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Identifying the dynamic gene regulatory network during latent HIV-1 reactivation using high-dimensional ordinary differential equations

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Abstract

Reactivation of latently infected cells has emerged as an important strategy for eradication of HIV. However, genetic mechanisms of regulation after reactivation remain unclear. We describe a five-step pipeline to study the dynamics of the gene regulatory network following a viral reactivation using high-dimensional ordinary differential equations. Our pipeline implements a combination of five different methods, by detecting temporally differentially expressed genes (step 1), clustering genes with similar temporal expression patterns into a small number of response modules (step2), performing a functional enrichment analysis within each gene response module (step 3), identifying a network structure based on the gene response modules using ordinary differential equations (ODE) and a high-dimensional variable selection technique (step 4), and obtaining a gene regulatory model based on refined parameter estimates using nonlinear least

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Supplementary material (Appendix) is available on request from the corresponding author, 'Hulin Wu'.

squares (step 5). We applied our pipeline to a time course gene expression data of latently infected T-cells following a latency-reversion.

Keywords

HIV; human immunodeficiency virus; gene regulatory network; ODEs; ordinary differential equations

1 Background

Introduction of highly active antiretroviral therapy (HAART) has dramatically reduced mortality of patients infected with human immunodeficiency virus (HIV) (Mocroft et al., 2003; Murphy et al., 2001). Yet, despite the prolonged life-span in HIV infected patients receiving HAART, the risk of latent infection still exists among these individuals (Dornadula et al., 1999; Havlir et al., 2005; Palmer et al., 2003, 2008). Latent infection is caused by rapid virological relapse of quiescent T cells (Lassen et al., 2004b,a), in interruption of HAART.

Reactivation of the latently infected cells has been discussed as a promising approach to eradicating HIV. These treatment approaches aim to reactivate the reservoirs that harbour the latently infected T cells while maintaining HAART, and actively eliminate the infected cells using cytotoxic drugs or the host immune system (Chun et al., 1997). Recently, wide range of latency-reversing agents have been developed to treat HIV-infected patients (Shirakawa et al., 2013; Kulkosky and Bray, 2006; Margolis, 2011; Xing et al., 2011; Doyon et al., 2013), and several clinical trials have been initiated to investigate the safety and efficacy of the latency-reversing agents (Archin et al., 2012; Rasmussen et al., 2013; Yin et al., 2011; Victoriano et al., 2011).

To develop treatment regimes for the eradication of HIV, it is critical to understand the biological processes underlying the virus reactivation. However, current approaches to study gene regulation after virus reactivation are not optimal for finding genes differentially expressed across time. Our pipeline proceeds in five steps, by detecting temporally differentially expressed genes (step 1), clustering genes with similar temporal expression patterns into a small number of gene response modules (step 2), performing a functional enrichment analysis within each gene response module (step 3), identifying a network structure based on the gene response modules using ordinary differential equations (ODEs) and a high-dimensional variable selection technique (step 4), and obtaining a gene regulatory model based on refined parameter estimates using nonlinear least squares (step 5).

The remainder of the paper is organised as follows. We first describe the motivating data and the methodology for the five-step analysis pipeline. Then we present an application of our pipeline to a time course gene expression data of latently infected T-cells following a latency-reversion. Finally, we discuss the performance of our methodology compared to existing methods in a simulation study.

2 Methods

2.1 Experimental data

We applied our pipeline to a time course experiment by Krishnan and Zeichner (2004). In this experiment, two cell lines were considered. ACH-2 is a cloned T-cell line (Folks et al., 1989) chronically infected with harbouring HIV-1 LAV strain. A3.01 is the corresponding parental uninfected cell line. Both cells were induced with phorbol myristyl acetate (PMA), an agent to induce viral reactivation. Total RNAs were obtained using UniGem2 microarrays prior to PMA induction and 0.5, 3, 6, 8, 12, 18, 24, 48, 72, and 96 hours after the PMA induction. The microarrays had 10,368 cDNA spots on each glass slide. The main objective of this experiment was to study change in cellular gene expression accompanying a viral reactivation in a latently infected cell, compared to an uninfected cell. Details of the experiment can be found in the original paper (Krishnan and Zeichner, 2004). The dataset was obtained from the Gene Expression Omnibus (GEO) database (accession number: GSE1441). The data consists of log of base 2 transformed ratio of normalised gene expression from ACH-2 cell to A3.01, for each time point. The ratio measure was used to minimise effects due to PMA induction (Krishnan and Zeichner, 2004; Caino et al., 2011). A total of 9,128 probes that met the intensity criteria, spot and the normalisation ratio were available in the publicly available dataset. Details of the data filtering and normalisation procedure is described in detail by Krishnan and Zeichner (Krishnan and Zeichner, 2004). We explored the gene regulatory network during the in vitro reactivation, using our pipeline. We describe the five steps of our pipeline in the following section.

2.2 Step 1: Identification of dynamic response genes

Dynamic response genes (DRGs) are genes with expressions that are differentially expressed over time. The DRGs are identified using the following procedure. First, we denote $X_{\lambda}(t)$ as the smooth function representing the centred expression levels of the λ th gene. In addition, we assume that each time course measurement represents discrete observations from this smooth function with measurement error, which can be written as the following.

$$Y_i - \mu_i = X_{\lambda}(t) + \epsilon_i(t),$$

for $i = 1, \dots, n$ where n is the number of genes. The average gene expression measurement over time for the λ th gene is denoted as μ_{λ} . We assume that the measurement error $\epsilon_{\lambda}(t)$ is independently and identically distributed with mean 0 and variance σ^2 .

We estimate the centred expression levels $X_{\lambda}(t)$ using a spline smoothing method (Green and Silverman, 1993; Ramsay and Silverman, 2005). In this approach, $X_{\lambda}(t)$ is estimated using a linear combination of L independent basis functions as follows.

$$\hat{X}_{\lambda}(t) \approx \sum_{l=1}^L c_{\lambda,l} B_{\lambda,l}(t),$$

where $B_{i,l}(t)$ are cubic B-spline basis functions and $c_{i,l}$ are the corresponding coefficients. The parameters for the cubic B-spline basis functions are obtained by minimising

$$\left[Y_i - \mu_i - \hat{X}_i(t)\right]^2 + \lambda \int_{t_0}^T \left[\frac{d^2}{dt^2} \hat{X}_i(t)\right]^2 dt,$$

for any $t \in [t_0, T]$, where $[t_0, T]$ is the interval of the time course experiment. The first term defines the squared difference between the observed centred gene expression measurement ($Y_i - \mu_i$) and the estimated smooth function of $\hat{X}_i(t)$, while the second term is the integral of the squared second derivative of the estimated function, which requires to be sufficiently smooth. The parameter λ controls the trade-off between the fit to the data and the smoothness requirement for $\hat{X}_i(t)$. This parameter is selected using the generalised cross-validation (Tibshirani, 1996).

Our objective is to identify a subset of the genes that change significantly with respect to time. To do this, we test the following hypothesis for each gene $i = 1, \dots, n$ to detect the DRGs,

$$H_0: \hat{X}_i(t) = 0$$

$$H_a: \hat{X}_i(t) \neq 0,$$

for any $t \in [t_0, T]$, where $[t_0, T]$ is the interval of the time course experiment. We use the conventional F-statistic, which compares the goodness-of-fit of the null model (H_0) to the alternative model (H_a):

$$F_i = \frac{\text{RSS}_i^0 - \text{RSS}_i^1}{\text{RSS}_i^1},$$

for $i = 1, \dots, n$, where $\text{RSS}_i^0 = (Y_i - \mu_i)^2$ and $\text{RSS}_i^1 = (Y_i - \mu_i - \hat{X}_i(t))^2$ are the residual sum of squares under the null and the alternative models for the i th gene. The genes with a large F-statistic can be considered as exhibiting notable changes with respect to time. We use a permutation test to generate a null distribution of the F-statistic ($F_1, \dots, F_n$), for genes $i = 1, \dots, n$, as described by Storey et al. (2005) and Wu and Wu (2013). Permutation samples are obtained by shuffling the time course measurements for each gene. The p-value for gene i is calculated as:

$$p_i = \frac{\sum_{b=1}^B \sum_{i=1}^n I\left\{F_i^{(b)} \geq F_i\right\}}{n \cdot B},$$

where b is the index for permutation sample and B is the number of permutation samples. We used $B = 10,000$ permutations controlling for the false discovery rate (FDR) by the Benjamini and Hochberg method (Benjamini and Hochberg, 1995) with $FDR = .01$.

2.3 Step 2: Identification of gene response modules (GRM)

The second step of the pipeline is to identify genes which share similar temporal gene expression patterns using a clustering method. This produces gene response modules that allow us to focus on the relationships between co-expressed or co-regulated genes rather than individual genes (Chuang et al., 2007; Von Dassow and Odell, 2002; von Dassow et al., 2000). The approach has been applied extensively in systems biology (Wong and Chang, 2005; Girvan and Newman, 2002), and have been found useful in understanding inter-related systems of biological processes (Han, 2008; Ravasz et al., 2002; Ihmels et al., 2002; Yook et al., 2004; Thieffry and Romero, 1999; Jeong et al., 2000; Wagner et al., 2007). We group the DRGs found in the first step of our pipeline as gene response modules (GRM). While many DRGs may follow similar temporal expression patterns, some DRGs may have very few or no co-expressed DRGs, exhibiting unique temporal response patterns. This implies that the size of clusters may be inhomogeneous (i.e., some clusters may contain many genes while others may be small or even singular). In order to identify inhomogeneous clusters, we introduce an iterative hierarchical clustering (IHC) method (Carey et al., 2016). The IHC algorithm implements the three steps as outlined below.

2.3.1 Initialisation—First, the *Initialisation* step clusters the DRGs using hierarchical clustering (Sokal and Michener, 1958). The clustering is based on the centred gene expression levels of DRGs. Initial clustering is achieved using a distance metric (to define a measure of distance between pairs of DRGs) and a linkage criterion (to determine average dissimilarity between clusters). We use the Spearman rank correlation as the distance metric for our hierarchical clustering with a pre-specified threshold α , and the mean linkage clustering (Sokal and Michener, 1958) is used to quantify the average dissimilarity in the time-course patterns of the DRGs between clusters.

2.3.2 Merging—Second, cluster centres are obtained as an average of all temporal gene expression patterns of member DRGs in the cluster. The *Merging* step considers each of the cluster centres (exemplars) as ‘new DRGs’, and use the same procedure described in the *Initialisation* step to merge the exemplars into a new set of clusters.

2.3.3 Pruning—Third, the *Pruning* step streamlines the clusters and removes inconsistencies by reassessing the cluster membership by each DRG. Spearman correlations are computed between the cluster centre and the centred gene expression levels of each DRG. If the Spearman correlation coefficient is less than α , then we remove the DRG from the cluster. The DRGs removed from the existing clusters are assigned into single-element clusters. The merging and pruning steps are repeated until our convergence criteria (between-cluster correlations less than α) is satisfied.

Based on the final cluster identification, module-wise centred response patterns are obtained as an average of temporal gene expression patterns for all DRGs in the GRM. We define four types of temporal GRMs based on the size of the cluster: single-gene modules (SGM) with only one gene in each cluster, small-size modules (SSM) that contain between 2–9 genes in each cluster, medium-size modules (MSM) that consist of 10–99 genes in each of the clusters and large-size modules (LSM) which contain at least 100 genes in each cluster.

2.4 Step 3: Obtain the functional enrichment analysis of the GRMs

The third step of our pipeline performs a functional enrichment analysis of the GRMs. Functional annotation is obtained using g:Profiler (Reimand et al., 2016), a web-based tool extract information on biological processes, molecular functions, cell components, and phenotypes related to a list of genes in a GRM. The g:Profiler maps gene lists by GRM and provides functional information based on various sources of databases such as the GO (Consortium, 2015; Ashburner et al., 2000), KEGG (Kanehisa et al., 2014), Online Mendelian Inheritance in Man (OMIM) resource (Amberger et al., 2015), CORUM (Ruepp et al., 2010), Human Protein Atlas (HPA) (Uhlén et al., 2015), microRNA target sites (Kozomara and Griffiths-Jones, 2013), Reactome (Fabregat et al., 2016), transcription factor (TF) binding sites (Wingender, 2008).

2.5 Step 4: Construction of the high-dimensional gene regulation network (GRN)

The fourth step of the pipeline is to construct a gene regulation network (GRN) using ODEs. Construction of high-dimensional GRN using ODEs have been discussed in the statistical literature (Hecker et al., 2009; Lu et al., 2011; Wu et al., 2014). The motivation for assembling a regulatory network is to understand systems of co-expressed genes. In ODEs, the regulations of GRMs are modelled using rate equations

$$\frac{\partial}{\partial t} M_q(t) = \beta_{0,q} + \sum_{p=1}^P \beta_{p,q} M_p(t),$$

for $q = 1, \dots, P$, where P is the number of response modules identified in the second step of our pipeline, $M_q(t)$ is the mean expression curve of the q th GRM, $\beta_{0,q}$ is the intercept for the q th GRM, and the coefficients $\{\beta_{p,q}\}_{p=1}^P$ quantify the regulation effects of the p th GRM on the instantaneous rate of change in q th GRM. This model can identify between-module regulations as well as self-module regulations.

Parameter estimation involves identifying the GRNs ($M_p(t)$) that are affecting the rate of change in the q th gene response (i.e., $\beta_{p,q} \neq 0$). In order to achieve this, we implement a two-stage smoothing-based method (Voit, 2000; Liang and Wu, 2008), which decouples the system of differential equations into a set of pseudo-regression models (Fang et al., 2011).

This method significantly reduces the computational cost. Let $\frac{\partial}{\partial t} \widehat{M}_q(t) = \sum_{l=1}^L \widehat{c}_{i,l} \frac{\partial}{\partial t} B_{i,l}(t)$, where $\frac{\partial}{\partial t} B_{i,l}(t)$ are the derivatives of the cubic B-spline basis functions and $\widehat{c}_{i,l}$ are the corresponding coefficients. The corresponding set of pseudo-linear regression models are

$$y_q = \beta_{0,q} + \sum_{p=1}^P \beta_{p,q} z_p + \delta_q,$$

where $y_q = \frac{\partial}{\partial t} \widehat{M}_q(t)$ and $z_p = \widehat{M}_p(t)$. The error term δ_q represents the combined estimation error for $\frac{\partial}{\partial t} \widehat{M}_q(t)$ and $\widehat{M}_q(t)$, as well as the error due to the substitution of the differential

equation variables by $\frac{\partial}{\partial t} \widehat{M}_q(t)$ and $\widehat{M}_q(t)$. These set of linear regression models are called ‘pseudo’ since the y_q and z_p are derived from the smoothing estimates rather than from a direct observation. Variable selection is performed using the least absolute shrinkage and selection operator (LASSO) (Tibshirani, 1996). The penalised objective function is defined as the following.

$$\delta_q + \theta \sum_{p=0}^P \|\beta_{p,q}\|,$$

where $\sum_{p=0}^P \|\beta_{p,q}\|$ is the LASSO penalty which shrinks the parameters $\beta_{p,q}$ to zero.

2.6 Step 5: Parameter refinement

The final step of the pipeline is to obtain refined parameter estimates for the GRN identified in the previous step. The parameter estimates obtained from the two-stage procedure are refined using a nonlinear least squares (NLS) method, using the estimates from the fourth step as initial estimates. This step is to avoid bias resulting from the approximation steps in the two-stage procedure using the estimated curves $(\widehat{M}_q)$ and its derivatives $(\frac{\partial}{\partial t} \widehat{M}_q)$.

3 Results

3.1 Data analysis

We applied our pipeline to a time course gene expression data collected by Krishnan and Zeichner (2004). Data obtained from the Gene Expression Omnibus database (accession number: GSE1441) included the log of base 2 transformed ratio of gene expression from ACH-2 cell to A3.01, for five independent experiments. We focused on the second replicate in the publicly available dataset, which was the only sample that has the complete time course data (microarray experiment prior to PMA induction and 0.5, 3, 6, 8, 12, 18, 24, 48, 72, and 96 hours after the PMA induction). Our main interest was to study the temporal pattern of gene expression in the latently infected ACH-2 cell line after viral reactivation with respect to the uninfected parental cell line A3.01. We analysed the normalised data for 9,128 probes that met the initial spot size, intensity criteria (Krishnan and Zeichner, 2004). Of the total 9128 probes, the first step of our pipeline have identified 3926 DRGs. The DRGs represent temporally differentially expressed genes in the latently infected cell (ACH-2) relative to the uninfected cell (A3.01), after the viral reactivation. The step 2 of our pipeline used a IHC clustering algorithm to identify gene modules sharing similar temporal expression patterns. Using this step, the 3926 DRGs have been clustered into 95 GRMs (with the threshold parameter of our IHC clustering algorithm set to $\alpha = .75$). There were 9 LSM with at least 100 genes in the cluster (Figure 1), 19 medium-size modules (MSM) that contain between 10–99 genes in each cluster (Figure 2), and 38 SSMs with 2–9 genes in the clusters (Figure 3). The remaining 24 were SGMs with only one gene in each cluster (Figure 4). A full list of genes in each module can be found in appendix (Appendix A). Following the identification of GRMs, our pipeline used the ODE modelling for constructing high-dimensional gene GRNs. Our gene regulatory network of the 95

GRMs mapped how different modules controlled the expression of other modules. The regulatory network represented the refined parameter estimates from the final step of our pipeline (parameter estimates can be found in Appendix B). Gene response modules with the most outward regulation were 39, 49, 57, 22, 58, and 9. This indicates these modules can be identified as ‘hubs’ in the regulatory network since they point to many other modules (full summary of outward regulation can be found in Appendix C). A list of genes in these ‘hub’ modules and their functions can be found in Table 1. Module 39 regulated all 95 GRMs and consisted of 9 genes sharing similar temporal expression patterns. Three genes (ARMCX5, GLRX, KPNA2) in module 39 were related to the microRNA hsa-miR-577, which has been found in HIV-1 infected cell line (Yeung et al., 2009). Other genes in module 39 were related to craniofacial dysmorphism, skeletal anomalies, mental retardation syndrome, and cerebrofaciothoracic dysplasia (TMCO1) or mitochondrial DNA depletion syndrome 3 (DGUOK). Module 49 was a SGM regulating 93 GRMs. The expression of gene NLE1 increased rapidly after viral reactivation in the latently infected cell with respect to the uninfected cell until around 6 h after PMA injection. The relative expression drops after around 6 h after reactivation and gradually increased until 96 h. Module 57 is also a SGM regulating 93 gene response modules. Temporal pattern of gene DNAJC8 in this module indicated a slow increase after viral reactivation, and then a sharp decrease between hours 3 and 6. A recent study that investigated gene expression of T cell lines with HIV-1 infection reported differential expression of this gene (DNAJC8) in a deep sequencing analysis (Peng et al., 2014). Module 22 was a small size module with two genes (TNFAIP3, CCNG2), where TNFAIP3 was related to the regulation of toll-like receptor 5 signalling pathway (GO accession numbers: 0034147, 0034148, and 0070429). Module 58 was also a small size module with three known (PBEF1, CTH, GRSF1) and one unknown gene (Incye clone ID:2115411). The gene CTH is known to be related to cystathioninuria or cystathionase deficiency (Online Mendelian Inheritance in Man (OMIM) number: 219500). A recent study by de Silly and colleagues (2012) indicate that this gene (CTH) is associated with immune tolerance after organ allotransplantation in rats (de Silly et al., 2011). Module 9 was a SGM responsible for regulating 86 gene response modules. This gene (ELF1) is known to be related to HIV-2 transcription following T-cell activation (Leiden et al., 1992). Full list of statistically significant ($\alpha = 0.05$) annotations based on functional enrichment analysis can be found in appendix (Appendix D). GRMs with the most inward regulation were 49, 59, 19, 64, and 70. Details of the inward regulation can be found in appendix (Appendix E).

Although our discovery was focused on the second replicate with the complete data, we examined the consistency of our findings using the remaining replicates in the experiment. In this consideration, we included replicates with at least six longitudinal gene expression measurements (replicates 1 and 3 in the original investigation (Krishnan and Zeichner, 2004)). Two replicates with less than six longitudinal measurements were not examined. An application of our pipeline to these replicates indicated that there was considerable overlap in the DRGs across the experiments. Specifically, there was 41.4% and 42.6% overlap in the genes with the highest value of the F statistic (as described in method section in step 1) with the DRGs found using only the second replicate. The complete list of overlapping genes can be found in Appendices F and G, for replicates 1 and 3, respectively. In addition, there were

notable similarities in the mean response pattern of the GRMs across the three replicates, especially for modules with at least 100 genes.

3.2 Simulation study

We evaluated the key steps of our analysis pipeline in comparison to existing methods in a simulation study. Two simulation studies were performed. The first simulation study evaluated the performance of our pipeline to correctly identify genes that changed significantly with respect to time (i.e., DRGs). The second simulation study examined the accuracy of our classification algorithm (IHC) to correctly group genes that follow similar temporal response patterns (i.e., GRMs).

In the evaluation of our method to identify DRGs, we simulated data for 1000 genes. We examined the performance of our method in comparison to a conventional method using the classical analysis of variance (ANOVA) in 200 simulated datasets. Data were generated in three different conditions, where the proportion of DRGs were 0.05, 0.2, and 0.5 with respect to the total number of genes. In other words, the number of DRGs were 50, 200, and 500, respectively for DRG proportions of 0.05, 0.2, and 0.5. In each of these scenarios, the non-differential genes had $X_i(t) = 0$, and the differential genes were generated as a linear combination of sine and cosine functions. In particular, non-differential gene response patterns were generated as $X_i(t) = \sum_{l=1}^3 \xi_{il} \phi_l(t)$, where $\phi_1(t) = -\sqrt{2/(b-a)} \cos(2\pi(t-a)/(b-a))$, $\phi_2(t) = \sqrt{2/(b-a)} \sin(2\pi(t-a)/(b-a))$, and $\phi_3(t) = -\sqrt{2/(b-a)} \cos(4\pi(t-a)/(b-a))$, $t \in [a, b]$. The coefficients ξ_{il} , $l = 1, 2, 3$ were generated from identically and independently distributed (i.i.d.) normal random variables, all with mean 0 and variances λ_l with $\lambda_1 = 4$, $\lambda_2 = 2$, and $\lambda_3 = 1$. To mimic the experimental condition in the real data analysis, we simulated data in $t \in [0, 96]$. For each gene, noisy signals were generated by adding identically and independently distributed (i.i.d) normal random variables with mean 0 and variance $\sigma^2 = 0.01$ to the response patterns. Finally, 11 observations were sampled at $t = 0.5, 3, 6, 8, 12, 18, 24, 48, 72$, and 96 hours, for each gene. Both methods in comparison used permutation tests to generate a null distribution of the F-statistic, and calculated the p-values for gene i as described in the methods section. Genes with p-values less than 0.05 were determined to be DRGs. Performance of our method to identify the DRGs compared to ANOVA is summarised in Table 2. Simulation results indicate that our method had higher true positive and lower false positive rates compared to ANOVA using time as a single factor.

In evaluation of methods to cluster DRGs with similar temporal response patterns, we simulated data for 300 DRGs. We examined the performance of our method in comparison to an existing method in 200 simulated datasets. The method in comparison clustered DRGs using the distance between periodograms (Montero and Vilar, 2014). The DRGs were generated as $X_i(t) = \sum_{l=1}^3 \xi_{il} \phi_l(t)$, where $\phi_1(t) = -\sqrt{2/(b-a)} \cos(2\pi(t-a)/(b-a))$, $\phi_2(t) = \sqrt{2/(b-a)} \sin(2\pi(t-a)/(b-a))$, and $\phi_3(t) = -\sqrt{2/(b-a)} \cos(4\pi(t-a)/(b-a))$, $t \in [a, b]$. The coefficients ξ_{il} , $l = 1, 2, 3$ were specified as $(\xi_{i1}, \xi_{i2}, \xi_{i3}) = (2, 2, 2)$ for the first 100 DRGs, $(\xi_{i1}, \xi_{i2}, \xi_{i3}) = (-2, -2, 2)$ for the second 100 DRGs, and $(\xi_{i1}, \xi_{i2}, \xi_{i3}) = (2, -2, -2)$ for the last 100 DRGs. The DRGs were simulated in $t \in [0, 96]$, and noisy signals

were generated by adding identically and independently distributed (i.i.d) normal random variables with mean 0 and variance $\sigma^2 = .02$ to the response patterns. The observations were sampled at $t = 0.5, 3, 6, 8, 12, 18, 24, 48, 72$, and 96 hours. Methods to correctly cluster the DRGs were evaluated using a metric called *purity* and similarity index. The *purity* index is calculated by dividing the number of correctly assigned DRGs by the total number. The similarity index quantifies the average proportion of overlapping DRGs between each of the identified clusters and truth (Montero and Vilar, 2014; Díaz and Vilar, 2010). Across the 200 simulated datasets, our proposed IHC method had an average *purity* of .98 and a similarity index of 0.979. The existing clustering method based on periodograms implemented through an R package TSclust showed lower classification accuracy with an average *purity* of .593 and a similarity index of 0.524. Whereas the IHC method correctly identified the 3 clusters most of the time (average number of clusters were 3.3 across the 200 simulated datasets), the method based on periodograms had an average cluster size of 6.0 across the 200 simulated datasets.

4 Discussion

In this study, we investigated temporal patterns of gene expression after viral reactivation in latently infected T-cell. We have used a functional data analysis approach to extract a subset of the measured genes representing significant temporal patterns after the viral reactivation. As indicated by the simulation study, the approach is more powerful in detecting dynamic response genes compared to the conventional approach based on analysis of variance. Whereas the original investigation (Krishnan and Zeichner, 2004) reported 1,740 genes with significant temporal alteration, our method has identified 3926. In addition, our novel clustering-based method showed good classification accuracy in the simulation study, and have identified 95 response modules in the real data analysis. The response modules exhibited distinct temporal patterns that are shared with many other genes or are unique to a single gene. A pathway analysis indicated that the hub genes in the network, which are critical in the regulatory function, are related to some of the biological dynamics discussed in the literature (Yeung et al., 2009; Leiden et al., 1992). We have also identified a handful of new genes that are found to be important in our regulatory network, but not yet reported in the HIV literature. Finally, a regulatory network was constructed using ODE to understand between module relations.

5 Conclusions

We present a novel application of a five-step pipeline to explore the regulatory relations between genes expressed in the critical period after the latent HIV reactivation. Our proposed pipeline is a combination of a series of advanced statistical methods to efficiently identify temporally varying patterns of gene expression over time. Our findings indicate that the response to latent HIV reactivation is an intricate network of regulatory feedback between genes sharing similar temporal patterns. The concordance of our pathway analysis with the existing literature shows the validity of our proposed pipeline. In addition, we identify some newly discovered genes that suggest the potential importance of the related pathways to the biological processes after latent HIV reactivation.

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Appendix

Appendix A.

Full list of genes in each module.

Module	Number of genes in module	Gene names or Incyte clone ID
1	16	86865.C6.FOSL2.SETMAR.RFX2.1954674.RPS3.SLC12A2.SETBP1.TheRNA.MGC52110.1534801.3729512.ZBTB17.PXMP2.ICT1
2	184	COL4A4.CEACAM1.MPPED2.CA4.INS.SLC6A4.PSCD3.VPS41.HSU79275.GUCY2C.PCYOX1.NRID2.CBARA1.PRKACA.ANPER.3031764.3492296.PDLIM5.CDC42EP1.2499851.MAP3K13.PDLIM1.172916.POU6F1.CDS2.EFNB2.ADCY8.KYNU.RICS.RYR3.NOL4.4248767.PLK3.APOD.Sepin2.MICAL3.CCDC94.2622788.ARSE.HERC1.KIT.MITF.EFNAL1.1638346.IRF8.AREG.1800286.ASAHL.MAP2K3.1656908.BAI2.MUC5AC.3176146.NFASC.KIF3C.HMGCS1.LILRB1.COG7.ZNF324.ANGPTL7.CLCA1.TMEM63A.DCX.CLIC2.COL9A1.UNC5C.RAB11FIP5.FXYD1.DPP9.2608629.HIST1H4H.1268175.PON2.LIMD1.3105607.ORC4L.OSGEP.SRC.SERPINA7.SULT4A1.AQP5.2505102.5311604.1505986.EP400.MXD4.KIAA0087.1841459.KIFC3.QDPR.NCAM1.FLJ36492.LPHN3.KIAA0701.DPP6.626672.STOML1.POSTN.ZCCHC2.CMAH.1302785.2230024.FAM120B.2605754.HMP19.LOC728772.PLEKHH2.HCFC2.C1QTNF5.2877956.LOC339535.FLJ38973.C12orf44.ITGA2.C12orf42.CREBBP.2678945.2818878.GTPBP8.LOC493869.CSPG5.3520224.AGTR2.TNFRSF10C.SETD4.2472966.MTHFD2L.TRAPP2.LELAC1.2510360.2707290.NPPB.1375813.C1orf75.PGF.ACACB.3278047.STATH.3136873.1965673.ARNTL.SAA4.SUFU.1208476.CCDC62.RCHY1.BDH2.ZNF238.HOXB2.2493672.CD5L.GATA1.LDB3.C9orf61.CAP2.PTPRB.ZNF133.CLIP4.YCAN.465496.BLR1.LOC729137.GNG4.MAP2.B3GAT1.LRRRC6.PCSK1.PRB3.MYOC.ZIC4.FCGRI1A.MMP7.SMAD1.1842016.TMEM16A.FCNI.SKAP1.NFKB2.CCL21.FHIT.PCDH7.WIZ.TRAF6.IL15RA
3	1	2446995
4	5	SLC43A1.GTF2H4.PPT2.RBM19.FNBP4
5	11	ICA1.MGC40405.TXNDC4.KIF2C.SLC27A2.SLC26A2.CCDC6.HAT1.2625593.CHAF1B.EEF1E1
6	3	SRP54.AKAP5.LMO7
7	3	UCK2.PSMD8.EIF3S9
8	1	SULT1A4
9	1	ELF1

Module	Number of genes in module	Gene names or Incyte clone ID
10	39	CDK3, TLE4, KIAA0363, KIAA0746, ZFP36L1, 487992, DUSP11, CTAG2, KAL1, SERPINB7, ADCY7, 688743, MFGE8, CLMN, RAP2A, MOSPD3, SLC25A16, DOPEY2, 2414525, BIRC3, MB, FGFR4, TGIF1, PHLPP, KLHL2, GPR65, FGFR1OP, CD8A, IL17RA, VAMP4, UBD, TAF12, MYD, 608148, SERPINE2, FOS, FKBP1A, CDYL, GRIK2
11	5	CPB2, LPA, APOC3, GAB2, CMYA5
12	1	DC2
13	9	SGK, TAPBP, RASA1, CX3CR1, MEAP3L, ARHGEF17, 2506194, 2745159, 1685511
14	4	SEC11A, RHEB, 2117221, HECW1
15	1	2817185
16	15	MEIS1, ABCC2, IFNB1, NHLH1, DENND2D, COPS7B, IFT122, GRIN2D, PLK4, BDNF, COV1, KIAA1166, SLC25A17, C2orf27, CRY1
17	10	STC2, IGFBP6, TP73L, MAP3K4, SOCS3, ZNF229, 223606, FOLR1, 1507151, MYH3
18	6	INSIG1, JHPK2, 1526570, ARL3, KBTBD2, 407748
19	1	2055538
20	1	C1orf41
21	1	CRAT
22	2	TNFAIP3, CCNG2
23	7	CPE, AP1S2, GPR56, C16orf75, SPOCK3, ATP6V1G1, BBC3
24	104	ANKRD15, MAPK4, AKR1C2, THBS4, PKP1, COL7A1, DUSP3, ALDH7A1, MLXIP, INPP1, ENPP2, USP15, KLK11, 1663943, 1623592, ULK1, ARID5A, RERE, FILIP1L, DTNB, ELAVL2, 2500225, CTNNA2, DYSF, 4923601, GRM5, ALPPL2, SAC3D1, 4327691, 3530812, 4112710, KCN9, MEF2A, POSTN, DISC1, CCR6, KIAA0738, TMEM16C, TNRC9, DST, EPB41L1, PRAC, C1orf173, IL27RA, TOB2, ANAPC7, MGC26647, FND5, MAPK10, B4GALT3, C16orf5, SLC03A1, SULT1E1, TREM2, KRT4, SGCE, ZCCHC14, SMPD1, LOC91461, ZNF500, 2639085, ZFYVE26, SPINK4, ST18, ADAM2, CCL8, TPST1, SYNJ2, CYP4V2, SLC6A1, BMP1, PSEN2, FKBP1B, IL6ST, SMAD3, CD38, PDE3A, DIO2, TNFSF8, TIE1, GSTA4, NR4A1, LAMA2, CSF1R, HPGD, ZBTB16, SALL2, TNFRSF9, LRRC8B, CDKN1A, EPAS1, GSTZ1, MAST4, GEM, NRCAM, SFTPB, ZNF585A, 547612, 194162, 340088, 2742708, HS3ST1, SMARCD2, TULP4
25	5	1655501, PON2, 698901, DEPD5, HPS6
26	27	F2R, 3033131, ASTN1, KIAA0692, 508322, PTK6, RARG, NPY2R, AURKA, LANCL2, RIMBP2, ORM1, C11orf41, 3052608, 3045817, ZNF473, GCKR, AURKC, TNFSF11, TNXB, 2173208, 1796616, ITTF1, 1528507, CMKLR1, PCCA, TIGD3

Module	Number of genes in module	Gene names or Incyte clone ID
27	1	BNIP2
28	299	3028411.LMAN1, AFE2, GRPR, VRK1, C3orf37, PROM1, FBXL5, SNN, APPBP2, HEXIM1, PEX3, OFD1, PDK1, 1942845, SMNDC1, PRPF4B, RBM15B, SEC24D, CAND1, STUB1, KCNN4, ITGAL, JFT88, 2429265, MAP4K5, RHOQ, KCTD12, XRCC4, CEACAM7, CXYorf3, 1886821, IL13RA1, PITPNM1, NFYB, ATP6V0D1, PEKFB3, TADA2L, EIF4E3, MPP6, SRCAP, PIAS1, 2640712, C9orf127, CCT6B, FCGRT, ROD1, 3074109, ARL6P5, SCEL, 2438502, HLA-DQB1, DGKQ, LRCH4, PPID, PEAAP5, FLNC, VAMP3, MPP2, IDS, MBD2, BCL6, VAT1, REEP2, UAP1, DNAL4, CD59, 5109040, 4690701, P2RY5, KIAA0143, BHMT, ALOX15B, CROCC, SPI00, RTF1, 2362945, 2288609, 968205, UROS, BTN3A1, EHHADH, STAB1, WDR47, IGI, IFI44, 2263146, XAF1, GPR160, RP13, 347D8, 3, MAP4K4, 2182201, CARD8, 1259532, CD36, HERC4, KIAA1212, GRLF1, ZNF395, CDH16, CLIC4, 334768, SLC22A9, 1290212, CRTAP, MESPI, ZNF83, 465591, ILDR1, ACCN2, MYEOV, SIP1, RHOG, RBL1, 1743234, C13orf23, AGR2, DFNA5, 1967582, DFFA, VIL1, ADHIC, SNX19, TMEM185A, SYNPO2, NDFIP2, CDO1, DLL4, SLIT3, ANKRD11, NFKBIE, CTGF, C1orf26, 240817, TXN2, SYNPO, THOC5, NSDHL, MAP2K5, 1967531, FLJ40869, FYB, MCTP2, KCNS1, CSMD1, GNAL, 2057812, PAX2, DAPK3, KIR2DL4, DSG3, GRM8, 2903239, ILIRB3, TP53BP2, 2251851, 2969890, 4215852, ABCD4, CCNT2, 2703593, THRAP2, 2994387, SCAMP1, FAM78A, SLC29A1, MYO9A, 986754, 23215, CCL17, KRT20, COX7A2L, ASS1, INSM1, TLR5, LY75, LCT, PDCD1, KCNJ8, TOB1, CYP2C18, TNNT1, THBS2, NPAS2, F5, TOPORS, EIF4A1, PDIA5, SNPH, NPY, GCH1, JGSF2, CEACAM8, SMARCA1, C1orf77, CD96, FUT8, RENBP, 2220137, C21orf2, APOE, CSF3, AKAP1, ITPR2, PTPRD, 3473202, EML1, IL18R1, 3970665, ZNF408, RANBP2, PDE5A, SLC11A2, CTSK, IQSEC1, MAP3K5, PSMB9, 2290350, METTL1, AXIN2, MMP11, AXL, KIAA1754, ACP5, HARS, C14orf32, C9orf100, IFNAR1, CAPN9, HLX1, CITED2, UBXD6, PTPRJ, TNFAIP6, CYP11A1, 2951537, 1995692, DLEU2, TNFSF13, C9orf19, HIST1H2BK, PTH, 1749727, 1507157, C1orf34, 2215239, NEFH, MVK, SEC61B, 3089644, 1223510, TXNDC10, 1332963, 1900378, 957311, 2223757, AOA1, 3352319, UGDH, 1426031, BCL2L2, RSP04, CFH, FOSB, CD79A, AUTS2, CCNU, PTCRA, VPS36, 1998708, ACAT1, Septin 4, SNRPA1, POP1, LBR, BTN3A3, UBXD8, NFE2, MORF4L2, CDX1, EPHX1, PTPN1, GPBP1, ZPBP, AGL, BAZ2B, IL3RA, SPOCK2, NMT2, PDZK1, 2310314, MS4A4A, CNN1, ALDH1A3, WIPF3, UBE2D1, ERBB3, MALL, LOC730092
29	24	PASK, ACADM, 4982124, ALPI, KCTD2, PEX13, NAGA, 1666815, ATP9B, CAST, PLN, 2312442, DYNLT3, ZNF165, ALMS1, AB12, CEPBG, COMMD1, TCF7L1, FOXRED1, MOBKL2C, 767348, TMEM55A, CLMN
30	3	LTBR, C20orf59, RRAGA
31	4	TAF4B, BNIP1, PSMC2, B4GALT2
32	1	2395712
33	2	HNRPA2B1, TRAFD1

Module	Number of genes in module	Gene names or Incyte clone ID
34	1	2008351
35	2	TFAP2C,DBN1
36	8	SERPINB3,ITIH3,CLCC1,SPIB,KIAA0485, CYP4F3,ZNF780A,2826117
37	1	ITGB7
38	2	VPS13B,ITGA8
39	9	PRCC,KPNA2,AMD1,TMCO1,NDUFS5, ARMCX5,GLRX,DGUOK,1686916
40	10	FBXO7,GAS8,YME1L1,HCCS,LOC643837, DOCK5,RSRC1,ZNF282,2824017,567779
41	1	PARP4
42	9	MRPL28,MTP18,SART1,MGLL, GYG1,PSMB4,P4HB,LPP,NCBP1
43	18	KAL1,ERAL1,IL8,TRIM23,MYO1C,PPM1D,ZNF184,HGS, TCN2,HTRA2,VDAC1,FARP1,NT5E, RPS6KA3,NEK3,NPM2,CXCL12,PTPRU
44	1	MOAP1
45	1	SSSCA1
46	9	2922438,TSPAN17,BRCA1,MPO,CLCN7, CDC2L5,MLC1,AHNAK,2955163
47	1	2902846

Module	Number of genes in module	Gene names or Incyte clone ID
		<p>CD70,ITGA3,NPR1,STRN3,EMD,YES1,ADAMI1,GDI1,ACVR1B,LTBP4,KHK,SLC20A2,CSF2,3118939,SGCA,POGZ,3124244,GOLGA3,4190790,HMGCS2,GTF2A2,UNC13B,CR2,SELE,BAD,LCMT2,APIS1,ENOSF1,EPB42,FDXR,SLC22A4,PAEP,ARHGAP11A,RXRA,JOSDI,ACD,MRPL49,RAB8A,GAS7,KLF5,CAPN2,TSR2,CSTA,DOC2A,CENPE,DGKG,DHRS2,ZBTB6,4093234,ITGA9,NRP2,COX11,MYO1D,CLEC2B,CNN3,CDC45L,SLC35D2,TOMM20,BCKDHB,OXAI1,TRIM13,FCGR2A,IMJDI1A,RAPGEF3,ANKRD12,SDHD,AUH,USP15,VAV1,LPFR4,AMPH,DDO,IRS1,TEAD3,CSNK1E,JUN,HRB,C14orf2,WFS1,PHF2,1979217,AHSG,TRPC3,SLC1A4,CDC2L2,ABHD2,PGR,1796576,AHCY,VBP1,POLD2,HRSP12,REEP5,DTX2,XAB1,MLH3,ESD,LPHN2,ERC5,HMGN3,TERF1,PCSK7,SCOI,ENPP4,HNRPH3,GNB3,TTCC28,SCRGI,PIAS2,SAPI8,OLEF1,CGB,SCAMP2,OPCML,BCL2L1,CDR2L,C6orf106,NPHI1,FBLN5,1540028,PXDN,BCL6,MGMT,PPP2R2A,1669879,4286401,PVT1,CHRNA5,RAB28,CD79B,IGBP1,NUP93,CST7,BAIAP2,CITED1,MED6,3434853,RNF40,HTR1D,HLEF,1879811,CD7,PEX11A,TBX19,2755432,SRPX,FBLN2,SEC63,CHST3,GP2,ZNF250,ACOX3,NEFH,VEGFB,BIN1,CDHL,RUNX1,CYP3A5,BCAT2,PHLDA2,EDG4,ATP2A2,AP4M1,KDR,GIPC1,PRCP,ARHGEF18,ADH1B,AP4M1,AOC3,KCNK3,NCSTN,STX6,CXCR3,ASPHD1,MAP4K1,KIAA0423,TMEM63A,TNFSF13,AQP8,2222804,MEP1B,MAP3K6,CLN3,KCNN3,NR2C1,IPO9,DNAJC10,ATP6V1F,GT2H4,2783671,FBLN2,VEGFB,PLRG1,FUT7,NNAT,NAPSA,1866654,ZNF804A,1645766,RGS1,DEDD,RAMP1,LY6H,MEGF6,2626971,RAC3,TCE7,CDC2L1,PDGFRA,KIAA0500,RGS1,SHB,SLC22A1,FASTK,NUP210,KIT,KIAA0251,ABCB6,2363832,CLCN7,RPS6KB1,GRIK5,BIRC5,HP2,185524,2743724,DIP,DCX,TRIP10,RDHI6,SEMA4F,CHRNA2,FBXO46,SLC30A4,NOS3,1478048,TACR2,PENK,SNAPC3,PAK1,3031581,DOK2,TDO2,HOXA11S,TOX,CDK5R1,RYR1,HSPG2,MYL6,3357679,TWFI,ZMYM3,PITPNB,ZMYND10,M-RIP,BRD8,WHDH1,2720976,KIAA0672,C19orf29,PFKFB1,3226017,GPR30,ATP6AP2,SMPDL3B,P2RY11,3043401,SPINT1,SLC19A1,PLXDC1,PIP,KIAA0753,3482091,EPN2A,AQP9,GPD1,ST8SIA1,2690251,TCEAL1,HLA-C,LEPR,SUPT3H,GTSE1,KIAA1727,C1orf95,RRBP1,CD5,TEK,SIGLEC5,SYNJ1,SPRR3,DMXL1,3344118,LOH3CR2A,CD84,SCNN1D,PCDH1,3500452,FDFTL,NAGPA,LOC283335,KCNA6,KLK8,2834237,NTSR1,ARHGEF5,ATP10B,3563211,CELSR3,KIAA0152,CDH1,TGFB1,PKD1,NCAPD2,C8orf72,CXCR6,PPGT,ARL4C,HOXD1,HIST1H1D,CCDC52,1511321,3599074,MBTPS2,1900968,KCNJ5,1668362,POLE2,ADAM21,1507769,DHODH,SDC4,ATAD3C,PCDHGC3,TSKAN1,TBC1D9B,PDE1A,HYAL1,NME4L,G1,ZNF516,GRIP2,TIMM8A,3461390,PNLIP,RER1,UPK1A,TCAENPTX2,EFNA3,SEMA3D,CCL18,TUBGCP2,DGCR11,PCK1,DDR1,4997978,3476658,4896093,HAX1,FKBP9,GTTF2E1,2237234,TIMM17B,CLDN11,RAD51AP1,RGS20,CSN1S1,ZNFX1,KCNK1,KRT8,LILRB3,SLC3A1,PVR,SAP30,CRY2,3074437,REG1B,CAS8,RHOB,TB3,KIAA0157,3369232,4177354,XAF1,CDH22,1869139,PDE6B,NUCB1,SLC7A1,SATB1,NCOR2,SOX3,HIST1H2AM,APC2,KCNB2,TNNI2,CLDN4,THBS3,CLDN7,ATP6V1E1,5262429,U1SNRNP,ATP2A2,4032372,FCN2,EMG1,SLC1A2,AMPD2,DCTD,LRR41,SRGN,ECH1,IL18,TACC1,IGL@,WISP1,LRBA,IER2,MCAM,DFNA5,GPR98,2131862,KIF3A,877574,KIF5A,SERPINC1,CREB5,AP3S1,CACNB3,TSPY1,DGCR14,CRAADD,SPIB,814763,SULT1A4,NCAPD2,CRRP,ST8SIA3,MDM2,TCEA2,LY6D,GAGE2,961082,S100P,64394,AGGF1,GABRA2,GAB1,RAE1,CCL18,PEPD,1366085,CCNC,CAMK1,CTNNA1,2291477,2040657,2424115,SNAP91,RBM4B,2621204,MAP3K14,MT1E,PHLDB1,MBD1,GARNL1,PLML,KLF4,CBFA2T3,CXCL6,PFKL,DVL1,IL8RA,1740889,PPFIA4,PRMT3,DOHH,PDPN,PITRM1,IKBKAP,NEBL,2112785,BAK1,ZNF365,NMB,ZNF415,SMC3,</p>

Module	Number of genes in module	Gene names or Incyte clone ID
49	1	NLE1
50	6	CGA,BDH1,LAMPI1,CFTR,CALCB,MAP3K3
51	1	ENSA
52	1	HIF1A
53	4	GUSB,RNF13,RNF103,MLN
54	336	PLXNA2,HOXB13,IGHA1,1806521,FZD2,FSTL3,GALT,1404153,ANGEL1,1795929,ST3GAL5,GFPT2,SPATA2L,FILPIL,EPHB1,SERPINB5,BICD1,PRTN3,2752460,1605140,TCL1A,1688845,HYOU1,LYRMI,ZNF787,POUF2,ELF5,1737140,CHRNA1,DTNA,ISG20,1701725,1726294,BLCAP,MBNL2,SURF5,HEPH,ARL4D,EP400,BCL9,JAK3,SMARCA2,RPS6KA5,NAT8,1900949,PTPRS,ASL,3352147,LOC91316,CYP11A1,2962371,FCER2,STAC,IKBK,AKAP4,ALB,3441835,3820247,TCF15,ZNF536,SLC10A1,HLA-DRB1,GABRA3,2478920,KIF21B,BMP2K,CHML,OCN,XVLB,MAGEA11,SGTB,2875553,LRP6,MTMR7,DKK1,5199207,5288472,LY6E,CILPRGS11,LOC51149,ABL1,HLA-DQA1,LRMP,ZNF432,SERPINB1,CCL13,NNAT,CRP,CAMK1,EHHADH,MCF2L,DPT,ERBB4,RNASE6,1740788,IL12A,UBOX5,SLC6A13,1217695,3448231,PDLM3,IL1B,BCKDHA,SLC14A2,4000648,995860,AFAP1L1,VTCN1,TMEM50B,1851319,FLJ32312,RASA4,GPRASP2,2225155,PTAR1,EMX208,2194153,XRN1,APC,2293931,GSST1,BRP44,2862153,407032,676007,AHCTF1,1412839,BMPER,KIAA1324,1724717,SNAPC5,KRTAP4-7,C20orf74,CTSF,3599962,2182589,2040650,3123244,LY6G5B,LIPIF,GSPT2,ZNF358,FST,2449986,734624,2753047,FBN1,PLEC1,SPR1A,PAPLN,CDH15,FLT3,WDR67,COL13A1,1641775,PYGM,IL10RB,ZC3H7B,CPZ,IFI15,TEAD1,MYOZ2,PTGER2,3035832,3509885,SEC14L1,PPPIR3A,3857518,VLDLR,MYL7,4179338,ITIH4,NPY6R,CORO2A,FLRT1,1998269,1743094,BTBD9,394433,CCNY,PPFIBP1,MAPK9,2818928,SDK2,ARID4A,2884655,SENP5,LOC284939,151026,INPP5E,CYR61,2514926,PTK2,CDKN1C,C2,3243995,SEC14L5,2108793,SASH1,PNLIPRP1,NRG1,CTNND2,COL11A1,SLC35E3,1638384,SLC35F5,2800618,CSAD,ADORA2B,SSX2IP,SNX13,CCNG1,CCNL2,SCGB3A2,EFEMP1,LOC285016,AMFR,SLC38A4,1220258,HTRA1,KIAA0247,GATAD1,SULF1,BRAF,767388,GZMK,TLK1,1865634,CDH5,SRD5A2,PPARA,ISLR,CAI,CYB5A,PLXNA3,ZNF239,MIA3,F8,MAPK12,LILRB5,MAP4,ALOX15,APOLI,HNTNEO1,ARID2,NPPA,1663543,C4orf7,C22orf16,ARHGAP27,HDAC5,MFAP3,TDRD6,IGHA1,TPM2,MYL10B,2752839,PDZK2,SIRT4,TTC14,MGC61598,448244,NEDD9,GPR146,GREB1,SPTLC2,MNDA,CENPH,HPICAL4,RIK2,XRCC3,RLF,POU4F2,99492,1967527,FPRL1,SIX1,2702231,ILIRN,CCRK,MYO7A,91090,GCAT,FEML1C,2256174,CREB3L1,PMF2,MMP2,1822388,4003773,3992991,FBXO42,TAF1C,ACTN2,CTNS,SEC23B,FLJ12886,PLEKHG1,LYST,2619,IDI1,899118,SNMPDL3A,A2M,ASCC1,COX15,FN1,3815547,TRIM22,2953987,RIT2,3099947,FZD5,PAPD4,DNAJC3
55	10	HIST2H2BE,PLS1,LRP2,2786904,4513815,2112288,PSITP4,ANGPT2,GMFR,FMOD
56	4	LOC644739,NGEF,SMARCB1,CTSG

Module	Number of genes in module	Gene names or Incyte clone ID
57	1	DNAJC8
58	4	PBEF1,CTH,GRSF1,2115411
59	1	NIPSNAP1
60	5	TFF2,2157845,TMEM90A,SOS2,FBXO28
61	11	ATP9A,IPO8,FARP2,FGF13,SERPINF2,LIMA1, WDR37,HYAL2,NFKBIL1,MYO1E,DCI
62	27	HHEX,RAB6A,PPP2R5E,RP6-213H19,1,LOC151507, TMEM131,LLBR,OIP5,CXADR,ARPC1A, 3097582,UQCRC2,RAD21,MERTK,ARF4,BTRC,LMO2, HERC3,KIF23,ATF6,TM9SF4,CAMK2N1, MGC42105,AIM1,UNC84B,ZNF85,OGT
63	3	NFIX,ST3GAL2,CACNB1
64	2	WDR43,RAD51
65	34	USP12,ATIC,TTC4,ABCG2,PRMT3,RRP15,2601553,CRISP1, WDR77,DLL1,NCK1,SEPHS2,NIPA2,SRP14,NEIL2,476348, SLC27A3,TOR1A,1906936,KCNQ2,ZNF22,SERP1,C3orf63, RAD54L,TUBGCP3,CLK3,RNF113A,392166, 1997717,EEF1A1,LCK,PKNOX1,2259392,MFNG
66	107	EIF2S1,LARP1,C11orf58,1901073,FEN1,PARP1,CCT4, NPEPPS,XPO1,KEAP1,ATP6AP1,BCAP31,HNRPU,HS6ST1, 1580853,CAPG,CD3D,RFC5,MCM3,HSPA9,MYL6,TPM3, DUT,H2AFZ,ATP6V1E1,Septin 7,ATP5C1,MRPL3, ARHGDI2,XRCC5,TXNL2,XRCC6,SFRS1,ILF2,KPNB1, TMEM28,ASCC3L1,PPIB,HNRPF,ATP5O,MAD2L1, MYCBP,PSMC4,EIF2AK1,VCP,1692195,HNRPK,TOPI, UQCRH,YWHAH,BZW1,PFAS,SLC25A5,33091,750770, TAF9,ACPI,SMARCC1,DDX39,SNRPE,SPCS2,PSMB10, LAPTM5,PHB2,PSMA4,YWHAH,VDAC2,CBFB,NPRBM10, RPL35,PAXIP1,CLINT1,PSME1,1922523,COPS8,RAN,ETFA, NUCB2,KATNB1,RPA2,1832406,EIF4H,NEDD8,TTC19,2930621, PSMC1,SUMO3,TPM4,ACTA2,ITM2A,FTL,IL23A,PPP1CA, CDC123,CDK9,2397815,UBE3A,EIF4G3,CALM2,PCNA, SRPR,GNAI3,RAB1F,YWHAZ,HISPPD1,CUGBP2
67	2	SCHIP1,693016
68	1	OSGIN1
69	1	HLA-DRB1
70	1	HEG1

Module	Number of genes in module	Gene names or Incyte clone ID
71	84	MBOAT5,SLC12A1,OLFAM4,MMP1,DDIT3,NPR3,FBN2,PVRL2, RBM28,PLAU,C1orf9,LOC653354,ENTPD5,MUC1,ZNF134, CXCR7,HNF4A,PAMCI,CTRC,ACAT1,BTRC,CLP1,PMS2L1, ITPKB,MSH4,DGCR4,TRAPPC6A,GLT8D1,ARSB,545124, DHRSX,ROM1,WDR45,1922533,NETO2,2672259,1679304, EPHA7,DEFB1,EYA2,TREH,GARNL1,1737280,LETM1,DISP1, EDA,BAT4,1507791,FBXO21,CTBP2,3878372,ZNF35, FAM113B,DAO,SMG1,EEA1,MOC53,SNAPC4,1308333, ICAM2,682741,CDK3,SHCBP1,262207,KCNE3,PRMT2, KCNAB1,GUC A2A, RGS2,DKFZP761N09121,CRHR1,MGST1, 4240009,RECQL5,TNFRSF17,IGF2,C20orf111,APOA1, SERPINB9,ACSM2,ARHGEF10,AMY2B,HIPK1,CCDC69
72	71	RANBP6,NDEL1,NR2F6,CTDP1,SRCAPI,PE,TGDS,MBL1P1, CPSF6,HOXA9,ACOT8,PSMF1,TOM1L1,USH1C,SOX5,CNGA1, PRKAR1B,2397966,RPP21,VAPB,KIAA0664,FLJ39779,ZNF398, 1875433,2785471,766891,PCNX,ECT2,CLCNKB,OPRL1,2751360, TRIM66,68729,TJP1,HNRPA6,C1orf57,THOC6,MINA,MPP6, MRRF,WDR59,C12orf30,BLVRB,IRX5,NDN,SCN9A,C12orf48, DCXR,BNC2,SFRP5,C6orf113,2455780,THAP6,COL18A1, PIM2,NR1H3,THADA,MTF1,TCF7,ACOX1,NAGLU,ZNF313, NBR1,MGC10433,XPC,MAML1,REG3A,PCBD1,ZNF45,IL10RA,TG
73	1	1870214
74	61	AKT2,GCG,BCL3,KIF13B,CRISP2,467798,MMP13,LUM, ALDH1A1,MMP10,IL6R,GLRB,CEACAM5,ARRB1,CEBPA, PTGES,SLC13A3,ATP2C2,GSTA3,C1orf95,PRR5,CRYAA, 4249388,CHRN3,PLXNB1,NDPERCC6,3080656,1830341, NR112,CYP26A1,CD300C,SSX3,C9,KCNC4,PKP2,BHLHB9, 963211,3255853,HAVCR1,TGFB2,LOH1,ICR2A,1908884, 1929565,HLA-DOB,2289203,1377330,RNF213,HLA-DPB1, TEX10,BMP7,FLT1,4116386,SLC26A4,CYP51A1, NMU,TMEM51,KIAA0574,ANKRD1,SYT17,IL11RA
75	4	SMARCC1,5288736,1457140,SNAPC5
76	16	NDUFS2,MARCKSL1,ACIN1,MCM7,HMGB2,SF3B2,DDX5, 1733490,YWHAQ,SARM1,CKS2,CNOT8, MATR3,AP3M1,1986833,IK
77	2	1579596,FBXO38
78	1	PPP3CB
79	2	FAM63A,ABTB1
80	2	CARTPT,PSME4

Module	Number of genes in module	Gene names or Incyte clone ID
81	129	GRIK1,TFAP2B,CBR1,CCDC130,SRPX2,NR3C2,PRSS8,ILIRL1, LPL,CYP27A1,CEBPA,CD27,NOTCH4,CRSP2,2449041,MAPRE2, SOC57,MPP3,SHROOM2,DSCAM,PROZ,3438934,4855492, FER,1861772,3243185,4984469,CDON,HELLS,ELA2B,E4F1, 1961734,B3GAT3,MYBL2,CD42EP2,KALRN,933905,ILIRB4, NGFR,IGSF6,SH3GLB1,TBKBPI,1753033,ARHGAP28,FAM20A, 2262766,1640094,997948,KIAA1377,GPR4,HSPA12A,2496526, CARD8,SLN,LOC400713,ODZ3,PSENNEN,RHD,HOXA7,PIP5K2B, 2189383,PAH,POMZP3,TNFSF9,TNFRSF10B,ZNF451,PDYN, SLC28A2,RBPMS,1505543,2959963,LEPR,1929364,CLIP2, C3orf14,FOXE1,CDH18,ACCN3,MRC2,PRLR,GAA,SLC16A5, PNLIPRP2,KEL,2705101,LASS1,POU1F1,FGFBP1,2322650, PRM1,CRAMPIL,NEURL,400275,ELASA,IRX5,STEAP4, INTS10,1728607,CLPS,UMOD,ODF2,SLC7A2,3553751,TST, CIITA,WT1,2462342,NRXN1,THRB,SDC2,PDE4B,FLJ22167, ALDH1L1,FXN,ATP9B,SPINK5,EMP2,HRG,SLC37A4,1968446, 995381,GRIA3,FBP1,PLAG1,KCNJ1,631136,RTN1,CCR1,MXI1
82	52	GPAA1,SORBS3,FRYL,443092,NFIB,BCAT1,TMCO3,2504786, UCHL3,HAGH,MAPK1,CG018,AGPS,SDS,IGFBP7,RIK1,CALB1, CYP2R1,BRD3,RP11-11C5.2,UBL4A,PREP,CD46,CLUAP1,TOM1L2, DNAJC4,1795967,LEP,DSG2,USP9Y,ZNF263,VARS, RAD23B,EMP1,ASCC3,KIAA0495,MACF1,ALDH5A1, PRKAR2A,DARC,SR140,RAD52,KPNA4,ZBTB7B,MPHOSPH1, SMPD2,DNAIB4,PDK3,POLR3G,MPV17,CCNH,PIK3CG
83	57	CSPG4,STX2,CYP17A1,RHOQ,2044956,PKP2,KERA,HSD17B2, 3421817,2160566,MSLN,ZNF443,5063036,IMPDH1,SLC1A7, DAPK2,TPSG1,AATK,ZMIZ2,KLF12,TNRC6C,SLC44A1,LRRK2, SUSD3,PLS3,1830024,PAPPA,FLJ44451,WWTR1,3407735, ITPKB,MEAP4,CES1,RGS9,DACT1,CCNL2,SPAG8,HLA-DRA, FAM38A,GZMB,PVALB,890629,CAMLG,ZNF277P,NEIL1, PIGL,JARID1C,UGT2B7,LGALS3,NAB1,ZMIZ2,MNRN1, C22orf9,123829,TMEM44,CACNA2D4,MARCKS
84	82	SLC12A4,KLHDC7A,RDX,ZKSCAN4,CDC34,POLD1,1697544, 2192092,HOXB2,EZHI,AKRIC4,ZNF460,5045640,C6orf120, 5084859,GBX2,1794536,2225273,LSM7,5089227,101010, SEL1L,ILIRL2,POLR2D,C6orf105,OMD,TRMT1,PLEKHA7, PPAPDC1B,KCTD1,DDAH2,LOC90784,RUFY1,TSC2,DLC1,CRSP9, EGR3,ARPC2,C16orf78,GYPB,CLSTN1,PROC,1554358,DGKD, PIK3R4,4049957,ACO1,3409234,HSPA4,SPRED2,TSEN2,GJB3, GYG2,1448135,TRAF3,ALAS1,LAG3,ESPL1,C2orf3,DAG1, TRIM27,TPD52,DAB2,KIAA0350,SLC31A2,BCS1L,ZNF211, TNFSF4,RAB7L1,GCK,963536,HK3,ZFYVE16,ZNF507,LOC92270, CDC14A,MYH11,RNF182,AKAP13,C9orf45,TBC1D16,MST1R
85	5	VAMP3,ZNF687,PDCCD2,POLR3G,ZNF317

Module	Number of genes in module	Gene names or Incyte clone ID
86	238	<p>NET1,REV3L,CTRB1,GK,SPON1,1849449,LTJF,2606307,FAT,2380042,DERL1,FAM89B,GPR37L1,1534748,NPC1,FAM13C1,ECM2,3911,ADRBK1,ZNFX1,STK17B,PCYT1A,SLC35B1,NCSTN,ETHE1,LRP8,CYLD,BST1,HOXD9,LOC653381,SFT2D2,KIAA0317,GPX2,DEDD,SLC25A20,INPP4A,GNAP,VP13D,UPK3A,OPN1SW,KDR,ATPAF2,RNASE1,SERF1A,SNAPC5,NPEF,HSJ17B6,STK17A,AKAP12,TFPI2,SPAG7,KRT83,LOC92312,SPARCL1,KIN,MNT,FLJ43806,SEMG1,SEC24B,TGFBRI,UQCRB,3606345,ZNF44,4914032,KCNQ3,E2F2,BHMT,NANS,HRH1,SMAD7,4588144,EDG2,1241709,LIMK2,ISGF3G,YPEL1,2289635,2040826,HIPK2,UBE2H,KRT31,MFN2,MMP23B,KIAA0748,PRMT2,3218865,FLJ10815,A,XIN1,546469,DBNDD1,C13orf16,LEPREL1,ZNF195,2136337,ITPKC,SERPINA12,Gcoml,C21orf34,ALDH6A1,NOTCH2NL,NFKBIZ,REG1,3127171,ITGA2,IGSF21,LPGAT1,ARHGEF9,CA3,PTGS1,SEMA6A,DP4,ZC3H8,GALNT14,KCNJ15,3144018,AYTL1,1686727,CBLN1,NAT2,182802,3190386,87235,GPC5,GOLGA1,NOVA1,PIK3R1,GRIA1,FRMPD4,TMF1,3526675,MAG1,CRIP2,CEP27,XDH,MAPKBPI,C11orf30,2911347,2924888,RAPEGFL1,1957596,532490,TFH3,HOXD10,2912987,PEG10,SCG5,ANXA3,DHCR7,ITPKA,EPHA4,TPD52L1,HOXB5,CASP5,IARS,RALGPS1,ADH4,DIAPH2,1485817,INHBB,1977267,SH3GL3,ZNF544,MATN3,KIAA0258,2183580,RANBP9,3341438,SORBS2,RAB3GAP1,DIO3,ZNF135,COBL,PCSK6,KIAA0265,NTRK2,TMEM142C,DNAJL1,PLCG2,NTRK3,81576,FGR,KHDRBS3,LIFR,APOC2,1534482,RRAS,DMD,TNXXB,2904011,C6orf137,CEP250,KRT7,GFRA2,87309,LOC81691,GP1,B4GALT4,ETFB,1980117,SLURP1,MCF2,NFRKB,1822809,INMT,TM4SF5,LOC728655,GATA6,SNX21,PIGY,828953,1653974,ZFYVE20,2447969,1635013,TSPAN6,RAB9B,PRKAR2A,DEFA1,MPHOSPH9,CRYM,ELL,168922,THBD,CDKL5,TBL1X,LSM8,TLE1,C5orf22,TUBB4,TFEC,SP110,ADRA1B,ZNF626,RAP1GAP,NR0B2,PPAP2B,3971258,ELL2</p>
87	103	<p>TEAM,COX7A2,CD247,ITGB2,MTR,462549,ACTR3,1238619,NDUFV2,496249,SMC4,HSF1,RBBP7,VDAC1,CHDIL,P4HA1,GUK1,BSG,POLA2,TGOLN2,PARK7,LOC728689,CIB1,RPS21,ANXA2,RBMX,WDR1,NDUFV1,MSH6,TMPO,CDIPT,HELZ,IFITM3,CDC2,KIAA1468,CHD1,SCYE1,EIF2AK3,CTR9,PRPSAP2,KIAA0286,2209136,SH2D1A,C19orf43,UTX,2508261,EEF1D,PRSSI,1517380,GM2A,CPT1B,3537526,SUMO1,IGSF1,GOLGB1,BANF1,FLJ10081,ARL6IP4,PCYT1B,MKRN1,DDX24,SNRPN,UQCRC2,VPS45,MTHFD2,TRIM24,1673780,SFRS11,IMMT,MYL2,GT2H2,LGALS8,C20orf3,B4GALT6,PNN,TMED10,ZNF384,1927093,RBM17,ZCCHC11,PDHB,SCARB2,MOBK1B,LONP1,TFE3,SNX17,ST13,HAX1,1879023,EIF2S1,PRKACB,PPP3CA,SRL,CSNK1G1,ANXA4,UNC5B,2060081,PAPSS1,BMI1,TYMS,ECT2,2957644,SMAD2</p>
88	6	C19orf57,TDRKH,INPP5D,DLEU1,RPE65,SLC29A2
89	30	<p>PRKAR1B,601416,NR1H2,CREBBP,DNAH17,COQ7,HIST1H2BG,SCGB2A,12380380,NAV3,SMARCA2,WNT5B,EPX,GNIG2,1808653,C20orf24,3736683,NOS2A,TP53BP1,S100A13,FABP7,CLDN1,SPSB1,KPTN,ATF7,FAM82A,ELL3,DCN,582423,BNC1</p>

Module	Number of genes in module	Gene names or Incyte clone ID
90	1	DNAJC1
91	5	SMYD2,SAPS2,2223152,CRSP8,HERC4
92	4	2366776,ETV6,662122,CLGN
93	1	TNFRSF14
94	33	ALG3,FKBP15,OGN,EIF3S9,STK24,CPNE6,NRXN3,APPL1,2243954, FNDC3B,KRT2.LST1,COG2,FUSIP1,ENTPD4,PIGA,CYP3A7,LOC442075, MT1M,ACVR2B,DPF1,SDCBP2,PEX19,POLRMT,PRAME,SYNJ1,OVGP1, GALNT10,1759794,STARD3,KRIT1,MTM1,AADAC
95	1	1930865

Note: Gene names or Incyte clone IDs were omitted if unknown

Appendix

Appendix B.

Parameter estimates for the ODE model.

Module	Outward regulated modules	Estimates (in the order of the modules presented in the previous column)
1	4,5,15,25,36,49,54,59, 63,64,68,70,74,81,92	0.137679455, -4.15E-05, 0.060364465, 0.016483193, 0.056384499, -0.000160529, 0.025890422, -0.000210467, 0.019958864, -4.01E-06, 0.011744476, 8.35E-06, 0.030315025, 0.030840919, 0.009656423
2	7,19,20,23,25,29,36,42, 63,68,81,85,91,92,94	0.006802491, -0.013630744, -9.41E-06, 0.033734825, 0.03699278, 0.085597536, 0.0024359, 0.00062263, 0.016270922, 0.003106411, 0.000294805, -0.004721464, 0.026409614, 0.076314638, 0.001980056
3	5,8,11,19,49,54,59,64, 70,81,92	-9.29E-05, -0.000102404, -0.000145515, 0.000197006, -0.000405325, 0.008610892, -0.000256693, -0.000523732, 5.04E-06, -0.00059317, -0.000481656

Module	Outward regulated modules	Estimates (in the order of the modules presented in the previous column)
4	3,8,11,19,20,35,46,47,49,50,53,57,59,64	3.16E-05, -0.000292174, -0.000156131, 6.33E-05, -1.69E-05, 2.72E-05, -3.16E-05, 4.69E-05, -0.000284288, 0.000122676, 4.23E-05, 0.000152769, -7.09E-05, -0.000332429
5	3,19,35,47,49,53,54,59,70,78	-3.36E-05, -0.000137163, -2.19E-05, -3.29E-05, 0.000205786, -3.18E-05, 8.93E-05, 0.000240518, 5.14E-05, -0.001617989
6	12,42,49,54,70,93	0.0014927, -0.000841839, -0.001377194, 0.000252319, 0.008726035, -0.000223249
7	19,49,59,64	-0.000137253, 0.000191749, 0.000254487, 1.57E-05
8	3,5,8,11,12,14,19,20,24,31,33,34,35,40,44,46,47,49,50,53,54,57,59,64,65,68,70,75,77,78,81,88,89,91,92,94	-4.73E-05, 0.00042991, 0.002483865, 0.000817131, -0.000593152, 0.001537503, -0.001930598, 6.48E-05, -0.002461206, -0.004605553, 0.001938618, 0.001330796, -3.46E-05, 0.00368251, -0.025636138, 9.72E-05, -9.48E-05, 0.000814801, -0.001719563, -8.00E-05, 5.73E-05, -0.00457052, 0.000234456, 0.005375551, 0.002794521, 0.001292074, -1.43E-05, -0.000692884, 0.002752506, -0.006895783, 0.00181819, 0.003229041, -0.005929392, 0.001676676, 0.000608358, 0.000921179
9	1,2,3,4,5,6,7,8,10,11,12,13,14,15,16,17,18,19,20,21,23,24,25,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,44,45,46,47,49,50,51,52,53,54,55,56,57,59,61,62,63,64,65,66,67,68,69,70,71,73,74,75,76,77,78,79,80,81,82,83,85,86,87,88,89,90,91,92,93,94,95	0.982576397, 0.004469551, 1.764585716, -0.429003524, -0.007489504, -0.642360296, 0.091715885, -0.023276905, 0.104231891, -0.703233062, 0.028838664, 1.428847488, -0.053853233, -0.458631744, -0.149533047, 0.295715065, 2.13368038, 0.074099213, -1.882032432, 1.537569982, -0.215122878, 0.053460672, -0.506528639, 1.928028015, 1.120469113, -0.116497853, -1.164210186, 2.239961887, -0.271930497, -0.019577615, -0.230753092, 2.150042142, -0.421002869, -1.625600213, -1.332038069, 0.030921134, -0.215861729, 2.052934342, 0.037311002, 1.42908015, -0.026875812, -0.533090981, 1.463895728, -0.017580618, 0.042527211, -0.719223123, -0.25019948, 1.598095857, -0.037060387, -0.130818199, -0.026609287, 0.09218147, 0.114693603, 0.731397691, 1.188004884, -0.442103947, -0.06336735, -0.092594845, 0.151674687, 0.007888131, -0.059277923, -0.346041078, 0.000365222, 0.004995832, -0.082863411, -0.64228879, 0.018408756, 0.165175783, -0.101206187, 1.546175608, 2.109620437, -0.16040185, -0.192850311, 0.318117342, 0.119851911, -0.666831734, 0.145012113, 1.192297121, -0.109293747, 0.108376285, 0.921892739, -0.067122883, -0.057410757, 0.405030573, -0.069397903, -0.757970304
10	3,8,11,12,14,19,24,33,34,35,47,49,50,53,57,59,64,65,67,68,70,71,75,81,84,88,89,91,92	4.63E-05, -0.000473182, -0.000667837, 0.003489616, -0.00321914, 0.000346152, 0.002389822, -0.005090306, -0.003153311, 4.57E-05, 0.000119727, -0.00106516, 0.002067469, 9.97E-05, 0.006222143, -0.000725634, -0.00186549, -0.004117332, -0.00212127, -0.003169136, 0.000110863, 0.00168536, 0.001192141, -0.001187501, 0.008541396, -0.003566774, 0.001885332, -0.002986136, -0.001315441
11	3,35,45,46,47,49,53,54,59	9.92E-06, 1.38E-05, -0.000363769, -4.60E-05, 1.07E-05, -6.66E-05, 1.19E-05, -7.20E-05, -5.04E-05
12	5,7,8,11,12,14,19,20,24,32,33,34,35,40,44,46,49,50,57,59,64,65,68,70,71,75,81,88,89,92,94	-0.000596189, 0.020933744, -0.005370727, -0.001336612, 0.00631084, -0.004586891, 0.002884601, -4.84E-05, 0.003560751, -0.016337798, -0.00425327, -0.005788789, 3.82E-05, -0.005539301, 0.004456814, -0.000153282, -0.001571354, 0.003056617, 0.00945076, -0.00073663, -0.008245214, -0.005839078, -0.003722144, 7.08E-05, 0.00101051, 0.001877505, -0.00189319, -0.006470606, 0.003564271, -0.001775306, -0.001735869
13	3,7,11,16,19,20,24,32,35,39,42,46,47,49,50,53,54,55,57,58,59,64,65,66,68,70,73,74,76,78,81,88,89,93	0.000157876, 0.003986768, -0.001145983, -0.006639107, -0.007290389, -0.000114691, 0.001006589, -0.015621479, 0.000135843, 0.009552482, 0.003168265, -0.000371977, 0.000244988, -0.001208913, 0.000736591, 0.000214717, -0.002311204, -0.021354826, 0.001223339, -0.001644099, 0.010615219, -1.65E-06, -0.00105753, 0.015484685, -0.001062004, -0.009846872, -0.002543397, -0.004828536, 0.009434757, 0.00414116, -0.001186165, -0.000763556, 0.003657377, 0.076886285
14	2,5,8,11,12,14,16,19,23,24,29,34,40,42,44,49,54,57,58,59,64,65,67,68,70,71,72,74,75,77,81,84,85,86,88,89,91,92,93,94	-0.009462792, 0.011585005, 0.024649934, 0.000548374, -0.014146294, 0.044503701, -0.000132746, -0.015440846, 0.03191466, -0.012257919, 0.018090747, 0.020186944, 0.008845294, 0.001014862, -0.006050177, 0.000554337, -0.000527428, -0.0055996, -0.0010979, 0.001734597, 0.08762698, 0.004757784, 0.000730763, 0.007670497, -0.02115388, -0.0017008, -0.01431963, -0.000335174, -0.001031673, 0.015368913,

Module	Outward regulated modules	Estimates (in the order of the modules presented in the previous column)
		0.001960482, -0.007143582, 0.00896727, -0.002865, 0.004999555, -0.014517901, 0.010671583, 0.001289392, 0.000267603, 0.034693658
15	3,5,6,8,11,12,14,15,19,20, 23,24,29,31,33,34,35,40, 44,46,47,48,49,50,53,57, 59,64,65,68,70,71,75,77, 78,81,84,88,89,91,92,94	6.78E-05, -0.011020376, -0.011409117, -0.009785933, -0.001751988, 0.015286085, -0.007680636, -0.005904778, 0.011105022, -6.26E-05, -0.012367243, 0.006268034, -0.014432849, 0.010144365, -0.00507279, -0.011955972, 4.93E-05, -0.019389499, 0.027516212, -0.000207733, 0.000127995, 0.011353236, -0.001440629, 0.002481385, 0.000109077, 0.017412802, -0.003315284, -0.021397906, -0.012763177, -0.008101797, 0.017957111, 0.001265929, 0.002510656, -0.015857245, 0.006715085, -0.007781061, 0.005182755, -0.010938541, 0.008148031, -0.006021431, -0.004303409, -0.014376765
16	3,5,8,11,12,14,19,24,33, 34,35,40,42,46,47,49,53, 54,57,59,64,65,68,70,71, 73,75,76,88,91,92,94	5.70E-05, -0.000184515, -0.002018479, -0.00063054, 0.003226358, -0.00081598, 0.002436535, 0.000377348, -0.001518009, -0.002191796, 2.90E-05, -0.000910082, 9.86E-05, -0.000160848, 0.000134886, -0.002972036, 0.000114221, -9.26E-05, 0.001365641, -0.000264583, -0.002136223, -0.000850657, -0.000548446, 0.014788487, 0.000143344, -0.000497164, 0.00046258, 0.001624347, -0.001202253, -0.002774312, -0.000967436, -0.000443677
17	1,2,3,4,5,6,7,8,10,11,12, 13,14,15,17,18,19,20,22, 23,24,25,26,27,28,29,30, 31,33,34,35,36,37,38,40, 41,42,44,46,47,48,49,50, 51,52,53,56,57,58,59, 60,62,63,64,65,66, 68,69,70,71,72,75,77, 78,79,80,81,82, 83,84,85,86,88,89,90, 91,92,94,95	-0.055895416, -0.052142451, -0.057781025, 0.016763339, 0.00594133, 0.135619272, 0.00089131, 0.009662432, -0.01791653, 0.088291824, -0.010951722, -0.015661696, 0.076187108, 0.037697769, -0.028760211, -0.043197473, -0.02188335, 0.231006429, -0.065514184, 0.048770623, -0.026120715, 0.074347246, 0.035343181, -0.03700682, -0.0238042, 0.038278963, 0.08350066, -0.00862119, 0.00458912, 0.068871984, -0.018297813, 0.066154687, 0.221464497, 0.142608811, 0.087162114, -0.063643626, 0.00036953, -0.518043803, 0.119071926, -0.027883329, -0.012097112, 0.00142241, -0.003071691, 0.044024876, 0.174742932, -0.008693515, 0.174509741, -0.011513889, -0.001184779, 0.004945773, -0.022860686, -0.020505722, 0.062976342, 0.008545135, 0.056692896, 0.000901716, 0.0118815, 0.131920424, -0.008933546, -0.002773533, -0.016937859, -0.048857343, 0.046367869, -0.061162002, -0.253335175, 0.101581548, 0.012785735, -0.00907535, -0.028041113, -0.005321392, 0.050675753, -0.027445139, 0.008841571, -0.03571411, -0.144817789, 0.017075982, 0.020953674, 0.061505835, 0.233503433
18	5,8,11,14,24,34,42,50,54, 55,57,64,65,70,71,73,75, 84,88	-0.000242871, -8.80E-05, -3.35E-05, -0.000548904, 0.000170116, -0.000473264, -0.000290151, 0.005262717, 0.000376144, 9.35E-05, 0.00123108, -0.000354889, -0.000502828, 4.40E-06, 0.000208883, 6.35E-05, 0.000137784, 0.002124579, -0.000545519
19	16,19,45,49,50,59	0.000416826, -0.000224435, 0.000183773, 0.000449718, -0.000521071, 0.000401637
20	2,3,5,6,8,10,11,12,14,15, 19,23,24,29,31,33,34,35, 40,44,45,46,47,48,49,50, 53,54,57,58,59,60,64,65, 68,70,71,72,75,77,78, 81,83,84,88,89,91,92,93,94	0.011901249, 3.30E-05, -0.002809687, -0.009986143, -0.003179156, 0.009355159, -0.000860938, 0.006517691, -0.004069126, -0.007053853, 0.008514415, -0.010812965, 0.003021045, -0.011407921, 0.003789049, -0.002466366, -0.005612737, 2.89E-05, -0.015201266, 0.007705365, -0.000495358, -0.000110859, 5.37E-05, 0.007456008, -0.001309364, 0.00172212, 4.82E-05, 6.81E-05, 0.011174222, 0.002424292, -0.002348666, 0.009101084, -0.004864561, -0.006419641, -0.005803866, 0.007704414, 0.003268246, 0.01264934, 0.014948, -0.010853972, 0.003497874, -0.008904152, 0.014741687, 0.00364931, -0.008176277, 0.004707277, -0.006656249, -0.002593079, -0.000286635, -0.011825945
21	5,7,8,11,12,14,16,19,20,24, 29,32,33,34,39,42,43,49,54, 55,57,58,59,64,65,66,67,70, 71,73,74,75,76,81,88,91,92, 93,94	-0.00819701, -0.013226151, -0.047832973, -0.000113613, 0.013096146, -0.00076686, 0.004821663, 0.003572431, 7.53E-06, 0.000289761, -0.001378101, 0.017825969, -0.007761643, -0.001126759, -0.011970339, -0.000800128, -0.013485791, -0.001029772, 0.000424807, 0.000690849, 0.016757982, 0.000842319, -0.008050864, -0.027220325, -0.000596893, -0.003172442, -0.008365428, 0.026205162, 0.001246953, 0.000348315, 0.000538398, 0.00022284, -0.003677258, -8.43E-05, -0.000631836, -0.009548558, -0.000584649, -0.00342129, -0.001270656

Module	Outward regulated modules	Estimates (in the order of the modules presented in the previous column)
22	1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,26,27,28,29,30,31,32,33,34,35,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,59,60,61,62,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,86,87,88,89,90,91,92,93,94,95	0.131852685, 0.139029996, 0.812994751, -0.021666019, -0.02775607, -0.218804997, 0.040333135, -0.04085326, -0.011203977, 0.139676306, -0.167850314, 0.022545251, 0.096818679, -0.029924273, -0.042221374, -0.091449189, 0.152353409, 0.456342041, 0.030761752, -0.616141763, 0.577345434, 0.098872296, -0.054420295, 0.06890192, -0.293170859, 0.29171365, 0.130112205, -0.046745526, -0.085381946, 0.652582733, -0.034918496, -0.014370334, -0.051226004, 0.589718416, -0.357978188, -0.384147319, 0.086337886, -0.173676609, 0.29155175, 0.004131992, 0.076283998, 1.062374048, -0.006564261, -0.124186666, 0.630533438, 0.096711323, -0.004995535, 0.00971954, -0.179454949, -0.235373871, 0.452692871, -0.001059441, -0.002756177, -0.149282942, 0.034292041, -0.002114717, 0.067531416, 0.115016723, 0.274656738, -0.084720456, -0.064343942, 0.032845603, 0.002511827, -0.020098369, -0.129972383, -0.090190786, 0.004836785, 0.145356571, -0.019633903, -0.001907418, 0.193874146, 0.021683128, -0.083254484, 0.952892227, 1.271360355, -0.25080692, -0.050713653, 0.083257805, 0.170134278, 0.029997581, 0.141601632, 0.081429028, -0.048748383, 0.10165526, 0.50338465, -0.019430329, -0.01992155, 0.04725836, -0.06361375, -0.394731824
23	3,7,16,19,32,35,39,42,46,47,49,53,54,55,58,59,66,68,71,73,74,76,91,93	3.85E-05, 0.004459252, -0.002731701, -0.000526629, -0.005892453, 2.90E-05, 0.002156383, 0.00057254, -5.03E-05, 8.30E-05, -0.000164992, 7.08E-05, -0.000403617, -0.000723088, -0.002409569, 0.009998886, 0.014167585, 0.000722244, -0.001674341, -0.000817169, -0.000870344, 0.004144414, 0.001056186, 0.025049112
24	59	3.51E-05
25	3,5,8,11,14,15,19,20,24,33,34,35,40,44,46,47,49,50,53,57,59,64,65,68,70,75,77,78,81,84,88,89,92,94	4.94E-05, -0.000378589, -0.000275685, -0.001144172, -0.003125488, -0.001466029, 0.000274226, -4.70E-05, 0.003598147, -0.001780638, -0.004072021, 3.04E-05, -0.007950248, 0.003687267, -0.000175512, 8.68E-05, -0.000720607, 0.001842119, 7.43E-05, 0.004270175, -0.000389031, -0.002516446, -0.007241427, -0.001183875, 4.58E-05, 0.001112647, -0.009697371, 0.007955885, -0.002366387, 0.003177026, -0.005687775, 0.00694357, -0.002274072, -0.003882532
26	5,8,11,12,14,19,24,33,34,40,49,54,57,59,64,65,68,70,71,75,77,88,92,94	-0.00229254, -0.003239383, -5.16E-05, 0.007815179, -0.001021068, 4.19E-07, 0.000241814, -0.000927974, -0.002960473, -0.003312107, -0.001061082, 0.000142721, 0.000856785, -7.30E-05, -0.003080351, -0.000680786, -0.000778503, 0.020505445, 0.000260806, 0.000420993, -0.004397945, -0.001135988, -0.000656277, -0.000843904
27	5,7,8,11,12,14,16,19,24,33,34,39,42,43,45,48,49,50,54,55,57,58,59,60,64,65,66,67,68,70,71,72,73,74,75,76,81,84,88,89,91,92,93	-0.000237613, -0.000606501, -0.031155996, -0.000231801, 0.005064897, -0.001904647, 0.001696034, 0.002440595, 0.000580017, -0.027505573, -0.002363519, -0.002207586, -0.00102114, 0.000313565, 0.001145903, 0.035991887, -0.000253298, 0.007689277, 0.067523154, 0.000299989, 0.00429184, 0.004573699, -0.004358719, 0.103816846, -0.00290201, -0.001304912, -0.007200361, -0.000964098, -0.002450274, 7.19E-05, 0.007841205, 0.023218112, 0.000122063, 0.041573619, 0.000511732, -0.01190031, -0.000933005, 0.027014754, -0.0015318, 0.000388361, -0.001846371, -0.000671935, -0.013056405
28	3,5,8,11,12,14,15,19,20,23,24,29,33,34,35,40,42,46,47,49,50,53,54,57,59,64,65,68,70,71,73,75,77,78,81,88,89,91,92,94	-0.000113256, 0.000479905, 0.000502001, 0.001356472, -0.002010502, 0.004037265, 0.004263712, -0.004203689, 3.54E-05, 0.003559489, -0.003533527, 0.000670124, 0.002906465, 0.004648369, -8.75E-05, 0.0059892, -0.000490501, 0.000248494, -0.000204275, 0.001459661, -0.002361404, -0.00017732, 0.000167142, -0.005805021, 0.00081917, 0.002032626, 0.007381233, 0.003846785, -8.47E-05, -0.000689521, 0.000199618, -0.001320525, 0.006777372, -0.004321756, 0.005411287, 0.007606822, -0.00585919, 0.003107723, 0.003217628, 0.006647561
30	1,2,3,4,5,6,8,10,11,12,13,14,15,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,33,34,35,36,37,38,40,41,44,45,46,47,49,50,51,52,53,54,56,57,58,59,60,61,62,63,64,65,68,69,70,71,72,75,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95	0.109225287, 0.049403233, 0.376820111, -0.059106102, -0.008492783, -0.16597638, -0.010506692, 0.060769394, -0.184360951, 0.012724545, 0.244447893, -0.011910616, -0.041017409, 0.08387852, 0.413496242, 0.01723138, -0.320575233, 0.378706635, 0.150678639, -0.030002665, 0.01064426, -0.104181919, -0.129494923, 0.22085633, 0.126591696, -0.020301398, -0.180541723, 0.203124068, -0.007914891, -0.017838028, 0.458960042, -0.060746488, -0.197500503, -0.183855485, -0.085976625, 0.199894111, 0.356037265, -0.00136201, -0.165796833, 0.318047022, -0.00340163, 0.006469425, -0.184470859, -0.122360458, 0.323728416, 9.25E-05, -0.099349725, 0.015727738,

Module	Outward regulated modules	Estimates (in the order of the modules presented in the previous column)
		0.002633098, -0.006169365, 0.016461708, 0.152669223, 0.208685935, -0.066812806, -0.025575829, -0.023913336, -0.012960062, -0.13561841, 0.000119026, 0.001936361, 0.031776544, 0.058204016, -0.025947377, 0.324675776, 0.349730032, -0.136884702, -0.030350127, 0.117990581, 0.071278358, 0.00956675, -0.088769341, 0.070412193, 0.204057938, -0.030290073, 0.019449035, 0.187321419, -0.010070777, -0.007478417, -0.000515585, -0.02505091, -0.16654171
31	5,8,11,14,16,19,24,33,34, 40,49,54,57,59,64,65,68, 75,81,84,88,89,91,92,93, 94	-0.000393734, -0.000380505, -0.000689216, -0.003385342, 0.00043452, 0.0054529, 0.003558104, -0.002878786, -0.003929319, -0.006942749, -0.00052108, 3.21E-05, 0.005129986, -0.000669442, -0.002689762, -0.005248032, -0.003736645, 0.000837375, -0.003032989, 0.002894799, -0.005333463, 0.005732245, -0.004401199, -0.002275607, -0.002997401, -0.004163244
32	1,2,3,4,5,6,7,8,10,11,12, 13,14,15,17,18,19,20,21, 22,23,24,25,26,27,28,29, 30,31,33,34,35,36,37,38, 39,40,41,44,45,46,47,48, 49,50,51,52,53,56,57,58, 59,60,61,62,63,64,65,66, 67,68,69,70,71,72,75,77, 78,79,80,81,82,83,84,85, 86,87,88,89,90,91,92,93, 94,95	0.80474525, 0.525234701, 1.802627264, -0.117491344, -0.141948292, -0.586554933, -0.015549637, -0.307242934, 0.579594939, -0.579682122, 0.08205854, 0.672204706, -0.277593061, -0.130450922, 0.506640046, 1.758596256, 0.048886863, -1.386558879, 1.689100449, 0.218486908, -0.098472154, 0.344744882, -0.239518933, -0.46418603, 1.310037985, 0.637938478, -0.175552871, -0.580388799, 1.51164714, -0.110697248, -0.225517501, 2.200371204, -0.145736133, -1.082893283, -0.90787985, -0.003897656, -0.50711741, 1.29034655, 2.023431638, -0.026004455, -0.726942636, 1.687148303, 0.239203218, -0.009831824, 0.051941854, -0.930669936, -0.60812212, 1.438385448, -0.348455499, 0.142457295, 0.004911635, -0.007577413, 0.538035285, 0.592878088, 0.851863189, -0.147457924, -0.405703449, -0.225181236, -0.003081905, -0.054576112, -0.028025468, -0.657183637, 0.16463966, 0.012390225, 0.447040308, 0.622637694, -0.098367398, 1.999802427, 2.093262075, -0.389150574, -0.117269494, 0.510355557, 0.675732117, 0.082291889, -0.26080726, 0.486341266, 0.594343514, -0.043535169, 0.392993216, 0.830877058, -0.045195508, -0.051884607, -0.000494405, -0.215442045, -0.713687569
33	2,4,5,8,10,11,12,14,15,17, 19,23,24,29,31,32,33,34, 40,42,43,46,49,50,54,55, 57,58,59,60,64,65,68,70, 71,72,75,77,78,81,83,84, 86,88,89,91,92,93,94	0.044955335, -0.031675883, -0.008893227, -0.008517247, 0.046630774, -0.001355343, 0.014107146, -0.011180296, -0.023489535, 0.022347454, 0.01880985, -0.032457791, 0.008155014, -0.02896372, 0.029049462, 0.006475258, -0.006030787, -0.017287131, -0.027577768, -0.00219952, 0.000705837, -0.000587998, -0.004527133, 0.009583314, 0.000594492, 0.008509786, 0.032409189, 0.05072632, -0.011117074, 0.023829756, -0.013655471, -0.019890452, -0.005838325, 0.00020194, 0.013248119, 0.045633708, 0.029211068, -0.034822896, 0.025915189, -0.023291378, 0.04888536, 0.013169639, 0.041458614, -0.092959862, 0.01906474, -0.007012611, -0.006573968, -0.000884101, -0.025248882
34	3,5,8,10,11,12,14,15,19,20, 23,24,29,31,33,34,35,40, 44,46,47,49,50,53,54,57, 59,64,65,68,71,75, 77,78,81,84,86,88,89, 91,92,94	-0.000255037, 0.011593365, 0.007702636, -0.020490419, 0.002703701, -0.003186543, 0.004464135, 0.007980355, -0.004355952, 0.000196407, 0.018233419, -0.004436151, 0.011059103, -0.025821175, 0.002611934, 0.005579664, -0.000184204, 0.015241599, -0.061389847, 0.000293189, -0.000474593, 0.001317598, -0.00499984, -0.000405828, 0.00037622, -0.007480489, 0.000300111, 0.01002001, 0.009786795, 0.00314421, -0.000843598, -0.001558283, 0.014338433, -0.014735733, 0.003030945, -0.004851904, -0.024669751, 0.006825467, -0.010594315, 0.00393986, 0.002394301, 0.002590542
35	5,8,11,14,19,20,24,33,34, 42,46,49,50,54,57,58, 59,64,65,68,70,71,73, 75,81,88,89,91,92	0.000210746, 0.000232646, 0.000602464, 0.001797096, -0.003580748, 8.74E-06, -0.00061783, 0.001921492, 0.00156299, 0.000193563, 3.57E-05, 0.000555321, -0.001622251, -0.000331916, -0.0034366, -0.000259518, 0.000467708, 0.000994618, 0.002130152, 0.002028292, -3.06E-05, -0.000309875, -0.00528519, -0.000442038, 0.001598603, 0.001952187, -0.001966569, 0.002532703, 0.000783421
36	3,7,20,35,47,49,53,54, 68,73,93	1.78E-05, 0.000862184, -1.08E-05, 1.99E-05, 3.95E-05, -0.000290438, 3.41E-05, -9.30E-05, 0.00060163, -0.000194031, 0.008991501
37	68	0.000349186

Module	Outward regulated modules	Estimates (in the order of the modules presented in the previous column)
38	3,5,8,11,12,14,19,20,23,24,29,33,34,35,40,44,46,47,48,49,50,53,54,57,58,59,64,65,68,70,71,75,77,78,81,84,88,89,91,92,94	3.11E-05, -0.000526036, -0.006079903, -0.001160836, 0.009263705, -0.005511276, 0.00771641, -2.07E-05, -0.01026494, 0.004805814, -0.011067194, -0.003670215, -0.008232472, 2.40E-05, -0.014103318, 0.006744445, -0.000188674, 4.97E-05, 0.008821866, -0.000808413, 0.002422466, 4.45E-05, 0.000102336, 0.007148702, 0.001216191, -0.002423801, -0.00895237, -0.006507145, -0.003799555, 0.012185817, 0.000949588, 0.002029997, -0.012040581, 0.005960335, -0.002766818, 0.004827472, -0.007789443, 0.005854302, -0.005784361, -0.003614641, -0.009511392
39	1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95	2.096198685, 1.180948607, 3.570353584, -0.578688063, -0.192781449, -1.229715888, -0.054778362, -0.705770853, -0.003466918, 1.063847245, -1.276887047, 0.224261686, 0.788071183, -0.817149207, -0.215811144, 0.011121045, 1.210154216, 2.003202208, 0.31416385, -2.563495314, 4.236000295, 0.540518747, -0.634741896, 0.678735235, -0.720330986, -0.567948026, 3.054718745, 1.451292726, -0.562470408, -1.370006729, 3.755844694, 0.030957018, -0.359709603, -0.732180095, 3.241673518, -0.810635868, -1.802630944, -0.966667766, -0.106007285, -0.879220209, 1.73850501, -0.130705824, 0.005022005, 5.134759274, -0.001979557, -1.206800807, 2.493458303, 0.59655701, -0.029743532, 0.429089176, -2.884673133, -0.973540373, 1.713892442, 0.010094222, 0.043002499, -1.058991592, 0.59233698, 0.154634238, -0.275610622, 1.274436918, 0.758592167, 1.751401334, -0.674322001, -0.137137768, -0.589433101, -0.207525929, 0.062223939, -0.107712117, -1.383887137, 0.174904613, 0.20804759, 1.266062959, 0.00750013, 0.110913249, 1.121527781, -0.235582938, -0.314200342, 3.755349491, 4.433851506, -0.600928416, -0.238006135, 1.018663458, 1.605921626, 0.630302797, -0.763420467, 1.410945684, 1.035264699, -0.244454675, 1.147223029, 1.462556812, -0.522016546, -0.252056739, -0.431830554, -0.624017569, -1.408256773
40	3,5,8,11,12,14,19,20,24,33,34,35,40,46,47,49,50,53,57,59,64,65,68,70,71,75,77,81,88,89,91,92,94	-2.72E-05, 0.000509551, 0.000799683, 0.001548536, -0.005041084, 0.004770169, -0.006136076, 1.34E-05, -0.004200614, 0.004083447, 0.006377868, -2.18E-05, 0.010846587, 0.000160401, -7.65E-05, 0.001190207, -0.002443611, -6.45E-05, -0.007765862, 0.000796975, 0.006081914, 0.006419486, 0.004285913, -6.80E-05, -0.00085036, -0.001802816, 0.008496124, 0.003015563, 0.007084906, -0.005556904, 0.004741129, 0.003107835, 0.004662348
41	1,2,3,4,5,6,8,10,11,12,13,14,15,17,19,20,21,22,23,24,25,27,28,29,30,31,32,33,34,35,36,40,42,43,44,46,47,48,49,50,51,53,54,57,58,59,60,61,62,63,64,65,66,68,69,70,71,72,75,77,78,79,81,82,83,84,86,87,88,89,91,92,93,94	0.234395072, 0.157126626, 0.057180833, -0.024454572, -0.010804468, -0.067391033, -0.021932591, 0.115901071, -0.085207645, 0.019843895, 0.082518913, -0.010431146, -0.014736887, 0.206147588, 0.018260717, -6.31E-05, 0.27888381, 0.091982451, -0.038722117, 0.086182429, -0.045751653, 0.179314048, 0.195998858, -0.031475501, -0.071804597, 0.150590478, 0.00256235, -0.009846161, -0.025054114, 0.00793362, -0.03820627, -0.0719045, -0.001501512, 0.054764966, 0.140656723, -0.085543983, 0.000168759, 0.068519398, -0.028659864, 0.028861807, -0.116812015, 0.000143026, 0.000424838, 0.037361151, 0.009780099, -0.00915308, 0.077886306, 0.152695143, 0.110968634, -0.051145749, -0.027479359, -0.027248071, -0.002352146, -0.012601091, -0.062101878, 0.023387301, 0.065434707, 0.148393867, 0.058533647, -0.038974238, 0.021746392, 0.111221588, -0.020691938, 0.076704655, 0.201421293, 0.118804724, 0.18398213, 0.08734827, -0.052294831, 0.165103926, -0.015879566, -0.006240769, -0.001003105, -0.034287324
42	4,5,7,9,14,16,19,23,29,32,36,39,42,49,50,54,58,59,63,66,68,71,81,84,91,92,94	-0.17645387, 0.00348673, -0.11157665, -0.011981193, -0.057742436, -0.073714404, 0.06390692, -0.169511675, -0.089948221, 0.077428121, -0.115464687, -0.018364435, -0.00356329, -0.024215032, 0.377469298, 0.000396542, 0.011776993, -0.029053401, -0.030790747, -0.022938447, -0.02305333, 0.008795795, -0.011868808, 0.073896987, -0.14734149, -0.033667615, -0.110356918
43	2,6,8,10,12,17,19,20,29,33,40,49,59,64,68,70,75,81,83,86,94	-0.008915051, 0.016971498, 0.001176857, -0.005693451, -0.001224783, -0.008321381, -3.04E-05, 0.042182325, 0.001710819, 0.00018161, 0.004178221, 1.37E-05, 5.25E-05, 1.84E-06, 0.001253576, -0.005699315, -0.005801252, 0.002224697, -0.008233076, -0.00111983, 0.001955911
44	3,5,9,19,20,32,35,42,49,50,54,55,57,58,66,70,71,73,74,76,84,93	2.62E-06, -2.86E-05, 0.000485965, 5.43E-05, -2.40E-05, -0.009508767, 4.26E-06, 0.002439955, -0.000187936, -0.001461419, -0.000142428, -0.04623274, 0.00047705, -0.031752866, 0.000692721,

Module	Outward regulated modules	Estimates (in the order of the modules presented in the previous column)
		-5.16E-06, -0.020218652, -0.000121889, -0.000216471, 0.000372411, -0.009792296, 0.000158032
45	3,5,8,11,12,14,19,24,29,33,34,35,40,44,45,46,47,49,53,57,59,64,65,68,70,71,75,77,81,88,89,91,92	1.90E-05, -0.004882947, -0.00610476, -0.000920639, 0.012562239, -0.003267856, 0.004257362, 0.003692059, -0.004693381, -0.003101042, -0.007569235, 2.20E-05, -0.012624063, 0.004903508, 0.023980134, -0.000136635, 4.94E-05, -0.000565972, 4.27E-05, 0.005291772, -0.000407152, -0.008478536, -0.004901623, -0.003892365, 0.018721881, 0.000535609, 0.001574714, -0.009266834, -0.001147411, -0.0082759, 0.003162787, -0.001970753, -0.00237139
46	19,49,50,59,64,71	0.000147463, -0.000460099, 0.001832719, -0.000219117, -2.07E-06, 0.000263776
47	16,32,42,43,49,54,55,58,59,66,71,73,74,76,93	0.000666836, 0.00148777, -0.000883843, 0.000201274, 5.91E-05, 0.00144487, 0.000741952, 0.002158262, 4.61E-05, -1.00E-05, 0.011587464, 0.000445837, 0.060609385, -0.000788803, -8.34E-05
48		2.54E-05
49	1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,44,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95	2.118903219, 1.351673282, 4.419417423, -0.462627637, -0.220721807, -1.165971183, -0.036958244, -0.626539803, 0.036989089, 1.51362927, -1.304874601, 0.38723268, 1.705221478, -0.644553217, -0.348754388, 0.100500284, 1.398099741, 3.367094439, 0.273564229, -2.576375467, 4.582419515, 0.864737582, -0.580509004, 0.998403675, -0.70059194, -0.634905136, 3.481160809, 1.847205195, -0.359965342, -1.331434209, 4.227141157, 0.016151207, -0.338538837, -0.604089352, 4.126106562, -0.575269591, -1.799954019, -1.191199719, -0.045576548, -1.014900705, 3.107852141, -0.028961649, 4.799972918, -1.367332439, 3.726059047, 0.936632117, -0.18873374, 0.794197299, -2.447803412, -1.025214296, 2.915762305, 0.053539551, 0.007996485, -0.866976299, 0.429747437, 0.2659745, -0.113270913, 1.615109162, 1.56762068, 2.355771048, -0.511891644, -0.448488548, -0.545131357, -0.037888424, -0.006922665, -0.207869419, -1.239368693, 0.322935236, 0.254632387, 1.487600858, 0.117482667, 0.002539622, 1.477366226, -0.008726875, -0.332124671, 4.678141832, 5.42721605, -0.807992653, -0.149983877, 1.456000342, 1.817863918, 0.667992071, -0.742064753, 1.486413771, 1.749858312, -0.168527702, 1.336466419, 2.344201522, -0.349540507, -0.444001409, -0.008513427, -0.436882163, -1.320585172
50	2,5,7,8,11,12,13,14,16,19,20,22,24,29,32,33,34,39,40,41,42,48,49,51,54,55,57,58,59,60,64,65,66,68,69,70,71,72,73,75,77,81,82,83,88,89,91,92,93,94	0.034276459, -0.027016514, -0.008827169, -0.026233095, -0.000414611, 0.012786268, 0.002612088, -0.060692878, 0.001255111, 0.022313622, 4.66E-05, 0.031650801, 0.046526794, -0.020658135, 0.011282414, -0.002330288, -0.054137912, -0.007943694, -0.053874592, 0.175280521, -0.005161537, 0.018653651, -0.000353418, -0.06491489, 0.001888066, 0.002778006, 0.029688005, 0.004222972, -0.0137526, 0.052135585, -0.001185865, -0.011566315, -0.007095342, -0.005224877, -0.008162258, 0.000106875, 0.008664526, 0.009717253, 0.001205773, 0.021873361, -0.012779096, -0.00202219, 0.048572566, 0.018723772, -0.002861373, 0.011248531, -0.016836651, -0.006386866, -0.002635586, -0.036726983
51	5,8,12,20,44,49,54,64,70	3.33E-05, 0.001780127, -0.00280947, 4.86E-06, -0.005068543, 8.85E-05, 6.03E-05, 0.0015418, -0.00437571
52	3,5,8,11,12,14,19,20,24,33,34,35,46,47,49,50,53,57,59,64,65,68,70,71,75,81,84,88,89,91,92,94	3.23E-05, -0.000354589, -0.000375425, -0.001087048, 0.001846538, -0.003460482, 0.005106643, -2.43E-05, 0.002606964, -0.002523121, -0.002686767, 2.57E-05, -0.00013925, 7.37E-05, -0.00082056, 0.003359135, 6.11E-05, 0.005101655, -0.000471496, -0.00230422, -0.004304881, -0.004776341, 1.24E-05, 0.00028317, 0.00100658, -0.002763931, 0.009834123, -0.004221548, 0.004812609, -0.003971791, -0.002088069, -0.003136919
53	8,12,34,35,39,42,43,46,50,54,55,58,59,64,66,70,71,73,74,75,76,84,93	0.002928542, -0.002971596, 0.000865918, -6.41E-06, -0.00159575, -0.00486199, 0.000235756, 9.82E-06, 0.00180799, 2.58E-05, 0.007293081, 0.00387434, -0.000909976, 0.00200679, -3.62E-05, -0.005727166, 0.005814147, 0.00016049, 0.000591568, -2.36E-05, -0.001227171, 0.000608664, -0.00127444
54	19,49,59,64	-0.000164761, 0.00016123, 0.000258545, 3.65E-06

Module	Outward regulated modules	Estimates (in the order of the modules presented in the previous column)
55	1,2,3,4,5,6,8,10,11,12,13,14,15,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,33,34,35,36,37,38,39,40,41,42,44,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,68,69,70,71,72,75,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95	0.260812259, 0.271612995, 0.51391289, -0.034435863, -0.043206523, -0.163003805, -0.096934432, 0.200672245, -0.207802768, 0.047339193, 0.208523512, -0.072887441, -0.054212103, 0.265871696, 0.447751459, 0.02159396, -0.419993675, 0.342190262, 0.09949447, -0.05350092, 0.260377514, -0.027581846, -0.098427409, 0.371691283, 0.21908264, -0.051814238, -0.104365595, 0.479463302, -0.043406967, -0.114522715, 0.586986327, -0.031012914, -0.240301595, -0.202853258, -0.005016694, -0.140658749, 0.36505767, -0.002588438, 1.354079519, -0.174456152, 0.443765405, 0.195977339, -0.005007455, 0.034556296, -0.338340741, -0.108449923, 0.31114144, 0.000167393, 0.001209969, -0.069858246, 0.048650401, 0.010045737, -0.006857476, 0.305689154, 0.206019066, 0.181912248, -0.044295664, -0.049006346, -0.064744274, -0.00485804, -0.013747374, -0.197256242, 0.086030122, 0.037406833, 0.313708522, 0.307112635, -0.05343784, 0.638442817, 0.688546823, -0.093411358, -0.027556174, 0.074106647, 0.297966346, 0.085470119, -0.057265059, 0.257819061, 0.112430658, -0.07313362, 0.245062667, 0.252120514, -0.016386536, -0.008794929, -0.001605081, -0.055400411, -0.10638786
56	5,8,11,12,14,19,23,24,29,33,34,40,46,49,50,54,57,58,59,64,65,68,70,71,75,77,81,84,88,89,91,92,93,94	0.004611786, 0.004512529, 0.001067492, -0.008071377, 0.004332418, -0.006241527, 0.003949934, -0.002955282, 0.006327755, 0.003103529, 0.005738824, 0.007073637, 0.000128374, 0.000898776, -0.001690683, -4.61E-05, -0.005568082, -0.002146957, 0.002993218, 0.005963386, 0.004679804, 0.004843331, -0.011125963, -0.004092835, -0.001512151, 0.006422199, 0.002078916, -0.00601778, 0.005276743, -0.003436027, 0.006144001, 0.002721692, 0.000457183, 0.006981622
57	1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,94,95	-0.573949415, -0.222593398, -0.911068943, 0.585972909, -0.001753823, 0.074395641, 0.0496691, -0.004044469, 0.008737105, -0.692744523, 0.218260483, 0.009328335, -0.323782443, 0.23493037, 0.096578425, 0.107074979, -0.266192068, -0.949792795, -0.272522458, -0.000622463, -1.154880753, -0.191744295, 0.613322445, -0.16273277, 0.287382831, 0.00423268, -0.844376219, -0.629356447, 0.209522381, 0.197363686, -0.997959639, -0.074573187, -0.007754204, 0.05211777, -0.627217268, 0.663329595, 0.611221643, 0.247862345, 0.123890385, -0.5395614, 0.05318547, -0.119433997, 0.012792144, 0.033730308, 0.359618609, -1.081720479, -0.25521701, 0.216000954, -0.867701903, 0.056499474, 0.31313126, -1.01866695, -0.001460105, -0.16053967, 0.547040504, 0.016163087, -0.456865145, 0.057404856, -0.565162258, -0.562133773, -0.692357023, 0.504849464, -0.011954885, 0.152340694, 0.001631888, -0.024839975, 0.290138719, 0.569608802, 0.125253286, -0.130362303, -0.529478887, -0.004103353, 0.04910466, -0.29711853, -0.067846497, 0.035626887, -0.856443488, -0.519879421, 0.307860935, 0.307180201, -0.426395722, -0.309439932, -0.464704804, 0.207227661, -0.561911668, -0.542737649, 0.106781855, -0.556947839, -0.703182698, 0.27546087, 0.257819156, 0.117278244, 0.318352667
58	1,2,3,4,5,6,8,10,11,12,13,14,15,16,17,18,19,20,22,23,24,25,27,28,29,30,31,33,34,35,36,37,38,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,91,92,93,94,95	0.140438386, 0.166736795, 0.183005138, -0.008153737, -0.043094291, -0.114494387, -0.121730095, 0.11401574, -0.134083915, 0.036405696, 0.18138528, -0.05090808, -0.015550008, 0.00123514, 0.10309818, 0.230816323, 0.012409027, -0.108365648, 0.105466663, -0.028605738, 0.064738266, -0.028355819, 0.137556017, 0.101207412, -0.026237052, -0.068095005, 0.055916458, -0.098280081, -0.036520135, 0.238395752, -0.016201115, -0.136201901, -0.121561066, -0.111396039, 0.213359871, -0.00151322, 0.007160299, 0.081039697, 0.004038439, -0.119727675, 0.216453595, 0.05399937, -0.006041325, 0.013734868, -0.116882852, -0.100502814, 0.176686387, 0.001023154, 0.000927353, -0.051551732, 0.05443892, 0.00524095, -0.005433894, 0.115803977, 0.126043912, 0.09316599, -0.031033048, -0.197190999, -0.024512842, -0.003481209, -0.007743137, -0.116915101, 0.098031215, 0.013335784, 0.09380189, 0.000348653, 0.004785129, 0.157943888, -0.00135388, -0.026244125, 0.182551973, 0.039437552, -0.089434061, -0.016372213, 0.121741428, 0.18687747, 0.03199222, -0.05878454, 0.078632513, 0.100833762, -0.070278462, 0.066479309, -0.010423745, -0.032704616, -0.001388215, -0.051003315, -0.068226764
59	5,7,8,12,16,33,44,45,54,57,64,70,73,74,81,92	0.000886758, -0.044502781, 0.022037519, -0.060366254, -0.017593261, 0.004259134, -0.033850911, -0.20872877, -0.009601812, -0.007904904, 0.026674448, -0.020304538, -0.035008329, -0.00676894, -0.025533347, -0.148073299

Module	Outward regulated modules	Estimates (in the order of the modules presented in the previous column)
60	3,5,8,11,12,14,19,20,24,33,34,35,40,44,46,47,49,50,53,54,57,59,64,65,67,68,70,71,73,75,77,78,81,84,88,89,91,92,94	4.51E-05, -0.000529256, -0.004395413, -0.001188689, 0.005093984, -0.004607357, 0.005640178, -5.39E-05, 0.003719562, -0.003159788, -0.005794626, 3.66E-05, -0.008317288, 0.00208287, -0.000140022, 8.52E-05, -0.001119686, 0.002685671, 7.20E-05, -5.68E-05, 0.006096445, -0.000596638, -0.006177001, -0.005338445, -0.000474538, -0.003676469, 0.002916662, 0.001038116, -0.000197263, 0.001695562, -0.010774526, 0.004451179, -0.002726482, 0.003437912, -0.006121033, 0.005127004, -0.004152828, -0.002890642, -0.004054818
61	2,3,4,5,6,8,9,10,11,12,14,15,17,19,20,22,23,24,26,29,31,33,34,35,36,38,40,43,44,46,47,48,49,50,51,52,53,54,56,57,58,59,60,61,63,64,65,68,69,70,71,72,75,77,78,79,80,81,82,83,84,86,88,89,91,92,94	-0.060150149, -0.000156114, 0.016228115, 0.020113344, 0.057196838, 0.040985355, -0.005508421, -0.046003051, 0.131268923, -0.038628174, 0.018888617, 0.101014835, -0.059580793, -0.027358729, 0.047029441, -0.124924308, 0.031083802, -0.01590883, 0.118141842, 0.041889049, -0.016521478, 0.013144542, 0.061506144, -0.000124823, 0.029041172, 0.101664027, 0.105182106, 0.053560588, -0.099945453, 0.115332847, -0.000279481, -0.040387907, 0.010112515, -0.007055906, 0.142175944, 0.048425493, -0.0002433, 0.021978346, 0.020655646, -0.025285984, -0.003086922, 0.005419306, -0.038374468, -0.0941491, 0.043527754, 0.083541659, 0.057904525, 0.018928462, 0.108012731, -0.050395008, -0.002624871, -0.055389415, -0.078569601, 0.067569212, -0.020974066, -0.069695049, 0.12303395, 0.026492299, -0.080339839, -0.085209467, -0.010758243, -0.035992719, 0.03743772, -0.022734414, 0.017934188, 0.011642874, 0.043072982
62	12,16,19,34,39,46,49,59,64,70,76,92	-0.002972244, 0.015777338, -0.000108529, 0.001503361, -0.004579984, 5.06E-05, 0.000257993, 0.000394518, 0.000928036, -0.000166041, -0.008572366, 0.000748644
63	3,5,8,11,14,16,19,20,24,33,34,35,40,42,46,47,49,53,57,59,64,65,68,73,74,75,76,77,78,81,88,89,91,92,93,94	3.94E-05, -0.000285961, -0.0002275, -0.000615183, -0.002171662, -0.000269281, 0.002355511, -1.71E-05, 0.001583304, -0.00185406, -0.00252462, 3.26E-05, -0.004723113, 0.000843757, -6.93E-05, 6.40E-05, -0.000462866, 5.63E-05, 0.00283295, -0.000175905, -0.000447943, -0.002711287, -0.002042667, -0.000262208, -0.000150749, 0.000962153, 0.001075476, -0.005966721, 0.000347105, -0.000983652, -0.003148764, 0.000307683, -0.001690466, -0.001261101, 0.000864812, -0.002095543
64	5,7,8,11,12,14,16,19,24,29,32,33,34,39,42,43,45,46,48,49,50,54,55,57,58,59,60,64,66,68,70,71,73,74,75,76,84,91,92,93	0.00035564, -0.004424425, 0.000455953, 0.000344804, 0.036412929, -0.032353283, 0.047175177, 0.006131898, 0.062658346, -0.001504184, 0.017785906, 0.001962411, -0.001935882, -0.007124073, -0.002887752, 0.000591192, 0.002326423, 4.00E-05, 0.038317477, 0.000705618, 0.025822405, 0.000565015, 0.039800901, 0.00661338, 0.073973952, -0.010651178, 0.089438056, 0.001356478, -0.002605331, 0.001181388, 0.0033102, 0.012906008, 0.078562495, 0.005347059, 0.013588124, -0.001954809, 0.019886833, -0.013851808, 0.000651116, -0.000771931
65	5,8,11,14,19,33,40,50,54,59,64,65,68,77,81,88,89,92,94	-0.003026879, -0.000198029, -0.000100108, -0.000386862, 0.004755479, -0.001008715, -0.003950404, 0.001349811, 0.000197263, -0.003931778, -0.002275162, -0.001905157, -0.003494549, -0.004634066, -0.001316685, -0.002211354, 0.002036026, -0.001313847, -0.002354299
66	1,2,3,4,6,7,9,10,11,12,13,14,17,18,19,21,22,23,24,25,26,27,28,30,31,32,34,35,36,37,39,40,41,42,43,44,46,47,48,49,50,51,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,75,76,78,79,81,82,83,84,85,86,87,89,90,91,92,93,94,95	0.966336074, 0.392564412, 2.014854362, -0.088941493, -0.112186287, -0.025712287, -0.023297036, 1.009188205, -0.211086474, 0.0136912, 0.840583499, -0.342485102, 0.545513676, 1.837372274, 0.123374945, 2.642995366, 0.139693826, -0.258174909, 0.460493916, -0.094049674, -0.019206116, 1.717770723, 1.184901803, -0.410053442, 1.982774683, 0.05947901, -0.094872531, 1.583961455, -0.301484622, -0.432079554, -0.122861238, -0.21622101, 1.763954463, -0.031234424, 0.125880246, 0.660988277, -0.336113817, 1.902535582, 0.53008456, -0.013011266, 0.810918899, -0.487759754, 1.88160764, 0.001397697, 0.045328279, -0.165368038, 0.112687878, 0.35763644, -0.052471593, 0.877962664, 1.06217531, 1.363450298, -0.115331214, -6.93E-05, -0.027928396, -0.033281248, 0.042886737, -0.189739008, -0.503942109, 0.00056441, 0.041704732, 1.087350752, 0.75034396, -0.024097218, 2.178851104, 1.841404355, -0.115589772, 0.837499134, 0.664896803, 0.595890794, -0.281112842, 0.83414188, 1.113406467, 0.837122502, 1.516060766, -0.22945382, -0.00403914, -0.00649751, -0.010152012, -0.008101705

Module	Outward regulated modules	Estimates (in the order of the modules presented in the previous column)
67	1,2,3,4,5,6,8,9,10,11,12,13,14,15,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,33,34,35,36,37,38,40,41,44,46,47,48,49,50,51,52,53,54,56,57,59,60,61,62,63,64,65,68,69,70,71,72,75,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,94,95	0.541949003, 0.242949559, 1.69231349, -0.088618549, -0.000581503, -0.472479379, -0.047594373, 0.000698203, 0.334873329, -0.441833158, 0.02533189, 0.373301456, -0.17450571, -0.062751812, 0.332390908, 1.451823726, 0.025927939, -1.461826889, 1.739694588, 0.092480978, -0.064122826, 0.165200127, -0.198601357, -0.465993614, 1.068842059, 0.401095598, -0.098602156, -0.543731768, 1.391960396, -0.003039744, -0.17936727, 2.084926655, -0.100110856, -0.968671999, -0.727975417, -0.301241565, 0.803611778, 2.404837813, -0.558210506, 1.355649283, 0.105240909, -0.001787043, 0.032438425, -0.851387035, -0.528383914, 1.125861067, -0.00022615, -0.27380041, 0.079449203, -0.000951894, 0.186116389, 0.260014447, 0.629886593, -0.089553394, -0.0107385, -0.205818112, -0.005579432, -0.510471759, 0.082045754, 0.001889903, 0.261872177, 0.491488129, -0.056029251, 1.799854449, 2.110769107, -0.258099255, -0.032171873, 0.210351664, 0.40984566, 0.025222859, -0.127151412, 0.32179312, 0.381659218, -0.012071922, 0.227263175, 0.713355164, -0.021009891, -0.002960114, -0.124867403, -0.648398707
68	5,8,11,12,14,15,19,20,24,29,33,34,35,46,49,50,57,59,64,65,68,70,71,74,75,77,81,88,89,91,92,93,94	-0.004741795, -0.005663638, -0.000702851, 0.007478292, -0.008681414, -0.02615621, 0.010292414, -3.32E-05, 0.00457001, -0.031007623, -0.001620941, -0.01053781, 8.14E-08, -0.000147418, -0.001289419, 0.001714563, 0.007543882, -0.000990031, -0.008056111, -0.002005509, -0.003605771, 0.000127684, 0.001704666, -4.16E-05, 0.002455752, -0.009243804, -0.001697841, -0.003275504, 0.000244485, -0.005236083, -0.004190489, 0.0748434, -0.023855336
69	1,2,3,4,5,6,8,10,11,12,13,14,17,18,19,20,23,24,27,28,29,30,31,33,34,35,36,37,38,40,41,44,46,47,48,49,50,51,53,57,59,60,61,62,64,65,68,69,70,71,72,75,77,78,79,81,82,83,84,86,87,88,89,91,92,93,94	-0.115152904, -0.06146274, -0.187656031, 0.007423997, 0.006262833, 0.051889978, 0.018675784, -0.038104065, 0.044745434, -0.011420427, -0.073997858, 0.005035184, -0.050979536, -0.190275991, -0.007814939, 0.021018043, 0.007612957, -0.015023029, -0.174871211, -0.061618994, 0.008149799, 0.03290018, -0.135966384, 0.003771772, 0.007389006, -0.254732177, 0.006464748, 0.073918036, 0.034292867, 0.03049606, -0.106369914, -0.27867825, 0.041748216, -0.196405235, -0.009466717, 0.001176886, -0.00323716, 0.126839725, -0.140551359, -0.029442665, 0.000648244, -0.003815518, -0.031374653, -0.056188977, 0.01433384, 0.012634669, 0.005468699, 0.024794282, -0.019409828, -0.000712531, -0.041782471, -0.007051882, 0.013284908, -0.215188958, -0.015581864, 0.003374752, -0.021963499, -0.055270745, -0.004131219, -0.043902016, -0.056634445, 0.008262242, -0.044090226, 0.005107745, 0.003380982, 0.000509132, 0.004298629
70	2,3,4,5,6,8,10,11,12,14,15,16,19,20,22,23,24,25,26,29,31,33,34,35,36,40,43,44,45,46,47,49,50,52,53,54,56,57,59,63,64,65,68,69,70,71,73,75,77,78,80,81,82,84,85,86,88,89,90,91,92,94,95	0.021886014, 0.000108175, -0.045114943, -0.027846173, -0.013615315, -0.007650383, 0.029969894, -0.00164153, 0.007237528, -0.009556399, -0.037049106, -0.000599076, 0.015243049, -6.37E-05, 0.050137127, -0.031570381, 0.005421493, -0.046179504, -0.033164848, -0.021133016, 0.025070024, -0.005651759, -0.02118408, 8.86E-05, -0.042437141, -0.020895937, -3.51E-05, 0.034183056, -0.001223753, -0.000312072, 0.000164044, -0.001902489, 0.005297376, -0.028716674, 0.000146651, -0.000517415, -0.077496314, 0.010072781, -0.001031092, -0.044239054, -0.013928871, -0.028050477, -0.011727741, -0.016848372, 7.08E-05, 0.001431597, -0.009465964, 0.002055117, -0.035001793, 0.014006204, -0.061621564, -0.038039956, 0.037825781, 0.014362972, -0.023763391, 0.02775335, -0.013995362, 0.015108287, 0.094815672, -0.013415833, -0.007676801, -0.02414172, -0.049178704
71	19,49,59	0.000175632, -0.000364697, -0.000247428
72	5,11,19,24,33,42,49,50,54,57,59,64,65,75,81,88,89	-0.000117391, -0.00022694, 0.003196113, 0.000614887, -0.001310605, -0.000399307, -0.000181772, 0.002708609, 0.001467992, 0.003019245, -0.001801539, -0.000509002, -0.00116345, 0.000275523, -0.001386458, -0.00116555, 0.000666581
73	3,5,7,11,14,19,23,24,29,31,32,33,34,35,40,42,47,49,50,53,54,55,57,58,59,64,65,66,68,70,71,73,75,76,77,81,84,88,89,91,92,93,94	-1.26E-05, 0.001491019, 0.003032384, 0.000396435, 0.002341894, -0.007798814, 0.014596068, -0.000820932, 0.006117995, -0.016921977, -0.001495147, 0.001609394, 0.000954724, -7.22E-06, 0.005778958, 0.002185051, -2.45E-05, 0.000661986, -0.003727072, -2.13E-05, -0.000271513, -0.000985936, -0.002377131, -0.001975148, 0.003863278, 0.000555715, 0.004018311, 0.003045946, 0.005644176,

Module	Outward regulated modules	Estimates (in the order of the modules presented in the previous column)
		1.63E-05, -0.002376499, -0.0006021, -0.000296299, 0.001038144, 0.007440048, 0.003273712, -0.007775471, 0.003641593, -0.006943854, 0.007529295, 0.001671755, 0.000723233, 0.005830406
74	54	-2.53E-05
75	1,2,3,4,5,6,8,9,10,11,12,13, 14,15,17,19,20,21,22,23, 24,25,27,28,29,30,31,33, 34,35,36,40,43,44,46,47, 48,49,50,51,53,54,55,57, 59,60,61,62,63,64,65,67, 68,69,71,72,74,75, 77,78,79,81,82,83,84, 85,86,87,88,89,91,92,94	0.063387785, 0.027953896, 5.43E-05, -0.023220434, -0.005366797, -0.071937188, -0.005605965, 0.006274247, 0.036236889, -0.080422421, 0.005014622, 0.110732542, -0.002847722, -0.052427746, 0.050612801, 0.005274609, -0.049213305, 0.142820903, 0.050436457, -0.02380335, 0.003994239, -0.054197417, 0.103412784, 0.064558943, -0.021639117, -0.086431868, 0.091827567, -0.001444672, -0.006705863, 3.80E-05, -0.021922136, -0.043434526, -0.035312124, 0.018253026, -0.076479007, 9.63E-05, 0.02206802, -0.000340255, 0.00134824, -0.095513502, 8.34E-05, -0.04195576, -0.008756824, 0.015744291, -0.002350056, 0.024056775, 0.07450948, 0.079919391, -0.031020115, -0.021633614, -0.014627168, -0.000632806, -0.003168757, -0.038850956, 0.000191361, 0.050145292, -0.04640418, 0.037008022, -0.02430295, 0.012700667, 0.102768523, -0.014151726, 0.047769669, 0.069377899, 0.006237827, -0.076093883, 0.039863134, 0.110775927, -0.011492541, 0.022295449, -0.004151645, -0.026289577, -0.013277026
76	9,19,45,49,50,59,67,81	-0.006199964, 0.000890728, -0.032753368, -0.000993465, 0.005241639, -0.001267657, 0.000332941, -0.072973233
77	1,2,3,4,5,6,7,8,10,11,12,13, 14,15,17,19,20,22,23,24, 25,26,27,28,29,30,31,32, 33,34,35,36,37,38,39,40, 41,42,44,46,47,48,49,50, 51,52,53,54,55,56,57,58, 59,60,61,63,64,65,66,68, 69,70,71,72,73,75,77,78, 79,80,81,82,83,84,85,86, 87,88,89,91,92,93,94,95	0.324555352, 0.2419679, 0.000205766, -0.044682935, -0.050530014, -0.311250961, -0.007168938, -0.148410092, 0.195279479, -0.247191621, 0.114724292, 0.310439437, -0.13354245, -0.180644064, 0.244800669, 0.050326328, -0.100879526, 0.184535517, -0.094811312, 0.118884602, -0.133438163, -0.110858705, 0.33115318, 0.250994619, -0.116874628, -0.214568477, 0.245450859, 0.007391851, -0.066118528, -0.123565393, 0.000149592, -0.080739801, -0.224217088, -0.226139341, -0.011991507, -0.303406887, 0.305119045, -0.004819217, 0.16470644, -0.305278758, 0.000411477, 0.143373953, -0.013216085, 0.052800933, -0.230087374, -0.112778918, 0.000350731, 0.001199808, 0.001829441, -0.008385797, 0.173149636, 0.016099721, -0.023397132, 0.138518204, 0.215360442, -0.071300759, -0.368501684, -0.073297694, -0.007520134, -0.033671274, -0.189137915, 0.204775595, 0.030014919, 0.240507593, 0.00075413, 0.200258589, -0.124174577, 0.045611225, 0.224398994, -0.085520345, -0.044624797, 0.192171039, 0.292859488, 0.084997947, -0.045036425, 0.164320673, 0.265678587, -0.055055332, 0.140871679, -0.071618427, -0.099843671, -0.002700906, -0.093671279, -0.087964734
78	5,8,11,12,14,16,19,24,33, 34,39,42,49,50,54,55,57, 58,59,64,65,66, 67,68,70,71,74, 75,76,81,84,88, 89,92,93,94	-0.000315901, -0.002470096, -0.000392772, 0.007286963, -0.003042686, 0.000189873, 0.004346628, 0.000824402, -0.002461273, -0.003517241, -0.003128299, -0.000302516, -0.000737012, 0.001136425, 0.000994066, 0.000251823, 0.004135324, 0.001491051, -0.001997093, -0.003200998, -0.002422346, -0.002838484, -0.000462036, -0.003188568, 0.004790718, 0.001200017, 0.021814245, 0.001141281, -0.010122064, -0.001247412, 0.001170625, -0.002209116, 0.000397597, -0.001243932, -0.008015218, -0.002615856
79	No outward regulation	
80	5,8,11,14,19,24,34, 40,46,49,50,59, 64,65,68,71,75,81, 88,89,91,92,94	0.001255914, 7.93E-05, 0.000586452, 0.000872333, -0.001989207, -0.000480778, 0.000647982, 0.005384774, 8.19E-05, 0.000304989, -0.001087392, 0.00019802, 0.000459734, 0.002191401, 0.000939502, -0.000104359, -0.000363585, 0.001144719, 0.002465329, -0.001951239, 0.003289843, 0.00128206, 0.001253081
81	16,32,39,42,49,54,55, 59,66,70,73,76,93	-0.000369652, -0.002643247, 0.002785408, 0.00041058, -0.000221102, -9.79E-05, -0.000240792, 0.015112736, 0.000652944, 2.21E-05, -0.000139034, 0.000463859, 0.000159977
82	5,7,12,19,29,32,39,42,49, 50,54,55,58,59,66,70,71	-0.004096424, -0.005853585, 0.001084158, -0.000136893, -0.002195489, 0.002903433, -0.000563778, -0.00897154, -0.003182872, 0.005337171, 5.07E-05, 0.000528703, 0.000835198, -0.005023799, -0.000443602, 0.007171532, 0.003791159

Module	Outward regulated modules	Estimates (in the order of the modules presented in the previous column)
83	5,8,11,12,14,19,23,24,29,33,34,40,42,46,49,50,54,57,58,59,64,65,68,70,71,75,77,81,84,88,89,91,92,93,94	0.001437584, 0.001831861, 0.000614649, -0.003656718, 0.003641795, -0.008902009, 0.011896535, -0.002741921, 0.011368362, 0.00372809, 0.004583515, 0.006551051, 0.001989395, 2.62E-05, 0.000657578, -0.00240878, -0.000185688, -0.005984412, -0.001822934, 0.004113201, 0.002919846, 0.004343576, 0.005808184, -0.005925999, -0.002846831, -0.001220607, 0.00983101, 0.00240227, -0.003719182, 0.004636709, -0.003607711, 0.004518612, 0.001831847, 0.000870147, 0.010363576
84	2,3,4,5,6,8,10,11,12,14,15,17,19,20,23,24,29,31,33,34,35,40,44,46,47,48,49,50,53,57,59,60,63,64,65,68,70,71,72,75,77,78,81,83,84,86,88,89,91,92,94	-0.034173362, -0.000100736, 0.014184374, 0.011054298, 0.033113835, 0.017572033, -0.031849746, 0.001628543, -0.014363165, 0.006275554, 0.015166537, -0.027812433, -0.006692416, 0.023668553, 0.014821441, -0.021934422, 0.012679291, -0.016479319, 0.003900396, 0.012117451, -7.97E-05, 0.040277293, -0.046332211, 0.000306567, -0.000182856, -0.026540151, 0.000996041, -0.002016973, -0.000158829, -0.027443498, 0.000452772, -0.021812537, 0.026362516, 0.025085692, 0.014931947, 0.00301004, -0.01761999, -0.000938524, -0.031724499, -0.036998111, 0.022473831, -0.013305447, 0.015778512, -0.037862842, -0.005096695, -0.026419135, 0.016307569, -0.010011142, 0.006608437, 0.004111445, 0.016090835
85	2,3,5,6,8,10,11,12,14,15,19,20,23,24,29,31,33,34,35,40,44,46,47,48,49,50,53,57,59,60,62,64,65,68,70,71,75,77,78,81,84,86,88,89,91,92,94	0.018918531, 0.000134633, -0.006894716, -0.021530759, -0.00697241, 0.023047194, -0.002418716, 0.00855521, -0.00886016, -0.012366417, 0.011261048, -7.74E-05, -0.015518672, 0.006124176, -0.010963114, 0.02093956, -0.006215515, -0.011679179, 0.000101066, -0.024179652, 0.023670414, -0.000336835, 0.000241069, 0.014196127, -0.001897499, 0.003939115, 0.00020846, 0.012240052, -0.001076913, 0.011591342, 0.100858317, -0.011077875, -0.016454644, -0.007756401, 0.000148551, 0.001554138, 0.018782542, -0.015092312, 0.007614413, -0.010956926, 0.00668879, 0.020309022, -0.017365945, 0.01305153, -0.00713773, -0.00589196, -0.008070931
86	3,14,19,24,35,46,47,49,50,53,59,64,65,68,70,71,81,89,91,92,94	-7.08E-06, 0.001238302, -0.002573762, -0.000451304, -6.46E-06, 1.85E-06, -1.27E-05, 0.000345741, -0.000137123, -1.14E-05, 0.000244107, 0.000602454, 0.001374922, 0.007495853, -4.46E-05, -0.000293031, 0.001464294, -0.000483139, 0.001196719, 0.000847448, 0.001691755
87	5,8,11,12,14,19,24,33,34,42,43,46,49,50,57,58,59,64,65,66,68,70,71,75,76,81,84,88,89,91,92,94	-0.000405485, -0.000442857, -0.001079206, 0.003205293, -0.00389072, 0.003805553, 0.003691098, -0.002895347, -0.003528843, -0.006703842, 0.000425258, -0.000141615, -0.001219005, 0.00420323, 0.005187135, 0.000367966, -0.011238715, -0.001498022, -0.003740626, -0.034652721, -0.003145338, 1.21E-05, 0.000841448, 0.001184566, -0.002100703, -0.001959106, 0.00405308, -0.003035273, 0.00352488, -0.005941643, -0.002461158, -0.003544
88	3,5,7,8,11,12,14,16,19,22,23,24,25,29,32,33,34,35,39,40,42,44,45,46,47,48,49,50,53,54,55,57,58,59,63,64,65,66,68,70,71,74,75,76,77,78,81,84,88,89,91,92,93,94	3.85E-05, -0.023532824, -0.019630684, -0.051361259, -0.002186379, 0.018134595, -0.038333839, 0.000838897, 0.017313387, 0.064686191, -0.013029191, 0.006666436, -0.014159842, -0.023218457, 0.008888874, -0.006561262, -0.032515956, 4.44E-05, -0.004159875, -0.025573261, -0.000874326, 0.012411394, -0.027223945, -0.000368195, 7.39E-05, 0.034554661, -0.003951669, 0.012399032, 6.63E-05, 0.000956326, 0.001008909, 0.029140982, 0.001872953, -0.010993972, -0.019246582, -0.014726556, -0.020862512, -0.002015254, -0.009163082, 0.02390919, 0.008531561, 0.000484449, 0.003594446, -0.00042595, -0.024892649, 0.007362066, -0.031145576, 0.018368314, -0.018175012, 0.003458151, -0.012967594, -0.057367227, -0.001315385, -0.018603254
89	3,6,8,11,12,14,15,19,24,33,34,35,46,47,49,50,53,57,59,64,65,68,70,71,75,77,81,88,89,91,92,94	-1.49E-05, 0.002346761, 0.000170238, 0.000423723, -0.001803472, 0.000883108, 0.006665408, -0.001336147, -0.000365871, 0.001408536, 0.00156105, -1.01E-05, 2.86E-05, -2.58E-05, 0.000102433, -0.000304854, -2.23E-05, -0.002530662, 9.12E-05, 0.000397151, 0.001837681, 0.001353601, -2.45E-05, -0.000137012, -0.000577651, 0.000968585, 0.000967718, 0.002365488, -0.001557199, 0.00033358, 0.000626334, 0.00081315
90	3,5,7,8,11,12,14,19,20,24,32,33,34,35,40,42,43,44,46,47,49,53,55,57,58,59,64,65,68,70,71,73,75,81,88,89,91,92,94	-6.95E-06, 0.004274374, -0.000754613, 0.00329264, 0.000972088, -0.006615041, 0.002773951, -0.003252816, 1.19E-05, -0.001937176, 0.002804779, 0.003556635, 0.003484702, -1.10E-05, 0.000962729, -0.003919449, 0.001459776, -0.005037848, 0.000117825, -9.17E-06, 0.000972883, -9.07E-06, 0.094251019, -0.005806259, 0.026930659, -0.000908847, 0.004863155, 0.003445154, 0.002562843, -0.010519312,

Module	Outward regulated modules	Estimates (in the order of the modules presented in the previous column)
		0.015293303, 0.000490691, -0.001320481, 0.001162978, 0.003292198, -0.000311891, 0.001894542, 0.002179181, 0.002758221
91	5,8,11,12,19,33,49,55,57, 58,59,64,67,70,71,75,84,93	0.00059568, 0.000555172, 0.000254223, -0.020445061, -0.000347659, 0.053462043, 0.000433297, -0.00031775, -0.004797482, -0.003629894, 0.004261129, 0.003140809, 0.000301821, -0.058836699, -0.008990721, -0.000208887, -0.006480615, 0.064375377
92	2,3,4,5,6,8,10,11,12,13,14, 15,17,19,20,22,23,24,25,26, 29,30,31,33,34,36,38,40,44, 46,47,48,49,50,51,52,53, 56,57,58,59,60,61,63,64,65, 68,69,70,71,72,75,77,78, 79,80,81,82,83,84,85, 86,87,88,89,91,92,94	-0.067895962, -0.000114292, 0.008940712, 0.014039006, 0.089297421, 0.022325786, -0.051544484, 0.124296165, -0.017787004, -0.126101664, 0.009382439, 0.018776235, -0.042645973, -0.013083375, 0.1183121, -0.119791668, 0.024144187, -0.097715833, 0.059732348, 0.116273475, 0.025442042, 0.064789013, -0.019363519, 0.005521054, 0.045987399, 0.04278387, 0.058821464, 0.064187852, -0.058710259, 0.11481008, -0.000209587, -0.104791907, 0.004205515, -0.002581586, 0.133200457, 0.062280969, -0.00018122, 0.064292746, -0.036228711, -0.002476541, 0.00307211, -0.134396968, -0.092678907, 0.025471812, 0.031150777, 0.03287539, 0.012519252, 0.099055915, -0.021994037, -0.005877669, -0.079189682, -0.065846001, 0.0265303, -0.01140088, -0.068755138, 0.086763365, 0.014873611, -0.084873317, -0.060984112, -0.035570262, 0.084769446, -0.040773015, -0.092324716, 0.021100162, -0.059667173, 0.010765145, 0.006294448, 0.018148739
93	3,7,19,20,24,31,35,39,42, 47,49,50,53,54,55,58,66,70, 71,73,74,76,78,81,89,93	3.75E-05, 0.000759, 2.00E-05, -1.46E-05, 0.007045777, 0.005630099, 3.11E-05, 0.000586527, 0.000520005, 6.90E-05, -0.000145095, -0.00180166, 5.92E-05, -0.004368303, -0.006941439, -0.003671298, 0.004836073, -2.12E-05, -0.010181074, -0.000590114, -0.000933748, 0.007022371, 0.002267097, -0.000664209, 0.001107351, 0.000601944
94	20,35,49,59,64,70,71	2.09E-06, -5.55E-05, -0.000144375, -0.000215981, -1.43E-05, 0.000147721, 0.000282723
95	3,5,8,11,12,14,19,20,23,24, 29,33,34,40,44,46,47,49,50, 53,57,59,64,65,68,70,71,75, 77,78,81,84,88,89,91,92,94	2.81E-05, -0.001940943, -0.001645714, -0.000779241, 0.002965223, -0.002893049, 0.003233981, -7.06E-06, -0.003523568, 0.002111156, -0.003800344, -0.002205338, -0.003810214, -0.005232111, 0.002751042, -0.000113394, 5.50E-05, -0.000676628, 0.001645059, 4.77E-05, 0.004082046, -0.000390694, -0.003256047, -0.003413248, -0.002259363, 6.72E-06, 0.000577668, 0.001017683, -0.005132528, 0.002680398, -0.001674741, 0.00211225, -0.003819801, 0.002834337, -0.00230663, -0.001938334, -0.002489782

Appendix

Appendix C.

Summary of outward regulation.

Module	Number of outward regulated modules	Outward regulated modules
1	15	4,5,15,25,36,49,54,59,63,64,68,70,74,81,92
2	15	7,19,20,23,25,29,36,42,63,68,81,85,91,92,94
3	11	5,8,11,19,49,54,59,64,70,81,92
4	14	3,8,11,19,20,35,46,47,49,50,53,57,59,64
5	10	3,19,35,47,49,53,54,59,70,78
6	6	12,42,49,54,70,93
8	36	3,5,8,11,12,14,19,20,24,31,33,34,35,40,44,46,47, 49,50,53,54,57,59,64,65,68,70,75,77,78,81,88,89,91,92,94
9	86	1,2,3,4,5,6,7,8,10,11,12,13,14,15,16,17,18,19,20,21, 23,24,25,27,28,29,30,31,32,33,34,35,36,37,38,39, 40,41,42,44,45,46,47,49,50,51,52,53,54,55,56,57, 59,61,62,63,64,65,66,67,68,69,70,71,73,74,75,76, 77,78,79,80,81,82,83,85,86,87,88,89,90,91,92,93,94,95

Module	Number of outward regulated modules	Outward regulated modules
10	29	3,8,11,12,14,19,24,33,34,35,47,49,50,53,57,59,64,65,67,68,70,71,75,81,84,88,89,91,92
11	9	3,35,45,46,47,49,53,54,59
12	31	5,7,8,11,12,14,19,20,24,32,33,34,35,40,44,46,49,50,57,59,64,65,68,70,71,75,81,88,89,92,94
13	34	3,7,11,16,19,20,24,32,35,39,42,46,47,49,50,53,54,55,57,58,59,64,65,66,68,70,73,74,76,78,81,88,89,93
14	40	2,5,8,11,12,14,16,19,23,24,29,34,40,42,44,49,54,57,58,59,64,65,67,68,70,71,72,74,75,77,81,84,85,86,88,89,91,92,93,94
15	42	3,5,6,8,11,12,14,15,19,20,23,24,29,31,33,34,35,40,44,46,47,48,49,50,53,57,59,64,65,68,70,71,75,77,78,81,84,88,89,91,92,94
16	32	3,5,8,11,12,14,19,24,33,34,35,40,42,46,47,49,53,54,57,59,64,65,68,70,71,73,75,76,88,91,92,94
17	79	1,2,3,4,5,6,7,8,10,11,12,13,14,15,17,18,19,20,22,23,24,25,26,27,28,29,30,31,33,34,35,36,37,38,40,41,42,44,46,47,48,49,50,51,52,53,56,57,58,59,60,62,63,64,65,66,68,69,70,71,72,75,77,78,79,80,81,82,83,84,85,86,88,89,90,91,92,94,95
18	19	5,8,11,14,24,34,42,50,54,55,57,64,65,70,71,73,75,84,88
19	6	16,19,45,49,50,59
20	50	2,3,5,6,8,10,11,12,14,15,19,23,24,29,31,33,34,35,40,44,45,46,47,48,49,50,53,54,57,58,59,60,64,65,68,70,71,72,75,77,78,81,83,84,88,89,91,92,93,94
21	39	5,7,8,11,12,14,16,19,20,24,29,32,33,34,39,42,43,49,54,55,57,58,59,64,65,66,67,70,71,73,74,75,76,81,88,91,92,93,94
22	90	1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,26,27,28,29,30,31,32,33,34,35,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,59,60,61,62,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,86,87,88,89,90,91,92,93,94,95
23	24	3,7,16,19,32,35,39,42,46,47,49,53,54,55,58,59,66,68,71,73,74,76,91,93
25	34	3,5,8,11,14,15,19,20,24,33,34,35,40,44,46,47,49,50,53,57,59,64,65,68,70,75,77,78,81,84,88,89,92,94
26	24	5,8,11,12,14,19,24,33,34,40,49,54,57,59,64,65,68,70,71,75,77,88,92,94
27	43	5,7,8,11,12,14,16,19,24,33,34,39,42,43,45,48,49,50,54,55,57,58,59,60,64,65,66,67,68,70,71,72,73,74,75,76,81,84,88,89,91,92,93
28	40	3,5,8,11,12,14,15,19,20,23,24,29,33,34,35,40,42,46,47,49,50,53,54,57,59,64,65,68,70,71,73,75,77,78,81,88,89,91,92,94
30	81	1,2,3,4,5,6,8,10,11,12,13,14,15,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,33,34,35,36,37,38,40,41,44,45,46,47,49,50,51,52,53,54,56,57,58,59,60,61,62,63,64,65,68,69,70,71,72,75,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95
31	26	5,8,11,14,16,19,24,33,34,40,49,54,57,59,64,65,68,75,81,84,88,89,91,92,93,94

Module	Number of outward regulated modules	Outward regulated modules
32	85	1,2,3,4,5,6,7,8,10,11,12,13,14,15,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,33,34,35,36,37,38,39,40,41,44,45,46,47,48,49,50,51,52,53,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,75,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95
33	49	2,4,5,8,10,11,12,14,15,17,19,23,24,29,31,32,33,34,40,42,43,46,49,50,54,55,57,58,59,60,64,65,68,70,71,72,75,77,78,81,83,84,86,88,89,91,92,93,94
34	42	3,5,8,10,11,12,14,15,19,20,23,24,29,31,33,34,35,40,44,46,47,49,50,53,54,57,59,64,65,68,71,75,77,78,81,84,86,88,89,91,92,94
35	29	5,8,11,14,19,20,24,33,34,42,46,49,50,54,57,58,59,64,65,68,70,71,73,75,81,88,89,91,92
36	11	3,7,20,35,47,49,53,54,68,73,93
38	41	3,5,8,11,12,14,19,20,23,24,29,33,34,35,40,44,46,47,48,49,50,53,54,57,58,59,64,65,68,70,71,75,77,78,81,84,88,89,91,92,94
39	95	1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95
40	33	3,5,8,11,12,14,19,20,24,33,34,35,40,46,47,49,50,53,57,59,64,65,68,70,71,75,77,81,88,89,91,92,94
41	74	1,2,3,4,5,6,8,10,11,12,13,14,15,17,19,20,21,22,23,24,25,27,28,29,30,31,32,33,34,35,36,40,42,43,44,46,47,48,49,50,51,53,54,57,58,59,60,61,62,63,64,65,66,68,69,70,71,72,75,77,78,79,81,82,83,84,86,87,88,89,91,92,93,94
42	27	4,5,7,9,14,16,19,23,29,32,36,39,42,49,50,54,58,59,63,66,68,71,81,84,91,92,94
43	21	2,6,8,10,12,17,19,20,29,33,40,49,59,64,68,70,75,81,83,86,94
44	22	3,5,9,19,20,32,35,42,49,50,54,55,57,58,66,70,71,73,74,76,84,93
45	33	3,5,8,11,12,14,19,24,29,33,34,35,40,44,45,46,47,49,53,57,59,64,65,68,70,71,75,77,81,88,89,91,92
46	6	19,49,50,59,64,71
47	15	16,32,42,43,49,54,55,58,59,66,71,73,74,76,93
49	93	1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,44,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95
50	50	2,5,7,8,11,12,13,14,16,19,20,22,24,29,32,33,34,39,40,41,42,48,49,51,54,55,57,58,59,60,64,65,66,68,69,70,71,72,73,75,77,81,82,83,88,89,91,92,93,94
51	9	5,8,12,20,44,49,54,64,70
52	32	3,5,8,11,12,14,19,20,24,33,34,35,46,47,49,50,53,57,59,64,65,68,70,71,75,81,84,88,89,91,92,94
53	23	8,12,34,35,39,42,43,46,50,54,55,58,59,64,66,70,71,73,74,75,76,84,93

Module	Number of outward regulated modules	Outward regulated modules
55	85	1,2,3,4,5,6,8,10,11,12,13,14,15,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,33,34,35,36,37,38,39,40,41,42,44,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,68,69,70,71,72,75,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95
56	34	5,8,11,12,14,19,23,24,29,33,34,40,46,49,50,54,57,58,59,64,65,68,70,71,75,77,81,84,88,89,91,92,93,94
57	93	1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,94,95
58	87	1,2,3,4,5,6,8,10,11,12,13,14,15,16,17,18,19,20,22,23,24,25,27,28,29,30,31,33,34,35,36,37,38,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,91,92,93,94,95
59	16	5,7,8,12,16,33,44,45,54,57,64,70,73,74,81,92
60	39	3,5,8,11,12,14,19,20,24,33,34,35,40,44,46,47,49,50,53,54,57,59,64,65,67,68,70,71,73,75,77,78,81,84,88,89,91,92,94
61	67	2,3,4,5,6,8,9,10,11,12,14,15,17,19,20,22,23,24,26,29,31,33,34,35,36,38,40,43,44,46,47,48,49,50,51,52,53,54,56,57,58,59,60,61,63,64,65,68,69,70,71,72,75,77,78,79,80,81,82,83,84,86,88,89,91,92,94
62	12	12,16,19,34,39,46,49,59,64,70,76,92
63	36	3,5,8,11,14,16,19,20,24,33,34,35,40,42,46,47,49,53,57,59,64,65,68,73,74,75,76,77,78,81,88,89,91,92,93,94
64	40	5,7,8,11,12,14,16,19,24,29,32,33,34,39,42,43,45,46,48,49,50,54,55,57,58,59,60,64,66,68,70,71,73,74,75,76,84,91,92,93
65	19	5,8,11,14,19,33,40,50,54,59,64,65,68,77,81,88,89,92,94
66	80	1,2,3,4,6,7,9,10,11,12,13,14,17,18,19,21,22,23,24,25,26,27,28,30,31,32,34,35,36,37,39,40,41,42,43,44,46,47,48,49,50,51,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,75,76,78,79,81,82,83,84,85,86,87,89,90,91,92,93,94,95
67	80	1,2,3,4,5,6,8,9,10,11,12,13,14,15,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,33,34,35,36,37,38,40,41,44,46,47,48,49,50,51,52,53,54,56,57,59,60,61,62,63,64,65,68,69,70,71,72,75,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,94,95
68	33	5,8,11,12,14,15,19,20,24,29,33,34,35,46,49,50,57,59,64,65,68,70,71,74,75,77,81,88,89,91,92,93,94
69	67	1,2,3,4,5,6,8,10,11,12,13,14,17,18,19,20,23,24,27,28,29,30,31,33,34,35,36,37,38,40,41,44,46,47,48,49,50,51,53,57,59,60,61,62,64,65,68,69,70,71,72,75,77,78,79,81,82,83,84,86,87,88,89,91,92,93,94
70	63	2,3,4,5,6,8,10,11,12,14,15,16,19,20,22,23,24,25,26,29,31,33,34,35,36,40,43,44,45,46,47,49,50,52,53,54,56,57,59,63,64,65,68,69,70,71,73,75,77,78,80,81,82,84,85,86,88,89,90,91,92,94,95

Module	Number of outward regulated modules	Outward regulated modules
72	17	5,11,19,24,33,42,49,50,54,57,59,64,65,75,81,88,89
73	43	3,5,7,11,14,19,23,24,29,31,32,33,34,35,40,42,47,49,50,53,54,55,57,58,59,64,65,66,68,70,71,73,75,76,77,81,84,88,89,91,92,93,94
75	73	1,2,3,4,5,6,8,9,10,11,12,13,14,15,17,19,20,21,22,23,24,25,27,28,29,30,31,33,34,35,36,40,43,44,46,47,48,49,50,51,53,54,55,57,59,60,61,62,63,64,65,67,68,69,71,72,74,75,77,78,79,81,82,83,84,85,86,87,88,89,91,92,94
76	8	9,19,45,49,50,59,67,81
77	84	1,2,3,4,5,6,7,8,10,11,12,13,14,15,17,19,20,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,44,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,63,64,65,66,68,69,70,71,72,73,75,77,78,79,80,81,82,83,84,85,86,87,88,89,91,92,93,94,95
78	36	5,8,11,12,14,16,19,24,33,34,39,42,49,50,54,55,57,58,59,64,65,66,67,68,70,71,74,75,76,81,84,88,89,92,93,94
80	23	5,8,11,14,19,24,34,40,46,49,50,59,64,65,68,71,75,81,88,89,91,92,94
81	13	16,32,39,42,49,54,55,59,66,70,73,76,93
82	17	5,7,12,19,29,32,39,42,49,50,54,55,58,59,66,70,71
83	35	5,8,11,12,14,19,23,24,29,33,34,40,42,46,49,50,54,57,58,59,64,65,68,70,71,75,77,81,84,88,89,91,92,93,94
84	51	2,3,4,5,6,8,10,11,12,14,15,17,19,20,23,24,29,31,33,34,35,40,44,46,47,48,49,50,53,57,59,60,63,64,65,68,70,71,72,75,77,78,81,83,84,86,88,89,91,92,94
85	47	2,3,5,6,8,10,11,12,14,15,19,20,23,24,29,31,33,34,35,40,44,46,47,48,49,50,53,57,59,60,62,64,65,68,70,71,75,77,78,81,84,86,88,89,91,92,94
86	21	3,14,19,24,35,46,47,49,50,53,59,64,65,68,70,71,81,89,91,92,94
87	32	5,8,11,12,14,19,24,33,34,42,43,46,49,50,57,58,59,64,65,66,68,70,71,75,76,81,84,88,89,91,92,94
88	54	3,5,7,8,11,12,14,16,19,22,23,24,25,29,32,33,34,35,39,40,42,44,45,46,47,48,49,50,53,54,55,57,58,59,63,64,65,66,68,70,71,74,75,76,77,78,81,84,88,89,91,92,93,94
89	32	3,6,8,11,12,14,15,19,24,33,34,35,46,47,49,50,53,57,59,64,65,68,70,71,75,77,81,88,89,91,92,94
90	39	3,5,7,8,11,12,14,19,20,24,32,33,34,35,40,42,43,44,46,47,49,53,55,57,58,59,64,65,68,70,71,73,75,81,88,89,91,92,94
91	18	5,8,11,12,19,33,49,55,57,58,59,64,67,70,71,75,84,93
92	68	2,3,4,5,6,8,10,11,12,13,14,15,17,19,20,22,23,24,25,26,29,30,31,33,34,36,38,40,44,46,47,48,49,50,51,52,53,56,57,58,59,60,61,63,64,65,68,69,70,71,72,75,77,78,79,80,81,82,83,84,85,86,87,88,89,91,92,94
93	26	3,7,19,20,24,31,35,39,42,47,49,50,53,54,55,58,66,70,71,73,74,76,78,81,89,93
94	7	20,35,49,59,64,70,71
95	37	3,5,8,11,12,14,19,20,23,24,29,33,34,40,44,46,47,49,50,53,57,59,64,65,68,70,71,75,77,78,81,84,88,89,91,92,94

Appendix

Appendix D.

Functional enrichment analysis.

Module	Terms	Description
Module 1	OMIM:616078	mental retardation, autosomal dominant 29; mrd29
Module 1	OMIM:612446	complement component 6 deficiency; c6d; c6 deficiency complement component 6 deficiency, subtotal, included; c6 deficiency, subtotal, included
Module 1	OMIM:269150	schinzel-giedion midface retraction syndrome; sgs
Module 2	GO:0051239	regulation of multicellular organismal process
Module 2	GO:0032502	developmental process
Module 2	GO:0048856	anatomical structure development
Module 2	GO:0009653	anatomical structure morphogenesis
Module 2	GO:0044767	single-organism developmental process
Module 2	GO:0044707	single-multicellular organism process
Module 2	GO:0007275	multicellular organism development
Module 2	GO:0048731	system development
Module 2	GO:0007399	nervous system development
Module 2	CORUM:2073	tnfrsf11a-traf6-src complex
Module 2	CORUM:2958	smad1-cbp complex
Module 2	HPA:005010_10	bronchus; respiratory epithelial cells
Module 2	HPA:007010_10	cerebral cortex; endothelial cells
Module 2	HPA:027010_10	pancreas; exocrine glandular cells
Module 2	HPA:006020_10	cerebellum; cells in granular layer
Module 2	HPA:021020_10	liver; hepatocytes
Module 2	HPA:001010_10	adrenal gland; glandular cells
Module 2	HPA:018010_10	hippocampus; glial cells
Module 2	HPA:022020_10	lung; pneumocytes
Module 2	HPA:007030_10	cerebral cortex; neuronal cells
Module 2	HPA:025010_10	oral mucosa; squamous epithelial cells
Module 2	HPA:035030_10	skin 1; keratinocytes
Module 2	HPA:012010_10	endometrium 2; cells in endometrial stroma
Module 2	HPA:039030_10	soft tissue 1; fibroblasts
Module 2	HPA:010010_10	duodenum; glandular cells
Module 2	HPA:037010_10	small intestine; glandular cells
Module 2	HPA:004010_10	breast; adipocytes
Module 2	HPA:004020_10	breast; glandular cells
Module 2	HPA:032010_10	salivary gland; glandular cells
Module 2	HPA:029020_10	placenta; trophoblastic cells
Module 2	HPA:048010_10	vagina; squamous epithelial cells
Module 2	HPA:042010_10	stomach 1; glandular cells
Module 2	HPA:045010_10	thyroid gland; glandular cells

Module	Terms	Description
Module 2	HPA:003010_10	bone marrow; hematopoietic cells
Module 2	HPA:044010_10	testis; leydig cells
Module 2	HPA:035010_10	skin 1; langerhans
Module 2	HPA:007020_10	cerebral cortex; glial cells
Module 2	HPA:029010_10	placenta; decidual cells
Module 2	HPA:021010_10	liver; bile duct cells
Module 2	HPA:034010_10	skeletal muscle; myocytes
Module 2	HPA:018020_10	hippocampus; neuronal cells
Module 2	HPA:002010_10	appendix; glandular cells
Module 2	HPA:035020_10	skin 1; fibroblasts
Module 2	HPA:006010_10	cerebellum; purkinje cells
Module 2	HPA:026020_10	ovary; ovarian stroma cells
Module 2	HPA:023010_10	lymph node; germinal center cells
Module 2	HPA:022010_10	lung; macrophages
Module 2	HPA:041010_10	spleen; cells in red pulp
Module 2	HPA:040040_10	soft tissue 2; peripheral nerve
Module 2	HPA:039010_10	soft tissue 1; adipocytes
Module 2	HPA:020010_10	lateral ventricle; glial cells
Module 2	HPA:009020_10	colon; glandular cells
Module 2	HPA:046010_10	tonsil; germinal center cells
Module 2	HPA:047010_10	urinary bladder; urothelial cells
Module 2	HPA:011010_10	endometrium 1; cells in endometrial stroma
Module 2	HPA:014010_10	esophagus; squamous epithelial cells
Module 2	HPA:031010_10	rectum; glandular cells
Module 2	HPA:012020_10	endometrium 2; glandular cells
Module 2	HPA:017010_10	heart muscle; myocytes
Module 2	HPA:006030_10	cerebellum; cells in molecular layer
Module 2	HPA:011020_10	endometrium 1; glandular cells
Module 2	HPA:041020_10	spleen; cells in white pulp
Module 2	HPA:019020_10	kidney; cells in tubules
Module 2	HPA:009010_10	colon; endothelial cells
Module 2	HPA:038010_10	smooth muscle; smooth muscle cells
Module 2	HPA:019010_10	kidney; cells in glomeruli
Module 2	HPA:040010_10	soft tissue 2; adipocytes
Module 2	HPA:004030_10	breast; myoepithelial cells
Module 2	HPA:043010_10	stomach 2; glandular cells
Module 2	HPA:007040_10	cerebral cortex; neuropil
Module 2	HPA:035040_10	skin 1; melanocytes
Module 2	HPA:016010_10	gallbladder; glandular cells

Module	Terms	Description
Module 2	HPA:023020_10	lymph node; non-germinal center cells
Module 2	HPA:044020_10	testis; cells in seminiferous ducts
Module 2	HPA:030010_10	prostate; glandular cells
Module 2	HPA:015010_10	fallopian tube; glandular cells
Module 2	HPA:013010_10	epididymis; glandular cells
Module 2	HPA:046020_10	tonsil; non-germinal center cells
Module 2	KEGG:05200	pathways in cancer
Module 3	-	-
Module 4	MI:hsa-miR-614	mi:hsa-mir-614
Module 5	CORUM:1149	histone h3.1 complex
Module 5	OMIM:226900	epiphyseal dysplasia, multiple, 4; edm4; multiple epiphyseal dysplasia, autosomal recessive; multiple epiphyseal dysplasia with clubfoot; multiple epiphyseal dysplasia with bilayered patellae
Module 5	OMIM:222600	diastrophic dysplasia; dtd; ddiastrophic dysplasia, broad bone-platyspondylic variant, included
Module 5	OMIM:256050	atelosteogenesis, type ii; ao2; aoi; neonatal osseous dysplasia ide la chapelle dysplasia, included; dlcd, included
Module 5	OMIM:600972	achondrogenesis, type ib; acg1b; achondrogenesis, fraccaro type
Module 6	-	-
Module 7	GO:0046035	cmp metabolic process
Module 7	GO:0009224	cmp biosynthetic process
Module 7	GO:0006238	cmp salvage
Module 8	-	-
Module 9	-	-
Module 10	GO:0044267	cellular protein metabolic process
Module 10	OMIM:142946	holoprosencephaly 4; hpe4
Module 10	OMIM:608957	cd8 deficiency, familial
Module 10	OMIM:613953	candidiasis, familial, 5; candf5; candidiasis, familial chronic mucocutaneous, autosomal recessive
Module 10	OMIM:611092	mental retardation, autosomal recessive 6; mrt6
Module 10	OMIM:615598	palmoplantar keratoderma, nagashima type; ppkn
Module 10	OMIM:308700	hypogonadotropic hypogonadism 1 with or without anosmia; hh1; kallmann syndrome 1; kal1; kms; hypogonadotropic hypogonadism and anosmia; hha; dysplasia olfactogenitalis of de morsier; anosmic hypogonadism
Module 10	OMIM:614714	porokeratosis 7, multiple types; porok7
Module 11	GO:0032994	protein-lipid complex
Module 11	GO:1990777	lipoprotein particle
Module 11	GO:0034358	plasma lipoprotein particle
Module 11	OMIM:614028	apolipoprotein c-iii deficiency; hyperalphalipoproteinemia 2; halp2
Module 11	REAC:174824	lipoprotein metabolism
Module 12	-	-
Module 13	CORUM:2578	sam68-p120gap complex
Module 13	CORUM:2581	rasgap-aurka/aurkb-survivin complex

Module	Terms	Description
Module 13	OMIM:613784	macular degeneration, age-related, 12; armd12
Module 13	OMIM:607339	coronary heart disease, susceptibility to, 1; chds1
Module 13	OMIM:608354	capillary malformation-arteriovenous malformation; cmavmcapillary malformation without arteriovenous malformation, included
Module 13	OMIM:608355	parkes weber syndrome; pkws
Module 14	-	-
Module 15	-	-
Module 16	OMIM:237500	dubin-johnson syndrome; djs; hyperbilirubinemia, dubin-johnson type; hblrdj; hyperbilirubinemia ii
Module 16	OMIM:616171	microcephaly and chorioretinopathy, autosomal recessive, 2; mccrp2
Module 16	OMIM:607499	bulimia nervosa, susceptibility to, 1; buln1; bn
Module 16	OMIM:610269	bulimia nervosa, susceptibility to, 2; buln2anorexia nervosa, susceptibility to, 2, included; anon2, included
Module 17	GO:0001890	placenta development
Module 17	HPA:018010_03	hippocampus; glial cells
Module 17	OMIM:613068	neurodegeneration due to cerebral folate transport deficiency
Module 17	OMIM:178110	arthrogryposis, distal, type 8; da8; multiple pterygium syndrome, autosomal dominant; pterygium syndrome, multiple, autosomal dominant
Module 17	OMIM:193700	arthrogryposis, distal, type 2a; da2a; freeman-sheldon syndrome; fss; whistling face-windmill vane hand syndrome; craniocarpotarsal dystrophy; craniocarpotarsal dysplasia
Module 18	HPA:046010_03	tonsil; germinal center cells
Module 19	-	-
Module 20	-	-
Module 21	GO:0004092	carnitine o-acetyltransferase activity
Module 22	GO:0070429	negative regulation of nucleotide-binding oligomerization domain containing 1 signaling pathway
Module 22	GO:0034147	regulation of toll-like receptor 5 signaling pathway
Module 22	GO:0034148	negative regulation of toll-like receptor 5 signaling pathway
Module 23	OMIM:304340	pettigrew syndrome; pgs; mental retardation, x-linked, syndromic 5; mrxs5; mental retardation, x-linked, with dandy-walker malformation, basal ganglia disease, and seizures; mental retardation, x-linked, syndromic, fried type; mrxf; mental retardation, x-linked 59; mrx59; mental retardation, x-linked, syndromic 21; mrxs21
Module 23	OMIM:615752	polymicrogyria, bilateral perisylvian, autosomal recessive; bppr; pmgr
Module 23	OMIM:606854	polymicrogyria, bilateral frontoparietal; bfpp; cerebellar ataxia with neuronal migration defect
Module 24	GO:0050794	regulation of cellular process
Module 24	GO:0070106	interleukin-27-mediated signaling pathway
Module 24	GO:0045509	interleukin-27 receptor activity
Module 25	OMIM:614075	hermansky-pudlak syndrome 6; hps6
Module 25	OMIM:604364	epilepsy, familial focal, with variable foci; ffevf; epilepsy, partial, with variable foci; fpevf
Module 26	GO:0031616	spindle pole centrosome
Module 26	GO:0032133	chromosome passenger complex
Module 26	GO:0035174	histone serine kinase activity

Module	Terms	Description
Module 26	OMIM:243060	spermatogenic failure 5; spgf5; male infertility with large-headed, multiflagellar, polyploid spermatozoa; infertility associated with multi-tailed spermatozoa and excessivedna
Module 26	OMIM:613463	fasting plasma glucose level quantitative trait locus 5; fgqtl5
Module 26	OMIM:259710	osteopetrosis, autosomal recessive 2; optb2; osteopetrosis, osteoclast-poor; osteopetrosis, mild autosomal recessive form
Module 27	CORUM:2029	bnip2-arhgap8 complex
Module 28	GO:0008150	biological_process
Module 28	GO:0065007	biological regulation
Module 28	GO:0065008	regulation of biological quality
Module 28	GO:0044699	single-organism process
Module 28	GO:0009987	cellular process
Module 28	GO:0044763	single-organism cellular process
Module 28	GO:0007154	cell communication
Module 28	GO:0023052	signaling
Module 28	GO:0044700	single organism signaling
Module 28	GO:0032501	multicellular organismal process
Module 28	GO:0044707	single-multicellular organism process
Module 28	GO:0002376	immune system process
Module 28	GO:0050896	response to stimulus
Module 28	GO:0006950	response to stress
Module 28	GO:0006952	defense response
Module 28	GO:0006955	immune response
Module 28	GO:0051716	cellular response to stimulus
Module 28	GO:0050789	regulation of biological process
Module 28	GO:0048583	regulation of response to stimulus
Module 28	GO:0050794	regulation of cellular process
Module 28	GO:0007165	signal transduction
Module 28	GO:0007166	cell surface receptor signaling pathway
Module 28	GO:0048518	positive regulation of biological process
Module 28	GO:0048584	positive regulation of response to stimulus
Module 28	GO:0048522	positive regulation of cellular process
Module 28	GO:0070887	cellular response to chemical stimulus
Module 28	GO:0010033	response to organic substance
Module 28	GO:0071310	cellular response to organic substance
Module 28	GO:0005575	cellular component
Module 28	GO:0005623	cell
Module 28	GO:0044464	cell part
Module 28	GO:0005829	cytosol
Module 28	GO:0005488	binding
Module 28	GO:0005515	protein binding

Module	Terms	Description
Module 28	HPA:025010_10	oral mucosa; squamous epithelial cells
Module 28	HPA:007030_10	cerebral cortex; neuronal cells
Module 28	HPA:010010_10	duodenum; glandular cells
Module 28	HPA:032010_10	salivary gland; glandular cells
Module 28	HPA:039030_10	soft tissue 1; fibroblasts
Module 28	HPA:039010	soft tissue 1; adipocytes
Module 28	HPA:039010_10	soft tissue 1; adipocytes
Module 28	HPA:006030_10	cerebellum; cells in molecular layer
Module 28	HPA:042010_10	stomach 1; glandular cells
Module 28	HPA:019010_10	kidney; cells in glomeruli
Module 28	HPA:041010_10	spleen; cells in red pulp
Module 28	HPA:035040_10	skin 1; melanocytes
Module 28	HPA:026020_10	ovary; ovarian stroma cells
Module 28	HPA:021010_10	liver; bile duct cells
Module 28	HPA:029020_10	placenta; trophoblastic cells
Module 28	HPA:046020_10	tonsil; non-germinal center cells
Module 28	HPA:004020_10	breast; glandular cells
Module 28	HPA:013010_10	epididymis; glandular cells
Module 28	HPA:040040_10	soft tissue 2; peripheral nerve
Module 28	HPA:023010_10	lymph node; germinal center cells
Module 28	HPA:041010_12	spleen; cells in red pulp
Module 28	HPA:033010_10	seminal vesicle; glandular cells
Module 28	HPA:040040_12	soft tissue 2; peripheral nerve
Module 28	HPA:040030_10	soft tissue 2; fibroblasts
Module 28	HPA:037010_10	small intestine; glandular cells
Module 28	HPA:046010_10	tonsil; germinal center cells
Module 28	HPA:046010_11	tonsil; germinal center cells
Module 28	HPA:012020_10	endometrium 2; glandular cells
Module 28	HPA:029010_10	placenta; decidual cells
Module 28	HPA:022020_10	lung; pneumocytes
Module 28	HPA:014010_10	esophagus; squamous epithelial cells
Module 28	HPA:035010_10	skin 1; langerhans
Module 28	HPA:007010_10	cerebral cortex; endothelial cells
Module 28	HPA:044020_10	testis; cells in seminiferous ducts
Module 28	HPA:007040_10	cerebral cortex; neuropil
Module 28	HPA:048010_10	vagina; squamous epithelial cells
Module 28	HPA:047010_10	urinary bladder; urothelial cells
Module 28	HPA:008010_10	cervix, uterine; glandular cells
Module 28	HPA:002010_10	appendix; glandular cells

Module	Terms	Description
Module 28	HPA:039040_10	soft tissue 1; peripheral nerve
Module 28	HPA:009010_10	colon; endothelial cells
Module 28	HPA:011010_10	endometrium 1; cells in endometrial stroma
Module 28	HPA:006010_10	cerebellum; purkinje cells
Module 28	HPA:041020_10	spleen; cells in white pulp
Module 28	HPA:036010_10	skin 2; epidermal cells
Module 28	HPA:038010_10	smooth muscle; smooth muscle cells
Module 28	HPA:015010_10	fallopian tube; glandular cells
Module 28	HPA:046030_10	tonsil; squamous epithelial cells
Module 28	HPA:004010_10	breast; adipocytes
Module 28	HPA:044010_10	testis; leydig cells
Module 28	HPA:018010_10	hippocampus; glial cells
Module 28	HPA:004030_10	breast; myoepithelial cells
Module 28	HPA:031010_10	rectum; glandular cells
Module 28	HPA:020020_10	lateral ventricle; neuronal cells
Module 28	HPA:011020_10	endometrium 1; glandular cells
Module 28	HPA:022010_10	lung; macrophages
Module 28	HPA:035020_10	skin 1; fibroblasts
Module 28	HPA:040010_10	soft tissue 2; adipocytes
Module 28	HPA:019020_10	kidney; cells in tubules
Module 28	HPA:019020_11	kidney; cells in tubules
Module 28	HPA:001010_10	adrenal gland; glandular cells
Module 28	HPA:037010_12	small intestine; glandular cells
Module 28	HPA:006020_10	cerebellum; cells in granular layer
Module 28	HPA:043010_10	stomach 2; glandular cells
Module 28	HPA:024010_10	nasopharynx; respiratory epithelial cells
Module 28	HPA:028010_10	parathyroid gland; glandular cells
Module 28	HPA:005010_10	bronchus; respiratory epithelial cells
Module 28	HPA:009030_10	colon; peripheral nerve/ganglion
Module 28	HPA:002020_10	appendix; lymphoid tissue
Module 28	HPA:008020_10	cervix, uterine; squamous epithelial cells
Module 28	HPA:027020_10	pancreas; islets of langerhans
Module 28	HPA:007020_10	cerebral cortex; glial cells
Module 28	HPA:018020_10	hippocampus; neuronal cells
Module 28	HPA:021020_10	liver; hepatocytes
Module 28	HPA:009020_10	colon; glandular cells
Module 28	HPA:023020_10	lymph node; non-germinal center cells
Module 28	HPA:003010_10	bone marrow; hematopoietic cells
Module 28	HPA:012010_10	endometrium 2; cells in endometrial stroma

Module	Terms	Description
Module 28	HPA:017010_10	heart muscle; myocytes
Module 28	HPA:030010_10	prostate; glandular cells
Module 28	HPA:034010_10	skeletal muscle; myocytes
Module 28	HPA:016010_10	gallbladder; glandular cells
Module 28	HPA:045010_10	thyroid gland; glandular cells
Module 28	HPA:027010_10	pancreas; exocrine glandular cells
Module 28	HPA:035030_10	skin 1; keratinocytes
Module 28	HPA:020010_10	lateral ventricle; glial cells
Module 29	HP:0001639	hypertrophic cardiomyopathy
Module 29	OMIM:616295	peeling skin with leukonychia, acral punctate keratoses, cheilitis, and knuckle pads; plack
Module 29	OMIM:203800	alstrom syndrome; alms; alss
Module 29	OMIM:201450	acyl-coa dehydrogenase, medium-chain, deficiency of; acadmd; acadm deficiency; mcad deficiency; mcadh deficiency; carnitine deficiency secondary to medium-chain acyl-coa dehydrogenase deficiency
Module 29	OMIM:614885	peroxisome biogenesis disorder 11b; pbd11b
Module 29	OMIM:609241	schindler disease, type i; neuroaxonal dystrophy, schindler type; alpha-n-acetylgalactosaminidase deficiency, type i; naga deficiency, type i; alpha-n-acetylgalactosaminidase deficiency, type iii, included; naga deficiency, type iii, included; schindler disease, type iii, included
Module 29	OMIM:609242	kanzaki disease; alpha-n-acetylgalactosaminidase deficiency, type ii; alpha-n-acetylgalactosaminidase deficiency, adult-onset; naga deficiency, type ii; schindler disease, type ii
Module 29	OMIM:614883	peroxisome biogenesis disorder 11a (zellweger); pbd11a peroxisome biogenesis disorder, complementation group 13, included; cg13, included; peroxisome biogenesis disorder, complementation group h, included; cgh, included
Module 29	OMIM:609909	cardiomyopathy, dilated, 1p; cmd1p
Module 29	OMIM:613874	cardiomyopathy, familial hypertrophic, 18; cmh18
Module 30	CORUM:5530	homodimeric complex 1btr
Module 31	OMIM:615841	spermatogenic failure 13; spgf13
Module 31	TF:M00772_1	factor: irf; motif: bncrsttcantyy; match class: 1
Module 32	-	-
Module 33	OMIM:615422	inclusion body myopathy with early-onset paget disease with or without frontotemporal dementia 2; ibmpfd2; multisystem proteinopathy 2; msp2
Module 34	-	-
Module 35	-	-
Module 36	-	-
Module 37	-	-
Module 38	CORUM:2439	itga8-itgb1 complex
Module 38	OMIM:216550	cohen syndrome; coh1; coh; hypotonia, obesity, and prominent incisors; pepper syndrome; chs1, formerly
Module 39	MI:hsa-miR-577	mi:hsa-miR-577
Module 39	OMIM:251880	mitochondrial dna depletion syndrome 3 (hepatocerebral type); mtdps3
Module 39	OMIM:213980	craniofacial dysmorphism, skeletal anomalies, and mental retardation syndrome; cfsmr; cerebrofaciothoracic dysplasia

Module	Terms	Description
Module 40	OMIM:260300	parkinson disease 15, autosomal recessive early-onset; park15; parkinsonian-pyramidal syndrome; pkps; pallidopyramidal syndrome; pallido-pyramidal syndrome
Module 41	-	-
Module 42	GO:0045292	mrna cis splicing, via spliceosome
Module 42	OMIM:613507	glycogen storage disease xv; gsd15; gsd xv; glycogenin deficiency; gyg1 deficiency
Module 42	OMIM:112240	cole-carpenter syndrome
Module 42	OMIM:616199	polyglucosan body myopathy 2; pgbm2
Module 42	TF :M02066_0	factor: pea3; motif: rccggaagyn; match class: 0
Module 42	TF :M02063_0	factor: c-ets-1; motif: accggawgtm; match class: 0
Module 43	OMIM:300844	mental retardation, x-linked 19; mrx19
Module 43	OMIM:308700	hypogonadotropic hypogonadism 1 with or without anosmia; hh1; kallmann syndrome 1; kal1; kms; hypogonadotropic hypogonadism and anosmia; hha; dysplasia olfactogenitalis of de morsier; anosmic hypogonadism
Module 43	OMIM:275350	transcobalamin ii deficiency; tc ii deficiency; tcn2 deficiency
Module 43	OMIM:303600	coffin-lowry syndrome; cls
Module 43	OMIM:610297	parkinson disease 13, autosomal dominant, susceptibility to; park13
Module 43	OMIM:211800	calcification of joints and arteries; calja; arterial calcification due to deficiency of cd73; acdc
Module 44	-	-
Module 45	-	-
Module 46	GO:0005773	vacuole
Module 46	GO:0000323	lytic vacuole
Module 46	GO:0005764	lysosome
Module 46	OMIM:254600	myeloperoxidase deficiency; mpod; mpo deficiency
Module 46	OMIM:614320	pancreatic cancer, susceptibility to, 4; pnca4
Module 46	OMIM:166600	osteopetrosis, autosomal dominant 2; opta2; osteopetrosis, autosomal dominant, type ii; marble bones, autosomal dominant; osteosclerosis fragilis generalisata; albers-schonberg disease, autosomal dominant
Module 46	OMIM:611490	osteopetrosis, autosomal recessive 4; optb4; osteopetrosis, infantile malignant 2
Module 46	OMIM:604370	breast-ovarian cancer, familial, susceptibility to, 1; brovca1 breast cancer, familial, susceptibility to, 1, included; ovarian cancer, familial, susceptibility to, 1, included
Module 46	REAC:6796648	tp53 regulates transcription of dna repair genes
Module 47	-	-
Module 48	GO:0008150	biological_process
Module 48	GO:0065007	biological regulation
Module 48	GO:0065008	regulation of biological quality
Module 48	GO:0050878	regulation of body fluid levels
Module 48	GO:0007599	hemostasis
Module 48	GO:0042592	homeostatic process
Module 48	GO:0048878	chemical homeostasis
Module 48	GO:0050801	ion homeostasis
Module 48	GO:0065009	regulation of molecular function
Module 48	GO:0044093	positive regulation of molecular function

Module	Terms	Description
Module 48	GO:0002376	immune system process
Module 48	GO:0050896	response to stimulus
Module 48	GO:0042221	response to chemical
Module 48	GO:1901698	response to nitrogen compound
Module 48	GO:1901700	response to oxygen-containing compound
Module 48	GO:0010033	response to organic substance
Module 48	GO:0014070	response to organic cyclic compound
Module 48	GO:0033993	response to lipid
Module 48	GO:0070848	response to growth factor
Module 48	GO:0010035	response to inorganic substance
Module 48	GO:0042493	response to drug
Module 48	GO:0009719	response to endogenous stimulus
Module 48	GO:0071495	cellular response to endogenous stimulus
Module 48	GO:0009725	response to hormone
Module 48	GO:0010243	response to organonitrogen compound
Module 48	GO:1901652	response to peptide
Module 48	GO:0043434	response to peptide hormone
Module 48	GO:0032868	response to insulin
Module 48	GO:0006950	response to stress
Module 48	GO:0006952	defense response
Module 48	GO:0009611	response to wounding
Module 48	GO:0042060	wound healing
Module 48	GO:0009628	response to abiotic stimulus
Module 48	GO:0009605	response to external stimulus
Module 48	GO:0051179	localization
Module 48	GO:0051674	localization of cell
Module 48	GO:0033036	macromolecule localization
Module 48	GO:0008104	protein localization
Module 48	GO:0051234	establishment of localization
Module 48	GO:0006810	transport
Module 48	GO:0071702	organic substance transport
Module 48	GO:0016192	vesicle-mediated transport
Module 48	GO:0006897	endocytosis
Module 48	GO:0045184	establishment of protein localization
Module 48	GO:0015031	protein transport
Module 48	GO:0051641	cellular localization
Module 48	GO:0070727	cellular macromolecule localization
Module 48	GO:0034613	cellular protein localization
Module 48	GO:0051649	establishment of localization in cell

Module	Terms	Description
Module 48	GO:0046907	intracellular transport
Module 48	GO:0016482	cytosolic transport
Module 48	GO:0071840	cellular component organization or biogenesis
Module 48	GO:0008152	metabolic process
Module 48	GO:0044238	primary metabolic process
Module 48	GO:0071704	organic substance metabolic process
Module 48	GO:0043170	macromolecule metabolic process
Module 48	GO:0043412	macromolecule modification
Module 48	GO:0019538	protein metabolic process
Module 48	GO:0006508	proteolysis
Module 48	GO:0036211	protein modification process
Module 48	GO:0044267	cellular protein metabolic process
Module 48	GO:0006464	cellular protein modification process
Module 48	GO:0018193	peptidyl-amino acid modification
Module 48	GO:0005975	carbohydrate metabolic process
Module 48	GO:0009056	catabolic process
Module 48	GO:0023052	signaling
Module 48	GO:0044699	single-organism process
Module 48	GO:0044710	single-organism metabolic process
Module 48	GO:0044712	single-organism catabolic process
Module 48	GO:0044281	small molecule metabolic process
Module 48	GO:0008283	cell proliferation
Module 48	GO:1902578	single-organism localization
Module 48	GO:0044765	single-organism transport
Module 48	GO:1902582	single-organism intracellular transport
Module 48	GO:0006811	ion transport
Module 48	GO:1902580	single-organism cellular localization
Module 48	GO:0044700	single organism signaling
Module 48	GO:0040011	locomotion
Module 48	GO:0042330	taxis
Module 48	GO:0006935	chemotaxis
Module 48	GO:0009987	cellular process
Module 48	GO:0044763	single-organism cellular process
Module 48	GO:0006928	movement of cell or subcellular component
Module 48	GO:0048870	cell motility
Module 48	GO:0016477	cell migration
Module 48	GO:0008219	cell death
Module 48	GO:0012501	programmed cell death
Module 48	GO:0006915	apoptotic process

Module	Terms	Description
Module 48	GO:0007154	cell communication
Module 48	GO:0007267	cell-cell signaling
Module 48	GO:0051716	cellular response to stimulus
Module 48	GO:0070887	cellular response to chemical stimulus
Module 48	GO:1901699	cellular response to nitrogen compound
Module 48	GO:1901701	cellular response to oxygen-containing compound
Module 48	GO:0071310	cellular response to organic substance
Module 48	GO:0071407	cellular response to organic cyclic compound
Module 48	GO:0071396	cellular response to lipid
Module 48	GO:0032870	cellular response to hormone stimulus
Module 48	GO:0071417	cellular response to organonitrogen compound
Module 48	GO:1901653	cellular response to peptide
Module 48	GO:0071375	cellular response to peptide hormone stimulus
Module 48	GO:0044237	cellular metabolic process
Module 48	GO:0006793	phosphorus metabolic process
Module 48	GO:0006796	phosphate-containing compound metabolic process
Module 48	GO:0016310	phosphorylation
Module 48	GO:0006468	protein phosphorylation
Module 48	GO:0018105	peptidyl-serine phosphorylation
Module 48	GO:0016043	cellular component organization
Module 48	GO:0032501	multicellular organismal process
Module 48	GO:0044707	single-multicellular organism process
Module 48	GO:0050817	coagulation
Module 48	GO:0007596	blood coagulation
Module 48	GO:0032502	developmental process
Module 48	GO:0048856	anatomical structure development
Module 48	GO:0009888	tissue development
Module 48	GO:0044767	single-organism developmental process
Module 48	GO:0048869	cellular developmental process
Module 48	GO:0030154	cell differentiation
Module 48	GO:0048468	cell development
Module 48	GO:0007275	multicellular organism development
Module 48	GO:0048731	system development
Module 48	GO:0048513	animal organ development
Module 48	GO:0007399	nervous system development
Module 48	GO:0022008	neurogenesis
Module 48	GO:0048699	generation of neurons
Module 48	GO:0030182	neuron differentiation
Module 48	GO:0009653	anatomical structure morphogenesis

Module	Terms	Description
Module 48	GO:0048646	anatomical structure formation involved in morphogenesis
Module 48	GO:0050789	regulation of biological process
Module 48	GO:0048583	regulation of response to stimulus
Module 48	GO:0080134	regulation of response to stress
Module 48	GO:0032101	regulation of response to external stimulus
Module 48	GO:0048518	positive regulation of biological process
Module 48	GO:0048584	positive regulation of response to stimulus
Module 48	GO:0048519	negative regulation of biological process
Module 48	GO:0032879	regulation of localization
Module 48	GO:0051049	regulation of transport
Module 48	GO:0050794	regulation of cellular process
Module 48	GO:0080135	regulation of cellular response to stress
Module 48	GO:0048522	positive regulation of cellular process
Module 48	GO:0048523	negative regulation of cellular process
Module 48	GO:0051128	regulation of cellular component organization
Module 48	GO:0010646	regulation of cell communication
Module 48	GO:0060341	regulation of cellular localization
Module 48	GO:0032386	regulation of intracellular transport
Module 48	GO:1903649	regulation of cytoplasmic transport
Module 48	GO:1903827	regulation of cellular protein localization
Module 48	GO:0051270	regulation of cellular component movement
Module 48	GO:0007165	signal transduction
Module 48	GO:0007166	cell surface receptor signaling pathway
Module 48	GO:0007167	enzyme linked receptor protein signaling pathway
Module 48	GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway
Module 48	GO:0019222	regulation of metabolic process
Module 48	GO:0050790	regulation of catalytic activity
Module 48	GO:0051336	regulation of hydrolase activity
Module 48	GO:0009893	positive regulation of metabolic process
Module 48	GO:0010604	positive regulation of macromolecule metabolic process
Module 48	GO:0043085	positive regulation of catalytic activity
Module 48	GO:0051347	positive regulation of transferase activity
Module 48	GO:0023051	regulation of signaling
Module 48	GO:0009966	regulation of signal transduction
Module 48	GO:0051174	regulation of phosphorus metabolic process
Module 48	GO:0019220	regulation of phosphate metabolic process
Module 48	GO:0042325	regulation of phosphorylation
Module 48	GO:0051246	regulation of protein metabolic process
Module 48	GO:0051247	positive regulation of protein metabolic process

Module	Terms	Description
Module 48	GO:0031325	positive regulation of cellular metabolic process
Module 48	GO:0010562	positive regulation of phosphorus metabolic process
Module 48	GO:0045937	positive regulation of phosphate metabolic process
Module 48	GO:0032268	regulation of cellular protein metabolic process
Module 48	GO:0048015	phosphatidylinositol-mediated signaling
Module 48	GO:0005575	cellular_component
Module 48	GO:0005623	cell
Module 48	GO:0005576	extracellular region
Module 48	GO:0043226	organelle
Module 48	GO:0043227	membrane-bounded organelle
Module 48	GO:0031982	vesicle
Module 48	GO:0044421	extracellular region part
Module 48	GO:0043230	extracellular organelle
Module 48	GO:1903561	extracellular vesicle
Module 48	GO:0070062	extracellular exosome
Module 48	GO:0044464	cell part
Module 48	GO:0044463	cell projection part
Module 48	GO:0044459	plasma membrane part
Module 48	GO:0005622	intracellular
Module 48	GO:0044424	intracellular part
Module 48	GO:0005737	cytoplasm
Module 48	GO:0044444	cytoplasmic part
Module 48	GO:0005829	cytosol
Module 48	GO:0043229	intracellular organelle
Module 48	GO:0043231	intracellular membrane-bounded organelle
Module 48	GO:0012505	endomembrane system
Module 48	GO:0044422	organelle part
Module 48	GO:0044446	intracellular organelle part
Module 48	GO:0098805	whole membrane
Module 48	GO:0098589	membrane region
Module 48	GO:0098590	plasma membrane region
Module 48	GO:0030554	adenyl nucleotide binding
Module 48	GO:0032559	adenyl ribonucleotide binding
Module 48	GO:0003674	molecular_function
Module 48	GO:0003824	catalytic activity
Module 48	GO:0005488	binding
Module 48	GO:0097367	carbohydrate derivative binding
Module 48	GO:0036094	small molecule binding
Module 48	GO:0043167	ion binding

Module	Terms	Description
Module 48	GO:0043168	anion binding
Module 48	GO:0005515	protein binding
Module 48	GO:0005102	receptor binding
Module 48	GO:0019899	enzyme binding
Module 48	GO:0016772	transferase activity, transferring phosphorus-containing groups
Module 48	GO:0016773	phosphotransferase activity, alcohol group as acceptor
Module 48	GO:0016301	kinase activity
Module 48	GO:0004672	protein kinase activity
Module 48	GO:0004674	protein serine/threonine kinase activity
Module 48	CORUM:2582	chromosomal passenger complex cpc (cdca8, aurkb, birc5)
Module 48	HPA:041010_10	spleen; cells in red pulp
Module 48	HPA:042010_10	stomach 1; glandular cells
Module 48	HPA:045010_10	thyroid gland; glandular cells
Module 48	HPA:018010_10	hippocampus; glial cells
Module 48	HPA:035020_10	skin 1; fibroblasts
Module 48	HPA:019020_10	kidney; cells in tubules
Module 48	HPA:035040_10	skin 1; melanocytes
Module 48	HPA:007040_10	cerebral cortex; neuropil
Module 48	HPA:036010_10	skin 2; epidermal cells
Module 48	HPA:010010_10	duodenum; glandular cells
Module 48	HPA:006010_10	cerebellum; purkinje cells
Module 48	HPA:001010_10	adrenal gland; glandular cells
Module 48	HPA:038010_10	smooth muscle; smooth muscle cells
Module 48	HPA:035010_10	skin 1; langerhans
Module 48	HPA:046030_10	tonsil; squamous epithelial cells
Module 48	HPA:011010_10	endometrium 1; cells in endometrial stroma
Module 48	HPA:046020_10	tonsil; non-germinal center cells
Module 48	HPA:040030_10	soft tissue 2; fibroblasts
Module 48	HPA:018020_10	hippocampus; neuronal cells
Module 48	HPA:027010_10	pancreas; exocrine glandular cells
Module 48	HPA:008020_10	cervix, uterine; squamous epithelial cells
Module 48	HPA:030010_10	prostate; glandular cells
Module 48	HPA:017010_10	heart muscle; myocytes
Module 48	HPA:044010_10	testis; leydig cells
Module 48	HPA:037010_10	small intestine; glandular cells
Module 48	HPA:021010_10	liver; bile duct cells
Module 48	HPA:015010_10	fallopian tube; glandular cells
Module 48	HPA:026020_10	ovary; ovarian stroma cells
Module 48	HPA:022010_10	lung; macrophages

Module	Terms	Description
Module 48	HPA:016010_10	gallbladder; glandular cells
Module 48	HPA:029020_10	placenta; trophoblastic cells
Module 48	HPA:013010_10	epididymis; glandular cells
Module 48	HPA:009030_10	colon; peripheral nerve/ganglion
Module 48	HPA:046010_10	tonsil; germinal center cells
Module 48	HPA:007020_10	cerebral cortex; glial cells
Module 48	HPA:025010_10	oral mucosa; squamous epithelial cells
Module 48	HPA:012010_10	endometrium 2; cells in endometrial stroma
Module 48	HPA:034010_10	skeletal muscle; myocytes
Module 48	HPA:006020_10	cerebellum; cells in granular layer
Module 48	HPA:043010_10	stomach 2; glandular cells
Module 48	HPA:032010_10	salivary gland; glandular cells
Module 48	HPA:011020_10	endometrium 1; glandular cells
Module 48	HPA:048010_10	vagina; squamous epithelial cells
Module 48	HPA:019010_10	kidney; cells in glomeruli
Module 48	HPA:022020_10	lung; pneumocytes
Module 48	HPA:008010_10	cervix, uterine; glandular cells
Module 48	HPA:021020_10	liver; hepatocytes
Module 48	HPA:029010_10	placenta; decidual cells
Module 48	HPA:040000	soft tissue 2
Module 48	HPA:031010_10	rectum; glandular cells
Module 48	HPA:014010_10	esophagus; squamous epithelial cells
Module 48	HPA:007010_10	cerebral cortex; endothelial cells
Module 48	HPA:009020_10	colon; glandular cells
Module 48	HPA:047010_10	urinary bladder; urothelial cells
Module 48	HPA:009010_10	colon; endothelial cells
Module 48	HPA:035030_10	skin 1; keratinocytes
Module 48	HPA:012020_10	endometrium 2; glandular cells
Module 48	HPA:044020_10	testis; cells in seminiferous ducts
Module 48	HPA:006030_10	cerebellum; cells in molecular layer
Module 48	HPA:041020_10	spleen; cells in white pulp
Module 48	HPA:027020_10	pancreas; islets of langerhans
Module 48	KEGG:04510	focal adhesion
Module 48	MI:hsa-miR-150	mi:hsa-mir-150
Module 48	MI:hsa-miR-554	mi:hsa-mir-554
Module 48	REAC:382551	transmembrane transport of small molecules
Module 48	REAC:425407	slc-mediated transmembrane transport
Module 48	REAC:109582	hemostasis
Module 48	TF:M02036_0	factor: wt1; motif: cgccccncn; match class: 0

Module	Terms	Description
Module 48	TF:M00196_0	factor: sp1; motif: ngggggcggggyn; match class: 0
Module 48	TF:M00196_1	factor: sp1; motif: ngggggcggggyn; match class: 1
Module 48	TF:M00378_1	factor: pax-4; motif: nnnnnyccacbb; match class: 1
Module 48	TF:M01240_1	factor: ben; motif: cagcgrnv; match class: 1
Module 48	TF:M07344_0	factor: zic1; motif: vgggggags; match class: 0
Module 48	TF:M01778_0	factor: plag1; motif: grggcnhnnrrggg; match class: 0
Module 48	TF:M00933_0	factor: sp1; motif: ccccgcccn; match class: 0
Module 48	TF:M00933_1	factor: sp1; motif: ccccgcccn; match class: 1
Module 48	TF:M07289_0	factor: gklf; motif: nnnrgngngggsn; match class: 0
Module 48	TF:M07289_1	factor: gklf; motif: nnnrgngngggsn; match class: 1
Module 48	TF:M01118_0	factor: wt1; motif: smcnccnsc; match class: 0
Module 48	TF:M01118_1	factor: wt1; motif: smcnccnsc; match class: 1
Module 48	TF:M04863_0	factor: tf3c-beta; motif: ccngagggtctctggaggag; match class: 0
Module 48	TF:M04863_1	factor: tf3c-beta; motif: ccngagggtctctggaggag; match class: 1
Module 48	TF:M07277_0	factor: bteb2; motif: rggnngkkgg; match class: 0
Module 48	TF:M07277_1	factor: bteb2; motif: rggnngkkgg; match class: 1
Module 48	TF:M07226_0	factor: sp1; motif: ncccccccc; match class: 0
Module 48	TF:M04760_0	factor: gr; motif: tctcgcgag; match class: 0
Module 48	TF:M05386_0	factor: klf17; motif: ngggcg; match class: 0
Module 48	TF:M05386_1	factor: klf17; motif: ngggcg; match class: 1
Module 48	TF:M01199_0	factor: rnf96; motif: bcccgcrcc; match class: 0
Module 48	TF:M01199_1	factor: rnf96; motif: bcccgcrcc; match class: 1
Module 48	TF:M04687_0	factor: brca1; motif: tmtcgcgag; match class: 0
Module 48	TF:M04687_1	factor: brca1; motif: tmtcgcgag; match class: 1
Module 48	TF:M07062_0	factor: rreb1; motif: grsdsgggtgkgg; match class: 0
Module 48	TF:M00695_0	factor: etf; motif: gvvgm; match class: 0
Module 48	TF:M00695_1	factor: etf; motif: gvvgm; match class: 1
Module 48	TF:M03893_0	factor: wt1; motif: gngggcgggg; match class: 0
Module 48	TF:M03893_1	factor: wt1; motif: gngggcgggg; match class: 1
Module 48	TF:M01104_0	factor: movo-b; motif: gngggg; match class: 0
Module 48	TF:M01104_1	factor: movo-b; motif: gngggg; match class: 1
Module 48	TF:M00931_0	factor: sp1; motif: gggcggggc; match class: 0
Module 48	TF:M00931_1	factor: sp1; motif: gggcggggc; match class: 1
Module 48	TF:M02089_0	factor: e2f-3; motif: ggcgggn; match class: 0
Module 48	TF:M02089_1	factor: e2f-3; motif: ggcgggn; match class: 1
Module 48	TF:M05439_0	factor: rreb-1; motif: gggwca; match class: 0
Module 48	TF:M05439_1	factor: rreb-1; motif: gggwca; match class: 1
Module 48	TF:M07208_0	factor: egr1; motif: ncncgccccgc; match class: 0
Module 48	TF:M07039_0	factor: etf; motif: ccccgcccn; match class: 0

Module	Terms	Description
Module 48	TF:M07039_1	factor: etf; motif: ccccgccccyn; match class: 1
Module 48	TF:M00333_0	factor: zf5; motif: nrngngcgcgcnw; match class: 0
Module 48	TF:M00333_1	factor: zf5; motif: nrngngcgcgcnw; match class: 1
Module 48	TF:M00986_0	factor: churchill; motif: cggggn; match class: 0
Module 48	TF:M00986_1	factor: churchill; motif: cggggn; match class: 1
Module 48	TF:M05499_0	factor: lkf; motif: ngggcg; match class: 0
Module 48	TF:M05499_1	factor: lkf; motif: ngggcg; match class: 1
Module 48	TF:M02023_0	factor: maz; motif: nkgggaggggrgr; match class: 0
Module 48	TF:M07129_0	factor: sp2; motif: gycccgccycynnnn; match class: 0
Module 48	TF:M07129_1	factor: sp2; motif: gycccgccycynnnn; match class: 1
Module 48	TF:M00800_0	factor: ap-2; motif: gscscrgcnrnnn; match class: 0
Module 48	TF:M01721_0	factor: pur1; motif: gggncagnn; match class: 0
Module 48	TF:M01858_0	factor: ap-2beta; motif: gcnnnggscngvgggn; match class: 0
Module 48	TF:M01858_1	factor: ap-2beta; motif: gcnnnggscngvgggn; match class: 1
Module 48	TF:M00649_0	factor: maz; motif: ggggaggg; match class: 0
Module 48	TF:M00649_1	factor: maz; motif: ggggaggg; match class: 1
Module 48	TF:M00008_0	factor: sp1; motif: gggcggggt; match class: 0
Module 48	TF:M00008_1	factor: sp1; motif: gggcggggt; match class: 1
Module 48	TF:M00189_0	factor: ap-2; motif: mkccscngcg; match class: 0
Module 48	TF:M00189_1	factor: ap-2; motif: mkccscngcg; match class: 1
Module 48	TF:M07250_0	factor: e2f1; motif: nnnsscgsaann; match class: 0
Module 48	TF:M07250_1	factor: e2f1; motif: nnnsscgsaann; match class: 1
Module 48	TF:M04595_1	factor: sall2; motif: ggggtgg; match class: 1
Module 48	TF:M01857_0	factor: ap-2alpha; motif: ngccynngsn; match class: 0
Module 48	TF:M01857_1	factor: ap-2alpha; motif: ngccynngsn; match class: 1
Module 48	TF:M07348_0	factor: ap-2alpha; motif: nscncrggsn; match class: 0
Module 48	TF:M07348_1	factor: ap-2alpha; motif: nscncrggsn; match class: 1
Module 48	TF:M03807_0	factor: sp2; motif: gnngggcggggsn; match class: 0
Module 48	TF:M03807_1	factor: sp2; motif: gnngggcggggsn; match class: 1
Module 48	TF:M01100_1	factor: lrf; motif: vnnrmccc; match class: 1
Module 48	TF:M05332_0	factor: sp2; motif: wggcg; match class: 0
Module 48	TF:M05361_0	factor: sp6; motif: wggcg; match class: 0
Module 48	TF:M00932_0	factor: sp1; motif: nngggcggggnn; match class: 0
Module 48	TF:M00932_1	factor: sp1; motif: nngggcggggnn; match class: 1
Module 48	TF:M07354_0	factor: egr-1; motif: gcggggcg; match class: 0
Module 48	TF:M07354_1	factor: egr-1; motif: gcggggcg; match class: 1
Module 48	TF:M03567_0	factor: sp2; motif: nysgccccccccc; match class: 0
Module 48	TF:M03567_1	factor: sp2; motif: nysgccccccccc; match class: 1
Module 48	TF:M05444_0	factor: cpbp; motif: ngggcg; match class: 0

Module	Terms	Description
Module 48	TF:M07040_0	factor: gklf; motif: nnrrgrngnsnnn; match class: 0
Module 48	TF:M07040_1	factor: gklf; motif: nnrrgrngnsnnn; match class: 1
Module 48	TF:M00915_0	factor: ap-2; motif: snnccncagcgn; match class: 0
Module 48	TF:M07329_0	factor: osx; motif: cccccccnnn; match class: 0
Module 48	TF:M07329_1	factor: osx; motif: cccccccnnn; match class: 1
Module 48	TF:M00982_0	factor: krox; motif: cccgcccccccc; match class: 0
Module 48	TF:M00982_1	factor: krox; motif: cccgcccccccc; match class: 1
Module 48	TF:M03814_0	factor: bteb2; motif: gnagggggngggssnn; match class: 0
Module 48	TF:M01873_0	factor: egr-1; motif: gcgggggcgg; match class: 0
Module 48	TF:M00430_0	factor: e2f-1; motif: ntsgcgg; match class: 0
Module 48	TF:M03920_0	factor: sp1; motif: rccmcrcccmc; match class: 0
Module 48	TF:M00803_0	factor: e2f; motif: ggcgsg; match class: 0
Module 48	TF:M00803_1	factor: e2f; motif: ggcgsg; match class: 1
Module 48	TF:M01175_0	factor: ckrox; motif: scctcccc; match class: 0
Module 48	TF:M01175_1	factor: ckrox; motif: scctcccc; match class: 1
Module 48	TF:M02281_0	factor: sp1; motif: cccckcccc; match class: 0
Module 48	TF:M02281_1	factor: sp1; motif: cccckcccc; match class: 1
Module 48	TF:M07063_0	factor: sp1; motif: ggggcggggc; match class: 0
Module 48	TF:M07063_1	factor: sp1; motif: ggggcggggc; match class: 1
Module 48	TF:M00716_0	factor: zf5; motif: gsgcgcg; match class: 0
Module 48	TF:M00716_1	factor: zf5; motif: gsgcgcg; match class: 1
Module 48	TF:M07395_0	factor: sp1; motif: nggggcgggggn; match class: 0
Module 48	TF:M07395_1	factor: sp1; motif: nggggcgggggn; match class: 1
Module 49	-	-
Module 50	MI:hsa-miR-449b	mi:hsa-mir-449b
Module 50	OMIM:277180	vas deferens, congenital bilateral aplasia of; cbavd; cavd
Module 51	MI:hsa-miR-629*	mi:hsa-mir-629*
Module 51	MI:hsa-miR-25*	mi:hsa-mir-25*
Module 51	MI:hsa-miR-32*	mi:hsa-mir-32*
Module 51	MI:hsa-miR-377*	mi:hsa-mir-377*
Module 52	GO:0072347	response to anesthetic
Module 52	GO:1903927	response to cyanide
Module 52	GO:1903928	cellular response to cyanide
Module 52	GO:0021502	neural fold elevation formation
Module 52	CORUM:5382	arnt-hif1a complex
Module 52	HPA:007040_13	cerebral cortex; neuropil
Module 52	REAC:8849473	ptk6 expression
Module 52	REAC:1234162	oxygen-dependent asparagine hydroxylation of hypoxia-inducible factor alpha

Module	Terms	Description
Module 53	HP:0004607	anterior beaking of lower thoracic vertebrae
Module 53	KEGG:00531	glycosaminoglycan degradation
Module 53	OMIM:253220	mucopolysaccharidosis, type vii; mps7; mps vii; sly syndrome; beta-glucuronidase deficiency; gusb deficiency
Module 53	TF:M00237_0	factor: ahr:arnt; motif: grgkatygcgtgmcwnscc; match class: 0
Module 54	GO:0030154	cell differentiation
Module 54	GO:0030510	regulation of bmp signaling pathway
Module 54	GO:0030514	negative regulation of bmp signaling pathway
Module 54	GO:0008150	biological_process
Module 54	GO:0023052	signaling
Module 54	GO:0022610	biological adhesion
Module 54	GO:0007155	cell adhesion
Module 54	GO:0002376	immune system process
Module 54	GO:0044700	single organism signaling
Module 54	GO:0007154	cell communication
Module 54	GO:0007165	signal transduction
Module 54	GO:0007166	cell surface receptor signaling pathway
Module 54	GO:0007167	enzyme linked receptor protein signaling pathway
Module 54	GO:0042325	regulation of phosphorylation
Module 54	GO:0006468	protein phosphorylation
Module 54	GO:0001932	regulation of protein phosphorylation
Module 54	GO:0043549	regulation of kinase activity
Module 54	GO:0045859	regulation of protein kinase activity
Module 54	GO:0071900	regulation of protein serine/threonine kinase activity
Module 54	GO:0023014	signal transduction by protein phosphorylation
Module 54	GO:0000165	mapk cascade
Module 54	GO:0043408	regulation of mapk cascade
Module 54	GO:0006952	defense response
Module 54	GO:0070887	cellular response to chemical stimulus
Module 54	GO:0010033	response to organic substance
Module 54	GO:0070848	response to growth factor
Module 54	GO:0071772	response to bmp
Module 54	GO:0071310	cellular response to organic substance
Module 54	GO:0071363	cellular response to growth factor stimulus
Module 54	GO:0071773	cellular response to bmp stimulus
Module 54	GO:0043062	extracellular structure organization
Module 54	GO:0030198	extracellular matrix organization
Module 54	GO:0005615	extracellular space
Module 54	KEGG:05145	toxoplasmosis
Module 54	KEGG:04670	leukocyte transendothelial migration

Module	Terms	Description
Module 54	REAC:1280215	cytokine signaling in immune system
Module 54	REAC:449147	signaling by interleukins
Module 55	OMIM:312600	retinitis pigmentosa 2; rp2
Module 56	GO:0051702	interaction with symbiont
Module 56	GO:0051851	modification by host of symbiont morphology or physiology
Module 56	OMIM:614608	mental retardation, autosomal dominant 15; mrd15
Module 56	OMIM:609322	rhabdoid tumor predisposition syndrome 1; rtpsl; brain tumor, posterior fossa, of infancy, familial malignant rhabdoid tumor, somatic, included; rhabdoid tumor, included; rdt, included; teratoid tumor, atypical, included; at/rt, included
Module 57	-	-
Module 58	OMIM:219500	cystathioninuria; cystathionase deficiency
Module 59	-	-
Module 60	OMIM:616559	noonan syndrome 9; ns9
Module 61	GO:0003014	renal system process
Module 61	OMIM:614131	focal segmental glomerulosclerosis 6; fsgs6; glomerulosclerosis, focal segmental, 6
Module 61	OMIM:262850	alpha-2-plasmin inhibitor deficiency; antiplasmin deficiency; plasmin inhibitor deficiency
Module 62	OMIM:215140	greenberg dysplasia; grbgd; hydrops-ectopic calcification-moth-eaten skeletal dysplasia; hem skeletal dysplasia; moth-eaten skeletal dysplasia; chondrodys trophy, hydropic and prenatally lethal type
Module 62	OMIM:169400	pelger-huet anomaly; pha
Module 62	OMIM:613862	retinitis pigmentosa 38; rp38; rod-cone dystrophy, childhood-onset
Module 62	OMIM:614701	cornelia de lange syndrome 4; cdls4
Module 62	OMIM:616517	achromatopsia 7; achm7
Module 62	OMIM:109720	primary biliary cirrhosis
Module 62	OMIM:613471	reynolds syndrome; primary biliary cirrhosis, scleroderma, raynaud disease, and telangiectasia
Module 62	OMIM:615160	mitochondrial complex iii deficiency, nuclear type 5; mc3dn5
Module 63	HP:0006642	large sternal ossification centers
Module 63	HP:0006048	distal widening of metacarpals
Module 63	HP:0009845	bullet-shaped middle phalanges of the hand
Module 63	OMIM:614753	sotos syndrome 2; sotos2
Module 63	OMIM:602535	marshall-smith syndrome; mrshss
Module 64	GO:1990426	homologous recombination-dependent replication fork processing
Module 64	GO:1902521	response to etoposide
Module 64	GO:1990414	replication-born double-strand break repair via sister chromatid exchange
Module 64	CORUM:2824	brca1-rad51 complex
Module 64	CORUM:5683	hrad51c-hxrcc3 complex
Module 64	OMIM:614508	mirror movements 2; mrmv2
Module 65	MI:hsa-miR-553	mi:hsa-mir-553
Module 65	OMIM:615758	immunodeficiency 22; imd22
Module 65	OMIM:608688	aicar transformylase/imp cyclohydrolase deficiency; atic deficiency; aica-ribosuria due to atic deficiency

Module	Terms	Description
Module 65	OMIM:300953	trichothiodystrophy 5, nonphotosensitive; ttd5
Module 65	OMIM:138900	serum uric acid concentration quantitative trait loci
Module 65	OMIM:128100	dystonia 1, torsion, autosomal dominant; dyt1; dystonia musculorum deformans 1; early-onset torsion dystonia; eotd
Module 65	OMIM:614490	blood group, junior system; jr
Module 66	GO:0002223	stimulatory c-type lectin receptor signaling pathway
Module 66	GO:0007167	enzyme linked receptor protein signaling pathway
Module 66	GO:0033365	protein localization to organelle
Module 66	GO:0072594	establishment of protein localization to organelle
Module 66	GO:0002474	antigen processing and presentation of peptide antigen via mhc class i
Module 66	GO:0007264	small gtpase mediated signal transduction
Module 66	GO:0051437	positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition
Module 66	GO:0051649	establishment of localization in cell
Module 66	GO:0046907	intracellular transport
Module 66	GO:1902582	single-organism intracellular transport
Module 66	GO:0006886	intracellular protein transport
Module 66	GO:0006605	protein targeting
Module 66	GO:0038061	nik/nf-kappaB signaling
Module 66	GO:0071156	regulation of cell cycle arrest
Module 66	GO:0070987	error-free translesion synthesis
Module 66	GO:0000209	protein polyubiquitination
Module 66	GO:0006367	transcription initiation from rna polymerase ii promoter
Module 66	GO:0070647	protein modification by small protein conjugation or removal
Module 66	GO:1903320	regulation of protein modification by small protein conjugation or removal
Module 66	GO:1903322	positive regulation of protein modification by small protein conjugation or removal
Module 66	GO:0032446	protein modification by small protein conjugation
Module 66	GO:0051704	multi-organism process
Module 66	GO:0044419	interspecies interaction between organisms
Module 66	GO:0044403	symbiosis, encompassing mutualism through parasitism
Module 66	GO:0065008	regulation of biological quality
Module 66	GO:0071840	cellular component organization or biogenesis
Module 66	GO:0009987	cellular process
Module 66	GO:0044764	multi-organism cellular process
Module 66	GO:0016032	viral process
Module 66	GO:0016043	cellular component organization
Module 66	GO:0051716	cellular response to stimulus
Module 66	GO:0033554	cellular response to stress
Module 66	GO:0006974	cellular response to dna damage stimulus
Module 66	GO:0051340	regulation of ligase activity

Module	Terms	Description
Module 66	GO:0042221	response to chemical
Module 66	GO:0070887	cellular response to chemical stimulus
Module 66	GO:0010033	response to organic substance
Module 66	GO:0071310	cellular response to organic substance
Module 66	GO:0044699	single-organism process
Module 66	GO:0044763	single-organism cellular process
Module 66	GO:0008219	cell death
Module 66	GO:0012501	programmed cell death
Module 66	GO:0010941	regulation of cell death
Module 66	GO:0043067	regulation of programmed cell death
Module 66	GO:0042981	regulation of apoptotic process
Module 66	GO:0007049	cell cycle
Module 66	GO:0000278	mitotic cell cycle
Module 66	GO:0022402	cell cycle process
Module 66	GO:0044770	cell cycle phase transition
Module 66	GO:0044843	cell cycle g1/s phase transition
Module 66	GO:1903047	mitotic cell cycle process
Module 66	GO:0044772	mitotic cell cycle phase transition
Module 66	GO:0000082	g1/s transition of mitotic cell cycle
Module 66	GO:0009719	response to endogenous stimulus
Module 66	GO:0071495	cellular response to endogenous stimulus
Module 66	GO:0009725	response to hormone
Module 66	GO:0032870	cellular response to hormone stimulus
Module 66	GO:0008152	metabolic process
Module 66	GO:0044238	primary metabolic process
Module 66	GO:0009058	biosynthetic process
Module 66	GO:0009056	catabolic process
Module 66	GO:0071704	organic substance metabolic process
Module 66	GO:0043170	macromolecule metabolic process
Module 66	GO:0010467	gene expression
Module 66	GO:0019538	protein metabolic process
Module 66	GO:1901575	organic substance catabolic process
Module 66	GO:0009057	macromolecule catabolic process
Module 66	GO:0030163	protein catabolic process
Module 66	GO:1901576	organic substance biosynthetic process
Module 66	GO:0009059	macromolecule biosynthetic process
Module 66	GO:1901360	organic cyclic compound metabolic process
Module 66	GO:1901362	organic cyclic compound biosynthetic process
Module 66	GO:0006807	nitrogen compound metabolic process

Module	Terms	Description
Module 66	GO:1901564	organonitrogen compound metabolic process
Module 66	GO:1901566	organonitrogen compound biosynthetic process
Module 66	GO:0044237	cellular metabolic process
Module 66	GO:0044248	cellular catabolic process
Module 66	GO:0044260	cellular macromolecule metabolic process
Module 66	GO:0044267	cellular protein metabolic process
Module 66	GO:0044265	cellular macromolecule catabolic process
Module 66	GO:0043632	modification-dependent macromolecule catabolic process
Module 66	GO:0044257	cellular protein catabolic process
Module 66	GO:0006259	dna metabolic process
Module 66	GO:0022616	dna strand elongation
Module 66	GO:0006725	cellular aromatic compound metabolic process
Module 66	GO:0046483	heterocycle metabolic process
Module 66	GO:0034641	cellular nitrogen compound metabolic process
Module 66	GO:0006139	nucleobase-containing compound metabolic process
Module 66	GO:0044249	cellular biosynthetic process
Module 66	GO:0019438	aromatic compound biosynthetic process
Module 66	GO:0018130	heterocycle biosynthetic process
Module 66	GO:0044271	cellular nitrogen compound biosynthetic process
Module 66	GO:0034654	nucleobase-containing compound biosynthetic process
Module 66	GO:0034645	cellular macromolecule biosynthetic process
Module 66	GO:0006260	dna replication
Module 66	GO:0006261	dna-dependent dna replication
Module 66	GO:0006271	dna strand elongation involved in dna replication
Module 66	GO:0048519	negative regulation of biological process
Module 66	GO:0051352	negative regulation of ligase activity
Module 66	GO:0048518	positive regulation of biological process
Module 66	GO:0048522	positive regulation of cellular process
Module 66	GO:0019222	regulation of metabolic process
Module 66	GO:0060255	regulation of macromolecule metabolic process
Module 66	GO:0010468	regulation of gene expression
Module 66	GO:0010608	posttranscriptional regulation of gene expression
Module 66	GO:0043487	regulation of rna stability
Module 66	GO:0043488	regulation of mrna stability
Module 66	GO:0080090	regulation of primary metabolic process
Module 66	GO:0051246	regulation of protein metabolic process
Module 66	GO:0030162	regulation of proteolysis
Module 66	GO:0009889	regulation of biosynthetic process
Module 66	GO:0051171	regulation of nitrogen compound metabolic process

Module	Terms	Description
Module 66	GO:0009894	regulation of catabolic process
Module 66	GO:0042176	regulation of protein catabolic process
Module 66	GO:0045732	positive regulation of protein catabolic process
Module 66	GO:0009893	positive regulation of metabolic process
Module 66	GO:0051173	positive regulation of nitrogen compound metabolic process
Module 66	GO:0010604	positive regulation of macromolecule metabolic process
Module 66	GO:0009891	positive regulation of biosynthetic process
Module 66	GO:0051276	chromosome organization
Module 66	GO:0032200	telomere organization
Module 66	GO:0000723	telomere maintenance
Module 66	GO:0000722	telomere maintenance via recombination
Module 66	GO:0048523	negative regulation of cellular process
Module 66	GO:0031323	regulation of cellular metabolic process
Module 66	GO:0031326	regulation of cellular biosynthetic process
Module 66	GO:0031329	regulation of cellular catabolic process
Module 66	GO:0031325	positive regulation of cellular metabolic process
Module 66	GO:0045935	positive regulation of nucleobase-containing compound metabolic process
Module 66	GO:0031331	positive regulation of cellular catabolic process
Module 66	GO:0031328	positive regulation of cellular biosynthetic process
Module 66	GO:0032268	regulation of cellular protein metabolic process
Module 66	GO:1903362	regulation of cellular protein catabolic process
Module 66	GO:1903364	positive regulation of cellular protein catabolic process
Module 66	GO:0006518	peptide metabolic process
Module 66	GO:0043043	peptide biosynthetic process
Module 66	GO:0006412	translation
Module 66	GO:0006413	translational initiation
Module 66	GO:0043434	response to peptide hormone
Module 66	GO:0032868	response to insulin
Module 66	GO:0072331	signal transduction by p53 class mediator
Module 66	GO:0030330	dna damage response, signal transduction by p53 class mediator
Module 66	GO:0010948	negative regulation of cell cycle process
Module 66	GO:1901988	negative regulation of cell cycle phase transition
Module 66	GO:1901991	negative regulation of mitotic cell cycle phase transition
Module 66	GO:0044783	g1 dna damage checkpoint
Module 66	GO:1902806	regulation of cell cycle g1/s phase transition
Module 66	GO:1902807	negative regulation of cell cycle g1/s phase transition
Module 66	GO:2000134	negative regulation of g1/s transition of mitotic cell cycle
Module 66	GO:1901653	cellular response to peptide
Module 66	GO:0071375	cellular response to peptide hormone stimulus

Module	Terms	Description
Module 66	GO:0032869	cellular response to insulin stimulus
Module 66	GO:0008286	insulin receptor signaling pathway
Module 66	GO:0051603	proteolysis involved in cellular protein catabolic process
Module 66	GO:1903050	regulation of proteolysis involved in cellular protein catabolic process
Module 66	GO:0010498	proteasomal protein catabolic process
Module 66	GO:0061136	regulation of proteasomal protein catabolic process
Module 66	GO:0019941	modification-dependent protein catabolic process
Module 66	GO:0006511	ubiquitin-dependent protein catabolic process
Module 66	GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process
Module 66	GO:0031145	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process
Module 66	GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic process
Module 66	GO:0007093	mitotic cell cycle checkpoint
Module 66	GO:0044774	mitotic dna integrity checkpoint
Module 66	GO:0044773	mitotic dna damage checkpoint
Module 66	GO:0044819	mitotic g1/s transition checkpoint
Module 66	GO:0031571	mitotic g1 dna damage checkpoint
Module 66	GO:0006281	dna repair
Module 66	GO:0006289	nucleotide-excision repair
Module 66	GO:0070911	global genome nucleotide-excision repair
Module 66	GO:0006302	double-strand break repair
Module 66	GO:0006284	base-excision repair
Module 66	GO:0072395	signal transduction involved in cell cycle checkpoint
Module 66	GO:0072401	signal transduction involved in dna integrity checkpoint
Module 66	GO:0072422	signal transduction involved in dna damage checkpoint
Module 66	GO:1902400	intracellular signal transduction involved in g1 dna damage checkpoint
Module 66	GO:0072413	signal transduction involved in mitotic cell cycle checkpoint
Module 66	GO:1902403	signal transduction involved in mitotic dna integrity checkpoint
Module 66	GO:1902402	signal transduction involved in mitotic dna damage checkpoint
Module 66	GO:0072431	signal transduction involved in mitotic g1 dna damage checkpoint
Module 66	GO:0006977	dna damage response, signal transduction by p53 class mediator resulting in cell cycle arrest
Module 66	GO:0031396	regulation of protein ubiquitination
Module 66	GO:0051438	regulation of ubiquitin-protein transferase activity
Module 66	GO:0051439	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
Module 66	GO:0051444	negative regulation of ubiquitin-protein transferase activity
Module 66	GO:0051436	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
Module 66	GO:2000058	regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process
Module 66	GO:0006521	regulation of cellular amino acid metabolic process
Module 66	GO:0031398	positive regulation of protein ubiquitination

Module	Terms	Description
Module 66	GO:0032201	telomere maintenance via semi-conservative replication
Module 66	GO:0032991	macromolecular complex
Module 66	GO:0043234	protein complex
Module 66	GO:0031974	membrane-enclosed lumen
Module 66	GO:0005576	extracellular region
Module 66	GO:0043226	organelle
Module 66	GO:0043228	non-membrane-bounded organelle
Module 66	GO:0043227	membrane-bounded organelle
Module 66	GO:0031982	vesicle
Module 66	GO:0044422	organelle part
Module 66	GO:0043233	organelle lumen
Module 66	GO:0044421	extracellular region part
Module 66	GO:0043230	extracellular organelle
Module 66	GO:1903561	extracellular vesicle
Module 66	GO:0070062	extracellular exosome
Module 66	GO:0005622	intracellular
Module 66	GO:0044424	intracellular part
Module 66	GO:0005737	cytoplasm
Module 66	GO:0044444	cytoplasmic part
Module 66	GO:0005829	cytosol
Module 66	GO:0043229	intracellular organelle
Module 66	GO:0043232	intracellular non-membrane-bounded organelle
Module 66	GO:0005694	chromosome
Module 66	GO:0044446	intracellular organelle part
Module 66	GO:0070013	intracellular organelle lumen
Module 66	GO:0044427	chromosomal part
Module 66	GO:0098687	chromosomal region
Module 66	GO:0000781	chromosome, telomeric region
Module 66	GO:0005657	replication fork
Module 66	GO:0043231	intracellular membrane-bounded organelle
Module 66	GO:0005634	nucleus
Module 66	GO:0044428	nuclear part
Module 66	GO:0031981	nuclear lumen
Module 66	GO:0005654	nucleoplasm
Module 66	GO:0000228	nuclear chromosome
Module 66	GO:0044454	nuclear chromosome part
Module 66	GO:0000784	nuclear chromosome, telomeric region
Module 66	GO:0000502	proteasome complex
Module 66	GO:0048770	pigment granule

Module	Terms	Description
Module 66	GO:0042470	melanosome
Module 66	GO:1901363	heterocyclic compound binding
Module 66	GO:0097159	organic cyclic compound binding
Module 66	GO:0003676	nucleic acid binding
Module 66	GO:0003723	rna binding
Module 66	GO:0044822	poly(a) rna binding
Module 66	GO:0005515	protein binding
Module 66	GO:0019899	enzyme binding
Module 66	GO:0044877	macromolecular complex binding
Module 66	GO:0044769	atpase activity, coupled to transmembrane movement of ions, rotational mechanism
Module 66	GO:0046933	proton-transporting atp synthase activity, rotational mechanism
Module 66	GO:0003684	damaged dna binding
Module 66	GO:0016817	hydrolase activity, acting on acid anhydrides
Module 66	GO:0016818	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides
Module 66	GO:0016462	pyrophosphatase activity
Module 66	GO:0017111	nucleoside-triphosphatase activity
Module 66	GO:0016887	atpase activity
Module 66	GO:0042623	atpase activity, coupled
Module 66	CORUM:5235	wrn-ku70-ku80-parp1 complex
Module 66	CORUM:1193	rap1 complex
Module 66	CORUM:4081	ku70/ku86 complex
Module 66	CORUM:328	ku antigen complex
Module 66	CORUM:5231	53bp1-containing complex
Module 66	CORUM:5179	ncoa6-dna-pk-ku-parp1 complex
Module 66	CORUM:5183	dna-pk-ku-eif2-nf90-nf45 complex
Module 66	CORUM:1092	pcna-ku antigen complex
Module 66	HPA:011010	endometrium 1; cells in endometrial stroma
Module 66	HPA:011010_10	endometrium 1; cells in endometrial stroma
Module 66	HPA:011010_01	endometrium 1; cells in endometrial stroma
Module 66	HPA:011010_02	endometrium 1; cells in endometrial stroma
Module 66	HPA:011010_11	endometrium 1; cells in endometrial stroma
Module 66	HPA:011010_12	endometrium 1; cells in endometrial stroma
Module 66	HPA:020020	lateral ventricle; neuronal cells
Module 66	HPA:020020_01	lateral ventricle; neuronal cells
Module 66	HPA:020020_02	lateral ventricle; neuronal cells
Module 66	HPA:020020_10	lateral ventricle; neuronal cells
Module 66	HPA:020020_11	lateral ventricle; neuronal cells
Module 66	HPA:020020_12	lateral ventricle; neuronal cells
Module 66	HPA:039040	soft tissue 1; peripheral nerve

Module	Terms	Description
Module 66	HPA:039040_10	soft tissue 1; peripheral nerve
Module 66	HPA:039040_11	soft tissue 1; peripheral nerve
Module 66	HPA:039040_12	soft tissue 1; peripheral nerve
Module 66	HPA:028010_01	parathyroid gland; glandular cells
Module 66	HPA:028010_10	parathyroid gland; glandular cells
Module 66	HPA:028010_11	parathyroid gland; glandular cells
Module 66	HPA:028010_12	parathyroid gland; glandular cells
Module 66	HPA:005010_10	bronchus; respiratory epithelial cells
Module 66	HPA:005010_11	bronchus; respiratory epithelial cells
Module 66	HPA:005010_12	bronchus; respiratory epithelial cells
Module 66	HPA:005010_13	bronchus; respiratory epithelial cells
Module 66	HPA:025010_10	oral mucosa; squamous epithelial cells
Module 66	HPA:025010_11	oral mucosa; squamous epithelial cells
Module 66	HPA:025010_12	oral mucosa; squamous epithelial cells
Module 66	HPA:025010_13	oral mucosa; squamous epithelial cells
Module 66	HPA:012010	endometrium 2; cells in endometrial stroma
Module 66	HPA:012010_10	endometrium 2; cells in endometrial stroma
Module 66	HPA:012010_01	endometrium 2; cells in endometrial stroma
Module 66	HPA:012010_02	endometrium 2; cells in endometrial stroma
Module 66	HPA:012010_11	endometrium 2; cells in endometrial stroma
Module 66	HPA:012010_12	endometrium 2; cells in endometrial stroma
Module 66	HPA:041020	spleen; cells in white pulp
Module 66	HPA:041020_01	spleen; cells in white pulp
Module 66	HPA:041020_02	spleen; cells in white pulp
Module 66	HPA:041020_10	spleen; cells in white pulp
Module 66	HPA:041020_11	spleen; cells in white pulp
Module 66	HPA:041020_12	spleen; cells in white pulp
Module 66	HPA:041020_13	spleen; cells in white pulp
Module 66	HPA:036010_10	skin 2; epidermal cells
Module 66	HPA:036010_11	skin 2; epidermal cells
Module 66	HPA:036010_02	skin 2; epidermal cells
Module 66	HPA:036010_12	skin 2; epidermal cells
Module 66	HPA:037010_10	small intestine; glandular cells
Module 66	HPA:037010_11	small intestine; glandular cells
Module 66	HPA:037010_02	small intestine; glandular cells
Module 66	HPA:037010_12	small intestine; glandular cells
Module 66	HPA:037010_13	small intestine; glandular cells
Module 66	HPA:040030_10	soft tissue 2; fibroblasts
Module 66	HPA:040030_11	soft tissue 2; fibroblasts

Module	Terms	Description
Module 66	HPA:040030_12	soft tissue 2; fibroblasts
Module 66	HPA:029010_10	placenta; decidual cells
Module 66	HPA:029010_11	placenta; decidual cells
Module 66	HPA:029010_12	placenta; decidual cells
Module 66	HPA:029010_13	placenta; decidual cells
Module 66	HPA:022020	lung; pneumocytes
Module 66	HPA:022020_10	lung; pneumocytes
Module 66	HPA:022020_11	lung; pneumocytes
Module 66	HPA:022020_12	lung; pneumocytes
Module 66	HPA:047010_10	urinary bladder; urothelial cells
Module 66	HPA:047010_02	urinary bladder; urothelial cells
Module 66	HPA:047010_11	urinary bladder; urothelial cells
Module 66	HPA:047010_12	urinary bladder; urothelial cells
Module 66	HPA:047010_13	urinary bladder; urothelial cells
Module 66	HPA:048010_10	vagina; squamous epithelial cells
Module 66	HPA:048010_11	vagina; squamous epithelial cells
Module 66	HPA:048010_12	vagina; squamous epithelial cells
Module 66	HPA:048010_13	vagina; squamous epithelial cells
Module 66	HPA:008020_10	cervix, uterine; squamous epithelial cells
Module 66	HPA:008020_11	cervix, uterine; squamous epithelial cells
Module 66	HPA:008020_12	cervix, uterine; squamous epithelial cells
Module 66	HPA:032010_10	salivary gland; glandular cells
Module 66	HPA:032010_11	salivary gland; glandular cells
Module 66	HPA:032010_12	salivary gland; glandular cells
Module 66	HPA:032010_13	salivary gland; glandular cells
Module 66	HPA:007010_10	cerebral cortex; endothelial cells
Module 66	HPA:007010_11	cerebral cortex; endothelial cells
Module 66	HPA:007010_12	cerebral cortex; endothelial cells
Module 66	HPA:009030_10	colon; peripheral nerve/ganglion
Module 66	HPA:009030_11	colon; peripheral nerve/ganglion
Module 66	HPA:009030_12	colon; peripheral nerve/ganglion
Module 66	HPA:009030_13	colon; peripheral nerve/ganglion
Module 66	HPA:034010_10	skeletal muscle; myocytes
Module 66	HPA:034010_11	skeletal muscle; myocytes
Module 66	HPA:007040_10	cerebral cortex; neuropil
Module 66	HPA:007040_11	cerebral cortex; neuropil
Module 66	HPA:009020_10	colon; glandular cells
Module 66	HPA:009020_11	colon; glandular cells
Module 66	HPA:009020_12	colon; glandular cells

Module	Terms	Description
Module 66	HPA:009020_13	colon; glandular cells
Module 66	HPA:021020_10	liver; hepatocytes
Module 66	HPA:021020_11	liver; hepatocytes
Module 66	HPA:040040_10	soft tissue 2; peripheral nerve
Module 66	HPA:040040_11	soft tissue 2; peripheral nerve
Module 66	HPA:040040_12	soft tissue 2; peripheral nerve
Module 66	HPA:023010_10	lymph node; germinal center cells
Module 66	HPA:023010_01	lymph node; germinal center cells
Module 66	HPA:023010_02	lymph node; germinal center cells
Module 66	HPA:023010_11	lymph node; germinal center cells
Module 66	HPA:023010_12	lymph node; germinal center cells
Module 66	HPA:023010_13	lymph node; germinal center cells
Module 66	HPA:033010_10	seminal vesicle; glandular cells
Module 66	HPA:033010_11	seminal vesicle; glandular cells
Module 66	HPA:033010_12	seminal vesicle; glandular cells
Module 66	HPA:033010_13	seminal vesicle; glandular cells
Module 66	HPA:001010_10	adrenal gland; glandular cells
Module 66	HPA:001010_11	adrenal gland; glandular cells
Module 66	HPA:001010_12	adrenal gland; glandular cells
Module 66	HPA:001010_13	adrenal gland; glandular cells
Module 66	HPA:041010_10	spleen; cells in red pulp
Module 66	HPA:041010_11	spleen; cells in red pulp
Module 66	HPA:041010_12	spleen; cells in red pulp
Module 66	HPA:003010_10	bone marrow; hematopoietic cells
Module 66	HPA:003010_01	bone marrow; hematopoietic cells
Module 66	HPA:003010_11	bone marrow; hematopoietic cells
Module 66	HPA:003010_12	bone marrow; hematopoietic cells
Module 66	HPA:003010_03	bone marrow; hematopoietic cells
Module 66	HPA:003010_13	bone marrow; hematopoietic cells
Module 66	HPA:029020_10	placenta; trophoblastic cells
Module 66	HPA:029020_11	placenta; trophoblastic cells
Module 66	HPA:029020_12	placenta; trophoblastic cells
Module 66	HPA:029020_13	placenta; trophoblastic cells
Module 66	HPA:009010_10	colon; endothelial cells
Module 66	HPA:009010_11	colon; endothelial cells
Module 66	HPA:009010_12	colon; endothelial cells
Module 66	HPA:019020_10	kidney; cells in tubules
Module 66	HPA:019020_11	kidney; cells in tubules
Module 66	HPA:019020_12	kidney; cells in tubules

Module	Terms	Description
Module 66	HPA:019020_13	kidney; cells in tubules
Module 66	HPA:039010	soft tissue 1; adipocytes
Module 66	HPA:039010_10	soft tissue 1; adipocytes
Module 66	HPA:039010_11	soft tissue 1; adipocytes
Module 66	HPA:039010_12	soft tissue 1; adipocytes
Module 66	HPA:012020_01	endometrium 2; glandular cells
Module 66	HPA:012020_02	endometrium 2; glandular cells
Module 66	HPA:012020_10	endometrium 2; glandular cells
Module 66	HPA:012020_11	endometrium 2; glandular cells
Module 66	HPA:012020_12	endometrium 2; glandular cells
Module 66	HPA:012020_13	endometrium 2; glandular cells
Module 66	HPA:013010_01	epididymis; glandular cells
Module 66	HPA:013010_10	epididymis; glandular cells
Module 66	HPA:013010_11	epididymis; glandular cells
Module 66	HPA:013010_12	epididymis; glandular cells
Module 66	HPA:013010_13	epididymis; glandular cells
Module 66	HPA:035010_10	skin 1; langerhans
Module 66	HPA:035010_01	skin 1; langerhans
Module 66	HPA:035010_02	skin 1; langerhans
Module 66	HPA:035010_11	skin 1; langerhans
Module 66	HPA:035010_12	skin 1; langerhans
Module 66	HPA:035010_13	skin 1; langerhans
Module 66	HPA:002010_10	appendix; glandular cells
Module 66	HPA:002010_11	appendix; glandular cells
Module 66	HPA:002010_02	appendix; glandular cells
Module 66	HPA:002010_12	appendix; glandular cells
Module 66	HPA:002010_13	appendix; glandular cells
Module 66	HPA:004010	breast; adipocytes
Module 66	HPA:004010_10	breast; adipocytes
Module 66	HPA:004010_11	breast; adipocytes
Module 66	HPA:004010_12	breast; adipocytes
Module 66	HPA:035040_01	skin 1; melanocytes
Module 66	HPA:035040_10	skin 1; melanocytes
Module 66	HPA:035040_11	skin 1; melanocytes
Module 66	HPA:035040_12	skin 1; melanocytes
Module 66	HPA:035040_13	skin 1; melanocytes
Module 66	HPA:043010_10	stomach 2; glandular cells
Module 66	HPA:043010_11	stomach 2; glandular cells
Module 66	HPA:043010_12	stomach 2; glandular cells

Module	Terms	Description
Module 66	HPA:043010_13	stomach 2; glandular cells
Module 66	HPA:046030_10	tonsil; squamous epithelial cells
Module 66	HPA:046030_11	tonsil; squamous epithelial cells
Module 66	HPA:046030_12	tonsil; squamous epithelial cells
Module 66	HPA:046030_13	tonsil; squamous epithelial cells
Module 66	HPA:016010_10	gallbladder; glandular cells
Module 66	HPA:016010_11	gallbladder; glandular cells
Module 66	HPA:016010_12	gallbladder; glandular cells
Module 66	HPA:007030_10	cerebral cortex; neuronal cells
Module 66	HPA:007030_11	cerebral cortex; neuronal cells
Module 66	HPA:007030_12	cerebral cortex; neuronal cells
Module 66	HPA:007030_13	cerebral cortex; neuronal cells
Module 66	HPA:035030_01	skin 1; keratinocytes
Module 66	HPA:035030_02	skin 1; keratinocytes
Module 66	HPA:035030_03	skin 1; keratinocytes
Module 66	HPA:035030_10	skin 1; keratinocytes
Module 66	HPA:035030_11	skin 1; keratinocytes
Module 66	HPA:035030_12	skin 1; keratinocytes
Module 66	HPA:035030_13	skin 1; keratinocytes
Module 66	HPA:017010_10	heart muscle; myocytes
Module 66	HPA:017010_11	heart muscle; myocytes
Module 66	HPA:046010	tonsil; germinal center cells
Module 66	HPA:046010_10	tonsil; germinal center cells
Module 66	HPA:046010_01	tonsil; germinal center cells
Module 66	HPA:046010_02	tonsil; germinal center cells
Module 66	HPA:046010_03	tonsil; germinal center cells
Module 66	HPA:046010_11	tonsil; germinal center cells
Module 66	HPA:046010_12	tonsil; germinal center cells
Module 66	HPA:046010_13	tonsil; germinal center cells
Module 66	HPA:022010_10	lung; macrophages
Module 66	HPA:022010_11	lung; macrophages
Module 66	HPA:022010_12	lung; macrophages
Module 66	HPA:022010_13	lung; macrophages
Module 66	HPA:011020_01	endometrium 1; glandular cells
Module 66	HPA:011020_02	endometrium 1; glandular cells
Module 66	HPA:011020_10	endometrium 1; glandular cells
Module 66	HPA:011020_11	endometrium 1; glandular cells
Module 66	HPA:011020_12	endometrium 1; glandular cells
Module 66	HPA:011020_13	endometrium 1; glandular cells

Module	Terms	Description
Module 66	HPA:035020_10	skin 1; fibroblasts
Module 66	HPA:035020_03	skin 1; fibroblasts
Module 66	HPA:035020_11	skin 1; fibroblasts
Module 66	HPA:035020_12	skin 1; fibroblasts
Module 66	HPA:035020_13	skin 1; fibroblasts
Module 66	HPA:038010_10	smooth muscle; smooth muscle cells
Module 66	HPA:038010_11	smooth muscle; smooth muscle cells
Module 66	HPA:006030	cerebellum; cells in molecular layer
Module 66	HPA:006030_01	cerebellum; cells in molecular layer
Module 66	HPA:006030_10	cerebellum; cells in molecular layer
Module 66	HPA:006030_11	cerebellum; cells in molecular layer
Module 66	HPA:006030_12	cerebellum; cells in molecular layer
Module 66	HPA:002020	appendix; lymphoid tissue
Module 66	HPA:002020_01	appendix; lymphoid tissue
Module 66	HPA:002020_02	appendix; lymphoid tissue
Module 66	HPA:002020_10	appendix; lymphoid tissue
Module 66	HPA:002020_11	appendix; lymphoid tissue
Module 66	HPA:002020_12	appendix; lymphoid tissue
Module 66	HPA:002020_13	appendix; lymphoid tissue
Module 66	HPA:019010_10	kidney; cells in glomeruli
Module 66	HPA:019010_11	kidney; cells in glomeruli
Module 66	HPA:019010_12	kidney; cells in glomeruli
Module 66	HPA:018020	hippocampus; neuronal cells
Module 66	HPA:018020_10	hippocampus; neuronal cells
Module 66	HPA:018020_01	hippocampus; neuronal cells
Module 66	HPA:018020_02	hippocampus; neuronal cells
Module 66	HPA:018020_11	hippocampus; neuronal cells
Module 66	HPA:018020_12	hippocampus; neuronal cells
Module 66	HPA:026020	ovary; ovarian stroma cells
Module 66	HPA:026020_10	ovary; ovarian stroma cells
Module 66	HPA:026020_01	ovary; ovarian stroma cells
Module 66	HPA:026020_02	ovary; ovarian stroma cells
Module 66	HPA:026020_11	ovary; ovarian stroma cells
Module 66	HPA:026020_12	ovary; ovarian stroma cells
Module 66	HPA:026020_13	ovary; ovarian stroma cells
Module 66	HPA:027010_10	pancreas; exocrine glandular cells
Module 66	HPA:027010_11	pancreas; exocrine glandular cells
Module 66	HPA:027010_12	pancreas; exocrine glandular cells
Module 66	HPA:023020_10	lymph node; non-germinal center cells

Module	Terms	Description
Module 66	HPA:023020_01	lymph node; non-germinal center cells
Module 66	HPA:023020_02	lymph node; non-germinal center cells
Module 66	HPA:023020_03	lymph node; non-germinal center cells
Module 66	HPA:023020_11	lymph node; non-germinal center cells
Module 66	HPA:023020_12	lymph node; non-germinal center cells
Module 66	HPA:023020_13	lymph node; non-germinal center cells
Module 66	HPA:018010	hippocampus; glial cells
Module 66	HPA:018010_01	hippocampus; glial cells
Module 66	HPA:018010_10	hippocampus; glial cells
Module 66	HPA:018010_11	hippocampus; glial cells
Module 66	HPA:018010_12	hippocampus; glial cells
Module 66	HPA:014010_02	esophagus; squamous epithelial cells
Module 66	HPA:014010_03	esophagus; squamous epithelial cells
Module 66	HPA:014010_10	esophagus; squamous epithelial cells
Module 66	HPA:014010_11	esophagus; squamous epithelial cells
Module 66	HPA:014010_12	esophagus; squamous epithelial cells
Module 66	HPA:014010_13	esophagus; squamous epithelial cells
Module 66	HPA:044020_10	testis; cells in seminiferous ducts
Module 66	HPA:044020_11	testis; cells in seminiferous ducts
Module 66	HPA:044020_12	testis; cells in seminiferous ducts
Module 66	HPA:044020_13	testis; cells in seminiferous ducts
Module 66	HPA:010010_10	duodenum; glandular cells
Module 66	HPA:010010_11	duodenum; glandular cells
Module 66	HPA:010010_12	duodenum; glandular cells
Module 66	HPA:010010_13	duodenum; glandular cells
Module 66	HPA:006010_02	cerebellum; purkinje cells
Module 66	HPA:006010_10	cerebellum; purkinje cells
Module 66	HPA:006010_11	cerebellum; purkinje cells
Module 66	HPA:006010_12	cerebellum; purkinje cells
Module 66	HPA:006010_13	cerebellum; purkinje cells
Module 66	HPA:027020_10	pancreas; islets of langerhans
Module 66	HPA:027020_11	pancreas; islets of langerhans
Module 66	HPA:027020_02	pancreas; islets of langerhans
Module 66	HPA:027020_12	pancreas; islets of langerhans
Module 66	HPA:024010_10	nasopharynx; respiratory epithelial cells
Module 66	HPA:024010_11	nasopharynx; respiratory epithelial cells
Module 66	HPA:024010_12	nasopharynx; respiratory epithelial cells
Module 66	HPA:024010_13	nasopharynx; respiratory epithelial cells
Module 66	HPA:020010_13	lateral ventricle; glial cells

Module	Terms	Description
Module 66	HPA:039020_10	soft tissue 1; chondrocytes
Module 66	HPA:039020_11	soft tissue 1; chondrocytes
Module 66	HPA:039020_12	soft tissue 1; chondrocytes
Module 66	HPA:042010_10	stomach 1; glandular cells
Module 66	HPA:042010_11	stomach 1; glandular cells
Module 66	HPA:042010_12	stomach 1; glandular cells
Module 66	HPA:042010_13	stomach 1; glandular cells
Module 66	HPA:026010_11	ovary; follicle cells
Module 66	HPA:026010_12	ovary; follicle cells
Module 66	HPA:046020_10	tonsil; non-germinal center cells
Module 66	HPA:046020_01	tonsil; non-germinal center cells
Module 66	HPA:046020_11	tonsil; non-germinal center cells
Module 66	HPA:046020_12	tonsil; non-germinal center cells
Module 66	HPA:046020_13	tonsil; non-germinal center cells
Module 66	HPA:004020_01	breast; glandular cells
Module 66	HPA:004020_02	breast; glandular cells
Module 66	HPA:004020_10	breast; glandular cells
Module 66	HPA:004020_11	breast; glandular cells
Module 66	HPA:004020_12	breast; glandular cells
Module 66	HPA:004020_13	breast; glandular cells
Module 66	HPA:030010_10	prostate; glandular cells
Module 66	HPA:030010_11	prostate; glandular cells
Module 66	HPA:030010_12	prostate; glandular cells
Module 66	HPA:006020_10	cerebellum; cells in granular layer
Module 66	HPA:006020_11	cerebellum; cells in granular layer
Module 66	HPA:006020_12	cerebellum; cells in granular layer
Module 66	HPA:006020_13	cerebellum; cells in granular layer
Module 66	HPA:040010	soft tissue 2; adipocytes
Module 66	HPA:040010_10	soft tissue 2; adipocytes
Module 66	HPA:040010_11	soft tissue 2; adipocytes
Module 66	HPA:040010_12	soft tissue 2; adipocytes
Module 66	HPA:039030_01	soft tissue 1; fibroblasts
Module 66	HPA:039030_10	soft tissue 1; fibroblasts
Module 66	HPA:039030_11	soft tissue 1; fibroblasts
Module 66	HPA:039030_12	soft tissue 1; fibroblasts
Module 66	HPA:004030_10	breast; myoepithelial cells
Module 66	HPA:004030_11	breast; myoepithelial cells
Module 66	HPA:004030_12	breast; myoepithelial cells
Module 66	HPA:015010_02	fallopian tube; glandular cells

Module	Terms	Description
Module 66	HPA:015010_10	fallopian tube; glandular cells
Module 66	HPA:015010_11	fallopian tube; glandular cells
Module 66	HPA:015010_12	fallopian tube; glandular cells
Module 66	HPA:007020	cerebral cortex; glial cells
Module 66	HPA:007020_10	cerebral cortex; glial cells
Module 66	HPA:007020_01	cerebral cortex; glial cells
Module 66	HPA:007020_11	cerebral cortex; glial cells
Module 66	HPA:007020_12	cerebral cortex; glial cells
Module 66	HPA:021010_10	liver; bile duct cells
Module 66	HPA:021010_11	liver; bile duct cells
Module 66	HPA:021010_12	liver; bile duct cells
Module 66	HPA:045010_10	thyroid gland; glandular cells
Module 66	HPA:045010_11	thyroid gland; glandular cells
Module 66	HPA:045010_02	thyroid gland; glandular cells
Module 66	HPA:045010_12	thyroid gland; glandular cells
Module 66	HPA:045010_13	thyroid gland; glandular cells
Module 66	HPA:017010_13	heart muscle; myocytes
Module 66	HPA:044010_10	testis; leydig cells
Module 66	HPA:044010_11	testis; leydig cells
Module 66	HPA:044010_12	testis; leydig cells
Module 66	HPA:044010_13	testis; leydig cells
Module 66	HPA:020010	lateral ventricle; glial cells
Module 66	HPA:020010_01	lateral ventricle; glial cells
Module 66	HPA:020010_10	lateral ventricle; glial cells
Module 66	HPA:020010_11	lateral ventricle; glial cells
Module 66	HPA:031010_10	rectum; glandular cells
Module 66	HPA:031010_11	rectum; glandular cells
Module 66	HPA:031010_12	rectum; glandular cells
Module 66	HPA:031010_13	rectum; glandular cells
Module 66	HPA:008010_10	cervix, uterine; glandular cells
Module 66	HPA:008010_11	cervix, uterine; glandular cells
Module 66	HPA:008010_12	cervix, uterine; glandular cells
Module 66	KEGG:03050	proteasome
Module 66	KEGG:04110	cell cycle
Module 66	KEGG:05169	epstein-barr virus infection
Module 66	KEGG:03450	non-homologous end-joining
Module 66	KEGG:03030	dna replication
Module 66	KEGG:04114	oocyte meiosis
Module 66	REAC:5610785	gli3 is processed to gli3r by the proteasome

Module	Terms	Description
Module 66	REAC:445355	smooth muscle contraction
Module 66	REAC:5676590	nik-->noncanonical nf-kb signaling
Module 66	REAC:1169091	activation of nf-kappab in b cells
Module 66	REAC:350562	regulation of ornithine decarboxylase (odc)
Module 66	REAC:73894	dna repair
Module 66	REAC:73884	base excision repair
Module 66	REAC:73933	resolution of abasic sites (ap sites)
Module 66	REAC:110373	resolution of ap sites via the multiple-nucleotide patch replacement pathway
Module 66	REAC:5651801	pcna-dependent long patch base excision repair
Module 66	REAC:5696398	nucleotide excision repair
Module 66	REAC:5696399	global genome nucleotide excision repair (gg-ner)
Module 66	REAC:5693532	dna double-strand break repair
Module 66	REAC:1236978	cross-presentation of soluble exogenous antigens (endosomes)
Module 66	REAC:5610783	degradation of gli2 by the proteasome
Module 66	REAC:4641257	degradation of axin
Module 66	REAC:1643685	disease
Module 66	REAC:5663205	infectious disease
Module 66	REAC:162906	hiv infection
Module 66	REAC:162909	host interactions of hiv factors
Module 66	REAC:180585	vif-mediated degradation of apobec3g
Module 66	REAC:180534	vpu mediated degradation of cd4
Module 66	REAC:162587	hiv life cycle
Module 66	REAC:162594	early phase of hiv life cycle
Module 66	REAC:8852276	the role of gtse1 in g2/m progression after g2 checkpoint
Module 66	REAC:202424	downstream tcr signaling
Module 66	REAC:69166	removal of the flap intermediate
Module 66	REAC:4608870	asymmetric localization of pcg proteins
Module 66	REAC:5387390	hh mutants abrogate ligand secretion
Module 66	REAC:5362768	hh mutants that don't undergo autocatalytic processing are degraded by erad
Module 66	REAC:75035	chk1/chk2(cds1) mediated inactivation of cyclin b:cdk1 complex
Module 66	REAC:180786	extension of telomeres
Module 66	REAC:174417	telomere c-strand (lagging strand) synthesis
Module 66	REAC:174414	processive synthesis on the c-strand of the telomere
Module 66	REAC:174437	removal of the flap intermediate from the c-strand
Module 66	REAC:5357801	programmed cell death
Module 66	REAC:109581	apoptosis
Module 66	REAC:169911	regulation of apoptosis
Module 66	REAC:211733	regulation of activated pak-2p34 by proteasome mediated degradation
Module 66	REAC:5607764	clec7a (dectin-1) signaling

Module	Terms	Description
Module 66	REAC:5607761	dectin-1 mediated noncanonical nf-kb signaling
Module 66	REAC:1236974	er-phagosome pathway
Module 66	REAC:5610780	degradation of gli1 by the proteasome
Module 66	REAC:5358346	hedgehog ligand biogenesis
Module 66	REAC:450531	regulation of mrna stability by proteins that bind au-rich elements
Module 66	REAC:450408	auf1 (hnmp d0) binds and destabilizes mrna
Module 66	REAC:4641258	degradation of dvl
Module 66	REAC:5687128	mapk6/mapk4 signaling
Module 66	REAC:1640170	cell cycle
Module 66	REAC:69620	cell cycle checkpoints
Module 66	REAC:69615	g1/s dna damage checkpoints
Module 66	REAC:69613	p53-independent g1/s dna damage checkpoint
Module 66	REAC:69610	p53-independent dna damage response
Module 66	REAC:69601	ubiquitin mediated degradation of phosphorylated cdc25a
Module 66	REAC:69580	p53-dependent g1/s dna damage checkpoint
Module 66	REAC:69563	p53-dependent g1 dna damage response
Module 66	REAC:69541	stabilization of p53
Module 66	REAC:349425	autodegradation of the e3 ubiquitin ligase cop1
Module 66	REAC:69481	g2/m checkpoints
Module 66	REAC:69278	cell cycle, mitotic
Module 66	REAC:69242	s phase
Module 66	REAC:75815	ubiquitin-dependent degradation of cyclin d
Module 66	REAC:69229	ubiquitin-dependent degradation of cyclin d1
Module 66	REAC:453279	mitotic g1-g1/s phases
Module 66	REAC:69206	g1/s transition
Module 66	REAC:69202	cyclin e associated events during g1/s transition
Module 66	REAC:453276	regulation of mitotic cell cycle
Module 66	REAC:174143	apc/c-mediated degradation of cell cycle proteins
Module 66	REAC:176814	activation of apc/c and apc/c:cdc20 mediated degradation of mitotic proteins
Module 66	REAC:176409	apc/c:cdc20 mediated degradation of mitotic proteins
Module 66	REAC:174154	apc/c:cdc20 mediated degradation of securin
Module 66	REAC:179419	apc:cdc20 mediated degradation of cell cycle proteins prior to satisfaction of the cell cycle checkpoint
Module 66	REAC:174184	cdc20:phospho-apc/c mediated degradation of cyclin a
Module 66	REAC:174084	autodegradation of cdh1 by cdh1:apc/c
Module 66	REAC:176408	regulation of apc/c activators between g1/s and early anaphase
Module 66	REAC:174113	scf-beta-trcp mediated degradation of emi1
Module 66	REAC:69306	dna replication
Module 66	REAC:68874	m/g1 transition
Module 66	REAC:69002	dna replication pre-initiation

Module	Terms	Description
Module 66	REAC:68867	assembly of the pre-replicative complex
Module 66	REAC:68827	cdt1 association with the cdc6:orc:origin complex
Module 66	REAC:69239	synthesis of dna
Module 66	REAC:69190	dna strand elongation
Module 66	REAC:69186	lagging strand synthesis
Module 66	REAC:69052	switching of origins to a post-replicative state
Module 66	REAC:69304	regulation of dna replication
Module 66	REAC:69300	removal of licensing factors from origins
Module 66	REAC:68949	orc1 removal from chromatin
Module 66	REAC:69017	cdk-mediated phosphorylation and removal of cdc6
Module 66	REAC:187577	scf(skp2)-mediated degradation of p27/p21
Module 66	REAC:5658442	regulation of ras by gaps
Module 66	REAC:110313	translesion synthesis by γ family dna polymerases bypasses lesions on dna template
Module 66	REAC:110320	translesion synthesis by polh
Module 66	TF:M02102_1	factor: nrf-1; motif: ygcgcmgtgcgc; match class: 1
Module 66	TF:M01258_0	factor: gabp; motif: cacttcggnnn; match class: 0
Module 66	TF:M02065_1	factor: er81; motif: rccggaaryn; match class: 1
Module 66	TF:M00803_1	factor: e2f; motif: ggcgsg; match class: 1
Module 67	TF:M07090_1	factor: c-fos; motif: nntgastcatn; match class: 1
Module 68	-	-
Module 69	-	-
Module 70	GO:0003017	lymph circulation
Module 71	MI:hsa-miR-619	mi:hsa-mir-619
Module 72	REAC:390247	beta-oxidation of very long chain fatty acids
Module 72	TF:M01588_0	factor: gklf; motif: gccmccccnnn; match class: 0
Module 73	-	-
Module 74	GO:0051240	positive regulation of multicellular organismal process
Module 74	GO:0032717	negative regulation of interleukin-8 production
Module 74	GO:0032879	regulation of localization
Module 74	GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling
Module 74	KEGG:05323	rheumatoid arthritis
Module 75	-	-
Module 76	HPA:046030_13	tonsil; squamous epithelial cells
Module 76	HPA:046010_03	tonsil; germinal center cells
Module 76	HPA:046010_11	tonsil; germinal center cells
Module 76	HPA:046010_12	tonsil; germinal center cells
Module 76	HPA:046010_13	tonsil; germinal center cells
Module 76	HPA:044020_13	testis; cells in seminiferous ducts
Module 76	HPA:023020_03	lymph node; non-germinal center cells

Module	Terms	Description
Module 76	HPA:023020_13	lymph node; non-germinal center cells
Module 76	HPA:026020_11	ovary; ovarian stroma cells
Module 76	HPA:048010_11	vagina; squamous epithelial cells
Module 76	HPA:002010_13	appendix; glandular cells
Module 76	HPA:025010_13	oral mucosa; squamous epithelial cells
Module 76	HPA:007020_03	cerebral cortex; glial cells
Module 76	HPA:007020_12	cerebral cortex; glial cells
Module 76	HPA:007020_13	cerebral cortex; glial cells
Module 76	HPA:043010_13	stomach 2; glandular cells
Module 76	HPA:009020_13	colon; glandular cells
Module 76	HPA:039010_02	soft tissue 1; adipocytes
Module 76	HPA:035040_12	skin 1; melanocytes
Module 76	HPA:023010_12	lymph node; germinal center cells
Module 76	HPA:023010_13	lymph node; germinal center cells
Module 76	HPA:002020_12	appendix; lymphoid tissue
Module 76	HPA:042010_12	stomach 1; glandular cells
Module 76	HPA:035030_12	skin 1; keratinocytes
Module 76	HPA:006020_12	cerebellum; cells in granular layer
Module 76	KEGG:03040	spliceosome
Module 77	OMIM:615575	neuropathy, distal hereditary motor, type iid; hmn2d; hmn iid; neuropathy, distal hereditary motor, type iid; dhmn2d; spinal muscular atrophy, distal, autosomal dominant, calf-predominant
Module 78	-	-
Module 79	MI:hsa-miR-744*	mi:hsa-mir-744*
Module 79	MI:hsa-miR-432*	mi:hsa-mir-432*
Module 80	GO:0032812	positive regulation of epinephrine secretion
Module 81	GO:0032502	developmental process
Module 81	GO:0048856	anatomical structure development
Module 81	GO:0050793	regulation of developmental process
Module 81	GO:0044699	single-organism process
Module 81	GO:0044763	single-organism cellular process
Module 81	GO:0044767	single-organism developmental process
Module 81	GO:0048869	cellular developmental process
Module 81	GO:0030154	cell differentiation
Module 81	GO:0032501	multicellular organismal process
Module 81	GO:0044707	single-multicellular organism process
Module 81	GO:0007275	multicellular organism development
Module 81	GO:0051239	regulation of multicellular organismal process
Module 81	GO:0048519	negative regulation of biological process

Module	Terms	Description
Module 81	GO:0071944	cell periphery
Module 81	GO:0005886	plasma membrane
Module 81	GO:0009986	cell surface
Module 82	KEGG:00290	valine, leucine and isoleucine biosynthesis
Module 83	KEGG:00983	drug metabolism - other enzymes
Module 83	KEGG:00140	steroid hormone biosynthesis
Module 83	OMIM:217300	cornea plana 2; cna2
Module 83	OMIM:180105	retinitis pigmentosa 10; rp10
Module 83	OMIM:607060	parkinson disease 8, autosomal dominant; park8
Module 83	OMIM:300910	bone mineral density quantitative trait locus 18; bmd18; osteoporosis and osteoporotic fractures, susceptibility to
Module 83	OMIM:280000	coloboma, congenital heart disease, ichthyosiform dermatosis, mental retardation, and ear anomalies syndrome; chime; chime syndrome; zunic neuroectodermal syndrome
Module 83	OMIM:610478	retinal cone dystrophy 4; rcd4
Module 83	OMIM:202110	adrenal hyperplasia, congenital, due to 17-alpha-hydroxylase deficiency; adrenal hyperplasia v; 17-@alpha-hydroxylase deficiency17,20-@lyase deficiency, isolated, included; 17-@alpha-hydroxylase/17,20-lyase deficiency, combined complete, included; 17-@alpha-hydroxylase/17,20-lyase deficiency, combined partial, included
Module 83	OMIM:609040	arrhythmogenic right ventricular dysplasia, familial, 9; arv9; arrhythmogenic right ventricular cardiomyopathy 9; arvc9
Module 83	OMIM:613837	leber congenital amaurosis 11; lca11
Module 84	GO:0043227	membrane-bounded organelle
Module 84	KEGG:00524	butirosin and neomycin biosynthesis
Module 85	-	-
Module 86	GO:0032502	developmental process
Module 86	GO:0048856	anatomical structure development
Module 86	GO:0044767	single-organism developmental process
Module 86	GO:0023052	signaling
Module 86	GO:0009987	cellular process
Module 86	GO:0065007	biological regulation
Module 86	GO:0050789	regulation of biological process
Module 86	GO:0050794	regulation of cellular process
Module 86	GO:0023051	regulation of signaling
Module 86	GO:0032501	multicellular organismal process
Module 86	GO:0051239	regulation of multicellular organismal process
Module 86	GO:0044700	single organism signaling
Module 86	GO:0044707	single-multicellular organism process
Module 86	GO:0051240	positive regulation of multicellular organismal process
Module 86	GO:0007154	cell communication
Module 86	GO:0010646	regulation of cell communication
Module 86	GO:0007165	signal transduction
Module 86	GO:0070848	response to growth factor

Module	Terms	Description
Module 86	GO:1900006	positive regulation of dendrite development
Module 86	GO:0006629	lipid metabolic process
Module 86	GO:0044255	cellular lipid metabolic process
Module 86	GO:0005575	cellular component
Module 86	GO:0043226	organelle
Module 86	GO:0043227	membrane-bounded organelle
Module 86	GO:0005623	cell
Module 86	GO:0044464	cell part
Module 86	GO:0005622	intracellular
Module 86	GO:0044424	intracellular part
Module 86	TF:M07039_1	factor: etf; motif: ccccgccccyn; match class: 1
Module 86	TF:M00932_1	factor: sp1; motif: nngggcgggggnn; match class: 1
Module 86	TF:M00933_1	factor: sp1; motif: ccccgccccn; match class: 1
Module 86	TF:M03567_1	factor: sp2; motif: nysgccccgccccy; match class: 1
Module 87	GO:0009987	cellular process
Module 87	GO:0044238	primary metabolic process
Module 87	GO:0006807	nitrogen compound metabolic process
Module 87	GO:0071704	organic substance metabolic process
Module 87	GO:1901360	organic cyclic compound metabolic process
Module 87	GO:0044237	cellular metabolic process
Module 87	GO:0046483	heterocycle metabolic process
Module 87	GO:0006725	cellular aromatic compound metabolic process
Module 87	GO:0034641	cellular nitrogen compound metabolic process
Module 87	GO:0006139	nucleobase-containing compound metabolic process
Module 87	GO:0031974	membrane-enclosed lumen
Module 87	GO:0043228	non-membrane-bounded organelle
Module 87	GO:0043227	membrane-bounded organelle
Module 87	GO:0044422	organelle part
Module 87	GO:0043233	organelle lumen
Module 87	GO:0005622	intracellular
Module 87	GO:0044424	intracellular part
Module 87	GO:0005737	cytoplasm
Module 87	GO:0044444	cytoplasmic part
Module 87	GO:0043229	intracellular organelle
Module 87	GO:0043232	intracellular non-membrane-bounded organelle
Module 87	GO:0044446	intracellular organelle part
Module 87	GO:0070013	intracellular organelle lumen
Module 87	GO:0044428	nuclear part
Module 87	GO:0031981	nuclear lumen

Module	Terms	Description
Module 87	GO:0043231	intracellular membrane-bounded organelle
Module 87	GO:0005739	mitochondrion
Module 87	GO:1990204	oxidoreductase complex
Module 87	GO:0032991	macromolecular complex
Module 87	GO:0043234	protein complex
Module 87	GO:0003723	rna binding
Module 87	GO:0097159	organic cyclic compound binding
Module 87	GO:1901363	heterocyclic compound binding
Module 87	HPA:039040_10	soft tissue 1; peripheral nerve
Module 87	HPA:029010	placenta; decidual cells
Module 87	HPA:029010_10	placenta; decidual cells
Module 87	HPA:029010_01	placenta; decidual cells
Module 87	HPA:029010_11	placenta; decidual cells
Module 87	HPA:029010_12	placenta; decidual cells
Module 87	HPA:029010_13	placenta; decidual cells
Module 87	HPA:040010_10	soft tissue 2; adipocytes
Module 87	HPA:040010_11	soft tissue 2; adipocytes
Module 87	HPA:040010_12	soft tissue 2; adipocytes
Module 87	HPA:048010_10	vagina; squamous epithelial cells
Module 87	HPA:048010_01	vagina; squamous epithelial cells
Module 87	HPA:048010_11	vagina; squamous epithelial cells
Module 87	HPA:048010_12	vagina; squamous epithelial cells
Module 87	HPA:018020	hippocampus; neuronal cells
Module 87	HPA:018020_01	hippocampus; neuronal cells
Module 87	HPA:018020_02	hippocampus; neuronal cells
Module 87	HPA:018020_10	hippocampus; neuronal cells
Module 87	HPA:018020_11	hippocampus; neuronal cells
Module 87	HPA:018020_12	hippocampus; neuronal cells
Module 87	HPA:017010_10	heart muscle; myocytes
Module 87	HPA:017010_11	heart muscle; myocytes
Module 87	HPA:017010_12	heart muscle; myocytes
Module 87	HPA:017010_13	heart muscle; myocytes
Module 87	HPA:009030_10	colon; peripheral nerve/ganglion
Module 87	HPA:009030_11	colon; peripheral nerve/ganglion
Module 87	HPA:009030_12	colon; peripheral nerve/ganglion
Module 87	HPA:033010_10	seminal vesicle; glandular cells
Module 87	HPA:033010_11	seminal vesicle; glandular cells
Module 87	HPA:033010_12	seminal vesicle; glandular cells
Module 87	HPA:033010_13	seminal vesicle; glandular cells

Module	Terms	Description
Module 87	HPA:021020_10	liver; hepatocytes
Module 87	HPA:021020_11	liver; hepatocytes
Module 87	HPA:021020_12	liver; hepatocytes
Module 87	HPA:007020_10	cerebral cortex; glial cells
Module 87	HPA:007020_11	cerebral cortex; glial cells
Module 87	HPA:007020_12	cerebral cortex; glial cells
Module 87	HPA:037010_10	small intestine; glandular cells
Module 87	HPA:037010_11	small intestine; glandular cells
Module 87	HPA:037010_12	small intestine; glandular cells
Module 87	HPA:020010	lateral ventricle; glial cells
Module 87	HPA:020010_10	lateral ventricle; glial cells
Module 87	HPA:020010_11	lateral ventricle; glial cells
Module 87	HPA:020010_12	lateral ventricle; glial cells
Module 87	HPA:035020_10	skin 1; fibroblasts
Module 87	HPA:035020_11	skin 1; fibroblasts
Module 87	HPA:035020_12	skin 1; fibroblasts
Module 87	HPA:030010_10	prostate; glandular cells
Module 87	HPA:030010_11	prostate; glandular cells
Module 87	HPA:030010_12	prostate; glandular cells
Module 87	HPA:009010_10	colon; endothelial cells
Module 87	HPA:009010_11	colon; endothelial cells
Module 87	HPA:003010_02	bone marrow; hematopoietic cells
Module 87	HPA:003010_10	bone marrow; hematopoietic cells
Module 87	HPA:003010_11	bone marrow; hematopoietic cells
Module 87	HPA:003010_12	bone marrow; hematopoietic cells
Module 87	HPA:025010_02	oral mucosa; squamous epithelial cells
Module 87	HPA:025010_10	oral mucosa; squamous epithelial cells
Module 87	HPA:025010_11	oral mucosa; squamous epithelial cells
Module 87	HPA:025010_12	oral mucosa; squamous epithelial cells
Module 87	HPA:012000	endometrium 2
Module 87	HPA:012010	endometrium 2; cells in endometrial stroma
Module 87	HPA:012010_10	endometrium 2; cells in endometrial stroma
Module 87	HPA:012010_01	endometrium 2; cells in endometrial stroma
Module 87	HPA:012010_02	endometrium 2; cells in endometrial stroma
Module 87	HPA:012010_11	endometrium 2; cells in endometrial stroma
Module 87	HPA:012010_12	endometrium 2; cells in endometrial stroma
Module 87	HPA:012020	endometrium 2; glandular cells
Module 87	HPA:012020_01	endometrium 2; glandular cells
Module 87	HPA:012020_10	endometrium 2; glandular cells

Module	Terms	Description
Module 87	HPA:012020_11	endometrium 2; glandular cells
Module 87	HPA:012020_12	endometrium 2; glandular cells
Module 87	HPA:039030_10	soft tissue 1; fibroblasts
Module 87	HPA:039030_11	soft tissue 1; fibroblasts
Module 87	HPA:039030_12	soft tissue 1; fibroblasts
Module 87	HPA:023000	lymph node
Module 87	HPA:023020	lymph node; non-germinal center cells
Module 87	HPA:023020_01	lymph node; non-germinal center cells
Module 87	HPA:023020_02	lymph node; non-germinal center cells
Module 87	HPA:023020_10	lymph node; non-germinal center cells
Module 87	HPA:023020_11	lymph node; non-germinal center cells
Module 87	HPA:023020_12	lymph node; non-germinal center cells
Module 87	HPA:023020_13	lymph node; non-germinal center cells
Module 87	HPA:006020_10	cerebellum; cells in granular layer
Module 87	HPA:006020_11	cerebellum; cells in granular layer
Module 87	HPA:006020_12	cerebellum; cells in granular layer
Module 87	HPA:029020_10	placenta; trophoblastic cells
Module 87	HPA:029020_02	placenta; trophoblastic cells
Module 87	HPA:029020_11	placenta; trophoblastic cells
Module 87	HPA:029020_12	placenta; trophoblastic cells
Module 87	HPA:027020_10	pancreas; islets of langerhans
Module 87	HPA:027020_11	pancreas; islets of langerhans
Module 87	HPA:027020_12	pancreas; islets of langerhans
Module 87	HPA:005010_10	bronchus; respiratory epithelial cells
Module 87	HPA:005010_11	bronchus; respiratory epithelial cells
Module 87	HPA:005010_12	bronchus; respiratory epithelial cells
Module 87	HPA:005010_13	bronchus; respiratory epithelial cells
Module 87	HPA:043010_10	stomach 2; glandular cells
Module 87	HPA:043010_11	stomach 2; glandular cells
Module 87	HPA:043010_12	stomach 2; glandular cells
Module 87	HPA:004010	breast; adipocytes
Module 87	HPA:004010_10	breast; adipocytes
Module 87	HPA:004010_11	breast; adipocytes
Module 87	HPA:004010_12	breast; adipocytes
Module 87	HPA:002020_10	appendix; lymphoid tissue
Module 87	HPA:002020_11	appendix; lymphoid tissue
Module 87	HPA:002020_12	appendix; lymphoid tissue
Module 87	HPA:002020_13	appendix; lymphoid tissue
Module 87	HPA:018010	hippocampus; glial cells

Module	Terms	Description
Module 87	HPA:018010_10	hippocampus; glial cells
Module 87	HPA:018010_11	hippocampus; glial cells
Module 87	HPA:018010_12	hippocampus; glial cells
Module 87	HPA:040030_10	soft tissue 2; fibroblasts
Module 87	HPA:040030_11	soft tissue 2; fibroblasts
Module 87	HPA:040030_12	soft tissue 2; fibroblasts
Module 87	HPA:008020_02	cervix, uterine; squamous epithelial cells
Module 87	HPA:008020_10	cervix, uterine; squamous epithelial cells
Module 87	HPA:008020_11	cervix, uterine; squamous epithelial cells
Module 87	HPA:008020_12	cervix, uterine; squamous epithelial cells
Module 87	HPA:013010_02	epididymis; glandular cells
Module 87	HPA:013010_03	epididymis; glandular cells
Module 87	HPA:013010_10	epididymis; glandular cells
Module 87	HPA:013010_11	epididymis; glandular cells
Module 87	HPA:013010_12	epididymis; glandular cells
Module 87	HPA:013010_13	epididymis; glandular cells
Module 87	HPA:010010_10	duodenum; glandular cells
Module 87	HPA:010010_11	duodenum; glandular cells
Module 87	HPA:010010_12	duodenum; glandular cells
Module 87	HPA:010010_13	duodenum; glandular cells
Module 87	HPA:026010_11	ovary; follicle cells
Module 87	HPA:023010_02	lymph node; germinal center cells
Module 87	HPA:023010_03	lymph node; germinal center cells
Module 87	HPA:023010_10	lymph node; germinal center cells
Module 87	HPA:023010_11	lymph node; germinal center cells
Module 87	HPA:023010_12	lymph node; germinal center cells
Module 87	HPA:023010_13	lymph node; germinal center cells
Module 87	HPA:020020_10	lateral ventricle; neuronal cells
Module 87	HPA:020020_11	lateral ventricle; neuronal cells
Module 87	HPA:020020_12	lateral ventricle; neuronal cells
Module 87	HPA:042010_10	stomach 1; glandular cells
Module 87	HPA:042010_11	stomach 1; glandular cells
Module 87	HPA:042010_12	stomach 1; glandular cells
Module 87	HPA:042010_13	stomach 1; glandular cells
Module 87	HPA:045000	thyroid gland
Module 87	HPA:045010	thyroid gland; glandular cells
Module 87	HPA:045010_10	thyroid gland; glandular cells
Module 87	HPA:045010_11	thyroid gland; glandular cells
Module 87	HPA:045010_12	thyroid gland; glandular cells

Module	Terms	Description
Module 87	HPA:045010_13	thyroid gland; glandular cells
Module 87	HPA:019010	kidney; cells in glomeruli
Module 87	HPA:019010_10	kidney; cells in glomeruli
Module 87	HPA:019010_11	kidney; cells in glomeruli
Module 87	HPA:019010_12	kidney; cells in glomeruli
Module 87	HPA:041010_10	spleen; cells in red pulp
Module 87	HPA:041010_11	spleen; cells in red pulp
Module 87	HPA:041010_12	spleen; cells in red pulp
Module 87	HPA:027010_10	pancreas; exocrine glandular cells
Module 87	HPA:027010_11	pancreas; exocrine glandular cells
Module 87	HPA:027010_12	pancreas; exocrine glandular cells
Module 87	HPA:026020	ovary; ovarian stroma cells
Module 87	HPA:026020_01	ovary; ovarian stroma cells
Module 87	HPA:026020_10	ovary; ovarian stroma cells
Module 87	HPA:026020_11	ovary; ovarian stroma cells
Module 87	HPA:026020_12	ovary; ovarian stroma cells
Module 87	HPA:008010_10	cervix, uterine; glandular cells
Module 87	HPA:008010_11	cervix, uterine; glandular cells
Module 87	HPA:008010_12	cervix, uterine; glandular cells
Module 87	HPA:007010_10	cerebral cortex; endothelial cells
Module 87	HPA:007010_11	cerebral cortex; endothelial cells
Module 87	HPA:007010_12	cerebral cortex; endothelial cells
Module 87	HPA:032010_10	salivary gland; glandular cells
Module 87	HPA:032010_11	salivary gland; glandular cells
Module 87	HPA:032010_12	salivary gland; glandular cells
Module 87	HPA:032010_13	salivary gland; glandular cells
Module 87	HPA:035010	skin 1; langerhans
Module 87	HPA:035010_10	skin 1; langerhans
Module 87	HPA:035010_11	skin 1; langerhans
Module 87	HPA:035010_12	skin 1; langerhans
Module 87	HPA:046010_01	tonsil; germinal center cells
Module 87	HPA:046010_10	tonsil; germinal center cells
Module 87	HPA:046010_11	tonsil; germinal center cells
Module 87	HPA:046010_12	tonsil; germinal center cells
Module 87	HPA:046010_13	tonsil; germinal center cells
Module 87	HPA:041020_10	spleen; cells in white pulp
Module 87	HPA:041020_11	spleen; cells in white pulp
Module 87	HPA:041020_12	spleen; cells in white pulp
Module 87	HPA:024000	nasopharynx

Module	Terms	Description
Module 87	HPA:024010	nasopharynx; respiratory epithelial cells
Module 87	HPA:024010_10	nasopharynx; respiratory epithelial cells
Module 87	HPA:024010_11	nasopharynx; respiratory epithelial cells
Module 87	HPA:024010_12	nasopharynx; respiratory epithelial cells
Module 87	HPA:024010_13	nasopharynx; respiratory epithelial cells
Module 87	HPA:014010_10	esophagus; squamous epithelial cells
Module 87	HPA:014010_11	esophagus; squamous epithelial cells
Module 87	HPA:014010_12	esophagus; squamous epithelial cells
Module 87	HPA:007040_10	cerebral cortex; neuropil
Module 87	HPA:007040_11	cerebral cortex; neuropil
Module 87	HPA:046030_10	tonsil; squamous epithelial cells
Module 87	HPA:046030_01	tonsil; squamous epithelial cells
Module 87	HPA:046030_02	tonsil; squamous epithelial cells
Module 87	HPA:046030_11	tonsil; squamous epithelial cells
Module 87	HPA:046030_12	tonsil; squamous epithelial cells
Module 87	HPA:035030	skin 1; keratinocytes
Module 87	HPA:035030_10	skin 1; keratinocytes
Module 87	HPA:035030_11	skin 1; keratinocytes
Module 87	HPA:035030_12	skin 1; keratinocytes
Module 87	HPA:021010	liver; bile duct cells
Module 87	HPA:021010_01	liver; bile duct cells
Module 87	HPA:021010_10	liver; bile duct cells
Module 87	HPA:021010_11	liver; bile duct cells
Module 87	HPA:021010_12	liver; bile duct cells
Module 87	HPA:039010_10	soft tissue 1; adipocytes
Module 87	HPA:039010_11	soft tissue 1; adipocytes
Module 87	HPA:039010_12	soft tissue 1; adipocytes
Module 87	HPA:031010_10	rectum; glandular cells
Module 87	HPA:031010_11	rectum; glandular cells
Module 87	HPA:031010_12	rectum; glandular cells
Module 87	HPA:031010_13	rectum; glandular cells
Module 87	HPA:004030_10	breast; myoepithelial cells
Module 87	HPA:004030_11	breast; myoepithelial cells
Module 87	HPA:004030_12	breast; myoepithelial cells
Module 87	HPA:034010_10	skeletal muscle; myocytes
Module 87	HPA:034010_11	skeletal muscle; myocytes
Module 87	HPA:034010_12	skeletal muscle; myocytes
Module 87	HPA:046020_10	tonsil; non-germinal center cells
Module 87	HPA:046020_11	tonsil; non-germinal center cells

Module	Terms	Description
Module 87	HPA:046020_12	tonsil; non-germinal center cells
Module 87	HPA:046020_13	tonsil; non-germinal center cells
Module 87	HPA:022010_10	lung; macrophages
Module 87	HPA:022010_11	lung; macrophages
Module 87	HPA:022010_12	lung; macrophages
Module 87	HPA:022010_13	lung; macrophages
Module 87	HPA:022020_10	lung; pneumocytes
Module 87	HPA:022020_11	lung; pneumocytes
Module 87	HPA:022020_12	lung; pneumocytes
Module 87	HPA:047010_10	urinary bladder; urothelial cells
Module 87	HPA:047010_11	urinary bladder; urothelial cells
Module 87	HPA:047010_12	urinary bladder; urothelial cells
Module 87	HPA:047010_13	urinary bladder; urothelial cells
Module 87	HPA:044020_10	testis; cells in seminiferous ducts
Module 87	HPA:044020_11	testis; cells in seminiferous ducts
Module 87	HPA:044020_12	testis; cells in seminiferous ducts
Module 87	HPA:036010_01	skin 2; epidermal cells
Module 87	HPA:036010_02	skin 2; epidermal cells
Module 87	HPA:036010_10	skin 2; epidermal cells
Module 87	HPA:036010_11	skin 2; epidermal cells
Module 87	HPA:036010_12	skin 2; epidermal cells
Module 87	HPA:011000	endometrium 1
Module 87	HPA:011010	endometrium 1; cells in endometrial stroma
Module 87	HPA:011010_10	endometrium 1; cells in endometrial stroma
Module 87	HPA:011010_11	endometrium 1; cells in endometrial stroma
Module 87	HPA:011010_12	endometrium 1; cells in endometrial stroma
Module 87	HPA:004020	breast; glandular cells
Module 87	HPA:004020_10	breast; glandular cells
Module 87	HPA:004020_01	breast; glandular cells
Module 87	HPA:004020_11	breast; glandular cells
Module 87	HPA:004020_12	breast; glandular cells
Module 87	HPA:004020_13	breast; glandular cells
Module 87	HPA:035040_10	skin 1; melanocytes
Module 87	HPA:035040_11	skin 1; melanocytes
Module 87	HPA:035040_12	skin 1; melanocytes
Module 87	HPA:002010_10	appendix; glandular cells
Module 87	HPA:002010_11	appendix; glandular cells
Module 87	HPA:002010_12	appendix; glandular cells
Module 87	HPA:015010_10	fallopian tube; glandular cells

Module	Terms	Description
Module 87	HPA:015010_11	fallopian tube; glandular cells
Module 87	HPA:015010_12	fallopian tube; glandular cells
Module 87	HPA:015010_13	fallopian tube; glandular cells
Module 87	HPA:009020_10	colon; glandular cells
Module 87	HPA:009020_11	colon; glandular cells
Module 87	HPA:009020_12	colon; glandular cells
Module 87	HPA:009020_13	colon; glandular cells
Module 87	HPA:007030_10	cerebral cortex; neuronal cells
Module 87	HPA:007030_11	cerebral cortex; neuronal cells
Module 87	HPA:007030_12	cerebral cortex; neuronal cells
Module 87	HPA:007030_13	cerebral cortex; neuronal cells
Module 87	HPA:006010_10	cerebellum; purkinje cells
Module 87	HPA:006010_11	cerebellum; purkinje cells
Module 87	HPA:006010_12	cerebellum; purkinje cells
Module 87	HPA:006010_13	cerebellum; purkinje cells
Module 87	HPA:016010_10	gallbladder; glandular cells
Module 87	HPA:016010_11	gallbladder; glandular cells
Module 87	HPA:016010_12	gallbladder; glandular cells
Module 87	HPA:016010_13	gallbladder; glandular cells
Module 87	HPA:040040_10	soft tissue 2; peripheral nerve
Module 87	HPA:040040_11	soft tissue 2; peripheral nerve
Module 87	HPA:006030	cerebellum; cells in molecular layer
Module 87	HPA:006030_10	cerebellum; cells in molecular layer
Module 87	HPA:006030_11	cerebellum; cells in molecular layer
Module 87	HPA:006030_12	cerebellum; cells in molecular layer
Module 87	HPA:011020_10	endometrium 1; glandular cells
Module 87	HPA:011020_11	endometrium 1; glandular cells
Module 87	HPA:011020_12	endometrium 1; glandular cells
Module 87	HPA:011020_13	endometrium 1; glandular cells
Module 87	HPA:039020	soft tissue 1; chondrocytes
Module 87	HPA:039020_01	soft tissue 1; chondrocytes
Module 87	HPA:039020_02	soft tissue 1; chondrocytes
Module 87	HPA:039020_10	soft tissue 1; chondrocytes
Module 87	HPA:039020_11	soft tissue 1; chondrocytes
Module 87	HPA:039020_12	soft tissue 1; chondrocytes
Module 87	HPA:039020_13	soft tissue 1; chondrocytes
Module 87	HPA:019020_10	kidney; cells in tubules
Module 87	HPA:019020_11	kidney; cells in tubules
Module 87	HPA:019020_12	kidney; cells in tubules

Module	Terms	Description
Module 87	HPA:019020_13	kidney; cells in tubules
Module 87	HPA:028000	parathyroid gland
Module 87	HPA:028010	parathyroid gland; glandular cells
Module 87	HPA:028010_10	parathyroid gland; glandular cells
Module 87	HPA:028010_01	parathyroid gland; glandular cells
Module 87	HPA:028010_02	parathyroid gland; glandular cells
Module 87	HPA:028010_11	parathyroid gland; glandular cells
Module 87	HPA:028010_12	parathyroid gland; glandular cells
Module 87	HPA:028010_13	parathyroid gland; glandular cells
Module 87	HPA:001010_10	adrenal gland; glandular cells
Module 87	HPA:001010_11	adrenal gland; glandular cells
Module 87	HPA:001010_12	adrenal gland; glandular cells
Module 87	HPA:038000	smooth muscle
Module 87	HPA:038010	smooth muscle; smooth muscle cells
Module 87	HPA:038010_01	smooth muscle; smooth muscle cells
Module 87	HPA:038010_10	smooth muscle; smooth muscle cells
Module 87	HPA:038010_11	smooth muscle; smooth muscle cells
Module 87	HPA:038010_12	smooth muscle; smooth muscle cells
Module 87	HPA:044010_10	testis; leydig cells
Module 87	HPA:044010_11	testis; leydig cells
Module 87	HPA:044010_12	testis; leydig cells
Module 87	KEGG:05010	alzheimer's disease
Module 87	KEGG:05012	parkinson's disease
Module 87	KEGG:04932	non-alcoholic fatty liver disease (nafld)
Module 87	KEGG:00670	one carbon pool by folate
Module 88	OMIM:613794	retinitis pigmentosa 20; rp20
Module 88	OMIM:204100	leber congenital amaurosis 2; lca2; amaurosis congenita of leber ii
Module 89	CORUM:3066	rna polymerase ii complex, chromatin structure modifying
Module 89	HPA:011010_12	endometrium 1; cells in endometrial stroma
Module 89	OMIM:615637	mental retardation, autosomal recessive 41; mrt41
Module 89	OMIM:610048	corneal dystrophy, congenital stromal; cscd; congenital stromal corneal dystrophy
Module 89	OMIM:261500	eosinophil peroxidase deficiency; epxd; eosinophil peroxidase deficiency, partial; peroxidase and phospholipid deficiency in eosinophils; presentey anomaly
Module 89	OMIM:607626	ichthyosis, leukocyte vacuoles, alopecia, and sclerosing cholangitis; ilvasc; ichthyosis-sclerosing cholangitis syndrome; neonatal ichthyosis-sclerosing cholangitis syndrome; nisch syndrome
Module 89	OMIM:601358	nicolaides-baraitser syndrome; ncbrs; sparse hair and mental retardation; nbs
Module 89	OMIM:180849	rubinstein-taybi syndrome
Module 90	-	-
Module 91	TF:M00953_1	factor: ar; motif: nnnngnrrgnacanngtgtctctnnnnnn; match class: 1

Module	Terms	Description
Module 92	OMIM:616216	thrombocytopenia 5; the5; thrombocytopenia 5 with increased susceptibility to malignancy; thrombocytopenia, autosomal dominant, 5
Module 92	TF:M06650_1	factor: znf670; motif: nntgtracccgn; match class: 1
Module 93	-	-
Module 94	GO:0012505	endomembrane system
Module 94	OMIM:615530	parkinson disease 20, early-onset; park20
Module 94	OMIM:146800	ichthyosis bullosa of siemens; ibs; ichthyosis, bullous typeichthyosis exfoliativa, included
Module 94	OMIM:300868	multiple congenital anomalies-hypotonia-seizures syndrome 2; mcahs2; epileptic encephalopathy, early infantile, 20; eiee20
Module 94	OMIM:613751	heterotaxy, visceral, 4, autosomal; htx4
Module 94	OMIM:616511	maturity-onset diabetes of the young, type 14; mody14
Module 94	OMIM:601110	congenital disorder of glycosylation, type id; cdg1d; cdg id; cdgid; carbohydrate-deficient glycoprotein syndrome, type iv, formerly; cdgs4, formerly; cdgs, type iv, formerly
Module 94	OMIM:310400	myopathy, centronuclear, x-linked; cnmx; myotubular myopathy, x-linked; mtmx; xlmtn; myotubular myopathy 1; mtm1
Module 94	OMIM:614886	peroxisome biogenesis disorder 12a (zellweger); pbd12peroxisome biogenesis disorder, complementation group 14, included; cg14, included; peroxisome biogenesis disorder, complementation group j, included; cgj, included
Module 95	-	-

Note: Annotations were omitted if unknown

Appendix

Appendix E.

Inward regulation.

Module	Number of inward regulated modules	Inward regulated modules
1	16	9,17,22,30,32,39,41,49,55,57,58,66,67,69,75,77
2	26	9,14,17,20,22,30,32,33,39,41,43,49,50,55,57,58,61,66,67,69,70,75,77,84,85,92
3	49	4,5,8,9,10,11,13,15,16,17,20,22,23,25,28,30,32,34,36,38,39,40,41,44,45,49,52,55,57,58,60,61,63,66,67,69,70,73,75,77,84,85,86,88,89,90,92,93,95
4	23	1,9,17,22,30,32,33,39,41,42,49,55,57,58,61,66,67,69,70,75,77,84,92
5	64	1,3,8,9,12,14,15,16,17,18,20,21,22,25,26,27,28,30,31,32,33,34,35,38,39,40,41,42,44,45,49,50,51,52,55,56,57,58,59,60,61,63,64,65,67,68,69,70,72,73,75,77,78,80,82,83,84,85,87,88,90,91,92,95

Module	Number of inward regulated modules	Inward regulated modules
6	25	9,15,17,20,22,30,32,39, 41,43,49,55,57,58,61,66, 67,69,70,75,77,84,85,89,92
7	25	2,9,12,13,17,21,22,23,27, 32,36,39,42,49,50,57,59, 64,66,73,77,82,88,90,93
8	63	3,4,8,9,10,12,14,15,16,17, 18,20,21,22,25,26,27,28, 30,31,32,33,34,35,38,39, 40,41,43,45,49,50,51,52, 53,55,56,57,58,59,60,61, 63,64,65,67,68,69,70,75, 77,78,80,83,84,85,87,88, 89,90,91,92,95
9	11	22,39,42,44,49,57,61, 66,67,75,76
10	25	9,17,20,22,30,32,33,34, 39,41,43,49,55,57,58,61, 66,67,69,70,75,77,84,85, 92
11	63	3,4,8,9,10,12,13,14,15, 16,17,18,20,21,22,25,26, 27,28,30,31,32,33,34,35, 38,39,40,41,45,49,50,52, 55,56,57,58,60,61,63,64, 65,66,67,68,69,70,72,73, 75,77,78,80,83,84,85,87, 88,89,90,91,92,95
12	58	6,8,9,10,12,14,15,16,17, 20,21,22,26,27,28,30,32, 33,34,38,39,40,41,43,45, 49,50,51,52,53,55,56,57, 58,59,60,61,62,64,66,67, 68,69,70,75,77,78,82,83, 84,85,87,88,89,90,91,92, 95
13	18	9,17,22,30,32,39,41,49,50, 55,57,58,66,67,69,75,77,92
14	60	8,9,10,12,14,15,16,17,18,20, 21,22,25,26,27,28,30,31,32, 33,34,35,38,39,40,41,42,45, 49,50,52,55,56,57,58,60,61, 63,64,65,66,67,68,69,70,73, 75,77,78,80,83,84,85,86, 87,88,89,90,92,95
15	28	1,9,15,17,20,22,25,28,30,32, 33,34,39,41,49,55,57,58,61, 67,68,70,75,77,84,85,89,92
16	24	9,13,14,19,21,22,23,27,31, 39,42,47,49,50,57,58,59, 62,63,64,70,78,81,88
17	21	9,17,22,30,32,33,39,41,43, 49,55,57,58,61,66,67,69, 75,77,84,92
18	13	9,17,22,30,32,39,49,55,57, 58,66,67,69

Module	Number of inward regulated modules	Inward regulated modules
19	78	2,3,4,5,7,8,9,10,12,13,14,15,16,17,19,20,21,22,23,25,26,27,28,30,31,32,33,34,35,38,39,40,41,42,43,44,45,46,49,50,52,54,55,56,57,58,60,61,62,63,64,65,66,67,68,69,70,71,72,73,75,76,77,78,80,82,83,84,85,86,87,88,89,90,91,92,93,95
20	46	2,4,8,9,12,13,15,17,21,22,25,28,30,32,34,35,36,38,39,40,41,43,44,49,50,51,52,55,57,58,60,61,63,67,68,69,70,75,77,84,85,90,92,93,94,95
21	12	9,22,30,32,39,41,49,55,57,66,67,75
22	19	17,22,30,32,39,41,49,50,55,57,58,61,66,67,70,75,77,88,92
23	35	2,9,14,15,17,20,22,28,30,32,33,34,38,39,41,42,49,55,56,57,58,61,66,67,69,70,73,75,77,83,84,85,88,92,95
24	61	8,9,10,12,13,14,15,16,17,18,20,21,22,25,26,27,28,30,31,32,33,34,35,38,39,40,41,45,49,50,52,55,56,57,58,60,61,63,64,66,67,68,69,70,72,73,75,77,78,80,83,84,85,86,87,88,89,90,92,93,95
25	19	1,2,9,17,30,32,39,41,49,55,57,58,66,67,70,75,77,88,92
26	14	17,22,30,32,39,49,55,57,61,66,67,70,77,92
27	16	9,17,22,30,32,39,41,49,55,57,58,66,67,69,75,77
28	16	9,17,22,30,32,39,41,49,55,57,58,66,67,69,75,77
29	41	2,9,14,15,17,20,21,22,28,30,32,33,34,38,39,41,42,43,45,49,50,55,56,57,58,61,64,67,68,69,70,73,75,77,82,83,84,85,88,92,95
30	17	9,17,22,30,32,39,41,49,55,57,58,66,67,69,75,77,92
31	28	8,9,15,17,20,22,30,32,33,34,39,41,49,55,57,58,61,66,67,69,70,73,75,77,84,85,92,93
32	23	9,12,13,21,22,23,33,39,41,42,44,47,49,50,57,64,66,73,77,81,82,88,90
33	58	8,9,10,12,15,16,17,20,21,22,25,26,27,28,30,31,32,33,34,35,38,39,40,41,43,45,49,50,52,55,56,57,58,59,60,61,63,64,65,67,68,69,70,72,73,75,77,78,83,84,85,87,88,89,90,91,92,95

Module	Number of inward regulated modules	Inward regulated modules
34	59	8,9,10,12,14,15,16,17,18,20,21,22,25,26,27,28,30,31,32,33,34,35,38,39,40,41,45,49,50,52,53,55,56,57,58,60,61,62,63,64,66,67,68,69,70,73,75,77,78,80,83,84,85,87,88,89,90,92,95
35	51	4,5,8,9,10,11,12,13,15,16,17,20,22,23,25,28,30,32,34,36,38,39,40,41,44,45,49,52,53,55,57,58,60,61,63,66,67,68,69,70,73,75,77,84,85,86,88,89,90,93,94
36	21	1,2,9,17,30,32,39,41,42,49,55,57,58,61,66,67,69,70,75,77,92
37	14	9,17,22,30,32,39,49,55,57,58,66,67,69,77
38	15	9,17,22,30,32,39,49,55,57,58,61,67,69,77,92
39	22	9,13,21,22,23,27,32,39,42,49,50,53,55,62,64,66,77,78,81,82,88,93
40	48	8,9,12,14,15,16,17,20,22,25,26,28,30,31,32,33,34,38,39,40,41,43,45,49,50,55,56,57,58,60,61,63,65,66,67,69,70,73,75,77,80,83,84,85,88,90,92,95
41	15	9,17,22,30,32,39,49,50,55,57,58,66,67,69,77
42	40	2,6,9,13,14,16,17,18,21,22,23,27,28,33,35,39,41,42,44,47,49,50,53,55,57,58,63,64,66,72,73,77,78,81,82,83,87,88,90,93
43	17	21,22,27,33,39,41,47,53,57,58,61,64,66,70,75,87,90
44	36	8,9,12,14,15,17,20,22,25,30,32,34,38,39,41,45,49,51,55,57,58,59,60,61,66,67,69,70,75,77,84,85,88,90,92,95
45	17	9,11,19,20,22,27,30,32,39,45,57,58,59,64,70,76,88
46	54	4,8,9,11,12,13,15,16,17,20,22,23,25,28,30,32,33,34,35,38,39,40,41,45,49,52,53,55,56,57,58,60,61,62,63,64,66,67,68,69,70,75,77,80,83,84,85,86,87,88,89,90,92,95
47	48	4,5,8,9,10,11,13,15,16,17,20,22,23,25,28,30,32,34,36,38,39,40,41,45,49,52,55,57,58,60,61,63,66,67,69,70,73,75,77,84,85,86,88,89,90,92,93,95
48	25	15,17,20,22,27,32,38,39,41,49,50,55,57,58,61,64,66,67,69,75,77,84,85,88,92
49	84	1,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,19,20,21,22,23,25,26,27,28,30,31,32,33,34,35,36,38,39,40,41,42,43,44,45,46,47,49,50,51,52,54,55,56,57,58,60,61,62,63,64,66,67,68,69,70,71,72,73,75,76,77,78,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95

Module	Number of inward regulated modules	Inward regulated modules
50	61	4,8,9,10,12,13,15,17,18,19,20,22,25,27,28,30,32,33,34,35,38,39,40,41,42,44,46,49,52,53,55,56,57,58,60,61,64,65,66,67,68,69,70,72,73,75,76,77,78,80,82,83,84,85,86,87,88,89,92,93,95
51	19	9,17,22,30,32,39,41,49,50,55,57,58,61,66,67,69,75,77,92
52	15	9,17,22,30,32,39,49,55,57,58,61,67,70,77,92
53	48	4,5,8,9,10,11,13,15,16,17,20,22,23,25,28,30,32,34,36,38,39,40,41,45,49,52,55,57,58,60,61,63,66,67,69,70,73,75,77,84,85,86,88,89,90,92,93,95
54	57	1,3,5,6,8,9,11,13,14,16,18,20,21,22,23,26,27,28,30,31,33,34,35,36,38,39,41,42,44,47,49,50,51,53,55,56,57,58,59,60,61,64,65,66,67,70,72,73,74,75,77,78,81,82,83,88,93
55	29	9,13,18,21,22,23,27,33,39,44,47,49,50,53,55,57,58,64,66,73,75,77,78,81,82,88,90,91,93
56	16	9,17,22,30,32,39,49,55,57,58,61,66,67,70,77,92
57	62	4,8,9,10,12,13,14,15,16,17,18,20,21,22,25,26,27,28,30,31,32,33,34,35,38,39,40,41,44,45,49,50,52,55,56,57,58,59,60,61,63,64,66,67,68,69,70,72,73,75,77,78,83,84,85,87,88,89,90,91,92,95
58	38	13,14,17,20,21,23,27,30,32,33,35,38,39,41,42,44,47,49,50,53,55,56,57,58,61,64,66,73,77,78,82,83,87,88,90,91,92,93
59	83	1,3,4,5,7,8,9,10,11,12,13,14,15,16,17,19,20,21,22,23,24,25,26,27,28,30,31,32,33,34,35,38,39,40,41,42,43,45,46,47,48,49,50,52,53,54,55,56,57,58,60,61,62,63,64,65,66,67,68,69,70,71,72,73,75,76,77,78,80,81,82,83,84,85,86,87,88,89,90,91,92,94,95
60	24	17,20,22,27,30,32,33,39,41,49,50,55,57,58,61,64,66,67,69,75,77,84,85,92
61	17	9,22,30,32,39,41,49,55,57,58,61,66,67,69,75,77,92
62	16	9,17,22,30,32,39,41,49,55,57,58,66,67,69,75,85
63	22	1,2,9,17,30,32,39,41,42,49,55,57,58,61,66,67,70,75,77,84,88,92
64	74	1,3,4,7,8,9,10,12,13,14,15,16,17,18,20,21,22,25,26,27,28,30,31,32,33,34,35,38,39,40,41,43,45,46,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,72,73,75,77,78,80,83,84,85,86,87,88,89,90,91,92,94,95
65	60	8,9,10,12,13,14,15,16,17,18,20,21,22,25,26,27,28,30,31,32,33,34,35,38,39,40,41,45,49,50,52,55,56,57,58,60,61,63,65,66,67,68,69,70,72,73,75,77,78,80,83,84,85,86,87,88,89,90,92,95

Module	Number of inward regulated modules	Inward regulated modules
66	29	9,13,17,21,22,23,27,32,39,41,42,44,47,49,50,53,55,57,58,64,66,73,77,78,81,82,87,88,93
67	16	9,10,14,21,22,27,32,39,49,57,60,66,75,76,78,91
68	65	1,2,8,9,10,12,13,14,15,16,17,20,22,23,25,26,27,28,30,31,32,33,34,35,36,37,38,39,40,41,42,43,45,49,50,52,55,56,57,58,60,61,63,64,65,66,67,68,69,70,73,75,77,78,80,83,84,85,86,87,88,89,90,92,95
69	20	9,17,22,30,32,39,41,49,50,55,57,58,61,66,67,69,70,75,77,92
70	69	1,3,5,6,8,9,10,12,13,14,15,16,17,18,20,21,22,25,26,27,28,30,32,33,35,38,39,40,41,43,44,45,49,50,51,52,53,55,56,57,58,59,60,61,62,64,66,67,68,69,70,73,77,78,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95
71	64	9,10,12,14,15,16,17,18,20,21,22,23,26,27,28,30,32,33,34,35,38,39,40,41,42,44,45,46,47,49,50,52,53,55,56,57,58,60,61,64,66,67,68,69,70,73,75,77,78,80,82,83,84,85,86,87,88,89,90,91,92,93,94,95
72	23	14,17,20,22,27,30,32,33,39,41,49,50,55,57,58,61,66,67,69,75,77,84,92
73	29	9,13,16,18,21,22,23,27,28,35,36,39,44,47,49,50,53,57,58,59,60,63,64,70,73,77,81,90,93
74	23	1,9,13,14,21,22,23,27,39,44,47,49,53,57,58,59,63,64,68,75,78,88,93
75	61	8,9,10,12,14,15,16,17,18,20,21,22,25,26,27,28,30,31,32,33,34,35,38,39,40,41,43,45,49,50,52,53,55,56,57,58,60,61,63,64,66,67,68,69,70,72,73,75,77,78,80,83,84,85,87,88,89,90,91,92,95
76	24	9,13,16,21,22,23,27,39,44,47,49,53,57,58,62,63,64,66,73,78,81,87,88,93
77	43	8,9,14,15,17,20,22,25,26,28,30,32,33,34,38,39,40,41,45,49,50,55,56,57,58,60,61,63,65,67,68,69,70,73,75,77,83,84,85,88,89,92,95
78	36	5,8,9,13,15,17,20,22,25,28,30,32,33,34,38,39,41,49,55,57,58,60,61,63,66,67,69,70,75,77,84,85,88,92,93,95
79	18	9,17,22,30,32,39,41,49,55,57,58,61,66,67,69,75,77,92
80	15	9,17,22,30,32,39,49,55,57,58,61,67,70,77,92
81	65	1,2,3,8,9,10,12,13,14,15,17,20,21,22,25,27,28,30,31,32,33,34,35,38,39,40,41,42,43,45,49,50,52,55,56,57,58,59,60,61,63,65,66,67,68,69,70,72,73,75,76,77,78,80,83,84,85,86,87,88,89,90,92,93,95
82	20	9,17,22,30,32,39,41,49,50,55,57,58,61,66,67,69,70,75,77,92

Module	Number of inward regulated modules	Inward regulated modules
83	23	9,17,20,22,30,32,33,39,41,43,49,50,55,57,58,61,66,67,69,75,77,84,92
84	45	10,14,15,17,18,20,22,25,27,30,31,32,33,34,38,39,41,42,44,49,52,53,55,56,57,58,60,61,64,66,67,69,70,73,75,77,78,83,84,85,87,88,91,92,95
85	17	2,9,14,17,30,32,39,49,55,57,58,66,67,70,75,77,92
86	25	9,14,17,22,30,32,33,34,39,41,43,49,55,57,58,61,66,67,69,70,75,77,84,85,92
87	16	9,22,30,32,39,41,49,55,57,58,66,67,69,75,77,92
88	58	8,9,10,12,13,14,15,16,17,18,20,21,22,25,26,27,28,30,31,32,33,34,35,38,39,40,41,45,49,50,52,55,56,57,58,60,61,63,65,67,68,69,70,72,73,75,77,78,80,83,84,85,87,88,89,90,92,95
89	57	8,9,10,12,13,14,15,17,20,22,25,27,28,30,31,32,33,34,35,38,39,40,41,45,49,50,52,55,56,57,58,60,61,63,65,66,67,68,69,70,72,73,75,77,78,80,83,84,85,86,87,88,89,90,92,93,95
90	12	9,17,22,30,32,39,49,55,57,66,67,70
91	56	2,8,9,10,14,15,16,17,20,21,22,23,27,28,30,31,32,33,34,35,38,39,40,41,42,45,49,50,52,55,56,57,58,60,61,63,64,66,67,68,69,70,73,75,77,80,83,84,85,86,87,88,89,90,92,95
92	64	1,2,3,8,9,10,12,14,15,16,17,20,21,22,25,26,27,28,30,31,32,33,34,35,38,39,40,41,42,45,49,50,52,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,73,75,77,78,80,83,84,85,86,87,88,89,90,92,95
93	37	6,9,13,14,20,21,22,23,27,30,31,32,33,36,39,41,44,47,49,50,53,55,56,58,63,64,66,68,69,73,77,78,81,83,88,91,93
94	56	2,8,9,12,14,15,16,17,20,21,22,25,26,28,30,31,32,33,34,38,39,40,41,42,43,49,50,52,55,56,57,58,60,61,63,65,66,67,68,69,70,73,75,77,78,80,83,84,85,86,87,88,89,90,92,95
95	14	9,17,22,30,32,39,49,55,57,58,66,67,70,77

Appendix

Appendix F.

Overlapping genes with replicate 1.

Gene name or Incyte clone ID	Description
1381654	asparagine synthetase
1593787	gamma-aminobutyric acid (GABA) A receptor, beta 1
MPDZ	Multiple PDZ domain protein
ACTB	Actin, beta

Gene name or Incyte clone ID	Description
MMP16	Matrix metalloproteinase 16 (membrane-inserted)
UBE1L	Ubiquitin-activating enzyme E1-like
2371441	nuclear receptor subfamily 5, group A, member 1
AKT2	V-akt murine thymoma viral oncogene homolog 2
EIF2S1	Eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa
3869412	homeo box D4
ALDH3B1	Aldehyde dehydrogenase 3 family, member B1
MBOAT5	Membrane bound O-acyltransferase domain containing 5
ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
KIAA0367	KIAA0367
PLXNA2	Plexin A2
1720056	prion protein (p27–30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)
PSCD3	Pleckstrin homology, Sec7 and coiled-coil domains 3
FUS	Fusion (involved in t(12;16) in malignant liposarcoma)
THBS4	Thrombospondin 4
HSU79275	Hypothetical protein HSU79275
NEDD4	Neural precursor cell expressed, developmentally down-regulated 4
RAB31	RAB31, member RAS oncogene family
SKIV2L2	Superkiller viralicidic activity 2-like 2 (S. cerevisiae)
LTBP4	Latent transforming growth factor beta binding protein 4
COL7A1	Collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive)
PPP1CC	Protein phosphatase 1, catalytic subunit, gamma isoform
PRDX2	Peroxiredoxin 2
PCYOX1	Prenylcysteine oxidase 1
MGEA5	Meningioma expressed antigen 5 (hyaluronidase)
H3F3B	H3 histone, family 3B (H3.3B)
1806521	TGFB inducible early growth response
CACNG3	Calcium channel, voltage-dependent, gamma subunit 3
GCG	Glucagon
DUSP3	Dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)
DNAJB2	DnaJ (Hsp40) homolog, subfamily B, member 2
ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2
3642720	calcium channel, voltage-dependent, alpha 2/delta subunit 2
CTSD	Cathepsin D
4190790	hepatocyte growth factor (hepapoietin A; scatter factor)
LARP1	La ribonucleoprotein domain family, member 1
JARID2	Jumonji, AT rich interactive domain 2
HDLBP	High density lipoprotein binding protein (vigilin)

Gene name or Incyte clone ID	Description
HMGCS2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)
CALCRL	Calcitonin receptor-like
2188753	tryptase, beta (tryptase II)
CDK3	Cyclin-dependent kinase 3
3031764	mitogen-activated protein kinase kinase 7
SELE	Selectin E (endothelial adhesion molecule 1)
FAM89B	Family with sequence similarity 89, member B
LCP1	Lymphocyte cytosolic protein 1 (L-plastin)
SFRS3	Splicing factor, arginine/serine-rich 3
OAT	Ornithine aminotransferase (gyrate atrophy)
ENO2	Enolase 2 (gamma, neuronal)
3074077	solute carrier family 1 (glial high affinity glutamate transporter), member 3
CDC42EP1	CDC42 effector protein (Rho GTPase binding) 1
RXRA	Retinoid X receptor, alpha
STK38	Serine/threonine kinase 38
3509376	phosphoglucomutase 5
G3BP2	GTPase activating protein (SH3 domain) binding protein 2
DMN	Desmuslin
DHRS2	Dehydrogenase/reductase (SDR family) member 2
ITGA9	Integrin, alpha 9
HESX1	HESX homeobox 1
ANGEL1	Angel homolog 1 (Drosophila)
NPC1	Niemann-Pick disease, type C1
TOP3B	Topoisomerase (DNA) III beta
INPP1	Inositol polyphosphate-1-phosphatase
LOC151162	Hypothetical protein LOC151162
RPS16	Ribosomal protein S16
TNNC2	Troponin C type 2 (fast)
MTR	5-methyltetrahydrofolate-homocysteine methyltransferase
CDC45L	CDC45 cell division cycle 45-like (S. cerevisiae)
SLC35D2	Solute carrier family 35, member D2
MTX2	Metaxin 2
2061432	spermine synthase
BCKDHB	Branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease)
WEE1	WEE1 homolog (S. pombe)
PPP1R7	Protein phosphatase 1, regulatory (inhibitor) subunit 7
ADAM9	ADAM metallopeptidase domain 9 (meltrin gamma)
STAT3	Signal transducer and activator of transcription 3 (acute-phase response factor)
ARNT2	Aryl-hydrocarbon receptor nuclear translocator 2

Gene name or Incyte clone ID	Description
C7orf24	Chromosome 7 open reading frame 24
PNMA1	Paraneoplastic antigen MA1
HNRPH1	Heterogeneous nuclear ribonucleoprotein H1 (H)
ATP6V1D	ATPase, H ⁺ transporting, lysosomal 34kDa, V1 subunit D
SCAP	SREBF chaperone
PTPRM	Protein tyrosine phosphatase, receptor type, M
SMO	Smoothed homolog (Drosophila)
PFKP	Phosphofructokinase, platelet
LRPPRC	Leucine-rich PPR-motif containing
SDHD	Succinate dehydrogenase complex, subunit D, integral membrane protein
GART	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
SSRP1	Structure specific recognition protein 1
MAST2	Microtubule associated serine/threonine kinase 2
DOCK2	Dedicator of cytokinesis 2
I238619	KIAA0117 protein
TMCC1	Transmembrane and coiled-coil domain family 1
UNC119	Unc-119 homolog (C. elegans)
LOC162427	Hypothetical protein LOC162427
LOC644739	Similar to Wiskott-Aldrich syndrome protein family member 4 (WASP-family protein member 4)
ATIC	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase
MAZ	MYC-associated zinc finger protein (purine-binding transcription factor)
SMG7	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)
ATP9A	ATPase, Class II, type 9A
ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5
CLCC1	Chloride channel CLIC-like 1
TCN1	Transcobalamin I (vitamin B12 binding protein, R binder family)
PIP5K1A	Phosphatidylinositol-4-phosphate 5-kinase, type I, alpha
KLHDC7A	Kelch domain containing 7A
EIF2S3	Eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa
GARS	Glycyl-tRNA synthetase
PQLC3	PQ loop repeat containing 3
ZNFX1	Zinc finger, NFX1-type containing 1
VAV3	Vav 3 oncogene
567189	hypothetical protein
CEP170	Centrosomal protein 170kDa
PEX3	Peroxisomal biogenesis factor 3
CUL3	Cullin 3
CEACAM5	Carcinoembryonic antigen-related cell adhesion molecule 5

Gene name or Incyte clone ID	Description
TAPBP	TAP binding protein (tapasin)
79797	Transcribed locus
GRK6	G protein-coupled receptor kinase 6
1979217	sterol regulatory element binding transcription factor 2
LAT	Linker for activation of T cells
DUSP6	Dual specificity phosphatase 6
CAPZA1	Capping protein (actin filament) muscle Z-line, alpha 1
AHSG	Alpha-2-HS-glycoprotein
SPR	Sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)
RDX	Radixin
PICK1	Protein interacting with PRKCA 1
AHCY	S-adenosylhomocysteine hydrolase
DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1
IFNGR2	Interferon gamma receptor 2 (interferon gamma transducer 1)
PDK1	Pyruvate dehydrogenase kinase, isozyme 1
PRCC	Papillary renal cell carcinoma (translocation-associated)
HRSP12	Heat-responsive protein 12
SEMA4D	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D
ATP2A3	ATPase, Ca++ transporting, ubiquitous
GANAB	Glucosidase, alpha; neutral AB
ERCC5	Excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))
TCEB2	Transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)
C8B	Complement component 8, beta polypeptide
SF3A1	Splicing factor 3a, subunit 1, 120kDa
SCO1	SCO cytochrome oxidase deficient homolog 1 (yeast)
ENPP4	Ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)
1996309	KIAA0631 protein
PPP2R5E	Protein phosphatase 2, regulatory subunit B', epsilon isoform
GFPT2	Glutamine-fructose-6-phosphate transaminase 2
1626927	DKFZP566I1024 protein
NOL4	Nucleolar protein 4
SPATA2L	Spermatogenesis associated 2-like
CYLD	Cylindromatosis (turban tumor syndrome)
SCRG1	Scrapie responsive protein 1
C10orf10	Chromosome 10 open reading frame 10
KIF22	Kinesin family member 22
H1FX	H1 histone family, member X
C5orf13	Chromosome 5 open reading frame 13

Gene name or Incyte clone ID	Description
BST1	Bone marrow stromal cell antigen 1
DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, <i>S. cerevisiae</i>)
CCK	Cholecystokinin
AFF1	AF4/FMR2 family, member 1
BCL6	B-cell CLL/lymphoma 6 (zinc finger protein 51)
MGMT	O-6-methylguanine-DNA methyltransferase
SERPINB5	Serpin peptidase inhibitor, clade B (ovalbumin), member 5
PPP2R2A	Protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform
PRKAR1A	Protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)
1663943	KIAA0726 gene product
CPNE1	Copine 1
RBBP7	Retinoblastoma binding protein 7
FASTK	Fas-activated serine/threonine kinase
ZNF609	Zinc finger protein 609
BAIAP2	BAI1-associated protein 2
MN1	Meningioma (disrupted in balanced translocation) 1
EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2
CITED1	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1
SHROOM2	Shroom family member 2
GPX2	Glutathione peroxidase 2 (gastrointestinal)
HHEX	Hematopoietically expressed homeobox
HIF1A	Hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
3434853	arginine vasopressin receptor 2 (nephrogenic diabetes insipidus)
ARSE	Arylsulfatase E (chondrodysplasia punctata 1)
UBQLN2	Ubiquilin 2
891949	Transcribed locus
PRKAR1B	Protein kinase, cAMP-dependent, regulatory, type I, beta
1605140	Incyte EST
1879811	heme oxygenase (decycling) 1
TCL1A	T-cell leukemia/lymphoma 1A
CD7	CD7 molecule
TBX19	T-box 19
PTGFR	Prostaglandin F receptor (FP)
H2AFY	H2A histone family, member Y
DBF4	DBF4 homolog (<i>S. cerevisiae</i>)
2755432	CDNA FLJ36210 fis, clone THYMU2000155
U2AF1	U2 small nuclear RNA auxiliary factor 1

Gene name or Incyte clone ID	Description
ARID5A	AT rich interactive domain 5A (MRF1-like)
RERE	Arginine-glutamic acid dipeptide (RE) repeats
EFNA1	Ephrin-A1
PES1	Pescadillo homolog 1, containing BRCT domain (zebrafish)
HS6ST1	Heparan sulfate 6-O-sulfotransferase 1
VEGFB	Vascular endothelial growth factor B
BIN1	Bridging integrator 1
CD2	CD2 molecule
DTYMK	Deoxythymidylate kinase (thymidylate kinase)
RHOD	Ras homolog gene family, member D
CIAO1	Cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)
1476214	ARTC1 mRNA, complete sequence
TCL1A	T-cell leukemia/lymphoma 1A
VDAC1	Voltage-dependent anion channel 1
VPS13D	Vacuolar protein sorting 13 homolog D (S. cerevisiae)
CDC23	Cell division cycle 23 homolog (S. cerevisiae)
IGFBP5	Insulin-like growth factor binding protein 5
H1FX	H1 histone family, member X
ATG7	ATG7 autophagy related 7 homolog (S. cerevisiae)
ARHGEF18	Rho/rac guanine nucleotide exchange factor (GEF) 18
TTK	TTK protein kinase
DPM2	Dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit
CD5	CD5 molecule
MYO1A	Myosin IA
NR1H2	Nuclear receptor subfamily 1, group H, member 2
CHD1L	Chromodomain helicase DNA binding protein 1-like
MARK3	MAP/microtubule affinity-regulating kinase 3
ARPC3	Actin related protein 2/3 complex, subunit 3, 21kDa
2222804	Incyte EST
POLD1	Polymerase (DNA directed), delta 1, catalytic subunit 125kDa
CREBBP	CREB binding protein (Rubinstein-Taybi syndrome)
PTPN13	Protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)
2447837	Human DNA sequence from clone RP5-1103G7 on chromosome 20p12.2-13. Contains up to five unknown novel genes, the gene for a novel protein kinase domains containing protein similar to phosphoprotein C8FW and the SOX22 gene for SRY (s
C19orf56	Chromosome 19 open reading frame 56
ICAM3	Intercellular adhesion molecule 3
RAMP1	Receptor (G protein-coupled) activity modifying protein 1
ISG20	Interferon stimulated exonuclease gene 20kDa

Gene name or Incyte clone ID	Description
2418918	hepatocellular carcinoma associated protein; breast cancer associated gene 1
HNF4A	Hepatocyte nuclear factor 4, alpha
SERPINA1	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1
VEGFB	Vascular endothelial growth factor B
CHES1	Checkpoint suppressor 1
TADA2L	Transcriptional adaptor 2 (ADA2 homolog, yeast)-like
ADA	Adenosine deaminase
MAP2K3	Mitogen-activated protein kinase kinase 3
RGS1	Regulator of G-protein signalling 1
STK24	Serine/threonine kinase 24 (STE20 homolog, yeast)
RABGGTB	Rab geranylgeranyltransferase, beta subunit
PTTG1IP	Pituitary tumor-transforming 1 interacting protein
NOLC1	Nucleolar and coiled-body phosphoprotein 1
SOCS2	Suppressor of cytokine signaling 2
MPP6	Membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)
2626971	Transcribed locus
MARCKSL1	MARCKS-like 1
CDC2L1	Cell division cycle 2-like 1 (PITSLRE proteins)
RGS1	Regulator of G-protein signalling 1
NUP210	Nucleoporin 210kDa
2503119	proteasome (prosome, macropain) subunit, beta type, 5
BAI2	Brain-specific angiogenesis inhibitor 2
STXBP3	Syntaxin binding protein 3
CYP7B1	Cytochrome P450, family 7, subfamily B, polypeptide 1
SPAG7	Sperm associated antigen 7
PRKCA	Protein kinase C, alpha
2743724	Incyte EST
ING1	Inhibitor of growth family, member 1
GSTA3	Glutathione S-transferase A3
EP400	E1A binding protein p400
ARFIP1	ADP-ribosylation factor interacting protein 1 (arfaptin 1)
3176146	Incyte EST
MGP	Matrix Gla protein
RFC5	Replication factor C (activator 1) 5, 36.5kDa
SLC30A4	Solute carrier family 30 (zinc transporter), member 4
VNN1	Vanin 1
3031581	Incyte EST
DNAH17	Dynein, axonemal, heavy chain 17
TOX	Thymus high mobility group box protein TOX

Gene name or Incyte clone ID	Description
NFASC	Neurofascin homolog (chicken)
2690019	Incyte EST
TAP2	Transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)
DCBLD1	Discoidin, CUB and LCCL domain containing 1
PARK7	Parkinson disease (autosomal recessive, early onset) 7
RASAL1	RAS protein activator like 1 (GAP1 like)
MRS2L	MRS2-like, magnesium homeostasis factor (<i>S. cerevisiae</i>)
PEX14	Peroxisomal biogenesis factor 14
1607471	Incyte EST
GPR30	G protein-coupled receptor 30
CALCA	Calcitonin/calcitonin-related polypeptide, alpha
CLCA1	Chloride channel, calcium activated, family member 1
SORBS3	Sorbin and SH3 domain containing 3
RGS7	Regulator of G-protein signalling 7
CLDN7	Claudin 7
SPINT1	Serine peptidase inhibitor, Kunitz type 1
SLC19A1	Solute carrier family 19 (folate transporter), member 1
PIP	Prolactin-induced protein
CXCL1	Chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)
AQP9	Aquaporin 9
CYP4F3	Cytochrome P450, family 4, subfamily F, polypeptide 3
DNM2	Dynamin 2
CLIC2	Chloride intracellular channel 2
ATP4B	ATPase, H ⁺ /K ⁺ exchanging, beta polypeptide
SDC4	Syndecan 4
WNT11	Wingless-type MMTV integration site family, member 11
HLA-C	Major histocompatibility complex, class I, C
ELAVL2	ELAV (embryonic lethal, abnormal vision, <i>Drosophila</i>)-like 2 (Hu antigen B)
CORO1A	Coronin, actin binding protein, 1A
RHOBTB2	Rho-related BTB domain containing 2
VDAC1	Voltage-dependent anion channel 1
CD5	CD5 molecule
BLZF1	Basic leucine zipper nuclear factor 1 (JEM-1)
DPP9	Dipeptidyl-peptidase 9
SCNN1D	Sodium channel, nonvoltage-gated 1, delta
GALNT2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)
FRAT2	Frequently rearranged in advanced T-cell lymphomas 2
COL2A1	Collagen, type II, alpha 1 (primary osteoarthritis, spondyloepiphyseal dysplasia, congenital)

Gene name or Incyte clone ID	Description
LOC92312	Hypothetical protein LOC92312
KLK8	Kallikrein-related peptidase 8
2608629	cytochrome P450, subfamily XXIA (steroid 21-hydroxylase, congenital adrenal hyperplasia), polypeptide 2
NTSR1	Neurotensin receptor 1 (high affinity)
LPHN1	Latrophilin 1
MBL1P1	Mannose-binding lectin (protein A) 1, pseudogene 1
GDF11	Growth differentiation factor 11
LOC91316	Similar to bK246H3.1 (immunoglobulin lambda-like polypeptide 1, pre-B-cell specific)
CELSR3	Cadherin, EGF LAG seven-pass G-type receptor 3 (flamingo homolog, Drosophila)
KIAA0152	KIAA0152
PKD1	Polycystic kidney disease 1 (autosomal dominant)
ARHGDI	Rho GDP dissociation inhibitor (GDI) alpha
C8orf72	Chromosome 8 open reading frame 72
PRTN3	Proteinase 3 (serine proteinase, neutrophil, Wegener granulomatosis autoantigen)
PER1	Period homolog 1 (Drosophila)
LIMD1	LIM domains containing 1
NFATC4	Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4
PRKCE	Protein kinase C, epsilon
ROD1	ROD1 regulator of differentiation 1 (S. pombe)
LMAN2	Lectin, mannose-binding 2
TPM3	Tropomyosin 3
EEF1G	Eukaryotic translation elongation factor 1 gamma
ACTG2	Actin, gamma 2, smooth muscle, enteric
DHODH	Dihydroorotate dehydrogenase
SCEL	Sciellin
PIP5K2A	Phosphatidylinositol-4-phosphate 5-kinase, type II, alpha
CIB1	Calcium and integrin binding 1 (calmyrin)
ATAD3C	ATPase family, AAA domain containing 3C
ZNF460	Zinc finger protein 460
PCDHGC3	Protocadherin gamma subfamily C, 3
ANKRD12	Ankyrin repeat domain 12
TIMM8A	Translocase of inner mitochondrial membrane 8 homolog A (yeast)
4923601	Incyte EST
NDUFC1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa
RAB28	RAB28, member RAS oncogene family
TUBGCP2	Tubulin, gamma complex associated protein 2
2538487	butyrophilin, subfamily 3, member A2
3031912	Incyte EST

Gene name or Incyte clone ID	Description
LOC55565	Hypothetical protein LOC55565
TRPA1	Transient receptor potential cation channel, subfamily A, member 1
TUBB	Tubulin, beta
3837384	adenosine A2b receptor pseudogene
RPS21	Ribosomal protein S21
MTF2	Metal response element binding transcription factor 2
NPC2	Niemann-Pick disease, type C2
ADAM10	ADAM metalloproteinase domain 10
HIST1H2BG	Histone cluster 1, H2bg
4896093	solute carrier family 28 (sodium-coupled nucleoside transporter), member 1
HAX1	HCLS1 associated protein X-1
FKBP9	FK506 binding protein 9, 63 kDa
GTF2E1	General transcription factor IIE, polypeptide 1, alpha 56kDa
NPY2R	Neuropeptide Y receptor Y2
3606345	Incyte EST
OCLN	Occludin
DUT	DUTP pyrophosphatase
NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)
2601553	Incyte EST
DOC2B	Double C2-like domains, beta
3933661	Incyte EST
FLJ30092	AF-1 specific protein phosphatase
5045640	hydroxysteroid (17-beta) dehydrogenase 1
PCDH8	Protocadherin 8
LRP6	Low density lipoprotein receptor-related protein 6
NME5	Non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)
PDE6B	Phosphodiesterase 6B, cGMP-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant)
SLC7A1	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
LRRFIP1	Leucine rich repeat (in FLII) interacting protein 1
4914032	Incyte EST
KCNC4	Potassium voltage-gated channel, Shaw-related subfamily, member 4
GALNT2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)
DCK	Deoxycytidine kinase
MMP11	Matrix metalloproteinase 11 (stromelysin 3)
E2F4	E2F transcription factor 4, p107/p130-binding
Septin 7	Septin 7
ATP5C1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
FAM130A1	Family with sequence similarity 130, member A1

Gene name or Incyte clone ID	Description
CUL5	Cullin 5
SSR4	Signal sequence receptor, delta (translocon-associated protein delta)
ACOT8	Acyl-CoA thioesterase 8
RBMX	RNA binding motif protein, X-linked
CLPTM1	Cleft lip and palate associated transmembrane protein 1
ALCAM	Activated leukocyte cell adhesion molecule
CLDN7	Claudin 7
C8A	Complement component 8, alpha polypeptide
FCN2	Ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin)
488205	Clone 24407 mRNA sequence
SACM1L	SAC1 suppressor of actin mutations 1-like (yeast)
SLC16A1	Solute carrier family 16, member 1 (monocarboxylic acid transporter 1)
PFDN5	Prefoldin subunit 5
ECH1	Enoyl Coenzyme A hydratase 1, peroxisomal
ABL1	V-abl Abelson murine leukemia viral oncogene homolog 1
LTB	Lymphotoxin beta (TNF superfamily, member 3)
CBS	Cystathionine-beta- synthase
ACIN1	Apoptotic chromatin condensation inducer 1
IER2	Immediate early response 2
5265684	Pp14571
TBCB	Tubulin folding cofactor B
4588144	intercellular adhesion molecule 4, Landsteiner-Wiener blood group
NDUFB7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa
EDG2	Endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2
SURF5	Surfeit 5
NHP2L1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
DGCR14	DiGeorge syndrome critical region gene 14
1997185	Homo sapiens clone 23904 mRNA sequence
LIMK2	LIM domain kinase 2
NNAT	Neuronatin
PPP3R1	Protein phosphatase 3 (formerly 2B), regulatory subunit B, alpha isoform
CRP	C-reactive protein, pentraxin-related
ST8SIA3	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3
961082	Transcribed locus
MBD4	Methyl-CpG binding domain protein 4
MARCKSL1	MARCKS-like 1
GSTM2	Glutathione S-transferase M2 (muscle)
SFRS1	Splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
IMPDH2	IMP (inosine monophosphate) dehydrogenase 2

Gene name or Incyte clone ID	Description
OSBPL3	Oxysterol binding protein-like 3
1366085	Incyte EST
CAMK1	Calcium/calmodulin-dependent protein kinase I
CTNNAL1	Catenin (cadherin-associated protein), alpha-like 1
EIF4A1	Eukaryotic translation initiation factor 4A, isoform 1
KIF1C	Kinesin family member 1C
FOXA3	Forkhead box A3
AHR	Aryl hydrocarbon receptor
KIAA0182	KIAA0182
LPHN3	Latrophilin 3
TMEM16C	Transmembrane protein 16C
DSCR3	Down syndrome critical region gene 3
CDK2AP1	CDK2-associated protein 1
1740788	CDNA FLJ42519 fis, clone BRACE3000787
PPFIA1	Protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1
RTF1	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)
RPL23A	Ribosomal protein L23a
POLR2D	Polymerase (RNA) II (DNA directed) polypeptide D
PDPN	Podoplanin
1740384	KIAA0403 protein
TADA3L	Transcriptional adaptor 3 (NGG1 homolog, yeast)-like
CXorf9	Chromosome X open reading frame 9
DHR SX	Dehydrogenase/reductase (SDR family) X-linked
ZNF415	Zinc finger protein 415
RAB6A	RAB6A, member RAS oncogene family
SMC3	Structural maintenance of chromosomes 3
PPP2R5E	Protein phosphatase 2, regulatory subunit B', epsilon isoform
1223725	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
PRKAR1B	Protein kinase, cAMP-dependent, regulatory, type I, beta
KPNB1	Karyopherin (importin) beta 1
TWF2	Twinfilin, actin-binding protein, homolog 2 (Drosophila)
EHHADH	Enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase
PECI	Peroxisomal D3,D2-enoyl-CoA isomerase
NHP2L1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
1781632	breast cell glutaminase
TMPO	Thymopoietin
ULK2	Unc-51-like kinase 2 (C. elegans)
ST5	Suppression of tumorigenicity 5

Gene name or Incyte clone ID	Description
GSS	Glutathione synthetase
ILK	Integrin-linked kinase
934100	NBR2
IFI44	Interferon-induced protein 44
SEPHS2	Selenophosphate synthetase 2
IER3	Immediate early response 3
SPRR1B	Small proline-rich protein 1B (cornifin)
SSBP1	Single-stranded DNA binding protein 1
2370225	Transcribed locus
ALF	TFIIA-alpha/beta-like factor
C12orf4	Chromosome 12 open reading frame 4
RPP21	Ribonuclease P 21kDa subunit
RRM2B	Ribonucleotide reductase M2 B (TP53 inducible)
TMEM56	Transmembrane protein 56
RAB3IL1	RAB3A interacting protein (rabin3)-like 1
FAM62B	Family with sequence similarity 62 (C2 domain containing) member B
2512249	CDNA FLJ11481 fis, clone HEMBA1001803
1477429	Transcribed locus
ALS2CR7	Amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 7
2966564	CDNA: FLJ22642 fis, clone HSI06970
2122652	Incyte EST
HMG20A	High-mobility group 20A
FUZ	Fuzzy homolog (Drosophila)
2743036	CDNA FLJ11602 fis, clone HEMBA1003908
2819864	Transcribed locus
LOC51255	Hypothetical protein LOC51255
LGI4	Leucine-rich repeat LGI family, member 4
FBF1	Fas (TNFRSF6) binding factor 1
C10orf83	Chromosome 10 open reading frame 83
RBM15	RNA binding motif protein 15
2606738	Transcribed locus, weakly similar to XP_517655.1 similar to KIAA0825 protein [Pan troglodytes]
2592657	ESTs
2374366	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
ASCC3L1	Activating signal cointegrator 1 complex subunit 3-like 1
C7orf29	Chromosome 7 open reading frame 29
ARL5B	ADP-ribosylation factor-like 5B
RASA4	RAS p21 protein activator 4
FZD7	Frizzled homolog 7 (Drosophila)

Gene name or Incyte clone ID	Description
GPRASP2	G protein-coupled receptor associated sorting protein 2
RASGRP3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
3846507	Transcribed locus
GAS2L3	Growth arrest-specific 2 like 3
OR51E2	Olfactory receptor, family 51, subfamily E, member 2
C20orf59	Chromosome 20 open reading frame 59
RNF139	Ring finger protein 139
2913207	Transcribed locus
HERC4	Hect domain and RLD 4
SLC12A2	Solute carrier family 12 (sodium/potassium/chloride transporters), member 2
ZNF473	Zinc finger protein 473
ARHGAP20	Rho GTPase activating protein 20
1848288	ribosomal protein S19
ASTN2	Astrotactin 2
2891379	ESTs
HOXD8	Homeobox D8
1398105	Transcribed locus
ZNF511	Zinc finger protein 511
ATP2C1	ATPase, Ca++ transporting, type 2C, member 1
2348251	CDNA FLJ14181 fis, clone NT2RP2004300
REEP1	Receptor accessory protein 1
SELI	Selenoprotein I
2155675	Transcribed locus, weakly similar to XP_001128517.1 hypothetical protein [Homo sapiens]
2877936	Transcribed locus
C6orf203	Chromosome 6 open reading frame 203
2718565	Transcribed locus
2262766	Incyte EST
SETBP1	SET binding protein 1
RPS29	Ribosomal protein S29
PPAPDC1B	Phosphatidic acid phosphatase type 2 domain containing 1B
334768	ESTs
GABBR1	Gamma-aminobutyric acid (GABA) B receptor, 1
MFGE8	Milk fat globule-EGF factor 8 protein
ATP1B2	ATPase, Na+/K+ transporting, beta 2 polypeptide
IGF2BP3	Insulin-like growth factor 2 mRNA binding protein 3
BLM	Bloom syndrome
1803882	Transcribed locus
RPP30	Ribonuclease P/MRP 30kDa subunit
CRTAP	Cartilage associated protein

Gene name or Incyte clone ID	Description
PAPOLA	Poly(A) polymerase alpha
CLIP3	CAP-GLY domain containing linker protein 3
KCTD1	Potassium channel tetramerisation domain containing 1
CABLES2	Cdk5 and Abl enzyme substrate 2
SGTA	Small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha
PEA15	Phosphoprotein enriched in astrocytes 15
FLJ38482	Hypothetical protein FLJ38482
GEMIN4	Gem (nuclear organelle) associated protein 4
2818878	Transcribed locus
3044614	Incyte EST
997948	Transcribed locus
TncRNA	Trophoblast-derived noncoding RNA
RBPM52	RNA binding protein with multiple splicing 2
RP11-561O23.4	COBW-like placental protein
LEPREL1	Leprecan-like 1
HEMGN	Hemogen
PPIB	Peptidylprolyl isomerase B (cyclophilin B)
ASL	Argininosuccinate lyase
CENTA2	Centaurin, alpha 2
2012680	CDNA clone IMAGE:5269981
695016	MRNA; cDNA DKFZp762N156 (from clone DKFZp762N156)
1494531	CDV-1 protein
1507281	Transcribed locus
TRAPPC1	Trafficking protein particle complex 1
HPS5	Hermansky-Pudlak syndrome 5
MYEOV	Myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas)
SIP1	Survival of motor neuron protein interacting protein 1
HELZ	Helicase with zinc finger
KRTAP4-7	Keratin associated protein 4-7
CSPG5	Chondroitin sulfate proteoglycan 5 (neuroglycan C)
RAB3C	RAB3C, member RAS oncogene family
3520224	Transcribed locus
1639638	Transcribed locus
1260330	Incyte EST
C1orf164	Chromosome 1 open reading frame 164
PSMB7	Proteasome (prosome, macropain) subunit, beta type, 7
C5orf33	Chromosome 5 open reading frame 33
NFKBIZ	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta
N4BP1	Nedd4 binding protein 1

Gene name or Incyte clone ID	Description
2054586	CDNA FLJ11614 fis, clone HEMBA1004015
LMOD3	Leiomodin 3 (fetal)
CDK9	Cyclin-dependent kinase 9 (CDC2-related kinase)
UBR1	Ubiquitin protein ligase E3 component n-recognin 1
SERPINF2	Serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 2
UBE3C	Ubiquitin protein ligase E3C
MAN1A2	Mannosidase, alpha, class 1A, member 2
DENND2D	DENN/MADD domain containing 2D
2291261	Transcribed locus, strongly similar to XP_516821.2 mediator of RNA polymerase II transcription, subunit 12 homolog (S. cerevisiae)-like [Pan troglodytes]
515055	Incyte EST
C1orf174	Chromosome 1 open reading frame 174
FREQ	Frequenin homolog (Drosophila)
385550	Transcribed locus
UBADC1	Ubiquitin associated domain containing 1
ADAM15	ADAM metallopeptidase domain 15 (metargidin)
HOXA4	Homeobox A4
LRRK2	Leucine-rich repeat kinase 2
SON	SON DNA binding protein
RANBP1	RAN binding protein 1
1649906	microtubule-associated protein 1B
PIGH	Phosphatidylinositol glycan anchor biosynthesis, class H
662122	Transcribed locus
IGSF21	Immunoglobulin superfamily, member 21
KIAA1183	KIAA1183 protein
C16orf5	Chromosome 16 open reading frame 5
TGS1	Trimethylguanosine synthase homolog (S. cerevisiae)
DNAJC1	DnaJ (Hsp40) homolog, subfamily C, member 1
2289203	Transcribed locus
IARS2	Isoleucyl-tRNA synthetase 2, mitochondrial
WSB2	WD repeat and SOCS box-containing 2
UNG	Uracil-DNA glycosylase
CUL2	Cullin 2
C17orf79	Chromosome 17 open reading frame 79
APIG2	Adaptor-related protein complex 1, gamma 2 subunit
GSPT2	G1 to S phase transition 2
3144431	Transcribed locus, moderately similar to XP_001072642.1 similar to CG4329-PA, isoform A [Rattus norvegicus]
LETM1	Leucine zipper-EF-hand containing transmembrane protein 1

Gene name or Incyte clone ID	Description
631100	polymerase (RNA) II (DNA directed) polypeptide A (220kD)
DNAJB14	DnaJ (Hsp40) homolog, subfamily B, member 14
HNRPM	Heterogeneous nuclear ribonucleoprotein M
LCP2	Lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)
MYBPC2	Myosin binding protein C, fast type
MDF1	MyoD family inhibitor
FGL1	Fibrinogen-like 1
PPP1R2	Protein phosphatase 1, regulatory (inhibitor) subunit 2
GOSR1	Golgi SNAP receptor complex member 1
2753047	Transcribed locus
WBSCR22	Williams Beuren syndrome chromosome region 22
SCN1B	Sodium channel, voltage-gated, type I, beta
1511658	fibrinogen, A alpha polypeptide
ZNF385	Zinc finger protein 385
GAB3	GRB2-associated binding protein 3
CCNA2	Cyclin A2
MGC15523	Hypothetical protein MGC15523
SPRR1A	Small proline-rich protein 1A
SFT2D1	SFT2 domain containing 1
2155690	CDNA: FLJ22049 fis, clone HEP09444
MLSTD1	Male sterility domain containing 1
MED6	Mediator of RNA polymerase II transcription, subunit 6 homolog (S. cerevisiae)
GPBP1L1	GC-rich promoter binding protein 1-like 1
RACGAP1	Rac GTPase activating protein 1
C14orf179	Chromosome 14 open reading frame 179
CRNKL1	Crooked neck pre-mRNA splicing factor-like 1 (Drosophila)
ATP5O	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)
EXOSC4	Exosome component 4
NUP85	Nucleoporin 85kDa
SESN2	Sestrin 2
EVA1	Epithelial V-like antigen 1
GALNT1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)
2346766	Clone HLS IMAGE 1534603 mRNA sequence
FLT3	Fms-related tyrosine kinase 3
2418337	Incyte EST
1802325	EST
MTP18	Mitochondrial protein 18 kDa
JUB	Jub, ajuba homolog (Xenopus laevis)

Gene name or Incyte clone ID	Description
2737804	hypothetical protein FLJ20693
ALS2CL	ALS2 C-terminal like
RNF185	Ring finger protein 185
IDH3B	Isocitrate dehydrogenase 3 (NAD+) beta
3142705	Transcribed locus
3684467	Transcribed locus
DNPEP	Aspartyl aminopeptidase
DISP1	Dispatched homolog 1 (Drosophila)
FUSIP1	FUS interacting protein (serine/arginine-rich) 1
ECD	Ecdysoneless homolog (Drosophila)
2472966	MRNA; cDNA DKFZp686P1116 (from clone DKFZp686P1116)
MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)
UVRAG	UV radiation resistance associated gene
NIPSNAP3A	Nipsnap homolog 3A (C. elegans)
PCGF5	Polycomb group ring finger 5
SECISBP2	SECIS binding protein 2
YRDC	YrdC domain containing (E. coli)
LOC126075	Hypothetical protein LOC126075
WWTR1	WW domain containing transcription regulator 1
CSRP1	Cysteine and glycine-rich protein 1
HMGB2	High-mobility group box 2
ASXL1	Additional sex combs like 1 (Drosophila)
2396760	CDNA clone IMAGE:5268696
BIRC3	Baculoviral IAP repeat-containing 3
GPR172A	G protein-coupled receptor 172A
2600279	CDNA FLJ40954 fis, clone UTERU2010525
PTPN18	Protein tyrosine phosphatase, non-receptor type 18 (brain-derived)
FAM46B	Family with sequence similarity 46, member B
RNF7	Ring finger protein 7
CHD1	Chromodomain helicase DNA binding protein 1
PSMC4	Proteasome (prosome, macropain) 26S subunit, ATPase, 4
DDX46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46
ZBTB20	Zinc finger and BTB domain containing 20
1605376	Incyte EST
VPS4B	Vacuolar protein sorting 4 homolog B (S. cerevisiae)
1909889	Transcribed locus
IREB2	Iron-responsive element binding protein 2
METTL4	Methyltransferase like 4
C11orf24	Chromosome 11 open reading frame 24

Gene name or Incyte clone ID	Description
1639524	Transcribed locus
EGLN1	Egl nine homolog 1 (C. elegans)
DEGS1	Degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)
ZBTB11	Zinc finger and BTB domain containing 11
ABHD13	Abhydrolase domain containing 13
UBE2C	Ubiquitin-conjugating enzyme E2C
2504786	Transcribed locus
RPL37A	Ribosomal protein L37a
LOC283624	Hypothetical protein LOC283624
GNAS	GNAS complex locus
DGKH	Diacylglycerol kinase, eta
ZNF292	Zinc finger protein 292
TBRG4	Transforming growth factor beta regulator 4
KIAA0319L	KIAA0319-like
3407735	Transcribed locus
APOA1	Apolipoprotein A-I
ITPKB	Inositol 1,4,5-trisphosphate 3-kinase B
1253625	Full-length cDNA clone CS0DL008YP09 of B cells (Ramos cell line) Cot 25-normalized of Homo sapiens (human)
KDEL1	KDEL (Lys-Asp-Glu-Leu) containing 1
CSNK2A2	Casein kinase 2, alpha prime polypeptide
SMC2	Structural maintenance of chromosomes 2
HDAC1	Histone deacetylase 1
1534801	Transcribed locus, strongly similar to XP_528003.2 hypothetical protein [Pan troglodytes]
FLNB	Filamin B, beta (actin binding protein 278)
WDR22	WD repeat domain 22
CPZ	Carboxypeptidase Z
GALNT14	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)
SELL	Selectin L (lymphocyte adhesion molecule 1)
SIRT1	Sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)
CCDC22	Coiled-coil domain containing 22
2674482	Incyte EST
CCDC56	Coiled-coil domain containing 56
DCTN1	Dynactin 1 (p150, glued homolog, Drosophila)
1822713	butyrophilin, subfamily 3, member A1
HMGB1	High-mobility group box 1
RP5-1022P6.2	Hypothetical protein KIAA1434
RAB13	RAB13, member RAS oncogene family
SF3B2	Splicing factor 3b, subunit 2, 145kDa

Gene name or Incyte clone ID	Description
2472778	CDNA FLJ41369 fis, clone BRCAN2006117
UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)
FLJ37464	Hypothetical protein FLJ37464
IMP4	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)
WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)
PGF	Placental growth factor, vascular endothelial growth factor-related protein
CTR9	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)
TEX261	Testis expressed sequence 261
VCP	Valosin-containing protein
KIFAP3	Kinesin-associated protein 3
1697306	Transcribed locus
HEXA	Hexosaminidase A (alpha polypeptide)
UTP11L	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)
MYOZ2	Myozenin 2
KIAA0404	Hypothetical protein LOC23130
1962190	Transcribed locus
MIDN	Midnolin
TXNDC9	Thioredoxin domain containing 9
C1orf21	Chromosome 1 open reading frame 21
FAM48A	Family with sequence similarity 48, member A
LRRC59	Leucine rich repeat containing 59
SIPA1L1	Signal-induced proliferation-associated 1 like 1
STAT3	Signal transducer and activator of transcription 3 (acute-phase response factor)
2496526	Incyte EST
SNRPB2	Small nuclear ribonucleoprotein polypeptide B''
3729512	CDNA FLJ45814 fis, clone NT2RP7018126
EPX	Eosinophil peroxidase
DMTF1	Cyclin D binding myb-like transcription factor 1
WDR37	WD repeat domain 37
VENTX	VENT homeobox homolog (Xenopus laevis)
KCNJ15	Potassium inwardly-rectifying channel, subfamily J, member 15
HCST	Hematopoietic cell signal transducer
ITPA	Inosine triphosphatase (nucleoside triphosphate pyrophosphatase)
DNAJC9	DnaJ (Hsp40) homolog, subfamily C, member 9
1863428	KIAA0036 gene product
STATH	Statherin
C1S	Complement component 1, s subcomponent
DGAT2	Diacylglycerol O-acyltransferase homolog 2 (mouse)
1601279	CDNA: FLJ23454 fis, clone HSI06959

Gene name or Incyte clone ID	Description
GNG12	Guanine nucleotide binding protein (G protein), gamma 12
2023744	Incyte EST
1686727	Incyte EST
3035832	nuclear receptor subfamily 2, group C, member 2
RAB11A	RAB11A, member RAS oncogene family
1907021	CDNA: FLJ22522 fis, clone HRC12491
MRPS5	Mitochondrial ribosomal protein S5
YARS	Tyrosyl-tRNA synthetase
RETSAT	Retinol saturase (all-trans-retinol 13,14-reductase)
GALE	UDP-galactose-4-epimerase
SREBF2	Sterol regulatory element binding transcription factor 2
LOC91461	Hypothetical protein BC007901
CDH4	Cadherin 4, type 1, R-cadherin (retinal)
C7orf42	Chromosome 7 open reading frame 42
C10orf46	Chromosome 10 open reading frame 46
NARS	Asparaginyl-tRNA synthetase
SNRPG	Small nuclear ribonucleoprotein polypeptide G
TANC2	Tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2
NUDT22	Nudix (nucleoside diphosphate linked moiety X)-type motif 22
1907369	TATA box binding protein (TBP)-associated factor, RNA polymerase II, N, 68kD (RNA-binding protein 56)
2506194	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2
CBLN1	Cerebellin 1 precursor
CDC25A	Cell division cycle 25 homolog A (S. pombe)
THOC1	THO complex 1
RBMS2	RNA binding motif, single stranded interacting protein 2
GABPA	GA binding protein transcription factor, alpha subunit 60kDa
PURA	Purine-rich element binding protein A
KNTC1	Kinetochore associated 1
SMYD5	SMYD family member 5
TMEM112B	Transmembrane protein 112B
LRRTM2	Leucine rich repeat transmembrane neuronal 2
IRAK1	Interleukin-1 receptor-associated kinase 1
GUCA2B	Guanylate cyclase activator 2B (uroguanylin)
KIF2C	Kinesin family member 2C
CLIP1	CAP-GLY domain containing linker protein 1
TNFAIP3	Tumor necrosis factor, alpha-induced protein 3
CD47	CD47 molecule
RHAG	Rh-associated glycoprotein

Gene name or Incyte clone ID	Description
C19orf47	Chromosome 19 open reading frame 47
Selenoprotein 15	15 kDa selenoprotein
SUPT6H	Suppressor of Ty 6 homolog (S. cerevisiae)
ELF4	E74-like factor 4 (ets domain transcription factor)
VLDLR	Very low density lipoprotein receptor
HNRPK	Heterogeneous nuclear ribonucleoprotein K
DDB2	Damage-specific DNA binding protein 2, 48kDa
RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)
DLG3	Discs, large homolog 3 (neuroendocrine-dlg, Drosophila)
OCA2	Oculocutaneous albinism II (pink-eye dilution homolog, mouse)
UQCRH	Ubiquinol-cytochrome c reductase hinge protein
IRX5	Iroquois homeobox protein 5
ABCB4	ATP-binding cassette, sub-family B (MDR/TAP), member 4
PRR3	Proline rich 3
ENTPD4	Ectonucleoside triphosphate diphosphohydrolase 4
LILRB3	Leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3
SRF	Serum response factor (c-fos serum response element-binding transcription factor)
4179338	apolipoprotein B (including Ag(x) antigen)
LSAMP	Limbic system-associated membrane protein
NDN	Necdin homolog (mouse)
YWHAH	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
CDS1	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 1
CALD1	Caldesmon 1
3149480	anti-Mullerian hormone receptor, type II
TNFSF10	Tumor necrosis factor (ligand) superfamily, member 10
TJP2	Tight junction protein 2 (zona occludens 2)
MAPK1	Mitogen-activated protein kinase 1
3421442	ribosomal protein S6 kinase, 90kD, polypeptide 2
1712327	wingless-type MMTV integration site family, member 5A
KIAA1128	KIAA1128
IL10	Interleukin 10
SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5
NEK2	NIMA (never in mitosis gene a)-related kinase 2
SUFU	Suppressor of fused homolog (Drosophila)
2930175	Transcribed locus
C9orf9	Chromosome 9 open reading frame 9
NARG1	NMDA receptor regulated 1

Gene name or Incyte clone ID	Description
RIT1	Ras-like without CAAX 1
WDR18	WD repeat domain 18
DKK3	Dickkopf homolog 3 (<i>Xenopus laevis</i>)
3206210	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle
SC4MOL	Sterol-C4-methyl oxidase-like
3045817	Transcribed locus
2247386	ESTs
GTPBP6	GTP binding protein 6 (putative)
C1orf96	Chromosome 1 open reading frame 96
ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7
CTSW	Cathepsin W
4106720	Transcribed locus
3927011	Transcribed locus
4217059	Homo sapiens, clone IMAGE:4414697, mRNA
MGAT1	Mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
ZNF37A	Zinc finger protein 37A
95901	Transcribed locus
TSEN2	TRNA splicing endonuclease 2 homolog (<i>S. cerevisiae</i>)
2959963	ESTs
2203704	CDNA FLJ42306 fis, clone TRACH2001646
RCHY1	Ring finger and CHY zinc finger domain containing 1
CDH3	Cadherin 3, type 1, P-cadherin (placental)
TNNI1	Troponin I type 1 (skeletal, slow)
ZNF22	Zinc finger protein 22 (KOX 15)
NKRF	NF-kappaB repressing factor
LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase
FAT3	FAT tumor suppressor homolog 3 (<i>Drosophila</i>)
RP11-50D16.3	Similar to RIKEN cDNA 8030451K01
2773862	Transcribed locus
MRPL44	Mitochondrial ribosomal protein L44
3736683	MRNA; cDNA DKFZp451K063 (from clone DKFZp451K063)
MUM1	Melanoma associated antigen (mutated) 1
HIF1A	Hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
2912987	Transcribed locus, strongly similar to XP_530610.1 hypothetical protein XP_530610 [Pan troglodytes]
ARID4A	AT rich interactive domain 4A (RBP1-like)
125776	Incyte EST
2245223	Homo sapiens, clone IMAGE:4346533, mRNA
ABCC1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1

Gene name or Incyte clone ID	Description
ECHS1	Enoyl Coenzyme A hydratase, short chain, 1, mitochondrial
2343492	Transcribed locus
SLC25A5	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
TSEN34	TRNA splicing endonuclease 34 homolog (S. cerevisiae)
PBLD	Phenazine biosynthesis-like protein domain containing
SLC27A2	Solute carrier family 27 (fatty acid transporter), member 2
CA10	Carbonic anhydrase X
CLPP	ClpP caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)
NEBL	Nebulette
TPBG	Trophoblast glycoprotein
ATP9B	ATPase, Class II, type 9B
AK3	Adenylate kinase 3
ABCF1	ATP-binding cassette, sub-family F (GCN20), member 1
2252991	Transcribed locus
AZU1	Azurocidin 1 (cationic antimicrobial protein 37)
UGT8	UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase)
ZZEF1	Zinc finger, ZZ-type with EF-hand domain 1
GPIAP1	GPI-anchored membrane protein 1
SF1	Splicing factor 1
PGK1	Phosphoglycerate kinase 1
GALNT12	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12 (GalNAc-T12)
BACH1	BTB and CNC homology 1, basic leucine zipper transcription factor 1
33091	Incyte EST
RAD21	RAD21 homolog (S. pombe)
EIF5B	Eukaryotic translation initiation factor 5B
KIAA0513	KIAA0513
CCT2	Chaperonin containing TCP1, subunit 2 (beta)
PSMC3	Proteasome (prosome, macropain) 26S subunit, ATPase, 3
ALOX5	Arachidonate 5-lipoxygenase
507022	Incyte EST
TNIK	TRAF2 and NCK interacting kinase
RPSA	Ribosomal protein SA
SRM	Spermidine synthase
SRP19	Signal recognition particle 19kDa
ZMYM3	Zinc finger, MYM-type 3
SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1
IL6ST	Interleukin 6 signal transducer (gp130, oncostatin M receptor)
PTPRG	Protein tyrosine phosphatase, receptor type, G

Gene name or Incyte clone ID	Description
VSNL1	Visinin-like 1
SPG7	Spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive)
SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1
750770	casein kinase 2, beta polypeptide
BIRC3	Baculoviral IAP repeat-containing 3
2832839	basic leucine zipper transcription factor, ATF-like
TAF9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa
MAL	Mal, T-cell differentiation protein
TROVE2	TROVE domain family, member 2
SLC25A46	Solute carrier family 25, member 46
ZNF238	Zinc finger protein 238
ANP32B	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member B
PLEKHC1	Pleckstrin homology domain containing, family C (with FERM domain) member 1
ZYX	Zyxin
DUSP2	Dual specificity phosphatase 2
CRK	V-crk sarcoma virus CT10 oncogene homolog (avian)
PTPRA	Protein tyrosine phosphatase, receptor type, A
GABRG3	Gamma-aminobutyric acid (GABA) A receptor, gamma 3
FABP1	Fatty acid binding protein 1, liver
CG018	Hypothetical gene CG018
I308333	fucosidase, alpha-L- 1, tissue
IARS	Isoleucyl-tRNA synthetase
FTH1	Ferritin, heavy polypeptide 1
GLMN	Glomulin, FKBP associated protein
ICAM2	Intercellular adhesion molecule 2
RPL19	Ribosomal protein L19
GZMA	Granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)
RNF10	Ring finger protein 10
SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
GNB2	Guanine nucleotide binding protein (G protein), beta polypeptide 2
PSMD6	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 6
PFDN4	Prefoldin subunit 4
PDCD1	Programmed cell death 1
SMAD3	SMAD family member 3
COX5A	Cytochrome c oxidase subunit Va
SCN4A	Sodium channel, voltage-gated, type IV, alpha subunit
MORC3	MORC family CW-type zinc finger 3
PSMB4	Proteasome (prosome, macropain) subunit, beta type, 4

Gene name or Incyte clone ID	Description
GTF3A	General transcription factor IIIA
SST	Somatostatin
ENTPD2	Ectonucleoside triphosphate diphosphohydrolase 2
NFKBIL1	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1
1986737	transmembrane 4 superfamily member 2
GPLOW	G patch domain and KOW motifs
EXOSC10	Exosome component 10
RRAGA	Ras-related GTP binding A
ITGAE	Integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)
C7	Complement component 7
RPS6KA3	Ribosomal protein S6 kinase, 90kDa, polypeptide 3
PLK1	Polo-like kinase 1 (Drosophila)
CHD9	Chromodomain helicase DNA binding protein 9
RASA4	RAS p21 protein activator 4
FAM107A	Family with sequence similarity 107, member A
CD38	CD38 molecule
1219391	protein tyrosine phosphatase, non-receptor type 7
ASCC3	Activating signal cointegrator 1 complex subunit 3
RP9	Retinitis pigmentosa 9 (autosomal dominant)
RHOC	Ras homolog gene family, member C
C4orf16	Chromosome 4 open reading frame 16
KIAA1279	KIAA1279
1517380	plexin B3
36829	enhancer of zeste (Drosophila) homolog 2
ATP6V0E1	ATPase, H ⁺ transporting, lysosomal 9kDa, V0 subunit e1
ZDHHC3	Zinc finger, DHHC-type containing 3
THBS2	Thrombospondin 2
OSBPL11	Oxysterol binding protein-like 11
NPAS2	Neuronal PAS domain protein 2
ALG12	Asparagine-linked glycosylation 12 homolog (S. cerevisiae, alpha-1,6-mannosyltransferase)
MEG3	Maternally expressed 3
F5	Coagulation factor V (proaccelerin, labile factor)
GM2A	GM2 ganglioside activator
PPP2R5C	Protein phosphatase 2, regulatory subunit B', gamma isoform
GABRG2	Gamma-aminobutyric acid (GABA) A receptor, gamma 2
RIPK1	Receptor (TNFRSF)-interacting serine-threonine kinase 1
TOPORS	Topoisomerase I binding, arginine/serine-rich
CALB1	Calbindin 1, 28kDa

Gene name or Incyte clone ID	Description
ACLY	ATP citrate lyase
RTN2	Reticulon 2
ZNF508	Zinc finger protein 508
AHCTF1	AT hook containing transcription factor 1
MPG	N-methylpurine-DNA glycosylase
IGF1R	Insulin-like growth factor 1 receptor
ALDH3B2	Aldehyde dehydrogenase 3 family, member B2
2022039	ESTs
2108793	CD151 antigen
SNRPB	Small nuclear ribonucleoprotein polypeptides B and B1
EREG	Epiregulin
NAALADL1	N-acetylated alpha-linked acidic dipeptidase-like 1
LSM5	LSM5 homolog, U6 small nuclear RNA associated (<i>S. cerevisiae</i>)
MPO	Myeloperoxidase
PELP1	Proline, glutamic acid and leucine rich protein 1
MLLT11	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, <i>Drosophila</i>); translocated to, 11
NRG1	Neuregulin 1
TNFSF11	Tumor necrosis factor (ligand) superfamily, member 11
LRRC58	Leucine rich repeat containing 58
EXO1	Exonuclease 1
998238	transaldolase 1
SLC22A18	Solute carrier family 22 (organic cation transporter), member 18
LAIR1	Leukocyte-associated immunoglobulin-like receptor 1
TMED1	Transmembrane emp24 protein transport domain containing 1
DAG1	Dystroglycan 1 (dystrophin-associated glycoprotein 1)
1746529	minichromosome maintenance deficient (<i>S. cerevisiae</i>) 5 (cell division cycle 46)
LIPC	Lipase, hepatic
MTMR15	Myotubularin related protein 15
2659262	Incyte EST
RENBP	Renin binding protein
2723965	Incyte EST
GATA1	GATA binding protein 1 (globin transcription factor 1)
FYTTD1	Forty-two-three domain containing 1
HLTF	Helicase-like transcription factor
1510847	protein kinase, interferon-inducible double stranded RNA dependent
SORBS2	Sorbin and SH3 domain containing 2
CHST12	Carbohydrate (chondroitin 4) sulfotransferase 12
ZNF33A	Zinc finger protein 33A

Gene name or Incyte clone ID	Description
FLI1	Friend leukemia virus integration 1
EPS8L1	EPS8-like 1
SPOCK1	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1
1511486	CD39-like 2
STX1A	Syntaxin 1A (brain)
SUMO1	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)
USP31	Ubiquitin specific peptidase 31
HDGF	Hepatoma-derived growth factor (high-mobility group protein 1-like)
TGS1	Trimethylguanosine synthase homolog (S. cerevisiae)
PREP	Prolyl endopeptidase
2382190	ESTs, Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]
C21orf66	Chromosome 21 open reading frame 66
NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)
KLHL2	Kelch-like 2, Mayven (Drosophila)
MRPS18B	Mitochondrial ribosomal protein S18B
1430749	glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase)
DPYD	Dihydropyrimidine dehydrogenase
ADCY2	Adenylate cyclase 2 (brain)
GSG1	Germ cell associated 1
MAP3K9	Mitogen-activated protein kinase kinase kinase 9
ARPP-21	Cyclic AMP-regulated phosphoprotein, 21 kD
PTPRD	Protein tyrosine phosphatase, receptor type, D
2736350	hypothetical protein KIAA1335
SHCBP1	SHC SH2-domain binding protein 1
CSTF3	Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa
ENSA	Endosulfine alpha
1781585	MRNA; cDNA DKFZp564M243 (from clone DKFZp564M243)
2245848	REMOVED FROM DATABASE
BOP1	Block of proliferation 1
GJB5	Gap junction protein, beta 5
TRAK2	Trafficking protein, kinesin binding 2
CAMK2B	Calcium/calmodulin-dependent protein kinase (CaM kinase) II beta
BAG4	BCL2-associated athanogene 4
TSNAX	Translin-associated factor X
CCL19	Chemokine (C-C motif) ligand 19
RNF128	Ring finger protein 128
HBZ	Hemoglobin, zeta
559786	Transcribed locus
1873338	Full-length cDNA clone CS0DM002YA18 of Fetal liver of Homo sapiens (human)

Gene name or Incyte clone ID	Description
PPP2CA	Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
DLEU1	Deleted in lymphocytic leukemia, 1
RILP	Rab interacting lysosomal protein
PLD1	Phospholipase D1, phosphatidylcholine-specific
EIF2B2	Eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa
DPF2	D4, zinc and double PHD fingers family 2
CHST13	Carbohydrate (chondroitin 4) sulfotransferase 13
ZNF408	Zinc finger protein 408
CD46	CD46 molecule, complement regulatory protein
4003377	CDNA FLJ37690 fis, clone BRHIP2014386
JARID1A	Jumonji, AT rich interactive domain 1A
KRT6A	Keratin 6A
HNRPLL	Heterogeneous nuclear ribonucleoprotein L-like
POLR2B	Polymerase (RNA) II (DNA directed) polypeptide B, 140kDa
RUFY2	RUN and FYVE domain containing 2
CAP2	CAP, adenylate cyclase-associated protein, 2 (yeast)
CECR4	Cat eye syndrome chromosome region, candidate 4
PDE5A	Phosphodiesterase 5A, cGMP-specific
WHDC1L1	WAS protein homology region 2 domain containing 1-like 1
LOC219854	Hypothetical protein LOC219854
DZIP3	Zinc finger DAZ interacting protein 3
1924012	CDNA FLJ41910 fis, clone PEBLM2007834
FGFR1OP	FGFR1 oncogene partner
LAPTM4B	Lysosomal associated protein transmembrane 4 beta
RPL7A	Ribosomal protein L7a
TBX15	T-box 15
CCNL2	Cyclin L2
LAPTM5	Lysosomal associated multispinning membrane protein 5
FES	Feline sarcoma oncogene
ELA3A	Elastase 3A, pancreatic
PITPNA	Phosphatidylinositol transfer protein, alpha
ITGA5	Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
IGSF11	Immunoglobulin superfamily, member 11
542944	CDNA FLJ11381 fis, clone HEMBA1000501
ZNF277P	Zinc finger protein 277 pseudogene
LOC285016	Hypothetical protein LOC285016
PSMD8	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 8
546616	ESTs
GSTA4	Glutathione S-transferase A4

Gene name or Incyte clone ID	Description
RAB11FIP1	RAB11 family interacting protein 1 (class I)
2327380	Transcribed locus
IHPK2	Inositol hexaphosphate kinase 2
CHMP2A	Chromatin modifying protein 2A
C18orf1	Chromosome 18 open reading frame 1
SLC38A4	Solute carrier family 38, member 4
NIPSNAP1	Nipsnap homolog 1 (C. elegans)
TAF7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa
RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5
MAPK3	Mitogen-activated protein kinase 3
2289974	Clone IMAGE:609899, mRNA sequence
NEIL1	Nei endonuclease VIII-like 1 (E. coli)
LOC220930	Hypothetical protein LOC220930
PSMB3	Proteasome (prosome, macropain) subunit, beta type, 3
321875	Transcribed locus, moderately similar to XP_517655.1 similar to KIAA0825 protein [Pan troglodytes]
EPHA2	EPH receptor A2
MLL4	Myeloid/lymphoid or mixed-lineage leukemia 4
PPP2R5D	Protein phosphatase 2, regulatory subunit B', delta isoform
OTUD3	OTU domain containing 3
TAP1	Transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)
RBBP8	Retinoblastoma binding protein 8
C2orf42	Chromosome 2 open reading frame 42
2253951	Transcribed locus
2373896	KIAA1046 protein
81576	Incyte EST
2625593	retinoid X receptor, beta
41087	Transcribed locus
LRPAP1	Low density lipoprotein receptor-related protein associated protein 1
FGR	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog
NUTF2	Nuclear transport factor 2
ZNF282	Zinc finger protein 282
INTS10	Integrator complex subunit 10
CEBPZ	CCAAT/enhancer binding protein zeta
344516	ESTs
JARID1C	Jumonji, AT rich interactive domain 1C
LOC348801	Hypothetical protein LOC348801
ISCU	Iron-sulfur cluster scaffold homolog (E. coli)
YY1	YY1 transcription factor

Gene name or Incyte clone ID	Description
6-Mar	Membrane-associated ring finger (C3HC4) 6
PAK4	P21(CDKN1A)-activated kinase 4
1605233	CDNA FLJ32531 fis, clone SMINT2000227
TPSAB1	Tryptase alpha/beta 1
TMEM185B	Transmembrane protein 185B
ARL6IP4	ADP-ribosylation-like factor 6 interacting protein 4
AKR7A2	Aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)
CLPS	Colipase, pancreatic
BRAF	V-raf murine sarcoma viral oncogene homolog B1
POLI	Polymerase (DNA directed) iota
PTOV1	Prostate tumor overexpressed gene 1
GZMK	Granzyme K (granzyme 3; tryptase II)
1528507	neutrophil cytosolic factor 4 (40kD)
RPS27	Ribosomal protein S27 (metallopanstimulin 1)
ECM1	Extracellular matrix protein 1
PLEKHM1	Pleckstrin homology domain containing, family M (with RUN domain) member 1
CASQ2	Calsequestrin 2 (cardiac muscle)
PRPF3	PRP3 pre-mRNA processing factor 3 homolog (S. cerevisiae)
UMOD	Uromodulin (uromucoid, Tamm-Horsfall glycoprotein)
TSN	Translin
NP	Nucleoside phosphorylase
CXCL10	Chemokine (C-X-C motif) ligand 10
SEC61B	Sec61 beta subunit
HARS	Histidyl-tRNA synthetase
392166	SFRS protein kinase 1
GGH	Gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)
RBBP6	Retinoblastoma binding protein 6
C5	Complement component 5
SRD5A2	Steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 2)
RFX5	Regulatory factor X, 5 (influences HLA class II expression)
MKRN1	Makorin, ring finger protein, 1
APLP2	Amyloid beta (A4) precursor-like protein 2
EDC4	Enhancer of mRNA decapping 4
CFLAR	CASP8 and FADD-like apoptosis regulator
SFRS4	Splicing factor, arginine/serine-rich 4
RPL38	Ribosomal protein L38
SLC25A17	Solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34kDa), member 17
RNASET2	Ribonuclease T2

Gene name or Incyte clone ID	Description
PRNPIP	Prion protein interacting protein
BDH1	3-hydroxybutyrate dehydrogenase, type 1
STAT5A	Signal transducer and activator of transcription 5A
PDE4A	Phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)
PUM1	Pumilio homolog 1 (Drosophila)
PA2G4	Proliferation-associated 2G4, 38kDa
ZNF629	Zinc finger protein 629
RPS15	Ribosomal protein S15
2904011	ciliary neurotrophic factor
NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa
RPA3	Replication protein A3, 14kDa
SEMA3E	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E
ATAD2B	ATPase family, AAA domain containing 2B
TTLL12	Tubulin tyrosine ligase-like family, member 12
PAXIP1	PAX interacting (with transcription-activation domain) protein 1
LENG4	Leukocyte receptor cluster (LRC) member 4
PPP1R10	Protein phosphatase 1, regulatory (inhibitor) subunit 10
ETFB	Electron-transfer-flavoprotein, beta polypeptide
HSF2	Heat shock transcription factor 2
C9orf100	Chromosome 9 open reading frame 100
RPA1	Replication protein A1, 70kDa
ANKHD1	Ankyrin repeat and KH domain containing 1
CLINT1	Clathrin interactor 1
SLC24A1	Solute carrier family 24 (sodium/potassium/calcium exchanger), member 1
CD44	CD44 molecule (Indian blood group)
KLF1	Kruppel-like factor 1 (erythroid)
ATP1B3	ATPase, Na ⁺ /K ⁺ transporting, beta 3 polypeptide
GUCA2A	Guanylate cyclase activator 2A (guanylin)
GFRA1	GDNF family receptor alpha 1
DNMT	Deoxynucleotidyltransferase, terminal
2961526	cytochrome P450, subfamily XIB (steroid 11-beta-hydroxylase), polypeptide 1
PABPC4	Poly(A) binding protein, cytoplasmic 4 (inducible form)
SDCBP	Syndecan binding protein (syntenin)
DNAJC7	DnaJ (Hsp40) homolog, subfamily C, member 7
ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltransferase 1
ELA2A	Elastase 2A
IRF1	Interferon regulatory factor 1
BTG3	BTG family, member 3
TNF	Tumor necrosis factor (TNF superfamily, member 2)

Gene name or Incyte clone ID	Description
MGAT2	Mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
KDELRL2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2
1538486	killer cell lectin-like receptor subfamily C, member 3
CHAF1B	Chromatin assembly factor 1, subunit B (p60)
RPL14	Ribosomal protein L14
CYP51A1	Cytochrome P450, family 51, subfamily A, polypeptide 1
RGS2	Regulator of G-protein signalling 2, 24kDa
CRHR1	Corticotropin releasing hormone receptor 1
NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
2414632	lamin B2
LIG1	Ligase I, DNA, ATP-dependent
2882957	collagen, type XI, alpha 2
4240009	chemokine (C-C motif) receptor 5
KATNB1	Katanin p80 (WD repeat containing) subunit B 1
HMMR	Hyaluronan-mediated motility receptor (RHAMM)
IFRD2	Interferon-related developmental regulator 2
MTF1	Metal-regulatory transcription factor 1
CD48	CD48 molecule
RNF144	Ring finger protein 144
LTA4H	Leukotriene A4 hydrolase
QARS	Glutamyl-tRNA synthetase
TRAP1	TNF receptor-associated protein 1
FBXO28	F-box protein 28
ANKRD28	Ankyrin repeat domain 28
182668	transcription factor AP-2 alpha (activating enhancer-binding protein 2 alpha)
NUP43	Nucleoporin 43kDa
ZNF331	Zinc finger protein 331
RPA2	Replication protein A2, 32kDa
ACOT2	Acyl-CoA thioesterase 2
TNFRSF9	Tumor necrosis factor receptor superfamily, member 9
OTUD4	OTU domain containing 4
1832406	splicing factor, arginine/serine-rich 9
GMPPB	GDP-mannose pyrophosphorylase B
SLIT3	Slit homolog 3 (Drosophila)
HIST1H2BK	Histone cluster 1, H2bk
C3AR1	Complement component 3a receptor 1
PTH	Parathyroid hormone
XPOT	Exportin, tRNA (nuclear export receptor for tRNAs)
PRKCD	Protein kinase C, delta

Gene name or Incyte clone ID	Description
SUPV3L1	Suppressor of var1, 3-like 1 (<i>S. cerevisiae</i>)
ADK	Adenosine kinase
HSD17B3	Hydroxysteroid (17-beta) dehydrogenase 3
UBE2D2	Ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)
ETV6	Ets variant gene 6 (TEL oncogene)
LCK	Lymphocyte-specific protein tyrosine kinase
NUDT2	Nudix (nucleoside diphosphate linked moiety X)-type motif 2
SDC2	Syndecan 2
PPP2R1B	Protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform
TADA1L	Transcriptional adaptor 1 (HF11 homolog, yeast)-like
CLK2	CDC-like kinase 2
ARID2	AT rich interactive domain 2 (ARID, RFX-like)
ADRM1	Adhesion regulating molecule 1
TMEM119	Transmembrane protein 119
RBM3	RNA binding motif (RNP1, RRM) protein 3
C6orf72	Chromosome 6 open reading frame 72
TSPYL4	TSPY-like 4
LOC401397	Hypothetical LOC401397
3236109	ESTs
SCN3B	Sodium channel, voltage-gated, type III, beta
1677133	KIAA0601 protein
ARF3	ADP-ribosylation factor 3
ABCA3	ATP-binding cassette, sub-family A (ABC1), member 3
1930865	Transcribed locus
PIM1	Pim-1 oncogene
SH3GL1	SH3-domain GRB2-like 1
MBD1	Methyl-CpG binding domain protein 1
ENTPD1	Ectonucleoside triphosphate diphosphohydrolase 1
EPAS1	Endothelial PAS domain protein 1
LGALS3BP	Lectin, galactoside-binding, soluble, 3 binding protein
413767	Full-length cDNA clone CS0DD001YA12 of Neuroblastoma Cot 50-normalized of Homo sapiens (human)
TICAM1	Toll-like receptor adaptor molecule 1
TNK2	Tyrosine kinase, non-receptor, 2
C15orf17	Chromosome 15 open reading frame 17
C22orf16	Chromosome 22 open reading frame 16
PUM2	Pumilio homolog 2 (<i>Drosophila</i>)
2447969	ESTs
SNRPA	Small nuclear ribonucleoprotein polypeptide A

Gene name or Incyte clone ID	Description
RBBP6	Retinoblastoma binding protein 6
LAD1	Ladinin 1
ZNF313	Zinc finger protein 313
EDEM2	ER degradation enhancer, mannosidase alpha-like 2
FLJ22167	Hypothetical protein FLJ22167
ALDH1L1	Aldehyde dehydrogenase 1 family, member L1
2627888	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
NTF5	Neurotrophin 5 (neurotrophin 4/5)
FXN	Frataxin
SERPINB9	Serpin peptidase inhibitor, clade B (ovalbumin), member 9
UBD	Ubiquitin D
PPP2R2C	Protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform
ANK3	Ankyrin 3, node of Ranvier (ankyrin G)
USP14	Ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)
GPIAP1	GPI-anchored membrane protein 1
C15orf24	Chromosome 15 open reading frame 24
TM9SF1	Transmembrane 9 superfamily member 1
DHPS	Deoxyhypusine synthase
1739690	Full length insert cDNA YN73H08
SMAD1	SMAD family member 1
MRPS6	Mitochondrial ribosomal protein S6
KIAA0574	KIAA0574 protein
DEFA1	Defensin, alpha 1
STX6	Syntaxin 6
EIF4E2	Eukaryotic translation initiation factor 4E family member 2
TMED9	Transmembrane emp24 protein transport domain containing 9
MYLPP	Fast skeletal myosin light chain 2
RPL7	Ribosomal protein L7
ZMIZ2	Zinc finger, MIZ-type containing 2
CENPC1	Centromere protein C 1
LOC147343	Hypothetical protein LOC147343
PSME3	Proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)
ZFP106	Zinc finger protein 106 homolog (mouse)
EIF1B	Eukaryotic translation initiation factor 1B
BTNL9	Butyrophilin-like 9
TCF12	Transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)
933477	Transcribed locus
TRUB1	TruB pseudouridine (psi) synthase homolog 1 (E. coli)

Gene name or Incyte clone ID	Description
535623	Transcribed locus
KIAA0495	KIAA0495
SFRP4	Secreted frizzled-related protein 4
HBG2	Hemoglobin, gamma G
UBC	Ubiquitin C
PCCB	Propionyl Coenzyme A carboxylase, beta polypeptide
CACNB1	Calcium channel, voltage-dependent, beta 1 subunit
C6orf106	Chromosome 6 open reading frame 106
C9orf58	Chromosome 9 open reading frame 58
PSCDBP	Pleckstrin homology, Sec7 and coiled-coil domains, binding protein
C1orf212	Chromosome 1 open reading frame 212
FUBP3	Far upstream element (FUSE) binding protein 3
225746	Incyte EST
KIAA1609	KIAA1609
IMPACT	Impact homolog (mouse)
PCDH11Y	Protocadherin 11 Y-linked
PSMC1	Proteasome (prosome, macropain) 26S subunit, ATPase, 1
SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
METTL7A	Methyltransferase like 7A
MVP	Major vault protein
FOXJ2	Forkhead box J2
MGC61598	Similar to ankyrin-repeat protein Nrarp
KIAA1840	KIAA1840
HADHB	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit
TRMU	TRNA 5-methylaminomethyl-2-thiouridylate methyltransferase
2666301	MRNA from chromosome 5q21-22, clone:843Ex
RSL1D1	Ribosomal L1 domain containing 1
RUNX3	Runt-related transcription factor 3
PDGFC	Platelet derived growth factor C
ABHD10	Abhydrolase domain containing 10
SLC9A1	Solute carrier family 9 (sodium/hydrogen exchanger), member 1 (antiporter, Na ⁺ /H ⁺ , amiloride sensitive)
MATR3	Matrin 3
BAP1	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)
TACC3	Transforming, acidic coiled-coil containing protein 3
CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)
HMG4	High mobility group nucleosomal binding domain 4
REXO1	REX1, RNA exonuclease 1 homolog (S. cerevisiae)

Gene name or Incyte clone ID	Description
TUSC3	Tumor suppressor candidate 3
D4S234E	DNA segment on chromosome 4 (unique) 234 expressed sequence
NDFIP2	Nedd4 family interacting protein 2
TARS	Threonyl-tRNA synthetase
SLC30A9	Solute carrier family 30 (zinc transporter), member 9
USP39	Ubiquitin specific peptidase 39
FAM127B	Family with sequence similarity 127, member B
FUBP1	Far upstream element (FUSE) binding protein 1
AACS	Acetoacetyl-CoA synthetase
HDGF2	Hepatoma-derived growth factor-related protein 2
FLJ22028	Hypothetical protein FLJ22028
NCAPH2	Non-SMC condensin II complex, subunit H2
TECT1	Tectonic 1
CFDP1	Craniofacial development protein 1
TTC35	Tetratricopeptide repeat domain 35
SERTAD2	SERTA domain containing 2
2288730	cyclin E2
MGC39584	Hypothetical gene supported by BC029568
ELAVL1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)
TXNL1	Thioredoxin-like 1
MLLT1	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1
RRM1	Ribonucleotide reductase M1 polypeptide
CEBPG	CCAAT/enhancer binding protein (C/EBP), gamma
1431969	CDNA FLJ41088 fis, clone ASTRO2002459
THEM2	Thioesterase superfamily member 2
SHC1	SHC (Src homology 2 domain containing) transforming protein 1
KLHDC4	Kelch domain containing 4
FOS	V-fos FBJ murine osteosarcoma viral oncogene homolog
2107270	DNA-binding transcriptional activator
SYT17	Synaptotagmin XVII
RAMP2	Receptor (G protein-coupled) activity modifying protein 2
GNAQ	Guanine nucleotide binding protein (G protein), q polypeptide
2747113	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1
RRAGB	Ras-related GTP binding B
SLC6A7	Solute carrier family 6 (neurotransmitter transporter, L-proline), member 7
HDAC7A	Histone deacetylase 7A
GAS1	Growth arrest-specific 1
ZNF177	Zinc finger protein 177

Gene name or Incyte clone ID	Description
TAS2R14	Taste receptor, type 2, member 14
DAZAP2	DAZ associated protein 2
GHRHR	Growth hormone releasing hormone receptor
EEF1E1	Eukaryotic translation elongation factor 1 epsilon 1
SSSCA1	Sjogren's syndrome/scleroderma autoantigen 1
ANXA1	Annexin A1
KRT6B	Keratin 6B
DAD1	Defender against cell death 1
ZAK	Sterile alpha motif and leucine zipper containing kinase AZK
TRIM31	Tripartite motif-containing 31
FTL	Ferritin, light polypeptide
RNF5	Ring finger protein 5
C1D	Nuclear DNA-binding protein
SLC17A3	Solute carrier family 17 (sodium phosphate), member 3
EPB41L2	Erythrocyte membrane protein band 4.1-like 2
TGM3	Transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)
RASGRF2	Ras protein-specific guanine nucleotide-releasing factor 2
PTPRD	Protein tyrosine phosphatase, receptor type, D
ACP6	Acid phosphatase 6, lysophosphatidic
2532692	proprotein convertase subtilisin/kexin type 2
C16orf53	Chromosome 16 open reading frame 53
BRE	Brain and reproductive organ-expressed (TNFRSF1A modulator)
ALDH6A1	Aldehyde dehydrogenase 6 family, member A1
SUSD5	Sushi domain containing 5
NCAN	Neurocan
DUSP26	Dual specificity phosphatase 26 (putative)
ZNF267	Zinc finger protein 267
RGAG4	Retrotransposon gag domain containing 4
1998708	Full-length cDNA clone CS0DF030YM05 of Fetal brain of Homo sapiens (human)
TRIAD3	TRIAD3 protein
SLC20A1	Solute carrier family 20 (phosphate transporter), member 1
TMED10	Transmembrane emp24-like trafficking protein 10 (yeast)
CCDC57	Coiled-coil domain containing 57
NCAPH	Non-SMC condensin I complex, subunit H
PPP3CB	Protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform
ACAT1	Acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)
SUV39H1	Suppressor of variegation 3-9 homolog 1 (Drosophila)
CMYA5	Cardiomyopathy associated 5
2926307	Incyte EST

Gene name or Incyte clone ID	Description
VANGL1	Vang-like 1 (van gogh, Drosophila)
Septin 4	Septin 4
CDK9	Cyclin-dependent kinase 9 (CDC2-related kinase)
FADD	Fas (TNFRSF6)-associated via death domain
PDHB	Pyruvate dehydrogenase (lipoamide) beta
ZBTB5	Zinc finger and BTB domain containing 5
1433260	Incyte EST
950186	guanylate cyclase 2D, membrane (retina-specific)
TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1
SMAD2	SMAD family member 2
PDGFD	Platelet derived growth factor D
2749278	Transcribed locus
KIAA0265	KIAA0265 protein
SOCS1	Suppressor of cytokine signaling 1
LOC257407	Hypothetical protein LOC257407
SCARB2	Scavenger receptor class B, member 2
KPNA4	Karyopherin alpha 4 (importin alpha 3)
CSNK1A1	Casein kinase 1, alpha 1
GMFG	Glia maturation factor, gamma
TMEM77	Transmembrane protein 77
1404401	CDNA clone IMAGE:4077090
2806295	Transcribed locus
DUSP8	Dual specificity phosphatase 8
1759794	phosphatidylinositol glycan, class C
CKMT2	Creatine kinase, mitochondrial 2 (sarcomeric)
GCAT	Glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)
FEM1C	Fem-1 homolog c (C. elegans)
UNC5A	Unc-5 homolog A (C. elegans)
PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)
MPHOSPH1	M-phase phosphoprotein 1
2799504	Transcribed locus
2648612	Incyte EST
CREB3L1	CAMP responsive element binding protein 3-like 1
PRMT1	Protein arginine methyltransferase 1
KIAA1688	KIAA1688 protein
2916261	Incyte EST
TRIM33	Tripartite motif-containing 33
VPS29	Vacuolar protein sorting 29 homolog (S. cerevisiae)
MOBK1B	MOB1, Mps One Binder kinase activator-like 1B (yeast)

Gene name or Incyte clone ID	Description
1372694	ESTs
C1orf194	Chromosome 1 open reading frame 194
YPEL4	Yippee-like 4 (Drosophila)
CRISPLD2	Cysteine-rich secretory protein LCCL domain containing 2
SNX17	Sorting nexin 17
DOK1	Docking protein 1, 62kDa (downstream of tyrosine kinase 1)
JOSD3	Josephin domain containing 3
MYH11	Myosin, heavy chain 11, smooth muscle
ZNF300	Zinc finger protein 300
GLCCI1	Glucocorticoid induced transcript 1
KALRN	Kalirin, RhoGEF kinase
SMPD2	Sphingomyelin phosphodiesterase 2, neutral membrane (neutral sphingomyelinase)
HSP90AB1	Heat shock protein 90kDa alpha (cytosolic), class B member 1
PHF7	PHD finger protein 7
CENPA	Centromere protein A
GFAP	Glial fibrillary acidic protein
PAG1	Phosphoprotein associated with glycosphingolipid microdomains 1
TIMELESS	Timeless homolog (Drosophila)
RBM15B	RNA binding motif protein 15B
RNF182	Ring finger protein 182
SAA1	Serum amyloid A1
ORC2L	Origin recognition complex, subunit 2-like (yeast)
CALM2	Calmodulin 2 (phosphorylase kinase, delta)
839947	ryanodine receptor 1 (skeletal)
2285350	Transcribed locus
2115411	Transcribed locus
EPRS	Glutamyl-prolyl-tRNA synthetase
MGC42105	Hypothetical protein MGC42105
NUBP1	Nucleotide binding protein 1 (MinD homolog, E. coli)
HIPK1	Homeodomain interacting protein kinase 1
TBL1X	Transducin (beta)-like 1X-linked
TIMM17A	Translocase of inner mitochondrial membrane 17 homolog A (yeast)
BLOC1S1	Biogenesis of lysosome-related organelles complex-1, subunit 1
2845548	Transcribed locus, weakly similar to XP_001064630.1 similar to apobec-1 complementation factor [Rattus norvegicus]
PPP1CB	Protein phosphatase 1, catalytic subunit, beta isoform
STARD3	START domain containing 3
TRIAP1	TP53 regulated inhibitor of apoptosis 1
TARP	TCR gamma alternate reading frame protein

Gene name or Incyte clone ID	Description
SRPR	Signal recognition particle receptor ('docking protein')
NOMO1	NODAL modulator 1
PDZD8	PDZ domain containing 8
NEK9	NIMA (never in mitosis gene a)- related kinase 9
IL3RA	Interleukin 3 receptor, alpha (low affinity)
SPOCK2	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2
2259550	Transcribed locus
TTN	Titin
PPP2R2B	Protein phosphatase 2 (formerly 2A), regulatory subunit B, beta isoform
2310314	Transcribed locus, strongly similar to NP_005236.2 tumor suppressor 1 precursor [Homo sapiens]
WDR42A	WD repeat domain 42A
C1QTNF1	C1q and tumor necrosis factor related protein 1
24744	Transcribed locus, strongly similar to NP_066953.1 isomerase A isoform 1 [Homo sapiens]
391601	CDNA FLJ34214 fis, clone FCBBF3021807
1756235	Incyte EST
SPATS2	Spermatogenesis associated, serine-rich 2
EIF3S9	Eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa
CDC42SE2	CDC42 small effector 2
ASCC1	Activating signal cointegrator 1 complex subunit 1
ABR	Active BCR-related gene
SP110	SP110 nuclear body protein
CCNH	Cyclin H
TAF11	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28kDa
HERPUD1	Homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1
ZNF45	Zinc finger protein 45
PRKACB	Protein kinase, cAMP-dependent, catalytic, beta
GFI1	Growth factor independent 1
ACOX2	Acyl-Coenzyme A oxidase 2, branched chain
PIK3CG	Phosphoinositide-3-kinase, catalytic, gamma polypeptide
SKIP	Skeletal muscle and kidney enriched inositol phosphatase
197870	fibroblast growth factor 1 (acidic)
ZNF410	Zinc finger protein 410
NR3C1	Nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)
IL13RA2	Interleukin 13 receptor, alpha 2
TRIP6	Thyroid hormone receptor interactor 6
SFRS10	Splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)
ESRRA	Estrogen-related receptor alpha
PRSS12	Protease, serine, 12 (neurotrypsin, motopsin)

Gene name or Incyte clone ID	Description
IRF8	Interferon regulatory factor 8
2954670	ESTs
KIAA0196	KIAA0196
22654	Incyte EST
COX8A	Cytochrome c oxidase subunit 8A (ubiquitous)
MDH1	Malate dehydrogenase 1, NAD (soluble)
TNIP1	TNFAIP3 interacting protein 1
BMP4	Bone morphogenetic protein 4
MRPS14	Mitochondrial ribosomal protein S14
TRIM22	Tripartite motif-containing 22
WDR20	WD repeat domain 20
NAP1L4	Nucleosome assembly protein 1-like 4
MBP	Myelin basic protein
SNCA	Synuclein, alpha (non A4 component of amyloid precursor)
RNF103	Ring finger protein 103
IL11RA	Interleukin 11 receptor, alpha
SAT1	Spermidine/spermine N1-acetyltransferase 1
DCK	Deoxycytidine kinase
C7orf28B	Chromosome 7 open reading frame 28B
2902846	KIAA0964 protein
RAC2	Ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)
RCN1	Reticulocalbin 1, EF-hand calcium binding domain
2055538	spectrin, beta, non-erythrocytic 1
IL32	Interleukin 32
ZNHIT1	Zinc finger, HIT type 1
TPO	Thyroid peroxidase
POLR3F	Polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa
991756	retinal degeneration, slow (retinitis pigmentosa 7)
ACAA1	Acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)
FOXG1B	Forkhead box G1B
SPHK1	Sphingosine kinase 1
ADAT1	Adenosine deaminase, tRNA-specific 1
1256859	Transcribed locus, moderately similar to XP_574914.2 similar to leucine rich repeat containing 34 [Rattus norvegicus]
BMI1	BMI1 polycomb ring finger oncogene
RABGGTA	Rab geranylgeranyltransferase, alpha subunit
TRA2A	Transformer-2 alpha
PCBP1	Poly(rC) binding protein 1
TYMS	Thymidylate synthetase

Gene name or Incyte clone ID	Description
BMP6	Bone morphogenetic protein 6
ECT2	Epithelial cell transforming sequence 2 oncogene
3099947	Transcribed locus, weakly similar to XP_001078693.1 hypothetical protein [Rattus norvegicus]
SMAD2	SMAD family member 2
UBE2S	Ubiquitin-conjugating enzyme E2S
LOC730092	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene
MEF2C	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)
RPP38	Ribonuclease P/MRP 38kDa subunit
SLC12A5	Solute carrier family 12, (potassium-chloride transporter) member 5
IPW	Imprinted in Prader-Willi syndrome
TULP4	Tubby like protein 4
SLC26A11	Solute carrier family 26, member 11
HES1	Hairy and enhancer of split 1, (Drosophila)
2874615	Transcribed locus
COX7B	Cytochrome c oxidase subunit VIIb
2899601	CDNA FLJ44256 fis, clone TKIDN2013287

Appendix

Appendix G.

Overlapping genes with replicate 3.

Gene name or Incyte clone ID	Description
FRAP1	FK506 binding protein 12-rapamycin associated protein 1
1830083	protein phosphatase 4, regulatory subunit 1
2365327	HIV TAT specific factor 1
TUBA4A	Tubulin, alpha 4a
1593787	gamma-aminobutyric acid (GABA) A receptor, beta 1
CTRB1	Chymotrypsinogen B1
LMAN1	Lectin, mannose-binding, 1
DEXI	Dexamethasone-induced transcript
ANKRD15	Ankyrin repeat domain 15
IGF2R	Insulin-like growth factor 2 receptor
GRIK1	Glutamate receptor, ionotropic, kainate 1
CTNND1	Catenin (cadherin-associated protein), delta 1
3869412	homeo box D4
AKR1C2	Aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)
3033131	8-oxoguanine DNA glycosylase

Gene name or Incyte clone ID	Description
DPYSL4	Dihydropyrimidinase-like 4
EVL	Enah/Vasp-like
TTRAP	TRAF and TNF receptor associated protein
STRN3	Striatin, calmodulin binding protein 3
CCKBR	Cholecystokinin B receptor
CBR1	Carbonyl reductase 1
1692960	adenosine deaminase, RNA-specific
SLC6A4	Solute carrier family 6 (neurotransmitter transporter, serotonin), member 4
PTTG1	Pituitary tumor-transforming 1
RORC	RAR-related orphan receptor C
TFAM	Transcription factor A, mitochondrial
OLFM4	Olfactomedin 4
ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3
DHX38	DEAH (Asp-Glu-Ala-His) box polypeptide 38
BTG2	BTG family, member 2
ACVR1B	Activin A receptor, type IB
MYD88	Myeloid differentiation primary response gene (88)
ENPP1	Ectonucleotide pyrophosphatase/phosphodiesterase 1
LTBP4	Latent transforming growth factor beta binding protein 4
MGEA5	Meningioma expressed antigen 5 (hyaluronidase)
1570216	protocadherin 2 (cadherin-like 2)
1297082	tachykinin receptor 1
SURF2	Surfeit 2
CTSD	Cathepsin D
CCDC95	Coiled-coil domain containing 95
ACTG1	Actin, gamma 1
CEACAM5	Carcinoembryonic antigen-related cell adhesion molecule 5
PRKACA	Protein kinase, cAMP-dependent, catalytic, alpha
SMN1	Survival of motor neuron 1, telomeric
MRPS27	Mitochondrial ribosomal protein S27
UBTF	Upstream binding transcription factor, RNA polymerase I
CR2	Complement component (3d/Epstein Barr virus) receptor 2
CD37	CD37 molecule
LCMT2	Leucine carboxyl methyltransferase 2
DERL1	Der1-like domain family, member 1
AAMP	Angio-associated, migratory cell protein
GUCY1B3	Guanylate cyclase 1, soluble, beta 3
MMP1	Matrix metalloproteinase 1 (interstitial collagenase)
SFRS3	Splicing factor, arginine/serine-rich 3

Gene name or Incyte clone ID	Description
INPP5B	Inositol polyphosphate-5-phosphatase, 75kDa
CRYAB	Crystallin, alpha B
DDIT3	DNA-damage-inducible transcript 3
ACD	Adrenocortical dysplasia homolog (mouse)
PDIA4	Protein disulfide isomerase family A, member 4
KLF5	Kruppel-like factor 5 (intestinal)
PTHRI	Parathyroid hormone receptor 1
PITX2	Paired-like homeodomain transcription factor 2
4093234	Clone 23676 mRNA sequence
MAP3K13	Mitogen-activated protein kinase kinase kinase 13
NISCH	Nischarin
DNAJC8	DnaJ (Hsp40) homolog, subfamily C, member 8
FAM13C1	Family with sequence similarity 13, member C1
TNNC2	Troponin C type 2 (fast)
IDH3A	Isocitrate dehydrogenase 3 (NAD+) alpha
MAPKAPK5	Mitogen-activated protein kinase-activated protein kinase 5
MTR	5-methyltetrahydrofolate-homocysteine methyltransferase
MMP13	Matrix metalloproteinase 13 (collagenase 3)
EDD1	E3 ubiquitin protein ligase, HECT domain containing, 1
YEATS4	YEATS domain containing 4
UBE1C	Ubiquitin-activating enzyme E1C (UBA3 homolog, yeast)
C3orf40	Chromosome 3 open reading frame 40
3911	sialic acid binding Ig-like lectin 6
SNUPN	Snurportin 1
C7orf24	Chromosome 7 open reading frame 24
RAB14	RAB14, member RAS oncogene family
ANKRD12	Ankyrin repeat domain 12
PNMA1	Paraneoplastic antigen MA1
HNRPH1	Heterogeneous nuclear ribonucleoprotein H1 (H)
ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D
PAWR	PRKC, apoptosis, WT1, regulator
LRPPRC	Leucine-rich PPR-motif containing
C14orf79	Chromosome 14 open reading frame 79
SNN	Stannin
MAST2	Microtubule associated serine/threonine kinase 2
VAV1	Vav 1 oncogene
HEXIM1	Hexamethylene bis-acetamide inducible 1
CDS2	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 2
RBM14	RNA binding motif protein 14

Gene name or Incyte clone ID	Description
DDO	D-aspartate oxidase
HCN3	Hyperpolarization activated cyclic nucleotide-gated potassium channel 3
TLR1	Toll-like receptor 1
GARS	Glycyl-tRNA synthetase
DCTN6	Dynactin 6
ETF1	Eukaryotic translation termination factor 1
PRPS1	Phosphoribosyl pyrophosphate synthetase 1
465152	karyopherin alpha 1 (importin alpha 5)
RNMT	RNA (guanine-7-) methyltransferase
PRPF6	PRP6 pre-mRNA processing factor 6 homolog (S. cerevisiae)
GLRB	Glycine receptor, beta
CUL3	Cullin 3
LARP1	La ribonucleoprotein domain family, member 1
2061226	cytochrome c oxidase subunit VIa polypeptide 1
B3GALNT1	Beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)
GRK6	G protein-coupled receptor kinase 6
RASA1	RAS p21 protein activator (GTPase activating protein) 1
UCK2	Uridine-cytidine kinase 2
PIK3CB	Phosphoinositide-3-kinase, catalytic, beta polypeptide
NOL1	Nucleolar protein 1, 120kDa
ZNF508	Zinc finger protein 508
DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked
IL1R1	Interleukin 1 receptor, type I
DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1
1942845	HLA-B associated transcript-3
PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
RBM15B	RNA binding motif protein 15B
SNCG	Synuclein, gamma (breast cancer-specific protein 1)
MLH3	MutL homolog 3 (E. coli)
GANAB	Glucosidase, alpha; neutral AB
LPHN2	Latrophilin 2
HMG3	High mobility group nucleosomal binding domain 3
C8B	Complement component 8, beta polypeptide
PKN2	Protein kinase N2
SF3A1	Splicing factor 3a, subunit 1, 120kDa
TERF1	Telomeric repeat binding factor (NIMA-interacting) 1
UBE2G1	Ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)
PCSK7	Proprotein convertase subtilisin/kexin type 7
SNAP25	Synaptosomal-associated protein, 25kDa

Gene name or Incyte clone ID	Description
NHSL1	NHS-like 1
GNB3	Guanine nucleotide binding protein (G protein), beta polypeptide 3
CASP7	Caspase 7, apoptosis-related cysteine peptidase
KCNN4	Potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4
ARRB1	Arrestin, beta 1
1858604	Protein P3
NOL4	Nucleolar protein 4
TTC28	Tetratricopeptide repeat domain 28
SCRG1	Scrapie responsive protein 1
C1orf9	Chromosome 1 open reading frame 9
BST1	Bone marrow stromal cell antigen 1
CSF2RB	Colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)
CCK	Cholecystokinin
CXCL12	Chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)
C6orf106	Chromosome 6 open reading frame 106
RGR	Retinal G protein coupled receptor
3186653	adenosine A2a receptor
HNRPU	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
BCL6	B-cell CLL/lymphoma 6 (zinc finger protein 51)
CREG1	Cellular repressor of E1A-stimulated genes 1
MAFG	V-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)
APOD	Apolipoprotein D
CD79B	CD79b molecule, immunoglobulin-associated beta
IGBP1	Immunoglobulin (CD79A) binding protein 1
BMS1L	BMS1-like, ribosome assembly protein (yeast)
NUP93	Nucleoporin 93kDa
AMD1	Adenosylmethionine decarboxylase 1
CDC34	Cell division cycle 34 homolog (S. cerevisiae)
PMM2	Phosphomannomutase 2
MUC1	Mucin 1, cell surface associated
CHN2	Chimerin (chimaerin) 2
ATP5D	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit
CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha
DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18
LMNA	Lamin A/C
HIF1A	Hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
3068764	Transcribed locus
OSGIN2	Oxidative stress induced growth inhibitor family member 2

Gene name or Incyte clone ID	Description
EXOC3	Exocyst complex component 3
HSF1	Heat shock transcription factor 1
HLF	Hepatic leukemia factor
PRKAR1B	Protein kinase, cAMP-dependent, regulatory, type I, beta
1821174	CD4 antigen (p55)
VAMP3	Vesicle-associated membrane protein 3 (cellubrevin)
PEX11A	Peroxisomal biogenesis factor 11A
UGT2B17	UDP glucuronosyltransferase 2 family, polypeptide B17
ARID5A	AT rich interactive domain 5A (MRF1-like)
GP2	Glycoprotein 2 (zymogen granule membrane)
RERE	Arginine-glutamic acid dipeptide (RE) repeats
EFNA1	Ephrin-A1
NELL2	NEL-like 2 (chicken)
HS6ST1	Heparan sulfate 6-O-sulfotransferase 1
1638346	tumor necrosis factor receptor superfamily, member 5
VEGFB	Vascular endothelial growth factor B
BIN1	Bridging integrator 1
1688845	KIAA0752 protein
CTAGE5	CTAGE family, member 5
IRF8	Interferon regulatory factor 8
CIAO1	Cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)
2446995	Transcribed locus
PRKAA2	Protein kinase, AMP-activated, alpha 2 catalytic subunit
LOC339123	Hypothetical LOC339123
IGFBP5	Insulin-like growth factor binding protein 5
POP7	Processing of precursor 7, ribonuclease P subunit (S. cerevisiae)
RREB1	Ras responsive element binding protein 1
H1FX	H1 histone family, member X
2169635	sodium channel, voltage-gated, type V, alpha polypeptide (long (electrocardiographic) QT syndrome 3)
ATG7	ATG7 autophagy related 7 homolog (S. cerevisiae)
ERLIN2	ER lipid raft associated 2
UPK3A	Uroplakin 3A
1468512	MRNA; cDNA DKFZp586F2224 (from clone DKFZp586F2224)
ZNF204	Zinc finger protein 204
UCHL5IP	UCHL5 interacting protein
PLEKHM2	Pleckstrin homology domain containing, family M (with RUN domain) member 2
2378205	Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (I

Gene name or Incyte clone ID	Description
ASPHD1	Aspartate beta-hydroxylase domain containing 1
CLDN1	Claudin 1
PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
2192092	Clone 24627 mRNA sequence
TNFSF13	Tumor necrosis factor (ligand) superfamily, member 13
MED6	Mediator of RNA polymerase II transcription, subunit 6 homolog (S. cerevisiae)
1800286	Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 ~complete genomic sequence
ERG	V-ets erythroblastosis virus E26 oncogene homolog (avian)
PASK	PAS domain containing serine/threonine kinase
MEP1B	Meprin A, beta
PCBP2	Poly(rC) binding protein 2
KIAA1641	KIAA1641
OSBPL3	Oxysterol binding protein-like 3
VAC14	Vac14 homolog (S. cerevisiae)
FOSL2	FOS-like antigen 2
2447837	Human DNA sequence from clone RP5-1103G7 on chromosome 20p12.2-13. Contains up to five unknown novel genes, the gene for a novel protein kinase domains containing protein similar to phosphoprotein C8FW an the SOX22 gene for SRY (s
SNAPC5	Small nuclear RNA activating complex, polypeptide 5, 19kDa
DTNA	Dystrobrevin, alpha
AMD1	Adenosylmethionine decarboxylase 1
RAMP1	Receptor (G protein-coupled) activity modifying protein 1
TRIM28	Tripartite motif-containing 28
1695917	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)
KIAA0859	KIAA0859
ADA	Adenosine deaminase
BSG	Basigin (Ok blood group)
ILF2	Interleukin enhancer binding factor 2, 45kDa
MAP2K3	Mitogen-activated protein kinase kinase 3
EIF4EBP1	Eukaryotic translation initiation factor 4E binding protein 1
PRMT3	Protein arginine methyltransferase 3
EIF4E3	Eukaryotic translation initiation factor 4E family member 3
ZNF804A	Zinc finger protein 804A
MAPRE2	Microtubule-associated protein, RP/EB family, member 2
RABGGTB	Rab geranylgeranyltransferase, beta subunit
LY6H	Lymphocyte antigen 6 complex, locus H
NOLC1	Nucleolar and coiled-body phosphoprotein 1
SOCS2	Suppressor of cytokine signaling 2
SIVA1	SIVA1, apoptosis-inducing factor

Gene name or Incyte clone ID	Description
MEGF6	Multiple EGF-like-domains 6
MPP6	Membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)
2626971	Transcribed locus
ATP2C2	ATPase, Ca++ transporting, type 2C, member 2
GIPC1	GIPC PDZ domain containing family, member 1
SRCAP	Snf2-related CBP activator protein
PDGFRA	Platelet-derived growth factor receptor, alpha polypeptide
SLC22A1	Solute carrier family 22 (organic cation transporter), member 1
KIAA0251	KIAA0251 protein
ABCB6	ATP-binding cassette, sub-family B (MDR/TAP), member 6
GRIK5	Glutamate receptor, ionotropic, kainate 5
KCND1	Potassium voltage-gated channel, Shal-related subfamily, member 1
UBE2A	Ubiquitin-conjugating enzyme E2A (RAD6 homolog)
SPAG7	Sperm associated antigen 7
HSD17B2	Hydroxysteroid (17-beta) dehydrogenase 2
2930448	KIAA0635 gene product
CHRNA2	Cholinergic receptor, nicotinic, alpha 2 (neuronal)
RFC5	Replication factor C (activator 1) 5, 36.5kDa
BCAT2	Branched chain aminotransferase 2, mitochondrial
JAK3	Janus kinase 3 (a protein tyrosine kinase, leukocyte)
POLD3	Polymerase (DNA-directed), delta 3, accessory subunit
PAK1	P21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)
DOK2	Docking protein 2, 56kDa
IL11	Interleukin 11
CDKN2D	Cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)
CDK5R1	Cyclin-dependent kinase 5, regulatory subunit 1 (p35)
CRSP2	Cofactor required for Sp1 transcriptional activation, subunit 2, 150kDa
TWF1	Twinfilin, actin-binding protein, homolog 1 (Drosophila)
MCM3	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae)
PITPNB	Phosphatidylinositol transfer protein, beta
PSMA6	Proteasome (prosome, macropain) subunit, alpha type, 6
KIAA0672	KIAA0672 gene product
PEX14	Peroxisomal biogenesis factor 14
PHTF2	Putative homeodomain transcription factor 2
HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
PHF20	PHD finger protein 20
ELF2	E74-like factor 2 (ets domain transcription factor)
SFRS2B	Splicing factor, arginine/serine-rich 2B
SPINT1	Serine peptidase inhibitor, Kunitz type 1

Gene name or Incyte clone ID	Description
PPM1D	Protein phosphatase 1D magnesium-dependent, delta isoform
PLXDC1	Plexin domain containing 1
PIP	Prolactin-induced protein
CXCL1	Chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)
GPD1	Glycerol-3-phosphate dehydrogenase 1 (soluble)
2994202	Human DNA sequence from PAC 75N13 on chromosome Xq21.1. Contains ZNF6 like gene, ESTs, STSs and CpG islands
C1orf95	Chromosome 1 open reading frame 95
HIST1H2AE	Histone cluster 1, H2ae
LEPR	Leptin receptor
RHOBTB2	Rho-related BTB domain containing 2
VDAC1	Voltage-dependent anion channel 1
PTPN11	Protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1)
SPRR3	Small proline-rich protein 3
CASP3	Caspase 3, apoptosis-related cysteine peptidase
KRT83	Keratin 83
FRAT2	Frequently rearranged in advanced T-cell lymphomas 2
FGF13	Fibroblast growth factor 13
ARHGEF5	Rho guanine nucleotide exchange factor (GEF) 5
HSPA9	Heat shock 70kDa protein 9 (mortalin)
FCGRT	Fc fragment of IgG, receptor, transporter, alpha
HNRPAB	Heterogeneous nuclear ribonucleoprotein A/B
ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha
SCARF1	Scavenger receptor class F, member 1
2500225	MRNA; cDNA DKFZp547P042 (from clone DKFZp547P042)
PON2	Paraoxonase 2
HOXD1	Homeobox D1
HIST1H1D	Histone cluster 1, H1d
3599074	Cri-du-chat region mRNA, clone NIBB11
RHBDL1	Rhomboid, veinlet-like 1 (Drosophila)
KCNJ5	Potassium inwardly-rectifying channel, subfamily J, member 5
SLC2A3P1	Solute carrier family 2 (facilitated glucose transporter), member 3 pseudogene 1
3553605	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound
GRM4	Glutamate receptor, metabotropic 4
TNRC5	Trinucleotide repeat containing 5
POLE2	Polymerase (DNA directed), epsilon 2 (p59 subunit)
TPM3	Tropomyosin 3
5167474	nebulin
ACAT1	Acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)

Gene name or Incyte clone ID	Description
AKAP4	A kinase (PRKA) anchor protein 4
AKR1C4	Aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4)
H3F3A	H3 histone, family 3A
PIP5K2A	Phosphatidylinositol-4-phosphate 5-kinase, type II, alpha
CIB1	Calcium and integrin binding 1 (calmyrin)
3438934	CDC14 (cell division cycle 14, <i>S. cerevisiae</i>) homolog B
SLC10A1	Solute carrier family 10 (sodium/bile acid cotransporter family), member 1
HYAL1	Hyaluronoglucosaminidase 1
GRIP2	Glutamate receptor interacting protein 2
PPID	Peptidylprolyl isomerase D (cyclophilin D)
S100A9	S100 calcium binding protein A9
CCL18	Chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)
NAALADL1	N-acetylated alpha-linked acidic dipeptidase-like 1
ZNF184	Zinc finger protein 184
S100A5	S100 calcium binding protein A5
2895226	Incyte EST
3617839	Transcribed locus
NR1I2	Nuclear receptor subfamily 1, group I, member 2
GRIN2A	Glutamate receptor, ionotropic, N-methyl D-aspartate 2A
1954674	prepronociceptin
TGFBR1	Transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)
VEGFA	Vascular endothelial growth factor A
FER	Fer (fps/fes related) tyrosine kinase (phosphoprotein NCP94)
UQCRB	Ubiquinol-cytochrome c reductase binding protein
GSTA2	Glutathione S-transferase A2
NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)
CNTN2	Contactin 2 (axonal)
1861772	Incyte EST
RPL31	Ribosomal protein L31
2601553	Incyte EST
C4BPB	Complement component 4 binding protein, beta
5092727	tubby (mouse) homolog
3933661	Incyte EST
5063036	Incyte EST
4912536	TATA box binding protein (TBP)-associated factor, RNA polymerase II, H, 30kD
SLC22A2	Solute carrier family 22 (organic cation transporter), member 2
4984469	Clone 24739 mRNA sequence

Gene name or Incyte clone ID	Description
UTP14A	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)
ATP6V1G1	ATPase, H ⁺ transporting, lysosomal 13kDa, V1 subunit G1
PCDH8	Protocadherin 8
XAF1	XIAP associated factor-1
DAZL	Deleted in azoospermia-like
CDH22	Cadherin-like 22
H2AFZ	H2A histone family, member Z
1869139	calcium binding protein P22
NME5	Non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)
BCAS2	Breast carcinoma amplified sequence 2
5311604	pre-T/NK cell associated protein
ZNF44	Zinc finger protein 44
DKK1	Dickkopf homolog 1 (Xenopus laevis)
RBMV1A1	RNA binding motif protein, Y-linked, family 1, member A1
443092	butyrate response factor 2 (EGF-response factor 2)
BCLAF1	BCL2-associated transcription factor 1
PKP2	Plakophilin 2
E2F2	E2F transcription factor 2
SFRS1	Splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
B3GNTL1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1
CLCN1	Chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant)
698901	translocase of inner mitochondrial membrane 8 (yeast) homolog A
ELA2B	Elastase 2B
PSMC5	Proteasome (prosome, macropain) 26S subunit, ATPase, 5
CDH2	Cadherin 2, type 1, N-cadherin (neuronal)
CDH2	Cadherin 2, type 1, N-cadherin (neuronal)
MRPL3	Mitochondrial ribosomal protein L3
BCL6	B-cell CLL/lymphoma 6 (zinc finger protein 51)
SLC16A1	Solute carrier family 16, member 1 (monocarboxylic acid transporter 1)
DCTD	DCMP deaminase
MCM7	MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)
NPM3	Nucleophosmin/nucleoplasmin, 3
NUP93	Nucleoporin 93kDa
ECH1	Enoyl Coenzyme A hydratase 1, peroxisomal
RPL9	Ribosomal protein L9
ATG16L2	ATG16 autophagy related 16-like 2 (S. cerevisiae)
550326	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase
WISP1	WNT1 inducible signaling pathway protein 1
COIL	Coilin

Gene name or Incyte clone ID	Description
CACNB1	Calcium channel, voltage-dependent, beta 1 subunit
UBE2A	Ubiquitin-conjugating enzyme E2A (RAD6 homolog)
RHEB	Ras homolog enriched in brain
DFNA5	Deafness, autosomal dominant 5
ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha
SQLE	Squalene epoxidase
XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kDa)
NDUFB7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa
294379	cytochrome P450, subfamily IIE (ethanol-inducible)
551626	transforming growth factor beta-activated kinase-binding protein 1
C22orf28	Chromosome 22 open reading frame 28
UAP1	UDP-N-acetylglucosamine pyrophosphorylase 1
GABRA6	Gamma-aminobutyric acid (GABA) A receptor, alpha 6
AP3S1	Adaptor-related protein complex 3, sigma 1 subunit
TSPY1	Testis specific protein, Y-linked 1
ZNF432	Zinc finger protein 432
CRADD	CASP2 and RIPK1 domain containing adaptor with death domain
S100A2	S100 calcium binding protein A2
FAM62A	Family with sequence similarity 62 (C2 domain containing), member A
RCVRN	Recoverin
348234	protein kinase, cGMP-dependent, type I
5043572	HLA-G histocompatibility antigen, class I, G
LY6D	Lymphocyte antigen 6 complex, locus D
CAMK1	Calcium/calmodulin-dependent protein kinase I
GRB7	Growth factor receptor-bound protein 7
961082	Transcribed locus
KIAA0143	KIAA0143 protein
DHRS3	Dehydrogenase/reductase (SDR family) member 3
PIWIL1	Piwi-like 1 (Drosophila)
64394	calpain-like protease
GAB1	GRB2-associated binding protein 1
FLJ36492	Hypothetical protein FLJ36492
CCL18	Chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)
SFRS1	Splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
MCM7	MCM7 minichromosome maintenance deficient 7 (<i>S. cerevisiae</i>)
DNAJC11	DnaJ (Hsp40) homolog, subfamily C, member 11
PDCD4	Programmed cell death 4 (neoplastic transformation inhibitor)
DUSP11	Dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)

Gene name or Incyte clone ID	Description
KIAA0913	KIAA0913
RNASE4	Ribonuclease, RNase A family, 4
LIG3	Ligase III, DNA, ATP-dependent
RIF1	RAP1 interacting factor homolog (yeast)
2040657	Incyte EST
PRRG2	Proline rich Gla (G-carboxyglutamic acid) 2
ALOX15B	Arachidonate 15-lipoxygenase, type B
CDC42EP2	CDC42 effector protein (Rho GTPase binding) 2
SDHB	Succinate dehydrogenase complex, subunit B, iron sulfur (Ip)
SCGB2A1	Secretoglobin, family 2A, member 1
MAP3K14	Mitogen-activated protein kinase kinase kinase 14
SPAG6	Sperm associated antigen 6
CHIT1	Chitinase 1 (chitotriosidase)
GCNT2	Glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)
CXCL6	Chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)
USH1C	Usher syndrome 1C (autosomal recessive, severe)
SOX5	SRY (sex determining region Y)-box 5
DLL1	Delta-like 1 (Drosophila)
DVL1	Dishevelled, dsh homolog 1 (Drosophila)
CPNE6	Copine VI (neuronal)
EIF3S2	Eukaryotic translation initiation factor 3, subunit 2 beta, 36kDa
NGFR	Nerve growth factor receptor (TNFR superfamily, member 16)
LDB2	LIM domain binding 2
RASGRP1	RAS guanyl releasing protein 1 (calcium and DAG-regulated)
UBE2L3	Ubiquitin-conjugating enzyme E2L 3
PRMT3	Protein arginine methyltransferase 3
PDPN	Podoplanin
IGSF6	Immunoglobulin superfamily, member 6
2112785	purinergic receptor P2X, ligand-gated ion channel, 4
UPK1B	Uroplakin 1B
1740384	KIAA0403 protein
TTC1	Tetratricopeptide repeat domain 1
CD164	CD164 molecule, sialomucin
CXorf9	Chromosome X open reading frame 9
CACNA2D1	Calcium channel, voltage-dependent, alpha 2/delta subunit 1
NHLH1	Nescient helix loop helix 1
DHRSX	Dehydrogenase/reductase (SDR family) X-linked
SLC6A13	Solute carrier family 6 (neurotransmitter transporter, GABA), member 13
KNG1	Kininogen 1

Gene name or Incyte clone ID	Description
963211	mannosidase, alpha, class 1A, member 1
CNR2	Cannabinoid receptor 2 (macrophage)
DDX12	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 12 (CHL1-like helicase homolog, <i>S. cerevisiae</i>)
2112288	adducin 2 (beta)
CYFIP1	Cytoplasmic FMR1 interacting protein 1
TRMT1	TRM1 tRNA methyltransferase 1 homolog (<i>S. cerevisiae</i>)
NOXA1	NADPH oxidase activator 1
S100B	S100 calcium binding protein B
NCK1	NCK adaptor protein 1
RPL12	Ribosomal protein L12
PECI	Peroxisomal D3,D2-enoyl-CoA isomerase
SLC1A1	Solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1
CDKN1A	Cyclin-dependent kinase inhibitor 1A (p21, Cip1)
GOT1	Glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)
ILK	Integrin-linked kinase
CACNB2	Calcium channel, voltage-dependent, beta 2 subunit
MMP23B	Matrix metalloproteinase 23B
IFI44	Interferon-induced protein 44
POSTN	Periostin, osteoblast specific factor
ABCC5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5
IER3	Immediate early response 3
EFCBP2	EF-hand calcium binding protein 2
CFP	Complement factor properdin
3145490	bromodomain, testis-specific
ELK1	ELK1, member of ETS oncogene family
MTA2	Metastasis associated 1 family, member 2
MAN2A2	Mannosidase, alpha, class 2A, member 2
SLC14A2	Solute carrier family 14 (urea transporter), member 2
NIPA2	Non imprinted in Prader-Willi/Angelman syndrome 2
CNOT2	CCR4-NOT transcription complex, subunit 2
C12orf4	Chromosome 12 open reading frame 4
PPP3CA	Protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform
LOC202347	Hypothetical protein LOC202347
NDUFB2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa
MRPL30	Mitochondrial ribosomal protein L30
KIAA1429	KIAA1429
RHOF	Ras homolog gene family, member F (in filopodia)
RPP21	Ribonuclease P 21kDa subunit

Gene name or Incyte clone ID	Description
THAP8	THAP domain containing 8
1798965	Transcribed locus, strongly similar to XP_001140330.1 similar to ankyrin repeat domain 10 isoform 3 [Pan troglodytes]
CPNE3	Copine III
2195489	Incyte EST
FAM62B	Family with sequence similarity 62 (C2 domain containing) member B
C20orf4	Chromosome 20 open reading frame 4
2512249	CDNA FLJ11481 fis, clone HEMBA1001803
S100PBP	S100P binding protein
NBPF1	Neuroblastoma breakpoint family, member 1
2597109	Transcribed locus, weakly similar to NP_608540.1 [Drosophila melanogaster]
2743036	CDNA FLJ11602 fis, clone HEMBA1003908
RBM25	RNA binding motif protein 25
CCDC92	Coiled-coil domain containing 92
GPR160	G protein-coupled receptor 160
C10orf83	Chromosome 10 open reading frame 83
2182201	Transcribed locus
2592657	ESTs
PRAC	Small nuclear protein PRAC
2378423	Transcribed locus
2590267	Transcribed locus
TMEPAI	Transmembrane, prostate androgen induced RNA
NCOR1	Nuclear receptor co-repressor 1
2544622	Transcribed locus, strongly similar to XP_001172939.1 hypothetical protein [Pan troglodytes]
2017475	CDNA FLJ33420 fis, clone BRACE2020028
LOC642346	Similar to golgi autoantigen, golgin subfamily a-like
XAGE1	X antigen family, member 1
GPRASP2	G protein-coupled receptor associated sorting protein 2
WRNIP1	Werner helicase interacting protein 1
3846507	Transcribed locus
MAP3K7IP2	Mitogen-activated protein kinase kinase kinase 7 interacting protein 2
ATP6V1C1	ATPase, H ⁺ transporting, lysosomal 42kDa, V1 subunit C1
OR51E2	Olfactory receptor, family 51, subfamily E, member 2
SLC12A2	Solute carrier family 12 (sodium/potassium/chloride transporters), member 2
RPESP	RPE-spondin
N4BP2	Nedd4 binding protein 2
1376651	CDNA FLJ31513 fis, clone NT2RI1000127
ZNF511	Zinc finger protein 511
ATCAY	Ataxia, cerebellar, Cayman type (caytaxin)

Gene name or Incyte clone ID	Description
PAG1	Phosphoprotein associated with glycosphingolipid microdomains 1
UBE2W	Ubiquitin-conjugating enzyme E2W (putative)
2831248	Incyte EST
IVNS1ABP	Influenza virus NS1A binding protein
3843969	Transcribed locus
FBXO32	F-box protein 32
TTC21B	Tetratricopeptide repeat domain 21B
SUCLA2	Succinate-CoA ligase, ADP-forming, beta subunit
LOC130074	P20
FLYWCH1	FLYWCH-type zinc finger 1
2219252	Full length insert cDNA Y137C01
ZC3H10	Zinc finger CCCH-type containing 10
LYAR	Hypothetical protein FLJ20425
RNASEH1	Ribonuclease H1
C9orf5	Chromosome 9 open reading frame 5
APOM	Apolipoprotein M
1436012	CDNA FLJ34311 fis, clone FEBRA2008255
1639661	Transcribed locus, moderately similar to XP_001054207.1 similar to MASK-4E-BP3 protein [Rattus norvegicus]
ZNF23	Zinc finger protein 23 (KOX 16)
1813721	Transcribed locus
FBXO8	F-box protein 8
BBS2	Bardet-Biedl syndrome 2
ITGA2	Integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)
C9orf85	Chromosome 9 open reading frame 85
SHROOM3	Shroom family member 3
APC	Adenomatosis polyposis coli
C11orf71	Chromosome 11 open reading frame 71
2513394	mannan-binding lectin serine protease 2
291636	Transcribed locus
WIPF1	WAS/WASL interacting protein family, member 1
FAM20A	Family with sequence similarity 20, member A
EWSR1	Ewing sarcoma breakpoint region 1
TAF4B	TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa
RPS29	Ribosomal protein S29
2556393	Transcribed locus
CD86	CD86 molecule
PPAPDC1B	Phosphatidic acid phosphatase type 2 domain containing 1B
TBC1D22A	TBC1 domain family, member 22A

Gene name or Incyte clone ID	Description
1405820	Transcribed locus
SGPP1	Sphingosine-1-phosphate phosphatase 1
GABBR1	Gamma-aminobutyric acid (GABA) B receptor, 1
MFGE8	Milk fat globule-EGF factor 8 protein
PAPOLA	Poly(A) polymerase alpha
407032	Transcribed locus, weakly similar to NP_071385.1 protein LOC63933 isoform 2 [Homo sapiens]
OR7E38P	Olfactory receptor, family 7, subfamily E, member 38 pseudogene
SFRS15	Splicing factor, arginine/serine-rich 15
SGTA	Small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha
TCF7L2	Transcription factor 7-like 2 (T-cell specific, HMG-box)
ACTL6A	Actin-like 6A
G3BP2	GTPase activating protein (SH3 domain) binding protein 2
FZD5	Frizzled homolog 5 (Drosophila)
694279	Transcribed locus
DCBLD1	Discoidin, CUB and LCCL domain containing 1
BMPER	BMP binding endothelial regulator
1478654	G protein-coupled receptor 37 (endothelin receptor type B-like)
3013507	Homo sapiens cDNA FLJ10022 fis, clone HEMBA1000588
DBNDD1	Dysbindin (dystrobrevin binding protein 1) domain containing 1
RPLP0-like	Similar to ribosomal protein P0
1640094	Transcribed locus
997948	Transcribed locus
TncRNA	Trophoblast-derived noncoding RNA
2673080	Transcribed locus
2738488	Incyte EST
ARSJ	Arylsulfatase family, member J
1908734	Transcribed locus
DOK5	Docking protein 5
ASL	Argininosuccinate lyase
CENTA2	Centaurin, alpha 2
2075522	CDNA clone IMAGE:4817413
1507281	Transcribed locus
TRAPPC1	Trafficking protein particle complex 1
PTCD2	Pentatricopeptide repeat domain 2
DNAH1	Dynein, axonemal, heavy chain 1
1465831	CDNA clone IMAGE:3878708
CDIPT	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)
CHRNA3	Cholinergic receptor, nicotinic, alpha 3

Gene name or Incyte clone ID	Description
PDCD6	Programmed cell death 6
C20orf74	Chromosome 20 open reading frame 74
1684421	CDNA FLJ41537 fis, clone BRTHA2017985
LOC51255	Hypothetical protein LOC51255
1481310	ESTs
3462557	homeo box D13
RAB3C	RAB3C, member RAS oncogene family
855928	Transcribed locus
1633393	Transcribed locus
LOC151146	Hypothetical protein LOC151146
TRIM66	Tripartite motif-containing 66
PRSS3	Protease, serine, 3 (mesotrypsin)
SEMA3A	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A
1639638	Transcribed locus
1260330	Incyte EST
MGC3207	Hypothetical protein MGC3207
SLC18A1	Solute carrier family 18 (vesicular monoamine), member 1
MGC26647	Hypothetical protein MGC26647
GPR137	G protein-coupled receptor 137
1997605	Transcribed locus
N4BP1	Nedd4 binding protein 1
SCNN1A	Sodium channel, nonvoltage-gated 1 alpha
LEPR	Leptin receptor
IFITM3	Interferon induced transmembrane protein 3 (1-8U)
TRABD	TraB domain containing
UBXD3	UBX domain containing 3
PILRA	Paired immunoglobulin-like type 2 receptor alpha
CCDC80	Coiled-coil domain containing 80
1403168	inositol(myo)-1(or 4)-monophosphatase 1
MAN1A2	Mannosidase, alpha, class 1A, member 2
ZNF226	Zinc finger protein 226
476348	Incyte EST
RPIA	Ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase)
ILF3	Interleukin enhancer binding factor 3, 90kDa
UROD	Uroporphyrinogen decarboxylase
PALM	Paralemmin
637283	Transcribed locus
TNNI3K	TNNI3 interacting kinase

Gene name or Incyte clone ID	Description
NXPH1	Neurexophilin 1
SON	SON DNA binding protein
1511484	N-acetylglucosaminyl transferase component Gpi1
RANBP1	RAN binding protein 1
CDC2	Cell division cycle 2, G1 to S and G2 to M
COL14A1	Collagen, type XIV, alpha 1 (undulin)
SLC6A6	Solute carrier family 6 (neurotransmitter transporter, taurine), member 6
GFER	Growth factor, augments liver regeneration (ERV1 homolog, <i>S. cerevisiae</i>)
NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa
C16orf5	Chromosome 16 open reading frame 5
68729	Incyte EST
C1orf41	Chromosome 1 open reading frame 41
1823641	ESTs
PPCS	Phosphopantothienoylcysteine synthetase
862356	ESTs
CCNB3	Cyclin B3
HNRPM	Heterogeneous nuclear ribonucleoprotein M
FGL1	Fibrinogen-like 1
SLC27A3	Solute carrier family 27 (fatty acid transporter), member 3
2754723	Incyte EST
GNPDA1	Glucosamine-6-phosphate deaminase 1
SCN1B	Sodium channel, voltage-gated, type I, beta
SNX19	Sorting nexin 19
CCNA1	Cyclin A1
606593	Transcribed locus
MRPL13	Mitochondrial ribosomal protein L13
MGC15523	Hypothetical protein MGC15523
NT5E	5'-nucleotidase, ecto (CD73)
ANKRD46	Ankyrin repeat domain 46
HNRPF	Heterogeneous nuclear ribonucleoprotein F
TATDN2	TatD DNase domain containing 2
PLXNC1	Plexin C1
MIA	Melanoma inhibitory activity
SEMA6A	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A
TMEM101	Transmembrane protein 101
SYK	Spleen tyrosine kinase
PDX1	Pancreatic and duodenal homeobox 1
C11orf2	Chromosome 11 open reading frame2
WDR81	WD repeat domain 81

Gene name or Incyte clone ID	Description
NUP85	Nucleoporin 85kDa
DDEF1	Development and differentiation enhancing factor 1
2414525	Full-length cDNA clone CS0DF007YP05 of Fetal brain of Homo sapiens (human)
1708552	Transcribed locus, strongly similar to XP_001147416.1 spermidine/spermine N1-acetyl transferase-like 1 [Pan troglodytes]
EVA1	Epithelial V-like antigen 1
FLT3	Fms-related tyrosine kinase 3
WDR67	WD repeat domain 67
MTP18	Mitochondrial protein 18 kDa
DDHD2	DDHD domain containing 2
RNF185	Ring finger protein 185
1701814	gastrulation brain homeo box 1
DDX55	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55
CLSTN1	Calsyntenin 1
DNPEP	Aspartyl aminopeptidase
TTYH1	Tweety homolog 1 (Drosophila)
DLL4	Delta-like 4 (Drosophila)
NFE2L3	Nuclear factor (erythroid-derived 2)-like 3
ACADL	Acyl-Coenzyme A dehydrogenase, long chain
1673167	erythropoietin receptor
RBM9	RNA binding motif protein 9
DKFZP686A01247	DKFZP686A01247 hypothetical protein
DAPP1	Dual adaptor of phosphotyrosine and 3-phosphoinositides
C20orf119	Chromosome 20 open reading frame 119
AKAP13	A kinase (PRKA) anchor protein 13
2766987	Transcribed locus
DHRS12	Dehydrogenase/reductase (SDR family) member 12
ZNF200	Zinc finger protein 200
ALDH16A1	Aldehyde dehydrogenase 16 family, member A1
ASXL1	Additional sex combs like 1 (Drosophila)
CORO2B	Coronin, actin binding protein, 2B
ELAC1	ElaC homolog 1 (E. coli)
2396760	CDNA clone IMAGE:5268696
C7orf36	Chromosome 7 open reading frame 36
CEP192	Centrosomal protein 192kDa
NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa
2399458	Transcribed locus
MYCBP	C-myc binding protein
DDX46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46

Gene name or Incyte clone ID	Description
1509519	Transcribed locus
FLJ20699	Hypothetical protein FLJ20699
IREB2	Iron-responsive element binding protein 2
SGIP1	SH3-domain GRB2-like (endophilin) interacting protein 1
EIF2AK1	Eukaryotic translation initiation factor 2-alpha kinase 1
CYS1	Cystin 1
MAGEA4	Melanoma antigen family A, 4
1621205	Transcribed locus
MS4A6A	Membrane-spanning 4-domains, subfamily A, member 6A
2350560	Transcribed locus
DHX36	DEAH (Asp-Glu-Ala-His) box polypeptide 36
LACTB2	Lactamase, beta 2
SHC2	SHC (Src homology 2 domain containing) transforming protein 2
CSNK2A2	Casein kinase 2, alpha prime polypeptide
ASNA1	ArsA arsenite transporter, ATP-binding, homolog 1 (bacterial)
HIST1H1C	Histone cluster 1, H1c
CEP63	Centrosomal protein 63kDa
GALNT14	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)
SELL	Selectin L (lymphocyte adhesion molecule 1)
PPP2R5A	Protein phosphatase 2, regulatory subunit B', alpha isoform
1673876	v-myc avian myelocytomatosis viral oncogene homolog
2674482	Incyte EST
SCYE1	Small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)
DDX23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23
FNIP1	Folliculin interacting protein 1
DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9
1822713	butyrophilin, subfamily 3, member A1
PSCD1	Pleckstrin homology, Sec7 and coiled-coil domains 1(cytohesin 1)
PDK4	Pyruvate dehydrogenase kinase, isozyme 4
SF3B2	Splicing factor 3b, subunit 2, 145kDa
MFAP4	Microfibrillar-associated protein 4
UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)
WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)
SP100	SP100 nuclear antigen
COL9A3	Collagen, type IX, alpha 3
CES1	Carboxylesterase 1 (monocyte/macrophage serine esterase 1)
240817	Transcribed locus
KIAA0284	KIAA0284

Gene name or Incyte clone ID	Description
MRPL54	Mitochondrial ribosomal protein L54
CTR9	Ctr9, Paf1/RNA polymerase II complex component, homolog (<i>S. cerevisiae</i>)
COBRA1	Cofactor of BRCA1
SYNPO	Synaptopodin
SF4	Splicing factor 4
ZCCHC14	Zinc finger, CCHC domain containing 14
WDR59	WD repeat domain 59
MIDN	Midnolin
1906936	Transcribed locus
1696224	heat shock 70kD protein 1
RDH10	Retinol dehydrogenase 10 (all-trans)
HCST	Hematopoietic cell signal transducer
GSTT1	Glutathione S-transferase theta 1
STATH	Statherin
DLG1	Discs, large homolog 1 (<i>Drosophila</i>)
NSDHL	NAD(P) dependent steroid dehydrogenase-like
MAP2K5	Mitogen-activated protein kinase kinase 5
RAB11A	RAB11A, member RAS oncogene family
WAC	WW domain containing adaptor with coiled-coil
HAGH	Hydroxyacylglutathione hydrolase
YARS	Tyrosyl-tRNA synthetase
GALE	UDP-galactose-4-epimerase
PABPN1	Poly(A) binding protein, nuclear 1
CTNNA1	Catenin (cadherin-associated protein), alpha 1, 102kDa
PRKRIP1	PRKR interacting protein 1 (IL11 inducible)
WDTC1	WD and tetratricopeptide repeats 1
ICMT	Isoprenylcysteine carboxyl methyltransferase
TNKS1BP1	Tankyrase 1 binding protein 1, 182kDa
BYSL	Bystin-like
NARS	Asparaginyl-tRNA synthetase
PTMS	Parathymosin
NUDT22	Nudix (nucleoside diphosphate linked moiety X)-type motif 22
GABRP	Gamma-aminobutyric acid (GABA) A receptor, pi
SEC14L1	SEC14-like 1 (<i>S. cerevisiae</i>)
NFATC1	Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1
DHX34	DEAH (Asp-Glu-Ala-His) box polypeptide 34
SLC1A5	Solute carrier family 1 (neutral amino acid transporter), member 5
SCNN1G	Sodium channel, nonvoltage-gated 1, gamma
FCGR3B	Fc fragment of IgG, low affinity IIIb, receptor (CD16b)

Gene name or Incyte clone ID	Description
CBLN1	Cerebellin 1 precursor
MYO5A	Myosin VA (heavy chain 12, myosin)
182802	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1
GABPA	GA binding protein transcription factor, alpha subunit 60kDa
NECAP2	NECAP endocytosis associated 2
FMO1	Flavin containing monooxygenase 1
ZBTB39	Zinc finger and BTB domain containing 39
SMYD5	SMYD family member 5
TMEM112B	Transmembrane protein 112B
SFRS1	Splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
80275	excision repair cross-complementing rodent repair deficiency, complementation group 4
SAA4	Serum amyloid A4, constitutive
DSC2	Desmocollin 2
TNFAIP3	Tumor necrosis factor, alpha-induced protein 3
STX8	Syntaxin 8
2201371	MRNA from chromosome 5q31-33 region
KIR2DL4	Killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4
2189383	Transcribed locus, weakly similar to NP_003119.2 beta, non-erythrocytic 1 isoform 1 [Homo sapiens]
CDC40	Cell division cycle 40 homolog (S. cerevisiae)
BPHL	Biphenyl hydrolase-like (serine hydrolase; breast epithelial mucin-associated antigen)
KLHL9	Kelch-like 9 (Drosophila)
DGKD	Diacylglycerol kinase, delta 130kDa
GABRB3	Gamma-aminobutyric acid (GABA) A receptor, beta 3
ELF4	E74-like factor 4 (ets domain transcription factor)
WNK1	WNK lysine deficient protein kinase 1
GOLGA1	Golgi autoantigen, golgin subfamily a, 1
DDB2	Damage-specific DNA binding protein 2, 48kDa
NSMAF	Neutral sphingomyelinase (N-SMase) activation associated factor
ADAM2	ADAM metalloproteinase domain 2 (fertilin beta)
ATP1A2	ATPase, Na ⁺ /K ⁺ transporting, alpha 2 (+) polypeptide
TNFRSF10B	Tumor necrosis factor receptor superfamily, member 10b
PRDX1	Peroxiredoxin 1
PRR3	Proline rich 3
MSR1	Macrophage scavenger receptor 1
SRF	Serum response factor (c-fos serum response element-binding transcription factor)
YWHAH	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
3149480	anti-Mullerian hormone receptor, type II
2251851	Clone 23908 mRNA sequence

Gene name or Incyte clone ID	Description
KCNH2	Potassium voltage-gated channel, subfamily H (eag-related), member 2
RBPMS	RNA binding protein with multiple splicing
MAP3K10	Mitogen-activated protein kinase kinase kinase 10
2209136	Clone 23728 mRNA sequence
KIAA1128	KIAA1128
IL10	Interleukin 10
SCN9A	Sodium channel, voltage-gated, type IX, alpha subunit
SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5
APBB1	Amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65)
FLRT1	Fibronectin leucine rich transmembrane protein 1
KCNQ2	Potassium voltage-gated channel, KQT-like subfamily, member 2
FGFR2	Fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)
KIF1B	Kinesin family member 1B
1998269	Incyte EST
1848981	Transcribed locus
HDAC9	Histone deacetylase 9
HSPA4	Heat shock 70kDa protein 4
2745159	Transcribed locus
KRT18	Keratin 18
C1orf2	Chromosome 1 open reading frame 2
TLR3	Toll-like receptor 3
CEP27	Centrosomal protein 27kDa
3045817	Transcribed locus
STX6	Syntaxin 6
MAGOH	Mago-nashi homolog, proliferation-associated (Drosophila)
APOD	Apolipoprotein D
RP13-401N8.2	Hypothetical gene supported by BC042812
CCNY	Cyclin Y
C6orf168	Chromosome 6 open reading frame 168
LOC283658	Hypothetical protein LOC283658
MAPK9	Mitogen-activated protein kinase 9
ANAPC10	Anaphase promoting complex subunit 10
KCNIP4	Kv channel interacting protein 4
4217059	Homo sapiens, clone IMAGE:4414697, mRNA
PFAS	Phosphoribosylformylglycinamide synthase (FGAR amidotransferase)
1842589	Transcribed locus
ZNF707	Zinc finger protein 707

Gene name or Incyte clone ID	Description
SCAMP1	Secretory carrier membrane protein 1
1208476	CDNA clone IMAGE:5301514
1612969	retinol-binding protein 1, cellular
2818928	Incyte EST
CCDC62	Coiled-coil domain containing 62
KIAA2026	KIAA2026
CRYZ	Crystallin, zeta (quinone reductase)
Septin 8	Septin 8
KRTAP4-7	Keratin associated protein 4–7
2156608	MRNA; cDNA DKFZp686L15210 (from clone DKFZp686L15210)
CLIP2	CAP-GLY domain containing linker protein 2
SLC26A8	Solute carrier family 26, member 8
ZNF22	Zinc finger protein 22 (KOX 15)
BDH2	3-hydroxybutyrate dehydrogenase, type 2
1282617	period (Drosophila) homolog 2
RABEPK	Rab9 effector protein with kelch motifs
FAT3	FAT tumor suppressor homolog 3 (Drosophila)
TMEM118	Transmembrane protein 118
2773862	Transcribed locus
MRPL44	Mitochondrial ribosomal protein L44
DNASE1	Deoxyribonuclease I
LMOD1	Leiomodulin 1 (smooth muscle)
NRP2	Neuropilin 2
TTC5	Tetratricopeptide repeat domain 5
ELAVL4	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)
1686856	Transcribed locus
2912987	Transcribed locus, strongly similar to XP_530610.1 hypothetical protein XP_530610 [Pan troglodytes]
CCNL2	Cyclin L2
3202075	Transcribed locus
ZBTB34	Zinc finger and BTB domain containing 34
SLC29A1	Solute carrier family 29 (nucleoside transporters), member 1
MRPL19	Mitochondrial ribosomal protein L19
SLC25A5	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
TSEN34	TRNA splicing endonuclease 34 homolog (S. cerevisiae)
MYO9A	Myosin IXA
SENP5	SUMO1/sentrin specific peptidase 5
LBP	Lipopolysaccharide binding protein
MAFG	V-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)

Gene name or Incyte clone ID	Description
PEG10	Paternally expressed 10
2060017	Incyte EST
CLPP	ClpP caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)
2826117	ESTs
POLR2H	Polymerase (RNA) II (DNA directed) polypeptide H
LOC153222	Adult retina protein
TTLL5	Tubulin tyrosine ligase-like family, member 5
COG8	Component of oligomeric golgi complex 8
REPS2	RALBP1 associated Eps domain containing 2
BDNF	Brain-derived neurotrophic factor
LOC284939	Hypothetical protein LOC284939
AZU1	Azurocidin 1 (cationic antimicrobial protein 37)
SGCB	Sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)
PGK1	Phosphoglycerate kinase 1
MEP1A	Meprin A, alpha (PABA peptide hydrolase)
PIIG	Peptidylprolyl isomerase G (cyclophilin G)
SSB	Sjogren syndrome antigen B (autoantigen La)
WNK1	WNK lysine deficient protein kinase 1
PSMC3	Proteasome (prosome, macropain) 26S subunit, ATPase, 3
BRCA1	Breast cancer 1, early onset
TNIK	TRAF2 and NCK interacting kinase
NOV	Nephroblastoma overexpressed gene
SRM	Spermidine synthase
ANXA3	Annexin A3
SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1
COX4I1	Cytochrome c oxidase subunit IV isoform 1
SDF2	Stromal cell-derived factor 2
CCL17	Chemokine (C-C motif) ligand 17
STXBP1	Syntaxin binding protein 1
SERPINA3	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3
GTF2F2	General transcription factor IIF, polypeptide 2, 30kDa
MGC17330	HGFL gene
COX7A2L	Cytochrome c oxidase subunit VIIa polypeptide 2 like
BIRC3	Baculoviral IAP repeat-containing 3
SLC15A2	Solute carrier family 15 (H+/peptide transporter), member 2
MAL	Mal, T-cell differentiation protein
PIP5K1B	Phosphatidylinositol-4-phosphate 5-kinase, type I, beta
TMEM115	Transmembrane protein 115

Gene name or Incyte clone ID	Description
RNASE4	Ribonuclease, RNase A family, 4
SLC25A46	Solute carrier family 25, member 46
ZNF238	Zinc finger protein 238
SLC39A6	Solute carrier family 39 (zinc transporter), member 6
CD40LG	CD40 ligand (TNF superfamily, member 5, hyper-IgM syndrome)
SGCB	Sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)
KIF2A	Kinesin heavy chain member 2A
LY75	Lymphocyte antigen 75
RND2	Rho family GTPase 2
SRGAP3	SLIT-ROBO Rho GTPase activating protein 3
LBA1	Lupus brain antigen 1
TDGF1	Teratocarcinoma-derived growth factor 1
FAM38A	Family with sequence similarity 38, member A
CASP5	Caspase 5, apoptosis-related cysteine peptidase
AGPS	Alkylglycerone phosphate synthase
23662	Incyte EST
LCT	Lactase
UPP1	Uridine phosphorylase 1
SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
HMGB1	High-mobility group box 1
PSMD6	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 6
ABCB10	ATP-binding cassette, sub-family B (MDR/TAP), member 10
SMAD3	SMAD family member 3
VPS72	Vacuolar protein sorting 72 homolog (<i>S. cerevisiae</i>)
ACHE	Acetylcholinesterase (Yt blood group)
TOB1	Transducer of ERBB2, 1
AURKB	Aurora kinase B
RALGPS1	Ral GEF with PH domain and SH3 binding motif 1
PRSS1	Protease, serine, 1 (trypsin 1)
RP11-56A21.1	Similar to KIAA0592 protein
CACNG1	Calcium channel, voltage-dependent, gamma subunit 1
PLP2	Proteolipid protein 2 (colonic epithelium-enriched)
TRAFD1	TRAF-type zinc finger domain containing 1
SLC16A5	Solute carrier family 16, member 5 (monocarboxylic acid transporter 6)
FGB	Fibrinogen beta chain
RPS6KA3	Ribosomal protein S6 kinase, 90kDa, polypeptide 3
PRKAR2B	Protein kinase, cAMP-dependent, regulatory, type II, beta
GFPT1	Glutamine-fructose-6-phosphate transaminase 1

Gene name or Incyte clone ID	Description
RELN	Reelin
TLN2	Talin 2
PPY	Pancreatic polypeptide
DIAPH2	Diaphanous homolog 2 (Drosophila)
TBC1D9	TBC1 domain family, member 9 (with GRAM domain)
ST6GALNAC6	ST6 (alpha-N-acetyl-neuraminy1-2,3-beta-galactosyl-1,3)-N-acetylglactosaminide alpha-2,6-sialyltransferase 6
PSME4	Proteasome (prosome, macropain) activator subunit 4
JAKMIP2	Janus kinase and microtubule interacting protein 2
ZDHHC3	Zinc finger, DHHC-type containing 3
C3orf63	Chromosome 3 open reading frame 63
BATF2	Basic leucine zipper transcription factor, ATF-like 2
NFU1	NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae)
ZNF415	Zinc finger protein 415
LAG3	Lymphocyte-activation gene 3
CALB1	Calbindin 1, 28kDa
MIPEP	Mitochondrial intermediate peptidase
HNF4A	Hepatocyte nuclear factor 4, alpha
APOA2	Apolipoprotein A-II
PDIA5	Protein disulfide isomerase family A, member 5
PDE6D	Phosphodiesterase 6D, cGMP-specific, rod, delta
AHCTF1	AT hook containing transcription factor 1
CPT1B	Carnitine palmitoyltransferase 1B (muscle)
MPG	N-methylpurine-DNA glycosylase
MOBP	Myelin-associated oligodendrocyte basic protein
RNASE3	Ribonuclease, RNase A family, 3 (eosinophil cationic protein)
818192	glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD)
ENC1	Ectodermal-neural cortex (with BTB-like domain)
SNRPE	Small nuclear ribonucleoprotein polypeptide E
STIL	SCL/TAL1 interrupting locus
SLC9A9	Solute carrier family 9 (sodium/hydrogen exchanger), member 9
SLC12A3	Solute carrier family 12 (sodium/chloride transporters), member 3
NUDCD2	NudC domain containing 2
POLR2F	Polymerase (RNA) II (DNA directed) polypeptide F
2298442	toll-like receptor 4
CNOT6	CCR4-NOT transcription complex, subunit 6
SASH1	SAM and SH3 domain containing 1
C1orf66	Chromosome 1 open reading frame 66
177171	period (Drosophila) homolog 1

Gene name or Incyte clone ID	Description
PHOX2B	Paired-like homeobox 2b
KIAA0258	KIAA0258
MSX1	Msh homeobox 1
JARID1D	Jumonji, AT rich interactive domain 1D
2183580	myosin IXB
RANBP9	RAN binding protein 9
TNFRSF8	Tumor necrosis factor receptor superfamily, member 8
PLEKHF2	Pleckstrin homology domain containing, family F (with FYVE domain) member 2
MTSS1	Metastasis suppressor 1
ZNF335	Zinc finger protein 335
EXO1	Exonuclease 1
CCDC45	Coiled-coil domain containing 45
MT1M	Metallothionein 1M
CRAMP1L	Crm, cramped-like (Drosophila)
SERPINA5	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5
HUS1	HUS1 checkpoint homolog (S. pombe)
EXTL1	Exostosins (multiple)-like 1
STK39	Serine threonine kinase 39 (STE20/SPS1 homolog, yeast)
SYN2	Synapsin II
CD5L	CD5 molecule-like
1746529	minichromosome maintenance deficient (S. cerevisiae) 5 (cell division cycle 46)
ATRNL1	Attractin-like 1
CCDC100	Coiled-coil domain containing 100
SLC35E3	Solute carrier family 35, member E3
NOD1	Nucleotide-binding oligomerization domain containing 1
HNT	Neurotrimin
2723965	Incyte EST
1638384	Incyte EST
PHF16	PHD finger protein 16
3763496	synaptotagmin 5
TLK2	Tousled-like kinase 2
BRPF3	Bromodomain and PHD finger containing, 3
HMG2	High mobility group AT-hook 2
LOC133874	Hypothetical gene LOC133874
UHRF1	Ubiquitin-like, containing PHD and RING finger domains, 1
NIP7	Nuclear import 7 homolog (S. cerevisiae)
RAB3GAP1	RAB3 GTPase activating protein subunit 1 (catalytic)
3358708	kallikrein 2, prostatic
1602726	CDNA FLJ36555 fis, clone TRACH2008716

Gene name or Incyte clone ID	Description
NEURL	Neuralized homolog (Drosophila)
PAX8	Paired box gene 8
PSMB10	Proteasome (prosome, macropain) subunit, beta type, 10
CLEC2B	C-type lectin domain family 2, member B
HDGF	Hepatoma-derived growth factor (high-mobility group protein 1-like)
2800618	Incyte EST
ADH1A	Alcohol dehydrogenase 1A (class I), alpha polypeptide
MCM2	MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae)
2382190	ESTs, Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]
NSF	N-ethylmaleimide-sensitive factor
TGM4	Transglutaminase 4 (prostate)
ITPR2	Inositol 1,4,5-triphosphate receptor, type 2
KLHL2	Kelch-like 2, Mayven (Drosophila)
MRPS18B	Mitochondrial ribosomal protein S18B
1486087	collagen, type IX, alpha 2
GSG1	Germ cell associated 1
CLCN5	Chloride channel 5 (nephrolithiasis 2, X-linked, Dent disease)
CHPT1	Choline phosphotransferase 1
CASP1	Caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
ARPP-21	Cyclic AMP-regulated phosphoprotein, 21 kD
2191490	ESTs
SHCBP1	SHC SH2-domain binding protein 1
ZNF135	Zinc finger protein 135
HAL	Histidine ammonia-lyase
EHMT2	Euchromatic histone-lysine N-methyltransferase 2
2397717	CDNA FLJ32568 fis, clone SPLEN2000098
PTPRCAP	Protein tyrosine phosphatase, receptor type, C-associated protein
3969907	KIAA0514 gene product
ADORA2B	Adenosine A2b receptor
ZNF512	Zinc finger protein 512
BET1	BET1 homolog (S. cerevisiae)
CAMK2B	Calcium/calmodulin-dependent protein kinase (CaM kinase) II beta
BANF1	Barrier to autointegration factor 1
CAMLG	Calcium modulating ligand
THNSL1	Threonine synthase-like 1 (bacterial)
CMYA5	Cardiomyopathy associated 5
CCDC93	Coiled-coil domain containing 93
COBL	Cordon-bleu homolog (mouse)
C1orf91	Chromosome 1 open reading frame 91

Gene name or Incyte clone ID	Description
ACVR2B	Activin A receptor, type IIB
APIG1	Adaptor-related protein complex 1, gamma 1 subunit
NOS3	Nitric oxide synthase 3 (endothelial cell)
559786	Transcribed locus
DNTTIP2	Deoxynucleotidyltransferase, terminal, interacting protein 2
ZNF131	Zinc finger protein 131
PKM2	Pyruvate kinase, muscle
RAI16	Retinoic acid induced 16
PLD1	Phospholipase D1, phosphatidylcholine-specific
KMO	Kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)
EIF2B2	Eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa
PDLIM2	PDZ and LIM domain 2 (mystique)
LARP7	La ribonucleoprotein domain family, member 7
KRT6A	Keratin 6A
SNX13	Sorting nexin 13
RUFY2	RUN and FYVE domain containing 2
4000275	Transcribed locus
CAP2	CAP, adenylate cyclase-associated protein, 2 (yeast)
CNKSRI	Connector enhancer of kinase suppressor of Ras 1
GPR65	G protein-coupled receptor 65
C20orf177	Chromosome 20 open reading frame 177
LAPTM4B	Lysosomal associated protein transmembrane 4 beta
NME1	Non-metastatic cells 1, protein (NM23A) expressed in
FES	Feline sarcoma oncogene
SCGB3A2	Secretoglobulin, family 3A, member 2
KIAA0265	KIAA0265 protein
PIK3CD	Phosphoinositide-3-kinase, catalytic, delta polypeptide
542944	CDNA FLJ11381 fis, clone HEMBA1000501
NTRK2	Neurotrophic tyrosine kinase, receptor, type 2
SLIT1	Slit homolog 1 (Drosophila)
DAB2	Disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)
TSEN54	TRNA splicing endonuclease 54 homolog (S. cerevisiae)
PIN1	Protein (peptidylprolyl cis/trans isomerase) NIMA-interacting 1
SCTR	Secretin receptor
546616	ESTs
1367516	Transcribed locus
RAB11FIP1	RAB11 family interacting protein 1 (class I)
SLC38A4	Solute carrier family 38, member 4
ADSL	Adenylosuccinate lyase

Gene name or Incyte clone ID	Description
ZNF202	Zinc finger protein 202
IQSEC1	IQ motif and Sec7 domain 1
CSNK2A1P	Casein kinase 2, alpha 1 polypeptide pseudogene
PIM2	Pim-2 oncogene
MAPK3	Mitogen-activated protein kinase 3
DTL	Denticleless homolog (Drosophila)
DTNBP1	Dystrobrevin binding protein 1
SLC17A5	Solute carrier family 17 (anion/sugar transporter), member 5
PSMD1	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 1
KIAA0247	KIAA0247
ERBB3	V-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)
LRRC51	Leucine rich repeat containing 51
RASSF2	Ras association (RalGDS/AF-6) domain family 2
DNASE1L1	Deoxyribonuclease I-like 1
FECH	Ferrochelatase (protoporphyrin)
NTRK3	Neurotrophic tyrosine kinase, receptor, type 3
2625593	retinoid X receptor, beta
LRPAP1	Low density lipoprotein receptor-related protein associated protein 1
LOC375295	Hypothetical gene supported by BC013438
ADI1	Acireductone dioxygenase 1
1324209	Transcribed locus, moderately similar to XP_001142857.1 hypothetical protein [Pan troglodytes]
METTL1	Methyltransferase like 1
LIFR	Leukemia inhibitory factor receptor alpha
NUTF2	Nuclear transport factor 2
PISD	Phosphatidylserine decarboxylase
KHDRBS3	KH domain containing, RNA binding, signal transduction associated 3
INTS10	Integrator complex subunit 10
HIP1	Huntingtin interacting protein 1
HPCAL1	Hippocalcin-like 1
PIK4CB	Phosphatidylinositol 4-kinase, catalytic, beta polypeptide
TM2D1	TM2 domain containing 1
HSD17B10	Hydroxysteroid (17-beta) dehydrogenase 10
MICAL2	Microtubule associated monooxygenase, calponin and LIM domain containing 2
PSMA5	Proteasome (prosome, macropain) subunit, alpha type, 5
TRERF1	Transcriptional regulating factor 1
NID1	Nidogen 1
1425861	CDNA FLJ44755 fis, clone BRACE3031161
ARL6IP4	ADP-ribosylation-like factor 6 interacting protein 4

Gene name or Incyte clone ID	Description
TTC32	Tetratricopeptide repeat domain 32
TBC1D22B	TBC1 domain family, member 22B
SULF1	Sulfatase 1
ATP6V0E2	ATPase, H ⁺ transporting V0 subunit e2
2323525	ESTs
TYK2	Tyrosine kinase 2
663057	Incyte EST
1728607	small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)
CLPS	Colipase, pancreatic
BRAF	V-raf murine sarcoma viral oncogene homolog B1
POLI	Polymerase (DNA directed) iota
PTOV1	Prostate tumor overexpressed gene 1
NFIC	Nuclear factor I/C (CCAAT-binding transcription factor)
EPS8	Epidermal growth factor receptor pathway substrate 8
CASQ2	Calsequestrin 2 (cardiac muscle)
TLK1	Tousled-like kinase 1
BCS1L	BCS1-like (yeast)
PCYT1B	Phosphate cytidylyltransferase 1, choline, beta
SEC61B	Sec61 beta subunit
ERCC1	Excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)
HARS	Histidyl-tRNA synthetase
RFX5	Regulatory factor X, 5 (influences HLA class II expression)
MKRN1	Makorin, ring finger protein, 1
PNPLA4	Patatin-like phospholipase domain containing 4
SFRS4	Splicing factor, arginine/serine-rich 4
FPR1	Formyl peptide receptor 1
GLB1	Galactosidase, beta 1
BDH1	3-hydroxybutyrate dehydrogenase, type 1
2590673	flavin containing monooxygenase 3
COCH	Coagulation factor C homolog, cochlin (<i>Limulus polyphemus</i>)
1669780	Incyte EST
YLPM1	YLP motif containing 1
UGP2	UDP-glucose pyrophosphorylase 2
TNXB	Tenascin XB
ISLR	Immunoglobulin superfamily containing leucine-rich repeat
ALG11	Asparagine-linked glycosylation 11 homolog (<i>S. cerevisiae</i> , alpha-1,2-mannosyltransferase)
IMPA2	Inositol(myo)-1(or 4)-monophosphatase 2
TGIF2	TGFB-induced factor homeobox 2

Gene name or Incyte clone ID	Description
2555590	v-myb avian myeloblastosis viral oncogene homolog
C6orf137	Chromosome 6 open reading frame 137
RTCD1	RNA terminal phosphate cyclase domain 1
TTLL4	Tubulin tyrosine ligase-like family, member 4
GFRA2	GDNF family receptor alpha 2
TTLL12	Tubulin tyrosine ligase-like family, member 12
ALMS1	Alstrom syndrome 1
PAXIP1	PAX interacting (with transcription-activation domain) protein 1
HRASLS3	HRAS-like suppressor 3
SLC7A2	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 2
UGT2B7	UDP glucuronosyltransferase 2 family, polypeptide B7
CNTNAP1	Contactin associated protein 1
TYRP1	Tyrosinase-related protein 1
MYBPH	Myosin binding protein H
SEMA5A	Sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A
TSC22D3	TSC22 domain family, member 3
KIAA0409	KIAA0409
RAB7L1	RAB7, member RAS oncogene family-like 1
PPP1R1A	Protein phosphatase 1, regulatory (inhibitor) subunit 1A
CCND3	Cyclin D3
BCHE	Butyrylcholinesterase
GCK	Glucokinase (hexokinase 4, maturity onset diabetes of the young 2)
F8A1	Coagulation factor VIII-associated (intronic transcript) 1
CDC27	Cell division cycle 27 homolog (S. cerevisiae)
KBTBD11	Kelch repeat and BTB (POZ) domain containing 11
MTTP	Microsomal triglyceride transfer protein
ZNF24	Zinc finger protein 24
IRF5	Interferon regulatory factor 5
EXOSC7	Exosome component 7
MYL6B	Myosin, light chain 6B, alkali, smooth muscle and non-muscle
KDELRL2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2
SLURP1	Secreted LY6/PLAUR domain containing 1
CYP51A1	Cytochrome P450, family 51, subfamily A, polypeptide 1
NBN	Nibrin
DKFZP761N09121	Hypothetical protein DKFZp761N09121
MORN2	MORN repeat containing 2
USP9Y	Ubiquitin specific peptidase 9, Y-linked (fat facets-like, Drosophila)
SLC39A14	Solute carrier family 39 (zinc transporter), member 14

Gene name or Incyte clone ID	Description
ELAVL3	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)
CSNK1D	Casein kinase 1, delta
1830303	KIAA0237 gene product
2986240	collagen, type X, alpha 1 (Schmid metaphyseal chondrodysplasia)
FAP	Fibroblast activation protein, alpha
CD48	CD48 molecule
RNF144	Ring finger protein 144
1985566	Homo sapiens chromosome 19, cosmid F22329
CD72	CD72 molecule
OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa
MAP2	Microtubule-associated protein 2
MAPK12	Mitogen-activated protein kinase 12
MAP4	Microtubule-associated protein 4
SLC12A7	Solute carrier family 12 (potassium/chloride transporters), member 7
ANKRD28	Ankyrin repeat domain 28
B3GAT1	Beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)
EMG1	EMG1 nucleolar protein homolog (S. cerevisiae)
IFIT3	Interferon-induced protein with tetratricopeptide repeats 3
NUP43	Nucleoporin 43kDa
1807264	phosphodiesterase I/nucleotide pyrophosphatase 3
CGGBP1	CGG triplet repeat binding protein 1
PLXND1	Plexin D1
CALR	Calreticulin
NUP62	Nucleoporin 62kDa
NRXN1	Neurexin 1
RPA2	Replication protein A2, 32kDa
TNFRSF17	Tumor necrosis factor receptor superfamily, member 17
ASPA	Aspartoacylase (Canavan disease)
FAM20B	Family with sequence similarity 20, member B
FBXO45	F-box protein 45
1435811	Transcribed locus
POMGNT1	Protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase
POLA1	Polymerase (DNA directed), alpha 1
CARS	CysteinyI-tRNA synthetase
EDIL3	EGF-like repeats and discoidin I-like domains 3
1507151	Transcribed locus
MEOX1	Mesenchyme homeobox 1
TMEM51	Transmembrane protein 51
PPM1G	Protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform

Gene name or Incyte clone ID	Description
NEO1	Neogenin homolog 1 (chicken)
GRIN2C	Glutamate receptor, ionotropic, N-methyl D-aspartate 2C
1822809	MRNA; cDNA DKFZp762M127 (from clone DKFZp762M127)
2652730	Full-length cDNA clone CS0CAP004YK17 of Thymus of Homo sapiens (human)
LIF	Leukemia inhibitory factor (cholinergic differentiation factor)
LOC728655	Hypothetical protein LOC728655
ADRM1	Adhesion regulating molecule 1
TMEM119	Transmembrane protein 119
RBM3	RNA binding motif (RNP1, RRM) protein 3
TM9SF4	Transmembrane 9 superfamily protein member 4
IGF2	Insulin-like growth factor 2 (somatomedin A)
DHX40	DEAH (Asp-Glu-Ala-His) box polypeptide 40
TCF7	Transcription factor 7 (T-cell specific, HMG-box)
SNX21	Sorting nexin family member 21
RAD23B	RAD23 homolog B (S. cerevisiae)
RAE1	RAE1 RNA export 1 homolog (S. pombe)
MOBK1A	MOB1, Mps One Binder kinase activator-like 1A (yeast)
1677133	KIAA0601 protein
NEDD8	Neural precursor cell expressed, developmentally down-regulated 8
2099962	Transcribed locus
2133481	Incyte EST
FRZB	Frizzled-related protein
ABCA3	ATP-binding cassette, sub-family A (ABC1), member 3
1930865	Transcribed locus
OSGIN1	Oxidative stress induced growth inhibitor 1
LGALS3	Lectin, galactoside-binding, soluble, 3
828953	Transcribed locus
TXNDC10	Thioredoxin domain containing 10
MEIS3P1	Meis homeobox 3 pseudogene 1
EIF5	Eukaryotic translation initiation factor 5
EPAS1	Endothelial PAS domain protein 1
LGALS3BP	Lectin, galactoside-binding, soluble, 3 binding protein
TEKT2	Tektin 2 (testicular)
1227602	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
851764	CDNA FLJ13446 fis, clone PLACE1002968
PTCD3	Pentatricopeptide repeat domain 3
1653974	MRNA full length insert cDNA clone EUROIMAGE 826033
PUM2	Pumilio homolog 2 (Drosophila)

Gene name or Incyte clone ID	Description
ARIH2	Ariadne homolog 2 (Drosophila)
LAD1	Ladinin 1
KIAA0355	KIAA0355
MTX3	Metaxin 3
OXSM	3-oxoacyl-ACP synthase, mitochondrial
MAP6D1	MAP6 domain containing 1
SFRS11	Splicing factor, arginine/serine-rich 11
PSMB6	Proteasome (prosome, macropain) subunit, beta type, 6
2627888	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
NTF5	Neurotrophin 5 (neurotrophin 4/5)
1332963	ESTs
ZDHC8	Zinc finger, DHHC-type containing 8
ISCA1	Iron-sulfur cluster assembly 1 homolog (S. cerevisiae)
Gcom1	GRINL1A combined protein
1900378	KIAA0365 gene product
DPP8	Dipeptidyl-peptidase 8
2373457	Transcribed locus
2223757	Transcribed locus
2925432	Transcribed locus
PRMT5	Protein arginine methyltransferase 5
SNRPD3	Small nuclear ribonucleoprotein D3 polypeptide 18kDa
UCP2	Uncoupling protein 2 (mitochondrial, proton carrier)
GSK3A	Glycogen synthase kinase 3 alpha
C22orf27	Chromosome 22 open reading frame 27
3352319	Incyte EST
HIF3A	Hypoxia inducible factor 3, alpha subunit
2916295	vesicle-associated membrane protein 2 (synaptobrevin 2)
870631	CDNA clone IMAGE:4814828
EPHA4	EPH receptor A4
MVD	Mevalonate (diphospho) decarboxylase
QPCT	Glutaminyl-peptide cyclotransferase (glutaminyl cyclase)
2754640	Transcribed locus
1367862	Incyte EST
HSF4	Heat shock transcription factor 4
hCG_1815491	HCG1815491
MYL2	Myosin, light chain 2, regulatory, cardiac, slow
ITIH2	Inter-alpha (globulin) inhibitor H2
CD24	CD24 molecule

Gene name or Incyte clone ID	Description
ABT1	Activator of basal transcription 1
ZMIZ2	Zinc finger, MIZ-type containing 2
2930621	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide
PYCR2	Pyrroline-5-carboxylate reductase family, member 2
TRA@	T cell receptor alpha locus
ITGBL1	Integrin, beta-like 1 (with EGF-like repeat domains)
SLCO3A1	Solute carrier organic anion transporter family, member 3A1
DKFZP686E2158	Hypothetical protein LOC643155
P2RX5	Purinergic receptor P2X, ligand-gated ion channel, 5
PPP1R12B	Protein phosphatase 1, regulatory (inhibitor) subunit 12B
RSPO4	R-spondin family, member 4
NTS	Neurotensin
KIAA0495	KIAA0495
MARCO	Macrophage receptor with collagenous structure
LDHA	Lactate dehydrogenase A
PRKAR2A	Protein kinase, cAMP-dependent, regulatory, type II, alpha
PCCB	Propionyl Coenzyme A carboxylase, beta polypeptide
PSCDBP	Pleckstrin homology, Sec7 and coiled-coil domains, binding protein
C1orf212	Chromosome 1 open reading frame 212
MEOX2	Mesenchyme homeobox 2
FUBP3	Far upstream element (FUSE) binding protein 3
NDRG1	N-myc downstream regulated gene 1
PCOLCE	Procollagen C-endopeptidase enhancer
PCDH11Y	Protocadherin 11 Y-linked
FCHO1	FCH domain only 1
SIRT4	Sirtuin (silent mating type information regulation 2 homolog) 4 (S. cerevisiae)
NOLC1	Nucleolar and coiled-body phosphoprotein 1
SUMO3	SMT3 suppressor of mif two 3 homolog 3 (S. cerevisiae)
CDH11	Cadherin 11, type 2, OB-cadherin (osteoblast)
1938947	CDNA clone IMAGE:3030163
TRMU	TRNA 5-methylaminomethyl-2-thiouridylate methyltransferase
NECAP2	NECAP endocytosis associated 2
PCF11	PCF11, cleavage and polyadenylation factor subunit, homolog (S. cerevisiae)
HSPA5	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
ATP8B1	ATPase, Class I, type 8B, member 1
DCN	Decorin
SAFB2	Scaffold attachment factor B2
GLIPR1	GLI pathogenesis-related 1 (glioma)

Gene name or Incyte clone ID	Description
RUNX3	Runt-related transcription factor 3
ANKRD1	Ankyrin repeat domain 1 (cardiac muscle)
ABLIM3	Actin binding LIM protein family, member 3
SLC9A1	Solute carrier family 9 (sodium/hydrogen exchanger), member 1 (antiporter, Na ⁺ /H ⁺ , amiloride sensitive)
TMEM16A	Transmembrane protein 16A
SLC41A1	Solute carrier family 41, member 1
GREB1	GREB1 protein
CDC14A	CDC14 cell division cycle 14 homolog A (<i>S. cerevisiae</i>)
ITPR1	Inositol 1,4,5-triphosphate receptor, type 1
1967543	Transcribed locus
C16orf58	Chromosome 16 open reading frame 58
RFXANK	Regulatory factor X-associated ankyrin-containing protein
VAMP5	Vesicle-associated membrane protein 5 (myobrevin)
TUSC3	Tumor suppressor candidate 3
SLC39A4	Solute carrier family 39 (zinc transporter), member 4
GOLGA8A	Golgi autoantigen, golgin subfamily a, 8A
TARS	Threonyl-tRNA synthetase
BIRC2	Baculoviral IAP repeat-containing 2
TCF21	Transcription factor 21
RIPK1	Receptor (TNFRSF)-interacting serine-threonine kinase 1
KLHL28	Kelch-like 28 (<i>Drosophila</i>)
EPHB3	EPH receptor B3
AKAP9	A kinase (PRKA) anchor protein (yotiao) 9
955697	Transcribed locus, moderately similar to XP_001070964.1 similar to FRG1 protein (FSDH region gene 1 protein) [<i>Rattus norvegicus</i>]
HPCAL4	Hippocalcin like 4
JAKMIP1	Janus kinase and microtubule interacting protein 1
RNPS1	RNA binding protein S1, serine-rich domain
BET1L	Blocked early in transport 1 homolog (<i>S. cerevisiae</i>)-like
THEM2	Thioesterase superfamily member 2
ARL3	ADP-ribosylation factor-like 3
HLA-DRB1	Major histocompatibility complex, class II, DR beta 1
SYT17	Synaptotagmin XVII
RAMP2	Receptor (G protein-coupled) activity modifying protein 2
ACTA2	Actin, alpha 2, smooth muscle, aorta
SR140	U2-associated SR140 protein
C20orf3	Chromosome 20 open reading frame 3
SLC6A7	Solute carrier family 6 (neurotransmitter transporter, L-proline), member 7
TAS2R14	Taste receptor, type 2, member 14

Gene name or Incyte clone ID	Description
THOC4	THO complex 4
BCL7B	B-cell CLL/lymphoma 7B
ANXA1	Annexin A1
ITM2A	Integral membrane protein 2A
HSPA14	Heat shock 70kDa protein 14
DAD1	Defender against cell death 1
POU2F1	POU domain, class 2, transcription factor 1
IL7R	Interleukin 7 receptor
567938	integrin, alpha X (antigen CD11C (p150), alpha polypeptide)
PNN	Pinin, desmosome associated protein
SLC17A3	Solute carrier family 17 (sodium phosphate), member 3
HBD	Hemoglobin, delta
627843	Transcribed locus
C16orf53	Chromosome 16 open reading frame 53
IFIT5	Interferon-induced protein with tetratricopeptide repeats 5
1772770	MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A)
ME1	Malic enzyme 1, NADP(+)-dependent, cytosolic
ALDH6A1	Aldehyde dehydrogenase 6 family, member A1
DNA2L	DNA2 DNA replication helicase 2-like (yeast)
COMMD1	Copper metabolism (Murr1) domain containing 1
LOC285986	Hypothetical protein LOC285986
3252932	CDNA clone IMAGE:4425104
RGAG4	Retrotransposon gag domain containing 4
TESK2	Testis-specific kinase 2
1781378	Transcribed locus
TMED10	Transmembrane emp24-like trafficking protein 10 (yeast)
DBC1	Deleted in bladder cancer 1
CCDC57	Coiled-coil domain containing 57
PPP1CA	Protein phosphatase 1, catalytic subunit, alpha isoform
TRPC4AP	Transient receptor potential cation channel, subfamily C, member 4 associated protein
CCRK	Cell cycle related kinase
PCDH7	Protocadherin 7
3187892	Transcribed locus
2258157	Transcribed locus
Septin 8	Septin 8
2926307	Incyte EST
Septin 4	Septin 4
CDK9	Cyclin-dependent kinase 9 (CDC2-related kinase)
ASGR1	Asialoglycoprotein receptor 1

Gene name or Incyte clone ID	Description
PDHB	Pyruvate dehydrogenase (lipoamide) beta
GRIA3	Glutamate receptor, ionotropic, AMPA 3
1289539	MRNA; cDNA DKFZp686G08203 (from clone DKFZp686G08203)
RAD52	RAD52 homolog (S. cerevisiae)
27177	Incyte EST
LSP1	Lymphocyte-specific protein 1
2239834	Transcribed locus
2806295	Transcribed locus
DUSP8	Dual specificity phosphatase 8
CKMT2	Creatine kinase, mitochondrial 2 (sarcomeric)
KIF1B	Kinesin family member 1B
GCAT	Glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)
CDYL	Chromodomain protein, Y-like
ORC6L	Origin recognition complex, subunit 6 like (yeast)
WDR26	WD repeat domain 26
FEM1C	Fem-1 homolog c (C. elegans)
2256174	Transcribed locus
BMP8B	Bone morphogenetic protein 8b (osteogenic protein 2)
EPM2AIP1	EPM2A (laforin) interacting protein 1
CHERP	Calcium homeostasis endoplasmic reticulum protein
CHAC2	ChaC, cation transport regulator homolog 2 (E. coli)
CAMK2N1	Calcium/calmodulin-dependent protein kinase II inhibitor 1
RNF13	Ring finger protein 13
BSCL2	Bernardinelli-Seip congenital lipodystrophy 2 (seipin)
METAP2	Methionyl aminopeptidase 2
CACNA2D4	Calcium channel, voltage-dependent, alpha 2/delta subunit 4
VPS29	Vacuolar protein sorting 29 homolog (S. cerevisiae)
631136	Incyte EST
MMP2	Matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)
SIAHBP1	Fuse-binding protein-interacting repressor
REG1A	Regenerating islet-derived 1 alpha (pancreatic stone protein, pancreatic thread protein)
CRISPLD2	Cysteine-rich secretory protein LCCL domain containing 2
ZNF300	Zinc finger protein 300
459890	Transcribed locus
STIP1	Stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)
PSMD5	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 5
SNAPC5	Small nuclear RNA activating complex, polypeptide 5, 19kDa
SPG20	Spastic paraplegia 20, spartin (Troyer syndrome)
SMPD2	Sphingomyelin phosphodiesterase 2, neutral membrane (neutral sphingomyelinase)

Gene name or Incyte clone ID	Description
GRIK2	Glutamate receptor, ionotropic, kainate 2
PHF7	PHD finger protein 7
EIF4G3	Eukaryotic translation initiation factor 4 gamma, 3
GFAP	Glial fibrillary acidic protein
IQGAP2	IQ motif containing GTPase activating protein 2
MAML1	Mastermind-like 1 (Drosophila)
G6PD	Glucose-6-phosphate dehydrogenase
CCNE1	Cyclin E1
BMPR1B	Bone morphogenetic protein receptor, type IB
EPHX1	Epoxide hydrolase 1, microsomal (xenobiotic)
HNRPC	Heterogeneous nuclear ribonucleoprotein C (C1/C2)
E2F6	E2F transcription factor 6
SAA1	Serum amyloid A1
CALM2	Calmodulin 2 (phosphorylase kinase, delta)
AZIN1	Antizyme inhibitor 1
ATP5F1	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit B1
EPRS	Glutamyl-prolyl-tRNA synthetase
APBA2BP	Amyloid beta (A4) precursor protein-binding, family A, member 2 binding protein
DNAJA2	DnaJ (Hsp40) homolog, subfamily A, member 2
COMMD10	COMM domain containing 10
MGC42105	Hypothetical protein MGC42105
TSTA3	Tissue specific transplantation antigen P35B
TBL1X	Transducin (beta)-like 1X-linked
L1CAM	L1 cell adhesion molecule
AIM1	Absent in melanoma 1
LSM8	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)
VIP	Vasoactive intestinal peptide
POLR3G	Polymerase (RNA) III (DNA directed) polypeptide G (32kD)
HAX1	HCLS1 associated protein X-1
COPS3	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)
2845548	Transcribed locus, weakly similar to XP_001064630.1 similar to apobec-1 complementation factor [Rattus norvegicus]
STARD4	START domain containing 4, sterol regulated
TRIAP1	TP53 regulated inhibitor of apoptosis 1
TARP	TCR gamma alternate reading frame protein
CUGBP1	CUG triplet repeat, RNA binding protein 1
MFAP5	Microfibrillar associated protein 5
194162	Incyte EST
SUPT5H	Suppressor of Ty 5 homolog (S. cerevisiae)

Gene name or Incyte clone ID	Description
ZPBP	Zona pellucida binding protein
PHEX	Phosphate regulating endopeptidase homolog, X-linked (hypophosphatemia, vitamin D resistant rickets)
NFATC3	Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3
CDC7	Cell division cycle 7 homolog (<i>S. cerevisiae</i>)
56919	thymopoietin
767348	Incyte EST
AGL	Amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)
SF3B3	Splicing factor 3b, subunit 3, 130kDa
POLM	Polymerase (DNA directed), mu
CYBB	Cytochrome b-245, beta polypeptide (chronic granulomatous disease)
2259550	Transcribed locus
RUVBL1	RuvB-like 1 (<i>E. coli</i>)
EXOC5	Exocyst complex component 5
PASK	PAS domain containing serine/threonine kinase
TMEM55A	Transmembrane protein 55A
MS4A4A	Membrane-spanning 4-domains, subfamily A, member 4
899118	CDNA clone IMAGE:6025865
CNN1	Calponin 1, basic, smooth muscle
POFUT1	Protein O-fucosyltransferase 1
MFNG	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase
UNC84B	Unc-84 homolog B (<i>C. elegans</i>)
SPATS2	Spermatogenesis associated, serine-rich 2
RABIF	RAB interacting factor
PAK2	P21 (CDKN1A)-activated kinase 2
EIF3S9	Eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa
CDC42SE2	CDC42 small effector 2
FOXN2	Forkhead box N2
ASCC1	Activating signal cointegrator 1 complex subunit 1
COX15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)
TBC1D16	TBC1 domain family, member 16
SLC34A1	Solute carrier family 34 (sodium phosphate), member 1
PZP	Pregnancy-zone protein
GFI1	Growth factor independent 1
PTPN14	Protein tyrosine phosphatase, non-receptor type 14
IL13RA2	Interleukin 13 receptor, alpha 2
SLC35B3	Solute carrier family 35, member B3
166337	arginase, liver
CPA2	Carboxypeptidase A2 (pancreatic)

Gene name or Incyte clone ID	Description
SLC18A2	Solute carrier family 18 (vesicular monoamine), member 2
NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa
PPIL5	Peptidylprolyl isomerase (cyclophilin)-like 5
FKBP11	FK506 binding protein 11, 19 kDa
3815547	ESTs
3880684	ESTs
ADFP	Adipose differentiation-related protein
CRIP1	Cysteine-rich protein 1 (intestinal)
MST1R	Macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
SNRPD2	Small nuclear ribonucleoprotein D2 polypeptide 16.5kDa
SPAG9	Sperm associated antigen 9
RIT2	Ras-like without CAAX 2
GJA1	Gap junction protein, alpha 1, 43kDa
MBP	Myelin basic protein
POLR3C	Polymerase (RNA) III (DNA directed) polypeptide C (62kD)
CDC16	Cell division cycle 16 homolog (S. cerevisiae)
FMOD	Fibromodulin
HOXB6	Homeobox B6
MRPL44	Mitochondrial ribosomal protein L44
LYPLA2	Lysophospholipase II
PTPDC1	Protein tyrosine phosphatase domain containing 1
2055538	spectrin, beta, non-erythrocytic 1
ZNHIT1	Zinc finger, HIT type 1
NAPA	N-ethylmaleimide-sensitive factor attachment protein, alpha
ACAA1	Acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)
LRRC17	Leucine rich repeat containing 17
EIF2B2	Eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa
DBNDD2	Dysbindin (dystrobrevin binding protein 1) domain containing 2
SPHK1	Sphingosine kinase 1
C7orf28A	Chromosome 7 open reading frame 28A
TFDP1	Transcription factor Dp-1
MALL	Mal, T-cell differentiation protein-like
CD14	CD14 molecule
GNG11	Guanine nucleotide binding protein (G protein), gamma 11
MAOA	Monoamine oxidase A
SMAD2	SMAD family member 2
RDBP	RD RNA binding protein
UBE2S	Ubiquitin-conjugating enzyme E2S
CACYBP	Calcyclin binding protein

Gene name or Incyte clone ID	Description
RNASE2	Ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)
IK	IK cytokine, down-regulator of HLA II
PGM1	Phosphoglucomutase 1
IL10RA	Interleukin 10 receptor, alpha
GALC	Galactosylceramidase
TG	Thyroglobulin
PPAT	Phosphoribosyl pyrophosphate amidotransferase
AXL	AXL receptor tyrosine kinase
HES1	Hairy and enhancer of split 1, (<i>Drosophila</i>)
2874615	Transcribed locus
2881469	Transcribed locus

Biography

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Figure 1.
Gene response modules (GRMs) with at least 100 genes in the clusters (LSMs) (see online version for colours)

Figure 2.
Gene response modules (GRMs) that contain between 10–99 genes in each cluster (MSMs)
(see online version for colours)

Figure 3. Gene response modules (GRMs) that contain between 2–9 genes in each cluster (SSMs) (see online version for colours)

Figure 4.
Single gene response modules (SGMs) (see online version for colours)

Table 1

Genes in hub modules

Module	Gene	Incyte Clone ID	Description
39	PRCC	IncytePD:461197	Papillary renal cell carcinoma (translocation-associated)
39	KPNA2	IncytePD:1574194	Karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
39	AMD1	IncytePD:1653934	Adenosylmethionine decarboxylase 1
39	TMCO1	IncytePD:1926540	Transmembrane and coiled-coil domains 1
39	NDUFS5	IncytePD:2503003	NADH dehydrogenase Fe-S protein 5, 15kDa (NADH-coenzyme Q)
39	ARMCX5	IncytePD:2353864	Armadillo repeat containing, X-linked 5
39	GLRX	IncytePD:1238577	Glutaredoxin (thioltransferase)
39	DGUOK	IncytePD:815619	Deoxyguanosine kinase
39		IncytePD:1686916	RNA binding motif, single stranded interacting protein 1
49	NLE1	IncytePD:3735019	Notchless homolog 1 (Drosophila)
57	DNAJC8	IncytePD:1627543	DnaJ (Hsp40) homolog, subfamily C, member 8
22	TNFAIP3	IncytePD:1878791	Tumour necrosis factor, alpha-induced protein 3
22	CCNG2	IncytePD:1922164	Cyclin G2
58	PBEF1	IncytePD:1641590	Pre-B-cell colony enhancing factor 1
58	CTH	IncytePD:666190	Cystathionase (cystathionine gamma-lyase)
58	GRSF1	IncytePD:1931925	G-rich RNA sequence binding factor 1
58		IncytePD:2115411	Transcribed locus
9	ELF1	IncytePD:1312824	E74-like factor 1 (ets domain transcription factor)

Table 2

Simulation study 1

Proportion of DRGs	Proposed method True positive	Proposed method False positive	ANOVA True positive	ANOVA False positive
0.05	0.756	0.049	0.030	0.050
0.2	0.745	0.046	0.033	0.049
0.5	0.732	0.038	0.032	0.049