

Correction notice

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Detecting early-warning signals for sudden deterioration of complex diseases by dynamical network biomarkers

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In the version of this Article initially published online, the table of contents was missing from the Supplementary Information file. Furthermore, two typographical errors were identified. In Theorem 1 on page 14, $SD(z_i)$ should be $SD(z_j)$ and in section A-2, $[0,1)$ should be $(0,1)$. These errors have been corrected.

Supplementary Information: Detecting early-warning signals for sudden deterioration of complex diseases by dynamical network biomarkers

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The Supplementary Information is organized as follows.

- In Section A, we derive the theoretical results based on generic bifurcations of a general discrete-time dynamical system, which is used to identify the model-independent dynamical network biomarker (DNB) and further construct the early-warning signal described in the main text. It should be noted that our method is a model-free approach, and the detection of early-warning signals is completely based on high-throughput biological data.

- In Section B, we adopt a five-gene system represented by stochastic dynamical equations to illustrate our method and numerically validate its effectiveness for identifying the pre-disease state.

- In Section C, we provide the details of the computational algorithm used for efficiently detecting a DNB of the pre-disease state based on high-throughput data.

- In Section D, three sets of real transcriptome data of diseases are used to test our method. The prediction results for these datasets are presented as examples in the main text. In particular, the detailed calculation process for acute lung injury is presented as a concrete example.

- In Section E, in order to verify the biological and statistical significance of the identified DNBs, we conduct bootstrap analysis respectively for the diseases of acute lung injury and HBV induced liver cancer.

- In Section F, to further validate the theoretical results and understand the dysfunctional implications of the DNBs, the functional analysis of each DNB is conducted although it is not generally required for the purpose of detecting the early-warning signals of the pre-disease state.

- In Section G, we present fold-change analysis of the disease data.

A Derivation of theoretical results for a dynamical network biomarker

The dynamics for the progression of complex diseases is very complicated either before or after sudden deterioration (see Fig.S1 (a)), and therefore the state equations are generally constructed in a high-dimensional space with a large number of variables and parameters (e.g., over thousands) (1–4). However, provided that the system driven by some known or unknown parameters approaches to the critical point (which is a very special phase during the dynamical progression), theoretically the system can be expressed in a very simple form, i.e., generally it can be expressed by one- or two-variable dynamical equations in an abstract phase space around a codimension-one bifurcation point (5, 6). This is generally guaranteed by the bifurcation theory and center manifold theory (5–8). Thus because of this special feature, during this special phase, unlike during other periods (i.e., a normal state before the transition, or a disease state after the transition), we can detect its signal, which is the main concept of this work (see Fig.S1 (a)).

In other words, no matter how complicated the system is and how many variables it has, provided that some factors drive the system to the critical state, we can usually express the system in this simple form using only one or two variables. However, unfortunately, these variables are generally unobservable because of the abstract phase space. If some factors first pass the critical value, a group of state variables would be driven to first move into the disease state. This group of variables corresponds to an observable subnetwork, i.e., a DNB, if it returns to the original state space. In this work, we construct this observable subnetwork (DNB) in the original state space through the unobservable variables in the abstract phase space, and we prove the conditions to identify the signal only by observing the DNB for the pre-disease state. It should be note that generally, we cannot express an entire complicated system in such a simple

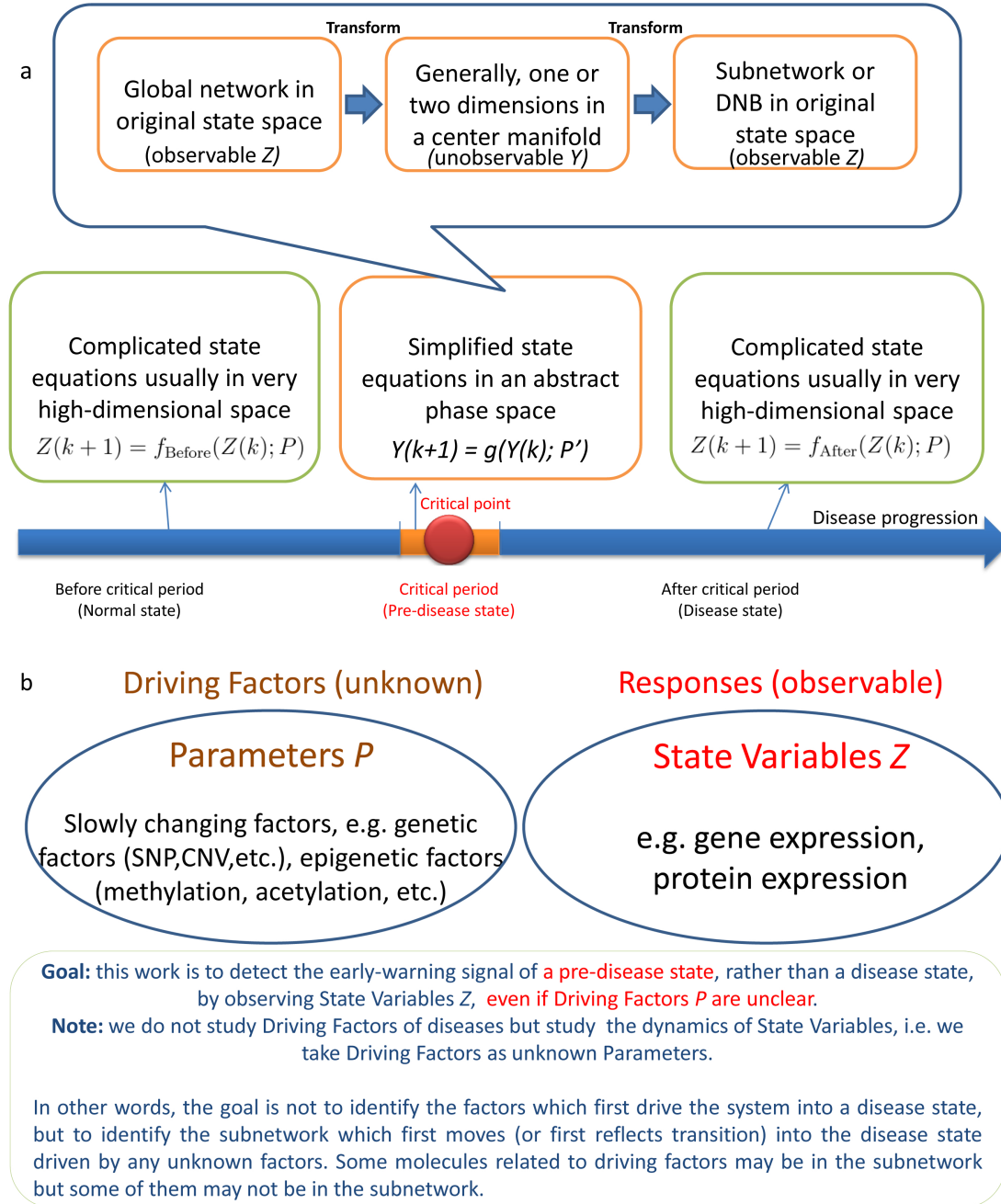


Figure S1: | **State spaces and state variables.** (a) State spaces in normal state, pre-disease state, and disease state. (b) State variables and parameters.

manner for either a normal state or a disease state, which has been also studied extensively by many researchers thus far.

In particular, in our model, the concentrations of proteins or mRNAs (e.g., protein expressions or gene expressions) are set as variables Z representing the dynamical state of the system, whereas the factors that drive the system from a normal state to a disease state are set as parameters P , representing slowly changing factors, e.g., genetic factors (SNP, CNV, etc.) and epigenetic factors (methylation, acetylation, etc.) (see Fig.S1 (b)).

A.1 A generic model in abstract phase space

Consider the following discrete-time dynamical system representing the dynamical evolution of an organism:

$$Z(k+1) = f(Z(k); P), \quad (\text{A1.1})$$

where $Z(k) = (z_1(k), \dots, z_n(k))$ is an n -dimensional state vector or variables at time instant k representing gene or protein expressions, and $P = (p_1, \dots, p_s)$ is an s -dimensional parameter vector or driving factors representing slowly changing factors, e.g., genetic factors (SNP, CNV, etc.) and epigenetic factors (methylation, acetylation, etc.) (see Fig.S1 (b)). $f : \mathbf{R}^n \times \mathbf{R}^s \rightarrow \mathbf{R}^n$ are generally nonlinear functions. Furthermore, assume that the following conditions hold for (A1.1).

1. $\bar{Z}$ is a fixed point of system (A1.1) such that $\bar{Z} = f(\bar{Z}; P)$.
2. There is a value P_c such that one or a complex-conjugate pair of the eigenvalues of the Jacobian matrix $\left. \frac{\partial f(Z; P_c)}{\partial Z} \right|_{Z=\bar{Z}}$ equal 1 in modulus.
3. When $P \neq P_c$, the eigenvalues of (A1.1) are generally not 1 in modulus.

The above three conditions along with other transversal conditions (I) imply that the system undergoes a transition at $\bar{Z}$ or a codimension-one bifurcation when P reaches the threshold

P_c . The bifurcation is generic from a mathematical viewpoint, *i.e.*, almost all bifurcations for a general system satisfy these conditions. It is noteworthy that most systems described by differential equations can be generally discretized and transformed into (A1.1), e.g., by the Euler scheme. Hence here and in what follows, for theoretical analysis we focus on the difference equations (A1.1).

For system (A1.1) near $\bar{Z}$, before P reaches P_c , suppose that the system is at a stable fixed point $\bar{Z}$ and therefore all the eigenvalues are within $[0, 1)$ in modulus. The parameter value P_c at which the state transition of the system occurs is called a bifurcation parameter value or a critical transition value.

Without loss of generality, we move the fixed point $\bar{Z}$ to the origin by setting variables $X = Z - \bar{Z}$. Thus in the vicinity of $X = 0$, system (A1.1) is rewritten as

$$X(k+1) = f(X(k) + \bar{Z}; P) - \bar{Z}, \quad (\text{A1.2})$$

where $X(k) = (x_1(k), \dots, x_n(k))$. Denote

$$J = \left. \frac{\partial f(Z(k); P)}{\partial Z} \right|_{Z=\bar{Z}}$$

as the Jacobian matrix of f , and $N(X(k); P)$ as the nonlinear part containing higher-order terms. It should be noted that $f(\bar{Z}; P) = \bar{Z}$. Thus, around the fixed point, we now have

$$X(k+1) = JX(k) + N(X(k); P), \quad (\text{A1.3})$$

where $J = J(P)$ is of full rank and is a function of parameter P . In the following, we omit P in J for simplicity. Note that when P tends to P_c , at least one of the eigenvalues equals 1 in modulus.

Because the Jacobian matrix J is of full rank, there is a full-rank matrix S satisfying $J = S\Lambda S^{-1}$, where Λ is in a normalized form that is discussed below. By defining variables $Y(k) =$

$S^{-1}X(k)$, a linearized equation of (A1.3) with the random perturbations can be rewritten as

$$Y(k+1) = \Lambda Y(k) + \zeta(k), \quad (\text{A1.4})$$

where $Y(k) = (y_1(k), \dots, y_n(k))$, and $\Lambda = \Lambda(P)$ is also a function of P . $\zeta(k) = (\zeta_1(k), \dots, \zeta_n(k))$ are Gaussian noises with zero means and covariances $\kappa_{ij} = \text{Cov}(\zeta_i, \zeta_j)$. It should be noted that among the eigenvalues of Λ , at least one eigenvalue equals 1 in modulus at $P = P_c$. Each of the eigenvalues characterizes the system's rate of change around the fixed point and the largest eigenvalue in modulus is called the dominant eigenvalue. Furthermore, when $P = P_c$, if the dominant eigenvalue is equal to 1, the bifurcation is a saddle-node (often called a fold bifurcation in maps), transcritical or pitchfork bifurcation. If the dominant eigenvalue is equal to -1 , it is a period-doubling (or flip) bifurcation, and if there is a pair of pure imaginary complex conjugate eigenvalues with modulus 1, it is a Neimark-Sacker bifurcation. All these bifurcations are codimension-one bifurcations and are generic for (A1.1).

A.2 Normalization analysis

As mentioned above, the Jacobian matrix Λ of system (A1.4) is in a normalized form. However, given a different nonlinear function f in (A1.1), the normalized form is different by diagonalization theory (17). We fix the value of parameter P before reaching P_c . Then either J or Λ is a constant matrix of full rank. Let us consider typical three cases as follows.

1° For matrix J , if the sum of the dimensions of its eigenspaces with real eigenvalues is equal to n , then there is a nonsingular matrix S satisfying $\Lambda = S^{-1}JS = \text{diag}(\lambda_1, \dots, \lambda_n)$, where all $|\lambda_i|$ ($i = 1, \dots, n$) are within $[0, 1)$ because of the stability of the given stable fixed point. In this case, the eigenvalues may be distinct or some of them may be identical. Without loss of generality, we may regard the first element $|\lambda_1|$ as being the nearest to 1, *i.e.*, the dominant eigenvalue.

2° If matrix J does not have linearly independent n eigenvectors, there is a nonsingular matrix S making

$$\Lambda = S^{-1}JS = \begin{bmatrix} G_1 & 0 & \dots & 0 \\ 0 & \ddots & \ddots & \vdots \\ \vdots & \ddots & \ddots & 0 \\ 0 & \dots & 0 & G_q \end{bmatrix}, \quad (\text{A1.5})$$

where

$$G_j = \begin{bmatrix} \lambda_j & 1 & 0 & \dots & 0 \\ 0 & \ddots & \ddots & \ddots & \vdots \\ \vdots & \ddots & \ddots & \ddots & 0 \\ \vdots & & \ddots & \ddots & 1 \\ 0 & \dots & \dots & 0 & \lambda_j \end{bmatrix},$$

where λ_j are real and $|\lambda_j| \in [0, 1)$. We can move the block with the largest eigenvalue in modulus, which is also the nearest to 1, to the first position of Jordan normal form Λ .

3° The complex conjugate eigenvalues are the third case. There is a nonsingular matrix S making $\Lambda = S^{-1}JS$ where the partitioned matrix Λ is of the form (A1.5), but

$$G_j = \begin{bmatrix} C_j & I & 0 & \dots & 0 \\ 0 & \ddots & \ddots & \ddots & \vdots \\ \vdots & \ddots & \ddots & \ddots & 0 \\ \vdots & & \ddots & \ddots & I \\ 0 & \dots & \dots & 0 & C_j \end{bmatrix}, \quad C_j = \begin{bmatrix} a_j & -b_j \\ b_j & a_j \end{bmatrix}$$

where I is the two-dimensional identity matrix, and a_j and b_j are real numbers. Each two-dimensional block matrix C_j has a pair of complex conjugated eigenvalues whose moduli are less than 1. We move the block, in which the eigenvalues have the largest modulus, to the first position of Λ .

Therefore, irrespective of which case occurs, the first element of Λ is the dominant eigenvalue, the one nearest to 1 in modulus, whose change actually leads to the state shift from the fixed point. Furthermore, all the eigenvalues (or their moduli) of matrix Λ are within $[0, 1)$. In addition, there is at least one dominant eigenvalue, approaching 1 in modulus when parameter $P \rightarrow P_c$. Now we discuss the statistical features of the three normalized forms.

In the above case 1, because Λ is a fully diagonalized matrix, we have

$$\begin{aligned}
\text{Var}(y_i) &= \text{Var}(y_i(k+1)) \\
&= \text{E}(y_i^2(k+1)) \\
&= \text{E}((\lambda_i y_i(k) + \zeta_i(k))^2) \\
&= \lambda_i^2 \text{E}(y_i^2(k)) + \kappa_{ii} \\
&= \lambda_i^2 \text{Var}(y_i) + \kappa_{ii},
\end{aligned}$$

where $\text{E}(y_i(k)) = 0$ and $\kappa_{ii} > 0$.

Therefore, we have

$$\text{Var}(y_i) = \frac{\kappa_{ii}}{1 - \lambda_i^2}.$$

Hence when $\lambda_1 \rightarrow 1$, $\text{Var}(y_1) \rightarrow +\infty$. The same result is obtained in (10), for a linearized equation with a single variable. Note that $0 \leq |\lambda_i| < 1$ before the critical transition.

Other λ_i ($i = 2, 3, \dots, n$) satisfy $0 \leq |\lambda_i| < 1$, and $\text{Var}(y_i)$ approaches some positive bounded value.

In case 2, suppose G_1 possesses the largest eigenvalue λ_1 . Based on the G_1 block, we obtain

$$\begin{cases}
y_1(k+1) = \lambda_1 y_1(k) + y_2 + \zeta_1(k), \\
y_2(k+1) = \lambda_1 y_2(k) + y_3 + \zeta_2(k), \\
\vdots \\
y_{j-1}(k+1) = \lambda_1 y_{j-1}(k) + y_j + \zeta_{j-1}(k), \\
y_j(k+1) = \lambda_1 y_j(k) + \zeta_j(k).
\end{cases}$$

Without loss of generality, we take $j = 2$ as an example. By analyzing the last equation,

$$\begin{aligned}
\text{Var}(y_2) &= \text{Var}(y_2(k+1)) \\
&= \text{E}((\lambda_1 y_2(k) + \zeta_2(k))^2) \\
&= \lambda_1^2 \text{Var}(y_2) + \kappa_{22}.
\end{aligned}$$

That is,

$$\text{Var}(y_2) = \frac{\kappa_{22}}{1 - \lambda_1^2}.$$

Hence when $\lambda_1 \rightarrow 1$, $\text{Var}(y_2) \rightarrow +\infty$. For y_1 ,

$$\begin{aligned} \text{Var}(y_1) &= \text{Var}(y_1(k+1)) \\ &= \text{E}((\lambda_1 y_1(k) + y_2(k) + \zeta_1(k))^2) \\ &= \lambda_1^2 \text{E}(y_1^2(k)) + \text{E}(y_2^2(k)) \\ &\quad + 2\lambda_1 \text{E}(y_1(k)y_2(k)) + \kappa_{11} \\ &= \lambda_1^2 \text{Var}(y_1) + \text{Var}(y_2) + 2\lambda_1 \text{E}(y_1 y_2) + \kappa_{11} \\ &= \lambda_1^2 \text{Var}(y_1) + 2\lambda_1 \text{E}(y_1 y_2) + \frac{\kappa_{22}}{1 - \lambda_1^2} + \kappa_{11}. \end{aligned}$$

Then,

$$\text{Var}(y_1) = \frac{\kappa_{11}}{1 - \lambda_1^2} + \frac{\kappa_{22}}{(1 - \lambda_1^2)^2} + \frac{2\lambda_1 \text{E}(y_1 y_2)}{1 - \lambda_1^2}.$$

By the Cauchy-Schwarz inequality, *i.e.*, $|\text{E}(y_1 y_2)|^2 \leq \text{E}(y_1^2) \text{E}(y_2^2)$ in the above equation, we have $\text{Var}(y_1) \rightarrow +\infty$ as $\lambda_1 \rightarrow 1$. Hence for the group composed of y_1 and y_2 , which are involved with the partitioned matrix G_1 , we have $\text{Var}(y_i) \rightarrow +\infty$ for $i = 1, 2$ as $\lambda_1 \rightarrow 1$.

In case 3, suppose the partitioned matrix G_1 possesses a pair of complex conjugate eigenvalues, which are the nearest to 1 in modulus. Because we have

$$G_1(y_1, y_2)^T = \begin{bmatrix} a_1 & -b_1 \\ b_1 & a_1 \end{bmatrix} \begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} a_1 y_1 - b_1 y_2 \\ b_1 y_1 + a_1 y_2 \end{bmatrix},$$

there are two variables y_1 and y_2 related to the largest eigenvalue pair. Hence,

$$\begin{cases} \text{Var}(y_1) = a_1^2 \text{E}(y_1^2) + b_1^2 \text{E}(y_2^2) - 2a_1 b_1 \text{E}(y_1 y_2) + \kappa_{11}, \\ \text{Var}(y_2) = b_1^2 \text{E}(y_1^2) + a_1^2 \text{E}(y_2^2) + 2a_1 b_1 \text{E}(y_1 y_2) + \kappa_{22}. \end{cases}$$

Noticing that $\text{E}(y_i^2) = \text{Var}(y_i)$ for $i = 1, 2$, we have

$$\text{Var}(y_1) + \text{Var}(y_2) = \frac{\kappa_{11} + \kappa_{22}}{1 - (a_1^2 + b_1^2)}.$$

Clearly, $\text{Var}(y_1) + \text{Var}(y_2) \rightarrow +\infty$, as $a_1^2 + b_1^2 \rightarrow 1$. Hence at least one of the variables, say, y_1 , has infinite variance when $a_1^2 + b_1^2 \rightarrow 1$.

From the above discussion, by an appropriate linear transformation of any normalized matrix Λ , we can always regard the first element λ_1 as the dominant eigenvalue, which approaches 1 in modulus as parameter $P \rightarrow P_c$. Further, any variable that is related to λ_1 , also has infinite variance as $P \rightarrow P_c$. Therefore, next, we derive theoretical results on the original variables Z using only the first case for simplicity, and the same conclusion can be obtained for the other two cases in a similar manner.

A.3 A dynamical network biomarker

We are now in a position to investigate other statistical characteristics, in particular for the original variables Z , so as to obtain the dynamical network biomarker (DNB). Because the covariance of y_i and y_j is

$$\text{Cov}(y_i, y_j) = \text{E}(y_i y_j) - \text{E}(y_i)\text{E}(y_j) = \text{E}(y_i y_j),$$

based on (A1.4) and the normalized Λ for case 1, we have

$$\begin{aligned} \text{Cov}(y_i, y_j) &= \text{Cov}(y_i(k+1), y_j(k+1)) \\ &= \text{E}(y_i(k+1) y_j(k+1)) \\ &= \text{E}((\lambda_i y_i(k) + \zeta_i(k)) (\lambda_j y_j(k) + \zeta_j(k))) \\ &= \lambda_i \lambda_j \text{E}(y_i y_j) + \kappa_{ij} \\ &= \lambda_i \lambda_j \text{Cov}(y_i, y_j) + \kappa_{ij}, \end{aligned}$$

where $\kappa_{ij} = \text{Cov}(\zeta_i, \zeta_j)$ is the covariance of the noise. Thus

$$\text{Cov}(y_i, y_j) = \frac{\kappa_{ij}}{1 - \lambda_i \lambda_j}.$$

For any $i \neq j$, $\text{Cov}(y_i, y_j)$ is convergent to a positive bounded value. It should be noted that, when $i = j$, it is the variance, *i.e.*, $\text{Cov}(y_i, y_i) = \text{Var}(y_i)$. Furthermore, the Pearson's correlation coefficient (PCC) can be expressed as

$$\begin{aligned} \text{PCC}(y_i, y_j) &= \frac{\text{Cov}(y_i, y_j)}{\sqrt{\text{Var}(y_i)\text{Var}(y_j)}} \\ &= \frac{\kappa_{ij}}{\sqrt{\kappa_{ii}\kappa_{jj}}} \frac{\sqrt{(1 - \lambda_i^2)(1 - \lambda_j^2)}}{1 - \lambda_i\lambda_j}. \end{aligned}$$

For the original variables Z that are assumed to be measured as high-throughput data, by $Z(k) - \bar{Z} = SY(k)$, we have

$$z_i(k) = s_{i1}y_1(k) + \cdots + s_{in}y_n(k) + \bar{z}_i,$$

$$z_j(k) = s_{j1}y_1(k) + \cdots + s_{jn}y_n(k) + \bar{z}_j.$$

Hence,

$$\begin{aligned} \text{Var}(z_i) &= s_{i1}^2 \text{Var}(y_1) + \sum_{k=2}^n s_{ik}^2 \text{Var}(y_k) \\ &\quad + \sum_{k,m=1, k \neq m}^n s_{ik}s_{im} \text{Cov}(y_k, y_m), \end{aligned}$$

$$\begin{aligned} \text{Cov}(z_i, z_j) &= \text{E}((s_{i1}y_1 + \cdots + s_{in}y_n)(s_{j1}y_1 + \cdots + s_{jn}y_n)) \\ &= s_{i1}s_{j1} \text{Var}(y_1) + \cdots + s_{in}s_{jn} \text{Var}(y_n) \\ &\quad + \sum_{k,m=1, k \neq m}^n s_{ik}s_{jm} \text{Cov}(y_k, y_m), \end{aligned}$$

and

$$\text{PCC}(z_i, z_j) = \frac{\text{Cov}(z_i, z_j)}{\sqrt{\text{Var}(z_i)\text{Var}(z_j)}},$$

where $\text{Cov}(y_k, y_m) \leq \sqrt{\text{Var}(y_k)\text{Var}(y_m)}$.

Notice that variable y_1 is related to the dominant eigenvalue λ_1 . Based on the above equations for $\text{Var}(z_i)$, $\text{Cov}(z_i, z_j)$ and $\text{PCC}(z_i, z_j)$, we can easily derive the following properties for $Z(k)$.

1° If a variable z_i is related to y_1 , that is, $s_{i1} \neq 0$, then the standard deviation $\text{SD}(z_i) = \sqrt{\text{Var}(z_i)}$ increases greatly as $\lambda_1 \rightarrow 1$.

2° If both variables z_i and z_j are related to y_1 , that is, both s_{i1} and s_{j1} are not vanishing, then $\text{Cov}(z_i, z_j)$ tends to infinity as $\lambda_1 \rightarrow 1$. Moreover, $|\text{PCC}(z_i, z_j)| \rightarrow 1$ as $\lambda_1 \rightarrow 1$.

3° If $s_{i1} \neq 0$ but $s_{j1} = 0$, then $|\text{PCC}(z_i, z_j)| \rightarrow 0$ as $\lambda_1 \rightarrow 1$.

4° If $s_{i1} = 0$, then $\text{SD}(z_i)$ is bounded as $\lambda_1 \rightarrow 1$.

5° If both s_{i1} and s_{j1} are vanishing, then $|\text{PCC}(z_i, z_j)| \rightarrow a$, $a \in (0, 1)$ as $\lambda_1 \rightarrow 1$.

If properties 1°-5° above are satisfied, all variables z_i with $s_{i1} \neq 0$ form a group, called the dominant group, that will first represent a transition to the disease state. As mentioned in the main text, the dominant group characterizes the dynamical features of the underlying system, and the molecules in the group are strongly and dynamically correlated in the pre-disease state. These molecules in the dominant group are expected to form a subnetwork or functional module from a network viewpoint. Hence, we also defined it as a DNB. Actually, each one of the first three conditions represents a criterion that can be used to detect the DNB or early-warning signals of the pre-disease state. Here we note that the three criteria are in fact the generic properties of the DNB members in dynamics whenever the system approaches a critical tipping point. Such critical behavior coincides with the phenomenon described by the so-called “critical slowing down” theory (10).

Unlike the traditional molecular biomarkers in medicine, whose expressions reflect the severity or presence of some disease state and which are required to have different but consistent (or constant) values in order to distinguish a disease state from a normal state, a DNB is a strongly correlated molecular network in which the concentrations of molecules, however, dy-

namically change without keeping constant values in the pre-disease state as shown in Fig.1h of the main text. In other words, the concentrations of molecules in the DNB tend to increasingly fluctuate when the system approaches the pre-disease state, although they change in a strongly collective manner, which is the key feature of a DNB. Hence, the existence of the DNB indicates that the system is in the pre-disease state. It is noteworthy that each individual may not have exactly the same DNB even for the same disease, that is, some molecule members in the DNB may differ from person to person. Unlike traditional biomarkers, a DNB is not composed of a group of fixed molecules even for the same disease and might have different members depending on individual variations that are detected by individual high-throughput data.

System (A1.1) is used to describe the progression of a disease. As the parameter P approaches the critical value P_c , which leads to $\lambda_1 \rightarrow 1$, the system reaches the pre-disease state. In order to obtain a strong signal of the pre-disease state, we combine the first three criteria to construct the following composite index:

$$I =: \frac{SD_d \cdot PCC_d}{PCC_o},$$

where PCC_d is the average Pearson's correlation coefficient of the dominant group in absolute value; PCC_o is the average Pearson's correlation coefficient of the dominant group with other molecules in absolute value; SD_d is the average standard deviation of the dominant group. Although the expression of each observable z_i may stochastically change at any time instant because of the perturbation, this composite index is expected to increase sharply whenever the system approaches a critical transition point, and therefore, it can serve as an effective early-warning signal to identify the pre-disease state. To summarize the above analysis, we have the following theorem.

Theorem 1 *Consider a stochastically perturbed linearized system of (A1.1):*

$$Z(k+1) = A(P)Z(k) + \varepsilon(k), \tag{A1.6}$$

where $\varepsilon(k)$ is the Gaussian noise and P is a parameter vector controlling the Jacobian matrix

A. When P approaches to the bifurcation point, the following results hold.

- If both z_i and z_j are in the dominant group, then

$$\text{PCC}(z_i, z_j) \rightarrow \pm 1,$$

while $\text{SD}(z_i) \rightarrow \infty$ and $\text{SD}(z_j) \rightarrow \infty$.

- If z_i is in the dominant group but z_j is not, then

$$\text{PCC}(z_i, z_j) \rightarrow 0,$$

while $\text{SD}(z_i) \rightarrow \infty$, and $\text{SD}(z_j)$ approaches a bounded value.

- If neither z_i nor z_j is in the dominant group, then

$$\text{PCC}(z_i, z_j) \rightarrow a, \quad a \in (-1, 1) \setminus \{0\},$$

while both $\text{SD}(z_i)$ and $\text{SD}(z_j)$ approach bounded values respectively.

Here PCC stands for the Pearson's correlation coefficient, and SD for the standard deviation.

These results in the theorem are rewritten in the main text as three conditions for the dominant group or the DNB. From the results, clearly the composite index $I =: (\text{SD}_d \cdot \text{PCC}_d) / \text{PCC}_o$ increases sharply when the system is approaching to the tipping point.

Remark 1 For nonlinear case (A1.1) at a fixed point, the dynamical behavior has the same tendency as that of the linearized case (A1.4) or (A1.6), that is, when the system is approaching to the tipping point, both indices $|\text{SD}|$ and $|\text{PCC}|$ in the dominant group increase sharply, while $|\text{PCC}|$ between the dominant group and other molecules decreases rapidly. The composite index I can serve as the early-warning indicator of the coming phase transition.

Actually, according to classical nonlinear dynamical systems theory (18), the Jacobian matrix $\left. \frac{\partial f(Z; P_c)}{\partial Z} \right|_{Z=\bar{Z}}$ of (A1.1) defines three subspaces:

1. The stable subspace, which is spanned by the generalized eigenvectors corresponding to the eigenvalues λ_i with $|\lambda_i| < 1$;
2. The unstable subspace, which is spanned by the generalized eigenvectors corresponding to the eigenvalues λ_i with $|\lambda_i| > 1$;
3. The center subspace, which is spanned by the generalized eigenvectors corresponding to the eigenvalues λ_i with $|\lambda_i| = 1$.

These spaces are all invariant subspaces of the linearized equations (A1.4) or (A1.6) without noise.

Corresponding to the linearized system (A1.6), the nonlinear system (A1.1) has invariant manifolds consisting of orbits of the nonlinear system. Under the condition that when the parameter P equals the critical value P_c , at least one of the eigenvalues of the Jacobian matrix $\left. \frac{\partial f(Z; P_c)}{\partial Z} \right|_{Z=\bar{Z}}$ equals 1 in modulus, there is an invariant center manifold tangent to the corresponding subspace. Locally, the center manifold is C^{r-1} if the nonlinear part f is a C^r function (r times continuously differentiable), and the orbits of (A1.1) can be approximated by the corresponding ones of (A1.6) without noise when the center manifold theory holds.

In fact, at any instant of disease progression, the expression of each variable (the concentration of one observable) may stochastically change due to perturbations. Hence in most complex diseases, it is difficult to identify the early-warning signal by solely focusing on one observable. As shown above, however, our detection of early-warning signals is based on a network of dynamically correlated observables from high-throughput data with over thousands of measurements for each sample. From time-course high-throughput data, based on the theoretical results, we can identify the dominant group or the DNB if the system approaches the pre-disease

state. Hence, the existence of the DNB implies that the system is in the pre-disease state. Again it is noteworthy that unlike traditional biomarkers, a DNB is not necessarily composed of fixed molecules even for the same disease but can have different members depending on individual variations that are detected by individual high-throughput data.

A.4 Summary

Mathematical models based on bifurcation theory and center manifold theory have successfully been applied to many fields for describing the catastrophic phenomena near the critical point, e.g., (9)–(13). For complex diseases, such as cancer, bifurcation theory has also been applied to describe the sudden changes in the dynamical relationship among molecules/cells and the phase changes in disease evolution (14)–(16). Generally, the dynamics for the progression of complex diseases is very complicated either before or after a sudden deterioration, and therefore the state equations are usually constructed in a high-dimensional space with a large number of variables and parameters. However, provided that the system driven by some (unknown) parameters approaches the critical point (which is a very special phase during the progression), as shown in this section, theoretically, the system can be expressed in a very simple form, i.e., generally it can be expressed by one- or two-variable equations in an abstract phase space around a codimension-one bifurcation point. This is guaranteed by the bifurcation theory and center manifold theory. Thus, because of this special feature, during this special phase (or period), unlike during other periods (i.e., before or after the transition), we can express the system in a simple form to detect the signal.

In other words, no matter how complicated the system is and how many variables it has, provided that some factors or parameters drive the system to the critical state, we can always express the system in this simple form (but, unfortunately, they are generally unobservable because of the abstract phase space). In this work, we constructed the relationship of the ob-

servable subnetwork (DNB) in the original state space with the unobservable variables of the abstract phase space, and we proved the conditions to identify the signal by only observing the DNB in the pre-disease state. Generally, we cannot express the complicated system in such a simple manner in either the normal state or the disease state although considerable efforts have been made thus far. In addition, next, we provide a computational algorithm to numerically identify the DNB based on the high-throughput data when the system reaches the critical state.

Note that we can roughly categorize the complex diseases into two types based on their progression features. One is those diseases with a sudden deterioration phase or transition during the progression, such as many cancers, where drastic changes are observed during the period from "a normal state" to "a disease state". The other one is those diseases with a relatively smooth or slow change during their progression. In this work, our method especially focuses on the former type.

B Numerical validation of detection of early-warning signals

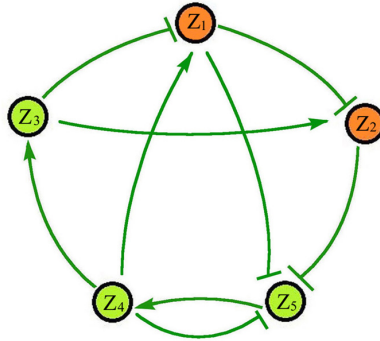


Figure S2: | **A five-gene regulatory network.** The arrow represents the positive regulation, and the blunted line denotes the negative regulation.

We used the five-gene network shown in Fig.S2 to demonstrate the theoretical results for detecting early-warning signals near a tipping point. Such a form of gene regulatory networks can be used to study the transcription, translation, diffusion, and translocation processes of

gene regulatory activities (1, 2, 19–22). The following five differential equations represent gene regulations among the five genes.

$$\left\{ \begin{array}{l} \frac{dz_1(t)}{dt} = (90|P| - 1236) + \frac{240-120|P|}{1+z_3(t)} + \\ \quad \frac{1488z_4(t)}{1+z_4(t)} - 30|P|z_1(t), \\ \frac{dz_2(t)}{dt} = (75|P| - 150) + \frac{60-30|P|}{1+z_1(t)} + \\ \quad \frac{(240-120|P|)z_3(t)}{1+z_3(t)} - 60z_2(t), \\ \frac{dz_3(t)}{dt} = -1056 + \frac{1488z_4(t)}{1+z_4(t)} - 60z_3(t), \\ \frac{dz_4(t)}{dt} = -600 + \frac{1350z_5(t)}{1+z_5(t)} - 100z_4(t), \\ \frac{dz_5(t)}{dt} = 108 + \frac{160}{1+z_1(t)} + \frac{40}{1+z_2(t)} + \frac{1488}{1+z_4(t)} - \\ \quad 300z_5(t), \end{array} \right. \quad (B1)$$

where P is a scalar control parameter, and $Z(t) = (z_1(t), z_2(t), z_3(t), z_4(t), z_5(t))$ are five nodes in the network (Fig.S2, or Fig.2a in the main text). z_i ($i = 1, \dots, 5$) respectively represents the concentration of mRNA- i . The gene regulations are represented by the Michaelis-Menten form except for the degradation rates, which are linearly proportional to the concentrations of the corresponding genes. The degradation rates for mRNAs are $(30P, 60, 60, 100, 300)$ in (B1). There is an equilibrium point $\bar{Z} = (\bar{z}_1, \bar{z}_2, \bar{z}_3, \bar{z}_4, \bar{z}_5) = (1, 0, 1, 3, 2)$ that is stable. The differential equations (B1) can be transformed into the difference equations $Z(k+1) = f(Z(k), p)$ by the Euler scheme (23), *i.e.*,

$$\left\{ \begin{array}{l} z_1(k+1) = z_1(k) + \left[(90|P| - 1236) + \frac{240-120|P|}{1+z_3(t)} + \right. \\ \quad \left. \frac{1488z_4(t)}{1+z_4(t)} - 30|P|z_1(t) \right] \Delta t, \\ z_2(k+1) = z_2(k) + \left[(75|P| - 150) + \frac{60-30|P|}{1+z_1(t)} + \right. \\ \quad \left. \frac{(240-120|P|)z_3(t)}{1+z_3(t)} - 60z_2(t) \right] \Delta t, \\ z_3(k+1) = z_3(k) + \left[-1056 + \frac{1488z_4(t)}{1+z_4(t)} - 60z_3(t) \right] \Delta t, \\ z_4(k+1) = z_4(k) + \left[-600 + \frac{1350z_5(t)}{1+z_5(t)} - 100z_4(t) \right] \Delta t, \\ z_5(k+1) = z_5(k) + \left[108 + \frac{160}{1+z_1(t)} + \frac{40}{1+z_2(t)} + \right. \\ \quad \left. \frac{1488}{1+z_4(t)} - 300z_5(t) \right] \Delta t, \end{array} \right. \quad (B2)$$

with a small time interval Δt . Note that $Z(k)$ is the vector of $Z(t)$ at the time instant $k\Delta t$.

By introducing $X = Z - \bar{Z}$, we obtain the linearized approximation of (B2) as follows:

$$\begin{cases} x_1(k+1) = x_1(k) + [-30|P| x_1(k) - (60 - 30|P|)x_3(k) + 93x_4(k)]\Delta t, \\ x_2(k+1) = x_2(k) + [-(60 - 30|P|)x_1(k) - 60x_2(k) + (60 - 30|P|)x_3(k)]\Delta t, \\ x_3(k+1) = x_3(k) + [-60x_3(k) + 93x_4(k)]\Delta t, \\ x_4(k+1) = x_4(k) + [-100x_4(k) + 150x_5(k)]\Delta t, \\ x_5(k+1) = x_5(k) + [-40x_1(k) - 40x_2(k) - 93x_4(k) - 300x_5(k)]\Delta t. \end{cases} \quad (\text{B3})$$

Therefore, representing the Jacobian matrix of (B2) by $J = \left. \frac{\partial f(Z(k);p)}{\partial Z} \right|_{Z=\bar{Z}}$, we have

$$J = e^{\Delta t \cdot A}, \quad (\text{B4})$$

where

$$A = \begin{bmatrix} -30|P| & 0 & 30|P| - 60 & 93 & 0 \\ 30|P| - 60 & -60 & 60 - 30|P| & 0 & 0 \\ 0 & 0 & -60 & 93 & 0 \\ 0 & 0 & 0 & -100 & 150 \\ -40 & -40 & 0 & -93 & -300 \end{bmatrix}.$$

From (B4), we obtain that there are 5 distinct eigenvalues $(0.74^{|P|}, 0.55, 0.37, 0.20, 0.14)$ by taking $\Delta t = 0.01$. Hence, the equilibrium point $\bar{Z}$ is stable when $P \in (0, 1]$. Obviously, there is a critical value $P_c = 0$, at which the system loses stability and undergoes a critical transition. We intend to detect the early-warning signals indicating the critical transition as the control parameter P approaches the critical value 0 from $P > 0$.

To analyze the system in a simple form, we transform $Z(k)$ into $Y(k) = (y_1(k), \dots, y_5(k))$, *i.e.*,

$$Y(k) = S^{-1}(Z(k) - \bar{Z})$$

with

$$S = \begin{bmatrix} -1 & 1 & -7/3 & 7/3 & -1 \\ 1 & -1 & 0 & 0 & 0 \\ 0 & 1 & -7/3 & 7/3 & -1 \\ 0 & 0 & 1 & -5/2 & 3/2 \\ 0 & 0 & 0 & 1 & -1 \end{bmatrix}. \quad (\text{B5})$$

The matrix S satisfies $S^{-1} J S = \Lambda$, where $\Lambda = \text{diag}(0.74^{|P|}, 0.55, 0.37, 0.20, 0.14)$ is a diagonal matrix. Hence, we obtain the linearized difference equations with additive noise $\zeta(k)$, $Y(k+1) = \Lambda Y(k) + \zeta(k)$ as follows:

$$\begin{cases} y_1((k+1)) = 0.74^{|P|} y_1(k) + \zeta_1(k), \\ y_2((k+1)) = 0.55 y_2(k) + \zeta_2(k), \\ y_3((k+1)) = 0.37 y_3(k) + \zeta_3(k), \\ y_4((k+1)) = 0.20 y_4(k) + \zeta_4(k), \\ y_5((k+1)) = 0.14 y_5(k) + \zeta_5(k), \end{cases} \quad (\text{B6})$$

where $\zeta_i(k)$ ($i = 1, 2, \dots, 5$) are Gaussian noises with zero means and covariances $\kappa_{ij} = \text{Cov}(\zeta_i, \zeta_j)$. For the control parameter $P \in (0, 1]$, it can be seen that the variable y_1 is related to the largest eigenvalue $0.74^{|P|}$, which is nearest to 1. Hence, when P approaches 0, the dominant eigenvalue $0.74^{|P|}$ tends to 1, which leads to a critical transition of system (B6) or (B2). Figure S3 shows that when $P \rightarrow 0$ the standard deviation of y_1 increases sharply.

Next, we study the dynamics using the original variables $Z(k)$, which are assumed to be quantitatively measured from the high-throughput devices. From the relationship $Z(k) - \bar{Z} = SY(k)$ and the matrix S in (B5), we have

$$\begin{aligned} z_1 - \bar{z}_1 &= -y_1 + y_2 - \frac{7}{3}y_3 + \frac{7}{3}y_4 - y_5, \\ z_2 - \bar{z}_2 &= y_1 - y_2, \\ z_3 - \bar{z}_3 &= y_2 - \frac{7}{3}y_3 + \frac{7}{3}y_4 - y_5, \\ z_4 - \bar{z}_4 &= y_3 - \frac{5}{2}y_4 + \frac{3}{2}y_5, \\ z_5 - \bar{z}_5 &= y_4 - y_5. \end{aligned} \quad (\text{B7})$$

It is clear that among $(z_1, z_2, z_3, z_4, z_5)$, the two variables z_1 and z_2 are directly related to y_1 , which corresponds to the dominant eigenvalue. Therefore, according to the theoretical results, $\{z_1, z_2\}$ constitute the dynamical dominant group or the DNB of the system when

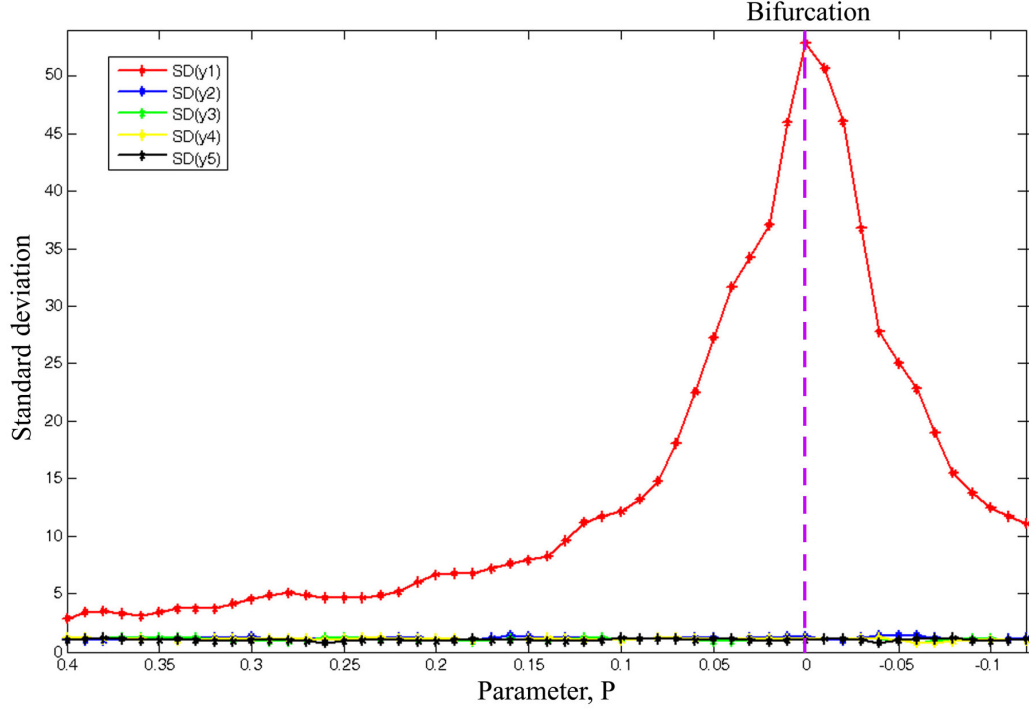


Figure S3: | **Standard deviation curves of $(y_1(t), y_2(t), y_3(t), y_4(t), y_5(t))$** . The horizontal axis represents the control parameter P , which varies from 0.4 to -0.1 and the critical threshold is $P = 0$ corresponding to the bifurcation point. The vertical axis represents the standard deviation.

$P \in (0, 1]$, which will reflect the breakdown of the system as $P \rightarrow 0$. Therefore, we use the DNB of $\{z_1, z_2\}$ to detect the early-warning signals based on their dynamical properties near the critical transition. We test this conjecture by numerical simulation, as shown in Fig.S4. From Fig.S4a, when the parameter P decreases from 0.4 to 0, $|\text{PCC}(z_1, z_2)|$ sharply increases around $P = 0.15$, whereas $|\text{PCC}(z_1, z_3)|$, $|\text{PCC}(z_1, z_4)|$, $|\text{PCC}(z_1, z_5)|$, $|\text{PCC}(z_2, z_3)|$, $|\text{PCC}(z_2, z_4)|$, and $|\text{PCC}(z_2, z_5)|$ approach zero. There are no significant changes in other PCC values ($|\text{PCC}(z_3, z_4)|$), $|\text{PCC}(z_3, z_5)|$ and $|\text{PCC}(z_4, z_5)|$). Meanwhile, Fig.S4b shows that the standard deviation curves of z_1 and z_2 increase drastically when parameter P decreases from 0.4 to 0, whereas the curves of other variables show little change with low values. These abrupt changes in the statistical indices show that variables $\{z_1, z_2\}$ satisfy all three criteria of the dom-

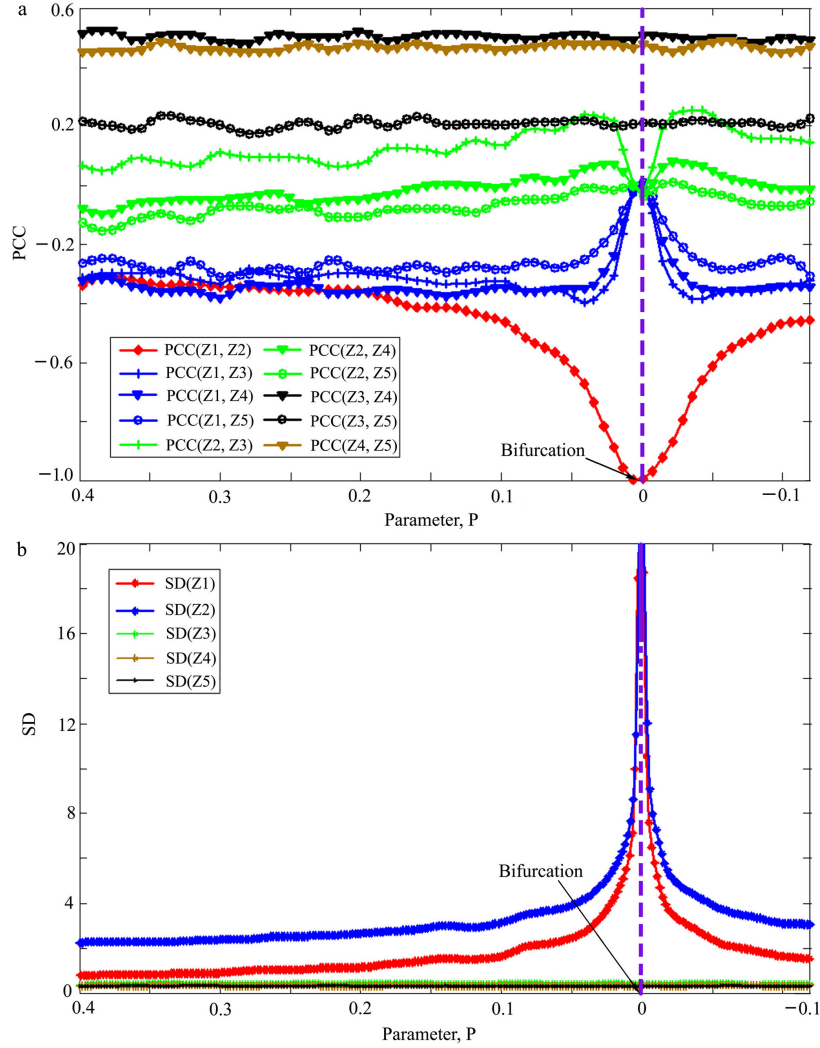


Figure S4: | **Early-warning signals of the five-gene network based on the dynamical network biomarker.** (a) PCC curves. Each curve is drawn for a pair of variables among $(z_1, z_2, z_3, z_4, z_5)$. The horizontal axis represents the control parameter P , which varies from 0.4 to -0.1. The vertical axis represents the PCC. (b) Standard deviation (SD) curves of $(z_1, z_2, z_3, z_4, z_5)$. The horizontal axis represents the control parameter P , which varies from 0.4 to -0.1. The vertical axis represents the standard deviation (SD). In the simulations based on (B3) with additive noise or based on (B6)-(B7), all the initial conditions are randomly set within the interval $[0, 1]$. The simulations were performed in MATLAB(R2009a) by using the Euler-Maruyama integration method with the Ito calculus (23).

inant group or the DNB in the theoretical result, which demonstrates that they do constitute the dynamical dominant group and can predict the critical transition. Therefore, their collective

dynamical properties provide a strong early-warning signal as shown in Fig.2f in the main text. It is noteworthy that, as indicated in Figs.S4a and b, when P passes over the critical value 0, the system approaches another state in which all the indices also return to “normal” again, although the disease state itself is not the focus of this work.

On the other hand, a gene regulatory network for a living organism is usually very complex, and it may involve thousands or more of variables and parameters. However, the DNB of such a system can not only sense the early-warning signals of the impending phase transition, but also provide a possible way to understand the underlying mechanism; that is, observing a certain module or subnetwork that is estimated only by a few samples, may be sufficient to study the dynamical behavior of the entire system in the pre-disease state.

C Algorithm for detecting early-warning signals by a dynamical network biomarker



Figure S5: | **Sampling periods (or time windows) and samples for the measured high-throughput data.** The entire period is divided into [period-1 ,..., period- T]. The interval between two consecutive periods (e.g., a month or a week) may be long, but the interval between two samples or sampling time points in each sampling period (e.g., a day or an hour) should be shorter so that the dynamical features can be reflected in the measured data. In each time period, we evaluate the composite index or DNB based on a few samples so as to check whether it is in the pre-disease state in this sampling period.

As shown in Fig.S5, we assumed that there are a few samples for one individual in each sampling period (or time window) from the practical viewpoint, but there are over thousands of measurements in each sample with high-throughput data, e.g., high-throughput expression data or high-throughput sequencing data. The entire period is divided into [period-1, ... , period- T].

The interval between two consecutive sampling periods (e.g., a month or a week) may be long, but the interval between two samples (or sampling time points) in each period (e.g., a day or an hour) should be shorter so that the dynamical features can be reflected in the measured data. In other words, we assume that there are a few samples in each period, whose intervals are not required to be equal but should be short so that the dynamic correlations remain among genes or proteins. At each time period, we evaluate the composite index or DNB based on a few samples so as to check whether it is in the pre-disease state. We assumed that there are two group samples, namely, the case samples and the control samples. The algorithm to detect a DNB for early-warning signals mainly includes the following steps with the objective of identifying the DNB carrying the most dynamical information from the high-throughput data for the entire study period and predicting the pre-disease state based on the DNB.

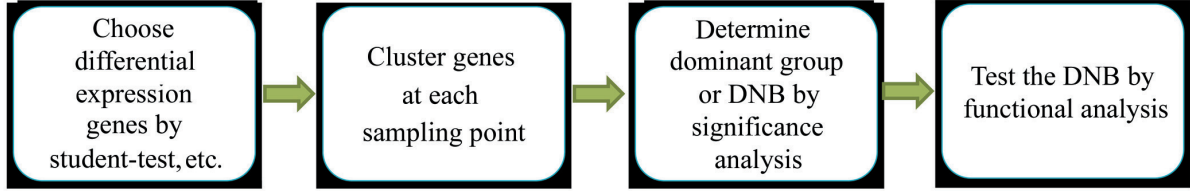


Figure S6: | **Flowchart of the algorithm.**

In order to state the algorithm clearly, in addition to the notation in Fig.S5, we denote the total number of measurements (genes or proteins) in each sample as N . The flowchart of the algorithm is shown in Fig.S6, and it is described as follows.

1° Choose differential expression genes from high-throughput physiological data.

1.1 At each sampling point (or period), by using the student t-test with significance level $p < 0.05$, choose those genes whose expressions show significant changes (in the sense of mean values) between the case samples (microarray data in the case group) and the control samples (microarray data in the control group).

1.2 By using the false discovery rate (FDR), correct the multiple comparisons or multiple student t-tests for the genes selected in **1.1** in each period.

1.3 The two-fold change method is then adopted to screen those genes selected in **1.2** that exhibit relatively significant changes in standard Deviation in each period.

After the above procedures, at each sampling time point of $t_1, t_2, \dots, t_T$, we obtain the differential-expression genes/proteins, numbered as $N_1, N_2, \dots, N_T$, respectively. These components have two main characteristics: they not only show significant differences in their expressions between the case group and the control group, but also show strong deviations from their mean values.

2° Cluster genes at each sampling time point by correlations.

At each sampling point of $t_1, t_2, \dots, t_T$, we cluster those differential expression genes se-

lected in **1.3** by their correlations in order to obtain a number of clusters. In every such cluster, genes (or proteins) are closely correlated at some period.

According to the theoretical results, if a time period is in or close to the pre-disease stage, then the clusters obtained in this period are potential dominant groups. Hence every cluster is a candidate of the DNB, whereas its corresponding period is a candidate of the transition point in the pre-disease state.

3° Determine the dominant group or the DNB by significance analysis.

3.1 Conduct a new type of data normalization for all genes or proteins in the selected clusters obtained in **2°**. Because there are S_i samples in period t_i for each gene or protein (see Fig.S5), the expression data are normalized in the following manner:

$$A = \frac{D_{\text{case}} - \text{mean}(N_{\text{control}})}{\text{SD}(N_{\text{control}})},$$

where A denotes the normalized expression data of each gene or protein for every case sample, D_{case} is the data of each gene or protein for every case sample, and $\text{mean}(N_{\text{control}})$ and $\text{SD}(N_{\text{control}})$ are the mean and SD of each gene or protein for all control samples, respectively.

3.2 For each cluster or group normalized in **3.1**, calculate four indices in each period: the standard deviation (i.e., SD_d in Eq.(2) of the main text), the average Pearson's correlation coefficient ($|\text{PCC}|$ in absolute value) among the cluster members (i.e., PCC_d in Eq.(2) of the main text), the average $|\text{PCC}|$ between the cluster members and other genes (i.e., PCC_o in Eq.(2) of the main text), and the composite index (i.e., I in Eq.(2) of the main text). We first screen clusters using the three criteria of a DNB (see Section A3).

Then, by significance analysis of the remaining clusters that satisfy the three criteria, we choose the cluster with the most significant change in the composite index between the two consecutive periods. This cluster is regarded as a candidate dominant group, and the corresponding period is also regarded as a candidate period of the pre-disease stage.

The selected genes in the candidate dominant group in 3° behave in a stochastic but strongly collective manner. In particular, in the candidate period, the average SD and $|\text{PCC}|$ of members in the group increase sharply, and the $|\text{PCC}|$ between members in the group and the others decreases greatly. Therefore, all three criteria for the DNB are satisfied, implying that it can be used to detect the early-warning signal for the pre-disease state. Note that we can replace $\text{mean}(N_{\text{control}})$ and $\text{SD}(N_{\text{control}})$ by $\text{mean}(N_{\text{case}})$ and $\text{SD}(N_{\text{case}})$ respectively to normalize expression data A in Step 3.1, when there are no control samples.

4° Functional analysis of the DNB.

In order to check whether the identified DNB for detecting the early-warning signal of a specific disease correctly predicts the impending critical transition, we conduct functional analysis of the specific disease, that is, we analyze the dysfunctional implication of the DNB based on GO enrichment or literature mining on the relations between the genes in the DNB and the specific diseases being studied.

It is noteworthy that because the prediction is based on a DNB, which may differ from person to person because of the widely existing individual variations (see the main text and section A in this SI), in the clinical test, it requires high-throughput data from the same individual during sampling periods. However, because of lack of such data, we use the physiological data (see section D) from a group of individuals instead. For each disease below, we approximately assume that the data are from the same individual to illustrate the plausibility of our method.

D Application to three sets of disease data

In this section, we applied our prediction method to detect the early-warning signals of diseases in three physiological datasets. The three datasets are described in Table S1. The name of a gene is represented by capital letters in this work.

Table.S1 Descriptions of the three datasets.

Experimental data	Descriptions
Genomic data about lung injury with carbonyl chloride inhalation exposure (24)	
Sampling points	9 sampling points 0, 0.5, 1, 4, 8, 12, 24, 48, 72 (h)
Number of observed objects	22690 genes
Groups	control group and case group
Genomic data about hepatic lesion caused by chronic hepatitis B (25)	
Sampling points	4 sampling periods F1, F2, F3, F4 (period)
Number of observed objects	8516 cDNAs
Groups	case group
Genomic data about transgenic B-cell lymphomagenesis (26)	
Sampling points	4 sampling periods normal activated, marginal lymphoma, transitional lymphoma, aggressive lymphoma (period)
Number of observed objects	13712 genes
Groups	case group

D.1 Dataset 1. Genomic data about the lung injury with carbonyl chloride inhalation exposure (i.e., acute lung injury)

The dataset was obtained from an experiment of a toxic-gas-induced lung injury such as pulmonary edema (24). The authors used a genomic approach to investigate the molecular mechanism of phosgene-induced lung injury. In the experiment, they determined the temporal effects of phosgene exposure on lung tissue antioxidant enzyme concentrations at the gene expression level, compared these results with those from air-exposed mice treated in a similar manner, and assessed the role of the GSH redox cycle in this oxidative lung injury model (24). In order to obtain two groups of data, namely control-group data and case-group data, two groups of CD-1 male mice were exposed to air and phosgene, respectively. Lung tissue was collected from air- or phosgene-exposed mice 0.5, 1, 4, 8, 12, 24, 48, and 72 h after exposure. The details of the experiment are available in the original paper (24).

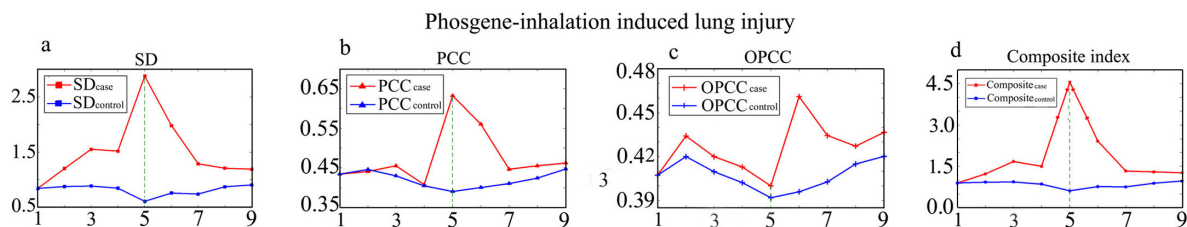


Figure S7: | Early-warning signals for acute lung injury. In all the figures, the horizontal axis represents the time period t . **(a)** Mean SD. **(b)** Mean PCC in the DNB. **(c)** Mean PCC between the DNB and other molecules (OPCC). **(d)** Composite index. The dotted green line indicates the pre-disease period. We show the curves of both the case group (red) and the control group (blue). Clearly, the composite index starts increasing drastically from the 4th time period (4h), and reaches the peak in the 5th time period (8h), while the OPCC decreases. This fact strongly suggests that the pre-disease state is near the 5th time period, and the system is driven into the disease state after the 5th time period. Our early-warning signals are consistent with the actual disease development in that the most prominent physiological effects occur within the first 8 hours after exposure, resulting in pulmonary edema, and ultimately reducing survival rates (see the original paper (24)).

Briefly, the authors found that most prominent physiological effects occur within the first 8 h after exposure, resulting in the common observation of enhanced BALF protein levels, increased pulmonary edema, and ultimately decreased survival rates (24). At the concentration delivered, 50%-60% mortality was routinely observed after 12 h and 60%-70% mortality was observed after 24 h. In addition, they found that the most severe phosgene-induced acute lung injury ranges from 4 to 12 h after exposure (24). The details of their findings are also available in the original paper (24). Early-warning signals of the lung injury based on the identified DNB are shown in Fig.S7, which indicates that the pre-disease state may start around the 4th time period (4h), and the system may turn into the disease state after the 5th time period (8h). The prediction based on the DNB is coincident with the actual disease development.

In order to explain our method more clearly, we considered acute lung injury as a concrete example to describe the computational procedure step-by-step. In GSE6136 data set, there are 22690 original probesets. We mapped them to the corresponding NCBI Entrez gene symbols by

using the GEO annotation. Meanwhile, all without-correct-corresponding gene symbols were screened out, and probes detecting the same genes were combined by the averaging method. There were 12871 genes left. Based on the algorithm in Supplementary Information C, we conducted the following computation.

1° Choose differential expression genes from the high-throughput gene data for acute lung injury. At each sampling point (or period), there are 6 case samples and 6 control samples with 12871 genes. At the 0 h sampling point, the case samples are considered to be identical to the control samples.

1.1 At each sampling point, by using the student t-test with significance level $p < 0.05$ we select $A = [0, 53, 184, 1325, 1327, 738, 980, 1263, 915]$ differential expression molecules for 9 periods or time points, respectively.

1.2-1.3 Based on set A of the selected differential expression molecules, by using the false discovery rate (FDR) ($p_i(k_i) < (k_i/controlsize(i)) \times 0.05$), and by two-fold change screening, we obtain $B = [0, 29, 72, 195, 269, 163, 173, 188, 176]$ genes respectively for the 9 sampling time points, respectively. For gene set B , each component member not only shows significant difference in the expressions between the case group and the control group but also shows strong deviation from the mean value.

2° For the selected gene set B in the above step, we cluster molecules at each sampling time point by correlations. For each sampling point, we obtain 40 clusters.

3° We determine the dominant group or the DNB using the three conditions and by significance analysis.

3.1 At each sampling point, we conduct a new type of data normalization for all genes in the

40 clusters obtained in 2°, that is, the expression data are normalized in the following manner:

$$A = \frac{D_{\text{case}} - \text{mean}(N_{\text{control}})}{\text{SD}(N_{\text{control}})}.$$

3.2 At each sampling point, for every cluster or group normalized in **3.1**, we calculate four indices in each period: the standard deviation (SD), average Pearson’s correlation coefficient (|PCC| in absolute value) of the cluster members, average |PCC| between the cluster members and other genes, and the composite index. We first screen clusters using the three conditions of the DNB. After screening, we obtain ‘the number of candidate DNB groups as [0,0,0,0,1,0,0,1,0] for the 9 periods.

The first cluster which is qualified to show a critical transition is the 111st group, containing 220 genes, which is obtained in the 5th sampling point (8 h). The obtained DNB is consistent with the real experimental phenomenon, and the illustrative indices, i.e., SD, PCC, and the composite index (see Fig.S7) start increasing sharply from the 4th time period (4 h) and reach peaks in the 5th time period (8 h, i.e., the pre-disease stage); meanwhile, the OPCC drastically decreases to the lowest value. These indices show that the pre-disease state starts near the 4th time period (4 h), and the system transitions to the disease state after the 5th time period (8 h). Our early-warning signals are coincident with the actual disease development that the most prominent physiological effects occur within the first 8 h after exposure, resulting in pulmonary edema and ultimately reducing survival rates (see the original paper (24)). The applicable computer program used for detecting the DNB from high-throughput data is described in the part “Supplementary computer program”.

4° Functional analysis of the DNB.

4.1 In order to determine whether the identified DNB for detecting the early-warning signal of a specific disease correctly predicts the impending critical transition, we conduct functional analysis, that is, we analyze the dysfunctional implication of the DNB based on GO enrichment

or literature studies of the relationships between the genes in the DNB and the specific diseases being studied. This is described in Section F.

4.2 In order to verify the biological significance of the DNB group, we also carry out bootstrap analysis respectively. The results are presented in Section E.

4.3 In addition, KEGG pathway enrichment analysis is also conducted. This is described in Section F.

Dynamical Evolution of DNB and Whole Molecular Network

In order to show the detailed progression of the DNB group as well as the whole molecular network along the sampling time series, we presented the dynamic process of the DNB for 8 time points (see Fig.S8) and the dynamics of the whole mouse network (see Fig.S9) to compare the dynamical changes between the members of the DNB and other genes. From Fig.S8, which shows the dynamic evolution of the DNB, it is obvious that the group of the DNB not only provides significant signals as the system approaches the critical point, but also forms a strongly correlated observable subnetwork. Clearly, there is a drastic change in the DNB at 8 h in terms of expression variations and network structure.

To show the dynamics of the whole molecular network, we constructed the whole mouse molecular interaction network (protein-protein interactions and TF-target regulations). In the whole network (Fig.S9), there are 4458 nodes (or genes) with 23616 links. Because there are too many links or interactions to show the network clearly, we randomly chose 9238 links with 3452 connected nodes to graphically illustrate the network in Fig.S9. Nodes are chosen by the following procedure:

1. All genes were mapped into the whole mouse molecular interaction network (protein-protein interactions and TF-target regulations) based on their interactions with expres-

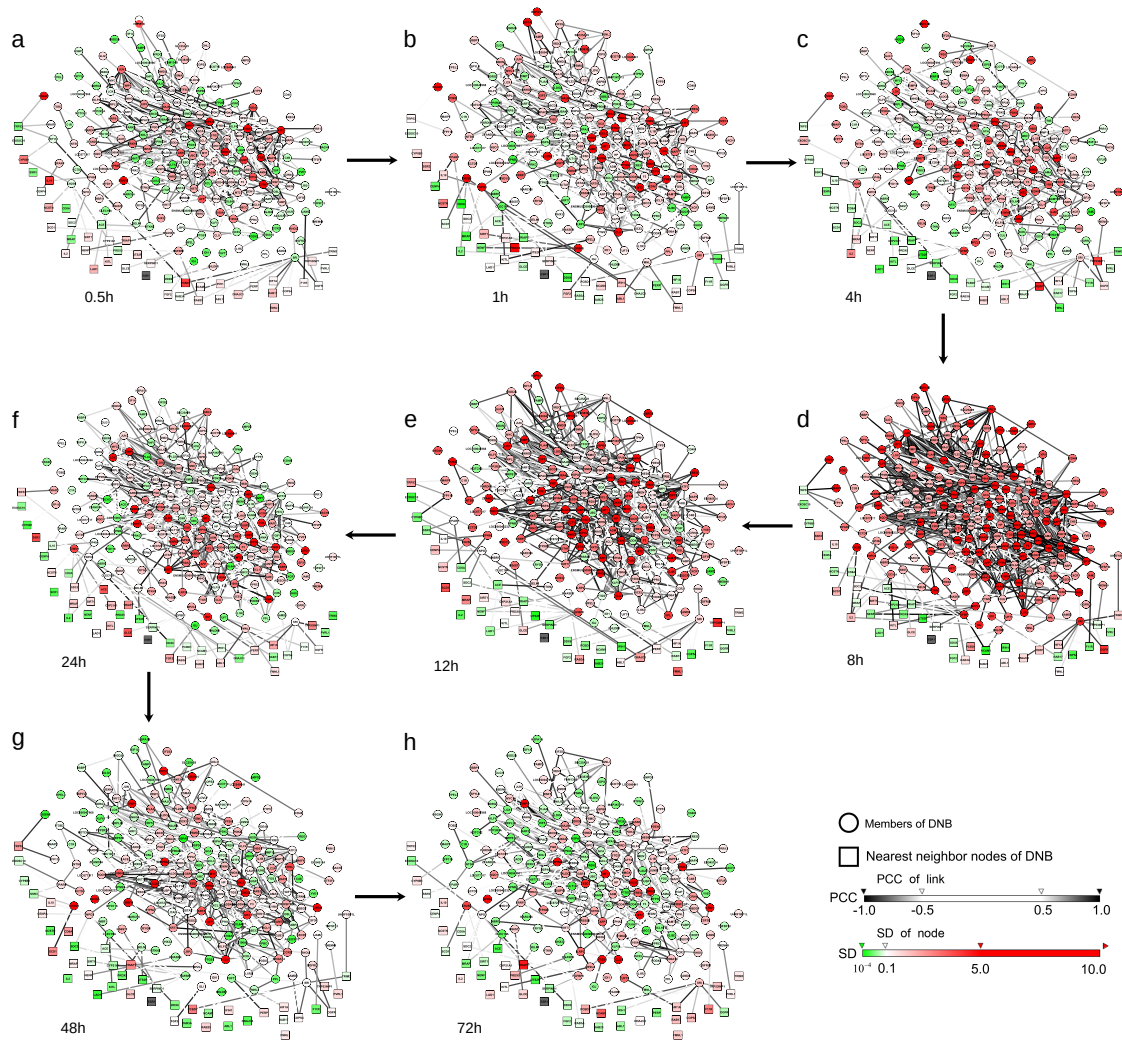


Figure S8: | Dynamic changes in the DNB (220 genes and 1167 links) subnetwork for acute lung injury at 8 time instants. For acute lung injury, we show the dynamic evolution of the network structure for the identified DNB subnetwork at 8 time instants. **(a)** The DNB at 0.5h. **(b)** The DNB at 1h. **(c)** The DNB at 4h. **(d)** The DNB at 8h. **(e)** The DNB at 12h. **(f)** The DNB at 24h. **(g)** The DNB at 48h. **(h)** The DNB at 72h. From these figures showing the dynamic evolution, it is obvious that the group of DNB not only provides significant signals as the system approaches the critical point, but also forms a strongly correlated observable subnetwork in terms of expression variations and network connections. The interactions in the network are based on the mouse molecular interaction network (protein-protein interactions and TF-target regulations) and gene expressions.

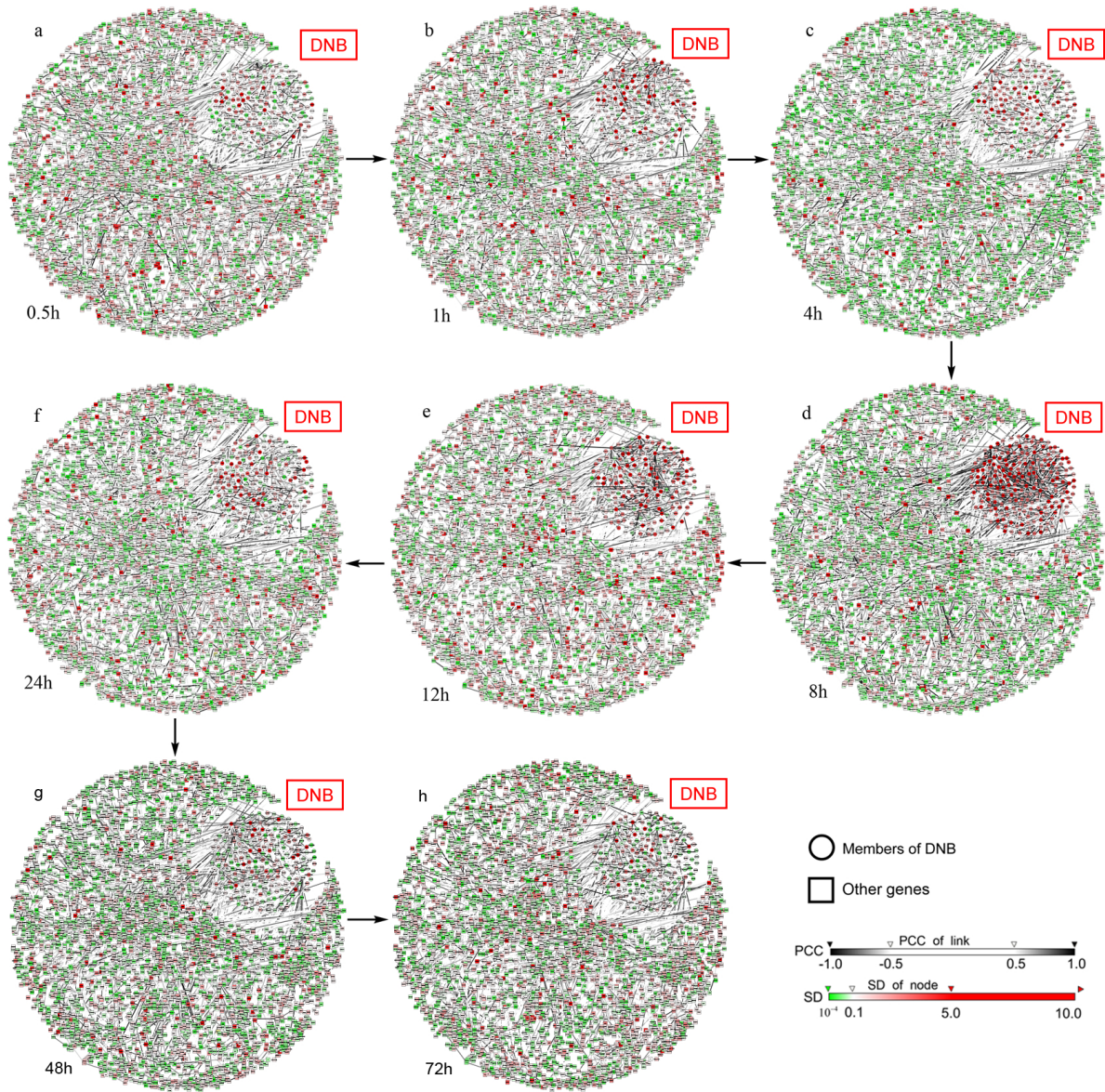


Figure S9: | Dynamical changes in the whole mouse network (3452 genes and 9238 links) including the detected DNB during the disease progression for acute lung injury. For acute lung injury, we show the dynamical evolution of the network structure for the whole mouse molecular interaction network (protein-protein interactions and TF-target regulations) including the identified DNB subnetwork. **(a)** Molecular network at 0.5h. **(b)** Molecular network at 1h. **(c)** Molecular network at 4h. **(d)** Molecular network at 8h. **(e)** Molecular network at 12h. **(f)** Molecular network at 24h. **(g)** Molecular network at 48h. **(h)** Molecular network at 72h. The network is constructed from the whole mapped mouse molecular interaction network (protein-protein interactions and TF-target regulations) based on the expression data.

sions.

2. Based on the links or interactions in the mapped network, 8000 links were chosen randomly after scrambling the gene order 5 times.
3. We then added the DNB subnetwork into the above mapped network, and removed the redundant links. 9238 links were left. By indicating the PCC values of each link and marking the standard deviations on nodes, we obtained the final network at each time instant.
4. All maps were constructed using Cytoscape (<http://www.cytoscape.org/>).

To compare the dynamics of the DNB with other genes, the dynamic process of the whole network including the DNB is also shown in Fig.S9, which clearly shows the significant signal of the DNB in the pre-disease state (8 h). In particular, before the disease state, there are no significant differences between the members of the DNB and other genes at all periods except at 8 h, during which the members of the DNB behave in a considerably different manner in terms of their expression variations and network connections by satisfying the three criteria. However, after the system is driven into the disease state, interestingly, the members of the DNB seem to behave in a manner similar to other genes again (e.g., figures for 24 h, 48 h and 72 h, i.e., Figs.S9 f, g and h). We list all the identified DNB members in the Supplementary Table ‘Identified DNBs’ and present the detailed functional analysis as well as KEGG enrichment analysis in Section F.

D.2 Dataset 2. Genomic data about the hepatic lesion caused by chronic hepatitis B (i.e., HBV induced liver cancer)

The data about hepatic lesion caused by chronic hepatitis B were obtained by courtesy of Drs. Masao Honda and Shuichi Kaneko of Kanazawa University, Japan. The details of the experi-

Table.S2 Clinical and virological characteristics of patients with hepatic lesion caused by chronic hepatitis B (or HBV induced liver cancer). (The detailed information can be available in Table 1 of (25).)

Clinical diagnosis	Patient no.	Age (yr)	Sex (M:F)	HBEAg/ HBsAg (+/+)	ALT at biopsy (IU/L)	Estimated duration of chronicity (yr)
Normal	6	57 $\pm$ 6	4:2	ND/0	27 $\pm$ 4	NA
Chronic hepatitis B	12	43 $\pm$ 16	10:2	6/12	67 $\pm$ 15	26 $\pm$ 4

ment are available in their original paper (25). In the analysis (25), the authors made gene expression microarrays and analyzed the gene expressions using labeled cDNAs prepared partly from 6 normal and 12 chronic hepatitis B liver tissues. The grading and staging of chronic hepatitis were histologically assessed according to the method described in (27)– (31). Some of the data description and the disease progression are shown in Table S2.

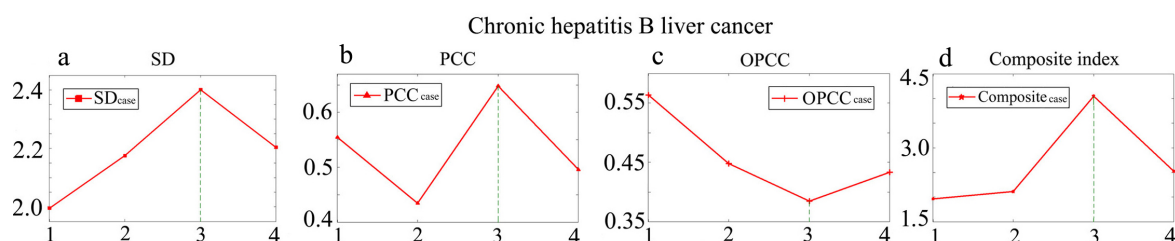


Figure S10: | **Early-warning signals for HBV induced liver cancer.** In all figures, the horizontal axis represents the time period t . (a) Mean SD in the DNB. (b) Mean PCC in the DNB. (c) Mean PCC between the DNB and other molecules (OPCC). (d) Composite index of the DNB. The dotted green line indicates the pre-disease period. Clearly, the composite index drastically increases from the second period (the F2 period), and reaches the peak in the third period (F3 period), meanwhile the OPCC decreases to the lowest level in the F3 period. These indices show that the pre-disease state is near the F3 period. The predicted result is consistent with the physiological data (see the original paper (25)).

Early-warning signals of the HBV induced liver cancer based on the DNB (42 nodes) are shown in Fig.S10, which indicates that the pre-disease state exists around the F3 period and the system transitions to the disease state after the F3 period. In addition, in order to show the detailed progression of the DNB group along the sampling time series, we presented the

dynamic process of the DNB for 4 sampling points (see Fig.S11). From these figures, which show the dynamic evolution, it is obviously that the DNB subnetwork is strongly correlated and provides significant signals as the system approaches the critical point. We list all the identified DNB members in the Supplementary Table ‘Identified DNBs’ and present a detailed functional analysis as well as the KEGG enrichment analysis in Section F.

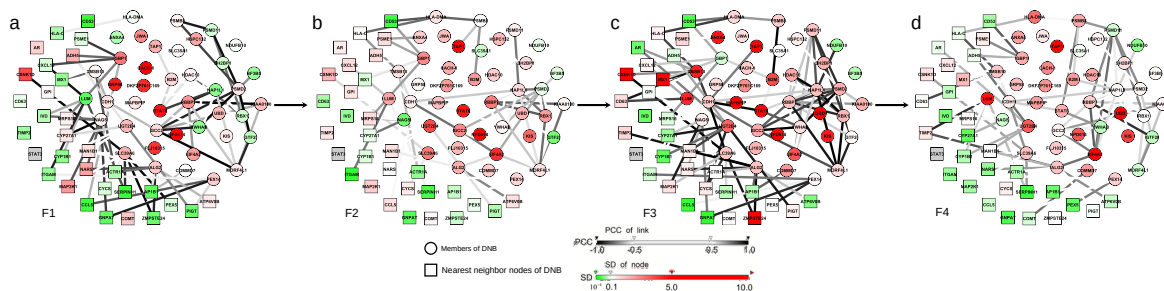


Figure S11: | **Dynamic changes in the identified DNB (42 genes and 90 links) for HBV induced liver cancer with 4 sampling points.** For HBV induced liver cancer, we show the dynamic evolution of the network structure for the identified DNB at 4 time instants. **(a)** The DNB at F1. **(b)** The DNB at F2. **(c)** The DNB at F3. **(d)** The DNB at F4.

D.3 Dataset 3. Genomic data about transgenic B-cell lymphomagenesis (i.e., lymphoma)

In the DNB of the B-cell lymphomagenesis, we found that the dysfunctional processes are also highly correlated to the signal transduction of the disease state. Previous studies have suggested that translocation plays an important role in B-cell lymphoma pathogenesis (26). Our results also indicated significant changes in abnormal translocation and transcription, such as that of *TOPBP1* and *AIFM1*. Moreover, genes regulating cell communication, such as *STRAP* and *RGS14*, and those regulating inflammatory response, such as *GPX1*, were expressed in a disorderly manner. Furthermore, some genes related to the formation of blood vessel for nutrition of tumor development, such as *GPX1*, became significantly disorder during disease progression. Among 22 genes and TFs in the identified DNB, 13 of them (p -value < 6.87e-

05) have been validated to be significantly related to B-cell lymphomagenesis. In particular, 8 out of the 13 genes have been treated as the master regulators of proliferation (Supplementary Table 'Identified DNBs'). The detailed functional analysis of the three diseases is presented in Supplementary Information E.

Table.S3 Clinical and pathological characteristics of samples for transgenic B-cell lymphomagenesis (or lymphoma). (The detailed information is available in Table 1 of (26).)

Group	Samples	Description	Splenomegaly	Flow Cytometry
P1	5	Resting	None	Normal resting
P2	3	Activated	None	Normal activated
P3	6	Marginal	+/-	Abnormal
P4	5	Transitional	+	Mixed
P5	7	Aggressive	+++	B-1 clones

In order to illustrate that the lymphoma is not only with rampant cellular proliferation but also involves additional transcriptional mobilization of many genes, the researchers compared the genome-wide transcriptional expression profiles of lymphomas with those of proliferating and resting normal B-cells. In this experiment (26), 26 samples of the whole genome expression profiles were generated. Based on clinical presentation, pathology and flow cytometry, the samples have been grouped into five major periods: P1, a normal resting period; P2, a normal activated period; P3, a marginal cases period; P4, a transitional cases period; and P5, an aggressive cases period, as summarized in Table S3.

According to the experimental data (26), we used the data from the normal resting period as the control group and data from other periods as the case group. The calculated early-warning signals of the B-cell lymphomagenesis based on the DNB (20 genes) are shown in Fig.S12, which indicates that the pre-disease state exists around the normal activated period, and the system transitions to the disease state around the transitional lymphoma period.

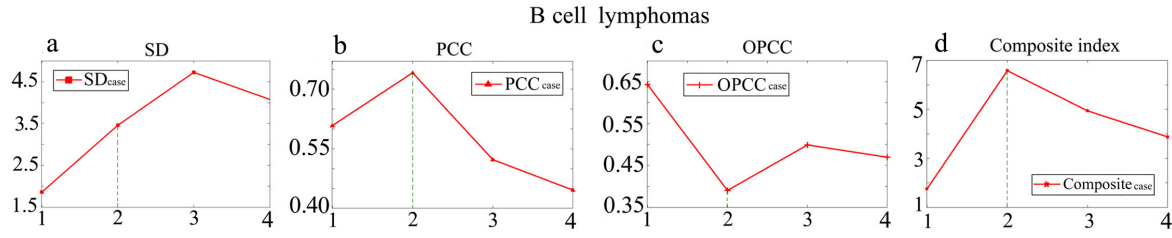


Figure S12: | **Early-warning signals for B-Cell Lymphomagenesis.** In all figures, the horizontal axis represents the time period t . **(a)** Mean SD in the DNB. **(b)** Mean PCC in the DNB. **(c)** Mean PCC between the DNB and other molecules (OPCC). **(d)** Composite index of the DNB. The dotted green line indicates the pre-disease period. Clearly, the composite index reaches the peak in the second period, which suggests that the pre-disease state is around the second period.

E Bootstrap analysis

In order to verify the biological and statistical significance of the DNB group, we carried out bootstrap analysis for the three diseases described in Section D. For each disease, we randomly chose 10 gene sets, each of which possesses the same number of members as the DNB group (see Table S4 for acute lung injury). Then, we calculated the three criteria for each gene set. We show the corresponding curves for the acute lung injury in Fig.S13e-h.

From the bootstrap results, it is obvious that the DNB group has the most significant signal, compared with the randomly chosen gene sets for the acute lung injury. For the other two diseases, we obtained a similar result as that of the acute lung injury. This provides evidence of the physiological importance of the DNB as well as the effectiveness of our proposed method.

Table.S4 Information about the bootstrap analysis for acute lung injury (the number overlapped with DNB).

	Sample 1	Sample 2	Sample 3	Sample 4	Sample 5	Sample 6	Sample 7	Sample 8	Sample 9	Sample 10
Overlap	6	3	2	0	3	4	2	3	4	5
Mean overlap:	3.2									

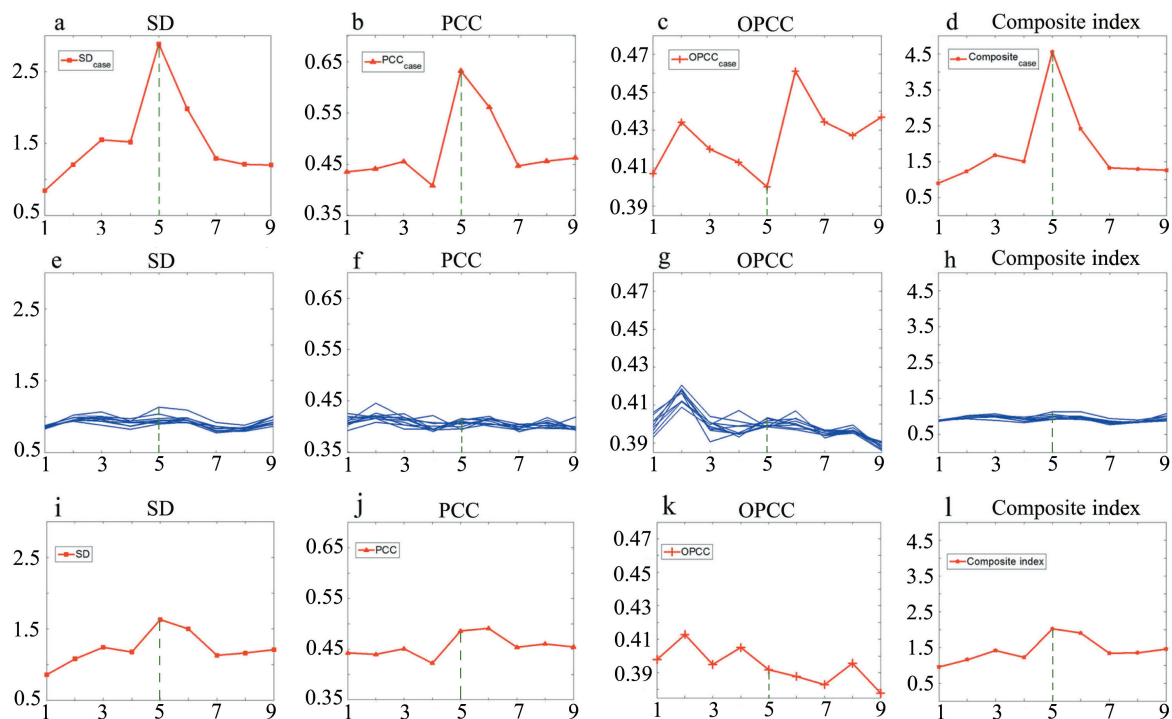


Figure S13: | **Comparison results of the DNB-based method, bootstrap analysis, and fold-change analysis.** In order to show the biological significance, we compared our method with the existing methods for acute lung injury. **(a)** Mean standard deviation (SD) for the case group data of the identified DNB. **(b)** Mean PCC for the case group data of the identified DNB. **(c)** Mean OPCC for the case group data of the identified DNB. **(d)** Composite index for the case group data of the identified DNB. **(e)** Mean standard deviation (SD) for the 10 sets of randomly selected genes (bootstrap analysis); each set of them has the same number of members as the identified DNB group. **(f)** Mean PCC for the 10 sets of randomly selected genes (bootstrap analysis). **(g)** Mean OPCC for the 10 sets of randomly selected genes (bootstrap analysis). **(h)** Composite indices for the 10 sets of randomly selected genes (bootstrap analysis). **(i)** SD by fold-change analysis. **(j)** PCC by fold-change analysis. **(k)** OPCC by fold-change analysis. **(l)** Composite index by fold-change analysis. The dotted green line indicates the pre-disease period.

F Functional analysis of the DNB

We identified the DNBs from the three high-throughput gene expression profiling datasets for phosgene-induced lung injury (or acute lung injury), hepatitis B virus (HBV) infection (or HBV induced liver cancer), and B-cell lymphomagenesis (or lymphoma) using our algorithm. This section provides detailed information about the data preprocessing and functional analyses of these DNBs for the three diseases.

It should be noted that the DNB subnetwork is not a set of disease genes or driving factors, but is used to provide the early-warning signal of the pre-disease state based on its dynamical features from observable data. However, some DNB members may be considerably relevant to the disease biomarkers, which were actually verified by the functional analysis. As shown in this section, we found that some reported disease-related genes are also included in the DNB. The other unreported molecules may be considered as novel candidates for indicating the disease. From this viewpoint, the DNB subnetwork also provides a clue to find new candidate biomarkers.

F.1 Data preprocessing

The gene expression profiling data were downloaded from the NCBI GEO (www.ncbi.nlm.nih.gov/geo) database (GSE6136, GSE2565) and obtained from the original authors (25). For the three datasets, a gene will not be considered in our analysis if it has a missing value in the samples or no correct corresponding symbol. The probe sets were mapped to the corresponding NCBI Entrez Gene symbols using the GEO annotation. If there are multiple probe sets corresponding to the same gene, we averaged them individually.

F.2 Functional linkage networks or molecular interaction networks

We identified the DNBs of three complex diseases individually. The published evidence suggests that many TFs may be the causal factors for target genes with large differential expressions. Thus, the TFs whose targets are in the identified DNB have been added, forming an extended DNB. The members (including genes and TFs) in the identified DNBs have been linked and correlated by the combined functional linkages among them from various databases of protein-protein interactions of STRING (string-db.org), FunCoup (funcoup.sbc.su.se), and BioGrid (thebiogrid.org), transcriptional regulations of TRED (rulai.cshl.edu/cgi-bin/TRED/tred.cgi?process=home), and metabolic pathways of KEGG (www.genome.jp/kegg). The molecular interaction network among these genes of each DNB is built as follows. First, we downloaded the available protein/gene linkage information of *Mus Musculus* and *Homo Sapiens* from STRING, FunCoup, BioGrid, TRED, and KEGG. We combined them without redundancy to obtain 3188881 functional linkages in 20868 proteins of human and 1729824 functional linkages in 17911 proteins of mouse. Then, the genes of the three DNBs were mapped into the integrated functional linkages, and their related functional linkages were extracted individually for the corresponding species. Finally, the extracted linkages of each DNB were integrated together to form a network of gene-linked DNB and visualized by Cytoscape. There are some DNB proteins that cannot be found directly by functional linkages. Thus, we added some of their neighbor proteins with high PCC to relate and connect them into a network. In total, there are 1443 interactions in 262 proteins including 47 TFs, 153 interactions in 56 proteins including 15 TFs, and 88 interactions in 22 proteins including 2 TFs in the DNB networks of lung injury, HBV infection, and B-cell lymphomas, respectively.

F.3 Acute lung injury

The phosgene-induced physiological experiment generated the genome-wide expressions of the case and control mice from the normal stage to the lung injury stage, *i.e.*, the expression data described the disease genesis process and were suitable for validating our theory. The detailed information of the experiment and the pathogenic mechanism can be referred to the original paper (24). In our results, the strongest signal of the transition point is obtained at 8 h, which is the critical point, and the identified genes by our method form a DNB. Interestingly, the pathway enrichment analysis and the GO functional analysis of genes (see Table 1 in main text and the Supplementary Table ‘KEGG enrichment analysis’) in the identified DNB are consistent with the identified mechanism of phosgene-induced lung injury, especially the parts pertaining to antioxidant reactions, response of DNA damage, metabolic processes, regulation of immune systems processes, and regulations of the cell cycle (24). Meanwhile, we also chose some significant genes and briefly explained their functions in the main text. *GCLC* and *ASNS*, which are associated with glutamine-metabolic activities, and *SRXN1*, *PGD*, *TXNLI*, *HMOX1*, *CYP51*, and *CH25H*, which participate in oxidation reduction, may protect against the oxidant-like activity of phosgene (24, 33). Moreover, some genes related to the regulation of inflammatory response and the response to wounding are abnormally active, *e.g.*, *ADM*, *LOX*, and *IL1B*, and these may be induced by tissue damage and irritation. Because of the denaturation of lipoids and proteins, many genes participating in cellular metabolism also become increasingly active. Furthermore, there are well-known genes regulating apoptosis, such as *MYC*, *JUN*, *FOSL1*, and *NOTCH2*, which may reduce the number of injured cells. Finally, we compared members in the DNB network with the genes identified by the previous study and with a Bonferroni-corrected $p < 0.001$ based on a three-way mixed model of ANOVA by Onto-Express. 43 out of the 262 members (hypergeometric test, p -value $< 7.89\text{e-}36$) have been validated with significantly close correlation with phosgene-induced lung injury (Supplementary Table ‘KEGG enrichment

analysis’).

F.4 HBV induced liver cancer

It is known that hepatitis B virus (HBV) can cause the disease hepatitis B and even lead to cirrhosis and hepatocellular carcinoma (HCC). The HBV life cycle between infecting the host and the host’s response to protect against HBV has also been studied (25, 32).

Based on the process of hepatitis B disease progression, we can identify the critical signals of phase transition using our method. We found that many genes in the DNB are related closely to the response of HBV infection *in vivo*, especially in the response of the immune system and dysfunctions associated with its performance in the life cycle (32). The results of pathway and GO functional enrichment analysis are shown in the Supplementary Table ‘KEGG enrichment analysis’. Based on our criteria, the genes in the DNB are significantly important for disease development. As mentioned above in the process of HBV infection, most parts of the functional analysis results validated the significant correlation between the disease evolution and the selected DNB. At the pathway enrichment level, the pathway of cancer and that of hepatitis C exist in the top 10, which directly indicates the close correlation between the DNB and this disease. Meanwhile, many other pathways related to immune system reactions (such as antigen processing and presentation and B-cell receptor signaling pathway), response to DNA abnormalities (cytosolic DNA-sensing pathway), and so on were listed in the result. *STAT6* is associated with the production of the corresponding antibody and the switch of antibody isotypes, which is consistent with the transition of antibodies in the virus infection period. *MORF4L1* is required for the activation of transcriptional programs and replicative senescence, apoptosis, and DNA repair. *RBX1* encodes ring-box 1, E3 ubiquitin protein ligase1 which interacts with cullin proteins. They play important roles in ubiquitination processes necessary for cell cycle progression, which contribute to the removal of infected cells (25, 32). Some genes

were also expressed in a disorder manner, which resulted from the HBV infection, especially the replication, transcription, translation and transport reactions. In particular, *TAPI*, *GCC2*, *CDH1* and *UGT2B4* help the viral proteins translate effectively and enable their entrance and release. *CDH1* has been validated to be the target of HBV X protein. The proteins encoded by *YWHAB* mediate signal transduction by binding to phosphoserine-containing proteins, which link the mitogenic signaling and cell cycle machinery. *RBBP7*, *HDAC10* and *NAP1L1* are associated with chromatin assembly and further regulate, and even participate in DNA replication and transcription, which helps the viral genomic replication (32). The genes in the identified DNB play crucial roles in the progression of HBV infection. 17 out of 56 members (p -value < 8.51e-04) have been identified as differential expression genes.

F.5 B-cell lymphomagenesis

B-cell lymphomagenesis has many subtypes. The data for this disease were obtained from the work by Lenburg *et al.* (26). The experimental model is the *E μ -BRD2* transgenic (Tg) mouse for diffusing large cell lymphoma (DLCL) which develops mature B-cell lymphomas with monoclonal immunoglobulin (Ig) genes after 28 weeks.

From the functional analysis of the identified DNB (Supplementary Table ‘Identified DNBs’), we found that the dysfunctional processes are strongly related to the signal transduction of disease states. As noted in the main text, the DNB genes are closely related to a dysfunctional immune system in that they respond to DNA damage and regulation of cell death, reflecting the significant changes in the disease state. The pathway enrichment to some extent reflected the mechanisms of B-cell lymphomagenesis, although the DNB provided such a small number of candidates that the pathway enrichment information was insufficient. However, the gene functional analysis also provided some evidence to show the relationship between DNB and this disease evolution. In particular, *TOPBP1* was expressed in a disorder manner, and the abnor-

mal phenomenon may result from DNA damage or abnormal translocation affected by B-cell lymphomas. *AIFM1* plays an important role in the death-receptor-induced apoptosis and in the general transcription machinery in the nucleus. The genes *IFT57* and *GPX1* participate in apoptosis, which is useful in reducing the number of irregular cells. Moreover, it is well known that the lymphomagenesis requires nutrition for forming new blood vessels more actively (26, 34). We actually found that these genes related to cellular metabolic processes and even to the disorder of blood vessels. In addition, 13 out of the 22 members (hypergeometric test, p -value $< 6.87\text{e-}05$) have been validated to be significantly related to B-cell lymphomas. In particular, 8 out of the 13 genes are validated as the master regulators of proliferation in germinal centers (34). It should be noted that compared to the other two diseases, the deterioration of B-cell lymphomagenesis appears to be much slower, and therefore the DNB signal is not so strong. One reason for this is that the sample size is too small to detect this critical transition, and the other is that our method assumes that the disease has drastic change from one state to another, which may not be the case with this disease.

Finally, it is noteworthy that because the samples are scarce, the DNB obtained above contains a number of molecules. However, with regard to clinical tests, the DNB is expected to be smaller with the increasing sample size.

G Fold-change analysis of disease data

One of the major targets in this work is to provide criteria to identify the pre-disease state, i.e., derive the conditions or criteria for the DNB. Theoretically, three criteria or conditions were derived from center manifold theory, and they are actually independent of numerical methods. In other words, there may exist many ways to numerically compute a DNB provided that they are based on our three new criteria, including the fold-change based method if it is effective. Here, we also tested the fold-change method for the data of the acute lung injury as shown in

Fig.S13. Clearly, all of those results also indicate the superiority of our numerical method (see Figs.S13 i-l although the fold-change also shows certain (non significant) signals (when using our new criteria). Specifically, for fold-change analysis, one criterion (i.e., Fig.S13i) reaches its peak in the pre-disease state, but the other two criteria are not at the maximum (Fig.S13j) and the minimum (Fig.S13k) at the pre-disease state. Note that Figs.S13 d, h and l are composite indices for detecting the pre-disease state, and (a, e, i), (b, f, j), and (c, g, k) in Figs.S13 correspond to the three criteria (i.e., internal-SD, internal-PCC, and outer-PCC) of the DNB respectively.

The procedure of the fold-change analysis is as follows. First, we applied fold change to the acute lung injury data of each sampling point to screen out molecules with significant differential expressions, that is, by setting the threshold two-fold in each time instant, we compared the differential expression of case-group data with that of control-group data. Then, we obtained nine groups of the selected genes for 9 time points. There is almost no overlap (only 4 genes) of the molecules for these nine groups with the gene expression data, and therefore we took the union of the genes in the nine groups (529 genes in total) to calculate SD, PCC, OPCC and the composite index as shown in Figs.S13i-l.

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H Supplementary Table ‘Identified DNBs’

See the Supplementary Table ‘Identified DNBs’ attached after the References.

I Supplementary Table ‘KEGG Enrichment analysis’

See the attached Supplementary Table ‘KEGG Enrichment analysis’ (After ‘Identified DNBs’).

J Supporting programme

See the attached Supporting programme (After ‘KEGG Enrichment analysis’).

Supplementary Table `Identified DNBs`

Identified DNB of Lung injury

Sample Name	Members Of DNB	GO: Term	P-value	Corrected P-value		R	T	G	O	Term Name	Contain Genes
Phosgene Inhalation	PHLDB1; E2F-2; MARCH6; CXCR7; ALS2CR13; SPNB2; GNL3; BTG2; ABCD3; SP3; C4B; EDN1; PPL; HOXB1; TCFAP2A; RTKN2; GSR; ZFP281; SERPINE1; WT1; BACH1; MPZL2; GTF2F2; PRSS22; UHRF1BP1L; HSPB8; TGIF1; C-MYC; USF2; TRIB3; MEN1; LOX; GP49A; RELB; NEDD4L; EGG667723; DHX32; CIR; REL; HMOX1; CEBPD; OGFRL1; FAM134B; TUFT1; PRR13; ZFP36; CCR2; GADD45G; TUBA4A;CLEC16A; ; TOB2; SULT1A1; CDKN1A; PPARA; TRP53; HOXA1; MT1; SAMD8; HSPA1B; TBC1D15; ANGPTL4; CSF3R; S100A14; EG383901; DNAJB4; BRCA1; FABP4; ADAMTS4; KRT8; E2F-1; LOC100047896; LOC640441; LRG1; ETV4; PDK2; STAT3; ADM; SRXN1; SLC25A29; COL6A3; SNHG6; EPHA2; GADD45A; INTS6; SELM; RHOU; ARF3; SMAD3; SNHG1; ATF3; PTGS2; TALD01; EIF5; DUSP1; EIF2S2; ENSMUSG00000040078; YRDC; LOC100046232; OSGIN1; NFKB1; FMNL3; ABCC1; NQO1; CYP51; NDRG1; SP1; HSPA9; IL1B; IMPACT; IL1R2; GSTA2; NOTCH2; TNPO3; DNAJC5; HOXC8; HES6; SRI; JUND1; DUSP16;	GO:0009987	4.20E-48	8.30E-45	BP	32911	228	8758	166	cellular process	SPNB2; BTG2; ABCD3; SP3; EDN1; HOXB1; TCFAP2A; GSR; WT1; BACH1; MPZL2; GTF2F2; TGIF1; TUBA4A; REL; HMOX1; CEBPD; PRR13; ZFP36; TRIB3; MEN1; LOX; RELB; NEDD4L; USF2; GADD45G; CCR2; SULT1A1; CDKN1A; PPARA; TRP53; HOXA1; MT1; SAMD8; HSPA1B; CSF3R; DNAJB4; BRCA1; FABP4; KRT8; LRG1; ETV4; PDK2; STAT3; ADM; SLC25A29; EPHA2; GADD45A; RHOU; ARF3; SMAD3; ATF3; PTGS2; TALD01; EIF5; DUSP1; EIF2S2; NFKB1; FMNL3; ABCC1; CYP51; NDRG1; SP1; HSPA9; IL1B; GSTA2; NOTCH2; DNAJC5; HOXC8; HES6; DUSP16; TUBB2C; LYVE1; CREB1; HSPA1A; EREG; HSPD1; HBEGF; MT2; PRKCI; PTPN21; FOS; TXNL1; JUNB; PTGS1; TIPARP; PTPN14; GTF3C1; PODXL; HS6ST1; MAFK; CLU; ERRF1; IDI1; EIF1A; KLF5; TSPYL4; AREG; MRPL28; PPA1; CEBPB; DDX39; BCL10; NFIC; MYC; THBS1; JUN; VAMP5; MRPS12; SOCS3; TXNRD1; TIMP1; SP2; AR; PRDX1; ACOT10; PGD; LRP2; ATF1; CEBPE; HSP90AB1; ETS1; LAMA3; PMAIP1; ASNS; ALDOA; TNFRSF12A; PPARG; CYR61; MAFF; ATF4; IFRD1; PDK4; PSMA5; RELA; HIF1A; FOSL1; HSPA8; RARB; AMPD3; STAT1; MYBL2; GCLC; PARD6B; GJB3; YPEL3; CH25H; SFP11; RPL22L1; EGR1; SLC2A1; CD48; LITAF; AFP; CEBPA; TNFSF12; USF1; PDE4B; HSP90AA1; ELOVL7; FGFBP1; S100A9; PPRC1; KLF6; KLF4; MYB
	GO:0048518	4.70E-42	9.20E-39	BP	32911	228	1851	80	positive regulation of biological process	BTG2; C4B; EDN1; HOXB1; RTKN2; SERPINE1; WT1; GTF2F2; TGIF1; REL; HMOX1; CEBPD; TRIB3; MEN1; RELB; USF2; CCR2; TOB2; CDKN1A; PPARA; TRP53; HOXA1; HSPA1B; BRCA1; FABP4; ETV4; STAT3; ADM; SMAD3; ATF3; PTGS2; DUSP1; NFKB1; ABCC1; NQO1; SP1; IL1B; NOTCH2; CREB1; EREG; HSPD1; HBEGF; PRKCI; FOS; JUNB; PTGS1; F3; CLU; KLF5; AREG; CEBPB; BCL10; NFIC; MYC; THBS1; JUN; SOCS3; AR; PRDX1; ATF1; ETS1; PMAIP1; TNFRSF12A; PPARG; CYR61; ATF4; RELA; HIF1A; FOSL1; RARB; STAT1; GCLC; SFP11; EGR1; CEBPA; USF1; HSP90AA1; FGFBP1; KLF6; KLF4	
	GO:0048522	6.80E-40	1.30E-36	BP	32911	228	1639	74	positive regulation of cellular process	EDN1; HOXB1; RTKN2; SERPINE1; WT1; GTF2F2; TGIF1; REL; HMOX1; CEBPD; TRIB3; MEN1; USF2; CCR2; CDKN1A; PPARA; TRP53; HOXA1; BRCA1; FABP4; ETV4; STAT3; ADM; SMAD3; ATF3; PTGS2; DUSP1; NFKB1; ABCC1; NQO1; SP1; IL1B; NOTCH2; CREB1; EREG; HSPD1; HBEGF; PRKCI; FOS; JUNB; F3; CLU; KLF5; AREG; CEBPB; BCL10; NFIC; MYC; THBS1; JUN; SOCS3; AR; PRDX1; ATF1; ETS1; PMAIP1; TNFRSF12A; PPARG; CYR61; ATF4; RELA; HIF1A; FOSL1; RARB; STAT1; GCLC; SFP11; EGR1; CEBPA; USF1; HSP90AA1; FGFBP1; KLF6; KLF4	
	GO:0008152	6.40E-39	1.20E-35	BP	32911	228	6447	134	metabolic process	SPNB2; BTG2; SP3; C4B; HOXB1; TCFAP2A; GSR; WT1; BACH1; GTF2F2; PRSS22; TGIF1; REL; HMOX1; CEBPD; PRR13; ZFP36; TRIB3; MEN1; LOX; RELB; NEDD4L; USF2; GADD45G; SULT1A1; PPARA; TRP53; HOXA1; SAMD8; HSPA1B; DNAJB4; BRCA1; FABP4; ADAMTS4; ETV4; PDK2; STAT3; ADM; SRXN1; EPHA2; RHOU; SMAD3; ATF3; PTGS2; TALD01; EIF5; DUSP1; EIF2S2; NFKB1; NQO1; CYP51; SP1; HSPA9; GSTA2; NOTCH2; DNAJC5; HOXC8; HES6; DUSP16; LYVE1; CREB1; HSPA1A; HSPD1; PRKCI; PTPN21; FOS; TXNL1; JUNB; PTGS1; TIPARP; PTPN14; GTF3C1; ESD; GPX2; HS6ST1; MAFK; IDI1; EIF1A; KLF5; TINAGL1; MRPL28; PPA1; CEBPB; DDX39; BCL10; NFIC; MYC; JUN; MRPS12; TXNRD1; SP2; AR; PRDX1; ACOT10; PGD; LRP2; ATF1; CEBPE; HSP90AB1; ETS1; ASNS; ALDOA; PPARG; CHI3L1; MAFF; ATF4; PDK4; PSMA5; RELA; HIF1A; HSPA8; RARB; PSMC1; AMPD3; STAT1; MYBL2; GCLC; CH25H; SFP11; RPL22L1; EGR1; LITAF; AFP; CEBPA; USF1; PDE4B; HSP90AA1; ELOVL7; PPRC1; KLF6; KLF4; MMP11; MYB; HP	

TUBB2C; RNASEK; LYVE1; CREB1; HSPA1A; EREG; HSPD1; HBEGF; MT2; PRKCI; PTPN21; FOS; TXNL1; CREG1; ZFAND2A; JUNB; PTGS1; TIPARP; PTPN14; F3; GTF3C1; PODXL; ESD; ZFP110; GPX2; MARCH6; HS6ST1; LOC677317; MAFK; CRYGN; CLU; LACE1; UBXN4; PSMD3; ERRFI1; IDI1; EIF1A; KLF5; NMD3; TSPYL4; LOC672215; AREG; LOC100047601; TINAGL1; SLC20A1; MRPL28; PPP2R2A; PPA1; CEBPB; HIGD2A; DDX39; BCL10; NFIC; E2F; SCEL; MYC; THBS1; JUN; VAMP5; MRPS12; SOCS3; CXCL16; TXNRD1; TIMP1; JAM2; SP2; S100A8; AR; RNF5; PRDX1; ACOT10; PLAUR; PGD; LRP2; ATF1; CEBPE; HSP90AB1; ETS1; LAMA3; PMAIP1; ASNS; ALDOA; PLAA; TNFRSF12A; PPARG; CYR61; CHI3L1; MAFF; ATF4; COPS3; IFRD1; KCTD9; GCA; GLG1; NBR1; CCRN4L; PDK4; LOC100047868; EG545124; PSMA5; HSBP1; RELA; HIF1A; FOSL1; HSPA8; RARB; PSMC1; AMPD3; STAT1; MYBL2; CARMD; GCLC; TMEM49; MYD116; PARD6B; GJB3; YPEL3; CH25H; SFPI1; RPL22L1; EGR1; SLC2A1; IGJ; CD48; LITAF; AFP; CEBPA; MAP3K7IP3; TNFSF12; USF1; PDE4B; UBC; HSP90AA1; ELOVL7; FGFBP1; KRT7; S100A9; PPRC1; KLF6; KLF4; SERPINA3N; MMP11; MYB; HP	GO:0065007	7.70E-37	1.50E-33	BP	32911	228	7046	137	biological regulation	CXCR7; SPNB2; GNL3; BTG2; SP3; C4B; EDN1; HOXB1; TCFAP2A; RTKN2; GSR; SERPINE1; WT1; BACH1; GTF2F2; TGIF1; REL; HMOX1; CEBPD; PRR13; ZFP36; TRIB3; MEN1; RELB; NEDD4L; USF2; GADD45G; CCR2; TOB2; SULT1A1; CDKN1A; PPARA; TRP53; HOXA1; MT1; HSPA1B; TBC1D15; ANGPTL4; BRCA1; FABP4; ETV4; PDK2; STAT3; ADM; EPHA2; GADD45A; RHOU; ARF3; SMAD3; ATF3; PTGS2; DUSP1; YRDC; NFKB1; ABCC1; NQO1; SP1; IL1B; IMPACT; NOTCH2; DNAJC5; HOXC8; HES6; DUSP16; LYVE1; CREB1; HSPA1A; EREG; HSPD1; HBEGF; MT2; PRKCI; FOS; TXNL1; CREG1; JUNB; PTGS1; TIPARP; F3; PODXL; GPX2; MAFK; CLU; PSMD3; ERRFI1; KLF5; AREG; MRPL28; PPP2R2A; CEBPB; BCL10; NFIC; MYC; THBS1; JUN; SOCS3; CXCL16; TXNRD1; TIMP1; SP2; AR; PRDX1; LRP2; ATF1; CEBPE; ETS1; LAMA3; PMAIP1; PLAA; TNFRSF12A; PPARG; CYR61; MAFF; ATF4; PDK4; RELA; HIF1A; FOSL1; HSPA8; RARB; STAT1; MYBL2; GCLC; SFPI1; EGR1; CD48; LITAF; AFP; CEBPA; USF1; HSP90AA1; FGFBP1; S100A9; PPRC1; KLF6; KLF4; MYB
GO:0044237	4.40E-36	8.60E-33	BP	32911	228	5339	119	cellular metabolic process	SPNB2; BTG2; SP3; HOXB1; TCFAP2A; GSR; WT1; BACH1; GTF2F2; TGIF1; REL; HMOX1; CEBPD; PRR13; ZFP36; TRIB3; MEN1; RELB; NEDD4L; USF2; GADD45G; SULT1A1; PPARA; TRP53; HOXA1; SAMD8; HSPA1B; DNAJB4; BRCA1; FABP4; ETV4; PDK2; STAT3; ADM; EPHA2; RHOU; SMAD3; ATF3; PTGS2; TALDO1; EIF5; DUSP1; EIF2S2; NFKB1; CYP51; SP1; HSPA9; GSTA2; NOTCH2; DNAJC5; HOXC8; HES6; DUSP16; CREB1; HSPA1A; HSPD1; PRKCI; PTPN21; FOS; TXNL1; JUNB; PTGS1; TIPARP; PTPN14; GTF3C1; HS6ST1; MAFK; IDI1; EIF1A; KLF5; MRPL28; PPA1; CEBPB; DDX39; BCL10; NFIC; MYC; JUN; MRPS12; TXNRD1; SP2; AR; PRDX1; ACOT10; PGD; ATF1; CEBPE; HSP90AB1; ETS1; ASNS; ALDOA; PPARG; MAFF; ATF4; PDK4; PSMA5; RELA; HIF1A; HSPA8; RARB; AMPD3; STAT1; MYBL2; GCLC; CH25H; SFPI1; RPL22L1; EGR1; LITAF; AFP; CEBPA; USF1; PDE4B; HSP90AA1; ELOVL7; PPRC1; KLF6; KLF4; MYB	
GO:0050789	2.50E-35	5.00E-32	BP	32911	228	6733	132	regulation of biological process	CXCR7; SPNB2; GNL3; BTG2; SP3; C4B; EDN1; HOXB1; TCFAP2A; RTKN2; GSR; SERPINE1; WT1; BACH1; GTF2F2; TGIF1; REL; HMOX1; CEBPD; PRR13; ZFP36; TRIB3; MEN1; RELB; NEDD4L; USF2; GADD45G; CCR2; TOB2; CDKN1A; PPARA; TRP53; HOXA1; HSPA1B; TBC1D15; ANGPTL4; BRCA1; FABP4; ETV4; PDK2; STAT3; ADM; EPHA2; GADD45A; RHOU; ARF3; SMAD3; ATF3; PTGS2; DUSP1; YRDC; NFKB1; ABCC1; NQO1; SP1; IL1B; IMPACT; NOTCH2; DNAJC5; HOXC8; HES6; DUSP16; LYVE1; CREB1; EREG; HSPD1; HBEGF; PRKCI; FOS; TXNL1; CREG1; JUNB; PTGS1; F3; PODXL; GPX2; MAFK; CLU; PSMD3; ERRFI1; KLF5; AREG; MRPL28; PPP2R2A; CEBPB; BCL10; NFIC; MYC; THBS1; JUN; SOCS3; CXCL16; TXNRD1; TIMP1; SP2; AR; PRDX1; LRP2; ATF1; CEBPE; ETS1; LAMA3; PMAIP1; PLAA; TNFRSF12A; PPARG; CYR61; MAFF; ATF4; PDK4; RELA; HIF1A; FOSL1; HSPA8; RARB; STAT1; MYBL2; GCLC; SFPI1; EGR1; CD48; LITAF; AFP; CEBPA; USF1; HSP90AA1; FGFBP1; S100A9; PPRC1; KLF6; KLF4; MYB	
GO:0044238	6.20E-35	1.20E-31	BP	32911	228	5580	120	primary metabolic process	SPNB2; BTG2; SP3; C4B; HOXB1; TCFAP2A; GSR; WT1; BACH1; GTF2F2; PRSS22; TGIF1; REL; CEBPD; PRR13; ZFP36; TRIB3; MEN1; RELB; NEDD4L; USF2; GADD45G; SULT1A1; PPARA; TRP53; HOXA1; SAMD8; HSPA1B; DNAJB4; BRCA1; FABP4; ADAMTS4; ETV4; PDK2; STAT3; ADM; EPHA2; RHOU; SMAD3; ATF3; PTGS2; TALDO1; EIF5; DUSP1; EIF2S2; NFKB1; CYP51; SP1; HSPA9; NOTCH2; DNAJC5; HOXC8; HES6; LYVE1; CREB1; HSPA1A; HSPD1; PRKCI; PTPN21; FOS; JUNB; PTGS1; TIPARP; PTPN14; GTF3C1; HS6ST1; MAFK; IDI1; EIF1A; KLF5; TINAGL1; MRPL28; CEBPB; DDX39; BCL10; NFIC; MYC; JUN; MRPS12; SP2; AR; PGD; ATF1; CEBPE; HSP90AB1; ETS1; ASNS; ALDOA; PPARG; CHI3L1; MAFF; ATF4; PDK4; PSMA5; RELA; HIF1A; HSPA8; RARB; PSMC1; AMPD3; STAT1; MYBL2; GCLC; CH25H; SFPI1; RPL22L1; EGR1; LITAF; AFP; CEBPA; USF1; PDE4B; HSP90AA1; ELOVL7; PPRC1; KLF6; KLF4; MMP11; MYB; HP	

									CXCR7; SPNB2; GNL3; BTG2; SP3; EDN1; HOXB1; TCFAP2A; RTKN2; GSR; SERPINE1; WT1; BACH1; GTF2F2; TGIF1; REL; HMOX1; CEBPD; PRR13; ZFP36; TRIB3; MEN1; RELB; USF2; GADD45G; CCR2; TOB2; CDKN1A; PPARA; TRP53; HOXA1; HSPA1B; TBCID15; ANGPTL4; BRCA1; FABP4; ETV4; PDK2; STAT3; ADM; EPHA2; GADD45A; RHOU; ARF3; SMAD3; ATF3; PTGS2; DUSP1; NFKB1; ABCC1; NQO1; SP1; IL1B; IMPACT; NOTCH2; DNAJC5; HOXC8; HES6; DUSP16; LVVE1; CREB1; EREG; HSPD1; HBEGF; PRKCI; FOS; TXNL1; CREG1; JUNB; PTGS1; F3; PODXL; MAFK; CLU; ERRF11; KLF5; AREG; MRPL28; PPP2R2A; CEBPB; BCL10; NFIC; MYC; THBS1; JUN; SOCS3; CXCL16; TXNRD1; TIMP1; SP2; AR; PRDX1; LRP2; ATF1; CEBPE; ETS1; LAMA3; PMAIP1; TNFRSF12A; PPARG; CYR61; MAFF; ATF4; PDK4; RELA; HIF1A; FOSL1; HSPA8; RARB; STAT1; MYBL2; GCLC; SFPI1; EGR1; CD48; LITAF; AFP; CEBPA; USF1; HSP90AA1; FGFBP1; S100A9; PPRC1; KLF6; KLF4; MYB
GO:0050794	7. 20E-34	1. 40E-30	BP	32911	228	6318	126	regulation of cellular process	BTG2; SP3; EDN1; HOXB1; TCFAP2A; SERPINE1; WT1; BACH1; GTF2F2; TGIF1; REL; HMOX1; CEBPD; PRR13; ZFP36; TRIB3; MEN1; RELB; USF2; GADD45G; TOB2; BRCA1; FABP4; ETV4; STAT3; GADD45A; SMAD3; ATF3; PTGS2; NFKB1; NQO1; SP1; IL1B; IMPACT; NOTCH2; HOXC8; HES6; DUSP16; CREB1; EREG; HBEGF; FOS; CREG1; JUNB; MAFK; PSMD3; ERRF11; KLF5; AREG; MRPL28; CEBPB; BCL10; NFIC; MYC; JUN; SOCS3; SP2; AR; ATF1; CEBPE; ETS1; PLAA; PPARG; MAFF; ATF4; RELA; HIF1A; FOSL1; RARB; STAT1; MYBL2; GCLC; SFPI1; EGR1; LITAF; CEBPA; USF1; HSP90AA1; S100A9; PPRC1; KLF6; KLF4; MYB
GO:0019222	7. 00E-33	1. 30E-29	BP	32911	228	3142	89	regulation of metabolic process	BTG2; SP3; EDN1; HOXB1; TCFAP2A; WT1; BACH1; GTF2F2; TGIF1; REL; HMOX1; CEBPD; PRR13; ZFP36; TRIB3; MEN1; RELB; USF2; GADD45G; CDKN1A; PPARA; TRP53; HOXA1; HSPA1B; TBCID15; BRCA1; FABP4; ETV4; STAT3; GADD45A; SMAD3; ATF3; PTGS2; NFKB1; NQO1; SP1; IL1B; IMPACT; NOTCH2; HOXC8; HES6; DUSP16; CREB1; EREG; HBEGF; FOS; CREG1; JUNB; MAFK; PSMD3; ERRF11; KLF5; AREG; MRPL28; CEBPB; BCL10; NFIC; MYC; JUN; SOCS3; SP2; AR; ATF1; CEBPE; ETS1; PLAA; PPARG; MAFF; ATF4; RELA; HIF1A; FOSL1; RARB; STAT1; MYBL2; GCLC; SFPI1; EGR1; LITAF; CEBPA; USF1; HSP90AA1; S100A9; PPRC1; KLF6; KLF4; MYB
GO:0031323	1. 00E-30	2. 00E-27	BP	32911	228	2749	81	regulation of cellular metabolic process	BTG2; SP3; EDN1; HOXB1; TCFAP2A; WT1; BACH1; GTF2F2; TGIF1; REL; HMOX1; CEBPD; PRR13; ZFP36; TRIB3; MEN1; RELB; USF2; GADD45G; CDKN1A; PPARA; TRP53; HOXA1; TBCID15; FABP4; ETV4; STAT3; GADD45A; SMAD3; ATF3; PTGS2; NFKB1; SP1; IL1B; IMPACT; NOTCH2; HOXC8; HES6; DUSP16; CREB1; EREG; HBEGF; FOS; CREG1; JUNB; MAFK; ERRF11; KLF5; AREG; MRPL28; CEBPB; BCL10; NFIC; MYC; JUN; SOCS3; SP2; AR; ATF1; CEBPE; ETS1; PPARG; MAFF; ATF4; RELA; HIF1A; FOSL1; RARB; STAT1; MYBL2; GCLC; SFPI1; EGR1; LITAF; CEBPA; USF1; HSP90AA1; PPRC1; KLF6; KLF4; MYB
GO:0032502	1. 10E-30	2. 30E-27	BP	32911	228	2682	80	developmental process	BTG2; SP3; EDN1; PPL; HOXB1; TCFAP2A; RTKN2; WT1; TGIF1; HMOX1; TUFT1; MEN1; LOX; RELB; GADD45G; CCR2; PPARA; TRP53; HOXA1; BRCA1; FABP4; KRT8; LRG1; ETV4; STAT3; ADM; EPHA2; SMAD3; PTGS2; NFKB1; SP1; IL1B; NOTCH2; HOXC8; HES6; CREB1; EREG; HBEGF; PRKCI; FOS; JUNB; PTGS1; TIPARP; HS6ST1; MAFK; CLU; ERRF11; KLF5; AREG; CEBPB; BCL10; NFIC; SCEL; MYC; THBS1; JUN; VAMP5; SOCS3; TXNRD1; TIMP1; AR; LRP2; CEBPE; HSP90AB1; TNFRSF12A; PPARG; CYR61; MAFF; COPPS3; IFRD1; RELA; HIF1A; RARB; GJB3; SFPI1; EGR1; CEBPA; KLF4; MYB; HP
GO:0044249	5. 60E-30	1. 10E-26	BP	32911	228	2599	78	cellular biosynthetic process	BTG2; SP3; HOXB1; TCFAP2A; WT1; BACH1; GTF2F2; TGIF1; REL; CEBPD; PRR13; TRIB3; RELB; USF2; PPARA; TRP53; HOXA1; SAMD8; BRCA1; ETV4; STAT3; SMAD3; ATF3; PTGS2; EIF5; EIF2S2; NFKB1; SP1; NOTCH2; HOXC8; HES6; CREB1; FOS; JUNB; PTGS1; GTRF3C1; HS6ST1; MAFK; IDI1; EIF1A; KLF5; MRPL28; CEBPB; NFIC; MYC; JUN; MRPS12; SP2; AR; PGD; ATF1; CEBPE; ETS1; ASNS; PPARG; MAFF; ATF4; PDK4; RELA; HIF1A; RARB; AMPD3; STAT1; MYBL2; GCLC; CH25H; SFPI1; RPL22L1; EGR1; LITAF; CEBPA; USF1; HSP90AA1; ELOVL7; PPRC1; KLF6; KLF4; MYB
GO:0050896	5. 70E-30	1. 10E-26	BP	32911	228	2388	75	response to stimulus	BTG2; C4B; EDN1; SERPINE1; HSPB8; HMOX1; TRIB3; LOX; RELB; USF2; CCR2; SULT1A1; CDKN1A; PPARA; TRP53; MT1; HSPA1B; CSF3R; BRCA1; FABP4; KRT8; STAT3; ADM; SRXN1; GADD45A; PTGS2; NFKB1; ABCC1; NQO1; HSPA9; IL1B; NOTCH2; CREB1; HSPA1A; HSPD1; MT2; PRKCI; FOS; PTGS1; GPX2; UBXN4; ERRF11; AREG; TINAGL1; PPP2R2A; CEBPB; BCL10; MYC; THBS1; JUN; TXNRD1; S100A8; AR; PROX1; LRP2; CEBPE; HSP90AB1; PMAIP1; PLAA; PPARG; CYR61; RELA; HIF1A; FOSL1; HSPA8; STAT1; GCLC; EGR1; IGJ; CD48; CEBPA; HSP90AA1; S100A9; KLF4; SERPINA3N

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GO:0051173	3.30E-28	6.50E-25	BP	32911	228	651	42	positive regulation of nitrogen compound metabolic process	HOXB1; WT1; GTF2F2; REL; CEBPD; MEN1; USF2; PPARA; TRP53; HOXA1; ETV4; STAT3; SMAD3; PTGS2; NFKB1; SP1; IL1B; CREB1; EREG; FOS; JUNB; KLF5; CEBPB; NFIC; MYC; JUN; AR; ATF1; ETS1; PPARG; ATF4; RELA; HIF1A; FOSL1; RARB; SFP11; EGR1; CEBPA; USF1; HSP90AA1; KLF6; KLF4
GO:0031326	5.10E-28	1.00E-24	BP	32911	228	2279	71	regulation of cellular biosynthetic process	BTG2; SP3; EDN1; HOXB1; TCFAP2A; WT1; BACH1; GTF2F2; TGIF1; REL; HMOX1; CEBPD; PRR13; TRIB3; MEN1; RELB; USF2; PPARA; TRP53; HOXA1; FABP4; ETV4; STAT3; SMAD3; ATF3; PTGS2; NFKB1; SP1; IL1B; IMPACT; NOTCH2; HOXC8; HES6; CREB1; EREG; HBEGF; FOS; CREG1; JUNB; MAFK; KLF5; MRPL28; CEBPB; BCL10; NFIC; MYC; JUN; SP2; AR; ATF1; CEBPE; ETS1; PPARG; MAFF; ATF4; RELA; HIF1A; FOSL1; RARB; STAT1; MYBL2; SFP11; EGR1; LITAF; CEBPA; USF1; HSP90AA1; PPRC1; KLF6; KLF4; MYB
GO:0045893	7.70E-28	1.50E-24	BP	32911	228	473	37	positive regulation of transcription, DNA-dependent	HOXB1; WT1; GTF2F2; REL; CEBPD; MEN1; USF2; PPARA; TRP53; HOXA1; STAT3; SMAD3; NFKB1; SP1; IL1B; CREB1; FOS; JUNB; CEBPB; NFIC; MYC; JUN; AR; ATF1; ETS1; PPARG; ATF4; RELA; HIF1A; FOSL1; RARB; SFP11; EGR1; CEBPA; USF1; KLF6; KLF4
GO:0034645	8.20E-28	1.60E-24	BP	32911	228	1960	66	cellular macromolecule biosynthetic process	BTG2; SP3; HOXB1; TCFAP2A; WT1; BACH1; GTF2F2; TGIF1; REL; CEBPD; PRR13; TRIB3; RELB; USF2; PPARA; TRP53; HOXA1; BRCA1; ETV4; STAT3; SMAD3; ATF3; EIF5; EIF2S2; NFKB1; SP1; NOTCH2; HOXC8; HES6; CREB1; FOS; JUNB; GTF3C1; HS6ST1; MAFK; EIF1A; KLF5; MRPL28; CEBPB; NFIC; MYC; JUN; MRPS12; SP2; AR; ATF1; CEBPE; ETS1; PPARG; MAFF; ATF4; RELA; HIF1A; RARB; STAT1; MYBL2; SFP11; RPL22L1; EGR1; LITAF; CEBPA; USF1; PPRC1; KLF6; KLF4; MYB
GO:0010468	8.90E-28	1.70E-24	BP	32911	228	2231	70	regulation of gene expression	BTG2; SP3; HOXB1; TCFAP2A; SERPINE1; WT1; BACH1; GTF2F2; TGIF1; REL; HMOX1; CEBPD; PRR13; ZFP36; TRIB3; MEN1; RELB; USF2; TOB2; PPARA; TRP53; HOXA1; BRCA1; FABP4; ETV4; STAT3; SMAD3; ATF3; NFKB1; SP1; IL1B; IMPACT; NOTCH2; HOXC8; HES6; CREB1; FOS; CREG1; JUNB; MAFK; KLF5; MRPL28; CEBPB; BCL10; NFIC; MYC; JUN; SP2; AR; ATF1; CEBPE; ETS1; PPARG; MAFF; ATF4; RELA; HIF1A; FOSL1; RARB; STAT1; MYBL2; SFP11; EGR1; LITAF; CEBPA; USF1; PPRC1; KLF6; KLF4; MYB
GO:0051254	9.70E-28	1.90E-24	BP	32911	228	476	37	positive regulation of RNA metabolic process	HOXB1; WT1; GTF2F2; REL; CEBPD; MEN1; USF2; PPARA; TRP53; HOXA1; STAT3; SMAD3; NFKB1; SP1; IL1B; CREB1; FOS; JUNB; CEBPB; NFIC; MYC; JUN; AR; ATF1; ETS1; PPARG; ATF4; RELA; HIF1A; FOSL1; RARB; SFP11; EGR1; CEBPA; USF1; KLF6; KLF4
GO:0010556	9.70E-28	1.90E-24	BP	32911	228	2166	69	regulation of macromolecule biosynthetic process	BTG2; SP3; HOXB1; TCFAP2A; WT1; BACH1; GTF2F2; TGIF1; REL; HMOX1; CEBPD; PRR13; TRIB3; MEN1; RELB; USF2; PPARA; TRP53; HOXA1; FABP4; ETV4; STAT3; SMAD3; ATF3; NFKB1; SP1; IL1B; IMPACT; NOTCH2; HOXC8; HES6; CREB1; EREG; HBEGF; FOS; CREG1; JUNB; MAFK; KLF5; MRPL28; CEBPB; BCL10; NFIC; MYC; JUN; SP2; AR; ATF1; CEBPE; ETS1; PPARG; MAFF; ATF4; RELA; HIF1A; FOSL1; RARB; STAT1; MYBL2; SFP11; EGR1; LITAF; CEBPA; USF1; S100A9; PPRC1; KLF6; KLF4; MYB
GO:0009059	1.20E-27	2.40E-24	BP	32911	228	1974	66	macromolecule biosynthetic process	BTG2; SP3; HOXB1; TCFAP2A; WT1; BACH1; GTF2F2; TGIF1; REL; CEBPD; PRR13; TRIB3; RELB; USF2; PPARA; TRP53; HOXA1; BRCA1; ETV4; STAT3; SMAD3; ATF3; EIF5; EIF2S2; NFKB1; SP1; NOTCH2; HOXC8; HES6; CREB1; FOS; JUNB; GTF3C1; HS6ST1; MAFK; EIF1A; KLF5; MRPL28; CEBPB; NFIC; MYC; JUN; MRPS12; SP2; AR; ATF1; CEBPE; ETS1; PPARG; MAFF; ATF4; RELA; HIF1A; RARB; STAT1; MYBL2; SFP11; RPL22L1; EGR1; LITAF; CEBPA; USF1; PPRC1; KLF6; KLF4; MYB
GO:0044260	1.40E-27	2.90E-24	BP	32911	228	3875	91	cellular macromolecule metabolic process	SPNB2; BTG2; SP3; HOXB1; TCFAP2A; WT1; BACH1; GTF2F2; TGIF1; REL; CEBPD; PRR13; ZFP36; TRIB3; MEN1; RELB; NEDD4L; USF2; GADD45G; PPARA; TRP53; HOXA1; HSPA1B; DNAJB4; BRCA1; ETV4; PDK2; STAT3; EPHA2; SMAD3; ATF3; EIF5; DUSP1; EIF2S2; NFKB1; SP1; HSPA9; NOTCH2; DNAJC5; HOXC8; HES6; CREB1; HSPA1A; HSPD1; PRKCI; PTPN21; FOS; JUNB; TIPARP; PTPN14; GTF3C1; HS6ST1; MAFK; EIF1A; KLF5; MRPL28; CEBPB; DDX39; BCL10; NFIC; MYC; JUN; MRPS12; SP2; AR; ATF1; CEBPE; HSP90AB1; ETS1; PPARG; MAFF; ATF4; PDK4; PSMA5; RELA; HIF1A; HSPA8; RARB; STAT1; MYBL2; SFP11; RPL22L1; EGR1; LITAF; CEBPA; USF1; HSP90AA1; PPRC1; KLF6; KLF4; MYB

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GO:0048523	4.40E-22	8.80E-19	BP	32911	228	1452	51	negative regulation of cellular process	SPNB2; BTG2; EDN1; WT1; TGIF1; HMOX1; ZFP36; TRIB3; MEN1; TOB2; CDKN1A; TRP53; HSPA1B; ANGPTL4; FABP4; ETV4; ADM; GADD45A; SMAD3; ATF3; PTGS2; NFKB1; IL1B; IMPACT; DNAJC5; HOXC8; EREG; HSPD1; HBEGF; PTGS1; CLU; ERRF1; AREG; CEBPB; NFIC; MYC; JUN; SOCS3; TIMP1; AR; ETS1; PMAIP1; PPARG; REL; FOSL1; RARB; GCLC; EGR1; CEBPA; KLF4
GO:0042981	6.30E-22	1.20E-18	BP	32911	228	653	36	regulation of apoptosis	BTG2; WT1; REL; HMOX1; MEN1; CDKN1A; TRP53; HSPA1B; ANGPTL4; BRCA1; SMAD3; PTGS2; DUSP1; NFKB1; ABCC1; NQO1; IL1B; NOTCH2; DNAJC5; CREB1; HSPD1; CLU; CEBPB; BCL10; MYC; JUN; TIMP1; PRDX1; ETS1; PMAIP1; HIF1A; FOSL1; RARB; STAT1; GCLC; SFP11
GO:0043067	9.90E-22	1.90E-18	BP	32911	228	662	36	regulation of programmed cell death	BTG2; WT1; REL; HMOX1; MEN1; CDKN1A; TRP53; HSPA1B; ANGPTL4; BRCA1; SMAD3; PTGS2; DUSP1; NFKB1; ABCC1; NQO1; IL1B; NOTCH2; DNAJC5; CREB1; HSPD1; CLU; CEBPB; BCL10; MYC; JUN; TIMP1; PRDX1; ETS1; PMAIP1; HIF1A; FOSL1; RARB; STAT1; GCLC; SFP11
GO:0090304	1.60E-21	3.20E-18	BP	32911	228	2322	63	nucleic acid metabolic process	BTG2; SP3; HOXB1; TCFAP2A; WT1; BACH1; GTF2F2; TGIF1; REL; CEBPD; PRR13; ZFP36; TRIB3; RELB; USF2; PPARA; TRP53; HOXA1; HSPA1B; BRCA1; ETV4; STAT3; SMAD3; ATF3; NFKB1; SP1; NOTCH2; HOXC8; HES6; CREB1; HSPA1A; FOS; JUNB; GTF3C1; MAFK; KLF5; CEBPB; DDX39; NFIC; MYC; JUN; SP2; AR; ATF1; CEBPE; ETS1; PPARG; MAFF; ATF4; REL; HIF1A; RARB; STAT1; MYBL2; SFP11; EGR1; LITAF; CEBPA; USF1; PPRC1; KLF6; KLF4; MYB
GO:0010941	1.90E-21	3.70E-18	BP	32911	228	675	36	regulation of cell death	BTG2; WT1; REL; HMOX1; MEN1; CDKN1A; TRP53; HSPA1B; ANGPTL4; BRCA1; SMAD3; PTGS2; DUSP1; NFKB1; ABCC1; NQO1; IL1B; NOTCH2; DNAJC5; CREB1; HSPD1; CLU; CEBPB; BCL10; MYC; JUN; TIMP1; PRDX1; ETS1; PMAIP1; HIF1A; FOSL1; RARB; STAT1; GCLC; SFP11
GO:0051239	1.10E-20	2.20E-17	BP	32911	228	1078	43	regulation of multicellular organismal process	EDN1; SERPINE1; TGIF1; REL; HMOX1; ZFP36; MEN1; CCR2; TOB2; TRP53; HSPA1B; ETV4; STAT3; ADM; EPHA2; SMAD3; PTGS2; NFKB1; IL1B; CREB1; EREG; HSPD1; HBEGF; PTGS1; ERRF1; AREG; CEBPB; MYC; THBS1; JUN; AR; ATF1; ETS1; LAMA3; TNFRSF12A; PPARG; MAFF; REL; HIF1A; RARB; EGR1; HSP90AA1; KLF4
GO:0048856	1.70E-20	3.40E-17	BP	32911	228	1515	50	anatomical structure development	SP3; EDN1; HOXB1; RTKN2; WT1; TGIF1; TUFT1; MEN1; LOX; CCR2; PPARA; TRP53; HOXA1; ADM; EPHA2; SMAD3; PTGS2; NFKB1; SP1; HES6; CREB1; PRKCI; FOS; JUNB; TIPARP; HS6ST1; MAFK; CLU; ERRF1; AREG; CEBPB; SCEL; THBS1; VAMP5; SOCS3; AR; LRP2; HSP90AB1; PPARG; CYR61; IFRD1; REL; HIF1A; RARB; GJB3; SFP11; CEBPA; KLF4; MYB; HP
GO:0042127	1.20E-19	2.50E-16	BP	32911	228	670	34	regulation of cell proliferation	GNL3; EDN1; RTKN2; SERPINE1; TGIF1; HMOX1; MEN1; CDKN1A; TRP53; FABP4; ETV4; ADM; SMAD3; ATF3; PTGS2; EREG; HBEGF; PTGS1; CLU; AREG; MYC; JUN; AR; ETS1; PMAIP1; PPARG; REL; HIF1A; FOSL1; RARB; STAT1; CEBPA; FGFBP1; KLF4
GO:0050793	3.80E-19	7.40E-16	BP	32911	228	794	36	regulation of developmental process	SERPINE1; TGIF1; ZFP36; TRIB3; MEN1; CCR2; TOB2; TRP53; ETV4; EPHA2; RHOU; SMAD3; PTGS2; IL1B; NOTCH2; JUNB; CLU; ERRF1; AREG; MYC; THBS1; JUN; SOCS3; AR; ATF1; ETS1; LAMA3; TNFRSF12A; PPARG; MAFF; REL; HIF1A; RARB; CEBPA; HSP90AA1; KLF4
GO:0051716	3.20E-18	6.20E-15	BP	32911	228	645	32	cellular response to stimulus	BTG2; HMOX1; TRIB3; USF2; CDKN1A; PPARA; TRP53; HSPA1B; CSF3R; BRCA1; FABP4; ADM; GADD45A; ABCC1; IL1B; HSPA1A; PRKCI; FOS; ERRF1; MYC; JUN; TXNRD1; AR; PRDX1; PMAIP1; PPARG; HIF1A; FOSL1; STAT1; EGR1; CEBPA; S100A9
GO:0048869	1.60E-17	3.20E-14	BP	32911	228	1443	45	cellular developmental process	BTG2; SP3; EDN1; WT1; MEN1; RELB; GADD45G; TRP53; HOXA1; FABP4; KRT8; LRG1; ETV4; STAT3; ADM; EPHA2; SMAD3; PTGS2; SP1; NOTCH2; HOXC8; HES6; CREB1; EREG; PRKCI; JUNB; PTGS1; TIPARP; CLU; CEBPB; JUN; VAMP5; SOCS3; TIMP1; AR; CEBPE; TNFRSF12A; PPARG; IFRD1; HIF1A; RARB; SFP11; EGR1; CEBPA; KLF4
GO:0030154	1.70E-16	3.40E-13	BP	32911	228	1083	38	cell differentiation	BTG2; SP3; WT1; RELB; GADD45G; TRP53; HOXA1; FABP4; KRT8; LRG1; ETV4; STAT3; EPHA2; SMAD3; PTGS2; SP1; NOTCH2; HOXC8; HES6; EREG; JUNB; PTGS1; TIPARP; CEBPB; JUN; VAMP5; SOCS3; AR; CEBPE; TNFRSF12A; PPARG; IFRD1; HIF1A; RARB; SFP11; EGR1; CEBPA; KLF4
GO:0010033	5.20E-16	1.00E-12	BP	32911	228	666	30	response to organic substance	HMOX1; TRIB3; LOX; SULT1A1; PPARA; HSPA1B; STAT3; ADM; PTGS2; IL1B; CREB1; HSPA1A; HSPD1; PRKCI; FOS; UBXN4; AREG; PPP2R2A; CEBPB; MYC; AR; PPARG; CYR61; REL; STAT1; EGR1; CD48; CEBPA; HSP90AA1; SERPINA3N

GO:0043068	1.80E-15	3.70E-12	BP	32911	228	292	21	positive regulation of programmed cell death	HMOX1; MEN1; CDKN1A; TRP53; BRCA1; SMAD3; PTGS2; DUSP1; NQO1; IL1B; NOTCH2; CEBPB; BCL10; MYC; JUN; PRDX1; PMAIP1; FOSL1; RARB; STAT1; SFP11
GO:0070887	2.10E-15	4.10E-12	BP	32911	228	224	19	cellular response to chemical stimulus	HMOX1; TRIB3; USF2; PPARA; CSF3R; FABP4; ABCC1; IL1B; PRKCI; MYC; TXNRD1; AR; PRDX1; PPARG; HIF1A; STAT1; EGR1; CEBPA; S100A9
GO:0048513	2.50E-15	5.00E-12	BP	32911	228	707	30	organ development	SP3; EDN1; RTKN2; WT1; MEN1; LOX; CCR2; ADM; SMAD3; NFKB1; SP1; CREB1; JUNB; TIPARP; HS6ST1; ERRF1; CEBPB; VAMP5; AR; HSP90AB1; PPARG; CYR61; RELA; HIF1A; GJB3; SFP11; CEBPA; KLF4; MYB; HP
GO:0010942	2.80E-15	5.50E-12	BP	32911	228	298	21	positive regulation of cell death	HMOX1; MEN1; CDKN1A; TRP53; BRCA1; SMAD3; PTGS2; DUSP1; NQO1; IL1B; NOTCH2; CEBPB; BCL10; MYC; JUN; PRDX1; PMAIP1; FOSL1; RARB; STAT1; SFP11
GO:0009653	4.80E-15	9.50E-12	BP	32911	228	893	33	anatomical structure morphogenesis	SP3; EDN1; HOXB1; TCFAP2A; WT1; TGIF1; MEN1; TRP53; HOXA1; KRT8; ETV4; ADM; EPHA2; SMAD3; SP1; NOTCH2; HOXC8; CREB1; EREG; TIPARP; CLU; ERRF1; AREG; BCL10; NFIC; MYC; SOCS3; TXNRD1; AR; RELA; HIF1A; RARB; KLF4
GO:0043065	1.80E-14	3.60E-11	BP	32911	228	289	20	positive regulation of apoptosis	HMOX1; MEN1; TRP53; BRCA1; SMAD3; PTGS2; DUSP1; NQO1; IL1B; NOTCH2; CEBPB; BCL10; MYC; JUN; PRDX1; PMAIP1; FOSL1; RARB; STAT1; SFP11
GO:0009892	1.40E-13	2.80E-10	BP	32911	228	656	27	negative regulation of metabolic process	EDN1; SERPINE1; WT1; TGIF1; TRIB3; MEN1; CDKN1A; TRP53; FABP4; SMAD3; ATF3; NFKB1; IL1B; IMPACT; HOXC8; HBEGF; ERRF1; NFIC; MYC; JUN; PPARG; RELA; RARB; GCLC; EGR1; CEBPA; KLF4
GO:0008285	3.90E-13	7.70E-10	BP	32911	228	260	18	negative regulation of cell proliferation	TGIF1; HMOX1; MEN1; CDKN1A; TRP53; ETV4; ADM; SMAD3; PTGS2; EREG; JUN; AR; PMAIP1; PPARG; FOSL1; RARB; CEBPA; KLF4
GO:0045595	1.20E-12	2.30E-09	BP	32911	228	554	24	regulation of cell differentiation	TGIF1; ZFP36; TRIB3; MEN1; TOB2; TRP53; SMAD3; JUNB; CLU; ERRF1; AREG; JUN; SOCS3; AR; ATF1; TNFRSF12A; PPARG; MAFF; RELA; HIF1A; RARB; CEBPA; HSP90AA1; KLF4
GO:0048646	1.30E-12	2.50E-09	BP	32911	228	363	20	anatomical structure formation involved in morphogenesis	HOXB1; TGIF1; HMOX1; TRP53; HOXA1; ADM; EPHA2; SMAD3; IL1B; EREG; HBEGF; HS6ST1; KLF5; BCL10; JUN; TXNRD1; AR; TNFRSF12A; CYR61; HIF1A
GO:0031324	3.90E-12	7.70E-09	BP	32911	228	586	24	negative regulation of cellular metabolic process	EDN1; WT1; TGIF1; TRIB3; MEN1; CDKN1A; TRP53; FABP4; SMAD3; ATF3; NFKB1; IMPACT; HOXC8; HBEGF; ERRF1; NFIC; MYC; JUN; PPARG; RARB; GCLC; EGR1; CEBPA; KLF4
GO:0065008	6.50E-12	1.20E-08	BP	32911	228	1160	33	regulation of biological quality	SPNB2; EDN1; GSR; HMOX1; MEN1; USF2; CCR2; SULT1A1; PPARA; TRP53; MT1; HSPA1B; FABP4; STAT3; ADM; RHOU; PTGS2; IL1B; CREB1; HSPA1A; MT2; TXNL1; PTGS1; TIPARP; F3; GPX2; JUN; TXNRD1; PRDX1; LRP2; HIF1A; EGR1; AFP
GO:0010605	8.80E-12	1.70E-08	BP	32911	228	609	24	negative regulation of macromolecule metabolic process	SERPINE1; WT1; TGIF1; TRIB3; MEN1; TRP53; FABP4; SMAD3; ATF3; NFKB1; IMPACT; HOXC8; HBEGF; ERRF1; NFIC; MYC; JUN; PPARG; RELA; RARB; GCLC; EGR1; CEBPA; KLF4
GO:0051094	1.10E-11	2.20E-08	BP	32911	228	362	19	positive regulation of developmental process	SERPINE1; TGIF1; MEN1; TOB2; SMAD3; PTGS2; IL1B; JUNB; CLU; MYC; JUN; SOCS3; ETS1; TNFRSF12A; PPARG; RELA; HIF1A; CEBPA; HSP90AA1
GO:0006979	1.40E-11	2.70E-08	BP	32911	228	108	12	response to oxidative stress	HMOX1; SRXN1; PTGS2; NFKB1; ABCC1; NQO1; PTGS1; GPX2; TXNRD1; PRDX1; HIF1A; GCLC
GO:0008284	3.20E-11	6.40E-08	BP	32911	228	385	19	positive regulation of cell proliferation	EDN1; RTKN2; TGIF1; CDKN1A; FABP4; ADM; ATF3; PTGS2; EREG; HBEGF; CLU; AREG; MYC; JUN; ETS1; RELA; HIF1A; STAT1; FGFBP1
GO:0001817	6.60E-11	1.20E-07	BP	32911	228	154	13	regulation of cytokine production	REL; HMOX1; CCR2; SMAD3; PTGS2; NFKB1; IL1B; CREB1; EREG; HSPD1; CEBPB; PPARG; RELA
GO:0044092	8.00E-11	1.50E-07	BP	32911	228	191	14	negative regulation of molecular function	SERPINE1; HMOX1; TRIB3; GADD45G; CDKN1A; HSPA1B; FABP4; GADD45A; NQO1; IL1B; DUSP16; ERRF1; MYC; PPARG
GO:0002376	8.20E-11	1.60E-07	BP	32911	228	564	22	immune system process	SP3; C4B; MEN1; RELB; GADD45G; CCR2; TRP53; CSF3R; SMAD3; NDRG1; IL1B; HSPD1; PODXL; TINAGL1; BCL10; PRDX1; RELA; SFP11; EGR1; IGJ; CEBPB; S100A9
GO:0048598	1.10E-10	2.10E-07	BP	32911	228	365	18	embryonic morphogenesis	SP3; EDN1; HOXB1; TCFAP2A; TGIF1; MEN1; TRP53; HOXA1; ADM; EPHA2; SMAD3; SP1; NOTCH2; BCL10; MYC; SOCS3; TXNRD1; RARB

GO:0009607	1.50E-10	2.90E-07	BP	32911	228	325	17	response to biotic stimulus	SERPINE1; TRP53; HSPA1B; KRT8; ADM; PTGS2; IL1B; HSPA1A; HSPD1; GPX2; UBXXN4; CEBPB; BCL10; CEBPE; RELA; STAT1; HSP90AA1
GO:0050790	1.70E-10	3.40E-07	BP	32911	228	705	24	regulation of catalytic activity	EDN1; SERPINE1; TRIB3; MEN1; GADD45G; CDKN1A; TRP53; HSPA1B; TBC1D15; FABP4; GADD45A; SMAD3; NQO1; IL1B; DUSP16; EREG; ERFF1; BCL10; MYC; AR; PLAA; PPARG; HIF1A; HSP90AA1
GO:0065009	1.80E-10	3.50E-07	BP	32911	228	831	26	regulation of molecular function	EDN1; SERPINE1; HMOX1; TRIB3; MEN1; GADD45G; CDKN1A; TRP53; HSPA1B; TBC1D15; FABP4; GADD45A; SMAD3; NQO1; IL1B; DUSP16; EREG; ERFF1; BCL10; MYC; AR; PLAA; PPARG; RELA; HIF1A; HSP90AA1
GO:0048583	3.00E-10	5.90E-07	BP	32911	228	439	19	regulation of response to stimulus	C4B; SERPINE1; HMOX1; ZFP36; CCR2; PPARG; HSPA1B; FABP4; SMAD3; PTGS2; IL1B; EREG; HSPD1; GPX2; BCL10; SOCS3; PRDX1; PPARG; RELA
GO:0051348	4.60E-10	9.00E-07	BP	32911	228	62	9	negative regulation of transferase activity	TRIB3; GADD45G; CDKN1A; FABP4; GADD45A; IL1B; DUSP16; ERFF1; PPARG
GO:0043066	5.60E-10	1.00E-06	BP	32911	228	307	16	negative regulation of apoptosis	BTG2; WT1; CDKN1A; TRP53; HSPA1B; ANGPTL4; SMAD3; NFKB1; DNJC5; HSPD1; CLU; CEBPB; MYC; TIMP1; ETS1; GCLC
GO:0048729	6.00E-10	1.10E-06	BP	32911	228	264	15	tissue morphogenesis	EDN1; TCFAP2A; WT1; TGIF1; ETV4; ADM; SMAD3; NOTCH2; ERFF1; AREG; BCL10; MYC; SOCS3; AR; KLF4
GO:0043069	7.00E-10	1.30E-06	BP	32911	228	312	16	negative regulation of programmed cell death	BTG2; WT1; CDKN1A; TRP53; HSPA1B; ANGPTL4; SMAD3; NFKB1; DNJC5; HSPD1; CLU; CEBPB; MYC; TIMP1; ETS1; GCLC
GO:0043086	8.50E-10	1.60E-06	BP	32911	228	153	12	negative regulation of catalytic activity	SERPINE1; TRIB3; GADD45G; CDKN1A; HSPA1B; FABP4; GADD45A; NQO1; IL1B; DUSP16; ERFF1; PPARC
GO:0051789	1.00E-09	2.00E-06	BP	32911	228	93	10	response to protein stimulus	HSPA1B; HSPA1A; HSPD1; FOS; UBXXN4; MYC; CYR61; EGRI; CD48; HSP90AA1
GO:0060548	1.10E-09	2.10E-06	BP	32911	228	322	16	negative regulation of cell death	BTG2; WT1; CDKN1A; TRP53; HSPA1B; ANGPTL4; SMAD3; NFKB1; DNJC5; HSPD1; CLU; CEBPB; MYC; TIMP1; ETS1; GCLC
GO:0044281	1.10E-09	2.30E-06	BP	32911	228	1343	32	small molecule metabolic process	BTG2; GSR; MEN1; SULT1A1; PPARG; BRCA1; FABP4; PDK2; RHOU; ATF3; PTGS2; TALD01; CYP51; PTGS1; IDI1; MYC; PGD; LRP2; ASNS; ALDOA; PPARG; ATF4; PDK4; HIF1A; HSPA8; AMPD3; GCLC; CH25H; CEBPA; USF1; PDE4B; ELOVL7
GO:0002682	1.30E-09	2.60E-06	BP	32911	228	375	17	regulation of immune system process	C4B; HMOX1; ZFP36; CCR2; TOB2; CDKN1A; TRP53; HSPA1B; SMAD3; EREG; HSPD1; GPX2; BCL10; JUN; RELA; HIF1A; HSP90AA1
GO:0032879	1.30E-09	2.70E-06	BP	32911	228	656	22	regulation of localization	EDN1; SERPINE1; HMOX1; TRIB3; NEDD4L; CCR2; TRP53; EPHA2; SMAD3; PTGS2; YRDC; ABCC1; IL1B; CREB1; HBEGF; PRKCI; PTGS1; F3; PRDX1; ETS1; LAMA3; HIF1A
GO:0009887	1.50E-09	3.10E-06	BP	32911	228	330	16	organ morphogenesis	SP3; HOXB1; TCFAP2A; MEN1; EPHA2; SMAD3; SP1; NOTCH2; HOXC8; EREG; TIPARP; NFIC; MYC; AR; RELA; RARB
GO:0048660	1.90E-09	3.80E-06	BP	32911	228	50	8	regulation of smooth muscle cell proliferation	TRP53; PTGS2; EREG; HBEGF; JUN; HIF1A; STAT1; KLF4
GO:0001525	2.10E-09	4.10E-06	BP	32911	228	131	11	angiogenesis	HMOX1; EPHA2; IL1B; EREG; HBEGF; HS6ST1; KLF5; JUN; TNFRSF12A; CYR61; HIF1A
GO:0031327	2.10E-09	4.10E-06	BP	32911	228	494	19	negative regulation of cellular biosynthetic process	EDN1; WT1; TGIF1; TRIB3; MEN1; TRP53; FABP4; SMAD3; ATF3; NFKB1; HOXC8; HBEGF; NFIC; MYC; PPARG; RARB; EGRI; CEBPA; KLF4
GO:0006366	2.30E-09	4.50E-06	BP	32911	228	51	8	transcription from RNA polymerase II promoter	GTF2F2; STAT3; SMAD3; CREB1; FOS; JUNB; MYC; JUN
GO:0048568	2.60E-09	5.10E-06	BP	32911	228	75	9	embryonic organ development	SP3; SP1; JUNB; HS6ST1; CEBPB; CYR61; HIF1A; CEBPA; MYB
GO:0006351	2.60E-09	5.10E-06	BP	32911	228	75	9	transcription, DNA-dependent	GTF2F2; TRP53; STAT3; SMAD3; CREB1; FOS; JUNB; MYC; JUN
GO:0009890	2.60E-09	5.20E-06	BP	32911	228	501	19	negative regulation of biosynthetic process	EDN1; WT1; TGIF1; TRIB3; MEN1; TRP53; FABP4; SMAD3; ATF3; NFKB1; HOXC8; HBEGF; NFIC; MYC; PPARG; RARB; EGRI; CEBPA; KLF4
GO:0045934	4.10E-09	8.00E-06	BP	32911	228	458	18	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	EDN1; WT1; TGIF1; TRIB3; MEN1; TRP53; FABP4; SMAD3; ATF3; NFKB1; HOXC8; NFIC; MYC; PPARG; RARB; EGRI; CEBPA; KLF4
GO:0032774	4.20E-09	8.30E-06	BP	32911	228	79	9	RNA biosynthetic process	GTF2F2; TRP53; STAT3; SMAD3; CREB1; FOS; JUNB; MYC; JUN
GO:0051172	5.50E-09	1.00E-05	BP	32911	228	467	18	negative regulation of nitrogen compound metabolic process	EDN1; WT1; TGIF1; TRIB3; MEN1; TRP53; FABP4; SMAD3; ATF3; NFKB1; HOXC8; NFIC; MYC; PPARG; RARB; EGRI; CEBPA; KLF4
GO:0006469	5.70E-09	1.10E-05	BP	32911	228	57	8	negative regulation of protein kinase activity	TRIB3; GADD45G; CDKN1A; FABP4; GADD45A; IL1B; DUSP16; ERFF1
GO:0045768	7.00E-09	1.30E-05	BP	32911	228	22	6	positive regulation of anti-apoptosis	BTG2; HMOX1; CDKN1A; ADM; DUSP1; HSPD1

GO:0033673	7.60E-09	1.50E-05	BP	32911	228	59	8	negative regulation of kinase activity	TRIB3; GADD45G; CDKN1A; FABP4; GADD45A; IL1B; DUSP16; ERFF1
GO:0010558	8.70E-09	1.70E-05	BP	32911	228	481	18	negative regulation of macromolecule biosynthetic process	WT1; TGIF1; TRIB3; MEN1; TRP53; FABP4; SMAD3; ATF3; NFKB1; HOXC8; HBEGF; NFIC; MYC; PPARG; RARB; EGR1; CEBPA; KLF4
GO:0016481	9.60E-09	1.80E-05	BP	32911	228	428	17	negative regulation of transcription	WT1; TGIF1; TRIB3; MEN1; TRP53; FABP4; SMAD3; ATF3; NFKB1; HOXC8; NFIC; MYC; PPARG; RARB; EGR1; CEBPA; KLF4
GO:0030334	1.20E-08	2.40E-05	BP	32911	228	155	11	regulation of cell migration	CCR2; TRP53; EPHA2; SMAD3; PTGS2; ABCC1; HBEGF; F3; ETS1; LAMA3; HIF1A
GO:0030335	1.30E-08	2.60E-05	BP	32911	228	90	9	positive regulation of cell migration	CCR2; TRP53; SMAD3; PTGS2; ABCC1; HBEGF; F3; ETS1; HIF1A
GO:0042592	1.30E-08	2.70E-05	BP	32911	228	616	20	homeostatic process	EDN1; GSR; MEN1; USF2; CCR2; TRP53; MT1; HSPA1B; FABP4; STAT3; ADM; IL1B; HSPA1A; MT2; TXNL1; GPX2; JUN; TXNRD1; PRDX1; HIF1A
GO:0019220	1.40E-08	2.80E-05	BP	32911	228	386	16	regulation of phosphate metabolic process	EDN1; TRIB3; GADD45G; CDKN1A; FABP4; GADD45A; SMAD3; IL1B; IMPACT; DUSP16; EREG; ERFF1; AREG; BCL10; JUN; SOCS3
GO:0051174	1.40E-08	2.80E-05	BP	32911	228	386	16	regulation of phosphorus metabolic process	EDN1; TRIB3; GADD45G; CDKN1A; FABP4; GADD45A; SMAD3; IL1B; IMPACT; DUSP16; EREG; ERFF1; AREG; BCL10; JUN; SOCS3
GO:0009611	1.50E-08	2.90E-05	BP	32911	228	240	13	response to wounding	SERPINE1; LOX; CCR2; PPARA; STAT3; ADM; PTGS2; IL1B; NOTCH2; THBS1; PLAA; PPARG; SERPINA3N
GO:0019538	2.10E-08	4.10E-05	BP	32911	228	2117	39	protein metabolic process	SPNB2; BTG2; C4B; PRSS22; TRIB3; MEN1; NEDD4L; GADD45G; DNAJB4; ADAMTS4; PDK2; EPHA2; EIF5; DUSP1; EIF2S2; HSPA9; DNAJC5; CREB1; HSPD1; PRKCI; PTPN21; TIPARP; PTPN14; EIF1A; TINAGL1; MRPL28; BCL10; MYC; MRPS12; HSP90AB1; PDK4; PSMA5; HIF1A; HSPA8; PSMC1; RPL22L1; HSP90AA1; MMP11; HP
GO:0040017	2.60E-08	5.10E-05	BP	32911	228	97	9	positive regulation of locomotion	CCR2; TRP53; SMAD3; PTGS2; ABCC1; HBEGF; F3; ETS1; HIF1A
GO:0051272	2.60E-08	5.10E-05	BP	32911	228	97	9	positive regulation of cellular component movement	CCR2; TRP53; SMAD3; PTGS2; ABCC1; HBEGF; F3; ETS1; HIF1A
GO:0040012	4.10E-08	8.10E-05	BP	32911	228	174	11	regulation of locomotion	CCR2; TRP53; EPHA2; SMAD3; PTGS2; ABCC1; HBEGF; F3; ETS1; LAMA3; HIF1A
GO:0045767	4.30E-08	8.40E-05	BP	32911	228	29	6	regulation of anti-apoptosis	BTG2; HMOX1; CDKN1A; ADM; DUSP1; HSPD1
GO:0032101	4.60E-08	9.10E-05	BP	32911	228	176	11	regulation of response to external stimulus	SERPINE1; ZFP36; CCR2; PPARA; FABP4; SMAD3; PTGS2; IL1B; HSPD1; GPX2; PPARG
GO:0009605	4.60E-08	9.10E-05	BP	32911	228	313	14	response to external stimulus	USF2; TRP53; CSF3R; ABCC1; IL1B; FOS; MYC; JUN; S100A8; CYR61; FOSL1; STAT1; S100A9; KLF4
GO:0010629	5.20E-08	1.00E-04	BP	32911	228	481	17	negative regulation of gene expression	WT1; TGIF1; TRIB3; MEN1; TRP53; FABP4; SMAD3; ATF3; NFKB1; HOXC8; NFIC; MYC; PPARG; RARB; EGR1; CEBPA; KLF4
GO:0009790	5.30E-08	1.00E-04	BP	32911	228	267	13	embryo development	SP3; EDN1; MEN1; TRP53; BRCA1; SMAD3; SP1; JUNB; SCEL; AR; MAFF; COPS3; MYB
GO:0050873	5.30E-08	1.00E-04	BP	32911	228	30	6	brown fat cell differentiation	FABP4; LRG1; PTGS2; CEBPB; PPARG; CEBPA
GO:0051270	5.50E-08	1.00E-04	BP	32911	228	179	11	regulation of cellular component movement	CCR2; TRP53; EPHA2; SMAD3; PTGS2; ABCC1; HBEGF; F3; ETS1; LAMA3; HIF1A
GO:0042325	5.80E-08	1.10E-04	BP	32911	228	371	15	regulation of phosphorylation	EDN1; TRIB3; GADD45G; CDKN1A; FABP4; GADD45A; IL1B; IMPACT; DUSP16; EREG; ERFF1; AREG; BCL10; JUN; SOCS3
GO:0006006	5.80E-08	1.10E-04	BP	32911	228	141	10	glucose metabolic process	PPARA; PDK2; ATF3; TALD01; MYC; PGD; ALDOA; ATF4; PDK4; USF1
GO:0009888	6.40E-08	1.20E-04	BP	32911	228	321	14	tissue development	EDN1; WT1; TUFT1; PPARA; SMAD3; PTGS2; JUNB; TIPARP; ERFF1; SCEL; THBS1; VAMP5; RELA; HIF1A
GO:0002009	1.00E-07	1.90E-04	BP	32911	228	234	12	morphogenesis of an epithelium	EDN1; TCFAP2A; WT1; TGIF1; ETV4; ADM; NOTCH2; AREG; BCL10; MYC; SOCS3; AR
GO:0010552	1.00E-07	2.10E-04	BP	32911	228	82	8	positive regulation of gene-specific transcription	TRP53; SMAD3; NFKB1; IL1B; CREB1; NFIC; PPARG; CEBPA
GO:0051338	1.00E-07	2.10E-04	BP	32911	228	236	12	regulation of transferase activity	EDN1; TRIB3; GADD45G; CDKN1A; FABP4; GADD45A; IL1B; DUSP16; EREG; ERFF1; BCL10; PPARG
GO:0016043	1.10E-07	2.20E-04	BP	32911	228	1894	35	cellular component organization	WT1; GTF2F2; TUBA4A; MEN1; LOX; TRP53; HSPA1B; ANGPTL4; BRCA1; KRT8; ADM; GADD45A; RHOU; SMAD3; FMNL3; TUBE2C; CREB1; HSPA1A; PRKCI; CLU; KLF5; TSPYL4; AREG; BCL10; MYC; JUN; LRP2; ATF1; CEBPE; LAMA3; PMAIP1; CYR61; HIF1A; CEBPA; S100A9
GO:0048661	1.10E-07	2.30E-04	BP	32911	228	34	6	positive regulation of smooth muscle cell differentiation	PTGS2; EREG; HBEGF; JUN; HIF1A; STAT1
GO:0010551	1.30E-07	2.60E-04	BP	32911	228	117	9	regulation of gene-specific transcription	TRP53; SMAD3; NFKB1; IL1B; CREB1; NFIC; MYC; PPARG; CEBPA
GO:0045892	1.40E-07	2.80E-04	BP	32911	228	343	14	negative regulation of transcription, DNA-dependent	WT1; TGIF1; MEN1; TRP53; SMAD3; NFKB1; HOXC8; NFIC; MYC; PPARG; RARB; EGR1; CEBPA; KLF4

GO:0001775	1.50E-07	2.90E-04	BP	32911	228	243	12	cell activation	SP3; RELB; GADD45G; TRP53; SMAD3; NDRG1; HSPD1; BCL10; TIMP1; SFP11; EGR1; CD48
GO:0051253	1.60E-07	3.10E-04	BP	32911	228	346	14	negative regulation of RNA metabolic process	WT1; TGIF1; MEN1; TRP53; SMAD3; NFKB1; HOXC8; NFIC; MYC; PPARG; RARB; EGR1; CEBPA; KLF4
GO:0001836	1.60E-07	3.20E-04	BP	32911	228	19	5	release of cytochrome c from mitochondria	TRP53; SMAD3; MYC; JUN; PMAIP1
GO:0002573	1.60E-07	3.30E-04	BP	32911	228	36	6	myeloid leukocyte differentiation	SP3; RELB; JUNB; CEBPE; SFP11; CEBPA
GO:0006917	1.70E-07	3.30E-04	BP	32911	228	158	10	induction of apoptosis	HMOX1; TRP53; BRCA1; CEBPB; BCL10; MYC; PRDX1; PMAIP1; STAT1; SFP11
GO:0012502	1.80E-07	3.50E-04	BP	32911	228	159	10	induction of programmed cell death	HMOX1; TRP53; BRCA1; CEBPB; BCL10; MYC; PRDX1; PMAIP1; STAT1; SFP11
GO:0043009	1.80E-07	3.60E-04	BP	32911	228	202	11	chordate embryonic development	SP3; EDN1; TRP53; BRCA1; SMAD3; SP1; JUNB; AR; MAFF; COPS3; MYB
GO:0080134	1.90E-07	3.80E-04	BP	32911	228	249	12	regulation of response to stress	SERPINE1; ZFP36; FABP4; PTGS2; IL1B; EREG; HSPD1; GPX2; BCL10; PRDX1; PPARG; RELA
GO:0032787	2.20E-07	4.30E-04	BP	32911	228	302	13	monocarboxylic acid metabolic process	PPARA; BRCA1; FABP4; ATF3; PTGS2; PTGS1; PGD; PPARG; ATF4; PDK4; HIF1A; CH25H; ELOVL7
GO:0009792	2.20E-07	4.50E-04	BP	32911	228	206	11	embryo development ending in birth or egg hatching	SP3; EDN1; TRP53; BRCA1; SMAD3; SP1; JUNB; AR; MAFF; COPS3; MYB
GO:0002521	2.30E-07	4.60E-04	BP	32911	228	125	9	leukocyte differentiation	SP3; RELB; GADD45G; TRP53; JUNB; CEBPE; SFP11; EGR1; CEBPA
GO:0033554	2.70E-07	5.40E-04	BP	32911	228	419	15	cellular response to stress	BTG2; HMOX1; CDKN1A; TRP53; HSPA1B; BRCA1; ADM; GADD45A; HSPA1A; ERFF11; JUN; TXNRD1; PRDX1; PMAIP1; HIF1A
GO:0019318	3.30E-07	6.60E-04	BP	32911	228	170	10	hexose metabolic process	PPARA; PDK2; ATF3; TALDO1; MYC; PGD; ALDOA; ATF4; PDK4; USF1
GO:0045597	3.30E-07	6.60E-04	BP	32911	228	262	12	positive regulation of cell differentiation	TGIF1; MEN1; JUNB; CLU; JUN; SOCS3; TNFRSF12A; PPARG; RELA; HIF1A; CEBPA; HSP90AA1
GO:0045765	3.40E-07	6.70E-04	BP	32911	228	65	7	regulation of angiogenesis	SERPINE1; CCR2; EPHA2; PTGS2; IL1B; THBS1; ETS1
GO:0001892	3.60E-07	7.10E-04	BP	32911	228	22	5	embryonic placenta development	SP3; SP1; CEBPB; HIF1A; CEBPA
GO:0000122	3.60E-07	7.10E-04	BP	32911	228	264	12	negative regulation of transcription from RNA polymerase II promoter	WT1; TGIF1; MEN1; TRP53; SMAD3; HOXC8; NFIC; MYC; PPARG; RARB; EGR1; CEBPA
GO:0048562	3.60E-07	7.20E-04	BP	32911	228	96	8	embryonic organ morphogenesis	SP3; HOXB1; TCFAP2A; MEN1; EPHA2; SMAD3; SP1; RARB
GO:0045859	4.00E-07	7.90E-04	BP	32911	228	218	11	regulation of protein kinase activity	EDN1; TRIB3; GADD45G; CDKN1A; FABP4; GADD45A; IL1B; DUSP16; EREG; ERFF11; BCL10
GO:0010035	4.00E-07	7.90E-04	BP	32911	228	133	9	response to inorganic substance	HMOX1; MT1; FABP4; MT2; TXNRD1; PRDX1; PPARG; GCLC; CEBPA
GO:0006066	4.10E-07	8.00E-04	BP	32911	228	374	14	alcohol metabolic process	SULT1A1; PPARA; PDK2; ATF3; TALDO1; CYP51; IDI1; MYC; PGD; ALDOA; ATF4; PDK4; CH25H; USF1
GO:0043193	4.30E-07	8.40E-04	BP	32911	228	98	8	positive regulation of gene-specific transcription	TRP53; SMAD3; NFKB1; IL1B; CREB1; NFIC; PPARG; CEBPA
GO:0045321	4.60E-07	9.00E-04	BP	32911	228	221	11	leukocyte activation	SP3; RELB; GADD45G; TRP53; SMAD3; NDRG1; HSPD1; BCL10; SFP11; EGR1; CD48
GO:0032501	5.40E-07	0.001	BP	32911	228	3092	46	multicellular organismal process	SP3; EDN1; HOXB1; GSR; WT1; REL; MEN1; USF2; GADD45G; CCR2; TRP53; HOXA1; FABP4; KRT8; ETV4; STAT3; ADM; PTGS2; SP1; IL1B; NOTCH2; HOXC8; HES6; CREB1; EREG; JUNB; TIPARP; F3; GPX2; AREG; MYC; JUN; VAMP5; SOCS3; AR; TNFRSF12A; IFRD1; HSBP1; RELA; HIF1A; STAT1; GJB3; EGR1; AFP; PDE4B; MMP11
GO:0043549	6.30E-07	0.0012	BP	32911	228	228	11	regulation of kinase activity	EDN1; TRIB3; GADD45G; CDKN1A; FABP4; GADD45A; IL1B; DUSP16; EREG; ERFF11; BCL10
GO:0051093	7.10E-07	0.0013	BP	32911	228	281	12	negative regulation of developmental process	SERPINE1; ZFP36; TRIB3; MEN1; CCR2; TOB2; TRP53; SMAD3; AREG; THBS1; RARB; KLF4
GO:0032583	7.40E-07	0.0014	BP	32911	228	143	9	regulation of gene-specific transcription	TRP53; SMAD3; NFKB1; IL1B; CREB1; NFIC; MYC; PPARG; CEBPA
GO:0030097	7.70E-07	0.0015	BP	32911	228	73	7	hemopoiesis	SP3; RTKN2; MEN1; CCR2; SP1; TIPARP; HIF1A
GO:0042110	7.80E-07	0.0015	BP	32911	228	106	8	T cell activation	SP3; RELB; GADD45G; TRP53; SMAD3; HSPD1; EGR1; CD48
GO:0061138	9.70E-07	0.0019	BP	32911	228	109	8	morphogenesis of a branching epithelium	EDN1; WT1; ETV4; ADM; AREG; MYC; SOCS3; AR
GO:0022603	9.80E-07	0.0019	BP	32911	228	290	12	regulation of anatomical structure morphogenesis	SERPINE1; CCR2; ETV4; EPHA2; RHOU; PTGS2; IL1B; MYC; THBS1; AR; ETS1; TNFRSF12A
GO:0001889	9.90E-07	0.0019	BP	32911	228	48	6	liver development	SP3; SMAD3; SP1; RELA; CEBPA; HP
GO:0051726	1.00E-06	0.0019	BP	32911	228	239	11	regulation of cell cycle	MEN1; GADD45G; CDKN1A; TRP53; GADD45A; EREG; JUNB; MYC; JUN; FOSL1; HSPA8

GO:0031347	1.00E-06	0.002	BP	32911	228	149	9	regulation of defense response	ZFP36; FABP4; PTGS2; IL1B; EREG; HSPD1; GPX2; PPARG; RELA
GO:0008637	1.00E-06	0.0021	BP	32911	228	27	5	apoptotic mitochondrial changes	TRP53; SMAD3; MYC; JUN; PMAIP1
GO:0071310	1.10E-06	0.0023	BP	32911	228	151	9	cellular response to organic substance	TRIB3; PPARA; PRKCI; MYC; AR; PPARG; STAT1; EGR1; CEBPA
GO:0048585	1.20E-06	0.0025	BP	32911	228	113	8	negative regulation of response to stimulus	SERPINE1; ZFP36; PPARA; IL1B; GPX2; SOCS3; PPARG; RELA
GO:0030099	1.30E-06	0.0025	BP	32911	228	79	7	myeloid cell differentiation	SP3; RELB; SP1; JUNB; CEBPE; SFPI1; CEBPA
GO:0044267	1.30E-06	0.0026	BP	32911	228	1556	29	cellular protein metabolic process	SPNB2; BTG2; TRIB3; MEN1; NEDD4L; GADD45G; DNAJB4; PDK2; EPHA2; EIF5; DUSP1; EIF2S2; HSPA9; DNAJC5; CREB1; HSPD1; PRKCI; PTPN21; TIPARP; PTPN14; EIF1A; MRPL28; BCL10; MRPS12; HSP90AB1; PDK4; HSPA8; RPL22L1; HSP90AA1
GO:0001701	1.30E-06	0.0026	BP	32911	228	198	10	in utero embryonic development	SP3; EDN1; TRP53; SMAD3; SP1; JUNB; AR; MAFF; COPS3; MYB
GO:0005996	1.30E-06	0.0026	BP	32911	228	198	10	monosaccharide metabolic process	PPARA; PDK2; ATF3; TALDO1; MYC; PGD; ALDOA; ATF4; PDK4; USF1
GO:0019221	1.40E-06	0.0028	BP	32911	228	80	7	cytokine-mediated signaling pathway	CCR2; KRT8; STAT3; EREG; STAT1; CEBPA; KLF6
GO:0023036	1.40E-06	0.0028	BP	32911	228	80	7	initiation of signal transduction	CCR2; KRT8; STAT3; EREG; STAT1; CEBPA; KLF6
GO:0023038	1.40E-06	0.0028	BP	32911	228	80	7	signal initiation by diffusible mediator	CCR2; KRT8; STAT3; EREG; STAT1; CEBPA; KLF6
GO:0023049	1.40E-06	0.0028	BP	32911	228	80	7	signal initiation by protein/peptide mediator	CCR2; KRT8; STAT3; EREG; STAT1; CEBPA; KLF6
GO:0035466	1.50E-06	0.003	BP	32911	228	614	17	regulation of signaling pathway	TGIF1; MEN1; CCR2; TRP53; SMAD3; IL1B; DUSP16; EREG; ERFF1; BCL10; SOCS3; AR; PRDX1; RELA; HIF1A; FGFBP1; KLF4
GO:0043523	1.70E-06	0.0034	BP	32911	228	118	8	regulation of neuron apoptosis	REL; TRP53; ABCC1; NQO1; DNAJC5; JUN; PMAIP1; GCLC
GO:0006952	2.00E-06	0.0039	BP	32911	228	428	14	defense response	SERPINE1; CCR2; HSPA1B; STAT3; PTGS2; IL1B; BCL10; THBS1; PRDX1; CEBPE; PLAA; PPARG; RELA; SERPINA3N
GO:0040008	2.10E-06	0.0041	BP	32911	228	312	12	regulation of growth	MEN1; TRP53; STAT3; CREB1; HBEGF; CREG1; SOCS3; AR; TNFRSF12A; PPARG; CYR61; HIF1A
GO:0030855	2.50E-06	0.0049	BP	32911	228	87	7	epithelial cell differentiation	WT1; PTGS2; PTGS1; CEBPB; JUN; AR; PPARG
GO:0051240	2.70E-06	0.0053	BP	32911	228	265	11	positive regulation of multicellular organismal process	EDN1; SERPINE1; ADM; SMAD3; PTGS2; IL1B; CREB1; EREG; HSPD1; PTGS1; MYC
GO:0051128	2.90E-06	0.0057	BP	32911	228	442	14	regulation of cellular component organization	SPNB2; SERPINE1; MEN1; TRP53; RHOU; SMAD3; EREG; PRKCI; PODXL; ATF1; ETS1; TNFRSF12A; HSP90AA1; S100A9
GO:0048534	3.40E-06	0.0068	BP	32911	228	129	8	hemopoietic or lymphoid organ development	SP3; RTKN2; MEN1; CCR2; NFKB1; SP1; TIPARP; HIF1A
GO:0008629	3.60E-06	0.007	BP	32911	228	34	5	induction of apoptosis by intracellular signals	HMOX1; TRP53; BRCA1; MYC; PMAIP1
GO:0031399	3.60E-06	0.0071	BP	32911	228	221	10	regulation of protein modification process	TRIB3; MEN1; TRP53; IL1B; IMPACT; ERFF1; BCL10; JUN; SOCS3; GCLC
GO:0008219	3.60E-06	0.0071	BP	32911	228	516	15	cell death	HMOX1; TRIB3; GADD45G; TRP53; KRT8; EPHA2; NFKB1; CLU; BCL10; MYC; PMAIP1; TNFRSF12A; YPEL3; LITAF; TNFSF12
GO:0042035	3.70E-06	0.0074	BP	32911	228	60	6	regulation of cytokine biosynthetic process	REL; NFKB1; IL1B; EREG; CEBPB; RELA
GO:0009725	3.90E-06	0.0077	BP	32911	228	223	10	response to hormone stimulus	HMOX1; TRIB3; LOX; SULT1A1; PPARA; PRKCI; AREG; AR; STAT1; SERPINA3N
GO:0019725	4.10E-06	0.0081	BP	32911	228	393	13	cellular homeostasis	EDN1; GSR; CCR2; TRP53; MT1; ADM; IL1B; MT2; TXNL1; JUN; TXNRD1; PRDX1; HIF1A
GO:0031668	4.10E-06	0.0081	BP	32911	228	35	5	cellular response to extracellular stimulus	USF2; TRP53; FOS; JUN; FOSL1
GO:0019752	4.20E-06	0.0082	BP	32911	228	522	15	carboxylic acid metabolic process	PPARA; BRCA1; FABP4; ATF3; PTGS2; PTGS1; PGD; ASNS; PPARG; ATF4; PDK4; HIF1A; GCLC; CH25H; ELOVL7
GO:0043436	4.20E-06	0.0082	BP	32911	228	522	15	oxoacid metabolic process	PPARA; BRCA1; FABP4; ATF3; PTGS2; PTGS1; PGD; ASNS; PPARG; ATF4; PDK4; HIF1A; GCLC; CH25H; ELOVL7
GO:0006082	4.30E-06	0.0084	BP	32911	228	523	15	organic acid metabolic process	PPARA; BRCA1; FABP4; ATF3; PTGS2; PTGS1; PGD; ASNS; PPARG; ATF4; PDK4; HIF1A; GCLC; CH25H; ELOVL7
GO:0001763	4.30E-06	0.0085	BP	32911	228	133	8	morphogenesis of a branching structure	EDN1; WT1; ETV4; ADM; AREG; MYC; SOCS3; AR
GO:0016265	4.70E-06	0.0092	BP	32911	228	527	15	death	HMOX1; TRIB3; GADD45G; TRP53; KRT8; EPHA2; NFKB1; CLU; BCL10; MYC; PMAIP1; TNFRSF12A; YPEL3; LITAF; TNFSF12
GO:0071496	4.80E-06	0.0094	BP	32911	228	36	5	cellular response to external stimulus	USF2; TRP53; FOS; JUN; FOSL1

GO:0048584	5.10E-06	0.0101	BP	32911	228	230	10	positive regulation of response to stimulus	C4B; CCR2; HSPA1B; FABP4; SMAD3; PTGS2; IL1B; EREG; HSPD1; RELA
GO:0048705	5.20E-06	0.0103	BP	32911	228	97	7	skeletal system morphogenesis	HOXB1; TCFAP2A; MEN1; SMAD3; HOXC8; TIPARP; MYC
GO:0010646	5.40E-06	0.0107	BP	32911	228	824	19	regulation of cell communication	EDN1; TGIF1; CCR2; TRP53; PTGS2; IL1B; DUSP16; CREB1; EREG; ERRF1; BCL10; SOCS3; AR; PRDX1; RELA; HIF1A; EGR1; FGFBP1; KLF4
GO:0045444	5.50E-06	0.0108	BP	32911	228	64	6	fat cell differentiation	FABP4; LRG1; PTGS2; CEBPB; PPARG; CEBPA
GO:0046649	5.70E-06	0.0112	BP	32911	228	183	9	lymphocyte activation	SP3; RELB; GADD45G; TRP53; SMAD3; HSPD1; SFPI1; EGR1; CD48
GO:0042180	5.70E-06	0.0113	BP	32911	228	536	15	cellular ketone metabolic process	PPARA; BRCA1; FABP4; ATF3; PTGS2; PTGS1; PGD; ASNS; PPARG; ATF4; PDK4; HIF1A; GCLC; CH25H; FLOV17
GO:0006916	6.00E-06	0.0118	BP	32911	228	99	7	anti-apoptosis	HSPA1B; NFKB1; HSPD1; CLU; CEBPB; MYC; ETS1
GO:0035239	6.30E-06	0.0125	BP	32911	228	140	8	tube morphogenesis	EDN1; WT1; ETV4; SMAD3; AREG; MYC; AR; HIF1A
GO:0050727	6.90E-06	0.0135	BP	32911	228	101	7	regulation of inflammatory response	ZFP36; FABP4; PTGS2; IL1B; HSPD1; GPX2; PPARG
GO:0051130	7.70E-06	0.0152	BP	32911	228	190	9	positive regulation of cellular component organization	SERPINE1; MEN1; TRP53; SMAD3; EREG; PRKCI; ATF1; TNFRSF12A; HSP90AA1
GO:0009991	7.80E-06	0.0154	BP	32911	228	103	7	response to extracellular stimulus	USF2; TRP53; FOS; JUN; FOSL1; STAT1; KLF4
GO:0060674	8.00E-06	0.0156	BP	32911	228	19	4	placenta blood vessel development	JUNB; HS6ST1; SOCS3; CYR61
GO:0001568	8.60E-06	0.0168	BP	32911	228	69	6	blood vessel development	LOX; EPHA2; JUNB; HS6ST1; SOCS3; CYR61
GO:0002684	8.70E-06	0.017	BP	32911	228	244	10	positive regulation of immune system process	C4B; CCR2; CDKN1A; TRP53; HSPA1B; EREG; HSPD1; BCL10; RELA; HSP90AA1
GO:0051246	1.00E-05	0.0203	BP	32911	228	428	13	regulation of protein metabolic process	SERPINE1; TRIB3; MEN1; TRP53; IL1B; IMPACT; PSMD3; ERRF1; BCL10; JUN; SOCS3; RELA; GCLC
GO:0030225	1.10E-05	0.022	BP	32911	228	7	3	macrophage differentiation	CEBPE; SFPI1; CEBPA
GO:0071636	1.10E-05	0.022	BP	32911	228	7	3	positive regulation of transforming growth	SMAD3; PTGS2; CREB1
GO:0001819	1.10E-05	0.0234	BP	32911	228	73	6	positive regulation of cytokine production	SMAD3; PTGS2; IL1B; CREB1; EREG; HSPD1
GO:0032103	1.10E-05	0.0234	BP	32911	228	73	6	positive regulation of response to external	CCR2; FABP4; SMAD3; PTGS2; IL1B; HSPD1
GO:0005975	1.20E-05	0.0247	BP	32911	228	436	13	carbohydrate metabolic process	PPARA; PDK2; ATF3; TALD01; LYVE1; HS6ST1; MYC; PGD; ALDOA; CHI3L1; ATF4; PDK4; USF1
GO:0009719	1.20E-05	0.025	BP	32911	228	255	10	response to endogenous stimulus	HMOX1; TRIB3; LOX; SULT1A1; PPARA; PRKCI; AREG; AR; STAT1; SERPINA3N
GO:0002274	1.60E-05	0.0325	BP	32911	228	46	5	myeloid leukocyte activation	RELB; NDRG1; BCL10; SFPI1; CD48
GO:0010574	1.70E-05	0.035	BP	32911	228	8	3	regulation of vascular endothelial growth factor	CCR2; PTGS2; IL1B
GO:0045075	1.70E-05	0.035	BP	32911	228	8	3	regulation of interleukin-12 biosynthetic process	REL; NFKB1; RELA
GO:0060136	1.70E-05	0.035	BP	32911	228	8	3	embryonic process involved in female pregnancy	SP3; SP1; JUNB
GO:0071285	1.70E-05	0.035	BP	32911	228	8	3	cellular response to lithium ion	FABP4; PPARG; CEBPA
GO:0071634	1.70E-05	0.035	BP	32911	228	8	3	regulation of transforming growth factor-beta	SMAD3; PTGS2; CREB1
GO:0006457	1.90E-05	0.0375	BP	32911	228	118	7	protein folding	DNAJB4; HSPA9; DNAJC5; HSPD1; HSP90AB1; HSPA8; HSP90AA1
GO:0002237	2.00E-05	0.0397	BP	32911	228	80	6	response to molecule of bacterial origin	ADM; PTGS2; IL1B; CEBPB; RELA; STAT1
GO:0007005	2.10E-05	0.0426	BP	32911	228	81	6	mitochondrion organization	TRP53; SMAD3; MYC; JUN; PMAIP1; CEBPA
GO:0009628	2.20E-05	0.0436	BP	32911	228	272	10	response to abiotic stimulus	HSPB8; CDKN1A; TRP53; HSPA1B; KRT8; HSPA1A; MYC; LRP2; PMAIP1; STAT1
GO:0023014	2.60E-05	0.0513	BP	32911	228	170	8	signal transmission via phosphorylation event	EDN1; REL; ZFP36; STAT3; ERRF1; BCL10; SOCS3; STAT1
GO:0007243	2.60E-05	0.0513	BP	32911	228	170	8	intracellular protein kinase cascade	EDN1; REL; ZFP36; STAT3; ERRF1; BCL10; SOCS3; STAT1
GO:0010226	2.60E-05	0.0523	BP	32911	228	9	3	response to lithium ion	FABP4; PPARG; CEBPA
GO:0071241	2.60E-05	0.0523	BP	32911	228	9	3	cellular response to inorganic substance	FABP4; PPARG; CEBPA
GO:0071248	2.60E-05	0.0523	BP	32911	228	9	3	cellular response to metal ion	FABP4; PPARG; CEBPA

GO:0031349	2.60E-05	0.0524	BP	32911	228	84	6	positive regulation of defense response	FABP4; PTGS2; IL1B; EREG; HSPD1; RELA
GO:0034097	3.00E-05	0.0596	BP	32911	228	52	5	response to cytokine stimulus	STAT3; PTGS2; PRKCI; STAT1; SERPINA3N
GO:0048545	3.00E-05	0.06	BP	32911	228	86	6	response to steroid hormone stimulus	HMOX1; LOX; SULT1A1; PPARA; AREG; AR
GO:0051051	3.40E-05	0.0667	BP	32911	228	129	7	negative regulation of transport	EDN1; HMOX1; NEDD4L; PTGS2; YRDC; IL1B; PTGS1
GO:0045596	3.40E-05	0.067	BP	32911	228	229	9	negative regulation of cell differentiation	ZFP36; TRIB3; MEN1; TOB2; TRP53; SMAD3; AREG; RARB; KLF4
GO:0045408	3.70E-05	0.0743	BP	32911	228	10	3	regulation of interleukin-6 biosynthetic process	IL1B; EREG; CEBPB
GO:0034599	4.00E-05	0.0789	BP	32911	228	28	4	cellular response to oxidative stress	HMOX1; TXNRD1; PRDX1; HIF1A
GO:0042060	4.00E-05	0.0789	BP	32911	228	28	4	wound healing	SERPINE1; LOX; PPARA; NOTCH2
GO:0006954	4.20E-05	0.0835	BP	32911	228	182	8	inflammatory response	CCR2; STAT3; PTGS2; IL1B; THBS1; PLAA; PPARG; SERPINA3N
GO:0021754	4.70E-05	0.0935	BP	32911	228	2	2	facial nucleus development	HOXB1; HOXA1
GO:0032916	4.70E-05	0.0935	BP	32911	228	2	2	positive regulation of transforming growth factor-beta3 production	SMAD3; CREB1
GO:0042908	4.70E-05	0.0935	BP	32911	228	2	2	xenobiotic transport	ABCC1; SLC2A1
GO:0045063	4.70E-05	0.0935	BP	32911	228	2	2	T-helper 1 cell differentiation	RELB; GADD45G
GO:0007098	4.70E-05	0.0935	BP	32911	228	2	2	centrosome cycle	BRCA1; GADD45A
GO:0008633	4.70E-05	0.0935	BP	32911	228	2	2	activation of pro-apoptotic gene products	SMAD3; MYC
GO:0050872	5.10E-05	0.1017	BP	32911	228	11	3	white fat cell differentiation	FABP4; PPARG; CEBPA
GO:0042493	5.30E-05	0.1053	BP	32911	228	95	6	response to drug	TRP53; ABCC1; CREB1; FOS; JUN; STAT1
GO:0048878	5.60E-05	0.1106	BP	32911	228	434	12	chemical homeostasis	EDN1; USF2; CCR2; TRP53; MT1; FABP4; STAT3; ADM; IL1B; MT2; JUN; HIF1A
GO:0030098	5.70E-05	0.1117	BP	32911	228	96	6	lymphocyte differentiation	SP3; RELB; GADD45G; TRP53; SFP11; EGR1
GO:0043525	6.00E-05	0.1193	BP	32911	228	31	4	positive regulation of neuron apoptosis	TRP53; NQO1; JUN; PMAIP1
GO:0030217	6.10E-05	0.1197	BP	32911	228	60	5	T cell differentiation	SP3; RELB; GADD45G; TRP53; EGR1
GO:0032102	6.60E-05	0.1297	BP	32911	228	61	5	negative regulation of response to external stimulus	SERPINE1; ZFP36; PPARA; GPX2; PPARG
GO:0002286	6.80E-05	0.1349	BP	32911	228	12	3	T cell activation involved in immune response	RELB; GADD45G; TRP53
GO:0060326	6.90E-05	0.1356	BP	32911	228	32	4	cell chemotaxis	CSF3R; ABCC1; IL1B; S100A9
GO:0008283	7.10E-05	0.1403	BP	32911	228	252	9	cell proliferation	GNL3; TRP53; JUNB; AREG; CEBPB; TXNRD1; PRDX1; LRP2; EGR1
GO:0045766	7.80E-05	0.1535	BP	32911	228	33	4	positive regulation of angiogenesis	SERPINE1; PTGS2; IL1B; ETS1
GO:0007167	8.50E-05	0.1679	BP	32911	228	258	9	enzyme linked receptor protein signaling pathway	TRP53; EPHA2; SMAD3; CREB1; EREG; HBEGF; TIPARP; AREG; EGR1
GO:0001829	8.90E-05	0.1745	BP	32911	228	13	3	trophectodermal cell differentiation	SP3; SP1; JUNB
GO:0046627	8.90E-05	0.1745	BP	32911	228	13	3	negative regulation of insulin receptor signaling pathway	IL1B; SOCS3; RELA

GO:0032496	8.90E-05	0.176	BP	32911	228	65	5	response to lipopolysaccharide	ADM; PTGS2; IL1B; CEBPB; STAT1
GO:0022414	9.10E-05	0.1794	BP	32911	228	604	14	reproductive process	SP3; GSR; WT1; MEN1; USF2; PTGS2; SP1; CREB1; EREG; JUNB; TIPARP; AREG; AR; AFP
GO:0044262	9.30E-05	0.184	BP	32911	228	323	10	cellular carbohydrate metabolic process	PPARA; PDK2; ATF3; TALD01; MYC; PGD; ALDOA; ATF4; PDK4; USF1
GO:0006631	9.40E-05	0.1859	BP	32911	228	204	8	fatty acid metabolic process	PPARA; BRCA1; FABP4; PTGS2; PTGS1; PPARG; CH25H; ELOVL7
GO:0019229	9.90E-05	0.1943	BP	32911	228	35	4	regulation of vasoconstriction	EDN1; HSPA1B; PTGS2; PTGS1
GO:0006915	1.00E-04	0.1996	BP	32911	228	462	12	apoptosis	TRIB3; GADD45G; TRP53; KRT8; EPHA2; NFKB1; BCL10; MYC; PMAIP1; TNFRSF12A; YPEL3; LITAF
GO:0048754	1.00E-04	0.2044	BP	32911	228	107	6	branching morphogenesis of a tube	EDN1; WT1; ETV4; AREG; MYC; AR
GO:0051098	1.00E-04	0.2044	BP	32911	228	107	6	regulation of binding	HMOX1; TRIB3; SMAD3; BCL10; MYC; RELA
GO:0051248	1.00E-04	0.2044	BP	32911	228	107	6	negative regulation of protein metabolic process	SERPINE1; IMPACT; ERFF1; JUN; RELA; GCLC
GO:0006275	1.10E-04	0.2174	BP	32911	228	36	4	regulation of DNA replication	TRP53; EREG; JUN; ATF1
GO:0010165	1.10E-04	0.221	BP	32911	228	14	3	response to X-ray	TRP53; LRP2; PMAIP1
GO:0048048	1.10E-04	0.221	BP	32911	228	14	3	embryonic eye morphogenesis	SP3; SP1; RARB
GO:0048609	1.10E-04	0.2304	BP	32911	228	332	10	reproductive process in a multicellular organism	SP3; GSR; MEN1; USF2; PTGS2; SP1; CREB1; EREG; JUNB; AFP
GO:0012501	1.10E-04	0.2343	BP	32911	228	470	12	programmed cell death	TRIB3; GADD45G; TRP53; KRT8; EPHA2; NFKB1; BCL10; MYC; PMAIP1; TNFRSF12A; YPEL3; LITAF
GO:0042330	1.20E-04	0.2382	BP	32911	228	110	6	taxis	CSF3R; ABCC1; IL1B; S100A8; CYR61; S100A9
GO:0006935	1.20E-04	0.2382	BP	32911	228	110	6	chemotaxis	CSF3R; ABCC1; IL1B; S100A8; CYR61; S100A9
GO:0003002	1.30E-04	0.2671	BP	32911	228	215	8	regionalization	BTG2; EDN1; HOXB1; TGIF1; TRP53; HOXA1; SMAD3; HOXC8
GO:0006629	1.30E-04	0.2678	BP	32911	228	707	15	lipid metabolic process	SULT1A1; PPARA; SAMD8; BRCA1; FABP4; ADM; PTGS2; CYP51; PTGS1; TIPARP; IDI1; PPARG; CH25H; AFP; ELOVL7
GO:0009056	1.30E-04	0.2693	BP	32911	228	789	16	catabolic process	HMOX1; ZFP36; RHOU; TALD01; GSTA2; LYVE1; MYC; TXNRD1; PRDX1; PGD; ALDOA; CHI3L1; PSMA5; HSPA8; PSMC1; PDE4B
GO:0030728	1.40E-04	0.2748	BP	32911	228	15	3	ovulation	PTGS2; EREG; AFP
GO:0045576	1.40E-04	0.2748	BP	32911	228	15	3	mast cell activation	NDRG1; BCL10; CD48
GO:0060716	1.40E-04	0.2748	BP	32911	228	15	3	labyrinthine layer blood vessel development	JUNB; HS6ST1; CYR61
GO:0010273	1.40E-04	0.2794	BP	32911	228	3	2	detoxification of copper ion	MT1; MT2
GO:0021570	1.40E-04	0.2794	BP	32911	228	3	2	rhombomere 4 development	HOXB1; HOXA1
GO:0021571	1.40E-04	0.2794	BP	32911	228	3	2	rhombomere 5 development	HOXB1; HOXA1
GO:0030219	1.40E-04	0.2794	BP	32911	228	3	2	megakaryocyte differentiation	SP3; SP1
GO:0032910	1.40E-04	0.2794	BP	32911	228	3	2	regulation of transforming growth factor-beta3	SMAD3; CREB1
GO:0042026	1.40E-04	0.2794	BP	32911	228	3	2	protein refolding	HSPD1; HSP90AA1
GO:0042108	1.50E-04	0.2986	BP	32911	228	39	4	positive regulation of cytokine biosynthetic	REL; IL1B; EREG; RELA
GO:0055114	1.50E-04	0.3117	BP	32911	228	637	14	oxidation reduction	GSR; HMOX1; LOX; SRXN1; PTGS2; NQO1; CYP51; TXNL1; PTGS1; GPX2; TXNRD1; PRDX1; PGD; CH25H
GO:0007173	1.70E-04	0.3366	BP	32911	228	16	3	epidermal growth factor receptor signaling pathway	EREG; HBEGF; AREG
GO:0044283	1.70E-04	0.3391	BP	32911	228	417	11	small molecule biosynthetic process	BRCA1; ATF3; PTGS2; PTGS1; PGD; ASNS; ATF4; AMPD3; GCLC; CH25H; ELOVL7
GO:0051049	1.70E-04	0.3444	BP	32911	228	490	12	regulation of transport	EDN1; SERPINE1; HMOX1; TRIB3; NEDD4L; PTGS2; YRDC; IL1B; CREB1; PRKCI; PTGS1; PRDX1
GO:0008202	1.70E-04	0.3514	BP	32911	228	168	7	steroid metabolic process	SULT1A1; ADM; CYP51; TIPARP; IDI1; CH25H; AFP
GO:0050776	1.80E-04	0.3536	BP	32911	228	224	8	regulation of immune response	C4B; HMOX1; CCR2; HSPA1B; SMAD3; EREG; GPX2; RELA

GO:0030003	2.00E-04	0.3988	BP	32911	228	228	8	cellular cation homeostasis	EDN1; CCR2; TRP53; MT1; ADM; IL1B; MT2; HIF1A
GO:0010553	2.00E-04	0.3999	BP	32911	228	42	4	negative regulation of gene-specific	SMAD3; NFIC; MYC; PPARG
GO:0023034	2.00E-04	0.4044	BP	32911	228	818	16	intracellular signaling pathway	EDN1; REL; HMOX1; ZFP36; TRP53; BRCA1; STAT3; RHOU; ARF3; DUSP1; PRKCI; ERRF1; BCL10; SOCS3;
GO:0045668	2.00E-04	0.4066	BP	32911	228	17	3	negative regulation of osteoblast differentiation	MEN1; SMAD3; AREG
GO:0010038	2.10E-04	0.4184	BP	32911	228	78	5	response to metal ion	MT1; FABP4; MT2; PPARG; CEBPA
GO:0006974	2.10E-04	0.425	BP	32911	228	292	9	response to DNA damage stimulus	BTG2; HMOX1; CDKN1A; TRP53; HSPA1B; BRCA1; GADD45A; HSPA1A; PMAIP1
GO:0006986	2.20E-04	0.4385	BP	32911	228	43	4	response to unfolded protein	HSPA1B; HSPA1A; UBXX4; HSP90AA1
GO:0032268	2.30E-04	0.4526	BP	32911	228	361	10	regulation of cellular protein metabolic process	TRIB3; MEN1; TRP53; IL1B; IMPACT; ERRF1; BCL10; JUN; SOCS3; GCLC
GO:0007389	2.40E-04	0.4699	BP	32911	228	296	9	pattern specification process	BTG2; EDN1; HOXB1; TGIF1; TRP53; HOXA1; SMAD3; NOTCH2; HOXC8
GO:0002285	2.40E-04	0.4854	BP	32911	228	18	3	lymphocyte activation involved in immune	RELB; GADD45G; TRP53
GO:0031669	2.40E-04	0.4854	BP	32911	228	18	3	cellular response to nutrient levels	USF2; TRP53; JUN
GO:0045987	2.40E-04	0.4854	BP	32911	228	18	3	positive regulation of smooth muscle contraction	EDN1; PTGS2; PTGS1
GO:0046626	2.40E-04	0.4854	BP	32911	228	18	3	regulation of insulin receptor signaling pathway	IL1B; SOCS3; RELA
GO:0042176	2.60E-04	0.5237	BP	32911	228	45	4	regulation of protein catabolic process	TRIB3; PSMD3; RELA; GCLC
GO:0050900	2.60E-04	0.5237	BP	32911	228	45	4	leukocyte migration	CSF3R; IL1B; PODXL; S100A9
GO:0035467	2.80E-04	0.5541	BP	32911	228	181	7	negative regulation of signaling pathway	TGIF1; TRP53; IL1B; ERRF1; SOCS3; RELA; KLF4
GO:0021612	2.80E-04	0.5562	BP	32911	228	4	2	facial nerve structural organization	HOXB1; HOXA1
GO:0002294	2.80E-04	0.5562	BP	32911	228	4	2	CD4-positive, alpha-beta T cell differentiation	RELB; GADD45G
GO:0042093	2.80E-04	0.5562	BP	32911	228	4	2	T-helper cell differentiation	RELB; GADD45G
GO:0043618	2.80E-04	0.5562	BP	32911	228	4	2	regulation of transcription from RNA	HMOX1; HIF1A
GO:0043619	2.80E-04	0.5562	BP	32911	228	4	2	regulation of transcription from RNA	HMOX1; HIF1A
GO:0045896	2.80E-04	0.5562	BP	32911	228	4	2	regulation of transcription, mitotic	JUNB; FOSL1
GO:0045897	2.80E-04	0.5562	BP	32911	228	4	2	positive regulation of transcription, mitotic	JUNB; FOSL1
GO:0046021	2.80E-04	0.5562	BP	32911	228	4	2	regulation of transcription from RNA	JUNB; FOSL1
GO:0046022	2.80E-04	0.5562	BP	32911	228	4	2	positive regulation of transcription from RNA	JUNB; FOSL1
GO:0032870	2.80E-04	0.5595	BP	32911	228	83	5	cellular response to hormone stimulus	TRIB3; PPARA; PRKCI; AR; STAT1
GO:0052548	2.80E-04	0.5595	BP	32911	228	83	5	regulation of endopeptidase activity	SERPINE1; MEN1; HSPA1B; BCL10; MYC
GO:0007259	2.90E-04	0.5735	BP	32911	228	19	3	JAK-STAT cascade	STAT3; SOCS3; STAT1
GO:0040011	3.10E-04	0.612	BP	32911	228	375	10	locomotion	CSF3R; ABCC1; IL1B; HBEGF; PODXL; S100A8; CYR61; HIF1A; HSP90AA1; S100A9
GO:0050729	3.10E-04	0.6202	BP	32911	228	47	4	positive regulation of inflammatory response	FABP4; PTGS2; IL1B; HSPD1
GO:0016052	3.10E-04	0.6251	BP	32911	228	85	5	carbohydrate catabolic process	TALDO1; LYVE1; PGD; ALDOA; CHI3L1
GO:0031667	3.30E-04	0.66	BP	32911	228	86	5	response to nutrient levels	USF2; TRP53; JUN; STAT1; KLF4
GO:0071495	3.30E-04	0.66	BP	32911	228	86	5	cellular response to endogenous stimulus	TRIB3; PPARA; PRKCI; AR; STAT1
GO:0010648	3.30E-04	0.665	BP	32911	228	246	8	negative regulation of cell communication	TGIF1; TRP53; PTGS2; IL1B; ERRF1; SOCS3; RELA; KLF4
GO:0045740	3.40E-04	0.6713	BP	32911	228	20	3	positive regulation of DNA replication	EREG; JUN; ATF1
GO:0044093	3.50E-04	0.6934	BP	32911	228	381	10	positive regulation of molecular function	EDN1; TRIB3; MEN1; GADD45G; SMAD3; IL1B; EREG; BCL10; MYC; RELA
GO:0051336	3.50E-04	0.7018	BP	32911	228	248	8	regulation of hydrolase activity	EDN1; SERPINE1; MEN1; HSPA1B; TBC1D15; SMAD3; BCL10; MYC
GO:0006873	3.60E-04	0.7236	BP	32911	228	314	9	cellular ion homeostasis	EDN1; CCR2; TRP53; MT1; ADM; IL1B; MT2; JUN; HIF1A
GO:0006633	3.90E-04	0.7735	BP	32911	228	89	5	fatty acid biosynthetic process	BRCA1; PTGS2; PTGS1; CH25H; ELOVL7
GO:0045933	3.90E-04	0.7792	BP	32911	228	21	3	positive regulation of muscle contraction	EDN1; PTGS2; PTGS1

GO:0008630	3.90E-04	0.7792	BP	32911	228	21	3	DNA damage response, signal transduction	HMOX1; TRP53; BRCA1
GO:0043408	3.90E-04	0.783	BP	32911	228	137	6	regulation of MAPKKK cascade	CCR2; IL1B; BCL10; AR; PRDX1; KLF4
GO:0001570	4.00E-04	0.7879	BP	32911	228	50	4	vasculogenesis	WT1; EPHA2; JUNB; TIPARP
GO:0042326	4.00E-04	0.7879	BP	32911	228	50	4	negative regulation of phosphorylation	CDKN1A; IMPACT; ERFF1; JUN
GO:0043085	4.00E-04	0.7931	BP	32911	228	318	9	positive regulation of catalytic activity	EDN1; TRIB3; MEN1; GADD45G; SMAD3; IL1B; EREG; BCL10; MYC
GO:0052547	4.10E-04	0.8144	BP	32911	228	90	5	regulation of peptidase activity	SERPINE1; MEN1; HSPA1B; BCL10; MYC
GO:0055082	4.40E-04	0.868	BP	32911	228	322	9	cellular chemical homeostasis	EDN1; CCR2; TRP53; MT1; ADM; IL1B; MT2; JUN; HIF1A
GO:0055080	4.50E-04	0.889	BP	32911	228	257	8	cation homeostasis	EDN1; CCR2; TRP53; MT1; ADM; IL1B; MT2; HIF1A
GO:0032655	4.50E-04	0.8976	BP	32911	228	22	3	regulation of interleukin-12 production	REL; NFKB1; RELA
GO:0022607	4.50E-04	0.8988	BP	32911	228	545	12	cellular component assembly	GTF2F2; TUBA4A; LOX; ANGPTL4; SMAD3; TUBB2C; KLF5; TSPYL4; BCL10; MYC; ATF1; LAMA3
GO:0008217	4.60E-04	0.9012	BP	32911	228	92	5	regulation of blood pressure	EDN1; HMOX1; PPARA; PTGS2; PTGS1
GO:0018106	4.70E-04	0.9228	BP	32911	228	5	2	peptidyl-histidine phosphorylation	PDK2; PDK4
GO:0021604	4.70E-04	0.9228	BP	32911	228	5	2	cranial nerve structural organization	HOXB1; HOXA1
GO:0002292	4.70E-04	0.9228	BP	32911	228	5	2	T cell differentiation involved in immune	RELB; GADD45G
GO:0002293	4.70E-04	0.9228	BP	32911	228	5	2	alpha-beta T cell differentiation involved	RELB; GADD45G
GO:0043401	4.70E-04	0.9228	BP	32911	228	5	2	steroid hormone mediated signaling pathway	PPARA; AR
GO:0043620	4.70E-04	0.9228	BP	32911	228	5	2	regulation of transcription in response	HMOX1; HIF1A
GO:0016477	4.70E-04	0.9356	BP	32911	228	259	8	cell migration	CSF3R; ABCC1; IL1B; HBEGF; PODXL; HIF1A; HSP90AA1; S100A9
GO:0006928	4.70E-04	0.9371	BP	32911	228	396	10	cellular component movement	HOXA1; CSF3R; ETV4; ABCC1; IL1B; HBEGF; PODXL; HIF1A; HSP90AA1; S100A9
GO:0048589	4.80E-04	0.9471	BP	32911	228	93	5	developmental growth	ADM; SMAD3; PTGS2; HBEGF; AR
GO:0044057	4.80E-04	0.9486	BP	32911	228	326	9	regulation of system process	EDN1; HSPA1B; ADM; PTGS2; IL1B; HBEGF; PTGS1; EGR1; KLF4
GO:0010563	5.00E-04	0.9857	BP	32911	228	53	4	negative regulation of phosphorus metabolic	CDKN1A; IMPACT; ERFF1; JUN
GO:0031400	5.00E-04	0.9857	BP	32911	228	53	4	negative regulation of protein modification	IMPACT; ERFF1; JUN; GCLC
GO:0032582	5.00E-04	0.9857	BP	32911	228	53	4	negative regulation of gene-specific	SMAD3; NFIC; MYC; PPARG
GO:0045936	5.00E-04	0.9857	BP	32911	228	53	4	negative regulation of phosphate metabolic	CDKN1A; IMPACT; ERFF1; JUN
GO:0030182	5.20E-04	1	BP	32911	228	144	6	neuron differentiation	BTG2; HOXA1; STAT3; EPHA2; HOXC8; CEBPB
GO:0001890	5.20E-04	1	BP	32911	228	23	3	placenta development	HSP90AB1; PPARG; GJB3
GO:0009952	5.40E-04	1	BP	32911	228	145	6	anterior/posterior pattern formation	BTG2; HOXB1; TRP53; HOXA1; SMAD3; HOXC8
GO:0001659	5.90E-04	1	BP	32911	228	24	3	temperature homeostasis	STAT3; IL1B; GPX2
GO:0030005	6.30E-04	1	BP	32911	228	207	7	cellular di-, tri-valent inorganic cation	EDN1; CCR2; MT1; ADM; IL1B; MT2; HIF1A
GO:0001501	6.40E-04	1	BP	32911	228	99	5	skeletal system development	SP3; EDN1; EPHA2; SMAD3; SP1
GO:0051186	6.50E-04	1	BP	32911	228	208	7	cofactor metabolic process	GSR; HMOX1; TALDO1; ACOT10; PGD; PDK4; GCLC
GO:0048731	6.60E-04	1	BP	32911	228	413	10	system development	SP3; EDN1; TRP53; HOXA1; EPHA2; SMAD3; SP1; HES6; FOS; MAFK
GO:0016053	6.60E-04	1	BP	32911	228	151	6	organic acid biosynthetic process	BRCA1; PTGS2; PTGS1; ASNS; CH25H; ELOVL7
GO:0046394	6.60E-04	1	BP	32911	228	151	6	carboxylic acid biosynthetic process	BRCA1; PTGS2; PTGS1; ASNS; CH25H; ELOVL7
GO:0051241	6.60E-04	1	BP	32911	228	151	6	negative regulation of multicellular organismal	HMOX1; HSPA1B; PTGS2; NFKB1; PPARG; KLF4
GO:0010827	6.70E-04	1	BP	32911	228	25	3	regulation of glucose transport	TRIB3; IL1B; PRKCI
GO:0010575	7.00E-04	1	BP	32911	228	6	2	positive regulation vascular endothelial	PTGS2; IL1B
GO:0019953	7.00E-04	1	BP	32911	228	6	2	sexual reproduction	STAT3; AFP
GO:0002287	7.00E-04	1	BP	32911	228	6	2	alpha-beta T cell activation involved in	RELB; GADD45G

GO:0000003	7.00E-04	1	BP	32911	228	6	2	reproduction	STAT3; AFP
GO:0030851	7.00E-04	1	BP	32911	228	6	2	granulocyte differentiation	SP3; SFPI1
GO:0043353	7.00E-04	1	BP	32911	228	6	2	enucleate erythrocyte differentiation	SP3; SP1
GO:0045084	7.00E-04	1	BP	32911	228	6	2	positive regulation of interleukin-12	REL; RELA
GO:0045410	7.00E-04	1	BP	32911	228	6	2	positive regulation of interleukin-6 biosynthetic	IL1B; EREG
GO:0007263	7.00E-04	1	BP	32911	228	6	2	nitric oxide mediated signal transduction	MT1; MT2
GO:0010638	7.00E-04	1	BP	32911	228	58	4	positive regulation of organelle organization	MEN1; TRP53; SMAD3; EREG
GO:0045454	7.00E-04	1	BP	32911	228	58	4	cell redox homeostasis	GSR; TXNL1; TXNRD1; PRDX1
GO:0050801	7.20E-04	1	BP	32911	228	345	9	ion homeostasis	EDN1; CCR2; TRP53; MT1; ADM; IL1B; MT2; JUN; HIF1A
GO:0051707	7.20E-04	1	BP	32911	228	212	7	response to other organism	SERPINE1; KRT8; GPX2; BCL10; CEBPE; RELA; STAT1
GO:0045637	7.50E-04	1	BP	32911	228	59	4	regulation of myeloid cell differentiation	ZFP36; TOB2; JUN; HIF1A
GO:0016525	7.50E-04	1	BP	32911	228	26	3	negative regulation of angiogenesis	SERPINE1; CCR2; THBS1
GO:0043281	8.00E-04	1	BP	32911	228	60	4	regulation of caspase activity	MEN1; HSPA1B; BCL10; MYC
GO:0044236	8.40E-04	1	BP	32911	228	27	3	multicellular organismal metabolic process	TIPARP; HIF1A; MMP11
GO:0055066	9.00E-04	1	BP	32911	228	220	7	di-, tri-valent inorganic cation homeostasis	EDN1; CCR2; MT1; ADM; IL1B; MT2; HIF1A
GO:0051345	9.10E-04	1	BP	32911	228	107	5	positive regulation of hydrolase activity	EDN1; MEN1; SMAD3; BCL10; MYC
GO:0016070	9.20E-04	1	BP	32911	228	591	12	RNA metabolic process	WT1; GTF2F2; ZFP36; TRP53; STAT3; SMAD3; CREB1; FOS; JUNB; DDX39; MYC; JUN
GO:0051704	9.30E-04	1	BP	32911	228	287	8	multi-organism process	SERPINE1; KRT8; IL1B; GPX2; BCL10; CEBPE; RELA; STAT1
GO:0048145	9.40E-04	1	BP	32911	228	28	3	regulation of fibroblast proliferation	TGIF1; TRP53; PMAIP1
GO:0048871	9.40E-04	1	BP	32911	228	28	3	multicellular organismal homeostasis	STAT3; IL1B; GPX2
GO:0034754	9.70E-04	1	BP	32911	228	63	4	cellular hormone metabolic process	SULT1A1; ADM; TIPARP; AFP
GO:0048704	9.70E-04	1	BP	32911	228	63	4	embryonic skeletal system morphogenesis	HOXB1; TCFAP2A; MEN1; SMAD3
GO:0018202	9.80E-04	1	BP	32911	228	7	2	peptidyl-histidine modification	PKD2; PKD4
GO:0021546	9.80E-04	1	BP	32911	228	7	2	rhombomere development	HOXB1; HOXA1
GO:0031023	9.80E-04	1	BP	32911	228	7	2	microtubule organizing center organization	BRCA1; GADD45A
GO:0046321	9.80E-04	1	BP	32911	228	7	2	positive regulation of fatty acid oxidation	PPARA; PPARG
GO:0046697	9.80E-04	1	BP	32911	228	7	2	decidualization	PTGS2; JUNB
GO:0048857	9.80E-04	1	BP	32911	228	7	2	neural nucleus development	HOXB1; HOXA1
GO:0051297	9.80E-04	1	BP	32911	228	7	2	centrosome organization	BRCA1; GADD45A
GO:0006882	9.80E-04	1	BP	32911	228	7	2	cellular zinc ion homeostasis	MT1; MT2
GO:0007176	9.80E-04	1	BP	32911	228	7	2	regulation of epidermal growth factor receptor	EREG; ERRFI1
GO:0043434	9.90E-04	1	BP	32911	228	109	5	response to peptide hormone stimulus	TRIB3; PPARA; PRKCI; STAT1; SERPINA3N
GO:0006955	9.90E-04	1	BP	32911	228	290	8	immune response	C4B; RELB; CCR2; IL1B; TINAGL1; BCL10; PRDX1; IGJ
GO:0006413	0.001	1	BP	32911	228	29	3	translational initiation	EIF5; EIF2S2; EIF1A
GO:0006953	0.001	1	BP	32911	228	29	3	acute-phase response	STAT3; IL1B; SERPINA3N
GO:0043623	0.001	1	BP	32911	228	65	4	cellular protein complex assembly	TUBA4A; SMAD3; TUBB2C; ATF1
GO:0006461	1.10E-03	1	BP	32911	228	296	8	protein complex assembly	GTF2F2; TUBA4A; ANGPTL4; SMAD3; TUBB2C; BCL10; MYC; ATF1
GO:0016126	0.0011	1	BP	32911	228	30	3	sterol biosynthetic process	CYP51; IDI1; CH25H
GO:0030595	0.0011	1	BP	32911	228	30	3	leukocyte chemotaxis	CSF3R; IL1B; S100A9
GO:0048870	1.20E-03	1	BP	32911	228	299	8	cell motility	CSF3R; ABCC1; IL1B; HBEGF; PODXL; HIF1A; HSP90AA1; S100A9

GO:0008610	1.20E-03	1	BP	32911	228	299	8	lipid biosynthetic process	SAMD8; BRCA1; PTGS2; CYP51; PTGS1; IDI1; CH25H; ELOVL7
GO:0006732	0.0012	1	BP	32911	228	171	6	coenzyme metabolic process	GSR; TALD01; ACOT10; PGD; PDK4; GCLC
GO:0009913	0.0012	1	BP	32911	228	31	3	epidermal cell differentiation	PTGS2; PTGS1; KLF4
GO:0035556	1.20E-03	1	BP	32911	228	531	11	intracellular signal transduction	EDN1; REL; HMOX1; ZFP36; STAT3; RHOU; ARF3; ERRFI1; BCL10; SOCS3; STAT1
GO:0065003	0.0012	1	BP	32911	228	375	9	macromolecular complex assembly	GTF2F2; TUBA4A; ANGPTL4; SMAD3; TUBB2C; TSPYL4; BCL10; MYC; ATF1
GO:0031058	0.0013	1	BP	32911	228	8	2	positive regulation of histone modification	MEN1; TRP53
GO:0043535	0.0013	1	BP	32911	228	8	2	regulation of blood vessel endothelial cell migration	EPHA2; PTGS2
GO:0048532	0.0013	1	BP	32911	228	8	2	anatomical structure arrangement	HOXB1; HOXA1
GO:0048596	0.0013	1	BP	32911	228	8	2	embryonic camera-type eye morphogenesis	SP3; SP1
GO:0055069	0.0013	1	BP	32911	228	8	2	zinc ion homeostasis	MT1; MT2
GO:0060670	0.0013	1	BP	32911	228	8	2	branching involved in embryonic placenta	ADM; SOCS3
GO:0045598	0.0014	1	BP	32911	228	32	3	regulation of fat cell differentiation	TRIB3; PPARG; CEBPA
GO:0006090	0.0014	1	BP	32911	228	32	3	pyruvate metabolic process	ATF3; ATF4; PDK4
GO:0032868	0.0015	1	BP	32911	228	71	4	response to insulin stimulus	TRIB3; PPARG; PRKCI; STAT1
GO:0051048	0.0015	1	BP	32911	228	71	4	negative regulation of secretion	EDN1; HMOX1; IL1B; PTGS1
GO:0009966	1.50E-03	1	BP	32911	228	462	10	regulation of signal transduction	CCR2; IL1B; DUSP16; EREG; ERRFI1; BCL10; SOCS3; AR; PRDX1; KLF4
GO:0010212	0.0015	1	BP	32911	228	33	3	response to ionizing radiation	TRP53; LRP2; PMAIP1
GO:0001707	0.0015	1	BP	32911	228	33	3	mesoderm formation	EPHA2; SMAD3; TXNRD1
GO:0001816	0.0015	1	BP	32911	228	33	3	cytokine production	REL; FABP4; PTGS2
GO:0001818	0.0015	1	BP	32911	228	33	3	negative regulation of cytokine production	HMOX1; NFKB1; PPARG
GO:0030218	0.0015	1	BP	32911	228	33	3	erythrocyte differentiation	SP3; SP1; SFPI1
GO:0009894	0.0015	1	BP	32911	228	178	6	regulation of catabolic process	TRIB3; TBC1D15; IL1B; PSMD3; RELA; GCLC
GO:0001932	0.0016	1	BP	32911	228	179	6	regulation of protein amino acid phosphorylation	IL1B; IMPACT; ERRFI1; BCL10; JUN; SOCS3
GO:0030155	0.0016	1	BP	32911	228	122	5	regulation of cell adhesion	SMAD3; PODXL; THBS1; LAMA3; CYR61
GO:0010594	0.0016	1	BP	32911	228	9	2	regulation of endothelial cell migration	EPHA2; PTGS2
GO:0001773	0.0016	1	BP	32911	228	9	2	myeloid dendritic cell activation	RELB; SFPI1
GO:0031622	0.0016	1	BP	32911	228	9	2	positive regulation of fever	PTGS2; IL1B
GO:0043011	0.0016	1	BP	32911	228	9	2	myeloid dendritic cell differentiation	RELB; SFPI1
GO:0043367	0.0016	1	BP	32911	228	9	2	CD4-positive, alpha beta T cell differentiation	RELB; GADD45G
GO:0048147	0.0016	1	BP	32911	228	9	2	negative regulation of fibroblast proliferation	TRP53; PMAIP1
GO:0048730	0.0016	1	BP	32911	228	9	2	epidermis morphogenesis	ERRFI1; KLF4
GO:0060216	0.0016	1	BP	32911	228	9	2	definitive hemopoiesis	SP3; SP1
GO:0061097	0.0016	1	BP	32911	228	9	2	regulation of protein tyrosine kinase activity	EREG; ERRFI1
GO:0019217	0.0016	1	BP	32911	228	34	3	regulation of fatty acid metabolic process	TRIB3; PPARG; PPARG
GO:0046364	0.0016	1	BP	32911	228	34	3	monosaccharide biosynthetic process	ATF3; PGD; ATF4
GO:0009411	0.0016	1	BP	32911	228	34	3	response to UV	CDKN1A; TRP53; PMAIP1
GO:0051052	0.0016	1	BP	32911	228	73	4	regulation of DNA metabolic process	TRP53; EREG; JUN; ATF1
GO:0007178	0.0016	1	BP	32911	228	73	4	transmembrane receptor protein serine/threonine	TRP53; SMAD3; CREB1; EGR1
GO:0006996	0.0016	1	BP	32911	228	997	16	organelle organization	MEN1; TRP53; HSPA1B; BRCA1; GADD45A; RHOU; SMAD3; FMNL3; HSPA1A; PRKCI; TSPYL4; MYC; JUN; PMAIP1; CEBPA; S100A9
GO:0023051	0.0017	1	BP	32911	228	470	10	regulation of signaling process	CCR2; IL1B; DUSP16; EREG; ERRFI1; BCL10; SOCS3; AR; PRDX1; KLF4

GO:0007610	0.0018	1	BP	32911	228	473	10	behavior	CSF3R; STAT3; PTGS2; ABCC1; IL1B; JUN; S100A8; CYR61; EGR1; S100A9
GO:0001933	0.0018	1	BP	32911	228	35	3	negative regulation of protein amino acid	IMPACT; ERRFI1; JUN
GO:0043280	0.0018	1	BP	32911	228	35	3	positive regulation of caspase activity	MEN1; BCL10; MYC
GO:0090257	0.0018	1	BP	32911	228	75	4	regulation of muscle system process	EDN1; PTGS2; PTGS1; KLF4
GO:0003006	0.0018	1	BP	32911	228	250	7	reproductive developmental process	WT1; PTGS2; EREG; JUNB; TIPARP; AREG; AR
GO:0030278	0.0019	1	BP	32911	228	76	4	regulation of ossification	MEN1; TOB2; SMAD3; AREG
GO:0010811	0.0019	1	BP	32911	228	36	3	positive regulation of cell-substrate adhesion	SMAD3; THBS1; CYR61
GO:0032675	0.0019	1	BP	32911	228	36	3	regulation of interleukin-6 production	IL1B; EREG; CEBPB
GO:0040007	0.002	1	BP	32911	228	187	6	growth	TRP53; ADM; SMAD3; PTGS2; HBEGF; AR
GO:0009617	0.002	1	BP	32911	228	128	5	response to bacterium	SERPINE1; GPX2; CEBPE; RELA; STAT1
GO:0001516	0.002	1	BP	32911	228	10	2	prostaglandin biosynthetic process	PTGS2; PTGS1
GO:0031620	0.002	1	BP	32911	228	10	2	regulation of fever	PTGS2; IL1B
GO:0032436	0.002	1	BP	32911	228	10	2	positive regulation of proteasomal ubiquitin-	TRIB3; GCLC
GO:0033598	0.002	1	BP	32911	228	10	2	mammary gland epithelial cell proliferation	AREG; CEBPB
GO:0045604	0.002	1	BP	32911	228	10	2	regulation of epidermal cell differentiation	ERRFI1; MAFF
GO:0046457	0.002	1	BP	32911	228	10	2	prostanoid biosynthetic process	PTGS2; PTGS1
GO:0002263	0.0021	1	BP	32911	228	37	3	cell activation involved in immune response	RELB; GADD45G; TRP53
GO:0002366	0.0021	1	BP	32911	228	37	3	leukocyte activation involved in immune	RELB; GADD45G; TRP53
GO:0002449	0.0021	1	BP	32911	228	37	3	lymphocyte mediated immunity	C4B; BCL10; PRDX1
GO:0042542	0.0021	1	BP	32911	228	37	3	response to hydrogen peroxide	HMOX1; TXNRD1; PRDX1
GO:0050728	0.0021	1	BP	32911	228	37	3	negative regulation of inflammatory response	ZFP36; GPX2; PPARG
GO:0043933	0.0021	1	BP	32911	228	404	9	macromolecular complex subunit organization	GTF2F2; TUBA4A; ANGPTL4; SMAD3; TUBB2C; TSPYL4; BCL10; MYC; ATF1
GO:0001704	0.0023	1	BP	32911	228	38	3	formation of primary germ layer	EPHA2; SMAD3; TXNRD1
GO:0048592	0.0023	1	BP	32911	228	38	3	eye morphogenesis	SP3; SP1; RARB
GO:0051781	0.0023	1	BP	32911	228	38	3	positive regulation of cell division	MEN1; IL1B; EREG
GO:0006940	0.0023	1	BP	32911	228	38	3	regulation of smooth muscle contraction	EDN1; PTGS2; PTGS1
GO:0009314	0.0023	1	BP	32911	228	132	5	response to radiation	CDKN1A; TRP53; MYC; LRP2; PMAIP1
GO:0023046	0.0023	1	BP	32911	228	2845	33	signaling process	CXCR7; EDN1; REL; HMOX1; ZFP36; CCR2; PPARA; TRP53; ANGPTL4; KRT8; PDK2; STAT3; ADM; RHOU; ARF3; NFKB1; LYVE1; EREG; ERRFI1; PPP2R2A; BCL10; SOCS3; CXCL16; AR; LRP2; PPARG; PDK4; HIF1A; STAT1; CD48; AFP; CEBPA; KLF6
GO:0002673	0.0024	1	BP	32911	228	39	3	regulation of acute inflammatory response	PTGS2; IL1B; PPARG
GO:0002076	0.0025	1	BP	32911	228	11	2	osteoblast development	MEN1; SMAD3
GO:0031652	0.0025	1	BP	32911	228	11	2	positive regulation of heat generation	PTGS2; IL1B
GO:0032872	0.0025	1	BP	32911	228	11	2	regulation of stress-activated MAPK cascade	IL1B; PRDX1
GO:0046688	0.0025	1	BP	32911	228	11	2	response to copper ion	MT1; MT2
GO:0006098	0.0025	1	BP	32911	228	11	2	pentose-phosphate shunt	TALDO1; PGD
GO:0006740	0.0025	1	BP	32911	228	11	2	NADPH regeneration	TALDO1; PGD
GO:0008209	0.0025	1	BP	32911	228	11	2	androgen metabolic process	ADM; TIPARP
GO:0044255	0.0025	1	BP	32911	228	496	10	cellular lipid metabolic process	PPARA; SAMD8; BRCA1; FABP4; PTGS2; PTGS1; IDI1; PPARG; CH25H; ELOVL7
GO:0010627	0.0025	1	BP	32911	228	197	6	regulation of intracellular protein	CCR2; IL1B; BCL10; AR; PRDX1; KLF4
GO:0010647	0.0027	1	BP	32911	228	267	7	positive regulation of cell communication	CCR2; PTGS2; IL1B; EREG; AR; HIF1A; FGFBP1

GO:0001558	0.0027	1	BP	32911	228	137	5	regulation of cell growth	TRP53; HBEGF; TNFRSF12A; PPARG; CYR61
GO:0045667	0.0028	1	BP	32911	228	41	3	regulation of osteoblast differentiation	MEN1; SMAD3; AREG
GO:0045787	0.0028	1	BP	32911	228	41	3	positive regulation of cell cycle	TRP53; EREG; FOSL1
GO:0030324	0.0029	1	BP	32911	228	85	4	lung development	SP3; LOX; SP1; CEBPA
GO:0031650	0.003	1	BP	32911	228	12	2	regulation of heat generation	PTGS2; IL1B
GO:0042058	0.003	1	BP	32911	228	12	2	regulation of epidermal growth factor receptor	EREG; ERRFI1
GO:0042089	0.003	1	BP	32911	228	12	2	cytokine biosynthetic process	GADD45G; CEBPE
GO:0045600	0.003	1	BP	32911	228	12	2	positive regulation of fat cell differentiation	PPARG; CEBPA
GO:0001657	0.003	1	BP	32911	228	42	3	ureteric bud development	WT1; SMAD3; RARB
GO:0002443	0.003	1	BP	32911	228	42	3	leukocyte mediated immunity	C4B; BCL10; PRDX1
GO:0002526	0.003	1	BP	32911	228	42	3	acute inflammatory response	STAT3; IL1B; SERPINA3N
GO:0042770	0.003	1	BP	32911	228	42	3	DNA damage response, signal transduction	HMOX1; TRP53; BRCA1
GO:0045834	0.003	1	BP	32911	228	42	3	positive regulation of lipid metabolic process	PPARA; IL1B; PPARG
GO:0007589	0.003	1	BP	32911	228	42	3	body fluid secretion	EDN1; USF2; CREB1
GO:0009896	0.003	1	BP	32911	228	42	3	positive regulation of catabolic process	TRIB3; IL1B; GCLC
GO:0034622	0.0031	1	BP	32911	228	142	5	cellular macromolecular complex assembly	TUBA4A; SMAD3; TUBB2C; TSPYL4; ATF1
GO:0010565	0.0033	1	BP	32911	228	43	3	regulation of cellular ketone metabolic process	TRIB3; PPARA; PPARG
GO:0002250	0.0033	1	BP	32911	228	43	3	adaptive immune response	C4B; RELB; BCL10
GO:0002460	0.0033	1	BP	32911	228	43	3	adaptive immune response based on somatic	C4B; RELB; BCL10
GO:0051054	0.0033	1	BP	32911	228	43	3	positive regulation of DNA metabolic process	EREG; JUN; ATF1
GO:0051302	0.0033	1	BP	32911	228	43	3	regulation of cell division	MEN1; IL1B; EREG
GO:0010952	0.0035	1	BP	32911	228	44	3	positive regulation of peptidase activity	MEN1; BCL10; MYC
GO:0007179	0.0035	1	BP	32911	228	44	3	transforming growth factor beta receptor signaling	TRP53; SMAD3; CREB1
GO:0042107	0.0035	1	BP	32911	228	13	2	cytokine metabolic process	GADD45G; CEBPE
GO:0042744	0.0035	1	BP	32911	228	13	2	hydrogen peroxide catabolic process	TXNRD1; PRDX1
GO:0046320	0.0035	1	BP	32911	228	13	2	regulation of fatty acid oxidation	PPARA; PPARG
GO:0051085	0.0035	1	BP	32911	228	13	2	chaperone mediated protein folding requiring cofactor	HSPD1; HSPA8
GO:0060706	0.0035	1	BP	32911	228	13	2	cell differentiation involved in embryonic	KRT8; SOCS3
GO:0006692	0.0035	1	BP	32911	228	13	2	prostanoid metabolic process	PTGS2; PTGS1
GO:0006693	0.0035	1	BP	32911	228	13	2	prostaglandin metabolic process	PTGS2; PTGS1
GO:0006968	0.0035	1	BP	32911	228	13	2	cellular defense response	CCR2; BCL10
GO:0008210	0.0035	1	BP	32911	228	13	2	estrogen metabolic process	SULT1A1; TIPARP
GO:0006796	0.0035	1	BP	32911	228	882	14	phosphate metabolic process	SPNB2; TRIB3; GADD45G; PDK2; EPHA2; DUSP1; DUSP16; CREB1; PRKCI; PTPN21; PTPN14; PPA1; RCT10; PDK4
GO:0016051	0.0035	1	BP	32911	228	90	4	carbohydrate biosynthetic process	ATF3; HS6ST1; PGD; ATF4
GO:0006793	0.0036	1	BP	32911	228	884	14	phosphorus metabolic process	SPNB2; TRIB3; GADD45G; PDK2; EPHA2; DUSP1; DUSP16; CREB1; PRKCI; PTPN21; PTPN14; PPA1; BCL10; PDK4
GO:0019216	0.0037	1	BP	32911	228	91	4	regulation of lipid metabolic process	TRIB3; PPARA; IL1B; PPARG
GO:0046165	0.0037	1	BP	32911	228	45	3	alcohol biosynthetic process	ATF3; PGD; ATF4
GO:0045926	0.0038	1	BP	32911	228	92	4	negative regulation of growth	MEN1; TRP53; PPARG; HIF1A
GO:0032434	0.0041	1	BP	32911	228	14	2	regulation of proteasomal ubiquitin-dependent	TRIB3; GCLC

GO:0048662	0.0041	1	BP	32911	228	14	2	negative regulation of smooth muscle cell	TRP53; KLF4
GO:0061077	0.0041	1	BP	32911	228	14	2	chaperone-mediated protein folding	HSPD1; HSPA8
GO:0071383	0.0041	1	BP	32911	228	14	2	cellular response to steroid hormone stimulus	PPARA; AR
GO:0071407	0.0041	1	BP	32911	228	14	2	cellular response to organic cyclic substance	PPARG; CEBPA
GO:0009267	0.0041	1	BP	32911	228	14	2	cellular response to starvation	TRP53; JUN
GO:0045860	0.0041	1	BP	32911	228	151	5	positive regulation of protein kinase activity	EDN1; GADD45G; IL1B; EREG; BCL10
GO:0031348	0.0042	1	BP	32911	228	47	3	negative regulation of defense response	ZFP36; GPX2; PPARG
GO:0009408	0.0042	1	BP	32911	228	47	3	response to heat	HSPB8; HSPA1B; HSPA1A
GO:0035468	0.0043	1	BP	32911	228	219	6	positive regulation of signaling pathway	CCR2; IL1B; EREG; AR; HIF1A; FGFBP1
GO:0032269	0.0043	1	BP	32911	228	95	4	negative regulation of cellular protein metabolic	IMPACT; ERRF1; JUN; GCLC
GO:0043687	0.0045	1	BP	32911	228	1005	15	post-translational protein modification	SPNB2; BTG2; TRIB3; MEN1; GADD45G; PDK2; EPHA2; DUSP1; CREB1; PRKCI; PTPN21; TIPARP; PTPN14; BCL10; PDK4
GO:0010817	0.0046	1	BP	32911	228	155	5	regulation of hormone levels	SULT1A1; ADM; TIPARP; LRP2; AFP
GO:0019321	0.0047	1	BP	32911	228	15	2	pentose metabolic process	TALD01; PGD
GO:0033993	0.0047	1	BP	32911	228	15	2	response to lipid	PPARG; EGR1
GO:0045833	0.0047	1	BP	32911	228	15	2	negative regulation of lipid metabolic process	TRIB3; IL1B
GO:0046632	0.0047	1	BP	32911	228	15	2	alpha-beta T cell differentiation	RELB; GADD45G
GO:0051084	0.0047	1	BP	32911	228	15	2	'de novo' posttranslational protein	HSPD1; HSPA8
GO:0061136	0.0047	1	BP	32911	228	15	2	regulation of proteasomal protein catabolic process	TRIB3; GCLC
GO:0006458	0.0047	1	BP	32911	228	15	2	'de novo' protein folding	HSPD1; HSPA8
GO:0032869	0.0047	1	BP	32911	228	49	3	cellular response to insulin stimulus	TRIB3; PRKCI; STAT1
GO:0016331	0.0048	1	BP	32911	228	98	4	morphogenesis of embryonic epithelium	TCFAP2A; TGIF1; ADM; BCL10
GO:0000302	0.005	1	BP	32911	228	50	3	response to reactive oxygen species	HMOX1; TXNRD1; PRDX1
GO:0071375	0.005	1	BP	32911	228	50	3	cellular response to peptide hormone stimulus	TRIB3; PRKCI; STAT1
GO:0007369	0.005	1	BP	32911	228	50	3	gastrulation	TRP53; SMAD3; TXNRD1
GO:0033043	0.0052	1	BP	32911	228	160	5	regulation of organelle organization	SPNB2; MEN1; TRP53; SMAD3; EREG
GO:0033674	0.0052	1	BP	32911	228	160	5	positive regulation of kinase activity	EDN1; GADD45G; IL1B; EREG; BCL10
GO:0008406	0.0053	1	BP	32911	228	51	3	gonad development	WT1; TIPARP; AR
GO:0010469	0.0053	1	BP	32911	228	16	2	regulation of receptor activity	EREG; ERRF1
GO:0015909	0.0053	1	BP	32911	228	16	2	long-chain fatty acid transport	ABCC1; PPARG
GO:0031056	0.0053	1	BP	32911	228	16	2	regulation of histone modification	MEN1; TRP53
GO:0060444	0.0053	1	BP	32911	228	16	2	branching involved in mammary gland duct	ETV4; AREG
GO:0006790	0.0054	1	BP	32911	228	101	4	sulfur metabolic process	GSR; SULT1A1; HS6ST1; GCLC
GO:0023052	0.0054	1	BP	32911	228	3239	35	signaling	CXCR7; EDN1; REL; HMOX1; ZFP36; CCR2; PPARA; TRP53; MT1; BRCA1; KRT8; STAT3; EPHA2; RHOU; ARF3; SMAD3; DUSP1; NOTCH2; CREB1; EREG; HBEGF; MT2; PRKCI; TIPARP; ERRF1; AREG; BCL10; SOCS3; AR; RELA; STAT1; EGR1; CEBPA; FGFBP1; KLF6
GO:0042445	0.0056	1	BP	32911	228	102	4	hormone metabolic process	SULT1A1; ADM; TIPARP; AFP
GO:0007050	0.0056	1	BP	32911	228	52	3	cell cycle arrest	MEN1; CDKN1A; GADD45A
GO:0023033	0.0057	1	BP	32911	228	3130	34	signaling pathway	CXCR7; EDN1; REL; HMOX1; ZFP36; CCR2; PPARA; TRP53; MT1; BRCA1; KRT8; STAT3; EPHA2; RHOU; ARF3; SMAD3; DUSP1; NOTCH2; CREB1; EREG; HBEGF; MT2; PRKCI; TIPARP; ERRF1; AREG; BCL10; SOCS3; AR; RELA; STAT1; EGR1; CEBPA; KLF6
GO:0010810	0.0059	1	BP	32911	228	53	3	regulation of cell-substrate adhesion	SMAD3; THBS1; CYR61

GO:0006007	0.0059	1	BP	32911	228	53	3	glucose catabolic process	TALDO1; PGD; ALDOA
GO:0006959	0.0059	1	BP	32911	228	53	3	humoral immune response	C4B; CCR2; IGJ
GO:0051347	0.0059	1	BP	32911	228	165	5	positive regulation of transferase activity	EDN1; GADD45G; IL1B; EREG; BCL10
GO:0002687	0.006	1	BP	32911	228	17	2	positive regulation of leukocyte migration	CCR2; TRP53
GO:0042474	0.006	1	BP	32911	228	17	2	middle ear morphogenesis	EDN1; MYC
GO:0042594	0.006	1	BP	32911	228	17	2	response to starvation	TRP53; JUN
GO:0045778	0.006	1	BP	32911	228	17	2	positive regulation of ossification	TOB2; SMAD3
GO:0045862	0.006	1	BP	32911	228	17	2	positive regulation of proteolysis	TRIB3; GCLC
GO:0060491	0.006	1	BP	32911	228	17	2	regulation of cell projection assembly	PODXL; HSP90AA1
GO:0060749	0.006	1	BP	32911	228	17	2	mammary gland alveolus development	AREG; AR
GO:0006739	0.006	1	BP	32911	228	17	2	NADP metabolic process	TALDO1; PGD
GO:0070301	0.006	1	BP	32911	228	17	2	cellular response to hydrogen peroxide	TXNRD1; PRDX1
GO:0009755	0.006	1	BP	32911	228	17	2	hormone-mediated signaling pathway	PPARA; AR
GO:0019320	0.0062	1	BP	32911	228	54	3	hexose catabolic process	TALDO1; PGD; ALDOA
GO:0032989	0.0063	1	BP	32911	228	237	6	cellular component morphogenesis	WT1; KRT8; ADM; CREB1; CLU; HIF1A
GO:0032844	0.0064	1	BP	32911	228	106	4	regulation of homeostatic process	PTGS2; IL1B; HIF1A; GCLC
GO:0051251	0.0064	1	BP	32911	228	106	4	positive regulation of lymphocyte activation	CDKN1A; HSPD1; BCL10; HSP90AA1
GO:0034621	0.0066	1	BP	32911	228	169	5	cellular macromolecular complex subunit	TUBA4A; SMAD3; TUBB2C; TSPYL4; ATF1
GO:0046365	0.0066	1	BP	32911	228	55	3	monosaccharide catabolic process	TALDO1; PGD; ALDOA
GO:0001944	0.0067	1	BP	32911	228	18	2	vasculature development	ERRFI1; SFPI1
GO:0043393	0.0067	1	BP	32911	228	18	2	regulation of protein binding	TRIB3; MYC
GO:0045687	0.0067	1	BP	32911	228	18	2	positive regulation of glial cell differentiation	PPARG; RELA
GO:0045923	0.0067	1	BP	32911	228	18	2	positive regulation of fatty acid metabolic	PPARA; PPARG
GO:0048701	0.0067	1	BP	32911	228	18	2	embryonic cranial skeleton morphogenesis	TCFAP2A; SMAD3
GO:0006026	0.0067	1	BP	32911	228	18	2	aminoglycan catabolic process	LYVE1; CHI3L1
GO:0010715	0.0069	1	BP	32911	228	1	1	regulation of extracellular matrix	ETS1
GO:0014038	0.0069	1	BP	32911	228	1	1	regulation of Schwann cell differentiation	RELA
GO:0014040	0.0069	1	BP	32911	228	1	1	positive regulation of Schwann cell	RELA
GO:0016109	0.0069	1	BP	32911	228	1	1	tetraterpenoid biosynthetic process	IDI1
GO:0016114	0.0069	1	BP	32911	228	1	1	terpenoid biosynthetic process	IDI1
GO:0016117	0.0069	1	BP	32911	228	1	1	carotenoid biosynthetic process	IDI1
GO:0001754	0.0069	1	BP	32911	228	1	1	eye photoreceptor cell differentiation	STAT3
GO:0018960	0.0069	1	BP	32911	228	1	1	4-nitrophenol metabolic process	SULT1A1
GO:0019102	0.0069	1	BP	32911	228	1	1	male somatic sex determination	AR
GO:0019520	0.0069	1	BP	32911	228	1	1	aldonic acid metabolic process	PGD
GO:0019521	0.0069	1	BP	32911	228	1	1	D-gluconate metabolic process	PGD
GO:0002041	0.0069	1	BP	32911	228	1	1	intussusceptive angiogenesis	CYR61
GO:0002236	0.0069	1	BP	32911	228	1	1	detection of misfolded protein	HSPD1
GO:0002248	0.0069	1	BP	32911	228	1	1	connective tissue replacement involved in	HIF1A
GO:0031581	0.0069	1	BP	32911	228	1	1	hemidesmosome assembly	LAMA3

GO:0033488	0.0069	1	BP	32911	228	1	1	cholesterol biosynthetic process via 24,25-	CYP51
GO:0034775	0.0069	1	BP	32911	228	1	1	glutathione transmembrane transport	ABCC1
GO:0035026	0.0069	1	BP	32911	228	1	1	leading edge cell differentiation	JUN
GO:0000429	0.0069	1	BP	32911	228	1	1	regulation of transcription from RNA	USF2
GO:0000430	0.0069	1	BP	32911	228	1	1	regulation of transcription from RNA	USF2
GO:0000432	0.0069	1	BP	32911	228	1	1	positive regulation of transcription from RNA	USF2
GO:0043215	0.0069	1	BP	32911	228	1	1	daunorubicin transport	ABCC1
GO:0000436	0.0069	1	BP	32911	228	1	1	positive regulation of transcription from RNA	USF2
GO:0045083	0.0069	1	BP	32911	228	1	1	negative regulation of interleukin-12	NFKB1
GO:0045113	0.0069	1	BP	32911	228	1	1	regulation of integrin biosynthetic process	S100A9
GO:0045583	0.0069	1	BP	32911	228	1	1	regulation of cytotoxic T cell differentiation	HSP90AA1
GO:0045585	0.0069	1	BP	32911	228	1	1	positive regulation of cytotoxic T cell	HSP90AA1
GO:0045991	0.0069	1	BP	32911	228	1	1	positive regulation of transcription by carbon	USF2
GO:0046016	0.0069	1	BP	32911	228	1	1	positive regulation of transcription by glucose	USF2
GO:0046530	0.0069	1	BP	32911	228	1	1	photoreceptor cell differentiation	STAT3
GO:0048160	0.0069	1	BP	32911	228	1	1	primary follicle stage	EREG
GO:0048194	0.0069	1	BP	32911	228	1	1	Golgi vesicle budding	PRKCI
GO:0048387	0.0069	1	BP	32911	228	1	1	negative regulation of retinoic acid receptor	TGIF1
GO:0051543	0.0069	1	BP	32911	228	1	1	regulation of elastin biosynthetic process	HBEGF
GO:0051545	0.0069	1	BP	32911	228	1	1	negative regulation of elastin biosynthetic	HBEGF
GO:0051547	0.0069	1	BP	32911	228	1	1	regulation of keratinocyte migration	HBEGF
GO:0051549	0.0069	1	BP	32911	228	1	1	positive regulation of keratinocyte migration	HBEGF
GO:0051599	0.0069	1	BP	32911	228	1	1	response to hydrostatic pressure	KRT8
GO:0051974	0.0069	1	BP	32911	228	1	1	negative regulation of telomerase activity	PPARG
GO:0060035	0.0069	1	BP	32911	228	1	1	notochord cell development	EPHA2
GO:0060520	0.0069	1	BP	32911	228	1	1	activation of prostate induction by androgen	AR
GO:0060598	0.0069	1	BP	32911	228	1	1	dichotomous subdivision of terminal units involved in mammary gland duct morphogenesis	AREG
GO:0061043	0.0069	1	BP	32911	228	1	1	regulation of vascular wound healing	SERPINE1
GO:0061044	0.0069	1	BP	32911	228	1	1	negative regulation of vascular wound healing	SERPINE1
GO:0061045	0.0069	1	BP	32911	228	1	1	negative regulation of wound healing	SERPINE1
GO:0006844	0.0069	1	BP	32911	228	1	1	acyl carnitine transport	SLC25A29
GO:0070164	0.0069	1	BP	32911	228	1	1	negative regulation of adiponectin secretion	IL1B
GO:0071503	0.0069	1	BP	32911	228	1	1	response to heparin	EGR1
GO:0071504	0.0069	1	BP	32911	228	1	1	cellular response to heparin	EGR1
GO:0007175	0.0069	1	BP	32911	228	1	1	negative regulation of epidermal growth factor receptor activity	ERRFI1
GO:0007183	0.0069	1	BP	32911	228	1	1	SMAD protein complex assembly	SMAD3
GO:0072110	0.0069	1	BP	32911	228	1	1	glomerular mesangial cell proliferation	EGR1
GO:0090095	0.0069	1	BP	32911	228	1	1	regulation of metanephric cap mesenchymal cell proliferation	MYC

GO:0090096	0.0069	1	BP	32911	228	1	1	positive regulation of metanephric cap mesenchymal cell proliferation	MYC
GO:0090271	0.0069	1	BP	32911	228	1	1	positive regulation of fibroblast growth factor production	PTGS2
GO:0001843	0.0069	1	BP	32911	228	56	3	neural tube closure	TGIF1; ADM; BCL10
GO:0002694	0.007	1	BP	32911	228	172	5	regulation of leukocyte activation	HMOX1; CDKN1A; HSPD1; BCL10; HSP90AA1
GO:0009057	0.0071	1	BP	32911	228	243	6	macromolecule catabolic process	ZFP36; LYVE1; MYC; CHI3L1; PSMA5; PSMC1
GO:0060606	0.0072	1	BP	32911	228	57	3	tube closure	TGIF1; ADM; BCL10
GO:0007249	0.0075	1	BP	32911	228	19	2	I-kappaB kinase/NF-kappaB cascade	REL; BCL10
GO:0007530	0.0075	1	BP	32911	228	19	2	sex determination	WT1; AR
GO:0051216	0.0076	1	BP	32911	228	58	3	cartilage development	EDN1; THBS1; HIF1A
GO:0007154	0.0076	1	BP	32911	228	324	7	cell communication	USF2; TRP53; FOS; JUN; FOSL1; GJB3; FGFBP1
GO:0002696	0.008	1	BP	32911	228	113	4	positive regulation of leukocyte activation	CDKN1A; HSPD1; BCL10; HSP90AA1
GO:0007626	0.008	1	BP	32911	228	249	6	locomotory behavior	CSF3R; ABCC1; IL1B; S100A8; CYR61; S100A9
GO:0050865	0.0081	1	BP	32911	228	178	5	regulation of cell activation	HMOX1; CDKN1A; HSPD1; BCL10; HSP90AA1
GO:0030593	0.0083	1	BP	32911	228	20	2	neutrophil chemotaxis	CSF3R; IL1B
GO:0032200	0.0083	1	BP	32911	228	20	2	telomere organization	HSPA1B; HSPA1A
GO:0032330	0.0083	1	BP	32911	228	20	2	regulation of chondrocyte differentiation	RELA; RARB
GO:0033044	0.0083	1	BP	32911	228	20	2	regulation of chromosome organization	MEN1; TRP53
GO:0045682	0.0083	1	BP	32911	228	20	2	regulation of epidermis development	ERRFI1; MAFF
GO:0046631	0.0083	1	BP	32911	228	20	2	alpha-beta T cell activation	RELB; GADD45G
GO:0051168	0.0083	1	BP	32911	228	20	2	nuclear export	HSPA9; NMD3
GO:0000060	0.0083	1	BP	32911	228	20	2	protein import into nucleus, translocation	SPNB2; TRP53
GO:0007006	0.0083	1	BP	32911	228	20	2	mitochondrial membrane organization	TRP53; PMAIP1
GO:0000723	0.0083	1	BP	32911	228	20	2	telomere maintenance	HSPA1B; HSPA1A
GO:0008045	0.0083	1	BP	32911	228	20	2	motor axon guidance	HOXA1; ETV4
GO:0090092	0.0083	1	BP	32911	228	60	3	regulation of transmembrane receptor	MEN1; TRP53; SMAD3
GO:0000904	0.0083	1	BP	32911	228	60	3	cell morphogenesis involved in	WT1; KRT8; HIF1A
GO:0050878	0.0085	1	BP	32911	228	115	4	regulation of body fluid levels	EDN1; USF2; CREB1; F3
GO:0006412	0.0086	1	BP	32911	228	253	6	translation	EIF5; EIF2S2; EIF1A; MRPL28; MRPS12; RPL22L1
GO:0044248	0.0086	1	BP	32911	228	592	10	cellular catabolic process	HMOX1; ZFP36; RHOU; GSTA2; MYC; TXNRD1; PRDX1; PSMA5; HSPA8; PDE4B
GO:0045785	0.0087	1	BP	32911	228	61	3	positive regulation of cell adhesion	SMAD3; THBS1; CYR61
GO:0007584	0.0087	1	BP	32911	228	61	3	response to nutrient	USF2; STAT1; KLF4
GO:0006464	0.0088	1	BP	32911	228	1186	16	protein modification process	SPNB2; BTG2; TRIB3; MEN1; NEDD4L; GADD45G; PDK2; EPHA2; DUSP1; CREB1; PRKCI; PTPN21; TIPARP; PTPN14; BCL10; PDK4
GO:0050767	0.0089	1	BP	32911	228	255	6	regulation of neurogenesis	TGIF1; TRP53; ATF1; TNFRSF12A; PPARG; RELA
GO:0044087	0.009	1	BP	32911	228	117	4	regulation of cellular component biogenesis	SPNB2; SMAD3; PODXL; HSP90AA1
GO:0006875	0.0091	1	BP	32911	228	183	5	cellular metal ion homeostasis	EDN1; CCR2; MT1; ADM; IL1B
GO:0007169	0.0091	1	BP	32911	228	183	5	transmembrane receptor protein tyrosine kinase signaling pathway	EPHA2; EREG; HBEGF; TIPARP; AREG
GO:0034637	0.0091	1	BP	32911	228	62	3	cellular carbohydrate biosynthetic process	ATF3; PGD; ATF4

GO:0070302	0.0091	1	BP	32911	228	62	3	regulation of stress-activated protein kinase signaling cascade	IL1B; BCL10; PRDX1
GO:0034614	0.0092	1	BP	32911	228	21	2	cellular response to reactive oxygen species	TXNRD1; PRDX1
GO:0050921	0.0092	1	BP	32911	228	21	2	positive regulation of chemotaxis	CCR2; SMAD3
GO:0006094	0.0092	1	BP	32911	228	21	2	gluconeogenesis	ATF3; ATF4
GO:0006805	0.0092	1	BP	32911	228	21	2	xenobiotic metabolic process	SULT1A1; GSTA2
GO:0050867	0.0093	1	BP	32911	228	118	4	positive regulation of cell activation	CDKN1A; HSPD1; BCL10; HSP90AA1
GO:0051099	0.0096	1	BP	32911	228	63	3	positive regulation of binding	TRIB3; BCL10; RELA
GO:0006937	0.0096	1	BP	32911	228	63	3	regulation of muscle contraction	EDN1; PTGS2; PTGS1
GO:0044275	0.01	1	BP	32911	228	64	3	cellular carbohydrate catabolic process	TALDO1; PGD; ALDOA
GO:0002685	0.01	1	BP	32911	228	22	2	regulation of leukocyte migration	CCR2; TRP53
GO:0031396	0.01	1	BP	32911	228	22	2	regulation of protein ubiquitination	TRIB3; GCLC
GO:0045907	0.01	1	BP	32911	228	22	2	positive regulation of vasoconstriction	PTGS2; PTGS1
GO:0060429	0.01	1	BP	32911	228	22	2	epithelium development	SMAD3; ERFF1
GO:0055065	0.0104	1	BP	32911	228	189	5	metal ion homeostasis	EDN1; CCR2; MT1; ADM; IL1B
GO:0006810	0.0106	1	BP	32911	228	2320	26	transport	SPNB2; ABCD3; EDN1; USF2; TRP53; FABP4; ADM; SLC25A29; ARF3; ABCC1; HSPA9; TNPO3; SRI; LYVE1; CREB1; TXNL1; NMD3; SLC20A1; VAMP5; LRP2; CEBPE; PPARG; KCTD9; SLC2A1; AFP; MYB
GO:0014015	0.0109	1	BP	32911	228	23	2	positive regulation of gliogenesis	PPARG; RELA
GO:0042743	0.0109	1	BP	32911	228	23	2	hydrogen peroxide metabolic process	TXNRD1; PRDX1
GO:0045429	0.0109	1	BP	32911	228	23	2	positive regulation of nitric oxide biosynthetic	PTGS2; HSP90AA1
GO:0007611	0.0113	1	BP	32911	228	125	4	learning or memory	PTGS2; IL1B; JUN; EGR1
GO:0046164	0.0113	1	BP	32911	228	67	3	alcohol catabolic process	TALDO1; PGD; ALDOA
GO:0051234	0.0117	1	BP	32911	228	2340	26	establishment of localization	SPNB2; ABCD3; EDN1; USF2; TRP53; FABP4; ADM; SLC25A29; ARF3; ABCC1; HSPA9; TNPO3; SRI; LYVE1; CREB1; TXNL1; NMD3; SLC20A1; VAMP5; LRP2; CEBPE; PPARG; KCTD9; SLC2A1; AFP; MYB
GO:0001666	0.0118	1	BP	32911	228	68	3	response to hypoxia	EDN1; PPARA; HIF1A
GO:0048468	0.0118	1	BP	32911	228	271	6	cell development	EDN1; WT1; MEN1; EPHA2; SMAD3; PRKCI
GO:0016064	0.0119	1	BP	32911	228	24	2	immunoglobulin mediated immune response	C4B; BCL10
GO:0002675	0.0119	1	BP	32911	228	24	2	positive regulation of acute inflammatory	PTGS2; IL1B
GO:0000272	0.0119	1	BP	32911	228	24	2	polysaccharide catabolic process	LYVE1; CHI3L1
GO:0032963	0.0119	1	BP	32911	228	24	2	collagen metabolic process	HIF1A; MMP11
GO:0043507	0.0119	1	BP	32911	228	24	2	positive regulation of JUN kinase activity	IL1B; BCL10
GO:0045638	0.0119	1	BP	32911	228	24	2	negative regulation of myeloid cell	ZFP36; TOB2
GO:0006695	0.0119	1	BP	32911	228	24	2	cholesterol biosynthetic process	CYP51; IDI1
GO:0007595	0.0119	1	BP	32911	228	24	2	lactation	USF2; CREB1
GO:0000082	0.0119	1	BP	32911	228	24	2	G1/S transition of mitotic cell cycle	RHO; MYB
GO:0060341	0.0124	1	BP	32911	228	274	6	regulation of cellular localization	EDN1; HMOX1; IL1B; CREB1; PTGS1; PRDX1
GO:0035295	0.0127	1	BP	32911	228	70	3	tube development	WT1; SMAD3; RARB
GO:0048608	0.0127	1	BP	32911	228	70	3	reproductive structure development	WT1; TIPARP; AR
GO:0070482	0.0127	1	BP	32911	228	70	3	response to oxygen levels	EDN1; PPARA; HIF1A

GO:0009266	0.0127	1	BP	32911	228	70	3	response to temperature stimulus	HSPB8; HSPA1B; HSPA1A
GO:0051960	0.0128	1	BP	32911	228	276	6	regulation of nervous system development	TGIF1; TRP53; ATF1; TNFRSF12A; PPARG; RELA
GO:0019319	0.0129	1	BP	32911	228	25	2	hexose biosynthetic process	ATF3; ATF4
GO:0043526	0.0129	1	BP	32911	228	25	2	neuroprotection	REL; ABCC1
GO:0044259	0.0129	1	BP	32911	228	25	2	multicellular organismal macromolecule metabolic process	HIF1A; MMP11
GO:0050920	0.0129	1	BP	32911	228	25	2	regulation of chemotaxis	CCR2; SMAD3
GO:0043412	0.0133	1	BP	32911	228	1243	16	macromolecule modification	SPNB2; BTG2; TRIB3; MEN1; NEDD4L; GADD45G; PDK2; EPHA2; DUSP1; CREB1; PRKCI; PTPN21; TIPARP; PTPN14; BCL10; PDK4
GO:0050870	0.0137	1	BP	32911	228	72	3	positive regulation of T cell activation	HSPD1; BCL10; HSP90AA1
GO:0051090	0.0137	1	BP	32911	228	72	3	regulation of transcription factor	HMOX1; BCL10; RELA
GO:0008203	0.0137	1	BP	32911	228	72	3	cholesterol metabolic process	CYP51; IDI1; CH25H
GO:0008544	0.0137	1	BP	32911	228	72	3	epidermis development	PPARA; SCEL; RELA
GO:0090046	0.0137	1	BP	32911	228	72	3	regulation of transcription regulator	HMOX1; BCL10; RELA
GO:0010692	0.0138	1	BP	32911	228	2	1	regulation of alkaline phosphatase activity	SMAD3
GO:0010694	0.0138	1	BP	32911	228	2	1	positive regulation of alkaline phosphatase activity	SMAD3
GO:0010700	0.0138	1	BP	32911	228	2	1	negative regulation of norepinephrine secretion	PTGS1
GO:0010755	0.0138	1	BP	32911	228	2	1	regulation of plasminogen activation	SERPINE1
GO:0010757	0.0138	1	BP	32911	228	2	1	negative regulation of plasminogen activation	SERPINE1
GO:0014028	0.0138	1	BP	32911	228	2	1	notochord formation	EPHA2
GO:0014740	0.0138	1	BP	32911	228	2	1	negative regulation of muscle hyperplasia	KLF4
GO:0001550	0.0138	1	BP	32911	228	2	1	ovarian cumulus expansion	EREG
GO:0015911	0.0138	1	BP	32911	228	2	1	plasma membrane long-chain fatty acid transport	ABCC1
GO:0016108	0.0138	1	BP	32911	228	2	1	tetraterpenoid metabolic process	IDI1
GO:0016116	0.0138	1	BP	32911	228	2	1	carotenoid metabolic process	IDI1
GO:0018993	0.0138	1	BP	32911	228	2	1	somatic sex determination	AR
GO:0019682	0.0138	1	BP	32911	228	2	1	glyceraldehyde-3-phosphate metabolic process	TALDO1
GO:0020028	0.0138	1	BP	32911	228	2	1	hemoglobin import	LRP2
GO:0021506	0.0138	1	BP	32911	228	2	1	anterior neuropore closure	TCFAP2A
GO:0022605	0.0138	1	BP	32911	228	2	1	oogenesis stage	EREG
GO:0030224	0.0138	1	BP	32911	228	2	1	monocyte differentiation	SP3
GO:0031062	0.0138	1	BP	32911	228	2	1	positive regulation of histone methylation	MEN1
GO:0031583	0.0138	1	BP	32911	228	2	1	activation of phospholipase D activity by G-protein coupled receptor protein signaling	EDN1
GO:0031915	0.0138	1	BP	32911	228	2	1	positive regulation of synaptic plasticity	PTGS2
GO:0031953	0.0138	1	BP	32911	228	2	1	negative regulation of protein amino acid autophosphorylation	JUN
GO:0032727	0.0138	1	BP	32911	228	2	1	positive regulation of interferon-alpha production	HSPD1
GO:0032764	0.0138	1	BP	32911	228	2	1	negative regulation of mast cell cytokine production	HMOX1

GO:0032925	0.0138	1	BP	32911	228	2	1	regulation of activin receptor signaling pathway	MEN1
GO:0033007	0.0138	1	BP	32911	228	2	1	negative regulation of mast cell activation involved in immune response	HMOX1
GO:0033015	0.0138	1	BP	32911	228	2	1	tetrapyrrole catabolic process	HMOX1
GO:0033753	0.0138	1	BP	32911	228	2	1	establishment of ribosome localization	NMD3
GO:0034635	0.0138	1	BP	32911	228	2	1	glutathione transport	ABCC1
GO:0042095	0.0138	1	BP	32911	228	2	1	interferon-gamma biosynthetic process	GADD45G
GO:0042167	0.0138	1	BP	32911	228	2	1	heme catabolic process	HMOX1
GO:0042700	0.0138	1	BP	32911	228	2	1	luteinizing hormone signaling pathway	EREG
GO:0042939	0.0138	1	BP	32911	228	2	1	tripeptide transport	ABCC1
GO:0043179	0.0138	1	BP	32911	228	2	1	rhythmic excitation	EDN1
GO:0043301	0.0138	1	BP	32911	228	2	1	negative regulation of leukocyte degranulation	HMOX1
GO:0043305	0.0138	1	BP	32911	228	2	1	negative regulation of mast cell degranulation	HMOX1
GO:0045657	0.0138	1	BP	32911	228	2	1	positive regulation of monocyte differentiation	JUN
GO:0045741	0.0138	1	BP	32911	228	2	1	positive regulation of epidermal growth factor receptor activity	EREG
GO:0045990	0.0138	1	BP	32911	228	2	1	regulation of transcription by carbon	USF2
GO:0046015	0.0138	1	BP	32911	228	2	1	regulation of transcription by glucose	USF2
GO:0046149	0.0138	1	BP	32911	228	2	1	pigment catabolic process	HMOX1
GO:0046661	0.0138	1	BP	32911	228	2	1	male sex differentiation	AR
GO:0048320	0.0138	1	BP	32911	228	2	1	axial mesoderm formation	EPHA2
GO:0048385	0.0138	1	BP	32911	228	2	1	regulation of retinoic acid receptor signaling	TGIF1
GO:0051365	0.0138	1	BP	32911	228	2	1	cellular response to potassium ion starvation	JUN
GO:0051541	0.0138	1	BP	32911	228	2	1	elastin metabolic process	HIF1A
GO:0051788	0.0138	1	BP	32911	228	2	1	response to misfolded protein	HSPD1
GO:0051972	0.0138	1	BP	32911	228	2	1	regulation of telomerase activity	PPARG
GO:0000054	0.0138	1	BP	32911	228	2	1	ribosomal subunit export from nucleus	NMD3
GO:0000055	0.0138	1	BP	32911	228	2	1	ribosomal large subunit export from nucleus	NMD3
GO:0060290	0.0138	1	BP	32911	228	2	1	transdifferentiation	SMAD3
GO:0060599	0.0138	1	BP	32911	228	2	1	lateral sprouting involved in mammary gland duct morphogenesis	AR
GO:0061099	0.0138	1	BP	32911	228	2	1	negative regulation of protein tyrosine kinase activity	ERRFI1
GO:0006529	0.0138	1	BP	32911	228	2	1	asparagine biosynthetic process	ASNS
GO:0006787	0.0138	1	BP	32911	228	2	1	porphyrin catabolic process	HMOX1
GO:0006788	0.0138	1	BP	32911	228	2	1	heme oxidation	HMOX1
GO:0006931	0.0138	1	BP	32911	228	2	1	substrate-bound cell migration, cell attachment to substrate	TNFRSF12A
GO:0070098	0.0138	1	BP	32911	228	2	1	chemokine-mediated signaling pathway	CCR2
GO:0070163	0.0138	1	BP	32911	228	2	1	regulation of adiponectin secretion	IL1B
GO:0071398	0.0138	1	BP	32911	228	2	1	cellular response to fatty acid	EGR1

									response to mycophenolic acid	EGR1
									cellular response to mycophenolic acid	EGR1
									cell proliferation involved in kidney	EGR1
									regulation of metanephros development	MYC
									adult somatic muscle development	IFRD1
									negative regulation of survival gene product expression	MYC
									positive regulation of establishment of protein localization in plasma membrane	PRKCI
									regulation of cell migration involved in sprouting angiogenesis	PTGS2
									positive regulation of cell migration involved in sprouting angiogenesis	PTGS2
									regulation of immune complex clearance by monocytes and macrophages	CCR2
									positive regulation of immune complex clearance by monocytes and macrophages	CCR2
									response to symbiont	GPX2
									response to symbiotic bacterium	GPX2
									keratinocyte differentiation	PTGS2; PTGS1
									positive regulation of cellular catabolic process	TRIB3; GCLC
									positive regulation of protein catabolic process	TRIB3; GCLC
									steroid biosynthetic process	CYP51; IDI1; CH25H
									B cell mediated immunity	C4B; BCL10
									negative regulation of MAP kinase activity	IL1B; DUSP16
									positive regulation of myeloid cell	JUN; HIF1A
									epithelial cell proliferation	AREG; CEBPB
									protein polymerization	TUBA4A; TUBB2C
									regulation of cartilage development	RELA; RARB
									regulation of pH	EDN1; TRP53
									activation of caspase activity	BCL10; MYC
									positive regulation of cell cycle process	TRP53; EREG
									positive regulation of MAPKKK cascade	CCR2; IL1B; AR
									positive regulation of cell projection	ATF1; TNFRSF12A; HSP90AA1
									fatty acid transport	ABCC1; PPARG
									regulation of transforming growth factor beta receptor signaling pathway	TRP53; SMAD3
									icosanoid biosynthetic process	PTGS2; PTGS1
									positive regulation of behavior	CCR2; SMAD3
									cell cycle process	MEN1; CDKN1A; BRCA1; GADD45A; RHOU; EREG; MYB
									regulation of cell development	TGIF1; TRP53; ATF1; TNFRSF12A; PPARG; RELA
									regulation of epithelial cell proliferation	ETV4; SMAD3; AR
									regulation of glial cell differentiation	PPARG; RELA

GO:0048286	0.0171	1	BP	32911	228	29	2	lung alveolus development	HS6ST1; ERRFI1
GO:0051092	0.0171	1	BP	32911	228	29	2	positive regulation of NF-kappaB transcription factor activity	BCL10; RELA
GO:0006636	0.0171	1	BP	32911	228	29	2	unsaturated fatty acid biosynthetic process	PTGS2; PTGS1
GO:0070372	0.0171	1	BP	32911	228	29	2	regulation of ERK1 and ERK2 cascade	IL1B; KLF4
GO:0001503	0.0176	1	BP	32911	228	79	3	ossification	SP3; MEN1; SP1
GO:0016125	0.0176	1	BP	32911	228	79	3	sterol metabolic process	CYP51; IDI1; CH25H
GO:0045786	0.0176	1	BP	32911	228	79	3	negative regulation of cell cycle	MEN1; CDKN1A; GADD45A
GO:0048469	0.0176	1	BP	32911	228	79	3	cell maturation	EREG; TIMP1; CEBPA
GO:0035148	0.0182	1	BP	32911	228	80	3	tube formation	TGIF1; ADM; BCL10
GO:0015758	0.0182	1	BP	32911	228	30	2	glucose transport	EDN1; SLC2A1
GO:0001947	0.0182	1	BP	32911	228	30	2	heart looping	SMAD3; HIF1A
GO:0043271	0.0182	1	BP	32911	228	30	2	negative regulation of ion transport	NEDD4L; PTGS2
GO:0045428	0.0182	1	BP	32911	228	30	2	regulation of nitric oxide biosynthetic process	PTGS2; HSP90AA1
GO:0006749	0.0182	1	BP	32911	228	30	2	glutathione metabolic process	GSR; GCLC
GO:0071445	0.0182	1	BP	32911	228	30	2	cellular response to protein stimulus	MYC; EGR1
GO:0048706	0.0194	1	BP	32911	228	31	2	embryonic skeletal system development	SP3; SP1
GO:0050680	0.0194	1	BP	32911	228	31	2	negative regulation of epithelial cell proliferation	ETV4; AR
GO:0051100	0.0194	1	BP	32911	228	31	2	negative regulation of binding	HMOX1; MYC
GO:0006352	0.0194	1	BP	32911	228	31	2	transcription initiation	GTF2F2; MYC
GO:0008645	0.0194	1	BP	32911	228	31	2	hexose transport	EDN1; SLC2A1
GO:0010561	0.0206	1	BP	32911	228	3	1	negative regulation of glycoprotein biosynthetic process	HBEGF
GO:0010766	0.0206	1	BP	32911	228	3	1	negative regulation of sodium ion transport	NEDD4L
GO:0014009	0.0206	1	BP	32911	228	3	1	glial cell proliferation	AREG
GO:0014060	0.0206	1	BP	32911	228	3	1	regulation of epinephrine secretion	PTGS1
GO:0014738	0.0206	1	BP	32911	228	3	1	regulation of muscle hyperplasia	KLF4
GO:0014745	0.0206	1	BP	32911	228	3	1	negative regulation of muscle adaptation	KLF4
GO:0014850	0.0206	1	BP	32911	228	3	1	response to muscle activity	HIF1A
GO:0001844	0.0206	1	BP	32911	228	3	1	protein insertion into mitochondrial membrane involved in induction of apoptosis	PMAIP1
GO:0002228	0.0206	1	BP	32911	228	3	1	natural killer cell mediated immunity	PRDX1
GO:0002309	0.0206	1	BP	32911	228	3	1	T cell proliferation involved in immune	TRP53
GO:0002520	0.0206	1	BP	32911	228	3	1	immune system development	SMAD3
GO:0002719	0.0206	1	BP	32911	228	3	1	negative regulation of cytokine production involved in immune response	HMOX1
GO:0031571	0.0206	1	BP	32911	228	3	1	G1/S DNA damage checkpoint	TRP53
GO:0032091	0.0206	1	BP	32911	228	3	1	negative regulation of protein binding	MYC
GO:0032227	0.0206	1	BP	32911	228	3	1	negative regulation of synaptic transmission, dopaminergic	PTGS2
GO:0032530	0.0206	1	BP	32911	228	3	1	regulation of microvillus organization	PODXL
GO:0032534	0.0206	1	BP	32911	228	3	1	regulation of microvillus assembly	PODXL

		GO:0032647	0.0206	1	BP	32911	228	3	1	regulation of interferon-alpha production	HSPD1
		GO:0032763	0.0206	1	BP	32911	228	3	1	regulation of mast cell cytokine production	HMOX1
		GO:0032811	0.0206	1	BP	32911	228	3	1	negative regulation of epinephrine secretion	PTGS1
		GO:0033148	0.0206	1	BP	32911	228	3	1	positive regulation of estrogen receptor signaling pathway	AR
		GO:0033600	0.0206	1	BP	32911	228	3	1	negative regulation of mammary gland epithelial cell proliferation	ETV4
		GO:0033687	0.0206	1	BP	32911	228	3	1	osteoblast proliferation	JUNB
		GO:0033700	0.0206	1	BP	32911	228	3	1	phospholipid efflux	ABCC1
		GO:0042059	0.0206	1	BP	32911	228	3	1	negative regulation of epidermal growth factor receptor signaling pathway	ERRFI1
		GO:0042149	0.0206	1	BP	32911	228	3	1	cellular response to glucose starvation	TRP53
		GO:0042267	0.0206	1	BP	32911	228	3	1	natural killer cell mediated cytotoxicity	PRDX1
		GO:0043568	0.0206	1	BP	32911	228	3	1	positive regulation of insulin-like growth factor receptor signaling pathway	AR
		GO:0045655	0.0206	1	BP	32911	228	3	1	regulation of monocyte differentiation	JUN
		GO:0046618	0.0206	1	BP	32911	228	3	1	drug export	ABCC1
		GO:0048251	0.0206	1	BP	32911	228	3	1	elastic fiber assembly	LOX
		GO:0048340	0.0206	1	BP	32911	228	3	1	paraxial mesoderm morphogenesis	SMAD3
		GO:0048570	0.0206	1	BP	32911	228	3	1	notochord morphogenesis	EPHA2
		GO:0050779	0.0206	1	BP	32911	228	3	1	RNA destabilization	ZFP36
		GO:0051204	0.0206	1	BP	32911	228	3	1	protein insertion into mitochondrial membrane	PMAIP1
		GO:0051298	0.0206	1	BP	32911	228	3	1	centrosome duplication	BRCA1
		GO:0051409	0.0206	1	BP	32911	228	3	1	response to nitrosative stress	GCLC
		GO:0051443	0.0206	1	BP	32911	228	3	1	positive regulation of ubiquitin-protein ligase activity	TRIB3
		GO:0051894	0.0206	1	BP	32911	228	3	1	positive regulation of focal adhesion assembly	SMAD3
		GO:0060397	0.0206	1	BP	32911	228	3	1	JAK-STAT cascade involved in growth hormone signaling pathway	STAT3
		GO:0060748	0.0206	1	BP	32911	228	3	1	tertiary branching involved in mammary gland duct morphogenesis	AR
		GO:0061098	0.0206	1	BP	32911	228	3	1	positive regulation of protein tyrosine kinase activity	EREG
		GO:0066900	0.0206	1	BP	32911	228	3	1	membrane budding	PRKCI
		GO:0066977	0.0206	1	BP	32911	228	3	1	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	TRP53
		GO:0070837	0.0206	1	BP	32911	228	3	1	dehydroascorbic acid transport	SLC2A1
		GO:0072112	0.0206	1	BP	32911	228	3	1	glomerular visceral epithelial cell differentiation	WT1
		GO:0072311	0.0206	1	BP	32911	228	3	1	glomerular epithelial cell differentiation	WT1
		GO:007525	0.0206	1	BP	32911	228	3	1	somatic muscle development	IFRD1
		GO:0090003	0.0206	1	BP	32911	228	3	1	regulation of establishment of protein localization in plasma membrane	PRKCI
		GO:0090270	0.0206	1	BP	32911	228	3	1	regulation of fibroblast growth factor production	PTGS2
		GO:0090501	0.0206	1	BP	32911	228	3	1	pentose-phosphate shunt, oxidative branch	PGD

GO:0009415	0.0206	1	BP	32911	228	3	1	response to water	KRT8
GO:0015749	0.0206	1	BP	32911	228	32	2	monosaccharide transport	EDN1; SLC2A1
GO:0043506	0.0206	1	BP	32911	228	32	2	regulation of JUN kinase activity	IL1B; BCL10
GO:0014070	0.0207	1	BP	32911	228	84	3	response to organic cyclic substance	PPP2R2A; PPARG; CEBPA
GO:0050778	0.0207	1	BP	32911	228	150	4	positive regulation of immune response	C4B; HSPA1B; EREG; RELA
GO:0031344	0.0211	1	BP	32911	228	151	4	regulation of cell projection organization	PODXL; ATF1; TNFRSF12A; HSP90AA1
GO:0032270	0.0211	1	BP	32911	228	151	4	positive regulation of cellular protein metabolic process	TRIB3; MEN1; TRP53; GCLC
GO:0007346	0.0213	1	BP	32911	228	85	3	regulation of mitotic cell cycle	TRP53; EREG; MYC
GO:0045995	0.0219	1	BP	32911	228	33	2	regulation of embryonic development	AR; LAMA3
GO:0051384	0.0219	1	BP	32911	228	33	2	response to glucocorticoid stimulus	SULT1A1; AREG
GO:0051101	0.0227	1	BP	32911	228	87	3	regulation of DNA binding	HMOX1; BCL10; RELA
GO:0051249	0.023	1	BP	32911	228	155	4	regulation of lymphocyte activation	CDKN1A; HSPD1; BCL10; HSP90AA1
GO:0031960	0.0231	1	BP	32911	228	34	2	response to corticosteroid stimulus	SULT1A1; AREG
GO:0045927	0.0241	1	BP	32911	228	89	3	positive regulation of growth	CREB1; HBEGF; TNFRSF12A
GO:0050769	0.0241	1	BP	32911	228	89	3	positive regulation of neurogenesis	TNFRSF12A; PPARG; RELA
GO:0080135	0.0241	1	BP	32911	228	89	3	regulation of cellular response to stress	IL1B; BCL10; PRDX1
GO:0060688	0.0244	1	BP	32911	228	35	2	regulation of morphogenesis of a	ETV4; AR
GO:0007165	0.0246	1	BP	32911	228	2738	28	signal transduction	CXCR7; EDN1; REL; HMOX1; ZFP36; CCR2; PPARA; TRP53; ANGPTL4; PDK2; STAT3; RHOU; ARF3; NFKB1; LYVE1; ERRFI1; PPP2R2A; BCL10; SOCS3; CXCL16; AR; LRP2; PPARG; PDK4; HIF1A; STAT1; CD48; AFP
GO:0023060	0.0252	1	BP	32911	228	2744	28	signal transmission	CXCR7; EDN1; REL; HMOX1; ZFP36; CCR2; PPARA; TRP53; ANGPTL4; PDK2; STAT3; RHOU; ARF3; NFKB1; LYVE1; ERRFI1; PPP2R2A; BCL10; SOCS3; CXCL16; AR; LRP2; PPARG; PDK4; HIF1A; STAT1; CD48; AFP
GO:0021700	0.0255	1	BP	32911	228	91	3	developmental maturation	EREG; TIMP1; CEBPA
GO:0001658	0.0257	1	BP	32911	228	36	2	branching involved in ureteric bud morphogenesis	WT1; MYC
GO:0044272	0.0257	1	BP	32911	228	36	2	sulfur compound biosynthetic process	HS6ST1; GCLC
GO:0048732	0.0269	1	BP	32911	228	93	3	gland development	WT1; SMAD3; CREB1
GO:0010758	0.0274	1	BP	32911	228	4	1	regulation of macrophage chemotaxis	CCR2
GO:0010759	0.0274	1	BP	32911	228	4	1	positive regulation of macrophage chemotaxis	CCR2
GO:0014067	0.0274	1	BP	32911	228	4	1	negative regulation of phosphoinositide 3-kinase cascade	KLF4
GO:0001660	0.0274	1	BP	32911	228	4	1	fever	IL1B
GO:0019322	0.0274	1	BP	32911	228	4	1	pentose biosynthetic process	PGD
GO:0021569	0.0274	1	BP	32911	228	4	1	rhombomere 3 development	HOXA1
GO:0002347	0.0274	1	BP	32911	228	4	1	response to tumor cell	TRP53
GO:0002701	0.0274	1	BP	32911	228	4	1	negative regulation of production of molecular mediator of immune response	HMOX1
GO:0000289	0.0274	1	BP	32911	228	4	1	nuclear-transcribed mRNA poly(A) tail shortening	ZFP36
GO:0002904	0.0274	1	BP	32911	228	4	1	positive regulation of B cell apoptosis	MYC
GO:0030033	0.0274	1	BP	32911	228	4	1	microvillus assembly	KLF5
GO:0030949	0.0274	1	BP	32911	228	4	1	positive regulation of vascular endothelial growth factor receptor signaling pathway	HIF1A
GO:0031063	0.0274	1	BP	32911	228	4	1	regulation of histone deacetylation	TRP53

GO:0031065	0.0274	1	BP	32911	228	4	1	positive regulation of histone deacetylation	TRP53
GO:0031584	0.0274	1	BP	32911	228	4	1	activation of phospholipase D activity	EDN1
GO:0031670	0.0274	1	BP	32911	228	4	1	cellular response to nutrient	USF2
GO:0032528	0.0274	1	BP	32911	228	4	1	microvillus organization	KLF5
GO:0032835	0.0274	1	BP	32911	228	4	1	glomerulus development	WT1
GO:0033004	0.0274	1	BP	32911	228	4	1	negative regulation of mast cell activation	HMOX1
GO:0033145	0.0274	1	BP	32911	228	4	1	positive regulation of steroid hormone receptor signaling pathway	AR
GO:0034101	0.0274	1	BP	32911	228	4	1	erythrocyte homeostasis	PRDX1
GO:0003417	0.0274	1	BP	32911	228	4	1	growth plate cartilage development	THBS1
GO:0034644	0.0274	1	BP	32911	228	4	1	cellular response to UV	TRP53
GO:0035313	0.0274	1	BP	32911	228	4	1	wound healing, spreading of epidermal cells	HBEGF
GO:0042448	0.0274	1	BP	32911	228	4	1	progesterone metabolic process	AFP
GO:0042541	0.0274	1	BP	32911	228	4	1	hemoglobin biosynthetic process	HIF1A
GO:0043536	0.0274	1	BP	32911	228	4	1	positive regulation of blood vessel endothelial cell migration	PTGS2
GO:0043589	0.0274	1	BP	32911	228	4	1	skin morphogenesis	ERRF1
GO:0044319	0.0274	1	BP	32911	228	4	1	wound healing, spreading of cells	HBEGF
GO:0045906	0.0274	1	BP	32911	228	4	1	negative regulation of vasoconstriction	HSPA1B
GO:0046685	0.0274	1	BP	32911	228	4	1	response to arsenic	GCLC
GO:0048332	0.0274	1	BP	32911	228	4	1	mesoderm morphogenesis	SMAD3
GO:0051351	0.0274	1	BP	32911	228	4	1	positive regulation of ligase activity	TRIB3
GO:0051923	0.0274	1	BP	32911	228	4	1	sulfation	SULT1A1
GO:0055012	0.0274	1	BP	32911	228	4	1	ventricular cardiac muscle cell differentiation	RARB
GO:0060024	0.0274	1	BP	32911	228	4	1	rhythmic synaptic transmission	EDN1
GO:0060708	0.0274	1	BP	32911	228	4	1	spongiotrophoblast differentiation	SOCS3
GO:0060712	0.0274	1	BP	32911	228	4	1	spongiotrophoblast layer development	ADM
GO:0060750	0.0274	1	BP	32911	228	4	1	epithelial cell proliferation involved in mammary gland duct elongation	AREG
GO:0006528	0.0274	1	BP	32911	228	4	1	asparagine metabolic process	ASNS
GO:0070423	0.0274	1	BP	32911	228	4	1	nucleotide-binding oligomerization domain containing signaling pathway	RELA
GO:0070431	0.0274	1	BP	32911	228	4	1	nucleotide-binding oligomerization domain containing 2 signaling pathway	RELA
GO:0070555	0.0274	1	BP	32911	228	4	1	response to interleukin-1	PRKCI
GO:0071156	0.0274	1	BP	32911	228	4	1	regulation of cell cycle arrest	TRP53
GO:0071158	0.0274	1	BP	32911	228	4	1	positive regulation of cell cycle arrest	TRP53
GO:0071622	0.0274	1	BP	32911	228	4	1	regulation of granulocyte chemotaxis	CCR2
GO:0071675	0.0274	1	BP	32911	228	4	1	regulation of mononuclear cell migration	CCR2
GO:0007182	0.0274	1	BP	32911	228	4	1	common-partner SMAD protein phosphorylation	SPNB2
GO:0085029	0.0274	1	BP	32911	228	4	1	extracellular matrix assembly	LOX
GO:0090184	0.0274	1	BP	32911	228	4	1	positive regulation of kidney development	MYC

GO:0090311	0.0274	1	BP	32911	228	4	1	regulation of protein amino acid deacetylation	TRP53
GO:0090312	0.0274	1	BP	32911	228	4	1	positive regulation of protein amino acid deacetylation	TRP53
GO:0009052	0.0274	1	BP	32911	228	4	1	pentose-phosphate shunt, non-oxidative branch	TALDO1
GO:0051046	0.0275	1	BP	32911	228	243	5	regulation of secretion	EDN1; HMOX1; IL1B; CREB1; PTGS1
GO:0060249	0.0277	1	BP	32911	228	94	3	anatomical structure homeostasis	HSPA1B; HSPA1A; HIF1A
GO:0014013	0.0285	1	BP	32911	228	38	2	regulation of gliogenesis	PPARG; RELA
GO:0046496	0.0285	1	BP	32911	228	38	2	nicotinamide nucleotide metabolic process	TALDO1; PGD
GO:0008584	0.0285	1	BP	32911	228	38	2	male gonad development	WT1; AR
GO:0030036	0.0287	1	BP	32911	228	166	4	actin cytoskeleton organization	RHO; FMNL3; PRKCI; S100A9
GO:0051247	0.0287	1	BP	32911	228	166	4	positive regulation of protein metabolic process	TRIB3; MEN1; TRP53; GCLC
GO:0016311	0.0298	1	BP	32911	228	168	4	dephosphorylation	DUSP1; DUSP16; PTPN21; PTPN14
GO:0042440	0.0299	1	BP	32911	228	39	2	pigment metabolic process	HMOX1; IDI1
GO:0043279	0.0299	1	BP	32911	228	39	2	response to alkaloid	PPP2R2A; MYC
GO:0043627	0.0299	1	BP	32911	228	39	2	response to estrogen stimulus	HMOX1; AREG
GO:0051899	0.0299	1	BP	32911	228	39	2	membrane depolarization	EDN1; JUN
GO:0055067	0.0299	1	BP	32911	228	39	2	monovalent inorganic cation homeostasis	EDN1; TRP53
GO:0055088	0.0299	1	BP	32911	228	39	2	lipid homeostasis	USF2; FABP4
GO:0060021	0.0299	1	BP	32911	228	39	2	palate development	MEN1; TIPARP
GO:0045165	0.03	1	BP	32911	228	97	3	cell fate commitment	MEN1; TRP53; PPARG
GO:0010720	0.0308	1	BP	32911	228	98	3	positive regulation of cell development	TNFRSF12A; PPARG; RELA
GO:0046883	0.0308	1	BP	32911	228	98	3	regulation of hormone secretion	EDN1; IL1B; CREB1
GO:0006874	0.0309	1	BP	32911	228	170	4	cellular calcium ion homeostasis	EDN1; CCR2; ADM; IL1B
GO:0006468	0.0309	1	BP	32911	228	625	9	protein amino acid phosphorylation	SPNB2; TRIB3; GADD45G; PDK2; EPHA2; CREB1; PRKCI; BCL10; PDK4
GO:0010466	0.0313	1	BP	32911	228	40	2	negative regulation of peptidase activity	SERPINE1; HSPA1B
GO:0002761	0.0313	1	BP	32911	228	40	2	regulation of myeloid leukocyte differentiation	TOB2; JUN
GO:0030162	0.0313	1	BP	32911	228	40	2	regulation of proteolysis	TRIB3; GCLC
GO:0031214	0.0313	1	BP	32911	228	40	2	biomineral formation	TUFT1; PTGS2
GO:0032846	0.0313	1	BP	32911	228	40	2	positive regulation of homeostatic process	PTGS2; IL1B
GO:0009100	0.0313	1	BP	32911	228	40	2	glycoprotein metabolic process	HS6ST1; HIF1A
GO:0009612	0.0313	1	BP	32911	228	40	2	response to mechanical stimulus	MYC; STAT1
GO:0044282	0.0317	1	BP	32911	228	340	6	small molecule catabolic process	RHO; TALDO1; PGD; ALDOA; HSPA8; PDE4B
GO:0044270	0.0321	1	BP	32911	228	172	4	cellular nitrogen compound catabolic process	HMOX1; RHO; HSPA8; PDE4B
GO:0043405	0.0324	1	BP	32911	228	100	3	regulation of MAP kinase activity	IL1B; DUSP16; BCL10
GO:0019362	0.0328	1	BP	32911	228	41	2	pyridine nucleotide metabolic process	TALDO1; PGD
GO:0045089	0.0328	1	BP	32911	228	41	2	positive regulation of innate immune response	EREG; RELA
GO:0046888	0.0328	1	BP	32911	228	41	2	negative regulation of hormone secretion	EDN1; IL1B
GO:0055074	0.0332	1	BP	32911	228	174	4	calcium ion homeostasis	EDN1; CCR2; ADM; IL1B
GO:0006470	0.0333	1	BP	32911	228	101	3	protein amino acid dephosphorylation	DUSP1; PTPN21; PTPN14
GO:0007204	0.0333	1	BP	32911	228	101	3	elevation of cytosolic calcium ion concentration	EDN1; ADM; IL1B
GO:0007275	0.0333	1	BP	32911	228	841	11	multicellular organismal development	HOXB1; GADD45G; HOXA1; KRT8; NOTCH2; HOXC8; HES6; EREG; VAMP5; TNFRSF12A; IFRD1

GO:0002252	0.0341	1	BP	32911	228	102	3	immune effector process	C4B; BCL10; PRDX1
GO:0010591	0.0341	1	BP	32911	228	5	1	regulation of lamellipodium assembly	HSP90AA1
GO:0010592	0.0341	1	BP	32911	228	5	1	positive regulation of lamellipodium assembly	HSP90AA1
GO:0010595	0.0341	1	BP	32911	228	5	1	positive regulation of endothelial cell migration	PTGS2
GO:0001779	0.0341	1	BP	32911	228	5	1	natural killer cell differentiation	SP3
GO:0001823	0.0341	1	BP	32911	228	5	1	mesonephros development	WT1
GO:0001832	0.0341	1	BP	32911	228	5	1	blastocyst growth	HBEGF
GO:0019852	0.0341	1	BP	32911	228	5	1	L-ascorbic acid metabolic process	GCLC
GO:0002051	0.0341	1	BP	32911	228	5	1	osteoblast fate commitment	MEN1
GO:0002326	0.0341	1	BP	32911	228	5	1	B cell lineage commitment	TRP53
GO:0000288	0.0341	1	BP	32911	228	5	1	nuclear-transcribed mRNA catabolic process, deadenylation-dependent	ZFP36
GO:0031077	0.0341	1	BP	32911	228	5	1	post-embryonic camera-type eye development	KLF4
GO:0032481	0.0341	1	BP	32911	228	5	1	positive regulation of type I interferon	HSPD1
GO:0032495	0.0341	1	BP	32911	228	5	1	response to muramyl dipeptide	RELA
GO:0033604	0.0341	1	BP	32911	228	5	1	negative regulation of catecholamine secretion	PTGS1
GO:0042088	0.0341	1	BP	32911	228	5	1	T-helper 1 type immune response	RELB
GO:0045080	0.0341	1	BP	32911	228	5	1	positive regulation of chemokine biosynthetic process	IL1B
GO:0045736	0.0341	1	BP	32911	228	5	1	negative regulation of cyclin-dependent protein kinase activity	CDKN1A
GO:0045742	0.0341	1	BP	32911	228	5	1	positive regulation of epidermal growth factor receptor signaling pathway	EREG
GO:0045743	0.0341	1	BP	32911	228	5	1	positive regulation of fibroblast growth factor receptor signaling pathway	FGFBP1
GO:0045920	0.0341	1	BP	32911	228	5	1	negative regulation of exocytosis	HMOX1
GO:0046621	0.0341	1	BP	32911	228	5	1	negative regulation of organ growth	MEN1
GO:0048808	0.0341	1	BP	32911	228	5	1	male genitalia morphogenesis	AR
GO:0051438	0.0341	1	BP	32911	228	5	1	regulation of ubiquitin-protein ligase activity	TRIB3
GO:0060428	0.0341	1	BP	32911	228	5	1	lung epithelium development	ERRFI1
GO:0060762	0.0341	1	BP	32911	228	5	1	regulation of branching involved in mammary gland duct morphogenesis	ETV4
GO:0061037	0.0341	1	BP	32911	228	5	1	negative regulation of cartilage development	RARB
GO:0006686	0.0341	1	BP	32911	228	5	1	sphingomyelin biosynthetic process	SAMD8
GO:0070542	0.0341	1	BP	32911	228	5	1	response to fatty acid	EGR1
GO:0071396	0.0341	1	BP	32911	228	5	1	cellular response to lipid	EGR1
GO:0007143	0.0341	1	BP	32911	228	5	1	female meiosis	EREG
GO:0071482	0.0341	1	BP	32911	228	5	1	cellular response to light stimulus	TRP53
GO:0007184	0.0341	1	BP	32911	228	5	1	SMAD protein nuclear translocation	SPNB2
GO:0009410	0.0341	1	BP	32911	228	5	1	response to xenobiotic stimulus	GCLC
GO:0015718	0.0343	1	BP	32911	228	42	2	monocarboxylic acid transport	ABCC1; PPARG
GO:0009636	0.0343	1	BP	32911	228	42	2	response to toxin	MT1; MT2
GO:0006753	0.0345	1	BP	32911	228	347	6	nucleoside phosphate metabolic process	RHOU; TALDO1; PGD; HSPA8; AMPD3; PDE4B

									nucleotide metabolic process	RHOU; TALD01; PGD; HSPA8; AMPD3; PDE4B
									cell morphogenesis	WT1; KRT8; HIF1A
									response to light stimulus	CDKN1A; TRP53; PMAIP1
									actin filament-based process	RHOU; FMNL3; PRKCI; S100A9
									heterocycle catabolic process	HMOX1; RHOU; HSPA8; PDE4B
									icosanoid metabolic process	PTGS2; PTGS1
									determination of left/right symmetry	TGIF1; NOTCH2
									muscle structure development	VAMP5; IFRD1; RARB
									biological adhesion	MPZL2; CSF3R; LYVE1; PODXL; THBS1; LAMA3; TNFRSF12A; CYR61
									cell adhesion	MPZL2; CSF3R; LYVE1; PODXL; THBS1; LAMA3; TNFRSF12A; CYR61
									unsaturated fatty acid metabolic process	PTGS2; PTGS1
									oxygen and reactive oxygen species metabolic process	TXNRD1; PRDX1
									specification of symmetry	TGIF1; NOTCH2
									determination of bilateral symmetry	TGIF1; NOTCH2
									somitogenesis	TRP53; SMAD3
									secretion	EDN1; USF2; ADM; CREB1; LRP2
									peptide metabolic process	GSR; GCLC
									negative regulation of glucose transport	IL1B
									positive regulation of phosphatase activity	SMAD3
									heparan sulfate proteoglycan biosynthetic	HS6ST1
									B cell apoptosis	MYC
									removal of superoxide radicals	PRDX1
									positive regulation of leukocyte chemotaxis	CCR2
									diuresis	EDN1
									androgen receptor signaling pathway	AR
									negative regulation of cyclic nucleotide biosynthetic process	EDN1
									negative regulation of nucleotide biosynthetic process	EDN1
									negative regulation of cAMP biosynthetic process	EDN1
									regulation of histone methylation	MEN1
									regulation of protein amino acid	JUN
									positive regulation of interleukin-1 beta production	SMAD3
									negative regulation of myeloid cell apoptosis	HSPA1B
									transcytosis	LRP2
									negative regulation of fatty acid biosynthetic	TRIB3
									ephrin receptor signaling pathway	EPHA2
									protein insertion into membrane	PMAIP1
									regulation of ligase activity	TRIB3
									negative regulation of protein kinase B signaling cascade	KLF4

GO:0060039	0.0408	1	BP	32911	228	6	1	pericardium development	SMAD3
GO:0060231	0.0408	1	BP	32911	228	6	1	mesenchymal to epithelial transition	WT1
GO:0060426	0.0408	1	BP	32911	228	6	1	lung vasculature development	ERRFI1
GO:0060685	0.0408	1	BP	32911	228	6	1	regulation of prostatic bud formation	AR
GO:0060707	0.0408	1	BP	32911	228	6	1	trophoblast giant cell differentiation	SOCS3
GO:0060710	0.0408	1	BP	32911	228	6	1	chorio-allantoic fusion	CYR61
GO:0060744	0.0408	1	BP	32911	228	6	1	mammary gland branching involved in thelarche	AREG
GO:0060686	0.0408	1	BP	32911	228	6	1	acetyl-CoA biosynthetic process from pyruvate	PDK4
GO:0060689	0.0408	1	BP	32911	228	6	1	lactate metabolic process	HIF1A
GO:0061005	0.0408	1	BP	32911	228	6	1	cell differentiation involved in kidney development	WT1
GO:0070230	0.0408	1	BP	32911	228	6	1	positive regulation of lymphocyte apoptosis	MYC
GO:0071450	0.0408	1	BP	32911	228	6	1	cellular response to oxygen radical	PRDX1
GO:0071451	0.0408	1	BP	32911	228	6	1	cellular response to superoxide	PRDX1
GO:0050795	0.0421	1	BP	32911	228	47	2	regulation of behavior	CCR2; SMAD3
GO:0051091	0.0421	1	BP	32911	228	47	2	positive regulation of transcription factor activity	BCL10; RELA
GO:0090047	0.0421	1	BP	32911	228	47	2	positive regulation of transcription regulator activity	BCL10; RELA
GO:0010740	0.0421	1	BP	32911	228	111	3	positive regulation of intracellular protein kinase cascade	CCR2; IL1B; AR
GO:0002697	0.0421	1	BP	32911	228	111	3	regulation of immune effector process	HMOX1; CCR2; HSPA1B
GO:0050863	0.0431	1	BP	32911	228	112	3	regulation of T cell activation	HSPD1; BCL10; HSP90AA1
GO:0051480	0.0431	1	BP	32911	228	112	3	cytosolic calcium ion homeostasis	EDN1; ADM; IL1B
GO:0030307	0.0437	1	BP	32911	228	48	2	positive regulation of cell growth	HBEGF; TNFRSF12A
GO:0033500	0.0437	1	BP	32911	228	48	2	carbohydrate homeostasis	STAT3; HIF1A
GO:0042593	0.0437	1	BP	32911	228	48	2	glucose homeostasis	STAT3; HIF1A
GO:0006022	0.0437	1	BP	32911	228	48	2	aminoglycan metabolic process	LYVE1; CHI3L1
GO:0006479	0.0437	1	BP	32911	228	48	2	protein amino acid methylation	BTG2; MEN1
GO:0008213	0.0437	1	BP	32911	228	48	2	protein amino acid alkylation	BTG2; MEN1
GO:0035282	0.0454	1	BP	32911	228	49	2	segmentation	TRP53; SMAD3
GO:0031401	0.047	1	BP	32911	228	116	3	positive regulation of protein modification	TRIB3; MEN1; TRP53
GO:0071216	0.0471	1	BP	32911	228	50	2	cellular response to biotic stimulus	TRP53; STAT1
GO:0010559	0.0475	1	BP	32911	228	7	1	regulation of glycoprotein biosynthetic process	HBEGF
GO:0001954	0.0475	1	BP	32911	228	7	1	positive regulation of cell-matrix adhesion	SMAD3
GO:0002360	0.0475	1	BP	32911	228	7	1	T cell lineage commitment	TRP53
GO:0002674	0.0475	1	BP	32911	228	7	1	negative regulation of acute inflammatory	PPARG
GO:0030147	0.0475	1	BP	32911	228	7	1	natriuresis	EDN1
GO:0030201	0.0475	1	BP	32911	228	7	1	heparan sulfate proteoglycan metabolic	HS6ST1
GO:0030501	0.0475	1	BP	32911	228	7	1	positive regulation of bone mineralization	SMAD3
GO:0030800	0.0475	1	BP	32911	228	7	1	negative regulation of cyclic nucleotide metabolic process	EDN1

GO:0030815	0.0475	1	BP	32911	228	7	1	negative regulation of cAMP metabolic process	EDN1
GO:0031397	0.0475	1	BP	32911	228	7	1	negative regulation of protein ubiquitination	GCLC
GO:0031575	0.0475	1	BP	32911	228	7	1	G1/S transition checkpoint	TRP53
GO:0031649	0.0475	1	BP	32911	228	7	1	heat generation	IL1B
GO:0032099	0.0475	1	BP	32911	228	7	1	negative regulation of appetite	PPARA
GO:0032303	0.0475	1	BP	32911	228	7	1	regulation of icosanoid secretion	IL1B
GO:0032305	0.0475	1	BP	32911	228	7	1	positive regulation of icosanoid secretion	IL1B
GO:0032306	0.0475	1	BP	32911	228	7	1	regulation of prostaglandin secretion	IL1B
GO:0032308	0.0475	1	BP	32911	228	7	1	positive regulation of prostaglandin secretion	IL1B
GO:0032732	0.0475	1	BP	32911	228	7	1	positive regulation of interleukin-1 production	SMAD3
GO:0033146	0.0475	1	BP	32911	228	7	1	regulation of estrogen receptor signaling pathway	AR
GO:0033599	0.0475	1	BP	32911	228	7	1	regulation of mammary gland epithelial cell proliferation	ETV4
GO:0035089	0.0475	1	BP	32911	228	7	1	establishment of apical/basal cell polarity	PRKCI
GO:0035428	0.0475	1	BP	32911	228	7	1	hexose transmembrane transport	SLC2A1
GO:0042178	0.0475	1	BP	32911	228	7	1	xenobiotic catabolic process	GSTA2
GO:0043249	0.0475	1	BP	32911	228	7	1	erythrocyte maturation	TIMP1
GO:0045073	0.0475	1	BP	32911	228	7	1	regulation of chemokine biosynthetic process	IL1B
GO:0045616	0.0475	1	BP	32911	228	7	1	regulation of keratinocyte differentiation	ERRFI1
GO:0045648	0.0475	1	BP	32911	228	7	1	positive regulation of erythrocyte	HIF1A
GO:0048260	0.0475	1	BP	32911	228	7	1	positive regulation of receptor-mediated endocytosis	SERPINE1
GO:0050996	0.0475	1	BP	32911	228	7	1	positive regulation of lipid catabolic process	IL1B
GO:0051893	0.0475	1	BP	32911	228	7	1	regulation of focal adhesion assembly	SMAD3
GO:0051900	0.0475	1	BP	32911	228	7	1	regulation of mitochondrial	GCLC
GO:0060002	0.0475	1	BP	32911	228	7	1	fructose 6-phosphate metabolic process	TALDO1
GO:0060601	0.0475	1	BP	32911	228	7	1	lateral sprouting from an epithelium	AR
GO:0061162	0.0475	1	BP	32911	228	7	1	establishment of monopolar cell polarity	PRKCI
GO:0060983	0.0475	1	BP	32911	228	7	1	ER overload response	TRP53
GO:0070169	0.0475	1	BP	32911	228	7	1	positive regulation of biomineral formation	SMAD3
GO:0070306	0.0475	1	BP	32911	228	7	1	lens fiber cell differentiation	SMAD3
GO:0071478	0.0475	1	BP	32911	228	7	1	cellular response to radiation	TRP53
GO:007406	0.0475	1	BP	32911	228	7	1	negative regulation of neuroblast proliferation	TRP53
GO:0080815	0.0475	1	BP	32911	228	7	1	blood circulation	STAT1
GO:0090109	0.0475	1	BP	32911	228	7	1	regulation of cell-substrate junction	SMAD3
GO:0016044	0.0477	1	BP	32911	228	283	5	cellular membrane organization	TRP53; PRKCI; LRP2; CEBPE; PMAIP1
GO:0061024	0.0477	1	BP	32911	228	283	5	membrane organization	TRP53; PRKCI; LRP2; CEBPE; PMAIP1
GO:0006733	0.0488	1	BP	32911	228	51	2	oxidoreduction coenzyme metabolic process	TALDO1; PGD
GO:0055086	0.0498	1	BP	32911	228	380	6	nucleobase, nucleoside and nucleotide metabolic	RHOU; TALDO1; PGD; HSPA8; AMPD3; PDE4B
GO:0090066	0.05	1	BP	32911	228	119	3	regulation of anatomical structure size	SPNB2; EDN1; CREB1

										SPNB2; GNL3; ABCD3; SP3; PPL; HOXB1; TCFAP2A; GSR; WT1; BACH1; GTF2F2; TGIF1; TUBA4A; REL; HMOX1; CEBPD; FAM134B; PRR13; ZFP36; DHX32; TRIB3; MEN1; LOX; RELB; NEDD4L; USF2; GADD45G; CCR2; SULT1A1; CDKN1A; PPARA; TRP53; HOXA1; MT1; HSPA1B; TBC1D15; S100A14; BRCA1; FABP4; KRT8; ETV4; PDK2; STAT3; SRXN1; SLC25A29; GADD45A; SELM; RHOU; ARF3; SMAD3; ATF3; PTGS2; TALDO1; DUSP1; NFKB1; ABCC1; NQO1; CYP51; NDRG1; SP1; HSPA9; IL1B; GSTA2; NOTCH2; TNPO3; HOXC8; HES6; SRI; DUSP16; TUBB2C; CREB1; HSPA1A; HSPD1; PRKCI; PTPN21; FOS; TXNL1; CREG1; ZFAND2A; JUNB; PTGS1; PTPN14; F3; GTF3C1; ESD; ZFP110; GPX2; MARCH6; MAFK; CLU; LACE1; UBXN4; PSMD3; ERRF11; IDI1; KLF5; NMD3; TSPYL4; AREG; TINAGL1; MRPL28; PPP2R2A; PPA1; CEBPB; HIGD2A; DDX39; BCL10; NFIC; SCEL; MYC; JUN; VAMP5; MRPS12; SOCS3; TXNRD1; SP2; S100A8; AR; RNF5; PRDX1; ACOT10; PGD; LRP2; ATF1; CEBPE; HSP90AB1; ETS1; PMAIP1; ALDOA; PPARG; MAFF; ATF4; COPS3; IFRD1; GCA; GLG1; NBRI; PDK4; PSMA5; HSBP1; RELA; HIF1A; FOSL1; HSPA8; RARB; PSMC1; STAT1; MYBL2; CARKD; GCLC; PARD6B; YPEL3; CH25H; SFP11; RPL22L1; EGR1; SLC2A1; LITAF; AFP; CEBPA; USF1; PDE4B; HSP90AA1; ELOVL7; KRT7; S100A9; PPRC1; KLF6; KLF4; MYB; HP
GO:0044424	1. 00E-46	2. 00E-44	CC	33355	227	9777	171	intracellular part	CXCR7; SPNB2; GNL3; ABCD3; SP3; PPL; HOXB1; TCFAP2A; RTKN2; GSR; SERPINE1; WT1; BACH1; MPZL2; GTF2F2; TGIF1; TUBA4A; REL; HMOX1; CEBPD; OGRFL1; FAM134B; PRR13; ZFP36; DHX32; TRIB3; MEN1; LOX; RELB; NEDD4L; USF2; GADD45G; CCR2; SULT1A1; CDKN1A; PPARA; TRP53; HOXA1; MT1; SAMD8; HSPA1B; TBC1D15; CSF3R; S100A14; BRCA1; FABP4; KRT8; ETV4; PDK2; STAT3; SRXN1; SLC25A29; COL6A3; EPHA2; GADD45A; SELM; RHOU; ARF3; SMAD3; ATF3; PTGS2; TALDO1; DUSP1; YRDC; NFKB1; ABCC1; NQO1; CYP51; NDRG1; SP1; HSPA9; IL1B; IL1R2; GSTA2; NOTCH2; TNPO3; DNAJC5; HOXC8; HES6; SRI; DUSP16; TUBB2C; RNASEK; LYVE1; CREB1; HSPA1A; EREG; HSPD1; HBEGF; PRKCI; PTPN21; FOS; TXNL1; CREG1; ZFAND2A; JUNB; PTGS1; PTPN14; F3; GTF3C1; PODXL; ESD; ZFP110; GPX2; MARCH6; HS6ST1; MAFK; CLU; LACE1; UBXN4; PSMD3; ERRF11; IDI1; KLF5; NMD3; TSPYL4; AREG; TINAGL1; SLC20A1; MRPL28; PPP2R2A; PPA1; CEBPB; HIGD2A; DDX39; BCL10; NFIC; SCEL; MYC; JUN; VAMP5; MRPS12; SOCS3; TXNRD1; JAM2; SP2; S100A8; AR; RNF5; PRDX1; ACOT10; PLAU; PGD; LRP2; ATF1; CEBPE; HSP90AB1; ETS1; LAMA3; PMAIP1; ASNS; ALDOA; TNFRSF12A; PPARG; MAFF; ATF4; COPS3; IFRD1; KCTD9; GCA; GLG1; NBRI; PDK4; PSMA5; HSBP1; RELA; HIF1A; FOSL1; HSPA8; RARB; PSMC1; STAT1; MYBL2; CARKD; GCLC; TMEM49; PARD6B; GJB3; YPEL3; CH25H; SFP11; RPL22L1; EGR1; SLC2A1; CD48; LITAF; AFP; CEBPA; USF1; PDE4B; HSP90AA1; ELOVL7; FGFBP1; KRT7; S100A9; PPRC1; KLF6; KLF4; SERPINA3N; MYB; HP	
GO:0044464	3. 40E-46	6. 90E-44	CC	33355	227	####	201	cell part	SPNB2; GNL3; ABCD3; SP3; PPL; HOXB1; TCFAP2A; GSR; WT1; BACH1; GTF2F2; TGIF1; REL; HMOX1; CEBPD; FAM134B; PRR13; ZFP36; DHX32; TRIB3; MEN1; LOX; RELB; USF2; GADD45G; CDKN1A; PPARA; TRP53; HOXA1; MT1; HSPA1B; TBC1D15; BRCA1; FABP4; ETV4; PDK2; STAT3; SLC25A29; GADD45A; SELM; RHOU; ARF3; SMAD3; ATF3; PTGS2; TALDO1; DUSP1; YRDC; NFKB1; ABCC1; NQO1; CYP51; NDRG1; SP1; HSPA9; IL1B; IL1R2; GSTA2; NOTCH2; TNPO3; DNAJC5; HOXC8; HES6; SRI; DUSP16; TUBB2C; RNASEK; LYVE1; CREB1; HSPA1A; EREG; HSPD1; HBEGF; PRKCI; PTPN21; FOS; TXNL1; CREG1; ZFAND2A; JUNB; PTGS1; PTPN14; F3; GTF3C1; PODXL; ESD; ZFP110; GPX2; MARCH6; HS6ST1; MAFK; CLU; LACE1; UBXN4; PSMD3; ERRF11; IDI1; KLF5; NMD3; TSPYL4; AREG; TINAGL1; SLC20A1; MRPL28; PPP2R2A; PPA1; CEBPB; HIGD2A; DDX39; BCL10; NFIC; SCEL; MYC; JUN; VAMP5; MRPS12; SOCS3; TXNRD1; JAM2; SP2; S100A8; AR; RNF5; PRDX1; ACOT10; PLAU; PGD; LRP2; ATF1; CEBPE; HSP90AB1; ETS1; LAMA3; PMAIP1; ASNS; ALDOA; TNFRSF12A; PPARG; MAFF; ATF4; COPS3; IFRD1; KCTD9; GCA; GLG1; NBRI; PDK4; PSMA5; HSBP1; RELA; HIF1A; FOSL1; HSPA8; RARB; PSMC1; STAT1; MYBL2; CARKD; GCLC; TMEM49; PARD6B; GJB3; YPEL3; CH25H; SFP11; RPL22L1; EGR1; SLC2A1; CD48; LITAF; AFP; CEBPA; USF1; PDE4B; HSP90AA1; ELOVL7; FGFBP1; KRT7; S100A9; PPRC1; KLF6; KLF4; SERPINA3N; MYB; HP	
GO:0043227	2. 40E-36	4. 90E-34	CC	33355	227	7147	136	membrane-bounded organelle	SPNB2; GNL3; ABCD3; SP3; PPL; HOXB1; TCFAP2A; GSR; WT1; BACH1; GTF2F2; TGIF1; REL; HMOX1; CEBPD; FAM134B; PRR13; ZFP36; DHX32; TRIB3; MEN1; LOX; RELB; USF2; GADD45G; CDKN1A; PPARA; TRP53; HOXA1; MT1; HSPA1B; TBC1D15; BRCA1; FABP4; ETV4; PDK2; STAT3; SLC25A29; GADD45A; SELM; RHOU; ARF3; SMAD3; ATF3; PTGS2; DUSP1; NFKB1; CYP51; NDRG1; SP1; HSPA9; IL1B; GSTA2; NOTCH2; TNPO3; HOXC8; HES6; SRI; DUSP16; CREB1; HSPA1A; HSPD1; PRKCI; FOS; ZFAND2A; JUNB; PTGS1; GTF3C1; ESD; ZFP110; MARCH6; MAFK; LACE1; UBXN4; ERRF11; IDI1; KLF5; NMD3; TSPYL4; AREG; MRPL28; CEBPB; HIGD2A; DDX39; NFIC; MYC; JUN; VAMP5; MRPS12; TXNRD1; SP2; AR; RNF5; PRDX1; ACOT10; LRP2; ATF1; CEBPE; HSP90AB1; ETS1; PMAIP1; ALDOA; PPARG; MAFF; ATF4; COPS3; IFRD1; GLG1; NBRI; PDK4; PSMA5; HSBP1; RELA; HIF1A; FOSL1; HSPA8; RARB; PSMC1; STAT1; MYBL2; CARKD; PARD6B; YPEL3; CH25H; SFP11; EGR1; LITAF; CEBPA; USF1; PDE4B; ELOVL7; PPRC1; KLF6; KLF4; MYB; HP	

	GO:0043231	1. 20E-35	2. 50E-33	CC	33355	227	7142	135	intracellular membrane-bounded organelle	SPNB2; GNL3; ABCD3; SP3; PPL; HOXB1; TCFAP2A; GSR; WT1; BACH1; GTF2F2; TGIF1; REL; HMOX1; CEBPD; FAM134B; PRR13; ZFP36; DHX32; TRIB3; MEN1; LOX; RELB; USF2; GADD45G; CDKN1A; PPARG; TRP53; HOXA1; MT1; HSPA1B; TBC1D15; BRCA1; FABP4; ETV4; PDK2; STAT3; SLC25A29; GADD45A; SELM; RHOU; ARF3; SMAD3; ATF3; PTGS2; DUSP1; NFKB1; CYP51; NDRG1; SP1; HSPA9; IL1B; GSTA2; NOTCH2; TNPO3; HOXC8; HES6; SRI; DUSP16; CREB1; HSPA1A; HSPD1; PRKCI; FOS; ZFAND2A; JUNB; PTGS1; GTF3C1; ESD; ZFP110; MARCH6; MAFK; LACE1; UBXL4; ERRFI1; IDI1; KLF5; NMD3; TSPYL4; AREG; MRPL28; CEBPB; HIGD2A; DDX39; NFIC; MYC; JUN; VAMP5; MRPS12; TXNRD1; SP2; AR; RNF5; PRDX1; ACOT10; LRP2; ATF1; CEBPE; HSP90AB1; ETS1; PMAIP1; ALDOA; PPARG; MAFF; ATF4; COPS3; IFRD1; GLG1; NBRI; PDK4; PSMA5; HSBP1; RELA; HIF1A; FOSL1; RARB; PSMC1; STAT1; MYBL2; CARND; PARDB6; YPEL3; CH25H; SFPI1; EGRI; LITAF; CEBPA; USF1; PDE4B; ELVOL7; PPRC1; KLF6; KLF4; MYB; HP
	GO:0043226	3. 60E-35	7. 30E-33	CC	33355	227	7883	141	organelle	SPNB2; GNL3; ABCD3; SP3; PPL; HOXB1; TCFAP2A; GSR; WT1; BACH1; GTF2F2; TGIF1; REL; HMOX1; CEBPD; FAM134B; PRR13; ZFP36; DHX32; TRIB3; MEN1; LOX; RELB; USF2; GADD45G; CDKN1A; PPARG; TRP53; HOXA1; MT1; HSPA1B; TBC1D15; BRCA1; FABP4; ETV4; PDK2; STAT3; SLC25A29; GADD45A; SELM; RHOU; ARF3; SMAD3; ATF3; PTGS2; DUSP1; NFKB1; CYP51; NDRG1; SP1; HSPA9; IL1B; GSTA2; NOTCH2; TNPO3; HOXC8; HES6; SRI; DUSP16; CREB1; HSPA1A; HSPD1; PRKCI; PTPN21; FOS; ZFAND2A; JUNB; PTGS1; PTPN14; GTF3C1; ESD; ZFP110; MARCH6; MAFK; LACE1; UBXL4; ERRFI1; IDI1; KLF5; NMD3; TSPYL4; AREG; MRPL28; CEBPB; HIGD2A; DDX39; NFIC; MYC; JUN; VAMP5; MRPS12; TXNRD1; SP2; S100A8; AR; RNF5; PRDX1; ACOT10; LRP2; ATF1; CEBPE; HSP90AB1; ETS1; PMAIP1; ALDOA; PPARG; MAFF; ATF4; COPS3; IFRD1; GLG1; NBRI; PDK4; PSMA5; HSBP1; RELA; HIF1A; FOSL1; HSPA8; RARB; PSMC1; STAT1; MYBL2; CARND; PARDB6; YPEL3; CH25H; SFPI1; RPL22L1; EGRI; LITAF; CEBPA; USF1; PDE4B; ELVOL7; S100A9; PPRC1; KLF6; KLF4; MYB; HP
	GO:0043229	1. 40E-34	3. 00E-32	CC	33355	227	7865	140	intracellular organelle	SPNB2; GNL3; ABCD3; SP3; PPL; HOXB1; TCFAP2A; GSR; WT1; BACH1; GTF2F2; TGIF1; REL; HMOX1; CEBPD; FAM134B; PRR13; ZFP36; DHX32; TRIB3; MEN1; LOX; RELB; USF2; GADD45G; CDKN1A; PPARG; TRP53; HOXA1; MT1; HSPA1B; TBC1D15; BRCA1; FABP4; ETV4; PDK2; STAT3; SLC25A29; GADD45A; SELM; RHOU; ARF3; SMAD3; ATF3; PTGS2; DUSP1; NFKB1; CYP51; NDRG1; SP1; HSPA9; IL1B; GSTA2; NOTCH2; TNPO3; HOXC8; HES6; SRI; DUSP16; CREB1; HSPA1A; HSPD1; PRKCI; PTPN21; FOS; ZFAND2A; JUNB; PTGS1; PTPN14; GTF3C1; ESD; ZFP110; MARCH6; MAFK; LACE1; UBXL4; ERRFI1; IDI1; KLF5; NMD3; TSPYL4; AREG; MRPL28; CEBPB; HIGD2A; DDX39; NFIC; MYC; JUN; VAMP5; MRPS12; TXNRD1; SP2; S100A8; AR; RNF5; PRDX1; ACOT10; LRP2; ATF1; CEBPE; HSP90AB1; ETS1; PMAIP1; ALDOA; PPARG; MAFF; ATF4; COPS3; IFRD1; GLG1; NBRI; PDK4; PSMA5; HSBP1; RELA; HIF1A; FOSL1; RARB; PSMC1; STAT1; MYBL2; CARND; PARDB6; YPEL3; CH25H; SFPI1; RPL22L1; EGRI; LITAF; CEBPA; USF1; PDE4B; ELVOL7; S100A9; PPRC1; KLF6; KLF4; MYB; HP
	GO:0005634	1. 90E-29	3. 90E-27	CC	33355	227	4243	97	nucleus	SPNB2; GNL3; SP3; PPL; HOXB1; TCFAP2A; WT1; BACH1; GTF2F2; TGIF1; REL; HMOX1; CEBPD; PRR13; ZFP36; DHX32; TRIB3; MEN1; LOX; RELB; USF2; GADD45G; CDKN1A; PPARG; TRP53; HOXA1; HSPA1B; BRCA1; FABP4; ETV4; STAT3; GADD45A; SMAD3; ATF3; PTGS2; DUSP1; NFKB1; NDRG1; SP1; GSTA2; NOTCH2; TNPO3; HOXC8; HES6; DUSP16; CREB1; PRKCI; FOS; ZFAND2A; JUNB; PTGS1; GTF3C1; ZFP110; MAFK; UBXL4; ERRFI1; KLF5; NMD3; TSPYL4; AREG; CEBPB; DDX39; NFIC; MYC; JUN; TXNRD1; SP2; AR; PRDX1; ATF1; CEBPE; ETS1; PPARG; MAFF; ATF4; COPS3; IFRD1; PSMA5; HSBP1; RELA; HIF1A; FOSL1; RARB; PSMC1; STAT1; MYBL2; PARDB6; YPEL3; SFPI1; EGRI; CEBPA; USF1; PDE4B; PPRC1; KLF6; KLF4; MYB
	GO:0005829	9. 50E-20	1. 90E-17	CC	33355	227	495	30	cytosol	GSR; HMOX1; ZFP36; RELB; CCR2; SUL1A1; CDKN1A; TRP53; MT1; HSPA1B; FABP4; SRXN1; TALDO1; NFKB1; GSTA2; HSPD1; GPX2; ERRFI1; BCL10; JUN; TXNRD1; PRDX1; PPARG; GCA; RELA; FOSL1; HSPA8; GCLC; PDE4B; HSP90AA1

[illegible]

GO:0005739	6.50E-07	1.30E-04	CC	33355	227	1355	27	mitochondrion	ABCD3; PPL; GSR; DHX32; TRP53; HSPA1B; TBC1D15; PDK2; SLC25A29; HSPA9; CREB1; HSPA1A; HSPD1; LACE1; IDI1; MRPL28; HIGD2A; MRPS12; TXNRD1; RNF5; PRDX1; ACOT10; HSP90AB1; PMAIP1; ALDOA; PDK4; CARKN
GO:0005615	1.60E-06	3.40E-04	CC	33355	227	559	16	extracellular space	EDN1; SERPINE1; ANGPTL4; ADM; COL6A3; IL1B; EREG; HBEGF; F3; AREG; THBS1; S100A8; LRP2; AFP; S100A9; HP
GO:0016020	7.00E-06	0.0014	CC	33355	227	5875	67	membrane	CXCR7; SPNB2; ABCD3; PPL; RTKN2; MPZL2; OGFRL1; FAM134B; CCR2; SAMD8; CSF3R; KRT8; STAT3; SLC25A29; COL6A3; EPHA2; RHOU; SMAD3; PTGS2; ABCC1; CYP51; IL1R2; GSTA2; NOTCH2; DNAJC5; SRI; RNASEK; LYVE1; EREG; HSPD1; HBEGF; PRKCI; PTGS1; F3; PODXL; MARCH6; HS6ST1; UBXN4; ERRF1; AREG; SLC20A1; HIGD2A; BCL10; SCEL; VAMP5; JAM2; S100A8; RNF5; PLAUR; LRP2; TNFRSF12A; ATF4; KCTD9; GCA; GLG1; PDK4; FOSL1; TMEM49; PARD6B; GJB3; CH25H; SLC2A1; CD48; LITAF; ELOVL7; FGFBP1; S100A9
GO:0044459	2.10E-05	0.0044	CC	33355	227	1454	25	plasma membrane part	PPL; GSR; HMOX1; HSPA1B; EPHA2; RHOU; PTGS2; ABCC1; NOTCH2; HSPD1; HBEGF; PRKCI; PODXL; ERRF1; BCL10; VAMP5; JAM2; LRP2; LAMA3; KCTD9; PARD6B; GJB3; SLC2A1; CD48; HSP90AA1
GO:0005886	9.60E-05	0.0194	CC	33355	227	2198	31	plasma membrane	CXCR7; SPNB2; PPL; RTKN2; CCR2; KRT8; STAT3; COL6A3; RHOU; SMAD3; ABCC1; NOTCH2; SRI; LYVE1; EREG; HBEGF; PODXL; ERRF1; VAMP5; JAM2; S100A8; PLAUR; TNFRSF12A; ATF4; GLG1; PARD6B; GJB3; SLC2A1; CD48; FGFBP1; S100A9
GO:0000267	2.40E-04	0.0503	CC	33355	227	1024	18	cell fraction	GSR; SERPINE1; HMOX1; TRP53; PTGS2; TALDO1; DUSP1; YRDC; CYP51; PRKCI; FOS; PTGS1; PGD; LRP2; ASNS; FOSL1; PDE4B; SERPINA3N
GO:0005625	3.10E-04	0.0644	CC	33355	227	313	9	soluble fraction	GSR; SERPINE1; TRP53; TALDO1; DUSP1; PRKCI; PGD; ASNS; PDE4B
GO:0005783	6.20E-04	0.1261	CC	33355	227	831	15	endoplasmic reticulum	HMOX1; TRP53; SELM; PTGS2; CYP51; SRI; HSPD1; PTGS1; MARCH6; UBXN4; RNF5; LRP2; CH25H;
GO:0031012	7.40E-04	0.1506	CC	33355	227	282	8	extracellular matrix	LOX; ANGPTL4; ADAMTS4; COL6A3; TIMP1; LAMA3; HSP90AA1; MMP11
GO:0000785	7.40E-04	0.1509	CC	33355	227	104	5	chromatin	TRP53; CREB1; JUN; PRDX1; KLF4
GO:0005759	0.0013	0.2707	CC	33355	227	32	3	mitochondrial matrix	HSPA1B; BRCA1; PRDX1
GO:0005911	0.0019	0.3926	CC	33355	227	189	6	cell-cell junction	PRKCI; JAM2; LAMA3; PARD6B; GJB3; SLC2A1
GO:0005901	0.0029	0.596	CC	33355	227	42	3	caveola	HMOX1; PTGS2; SLC2A1
GO:0005792	0.0031	0.6371	CC	33355	227	279	7	microsome	HMOX1; PTGS2; TALDO1; CYP51; PTGS1; PGD; FOSL1
GO:0016324	0.0034	0.6929	CC	33355	227	147	5	apical plasma membrane	HSPA1B; PRKCI; PODXL; LRP2; HSP90AA1
GO:0042598	0.0035	0.7298	CC	33355	227	286	7	vesicular fraction	HMOX1; PTGS2; TALDO1; CYP51; PTGS1; PGD; FOSL1
GO:0045121	0.0036	0.7339	CC	33355	227	149	5	membrane raft	HMOX1; PTGS2; HSPD1; BCL10; SLC2A1
GO:0016323	0.0038	0.7716	CC	33355	227	93	4	basolateral plasma membrane	HSPA1B; ABCC1; SLC2A1; HSP90AA1
GO:0000127	0.0068	1	CC	33355	227	1	1	transcription factor TFIIIC complex	GTF3C1
GO:0035189	0.0068	1	CC	33355	227	1	1	Rb-E2F complex	CEBPA
GO:0045298	0.0068	1	CC	33355	227	1	1	tubulin complex	TUBB2C
GO:0005608	0.0068	1	CC	33355	227	1	1	laminin-3 complex	LAMA3
GO:0005674	0.0068	1	CC	33355	227	1	1	transcription factor TFIIIF complex	GTF2F2
GO:0009986	0.0072	1	CC	33355	227	176	5	cell surface	HSPD1; F3; TNFRSF12A; HSP90AA1; FGFBP1
GO:0000502	0.0076	1	CC	33355	227	59	3	proteasome complex	PSMD3; PSMA5; PSMC1
GO:0005578	0.0084	1	CC	33355	227	256	6	proteinaceous extracellular matrix	LOX; ANGPTL4; ADAMTS4; TIMP1; LAMA3; MMP11
GO:0045177	0.0091	1	CC	33355	227	63	3	apical part of cell	PRKCI; LRP2; PARD6B
GO:0005626	0.0098	1	CC	33355	227	809	12	insoluble fraction	HMOX1; PTGS2; TALDO1; YRDC; CYP51; PRKCI; FOS; PTGS1; PGD; LRP2; FOSL1; PDE4B
GO:0005730	0.0115	1	CC	33355	227	128	4	nucleolus	GNL3; HMOX1; MYC; PRDX1
GO:0016235	0.0135	1	CC	33355	227	2	1	aggresome	CLU

GO:0017109	0.0135	1	CC	33355	227	2	1	glutamate-cysteine ligase complex	GCLC
GO:0016363	0.0144	1	CC	33355	227	27	2	nuclear matrix	CEBPB; CEBPA
GO:0005923	0.0146	1	CC	33355	227	75	3	tight junction	PRKCI; JAM2; PARD6B
GO:0070160	0.0146	1	CC	33355	227	75	3	occluding junction	PRKCI; JAM2; PARD6B
GO:0005624	0.0172	1	CC	33355	227	772	11	membrane fraction	HMOX1; PTGS2; TALDO1; YRDC; CYP51; PRKCI; FOS; PTGS1; PGD; LRP2; FOXL1
GO:0044438	0.0188	1	CC	33355	227	31	2	microbody part	ABCD3; PRDX1
GO:0044439	0.0188	1	CC	33355	227	31	2	peroxisomal part	ABCD3; PRDX1
GO:0032437	0.0202	1	CC	33355	227	3	1	cuticular plate	SPNB2
GO:0008091	0.0202	1	CC	33355	227	3	1	spectrin	SPNB2
GO:0045095	0.0236	1	CC	33355	227	35	2	keratin filament	KRT8; KRT7
GO:0030054	0.0241	1	CC	33355	227	510	8	cell junction	PPL; RHOU; PRKCI; JAM2; LAMA3; PARD6B; GJB3; SLC2A1
GO:0031234	0.0269	1	CC	33355	227	4	1	extrinsic to internal side of plasma membrane	ERRF11
GO:0005610	0.0269	1	CC	33355	227	4	1	laminin-5 complex	LAMA3
GO:0043228	0.0292	1	CC	33355	227	1278	15	non-membrane-bounded organelle	SPNB2; GNL3; PPL; HMOX1; BRCA1; PTPN21; PTPN14; MRPL28; MYC; MRPS12; S100A8; PRDX1; HSBP1; RPL22L1; S100A9
GO:0043232	0.0292	1	CC	33355	227	1278	15	intracellular non-membrane-bounded organelle	SPNB2; GNL3; PPL; HMOX1; BRCA1; PTPN21; PTPN14; MRPL28; MYC; MRPS12; S100A8; PRDX1; HSBP1; RPL22L1; S100A9
GO:0044420	0.0334	1	CC	33355	227	103	3	extracellular matrix part	LOX; TIMP1; LAMA3
GO:0030056	0.0335	1	CC	33355	227	5	1	hemidesmosome	LAMA3
GO:0043230	0.0335	1	CC	33355	227	5	1	extracellular organelle	HSPA8
GO:0005797	0.0335	1	CC	33355	227	5	1	Golgi medial cisterna	GLG1
GO:0065010	0.0335	1	CC	33355	227	5	1	extracellular membrane-bounded organelle	HSPA8
GO:0070062	0.0335	1	CC	33355	227	5	1	extracellular vesicular exosome	HSPA8
GO:0044429	0.0392	1	CC	33355	227	461	7	mitochondrial part	ABCD3; HSPA1B; BRCA1; SLC25A29; HSPD1; PRDX1; PDK4
GO:0030061	0.0401	1	CC	33355	227	6	1	mitochondrial crista	HSPD1
GO:0005719	0.0401	1	CC	33355	227	6	1	nuclear euchromatin	PRDX1
GO:0000791	0.0401	1	CC	33355	227	6	1	euchromatin	PRDX1
GO:0005794	0.0424	1	CC	33355	227	675	9	Golgi apparatus	FAM134B; SELM; RHOU; ARF3; HSPD1; VAMP5; LRP2; GLG1; HP
GO:0042995	0.0434	1	CC	33355	227	785	10	cell projection	CCR2; RHOU; PODXL; MYC; AR; LRP2; ALDOA; TNFRSF12A; HIF1A; STAT1
GO:0019861	0.0439	1	CC	33355	227	49	2	flagellum	ALDOA; HIF1A
GO:0030018	0.0439	1	CC	33355	227	49	2	Z disc	KRT8; SRI
GO:0031907	0.0466	1	CC	33355	227	7	1	microbody lumen	PRDX1
GO:0042588	0.0466	1	CC	33355	227	7	1	zymogen granule	HSPD1
GO:0045254	0.0466	1	CC	33355	227	7	1	pyruvate dehydrogenase complex	PDK2
GO:0005606	0.0466	1	CC	33355	227	7	1	laminin-1 complex	LAMA3
GO:0005782	0.0466	1	CC	33355	227	7	1	peroxisomal matrix	PRDX1
GO:0000790	0.0489	1	CC	33355	227	52	2	nuclear chromatin	JUN; PRDX1

[illegible]

GO:0003676	2.20E-21	9.60E-19	MF	32949	225	2450	64	nucleic acid binding	SP3; HOXB1; TCFAP2A; WT1; BACH1; GTF2F2; TGIF1; REL; CEBPD; ZFP36; MEN1; RELB; USF2; PPARA; TRP53; HOXA1; BRCA1; ETV4; STAT3; SRXN1; SMAD3; ATF3; EIF5; EIF2S2; NFKB1; SP1; HOXC8; HES6; CREB1; FOS; JUNB; TIPARP; GTF3C1; MAFK; EIF1A; KLF5; MRPL28; CEBPB; DDX39; NFIC; MYC; JUN; SP2; AR; ATF1; CEBPE; ETS1; PPARG; MAFF; ATF4; RELA; HIF1A; FOSL1; RARB; STAT1; MYBL2; SFP11; EGR1; CEBPA; USF1; PPRC1; KLF6; KLF4; MYB
GO:0003690	1.50E-19	6.40E-17	MF	32949	225	78	16	double-stranded DNA binding	SP3; WT1; USF2; SMAD3; NFKB1; SP1; CREB1; FOS; JUNB; NFIC; MYC; JUN; EGR1; USF1; KLF6; KLF4
GO:0016563	1.10E-17	4.90E-15	MF	32949	225	263	22	transcription activator activity	WT1; USF2; PPARA; ETV4; STAT3; SMAD3; NFKB1; SP1; JUNB; CEBPB; NFIC; MYC; AR; ETS1; PPARG; ATF4; RELA; FOSL1; RARB; SFP11; EGR1; USF1
GO:0043566	1.80E-16	7.90E-14	MF	32949	225	119	16	structure-specific DNA binding	SP3; WT1; USF2; SMAD3; NFKB1; SP1; CREB1; FOS; JUNB; NFIC; MYC; JUN; EGR1; USF1; KLF6; KLF4
GO:0003702	7.80E-14	3.30E-11	MF	32949	225	117	14	RNA polymerase II transcription factor activity	GTF2F2; CEBPD; USF2; PPARA; SMAD3; CREB1; CEBPB; JUN; ATF1; ATF4; RELA; HIF1A; CEBPA; KLF4
GO:0046982	4.60E-12	1.90E-09	MF	32949	225	190	15	protein heterodimerization activity	CEBPD; USF2; PPARA; PDK2; HSPD1; FOS; CEBPB; BCL10; MYC; JUN; ATF1; CEBPE; HIF1A; GCLC;
GO:0042803	1.70E-11	7.10E-09	MF	32949	225	246	16	protein homodimerization activity	GSR; CEBPD; USF2; CCR2; SULT1A1; PDK2; NFKB1; CEBPB; BCL10; JUN; PRDX1; CEBPE; ASNS; CEBPA;
GO:0003704	2.90E-11	1.20E-08	MF	32949	225	19	7	specific RNA polymerase II transcription factor activity	CEBPD; PPARA; SMAD3; CREB1; ATF4; HIF1A; CEBPA
GO:0043169	8.80E-10	3.70E-07	MF	32949	225	3201	53	cation binding	SP3; WT1; HMOX1; ZFP36; LOX; CDKN1A; PPARA; TRP53; MT1; S100A14; BRCA1; ADAMTS4; STAT3; RHOU; PTGS2; EIF2S2; CYP51; SP1; NOTCH2; SRI; MT2; PRKCI; ZFAND2A; PTGS1; TIPARP; ZFP110; MARCH6; IDI1; KLF5; PPA1; SCEL; THBS1; TIMP1; SP2; S100A8; AR; RNF5; PRDX1; LRP2; PPARG; CHI3L1; GCA; NBR1; RARB; STAT1; CH25H; EGR1; AFP; PDE4B; S100A9; KLF6; KLF4; MMP11
GO:0043167	9.70E-10	4.00E-07	MF	32949	225	3210	53	ion binding	SP3; WT1; HMOX1; ZFP36; LOX; CDKN1A; PPARA; TRP53; MT1; S100A14; BRCA1; ADAMTS4; STAT3; RHOU; PTGS2; EIF2S2; CYP51; SP1; NOTCH2; SRI; MT2; PRKCI; ZFAND2A; PTGS1; TIPARP; ZFP110; MARCH6; IDI1; KLF5; PPA1; SCEL; THBS1; TIMP1; SP2; S100A8; AR; RNF5; PRDX1; LRP2; PPARG; CHI3L1; GCA; NBR1; RARB; STAT1; CH25H; EGR1; AFP; PDE4B; S100A9; KLF6; KLF4; MMP11
GO:0046872	1.70E-09	7.40E-07	MF	32949	225	3166	52	metal ion binding	SP3; WT1; HMOX1; ZFP36; LOX; CDKN1A; PPARA; TRP53; MT1; S100A14; BRCA1; ADAMTS4; STAT3; RHOU; PTGS2; EIF2S2; CYP51; SP1; NOTCH2; SRI; MT2; PRKCI; ZFAND2A; PTGS1; TIPARP; ZFP110; MARCH6; IDI1; KLF5; PPA1; SCEL; THBS1; TIMP1; SP2; S100A8; AR; RNF5; PRDX1; LRP2; PPARG; GCA; NBR1; RARB; STAT1; CH25H; EGR1; AFP; PDE4B; S100A9; KLF6; KLF4; MMP11
GO:0042802	4.80E-09	2.00E-06	MF	32949	225	362	16	identical protein binding	GSR; CEBPD; USF2; CCR2; SULT1A1; PDK2; NFKB1; CEBPB; BCL10; JUN; PRDX1; CEBPE; ASNS; CEBPA; HSP90AA1; HP
GO:0046914	6.60E-09	2.80E-06	MF	32949	225	1546	33	transition metal ion binding	SP3; WT1; HMOX1; ZFP36; LOX; PPARA; TRP53; MT1; BRCA1; ADAMTS4; PTGS2; CYP51; SP1; MT2; PRKCI; ZFAND2A; PTGS1; TIPARP; MARCH6; KLF5; SCEL; SP2; AR; RNF5; PRDX1; PPARG; NBR1; RARB; CH25H; EGR1; KLF6; KLF4; MMP11
GO:0016209	8.00E-09	3.30E-06	MF	32949	225	39	7	antioxidant activity	GSR; SRXN1; PTGS2; PTGS1; GPX2; TXNRD1; PRDX1
GO:0035326	2.10E-07	9.10E-05	MF	32949	225	38	6	enhancer binding	SP1; CREB1; CEBPB; ATF1; RELA; CEBPA
GO:0016564	3.80E-07	1.60E-04	MF	32949	225	220	11	transcription repressor activity	WT1; TGIF1; TRIB3; TRP53; FABP4; SMAD3; ATF3; NFKB1; HOXC8; PPARG; KLF4
GO:0003824	5.90E-07	2.50E-04	MF	32949	225	4892	62	catalytic activity	ABCD3; GSR; SERPINE1; GTF2F2; PRSS22; TUBA4A; HMOX1; DHX32; TRIB3; LOX; NEDD4L; SULT1A1; CDKN1A; BRCA1; ADAMTS4; PDK2; SRXN1; EPHA2; RHOU; PTGS2; TALD01; DUSP1; ABCC1; NQO1; CYP51; GSTA2; DUSP16; TUBB2C; RNASEK; PRKCI; PTPN21; PTGS1; TIPARP; PTPN14; ESD; GPX2; MARCH6; HS6ST1; IDI1; TINAGL1; PPA1; DDX39; TXNRD1; RNF5; PRDX1; ACOT10; PLAUR; PGD; ASNS; ALDOA; CHI3L1; PDK4; PSMA5; HSPA8; PSMC1; AMPD3; GCLC; CH25H; AFP; PDE4B; MMP11; HP
GO:0019899	7.20E-07	3.00E-04	MF	32949	225	398	14	enzyme binding	TGIF1; HMOX1; TRIB3; TRP53; HSPA1B; STAT3; FMNL3; SP1; HSPA9; HSPD1; F3; ERRF11; HIF1A; SLC2A1

GO:0008270	1.30E-06	5.60E-04	MF	32949	225	1318	26	zinc ion binding	SP3; WT1; ZFP36; PPARA; TRP53; MT1; BRCA1; ADAMTS4; SP1; MT2; PRKCI; ZFAND2A; TIPARP; MARCH6; KLF5; SCEL; SP2; AR; RNF5; PPARG; NBR1; RARB; EGR1; KLF6; KLF4; MMP11
GO:0016566	2.40E-06	0.001	MF	32949	225	32	5	specific transcriptional repressor activity	WT1; TGIF1; SMAD3; NFKB1; PPARG
GO:0051082	3.80E-06	0.0016	MF	32949	225	61	6	unfolded protein binding	DNAJB4; HSPA9; DNAJC5; HSP90AB1; HSPA8; HSP90AA1
GO:0003705	4.50E-06	0.0018	MF	32949	225	36	5	RNA polymerase II transcription factor activity, enhancer binding	CREB1; CEBPB; ATF1; RELA; CEBPA
GO:0008134	7.90E-06	0.0033	MF	32949	225	245	10	transcription factor binding	TRIB3; TOB2; HSPA1B; STAT3; SMAD3; HES6; CREB1; CREG1; CEBPB; RELA
GO:0017076	1.20E-05	0.0053	MF	32949	225	1776	29	purine nucleotide binding	GNL3; ABCD3; GSR; GTF2F2; TUBA4A; DHX32; TRIB3; SULT1A1; PDK2; SRXN1; EPHA2; RHOU; ARF3; EIF5; ABCC1; HSPA9; TUBB2C; HSPD1; PRKCI; LACE1; DDX39; TXNRD1; HSP90AB1; ASNS; PDK4; HSPA8; PSMC1; GCLC; HSP90AA1
GO:0000166	2.60E-05	0.0112	MF	32949	225	2046	31	nucleotide binding	GNL3; ABCD3; GSR; GTF2F2; TUBA4A; DHX32; TRIB3; SULT1A1; PDK2; SRXN1; EPHA2; RHOU; ARF3; EIF5; ABCC1; HSPA9; TUBB2C; HSPD1; PRKCI; LACE1; DDX39; TXNRD1; PGD; HSP90AB1; ASNS; PDK4; HSPA8; PSMC1; GCLC; HSP90AA1; PPRC1
GO:0016787	4.30E-05	0.0182	MF	32949	225	2099	31	hydrolase activity	ABCD3; SERPINE1; GTF2F2; PRSS22; TUBA4A; HMOX1; DHX32; ADAMTS4; RHOU; DUSP1; ABCC1; DUSP16; TUBB2C; RNASEK; PTPN21; PTPN14; ESD; IDI1; TINAGL1; PPA1; DDX39; ACOT10; CHI3L1; PSMA5; HSPA8; PSMC1; AMPD3; AFP; PDE4B; MMP11; HP
GO:0016684	4.30E-05	0.0184	MF	32949	225	29	4	oxidoreductase activity, acting on peroxide as acceptor	PTGS2; PTGS1; GPX2; PRDX1
GO:0004601	4.30E-05	0.0184	MF	32949	225	29	4	peroxidase activity	PTGS2; PTGS1; GPX2; PRDX1
GO:0003706	4.60E-05	0.0194	MF	32949	225	2	2	ligand-regulated transcription factor activity	PPARA; SMAD3
GO:0004666	4.60E-05	0.0194	MF	32949	225	2	2	prostaglandin-endoperoxide synthase activity	PTGS2; PTGS1
GO:0005154	6.60E-05	0.0276	MF	32949	225	12	3	epidermal growth factor receptor binding	EREG; HBEGF; AREG
GO:0010843	1.00E-04	0.0437	MF	32949	225	68	5	promoter binding	CEBPD; ATF1; PPARG; CEBPA; KLF4
GO:0002020	1.00E-04	0.0453	MF	32949	225	14	3	protease binding	HSPA1B; HSPD1; F3
GO:0032555	1.10E-04	0.0468	MF	32949	225	1703	26	purine ribonucleotide binding	GNL3; ABCD3; GTF2F2; TUBA4A; DHX32; TRIB3; PDK2; SRXN1; EPHA2; RHOU; ARF3; EIF5; ABCC1; HSPA9; TUBB2C; HSPD1; PRKCI; LACE1; DDX39; HSP90AB1; ASNS; PDK4; HSPA8; PSMC1; GCLC; HSP90AA1
GO:0032553	1.10E-04	0.0473	MF	32949	225	1704	26	ribonucleotide binding	GNL3; ABCD3; GTF2F2; TUBA4A; DHX32; TRIB3; PDK2; SRXN1; EPHA2; RHOU; ARF3; EIF5; ABCC1; HSPA9; TUBB2C; HSPD1; PRKCI; LACE1; DDX39; HSP90AB1; ASNS; PDK4; HSPA8; PSMC1; GCLC; HSP90AA1
GO:0044212	1.10E-04	0.0501	MF	32949	225	70	5	DNA regulatory region binding	CEBPD; ATF1; PPARG; CEBPA; KLF4
GO:0005198	1.60E-04	0.0688	MF	32949	225	351	10	structural molecule activity	SPNB2; TUBA4A; KRT8; TUBB2C; CRYGN; MRPL28; THBS1; MRPS12; RPL22L1; KRT7
GO:0030554	2.00E-04	0.0878	MF	32949	225	1475	23	adenyl nucleotide binding	ABCD3; GSR; GTF2F2; DHX32; TRIB3; SULT1A1; PDK2; SRXN1; EPHA2; ABCC1; HSPA9; HSPD1; PRKCI; LACE1; DDX39; TXNRD1; HSP90AB1; ASNS; PDK4; HSPA8; PSMC1; GCLC; HSP90AA1
GO:0032403	2.10E-04	0.0896	MF	32949	225	233	8	protein complex binding	SPNB2; CDKN1A; PDK2; HSPD1; ATF1; RELA; HIF1A; CEBPA
GO:0001883	2.50E-04	0.1074	MF	32949	225	1496	23	purine nucleoside binding	ABCD3; GSR; GTF2F2; DHX32; TRIB3; SULT1A1; PDK2; SRXN1; EPHA2; ABCC1; HSPA9; HSPD1; PRKCI; LACE1; DDX39; TXNRD1; HSP90AB1; ASNS; PDK4; HSPA8; PSMC1; GCLC; HSP90AA1
GO:0001882	2.70E-04	0.1137	MF	32949	225	1502	23	nucleoside binding	ABCD3; GSR; GTF2F2; DHX32; TRIB3; SULT1A1; PDK2; SRXN1; EPHA2; ABCC1; HSPA9; HSPD1; PRKCI; LACE1; DDX39; TXNRD1; HSP90AB1; ASNS; PDK4; HSPA8; PSMC1; GCLC; HSP90AA1
GO:0003707	2.70E-04	0.1155	MF	32949	225	46	4	steroid hormone receptor activity	PPARA; AR; PPARG; RARB
GO:0042910	2.70E-04	0.1156	MF	32949	225	4	2	xenobiotic transporter activity	ABCC1; SLC2A1
GO:0004740	2.70E-04	0.1156	MF	32949	225	4	2	pyruvate dehydrogenase (acetyl-transferring) kinase activity	PDK2; PDK4

GO:0016705	3.40E-04	0.1435	MF	32949	225	135	6	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	HMOX1; PTGS2; CYP51; PTGS1; PRDX1; CH25H
GO:0004879	3.50E-04	0.1477	MF	32949	225	49	4	ligand-dependent nuclear receptor activity	PPARA; AR; PPARG; RARB
GO:0005509	3.50E-04	0.1506	MF	32949	225	461	11	calcium ion binding	S100A14; STAT3; NOTCH2; SRI; THBS1; S100A8; LRP2; GCA; STAT1; S100A9; MMP11
GO:0030492	4.50E-04	0.1919	MF	32949	225	5	2	hemoglobin binding	LRP2; HP
GO:0030234	6.70E-04	0.2823	MF	32949	225	661	13	enzyme regulator activity	SERPINE1; TRIB3; CDKN1A; TRP53; TBC1D15; PSMD3; PPP2R2A; BCL10; TIMP1; PLAA; HSP90AA1; KLF4; SERPINA3N
GO:0016668	6.80E-04	0.2865	MF	32949	225	6	2	oxidoreductase activity, acting on sulfur group of donors, NAD or NADP as acceptor	GSR; TXNRD1
GO:0020037	7.50E-04	0.3161	MF	32949	225	104	5	heme binding	HMOX1; PTGS2; CYP51; PTGS1; PRDX1
GO:0003682	7.80E-04	0.3294	MF	32949	225	158	6	chromatin binding	SP3; TGIF1; MEN1; TRP53; PPARG; RELA
GO:0016491	8.60E-04	0.3608	MF	32949	225	679	13	oxidoreductase activity	GSR; HMOX1; LOX; SRXN1; PTGS2; NQO1; CYP51; PTGS1; GPX2; TXNRD1; PRDX1; PGD; CH25H
GO:0050661	0.001	0.4219	MF	32949	225	29	3	NADP or NADPH binding	GSR; TXNRD1; PGD
GO:0046906	0.001	0.424	MF	32949	225	111	5	tetrapyrrole binding	HMOX1; PTGS2; CYP51; PTGS1; PRDX1
GO:0070851	0.001	0.4334	MF	32949	225	65	4	growth factor receptor binding	IL1B; EREG; HBEGF; AREG
GO:0005506	0.0011	0.4957	MF	32949	225	171	6	iron ion binding	HMOX1; PTGS2; CYP51; PTGS1; PRDX1; CH25H
GO:0050840	0.0012	0.5138	MF	32949	225	31	3	extracellular matrix binding	TINAGL1; THBS1; CYR61
GO:0005524	0.0012	0.5395	MF	32949	225	1376	20	ATP binding	ABCD3; GTF2F2; DHX32; TRIB3; PDK2; SRXN1; EPHA2; ABCC1; HSPA9; HSPD1; PRKCI; LACE1; DDX39; HSP90AB1; ASNS; PDK4; HSPA8; PSMC1; GCLC; HSP90AA1
GO:0016667	0.0013	0.5641	MF	32949	225	32	3	oxidoreductase activity, acting on sulfur group of	GSR; SRXN1; TXNRD1
GO:0032559	0.0016	0.6728	MF	32949	225	1402	20	adenyl ribonucleotide binding	ABCD3; GTF2F2; DHX32; TRIB3; PDK2; SRXN1; EPHA2; ABCC1; HSPA9; HSPD1; PRKCI; LACE1; DDX39; HSP90AB1; ASNS; PDK4; HSPA8; PSMC1; GCLC; HSP90AA1
GO:0043295	0.0016	0.6784	MF	32949	225	9	2	glutathione binding	GSR; GSTA2
GO:0005102	0.0018	0.7945	MF	32949	225	742	13	receptor binding	EDN1; TOB2; ANGPTL4; ADM; IL1B; EREG; HBEGF; AREG; CXCL16; AR; LAMA3; ATF4; HSPA8
GO:0000155	0.002	0.8443	MF	32949	225	10	2	two-component sensor activity	PDK2; PDK4
GO:0004673	0.002	0.8443	MF	32949	225	10	2	protein histidine kinase activity	PDK2; PDK4
GO:0001871	0.0024	1	MF	32949	225	136	5	pattern binding	LYVE1; HBEGF; TINAGL1; THBS1; CYR61
GO:0030247	0.0024	1	MF	32949	225	136	5	polysaccharide binding	LYVE1; HBEGF; TINAGL1; THBS1; CYR61
GO:0016462	0.0028	1	MF	32949	225	598	11	pyrophosphatase activity	ABCD3; GTF2F2; TUBA4A; DHX32; RHOU; ABCC1; TUBB2C; PPA1; DDX39; HSPA8; PSMC1
GO:0030246	0.0029	1	MF	32949	225	350	8	carbohydrate binding	TALDO1; LYVE1; HBEGF; TINAGL1; THBS1; PGD; CYR61; GLG1
GO:0016818	0.0029	1	MF	32949	225	601	11	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	ABCD3; GTF2F2; TUBA4A; DHX32; RHOU; ABCC1; TUBB2C; PPA1; DDX39; HSPA8; PSMC1
GO:0016817	0.003	1	MF	32949	225	602	11	hydrolase activity, acting on acid anhydrides	ABCD3; GTF2F2; TUBA4A; DHX32; RHOU; ABCC1; TUBB2C; PPA1; DDX39; HSPA8; PSMC1
GO:0016775	0.004	1	MF	32949	225	14	2	phosphotransferase activity, nitrogenous group as acceptor	PDK2; PDK4
GO:0016651	0.0045	1	MF	32949	225	49	3	oxidoreductase activity, acting on NADH or NADPH	GSR; NQO1; TXNRD1
GO:0017111	0.006	1	MF	32949	225	569	10	nucleoside-triphosphatase activity	ABCD3; GTF2F2; TUBA4A; DHX32; RHOU; ABCC1; TUBB2C; DDX39; HSPA8; PSMC1
GO:0019900	0.0062	1	MF	32949	225	169	5	kinase binding	TGIF1; TRIB3; STAT3; ERRF11; SLC2A1
GO:0015038	0.0068	1	MF	32949	225	1	1	glutathione disulfide oxidoreductase activity	GSR
GO:0015227	0.0068	1	MF	32949	225	1	1	acyl carnitine transporter activity	SLC25A29
GO:0015431	0.0068	1	MF	32949	225	1	1	glutathione S-conjugate-exporting ATPase activity	ABCC1

GO:0015562	0.0068	1	MF	32949	225	1	1	efflux transmembrane transporter activity	ABCC1
GO:0001567	0.0068	1	MF	32949	225	1	1	cholesterol 25-hydroxylase activity	CH25H
GO:0018738	0.0068	1	MF	32949	225	1	1	S-formylglutathione hydrolase activity	ESD
GO:0030377	0.0068	1	MF	32949	225	1	1	U-plasminogen activator receptor activity	PLAUR
GO:0031700	0.0068	1	MF	32949	225	1	1	adrenomedullin receptor binding	ADM
GO:0031707	0.0068	1	MF	32949	225	1	1	endothelin A receptor binding	EDN1
GO:0031708	0.0068	1	MF	32949	225	1	1	endothelin B receptor binding	EDN1
GO:0032542	0.0068	1	MF	32949	225	1	1	sulfiredoxin activity	SRXN1
GO:0034040	0.0068	1	MF	32949	225	1	1	lipid-transporting ATPase activity	ABCC1
GO:0034634	0.0068	1	MF	32949	225	1	1	glutathione transmembrane transporter activity	ABCC1
GO:0003709	0.0068	1	MF	32949	225	1	1	RNA polymerase III transcription factor activity	GTF3C1
GO:0003955	0.0068	1	MF	32949	225	1	1	NAD(P)H dehydrogenase (quinone) activity	NQO1
GO:0042954	0.0068	1	MF	32949	225	1	1	lipoprotein transporter activity	LRP2
GO:0004362	0.0068	1	MF	32949	225	1	1	glutathione-disulfide reductase activity	GSR
GO:0004452	0.0068	1	MF	32949	225	1	1	isopentenyl-diphosphate delta-isomerase activity	IDI1
GO:0046624	0.0068	1	MF	32949	225	1	1	sphingolipid transporter activity	ABCC1
GO:0004801	0.0068	1	MF	32949	225	1	1	transaldolase activity	TALDO1
GO:0004882	0.0068	1	MF	32949	225	1	1	androgen receptor activity	AR
GO:0050656	0.0068	1	MF	32949	225	1	1	3'-phosphoadenosine 5'-phosphosulfate binding	SULT1A1
GO:0005316	0.0068	1	MF	32949	225	1	1	high affinity inorganic phosphate:sodium symporter activity	SLC20A1
GO:0070410	0.0068	1	MF	32949	225	1	1	co-SMAD binding	TGIF1
GO:0070974	0.0068	1	MF	32949	225	1	1	POU domain binding	AR
GO:0008114	0.0068	1	MF	32949	225	1	1	phosphogluconate 2-dehydrogenase activity	PGD
GO:0008398	0.0068	1	MF	32949	225	1	1	sterol 14-demethylase activity	CYP51
GO:0003743	0.008	1	MF	32949	225	60	3	translation initiation factor activity	EIF5; EIF2S2; EIF1A
GO:0004860	0.0081	1	MF	32949	225	20	2	protein kinase inhibitor activity	TRIB3; CDKN1A
GO:0005539	0.0091	1	MF	32949	225	119	4	glycosaminoglycan binding	LYVE1; HBEGF; THBS1; CYR61
GO:0019210	0.0098	1	MF	32949	225	22	2	kinase inhibitor activity	TRIB3; CDKN1A
GO:0042623	0.0098	1	MF	32949	225	189	5	ATPase activity, coupled	ABCD3; GTF2F2; ABCC1; DDX39; HSPA8
GO:0004175	0.0103	1	MF	32949	225	348	7	endopeptidase activity	SERPINE1; PRSS22; ADAMTS4; TINAGL1; PSMA5; MMP11; HP
GO:0019207	0.0109	1	MF	32949	225	67	3	kinase regulator activity	TRIB3; CDKN1A; KLF4
GO:0031072	0.0122	1	MF	32949	225	70	3	heat shock protein binding	DNAJB4; NFKB1; DNAJC5
GO:0031625	0.0125	1	MF	32949	225	25	2	ubiquitin protein ligase binding	TRIB3; TRP53
GO:0046332	0.0125	1	MF	32949	225	25	2	SMAD binding	TGIF1; SMAD3
GO:0015037	0.0136	1	MF	32949	225	2	1	peptide disulfide oxidoreductase activity	GSR
GO:0016005	0.0136	1	MF	32949	225	2	1	phospholipase A2 activator activity	PLAA
GO:0017067	0.0136	1	MF	32949	225	2	1	tyrosine-ester sulfotransferase activity	SULT1A1
GO:0030235	0.0136	1	MF	32949	225	2	1	nitric-oxide synthase regulator activity	HSP90AA1
GO:0031705	0.0136	1	MF	32949	225	2	1	bombesin receptor binding	EDN1

GO:0004066	0.0136	1	MF	32949	225	2	1	asparagine synthase (glutamine-hydrolyzing) activity	ASNS
GO:0004357	0.0136	1	MF	32949	225	2	1	glutamate-cysteine ligase activity	GCLC
GO:0004392	0.0136	1	MF	32949	225	2	1	heme oxygenase (decyclizing) activity	HMOX1
GO:0004720	0.0136	1	MF	32949	225	2	1	protein-lysine 6-oxidase activity	LOX
GO:0004910	0.0136	1	MF	32949	225	2	1	interleukin-1, Type II, blocking receptor activity	IL1R2
GO:0005497	0.0136	1	MF	32949	225	2	1	androgen binding	AR
GO:0070215	0.0136	1	MF	32949	225	2	1	MDM2 binding	PPARA
GO:0008083	0.0139	1	MF	32949	225	135	4	growth factor activity	IL1B; EREG; HBEGF; AREG
GO:0004857	0.0143	1	MF	32949	225	208	5	enzyme inhibitor activity	SERPINE1; TRIB3; CDKN1A; TIMP1; SERPINA3N
GO:0019838	0.0164	1	MF	32949	225	78	3	growth factor binding	IL1R2; CYR61; FGFBP1
GO:0019955	0.0193	1	MF	32949	225	83	3	cytokine binding	CCR2; CSF3R; IL1R2
GO:0042578	0.0198	1	MF	32949	225	309	6	phosphoric ester hydrolase activity	HMOX1; DUSP1; DUSP16; PTPN21; PTPN14; PDE4B
GO:0019871	0.0203	1	MF	32949	225	3	1	sodium channel inhibitor activity	NEDD4L
GO:0033300	0.0203	1	MF	32949	225	3	1	dehydroascorbic acid transporter activity	SLC2A1
GO:0035033	0.0203	1	MF	32949	225	3	1	histone deacetylase regulator activity	TRP53
GO:0003876	0.0203	1	MF	32949	225	3	1	AMP deaminase activity	AMPD3
GO:0004566	0.0203	1	MF	32949	225	3	1	beta-glucuronidase activity	AFP
GO:0004616	0.0203	1	MF	32949	225	3	1	phosphogluconate dehydrogenase (decarboxylating) activity	PGD
GO:0051787	0.0203	1	MF	32949	225	3	1	misfolded protein binding	HSPD1
GO:0005315	0.0203	1	MF	32949	225	3	1	inorganic phosphate transmembrane transporter activity	SLC20A1
GO:0005436	0.0203	1	MF	32949	225	3	1	sodium:phosphate symporter activity	SLC20A1
GO:0055103	0.0203	1	MF	32949	225	3	1	ligase regulator activity	TRIB3
GO:0055106	0.0203	1	MF	32949	225	3	1	ubiquitin-protein ligase regulator activity	TRIB3
GO:0070742	0.0203	1	MF	32949	225	3	1	C2H2 zinc finger domain binding	WT1
GO:0008330	0.0203	1	MF	32949	225	3	1	protein tyrosine/threonine phosphatase activity	DUSP1
GO:0008559	0.0203	1	MF	32949	225	3	1	xenobiotic-transporting ATPase activity	ABCC1
GO:0016887	0.0212	1	MF	32949	225	230	5	ATPase activity	ABCD3; GTF2F2; ABCC1; DDX39; HSPA8
GO:0004725	0.0218	1	MF	32949	225	87	3	protein tyrosine phosphatase activity	DUSP1; PTPN21; PTPN14
GO:0048037	0.0219	1	MF	32949	225	232	5	cofactor binding	GSR; NQO1; TXNRD1; PGD; ASNS
GO:0061134	0.022	1	MF	32949	225	155	4	peptidase regulator activity	SERPINE1; BCL10; TIMP1; SERPINA3N
GO:0005525	0.0222	1	MF	32949	225	317	6	GTP binding	GNL3; TUBA4A; RHOU; ARF3; EIF5; TUBB2C
GO:0008201	0.0239	1	MF	32949	225	90	3	heparin binding	HBEGF; THBS1; CYR61
GO:0005044	0.0264	1	MF	32949	225	37	2	scavenger receptor activity	TINAGL1; CXCL16
GO:0008135	0.0267	1	MF	32949	225	94	3	translation factor activity, nucleic acid	EIF5; EIF2S2; EIF1A
GO:0016004	0.027	1	MF	32949	225	4	1	phospholipase activator activity	PLAA
GO:0016744	0.027	1	MF	32949	225	4	1	transferase activity, transferring aldehyde or	TALDO1
GO:0004062	0.027	1	MF	32949	225	4	1	aryl sulfotransferase activity	SULT1A1
GO:0042809	0.027	1	MF	32949	225	4	1	vitamin D receptor binding	TOB2

									GO:0043023	0.027	1	MF	32949	225	4	1	ribosomal large subunit binding	NMD3
									GO:0043559	0.027	1	MF	32949	225	4	1	insulin binding	HSPD1
									GO:0004427	0.027	1	MF	32949	225	4	1	inorganic diphosphatase activity	PPA1
									GO:0004791	0.027	1	MF	32949	225	4	1	thioredoxin-disulfide reductase activity	TXNRD1
									GO:0050544	0.027	1	MF	32949	225	4	1	arachidonic acid binding	PPARG
									GO:0005324	0.027	1	MF	32949	225	4	1	long-chain fatty acid transporter activity	ABCC1
									GO:0055056	0.027	1	MF	32949	225	4	1	D-glucose transmembrane transporter activity	SLC2A1
									GO:0060229	0.027	1	MF	32949	225	4	1	lipase activator activity	PLAA
									GO:0008656	0.027	1	MF	32949	225	4	1	caspase activator activity	BCL10
									GO:0019001	0.0273	1	MF	32949	225	333	6	guanyl nucleotide binding	GNL3; TUBA4A; RHOU; ARF3; EIF5; TUBB2C
									GO:0032561	0.0273	1	MF	32949	225	333	6	guanyl ribonucleotide binding	GNL3; TUBA4A; RHOU; ARF3; EIF5; TUBB2C
									GO:0008289	0.0273	1	MF	32949	225	333	6	lipid binding	PPARA; FABP4; PTGS2; PTGS1; AR; PPARG
									GO:0050662	0.0274	1	MF	32949	225	166	4	coenzyme binding	GSR; NQO1; TXNRD1; PGD
									GO:0005507	0.0291	1	MF	32949	225	39	2	copper ion binding	LOX; MT1
									GO:0004332	0.0336	1	MF	32949	225	5	1	fructose-bisphosphate aldolase activity	ALDOA
									GO:0050542	0.0336	1	MF	32949	225	5	1	icosanoid binding	PPARG
									GO:0050543	0.0336	1	MF	32949	225	5	1	icosatetraenoic acid binding	PPARG
									GO:0016788	0.0345	1	MF	32949	225	647	9	hydrolase activity, acting on ester bonds	HMOX1; DUSP1; DUSP16; RNASEK; PTPN21; PTPN14; ESD; ACOT10; PDE4B
									GO:0003735	0.0354	1	MF	32949	225	105	3	structural constituent of ribosome	MRPL28; MRPS12; RPL22L1
									GO:0001664	0.0371	1	MF	32949	225	107	3	G-protein-coupled receptor binding	EDN1; ADM; CXCL16
									GO:0008146	0.0379	1	MF	32949	225	45	2	sulfotransferase activity	SULT1A1; HS6ST1
									GO:0016874	0.0391	1	MF	32949	225	363	6	ligase activity	NEDD4L; BRCA1; MARCH6; RNF5; ASNS; GCLC
									GO:0016505	0.0402	1	MF	32949	225	6	1	apoptotic protease activator activity	BCL10
									GO:0030332	0.0402	1	MF	32949	225	6	1	cyclin binding	CDKN1A
									GO:0035014	0.0402	1	MF	32949	225	6	1	phosphoinositide 3-kinase regulator activity	KLF4
									GO:0035035	0.0402	1	MF	32949	225	6	1	histone acetyltransferase binding	SP1
									GO:0003708	0.0402	1	MF	32949	225	6	1	retinoic acid receptor activity	RARB
									GO:0004861	0.0402	1	MF	32949	225	6	1	cyclin-dependent protein kinase inhibitor activity	CDKN1A
									GO:0051059	0.0402	1	MF	32949	225	6	1	NF-kappaB binding	HSPA1B
									GO:0008432	0.0402	1	MF	32949	225	6	1	JUN kinase binding	TGIF1
									GO:0004896	0.0442	1	MF	32949	225	49	2	cytokine receptor activity	CSF3R; IL1R2
									GO:0017091	0.0468	1	MF	32949	225	7	1	AU-rich element binding	ZFP36
									GO:0019966	0.0468	1	MF	32949	225	7	1	interleukin-1 binding	IL1R2
									GO:0043028	0.0468	1	MF	32949	225	7	1	caspase regulator activity	BCL10
									GO:0043499	0.0468	1	MF	32949	225	7	1	eukaryotic cell surface binding	CD48
									GO:0004630	0.0468	1	MF	32949	225	7	1	phospholipase D activity	HMOX1
									GO:0004908	0.0468	1	MF	32949	225	7	1	interleukin-1 receptor activity	IL1R2
									GO:0005041	0.0468	1	MF	32949	225	7	1	low-density lipoprotein receptor activity	CXCL16
									GO:0050811	0.0468	1	MF	32949	225	7	1	GABA receptor binding	ATF4
									GO:0005149	0.0468	1	MF	32949	225	7	1	interleukin-1 receptor binding	IL1B

		GO:0051920	0.0468	1	MF	32949	225	7	1	peroxiredoxin activity	PRDX1
		GO:0016782	0.0475	1	MF	32949	225	51	2	transferase activity, transferring sulfur- containing groups	SULT1A1; HS6ST1

Identified DNB of HBV

Sample Name	Members Of DNB	GO: term	P-value	Corrected P-value		R	T	G	O	Term Name	Contain Genes
Chronic Hepatitis B	DKFZP761C169; PSMB8; KIS; JWA; HSPC132; STAT6; E2F-2; HLA-DMA; RARA; FLJ10315; PSMD11; SLC35A1; NP0014; CDH1; E2F-1; NFKB1; UBD; C-MYC; USF2; CACH-1; GCC2; SH2BP1; SF3B5; COMMD7; KIAA0100; NAGS; PEX14; EIF4A2; ANXA4; HOXD9; WT1; NDUFB10; GTF2I; USF1; GBP1; PPARA; TMSB10; RBBP7; MAPBP1P; GRP58; LUM; NAP1L1; RBX1; STAT1; PSMD2; YWHAB; TAP1; AR; UGT2B4; MORF4L1; ESR1; SLC39A6; B2M; ALG2; HDAC10; SPI1	GO:0032583	2.90E-09	2.60E-06	BP	14791	41	199	9	regulation of gene-specific transcription	RARA; NFKB1; USF2; PEX14; WT1; USF1; PPARA; AR; SPI1
		GO:0048519	7.70E-09	7.00E-06	BP	14791	41	1983	21	negative regulation of biological process	PSMB8; STAT6; RARA; PSMD11; NFKB1; UBD; COMMD7; PEX14; ANXA4; WT1; USF1; PPARA; TMSB10; RBBP7; PSMD2; YWHAB; TAP1; AR; ESR1; HDAC10; SPI1
		GO:0010604	1.00E-07	1.00E-04	BP	14791	41	939	14	positive regulation of macromolecule metabolic process	PSMB8; STAT6; RARA; PSMD11; NFKB1; USF2; HOXD9; WT1; USF1; PPARA; PSMD2; AR; ESR1; SPI1
		GO:0048518	2.60E-07	2.40E-04	BP	14791	41	2188	20	positive regulation of biological process	PSMB8; STAT6; RARA; PSMD11; CDH1; NFKB1; UBD; USF2; HOXD9; WT1; USF1; PPARA; NAP1L1; STAT1; PSMD2; YWHAB; AR; ESR1; B2M; SPI1
		GO:0009893	2.80E-07	2.60E-04	BP	14791	41	1015	14	positive regulation of metabolic process	PSMB8; STAT6; RARA; PSMD11; NFKB1; USF2; HOXD9; WT1; USF1; PPARA; PSMD2; AR; ESR1; SPI1
		GO:0048523	4.50E-07	4.10E-04	BP	14791	41	1815	18	negative regulation of cellular process	PSMB8; RARA; PSMD11; NFKB1; UBD; COMMD7; PEX14; ANXA4; WT1; PPARA; TMSB10; RBBP7; PSMD2; YWHAB; AR; ESR1; HDAC10; SPI1
		GO:0010628	5.30E-07	4.80E-04	BP	14791	41	608	11	positive regulation of gene expression	STAT6; RARA; NFKB1; USF2; HOXD9; WT1; USF1; PPARA; AR; ESR1; SPI1
		GO:0031324	7.20E-07	6.50E-04	BP	14791	41	771	12	negative regulation of cellular metabolic process	PSMB8; RARA; PSMD11; NFKB1; COMMD7; PEX14; WT1; PPARA; PSMD2; YWHAB; HDAC10; SPI1
		GO:0010605	9.30E-07	8.50E-04	BP	14791	41	790	12	negative regulation of macromolecule metabolic process	PSMB8; RARA; PSMD11; NFKB1; COMMD7; PEX14; WT1; PPARA; PSMD2; YWHAB; HDAC10; SPI1
		GO:0031325	1.10E-06	0.001	BP	14791	41	965	13	positive regulation of cellular metabolic process	PSMB8; STAT6; RARA; PSMD11; NFKB1; USF2; HOXD9; WT1; USF1; PPARA; PSMD2; AR; SPI1
		GO:0043193	1.50E-06	0.0013	BP	14791	41	131	6	positive regulation of gene-specific transcription	RARA; USF2; WT1; USF1; AR; SPI1
		GO:0048522	1.70E-06	0.0015	BP	14791	41	1984	18	positive regulation of cellular process	PSMB8; STAT6; RARA; PSMD11; NFKB1; UBD; USF2; HOXD9; WT1; USF1; PPARA; NAP1L1; STAT1; PSMD2; YWHAB; AR; ESR1; SPI1
		GO:0009892	1.80E-06	0.0017	BP	14791	41	845	12	negative regulation of metabolic process	PSMB8; RARA; PSMD11; NFKB1; COMMD7; PEX14; WT1; PPARA; PSMD2; YWHAB; HDAC10; SPI1
		GO:0032582	2.70E-06	0.0025	BP	14791	41	81	5	negative regulation of gene-specific transcription	RARA; NFKB1; PEX14; WT1; PPARA
		GO:0006351	2.90E-06	0.0027	BP	14791	41	231	7	transcription, DNA-dependent	NFKB1; USF2; USF1; PPARA; STAT1; AR; ESR1
		GO:0045941	3.00E-06	0.0027	BP	14791	41	582	10	positive regulation of transcription	STAT6; RARA; NFKB1; USF2; HOXD9; WT1; USF1; PPARA; AR; SPI1
		GO:0032774	3.30E-06	0.003	BP	14791	41	235	7	RNA biosynthetic process	NFKB1; USF2; USF1; PPARA; STAT1; AR; ESR1
		GO:0006357	3.60E-06	0.0033	BP	14791	41	741	11	regulation of transcription from RNA polymerase II promoter	STAT6; RARA; NFKB1; USF2; HOXD9; WT1; USF1; PPARA; AR; HDAC10; SPI1
		GO:0060255	4.70E-06	0.0043	BP	14791	41	3403	23	regulation of macromolecule metabolic process	PSMB8; STAT6; RARA; PSMD11; NFKB1; USF2; COMMD7; PEX14; EIF4A2; HOXD9; WT1; GTF2I; USF1; PPARA; RBBP7; STAT1; PSMD2; YWHAB; AR; MORF4L1; ESR1; HDAC10; SPI1
		GO:0016481	5.90E-06	0.0054	BP	14791	41	489	9	negative regulation of transcription	RARA; NFKB1; COMMD7; PEX14; WT1; PPARA; YWHAB; HDAC10; SPI1
		GO:0045893	6.40E-06	0.0059	BP	14791	41	494	9	positive regulation of transcription, DNA-dependent	STAT6; RARA; USF2; HOXD9; WT1; USF1; PPARA; AR; SPI1
		GO:0051254	7.10E-06	0.0065	BP	14791	41	500	9	positive regulation of RNA metabolic process	STAT6; RARA; USF2; HOXD9; WT1; USF1; PPARA; AR; SPI1
		GO:0019083	7.40E-06	0.0068	BP	14791	41	2	2	viral transcription	USF2; USF1
		GO:0019086	7.40E-06	0.0068	BP	14791	41	2	2	late viral mRNA transcription	USF2; USF1
		GO:0000429	7.40E-06	0.0068	BP	14791	41	2	2	regulation of transcription from RNA polymerase II promoter by carbon metabolism	USF2; USF1

GO:000430	7.40E-06	0.0068	BP	14791	41	2	2	regulation of transcription from RNA polymerase II promoter by glucose	USF2; USF1
GO:000432	7.40E-06	0.0068	BP	14791	41	2	2	positive regulation of transcription from RNA polymerase II promoter by glucose	USF2; USF1
GO:000436	7.40E-06	0.0068	BP	14791	41	2	2	positive regulation of transcription from RNA polymerase II promoter by carbon catabolites	USF2; USF1
GO:0045991	7.40E-06	0.0068	BP	14791	41	2	2	positive regulation of transcription by carbon catabolites	USF2; USF1
GO:0046016	7.40E-06	0.0068	BP	14791	41	2	2	positive regulation of transcription by glucose	USF2; USF1
GO:0045944	8.60E-06	0.0079	BP	14791	41	384	8	positive regulation of transcription from RNA polymerase II promoter	STAT6; RARA; USF2; HOXD9; WT1; USF1; PPARA; AR
GO:0045935	9.50E-06	0.0087	BP	14791	41	662	10	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	STAT6; RARA; NFKB1; USF2; HOXD9; WT1; USF1; PPARA; AR; SPI1
GO:0006350	1.10E-05	0.0107	BP	14791	41	285	7	transcription	NFKB1; USF2; USF1; PPARA; STAT1; AR; ESR1
GO:0080090	1.20E-05	0.011	BP	14791	41	3585	23	regulation of primary metabolic process	PSMB8; STAT6; RARA; PSMD11; NFKB1; USF2; COMMD7; PEX14; EIF4A2; HOXD9; WT1; GTF2I; USF1; PPARA; RBBP7; STAT1; PSMD2; YWHAB; AR; MORF4L1; ESR1; HDAC10; SPI1
GO:0010557	1.20E-05	0.0114	BP	14791	41	683	10	positive regulation of macromolecule biosynthetic process	STAT6; RARA; NFKB1; USF2; HOXD9; WT1; USF1; PPARA; AR; SPI1
GO:0051173	1.20E-05	0.0114	BP	14791	41	683	10	positive regulation of nitrogen compound metabolic process	STAT6; RARA; NFKB1; USF2; HOXD9; WT1; USF1; PPARA; AR; SPI1
GO:0032269	1.30E-05	0.0124	BP	14791	41	192	6	negative regulation of cellular protein metabolic process	PSMB8; PSMD11; NFKB1; WT1; PSMD2; YWHAB
GO:0010629	1.30E-05	0.0126	BP	14791	41	543	9	negative regulation of gene expression	RARA; NFKB1; COMMD7; PEX14; WT1; PPARA; YWHAB; HDAC10; SPI1
GO:0045934	1.50E-05	0.014	BP	14791	41	550	9	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RARA; NFKB1; COMMD7; PEX14; WT1; PPARA; YWHAB; HDAC10; SPI1
GO:0051172	1.70E-05	0.0155	BP	14791	41	557	9	negative regulation of nitrogen compound metabolic process	RARA; NFKB1; COMMD7; PEX14; WT1; PPARA; YWHAB; HDAC10; SPI1
GO:0051248	1.90E-05	0.0175	BP	14791	41	204	6	negative regulation of protein metabolic process	PSMB8; PSMD11; NFKB1; WT1; PSMD2; YWHAB
GO:0031328	2.10E-05	0.0197	BP	14791	41	727	10	positive regulation of cellular biosynthetic process	STAT6; RARA; NFKB1; USF2; HOXD9; WT1; USF1; PPARA; AR; SPI1
GO:0045990	2.20E-05	0.0204	BP	14791	41	3	2	regulation of transcription by carbon catabolites	USF2; USF1
GO:0046015	2.20E-05	0.0204	BP	14791	41	3	2	regulation of transcription by glucose	USF2; USF1
GO:0009891	2.50E-05	0.023	BP	14791	41	740	10	positive regulation of biosynthetic process	STAT6; RARA; NFKB1; USF2; HOXD9; WT1; USF1; PPARA; AR; SPI1
GO:0019222	2.60E-05	0.0241	BP	14791	41	4046	24	regulation of metabolic process	PSMB8; STAT6; RARA; PSMD11; CDH1; NFKB1; USF2; COMMD7; PEX14; EIF4A2; HOXD9; WT1; GTF2I; USF1; PPARA; RBBP7; STAT1; PSMD2; YWHAB; AR; MORF4L1; ESR1; HDAC10; SPI1
GO:0010558	2.60E-05	0.0241	BP	14791	41	589	9	negative regulation of macromolecule biosynthetic process	RARA; NFKB1; COMMD7; PEX14; WT1; PPARA; YWHAB; HDAC10; SPI1
GO:0010556	2.70E-05	0.0254	BP	14791	41	2923	20	regulation of macromolecule biosynthetic process	STAT6; RARA; NFKB1; USF2; COMMD7; PEX14; EIF4A2; HOXD9; WT1; GTF2I; USF1; PPARA; RBBP7; STAT1; YWHAB; AR; MORF4L1; ESR1; HDAC10; SPI1
GO:0045449	2.80E-05	0.0263	BP	14791	41	2668	19	regulation of transcription	STAT6; RARA; NFKB1; USF2; COMMD7; PEX14; HOXD9; WT1; GTF2I; USF1; PPARA; RBBP7; STAT1; YWHAB; AR; MORF4L1; ESR1; HDAC10; SPI1

GO:0031323	2.80E-05	0.0263	BP	14791	41	3768	23	regulation of cellular metabolic process	PSMB8; STAT6; RARA; PSMD11; NFKB1; USF2; COMMD7; PEX14; EIF4A2; HOXD9; WT1; GTF2I; USF1; PPARA; RBBP7; STAT1; PSMD2; YWHAB; AR; MORF4L1; ESR1; HDAC10; SPI1
GO:0034645	2.90E-05	0.0267	BP	14791	41	753	10	cellular macromolecule biosynthetic process	NFKB1; USF2; EIF4A2; USF1; PPARA; RBBP7; NAP1L1; STAT1; AR; ESR1
GO:0031327	3.30E-05	0.0302	BP	14791	41	606	9	negative regulation of cellular biosynthetic process	RARA; NFKB1; COMMD7; PEX14; WT1; PPARA; YWHAB; HDAC10; SPI1
GO:0010468	3.50E-05	0.032	BP	14791	41	2968	20	regulation of gene expression	STAT6; RARA; NFKB1; USF2; COMMD7; PEX14; EIF4A2; HOXD9; WT1; GTF2I; USF1; PPARA; RBBP7; STAT1; YWHAB; AR; MORF4L1; ESR1; HDAC10; SPI1
GO:0009890	3.90E-05	0.0357	BP	14791	41	619	9	negative regulation of biosynthetic process	RARA; NFKB1; COMMD7; PEX14; WT1; PPARA; YWHAB; HDAC10; SPI1
GO:0009059	4.10E-05	0.0381	BP	14791	41	785	10	macromolecule biosynthetic process	NFKB1; USF2; EIF4A2; USF1; PPARA; RBBP7; NAP1L1; STAT1; AR; ESR1
GO:0010551	5.20E-05	0.0479	BP	14791	41	148	5	regulation of gene-specific transcription from RNA polymerase II promoter	NFKB1; USF2; USF1; PPARA; AR
GO:0031326	5.80E-05	0.0536	BP	14791	41	3071	20	regulation of cellular biosynthetic process	STAT6; RARA; NFKB1; USF2; COMMD7; PEX14; EIF4A2; HOXD9; WT1; GTF2I; USF1; PPARA; RBBP7; STAT1; YWHAB; AR; MORF4L1; ESR1; HDAC10; SPI1
GO:0060688	6.10E-05	0.0563	BP	14791	41	28	3	regulation of morphogenesis of a branching structure	CDH1; AR; ESR1
GO:0009889	6.50E-05	0.06	BP	14791	41	3094	20	regulation of biosynthetic process	STAT6; RARA; NFKB1; USF2; COMMD7; PEX14; EIF4A2; HOXD9; WT1; GTF2I; USF1; PPARA; RBBP7; STAT1; YWHAB; AR; MORF4L1; ESR1; HDAC10; SPI1
GO:0048732	7.90E-05	0.0727	BP	14791	41	83	4	gland development	CDH1; HOXD9; WT1; AR
GO:0090304	8.10E-05	0.0743	BP	14791	41	1431	13	nucleic acid metabolic process	NFKB1; USF2; SF3B5; WT1; USF1; PPARA; RBBP7; NAP1L1; RBX1; STAT1; AR; MORF4L1; ESR1
GO:0010033	8.10E-05	0.0746	BP	14791	41	850	10	response to organic substance	STAT6; RARA; CDH1; UBD; USF1; PPARA; STAT1; AR; ESR1; B2M
GO:0044260	8.50E-05	0.0776	BP	14791	41	3428	21	cellular macromolecule metabolic process	PSMB8; PSMD11; SLC35A1; NFKB1; UBD; USF2; SF3B5; EIF4A2; WT1; USF1; PPARA; RBBP7; NAP1L1; RBX1; STAT1; PSMD2; AR; MORF4L1; ESR1; ALG2; HDAC10
GO:0045892	8.50E-05	0.0781	BP	14791	41	389	7	negative regulation of transcription, DNA-dependent	RARA; NFKB1; PEX14; WT1; PPARA; HDAC10; SPI1
GO:0065009	8.90E-05	0.082	BP	14791	41	1043	11	regulation of molecular function	PSMB8; RARA; PSMD11; CDH1; NFKB1; COMMD7; PEX14; STAT1; PSMD2; YWHAB; AR
GO:0051253	9.50E-05	0.0874	BP	14791	41	396	7	negative regulation of RNA metabolic process	RARA; NFKB1; PEX14; WT1; PPARA; HDAC10; SPI1
GO:0009299	1.10E-04	0.1019	BP	14791	41	6	2	mRNA transcription	USF2; USF1
GO:0008584	1.90E-04	0.1788	BP	14791	41	41	3	male gonad development	WT1; AR; ESR1
GO:0019219	2.00E-04	0.1873	BP	14791	41	3064	19	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	STAT6; RARA; NFKB1; USF2; COMMD7; PEX14; HOXD9; WT1; GTF2I; USF1; PPARA; RBBP7; STAT1; YWHAB; AR; MORF4L1; ESR1; HDAC10; SPI1
GO:0006355	2.10E-04	0.1995	BP	14791	41	1804	14	regulation of transcription, DNA-dependent	STAT6; RARA; NFKB1; USF2; PEX14; HOXD9; WT1; USF1; PPARA; STAT1; AR; ESR1; HDAC10; SPI1
GO:0051171	2.30E-04	0.2113	BP	14791	41	3091	19	regulation of nitrogen compound metabolic process	STAT6; RARA; NFKB1; USF2; COMMD7; PEX14; HOXD9; WT1; GTF2I; USF1; PPARA; RBBP7; STAT1; YWHAB; AR; MORF4L1; ESR1; HDAC10; SPI1
GO:0043170	2.40E-04	0.2257	BP	14791	41	3975	22	macromolecule metabolic process	PSMB8; PSMD11; SLC35A1; CDH1; NFKB1; UBD; USF2; SF3B5; EIF4A2; WT1; USF1; PPARA; RBBP7; NAP1L1; RBX1; STAT1; PSMD2; AR; MORF4L1; ESR1; ALG2; HDAC10
GO:0060736	2.60E-04	0.2433	BP	14791	41	9	2	prostate gland growth	AR; ESR1
GO:0051252	2.90E-04	0.265	BP	14791	41	1853	14	regulation of RNA metabolic process	STAT6; RARA; NFKB1; USF2; PEX14; HOXD9; WT1; USF1; PPARA; STAT1; AR; ESR1; HDAC10; SPI1
GO:0042221	2.90E-04	0.2668	BP	14791	41	1402	12	response to chemical stimulus	STAT6; RARA; CDH1; UBD; USF2; USF1; PPARA; STAT1; AR; ESR1; B2M; ALG2

GO:0002828	3.30E-04	0.3037	BP	14791	41	10	2	regulation of T-helper 2 type immune response	STAT6; RARA
GO:0002706	3.50E-04	0.3231	BP	14791	41	50	3	regulation of lymphocyte mediated immunity	STAT6; TAP1; B2M
GO:0002822	3.50E-04	0.3231	BP	14791	41	50	3	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	STAT6; RARA; B2M
GO:0032868	3.60E-04	0.3318	BP	14791	41	123	4	response to insulin stimulus	USF1; PPARA; STAT1; AR
GO:0002819	3.70E-04	0.3427	BP	14791	41	51	3	regulation of adaptive immune response	STAT6; RARA; B2M
GO:0008406	3.90E-04	0.3629	BP	14791	41	52	3	gonad development	WT1; AR; ESR1
GO:0031400	4.30E-04	0.3976	BP	14791	41	129	4	negative regulation of protein modification process	PSMB8; PSMD11; PSMD2; YWHAB
GO:0044092	4.70E-04	0.4349	BP	14791	41	366	6	negative regulation of molecular function	PSMB8; PSMD11; NFKB1; COMMD7; PEX14; PSMD2
GO:0030520	4.80E-04	0.4438	BP	14791	41	12	2	estrogen receptor signaling pathway	RARA; ESR1
GO:0060749	4.80E-04	0.4438	BP	14791	41	12	2	mammary gland alveolus development	AR; ESR1
GO:0031670	5.70E-04	0.5236	BP	14791	41	13	2	cellular response to nutrient	USF2; USF1
GO:0002703	5.70E-04	0.5268	BP	14791	41	59	3	regulation of leukocyte mediated immunity	STAT6; TAP1; B2M
GO:0032268	6.20E-04	0.5672	BP	14791	41	538	7	regulation of cellular protein metabolic process	PSMB8; PSMD11; NFKB1; EIF4A2; WT1; PSMD2; YWHAB
GO:0030518	6.30E-04	0.5809	BP	14791	41	61	3	steroid hormone receptor signaling pathway	RARA; AR; ESR1
GO:0051436	6.60E-04	0.6093	BP	14791	41	62	3	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	PSMB8; PSMD11; PSMD2
GO:0031145	6.90E-04	0.6386	BP	14791	41	63	3	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	PSMB8; PSMD11; PSMD2
GO:0048608	6.90E-04	0.6386	BP	14791	41	63	3	reproductive structure development	WT1; AR; ESR1
GO:0006139	7.00E-04	0.6432	BP	14791	41	1776	13	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	NFKB1; USF2; SF3B5; WT1; USF1; PPARA; RBBP7; NAP1L1; RBX1; STAT1; AR; MORF4L1; ESR1
GO:0051437	7.60E-04	0.6997	BP	14791	41	65	3	positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	PSMB8; PSMD11; PSMD2
GO:0051352	8.00E-04	0.7316	BP	14791	41	66	3	negative regulation of ligase activity	PSMB8; PSMD11; PSMD2
GO:0051444	8.00E-04	0.7316	BP	14791	41	66	3	negative regulation of ubiquitin-protein ligase activity	PSMB8; PSMD11; PSMD2
GO:0016070	8.10E-04	0.7432	BP	14791	41	927	9	RNA metabolic process	NFKB1; USF2; SF3B5; WT1; USF1; PPARA; STAT1; AR; ESR1
GO:0007584	8.20E-04	0.7557	BP	14791	41	153	4	response to nutrient	RARA; USF2; USF1; STAT1

GO:0051439	8.70E-04	0.7982	BP	14791	41	68	3	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	PSMB8; PSMD11; PSMD2
GO:0009058	8.70E-04	0.7996	BP	14791	41	1581	12	biosynthetic process	NFKB1; USF2; NAGS; EIF4A2; USF1; PPARA; RBBP7; NAP1L1; STAT1; AR; ESR1; ALG2
GO:0051603	8.80E-04	0.807	BP	14791	41	272	5	proteolysis involved in cellular protein catabolic process	PSMB8; PSMD11; NFKB1; UBD; PSMD2
GO:0044237	8.80E-04	0.8078	BP	14791	41	4963	24	cellular metabolic process	PSMB8; PSMD11; SLC35A1; NFKB1; UBD; USF2; SF3B5; NAGS; EIF4A2; WT1; NDUFB10; USF1; PPARA; RBBP7; NAP1L1; RBX1; STAT1; PSMD2; AR; UGT2B4; MORF4L1; ESR1; ALG2; HDAC10
GO:0034641	9.00E-04	0.827	BP	14791	41	2069	14	cellular nitrogen compound metabolic process	NFKB1; USF2; SF3B5; NAGS; WT1; USF1; PPARA; RBBP7; NAP1L1; RBX1; STAT1; AR; MORF4L1; ESR1
GO:0019221	9.10E-04	0.8329	BP	14791	41	69	3	cytokine-mediated signaling pathway	STAT6; COMMD7; STAT1
GO:0023036	9.50E-04	0.8685	BP	14791	41	70	3	initiation of signal transduction	STAT6; COMMD7; STAT1
GO:0023038	9.50E-04	0.8685	BP	14791	41	70	3	signal initiation by diffusible mediator	STAT6; COMMD7; STAT1
GO:0023049	9.50E-04	0.8685	BP	14791	41	70	3	signal initiation by protein/peptide mediator	STAT6; COMMD7; STAT1
GO:0051443	9.50E-04	0.8685	BP	14791	41	70	3	positive regulation of ubiquitin-protein ligase activity	PSMB8; PSMD11; PSMD2
GO:0016575	9.90E-04	0.9066	BP	14791	41	17	2	histone deacetylation	MORF4L1; HDAC10
GO:0000122	0.001	0.9335	BP	14791	41	281	5	negative regulation of transcription from RNA polymerase II promoter	NFKB1; WT1; PPARA; HDAC10; SPI1
GO:0051351	0.001	0.9811	BP	14791	41	73	3	positive regulation of ligase activity	PSMB8; PSMD11; PSMD2
GO:0065007	0.0011	1	BP	14791	41	7547	31	biological regulation	PSMB8; STAT6; RARA; PSMD11; CDH1; NFKB1; UBD; USF2; COMMD7; PEX14; EIF4A2; ANXA4; HOXD9; WT1; GTF2I; USF1; PPARA; TMSB10; RBBP7; NAP1L1; STAT1; PSMD2; YWHAB; TAP1; AR; UGT2B4; MORF4L1; ESR1; B2M; HDAC10; SPI1
GO:0007530	0.0011	1	BP	14791	41	18	2	sex determination	WT1; AR
GO:0050793	0.0011	1	BP	14791	41	776	8	regulation of developmental process	STAT6; RARA; CDH1; NFKB1; PPARA; AR; ESR1; SPI1
GO:0031397	0.0011	1	BP	14791	41	75	3	negative regulation of protein ubiquitination	PSMB8; PSMD11; PSMD2
GO:0009725	0.0012	1	BP	14791	41	440	6	response to hormone stimulus	RARA; USF1; PPARA; STAT1; AR; ESR1
GO:0030522	0.0012	1	BP	14791	41	77	3	intracellular receptor mediated signaling pathway	RARA; AR; ESR1
GO:0051246	0.0012	1	BP	14791	41	610	7	regulation of protein metabolic process	PSMB8; PSMD11; NFKB1; EIF4A2; WT1; PSMD2; YWHAB
GO:0050789	0.0013	1	BP	14791	41	7226	30	regulation of biological process	PSMB8; STAT6; RARA; PSMD11; CDH1; NFKB1; UBD; USF2; COMMD7; PEX14; EIF4A2; ANXA4; HOXD9; WT1; GTF2I; USF1; PPARA; TMSB10; RBBP7; NAP1L1; STAT1; PSMD2; YWHAB; TAP1; AR; MORF4L1; ESR1; B2M; HDAC10; SPI1
GO:0051438	0.0014	1	BP	14791	41	80	3	regulation of ubiquitin-protein ligase activity	PSMB8; PSMD11; PSMD2
GO:0051340	0.0015	1	BP	14791	41	83	3	regulation of ligase activity	PSMB8; PSMD11; PSMD2
GO:0006807	0.0015	1	BP	14791	41	2186	14	nitrogen compound metabolic process	NFKB1; USF2; SF3B5; NAGS; WT1; USF1; PPARA; RBBP7; NAP1L1; RBX1; STAT1; AR; MORF4L1; ESR1

GO:0044249	0.0016	1	BP	14791	41	1458	11	cellular biosynthetic process	NFKB1; USF2; NAGS; EIF4A2; USF1; PPARA; RBBP7; NAP1L1; STAT1; AR; ESR1
GO:0006476	0.0016	1	BP	14791	41	22	2	protein amino acid deacetylation	MORF4L1; HDAC10
GO:0043434	0.0017	1	BP	14791	41	187	4	response to peptide hormone stimulus	USF1; PPARA; STAT1; AR
GO:0006366	0.0017	1	BP	14791	41	188	4	transcription from RNA polymerase II promoter	NFKB1; USF1; PPARA; STAT1
GO:0060740	0.0018	1	BP	14791	41	23	2	prostate gland epithelium morphogenesis	AR; ESR1
GO:0048754	0.0018	1	BP	14791	41	88	3	branching morphogenesis of a tube	WT1; AR; ESR1
GO:0050896	0.0018	1	BP	14791	41	3619	19	response to stimulus	STAT6; HLA-DMA; RARA; CDH1; NFKB1; UBD; USF2; HOXD9; USF1; PPARA; RBBP7; RBX1; STAT1; TAP1; AR; MORF4L1; ESR1; B2M; ALG2
GO:0042981	0.0019	1	BP	14791	41	842	8	regulation of apoptosis	CDH1; NFKB1; UBD; ANXA4; WT1; STAT1; YWHAB; ESR1
GO:0061138	0.0019	1	BP	14791	41	90	3	morphogenesis of a branching epithelium	WT1; AR; ESR1
GO:0051716	0.0019	1	BP	14791	41	847	8	cellular response to stimulus	RARA; CDH1; USF2; USF1; RBBP7; RBX1; STAT1; MORF4L1
GO:0001910	0.0019	1	BP	14791	41	24	2	regulation of leukocyte mediated cytotoxicity	TAP1; B2M
GO:0043067	0.002	1	BP	14791	41	850	8	regulation of programmed cell death	CDH1; NFKB1; UBD; ANXA4; WT1; STAT1; YWHAB; ESR1
GO:0070887	0.002	1	BP	14791	41	329	5	cellular response to chemical stimulus	RARA; CDH1; USF2; USF1; STAT1
GO:0009719	0.002	1	BP	14791	41	486	6	response to endogenous stimulus	RARA; USF1; PPARA; STAT1; AR; ESR1
GO:0010941	0.0021	1	BP	14791	41	856	8	regulation of cell death	CDH1; NFKB1; UBD; ANXA4; WT1; STAT1; YWHAB; ESR1
GO:0031398	0.0021	1	BP	14791	41	93	3	positive regulation of protein ubiquitination	PSMB8; PSMD11; PSMD2
GO:0010743	0.0021	1	BP	14791	41	25	2	regulation of macrophage derived foam cell differentiation	NFKB1; PPARA
GO:0010883	0.0021	1	BP	14791	41	25	2	regulation of lipid storage	NFKB1; PPARA
GO:0044238	0.0022	1	BP	14791	41	5258	24	primary metabolic process	PSMB8; PSMD11; SLC35A1; CDH1; NFKB1; UBD; USF2; SF3B5; NAGS; EIF4A2; WT1; USF1; PPARA; RBBP7; NAP1L1; RBX1; STAT1; PSMD2; AR; UGT2B4; MORF4L1; ESR1; ALG2; HDAC10
GO:0031667	0.0023	1	BP	14791	41	203	4	response to nutrient levels	RARA; USF2; USF1; STAT1
GO:0010552	0.0024	1	BP	14791	41	97	3	positive regulation of gene-specific transcription from RNA polymerase II promoter	USF2; USF1; AR
GO:0050777	0.0025	1	BP	14791	41	27	2	negative regulation of immune response	STAT6; TAP1
GO:0048583	0.0026	1	BP	14791	41	510	6	regulation of response to stimulus	STAT6; RARA; USF1; PPARA; TAP1; B2M
GO:0031341	0.0027	1	BP	14791	41	28	2	regulation of cell killing	TAP1; B2M
GO:0010286	0.0027	1	BP	14791	41	1	1	heat acclimation	RBBP7

GO:0015782	0.0027	1	BP	14791	41	1	1	CMP-sialic acid transport	SLC35A1
GO:0019102	0.0027	1	BP	14791	41	1	1	male somatic sex determination	AR
GO:0002477	0.0027	1	BP	14791	41	1	1	antigen processing and presentation of exogenous peptide antigen via MHC class Ib	B2M
GO:0002481	0.0027	1	BP	14791	41	1	1	antigen processing and presentation of exogenous protein antigen via MHC class Ib, TAP-dependent	B2M
GO:0032736	0.0027	1	BP	14791	41	1	1	positive regulation of interleukin-13 production	RARA
GO:0032754	0.0027	1	BP	14791	41	1	1	positive regulation of interleukin-5 production	RARA
GO:0033577	0.0027	1	BP	14791	41	1	1	protein amino acid glycosylation in endoplasmic reticulum	ALG2
GO:0034499	0.0027	1	BP	14791	41	1	1	late endosome to Golgi transport	GCC2
GO:0035415	0.0027	1	BP	14791	41	1	1	regulation of mitotic prometaphase	UBD
GO:0035417	0.0027	1	BP	14791	41	1	1	negative regulation of mitotic prometaphase	UBD
GO:0042270	0.0027	1	BP	14791	41	1	1	protection from natural killer cell mediated cytotoxicity	TAP1
GO:0060520	0.0027	1	BP	14791	41	1	1	activation of prostate induction by androgen receptor signaling pathway	AR
GO:0006711	0.0027	1	BP	14791	41	1	1	estrogen catabolic process	UGT2B4
GO:0070370	0.0027	1	BP	14791	41	1	1	cellular heat acclimation	RBBP7
GO:0090161	0.0027	1	BP	14791	41	1	1	Golgi ribbon formation	GCC2
GO:0050790	0.0028	1	BP	14791	41	898	8	regulation of catalytic activity	PSMB8; PSMD11; CDH1; NFKB1; STAT1; PSMD2; YWHAB; AR
GO:0002697	0.0028	1	BP	14791	41	103	3	regulation of immune effector process	STAT6; TAP1; B2M
GO:0071310	0.0029	1	BP	14791	41	217	4	cellular response to organic substance	RARA; CDH1; USF1; STAT1
GO:0034097	0.003	1	BP	14791	41	105	3	response to cytokine stimulus	STAT6; UBD; STAT1
GO:0009991	0.0032	1	BP	14791	41	222	4	response to extracellular stimulus	RARA; USF2; USF1; STAT1
GO:0010498	0.0033	1	BP	14791	41	109	3	proteasomal protein catabolic process	PSMB8; PSMD11; PSMD2
GO:0043161	0.0033	1	BP	14791	41	109	3	proteasomal ubiquitin-dependent protein catabolic process	PSMB8; PSMD11; PSMD2
GO:0009987	0.0035	1	BP	14791	41	9216	34	cellular process	PSMB8; RARA; PSMD11; SLC35A1; CDH1; NFKB1; UBD; USF2; GCC2; SF3B5; NAGS; PEX14; EIF4A2; HOXD9; WT1; NDUFB10; USF1; PPARA; TMSB10; RBBP7; LUM; NAP1L1; RBX1; STAT1; PSMD2; YWHAB; TAP1; AR; UGT2B4; MORF4L1; ESR1; SLC39A6; ALG2; HDAC10
GO:0050776	0.0036	1	BP	14791	41	229	4	regulation of immune response	STAT6; RARA; TAP1; B2M

GO:0001763	0.0037	1	BP	14791	41	113	3	morphogenesis of a branching structure	WT1; AR; ESR1
GO:0031396	0.0038	1	BP	14791	41	114	3	regulation of protein ubiquitination	PSMB8; PSMD11; PSMD2
GO:0050794	0.0041	1	BP	14791	41	6896	28	regulation of cellular process	PSMB8; STAT6; RARA; PSMD11; CDH1; NFKB1; UBD; USF2; COMMD7; PEX14; EIF4A2; ANXA4; HOXD9; WT1; GTF21; USF1; PPARA; TMSB10; RBBP7; NAP1L1; STAT1; PSMD2; YWHAB; AR; MORF4L1; ESR1; HDAC10; SPI1
GO:0010035	0.0041	1	BP	14791	41	238	4	response to inorganic substance	CDH1; STAT1; B2M; ALG2
GO:0006511	0.0041	1	BP	14791	41	238	4	ubiquitin-dependent protein catabolic process	PSMB8; PSMD11; UBD; PSMD2
GO:0035239	0.0044	1	BP	14791	41	120	3	tube morphogenesis	WT1; AR; ESR1
GO:0019941	0.0044	1	BP	14791	41	243	4	modification-dependent protein catabolic process	PSMB8; PSMD11; UBD; PSMD2
GO:0043632	0.0044	1	BP	14791	41	243	4	modification-dependent macromolecule catabolic process	PSMB8; PSMD11; UBD; PSMD2
GO:0048585	0.0047	1	BP	14791	41	123	3	negative regulation of response to stimulus	STAT6; PPARA; TAP1
GO:0031669	0.0054	1	BP	14791	41	40	2	cellular response to nutrient levels	USF2; USF1
GO:0010957	0.0055	1	BP	14791	41	2	1	negative regulation of vitamin D biosynthetic process	NFKB1
GO:0018993	0.0055	1	BP	14791	41	2	1	somatic sex determination	AR
GO:0002428	0.0055	1	BP	14791	41	2	1	antigen processing and presentation of peptide antigen via MHC class Ib	B2M
GO:0002716	0.0055	1	BP	14791	41	2	1	negative regulation of natural killer cell mediated immunity	TAP1
GO:0045953	0.0055	1	BP	14791	41	2	1	negative regulation of natural killer cell mediated cytotoxicity	TAP1
GO:0046137	0.0055	1	BP	14791	41	2	1	negative regulation of vitamin metabolic process	NFKB1
GO:0046661	0.0055	1	BP	14791	41	2	1	male sex differentiation	AR
GO:0046967	0.0055	1	BP	14791	41	2	1	cytosol to ER transport	TAP1
GO:0048295	0.0055	1	BP	14791	41	2	1	positive regulation of isotype switching to IgE isotypes	STAT6
GO:0048386	0.0055	1	BP	14791	41	2	1	positive regulation of retinoic acid receptor signaling pathway	ESR1
GO:0060523	0.0055	1	BP	14791	41	2	1	prostate epithelial cord elongation	ESR1
GO:0060599	0.0055	1	BP	14791	41	2	1	lateral sprouting involved in mammary gland duct morphogenesis	AR
GO:0060737	0.0055	1	BP	14791	41	2	1	prostate gland morphogenetic growth	ESR1
GO:0071285	0.0055	1	BP	14791	41	2	1	cellular response to lithium ion	CDH1
GO:0071391	0.0055	1	BP	14791	41	2	1	cellular response to estrogen stimulus	RARA

GO:0002682	0.0057	1	BP	14791	41	418	5	regulation of immune system process	STAT6; RARA; TAP1; B2M; SPI1
GO:0044093	0.0069	1	BP	14791	41	623	6	positive regulation of molecular function	PSMB8; RARA; PSMD11; STAT1; PSMD2; YWHAB
GO:0019882	0.007	1	BP	14791	41	142	3	antigen processing and presentation	HLA-DMA; TAP1; B2M
GO:0008152	0.0071	1	BP	14791	41	6033	25	metabolic process	PSMB8; PSMD11; SLC35A1; CDH1; NFKB1; UBD; USF2; SF3B5; NAGS; EIF4A2; WT1; NDUFB10; USF1; PPARA; RBBP7; NAP1L1; RBX1; STAT1; PSMD2; AR; UGT2B4; MORF4L1; ESR1; ALG2; HDAC10
GO:0042127	0.0076	1	BP	14791	41	839	7	regulation of cell proliferation	STAT6; RARA; WT1; NAP1L1; STAT1; AR; ESR1
GO:0010956	0.0082	1	BP	14791	41	3	1	negative regulation of calcidiol 1-monooxygenase activity	NFKB1
GO:0001547	0.0082	1	BP	14791	41	3	1	antral ovarian follicle growth	ESR1
GO:0032656	0.0082	1	BP	14791	41	3	1	regulation of interleukin-13 production	RARA
GO:0032674	0.0082	1	BP	14791	41	3	1	regulation of interleukin-5 production	RARA
GO:0032753	0.0082	1	BP	14791	41	3	1	positive regulation of interleukin-4 production	RARA
GO:0034067	0.0082	1	BP	14791	41	3	1	protein localization in Golgi apparatus	GCC2
GO:0045630	0.0082	1	BP	14791	41	3	1	positive regulation of T-helper 2 cell differentiation	RARA
GO:0048935	0.0082	1	BP	14791	41	3	1	peripheral nervous system neuron development	HOXD9
GO:0060065	0.0082	1	BP	14791	41	3	1	uterus development	ESR1
GO:0060605	0.0082	1	BP	14791	41	3	1	tube lumen cavitation	CDH1
GO:0060662	0.0082	1	BP	14791	41	3	1	salivary gland cavitation	CDH1
GO:0060745	0.0082	1	BP	14791	41	3	1	mammary gland branching involved in pregnancy	ESR1
GO:0060748	0.0082	1	BP	14791	41	3	1	tertiary branching involved in mammary gland duct morphogenesis	AR
GO:0060750	0.0082	1	BP	14791	41	3	1	epithelial cell proliferation involved in mammary gland duct morphogenesis	ESR1
GO:0010038	0.0086	1	BP	14791	41	153	3	response to metal ion	CDH1; B2M; ALG2
GO:0043086	0.0089	1	BP	14791	41	297	4	negative regulation of catalytic activity	PSMB8; PSMD11; NFKB1; PSMD2
GO:0043433	0.0091	1	BP	14791	41	52	2	negative regulation of transcription factor activity	COMMD7; PEX14
GO:0090048	0.0091	1	BP	14791	41	52	2	negative regulation of transcription regulator activity	COMMD7; PEX14
GO:0043062	0.0094	1	BP	14791	41	158	3	extracellular structure organization	CDH1; WT1; LUM
GO:0032870	0.0096	1	BP	14791	41	159	3	cellular response to hormone stimulus	RARA; USF1; STAT1

GO:0071495	0.0099	1	BP	14791	41	161	3	cellular response to endogenous stimulus	RARA; USF1; STAT1
GO:0010891	0.011	1	BP	14791	41	4	1	negative regulation of sequestering of triglyceride	PPARA
GO:0019060	0.011	1	BP	14791	41	4	1	intracellular transport of viral proteins in host cell	TAP1
GO:0001911	0.011	1	BP	14791	41	4	1	negative regulation of leukocyte mediated cytotoxicity	TAP1
GO:0002475	0.011	1	BP	14791	41	4	1	antigen processing and presentation via MHC class Ib	B2M
GO:0002829	0.011	1	BP	14791	41	4	1	negative regulation of T-helper 2 type immune response	STAT6
GO:0030581	0.011	1	BP	14791	41	4	1	symbiont intracellular protein transport in host	TAP1
GO:0030656	0.011	1	BP	14791	41	4	1	regulation of vitamin metabolic process	NFKB1
GO:0032096	0.011	1	BP	14791	41	4	1	negative regulation of response to food	PPARA
GO:0032099	0.011	1	BP	14791	41	4	1	negative regulation of appetite	PPARA
GO:0033145	0.011	1	BP	14791	41	4	1	positive regulation of steroid hormone receptor signaling pathway	AR
GO:0033148	0.011	1	BP	14791	41	4	1	positive regulation of estrogen receptor signaling pathway	AR
GO:0035305	0.011	1	BP	14791	41	4	1	negative regulation of dephosphorylation	YWHAB
GO:0035308	0.011	1	BP	14791	41	4	1	negative regulation of protein amino acid dephosphorylation	YWHAB
GO:0048293	0.011	1	BP	14791	41	4	1	regulation of isotype switching to IgE isotypes	STAT6
GO:0051708	0.011	1	BP	14791	41	4	1	intracellular protein transport in other organism involved in symbiotic interaction	TAP1
GO:0060068	0.011	1	BP	14791	41	4	1	vagina development	ESR1
GO:0060556	0.011	1	BP	14791	41	4	1	regulation of vitamin D biosynthetic process	NFKB1
GO:0006488	0.011	1	BP	14791	41	4	1	dolichol-linked oligosaccharide biosynthetic process	ALG2
GO:0006526	0.011	1	BP	14791	41	4	1	arginine biosynthetic process	NAGS
GO:0070841	0.011	1	BP	14791	41	4	1	inclusion body assembly	UBD
GO:0070842	0.011	1	BP	14791	41	4	1	aggresome assembly	UBD
GO:0016043	0.0111	1	BP	14791	41	2417	13	cellular component organization	CDH1; UBD; GCC2; PEX14; WT1; GTF2I; TMSB10; RBBP7; LUM; NAP1L1; YWHAB; MORF4L1; HDAC10
GO:0006605	0.0111	1	BP	14791	41	168	3	protein targeting	GCC2; PEX14; YWHAB
GO:0031668	0.0112	1	BP	14791	41	58	2	cellular response to extracellular stimulus	USF2; USF1

GO:0071496	0.0112	1	BP	14791	41	58	2	cellular response to external stimulus	USF2; USF1
GO:0043392	0.0119	1	BP	14791	41	60	2	negative regulation of DNA binding	COMMD7; PEX14
GO:0034754	0.0123	1	BP	14791	41	61	2	cellular hormone metabolic process	UGT2B4; ESR1
GO:0010553	0.0127	1	BP	14791	41	62	2	negative regulation of gene-specific transcription from RNA polymerase II promoter	NFKB1; PPARA
GO:0032355	0.0127	1	BP	14791	41	62	2	response to estradiol stimulus	RARA; ESR1
GO:0055088	0.0127	1	BP	14791	41	62	2	lipid homeostasis	USF2; USF1
GO:0002009	0.0132	1	BP	14791	41	179	3	morphogenesis of an epithelium	WT1; AR; ESR1
GO:0010871	0.0137	1	BP	14791	41	5	1	negative regulation of receptor biosynthetic process	PPARA
GO:0015781	0.0137	1	BP	14791	41	5	1	pyrimidine nucleotide-sugar transport	SLC35A1
GO:0001916	0.0137	1	BP	14791	41	5	1	positive regulation of T cell mediated cytotoxicity	B2M
GO:0031342	0.0137	1	BP	14791	41	5	1	negative regulation of cell killing	TAP1
GO:0032835	0.0137	1	BP	14791	41	5	1	glomerulus development	WT1
GO:0032836	0.0137	1	BP	14791	41	5	1	glomerular basement membrane development	WT1
GO:0043001	0.0137	1	BP	14791	41	5	1	Golgi to plasma membrane protein transport	GCC2
GO:0060601	0.0137	1	BP	14791	41	5	1	lateral sprouting from an epithelium	AR
GO:0071680	0.0137	1	BP	14791	41	5	1	response to indole-3-methanol	CDH1
GO:0071681	0.0137	1	BP	14791	41	5	1	cellular response to indole-3-methanol	CDH1
GO:0051098	0.0138	1	BP	14791	41	182	3	regulation of binding	RARA; COMMD7; PEX14
GO:0045185	0.0147	1	BP	14791	41	67	2	maintenance of protein location	TMSB10; YWHAB
GO:0051259	0.0151	1	BP	14791	41	188	3	protein oligomerization	CDH1; PEX14; YWHAB
GO:0031399	0.0152	1	BP	14791	41	347	4	regulation of protein modification process	PSMB8; PSMD11; PSMD2; YWHAB
GO:0040008	0.0152	1	BP	14791	41	347	4	regulation of growth	WT1; RBBP7; AR; MORF4L1
GO:0019538	0.0159	1	BP	14791	41	2528	13	protein metabolic process	PSMB8; PSMD11; SLC35A1; CDH1; NFKB1; UBD; EIF4A2; RBX1; STAT1; PSMD2; MORF4L1; ALG2; HDAC10
GO:0045595	0.0164	1	BP	14791	41	543	5	regulation of cell differentiation	RARA; NFKB1; PPARA; AR; SPI1
GO:0010887	0.0165	1	BP	14791	41	6	1	negative regulation of cholesterol storage	PPARA
GO:0015780	0.0165	1	BP	14791	41	6	1	nucleotide-sugar transport	SLC35A1

GO:0019885	0.0165	1	BP	14791	41	6	1	antigen processing and presentation of endogenous peptide antigen via MHC class I	TAP1
GO:0002478	0.0165	1	BP	14791	41	6	1	antigen processing and presentation of exogenous peptide antigen	B2M
GO:0002483	0.0165	1	BP	14791	41	6	1	antigen processing and presentation of endogenous peptide antigen	TAP1
GO:0030850	0.0165	1	BP	14791	41	6	1	prostate gland development	AR
GO:0045628	0.0165	1	BP	14791	41	6	1	regulation of T-helper 2 cell differentiation	RARA
GO:0045824	0.0165	1	BP	14791	41	6	1	negative regulation of innate immune response	TAP1
GO:0060527	0.0165	1	BP	14791	41	6	1	prostate epithelial cord arborization involved in prostate glandular acinus morphogenesis	ESR1
GO:0060685	0.0165	1	BP	14791	41	6	1	regulation of prostatic bud formation	AR
GO:0060687	0.0165	1	BP	14791	41	6	1	regulation of branching involved in prostate gland morphogenesis	ESR1
GO:0071383	0.0165	1	BP	14791	41	6	1	cellular response to steroid hormone stimulus	RARA
GO:0007260	0.0165	1	BP	14791	41	6	1	tyrosine phosphorylation of STAT protein	STAT1
GO:0043085	0.0167	1	BP	14791	41	545	5	positive regulation of catalytic activity	PSMB8; PSMD11; STAT1; PSMD2; YWHAB
GO:0051100	0.0169	1	BP	14791	41	72	2	negative regulation of binding	COMMD7; PEX14
GO:0006886	0.017	1	BP	14791	41	359	4	intracellular protein transport	GCC2; PEX14; YWHAB; TAP1
GO:0006916	0.018	1	BP	14791	41	201	3	anti-apoptosis	NFKB1; ANXA4; ESR1
GO:0032869	0.0183	1	BP	14791	41	75	2	cellular response to insulin stimulus	USF1; STAT1
GO:0043066	0.0189	1	BP	14791	41	371	4	negative regulation of apoptosis	NFKB1; ANXA4; WT1; ESR1
GO:0016558	0.0192	1	BP	14791	41	7	1	protein import into peroxisome matrix	PEX14
GO:0001914	0.0192	1	BP	14791	41	7	1	regulation of T cell mediated cytotoxicity	B2M
GO:0019884	0.0192	1	BP	14791	41	7	1	antigen processing and presentation of exogenous antigen	B2M
GO:0032000	0.0192	1	BP	14791	41	7	1	positive regulation of fatty acid beta-oxidation	PPARA
GO:0032105	0.0192	1	BP	14791	41	7	1	negative regulation of response to extracellular stimulus	PPARA
GO:0032108	0.0192	1	BP	14791	41	7	1	negative regulation of response to nutrient levels	PPARA
GO:0032372	0.0192	1	BP	14791	41	7	1	negative regulation of sterol transport	NFKB1
GO:0032375	0.0192	1	BP	14791	41	7	1	negative regulation of cholesterol transport	NFKB1

GO:0032689	0.0192	1	BP	14791	41	7	1	negative regulation of interferon-gamma production	RARA
GO:0033146	0.0192	1	BP	14791	41	7	1	regulation of estrogen receptor signaling pathway	AR
GO:0003401	0.0192	1	BP	14791	41	7	1	axis elongation	ESR1
GO:0035304	0.0192	1	BP	14791	41	7	1	regulation of protein amino acid dephosphorylation	YWHA
GO:0043568	0.0192	1	BP	14791	41	7	1	positive regulation of insulin-like growth factor receptor signaling pathway	AR
GO:0045116	0.0192	1	BP	14791	41	7	1	protein neddylation	RBX1
GO:0045624	0.0192	1	BP	14791	41	7	1	positive regulation of T-helper cell differentiation	RARA
GO:0060558	0.0192	1	BP	14791	41	7	1	regulation of calcidiol 1-monooxygenase activity	NFKB1
GO:0060602	0.0192	1	BP	14791	41	7	1	branch elongation of an epithelium	ESR1
GO:0006622	0.0192	1	BP	14791	41	7	1	protein targeting to lysosome	GCC2
GO:0006623	0.0192	1	BP	14791	41	7	1	protein targeting to vacuole	GCC2
GO:0043069	0.0198	1	BP	14791	41	376	4	negative regulation of programmed cell death	NFKB1; ANXA4; WT1; ESR1
GO:0044265	0.02	1	BP	14791	41	377	4	cellular macromolecule catabolic process	PSMB8; PSMD11; UBD; PSMD2
GO:0071375	0.0201	1	BP	14791	41	79	2	cellular response to peptide hormone stimulus	USF1; STAT1
GO:0048729	0.021	1	BP	14791	41	213	3	tissue morphogenesis	WT1; AR; ESR1
GO:0060548	0.021	1	BP	14791	41	383	4	negative regulation of cell death	NFKB1; ANXA4; WT1; ESR1
GO:0010894	0.0219	1	BP	14791	41	8	1	negative regulation of steroid biosynthetic process	NFKB1
GO:0001823	0.0219	1	BP	14791	41	8	1	mesonephros development	WT1
GO:0019883	0.0219	1	BP	14791	41	8	1	antigen processing and presentation of endogenous antigen	TAP1
GO:0002704	0.0219	1	BP	14791	41	8	1	negative regulation of leukocyte mediated immunity	TAP1
GO:0002707	0.0219	1	BP	14791	41	8	1	negative regulation of lymphocyte mediated immunity	TAP1
GO:0032098	0.0219	1	BP	14791	41	8	1	regulation of appetite	PPARA
GO:0033209	0.0219	1	BP	14791	41	8	1	tumor necrosis factor-mediated signaling pathway	COMMD7
GO:0042989	0.0219	1	BP	14791	41	8	1	sequestering of actin monomers	TMSB10
GO:0045830	0.0219	1	BP	14791	41	8	1	positive regulation of isotype switching	STAT6
GO:0045939	0.0219	1	BP	14791	41	8	1	negative regulation of steroid metabolic process	NFKB1

GO:0048385	0.0219	1	BP	14791	41	8	1	regulation of retinoic acid receptor signaling pathway	ESR1
GO:0060231	0.0219	1	BP	14791	41	8	1	mesenchymal to epithelial transition	WT1
GO:0060742	0.0219	1	BP	14791	41	8	1	epithelial cell differentiation involved in prostate gland development	AR
GO:0044419	0.0221	1	BP	14791	41	389	4	interspecies interaction between organisms	PSMB8; EIF4A2; STAT1; TAP1
GO:0002474	0.0226	1	BP	14791	41	84	2	antigen processing and presentation of peptide antigen via MHC class I	TAP1; B2M
GO:0051235	0.0226	1	BP	14791	41	84	2	maintenance of location	TMSB10; YWHAB
GO:0051239	0.0236	1	BP	14791	41	1047	7	regulation of multicellular organismal process	STAT6; RARA; CDH1; USF1; AR; ESR1; SPI1
GO:0031401	0.0242	1	BP	14791	41	225	3	positive regulation of protein modification process	PSMB8; PSMD11; PSMD2
GO:0010889	0.0246	1	BP	14791	41	9	1	regulation of sequestering of triglyceride	PPARA
GO:0032095	0.0246	1	BP	14791	41	9	1	regulation of response to food	PPARA
GO:0032673	0.0246	1	BP	14791	41	9	1	regulation of interleukin-4 production	RARA
GO:0033598	0.0246	1	BP	14791	41	9	1	mammary gland epithelial cell proliferation	ESR1
GO:0042447	0.0246	1	BP	14791	41	9	1	hormone catabolic process	UGT2B4
GO:0043011	0.0246	1	BP	14791	41	9	1	myeloid dendritic cell differentiation	UBD
GO:0043372	0.0246	1	BP	14791	41	9	1	positive regulation of CD4-positive, alpha beta T cell differentiation	RARA
GO:0045911	0.0246	1	BP	14791	41	9	1	positive regulation of DNA recombination	STAT6
GO:0006893	0.0246	1	BP	14791	41	9	1	Golgi to plasma membrane transport	GCC2
GO:0071241	0.0246	1	BP	14791	41	9	1	cellular response to inorganic substance	CDH1
GO:0071248	0.0246	1	BP	14791	41	9	1	cellular response to metal ion	CDH1
GO:0002683	0.0252	1	BP	14791	41	89	2	negative regulation of immune system process	STAT6; TAP1
GO:0048468	0.0253	1	BP	14791	41	229	3	cell development	HOXD9; WT1; ESR1
GO:0043281	0.0257	1	BP	14791	41	90	2	regulation of caspase activity	CDH1; STAT1
GO:0048002	0.0257	1	BP	14791	41	90	2	antigen processing and presentation of peptide antigen	TAP1; B2M
GO:0006325	0.0262	1	BP	14791	41	410	4	chromatin organization	RBBP7; NAP1L1; MORF4L1; HDAC10
GO:0010226	0.0273	1	BP	14791	41	10	1	response to lithium ion	CDH1
GO:0010453	0.0273	1	BP	14791	41	10	1	regulation of cell fate commitment	AR

GO:0010869	0.0273	1	BP	14791	41	10	1	regulation of receptor biosynthetic process	PPARA
GO:0001773	0.0273	1	BP	14791	41	10	1	myeloid dendritic cell activation	UBD
GO:0002820	0.0273	1	BP	14791	41	10	1	negative regulation of adaptive immune response	STAT6
GO:0002823	0.0273	1	BP	14791	41	10	1	negative regulation of adaptive immune response based on somatic recombination of immune	STAT6
GO:0030238	0.0273	1	BP	14791	41	10	1	male sex determination	AR
GO:0031663	0.0273	1	BP	14791	41	10	1	lipopolysaccharide-mediated signaling pathway	STAT1
GO:0042659	0.0273	1	BP	14791	41	10	1	regulation of cell fate specification	AR
GO:0046321	0.0273	1	BP	14791	41	10	1	positive regulation of fatty acid oxidation	PPARA
GO:0000050	0.0273	1	BP	14791	41	10	1	urea cycle	NAGS
GO:0051918	0.0273	1	BP	14791	41	10	1	negative regulation of fibrinolysis	USF1
GO:0060442	0.0273	1	BP	14791	41	10	1	branching involved in prostate gland morphogenesis	ESR1
GO:0060693	0.0273	1	BP	14791	41	10	1	regulation of branching involved in salivary gland morphogenesis	CDH1
GO:0008210	0.0273	1	BP	14791	41	10	1	estrogen metabolic process	UGT2B4
GO:0042493	0.0279	1	BP	14791	41	238	3	response to drug	CDH1; STAT1; B2M
GO:0052548	0.029	1	BP	14791	41	96	2	regulation of endopeptidase activity	CDH1; STAT1
GO:0003006	0.0295	1	BP	14791	41	243	3	reproductive developmental process	WT1; AR; ESR1
GO:0001829	0.03	1	BP	14791	41	11	1	trophoblast cell differentiation	CDH1
GO:0019627	0.03	1	BP	14791	41	11	1	urea metabolic process	NAGS
GO:0002076	0.03	1	BP	14791	41	11	1	osteoblast development	ESR1
GO:0002711	0.03	1	BP	14791	41	11	1	positive regulation of T cell mediated immunity	B2M
GO:0031293	0.03	1	BP	14791	41	11	1	membrane protein intracellular domain proteolysis	NFKB1
GO:0031998	0.03	1	BP	14791	41	11	1	regulation of fatty acid beta-oxidation	PPARA
GO:0032769	0.03	1	BP	14791	41	11	1	negative regulation of monooxygenase activity	NFKB1
GO:0043330	0.03	1	BP	14791	41	11	1	response to exogenous dsRNA	STAT1
GO:0043604	0.03	1	BP	14791	41	11	1	amide biosynthetic process	NAGS
GO:0045622	0.03	1	BP	14791	41	11	1	regulation of T-helper cell differentiation	RARA

GO:0048589	0.0307	1	BP	14791	41	99	2	developmental growth	AR; ESR1
GO:0052547	0.0318	1	BP	14791	41	101	2	regulation of peptidase activity	CDH1; STAT1
GO:0030198	0.0324	1	BP	14791	41	102	2	extracellular matrix organization	WT1; LUM
GO:0030308	0.0324	1	BP	14791	41	102	2	negative regulation of cell growth	WT1; RBBP7
GO:0043065	0.0326	1	BP	14791	41	439	4	positive regulation of apoptosis	UBD; WT1; STAT1; YWHAB
GO:0010745	0.0327	1	BP	14791	41	12	1	negative regulation of macrophage derived foam cell differentiation	PPARA
GO:0010885	0.0327	1	BP	14791	41	12	1	regulation of cholesterol storage	PPARA
GO:0010888	0.0327	1	BP	14791	41	12	1	negative regulation of lipid storage	PPARA
GO:0002064	0.0327	1	BP	14791	41	12	1	epithelial cell development	ESR1
GO:0030325	0.0327	1	BP	14791	41	12	1	adrenal gland development	WT1
GO:0043968	0.0327	1	BP	14791	41	12	1	histone H2A acetylation	MORF4L1
GO:0045191	0.0327	1	BP	14791	41	12	1	regulation of isotype switching	STAT6
GO:0045885	0.0327	1	BP	14791	41	12	1	positive regulation of survival gene product expression	ESR1
GO:0048384	0.0327	1	BP	14791	41	12	1	retinoic acid receptor signaling pathway	RARA
GO:0060444	0.0327	1	BP	14791	41	12	1	branching involved in mammary gland duct morphogenesis	ESR1
GO:0060571	0.0327	1	BP	14791	41	12	1	morphogenesis of an epithelial fold	AR
GO:0051260	0.033	1	BP	14791	41	103	2	protein homooligomerization	CDH1; PEX14
GO:0043068	0.0333	1	BP	14791	41	442	4	positive regulation of programmed cell death	UBD; WT1; STAT1; YWHAB
GO:0051251	0.0336	1	BP	14791	41	104	2	positive regulation of lymphocyte activation	STAT6; RARA
GO:0030855	0.0342	1	BP	14791	41	105	2	epithelial cell differentiation	WT1; AR
GO:0010942	0.0343	1	BP	14791	41	446	4	positive regulation of cell death	UBD; WT1; STAT1; YWHAB
GO:0009057	0.0345	1	BP	14791	41	447	4	macromolecule catabolic process	PSMB8; PSMD11; UBD; PSMD2
GO:0042445	0.0348	1	BP	14791	41	106	2	hormone metabolic process	UGT2B4; ESR1
GO:0010744	0.0354	1	BP	14791	41	13	1	positive regulation of macrophage derived foam cell differentiation	NFKB1
GO:0010884	0.0354	1	BP	14791	41	13	1	positive regulation of lipid storage	NFKB1
GO:0043370	0.0354	1	BP	14791	41	13	1	regulation of CD4-positive, alpha beta T cell differentiation	RARA

GO:0043567	0.0354	1	BP	14791	41	13	1	regulation of insulin-like growth factor receptor signaling pathway	AR
GO:0051917	0.0354	1	BP	14791	41	13	1	regulation of fibrinolysis	USF1
GO:0006525	0.0354	1	BP	14791	41	13	1	arginine metabolic process	NAGS
GO:0006625	0.0354	1	BP	14791	41	13	1	protein targeting to peroxisome	PEX14
GO:0009312	0.0354	1	BP	14791	41	13	1	oligosaccharide biosynthetic process	ALG2
GO:0002684	0.0357	1	BP	14791	41	262	3	positive regulation of immune system process	STAT6; RARA; B2M
GO:0008284	0.0357	1	BP	14791	41	452	4	positive regulation of cell proliferation	RARA; NAP1L1; STAT1; ESR1
GO:0022607	0.0357	1	BP	14791	41	897	6	cellular component assembly	CDH1; UBD; PEX14; GTF2I; NAP1L1; YWHAB
GO:0065003	0.0362	1	BP	14791	41	668	5	macromolecular complex assembly	CDH1; PEX14; GTF2I; NAP1L1; YWHAB
GO:0030194	0.0381	1	BP	14791	41	14	1	positive regulation of blood coagulation	USF1
GO:0032104	0.0381	1	BP	14791	41	14	1	regulation of response to extracellular stimulus	PPARA
GO:0032107	0.0381	1	BP	14791	41	14	1	regulation of response to nutrient levels	PPARA
GO:0003382	0.0381	1	BP	14791	41	14	1	epithelial cell morphogenesis	WT1
GO:0043574	0.0381	1	BP	14791	41	14	1	peroxisomal transport	PEX14
GO:0048645	0.0381	1	BP	14791	41	14	1	organ formation	AR
GO:0060135	0.0381	1	BP	14791	41	14	1	maternal process involved in female pregnancy	ESR1
GO:0060560	0.0381	1	BP	14791	41	14	1	developmental growth involved in morphogenesis	ESR1
GO:0008209	0.0381	1	BP	14791	41	14	1	androgen metabolic process	ESR1
GO:0043627	0.039	1	BP	14791	41	113	2	response to estrogen stimulus	RARA; ESR1
GO:0002696	0.0403	1	BP	14791	41	115	2	positive regulation of leukocyte activation	STAT6; RARA
GO:0032369	0.0408	1	BP	14791	41	15	1	negative regulation of lipid transport	NFKB1
GO:0032720	0.0408	1	BP	14791	41	15	1	negative regulation of tumor necrosis factor production	RARA
GO:0043526	0.0408	1	BP	14791	41	15	1	neuroprotection	ESR1
GO:0051354	0.0408	1	BP	14791	41	15	1	negative regulation of oxidoreductase activity	NFKB1
GO:0032270	0.0429	1	BP	14791	41	282	3	positive regulation of cellular protein metabolic process	PSMB8; PSMD11; PSMD2
GO:0034341	0.0434	1	BP	14791	41	16	1	response to interferon-gamma	UBD

GO:0034605	0.0434	1	BP	14791	41	16	1	cellular response to heat	RBBP7
GO:0050996	0.0434	1	BP	14791	41	16	1	positive regulation of lipid catabolic process	PPARA
GO:0006536	0.0434	1	BP	14791	41	16	1	glutamate metabolic process	NAGS
GO:0050867	0.0435	1	BP	14791	41	120	2	positive regulation of cell activation	STAT6; RARA
GO:0051090	0.0442	1	BP	14791	41	121	2	regulation of transcription factor activity	COMMD7; PEX14
GO:0090046	0.0442	1	BP	14791	41	121	2	regulation of transcription regulator activity	COMMD7; PEX14
GO:0006508	0.0445	1	BP	14791	41	707	5	proteolysis	PSMB8; PSMD11; NFKB1; UBD; PSMD2
GO:0048513	0.0452	1	BP	14791	41	710	5	organ development	CDH1; HOXD9; WT1; AR; ESR1
GO:0002698	0.0461	1	BP	14791	41	17	1	negative regulation of immune effector process	TAP1
GO:0002709	0.0461	1	BP	14791	41	17	1	regulation of T cell mediated immunity	B2M
GO:0030539	0.0461	1	BP	14791	41	17	1	male genitalia development	WT1
GO:0033365	0.0461	1	BP	14791	41	17	1	protein localization in organelle	GCC2
GO:0042993	0.0461	1	BP	14791	41	17	1	positive regulation of transcription factor import into nucleus	CDH1
GO:0046686	0.0461	1	BP	14791	41	17	1	response to cadmium ion	B2M
GO:0050820	0.0461	1	BP	14791	41	17	1	positive regulation of coagulation	USF1
GO:0051220	0.0461	1	BP	14791	41	17	1	cytoplasmic sequestering of protein	YWHAB
GO:0007031	0.0461	1	BP	14791	41	17	1	peroxisome organization	PEX14
GO:0071222	0.0461	1	BP	14791	41	17	1	cellular response to lipopolysaccharide	STAT1
GO:0009084	0.0461	1	BP	14791	41	17	1	glutamine family amino acid biosynthetic process	NAGS
GO:0045926	0.0462	1	BP	14791	41	124	2	negative regulation of growth	WT1; RBBP7
GO:0043933	0.0463	1	BP	14791	41	715	5	macromolecular complex subunit organization	CDH1; PEX14; GTF2I; NAP1L1; YWHAB
GO:0019216	0.0475	1	BP	14791	41	126	2	regulation of lipid metabolic process	NFKB1; PPARA
GO:0002237	0.0475	1	BP	14791	41	126	2	response to molecule of bacterial origin	STAT1; B2M
GO:0001912	0.0487	1	BP	14791	41	18	1	positive regulation of leukocyte mediated cytotoxicity	B2M
GO:0021983	0.0487	1	BP	14791	41	18	1	pituitary gland development	CDH1
GO:0002715	0.0487	1	BP	14791	41	18	1	regulation of natural killer cell mediated immunity	TAP1

GO:0033143	0.0487	1	BP	14791	41	18	1	regulation of steroid hormone receptor signaling pathway	AR
GO:0042269	0.0487	1	BP	14791	41	18	1	regulation of natural killer cell mediated cytotoxicity	TAP1
GO:0043331	0.0487	1	BP	14791	41	18	1	response to dsRNA	STAT1
GO:0046638	0.0487	1	BP	14791	41	18	1	positive regulation of alpha-beta T cell differentiation	RARA
GO:0022603	0.0487	1	BP	14791	41	297	3	regulation of anatomical structure morphogenesis	CDH1; AR; ESR1
GO:0006461	0.0488	1	BP	14791	41	500	4	protein complex assembly	CDH1; PEX14; GTF2I; YWHAB
GO:0009605	0.0488	1	BP	14791	41	500	4	response to external stimulus	RARA; USF2; USF1; STAT1
GO:0051247	0.0496	1	BP	14791	41	299	3	positive regulation of protein metabolic process	PSMB8; PSMD11; PSMD2
GO:0043234	1.60E-05	0.0023	CC	16768	43	2748	19	protein complex	PSMB8; HLA-DMA; PSMD11; CDH1; NFKB1; PEX14; EIF4A2; NDUFB10; USF1; RBBP7; NAP1L1; RBX1; PSMD2; YWHAB; TAP1; MORF4L1; ESR1; B2M; HDAC10
GO:0016585	5.90E-05	0.0086	CC	16768	43	83	4	chromatin remodeling complex	RBBP7; MORF4L1; ESR1; HDAC10
GO:0032991	6.50E-05	0.0096	CC	16768	43	3312	20	macromolecular complex	PSMB8; HLA-DMA; PSMD11; CDH1; NFKB1; SF3B5; PEX14; EIF4A2; NDUFB10; USF1; RBBP7; NAP1L1; RBX1; PSMD2; YWHAB; TAP1; MORF4L1; ESR1; B2M; HDAC10
GO:0044424	1.50E-04	0.0219	CC	16768	43	####	39	intracellular part	PSMB8; STAT6; HLA-DMA; RARA; PSMD11; SLC35A1; CDH1; NFKB1; UBD; USF2; GCC2; SF3B5; NAGS; PEX14; EIF4A2; ANXA4; HOXD9; WT1; NDUFB10; GTF2I; USF1; PPARA; TMSB10; RBBP7; NAP1L1; RBX1; STAT1; PSMD2; YWHAB; TAP1; AR; UGT2B4; MORF4L1; ESR1; SLC39A6; B2M; ALG2; HDAC10; SPI1
GO:0000118	2.00E-04	0.0301	CC	16768	43	45	3	histone deacetylase complex	RBBP7; MORF4L1; HDAC10
GO:0043229	2.50E-04	0.0369	CC	16768	43	8759	34	intracellular organelle	PSMB8; STAT6; HLA-DMA; RARA; SLC35A1; CDH1; NFKB1; UBD; USF2; GCC2; SF3B5; NAGS; PEX14; HOXD9; WT1; NDUFB10; GTF2I; USF1; PPARA; TMSB10; RBBP7; NAP1L1; RBX1; STAT1; YWHAB; TAP1; AR; UGT2B4; MORF4L1; ESR1; SLC39A6; ALG2; HDAC10; SPI1
GO:0043226	2.60E-04	0.0384	CC	16768	43	8773	34	organelle	PSMB8; STAT6; HLA-DMA; RARA; SLC35A1; CDH1; NFKB1; UBD; USF2; GCC2; SF3B5; NAGS; PEX14; HOXD9; WT1; NDUFB10; GTF2I; USF1; PPARA; TMSB10; RBBP7; NAP1L1; RBX1; STAT1; YWHAB; TAP1; AR; UGT2B4; MORF4L1; ESR1; SLC39A6; ALG2; HDAC10; SPI1
GO:0043231	3.20E-04	0.0478	CC	16768	43	7996	32	intracellular membrane-bounded organelle	PSMB8; STAT6; HLA-DMA; RARA; SLC35A1; NFKB1; UBD; USF2; GCC2; SF3B5; NAGS; PEX14; HOXD9; WT1; NDUFB10; GTF2I; USF1; PPARA; RBBP7; NAP1L1; RBX1; STAT1; YWHAB; TAP1; AR; UGT2B4; MORF4L1; ESR1; SLC39A6; ALG2; HDAC10; SPI1
GO:0043227	3.20E-04	0.048	CC	16768	43	7998	32	membrane-bounded organelle	PSMB8; STAT6; HLA-DMA; RARA; SLC35A1; NFKB1; UBD; USF2; GCC2; SF3B5; NAGS; PEX14; HOXD9; WT1; NDUFB10; GTF2I; USF1; PPARA; RBBP7; NAP1L1; RBX1; STAT1; YWHAB; TAP1; AR; UGT2B4; MORF4L1; ESR1; SLC39A6; ALG2; HDAC10; SPI1
GO:0005634	3.70E-04	0.055	CC	16768	43	5037	24	nucleus	PSMB8; STAT6; RARA; NFKB1; UBD; USF2; SF3B5; PEX14; HOXD9; WT1; GTF2I; USF1; PPARA; RBBP7; NAP1L1; RBX1; STAT1; YWHAB; AR; MORF4L1; ESR1; ALG2; HDAC10; SPI1
GO:0000502	4.10E-04	0.0609	CC	16768	43	57	3	proteasome complex	PSMB8; PSMD11; PSMD2
GO:0044428	0.0026	0.3876	CC	16768	43	1932	12	nuclear part	STAT6; NFKB1; SF3B5; WT1; USF1; RBBP7; NAP1L1; STAT1; YWHAB; MORF4L1; ESR1; HDAC10
GO:0044451	0.0038	0.5621	CC	16768	43	594	6	nucleoplasm part	WT1; USF1; RBBP7; YWHAB; MORF4L1; HDAC10
GO:0017053	0.0054	0.7922	CC	16768	43	43	2	transcriptional repressor complex	RBBP7; YWHAB

GO:0044446	0.0069	1	CC	16768	43	5015	21	intracellular organelle part	STAT6; HLA-DMA; SLC35A1; NFKB1; GCC2; SF3B5; NAGS; PEX14; WT1; NDUFB10; USF1; RBBP7; NAP1L1; STAT1; YWHAB; TAP1; UGT2B4; MORF4L1; ESR1; B2M; HDAC10
GO:0030891	0.0076	1	CC	16768	43	3	1	VCB complex	RBX1
GO:0042825	0.0076	1	CC	16768	43	3	1	TAP complex	TAP1
GO:0044422	0.0081	1	CC	16768	43	5082	21	organelle part	STAT6; HLA-DMA; SLC35A1; NFKB1; GCC2; SF3B5; NAGS; PEX14; WT1; NDUFB10; USF1; RBBP7; NAP1L1; STAT1; YWHAB; TAP1; UGT2B4; MORF4L1; ESR1; B2M; HDAC10
GO:0000153	0.0127	1	CC	16768	43	5	1	cytoplasmic ubiquitin ligase complex	RBX1
GO:0033256	0.0127	1	CC	16768	43	5	1	I-kappaB/NF-kappaB complex	NFKB1
GO:0043296	0.0152	1	CC	16768	43	6	1	apical junction complex	CDH1
GO:0016235	0.0178	1	CC	16768	43	7	1	aggresome	UBD
GO:0005678	0.0178	1	CC	16768	43	7	1	chromatin assembly complex	NAP1L1
GO:0016342	0.0203	1	CC	16768	43	8	1	catenin complex	CDH1
GO:0016580	0.0203	1	CC	16768	43	8	1	Sin3 complex	MORF4L1
GO:0005838	0.0203	1	CC	16768	43	8	1	proteasome regulatory particle	PSMD2
GO:0070822	0.0203	1	CC	16768	43	8	1	Sin3-type complex	MORF4L1
GO:0042470	0.0213	1	CC	16768	43	88	2	melanosome	NAP1L1; YWHAB
GO:0048770	0.0213	1	CC	16768	43	88	2	pigment granule	NAP1L2; YWHAB
GO:0016281	0.0228	1	CC	16768	43	9	1	eukaryotic translation initiation factor 4F complex	EIF4A2
GO:0035098	0.0228	1	CC	16768	43	9	1	ESC/E(Z) complex	RBBP7
GO:0019005	0.0278	1	CC	16768	43	11	1	SCF ubiquitin ligase complex	RBX1
GO:0005583	0.0278	1	CC	16768	43	11	1	fibrillar collagen	LUM
GO:0016581	0.0353	1	CC	16768	43	14	1	NuRD complex	RBBP7
GO:0035267	0.0353	1	CC	16768	43	14	1	NuA4 histone acetyltransferase complex	MORF4L1
GO:0005839	0.0353	1	CC	16768	43	14	1	proteasome core complex	PSMB8
GO:0042611	0.0367	1	CC	16768	43	118	2	MHC protein complex	HLA-DMA; B2M
GO:0043189	0.0377	1	CC	16768	43	15	1	H4/H2A histone acetyltransferase complex	MORF4L1
GO:0016328	0.0402	1	CC	16768	43	16	1	lateral plasma membrane	CDH1
GO:0043005	0.041	1	CC	16768	43	299	3	neuron projection	STAT1; AR; ESR1

GO:0030425	0.0425	1	CC	16768	43	128	2	dendrite	STAT1; AR
GO:0030424	0.0432	1	CC	16768	43	129	2	axon	STAT1; AR
GO:0016234	0.0451	1	CC	16768	43	18	1	inclusion body	UBD
GO:0030315	0.0476	1	CC	16768	43	19	1	T-tubule	ESR1
GO:0031519	0.0476	1	CC	16768	43	19	1	PcG protein complex	RBBP7
GO:0048471	0.0481	1	CC	16768	43	319	3	perinuclear region of cytoplasm	CDH1; YWHAB; ALG2
GO:0043565	3.40E-08	6.70E-06	MF	15767	40	639	12	sequence-specific DNA binding	STAT6; RARA; NFKB1; USF2; HOXD9; WT1; USF1; PPARA; STAT1; AR; ESR1; SPI1
GO:0030528	4.90E-08	9.50E-06	MF	15767	40	1518	17	transcription regulator activity	STAT6; RARA; CDH1; NFKB1; USF2; PEX14; HOXD9; WT1; GTF2I; USF1; PPARA; STAT1; YWHAB; AR; ESR1; HDAC10; SPI1
GO:0003700	4.50E-07	8.80E-05	MF	15767	40	977	13	transcription factor activity	STAT6; RARA; NFKB1; USF2; HOXD9; WT1; GTF2I; USF1; PPARA; STAT1; AR; ESR1; SPI1
GO:0003707	6.90E-06	0.0013	MF	15767	40	49	4	steroid hormone receptor activity	RARA; PPARA; AR; ESR1
GO:0016563	8.40E-06	0.0016	MF	15767	40	419	8	transcription activator activity	RARA; CDH1; USF2; HOXD9; WT1; USF1; PPARA; AR
GO:0004879	8.80E-06	0.0016	MF	15767	40	52	4	ligand-dependent nuclear receptor activity	RARA; PPARA; AR; ESR1
GO:0008134	3.80E-05	0.0074	MF	15767	40	517	8	transcription factor binding	RARA; USF2; COMMD7; PEX14; USF1; YWHAB; AR; ESR1
GO:0005515	4.10E-05	0.008	MF	15767	40	8097	33	protein binding	PSMB8; STAT6; RARA; PSMD11; CDH1; NFKB1; UBD; USF2; GCC2; COMMD7; PEX14; EIF4A2; WT1; NDUFB10; GTF2I; USF1; PPARA; TMSB10; RBBP7; LUM; NAP1L1; RBX1; STAT1; PSMD2; YWHAB; TAP1; AR; MORF4L1; ESR1; B2M; ALG2; HDAC10; SPI1
GO:0042826	1.50E-04	0.0291	MF	15767	40	41	3	histone deacetylase binding	USF1; YWHAB; HDAC10
GO:0043425	1.70E-04	0.0335	MF	15767	40	8	2	bHLH transcription factor binding	USF2; USF1
GO:0010843	1.70E-04	0.0337	MF	15767	40	111	4	promoter binding	NFKB1; WT1; AR; ESR1
GO:0044212	2.00E-04	0.0386	MF	15767	40	115	4	DNA regulatory region binding	NFKB1; WT1; AR; ESR1
GO:0003702	3.20E-04	0.0632	MF	15767	40	239	5	RNA polymerase II transcription factor activity	USF2; HOXD9; GTF2I; USF1; PPARA
GO:0019904	3.70E-04	0.0717	MF	15767	40	382	6	protein domain specific binding	RARA; CDH1; WT1; PPARA; YWHAB; AR
GO:0047485	9.00E-04	0.1737	MF	15767	40	75	3	protein N-terminus binding	PEX14; MORF4L1; ALG2
GO:0016564	0.0013	0.2676	MF	15767	40	329	5	transcription repressor activity	RARA; PEX14; WT1; YWHAB; HDAC10
GO:0046982	0.0015	0.3043	MF	15767	40	199	4	protein heterodimerization activity	USF2; USF1; TAP1; ALG2
GO:0003690	0.0021	0.4212	MF	15767	40	102	3	double-stranded DNA binding	USF2; WT1; USF1
GO:0034056	0.0025	0.4896	MF	15767	40	1	1	estrogen response element binding	ESR1

GO:0003991	0.0025	0.4896	MF	15767	40	1	1	acetylglutamate kinase activity	NAGS
GO:0004042	0.0025	0.4896	MF	15767	40	1	1	acetyl-CoA:L-glutamate N-acetyltransferase activity	NAGS
GO:0005456	0.0025	0.4896	MF	15767	40	1	1	CMP-sialic acid transmembrane transporter activity	SLC35A1
GO:0070974	0.0025	0.4896	MF	15767	40	1	1	POU domain binding	AR
GO:0008289	0.0036	0.6966	MF	15767	40	410	5	lipid binding	RARA; ANXA4; PPARA; AR; ESR1
GO:0016566	0.0041	0.8036	MF	15767	40	38	2	specific transcriptional repressor activity	WT1; HDAC10
GO:0035326	0.0043	0.8457	MF	15767	40	39	2	enhancer binding	USF2; USF1
GO:0003705	0.0043	0.8457	MF	15767	40	39	2	RNA polymerase II transcription factor activity, enhancer binding	USF2; USF1
GO:0003677	0.0044	0.8539	MF	15767	40	2375	13	DNA binding	STAT6; RARA; NFKB1; USF2; HOXD9; WT1; GTF2I; USF1; PPARA; STAT1; AR; ESR1; SPI1
GO:0008013	0.0046	0.8888	MF	15767	40	40	2	beta-catenin binding	CDH1; AR
GO:0030284	0.005	0.978	MF	15767	40	2	1	estrogen receptor activity	ESR1
GO:0046979	0.005	0.978	MF	15767	40	2	1	TAP2 binding	TAP1
GO:0004882	0.005	0.978	MF	15767	40	2	1	androgen receptor activity	AR
GO:0003714	0.0057	1	MF	15767	40	144	3	transcription corepressor activity	RARA; PEX14; YWHAB
GO:0043566	0.0065	1	MF	15767	40	151	3	structure-specific DNA binding	USF2; WT1; USF1
GO:0000033	0.0075	1	MF	15767	40	3	1	alpha-1,3-mannosyltransferase activity	ALG2
GO:0043495	0.0075	1	MF	15767	40	3	1	protein anchor	ALG2
GO:0046977	0.0075	1	MF	15767	40	3	1	TAP binding	TAP1
GO:0046978	0.0075	1	MF	15767	40	3	1	TAP1 binding	TAP1
GO:0042562	0.0076	1	MF	15767	40	52	2	hormone binding	AR; ESR1
GO:0016774	0.0101	1	MF	15767	40	4	1	phosphotransferase activity, carboxyl group as acceptor	NAGS
GO:0019788	0.0101	1	MF	15767	40	4	1	NEDD8 ligase activity	RBX1
GO:0050815	0.0101	1	MF	15767	40	4	1	phosphoserine binding	YWHAB
GO:0005497	0.0101	1	MF	15767	40	4	1	androgen binding	AR
GO:0005496	0.0114	1	MF	15767	40	64	2	steroid binding	AR; ESR1
GO:0042153	0.0126	1	MF	15767	40	5	1	RPTP-like protein binding	CDH1

		GO:0046983	0.0133	1	MF	15767	40	563	5	protein dimerization activity	USF2; USF1; TAP1; AR; ALG2
		GO:0015165	0.0151	1	MF	15767	40	6	1	pyrimidine nucleotide sugar transmembrane transporter activity	SLC35A1
		GO:0030235	0.0151	1	MF	15767	40	6	1	nitric-oxide synthase regulator activity	ESR1
		GO:0003708	0.0151	1	MF	15767	40	6	1	retinoic acid receptor activity	RARA
		GO:0005062	0.0151	1	MF	15767	40	6	1	hematopoietin/interferon-class (D200-domain) cytokine receptor signal transduction activity	STAT1
		GO:0001972	0.0176	1	MF	15767	40	7	1	retinoic acid binding	RARA
		GO:0070628	0.0176	1	MF	15767	40	7	1	proteasome binding	UBD
		GO:0005338	0.0201	1	MF	15767	40	8	1	nucleotide-sugar transmembrane transporter activity	SLC35A1
		GO:0070742	0.0201	1	MF	15767	40	8	1	C2H2 zinc finger domain binding	WT1
		GO:0003706	0.0226	1	MF	15767	40	9	1	ligand-regulated transcription factor activity	PPARA
		GO:0005351	0.0226	1	MF	15767	40	9	1	sugar:hydrogen symporter activity	SLC35A1
		GO:0005402	0.0226	1	MF	15767	40	9	1	cation:sugar symporter activity	SLC35A1
		GO:0032403	0.0234	1	MF	15767	40	243	3	protein complex binding	UBD; YWHAB; ESR1
		GO:0015197	0.025	1	MF	15767	40	10	1	peptide transporter activity	TAP1
		GO:0045295	0.0275	1	MF	15767	40	11	1	gamma-catenin binding	CDH1
		GO:0003676	0.0313	1	MF	15767	40	3348	14	nucleic acid binding	STAT6; RARA; NFKB1; USF2; EIF4A2; HOXD9; WT1; GTF2I; USF1; PPARA; STAT1; AR; ESR1; SPI1
		GO:0004859	0.0324	1	MF	15767	40	13	1	phospholipase inhibitor activity	ANXA4
		GO:0045309	0.0374	1	MF	15767	40	15	1	protein phosphorylated amino acid binding	YWHAB
		GO:0000030	0.0398	1	MF	15767	40	16	1	mannosyltransferase activity	ALG2
		GO:0042605	0.0398	1	MF	15767	40	16	1	peptide antigen binding	TAP1
		GO:0004407	0.0398	1	MF	15767	40	16	1	histone deacetylase activity	HDAC10
		GO:0055102	0.0398	1	MF	15767	40	16	1	lipase inhibitor activity	ANXA4
		GO:0015295	0.0422	1	MF	15767	40	17	1	solute:hydrogen symporter activity	SLC35A1
		GO:0033558	0.0422	1	MF	15767	40	17	1	protein deacetylase activity	HDAC10
		GO:0051059	0.0422	1	MF	15767	40	17	1	NF-kappaB binding	COMMD7
		GO:0043531	0.0471	1	MF	15767	40	19	1	ADP binding	TAP1
		GO:0019213	0.0495	1	MF	15767	40	20	1	deacetylase activity	HDAC10

Identified DNB of B-cell lymphomagenesis

Sample Name	Members Of DNB	GO: Term	P-value	Corrected P-value		R	T	G	O	Term Name	Contain Genes
B Cell Lymphomas	STRAP; LYAR; TCP1; 1110038D17RIK; 1500011H22RIK; ENOPH1; GRSF1; IFT57; EIF4A3; TOPBP1; EIF1AX; DHFR; LOC100047898; GPX1; AIFM1; PHF1; WDR45; RGS14; YPEL5; LOC100044266; SP1; E2F	GO:0044237	9.60E-06	0.0036	BP	32911	17	5339	11	cellular metabolic process	EIF1AX; DHFR; AIFM1; PHF1; GPX1; TOPBP1; ENOPH1; IFT57; TCP1; SP1; STRAP
		GO:0044238	1.40E-05	0.0056	BP	32911	17	5580	11	primary metabolic process	EIF1AX; DHFR; AIFM1; PHF1; GPX1; TOPBP1; ENOPH1; IFT57; TCP1; SP1; STRAP
		GO:0044260	4.30E-05	0.0161	BP	32911	17	3875	9	cellular macromolecule metabolic process	EIF1AX; AIFM1; PHF1; GPX1; TOPBP1; IFT57; TCP1; SP1; STRAP
		GO:0034641	4.60E-05	0.0174	BP	32911	17	2937	8	cellular nitrogen compound metabolic process	DHFR; AIFM1; PHF1; TOPBP1; ENOPH1; IFT57; SP1; STRAP
		GO:0006807	5.70E-05	0.0214	BP	32911	17	3023	8	nitrogen compound metabolic process	DHFR; AIFM1; PHF1; TOPBP1; ENOPH1; IFT57; SP1; STRAP
		GO:0008152	6.10E-05	0.0231	BP	32911	17	6447	11	metabolic process	EIF1AX; DHFR; AIFM1; PHF1; GPX1; TOPBP1; ENOPH1; IFT57; TCP1; SP1; STRAP
		GO:0043170	1.10E-04	0.0444	BP	32911	17	4397	9	macromolecule metabolic process	EIF1AX; AIFM1; PHF1; GPX1; TOPBP1; IFT57; TCP1; SP1; STRAP
		GO:0009987	1.90E-04	0.0718	BP	32911	17	8758	12	cellular process	EIF1AX; DHFR; AIFM1; PHF1; GPX1; TOPBP1; ENOPH1; IFT57; TCP1; RGS14; SP1; STRAP
		GO:0008652	2.10E-04	0.0803	BP	32911	17	42	2	cellular amino acid biosynthetic process	DHFR; ENOPH1
		GO:0006139	2.30E-04	0.0883	BP	32911	17	2708	7	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	DHFR; AIFM1; PHF1; TOPBP1; IFT57; SP1; STRAP
		GO:0006519	4.80E-04	0.1812	BP	32911	17	304	3	cellular amino acid and derivative metabolic process	DHFR; GPX1; ENOPH1
		GO:0018158	5.10E-04	0.1942	BP	32911	17	1	1	protein amino acid oxidation	GPX1
		GO:0030263	5.10E-04	0.1942	BP	32911	17	1	1	apoptotic chromosome condensation	AIFM1
		GO:0031427	5.10E-04	0.1942	BP	32911	17	1	1	response to methotrexate	DHFR
		GO:0046452	5.10E-04	0.1942	BP	32911	17	1	1	dihydrofolate metabolic process	DHFR
		GO:0006982	5.10E-04	0.1942	BP	32911	17	1	1	response to lipid hydroperoxide	GPX1
		GO:0009309	5.90E-04	0.2233	BP	32911	17	70	2	amine biosynthetic process	DHFR; ENOPH1
		GO:0090304	7.60E-04	0.2891	BP	32911	17	2322	6	nucleic acid metabolic process	AIFM1; PHF1; TOPBP1; IFT57; SP1; STRAP
		GO:0019509	0.001	0.3883	BP	32911	17	2	1	L-methionine salvage from methylthioadenosine	ENOPH1
		GO:0043102	0.001	0.3883	BP	32911	17	2	1	amino acid salvage	ENOPH1
		GO:0071265	0.001	0.3883	BP	32911	17	2	1	L-methionine biosynthetic process	ENOPH1
		GO:0071267	0.001	0.3883	BP	32911	17	2	1	L-methionine salvage	ENOPH1
		GO:0009608	0.001	0.3883	BP	32911	17	2	1	response to symbiont	GPX1
		GO:0009609	0.001	0.3883	BP	32911	17	2	1	response to symbiotic bacterium	GPX1
		GO:0006790	0.0012	0.4627	BP	32911	17	101	2	sulfur metabolic process	GPX1; ENOPH1
		GO:0044249	0.0013	0.5233	BP	32911	17	2599	6	cellular biosynthetic process	EIF1AX; DHFR; PHF1; ENOPH1; IFT57; SP1
		GO:0030219	0.0015	0.5823	BP	32911	17	3	1	megakaryocyte differentiation	SP1
		GO:0046654	0.0015	0.5823	BP	32911	17	3	1	tetrahydrofolate biosynthetic process	DHFR
		GO:0060055	0.0015	0.5823	BP	32911	17	3	1	angiogenesis involved in wound healing	GPX1
		GO:0006915	0.0016	0.6069	BP	32911	17	462	3	apoptosis	AIFM1; GPX1; IFT57

GO:0009058	0.0016	0.6333	BP	32911	17	2696	6	biosynthetic process	EIF1AX; DHFR; PHF1; ENOPH1; IFT57; SP1
GO:0012501	0.0016	0.6374	BP	32911	17	470	3	programmed cell death	AIFM1; GPX1; IFT57
GO:0003015	0.002	0.7763	BP	32911	17	4	1	heart process	GPX1
GO:0033194	0.002	0.7763	BP	32911	17	4	1	response to hydroperoxide	GPX1
GO:0051450	0.002	0.7763	BP	32911	17	4	1	myoblast proliferation	GPX1
GO:0060047	0.002	0.7763	BP	32911	17	4	1	heart contraction	GPX1
GO:0006545	0.002	0.7763	BP	32911	17	4	1	glycine biosynthetic process	DHFR
GO:0008219	0.0022	0.8317	BP	32911	17	516	3	cell death	AIFM1; GPX1; IFT57
GO:0016265	0.0023	0.883	BP	32911	17	527	3	death	AIFM1; GPX1; IFT57
GO:0001885	0.0025	0.9701	BP	32911	17	5	1	endothelial cell development	GPX1
GO:0009410	0.0025	0.9701	BP	32911	17	5	1	response to xenobiotic stimulus	GPX1
GO:0016053	0.0027	1	BP	32911	17	151	2	organic acid biosynthetic process	DHFR; ENOPH1
GO:0046394	0.0027	1	BP	32911	17	151	2	carboxylic acid biosynthetic process	DHFR; ENOPH1
GO:0043094	0.003	1	BP	32911	17	6	1	cellular metabolic compound salvage	ENOPH1
GO:0043353	0.003	1	BP	32911	17	6	1	enucleate erythrocyte differentiation	SP1
GO:0043534	0.003	1	BP	32911	17	6	1	blood vessel endothelial cell migration	GPX1
GO:0008631	0.003	1	BP	32911	17	6	1	induction of apoptosis by oxidative stress	GPX1
GO:0006732	0.0034	1	BP	32911	17	171	2	coenzyme metabolic process	DHFR; GPX1
GO:0009396	0.0036	1	BP	32911	17	7	1	folic acid and derivative biosynthetic process	DHFR
GO:0035466	0.0036	1	BP	32911	17	614	3	regulation of signaling pathway	GPX1; RGS14; STRAP
GO:0006520	0.0039	1	BP	32911	17	183	2	cellular amino acid metabolic process	DHFR; ENOPH1
GO:0055114	0.004	1	BP	32911	17	637	3	oxidation reduction	DHFR; AIFM1; GPX1
GO:0043403	0.0041	1	BP	32911	17	8	1	skeletal muscle tissue regeneration	GPX1
GO:0046653	0.0041	1	BP	32911	17	8	1	tetrahydrofolate metabolic process	DHFR
GO:0048596	0.0041	1	BP	32911	17	8	1	embryonic camera-type eye morphogenesis	SP1
GO:0051702	0.0041	1	BP	32911	17	8	1	interaction with symbiont	GPX1
GO:0060136	0.0041	1	BP	32911	17	8	1	embryonic process involved in female pregnancy	SP1
GO:0007131	0.0041	1	BP	32911	17	8	1	reciprocal meiotic recombination	TOPBP1
GO:0014902	0.0046	1	BP	32911	17	9	1	myotube differentiation	GPX1
GO:0051897	0.0046	1	BP	32911	17	9	1	positive regulation of protein kinase B signaling cascade	GPX1
GO:0060216	0.0046	1	BP	32911	17	9	1	definitive hemopoiesis	SP1

GO:0009086	0.0046	1	BP	32911	17	9	1	methionine biosynthetic process	ENOPH1
GO:0051186	0.005	1	BP	32911	17	208	2	cofactor metabolic process	DHFR; GPX1
GO:0006309	0.0051	1	BP	32911	17	10	1	DNA fragmentation involved in apoptotic nuclear change	AIFM1
GO:0006555	0.0051	1	BP	32911	17	10	1	methionine metabolic process	ENOPH1
GO:0000737	0.0051	1	BP	32911	17	10	1	DNA catabolic process, endonucleolytic	AIFM1
GO:0009070	0.0051	1	BP	32911	17	10	1	serine family amino acid biosynthetic process	DHFR
GO:0002862	0.0056	1	BP	32911	17	11	1	negative regulation of inflammatory response to antigenic stimulus	GPX1
GO:0043542	0.0056	1	BP	32911	17	11	1	endothelial cell migration	GPX1
GO:0000097	0.0056	1	BP	32911	17	11	1	sulfur amino acid biosynthetic process	ENOPH1
GO:0001829	0.0066	1	BP	32911	17	13	1	trophectodermal cell differentiation	SP1
GO:0042744	0.0066	1	BP	32911	17	13	1	hydrogen peroxide catabolic process	GPX1
GO:0048741	0.0066	1	BP	32911	17	13	1	skeletal muscle fiber development	GPX1
GO:0006544	0.0066	1	BP	32911	17	13	1	glycine metabolic process	DHFR
GO:0010648	0.007	1	BP	32911	17	246	2	negative regulation of cell communication	RGS14; STRAP
GO:0042246	0.0072	1	BP	32911	17	14	1	tissue regeneration	GPX1
GO:0048048	0.0072	1	BP	32911	17	14	1	embryonic eye morphogenesis	SP1
GO:0006308	0.0072	1	BP	32911	17	14	1	DNA catabolic process	AIFM1
GO:0006760	0.0072	1	BP	32911	17	14	1	folic acid and derivative metabolic process	DHFR
GO:0044106	0.0073	1	BP	32911	17	251	2	cellular amine metabolic process	DHFR; ENOPH1
GO:0002064	0.0077	1	BP	32911	17	15	1	epithelial cell development	GPX1
GO:0042559	0.0077	1	BP	32911	17	15	1	pteridine and derivative biosynthetic process	DHFR
GO:0051402	0.0077	1	BP	32911	17	15	1	neuron apoptosis	AIFM1
GO:0051896	0.0077	1	BP	32911	17	15	1	regulation of protein kinase B signaling cascade	GPX1
GO:0009067	0.0077	1	BP	32911	17	15	1	aspartate family amino acid biosynthetic process	ENOPH1
GO:0010646	0.0081	1	BP	32911	17	824	3	regulation of cell communication	GPX1; RGS14; STRAP
GO:0070997	0.0082	1	BP	32911	17	16	1	neuron death	AIFM1
GO:0090305	0.0082	1	BP	32911	17	16	1	nucleic acid phosphodiester bond hydrolysis	AIFM1
GO:0010332	0.0087	1	BP	32911	17	17	1	response to gamma radiation	GPX1
GO:0019438	0.0087	1	BP	32911	17	17	1	aromatic compound biosynthetic process	DHFR
GO:0030261	0.0087	1	BP	32911	17	17	1	chromosome condensation	AIFM1
GO:0030512	0.0087	1	BP	32911	17	17	1	negative regulation of transforming growth factor beta receptor	STRAP

GO:0070301	0.0087	1	BP	32911	17	17	1	cellular response to hydrogen peroxide	GPX1
GO:0000096	0.0092	1	BP	32911	17	18	1	sulfur amino acid metabolic process	ENOPH1
GO:0044271	0.0098	1	BP	32911	17	294	2	cellular nitrogen compound biosynthetic process	DHFR; ENOPH1
GO:0009653	0.0101	1	BP	32911	17	893	3	anatomical structure morphogenesis	GPX1; SP1; GRSF1
GO:0042311	0.0102	1	BP	32911	17	20	1	vasodilation	GPX1
GO:0034614	0.0107	1	BP	32911	17	21	1	cellular response to reactive oxygen species	GPX1
GO:0009066	0.0107	1	BP	32911	17	21	1	aspartate family amino acid metabolic process	ENOPH1
GO:0001892	0.0113	1	BP	32911	17	22	1	embryonic placenta development	SP1
GO:0006323	0.0113	1	BP	32911	17	22	1	DNA packaging	AIFM1
GO:0009069	0.0113	1	BP	32911	17	22	1	serine family amino acid metabolic process	DHFR
GO:0042558	0.0118	1	BP	32911	17	23	1	pteridine and derivative metabolic process	DHFR
GO:0042743	0.0118	1	BP	32911	17	23	1	hydrogen peroxide metabolic process	GPX1
GO:0048747	0.0118	1	BP	32911	17	23	1	muscle fiber development	GPX1
GO:0001659	0.0123	1	BP	32911	17	24	1	temperature homeostasis	GPX1
GO:0055002	0.0123	1	BP	32911	17	24	1	striated muscle cell development	GPX1
GO:0006752	0.0123	1	BP	32911	17	24	1	group transfer coenzyme metabolic process	DHFR
GO:0009308	0.0124	1	BP	32911	17	332	2	amine metabolic process	DHFR; ENOPH1
GO:0002861	0.0133	1	BP	32911	17	26	1	regulation of inflammatory response to antigenic stimulus	GPX1
GO:0006996	0.0137	1	BP	32911	17	997	3	organelle organization	AIFM1; PHF1; RGS14
GO:0006919	0.0138	1	BP	32911	17	27	1	activation of caspase activity	IFT57
GO:0008637	0.0138	1	BP	32911	17	27	1	apoptotic mitochondrial changes	AIFM1
GO:0017015	0.0143	1	BP	32911	17	28	1	regulation of transforming growth factor beta receptor	STRAP
GO:0034599	0.0143	1	BP	32911	17	28	1	cellular response to oxidative stress	GPX1
GO:0048871	0.0143	1	BP	32911	17	28	1	multicellular organismal homeostasis	GPX1
GO:0051276	0.0144	1	BP	32911	17	359	2	chromosome organization	AIFM1; PHF1
GO:0051146	0.0148	1	BP	32911	17	29	1	striated muscle cell differentiation	GPX1
GO:0006413	0.0148	1	BP	32911	17	29	1	translational initiation	EIF1AX
GO:0048598	0.0149	1	BP	32911	17	365	2	embryonic morphogenesis	SP1; GRSF1
GO:0006749	0.0153	1	BP	32911	17	30	1	glutathione metabolic process	GPX1
GO:0022402	0.0158	1	BP	32911	17	376	2	cell cycle process	TOPBP1; RGS14
GO:0048706	0.0158	1	BP	32911	17	31	1	embryonic skeletal system development	SP1

GO:0008277	0.0158	1	BP	32911	17	31	1	regulation of G-protein coupled receptor protein signaling pathway	RGS14
GO:0034645	0.0159	1	BP	32911	17	1960	4	cellular macromolecule biosynthetic process	EIF1AX; PHF1; IFT57; SP1
GO:0009059	0.0163	1	BP	32911	17	1974	4	macromolecule biosynthetic process	EIF1AX; PHF1; IFT57; SP1
GO:0045449	0.0164	1	BP	32911	17	1978	4	regulation of transcription	PHF1; IFT57; SP1; STRAP
GO:0006259	0.0168	1	BP	32911	17	389	2	DNA metabolic process	AIFM1; TOPBP1
GO:0010212	0.0169	1	BP	32911	17	33	1	response to ionizing radiation	GPX1
GO:0030218	0.0169	1	BP	32911	17	33	1	erythrocyte differentiation	SP1
GO:0044419	0.0169	1	BP	32911	17	33	1	interspecies interaction between organisms	GPX1
GO:0071103	0.0169	1	BP	32911	17	33	1	DNA conformation change	AIFM1
GO:0031099	0.0174	1	BP	32911	17	34	1	regeneration	GPX1
GO:0055001	0.0174	1	BP	32911	17	34	1	muscle cell development	GPX1
GO:0008629	0.0174	1	BP	32911	17	34	1	induction of apoptosis by intracellular signals	GPX1
GO:0043280	0.0179	1	BP	32911	17	35	1	positive regulation of caspase activity	IFT57
GO:0019222	0.0183	1	BP	32911	17	3142	5	regulation of metabolic process	PHF1; IFT57; RGS14; SP1; STRAP
GO:0044272	0.0184	1	BP	32911	17	36	1	sulfur compound biosynthetic process	ENOPH1
GO:0090101	0.0184	1	BP	32911	17	36	1	negative regulation of transmembrane receptor protein serine/threonine	STRAP
GO:0042542	0.0189	1	BP	32911	17	37	1	response to hydrogen peroxide	GPX1
GO:0050728	0.0189	1	BP	32911	17	37	1	negative regulation of inflammatory response	GPX1
GO:0044283	0.0192	1	BP	32911	17	417	2	small molecule biosynthetic process	DHFR; ENOPH1
GO:0033554	0.0193	1	BP	32911	17	419	2	cellular response to stress	GPX1; TOPBP1
GO:0048592	0.0194	1	BP	32911	17	38	1	eye morphogenesis	SP1
GO:0050777	0.0204	1	BP	32911	17	40	1	negative regulation of immune response	GPX1
GO:0006641	0.0204	1	BP	32911	17	40	1	triglyceride metabolic process	GPX1
GO:0009636	0.0214	1	BP	32911	17	42	1	response to toxin	GPX1
GO:0010556	0.0223	1	BP	32911	17	2166	4	regulation of macromolecule biosynthetic process	PHF1; IFT57; SP1; STRAP
GO:0010952	0.0224	1	BP	32911	17	44	1	positive regulation of peptidase activity	IFT57
GO:0050880	0.0224	1	BP	32911	17	44	1	regulation of blood vessel size	GPX1
GO:0006800	0.0224	1	BP	32911	17	44	1	oxygen and reactive oxygen species metabolic process	GPX1
GO:0035150	0.0229	1	BP	32911	17	45	1	regulation of tube size	GPX1
GO:0009966	0.0232	1	BP	32911	17	462	2	regulation of signal transduction	GPX1; RGS14
GO:0006518	0.0235	1	BP	32911	17	46	1	peptide metabolic process	GPX1

GO:0031348	0.024	1	BP	32911	17	47	1	negative regulation of defense response	GPX1
GO:0006639	0.024	1	BP	32911	17	47	1	acylglycerol metabolic process	GPX1
GO:0023051	0.024	1	BP	32911	17	470	2	regulation of signaling process	GPX1; RGS14
GO:0019219	0.0244	1	BP	32911	17	2226	4	regulation of nucleobase, nucleoside, nucleotide and nucleic	PHF1; IFT57; SP1; STRAP
GO:0001889	0.0245	1	BP	32911	17	48	1	liver development	SP1
GO:0010468	0.0245	1	BP	32911	17	2231	4	regulation of gene expression	PHF1; IFT57; SP1; STRAP
GO:0003018	0.025	1	BP	32911	17	49	1	vascular process in circulatory system	GPX1
GO:0006638	0.025	1	BP	32911	17	49	1	neutral lipid metabolic process	GPX1
GO:0006662	0.025	1	BP	32911	17	49	1	glycerol ether metabolic process	GPX1
GO:0051171	0.0253	1	BP	32911	17	2253	4	regulation of nitrogen compound metabolic process	PHF1; IFT57; SP1; STRAP
GO:0000302	0.0255	1	BP	32911	17	50	1	response to reactive oxygen species	GPX1
GO:0031326	0.0263	1	BP	32911	17	2279	4	regulation of cellular biosynthetic process	PHF1; IFT57; SP1; STRAP
GO:0018904	0.0265	1	BP	32911	17	52	1	organic ether metabolic process	GPX1
GO:0042692	0.027	1	BP	32911	17	53	1	muscle cell differentiation	GPX1
GO:0009889	0.0271	1	BP	32911	17	2301	4	regulation of biosynthetic process	PHF1; IFT57; SP1; STRAP
GO:0018130	0.0275	1	BP	32911	17	54	1	heterocycle biosynthetic process	DHFR
GO:0019752	0.0291	1	BP	32911	17	522	2	carboxylic acid metabolic process	DHFR; ENOPH1
GO:0043436	0.0291	1	BP	32911	17	522	2	oxoacid metabolic process	DHFR; ENOPH1
GO:0006082	0.0292	1	BP	32911	17	523	2	organic acid metabolic process	DHFR; ENOPH1
GO:0003013	0.0295	1	BP	32911	17	58	1	circulatory system process	GPX1
GO:0045454	0.0295	1	BP	32911	17	58	1	cell redox homeostasis	AIFM1
GO:0044281	0.03	1	BP	32911	17	1343	3	small molecule metabolic process	DHFR; GPX1; ENOPH1
GO:0043281	0.0305	1	BP	32911	17	60	1	regulation of caspase activity	IFT57
GO:0090092	0.0305	1	BP	32911	17	60	1	regulation of transmembrane receptor protein serine/threonine	STRAP
GO:0050794	0.0306	1	BP	32911	17	6318	7	regulation of cellular process	AIFM1; PHF1; GPX1; IFT57; RGS14; SP1; STRAP
GO:0042180	0.0306	1	BP	32911	17	536	2	cellular ketone metabolic process	DHFR; ENOPH1
GO:0032102	0.031	1	BP	32911	17	61	1	negative regulation of response to external stimulus	GPX1
GO:0045444	0.0325	1	BP	32911	17	64	1	fat cell differentiation	GPX1
GO:0009108	0.034	1	BP	32911	17	67	1	coenzyme biosynthetic process	DHFR
GO:0006310	0.0355	1	BP	32911	17	70	1	DNA recombination	TOPBP1
GO:0048523	0.0366	1	BP	32911	17	1452	3	negative regulation of cellular process	GPX1; RGS14; STRAP

GO:0044248	0.0367	1	BP	32911	17	592	2	cellular catabolic process	AIFM1; GPX1
GO:0060255	0.0369	1	BP	32911	17	2531	4	regulation of macromolecule metabolic process	PHF1; IFT57; SP1; STRAP
GO:0030097	0.037	1	BP	32911	17	73	1	hemopoiesis	SP1
GO:0048568	0.038	1	BP	32911	17	75	1	embryonic organ development	SP1
GO:0042592	0.0395	1	BP	32911	17	616	2	homeostatic process	AIFM1; GPX1
GO:0001503	0.04	1	BP	32911	17	79	1	ossification	SP1
GO:0030099	0.04	1	BP	32911	17	79	1	myeloid cell differentiation	SP1
GO:0007005	0.041	1	BP	32911	17	81	1	mitochondrion organization	AIFM1
GO:0080090	0.0414	1	BP	32911	17	2625	4	regulation of primary metabolic process	PHF1; IFT57; SP1; STRAP
GO:0052548	0.042	1	BP	32911	17	83	1	regulation of endopeptidase activity	IFT57
GO:0050789	0.042	1	BP	32911	17	6733	7	regulation of biological process	AIFM1; PHF1; GPX1; IFT57; RGS14; SP1; STRAP
GO:0014070	0.0425	1	BP	32911	17	84	1	response to organic cyclic substance	DHFR
GO:0051716	0.0429	1	BP	32911	17	645	2	cellular response to stimulus	GPX1; TOPBP1
GO:0030324	0.043	1	BP	32911	17	85	1	lung development	SP1
GO:0009968	0.0435	1	BP	32911	17	86	1	negative regulation of signal transduction	RGS14
GO:0044267	0.0436	1	BP	32911	17	1556	3	cellular protein metabolic process	EIF1AX; GPX1; TCP1
GO:0042981	0.0439	1	BP	32911	17	653	2	regulation of apoptosis	GPX1; IFT57
GO:0023057	0.044	1	BP	32911	17	87	1	negative regulation of signaling process	RGS14
GO:0006350	0.044	1	BP	32911	17	1561	3	transcription	PHF1; IFT57; SP1
GO:0002683	0.045	1	BP	32911	17	89	1	negative regulation of immune system process	GPX1
GO:0043067	0.045	1	BP	32911	17	662	2	regulation of programmed cell death	GPX1; IFT57
GO:0052547	0.0454	1	BP	32911	17	90	1	regulation of peptidase activity	IFT57
GO:0010941	0.0466	1	BP	32911	17	675	2	regulation of cell death	GPX1; IFT57
GO:0006357	0.0468	1	BP	32911	17	677	2	regulation of transcription from RNA polymerase II promoter	SP1; STRAP
GO:0048589	0.0469	1	BP	32911	17	93	1	developmental growth	GPX1
GO:0051188	0.0469	1	BP	32911	17	93	1	cofactor biosynthetic process	DHFR
GO:0031323	0.0479	1	BP	32911	17	2749	4	regulation of cellular metabolic process	PHF1; IFT57; SP1; STRAP
GO:0048562	0.0484	1	BP	32911	17	96	1	embryonic organ morphogenesis	SP1
GO:0007605	0.0489	1	BP	32911	17	97	1	sensory perception of sound	GPX1
GO:0016331	0.0494	1	BP	32911	17	98	1	morphogenesis of embryonic epithelium	GRSF1
GO:0048519	0.0495	1	BP	32911	17	1637	3	negative regulation of biological process	GPX1; RGS14; STRAP

GO:0001501	0.0499	1	BP	32911	17	99	1	skeletal system development	SP1
GO:0005737	7.20E-05	0.0047	CC	33355	18	3897	9	cytoplasm	AIFM1; GPX1; TOPBP1; ENOPH1; IFT57; TCP1; SP1; STRAP; GRSF1
GO:0043229	1.20E-04	0.0081	CC	33355	18	7865	12	intracellular organelle	AIFM1; PHF1; GPX1; TOPBP1; ENOPH1; IFT57; TCP1; RGS14; SP1; STRAP; GRSF1; LYAR
GO:0043226	1.20E-04	0.0083	CC	33355	18	7883	12	organelle	AIFM1; PHF1; GPX1; TOPBP1; ENOPH1; IFT57; TCP1; RGS14; SP1; STRAP; GRSF1; LYAR
GO:0005634	1.40E-04	0.0092	CC	33355	18	4243	9	nucleus	AIFM1; PHF1; GPX1; TOPBP1; ENOPH1; RGS14; SP1; STRAP; LYAR
GO:0043231	3.00E-04	0.0195	CC	33355	18	7142	11	intracellular membrane-bounded organelle	AIFM1; PHF1; GPX1; TOPBP1; ENOPH1; IFT57; RGS14; SP1; STRAP; GRSF1; LYAR
GO:0043227	3.00E-04	0.0196	CC	33355	18	7147	11	membrane-bounded organelle	AIFM1; PHF1; GPX1; TOPBP1; ENOPH1; IFT57; RGS14; SP1; STRAP; GRSF1; LYAR
GO:0005625	6.00E-04	0.0391	CC	33355	18	313	3	soluble fraction	DHFR; AIFM1; GPX1
GO:0005815	8.40E-04	0.0551	CC	33355	18	80	2	microtubule organizing center	IFT57; TCP1
GO:0044424	0.0011	0.0738	CC	33355	18	9777	12	intracellular part	AIFM1; PHF1; GPX1; TOPBP1; ENOPH1; IFT57; TCP1; RGS14; SP1; STRAP; GRSF1; LYAR
GO:0044446	0.0021	0.1398	CC	33355	18	2685	6	intracellular organelle part	AIFM1; TOPBP1; IFT57; TCP1; RGS14; STRAP
GO:0044422	0.0024	0.1613	CC	33355	18	2761	6	organelle part	AIFM1; TOPBP1; IFT57; TCP1; RGS14; STRAP
GO:0000242	0.0037	0.2451	CC	33355	18	7	1	pericentriolar material	TCP1
GO:0005832	0.0037	0.2451	CC	33355	18	7	1	chaperonin-containing T-complex	TCP1
GO:0043228	0.0042	0.2773	CC	33355	18	1278	4	non-membrane-bounded organelle	TOPBP1; IFT57; TCP1; RGS14
GO:0043232	0.0042	0.2773	CC	33355	18	1278	4	intracellular non-membrane-bounded organelle	TOPBP1; IFT57; TCP1; RGS14
GO:0005856	0.0062	0.4091	CC	33355	18	715	3	cytoskeleton	TOPBP1; IFT57; TCP1
GO:0044430	0.0063	0.4155	CC	33355	18	719	3	cytoskeletal part	IFT57; TCP1; RGS14
GO:0001673	0.0096	0.6286	CC	33355	18	18	1	male germ cell nucleus	TOPBP1
GO:0044450	0.0102	0.6634	CC	33355	18	19	1	microtubule organizing center part	TCP1
GO:0005932	0.0102	0.6634	CC	33355	18	19	1	microtubule basal body	IFT57
GO:0005758	0.0107	0.6981	CC	33355	18	20	1	mitochondrial intermembrane space	AIFM1
GO:0000794	0.0107	0.6981	CC	33355	18	20	1	condensed nuclear chromosome	TOPBP1
GO:0043073	0.0112	0.7328	CC	33355	18	21	1	germ cell nucleus	TOPBP1
GO:0044428	0.0125	0.8141	CC	33355	18	920	3	nuclear part	TOPBP1; TCP1; STRAP
GO:0044464	0.0129	0.8435	CC	33355	18	14486	13	cell part	DHFR; AIFM1; PHF1; GPX1; TOPBP1; ENOPH1; IFT57; TCP1; RGS14; SP1; STRAP; GRSF1; LYAR
GO:0005819	0.015	0.9754	CC	33355	18	28	1	spindle	RGS14
GO:0031970	0.0155	1	CC	33355	18	29	1	organelle envelope lumen	AIFM1
GO:0000267	0.0166	1	CC	33355	18	1024	3	cell fraction	DHFR; AIFM1; GPX1
GO:0000228	0.0171	1	CC	33355	18	32	1	nuclear chromosome	TOPBP1
GO:0000793	0.0176	1	CC	33355	18	33	1	condensed chromosome	TOPBP1

GO:0005720	0.0187	1	CC	33355	18	35	1	nuclear heterochromatin	TCP1
GO:0019861	0.0261	1	CC	33355	18	49	1	flagellum	IFT57
GO:0000790	0.0276	1	CC	33355	18	52	1	nuclear chromatin	TCP1
GO:0000792	0.0276	1	CC	33355	18	52	1	heterochromatin	TCP1
GO:0032993	0.0303	1	CC	33355	18	57	1	protein-DNA complex	SP1
GO:0005739	0.0345	1	CC	33355	18	1355	3	mitochondrion	AIFM1; GPX1; GRSF1
GO:0031974	0.0381	1	CC	33355	18	72	1	membrane-enclosed lumen	AIFM1
GO:0005741	0.0443	1	CC	33355	18	84	1	mitochondrial outer membrane	AIFM1
GO:0044445	0.0464	1	CC	33355	18	88	1	cytosolic part	TCP1
GO:0031968	0.049	1	CC	33355	18	93	1	organelle outer membrane	AIFM1
GO:0019867	0.05	1	CC	33355	18	95	1	outer membrane	AIFM1
GO:0016645	7.00E-05	0.005	MF	32949	18	23	2	oxidoreductase activity, acting on the CH-NH group of donors	DHFR; AIFM1
GO:0003676	1.90E-04	0.0137	MF	32949	18	2450	7	nucleic acid binding	EIF1AX; AIFM1; PHF1; TOPBP1; IFT57; SP1; GRSF1
GO:0005488	4.30E-04	0.0311	MF	32949	18	10322	13	binding	EIF1AX; DHFR; AIFM1; PHF1; GPX1; TOPBP1; ENOPH1; IFT57; TCP1; SP1; STRAP; GRSF1; LYAR
GO:0004146	5.40E-04	0.0393	MF	32949	18	1	1	dihydrofolate reductase activity	DHFR
GO:0043874	5.40E-04	0.0393	MF	32949	18	1	1	acireductone synthase activity	ENOPH1
GO:0051871	5.40E-04	0.0393	MF	32949	18	1	1	dihydrofolic acid binding	DHFR
GO:0016649	0.001	0.0786	MF	32949	18	2	1	oxidoreductase activity, acting on the CH-NH group of donors, quinone electron-transferring-flavoprotein	AIFM1
GO:0004174	0.001	0.0786	MF	32949	18	2	1	dehydrogenase activity phospholipid-hydroperoxide	AIFM1
GO:0047066	0.001	0.0786	MF	32949	18	2	1	glutathione peroxidase	GPX1
GO:0008967	0.0016	0.1179	MF	32949	18	3	1	phosphoglycolate phosphatase activity	ENOPH1
GO:0035035	0.0032	0.2356	MF	32949	18	6	1	histone acetyltransferase binding	SP1
GO:0050662	0.0036	0.2635	MF	32949	18	166	2	coenzyme binding	DHFR; AIFM1
GO:0043295	0.0049	0.3532	MF	32949	18	9	1	glutathione binding	GPX1
GO:0016491	0.0056	0.4063	MF	32949	18	679	3	oxidoreductase activity	DHFR; AIFM1; GPX1
GO:0048037	0.007	0.5048	MF	32949	18	232	2	cofactor binding	DHFR; AIFM1
GO:0004602	0.007	0.5097	MF	32949	18	13	1	glutathione peroxidase activity	GPX1
GO:0016646	0.0076	0.5488	MF	32949	18	14	1	oxidoreductase activity, acting on the CH-NH group of donors, NAD or	DHFR
GO:0008430	0.0081	0.5878	MF	32949	18	15	1	selenium binding	GPX1
GO:0003677	0.0116	0.8353	MF	32949	18	1680	4	DNA binding	AIFM1; TOPBP1; IFT57; SP1
GO:0016684	0.0157	1	MF	32949	18	29	1	oxidoreductase activity, acting on peroxide as acceptor	GPX1

		GO:0004601	0.0157	1	MF	32949	18	29	1	peroxidase activity	GPX1
		GO:0050661	0.0157	1	MF	32949	18	29	1	NADP or NADPH binding	DHFR
		GO:0035326	0.0205	1	MF	32949	18	38	1	enhancer binding	SP1
		GO:0016209	0.021	1	MF	32949	18	39	1	antioxidant activity	GPX1
		GO:0000166	0.0225	1	MF	32949	18	2046	4	nucleotide binding	DHFR; AIFM1; TCP1; GRSF1
		GO:0003743	0.0322	1	MF	32949	18	60	1	translation initiation factor activity	EIF1AX
		GO:0051082	0.0328	1	MF	32949	18	61	1	unfolded protein binding	TCP1
		GO:0050660	0.0365	1	MF	32949	18	68	1	FAD binding	AIFM1
		GO:0003690	0.0417	1	MF	32949	18	78	1	double-stranded DNA binding	SP1
		GO:0003723	0.0421	1	MF	32949	18	603	2	RNA binding	EIF1AX; GRSF1

Supplementary Table `KEGG Enrichment analysis'

Lung injury pathway enrichment

pathway_term	members	overlap_ members_ background	ove- rlap	DNB	backg- round	p-value
Pathways_in_cancer	254	240	17	262	12878	1.54E-06
MAPK_signaling_pathway	263	233	16	262	12878	4.42E-06
p53_signaling_pathway	56	50	7	262	12878	6.57E-06
Chronic_myeloid_leukemia	54	47	6	262	12878	4.08E-05
Toxoplasmosis	90	83	8	262	12878	4.38E-05
Hepatitis_C	74	65	7	262	12878	4.71E-05
Adipocytokine_signaling_pathway	61	52	6	262	12878	7.95E-05
Acute_myeloid_leukemia	57	52	6	262	12878	7.95E-05
Leishmaniasis	37	37	5	262	12878	9.02E-05
Cell_cycle	62	55	6	262	12878	0.000114
NOD-like_receptor_signaling_pathway	36	29	4	262	12878	0.000264
ErbB_signaling_pathway	83	70	6	262	12878	0.000518
Protein_processing_in_endoplasmic_reticul	133	115	8	262	12878	0.000525
Prostate_cancer	79	71	6	262	12878	0.000565
Toll-like_receptor_signaling_pathway	91	77	6	262	12878	0.00092
Pentose_phosphate_pathway	28	24	3	262	12878	0.001282
Pancreatic_cancer	66	60	5	262	12878	0.001305
Amoebiasis	56	41	4	262	12878	0.001362
Colorectal_cancer	47	41	4	262	12878	0.001362
Glutathione_metabolism	46	42	4	262	12878	0.001521
Chagas_disease_(American_trypanosomiasis)	79	71	5	262	12878	0.003091
Renal_cell_carcinoma	61	53	4	262	12878	0.004268
Cytosolic_DNA-sensing_pathway	20	18	2	262	12878	0.005397
B_cell_receptor_signaling_pathway	68	57	4	262	12878	0.005826
Nitrogen_metabolism	9	6	1	262	12878	0.005855
Neurotrophin_signaling_pathway	126	107	6	262	12878	0.005913
T_cell_receptor_signaling_pathway	96	83	5	262	12878	0.00664
Jak-STAT_signaling_pathway	102	86	5	262	12878	0.00786
Cytokine-cytokine_receptor_interaction	129	117	6	262	12878	0.009464
Small_cell_lung_cancer	48	43	3	262	12878	0.010968
Apoptosis	80	69	4	262	12878	0.01282
Sulfur_metabolism	10	9	1	262	12878	0.01349
Thyroid_cancer	29	25	2	262	12878	0.013684
Tight_junction	121	104	5	262	12878	0.018721
Dorso-ventral_axis_formation	11	11	1	262	12878	0.02006
Complement_and_coagulation_cascades	59	52	3	262	12878	0.020854
Phagosome	44	32	2	262	12878	0.02657
Terpenoid_backbone_biosynthesis	14	13	1	262	12878	0.027692
TGF-beta_signaling_pathway	67	57	3	262	12878	0.028117
RIG-I-like_receptor_signaling_pathway	41	35	2	262	12878	0.033529
Chemokine_signaling_pathway	181	154	6	262	12878	0.036031
Primary_bile_acid_biosynthesis	15	15	1	262	12878	0.036291
Staphylococcus_aureus_infection	15	15	1	262	12878	0.036291
RNA_transport	118	93	4	262	12878	0.040048
Steroid_biosynthesis	18	17	1	262	12878	0.045765
Prion_diseases	17	17	1	262	12878	0.045765
Arachidonic_acid_metabolism	85	68	3	262	12878	0.048786
ECM-receptor_interaction	48	41	2	262	12878	0.049965

HBV pathway enrichment

pathway_term	members	overlap_ members_ background	ove- rlap	DNB	backg- round	p-value
Acute_myeloid_leukemia	57	20	3	56	4082	0.000128
Pathways_in_cancer	255	78	5	56	4082	0.000551
Leishmaniasis	39	17	2	56	4082	0.001434
Pentose_and_glucuronate_interconversions	27	6	1	56	4082	0.002669
Antigen_processing_and_presentation	61	23	2	56	4082	0.00351
Cytosolic_DNA-sensing_pathway	20	7	1	56	4082	0.003702
Adipocytokine_signaling_pathway	61	25	2	56	4082	0.004466
Hepatitis_C	74	27	2	56	4082	0.005563
Pancreatic_cancer	66	28	2	56	4082	0.006167
Toll-like_receptor_signaling_pathway	92	29	2	56	4082	0.006808
Thyroid_cancer	28	10	1	56	4082	0.007716
RIG-I-like_receptor_signaling_pathway	38	11	1	56	4082	0.009344
Porphyrin_and_chlorophyll_metabolism	40	12	1	56	4082	0.011109
NOD-like_receptor_signaling_pathway	39	12	1	56	4082	0.011109
Oocyte_meiosis	92	35	2	56	4082	0.011468
Neurotrophin_signaling_pathway	122	35	2	56	4082	0.011468
Toxoplasmosis	89	35	2	56	4082	0.011468
Cell_adhesion_molecules_(CAMs)	106	36	2	56	4082	0.012384
Osteoclast_differentiation	101	38	2	56	4082	0.014336
Arginine_and_proline_metabolism	53	15	1	56	4082	0.017193
Small_cell_lung_cancer	46	15	1	56	4082	0.017193
Jak-STAT_signaling_pathway	99	42	2	56	4082	0.018732
Steroid_hormone_biosynthesis	53	17	1	56	4082	0.021864
Chronic_myeloid_leukemia	54	17	1	56	4082	0.021864
Epithelial_cell_signaling_in_Helicobacter_pylori_infection	36	18	1	56	4082	0.024373
Starch_and_sucrose_metabolism	52	19	1	56	4082	0.026992
N-Glycan_biosynthesis	43	19	1	56	4082	0.026992
Shigellosis	41	19	1	56	4082	0.026992
Retinol_metabolism	64	23	1	56	4082	0.038507
B_cell_receptor_signaling_pathway	67	23	1	56	4082	0.038507
Bacterial_invasion_of_epithelial_cells	56	23	1	56	4082	0.038507
Amoebiasis	43	24	1	56	4082	0.041628
Adherens_junction	63	25	1	56	4082	0.044839
Chemokine_signaling_pathway	185	60	2	56	4082	0.046592
Cell_cycle	61	26	1	56	4082	0.048138

```

clear;
clc;
close all;

fpi=fopen('lung_injury_control.txt');
hline1 = textscan(fpi, '%s', 1, 'delimiter', '\n');
field1=textscan(hline1{1}{1}, '%s');
format='%s';
% format=[format, ' %s'];
for i=2:57
    format=[format, ' %f'];
end
plines =textscan(fpi, format,1000000,'delimiter', '\t');
pipi=plines{1};
controlprofile = [];
for i = 2 : 57
    controlprofile = [controlprofile, plines{i}];
end
fclose(fpi);

fpi=fopen('lung_injury_case.txt');
hline2 = textscan(fpi, '%s', 1, 'delimiter', '\n');
field2=textscan(hline2{1}{1}, '%s');
clear format;
format='%s';
% format=[format, ' %s'];
for i=2:55
    format=[format, ' %f'];
end
mlines =textscan(fpi, format,1000000,'delimiter', '\t');
mipi=mlines{1};
caseprofile = [];
for i = 2 : 55
    caseprofile = [caseprofile, mlines{i}];
end
fclose(fpi);

controlsize=size(controlprofile);
casesize=size(caseprofile);
tempcontrol1=controlprofile(:,1:6);
tempcontrol2=controlprofile(:,7:12);
tempcontrol3=controlprofile(:,13:18);
tempcontrol4=controlprofile(:,19:24);
tempcontrol5=controlprofile(:,25:30);
tempcontrol6=controlprofile(:,31:36);
tempcontrol7=controlprofile(:,37:42);
tempcontrol8=controlprofile(:,43:48);
tempcontrol9=controlprofile(:,51:56);
tempcase1=caseprofile(:,1:6);
tempcase2=caseprofile(:,7:12);
tempcase3=caseprofile(:,13:18);
tempcase4=caseprofile(:,19:24);
tempcase5=caseprofile(:,25:30);
tempcase6=caseprofile(:,31:36);
tempcase7=caseprofile(:,37:42);
tempcase8=caseprofile(:,43:48);

```

%22690*56

```

tempcase9=caseprofile(:,49:54);
j1=0;
j2=0;
j3=0;
j4=0;
j5=0;
j6=0;
j7=0;
j8=0;
j9=0;
for i=1:controlsize(1)
    [h1,pvalue1(i),ci1]=ttest2(tempcontrol1(i,:),tempcase1(i,:),0.05);
    [h2,pvalue2(i),ci2]=ttest2(tempcontrol2(i,:),tempcase2(i,:),0.05);
    [h3,pvalue3(i),ci3]=ttest2(tempcontrol3(i,:),tempcase3(i,:),0.05);
    [h4,pvalue4(i),ci4]=ttest2(tempcontrol4(i,:),tempcase4(i,:),0.05);
    [h5,pvalue5(i),ci5]=ttest2(tempcontrol5(i,:),tempcase5(i,:),0.05);
    [h6,pvalue6(i),ci6]=ttest2(tempcontrol6(i,:),tempcase6(i,:),0.05);
    [h7,pvalue7(i),ci7]=ttest2(tempcontrol7(i,:),tempcase7(i,:),0.05);
    [h8,pvalue8(i),ci8]=ttest2(tempcontrol8(i,:),tempcase8(i,:),0.05);
    [h9,pvalue9(i),ci9]=ttest2(tempcontrol9(i,:),tempcase9(i,:),0.05);

    if mod(i,100)==0
        i
        pv=[pvalue1(i) pvalue2(i) pvalue3(i) pvalue4(i) pvalue5(i) ...
            pvalue6(i) pvalue7(i) pvalue8(i) pvalue9(i)]
    end
end
[p1,idx1]=sort(pvalue1);
[p2,idx2]=sort(pvalue2);
[p3,idx3]=sort(pvalue3);
[p4,idx4]=sort(pvalue4);
[p5,idx5]=sort(pvalue5);
[p6,idx6]=sort(pvalue6);
[p7,idx7]=sort(pvalue7);
[p8,idx8]=sort(pvalue8);
[p9,idx9]=sort(pvalue9);
qthresh=0.05;

k1=1;
j1=0;
while p1(k1)<(k1/controlsize(1))*qthresh
    if std(tempcase1(idx1(k1),:))/std(tempcontrol1(idx1(k1),:))<2
        k1=k1+1;
        continue
    end
    j1=j1+1;
    index1(j1)=idx1(k1);
    usefulRNA1_id(j1)=pipi(idx1(k1));
    usefulRNA1_pig(j1,:)=tempcontrol1(idx1(k1),:);
    usefulRNA1_mimi(j1,:)=tempcase1(idx1(k1),:);

    usefulRNA1_z(j1,:)=(tempcase1(idx1(k1),:)-mean(tempcontrol1(idx1(k1),:)))/std(tempcontrol1(idx1(k1),:));
    usefulRNA1_healthy(j1,:)=controlprofile(idx1(k1),:);
    usefulRNA1_sick(j1,:)=caseprofile(idx1(k1),:);
    k1=k1+1;
end

```

```

end

k2=1;
j2=0;
while p2(k2)<(k2/controlsizel(1))*qthresh
    if std(tempcase2(idx2(k2),:))/std(tempcontrol2(idx2(k2),:))<2
        k2=k2+1;
        continue
    end
    j2=j2+1;
    index2(j2)=idx2(k2);
    usefulRNA2_id(j2)=pipi(idx2(k2));
    usefulRNA2_pig(j2,:)=tempcontrol2(idx2(k2),:);
    usefulRNA2_mimi(j2,:)=tempcase2(idx2(k2),:);

    usefulRNA2_z(j2,:)=(tempcase2(idx2(k2),:)-mean(tempcontrol2(idx2(k2),:)))/std(tempcontrol2(idx2(k2),:));
    usefulRNA2_healthy(j2,:)=controlprofile(idx2(k2),:);
    usefulRNA2_sick(j2,:)=caseprofile(idx2(k2),:);
    k2=k2+1;
end

k3=1;
j3=0;
while p3(k3)<(k3/controlsizel(1))*qthresh
    if std(tempcase3(idx3(k3),:))/std(tempcontrol3(idx3(k3),:))<2
        k3=k3+1;
        continue
    end
    j3=j3+1;
    index3(j3)=idx3(k3);
    usefulRNA3_id(j3)=pipi(idx3(k3));
    usefulRNA3_pig(j3,:)=tempcontrol3(idx3(k3),:);
    usefulRNA3_mimi(j3,:)=tempcase3(idx3(k3),:);

    usefulRNA3_z(j3,:)=(tempcase3(idx3(k3),:)-mean(tempcontrol3(idx3(k3),:)))/std(tempcontrol3(idx3(k3),:));
    usefulRNA3_healthy(j3,:)=controlprofile(idx3(k3),:);
    usefulRNA3_sick(j3,:)=caseprofile(idx3(k3),:);
    k3=k3+1;
end

k3=k3-1;

k4=1;
j4=0;
while p4(k4)<(k4/controlsizel(1))*qthresh
    if std(tempcase4(idx4(k4),:))/std(tempcontrol4(idx4(k4),:))<2
        k4=k4+1;
        continue
    end
    j4=j4+1;
    index4(j4)=idx4(k4);
    usefulRNA4_id(j4)=pipi(idx4(k4));
    usefulRNA4_pig(j4,:)=tempcontrol4(idx4(k4),:);
    usefulRNA4_mimi(j4,:)=tempcase4(idx4(k4),:);

```

```

usefulRNA4_z(j4,:)=(tempcase4(idx4(k4),:)-mean(tempcontrol4(idx4(k4),:))
)/std(tempcontrol4(idx4(k4),:));
    usefulRNA4_healthy(j4,:)=controlprofile(idx4(k4),:);
    usefulRNA4_sick(j4,:)=caseprofile(idx4(k4),:);
    k4=k4+1;

```

end

```

k5=1;
j5=0;
while p5(k5)<(k5/controlsize(1))*qthresh
    if std(tempcase5(idx5(k5),:))/std(tempcontrol5(idx5(k5),:))<2
        k5=k5+1;
        continue
    end
    j5=j5+1;
    index5(j5)=idx5(k5);
    usefulRNA5_id(j5)=pipi(idx5(k5));
    usefulRNA5_pig(j5,:)=tempcontrol5(idx5(k5),:);
    usefulRNA5_mimi(j5,:)=tempcase5(idx5(k5),:);

```

```

usefulRNA5_z(j5,:)=(tempcase5(idx5(k5),:)-mean(tempcontrol5(idx5(k5),:))
)/std(tempcontrol5(idx5(k5),:));
    usefulRNA5_healthy(j5,:)=controlprofile(idx5(k5),:);
    usefulRNA5_sick(j5,:)=caseprofile(idx5(k5),:);
    k5=k5+1;

```

end

```

k6=1;
j6=0;
while p6(k6)<(k6/controlsize(1))*qthresh
    if std(tempcase6(idx6(k6),:))/std(tempcontrol6(idx6(k6),:))<2
        k6=k6+1;
        continue
    end
    j6=j6+1;
    index6(j6)=idx6(k6);
    usefulRNA6_id(j6)=pipi(idx6(k6));
    usefulRNA6_pig(j6,:)=tempcontrol6(idx6(k6),:);
    usefulRNA6_mimi(j6,:)=tempcase6(idx6(k6),:);

```

```

usefulRNA6_z(j6,:)=(tempcase6(idx6(k6),:)-mean(tempcontrol6(idx6(k6),:))
)/std(tempcontrol6(idx6(k6),:));
    usefulRNA6_healthy(j6,:)=controlprofile(idx6(k6),:);
    usefulRNA6_sick(j6,:)=caseprofile(idx6(k6),:);
    k6=k6+1;

```

end

```

k7=1;
j7=0;
while p7(k7)<(k7/controlsize(1))*qthresh
    if std(tempcase7(idx7(k7),:))/std(tempcontrol7(idx7(k7),:))<2
        k7=k7+1;
        continue
    end
    j7=j7+1;
    index7(j7)=idx7(k7);

```

```

        usefulRNA7_id(j7)=pipi(idx7(k7));
        usefulRNA7_pig(j7,:)=tempcontrol7(idx7(k7),:);
        usefulRNA7_mimi(j7,:)=tempcase7(idx7(k7),:);

        usefulRNA7_z(j7,:)=(tempcase7(idx7(k7),:)-mean(tempcontrol7(idx7(k7),:)))/std(tempcontrol7(idx7(k7),:));
        usefulRNA7_healthy(j7,:)=controlprofile(idx7(k7),:);
        usefulRNA7_sick(j7,:)=caseprofile(idx7(k7),:);
        k7=k7+1;
    end

    k8=1;
    j8=0;
    while p8(k8)<(k8/controlsize(1))*qthresh
        if std(tempcase8(idx8(k8),:))/std(tempcontrol8(idx8(k8),:))<2
            k8=k8+1;
            continue
        end
        j8=j8+1;
        index8(j8)=idx8(k8);
        usefulRNA8_id(j8)=pipi(idx8(k8));
        usefulRNA8_pig(j8,:)=tempcontrol8(idx8(k8),:);
        usefulRNA8_mimi(j8,:)=tempcase8(idx8(k8),:);

        usefulRNA8_z(j8,:)=(tempcase8(idx8(k8),:)-mean(tempcontrol8(idx8(k8),:)))/std(tempcontrol8(idx8(k8),:));
        usefulRNA8_healthy(j8,:)=controlprofile(idx8(k8),:);
        usefulRNA8_sick(j8,:)=caseprofile(idx8(k8),:);
        k8=k8+1;
    end

    k9=1;
    j9=0;
    while p9(k9)<(k9/controlsize(1))*qthresh
        if std(tempcase9(idx9(k9),:))/std(tempcontrol9(idx9(k9),:))<2
            k9=k9+1;
            continue
        end
        j9=j9+1;
        index9(j9)=idx9(k9);
        usefulRNA9_id(j9)=pipi(idx9(k9));
        usefulRNA9_pig(j9,:)=tempcontrol9(idx9(k9),:);
        usefulRNA9_mimi(j9,:)=tempcase9(idx9(k9),:);

        usefulRNA9_z(j9,:)=(tempcase9(idx9(k9),:)-mean(tempcontrol9(idx9(k9),:)))/std(tempcontrol9(idx9(k9),:));
        usefulRNA9_healthy(j9,:)=controlprofile(idx9(k9),:);
        usefulRNA9_sick(j9,:)=caseprofile(idx9(k9),:);
        k9=k9+1;
    end

    Y2=pdist(usefulRNA2_z,@cofun);
    Z2=linkage(Y2);
    T2=cluster(Z2,'maxclust',40);
    num2=max(T2);
    groupnum2=zeros(1,num2);

```

```

for i=1:length(T2)
    groupnum2(T2(i))=groupnum2(T2(i))+1;
end

Y3=pdist(usableRNA3_z,@cofun);
Z3=linkage(Y3);
T3=cluster(Z3,'maxclust',40);
num3=max(T3);
groupnum3=zeros(1,num3);
for i=1:length(T3)
    groupnum3(T3(i))=groupnum3(T3(i))+1;
end

Y4=pdist(usableRNA4_z,@cofun);
Z4=linkage(Y4);
T4=cluster(Z4,'maxclust',40);
num4=max(T4);
groupnum4=zeros(1,num4);
for i=1:length(T4)
    groupnum4(T4(i))=groupnum4(T4(i))+1;
end

Y5=pdist(usableRNA5_z,@cofun);
Z5=linkage(Y5);
T5=cluster(Z5,'maxclust',40);
num5=max(T5);
groupnum5=zeros(1,num5);
for i=1:length(T5)
    groupnum5(T5(i))=groupnum5(T5(i))+1;
end

Y6=pdist(usableRNA6_z,@cofun);
Z6=linkage(Y6);
T6=cluster(Z6,'maxclust',40);
num6=max(T6);
groupnum6=zeros(1,num6);
for i=1:length(T6)
    groupnum6(T6(i))=groupnum6(T6(i))+1;
end

Y7=pdist(usableRNA7_z,@cofun);
Z7=linkage(Y7);
T7=cluster(Z7,'maxclust',40);
num7=max(T7);
groupnum7=zeros(1,num7);
for i=1:length(T7)
    groupnum7(T7(i))=groupnum7(T7(i))+1;
end

Y8=pdist(usableRNA8_z,@cofun);
Z8=linkage(Y8);
T8=cluster(Z8,'maxclust',40);
num8=max(T8);
groupnum8=zeros(1,num8);
for i=1:length(T8)
    groupnum8(T8(i))=groupnum8(T8(i))+1;
end

```

```

end

mkdir('cluster_gene_group');
path=cd;
newpath=strcat(path,'\','cluster_gene_group','\');

totalgroupnum=num6+num5+num4+num3+num2;
clear A;

validgroupnum=0;
filename=strcat(newpath,'time',int2str(2),'.txt');
fpi=fopen(filename,'wt');
candidategroup2=0;
for i=1:num2
    fprintf(fpi,'µÜ%d×é:\n',i);
    clear tm;
    clear k; clear tmm; clear tp; clear zjj;
    k=0; stdRNA=0;
    stdRNA1=0; stdRNA2=0; stdRNA3=0; stdRNA4=0; stdRNA5=0; stdRNA6=0;
    stdRNA7=0; stdRNA8=0; stdRNA9=0;
    stdRNA_c1=0; stdRNA_c2=0; stdRNA_c3=0; stdRNA_c4=0; stdRNA_c5=0;
    stdRNA_c6=0; stdRNA_c7=0; stdRNA_c8=0; stdRNA_c9=0;
    mixpcc1=0; mixpcc2=0; mixpcc3=0; mixpcc4=0; mixpcc5=0; mixpcc6=0;
    mixpcc7=0; mixpcc8=0; mixpcc9=0;
    mixpcc_c1=0; mixpcc_c2=0; mixpcc_c3=0; mixpcc_c4=0; mixpcc_c5=0;
    mixpcc_c6=0; mixpcc_c7=0; mixpcc_c8=0; mixpcc_c9=0;
    pccall1=0; pccall2=0; pccall3=0; pccall4=0; pccall5=0; pccall6=0;
    pccall7=0; pccall8=0; pccall9=0;
    pccall_c1=0; pccall_c2=0; pccall_c3=0; pccall_c4=0; pccall_c5=0;
    pccall_c6=0; pccall_c7=0; pccall_c8=0; pccall_c9=0;

    for j=1:length(T2)
        if i==T2(j)
            fprintf(fpi,'%d\t%s\n',j,usefulRNA2_id{j});
            k=k+1;
            %           tm(k,:)=usefulRNA2_z(j,:);
            tmm(k,:)=usefulRNA2_sick(j,:);
            zjj(k,:)=usefulRNA2_healthy(j,:);
            tp(k,:)=(tmm(k,:)-mean(zjj(k,:)))/(std(zjj(k,:))); %
        case z-score
            tm(k,:)=(zjj(k,:)-mean(zjj(k,:)))/(std(zjj(k,:))); %
        control z-score

            stdRNA1=stdRNA1+std(tp(k,1:6)); % case std
            stdRNA2=stdRNA2+std(tp(k,7:12));
            stdRNA3=stdRNA3+std(tp(k,13:18));
            stdRNA4=stdRNA4+std(tp(k,19:24));
            stdRNA5=stdRNA5+std(tp(k,25:30));
            stdRNA6=stdRNA6+std(tp(k,31:36));
            stdRNA7=stdRNA7+std(tp(k,37:42));
            stdRNA8=stdRNA8+std(tp(k,43:48));
            stdRNA9=stdRNA9+std(tp(k,49:54));

            stdRNA_c1=stdRNA_c1+std(tm(k,1:6)); % control std
            stdRNA_c2=stdRNA_c2+std(tm(k,7:12));
            stdRNA_c3=stdRNA_c3+std(tm(k,13:18));

```

```

        stdRNA_c4=stdRNA_c4+std(tm(k,19:24));
        stdRNA_c5=stdRNA_c5+std(tm(k,25:30));
        stdRNA_c6=stdRNA_c6+std(tm(k,31:36));
        stdRNA_c7=stdRNA_c7+std(tm(k,37:42));
        stdRNA_c9=stdRNA_c9+std(tm(k,51:56));
        stdRNA_c8=stdRNA_c8+std(tm(k,43:48));
    end
end
if k<2
    fprintf(fpi,'\n');
    continue
end

if k<10
    continue;
end

pccall1=corr(tp(:,1:6));
pccall2=corr(tp(:,7:12));
pccall3=corr(tp(:,13:18));
pccall4=corr(tp(:,19:24));
pccall5=corr(tp(:,25:30));
pccall6=corr(tp(:,31:36));
pccall7=corr(tp(:,37:42));
pccall8=corr(tp(:,43:48));
pccall9=corr(tp(:,49:54));
sumpccall(1)=(sum(sum(abs(pccall1)))-k)/2;
sumpccall(2)=(sum(sum(abs(pccall2)))-k)/2;
sumpccall(3)=(sum(sum(abs(pccall3)))-k)/2;
sumpccall(4)=(sum(sum(abs(pccall4)))-k)/2;
sumpccall(5)=(sum(sum(abs(pccall5)))-k)/2;
sumpccall(6)=(sum(sum(abs(pccall6)))-k)/2;
sumpccall(7)=(sum(sum(abs(pccall7)))-k)/2;
sumpccall(8)=(sum(sum(abs(pccall8)))-k)/2;
sumpccall(9)=(sum(sum(abs(pccall9)))-k)/2;
%      sumpcc=(sum(sum(abs(pcc)))-k)/2;

pccall_c1=corr(tm(:,1:6));
pccall_c2=corr(tm(:,7:12));
pccall_c3=corr(tm(:,13:18));
pccall_c4=corr(tm(:,19:24));
pccall_c5=corr(tm(:,25:30));
pccall_c6=corr(tm(:,31:36));
pccall_c7=corr(tm(:,37:42));
pccall_c8=corr(tm(:,43:48));
pccall_c9=corr(tm(:,51:56));
sumpccall_c(1)=(sum(sum(abs(pccall_c1)))-k)/2;
sumpccall_c(2)=(sum(sum(abs(pccall_c2)))-k)/2;
sumpccall_c(3)=(sum(sum(abs(pccall_c3)))-k)/2;
sumpccall_c(4)=(sum(sum(abs(pccall_c4)))-k)/2;
sumpccall_c(5)=(sum(sum(abs(pccall_c5)))-k)/2;
sumpccall_c(6)=(sum(sum(abs(pccall_c6)))-k)/2;
sumpccall_c(7)=(sum(sum(abs(pccall_c7)))-k)/2;
sumpccall_c(8)=(sum(sum(abs(pccall_c8)))-k)/2;
sumpccall_c(9)=(sum(sum(abs(pccall_c9)))-k)/2;
%      sumpcc=(sum(sum(abs(pcc)))-k)/2;

```

```

avestd1=stdRNA1/k;
avestd2=stdRNA2/k;
avestd3=stdRNA3/k;
avestd4=stdRNA4/k;
avestd5=stdRNA5/k;
avestd6=stdRNA6/k;
avestd7=stdRNA6/k;
avestd8=stdRNA6/k;
avestd9=stdRNA6/k;
avepcc1=sumpccall(1)/(k*(k-1))*2;
avepcc2=sumpccall(2)/(k*(k-1))*2;
avepcc3=sumpccall(3)/(k*(k-1))*2;
avepcc4=sumpccall(4)/(k*(k-1))*2;
avepcc5=sumpccall(5)/(k*(k-1))*2;
avepcc6=sumpccall(6)/(k*(k-1))*2;
avepcc7=sumpccall(7)/(k*(k-1))*2;
avepcc8=sumpccall(8)/(k*(k-1))*2;
avepcc9=sumpccall(9)/(k*(k-1))*2;

line=line+1;
fprintf(fpi, '\n');
validgroupnum=validgroupnum+1;
stdrna=[stdRNA1 stdRNA2 stdRNA3 stdRNA4 stdRNA5 stdRNA6 stdRNA7 stdRNA8
stdRNA9];
stdrna_c=[stdRNA_c1 stdRNA_c2 stdRNA_c3 stdRNA_c4 stdRNA_c5 stdRNA_c6
stdRNA_c7 stdRNA_c8 stdRNA_c9];
stdrna=stdrna/k;
stdrna_c=stdrna_c/k;
pccrna=sumpccall;
pccrna_c=sumpccall_c;
pccrna=pccrna/(k*(k-1))*2;
pccrna_c=pccrna_c/(k*(k-1))*2;

othergenes_mimi=setdiff(usefulRNA2_sick, tmm, 'rows');
othergenes_pig=setdiff(usefulRNA2_healthy, zjj, 'rows');
mimisize=size(othergenes_mimi);

for ii=1:k
    for jj=1:mimisize(1)

zscoretp=(othergenes_mimi(jj,:)-mean(othergenes_pig(jj,:)))/std(otherge
nes_pig(jj,:));

mixpcc1=mixpcc1+abs(corr(tp(ii,1:6)', zscoretp(1:6)'));
    % case outpcc
    mixpcc2=mixpcc2+abs(corr(tp(ii,7:12)', zscoretp(7:12)'));
    mixpcc3=mixpcc3+abs(corr(tp(ii,13:18)', zscoretp(13:18)'));
    mixpcc4=mixpcc4+abs(corr(tp(ii,19:24)', zscoretp(19:24)'));
    mixpcc5=mixpcc5+abs(corr(tp(ii,25:30)', zscoretp(25:30)'));
    mixpcc6=mixpcc6+abs(corr(tp(ii,31:36)', zscoretp(31:36)'));
    mixpcc7=mixpcc7+abs(corr(tp(ii,37:42)', zscoretp(37:42)'));
    mixpcc8=mixpcc8+abs(corr(tp(ii,43:48)', zscoretp(43:48)'));
    mixpcc9=mixpcc9+abs(corr(tp(ii,49:54)', zscoretp(49:54)'));

```

```

zscoretm=(othergenes_pig(jj,:)-mean(othergenes_pig(jj,:)))/std(othergenes_pig(jj,:));

mixpcc_c1=mixpcc_c1+abs(corr(tm(ii,1:6)',zscoretm(1:6)'));
    % control outpcc
    mixpcc_c2=mixpcc_c2+abs(corr(tm(ii,7:12)',zscoretm(7:12)'));

mixpcc_c3=mixpcc_c3+abs(corr(tm(ii,13:18)',zscoretm(13:18)'));

mixpcc_c4=mixpcc_c4+abs(corr(tm(ii,19:24)',zscoretm(19:24)'));

mixpcc_c5=mixpcc_c5+abs(corr(tm(ii,25:30)',zscoretm(25:30)'));

mixpcc_c6=mixpcc_c6+abs(corr(tm(ii,31:36)',zscoretm(31:36)'));

mixpcc_c7=mixpcc_c7+abs(corr(tm(ii,37:42)',zscoretm(37:42)'));

mixpcc_c8=mixpcc_c8+abs(corr(tm(ii,43:48)',zscoretm(43:48)'));

mixpcc_c9=mixpcc_c9+abs(corr(tm(ii,51:56)',zscoretm(51:56)'));
    end
    end
    mixpcc=[mixpcc1 mixpcc2 mixpcc3 mixpcc4 mixpcc5 mixpcc6 mixpcc7 mixpcc8
mixpcc9];
    mixpcc_c=[mixpcc_c1 mixpcc_c2 mixpcc_c3 mixpcc_c4 mixpcc_c5 mixpcc_c6
mixpcc_c7 mixpcc_c8 mixpcc_c9];
    mixpcc=mixpcc/k/mimisize(1);
    mixpcc_c=mixpcc_c/k/mimisize(1);

    tag=0;
    for time=2:8
        if
            (stdrna(time)>stdrna(time-1)) && (stdrna(time)>stdrna(time+1)) && ...

            (pccrna(time)>pccrna(time-1)) && (pccrna(time)>pccrna(time+1)) && ...

            (mixpcc(time)<mixpcc(time-1)) && (mixpcc(time)<mixpcc(time+1))
                tag=1;
                break;
            end
        end
        if tag==0
            continue;
        end

        candidategroup2=candidategroup2+1;

        compositindex=zeros(9,1);
        compositindex_c=zeros(9,1);
        for s=1:9
            compositindex(s)=(stdrna(s)/k)*(pccrna(s)/(k*(k-1))*2)/mixpcc(s);

            compositindex_c(s)=(stdrna_c(s)/k)*(pccrna_c(s)/(k*(k-1))*2)/mixpcc_c(s);
        end
    end

```

```

figure(i);
t=[1 2 3 4 5 6 7 8 9];

subplot(1,4,1);
plot(t,stdrna,'r', t,stdrna_c,'b');
title('std2');
legend('SD_{case}','SD_{control}',2);

subplot(1,4,2);
plot(t,pccrna,'r',t,pccrna_c,'b');
title('inpcc2');
legend('PCC_{case}','PCC_{control}',2);

subplot(1,4,3);
plot(t,mixpcc,'r',t,mixpcc_c,'b');
title('outpcc2');
legend('OPCC_{case}','OPCC_{control}',2);

subplot(1,4,4);
plot(t,compositindex,'r',t,compositindex_c,'b')
title('composite index');
legend('Composite_{case}','Composite_{control}',2);

end
fclose(fpi);

filename=strcat(newpath,'time',int2str(3),'.txt');
fpi=fopen(filename,'wt');
candidategroup3=0;
for i=num2+1:num3+num2
    fprintf(fpi,'µŮ%d×é:\n',i);
    clear tm;
    clear k; clear tmm; clear tp; clear zjj;
    k=0; stdRNA=0;
    stdRNA1=0; stdRNA2=0; stdRNA3=0; stdRNA4=0; stdRNA5=0; stdRNA6=0;
    stdRNA7=0; stdRNA8=0; stdRNA9=0;
    stdRNA_c1=0; stdRNA_c2=0; stdRNA_c3=0; stdRNA_c4=0; stdRNA_c5=0;
    stdRNA_c6=0; stdRNA_c7=0; stdRNA_c8=0; stdRNA_c9=0;
    mixpcc1=0; mixpcc2=0; mixpcc3=0; mixpcc4=0; mixpcc5=0; mixpcc6=0;
    mixpcc7=0; mixpcc8=0; mixpcc9=0;
    mixpcc_c1=0; mixpcc_c2=0; mixpcc_c3=0; mixpcc_c4=0; mixpcc_c5=0;
    mixpcc_c6=0; mixpcc_c7=0; mixpcc_c8=0; mixpcc_c9=0;
    pccall1=0; pccall2=0; pccall3=0; pccall4=0; pccall5=0; pccall6=0;
    pccall7=0; pccall8=0; pccall9=0;
    pccall_c1=0; pccall_c2=0; pccall_c3=0; pccall_c4=0; pccall_c5=0;
    pccall_c6=0; pccall_c7=0; pccall_c8=0; pccall_c9=0;

    for j=1:length(T3)
        if i==T3(j)+num2
            fprintf(fpi,'%d\t%s\n',j,usefulRNA3_id{j});
            k=k+1;
            tmm(k,:)=usefulRNA3_sick(j,:);
            zjj(k,:)=usefulRNA3_healthy(j,:);
            tp(k,:)=(tmm(k,:)-mean(zjj(k,:)))/(std(zjj(k,:)));
        end
    end
case z-score

```

```

        tm(k,:)=(zjj(k,:)-mean(zjj(k,:)))/(std(zjj(k,:))); %
control z-score

        stdRNA1=stdRNA1+std(tp(k,1:6)); % case std
        stdRNA2=stdRNA2+std(tp(k,7:12));
        stdRNA3=stdRNA3+std(tp(k,13:18));
        stdRNA4=stdRNA4+std(tp(k,19:24));
        stdRNA5=stdRNA5+std(tp(k,25:30));
        stdRNA6=stdRNA6+std(tp(k,31:36));
        stdRNA7=stdRNA7+std(tp(k,37:42));
        stdRNA8=stdRNA8+std(tp(k,43:48));
        stdRNA9=stdRNA9+std(tp(k,49:54));

        stdRNA_c1=stdRNA_c1+std(tm(k,1:6)); % control std
        stdRNA_c2=stdRNA_c2+std(tm(k,7:12));
        stdRNA_c3=stdRNA_c3+std(tm(k,13:18));
        stdRNA_c4=stdRNA_c4+std(tm(k,19:24));
        stdRNA_c5=stdRNA_c5+std(tm(k,25:30));
        stdRNA_c6=stdRNA_c6+std(tm(k,31:36));
        stdRNA_c7=stdRNA_c7+std(tm(k,37:42));
        stdRNA_c9=stdRNA_c9+std(tm(k,51:56));
        stdRNA_c8=stdRNA_c8+std(tm(k,43:48));
    end
end
if k<2
    fprintf(fpi,'\n');
    continue
end

if k<10
    continue;
end

pccall1=corr(tp(:,1:6)'); % case pcc
pccall2=corr(tp(:,7:12)');
pccall3=corr(tp(:,13:18)');
pccall4=corr(tp(:,19:24)');
pccall5=corr(tp(:,25:30)');
pccall6=corr(tp(:,31:36)');
pccall7=corr(tp(:,37:42)');
pccall8=corr(tp(:,43:48)');
pccall9=corr(tp(:,49:54)');
sumpccall(1)=(sum(sum(abs(pccall1)))-k)/2;
sumpccall(2)=(sum(sum(abs(pccall2)))-k)/2;
sumpccall(3)=(sum(sum(abs(pccall3)))-k)/2;
sumpccall(4)=(sum(sum(abs(pccall4)))-k)/2;
sumpccall(5)=(sum(sum(abs(pccall5)))-k)/2;
sumpccall(6)=(sum(sum(abs(pccall6)))-k)/2;
sumpccall(7)=(sum(sum(abs(pccall7)))-k)/2;
sumpccall(8)=(sum(sum(abs(pccall8)))-k)/2;
sumpccall(9)=(sum(sum(abs(pccall9)))-k)/2;
% sumpcc=(sum(sum(abs(pcc)))-k)/2;

pccall_c1=corr(tm(:,1:6)'); % control pcc
pccall_c2=corr(tm(:,7:12)');
pccall_c3=corr(tm(:,13:18)');

```

```

pccall_c4=corr(tm(:,19:24)');
pccall_c5=corr(tm(:,25:30)');
pccall_c6=corr(tm(:,31:36)');
pccall_c7=corr(tm(:,37:42)');
pccall_c8=corr(tm(:,43:48)');
pccall_c9=corr(tm(:,51:56)');
sumpccall_c(1)=(sum(sum(abs(pccall_c1)))-k)/2;
sumpccall_c(2)=(sum(sum(abs(pccall_c2)))-k)/2;
sumpccall_c(3)=(sum(sum(abs(pccall_c3)))-k)/2;
sumpccall_c(4)=(sum(sum(abs(pccall_c4)))-k)/2;
sumpccall_c(5)=(sum(sum(abs(pccall_c5)))-k)/2;
sumpccall_c(6)=(sum(sum(abs(pccall_c6)))-k)/2;
sumpccall_c(7)=(sum(sum(abs(pccall_c7)))-k)/2;
sumpccall_c(8)=(sum(sum(abs(pccall_c8)))-k)/2;
sumpccall_c(9)=(sum(sum(abs(pccall_c9)))-k)/2;
%    sumpcc=(sum(sum(abs(pcc)))-k)/2;

avestd1=stdRNA1/k;
avestd2=stdRNA2/k;
avestd3=stdRNA3/k;
avestd4=stdRNA4/k;
avestd5=stdRNA5/k;
avestd6=stdRNA6/k;
avestd7=stdRNA6/k;
avestd8=stdRNA6/k;
avestd9=stdRNA6/k;
avepcc1=sumpccall(1)/(k*(k-1))*2;
avepcc2=sumpccall(2)/(k*(k-1))*2;
avepcc3=sumpccall(3)/(k*(k-1))*2;
avepcc4=sumpccall(4)/(k*(k-1))*2;
avepcc5=sumpccall(5)/(k*(k-1))*2;
avepcc6=sumpccall(6)/(k*(k-1))*2;
avepcc7=sumpccall(7)/(k*(k-1))*2;
avepcc8=sumpccall(8)/(k*(k-1))*2;
avepcc9=sumpccall(9)/(k*(k-1))*2;

line=line+1;
fprintf(fpi,'\n');
validgroupnum=validgroupnum+1;
stdrna=[stdRNA1 stdRNA2 stdRNA3 stdRNA4 stdRNA5 stdRNA6 stdRNA7 stdRNA8
stdRNA9];
stdrna_c=[stdRNA_c1 stdRNA_c2 stdRNA_c3 stdRNA_c4 stdRNA_c5 stdRNA_c6
stdRNA_c7 stdRNA_c8 stdRNA_c9];
stdrna=stdrna/k;
stdrna_c=stdrna_c/k;
pccrna=sumpccall;
pccrna_c=sumpccall_c;
pccrna=pccrna/(k*(k-1))*2;
pccrna_c=pccrna_c/(k*(k-1))*2;

othergenes_mimi=setdiff(usefulRNA3_sick, tmm, 'rows');
othergenes_pig=setdiff(usefulRNA3_healthy, zjj, 'rows');
mimisize=size(othergenes_mimi);

for ii=1:k
    for jj=1:mimisize(1)

```

```

zscoretp=(othergenes_mimi(jj,:)-mean(othergenes_pig(jj,:)))/std(othergenes_pig(jj,:));

mixpcc1=mixpcc1+abs(corr(tp(ii,1:6)',zscoretp(1:6)'));
    % case outpcc
    mixpcc2=mixpcc2+abs(corr(tp(ii,7:12)',zscoretp(7:12)'));
    mixpcc3=mixpcc3+abs(corr(tp(ii,13:18)',zscoretp(13:18)'));
    mixpcc4=mixpcc4+abs(corr(tp(ii,19:24)',zscoretp(19:24)'));
    mixpcc5=mixpcc5+abs(corr(tp(ii,25:30)',zscoretp(25:30)'));
    mixpcc6=mixpcc6+abs(corr(tp(ii,31:36)',zscoretp(31:36)'));
    mixpcc7=mixpcc7+abs(corr(tp(ii,37:42)',zscoretp(37:42)'));
    mixpcc8=mixpcc8+abs(corr(tp(ii,43:48)',zscoretp(43:48)'));
    mixpcc9=mixpcc9+abs(corr(tp(ii,49:54)',zscoretp(49:54)'));

zscoretm=(othergenes_pig(jj,:)-mean(othergenes_pig(jj,:)))/std(othergenes_pig(jj,:));

mixpcc_c1=mixpcc_c1+abs(corr(tm(ii,1:6)',zscoretm(1:6)'));
    % control outpcc
    mixpcc_c2=mixpcc_c2+abs(corr(tm(ii,7:12)',zscoretm(7:12)'));

mixpcc_c3=mixpcc_c3+abs(corr(tm(ii,13:18)',zscoretm(13:18)'));

mixpcc_c4=mixpcc_c4+abs(corr(tm(ii,19:24)',zscoretm(19:24)'));

mixpcc_c5=mixpcc_c5+abs(corr(tm(ii,25:30)',zscoretm(25:30)'));

mixpcc_c6=mixpcc_c6+abs(corr(tm(ii,31:36)',zscoretm(31:36)'));

mixpcc_c7=mixpcc_c7+abs(corr(tm(ii,37:42)',zscoretm(37:42)'));

mixpcc_c8=mixpcc_c8+abs(corr(tm(ii,43:48)',zscoretm(43:48)'));

mixpcc_c9=mixpcc_c9+abs(corr(tm(ii,51:56)',zscoretm(51:56)'));
end
end
mixpcc=[mixpcc1 mixpcc2 mixpcc3 mixpcc4 mixpcc5 mixpcc6 mixpcc7 mixpcc8
mixpcc9];
mixpcc_c=[mixpcc_c1 mixpcc_c2 mixpcc_c3 mixpcc_c4 mixpcc_c5 mixpcc_c6
mixpcc_c7 mixpcc_c8 mixpcc_c9];
mixpcc=mixpcc/k/mimimize(1);
mixpcc_c=mixpcc_c/k/mimimize(1);

tag=0;
for time=2:8
    if
        (stdrna(time)>stdrna(time-1)) && (stdrna(time)>stdrna(time+1)) && ...
        (pccrna(time)>pccrna(time-1)) && (pccrna(time)>pccrna(time+1)) && ...
        (mixpcc(time)<mixpcc(time-1)) && (mixpcc(time)<mixpcc(time+1))
        tag=1;
        break;
    end
end

```

```

end
if tag==0
    continue;
end

candidategroup3=candidategroup3+1;

compositindex=zeros(9,1);
compositindex_c=zeros(9,1);
for s=1:9
    compositindex(s)=(stdrna(s)/k)*(pccrna(s)/(k*(k-1))*2)/mixpcc(s);
compositindex_c(s)=(stdrna_c(s)/k)*(pccrna_c(s)/(k*(k-1))*2)/mixpcc_c(s);
end

figure(i);
t=[1 2 3 4 5 6 7 8 9];
subplot(1,4,1);
plot(t,stdrna,'r', t,stdrna_c,'b');
title('std3');
legend('SD_{case}','SD_{control}',2);

subplot(1,4,2);
plot(t,pccrna,'r',t,pccrna_c,'b');
title('inpcc3');
legend('PCC_{case}','PCC_{control}',2);

subplot(1,4,3);
plot(t,mixpcc,'r',t,mixpcc_c,'b');
title('outpcc3');
legend('OPCC_{case}','OPCC_{control}',2);

subplot(1,4,4);
plot(t,compositindex,'r',t,compositindex_c,'b')
title('composite index');
legend('Composite_{case}','Composite_{control}',2);
end
fclose(fpi);

filename=strcat(newpath,'time',int2str(4),'.txt');
fpi=fopen(filename,'wt');
candidategroup4=0;
for i=num2+num3+1:num4+num3+num2
    fprintf(fpi,'µŮ%d×é:\n',i);
    clear tmm;
    clear k; clear tmm; clear tp; clear zjj;
    clear k; clear tmm; clear tp; clear zjj;
    k=0; stdRNA=0;
    stdRNA1=0; stdRNA2=0; stdRNA3=0; stdRNA4=0; stdRNA5=0; stdRNA6=0;
    stdRNA7=0; stdRNA8=0; stdRNA9=0;
    stdRNA_c1=0; stdRNA_c2=0; stdRNA_c3=0; stdRNA_c4=0; stdRNA_c5=0;
    stdRNA_c6=0; stdRNA_c7=0; stdRNA_c8=0; stdRNA_c9=0;
    mixpcc1=0; mixpcc2=0; mixpcc3=0; mixpcc4=0; mixpcc5=0; mixpcc6=0;

```

```

mixpcc7=0; mixpcc8=0; mixpcc9=0;
mixpcc_c1=0; mixpcc_c2=0; mixpcc_c3=0; mixpcc_c4=0; mixpcc_c5=0;
mixpcc_c6=0; mixpcc_c7=0; mixpcc_c8=0; mixpcc_c9=0;
pccall1=0; pccall2=0; pccall3=0; pccall4=0; pccall5=0; pccall6=0;
pccall7=0; pccall8=0; pccall9=0;
pccall_c1=0; pccall_c2=0; pccall_c3=0; pccall_c4=0; pccall_c5=0;
pccall_c6=0; pccall_c7=0; pccall_c8=0; pccall_c9=0;

for j=1:length(T4)
    if i==T4(j)+num2+num3
        fprintf(fpi, '%d\t%s\n', j, usefulRNA4_id{j});
        k=k+1;
        tmm(k,:)=usefulRNA4_sick(j,:);
        zjj(k,:)=usefulRNA4_healthy(j,:);
        tp(k,:)=(tmm(k,:)-mean(zjj(k,:)))/(std(zjj(k,:))); %
case z-score
        tm(k,:)=(zjj(k,:)-mean(zjj(k,:)))/(std(zjj(k,:))); %
control z-score

        stdRNA1=stdRNA1+std(tp(k,1:6)); % case std
        stdRNA2=stdRNA2+std(tp(k,7:12));
        stdRNA3=stdRNA3+std(tp(k,13:18));
        stdRNA4=stdRNA4+std(tp(k,19:24));
        stdRNA5=stdRNA5+std(tp(k,25:30));
        stdRNA6=stdRNA6+std(tp(k,31:36));
        stdRNA7=stdRNA7+std(tp(k,37:42));
        stdRNA8=stdRNA8+std(tp(k,43:48));
        stdRNA9=stdRNA9+std(tp(k,49:54));

        stdRNA_c1=stdRNA_c1+std(tm(k,1:6)); % control std
        stdRNA_c2=stdRNA_c2+std(tm(k,7:12));
        stdRNA_c3=stdRNA_c3+std(tm(k,13:18));
        stdRNA_c4=stdRNA_c4+std(tm(k,19:24));
        stdRNA_c5=stdRNA_c5+std(tm(k,25:30));
        stdRNA_c6=stdRNA_c6+std(tm(k,31:36));
        stdRNA_c7=stdRNA_c7+std(tm(k,37:42));
        stdRNA_c9=stdRNA_c9+std(tm(k,51:56));
        stdRNA_c8=stdRNA_c8+std(tm(k,43:48));
    end
end
if k<2
    fprintf(fpi, '\n');
    continue
end

if k<10
    continue;
end

pccall1=corr(tp(:,1:6)'); % case pcc
pccall2=corr(tp(:,7:12)');
pccall3=corr(tp(:,13:18)');
pccall4=corr(tp(:,19:24)');
pccall5=corr(tp(:,25:30)');
pccall6=corr(tp(:,31:36)');
pccall7=corr(tp(:,37:42)');

```

```

pccall18=corr(tp(:,43:48)');
pccall19=corr(tp(:,49:54)');
sumpccall1=(sum(sum(abs(pccall11)))-k)/2;
sumpccall2=(sum(sum(abs(pccall12)))-k)/2;
sumpccall3=(sum(sum(abs(pccall13)))-k)/2;
sumpccall4=(sum(sum(abs(pccall14)))-k)/2;
sumpccall5=(sum(sum(abs(pccall15)))-k)/2;
sumpccall6=(sum(sum(abs(pccall16)))-k)/2;
sumpccall7=(sum(sum(abs(pccall17)))-k)/2;
sumpccall8=(sum(sum(abs(pccall18)))-k)/2;
sumpccall9=(sum(sum(abs(pccall19)))-k)/2;
%      sumpcc=(sum(sum(abs(pcc)))-k)/2;

pccall_c1=corr(tm(:,1:6)'); % control pcc
pccall_c2=corr(tm(:,7:12)');
pccall_c3=corr(tm(:,13:18)');
pccall_c4=corr(tm(:,19:24)');
pccall_c5=corr(tm(:,25:30)');
pccall_c6=corr(tm(:,31:36)');
pccall_c7=corr(tm(:,37:42)');
pccall_c8=corr(tm(:,43:48)');
pccall_c9=corr(tm(:,51:56)');
sumpccall_c1=(sum(sum(abs(pccall_c1)))-k)/2;
sumpccall_c2=(sum(sum(abs(pccall_c2)))-k)/2;
sumpccall_c3=(sum(sum(abs(pccall_c3)))-k)/2;
sumpccall_c4=(sum(sum(abs(pccall_c4)))-k)/2;
sumpccall_c5=(sum(sum(abs(pccall_c5)))-k)/2;
sumpccall_c6=(sum(sum(abs(pccall_c6)))-k)/2;
sumpccall_c7=(sum(sum(abs(pccall_c7)))-k)/2;
sumpccall_c8=(sum(sum(abs(pccall_c8)))-k)/2;
sumpccall_c9=(sum(sum(abs(pccall_c9)))-k)/2;

line=line+1;
fprintf(fpi, '\n');
validgroupnum=validgroupnum+1;
stdrna=[stdRNA1 stdRNA2 stdRNA3 stdRNA4 stdRNA5 stdRNA6 stdRNA7 stdRNA8
stdRNA9];
stdrna_c=[stdRNA_c1 stdRNA_c2 stdRNA_c3 stdRNA_c4 stdRNA_c5 stdRNA_c6
stdRNA_c7 stdRNA_c8 stdRNA_c9];
stdrna=stdrna/k;
stdrna_c=stdrna_c/k;
pccrna=sumpccall;
pccrna_c=sumpccall_c;
pccrna=pccrna/(k*(k-1))*2;
pccrna_c=pccrna_c/(k*(k-1))*2;

othergenes_mimi=setdiff(usefulRNA4_sick, tmm, 'rows');
othergenes_pig=setdiff(usefulRNA4_healthy, zjj, 'rows');
mimisize=size(othergenes_mimi);

for ii=1:k
    for jj=1:mimisize(1)

zscoretp=(othergenes_mimi(jj,:)-mean(othergenes_pig(jj,:)))/std(otherge
nes_pig(jj,:));

```

```

mixpcc1=mixpcc1+abs(corr(tp(ii,1:6)',zscoretp(1:6)'));
    % case outpcc
    mixpcc2=mixpcc2+abs(corr(tp(ii,7:12)',zscoretp(7:12)'));
    mixpcc3=mixpcc3+abs(corr(tp(ii,13:18)',zscoretp(13:18)'));
    mixpcc4=mixpcc4+abs(corr(tp(ii,19:24)',zscoretp(19:24)'));
    mixpcc5=mixpcc5+abs(corr(tp(ii,25:30)',zscoretp(25:30)'));
    mixpcc6=mixpcc6+abs(corr(tp(ii,31:36)',zscoretp(31:36)'));
    mixpcc7=mixpcc7+abs(corr(tp(ii,37:42)',zscoretp(37:42)'));
    mixpcc8=mixpcc8+abs(corr(tp(ii,43:48)',zscoretp(43:48)'));
    mixpcc9=mixpcc9+abs(corr(tp(ii,49:54)',zscoretp(49:54)'));

zscoretm=(othergenes_pig(jj,:)-mean(othergenes_pig(jj,:)))/std(othergenes_pig(jj,:));

mixpcc_c1=mixpcc_c1+abs(corr(tm(ii,1:6)',zscoretm(1:6)'));
    % control outpcc
    mixpcc_c2=mixpcc_c2+abs(corr(tm(ii,7:12)',zscoretm(7:12)'));

mixpcc_c3=mixpcc_c3+abs(corr(tm(ii,13:18)',zscoretm(13:18)'));
mixpcc_c4=mixpcc_c4+abs(corr(tm(ii,19:24)',zscoretm(19:24)'));
mixpcc_c5=mixpcc_c5+abs(corr(tm(ii,25:30)',zscoretm(25:30)'));
mixpcc_c6=mixpcc_c6+abs(corr(tm(ii,31:36)',zscoretm(31:36)'));
mixpcc_c7=mixpcc_c7+abs(corr(tm(ii,37:42)',zscoretm(37:42)'));
mixpcc_c8=mixpcc_c8+abs(corr(tm(ii,43:48)',zscoretm(43:48)'));
mixpcc_c9=mixpcc_c9+abs(corr(tm(ii,51:56)',zscoretm(51:56)'));
end
end
mixpcc=[mixpcc1 mixpcc2 mixpcc3 mixpcc4 mixpcc5 mixpcc6 mixpcc7 mixpcc8 mixpcc9];
mixpcc_c=[mixpcc_c1 mixpcc_c2 mixpcc_c3 mixpcc_c4 mixpcc_c5 mixpcc_c6 mixpcc_c7 mixpcc_c8 mixpcc_c9];
mixpcc=mixpcc/k/mimisize(1);
mixpcc_c=mixpcc_c/k/mimisize(1);

tag=0;
for time=2:8
    if
        (stdrna(time)>stdrna(time-1)) && (stdrna(time)>stdrna(time+1)) &&...

        (pccrna(time)>pccrna(time-1)) && (pccrna(time)>pccrna(time+1)) &&...

        (mixpcc(time)<mixpcc(time+1)) && (mixpcc(time)<mixpcc(time+1))
            tag=1;
            break;
        end
    end
    if tag==0
        continue;
    end
end

```

```

candidategroup4=candidategroup4+1;
compositindex_c=zeros(9,1);
compositindex=zeros(9,1);
for s=1:9
    compositindex(s)=(stdrna(s)/k)*(pccrna(s)/(k*(k-1))*2)/mixpcc(s);

compositindex_c(s)=(stdrna_c(s)/k)*(pccrna_c(s)/(k*(k-1))*2)/mixpcc_c(s);
end

figure(i);
t=[1 2 3 4 5 6 7 8 9];
subplot(1,4,1);
plot(t,stdrna,'r', t,stdrna_c,'b');
title('std4');
legend('SD_{case}','SD_{control}',2);

subplot(1,4,2);
plot(t,pccrna,'r',t,pccrna_c,'b');
title('inpcc4');
legend('PCC_{case}','PCC_{control}',2);

subplot(1,4,3);
plot(t,mixpcc,'r',t,mixpcc_c,'b');
title('outpcc4');
legend('OPCC_{case}','OPCC_{control}',2);

subplot(1,4,4);
plot(t,compositindex,'r',t,compositindex_c,'b')
title('composite index');
legend('Composite_{case}','Composite_{control}',2);

end
fclose(fpi);

filename=strcat(newpath,'time',int2str(5),'.txt');
fpi=fopen(filename,'wt');
candidategroup5=0;
for i=num2+num3+num4+1:num5+num4+num3+num2
    fprintf(fpi,'µÛ%dxé:\n',i);
    clear tm;
    clear k; clear tmm; clear tp; clear zjj;
    clear k; clear tmm; clear tp; clear zjj;
    k=0; stdRNA=0;
    stdRNA1=0; stdRNA2=0; stdRNA3=0; stdRNA4=0; stdRNA5=0; stdRNA6=0;
    stdRNA7=0; stdRNA8=0; stdRNA9=0;
    stdRNA_c1=0; stdRNA_c2=0; stdRNA_c3=0; stdRNA_c4=0; stdRNA_c5=0;
    stdRNA_c6=0; stdRNA_c7=0; stdRNA_c8=0; stdRNA_c9=0;
    mixpcc1=0; mixpcc2=0; mixpcc3=0; mixpcc4=0; mixpcc5=0; mixpcc6=0;
    mixpcc7=0; mixpcc8=0; mixpcc9=0;
    mixpcc_c1=0; mixpcc_c2=0; mixpcc_c3=0; mixpcc_c4=0; mixpcc_c5=0;
    mixpcc_c6=0; mixpcc_c7=0; mixpcc_c8=0; mixpcc_c9=0;
    pccall1=0; pccall2=0; pccall3=0; pccall4=0; pccall5=0; pccall6=0;

```

```

pccall17=0; pccall18=0; pccall19=0;
    pccall_c1=0; pccall_c2=0; pccall_c3=0; pccall_c4=0; pccall_c5=0;
pccall_c6=0; pccall_c7=0; pccall_c8=0; pccall_c9=0;

    for j=1:length(T5)
        if i==T5(j)+num2+num3+num4
            fprintf(fpi, '%d\t%s\n', j, usefulRNA5_id{j});
            k=k+1;
            tmm(k,:)=usefulRNA5_sick(j,:);
            zjj(k,:)=usefulRNA5_healthy(j,:);
            tp(k,:)=(tmm(k,:)-mean(zjj(k,:)))/(std(zjj(k,:))); %
case z-score
            tm(k,:)=(zjj(k,:)-mean(zjj(k,:)))/(std(zjj(k,:))); %
control z-score

            stdRNA1=stdRNA1+std(tp(k,1:6)); % case std
            stdRNA2=stdRNA2+std(tp(k,7:12));
            stdRNA3=stdRNA3+std(tp(k,13:18));
            stdRNA4=stdRNA4+std(tp(k,19:24));
            stdRNA5=stdRNA5+std(tp(k,25:30));
            stdRNA6=stdRNA6+std(tp(k,31:36));
            stdRNA7=stdRNA7+std(tp(k,37:42));
            stdRNA8=stdRNA8+std(tp(k,43:48));
            stdRNA9=stdRNA9+std(tp(k,49:54));

            stdRNA_c1=stdRNA_c1+std(tm(k,1:6)); % control std
            stdRNA_c2=stdRNA_c2+std(tm(k,7:12));
            stdRNA_c3=stdRNA_c3+std(tm(k,13:18));
            stdRNA_c4=stdRNA_c4+std(tm(k,19:24));
            stdRNA_c5=stdRNA_c5+std(tm(k,25:30));
            stdRNA_c6=stdRNA_c6+std(tm(k,31:36));
            stdRNA_c7=stdRNA_c7+std(tm(k,37:42));
            stdRNA_c9=stdRNA_c9+std(tm(k,51:56));
            stdRNA_c8=stdRNA_c8+std(tm(k,43:48));
        end
    end
    if k<2
        fprintf(fpi, '\n');
        continue
    end

    if k<10
        continue;
    end

    pccall1=corr(tp(:,1:6)); % case pcc
    pccall2=corr(tp(:,7:12));
    pccall3=corr(tp(:,13:18));
    pccall4=corr(tp(:,19:24));
    pccall5=corr(tp(:,25:30));
    pccall6=corr(tp(:,31:36));
    pccall7=corr(tp(:,37:42));
    pccall8=corr(tp(:,43:48));
    pccall9=corr(tp(:,49:54));
    sumpccall(1)=(sum(sum(abs(pccall1)))-k)/2;
    sumpccall(2)=(sum(sum(abs(pccall2)))-k)/2;

```

```

sumppccall(3)=(sum(sum(abs(pccall3)))-k)/2;
sumppccall(4)=(sum(sum(abs(pccall4)))-k)/2;
sumppccall(5)=(sum(sum(abs(pccall5)))-k)/2;
sumppccall(6)=(sum(sum(abs(pccall6)))-k)/2;
sumppccall(7)=(sum(sum(abs(pccall7)))-k)/2;
sumppccall(8)=(sum(sum(abs(pccall8)))-k)/2;
sumppccall(9)=(sum(sum(abs(pccall9)))-k)/2;
%      sumppcc=(sum(sum(abs(pcc)))-k)/2;

pccall_c1=corr(tm(:,1:6)'); % control pcc
pccall_c2=corr(tm(:,7:12)');
pccall_c3=corr(tm(:,13:18)');
pccall_c4=corr(tm(:,19:24)');
pccall_c5=corr(tm(:,25:30)');
pccall_c6=corr(tm(:,31:36)');
pccall_c7=corr(tm(:,37:42)');
pccall_c8=corr(tm(:,43:48)');
pccall_c9=corr(tm(:,51:56)');
sumppccall_c(1)=(sum(sum(abs(pccall_c1)))-k)/2;
sumppccall_c(2)=(sum(sum(abs(pccall_c2)))-k)/2;
sumppccall_c(3)=(sum(sum(abs(pccall_c3)))-k)/2;
sumppccall_c(4)=(sum(sum(abs(pccall_c4)))-k)/2;
sumppccall_c(5)=(sum(sum(abs(pccall_c5)))-k)/2;
sumppccall_c(6)=(sum(sum(abs(pccall_c6)))-k)/2;
sumppccall_c(7)=(sum(sum(abs(pccall_c7)))-k)/2;
sumppccall_c(8)=(sum(sum(abs(pccall_c8)))-k)/2;
sumppccall_c(9)=(sum(sum(abs(pccall_c9)))-k)/2;

line=line+1;
fprintf(fpi,'\n');
validgroupnum=validgroupnum+1;
stdrna=[stdRNA1 stdRNA2 stdRNA3 stdRNA4 stdRNA5 stdRNA6 stdRNA7 stdRNA8
stdRNA9];
stdrna_c=[stdRNA_c1 stdRNA_c2 stdRNA_c3 stdRNA_c4 stdRNA_c5 stdRNA_c6
stdRNA_c7 stdRNA_c8 stdRNA_c9];
stdrna=stdrna/k;
stdrna_c=stdrna_c/k;
pccrna=sumppccall;
pccrna_c=sumppccall_c;
pccrna=pccrna/(k*(k-1))*2;
pccrna_c=pccrna_c/(k*(k-1))*2;

%      othergenes_mimi=setdiff(caseprofile, tmm, 'rows');
%      othergenes_pig=setdiff(controlprofile, zjj, 'rows');
othergenes_mimi=setdiff(usableRNA5_sick, tmm, 'rows');
othergenes_pig=setdiff(usableRNA5_healthy, zjj, 'rows');
mimisize=size(othergenes_mimi);

for ii=1:k
    for jj=1:mimisize(1)

zscoretp=(othergenes_mimi(jj,:)-mean(othergenes_pig(jj,:)))/std(otherge
nes_pig(jj,:));

mixpccl=mixpccl+abs(corr(tp(ii,1:6)', zscoretp(1:6)'));
% case outpcc

```

```

mixpcc2=mixpcc2+abs(corr(tp(ii,7:12)',zscoretp(7:12)'));
mixpcc3=mixpcc3+abs(corr(tp(ii,13:18)',zscoretp(13:18)'));
mixpcc4=mixpcc4+abs(corr(tp(ii,19:24)',zscoretp(19:24)'));
mixpcc5=mixpcc5+abs(corr(tp(ii,25:30)',zscoretp(25:30)'));
mixpcc6=mixpcc6+abs(corr(tp(ii,31:36)',zscoretp(31:36)'));
mixpcc7=mixpcc7+abs(corr(tp(ii,37:42)',zscoretp(37:42)'));
mixpcc8=mixpcc8+abs(corr(tp(ii,43:48)',zscoretp(43:48)'));
mixpcc9=mixpcc9+abs(corr(tp(ii,49:54)',zscoretp(49:54)'));

zscoretm=(othergenes_pig(jj,:)-mean(othergenes_pig(jj,:)))/std(othergenes_pig(jj,:));

mixpcc_c1=mixpcc_c1+abs(corr(tm(ii,1:6)',zscoretm(1:6)'));
    % control outpcc
    mixpcc_c2=mixpcc_c2+abs(corr(tm(ii,7:12)',zscoretm(7:12)'));

mixpcc_c3=mixpcc_c3+abs(corr(tm(ii,13:18)',zscoretm(13:18)'));
mixpcc_c4=mixpcc_c4+abs(corr(tm(ii,19:24)',zscoretm(19:24)'));
mixpcc_c5=mixpcc_c5+abs(corr(tm(ii,25:30)',zscoretm(25:30)'));
mixpcc_c6=mixpcc_c6+abs(corr(tm(ii,31:36)',zscoretm(31:36)'));
mixpcc_c7=mixpcc_c7+abs(corr(tm(ii,37:42)',zscoretm(37:42)'));
mixpcc_c8=mixpcc_c8+abs(corr(tm(ii,43:48)',zscoretm(43:48)'));
mixpcc_c9=mixpcc_c9+abs(corr(tm(ii,51:56)',zscoretm(51:56)'));
end
end
mixpcc=[mixpcc1 mixpcc2 mixpcc3 mixpcc4 mixpcc5 mixpcc6 mixpcc7 mixpcc8
mixpcc9];
mixpcc_c=[mixpcc_c1 mixpcc_c2 mixpcc_c3 mixpcc_c4 mixpcc_c5 mixpcc_c6
mixpcc_c7 mixpcc_c8 mixpcc_c9];
mixpcc=mixpcc/k/mimisize(1);
mixpcc_c=mixpcc_c/k/mimisize(1);

tag=0;
for time=2:8
    if
        (stdrna(time)>stdrna(time-1)) && (stdrna(time)>stdrna(time+1)) && ...
        (pccrna(time)>pccrna(time-1)) && (pccrna(time)>pccrna(time+1)) && ...
        (mixpcc(time)<mixpcc(time+1)) && (mixpcc(time)<mixpcc(time+1))
            tag=1;
            break;
        end
    end
    if tag==0
        continue;
    end
    candidategroup5=candidategroup5+1;

```

```

compositindex=zeros(9,1);
compositindex_c=zeros(9,1);
for s=1:9
    compositindex(s)=(stdrna(s)/k)*(pccrna(s)/(k*(k-1))*2)/mixpcc(s);

compositindex_c(s)=(stdrna_c(s)/k)*(pccrna_c(s)/(k*(k-1))*2)/mixpcc_c(s);
end

figure(i);
t=[1 2 3 4 5 6 7 8 9];
subplot(1,4,1);
plot(t,stdrna,'r', t,stdrna_c,'b');
title('std5');
legend('SD_{case}','SD_{control}',2);

subplot(1,4,2);
plot(t,pccrna,'r',t,pccrna_c,'b');
title('inpcc5');
legend('PCC_{case}','PCC_{control}',2);

subplot(1,4,3);
plot(t,mixpcc,'r',t,mixpcc_c,'b');
title('outpcc5');
legend('OPCC_{case}','OPCC_{control}',2);

subplot(1,4,4);
plot(t,compositindex,'r',t,compositindex_c,'b')
title('composite index');
legend('Composite_{case}','Composite_{control}',2);
end
fclose(fpi);

filename=strcat(newpath,'time',int2str(6),'.txt');
fpi=fopen(filename,'wt');
candidategroup6=0;
for i=num2+num3+num4+num5+1:num6+num5+num4+num3+num2
    fprintf(fpi,'µŮ%d×é:\n',i);
    clear tm;
    clear k; clear tmm; clear tp; clear zjj;
    clear k; clear tmm; clear tp; clear zjj;
    k=0; stdRNA=0;
    stdRNA1=0; stdRNA2=0; stdRNA3=0; stdRNA4=0; stdRNA5=0; stdRNA6=0;
    stdRNA7=0; stdRNA8=0; stdRNA9=0;
    stdRNA_c1=0; stdRNA_c2=0; stdRNA_c3=0; stdRNA_c4=0; stdRNA_c5=0;
    stdRNA_c6=0; stdRNA_c7=0; stdRNA_c8=0; stdRNA_c9=0;
    mixpcc1=0; mixpcc2=0; mixpcc3=0; mixpcc4=0; mixpcc5=0; mixpcc6=0;
    mixpcc7=0; mixpcc8=0; mixpcc9=0;
    mixpcc_c1=0; mixpcc_c2=0; mixpcc_c3=0; mixpcc_c4=0; mixpcc_c5=0;
    mixpcc_c6=0; mixpcc_c7=0; mixpcc_c8=0; mixpcc_c9=0;
    pccall1=0; pccall2=0; pccall3=0; pccall4=0; pccall5=0; pccall6=0;
    pccall7=0; pccall8=0; pccall9=0;
    pccall_c1=0; pccall_c2=0; pccall_c3=0; pccall_c4=0; pccall_c5=0;
    pccall_c6=0; pccall_c7=0; pccall_c8=0; pccall_c9=0;

    for j=1:length(T6)

```

```

if i==T6(j)+num2+num3+num4+num5
    fprintf(fpi, '%d\t%s\n', j, usefulRNA6_id{j});
    k=k+1;
    tmm(k,:)=usefulRNA6_sick(j,:);
    zjj(k,:)=usefulRNA6_healthy(j,:);
    tp(k,:)=(tmm(k,:)-mean(zjj(k,:)))/(std(zjj(k,:))); %
case z-score
    tm(k,:)=(zjj(k,:)-mean(zjj(k,:)))/(std(zjj(k,:))); %
control z-score

    stdRNA1=stdRNA1+std(tp(k,1:6)); % case std
    stdRNA2=stdRNA2+std(tp(k,7:12));
    stdRNA3=stdRNA3+std(tp(k,13:18));
    stdRNA4=stdRNA4+std(tp(k,19:24));
    stdRNA5=stdRNA5+std(tp(k,25:30));
    stdRNA6=stdRNA6+std(tp(k,31:36));
    stdRNA7=stdRNA7+std(tp(k,37:42));
    stdRNA8=stdRNA8+std(tp(k,43:48));
    stdRNA9=stdRNA9+std(tp(k,49:54));

    stdRNA_c1=stdRNA_c1+std(tm(k,1:6)); % control std
    stdRNA_c2=stdRNA_c2+std(tm(k,7:12));
    stdRNA_c3=stdRNA_c3+std(tm(k,13:18));
    stdRNA_c4=stdRNA_c4+std(tm(k,19:24));
    stdRNA_c5=stdRNA_c5+std(tm(k,25:30));
    stdRNA_c6=stdRNA_c6+std(tm(k,31:36));
    stdRNA_c7=stdRNA_c7+std(tm(k,37:42));
    stdRNA_c9=stdRNA_c9+std(tm(k,51:56));
    stdRNA_c8=stdRNA_c8+std(tm(k,43:48));
end
end
if k<2
    fprintf(fpi, '\n');
    continue
end

if k<10
    continue;
end

pccall1=corr(tp(:,1:6)); % case pcc
pccall2=corr(tp(:,7:12));
pccall3=corr(tp(:,13:18));
pccall4=corr(tp(:,19:24));
pccall5=corr(tp(:,25:30));
pccall6=corr(tp(:,31:36));
pccall7=corr(tp(:,37:42));
pccall8=corr(tp(:,43:48));
pccall9=corr(tp(:,49:54));
sumpccall(1)=(sum(sum(abs(pccall1)))-k)/2;
sumpccall(2)=(sum(sum(abs(pccall2)))-k)/2;
sumpccall(3)=(sum(sum(abs(pccall3)))-k)/2;
sumpccall(4)=(sum(sum(abs(pccall4)))-k)/2;
sumpccall(5)=(sum(sum(abs(pccall5)))-k)/2;
sumpccall(6)=(sum(sum(abs(pccall6)))-k)/2;
sumpccall(7)=(sum(sum(abs(pccall7)))-k)/2;

```

```

sumpccall(8)=(sum(sum(abs(pccall8)))-k)/2;
sumpccall(9)=(sum(sum(abs(pccall9)))-k)/2;
%      sumpcc=(sum(sum(abs(pcc)))-k)/2;

pccall_c1=corr(tm(:,1:6)'); % control pcc
pccall_c2=corr(tm(:,7:12)');
pccall_c3=corr(tm(:,13:18)');
pccall_c4=corr(tm(:,19:24)');
pccall_c5=corr(tm(:,25:30)');
pccall_c6=corr(tm(:,31:36)');
pccall_c7=corr(tm(:,37:42)');
pccall_c8=corr(tm(:,43:48)');
pccall_c9=corr(tm(:,51:56)');
sumpccall_c(1)=(sum(sum(abs(pccall_c1)))-k)/2;
sumpccall_c(2)=(sum(sum(abs(pccall_c2)))-k)/2;
sumpccall_c(3)=(sum(sum(abs(pccall_c3)))-k)/2;
sumpccall_c(4)=(sum(sum(abs(pccall_c4)))-k)/2;
sumpccall_c(5)=(sum(sum(abs(pccall_c5)))-k)/2;
sumpccall_c(6)=(sum(sum(abs(pccall_c6)))-k)/2;
sumpccall_c(7)=(sum(sum(abs(pccall_c7)))-k)/2;
sumpccall_c(8)=(sum(sum(abs(pccall_c8)))-k)/2;
sumpccall_c(9)=(sum(sum(abs(pccall_c9)))-k)/2;

line=line+1;
fprintf(fpi,'\n');
validgroupnum=validgroupnum+1;
stdrna=[stdRNA1 stdRNA2 stdRNA3 stdRNA4 stdRNA5 stdRNA6 stdRNA7 stdRNA8
stdRNA9];
stdrna_c=[stdRNA_c1 stdRNA_c2 stdRNA_c3 stdRNA_c4 stdRNA_c5 stdRNA_c6
stdRNA_c7 stdRNA_c8 stdRNA_c9];
stdrna=stdrna/k;
stdrna_c=stdrna_c/k;
pccrna=sumpccall;
pccrna_c=sumpccall_c;
pccrna=pccrna/(k*(k-1))*2;
pccrna_c=pccrna_c/(k*(k-1))*2;

othergenes_mimi=setdiff(usefulRNA6_sick, tmm, 'rows');
othergenes_pig=setdiff(usefulRNA6_healthy, zjj, 'rows');
mimisize=size(othergenes_mimi);

for ii=1:k
    for jj=1:mimisize(1)

zscoretp=(othergenes_mimi(jj,:)-mean(othergenes_pig(jj,:)))/std(otherge
nes_pig(jj,:));

mixpcc1=mixpcc1+abs(corr(tp(ii,1:6)', zscoretp(1:6)'));
% case outpcc
mixpcc2=mixpcc2+abs(corr(tp(ii,7:12)', zscoretp(7:12)'));
mixpcc3=mixpcc3+abs(corr(tp(ii,13:18)', zscoretp(13:18)'));
mixpcc4=mixpcc4+abs(corr(tp(ii,19:24)', zscoretp(19:24)'));
mixpcc5=mixpcc5+abs(corr(tp(ii,25:30)', zscoretp(25:30)'));
mixpcc6=mixpcc6+abs(corr(tp(ii,31:36)', zscoretp(31:36)'));
mixpcc7=mixpcc7+abs(corr(tp(ii,37:42)', zscoretp(37:42)'));

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```

mixpcc8=mixpcc8+abs(corr(tp(ii,43:48)',zscoretp(43:48)'));
mixpcc9=mixpcc9+abs(corr(tp(ii,49:54)',zscoretp(49:54)'));

zscoretm=(othergenes_pig(jj,:)-mean(othergenes_pig(jj,:)))/std(othergenes_pig(jj,:));

mixpcc_c1=mixpcc_c1+abs(corr(tm(ii,1:6)',zscoretm(1:6)'));
    % control outpcc
    mixpcc_c2=mixpcc_c2+abs(corr(tm(ii,7:12)',zscoretm(7:12)'));

mixpcc_c3=mixpcc_c3+abs(corr(tm(ii,13:18)',zscoretm(13:18)'));
mixpcc_c4=mixpcc_c4+abs(corr(tm(ii,19:24)',zscoretm(19:24)'));
mixpcc_c5=mixpcc_c5+abs(corr(tm(ii,25:30)',zscoretm(25:30)'));
mixpcc_c6=mixpcc_c6+abs(corr(tm(ii,31:36)',zscoretm(31:36)'));
mixpcc_c7=mixpcc_c7+abs(corr(tm(ii,37:42)',zscoretm(37:42)'));
mixpcc_c8=mixpcc_c8+abs(corr(tm(ii,43:48)',zscoretm(43:48)'));
mixpcc_c9=mixpcc_c9+abs(corr(tm(ii,51:56)',zscoretm(51:56)'));
end
end
mixpcc=[mixpcc1 mixpcc2 mixpcc3 mixpcc4 mixpcc5 mixpcc6 mixpcc7 mixpcc8
mixpcc9];
mixpcc_c=[mixpcc_c1 mixpcc_c2 mixpcc_c3 mixpcc_c4 mixpcc_c5 mixpcc_c6
mixpcc_c7 mixpcc_c8 mixpcc_c9];
mixpcc=mixpcc/k/mimisize(1);
mixpcc_c=mixpcc_c/k/mimisize(1);

tag=0;
for time=2:8
    if
        (stdrna(time)>stdrna(time-1)) && (stdrna(time)>stdrna(time+1)) && ...
        (pccrna(time)>pccrna(time-1)) && (pccrna(time)>pccrna(time+1)) && ...
        (mixpcc(time)<mixpcc(time+1)) && (mixpcc(time)<mixpcc(time+1))
            tag=1;
            break;
        end
    end
    if tag==0
        continue;
    end

candidategroup6=candidategroup6+1;

compositindex=zeros(9,1);
compositindex_c=zeros(9,1);
for s=1:9
    compositindex(s)=(stdrna(s)/k)*(pccrna(s)/(k*(k-1))*2)/mixpcc(s);

```

```

compositindex_c(s)=(stdrna_c(s)/k)*(pccrna_c(s)/(k*(k-1))*2)/mixpcc_c(s
);
    end

    figure(i);
    t=[1 2 3 4 5 6 7 8 9];
    subplot(1,4,1);
    plot(t,stdrna,'r', t,stdrna_c,'b');
    title('std6');
    legend('SD_{case}','SD_{control}',2);

    subplot(1,4,2);
    plot(t,pccrna,'r',t,pccrna_c,'b');
    title('inpcc6');
    legend('PCC_{case}','PCC_{control}',2);

    subplot(1,4,3);
    plot(t,mixpcc,'r',t,mixpcc_c,'b');
    title('outpcc6');
    legend('OPCC_{case}','OPCC_{control}',2);

    subplot(1,4,4);
    plot(t,compositindex,'r',t,compositindex_c,'b')
    title('composite index');
    legend('Composite_{case}','Composite_{control}',2);
end
fclose(fpi);

filename=strcat(newpath,'time',int2str(7),'.txt');
fpi=fopen(filename,'wt');
candidategroup7=0;
for i=num2+num3+num4+num5+num6+1:num7+num6+num5+num4+num3+num2
    fprintf(fpi,'µŮ%d×é:\n',i);
    clear tm;
    clear k; clear tmm; clear tp; clear zjj;
    clear k; clear tmm; clear tp; clear zjj;
    k=0; stdRNA=0;
    stdRNA1=0; stdRNA2=0; stdRNA3=0; stdRNA4=0; stdRNA5=0; stdRNA6=0;
    stdRNA7=0; stdRNA8=0; stdRNA9=0;
    stdRNA_c1=0; stdRNA_c2=0; stdRNA_c3=0; stdRNA_c4=0; stdRNA_c5=0;
    stdRNA_c6=0; stdRNA_c7=0; stdRNA_c8=0; stdRNA_c9=0;
    mixpcc1=0; mixpcc2=0; mixpcc3=0; mixpcc4=0; mixpcc5=0; mixpcc6=0;
    mixpcc7=0; mixpcc8=0; mixpcc9=0;
    mixpcc_c1=0; mixpcc_c2=0; mixpcc_c3=0; mixpcc_c4=0; mixpcc_c5=0;
    mixpcc_c6=0; mixpcc_c7=0; mixpcc_c8=0; mixpcc_c9=0;
    pccall1=0; pccall2=0; pccall3=0; pccall4=0; pccall5=0; pccall6=0;
    pccall7=0; pccall8=0; pccall9=0;
    pccall_c1=0; pccall_c2=0; pccall_c3=0; pccall_c4=0; pccall_c5=0;
    pccall_c6=0; pccall_c7=0; pccall_c8=0; pccall_c9=0;

    for j=1:length(T7)
        if i==T7(j)+num2+num3+num4+num5+num6
            fprintf(fpi,'%d\t%s\n',j,usefulRNA7_id{j});
            k=k+1;
            tmm(k,:)=usefulRNA7_sick(j,:);
            zjj(k,:)=usefulRNA7_healthy(j,:);

```

```

        tp(k,:)=(tmm(k,:)-mean(zjj(k,:)))/(std(zjj(k,:))); %
case z-score
        tm(k,:)=(zjj(k,:)-mean(zjj(k,:)))/(std(zjj(k,:))); %
control z-score

        stdRNA1=stdRNA1+std(tp(k,1:6)); % case std
        stdRNA2=stdRNA2+std(tp(k,7:12));
        stdRNA3=stdRNA3+std(tp(k,13:18));
        stdRNA4=stdRNA4+std(tp(k,19:24));
        stdRNA5=stdRNA5+std(tp(k,25:30));
        stdRNA6=stdRNA6+std(tp(k,31:36));
        stdRNA7=stdRNA7+std(tp(k,37:42));
        stdRNA8=stdRNA8+std(tp(k,43:48));
        stdRNA9=stdRNA9+std(tp(k,49:54));

        stdRNA_c1=stdRNA_c1+std(tm(k,1:6)); % control std
        stdRNA_c2=stdRNA_c2+std(tm(k,7:12));
        stdRNA_c3=stdRNA_c3+std(tm(k,13:18));
        stdRNA_c4=stdRNA_c4+std(tm(k,19:24));
        stdRNA_c5=stdRNA_c5+std(tm(k,25:30));
        stdRNA_c6=stdRNA_c6+std(tm(k,31:36));
        stdRNA_c7=stdRNA_c7+std(tm(k,37:42));
        stdRNA_c9=stdRNA_c9+std(tm(k,51:56));
        stdRNA_c8=stdRNA_c8+std(tm(k,43:48));
    end
end
if k<2
    fprintf(fpi,'\n');
    continue
end

if k<10
    continue;
end

pccall1=corr(tp(:,1:6)'); % case pcc
pccall2=corr(tp(:,7:12)');
pccall3=corr(tp(:,13:18)');
pccall4=corr(tp(:,19:24)');
pccall5=corr(tp(:,25:30)');
pccall6=corr(tp(:,31:36)');
pccall7=corr(tp(:,37:42)');
pccall8=corr(tp(:,43:48)');
pccall9=corr(tp(:,49:54)');
sumpccall(1)=(sum(sum(abs(pccall1)))-k)/2;
sumpccall(2)=(sum(sum(abs(pccall2)))-k)/2;
sumpccall(3)=(sum(sum(abs(pccall3)))-k)/2;
sumpccall(4)=(sum(sum(abs(pccall4)))-k)/2;
sumpccall(5)=(sum(sum(abs(pccall5)))-k)/2;
sumpccall(6)=(sum(sum(abs(pccall6)))-k)/2;
sumpccall(7)=(sum(sum(abs(pccall7)))-k)/2;
sumpccall(8)=(sum(sum(abs(pccall8)))-k)/2;
sumpccall(9)=(sum(sum(abs(pccall9)))-k)/2;
% sumppcc=(sum(sum(abs(pcc)))-k)/2;

pccall_c1=corr(tm(:,1:6)'); % control pcc

```

```

pccall_c2=corr(tm(:,7:12)');
pccall_c3=corr(tm(:,13:18)');
pccall_c4=corr(tm(:,19:24)');
pccall_c5=corr(tm(:,25:30)');
pccall_c6=corr(tm(:,31:36)');
pccall_c7=corr(tm(:,37:42)');
pccall_c8=corr(tm(:,43:48)');
pccall_c9=corr(tm(:,51:56)');
sumpccall_c(1)=(sum(sum(abs(pccall_c1)))-k)/2;
sumpccall_c(2)=(sum(sum(abs(pccall_c2)))-k)/2;
sumpccall_c(3)=(sum(sum(abs(pccall_c3)))-k)/2;
sumpccall_c(4)=(sum(sum(abs(pccall_c4)))-k)/2;
sumpccall_c(5)=(sum(sum(abs(pccall_c5)))-k)/2;
sumpccall_c(6)=(sum(sum(abs(pccall_c6)))-k)/2;
sumpccall_c(7)=(sum(sum(abs(pccall_c7)))-k)/2;
sumpccall_c(8)=(sum(sum(abs(pccall_c8)))-k)/2;
sumpccall_c(9)=(sum(sum(abs(pccall_c9)))-k)/2;

line=line+1;
fprintf(fpi, '\n');
validgroupnum=validgroupnum+1;
stdrna=[stdRNA1 stdRNA2 stdRNA3 stdRNA4 stdRNA5 stdRNA6 stdRNA7 stdRNA8
stdRNA9];
stdrna_c=[stdRNA_c1 stdRNA_c2 stdRNA_c3 stdRNA_c4 stdRNA_c5 stdRNA_c6
stdRNA_c7 stdRNA_c8 stdRNA_c9];
stdrna=stdrna/k;
stdrna_c=stdrna_c/k;
pccrna=sumpccall;
pccrna_c=sumpccall_c;
pccrna=pccrna/(k*(k-1))*2;
pccrna_c=pccrna_c/(k*(k-1))*2;

othergenes_mimi=setdiff(usefulRNA7_sick, tmm, 'rows');
othergenes_pig=setdiff(usefulRNA7_healthy, zjj, 'rows');
mimisize=size(othergenes_mimi);

for ii=1:k
    for jj=1:mimisize(1)

zscoretp=(othergenes_mimi(jj,:)-mean(othergenes_pig(jj,:)))/std(othergenes_pig(jj,:));

mixpcc1=mixpcc1+abs(corr(tp(ii,1:6)', zscoretp(1:6)'));
    % case outpcc
    mixpcc2=mixpcc2+abs(corr(tp(ii,7:12)', zscoretp(7:12)'));
    mixpcc3=mixpcc3+abs(corr(tp(ii,13:18)', zscoretp(13:18)'));
    mixpcc4=mixpcc4+abs(corr(tp(ii,19:24)', zscoretp(19:24)'));
    mixpcc5=mixpcc5+abs(corr(tp(ii,25:30)', zscoretp(25:30)'));
    mixpcc6=mixpcc6+abs(corr(tp(ii,31:36)', zscoretp(31:36)'));
    mixpcc7=mixpcc7+abs(corr(tp(ii,37:42)', zscoretp(37:42)'));
    mixpcc8=mixpcc8+abs(corr(tp(ii,43:48)', zscoretp(43:48)'));
    mixpcc9=mixpcc9+abs(corr(tp(ii,49:54)', zscoretp(49:54)'));

zscoretm=(othergenes_pig(jj,:)-mean(othergenes_pig(jj,:)))/std(othergenes_pig(jj,:));

```

```

es_pig(jj,:));

mixpcc_c1=mixpcc_c1+abs(corr(tm(ii,1:6)',zscoretm(1:6)'));
    % control outpcc
    mixpcc_c2=mixpcc_c2+abs(corr(tm(ii,7:12)',zscoretm(7:12)'));

mixpcc_c3=mixpcc_c3+abs(corr(tm(ii,13:18)',zscoretm(13:18)'));
mixpcc_c4=mixpcc_c4+abs(corr(tm(ii,19:24)',zscoretm(19:24)'));
mixpcc_c5=mixpcc_c5+abs(corr(tm(ii,25:30)',zscoretm(25:30)'));
mixpcc_c6=mixpcc_c6+abs(corr(tm(ii,31:36)',zscoretm(31:36)'));
mixpcc_c7=mixpcc_c7+abs(corr(tm(ii,37:42)',zscoretm(37:42)'));
mixpcc_c8=mixpcc_c8+abs(corr(tm(ii,43:48)',zscoretm(43:48)'));
mixpcc_c9=mixpcc_c9+abs(corr(tm(ii,51:56)',zscoretm(51:56)'));
    end
    end
    mixpcc=[mixpcc1 mixpcc2 mixpcc3 mixpcc4 mixpcc5 mixpcc6 mixpcc7 mixpcc8
mixpcc9];
    mixpcc_c=[mixpcc_c1 mixpcc_c2 mixpcc_c3 mixpcc_c4 mixpcc_c5 mixpcc_c6
mixpcc_c7 mixpcc_c8 mixpcc_c9];
    mixpcc=mixpcc/k/mimisize(1);
    mixpcc_c=mixpcc_c/k/mimisize(1);

    tag=0;
    for time=2:8
        if
            (stdrna(time)>stdrna(time-1)) && (stdrna(time)>stdrna(time+1)) && ...
            (pccrna(time)>pccrna(time-1)) && (pccrna(time)>pccrna(time+1)) && ...
            (mixpcc(time)<mixpcc(time+1)) && (mixpcc(time)<mixpcc(time+1))
                tag=1;
                break;
            end
        end
        if tag==0
            continue;
        end

        candidategroup6=candidategroup6+1;

        compositindex=zeros(9,1);
        compositindex_c=zeros(9,1);
        for s=1:9
            compositindex(s)=(stdrna(s)/k)*(pccrna(s)/(k*(k-1))^2)/mixpcc(s);
            compositindex_c(s)=(stdrna_c(s)/k)*(pccrna_c(s)/(k*(k-1))^2)/mixpcc_c(s);
        end

        figure(i);

```

```

t=[1 2 3 4 5 6 7 8 9];
subplot(1,4,1);
plot(t,stdrna,'r', t,stdrna_c,'b');
title('std7');
legend('SD_{case}','SD_{control}',2);

subplot(1,4,2);
plot(t,pccrna,'r',t,pccrna_c,'b');
title('inpcc7');
legend('PCC_{case}','PCC_{control}',2);

subplot(1,4,3);
plot(t,mixpcc,'r',t,mixpcc_c,'b');
title('outpcc7');
legend('OPCC_{case}','OPCC_{control}',2);

subplot(1,4,4);
plot(t,compositindex,'r',t,compositindex_c,'b')
title('composite index');
legend('Composite_{case}','Composite_{control}',2);
end
fclose(fpi);

filename=strcat(newpath,'time',int2str(8),'.txt');
fpi=fopen(filename,'wt');
candidategroup8=0;
for i=num2+num3+num4+num5+num6+num7+1:num8+num7+num6+num5+num4+num3+num2
    fprintf(fpi,'µŮ%d×é:\n',i);
    clear tm;
    clear k; clear tmm; clear tp; clear zjj;
    k=0; stdRNA=0;
    stdRNA1=0; stdRNA2=0; stdRNA3=0; stdRNA4=0; stdRNA5=0; stdRNA6=0;
stdRNA7=0; stdRNA8=0; stdRNA9=0;
    stdRNA_c1=0; stdRNA_c2=0; stdRNA_c3=0; stdRNA_c4=0; stdRNA_c5=0;
stdRNA_c6=0; stdRNA_c7=0; stdRNA_c8=0; stdRNA_c9=0;
    mixpcc1=0; mixpcc2=0; mixpcc3=0; mixpcc4=0; mixpcc5=0; mixpcc6=0;
mixpcc7=0; mixpcc8=0; mixpcc9=0;
    mixpcc_c1=0; mixpcc_c2=0; mixpcc_c3=0; mixpcc_c4=0; mixpcc_c5=0;
mixpcc_c6=0; mixpcc_c7=0; mixpcc_c8=0; mixpcc_c9=0;
    pccall1=0; pccall2=0; pccall3=0; pccall4=0; pccall5=0; pccall6=0;
pccall7=0; pccall8=0; pccall9=0;
    pccall_c1=0; pccall_c2=0; pccall_c3=0; pccall_c4=0; pccall_c5=0;
pccall_c6=0; pccall_c7=0; pccall_c8=0; pccall_c9=0;

    for j=1:length(T8)
        if i==T8(j)+num2+num3+num4+num5+num6+num7
            fprintf(fpi,'%d\t%s\n',j,usefulRNA8_id{j});
            k=k+1;
            tmm(k,:)=usefulRNA8_sick(j,:);
            zjj(k,:)=usefulRNA8_healthy(j,:);
            tp(k,:)=(tmm(k,:)-mean(zjj(k,:)))/(std(zjj(k,:))); %
case z-score
            tm(k,:)=(zjj(k,:)-mean(zjj(k,:)))/(std(zjj(k,:))); %
control z-score

            stdRNA1=stdRNA1+std(tp(k,1:6)); % case std

```

```

stdRNA2=stdRNA2+std(tp(k,7:12));
stdRNA3=stdRNA3+std(tp(k,13:18));
stdRNA4=stdRNA4+std(tp(k,19:24));
stdRNA5=stdRNA5+std(tp(k,25:30));
stdRNA6=stdRNA6+std(tp(k,31:36));
stdRNA7=stdRNA7+std(tp(k,37:42));
stdRNA8=stdRNA8+std(tp(k,43:48));
stdRNA9=stdRNA9+std(tp(k,49:54));

stdRNA_c1=stdRNA_c1+std(tm(k,1:6));           % control std
stdRNA_c2=stdRNA_c2+std(tm(k,7:12));
stdRNA_c3=stdRNA_c3+std(tm(k,13:18));
stdRNA_c4=stdRNA_c4+std(tm(k,19:24));
stdRNA_c5=stdRNA_c5+std(tm(k,25:30));
stdRNA_c6=stdRNA_c6+std(tm(k,31:36));
stdRNA_c7=stdRNA_c7+std(tm(k,37:42));
stdRNA_c9=stdRNA_c9+std(tm(k,51:56));
stdRNA_c8=stdRNA_c8+std(tm(k,43:48));
end
end
if k<2
    fprintf(fpi,'\n');
    continue
end

if k<10
    continue;
end

pccall1=corr(tp(:,1:6)');           % case pcc
pccall2=corr(tp(:,7:12)');
pccall3=corr(tp(:,13:18)');
pccall4=corr(tp(:,19:24)');
pccall5=corr(tp(:,25:30)');
pccall6=corr(tp(:,31:36)');
pccall7=corr(tp(:,37:42)');
pccall8=corr(tp(:,43:48)');
pccall9=corr(tp(:,49:54)');
sumpccall(1)=(sum(sum(abs(pccall1)))-k)/2;
sumpccall(2)=(sum(sum(abs(pccall2)))-k)/2;
sumpccall(3)=(sum(sum(abs(pccall3)))-k)/2;
sumpccall(4)=(sum(sum(abs(pccall4)))-k)/2;
sumpccall(5)=(sum(sum(abs(pccall5)))-k)/2;
sumpccall(6)=(sum(sum(abs(pccall6)))-k)/2;
sumpccall(7)=(sum(sum(abs(pccall7)))-k)/2;
sumpccall(8)=(sum(sum(abs(pccall8)))-k)/2;
sumpccall(9)=(sum(sum(abs(pccall9)))-k)/2;
%     sumpcc=(sum(sum(abs(pcc)))-k)/2;

pccall_c1=corr(tm(:,1:6)');           % control pcc
pccall_c2=corr(tm(:,7:12)');
pccall_c3=corr(tm(:,13:18)');
pccall_c4=corr(tm(:,19:24)');
pccall_c5=corr(tm(:,25:30)');
pccall_c6=corr(tm(:,31:36)');
pccall_c7=corr(tm(:,37:42)');

```

```

pccall_c8=corr(tm(:,43:48)');
pccall_c9=corr(tm(:,51:56)');
sumpccall_c(1)=(sum(sum(abs(pccall_c1)))-k)/2;
sumpccall_c(2)=(sum(sum(abs(pccall_c2)))-k)/2;
sumpccall_c(3)=(sum(sum(abs(pccall_c3)))-k)/2;
sumpccall_c(4)=(sum(sum(abs(pccall_c4)))-k)/2;
sumpccall_c(5)=(sum(sum(abs(pccall_c5)))-k)/2;
sumpccall_c(6)=(sum(sum(abs(pccall_c6)))-k)/2;
sumpccall_c(7)=(sum(sum(abs(pccall_c7)))-k)/2;
sumpccall_c(8)=(sum(sum(abs(pccall_c8)))-k)/2;
sumpccall_c(9)=(sum(sum(abs(pccall_c9)))-k)/2;
%      sumpcc=(sum(sum(abs(pcc)))-k)/2;

avestd1=stdRNA1/k;
avestd2=stdRNA2/k;
avestd3=stdRNA3/k;
avestd4=stdRNA4/k;
avestd5=stdRNA5/k;
avestd6=stdRNA6/k;
avestd7=stdRNA6/k;
avestd8=stdRNA6/k;
avestd9=stdRNA6/k;
avepcc1=sumpccall(1)/(k*(k-1))*2;
avepcc2=sumpccall(2)/(k*(k-1))*2;
avepcc3=sumpccall(3)/(k*(k-1))*2;
avepcc4=sumpccall(4)/(k*(k-1))*2;
avepcc5=sumpccall(5)/(k*(k-1))*2;
avepcc6=sumpccall(6)/(k*(k-1))*2;
avepcc7=sumpccall(7)/(k*(k-1))*2;
avepcc8=sumpccall(8)/(k*(k-1))*2;
avepcc9=sumpccall(9)/(k*(k-1))*2;

line=line+1;
fprintf(fpi, '\n');
validgroupnum=validgroupnum+1;
stdrna=[stdRNA1 stdRNA2 stdRNA3 stdRNA4 stdRNA5 stdRNA6 stdRNA7 stdRNA8
stdRNA9];
stdrna_c=[stdRNA_c1 stdRNA_c2 stdRNA_c3 stdRNA_c4 stdRNA_c5 stdRNA_c6
stdRNA_c7 stdRNA_c8 stdRNA_c9];
stdrna=stdrna/k;
stdrna_c=stdrna_c/k;
pccrna=sumpccall;
pccrna_c=sumpccall_c;
pccrna=pccrna/(k*(k-1))*2;
pccrna_c=pccrna_c/(k*(k-1))*2;

othergenes_mimi=setdiff(usefulRNA8_sick, tmm, 'rows');
othergenes_pig=setdiff(usefulRNA8_healthy, zjj, 'rows');
mimisize=size(othergenes_mimi);

for ii=1:k
    for jj=1:mimisize(1)

zscoretp=(othergenes_mimi(jj,:)-mean(othergenes_pig(jj,:)))/std(otherge
nes_pig(jj,:));

```

```

mixpcc1=mixpcc1+abs(corr(tp(ii,1:6)',zscoretp(1:6)'));
    % case outpcc
    mixpcc2=mixpcc2+abs(corr(tp(ii,7:12)',zscoretp(7:12)'));
    mixpcc3=mixpcc3+abs(corr(tp(ii,13:18)',zscoretp(13:18)'));
    mixpcc4=mixpcc4+abs(corr(tp(ii,19:24)',zscoretp(19:24)'));
    mixpcc5=mixpcc5+abs(corr(tp(ii,25:30)',zscoretp(25:30)'));
    mixpcc6=mixpcc6+abs(corr(tp(ii,31:36)',zscoretp(31:36)'));
    mixpcc7=mixpcc7+abs(corr(tp(ii,37:42)',zscoretp(37:42)'));
    mixpcc8=mixpcc8+abs(corr(tp(ii,43:48)',zscoretp(43:48)'));
    mixpcc9=mixpcc9+abs(corr(tp(ii,49:54)',zscoretp(49:54)'));

zscoretm=(othergenes_pig(jj,:)-mean(othergenes_pig(jj,:)))/std(othergenes_pig(jj,:));

mixpcc_c1=mixpcc_c1+abs(corr(tm(ii,1:6)',zscoretm(1:6)'));
    % control outpcc
    mixpcc_c2=mixpcc_c2+abs(corr(tm(ii,7:12)',zscoretm(7:12)'));

mixpcc_c3=mixpcc_c3+abs(corr(tm(ii,13:18)',zscoretm(13:18)'));
mixpcc_c4=mixpcc_c4+abs(corr(tm(ii,19:24)',zscoretm(19:24)'));
mixpcc_c5=mixpcc_c5+abs(corr(tm(ii,25:30)',zscoretm(25:30)'));
mixpcc_c6=mixpcc_c6+abs(corr(tm(ii,31:36)',zscoretm(31:36)'));
mixpcc_c7=mixpcc_c7+abs(corr(tm(ii,37:42)',zscoretm(37:42)'));
mixpcc_c8=mixpcc_c8+abs(corr(tm(ii,43:48)',zscoretm(43:48)'));
mixpcc_c9=mixpcc_c9+abs(corr(tm(ii,51:56)',zscoretm(51:56)'));
    end
end
mixpcc=[mixpcc1 mixpcc2 mixpcc3 mixpcc4 mixpcc5 mixpcc6 mixpcc7 mixpcc8
mixpcc9];
mixpcc_c=[mixpcc_c1 mixpcc_c2 mixpcc_c3 mixpcc_c4 mixpcc_c5 mixpcc_c6
mixpcc_c7 mixpcc_c8 mixpcc_c9];
mixpcc=mixpcc/k/mimisize(1);
mixpcc_c=mixpcc_c/k/mimisize(1);

tag=0;
for time=2:8
    if
        (stdrna(time)>stdrna(time-1)) && (stdrna(time)>stdrna(time+1)) &&...

        (pccrna(time)>pccrna(time-1)) && (pccrna(time)>pccrna(time+1)) &&...

        (mixpcc(time)<mixpcc(time-1)) && (mixpcc(time)<mixpcc(time+1))
            tag=1;
            break;
        end
    end
    if tag==0
        continue;
    end
end

```

```

candidategroup8=candidategroup8+1;

compositindex=zeros(9,1);
compositindex_c=zeros(9,1);
for s=1:9
    compositindex(s)=(stdrna(s)/k)*(pccrna(s)/(k*(k-1))*2)/mixpcc(s);
compositindex_c(s)=(stdrna_c(s)/k)*(pccrna_c(s)/(k*(k-1))*2)/mixpcc_c(s);
end

figure(i);
t=[1 2 3 4 5 6 7 8 9];
subplot(1,4,1);
plot(t,stdrna,'r', t,stdrna_c,'b');
title('std8');
legend('SD_{case}','SD_{control}',2);

subplot(1,4,2);
plot(t,pccrna,'r',t,pccrna_c,'b');
title('inpcc8');
legend('PCC_{case}','PCC_{control}',2);

subplot(1,4,3);
plot(t,mixpcc,'r',t,mixpcc_c,'b');
title('outpcc8');
legend('OPCC_{case}','OPCC_{control}',2);

subplot(1,4,4);
plot(t,compositindex,'r',t,compositindex_c,'b')
title('composite index');
legend('Composite_{case}','Composite_{control}',2);
end
fclose(fpi);

clc;

disp('t-test:');
[k1 k2 k3 k4 k5 k6 k7 k8 k9]
disp('two-fold-change:');
[j1 j2 j3 j4 j5 j6 j7 j8 j9]

candidategroup_in_each_time_point=[candidategroup2 candidategroup3
candidategroup4...
candidategroup5 candidategroup6 candidategroup7 candidategroup8];
disp('the number of selected groups:');
sum(cans)

```