

Supplementary Materials: Identifying critical transitions and their leading biomolecular networks in complex diseases

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In this study, we developed a novel computational method by first constructing a state-transition-based local network entropy (SNE) and then theoretically proving that the SNE can provide a general early warning indicator for identifying critical transitions and their leading biomolecular networks (or leading networks) during disease progression. SNE is based on dynamical network biomarker (DNB) (*1*), by using high throughput data (e.g., gene or protein expression data) even with a small number of samples. Figure S1 shows the main differences between the traditional biomarkers and a type of dynamical network biomarker (DNB), which can effectively signal the pre-disease state from its critical behavior in dynamics.

Completely different from traditional static approaches, a dynamical network biomarker (DNB, or a dynamical network of biomarkers) is able to characterize pre-disease phenotypes, for which traditional biomarkers failed. Figure 1 (the main text) and Figure S1 illustrate major features of the two types of biomarkers. Note that a DNB is a group of molecules which are highly unstable but strongly correlated without consistent values for the pre-disease samples, and thus it is a new concept different from the conventional biomarkers which are required to keep consistent values for the respective disease and normal samples. A DNB is also called as the leading network because it makes the first move into the disease state, which implies that the DNB is highly related to causal or driver factors (or genes) to the disease. It is also the first theoretical result to ensure such a causality feature. Note that DNB or the leading network in this paper is not for identifying the critical transition phenomenon but for detecting the state just before the critical transition, and therefore, it is of great importance for early diagnosis of complex diseases. Hence, without confusion, identifying the critical transition in this paper means identifying the state just before the critical transition.

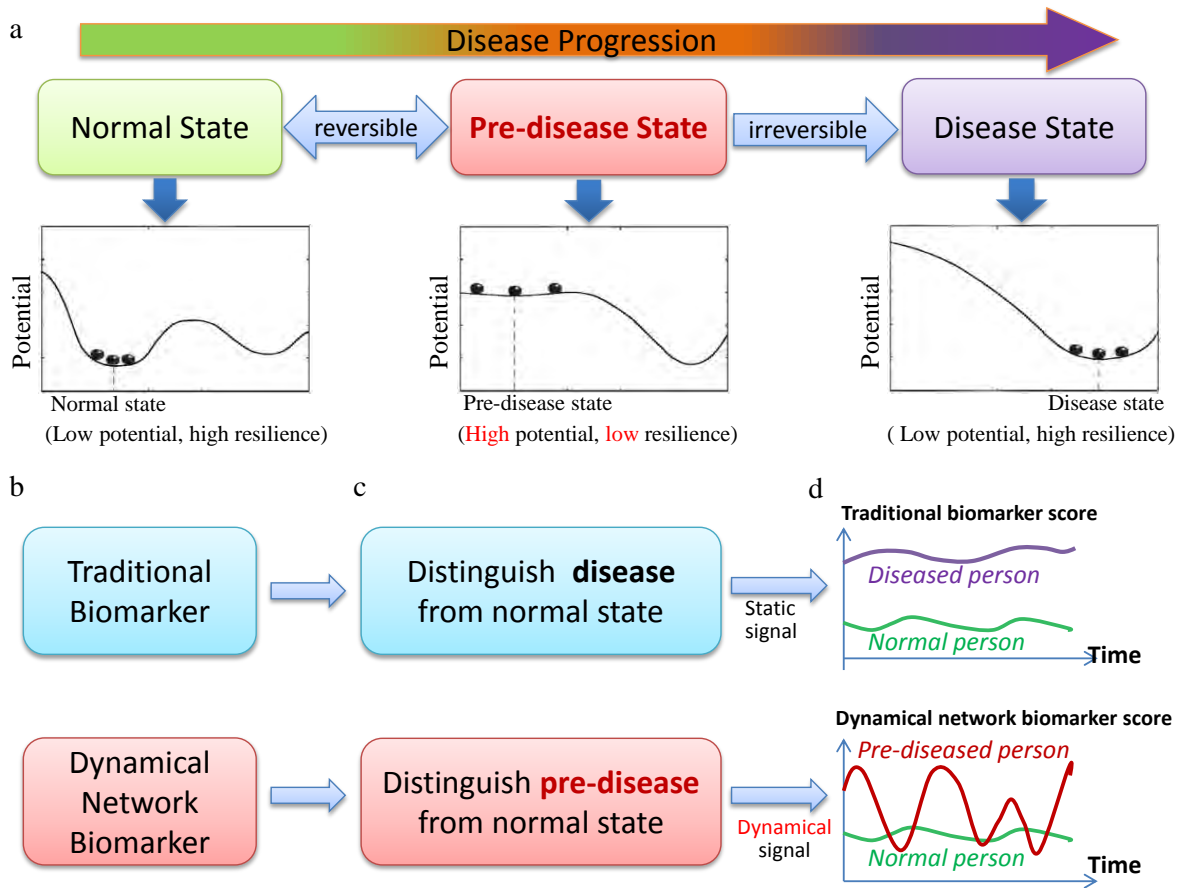


Figure S1: | **Disease states and biomarkers.** (a) Three stages during disease progression, i.e., a normal state, a pre-disease state, and a disease state. A normal state is a relatively healthy stage including the chronic inflammation period or the period during which the disease is under control, whereas a pre-disease state is the limit of the normal state just before the critical transition. At this stage, the pre-disease state is considered to be reversible to the normal state if appropriately treated. However, if the system passes over the critical (bifurcation) point to the disease state, it usually becomes irreversible to the normal state. (b) Two types of biomarkers, i.e., traditional biomarkers, and newly developed dynamical network biomarkers (DNBs). (c) Main targets of the two biomarkers. The traditional biomarkers are indicators on the disease state, whereas the dynamical network biomarkers signal the pre-disease state. (d) Comparison of the major features of the two biomarkers. The traditional biomarkers are static measurements on the disease, whereas dynamical network biomarkers are dynamical measurements on the pre-disease, thus providing the early-warning signals for the pre-disease state.

A Statistical properties near a critical transition point

For a dynamical system or dynamical network, e.g., a protein-protein interaction (PPI) network, a gene regulatory network, or a correlation network, it is assumed that we can measure the variables at different time points or different periods (even for a small number of samples). In this section, we aim to theoretically prove several generic properties of such a dynamical network when the system approaches the critical transition point. In particular, we focus on the analysis of variation equations for the original network.

A.1 The leading networks during critical transitions

We consider the following discrete-time dynamical system that represents the dynamical evolution of a network:

$$Z(t+1) = f(Z(t); P), \quad (\text{S1})$$

where $Z(t) = (z_1(t), \dots, z_n(t))$ is an n -dimensional state vector or variables at time instant t that represents gene or protein expressions, while $P = (p_1, \dots, p_s)$ is a parameter vector or driving factors that represent slowly changing factors, e.g., genetic factors (SNP, CNV, etc.) and epigenetic factors (methylation, acetylation, etc.). $f : \mathbf{R}^n \times \mathbf{R}^s \rightarrow \mathbf{R}^n$ are generally nonlinear functions.

Furthermore, we assume that the following conditions hold for Eq.(S1).

1. \bar{Z} is a fixed point of system (S1) such that $\bar{Z} = f(\bar{Z}; P)$.
2. There is a value P_c such that one or a pair of the eigenvalues of the Jacobian matrix $\left. \frac{\partial f(Z; P_c)}{\partial Z} \right|_{Z=\bar{Z}}$ is equal to 1 in the modulus.
3. When $P \neq P_c$, the eigenvalues of (S1) are not always equal to 1 in the modulus.

The above three conditions with other transverse conditions (2) imply that the system undergoes a phase change at \bar{Z} or a codimension-one bifurcation when P reaches the threshold P_c . From a mathematical perspective, the bifurcation is generic, *i.e.* almost all of the bifurcations in a general system satisfy these conditions. It is notable that most of the systems described by differential equations can be generally discretized and transformed into Eq.(S1), e.g., using methods such as the Euler scheme and the Poincaré section. Thus, we focus on difference equations (S1) during our theoretical analysis in this section.

It is known that the dynamics of complex disease progression is highly complex before or after a sudden deterioration, so the state equations of systems are generally constructed in a very high-dimensional space using a large number of variables and parameters (1–5). However, if a system driven by known or unknown parameters approaches a critical point, which is a very special phase during the dynamical progression, it is theoretically guaranteed that the system will eventually be constrained to one- or two-dimensional space (*i.e.*, the center manifold), which can be expressed in a simple form around a codimension-one bifurcation point (1, 6, 7). This is generally guaranteed by the bifurcation theory and center manifold theory (6–9). Thus, we can detect the signal of any dynamical system only during this special phase and not in other periods (*i.e.*, neither the normal state before a transition nor a disease state after the transition), which is the theoretical foundation of this study (1).

For system (S1) near \bar{Z} and before P reaches P_c , we assume that the system is at a stable fixed point \bar{Z} so all of the eigenvalues are within $(0, 1)$ in the modulus. The parameter value P_c when the state shift of the system occurs, is known as a bifurcation parameter value or a critical transition value.

This theoretical result was derived based on a consideration of the linearized equations for Eq.(S1) and the noise perturbations near \bar{Z} . Specifically, by introducing new variables

$Y(t) = (y_1(t), \dots, y_n(t))$ and a transformation matrix S , i.e. $Y(t) = S^{-1}(Z(t) - \bar{Z})$, we have

$$Y(t+1) = \Lambda Y(t) + \zeta(t). \quad (\text{S2})$$

where $\Lambda(P)$ is the diagonalized matrix of $\left. \frac{\partial f(Z;P)}{\partial Z} \right|_{Z=\bar{Z}}$. $\zeta(t) = (\zeta_1(t), \dots, \zeta_n(t))$ are small Gaussian noises with zero means. We denote σ_i as the small standard deviation of ζ_i for all k . Without any loss of generality, the diagonalized matrix $\Lambda(P) = \text{diag}(\lambda_1(P), \dots, \lambda_n(P))$ for each $|\lambda_i|$ is between 0 and 1. (In fact, three typical cases arising during the diagonalization process (I), but we only illustrate the diagonal case with different real eigenvalues for simplicity. The derivations of the other two cases are similar). Of the eigenvalues of Λ , the largest one (in the modulus), say λ_1 , approaches 1 in the modulus when parameter $P \rightarrow P_c$. The eigenvalue λ_1 characterizes the system's rate of change around a fixed point and it is known as the dominant eigenvalue. The normal state corresponds to a period where $|\lambda_1| < 1$, whereas the pre-disease stage corresponds to the period with $|\lambda_1| \rightarrow 1$. Without loss of generality, we assume that the first variable y_1 in Y corresponds to λ_1 , namely $(y_1, 0, \dots, 0)$ is the eigenvector of λ_1 . Close to a fixed point, we have shown that there is a dominant group or a DNB that satisfies the following conditions when the system approaches a critical transition point (I).

Theorem 1 *We consider a stochastically perturbed linear system for Eq.(S1), i.e., Eq.(S14). When P approaches the bifurcation point, the following results hold.*

- *If both i and j are in the dominant group, then*

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

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

- *if i is in the dominant group but j is not, then*

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

while $SD(z_i) \rightarrow \infty$, and $SD(z_j)$ approaches a bounded value;

- if neither i nor j is in the dominant group, then $PCC(z_i, z_j)$ approaches a constant, while both $SD(z_i)$ and $SD(z_j)$ approach bounded values,

where PCC is Pearson's correlation coefficient and SD is the standard deviation.

This theorem is the theoretical basis for whole the analysis of this work (I). In other words, all of the results in this paper are derived mainly based on this theorem. The DNB is the sub-network that makes the first move from one state toward another state at the critical transition point, so we refer to the DNB as the **leading network** in this critical transition. For a general discrete-time dynamical system in this paper, the critical transition includes all codimension-one bifurcations except the super-critical Neimark-Sacker bifurcation, i.e., it includes saddle-node bifurcation (including transcritical and pitchfork bifurcation) if the dominant eigenvalue is equal to 1; period-doubling (or flip) bifurcation if the dominant eigenvalue is equal to -1 ; sub-critical Neimark-Sacker bifurcation if there is a pair of pure imaginary complex conjugate eigenvalues with modulus 1. In this work, we do not study the super-critical Neimark-Sacker bifurcation which is not the catastrophic-type bifurcation. In other words, i.e., there is no drastic change of the state for the super-critical Hopf bifurcation because the amplitude of the periodic solution after the critical transition point increases with the bifurcation parameter in a polynomial manner, rather than an exponential or drastic manner.

A.2 Variation variables

In contrast to the analysis of the original variables Z in (I) or Theorem 1, in this work we focus on the variation equation for Eq.(S1) with variation variables ΔZ .

We note that

$$z_i(t) = s_{i1}y_1(t) + \cdots + s_{in}y_n(t) + \bar{z}_i, \quad (\text{S3})$$

and we let the variation variables be

$$\Delta Z(t) = Z(t) - Z(t - 1), \quad (\text{S4})$$

then from Eq.(S3) we have

$$\Delta z_i(t) = s_{i1}\Delta y_1(t) + \cdots + s_{in}\Delta y_n(t), \quad (\text{S5})$$

where

$$\Delta Y(t) = Y(t) - Y(t - 1). \quad (\text{S6})$$

We refer to $\Delta z_i(t)$ and $\Delta y_i(t)$ as the variation variables for $z_i(t)$ and $y_i(t)$, respectively. From Eq.(S2) and Eq.(S6), it clearly holds that

$$\Delta Y(t + 1) = \Lambda \Delta Y(t) + \xi(t), \quad (\text{S7})$$

where $\xi(t) = \zeta(t) - \zeta(t - 1)$ are Gaussian noises with zero means and covariances $\kappa_{ij} = \text{Cov}(\xi_i, \xi_j)$. It is clear that the standard deviation of $\xi_i(t)$ is $\sqrt{2}\sigma_i$ for all t . Obviously, variable Δy_1 corresponds to the dominant eigenvalue λ_1 .

For any integer $T > 0$, by iteration we have

$$\begin{aligned} & \Delta Y(t + T) \\ &= \Lambda \Delta Y(t + T - 1) + \xi(t + T - 1) \\ &= \Lambda[\Lambda \Delta Y(t + T - 2) + \xi(t + T - 2)] + \xi(t + T - 1) \\ & \dots \\ &= \Lambda^T \Delta Y(t) + \Lambda^{T-1} \xi(t) + \Lambda^{T-2} \xi(t + 1) + \cdots + \Lambda \xi(t + T - 2) + \xi(t + T - 1). \end{aligned}$$

Clearly, the summation of the coefficients for the covariance matrices for T Gaussian noises is

$$(1 - \Lambda^T)(I - \Lambda)^{-1},$$

where I is the n -dimensional identity matrix.

Note that when the system is in a normal state, $|\lambda_i| < 1$. Because when T is large enough, it holds that

$$\Delta Y(t + T) = \varepsilon(t), \quad (\text{S8})$$

where $\varepsilon(t) = (\varepsilon_1(t), \dots, \varepsilon_n(t))$ are small Gaussian noises with zero means. Based on the law of large numbers (10), the covariances are $\kappa_{ij}/(1 - \lambda_i)$ and the deviation of $\varepsilon_i(t)$ is $\sqrt{\kappa_{ii}/(1 - \lambda_i)}$ for all t , which is a bounded value when $\lambda_i \neq 1$. In the original variables Z from Eq.(S5) and Eq.(S8), it holds that

$$\begin{aligned} \Delta z_i(t + T) &= s_{i1}\Delta y_1(t + T) + \dots + s_{in}\Delta y_n(t + T) \\ &= s_{i1}\varepsilon_1(t) + \dots + s_{in}\varepsilon_n(t). \end{aligned} \quad (\text{S9})$$

Therefore, when the system is in a normal state, or equivalently $|\lambda_i| < 1$, any variation variable $\Delta z_i(t + T)$ is statistically independent of its initial variable $\Delta z_i(t)$ for a sufficiently long T , which generally holds because biochemical reactions occur within a very short time interval (i.e., sub-ms time). Thus, any two samples can be considered as having a long T because there are large numbers of biochemical reactions during their observation intervals. Hence, the variation variables for any two samples are statistically independent when the system is in its normal state.

Next, we discuss the case close to a critical transition when the dominant eigenvalue $\lambda_1 \rightarrow 1$ (for $\lambda_1 \rightarrow -1$, the derivation is similar so it is omitted). Note that the variation variable y_1 is related to the dominant eigenvalue λ_1 . Since

$$y_1(t + T) = \lambda_1 y_1(t + T - 1) + \zeta_1(t + T - 1) \quad (\text{S10})$$

holds for any integer T , we have

$$\begin{aligned}
& [\Delta y_1(t+T) + \Delta y_1(t+T-1) + \cdots + \Delta y_1(t+1)] \\
& = [y_1(t+T) - y_1(t+T-1)] + [y_1(t+T-1) - y_1(t+T-2)] \\
& \quad + [y_1(t+T-2) - \cdots - y_1(t+2)] + [y_1(t+1) - y_1(t)] \\
& = \lambda_1 [\Delta y_1(t+T-1) + \cdots + \Delta y_1(t+1) + \Delta y_1(t)] \\
& \quad + [\zeta_1(t+T-1) - \zeta_1(t+T-1) + \zeta_1(t+T-1) - \cdots - \zeta_1(t) + \zeta_1(t) - \zeta_1(t-1)] \\
& = \lambda_1 [\Delta y_1(t+T-1) + \cdots + \Delta y_1(t)] + [\zeta_1(t+T-1) - \zeta_1(t-1)].
\end{aligned}$$

Therefore,

$$\begin{aligned}
& \Delta y_1(t+T) + \Delta y_1(t+T-1) + \cdots + \Delta y_1(t+1) \\
& = \lambda_1 [\Delta y_1(t+T-1) + \cdots + \Delta y_1(t)] + [\zeta_1(t+T-1) - \zeta_1(t-1)],
\end{aligned}$$

or

$$\begin{aligned}
\Delta y_1(t+T) & = (\lambda_1 - 1)\Delta y_1(t+T-1) + \cdots + (\lambda_1 - 1)\Delta y_1(t+1) \\
& \quad + \lambda_1 \Delta y_1(t) + [\zeta_1(t+T-1) - \zeta_1(t-1)].
\end{aligned}$$

Thus, when $\lambda_1 \rightarrow 1$ we have

$$\Delta y_1(t+T) = \Delta y_1(t) + [\zeta_1(t+T-1) - \zeta_1(t-1)], \tag{S11}$$

which means that $\Delta y_1(t+T)$ depends greatly on $\Delta y_1(t)$ for a small noise. In other words, the dominant variables $\Delta y_1(t)$ are highly dependent on each other (or dependent on their previous state) for any two samples near the critical transition. It is clear that the same result holds when $\lambda_1 \rightarrow -1$. However, because $|\lambda_i| < |\lambda_1|$, $i = 2, 3, \dots, n$, the other variables $\Delta y_i(t+T)$ satisfy Eq.(S8), i.e.,

$$\Delta y_i(t+T) = \varepsilon_i(t), \quad i = 2, 3, \dots, n. \tag{S12}$$

Note that the variable Δy_1 is related to the dominant eigenvalue λ_1 . There is a special group of variables z_j , in which the variables Δz_j are related to Δy_1 , *i.e.*, Δz_j in Eq.(S5) with $s_{j1} \neq 0$, which is known as the dominant group. These variables z_j are known as the dominant group members or DNB members (I). For any two DNB members z_j and z_i with $s_{j1} \neq 0$ and $s_{i1} \neq 0$ in Eq.(S5), when $|\lambda_1| \rightarrow 1$, from Eq.(S11) and Eq.(S12) we have

$$\begin{aligned}
\Delta z_j(t+T) &= s_{j1}\Delta y_1(t+T) + s_{j2}\Delta y_2(t+T) + \cdots + s_{jn}\Delta y_n(t+T) \\
&= s_{j1}[\Delta y_1(t) + (\zeta_1(t+T-1) - \zeta_1(t-1))] + s_{j2}\varepsilon_2(t) + \cdots + s_{jn}\varepsilon_n(t) \\
&= \frac{s_{j1}}{s_{i1}}\Delta z_i(t) + s_{j1}(\zeta_1(t+T-1) - \zeta_1(t-1)) \\
&\quad + (N(t) + \frac{s_{j1}}{s_{i1}}(s_{j2} - s_{i2})\varepsilon_2(t) + \cdots + \frac{s_{j1}}{s_{i1}}(s_{jn} - s_{in})\varepsilon_n(t)) \\
&= \frac{s_{j1}}{s_{i1}}\Delta z_i(t) + N(t) + \rho_j(t), \tag{S13}
\end{aligned}$$

where $\rho_j(t) = s_{j1}(\zeta_1(t+T-1) - \zeta_1(t-1)) + (\frac{s_{j1}}{s_{i1}}(s_{j2} - s_{i2})\varepsilon_2(t) + \cdots + \frac{s_{j1}}{s_{i1}}(s_{jn} - s_{in})\varepsilon_n(t))$ is Gaussian noise which is assumed to be small, $N(t) = -(\frac{s_{j1}s_{i2}}{s_{i1}}\Delta y_2(t) + \cdots + \frac{s_{j1}s_{in}}{s_{i1}}\Delta y_n(t))$. From Eq.(S13), it is clear that when $|\lambda_1| \rightarrow 1$ for any two DNB members, the variable $\Delta z_j(t+T)$ is correlated to $\Delta z_i(t)$, where it also holds for $i = j$, *i.e.*, for any DNB member, that the variable $\Delta z_j(t+T)$ is correlated to its previous $\Delta z_j(t)$. By contrast, as suggested by Eq.(S9), for any non-DNB member z_k , $\Delta z_k(t+T)$ is statistically independent of $\Delta z_k(t)$.

Thus, near any fixed point, we derive the following theorem for any two samples (*i.e.*, at time t and time $t+T$).

Theorem 2 *For a stochastically perturbed linear system of Eq.(S1):*

$$Z(t+1) = A(P)Z(t) + \varepsilon(t), \tag{S14}$$

where $\varepsilon(t)$ is the Gaussian noise and P is a parameter vector that controls the Jacobian matrix A . We denote the variation variable as $\Delta z_i(t) = z_i(t) - z_i(t-1)$ and assume T to be sufficiently large.

1. When P is not in the vicinity of a critical transition point or a bifurcation point, the following holds.

- For any i and j including $i = j$, $\Delta z_i(t + T)$ is statistically independent of $\Delta z_j(t)$, where $i, j = 1, 2, \dots, n$.

2. When P approaches to a critical transition point, the following holds.

- If both i and j are in the dominant group, or DNB members, then there is a strong correlation between $\Delta z_i(t + T)$ and $\Delta z_j(t)$;
- If neither i nor j is in the dominant group, then $\Delta z_i(t + T)$ is statistically independent of $\Delta z_j(t)$. Note that this also holds for $i = j$.

Remark 1 For a nonlinear case (S1) at a fixed point, the dynamical behavior has the same trend described in Theorem 1 and Theorem 2.

Clearly, the conditions in Theorem 1 or 2 can be used to detect the DNB (or the leading network) and the critical transition. In particular, the expression of each node in a network may change stochastically at any time instant due to perturbation, but the above theorem and remark guarantee that, for a group of nodes, some statistical indices will change drastically whenever the system approaches a critical transition point, which provides a reliable early warning signal for identifying the pre-disease state.

A.3 State transition variables

Next, we further discretize the variable $\Delta Z_i(t)$ as $x_i(t)$ to derive similar theoretical results to Theorem 2.

Definition 1 For any original variables z_i in Eq.(S1) at time point t , we define the transition state variable $x_i : \Delta z_i(t) \mapsto \{0, 1\}$ as

$$x_i(t) = \begin{cases} 1, & \text{if } |\Delta z_i(t)| > d_i, \\ 0, & \text{if } |\Delta z_i(t)| \leq d_i, \end{cases} \quad (\text{S15})$$

where the threshold $d_i \in \mathbb{R}^+$ is a positive constant or the threshold for discretization. Then, $x_i(t) \in \{0, 1\}$ is defined for measuring whether node i experiences a large change at sampling point t , i.e., if $|z_i(t) - z_i(t-1)|$ is sufficiently large ($> d_i$), then $x_i(t) = 1$, otherwise $x_i(t) = 0$.

Thus, $X(t) = (x_1(t), \dots, x_n(t))$ is the transition state for the network at t . We will discuss how we determine d_i to construct the transition state space in Section C. Based on Theorem 2, we derive the following result.

Theorem 3 We consider a stochastically perturbed linear system for Eq.(S1), i.e., Eq.(S14).

When P approaches the bifurcation point, the following results hold for a sufficiently large T .

- If both i and j are in the dominant group or DNB members, the correlation between the transition states $x_i(t+T)$ and $x_j(t)$ increases drastically and

$$p(x_i(t+T) = 1 | x_j(t) = \gamma) \rightarrow 1,$$

$$p(x_i(t+T) = 0 | x_j(t) = \gamma) \rightarrow 0,$$

where $\gamma \in \{0, 1\}$.

- If neither i nor j is in the dominant group, or DNB members, then the transition state $x_i(t+T)$ is statistically independent of $x_j(t)$ and

$$p(x_i(t+T) = \gamma_i | x_j(t) = \gamma_j) = p(x_i(t+T) = \gamma_i) \rightarrow a,$$

where $\gamma_i, \gamma_j \in \{0, 1\}$, a is a constant within $(0, 1)$. In other words, there is no significant change in the conditional probability.

Next, we construct a SNE to identify the critical transition and its leading network (or DNB) based on Theorem 3.

B Constructing the SNE

B.1 Markov process

In general, it is difficult to analyze a large network directly because of its complexity. Then, we will focus on the local structure of a network to analyze its dynamical properties. Specifically, there is a local network for each node, i.e., the local network is centered on node i with its m linked first-order neighbor nodes i_1, i_2, \dots, i_m . The local network centered on node i has the local transition state $X^i(t) = (x_i(t), x_{i_1}(t), \dots, x_{i_m}(t))$ at time t (see Fig.S2 a). The following description and derivation are all based on a local node, i.e., i , to simplify the notation, so we omit i and denote $X^i(t)$ as $X(t)$, while we also denote the transition state simply as a state.

Given the current state $X(t)$ at time t for this local network, then at the next time point $t + 1$ there is a total of 2^{m+1} possible state transitions (or possible transition states) for state $X(t + 1)$ (see Fig.S2 b), each of which is a stochastic event that is denoted, respectively, as $\{A_u\}_{u=1,2,\dots,2^{m+1}}$, where

$$A_u = \{x_i = \gamma_0, x_{i_1} = \gamma_1, \dots, x_{i_m} = \gamma_m\}, \quad (\text{S16})$$

with $\gamma_l \in \{0, 1\}$ for $l \in \{0, 1, 2, \dots, m\}$. The next state depends on the current state and its transition functions related to Eq.(S14).

Obviously, for this local subnetwork, the discrete stochastic process

$$\{X(t + i)\}_{i=0,1,\dots} = \{X(t), X(t + 1), \dots, X(t + i), \dots\} \quad (\text{S17})$$

with

$$X(t + i) = A_u, \quad u \in \{1, 2, \dots, 2^{m+1}\},$$

is a stochastic Markov process during a period or phase of the system (see Fig.S3), i.e., during the normal stage or during the pre-disease stage. This stochastic process is defined or given by a Markov matrix $P = (p_{u,v})$, which describes the transition rates from state v to state u as follows

$$p_{u,v}(t) = \Pr(X(t+1) = A_u | X(t) = A_v), \quad (\text{S18})$$

where $u, v \in \{1, 2, \dots, 2^{m+1}\}$ and $\sum_u p_{u,v}(t) = 1$. This can actually be determined based on the topological structure of the local network, or Eq.(S14).

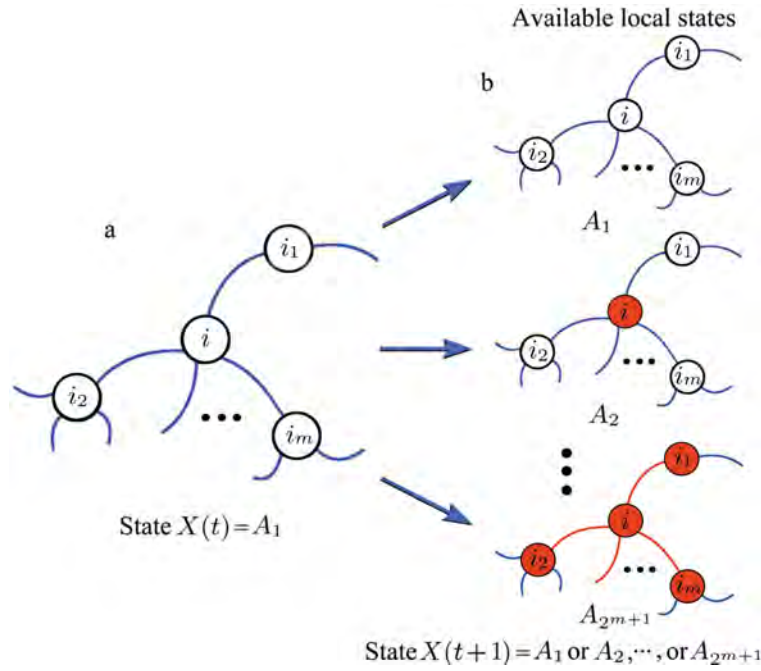


Figure S2: | **Local network centered on node i with m linked first-order neighbor nodes.** The outline shows the local network structure for node i , which is linked to m neighbor nodes i_1, i_2, \dots, i_m . Each edge $i - i_k$ of $k = 1, 2, \dots, m$ indicates how the neighbor i_k may influence i directly and lead to a state transition in i . **(a)** is the state of this local network at time t . **(b)** is the next time point $t + 1$, which has 2^{m+1} possible states $\{A_1, A_2, \dots, A_{2^{m+1}}\}$ for this local structure.

B.2 SNE

For a local structure centered on node i and its m linked first-order neighbor nodes i_1, i_2, \dots, i_m , we already know that its state transition process is a stochastic Markov process, as shown in (S17). Within a period or phase, we assume that there is no change in the transition matrix, i.e., the transition probabilities $p_{u,v}(t)$ in (S18) between any two possible states A_v and A_u . Thus, the process $\{X(t)\}_{t \in [t_1, t_2]}$ is a stationary stochastic Markov process during a specific period, i.e., the normal stage or the pre-disease stage. Thus, there is a stationary distribution $\pi = (\pi_1, \dots, \pi_{2m+1})$ that satisfies

$$\sum_v \pi_v p_{u,v} = \pi_u.$$

Therefore, we can define the local network entropy, i.e., the SNE, as

$$H_i(t) = H(\chi) = - \sum_{u,v} \pi_v p_{u,v} \log p_{u,v}, \quad (\text{S19})$$

where the subscript index i indicates the center node i of this local network, while χ represents the state-transition process $X(t), X(t+1), \dots, X(t+T), \dots$ of the local network.

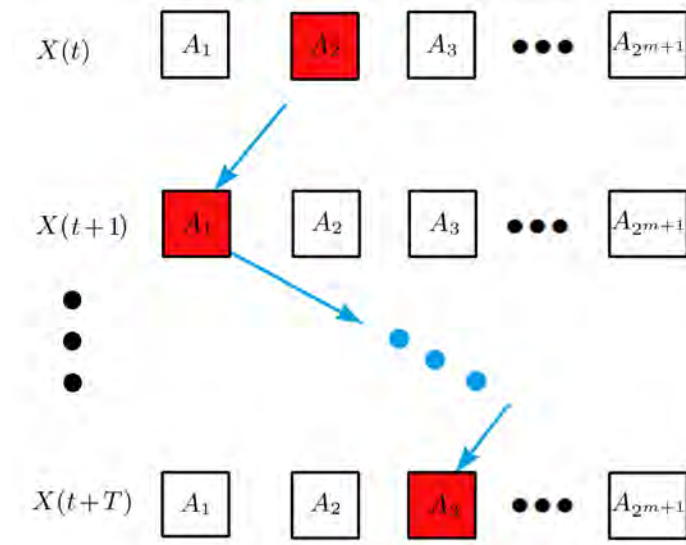


Figure S3: | **Outline of the state transition process.** The outline shows the essential stochastic Markov process of the state transition process in a local structure.

Next, we prove that the entropy Eq.(S19) is equivalent to the so-called entropy rate defined in previous studies (I1), (I2), i.e.,

$$H(\chi) = \lim_{T \rightarrow \infty} \frac{1}{T} H(X(t), X(t+1), \dots, X(t+T)), \quad (\text{S20})$$

when the limit exists.

Note that the stochastic process $X(t), X(t+1), \dots$ is a stochastic Markov process during a period, where the step size between any two adjacent sampling times is a small unit δt . Based on the Markov chains property, we have

$$\begin{aligned} H(\chi) &= - \sum_{u,v} \pi_v p_{u,v} \log p_{u,v} = \sum_v \pi_v \left(\sum_u -p_{u,v} \log p_{u,v} \right) \\ &= H(X(t+1) | X(t)) \\ &= H(X(t+T) | X(t+T-1)) \\ &= H(X(t+T) | X(t+T-1), X(t+T-2), \dots, X(t)), \end{aligned}$$

where T is sufficiently large. Therefore,

$$H(\chi) = \lim_{T \rightarrow \infty} H(X(t+T) | X(t+T-1), \dots, X(t)), \quad (\text{S21})$$

provided that the limit exists.

Based on the chain rule (I3), we have

$$\begin{aligned} &\frac{1}{T} H(X(t), X(t+1), \dots, X(t+T)) \\ &= \frac{1}{T} \sum_{i=0}^{T-1} H(X(t+i) | X(t+i-1), X(t+i-2), \dots, X(t)), \end{aligned} \quad (\text{S22})$$

which means that the entropy rate is the time average of the conditional entropies.

Based on Cesàro's mean (I4), because $H(X(t+T) | X(t+T-1), \dots, X(t)) \rightarrow H(\chi)$ as $T \rightarrow \infty$ (see (S21)), from (S22) we derive $\frac{1}{T} H(X(t), X(t+1), \dots, X(t+T)) \rightarrow H(\chi)$ as $T \rightarrow \infty$, which proves Eq.(S20), i.e.,

$$H_i(t) = H(\chi) = \lim_{T \rightarrow \infty} \frac{1}{T} H(X(t), X(t+1), \dots, X(t+T)). \quad (\text{S23})$$

Therefore, the SNE is actually the conditional entropy while it also describes the average transition entropy, depending on the state transition.

Thus, we note that the SNE is the conditional entropy, i.e., $H_i(t) = H(X(t) | X(t-1)) = H(X(t), X(t-1)) - H(X(t-1))$. We also note that $X(t)$ (or $Z(t) - Z(t-1)$) are variation variables. Clearly, in a normal state (or a disease state), a system recovers from a small perturbation quickly because of high resilience, i.e., $X(t)$ and $X(t-1)$ are almost independent. Thus, we have $H_i(t) \approx H(X(t))$ due to $H(X(t), X(t-1)) \approx H(X(t)) + H(X(t-1)) > 0$, which results in a high SNE. By contrast, the system has difficulty recovering from a small perturbation in a pre-disease state because of low resilience, i.e., $X(t)$ and $X(t-1)$ are strongly correlated, which implies that $H_i(t)$ rapidly approaches the minimum, $H_i(t) \approx 0$ due to $H(X(t), X(t-1)) \approx H(X(t-1))$ (Fig. 1 g in the main text).

We combine the SNEs for all nodes and define the average network entropy for the whole network with n nodes as the average SNE (i.e., ANE) as follows:

$$H(t) = \frac{1}{n} \sum_{i=1}^n H_i(t). \quad (\text{S24})$$

B.3 Robustness

Next, we show that the SNE is positively correlated with the robustness of the network. Thus, the SNE is used to quantify the robustness of a network in this study. We denote $p_\epsilon(t)$ as the probability that a sample deviates (in the mean sense) by more than ϵ from its unperturbed value at any sampling time t . If t is sufficiently large, the perturbed observables may recover from small perturbations and return to their equilibrium state, which means that $p_\epsilon(t)$ will converge to zero as $t \rightarrow \infty$. We define the fluctuation decay rate R as the rate of this convergence on a logarithmic scale as follows:

$$R = \lim_{t \rightarrow \infty} \left(-\frac{1}{t} \log(p_\epsilon(t)) \right). \quad (\text{S25})$$

A large value of R results in small deviations of the observables from the equilibrium state whereas a small value of R corresponds to large fluctuations around the mean value. Thus, R may characterize the insensitivity to perturbations, which represents the capacity to withstand random changes, i.e., robustness. According to the fluctuation theorem (15), the R used in (S25) is positively correlated with the SNE defined by Eq.(S19).

Therefore, the system is highly robust in its normal state when the average network entropy (S24) reaches a relatively high level. However, when the system approaches the critical transition point in the pre-disease state, the SNE reaches a low level and the robustness of the system is reduced accordingly (see Fig. 1g in the main text). This critical phenomenon coincides with the “critical slowing down” or weak resilience (16, 17), which is a generic dynamical phenomenon that occurs near a bifurcation point when the system becomes increasingly slow at recovering from small perturbations and reverting to its equilibrium state (18), (19). Clearly, the SNE can be used to quantify robustness and identify this critical stage.

C Constructing the transition state space and analyzing the SNE

We construct the transition state space x_i from (S15) by determining the threshold d_i and we then analyze the SNE by decomposing the network based on the DNB or the leading network.

C.1 Constructing the transition state space

In a local network centered on node i with m linked first-order neighbors i_1, i_2, \dots, i_m , we first need to determine the threshold parameters $d = \{d_i, d_{i_1}, \dots, d_{i_m}\}$, which measures whether the state $z_i(t)$ has a large change or a state transition from its former state $z_i(t - 1)$. Note that a system is in a stable state during its normal state (see Fig. 1(b) in the main text), whereas a system is sensitive to perturbation in its pre-disease state (see Fig. 1(c) in the main text). Thus,

d_i should be set to distinguish the "small changes" in normal state from the "large changes" in pre-disease state. For this local network, therefore, we select $d = \{d_i, d_{i_1}, \dots, d_{i_m}\}$ when the system is in a normal state such that for each node k , $p(|z_k(t_0)| > d_k) = \alpha$, if time point t_0 is in a normal state (see Fig.S4). Obviously, for such thresholds d , it holds that

$$p(|z_i(t_0)| > d_i, |z_{i_1}(t_0)| > d_{i_1}, \dots, |z_{i_m}(t_0)| > d_{i_m}) \leq \alpha. \quad (\text{S26})$$

With such a distribution, genes with large deviations clearly correspond to high probabilities.

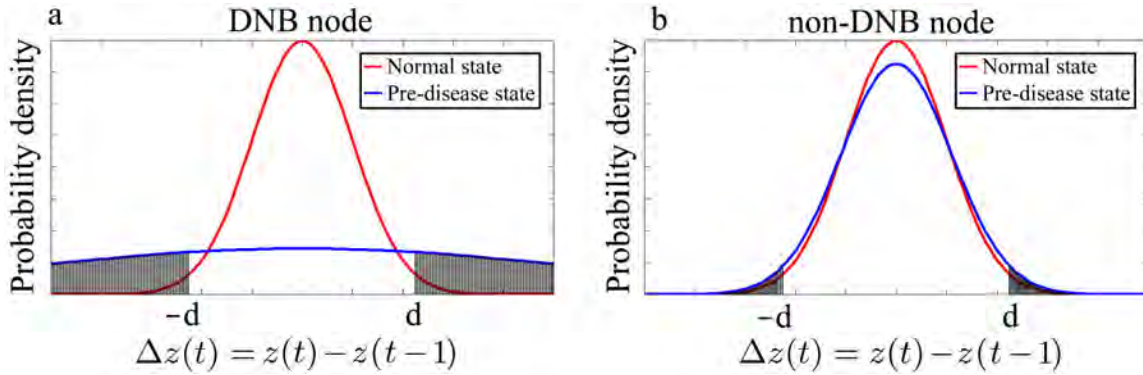


Figure S4: | **Outline of the choice of threshold d .** Given thresholds d_i and d_j for DNB node i and non-DNB node j , respectively, there is a large difference between $p(|\Delta z_i| > d_i)$ and $p(|\Delta z_j| > d_j)$ when the system is in a pre-disease state. **(a)** For a DNB node i , the standard deviation of Δz_i increases drastically as the system approaches a critical point, so it is more likely to be $|\Delta z_i| > d_i$, indicating a large state transition in i in a pre-disease state. **(b)**, For a non-DNB node j , the standard deviation of Δz_j is small, so there is no significant difference in the probability of a random event $\{|\Delta z_j| > d_j\}$, even when the system is in a pre-disease state.

C.2 Analyzing SNE

Based on the transition state space defined above, we can now discuss what happens to the SNE in Eq.(S19) when the system approaches a critical transition point from a normal state.

For a local network centered on node i with m linked first-order neighbors i_1, i_2, \dots, i_m (see Fig.S2 a), let χ denote the state-transition process of the local network, $p_{u,v}^{\text{nor}}(t)$ denotes the

transition probabilities in the normal state, and $p_{u,v}^{\text{pre}}(t)$ those in the pre-disease state. Correspondingly, let

$$H^{\text{nor}}(\chi) = - \sum_{u,v} \pi_v^{\text{nor}} p_{u,v}^{\text{nor}} \log p_{u,v}^{\text{nor}}$$

and

$$H^{\text{pre}}(\chi) = - \sum_{u,v} \pi_v^{\text{pre}} p_{u,v}^{\text{pre}} \log p_{u,v}^{\text{pre}}$$

represent the SNEs in the normal state and the pre-disease state, respectively.

Based on the transition state defined in Eq.(S15), for node i when the system is in a normal state, it holds that

$$p^{\text{nor}}(x_i(t) = 1) = p^{\text{nor}}(|\Delta z_i| > d_i) = \alpha, \quad (\text{S27})$$

which represents the probability of large state transition at t , namely, $p^{\text{nor}}(x_i(t) = 0) = p^{\text{nor}}(|\Delta z_i| \leq d_i) = 1 - \alpha$. Here, node i can be either a DNB member or a non-DNB node.

When the system is in a pre-disease state and there is at least one DNB member in the local network, e.g., node j , then based on Theorem 1, there is $\text{SD}(z_j) \rightarrow \infty$, which means

$$\text{SD}(\Delta z_j) \rightarrow \infty. \quad (\text{S28})$$

This is straightforward because

$$\Delta Z(t) = Z(t) - Z(t-1),$$

and $\text{SD}(\Delta z_j) = \sqrt{2} \cdot \text{SD}(z_j)$.

Therefore, it holds that

$$p^{\text{pre}}(x_j(t) = 1) = p^{\text{pre}}(|\Delta z_j(t)| > d_j) \rightarrow 1, \quad (\text{S29})$$

for a given constant threshold d_j , and

$$p^{\text{pre}}(x_j(t) = 0) = p^{\text{pre}}(|\Delta z_j(t)| \leq d_j) \rightarrow 0. \quad (\text{S30})$$

Note that in Section B we defined the dominant-group, or the DNB, as a group of nodes that make the first move toward the disease state, thereby indicating a sudden deterioration. Then, the nodes in the network can be categorized into four groups according to the local structure of the DNB or the leading network:

- Type 1: A DNB core node is a DNB node that is linked with DNB nodes only, i.e., in Fig.S2a if node i and its linked neighbors i_1, i_2, \dots, i_m are all DNB members, then i is a Type 1 node (see the red nodes shown in Fig. 2a in the main text).
- Type 2: A DNB boundary node is a DNB node that is linked with at least one non-DNB node, i.e., in Fig.S2a if node i is a DNB node and some of its linked neighbors are non-DNB nodes, then i is a Type 2 node (see the orange nodes shown in Fig. 2a in the main text).
- Type 3: A non-DNB core node is a non-DNB node that is linked with at least one DNB node, i.e., in Fig.S2a if node i is a non-DNB node and some of its linked neighbors are DNB nodes, then i is a Type 3 node (see the blue nodes shown in Fig. 2a in the main text).
- Type 4: A non-DNB boundary node is a non-DNB node that has no links with DNB nodes, i.e., in Fig.S2a if node i is a non-DNB node, and its linked neighbors i_1, i_2, \dots, i_m are all non-DNB members, then i is a Type 4 node (see the purple nodes shown in Fig. 2a in the main text).

Next, we prove that the SNE has the following generic properties in terms of its dynamics, which correspond to these four types of nodes when the system is near a critical transition (see Table S1).

Table S1: SNE and node types

Type	Node	State transition for the center node	SNE for local network
1	DNB	$p(z(t) - z(t-1) > d) \rightarrow 1$	decreases drastically to 0
2	DNB	$p(z(t) - z(t-1) > d) \rightarrow 1$	decreases
3	non-DNB	$p(z(t) - z(t-1) > d) \rightarrow \beta$	decreases
4	non-DNB	$p(z(t) - z(t-1) > d) \rightarrow \beta$	has no significant change

* $\beta \in (0, 1)$ is a constant.

C.2.1 SNE for Type 1 nodes

We assume that DNB node i is of Type 1 and all of its neighbors are DNB members i_1, i_2, \dots, i_m . From Eq.(S29), we know that when a system is near a critical point, it is more likely that DNB node i has a large state transition at any time t . The same property holds for other DND nodes i_l ($l = 1, 2, \dots, m$).

We define the event $A_1 = \{x_i = 1, x_{i_1} = 1, \dots, x_{i_m} = 1\}$ (see Fig.S2). When the system approaches the critical point, from Theorem 3 we have

$$p_{1,v}^{\text{pre}} = p^{\text{pre}}(X(t+1) = A_1 | X(t) = A_v) \rightarrow 1, \quad (\text{S31})$$

while the probability of other transitions approaches 0, because $p_{s,v}^{\text{pre}} = p^{\text{pre}}(X(t+1) = A_s | X(t) = A_v) = p^{\text{pre}}(x_{i_l}(t+1) = 0, \dots, | X(t) = A_v) \leq p^{\text{pre}}(x_{i_l}(t+1) = 0 | X(t) = A_v) \rightarrow 0$, for any $l \in \{1, \dots, m\}$, $u \in \{1, 2, \dots, 2^{m+1}\}$, $s \in \{2, 3, \dots, 2^{m+1}\}$.

Equation (S31) implies that if any DNB node has a state transition, then its DNB neighbors will probably have a state transition as well. They change dynamically in a highly collective manner.

Therefore, when the system approaches a critical point, the SNE for type 1 node

$$H^{\text{pre}} = - \sum_{u,v} \pi_v^{\text{pre}} p_{u,v}^{\text{pre}} \log p_{u,v}^{\text{pre}} \rightarrow 0,$$

suggesting that the SNE decreases drastically for Type 1 nodes.

C.2.2 SNE for Type 2 nodes

We assume that node i is a Type 2 node, *i.e.*, a DNB boundary node linked with at least one non-DNB node. Thus, we assume that some of its neighbors, *i.e.*, i_1, i_2, \dots, i_h , are DNB nodes whereas others $i_{h+1}, i_{h+2}, \dots, i_m$ are non-DNB nodes. Therefore, when a system approaches a critical point, Eq.(S29) holds for i and i_l ($l = 1, 2, \dots, h$).

For i_{h+r} ($r = 1, 2, \dots, m - h$), Theorem 1 shows that even when the system is in a pre-disease state, $\text{SD}(z_{i_{h+r}})$ approaches bounded values. Thus, it holds that

$$p^{\text{pre}}(x_{i_{h+r}}(t) = 1) \rightarrow \beta_{i_{h+r}}, \quad (\text{S32})$$

where $\beta_{i_{h+r}}$ are positive constants.

Definition 2 Let B_1 represent the event $\{x_i = 1, x_{i_1} = 1, \dots, x_{i_h} = 1\}$. Let $\{B_s\}_{s=2,3,\dots,2^{h+1}}$ denote random events $\{x_i = \gamma_0, x_{i_1} = \gamma_1, \dots, x_{i_h} = \gamma_h\}$ with $\gamma_l \in \{0, 1\}$ for $l \in \{0, 1, 2, \dots, h\}$ and at least one $\gamma_l = 0$. Let $\{C_k\}_{k=1,2,\dots,2^{m-h}}$ represent random events $\{x_{i_{h+1}} = \gamma_{h+1}, \dots, x_{i_m} = \gamma_m\}$ with $\gamma_{h+r} \in \{0, 1\}$ for $r \in \{1, 2, \dots, m - h\}$. Obviously, $A_u = \{B_s, C_k\}$, where $u \in \{1, 2, \dots, 2^{m+1}\}$, $s \in \{1, 2, \dots, 2^{h+1}\}$, $k \in \{1, 2, \dots, 2^{m-h}\}$.

For any random event B_s ($s \geq 2$), there is at least one DNB node, *i.e.*, $i_l, l \in \{0, 1, 2, \dots, h\}$, that satisfies $x_{i_l} = 0$ ($x_{i_0} = x_i$). Because $p^{\text{pre}}(x_{i_l} = 0, \dots) \leq p^{\text{pre}}(x_{i_l} = 0) \rightarrow 0$ from Eq.(S30), we know that there are $(2^{m+1} - 2^{m-h})$ probabilities vanishing, *i.e.*,

$$p^{\text{pre}}(B_s, C_k) = 0, \quad s = 2, 3, \dots, 2^{h+1}, \quad k = 1, 2, \dots, 2^{m-h}, \quad (\text{S33})$$

and only 2^{m-h} non-zero probabilities remaining, i.e.,

$$p_k^{\text{pre}} := p^{\text{pre}}(B_1, C_k),$$

that satisfy $\sum_{k=1}^{2^{m-h}} p_k^{\text{pre}} = 1$.

In a pre-disease state, note that $\text{PCC}(z_{i_l}, z_{i_{h+r}}) \rightarrow 0$, $l = 1, 2, \dots, h$; $r = 1, 2, \dots, m - h$, and the correlations among non-DNB nodes i_{h+r} ($r = 1, 2, \dots, m - h$) are similar to those in a normal state. For any random event C_k , from Eq.(S33) we have

$$\begin{aligned} & p^{\text{pre}}(B_1, C_k) \\ &= p^{\text{pre}}(B_1, C_k) + \sum_{s=2}^{2^{h+1}} p^{\text{pre}}(B_s, C_k) \\ &= p^{\text{pre}}(C_k) = p^{\text{nor}}(C_k) \\ &= \sum_{s=1}^{2^{h+1}} p^{\text{nor}}(B_s, C_k). \end{aligned}$$

Thus, $p_k^{\text{pre}} = \sum_{s_k=1}^{2^{h+1}} p_{s_k}^{\text{nor}}$, which suggests

$$\begin{aligned} p_k^{\text{pre}} \cdot \log(p_k^{\text{pre}}) &= \left(\sum_{s_k=1}^{2^{h+1}} p_{s_k}^{\text{nor}} \right) \cdot \log \left(\sum_{s_k=1}^{2^{h+1}} p_{s_k}^{\text{nor}} \right) \\ &= \sum_{s_k=1}^{2^{h+1}} \left(p_{s_k}^{\text{nor}} \cdot \log \left(\sum_{s_k=1}^{2^{h+1}} p_{s_k}^{\text{nor}} \right) \right) \\ &> \sum_{s_k=1}^{2^{h+1}} (p_{s_k}^{\text{nor}} \cdot \log(p_{s_k}^{\text{nor}})). \end{aligned}$$

Therefore,

$$\begin{aligned}
& - \sum_{k=1}^{2^{m-h}} p_k^{\text{pre}} \log p_k^{\text{pre}} \\
& < - \sum_{k=1}^{2^{m-h}} \left(\sum_{s_k=1}^{2^{h+1}} (p_{s_k}^{\text{nor}} \cdot \log p_{s_k}^{\text{nor}}) \right) \\
& = - \sum_{k=1}^{2^{m+1}} p_k^{\text{nor}} \log p_k^{\text{nor}},
\end{aligned}$$

which infers $H^{\text{pre}} < H^{\text{nor}}$. Thus, for any Type 2 node, the SNE will decrease when the system approaches a critical point.

C.2.3 SNE for Type 3 nodes

We assume that node i is a Type 3 node, *i.e.*, a non-DNB node linked with non-DNB nodes and at least one DNB one. Therefore, we assume that some of the neighbors i_1, i_2, \dots, i_h are DNB nodes, whereas others $i_{h+1}, i_{h+2}, \dots, i_m$ are non-DNB nodes. As with Type 2 nodes, we know that the SNE will decrease when the system approaches a critical point.

C.2.4 SNE for Type 4 nodes

We assume that node i is a Type 4 node, *i.e.*, i is a non-DNB node linked with non-DNB nodes alone, i_1, i_2, \dots, i_m . Therefore, Eq.(S32) holds for i and i_l ($l = 1, 2, \dots, m$).

There are no significant changes in the correlations among i and its neighbors even in a pre-disease state. Thus, we may assume that the correlations between i and i_{h+r} ($r = 1, 2, \dots, m-h$) are the same as those in a normal state. Therefore,

$$p^{\text{pre}}(X(t+1) = A_u | X(t) = A_v) = p^{\text{nor}}(X(t+1) = A_u | X(t) = A_v),$$

where $u, v \in \{1, 2, \dots, 2^{m+1}\}$. Thus, the SNE of a Type 4 node remains the same as that in its normal state and it can be viewed as invariant.

Based on these four cases, we conclude that the average SNE (S24) decreases drastically as the system approaches a critical transition point. This critical phenomenon coincides with the physical meaning of the conditional entropy in terms of the low resilience or robustness in a pre-disease state, i.e., the next state transition depends greatly on its current state, which implies a low conditional entropy due to this dependence near the pre-disease state. We adopt an efficient strategy for estimating the average SNE using only those nodes with decreasing SNEs, rather than all of the nodes in the network. Using such a scheme, the average SNE is more sensitive to a pre-disease state.

Remark 2 *Near a critical transition point, the decreasing value of an SNE depends on the ratio of the number of DNB nodes to the number of non-DNB nodes in the local network. If the ratio of DNB nodes is higher, the SNE is smaller in the local network. In particular, the SNE decreases drastically for a Type 1 node because all of the nodes in the local network that are centered on a DNB core node are DNB nodes. The decrease in SNEs for Type 2 or Type 3 nodes results from the DNB nodes in the local network.*

The derivation of the SNE is based on the properties of the DNB, but there are several advantages in using the SNE to detect a critical transition. **(1)** It is easier to detect DNB nodes directly, rather than a dominant group in the overall network, which is generally a difficult task because of the scale of datasets. **(2)** We only need to focus on the local structure of a network node by node, which significantly reduces the computational complexity. Therefore, predictions based on the SNE method are DNB-free.

C.3 The leading network and SNE network

After we calculate the SNE for each node, it is reasonable to ignore any nodes with increasing SNEs because this may be caused by noise and data errors. In a pre-disease state, the remaining

nodes with decreasing SNEs form a subnetwork, which we use as our index or criterion for detecting a critical transition and the leading network in the transition to a disease state. Our analysis and computations are based on local structure, i.e., one node and its linked neighbors, but the final subnetwork is of the most critical information for determining the dynamics of the original overall network. Clearly, this method simplifies the computation and it also helps us to avoid the effect of noise, thereby providing a more accurate and reliable early warning signal.

In this study, we adopted the following definitions of different networks.

- An overall network is formed of Type 1, Type 2, Type 3, and Type 4 nodes, i.e., a network includes all genes.
- An SNE network is formed of Type 1, Type 2, and Type 3 nodes, i.e., the DNB and its first-order neighbors.
- A leading network is formed of Type 1 and Type 2 nodes, i.e., the DNB.

A leading network is formed of Type 1 and Type 2 nodes, so critical behavior in their dynamics drives the system toward a phase transition. Therefore, Type 1 and Type 2 nodes that are directly related to the dominant eigenvalue behave in a strongly collective manner, carrying most of the dynamical information when the system is in a pre-disease state. In addition, their critical characteristics are little distorted by noise because of their overwhelming trend as a system approaches a critical point.

Type 3 and Type 4 nodes, in contrast, are irrelevant to the dominant eigenvalue, and loses the correlations with Type 1 and Type 2 nodes as a system approaches a critical point, and they are much more likely to be influenced by the widespread noise and data errors, resulting in the fluctuations (i.e., possible increasing or decreasing) SNEs. Therefore, in the computational algorithm, we ignore those Type 3 and Type 4 nodes (in particular, Type 4 nodes) that form most of nodes in the network, with increasing SNEs.

In our algorithm, therefore, we only select nodes with decreasing SNEs (i.e., Type 1 and Type 2, and some Type 3) to calculate the average SNE as our index or criterion for detecting critical transitions and the leading network in an efficient and accurate manner. Based on the definition of the four types of nodes that form the entire network, the DNB or leading network is composed of Type 1 and Type 2 nodes, while the SNE network is composed of Type 1, Type 2, and Type 3 nodes because of the decrease in their SNEs near the critical transition.

D Numerical validation of leading networks detected by SNE

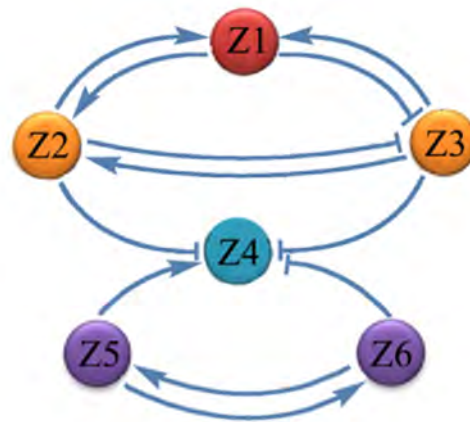


Figure S5: | **A model of a six-gene regulatory network.** In this sketch of a regulatory network, the arrow represents positive regulation, whereas the blunt line denotes negative regulation.

In this section, we use a six-gene network (see Fig.S5 or Fig.3a in the main text) to conduct a numerical simulation and theoretically demonstrate the detection of early-warning signals using the SNE near a critical point. These types of gene regulatory networks are often used to study transcription, translation, diffusion, and translocation processes that affect gene regulatory activities (2, 5, 20–22). The following six differential equations represent the gene regulation of six genes in a network where gene regulation is represented in a Michaelis-Menten form, with

the exception of the degradation rates, which are linearly proportional to the concentrations of the corresponding genes.

$$\left\{ \begin{array}{l} \frac{dz_1(t)}{dt} = \frac{(5-2|P|)z_2}{5(1+z_2(t))} + \frac{(5-2|P|)z_3}{5(1+z_3(t))} - \frac{2*|P|}{5} z_1(t) + \zeta_1(t), \\ \frac{dz_2(t)}{dt} = \frac{(2-|P|)z_1}{5(1+z_1(t))} + \frac{(2-|P|)z_3}{5(1+z_3(t))} - \frac{|P|+2}{5} z_2(t) + \zeta_2(t), \\ \frac{dz_3(t)}{dt} = \left(\frac{2|P|}{5} - 1\right) + \frac{(2-|P|)}{5(1+z_1(t))} + \frac{(3-|P|)}{5(1+z_2(t))} - \frac{7-|P|}{5} z_3(t) + \zeta_3(t), \\ \frac{dz_4(t)}{dt} = -\frac{1}{2} + \frac{1}{10(1+z_2(t))} + \frac{1}{10(1+z_3(t))} + \frac{3z_5(t)}{10(1+z_5(t))} \\ \quad + \frac{3}{10(1+z_6(t))} - \frac{8}{5} z_4(t) + \zeta_4(t), \\ \frac{dz_5(t)}{dt} = \frac{z_6(t)}{10(1+z_6(t))} - \frac{21}{10} z_5(t) + \zeta_5(t), \\ \frac{dz_6(t)}{dt} = \frac{z_5(t)}{10(1+z_5(t))} - \frac{21}{10} z_6(t) + \zeta_6(t), \end{array} \right. \quad (\text{S34})$$

where P is a scalar control parameter and $\zeta_i(t)$ ($i = 1, 2, \dots, 5$) are Gaussian noises with zero means and covariances $\kappa_{ij} = \text{Cov}(\zeta_i, \zeta_j)$. z_i ($i = 1, \dots, 5$) represent the concentrations of mRNA- i . In Eq.(S34), the degradation rates of mRNAs are $(\frac{2*|P|}{5}, \frac{|P|+2}{5}, \frac{7-|P|}{5}, \frac{8}{5}, \frac{21}{10}, \frac{21}{10})$. There is a stable equilibrium point $\bar{Z} = (\bar{z}_1, \bar{z}_2, \bar{z}_3, \bar{z}_4, \bar{z}_5, \bar{z}_6) = (0, 0, 0, 0, 0, 0)$. The differential equations Eq.(S34) can be transformed into the difference equations $Z(k+1) = f(Z(k), P)$ using the Euler scheme (23), *i.e.*,

$$\left\{ \begin{array}{l} z_1(k+1) = z_1(k) + \left[\frac{(5-2|P|)z_2}{5(1+z_2(t))} + \frac{(5-2|P|)z_3}{5(1+z_3(t))} - \frac{2*|P|}{5} z_1(t) + \zeta_1(t) \right] \Delta t, \\ z_2(k+1) = z_2(k) + \left[\frac{(2-|P|)z_1}{5(1+z_1(t))} + \frac{(2-|P|)z_3}{5(1+z_3(t))} - \frac{|P|+2}{5} z_2(t) + \zeta_2(t) \right] \Delta t, \\ z_3(k+1) = z_3(k) + \left[\left(\frac{2|P|}{5} - 1\right) + \frac{(2-|P|)}{5(1+z_1(t))} + \frac{(3-|P|)}{5(1+z_2(t))} - \frac{7-|P|}{5} z_3(t) + \zeta_3(t) \right] \Delta t, \\ z_4(k+1) = z_4(k) + \left[-\frac{1}{2} + \frac{1}{10(1+z_2(t))} + \frac{1}{10(1+z_3(t))} + \frac{3z_5(t)}{10(1+z_5(t))} \right. \\ \quad \left. + \frac{3}{10(1+z_6(t))} - \frac{8}{5} z_4(t) \right] \Delta t, \\ z_5(k+1) = z_5(k) + \left[\frac{z_6(t)}{10(1+z_6(t))} - \frac{21}{10} z_5(t) \right] \Delta t, \\ z_6(k+1) = z_6(k) + \left[\frac{z_5(t)}{10(1+z_5(t))} - \frac{21}{10} z_6(t) \right] \Delta t, \end{array} \right. \quad (\text{S35})$$

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

We denote the Jacobian matrix of Eq.(S35) as $J = \frac{\partial f(Z(k); P)}{\partial Z} \Big|_{Z=\bar{Z}}$, where

$$J = e^{\Delta t \cdot A} \quad (\text{S36})$$

with

$$A = \begin{bmatrix} \frac{-2*|P|}{(2-|P|)^5} & 1 - \frac{2|P|}{(2+|P|)^5} & 1 - \frac{2|P|}{(2-|P|)^5} & 0 & 0 & 0 \\ \frac{5}{(2-|P|)^5} & -\frac{5}{(2+|P|)^5} & \frac{5}{(2-|P|)^5} & 0 & 0 & 0 \\ -\frac{(2-|P|)}{5} & -\frac{(3-|P|)}{5} & \frac{(7-|P|)}{5} & 0 & 0 & 0 \\ 0 & -\frac{1}{10} & -\frac{1}{10} & -\frac{8}{5} & \frac{3}{10} & -\frac{3}{10} \\ 0 & 0 & 0 & 0 & -\frac{21}{10} & \frac{1}{10} \\ 0 & 0 & 0 & 0 & \frac{1}{10} & -\frac{21}{10} \end{bmatrix}.$$

From Eq.(S36), we obtain six distinct eigenvalues $(0.74^{|P|}, 0.55, 0.37, 0.20, 0.14)$ by taking $\Delta t = 1$. Thus, the equilibrium point \bar{Z} is stable when $P \in (0, 1]$. Obviously, there is a critical value $P_c = 0$, where the system loses stability and undergoes a critical transition. We aimed to detect early warning signals that indicate the critical transition as a control parameter P approaches a critical value 0 from $P > 0$.

We then diagonalize the Jacobian matrix J using matrix S

$$S = \begin{bmatrix} -2 & 0 & 6 & 0 & 0 & 0 \\ -1 & -1 & 0 & 0 & 0 & 0 \\ 1 & 1 & -6 & 0 & 0 & 0 \\ 0 & 0 & 1 & -1 & 0 & -1 \\ 0 & 0 & 0 & 0 & -1 & 1 \\ 0 & 0 & 0 & 0 & -1 & -1 \end{bmatrix}, \quad (\text{S37})$$

which satisfies $S^{-1} J S = \Lambda$ where $\Lambda = \text{diag}(0.67^{|P|}, 0.45, 0.37, 0.20, 0.14, 0.09)$ is a diagonal matrix. We denote $(y_1, 0, 0, 0, 0, 0)$, $(0, y_2, 0, 0, 0, 0)$, $(0, 0, y_3, 0, 0, 0)$, $(0, 0, 0, y_4, 0, 0)$, $(0, 0, 0, 0, y_5, 0)$, $(0, 0, 0, 0, 0, y_6)$, respectively, as the eigenvectors of Λ with eigenvalue λ_i ($i = 1, 2, \dots, 6$). Note that the variable y_1 is related to the largest eigenvalue $0.67^{|P|}$, which is nearest to 1. Thus, as P approaches 0, the dominant eigenvalue $0.67^{|P|}$ tends to 1, which leads to a critical transition in the system Eq.(S35). Thus, from the relationship

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

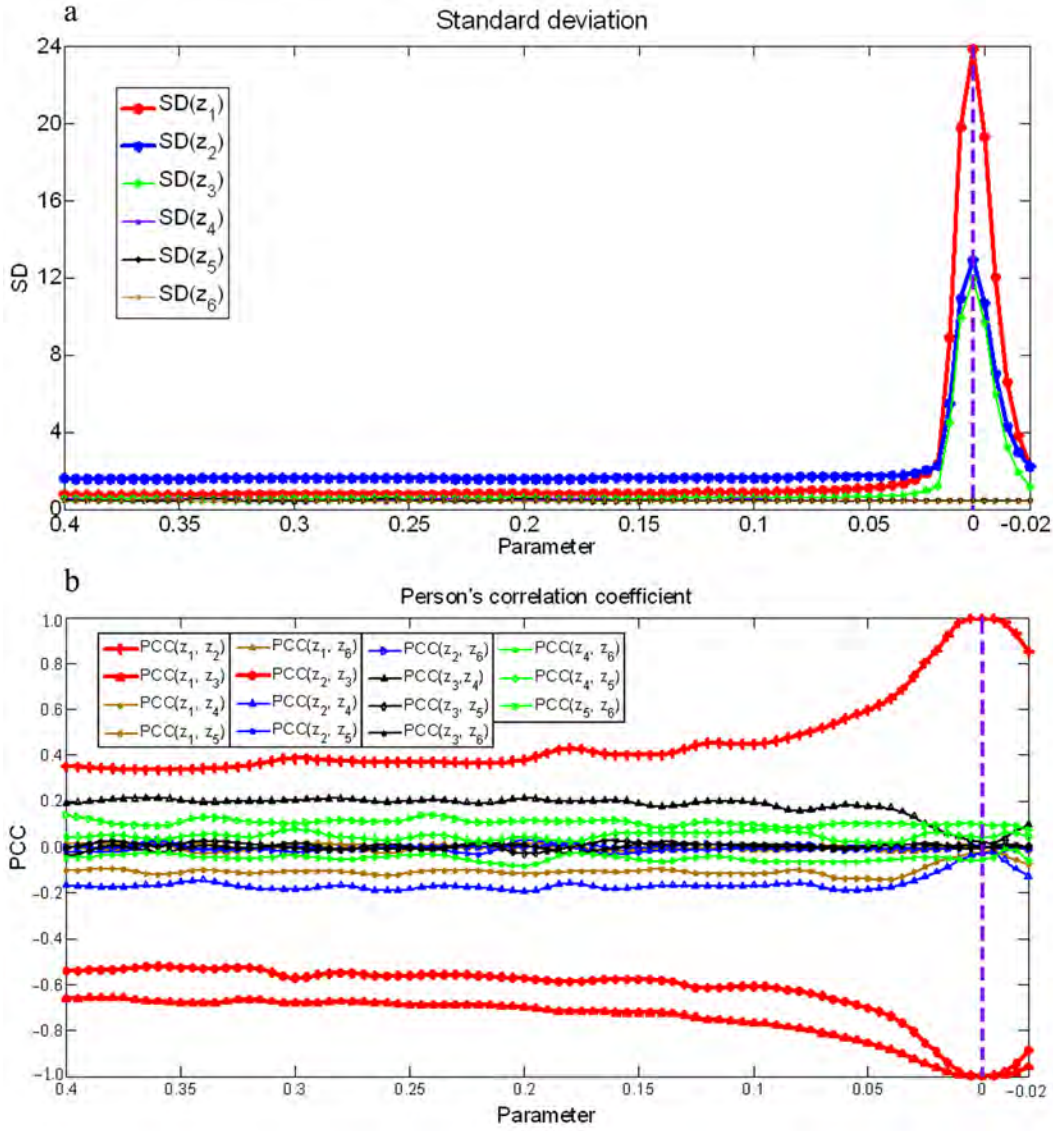


Figure S6: | **Early warning signals in a six-gene network based on a dynamical network biomarker.** (a) Standard deviation (SD) curves for $(z_1, z_2, z_3, z_4, z_5, z_6)$. The horizontal axis represents a control parameter P that varies from 0.4 to -0.1. The vertical axis represents the standard deviation (SD). (b) PCC curves. Each curve is drawn for a pair of variables from $(z_1, z_2, z_3, z_4, z_5, z_6)$. The horizontal axis represents a control parameter P that varies from 0.4 to -0.02. The vertical axis represents the PCC. In simulations based on Eq.(S35) with additive noise, all of the initial conditions are randomly set within the interval $[0, 1]$. The simulations were performed in MATLAB(R2009a) using the Euler-Maruyama integration method with the Ito calculus (23). The system undergoes a bifurcation at $P = 0$.

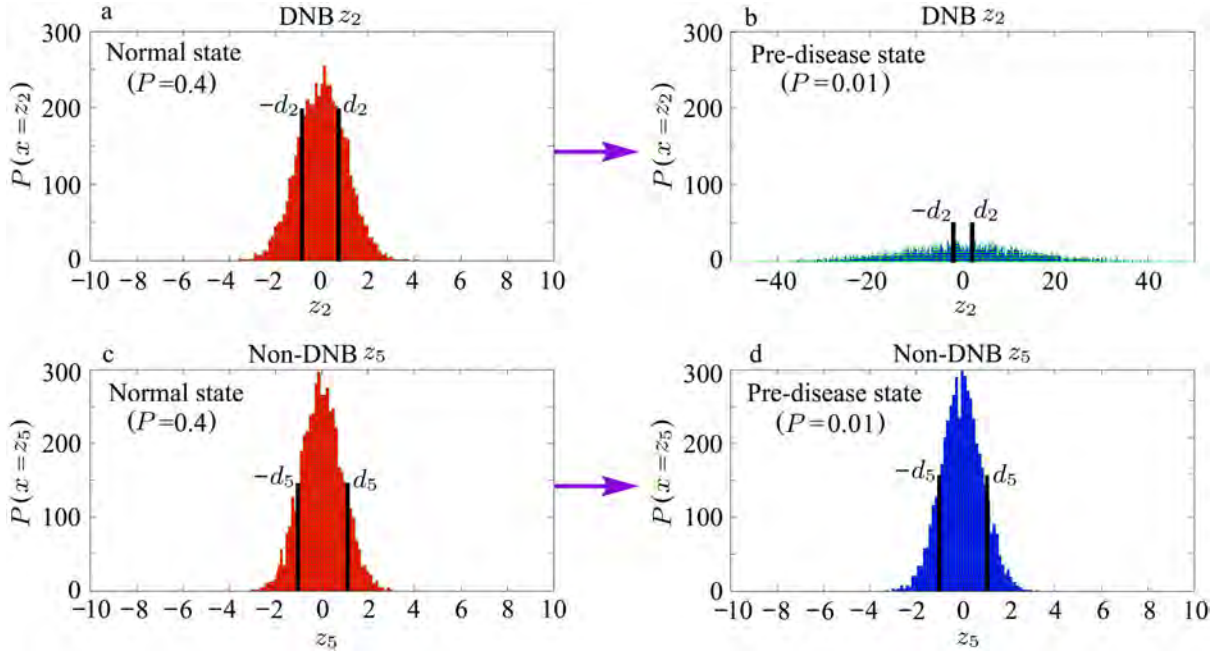


Figure S7: | **Comparison of a DNB node z_2 and a non-DNB node z_5 .** We use a DNB node z_2 and a non-DNB node z_5 as examples. **(a)** In a normal state ($P = 0.4$), the distribution of DNB node z_2 . **(b)** In a pre-disease state ($P = 0.01$), the distribution of DNB node z_2 . **(c)** In a normal state ($P = 0.4$), the distribution of non-DNB nodes z_5 . **(d)** In a pre-disease state ($P = 0.01$), the distribution of non-DNB node z_5 .

or

$$z_1 - \bar{z}_1 = 2y_1 - 6y_3,$$

$$z_2 - \bar{z}_2 = -y_1 - y_2,$$

$$z_3 - \bar{z}_3 = -y_1 + y_2 - 6y_3,$$

$$z_4 - \bar{z}_4 = y_3 - y_4 - y_6,$$

$$z_5 - \bar{z}_5 = -y_5 + y_6,$$

$$z_6 - \bar{z}_6 = -y_5 - y_6,$$

it is clear that among $(z_1, z_2, z_3, z_4, z_5, z_6)$, the three variables z_1, z_2 , and z_3 are related directly to y_1 , which corresponds to the dominant eigenvalue. Therefore, according to the theoretical

results in Section B, $\{z_1, z_2, z_3\}$ constitute the dynamical dominant group or the DNB of the system when $P \in (0, 1]$ and this will reflect the breakdown of the system as $P \rightarrow 0$. We simulated the SD and PCC curves for $(z_1, z_2, z_3, z_4, z_5, z_6)$, as shown in Fig.S6. In addition, we compared the distributions of the expressions for a DNB member z_2 and a non-DNB member z_5 , as shown in Fig.S7.

Based on the theoretical model, we collected time-course data of the six-gene expressions. Then, using the time-course data, we identified the DNB as well as the PCCs and SDs of genes shown in Figures S6 and S7. Finally, we simulated the SNE curves for z_i ($i = 1, 2, \dots, 6$), as shown in Fig.3e in the main text. The mean entropy curve is shown in Fig. 3f in the main text.

E Algorithm for calculating the SNE

We assume a set of samples for one individual in each sampling period (or time window) from a practical viewpoint, whereas there are many thousands of measurements for each sample in high-throughput data, i.e., high-throughput expression data or high-throughput sequencing data. The overall 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) at each period (e.g., a day or an hour) should be shorter so the dynamical features can be reflected in the measured data. In other words, we assume that there are few samples in each period and the intervals need not be equal, although they should be short so that dynamic correlations remain among genes or proteins. For each time period, we evaluate the composite index or the DNB based on a few samples to check whether it is in a pre-disease state in this time period.

We assume that there are two groups of samples, *i.e.*, the case samples and the control samples. The algorithm to detect a DNB and the leading network contains the following steps, using high-throughput data throughout the whole study period.

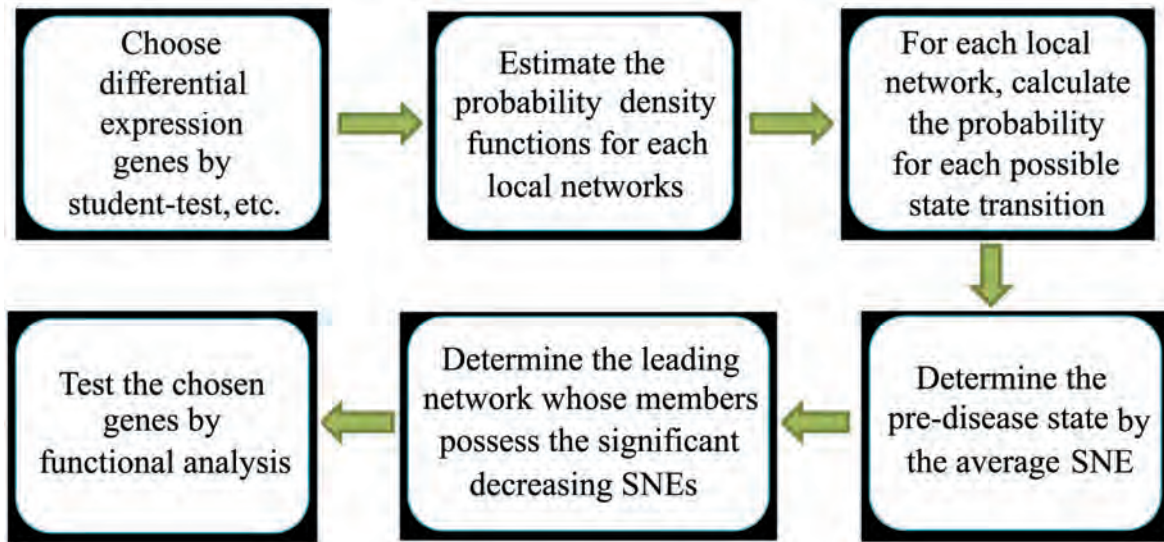


Figure S8: | **Flowchart for the algorithm.**

To define the algorithm clearly, we denote the total number of measurements (genes or proteins) for each sample as N . The flowchart of the algorithm is shown in Fig.S8, which is described as follows.

- **1°** Selection of differentially expressed genes in high-throughput biological data.
 - **1.1** To reflect the state transition in the local network, we determine the differences between samples at two adjacent time points. At each sampling point (or period), we use the Student’s t-test with a significance level of $p < 0.05$ to select genes where the expression changes significantly (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** A false discovery rate (FDR) is used to correct multiple comparisons or multiple t-tests of genes selected in **1.1** during each period.

Next, at each sampling time point t_1, t_2, \dots, t_T , we identify the differentially expressed

genes/proteins with the numbers N_1, N_2, \dots, N_T . These components have two main characteristics, *i.e.*, they have significant differences in their expressions between the case group and the control group, while they also have strong deviations from their mean values.

- **2°** Calculate the SNE for each local network.
 - **2.1** We conduct a new type of data normalization for all the differential expression genes obtained in **1°**. There are S_k samples at t_k for each gene or protein, so the expression data are normalized as follows:

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

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

- **2.2** Using the PPI network, we consider every local network that is centered on each node. In a local network with N nodes, we first need to determine the threshold parameters $d = \{d_1, \dots, d_N\}$ as introduced in section C, *i.e.*, we select $d = \{d_1, \dots, d_N\}$ when the system is in the first time point t_1 (a normal state) such that for each node k , $p(|z_k(t_1)| > d_k) = \alpha$ (see Fig.S4), where α is usually set as 1/2 to insure the highest entropy in a normal state.

Using the samples at each time point t_k , we calculate the probability density function for each local network. For the i th local network with N nodes, we assume that the samples follow a multivariate normal distribution

$$f_{t_k}(Z) = \frac{1}{(2\pi)^{N/2} |\Sigma(t_k)|^{1/2}} \exp\left(-\frac{1}{2}(Z - \mu(t_k))^T \Sigma(t_k)^{-1} (Z - \mu(t_k))\right), \quad (\text{S38})$$

where $Z = (z_1, \dots, z_N)$, $\mu(t_k) = (\mu_1(t_k), \dots, \mu_N(t_k))$ are the means and $\Sigma(t_k)$ is the covariance matrix for the local network at t_k . Then we integrate this probability density function (S38) in different integration domains and we obtain the transition probabilities at time point t_k as $p_{u,v}(t_k)$ in Eq.(S18) or Eq.(1) of the main text, that is,

$$\begin{aligned} p_{u,v}(t_k) &= \Pr(X(t_k) = A_u | X(t_{k-1}) = A_v) \\ &= \frac{\Pr(X(t_k) = A_u, X(t_{k-1}) = A_v)}{\Pr(X(t_{k-1}) = A_v)} \\ &= \frac{\int \dots \int_{Z \in \Omega_v} \int_{\tilde{Z} \in \Omega_u} f_{t_k}(Z, \tilde{Z}) dz_1 \dots dz_N d\tilde{z}_1 \dots d\tilde{z}_N}{\int \dots \int_{Z \in \Omega_v} f_{t_k}(Z) dz_1 \dots dz_N}, \end{aligned}$$

where $Z = (z_1, \dots, z_N)$, $\tilde{Z} = (\tilde{z}_1, \dots, \tilde{z}_N)$, Ω_v and Ω_u are the integration domains respectively corresponding to states A_v and A_u . It is also suitable to use the conditional multivariate normal distributions or the Gaussian kernel estimators to calculate the probabilities (24). Then by using

$$\sum_v \pi_v(t_k) p_{u,v}(t_k) = \pi_u(t_k),$$

we decide the stationary distribution $\pi(t_k)$.

- **3°** Using the probabilities obtained in **2°**, we calculate the SNE for each local network at time point t_k by

$$H_i(t_k) = - \sum_{u,v} \pi_v(t_k) p_{u,v}(t_k) \log p_{u,v}(t_k),$$

where H_i denotes the SNE for the i th local network.

- **3.1** At each time point t_k , we screen out those nodes with increasing SNEs at t_k and we have the node set M_{t_k} with n nodes, in which all nodes have decreasing SNEs at t_k (as shown in Fig. 3e in the main text). Therefore, the average network entropy

got from

$$H(t) = \frac{1}{n} \sum_{i=1}^n H_i(t)$$

decreases at t_k (as shown in Fig. 3f in the main text), and time point t_k is a candidate of a critical transition point.

- **3.2** To determine the critical transition point among all candidate time points, a significance analysis is conducted using the average network entropies respectively obtained from node sets M_{t_k} ($k = 1, 2, \dots, T$). We select the first candidate time point t_j that satisfies the following two significance conditions. First, the node set M_{t_j} should possess many nodes. Second, the change at t_j in the average network entropy from the case data is twice (or more) larger than that of the control data.
- **3.3** Among nodes in set M_{t_j} , we further select the leading network. It can be done by setting a threshold for the changes in the SNE between adjacent sampling points to obtain nodes with the most significant decreasing SNEs.

Each single gene in the selected candidate dominant group in **3°** behaves in a stochastic manner, but their average network entropy is expected to decrease sharply close to the critical transition point. By setting a threshold and selecting the nodes with the most significant changes in the SNE, we assume that the DNB core and DNB boundary are selected so that they form a subnetwork, which will move first toward a disease state and provide a reliable early warning signal. This subnetwork is the so-called leading network.

- **4°** Functional analysis of the genes selected in **3.2**. To determine whether the leading network identified for the detection of an early warning signal of a specific disease correctly predicts an impending critical transition, we conducted a functional analysis of the specific disease, i.e., we analyzed the dysfunctional implications of the extended leading

network (extended by adding the related TFs) based on GO enrichment or literature mining for the relationships between genes in the extended leading network and the specific diseases being studied.

It is notable that the predictions are based on a leading network, which may differ because of large individual variations (see the main text and Section A in this SI) in clinical tests, so high-throughput data are required from the same individual during a sampling period. However, such data were not available, so we used biological data (see Section F) from a group of individuals.

F Application to two different diseases

In this section, we applied our method to the detection of early warning signals and the leading networks in diseases using two experimental datasets. The two datasets are described in Table S2.

Table S2: Descriptions of the two datasets

Experimental data	Descriptions
Genomic data on lung injury due to carbonyl chloride inhalation exposure (GSE6136) (25)	
Sampling points	9 sampling points 0.5, 1, 4, 8, 12, 24, 48, 72 (hours)
Number of observations	PPI network with 4458 RNAs
Groups	control group and case group
Genomic data on hepatic lesions due to chronic hepatitis C (GSE6764) (26)	
Sampling points	7 sampling periods cirrhosis, low-grade dysplastic liver tissue, high-grade dysplastic liver tissue, very early HCC, early HCC, advanced HCC, very advanced HCC (period)
Number of observations	PPI network with 9513 cDNAs
Groups	control group and case group

F.1 Dataset 1: Genomic data related to liver cancer (26)

To explain our method more clearly, we used hepatocellular carcinoma (HCC) as a concrete example to describe our computational procedure step by step. We used the dataset for HCV-induced dysplasia and HCC from (26).

Early warning signals of liver cancer were identified based on the detection of a leading network, as shown in Figs.4 a and 4 c-f in the main text, which indicated that the pre-disease or the pre-deterioration state may have occurred around the fourth time period (a very early HCC stage), while the system may have switched into the disease state after the fourth time period. The prediction based on the SNE coincided with the actual disease development.

We listed all of the dominant-group members which we identified in the Supplementary Table ‘Identified extended leading network’. We provided a detailed functional analysis and the KEGG enrichment analysis in Section H.

In the HCC dataset GSE6764, there were 20320 original probesets, which we mapped to the PPI network. We screened out all probesets with incorrect corresponding gene symbols while probeset that detected the same genes were combined using the averaging method, leaving 9513 genes. Using the algorithm in Section E, we conducted the following computations.

1° We selected differentially expressed genes from high-throughput genomic data related to hepatic lesions. In the case condition, there were seven sampling time points, i.e., cirrhosis (10 samples), low grade dysplastic liver tissue (10 samples), high grade dysplastic liver tissue (7 samples), very early HCC (8 samples), early HCC (10 samples), advanced HCC (7 samples), and very advanced HCC (10 samples). There were 10 samples in the control.

1.1 At each sampling point, we used the Student’s t-test with a significance level of $p < 0.05$ to select $A = [184, 312, 1063, 546, 249, 433]$ of differentially expressed genes for seven periods or time points.

1.2-1.3 We used set A of the differentially expressed genes and based on the false discovery rate (FDR), we obtained 2291 genes from the seven sampling time points, i.e., a PPI network with 2291 nodes that was denoted as gene set B . In gene set B , each component member had significantly different expression in the case group and the control group for at least one sampling point.

2° In the selected PPI network from the above step, there were 2291 local networks, i.e., each node as a center and its first-order neighbors as leaves in a local network. We calculated the state-transition probabilities for each local network.

3° We used the probabilities from **2°** to calculate the SNE for each local network.

3.1 At each time point t_i , we screened out any nodes with an increasing SNE at t_i , to yield the remaining nodes at t_i . Thus, for each sampling point at t_1, t_2, \dots, t_T , we had a set of nodes A_{t_i} ($i = 1, 2, \dots, T$) that all had decreasing SNEs at t_i , i.e.,

- cirrhosis (nodes: 0, overall changes 0)
- low grade dysplastic liver tissue (nodes: 740, overall changes -987)
- high grade dysplastic liver tissue (nodes: 764, overall changes -883)
- very early HCC (nodes: 1258, overall changes -3592)
- early HCC (nodes: 926, overall changes -713)
- advanced HCC (nodes: 738, overall changes -486)
- very advanced HCC (nodes: 813, overall changes -857).

3.2 From **3.1**, it is clear that the SNEs decrease most significantly from the fourth sampling point (very early HCC). Thus, we regarded the “very early HCC” as the critical sampling point and there was sudden deterioration around this point.

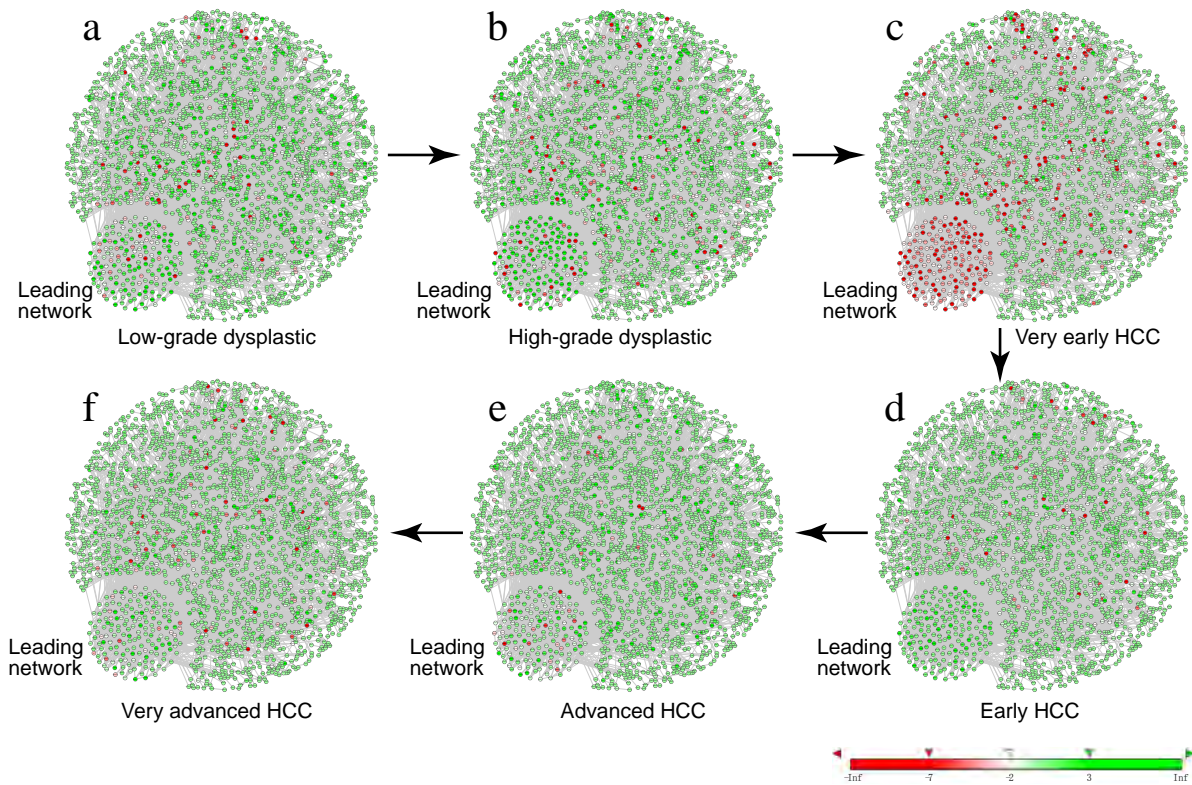


Figure S9: | **Dynamical changes in the overall human PPI network (2291 genes) including the leading network (167 genes) we identified during the disease progression of HCC.** For HCC, we determined the dynamical evolution of the network structure of the entire Homo molecular interaction network (protein-protein interactions and TF-target regulations), including the leading network we identified, in terms of SNE. **(a)** Molecular network during the low grade dysplastic stage. **(b)** Molecular network during the high grade dysplastic stage. **(c)** Molecular network during the very early HCC stage. **(d)** Molecular network during the early HCC stage. **(e)** Molecular network during the advanced HCC stage. **(f)** Molecular network during the very advanced HCC stage. Clearly, the very early HCC stage was the critical transition point according to our criterion, which corresponded to the pre-disease or pre-deterioration state when the genes of the leading network behaved significantly differently from others.

3.3 We also selected a leading network with 167 nodes based on a twofold change selection method, i.e., we set twofold as the threshold to select nodes with the most significant changes in the SNE.

4° Functional analysis of the genes selected in **3.2**. To confirm whether the leading network identified for the detection of an early warning signal of a specific disease correctly predicted the impending critical transition, we conducted a functional analysis of the specific diseases.

Thus, we analyzed the dysfunctional implications of the extended leading network (extended by adding related TFs) based on GO enrichment or literature mining for the relationships between the genes in the extended leading network and the specific disease being studied.

To identify the dynamics of the overall molecular network, we constructed the entire Homo molecular interaction network (protein-protein interactions and TF-target regulations). In the overall network (Fig.S9), there were 1319 nodes (or genes). We graphically illustrated the network in Fig.S9, where the leading network is also indicated. In addition, the heat maps of the gene expression and SNE of the leading network are shown in Figs.S11 a and b, respectively.

F.2 Dataset 2: Genomic data related to lung injury after carbonyl chloride inhalation (25)

This dataset was obtained in an experiment on toxic gas-induced lung injury effects, i.e., pulmonary edema (25). A genomic approach was used to investigate the molecular mechanism of phosgene-induced lung injury. The experiments determined the temporal effects of phosgene exposure on lung tissue antioxidant enzyme concentrations and the gene expression level, and these results were compared with those from air-exposed mice treated in a similar manner to assess the role of the GSH redox cycle in this oxidative lung injury model (25). To produce two groups of data, i.e., the control group data and case group data, two groups of CD-1 male mice were exposed to air or phosgene, respectively. Lung tissues were collected from air- or phosgene-exposed mice at 0.5, 1, 4, 8, 12, 24, 48, and 72 h after exposure. The details of the experiment are available in the original paper (25).

Briefly, the authors found that the main physiological effects occurred within the first 8 h after exposure, resulting in common observations of enhanced BALF protein levels, increased pulmonary edema, and ultimately decreased survival rates (25). At the concentration delivered, 50%-60% mortality was routinely observed after 12 h while 60%-70% mortality was observed

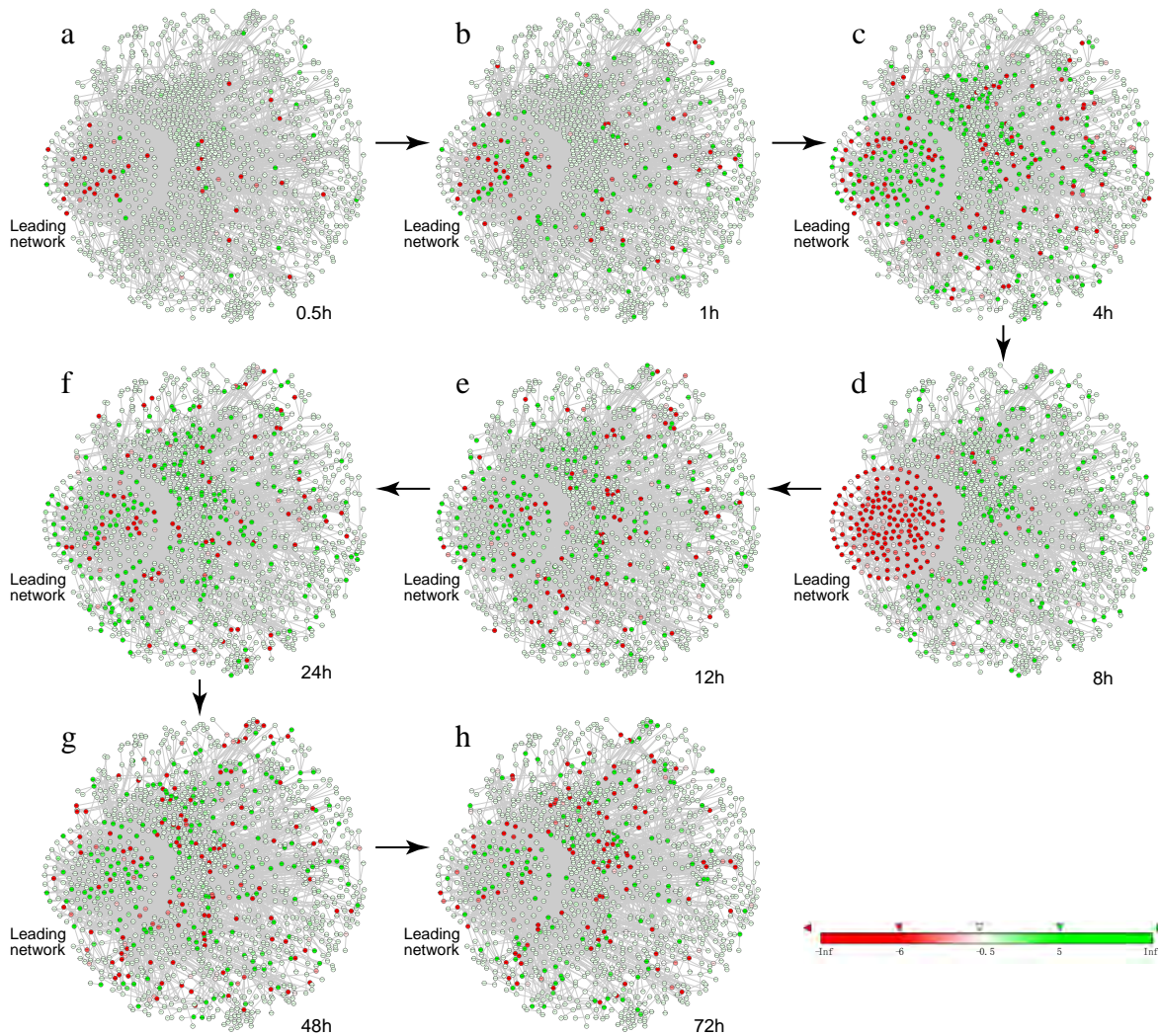


Figure S10: | **Dynamical changes in the overall mouse PPI network (1319 genes) including the leading network (178 genes) we detected during the progression of acute lung injury.** For acute lung injury, we show the dynamical evolution of the network structure for the overall mouse molecular interaction network (protein-protein interactions and TF-target regulations), including the leading network which we identified, in terms of the SNE. **(a)** Molecular network at 0.5 h. **(b)** Molecular network at 1 h. **(c)** Molecular network at 4 h. **(d)** Molecular network at 8 h. **(e)** Molecular network at 12 h. **(f)** Molecular network at 24 h. **(g)** Molecular network at 48 h. **(h)** Molecular network at 72 h. The network was constructed from the overall mapped mouse molecular interaction network (protein-protein interactions and TF-target regulations) based on the expression data. Clearly, the stage at 8 h was the critical transition point according to our criterion, which corresponded to the pre-disease or pre-deterioration state, where the genes in the leading network behaved significantly differently from others.

after 24 h. In addition, they found that the most severe phosgene-induced acute lung injury ranged from 4 to 12 h after exposure (25). The detailed results are also available in the original paper (25). Early warning signals of lung injury based on the leading network which we identified are shown in Figs.4b, and 4g-j in the main text, which showed that the pre-disease state may start around the fourth time period (8 h), while the system may enter the disease state after the fourth time period (8 h). Our prediction based on the SNE agreed with the actual disease development.

To examine the dynamics of the overall molecular network, we constructed the entire mouse molecular interaction network (protein-protein interactions and TF-target regulations). There were 1319 nodes (or genes) in the overall network (Fig.S10). We graphically illustrate the network in Fig.S10, where the leading network is also indicated. In addition, the heat maps of the gene expression and SNE in the leading network are shown in Figs.S11 c and d, respectively.

We listed all of the dominant-group members that we identified in Supplementary Table ‘Identified extended leading network’ and we also provided a detailed functional analysis and the KEGG enrichment analysis in Section H.

G Bootstrap analysis and cross validation

To verify the biological and statistical significance of the SNE group, we performed bootstrap analyses for the two diseases individually described in Section D. For each disease, we randomly selected 10 gene sets, each of which possessed the same number of members as the SNE group (see Table S3 for HCC, and Table S4 for lung injury). Next, we calculated the criterion for each gene set. The corresponding curves for HCC and acute lung injury are respectively shown in Figs.S12a and b, where the red curves represent the respective average SNE and the blue ones are the average SNEs for randomly chosen gene sets of the same numbers with the leading networks.

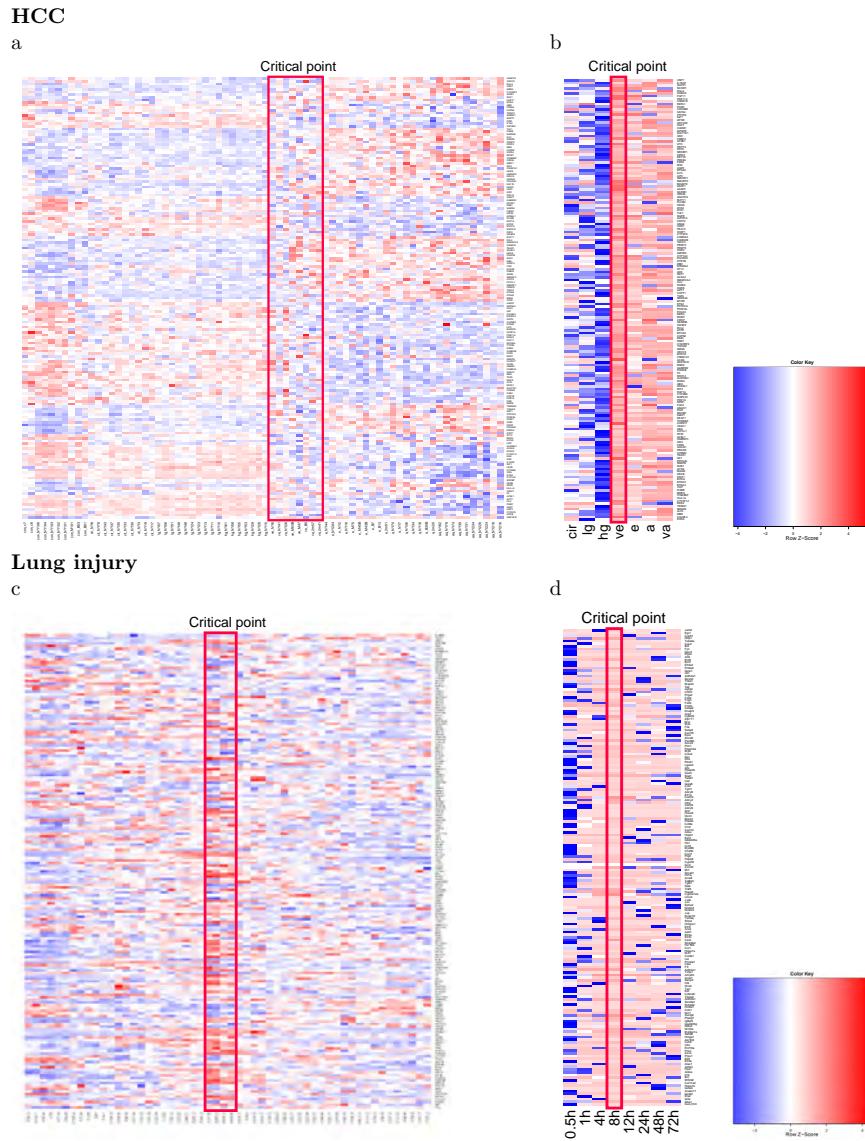


Figure S11: | **Heat maps of the SNEs and gene expression in the leading networks.** The heat maps of the SNEs and gene expression are shown for the leading networks in HCC liver cancer and acute lung injury. **(a)** Heat map of gene expression for the leading network of HCC. **(b)** Heat map of the SNE for the leading network of HCC. **(c)** Heat map of gene expression for the leading network of lung injury. **(d)** Heat map of the SNE for the leading network of lung injury.

The bootstrap results clearly show that the identified leading network produced the most significant signal compared with randomly chosen gene sets for both HCC and acute lung injury. This provides more reliable evidence of the physiological importance of the SNE, as well as the effectiveness of our method.

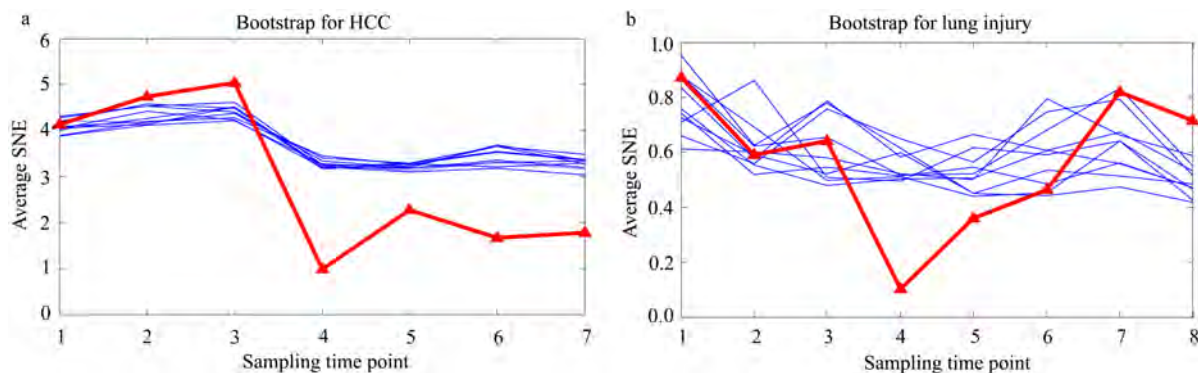


Figure S12: | **Comparison of the SNE-based method and the bootstrap analysis.** To demonstrate biological significance, we compared our method with the bootstrap analysis using the acute lung injury and HCC datasets. **(a)** The bootstrap results for HCC. **(b)** The bootstrap results for lung injury. The red curve and the blue curve show the average SNEs for respectively identified leading networks and randomly chosen gene sets of the same number of members with the leading networks.

Table S3: Information on the bootstrap analysis of HCC (the number that overlapped with the leading network).

	Sample 1	Sample 2	Sample 3	Sample 4	Sample 5	Sample 6	Sample 7	Sample 8	Sample 9	Sample 10
Overlap	13	12	17	9	15	10	11	13	19	11
Leading network:	167			Background:			2291			
Mean overlap:	13			Mean overlap rate:			0.08			

For the lung injury dataset, we also applied a DNB-based method to detect the early warning signal and a group of nodes (I). We compared the SNE-based method and the DNB-methods using statistical indices to evaluate the identified genes, i.e., the precision (P), recall (R), and F-measure (F). Thus, for the lung injury dataset, we compared a leading network composed of

Table S4: Information on the bootstrap analysis of acute lung injury (the number that overlapped with the leading network).

	Sample 1	Sample 2	Sample 3	Sample 4	Sample 5	Sample 6	Sample 7	Sample 8	Sample 9	Sample 10
Overlap	28	24	23	23	18	22	22	22	23	28
Leading network:	178			Background: 1319						
Mean overlap:	23.3			Mean overlap rate: 0.13						

178 nodes whereas the DNB subnetwork was composed of 220 genes (I), so the overlap was 60 genes.

$$P = \frac{t_p}{t_p + f_p} = 60/178 = 0.34,$$

$$R = \frac{t_p}{t_p + f_n} = 60/220 = 0.27,$$

$$F = \frac{2 * P * R}{P + R} = 2 * 0.34 * 0.27 / (0.34 + 0.27) = 0.30,$$

where t_p is the true positive, which represents the overlap with the SNE method, while f_n is the false negative, which represents the other DNB nodes that are not identified by the SNE. f_p is the false positive, which represents other members of the leading network that have no relationship with the DNB.

The bootstrap results also showed that $P_{\text{MAX}} = 0.027$, $R_{\text{MAX}} = 0.039$, and $F_{\text{MAX}} = 0.042$, which demonstrated that the leading network was the most biologically significant (see Fig.S12b).

We also carried out a cross validation for the two diseases, respectively to demonstrate the correctness of the identified leading networks (see Fig.S13), where the red curves represent the average SNEs of the identified leading networks with all samples, and the green curves represent the average SNEs of the identified leading networks with leave-one-out cross validation. From Fig.S13, it can be seen that the average SNE curves (green line) with leave-one-out cross validation have the same trends to those (red line) of the leading networks with all samples,

which validates the correctness of the identified pre-disease states. Note that the average SNE curves (green line) with the leave-one-out cross validation for n samples were calculated in the following way.

- First, calculate the leading network for $n - 1$ samples by excluding sample- i , and then calculate its average SNE : SNE_i for $i = 1, \dots, n$;
- Finally, the average SNE with the leave-one-out cross validation is obtained by $\sum_i^n SNE_i/n$.

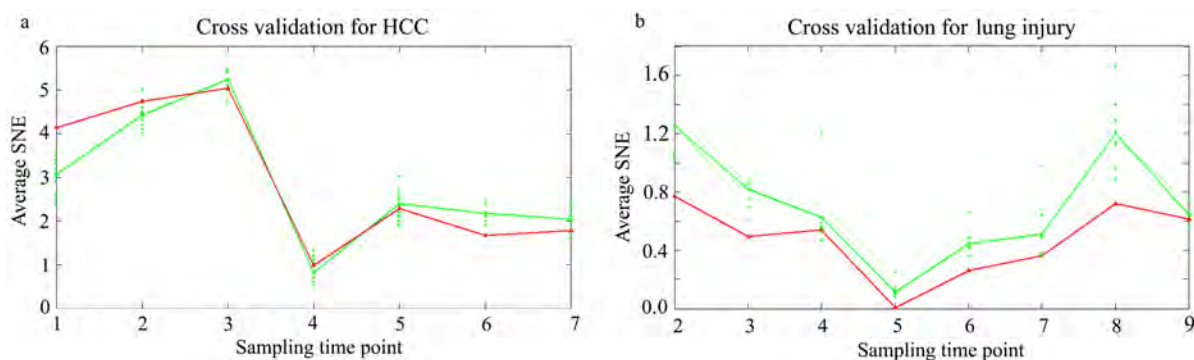


Figure S13: | **Cross validation results for the two diseases** To demonstrate the effectiveness of the identified leading networks, we carried out cross validations for (a) HCC and (b) acute lung injury. The red curves represent the average SNEs of the identified leading networks with all samples, while the green ones are the average SNEs of the leading networks for the leave-one-out cross-validation.

H Functional analysis of the leading networks

In the high-throughput gene expression profiling datasets for HCC induced by HCV infection and acute lung injury induced by phosgene gas, we identified the leading networks using our SNE algorithm and the corresponding networks, including the protein-protein and the TF-target interactions.

It is considered that TFs with high differential expression of their target genes might be causal factors. Bearing this in mind, we included TFs that had relevant targets in the leading

networks and proteins or genes adjacent to any member of the leading networks. We then treated them as the extended leading networks. In this section, we describe the data processing in detail and present the functional analysis results (g:profiler: <http://biit.cs.ut.ee/gprofiler/> and NOA: <http://app.aporc.org/NOA/>) (27, 28) for the leading networks of the two diseases.

Based on the functional analysis, we identified the relationships among members of the leading networks and the complex diseases. Several genes that had been verified in other published studies were also identified. Some newly identified genes may be treated as novel biomarker candidates.

H.1 Data preprocessing

Two gene expression profiling datasets were downloaded from the NCBI GEO database (access ID: GSE6764, GSE2565) (www.ncbi.nlm.nih.gov/geo). In these datasets, probesets without corresponding gene symbols were ignored during our analysis. The expression values of probe sets that mapped to the same gene were averaged.

For each disease dataset, the expression profiling information was mapped to the integrated networks. For each species, we downloaded the biomolecular interaction networks from various databases, including BioGrid (www.thebiogrid.org), TRED (www.rulai.cshl.edu/cgi-bin/TRED/), KEGG (www.genome.jp/kegg), and HPRD (www.hprd.org). First, we downloaded and combined the available functional linkage information on *Mus musculus* and *Homo sapiens* from these databases. After deleting any redundancy, we found 65625 linkages in 11451 human proteins/genes and 37950 linkages in mouse 6683 proteins/genes. Next, the genes evaluated in these microarray datasets were mapped to the integrated functional linkage networks. The leading networks in the two diseases were identified using the SNE algorithm. Overall, there were 167 proteins including four TFs in the leading network we identified for HCC, while 182 proteins including 16 TFs were identified in the leading network for acute lung injury.

These networks were then visualized using Cytoscape (www.cytoscape.org).

H.2 HCC induced by HCV infection

Greater attention is being paid to the study of HCC because it is one of the highest fatal-ratio diseases and increasing numbers of patients are suffering from hepatitis C virus (HCV) infections worldwide. The main cause of HCC via HCV infection is far from clear, but some of the mechanisms and phenomena that occur during HCV infection and hepatitis C disease progression have been identified based on major studies of its molecular mechanisms (29–35) and pathogenesis (36–38). When HCV invades the host cell, it recruits the necessary molecules to replicate itself, then translates and processes its proteins for packaging, before releasing its copies via host lipid transport systems (29–35). In the infected host, some metabolic pathways respond to these interruptions and become increasingly disordered. The following results show that some reported phenomena were consistent with our investigations, which also provided some novel insights.

According to our algorithm, the critical point of the disease occurred between the high grade dysplastic stage and the very early cancer stage.

Interestingly, we found that many of genes in the identified leading network were consistent with the response to HCV infection *in vivo*, particularly the activation of the immune system and dysfunctions associated with basic cell metabolism in the hosts (29–39). The GO and pathway enrichment analysis results are shown in the Supplementary Table ‘KEGG enrichment analysis’. According to these results, genes in the leading network had significantly important roles during disease development. The most enriched functions indicated the leading network’s significant relationship with disease evolution. At the pathway level, the pathways involved in cancer and Hepatitis C appear to be significant, which provides clear evidence that most of the genes selected by the SNE were directly related to HCC. Some enriched pathways were

related to dysfunctions of basic cell metabolism that might be interrupted by the reproduction and release of HCV. Some pathways shared common characteristics with cancer, especially the signaling pathways involved in cell growth, such as transcriptional misregulation in cancer, purine metabolism, Wnt signaling pathway, TGF-beta signaling pathway, and others. These dysfunctional pathways indicated the cell status when HCV invades host cells (30–34) and exploits the host resources for replication. At the GO function level, some genes were also related to other important biological processes. For example, CLU, IL1B, and TNF lead to inflammatory response (37, 40). The regulation of anti-apoptosis and growth may also become dysfunctional (38, 39). Self-reproduction and release also required the interruption of the RNA biosynthetic process and gene expression was enriched in the genes CD81, POLR1A, POLR1E, TCERG1, AR, STAT1, etc. Transport activity was enriched in DRD2, PPARG, JPH2, SNCA, etc., which are important for the release of new viruses after their production (30, 30–32, 40). We also compared the members of the leading network we identified with those reported in a previous study (38). We found that 5/167 genes (hypergeometric test, p-value < 0.02) were validated to have a close correspondence with HCC induced by HCV infection between the dysplastic stage and very early stage of HCC.

H.3 Acute lung injury

Phosgene gas is one of the most important and common chemical industry gases (41). Some pathogenic mechanisms of the acute lung injury induced by phosgene have been identified (42, 43). According to the results of the former study (42), a major change in the entropy of the core dynamical network biomarker (DNB) occurs from 4 h to 8 h. The pathway enrichment analysis and GO functional analysis (shown in Supplementary Table ‘Identified extended leading network’) showed that genes in the leading network we identified were closely related to the mechanism of disease progression (42, 43). Dysfunctions of glutathione metabolism and

the chemokine signaling pathway related to inflammatory immune response were activated in vivo, which also reflected protection against the oxidant-like activity of phosgene. Pathways affected by the oxidant reaction became disordered, especially signal transduction via protein-modified activation, such as the MAPK signaling pathway and Wnt signaling pathway. The decrease in PH induced by the HCl-release reaction meant that affected were some pathways that were sensitive to intracellular conditions and related to communication or transport channels, e.g., gap junctions. Some signaling pathways may also be relevant to repair, survival, apoptosis, and reproduction, such as the GnRH signaling pathway, MAPK signaling pathway, and TGF-beta signaling pathway (42, 43). At the GO function level, some biological processes were also highly related to acute lung injury. For example, the expression profiles of some genes were related to abnormal changes in primary metabolic processes. This indicated the denaturation of lipoids, proteins, and nucleic acids that may have been oxidized by phosgene (42, 43). Some well-known genes that regulate or are directly involved in apoptosis were also included in the leading network, such as JUN, NOTCH2, and MYC. Some genes in the leading network were also related to inflammatory response, wounding induced by oxidant damage, and irritation, such as IL1B, PTGS2, CCL2, and MYD88. Overall, 39/178 genes included in the leading network ($p\text{-value} < 8.45e-15$) have been described as important disease-related genes (42).

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I Supplementary Table ‘Identified extended leading network’

See the Supplementary Table ‘Identified extended leading network’ attached after the References.

J Supplementary Table ‘KEGG Enrichment analysis’

See the attached Supplementary Table ‘KEGG Enrichment analysis’ (After ‘Identified extended leading network’).

Supplementary Table 'Identified extended leading networks'

Identified extended leading networks of HBV

HCV-induced HCC								Term Name	Contain Genes
GO Term	P-value	Corrected P-value	R	T	G	O			
GO:0048518	1.70E-28	6.40E-25	14791	601	2188	194	BP	positive regulation of biological process	SMARCC2; HIPK2; L1CAM; ARHGEF12; SP1; F3; AR; MX1; BNIPL; APOB; APOH; CYP27B1; HOXB9; BLM; PPARG; PPARG; COL4A3; PPARA; ANAPC5; ANAPC7; PDE6H; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; PRKDC; TAF11; AKAP12; REL; TSC1; SPI1; RXRA; LEPR; LEF1; TP73; ERCC1; EGFR; IGF1R; NGFR; UBTIF; PGR; JAG1; NOS1; CYR61; SNCA; JUN; SFTPD; LIF; AVPR1A; RARA; RARB; RARG; REL; CDKN2B; WT1; HOMER1; DBH; SCARB1; ELK1; MASP1; USF1; TCF4; IGF1; F10; SST; IRF8; NFKB1; CSNK1E; NSD1; RALA; EPHX2; ZFH3; USF2; SKP1; CADM1; NTF3; CITED2; CLU; PDCD5; HOXA5; HOXA1; CDK7; TAF9B; LPAR1; ITGB3BP; PRSS2; SMARCA4; CEBPA; CEBPG; CAMP; ETS1; SUZ12; VIPR1; PSME1; SMAD3; ILF3; BCL2; CAV3; GHR; ZFPM2; BRCA1; ERBB4; CREB1; CTSG; MASP2; CRX; HIF1A; XRC5; SMURF1; DAXX; CDC16; EGRI; EGR4; RPS3A; FCN2; FOS; RAD50; TP53INP1; PAX8; ESR2; ESR1; PAX1; FGF23; CCR4; IL1B; STAT3; STAT1; IFNB1; ING2; TAL1; COMT; TP53; WNT2; IL6; MAP2K3; TEAD1; TFAP2A; NAP1L1; GDF5; PDPK1; POU3F2; CEBPB; TP53BP2; SQSTM1; DRD2; C1S; HTR1A; PICALM; HBB; NKX2-1; ETS2; ITSN1; NTRK3; PPP2CA; EEF1D; MST1R; GSK3B; TERF1; POU2F1; TGFA; HRAS; FGF5; FGF4; TAF7; PEX5; CDC23; TNF; NCAM1; MAP1B; NBN; DUSP1; ACHE; ADK; SOS1; STAT5B; STAT5A; SREBF1; PSMB4; RIPK2; ADRBK1; GLI2; TRAF5; NDEL1; CLTCL1; NPM1; NFIC; PEXT; ATF1; AXIN1; HOXC11; NEDD4L; ATF6; IGF2R
GO:0048522	5.90E-26	2.20E-22	14791	601	1984	177	BP	positive regulation of cellular process	SMARCC2; HIPK2; L1CAM; ARHGEF12; SP1; F3; AR; MX1; BNIPL; APOB; CYP27B1; HOXB9; BLM; PPARG; PPARG; COL4A3; PPARA; ANAPC5; ANAPC7; PDE6H; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; PRKDC; TAF11; AKAP12; REL; TSC1; SPI1; RXRA; LEPR; LEF1; TP73; EGFR; IGF1R; NGFR; UBTIF; PGR; JAG1; CYR61; SNCA; JUN; SFTPD; LIF; AVPR1A; RARA; RARB; RARG; REL; CDKN2B; WT1; SCARB1; ELK1; USF1; TCF4; IGF1; F10; SST; IRF8; NFKB1; CSNK1E; NSD1; RALA; ZFH3; USF2; SKP1; CADM1; NTF3; CITED2; CLU; PDCD5; HOXA5; HOXA1; CDK7; TAF9B; LPAR1; ITGB3BP; PRSS2; SMARCA4; CEBPA; CEBPG; CAMP; ETS1; SUZ12; VIPR1; PSME1; SMAD3; ILF3; BCL2; CAV3; GHR; ZFPM2; BRCA1; ERBB4; CREB1; CRX; HIF1A; XRC5; SMURF1; DAXX; CDC16; EGRI; EGR4; RPS3A; FOS; RAD50; TP53INP1; PAX8; ESR2; ESR1; PAX1; FGF23; IL1B; STAT3; STAT1; IFNB1; ING2; TAL1; COMT; TP53; WNT2; IL6; MAP2K3; TEAD1; NAP1L1; GDF5; PDPK1; POU3F2; CEBPB; TP53BP2; SQSTM1; DRD2; HTR1A; PICALM; HBB; NKX2-1; ETS2; ITSN1; NTRK3; PPP2CA; EEF1D; MST1R; TERF1; POU2F1; TGFA; HRAS; FGF5; FGF4; TAF7; CDC23; TNF; NCAM1; MAP1B; NBN; DUSP1; ACHE; ADK; SOS1; STAT5B; STAT5A; SREBF1; PSMB4; RIPK2; ADRBK1; GLI2; TRAF5; NDEL1; NPM1; NFIC; PEXT; ATF1; AXIN1; NEDD4L; ATF6; IGF2R
GO:0065007	4.10E-24	1.50E-20	14791	601	7547	426	BP	biological regulation	SMARCC2; PPAP2A; PCSK2; SCG5; HIPK2; L1CAM; DLG1; PIK3CB; SV2A; ARHGEF12; SP1; SP3; CAMK2A; CAMK2B; F3; SULT1E1; JPH2; WHSC2; AKAP8; AR; HHIP; TSG101; UBE2D2; RIT2; RAB6B; MX1; FZD10; BNIPL; APOB; MST1; APOH; CYP27B1; GTF2I; SMG5; HOXB8; HOXB9; SENP2; BLM; PPARG; PPARG; COL4A3; PPARA; GDI1; ANAPC5; ANAPC7; CSNK1A1; KCNH2; ITGAV; SIGIRR; TRDMT1; PDE6H; SMAD9; RALBP1; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; AKAP12; REL; TSC1; SPI1; IRF3; RXRA; LEPR; LTF; LEF1; SRPK1; PDE10A; BDKRB2; F5; APBA2; TP73; ERCC1; EGFR; IGF1R; RBM9; ERG; NGFR; ABAT; GF11B; PPF1A1; PDE1A; UBTIF; PGR; CNOT3; JAG1; CNOT4; NOS1; CYR61; SNCA; RTN1; JUN; FZD8; HGF; HOXB13; HEXB; ANK3; RGS10; SFTPD; LIF; AVPR1A; COL11A2; RARA; CATSPER1; DAB1; SON; EIF3H; RARB; RARG; PEA15; NFE2L1; SAG; RAB1F; REL; FGB; CDKN2B; WT1; LIPC; HOMER1; TPR; PDE8A; ADCY1; DBH; PTGES3; SCARB1; ELK1; GNG2; RHO; MAPK10; VLDLR; PROS1; MASP1; USF1; AP2B1; GTF2E1; TIRAP; PRKG1; BMX; TCF4; IGF1; KCNK3; IGFBP6; F10; EPOR; SST; IRF8; NFKB1; CSNK1E; NSD1; RALA; EPHX2; PI4KB; IL1RAP; TCEG1; ZFH3; FAPB3; PGAM1; GMN; PDE11A; MLF1; USF2; SKP1; ADAP1; CHTP1; FANCC; CADM1; NTF3; ASCL3; CITED2; CLU; UHRF1; PDCD5; KEAP1; HOXA5; PPAT; HOXA1; CDK7; F2RL3; TAF9B; LPAR1; GTF2H4; TCEB3; MSH2; MSH3; ITGB3BP; PRSS2; MYBL1; SMARCA4; YWHAZ; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; CAMP; ARHGAP1; ETS1; MED15; SUZ12; VIPR1; PRKDC; PSME1; SMAD3; MCL1; CTNNA2; ABI3; ILF3; BCL2; PLCD3; WWP1; CAV3; GHR; CACNA1F; ZFPM2; MAGI2; TRPV4; BRCA1; CETP; ERBB4; CREB1; CTSG; NR2C2; BRD8; BRD7; ADCY5; PRMT5; MASP2; KPNA2; GNAO1; CRX; PLCB2; HIF1A; XRC5; SMURF1; DAXX; SMURF2; CDC16; NONO; EGRI; NT5E; EGR4; XDH; RPH3AL; RPS3A; FCN2; FOS; RAD50; TRRAP; SFPQ; PAX6; TP53INP1; NFKB2; PAX2; PAX8; ESR2; TOLLIP; ESR1; ACAD8; STK36; PAX1; FGF23; SYN1; YY1; CCR4; IL1B; STAT3; RBM8A; STAT1; ZHX2; ZHX3; ZHX1; IFNB1; PDE7B; ING2; IGBP1; TAL1; ACACB; LCAT; COMT; EIF2C2; TP53; NRBF2; SFRP2; CYP1A2; MYB; WNT2; IL6; RHEB; ASAP1; ASAP2; EIF5; MAP2K3; RUNX1T1; TEAD1; CAMLG; KLF11; WASF2; TFAP2A; NAP1L1; AMHR2; GDF5; PDPK1; BCAN; POU3F2; CEBPB; PKN1; MCM7; TP53BP2; VWF; DUSP12; SQSTM1; DRD2; RDH12; C1S; HTR1A; PICALM; KCNE2; KCNE1; ISL1; HBB; NKX2-1; ETS2; CACNA2D1; ITSN1; ITSN2; NTRK2; NTRK3; MICALL1; GOT1; GABRR2; SYT9; ENPP7; FLI1; RAPIA; SNAPC5; SRGAP2; SOCS2; PPP2CA; EEF1D; PPP2CB; MST1R; GSK3B; TERF1; SLC4A1; ACSL1; STMN1; POU2F1; PABPC1; MAPKAPK5; TGFA; PLXNB3; HTR1B; ELK4; MED30; CHRM2; HRAS; FGF5; FGF4; POLR2K; TAF7; PEX5; ETV4; CDC23; TNFAIP3; SHBG; TNF; EPHA3; EPHA2; SDCBP; ACR; GNRHR; ATP5B; NCAM1; NCOR1; FZD6; MAP1B; NBN; SRD5A2; FGF11; DUSP1; CRHBP; TGS1; BCOR; ACHE; ADK; HEY1; SOS1; TACC3; IGFALS; GDF9; STAT5B; STAT5A; SREBF1; PSMB4; CHGA; RIPK2; GRIN2C; DGKQ; ADRBK1; GLI2; FSHR; SIN3A; TRAF5; RAD21; DNMT3L; PLAT; NDEL1; DACH1; CLTCL1; NPM1; NFIC; INPP1; PEXT; ATF1; AXIN1; SUB1; HOXC11; NEDD4L; TGIF1; ATF6; ATF2; IGF2R

GO:0006357	5.00E-23	1.80E-19	14791	601	741	93	BP	regulation of transcription from RNA polymerase II promoter	SMARCC2; HIPK2; SP1; AR; HOXB9; PPARG; PPARG; PPARA; SMAD4; SMAD7; SMAD1; PRKDC; SPI1; RXRA; LEF1; GF1B; JUN; LIF; RARA; RARB; RARG; REL; WT1; ELK1; USF1; IGF1; IRF8; NFKB1; NSD1; ZFH3; USF2; NTF3; ASCL3; CITED2; UHRF1; HOXA5; HOXA1; CDK7; TAF9B; TCEB3; SMARCA4; CEBPA; CEBPG; ETS1; MED15; SUZ12; SMAD3; ZFPM2; BRCA1; CREB1; BRD8; BRD7; CRX; HIF1A; EGR1; FOS; PAX8; ESR2; PAX1; YY1; IL1B; STAT3; ZHX2; IGBP1; TAL1; TP53; IL6; TEAD1; KLF11; TPAP2A; POU3F2; CEBPB; PKM1; SQSTM1; NKX2-1; POU2F1; TAF7; TNF; NCOB1; BCOR; HEY1; STAT5B; STAT5A; SREBF1; DGKQ; GLI2; SIN3A; RAD21; NFIC; ATF1; SUB1; TGIF1; ATF6
GO:0031325	1.00E-22	3.90E-19	14791	601	965	108	BP	positive regulation of cellular metabolic process	SMARCC2; HIPK2; SP1; AR; HOXB9; BLM; PPARG; PPARA; ANAPC5; ANAPC7; SMAD9; SMAD4; SMAD7; SMAD1; PRKDC; TAF11; AKAP12; REL; SPI1; RXRA; LEF1; TP73; EGFR; IGF1R; UBTf; PGR; SNCA; JUN; LIF; AVPR1A; RARA; RARB; RARG; REL; WT1; ELK1; USF1; TCF4; IGF1; IRF8; NFKB1; CSNK1E; NSD1; USF2; SKP1; NTF3; CITED2; HOXA5; HOXA1; CDK7; SMARCA4; CEBPA; CEBPG; CAMP; ETS1; PSME1; SMAD3; ILF3; BCL2; GHR; ZFPM2; BRCA1; CREB1; CRX; HIF1A; SMURF1; CDC16; EGR1; EGR4; FOS; RAD50; PAX8; ESR2; PAX1; FGF23; IL1B; STAT3; ING2; COMT; TP53; IL6; MAP2K3; TEAD1; POU3F2; CEBPB; SQSTM1; PICALM; HBB; NKX2-1; ETS2; POU2F1; HRAS; TAF7; CDC23; TNF; NBN; STAT5B; STAT5A; SREBF1; PSMB4; RIPK2; GLI2; NPM1; NFIC; PEMT; ATF1; AXIN1; ATF6
GO:0045941	2.40E-22	9.10E-19	14791	601	582	80	BP	positive regulation of transcription	SMARCC2; HIPK2; SP1; AR; HOXB9; BLM; PPARG; PPARA; SMAD9; SMAD4; SMAD1; PRKDC; TAF11; REL; SPI1; RXRA; LEF1; TP73; UBTf; PGR; JUN; LIF; RARA; RARB; RARG; REL; WT1; ELK1; USF1; TCF4; IGF1; IRF8; NFKB1; NSD1; USF2; NTF3; CITED2; HOXA5; HOXA1; CDK7; SMARCA4; CEBPA; ETS1; SMAD3; ILF3; ZFPM2; BRCA1; CREB1; CRX; HIF1A; EGR1; EGR4; FOS; PAX8; ESR2; PAX1; FGF23; IL1B; STAT3; ING2; TP53; IL6; MAP2K3; TEAD1; POU3F2; CEBPB; SQSTM1; PICALM; NKX2-1; ETS2; POU2F1; TAF7; TNF; STAT5B; STAT5A; SREBF1; GLI2; NFIC; ATF1; ATF6
GO:0045893	2.70E-22	1.00E-18	14791	601	494	73	BP	positive regulation of transcription, DNA-dependent	SMARCC2; HIPK2; SP1; AR; HOXB9; PPARG; PPARA; SMAD4; SMAD1; PRKDC; REL; SPI1; RXRA; LEF1; TP73; UBTf; PGR; JUN; LIF; RARA; RARB; RARG; REL; WT1; ELK1; USF1; TCF4; IGF1; IRF8; NSD1; USF2; NTF3; CITED2; HOXA5; HOXA1; CDK7; SMARCA4; CEBPA; CREB1; CRX; HIF1A; EGR1; FOS; PAX8; ESR2; PAX1; FGF23; IL1B; STAT3; TP53; IL6; MAP2K3; TEAD1; POU3F2; CEBPB; SQSTM1; NKX2-1; ETS2; POU2F1; TAF7; TNF; STAT5B; STAT5A; SREBF1; GLI2; NFIC; ATF1; ATF6
GO:0032502	2.70E-22	1.00E-18	14791	601	3032	224	BP	developmental process	SMARCC2; PCSK2; HIPK2; L1CAM; SP1; SP3; F3; DDX41; WHSC2; AR; HHIP; TSG101; FZD10; APOB; DRP2; APOH; ZIC2; CYP27B1; HOXB8; HOXB9; DSP; BLM; PPARG; PPARG; PPARA; ITGAV; SMAD9; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TSC1; RXRA; LEPR; LEF1; SRPK1; APBA2; TP73; ERC1; EGFR; IGF1R; ERG; NGFR; GF1B; PGR; JAG1; NOS1; CYR61; RTN1; JUN; FZD8; HGF; TRIP13; HOXB13; HEXB; WNT16; MLPH; SFTPD; LIF; AVPR1A; COL11A2; CATSPER1; PKP2; DAB1; RARB; RARG; WNT10A; NFE2L1; REL; CDKN2B; WT1; HOMER1; PTGES3; VLDLR; BMX; IGF1; KCNK3; EPOR; IRF8; NSD1; ZFH3; GGN; MLI1; FANCC; CADM1; NTF3; CITED2; CLU; COL17A1; KEAP1; HOXA5; PPAT; HOXA1; MSH2; SMARCA4; ZNF7; CEBPA; CEBPG; CEBPE; DVL2; PRKCD; SMAD3; MCL1; CTNNA2; MMP8; BCL2; PLCD3; WWP1; CAV3; GHR; CACNA1F; ZFPM2; BMP8A; ERBB4; CREB1; NR2C2; GNAO1; CRX; HIF1A; XRC5; SMURF1; EGR1; RPS3A; RICS8A; FOS; PAX6; NFKB2; PAX2; PAX8; ESR2; ESR1; STK36; PAX1; FGF22; FGF23; YY1; IL1B; STAT3; TAL1; EFNA5; LGALS3; TP53; SFRP2; CYP11A2; WNT2; IL6; TEAD1; WAF2; TAFAP2A; AMHR2; NEFH; GDF5; PPL; BCAN; POU3F2; CEBPB; VWF; SQSTM1; DRD2; WNT9B; C1S; ALPL; KCNE1; ISL1; NKX2-1; ETS2; NTRK2; NTRK3; CAPN2; FLI1; BMP5; SOCS2; PPP2CA; MST1R; STMN1; POU2F1; PLXNB3; ODF1; CHR2; HRAS; FGF5; FGF4; PEX5; SDC1; SHBG; TNF; ACAN; EPHA2; GNRHR; ATP5B; FZD6; MAP1B; NBN; SRD5A2; FGF11; BCOR; ACHE; HEY1; TACC3; GDF9; STAT5B; STAT5A; ADAM12; PAPSS1; ADRBK1; GLI2; FSHR; SIN3A; DNMT3L; PLAT; ALDH6A1; NDEL1; DACH1; CLTCL1; NPM1; AXIN1; HOXC11; TGIF1; DNMT1; MYO7A; IGF2R
GO:0051173	5.50E-22	2.00E-18	14791	601	683	87	BP	positive regulation of nitrogen compound metabolic process	SMARCC2; HIPK2; SP1; AR; HOXB9; BLM; PPARG; PPARA; SMAD9; SMAD4; SMAD1; PRKDC; TAF11; AKAP12; REL; SPI1; RXRA; LEF1; TP73; EGFR; IGF1R; UBTf; PGR; JUN; LIF; RARA; RARB; RARG; REL; WT1; ELK1; USF1; TCF4; IGF1; IRF8; NFKB1; NSD1; USF2; NTF3; CITED2; HOXA5; HOXA1; CDK7; SMARCA4; CEBPA; CEBPG; ETS1; SMAD3; ILF3; ZFPM2; BRCA1; CREB1; CRX; HIF1A; EGR1; EGR4; FOS; PAX8; ESR2; PAX1; FGF23; IL1B; STAT3; ING2; COMT; TP53; IL6; MAP2K3; TEAD1; POU3F2; CEBPB; SQSTM1; PICALM; HBB; NKX2-1; ETS2; POU2F1; HRAS; TAF7; TNF; STAT5B; STAT5A; SREBF1; GLI2; NFIC; ATF1; ATF6
GO:0051254	5.60E-22	2.00E-18	14791	601	500	73	BP	positive regulation of RNA metabolic process	SMARCC2; HIPK2; SP1; AR; HOXB9; PPARG; PPARA; SMAD4; SMAD1; PRKDC; REL; SPI1; RXRA; LEF1; TP73; UBTf; PGR; JUN; LIF; RARA; RARB; RARG; REL; WT1; ELK1; USF1; TCF4; IGF1; IRF8; NSD1; USF2; NTF3; CITED2; HOXA5; HOXA1; CDK7; SMARCA4; CEBPA; ETS1; SMAD3; ILF3; ZFPM2; BRCA1; CREB1; CRX; HIF1A; EGR1; FOS; PAX8; ESR2; PAX1; FGF23; IL1B; STAT3; TP53; IL6; MAP2K3; TEAD1; POU3F2; CEBPB; SQSTM1; NKX2-1; ETS2; POU2F1; TAF7; TNF; STAT5B; STAT5A; SREBF1; GLI2; NFIC; ATF1; ATF6
GO:0010628	1.00E-21	3.70E-18	14791	601	608	81	BP	positive regulation of gene expression	SMARCC2; HIPK2; SP1; AR; HOXB9; BLM; PPARG; PPARA; SMAD9; SMAD4; SMAD1; PRKDC; TAF11; REL; SPI1; RXRA; LEF1; TP73; UBTf; PGR; JUN; LIF; RARA; RARB; RARG; REL; WT1; ELK1; USF1; TCF4; IGF1; IRF8; NFKB1; NSD1; USF2; NTF3; CITED2; HOXA5; HOXA1; CDK7; SMARCA4; CEBPA; ETS1; SMAD3; ILF3; ZFPM2; BRCA1; CREB1; CRX; HIF1A; EGR1; EGR4; FOS; PAX8; ESR2; ESR1; PAX1; FGF23; IL1B; STAT3; ING2; TP53; IL6; MAP2K3; TEAD1; POU3F2; CEBPB; SQSTM1; PICALM; NKX2-1; ETS2; POU2F1; TAF7; TNF; STAT5B; STAT5A; SREBF1; GLI2; NFIC; ATF1; ATF6

GO:0009893	1.70E-21	6.50E-18	14791	601	1015	109	BP	positive regulation of metabolic process	SMARCC2; HIPK2; SP1; AR; HOXB9; BLM; PPARG; PPARA; ANAPC5; ANAPC7; SMAD9; SMAD4; SMAD7; SMAD1; PRKDC; TAF11; AKAP12; REL; SPI1; RXRA; LEF1; TP73; EGFR; IGF1R; UBTf; PGR; SNCA; JUN; LIF; AVPR1A; RARA; RARB; RARG; REL; WT1; ELK1; USF1; TCF4; IGF1; IRF8; NFKB1; CSNK1E; NSD1; USF2; SKP1; NTF3; CITED2; HOXA5; HOXA1; CDK7; SMARCA4; CEBPA; CEBPG; CAMP; ETS1; PSME1; SMAD3; ILF3; BCL2; GHR; ZFPM2; BRCA1; CREB1; CRX; HIF1A; SMURF1; CDC16; EGR1; EGR4; FOS; RAD50; PAX8; ESR2; ESR1; PAX1; FGF23; IL1B; STAT3; ING2; COMT; TP53; IL6; MAP2K3; TEAD1; POU3F2; CEBPB; SQSTM1; PICALM; HBB; NKX2-1; ETS2; POU2F1; HRAS; TAF7; CDC23; TNF; NBN; STAT5B; STAT5A; SREBF1; PSMB4; RIPK2; GLI2; NPM1; NFIC; PEXT; ATF1; AXIN1; ATF6
GO:0031328	2.70E-21	1.00E-17	14791	601	727	89	BP	positive regulation of cellular biosynthetic process	SMARCC2; HIPK2; SP1; AR; HOXB9; BLM; PPARG; PPARA; SMAD9; SMAD4; SMAD1; PRKDC; TAF11; AKAP12; REL; SPI1; RXRA; LEF1; TP73; EGFR; IGF1R; UBTf; PGR; SNCA; JUN; LIF; AVPR1A; RARA; RARB; RARG; REL; WT1; ELK1; USF1; TCF4; IGF1; IRF8; NFKB1; NSD1; USF2; NTF3; CITED2; HOXA5; HOXA1; CDK7; BRCA1; CREB1; CRX; HIF1A; EGR1; EGR4; FOS; PAX8; ESR2; PAX1; FGF23; IL1B; STAT3; ING2; TP53; IL6; MAP2K3; TEAD1; POU3F2; CEBPB; SQSTM1; PICALM; HBB; NKX2-1; ETS2; POU2F1; HRAS; TAF7; TNF; STAT5B; STAT5A; SREBF1; GLI2; NPM1; NFIC; ATF1; ATF6
GO:0045935	4.00E-21	1.40E-17	14791	601	662	84	BP	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	SMARCC2; HIPK2; SP1; AR; HOXB9; BLM; PPARG; PPARA; SMAD9; SMAD4; SMAD1; PRKDC; TAF11; AKAP12; REL; SPI1; RXRA; LEF1; TP73; IGF1R; UBTf; PGR; JUN; LIF; RARA; RARB; RARG; REL; WT1; ELK1; USF1; TCF4; IGF1; IRF8; NFKB1; NSD1; USF2; NTF3; CITED2; HOXA5; HOXA1; CDK7; SMARCA4; CEBPA; CEBPG; ETS1; SMAD3; ILF3; ZFPM2; BRCA1; CREB1; CRX; HIF1A; EGR1; EGR4; FOS; PAX8; ESR2; PAX1; FGF23; IL1B; STAT3; ING2; TP53; IL6; MAP2K3; TEAD1; POU3F2; CEBPB; SQSTM1; PICALM; NKX2-1; ETS2; POU2F1; HRAS; TAF7; TNF; STAT5B; STAT5A; SREBF1; GLI2; NFIC; ATF1; ATF6
GO:0010604	5.60E-21	2.10E-17	14791	601	939	103	BP	positive regulation of macromolecule metabolic process	SMARCC2; HIPK2; SP1; AR; HOXB9; BLM; PPARG; PPARA; ANAPC5; ANAPC7; SMAD9; SMAD4; SMAD7; SMAD1; PRKDC; TAF11; REL; SPI1; RXRA; LEF1; TP73; IGF1R; UBTf; PGR; SNCA; JUN; LIF; RARA; RARB; RARG; REL; WT1; ELK1; USF1; TCF4; IGF1; IRF8; NFKB1; CSNK1E; NSD1; USF2; SKP1; NTF3; CITED2; HOXA5; HOXA1; CDK7; SMARCA4; CEBPA; CEBPG; CAMP; ETS1; PSME1; SMAD3; ILF3; BCL2; GHR; ZFPM2; BRCA1; CREB1; CRX; HIF1A; SMURF1; CDC16; EGR1; EGR4; FOS; RAD50; PAX8; ESR2; ESR1; PAX1; FGF23; IL1B; STAT3; ING2; TP53; IL6; MAP2K3; TEAD1; POU3F2; CEBPB; SQSTM1; PICALM; NKX2-1; ETS2; POU2F1; HRAS; TAF7; CDC23; TNF; NBN; STAT5B; STAT5A; SREBF1; PSMB4; RIPK2; GLI2; NFIC; PEXT; ATF1; AXIN1; ATF6
GO:0019222	7.90E-21	2.90E-17	14791	601	4046	269	BP	regulation of metabolic process	SMARCC2; PPAP2A; HIPK2; PIK3CB; SP1; SP3; CAMK2A; F3; WHSC2; AR; TSG101; UBE2D2; APOB; APOH; CYP27B1; GTF2I; SMG5; HOXB8; HOXB9; BLM; PPARG; PPARD; COL4A3; PPARA; GD11; ANAPC5; ANAPC7; KCNH2; ITGAV; SIGIRR; TRDMT1; PDE6H; SMAD9; RALBP1; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; AKAP12; REL; TSC1; SPI1; IRF3; RXRA; LEPR; LEF1; SRPK1; BDKRB2; APBA2; TP73; ERC1; EGFR; IGF1R; RBM9; ERG; NGFR; GF11B; UBTf; PGR; CNOT3; CNOT4; SNCA; JUN; HGF; HOXB13; HEBX; SFTPD; LIF; AVPR1A; RARA; DAB1; EIF3H; RARB; RARG; NFE2L1; REL; CDKN2B; WT1; HOMER1; PDE8A; ADCY1; SCARB1; ELK1; VLDLR; MASP1; USF1; GTF2E1; TCF4; IGF1; IRF8; NFKB1; CSNK1E; NSD1; TCEG1; ZPHX3; PGAM1; GMNN; USF2; SKP1; ADAP1; NTF3; ASCL3; CITED2; UHRF1; KEAP1; HOXA5; HOXA1; CDK7; F2RL3; TAF9B; LPAR1; GTF2H4; TCEB3; MSH2; MSH3; ITGB3BP; MYBL1; SMARCA4; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; CAMP; ETS1; MED15; SUZ12; PRKCD; PSME1; SMAD3; ILF3; BCL2; WWP1; CAV3; GHR; ZFPM2; BRCA1; ERBB4; CREB1; NR2C2; BRD8; BRD7; ADCY5; PRMT5; KPNA2; GNAO1; CRX; PLCB2; HIF1A; SMURF1; DAXX; SMURF2; CDC16; NONO; EGR1; EGR4; FOS; RAD50; TRRAP; SFPQ; PAX6; NFKB2; PAX2; PAX8; ESR2; ESR1; ACAD8; STK36; PAX1; FGF23; YY1; IL1B; STAT3; RBMSA; STAT1; ZHX2; ZHX3; ZHX1; IFNB1; ING2; IGBP1; TAL1; ACACB; COMT; EIF2C2; TP53; NRBPF; CYP1A2; MYB; IL6; ASAP1; ASAP2; EIF5; MAP2K3; RUNX1T1; TEAD1; KLF11; TFAP2A; PDPK1; POU3F2; CEBPB; PKN1; MCM7; DUSP12; SQSTM1; DRD2; HTR1A; PICALM; ISL1; HBB; NKX2-1; ETS2; NTRK2; ENPP7; FLI1; SNAPC5; PPP2CA; PPP2CB; TERF1; ACSL1; POU2F1; PABPC1; TGFA; HTR1B; ELK4; MED30; CHRM2; HRAS; POLR2K; TAF7; ETV4; CDC23; TNF; ACR; NCOR1; NBN; TGS1; BCOR; HEY1; STAT5B; STAT5A; SREBF1; PSMB4; RIPK2; GRIN2C; DGKQ; GLI2; FSHR; SIN3A; RAD21; DNMT3L; PLAT; NDEL1; DACHI; NPM1; NFIC; PEXT; ATF1; AXIN1; SUB1; HOXC11; NEDD4L; TGIF1; ATF6; ATF2
GO:0009891	9.00E-21	3.30E-17	14791	601	740	89	BP	positive regulation of biosynthetic process	SMARCC2; HIPK2; SP1; AR; HOXB9; BLM; PPARG; PPARA; SMAD9; SMAD4; SMAD1; PRKDC; TAF11; AKAP12; REL; SPI1; RXRA; LEF1; TP73; EGFR; IGF1R; UBTf; PGR; SNCA; JUN; LIF; AVPR1A; RARA; RARB; RARG; REL; WT1; ELK1; USF1; TCF4; IGF1; IRF8; NFKB1; NSD1; USF2; NTF3; CITED2; HOXA5; HOXA1; CDK7; SMARCA4; CEBPA; CEBPG; ETS1; SMAD3; ILF3; ZFPM2; BRCA1; CREB1; CRX; HIF1A; EGR1; EGR4; FOS; PAX8; ESR2; PAX1; FGF23; IL1B; STAT3; ING2; TP53; IL6; MAP2K3; TEAD1; POU3F2; CEBPB; SQSTM1; PICALM; HBB; NKX2-1; ETS2; POU2F1; HRAS; TAF7; TNF; STAT5B; STAT5A; SREBF1; GLI2; NPM1; NFIC; ATF1; ATF6

GO:0048523	1. 80E-20	6. 70E-17	14791	601	1815	155	BP	negative regulation of cellular process	SMARCC2; PPAP2A; HIPK2; DLG1; F3; AR; HHIP; TSG101; BNIPL; APOH; CYP27B1; BLM; PPARG; PPAR; COL4A3; PPARA; ANAPC5; ANAPC7; ITGAV; SIGIRR; SMAD4; TLE1; SMAD7; SMAD1; TSC1; SP1; RXRA; LEF1; BDKRB2; TP73; EGFR; IGF1R; RBM9; NGFR; GF11B; UBT; PGR; JAG1; NOS1; SNCA; JUN; HGF; RGS10; SFTPD; LIF; AVPR1A; RARA; DAB1; SON; RARB; RARG; PEA15; REL; CDKN2B; WT1; TPR; IGF1; IGFBP6; SST; IRF8; NFKB1; NSD1; ZFH3; FABP3; GMN; MLF1; CITED2; CLU; HOXA5; TAF9B; MSH2; MSH3; SMARCA4; YWHAZ; CEPA; ETS1; SUZ12; PRKCD; PSME1; SMAD3; MCL1; ILF3; BCL2; WWP1; CAV3; ZFP2; BRCA1; CETP; XRCC5; SMURF1; DAXX; SMURF2; CDC16; EGRI; RPH3AL; TP53INP1; ESR2; ESR1; FGF23; IL1B; STAT3; ZHX2; ZHX3; ZHX1; IFNB1; IGBP1; COMT; EIF2C2; TP53; SFRP2; IL6; KLF11; CEBPB; TP53BP2; SQSTM1; DRD2; PICALM; NKX2-1; ITSN1; ENPP7; SOCS2; PPP2CA; PPP2CB; GSK3B; TERF1; POU2F1; HTR1B; HRAS; FGF4; TAF7; CDC23; TNFAIP3; TNF; GNRHR; ATP5B; NCOR1; MAP1B; NBN; BCOR; ACHE; HEY1; GDF9; STAT5B; STAT5A; PSMB4; RIPK2; ADRBK1; GLI2; SIN3A; PLAT; NPM1; NFIC; PENT; AXIN1; TGIF1
GO:0050789	2. 90E-20	1. 10E-16	14791	601	7226	403	BP	regulation of biological process	SMARCC2; PPAP2A; SCG5; HIPK2; L1CAM; DLG1; PIK3CB; ARHGFE12; SP1; SP3; CAMK2A; CAMK2B; F3; JPH2; WHSC2; AKAP8; AR; HHIP; TSG101; UBE2D2; RIT2; RAB6B; MX1; FZD10; BNIPL; APOB; APOH; CYP27B1; GTF2I; SMG5; HOXB8; HOXB9; SENP2; BLM; PPARG; PPAR; COL4A3; PPARA; GD11; ANAPC5; ANAPC7; CSNK1A1; KCNH2; ITGAV; SIGIRR; TRDM1; PDE6H; SMAD9; RALBP1; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; AKAP12; REL; TSC1; SP1; IRF3; RXRA; LEPR; LEF1; SRPK1; PDE10A; BDKRB2; APBA2; TP73; ERC1; EGFR; IGF1R; RBM9; ERG; NGFR; GF11B; PPF1A1; PDE1A; UBT; PGR; CNOT3; JAG1; CNOT4; NOS1; CYR61; SNCA; RTN1; JUN; FZD8; HGF; HOXB13; HEXB; ANK3; RGS10; SFTPD; LIF; AVPR1A; RARA; CATSPER1; DAB1; SON; EIF3H; RARB; RARG; PEA15; NFE2L1; SAG; RAB1F; REL; FGB; CDKN2B; WT1; HOMER1; TPR; PDE8A; ADCY1; DBH; PTGES3; SCARB1; ELK1; GNG2; RHO; MAPK10; VLDLR; MASP1; USF1; AP2B1; GTF2E1; TIRAP; PRKG1; BMX; TCF4; IGF1; IGFBP6; F10; EPOR; SST; IRF8; NFKB1; CSNK1E; NSD1; RALA; EPHX2; PI4KB; IL1RAP; TCERG1; ZFH3; FABP3; PGAM1; GMN; PDE11A; MLF1; USF2; SKP1; ADAP1; CHPT1; CADM1; NTF3; ASCL3; CITED2; CLU; UHRF1; PDCD5; KEAP1; HOXA5; HOXA1; CDK7; F2RL3; TAF9B; LPAR1; GTF2H4; TCEB3; MSH2; MSH3; ITGB3BP; PRSS2; MYBL1; SMARCA4; YWHAZ; ZNF7; CEPA; CEBPG; CEBPE; CEBPD; CAMP; ARHGAP1; ETS1; MED15; SUZ12; VIPR1; PRKDC; PSME1; SMAD3; MCL1; CTNNA2; ABT3; ILF3; BCL2; PLCD3; WWP1; CAV3; GHR; ZFP2; MAGI2; TRPV4; BRCA1; CETP; ERBB4; CREB1; CTSG; NR2C2; BRD8; BRD7; ADCY5; PRMT5; MASP2; KPN2; GNAO1; CRX; PLCB2; HIF1A; XRCC5; SMURF1; DAXX; SMURF2; CDC16; NONO; EGRI; NT5E; EGR4; XDH; RPH3AL; RPS3A; FCN2; FOS; RAD50; TRRAP; SFPQ; PAX6; TP53INP1; NFKB2; PAX2; PAX8; ESR2; TOLLIP; ESR1; ACAD8; STRK3; PAX1; FGF23; YY1; CCR4; IL1B; STAT3; RBM8A; STAT1; ZHX2; ZHX3; ZHX1; IFNB1; PDE7B; ING2; IGBP1; TAL1; ACACB; COMT; EIF2C2; TP53; NRFB2; SFRP2; CYP11A2; MYB; WNT2; IL6; RHEB; ASAP1; ASAP2; EIF5; MAP2K3; RUNX1T1; TEAD1; CAMLG; KLF11; WASF2; TFAP2A; NAP1L1; AMHR2; GDF5; PDPK1; BCAN; POU3F2; CEBPB; PKN1; MCM7; TP53BP2; DUSP12; SQSTM1; DRD2; CIS; HTR1A; PICALM; KCNE2; KCNE1; ISL1; HBB; NKX2-1; ETS2; CACNA2D1; ITSN1; ITSN2; NTRK2; NTRK3; MICAL1; GABRR2; SYT9; ENPP7; FLI1; RAPIA; SNAPC5; SRGAP2; SOCS2; PPP2CA; EEF1D; PPP2CB; MST1R; GSK3B; TERF1; ACSL1; STMN1; POU2F1; PABPC1; MAPKAPK5; TGFA; PLXNB3; HTR1B; ELK4; MED30; CHRM2; HRAS; FGF5; FGF4; POLR2K; TAF7; PEX5; ETV4; CDC23; TNFAIP3; TNF; EPHA3; EPHA2; SDCBP; ACR; GNRHR; ATP5B; NCAM1; NCOR1; FZD6; MAP1B; NBN; FGF11; DUSP1; CRHBP; TGS1; BCOR; ACHE; ADK; HEY1; SOS1; TACC3; IGFALS; GDF9; STAT5B; STAT5A; SREBF1; PSMB4; RIPK2; GRIN2C; DGKQ; ADRBK1; GLI2; FSHR; SIN3A; TRAF5; RAD21; DNMT3L; PLAT; NDEL1; DACH1; CLTCL1; NPM1; NFIC; INPP1; PENT; ATF1; AXIN1; SUB1; HOXC11; NEDD4L; TGIF1; ATF6; ATF2; IGF2R
GO:0048519	6. 40E-20	2. 40E-16	14791	601	1983	163	BP	negative regulation of biological process	SMARCC2; PPAP2A; HIPK2; DLG1; F3; AR; HHIP; TSG101; BNIPL; APOH; CYP27B1; BLM; PPARG; PPAR; COL4A3; PPARA; ANAPC5; ANAPC7; ITGAV; SIGIRR; SMAD4; TLE1; SMAD7; SMAD1; TSC1; SP1; RXRA; LEF1; BDKRB2; TP73; EGFR; IGF1R; RBM9; NGFR; GF11B; UBT; PGR; JAG1; NOS1; SNCA; JUN; HGF; RGS10; SFTPD; LIF; AVPR1A; RARA; DAB1; SON; RARB; RARG; PEA15; REL; CDKN2B; WT1; TPR; MASP1; USF1; IGF1; IGFBP6; SST; IRF8; NFKB1; NSD1; ZFH3; FABP3; GMN; MLF1; CITED2; CLU; HOXA5; TAF9B; MSH2; MSH3; SMARCA4; YWHAZ; CEPA; ETS1; SUZ12; PRKCD; PSME1; SMAD3; MCL1; CTNNA2; ILF3; BCL2; WWP1; CAV3; ZFP2; BRCA1; CETP; CTSG; GNAO1; XRCC5; SMURF1; DAXX; SMURF2; CDC16; EGRI; NT5E; RPH3AL; TP53INP1; ESR2; ESR1; FGF23; IL1B; STAT3; ZHX2; ZHX3; ZHX1; IFNB1; IGBP1; COMT; EIF2C2; TP53; SFRP2; IL6; KLF11; CEBPB; TP53BP2; SQSTM1; DRD2; PICALM; NKX2-1; ITSN1; ENPP7; SOCS2; PPP2CA; PPP2CB; GSK3B; TERF1; POU2F1; HTR1B; HRAS; FGF4; TAF7; CDC23; TNFAIP3; TNF; GNRHR; ATP5B; NCOR1; MAP1B; NBN; BCOR; ACHE; HEY1; TACC3; GDF9; STAT5B; STAT5A; PSMB4; RIPK2; GRIN2C; ADRBK1; GLI2; SIN3A; PLAT; NPM1; NFIC; PENT; AXIN1; TGIF1
GO:0010557	1. 10E-19	4. 20E-16	14791	601	683	83	BP	positive regulation of macromolecule biosynthetic process	SMARCC2; HIPK2; SP1; AR; HOXB9; BLM; PPARG; PPARA; SMAD9; SMAD4; SMAD1; PRKDC; TAF11; REL; SP1; RXRA; LEF1; TP73; IGF1R; UBT; PGR; JUN; LIF; RARA; RARB; RARG; REL; WT1; ELK1; USF1; TCF4; IGF1; IRF8; NFKB1; NSD1; USF2; NTF3; CITED2; HOXA5; HOXA1; CDK7; SMARCA4; CEPA; CEBPG; ETS1; SMAD3; ILF3; ZFP2; BRCA1; CREB1; CRX; HIF1A; EGRI; EGR4; FOS; PAX8; ESR2; PAX1; FGF23; IL1B; STAT3; ING2; TP53; IL6; MAP2K3; TEAD1; POU3F2; CEBPB; SQSTM1; PICALM; NKX2-1; ETS2; POU2F1; HRAS; TAF7; TNF; STAT5B; STAT5A; SREBF1; GLI2; NFIC; ATF1; ATF6

GO:0045944	1. 10E-19	4. 20E-16	14791	601	384	60	BP	positive regulation of transcription from RNA polymerase II promoter	HIPK2; SP1; AR; HOXB9; PPARG; PPARA; SMAD4; SMAD1; PRKDC; RXRA; LEF1; JUN; LIF; RARA; RARB; RARG; RELA; WT1; ELK1; USF1; IGF1; USF2; NTF3; CITED2; HOXA5; HOXA1; CDK7; SMARCA4; CEBPA; ETS1; SMAD3; ZFPM2; BRCA1; CREB1; CRX; HIF1A; EGR1; FOS; PAX8; ESR2; PAX1; IL1B; STAT3; TP53; IL6; TEAD1; POU3F2; CEBPB; SQSTM1; NKX2-1; POU2F1; TAF7; TNF; STAT5B; STAT5A; SREBF1; GLI2; NFIC; ATF1; ATF6
GO:0032583	5. 70E-19	2. 10E-15	14791	601	199	42	BP	regulation of gene-specific transcription	AR; PPARG; PPARA; SMAD7; PRKDC; SPI1; RXRA; LIF; RARA; RELA; WT1; USF1; IGF1; NFKB1; USF2; CITED2; TAF9B; SMARCA4; CEBPA; ETS1; SMAD3; BRCA1; CREB1; HIF1A; ESR2; FGF23; IL1B; IGBP1; TAL1; TP53; IL6; PKN1; NKX2-1; TAF7; TNF; NCOR1; BCOR; HEY1; DGKQ; RAD21; NFIC; ATF6
GO:0010033	7. 40E-19	2. 70E-15	14791	601	850	93	BP	response to organic substance	F3; AR; APOB; CYP27B1; PPARG; PPARD; COL4A3; PPARA; KHK; TRDMT1; ASH2L; SMAD1; PRKDC; TSC1; RXRA; LEPR; LEF1; EGFR; IGF1R; ABAT; CYR61; SNCA; JUN; AVPR1A; RARA; RELA; CDKN2B; ADCY1; DBH; SCARB1; GNG2; VLDLR; USF1; SST; FABP3; CLU; PPAT; TAF9B; MSH2; AGRP; CEBPA; CAMP; MCL1; BCL2; GHR; BRCA1; ERBB4; CREB1; CTSG; ADCY5; GNAO1; EGR1; FOS; LCT; ESR2; ESR1; CCR4; IL1B; STAT3; STAT1; IGBP1; LCAT; COMT; AGXT; IL6; AP3S1; PDPK1; HSPB3; DRD2; CIS; ALPL; NKX2-1; GOT1; SOCS2; PPP2CA; HTR1B; GYS2; SDC1; TNF; EPHA3; ACR; MAP1B; SRD5A2; DUSP1; STAT5B; STAT5A; RIPK2; DGKQ; ADRBK1; PLAT; PEMT; ATF1; ATF6
GO:0009987	2. 10E-18	7. 90E-15	14791	601	9216	472	BP	cellular process	SMARCC2; PPAP2A; STK16; P4HA2; HIPK2; LICAM; DLG1; PIK3CB; SV2A; CYP2C9; ARHGEF12; SP1; SP3; CAMK2A; CAMK2B; F3; SULT1E1; JPH2; AKAP3; DDX41; AKAP8; AR; TSG101; ITGA3; UBE2D2; RIT2; RAB6B; POLR1A; POLR1E; HIP1R; BNIPL; APOB; XP07; APOH; ZIC2; CYP27B1; H3F3A; SMG5; SENP2; DSP; BLM; PPARG; PPARD; COL4A4; COL4A3; PPARA; ANAPC5; ANAPC7; PPID; CSNK1A1; KCNH2; ITGAV; KHK; TRDMT1; PDE6H; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; PRKDC; TAF11; ADSS1; TSC1; KIF3A; IRF3; RXRA; LEPR; LTF; LEF1; SRPK1; BDKRB2; F5; APBA2; AK7; TP73; GEMIN5; RBM7; ERC1; EGFR; IGF1R; RBM9; ERG; NGFR; ABAT; GF11B; PPF1A1; UBTG; ACAA2; PGR; JAG1; NOS1; CYR61; SNCA; RTN1; YARS2; JUN; HGF; TRIP13; HOXB13; EXOC2; HEXB; CYB5A; RBMX; WNT16; MLPH; SFTPD; LIF; AVPR1A; COL11A2; RARA; CATSPER1; PKP3; PKP2; DAB1; EIF3H; B3GNT6; RARB; EIF3L; NFE2L1; SAG; ORC6L; EIF3G; RAB1F; FGB; CDKN2B; WT1; LIPC; CENPJ; LPO; HOMER1; TPR; PDE8A; ADCY1; DBH; PTGES3; SCARB2; SCARB1; GNG2; RHO; MAPK10; VLDLR; SNX9; PPOX; CNTN1; USF1; AP2B1; GTF2E1; PRKG1; BMX; IGF1; KCNK3; AGMAT; EPOR; SST; IRF8; NFKB1; CSNK1E; SARDH; NSD1; WDHV1; RALA; EPHX2; PI4KB; TCERG1; ZFH3; FABP3; PDE11A; MLF1; USF2; SKP1; CHPT1; FANCC; CADM1; NTF3; HNRNPA1; MTHFS; CITED2; CLU; UHRF1; COL17A1; PDCD5; DLST; GRIK5; STX6; HOXA5; PPAT; CNGA4; HOXA1; CDK7; TAF9B; LPAR1; DSCC1; GTF2H4; TCEB3; MSH2; MSH3; AGRP; USP7; ITGB3BP; SLC5A5; SMARCA4; YWHAZ; CEBPA; CEBPG; CEBPE; CEBPD; CAMP; DVL2; ETS1; SUZ12; VIPR1; RUFY1; PRKCD; PSME1; SMAD3; MCL1; CTNNA2; AB13; CSTF2; GOLGB1; ILF3; BCL2; WWP1; CAV3; SNRNP200; GHR; CACNA1F; ZFPM2; MAGI3; DLGAP4; TRPV4; BRCA1; CETP; BMP8A; ERBB4; PRMT3; CREB1; BRD8; ADCY5; DZIP3; PRMT5; PPF1BP1; KPN2A; GBA; GNAO1; PLCB2; HIF1A; XRCC5; PRPF3; SMURF1; DAXX; SMURF2; CDC16; NONO; EGR1; NT5E; XDH; RPH3AL; RPS3A; FOS; RAD50; TRRAP; SFPQ; PAX6; TP53INP1; NFKB2; PAX2; PAX8; ESR2; TOLLIP; ESR1; ACAD8; POLE2; STK36; PAX1; FGF22; FGF23; SYN1; LCMT1; CCR4; IL1B; HARS; VPS45; STAT3; RBM8A; STAT1; ZHX2; IFNB1; PDE7B; ICAM3; ING2; MARK3; MNAT2; IGBP1; TAL1; ACACB; LCAT; EFNA5; EFNA4; COMT; EIF2C2; LGALS3; TP53; SFRP2; CYP1A2; WNT2; AGXT; IL6; AP3S1; HARS2; EIF5; EIF6; MAP2K3; RUNX1T1; CAMLG; KLF11; WASF2; NAP1L1; AMHR2; NEFH; GDF5; PDPK1; BCAN; POU3F2; AADAT; CEBPB; PKN1; MCM7; HADHA; TP53BP2; DUSP14; VWF; DUSP12; SQSTM1; DRD2; PON3; WNT9B; RDH12; CIS; PICCALM; ALPL; KCNE1; ISL1; DHX16; FBP2; NKX2-1; UGP2; ITSN1; ITSN2; NTRK2; NTRK3; MICAL1; CAPN2; GOT1; GABRR2; ENPP7; SNAPC5; KCTD13; BMP5; SOCS2; PPP2CA; EEF1D; PPP2CB; MST1R; GSK3B; TERF1; SLC4A1; TRIM39; ACSL1; STMN1; POU2F1; PABPC1; G6PC2; ST13; CLTB; MAPKAPK5; VDCA1; TGFA; GUCY1A3; HTR1B; ODF1; NACA; PGM1; GYS2; HRAS; FGF5; FGF4; POLR2H; POLR2K; POLR2J; PEX5; SDC1; CDC23; TNFAIP3; SHBG; TNF; BAT1; CLDN11; CLDN17; EPHA8; ACAN; CLDN19; EPHA3; EPHA2; SDCBP; ACR; RBKS; ATP5B; NCAM1; NCOR1; AKR1B10; MAP1B; CACNB2; CYP2B6; POLD2; NBN; SRD5A2; FGF11; HNRNPC; DUSP1; SGPP1; ASL; PCMT1; TGS1; BCOR; ACHE; FADS2; ADK; SOS1; TACC3; IGFALS; GDF9; STAT5B; STAT5A; SREBF1; PSMB4; MKI67; ADAM12; RIPK2; DERA; PAPSS1; GRIN2C; SVEP1; ADRBK1; GLI2; FSHR; SIN3A; RAD21; DNMT3L; PLAT; ALDH6A1; GGT1; NDEL1; CLTCL1; SNRPA; NPM1; SNRPE; NFIC; INP1; PTPRS; PEMT; ATF1; AXIN1; HOXC11; NEDD4L; UPP3A; DNML1; ATF6; MYO7A; FSD1; IGF2R

GO:0080090	5.50E-18	2.00E-14	14791	601	3585	239	BP	regulation of primary metabolic process	<p>SMARCC2; PPAP2A; HIPK2; SP1; SP3; CAMK2A; WHSC2; AR; TSG101; UBE2D2; APOB; GTF2I; HOXB8; HOXB9; BLM; PPARG; PPARG; PPARA; GDI1; ANAPC5; ANAPC7; KCNH2; ITGAV; SIGIRR; SMAD9; RALBP1; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; AKAP12; REL; TSCI; SP11; IRF3; RXRA; LEF1; SRPK1; BDKRB2; TP73; ERC1; EGFR; IGF1R; RBM9; ERG; GF11B; UBTFF; PGR; CNOT3; CNOT4; SNCA; JUN; HOXB13; LIF; AVPRIA; RARA; EIF3H; RARB; RARG; NFE2L1; RELA; WT1; PDE8A; ADCY1; ELK1; MASP1; USF1; GTF2E1; TCF4; IGF1; IRF8; NFKB1; CSNK1E; NSD1; TCERG1; ZFH3; PGAM1; GMNN; USF2; SKP1; ADAP1; NTF3; ASCL3; CITED2; UHRF1; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; GTF2H4; TCEB3; MSH2; MSH3; ITGB3BP; MYBL1; SMARCA4; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; CAMP; ETS1; MED15; SUZ12; PRKCD; PSME1; SMAD3; ILF3; BCL2; WWP1; GHR; ZFPM2; BRCA1; ERBB4; CREB1; NR2C2; BRD8; BRD7; ADCY5; PRMT5; KPNA2; GNA01; CRX; HIF1A; SMURF1; DAXX; SMURF2; CDC16; NONO; EGR1; EGR4; FOS; RAD50; TRRAP; SFPQ; PAX6; NFKB2; PAX2; PAX8; ESR2; ESR1; ACAD8; STK36; PAX1; FGF23; YY1; IL1B; STAT3; RBM8A; STAT1; ZHX2; ZHX3; ZHX1; IPNB1; ING2; IGBP1; TAL1; ACACB; COMT; EIF2C2; TP53; NRBF2; MYB; IL6; ASAP1; ASAP2; EIF5; MAP2K3; RUNX1T1; TEAD1; KLF11; TFAP2A; POU3F2; CEBPB; PKN1; MCM7; DUSP12; SQSTM1; DRD2; HTR1A; PICALM; ISL1; NKX2-1; ETS2; NTRK2; ENPP7; FLI1; SNAPC5; PPP2CA; TERF1; ACSL1; POU2F1; PABPC1; HTR1B; ELK4; MED30; HRAS; POLR2K; TAF7; ETV4; CDC23; TNF; ACR; NCOR1; NBN; TGS1; BCOR; HEY1; STAT5B; STAT5A; SREBF1; PSMB4; RIPK2; GRIN2C; DKGQ; GLI2; FSHR; SIN3A; RAD21; PLAT; NDEL1; DACH1; NPM1; NFIC; PEMT; ATF1; AXIN1; SUB1; HOXC11; NEDD4L; TGIF1; ATF6; ATF2</p>
GO:0050794	5.70E-18	2.10E-14	14791	601	6896	383	BP	regulation of cellular process	<p>SMARCC2; PPAP2A; SCG5; HIPK2; L1CAM; DLG1; PIK3CB; ARHGFE12; SP1; SP3; CAMK2A; CAMK2B; F3; JPH2; WHSC2; AKAP8; AR; HHIIP; TSG101; RIT2; RAB6B; MX1; FZD10; BNIPL; APOB; APOH; CYP27B1; GTF2I; SMG5; HOXB8; HOXB9; BLM; PPARG; PPARG; COL4A3; PPARA; GDI1; ANAPC5; ANAPC7; CSNK1A1; KCNH2; ITGAV; SIGIRR; PDE6H; SMAD9; RALBP1; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; AKAP12; REL; TSCI; SP11; IRF3; RXRA; LEPR; LEF1; SRPK1; PDE10A; BDKRB2; TP73; ERC1; EGFR; IGF1R; RBM9; ERG; NGFR; GF11B; PPF1A1; PDE1A; UBTFF; PGR; CNOT3; JAG1; CNOT4; NOS1; CYR61; SNCA; RTN1; JUN; EZD8; HGF; HOXB13; HEXB; ANK3; RGS10; SFTPD; LIF; AVPRIA; RARA; CATSPER1; DAB1; SON; EIF3H; RARB; RARG; PEA15; NFE2L1; SAG; RAB1F; RELA; FGB; CDKN2B; WT1; HOMER1; TPR; PDE8A; ADCY1; DBH; PTGES3; SCARB1; ELK1; GNG2; RHO; MAPK10; VLDLR; USF1; GTF2E1; TIRAP; PRKG1; BMX; TCF4; IGF1; IGFBP6; F10; EPOR; SST; IRF8; NFKB1; CSNK1E; NSD1; RALA; PI4KB; IL1RAP; TCERG1; ZFH3; FBP3; PGAM1; GMNN; PDE11A; MLF1; USF2; SKP1; ADAP1; CHPT1; CADM1; NTF3; ASCL3; CITED2; CLU; UHRF1; PDCD5; KEAP1; HOXA5; HOXA1; CDK7; F2RL3; TAF9B; LPAR1; GTF2H4; TCEB3; MSH2; MSH3; ITGB3BP; PRSS2; MYBL1; SMARCA4; YWHAZ; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; CAMP; ARHGAP1; ETS1; MED15; SUZ12; VIPR1; PRKCD; PSME1; SMAD3; MCL1; CTNNA2; ABI3; ILF3; BCL2; PLCD3; WWP1; CAV3; GHR; ZFPM2; MAGI2; BRCA1; CETP; ERBB4; CREB1; NR2C2; BRD8; BRD7; ADCY5; PRMT5; KPNA2; GNA01; CRX; PLCB2; HIF1A; XRCC5; SMURF1; DAXX; SMURF2; CDC16; NONO; EGR1; EGR4; XDH; RPH3AL; RPS3A; FCN2; FOS; RAD50; TRRAP; SFPQ; PAX6; TP53INP1; NFKB2; PAX2; PAX8; ESR2; TOLLIP; ESR1; ACAD8; STK36; PAX1; FGF23; YY1; CCR4; IL1B; STAT3; RBM8A; STAT1; ZHX2; ZHX3; ZHX1; IPNB1; PDE7B; ING2; IGBP1; TAL1; ACACB; COMT; EIF2C2; TP53; NRBF2; SFRP2; MYB; WNT2; IL6; RHEB; ASAP1; ASAP2; EIF5; MAP2K3; RUNX1T1; TEAD1; CAMLG; KLF11; WASF2; TFAP2A; NAP1L1; AMHR2; GDF5; PDPK1; BCAN; POU3F2; CEBPB; PKN1; MCM7; TP53BP2; DUSP12; SQSTM1; DRD2; HTR1A; PICALM; ISL1; HBB; NKX2-1; ETS2; ITSN1; ITSN2; NTRK2; NTRK3; MICAL1; GABRR2; SYT9; ENPP7; FLI1; RAPIA; SNAPC5; SRGAP2; SOCS2; PPP2CA; EEF1D; PPP2CB; MST1R; GSK3B; TERF1; ACSL1; STMN1; POU2F1; PABPC1; MAPKAPK5; TGFA; PLXNB3; HTR1B; ELK4; MED30; CHRM2; HRAS; FGF5; FGF4; POLR2K; TAF7; ETV4; CDC23; TNFAIP3; TNF; EPHA3; EPHA2; SDCBP; ACR; GNRHR; ATP5B; NCAM1; NCOR1; FZD6; MAP1B; NBN; FGF11; DUSP1; CRHBP; TGS1; BCOR; ACHE; ADK; HEY1; SOS1; TACC3; IGFALS; GDF9; STAT5B; STAT5A; SREBF1; PSMB4; RIPK2; DKGQ; ADRBK1; GLI2; FSHR; SIN3A; TRAF5; RAD21; PLAT; NDEL1; DACH1; NPM1; NFIC; INPP1; PEMT; ATF1; AXIN1; SUB1; HOXC11; NEDD4L; TGIF1; ATF6; ATF2; IGF2R</p>

GO:0031323	9.00E-18	3.30E-14	14791	601	3768	247	BP	regulation of cellular metabolic process	SMARCC2; PPAP2A; HIPK2; PIK3CB; SP1; SP3; CAMK2A; WHSC2; AR; TSG101; GTF2I; SMG5; HOXB8; HOXB9; BLM; PPARG; PPAR; PPARA; GD11; ANAPC5; ANAPC7; KCNH2; ITGAV; SIGIRR; PDEGH; SMAD9; RALBP1; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; AKAP12; REL; TSC1; SPI1; IRF3; RXRA; LEF1; SRPK1; BDKRB2; TP73; ERCC1; EGFR; IGF1R; RBM9; ERG; GFI1B; UBTf; PGR; CNOT3; CNOT4; SNCA; JUN; HGF; HOXB13; HEXB; SFTPD; LIF; AVPR1A; RARA; DAB1; EIF3H; RARB; RARG; NFE2L1; REL; CDKN2B; WT1; PDE8A; ADCY1; ELK1; VLDLR; USF1; GTF2E1; TCF4; IGF1; IRF8; NFKB1; CSNK1E; NSD1; TCERG1; ZFXH3; PGAM1; GNN; USF2; SKP1; ADAP1; NTF3; ASCL3; CITED2; UHRF1; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; GTF2H4; TCEB3; MSH2; MSH3; ITGB3BP; MYBL1; SMARCA4; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; CAMP; ETS1; MED15; SUZ12; PRKCD; PSME1; SMAD3; ILF3; BCL2; WWP1; CAV3; GHR; ZFP2M; BRCA1; ERBB4; CREB1; NR2C2; BRD8; BRD7; ADCY5; PRMT5; KPNA2; GNAO1; CRX; HIF1A; SMURF1; DAXX; SMURF2; CDC16; NONO; EGRI; EGR4; FOS; RAD50; TRRAP; SFPQ; PAX6; NFKB2; PAX2; PAX8; ESR2; ESRI; ACAD8; STK36; PAX1; FGF23; YY1; IL1B; STAT3; RBM8A; STAT1; ZHX2; ZHX3; ZHX1; IFNB1; ING2; IGBP1; TAL1; ACACB; COMT; EIF2C2; TP53; NRB2; MYB; IL6; ASAP1; ASAP2; EIF5; MAP2K3; RUNX1T1; TEAD1; KLF11; TFAP2A; PDPK1; POU3F2; CEBPB; PKN1; MCM7; DUSP12; SQSTM1; DRD2; HTR1A; PICALM; ISL1; HBB; NKX2-1; ETS2; NTRK2; ENPP7; FLI1; SNAPC5; PPP2CA; TERF1; ACSL1; POU2F1; PABPC1; TGFA; HTR1B; ELK4; MED30; HRAS; POLR2K; TAF7; ETV4; CDC23; TNF; ACR; NCOR1; NBN; TGS1; BCOR; HEY1; STAT5B; STAT5A; SREBF1; PSMB4; RIPK2; DGKQ; GLI2; FSHR; SIN3A; RAD21; PLAT; NDEL1; DACH1; NPM1; NFIC; PEXT; ATF1; AXIN1; SUB1; HOXC11; TGIF1; ATF6; ATF2
GO:0031324	1.80E-17	6.80E-14	14791	601	771	85	BP	negative regulation of cellular metabolic process	SMARCC2; HIPK2; TSG101; BLM; PPARG; PPAR; PPARA; ANAPC5; ANAPC7; ITGAV; SIGIRR; SMAD4; TLE1; SMAD7; TSC1; SPI1; RXRA; LEF1; BDKRB2; RBM9; GFI1B; UBTf; PGR; SNCA; JUN; SFTPD; RARA; RARB; RARG; REL; CDKN2B; WT1; IRF8; NFKB1; NSD1; ZFXH3; GNN; CITED2; TAF9B; MSH2; MSH3; SMARCA4; CEBPA; SUZ12; PRKCD; PSME1; SMAD3; ILF3; WWP1; ZFP2M; BRCA1; DAXX; SMURF2; CDC16; EGRI; STAT3; ZHX2; ZHX3; ZHX1; IFNB1; IGBP1; COMT; EIF2C2; TP53; IL6; KLF11; NKX2-1; ENPP7; PPP2CA; TERF1; POU2F1; HTR1B; TAF7; CDC23; TNF; NCOR1; BCOR; HEY1; PSMB4; GLI2; SIN3A; PLAT; NPM1; NFIC; TGIF1
GO:0042221	2.30E-17	8.60E-14	14791	601	1402	124	BP	response to chemical stimulus	PIK3CB; F3; AR; APOB; CYP27B1; PPARG; PPAR; COL4A3; PPARA; KHK; GPX5; TRDMT1; SMAD9; RALBP1; ASH2L; SMAD4; SMAD1; PRKDC; TSC1; RXRA; LEPR; LEF1; BDKRB2; EGFR; IGF1R; ABAT; DEFA1; NOS1; CYR61; SNCA; JUN; SFTPD; AVPR1A; RARA; RARG; REL; FGB; CDKN2B; LPO; ADCY1; DBH; SCARB1; GNG2; VLDLR; USF1; KCNK3; SST; RALA; EPHX2; FABP3; USF2; FANCC; CITED2; CLU; PPAT; TAF9B; MSH2; AGRP; YWHAZ; CEBPA; CAMP; ETS1; SMAD3; MCL1; BCL2; GHR; BRCA1; ERBB4; CREB1; CTSG; ADCY5; GNAO1; PLCB2; HIF1A; EGRI; FOS; LCT; ESR2; ESRI; CCR4; IL1B; STAT3; STAT1; IGBP1; LCAT; COMT; TP53; AGXT; IL6; AP3S1; PDPK1; HSPB3; HADHA; DRD2; C1S; ALPL; NKX2-1; CAPN2; GOT1; SOCS2; PPP2CA; PPP2CB; HTR1B; GYS2; HRAS; SDC1; TNF; EPHA3; ACR; MAP1B; NBN; SRD5A2; DUSP1; STAT5B; STAT5A; RIPK2; DGKQ; ADRBK1; PLAT; PEXT; ATF1; NEDD4L; ATF6; IGF2R
GO:0048856	1.30E-16	4.90E-13	14791	601	1717	140	BP	anatomical structure development	SMARCC2; PCSK2; L1CAM; SP1; SP3; AR; HHIP; APOB; DRP2; ZIC2; CYP27B1; HOXB8; HOXB9; DSP; PPARG; PPAR; PPARA; ITGAV; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; PRKDC; TSC1; RXRA; LEF1; APBA2; TP73; EGFR; IGF1R; NGFR; PGR; JAG1; CYR61; HGF; TRIP13; HOXB13; HEXB; SFTPD; LIF; AVPR1A; COL11A2; PKP2; DAB1; RARB; RARG; REL; WT1; HOMER1; PTGES3; VLDLR; BMX; IGF1; KCNK3; EPOR; ZFXH3; FANCC; CADM1; NTF3; CITED2; CLU; COL17A1; HOXA5; HOXA1; MSH2; SMARCA4; CEBPA; CEBPG; DVL2; SMAD3; BCL2; PLCD3; WWP1; CAV3; GHR; ZFP2M; BMP8A; ERBB4; CREB1; NR2C2; GNAO1; SMURF1; FOS; PAX6; NFKB2; PAX8; ESR2; ESRI; PAX1; STAT3; TAL1; EFN5; LGALS3; TP53; SFRP2; CYP1A2; WNT2; IL6; TEAD1; TFAP2A; NEMF; BCAN; POU3F2; CEBPB; VWF; DRD2; ALPL; NKX2-1; ETS2; NTRK2; NTRK3; CAPN2; BMP5; PPP2CA; STMN1; CHRM2; HRAS; FGF5; PEX5; SDC1; ACAN; EPHA2; MAP1B; SRD5A2; FGF11; BCOR; ACHE; HEY1; TACC3; STAT5B; STAT5A; PAPS1; ADRBK1; GLI2; FSHR; NDEL1; HOXC11; MYO7A; IGF2R
GO:0009892	1.60E-16	6.00E-13	14791	601	845	88	BP	negative regulation of metabolic process	SMARCC2; HIPK2; TSG101; BLM; PPARG; PPAR; PPARA; ANAPC5; ANAPC7; ITGAV; SIGIRR; SMAD4; TLE1; SMAD7; TSC1; SPI1; RXRA; LEF1; BDKRB2; RBM9; GFI1B; UBTf; PGR; SNCA; JUN; SFTPD; RARA; RARB; RARG; REL; CDKN2B; WT1; MASP1; IRF8; NFKB1; NSD1; ZFXH3; GNN; CITED2; TAF9B; MSH2; MSH3; SMARCA4; CEBPA; SUZ12; PRKCD; PSME1; SMAD3; ILF3; WWP1; ZFP2M; BRCA1; DAXX; SMURF2; CDC16; EGRI; IL1B; STAT3; ZHX2; ZHX3; ZHX1; IFNB1; IGBP1; COMT; EIF2C2; TP53; IL6; KLF11; NKX2-1; ENPP7; PPP2CA; TERF1; POU2F1; HTR1B; TAF7; CDC23; TNF; NCOR1; BCOR; HEY1; PSMB4; GRIN2C; GLI2; SIN3A; PLAT; NPM1; NFIC; TGIF1
GO:0009719	1.90E-16	7.00E-13	14791	601	486	63	BP	response to endogenous stimulus	F3; AR; CYP27B1; PPARG; PPARA; KHK; TRDMT1; ASH2L; SMAD1; PRKDC; TSC1; RXRA; LEPR; IGF1R; AVPR1A; RARA; REL; ADCY1; DBH; GNG2; VLDLR; USF1; SST; FABP3; PPAT; MSH2; AGRP; CEBPA; BCL2; GHR; BRCA1; ERBB4; ADCY5; GNAO1; EGRI; FOS; LCT; ESR2; ESRI; IL1B; STAT3; STAT1; LCAT; AGXT; IL6; AP3S1; PDPK1; DRD2; ALPL; NKX2-1; GOT1; SOCS2; HTR1B; SDC1; TNF; ACR; MAP1B; SRD5A2; DUSP1; STAT5B; STAT5A; PLAT; PEXT
GO:0010605	2.50E-16	9.50E-13	14791	601	790	84	BP	negative regulation of macromolecule metabolic process	SMARCC2; HIPK2; TSG101; BLM; PPARG; PPAR; PPARA; ANAPC5; ANAPC7; ITGAV; SIGIRR; SMAD4; TLE1; SMAD7; TSC1; SPI1; RXRA; LEF1; BDKRB2; RBM9; GFI1B; UBTf; PGR; SNCA; JUN; SFTPD; RARA; RARB; RARG; REL; WT1; MASP1; IRF8; NFKB1; NSD1; ZFXH3; GNN; CITED2; TAF9B; MSH2; MSH3; SMARCA4; CEBPA; SUZ12; PRKCD; PSME1; SMAD3; ILF3; WWP1; ZFP2M; BRCA1; DAXX; SMURF2; CDC16; EGRI; STAT3; ZHX2; ZHX3; ZHX1; IFNB1; IGBP1; EIF2C2; TP53; IL6; KLF11; NKX2-1; ENPP7; PPP2CA; TERF1; POU2F1; TAF7; CDC23; TNF; NCOR1; BCOR; HEY1; PSMB4; GRIN2C; GLI2; SIN3A; PLAT; NPM1; NFIC; TGIF1

GO:0060255	6. 30E-16	2. 30E-12	14791	601	3403	224	BP	regulation of macromolecule metabolic process	SMARCC2; HIPK2; SP1; SP3; CAMK2A; WHSC2; AR; TSG101; UBE2D2; GTF2I; HOXB8; HOXB9; BLM; PPARG; PPARG; PPARG; PPARG; ANAPC5; ANAPC7; KCNH2; ITGAV; SIGIRR; TRMT1; SMAD9; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; REL; TSC1; SPI1; IRF3; RXRA; LEF1; SRPK1; BDKRB2; APBA2; TP73; ERG1; EGFR; IGF1R; RBM9; ERG; NGFR; GF11B; UBTf; PGR; CNOT3; CNOT4; SNCA; JUN; HOXB13; SFTPD; LIF; RARA; EIF3H; RARB; RARG; NFE2L1; REL; WT1; PDE8A; ELK1; MASP1; USF1; GTF2E1; TCF4; IGF1; IRF8; NFKB1; CSNK1E; NSD1; TCERG1; ZFH3; PGAM1; GMNN; USF2; SKP1; NTF3; ASCL3; CITED2; UHRF1; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; GTF2H4; TCEB3; MSH2; MSH3; ITGB3BP; MYBL1; SMARCA4; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; CAMP; ETS1; MED15; SUZ12; PRKCD; PSME1; SMAD3; ILF3; BCL2; WWP1; GHR; ZFPM2; BRCA1; ERBB4; CREB1; NR2C2; BRD8; BRD7; PRMT5; KPNA2; CRX; HIF1A; SMURF1; DAXX; SMURF2; CDC16; NONO; EGR1; EGR4; FOS; RAD50; TRRAP; SFPQ; PAX6; NFKB2; PAX2; PAX8; ESR2; ESR1; ACAD8; STK36; PAX1; FGF23; YY1; IL1B; STAT3; RBM8A; STAT1; ZHX2; ZHX3; ZHX1; IFNB1; ING2; IGBP1; TAL1; EIF2C2; TP53; NRBF2; CYP1A2; MYB; IL6; EIF5; MAP2K3; RUNX1T1; TEAD1; KLF11; TFAP2A; POU3F2; CEBPB; PKN1; MCM7; SQSTM1; DRD2; PICALM; ISL1; NKX2-1; ETS2; ENPP7; FLI1; SNAPC5; PPP2CA; PPP2CB; TERF1; POU2F1; PABPC1; ELK4; MED30; HRAS; POLR2K; TAF7; ETV4; CDC23; TNF; NCOR1; NBN; TGS1; BCOR; HEY1; STAT5B; STAT5A; SREBF1; PSMB4; RIPK2; GRIN2C; DGKQ; GLI2; SIN3A; RAD21; DNMT3L; PLAT; DACH1; NPM1; NFIC; PEMT; ATF1; AXIN1; SUB1; HOXC11; NEDD4L; TGIF1; ATF6; ATF2
GO:0051171	1. 30E-15	4. 80E-12	14791	601	3091	208	BP	regulation of nitrogen compound metabolic process	SMARCC2; HIPK2; SP1; SP3; CAMK2A; WHSC2; AR; TSG101; GTF2I; HOXB8; HOXB9; BLM; PPARG; PPARG; PPARG; PPARG; GDI1; KCNH2; SIGIRR; SMAD9; RALBP1; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; AKAP12; REL; TSC1; SPI1; IRF3; RXRA; LEF1; SRPK1; TP73; ERG1; EGFR; IGF1R; RBM9; ERG; GF11B; UBTf; PGR; CNOT3; CNOT4; JUN; HOXB13; LIF; RARA; RARB; RARG; NFE2L1; REL; WT1; PDE8A; ADCY1; ELK1; USF1; GTF2E1; TCF4; IGF1; IRF8; NFKB1; NSD1; TCERG1; ZFH3; PGAM1; GMNN; USF2; ADAP1; NTF3; ASCL3; CITED2; UHRF1; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; GTF2H4; TCEB3; MSH2; MSH3; ITGB3BP; MYBL1; SMARCA4; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; ETS1; MED15; SUZ12; SMAD3; ILF3; WWP1; ZFPM2; BRCA1; ERBB4; CREB1; NR2C2; BRD8; BRD7; ADCY5; PRMT5; KPNA2; GNAO1; CRX; HIF1A; DAXX; SMURF2; NONO; EGR1; EGR4; FOS; RAD50; TRRAP; SFPQ; PAX6; NFKB2; PAX2; PAX8; ESR2; ESR1; ACAD8; STK36; PAX1; FGF23; YY1; IL1B; STAT3; STAT1; ZHX2; ZHX3; ZHX1; IFNB1; ING2; IGBP1; TAL1; COMT; EIF2C2; TP53; NRBF2; MYB; IL6; ASAP1; ASAP2; MAP2K3; RUNX1T1; TEAD1; KLF11; TFAP2A; POU3F2; CEBPB; PKN1; MCM7; SQSTM1; DRD2; HTR1A; PICALM; ISL1; HBB; NKX2-1; ETS2; NTRK2; ENPP7; FLI1; SNAPC5; PPP2CA; TERF1; POU2F1; PABPC1; HTR1B; ELK4; MED30; HRAS; POLR2K; TAF7; ETV4; TNF; ACR; NCOR1; NBN; TGS1; BCOR; HEY1; STAT5B; STAT5A; SREBF1; RIPK2; DGKQ; GLI2; FSHR; SIN3A; RAD21; NDEL1; DACH1; NPM1; NFIC; ATF1; SUB1; HOXC11; TGIF1; ATF6; ATF2
GO:0051172	3. 10E-15	1. 10E-11	14791	601	557	66	BP	negative regulation of nitrogen compound metabolic process	SMARCC2; HIPK2; TSG101; BLM; PPARG; PPARG; PPARG; SMAD4; TLE1; SMAD7; SPI1; RXRA; LEF1; RBM9; GF11B; UBTf; PGR; RARA; RARB; RARG; REL; WT1; IRF8; NFKB1; NSD1; ZFH3; GMNN; CITED2; TAF9B; MSH2; MSH3; SMARCA4; CEBPA; SUZ12; SMAD3; ILF3; WWP1; ZFPM2; BRCA1; DAXX; SMURF2; EGR1; STAT3; ZHX2; ZHX3; ZHX1; IFNB1; IGBP1; COMT; TP53; KLF11; NKX2-1; ENPP7; TERF1; POU2F1; HTR1B; TAF7; TNF; NCOR1; BCOR; HEY1; GLI2; SIN3A; NPM1; NFIC; TGIF1
GO:0019219	4. 40E-15	1. 60E-11	14791	601	3064	205	BP	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	SMARCC2; HIPK2; SP1; SP3; CAMK2A; WHSC2; AR; TSG101; GTF2I; HOXB8; HOXB9; BLM; PPARG; PPARG; PPARG; GDI1; KCNH2; SIGIRR; SMAD9; RALBP1; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; AKAP12; REL; TSC1; SPI1; IRF3; RXRA; LEF1; SRPK1; TP73; ERG1; IGF1R; RBM9; ERG; GF11B; UBTf; PGR; CNOT3; CNOT4; JUN; HOXB13; LIF; RARA; RARB; RARG; NFE2L1; REL; WT1; PDE8A; ADCY1; ELK1; USF1; GTF2E1; TCF4; IGF1; IRF8; NFKB1; NSD1; TCERG1; ZFH3; PGAM1; GMNN; USF2; ADAP1; NTF3; ASCL3; CITED2; UHRF1; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; GTF2H4; TCEB3; MSH2; MSH3; ITGB3BP; MYBL1; SMARCA4; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; ETS1; MED15; SUZ12; SMAD3; ILF3; WWP1; ZFPM2; BRCA1; ERBB4; CREB1; NR2C2; BRD8; BRD7; ADCY5; PRMT5; KPNA2; GNAO1; CRX; HIF1A; DAXX; SMURF2; NONO; EGR1; EGR4; FOS; RAD50; TRRAP; SFPQ; PAX6; NFKB2; PAX2; PAX8; ESR2; ESR1; ACAD8; STK36; PAX1; FGF23; YY1; IL1B; STAT3; STAT1; ZHX2; ZHX3; ZHX1; IFNB1; ING2; IGBP1; TAL1; EIF2C2; TP53; NRBF2; MYB; IL6; ASAP1; ASAP2; MAP2K3; RUNX1T1; TEAD1; KLF11; TFAP2A; POU3F2; CEBPB; PKN1; MCM7; SQSTM1; DRD2; HTR1A; PICALM; ISL1; NKX2-1; ETS2; NTRK2; ENPP7; FLI1; SNAPC5; PPP2CA; TERF1; POU2F1; PABPC1; HTR1B; ELK4; MED30; HRAS; POLR2K; TAF7; ETV4; TNF; ACR; NCOR1; NBN; TGS1; BCOR; HEY1; STAT5B; STAT5A; SREBF1; RIPK2; DGKQ; GLI2; FSHR; SIN3A; RAD21; NDEL1; DACH1; NPM1; NFIC; ATF1; SUB1; HOXC11; TGIF1; ATF6; ATF2
GO:0010551	4. 60E-15	1. 70E-11	14791	601	148	32	BP	regulation of gene-specific transcription from RNA polymerase II promoter	AR; PPARG; PPARG; SMAD7; PRKDC; RXRA; LIF; USF1; IGF1; NFKB1; USF2; CITED2; TAF9B; SMARCA4; CEBPA; ETS1; SMAD3; BRCA1; CREB1; IL1B; IGBP1; TAL1; TP53; PKN1; NKX2-1; TAF7; NCOR1; BCOR; HEY1; DGKQ; RAD21; NFIC

GO:0045934	5.90E-15	2.20E-11	14791	601	550	65	BP	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	SMARCC2; HIPK2; TSG101; BLM; PPARG; PPAR; PPARA; SMAD4; TLE1; SMAD7; SPI1; RXRA; LEF1; RBM9; GF11B; UBT; PGR; RARA; RARB; RARG; REL; WT1; IRF8; NFKB1; NSD1; ZFH3; GMN; CITED2; TAF9B; MSH2; MSH3; SMARCA4; CEBPA; SUZ12; SMAD3; ILF3; WWP1; ZFPM2; BRCA1; DAXX; SMURF2; EGR1; STAT3; ZHX2; ZHX3; ZHX1; IFNB1; IGBP1; TP53; KLF11; NKX2-1; ENPP7; TERF1; POU2F1; HTR1B; TAF7; TNF; NCOR1; BCOR; HEY1; GLI2; SIN3A; NPM1; NFIC; TGIF1
GO:0042127	8.70E-15	3.20E-11	14791	601	839	84	BP	regulation of cell proliferation	PPAP2A; HIPK2; F3; AR; TSG101; BNIPL; APOH; CYP27B1; BLM; PPARG; PPAR; COL4A3; ASH2L; SMAD4; SMAD1; TSC1; RXRA; BDKRB2; EGFR; IGF1R; RBM9; NGFR; PGR; JAG1; JUN; SFTPD; LIF; AVPR1A; RARA; RARB; RARG; REL; CDKN2B; WT1; DBH; IGF1; IGFBP6; SST; FABP3; CLU; HOXA5; CEBPA; CAMP; ETS1; SUZ12; VIPR1; SMAD3; BCL2; PLCD3; BRCA1; ERBB4; HIF1A; EGR4; ESR2; ESR1; IL1B; STAT1; IFNB1; COMT; TP53; SFRP2; WNT2; IL6; KLF11; NAP1L1; POU3F2; DRD2; HTR1A; ENPP7; MST1R; TGFA; HRAS; FGF5; FGF4; TNF; GNRHR; NBN; ADK; STAT5B; STAT5A; RIPK2; GLI2; NPM1; PENT
GO:0010558	1.40E-14	5.40E-11	14791	601	589	67	BP	negative regulation of macromolecule biosynthetic process	SMARCC2; HIPK2; TSG101; BLM; PPARG; PPAR; PPARA; ITGAV; SIGIRR; SMAD4; TLE1; SMAD7; TSC1; SPI1; RXRA; LEF1; RBM9; GF11B; UBT; PGR; SFTPD; RARA; RARB; RARG; REL; WT1; IRF8; NFKB1; NSD1; ZFH3; GMN; CITED2; TAF9B; SMARCA4; CEBPA; SUZ12; SMAD3; ILF3; WWP1; ZFPM2; BRCA1; DAXX; SMURF2; EGR1; STAT3; ZHX2; ZHX3; ZHX1; IFNB1; IGBP1; EIF2C2; TP53; IL6; KLF11; NKX2-1; ENPP7; TERF1; POU2F1; TAF7; TNF; NCOR1; BCOR; HEY1; GLI2; SIN3A; NFIC; TGIF1
GO:0009725	2.20E-14	8.20E-11	14791	601	440	56	BP	response to hormone stimulus	F3; AR; CYP27B1; PPARG; PPARA; KHK; ASH2L; PRKDC; TSC1; RXRA; LEPR; IGF1R; AVPR1A; RARA; REL; ADCY1; GNG2; VLDLR; USF1; SST; FABP3; PPAT; AGRP; CEBPA; BCL2; GHR; BRCA1; ERBB4; ADCY5; EGR1; FOS; LCT; ESR2; ESR1; IL1B; STAT3; STAT1; LCAT; AGXT; IL6; AP3S1; PDPK1; ALPL; NKX2-1; GOT1; SOCS2; HTR1B; SDC1; TNF; ACR; MAP1B; SRD5A2; DUSP1; STAT5B; STAT5A; PIAT
GO:0009890	5.00E-14	1.80E-10	14791	601	619	68	BP	negative regulation of biosynthetic process	SMARCC2; HIPK2; TSG101; BLM; PPARG; PPAR; PPARA; ITGAV; SIGIRR; SMAD4; TLE1; SMAD7; TSC1; SPI1; RXRA; LEF1; RBM9; GF11B; UBT; PGR; SFTPD; RARA; RARB; RARG; REL; WT1; IRF8; NFKB1; NSD1; ZFH3; GMN; CITED2; TAF9B; SMARCA4; CEBPA; SUZ12; SMAD3; ILF3; WWP1; ZFPM2; BRCA1; DAXX; SMURF2; EGR1; STAT3; ZHX2; ZHX3; ZHX1; IFNB1; IGBP1; EIF2C2; TP53; IL6; KLF11; NKX2-1; ENPP7; TERF1; POU2F1; HTR1B; TAF7; TNF; NCOR1; BCOR; HEY1; GLI2; SIN3A; NFIC; TGIF1
GO:0051253	5.60E-14	2.10E-10	14791	601	396	52	BP	negative regulation of RNA metabolic process	SMARCC2; HIPK2; TSG101; PPARG; PPAR; PPARA; SMAD4; SMAD7; SPI1; RXRA; LEF1; GF11B; UBT; PGR; RARA; RARB; RARG; REL; WT1; IRF8; NFKB1; NSD1; ZFH3; CITED2; TAF9B; SMARCA4; CEBPA; SUZ12; SMAD3; ILF3; ZFPM2; DAXX; EGR1; STAT3; ZHX2; ZHX3; ZHX1; IGBP1; TP53; KLF11; NKX2-1; POU2F1; TAF7; TNF; NCOR1; BCOR; HEY1; GLI2; SIN3A; NPM1; NFIC; TGIF1
GO:0031327	5.80E-14	2.10E-10	14791	601	606	67	BP	negative regulation of cellular biosynthetic process	SMARCC2; HIPK2; TSG101; BLM; PPARG; PPAR; PPARA; SIGIRR; SMAD4; TLE1; SMAD7; TSC1; SPI1; RXRA; LEF1; RBM9; GF11B; UBT; PGR; SFTPD; RARA; RARB; RARG; REL; WT1; IRF8; NFKB1; NSD1; ZFH3; GMN; CITED2; TAF9B; SMARCA4; CEBPA; SUZ12; SMAD3; ILF3; WWP1; ZFPM2; BRCA1; DAXX; SMURF2; EGR1; STAT3; ZHX2; ZHX3; ZHX1; IFNB1; IGBP1; EIF2C2; TP53; IL6; KLF11; NKX2-1; ENPP7; TERF1; POU2F1; HTR1B; TAF7; TNF; NCOR1; BCOR; HEY1; GLI2; SIN3A; NFIC; TGIF1
GO:0006950	6.20E-14	2.30E-10	14791	601	1591	126	BP	response to stress	HIPK2; IFNA10; F3; MX1; DSP; BLM; PPARG; PPAR; PPARA; GPX5; SIGIRR; SMAD9; SMAD4; SMAD7; SMAD1; PRKDC; RXRA; LTF; BDKRB2; TP73; IFNA21; EGFR; NGFR; ABAT; DEFA1; NOS1; SNCA; JUN; TRIP13; HOXB13; SFTPD; AVPR1A; NFE2L1; REL; LPO; DBH; SCARB1; MAPK10; VLDLR; MASP1; USF1; TIRAP; KCN3; SST; IRF8; NFKB1; CSNK1E; EPHX2; IL1RAP; FANCC; CITED2; CLU; UHRF1; CDK7; F2RL3; GTF2H4; MSH2; MSH3; MGLL; CEBPA; CEBPG; CEBPE; CAMP; SMAD3; BCL2; TRPV4; BRCA1; ERBB4; CTSG; MASP2; GNAO1; HIF1A; XRCC5; NANO; FCN2; FOS; RAD50; SFPQ; PAX6; TP53INP1; KIR3DL2; LCT; ESR2; TOLLIP; POLE2; CCR4; IL1B; STAT3; STAT1; IFNB1; COMT; TP53; IL6; CAMLG; PDPK1; HSPB3; CEBPB; PKN1; MCM7; VWF; SQSTM1; C1S; NKX2-1; CAPN2; PPP2CB; MST1R; GSK3B; HLA-G; VDCA1; SDC1; TNF; EPHA3; MAP1B; NBN; DUSP1; ACHE; TACC3; STAT5B; SREBF1; RIPK2; GRIN2C; ADRBK1; RAD21; PLAT; NPM1; ATF6
GO:0044093	6.90E-14	2.50E-10	14791	601	623	68	BP	positive regulation of molecular function	PPAP2A; HIPK2; PIK3CB; CAMK2A; F3; APOH; CYP27B1; PPARG; COL4A3; ANAPC5; ANAPC7; PDE6H; RALBP1; TSC1; ERC1; EGFR; HGF; AVPR1A; RARA; DAB1; REL; HOMER1; ADCY1; SCARB1; VLDLR; SKP1; F2RL3; LPAR1; MSH2; MSH3; SMARCA4; CEBPG; PSME1; SMAD3; BCL2; GHR; ADCY5; GNAO1; PLCB2; HIF1A; DAXX; CDC16; RAD50; FGF23; IL1B; STAT1; IFNB1; TP53; IL6; MAP2K3; PDPK1; PKN1; DUSP12; DRD2; NTRK2; TERF1; TGFA; CHRM2; CDC23; TNF; ACR; NBN; PSMB4; RIPK2; DGKQ; FSHR; NDEL1; NPM1
GO:0051252	7.00E-14	2.60E-10	14791	601	1853	140	BP	regulation of RNA metabolic process	SMARCC2; HIPK2; SPI1; SPI3; AR; TSG101; HOXB8; HOXB9; PPARG; PPAR; PPARA; KCNH2; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; PRKDC; REL; SPI1; IRF3; RXRA; LEF1; SRPK1; TP73; ERC1; ERG; GF11B; UBT; PGR; JUN; HOXB13; LIF; RARA; RARB; RARG; NFE2L1; REL; WT1; PDE8A; ELK1; USF1; TCF4; IGF1; IRF8; NFKB1; NSD1; ZFH3; USF2; NTF3; ASCL3; CITED2; UHRF1; HOXA5; HOXA1; CDK7; TAF9B; GTF2H4; TCEB3; MYBL1; SMARCA4; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; ETS1; MED15; SUZ12; SMAD3; ILF3; ZFPM2; BRCA1; CREB1; NR2C2; BRD8; BRD7; CRX; HIF1A; DAXX; EGR1; FOS; PAX6; NFKB2; PAX8; ESR2; ESR1; PAX1; FGF23; YY1; IL1B; STAT3; STAT1; ZHX2; ZHX3; ZHX1; ING2; IGBP1; TAL1; TP53; MYB; IL6; MAP2K3; RUNX1T1; TEAD1; KLF11; TFAP2A; POU3F2; CEBPB; PKN1; SQSTM1; ISL1; NKX2-1; ETS2; FLI1; POU2F1; PABPC1; ELK4; POLR2K; TAF7; ETV4; TNF; NCOR1; BCOR; HEY1; STAT5B; STAT5A; SREBF1; DGKQ; GLI2; SIN3A; RAD21; NPM1; NFIC; ATF1; SUB1; HOXC11; TGIF1; ATF6; ATF2

GO:0010941	7. 70E-14	2. 80E-10	14791	601	856	83	BP	regulation of cell death	HIPK2; ARHGEF12; F3; MX1; BNIPL; APOH; PPARG; COL4A3; SMAD4; PRKDC; RXRA; BDKRB2; TP73; EGFR; IGF1R; NGFR; SNCA; JUN; HGF; SON; RARB; RARG; PEA15; REL; WT1; DBH; IGF1; SST; NFKB1; CADM1; NTF3; CITED2; CLU; PDCD5; HOXA5; TAF9B; MSH2; ITGB3BP; YWHAZ; CEBPG; ETS1; SMAD3; MCL1; BCL2; GHR; BRCA1; CREB1; XRCC5; DAXX; RPS3A; TP53INP1; ESR2; ESR1; IL1B; STAT1; IFNB1; IGBP1; TP53; SFRP2; IL6; GDF5; CEBPB; TP53BP2; SQSTM1; ITSN1; SOCS2; PPP2CA; PPP2CB; GSK3B; TERF1; HRAS; FGF4; TNFAIP3; TNF; DUSP1; SOS1; STAT5B; STAT5A; RIPK2; SIN3A; TRAF5; NPM1; IGF2R
GO:0042981	8. 80E-14	3. 20E-10	14791	601	842	82	BP	regulation of apoptosis	HIPK2; ARHGEF12; F3; MX1; BNIPL; APOH; PPARG; COL4A3; PRKDC; RXRA; BDKRB2; TP73; EGFR; IGF1R; NGFR; SNCA; JUN; HGF; SON; RARB; RARG; PEA15; REL; WT1; DBH; IGF1; SST; NFKB1; CADM1; NTF3; CITED2; CLU; PDCD5; HOXA5; TAF9B; MSH2; ITGB3BP; YWHAZ; CEBPG; ETS1; SMAD3; MCL1; BCL2; GHR; BRCA1; CREB1; XRCC5; DAXX; RPS3A; TP53INP1; ESR2; ESR1; IL1B; STAT1; IFNB1; IGBP1; TP53; SFRP2; IL6; GDF5; CEBPB; TP53BP2; SQSTM1; ITSN1; SOCS2; PPP2CA; PPP2CB; GSK3B; TERF1; HRAS; FGF4; TNFAIP3; TNF; DUSP1; SOS1; STAT5B; STAT5A; RIPK2; SIN3A; TRAF5; NPM1; IGF2R
GO:0006355	9. 60E-14	3. 50E-10	14791	601	1804	137	BP	regulation of transcription, DNA-dependent	SMARCC2; HIPK2; SP1; SP3; AR; TSG101; HOXB8; HOXB9; PPARG; PPARG; PPARA; KCNH2; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; PRKDC; REL; SPI1; IRF3; RXRA; LEF1; TP73; ERC1; ERG; GFI1B; UBTf; PGR; JUN; HOXB13; LIF; RARA; RARB; RARG; NFE2L1; REL; WT1; PDE8A; ELK1; USF1; TCF4; IGF1; IRF8; NFKB1; NSD1; ZFH3; USF2; NTF3; ASCL3; CITED2; UHRF1; HOXA5; HOXA1; CDK7; TAF9B; GTF2H4; TCEB3; MYBL1; SMARCA4; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; ETS1; MED15; SUZ12; SMAD3; ILF3; ZFPM2; BRCA1; CREB1; NR2C2; BRD8; BRD7; CRX; HIF1A; DAXX; EGR1; FOS; PAX6; NFKB2; PAX8; ESR2; ESR1; PAX1; FGF23; YY1; IL1B; STAT3; STAT1; ZHX2; ZHX3; ZHX1; ING2; IGBP1; TAL1; TP53; MYB; IL6; MAP2K3; RUNX1T1; TEAD1; KLF11; TFAP2A; POU3F2; CEBPB; PKN1; SQSTM1; ISL1; NKX2-1; ETS2; FLI1; POU2F1; ELK4; POLR2K; TAF7; ETV4; TNF; NCOR1; BCOR; HEY1; STAT5B; STAT5A; SREBF1; DGKQ; GLI2; SIN3A; RAD21; NFIC; ATF1; SUB1; HOXC11; TGIF1; ATF6; ATF2
GO:0009889	1. 00E-13	3. 80E-10	14791	601	3094	202	BP	regulation of biosynthetic process	SMARCC2; HIPK2; SP1; SP3; CAMK2A; WHSC2; AR; TSG101; APOB; GTF2I; HOXB8; HOXB9; BLM; PPARG; PPARG; PPARA; KCNH2; ITGA; SIGIRR; SMAD9; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; AKAP12; REL; TSC1; SPI1; IRF3; RXRA; LEF1; TP73; ERC1; EGFR; IGF1R; RBM9; ERG; GFI1B; UBTf; PGR; CNOT3; CNOT4; SNCA; JUN; HOXB13; SFTPD; LIF; AVPRIA; RARA; EIF3H; RARB; RARG; NFE2L1; REL; WT1; PDE8A; ADCY1; ELK1; USF1; GTF2E1; TCF4; IGF1; IRF8; NFKB1; NSD1; TCERG1; ZFH3; GMN; USF2; NTF3; ASCL3; CITED2; UHRF1; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; GTF2H4; TCEB3; ITGB3BP; MYBL1; SMARCA4; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; ETS1; MED15; SUZ12; SMAD3; ILF3; BCL2; WWP1; ZFPM2; BRCA1; ERBB4; CREB1; NR2C2; BRD8; BRD7; ADCY5; PRMT5; CRX; HIF1A; DAXX; SMURF2; NONO; EGR1; EGR4; FOS; TRRAP; SFPQ; PAX6; NFKB2; PAX2; PAX8; ESR2; ESR1; ACAD8; STK36; PAX1; FGF23; YY1; IL1B; STAT3; RBM8A; STAT1; ZHX2; ZHX3; ZHX1; IFNB1; ING2; IGBP1; TAL1; EIF2C2; TP53; NRFB2; MYB; IL6; EIF5; MAP2K3; RUNX1T1; TEAD1; KLF11; TFAP2A; POU3F2; CEBPB; PKN1; MCM7; SQSTM1; DRD2; HTR1A; PICALM; ISL1; HBB; NKX2-1; ETS2; NTRK2; ENPP7; FLI1; SNAPC5; PPP2CA; TERF1; POU2F1; HTR1B; ELK4; MED30; HRAS; POLR2K; TAF7; ETV4; TNF; ACR; NCOR1; NBN; TGS1; BCOR; HEY1; STAT5B; STAT5A; SREBF1; RIPK2; DGKQ; GLI2; FSHR; SIN3A; RAD21; DACH1; NPM1; NFIC; ATF1; SUB1; HOXC11; TGIF1; ATF6; ATF2
GO:0045892	1. 00E-13	3. 90E-10	14791	601	389	51	BP	negative regulation of transcription, DNA-dependent	SMARCC2; HIPK2; TSG101; PPARG; PPARG; PPARA; SMAD4; SMAD7; SPI1; RXRA; LEF1; GFI1B; UBTf; PGR; RARA; RARB; RARG; REL; WT1; IRF8; NFKB1; NSD1; ZFH3; CITED2; TAF9B; SMARCA4; CEBPA; SUZ12; SMAD3; ILF3; ZFPM2; DAXX; EGR1; STAT3; ZHX2; ZHX3; ZHX1; IGBP1; TP53; KLF11; NKX2-1; POU2F1; TAF7; TNF; NCOR1; BCOR; HEY1; GLI2; SIN3A; NFIC; TGIF1
GO:0043067	1. 40E-13	5. 40E-10	14791	601	850	82	BP	regulation of programmed cell death	HIPK2; ARHGEF12; F3; MX1; BNIPL; APOH; PPARG; COL4A3; PRKDC; RXRA; BDKRB2; TP73; EGFR; IGF1R; NGFR; SNCA; JUN; HGF; SON; RARB; RARG; PEA15; REL; WT1; DBH; IGF1; SST; NFKB1; CADM1; NTF3; CITED2; CLU; PDCD5; HOXA5; TAF9B; MSH2; ITGB3BP; YWHAZ; CEBPG; ETS1; SMAD3; MCL1; BCL2; GHR; BRCA1; CREB1; XRCC5; DAXX; RPS3A; TP53INP1; ESR2; ESR1; IL1B; STAT1; IFNB1; IGBP1; TP53; SFRP2; IL6; GDF5; CEBPB; TP53BP2; SQSTM1; ITSN1; SOCS2; PPP2CA; PPP2CB; GSK3B; TERF1; HRAS; FGF4; TNFAIP3; TNF; DUSP1; SOS1; STAT5B; STAT5A; RIPK2; SIN3A; TRAF5; NPM1; IGF2R
GO:0031326	1. 90E-13	7. 10E-10	14791	601	3071	200	BP	regulation of cellular biosynthetic process	SMARCC2; HIPK2; SP1; SP3; CAMK2A; WHSC2; AR; TSG101; GTF2I; HOXB8; HOXB9; BLM; PPARG; PPARG; PPARA; KCNH2; SIGIRR; SMAD9; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; AKAP12; REL; TSC1; SPI1; IRF3; RXRA; LEF1; TP73; ERC1; EGFR; IGF1R; RBM9; ERG; GFI1B; UBTf; PGR; CNOT3; CNOT4; SNCA; JUN; HOXB13; SFTPD; LIF; AVPRIA; RARA; EIF3H; RARB; RARG; NFE2L1; REL; WT1; PDE8A; ADCY1; ELK1; USF1; GTF2E1; TCF4; IGF1; IRF8; NFKB1; NSD1; TCERG1; ZFH3; GMN; USF2; NTF3; ASCL3; CITED2; UHRF1; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; GTF2H4; TCEB3; ITGB3BP; MYBL1; SMARCA4; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; ETS1; MED15; SUZ12; SMAD3; ILF3; BCL2; WWP1; ZFPM2; BRCA1; ERBB4; CREB1; NR2C2; BRD8; BRD7; ADCY5; PRMT5; CRX; HIF1A; DAXX; SMURF2; NONO; EGR1; EGR4; FOS; TRRAP; SFPQ; PAX6; NFKB2; PAX2; PAX8; ESR2; ESR1; ACAD8; STK36; PAX1; FGF23; YY1; IL1B; STAT3; RBM8A; STAT1; ZHX2; ZHX3; ZHX1; IFNB1; ING2; IGBP1; TAL1; EIF2C2; TP53; NRFB2; MYB; IL6; EIF5; MAP2K3; RUNX1T1; TEAD1; KLF11; TFAP2A; POU3F2; CEBPB; PKN1; MCM7; SQSTM1; DRD2; HTR1A; PICALM; ISL1; HBB; NKX2-1; ETS2; NTRK2; ENPP7; FLI1; SNAPC5; PPP2CA; TERF1; POU2F1; HTR1B; ELK4; MED30; HRAS; POLR2K; TAF7; ETV4; TNF; ACR; NCOR1; NBN; TGS1; BCOR; HEY1; STAT5B; STAT5A; SREBF1; RIPK2; DGKQ; GLI2; FSHR; SIN3A; RAD21; DACH1; NPM1; NFIC; ATF1; SUB1; HOXC11; TGIF1; ATF6; ATF2

GO:0065009	3.00E-13	1.10E-09	14791	601	1043	93	BP	regulation of molecular function	PPAP2A; HIPK2; PIK3CB; CAMK2A; F3; JPH2; AR; APOH; CYP27B1; BLM; PPARG; COL4A3; GDI1; ANAPC5; ANAPC7; SIGIRR; PDE6H; RALBP1; SMAD4; SMAD7; TSC1; LEPR; TP73; ERCC1; EGFR; SNCA; JUN; HGF; AVPR1A; RARA; CATSPER1; DAB1; RELA; CDKN2B; HOMER1; ADCY1; SCARB1; VLDLR; NFKB1; SKP1; ADAP1; CDK7; F2RL3; LPAR1; MSH2; MSH3; SMARCA4; CEBPG; PRKCD; PSME1; SMAD3; BCL2; CAV3; GHR; ADCY5; GNAO1; PLCB2; HIF1A; DAXX; CDC16; RAD50; STK36; FGF23; IL1B; STAT1; IFNB1; IGBP1; TP53; IL6; ASAP1; ASAP2; MAP2K3; PDPK1; PKN1; DUSP12; DRD2; HTR1A; NTRK2; PPP2CA; TERF1; TGFA; CHRM2; TAF7; CDC23; TNF; ACR; NBN; PSMB4; RIPK2; DGKQ; FSHR; NDEL1; NPM1
GO:0065008	3.20E-13	1.20E-09	14791	601	1285	107	BP	regulation of biological quality	PCSK2; SCG5; PIK3CB; SY2A; SP1; F3; SULT1E1; JPH2; APOB; MST1; APOH; CYP27B1; BLM; PPARG; PPARA; KCNH2; SMAD7; SMAD1; PRKDC; TAF11; TSC1; LTF; BDKRB2; F5; TP73; ABAT; NOS1; SNCA; JUN; HEXB; SFTPD; AVPR1A; COL11A2; RARG; LIPC; DBH; PTGES3; SCARB1; PROS1; USF1; IGF1; KCNK3; F10; EPOR; EPHX2; USF2; FANCC; PPAT; F2RL3; LPAR1; YWHAZ; PRKCD; MCL1; BCL2; CAV3; CACNA1F; TRPV4; CETP; ERBB4; CREB1; CTSG; HIF1A; XRC5; EGR1; XDH; RPH3AL; RAD50; ESRI; FGF23; SYN1; CCR4; IL1B; STAT3; LCAT; COMT; TP53; IL6; BCAN; VWF; DRD2; RDH12; KCNE1; HBB; NKX2-1; GOT1; FLI1; TERF1; SLC4A1; HRAS; SHBG; TNF; EPHA3; ATP5B; MAP1B; NBN; SRD5A2; CRHBP; ACHE; TACC3; STAT5B; STAT5A; CHGA; GRIN2C; ADRBK1; PLAT; NPM1; NEDD4L
GO:0043193	3.30E-13	1.20E-09	14791	601	131	28	BP	positive regulation of gene-specific transcription	AR; PPARG; PRKDC; SPI1; RXRA; LIF; RARA; WT1; USF1; IGF1; USF2; CITED2; SMARCA4; CEBPA; ETS1; SMAD3; BRCA1; CREB1; HIF1A; ESR2; FGF23; IL1B; TP53; IL6; NKX2-1; TNF; NFIC; ATF6
GO:0016481	5.60E-13	2.10E-09	14791	601	489	57	BP	negative regulation of transcription	SMARCC2; HIPK2; TSG101; PPARG; PPARD; PPARA; SMAD4; TLE1; SMAD7; SPI1; RXRA; LEF1; RBM9; GF11B; UBTG; PGR; RARA; RARB; RARG; RELA; WT1; IRF8; NFKB1; NSD1; ZFXH3; CITED2; TAF9B; SMARCA4; CEBPA; SUZ12; SMAD3; ILF3; WWP1; ZFPM2; BRCA1; ERBB4; CREB1; NR2C2; BRD8; BRD7; ZHX3; ZHX1; IFNB1; IGBP1; TP53; KLF11; NKX2-1; POU2F1; TAF7; TNF; NCOR1; BCOR; HEY1; GLI2; SIN3A; NFIC; TGIF1
GO:0010468	7.70E-13	2.80E-09	14791	601	2968	193	BP	regulation of gene expression	SMARCC2; HIPK2; SP1; SP3; CAMK2A; WHSC2; AR; TSG101; GTF2I; HOXB8; HOXB9; BLM; PPARG; PPARD; PPARA; KCNH2; SIGIRR; TRDM1; SMAD9; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; REL; TSC1; SPI1; IRF3; RXRA; LEF1; SRPK1; APBA2; TP73; ERCC1; RBM9; ERG; NGFR; GF11B; UBTG; PGR; CNOT3; CNOT4; JUN; HOXB13; LIF; RARA; EIF3H; RARB; RARG; NFE2L1; RELA; WT1; PDE8A; ELK1; MASP1; USF1; GTF2E1; TCF4; IGF1; IRF8; NFKB1; NSD1; TCEG1; ZFXH3; GNN; USF2; NTF3; ASCL3; CITED2; UHRF1; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; GTF2H4; TCEB3; ITGB3BP; MYBL1; SMARCA4; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; ETS1; MED15; SUZ12; PRKCD; SMAD3; ILF3; BCL2; WWP1; ZFPM2; BRCA1; ERBB4; CREB1; NR2C2; BRD8; BRD7; PRMT5; CRX; HIF1A; DAXX; SMURF2; NONO; EGR1; EGR4; FOS; TRRAP; SFPQ; PAX6; NFKB2; PAX2; PAX8; ESR2; ESR1; ACAD8; STK36; PAX1; FGF23; YY1; IL1B; STAT3; RBM8A; STAT1; ZHX2; ZHX3; ZHX1; IFNB1; ING2; IGBP1; TALL1; EIF2C2; TP53; NRBF2; CYP1A2; MYB; IL6; EIF5; MAP2K3; RUNX1T1; TEAD1; KLF11; TFAP2A; POU3F2; CEBPB; PKN1; MCM7; SQSTM1; DRD2; PICALM; ISL1; NKX2-1; ETS2; FLI1; SNAPC5; PPP2CA; PPP2CB; TERF1; POU2F1; PABPC1; ELK4; MED30; POLR2K; TAF7; ETV4; TNF; NCOR1; TGS1; BCOR; HEY1; STAT5B; STAT5A; SREBF1; RIPK2; DGKQ; GLI2; SIN3A; RAD21; DNMT3L; DACH1; NPM1; NFIC; ATF1; SUB1; HOXC11; TGIF1; ATF6; ATF2
GO:0051239	9.80E-13	3.60E-09	14791	601	1047	92	BP	regulation of multicellular organismal process	F3; AR; APOH; CYP27B1; PPARG; COL4A3; KCNH2; SIGIRR; SMAD4; SMAD7; SMAD1; REL; SPI1; RXRA; LEF1; BDKRB2; EGFR; NGFR; JAG1; NOS1; SNCA; JUN; HGF; SFTPD; LIF; AVPR1A; RARA; RELA; CDKN2B; DBH; USF1; IGF1; EPHX2; ZFXH3; CADM1; NTF3; KEAP1; HOXA5; CEBPG; CAMP; ETS1; SMAD3; BCL2; CAV3; GHR; ERBB4; CREB1; GNAO1; CRX; HIF1A; XRC5; SMURF1; EGR1; XDH; ESRI; FGF23; IL1B; STAT3; TALL1; TP53; SFRP2; WNT2; IL6; TFAP2A; GDF5; BCAN; POU3F2; CEBPB; DRD2; KCNE2; KCNE1; NKX2-1; NTRK3; HTR1B; CHRM2; HRAS; PEX5; TNF; EPHA2; MAP1B; NBN; BCOR; ACHE; STAT5B; STAT5A; RIPK2; ADRBK1; GLI2; PLAT; NDEL1; ATF1; HOXC11
GO:0048545	1.10E-12	4.10E-09	14791	601	223	36	BP	response to steroid hormone stimulus	F3; CYP27B1; PPARG; ASH2L; RXRA; LEPR; AVPR1A; RARA; RELA; SST; CEBPA; BCL2; GHR; BRCA1; ERBB4; FOS; LCT; ESR2; ESR1; IL1B; STAT3; LCAT; AGXT; IL6; ALPL; GOT1; SOCS2; HTR1B; SDC1; TNF; ACR; MAP1B; SRD5A2; DUSP1; STAT5B; PLAT
GO:0048513	1.30E-12	5.10E-09	14791	601	710	71	BP	organ development	SP1; SP3; AR; HHIP; ZIC2; HOXB9; PPARG; PPARD; ASH2L; SMAD4; SMAD1; PRKDC; TSC1; RXRA; LEF1; EGFR; IGF1R; PGR; JAG1; CYR61; HGF; LIF; PKP2; RARG; RELA; WT1; IGF1; KCNK3; EPOR; ZFXH3; CADM1; NTF3; CITED2; HOXA5; MSH2; CEBPA; CEBPG; DVL2; SMAD3; BCL2; PLCD3; CAV3; ZFPM2; ERBB4; CREB1; PAX6; NFKB2; PAX8; ESR2; ESRI; PAX1; TALL1; EFNA5; CYP1A2; WNT2; TEAD1; CEBPB; VWF; NKX2-1; BMP5; SRD5A2; BCOR; ACHE; TACC3; STAT5B; STAT5A; ADRBK1; GLI2; FSHR; HOXC11; IGF2R
GO:0045597	1.50E-12	5.80E-09	14791	601	249	38	BP	positive regulation of cell differentiation	APOB; CYP27B1; PPARG; PPARD; SMAD9; SMAD4; SMAD1; NGFR; JAG1; JUN; LIF; RARA; RELA; CDKN2B; NFKB1; ZFXH3; NTF3; CLU; HOXA5; CEBPA; ETS1; SMAD3; BCL2; GHR; CRX; HIF1A; XRC5; TALL1; IL6; GDF5; DRD2; NTRK3; MAP1B; STAT5B; STAT5A; RIPK2; GLI2; NDEL1
GO:0051094	1.80E-12	6.90E-09	14791	601	338	45	BP	positive regulation of developmental process	F3; APOB; CYP27B1; PPARG; PPARD; SMAD9; SMAD4; SMAD1; NGFR; JAG1; JUN; LIF; RARA; RELA; CDKN2B; NFKB1; ZFXH3; NTF3; CLU; HOXA5; CEBPA; CAMP; ETS1; SMAD3; BCL2; GHR; CRX; HIF1A; XRC5; IL1B; TALL1; WNT2; IL6; TFAP2A; GDF5; DRD2; NTRK3; TNF; MAP1B; STAT5B; STAT5A; RIPK2; GLI2; NDEL1; HOXC11

GO:0009653	2.70E-12	1.00E-08	14791	601	881	81	BP	anatomical structure morphogenesis	SP1; SP3; AR; HHIP; APOB; APOH; ZIC2; HOXB8; PPARG; SMAD4; TLE2; TLE1; SMAD7; TSC1; RXRA; LEF1; TP73; EGFR; IGF1R; NGFR; PGR; JAG1; CYR61; HGF; HOXB13; LIF; COL11A2; RARB; RARG; NFE2L1; REL; WT1; IGF1; NSD1; GMNN; CLU; HOXA5; PPAT; HOXA1; CEBPA; DVL2; SMAD3; CTNNA2; BCL2; CACNA1F; ERBB4; CREB1; CRX; HIF1A; PAX6; PAX2; PAX8; ESR2; ESR1; PAX1; YY1; TP53; SFRP2; TFAP2A; GDF5; DRD2; NKX2-1; FLI1; HRAS; FGF4; SDC1; TNF; EPHA2; FZD6; MAP1B; BCOR; HEY1; STAT5A; GLI2; PLAT; NDEL1; CLTCL1; HOXC11; DNML1; MYO7A; IGF2R
GO:0045449	3.90E-12	1.40E-08	14791	601	2668	176	BP	regulation of transcription	SMARCC2; HIPK2; SP1; SP3; CAMK2A; WHSC2; AR; TSG101; GTF2I; HOXB8; HOXB9; BLM; PPARG; PPAR; PPARA; KCNH2; SIGIRR; SMAD9; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; REL; SPI1; IRF3; RXRA; LEF1; TP73; ERC1; RBM9; ERG; GFI1B; UBT; PGR; CNOT3; CNOT4; JUN; HOXB13; LIF; RARA; RARB; RARG; NFE2L1; REL; WT1; PDE8A; ELK1; USF1; GTF2E1; TCF4; IGF1; IRF8; NFKB1; NSD1; TCERG1; ZFH3; USF2; NTF3; ASCL3; CITED2; UHRF1; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; GTF2H4; TCEB3; ITGB3BP; MYBL1; SMARCA4; ZNF7; CEBPA; CEBPG; CEBPE; ETS1; MED15; SUZ12; SMAD3; ILF3; WWP1; ZFPM2; BRCA1; ERBB4; CREB1; NR2C2; BRD8; BRD7; PRMT5; CRX; HIF1A; DAXX; SMURF2; NONO; EGR1; EGR4; FOS; TRRAP; SFPQ; PAX6; NFKB2; PAX2; PAX8; ESR2; ESR1; ACAD8; STK36; PAX1; FGF23; YY1; IL1B; STAT3; STAT1; ZHX2; ZHX3; ZHX1; IFNB1; ING2; IGBP1; TAL1; EIF2C2; TP53; NRBF2; MYB; IL6; MAP2K3; RUNX1T1; TEAD1; KLF11; TFAP2A; POU3F2; CEBPB; PKN1; MCM7; SQSTM1; PICALM; ISL1; NKX2-1; ETS2; FLI1; SNAPC5; PPP2CA; TERF1; POU2F1; ELK4; MED30; POLR2K; TAF7; ETV4; TNF; NCOR1; TGS1; BCOR; HEY1; STAT5B; STAT5A; SREBF1; RIPK2; DGKQ; GLI2; SIN3A; RAD21; DACH1; NPM1; NFIC; ATF1; SUB1; HOXC11; TGIF1; ATF6; ATF2
GO:0010629	4.30E-12	1.60E-08	14791	601	543	59	BP	negative regulation of gene expression	SMARCC2; HIPK2; TSG101; PPARG; PPAR; PPARA; SMAD4; TLE1; SMAD7; SPI1; RXRA; LEF1; RBM9; GFI1B; UBT; PGR; RARA; RARB; RARG; REL; WT1; IRF8; NFKB1; NSD1; ZFH3; GMNN; CITED2; TAF9B; SMARCA4; CEBPA; SUZ12; SMAD3; ILF3; WWP1; ZFPM2; BRCA1; DAXX; SMURF2; EGR1; STAT3; ZHX2; ZHX3; ZHX1; IFNB1; IGBP1; EIF2C2; TP53; KLF11; NKX2-1; POU2F1; TAF7; TNF; NCOR1; BCOR; HEY1; GLI2; SIN3A; NFIC; TGIF1
GO:0048869	4.60E-12	1.70E-08	14791	601	1394	110	BP	cellular developmental process	L1CAM; SP1; SP3; AR; TSG101; ZIC2; DSP; BLM; PPARG; PPAR; PPARA; SMAD4; SMAD1; PRKDC; TSC1; RXRA; LEF1; SRPK1; TP73; EGFR; IGF1R; NGFR; PGR; JAG1; RTN1; JUN; HGF; TRIP13; HOXB13; MLPH; LIF; AVPR1A; COL11A2; CATSPER1; DAB1; RARB; CDKN2B; WT1; HOMER1; IGF1; IRF8; MLF1; FANCC; CADM1; NTF3; CITED2; CLU; HOXA5; HOXA1; MSH2; CEBPA; CEBPG; CEBPE; SMAD3; MCL1; CTNNA2; BCL2; CAV3; CACNA1F; ZFPM2; BMP8A; CREB1; HIF1A; XRC5; SMURF1; EGR1; RPS3A; PAX6; NFKB2; PAX2; PAX8; ESR2; ESR1; PAX1; FGF22; FGF23; STAT3; TAL1; EFNA5; LGALS3; TP53; SFRP2; POU3F2; CEBPB; SQSTM1; DRD2; CIS; KCNE1; NKX2-1; NTRK2; NTRK3; BMP5; STMN1; ODF1; HRAS; FGF5; FGF4; PEX5; SDC1; EPHA2; MAP1B; SRD5A2; ACHE; TACC3; STAT5B; STAT5A; GLI2; ALDH6A1; NDEL1; DNML1; MYO7A
GO:0043085	5.00E-12	1.80E-08	14791	601	545	59	BP	positive regulation of catalytic activity	PPAP2A; PIK3CB; F3; APOH; CYP27B1; PPARG; PPAR; PPARA; ANAPC5; ANAPC7; PDE6H; RALBP1; TSC1; EGFR; HGF; AVPR1A; DAB1; HOMER1; ADCY1; SCARB1; VLDLR; SKP1; F2RL3; LPAR1; MSH2; MSH3; PSME1; SMAD3; BCL2; GHR; ADCY5; GNAO1; PLCB2; HIF1A; DAXX; CDC16; RAD50; FGF23; IL1B; STAT1; IFNB1; TP53; MAP2K3; PDPK1; PKN1; DUSP12; DRD2; NTRK2; TERF1; TGF; CHRM2; CDC23; TNF; ACR; NBN; PSMB4; DGKQ; FSHR; NDEL1; NPM1
GO:0010556	5.10E-12	1.80E-08	14791	601	2923	188	BP	regulation of macromolecule biosynthetic process	SMARCC2; HIPK2; SP1; SP3; CAMK2A; WHSC2; AR; TSG101; GTF2I; HOXB8; HOXB9; BLM; PPARG; PPAR; PPARA; KCNH2; ITGAV; SIGIRR; SMAD9; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; REL; TSC1; SPI1; IRF3; RXRA; LEF1; TP73; ERC1; IGF1R; RBM9; ERG; GFI1B; UBT; PGR; CNOT3; CNOT4; JUN; HOXB13; SFTPD; LIF; RARA; EIF3H; RARB; RARG; NFE2L1; REL; WT1; PDE8A; ELK1; USF1; GTF2E1; TCF4; IGF1; IRF8; NFKB1; NSD1; TCERG1; ZFH3; GMNN; USF2; NTF3; ASCL3; CITED2; UHRF1; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; GTF2H4; TCEB3; ITGB3BP; MYBL1; SMARCA4; ZNF7; CEBPA; CEBPG; CEBPE; ETS1; MED15; SUZ12; SMAD3; ILF3; BCL2; WWP1; ZFPM2; BRCA1; ERBB4; CREB1; NR2C2; BRD8; BRD7; PRMT5; CRX; HIF1A; DAXX; SMURF2; NONO; EGR1; EGR4; FOS; TRRAP; SFPQ; PAX6; NFKB2; PAX2; PAX8; ESR2; ESR1; ACAD8; STK36; PAX1; FGF23; YY1; IL1B; STAT3; RBMSA; STAT1; ZHX2; ZHX3; ZHX1; IFNB1; ING2; IGBP1; TAL1; EIF2C2; TP53; NRBF2; MYB; IL6; EIF5; MAP2K3; RUNX1T1; TEAD1; KLF11; TFAP2A; POU3F2; CEBPB; PKN1; MCM7; SQSTM1; PICALM; ISL1; NKX2-1; ETS2; ENPP7; FLI1; SNAPC5; PPP2CA; TERF1; POU2F1; ELK4; MED30; HRAS; POLR2K; TAF7; ETV4; TNF; NCOR1; NBN; TGS1; BCOR; HEY1; STAT5B; STAT5A; SREBF1; RIPK2; DGKQ; GLI2; SIN3A; RAD21; DACH1; NPM1; NFIC; ATF1; SUB1; HOXC11; TGIF1; ATF6; ATF2
GO:0050793	1.20E-11	4.60E-08	14791	601	776	73	BP	regulation of developmental process	F3; AR; APOB; APOH; CYP27B1; PPARG; PPAR; PPARA; ITGAV; SMAD9; SMAD4; SMAD7; SMAD1; SPI1; RXRA; LEF1; NGFR; JAG1; JUN; HGF; LIF; RARA; REL; CDKN2B; IGF1; NFKB1; ZFH3; NTF3; CLU; KEAP1; HOXA5; CEBPA; CAMP; ETS1; SMAD3; BCL2; CAV3; GHR; CETP; CRX; HIF1A; XRC5; SMURF1; XDH; ESR1; FGF23; IL1B; TAL1; TP53; SFRP2; WNT2; IL6; TFAP2A; GDF5; POU3F2; DRD2; NKX2-1; NTRK3; PPP2CA; FGF4; TNF; EPHA2; MAP1B; NBN; BCOR; STAT5B; STAT5A; RIPK2; GLI2; NDEL1; ATF1; HOXC11
GO:0045595	1.30E-11	4.90E-08	14791	601	543	58	BP	regulation of cell differentiation	AR; APOB; CYP27B1; PPARG; PPAR; PPARA; ITGAV; SMAD9; SMAD4; SMAD7; SMAD1; SPI1; NGFR; JAG1; JUN; LIF; RARA; REL; CDKN2B; IGF1; NFKB1; ZFH3; NTF3; CLU; KEAP1; HOXA5; CEBPA; ETS1; SMAD3; BCL2; CAV3; GHR; CETP; CRX; HIF1A; XRC5; XDH; FGF23; TAL1; TP53; SFRP2; IL6; GDF5; POU3F2; DRD2; NKX2-1; NTRK3; PPP2CA; FGF4; TNF; MAP1B; NBN; STAT5B; STAT5A; RIPK2; GLI2; NDEL1; ATF1

GO:0044238	1.50E-11	5.50E-08	14791	601	5258	292	BP	primary metabolic process	PPAP2A; PCSK2; SCG5; STK16; P4HA2; HIPK2; PIK3CB; CYP2C9; CAMK2A; CAMK2B; F3; SULT1E1; OSBPL3; CNBP1; DDX41; AR; TSG101; UBE2D2; POLR1A; POLR1E; APOD; APOB; MST1; APOH; CYP27B1; SMG5; SENP2; DSP; BLM; PPARG; PPAR; PPARA; ANAPC5; ANAPC7; PPID; CSNK1A1; KHK; GPX5; TRDMT1; PDE6H; ACP6; SMAD9; ASH2L; SMAD7; SMAD1; PRKDC; TAF11; ADSSL1; IRF3; RXRA; LEPR; SRPK1; AK7; TP73; GEMIN5; ERC1; EGFR; IGF1R; RBM9; ERG; NGFR; ABAT; ACAA2; NOS1; SNCA; YARS2; HGF; TRIP13; HEXB; RBMX; B3GNT6; NFE2L1; ORC6L; RELA; WT1; LIPC; TPR; PDE8A; ADCY1; DBH; PTGES3; SCARB1; RHO; MAPK10; VLDLR; MASP1; USF1; GTF2E1; PRKG1; BMX; IGF1; AGMAT; F10; NFKB1; CSNK1E; SARDH; NSD1; WDHV1; PI4KB; TCERG1; ZFH3; FABP3; PDE11A; MLF1; USF2; SKP1; CHPT1; FANCC; HNRNPA1; CLU; UHRF1; DLST; PPAT; CDK7; DSCC1; GTF2H4; TCEB3; MSH2; MSH3; MGLL; USP7; PRSS2; CEBPA; CEBPG; CEBPD; DVL2; ETS1; SUZ12; PRKCD; PSME1; SMAD3; ABI3; CSTF2; MMP8; BCL2; PLCD3; WWP1; CAV3; SNRNP200; GHR; BRCA1; CETP; ERBB4; PRMT3; CREB1; CTSG; BRD8; ADCY5; DZ1P3; PRMT5; MASP2; KPNA2; GBA; PLCB2; HIF1A; XRC5; PRPF3; SMURF1; DAXX; SMURF2; CDC16; NONO; NT5E; XDH; RPS3A; FCN2; FOS; RAD50; TRRAP; SFPQ; PAX2; LCT; ESR1; ACAD8; CTSL1; POLE2; STK36; PAX1; FGF23; LCMT1; IL1B; HARS; RBM8A; STAT1; ZHX2; MARK3; NMNAT2; ACACB; LCAT; COMT; EIF2C2; TP53; CYP1A2; AGXT; HARS2; EIF6; MAP2K3; KLF11; NAP1L1; AMHR2; PDPK1; AADAT; AMY2B; CEBPB; PKN1; MCM7; HADHA; DUSP14; DUSP12; SQSTM1; DRD2; RDH12; C1S; DHX16; FBP2; NKX2-1; UGP2; NTRK2; NTRK3; CAPN2; GOT1; ENPP7; SNAPC5; KCTD13; PPP2CA; PPP2CB; MST1R; GSK3B; TERF1; ACSL1; PABPC1; G6PC2; ST13; MAPKAPK5; TGFA; GUCY1A3; NACA; PGM1; GYS2; POLR2H; POLR2K; POLR2J; PEX5; CDC23; TNF; BAT1; EPHA8; ACAN; EPHA3; EPHA2; ACR; RBKS; ATP5B; NCOR1; AKR1B10; CYP2B6; POLD2; NBN; SRD5A2; HNRNPC; DUSP1; SGPP1; ASL; PCMT1; TGS1; ACHE; FADS2; ADK; STAT5B; STAT5A; SREBF1; PSMB4; ADAM12; RIPK2; DERA; PAPSS1; ADRBK1; SIN3A; RAD21; DNMT3L; PLAT; ALDH6A1; GGT1; SNRPA; SNRPE; NFIC; PTPRS; PEMT; AXIN1; NEDD4L; UPF3A; ATF6
GO:0000122	1.60E-11	6.00E-08	14791	601	281	39	BP	negative regulation of transcription from RNA polymerase II promoter	HIPK2; PPARG; PPAR; PPARA; SMAD7; SPI1; RXRA; LEF1; GFI1B; RARB; RARG; WT1; IRF8; NFKB1; NSD1; ZFH3; CITED2; TAF9B; SMARCA4; CEBPA; SUZ12; SMAD3; ZFPM2; EGRI; STAT3; ZHX2; IGBP1; TP53; KLF11; NKX2-1; TAF7; TNF; NCOR1; BCOR; HEY1; GLI2; SIN3A; NFIC; TGIF1
GO:0060548	3.90E-11	1.40E-07	14791	601	383	46	BP	negative regulation of cell death	HIPK2; F3; APOH; SMAD4; BDKRB2; TP73; EGFR; IGF1R; NGFR; SNCA; HGF; SON; PEA15; RELA; WT1; IGF1; NFKB1; CITED2; CLU; TAF9B; MSH2; YWHAZ; SMAD3; MCL1; BCL2; XRC5; ESR2; ESR1; IL1B; TP53; IL6; CEBPB; SQSTM1; ITSN1; SOCS2; PPP2CB; GSK3B; HRAS; FGF4; TNFAIP3; TNF; STAT5B; STAT5A; RIPK2; SIN3A; NPM1
GO:0043066	4.60E-11	1.70E-07	14791	601	371	45	BP	negative regulation of apoptosis	HIPK2; F3; APOH; BDKRB2; TP73; EGFR; IGF1R; NGFR; SNCA; HGF; SON; PEA15; RELA; WT1; IGF1; NFKB1; CITED2; CLU; TAF9B; MSH2; YWHAZ; SMAD3; MCL1; BCL2; XRC5; ESR2; ESR1; IL1B; TP53; IL6; CEBPB; SQSTM1; ITSN1; SOCS2; PPP2CB; GSK3B; HRAS; FGF4; TNFAIP3; TNF; STAT5B; STAT5A; RIPK2; SIN3A; NPM1
GO:0006807	6.30E-11	2.30E-07	14791	601	2186	148	BP	nitrogen compound metabolic process	P4HA2; CYP2C9; DDX41; AR; POLR1A; POLR1E; SMG5; BLM; PPARA; TRDMT1; ASH2L; SMAD1; PRKDC; TAF11; ADSSL1; IRF3; SRPK1; AK7; TP73; GEMIN5; RBM9; ABAT; NOS1; SNCA; YARS2; TRIP13; HEXB; RBMX; NFE2L1; ORC6L; WT1; LIPC; TPR; PDE8A; ADCY1; DBH; PTGES3; PPOX; USF1; GTF2E1; IGF1; AGMAT; NFKB1; CSNK1E; SARDH; TCERG1; ZFH3; FABP3; PDE11A; MLF1; USF2; CHPT1; FANCC; HNRNPA1; MTHFS; UHRF1; DLST; PPAT; CDK7; DSCC1; GTF2H4; TCEB3; MSH2; MSH3; CEBPA; CEBPG; CEBPD; DVL2; ETS1; SMAD3; CSTF2; SNRNP200; GHR; BRCA1; CETP; CREB1; ADCY5; KPNA2; HIF1A; XRC5; PRPF3; NONO; NT5E; XDH; FOS; RAD50; SFPQ; PAX2; ESR1; ACAD8; POLE2; PAX1; HARS; RBM8A; STAT1; ZHX2; NMNAT2; LCAT; COMT; EIF2C2; TP53; CYP1A2; AGXT; HARS2; KLF11; NAP1L1; AADAT; CEBPB; MCM7; DRD2; DHX16; UGP2; GOT1; SNAPC5; KCTD13; PPP2CA; TERF1; PABPC1; GUCY1A3; NACA; POLR2H; POLR2K; POLR2J; BAT1; ATP5B; NCOR1; POLD2; NBN; HNRNPC; SGPP1; ASL; TGS1; ACHE; ADK; STAT5B; STAT5A; DERA; PAPSS1; SIN3A; RAD21; DNMT3L; ALDH6A1; GGT1; SNRPA; SNRPE; NFIC; PEMT; UPF3A
GO:0006351	6.60E-11	2.40E-07	14791	601	231	34	BP	transcription, DNA-dependent	AR; POLR1A; POLR1E; PPARA; ASH2L; IRF3; TRIP13; NFE2L1; USF1; NFKB1; TCERG1; ZFH3; USF2; CDK7; GTF2H4; CEBPA; CEBPD; DVL2; ETS1; CREB1; HIF1A; PAX2; ESR1; PAX1; STAT1; TP53; KLF11; CEBPB; SNAPC5; POLR2H; POLR2K; POLR2J; NCOR1; NFIC
GO:0034641	6.80E-11	2.50E-07	14791	601	2069	142	BP	cellular nitrogen compound metabolic process	CYP2C9; DDX41; AR; POLR1A; POLR1E; SMG5; BLM; PPARA; TRDMT1; ASH2L; SMAD1; PRKDC; TAF11; ADSSL1; IRF3; SRPK1; AK7; TP73; GEMIN5; RBM9; NOS1; SNCA; YARS2; TRIP13; RBMX; NFE2L1; ORC6L; WT1; LIPC; TPR; PDE8A; ADCY1; DBH; PTGES3; PPOX; USF1; GTF2E1; IGF1; AGMAT; NFKB1; CSNK1E; SARDH; TCERG1; ZFH3; FABP3; PDE11A; MLF1; USF2; CHPT1; FANCC; HNRNPA1; UHRF1; DLST; PPAT; CDK7; DSCC1; GTF2H4; TCEB3; MSH2; MSH3; CEBPA; CEBPG; CEBPD; DVL2; ETS1; SMAD3; CSTF2; SNRNP200; GHR; BRCA1; CETP; CREB1; ADCY5; KPNA2; HIF1A; XRC5; PRPF3; NONO; NT5E; XDH; FOS; RAD50; SFPQ; PAX2; ESR1; ACAD8; POLE2; PAX1; HARS; RBM8A; STAT1; ZHX2; NMNAT2; LCAT; COMT; EIF2C2; TP53; AGXT; HARS2; KLF11; NAP1L1; AADAT; CEBPB; MCM7; DRD2; DHX16; UGP2; GOT1; SNAPC5; KCTD13; PPP2CA; TERF1; PABPC1; GUCY1A3; NACA; POLR2H; POLR2K; POLR2J; BAT1; ATP5B; NCOR1; POLD2; NBN; HNRNPC; ASL; TGS1; ACHE; ADK; STAT5B; STAT5A; DERA; PAPSS1; SIN3A; RAD21; DNMT3L; ALDH6A1; GGT1; SNRPA; SNRPE; NFIC; PEMT; UPF3A

GO:0043069	7.30E-11	2.70E-07	14791	601	376	45	BP	negative regulation of programmed cell death	HIPK2; F3; APOH; BDKRB2; TP73; EGFR; IGF1R; NGFR; SNCA; HGF; SON; PEA15; RELA; WT1; IGF1; NFKB1; CITED2; CLU; TAF9B; MSH2; YWHAZ; SMAD3; MCL1; BCL2; XRCC5; ESR2; ESR1; IL1B; TP53; IL6; CEBPB; SQSTM1; ITSN1; SOCS2; PPP2CB; GSK3B; HRAS; FGF4; TNFAIP3; TNF; STAT5B; STAT5A; RIPK2; SIN3A; NPM1
GO:0032774	1.00E-10	3.90E-07	14791	601	235	34	BP	RNA biosynthetic process	AR; POLR1A; POLR1E; PPARA; ASH2L; IRF3; TRIP13; NFE2L1; USF1; NFKB1; TCERG1; ZFH3; USF2; CDK7; GTF2H4; CEBPA; CEBPD; DVL2; ETS1; CREB1; HIF1A; PAX2; ESR1; PAX1; STAT1; TP53; KLF11; CEBPB; SNAPC5; POLR2H; POLR2K; POLR2J; NCOR1; NFIC
GO:0023052	1.40E-10	5.50E-07	14791	601	2825	178	BP	signaling	PPAP2A; SCG5; HIPK2; L1CAM; PIK3CB; ARHGEF12; AKAP3; AR; ITGA3; RIT2; RAB6B; FZD10; BLM; COL4A3; GDI1; CSNK1A1; ITGAV; SMAD9; RALBP1; SMAD4; TLE2; SMAD7; SMAD1; AKAP12; IRF3; RXRA; LEPR; LEF1; SRPK1; BDKRB2; APBA2; TP73; EGFR; IGF1R; RBM9; PGR; JAG1; SNCA; JUN; FZD8; HGF; WNT16; LIF; AVPR1A; RARA; DAB1; RARG; WNT10A; SAG; RAB1F; RELA; HOMER1; ADCY1; DBH; PTGES3; GNG2; RHO; MAPK10; CNTN1; TIRAP; BMX; IGF1; KCNK3; SST; RALA; PI4KB; ADAP1; NTF3; GRIK5; HOXA5; CDK7; F2RL3; LPAR1; MSH2; AGRP; CEBPA; ARHGAP1; DVL2; VIPR1; PRKCD; SMAD3; PLCD3; GHR; MAGI3; DLGAP4; TRPV4; BRCA1; ERBB4; CREB1; BRD8; BRD7; ADCY5; GNAO1; SMURF1; DAXX; SMURF2; FOS; ESR2; TOLLIP; ESR1; FGF22; FGF23; SYN1; CCR4; IL1B; STAT3; STAT1; IFNB1; PDE7B; EFNA5; EFNA4; TP53; SFRP2; WNT2; IL6; AP3S1; RHEB; TEAD1; CAMLG; WASF2; AMHR2; GDF5; PDPK1; SQSTM1; DRD2; WNT9B; HTR1A; NKX2-1; ITSN1; NTRK2; NTRK3; GABRR2; RAP1A; SOCS2; PPP2CA; MST1R; GSK3B; STMN1; POU2F1; VDACL1; GUCY1A3; HTR1B; MED30; CHRM2; HRAS; FGF5; FGF4; TAF7; SDC1; MPL; TNF; EPHA8; EPHA3; EPHA2; SDCBP; GNRHR; NCAM1; FZD6; CACNB2; NBN; SRD5A2; FGF11; HEY1; SOS1; GDF9; STAT5B; STAT5A; RIPK2; GRIN2C; DGKQ; ADRBK1; GLI2; FSHR; PLAT; AXIN1; HOXC11; ATF6; IGF2R
GO:0044237	1.60E-10	6.00E-07	14791	601	4963	275	BP	cellular metabolic process	PPAP2A; STK16; P4HA2; HIPK2; PIK3CB; CYP2C9; CAMK2A; CAMK2B; SULT1E1; DDX41; AR; TSG101; UBE2D2; POLR1A; POLR1E; APOB; APOH; CYP27B1; SMG5; SENP2; DSP; BLM; PPARG; PPARC; PPARA; ANAPC5; ANAPC7; PPID; CSNK1A1; KHK; TRDMT1; PDE6H; SMAD9; ASH2L; SMAD7; SMAD1; PRKDC; TAF11; ADSSL1; IRF3; LEPR; SRPK1; AK7; TP73; GEMIN5; ERC1; EGFR; IGF1R; RBM9; ERG; ABAT; ACAA2; NOS1; SNCA; YARS2; HGF; TRIP13; HEXB; CYB5A; RBMX; SFTPD; AVPR1A; B3GNT6; NFE2L1; ORC6L; WT1; LIPC; LPO; TPR; PDE8A; ADCY1; DBH; PTGES3; SCARB1; RHO; MAPK10; PPOX; USF1; GTF2E1; PRKGI; BMX; IGF1; AGMAT; NFKB1; CSNK1E; SARDH; NSD1; WDYHV1; EPHX2; PI4KB; TCERG1; ZFH3; FABP3; PDE11A; MLF1; USF2; SKP1; CHPT1; FANCC; HNRNP1A; MTHFS; UHRF1; DLST; PPAT; CDK7; DSCC1; GTF2H4; TCEB3; MSH2; MSH3; USP7; CEBPA; CEBPG; CEBPD; DVL2; ETS1; SUZ12; PRKCD; PSME1; SMAD3; ABI3; CSTF2; BCL2; WWP1; CAV3; SNRNP200; GHR; BRCA1; CETP; ERBB4; PRMT3; CREB1; BRD8; ADCY5; DZIP3; PRMT5; KPNA2; GBA; PLCB2; HIF1A; XRCC5; PRPF3; SMURF1; DAXX; SMURF2; CDC16; NONO; NTF5; XDH; RPS3A; FOS; RAD50; TRRAP; SFPQ; PAX2; TOLLIP; ESR1; ACAD8; POLE2; STK36; PAX1; FGF23; LCMT1; IL1B; HARS; RBM8A; STAT1; ZHX2; MARK3; MNAT2; ACACB; LCAT; COMT; EIF2C2; TP53; CYP1A2; AGXT; HARS2; EIF6; MAP2K3; RUNX1T1; CAMLG; KLF11; NAP1L1; AMHR2; PDPK1; AADAT; CEBPB; PKN1; MCM7; HADHA; DUSP14; DUSP12; SQSTM1; DRD2; PON3; RDH12; PICALM; ALPL; ISL1; DHX16; FBP2; NKX2-1; UGP2; NTRK2; NTRK3; GOT1; ENPP7; SNAPC5; KCTD13; PPP2CA; EIF1D; PPP2CB; MST1R; GSK3B; TERF1; ACSL1; PABPC1; G6PC2; ST13; MAPKAPK5; TGFA; GUCY1A3; NACA; PGM1; GYS2; POLR2H; POLR2K; POLR2J; PEX5; CDC23; TNF; BAT1; EPHA8; EPHA3; EPHA2; RBK5; ATP5B; NCOR1; AKR1B10; CYP2B6; POLD2; NBN; SRD5A2; HNRNPC; DUSP1; SGPP1; ASL; PCMT1; TGS1; ACHE; FADS2; ADK; STAT5B; STAT5A; PSMB4; RIPK2; DERA; PAPSS1; ADRBK1; SIN3A; RAD21; DNMT3L; PLAT; ALDH6A1; GGT1; SNRPA; SNRPE; NFIC; INPP1; PTPRS; PEMT; NEDD4L; UPF3A; ATF6
GO:0050790	2.80E-10	1.00E-06	14791	601	898	77	BP	regulation of catalytic activity	PPAP2A; PIK3CB; F3; AR; APOH; CYP27B1; BLM; PPARG; COL4A3; GDI1; ANAPC5; ANAPC7; PDE6H; RALBP1; SMAD7; TSC1; LEPR; TP73; EGFR; SNCA; HGF; AVPR1A; DAB1; CDKN2B; HOMER1; ADCY1; SCARB1; VLDLR; NFKB1; SKP1; ADAP1; CDK7; F2RL3; LPAR1; MSH2; MSH3; PSME1; SMAD3; BCL2; CAV3; GHR; ADCY5; GNAO1; PLCB2; HIF1A; DAXX; CDC16; RAD50; FGF23; IL1B; STAT1; IFNB1; IGBP1; TP53; ASAP1; ASAP2; MAP2K3; PDPK1; PKN1; DUSP12; DRD2; HTR1A; NTRK2; PPP2CA; TERF1; TGFA; CHRM2; TAF7; CDC23; TNF; ACR; NBN; PSMB4; DGKQ; FSHR; NDEL1; NPM1
GO:0035466	2.80E-10	1.00E-06	14791	601	881	76	BP	regulation of signaling pathway	HIPK2; L1CAM; PIK3CB; ARHGEF12; F3; AR; HHIP; CYP27B1; SENP2; PPARC; SIGIRR; PDE6H; SMAD4; TLE1; SMAD7; AKAP12; REL; TSC1; LEPR; LEF1; TP73; EGFR; IGF1R; NGFR; JAG1; SNCA; HGF; LIF; RELA; CDKN2B; IGF1; F10; CITED2; LPAR1; PRKCD; SMAD3; CAV3; GHR; HIF1A; SMURF1; DAXX; SMURF2; RPH3AL; ESR2; ESR1; FGF23; IL1B; ING2; IGBP1; TP53; SFRP2; WNT2; IL6; PKN1; SQSTM1; DRD2; NKX2-1; ITSN1; ITSN2; PPP2CA; EIF1D; PPP2CB; TGFA; HRAS; FGF4; TNFAIP3; TNF; NCAM1; NCOR1; SOS1; RIPK2; ADRBK1; GLI2; TRAF5; NPM1; AXIN1
GO:0030154	3.90E-10	1.40E-06	14791	601	1061	86	BP	cell differentiation	L1CAM; SP1; SP3; AR; TSG101; ZIC2; DSP; BLM; PPARG; PPARC; PRKDC; TSC1; RXRA; SRPK1; NGFR; JAG1; RTN1; JUN; MLPH; LIF; AVPR1A; COL11A2; CATSPER1; DAB1; RARB; CDKN2B; WT1; IGF1; IRF8; MLF1; CADM1; NTF3; CITED2; HOXA5; HOXA1; MSH2; CEBPA; CEBPG; CEBPE; SMAD3; MCL1; CTNNA2; BCL2; CAV3; ZFPM2; BMP8A; XRCC5; SMURF1; EGR1; RPS3A; PAX6; NFKB2; PAX2; PAX8; PAX1; FGF22; FGF23; STAT3; TAL1; EFNA5; LGALS3; TP53; SFRP2; POU3F2; CEBPB; SQSTM1; CIS; NKX2-1; NTRK2; NTRK3; BMP5; STMN1; ODF1; HRAS; FGF5; FGF4; PEX5; EPHA2; SRD5A2; TACC3; STAT5B; STAT5A; GLI2; ALDH6A1; NDEL1; MYO7A

GO:0010646	5.10E-10	1.80E-06	14791	601	1031	84	BP	regulation of cell communication	SCG5; HIPK2; LICAM; PIK3CB; ARHGEF12; F3; AR; HHIP; CYP27B1; PPARD; SIGIRR; PDE6H; SMAD4; TLE1; SMAD7; AKAP12; REL; TSC1; LEPR; TP73; EGFR; IGF1R; NGFR; JAG1; SNCA; HGF; RGS10; LIF; AVPR1A; REL; CDKN2B; IGF1; F10; NTF3; CITED2; LPAR1; PRKCD; CAV3; GHR; ERBB4; CREB1; HIF1A; SMURF1; DAXX; EGRI; RPH3AL; ESR2; ESR1; FGF23; IL1B; ING2; IGBP1; TP53; SFRP2; WNT2; IL6; BCAN; PKN1; SQSTM1; DRD2; NKX2-1; ITSN1; ITSN2; SYT9; SOCS2; PPP2CA; EEF1D; PPP2CB; TGFA; HTR1B; HRAS; FGF4; TNFAIP3; TNF; NCAM1; NCOR1; MAP1B; ACHE; SOS1; RIPK2; ADRBK1; TRAF5; PLAT; AXIN1
GO:0008285	9.00E-10	3.30E-06	14791	601	377	43	BP	negative regulation of cell proliferation	PPAP2A; AR; TSG101; BNIPL; APOH; CYP27B1; PPARG; PPARD; COL4A3; SMAD4; SMAD1; TSC1; RXRA; BDKRB2; JUN; SFTPD; LIF; RARB; RARG; CDKN2B; WT1; IGF1; IGFBP6; SST; FABP3; CEBPA; ETS1; SMAD3; BCL2; ESR2; IL1B; IFN1; COMT; TP53; IL6; KLF11; DRD2; ENPP7; HRAS; TNF; GNRHR; NPM1; PENT
GO:0008152	1.00E-09	3.80E-06	14791	601	6033	317	BP	metabolic process	PPAP2A; PCSK2; SCG5; STK16; P4HA2; HIPK2; PIK3CB; CYP2C9; CAMK2A; CAMK2B; F3; SULT1E1; OSBPL3; CNDP1; DDX41; AR; TSG101; UBE2D2; POLR1A; POLR1E; APOD; APOB; MST1; APOH; CYP27B1; SMG5; UCK1; SENP2; DSP; BLM; PPARG; PPARD; PPARA; ANAPC5; ANAPC7; PPID; CSNK1A1; KHK; GPX5; TRDMT1; PDE6H; ACP6; SMAD9; ASH2L; SMAD7; SMAD1; PRKDC; TAF11; ADSSL1; IRF3; RXRA; LEPR; SRPK1; F5; AK7; TP73; GEMIN5; ERC1; EGFR; IGF1R; RBM9; ERG; NGFR; ABAT; ACAA2; NOS1; SNCA; YARS2; HGF; TRIP13; HEXB; CYB5A; RBMX; SFTPD; AVPR1A; GSTA4; B3GNT6; NFE2L1; ORC6L; REL; WT1; LIPC; LPO; TPR; PDE8A; ADCY1; DBH; PTGES3; SCARB1; RHO; MAPK10; VLDLR; MASP1; PPOX; USF1; GTF2E1; PRKG1; BMX; IGF1; AGMAT; F10; NFKB1; CSNK1E; SARDH; NSD1; WDHV1; EPHX2; PI4KB; TCERG1; ZFH3; FABP3; PGAM1; PDE11A; MLF1; USF2; SKP1; CHPT1; FANCC; HNRNP1; MTHFS; CLU; UHRF1; DLST; PPAT; CDK7; DSCC1; GTF2H4; TCEB3; MSH2; MSH3; MGLL; USP7; PRSS2; CEBPA; CEBPG; CEBPE; CEBPD; DVL2; ETS1; SUZ12; PRKCD; PSM1; SMAD3; ABI3; CSTF2; MMP8; BCL2; PLCD3; WWP1; CAV3; SNRNP200; GHR; CYP4F12; BRCA1; CETP; ERBB4; PRMT3; CREB1; CTSG; BRD8; ADCY5; DZIP3; PRMT5; MASP2; KPNA2; GBA; PLCB2; HIF1A; XRCC5; PRPF3; SMURF1; DAXX; SMURF2; CDC16; NONO; NT5E; XDH; RPS3A; FCN2; FOS; RAD50; TRRAP; SFPQ; PAX2; LCT; TOLLIP; ESRI; ACAD8; CTS1; POLE2; STK36; PAX1; FGF23; LCMT1; IL1B; HARS; RBMSA; STAT1; ZHX2; MARK3; NMNAT2; ACACB; LCAT; COMT; EIF2C2; TP53; CYP1A2; AGXT; HARS2; EIF6; MAP2K3; RUNX1T1; CAMLG; KLF11; NAP1L1; AMHR2; PDPK1; AADAT; AMY2B; CEBPB; PKN1; MCM7; HADHA; DUSP14; DUSP12; SQSTM1; DRD2; PON3; RDH14; RDH12; CIS; PICCALM; ALPL; ISL1; DHX16; FBP2; NKX2-1; UGP2; NTRK2; NTRK3; MICAL1; CAPN2; GOT1; ENPP7; SNAPC5; KCTD13; PPP2CA; EEF1D; PPP2CB; MST1R; GSK3B; TERF1; ACSL1; PABPC1; G6PC2; ST13; MAPKAPK5; TGFA; GUCY1A3; NACA; PG1; GYS2; POLR2H; POLR2K; POLR2J; PEX5; CDC23; TNF; BAT1; EPHA8; ACAN; EPHA3; EPHA2; ACR; RBKS; ATP5B; NCOR1; AKR1B10; CYP2B6; POLD2; NBN; SRD5A2; HNRNPC; DUSP1; SGPP1; ASL; PCMT1; CRHBP; TGS1; ACHE; FADS2; ADK; STAT5B; STAT5A; SREBF1; PSMB4; ADAM12; RIPK2; DERA; PAPSS1; ADRBK1; SIN3A; RAD21; DNMT3L; PLAT; ALDH6A1; GGT1; SNRPA; SNRPE; NFIC; INPP1; PTPRS; PENT; AXIN1; NEDD4L; UPF3A; ATF6
GO:0003006	1.00E-09	4.00E-06	14791	601	243	33	BP	reproductive developmental process	AR; CYP27B1; PPARD; SMAD9; PRKDC; RXRA; IGF1R; PGR; TRIP13; HOXB13; LIF; RARG; WT1; IGF1; EPOR; FANCC; CITED2; MSH2; BCL2; ESR2; ESR1; AMHR2; NKX2-1; BMP5; SDC1; SHBG; SRD5A2; GDF9; STAT5B; STAT5A; GLI2; FSHR; AXIN1
GO:0022414	1.10E-09	4.00E-06	14791	601	771	68	BP	reproductive process	PPAP2A; HIPK2; SP1; SP3; SULT1E1; AKAP3; AR; TSG101; APOB; CYP27B1; PPARD; SMAD9; SMAD1; PRKDC; RXRA; LEPR; EGFR; IGF1R; ABAT; PGR; TRIP13; HOXB13; HEXB; LIF; AVPR1A; CATSPER1; RARG; WT1; DBH; IGF1; EPOR; USF2; FANCC; CADM1; CITED2; PPAT; MSH2; SMAD3; BCL2; CREB1; XRCC5; XDH; FOS; ESR2; ESR1; IL1B; COMT; ELSBPB1; AMHR2; NKX2-1; BMP5; MST1R; ODF1; SDC1; SHBG; BAT1; CLDN11; ACR; SRD5A2; CRHBP; GDF9; STAT5B; STAT5A; GLI2; FSHR; DNMT3L; AXIN1; IGF2R
GO:0006350	1.40E-09	5.20E-06	14791	601	285	36	BP	transcription	AR; POLR1A; POLR1E; PPARA; ASH2L; IRF3; TRIP13; NFE2L1; USF1; NFKB1; TCERG1; ZFH3; MLF1; USF2; CDK7; GTF2H4; CEBPA; CEBPD; DVL2; ETS1; CREB1; HIF1A; PAX2; ESRI; PAX1; STAT1; TP53; KLF11; CEBPB; SNAPC5; NACA; POLR2H; POLR2K; POLR2J; NCOR1; NFIC
GO:0009887	1.80E-09	6.80E-06	14791	601	343	40	BP	organ morphogenesis	SP1; SP3; HHIP; APOH; HOXB8; PPARG; TLE2; TLE1; LEF1; IGF1R; JAG1; HGF; LIF; COL11A2; RARB; RARG; REL; GMN; HOXA5; PPAT; CEBPA; SMAD3; CTNNA2; BCL2; ERBB4; CRX; PAX6; YY1; TFAP2A; NKX2-1; FLI1; HRAS; FGF4; SDC1; TNF; BCOR; HEY1; GLI2; MYO7A; IGF2R
GO:0051704	1.80E-09	6.90E-06	14791	601	714	64	BP	multi-organism process	HIPK2; DLG1; IFNA10; SP1; SULT1E1; TSG101; MX1; APOB; ITGAV; TAF11; IRF3; RXRA; LEPR; LTF; SRPK1; IFNA21; ABAT; DEFA1; JUN; AVPR1A; REL; SCARB1; GTF2E1; IRF8; RALA; HNRNP1; CLU; USP7; CEBPA; CEBPE; CAMP; SMAD3; BCL2; WWP1; MAGI3; CREB1; CTSG; KPNA2; DAXX; FOS; CCR4; IL1B; STAT3; STAT1; IFN1; COMT; TP53; IL6; MST1R; STMN1; VDACL1; NACA; CHR2; HRAS; TNF; BAT1; FBLN1; CRHBP; STAT5B; STAT5A; PSMB4; RIPK2; NPM1; NEDD4L
GO:0043434	2.20E-09	8.20E-06	14791	601	187	28	BP	response to peptide hormone stimulus	AR; PPARG; PPARA; KHK; PRKDC; TSC1; RXRA; IGF1R; REL; VLDLR; USF1; FABP3; PPAT; AGRP; BCL2; GHR; EGRI; STAT3; STAT1; AP3S1; PDPK1; GOT1; SOCS2; MAP1B; SRD5A2; STAT5B; STAT5A; PLAT
GO:0032582	2.90E-09	1.00E-05	14791	601	81	18	BP	negative regulation of gene-specific transcription	PPARG; PPARA; SMAD7; RXRA; RARA; REL; WT1; NFKB1; TAF9B; SMARCA4; SMAD3; IGBP1; TAF7; TNF; NCOR1; BCOR; HEY1; NFIC

GO:0023033	4.50E-09	1.60E-05	14791	601	2547	159	BP	signaling pathway	PPAP2A; SCG5; HIPK2; L1CAM; PIK3CB; ARHGEF12; AKAP3; AR; ITGA3; RIT2; RAB6B; FZD10; BLM; COL4A3; GDI1; CSNK1A1; ITGAV; SMAD9; RALBP1; SMAD4; TLE2; SMAD7; SMAD1; AKAP12; IRF3; RXRA; LEPR; LEF1; SRPK1; BDKRB2; TP73; EGFR; IGF1R; RBM9; PGR; JAG1; JUN; FZD8; HGF; WNT16; LIF; AVPR1A; RARA; DAB1; RARG; WNT10A; SAG; RAB1F; RELA; HOMER1; ADCY1; PTGES3; GNG2; RHO; MAPK10; CNTN1; TIRAP; BMX; IGF1; SST; RALA; PI4KB; ADAP1; CDK7; F2RL3; LPAR1; MSH2; AGRP; CEBPA; ARHGAP1; DVL2; VIPR1; PRKCD; SMAD3; PLCD3; GHR; MAG13; TRPV4; BRCA1; ERBB4; CREB1; BRD8; BRD7; ADCY5; GNAO1; SMURF1; DAXX; SMURF2; FOS; ESR2; TOLLIP; ESR1; FGF22; FGF23; CCR4; IL1B; STAT3; STAT1; IFNB1; TP53; SFRP2; WNT2; IL6; AP3S1; RHEB; TEAD1; CAMLG; WASF2; AMHR2; GDF5; PDPK1; SQSTM1; DRD2; WNT9B; HTR1A; ITSN1; NTRK2; NTRK3; GABRR2; RAPIA; SOCS2; PPP2CA; MST1R; GSK3B; STMN1; GUCY1A3; HTR1B; MED30; CHRM2; HRAS; FGF5; FGF4; TAF7; SDC1; MPL; TNF; EPHA8; EPHA3; EPHA2; SDCBP; GNRHR; NCAM1; FZD6; NBN; HEY1; SOS1; GDF9; STAT5B; STAT5A; RIPK2; GRIN2C; DGKQ; ADRBK1; GLI2; FSHR; PLAT; AXIN1; ATF6; IGF2R
GO:0070887	6.20E-09	2.30E-05	14791	601	329	38	BP	cellular response to chemical stimulus	F3; PPARG; PRKDC; RXRA; IGF1R; SNCA; SFTPD; AVPR1A; RARA; CDKN2B; LPO; ADCY1; GNG2; VLDLR; USF1; KCNK3; USF2; FANCC; PPAT; AGRP; CAMP; GHR; BRCA1; ADCY5; HIF1A; EGRI; FOS; IL1B; STAT3; STAT1; IL6; AP3S1; PDPK1; GOT1; SOCS2; DUSP1; STAT5B; ATF6
GO:0009991	7.00E-09	2.60E-05	14791	601	222	30	BP	response to extracellular stimulus	CYP27B1; PPARG; RXRA; LEPR; IGF1R; JUN; AVPR1A; RARA; RARG; RELA; CDKN2B; VLDLR; USF1; SST; USF2; CEBPA; BCL2; GHR; FOS; LCT; IL1B; STAT1; TP53; SFRP2; ALPL; MAP1B; DUSP1; SREBF1; PEMT; IGF2R
GO:0050896	8.00E-09	2.90E-05	14791	601	3619	208	BP	response to stimulus	HIPK2; PIK3CB; IFNA10; F3; AR; MX1; APOB; CYP27B1; HOXB8; DSP; BLM; PPARG; PPARC; COL4A3; PPARA; KHK; GPX5; SIGIRR; TRDMT1; PDE6H; SMAD9; RALBP1; ASH2L; SMAD4; SMAD7; SMAD1; PRKDC; TSC1; IRF3; RXRA; LEPR; LTF; LEF1; BDKRB2; APBA2; TP73; IFNA21; EGFR; IGF1R; NGFR; ABAT; DEFA1; NOS1; CYR61; SNCA; JUN; TRIP13; HOXB13; HEXB; SFTPD; LIF; AVPR1A; RARA; RARG; NFE2L1; SAG; RELA; FGB; CDKN2B; LPO; ADCY1; DBH; SCARB1; GNG2; RHO; MAPK10; VLDLR; MASP1; USF1; TIRAP; KCNK3; SST; IRF8; NFKB1; CSNK1E; RALA; EPHX2; IL1RAP; FABP3; USF2; FANCC; CADM1; CITED2; CLU; UHRF1; PPAT; CNGA4; CDK7; F2RL3; TAF9B; GTF2H4; MSH2; MSH3; MGLL; AGRP; YWHAZ; CEBPA; CEBPG; CEBPE; CAMP; ETS1; VIPR1; PRKCD; SMAD3; MCL1; BCL2; GHR; CACNA1F; TRPV4; BRCA1; ERBB4; CREB1; CTSG; ADCY5; MASP2; GNAO1; CRX; PLCB2; HIF1A; XRCC5; PRPF3; NONO; EGR1; FCN2; RIC8A; FOS; RAD50; SFPQ; PAX6; TP53INP1; NFKB2; KIR3DL2; LCT; ESR2; TOLLIP; ESR1; POLE2; CCR4; IL1B; STAT3; STAT1; IFNB1; IGBP1; LCAT; COMT; TP53; SFRP2; AGXT; IL6; AP3S1; CAMLG; PDPK1; HSPB3; CEBPB; PKN1; MCM7; HADHA; VWF; SQSTM1; DRD2; PON3; RDH12; C1S; HTR1A; ALPL; NKX2-1; CAPN2; GOT1; SOCS2; PPP2CA; PPP2CB; MST1R; GSK3B; STMN1; HLA-G; VDACC1; HTR1B; CHRM2; GYS2; HRAS; SDC1; TNF; CLDN19; EPHA3; ACR; MAP1B; NBN; SRD5A2; DUSP1; CRHBP; ACHE; TACC3; STAT5B; STAT5A; SREBF1; RIPK2; GRIN2C; DGKQ; ADRBK1; RAD21; PLAT; NPM1; PEMT; ATF1; NEDD4L; ATF6; MYO7A; IGF2R
GO:0007167	9.60E-09	3.50E-05	14791	601	320	37	BP	enzyme linked receptor protein signaling pathway	AKAP3; SMAD9; SMAD4; SMAD7; SMAD1; LEF1; BDKRB2; EGFR; IGF1R; JUN; HGF; SMAD3; GHR; ERBB4; CREB1; SMURF1; SMURF2; FOS; FGF22; FGF23; AP3S1; CAMLG; AMHR2; GDF5; NTRK2; NTRK3; SOCS2; MST1R; FGF5; FGF4; EPHA8; EPHA3; EPHA2; SOS1; GDF9; PLAT
GO:0010552	1.00E-08	3.70E-05	14791	601	97	19	BP	positive regulation of gene-specific transcription from RNA polymerase II promoter	AR; PPARG; PRKDC; RXRA; LIF; USF1; IGF1; USF2; CITED2; SMARCA4; CEBPA; ETS1; SMAD3; BRCA1; CREB1; IL1B; TP53; NKX2-1; NFIC
GO:0006366	1.00E-08	3.90E-05	14791	601	188	27	BP	transcription from RNA polymerase II promoter	PPARA; ASH2L; IRF3; TRIP13; NFE2L1; USF1; NFKB1; TCERG1; ZFXH3; CDK7; GTF2H4; CEBPA; CEBPD; DVL2; ETS1; HIF1A; PAX2; PAX1; STAT1; KLF11; CEBPB; SNAPC5; POLR2H; POLR2K; POLR2J; NCOR1; NFIC
GO:0032501	1.10E-08	4.10E-05	14791	601	2706	165	BP	multicellular organismal process	HIPK2; L1CAM; SP1; SP3; F3; DDX41; WHSC2; AR; FZD10; APOB; MST1; APOH; ZIC2; HOXB8; HOXB9; PPARC; COL4A3; KCNH2; PDE6H; SMAD4; TLE1; SMAD1; REL; LEPR; BDKRB2; F5; APBA2; TP73; ERC1; EGFR; ERG; NGFR; ABAT; GF11B; PGR; JAG1; NOS1; SNCA; JUN; FZD8; HOXB13; HEXB; WNT16; SFTPD; LIF; AVPR1A; COL11A2; CATSPER1; DAB1; WNT10A; SAG; RELA; WT1; LIPC; HOMER1; ADCY1; DBH; SCARB1; RHO; VLDLR; PROS1; IGF1; F10; SST; MLF1; USF2; CADM1; CITED2; HOXA5; PPAT; CNGA4; HOXA1; F2RL3; MSH2; AGRP; PRSS2; ZNF7; DVL2; VIPR1; PRKCD; MCL1; CTNNA2; MMP8; BCL2; GHR; CACNA1F; BMP8A; CREB1; ADCY5; GNAO1; CRX; HIF1A; PRPF3; EGR1; XDH; RIC8A; FOS; PAX6; PAX2; PAX8; ESR2; ESR1; IL1B; STAT3; STAT1; TAL1; EFNAA5; COMT; TP53; SFRP2; WNT2; AMY2B; VWF; DRD2; WNT9B; RDH12; KCNE2; KCNE1; ISL1; HBB; NKX2-1; NTRK2; NTRK3; GABRR2; FLI1; MST1R; ACSL1; STMN1; VDACC1; PLXNB3; GUCY1A3; ODF1; HRAS; PEX5; TNF; CLDN11; CLDN19; EPHA3; EPHA2; ACR; GNRHR; AKR1B10; FZD6; CACNB2; NBN; CRHBP; HEY1; GDF9; STAT5B; STAT5A; GRIN2C; ADRBK1; GLI2; FSHR; DNMT3L; PLAT; NDEL1; DACH1; AXIN1; HOXC11; NEDD4L; TGIF1; DNMT1; MYO7A; IGF2R
GO:0009611	1.10E-08	4.20E-05	14791	601	380	41	BP	response to wounding	F3; DSP; PPARC; PPARA; SIGIRR; SMAD1; RXRA; BDKRB2; TP73; NGFR; HOXB13; NFE2L1; RELA; SCARB1; TIRAP; NFKB1; EPHX2; IL1RAP; CLU; F2RL3; MGLL; CEBPA; SMAD3; BCL2; FOS; PAX6; TOLLIP; CCR4; IL1B; STAT3; IL6; CEBPB; VWF; SDC1; TNF; EPHA3; MAP1B; ACHE; STAT5B; RIPK2; GRIN2C

GO:0006139	1.50E-08	5.70E-05	14791	601	1776	119	BP	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	DDX41; AR; POLR1A; POLR1E; SMG5; BLM; PPARA; TRDMT1; ASH2L; SMAD1; PRKDC; TAF11; ADSSL1; IRF3; SRPK1; AK7; TP73; GEMIN5; RBM9; YARS2; TRIP13; RBMX; NFE2L1; ORC6L; WT1; TPR; PDE8A; ADCY1; PTGES3; USF1; GTF2E1; IGF1; NFKB1; CSNK1E; TCERG1; ZFXH3; PDE11A; MLF1; USF2; FANCC; HNRNP1A; UHRF1; DLST; PPAT; CDK7; DSCC1; GTF2H4; TCEB3; MSH2; MSH3; CEBPA; CEBPG; CEBPD; DVL2; ETS1; SMAD3; CSTF2; SNRNP200; BRCA1; CREB1; ADCY5; KPNA2; HIF1A; XRCC5; PRPF3; NONO; NT5E; XDH; FOS; RAD50; SFPQ; PAX2; ESR1; POLE2; PAX1; HARS; RBM8A; STAT1; ZHX2; MNAT2; EIF2C2; TP53; HARS2; KLF11; NAP1L1; CEBPB; MCM7; DHX16; UGP2; SNAPC5; KCTD13; PPP2CA; TERF1; PABPC1; GUCY1A3; NACA; POLR2H; POLR2K; POLR2J; BAT1; ATP5B; NCOR1; POLD2; NBN; HNRNPC; TGS1; ACHE; ADK; DERA; PAPSS1; SIN3A; RAD21; DNMT3L; ALDH6A1; SNRPA; SNRPE; NFIC; PEMT; UPF3A
GO:0090304	1.80E-08	6.80E-05	14791	601	1431	101	BP	nucleic acid metabolic process	DDX41; AR; POLR1A; POLR1E; SMG5; BLM; PPARA; TRDMT1; ASH2L; SMAD1; PRKDC; TAF11; IRF3; SRPK1; TP73; GEMIN5; RBM9; YARS2; TRIP13; RBMX; NFE2L1; ORC6L; WT1; TPR; PTGES3; USF1; GTF2E1; IGF1; NFKB1; CSNK1E; TCERG1; ZFXH3; MLF1; USF2; FANCC; HNRNP1A; UHRF1; CDK7; DSCC1; GTF2H4; TCEB3; MSH2; MSH3; CEBPA; CEBPG; CEBPD; DVL2; ETS1; SMAD3; CSTF2; SNRNP200; BRCA1; CREB1; KPNA2; HIF1A; XRCC5; PRPF3; NONO; NT5E; FOS; RAD50; SFPQ; PAX2; ESR1; POLE2; PAX1; HARS; RBM8A; STAT1; ZHX2; EIF2C2; TP53; HARS2; KLF11; NAP1L1; CEBPB; MCM7; DHX16; SNAPC5; KCTD13; PPP2CA; TERF1; PABPC1; NACA; POLR2H; POLR2K; POLR2J; BAT1; NCOR1; POLD2; NBN; HNRNPC; TGS1; ACHE; SIN3A; RAD21; DNMT3L; SNRPA; SNRPE; NFIC; UPF3A
GO:0051716	2.10E-08	8.00E-05	14791	601	847	69	BP	cellular response to stimulus	HIPK2; F3; BLM; PPARG; PRKDC; RXRA; LEPR; TP73; IGF1R; SNCA; JUN; TRIP13; SFTPD; AVPR1A; RARA; SAG; CDKN2B; LPO; ADCY1; GNG2; RHO; MAPK10; VLDLR; USF1; KCNK3; CSNK1E; USF2; FANCC; UHRF1; PPAT; CDK7; GTF2H4; MSH2; MSH3; AGRP; CAMP; BCL2; GHR; TRPV4; BRCA1; ADCY5; HIF1A; XRCC5; NONO; EGFR; FOS; RAD50; SFPQ; POLE2; IL1B; STAT3; STAT1; TP53; SFRP2; IL6; AP3S1; PDPK1; MCM7; GOT1; SOCS2; GSK3B; MAP1B; NBN; DUSP1; STAT5B; SREBF1; RIPK2; RAD21; ATF6
GO:0032868	2.10E-08	8.10E-05	14791	601	123	21	BP	response to insulin stimulus	AR; PPARG; PPARA; KHK; PRKDC; TSC1; RXRA; IGF1R; RELA; VLDLR; USF1; FABP3; PPAT; AGRP; BCL2; GHR; EGFR; STAT1; AP3S1; PDPK1; GOT1
GO:0042592	2.40E-08	9.20E-05	14791	601	678	59	BP	homeostatic process	PIK3CB; SV2A; JPH2; APOB; CYP27B1; BLM; PPARG; KCNH2; SMAD1; PRKDC; LTF; BDKRB2; SNCA; JUN; HEXB; SFTPD; AVPR1A; COL11A2; LIPC; DBH; PTGES3; SCARB1; USF1; IGF1; KCNK3; EPOR; EPHX2; USF2; FANCC; LPAR1; MCL1; BCL2; CAV3; CACNA1F; TRPV4; CETP; ERBB4; HIF1A; XRCC5; RPH3AL; RAD50; FGF23; CCR4; IL1B; STAT3; LCAT; DRD2; KCNE1; GOT1; TERF1; SLC4A1; EPHA3; ATP5B; NBN; STAT5B; STAT5A; GRIN2C; NPM1; NEDD4L
GO:0023046	2.50E-08	9.60E-05	14791	601	2569	157	BP	signaling process	HIPK2; DLG1; PIK3CB; CAMK2B; AKAP8; AR; RIT2; RAB6B; MX1; FZD10; GTF2I; BLM; PPARG; GDI1; CSNK1A1; KCNH2; SIGIRR; RALBP1; SMAD4; TLE2; TLE1; SMAD1; AKAP12; IRF3; LEPR; SRPK1; PDE10A; BDKRB2; EGFR; IGF1R; ERG; NGFR; PPF1A1; PDE1A; PGR; RTN1; JUN; FZD8; ANK3; AVPR1A; RARA; DAB1; RARB; SAG; RAB1F; RELA; FGB; CDKN2B; HOMER1; TPR; PDE8A; ADCY1; PTGES3; GNG2; RHO; MAPK10; VLDLR; TIRAP; PRKG1; BMX; IGF1; IGFBP6; EPOR; NFKB1; CSNK1E; RALA; PI4KB; IL1RAP; PDE11A; NTF3; F2RL3; LPAR1; MSH2; ITGB3BP; YWHAZ; CEBPA; ARHGAP1; VIPR1; PRKCD; PLCD3; WWP1; GHR; MAGI2; TRPV4; BRCA1; ERBB4; CREB1; BRD8; ADCY5; GNAO1; PLCB2; HIF1A; FCN2; FOS; TRRAP; NFKB2; ESR2; TOLLIP; ESR1; SYN1; CCR4; IL1B; STAT3; STAT1; PDE7B; ING2; IGBP1; TP53; IL6; RHEB; MAP2K3; TEAD1; CAMLG; WASF2; AMHR2; PKN1; TP53BP2; DRD2; HTR1A; ITSN1; MICALL1; GABRR2; RAPIA; SRGAP2; SOCS2; PPP2CA; MST1R; TERF1; STMN1; MAPKAPK5; PLXNB3; HTR1B; CHRM2; HRAS; FGF4; TNF; EPHA3; EPHA2; SDCBP; GNRHR; FZD6; NBN; FGF11; CRHBP; SOS1; IGFALS; STAT5B; STAT5A; RIPK2; DGKQ; ADRBK1; FSHR; TRAF5; NPM1; INPP1; ATF6; IGF2R
GO:0048732	2.90E-08	1.10E-04	14791	601	83	17	BP	gland development	AR; HOXB9; LEF1; IGF1R; PGR; RARG; WT1; IGF1; CITED2; HOXA5; SMAD3; ERBB4; CREB1; PAX8; PAX1; NKX2-1; GLI2
GO:0009059	3.10E-08	1.10E-04	14791	601	785	65	BP	macromolecule biosynthetic process	AR; POLR1A; POLR1E; APOB; BLM; PPARG; PPARA; ASH2L; IRF3; EGFR; YARS2; TRIP13; B3GNT6; NFE2L1; ORC6L; TPR; PTGES3; USF1; IGF1; NFKB1; TCERG1; ZFXH3; MLF1; USF2; CDK7; DSCC1; GTF2H4; CEBPA; CEBPD; DVL2; ETS1; CREB1; HIF1A; RPS3A; RAD50; PAX2; ESR1; POLE2; PAX1; HARS; STAT1; LCAT; EIF2C2; TP53; HARS2; EIF6; KLF11; NAP1L1; CEBPB; MCM7; SNAPC5; KCTD13; EIF1D; TERF1; NACA; GYS2; POLR2H; POLR2K; POLR2J; TNF; NCOR1; POLD2; ACHE; SIN3A; NFIC
GO:0008283	3.30E-08	1.20E-04	14791	601	425	43	BP	cell proliferation	DLG1; AR; HHIP; PPARD; COL4A3; RXRA; EGFR; ERG; GF11B; CYR61; HGF; PTGES3; SCARB1; GNG2; IGF1; CADM1; CITED2; UHRF1; CDK7; PRKDC; BCL2; ERBB4; PRMT5; XRCC5; CDC16; ESR1; IFNB1; TAL1; TP53; CEBPB; MCM7; TGFA; FGF5; FGF4; MPL; TNF; ACHE; TACC3; MKI67; RIPK2; GLI2; NDEL1; ^{DNMT}
GO:0009607	3.40E-08	1.20E-04	14791	601	441	44	BP	response to biotic stimulus	IFNA10; F3; MX1; APOB; CYP27B1; IRF3; LTF; TP73; IFNA21; DEFA1; SNCA; JUN; RELA; SCARB1; VLDLR; IRF8; CLU; CEBPE; CAMP; SMAD3; BCL2; CTSG; FOS; CCR4; IL1B; STAT1; IFNB1; IGBP1; COMT; TP53; IL6; HSPB3; ALPL; NKX2-1; MST1R; GSK3B; STMN1; CHRM2; TNF; EPHA3; ACR; STAT5B; RIPK2; ^{AT2C}
GO:0034645	3.50E-08	1.30E-04	14791	601	753	63	BP	cellular macromolecule biosynthetic process	AR; POLR1A; POLR1E; APOB; BLM; PPARA; ASH2L; IRF3; EGFR; YARS2; TRIP13; B3GNT6; NFE2L1; ORC6L; TPR; PTGES3; USF1; IGF1; NFKB1; TCERG1; ZFXH3; MLF1; USF2; CDK7; DSCC1; GTF2H4; CEBPA; CEBPD; DVL2; ETS1; CREB1; HIF1A; RPS3A; RAD50; PAX2; ESR1; POLE2; PAX1; HARS; STAT1; LCAT; EIF2C2; TP53; HARS2; EIF6; KLF11; NAP1L1; CEBPB; MCM7; SNAPC5; KCTD13; EIF1D; TERF1; NACA; GYS2; POLR2H; POLR2K; POLR2J; NCOR1; POLD2; ACHE; SIN3A; NFIC
GO:0042493	3.50E-08	1.30E-04	14791	601	238	30	BP	response to drug	PPARG; SMAD1; BDKRB2; ABAT; SNCA; JUN; RELA; KCNK3; SST; FABP3; MSH2; YWHAZ; BCL2; ERBB4; CREB1; GNAO1; FOS; LCT; IL1B; STAT3; STAT1; COMT; TP53; HADHA; DRD2; TNF; MAP1B; NBN; SRD5A2; PEMT

GO:0016043	3.90E-08	1.40E-04	14791	601	2417	149	BP	cellular component organization	SMARCC2; STK16; L1CAM; DLG1; AKAP8; HIP1R; APOB; H3F3A; GTF2I; DSP; BLM; COL4A4; COL4A3; ANAPC7; CSNK1A1; KCNH2; ITGAV; ASH2L; SMAD4; SMAD7; SMAD1; PRKDC; TAF11; TSCI; KIF3A; RXRA; LEF1; AK7; TP73; GEMIN5; EGFR; IGF1R; GF11B; CYR61; SNCA; JUN; HGF; HEXB; SFTPD; COL11A2; CATSPER1; RAB1F; FGB; WT1; LIPC; CENPJ; PTGES3; SCARB1; VLDLR; GTF2E1; PRKG1; IRF8; NSD1; RALA; PI4KB; IL1RAP; FANCC; CADM1; CLU; COL17A1; STX6; PPAT; CDK7; TAF9B; GTF2H4; MSH2; MSH3; SMARCA4; CEBPA; CEBPE; ETS1; SUZ12; RUFY1; SMAD3; CTNNA2; GOLGB1; BCL2; CAV3; SNRNP200; GHR; CACNA1F; CETP; ERBB4; TRIM21; CREB1; BRD8; PRMT5; GBA; GNAO1; HIF1A; XRCC5; CDC16; RAD50; TRRAP; NFKB2; PAX2; ING2; LCAT; LGALS3; TP53; IL6; EIF6; WASF2; NAP1L1; NEFH; PDPK1; PKN1; VWF; DRD2; RDH12; PICALM; ITSN1; ITSN2; MICAL1; SNAPC5; TERF1; STMN1; MED30; HRAS; POLR2H; POLR2K; POLR2J; TAF7; PEX5; CDC23; TNF; BAT1; CLDN19; SDCBP; ATP5B; NCOR1; MAP1B; CACNB2; NBN; TGS1; BCOR; ACHE; TACC3; GLI2; RAD21; NDEL1; CLTCL1; NPM1; SNRPE; ATF1; DNML1; MYO7A; FSD1; IGF2R
GO:0006916	4.50E-08	1.60E-04	14791	601	201	27	BP	anti-apoptosis	F3; IGF1R; NGFR; SNCA; HGF; SON; PEA15; RELA; IGF1; NFKB1; CITED2; CLU; YWHAZ; MCL1; BCL2; ESR2; ESR1; IL1B; CEBPB; SQSTM1; SOCS2; TNFAIP3; TNF; STAT5B; STAT5A; RIPK2; NPM1
GO:0010647	4.90E-08	1.80E-04	14791	601	400	41	BP	positive regulation of cell communication	HIPK2; L1CAM; F3; AR; CYP27B1; PPARC; PDE6H; SMAD4; AKAP12; REL; LEPR; EGFR; IGF1R; JAG1; SNCA; LIF; RELA; CDKN2B; IGF1; F10; CITED2; LPAR1; GHR; ERBB4; HIF1A; ESR1; FGF23; IL1B; ING2; WNT2; IL6; ITSN1; EEF1D; TGFA; HRAS; FGF4; TNF; NCAM1; RIPK2; TRAF5; AXIN1
GO:0031667	5.60E-08	2.00E-04	14791	601	203	27	BP	response to nutrient levels	CYP27B1; PPARC; RXRA; LEPR; IGF1R; JUN; RARA; RARG; RELA; CDKN2B; VLDLR; USF1; SST; USF2; CEBPA; BCL2; GHR; LCT; IL1B; STAT1; TP53; ALPL; MAP1B; DUSP1; SREBF1; PEMT; IGF2R
GO:0008284	7.10E-08	2.60E-04	14791	601	452	44	BP	positive regulation of cell proliferation	HIPK2; F3; BLM; PPARC; ASH2L; EGFR; IGF1R; NGFR; JUN; LIF; AVPR1A; RARA; RELA; IGF1; CLU; CAMP; SUZ12; VIPR1; BCL2; ERBB4; HIF1A; EGR4; ESR1; IL1B; STAT1; WNT2; IL6; NAP1L1; POU3F2; DRD2; HTR1A; MST1R; TGFA; HRAS; FGF5; FGF4; TNF; NBN; ADK; STAT5B; STAT5A; RIPK2; GLI2; NPM1
GO:0009605	7.30E-08	2.70E-04	14791	601	500	47	BP	response to external stimulus	PIK3CB; F3; CYP27B1; PPARC; RALBP1; RXRA; LEPR; IGF1R; NGFR; DEFA1; CYR61; JUN; SFTPD; AVPR1A; RARA; RARG; SAG; RELA; CDKN2B; RHO; VLDLR; USF1; SST; RALA; USF2; CEBPA; BCL2; GHR; CACNA1F; TRPV4; FOS; LCT; CCR4; IL1B; STAT1; TP53; SFRP2; IL6; PON3; ALPL; HRAS; TNF; MAP1B; DUSP1; SREBF1; PEMT; IGF2R
GO:0007165	7.60E-08	2.80E-04	14791	601	2484	151	BP	signal transduction	HIPK2; DLG1; PIK3CB; CAMK2B; AKAP8; AR; RIT2; RAB6B; MX1; FZD10; GTF2I; BLM; PPARC; GDI1; CSNK1A1; KCNH2; SIGIRR; RALBP1; SMAD4; TLE2; TLE1; SMAD1; AKAP12; IRF3; SRPK1; PDE10A; BDKRB2; EGFR; IGF1R; ERG; NGFR; PPF1A1; PDE1A; PGR; RTN1; JUN; FZD8; ANK3; AVPR1A; RARA; DAB1; RARB; SAG; RAB1F; FGB; CDKN2B; HOMER1; TPR; PDE8A; ADCY1; PTGES3; GNG2; RHO; MAPK10; VLDLR; TIRAP; PRKG1; BMX; IGF1; IGFBP6; EPOR; NFKB1; CSNK1E; RALA; PI4KB; IL1RAP; PDE11A; NTF3; F2RL3; LPAR1; MSH2; ITGB3BP; YWHAZ; ARHGAP1; VIPR1; PRKDC; PLCD3; WWP1; GHR; MAGI2; BRCA1; ERBB4; CREB1; BRD8; ADCY5; GNAO1; PLCB2; HIF1A; FCN2; FOS; TRRAP; NFKB2; ESR2; TOLLIP; ESR1; CCR4; IL1B; STAT3; STAT1; PDE7B; ING2; IGBP1; TP53; RHEB; MAP2K3; TEAD1; CAMLG; WASF2; AMHR2; PKN1; TP53BP2; DRD2; HTR1A; ITSN1; MICAL1; GABRR2; RAP1A; SRGAP2; SOCS2; PPP2CA; MST1R; TERF1; STMN1; MAPKAPK5; PLXNB3; HTR1B; CHRM2; HRAS; FGF4; TNF; EPHA3; EPHA2; SDCBP; GNRHR; FZD6; NBN; FGF11; CRHBP; SOS1; IGFALS; STAT5B; STAT5A; RIPK2; DGKQ; ADRBK1; FSHR; TRAF5; NPM1; INPP1; ATF6; IGF2R
GO:0043065	8.40E-08	3.10E-04	14791	601	439	43	BP	positive regulation of apoptosis	HIPK2; ARHGEF12; MX1; BNIP1; PPARC; COL4A3; PRKDC; RXRA; TP73; NGFR; JUN; RARB; RARG; WT1; SST; CADM1; PDCD5; HOXA5; ITGB3BP; CEBPB; ETS1; SMAD3; BCL2; BRCA1; DAXX; RPS3A; TP53INP1; ESR2; IL1B; STAT1; IFN1B; TP53; CEBPB; TP53BP2; SQSTM1; ITSN1; PPP2CA; TERF1; TNF; DUSP1; SOS1; DDX9; ICF9D
GO:0023034	8.80E-08	3.20E-04	14791	601	1041	78	BP	intracellular signaling pathway	PPAP2A; HIPK2; PIK3CB; AR; RIT2; RAB6B; BLM; GDI1; RALBP1; SMAD1; IRF3; RXRA; SRPK1; TP73; EGFR; IGF1R; RBM9; PGR; AVPR1A; RARA; DAB1; RARG; RAB1F; HOMER1; ADCY1; PTGES3; MAPK10; TIRAP; BMX; IGF1; RALA; PI4KB; CDK7; F2RL3; MSH2; ARHGAP1; DVL2; VIPR1; PRKDC; PLCD3; GHR; MAGI3; BRCA1; ADCY5; DAXX; ESR2; TOLLIP; ESR1; STAT3; STAT1; TP53; RHEB; TEAD1; WASF2; PDPK1; SQSTM1; DRD2; HTR1A; ITSN1; RAP1A; SOCS2; PPP2CA; GSK3B; STMN1; HTR1B; MED30; CHRM2; HRAS; TAF7; TNF; SDCBP; NBN; SOS1; STAT5B; STAT5A; DGKQ; FSHR; ATF6
GO:0023060	8.90E-08	3.30E-04	14791	601	2490	151	BP	signal transmission	HIPK2; DLG1; PIK3CB; CAMK2B; AKAP8; AR; RIT2; RAB6B; MX1; FZD10; GTF2I; BLM; PPARC; GDI1; CSNK1A1; KCNH2; SIGIRR; RALBP1; SMAD4; TLE2; TLE1; SMAD1; AKAP12; IRF3; SRPK1; PDE10A; BDKRB2; EGFR; IGF1R; ERG; NGFR; PPF1A1; PDE1A; PGR; RTN1; JUN; FZD8; ANK3; AVPR1A; RARA; DAB1; RARB; SAG; RAB1F; FGB; CDKN2B; HOMER1; TPR; PDE8A; ADCY1; PTGES3; GNG2; RHO; MAPK10; VLDLR; TIRAP; PRKG1; BMX; IGF1; IGFBP6; EPOR; NFKB1; CSNK1E; RALA; PI4KB; IL1RAP; PDE11A; NTF3; F2RL3; LPAR1; MSH2; ITGB3BP; YWHAZ; ARHGAP1; VIPR1; PRKDC; PLCD3; WWP1; GHR; MAGI2; BRCA1; ERBB4; CREB1; BRD8; ADCY5; GNAO1; PLCB2; HIF1A; FCN2; FOS; TRRAP; NFKB2; ESR2; TOLLIP; ESR1; CCR4; IL1B; STAT3; STAT1; PDE7B; ING2; IGBP1; TP53; RHEB; MAP2K3; TEAD1; CAMLG; WASF2; AMHR2; PKN1; TP53BP2; DRD2; HTR1A; ITSN1; MICAL1; GABRR2; RAP1A; SRGAP2; SOCS2; PPP2CA; MST1R; TERF1; STMN1; MAPKAPK5; PLXNB3; HTR1B; CHRM2; HRAS; FGF4; TNF; EPHA3; EPHA2; SDCBP; GNRHR; FZD6; NBN; FGF11; CRHBP; SOS1; IGFALS; STAT5B; STAT5A; RIPK2; DGKQ; ADRBK1; FSHR; TRAF5; NPM1; INPP1; ATF6; IGF2R
GO:0035468	9.50E-08	3.50E-04	14791	601	364	38	BP	positive regulation of signaling pathway	HIPK2; L1CAM; F3; AR; CYP27B1; PPARC; PDE6H; SMAD4; AKAP12; REL; LEPR; IGF1R; JAG1; LIF; RELA; CDKN2B; IGF1; F10; CITED2; LPAR1; GHR; HIF1A; ESR1; FGF23; IL1B; ING2; WNT2; IL6; ITSN1; EEF1D; TGFA; HRAS; FGF4; TNF; NCAM1; RIPK2; TRAF5; AXIN1

GO:0043068	1.00E-07	3.80E-04	14791	601	442	43	BP	positive regulation of programmed cell death	HIPK2; ARHGEF12; MX1; BNIPL; PPARG; COL4A3; PRKDC; RXRA; TP73; NGFR; JUN; RARB; RARG; WT1; SST; CADM1; PDCD5; HOXA5; ITGB3BP; CEBPG; ETS1; SMAD3; BCL2; BRCA1; DAXX; RPS3A; TP53INP1; ESR2; IL1B; STAT1; IFNB1; TP53; CEBPB; TP53BP2; SQSTM1; ITSN1; PPP2CA; TERF1; TNF; DUSP1; SOS1; RIPK2; IGF2R
GO:0044260	1.20E-07	4.40E-04	14791	601	3428	194	BP	cellular macromolecule metabolic process	STK16; P4HA2; HIPK2; PIK3CB; CAMK2A; CAMK2B; DDX41; AR; TSG101; UBE2D2; POLR1A; POLR1E; APOB; SMG5; SENP2; DSP; BLM; PPARG; PPARA; ANAPC5; ANAPC7; PPID; CSNK1A1; TRDMT1; PDE6H; SMAD9; ASH2L; SMAD7; SMAD1; PRKDC; TAF11; IRF3; SRPK1; TP73; GEMIN5; ERC1; EGFR; IGF1R; RBM9; ERG; SNCA; YARS2; HGF; TRIP13; HEXB; RBMX; B3GNT6; NFE2L1; ORC6L; WT1; TPR; PTGES3; RHO; MAPK10; USF1; GTF2E1; PRKG1; BMX; IGF1; NFKB1; CSNK1E; NSD1; WDYHV1; TCERG1; ZFXH3; MLF1; USF2; SKP1; FANCC; HNRNPA1; UHRF1; CDK7; DSCC1; GTF2H4; TCEB3; MSH2; MSH3; USP7; CEBPA; CEBPG; CEBPD; DVL2; ETS1; SUZ12; PRKCD; PSME1; SMAD3; ABI3; CSTF2; BCL2; WWP1; SNRNP200; GHR; BRCA1; ERBB4; PRMT3; CREB1; BRD8; DZIP3; PRMT5; KPNA2; HIF1A; XRCC5; PRPF3; SMURF1; DAXX; SMURF2; CDC16; NONO; NT5E; RPS3A; FOS; RAD50; TRRAP; SFPQ; PAX2; ESR1; POLE2; STK36; PAX1; LCMT1; IL1B; HARS; RBM8A; STAT1; ZHX2; MARK3; LCAT; EIF2C2; TP53; HARS2; EIF6; MAP2K3; CAMLG; KLF11; NAP1L1; AMHR2; PDPK1; CEBPB; PKN1; MCM7; DUSP14; DUSP12; SQSTM1; PICALM; DHX16; NTRK2; NTRK3; SNAPC5; KCTD13; PPP2CA; EEF1D; PPP2CB; MST1R; GSK3B; TERF1; PABPC1; ST13; MAPKAPK5; TGFA; NACA; GYS2; POLR2H; POLR2K; POLR2J; CDC23; TNF; BAT1; EPHA8; EPHA3; EPHA2; NCOR1; POLD2; NBN; HNRNPC; DUSP1; PCMT1; TGS1; ACHE; STAT5A; PSMB4; RIPK2; ADRBK1; SIN3A; RAD21; DNMT3L; PLAT; SNRPA; SNRPE; NFIC; PTPRS; NEDD4L; UPP3A; ATF6
GO:0010035	1.20E-07	4.60E-04	14791	601	238	29	BP	response to inorganic substance	F3; APOB; KHK; RXRA; LEF1; EGFR; ABAT; SNCA; JUN; AVPR1A; RELA; FGB; LPO; KCN3; FANCC; BCL2; ERBB4; GNAO1; FOS; LCT; STAT1; LCAT; PPP2CB; SDC1; MAP1B; DUSP1; ADRBK1; ADRBK1; ATF1; NEDD4L
GO:0010942	1.30E-07	4.90E-04	14791	601	446	43	BP	positive regulation of cell death	HIPK2; ARHGEF12; MX1; BNIPL; PPARG; COL4A3; PRKDC; RXRA; TP73; NGFR; JUN; RARB; RARG; WT1; SST; CADM1; PDCD5; HOXA5; ITGB3BP; CEBPG; ETS1; SMAD3; BCL2; BRCA1; DAXX; RPS3A; TP53INP1; ESR2; IL1B; STAT1; IFNB1; TP53; CEBPB; TP53BP2; SQSTM1; ITSN1; PPP2CA; TERF1; TNF; DUSP1; SOS1; DDX41; IGF2R
GO:0010553	1.30E-07	5.10E-04	14791	601	62	14	BP	negative regulation of gene-specific transcription from RNA polymerase II promoter	PPARG; PPARA; SMAD7; RXRA; NFKB1; TAF9B; SMARCA4; SMAD3; IGBP1; TAF7; NCOR1; BCOR; HEY1; NFIC
GO:0032879	1.30E-07	5.10E-04	14791	601	712	59	BP	regulation of localization	SCG5; F3; JPH2; APOB; APOH; PPARG; PPARA; ITGAV; SMAD4; SMAD7; EGFR; IGF1R; JAG1; NOS1; SNCA; SFTPD; LIF; AVPR1A; CATSPER1; PEA15; HOMER1; SCARB1; IGF1; F10; SST; NFKB1; RALA; CADM1; CITED2; ETS1; SMAD3; ABI3; BCL2; CAV3; CETP; ERBB4; CREB1; GNAO1; HIF1A; RPH3AL; FGF23; IL1B; IL6; PDPK1; DRD2; PICALM; NKX2-1; CACNA2D1; SYT9; GSK3B; HTR1B; TNF; EPHA2; ACHE; TACC3; STAT5B; ADRBK1; CLTCL1; NEDD4L
GO:0060740	1.30E-07	5.10E-04	14791	601	23	9	BP	prostate gland epithelium morphogenesis	AR; IGF1R; HOXB13; RARG; IGF1; ESR2; ESR1; STAT5A; GLI2
GO:0010648	1.40E-07	5.20E-04	14791	601	310	34	BP	negative regulation of cell communication	HIPK2; HHIP; SIGIRR; TLE1; SMAD7; TSC1; IGF1R; NGFR; SNCA; RGS10; LIF; AVPR1A; RELA; IGF1; PRKDC; CAV3; SMURF1; RPH3AL; ESR2; IL1B; IGBP1; TP53; SFRP2; DRD2; NKX2-1; SOCS2; PPP2CA; PPP2CB; HTR1B; TNFAIP3; NCOR1; ACHE; ADRBK1; AXIN1
GO:0043170	1.50E-07	5.90E-04	14791	601	3975	218	BP	macromolecule metabolic process	PCSK2; SCG5; STK16; P4HA2; HIPK2; PIK3CB; CAMK2A; CAMK2B; F3; CNDP1; DDX41; AR; TSG101; UBE2D2; POLR1A; POLR1E; APOB; MST1; APOH; SMG5; SENP2; DSP; BLM; PPARG; PPARA; ANAPC5; ANAPC7; PPID; CSNK1A1; TRDMT1; PDE6H; SMAD9; ASH2L; SMAD7; SMAD1; PRKDC; TAF11; IRF3; SRPK1; TP73; GEMIN5; ERC1; EGFR; IGF1R; RBM9; ERG; NGFR; SNCA; YARS2; HGF; TRIP13; HEXB; RBMX; B3GNT6; NFE2L1; ORC6L; RELA; WT1; TPR; PTGES3; RHO; MAPK10; MASP1; USF1; GTF2E1; PRKG1; BMX; IGF1; F10; NFKB1; CSNK1E; NSD1; WDYHV1; TCERG1; ZFXH3; MLF1; USF2; SKP1; FANCC; HNRNPA1; CLU; UHRF1; CDK7; DSCC1; GTF2H4; TCEB3; MSH2; MSH3; USP7; PRSS2; CEBPA; CEBPG; CEBPE; CEBPD; DVL2; ETS1; SUZ12; PRKCD; PSME1; SMAD3; ABI3; CSTF2; MMP8; BCL2; WWP1; SNRNP200; GHR; BRCA1; ERBB4; PRMT3; CREB1; CTSG; BRD8; DZIP3; PRMT5; MASP2; KPNA2; HIF1A; XRCC5; PRPF3; SMURF1; DAXX; SMURF2; CDC16; NONO; NT5E; RPS3A; FCN2; FOS; RAD50; TRRAP; SFPQ; PAX2; ESR1; CTSL1; POLE2; STK36; PAX1; LCMT1; IL1B; HARS; RBM8A; STAT1; ZHX2; MARK3; LCAT; EIF2C2; TP53; HARS2; EIF6; MAP2K3; CAMLG; KLF11; NAP1L1; AMHR2; PDPK1; CEBPB; PKN1; MCM7; DUSP14; DUSP12; SQSTM1; C1S; PICALM; DHX16; NTRK2; NTRK3; CAPN2; SNAPC5; KCTD13; PPP2CA; EEF1D; PPP2CB; MST1R; GSK3B; TERF1; PABPC1; ST13; MAPKAPK5; TGFA; NACA; GYS2; POLR2H; POLR2K; POLR2J; CDC23; TNF; BAT1; EPHA8; ACAN; EPHA3; EPHA2; ACR; NCOR1; POLD2; NBN; HNRNPC; DUSP1; PCMT1; TGS1; ACHE; STAT5A; PSMB4; ADAM12; RIPK2; ADRBK1; SIN3A; RAD21; DNMT3L; PLAT; SNRPA; SNRPE; NFIC; PTPRS; AXIN1; NEDD4L; UPP3A; ATF6
GO:0014070	1.70E-07	6.30E-04	14791	601	150	22	BP	response to organic cyclic substance	PPARG; RXRA; LEPR; LEF1; ABAT; JUN; RELA; CDKN2B; TAF9B; MSH2; BCL2; GHR; GNAO1; FOS; IL1B; STAT3; STAT1; COMT; DRD2; HTR1B; ADRBK1; ATF1

GO:0010627	1.70E-07	6.50E-04	14791	601	313	34	BP	regulation of intracellular protein kinase cascade	HIPK2; F3; AR; AKAP12; REL; LEPR; TP73; IGF1R; LIF; REL; IGF1; F10; LPAR1; CAV3; GHR; DAXX; FGF23; IL1B; IGBP1; IL6; PKN1; SQSTM1; DRD2; ITSN1; PPP2CA; EEF1D; HRAS; FGF4; TNFAIP3; TNF; NCOR1; RIPK2; TRAF5; AXIN1
GO:0035467	1.90E-07	7.30E-04	14791	601	243	29	BP	negative regulation of signaling pathway	HIPK2; HHIP; SIGIRR; TLE1; SMAD7; TSC1; IGF1R; NGFR; SNCA; LIF; REL; IGF1; PRKCD; CAV3; SMURF1; RPH3AL; ESR2; IL1B; IGBP1; TP53; SFRP2; DRD2; NKX2-1; PPP2CA; PPP2CB; TNFAIP3; NCOR1; ADRBK1; AXIN1
GO:0007584	2.40E-07	8.90E-04	14791	601	153	22	BP	response to nutrient	CYP27B1; PPARG; RXRA; IGF1R; RARA; RARG; REL; CDKN2B; VLDLR; USF1; SST; USF2; CEBPA; BCL2; LCT; IL1B; STAT1; ALPL; MAP1B; DUSP1; PEMT; TCF7L2
GO:0031399	2.40E-07	9.00E-04	14791	601	347	36	BP	regulation of protein modification process	ANAPC5; ANAPC7; SMAD4; SMAD7; TSC1; BDKRB2; TP73; EGFR; SNCA; JUN; LIF; IGF1; SKP1; CAMP; PRKCD; PSME1; BCL2; GHR; BRCA1; SMURF1; DAXX; CDC16; RAD50; IL1B; TP53; IL6; PKN1; PPP2CA; TAF7; CDC23; TNF; NBN; BCOR; PSMB4; RIPK2; AXIN1
GO:0040008	2.40E-07	9.00E-04	14791	601	347	36	BP	regulation of growth	AR; TSG101; BNIPL; CYP27B1; PPARG; SMAD4; TP73; CYR61; HOXB13; AVPR1A; WT1; IGF1; IGFBP6; CHPT1; TAF9B; PRSS2; SMAD3; BCL2; GHR; CREB1; CTSG; BRD8; ESR2; STAT3; ING2; TP53; GDF5; POU3F2; NTRK3; SOCS2; PPP2CA; PEX5; MAP1B; GDF9; STAT5B; STAT5A
GO:0044281	2.90E-07	0.001	14791	601	1396	95	BP	small molecule metabolic process	P4HA2; CYP2C9; APOB; APOH; CYP27B1; PPARG; PPARA; KHK; TRMT1; ASH2L; ADSSL1; RXRA; LEPR; ABAT; ACA2; NOS1; SNCA; YARS2; HEXB; LIPC; TPR; PDE8A; ADCY1; DBH; PTGES3; SCARB1; VLDLR; USF1; IGF1; AGMAT; SARDH; NSD1; FABP3; PDE11A; CHPT1; MTHFS; DLST; PPAT; CEBPA; SUZ12; CAV3; GHR; CETP; PRMT3; ADCY5; PRMT5; NT5E; XDH; FOS; ACAD8; FGF23; LCMT1; HARS; MNAT2; ACACB; LCAT; COMT; CYP1A2; AGXT; HARS2; AADAT; HADHA; DRD2; PON3; RDH12; FBP2; UGP2; GOT1; GSK3B; ACSL1; G6PC2; GUCY1A3; PGM1; GYS2; PEX5; TNF; RBKS; ATP5B; CYP2B6; SGPPI; ASL; PCMT1; TGS1; ACHE; FADS2; ADK; STAT5B; STAT5A; SREBF1; DERA; PAPSS1; DNMT3L; ALDH6A1; GGT1; PEMT
GO:0048878	3.10E-07	0.0011	14791	601	476	44	BP	chemical homeostasis	PIK3CB; SV2A; JPH2; APOB; CYP27B1; PPARG; KCNH2; LTF; BDKRB2; SNCA; JUN; HEXB; SFTPD; AVPR1A; LIPC; DBH; SCARB1; USF1; IGF1; KCNK3; EPOR; EPHX2; USF2; LPAR1; BCL2; CAV3; CACNA1F; TRPV4; CETP; ERBB4; HIF1A; RPH3AL; FGF23; CCR4; IL1B; STAT3; LCAT; DRD2; KCNE1; GOT1; SLC4A1; ATP8B; CP110C; NEDD4
GO:0016070	3.20E-07	0.0012	14791	601	927	70	BP	RNA metabolic process	DDX41; AR; POLR1A; POLR1E; SMG5; PPARA; TRMT1; ASH2L; SMAD1; TAF11; IRF3; SRPK1; GEMIN5; RBM9; YARS2; TRIP13; RBMX; NFE2L1; WT1; TPR; USF1; GTF2E1; NFKB1; TCERG1; ZFH3; USF2; HNRNPAL1; CDK7; GTF2H4; TCEB3; CEBPA; CEBPG; CEBPD; DVL2; ETS1; SMAD3; CSTF2; SNRNP200; CREB1; HIF1A; PRPF3; NONO; SFPQ; PAX2; ESR1; PAX1; HARS; RBM8A; STAT1; ZHX2; EIF2C2; TP53; HARS2; KLF11; CEBPB; DHX16; SNAPC5; PPP2CA; PABPC1; POLR2H; POLR2K; POLR2J; BAT1; NCOR1; HNRNPC; TGS1; SNRPA; SNRPE; NFIC; UPF3A
GO:0044249	3.30E-07	0.0012	14791	601	1458	98	BP	cellular biosynthetic process	AR; POLR1A; POLR1E; APOB; CYP27B1; BLM; PPARA; ASH2L; ADSSL1; IRF3; EGFR; NOS1; SNCA; YARS2; TRIP13; HEXB; B3GNT6; NFE2L1; ORC6L; LIPC; TPR; ADCY1; DBH; PTGES3; SCARB1; PPOX; USF1; IGF1; AGMAT; NFKB1; PI4KB; TCERG1; ZFH3; FABP3; MLF1; USF2; CHPT1; MTHFS; PPAT; CDK7; DSCC1; GTF2H4; CEBPA; CEBPD; DVL2; ETS1; CREB1; ADCY5; HIF1A; NT5E; RPS3A; RAD50; PAX2; ESR1; POLE2; PAX1; HARS; STAT1; MNAT2; ACACB; LCAT; EIF2C2; TP53; CYP1A2; AGXT; HARS2; EIF6; KLF11; NAP1L1; CEBPB; MCM7; FBP2; UGP2; GOT1; SNAPC5; KCTD13; EEF1D; TERF1; G6PC2; GUCY1A3; NACA; GYS2; POLR2H; POLR2K; POLR2J; ATP5B; NCOR1; POLD2; SRD5A2; ASL; ACHE; FADS2; ADK; PAPSS1; SIN3A; GGT1; NFIC; PEMT
GO:0007154	3.30E-07	0.0012	14791	601	627	53	BP	cell communication	AR; RIT2; LEPR; APBA2; PGR; JAG1; SNCA; JUN; HGF; WNT16; AVPR1A; CDKN2B; HOMER1; DBH; SNX9; USF1; KCNK3; SST; USF2; NTF3; GRIK5; HOXA5; VIPR1; DLGAP4; FOS; ESR2; TOLLIP; SYN1; IL1B; PDE7B; EFNA5; EFNA4; TP53; SFRP2; WNT2; GDF5; DRD2; WNT9B; NKX2-1; GABRR2; POU2F1; VDCA1; HTR1B; FGF5; FGF4; SDCBP; CACNB2; SRD5A2; FGF11; SREBF1; PLAT; HOXC11; DNMT1
GO:0051246	3.30E-07	0.0012	14791	601	610	52	BP	regulation of protein metabolic process	TSG101; UBE2D2; ANAPC5; ANAPC7; ITGAV; SMAD4; SMAD7; TSC1; BDKRB2; TP73; EGFR; SNCA; JUN; LIF; EIF3H; REL; WT1; MASP1; IGF1; NFKB1; CSNK1E; SKP1; CAMP; PRKCD; PSME1; BCL2; GHR; BRCA1; SMURF1; DAXX; CDC16; RAD50; IL1B; RBM8A; EIF2C2; TP53; IL6; EIF5; PKN1; PPP2CA; TAF7; CDC23; TNF; NBN; BCOR; PSMB4; RIPK2; GRIN2C; PLAT; PEMT; AXIN1; NEDD4
GO:0048583	3.30E-07	0.0012	14791	601	510	46	BP	regulation of response to stimulus	HIPK2; F3; APOH; CYP27B1; PPARG; PPARA; SIGIRR; TP73; RARA; REL; MASP1; USF1; AP2B1; CADM1; CLU; CEBPG; PRKCD; SMAD3; CTNNA2; TRPV4; BRCA1; CTSG; MASP2; DAXX; NT5E; FCN2; ESR2; CCR4; IL1B; IFNB1; IGBP1; IL6; PKN1; DRD2; CIS; HTR1A; NTRK3; TNF; NCOR1; STAT5B; STAT5A; PSMB4; RIPK2; NDEL1; NPML1; AXIN1
GO:0001889	3.40E-07	0.0012	14791	601	57	13	BP	liver development	SP1; SP3; RXRA; HGF; REL; CADM1; CITED2; CEBPA; CEBPG; SMAD3; VWF; STAT5B; IGF2R
GO:0030522	3.80E-07	0.0014	14791	601	77	15	BP	intracellular receptor mediated signaling pathway	PPAP2A; AR; RXRA; RBM9; PGR; RARA; RARG; PTGES3; CDK7; BRCA1; DAXX; ESR2; ESR1; MED30; TAF7
GO:0032870	4.70E-07	0.0017	14791	601	159	22	BP	cellular response to hormone stimulus	PPARG; PRKDC; RXRA; IGF1R; RARA; ADCY1; GNG2; VLDLR; USF1; PPAT; AGRP; GHR; ADCY5; FOS; STAT3; STAT1; AP3S1; PDPK1; GOT1; SOCS2; DUSP1; STAT5B

GO:0071495	5.90E-07	0.0022	14791	601	161	22	BP	cellular response to endogenous stimulus	PPARG; PRKDC; RXRA; IGF1R; RARA; ADCY1; GNG2; VLDLR; USF1; PPAT; AGRP; GHR; ADCY5; FOS; STAT3; STAT1; AP3S1; PDPK1; GOT1; SOCS2; DUSP1; STAT5B
GO:0002237	7.60E-07	0.0028	14791	601	126	19	BP	response to molecule of bacterial origin	F3; CYP27B1; SNCA; JUN; RELA; SCARB1; VLDLR; CAMP; CTSG; FOS; IL1B; STAT1; COMT; IL6; ALPL; NKX2-1; EPHA3; STAT5B; RIPK2
GO:0030518	7.80E-07	0.0029	14791	601	61	13	BP	steroid hormone receptor signaling pathway	PPAP2A; AR; RBM9; PGR; RARA; PTGES3; CDK7; BRCA1; DAXX; ESR2; ESR1; MED30; TAF7
GO:0071310	7.80E-07	0.0029	14791	601	217	26	BP	cellular response to organic substance	PPARG; PRKDC; RXRA; IGF1R; RARA; ADCY1; GNG2; VLDLR; USF1; PPAT; AGRP; CAMP; GHR; BRCA1; ADCY5; EGRI; FOS; STAT3; STAT1; AP3S1; PDPK1; GOT1; SOCS2; DUSP1; STAT5B; ATF6
GO:0031960	7.90E-07	0.0029	14791	601	103	17	BP	response to corticosteroid stimulus	RXRA; AVPRIA; CEBPA; BCL2; GHR; FOS; IL1B; LCAT; AGXT; IL6; ALPL; GOT1; HTR1B; SDC1; TNF; DUSP1; PLAT
GO:0032496	8.40E-07	0.0031	14791	601	115	18	BP	response to lipopolysaccharide	F3; CYP27B1; SNCA; JUN; RELA; SCARB1; VLDLR; CAMP; CTSG; FOS; IL1B; STAT1; COMT; ALPL; NKX2-1; EPHA3; STAT5B; RIPK2
GO:0051345	9.70E-07	0.0035	14791	601	192	24	BP	positive regulation of hydrolase activity	F3; APOH; PPARG; COL4A3; RALBP1; TSC1; EGFR; AVPRIA; HOMER1; F2RL3; LPAR1; MSH2; MSH3; SMAD3; GNAO1; PLCB2; STAT1; IFNB1; TP53; DRD2; TERF1; CHR2; TNF; NDEL1
GO:0032768	9.80E-07	0.0036	14791	601	28	9	BP	regulation of monooxygenase activity	CYP27B1; EGFR; SNCA; SCARB1; NFKB1; CAV3; HIF1A; IL1B; TNF
GO:0034097	1.00E-06	0.0038	14791	601	105	17	BP	response to cytokine stimulus	CYP27B1; SNCA; JUN; RELA; CDKN2B; CAMP; MCL1; BCL2; GHR; GNAO1; FOS; STAT3; STAT1; IGBP1; EPHA3; STAT5B; RIPK2
GO:0051726	1.20E-06	0.0045	14791	601	435	40	BP	regulation of cell cycle	DLG1; TSG101; CYP27B1; BLM; TP73; EGFR; NGFR; JUN; LIF; RARA; CDKN2B; TPR; IGF1; GMN; MLF1; CITED2; CDK7; MSH2; SMARCA4; ETS1; SMAD3; BCL2; BRCA1; PRMT5; CDC16; TRAP; TP53INP1; IL1B; TP53; TP53BP2; TERF1; TGFA; HRAS; CDC23; TNF; NBN; TACC3; STAT5B; STAT5A; NPM1
GO:0051052	1.20E-06	0.0046	14791	601	130	19	BP	regulation of DNA metabolic process	BLM; IGF1R; JUN; IGF1; GMN; MSH2; MSH3; CEBPG; BRCA1; KPNA2; RAD50; TP53; ENPP7; PPP2CA; TERF1; HRAS; NBN; GLI2; ATF1
GO:0009058	1.20E-06	0.0046	14791	601	1581	102	BP	biosynthetic process	AR; POLR1A; POLR1E; APOB; CYP27B1; BLM; PPARG; PPARA; ASH2L; ADSSL1; IRF3; EGFR; ACAA2; NOS1; SNCA; YARS2; TRIP13; HEXB; B3GNT6; NFE2L1; ORC6L; LIPC; TPR; ADCY1; DBH; PTGES3; SCARB1; PPOX; USF1; IGF1; AGMAT; NFKB1; PI4KB; TCERG1; ZFXH3; FABP3; MLF1; USF2; CHPT1; MTHFS; PPAT; CDK7; DSCC1; GTF2H4; CEBPA; CEBPD; DVL2; ETS1; CREB1; ADCY5; HIF1A; NT5E; RPS3A; RAD50; PAX2; ESR1; POLE2; PAX1; HARS; STAT1; MNAT2; ACACB; LCAT; EIF2C2; TP53; CYP1A2; AGXT; HARS2; EIF6; KLF11; NAP1L1; AADAT; CEBPB; MCM7; FBP2; UGP2; GOT1; SNAPC5; KCTD13; EEF1D; TERF1; G6PC2; GUCY1A3; NACA; GYS2; POLR2H; POLR2K; POLR2J; TNF; ATP5B; NCOR1; POLD2; SRD5A2; ASL; ACHE; FADS2; ADK; PAPSS1; SIN3A; GGT1; NFIC; PEMT
GO:0051384	1.40E-06	0.0054	14791	601	96	16	BP	response to glucocorticoid stimulus	RXRA; AVPRIA; CEBPA; BCL2; GHR; FOS; IL1B; LCAT; AGXT; IL6; ALPL; GOT1; SDC1; TNF; DUSP1; PLAT
GO:0022603	1.40E-06	0.0054	14791	601	297	31	BP	regulation of anatomical structure morphogenesis	F3; AR; APOH; COL4A3; SMAD4; SMAD7; SMAD1; RXRA; NGFR; HGF; HOXA5; CAMP; SMAD3; BCL2; CAV3; HIF1A; ESR1; IL1B; SFRP2; WNT2; IL6; TFAP2A; POU3F2; NKX2-1; NTRK3; TNF; EPHA2; MAP1B; BCOR; NDEL1; HOXC11
GO:0032268	1.50E-06	0.0056	14791	601	538	46	BP	regulation of cellular protein metabolic process	ANAPC5; ANAPC7; ITGAV; SMAD4; SMAD7; TSC1; BDKRB2; TP73; EGFR; SNCA; JUN; LIF; EIF3H; WT1; IGF1; NFKB1; CSNK1E; SKP1; CAMP; PRKCD; PSME1; BCL2; GHR; BRCA1; SMURF1; DAXX; CDC16; RAD50; IL1B; RBM8A; EIF2C2; TP53; IL6; EIF5; PKN1; PPP2CA; TAF7; CDC23; TNF; NBN; BCOR; PSMB4; RIPK2; PLAT; PEMT; AXIN1
GO:0006952	1.70E-06	0.0064	14791	601	592	49	BP	defense response	IFNA10; MX1; PPARG; SIGIRR; SMAD1; RXRA; LTF; BDKRB2; TP73; IFNA21; DEFA1; SFTPD; NFE2L1; RELA; MASP1; TIRAP; IRF8; NFKB1; EPHX2; IL1RAP; CLU; MGLL; CEBPA; CEBPG; CEBPE; CAMP; BCL2; CTSG; MASP2; FCN2; FOS; KIR3DL2; ESR2; TOLLIP; CCR4; IL1B; STAT3; IFNB1; IL6; CAMLG; CEBPB; C1S; MST1R; HLA-G; VDCA1; TNF; EPHA3; STAT5B; RIPK2
GO:0048729	1.80E-06	0.0069	14791	601	213	25	BP	tissue morphogenesis	AR; ZIC2; SMAD4; SMAD7; TSC1; RXRA; EGFR; IGF1R; PGR; JAG1; HOXB13; RARG; WT1; IGF1; HOXA5; DVL2; SMAD3; BCL2; ESR2; ESR1; TFAP2A; NKX2-1; FZD6; STAT5A; GLI2
GO:0033273	1.90E-06	0.0073	14791	601	87	15	BP	response to vitamin	CYP27B1; PPARG; RXRA; IGF1R; RARA; RARG; RELA; CEBPA; BCL2; IL1B; ALPL; MAP1B; DUSP1; PEMT; IGF2R

GO:0006793	2.40E-06	0.0089	14791	601	886	65	BP	phosphorus metabolic process	PPAP2A; STK16; HIPK2; PIK3CB; CAMK2A; CAMK2B; CSNK1A1; PDE6H; SMAD9; SMAD7; SMAD1; PRKDC; SRPK1; ERC1; EGFR; IGF1R; ERG; HGF; RHO; MAPK10; PRKG1; BMX; CSNK1E; PI4KB; CDK7; MSH2; PRKCD; ABI3; BCL2; GHR; ERBB4; CREB1; DAXX; TOLLIP; STK36; FGF23; IL1B; STAT1; MARK3; MAP2K3; AMHR2; PDPK1; PKN1; DUSP14; DUSP12; ALPL; UGP2; NTRK2; NTRK3; PPP2CA; PPP2CB; MST1R; GSK3B; MAPKAPK5; TGFA; TNF; EPHA8; EPHA3; EPHA2; DUSP1; STAT5A; RIPK2; ADRBK1; INPP1; PTPRS
GO:0006796	2.40E-06	0.0089	14791	601	886	65	BP	phosphate metabolic process	PPAP2A; STK16; HIPK2; PIK3CB; CAMK2A; CAMK2B; CSNK1A1; PDE6H; SMAD9; SMAD7; SMAD1; PRKDC; SRPK1; ERC1; EGFR; IGF1R; ERG; HGF; RHO; MAPK10; PRKG1; BMX; CSNK1E; PI4KB; CDK7; MSH2; PRKCD; ABI3; BCL2; GHR; ERBB4; CREB1; DAXX; TOLLIP; STK36; FGF23; IL1B; STAT1; MARK3; MAP2K3; AMHR2; PDPK1; PKN1; DUSP14; DUSP12; ALPL; UGP2; NTRK2; NTRK3; PPP2CA; PPP2CB; MST1R; GSK3B; MAPKAPK5; TGFA; TNF; EPHA8; EPHA3; EPHA2; DUSP1; STAT5A; RIPK2; ADRBK1; INPP1; PTPRS
GO:0023051	2.40E-06	0.009	14791	601	669	53	BP	regulation of signaling process	HIPK2; L1CAM; PIK3CB; ARHGFE12; F3; AR; HHIP; PPARD; SIGIRR; PDE6H; AKAP12; REL; TSC1; LEPR; TP73; EGFR; IGF1R; SNCA; HGF; RGS10; LIF; REL; IGF1; F10; LPAR1; PRKCD; CAV3; GHR; DAXX; FGF23; IL1B; IGBP1; IL6; PKN1; SQSTM1; DRD2; ITSN1; ITSN2; SOCS2; PPP2CA; EEF1D; PPP2CB; TGFA; HRAS; FGF4; TNFAIP3; TNF; NCAM1; NCOR1; SOS1; RIPK2; TRAF5; AXIN1
GO:0048731	2.40E-06	0.0092	14791	601	652	52	BP	system development	SMARCC2; PCSK2; L1CAM; SP1; SP3; APOB; DRP2; HOXB9; TSC1; APBA2; NGFR; JAG1; HEXB; COL11A2; DAB1; VLDLR; IGF1; NTF3; CITED2; HOXA1; SMARCA4; SMAD3; BCL2; WWP1; NR2C2; FOS; PAX6; PAX1; STAT3; EFNA5; LGALS3; TP53; NEFH; ALPL; NKX2-1; ETS2; NTRK2; NTRK3; BMP5; STMN1; CHRM2; FGF5; ACAN; EPHA2; MAP1B; FGF11; ACHE; HEY1; PAPSS1; GLI2; NDF1; HOXC11
GO:0007346	2.50E-06	0.0094	14791	601	162	21	BP	regulation of mitotic cell cycle	DLG1; EGFR; CDKN2B; TPR; IGF1; SMARCA4; SMAD3; BCL2; PRMT5; CDC16; TRRAP; IL1B; TP53; TERF1; TGFA; HRAS; CDC23; TNF; NBN; STAT5B; STAT5A
GO:0051179	2.70E-06	0.0101	14791	601	176	22	BP	localization	AKAP3; SMAD7; EGFR; HEXB; MLPH; RALA; CAV3; SMURF1; IL1B; TP53; SQSTM1; DRD2; TNF; TGS1; TACC3; STAT5B; STAT5A; GRIN2C; SIN3A; NDEL1;
GO:0043627	2.90E-06	0.011	14791	601	113	17	BP	response to estrogen stimulus	F3; CYP27B1; PPARG; ASH2L; LEPR; RARA; BCL2; GHR; BRCA1; LCT; ESR1; IL1B; STAT3; SOCS2; MAP1B; DUSP1; STAT5B
GO:0016310	3.00E-06	0.0113	14791	601	710	55	BP	phosphorylation	STK16; HIPK2; PIK3CB; CAMK2A; CAMK2B; CSNK1A1; PDE6H; SMAD9; SMAD7; SMAD1; PRKDC; SRPK1; ERC1; EGFR; IGF1R; ERG; HGF; RHO; MAPK10; PRKG1; BMX; CSNK1E; PI4KB; CDK7; MSH2; PRKCD; ABI3; BCL2; GHR; ERBB4; CREB1; DAXX; TOLLIP; STK36; IL1B; STAT1; MARK3; MAP2K3; AMHR2; PDPK1; PKN1; UGP2; NTRK2; NTRK3; MST1R; GSK3B; MAPKAPK5; TGFA; TNF; EPHA8; EPHA3; EPHA2; STAT5A; RIPK2; ADRBK1
GO:0002009	3.60E-06	0.0134	14791	601	179	22	BP	morphogenesis of an epithelium	AR; ZIC2; SMAD4; TSC1; EGFR; IGF1R; PGR; JAG1; HOXB13; RARG; WT1; IGF1; HOXA5; DVL2; BCL2; ESR2; ESR1; TFAP2A; NKX2-1; FZD6; STAT5A; GLI2
GO:0009966	3.80E-06	0.0143	14791	601	662	52	BP	regulation of signal transduction	HIPK2; L1CAM; PIK3CB; ARHGFE12; F3; AR; HHIP; PPARD; SIGIRR; PDE6H; AKAP12; REL; TSC1; LEPR; TP73; EGFR; IGF1R; HGF; RGS10; LIF; REL; IGF1; F10; LPAR1; PRKCD; CAV3; GHR; DAXX; FGF23; IL1B; IGBP1; IL6; PKN1; SQSTM1; DRD2; ITSN1; ITSN2; SOCS2; PPP2CA; EEF1D; PPP2CB; TGFA; HRAS; FGF4; TNFAIP3; TNF; NCAM1; NCOR1; SOS1; RIPK2; TRAF5; AXIN1
GO:0043408	4.20E-06	0.0159	14791	601	154	20	BP	regulation of MAPKKK cascade	HIPK2; AR; LEPR; TP73; IGF1R; LIF; IGF1; CAV3; DAXX; FGF23; IL1B; IGBP1; IL6; PKN1; HRAS; FGF4; TNF; NCOR1; RIPK2; AXIN1
GO:0006917	4.40E-06	0.0163	14791	601	313	31	BP	induction of apoptosis	HIPK2; ARHGFE12; MX1; BNIPL; PPARG; COL4A3; TP73; NGFR; WT1; SST; CADM1; PDCD5; ITGB3BP; CEBPG; ETS1; SMAD3; BRCA1; DAXX; RPS3A; TP53INP1; STAT1; IFNB1; TP53; CEBPB; TP53BP2; SQSTM1; ITSN1; PPP2CA; TRAF5; AXIN1
GO:0012502	4.70E-06	0.0175	14791	601	314	31	BP	induction of programmed cell death	HIPK2; ARHGFE12; MX1; BNIPL; PPARG; COL4A3; TP73; NGFR; WT1; SST; CADM1; PDCD5; ITGB3BP; CEBPG; ETS1; SMAD3; BRCA1; DAXX; RPS3A; TP53INP1; STAT1; IFNB1; TP53; CEBPB; TP53BP2; SQSTM1; ITSN1; PPP2CA; TRAF5; AXIN1
GO:0051098	4.70E-06	0.0176	14791	601	182	22	BP	regulation of binding	HIPK2; CAMK2A; BLM; PPARG; SIGIRR; SMAD4; SMAD7; ERC1; JUN; RNA; REL; SMARCA4; CEBPG; PRKCD; SMAD3; BCL2; STK36; IL1B; IL6; TNF; RPTK9; NPM1
GO:0019220	5.20E-06	0.0195	14791	601	529	44	BP	regulation of phosphate metabolic process	PPAP2A; PIK3CB; SMG5; BLM; PDE6H; SMAD4; SMAD7; TSC1; BDKRB2; TP73; EGFR; JUN; HGF; LIF; DAB1; CDKN2B; ADCY1; VLDLR; IGF1; CDK7; CAMP; PRKCD; SMAD3; BCL2; CAV3; GHR; ADCY5; DAXX; RAD50; IL1B; IL6; MAP2K3; PDPK1; PKN1; MCM7; DUSP12; PPP2CA; TGFA; TAF7; TNF; NBN; DGKQ; NPM1; AXIN1
GO:0051174	5.20E-06	0.0195	14791	601	529	44	BP	regulation of phosphorus metabolic process	PPAP2A; PIK3CB; SMG5; BLM; PDE6H; SMAD4; SMAD7; TSC1; BDKRB2; TP73; EGFR; JUN; HGF; LIF; DAB1; CDKN2B; ADCY1; VLDLR; IGF1; CDK7; CAMP; PRKCD; SMAD3; BCL2; CAV3; GHR; ADCY5; DAXX; RAD50; IL1B; IL6; MAP2K3; PDPK1; PKN1; MCM7; DUSP12; PPP2CA; TGFA; TAF7; TNF; NBN; DGKQ; NPM1; AXIN1
GO:0007178	5.40E-06	0.02	14791	601	94	15	BP	transmembrane receptor protein serine/threonine kinase signaling pathway	AKAP3; SMAD9; SMAD4; SMAD7; SMAD1; LEF1; JUN; SMAD3; CREB1; SMURF1; SMURF2; FOS; AMHR2; GDF5; GDF9

GO:0007166	5.80E-06	0.0216	14791	601	1800	110	BP	cell surface receptor linked signaling pathway	PPAP2A; SCG5; HIPK2; LICAM; PIK3CB; ARHGEF12; AKAP3; ITGA3; FZD10; COL4A3; CSNK1A1; ITGAV; SMAD9; SMAD4; TLE2; SMAD7; SMAD1; AKAP12; LEPR; LEF1; BDKRB2; EGFR; IGF1R; JAG1; JUN; FZD8; HGF; WNT16; LIF; AVPR1A; RARG; WNT10A; SAG; RELA; HOMER1; ADCY1; GNG2; RHO; CNTN1; SST; ADAP1; F2RL3; LPAR1; AGRP; CEBA; DVL2; VIPR1; SMAD3; GHR; ERBB4; CREB1; BRD8; BRD7; ADCY5; GNAO1; SMURF1; SMURF2; FOS; FGF22; FGF23; CCR4; IL1B; STAT3; STAT1; IFNB1; SFRP2; WNT2; IL6; AP3S1; CAMLG; WASF2; AMHR2; GDF5; DRD2; WNT9B; HTR1A; NTRK2; NTRK3; GABRR2; SOCS2; MST1R; GSK3B; HTR1B; CHRM2; HRAS; FGF5; FGF4; SDC1; MPL; TNF; EPHA8; EPHA3; EPHA2; GNRHR; NCAM1; FZD6; HEY1; SOS1; GDF9; STAT5B; STAT5A; RIPK2; GRIN2C; DGKQ; ADRBK1; GLI2; FSHR; PLAT; AXIN1; IGF2R
GO:0051341	6.40E-06	0.024	14791	601	43	10	BP	regulation of oxidoreductase activity	CYP27B1; EGFR; SNCA; SCARB1; NFKB1; CAV3; HIF1A; FGF23; IL1B; TNF
GO:0023056	6.60E-06	0.0245	14791	601	273	28	BP	positive regulation of signaling process	HIPK2; LICAM; F3; AR; PPARD; AKAP12; REL; LEPR; IGF1R; SNCA; LIF; RELA; IGF1; F10; LPAR1; GHR; FGF23; IL1B; IL6; ITSN1; EEF1D; HRAS; FGF4; TNF; NCAM1; RIPK2; TRAF5; AXIN1
GO:0010740	6.60E-06	0.0246	14791	601	214	24	BP	positive regulation of intracellular protein kinase cascade	HIPK2; F3; AR; AKAP12; REL; LEPR; IGF1R; LIF; RELA; IGF1; F10; LPAR1; GHR; FGF23; IL1B; IL6; ITSN1; EEF1D; HRAS; FGF4; TNF; RIPK2; TRAF5; AXIN1
GO:0009888	7.00E-06	0.0262	14791	601	368	34	BP	tissue development	CYP27B1; DSP; PPARD; PPARA; SMAD4; LEF1; EGFR; NGFR; HOXB13; LIF; COL11A2; RARG; RELA; WT1; PTGES3; BMX; EPOR; NTF3; CITED2; COL17A1; HOXA5; SMAD3; GHR; ZFPM2; BMP8A; SMURF1; SFRP2; TFAP2A; POU3F2; ALPL; NKX2-1; BMP5; PPP2CA; HOXC11
GO:0009628	7.20E-06	0.027	14791	601	401	36	BP	response to abiotic stimulus	F3; BLM; PPARG; PRKDC; BDKRB2; EGFR; NGFR; NOS1; JUN; AVPR1A; SAG; RELA; DBH; RHO; USF1; SST; MSH2; BCL2; CACNA1F; TRPV4; BRCA1; RIC8A; FOS; CCR4; IL1B; STAT1; TP53; PDPK1; HSPB3; PKN1; DRD2; NKX2-1; HRAS; TNF; MAP1B; DUSP1
GO:0017015	7.30E-06	0.0271	14791	601	53	11	BP	regulation of transforming growth factor beta receptor signaling pathway	HIPK2; SMAD4; SMAD7; CDKN2B; CITED2; SMAD3; SMURF1; SMURF2; ING2; TP53; NKX2-1
GO:0080134	7.70E-06	0.0286	14791	601	306	30	BP	regulation of response to stress	HIPK2; F3; APOH; PPARG; TP73; RELA; MASP1; USF1; AP2B1; CADM1; CEBPG; TRPV4; BRCA1; DAXX; NT5E; IL1B; IFNB1; IGBP1; IL6; PKN1; NTRK3; TNF; NCOR1; STAT5B; STAT5A; PSMB4; RIPK2; NDEL1; NPM1; AXIN1
GO:0006275	7.70E-06	0.0286	14791	601	74	13	BP	regulation of DNA replication	BLM; IGF1R; JUN; IGF1; GMNN; TP53; ENPP7; PPP2CA; TERF1; HRAS; NBN; GLI2; ATF1
GO:0045646	8.60E-06	0.0319	14791	601	20	7	BP	regulation of erythrocyte differentiation	SPI1; HOXA5; ETS1; HIF1A; TAL1; STAT5B; STAT5A
GO:0042325	8.60E-06	0.0321	14791	601	505	42	BP	regulation of phosphorylation	PPAP2A; PIK3CB; BLM; PDE6H; SMAD4; SMAD7; TSC1; BDKRB2; TP73; EGFR; JUN; HGF; LIF; DAB1; CDKN2B; ADCY1; VLDLR; IGF1; CDK7; CAMP; PRKCD; BCL2; CAV3; GHR; ADCY5; DAXX; RAD50; IL1B; IL6; MAP2K3; PDPK1; PKN1; MCM7; DUSP12; PPP2CA; TGFA; TAF7; TNF; NBN; DGKQ; NPM1; AXIN1
GO:0000302	8.70E-06	0.0323	14791	601	86	14	BP	response to reactive oxygen species	F3; JUN; RELA; LPO; FANCC; BCL2; ERBB4; GNAO1; FOS; STAT1; PPP2CB; SDC1; DUSP1; ADRBK1
GO:0051248	9.40E-06	0.035	14791	601	204	23	BP	negative regulation of protein metabolic process	ANAPC5; ANAPC7; ITGAV; SMAD7; TSC1; BDKRB2; SNCA; JUN; RELA; WT1; MASP1; NFKB1; PRKCD; PSME1; CDC16; EIF2C2; PPP2CA; TAF7; CDC23; BCOR; PSMB4; GRIN2C; PLAT
GO:0001775	9.40E-06	0.0351	14791	601	263	27	BP	cell activation	PIK3CB; SP3; BLM; PRKDC; EGFR; SNCA; FGB; CADM1; MSH2; CEBPG; PRKCD; SMAD3; BCL2; EGRI; NFKB2; TOLLIP; PAX1; IFNB1; IGBP1; TP53; IL6; VWF; TNF; NBN; STAT5B; STAT5A; RIPK2
GO:0006468	9.80E-06	0.0364	14791	601	666	51	BP	protein amino acid phosphorylation	STK16; HIPK2; PIK3CB; CAMK2A; CAMK2B; CSNK1A1; PDE6H; SMAD9; SMAD7; SMAD1; PRKDC; SRPK1; ERC1; EGFR; IGF1R; ERG; HGF; RHO; MAPK10; PRKG1; BMX; CSNK1E; CDK7; PRKCD; ABI3; BCL2; GHR; ERBB4; CREB1; DAXX; STK36; IL1B; STAT1; MARK3; MAP2K3; AMHR2; PDPK1; PKN1; NTRK2; NTRK3; MST1R; GSK3B; MAPKAPK5; TGFA; TNF; EPHA8; EPHA3; EPHA2; STAT5A; RIPK2; ADRBK1
GO:0006970	1.00E-05	0.037	14791	601	36	9	BP	response to osmotic stress	BDKRB2; EGFR; SST; TRPV4; TP53; PDPK1; PKN1; NKX2-1; TNF
GO:0042542	1.00E-05	0.0376	14791	601	65	12	BP	response to hydrogen peroxide	F3; JUN; RELA; LPO; BCL2; ERBB4; GNAO1; STAT1; PPP2CB; SDC1; DUSP1; ADRBK1
GO:0008202	1.10E-05	0.0411	14791	601	206	23	BP	steroid metabolic process	CYP2C9; SULT1E1; OSBPL3; APOB; CYP27B1; PPARD; RXRA; LEPR; ACAA2; LIPC; SCARB1; VLDLR; CETP; ESRI; FGF23; LCAT; COMT; CYP1A2; AKR1B10; CYP2B6; SRD5A2; STAT5B; SREBF1

GO:0045786	1. 10E-05	0. 0423	14791	601	178	21	BP	negative regulation of cell cycle	DLG1; TSG101; CYP27B1; TP73; EGFR; NGFR; CDKN2B; TPR; GMNN; MLF1; MSH2; SMARCA4; ETS1; SMAD3; BCL2; TP53INP1; TP53; TP53BP2; TERF1; HRAS; NBN
GO:0007267	1. 10E-05	0. 0434	14791	601	477	40	BP	cell-cell signaling	AR; RIT2; APBA2; PGR; SNCA; HGF; WNT16; HOMER1; DBH; KCNK3; SST; NTF3; GRIK5; HOXA5; VIPR1; DLGAP4; ESR2; TOLLIP; SYN1; IL1B; PDE7B; EFNA5; EFNA4; WNT2; GDF5; DRD2; WNT9B; NKX2-1; GABRR2; POU2F1; VDACL1; HTRIB; FGF5; FGF4; SDCBP; CACNB2; SRD5A2; FGF11; PLAT; HOXC11
GO:0006573	1. 30E-05	0. 0483	14791	601	5	4	BP	valine metabolic process	GHR; STAT5B; STAT5A; ALDH6A1
GO:0043523	1. 30E-05	0. 0487	14791	601	89	14	BP	regulation of neuron apoptosis	HIPK2; TP73; SNCA; JUN; NTF3; MSH2; BCL2; GHR; ESR2; ESR1; TP53; ITSN1; HRAS; TNF
GO:0009967	1. 30E-05	0. 0495	14791	601	268	27	BP	positive regulation of signal transduction	HIPK2; L1CAM; F3; AR; PPARC; AKAP12; REL; LEPR; IGF1R; LIF; RELA; IGF1; F10; LPAR1; GHR; FGF23; IL1B; IL6; ITSN1; EEF1D; HRAS; FGF4; TNF; NCAM1; RIPK2; TRAF5; AXIN1
GO:0006629	1. 30E-05	0. 0502	14791	601	821	59	BP	lipid metabolic process	PPAP2A; PIK3CB; CYP2C9; SULT1E1; OSBPL3; APOD; APOB; APOH; CYP27B1; PPARG; PPARC; PPARA; GPX5; ACP6; RXRA; LEPR; ACAA2; SNCA; HEXB; LIPC; PTGES3; SCARB1; VLDLR; PI4KB; FABP3; CHPT1; CLU; MGLL; PLCD3; CAV3; GHR; CETP; GBA; PLCB2; ESR1; ACAD8; FGF23; ACACB; LCAT; COMT; CYP11A2; HADHA; DRD2; RDH12; NKX2-1; ENPP7; PPP2CA; ACSL1; PEX5; ATP5B; AKR1B10; CYP2B6; SRD5A2; SGGP1; FADS2; STAT5B; STAT5A; SREBF1; PEMT
GO:0051093	1. 30E-05	0. 0515	14791	601	284	28	BP	negative regulation of developmental process	APOH; PPARG; COL4A3; PPARA; ITGAV; SMAD7; LEF1; NGFR; JAG1; LIF; IGF1; ZFXH3; HOXA5; SMAD3; BCL2; CETP; SMURF1; FGF23; TP53; SFRP2; NKX2-1; FGF4; TNF; NBN; BCOR; STAT5B; STAT5A; GLI2
GO:0031401	1. 50E-05	0. 0578	14791	601	225	24	BP	positive regulation of protein modification process	ANAPC5; ANAPC7; SMAD4; SMAD7; LIF; IGF1; SKP1; CAMP; PSME1; BCL2; GHR; BRCA1; SMURF1; CDC16; RAD50; IL1B; TP53; IL6; CDC23; TNF; NBN; PSMB4; RIPK2; AXIN1
GO:0043410	1. 60E-05	0. 0599	14791	601	79	13	BP	positive regulation of MAPKKK cascade	HIPK2; AR; LEPR; IGF1R; LIF; FGF23; IL1B; IL6; HRAS; FGF4; TNF; RIPK2; AXIN1
GO:0071375	1. 60E-05	0. 0599	14791	601	79	13	BP	cellular response to peptide hormone stimulus	PPARG; PRKDC; RXRA; IGF1R; VLDLR; USF1; PPAT; GHR; STAT1; AP3S1; PDPK1; GOT1; SOCS2
GO:0016055	1. 60E-05	0. 0612	14791	601	128	17	BP	Wnt receptor signaling pathway	FZD10; CSNK1A1; TLE2; LEF1; FZD8; WNT16; RARG; WNT10A; DVL2; BRD7; SFRP2; WNT2; WNT9B; GSK3B; SDC1; FZD6; AXIN1
GO:0001657	2. 00E-05	0. 0747	14791	601	39	9	BP	ureteric bud development	SMAD9; SMAD4; SMAD7; SMAD1; RARB; WT1; SMAD3; BCL2; SDC1
GO:0040014	2. 20E-05	0. 0826	14791	601	49	10	BP	regulation of multicellular organism growth	IGF1; BCL2; GHR; CREB1; STAT3; GDF5; POU3F2; PEX5; STAT5B; STAT5A
GO:0044419	2. 20E-05	0. 0847	14791	601	389	34	BP	interspecies interaction between organisms	HIPK2; DLG1; SP1; TSG101; ITGAV; TAF11; IRF3; RXRA; SRPK1; JUN; RELA; SCARB1; GTF2E1; RALA; HNRNP1A1; USP7; CEBPA; SMAD3; WWP1; MAGI3; CREB1; CTSG; KPNA2; DAXX; STAT3; STAT1; TP53; VDACL1; NACA; BAT1; FBLN1; PSMB4; NPM1; NEDD4L
GO:0043687	2. 20E-05	0. 0848	14791	601	1243	80	BP	post-translational protein modification	STK16; HIPK2; PIK3CB; CAMK2A; CAMK2B; TSG101; UBE2D2; SENP2; DSP; ANAPC5; ANAPC7; CSNK1A1; PDE6H; SMAD9; ASH2L; SMAD7; SMAD1; PRKDC; SRPK1; ERC1; EGFR; IGF1R; ERG; HGF; RHO; MAPK10; PRKG1; BMX; CSNK1E; NSD1; CDK7; USP7; SUZ12; PRKCD; ABI3; BCL2; WWP1; GHR; BRCA1; ERBB4; PRMT3; CREB1; BRD8; DZIP3; PRMT5; SMURF1; DAXX; CDC16; TRRAP; STK36; LCMT1; IL1B; STAT1; MARK3; MAP2K3; AMHR2; PDPK1; PKN1; DUSP14; DUSP12; NTRK2; NTRK3; PPP2CA; PPP2CB; MST1R; GSK3B; MAPKAPK5; TGFA; CDC23; TNF; EPHA8; EPHA3; EPHA2; DUSP1; PCMT1; STAT5A; RIPK2; ADRBK1; PTPRS; NEDD4L
GO:0002070	2. 30E-05	0. 0858	14791	601	10	5	BP	epithelial cell maturation	PGR; HOXB13; HOXA5; ESR2; KCNE1
GO:0044106	2. 30E-05	0. 0869	14791	601	308	29	BP	cellular amine metabolic process	NOS1; SNCA; YARS2; LIPC; TPR; DBH; AGMAT; SARDH; FABP3; CHPT1; PPAT; GHR; CETP; ACAD8; HARS; LCAT; COMT; AGXT; HARS2; AADAT; DRD2; GOT1; ASL; ACHE; STAT5B; STAT5A; ALDH6A1; GGT1; PEMT
GO:0022029	2. 40E-05	0. 0918	14791	601	16	6	BP	telencephalon cell migration	EGFR; DAB1; POU3F2; DRD2; NKX2-1; PEX5
GO:0006103	2. 40E-05	0. 0918	14791	601	16	6	BP	2-oxoglutarate metabolic process	DLST; GHR; AADAT; GOT1; STAT5B; STAT5A
GO:0050878	2. 60E-05	0. 0976	14791	601	146	18	BP	regulation of body fluid levels	F3; MST1; APOH; F5; TP73; PROS1; F10; USF2; PPAT; F2RL3; CREB1; XDH; VWF; DRD2; FL11; STAT5B; STAT5A; PLAT

GO:0010720	2.70E-05	0.1035	14791	601	83	13	BP	positive regulation of cell development	PPARG; SMAD4; SMAD1; NGFR; RELA; NTF3; SMAD3; BCL2; XRCC5; DRD2; NTRK3; MAP1B; NDEL1
GO:0051130	2.90E-05	0.111	14791	601	219	23	BP	positive regulation of cellular component organization	SMAD4; SMAD1; TSC1; NGFR; SNCA; SFTPD; IGF1; RALA; SMAD3; CAV3; IL1B; TP53; PDPK1; NTRK3; GSK3B; TERF1; TGFA; TNF; MAP1B; NDEL1; NPM1; ATF1; NEDD4L
GO:0048610	3.20E-05	0.1192	14791	601	162	19	BP	reproductive cellular process	PPAP2A; AKAP3; AR; PRKDC; RXRA; TRIP13; HOXB13; WT1; FANCC; MSH2; BCL2; ESR2; NKX2-1; SDC1; SHBG; ACR; GDF9; STAT5A; FSHR
GO:0040018	3.30E-05	0.1237	14791	601	24	7	BP	positive regulation of multicellular organism growth	BCL2; GHR; CREB1; POU3F2; PEX5; STAT5B; STAT5A
GO:0051049	3.40E-05	0.1283	14791	601	500	40	BP	regulation of transport	SCG5; JPH2; PPARG; ITGAV; SMAD4; NOS1; SNCA; SFTPD; LIF; AVPRIA; CATSPER1; PEA15; HOMER1; SCARB1; NFKB1; RALA; CADM1; SMAD3; BCL2; CAV3; CETP; ERBB4; CREB1; GNAO1; RPH3AL; FGF23; IL1B; IL6; DRD2; PICALM; CACNA2D1; SYT9; GSK3B; HTR1B; TNF; ACHE; TACC3; ADRBK1; CACNA1C; NEDD4L
GO:0021885	3.70E-05	0.1371	14791	601	17	6	BP	forebrain cell migration	EGFR; DAB1; POU3F2; DRD2; NKX2-1; PEX5
GO:0007610	3.90E-05	0.1462	14791	601	468	38	BP	behavior	HIPK2; PIK3CB; HOXB8; RALBP1; LEPR; APBA2; ABAT; DEFA1; CYR61; SNCA; JUN; HEXB; SFTPD; AVPRIA; ADCY1; DBH; VLDLR; RALA; AGRP; BCL2; ADCY5; GNAO1; EGRI; RIC8A; FOS; ESR2; CCR4; IL1B; STAT3; COMT; IL6; DRD2; HTR1A; NKX2-1; VDAC1; HTR1B; HRAS; CRHBP
GO:0048568	4.00E-05	0.1515	14791	601	63	11	BP	embryonic organ development	SP1; SP3; EGFR; CYR61; CITED2; CEBPA; PLCD3; ZFPM2; WNT2; CEBPB; GLI2
GO:0051240	4.20E-05	0.1557	14791	601	270	26	BP	positive regulation of multicellular organismal process	F3; APOH; EGFR; NOS1; SNCA; AVPRIA; RARA; DBH; USF1; EPHX2; SMAD3; BCL2; GHR; ERBB4; CREB1; CRX; HIF1A; IL1B; IL6; TFAP2A; POU3F2; PEX5; TNF; STAT5B; STAT5A; RIPK2
GO:0032869	4.50E-05	0.1686	14791	601	75	12	BP	cellular response to insulin stimulus	PPARG; PRKDC; RXRA; IGF1R; VLDLR; USF1; PPAT; GHR; STAT1; AP3S1; PDPK1; GOT1
GO:0042439	5.00E-05	0.1868	14791	601	34	8	BP	ethanolamine and derivative metabolic process	LIPC; DBH; FABP3; CHPT1; CETP; LCAT; ACHE; PENT
GO:0048584	5.30E-05	0.1966	14791	601	258	25	BP	positive regulation of response to stimulus	HIPK2; F3; CYP27B1; RELA; MASP1; CADM1; CLU; CEBPG; SMAD3; BRCA1; CTSG; MASP2; FCN2; CCR4; IL1B; IFNB1; IL6; CIS; NTRK3; TNF; STAT5B; STAT5A; RIPK2; NDEL1; AXIN1
GO:0001892	5.30E-05	0.1986	14791	601	18	6	BP	embryonic placenta development	SP1; SP3; EGFR; CITED2; CEBPA; CEBPB
GO:0030879	5.90E-05	0.219	14791	601	26	7	BP	mammary gland development	HOXB9; LEF1; IGF1R; PGR; IGF1; ERBB4; GLI2
GO:0006575	6.20E-05	0.2323	14791	601	170	19	BP	cellular amino acid derivative metabolic process	P4HA2; ABAT; SNCA; LIPC; DBH; AGMAT; FABP3; CHPT1; GHR; CETP; LCAT; COMT; AADAT; DRD2; ACHE; STAT5B; STAT5A; GGT1; PENT
GO:0043279	6.30E-05	0.2361	14791	601	55	10	BP	response to alkaloid	PPARG; LEPR; ABAT; RELA; BCL2; GHR; GNAO1; IL1B; DRD2; HTR1B
GO:0007179	6.30E-05	0.2361	14791	601	55	10	BP	transforming growth factor beta receptor signaling pathway	SMAD9; SMAD4; SMAD1; JUN; SMAD3; CREB1; FOS; AMHR2; GDF5; GDF9
GO:0046449	6.60E-05	0.2473	14791	601	3	3	BP	creatinine metabolic process	GHR; STAT5B; STAT5A
GO:0046543	6.60E-05	0.2473	14791	601	3	3	BP	development of secondary female sexual characteristics	NKX2-1; STAT5B; STAT5A

GO:0048646	6.70E-05	0.2505	14791	601	310	28	BP	anatomical structure formation involved in morphogenesis	AR; ZIC2; SMAD4; PRKDC; TSC1; LEPR; LEF1; JAG1; NOS1; CYR61; JUN; HOXB13; HOXA1; DVL2; SMAD3; PLCD3; PAX1; TP53; SFRP2; WASF2; NKX2-1; CAPN2; POU2F1; EPHA2; ATP5B; FZD6; ADAM12; GLI2
GO:0021795	6.80E-05	0.2519	14791	601	12	5	BP	cerebral cortex cell migration	EGFR; DAB1; POU3F2; NKX2-1; PEX5
GO:0030520	6.80E-05	0.2519	14791	601	12	5	BP	estrogen receptor signaling pathway	RBM9; RARA; ESR2; ESR1; TAF7
GO:0006519	6.90E-05	0.2559	14791	601	360	31	BP	cellular amino acid and derivative metabolic process	P4HA2; ABAT; NOS1; SNCA; YARS2; LIPC; TPR; DBH; AGMAT; SARDH; FABP3; CHPT1; PPAT; GHR; CETP; ACAD8; HARS; LCAT; COMT; AGXT; HARS2; AADAT; DRD2; GOT1; ASL; ACHE; STAT5B; STAT5A; ALDH6A1; GGT1; PEMT
GO:0033135	7.50E-05	0.2803	14791	601	19	6	BP	regulation of peptidyl-serine phosphorylation	SMAD7; BDKRB2; LIF; BCL2; IL6; AXIN1
GO:0043603	7.50E-05	0.2803	14791	601	19	6	BP	cellular amide metabolic process	CYP2C9; CEBPA; GHR; ASL; STAT5B; STAT5A
GO:0045639	7.80E-05	0.2899	14791	601	36	8	BP	positive regulation of myeloid cell differentiation	JAG1; JUN; LIF; HOXA5; ETS1; HIF1A; TAL1; STAT5A
GO:0008015	8.10E-05	0.3016	14791	601	46	9	BP	blood circulation	COL4A3; KCNH2; BDKRB2; AVPR1A; STAT1; KCNE2; KCNE1; FLI1; GUCY1A3
GO:0060558	8.50E-05	0.3173	14791	601	7	4	BP	regulation of calcidiol 1-monooxygenase activity	CYP27B1; NFKB1; IL1B; TNF
GO:0032270	8.70E-05	0.3226	14791	601	282	26	BP	positive regulation of cellular protein metabolic process	ANAPC5; ANAPC7; SMAD4; SMAD7; LIF; IGF1; CSNK1E; SKP1; CAMP; PSME1; BCL2; GHR; BRCA1; SMURF1; CDC16; RAD50; IL1B; TP53; IL6; CDC23; TNF; NBN; PSMB4; RIPK2; PEMT; AXIN1
GO:0035295	8.70E-05	0.3241	14791	601	57	10	BP	tube development	SMAD9; SMAD4; SMAD7; SMAD1; RARB; WT1; SMAD3; BCL2; SDC1; GLI2
GO:0006302	8.70E-05	0.3241	14791	601	57	10	BP	double-strand break repair	BLM; PRKDC; TRIP13; MSH2; BRCA1; XRCC5; RAD50; TP53; NBN; RAD21
GO:0001932	8.70E-05	0.3257	14791	601	204	21	BP	regulation of protein amino acid phosphorylation	SMAD4; SMAD7; BDKRB2; TP73; EGFR; JUN; LIF; IGF1; CAMP; PRKDC; BCL2; GHR; DAXX; RAD50; IL1B; IL6; PKN1; PPP2CA; TNF; NBN; AXIN1
GO:0031668	1.00E-04	0.3776	14791	601	58	10	BP	cellular response to extracellular stimulus	LEPR; JUN; AVPR1A; CDKN2B; USF1; USF2; FOS; TP53; SFRP2; SREBF1
GO:0071496	1.00E-04	0.3776	14791	601	58	10	BP	cellular response to external stimulus	LEPR; JUN; AVPR1A; CDKN2B; USF1; USF2; FOS; TP53; SFRP2; SREBF1
GO:0040012	1.00E-04	0.3788	14791	601	237	23	BP	regulation of locomotion	F3; APOH; SMAD7; EGFR; IGF1R; JAG1; SNCA; SCARB1; IGF1; F10; SST; CITED2; SMAD3; ABI3; BCL2; ERBB4; HIF1A; CCR4; IFNB1; IL6; DRD2; NKX2-1; EPHA2
GO:0022402	1.00E-04	0.3884	14791	601	562	42	BP	cell cycle process	CAMK2B; AKAP8; TSG101; CYP27B1; BLM; ANAPC5; ANAPC7; CSNK1A1; TP73; RBM7; GF11B; HGF; TRIP13; CDKN2B; CENPJ; MLF1; SKP1; DSCC1; MSH2; PSME1; SMAD3; ILF3; BCL2; KPNA2; DAXX; CDC16; RAD50; TP53INP1; TP53; PPP2CA; TERF1; STMN1; HRAS; CDC23; NBN; PSMB4; MKI67; SIN3A; RAD21; C17orf11; NDM1; ESD1
GO:0022409	1.00E-04	0.3958	14791	601	13	5	BP	positive regulation of cell-cell adhesion	L1CAM; SMAD7; CITED2; IL1B; TNF
GO:0001501	1.00E-04	0.398	14791	601	148	17	BP	skeletal system development	SP1; SP3; HOXB9; HEXB; COL11A2; IGF1; SMAD3; PAX1; LGALS3; ALPL; ETS2; BMP5; ACAN; EPHA2; PAPS1; GLI2; HOXC11

GO:0007169	1.00E-04	0.4014	14791	601	207	21	BP	transmembrane receptor protein tyrosine kinase signaling pathway	BDKRB2; EGFR; IGF1R; HGF; GHR; ERBB4; FGF22; FGF23; AP3S1; CAMLG; NTRK2; NTRK3; SOCS2; MST1R; FGF5; FGF4; EPHA8; EPHA3; EPHA2; SOS1; PLAT
GO:0032269	1.00E-04	0.4047	14791	601	192	20	BP	negative regulation of cellular protein metabolic process	ANAPC5; ANAPC7; ITGAV; SMAD7; TSC1; BDKRB2; SNCA; JUN; WT1; NFKB1; PRKCD; PSME1; CDC16; EIF2C2; PPP2CA; TAF7; CDC23; BCOR; PSMB4; PLAT
GO:0006352	1.10E-04	0.4128	14791	601	82	12	BP	transcription initiation	GTF2I; TAF11; GTF2E1; CDK7; TAF9B; GTF2H4; SNAPC5; MED30; POLR2H; POLR2K; POLR2J; TAF7
GO:0051336	1.20E-04	0.4451	14791	601	371	31	BP	regulation of hydrolase activity	F3; APOH; PPARG; COL4A3; GDI1; RALBP1; TSC1; LEPR; EGFR; SNCA; AVPR1A; HOMER1; ADAP1; F2RL3; LPAR1; MSH2; MSH3; SMAD3; GNAO1; PLCB2; STAT1; IFNB1; IGBP1; TP53; ASAP1; ASAP2; DRD2; TERF1; CHRM2; TNF; NDEL1
GO:0043388	1.20E-04	0.4651	14791	601	83	12	BP	positive regulation of DNA binding	HIPK2; CAMK2A; PPARG; ERC1; RELA; SMARCA4; CEBPG; IL1B; IL6; TNF; RIPK2; NPM1
GO:0050678	1.20E-04	0.4651	14791	601	83	12	BP	regulation of epithelial cell proliferation	AR; PPARD; EGFR; PGR; CDKN2B; IGF1; HOXA5; SMAD3; ERBB4; ESR2; WNT2; TGFA
GO:0048661	1.20E-04	0.4674	14791	601	29	7	BP	positive regulation of smooth muscle cell proliferation	EGFR; JUN; IGF1; STAT1; IL6; TNF; STAT5B
GO:0008637	1.20E-04	0.4674	14791	601	29	7	BP	apoptotic mitochondrial changes	TP73; JUN; CLU; SMAD3; BCL2; TP53; DNML
GO:0002252	1.30E-04	0.4852	14791	601	109	14	BP	immune effector process	RELA; DBH; MASP1; CADM1; CLU; MSH2; CEBPG; PRKCD; BCL2; CTSG; MASP2; FCN2; IL6; C1S
GO:0001558	1.30E-04	0.4923	14791	601	210	21	BP	regulation of cell growth	TSG101; CYP27B1; PPARG; SMAD4; TP73; CYR61; AVPR1A; WT1; IGFBP6; CHPT1; TAF9B; PRSS2; SMAD3; BCL2; ESR2; TP53; NTRK3; SOCS2; PPP2CA; MAP1B; CHFG
GO:0009308	1.30E-04	0.5034	14791	601	408	33	BP	amine metabolic process	P4HA2; ABAT; NOS1; SNCA; YARS2; HEXB; LIPC; TPR; DBH; AGMAT; SARDH; FABP3; CHPT1; PPAT; GHR; CETP; ACAD8; HARS; LCAT; COMT; AGXT; HARS2; AADAT; DRD2; GOT1; SGPP1; ASL; ACHE; STAT5B; STAT5A; ALDH6A1; GGT1; PSM1
GO:0030217	1.30E-04	0.5046	14791	601	49	9	BP	T cell differentiation	SP3; BLM; PRKDC; BCL2; EGR1; PAX1; TP53; STAT5B; STAT5A
GO:0051591	1.30E-04	0.5046	14791	601	49	9	BP	response to cAMP	JUN; RELA; FOS; STAT1; AGXT; C1S; SDC1; DUSP1; PLAT
GO:0051338	1.30E-04	0.5105	14791	601	391	32	BP	regulation of transferase activity	PPAP2A; PIK3CB; BLM; PPARG; PDE6H; TSC1; TP73; EGFR; HGF; DAB1; CDKN2B; ADCY1; VLDLR; CDK7; CAV3; GHR; ADCY5; DAXX; RAD50; IL1B; MAP2K3; PDPK1; PKN1; DUSP12; PPP2CA; TERF1; TGFA; TAF7; TNF; NBN; DGRQ; NPM1
GO:0045927	1.40E-04	0.5229	14791	601	84	12	BP	positive regulation of growth	AVPR1A; TAF9B; PRSS2; BCL2; GHR; CREB1; POU3F2; NTRK3; PEX5; MAP1B; STAT5B; STAT5A
GO:0001836	1.40E-04	0.5231	14791	601	21	6	BP	release of cytochrome c from mitochondria	TP73; JUN; CLU; SMAD3; BCL2; TP53
GO:0046470	1.40E-04	0.5231	14791	601	21	6	BP	phosphatidylcholine metabolic process	LIPC; FABP3; CHPT1; CETP; LCAT; PEMT
GO:0044248	1.40E-04	0.5281	14791	601	719	50	BP	cellular catabolic process	CYP2C9; TSG101; UBE2D2; APOB; CYP27B1; SMG5; PPARD; ANAPC5; ANAPC7; ABAT; NOS1; HEXB; LIPC; LPO; DBH; SARDH; EPHX2; PDE11A; SKP1; DLST; CDK7; GTF2H4; USP7; PSME1; SMURF1; SMURF2; CDC16; NT5E; XDH; ACAD8; FGF23; RBM8A; ZHX2; COMT; CYP1A2; HADHA; SQSTM1; PON3; GOT1; PPP2CB; PEX5; CDC23; ATP5B; CYP2B6; ASL; ACHE; PSMB4; DERA; ALDH6A1; UPF3A
GO:0006953	1.40E-04	0.5293	14791	601	39	8	BP	acute-phase response	SIGIRR; CEBPA; IL1B; STAT3; IL6; CEBPB; EPHA3; STAT5B
GO:0051091	1.40E-04	0.5344	14791	601	72	11	BP	positive regulation of transcription factor activity	CAMK2A; PPARG; ERC1; RELA; SMARCA4; CEBPG; IL1B; IL6; TNF; RIPK2; NPM1

GO:0090047	1.40E-04	0.5344	14791	601	72	11	BP	positive regulation of transcription regulator activity	CAMK2A; PPARG; ERC1; RELA; SMARCA4; CEBPG; IL1B; IL6; TNF; RIPK2; NPM1
GO:0003002	1.40E-04	0.5393	14791	601	181	19	BP	regionalization	HIPK2; HHIP; HOXB8; HOXB9; SMAD4; PRKDC; LEF1; RARG; HOXA5; HOXA1; DVL2; SMAD3; PAX1; YY1; TP53; SFRP2; NKX2-1; GLI2; HOXC11
GO:0051099	1.40E-04	0.5423	14791	601	97	13	BP	positive regulation of binding	HIPK2; CAMK2A; PPARG; ERC1; RARA; RELA; SMARCA4; CEBPG; IL1B; IL6; TNF; RIPK2; NPM1
GO:0007389	1.40E-04	0.5529	14791	601	259	24	BP	pattern specification process	HIPK2; HHIP; HOXB8; HOXB9; SMAD4; SMAD1; PRKDC; LEF1; RARG; CITED2; HOXA5; HOXA1; DVL2; SMAD3; PAX1; YY1; TP53; SFRP2; NKX2-1; BMP5; BCOR; GLI2; AXIN1; HOXC11
GO:0009615	1.50E-04	0.5643	14791	601	138	16	BP	response to virus	IFNA10; MX1; APOB; IRF3; IFNA21; DEFA1; RELA; CLU; BCL2; STAT1; IFNB1; IL6; MST1R; STMN1; CHRM2; TNF
GO:0000723	1.50E-04	0.5884	14791	601	30	7	BP	telomere maintenance	BLM; PRKDC; PTGES3; XRCC5; RAD50; TERF1; NBN
GO:0030511	1.60E-04	0.5951	14791	601	14	5	BP	positive regulation of transforming growth factor beta receptor signaling pathway	HIPK2; SMAD4; CDKN2B; CITED2; ING2
GO:0046697	1.60E-04	0.5951	14791	601	14	5	BP	decidualization	CYP27B1; PPARG; LIF; EPOR; CITED2
GO:0045637	1.60E-04	0.6065	14791	601	73	11	BP	regulation of myeloid cell differentiation	SPI1; JAG1; JUN; LIF; HOXA5; ETS1; HIF1A; TAL1; TNF; STAT5B; STAT5A
GO:0080135	1.60E-04	0.6129	14791	601	125	15	BP	regulation of cellular response to stress	HIPK2; TP73; CEBPG; BRCA1; DAXX; IL1B; IGBP1; PKN1; NTRK3; TNF; NCOR1; RIPK2; NDEL1; NPM1; AXIN1
GO:0048468	1.60E-04	0.6164	14791	601	229	22	BP	cell development	LEF1; TP73; TRIP13; LIF; WT1; HOMER1; IGF1; FANCC; NTF3; MSH2; SMAD3; BCL2; ESR1; SFRP2; POU3F2; PEX5; SDC1; EPHA2; MAP1B; ACHE; GLI2; MYO7A
GO:0051707	1.70E-04	0.6589	14791	601	262	24	BP	response to other organism	IFNA10; MX1; APOB; IRF3; LTF; IFNA21; DEFA1; RELA; IRF8; CLU; CEBPE; CAMP; SMAD3; BCL2; CTSG; CCR4; STAT1; IFNB1; IL6; MST1R; STMN1; CHRM2; TNF; RIPK2
GO:0006979	1.80E-04	0.6692	14791	601	184	19	BP	response to oxidative stress	F3; GPX5; EGFR; SNCA; JUN; RELA; LPO; FANCC; CLU; BCL2; ERBB4; GNAO1; HIF1A; FOS; STAT1; PPP2CB; SDC1; DUSP1; ADRBK1
GO:0009952	1.80E-04	0.6703	14791	601	126	15	BP	anterior/posterior pattern formation	HIPK2; HOXB8; HOXB9; SMAD4; PRKDC; LEF1; RARG; HOXA5; HOXA1; SMAD3; PAX1; YY1; TP53; SFRP2; HOXC11
GO:0032355	1.80E-04	0.6724	14791	601	62	10	BP	response to estradiol stimulus	F3; RARA; GHR; ESR1; IL1B; STAT3; SOCS2; MAP1B; DUSP1; STAT5B
GO:0055088	1.80E-04	0.6724	14791	601	62	10	BP	lipid homeostasis	APOB; PPARG; LIPC; SCARB1; USF1; USF2; CAV3; CETP; LCAT; GOT1
GO:0007611	1.90E-04	0.7151	14791	601	113	14	BP	learning or memory	JUN; ADCY1; DBH; VLDLR; EGR1; RIC8A; FOS; ESR2; IL1B; COMT; DRD2; VDAC1; HRAS; CRHBP
GO:0044057	1.90E-04	0.7209	14791	601	313	27	BP	regulation of system process	KCNH2; SMAD7; BDKRB2; EGFR; NOS1; SNCA; AVPR1A; DBH; EPHX2; NTF3; CAV3; ERBB4; GNAO1; EGR1; IL1B; BCAN; DRD2; KCNE2; KCNE1; HTR1B; CHRM2; HRAS; TNF; MAP1B; ACHE; ADRBK1; PLAT
GO:0032200	1.90E-04	0.7337	14791	601	31	7	BP	telomere organization	BLM; PRKDC; PTGES3; XRCC5; RAD50; TERF1; NBN
GO:0060284	2.00E-04	0.7454	14791	601	248	23	BP	regulation of cell development	PPARG; SMAD4; SMAD7; SMAD1; NGFR; RELA; ZFXH3; NTF3; SMAD3; BCL2; CAV3; CRX; XRCC5; TP53; POU3F2; DRD2; NKX2-1; NTRK3; MAP1B; NBN; GLI2; NDEL1; ATF1
GO:0002521	2.10E-04	0.7854	14791	601	114	14	BP	leukocyte differentiation	SP3; BLM; PPARG; PRKDC; MSH2; CEBPA; CEBPG; CEBPE; BCL2; EGR1; PAX1; TP53; STAT5B; STAT5A
GO:0051101	2.10E-04	0.788	14791	601	142	16	BP	regulation of DNA binding	HIPK2; CAMK2A; PPARG; SIGIRR; SMAD7; ERC1; JUN; RELA; SMARCA4; CEBPG; STK36; IL1B; IL6; TNF; RIPK2; NPM1
GO:0051247	2.20E-04	0.8301	14791	601	299	26	BP	positive regulation of protein metabolic process	ANAPC5; ANAPC7; SMAD4; SMAD7; LIF; IGF1; CSNK1E; SKP1; CAMP; PSME1; BCL2; GHR; BRCA1; SMURF1; CDC16; RAD50; IL1B; TP53; IL6; CDC23; TNF; NBN; PSMB4; RIPK2; PEXT; AXIN1

GO:0009968	2.30E-04	0.8617	14791	601	115	14	BP	negative regulation of signal transduction	HHIP; TSC1; IGF1R; RGS10; LIF; IGF1; CAV3; IGBP1; DRD2; SOCS2; PPP2CA; PPP2CB; TNFAIP3; NCOR1
GO:0055065	2.30E-04	0.8623	14791	601	203	20	BP	metal ion homeostasis	PIK3CB; SV2A; JPH2; CYP27B1; BDKRB2; SNCA; HEXB; AVPR1A; KCNK3; EPOR; EPHX2; LPAR1; BCL2; CAV3; CACNA1F; TRPV4; CCR4; IL1B; DRD2; NEDD4L
GO:0033077	2.30E-04	0.863	14791	601	15	5	BP	T cell differentiation in the thymus	PRKDC; BCL2; TP53; STAT5B; STAT5A
GO:0006972	2.30E-04	0.863	14791	601	15	5	BP	hyperosmotic response	SST; TRPV4; PDPK1; PKN1; NKX2-1
GO:0043933	2.30E-04	0.8688	14791	601	715	49	BP	macromolecular complex subunit organization	STK16; APOB; H3F3A; GTF2I; BLM; KCNH2; SMAD4; SMAD1; TAF11; TSC1; GEMIN5; IGF1R; FGB; LIPC; CENPJ; SCARB1; GTF2E1; IL1RAP; FANCC; PPAT; CDK7; TAF9B; GTF2H4; SMAD3; SNRNP200; CETP; TRIM21; PRMT5; LCAT; TP53; EIF6; NAP1L1; VWF; PICALM; SNAPC5; TERF1; STMN1; MED30; HRAS; POLR2H; POLR2K; POLR2J; TAF7; PEX5; BAT1; TGS1; NPM1; SNRPE; ATF1
GO:0031400	2.30E-04	0.871	14791	601	129	15	BP	negative regulation of protein modification process	ANAPC5; ANAPC7; SMAD7; TSC1; BDKRB2; SNCA; JUN; PRKCD; PSME1; CDC16; PPP2CA; TAF7; CDC23; BCOR; PSMB4
GO:0051270	2.40E-04	0.8918	14791	601	235	22	BP	regulation of cellular component movement	F3; APOH; SMAD7; EGFR; IGF1R; JAG1; SCARB1; IGF1; F10; SST; CITED2; ETS1; SMAD3; ABI3; BCL2; ERBB4; HIF1A; IL6; DRD2; NKX2-1; EPHA2; STAT5B
GO:0045768	2.40E-04	0.9066	14791	601	32	7	BP	positive regulation of anti-apoptosis	SMAD7; SMAD1; ERC1; IGF1R; ERBB4; IL6; DUSP1
GO:0032642	2.40E-04	0.9079	14791	601	23	6	BP	regulation of chemokine production	SIGIRR; HIF1A; IL1B; IL6; TNF; RIPK2
GO:0048660	2.40E-04	0.9121	14791	601	42	8	BP	regulation of smooth muscle cell proliferation	EGFR; JUN; IGF1; STAT1; COMT; IL6; TNF; STAT5B
GO:0010741	2.50E-04	0.9419	14791	601	53	9	BP	negative regulation of intracellular protein kinase cascade	IGF1R; LIF; IGF1; CAV3; IGBP1; DRD2; PPP2CA; TNFAIP3; NCOR1
GO:0006898	2.50E-04	0.9419	14791	601	53	9	BP	receptor-mediated endocytosis	HIP1R; SNCA; SFTPD; PI4KB; GHR; PICALM; ATP5B; CLTCL1; IGF2R
GO:0055074	2.50E-04	0.9472	14791	601	189	19	BP	calcium ion homeostasis	PIK3CB; SV2A; JPH2; CYP27B1; BDKRB2; SNCA; HEXB; AVPR1A; KCNK3; EPOR; EPHX2; LPAR1; BCL2; CAV3; CACNA1F; TRPV4; CCR4; IL1B; DRD2
GO:0019530	2.50E-04	0.9594	14791	601	4	3	BP	taurine metabolic process	GHR; STAT5B; STAT5A
GO:0000255	2.50E-04	0.9594	14791	601	4	3	BP	allantoin metabolic process	GHR; STAT5B; STAT5A
GO:0030219	2.50E-04	0.9594	14791	601	4	3	BP	megakaryocyte differentiation	SP1; SP3; CDKN2B
GO:0032909	2.50E-04	0.9594	14791	601	4	3	BP	regulation of transforming growth factor-beta2 production	SMAD4; SMAD3; HIF1A
GO:0043923	2.50E-04	0.9594	14791	601	4	3	BP	positive regulation by host of viral transcription	SP1; TAF11; JUN
GO:0045136	2.50E-04	0.9594	14791	601	4	3	BP	development of secondary sexual characteristics	NKX2-1; STAT5B; STAT5A

GO:0060397	2.50E-04	0.9594	14791	601	4	3	BP	JAK-STAT cascade involved in growth hormone signaling pathway	STAT3; STAT5B; STAT5A
GO:0006549	2.50E-04	0.9594	14791	601	4	3	BP	isoleucine metabolic process	GHR; STAT5B; STAT5A
GO:0042180	2.60E-04	0.9783	14791	601	568	41	BP	cellular ketone metabolic process	P4HA2; CYP2C9; PPARD; PPARA; ACAA2; NOS1; SNCA; YARS2; LIPC; TPR; DBH; PTGES3; IGF1; SARDH; FABP3; MTHFS; DLST; PPAT; GHR; ACAD8; HARS; ACACB; CYP1A2; AGXT; HARS2; AADAT; HADHA; PON3; FBP2; UGP2; GOT1; ACSL1; G6PC2; PEX5; CYP2B6; ASL; FADS2; STAT5B; STAT5A; ALDH6A1; GGT1
GO:0042035	2.60E-04	0.9835	14791	601	77	11	BP	regulation of cytokine biosynthetic process	SIGIRR; REL; SFTPD; REL; CEBPG; IL1B; IL6; CEBPB; TNF; STAT5B; STAT5A
GO:0030155	2.70E-04	1	14791	601	145	16	BP	regulation of cell adhesion	L1CAM; PIK3CB; SMAD7; TSC1; CYR61; DAB1; CITED2; PRSS2; SMAD3; BCL2; IL1B; PPP2CA; TNF; ATP5B; STAT5B; STAT5A
GO:0023057	2.70E-04	1	14791	601	117	14	BP	negative regulation of signaling process	HHIP; TSC1; IGF1R; RGS10; LIF; IGF1; CAV3; IGBP1; DRD2; SOCS2; PPP2CA; PPP2CB; TNFAIP3; NCOR1
GO:0006954	2.70E-04	1	14791	601	270	24	BP	inflammatory response	SIGIRR; SMAD1; RXRA; BDKRB2; TP73; NFE2L1; REL; TIRAP; NFKB1; EPHX2; IL1RAP; MGLL; CEBPA; FOS; TOLLIP; CCR4; IL1B; STAT3; IL6; CEBPB; TNF; EPHA3; STAT5B; RIPK2
GO:0040007	2.90E-04	1	14791	601	191	19	BP	growth	AR; PPARD; SMAD4; APBA2; IGF1; HOXA5; SMAD3; BCL2; CAV3; BMP8A; ESRI; TP53; GDF5; BMP5; SHBG; NBN; GDF9; GLI2; NPM1
GO:0022607	2.90E-04	1	14791	601	897	58	BP	cellular component assembly	STK16; APOB; H3F3A; GTF2I; BLM; KCNH2; SMAD4; SMAD7; SMAD1; TAF11; TSC1; GEMIN5; IGF1R; FGB; CENPJ; GTF2E1; IL1RAP; FANCC; CADM1; COL17A1; PPAT; CDK7; TAF9B; GTF2H4; SMAD3; BCL2; SNRNP200; TRIM21; PRMT5; TP53; EIF6; WASF2; NAP1L1; NEFH; PDPK1; VWF; DRD2; PICALM; SNAPC5; TERF1; MED30; HRAS; POLR2H; POLR2K; POLR2J; TAF7; PEX5; BAT1; CLDN19; SDCBP; NCOR1; MAP1B; TGS1; ACHE; NPM1; SNRPE; ATF1; MYO7A
GO:0043414	2.90E-04	1	14791	601	78	11	BP	macromolecule methylation	TRDMT1; ASH2L; NSD1; SUZ12; PRMT3; PRMT5; FOS; LCMT1; PCMT1; TGS1; DNMT3L
GO:0008219	3.00E-04	1	14791	601	628	44	BP	cell death	HIPK2; L1CAM; ARHGEF12; DDX41; AR; BNIPL; PPARD; PRKDC; NGFR; SNCA; NFKB1; CADM1; CLU; PDCD5; TAF9B; ITGB3BP; MCL1; BCL2; MAGI3; BRCA1; GBA; DAXX; TP53INP1; IL1B; TP53; SFRP2; IL6; KLF11; NEFH; TP53BP2; SQSTM1; ITSN1; TRIM39; VDAC1; HRAS; TNFAIP3; TNF; EPHA2; SGPP1; SOS1; RIPK2; GLI2; RAD21; AXIN1
GO:0019752	3.10E-04	1	14791	601	554	40	BP	carboxylic acid metabolic process	P4HA2; CYP2C9; PPARD; PPARA; ACAA2; NOS1; SNCA; YARS2; LIPC; TPR; DBH; PTGES3; IGF1; SARDH; FABP3; MTHFS; DLST; PPAT; GHR; ACAD8; HARS; ACACB; CYP1A2; AGXT; HARS2; AADAT; HADHA; PON3; FBP2; UGP2; GOT1; ACSL1; G6PC2; PEX5; ASL; FADS2; STAT5B; STAT5A; ALDH6A1; GGT1
GO:0043436	3.10E-04	1	14791	601	554	40	BP	oxoacid metabolic process	P4HA2; CYP2C9; PPARD; PPARA; ACAA2; NOS1; SNCA; YARS2; LIPC; TPR; DBH; PTGES3; IGF1; SARDH; FABP3; MTHFS; DLST; PPAT; GHR; ACAD8; HARS; ACACB; CYP1A2; AGXT; HARS2; AADAT; HADHA; PON3; FBP2; UGP2; GOT1; ACSL1; G6PC2; PEX5; ASL; FADS2; STAT5B; STAT5A; ALDH6A1; GGT1
GO:0033674	3.20E-04	1	14791	601	240	22	BP	positive regulation of kinase activity	PPAP2A; PIK3CB; PDE6H; EGFR; HGF; DAB1; ADCY1; VLDLR; GHR; ADCY5; DAXX; RAD50; IL1B; MAP2K3; PDPK1; PKN1; DUSP12; TGFA; TNF; NBN; DGKQ; NPM1
GO:0030855	3.20E-04	1	14791	601	105	13	BP	epithelial cell differentiation	AR; TSG101; DSP; PPARG; RXRA; JAG1; JUN; WT1; IGF1; HOXA5; CEBPB; NKX2-1; STAT5A
GO:0014072	3.20E-04	1	14791	601	16	5	BP	response to isoquinoline alkaloid	RELA; GHR; GNAO1; IL1B; DRD2
GO:0031575	3.20E-04	1	14791	601	16	5	BP	G1/S transition checkpoint	DLG1; CDKN2B; TP53; HRAS; NBN
GO:0043278	3.20E-04	1	14791	601	16	5	BP	response to morphine	RELA; GHR; GNAO1; IL1B; DRD2
GO:0043691	3.20E-04	1	14791	601	16	5	BP	reverse cholesterol transport	LIPC; SCARB1; CLU; CETP; LCAT
GO:0009651	3.20E-04	1	14791	601	16	5	BP	response to salt stress	BDKRB2; TRPV4; TP53; NKX2-1; TNF
GO:0043549	3.40E-04	1	14791	601	376	30	BP	regulation of kinase activity	PPAP2A; PIK3CB; BLM; PDE6H; TSC1; TP73; EGFR; HGF; DAB1; CDKN2B; ADCY1; VLDLR; CDK7; CAV3; GHR; ADCY5; DAXX; RAD50; IL1B; MAP2K3; PDPK1; PKN1; DUSP12; PPP2CA; TGFA; TAF7; TNF; NBN; DGKQ; NPM1
GO:0046649	3.40E-04	1	14791	601	178	18	BP	lymphocyte activation	SP3; BLM; PRKDC; CADM1; MSH2; CEBPG; PRKCD; SMAD3; BCL2; EGRI; PAX1; IFNB1; IGBP1; TP53; NBN; STAT5B; STAT5A; RIPK2
GO:0007093	3.40E-04	1	14791	601	44	8	BP	mitotic cell cycle checkpoint	DLG1; CDKN2B; TPR; TRRAP; TP53; TERF1; HRAS; NBN

GO:0006367	3.40E-04	1	14791	601	67	10	BP	transcription initiation from RNA polymerase II promoter	GTF2I; TAF11; GTF2E1; CDK7; GTF2H4; MED30; POLR2H; POLR2K; POLR2J; TAF7
GO:0012501	3.50E-04	1	14791	601	502	37	BP	programmed cell death	HIPK2; ARHGEF12; DDX41; BNIPL; PPAR; PRKDC; NGFR; NFKB1; CADM1; PDCD5; TAF9B; ITGB3BP; MCL1; BCL2; MAGI3; BRCA1; DAXX; TP53INP1; IL1B; TP53; IL6; KLF11; TP53BP2; SQSTM1; ITSN1; TRIM39; VDACL1; HRAS; TNFAIP3; TNF; EPHA2; SGPP1; SOS1; RIPK2; GLI2; RAD21; AXIN1
GO:0006873	3.50E-04	1	14791	601	325	27	BP	cellular ion homeostasis	PIK3CB; SV2A; JPH2; KCNH2; LTF; BDKRB2; SNCA; JUN; HEXB; AVPRIA; KCNK3; EPOR; EPHX2; LPAR1; BCL2; CAV3; CACNA1F; TRPV4; FGF23; CCR4; IL1B; DRD2; KCNE1; SLC4A1; ATP5B; GRIN2C; NEDD4L
GO:0043112	3.60E-04	1	14791	601	34	7	BP	receptor metabolic process	PPARG; SNCA; GHR; SMURF1; CAMLG; PICALM; TNF
GO:0031398	3.70E-04	1	14791	601	93	12	BP	positive regulation of protein ubiquitination	ANAPC5; ANAPC7; SMAD7; SKP1; PSME1; BRCA1; SMURF1; CDC16; CDC23; PSMB4; RIPK2; AXIN1
GO:0016265	3.80E-04	1	14791	601	635	44	BP	death	HIPK2; LICAM; ARHGEF12; DDX41; AR; BNIPL; PPAR; PRKDC; NGFR; SNCA; NFKB1; CADM1; CLU; PDCD5; TAF9B; ITGB3BP; MCL1; BCL2; MAGI3; BRCA1; GBA; DAXX; TP53INP1; IL1B; TP53; SFRP2; IL6; KLF11; NEFH; TP53BP2; SQSTM1; ITSN1; TRIM39; VDACL1; HRAS; TNFAIP3; TNF; EPHA2; SGPP1; SOS1; RIPK2; GLI2; RAD21; AXIN1
GO:0045787	3.90E-04	1	14791	601	68	10	BP	positive regulation of cell cycle	EGFR; RARA; IGF1; CITED2; IL1B; TERF1; TGFA; TNF; STAT5B; STAT5A
GO:0051090	3.90E-04	1	14791	601	121	14	BP	regulation of transcription factor activity	CAMK2A; PPARG; SIGIRR; SMAD7; ERC1; RELA; SMARCA4; CEBPG; STK36; IL1B; IL6; TNF; RIPK2; NPM1
GO:0090046	3.90E-04	1	14791	601	121	14	BP	regulation of transcription regulator activity	CAMK2A; PPARG; SIGIRR; SMAD7; ERC1; RELA; SMARCA4; CEBPG; STK36; IL1B; IL6; TNF; RIPK2; NPM1
GO:0001666	3.90E-04	1	14791	601	150	16	BP	response to hypoxia	PPARA; SMAD9; SMAD4; ABAT; NOS1; VLDLR; USF1; KCNK3; CITED2; SMAD3; BCL2; HIF1A; LCT; CAPN2; STAT5B; PLAT
GO:0006082	4.00E-04	1	14791	601	561	40	BP	organic acid metabolic process	P4HA2; CYP2C9; PPAR; PPARA; ACAA2; NOS1; SNCA; YARS2; LIPC; TPR; DBH; PTGES3; IGF1; SARDH; FABP3; MTHFS; DLST; PPAT; GHR; ACAD8; HARS; ACACB; CYP1A2; AGXT; HARS2; AADAT; HADHA; PON3; FBP2; UGP2; GOT1; ACSL1; G6PC2; PEX5; ASL; FADS2; STAT5B; STAT5A; ALDH6A1; GGT1
GO:0010743	4.00E-04	1	14791	601	25	6	BP	regulation of macrophage derived foam cell differentiation	APOB; PPARG; PPARA; ITGAV; NFKB1; CETP
GO:0010883	4.00E-04	1	14791	601	25	6	BP	regulation of lipid storage	APOB; PPARG; PPARA; ITGAV; SCARB1; NFKB1
GO:0006066	4.00E-04	1	14791	601	433	33	BP	alcohol metabolic process	APOB; PPAR; KHK; RXRA; LEPR; ACAA2; SNCA; HEXB; LIPC; DBH; PTGES3; SCARB1; VLDLR; USF1; FABP3; CHPT1; CETP; LCAT; COMT; DRD2; FBP2; UGP2; GOT1; GSK3B; G6PC2; PGM1; GYS2; TNF; RBKS; SGPP1; ACHE; SREBF1; PEMT
GO:0030334	4.10E-04	1	14791	601	212	20	BP	regulation of cell migration	F3; APOH; SMAD7; EGFR; IGF1R; JAG1; SCARB1; IGF1; F10; SST; CITED2; SMAD3; ABI3; BCL2; ERBB4; HIF1A; IL6; DRD2; NXK2-1; EPHA2
GO:0045596	4.30E-04	1	14791	601	229	21	BP	negative regulation of cell differentiation	PPARG; PPARA; ITGAV; SMAD7; NGFR; JAG1; LIF; IGF1; ZFH3; HOXA5; SMAD3; CETP; FGF23; TP53; SFRP2; NXK2-1; FGF4; NBN; STAT5B; STAT5A; GLI2
GO:0019221	4.40E-04	1	14791	601	69	10	BP	cytokine-mediated signaling pathway	LEPR; RELA; CEBPA; IL1B; STAT3; STAT1; IL6; TNF; STAT5B; STAT5A
GO:0050769	4.40E-04	1	14791	601	69	10	BP	positive regulation of neurogenesis	PPARG; SMAD1; NGFR; RELA; NTF3; XRCC5; DRD2; NTRK3; MAP1B; NDEL1
GO:0006919	4.40E-04	1	14791	601	57	9	BP	activation of caspase activity	F3; PPARG; COL4A3; SMAD3; STAT1; IFNB1; TP53; TERF1; TNF
GO:0010876	4.40E-04	1	14791	601	17	5	BP	lipid localization	HEXB; IL1B; TNF; STAT5B; STAT5A
GO:0019915	4.40E-04	1	14791	601	17	5	BP	lipid storage	HEXB; IL1B; TNF; STAT5B; STAT5A
GO:0051702	4.40E-04	1	14791	601	17	5	BP	interaction with symbiont	SP1; TAF11; JUN; SCARB1; CTSG

GO:0009081	4.40E-04	1	14791	601	17	5	BP	branched chain family amino acid metabolic process	GHR; ACAD8; STAT5B; STAT5A; ALDH6A1
GO:0008016	4.60E-04	1	14791	601	82	11	BP	regulation of heart contraction	KCNH2; SMAD7; NOS1; AVPR1A; CAV3; GNAO1; DRD2; KCNE2; KCNE1; CHRM2; ADRBK1
GO:0010869	4.60E-04	1	14791	601	10	4	BP	regulation of receptor biosynthetic process	PPARG; PPARA; ITGAV; HOXA5
GO:0048585	4.60E-04	1	14791	601	123	14	BP	negative regulation of response to stimulus	PPARG; PPARA; SIGIRR; RELA; MASP1; PRKCD; CTNNA2; NT5E; ESR2; IL1B; IGBP1; DRD2; NCOR1; PSMB4
GO:0055082	4.70E-04	1	14791	601	331	27	BP	cellular chemical homeostasis	PIK3CB; SV2A; JPH2; KCNH2; LTF; BDKRB2; SNCA; JUN; HEXB; AVPR1A; KCNK3; EPOR; EPHX2; LPAR1; BCL2; CAV3; CACNA1F; TRPV4; FGF23; CCR4; IL1B; DRD2; KCNE1; SLC4A1; ATP5B; GRIN2C; NEDD4L
GO:0044092	4.70E-04	1	14791	601	366	29	BP	negative regulation of molecular function	CYP27B1; PPARG; ANAPC5; ANAPC7; SIGIRR; SMAD7; LEPR; TP73; SNCA; JUN; ADCY1; NFKB1; CEBPG; PRKCD; PSME1; CAV3; ADCY5; CDC16; IL1B; IGBP1; TP53; PDPK1; DRD2; HTR1A; PPP2CA; TERF1; TAF7; CDC23; PSMB4
GO:0043086	4.70E-04	1	14791	601	297	25	BP	negative regulation of catalytic activity	CYP27B1; PPARG; ANAPC5; ANAPC7; SMAD7; LEPR; TP73; SNCA; ADCY1; NFKB1; PSME1; CAV3; ADCY5; CDC16; IL1B; IGBP1; TP53; PDPK1; DRD2; HTR1A; PPP2CA; TERF1; TAF7; CDC23; PSMB4
GO:0001817	4.90E-04	1	14791	601	199	19	BP	regulation of cytokine production	PPARG; SIGIRR; SMAD4; REL; SFTPD; RARA; RELA; CADM1; CEBPG; SMAD3; CREB1; HIF1A; IL1B; IL6; CEBPB; TNF; STAT5B; STAT5A; RIPK2
GO:0006897	4.90E-04	1	14791	601	199	19	BP	endocytosis	HIP1R; ITGAV; SNCA; SFTPD; VLDLR; IRF8; PI4KB; CEBPE; RUFY1; GHR; WASF2; PICALM; ITSN1; ITSN2; HRAS; ATP5B; CLTCL1; MYO7A; IGF2R
GO:0009314	4.90E-04	1	14791	601	215	20	BP	response to radiation	BLM; PRKDC; EGFR; SAG; RELA; DBH; RHO; USF1; MSH2; BCL2; CACNA1F; BRCA1; RIC8A; FOS; CCR4; IL1B; TP53; DRD2; HRAS; DUSP1
GO:0010038	4.90E-04	1	14791	601	153	16	BP	response to metal ion	APOB; KHK; RXRA; LEF1; EGFR; ABAT; SNCA; FGB; KCNK3; BCL2; LCT; LCAT; SDC1; DUSP1; ATF1; NEDD4L
GO:0023036	5.00E-04	1	14791	601	70	10	BP	initiation of signal transduction	LEPR; RELA; CEBPA; IL1B; STAT3; STAT1; IL6; TNF; STAT5B; STAT5A
GO:0023038	5.00E-04	1	14791	601	70	10	BP	signal initiation by diffusible mediator	LEPR; RELA; CEBPA; IL1B; STAT3; STAT1; IL6; TNF; STAT5B; STAT5A
GO:0023049	5.00E-04	1	14791	601	70	10	BP	signal initiation by protein/peptide mediator	LEPR; RELA; CEBPA; IL1B; STAT3; STAT1; IL6; TNF; STAT5B; STAT5A
GO:0051783	5.10E-04	1	14791	601	58	9	BP	regulation of nuclear division	TPR; IGF1; PRMT5; CDC16; IL1B; TERF1; TGFA; CDC23; TNF
GO:0007088	5.10E-04	1	14791	601	58	9	BP	regulation of mitosis	TPR; IGF1; PRMT5; CDC16; IL1B; TERF1; TGFA; CDC23; TNF
GO:0048812	5.10E-04	1	14791	601	110	13	BP	neuron projection	RXRA; EGFR; IGF1R; CLU; CTNNA2; BCL2; CACNA1F; CREB1; PAX2; DRD2; MAP1B; GLI2; NDEL1
GO:0030098	5.10E-04	1	14791	601	83	11	BP	morphogenesis lymphocyte differentiation	SP3; BLM; PRKDC; MSH2; CEBPG; BCL2; EGR1; PAX1; TP53; STAT5B; STAT5A
GO:0051347	5.30E-04	1	14791	601	249	22	BP	positive regulation of transferase activity	PPAP2A; PIK3CB; PDEGH; EGFR; HGF; DAB1; ADCY1; VLDLR; GHR; ADCY5; DAXX; RAD50; IL1B; MAP2K3; PDPK1; PKN1; DUSP12; TGFA; TNF; NBN; DGKQ; NPM1
GO:0006576	5.50E-04	1	14791	601	97	12	BP	cellular biogenic amine metabolic process	SNCA; LIPC; DBH; AGMAT; FABP3; CHPT1; CETP; LCAT; COMT; DRD2; ACHE; PEMT
GO:0032844	5.50E-04	1	14791	601	125	14	BP	regulation of homeostatic process	SMAD7; SPI1; NOS1; SNCA; AVPR1A; HOXA5; ETS1; BCL2; HIF1A; TAL1; DRD2; TERF1; STAT5B; STAT5A

GO:0016044	5.80E-04	1	14791	601	353	28	BP	cellular membrane organization	HIP1R; ITGAV; SNCA; SFTPD; CATSPER1; RABIF; VLDLR; IRF8; PI4KB; STX6; CEBPE; RUFY1; BCL2; CAV3; GHR; TP53; WASF2; PICALM; ITSN1; ITSN2; HRAS; PEX5; ATP5B; NDEL1; CLTCL1; DNML1; MYO7A; IGF2R
GO:0019216	5.90E-04	1	14791	601	126	14	BP	regulation of lipid metabolic process	PPAP2A; APOB; PPARG; PPARA; SNCA; AVPR1A; NFKB1; BRCA1; IL1B; ACACB; ACSL1; TNF; STAT5B; STAT5A
GO:0033036	6.10E-04	1	14791	601	141	15	BP	macromolecule localization	AKAP3; EGFR; HEXB; CAV3; SMURF1; IL1B; TP53; SQSTM1; DRD2; TNF; STAT5B; STAT5A; GRIN2C; SIN3A; NPM1
GO:0006928	6.10E-04	1	14791	601	462	34	BP	cellular component movement	PPAP2A; L1CAM; AKAP3; APOB; PPARG; EGFR; NGFR; SFTPD; CATSPER1; DAB1; DBH; SCARB1; IGF1; NTF3; HOXA5; HOXA1; ETS1; CTNNA2; ABI3; ESR2; CCR4; IL1B; STAT3; EFNA5; IL6; WASF2; POU3F2; DRD2; NKX2-1; MST1R; PEX5; GLI2; PLAT; NDEL1
GO:0032101	6.20E-04	1	14791	601	187	18	BP	regulation of response to external stimulus	F3; APOH; CYP27B1; PPARG; PPARA; MASP1; USF1; SMAD3; CTNNA2; NT5E; CCR4; IL6; DRD2; NTRK3; STAT5B; STAT5A; PSMB4; NDEL1
GO:0051353	6.20E-04	1	14791	601	27	6	BP	positive regulation of oxidoreductase activity	CYP27B1; SCARB1; HIF1A; FGF23; IL1B; TNF
GO:0070555	6.20E-04	1	14791	601	27	6	BP	response to interleukin-1	SNCA; RELA; CAMP; GHR; IGBP1; RIPK2
GO:0031100	6.20E-04	1	14791	601	37	7	BP	organ regeneration	APOH; PPARG; HGF; LIF; PPAT; CEBPA; IGF2R
GO:0010871	6.20E-04	1	14791	601	5	3	BP	negative regulation of receptor biosynthetic process	PPARG; PPARA; ITGAV
GO:0002326	6.20E-04	1	14791	601	5	3	BP	B cell lineage commitment	PRKDC; BCL2; TP53
GO:0002360	6.20E-04	1	14791	601	5	3	BP	T cell lineage commitment	PRKDC; BCL2; TP53
GO:0032836	6.20E-04	1	14791	601	5	3	BP	glomerular basement membrane development	COL4A4; COL4A3; WT1
GO:0033033	6.20E-04	1	14791	601	5	3	BP	negative regulation of myeloid cell apoptosis	APOH; BCL2; STAT5A
GO:0048609	6.20E-04	1	14791	601	408	31	BP	reproductive process in a multicellular organism	SP1; SP3; APOB; SMAD1; LEPR; EGFR; PGR; HEXB; LIF; AVPR1A; CATSPER1; DBH; USF2; CADM1; CITED2; PPAT; MSH2; CREB1; XDH; ESR1; IL1B; COMT; ODF1; CLDN11; ACR; GDF9; STAT5B; STAT5A; FSHR; DNMT3L; IGF2R
GO:0051092	6.30E-04	1	14791	601	48	8	BP	positive regulation of NF-kappaB transcription factor activity	CAMK2A; ERC1; RELA; IL1B; IL6; TNF; RIPK2; NPM1
GO:0006368	6.30E-04	1	14791	601	48	8	BP	RNA elongation from RNA polymerase II promoter	TAF11; GTF2E1; CDK7; GTF2H4; TCEB3; POLR2H; POLR2K; POLR2J
GO:0061024	6.30E-04	1	14791	601	355	28	BP	membrane organization	HIP1R; ITGAV; SNCA; SFTPD; CATSPER1; RABIF; VLDLR; IRF8; PI4KB; STX6; CEBPE; RUFY1; BCL2; CAV3; GHR; TP53; WASF2; PICALM; ITSN1; ITSN2; HRAS; PEX5; ATP5B; NDEL1; CLTCL1; DNML1; MYO7A; IGF2R
GO:0043412	6.70E-04	1	14791	601	1569	89	BP	macromolecule modification	STK16; P4HA2; HIPK2; PIK3CB; CAMK2A; CAMK2B; TSG101; UBE2D2; SENP2; DSP; ANAPC5; ANAPC7; CSNK1A1; TRDMT1; PDE6H; SMAD9; ASH2L; SMAD7; SMAD1; PRKDC; SRPK1; ERC1; EGFR; IGF1R; ERG; HGF; B3GNT6; RHO; MAPK10; PRKG1; BMX; CSNK1E; NSD1; WDVHV1; CDK7; USP7; SUZ12; PRKCD; ABI3; BCL2; WWP1; GHR; BRCA1; ERBB4; PRMT3; CREB1; BRD8; DZIP3; PRMT5; SMURF1; DAXX; SMURF2; CDC16; FOS; TRRAP; STK36; LCM1; IL1B; STAT1; MARK3; MAP2K3; AMHR2; PDPK1; PKN1; DUSP14; DUSP12; NTRK2; NTRK3; PPP2CA; PPP2CB; MST1R; GSK3B; MAPKAPK5; TGFA; CDC23; TNF; EPHA8; EPHA3; EPHA2; DUSP1; PCMT1; TGS1; STAT5A; RIPK2; ADRBK1; DNMT3L; PLAT; PTPRS; NEDD4L
GO:0032259	6.90E-04	1	14791	601	86	11	BP	methylation	TRDMT1; ASH2L; NSD1; SUZ12; PRMT3; PRMT5; FOS; LCM1; PCMT1; TGS1; DNMT3L
GO:0007409	6.90E-04	1	14791	601	86	11	BP	axonogenesis	RXRA; IGF1R; CTNNA2; BCL2; CACNA1F; CREB1; PAX2; DRD2; MAP1B; GLI2; NDF1
GO:0002076	7.00E-04	1	14791	601	11	4	BP	osteoblast development	SMAD3; ESR1; ACHE; GLI2

GO:0032494	7.00E-04	1	14791	601	11	4	BP	response to peptidoglycan	RELA; CAMP; IL6; RIPK2
GO:0032769	7.00E-04	1	14791	601	11	4	BP	negative regulation of monoxygenase activity	CYP27B1; SNCA; NFKB1; CAV3
GO:0045073	7.00E-04	1	14791	601	11	4	BP	regulation of chemokine biosynthetic process	SIGIRR; IL1B; IL6; TNF
GO:0006107	7.00E-04	1	14791	601	11	4	BP	oxaloacetate metabolic process	GHR; GOT1; STAT5B; STAT5A
GO:0071634	7.00E-04	1	14791	601	11	4	BP	regulation of transforming growth factor-beta production	SMAD4; SMAD3; CREB1; HIF1A
GO:0009416	7.10E-04	1	14791	601	143	15	BP	response to light stimulus	EGFR; SAG; RELA; DBH; RHO; USF1; MSH2; BCL2; CACNA1F; RIC8A; FOS; TP53; DRD2; HRAS; DUSP1
GO:0031396	7.20E-04	1	14791	601	114	13	BP	regulation of protein ubiquitination	ANAPC5; ANAPC7; SMAD7; TSC1; SKP1; PSME1; BRCA1; SMURF1; CDC16; CDC23; PSMB4; RIPK2; AXIN1
GO:0002526	7.30E-04	1	14791	601	49	8	BP	acute inflammatory response	SIGIRR; CEBPA; IL1B; STAT3; IL6; CEBPB; EPHA3; STAT5B
GO:0070372	7.40E-04	1	14791	601	38	7	BP	regulation of ERK1 and ERK2 cascade	LIF; IGF1; FGF23; IL1B; HRAS; FGF4; RIPK2
GO:0006259	7.50E-04	1	14791	601	523	37	BP	DNA metabolic process	BLM; TRDMT1; PRKDC; TP73; TRIP13; ORC6L; PTGES3; IGF1; CSNK1E; FANCC; UHRF1; CDK7; DSCC1; GTF2H4; MSH2; MSH3; BRCA1; KPNA2; XRCC5; NONO; NT5E; FOS; RAD50; SFPQ; POLE2; TP53; NAP1L1; MCM7; KCTD13; TERF1; POLD2; NBN; ACHE; SIN3A; RAD21; DNMT3L; NFIC
GO:0070482	7.50E-04	1	14791	601	159	16	BP	response to oxygen levels	PPARA; SMAD9; SMAD4; ABAT; NOS1; VLDLR; USF1; KCNK3; CITED2; SMAD3; BCL2; HIF1A; LCT; CAPN2; STAT5B; PLAT
GO:0006464	7.50E-04	1	14791	601	1490	85	BP	protein modification process	STK16; P4HA2; HIPK2; PIK3CB; CAMK2A; CAMK2B; TSG101; UBE2D2; SENP2; DSP; ANAPC5; ANAPC7; CSNK1A1; PDE6H; SMAD9; ASH2L; SMAD7; SMAD1; PRKDC; SRPK1; ERC1; EGFR; IGF1R; ERG; HGF; B3GNT6; RHO; MAPK10; PRKG1; BMX; CSNK1E; NSD1; WDHV1; CDK7; USP7; SUZ12; PRKCD; ABI3; BCL2; WWP1; GHR; BRCA1; ERBB4; PRMT3; CREB1; BRD8; DZIP3; PRMT5; SMURF1; DAXX; SMURF2; CDC16; TRRAP; STK36; LCMT1; IL1B; STAT1; MARK3; MAP2K3; AMHR2; PDPK1; PKN1; DUSP14; DUSP12; NTRK2; NTRK3; PPP2CA; PPP2CB; MST1R; GSK3B; MAPKAPK5; TGFA; CDC23; TNF; EPHA8; EPHA3; EPHA2; DUSP1; PCMT1; STAT5A; RIPK2; ADRBK1; PLAT; PTPRS; NEDD4L
GO:0007275	7.60E-04	1	14791	601	912	57	BP	multicellular organismal development	L1CAM; DDX41; WHSC2; FZD10; ZIC2; HOXB8; HOXB9; TLE1; LEPR; ERC1; ERG; NGFR; GFI1B; JAG1; FZD8; HOXB13; WNT16; LIF; CATSPER1; DAB1; WNT10A; MLF1; CADM1; HOXA1; ZNF7; DVL2; MCL1; CTNNA2; BMP8A; CRX; PAX6; PAX2; PAX8; TAL1; EFNA5; TP53; SFRP2; WNT2; WNT9B; ISL1; NTRK2; NTRK3; MST1R; STMN1; PLXNB3; ODF1; TNF; EPHA2; GNRHR; FZD6; HEY1; NDEL1; DACH1; AXIN1; HOXC11; TGIF1; DNML
GO:0050792	7.60E-04	1	14791	601	28	6	BP	regulation of viral reproduction	SP1; TAF11; JUN; BCL2; IFNB1; TNF
GO:0060688	7.60E-04	1	14791	601	28	6	BP	regulation of morphogenesis of a branching structure	AR; RXRA; HGF; ESR1; WNT2; TNF
GO:0007259	7.60E-04	1	14791	601	28	6	BP	JAK-STAT cascade	GHR; STAT3; STAT1; SOCS2; STAT5B; STAT5A
GO:0046330	7.80E-04	1	14791	601	19	5	BP	positive regulation of JNK cascade	HIPK2; IL1B; TNF; RIPK2; AXIN1
GO:0050801	7.90E-04	1	14791	601	360	28	BP	ion homeostasis	PIK3CB; SV2A; JPH2; CYP27B1; KCNH2; LTF; BDKRB2; SNCA; JUN; HEXB; AVPR1A; KCNK3; EPOR; EPHX2; LPAR1; BCL2; CAV3; CACNA1F; TRPV4; FGF23; CCR4; IL1B; DRD2; KCNE1; SLC4A1; ATP5B; GRIN2C; NEDD4L
GO:0032990	8.10E-04	1	14791	601	130	14	BP	cell part morphogenesis	RXRA; EGFR; IGF1R; CLU; CTNNA2; BCL2; CACNA1F; CREB1; PAX2; DRD2; MAP1B; GLI2; NDEL1; DNML
GO:0045321	8.20E-04	1	14791	601	224	20	BP	leukocyte activation	SP3; BLM; PRKDC; SNCA; CADM1; MSH2; CEBPG; PRKCD; SMAD3; BCL2; EGR1; TOLLIP; PAX1; IFNB1; IGBP1; TP53; NBN; STAT5B; STAT5A; RIPK2
GO:0030324	8.40E-04	1	14791	601	62	9	BP	lung development	SP1; SP3; HHIP; CEBPA; ZFPM2; CYP1A2; WNT2; NKX2-1; GLI2
GO:0042692	8.40E-04	1	14791	601	50	8	BP	muscle cell differentiation	TSC1; RXRA; JAG1; AVPR1A; RARB; IGF1; NTF3; HRAS

GO:0010324	8.40E-04	1	14791	601	208	19	BP	membrane invagination	HIP1R; ITGAV; SNCA; SFTPD; VLDLR; IRF8; PI4KB; CEBPE; RUFY1; GHR; WASF2; PICALM; ITSN1; ITSN2; HRAS; ATP5B; CLTCL1; MYO7A; IGF2R
GO:0006875	8.40E-04	1	14791	601	192	18	BP	cellular metal ion homeostasis	PIK3CB; SV2A; JPH2; BDKRB2; HEXB; AVPR1A; KCNK3; EPOR; EPHX2; LPAR1; BCL2; CAV3; CACNA1F; TRPV4; CCR4; IL1B; DRD2; NEDD4L
GO:0051924	8.70E-04	1	14791	601	75	10	BP	regulation of calcium ion transport	JPH2; NOS1; SNCA; CATSPER1; HOMER1; BCL2; CAV3; GNAO1; DRD2; CACNA2D1
GO:0045767	8.70E-04	1	14791	601	39	7	BP	regulation of anti-apoptosis	SMAD7; SMAD1; ERC1; IGF1R; ERBB4; IL6; DUSP1
GO:0051128	9.30E-04	1	14791	601	529	37	BP	regulation of cellular component organization	SMAD4; SMAD7; SMAD1; TSC1; NGFR; SNCA; SFTPD; TPR; SCARB1; IGF1; RALA; CLU; SMAD3; CTNNA2; CAV3; BRCA1; PRMT5; CDC16; IL1B; TP53; PDPK1; POU3F2; PICALM; NX2-1; NTRK3; GSK3B; TERF1; TGFA; TAF7; CDC23; TNF; MAP1B; BCR; NDEL1; NPM1; ATF1; NEDD4L
GO:0007595	9.30E-04	1	14791	601	29	6	BP	lactation	USF2; PPAT; CREB1; XDH; STAT5B; STAT5A
GO:0002682	9.30E-04	1	14791	601	418	31	BP	regulation of immune system process	BLM; SPI1; JAG1; SNCA; JUN; SFTPD; LIF; RARA; RELA; MASP1; AP2B1; CADM1; CLU; HOXA5; ETS1; SMAD3; CTSG; MASP2; HIF1A; FCN2; IL1B; IFNB1; TAL1; IL6; CIS; TNF; ADK; STAT5B; STAT5A; PSMB4; RIPK2
GO:0048608	9.40E-04	1	14791	601	63	9	BP	reproductive structure development	AR; RARG; WT1; MSH2; BCL2; ESR2; ESR1; SRD5A2; FSHR
GO:0006915	9.40E-04	1	14791	601	492	35	BP	apoptosis	HIPK2; ARHGEF12; DDX41; BNIPL; PPARD; NGFR; NFKB1; CADM1; PDCD5; ITGB3BP; MCL1; BCL2; MAGI3; BRCA1; DAXX; TP53INP1; IL1B; TP53; IL6; KLF11; TP53BP2; SQSTM1; ITSN1; TRIM39; VDAC1; HRAS; TNFAIP3; TNF; EPHA2; SGPP1; SOS1; RIPK2; GLI2; RAD21; AXIN1
GO:0008380	9.50E-04	1	14791	601	277	23	BP	RNA splicing	DDX41; SRPK1; GEMIN5; RBM9; RBMX; WT1; HNRNP1A; CSTF2; SNRNP200; PRPF3; NONO; SFPQ; RBM8A; DHX16; PPP2CA; PABPC1; POLR2H; POLR2K; POLR2J; BAT1; HNRNPC; SNRPA; SNRPE
GO:0006354	9.60E-04	1	14791	601	51	8	BP	RNA elongation	TAF11; GTF2E1; CDK7; GTF2H4; TCEB3; POLR2H; POLR2K; POLR2J
GO:0007268	0.001	1	14791	601	211	19	BP	synaptic transmission	RIT2; APBA2; SNCA; HOMER1; DBH; KCNK3; SST; NTF3; GRIK5; VIPR1; SYN1; PDE7B; DRD2; GABRR2; VDAC1; HTR1B; SDCBP; CACNB2; PLAT
GO:0048858	0.001	1	14791	601	118	13	BP	cell projection morphogenesis	RXRA; EGFR; IGF1R; CLU; CTNNA2; BCL2; CACNA1F; CREB1; PAX2; DRD2; MAP1B; GLI2; NDEL1
GO:0035556	0.001	1	14791	601	724	47	BP	intracellular signal transduction	PIK3CB; RIT2; RAB6B; GDI1; RALBP1; SMAD1; IRF3; SRPK1; EGFR; IGF1R; AVPR1A; DAB1; RABIF; HOMER1; ADCY1; MAPK10; TIRAP; IGF1; RALA; PI4KB; F2RL3; ARHGAP1; VIPR1; GHR; ADCY5; STAT3; STAT1; TP53; RHEB; TEAD1; WASF2; DRD2; HTR1A; ITSN1; RAP1A; SOCS2; PPP2CA; HTR1B; CHRM2; HRAS; TNF; SDCBP; SOS1; STAT5B; STAT5A; DGKQ; FSHR
GO:0001659	0.001	1	14791	601	20	5	BP	temperature homeostasis	DBH; IL1B; STAT3; DRD2; EPHA3
GO:0008361	0.001	1	14791	601	20	5	BP	regulation of cell size	TSC1; TP73; RARG; CAV3; CREB1
GO:0031669	0.001	1	14791	601	40	7	BP	cellular response to nutrient levels	LEPR; JUN; CDKN2B; USF1; USF2; TP53; SREBF1
GO:0043281	0.001	1	14791	601	90	11	BP	regulation of caspase activity	F3; PPARG; COL4A3; SNCA; SMAD3; STAT1; IFNB1; IGBP1; TP53; TERF1; TNF
GO:0010745	0.001	1	14791	601	12	4	BP	negative regulation of macrophage derived foam cell differentiation	PPARG; PPARA; ITGAV; CETP
GO:0010885	0.001	1	14791	601	12	4	BP	regulation of cholesterol storage	APOB; PPARG; PPARA; SCARB1
GO:0045885	0.001	1	14791	601	12	4	BP	positive regulation of survival gene product expression	ESR2; ESR1; STAT5B; STAT5A
GO:0051851	0.001	1	14791	601	12	4	BP	modification by host of symbiont morphology or physiology	SP1; TAF11; JUN; CTSG
GO:0043269	0.001	1	14791	601	104	12	BP	regulation of ion transport	JPH2; NOS1; SNCA; CATSPER1; HOMER1; BCL2; CAV3; GNAO1; FGF23; DRD2; CACNA2D1; TNF
GO:0021700	0.001	1	14791	601	77	10	BP	developmental maturation	PPARG; PGR; TRIP13; HOXB13; HOXA5; CEBPA; ERBB4; ESR2; KCNE1; MAP1B

GO:0070302	0.001	1	14791	601	77	10	BP	regulation of stress-activated protein kinase signaling cascade	HIPK2; TP73; DAXX; IL1B; IGBP1; PKN1; TNF; NCOR1; RIPK2; AXIN1
GO:0006869	0.001	1	14791	601	149	15	BP	lipid transport	OSBPPL3; APOB; APOH; PPARG; PPAR; PPARA; BDKRB2; LIPC; SCARB1; VLDLR; FABP3; CLU; CETP; LCAT; DRD2
GO:0032787	0.001	1	14791	601	297	24	BP	monocarboxylic acid metabolic process	P4HA2; CYP2C9; PPAR; PPARA; ACAA2; SNCA; LIPC; PTGES3; IGF1; FABP3; MTHFS; GHR; ACACB; CYP1A2; AGXT; HADHA; FBP2; UGP2; ACSL1; G6PC2; PEX5; FADS2; STAT5B; STAT5A
GO:0065003	0.001	1	14791	601	668	44	BP	macromolecular complex assembly	STK16; APOB; H3F3A; GTF2I; BLM; KCNH2; SMAD4; SMAD1; TAF11; TSC1; GEMIN5; IGF1R; FGB; CENPJ; GTF2E1; IL1RAP; FANCC; PPAT; CDK7; TAF9B; GTF2H4; SMAD3; SNRNP200; TRIM21; PRMT5; TP53; EIF6; NAP1L1; VWF; PICALM; SNAPC5; TERF1; MED30; HRAS; POLR2H; POLR2K; POLR2J; TAF7; PEX5; BAT1; TGS1; NPM1; SNRPE; ATF1
GO:0007568	0.0011	1	14791	601	134	14	BP	aging	F3; RXRA; JUN; RELA; PRKCD; BCL2; GNAO1; FOS; IL1B; TP53; SOCS2; HRAS; ADRBK1; NPM1
GO:0008203	0.0011	1	14791	601	91	11	BP	cholesterol metabolic process	APOB; PPAR; RXRA; LEPR; ACAA2; LIPC; SCARB1; VLDLR; CETP; LCAT; SREBF1
GO:0006874	0.0011	1	14791	601	181	17	BP	cellular calcium ion homeostasis	PIK3CB; SV2A; JPH2; BDKRB2; HEXB; AVPR1A; KCNK3; EPOR; EPHX2; LPAR1; BCL2; CAV3; CACNA1F; TRPV4; CCR4; IL1B; DRD2
GO:0010243	0.0011	1	14791	601	78	10	BP	response to organic nitrogen	TRDMT1; SMAD1; RELA; DBH; SST; MSH2; GNAO1; IL1B; DRD2; PENT
GO:0031099	0.0011	1	14791	601	78	10	BP	regeneration	APOH; PPARG; RXRA; HGF; LIF; PPAT; CEBPA; BCL2; MAP1B; IGF2R
GO:0045471	0.0011	1	14791	601	78	10	BP	response to ethanol	ABAT; DBH; BCL2; LCT; STAT3; DRD2; NKX2-1; HTR1B; STAT5B; PENT
GO:0001867	0.0012	1	14791	601	6	3	BP	complement activation, lectin pathway	MASP1; MASP2; FCN2
GO:0043353	0.0012	1	14791	601	6	3	BP	enucleate erythrocyte differentiation	SP1; SP3; CEBPG
GO:0045647	0.0012	1	14791	601	6	3	BP	negative regulation of erythrocyte differentiation	HOXA5; STAT5B; STAT5A
GO:0060033	0.0012	1	14791	601	6	3	BP	anatomical structure regression	SMAD9; AMHR2; GLI2
GO:0060479	0.0012	1	14791	601	6	3	BP	lung cell differentiation	IGF1; HOXA5; NKX2-1
GO:0060487	0.0012	1	14791	601	6	3	BP	lung epithelial cell differentiation	IGF1; HOXA5; NKX2-1
GO:0060527	0.0012	1	14791	601	6	3	BP	prostate epithelial cord arborization involved in prostate glandular acinus morphogenesis	HOXB13; IGF1; ESR1
GO:0009299	0.0012	1	14791	601	6	3	BP	mRNA transcription	USF1; USF2; HIF1A
GO:0040011	0.0012	1	14791	601	425	31	BP	locomotion	PPAP2A; PIK3CB; APOB; PPAR; RALBP1; EGFR; DEFA1; CYR61; SFTPD; CATSPER1; DAB1; DBH; SCARB1; RALA; HOXA5; ETS1; CTNNA2; WWP1; ESR2; CCR4; IL1B; IL6; WASF2; POU3F2; DRD2; NKX2-1; HRAS; PEX5; GRIN2C; POU3F1; ARHGAP10
GO:0000075	0.0012	1	14791	601	92	11	BP	cell cycle checkpoint	DLG1; BLM; CDKN2B; TPR; MSH2; BRCA1; TRRAP; TP53; TERF1; HRAS; NBN
GO:0042060	0.0012	1	14791	601	53	8	BP	wound healing	DSP; PPAR; PPARA; SMAD1; SCARB1; SMAD3; IL1B; SDC1
GO:0006461	0.0012	1	14791	601	500	35	BP	protein complex assembly	STK16; GTF2I; BLM; KCNH2; SMAD4; SMAD1; TAF11; TSC1; GEMIN5; IGF1R; FGB; CENPJ; GTF2E1; IL1RAP; FANCC; PPAT; CDK7; TAF9B; GTF2H4; SMAD3; TRIM21; TP53; VWF; PICALM; SNAPC5; TERF1; MED30; HRAS; POLR2H; POLR2K; POLR2J; TAF7; PEX5; NPM1; ATF1
GO:0034367	0.0012	1	14791	601	21	5	BP	macromolecular complex remodeling	APOB; LIPC; SCARB1; CETP; LCAT

GO:0034368	0.0012	1	14791	601	21	5	BP	protein-lipid complex remodeling	APOB; LIPC; SCARB1; CETP; LCAT
GO:0034369	0.0012	1	14791	601	21	5	BP	plasma lipoprotein particle remodeling	APOB; LIPC; SCARB1; CETP; LCAT
GO:0042133	0.0012	1	14791	601	21	5	BP	neurotransmitter metabolic process	ABAT; NOS1; DBH; COMT; ACHE
GO:0060249	0.0013	1	14791	601	107	12	BP	anatomical structure homeostasis	BLM; PRKDC; SFTPD; COL11A2; PTGES3; BCL2; CAV3; ERBB4; XRCC5; RAD50; TERF1; NBN
GO:0010952	0.0013	1	14791	601	66	9	BP	positive regulation of peptidase activity	F3; PPARG; COL4A3; SMAD3; STAT1; IFNB1; TP53; TERF1; TNF
GO:0043280	0.0013	1	14791	601	66	9	BP	positive regulation of caspase activity	F3; PPARG; COL4A3; SMAD3; STAT1; IFNB1; TP53; TERF1; TNF
GO:0048598	0.0013	1	14791	601	284	23	BP	embryonic morphogenesis	SP1; SP3; ZIC2; HOXB8; SMAD4; TSC1; LEF1; RARB; RARG; NSD1; HOXA5; HOXA1; DVL2; SMAD3; TP53; SFRP2; TFAP2A; GDF5; FGF4; FZD6; GLI2; HOXC11; MYO7A
GO:0002443	0.0013	1	14791	601	31	6	BP	leukocyte mediated immunity	DBH; CADM1; MSH2; CEBPG; PRKCD; IL6
GO:0042102	0.0013	1	14791	601	42	7	BP	positive regulation of T cell proliferation	BLM; IL1B; IL6; ADK; STAT5B; STAT5A; RIPK2
GO:0033138	0.0014	1	14791	601	13	4	BP	regulation of peptidyl-serine phosphorylation	LIF; BCL2; IL6; AXIN1
GO:0034375	0.0014	1	14791	601	13	4	BP	high-density lipoprotein particle remodeling	LIPC; SCARB1; CETP; LCAT
GO:0046782	0.0014	1	14791	601	13	4	BP	regulation of viral transcription	SP1; TAF11; JUN; IFNB1
GO:0048048	0.0014	1	14791	601	13	4	BP	embryonic eye morphogenesis	SP1; SP3; RARB; RARG
GO:0090092	0.0014	1	14791	601	94	11	BP	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	HIPK2; SMAD4; SMAD7; CDKN2B; CITED2; SMAD3; SMURF1; SMURF2; ING2; TP53; NXX2-1
GO:0010517	0.0014	1	14791	601	67	9	BP	di-, tri-valent inorganic cation homeostasis	EGFR; SNCA; AVPR1A; HOMER1; F2RL3; LPAR1; PLCB2; DRD2; CHRM2
GO:0055066	0.0014	1	14791	601	235	20	BP	inorganic cation homeostasis	PIK3CB; SV2A; JPH2; CYP27B1; LTF; BDKRB2; SNCA; HEXB; AVPR1A; KCNK3; EPOR; EPHX2; LPAR1; BCL2; CAV3; CACNA1F; TRPV4; CCR4; IL1B; DRD2
GO:0001701	0.0015	1	14791	601	139	14	BP	in utero embryonic development	AR; APOB; SMAD4; APBA2; KEAP1; MSH2; SMAD3; ZFPM2; RIC8A; TP53; NBN; GLI2; SIN3A; DNMT3L
GO:0032409	0.0015	1	14791	601	43	7	BP	regulation of transporter activity	JPH2; PPARG; SNCA; CATSPER1; HOMER1; CAV3; DRD2
GO:0007612	0.0015	1	14791	601	55	8	BP	learning	JUN; DBH; RIC8A; FOS; COMT; DRD2; VDAC1; HRAS
GO:0045930	0.0016	1	14791	601	22	5	BP	negative regulation of mitotic cell cycle	DLG1; EGFR; SMARCA4; SMAD3; BCL2

GO:0033554	0.0016	1	14791	601	546	37	BP	cellular response to stress	HIPK2; F3; BLM; PRKDC; RXRA; TP73; SNCA; JUN; TRIP13; AVPRIA; LPO; MAPK10; CSNK1E; FANCC; UHRF1; CDK7; GTF2H4; MSH2; MSH3; BCL2; TRPV4; BRCA1; HIF1A; XRCC5; NONO; FOS; RAD50; SFPQ; POLE2; TP53; MCM7; GSK3B; MAP1B; NBN; SREBF1; RAD21; ATF6
GO:0045785	0.0016	1	14791	601	68	9	BP	positive regulation of cell adhesion	L1CAM; SMAD7; TSC1; CYR61; CITED2; PRSS2; SMAD3; IL1B; TNF
GO:0046328	0.0016	1	14791	601	68	9	BP	regulation of JNK cascade	HIPK2; TP73; DAXX; IL1B; PKN1; TNF; NCOR1; RIPK2; AXIN1
GO:0010719	0.0016	1	14791	601	2	2	BP	negative regulation of epithelial to mesenchymal transition	SMAD7; NKX2-1
GO:0019083	0.0016	1	14791	601	2	2	BP	viral transcription	USF1; USF2
GO:0019086	0.0016	1	14791	601	2	2	BP	late viral mRNA transcription	USF1; USF2
GO:0021942	0.0016	1	14791	601	2	2	BP	radial glia guided migration of Purkinje cell	DAB1; CTNNA2
GO:0002439	0.0016	1	14791	601	2	2	BP	chronic inflammatory response to antigenic stimulus	IL1B; TNF
GO:0002520	0.0016	1	14791	601	2	2	BP	immune system development	SMAD3; BCL2
GO:0032916	0.0016	1	14791	601	2	2	BP	positive regulation of transforming growth factor-beta3 production	SMAD3; CREB1
GO:0034116	0.0016	1	14791	601	2	2	BP	positive regulation of heterotypic cell-cell adhesion	IL1B; TNF
GO:0000429	0.0016	1	14791	601	2	2	BP	regulation of transcription from RNA polymerase II promoter by carbon catabolites	USF1; USF2
GO:0000430	0.0016	1	14791	601	2	2	BP	regulation of transcription from RNA polymerase II promoter by glucose	USF1; USF2
GO:0000432	0.0016	1	14791	601	2	2	BP	positive regulation of transcription from RNA polymerase II promoter by glucose	USF1; USF2
GO:0000436	0.0016	1	14791	601	2	2	BP	positive regulation of transcription from RNA polymerase II promoter by carbon catabolites	USF1; USF2

GO:0045991	0.0016	1	14791	601	2	2	BP	positive regulation of transcription by carbon catabolites	USF1; USF2
GO:0046016	0.0016	1	14791	601	2	2	BP	positive regulation of transcription by glucose	USF1; USF2
GO:0046544	0.0016	1	14791	601	2	2	BP	development of secondary male sexual characteristics	STAT5B; STAT5A
GO:0051029	0.0016	1	14791	601	2	2	BP	rRNA transport	TSC1; NPM1
GO:0055098	0.0016	1	14791	601	2	2	BP	response to low-density lipoprotein stimulus	F3; PPARG
GO:0006407	0.0016	1	14791	601	2	2	BP	rRNA export from nucleus	TSC1; NPM1
GO:0006427	0.0016	1	14791	601	2	2	BP	histidyl-tRNA aminoacylation	HARS; HARS2
GO:0043009	0.0016	1	14791	601	140	14	BP	chordate embryonic development	AR; APOB; SMAD4; APBA2; KEAP1; MSH2; SMAD3; ZFPM2; RIC8A; TP53; NBN; GLI2; SIN3A; DNMT3L
GO:0051969	0.0016	1	14791	601	140	14	BP	regulation of transmission of nerve impulse	EGFR; SNCA; AVPR1A; NTF3; ERBB4; EGR1; BCAN; DRD2; HTR1B; HRAS; TNF; MAP1B; ACHE; PLAT
GO:0042110	0.0016	1	14791	601	110	12	BP	T cell activation	SP3; BLM; PRKDC; CADM1; SMAD3; BCL2; EGR1; PAX1; TP53; STAT5B; STAT5A; RIPK2
GO:0052548	0.0017	1	14791	601	96	11	BP	regulation of endopeptidase activity	F3; PPARG; COL4A3; SNCA; SMAD3; STAT1; IFNB1; IGBP1; TP53; TERF1; TNF
GO:0045859	0.0018	1	14791	601	362	27	BP	regulation of protein kinase activity	PPAP2A; PIK3CB; BLM; PDE6H; TSC1; TP73; EGFR; HGF; DAB1; CDKN2B; ADCY1; VLDLR; CDK7; CAV3; GHR; ADCY5; DAXX; IL1B; MAP2K3; PDPK1; PKN1; PPP2CA; TGFA; TAF7; TNF; DGKQ; NPM1
GO:0006310	0.0018	1	14791	601	111	12	BP	DNA recombination	BLM; PRKDC; TRIP13; MSH2; MSH3; BRCA1; XRCC5; NONO; RAD50; SFPQ; NBN; RAD21
GO:0007565	0.0018	1	14791	601	69	9	BP	female pregnancy	SULT1E1; RXRA; LEPR; BCL2; FOS; COMT; CRHBP; STAT5B; STAT5A
GO:0042327	0.0018	1	14791	601	126	13	BP	positive regulation of phosphorylation	SMAD4; EGFR; LIF; IGF1; CAMP; BCL2; GHR; RAD50; IL1B; IL6; TNF; NBN; AXIN1
GO:0015908	0.0019	1	14791	601	33	6	BP	fatty acid transport	PPARG; PPARC; PPARA; BDKRB2; FABP3; DRD2
GO:0033555	0.0019	1	14791	601	33	6	BP	multicellular organismal response to stress	NOS1; DBH; BCL2; ESR2; COMT; VDAC1
GO:0043409	0.0019	1	14791	601	33	6	BP	negative regulation of MAPKKK cascade	IGF1R; LIF; IGF1; CAV3; IGBP1; NCOR1
GO:0045740	0.0019	1	14791	601	33	6	BP	positive regulation of DNA replication	IGF1R; JUN; IGF1; HRAS; GLI2; ATF1
GO:0007599	0.0019	1	14791	601	83	10	BP	hemostasis	F3; MST1; APOH; F5; PROS1; F10; F2RL3; VWF; FLI1; PLAT
GO:0010717	0.0019	1	14791	601	14	4	BP	regulation of epithelial to mesenchymal transition	SMAD4; SMAD7; SMAD3; NKX2-1
GO:0030878	0.0019	1	14791	601	14	4	BP	thyroid gland development	HOXA5; SMAD3; PAX8; NKX2-1
GO:0030902	0.0019	1	14791	601	14	4	BP	hindbrain development	SMAD9; SMAD1; HOXA1; GLI2
GO:0032770	0.0019	1	14791	601	14	4	BP	positive regulation of monooxygenase activity	SCARB1; HIF1A; IL1B; TNF

GO:0006656	0.0019	1	14791	601	14	4	BP	phosphatidylcholine biosynthetic process	FABP3; CHPT1; LCAT; PEMT
GO:0070979	0.0019	1	14791	601	14	4	BP	protein K11-linked ubiquitination	ANAPC5; ANAPC7; CDC16; CDC23
GO:0043062	0.0019	1	14791	601	158	15	BP	extracellular structure organization	COL4A4; COL4A3; TSC1; CYR61; COL11A2; WT1; CADM1; ERBB4; NFKB2; LGALS3; DRD2; TNF; MAP1B; CACNB2; ACHE
GO:0032989	0.0019	1	14791	601	207	18	BP	cellular component morphogenesis	RXRA; LEF1; EGFR; IGF1R; HGF; WT1; CLU; CTNNA2; BCL2; CACNA1F; CREB1; HIF1A; PAX2; DRD2; MAP1B; GLI2; NDEL1; DNML
GO:0048871	0.0019	1	14791	601	23	5	BP	multicellular organismal homeostasis	DBH; IL1B; STAT3; DRD2; EPHA3
GO:0006706	0.0019	1	14791	601	23	5	BP	steroid catabolic process	CYP27B1; SCARB1; FGF23; CYP1A2; SRD5A2
GO:0060193	0.002	1	14791	601	70	9	BP	positive regulation of lipase activity	APOH; EGFR; AVPR1A; HOMER1; F2RL3; LPAR1; PLCB2; DRD2; CHRM2
GO:0009792	0.002	1	14791	601	143	14	BP	embryo development ending in birth or egg hatching	AR; APOB; SMAD4; APBA2; KEAP1; MSH2; SMAD3; ZFPM2; RICS8A; TP53; NBN; GLI2; SIN3A; DNMT3L
GO:0010829	0.002	1	14791	601	7	3	BP	negative regulation of glucose transport	PEA15; IL1B; TNF
GO:0031116	0.002	1	14791	601	7	3	BP	positive regulation of microtubule polymerization	CAV3; TERF1; MAP1B
GO:0034372	0.002	1	14791	601	7	3	BP	very-low-density lipoprotein particle remodeling	LIPC; CETP; LCAT
GO:0043921	0.002	1	14791	601	7	3	BP	modulation by host of viral transcription	SP1; TAF11; JUN
GO:0050434	0.002	1	14791	601	7	3	BP	positive regulation of viral transcription	SP1; TAF11; JUN
GO:0051095	0.002	1	14791	601	7	3	BP	regulation of helicase activity	MSH2; MSH3; TP53
GO:0052312	0.002	1	14791	601	7	3	BP	modulation of transcription in other organism	SP1; TAF11; JUN
GO:0052472	0.002	1	14791	601	7	3	BP	involved in symbiotic interaction	SP1; TAF11; JUN
GO:0060136	0.002	1	14791	601	7	3	BP	modulation by host of symbiont transcription	SP1; TAF11; JUN
GO:0060136	0.002	1	14791	601	7	3	BP	embryonic process involved in female pregnancy	SP1; SP3; CITED2
GO:0006101	0.002	1	14791	601	7	3	BP	citrate metabolic process	GHR; STAT5B; STAT5A

GO:0030509	0.002	1	14791	601	45	7	BP	BMP signaling pathway	SMAD9; SMAD4; SMAD7; SMAD1; LEF1; SMURF1; SMURF2
GO:0044255	0.0021	1	14791	601	535	36	BP	cellular lipid metabolic process	PPAP2A; PIK3CB; CYP2C9; APOB; APOH; PPARC; PPARA; ACAA2; SNCA; HEXB; LIPC; PTGES3; PI4KB; FABP3; CHTP1; CAV3; GHR; CETP; GBA; PLCB2; ACACB; LCAT; CYP1A2; HADHA; DRD2; RDH12; NKX2-1; ENPP7; PPP2CA; ACSL1; PEX5; SGPP1; FADS2; STAT5B; STAT5A; PENT
GO:0001763	0.0021	1	14791	601	113	12	BP	morphogenesis of a branching structure	AR; SMAD4; PGR; HOXB13; WT1; IGF1; HOXA5; BCL2; ESR1; DRD2; NKX2-1; GLI2
GO:0030182	0.0021	1	14791	601	113	12	BP	neuron differentiation	JAG1; RTN1; NTF3; HOXA1; STAT3; POU3F2; CEBPB; NKX2-1; NTRK3; PEX5; EPHA2; MYO7A
GO:0019932	0.0022	1	14791	601	226	19	BP	second-messenger-mediated signaling	PIK3CB; EGFR; IGF1R; AVPR1A; HOMER1; ADCY1; IGF1; PI4KB; F2RL3; VIPR1; ADCY5; WASF2; DRD2; HTR1A; PPP2CA; HTR1B; CHRM2; TNF; FSHR
GO:0009123	0.0022	1	14791	601	71	9	BP	nucleoside monophosphate metabolic process	ADSSL1; PDE8A; ADCY1; PDE11A; PPAT; ADCY5; NT5E; GUCY1A3; ADK
GO:0048589	0.0022	1	14791	601	99	11	BP	developmental growth	AR; PPARC; SMAD4; IGF1; SMAD3; BCL2; ESR1; SHBG; NBN; GDF9; GLI2
GO:0010863	0.0022	1	14791	601	58	8	BP	positive regulation of phospholipase C activity	EGFR; AVPR1A; HOMER1; F2RL3; LPAR1; PLCB2; DRD2; CHRM2
GO:0007202	0.0022	1	14791	601	58	8	BP	activation of phospholipase C activity	EGFR; AVPR1A; HOMER1; F2RL3; LPAR1; PLCB2; DRD2; CHRM2
GO:0010562	0.0022	1	14791	601	129	13	BP	positive regulation of phosphorus metabolic process	SMAD4; EGFR; LIF; IGF1; CAMP; BCL2; GHR; RAD50; IL1B; IL6; TNF; NBN; AXIN1
GO:0045937	0.0022	1	14791	601	129	13	BP	positive regulation of phosphate metabolic process	SMAD4; EGFR; LIF; IGF1; CAMP; BCL2; GHR; RAD50; IL1B; IL6; TNF; NBN; AXIN1
GO:0055080	0.0023	1	14791	601	279	22	BP	cation homeostasis	PIK3CB; SV2A; JPH2; CYP27B1; LTF; BDKRB2; SNCA; HEXB; AVPR1A; KCNK3; EPOR; EPHX2; LPAR1; BCL2; CAV3; CACNA1F; TRPV4; CCR4; IL1B; DRD2; ATP5B; NEDD4
GO:0014075	0.0023	1	14791	601	46	7	BP	response to amine stimulus	TRDMT1; RELA; DBH; SST; MSH2; DRD2; PENT
GO:0032886	0.0023	1	14791	601	46	7	BP	regulation of microtubule-based process	CAV3; BRCA1; IGBP1; TERF1; MAP1B; TACC3; NPM1
GO:0051053	0.0023	1	14791	601	46	7	BP	negative regulation of DNA metabolic process	BLM; GMNN; MSH2; MSH3; TP53; ENPP7; TERF1
GO:0050804	0.0024	1	14791	601	130	13	BP	regulation of synaptic transmission	EGFR; SNCA; NTF3; ERBB4; EGR1; BCAN; DRD2; HTR1B; HRAS; TNF; MAP1B; ACHE; PLAT
GO:0016125	0.0024	1	14791	601	100	11	BP	sterol metabolic process	APOB; PPARC; RXRA; LEPR; ACAA2; LIPC; SCARB1; VLDLR; CETP; LCAT; SREBF1
GO:0045840	0.0024	1	14791	601	24	5	BP	positive regulation of mitosis	IGF1; IL1B; TERF1; TGFA; TNF
GO:0051146	0.0024	1	14791	601	24	5	BP	striated muscle cell differentiation	TSC1; RXRA; AVPR1A; RARB; HRAS
GO:0051785	0.0024	1	14791	601	24	5	BP	positive regulation of nuclear division	IGF1; IL1B; TERF1; TGFA; TNF
GO:0060070	0.0024	1	14791	601	24	5	BP	canonical Wnt receptor signaling pathway	FZD8; RARG; GSK3B; SDC1; AXIN1

GO:0030003	0.0024	1	14791	601	245	20	BP	cellular cation homeostasis	PIK3CB; SV2A; JPH2; LTF; BDKRB2; HEXB; AVPR1A; KCNK3; EPOR; EPHX2; LPAR1; BCL2; CAV3; CACNA1F; TRPV4; CCR4; IL1B; DRD2; ATP5B; NEDD4L
GO:0001934	0.0024	1	14791	601	115	12	BP	positive regulation of protein amino acid phosphorylation	SMAD4; LIF; IGF1; CAMP; BCL2; GHR; RAD50; IL1B; IL6; TNF; NBN; AXIN1
GO:0060191	0.0025	1	14791	601	86	10	BP	regulation of lipase activity	APOH; EGFR; SNCA; AVPR1A; HOMER1; F2RL3; LPAR1; PLCB2; DRD2; CHRM2
GO:0007589	0.0025	1	14791	601	59	8	BP	body fluid secretion	TP73; USF2; PPAT; CREB1; XDH; DRD2; STAT5B; STAT5A
GO:0009612	0.0025	1	14791	601	59	8	BP	response to mechanical stimulus	F3; JUN; RELA; TRPV4; FOS; STAT1; TNF; MAP1B
GO:0032722	0.0025	1	14791	601	15	4	BP	positive regulation of chemokine production	HIF1A; IL6; TNF; RIPK2
GO:0045744	0.0025	1	14791	601	15	4	BP	negative regulation of G-protein coupled receptor protein signaling pathway	SNCA; RPH3AL; DRD2; ADRBK1
GO:0051354	0.0025	1	14791	601	15	4	BP	negative regulation of oxidoreductase activity	CYP27B1; SNCA; NFKB1; CAV3
GO:0050776	0.0025	1	14791	601	229	19	BP	regulation of immune response	RARA; RELA; MASP1; AP2B1; CADM1; CLU; SMAD3; CTSG; MASP2; FCN2; IL1B; IFNB1; IL6; C1S; TNF; STAT5B; STAT5A; PSMB4; RIPK2
GO:0052547	0.0026	1	14791	601	101	11	BP	regulation of peptidase activity	F3; PPARG; COL4A3; SNCA; SMAD3; STAT1; IFNB1; IGBP1; TP53; TERF1; TNF
GO:0006479	0.0027	1	14791	601	47	7	BP	protein amino acid methylation	ASH2L; NSD1; SUZ12; PRMT3; PRMT5; LCMT1; PCMT1
GO:0008213	0.0027	1	14791	601	47	7	BP	protein amino acid alkylation	ASH2L; NSD1; SUZ12; PRMT3; PRMT5; LCMT1; PCMT1
GO:0022602	0.0027	1	14791	601	73	9	BP	ovulation cycle process	LEPR; PGR; BCL2; ESR2; ESR1; NKX2-1; STAT5B; STAT5A; FSHR
GO:0045165	0.0027	1	14791	601	73	9	BP	cell fate commitment	PPARG; SMAD4; SMAD1; PRKDC; BCL2; PAX6; TAL1; TP53; NKX2-1
GO:0010959	0.0027	1	14791	601	87	10	BP	regulation of metal ion transport	JPH2; NOS1; SNCA; CATSPER1; HOMER1; BCL2; CAV3; GNAO1; DRD2; CACNA2D1
GO:0007005	0.0027	1	14791	601	87	10	BP	mitochondrion organization	TP73; SNCA; JUN; CLU; CEBPA; SMAD3; BCL2; TP53; PEX5; DNMI1
GO:0048870	0.0028	1	14791	601	301	23	BP	cell motility	PPAP2A; APOB; PPARG; EGFR; SFTPD; CATSPER1; DAB1; DBH; SCARB1; HOXA5; ETS1; CTNNA2; ESR2; CCR4; IL1B; IL6; WASF2; POU3F2; DRD2; NKX2-1; PEX5; PLAT; NDEL1
GO:0010817	0.0028	1	14791	601	148	14	BP	regulation of hormone levels	PCSK2; SCG5; SULT1E1; SCARB1; YWHAZ; TRPV4; ESR1; COMT; IL6; RDH12; SHBG; SRD5A2; CRHBP; STAT5B
GO:0030308	0.0028	1	14791	601	102	11	BP	negative regulation of cell growth	CYP27B1; PPARG; SMAD4; TP73; WT1; SMAD3; BCL2; ESR2; TP53; PPP2CA; GDF9
GO:0045860	0.0028	1	14791	601	231	19	BP	positive regulation of protein kinase activity	PPAP2A; PIK3CB; PDEGH; EGFR; HGF; DAB1; ADCY1; VLDLR; GHR; ADCY5; DAXX; IL1B; MAP2K3; PDPK1; PKN1; TGFA; TNF; DGKQ; NPM1
GO:0007006	0.0029	1	14791	601	25	5	BP	mitochondrial membrane organization	SNCA; BCL2; TP53; PEX5; DNMI1

GO:0070304	0.0029	1	14791	601	25	5	BP	positive regulation of stress-activated protein kinase signaling cascade	HIPK2; IL1B; TNF; RIPK2; AXIN1
GO:0048754	0.0029	1	14791	601	88	10	BP	branching morphogenesis of a tube	AR; SMAD4; PGR; WT1; IGF1; HOXA5; BCL2; ESR1; NKX2-1; GLI2
GO:0010564	0.0029	1	14791	601	133	13	BP	regulation of cell cycle process	LIF; TPR; IGF1; SMARCA4; BRCA1; PRMT5; CDC16; IL1B; TERF1; TGFA; CDC23; TNF; NPM1
GO:0001756	0.003	1	14791	601	36	6	BP	somitogenesis	PRKDC; LEF1; SMAD3; PAX1; TP53; SFRP2
GO:0000377	0.003	1	14791	601	48	7	BP	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	GEMIN5; HNRNPA1; PRPF3; SFPQ; BAT1; HNRNPC; SNRPA
GO:0000398	0.003	1	14791	601	48	7	BP	nuclear mRNA splicing, via spliceosome	GEMIN5; HNRNPA1; PRPF3; SFPQ; BAT1; HNRNPC; SNRPA
GO:0051272	0.0031	1	14791	601	134	13	BP	positive regulation of cellular component movement	F3; EGFR; IGF1R; SCARB1; IGF1; F10; ETS1; SMAD3; BCL2; ERBB4; HIF1A; IL6; STAT5B
GO:0031644	0.0032	1	14791	601	150	14	BP	regulation of neurological system process	EGFR; SNCA; AVPR1A; NTF3; ERBB4; EGR1; BCAN; DRD2; HTR1B; HRAS; TNF; MAP1B; ACHE; PLAT
GO:0010224	0.0032	1	14791	601	8	3	BP	response to UV-B	RELA; MSH2; BCL2
GO:0010470	0.0032	1	14791	601	8	3	BP	regulation of gastrulation	IL1B; SFRP2; TNF
GO:0031112	0.0032	1	14791	601	8	3	BP	positive regulation of microtubule polymerization or depolymerization	CAV3; TERF1; MAP1B
GO:0042738	0.0032	1	14791	601	8	3	BP	exogenous drug catabolic process	CYP2C9; CYP1A2; CYP2B6
GO:0045600	0.0032	1	14791	601	8	3	BP	positive regulation of fat cell differentiation	PPARG; PPARD; CEBPA
GO:0045910	0.0032	1	14791	601	8	3	BP	negative regulation of DNA recombination	BLM; MSH2; MSH3
GO:0060349	0.0032	1	14791	601	8	3	BP	bone morphogenesis	RARG; PAX1; SFRP2
GO:0060742	0.0032	1	14791	601	8	3	BP	epithelial cell differentiation involved in prostate gland development	AR; RXRA; STAT5A
GO:0007183	0.0032	1	14791	601	8	3	BP	SMAD protein complex assembly	SMAD4; SMAD1; SMAD3
GO:0010638	0.0032	1	14791	601	89	10	BP	positive regulation of organelle organization	IGF1; SMAD3; CAV3; IL1B; TP53; TERF1; TGFA; TNF; MAP1B; NPM1

GO:0008217	0.0032	1	14791	601	89	10	BP	regulation of blood pressure	PPARG; PPARA; BDKRB2; ABAT; AVPR1A; EPHX2; DRD2; HBB; NKX2-1; CHGA
GO:0016447	0.0033	1	14791	601	16	4	BP	somatic recombination of immunoglobulin gene segments	PRKDC; MSH2; MSH3; NBN
GO:0060395	0.0033	1	14791	601	16	4	BP	SMAD protein signal transduction	HIPK2; SMAD4; JUN; FOS
GO:0033043	0.0034	1	14791	601	235	19	BP	regulation of organelle organization	TSC1; SNCA; TPR; IGF1; SMAD3; CAV3; BRCA1; PRMT5; CDC16; IL1B; TP53; TERF1; TGFA; TAF7; CDC23; TNF; MAP1B; BCOR; NPM1
GO:0015918	0.0034	1	14791	601	37	6	BP	sterol transport	APOB; LIPC; SCARB1; CLU; CETP; LCAT
GO:0030301	0.0034	1	14791	601	37	6	BP	cholesterol transport	APOB; LIPC; SCARB1; CLU; CETP; LCAT
GO:0061138	0.0035	1	14791	601	90	10	BP	morphogenesis of a branching epithelium	AR; SMAD4; PGR; HOXB13; WT1; IGF1; HOXA5; BCL2; ESR1; NKX2-1
GO:0043271	0.0035	1	14791	601	26	5	BP	negative regulation of ion transport	NOS1; BCL2; GNAO1; DRD2; TNF
GO:0050817	0.0035	1	14791	601	76	9	BP	coagulation	F3; MST1; APOH; F5; PROS1; F10; F2RL3; VWF; PLAT
GO:0007596	0.0035	1	14791	601	76	9	BP	blood coagulation	F3; MST1; APOH; F5; PROS1; F10; F2RL3; VWF; PLAT
GO:0051960	0.0036	1	14791	601	219	18	BP	regulation of nervous system development	PPARG; SMAD1; NGFR; RELA; IGF1; NTF3; BCL2; CRX; XRCC5; TP53; POU3F2; DRD2; NTRK3; MAP1B; NBN; GLI2; NDEL1; ATF1
GO:0044282	0.0037	1	14791	601	272	21	BP	small molecule catabolic process	CYP27B1; PPARD; ABAT; NOS1; DBH; SARDH; PDE11A; NT5E; XDH; ACAD8; FGF23; COMT; HADHA; PON3; GOT1; PEX5; ATP5B; ASL; ACHE; DERA; ALDH6A1
GO:0051641	0.0037	1	14791	601	91	10	BP	cellular localization	SMAD7; EGFR; MLPH; RALA; SMURF1; TGS1; TACC3; SIN3A; NDEL1; MYO7A
GO:0010518	0.0038	1	14791	601	63	8	BP	positive regulation of phospholipase activity	EGFR; AVPR1A; HOMER1; F2RL3; LPAR1; PLCB2; DRD2; CHRM2
GO:0030005	0.0038	1	14791	601	220	18	BP	cellular di-, tri-valent inorganic cation homeostasis	PIK3CB; SV2A; JPH2; LTF; BDKRB2; HEXB; AVPR1A; KCNK3; EPOR; EPHX2; LPAR1; BCL2; CAV3; CACNA1F; TRPV4; CCR4; IL1B; DRD2
GO:0031331	0.0038	1	14791	601	50	7	BP	positive regulation of cellular catabolic process	PPARA; SMAD7; IGF1; CSNK1E; HIF1A; IL1B; TNF
GO:0007626	0.0039	1	14791	601	273	21	BP	locomotory behavior	HIPK2; PIK3CB; HOXB8; RALBP1; APBA2; ABAT; DEFA1; CYR61; SNCA; HEXB; SFTPD; DBH; RALA; ADCY5; GNAO1; CCR4; IL1B; IL6; DRD2; NKX2-1; HRAS
GO:0000187	0.0039	1	14791	601	77	9	BP	activation of MAPK activity	PIK3CB; PDE6H; HGF; GHR; DAXX; IL1B; PKN1; TGFA; TNF
GO:0006959	0.0039	1	14791	601	77	9	BP	humoral immune response	LTF; MASP1; CLU; BCL2; MASP2; FCN2; IL6; C1S; TNF
GO:0019725	0.0039	1	14791	601	421	29	BP	cellular homeostasis	PIK3CB; SV2A; JPH2; KCNH2; LTF; BDKRB2; SNCA; JUN; HEXB; AVPR1A; KCNK3; EPOR; EPHX2; LPAR1; MCL1; BCL2; CAV3; CACNA1F; TRPV4; FGF23; CCR4; IL1B; DRD2; KCNE1; SLC4A1; ATP5B; GRIN2C; NPM1; NEDD4L
GO:0010769	0.0041	1	14791	601	92	10	BP	regulation of cell morphogenesis involved in differentiation	SMAD4; SMAD7; SMAD1; NGFR; SMAD3; POU3F2; NKX2-1; NTRK3; MAP1B; NDEL1
GO:0001101	0.0041	1	14791	601	27	5	BP	response to acid	RELA; SST; MSH2; BCL2; PENT
GO:0000018	0.0041	1	14791	601	27	5	BP	regulation of DNA recombination	BLM; MSH2; MSH3; KPNA2; RAD50

GO:0022407	0.0041	1	14791	601	27	5	BP	regulation of cell-cell adhesion	L1CAM; SMAD7; CITED2; IL1B; TNF
GO:0030279	0.0042	1	14791	601	17	4	BP	negative regulation of ossification	BCL2; SMURF1; FGF23; BCOR
GO:0033280	0.0042	1	14791	601	17	4	BP	response to vitamin D	CYP27B1; RXRA; IL1B; ALPL
GO:0034381	0.0042	1	14791	601	17	4	BP	lipoprotein particle clearance	APOB; LIPC; SCARB1; VLDLR
GO:0042490	0.0042	1	14791	601	17	4	BP	mechanoreceptor differentiation	JAG1; NTF3; NTRK3; MYO7A
GO:0042516	0.0042	1	14791	601	17	4	BP	regulation of tyrosine phosphorylation of Stat3 protein	LIF; GHR; IL6; PPP2CA
GO:0048524	0.0042	1	14791	601	17	4	BP	positive regulation of viral reproduction	SP1; TAF11; JUN; IFNB1
GO:0051926	0.0042	1	14791	601	17	4	BP	negative regulation of calcium ion transport	NOS1; BCL2; GNAO1; DRD2
GO:0007492	0.0042	1	14791	601	17	4	BP	endoderm development	SMAD4; SMAD3; NKX2-1; HOXC11
GO:0051054	0.0042	1	14791	601	64	8	BP	positive regulation of DNA metabolic process	IGF1R; JUN; IGF1; CEBPG; BRCA1; HRAS; GLI2; ATF1
GO:0050767	0.0042	1	14791	601	205	17	BP	regulation of neurogenesis	PPARG; SMAD1; NGFR; RELA; NTF3; BCL2; CRX; XRCC5; TP53; POU3F2; DRD2; NTRK3; MAP1B; NBN; GLI2; NDEL1; ATF1
GO:0051605	0.0042	1	14791	601	78	9	BP	protein maturation by peptide bond cleavage	PCSK2; SCG5; F3; APOH; MASP1; CLU; MASP2; FCN2; C1S
GO:0051051	0.0043	1	14791	601	155	14	BP	negative regulation of transport	ITGAV; NOS1; SNCA; LIF; PEA15; NFKB1; BCL2; GNAO1; FGF23; IL1B; DRD2; PICALM; TNF; TACC3
GO:0042108	0.0043	1	14791	601	51	7	BP	positive regulation of cytokine biosynthetic process	REL; RELA; CEBPG; IL1B; TNF; STAT5B; STAT5A
GO:0043524	0.0043	1	14791	601	51	7	BP	negative regulation of neuron apoptosis	HIPK2; TP73; SNCA; MSH2; BCL2; ITSN1; HRAS
GO:0007399	0.0045	1	14791	601	387	27	BP	nervous system development	SMARCC2; PCSK2; L1CAM; APOB; TSC1; APBA2; JAG1; DAB1; VLDLR; IGF1; NTF3; HOXA1; SMARCA4; NR2C2; FOS; STAT3; EFNA5; NEFH; NTRK2; NTRK3; STMN1; CHRM2; FGF5; FGF11; ACHE; HEY1; NDEL1
GO:0046651	0.0045	1	14791	601	39	6	BP	lymphocyte proliferation	CADM1; PRKCD; BCL2; IFNB1; TP53; RIPK2
GO:0045926	0.0045	1	14791	601	124	12	BP	negative regulation of growth	CYP27B1; PPARG; SMAD4; TP73; WT1; SMAD3; BCL2; CTSG; ESR2; TP53; PPP2CA; GDF9
GO:0006730	0.0046	1	14791	601	140	13	BP	one-carbon metabolic process	CYP2C9; TRDMT1; ASH2L; NSD1; SUZ12; PRMT3; PRMT5; FOS; LCMT1; CYP1A2; PCMT1; TGS1; DNMT3L
GO:0031113	0.0046	1	14791	601	9	3	BP	regulation of microtubule polymerization	CAV3; TERF1; MAP1B
GO:0034370	0.0046	1	14791	601	9	3	BP	triglyceride-rich lipoprotein particle remodeling	LIPC; CETP; LCAT

GO:0034374	0.0046	1	14791	601	9	3	BP	low-density lipoprotein particle remodeling	APOB; LIPC; CETP
GO:0042135	0.0046	1	14791	601	9	3	BP	neurotransmitter catabolic process	ABAT; COMT; ACHE
GO:0042772	0.0046	1	14791	601	9	3	BP	DNA damage response, signal transduction resulting in transcription	HIPK2; BRCA1; TP53
GO:0060736	0.0046	1	14791	601	9	3	BP	prostate gland growth	AR; IGF1; ESR1
GO:0006599	0.0046	1	14791	601	9	3	BP	phosphagen metabolic process	GHR; STAT5B; STAT5A
GO:0006600	0.0046	1	14791	601	9	3	BP	creatine metabolic process	GHR; STAT5B; STAT5A
GO:0006978	0.0046	1	14791	601	9	3	BP	DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator	HIPK2; BRCA1; TP53
GO:0010771	0.0048	1	14791	601	3	2	BP	negative regulation of cell morphogenesis involved in differentiation	SMAD7; NKX2-1
GO:0010956	0.0048	1	14791	601	3	2	BP	negative regulation of calcidiol 1-monoxygenase activity	CYP27B1; NFKB1
GO:0010979	0.0048	1	14791	601	3	2	BP	regulation of vitamin D 24-hydroxylase activity	CYP27B1; FGF23
GO:0010980	0.0048	1	14791	601	3	2	BP	positive regulation of vitamin D 24-hydroxylase activity	CYP27B1; FGF23
GO:0016056	0.0048	1	14791	601	3	2	BP	rhodopsin mediated signaling pathway	SAG; RHO
GO:0001660	0.0048	1	14791	601	3	2	BP	fever	IL1B; EPHA3
GO:0021932	0.0048	1	14791	601	3	2	BP	hindbrain radial glia guided cell migration	DAB1; CTNNA2
GO:0030730	0.0048	1	14791	601	3	2	BP	sequestering of triglyceride	IL1B; TNF
GO:0032823	0.0048	1	14791	601	3	2	BP	regulation of natural killer cell differentiation	STAT5B; STAT5A

GO:0032825	0.0048	1	14791	601	3	2	BP	positive regulation of natural killer cell differentiation	STAT5B; STAT5A
GO:0032910	0.0048	1	14791	601	3	2	BP	regulation of transforming growth factor-beta3 production	SMAD3; CREB1
GO:0034114	0.0048	1	14791	601	3	2	BP	regulation of heterotypic cell-cell adhesion	IL1B; TNF
GO:0034392	0.0048	1	14791	601	3	2	BP	negative regulation of smooth muscle cell apoptosis	APOH; IGF1
GO:0035067	0.0048	1	14791	601	3	2	BP	negative regulation of histone acetylation	SNCA; TAF7
GO:0042369	0.0048	1	14791	601	3	2	BP	vitamin D catabolic process	CYP27B1; FGF23
GO:0043570	0.0048	1	14791	601	3	2	BP	maintenance of DNA repeat elements	MSH2; MSH3
GO:0045079	0.0048	1	14791	601	3	2	BP	negative regulation of chemokine biosynthetic process	SIGIRR; IL6
GO:0045990	0.0048	1	14791	601	3	2	BP	regulation of transcription by carbon catabolites	USF1; USF2
GO:0046015	0.0048	1	14791	601	3	2	BP	regulation of transcription by glucose	USF1; USF2
GO:0046085	0.0048	1	14791	601	3	2	BP	adenosine metabolic process	NT5E; ADK
GO:0048680	0.0048	1	14791	601	3	2	BP	positive regulation of axon regeneration	NTRK3; NDEL1
GO:0051450	0.0048	1	14791	601	3	2	BP	myoblast proliferation	HGF; IGF1
GO:0055012	0.0048	1	14791	601	3	2	BP	ventricular cardiac muscle cell differentiation	RXRA; RARB
GO:0060065	0.0048	1	14791	601	3	2	BP	uterus development	ESR2; ESR1
GO:0060510	0.0048	1	14791	601	3	2	BP	Type II pneumocyte differentiation	IGF1; NKX2-1
GO:0060559	0.0048	1	14791	601	3	2	BP	positive regulation of calcidiol 1-monooxygenase activity	IL1B; TNF
GO:0060748	0.0048	1	14791	601	3	2	BP	tertiary branching involved in mammary gland duct morphogenesis	AR; PGR

GO:0060766	0.0048	1	14791	601	3	2	BP	negative regulation of androgen receptor signaling pathway	IGF1; ESR2
GO:0070102	0.0048	1	14791	601	3	2	BP	interleukin-6-mediated signaling pathway	STAT3; IL6
GO:0070572	0.0048	1	14791	601	3	2	BP	positive regulation of neuron projection regeneration	NTRK3; NDEL1
GO:0070587	0.0048	1	14791	601	3	2	BP	regulation of cell-cell adhesion involved in gastrulation	IL1B; TNF
GO:0009586	0.0048	1	14791	601	3	2	BP	rhodopsin mediated phototransduction	SAG; RHO
GO:0033189	0.0048	1	14791	601	52	7	BP	response to vitamin A	PPARG; RXRA; RARA; RARG; MAP1B; DUSP1; IGF2R
GO:0008406	0.0048	1	14791	601	52	7	BP	gonad development	AR; WT1; MSH2; BCL2; ESR1; SRD5A2; FSHR
GO:0048534	0.005	1	14791	601	110	11	BP	hemopoietic or lymphoid organ development	SPI1; SP3; ASH2L; JAG1; BCL2; NFKB2; PAX1; TAL1; TACC3; STAT5B; STAT5A
GO:0042129	0.0051	1	14791	601	66	8	BP	regulation of T cell proliferation	BLM; SFTPD; IL1B; IL6; ADK; STAT5B; STAT5A; RIPK2
GO:0048469	0.0051	1	14791	601	66	8	BP	cell maturation	PPARG; PGR; TRIP13; HOXB13; HOXA5; CEBPA; ESR2; KCNE1
GO:0003013	0.0051	1	14791	601	95	10	BP	circulatory system process	COL4A3; KCNH2; BDKRB2; AVPR1A; STAT1; KCNE2; KCNE1; HBB; FL11; GUCY1A3
GO:0030521	0.0051	1	14791	601	40	6	BP	androgen receptor signaling pathway	PPAP2A; AR; CDK7; BRCA1; DAXX; MED30
GO:0035282	0.0051	1	14791	601	40	6	BP	segmentation	PRKDC; LEF1; SMAD3; PAX1; TP53; SFRP2
GO:0007272	0.0051	1	14791	601	40	6	BP	ensheathment of neurons	PPARD; TSC1; HEXB; NTF3; POU3F2; CLDN11
GO:0008366	0.0051	1	14791	601	40	6	BP	axon ensheathment	PPARD; TSC1; HEXB; NTF3; POU3F2; CLDN11
GO:0042596	0.0052	1	14791	601	18	4	BP	fear response	DBH; BCL2; ESR2; VDAC1
GO:0050999	0.0052	1	14791	601	18	4	BP	regulation of nitric-oxide synthase activity	EGFR; SCARB1; CAV3; HIF1A
GO:0009056	0.0052	1	14791	601	953	55	BP	catabolic process	CYP2C9; TSG101; UBE2D2; APOB; CYP27B1; SMG5; PPARD; ANAPC5; ANAPC7; ABAT; NOS1; HEXB; LIPC; LPO; DBH; SCARB1; SARDH; EPHX2; PDE11A; SKP1; DLST; CDK7; GTF2H4; USP7; PSME1; PLCD3; PLCB2; SMURF1; SMURF2; CDC16; NT5E; XDH; ACAD8; FGF23; RBM8A; ZHX2; COMT; CYP11A2; HADHA; SQSTM1; PON3; GOT1; PPP2CB; PEX5; CDC23; ATP5B; CYP2B6; SRD5A2; ASL; ACHE; PSMB4; DERA; ALDH6A1; AXIN1; IIPF3A
GO:0044267	0.0054	1	14791	601	1883	98	BP	cellular protein metabolic process	STK16; P4HA2; HIPK2; PIK3CB; CAMK2A; CAMK2B; TSG101; UBE2D2; SENP2; DSP; ANAPC5; ANAPC7; PPIID; CSNK1A1; PDE6H; SMAD9; ASH2L; SMAD7; SMAD1; PRKDC; SRPK1; ERC1; EGFR; IGF1R; ERG; YARS2; HGF; HEXB; B3GNT6; TPR; PTGES3; RHO; MAPK10; PRKG1; BMX; CSNK1E; NSD1; WDIHV1; CDK7; USP7; SUZ12; PRKCD; ABI3; BCL2; WWP1; GHR; BRCA1; ERBB4; PRMT3; CREB1; BRD8; DZIP3; PRMT5; SMURF1; DAXX; SMURF2; CDC16; RPS3A; TRRAP; STK36; LCMT1; IL1B; HARS; STAT1; MARK3; EIF2C2; HARS2; EIF6; MAP2K3; AMHR2; PDPK1; PKN1; DUSP14; DUSP12; NTRK2; NTRK3; PPP2CA; PPP2CB; MST1R; GSK3B; ST13; MAPKAPK5; TGFA; NACA; CDC23; TNF; EPHA8; EPHA3; EPHA2; DUSP1; PCMT1; STAT5A; RIPK2; ADRBK1; PLAT; PTPRS; NEDD4L; ATF6
GO:0007050	0.0054	1	14791	601	111	11	BP	cell cycle arrest	TSG101; CYP27B1; TP73; CDKN2B; MLF1; MSH2; SMAD3; TP53INP1; TP53; HRAS; NBN

GO:0032103	0.0054	1	14791	601	81	9	BP	positive regulation of response to external stimulus	F3; CYP27B1; SMAD3; CCR4; IL6; NTRK3; STAT5B; STAT5A; NDEL1
GO:0009310	0.0054	1	14791	601	81	9	BP	amine catabolic process	NOS1; DBH; SARDH; ACAD8; COMT; GOT1; ASL; ACHE; ALDH6A1
GO:0006520	0.0055	1	14791	601	228	18	BP	cellular amino acid metabolic process	NOS1; YARS2; TPR; DBH; SARDH; PPAT; GHR; ACAD8; HARS; AGXT; HARS2; AADAT; GOT1; ASL; STAT5B; STAT5A; ALDH6A1; GGT1
GO:0009790	0.0056	1	14791	601	211	17	BP	embryo development	AR; APOB; SMAD4; TSC1; APBA2; EPOR; KEAP1; MSH2; SMAD3; ZFPM2; RIC8A; TP53; MAP1B; NBN; GLI2; SIN3A; DNMT3L
GO:0050778	0.0058	1	14791	601	144	13	BP	positive regulation of immune response	RELA; MASP1; CADM1; CLU; CTSG; MASP2; FCN2; IL1B; IFNB1; C1S; STAT5B; STAT5A; RIPK2
GO:0002541	0.0058	1	14791	601	41	6	BP	activation of plasma proteins involved in acute inflammatory response	F3; MASP1; CLU; MASP2; FCN2; C1S
GO:0032943	0.0058	1	14791	601	41	6	BP	mononuclear cell proliferation	CADM1; PRKDC; BCL2; IFNB1; TP53; RIPK2
GO:0008584	0.0058	1	14791	601	41	6	BP	male gonad development	AR; WT1; MSH2; BCL2; ESR1; SRD5A2
GO:0030030	0.0058	1	14791	601	283	21	BP	cell projection organization	LICAM; TSC1; RXRA; AK7; EGFR; IGF1R; CLU; CTNNA2; BCL2; CACNA1F; CREB1; GNAO1; PAX2; IL6; WASF2; DRD2; SDCBP; MAP1B; GLI2; NDEL1; MVO7A
GO:0030099	0.0059	1	14791	601	82	9	BP	myeloid cell differentiation	SP1; SP3; PPARG; CDKN2B; IRF8; CEBPA; CEBPG; CEBPE; TAL1
GO:0030278	0.0059	1	14791	601	82	9	BP	regulation of ossification	CYP27B1; SMAD1; SMAD3; BCL2; SMURF1; FGF23; IL6; TFAP2A; BCOR
GO:0016445	0.0064	1	14791	601	19	4	BP	somatic diversification of immunoglobulins	PRKDC; MSH2; MSH3; NBN
GO:0032228	0.0064	1	14791	601	19	4	BP	regulation of synaptic transmission, GABAergic	ERBB4; DRD2; HTR1B; HRAS
GO:0045076	0.0064	1	14791	601	19	4	BP	regulation of interleukin-2 biosynthetic process	SFTPD; IL1B; STAT5B; STAT5A
GO:0014911	0.0064	1	14791	601	10	3	BP	positive regulation of smooth muscle cell migration	F3; IGF1; BCL2
GO:2000027	0.0064	1	14791	601	10	3	BP	regulation of organ morphogenesis	NGFR; TFAP2A; BCOR
GO:0031057	0.0064	1	14791	601	10	3	BP	negative regulation of histone modification	SNCA; TAF7; BCOR
GO:0031952	0.0064	1	14791	601	10	3	BP	regulation of protein amino acid autophosphorylation	JUN; RAD50; NBN
GO:0033057	0.0064	1	14791	601	10	3	BP	reproductive behavior in a multicellular organism	HEXB; AVPR1A; DBH
GO:0042481	0.0064	1	14791	601	10	3	BP	regulation of odontogenesis	NGFR; TFAP2A; BCOR
GO:0042737	0.0064	1	14791	601	10	3	BP	drug catabolic process	CYP2C9; CYP1A2; CYP2B6

GO:0050908	0.0064	1	14791	601	10	3	BP	detection of light stimulus involved in visual perception	SAG; RHO; CACNA1F
GO:0050962	0.0064	1	14791	601	10	3	BP	detection of light stimulus involved in sensory perception	SAG; RHO; CACNA1F
GO:0055117	0.0064	1	14791	601	10	3	BP	regulation of cardiac muscle contraction	SMAD7; NOS1; CAV3
GO:0060442	0.0064	1	14791	601	10	3	BP	branching involved in prostate gland morphogenesis	HOXB13; IGF1; ESR1
GO:0006105	0.0064	1	14791	601	10	3	BP	succinate metabolic process	GHR; STAT5B; STAT5A
GO:0043405	0.0065	1	14791	601	146	13	BP	regulation of MAP kinase activity	PIK3CB; PDE6H; TP73; EGFR; HGF; CAV3; GHR; DAXX; IL1B; PKN1; PPP2CA; TGFA; TNF
GO:0043648	0.0066	1	14791	601	42	6	BP	dicarboxylic acid metabolic process	DLST; GHR; AADAT; GOT1; STAT5B; STAT5A
GO:0051216	0.0066	1	14791	601	42	6	BP	cartilage development	COL11A2; RARG; GHR; BMP8A; SFRP2; BMP5
GO:0070661	0.0066	1	14791	601	42	6	BP	leukocyte proliferation	CADM1; PRKCD; BCL2; IFNB1; TP53; RIPK2
GO:0016477	0.0066	1	14791	601	268	20	BP	cell migration	PPAP2A; PPARD; EGFR; SFTPD; DAB1; DBH; SCARB1; HOXA5; CTNNA2; ESR2; CCR4; IL1B; IL6; WASF2; POU3F2; DRD2; NKX2-1; PEX5; PLAT; NDEL1
GO:0009617	0.0066	1	14791	601	130	12	BP	response to bacterium	LTF; DEFA1; RELA; IRF8; CEBPE; CAMP; CCR4; STAT1; IFNB1; IL6; TNF; RIPK2
GO:0032663	0.0066	1	14791	601	30	5	BP	regulation of interleukin-2 production	SFTPD; IL1B; STAT5B; STAT5A; RIPK2
GO:0042509	0.0066	1	14791	601	30	5	BP	regulation of tyrosine phosphorylation of STAT protein	LIF; IGF1; GHR; IL6; PPP2CA
GO:0045995	0.0066	1	14791	601	30	5	BP	regulation of embryonic development	AR; IL1B; SFRP2; WNT2; TNF
GO:0051896	0.0066	1	14791	601	30	5	BP	regulation of protein kinase B signaling cascade	F3; IGF1R; F10; DRD2; ITSN1
GO:0070374	0.0066	1	14791	601	30	5	BP	positive regulation of ERK1 and ERK2 cascade	FGF23; IL1B; HRAS; FGF4; RIPK2
GO:0019538	0.0068	1	14791	601	2528	126	BP	protein metabolic process	PCSK2; SCG5; STK16; P4HA2; HIPK2; PIK3CB; CAMK2A; CAMK2B; F3; CNDP1; TSG101; UBE2D2; MST1; APOH; SENP2; DSP; ANAPC5; ANAPC7; PPID; CSNK1A1; PDE6H; SMAD9; ASH2L; SMAD7; SMAD1; PRKDC; SRPK1; ERC1; EGFR; IGF1R; ERG; NGFR; YARS2; HGF; HEXB; B3GNT6; RELA; TPR; PTGES3; RHO; MAPK10; MASP1; PRKG1; BMX; F10; NFKB1; CSNK1E; NSD1; WDHV1; SKP1; CLU; CDK7; USP7; PRSS2; SUZ12; PRKCD; PSME1; ABI3; MMP8; BCL2; WWP1; GHR; BRCA1; ERBB4; PRMT3; CREB1; CTSG; BRD8; DZIP3; PRMT5; MASP2; SMURF1; DAXX; SMURF2; CDC16; RPS3A; FCN2; TRRAP; CTSL1; STK36; LCMT1; IL1B; HARS; STAT1; MARK3; EIF2C2; HARS2; EIF6; MAP2K3; AMHR2; PDPK1; PKN1; DUSP14; DUSP12; SQSTM1; C1S; NTRK2; NTRK3; CAPN2; PPP2CA; PPP2CB; MST1R; GSK3B; ST13; MAPKAPK5; TGFA; NACA; CDC23; TNF; EPHAS; ACAN; EPHA3; EPHA2; ACR; DUSP1; PCMT1; STAT5A; PSMB4; ADAM12; RIPK2; ADRBK1; PLAT; PTPRS; AXIN1; NEDD4L; ATF6
GO:0019217	0.0072	1	14791	601	56	7	BP	regulation of fatty acid metabolic process	PPARG; PPARA; SNCA; AVPR1A; BRCA1; ACACB; ACSL1
GO:0048511	0.0073	1	14791	601	148	13	BP	rhythmic process	LEPR; EGFR; PGR; JUN; BCL2; CRX; ESR2; ESR1; DRD2; NKX2-1; STAT5B; STAT5A; FSHR

G0:0048592	0.0077	1	14791	601	31	5	BP	eye morphogenesis	SP1; SP3; RARB; RARG; YY1
G0:0017144	0.0077	1	14791	601	20	4	BP	drug metabolic process	CYP2C9; EPHX2; CYP1A2; CYP2B6
G0:0018107	0.0077	1	14791	601	20	4	BP	peptidyl-threonine phosphorylation	BCL2; PDPK1; PKN1; ADRBK1
G0:0042417	0.0077	1	14791	601	20	4	BP	dopamine metabolic process	SNCA; DBH; COMT; DRD2
G0:0043200	0.0077	1	14791	601	20	4	BP	response to amino acid stimulus	RELA; SST; MSH2; PENT
G0:0045884	0.0077	1	14791	601	20	4	BP	regulation of survival gene product expression	ESR2; ESR1; STAT5B; STAT5A
G0:0048169	0.0077	1	14791	601	20	4	BP	regulation of long-term neuronal synaptic plasticity	SNCA; EGR1; DRD2; HRAS
G0:0042632	0.0083	1	14791	601	44	6	BP	cholesterol homeostasis	APOB; LIPC; SCARB1; CAV3; CETP; LCAT
G0:0055092	0.0083	1	14791	601	44	6	BP	sterol homeostasis	APOB; LIPC; SCARB1; CAV3; CETP; LCAT
G0:0040017	0.0084	1	14791	601	134	12	BP	positive regulation of locomotion	F3; EGFR; IGF1R; SCARB1; IGF1; F10; SMAD3; BCL2; ERBB4; HIF1A; CCR4; IL6
G0:0016054	0.0085	1	14791	601	118	11	BP	organic acid catabolic process	PPARD; NOS1; DBH; SARDH; ACAD8; HADHA; PON3; GOT1; PEX5; ASL; ALDH6A1
G0:0046395	0.0085	1	14791	601	118	11	BP	carboxylic acid catabolic process	PPARD; NOS1; DBH; SARDH; ACAD8; HADHA; PON3; GOT1; PEX5; ASL; ALDH6A1
G0:0042113	0.0086	1	14791	601	72	8	BP	B cell activation	SP3; MSH2; CEBPG; PRKCD; BCL2; IFNB1; IGBP1; NBN
G0:0001829	0.0086	1	14791	601	11	3	BP	trophectodermal cell differentiation	SP1; SP3; CITED2
G0:0001909	0.0086	1	14791	601	11	3	BP	leukocyte mediated cytotoxicity	CADM1; CEBPG; CTSG
G0:0019627	0.0086	1	14791	601	11	3	BP	urea metabolic process	CYP2C9; CEBPA; ASL
G0:0031103	0.0086	1	14791	601	11	3	BP	axon regeneration	RXRA; BCL2; MAP1B
G0:0031293	0.0086	1	14791	601	11	3	BP	membrane protein intracellular domain proteolysis	NGFR; RELA; NFKB1
G0:0033032	0.0086	1	14791	601	11	3	BP	regulation of myeloid cell apoptosis	APOH; BCL2; STAT5A
G0:0034405	0.0086	1	14791	601	11	3	BP	response to fluid shear stress	F3; SMAD7; CITED2
G0:0042517	0.0086	1	14791	601	11	3	BP	positive regulation of tyrosine phosphorylation of Stat3 protein	LIF; GHR; IL6
G0:0055007	0.0086	1	14791	601	11	3	BP	cardiac muscle cell differentiation	TSC1; RXRA; RARB
G0:0007520	0.0086	1	14791	601	11	3	BP	myoblast fusion	NOS1; CAPN2; ADAM12

GO:0045765	0.0087	1	14791	601	87	9	BP	regulation of angiogenesis	F3; APOH; COL4A3; HOXA5; CAMP; HIF1A; IL1B; IL6; EPHA2
GO:0007155	0.0087	1	14791	601	707	42	BP	cell adhesion	L1CAM; DLG1; PIK3CB; ITGA3; DSP; PPARD; COL4A3; ITGAV; TSC1; LEF1; F5; EGFR; PPF1A1; CYR61; COL11A2; PKP3; PKP2; DAB1; SCARB2; SCARB1; CNTN1; CADM1; COL17A1; ITGB3BP; CTNNA2; BCL2; PPF1BP1; ICAM3; BCAN; VWF; FGF4; TNF; CLDN11; CLDN17; ACAN; CLDN19; NCAM1; ACHE; IGFALS; ADAM12; SVEP1; PTPRS
GO:0048167	0.0088	1	14791	601	58	7	BP	regulation of synaptic plasticity	SNCA; EGR1; BCAN; DRD2; HRAS; MAP1B; PLAT
GO:0050808	0.0088	1	14791	601	58	7	BP	synapse organization	TSC1; CADM1; ERBB4; DRD2; MAP1B; CACNB2; ACHE
GO:0051168	0.0088	1	14791	601	58	7	BP	nuclear export	XP07; SMG5; TSC1; HNRNPA1; SMURF1; BAT1; NPM1
GO:0030500	0.0088	1	14791	601	32	5	BP	regulation of bone mineralization	CYP27B1; SMAD3; FGF23; TFAP2A; BCOR
GO:0032412	0.0088	1	14791	601	32	5	BP	regulation of ion transmembrane transporter activity	JPH2; CATSPER1; HOMER1; CAV3; DRD2
GO:0022610	0.0089	1	14791	601	708	42	BP	biological adhesion	L1CAM; DLG1; PIK3CB; ITGA3; DSP; PPARD; COL4A3; ITGAV; TSC1; LEF1; F5; EGFR; PPF1A1; CYR61; COL11A2; PKP3; PKP2; DAB1; SCARB2; SCARB1; CNTN1; CADM1; COL17A1; ITGB3BP; CTNNA2; BCL2; PPF1BP1; ICAM3; BCAN; VWF; FGF4; TNF; CLDN11; CLDN17; ACAN; CLDN19; NCAM1; ACHE; IGFALS; ADAM12; SVEP1; PTPRS
GO:0043406	0.009	1	14791	601	103	10	BP	positive regulation of MAP kinase activity	PIK3CB; PDE6H; EGFR; HGF; GHR; DAXX; IL1B; PKN1; TGFA; TNF
GO:0016567	0.009	1	14791	601	152	13	BP	protein ubiquitination	TSG101; UBE2D2; ANAPC5; ANAPC7; SUZ12; BCL2; WWP1; BRCA1; DZIP3; SMURF1; CDC16; CDC23; NEDD4L
GO:0008544	0.009	1	14791	601	119	11	BP	epidermis development	DSP; PPARA; LEF1; EGFR; NGFR; HOXB13; RELA; PTGES3; NTF3; COL17A1; POU3F2
GO:0070647	0.0091	1	14791	601	204	16	BP	protein modification by small protein conjugation or removal	TSG101; UBE2D2; SENP2; ANAPC5; ANAPC7; USP7; SUZ12; BCL2; WWP1; BRCA1; DZIP3; SMURF1; CDC16; TRRAP; CDC23; NEDD4L
GO:0021766	0.0093	1	14791	601	21	4	BP	hippocampus development	TSC1; TP73; BCAN; NKX2-1
GO:0031128	0.0093	1	14791	601	21	4	BP	developmental induction	WNT2; NKX2-1; POU2F1; HOXC11
GO:0045776	0.0093	1	14791	601	21	4	BP	negative regulation of blood pressure	PPARA; BDKRB2; ABAT; DRD2
GO:0051817	0.0093	1	14791	601	21	4	BP	modification of morphology or physiology of other organism involved in symbiotic interaction	SP1; TAF11; JUN; CTSG
GO:0051897	0.0093	1	14791	601	21	4	BP	positive regulation of protein kinase B signaling cascade	F3; IGF1R; F10; ITSN1
GO:0007223	0.0093	1	14791	601	21	4	BP	Wnt receptor signaling pathway, calcium modulating pathway	WNT16; WNT10A; WNT2; WNT9B
GO:0010523	0.0093	1	14791	601	4	2	BP	negative regulation of calcium ion transport into cytosol	NOS1; BCL2

GO:0010640	0.0093	1	14791	601	4	2	BP	regulation of platelet-derived growth factor receptor signaling pathway	F3; SNCA
GO:0010799	0.0093	1	14791	601	4	2	BP	regulation of peptidyl-threonine phosphorylation	SMAD7; AXIN1
GO:0010891	0.0093	1	14791	601	4	2	BP	regulation of sequestering of triglyceride	PPARG; PPARA
GO:0001553	0.0093	1	14791	601	4	2	BP	luteinization	STAT5B; STAT5A
GO:0001880	0.0093	1	14791	601	4	2	BP	Mullerian duct regression	SMAD9; AMHR2
GO:0000019	0.0093	1	14791	601	4	2	BP	regulation of mitotic recombination	BLM; RAD50
GO:0021799	0.0093	1	14791	601	4	2	BP	cerebral cortex radially oriented cell migration	DAB1; POU3F2
GO:0030579	0.0093	1	14791	601	4	2	BP	ubiquitin-dependent SMAD protein catabolic process	SMURF1; SMURF2
GO:0030656	0.0093	1	14791	601	4	2	BP	regulation of vitamin metabolic process	NFKB1; TNF
GO:0032800	0.0093	1	14791	601	4	2	BP	receptor biosynthetic process	PPARG; TNF
GO:0033591	0.0093	1	14791	601	4	2	BP	response to L-ascorbic acid	BCL2; IL1B
GO:0034332	0.0093	1	14791	601	4	2	BP	adherens junction organization	DSP; SMAD7
GO:0042420	0.0093	1	14791	601	4	2	BP	dopamine catabolic process	DBH; COMT
GO:0043089	0.0093	1	14791	601	4	2	BP	positive regulation of Cdc42 GTPase activity	RALBP1; NDEL1
GO:0044070	0.0093	1	14791	601	4	2	BP	regulation of anion transport	FGF23; TNF
GO:0045586	0.0093	1	14791	601	4	2	BP	regulation of gamma-delta T cell differentiation	STAT5B; STAT5A
GO:0045588	0.0093	1	14791	601	4	2	BP	positive regulation of gamma-delta T cell differentiation	STAT5B; STAT5A
GO:0046113	0.0093	1	14791	601	4	2	BP	nucleobase catabolic process	XDH; ALDH6A1
GO:0046643	0.0093	1	14791	601	4	2	BP	regulation of gamma-delta T cell activation	STAT5B; STAT5A
GO:0046645	0.0093	1	14791	601	4	2	BP	positive regulation of gamma-delta T cell activation	STAT5B; STAT5A

GO:0055094	0.0093	1	14791	601	4	2	BP	response to lipoprotein stimulus	F3; PPARG
GO:0060068	0.0093	1	14791	601	4	2	BP	vagina development	ESR2; ESR1
GO:0060396	0.0093	1	14791	601	4	2	BP	growth hormone receptor signaling pathway	GHR; SOCS2
GO:0060430	0.0093	1	14791	601	4	2	BP	lung saccule development	PTGES3; NKX2-1
GO:0060463	0.0093	1	14791	601	4	2	BP	lung lobe morphogenesis	LIF; IGF1
GO:0060556	0.0093	1	14791	601	4	2	BP	regulation of vitamin D biosynthetic process	NFKB1; TNF
GO:0060743	0.0093	1	14791	601	4	2	BP	epithelial cell maturation involved in prostate gland development	HOXB13; ESR2
GO:0061046	0.0093	1	14791	601	4	2	BP	regulation of branching involved in lung morphogenesis	WNT2; TNF
GO:0070423	0.0093	1	14791	601	4	2	BP	nucleotide-binding oligomerization domain containing signaling pathway	RELA; RIPK2
GO:0070431	0.0093	1	14791	601	4	2	BP	nucleotide-binding oligomerization domain containing 2 signaling pathway	RELA; RIPK2
GO:0071378	0.0093	1	14791	601	4	2	BP	cellular response to growth hormone stimulus	GHR; SOCS2
GO:0006281	0.0094	1	14791	601	277	20	BP	DNA repair	BLM; PRKDC; TP73; TRIP13; CSNK1E; FANCC; UHRF1; CDK7; GTF2H4; MSH2; MSH3; BRCA1; XRCC5; NONO; RAD50; SFPQ; POLE2; TP53; NBN; RAD21
GO:0060341	0.0095	1	14791	601	296	21	BP	regulation of cellular localization	SCG5; SMAD4; SNCA; LIF; AVPR1A; RALA; CADM1; SMAD3; CREB1; RPH3AL; FGF23; IL1B; IL6; DRD2; SYT9; GSK3B; HTR1B; TNF; ACHE; TACC3; ADRBK1
GO:0035239	0.0096	1	14791	601	120	11	BP	tube morphogenesis	AR; SMAD4; PGR; WT1; IGF1; HOXA5; SMAD3; BCL2; ESR1; NKX2-1; GLI2
GO:0001822	0.01	1	14791	601	89	9	BP	kidney development	SMAD4; SMAD1; TSC1; LEF1; WT1; BCL2; PAX8; GLI2; HOXC11
GO:0030856	0.01	1	14791	601	33	5	BP	regulation of epithelial cell differentiation	CYP27B1; CDKN2B; XDH; STAT5B; STAT5A
GO:0008306	0.01	1	14791	601	33	5	BP	associative learning	DBH; RIC8A; FOS; DRD2; HRAS
GO:0048562	0.0101	1	14791	601	74	8	BP	embryonic organ morphogenesis	SP1; SP3; HOXB8; RARB; RARG; HOXA5; SMAD3; TFAP2A
GO:0051480	0.0102	1	14791	601	121	11	BP	cytosolic calcium ion homeostasis	JPH2; BDKRB2; AVPR1A; KCNK3; EPOR; LPAR1; CAV3; TRPV4; CCR4; IL1B; DRD2
GO:0016485	0.0103	1	14791	601	105	10	BP	protein processing	PCSK2; SCG5; F3; APOH; MASP1; CLU; MASP2; FCN2; CIS; CAPN2

GO:0031397	0.0109	1	14791	601	75	8	BP	negative regulation of protein ubiquitination	ANAPC5; ANAPC7; SMAD7; TSC1; PSME1; CDC16; CDC23; PSMB4
GO:0042445	0.0109	1	14791	601	106	10	BP	hormone metabolic process	PCSK2; SCG5; SULT1E1; SCARB1; ESR1; COMT; RDH12; SRD5A2; CRHBP; STAT5B
GO:0016338	0.011	1	14791	601	22	4	BP	calcium-independent cell-cell adhesion	CADM1; CLDN11; CLDN17; CLDN19
GO:0001890	0.011	1	14791	601	22	4	BP	placenta development	PPARG; PPARC; RXRA; VWF
GO:0031056	0.011	1	14791	601	22	4	BP	regulation of histone modification	SNCA; TP53; TAF7; BCOR
GO:0032755	0.011	1	14791	601	22	4	BP	positive regulation of interleukin-6 production	IL1B; IL6; TNF; RIPK2
GO:0035567	0.011	1	14791	601	22	4	BP	non-canonical Wnt receptor signaling pathway	WNT16; WNT10A; WNT2; WNT9B
GO:0042219	0.011	1	14791	601	22	4	BP	cellular amino acid derivative catabolic process	ABAT; DBH; COMT; ACHE
GO:0045682	0.011	1	14791	601	22	4	BP	regulation of epidermis development	CYP27B1; NGFR; KEAP1; TNF
GO:0051385	0.011	1	14791	601	22	4	BP	response to mineralocorticoid stimulus	AVPR1A; BCL2; FOS; HTR1B
GO:0051129	0.011	1	14791	601	173	14	BP	negative regulation of cellular component organization	SMAD7; NGFR; SNCA; TPR; CLU; CAV3; BRCA1; PICALM; NKX2-1; TERF1; TAF7; MAP1B; BCOR; NPM1
GO:0006725	0.0111	1	14791	601	139	12	BP	cellular aromatic compound metabolic process	SNCA; DBH; EPHX2; MTHFS; PPAT; XDH; COMT; CYP1A2; DRD2; PON3; ALDH6A1; PEMT
GO:0010888	0.0111	1	14791	601	12	3	BP	negative regulation of lipid storage	PPARG; PPARA; ITGAV
GO:0042100	0.0111	1	14791	601	12	3	BP	B cell proliferation	PRKCD; BCL2; IFNB1
GO:0045648	0.0111	1	14791	601	12	3	BP	positive regulation of erythrocyte differentiation	ETS1; HIF1A; TAL1
GO:0048384	0.0111	1	14791	601	12	3	BP	retinoic acid receptor signaling pathway	RXRA; RARA; RARG
GO:0060571	0.0111	1	14791	601	12	3	BP	morphogenesis of an epithelial fold	AR; EGFR; GLI2
GO:0060749	0.0111	1	14791	601	12	3	BP	mammary gland alveolus development	AR; HOXA5; ESR1
GO:0006110	0.0111	1	14791	601	12	3	BP	regulation of glycolysis	IGF1; PGAM1; HIF1A
GO:0000768	0.0111	1	14791	601	12	3	BP	syncytium formation by plasma membrane fusion	NOS1; CAPN2; ADAM12

GO:0010827	0.0114	1	14791	601	34	5	BP	regulation of glucose transport	PEA15; ERBB4; IL1B; TNF; CLTCL1
GO:0022898	0.0114	1	14791	601	34	5	BP	regulation of transmembrane transporter activity	JPH2; CATSPER1; HOMER1; CAV3; DRD2
GO:0034765	0.0114	1	14791	601	34	5	BP	regulation of ion transmembrane transport	JPH2; CATSPER1; HOMER1; CAV3; DRD2
GO:0008156	0.0114	1	14791	601	34	5	BP	negative regulation of DNA replication	BLM; GMN; TP53; ENPP7; TERF1
GO:0071216	0.0114	1	14791	601	47	6	BP	cellular response to biotic stimulus	CAMP; STAT1; TP53; GSK3B; RIPK2; ATF6
GO:0034754	0.0115	1	14791	601	61	7	BP	cellular hormone metabolic process	SULT1E1; SCARB1; ESR1; COMT; RDH12; SRD5A2; STAT5B
GO:0000375	0.0115	1	14791	601	61	7	BP	RNA splicing, via transesterification reactions	GEMIN5; HNRNPA1; PRPF3; SFPQ; BAT1; HNRNPC; SNRPA
GO:0050870	0.0118	1	14791	601	76	8	BP	positive regulation of T cell activation	BLM; RARA; IL1B; IL6; ADK; STAT5B; STAT5A; RIPK2
GO:0006886	0.0118	1	14791	601	359	24	BP	intracellular protein transport	SCG5; XP07; AKAP12; JUN; MLPH; TPR; SNX9; AP2B1; STX6; YWHAZ; KPNA2; SMURF1; RPH3AL; VPS45; TP53; AGXT; AP3S1; CLTB; PEX5; TNF; SDCBP; TOMM20; CLTCL1; NPM1
GO:0006644	0.0118	1	14791	601	192	15	BP	phospholipid metabolic process	PIK3CB; SNCA; HEXB; LIPC; PI4KB; FABP3; CHPT1; CETP; PLCB2; LCAT; DRD2; NKX2-1; ENPP7; SGPP1; PEMT
GO:0051241	0.0121	1	14791	601	175	14	BP	negative regulation of multicellular organismal process	APOH; PPARG; NGFR; AVPR1A; RARA; CAV3; FGF23; IL6; DRD2; HTR1B; TNF; BCOR; ACHE; ADRBK1
GO:0006638	0.0126	1	14791	601	48	6	BP	neutral lipid metabolic process	APOB; APOH; SNCA; LIPC; CAV3; CETP
GO:0022618	0.0127	1	14791	601	77	8	BP	ribonucleoprotein complex assembly	GEMIN5; SNRNP200; PRMT5; EIF6; BAT1; TGS1; NPM1; SNRPE
GO:0030335	0.0128	1	14791	601	125	11	BP	positive regulation of cell migration	F3; EGFR; IGF1R; SCARB1; IGF1; F10; SMAD3; BCL2; ERBB4; HIF1A; IL6
GO:0007507	0.0128	1	14791	601	125	11	BP	heart development	PRKDC; RXRA; PKP2; WT1; EPOR; CITED2; DVL2; TEAD1; BCOR; ADRBK1; GLI2
GO:0048168	0.0128	1	14791	601	35	5	BP	regulation of neuronal synaptic plasticity	SNCA; EGR1; BCAN; DRD2; HRAS
GO:0051952	0.0128	1	14791	601	35	5	BP	regulation of amine transport	SNCA; DRD2; HTR1B; TNF; ADRBK1
GO:0070167	0.0128	1	14791	601	35	5	BP	regulation of biomaterial formation	CYP27B1; SMAD3; FGF23; TFAP2A; BCOR
GO:0008543	0.0128	1	14791	601	35	5	BP	fibroblast growth factor receptor signaling pathway	FGF22; FGF23; FGF5; FGF4; SOS1
GO:0018210	0.0129	1	14791	601	23	4	BP	peptidyl-threonine modification	BCL2; PDPK1; PKN1; ADRBK1

GO:0042531	0.0129	1	14791	601	23	4	BP	positive regulation of tyrosine phosphorylation of STAT protein	LIF; IGF1; GHR; IL6
GO:0050885	0.0129	1	14791	601	23	4	BP	neuromuscular process controlling balance	HEXB; ADCY5; NBN; GRIN2C
GO:0006942	0.0129	1	14791	601	23	4	BP	regulation of striated muscle contraction	SMAD7; NOS1; CAV3; ADRBK1
GO:0018193	0.0129	1	14791	601	159	13	BP	peptidyl-amino acid modification	P4HA2; PRKDC; ABI3; BCL2; GHR; ERBB4; PRMT5; STAT1; PDPK1; PKN1; GSK3B; STAT5A; ADRBK1
GO:0010565	0.0136	1	14791	601	78	8	BP	regulation of cellular ketone metabolic process	PPARG; PPARA; SNCA; AVPR1A; BRCA1; ACACB; COMT; ACSL1
GO:0009743	0.0136	1	14791	601	78	8	BP	response to carbohydrate stimulus	APOB; PPARD; COL4A3; KHK; EGR1; LCT; GYS2; MAP1B
GO:0030307	0.0139	1	14791	601	49	6	BP	positive regulation of cell growth	AVPR1A; TAF9B; PRSS2; BCL2; NTRK3; MAP1B
GO:0045089	0.0139	1	14791	601	49	6	BP	positive regulation of innate immune response	RELA; CADM1; IFNB1; STAT5B; STAT5A; RIPK2
GO:0051302	0.0139	1	14791	601	49	6	BP	regulation of cell division	BLM; IGF1R; IL1B; TGFA; FGF5; FGF4
GO:0010884	0.014	1	14791	601	13	3	BP	positive regulation of lipid storage	APOB; SCARB1; NFKB1
GO:0031102	0.014	1	14791	601	13	3	BP	neuron projection regeneration	RXRA; BCL2; MAP1B
GO:0031670	0.014	1	14791	601	13	3	BP	cellular response to nutrient	CDKN2B; USF1; USF2
GO:0032330	0.014	1	14791	601	13	3	BP	regulation of chondrocyte differentiation	RELA; GDF5; GLI2
GO:0043029	0.014	1	14791	601	13	3	BP	T cell homeostasis	BCL2; STAT5B; STAT5A
GO:0045086	0.014	1	14791	601	13	3	BP	positive regulation of interleukin-2 biosynthetic process	IL1B; STAT5B; STAT5A
GO:0045687	0.014	1	14791	601	13	3	BP	positive regulation of glial cell differentiation	PPARG; RELA; NTF3
GO:0060716	0.014	1	14791	601	13	3	BP	labyrinthine layer blood vessel development	CYR61; PLCD3; WNT2
GO:0045087	0.0144	1	14791	601	144	12	BP	innate immune response	PPARG; SIGIRR; SFTPD; MASP1; TIRAP; IL1RAP; CLU; CEBPG; MASP2; FCN2; TOLLIP; C1S
GO:0001933	0.0144	1	14791	601	36	5	BP	negative regulation of protein amino acid phosphorylation	SMAD7; BDKRB2; JUN; PRKCD; PPP2CA
GO:0046425	0.0144	1	14791	601	36	5	BP	regulation of JAK-STAT cascade	LIF; IGF1; GHR; IL6; PPP2CA

GO:0048015	0.0147	1	14791	601	79	8	BP	phosphoinositid e-mediated signaling positive regulation of cell projection organization	PIK3CB; IGF1R; HOMER1; IGF1; PI4KB; F2RL3; DRD2; CHRM2
GO:0031346	0.0147	1	14791	601	64	7	BP	positive regulation of lymphocyte proliferation	SMAD1; NGFR; RALA; NTRK3; MAP1B; NDEL1; ATF1
GO:0050671	0.0147	1	14791	601	64	7	BP	nucleic acid transport	BLM; IL1B; IL6; ADK; STAT5B; STAT5A; RIPK2
GO:0050657	0.0148	1	14791	601	111	10	BP	RNA transport	XP07; SMG5; SENP2; TSC1; TPR; HNRNPA1; RBMSA; BAT1; NPM1; UPF3A
GO:0050658	0.0148	1	14791	601	111	10	BP	establishment of RNA localization	XP07; SMG5; SENP2; TSC1; TPR; HNRNPA1; RBMSA; BAT1; NPM1; UPF3A
GO:0051236	0.0148	1	14791	601	111	10	BP	long-chain fatty acid transport	PPARG; BDKRB2; FABP3; DRD2
GO:0015909	0.015	1	14791	601	24	4	BP	somatic cell DNA recombination	PRKDC; MSH2; MSH3; NBN
GO:0001776	0.015	1	14791	601	24	4	BP	leukocyte homeostasis	FANCC; BCL2; STAT5B; STAT5A
GO:0002449	0.015	1	14791	601	24	4	BP	lymphocyte mediated immunity	CADM1; MSH2; CEBPG; PRKCD
GO:0002562	0.015	1	14791	601	24	4	BP	somatic diversification of immune receptors via germline recombination within a single locus	PRKDC; MSH2; MSH3; NBN
GO:0045168	0.015	1	14791	601	24	4	BP	cell-cell signaling involved in cell fate commitment	WNT2; NKX2-1; POU2F1; HOXC11
GO:0048286	0.015	1	14791	601	24	4	BP	lung alveolus development	SFTPD; LIF; IGF1; HOXA5
GO:0051640	0.015	1	14791	601	24	4	BP	organelle localization	MLPH; TACC3; NDEL1; MYO7A
GO:0008542	0.015	1	14791	601	24	4	BP	visual learning	DBH; RIC8A; DRD2; HRAS
GO:0019614	0.0151	1	14791	601	5	2	BP	catechol catabolic process	DBH; COMT
GO:0021535	0.0151	1	14791	601	5	2	BP	cell migration in hindbrain	DAB1; CTNNA2
GO:0002347	0.0151	1	14791	601	5	2	BP	response to tumor cell	TP73; TP53
GO:0030224	0.0151	1	14791	601	5	2	BP	monocyte differentiation	SP3; PPARG
GO:0031053	0.0151	1	14791	601	5	2	BP	primary microRNA processing	SMAD1; SMAD3
GO:0031649	0.0151	1	14791	601	5	2	BP	heat generation	IL1B; EPHA3
GO:0031954	0.0151	1	14791	601	5	2	BP	positive regulation of protein amino acid autophosphoryla tion	RAD50; NBN
GO:0032835	0.0151	1	14791	601	5	2	BP	glomerulus development	WT1; BCL2

GO:0032847	0.0151	1	14791	601	5	2	BP	regulation of cellular pH reduction	AVPR1A; BCL2
GO:0034313	0.0151	1	14791	601	5	2	BP	diol catabolic process	DBH; COMT
GO:0034339	0.0151	1	14791	601	5	2	BP	regulation of transcription from RNA polymerase II promoter by nuclear hormone receptor	PKN1; DGKQ
GO:0000380	0.0151	1	14791	601	5	2	BP	alternative nuclear mRNA splicing, via spliceosome	HNRNPA1; SFPQ
GO:0042158	0.0151	1	14791	601	5	2	BP	lipoprotein biosynthetic process	APOB; LCAT
GO:0042424	0.0151	1	14791	601	5	2	BP	catecholamine catabolic process	DBH; COMT
GO:0046827	0.0151	1	14791	601	5	2	BP	positive regulation of protein export from nucleus	IL1B; GSK3B
GO:0048149	0.0151	1	14791	601	5	2	BP	behavioral response to ethanol	DBH; DRD2
GO:0051096	0.0151	1	14791	601	5	2	BP	positive regulation of helicase activity	MSH2; MSH3
GO:0051797	0.0151	1	14791	601	5	2	BP	regulation of hair follicle development	NGFR; TNF
GO:0051894	0.0151	1	14791	601	5	2	BP	positive regulation of focal adhesion assembly	TSC1; SMAD3
GO:0051974	0.0151	1	14791	601	5	2	BP	negative regulation of telomerase activity	PPARG; TERF1
GO:0060216	0.0151	1	14791	601	5	2	BP	definitive hemopoiesis	SP1; SP3
GO:0060601	0.0151	1	14791	601	5	2	BP	lateral sprouting from an epithelium	AR; GLI2
GO:0060710	0.0151	1	14791	601	5	2	BP	chorio-allantoic fusion	LEF1; CYR61
GO:0006356	0.0151	1	14791	601	5	2	BP	regulation of transcription from RNA polymerase I promoter	UBTF; POLR2K
GO:0006702	0.0151	1	14791	601	5	2	BP	androgen biosynthetic process	SCARB1; SRD5A2
GO:0070170	0.0151	1	14791	601	5	2	BP	regulation of tooth mineralization	TFAP2A; BCOR

GO:0007195	0.0151	1	14791	601	5	2	BP	inhibition of adenylate cyclase activity by dopamine receptor signaling pathway	ADCY5; DRD2
GO:0007341	0.0151	1	14791	601	5	2	BP	penetration of zona pellucida blood	HEXB; ACR
GO:0007598	0.0151	1	14791	601	5	2	BP	coagulation, extrinsic pathway	F3; F10
GO:0042326	0.0152	1	14791	601	50	6	BP	negative regulation of phosphorylation	SMAD7; BDKRB2; JUN; CDKN2B; PRKCD; PPP2CA
GO:0009894	0.0154	1	14791	601	272	19	BP	regulation of catabolic process	PPARA; GDI1; RALBP1; SMAD7; TSC1; RELA; IGF1; CSNK1E; PGAM1; ADAP1; GNAO1; HIF1A; IL1B; ASAP1; ASAP2; TNF; GRIN2C; NDEL1; NEDD4L
GO:0007204	0.0157	1	14791	601	112	10	BP	elevation of cytosolic calcium ion concentration	JPH2; BDKRB2; AVPR1A; EPOR; LPAR1; CAV3; TRPV4; CCR4; IL1B; DRD2
GO:0051222	0.0157	1	14791	601	80	8	BP	positive regulation of protein transport	SMAD4; CADM1; SMAD3; IL1B; IL6; GSK3B; TNF; ACHE
GO:0051438	0.0157	1	14791	601	80	8	BP	regulation of ubiquitin-protein ligase activity	ANAPC5; ANAPC7; SMAD7; SKP1; PSME1; CDC16; CDC23; PSMB4
GO:0010639	0.016	1	14791	601	96	9	BP	negative regulation of organelle organization	SNCA; TPR; CAV3; BRCA1; TERF1; TAF7; MAP1B; BCOR; NPM1
GO:0032946	0.016	1	14791	601	65	7	BP	positive regulation of mononuclear cell proliferation	BLM; IL1B; IL6; ADK; STAT5B; STAT5A; RIPK2
GO:0042176	0.016	1	14791	601	65	7	BP	regulation of protein catabolic process	SMAD7; RELA; CSNK1E; IL1B; TNF; GRIN2C; NEDD4L
GO:0051437	0.016	1	14791	601	65	7	BP	positive regulation of ubiquitin-protein ligase activity	ANAPC5; ANAPC7; SKP1; PSME1; CDC16; CDC23; PSMB4
GO:0050905	0.0162	1	14791	601	37	5	BP	activity involved in mitotic cell cycle	HEXB; ADCY5; PEX5; NBN; GRIN2C
GO:0090100	0.0162	1	14791	601	37	5	BP	neuromuscular process	HIPK2; SMAD4; CDKN2B; CITED2; ING2
GO:0051046	0.0162	1	14791	601	236	17	BP	positive regulation of transmembrane receptor protein signaling pathway	SCG5; SNCA; LIF; AVPR1A; RALA; CADM1; CREB1; RPH3AL; FGF23; IL1B; IL6; DRD2; SYT9; HTR1B; TNF; ACHE; ADRBK1
GO:0032880	0.0164	1	14791	601	164	13	BP	regulation of protein localization	SMAD4; CADM1; SMAD3; BCL2; IL1B; IL6; PDPK1; DRD2; PICALM; GSK3B; TNF; ACHE; TACC3

GO:0033500	0.0167	1	14791	601	51	6	BP	carbohydrate homeostasis	PPARG; DBH; USF1; CAV3; RPH3AL; STAT3
GO:0042593	0.0167	1	14791	601	51	6	BP	glucose homeostasis	PPARG; DBH; USF1; CAV3; RPH3AL; STAT3
GO:0046483	0.0172	1	14791	601	352	23	BP	heterocycle metabolic process	P4HA2; ADSSL1; NFE2L1; ADCY1; DBH; PPOX; PDE11A; MTHFS; PPAT; GHR; ADCY5; NT5E; XDH; CYP1A2; GUCY1A3; RBKS; ATP5B; ADK; STAT5B; STAT5A; DERA; PAPSS1; ALDH6A1
GO:0051352	0.0173	1	14791	601	66	7	BP	negative regulation of ligase activity	ANAPC5; ANAPC7; SMAD7; PSME1; CDC16; CDC23; PSMB4
GO:0051444	0.0173	1	14791	601	66	7	BP	negative regulation of ubiquitin-protein ligase activity	ANAPC5; ANAPC7; SMAD7; PSME1; CDC16; CDC23; PSMB4
GO:0070665	0.0173	1	14791	601	66	7	BP	positive regulation of leukocyte proliferation	BLM; IL1B; IL6; ADK; STAT5B; STAT5A; RIPK2
GO:0009896	0.0173	1	14791	601	66	7	BP	positive regulation of catabolic process	PPARA; SMAD7; IGF1; CSNK1E; HIF1A; IL1B; TNF
GO:0035137	0.0173	1	14791	601	25	4	BP	hindlimb morphogenesis	RARB; RARG; GDF5; FGF4
GO:0045429	0.0173	1	14791	601	25	4	BP	positive regulation of nitric oxide biosynthetic process	EGFR; IL1B; HBB; TNF
GO:0050873	0.0173	1	14791	601	25	4	BP	brown fat cell differentiation	PPARG; CEBPA; CEBPB; ALDH6A1
GO:0007548	0.0173	1	14791	601	25	4	BP	sex differentiation	AR; AMHR2; SRD5A2; STAT5B
GO:0006260	0.0173	1	14791	601	183	14	BP	DNA replication	BLM; ORC6L; IGF1; DSCC1; RAD50; POLE2; NAP1L1; MCM7; KCTD13; TERF1; POLD2; ACHB; SIN3A; NFIC
GO:0010039	0.0173	1	14791	601	14	3	BP	response to iron ion	ABAT; SNCA; BCL2
GO:0010976	0.0173	1	14791	601	14	3	BP	positive regulation of neuron projection development	NTRK3; NDEL1; ATF1
GO:0014015	0.0173	1	14791	601	14	3	BP	positive regulation of gliogenesis	PPARG; RELA; NTF3
GO:0001662	0.0173	1	14791	601	14	3	BP	behavioral fear response	BCL2; ESR2; VDAC1
GO:0030194	0.0173	1	14791	601	14	3	BP	positive regulation of blood coagulation maternal process	F3; APOH; USF1
GO:0060135	0.0173	1	14791	601	14	3	BP	involved in female pregnancy	LIF; PPAT; ESR1
GO:0006949	0.0173	1	14791	601	14	3	BP	syncytium formation	NOS1; CAPN2; ADAM12
GO:0070328	0.0173	1	14791	601	14	3	BP	triglyceride homeostasis	LIPC; SCARB1; CETP
GO:0008209	0.0173	1	14791	601	14	3	BP	androgen metabolic process	SCARB1; ESR1; SRD5A2
GO:0034762	0.018	1	14791	601	38	5	BP	regulation of transmembrane transport	JPH2; CATSPER1; HOMER1; CAV3; DRD2

GO:0070507	0.018	1	14791	601	38	5	BP	regulation of microtubule cytoskeleton organization	CAV3; BRCA1; TERF1; MAP1B; NPM1
GO:0009266	0.018	1	14791	601	98	9	BP	response to temperature stimulus	F3; PPARG; NGFR; NOS1; SST; BCL2; FOS; IL1B; HSPB3
GO:0018904	0.0183	1	14791	601	52	6	BP	organic ether metabolic process	APOB; APOH; LIPC; CAV3; CETP; CYP1A2
GO:0009124	0.0183	1	14791	601	52	6	BP	nucleoside monophosphate biosynthetic process	ADSSL1; ADCY1; PPAT; ADCY5; GUCY1A3; ADK
GO:0051604	0.0186	1	14791	601	115	10	BP	protein maturation	PCSK2; SCG5; F3; APOH; MASP1; CLU; MASP2; FCN2; CIS; CAPN2
GO:0010212	0.0186	1	14791	601	67	7	BP	response to ionizing radiation	BLM; PRKDC; MSH2; BCL2; BRCA1; IL1B; TP53
GO:0030097	0.0186	1	14791	601	67	7	BP	hemopoiesis	SP1; SP3; ASH2L; JAG1; BCL2; TAL1; TACC3
GO:0046907	0.0188	1	14791	601	659	38	BP	intracellular transport	SCG5; RAB6B; XP07; SMG5; AKAP12; TSC1; ERC1; JUN; MLPH; TPR; SNX9; AP2B1; ENAH; HNRNPA1; STX6; YWHAZ; KPNA2; SMURF1; RPH3AL; VPS45; TP53; AGXT; AP3S1; WASF2; SQSTM1; PICALM; CLTB; PEX5; TNF; BAT1; SDCBP; ATP5B; TGS1; TOMM20; NDEL1; CLTCL1; NPM1; MYO7A
GO:0046883	0.0193	1	14791	601	83	8	BP	regulation of hormone secretion	SCG5; LIF; CREB1; FGF23; IL1B; DRD2; SYT9; TNF
GO:0051340	0.0193	1	14791	601	83	8	BP	regulation of ligase activity	ANAPC5; ANAPC7; SMAD7; SKP1; PSME1; CDC16; CDC23; PSMB4
GO:0019637	0.0195	1	14791	601	204	15	BP	organophosphate metabolic process	PIK3CB; SNCA; HEXB; LIPC; PI4KB; FABP3; CHPT1; CETP; PLCB2; LCAT; DRD2; NKX2-1; ENPP7; SGPP1; PEMT
GO:0032446	0.0196	1	14791	601	168	13	BP	protein modification by small protein conjugation	TSG101; UBE2D2; ANAPC5; ANAPC7; SUZ12; BCL2; WWP1; BRCA1; DZIP3; SMURF1; CDC16; CDC23; NEDD4L
GO:0010332	0.0198	1	14791	601	26	4	BP	response to gamma radiation	PRKDC; BCL2; IL1B; TP53
GO:0002200	0.0198	1	14791	601	26	4	BP	somatic diversification of immune receptors	PRKDC; MSH2; MSH3; NBN
GO:0030168	0.0198	1	14791	601	26	4	BP	platelet activation	PIK3CB; FGB; IL6; VWF
GO:0000387	0.0198	1	14791	601	26	4	BP	spliceosomal snRNP assembly	GEMIN5; PRMT5; TGS1; SNRPE
GO:0009161	0.0198	1	14791	601	26	4	BP	ribonucleoside monophosphate metabolic process	ADSSL1; PPAT; NT5E; ADK
GO:0015718	0.0199	1	14791	601	53	6	BP	monocarboxylic acid transport	PPARG; PPARC; PPARA; BDKRB2; FABP3; DRD2
GO:0010948	0.02	1	14791	601	39	5	BP	negative regulation of cell cycle process	LIF; TPR; SMARCA4; BRCA1; TERF1
GO:0019218	0.02	1	14791	601	39	5	BP	regulation of steroid metabolic process	APOB; NFKB1; TNF; STAT5B; STAT5A
GO:0006413	0.02	1	14791	601	39	5	BP	translational initiation	EIF3H; EIF3L; EIF3G; RPS3A; EIF5
GO:0090316	0.02	1	14791	601	39	5	BP	positive regulation of intracellular protein transport	SMAD4; SMAD3; IL1B; GSK3B; TNF

G0:0051439	0.0201	1	14791	601	68	7	BP	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	ANAPC5; ANAPC7; SKP1; PSME1; CDC16; CDC23; PSMB4
G0:0010165	0.021	1	14791	601	15	3	BP	response to X-ray	BLM; MSH2; TP53
G0:0010574	0.021	1	14791	601	15	3	BP	regulation of vascular endothelial growth factor production	HIF1A; IL1B; IL6
G0:0014048	0.021	1	14791	601	15	3	BP	regulation of glutamate secretion	SNCA; AVPR1A; IL1B
G0:0002209	0.021	1	14791	601	15	3	BP	behavioral defense response	BCL2; ESR2; VDAC1
G0:0002717	0.021	1	14791	601	15	3	BP	positive regulation of natural killer cell mediated immunity	CADM1; STAT5B; STAT5A
G0:0031572	0.021	1	14791	601	15	3	BP	G2/M transition DNA damage checkpoint	BLM; BRCA1; NBN
G0:0031623	0.021	1	14791	601	15	3	BP	receptor internalization	SNCA; GHR; PICALM
G0:0043526	0.021	1	14791	601	15	3	BP	neuroprotection	GHR; ESR2; ESR1
G0:0045954	0.021	1	14791	601	15	3	BP	positive regulation of natural killer cell mediated cytotoxicity	CADM1; STAT5B; STAT5A
G0:0060562	0.021	1	14791	601	15	3	BP	epithelial tube morphogenesis	HOXA5; NKX2-1; GLI2
G0:0061035	0.021	1	14791	601	15	3	BP	regulation of cartilage development	RELA; GDF5; GLI2
G0:0006631	0.0211	1	14791	601	206	15	BP	fatty acid metabolic process	PPARD; PPARA; ACAA2; SNCA; LIPC; PTGES3; FABP3; GHR; ACACB; HADHA; ACSL1; PEX5; FADS2; STAT5B; STAT5A
G0:0010563	0.0217	1	14791	601	54	6	BP	negative regulation of phosphorus metabolic process	SMAD7; BDKRB2; JUN; CDKN2B; PRKCD; PPP2CA
G0:0034599	0.0217	1	14791	601	54	6	BP	cellular response to oxidative stress	F3; SNCA; LP0; FANCC; HIF1A; FOS
G0:0045936	0.0217	1	14791	601	54	6	BP	negative regulation of phosphate metabolic process	SMAD7; BDKRB2; JUN; CDKN2B; PRKCD; PPP2CA
G0:0022404	0.0221	1	14791	601	40	5	BP	molting cycle process	PPARD; EGFR; NGFR; RELA; BCL2
G0:0022405	0.0221	1	14791	601	40	5	BP	hair cycle process	PPARD; EGFR; NGFR; RELA; BCL2
G0:0032526	0.0221	1	14791	601	40	5	BP	response to retinoic acid	RXRA; RARA; RARG; DUSP1; IGF2R
G0:0048145	0.0221	1	14791	601	40	5	BP	regulation of fibroblast proliferation	NGFR; IGF1; ESR1; TP53; NBN

GO:0051781	0.0221	1	14791	601	40	5	BP	positive regulation of cell division	IGF1R; IL1B; TGFA; FGF5; FGF4
GO:0006956	0.0221	1	14791	601	40	5	BP	complement activation	MASP1; CLU; MASP2; FCN2; C1S
GO:0010656	0.0221	1	14791	601	6	2	BP	negative regulation of muscle cell apoptosis	APOH; IGF1
GO:0010824	0.0221	1	14791	601	6	2	BP	regulation of centrosome duplication	BRCA1; NPM1
GO:0010886	0.0221	1	14791	601	6	2	BP	positive regulation of cholesterol storage	APOB; SCARB1
GO:0010887	0.0221	1	14791	601	6	2	BP	negative regulation of cholesterol storage	PPARG; PPARA
GO:0016098	0.0221	1	14791	601	6	2	BP	monoterpenoid metabolic process	CYP2C9; CYP1A2
GO:0021895	0.0221	1	14791	601	6	2	BP	cerebral cortex neuron differentiation	NKX2-1; PEX5
GO:0002437	0.0221	1	14791	601	6	2	BP	inflammatory response to antigenic stimulus	IL1B; TNF
GO:0002544	0.0221	1	14791	601	6	2	BP	chronic inflammatory response	IL1B; TNF
GO:0031017	0.0221	1	14791	601	6	2	BP	exocrine pancreas development	IGF1R; IGF1
GO:0034391	0.0221	1	14791	601	6	2	BP	regulation of smooth muscle cell apoptosis	APOH; IGF1
GO:0042634	0.0221	1	14791	601	6	2	BP	regulation of hair cycle	NGFR; TNF
GO:0045579	0.0221	1	14791	601	6	2	BP	positive regulation of B cell differentiation	STAT5B; STAT5A
GO:0046033	0.0221	1	14791	601	6	2	BP	AMP metabolic process	ADSSL1; NT5E
GO:0046325	0.0221	1	14791	601	6	2	BP	negative regulation of glucose import	PEA15; TNF
GO:0048537	0.0221	1	14791	601	6	2	BP	mucosal-associated lymphoid tissue development	STAT5B; STAT5A
GO:0048541	0.0221	1	14791	601	6	2	BP	Peyer's patch development	STAT5B; STAT5A
GO:0051580	0.0221	1	14791	601	6	2	BP	regulation of neurotransmitter uptake	SNCA; DRD2
GO:0051584	0.0221	1	14791	601	6	2	BP	regulation of dopamine uptake	SNCA; DRD2
GO:0051590	0.0221	1	14791	601	6	2	BP	positive regulation of neurotransmitter transport	SNCA; DRD2
GO:0051875	0.0221	1	14791	601	6	2	BP	pigment granule localization	MLPH; MYO7A

GO:0051940	0.0221	1	14791	601	6	2	BP	regulation of catecholamine uptake involved in synaptic transmission	SNCA; DRD2
GO:0051967	0.0221	1	14791	601	6	2	BP	negative regulation of synaptic transmission, glutamatergic	DRD2; HTR1B
GO:0060416	0.0221	1	14791	601	6	2	BP	response to growth hormone stimulus	GHR; SOCS2
GO:0060426	0.0221	1	14791	601	6	2	BP	lung vasculature development	LIF; IGF1
GO:0060687	0.0221	1	14791	601	6	2	BP	regulation of branching involved in prostate gland morphogenesis	RXRA; ESR1
GO:0060765	0.0221	1	14791	601	6	2	BP	regulation of androgen receptor signaling pathway	IGF1; ESR2
GO:0071636	0.0221	1	14791	601	6	2	BP	positive regulation of transforming growth factor-beta production	SMAD3; CREB1
GO:0031347	0.0222	1	14791	601	153	12	BP	regulation of defense response	PPARG; RELA; MASP1; AP2B1; CADM1; NT5E; IFNB1; IL6; STAT5B; STAT5A; PSMB4; RIPK2
GO:0030330	0.0225	1	14791	601	27	4	BP	DNA damage response, signal transduction by p53 class mediator	HIPK2; BRCA1; TP53; NBN
GO:0046427	0.0225	1	14791	601	27	4	BP	positive regulation of JAK-STAT cascade	LIF; IGF1; GHR; IL6
GO:0050806	0.0225	1	14791	601	27	4	BP	positive regulation of synaptic transmission	EGFR; SNCA; ERBB4; TNF
GO:0007632	0.0225	1	14791	601	27	4	BP	visual behavior	DBH; RIC8A; DRD2; HRAS
GO:0051050	0.0225	1	14791	601	264	18	BP	positive regulation of transport	SMAD4; SNCA; SFTPD; AVPR1A; HOMER1; CADM1; SMAD3; ERBB4; CREB1; IL1B; IL6; DRD2; GSK3B; TNF; ACHE; ADRBK1; CLTCL1; NEDD4L
GO:0022403	0.0226	1	14791	601	322	21	BP	cell cycle phase	AKAP8; BLM; ANAPC5; ANAPC7; CSNK1A1; RBM7; HGF; TRIP13; ILF3; KPNA2; CDC16; RAD50; PPP2CA; TERF1; CDC23; NBN; MKI67; SIN3A; RAD21; CLTCL1; RSN1
GO:0006913	0.023	1	14791	601	119	10	BP	nucleocytoplasmic transport	XP07; SMG5; TSC1; TPR; HNRNPA1; KPNA2; SMURF1; BAT1; TGS1; NPM1
GO:0030258	0.0232	1	14791	601	70	7	BP	lipid modification	PPAP2A; PIK3CB; PPAR; PI4KB; LCAT; HADHA; PEX5
GO:0034330	0.0232	1	14791	601	70	7	BP	cell junction organization	DSP; SMAD7; COL17A1; SMAD3; BCL2; PDPK1; CLDN19
GO:0051443	0.0232	1	14791	601	70	7	BP	positive regulation of ubiquitin-protein ligase activity	ANAPC5; ANAPC7; SKP1; PSME1; CDC16; CDC23; PSMB4
GO:0009063	0.0232	1	14791	601	70	7	BP	cellular amino acid catabolic process	NOS1; DBH; SARDH; ACAD8; GOT1; ASL; ALDH6A1

GO:0009791	0.0235	1	14791	601	55	6	BP	post-embryonic development	APOB; TP73; BCL2; STK36; CYP11A2; IGF2R
GO:0051169	0.0242	1	14791	601	120	10	BP	nuclear transport	XP07; SMG5; TSC1; TPR; HNRNPA1; KPNA2; SMURF1; BAT1; TGS1; NPM1
GO:0008104	0.0242	1	14791	601	120	10	BP	protein localization	AKAP3; EGFR; CAV3; SMURF1; TP53; SQSTM1; DRD2; GRIN2C; SIN3A; NPM1
GO:0018108	0.0244	1	14791	601	41	5	BP	peptidyl-tyrosine phosphorylation	ABI3; GHR; ERBB4; STAT1; STAT5A
GO:0033044	0.0244	1	14791	601	41	5	BP	regulation of chromosome organization	SNCA; TP53; TERF1; TAF7; BCOR
GO:0006641	0.0244	1	14791	601	41	5	BP	triglyceride metabolic process	APOB; APOH; LIPC; CAV3; CETP
GO:0030111	0.0248	1	14791	601	71	7	BP	regulation of Wnt receptor signaling pathway	SENP2; TLE1; LEF1; SFRP2; WNT2; PPP2CA; AXIN1
GO:0019098	0.0251	1	14791	601	16	3	BP	reproductive behavior	HEXB; AVPR1A; DBH
GO:0002244	0.0251	1	14791	601	16	3	BP	hemopoietic progenitor cell differentiation	PRKDC; MLF1; BCL2
GO:0030728	0.0251	1	14791	601	16	3	BP	ovulation	LEPR; PGR; IL1B
GO:0032872	0.0251	1	14791	601	16	3	BP	regulation of stress-activated MAPK cascade	IL1B; IGBP1; RIPK2
GO:0042402	0.0251	1	14791	601	16	3	BP	cellular biogenic amine catabolic process	DBH; COMT; ACHE
GO:0051925	0.0251	1	14791	601	16	3	BP	regulation of calcium ion transport via voltage-gated calcium channel activity	CATSPER1; CAV3; DRD2
GO:0009584	0.0251	1	14791	601	16	3	BP	detection of visible light	SAG; RHO; CACNA1F
GO:0016571	0.0254	1	14791	601	28	4	BP	histone methylation	ASH2L; NSD1; SUZ12; PRMT5
GO:0002705	0.0254	1	14791	601	28	4	BP	positive regulation of leukocyte mediated immunity	CADM1; IL1B; STAT5B; STAT5A
GO:0002708	0.0254	1	14791	601	28	4	BP	positive regulation of lymphocyte mediated immunity	CADM1; IL1B; STAT5B; STAT5A
GO:0043547	0.0254	1	14791	601	28	4	BP	positive regulation of GTPase activity	RALBP1; TSC1; GNAO1; NDEL1
GO:0043588	0.0254	1	14791	601	28	4	BP	skin development	DSP; LEF1; NGFR; PTGES3
GO:0045582	0.0254	1	14791	601	28	4	BP	positive regulation of T cell differentiation	RARA; STAT5B; STAT5A; RIPK2
GO:0046677	0.0254	1	14791	601	28	4	BP	response to antibiotic	ETS1; CCR4; ALPL; PPP2CB
GO:0051970	0.0254	1	14791	601	28	4	BP	negative regulation of transmission of nerve impulse	AVPR1A; DRD2; HTR1B; ACHE

GO:0007270	0.0254	1	14791	601	28	4	BP	nerve-nerve synaptic transmission	SNCA; DRD2; VDAC1; PLAT
GO:0001505	0.0255	1	14791	601	56	6	BP	regulation of neurotransmitter levels	ABAT; NOS1; DBH; SYN1; COMT; ACHE
GO:0032102	0.0255	1	14791	601	56	6	BP	negative regulation of response to external stimulus	PPARG; PPARA; CTNNA2; NT5E; DRD2; PSMB4
GO:0007586	0.0255	1	14791	601	56	6	BP	digestion	SST; PRSS2; VIPR1; AMY2B; ACSL1; AKR1B10
GO:0016337	0.0262	1	14791	601	288	19	BP	cell-cell adhesion	L1CAM; DLG1; PIK3CB; DSP; LEF1; EGFR; CYR61; PKP2; DAB1; CADM1; CTNNA2; BCL2; ICAM3; FGF4; TNF; CLDN11; CLDN17; CLDN19; NCAM1
GO:0032388	0.0268	1	14791	601	42	5	BP	positive regulation of intracellular transport	SMAD4; SMAD3; IL1B; GSK3B; TNF
GO:0032675	0.0268	1	14791	601	42	5	BP	regulation of interleukin-6 production	IL1B; IL6; CEBPB; TNF; RIPK2
GO:0042303	0.0268	1	14791	601	42	5	BP	molting cycle	PPARD; EGFR; NGFR; RELA; BCL2
GO:0050679	0.0268	1	14791	601	42	5	BP	positive regulation of epithelial cell proliferation	EGFR; IGF1; ERBB4; WNT2; TGFA
GO:0006405	0.0268	1	14791	601	42	5	BP	RNA export from nucleus	SMG5; TSC1; HNRNPA1; BAT1; NPM1
GO:0009187	0.0268	1	14791	601	42	5	BP	cyclic nucleotide metabolic process	PDE8A; ADCY1; PDE11A; ADCY5; GUCY1A3
GO:0051351	0.0284	1	14791	601	73	7	BP	positive regulation of ligase activity	ANAPC5; ANAPC7; SKP1; PSME1; CDC16; CDC23; PSMB4
GO:0001656	0.0286	1	14791	601	29	4	BP	metanephros development	WT1; BCL2; PAX8; HOXC11
GO:0046824	0.0286	1	14791	601	29	4	BP	positive regulation of nucleocytoplasmic transport	SMAD3; IL1B; GSK3B; TNF
GO:0051603	0.0292	1	14791	601	272	18	BP	proteolysis involved in cellular protein catabolic process	TSG101; UBE2D2; ANAPC5; ANAPC7; NGFR; RELA; NFKB1; SKP1; USP7; PSME1; SMURF1; SMURF2; CDC16; SQSTM1; PPP2CB; CDC23; ACR; PSMB4
GO:0010675	0.0293	1	14791	601	43	5	BP	regulation of cellular carbohydrate metabolic process	SNCA; IGF1; PGAM1; HIF1A; DUSP12
GO:0018212	0.0293	1	14791	601	43	5	BP	peptidyl-tyrosine modification	ABI3; GHR; ERBB4; STAT1; STAT5A
GO:0090068	0.0293	1	14791	601	43	5	BP	positive regulation of cell cycle process	IGF1; IL1B; TERF1; TGFA; TNF
GO:0043122	0.0296	1	14791	601	124	10	BP	regulation of I-kappaB kinase/NF-kappaB cascade	REL; RELA; LPAR1; IL1B; SQSTM1; EEF1D; TNFAIP3; TNF; RIPK2; TRAF5
GO:0019048	0.0296	1	14791	601	17	3	BP	virus-host interaction	HIPK2; SMAD3; BAT1
GO:0030539	0.0296	1	14791	601	17	3	BP	male genitalia development	WT1; BMP5; SRD5A2

GO:0032321	0.0296	1	14791	601	17	3	BP	positive regulation of Rho GTPase activity	RALBP1; TSC1; NDEL1
GO:0035116	0.0296	1	14791	601	17	3	BP	embryonic hindlimb morphogenesis	RARB; RARG; FGF4
GO:0043470	0.0296	1	14791	601	17	3	BP	regulation of carbohydrate catabolic process	IGF1; PGAM1; HIF1A
GO:0043471	0.0296	1	14791	601	17	3	BP	regulation of cellular carbohydrate catabolic process	IGF1; PGAM1; HIF1A
GO:0046627	0.0296	1	14791	601	17	3	BP	negative regulation of insulin receptor signaling pathway	RELA; PRKCD; IL1B
GO:0050820	0.0296	1	14791	601	17	3	BP	positive regulation of coagulation	F3; APOH; USF1
GO:0071222	0.0296	1	14791	601	17	3	BP	cellular response to lipopolysaccharide	CAMP; STAT1; RIPK2
GO:0001764	0.0297	1	14791	601	58	6	BP	neuron migration	DAB1; ESR2; CCR4; NKX2-1; PEX5; NDEL1
GO:0045088	0.0297	1	14791	601	58	6	BP	regulation of innate immune response	RELA; CADM1; IFNB1; STAT5B; STAT5A; RIPK2
GO:0046486	0.0301	1	14791	601	160	12	BP	glycerolipid metabolic process	PIK3CB; APOB; APOH; LIPC; PI4KB; FABP3; CHPT1; CAV3; CETP; LCAT; DRD2; PEMT
GO:0010269	0.0302	1	14791	601	7	2	BP	response to selenium ion	APOB; RXRA
GO:0002320	0.0302	1	14791	601	7	2	BP	lymphoid progenitor cell differentiation	PRKDC; BCL2
GO:0030502	0.0302	1	14791	601	7	2	BP	negative regulation of bone mineralization	FGF23; BCOR
GO:0031000	0.0302	1	14791	601	7	2	BP	response to caffeine	PPARG; BCL2
GO:0033137	0.0302	1	14791	601	7	2	BP	negative regulation of peptidyl-serine phosphorylation	SMAD7; BDKRB2
GO:0034109	0.0302	1	14791	601	7	2	BP	homotypic cell-cell adhesion	L1CAM; NCAM1
GO:0042359	0.0302	1	14791	601	7	2	BP	vitamin D metabolic process	CYP27B1; FGF23
GO:0042363	0.0302	1	14791	601	7	2	BP	fat-soluble vitamin catabolic process	CYP27B1; FGF23
GO:0042538	0.0302	1	14791	601	7	2	BP	hyperosmotic salinity response	TRPV4; NKX2-1
GO:0042711	0.0302	1	14791	601	7	2	BP	maternal behavior	AVPR1A; DBH

GO:0043568	0.0302	1	14791	601	7	2	BP	positive regulation of insulin-like growth factor receptor signaling pathway	AR; IGF1
GO:0043903	0.0302	1	14791	601	7	2	BP	regulation of symbiosis, encompassing mutualism through parasitism	CTSG; IFNB1
GO:0045084	0.0302	1	14791	601	7	2	BP	positive regulation of interleukin-12 biosynthetic process	REL; RELA
GO:0045624	0.0302	1	14791	601	7	2	BP	positive regulation of T-helper cell differentiation	RARA; RIPK2
GO:0045792	0.0302	1	14791	601	7	2	BP	negative regulation of cell size	TSC1; CAV3
GO:0045821	0.0302	1	14791	601	7	2	BP	positive regulation of glycolysis	IGF1; HIF1A
GO:0046605	0.0302	1	14791	601	7	2	BP	regulation of centrosome cycle	BRCA1; NPM1
GO:0046641	0.0302	1	14791	601	7	2	BP	positive regulation of alpha-beta T cell proliferation	BLM; RIPK2
GO:0048488	0.0302	1	14791	601	7	2	BP	synaptic vesicle endocytosis	SNCA; ITSN1
GO:0048525	0.0302	1	14791	601	7	2	BP	negative regulation of viral reproduction	IFNB1; TNF
GO:0048679	0.0302	1	14791	601	7	2	BP	regulation of axon regeneration	NTRK3; NDEL1
GO:0051319	0.0302	1	14791	601	7	2	BP	G2 phase	BLM; KPNA2
GO:0051648	0.0302	1	14791	601	7	2	BP	vesicle localization	MLPH; MYO7A
GO:0060746	0.0302	1	14791	601	7	2	BP	parental behavior	AVPR1A; DBH
GO:0070570	0.0302	1	14791	601	7	2	BP	regulation of neuron projection regeneration	NTRK3; NDEL1
GO:0000085	0.0302	1	14791	601	7	2	BP	G2 phase of mitotic cell cycle	BLM; KPNA2
GO:0006996	0.0304	1	14791	601	1292	66	BP	organelle organization	SMARCC2; DLG1; AKAP8; H3F3A; BLM; ANAPC7; CSNK1A1; ASH2L; PRKDC; KIF3A; TP73; GF11B; SNCA; JUN; HGF; HEXB; CENPJ; PTGES3; PRKG1; NSD1; RALA; CLU; STX6; MSH2; MSH3; SMARCA4; CEBPA; ETS1; SUZ12; SMAD3; GOLGB1; BCL2; BRD8; PRMT5; GBA; XRCC5; CDC16; RAD50; TRRAP; ING2; TP53; WASF2; NAP1L1; NEFH; PDPK1; PKN1; PICALM; MICAL1; TERF1; STMN1; HRAS; PEX5; CDC23; SDCBP; NCOR1; MAP1B; NBN; BCOR; TACC3; RAD21; NDEL1; CLTCL1; NPM1; DNML1; MYO7A; FSD1
GO:0031329	0.0306	1	14791	601	235	16	BP	regulation of cellular catabolic process	PPARA; GDI1; RALBP1; SMAD7; TSC1; IGF1; CSNK1E; PGAM1; ADAP1; GNAO1; HIF1A; IL1B; ASAP1; ASAP2; TNF; NDEL1

GO:0016192	0.0308	1	14791	601	557	32	BP	vesicle-mediated transport	AKAP3; RAB6B; HIP1R; ITGAV; ERC1; SNCA; EXOC2; SFTPD; VLDLR; AP2B1; IRF8; PI4KB; STX6; CEBPE; RUFY1; GHR; RPH3AL; VPS45; AP3S1; WASF2; SQSTM1; PICALM; ITSN1; ITS2; CLTB; HRAS; ACR; ATP5B; FSHR; CLTCL1; MYO7A; IGF2R
GO:0061061	0.0314	1	14791	601	143	11	BP	muscle structure development	TSC1; RXRA; JAG1; AVPR1A; RARB; IGF1; ZFH3; NTF3; CAV3; HRAS; ACHE
GO:0008624	0.0316	1	14791	601	108	9	BP	induction of apoptosis by extracellular signals	ARHGEF12; NGFR; SST; ITGB3BP; DAXX; SQSTM1; ITSN1; TNF; SOS1
GO:0030512	0.0319	1	14791	601	30	4	BP	negative regulation of transforming growth factor beta receptor signaling pathway	SMAD7; SMURF1; TP53; NKX2-1
GO:0050772	0.0319	1	14791	601	30	4	BP	positive regulation of axonogenesis	NGFR; NTRK3; MAP1B; NDEL1
GO:0051971	0.0319	1	14791	601	30	4	BP	positive regulation of transmission of nerve impulse	EGFR; SNCA; ERBB4; TNF
GO:0008630	0.0319	1	14791	601	30	4	BP	DNA damage response, signal transduction resulting in induction of apoptosis	HIPK2; TP73; BRCA1; TP53
GO:0042476	0.032	1	14791	601	59	6	BP	odontogenesis	LEF1; ERBB4; FGF4; SDC1; BCOR; GLI2
GO:2000021	0.032	1	14791	601	44	5	BP	regulation of ion homeostasis	SMAD7; NOS1; SNCA; AVPR1A; BCL2
GO:0006109	0.032	1	14791	601	44	5	BP	regulation of carbohydrate metabolic process	SNCA; IGF1; PGAM1; HIF1A; DUSP12
GO:0016042	0.0322	1	14791	601	180	13	BP	lipid catabolic process	APOB; CYP27B1; PPARD; HEXB; LIPC; SCARB1; PLCD3; PLCB2; FGF23; CYP1A2; HADHA; PEX5; SRD5A2
GO:0015931	0.0341	1	14791	601	127	10	BP	nucleobase, nucleoside, nucleotide and nucleic acid transport	XP07; SMG5; SENP2; TSC1; TPR; HNRNPA1; RBM8A; BAT1; NPM1; UPF3A
GO:0070201	0.0343	1	14791	601	145	11	BP	regulation of establishment of protein localization	SMAD4; CADM1; SMAD3; IL1B; IL6; PDPK1; DRD2; GSK3B; TNF; ACHE; TACC3
GO:0001568	0.0343	1	14791	601	60	6	BP	blood vessel development	ITGAV; CYR61; CITED2; PLCD3; WNT2; EPHA2
GO:0030534	0.0344	1	14791	601	76	7	BP	adult behavior	HIPK2; HOXB8; ABAT; SNCA; DBH; AGRP; DRD2
GO:0001837	0.0345	1	14791	601	18	3	BP	epithelial to mesenchymal transition	LEF1; HGF; HIF1A
GO:0001912	0.0345	1	14791	601	18	3	BP	positive regulation of leukocyte mediated cytotoxicity	CADM1; STAT5B; STAT5A
GO:0021983	0.0345	1	14791	601	18	3	BP	pituitary gland development	CREB1; NKX2-1; GLI2
GO:0002715	0.0345	1	14791	601	18	3	BP	regulation of natural killer cell mediated immunity	CADM1; STAT5B; STAT5A

GO:0033143	0.0345	1	14791	601	18	3	BP	regulation of steroid hormone receptor signaling pathway	AR; IGF1; ESR2
GO:0035176	0.0345	1	14791	601	18	3	BP	social behavior	AVPR1A; IL1B; HRAS
GO:0042269	0.0345	1	14791	601	18	3	BP	regulation of natural killer cell mediated cytotoxicity	CADM1; STAT5B; STAT5A
GO:0046717	0.0345	1	14791	601	18	3	BP	acid secretion	BDKRB2; AGXT; DRD2
GO:0051412	0.0345	1	14791	601	18	3	BP	response to corticosterone stimulus	AVPR1A; BCL2; FOS
GO:0060674	0.0345	1	14791	601	18	3	BP	placenta blood vessel development	CYR61; PLCD3; WNT2
GO:0007212	0.0345	1	14791	601	18	3	BP	dopamine receptor signaling pathway	ADCY5; GNAO1; DRD2
GO:0007530	0.0345	1	14791	601	18	3	BP	sex determination	AR; IGF1R; WT1
GO:0009303	0.0345	1	14791	601	18	3	BP	rRNA transcription	POLR1A; POLR1E; TP53
GO:0000077	0.0349	1	14791	601	45	5	BP	DNA damage checkpoint	BLM; MSH2; BRCA1; TP53; NBN
GO:0050670	0.0352	1	14791	601	93	8	BP	regulation of lymphocyte proliferation	BLM; SFTPD; IL1B; IL6; ADK; STAT5B; STAT5A; RIPK2
GO:0001906	0.0355	1	14791	601	31	4	BP	cell killing	DEFA1; CADM1; CEBPG; CTSG
GO:0002250	0.0355	1	14791	601	31	4	BP	adaptive immune response	CADM1; MSH2; PRKCD; NFKB2
GO:0002460	0.0355	1	14791	601	31	4	BP	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	CADM1; MSH2; PRKCD; NFKB2
GO:0030218	0.0355	1	14791	601	31	4	BP	erythrocyte differentiation	SP1; SP3; CEBPG; TAL1
GO:0031645	0.0355	1	14791	601	31	4	BP	negative regulation of neurological system process	AVPR1A; DRD2; HTR1B; ACHE
GO:0045428	0.0355	1	14791	601	31	4	BP	regulation of nitric oxide biosynthetic process	EGFR; IL1B; HBB; TNF
GO:0045621	0.0355	1	14791	601	31	4	BP	positive regulation of lymphocyte differentiation	RARA; STAT5B; STAT5A; RIPK2
GO:0046324	0.0355	1	14791	601	31	4	BP	regulation of glucose import	PEA15; ERBB4; TNF; CLTCL1
GO:0007338	0.0355	1	14791	601	31	4	BP	single fertilization	AKAP3; ELSBP1; MST1R; ACR
GO:0031349	0.0366	1	14791	601	77	7	BP	positive regulation of defense response	RELA; CADM1; IFNB1; IL6; STAT5B; STAT5A; RIPK2

GO:0050730	0.0366	1	14791	601	77	7	BP	regulation of peptidyl-tyrosine phosphorylation	EGFR; LIF; IGF1; PRKCD; GHR; IL6; PPP2CA
GO:0009411	0.0368	1	14791	601	61	6	BP	response to UV	EGFR; RELA; USF1; MSH2; BCL2; TP53
GO:0032944	0.0372	1	14791	601	94	8	BP	regulation of mononuclear cell proliferation	BLM; SFTPD; IL1B; IL6; ADK; STAT5B; STAT5A; RIPK2
GO:0046903	0.0386	1	14791	601	301	19	BP	secretion	AKAP3; BDKRB2; TP73; EXOC2; USF2; PPAT; YWHAZ; TRPV4; CREB1; XDH; RPH3AL; SYN1; AGXT; IL6; DRD2; ACR; STAT5B; STAT5A; NEDD4L
GO:0002684	0.0391	1	14791	601	262	17	BP	positive regulation of immune system process	BLM; RARA; RELA; MASP1; CADM1; CLU; CTSG; MASP2; FCN2; IL1B; IFNB1; IL6; CIS; ADK; STAT5B; STAT5A; RIPK2
GO:0016540	0.0392	1	14791	601	8	2	BP	protein autoprocesing	PCSK2; CAPN2
GO:0019433	0.0392	1	14791	601	8	2	BP	triglyceride catabolic process	APOB; LIPC
GO:0019953	0.0392	1	14791	601	8	2	BP	sexual reproduction	HEXB; STAT3
GO:0031109	0.0392	1	14791	601	8	2	BP	microtubule polymerization or depolymerization	CENPJ; STMN1
GO:0032332	0.0392	1	14791	601	8	2	BP	positive regulation of chondrocyte differentiation	RELA; GDF5
GO:0032816	0.0392	1	14791	601	8	2	BP	positive regulation of natural killer cell activation	STAT5B; STAT5A
GO:0034285	0.0392	1	14791	601	8	2	BP	response to disaccharide stimulus	KHK; LCT
GO:0035065	0.0392	1	14791	601	8	2	BP	regulation of histone acetylation	SNCA; TAF7
GO:0035121	0.0392	1	14791	601	8	2	BP	tail morphogenesis	SFRP2; EPHA2
GO:0045075	0.0392	1	14791	601	8	2	BP	regulation of interleukin-12 biosynthetic process	REL; RELA
GO:0045080	0.0392	1	14791	601	8	2	BP	positive regulation of chemokine biosynthetic process	IL1B; TNF
GO:0048148	0.0392	1	14791	601	8	2	BP	behavioral response to cocaine	ABAT; DRD2
GO:0048532	0.0392	1	14791	601	8	2	BP	anatomical structure arrangement	DAB1; HOXA1
GO:0048596	0.0392	1	14791	601	8	2	BP	embryonic camera-type eye morphogenesis	SP1; SP3
GO:0048635	0.0392	1	14791	601	8	2	BP	negative regulation of muscle organ development	LEF1; NGFR
GO:0048857	0.0392	1	14791	601	8	2	BP	neural nucleus development	HOXA1; BCL2

GO:0050732	0.0392	1	14791	601	8	2	BP	negative regulation of peptidyl-tyrosine phosphorylation	PRKCD; PPP2CA
GO:0050746	0.0392	1	14791	601	8	2	BP	regulation of lipoprotein metabolic process	ITGAV; PEMT
GO:0051898	0.0392	1	14791	601	8	2	BP	negative regulation of protein kinase B signaling cascade	IGF1R; DRD2
GO:0060052	0.0392	1	14791	601	8	2	BP	neurofilament cytoskeleton organization	NEFH; NDEL1
GO:0060134	0.0392	1	14791	601	8	2	BP	prepulse inhibition	CTNNA2; DRD2
GO:0060231	0.0392	1	14791	601	8	2	BP	mesenchymal to epithelial transition	WT1; PAX2
GO:0060638	0.0392	1	14791	601	8	2	BP	mesenchymal-epithelial cell signaling	HGF; HOXA5
GO:0060644	0.0392	1	14791	601	8	2	BP	mammary gland epithelial cell differentiation	HOXA5; CEBPB
GO:0006301	0.0392	1	14791	601	8	2	BP	postreplication repair	MSH2; BRCA1
GO:0006527	0.0392	1	14791	601	8	2	BP	arginine catabolic process	NOS1; ASL
GO:0070168	0.0392	1	14791	601	8	2	BP	negative regulation of biomineral formation	FGF23; BCOR
GO:0009111	0.0392	1	14791	601	8	2	BP	vitamin catabolic process	CYP27B1; FGF23
GO:0009744	0.0392	1	14791	601	8	2	BP	response to sucrose stimulus	KHK; LCT
GO:0070663	0.0392	1	14791	601	95	8	BP	regulation of leukocyte proliferation	BLM; SFTPD; IL1B; IL6; ADK; STAT5B; STAT5A; RIPK2
GO:0010001	0.0394	1	14791	601	32	4	BP	glial cell differentiation	IGF1; C1S; NKX2-1; FGF5
GO:0001843	0.0394	1	14791	601	32	4	BP	neural tube closure	ZIC2; TSC1; DVL2; FZD6
GO:0031334	0.0394	1	14791	601	32	4	BP	positive regulation of protein complex assembly	CAV3; GSK3B; TERF1; MAP1B
GO:0031646	0.0394	1	14791	601	32	4	BP	positive regulation of neurological system process	EGFR; SNCA; ERBB4; TNF
GO:0060606	0.0394	1	14791	601	32	4	BP	tube closure	ZIC2; TSC1; DVL2; FZD6
GO:0007569	0.0394	1	14791	601	32	4	BP	cell aging	BCL2; TP53; HRAS; NPM1
GO:0051436	0.0394	1	14791	601	62	6	BP	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	ANAPC5; ANAPC7; PSME1; CDC16; CDC23; PSMB4

GO:0022612	0.0398	1	14791	601	19	3	BP	gland morphogenesis	EGFR; BCL2; TNF
GO:0002763	0.0398	1	14791	601	19	3	BP	positive regulation of myeloid leukocyte differentiation	JUN; LIF; STAT5A
GO:0032392	0.0398	1	14791	601	19	3	BP	DNA geometric change	RAD50; MCM7; NBN
GO:0032508	0.0398	1	14791	601	19	3	BP	DNA duplex unwinding	RAD50; MCM7; NBN
GO:0033619	0.0398	1	14791	601	19	3	BP	membrane protein proteolysis	NGFR; RELA; NFKB1
GO:0034612	0.0398	1	14791	601	19	3	BP	response to tumor necrosis factor	CYP27B1; CAMP; IGBP1
GO:0035051	0.0398	1	14791	601	19	3	BP	cardiac cell differentiation	TSC1; RXRA; RARB
GO:0045931	0.0398	1	14791	601	19	3	BP	positive regulation of mitotic cell cycle	TERF1; STAT5B; STAT5A
GO:0051966	0.0398	1	14791	601	19	3	BP	regulation of synaptic transmission, glutamatergic	EGFR; DRD2; HTR1B
GO:0009065	0.0398	1	14791	601	19	3	BP	glutamine family amino acid catabolic process	NOS1; GOT1; ASL
GO:0009126	0.0398	1	14791	601	19	3	BP	purine nucleoside monophosphate metabolic process	ADSSL1; PPAT; NT5E
GO:0009167	0.0398	1	14791	601	19	3	BP	purine ribonucleoside monophosphate metabolic process	ADSSL1; PPAT; NT5E
GO:0010045	0.0406	1	14791	601	1	1	BP	response to nickel ion	LCT
GO:0010501	0.0406	1	14791	601	1	1	BP	RNA secondary structure unwinding	BAT1
GO:0010801	0.0406	1	14791	601	1	1	BP	negative regulation of peptidyl-threonine phosphorylation	SMAD7
GO:0000114	0.0406	1	14791	601	1	1	BP	regulation of transcription involved in G1 phase of mitotic cell cycle	GFI1B
GO:0014038	0.0406	1	14791	601	1	1	BP	regulation of Schwann cell differentiation	RELA
GO:0014040	0.0406	1	14791	601	1	1	BP	positive regulation of Schwann cell differentiation	RELA
GO:0014041	0.0406	1	14791	601	1	1	BP	regulation of neuron maturation	BCL2

GO:0014042	0.0406	1	14791	601	1	1	BP	positive regulation of neuron maturation	BCL2
GO:0014834	0.0406	1	14791	601	1	1	BP	satellite cell maintenance involved in skeletal muscle regeneration	IGF1
GO:0014904	0.0406	1	14791	601	1	1	BP	myotube cell development	IGF1
GO:0001555	0.0406	1	14791	601	1	1	BP	oocyte growth	GDF9
GO:0015846	0.0406	1	14791	601	1	1	BP	polyamine transport	TAF7
GO:0016238	0.0406	1	14791	601	1	1	BP	chaperone-mediated autophagy	SQSTM1
GO:0016269	0.0406	1	14791	601	1	1	BP	O-glycan processing, core 3	B3GNT6
GO:0001754	0.0406	1	14791	601	1	1	BP	eye photoreceptor cell differentiation	STAT3
GO:0019102	0.0406	1	14791	601	1	1	BP	male somatic sex determination	AR
GO:0019265	0.0406	1	14791	601	1	1	BP	glycine biosynthetic process, by transamination of glyoxylate	AGXT
GO:0019484	0.0406	1	14791	601	1	1	BP	beta-alanine catabolic process	ALDH6A1
GO:0002037	0.0406	1	14791	601	1	1	BP	negative regulation of L-glutamate transport	TNF
GO:0002041	0.0406	1	14791	601	1	1	BP	intussusceptive angiogenesis	CYR61
GO:0002077	0.0406	1	14791	601	1	1	BP	acrosome matrix dispersal	ACR
GO:0021506	0.0406	1	14791	601	1	1	BP	anterior neuropore closure	TFAP2A
GO:0021508	0.0406	1	14791	601	1	1	BP	floor plate formation	GLI2
GO:0021517	0.0406	1	14791	601	1	1	BP	ventral spinal cord development	GLI2
GO:0021747	0.0406	1	14791	601	1	1	BP	cochlear nucleus development	BCL2
GO:0021813	0.0406	1	14791	601	1	1	BP	cell-cell adhesion involved in neuronal-glia interactions involved in cerebral cortex radial glia guided migration	DAB1
GO:0002441	0.0406	1	14791	601	1	1	BP	histamine secretion involved in inflammatory response	YWHAZ

GO:0002543	0.0406	1	14791	601	1	1	BP	activation of blood coagulation via clotting cascade	F3
GO:0002553	0.0406	1	14791	601	1	1	BP	histamine secretion by mast cell	YWHAZ
GO:0000296	0.0406	1	14791	601	1	1	BP	spermine transport	TAF7
GO:0003108	0.0406	1	14791	601	1	1	BP	negative regulation of the force of heart contraction by chemical signal	ADRBK1
GO:0031337	0.0406	1	14791	601	1	1	BP	positive regulation of sulfur amino acid metabolic process	COMT
GO:0032223	0.0406	1	14791	601	1	1	BP	negative regulation of synaptic transmission, cholinergic	ACHE
GO:0032460	0.0406	1	14791	601	1	1	BP	negative regulation of protein oligomerization	CLU
GO:0032462	0.0406	1	14791	601	1	1	BP	regulation of protein homooligomerization	CLU
GO:0032463	0.0406	1	14791	601	1	1	BP	negative regulation of protein homooligomerization	CLU
GO:0032613	0.0406	1	14791	601	1	1	BP	interleukin-10 production	PRKCD
GO:0032615	0.0406	1	14791	601	1	1	BP	interleukin-12 production	PRKCD
GO:0032736	0.0406	1	14791	601	1	1	BP	positive regulation of interleukin-13 production	RARA
GO:0032754	0.0406	1	14791	601	1	1	BP	positive regulation of interleukin-5 production	RARA
GO:0032817	0.0406	1	14791	601	1	1	BP	regulation of natural killer cell proliferation	STAT5B
GO:0032819	0.0406	1	14791	601	1	1	BP	positive regulation of natural killer cell proliferation	STAT5B
GO:0032848	0.0406	1	14791	601	1	1	BP	negative regulation of cellular pH reduction	BCL2
GO:0032864	0.0406	1	14791	601	1	1	BP	activation of Cdc42 GTPase activity	NDEL1

GO:0033091	0.0406	1	14791	601	1	1	BP	positive regulation of immature T cell proliferation	RIPK2
GO:0033274	0.0406	1	14791	601	1	1	BP	response to vitamin B2	CEBPA
GO:0033292	0.0406	1	14791	601	1	1	BP	T-tubule organization	CAV3
GO:0033866	0.0406	1	14791	601	1	1	BP	nucleoside bisphosphate biosynthetic process	PAPSS1
GO:0034030	0.0406	1	14791	601	1	1	BP	ribonucleoside bisphosphate biosynthetic process	PAPSS1
GO:0034033	0.0406	1	14791	601	1	1	BP	purine nucleoside bisphosphate biosynthetic process	PAPSS1
GO:0034036	0.0406	1	14791	601	1	1	BP	purine ribonucleoside bisphosphate biosynthetic process	PAPSS1
GO:0034196	0.0406	1	14791	601	1	1	BP	acylglycerol transport	APOH
GO:0034197	0.0406	1	14791	601	1	1	BP	triglyceride transport	APOH
GO:0034230	0.0406	1	14791	601	1	1	BP	enkephalin processing	PCSK2
GO:0034231	0.0406	1	14791	601	1	1	BP	islet amyloid polypeptide processing	PCSK2
GO:0034248	0.0406	1	14791	601	1	1	BP	regulation of cellular amide metabolic process	PGAM1
GO:0034333	0.0406	1	14791	601	1	1	BP	adherens junction assembly	SMAD7
GO:0034373	0.0406	1	14791	601	1	1	BP	intermediate-density lipoprotein particle remodeling	LIPC
GO:0034638	0.0406	1	14791	601	1	1	BP	phosphatidylcholine catabolic process	LIPC
GO:0035026	0.0406	1	14791	601	1	1	BP	leading edge cell differentiation	JUN
GO:0035407	0.0406	1	14791	601	1	1	BP	histone H3-T11 phosphorylation	PKN1
GO:0000414	0.0406	1	14791	601	1	1	BP	regulation of histone H3-K36 methylation	BCOR
GO:0000415	0.0406	1	14791	601	1	1	BP	negative regulation of histone H3-K36 methylation	BCOR
GO:0042256	0.0406	1	14791	601	1	1	BP	mature ribosome assembly	EIF6
GO:0042309	0.0406	1	14791	601	1	1	BP	homiothermy	DBH
GO:0042368	0.0406	1	14791	601	1	1	BP	vitamin D biosynthetic process	CYP27B1

G0:0042450	0.0406	1	14791	601	1	1	BP	arginine biosynthetic process via ornithine	ASL
G0:0042696	0.0406	1	14791	601	1	1	BP	menarche	NKX2-1
G0:0043369	0.0406	1	14791	601	1	1	BP	CD4-positive or CD8-positive, alpha-beta T cell lineage commitment	BCL2
G0:0043375	0.0406	1	14791	601	1	1	BP	CD8-positive, alpha-beta T cell lineage commitment	BCL2
G0:0043455	0.0406	1	14791	601	1	1	BP	regulation of secondary metabolic process	PGAM1
G0:0043456	0.0406	1	14791	601	1	1	BP	regulation of pentose-phosphate shunt	PGAM1
G0:0045713	0.0406	1	14791	601	1	1	BP	low-density lipoprotein receptor biosynthetic process	PPARG
G0:0045764	0.0406	1	14791	601	1	1	BP	positive regulation of cellular amino acid metabolic process	COMT
G0:0045914	0.0406	1	14791	601	1	1	BP	negative regulation of catecholamine metabolic process	COMT
G0:0045963	0.0406	1	14791	601	1	1	BP	negative regulation of dopamine metabolic process	COMT
G0:0045994	0.0406	1	14791	601	1	1	BP	positive regulation of translational initiation by iron	TNF
G0:0046086	0.0406	1	14791	601	1	1	BP	adenosine biosynthetic process	NT5E
G0:0046333	0.0406	1	14791	601	1	1	BP	octopamine metabolic process	DBH
G0:0046530	0.0406	1	14791	601	1	1	BP	photoreceptor cell differentiation	STAT3
G0:0046597	0.0406	1	14791	601	1	1	BP	negative regulation of virion penetration into host cell	IFNB1
G0:0046600	0.0406	1	14791	601	1	1	BP	negative regulation of centriole replication	BRCA1
G0:0046606	0.0406	1	14791	601	1	1	BP	negative regulation of centrosome cycle	BRCA1

GO:0046724	0.0406	1	14791	601	1	1	BP	oxalic acid secretion	AGXT
GO:0047484	0.0406	1	14791	601	1	1	BP	regulation of response to osmotic stress	TRPV4
GO:0048320	0.0406	1	14791	601	1	1	BP	axial mesoderm formation	EPHA2
GO:0048686	0.0406	1	14791	601	1	1	BP	regulation of sprouting of injured axon	NTRK3
GO:0048687	0.0406	1	14791	601	1	1	BP	positive regulation of sprouting of injured axon	NTRK3
GO:0048690	0.0406	1	14791	601	1	1	BP	regulation of axon extension involved in regeneration	NTRK3
GO:0048691	0.0406	1	14791	601	1	1	BP	positive regulation of axon extension involved in regeneration	NTRK3
GO:0048743	0.0406	1	14791	601	1	1	BP	regulation of skeletal muscle fiber development	BCL2
GO:0050428	0.0406	1	14791	601	1	1	BP	3'-phosphoadenosine 5'-phosphosulfate biosynthetic process	PAPSS1
GO:0050668	0.0406	1	14791	601	1	1	BP	positive regulation of homocysteine metabolic process	COMT
GO:0050747	0.0406	1	14791	601	1	1	BP	positive regulation of lipoprotein metabolic process	PEMT
GO:0050812	0.0406	1	14791	601	1	1	BP	regulation of acyl-CoA biosynthetic process	SNCA
GO:0051572	0.0406	1	14791	601	1	1	BP	negative regulation of histone H3-K4 methylation	BCOR
GO:0051581	0.0406	1	14791	601	1	1	BP	negative regulation of neurotransmitter uptake	SNCA
GO:0051585	0.0406	1	14791	601	1	1	BP	negative regulation of dopamine uptake	SNCA
GO:0051611	0.0406	1	14791	601	1	1	BP	regulation of serotonin uptake	SNCA
GO:0051612	0.0406	1	14791	601	1	1	BP	negative regulation of serotonin uptake	SNCA
GO:0051621	0.0406	1	14791	601	1	1	BP	regulation of norepinephrine uptake	SNCA

GO:0051622	0.0406	1	14791	601	1	1	BP	negative regulation of norepinephrine uptake	SNCA
GO:0051799	0.0406	1	14791	601	1	1	BP	negative regulation of hair follicle development	NGFR
GO:0051913	0.0406	1	14791	601	1	1	BP	regulation of synaptic plasticity by chemical substance	MAP1B
GO:0051914	0.0406	1	14791	601	1	1	BP	positive regulation of synaptic plasticity by chemical substance	MAP1B
GO:0051915	0.0406	1	14791	601	1	1	BP	induction of synaptic plasticity by chemical substance	MAP1B
GO:0051945	0.0406	1	14791	601	1	1	BP	negative regulation of catecholamine uptake involved in synaptic transmission	SNCA
GO:0000055	0.0406	1	14791	601	1	1	BP	ribosomal large subunit export from nucleus	NPM1
GO:0060035	0.0406	1	14791	601	1	1	BP	notochord cell development	EPHA2
GO:0060074	0.0406	1	14791	601	1	1	BP	synapse maturation	ERBB4
GO:0060290	0.0406	1	14791	601	1	1	BP	transdifferentiation	SMAD3
GO:0060299	0.0406	1	14791	601	1	1	BP	negative regulation of sarcomere organization	CAV3
GO:0060306	0.0406	1	14791	601	1	1	BP	regulation of membrane repolarization	CAV3
GO:0060307	0.0406	1	14791	601	1	1	BP	regulation of ventricular cardiomyocyte membrane repolarization	CAV3
GO:0060353	0.0406	1	14791	601	1	1	BP	regulation of cell adhesion molecule production	IL1B
GO:0060355	0.0406	1	14791	601	1	1	BP	positive regulation of cell adhesion molecule production	IL1B
GO:0060373	0.0406	1	14791	601	1	1	BP	regulation of ventricular cardiomyocyte membrane depolarization	SMAD7
GO:0060375	0.0406	1	14791	601	1	1	BP	regulation of mast cell differentiation	STAT5A

GO:0060376	0.0406	1	14791	601	1	1	BP	positive regulation of mast cell differentiation	STAT5A
GO:0060480	0.0406	1	14791	601	1	1	BP	lung goblet cell differentiation	HOXA5
GO:0060520	0.0406	1	14791	601	1	1	BP	activation of prostate induction by androgen receptor signaling pathway	AR
GO:0060534	0.0406	1	14791	601	1	1	BP	trachea cartilage development	RARG
GO:0060535	0.0406	1	14791	601	1	1	BP	trachea cartilage morphogenesis	HOXA5
GO:0060536	0.0406	1	14791	601	1	1	BP	cartilage morphogenesis	HOXA5
GO:0060574	0.0406	1	14791	601	1	1	BP	intestinal epithelial cell maturation	HOXA5
GO:0060764	0.0406	1	14791	601	1	1	BP	cell-cell signaling involved in mammary gland development	HOXA5
GO:0061048	0.0406	1	14791	601	1	1	BP	negative regulation of branching involved in lung morphogenesis	TNF
GO:0006175	0.0406	1	14791	601	1	1	BP	dATP biosynthetic process	ADK
GO:0065001	0.0406	1	14791	601	1	1	BP	specification of axis polarity	BCOR
GO:0006574	0.0406	1	14791	601	1	1	BP	valine catabolic process	ALDH6A1
GO:0006657	0.0406	1	14791	601	1	1	BP	CDP-choline pathway	CHPT1
GO:0006808	0.0406	1	14791	601	1	1	BP	regulation of nitrogen utilization	BCL2
GO:0006933	0.0406	1	14791	601	1	1	BP	negative regulation of cell adhesion involved in substrate-bound cell migration	ATP5B
GO:0006990	0.0406	1	14791	601	1	1	BP	positive regulation of gene-specific transcription involved in unfolded protein response	ATF6
GO:0070091	0.0406	1	14791	601	1	1	BP	glucagon secretion	IL6

GO:0070164	0.0406	1	14791	601	1	1	BP	negative regulation of adiponectin secretion	IL1B
GO:0070314	0.0406	1	14791	601	1	1	BP	G1 to G0 transition	CYP27B1
GO:0070384	0.0406	1	14791	601	1	1	BP	Harderian gland development	RARG
GO:0070494	0.0406	1	14791	601	1	1	BP	regulation of thrombin receptor signaling pathway	SNCA
GO:0070495	0.0406	1	14791	601	1	1	BP	negative regulation of thrombin receptor signaling pathway	SNCA
GO:0070564	0.0406	1	14791	601	1	1	BP	positive regulation of vitamin D receptor signaling pathway	CYP27B1
GO:0070671	0.0406	1	14791	601	1	1	BP	response to interleukin-12	RIPK2
GO:0070673	0.0406	1	14791	601	1	1	BP	response to interleukin-18	RIPK2
GO:0071166	0.0406	1	14791	601	1	1	BP	ribonucleoprotein complex localization	TGS1
GO:0071167	0.0406	1	14791	601	1	1	BP	ribonucleoprotein complex import into nucleus	TGS1
GO:0071224	0.0406	1	14791	601	1	1	BP	cellular response to peptidoglycan	CAMP
GO:0071294	0.0406	1	14791	601	1	1	BP	cellular response to zinc ion	KCNK3
GO:0071529	0.0406	1	14791	601	1	1	BP	cementum mineralization	ALPL
GO:0071615	0.0406	1	14791	601	1	1	BP	oxidative deethylation	CYP1A2
GO:0007198	0.0406	1	14791	601	1	1	BP	inhibition of adenylate cyclase activity by serotonin receptor signaling pathway	HTR1A
GO:0007231	0.0406	1	14791	601	1	1	BP	osmosensory signaling pathway	TRPV4
GO:0007285	0.0406	1	14791	601	1	1	BP	primary spermatocyte growth	SHBG
GO:0007447	0.0406	1	14791	601	1	1	BP	imaginal disc pattern formation	DVL2
GO:0008049	0.0406	1	14791	601	1	1	BP	male courtship behavior	HEXB
GO:0090103	0.0406	1	14791	601	1	1	BP	cochlea morphogenesis	GLI2

GO:0009115	0.0406	1	14791	601	1	1	BP	xanthine catabolic process	XDH
GO:0009216	0.0406	1	14791	601	1	1	BP	purine deoxyribonucleoside triphosphate biosynthetic process	ADK
GO:0009403	0.0406	1	14791	601	1	1	BP	toxin biosynthetic process	CYP1A2
GO:0009441	0.0406	1	14791	601	1	1	BP	glycolate metabolic process	IGF1
GO:0009445	0.0406	1	14791	601	1	1	BP	putrescine metabolic process	AGMAT
GO:0009446	0.0406	1	14791	601	1	1	BP	putrescine biosynthetic process	AGMAT
GO:0006140	0.0407	1	14791	601	283	18	BP	regulation of nucleotide metabolic process	GDI1; RALBP1; AKAP12; TSC1; ADCY1; PGAM1; ADAP1; ADCY5; GNAO1; ASAP1; ASAP2; DRD2; HTR1A; NTRK2; HTR1B; ACR; FSHR; NDEL1
GO:0006639	0.041	1	14791	601	47	5	BP	acylglycerol metabolic process	APOB; APOH; LIPC; CAV3; CETP
GO:0090101	0.041	1	14791	601	47	5	BP	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	HIPK2; SMAD7; SMURF1; TP53; NKX2-1
GO:0016071	0.0416	1	14791	601	364	22	BP	mRNA metabolic process	DDX41; SMG5; GEMIN5; RBM9; RBMX; HNRNPA1; CEBPG; CSTF2; SNRNP200; PRPF3; NONO; SFPQ; RBM8A; ZHX2; EIF2C2; DHX16; PABPC1; BAT1; HNRNPC; SNRPA; SNRPE; UPF3A
GO:0031145	0.0422	1	14791	601	63	6	BP	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	ANAPC5; ANAPC7; PSME1; CDC16; CDC23; PSMB4
GO:0034655	0.0422	1	14791	601	63	6	BP	nucleobase, nucleoside, nucleotide and nucleic acid catabolic process	PDE11A; NT5E; XDH; ATP5B; DERA; ALDH6A1
GO:0034656	0.0422	1	14791	601	63	6	BP	nucleobase, nucleoside and nucleotide catabolic process	PDE11A; NT5E; XDH; ATP5B; DERA; ALDH6A1
GO:0030817	0.0425	1	14791	601	114	9	BP	regulation of cAMP biosynthetic process	AKAP12; ADCY1; ADCY5; DRD2; HTR1A; NTRK2; HTR1B; ACR; FSHR
GO:0051649	0.0425	1	14791	601	852	45	BP	establishment of localization in cell	SCG5; AKAP3; RAB6B; XP07; SMG5; AKAP12; TSC1; ERC1; JUN; EXOC2; MLPH; TPR; SNX9; AP2B1; ENAH; HNRNPA1; STX6; YWHAZ; TRPV4; KPNA2; SMURF1; RPH3AL; SYN1; VPS45; TP53; AGXT; IL6; AP3S1; WASF2; SQSTM1; PICALM; CLTB; PEX5; CDC23; TNF; BAT1; SDCBP; ACR; ATP5B; TGS1; TOMM20; NDEL1; CLTCL1; NPM1; MYO7A

GO:0001952	0.0434	1	14791	601	33	4	BP	regulation of cell-matrix adhesion	PIK3CB; TSC1; SMAD3; BCL2
GO:0045862	0.0434	1	14791	601	33	4	BP	positive regulation of proteolysis	SMAD7; CSNK1E; IL1B; TNF
GO:0046320	0.0434	1	14791	601	33	4	BP	regulation of fatty acid oxidation	PPARG; PPARA; ACACB; ACSL1
GO:0050906	0.0434	1	14791	601	33	4	BP	detection of stimulus involved in sensory perception	SAG; RHO; CACNA1F; PLCB2
GO:0009566	0.0443	1	14791	601	48	5	BP	fertilization	AKAP3; APOB; ELSBPB1; MST1R; ACR
GO:0007187	0.0445	1	14791	601	115	9	BP	G-protein signaling, coupled to cyclic nucleotide second messenger	ADCY1; VIPR1; ADCY5; WASF2; DRD2; HTR1A; HTR1B; CHRM2; FSHR
GO:0006816	0.0445	1	14791	601	133	10	BP	calcium ion transport	CAMK2B; JPH2; CYP27B1; CATSPER1; CACNG6; CACNA1F; TRPV4; DRD2; CACNA2D1; CACNB2
GO:0016331	0.045	1	14791	601	64	6	BP	morphogenesis of embryonic epithelium	ZIC2; TSC1; DVL2; TFAP2A; FZD6; GLI2
GO:0014910	0.0454	1	14791	601	20	3	BP	regulation of smooth muscle cell migration	F3; IGF1; BCL2
GO:0001975	0.0454	1	14791	601	20	3	BP	response to amphetamine	TRDMT1; DBH; DRD2
GO:0002260	0.0454	1	14791	601	20	3	BP	lymphocyte homeostasis	BCL2; STAT5B; STAT5A
GO:0003156	0.0454	1	14791	601	20	3	BP	regulation of organ formation	AR; WNT2; HOXC11
GO:0031576	0.0454	1	14791	601	20	3	BP	G2/M transition checkpoint	BLM; BRCA1; NBN
GO:0035094	0.0454	1	14791	601	20	3	BP	response to nicotine	LEPR; ABAT; BCL2
GO:0043525	0.0454	1	14791	601	20	3	BP	positive regulation of neuron apoptosis	JUN; TP53; TNF
GO:0071219	0.0454	1	14791	601	20	3	BP	cellular response to molecule of bacterial origin	CAMP; STAT1; RIPK2
GO:0000086	0.0454	1	14791	601	20	3	BP	G2/M transition of mitotic cell cycle	ANAPC5; CDKN2B; TERF1
GO:0030814	0.0466	1	14791	601	116	9	BP	regulation of cAMP metabolic process	AKAP12; ADCY1; ADCY5; DRD2; HTR1A; NTRK2; HTR1B; ACR; FSHR
GO:0051789	0.0466	1	14791	601	116	9	BP	response to protein stimulus	CYR61; CLU; BCL2; EGR1; FOS; CCR4; HSPB3; MAP1B; ATF6
GO:0006650	0.0466	1	14791	601	116	9	BP	glycerophospholipid metabolic process	PIK3CB; LIPC; PI4KB; FABP3; CHPT1; CETP; LCAT; DRD2; PEMT
GO:0007420	0.0466	1	14791	601	116	9	BP	brain development	ZIC2; PRKDC; IGF1R; KCNK3; EPOR; NTF3; ESR2; EFNA5; NKX2-1
GO:0033993	0.0477	1	14791	601	34	4	BP	response to lipid	PPARG; EGFR; FABP3; EGR1
GO:0034311	0.0477	1	14791	601	34	4	BP	diol metabolic process	SNCA; DBH; COMT; DRD2

GO:0045833	0.0477	1	14791	601	34	4	BP	negative regulation of lipid metabolic process	NFKB1; BRCA1; IL1B; TNF
GO:0050680	0.0477	1	14791	601	34	4	BP	negative regulation of epithelial cell proliferation	AR; PPARC; CDKN2B; ESR2
GO:0051899	0.0477	1	14791	601	34	4	BP	membrane depolarization	SNCA; JUN; KCNE1; GRIN2C
GO:0060021	0.0477	1	14791	601	34	4	BP	palate development	SMAD4; LEF1; COL11A2; BCOR
GO:0006584	0.0477	1	14791	601	34	4	BP	catecholamine metabolic process	SNCA; DBH; COMT; DRD2
GO:0006775	0.0477	1	14791	601	34	4	BP	fat-soluble vitamin metabolic process	CYP27B1; PPARC; FGF23; RDH12
GO:0006909	0.0477	1	14791	601	34	4	BP	phagocytosis	ITGAV; IRF8; CEBPE; MYO7A
GO:0007416	0.0477	1	14791	601	34	4	BP	synapse assembly	CADM1; DRD2; MAP1B; ACHE
GO:0009712	0.0477	1	14791	601	34	4	BP	catechol metabolic process	SNCA; DBH; COMT; DRD2
GO:0031570	0.0478	1	14791	601	49	5	BP	DNA integrity checkpoint	BLM; MSH2; BRCA1; TP53; NBN
GO:0045834	0.0478	1	14791	601	49	5	BP	positive regulation of lipid metabolic process	PPARG; PPARA; AVPR1A; IL1B; TNF
GO:0030336	0.048	1	14791	601	65	6	BP	negative regulation of cell migration	APOH; SMAD7; CITED2; BCL2; DRD2; NKX2-1
GO:0006800	0.048	1	14791	601	65	6	BP	oxygen and reactive oxygen species metabolic process	SFTPD; LPO; EPHX2; FANCC; BCL2; CYP1A2
GO:0007631	0.048	1	14791	601	65	6	BP	feeding behavior	LEPR; AGRP; FOS; STAT3; NKX2-1; HTR1B
GO:0006974	0.0482	1	14791	601	370	22	BP	response to DNA damage stimulus	HIPK2; BLM; PRKDC; TP73; TRIP13; CSNK1E; FANCC; UHRF1; CDK7; GTF2H4; MSH2; MSH3; BRCA1; XRCC5; NONO; RAD50; SFPQ; POLE2; TP53; MCM7; NBN; RAD91
GO:0042742	0.0487	1	14791	601	117	9	BP	defense response to bacterium	LTF; DEFA1; IRF8; CEBPE; CAMP; IFNB1; IL6; TNF; RIPK2
GO:0046700	0.0488	1	14791	601	82	7	BP	heterocycle catabolic process	DBH; PDE11A; NT5E; XDH; ATP5B; DERA; ALDH6A1
GO:0010660	0.049	1	14791	601	9	2	BP	regulation of muscle cell apoptosis	APOH; IGF1
GO:0010889	0.049	1	14791	601	9	2	BP	regulation of sequestering of triglyceride	PPARG; PPARA
GO:0000160	0.049	1	14791	601	9	2	BP	two-component signal transduction system	KCNH2; PDE8A
GO:0021537	0.049	1	14791	601	9	2	BP	(phosphorelay) telencephalon development	AVPR1A; ERBB4
GO:0000003	0.049	1	14791	601	9	2	BP	reproduction	HEXB; STAT3
GO:0030225	0.049	1	14791	601	9	2	BP	macrophage differentiation	CEBPA; CEBPE
GO:0003254	0.049	1	14791	601	9	2	BP	regulation of membrane depolarization	SMAD7; BCL2

GO:0032814	0.049	1	14791	601	9	2	BP	regulation of natural killer cell activation	STAT5B; STAT5A
GO:0033144	0.049	1	14791	601	9	2	BP	negative regulation of steroid hormone receptor signaling pathway	IGF1; ESR2
GO:0033598	0.049	1	14791	601	9	2	BP	mammary gland epithelial cell proliferation	ESR1; CEBPB
GO:0042451	0.049	1	14791	601	9	2	BP	purine nucleoside biosynthetic process	NT5E; ADK
GO:0042455	0.049	1	14791	601	9	2	BP	ribonucleoside biosynthetic process	NT5E; ADK
GO:0042491	0.049	1	14791	601	9	2	BP	auditory receptor cell differentiation	JAG1; MYO7A
GO:0042953	0.049	1	14791	601	9	2	BP	lipoprotein transport	APOB; PPARG
GO:0043129	0.049	1	14791	601	9	2	BP	surfactant homeostasis	SFTPD; ERBB4
GO:0043372	0.049	1	14791	601	9	2	BP	positive regulation of CD4-positive, alpha beta T cell differentiation	RARA; RIPK2
GO:0044269	0.049	1	14791	601	9	2	BP	glycerol ether catabolic process	APOB; LIPC
GO:0045684	0.049	1	14791	601	9	2	BP	positive regulation of epidermis development	CYP27B1; TNF
GO:0046129	0.049	1	14791	601	9	2	BP	purine ribonucleoside biosynthetic process	NT5E; ADK
GO:0046461	0.049	1	14791	601	9	2	BP	neutral lipid catabolic process	APOB; LIPC
GO:0046464	0.049	1	14791	601	9	2	BP	acylglycerol catabolic process	APOB; LIPC
GO:0046902	0.049	1	14791	601	9	2	BP	regulation of mitochondrial membrane permeability	BCL2; TP53
GO:0048009	0.049	1	14791	601	9	2	BP	insulin-like growth factor receptor signaling pathway	IGF1R; GHR
GO:0048875	0.049	1	14791	601	9	2	BP	chemical homeostasis within a tissue	SFTPD; ERBB4
GO:0051000	0.049	1	14791	601	9	2	BP	positive regulation of nitric-oxide synthase activity	SCARB1; HIF1A
GO:0051023	0.049	1	14791	601	9	2	BP	regulation of immunoglobulin secretion	IL6; TNF

GO:0051044	0.049	1	14791	601	9	2	BP	positive regulation of membrane protein ectodomain proteolysis	IL1B; TNF
GO:0051953	0.049	1	14791	601	9	2	BP	negative regulation of amine transport	SNCA; TNF
GO:0051972	0.049	1	14791	601	9	2	BP	regulation of telomerase activity	PPARG; TERF1
GO:0070373	0.049	1	14791	601	9	2	BP	negative regulation of ERK1 and ERK2 cascade	LIF; IGF1
GO:0007603	0.049	1	14791	601	9	2	BP	phototransduction, visible light	SAG; RHO
GO:0007625	0.049	1	14791	601	9	2	BP	grooming behavior	HOXB8; AVPR1A
GO:0009163	0.049	1	14791	601	9	2	BP	nucleoside biosynthetic process	NT5E; ADK
GO:0044428	5.40E-21	2.70E-18	16768	594	1932	149	CC	nuclear part	SMARCC2; HIPK2; SP1; CAMK2A; CAMK2B; DDX41; WHSC2; AKAP8; TSG101; POLR1A; POLR1E; XP07; H3F3A; SENP2; BLM; ANAPC5; ANAPC7; KCNH2; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; PRKDC; TAF11; IRF3; LEF1; GEMIN5; RBM9; NGFR; UBTf; JUN; COPS7B; HOXB13; RBMX; SON; EIF3L; RARG; ORC6L; RELA; WT1; TPR; PTGES3; MAPK10; USF1; GTF2E1; NFKB1; ZFH3; GMN; MLF1; SKP1; ADAP1; ASCL3; HNRNP1A; CITED2; KEAP1; CDK7; TAF9B; DSCC1; MATR3; GTF2H4; TCEB3; MSH2; MSH3; ITGB3BP; MYBL1; SMARCA4; CEBPA; CEBPG; CEBPE; MED15; SUZ12; SMAD3; MCL1; CSTF2; ILF3; BCL2; SNRNP200; BRCA1; CREB1; NR2C2; BRD8; KPNA2; CRX; HIF1A; XRCC5; PRPF3; DAXX; CDC16; NONO; RPS3A; FOS; RAD50; TRRAP; SFPQ; PAX8; ESR1; POLE2; FGF22; SYN1; YY1; STAT3; RBM8A; STAT1; ING2; TAL1; TP53; MYB; RHEB; EIF6; NAP1L1; POU3F2; CEBPB; MCM7; SQSTM1; NKX2-1; TERF1; POU2F1; PABPC1; MED30; POLR2H; POLR2K; POLR2J; TAF7; ETV4; CDC23; BAT1; NCOR1; POLD2; NBN; HNRNPC; TGS1; BCOR; SREBF1; MKI67; DGKQ; SIN3A; RAD21; DNMT3L; NDEL1; DACH1; SNRPA; NPM1; SNRPE; ATF1; SUB1; ATF6; ATF2; IGF2R
GO:0005654	4.50E-17	2.20E-14	16768	594	465	58	CC	nucleoplasm	SMARCC2; CAMK2A; CAMK2B; WHSC2; POLR1A; ANAPC5; ANAPC7; SMAD9; SMAD4; SMAD1; PRKDC; TAF11; IRF3; GEMIN5; NGFR; UBTf; JUN; EIF3L; ORC6L; RELA; WT1; TPR; MAPK10; GTF2E1; NFKB1; GMN; SKP1; HNRNP1A; CDK7; DSCC1; GTF2H4; TCEB3; ITGB3BP; SMAD3; MCL1; BRCA1; CREB1; KPNA2; XRCC5; CDC16; SFPQ; PAX8; POLE2; TP53; MCM7; SQSTM1; NKX2-1; TERF1; POLR2H; POLR2K; POLR2J; CDC23; POLD2; NBN; NPM1; SNRPE; ATF6; ATF2
GO:0005667	2.20E-14	1.10E-11	16768	594	200	34	CC	transcription factor complex	SMAD9; SMAD4; SMAD7; SMAD1; PRKDC; TAF11; LEF1; JUN; HOXB13; RARG; RELA; USF1; ZFH3; ASCL3; CDK7; TAF9B; GTF2H4; CEBPA; SMAD3; CREB1; CRX; HIF1A; FOS; TRRAP; YY1; ING2; TP53; POU3F2; NKX2-1; POU2F1; TAF7; DACH1; ATF1; SUB1

GO:0044424	3.40E-14	1.60E-11	16768	594	####	472	CC	intracellular part	<p>SMARCC2; PCSK2; SCG5; P4HA2; HIPK2; DLG1; PIK3CB; SV2A; CYP2C9; ARHGFEF12; SP1; SP3; CAMK2A; CAMK2B; F3; SULT1E1; JPH2; AKAP3; DDX41; WHSC2; AKAP8; AR; HHIP; TSG101; RAB6B; MX1; POLR1A; POLR1E; IFIT1; HIP1R; BNIPL; APOB; XP07; DRP2; ZIC2; CYP27B1; H3F3A; GTF2I; SMG5; HOXB8; HOXB9; SENP2; DSP; BLM; PPARG; PPAR; PPARA; GDI1; ANAPC5; ANAPC7; PPID; CSNK1A1; KCNH2; KHK; TRDMT1; ACP6; SMAD9; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; AKAP12; REL; ADSSL1; TSC1; SPI1; KIF3A; IRF3; RXRA; LTF; LEF1; SRPK1; PDE10A; BDKRB2; ACPP; F5; TP73; GEMIN5; ERC1; EGFR; RBM9; ERG; NGR; ABAT; AFAP1; GF11B; PPF1A1; PDE1A; UBT; ACAA2; PGR; CNOT3; CNOT4; NOS1; SNCA; RTN1; YARS2; JUN; HGF; TRIP13; COPS7B; HOXB13; EXOC2; HEXB; CYB5A; RBMX; ANK3; MLPH; SFTPD; AVPRIA; GSTA4; RARA; CATSPER1; PKP3; PKP2; DAB1; SON; EIF3H; B3GNT6; RARB; EIF3L; RARG; PEA15; NFE2L1; ORC6L; EIF3G; REL; FGB; CDKN2B; WT1; CENPJ; HOMER1; TPR; DBH; PTGES3; SCARB2; SCARB1; ELK1; GNG2; RHO; MAPK10; VLDLR; SNX9; PPOX; USF1; AP2B1; GTF2E1; TIRAP; BMX; TCF4; IGF1; IGF2BP6; AGMAT; IRF8; NFKB1; CSNK1E; SARDH; NSD1; WDHV1; RALA; EPHX2; PI4KB; TCERG1; ZFH3; FAPB3; PGAM1; GANN; PDE11A; MLF1; USF2; SKP1; ADAP1; CHPT1; FANCC; ENAH; CADM1; NTF3; ASCL3; HNRNP1A; MTHFS; CITED2; CLU; UHRF1; DLST; STX6; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; LPAR1; DSCC1; MATR3; GTF2H4; TCEB3; MSH2; MSH3; USP7; ITGB3BP; MYBL1; SMARCA4; YWHAZ; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; CAMP; ARHGAP1; DVL2; ETS1; MED15; SUZ12; RUFY1; PRKDC; PSME1; SMAD3; MCL1; CTNNA2; ABI3; CSTF2; GOLGB1; ILF3; BCL2; IMMT; PLCD3; TRIM11; WWP1; CAV3; SNRNP200; GHR; CYP4F12; ZFPM2; MAGI3; EIF4ENIF1; BRCA1; ERBB4; PRMT3; TRIM21; CREB1; CTSG; NR2C2; BRD8; BRD7; DZIP3; PRMT5; KPNA2; GBA; CRX; PLCB2; HIF1A; XRC5; PRPF3; SMURF1; DAXX; SMURF2; CDC16; NONO; EGR1; EGR4; XDH; RPH3AL; RPS3A; R1C8A; FOS; RAD50; TRRAP; SFPQ; PAX6; TP53INP1; NFKB2; PAX2; PAX8; ESR2; TOLLIP; ESR1; ACAD8; CTSL1; POLE2; STK36; PAX1; FGF22; SYM1; YY1; IL1B; HARS; VPS45; STAT3; RBM8A; STAT1; ZHX2; ZHX3; ZHX1; ING2; NMNAT2; IGBP1; TAL1; ACACB; COMT; EIF2C2; LGALS3; TP53; NRBF2; CYP11A2; MYB; WNT2; AGXT; AP3S1; RHEB; ASAP1; ASAP2; HARS2; SNTB2; ANTXR2; EIF5; EIF6; RUNX1T1; TEAD1; CAMLG; ZMYND19; KLF11; WASF2; TFAP2A; NAP1L1; NEFH; PPL; PDPK1; BCAN; POU3F2; AADAT; CEBPB; PKN1; MCM7; HADHA; TP53BP2; VWF; DUSP12; SQSTM1; RDH14; PICCALM; KCNE2; KCNE1; ISL1; HBB; DHX16; NKX2-1; UGP2; ETS2; CACNA2D1; ITSN1; ITSN2; NTRK3; GNB2L1; MICAL1; CAPN2; GOT1; SYT9; ENPP7; FLI1; RAPIA; SNAPC5; SRGAP2; KCTD13; SOCS2; PPP2CA; EEF1D; PPP2CB; MST1R; GSK3B; TERF1; SLC4A1; TRIM39; ACSL1; STMN1; POU2F1; PABPC1; G6PC2; ST13; CLTB; MAPKAPK5; VDAC1; GUCY1A3; ODF1; NACA; ELK4; MED30; PGM1; GYS2; HRAS; POLR2H; POLR2K; POLR2J; TAF7; PEX5; ETV4; SDC1; CDC23; TNFAIP3; TNF; BAT1; CLDN17; CLDN19; SDCBP; ACR; ATP5B; NCOR1; AKR1B10; MAP1B; CYP2B6; POLD2; NBN; SRD5A2; HNRNPC; DUSP1; SGPP1; ASL; PCMT1; TGS1; GOLM1; BCOR; ACHE; FADS2; ADK; HEY1; SOS1; TACC3; GALNT14; STAT5B; STAT5A; SREBF1; PSMB4; TOMM20; MKI67; RIPK2; DERA; GRIN2C; DGKQ; SVEP1; ADRBK1; GLI2; FSHR; SIN3A; TRAF5; RAD21; DNMT3L; PLAT; ALDH6A1; NDEL1; DACH1; CLTCL1; SNRPA; NPM1; SNRPE; NFIC; PENT; ATF1; AXIN1; SUB1; HOXC11; NEDD4L; UPF3A; TGF1; DNMLL; ATF6; MYO7A; FSD1; ATF2; IGF2R</p>
GO:0044451	6.20E-14	3.10E-11	16768	594	594	61	CC	nucleoplasm part	<p>SMARCC2; HIPK2; BLM; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; PRKDC; TAF11; LEF1; GEMIN5; JUN; HOXB13; SON; RARG; REL; WT1; USF1; ZFH3; ASCL3; CDK7; TAF9B; GTF2H4; TCEB3; CEBPA; MED15; SUZ12; SMAD3; CREB1; BRD8; CRX; HIF1A; PRPF3; DAXX; NONO; FOS; TRRAP; SFPQ; YY1; RBM8A; ING2; TAL1; TP53; POU3F2; MCM7; NKX2-1; POU2F1; MED30; POLR2H; POLR2J; TAF7; BAT1; NCOR1; TGS1; DGKQ; SIN3A; DACH1; NPM1; ATF1; SUB1</p>

GO:0043231	4. 80E-11	2. 40E-08	16768	594	7996	361	CC	intracellular membrane-bounded organelle	<p>SMARCC2; PCSK2; SCG5; P4HA2; HIPK2; DLG1; SV2A; CYP2C9; SP1; SP3; AKAP3; DDX41; WHSC2; AKAP8; AR; TSG101; RAB6B; POLR1A; POLR1E; HIP1R; BNIPL; APOB; XP07; ZIC2; CYP27B1; H3F3A; GTF2I; SMG5; HOXB8; HOXB9; SENP2; DSP; BLM; PPARG; PPAR; PPARA; TRDM1; ACP6; SMAD9; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; REL; SPI1; IRF3; RXRA; LTF; LEF1; SRPK1; BDKRB2; TP73; GEMIN5; ERC1; EGFR; RBM9; ERG; NGFR; ABAT; GF11B; UBTf; ACAA2; PGR; CNOT3; CNOT4; NOS1; SNCA; RTN1; YARS2; JUN; TRIP13; COPS7B; HOXB13; HEXB; CYB5A; RBMX; MLPH; SFTPD; AVPRIA; RARA; PKP3; PKP2; SON; B3GNT6; RARB; RARG; NFE2L1; ORC6L; REL; FGB; CDKN2B; WT1; TPR; DBH; ELK1; GNG2; MAPK10; VLDLR; PPOX; USF1; GTF2E1; TCF4; IGFBP6; AGMAT; IRF8; NFKB1; CSNK1E; SARDH; NSD1; WDYHV1; RALA; EPHX2; PI4KB; TCERG1; ZFH3; GMNN; MLF1; USF2; ADAP1; CHPT1; FANCC; CADM1; NTF3; ASCL3; HNRNPA1; MTHFS; CITED2; CLU; UHRF1; DLST; STX6; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; LPAR1; DSCC1; MATR3; GTF2H4; TCEB3; MSH2; USP7; ITGB3BP; MYBL1; SMARCA4; YWHAZ; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; CAMP; ARHGAP1; DVL2; ETS1; MED15; SUZ12; RUFY1; PRKCD; SMAD3; MCL1; CSTF2; GOLGB1; ILF3; BCL2; IMMT; TRIM11; CAV3; SNRN200; GHR; ZFPM2; MAGI3; EIF4ENIF1; BRCA1; ERBB4; TRIM21; CREB1; CTSG; NR2C2; BRD8; BRD7; PRMT5; KPNA2; CRX; PLCB2; HIF1A; XRC5; PRPF3; DAXX; SMURF2; CDC16; NONO; EGR1; EGR4; XDH; RPS3A; FOS; RAD50; TRRAP; SFPQ; PAX6; TP53INP1; NFKB2; PAX2; PAX8; ESR2; ESR1; ACAD8; CTSL; POLE2; STK36; PAX1; PGP22; SYN1; YY1; IL1B; VPS45; STAT3; RBM8A; STAT1; ZHX2; ZHX3; ZHX1; ING2; MNAT2; TALL1; ACACB; COMT; EIF2C2; LGALS3; TP53; NRBF2; MYB; AGXT; AP3S1; ASAP2; HARS2; ANXR2; EIF6; RUNX1T1; TEAD1; CAMLG; KLF11; WASF2; TFAP2A; NAP1L1; NEFH; PPL; PDPK1; POU3F2; AADAT; CEBPB; PKN1; MCM7; HADHA; TP53BP2; VWF; DUSP12; SQSTM1; RDH14; PICALM; KCNE2; KCNE1; ISL1; DHX16; NKX2-1; ETS2; CACNA2D1; ITSN1; GOT1; SYT9; ENPP7; FLI1; SNAPC5; KCTD13; PPP2CA; PPP2CB; GSK3B; TERF1; TRIM39; ACSL1; POU2F1; PABPC1; G6PC2; MAPKAPK5; VDAC1; NACA; ELK4; MED30; HRAS; POLR2H; POLR2K; POLR2J; TAF7; PEX5; ETV4; TNFAIP3; TNF; BAT1; CLDN17; CLDN19; SDCBP; ACR; ATP5B; NCOR1; CYP2B6; POLD2; NBN; SRD5A2; HNRNPC; DUSP1; SGPP1; PCMT1; TGS1; GOLM1; BCOR; ACHE; FADS2; ADK; HEY1; GALNT14; STAT5B; STAT5A; SREBF1; PSMB4; TOMM20; MKI67; DGKQ; GLI2; FSHR; SIN3A; RAD21; DNMT3L; PLAT; ALDH6A1; DACH1; CLTCL1; SNRPA; NPM1; SNRPE; NFIC; PEMT; ATF1; AXIN1; SUB1; HOXC11; UPF3A; TGIF1; DNML1; ATF6; MYO7A; FSD1; ATF2; IGF2R</p>
GO:0043227	5. 00E-11	2. 40E-08	16768	594	7998	361	CC	membrane-bounded organelle	<p>SMARCC2; PCSK2; SCG5; P4HA2; HIPK2; DLG1; SV2A; CYP2C9; SP1; SP3; AKAP3; DDX41; WHSC2; AKAP8; AR; TSG101; RAB6B; POLR1A; POLR1E; HIP1R; BNIPL; APOB; XP07; ZIC2; CYP27B1; H3F3A; GTF2I; SMG5; HOXB8; HOXB9; SENP2; DSP; BLM; PPARG; PPAR; PPARA; TRDM1; ACP6; SMAD9; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; REL; SPI1; IRF3; RXRA; LTF; LEF1; SRPK1; BDKRB2; TP73; GEMIN5; ERC1; EGFR; RBM9; ERG; NGFR; ABAT; GF11B; UBTf; ACAA2; PGR; CNOT3; CNOT4; NOS1; SNCA; RTN1; YARS2; JUN; TRIP13; COPS7B; HOXB13; HEXB; CYB5A; RBMX; MLPH; SFTPD; AVPRIA; RARA; PKP3; PKP2; SON; B3GNT6; RARB; RARG; NFE2L1; ORC6L; REL; FGB; CDKN2B; WT1; TPR; DBH; ELK1; GNG2; MAPK10; VLDLR; PPOX; USF1; GTF2E1; TCF4; IGFBP6; AGMAT; IRF8; NFKB1; CSNK1E; SARDH; NSD1; WDYHV1; RALA; EPHX2; PI4KB; TCERG1; ZFH3; GMNN; MLF1; USF2; ADAP1; CHPT1; FANCC; CADM1; NTF3; ASCL3; HNRNPA1; MTHFS; CITED2; CLU; UHRF1; DLST; STX6; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; LPAR1; DSCC1; MATR3; GTF2H4; TCEB3; MSH2; USP7; ITGB3BP; MYBL1; SMARCA4; YWHAZ; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; CAMP; ARHGAP1; DVL2; ETS1; MED15; SUZ12; RUFY1; PRKCD; SMAD3; MCL1; CSTF2; GOLGB1; ILF3; BCL2; IMMT; TRIM11; CAV3; SNRN200;</p>
GO:0005634	1. 50E-10	7. 60E-08	16768	594	5037	250	CC	nucleus	<p>SMARCC2; HIPK2; SP1; SP3; DDX41; WHSC2; AKAP8; AR; TSG101; POLR1A; POLR1E; BNIPL; XP07; ZIC2; H3F3A; GTF2I; SMG5; HOXB8; HOXB9; SENP2; BLM; PPARG; PPAR; PPARA; TRDM1; SMAD9; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; REL; SPI1; IRF3; RXRA; LEF1; SRPK1; TP73; GEMIN5; EGFR; RBM9; ERG; NGFR; GF11B; UBTf; PGR; CNOT3; CNOT4; SNCA; JUN; TRIP13; COPS7B; HOXB13; RBMX; RARA; PKP3; PKP2; SON; RARB; RARG; NFE2L1; ORC6L; REL; CDKN2B; WT1; TPR; ELK1; VLDLR; USF1; GTF2E1; TCF4; IRF8; NFKB1; CSNK1E; NSD1; WDYHV1; TCERG1; ZFH3; GMNN; MLF1; USF2; ADAP1; FANCC; ASCL3; HNRNPA1; CITED2; UHRF1; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; DSCC1; MATR3; GTF2H4; TCEB3; MSH2; USP7; ITGB3BP; MYBL1; SMARCA4; YWHAZ; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; DVL2; ETS1; MED15; SUZ12; PRKCD; SMAD3; MCL1; CSTF2; ILF3; BCL2; TRIM11; SNRN200; GHR; ZFPM2; MAGI3; EIF4ENIF1; BRCA1; ERBB4; TRIM21; CREB1; NR2C2; BRD8; BRD7; PRMT5; KPNA2; CRX; HIF1A; XRC5; PRPF3; DAXX; SMURF2; CDC16; NONO; EGR1; EGR4; RPS3A; FOS; RAD50; TRRAP; SFPQ; PAX6; TP53INP1; NFKB2; PAX2; PAX8; ESR2; ESR1; POLE2; STK36; PAX1; YY1; STAT3; RBM8A; STAT1; ZHX2; ZHX3; ZHX1; ING2; TALL1; EIF2C2; LGALS3; TP53; NRBF2; MYB; EIF6; RUNX1T1; TEAD1; KLF11; TFAP2A; NAP1L1; PPL; POU3F2; CEBPB; PKN1; MCM7; TP53BP2; DUSP12; SQSTM1; PICALM; ISL1; DHX16; NKX2-1; ETS2; FLI1; SNAPC5; KCTD13; PPP2CA; PPP2CB; GSK3B; TERF1; POU2F1; PABPC1; MAPKAPK5; NACA; ELK4; MED30; POLR2H; POLR2K; POLR2J; TAF7; ETV4; TNFAIP3; BAT1; CLDN19; SDCBP; NCOR1; POLD2; NBN; HNRNPC; DUSP1; TGS1; BCOR; ACHE; ADK; HEY1; STAT5B; STAT5A; SREBF1; PSMB4; MKI67; DGKQ; GLI2; SIN3A; RAD21; DNMT3L; DACH1; SNRPA; NPM1; SNRPE; NFIC; ATF1; AXIN1; SUB1; HOXC11; UPF3A; TGIF1; ATF6; FSD1; ATF2; IGF2R</p>

G0:0044446	5.00E-10	2.40E-07	16768	594	5015	247	CC	intracellular organelle part	<p>SMARCC2; P4HA2; HIPK2; DLG1; SV2A; CYP2C9; SP1; CAMK2A; CAMK2B; JPH2; DDX41; WHSC2; AKAP8; TSG101; RAB6B; POLR1A; POLR1E; HIP1R; APOB; XP07; CYP27B1; H3F3A; SENP2; BLM; ANAPC5; ANAPC7; CSNK1A1; KCNH2; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; PRKDC; TAF11; TSC1; KIF3A; IRF3; LEF1; ACPP; F5; GEMIN5; ERC1; EGFR; RBM9; NGFR; ABAT; UBTf; ACAA2; SNCA; RTN1; YARS2; JUN; HGF; COPS7B; HOXB13; CYB5A; RBMX; CATSPER1; SON; B3GNT6; EIF3L; RARG; PEA15; ORC6L; RELA; FGB; WT1; CENPJ; HOMER1; TPR; DBH; PTGES3; SCARB2; RHO; MAPK10; PPOX; USF1; AP2B1; GTF2E1; IGF1; NFKB1; SARDH; PI4KB; ZFXH3; GMNN; MLF1; SKP1; ADAP1; CHPT1; FANCC; ASCL3; HNRNPA1; CITED2; STX6; KEAP1; CDK7; TAF9B; DSCC1; MATR3; GTF2H4; TCEB3; MSH2; MSH3; ITGB3BP; MYBL1; SMARCA4; YWHAZ; CEBPA; CEBPG; CEBPE; ARHGAP1; MED15; SUZ12; RUFY1; SMAD3; MCL1; CSTF2; GOLGB1; ILF3; BCL2; IMMT; CAV3; SNRNP200; CYP4F12; BRCA1; ERBB4; CREB1; NR2C2; BRD8; KPNA2; GBA; CRX; HIF1A; XRC5; PRPF3; DAXX; CDC16; NONO; RPH3AL; RPS3A; FOS; RAD50; TRRAP; SFPQ; PAX2; PAX8; ESRI; POLE2; FGF22; SYN1; YY1; VPS45; STAT3; RBM8A; STAT1; ING2; IGBP1; TAL1; LGALS3; TP53; CYP1A2; MYB; AGXT; AP3S1; RHEB; ASAP2; HARS2; SNTB2; ANTXR2; EIF6; NAP1L1; NEFH; BCAN; POU3F2; CEBPB; MCM7; HADHA; SQSTM1; PICALM; NKX2-1; MICAL1; SYT9; SRGAP2; PPP2CA; PPP2CB; MST1R; TERF1; ACSL1; STMN1; POU2F1; PABPC1; G6PC2; CLTB; VDACL1; MED30; GYS2; HRAS; POLR2H; POLR2K; POLR2J; TAF7; PEX5; ETV4; CDC23; TNFAIP3; BAT1; SDCBP; ACR; ATP5B; NCOR1; MAP1B; CYP2B6; POLD2; NBN; SRD5A2; HNRNPC; SGPP1; TGS1; BCOR; FADS2; TACC3; GALNT14; SREBF1; PSMB4; TOMM20; MKI67; GRIN2C; DGKQ; SIN3A; RAD21; DNMT3L; NDEL1; DACH1; CLTCL1; SNRPA; NPM1; SNRPE; PEMT; ATF1; SUB1; DNML1; ATF6; MYO7A; FSD1; ATF2; IGF2R</p>
G0:0044422	6.90E-10	3.40E-07	16768	594	5082	249	CC	organelle part	<p>SMARCC2; P4HA2; HIPK2; DLG1; SV2A; CYP2C9; SP1; CAMK2A; CAMK2B; JPH2; DDX41; WHSC2; AKAP8; TSG101; RAB6B; POLR1A; POLR1E; HIP1R; APOB; XP07; CYP27B1; H3F3A; SENP2; BLM; ANAPC5; ANAPC7; CSNK1A1; KCNH2; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; PRKDC; TAF11; TSC1; KIF3A; IRF3; LEF1; ACPP; F5; GEMIN5; ERC1; EGFR; RBM9; NGFR; ABAT; UBTf; ACAA2; SNCA; RTN1; YARS2; JUN; HGF; COPS7B; HOXB13; CYB5A; RBMX; CATSPER1; SON; B3GNT6; EIF3L; RARG; PEA15; ORC6L; RELA; FGB; WT1; CENPJ; HOMER1; TPR; DBH; PTGES3; SCARB2; RHO; MAPK10; PPOX; USF1; AP2B1; GTF2E1; IGF1; NFKB1; SARDH; PI4KB; ZFXH3; GMNN; MLF1; SKP1; ADAP1; CHPT1; FANCC; ASCL3; HNRNPA1; CITED2; STX6; KEAP1; CDK7; TAF9B; DSCC1; MATR3; GTF2H4; TCEB3; MSH2; MSH3; ITGB3BP; MYBL1; SMARCA4; YWHAZ; CEBPA; CEBPG; CEBPE; ARHGAP1; MED15; SUZ12; RUFY1; SMAD3; MCL1; CSTF2; GOLGB1; ILF3; BCL2; IMMT; CAV3; SNRNP200; CYP4F12; BRCA1; ERBB4; CREB1; NR2C2; BRD8; KPNA2; GBA; CRX; HIF1A; XRC5; PRPF3; DAXX; CDC16; NONO; RPH3AL; RPS3A; FOS; RAD50; TRRAP; SFPQ; PAX2; PAX8; ESRI; POLE2; FGF22; SYN1; YY1; VPS45; STAT3; RBM8A; STAT1; ING2; IGBP1; TAL1; LGALS3; TP53; CYP1A2; MYB; AGXT; AP3S1; RHEB; ASAP2; HARS2; SNTB2; ANTXR2; EIF6; NAP1L1; NEFH; BCAN; POU3F2; CEBPB; MCM7; HADHA; SQSTM1; PICALM; NKX2-1; MICAL1; SYT9; SRGAP2; PPP2CA; PPP2CB; MST1R; TERF1; SLC4A1; ACSL1; STMN1; POU2F1; PABPC1; G6PC2; CLTB; VDACL1; ODF1; MED30; GYS2; HRAS; POLR2H; POLR2K; POLR2J; TAF7; PEX5; ETV4; CDC23; TNFAIP3; BAT1; SDCBP; ACR; ATP5B; NCOR1; MAP1B; CYP2B6; POLD2; NBN; SRD5A2; HNRNPC; SGPP1; TGS1; BCOR; FADS2; TACC3; GALNT14; SREBF1; PSMB4; TOMM20; MKI67; GRIN2C; DGKQ; SIN3A; RAD21; DNMT3L; NDEL1; DACH1; CLTCL1; SNRPA; NPM1; SNRPE; PEMT; ATF1; SUB1; DNML1; ATF6; MYO7A; FSD1; ATF2; IGF2R</p>

GO:0043226	1. 20E-09	6. 10E-07	16768	594	8773	382	CC	organelle	<p>SMARCC2; PCSK2; SCG5; P4HA2; HIPK2; DLG1; SV2A; CYP2C9; SP1; SP3; AKAP3; DDX41; WHSC2; AKAP8; AR; TSG101; RAB6B; POLR1A; POLR1E; HIP1R; BNIPL; APOB; XPO7; DRP2; ZIC2; CYP27B1; H3F3A; GTF2I; SMG5; HOXB8; HOXB9; SENP2; DSP; BLM; PPARG; PPAR; PPARA; CSNK1A1; TRDM1; ACP6; SMAD9; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; AKAP12; REL; SPI1; IRF3; RXRA; LTF; LEF1; SRPK1; BDKRB2; TP73; GEMIN5; ERC1; EGFR; RBM9; ERG; NGFR; ABAT; AFAP1; GF11B; UBTf; ACAA2; PGR; CNOT3; CNOT4; NOS1; SNCA; RTN1; YARS2; JUN; TRIP13; COPS7B; HOXB13; HEXB; CYB5A; RBMX; ANK3; MLPH; SFTPD; AVPR1A; RARA; CATSPER1; PKP3; PKP2; SON; B3GNT6; RARB; EIF3L; RARG; NFE2L1; ORC6L; REL; FGB; CDKN2B; WT1; CENPJ; TPR; DBH; ELK1; GNG2; MAPK10; VLDLR; PPOX; USF1; GTF2E1; TCF4; IGFBP6; AGMAT; IRF8; NFKB1; CSNK1E; SARDH; NSD1; WDYHV1; RALA; EPHX2; PI4KB; TCERG1; ZFH3; GMNN; MLF1; USF2; ADAP1; CHPT1; FANCC; ENAH; CADM1; NTF3; ASCL3; HNRNP1A; MTHFS; CITED2; CLU; UHRF1; DLST; STX6; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; LPAR1; DSCC1; MATR3; GTF2H4; TCEB3; MSH2; USP7; ITGB3BP; MYBL1; SMARCA4; YWHAZ; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; CAMP; ARHGAP1; DVL2; ETS1; MED15; SUZ12; RUFY1; PRKCD; SMAD3; MCL1; CTNNA2; CSTF2; GOLGB1; ILF3; BCL2; IMMT; TRIM11; CAV3; SNRNP200; GHR; CYP4F12; ZFPM2; MAG13; EIF4ENIF1; BRCA1; ERBB4; ERBB4; TRIM21; CREB1; CTSG; NR2C2; BRD8; BRD7; PRMT5; KPNA2; CRX; PLCB2; HIF1A; XRCC5; PRPF3; DAXX; SMURF2; CDC16; NONO; EGRI; EGRA; XDH; RPH3AL; RPS3A; FOS; RAD50; TRRAP; SFPQ; PAX6; TP53INP1; NFKB2; PAX2; PAX8; ESR2; ESR1; ACAD8; CTS1; POLE2; STK36; PAX1; FGF22; SYN1; YY1; IL1B; VPS45; STAT3; RBM8A; STAT1; ZHX2; ZHX3; ZHX1; ING2; NMNAT2; IGBP1; TAL1; ACACB; COMT; EIF2C2; LGALS3; TP53; NRBF2; CYP1A2; MYB; AGXT; AP3S1; ASAP2; HARS2; SNTB2; ANTXR2; EIF6; RUNX1T1; TEAD1; CAMLG; KLF11; WASF2; TFAP2A; NAP1L1; NEFH; PPL; PDPK1; POU3F2; AADAT; CEBPB; PKN1; MCM7; HADHA; TP53BP2; VWF; DUSP12; SQSTM1; RDH14; PICALM; KCNE2; KCNE1; ISL1; DHX16; NKX2-1; ETS2; CACNA2D1; ITSN1; MICAL1; GOT1; SYT9; ENPP7; FLI1; SNAPC5; KCTD13; PPP2CA; PPP2CB; GSK3B; TERF1; SLC4A1; TRIM39; ACSL1; POU2F1; PABPC1; G6PC2; CLTB; MAPKAPK5; VDACL1; NACA; ELK4; MED30; GYS2; HRAS; POLR2H; POLR2K; POLR2J; TAF7; PEX5; ETV4; TNFAIP3; TNF; BAT1; CLDN17; CLDN19; SDCBP; ACR; ATP5B; NCOR1; MAP1B; CYP2B6; POLD2; NBN; SRD5A2; HNRNPC; DUSP1; SGPP1; PCMT1; TGS1; GOLM1; BCOR; ACHE; FADS2; ADK; HEY1; TACC3; GALNT14; STAT5B; STAT5A; SREBF1; PSMB4; TOMM20; MKI67; DGKQ; GLI2; FSHR; SIN3A; RAD21; DNMT3L; PLAT; ALDH6A1; NDEL1; DACH1; CLTCL1; SNRPA; NPM1; SNRPE; NFIC; PEMT; ATF1; AXIN1; SUB1; HOXC11; UPF3A; TGIF1; DNML1; ATF6; MYO7A; FSD1; ATF2; IGF2R</p>
GO:0043229	1. 60E-09	7. 90E-07	16768	594	8759	381	CC	intracellular organelle	<p>SMARCC2; PCSK2; SCG5; P4HA2; HIPK2; DLG1; SV2A; CYP2C9; SP1; SP3; AKAP3; DDX41; WHSC2; AKAP8; AR; TSG101; RAB6B; POLR1A; POLR1E; HIP1R; BNIPL; APOB; XPO7; DRP2; ZIC2; CYP27B1; H3F3A; GTF2I; SMG5; HOXB8; HOXB9; SENP2; DSP; BLM; PPARG; PPAR; PPARA; CSNK1A1; TRDM1; ACP6; SMAD9; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; AKAP12; REL; SPI1; IRF3; RXRA; LTF; LEF1; SRPK1; BDKRB2; TP73; GEMIN5; ERC1; EGFR; RBM9; ERG; NGFR; ABAT; AFAP1; GF11B; UBTf; ACAA2; PGR; CNOT3; CNOT4; NOS1; SNCA; RTN1; YARS2; JUN; TRIP13; COPS7B; HOXB13; HEXB; CYB5A; RBMX; ANK3; MLPH; SFTPD; AVPR1A; RARA; CATSPER1; PKP3; PKP2; SON; B3GNT6; RARB; EIF3L; RARG; NFE2L1; ORC6L; REL; FGB; CDKN2B; WT1; CENPJ; TPR; DBH; ELK1; GNG2; MAPK10; VLDLR; PPOX; USF1; GTF2E1; TCF4; IGFBP6; AGMAT; IRF8; NFKB1; CSNK1E; SARDH; NSD1; WDYHV1; RALA; EPHX2; PI4KB; TCERG1; ZFH3; GMNN; MLF1; USF2; ADAP1; CHPT1; FANCC; ENAH; CADM1; NTF3; ASCL3; HNRNP1A; MTHFS; CITED2; CLU; UHRF1; DLST; STX6; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; LPAR1; DSCC1; MATR3; GTF2H4; TCEB3; MSH2; USP7; ITGB3BP; MYBL1; SMARCA4; YWHAZ; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; CAMP; ARHGAP1; DVL2; ETS1; MED15; SUZ12; RUFY1; PRKCD; SMAD3; MCL1; CTNNA2; CSTF2; GOLGB1; ILF3; BCL2; IMMT; TRIM11; CAV3; SNRNP200; GHR; CYP4F12; ZFPM2; MAG13; EIF4ENIF1; BRCA1; ERBB4; TRIM21; CREB1; CTSG; NR2C2; BRD8; BRD7; PRMT5; KPNA2; CRX; PLCB2; HIF1A; XRCC5; PRPF3; DAXX; SMURF2; CDC16; NONO; EGRI; EGRA; XDH; RPH3AL; RPS3A; FOS; RAD50; TRRAP; SFPQ; PAX6; TP53INP1; NFKB2; PAX2; PAX8; ESR2; ESR1; ACAD8; CTS1; POLE2; STK36; PAX1; FGF22; SYN1; YY1; IL1B; VPS45; STAT3; RBM8A; STAT1; ZHX2; ZHX3; ZHX1; ING2; NMNAT2; IGBP1; TAL1; ACACB; COMT; EIF2C2; LGALS3; TP53; NRBF2; CYP1A2; MYB; AGXT; AP3S1; ASAP2; HARS2; SNTB2; ANTXR2; EIF6; RUNX1T1; TEAD1; CAMLG; KLF11; WASF2; TFAP2A; NAP1L1; NEFH; PPL; PDPK1; POU3F2; AADAT; CEBPB; PKN1; MCM7; HADHA; TP53BP2; VWF; DUSP12; SQSTM1; RDH14; PICALM; KCNE2; KCNE1; ISL1; DHX16; NKX2-1; ETS2; CACNA2D1; ITSN1; MICAL1; GOT1; SYT9; ENPP7; FLI1; SNAPC5; KCTD13; PPP2CA; PPP2CB; GSK3B; TERF1; SLC4A1; TRIM39; ACSL1; POU2F1; PABPC1; G6PC2; CLTB; MAPKAPK5; VDACL1; NACA; ELK4; MED30; GYS2; HRAS; POLR2H; POLR2K; POLR2J; TAF7; PEX5; ETV4; TNFAIP3; TNF; BAT1; CLDN17; CLDN19; SDCBP; ACR; ATP5B; NCOR1; MAP1B; CYP2B6; POLD2; NBN; SRD5A2; HNRNPC; DUSP1; SGPP1; PCMT1; TGS1; GOLM1; BCOR; ACHE; FADS2; ADK; HEY1; TACC3; GALNT14; STAT5B; STAT5A; SREBF1; PSMB4; TOMM20; MKI67; DGKQ; GLI2; FSHR; SIN3A; RAD21; DNMT3L; PLAT; ALDH6A1; NDEL1; DACH1; CLTCL1; SNRPA; NPM1; SNRPE; NFIC; PEMT; ATF1; AXIN1; SUB1; HOXC11; UPF3A; TGIF1; DNML1; ATF6; MYO7A; FSD1; ATF2; IGF2R</p>

GO:0032991	1. 60E-09	8. 30E-07	16768	594	3312	177	CC	macromolecular complex	<p>SMARCC2; PIK3CB; SP1; DDX41; ITGA3; POLR1A; APOB; XP07; APOH; H3F3A; SENP2; ANAPC5; ANAPC7; CSNK1A1; KCNH2; ITGAV; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; PRKDC; TAF11; TSC1; KIF3A; LEF1; GEMIN5; ERC1; EGFR; ERG; ABAT; JUN; COPS7B; HOXB13; EXOC2; RBM8; EIF3H; EIF3L; RARG; PEA15; ORC6L; EIF3G; RELA; FGB; LIPC; CENPJ; TPR; PTGES3; GNG2; VLDLR; USF1; AP2B1; IGF1; NFKB1; ZFH3; SKP1; ASCL3; HNRNP1A; CLU; DLST; CNGA4; CDK7; TAF9B; GTF2H4; TCEB3; MSH2; MSH3; SMARCA4; YWHAZ; CEBPA; MED15; SUZ12; PSME1; SMAD3; ILF3; BCL2; CACNG6; WWP1; CAV3; SNRNP200; GHR; CACNA1F; MAGI2; BRCA1; CETP; TRIM21; CREB1; BRD8; KPNA2; GNAO1; CRX; HIF1A; XRC5; PRPF3; SMURF2; CDC16; RPS3A; FOS; RAD50; TRRAP; NFKB2; TOLLIP; ESR1; YY1; RBM8A; ING2; TALL1; LCAT; EIF2C2; TP53; IL6; AP3S1; RHEB; SNTB2; EIF6; NAP1L1; NEFH; POU3F2; MCM7; HADHA; PICALM; KCNE2; KCNE1; HBB; NKX2-1; CACNA2D1; MICAL1; GABRR2; RAPIA; KCTD13; PPP2CA; EEF1D; PPP2CB; GSK3B; TERF1; STMN1; POU2F1; PABPC1; HLA-G; CLTB; VDACL1; GUCY1A3; NACA; MED30; POLR2H; POLR2J; TAF7; PEX5; SDC1; CDC23; BAT1; SDCBP; ACR; ATP5B; NCOR1; MAP1B; CACNB2; NBN; HNRNPC; TGS1; BCOR; PSMB4; TOMM20; GRIN2C; SIN3A; RAD21; NDEL1; DACH1; CLTCL1; SNRPA; NPM1; SNRPE; ATF1; AXIN1; SUB1; MYO7A; FSD1</p> <p>HIPK2; SV2A; ARHGEF12; SP1; F3; SULT1E1; AR; HHIP; TSG101; MX1; IFIT1; HIP1R; XP07; DRP2; CYP27B1; GTF2I; SMG5; SENP2; DSP; BLM; GDI1; PPID; CSNK1A1; KCNH2; KHK; SMAD9; SMAD4; SMAD7; SMAD1; AKAP12; ADSSL1; TSC1; IRF3; LTF; LEF1; SRPK1; PDE10A; GEMIN5; ERC1; EGFR; RBM9; ERG; NGFR; AFAP1; PPF1A1; PGR; CNOT3; CNOT4; NOS1; SNCA; YARS2; COPS7B; CYB5A; ANK3; MLPH; GSTA4; EIF3H; RARB; EIF3L; PEA15; EIF3G; RELA; CDKN2B; WT1; CENPJ; HOMER1; TPR; DBH; PTGES3; SCARB1; MAPK10; SNX9; TIRAP; BMX; IGFBP6; NFKB1; CSNK1E; SARDH; WDHV1; EPHX2; PI4KB; FABP3; PDE11A; MLF1; ADAP1; FANCC; ENAH; HNRNP1A; MTHFS; CITED2; KEAP1; CDK7; TCEB3; ITGB3BP; YWHAZ; CAMP; ARHGAP1; DVL2; MED15; RUFY1; PRKCD; PSME1; SMAD3; MCL1; CTNNA2; ABI3; ILF3; BCL2; PLCD3; TRIM11; CAV3; GHR; ZFPM2; EIF4ENIF1; BRCA1; ERBB4; PRMT3; TRIM21; BRD7; DZIP3; PRMT5; KPNA2; HIF1A; XRC5; SMURF1; DAXX; SMURF2; CDC16; EGRI; XDH; RPH3AL; RPS3A; R1CSA; PAX6; NFKB2; ESR2; TOLLIP; ESR1; STK36; HARS; STAT3; RBM8A; STAT1; ZHX3; NMNAT2; IGBP1; ACACB; COMT; EIF2C2; LGALS3; TP53; NRB2; WNT2; ASAP1; ASAP2; HARS2; SNTB2; EIF5; EIF6; ZMYND19; WASF2; PPL; PDPK1; CEBPB; PKN1; MCM7; TP53BP2; DUSP12; SQSTM1; UGP2; ITSN2; NTRK3; GNB2L1; MICAL1; CAPN2; GOT1; SOCS2; PPP2CA; PPP2CB; GSK3B; TERF1; TRIM39; STMN1; PABPC1; ST13; MAPKAPK5; GUCY1A3; NACA; PGM1; GYS2; HRAS; TAF7; PEX5; SDC1; TNFAIP3; CLDN19; SDCBP; AKR1B10; SRD5A2; ASL; PCMT1; TGS1; TACC3; STAT5B; STAT5A; PSMB4; MKI67; RIPK2; DERA; DGKQ; SVEP1; ADRBK1; GLI2; TRAF5; DNMT3L; PLAT; NDEL1; DACH1; NPM1; AXIN1; NEDD4L; UPF3A; DNML1; MYO7A; FSD1; IGF2R</p> <p>DLG1; PIK3CB; ARHGEF12; CAMK2A; CAMK2B; SULT1E1; MX1; BNIPL; PPARG; ANAPC5; ANAPC7; CSNK1A1; SMAD9; SMAD4; SMAD7; SMAD1; TSC1; IRF3; GEMIN5; NGFR; PDE1A; SNCA; JUN; EIF3H; EIF3G; RELA; CENPJ; PTGES3; AP2B1; BMX; NFKB1; CSNK1E; WDHV1; EPHX2; FABP3; PGM1; PDE11A; SKP1; FANCC; ENAH; MTHFS; CDK7; ITGB3BP; PRKCD; SMAD3; BCL2; EIF4ENIF1; PLCB2; CDC16; RPS3A; HARS; ACACB; COMT; TP53; RHEB; EIF5; PDPK1; SQSTM1; ITSN1; GOT1; RAPIA; PPP2CA; EEF1D; GSK3B; TRIM39; ACSL1; PABPC1; PGM1; GYS2; HRAS; PEX5; CDC23; SDCBP; MAP1B; ADK; SOS1; STAT5B; RIPK2; DGKQ; ADRBK1; DNMT3L; NPM1; SNRPE; AXIN1; DNML1; MYO7A</p>
GO:0005737	2. 30E-09	1. 10E-06	16768	594	4549	226	CC	cytoplasm	<p>SMARCC2; PIK3CB; ITGA3; POLR1A; XP07; SENP2; ANAPC5; ANAPC7; CSNK1A1; KCNH2; ITGAV; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; PRKDC; TAF11; TSC1; KIF3A; LEF1; ERC1; EGFR; ABAT; JUN; COPS7B; HOXB13; EXOC2; EIF3H; EIF3L; RARG; PEA15; ORC6L; EIF3G; RELA; FGB; CENPJ; TPR; GNG2; USF1; AP2B1; IGF1; NFKB1; ZFH3; SKP1; ASCL3; DLST; CNGA4; CDK7; TAF9B; GTF2H4; TCEB3; MSH2; MSH3; SMARCA4; YWHAZ; CEBPA; MED15; SUZ12; PSME1; SMAD3; BCL2; CACNG6; WWP1; CAV3; GHR; CACNA1F; MAGI2; BRCA1; CREB1; BRD8; KPNA2; GNAO1; CRX; HIF1A; XRC5; SMURF2; CDC16; FOS; RAD50; TRRAP; NFKB2; TOLLIP; ESR1; YY1; RBM8A; ING2; TALL1; EIF2C2; TP53; IL6; AP3S1; SNTB2; EIF6; NAP1L1; NEFH; POU3F2; MCM7; HADHA; PICALM; KCNE2; KCNE1; HBB; NKX2-1; CACNA2D1; MICAL1; GABRR2; RAPIA; KCTD13; PPP2CA; EEF1D; PPP2CB; GSK3B; STMN1; POU2F1; HLA-G; CLTB; VDACL1; GUCY1A3; NACA; MED30; POLR2H; POLR2J; TAF7; PEX5; SDC1; CDC23; BAT1; SDCBP; ACR; ATP5B; NCOR1; MAP1B; CACNB2; NBN; BCOR; PSMB4; TOMM20; GRIN2C; SIN3A; RAD21; NDEL1; DACH1; CLTCL1; ATF1; AXIN1; SUB1; MYO7A; FSD1</p> <p>PPAP2A; PCSK2; LICAM; CYP2C9; JPH2; APOB; GDI1; TSC1; IGF1R; ABAT; SNCA; HEXB; CYB5A; FGB; HOMER1; DBH; SCARB2; SCARB1; VLDLR; SNX9; CNTN1; F10; EPHX2; PDE11A; CHPT1; CADM1; DLST; STX6; PPAT; CDK7; ITGB3BP; YWHAZ; BCL2; CAV3; CYP4F12; MAGI2; DLGAP4; GNAO1; NT5E; FOS; IL13RA2; LCT; COMT; TP53; CYP1A2; SNTB2; ZMYND19; PON3; NKX2-1; ITSN1; CAPN2; GOT1; PPP2CA; ACSL1; CHRM2; GYS2; HRAS; FBLN1; MAP1B; CYP2B6; SRD5A2; DUSP1; SGPP1; CRHBP; FADS2; IGFALS; ADRBK1; GLI2; PEMT; ATF2; IGF2R</p>
GO:0005829	3. 40E-09	1. 60E-06	16768	594	1269	86	CC	cytosol	<p>SMARCC2; PIK3CB; ITGA3; POLR1A; XP07; SENP2; ANAPC5; ANAPC7; CSNK1A1; KCNH2; ITGAV; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; PRKDC; TAF11; TSC1; KIF3A; LEF1; ERC1; EGFR; ABAT; JUN; COPS7B; HOXB13; EXOC2; EIF3H; EIF3L; RARG; PEA15; ORC6L; EIF3G; RELA; FGB; CENPJ; TPR; GNG2; USF1; AP2B1; IGF1; NFKB1; ZFH3; SKP1; ASCL3; DLST; CNGA4; CDK7; TAF9B; GTF2H4; TCEB3; MSH2; MSH3; SMARCA4; YWHAZ; CEBPA; MED15; SUZ12; PSME1; SMAD3; BCL2; CACNG6; WWP1; CAV3; GHR; CACNA1F; MAGI2; BRCA1; CREB1; BRD8; KPNA2; GNAO1; CRX; HIF1A; XRC5; SMURF2; CDC16; FOS; RAD50; TRRAP; NFKB2; TOLLIP; ESR1; YY1; RBM8A; ING2; TALL1; EIF2C2; TP53; IL6; AP3S1; SNTB2; EIF6; NAP1L1; NEFH; POU3F2; MCM7; HADHA; PICALM; KCNE2; KCNE1; HBB; NKX2-1; CACNA2D1; MICAL1; GABRR2; RAPIA; KCTD13; PPP2CA; EEF1D; PPP2CB; GSK3B; STMN1; POU2F1; HLA-G; CLTB; VDACL1; GUCY1A3; NACA; MED30; POLR2H; POLR2J; TAF7; PEX5; SDC1; CDC23; BAT1; SDCBP; ACR; ATP5B; NCOR1; MAP1B; CACNB2; NBN; BCOR; PSMB4; TOMM20; GRIN2C; SIN3A; RAD21; NDEL1; DACH1; CLTCL1; ATF1; AXIN1; SUB1; MYO7A; FSD1</p>
GO:0043234	2. 30E-08	1. 10E-05	16768	594	2748	149	CC	protein complex	<p>SMARCC2; PIK3CB; ITGA3; POLR1A; XP07; SENP2; ANAPC5; ANAPC7; CSNK1A1; KCNH2; ITGAV; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; PRKDC; TAF11; TSC1; KIF3A; LEF1; ERC1; EGFR; ABAT; JUN; COPS7B; HOXB13; EXOC2; EIF3H; EIF3L; RARG; PEA15; ORC6L; EIF3G; RELA; FGB; CENPJ; TPR; GNG2; USF1; AP2B1; IGF1; NFKB1; ZFH3; SKP1; ASCL3; DLST; CNGA4; CDK7; TAF9B; GTF2H4; TCEB3; MSH2; MSH3; SMARCA4; YWHAZ; CEBPA; MED15; SUZ12; PSME1; SMAD3; BCL2; CACNG6; WWP1; CAV3; GHR; CACNA1F; MAGI2; BRCA1; CREB1; BRD8; KPNA2; GNAO1; CRX; HIF1A; XRC5; SMURF2; CDC16; FOS; RAD50; TRRAP; NFKB2; TOLLIP; ESR1; YY1; RBM8A; ING2; TALL1; EIF2C2; TP53; IL6; AP3S1; SNTB2; EIF6; NAP1L1; NEFH; POU3F2; MCM7; HADHA; PICALM; KCNE2; KCNE1; HBB; NKX2-1; CACNA2D1; MICAL1; GABRR2; RAPIA; KCTD13; PPP2CA; EEF1D; PPP2CB; GSK3B; STMN1; POU2F1; HLA-G; CLTB; VDACL1; GUCY1A3; NACA; MED30; POLR2H; POLR2J; TAF7; PEX5; SDC1; CDC23; BAT1; SDCBP; ACR; ATP5B; NCOR1; MAP1B; CACNB2; NBN; BCOR; PSMB4; TOMM20; GRIN2C; SIN3A; RAD21; NDEL1; DACH1; CLTCL1; ATF1; AXIN1; SUB1; MYO7A; FSD1</p>
GO:0000267	3. 00E-07	1. 50E-04	16768	594	1080	71	CC	cell fraction	<p>SMARCC2; PIK3CB; ITGA3; POLR1A; XP07; SENP2; ANAPC5; ANAPC7; CSNK1A1; KCNH2; ITGAV; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; PRKDC; TAF11; TSC1; KIF3A; LEF1; ERC1; EGFR; ABAT; JUN; COPS7B; HOXB13; EXOC2; EIF3H; EIF3L; RARG; PEA15; ORC6L; EIF3G; RELA; FGB; CENPJ; TPR; GNG2; USF1; AP2B1; IGF1; NFKB1; ZFH3; SKP1; ASCL3; DLST; CNGA4; CDK7; TAF9B; GTF2H4; TCEB3; MSH2; MSH3; SMARCA4; YWHAZ; CEBPA; MED15; SUZ12; PSME1; SMAD3; BCL2; CACNG6; WWP1; CAV3; GHR; CACNA1F; MAGI2; BRCA1; CREB1; BRD8; KPNA2; GNAO1; CRX; HIF1A; XRC5; SMURF2; CDC16; FOS; RAD50; TRRAP; NFKB2; TOLLIP; ESR1; YY1; RBM8A; ING2; TALL1; EIF2C2; TP53; IL6; AP3S1; SNTB2; EIF6; NAP1L1; NEFH; POU3F2; MCM7; HADHA; PICALM; KCNE2; KCNE1; HBB; NKX2-1; CACNA2D1; MICAL1; GABRR2; RAPIA; KCTD13; PPP2CA; EEF1D; PPP2CB; GSK3B; STMN1; POU2F1; HLA-G; CLTB; VDACL1; GUCY1A3; NACA; MED30; POLR2H; POLR2J; TAF7; PEX5; SDC1; CDC23; BAT1; SDCBP; ACR; ATP5B; NCOR1; MAP1B; CACNB2; NBN; BCOR; PSMB4; TOMM20; GRIN2C; SIN3A; RAD21; NDEL1; DACH1; CLTCL1; ATF1; AXIN1; SUB1; MYO7A; FSD1</p>

GO:0044444	6. 70E-07	3. 30E-04	16768	594	5164	238	CC	cytoplasmic part	PCSK2; SCG5; P4HA2; DLG1; PIK3CB; SV2A; CYP2C9; ARHGEF12; CAMK2A; CAMK2B; SULT1E1; JPH2; AKAP3; AKAP8; TSG101; RAB6B; MX1; HIP1R; BNIPL; APOB; CYP27B1; DSP; PPARG; ANAPC5; ANAPC7; CSNK1A1; ACP6; SMAD9; SMAD4; SMAD7; SMAD1; AKAP12; TSC1; IRF3; LTF; BDKRB2; ACP2; F5; GEMIN5; ERC1; EGFR; NGFR; ABAT; PDE1A; ACAA2; NOS1; SNCA; RTN1; YARS2; JUN; HGF; EXOC2; HEXB; CYB5A; MLPH; SFTPD; AVPR1A; DAB1; EIF3H; B3GNT6; EIF3L; EIF3G; RELA; FGB; CENPJ; HOMER1; DBH; PTGES3; SCARB2; GNG2; MAPK10; PPOX; AP2B1; BMX; IGF1; IGFBP6; AGMAT; NFKB1; CSNK1E; SARDH; WDHV1; RALA; EPHX2; PI4KB; ZFXH3; FABP3; PGAM1; PDE11A; SKP1; CHPT1; FANCC; ENAH; CADM1; NTF3; MTHFS; CLU; DLST; STX6; KEAP1; CDK7; LPAR1; ITGB3BP; YWHAZ; CAMP; ARHGAP1; MED15; RUFY1; PRKCD; SMAD3; MCL1; GOLGB1; ILF3; BCL2; IMMT; CAV3; GHR; CYP4F12; EIF4ENIF1; BRCA1; CREB1; CTSG; BRD8; GBA; PLCB2; DAXX; CDC16; XDH; RPH3AL; RPS3A; PAX2; ESR2; ACAD8; CTSL1; FGF22; SYN1; IL1B; HARS; VPS45; MNAT2; IGBP1; ACACB; COMT; EIF2C2; LGALS3; TP53; CYP1A2; AGXT; AP3S1; RHEB; ASAP2; HARS2; SNTB2; ANTXR2; EIF5; CAMLG; WASF2; NAP1L1; NEFH; PPL; PDPK1; BCAN; AADAT; PKN1; HADHA; TP53BP2; VWF; SQSTM1; RDH14; PICALM; KCNE2; KCNE1; HBB; CACNA2D1; ITSN1; GOT1; SYT9; ENPP7; RAPIA; SRGAP2; PPP2CA; EEF1D; GSK3B; SLC4A1; TRIM39; ACSL1; PABPC1; G6PC2; CLTB; VDACL1; GUCY1A3; NACA; PGM1; GYS2; HRAS; TAF7; PEX5; CDC23; TNFAIP3; TNF; CLDN17; SDCBP; ACR; ATP5B; MAP1B; CYP2B6; NBN; SRD5A2; SGPP1; PCMT1; GOLM1; ACHE; FADS2; ADK; SOS1; TACC3; GALNT14; STAT5B; SREBF1; PSMB4; TOMM20; RIPK2; DGKQ; ADRBK1; FSHR; DNMT3L; PLAT; ALDH6A1; NDEL1; CLTCL1; NPM1; SNRPE; PEMT; AXIN1; DNML1; ATF6; MYO7A; FSD1; IGF2R
GO:0044421	7. 10E-07	3. 50E-04	16768	594	979	65	CC	extracellular region part	PCSK2; MFAP1; IFNA10; F3; APOD; APOB; APOH; COL4A4; COL4A3; LEPR; IFNA21; EGFR; DEFA1; SNCA; HGF; WNT16; SFTPD; LIF; COL11A2; WNT10A; FGB; LIPC; LPO; VLDLR; MASP1; IGF1; IGFBP6; SST; CLU; COL17A1; PRSS2; CAMP; MMP8; GHR; CETP; BMP8A; FCN2; IL13RA2; FGF22; FGF23; IL1B; IFNB1; LCAT; EFNA5; LGALS3; WNT2; IL6; GDF5; BCAN; VWF; PON3; WNT9B; ALPL; BMP5; TGFA; FGF5; TNF; FBLN1; ACAN; CRHBP; ACHE; IGFALS; GDF9; PLAT; IGF2R
GO:0005615	1. 40E-06	7. 20E-04	16768	594	693	50	CC	extracellular space	PCSK2; IFNA10; F3; APOD; APOB; APOH; LEPR; IFNA21; EGFR; DEFA1; HGF; SFTPD; LIF; FGB; LIPC; LPO; VLDLR; MASP1; IGF1; IGFBP6; SST; CLU; PRSS2; CAMP; MMP8; GHR; CETP; BMP8A; FCN2; IL13RA2; FGF22; FGF23; IL1B; IFNB1; LCAT; EFNA5; IL6; GDF5; PON3; ALPL; BMP5; TGFA; FGF5; TNF; FBLN1; CRHBP; IGFALS; GDF9; PLAT; IGF2R
GO:0016023	2. 50E-06	0. 0012	16768	594	438	36	CC	cytoplasmic membrane-bounded vesicle	PCSK2; SCG5; AKAP3; RAB6B; HIP1R; LTF; EGFR; HEXB; MLPH; SFTPD; FGB; DBH; RALA; CADM1; NTF3; STX6; LPAR1; YWHAZ; CAMP; CTSG; IL1B; AP3S1; NAP1L1; PDPK1; PKN1; VWF; PICALM; ITSN1; SYT9; SDCBP; ACR; PLAT; CLTCL1; AXIN1; MYO7A; IGF2R
GO:0031988	4. 10E-06	0. 002	16768	594	447	36	CC	membrane-bounded vesicle	PCSK2; SCG5; AKAP3; RAB6B; HIP1R; LTF; EGFR; HEXB; MLPH; SFTPD; FGB; DBH; RALA; CADM1; NTF3; STX6; LPAR1; YWHAZ; CAMP; CTSG; IL1B; AP3S1; NAP1L1; PDPK1; PKN1; VWF; PICALM; ITSN1; SYT9; SDCBP; ACR; PLAT; CLTCL1; AXIN1; MYO7A; IGF2R
GO:0005626	5. 70E-06	0. 0028	16768	594	830	55	CC	insoluble fraction	PPAP2A; L1CAM; CYP2C9; JPH2; APOB; GDI1; TSC1; IGF1R; ABAT; SNCA; CYB5A; HOMER1; DBH; SCARB2; SCARB1; VLDLR; SNX9; CNTN1; F10; CHPT1; CADM1; DLST; STX6; CDK7; ITGB3BP; BCL2; CAV3; CYP4F12; MAG12; DLGAP4; GNAO1; NT5E; FOS; LCT; COMT; TP53; CYP1A2; SNTB2; ZMYND19; PON3; ITSN1; CAPN2; ACSL1; CHRM2; GYS2; HRAS; CYP2B6; SRD5A2; SGPP1; FADS2; ADRBK1; GLI2; PEMT; ATF2; IGF2R
GO:0031410	9. 90E-06	0. 0049	16768	594	581	42	CC	cytoplasmic vesicle	PCSK2; SCG5; SV2A; AKAP3; RAB6B; HIP1R; LTF; EGFR; HEXB; MLPH; SFTPD; AVPR1A; FGB; DBH; RALA; CADM1; NTF3; STX6; LPAR1; YWHAZ; CAMP; CTSG; RPH3AL; IL1B; AP3S1; SNTB2; NAP1L1; PDPK1; PKN1; VWF; PICALM; ITSN1; SYT9; CLTB; SDCBP; ACR; SREBF1; PLAT; CLTCL1; AXIN1; MYO7A; IGF2R
GO:0031982	1. 00E-05	0. 0051	16768	594	602	43	CC	vesicle	PCSK2; SCG5; SV2A; AKAP3; RAB6B; HIP1R; LTF; EGFR; HEXB; MLPH; SFTPD; AVPR1A; FGB; DBH; RALA; CADM1; NTF3; STX6; LPAR1; YWHAZ; CAMP; CETP; CTSG; RPH3AL; IL1B; AP3S1; SNTB2; NAP1L1; PDPK1; PKN1; VWF; PICALM; ITSN1; SYT9; CLTB; SDCBP; ACR; SREBF1; PLAT; CLTCL1; AXIN1; MYO7A; IGF2R
GO:0005624	1. 70E-05	0. 0087	16768	594	800	52	CC	membrane fraction	PPAP2A; L1CAM; CYP2C9; JPH2; APOB; GDI1; TSC1; IGF1R; ABAT; SNCA; CYB5A; HOMER1; DBH; SCARB2; SCARB1; VLDLR; SNX9; CNTN1; F10; CHPT1; CADM1; DLST; STX6; CDK7; ITGB3BP; BCL2; CAV3; CYP4F12; MAG12; DLGAP4; GNAO1; NT5E; FOS; LCT; COMT; CYP1A2; SNTB2; ZMYND19; PON3; ITSN1; ACSL1; CHRM2; HRAS; CYP2B6; SRD5A2; SGPP1; FADS2; ADRBK1; GLI2; PEMT; ATF2; IGF2R
GO:0044459	3. 80E-05	0. 019	16768	594	2081	107	CC	plasma membrane part	PPAP2A; L1CAM; DLG1; SV2A; CAMK2A; F3; HHIP; ITGA3; FZD10; DSP; KCNH2; ITGAV; SMAD7; BDKRB2; EGFR; IGF1R; NGFR; AFAP1; JAG1; ANK3; AVPR1A; CATSPER1; PKP3; PKP2; FGB; HOMER1; SCARB2; SCARB1; GNG2; RHO; KCNK3; F10; EPOR; IL1RAP; ENAH; CADM1; COL17A1; GRIK5; KEAP1; F2RL3; LPAR1; VIPR1; CTNNA2; CACNG6; CAV3; GHR; CACNA1F; MAGI3; MAGI2; ERBB4; KIR3DL2; LCT; TOLLIP; ESR1; SYN1; CCR4; ICAM3; EFNA5; EFNA4; IL6; SNTB2; AMHR2; PPL; VWF; DRD2; HTR1A; PICALM; KCNE2; KCNE1; CACNA2D1; ITSN1; NTRK2; NTRK3; GABRR2; SYT9; KCTD13; MST1R; SLC4A1; HLA-G; CLTB; HTR1B; CHRM2; SDC1; MPL; TNF; CLDN11; CLDN17; EPHA8; CLDN19; EPHA3; EPHA2; SDCBP; GNRHR; NCAM1; FZD6; CACNB2; GOLM1; ACHE; FADS2; GRIN2C; ADRBK1; CLTCL1; PTPRS; PEMT; AXIN1; MYO7A; IGF2R
GO:0044433	4. 10E-05	0. 0206	16768	594	273	24	CC	cytoplasmic vesicle part	SV2A; CAMK2A; CAMK2B; HIP1R; APOB; F5; EGFR; SNCA; HGF; FGB; DBH; AP2B1; IGF1; RPH3AL; SYN1; AP3S1; SNTB2; BCAN; PICALM; SYT9; CLTB; ACR; SREBF1; CLTCL1
GO:0016363	6. 70E-05	0. 0335	16768	594	63	10	CC	nuclear matrix	AKAP8; BLM; MATR3; CEBPA; NONO; SFPQ; YY1; TP53; MYB; CEBPB
GO:0044427	1. 00E-04	0. 0497	16768	594	401	30	CC	chromosomal part	SMARCC2; H3F3A; BLM; CSNK1A1; JUN; ORC6L; TPR; PTGES3; FANCC; CITED2; DSCC1; ITGB3BP; SUZ12; CREB1; XRCC5; DAXX; RAD50; SYN1; TAL1; TP53; MCM7; PPP2CA; PPP2CB; TERF1; NBN; MKI67; SIN3A; RAD21; DNMT3L; NDEL1

GO:0032994	1.50E-04	0.0779	16768	594	34	7	CC	protein-lipid complex	APOB; APOH; LIPC; VLDLR; CLU; CETP; LCAT
GO:0034358	1.50E-04	0.0779	16768	594	34	7	CC	plasma lipoprotein particle	APOB; APOH; LIPC; VLDLR; CLU; CETP; LCAT
GO:0030141	3.50E-04	0.1769	16768	594	121	13	CC	stored secretory granule	PCSK2; SCG5; AKAP3; LTF; HEXB; FGB; DBH; CAMP; CTSG; IL1B; VWF; SYT9; PLAT
GO:0044454	4.20E-04	0.2077	16768	594	123	13	CC	nuclear chromosome part	H3F3A; BLM; JUN; ORC6L; CITED2; SUZ12; XRCC5; RAD50; SYN1; MCM7; TERF1; NBN; DNMT3L
GO:0005625	4.60E-04	0.2318	16768	594	320	24	CC	soluble fraction	PCSK2; HEXB; FGB; DBH; SNX9; EPHX2; PDE11A; PPAT; YWHAZ; CAV3; IL13RA2; COMT; NKX2-1; CAPN2; GOT1; PPP2CA; GYS2; HRAS; FBLN1; MAP1B; DUSP1; CRHPB; IGFALS; ADRBK1
GO:0042598	6.10E-04	0.3017	16768	594	250	20	CC	vesicular fraction	CYP2C9; JPH2; APOB; TSC1; IGF1R; CYB5A; SNX9; F10; CHPT1; DLST; BCL2; CAV3; CYP4F12; COMT; CYP1A2; PON3; ACSL1; HRAS; CYP2B6; SRD5A2
GO:0030424	6.60E-04	0.3283	16768	594	129	13	CC	axon	AR; RXRA; SNCA; DBH; CADM1; CTNNA2; STAT1; NEFH; DRD2; NCAM1; MAP1B; ADRBK1; NDEL1
GO:0045202	7.80E-04	0.3875	16768	594	293	22	CC	synapse	DLG1; SV2A; CAMK2A; HOMER1; ENAH; CADM1; GRIK5; CAV3; MAG12; DLGAP4; SYN1; SNTB2; BCAN; ITSN1; GABRR2; SYT9; CHRM2; ACHE; GRIN2C; ADRBK1;
GO:0030132	8.10E-04	0.4033	16768	594	6	3	CC	clathrin coat of coated pit	PICALM; CLTB; CLTCL1
GO:0005730	8.40E-04	0.4151	16768	594	733	43	CC	nucleolus	SMARCC2; SP1; AKAP8; TSG101; POLR1A; POLR1E; BLM; SMAD4; LEF1; RBM9; UBTB; EIF3L; MLF1; ADAP1; HNRNPA1; KEAP1; MYBL1; CEBPG; CEBPE; CSTF2; ILF3; NR2C2; BRD8; HIF1A; RPS3A; FOS; FGF22; STAT3; RBMSA; STAT1; ING2; TP53; EIF6; POLR2H; TAF7; ETV4; NBN; MKI67; SIN3A; RAD21; NPM1; SIRI1; ATF9
GO:0030659	8.70E-04	0.4321	16768	594	202	17	CC	cytoplasmic vesicle membrane	SV2A; CAMK2A; CAMK2B; HIP1R; APOB; SNCA; DBH; AP2B1; RPH3AL; SYN1; AP3S1; SNTB2; BCAN; SYT9; CLTB; SREBF1; CLTCL1
GO:0009986	9.10E-04	0.4517	16768	594	221	18	CC	cell surface	F3; HHIP; APOH; RARA; SCARB1; RALA; LPAR1; CAV3; GHR; CTSG; FGF22; TGFA; SDC1; TNF; ATP5B; FSHR; PLAT; IGF2R
GO:0005792	0.001	0.5372	16768	594	243	19	CC	microsome	CYP2C9; JPH2; APOB; TSC1; IGF1R; CYB5A; SNX9; F10; CHPT1; DLST; BCL2; CYP4F12; COMT; CYP1A2; PON3; ACSL1; HRAS; CYP2B6; SRD5A2
GO:0005681	0.001	0.539	16768	594	136	13	CC	spliceosomal complex	DDX41; GEMIN5; RBMX; HNRNPA1; SNRNP200; PRPF3; RBMSA; RHEB; PABPC1; BAT1; HNRNPC; SNRPA; SNRPE
GO:0032302	0.0012	0.6189	16768	594	2	2	CC	MutSbeta complex	MSH2; MSH3
GO:0034364	0.0013	0.658	16768	594	24	5	CC	high-density lipoprotein particle	APOH; LIPC; CLU; CETP; LCAT
GO:0012506	0.0016	0.8124	16768	594	214	17	CC	vesicle membrane	SV2A; CAMK2A; CAMK2B; HIP1R; APOB; SNCA; DBH; AP2B1; RPH3AL; SYN1; AP3S1; SNTB2; BCAN; SYT9; CLTB; SREBF1; CLTCL1
GO:0000781	0.0017	0.8674	16768	594	37	6	CC	chromosome, telomeric region	BLM; PTGES3; XRCC5; RAD50; TERF1; NBN
GO:0030139	0.002	0.9998	16768	594	38	6	CC	endocytic vesicle	EGFR; SFTPD; RALA; LPAR1; ITSN1; IGF2R
GO:0000152	0.0023	1	16768	594	27	5	CC	nuclear ubiquitin ligase complex	ANAPC5; ANAPC7; BRCA1; CDC16; CDC23
GO:0031983	0.0023	1	16768	594	39	6	CC	vesicle lumen	APOB; F5; HGF; FGB; DBH; IGF1
GO:0005886	0.003	1	16768	594	3063	135	CC	plasma membrane	PPAP2A; L1CAM; DLG1; CAMK2A; CAMK2B; F3; JPH2; HHIP; TSG101; ITGA3; RIT2; APOB; DRP2; DSP; KCNH2; ITGAV; SMAD7; LEPR; BDKRB2; F5; APBA2; EGFR; IGF1R; NGFR; JAG1; NOS1; SNCA; AVPR1A; CATSPER1; PKP2; FGB; HOMER1; ADCY1; SCARB1; GNG2; RHO; MAPK10; VLDLR; SNX9; CNTN1; AP2B1; TIRAP; KCNK3; F10; EPOR; RALA; IL1RAP; ADAP1; CADM1; NTF3; MTHFS; COL17A1; DLST; GRIK5; STX6; F2RL3; LPAR1; SLC5A5; VIPR1; PRKCD; SMAD3; CTNNA2; CAV3; GHR; MAG13; MAG12; TRPV4; ERBB4; CTSG; ADCY5; PPF1BP1; GNAO1; PLCB2; SMURF1; SMURF2; NT5E; KIR3DL2; KIR3DL3; LCT; ESR1; CCR4; STAT3; ICAM3; EFNA5; EFNA4; COMT; LGALS3; RHEB; ASAP2; ANTXR2; ZMYND19; PPL; PDPK1; PKN1; DRD2; HTR1A; PICALM; ALPL; KCNE2; KCNE1; ITSN1; GNB2L1; CAPN2; GABRR2; RAPIA; PPP2CA; MST1R; VDACL1; TGFA; PLXNB3; HTR1B; CHRM2; HRAS; MPL; TNF; CLDN11; CLDN17; EPHA8; CLDN19; EPHA3; EPHA2; SDCBP; GNRHR; ATP5B; NCAM1; FZD6; MAP1B; CACNB2; ACHE; ADAM12; GRIN2C; DGKQ; ADRBK1; FSHR; PENT
GO:0016604	0.0033	1	16768	594	191	15	CC	nuclear body	HIPK2; BLM; GEMIN5; SON; WT1; PRPF3; DAXX; NONO; SFPQ; RBMSA; TP53; BAT1; TGS1; DGKQ; NPM1
GO:0030054	0.0033	1	16768	594	520	31	CC	cell junction	DLG1; SV2A; CAMK2A; DSP; SMAD7; AFAP1; PKP3; PKP2; HOMER1; ENAH; CADM1; COL17A1; GRIK5; KEAP1; CTNNA2; MAG13; MAG12; SYN1; SNTB2; PPL; ITSN1; GABRR2; SYT9; CHRM2; SDC1; CLDN11; CLDN17; CLDN19; SDCBP; NPM1; GNAO1; GNA01
GO:0045120	0.0044	1	16768	594	10	3	CC	pronucleus	AKAP8; BLM; RAD50
GO:0031226	0.0044	1	16768	594	1036	53	CC	intrinsic to plasma membrane	PPAP2A; F3; HHIP; FZD10; ITGAV; BDKRB2; IGF1R; NGFR; JAG1; AVPR1A; HOMER1; SCARB2; SCARB1; RHO; KCNK3; F10; EPOR; IL1RAP; COL17A1; F2RL3; LPAR1; VIPR1; GHR; KIR3DL2; LCT; CCR4; ICAM3; EFNA5; EFNA4; AMHR2; DRD2; HTR1A; NTRK2; NTRK3; GABRR2; MST1R; SLC4A1; HTR1B; CHRM2; SDC1; MPL; TNF; EPHA8; EPHA3; EPHA2; GNRHR; FZD6; CACNB2; G0LM1; FADS2; GRIN2C; PTPRS; IGF2R

GO:0005911	0.0046	1	16768	594	179	14	CC	cell-cell junction	DLG1; DSP; SMAD7; PKP3; PKP2; CADM1; COL17A1; KEAP1; CTNNA2; MAGI3; PPL; CLDN11; CLDN17; CLDN19
GO:0030057	0.0048	1	16768	594	20	4	CC	desmosome	DSP; PKP3; PKP2; PPL
GO:0005669	0.0048	1	16768	594	20	4	CC	transcription factor TFIID complex	TAF11; TAF9B; TP53; TAF7
GO:0030658	0.0068	1	16768	594	22	4	CC	transport vesicle membrane	DBH; RPH3AL; SNTB2; SREBF1
GO:0005891	0.0068	1	16768	594	22	4	CC	voltage-gated calcium channel complex	CACNG6; CACNA1F; CACNA2D1; CACNB2
GO:0005901	0.0073	1	16768	594	49	6	CC	caveola	IGF1R; SCARB1; CAV3; ERBB4; EFNA5; ADRBK1
GO:0005657	0.0076	1	16768	594	12	3	CC	replication fork	BLM; TP53; NBN
GO:0030662	0.0079	1	16768	594	65	7	CC	coated vesicle membrane	SV2A; HIP1R; APOB; SYN1; BCAN; SYT9; SREBF1
GO:0005680	0.008	1	16768	594	23	4	CC	anaphase-promoting complex	ANAPC5; ANAPC7; CDC16; CDC23
GO:0060205	0.0093	1	16768	594	37	5	CC	cytoplasmic membrane-bounded vesicle lumen	F5; HGF; FGB; DBH; IGF1
GO:0043005	0.0104	1	16768	594	299	19	CC	neuron projection	AR; RXRA; IGF1R; PGR; NOS1; SNCA; DBH; CADM1; CTNNA2; ESR2; ESR1; STAT1; NEFH; DRD2; CHRM2; NCAM1; MAP1B; ADRBK1; NDEL1
GO:0000785	0.0105	1	16768	594	139	11	CC	chromatin	SMARCC2; H3F3A; JUN; FANCC; CITED2; DSCC1; SUZ12; CREB1; DAXX; MCM7; DNMT3I
GO:0044456	0.0113	1	16768	594	239	16	CC	synapse part	L1CAM; DLG1; CAMK2A; ERC1; HOMER1; CADM1; GRIK5; YWHAZ; DLGAP4; ERBB4; SYN1; PICALM; GABRR2; CHRM2; MAP1B; GRIN2C
GO:0005887	0.0113	1	16768	594	1015	50	CC	integral to plasma membrane	PPAP2A; HHIP; FZD10; ITGAV; BDKRB2; IGF1R; NGFR; JAG1; AVPR1A; HOMER1; SCARB2; SCARB1; RHO; KCNK3; EPOR; IL1RAP; COL17A1; F2RL3; LPAR1; VIPR1; GHR; KIR3DL2; LCT; CCR4; ICAM3; EFNA4; AMHR2; DRD2; HTR1A; NTRK2; NTRK3; GABRR2; MST1R; SLC4A1; HTR1B; CHRM2; SDC1; MPL; TNF; EPHA8; EPHA3; EPHA2; GNRHR; FZD6; CACNB2; GOLM1; FADS2; GRIN2C; PTPRS; IGF2R
GO:0030870	0.0116	1	16768	594	5	2	CC	Mre11 complex	RAD50; NBN
GO:0031304	0.0116	1	16768	594	5	2	CC	intrinsic to mitochondrial inner membrane	PPOX; IMMT
GO:0033256	0.0116	1	16768	594	5	2	CC	I-kappaB/NF-kappaB complex	NFKB1; NFKB2
GO:0033276	0.012	1	16768	594	14	3	CC	transcription factor TFIIIC complex	TAF9B; TRRAP; TAF7
GO:0005852	0.012	1	16768	594	14	3	CC	eukaryotic translation initiation factor 3 complex	EIF3H; EIF3L; EIF3G
GO:0005576	0.0134	1	16768	594	2027	90	CC	extracellular region	SCG5; MFAP1; IFNA10; CNDP1; HHIP; APOD; APOB; MST1; APOH; COL4A4; COL4A3; GPX5; ACP6; LEPR; LTF; ACP; F5; IFNA21; EGFR; DEFA1; JAG1; CYR61; HGF; WNT16; SFTPD; LIF; COL11A2; WNT10A; FGB; LIPC; LPO; DBH; PROS1; MASP1; IGF1; IGFBP6; F10; EPOR; SST; IL1RAP; NTF3; CLU; COL17A1; AGRP; PRSS2; CAMP; MMP8; GHR; CETP; BMP8A; MASP2; XDH; FCN2; CTSL1; FGF22; FGF23; IL1B; IFNB1; LCAT; EFNA4; SFRP2; WNT2; IL6; ELSBP1; ANTXR2; GDF5; BCAN; AMY2B; VWF; PON3; WNT9B; C1S; BMP5; TGFA; FGF5; FGF4; SHBG; TNF; FBLN1; ACAN; EPHA3; NCAM1; CRHBP; ACHE; IGFALS; GDF9; CHGA; ADAM12; SVEP1; PLAT
GO:0016323	0.0136	1	16768	594	107	9	CC	basolateral plasma membrane	DLG1; DSP; EGFR; ANK3; CADM1; CTNNA2; ERBB4; SLC4A1; CLDN19
GO:0030118	0.0146	1	16768	594	15	3	CC	clathrin coat	PICALM; CLTB; CLTCL1
GO:0005905	0.0158	1	16768	594	42	5	CC	coated pit	HIP1R; VLDLR; AP2B1; PICALM; CLTCL1
GO:0019717	0.0162	1	16768	594	92	8	CC	synaptosome	ABAT; SNCA; CADM1; MAGI2; GNAO1; FOS; ZMYND19; ITSN1
GO:0030665	0.0163	1	16768	594	58	6	CC	clathrin coated vesicle membrane	SV2A; HIP1R; APOB; SYN1; BCAN; SYT9
GO:0030122	0.017	1	16768	594	6	2	CC	AP-2 adaptor complex	EGFR; PICALM
GO:0030877	0.017	1	16768	594	6	2	CC	beta-catenin destruction complex	GSK3B; AXIN1

GO:0032300	0.017	1	16768	594	6	2	CC	mismatch repair complex	MSH2; MSH3
GO:0042382	0.017	1	16768	594	6	2	CC	paraspeckles	NONO; SFPQ
GO:0005587	0.017	1	16768	594	6	2	CC	collagen type IV	COL4A4; COL4A3
GO:0000784	0.0175	1	16768	594	16	3	CC	nuclear chromosome, telomeric region	XRCC5; RAD50; NBN
GO:0034704	0.0205	1	16768	594	30	4	CC	calcium channel complex	CACNG6; CACNA1F; CACNA2D1; CACNB2
GO:0030119	0.0229	1	16768	594	31	4	CC	AP-type membrane coat adaptor complex	EGFR; AP2B1; AP3S1; PICALM
GO:0030935	0.0233	1	16768	594	7	2	CC	sheet-forming collagen	COL4A4; COL4A3
GO:0070419	0.0233	1	16768	594	7	2	CC	nonhomologous end joining complex	PRKDC; XRCC5
GO:0043228	0.0239	1	16768	594	2051	89	CC	non-membrane-bounded organelle	SMARCC2; SP1; AKAP8; TSG101; POLR1A; POLR1E; HIP1R; DRP2; H3F3A; DSP; BLM; CSNK1A1; SMAD4; AKAP12; LEF1; RBM9; AFAP1; UBTf; NOS1; SNCA; JUN; ANK3; MLPH; EIF3L; CENPJ; TPR; MLF1; ADAP1; ENAH; HNRNP1; KEAP1; CDK7; ITGB3BP; MYBL1; CEBPG; CEBPE; ARHGAP1; CTNNA2; CSTF2; ILF3; NR2C2; BRD8; HIF1A; XRCC5; CDC16; RPS3A; FOS; RAD50; FGF22; STAT3; RBM8A; STAT1; ING2; IGBP1; TP53; SNTB2; EIF6; WASF2; PPL; HADHA; MICAL1; PPP2CA; PPP2CB; TERF1; SLC4A1; VDACL1; GYS2; POLR2H; TAF7; ETV4; TNFAIP3; SDCBP; ATP5B; MAP1B; NBN; TACC3; PSMB4; MKI67; DGKQ; SIN3A; RAD21; DNMT3L; NDEL1; CLTCL1; NPM1; SUB1; MYO7A; FSD1; ATF2
GO:0043232	0.0239	1	16768	594	2051	89	CC	intracellular non-membrane-bounded organelle	SMARCC2; SP1; AKAP8; TSG101; POLR1A; POLR1E; HIP1R; DRP2; H3F3A; DSP; BLM; CSNK1A1; SMAD4; AKAP12; LEF1; RBM9; AFAP1; UBTf; NOS1; SNCA; JUN; ANK3; MLPH; EIF3L; CENPJ; TPR; MLF1; ADAP1; ENAH; HNRNP1; KEAP1; CDK7; ITGB3BP; MYBL1; CEBPG; CEBPE; ARHGAP1; CTNNA2; CSTF2; ILF3; NR2C2; BRD8; HIF1A; XRCC5; CDC16; RPS3A; FOS; RAD50; FGF22; STAT3; RBM8A; STAT1; ING2; IGBP1; TP53; SNTB2; EIF6; WASF2; PPL; HADHA; MICAL1; PPP2CA; PPP2CB; TERF1; SLC4A1; VDACL1; GYS2; POLR2H; TAF7; ETV4; TNFAIP3; SDCBP; ATP5B; MAP1B; NBN; TACC3; PSMB4; MKI67; DGKQ; SIN3A; RAD21; DNMT3L; NDEL1; CLTCL1; NPM1; SUB1; MYO7A; FSD1; ATF2
GO:0070161	0.0241	1	16768	594	157	11	CC	anchoring junction	DSP; SMAD7; AFAP1; PKP3; PKP2; ENAH; KEAP1; CTNNA2; PPL; SDC1; SDCBP
GO:0042995	0.0254	1	16768	594	652	33	CC	cell projection	AKAP3; AR; TSC1; RXRA; IGF1R; PGR; NOS1; SNCA; CATSPER1; DBH; ENAH; CADM1; CAMP; CTNNA2; ABI3; TRPV4; LCT; ESR2; ESR1; STAT1; WASF2; NEFH; DRD2; ITSN1; ENPP7; CHRM2; SDC1; NCAM1; MAP1B; ADRBK1; GLI2; NFE2L3; NFE2L1
GO:0030532	0.0255	1	16768	594	32	4	CC	small nuclear ribonucleoprotein complex	SNRNP200; BAT1; TGS1; SNRPE
GO:0005741	0.026	1	16768	594	82	7	CC	mitochondrial outer membrane	CYB5A; PI4KB; MCL1; BCL2; ACSL1; VDACL1; DNMLL
GO:0016585	0.0276	1	16768	594	83	7	CC	chromatin remodeling complex	SMARCC2; SMARCA4; ESR1; ING2; TAL1; NCOR1; SIN3A
GO:0030315	0.028	1	16768	594	19	3	CC	T-tubule	CAV3; ESR1; CACNA2D1
GO:0031519	0.028	1	16768	594	19	3	CC	PcG protein complex	SUZ12; YY1; BCOR
GO:0000790	0.029	1	16768	594	49	5	CC	nuclear chromatin	H3F3A; JUN; CITED2; SUZ12; DNMT3L
GO:0005813	0.0294	1	16768	594	122	9	CC	centrosome	KEAP1; ARHGAP1; CDC16; IGBP1; TNFAIP3; TACC3; PSMB4; NDEL1; NPM1
GO:0016580	0.0304	1	16768	594	8	2	CC	Sin3 complex	ING2; SIN3A
GO:0031233	0.0304	1	16768	594	8	2	CC	intrinsic to external side of plasma membrane	F3; F10
GO:0070822	0.0304	1	16768	594	8	2	CC	Sin3-type complex	ING2; SIN3A
GO:0030666	0.0311	1	16768	594	34	4	CC	endocytic vesicle membrane	CAMK2A; CAMK2B; APOB; AP2B1
GO:0043204	0.0311	1	16768	594	34	4	CC	perikaryon	PDE11A; ESR2; ESR1; MAP1B
GO:0000159	0.0321	1	16768	594	20	3	CC	protein phosphatase type 2A complex	BCL2; PPP2CA; PPP2CB

GO:0034361	0.0321	1	16768	594	20	3	CC	very-low-density lipoprotein particle	APOB; APOH; VLDLR
GO:0034385	0.0321	1	16768	594	20	3	CC	triglyceride-rich lipoprotein particle	APOB; APOH; VLDLR
GO:0030136	0.0327	1	16768	594	86	7	CC	clathrin-coated vesicle	HIP1R; CADM1; STX6; VWF; PICALM; CLTCL1; IGF2R
GO:0016605	0.0342	1	16768	594	35	4	CC	PML body	HIPK2; BLM; DAXX; TP53
GO:0042734	0.0342	1	16768	594	35	4	CC	presynaptic membrane	L1CAM; CAMK2A; ERC1; PICALM
GO:0001650	0.0354	1	16768	594	1	1	CC	fibrillar center	EIF3L
GO:0016528	0.0354	1	16768	594	1	1	CC	sarcoplasm	FABP3
GO:0031904	0.0354	1	16768	594	1	1	CC	endosome lumen	APOB
GO:0032144	0.0354	1	16768	594	1	1	CC	4-aminobutyrate transaminase complex	ABAT
GO:0032280	0.0354	1	16768	594	1	1	CC	symmetric synapse	CHRM2
GO:0033193	0.0354	1	16768	594	1	1	CC	Lsd1/2 complex	TAL1
GO:0034359	0.0354	1	16768	594	1	1	CC	mature chylomicron	APOB
GO:0034360	0.0354	1	16768	594	1	1	CC	chylomicron remnant	APOB
GO:0034466	0.0354	1	16768	594	1	1	CC	chromaffin granule lumen	DBH
GO:0042555	0.0354	1	16768	594	1	1	CC	MCM complex	MCM7
GO:0042583	0.0354	1	16768	594	1	1	CC	chromaffin granule	DBH
GO:0043265	0.0354	1	16768	594	1	1	CC	ectoplasm	GYS2
GO:0045092	0.0354	1	16768	594	1	1	CC	interleukin-18 receptor complex	TOLLIP
GO:0045267	0.0354	1	16768	594	1	1	CC	proton-transporting ATP synthase, catalytic core	ATP5B
GO:0005754	0.0354	1	16768	594	1	1	CC	mitochondrial proton-transporting ATP synthase, catalytic core	ATP5B
GO:0005854	0.0354	1	16768	594	1	1	CC	nascent polypeptide-associated complex	NACA
GO:0005895	0.0354	1	16768	594	1	1	CC	interleukin-5 receptor complex	SDCBP
GO:0060342	0.0354	1	16768	594	1	1	CC	photoreceptor inner segment membrane	RHO
GO:0070195	0.0354	1	16768	594	1	1	CC	growth hormone receptor complex	GHR
GO:0008024	0.0354	1	16768	594	1	1	CC	positive transcription elongation factor complex	TAF7
GO:0008275	0.0354	1	16768	594	1	1	CC	gamma-tubulin small complex	CENPJ
GO:0031093	0.0374	1	16768	594	36	4	CC	platelet alpha granule lumen	F5; HGF; FGB; IGF1

GO:0030130	0.0382	1	16768	594	9	2	CC	clathrin coat of trans-Golgi network vesicle	CLTB; CLTCL1
GO:0043205	0.0382	1	16768	594	9	2	CC	fibril	MFAP1; SNCA
GO:0000151	0.0435	1	16768	594	111	8	CC	ubiquitin ligase complex	ANAPC5; ANAPC7; SKP1; WWP1; BRCA1; SMURF2; CDC16; CDC23
GO:0005913	0.0444	1	16768	594	38	4	CC	cell-cell adherens junction	DSP; SMAD7; KEAP1; CTNNA2
GO:0033267	0.0444	1	16768	594	73	6	CC	axon part	L1CAM; ESR1; NEFH; HTR1A; GOT1; CHRM2
GO:0070461	0.0462	1	16768	594	23	3	CC	SAGA-type complex	TAF9B; TRRAP; TAF7
GO:0031091	0.0466	1	16768	594	10	2	CC	platelet alpha granule	FGB; VWF
GO:0030135	0.0469	1	16768	594	93	7	CC	coated vesicle	HIP1R; CADM1; STX6; VWF; PICALM; CLTCL1; IGF2R
GO:0000775	0.0476	1	16768	594	56	5	CC	chromosome, centromeric region	DSCC1; ITGB3BP; PPP2CA; PPP2CB; MKI67
GO:0043235	0.0495	1	16768	594	114	8	CC	receptor complex	ITGA3; ITGAV; SMAD3; GHR; TOLLIP; IL6; SDCBP; GRIN2C
GO:0030027	0.0496	1	16768	594	75	6	CC	lamellipodium	TSC1; ENAH; CTNNA2; ABI3; WASF2; ITSN1
GO:0005515	9.50E-46	9.50E-43	15767	609	8097	479	MF	protein binding	SMARCC2; PPP3R2; PCSK2; SCG5; STK16; P4HA2; HIPK2; L1CAM; DLG1; PIK3CB; SV2A; IFNA10; ARHGAP12; SP1; SP3; CAMK2A; CAMK2B; F3; OSBP1; CNDP1; JPH2; AKAP3; DDX41; AKAP8; AR; HHIP; TSG101; ITGA3; UBE2D2; RIT2; RAB6B; MX1; POLR1A; POLR1E; FZD10; HIP1R; BNIPL; APOD; APOB; XP07; DRP2; APOH; ZIC2; GTF2I; SMG5; HOXB9; SENP2; DSP; BLM; PPARG; PPARG; COL4A4; COL4A3; PPARA; GDI1; ANAPC7; PPID; CSNK1A1; ITGAV; KHK; SIGIRR; ACP6; SMAD9; RALBP1; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; AKAP12; REL; TSC1; SPI1; KIF3A; IRF3; RXRA; LEPR; LTF; LEP1; SRPK1; BDKRB2; APBA2; TP73; GEMIN5; IFNA21; RBM7; ERC1; EGFR; IGF1R; RBM9; ERG; NGFR; ABAT; AFAP1; GF11B; PPF1A1; PDE1A; UBTB; PGR; CNOT3; JAG1; CNOT4; NOS1; CYR61; SNCA; YARS2; JUN; FZD8; HGF; TRIP13; HOXB13; EXOC2; HEXB; CYB5A; RBMX; ANK3; RGS10; MLPH; SFTPD; LIF; AVPR1A; COL11A2; RARA; CATSPER1; DAB1; SON; EIF3H; RARB; EIF3L; RARG; PEA15; NFE2L1; FBNP4; SAG; ORC6L; EIF3G; REL; FGB; CDKN2B; WT1; LIPC; CENPJ; HOMER1; TPR; ADCY1; PTGES3; SCARB2; SCARB1; ELK1; RHO; MAPK10; VLDLR; SNX9; MASP1; CNTN1; USF1; AP2B1; GTF2E1; TIRAP; BMX; ORAI2; TCF4; IGF1; KCNK3; IGFBP6; F10; EPOR; SST; IRF8; NFKB1; CSNK1E; NSD1; WDHV1; RALA; EPHX2; PI4KB; IL1RAP; TCERG1; ZFH3; PGAM1; GMN; MLF1; USF2; SKP1; ADAP1; FANCC; ENAH; CADM1; NTF3; ASCL3; HNRNP1; CITED2; CLU; UHRF1; DLST; STX6; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; LPAR1; DSCC1; MATR3; GTF2H4; TCEB3; MSH2; MSH3; AGRP; USP7; ITGB3BP; PRSS2; SMARCA4; YWHAZ; CEBPA; CEBPG; CEBPE; CEBPD; ARHGAP1; DVL2; ETS1; MED15; SUZ12; RUFY1; PRKCD; SMAD3; MCL1; CTNNA2; ABI3; CSTF2; GOLGB1; ILF3; BCL2; IMMT; TRIM11; WWP1; CAV3; SNRNP200; GHR; CACNA1F; ZFPM2; MAGI3; MAGI2; DLGAP4; EIF4ENIF1; TRPV4; BRCA1; BMP8A; ERBB4; TRIM21; CREB1; NR2C2; BRD7; DZIP3; PRMT5; PPF1BP1; MASP2; KPNA2; GBA; GNAO1; CRX; PLCB2; HIF1A; XRCC5; PRPF3; SMURF1; DAXX; SMURF2; CDC16; NONO; EGR1; XDH; RPH3AL; RPS3A; FCN2; R1CSA; FOS; RAD50; TRRAP; SFPQ; PAX6; NFKB2; PAX8; IL13RA2; ESR2; TOLLIP; ESR1; CTSL1; STK36; FGF22; FGF23; SYN1; LCMT1; YY1; CCR4; IL1B; VPS45; STAT3; RBM8A; STAT1; ZHX2; ZHX3; ZHX1; IFNB1; ICAM3; ING2; MARK3; IGBP1; TAL1; ACACB; LCAT; EFN5; COMT; EIF2C2; LGALS3; TP53; NRBF2; SFRP2; CYP11A2; MYB; WNT2; AGXT; RALYL; IL6; AP3S1; RHEB; ASAP1; ASAP2; SNTB2; ANTXR2; EIF6; MAP2K3; RUNX1T1; TEAD1; CAMLG; WASF2; TFAP2A; NAP1L1; NEFH; GDF5; PPL; PDPK1; POU3F2; AADAT; CEBPB; PRK1; MCM7; TP53BP2; VWF; DUSP12; SQSTM1; DRD2; PON3; HTR1A; PICALM; HBB; NKX2-1; UGP2; ETS2; CACNA2D1; ITSN1; ITSN2; NTRK2; NTRK3; GNB2L1; MICAL1; CAPN2; GABRR2; SYT9; FLN1; RAPIA; SRGAP2; KCTD13; BMP5; SOCS2; PPP2CA; EEF1D; PPP2CB; MST1R; GSK3B; TERF1; SLC4A1; TRIM39; STMN1; POU2F1; PABPC1; ST13; CLTB; MAPKAPK5; VDACL1; TGFA; PLXNB3; HTR1B; ELK4; MED30; CHRM2; GYS2; HRAS; FGF5; FGF4; POLR2H; POLR2J; TAF7; PEX5; SDC1; MPL; TNFAIP3; SHBG; TNF; BAT1; FBLN1; CLDN11; CLDN17; EPHA8; ACAN; CLDN19; EPHA3; EPHA2; SDCBP; ACR; GNRHR; ATP5B; NCOR1; AKR1B10; MAP1B; CACNB2; POLD2; NBN; FGF11; HNRNPC; DUSP1; PCMT1; BCOR; ACHE; SOS1; TACC3; IGFALS; GDF9; STAT5B; STAT5A; SREBF1; TOMM20; MKI67; CHGA; ADAM12; RIPK2; DERA; GRIN2C; DGKQ; ADRBK1; GLI2; FSHR; SIN3A; TRAF5; RAD21; DNMT3L; PLAT; GGT1; NDEL1; DACH1; CLTCL1; SNRPA; NPM1; SNRPE; PTPRS; ATF1; AXIN1; SUB1; NEDD4L; UPF3A; TGIF1; DNML1; ATF6; MYO7A; ATF2; IGF2R

GO:0005488	1.60E-25	1.70E-22	15767	609	####	575	MF	binding	<p>SMARCC2; PPP3R2; PCSK2; SCG5; STK16; P4HA2; HIPK2; LICAM; DLG1; PIK3CB; SV2A; IFNA10; CYP2C9; ARHGFE12; SP1; SP3; CAMK2A; CAMK2B; F3; SULT1E1; OSBP1; CNBP1; JPH2; AKAP3; DDX41; AKAP8; AR; HHP1; TSG101; ITGA3; UBE2D2; RIT2; RAB6B; MX1; POLR1A; POLR1E; FZD10; IFIT3; IFIT1; HIP1R; BNIPL; APOD; APOB; XPO7; DRP2; MST1; APOH; ZIC2; CYP27B1; H3F3A; GTF2I; SMG5; HOXB8; HOXB9; UCK1; SENP2; DSP; BLM; PPARG; PPARC; COL4A4; COL4A3; PPARA; GD11; ANAPC5; ANAPC7; PPID; CSNK1A1; ITGAV; KHK; SIGIRR; TRDM1; PDE6H; ACP6; SMAD9; RALBP1; ASH2L; SMAD4; TLE2; TLE1; SMAD7; SMAD1; PRKDC; TAF11; AKAP12; REL; ADSSL1; TSC1; SPI1; KIF3A; IRF3; RXRA; LEPR; LTF; LEF1; SRPK1; PDE10A; BDKRB2; F5; APBA2; AK7; TP73; GEMIN5; IFNA21; RBM7; ERC1; EGFR; IGF1R; RBM9; ERG; NGFR; ABAT; AFAP1; GF11B; PPF1A1; PDE1A; UBTB; PGR; CNOT3; JAG1; CNOT4; NOS1; CYR61; SNCA; YARS2; JUN; FZD8; HGF; TRIP13; HOXB13; EXOC2; HEXB; CYB5A; RBM3; ANK3; RGS10; MLPH; SFTPD; LIF; AVPR1A; COL11A2; RARA; CATSPER1; PKP3; PKP2; DAB1; SON; EIF3H; RARB; EIF3L; RARG; PEA15; NFE2L1; FBNP4; SAG; ORC6L; EIF3G; RAB1F; REL; FGB; CDKN2B; WT1; LIPC; CENPJ; RBM41; LPO; HOMER1; TPR; PDE8A; ADCY1; DBH; PTGES3; SCARB2; SCARB1; ELK1; RHO; MAPK10; VLDLR; SNX9; PROS1; MASP1; PPOX; CNTN1; USF1; AP2B1; GTF2E1; TIRAP; PRKG1; BMX; ORAI2; TCF4; IGF1; KCNK3; IGF1R; AGMAT; F10; EPOR; CALML3; SST; IRF8; NFKB1; CSNK1E; SARDH; NSD1; WDHV1; RALA; EPHX2; P14KB; IL1RAP; TCEG1; ZFH3; FAP3; PGAM1; GMN; PDE11A; MLF1; USF2; SKP1; ADAP1; CHPT1; FANCC; ENAH; CADM1; NTF3; ASCL3; HNRNP1A1; MTHFS; CITED2; CLU; UHRF1; PDCD5; DLST; STX6; KEAP1; HOXA5; PPAT; CNGA4; HOXA1; CDK7; F2RL3; TAF9B; LPAR1; DSCC1; MATR3; GTF2H4; TCEB3; MSH2; MSH3; AGRP; USP7; ITGB3BP; PRSS2; MYBL1; SMARCA4; YWHAZ; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; ARHGAP1; DVL2; ETS1; MED15; SUZ12; RUFY1; PRKCD; SMAD3; MCL1; CTNNA2; ABI3; CSTF2; GOLGB1; ILF3; MMP8; BCL2; IMMT; PLCD3; TRIM11; WWP1; CAV3; SNRNP200; GHR; CYP4F12; CACNA1F; ZFPM2; MAGI3; MAGI2; DLGAP4; EIF4ENIF1; TRPV4; BRCA1; CETP; BMP8A; ERBB4; PRMT3; TRIM21; CREB1; CTSG; NR2C2; BRD8; BRD7; ADCY5; DZIP3; PRMT5; PPF1B1; MASP2; KPNA2; GBA; GNAO1; CRX; PLCB2; HIF1A; XRCC5; PRPF3; SMURF1; DAXX; SMURF2; CDC16; NONO; EGR1; NT5E; EGR4; XDH; RPH3AL; RPS3A; FCN2; RIC8A; FOS; RAD50; TRRAP; SFPQ; PAX6; NFKB2; PAX2; PAX8; IL13RA2; LCT; ESR2; TOLLIP; ESRI; ACAD8; CTS1; POLE2; STK36; PAX1; FGF22; FGF23; SYN1; LCM1; YY1; CCR4; IL1B; HARS; VPS45; STAT3; RBM8A; STAT1; ZHX2; ZHX3; ZHX1; IFNB1; PDE7B; ICAM3; ING2; MARK3; MNAT2; IGBP1; TAL1; ACACB; LCAT; EFNA5; COMT; EIF2C2; LGALS3; TP53; NRBF2; SFRP2; CYP1A2; MYB; WNT2; AGXT; RALYL; IL6; AP3S1; RHEB; ASAP1; ASAP2; HARS2; SNTB2; ANTXR2; EIF5; EIF6; MAP2K3; RUNX1T1; TEAD1; CAMLG; ZMYND19; KLF11; WASF2; TFAP2A; NAP1L1; AMHR2; NEFH; GDF5; PPL; PDPK1; BCAN; POU3F2; AADAT; AMY2B; CEBPB; PKN1; MCM7; HADHA; TP53BP2; VWF; DUSP12; SQSTM1; DRD2; PON3; RDH14; RDH12; C1S; HTR1A; PICALM; ALPL; ISL1; HBB; DHX16; FBP2; NKX2-1; UGP2; ETS2; CACNA2D1; ITSN1; ITSN2; NTRK2; NTRK3; GNB2L1; MICAL1; CAPN2; GOT1; GABRR2; SYT9; FLI1; RAP1A; SNAPC5; SRGAP2; KCTD13; BMP5; SOCS2; PPP2CA; EEF1D; PPP2CB; MST1R; GSK3B; TERF1; SLC4A1; TRIM39; ACSL1; STMN1; POU2F1; PABPC1; ST13; CLTB; MAPKAPK5; VDACL1; TGFA; PLXNB3; GUCY1A3; HTR1B; NACA; ELK4; MED30; PGM1; CHRM2; GYS2; HRAS; FGF5; FGF4; POLR2H; POLR2K; POLR2J; TAF7; PEX5; ETV4; SDC1; MPL; CDC23; TNFAIP3; SHBG; TNF; BAT1; FBLN1; CLDN11; CLDN17; EPHAS; ACAN; CLDN19; EPHA3; EPHA2; SDCBP; ACR; RBKS; GNRHR; ATP5B; NCOR1; AKR1B10; MAP1B; CACNB2; CYP2B6; POLD2; NRN; RCF11; HNRNP1; DUSP1; DCMT1; CRHRP; BCOR; ACHF; FADS9; ADK</p> <p>SP1; AR; HOXB8; HOXB9; PPARG; PPARC; PPARD; PPARA; ASH2L; SMAD4; SMAD7; SPI1; RXRA; LEF1; ERG; PGR; JUN; HOXB13; RARA; RARB; RARG; NFE2L1; REL; WT1; ELK1; USF1; IRF8; NFKB1; ZFH3; USF2; HOXA5; HOXA1; MSH2; MSH3; CEBPA; CEBPG; CEBPE; CEBPD; ETS1; SMAD3; BCL2; CREB1; NR2C2; CRX; HIF1A; XRCC5; EGR1; FOS; PAX6; PAX2; PAX8; ESR2; ESRI; STAT3; STAT1; ZHX2; ZHX3; ZHX1; TAL1; TP53; POU3F2; CEBPB; ISL1; NKX2-1; ETS2; FLI1; TERF1; POU2F1; ELK4; TAF7; ETV4; TNF; NCOR1; BCOR; STAT5B; SREBF1; GLI2; ATF1; HOXC11; TGIF1; ATF6; ATF2</p> <p>SMARCC2; HIPK2; SP1; SP3; AR; TSG101; GTF2I; HOXB8; HOXB9; PPARG; PPARC; PPARA; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; TAF11; REL; SPI1; IRF3; RXRA; LEF1; TP73; RBM9; ERG; GF11B; UBTB; PGR; CNOT3; JUN; TRIP13; HOXB13; RARA; RARB; RARG; NFE2L1; REL; WT1; PDE8A; ELK1; USF1; GTF2E1; TCF4; IRF8; NFKB1; NSD1; TCEG1; ZFH3; GMN; USF2; ASCL3; CITED2; UHRF1; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; GTF2H4; TCEB3; MYBL1; SMARCA4; CEBPA; CEBPG; CEBPE; CEBPD; ETS1; MED15; SMAD3; ILF3; BCL2; ZFPM2; BRCA1; CREB1; NR2C2; BRD8; CRX; HIF1A; DAXX; EGR1; EGR4; FOS; TRRAP; PAX6; NFKB2; PAX8; ESR2; ESRI; YY1; STAT3; STAT1; ZHX2; ZHX3; ZHX1; IFNB1; ING2; TAL1; TP53; MYB; RUNX1T1; TEAD1; KLF11; TFAP2A; POU3F2; CEBPB; PKN1; ISL1; NKX2-1; ETS2; FLI1; SNAPC5; POU2F1; ELK4; MED30; TAF7; ETV4; TNF; NCOR1; BCOR; HEY1; STAT5B; STAT5A; SREBF1; GLI2; SIN3A; DNMT3L; DACH1; NPM1; NFIC; ATF1; SUB1; HOXC11; TGIF1; ATF6; ATF2</p> <p>SMARCC2; SP1; SP3; AR; TSG101; HOXB9; PPARG; PPARC; PPARD; PPARA; SMAD4; TAF11; RXRA; LEF1; PGR; JUN; RARA; RARB; REL; WT1; ELK1; USF1; TCEG1; USF2; CITED2; CDK7; MYBL1; SMARCA4; CEBPE; SMAD3; ILF3; BCL2; BRCA1; NR2C2; CRX; EGR1; EGR4; TRRAP; NFKB2; PAX8; ESR2; YY1; STAT3; ING2; TP53; MYB; TEAD1; TFAP2A; CEBPB; PKN1; NKX2-1; POU2F1; MED30; TAF7; ETV4; TNF; GLI2; NPM1; SUB1; ATF6; ATF2</p> <p>SMARCC2; HIPK2; AR; TSG101; PPARG; PPARC; PPARD; TLE1; PRKDC; TAF11; IRF3; RXRA; TP73; RBM9; JUN; TRIP13; RARA; RARG; NFE2L1; REL; USF1; NSD1; TCEG1; GMN; USF2; CITED2; CDK7; TAF9B; YWHAZ; CEBPA; CEBPG; ETS1; SMAD3; BCL2; ZFPM2; BRCA1; CREB1; NR2C2; BRD7; HIF1A; DAXX; TRRAP; NFKB2; ESR2; ESRI; STK36; YY1; STAT3; IFNB1; TP53; TFAP2A; CEBPB; PKN1; TP53BP2; GSK3B; ELK4; MED30; TAF7; NCOR1; NBN; BCOR; SIN3A; NPM1; SUB1; TGIF1; ATF6; ATF2</p>
GO:0043565	1.10E-21	1.10E-18	15767	609	639	81	MF	sequence-specific DNA binding	<p>SMARCC2; HIPK2; SP1; SP3; AR; TSG101; GTF2I; HOXB8; HOXB9; PPARG; PPARC; PPARA; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; TAF11; REL; SPI1; IRF3; RXRA; LEF1; TP73; RBM9; ERG; GF11B; UBTB; PGR; CNOT3; JUN; TRIP13; HOXB13; RARA; RARB; RARG; NFE2L1; REL; WT1; PDE8A; ELK1; USF1; GTF2E1; TCF4; IRF8; NFKB1; NSD1; TCEG1; ZFH3; GMN; USF2; ASCL3; CITED2; UHRF1; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; GTF2H4; TCEB3; MYBL1; SMARCA4; CEBPA; CEBPG; CEBPE; CEBPD; ETS1; MED15; SMAD3; ILF3; BCL2; ZFPM2; BRCA1; CREB1; NR2C2; BRD8; CRX; HIF1A; DAXX; EGR1; EGR4; FOS; TRRAP; PAX6; NFKB2; PAX8; ESR2; ESRI; YY1; STAT3; STAT1; ZHX2; ZHX3; ZHX1; IFNB1; ING2; TAL1; TP53; MYB; RUNX1T1; TEAD1; KLF11; TFAP2A; POU3F2; CEBPB; PKN1; ISL1; NKX2-1; ETS2; FLI1; TERF1; POU2F1; ELK4; TAF7; ETV4; TNF; NCOR1; BCOR; STAT5B; SREBF1; GLI2; ATF1; HOXC11; TGIF1; ATF6; ATF2</p>
GO:0030528	1.60E-21	1.60E-18	15767	609	1518	136	MF	transcription regulator activity	<p>SMARCC2; HIPK2; SP1; SP3; AR; TSG101; GTF2I; HOXB8; HOXB9; PPARG; PPARC; PPARA; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; TAF11; REL; SPI1; IRF3; RXRA; LEF1; TP73; RBM9; ERG; GF11B; UBTB; PGR; CNOT3; JUN; TRIP13; HOXB13; RARA; RARB; RARG; NFE2L1; REL; WT1; PDE8A; ELK1; USF1; GTF2E1; TCF4; IRF8; NFKB1; NSD1; TCEG1; ZFH3; GMN; USF2; ASCL3; CITED2; UHRF1; KEAP1; HOXA5; HOXA1; CDK7; TAF9B; GTF2H4; TCEB3; MYBL1; SMARCA4; CEBPA; CEBPG; CEBPE; CEBPD; ETS1; MED15; SMAD3; ILF3; BCL2; ZFPM2; BRCA1; CREB1; NR2C2; BRD8; CRX; HIF1A; DAXX; EGR1; EGR4; FOS; TRRAP; PAX6; NFKB2; PAX8; ESR2; ESRI; YY1; STAT3; STAT1; ZHX2; ZHX3; ZHX1; IFNB1; ING2; TAL1; TP53; MYB; RUNX1T1; TEAD1; KLF11; TFAP2A; POU3F2; CEBPB; PKN1; ISL1; NKX2-1; ETS2; FLI1; SNAPC5; POU2F1; ELK4; MED30; TAF7; ETV4; TNF; NCOR1; BCOR; HEY1; STAT5B; STAT5A; SREBF1; GLI2; SIN3A; DNMT3L; DACH1; NPM1; NFIC; ATF1; SUB1; HOXC11; TGIF1; ATF6; ATF2</p>
GO:0016563	8.50E-19	8.60E-16	15767	609	419	60	MF	transcription activator activity	<p>SMARCC2; SP1; SP3; AR; TSG101; HOXB9; PPARG; PPARC; PPARD; PPARA; SMAD4; TAF11; RXRA; LEF1; PGR; JUN; RARA; RARB; REL; WT1; ELK1; USF1; TCEG1; USF2; CITED2; CDK7; MYBL1; SMARCA4; CEBPE; SMAD3; ILF3; BCL2; BRCA1; NR2C2; CRX; EGR1; EGR4; TRRAP; NFKB2; PAX8; ESR2; YY1; STAT3; ING2; TP53; MYB; TEAD1; TFAP2A; CEBPB; PKN1; NKX2-1; POU2F1; MED30; TAF7; ETV4; TNF; GLI2; NPM1; SUB1; ATF6; ATF2</p>
GO:0008134	6.30E-18	6.30E-15	15767	609	517	66	MF	transcription factor binding	<p>SMARCC2; HIPK2; AR; TSG101; PPARG; PPARC; PPARD; TLE1; PRKDC; TAF11; IRF3; RXRA; TP73; RBM9; JUN; TRIP13; RARA; RARG; NFE2L1; REL; USF1; NSD1; TCEG1; GMN; USF2; CITED2; CDK7; TAF9B; YWHAZ; CEBPA; CEBPG; ETS1; SMAD3; BCL2; ZFPM2; BRCA1; CREB1; NR2C2; BRD7; HIF1A; DAXX; TRRAP; NFKB2; ESR2; ESRI; STK36; YY1; STAT3; IFNB1; TP53; TFAP2A; CEBPB; PKN1; TP53BP2; GSK3B; ELK4; MED30; TAF7; NCOR1; NBN; BCOR; SIN3A; NPM1; SUB1; TGIF1; ATF6; ATF2</p>

GO:0003700	3.20E-17	3.20E-14	15767	609	977	95	MF	transcription factor activity	SP1; AR; GTF2I; HOXB8; HOXB9; PPARG; PPAR; PPARA; SMAD9; SMAD4; SMAD7; SMAD1; REL; SPI1; IRF3; RXRA; LEF1; TP73; ERG; PGR; JUN; HOXB13; RARA; RARB; RARG; NFE2L1; RELA; WT1; ELK1; USF1; TCF4; IRF8; NFKB1; ZFXH3; USF2; CITED2; UHRF1; HOXA5; HOXA1; GTF2H4; CEBPA; CEBPG; CEBPE; CEBPD; ETS1; SMAD3; CREB1; NR2C2; BRD8; CRX; HIF1A; EGR1; EGR4; FOS; PAX6; NFKB2; PAX8; ESR2; ESR1; YY1; STAT3; STAT1; ZHX2; ZHX3; ZHX1; TAL1; TP53; RUNX1T1; TEAD1; KLF11; TFAP2A; POU3F2; CEBPB; ISL1; NKX2-1; ETS2; FLI1; SNAPC5; POU2F1; ELK4; TAF7; ETV4; HEY1; STAT5B; STAT5A; SREBF1; GLI2; SIN3A; DACH1; NFIC; ATF1; HOXC11; TGIF1; ATF6; ATF2
GO:0044212	3.20E-16	3.20E-13	15767	609	115	29	MF	DNA regulatory region binding	SP1; AR; PPARG; ASH2L; SMAD4; SMAD7; RXRA; LEF1; JUN; RELA; WT1; NFKB1; ZFXH3; CEBPA; SMAD3; XRCC5; FOS; PAX2; ESR1; TAL1; TP53; NKX2-1; TAF7; TNF; NCOR1; BCOR; SREBF1; GLI2; ATF1
GO:0010843	1.00E-15	1.00E-12	15767	609	111	28	MF	promoter binding	SP1; AR; PPARG; ASH2L; SMAD4; SMAD7; RXRA; JUN; RELA; WT1; NFKB1; ZFXH3; CEBPA; SMAD3; XRCC5; FOS; PAX2; ESR1; TAL1; TP53; NKX2-1; TAF7; TNF; NCOR1; BCOR; SREBF1; GLI2; ATF1
GO:0003702	9.20E-14	9.20E-11	15767	609	239	38	MF	RNA polymerase II transcription factor activity	SP1; GTF2I; PPARA; SMAD1; TAF11; IRF3; RXRA; LEF1; GF11B; JUN; RELA; USF1; GTF2E1; IRF8; TCEG1; ZFXH3; USF2; UHRF1; HOXA1; GTF2H4; CEBPA; ETS1; MED15; SMAD3; ZFPM2; CREB1; HIF1A; FOS; CEBPB; ISL1; NKX2-1; MED30; TAF7; SREBF1; ATF1; HOXC11; ATF6; ATF2
GO:0003677	2.70E-11	2.70E-08	15767	609	2375	153	MF	DNA binding	SMARCC2; SP1; SP3; AKAP8; AR; TSG101; POLR1A; POLR1E; ZIC2; H3F3A; GTF2I; HOXB8; HOXB9; BLM; PPARG; PPAR; PPARA; TRDM1; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; PRKDC; TAF11; REL; SPI1; IRF3; RXRA; LEF1; TP73; EGFR; ERG; GF11B; UBT; PGR; JUN; HOXB13; RARA; SON; RARB; RARG; NFE2L1; ORC6L; RELA; WT1; ELK1; USF1; TCF4; IRF8; NFKB1; ZFXH3; MLF1; USF2; ASCL3; HNRNPA1; CITED2; UHRF1; PDCD5; HOXA5; HOXA1; TAF9B; DSCC1; GTF2H4; TCEB3; MSH2; MSH3; MYBL1; SMARCA4; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; ETS1; SMAD3; ILF3; BCL2; ZFPM2; BRCA1; TRIM21; CREB1; NR2C2; BRD8; CRX; HIF1A; XRCC5; NONO; EGR1; EGR4; FOS; RAD50; SFPQ; PAX6; NFKB2; PAX2; PAX8; ESR2; ESR1; POLE2; PAX1; YY1; STAT3; STAT1; ZHX2; ZHX3; ZHX1; ING2; TAL1; TP53; MYB; RUNX1T1; TEAD1; KLF11; TFAP2A; POU3F2; CEBPB; MCM7; ISL1; NKX2-1; ETS2; FLI1; SNAPC5; TERF1; POU2F1; NACA; ELK4; POLR2K; POLR2J; TAF7; ETV4; TNFAIP3; TNF; ACR; NCOR1; POLD2; NBN; BCOR; HEY1; SOS1; STAT5B; STAT5A; SREBF1; GLI2; SIN3A; DACH1; NFIC; ATF1; SUB1; HOXC11; TGIF1; ATF6; ATF2
GO:0003690	2.50E-10	2.60E-07	15767	609	102	21	MF	double-stranded DNA binding	SP1; SP3; AKAP8; BLM; RXRA; EGFR; JUN; WT1; USF1; USF2; MSH2; MSH3; CEBPG; SMAD3; CREB1; XRCC5; EGR1; FOS; TP53; TERF1; STAT5B
GO:0046983	6.30E-10	6.40E-07	15767	609	563	54	MF	protein dimerization activity	SP1; AR; APOB; SMAD4; BDKRB2; EGFR; ABAT; JUN; HGF; HEXB; NFE2L1; MASP1; USF1; TCF4; KCNK3; EPHX2; USF2; CADM1; MSH2; MSH3; CEBPA; CEBPG; CEBPE; CEBPD; SMAD3; MCL1; BCL2; GHR; CREB1; HIF1A; DAXX; XDH; FOS; STAT3; TP53; AGXT; TFAP2A; AADAT; CEBPB; VWF; PON3; TERF1; SLC4A1; GYS2; POLR2J; SHBG; SDCBP; ACHE; NPM1; ATF1; AXIN1; ATF6; MYO7A; ATF2
GO:0035326	1.20E-09	1.20E-06	15767	609	39	13	MF	enhancer binding	LEF1; JUN; RELA; USF1; IRF8; ZFXH3; USF2; CEBPA; CREB1; HIF1A; CEBPB; NKX2-1; ATF1
GO:0003705	1.20E-09	1.20E-06	15767	609	39	13	MF	RNA polymerase II transcription factor activity, enhancer binding	LEF1; JUN; RELA; USF1; IRF8; ZFXH3; USF2; CEBPA; CREB1; HIF1A; CEBPB; NKX2-1; ATF1
GO:0019899	2.30E-09	2.30E-06	15767	609	584	54	MF	enzyme binding	DLG1; SP1; F3; APOB; SMG5; RALBP1; SMAD7; SMAD1; AKAP12; BDKRB2; ERC1; EGFR; IGF1R; ABAT; SNCA; EXOC2; CYB5A; MLPH; AVPR1A; RELA; CDKN2B; USF1; ZFXH3; PGAM1; GNN; PRKCD; SMAD3; BCL2; CAV3; GHR; MAGI2; BRCA1; KPNA2; HIF1A; RPH3AL; TOLLIP; STAT3; TAL1; TP53; CYP1A2; PDPK1; PKN1; VWF; DUSP12; SQSTM1; GNB2L1; RAP1A; GSK3B; TAF7; NCOR1; BCOR; DGKB; DNMT3A; TGF2R
GO:0043566	3.50E-09	3.60E-06	15767	609	151	24	MF	structure-specific DNA binding	SP1; SP3; AKAP8; BLM; RXRA; EGFR; JUN; WT1; USF1; USF2; HNRNPA1; MSH2; MSH3; CEBPG; SMAD3; CREB1; XRCC5; EGR1; FOS; TP53; MCM7; TERF1; STAT5B; SUB1
GO:0003712	6.50E-09	6.60E-06	15767	609	361	39	MF	transcription cofactor activity	SMARCC2; HIPK2; TSG101; TAF11; IRF3; RXRA; RBM9; JUN; TRIP13; RARA; NFE2L1; NSD1; TCEG1; GNN; CITED2; CDK7; TAF9B; ZFPM2; BRCA1; CREB1; NR2C2; TRRAP; NFKB2; ESR2; YY1; IFNB1; TFAP2A; PKN1; ELK4; MED30; TAF7; NCOR1; BCOR; SIN3A; NPM1; SUB1; TGIF1; ATF6; ATF2
GO:0042802	2.40E-08	2.40E-05	15767	609	677	57	MF	identical protein binding	L1CAM; SP1; BNIPL; SMAD4; SMAD1; EGFR; IGF1R; ABAT; SNCA; TRIP13; HEXB; RELA; MASP1; USF1; KCNK3; EPHX2; USF2; CADM1; MSH2; MSH3; SMARCA4; CEBPA; CEBPE; DVL2; SMAD3; BCL2; GHR; TRPV4; BRCA1; DAXX; SMURF2; NONO; XDH; AGXT; RALYL; POU3F2; AADAT; CEBPB; VWF; PON3; KCTD13; TERF1; SLC4A1; TRIM39; MED30; GYS2; SHBG; TNF; BAT1; CLDN11; CLDN17; CLDN19; HNRNPC; PCMT1; ACHE; NPM1; AXIN1
GO:0004879	5.90E-08	5.90E-05	15767	609	52	13	MF	ligand-dependent nuclear receptor activity	AR; PPARG; PPAR; PPARA; RXRA; PGR; RARA; RARB; RARG; NR2C2; BRD8; ESR2; ESR1

GO:0003676	1.90E-07	1.90E-04	15767	609	3348	182	MF	nucleic acid binding	SMARCC2; SP1; SP3; DDX41; AKAP8; AR; TSG101; POLR1A; POLR1E; ZIC2; H3F3A; GTF2I; HOXB8; HOXB9; BLM; PPARG; PPAR; PPARA; TRDMT1; SMAD9; ASH2L; SMAD4; SMAD7; SMAD1; PRKDC; TAF11; REL; SPI1; IRF3; RXRA; LEF1; TP73; GEMIN5; RBM7; EGFR; RBM9; ERG; GFI1B; UBT; PGR; CNOT4; JUN; HOXB13; RBM; RARA; SON; EIF3H; RARB; EIF3L; RARG; NFE2L1; ORC6L; EIF3G; REL; WT1; RBM41; ELK1; USF1; TCF4; IRF8; NFKB1; ZFXH3; MLF1; USF2; ASCL3; HNRNPA1; CITED2; UHRF1; PDCD5; HOXA5; HOXA1; TAF9B; DSCC1; MATR3; GTF2H4; TCEB3; MSH2; MSH3; MYBL1; SMARCA4; ZNF7; CEBPA; CEBPG; CEBPE; CEBPD; ETS1; SMAD3; CSTF2; ILF3; BCL2; SNRNP200; ZFPM2; BRCA1; TRIM21; CREB1; NR2C2; BRD8; DZIP3; CRX; HIF1A; XRCC5; NONO; EGR1; EGR4; RPS3A; FOS; RAD50; SFPQ; PAX6; NFKB2; PAX2; PAX8; ESR2; ESR1; POLE2; PAX1; YY1; STAT3; RBM8A; STAT1; ZHX2; ZHX3; ZHX1; ING2; TAL1; EIF2C2; TP53; MYB; RALYL; EIF5; EIF6; RUNX1T1; TEAD1; KLF11; TFAP2A; POU3F2; CEBPB; MCM7; ISL1; DHX16; NKX2-1; ETS2; FLI1; SNAPC5; EEF1D; TERF1; POU2F1; PABPC1; NACA; ELK4; POLR2K; POLR2J; TAF7; ETV4; TNFAIP3; TNF; BAT1; ACR; NCOR1; POLD2; NBN; HNRNPC; BCOR; HEY1; SOS1; STAT5B; STAT5A; SREBF1; GLI2; SIN3A; DACH1; SNRPA; NPM1; SNRPE; NFIC; ATF1; SUB1; HOXC11; UPF3A; TGIF1; ATF6; ATF2
GO:0008022	2.20E-07	2.20E-04	15767	609	147	21	MF	protein C-terminus binding	DLG1; SP1; TCF4; KCNK3; CADM1; CDK7; MSH2; USP7; ITGB3BP; PRKDC; TRIM11; CAV3; XRCC5; PPP2CA; PPP2CB; SLC4A1; PABPC1; HRAS; PEX5; SDC1; MKI67
GO:0003707	2.40E-07	2.40E-04	15767	609	49	12	MF	steroid hormone receptor activity	AR; PPARG; PPAR; RXRA; PGR; RARA; RARB; RARG; NR2C2; ESR2; ESR1
GO:0005071	1.20E-06	0.0012	15767	609	11	6	MF	transmembrane receptor protein serine/threonine kinase signaling protein activity	SMAD9; SMAD4; SMAD7; SMAD1; SMAD3; AMHR2
GO:0005102	2.00E-06	0.0021	15767	609	927	65	MF	receptor binding	LICAM; IFNA10; ARHGEF12; AR; APOB; PPARG; COL4A3; SMAD7; TAF11; RXRA; BDKRB2; IFNA21; IGF1R; PGR; JAG1; HGF; LIF; AVPR1A; RARA; RARG; FGB; IGF1; SST; NSD1; RALA; CADM1; NTF3; CDK7; AGRP; SMAD3; BRCA1; BMP8A; GNAO1; DAXX; FCN2; ESR2; TOLLIP; FGF22; FGF23; IL1B; IFNB1; ICAM3; EFN5; WNT2; IL6; GDF5; PDPK1; PKN1; VWF; SQSTM1; GNB2L1; BMP5; SOCS2; TGFA; MED30; FGF5; FGF4; TAF7; TNF; SDCBP; ATP5B; FGF11; GDF9; STAT5B; ADRBK1
GO:0046982	2.70E-06	0.0027	15767	609	199	23	MF	protein heterodimerization activity	APOB; BDKRB2; EGFR; JUN; HGF; HEXB; USF1; TCF4; KCNK3; USF2; CEBPA; CEBPG; CEBPE; MCL1; BCL2; HIF1A; FOS; TP53; CEBPB; TERF1; SDCBP; NPM1; ATF1
GO:0042562	3.70E-06	0.0037	15767	609	52	11	MF	hormone binding	AR; LEPR; IGF1R; PGR; AVPR1A; GHR; ESR2; ESR1; AMHR2; SHBG; CRHBP
GO:0046332	9.70E-06	0.0098	15767	609	47	10	MF	SMAD binding	HIPK2; SMAD4; SMAD7; SMAD1; JUN; SMAD3; SMURF1; SMURF2; FOS; AXIN1
GO:0003713	1.00E-05	0.0101	15767	609	215	23	MF	transcription coactivator activity	SMARCC2; TSG101; TAF11; RXRA; JUN; RARA; TCERG1; CITED2; CDK7; BRCA1; NR2C2; TRRAP; NFKB2; ESR2; YY1; TFAP2A; PKN1; MED30; TAF7; NPM1; SUB1; ATF6; ATF2
GO:0005072	1.80E-05	0.0182	15767	609	10	5	MF	transforming growth factor beta receptor, cytoplasmic mediator activity	SMAD9; SMAD4; SMAD7; SMAD1; SMAD3
GO:0070411	1.80E-05	0.0182	15767	609	10	5	MF	I-SMAD binding	SMAD4; SMAD7; SMAD1; SMURF1; AXIN1
GO:0070412	1.80E-05	0.0182	15767	609	10	5	MF	R-SMAD binding	SMAD4; JUN; SMAD3; SMURF1; FOS
GO:0003708	3.10E-05	0.0312	15767	609	6	4	MF	retinoic acid receptor activity	RXRA; RARA; RARB; RARG
GO:0016564	3.10E-05	0.0321	15767	609	329	29	MF	transcription repressor activity	HIPK2; SP3; TSG101; PPARG; PPAR; RBM9; JUN; RARA; REL; WT1; NSD1; ZFXH3; GMN; CITED2; TAF9B; SMAD3; ILF3; ZFPM2; DAXX; YY1; IFNB1; POU2F1; TAF7; TNF; NCOR1; BCOR; SIN3A; DNMT3L; TGIF1
GO:0019904	3.40E-05	0.0349	15767	609	382	32	MF	protein domain specific binding	AR; PPARA; ERC1; RARA; SON; WT1; CENPJ; GMN; MLF1; ENAH; CADM1; CITED2; YWHAZ; CEBPA; ARHGAP1; BCL2; TRIM11; GHR; DLGAP4; RPH3AL; IL1B; TP53BP2; SQSTM1; MICAL1; PPP2CB; POLR2J; TACC3; ADAM12; RIPK2; GRIN2C; AXIN1; MYO7A
GO:0004714	3.40E-05	0.0351	15767	609	65	11	MF	transmembrane receptor protein tyrosine kinase activity	EGFR; IGF1R; ERBB4; EFNA4; NTRK2; NTRK3; MST1R; EPHA8; EPHA3; EPHA2; IGF2R
GO:0051427	3.50E-05	0.0356	15767	609	89	13	MF	hormone receptor binding	PPARG; TAF11; RXRA; RARG; NSD1; CDK7; BRCA1; DAXX; PKN1; SOCS2; MED30; TAF7; STAT5B

GO:0035257	4.10E-05	0.0419	15767	609	78	12	MF	nuclear hormone receptor binding	PPARG; TAF11; RXRA; RARG; NSD1; CDK7; BRCA1; DAXX; PKN1; MED30; TAF7; STAT5B
GO:0016772	4.20E-05	0.0422	15767	609	917	60	MF	transferase activity, transferring phosphorus-containing groups	STK16; HIPK2; DLG1; PIK3CB; CAMK2A; CAMK2B; POLR1A; POLR1E; UCK1; CSNK1A1; KCNH2; KHK; PRKDC; SRPK1; AK7; EGFR; IGF1R; PTGES3; MAPK10; PRKG1; BMX; CSNK1E; PI4KB; CHTP1; CDK7; GTF2H4; PRKCD; MAG13; ERBB4; TRRAP; POLE2; STK36; MARK3; NMNAT2; EFNA4; MAP2K3; AMHR2; PDPK1; PKN1; UGP2; NTRK2; NTRK3; MST1R; GSK3B; MAPKAPK5; TGFA; POLR2H; POLR2K; POLR2J; EPHA8; EPHA3; EPHA2; RBKS; POLD2; ADK; RIPK2; PAPSS1; DGKQ; ADRBK1; IGF2R
GO:0042803	4.50E-05	0.046	15767	609	370	31	MF	protein homodimerization activity	SP1; SMAD4; ABAT; HEXB; MASP1; USF1; KCNK3; EPHX2; USF2; CADM1; MSH2; MSH3; CEBPA; CEBPE; SMAD3; BCL2; GHR; DAXX; XDH; AGXT; AADAT; CEBPB; VWF; PON3; TERF1; SLC4A1; GYS2; SHBG; ACHE; NPM1; AXIN1
GO:0042578	6.80E-05	0.0684	15767	609	343	29	MF	phosphoric ester hydrolase activity	PPAP2A; DLG1; PDE6H; ACP6; PDE10A; ACPT; BDKRB2; ACP; PDE1A; PDE8A; PGAM1; PDE11A; PLCD3; PLCB2; NTSE; PDE7B; DUSP14; DUSP12; PON3; ALPL; FBP2; ENPP7; PPP2CA; PPP2CB; G6PC2; DUSP1; SGPP1; INPP1; PTPRS
GO:0019199	6.90E-05	0.0695	15767	609	82	12	MF	transmembrane receptor protein kinase activity	EGFR; IGF1R; ERBB4; EFNA4; AMHR2; NTRK2; NTRK3; MST1R; EPHA8; EPHA3; EPHA2; IGF2R
GO:0032403	7.00E-05	0.0711	15767	609	243	23	MF	protein complex binding	PCSK2; L1CAM; COL4A3; SMAD7; IGF1R; RELA; IGF1; CDK7; MSH2; YWHAZ; CEBPA; CAV3; MAGI2; GNAO1; SMURF1; ESR1; ICAM3; ING2; LGALS3; PDPK1; VWF; MAP1B; ATF1
GO:0047485	1.30E-04	0.1358	15767	609	75	11	MF	protein N-terminus binding	TAF11; TSC1; RELA; SMARCA4; DAXX; TP53; VWF; PEX5; SDCBP; NBN; GRIN2C
GO:0043121	1.30E-04	0.137	15767	609	8	4	MF	neurotrophin binding	NGFR; NTF3; NTRK2; NTRK3
GO:0031406	1.40E-04	0.1424	15767	609	144	16	MF	carboxylic acid binding	P4HA2; PPARG; PPAR; NOS1; SNCA; RARA; DBH; FABP3; MTHFS; DLST; ACACB; AGXT; HADHA; GOT1; ALDH6A1; IGF2R
GO:0042826	1.40E-04	0.147	15767	609	41	8	MF	histone deacetylase binding	SP1; USF1; GMN; KPNA2; TAL1; PKN1; NCOR1; BCOR
GO:0008144	1.50E-04	0.1591	15767	609	64	10	MF	drug binding	CYP2C9; PPARG; PPAR; PPARA; PPID; DRD2; HTR1A; HTR1B; CHR2; ACR
GO:0003704	1.70E-04	0.1756	15767	609	42	8	MF	specific RNA polymerase II transcription factor activity	PPARA; RXRA; GFI1B; CEBPA; SMAD3; CREB1; FOS; NKX2-1
GO:0008083	2.20E-04	0.2245	15767	609	165	17	MF	growth factor activity	JAG1; HGF; LIF; IGF1; NTF3; BMP8A; FGF22; FGF23; IL1B; IL6; GDF5; BMP5; TGFA; FGF5; FGF4; FGF11; GDF9
GO:0033293	2.30E-04	0.2353	15767	609	55	9	MF	monocarboxylic acid binding	PPARG; PPAR; SNCA; RARA; FABP3; ACACB; HADHA; ALDH6A1; IGF2R
GO:0004114	2.40E-04	0.2417	15767	609	24	6	MF	3',5'-cyclic-nucleotide phosphodiesterase activity	PDE6H; PDE10A; PDE1A; PDE8A; PDE11A; PDE7B
GO:0016773	2.70E-04	0.2805	15767	609	717	47	MF	phosphotransferase activity, alcohol group as acceptor	STK16; HIPK2; PIK3CB; CAMK2A; CAMK2B; UCK1; CSNK1A1; KCNH2; KHK; PRKDC; SRPK1; EGFR; IGF1R; MAPK10; PRKG1; BMX; CSNK1E; PI4KB; CDK7; GTF2H4; PRKCD; ERBB4; TRRAP; STK36; MARK3; EFNA4; MAP2K3; AMHR2; PDPK1; PKN1; NTRK2; NTRK3; MST1R; GSK3B; MAPKAPK5; TGFA; POLR2H; POLR2J; EPHA8; EPHA3; EPHA2; RBKS; RIPK2; PAPSS1; DGKQ; ADRBK1; IGF2R
GO:0008289	2.90E-04	0.2959	15767	609	410	31	MF	lipid binding	F3; SULT1E1; AR; HIP1R; APOD; APOB; APOH; PPARG; PPAR; PPARA; RXRA; PGR; SNCA; RARA; SCARB1; SNX9; F10; FABP3; CHTP1; RUFY1; CETP; PLCB2; ESR2; ESR1; HADHA; PICALM; SHBG; MAP1B; ALDH6A1; PEMT; IGF2R
GO:0004112	3.00E-04	0.3078	15767	609	25	6	MF	cyclic-nucleotide phosphodiesterase activity	PDE6H; PDE10A; PDE1A; PDE8A; PDE11A; PDE7B
GO:0016301	3.20E-04	0.3228	15767	609	782	50	MF	kinase activity	STK16; HIPK2; DLG1; PIK3CB; CAMK2A; CAMK2B; UCK1; CSNK1A1; KCNH2; KHK; PRKDC; SRPK1; AK7; EGFR; IGF1R; MAPK10; PRKG1; BMX; CSNK1E; PI4KB; CDK7; GTF2H4; PRKCD; MAG13; ERBB4; STK36; MARK3; EFNA4; MAP2K3; AMHR2; PDPK1; PKN1; NTRK2; NTRK3; MST1R; GSK3B; MAPKAPK5; TGFA; POLR2H; POLR2J; EPHA8; EPHA3; EPHA2; RBKS; ADK; RIPK2; PAPSS1; DGKQ; ADRBK1; IGF2R
GO:0051059	3.50E-04	0.3575	15767	609	17	5	MF	NF-kappaB binding	PPARD; RELA; TP53BP2; GSK3B; NPM1
GO:0003714	4.50E-04	0.4598	15767	609	144	15	MF	transcription corepressor activity	HIPK2; TSG101; RBM9; RARA; NSD1; GMN; CITED2; TAF9B; ZFPM2; YY1; IFNB1; NCOR1; BCOR; SIN3A; TGIF1

GO:0030618	5.40E-04	0.5441	15767	609	5	3	MF	transforming growth factor beta receptor, pathway-specific cytoplasmic mediator activity	SMAD9; SMAD1; SMAD3
GO:0005030	5.40E-04	0.5441	15767	609	5	3	MF	neurotrophin receptor activity	NGFR; NTRK2; NTRK3
GO:0034185	5.80E-04	0.5888	15767	609	11	4	MF	apolipoprotein binding	LIPC; SCARB1; VLDLR; LCAT
GO:0004871	7.70E-04	0.7774	15767	609	2155	111	MF	signal transducer activity	AR; ITGA3; FZD10; PPARG; PPARC; PPARA; KCNH2; ITGAV; SIGIRR; SMAD9; SMAD4; SMAD7; SMAD1; RXRA; LEPR; BDKRB2; EGFR; IGF1R; ERG; NGFR; PPF1A1; PGR; RTN1; FZD8; RGS10; WNT16; AVPR1A; RARA; RARB; RARG; WNT10A; PDE8A; SCARB2; SCARB1; GNG2; RHO; MAPK10; VLDLR; TIRAP; BMX; EPOR; IL1RAP; GRIK5; F2RL3; LPAR1; ITGB3BP; ARHGAP1; DVL2; VIPR1; SMAD3; PLCD3; GHR; MAGI2; TRPV4; ERBB4; NR2C2; BRD8; GNAO1; PLCB2; HIF1A; DAXX; KIR3DL2; KIR3DL3; PAX8; IL13RA2; ESR2; TOLLIP; ESR1; CCR4; STAT3; STAT1; EFNA4; WNT2; ANTXR2; AMHR2; TP53BP2; DRD2; WNT9B; HTR1A; ITSN2; NTRK2; NTRK3; GABRR2; SOCS2; EEF1D; MST1R; STMN1; HLA-G; TGFA; PLXNB3; GUCY1A3; HTR1B; MED30; CHRM2; MPL; EPHA8; EPHA3; EPHA2; GNRHR; ATP5B; FZD6; STAT5B; STAT5A; RIPK2; GRIN2C; ADRBK1; FSHR; CLTCL1; PTPRS; AXIN1; IGF2R
GO:0060089	7.70E-04	0.7774	15767	609	2155	111	MF	molecular transducer activity	AR; ITGA3; FZD10; PPARG; PPARC; PPARA; KCNH2; ITGAV; SIGIRR; SMAD9; SMAD4; SMAD7; SMAD1; RXRA; LEPR; BDKRB2; EGFR; IGF1R; ERG; NGFR; PPF1A1; PGR; RTN1; FZD8; RGS10; WNT16; AVPR1A; RARA; RARB; RARG; WNT10A; PDE8A; SCARB2; SCARB1; GNG2; RHO; MAPK10; VLDLR; TIRAP; BMX; EPOR; IL1RAP; GRIK5; F2RL3; LPAR1; ITGB3BP; ARHGAP1; DVL2; VIPR1; SMAD3; PLCD3; GHR; MAGI2; TRPV4; ERBB4; NR2C2; BRD8; GNAO1; PLCB2; HIF1A; DAXX; KIR3DL2; KIR3DL3; PAX8; IL13RA2; ESR2; TOLLIP; ESR1; CCR4; STAT3; STAT1; EFNA4; WNT2; ANTXR2; AMHR2; TP53BP2; DRD2; WNT9B; HTR1A; ITSN2; NTRK2; NTRK3; GABRR2; SOCS2; EEF1D; MST1R; STMN1; HLA-G; TGFA; PLXNB3; GUCY1A3; HTR1B; MED30; CHRM2; MPL; EPHA8; EPHA3; EPHA2; GNRHR; ATP5B; FZD6; STAT5B; STAT5A; RIPK2; GRIN2C; ADRBK1; FSHR; CLTCL1; PTPRS; AXIN1; IGF2R
GO:0019900	8.10E-04	0.8177	15767	609	201	18	MF	kinase binding	DLG1; SMAD1; IGF1R; AVPR1A; RELA; CDKN2B; USF1; PGAM1; SMAD3; GHR; TOLLIP; STAT3; PDPK1; PKN1; DUSP12; SQSTM1; GSK3B; DGKQ
GO:0016500	8.50E-04	0.8564	15767	609	12	4	MF	protein-hormone receptor activity	LEPR; PAX8; GNRHR; FSHR
GO:0030553	8.50E-04	0.8564	15767	609	12	4	MF	cGMP binding	PDE6H; PDE10A; PRKG1; PDE11A
GO:0050542	0.001	1	15767	609	6	3	MF	icosanoid binding	PPARG; SNCA; FABP3
GO:0050543	0.001	1	15767	609	6	3	MF	icosatetraenoic acid binding	PPARG; SNCA; FABP3
GO:0004672	0.001	1	15767	609	600	39	MF	protein kinase activity	STK16; HIPK2; CAMK2A; CAMK2B; CSNK1A1; KCNH2; PRKDC; SRPK1; EGFR; IGF1R; MAPK10; PRKG1; BMX; CSNK1E; CDK7; GTF2H4; PRKCD; ERBB4; STK36; MARK3; EFNA4; MAP2K3; AMHR2; PDPK1; PKN1; NTRK2; NTRK3; MST1R; GSK3B; MAPKAPK5; TGFA; POLR2H; POLR2J; EPHA8; EPHA3; EPHA2; RIPK2; ADRBK1; ¹⁷⁷⁹⁹
GO:0019002	0.0011	1	15767	609	13	4	MF	GMP binding	PDE6H; PDE10A; PRKG1; PDE11A
GO:0051018	0.0011	1	15767	609	13	4	MF	protein kinase A binding	AKAP3; AKAP8; AKAP12; GSK3B
GO:0002039	0.0012	1	15767	609	22	5	MF	p53 binding	BLM; TP73; USP7; SMARCA4; GSK3B
GO:0030284	0.0014	1	15767	609	2	2	MF	estrogen receptor activity	ESR2; ESR1
GO:0031753	0.0014	1	15767	609	2	2	MF	endothelial differentiation G-protein coupled receptor binding	RALA; ADRBK1
GO:0031755	0.0014	1	15767	609	2	2	MF	Edg-2 lysophosphatidic acid receptor binding	RALA; ADRBK1
GO:0032181	0.0014	1	15767	609	2	2	MF	dinucleotide repeat insertion binding	MSH2; MSH3
GO:0004821	0.0014	1	15767	609	2	2	MF	histidine-tRNA ligase activity	HARS; HARS2

GO:0008081	0.0015	1	15767	609	85	10	MF	phosphoric diester hydrolase activity	PDE6H; PDE10A; BDKRB2; PDE1A; PDE8A; PDE11A; PLCD3; PLCB2; PDE7B; ENPP7
GO:0004708	0.0021	1	15767	609	15	4	MF	MAP kinase activity	MAPK10; MAP2K3; MAPKAPK5; TGFA
GO:0005520	0.0023	1	15767	609	25	5	MF	insulin-like growth factor binding	IGF1R; CYR61; IGFBP6; IGFALS; IGF2R
GO:0005504	0.0027	1	15767	609	37	6	MF	fatty acid binding	PPARG; PPARC; SNCA; FABP3; HADHA; ALDH6A1
GO:0000166	0.0027	1	15767	609	2283	113	MF	nucleotide binding	SCG5; STK16; HIPK2; PIK3CB; CAMK2A; CAMK2B; DDX41; UBE2D2; RIT2; RAB6B; MX1; UCK1; BLM; CSNK1A1; KHK; PDE6H; PRKDC; ADSSL1; KIF3A; SRPK1; PDE10A; AK7; RBM7; EGFR; IGF1R; RBM9; CNOT4; NOS1; YARS2; TRIP13; RBMX; EIF3G; RBM41; TPR; ADCY1; MAPK10; PPOX; PRKG1; BMX; CSNK1E; SARDH; RALA; PI4KB; PDE11A; HNRNPAL; MTHFS; CNGA4; CDK7; MATR3; MSH2; MSH3; SMARCA4; PRKCD; CSTF2; SNRNP200; MAGI3; ERBB4; ADCY5; GNAO1; XRCC5; NONO; NT5E; XDH; RAD50; SFPQ; ACAD8; STK36; SYN1; HARS; RBMSA; MARK3; NMNAT2; ACACB; TP53; RALYL; RHEB; HARS2; EIF5; MAP2K3; AMHR2; PDPK1; PKN1; MCM7; HADHA; DHX16; NTRK2; NTRK3; RAP1A; MST1R; GSK3B; ACSL1; PABPC1; MAPKAPK5; GUCY1A3; HRAS; BAT1; EPHA8; EPHA3; EPHA2; RBKS; ATP5B; HNRNPC; ADK; MKI67; RIPK2; PAPSS1; DGKQ; ADRBK1; DACH1; SNRPA; UPF3A; DNML1; MYO7A
GO:0042809	0.0027	1	15767	609	16	4	MF	vitamin D receptor binding	TAF11; RXRA; MED30; TAF7
GO:0033613	0.0027	1	15767	609	8	3	MF	transcription activator binding protein	PPARG; RELA; DGKQ
GO:0004713	0.0028	1	15767	609	139	13	MF	tyrosine kinase activity	EGFR; IGF1R; BMX; ERBB4; EFNA4; MAP2K3; NTRK2; NTRK3; MST1R; EPHA8; EPHA3; EPHA2; IGF2R
GO:0005496	0.0031	1	15767	609	64	8	MF	steroid binding	SULT1E1; AR; RXRA; PGR; CETP; ESR2; ESR1; SHBG
GO:0030551	0.0033	1	15767	609	27	5	MF	cyclic nucleotide binding	PDE6H; PDE10A; PRKG1; PDE11A; CNGA4
GO:0005245	0.0033	1	15767	609	27	5	MF	voltage-gated calcium channel activity	CATSPER1; CACNG6; CACNA1F; CACNA2D1; CACNB2
GO:0016740	0.0034	1	15767	609	1720	88	MF	transferase activity	STK16; HIPK2; DLG1; PIK3CB; CAMK2A; CAMK2B; SULT1E1; POLR1A; POLR1E; UCK1; CSNK1A1; KCNH2; KHK; TRDM1; ASH2L; PRKDC; SRPK1; AK7; EGFR; IGF1R; ABAT; ACAA2; GSTA4; B3GNT6; PTGES3; MAPK10; PRKG1; BMX; CSNK1E; SARDH; NSD1; PI4KB; CHPT1; DLST; PPAT; CDK7; GTF2H4; SUZ12; PRKCD; MAGI3; ERBB4; PRMT3; PRMT5; TRRAP; LCT; POLE2; STK36; LCMT1; MARK3; NMNAT2; LCAT; EFNA4; COMT; AGXT; MAP2K3; AMHR2; PDPK1; AADAT; PKN1; HADHA; UGP2; NTRK2; NTRK3; GOT1; MST1R; GSK3B; MAPKAPK5; TGFA; GYS2; POLR2H; POLR2K; POLR2J; EPHA8; EPHA3; EPHA2; RBKS; POLD2; PCMT1; TGS1; ADK; GALNT14; RIPK2; PAPSS1; DGKQ; ADRBK1; GGT1; PEMT; IGF2R
GO:0004712	0.0035	1	15767	609	17	4	MF	protein serine/threonine/tyrosine kinase activity	MAPK10; MAP2K3; MAPKAPK5; TGFA
GO:0005003	0.0035	1	15767	609	17	4	MF	ephrin receptor activity	EFNA4; EPHA8; EPHA3; EPHA2
GO:0019838	0.004	1	15767	609	112	11	MF	growth factor binding	IGF1R; NGFR; CYR61; IGFBP6; IL1RAP; NTF3; GHR; NTRK2; NTRK3; IGFALS; IGF2R
GO:0003706	0.004	1	15767	609	9	3	MF	ligand-regulated transcription factor activity	PPARA; RXRA; SMAD3
GO:0046965	0.004	1	15767	609	9	3	MF	retinoid X receptor binding	PPARG; RARG; NSD1
GO:0005057	0.0041	1	15767	609	162	14	MF	receptor signaling protein activity	SMAD9; SMAD4; SMAD7; SMAD1; EGFR; MAPK10; SMAD3; ERBB4; DAXX; ESR2; STAT3; STAT1; AMHR2; SOCS2
GO:0017160	0.0043	1	15767	609	3	2	MF	Ral GTPase binding	RALBP1; EXOC2
GO:0032139	0.0043	1	15767	609	3	2	MF	dinucleotide insertion or deletion binding	MSH2; MSH3

GO:0032142	0.0043	1	15767	609	3	2	MF	single guanine insertion binding	MSH2; MSH3
GO:0032356	0.0043	1	15767	609	3	2	MF	oxidized DNA binding	MSH2; MSH3
GO:0032357	0.0043	1	15767	609	3	2	MF	oxidized purine DNA binding	MSH2; MSH3
GO:0034186	0.0043	1	15767	609	3	2	MF	apolipoprotein A-I binding	SCARB1; LCAT
GO:0017046	0.0046	1	15767	609	29	5	MF	peptide hormone binding	LEPR; IGF1R; AVPR1A; GHR; CRHBP
GO:0050681	0.0046	1	15767	609	29	5	MF	androgen receptor binding	NSD1; CDK7; BRCA1; DAXX; PKN1
GO:0016791	0.0052	1	15767	609	257	19	MF	phosphatase activity	PPAP2A; DLG1; ACP6; ACPT; ACP; PGAM1; NT5E; DUSP14; DUSP12; PON3; ALPL; FBP2; PPP2CA; PPP2CB; G6PC2; DUSP1; SGPP1; INPP1; PTPRS
GO:0051087	0.0054	1	15767	609	30	5	MF	chaperone binding	TSC1; FGB; DLST; TP53; VWF
GO:0016725	0.0056	1	15767	609	10	3	MF	oxidoreductase activity, acting on CH or CH2 groups	CYP2C9; XDH; CYP1A2
GO:0035035	0.0056	1	15767	609	10	3	MF	histone acetyltransferase binding	SP1; HIF1A; TAF7
GO:0042813	0.0056	1	15767	609	10	3	MF	Wnt receptor activity	FZD10; FZD8; FZD6
GO:0019901	0.0059	1	15767	609	169	14	MF	protein kinase binding	DLG1; SMAD1; AVPR1A; RELA; CDKN2B; USF1; PGAM1; SMAD3; GHR; STAT3; PDPK1; PKN1; SQSTM1; GSK3B
GO:0003682	0.0062	1	15767	609	170	14	MF	chromatin binding	SMARCC2; SP3; PPARG; SMAD4; LEF1; NSD1; SUZ12; CRX; ING2; TP53; PKN1; SVEP1; GLI2; SIN3A
GO:0035258	0.0065	1	15767	609	44	6	MF	steroid hormone receptor binding	NSD1; CDK7; BRCA1; DAXX; PKN1; STAT5B
GO:0005506	0.0066	1	15767	609	207	16	MF	iron ion binding	P4HA2; CYP2C9; CYP27B1; LTF; NOS1; SNCA; CYB5A; LPO; CYP4F12; NT5E; XDH; CYP1A2; HBB; GUCY1A3; CYP2B6; FADS2
GO:0008276	0.0067	1	15767	609	58	7	MF	protein methyltransferase activity	ASH2L; NSD1; SUZ12; PRMT3; PRMT5; LCMT1; PCMT1
GO:0003697	0.0074	1	15767	609	59	7	MF	single-stranded DNA binding	BLM; HNRNPA1; MSH2; MSH3; TP53; MCM7; SUB1
GO:0003993	0.0075	1	15767	609	11	3	MF	acid phosphatase activity	ACP6; ACPT; ACP
GO:0042974	0.0075	1	15767	609	11	3	MF	retinoic acid receptor binding	PPARG; RARG; NSD1
GO:0004926	0.0075	1	15767	609	11	3	MF	non-G-protein coupled 7TM receptor activity	FZD10; FZD8; FZD6
GO:0008171	0.0075	1	15767	609	11	3	MF	O-methyltransferase activity	LCMT1; COMT; PCMT1
GO:0008483	0.0078	1	15767	609	21	4	MF	transaminase activity	ABAT; AGXT; AADAT; GOT1
GO:0008757	0.0078	1	15767	609	90	9	MF	S-adenosylmethionine-dependent methyltransferase activity	TRDMT1; ASH2L; NSD1; PRMT3; PRMT5; LCMT1; COMT; PCMT1; PEMT
GO:0031995	0.0084	1	15767	609	4	2	MF	insulin-like growth factor II binding	IGFBP6; IGF2R
GO:0032137	0.0084	1	15767	609	4	2	MF	guanine/thymine mispair binding	MSH2; MSH3

GO:0032138	0.0084	1	15767	609	4	2	MF	single base insertion or deletion binding	MSH2; MSH3
GO:0033695	0.0084	1	15767	609	4	2	MF	oxidoreductase activity, acting on CH or CH2 groups, quinone or similar compound as acceptor	CYP2C9; CYP1A2
GO:0034875	0.0084	1	15767	609	4	2	MF	caffeine oxidase activity	CYP2C9; CYP1A2
GO:0003988	0.0084	1	15767	609	4	2	MF	acetyl-CoA C-acyltransferase activity	ACAA2; HADHA
GO:0005010	0.0084	1	15767	609	4	2	MF	insulin-like growth factor receptor activity	IGF1R; IGF2R
GO:0050544	0.0084	1	15767	609	4	2	MF	arachidonic acid binding	PPARG; SNCA
GO:0005497	0.0084	1	15767	609	4	2	MF	androgen binding	AR; SHBG
GO:0000739	0.0084	1	15767	609	4	2	MF	DNA strand annealing activity	BLM; TP53
GO:0020037	0.0085	1	15767	609	124	11	MF	heme binding	CYP2C9; CYP27B1; NOS1; CYB5A; LP0; CYP4F12; CYP1A2; HBB; GUCY1A3; CYP2B6; FADS2
GO:0004252	0.0092	1	15767	609	160	13	MF	serine-type endopeptidase activity	PCSK2; MST1; LTF; HGF; MASP1; F10; PRSS2; MMP8; CTSG; MASP2; C1S; ACR; PLAT
GO:0008094	0.0096	1	15767	609	62	7	MF	DNA-dependent ATPase activity	BLM; CDK7; GTF2H4; SMARCA4; XRCC5; RAD50; NBN
GO:0030275	0.0097	1	15767	609	12	3	MF	LRR domain binding	ERC1; GMNN; POLR2J
GO:0043560	0.0097	1	15767	609	12	3	MF	insulin receptor substrate binding	PIK3CB; IGF1R; PRKCD
GO:0016779	0.0107	1	15767	609	128	11	MF	nucleotidyltransferase activity	POLR1A; POLR1E; PTGES3; POLE2; NMNAT2; UGP2; POLR2H; POLR2K; POLR2J; POLD2; PAPSS1
GO:0002020	0.0108	1	15767	609	23	4	MF	protease binding	F3; BDKRB2; BCL2; VWF
GO:0019902	0.011	1	15767	609	49	6	MF	phosphatase binding	DLG1; SMG5; EGFR; GHR; MAG12; GNB2L1
GO:0030674	0.011	1	15767	609	95	9	MF	protein binding, bridging	DSP; COL11A2; FGB; ARHGAP1; RAD50; TP53BP2; ITSN2; SOCS2; ST13

GO:0003824	0.0126	1	15767	609	5225	228	MF	catalytic activity	PPAP2A; PCSK2; STK16; P4HA2; HIPK2; DLG1; PIK3CB; CYP2C9; CAMK2A; CAMK2B; SULT1E1; CNDP1; DDX41; HHIP; TSG101; UBE2D2; RIT2; RAB6B; MX1; POLR1A; POLR1E; MST1; CYP27B1; UCK1; SENP2; BLM; ANAPC5; PPD; CSNK1A1; KCN2; KHK; GPX5; TRDMT1; PDE6H; ACP6; RALBP1; ASH2L; PRKDC; ADSSL1; KIF3A; LTF; SRPK1; PDE10A; ACP7; BDKRB2; ACP6; F5; AK7; EGFR; IGF1R; NGFR; ABAT; PDE1A; ACAA2; CNOT4; NOS1; YARS2; HGF; TRIP13; HEXB; CYB5A; GSTA4; B3GNT6; LIPC; LPO; TPR; PDE8A; ADCY1; DBH; PTGES3; MAPK10; MASP1; PPOX; PRKG1; BMX; AGMAT; F10; CSNK1E; SARDB; NSD1; WDYHV1; RALA; EPHX2; PI4KB; PGAM1; PDE11A; CHPT1; MTHFS; UHRF1; DLST; PPAT; CDK7; GTF2H4; MSH2; MGLL; USP7; PRSS2; SMARCA4; SUZ12; PRKCD; MMP8; PLCD3; TRIM11; WWP1; SNRNP200; CYP4F12; MAGI3; BRCA1; ERBB4; PRMT3; CTSG; ADCY5; DZIP3; PRMT5; MASP2; GBA; GNAO1; PLCB2; XRCC5; SMURF1; SMURF2; NT5E; XDH; RAD50; TRRAP; LCT; ACAD8; CTSL1; POLE2; STK36; SYN1; LCMT1; HARS; PDE7B; MARK3; MNAT2; ACACB; LCAT; EFN4; COMT; EIF2C2; CYP1A2; AGXT; RHEB; HARS2; EIF5; MAP2K3; AMHR2; PDPK1; AADAT; AMY2B; PKN1; MCM7; HADHA; DUSP14; DUSP12; PON3; RDH14; RDH12; C1S; ALPL; DHX16; FBP2; UGP2; NTRK2; NTRK3; MICAL1; CAPN2; GOT1; ENPP7; RAP1A; PPP2CA; PPP2CB; MST1R; GSK3B; ACSL1; G6PC2; MAPKAPK5; TGFA; GUCY1A3; PGMI; GYS2; HRAS; POLR2H; POLR2K; POLR2J; CDC23; TNFAIP3; BAT1; EPHA8; EPHA3; EPHA2; ACR; RBKS; ATP5B; AKR1B10; CYP2B6; POLD2; NBN; SRD5A2; DUSP1; SGPP1; ASL; PCMT1; TGS1; BCOR; ACHE; FADS2; ADK; GALNT14; PSMB4; ADAM12; RIPK2; DERA; PAPSS1; DGKQ; ADRBK1; PLAT; ALDH6A1; GGT1; NDEL1; INPP1; PTPRS; PEMT; NEDD4L; DNML1; MYO7A; IGF2R
GO:0017171	0.0127	1	15767	609	185	14	MF	serine hydrolase activity	PCSK2; MST1; LTF; HGF; MASP1; F10; PRSS2; MMP8; CTSG; MASP2; C1S; ACR; ACHE; PLAT
GO:0030554	0.0127	1	15767	609	1598	79	MF	adenyl nucleotide binding	STK16; HIPK2; PIK3CB; CAMK2A; CAMK2B; DDX41; UBE2D2; UCK1; BLM; CSNK1A1; KHK; PRKDC; KIF3A; SRPK1; PDE10A; AK7; EGFR; IGF1R; NOS1; YARS2; TRIP13; TPR; ADCY1; MAPK10; PPOX; PRKG1; BMX; CSNK1E; SARDB; PI4KB; PDE11A; MTHFS; CNGA4; CDK7; MSH2; MSH3; SMARCA4; PRKCD; SNRNP200; MAGI3; ERBB4; ADCY5; XRCC5; XDH; RAD50; ACAD8; STK36; SYN1; HARS; MARK3; MNAT2; ACACB; TP53; HARS2; MAP2K3; AMHR2; PDPK1; PKN1; MCM7; DHX16; NTRK2; NTRK3; MST1R; GSK3B; ACSL1; MAPKAPK5; BAT1; EPHA8; EPHA3; EPHA2; RBKS; ATP5B; ADK; MKI67; RIPK2; PAPSS1; DGKQ; ADRBK1; MYO7A
GO:0005518	0.0132	1	15767	609	37	5	MF	collagen binding	SMAD4; SMAD7; SMAD3; VWF; ACHE
GO:0046906	0.0133	1	15767	609	132	11	MF	tetrapyrrole binding	CYP2C9; CYP27B1; NOS1; CYB5A; LPO; CYP4F12; CYP1A2; HBB; GUCY1A3; CYP2B6; FADS2
GO:0010340	0.0137	1	15767	609	5	2	MF	carboxyl-O-methyltransferase activity	LCMT1; PCMT1
GO:0001965	0.0137	1	15767	609	5	2	MF	G-protein alpha-subunit binding	HTR1A; IGF2R
GO:0032135	0.0137	1	15767	609	5	2	MF	DNA insertion or deletion binding	MSH2; MSH3
GO:0003691	0.0137	1	15767	609	5	2	MF	double-stranded telomeric DNA binding	XRCC5; TERF1
GO:0042392	0.0137	1	15767	609	5	2	MF	sphingosine-1-phosphate phosphatase activity	PPAP2A; SGPP1
GO:0048406	0.0137	1	15767	609	5	2	MF	nerve growth factor binding protein	NGFR; NTF3
GO:0051998	0.0137	1	15767	609	5	2	MF	carboxyl O-methyltransferase activity	LCMT1; PCMT1
GO:0046966	0.0146	1	15767	609	25	4	MF	thyroid hormone receptor binding	TAF11; NSD1; MED30; TAF7
GO:0016566	0.0147	1	15767	609	38	5	MF	specific transcriptional repressor activity	PPARG; WT1; SMAD3; YY1; TAF7
GO:0001883	0.0152	1	15767	609	1634	80	MF	purine nucleoside binding	STK16; HIPK2; PIK3CB; CAMK2A; CAMK2B; DDX41; UBE2D2; UCK1; BLM; CSNK1A1; KHK; PDE6H; PRKDC; KIF3A; SRPK1; PDE10A; AK7; EGFR; IGF1R; NOS1; YARS2; TRIP13; TPR; ADCY1; MAPK10; PPOX; PRKG1; BMX; CSNK1E; SARDB; PI4KB; PDE11A; MTHFS; CNGA4; CDK7; MSH2; MSH3; SMARCA4; PRKCD; SNRNP200; MAGI3; ERBB4; ADCY5; XRCC5; XDH; RAD50; ACAD8; STK36; SYN1; HARS; MARK3; MNAT2; ACACB; TP53; HARS2; MAP2K3; AMHR2; PDPK1; PKN1; MCM7; DHX16; NTRK2; NTRK3; MST1R; GSK3B; ACSL1; MAPKAPK5; BAT1; EPHA8; EPHA3; EPHA2; RBKS; ATP5B; ADK; MKI67; RIPK2; PAPSS1; DGKQ; ADRBK1; MYO7A

GO:0003743	0.0159	1	15767	609	53	6	MF	translation initiation factor activity	EIF3H; EIF3L; EIF3G; EIF2C2; EIF5; EIF6
GO:0015459	0.0167	1	15767	609	26	4	MF	potassium channel regulator activity	DLG1; DRD2; KCNE2; KCNE1
GO:0001882	0.0174	1	15767	609	1644	80	MF	nucleoside binding	STK16; HIPK2; PIK3CB; CAMK2A; CAMK2B; DDX41; UBE2D2; UCK1; BLM; CSNK1A1; KHK; PDE6H; PRKDC; KIF3A; SRPK1; PDE10A; AK7; EGFR; IGF1R; NOS1; YARS2; TRIP13; TPR; ADCY1; MAPK10; PPOX; PRKG1; BMX; CSNK1E; SARDH; PI4KB; PDE11A; MTHFS; CNGA4; CDK7; MSH2; MSH3; SMARCA4; PRKCD; SNRNP200; MAGI3; ERBB4; ADCY5; XRCC5; XDH; RAD50; ACAD8; STK36; SYN1; HARS; MARK3; MNAT2; ACACB; TP53; HARS2; MAP2K3; AMHR2; PDPK1; PKN1; MCM7; DHX16; NTRK2; NTRK3; MST1R; GSK3B; ACSL1; MAPKAPK5; BAT1; EPHA8; EPHA3; EPHA2; RBKS; ATP5B; ADK; MKI67; RIPK2; PAPSS1; DGKQ; ADRBK1; MYO7A
GO:0008013	0.0182	1	15767	609	40	5	MF	beta-catenin binding	AR; SMAD7; LEF1; GSK3B; AXIN1
GO:0030228	0.0184	1	15767	609	15	3	MF	lipoprotein receptor activity	SCARB1; VLDLR; ATP5B
GO:0017076	0.019	1	15767	609	1957	93	MF	purine nucleotide binding	SCG5; STK16; HIPK2; PIK3CB; CAMK2A; CAMK2B; DDX41; UBE2D2; RIT2; RAB6B; MX1; UCK1; BLM; CSNK1A1; KHK; PDE6H; PRKDC; ADSSL1; KIF3A; SRPK1; PDE10A; AK7; EGFR; IGF1R; NOS1; YARS2; TRIP13; TPR; ADCY1; MAPK10; PPOX; PRKG1; BMX; CSNK1E; SARDH; RALA; PI4KB; PDE11A; MTHFS; CNGA4; CDK7; MSH2; MSH3; SMARCA4; PRKCD; SNRNP200; MAGI3; ERBB4; ADCY5; GNAO1; XRCC5; XDH; RAD50; ACAD8; STK36; SYN1; HARS; MARK3; MNAT2; ACACB; TP53; RHEB; HARS2; EIF5; MAP2K3; AMHR2; PDPK1; PKN1; MCM7; DHX16; NTRK2; NTRK3; RAP1A; MST1R; GSK3B; ACSL1; MAPKAPK5; GUCY1A3; HRAS; BAT1; EPHA8; EPHA3; EPHA2; RBKS; ATP5B; ADK; MKI67; RIPK2; PAPSS1; DGKQ; ADRBK1; DNMI1; MYO7A
GO:0019237	0.0201	1	15767	609	6	2	MF	centromeric DNA binding	MSH2; MSH3
GO:0030235	0.0201	1	15767	609	6	2	MF	nitric-oxide synthase regulator activity	EGFR; ESRI
GO:0031994	0.0201	1	15767	609	6	2	MF	insulin-like growth factor I binding	IGF1R; IGFBP6
GO:0005062	0.0201	1	15767	609	6	2	MF	hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity	STAT3; STAT1
GO:0016247	0.0204	1	15767	609	56	6	MF	channel regulator activity	DLG1; CAV3; DRD2; KCNE2; KCNE1; NEDD4L
GO:0004896	0.0204	1	15767	609	56	6	MF	cytokine receptor activity	LEPR; EPOR; IL1RAP; GHR; IL13RA2; MPL
GO:0032559	0.0205	1	15767	609	1516	74	MF	adenyl ribonucleotide binding	STK16; HIPK2; PIK3CB; CAMK2A; CAMK2B; DDX41; UBE2D2; UCK1; BLM; CSNK1A1; KHK; PRKDC; KIF3A; SRPK1; PDE10A; AK7; EGFR; IGF1R; YARS2; TRIP13; TPR; ADCY1; MAPK10; PRKG1; BMX; CSNK1E; PI4KB; PDE11A; MTHFS; CNGA4; CDK7; MSH2; MSH3; SMARCA4; PRKCD; SNRNP200; MAGI3; ERBB4; ADCY5; XRCC5; RAD50; STK36; SYN1; HARS; MARK3; MNAT2; ACACB; TP53; HARS2; MAP2K3; AMHR2; PDPK1; PKN1; MCM7; DHX16; NTRK2; NTRK3; MST1R; GSK3B; ACSL1; MAPKAPK5; BAT1; EPHA8; EPHA3; EPHA2; RBKS; ATP5B; ADK; MKI67; RIPK2; PAPSS1; DGKQ; ADRBK1; MYO7A
GO:0043499	0.022	1	15767	609	16	3	MF	eukaryotic cell surface binding	APOH; FGB; ATP5B
GO:0034062	0.0221	1	15767	609	42	5	MF	RNA polymerase activity	POLR1A; POLR1E; POLR2H; POLR2K; POLR2J
GO:0003899	0.0221	1	15767	609	42	5	MF	DNA-directed RNA polymerase activity	POLR1A; POLR1E; POLR2H; POLR2K; POLR2J
GO:0043498	0.0221	1	15767	609	42	5	MF	cell surface binding	F3; APOH; SFTPD; FGB; ATP5B
GO:0019825	0.0242	1	15767	609	43	5	MF	oxygen binding	CYP2C9; CYP4F12; CYP1A2; HBB; CYP2B6
GO:0005100	0.0243	1	15767	609	29	4	MF	Rho GTPase activator activity	RALBP1; JUN; ARHGAP1; SOS1

GO:0008236	0.0244	1	15767	609	182	13	MF	serine-type peptidase activity	PCSK2; MST1; LTF; HGF; MASP1; F10; PRSS2; MMP8; CTSG; MASP2; C1S; ACR; PLAT
GO:0030552	0.026	1	15767	609	17	3	MF	cAMP binding transferase activity,	PDE10A; PDE11A; CNGA4
GO:0016769	0.0272	1	15767	609	30	4	MF	transferring nitrogenous groups	ABAT; AGXT; AADAT; GOT1
GO:0004003	0.0272	1	15767	609	30	4	MF	ATP-dependent DNA helicase activity	BLM; XRCC5; RAD50; NBN
GO:0004497	0.0272	1	15767	609	93	8	MF	monooxygenase activity	CYP2C9; CYP27B1; NOS1; DBH; CYP4F12; CYP1A2; MICAL1; CYP2B6
GO:0016273	0.0274	1	15767	609	7	2	MF	arginine N- methyltransfera se activity	PRMT3; PRMT5
GO:0016274	0.0274	1	15767	609	7	2	MF	protein- arginine N- methyltransfera se activity	PRMT3; PRMT5
GO:0017080	0.0274	1	15767	609	7	2	MF	sodium channel regulator activity	CAV3; NEDD4L
GO:0001972	0.0274	1	15767	609	7	2	MF	retinoic acid binding	RARA; IGF2R
GO:0030274	0.0274	1	15767	609	7	2	MF	LIM domain binding	RPH3AL; RIPK2
GO:0032553	0.0287	1	15767	609	1873	88	MF	ribonucleotide binding	SCG5; STK16; HIPK2; PIK3CB; CAMK2A; CAMK2B; DDX41; UBE2D2; RIT2; RAB6B; MX1; UCK1; BLM; CSNK1A1; KHK; PDE6H; PRKDC; ADSSL1; KIF3A; SRPK1; PDE10A; AK7; EGFR; IGF1R; YARS2; TRIP13; TPR; ADCY1; MAPK10; PRKG1; BMX; CSNK1E; RALA; PI4KB; PDE11A; MTHFS; CNGA4; CDK7; MSH2; MSH3; SMARCA4; PRKCD; SNRNP200; MAG13; ERBB4; ADCY5; GNAO1; XRCC5; RAD50; STK36; SYN1; HARS; MARK3; MNAT2; ACACB; TP53; RHEB; HARS2; EIF5; MAP2K3; AMHR2; PDPK1; PKN1; MCM7; DHX16; NTRK2; NTRK3; RAP1A; MST1R; GSK3B; ACSL1; MAPKAPK5; GUCY1A3; HRAS; BAT1; EPHA8; EPHA3; EPHA2; RBKS; ATP5B; ADK; MKI67; RIPK2; PAPSS1; DGKQ; ADRBK1; DNML1; MYO7A
GO:0032555	0.0287	1	15767	609	1873	88	MF	purine ribonucleotide binding	SCG5; STK16; HIPK2; PIK3CB; CAMK2A; CAMK2B; DDX41; UBE2D2; RIT2; RAB6B; MX1; UCK1; BLM; CSNK1A1; KHK; PDE6H; PRKDC; ADSSL1; KIF3A; SRPK1; PDE10A; AK7; EGFR; IGF1R; YARS2; TRIP13; TPR; ADCY1; MAPK10; PRKG1; BMX; CSNK1E; RALA; PI4KB; PDE11A; MTHFS; CNGA4; CDK7; MSH2; MSH3; SMARCA4; PRKCD; SNRNP200; MAG13; ERBB4; ADCY5; GNAO1; XRCC5; RAD50; STK36; SYN1; HARS; MARK3; MNAT2; ACACB; TP53; RHEB; HARS2; EIF5; MAP2K3; AMHR2; PDPK1; PKN1; MCM7; DHX16; NTRK2; NTRK3; RAP1A; MST1R; GSK3B; ACSL1; MAPKAPK5; GUCY1A3; HRAS; BAT1; EPHA8; EPHA3; EPHA2; RBKS; ATP5B; ADK; MKI67; RIPK2; PAPSS1; DGKQ; ADRBK1; DNML1; MYO7A
GO:0003678	0.0289	1	15767	609	45	5	MF	DNA helicase activity	BLM; XRCC5; RAD50; MCM7; NBN
GO:0043176	0.0324	1	15767	609	114	9	MF	amine binding	NOS1; MTHFS; CETP; AGXT; DRD2; HTR1A; HTR1B; CHRM2; ACHE
GO:0048306	0.0336	1	15767	609	32	4	MF	calcium- dependent protein binding	TSG101; MASP1; MASP2; FCN2
GO:0015270	0.0357	1	15767	609	8	2	MF	dihydropyridine -sensitive calcium channel activity	CACNA1F; CACNA2D1
GO:0043425	0.0357	1	15767	609	8	2	MF	bHLH transcription factor binding	USF1; USF2
GO:0047555	0.0357	1	15767	609	8	2	MF	3',5'-cyclic- GMP phosphodiestera se activity	PDE10A; PDE11A
GO:0070410	0.0357	1	15767	609	8	2	MF	co-SMAD binding	SMAD1; SMAD3
GO:0019205	0.0369	1	15767	609	48	5	MF	nucleobase, nucleoside, nucleotide kinase activity	DLG1; UCK1; AK7; MAG13; ADK

GO:0005524	0.0379	1	15767	609	1493	71	MF	ATP binding	STK16; HIPK2; PIK3CB; CAMK2A; CAMK2B; DDX41; UBE2D2; UCK1; BLM; CSNK1A1; KHK; PRKDC; KIF3A; SRPK1; AK7; EGFR; IGF1R; YARS2; TRIP13; TPR; ADCY1; MAPK10; PRKG1; BMX; CSNK1E; PI4KB; MTHFS; CDK7; MSH2; MSH3; SMARCA4; PRKCD; SNRNP200; MAG13; ERBB4; ADCY5; XRC5; RAD50; STK36; SYN1; HARS; MARK3; MNAT2; ACACB; TP53; HARS2; MAP2K3; AMHR2; PDPK1; PKN1; MCM7; DHX16; NTRK2; NTRK3; MST1R; GSK3B; ACSL1; MAPKAPK5; BAT1; EPHA8; EPHA3; EPHA2; RBKS; ATP5B; ADK; MKI67; RIPK2; PAPSS1; DGKQ; ADRBK1; MYO7A
GO:0015266	0.0386	1	15767	609	1	1	MF	protein channel activity	MCL1
GO:0015373	0.0386	1	15767	609	1	1	MF	monovalent anion:sodium symporter activity	SLC5A5
GO:0000016	0.0386	1	15767	609	1	1	MF	lactase activity	LCT
GO:0016231	0.0386	1	15767	609	1	1	MF	beta-N-acetylglucosaminidase activity	HEXB
GO:0001670	0.0386	1	15767	609	1	1	MF	dopamine D2 receptor activity	DRD2
GO:0016727	0.0386	1	15767	609	1	1	MF	oxidoreductase activity, acting on CH or CH2 groups, oxygen as acceptor	XDH
GO:0016751	0.0386	1	15767	609	1	1	MF	S-succinyltransferase activity	DLST
GO:0016929	0.0386	1	15767	609	1	1	MF	SUMO-specific protease activity	SEN2
GO:0017047	0.0386	1	15767	609	1	1	MF	adrenocorticotropic hormone binding	CRHBP
GO:0018478	0.0386	1	15767	609	1	1	MF	malonate-semialdehyde dehydrogenase (acetylating) activity	ALDH6A1
GO:0030616	0.0386	1	15767	609	1	1	MF	transforming growth factor beta receptor, common-partner cytoplasmic mediator activity	SMAD4
GO:0030621	0.0386	1	15767	609	1	1	MF	U4 snRNA binding	BAT1
GO:0031852	0.0386	1	15767	609	1	1	MF	mu-type opioid receptor binding	GNAO1
GO:0032145	0.0386	1	15767	609	1	1	MF	succinate-semialdehyde dehydrogenase binding	ABAT
GO:0034056	0.0386	1	15767	609	1	1	MF	estrogen response element binding	ESR1
GO:0035325	0.0386	1	15767	609	1	1	MF	Toll-like receptor binding	TOLLIP
GO:0035402	0.0386	1	15767	609	1	1	MF	histone kinase activity (H3-T11 specific)	PKN1
GO:0003867	0.0386	1	15767	609	1	1	MF	4-aminobutyrate transaminase activity	ABAT

GO:0003983	0.0386	1	15767	609	1	1	MF	UTP:glucose-1-phosphate uridylyltransferase activity	UGP2
GO:0004001	0.0386	1	15767	609	1	1	MF	adenosine kinase activity	ADK
GO:0004040	0.0386	1	15767	609	1	1	MF	amidase activity	ACR
GO:0004044	0.0386	1	15767	609	1	1	MF	amidophosphoribosyltransferase activity	PPAT
GO:0004056	0.0386	1	15767	609	1	1	MF	argininosuccinate lyase activity	ASL
GO:0004139	0.0386	1	15767	609	1	1	MF	deoxyribose- phosphate aldolase activity	DERA
GO:0004149	0.0386	1	15767	609	1	1	MF	dihydrolipoyllysine-residue succinyltransferase activity	DLST
GO:0004304	0.0386	1	15767	609	1	1	MF	estrone sulfotransferase activity	SULT1E1
GO:0004441	0.0386	1	15767	609	1	1	MF	inositol-1,4- bisphosphate 1- phosphatase activity	INPP1
GO:0004454	0.0386	1	15767	609	1	1	MF	ketoheokinase activity	KHK
GO:0004491	0.0386	1	15767	609	1	1	MF	methylmalonate- semialdehyde dehydrogenase (acylating) activity	ALDH6A1
GO:0004498	0.0386	1	15767	609	1	1	MF	calcidiol 1- monooxygenase activity	CYP27B1
GO:0004608	0.0386	1	15767	609	1	1	MF	phosphatidylethanolamine N- methyltransferase activity	PEMT
GO:0004676	0.0386	1	15767	609	1	1	MF	3- phosphoinositide-dependent protein kinase activity	PDPK1
GO:0046975	0.0386	1	15767	609	1	1	MF	histone methyltransferase activity (H3-K36 specific)	NSD1
GO:0004729	0.0386	1	15767	609	1	1	MF	oxygen- dependent protoporphyrinogen oxidase activity	PPOX
GO:0047298	0.0386	1	15767	609	1	1	MF	(S)-3-amino-2- methylpropionate transaminase activity	ABAT
GO:0004747	0.0386	1	15767	609	1	1	MF	ribokinase activity	RBKS
GO:0047536	0.0386	1	15767	609	1	1	MF	2-aminoadipate transaminase activity	AADAT

GO:0004760	0.0386	1	15767	609	1	1	MF	serine-pyruvate transaminase activity	AGXT
GO:0004855	0.0386	1	15767	609	1	1	MF	xanthine oxidase activity	XDH
GO:0004900	0.0386	1	15767	609	1	1	MF	erythropoietin receptor activity	EPOR
GO:0004903	0.0386	1	15767	609	1	1	MF	growth hormone receptor activity	GHR
GO:0004963	0.0386	1	15767	609	1	1	MF	follicle- stimulating hormone receptor activity	FSHR
GO:0005034	0.0386	1	15767	609	1	1	MF	osmosensor activity	TRPV4
GO:0005052	0.0386	1	15767	609	1	1	MF	peroxisome matrix targeting signal-1 binding	PEX5
GO:0051748	0.0386	1	15767	609	1	1	MF	UTP- monosaccharide- 1-phosphate uridylyltransfe rase activity	UGP2
GO:0005252	0.0386	1	15767	609	1	1	MF	open rectifier potassium channel activity	KCNK3
GO:0060961	0.0386	1	15767	609	1	1	MF	phospholipase D inhibitor activity	SNCA
GO:0070012	0.0386	1	15767	609	1	1	MF	oligopeptidase activity	NDEL1
GO:0070506	0.0386	1	15767	609	1	1	MF	high-density lipoprotein receptor activity	SCARB1
GO:0070539	0.0386	1	15767	609	1	1	MF	linoleic acid binding	PPARD
GO:0070551	0.0386	1	15767	609	1	1	MF	endoribonucleas e activity, cleaving siRNA- paired mRNA	EIF2C2
GO:0070773	0.0386	1	15767	609	1	1	MF	protein N- terminal glutamine amidohydrolase activity	WDYHV1
GO:0070818	0.0386	1	15767	609	1	1	MF	protoporphyrino gen oxidase activity	PPOX
GO:0070974	0.0386	1	15767	609	1	1	MF	POU domain binding RNA	AR
GO:0071164	0.0386	1	15767	609	1	1	MF	trimethylguanos ine synthase activity	TGS1
GO:0008480	0.0386	1	15767	609	1	1	MF	sarcosine dehydrogenase activity	SARDH
GO:0008507	0.0386	1	15767	609	1	1	MF	sodium:iodide symporter activity	SLC5A5

GO:0008783	0.0386	1	15767	609	1	1	MF	agmatinase activity	AGMAT
GO:0009917	0.0386	1	15767	609	1	1	MF	sterol 5-alpha reductase activity	SRD5A2
GO:0016251	0.0398	1	15767	609	49	5	MF	general RNA polymerase II transcription factor activity	GTF2I; TAF11; MED15; MED30; TAF7
GO:0016874	0.0405	1	15767	609	403	23	MF	ligase activity	TSG101; UBE2D2; ANAPC5; ADSSL1; CNOT4; YARS2; TPR; MTHFS; UHRF1; TRIM11; WWP1; BRCA1; DZIP3; SMURF1; SMURF2; HARS; ACACB; HARS2; ACSL1; CDC23; TNFAIP3; BCOR; NEDD4L
GO:0008168	0.0405	1	15767	609	176	12	MF	methyltransferase activity	TRDMT1; ASH2L; SARDH; NSD1; SUZ12; PRMT3; PRMT5; LCMT1; COMT; PCMT1; TGS1; PEMT
GO:0016788	0.0432	1	15767	609	715	37	MF	hydrolase activity, acting on ester bonds	PPAP2A; DLG1; PDE6H; ACP6; PDE10A; ACPT; BDKRB2; ACP; PDE1A; LIPC; PDE8A; PGAM1; PDE11A; MGLL; USP7; PLCD3; PLCB2; NT5E; RAD50; PDE7B; LCAT; EIF2C2; DUSP14; DUSP12; PON3; ALPL; FBP2; ENPP7; PPP2CA; PPP2CB; G6PC2; DUSP1; SGPP1; ACHE; ALDH6A1; INPP1; PTPRS
GO:0017016	0.0435	1	15767	609	84	7	MF	Ras GTPase binding	RALBP1; ERC1; EXOC2; MLPH; RPH3AL; PKN1; RAP1A
GO:0005201	0.0435	1	15767	609	84	7	MF	extracellular matrix structural constituent	COL4A4; COL4A3; WNT16; COL11A2; WNT9B; FBLN1; ACAN
GO:0051378	0.0447	1	15767	609	9	2	MF	serotonin binding	HTR1A; HTR1B
GO:0008034	0.0447	1	15767	609	35	4	MF	lipoprotein binding	LIPC; SCARB1; VLDLR; ATP5B
GO:0016741	0.0451	1	15767	609	179	12	MF	transferase activity, transferring one-carbon groups	TRDMT1; ASH2L; SARDH; NSD1; SUZ12; PRMT3; PRMT5; LCMT1; COMT; PCMT1; TGS1; PEMT
GO:0030169	0.0454	1	15767	609	21	3	MF	low-density lipoprotein binding	LIPC; SCARB1; VLDLR
GO:0004620	0.0459	1	15767	609	85	7	MF	phospholipase activity	BDKRB2; LIPC; MGLL; PLCD3; PLCB2; LCAT; ENPP7
GO:0004674	0.0468	1	15767	609	431	24	MF	protein serine/threonine kinase activity	STK16; HIPK2; CAMK2A; CAMK2B; CSNK1A1; PRKDC; SRPK1; EGFR; MAPK10; PRKG1; CSNK1E; CDK7; GTF2H4; PRKCD; STK36; MARK3; MAP2K3; AMHR2; PDPK1; PKN1; GSK3B; MAPKAPK5; RIPK2; ADRBK1
GO:0008565	0.0484	1	15767	609	86	7	MF	protein transporter activity	XP07; AP2B1; MCL1; EIF4ENIF1; KPNA2; AP3S1; TOMM20

Identified extended leading networks of Lung injury

Phosgene-induced Lung Injury									
GO Term	P-value	Corrected P-value	R	T	G	O		Term Name	Contain Genes
GO:0009987	2.40E-54	5.00E-51	32911	172	8758	143	BP	cellular process	SPNB2; EGR1; CYP51; NRIP1; TUBA4A; BID; FYN; SP1; ATF4; RELA; BCL3; EIF2S2; PTDSS2; GSTO1; IDI1; ALDH3A1; SLC2A1; THBS1; MAPK3; TEK; CAV2; PTGS2; FZD2; GATA5; FZD4; CEBPD; DNAJC5; ARG2; MYC; CXCL12; EPOR; SOCS6; NT5C2; SOCS3; FOS; MYLK; CKAR; GSR; DLL4; LGALS3; AFP; CALM3; GAMT; STAT1; CERK; JUN; IRS2; CCL2; TGM1; ADCY6; EIF1A; PPAP2B; ADCY2; TALDO1; ADCY8; ADCY9; SRM; HOXA5; PDE4B; CCT6A; MYB; ADSS; EGR2; GADD45A; HK1; CCT5; MYD88; CH25H; CXCL1; MKNK1; CYP2F2; CCND3; MT1; PARD6B; HIF1A; ACADL; TUBB2C; TGFB1; SQLE; TRAF5; HSPA5; CYP4A12A; HSPA8; SMAD1; NOTCH2; NOTCH3; JUP; DUSP16; SFRP2; HMGCS1; EPHA2; ADD1; EIF3A; EIF3C; EIF3E; CCR1; HSPA1A; MCL1; JUNB; COL3A1; PIMI; IVD; CTPS; ALDH4A1; TIMP1; AMPD3; ACS1; SENP2; WNT2; TIE1; KDR; CDKN2B; TBXA2R; ALDH3B1; ST3GAL2; HMOX1; CD01; SUCLG2; IGFBP5; GADD45G; ARSA; WNT3A; MYBBP1A; SETD8; CSF3R; PRKCI; ASNS; PRPS1; EIF5; GCLC; ALAS1; ADRB3; PPA1; ALDOA; IL1B; BCR; MTHFD2; COL11A2; HSPA1B; ANAPC11; GSTA2; GBE1; GUCY1B3
GO:0044237	1.20E-37	2.60E-34	32911	172	5339	102	BP	cellular metabolic process	SPNB2; EGR1; CYP51; NRIP1; FYN; SP1; ATF4; RELA; BCL3; EIF2S2; PTDSS2; GSTO1; IDI1; ALDH3A1; MAPK3; TEK; PTGS2; GATA5; CEBPD; DNAJC5; ARG2; MYC; NT5C2; FOS; MYLK; GSR; AFP; GAMT; STAT1; CERK; JUN; TGM1; ADCY6; EIF1A; PPAP2B; ADCY2; TALDO1; ADCY8; ADCY9; SRM; HOXA5; PDE4B; CCT6A; MYB; ADSS; EGR2; HK1; CCT5; CH25H; MKNK1; CYP2F2; CCND3; HIF1A; ACADL; TGFB1; SQLE; CYP4A12A; HSPA8; SMAD1; NOTCH2; NOTCH3; DUSP16; HMGCS1; EPHA2; ADD1; EIF3A; EIF3C; EIF3E; HSPA1A; JUNB; PIMI; IVD; CTPS; ALDH4A1; AMPD3; ACS1; SENP2; TIE1; KDR; ALDH3B1; HMOX1; CD01; SUCLG2; GADD45G; ARSA; MYBBP1A; SETD8; PRKCI; ASNS; PRPS1; EIF5; GCLC; ALAS1; PPA1; ALDOA; BCR; MTHFD2; HSPA1B; GSTA2; GBE1; GUCY1B3
GO:0008152	3.60E-36	7.30E-33	32911	172	6447	109	BP	metabolic process	SPNB2; EGR1; CYP51; NRIP1; FYN; SP1; GPX2; ATF4; RELA; BCL3; EIF2S2; PTDSS2; GSTO1; IDI1; ALDH3A1; MAPK3; TEK; PTGS2; GATA5; CEBPD; DNAJC5; ARG2; CYP2J9; MYC; NT5C2; FOS; MYLK; GSR; AFP; GAMT; STAT1; CERK; JUN; TGM1; ADCY6; EIF1A; PPAP2B; ADCY2; TALDO1; ADCY8; ADCY9; SRM; HOXA5; PDE4B; CCT6A; MYB; ADSS; EGR2; HK1; CCT5; MYD88; CH25H; MKNK1; CYP2F2; CCND3; HIF1A; ACADL; TGFB1; SQLE; HSPA5; CYP4A12A; HSPA8; SMAD1; NOTCH2; NOTCH3; DUSP16; HMGCS1; EPHA2; ADD1; EIF3A; EIF3C; EIF3E; HSPA1A; JUNB; PIMI; IVD; CTPS; ALDH4A1; AMPD3; ACS1; SENP2; TIE1; KDR; ALDH3B1; ST3GAL2; HMOX1; CD01; SUCLG2; PLA2G7; GADD45G; ARSA; MYBBP1A; SETD8; AKR1B8; PRKCI; ASNS; PRPS1; EIF5; GCLC; ALAS1; PPA1; ALDOA; BCR; MTHFD2; HSPA1B; GSTA4; GSTA2; GBE1; GUCY1B3
GO:0065007	3.80E-27	7.70E-24	32911	172	7046	102	BP	biological regulation	SPNB2; EGR1; NRIP1; AGFG2; BID; FYN; SP1; GPX2; RGS3; ATF4; RELA; BCL3; ALDH3A1; THBS1; MAPK3; TEK; CAV2; PTGS2; FZD2; GATA5; FZD4; CEBPD; DNAJC5; ARG2; MYC; CXCL12; CXCL16; EPOR; SOCS6; SOCS3; FOS; PPP2R2A; CKAR; GSR; DLL4; RBCK1; AFP; GAMT; STAT1; CERK; IL2RG; JUN; IRS2; CCL2; ADCY6; PPAP2B; ADCY2; ADCY8; ADCY9; HOXA5; MYB; EGR2; GADD45A; HK1; MYD88; PTGFR; MKNK1; CCND3; MT1; HIF1A; ACADL; TGFB1; TRAF5; HSPA5; LMO2; HSPA8; SMAD1; NOTCH2; NOTCH3; DUSP16; YWHAQ; SFRP2; EPHA2; ADD1; EIF3C; CCR1; HSPA1A; MCL1; JUNB; F3; TIMP1; SENP2; WNT2; TIE1; KDR; CDKN2B; TBXA2R; HMOX1; CD01; IGFBP5; GADD45G; WNT3A; MYBBP1A; SETD8; PRKCI; GCLC; ADRB3; IL1B; BCR; COL11A2; HSPA1B; ETS2
GO:0044238	4.60E-27	9.40E-24	32911	172	5580	91	BP	primary metabolic process	SPNB2; EGR1; CYP51; NRIP1; FYN; SP1; ATF4; RELA; BCL3; EIF2S2; PTDSS2; IDI1; MAPK3; TEK; PTGS2; GATA5; CEBPD; DNAJC5; ARG2; MYC; NT5C2; FOS; MYLK; GSR; AFP; GAMT; STAT1; CERK; JUN; TGM1; ADCY6; EIF1A; PPAP2B; ADCY2; TALDO1; ADCY8; ADCY9; SRM; HOXA5; PDE4B; CCT6A; MYB; ADSS; EGR2; HK1; CCT5; CH25H; MKNK1; CCND3; HIF1A; ACADL; TGFB1; SQLE; HSPA5; CYP4A12A; HSPA8; SMAD1; NOTCH2; NOTCH3; HMGCS1; EPHA2; ADD1; EIF3A; EIF3C; EIF3E; HSPA1A; JUNB; PIMI; IVD; CTPS; ALDH4A1; AMPD3; SENP2; TIE1; KDR; ST3GAL2; CD01; PLA2G7; GADD45G; MYBBP1A; SETD8; PRKCI; ASNS; PRPS1; EIF5; GCLC; ALDOA; BCR; HSPA1B; GBE1; GUCY1B3
GO:0050794	3.70E-25	7.50E-22	32911	172	6318	94	BP	regulation of cellular process	SPNB2; EGR1; NRIP1; AGFG2; BID; FYN; SP1; RGS3; ATF4; RELA; BCL3; ALDH3A1; THBS1; MAPK3; TEK; CAV2; PTGS2; FZD2; GATA5; FZD4; CEBPD; DNAJC5; MYC; CXCL12; CXCL16; EPOR; SOCS6; SOCS3; FOS; PPP2R2A; CKAR; GSR; DLL4; RBCK1; AFP; STAT1; CERK; IL2RG; JUN; IRS2; CCL2; ADCY6; PPAP2B; ADCY2; ADCY8; ADCY9; HOXA5; MYB; EGR2; GADD45A; HK1; MYD88; PTGFR; MKNK1; CCND3; HIF1A; ACADL; TGFB1; TRAF5; HSPA5; LMO2; HSPA8; SMAD1; NOTCH2; NOTCH3; DUSP16; YWHAQ; SFRP2; EPHA2; EIF3C; CCR1; MCL1; JUNB; F3; TIMP1; SENP2; WNT2; TIE1; KDR; CDKN2B; TBXA2R; HMOX1; IGFBP5; GADD45G; WNT3A; MYBBP1A; SETD8; PRKCI; GCLC; ADRB3; IL1B; BCR; HSPA1B; GBE1; GUCY1B3

GO:0050789	3.80E-25	7.80E-22	32911	172	6733	97	BP	regulation of biological process	SPNB2; EGR1; NR1P1; AGFG2; BID; FYN; SP1; GPX2; RGS3; ATF4; RELA; BCL3; ALDH3A1; THBS1; MAPK3; TEK; CAV2; PTGS2; FZD2; GATA5; FZD4; CEBPD; DNJC5; ARG2; MYC; CXCL12; CXCL16; EPOR; SOCS6; SOCS3; FOS; PPP2R2A; CCKAR; GSR; DLL4; RBCK1; AFP; GAMT; STAT1; CERK; IL2RG; JUN; IRS2; CCL2; ADCY6; PPAP2B; ADCY2; ADCY8; ADCY9; HOXA5; MYB; EGR2; GADD45A; HK1; MYD88; PTGFR; MKNK1; CCND3; HIF1A; ACADL; TGFB1; TRAF5; HSPA5; LMO2; HSPA8; SMAD1; NOTCH2; NOTCH3; DUSP16; YWHAQ; SFRP2; EPHA2; EIF3C; CCR1; MCL1; JUNB; F3; TIMP1; SENP2; WNT2; TIE1; KDR; CDKN2B; TBXA2R; HMOX1; IGFBP5; GADD45G; WNT3A; MYBBP1A; SETD8; PRKCI; GCLC; ADRB3; IL1B; BCR; HSPA1B; ETS2
GO:0042221	4.30E-24	8.70E-21	32911	172	1061	41	BP	response to chemical stimulus	EGR1; FYN; GPX2; RELA; ALDH3A1; MAPK3; TEK; PTGS2; MYC; CXCL12; FOS; PPP2R2A; STAT1; JUN; IRS2; CCL2; EGR2; MYD88; CXCL1; CYP2F2; CCND3; MT1; HIF1A; TGFB1; SQLE; SMAD1; HMGCS1; CCR1; HSPA1A; MCL1; TIE1; KDR; HMOX1; CD01; ARSA; WNT3A; CSF3R; PRKCI; GCLC; IL1B; HSPA1B
GO:0048518	1.40E-22	2.80E-19	32911	172	1851	50	BP	positive regulation of biological process	EGR1; BID; SP1; ATF4; RELA; BCL3; ALDH3A1; THBS1; MAPK3; TEK; CAV2; PTGS2; GATA5; CEBPD; MYC; CXCL12; SOCS3; FOS; CCKAR; RBCK1; STAT1; IL2RG; JUN; IRS2; CCL2; HOXA5; EGR2; MYD88; CCND3; HIF1A; TGFB1; TRAF5; HSPA5; SMAD1; NOTCH2; SFRP2; EIF3C; JUNB; F3; WNT2; KDR; TBXA2R; HMOX1; WNT3A; PRKCI; GCLC; ADRB3; IL1B; HSPA1B; ETS2
GO:0048522	3.10E-22	6.30E-19	32911	172	1639	47	BP	positive regulation of cellular process	EGR1; BID; SP1; ATF4; RELA; BCL3; ALDH3A1; THBS1; MAPK3; TEK; CAV2; PTGS2; GATA5; CEBPD; MYC; CXCL12; SOCS3; FOS; CCKAR; RBCK1; STAT1; IL2RG; JUN; IRS2; CCL2; HOXA5; EGR2; MYD88; CCND3; HIF1A; TGFB1; TRAF5; HSPA5; SMAD1; NOTCH2; SFRP2; EIF3C; JUNB; F3; WNT2; KDR; HMOX1; WNT3A; PRKCI; GCLC; IL1B; ETS2
GO:0050896	1.00E-21	2.10E-18	32911	172	2388	55	BP	response to stimulus	EGR1; FYN; GPX2; RELA; BCL3; ALDH3A1; THBS1; MAPK3; TEK; PTGS2; MYC; CXCL12; FOS; PPP2R2A; CCKAR; STAT1; JUN; IRS2; FCGRT; CCL2; ADCY8; HSPB1; EGR2; GADD45A; MYD88; CXCL1; MKNK1; CYP2F2; CCND3; MT1; HIF1A; TGFB1; SQLE; HSPA5; HSPA8; SMAD1; NOTCH2; SFRP2; HMGCS1; CCR1; HSPA1A; MCL1; TIE1; KDR; HMOX1; CD01; PLA2G7; ARSA; WNT3A; CSF3R; PRKCI; GCLC; ADRB3; IL1B; HSPA1B
GO:0032502	1.20E-21	2.50E-18	32911	172	2682	58	BP	developmental process	EGR1; FYN; SP1; RELA; BCL3; THBS1; MAPK3; TEK; CAV2; PTGS2; FZD2; GATA5; FZD4; ARG2; MYC; CXCL12; EPOR; SOCS3; FOS; CCKAR; DLL4; LGALS3; GAMT; JUN; IRS2; TGM1; PPAP2B; HOXA5; MYB; EGR2; HIF1A; TGFB1; HSPA5; SMAD1; NOTCH2; NOTCH3; JUP; SFRP2; EPHA2; ADD1; CCR1; MCL1; JUNB; COL3A1; TIMP1; WNT2; TIE1; KDR; HMOX1; IGFBP5; GADD45G; ARSA; WNT3A; PRKCI; ADRB3; IL1B; BCR; COL11A2
GO:0009058	5.20E-20	1.00E-16	32911	172	2696	56	BP	biosynthetic process	EGR1; CYP51; NR1P1; SP1; ATF4; RELA; BCL3; EIF2S2; PTDSS2; GSTO1; IDI1; PTGS2; GATA5; CEBPD; ARG2; MYC; FOS; GAMT; STAT1; JUN; ADCY6; EIF1A; ADCY2; ADCY8; ADCY9; SRM; HOXA5; MYB; ADSS; EGR2; CH25H; CCND3; HIF1A; SMAD1; NOTCH2; NOTCH3; HMGCS1; EIF3A; EIF3C; EIF3E; JUNB; CTPS; ALDH4A1; AMPD3; ACSS1; SENP2; MYBBP1A; SETD8; ASNS; PRPS1; EIF5; GCLC; ALAS1; MTHFD2; GBE1; GUCY1B3
GO:0044281	1.90E-19	3.90E-16	32911	172	1343	40	BP	small molecule metabolic process	CYP51; ATF4; GSTO1; IDI1; PTGS2; ARG2; MYC; NT5C2; GSR; GAMT; ADCY6; ADCY2; TALDO1; ADCY8; ADCY9; SRM; PDE4B; ADSS; HK1; CH25H; HIF1A; ACADL; SQLE; CYP4A12A; HSPA8; HMGCS1; IVD; CTPS; ALDH4A1; AMPD3; ACSS1; CD01; SUCLG2; ASNS; PRPS1; GCLC; ALDOA; MTHFD2; GBE1; GUCY1B3
GO:0044249	3.00E-19	6.10E-16	32911	172	2599	54	BP	cellular biosynthetic process	EGR1; NR1P1; SP1; ATF4; RELA; BCL3; EIF2S2; PTDSS2; GSTO1; IDI1; PTGS2; GATA5; CEBPD; ARG2; MYC; FOS; GAMT; STAT1; JUN; ADCY6; EIF1A; ADCY2; ADCY8; ADCY9; SRM; HOXA5; MYB; ADSS; EGR2; CH25H; HIF1A; SMAD1; NOTCH2; NOTCH3; HMGCS1; EIF3A; EIF3C; EIF3E; JUNB; CTPS; ALDH4A1; AMPD3; ACSS1; SENP2; MYBBP1A; SETD8; ASNS; PRPS1; EIF5; GCLC; ALAS1; MTHFD2; GBE1; GUCY1B3
GO:0048519	7.20E-19	1.40E-15	32911	172	1637	43	BP	negative regulation of biological process	SPNB2; EGR1; NR1P1; GPX2; RGS3; RELA; BCL3; THBS1; TEK; CAV2; PTGS2; DNJC5; ARG2; MYC; SOCS6; SOCS3; DLL4; JUN; IRS2; CCL2; PPAP2B; GADD45A; HK1; MYD88; HIF1A; ACADL; TGFB1; HSPA5; LMO2; SMAD1; NOTCH3; SFRP2; MCL1; TIMP1; TIE1; CDKN2B; HMOX1; WNT3A; MYBBP1A; GCLC; ADRB3; IL1B; HSPA1B
GO:0010033	1.70E-18	3.40E-15	32911	172	666	29	BP	response to organic substance	EGR1; FYN; RELA; ALDH3A1; MAPK3; TEK; PTGS2; MYC; FOS; PPP2R2A; STAT1; IRS2; EGR2; MYD88; CCND3; TGFB1; SQLE; SMAD1; HMGCS1; CCR1; HSPA1A; MCL1; HMOX1; CD01; ARSA; WNT3A; PRKCI; IL1B; HSPA1B
GO:0051239	2.70E-17	5.50E-14	32911	172	1078	34	BP	regulation of multicellular organismal process	EGR1; RELA; BCL3; THBS1; TEK; PTGS2; ARG2; MYC; CXCL12; GAMT; IL2RG; JUN; CCL2; HOXA5; EGR2; MYD88; HIF1A; TGFB1; HSPA5; LMO2; SMAD1; NOTCH3; SFRP2; EPHA2; CCR1; WNT2; TIE1; KDR; TBXA2R; HMOX1; WNT3A; ADRB3; IL1B; HSPA1B
GO:0019222	5.60E-17	1.10E-13	32911	172	3142	56	BP	regulation of metabolic process	EGR1; NR1P1; AGFG2; SP1; RGS3; ATF4; RELA; BCL3; MAPK3; TEK; PTGS2; GATA5; CEBPD; ARG2; MYC; SOCS3; FOS; STAT1; CERK; IL2RG; JUN; IRS2; ADCY6; PPAP2B; ADCY2; ADCY9; HOXA5; MYB; EGR2; GADD45A; MYD88; MKNK1; HIF1A; ACADL; TGFB1; HSPA5; SMAD1; NOTCH2; NOTCH3; DUSP16; SFRP2; EIF3C; JUNB; SENP2; WNT2; HMOX1; GADD45G; WNT3A; MYBBP1A; SETD8; GCLC; ADRB3; IL1B; BCR; HSPA1B; ETS2
GO:0050793	1.80E-16	3.60E-13	32911	172	794	29	BP	regulation of developmental process	FYN; RELA; THBS1; TEK; PTGS2; MYC; CXCL12; SOCS3; IL2RG; JUN; CCL2; HOXA5; EGR2; HIF1A; TGFB1; HSPA5; LMO2; SMAD1; NOTCH2; NOTCH3; SFRP2; EPHA2; JUNB; WNT2; TIE1; KDR; TBXA2R; WNT3A; IL1B

GO:0031323	4.40E-16	8.90E-13	32911	172	2749	51	BP	regulation of cellular metabolic process	EGR1; NR1P1; AGFG2; SP1; ATF4; RELA; BCL3; MAPK3; TEK; PTGS2; GATA5; CEBPD; MYC; SOCS3; FOS; STAT1; CERK; JUN; IRS2; ADCY6; PPAP2B; ADCY2; ADCY9; HOXA5; MYB; EGR2; GADD45A; MYD88; MKNK1; HIF1A; ACADL; TGFB1; HSPA5; SMAD1; NOTCH2; NOTCH3; DUSP16; SFRP2; EIF3C; JUNB; SENP2; WNT2; HMOX1; GADD45G; WNT3A; MYBBP1A; SETD8; GCLC; ADRB3; IL1B; ETS2
GO:0065009	5.90E-16	1.10E-12	32911	172	831	29	BP	regulation of molecular function	AGFG2; RGS3; RELA; MAPK3; ARG2; MYC; CXCL12; CCKAR; CERK; IRS2; ADCY6; PPAP2B; ADCY2; ADCY9; GADD45A; HK1; MYD88; HIF1A; TGFB1; HSPA5; DUSP16; SFRP2; HMOX1; GADD45G; WNT3A; ADRB3; IL1B; BCR; HSPA1B
GO:0048869	6.60E-16	1.30E-12	32911	172	1443	37	BP	cellular developmental process	EGR1; SP1; BCL3; CAV2; PTGS2; FZD2; GATA5; FZD4; CXCL12; SOCS3; CCKAR; DLL4; LGALS3; JUN; HOXA5; EGR2; HIF1A; TGFB1; SMAD1; NOTCH2; NOTCH3; SFRP2; EPHA2; ADD1; CCR1; MCL1; JUNB; TIMP1; WNT2; TIE1; KDR; IGFBP5; GADD45G; WNT3A; ADRB3; ADRB2; COL11A2
GO:0051716	7.40E-16	1.40E-12	32911	172	645	26	BP	cellular response to stimulus	EGR1; BCL3; MAPK3; MYC; FOS; STAT1; JUN; IRS2; CCL2; GADD45A; MYD88; CXCL1; HIF1A; TGFB1; HSPA5; SMAD1; SFRP2; HMGCS1; CCR1; HSPA1A; HMOX1; WNT3A; CSF3R; PRKCI; IL1B; HSPA1B
GO:0048856	3.00E-15	6.10E-12	32911	172	1515	37	BP	anatomical structure development	FYN; SP1; RELA; BCL3; THBS1; MAPK3; TEK; CAV2; PTGS2; ARG2; CXCL12; EPOR; SOCS3; FOS; CCKAR; LGALS3; IRS2; PPAP2B; HOXA5; MYB; EGR2; HIF1A; TGFB1; HSPA5; SMAD1; NOTCH3; JUP; SFRP2; EPHA2; JUNB; COL3A1; WNT2; KDR; ARSA; WNT3A; DDIT4; DKO
GO:0048523	4.90E-15	9.80E-12	32911	172	1452	36	BP	negative regulation of cellular process	SPNB2; EGR1; NR1P1; RGS3; RELA; BCL3; TEK; CAV2; PTGS2; DNJC5; MYC; SOCS6; SOCS3; DLL4; JUN; IRS2; PPAP2B; GADD45A; HK1; ACADL; TGFB1; HSPA5; LMO2; SMAD1; NOTCH3; SFRP2; MCL1; TIMP1; TIE1; CDKN2B; HMOX1; WNT3A; MYBBP1A; GCLC; IL1B; HSPA1B
GO:0065008	1.10E-14	2.20E-11	32911	172	1160	32	BP	regulation of biological quality	SPNB2; EGR1; BID; FYN; GPX2; PTGS2; FZD2; FZD4; EPOR; SOCS6; CCKAR; GSR; AFP; JUN; CCL4; PPAP2B; MT1; HIF1A; ACADL; TGFB1; SMAD1; ADD1; HSPA1A; F3; KDR; TBXA2R; HMOX1; CDO1; ADRB3; IL1B; COL11A2; HSPA1B
GO:0009893	3.20E-14	6.40E-11	32911	172	898	28	BP	positive regulation of metabolic process	EGR1; SP1; ATF4; RELA; BCL3; MAPK3; TEK; PTGS2; GATA5; CEBPD; MYC; FOS; JUN; HOXA5; EGR2; MYD88; HIF1A; TGFB1; HSPA5; SMAD1; EIF3C; JUNB; WNT2; WNT3A; GCLC; ADRB3; IL1B; ETS2
GO:0031325	3.70E-14	7.50E-11	32911	172	832	27	BP	positive regulation of cellular metabolic process	EGR1; SP1; ATF4; RELA; BCL3; MAPK3; TEK; PTGS2; GATA5; CEBPD; MYC; FOS; JUN; HOXA5; EGR2; MYD88; HIF1A; TGFB1; HSPA5; SMAD1; EIF3C; JUNB; WNT2; WNT3A; GCLC; IL1B; ETS2
GO:0070887	6.60E-14	1.30E-10	32911	172	224	16	BP	cellular response to chemical stimulus	EGR1; MYC; STAT1; IRS2; CCL2; CXCL1; HIF1A; TGFB1; SMAD1; HMGCS1; CCR1; HMOX1; WNT3A; CSF3R; PRKCI; IL1B
GO:0051094	7.20E-14	1.40E-10	32911	172	362	19	BP	positive regulation of developmental process	RELA; TEK; PTGS2; MYC; CXCL12; SOCS3; IL2RG; JUN; HIF1A; TGFB1; HSPA5; SMAD1; SFRP2; JUNB; WNT2; KDR; TBXA2R; WNT3A; IL1B
GO:0030154	7.60E-14	1.50E-10	32911	172	1083	30	BP	cell differentiation	EGR1; SP1; BCL3; PTGS2; FZD2; GATA5; FZD4; SOCS3; DLL4; LGALS3; JUN; HOXA5; EGR2; HIF1A; TGFB1; NOTCH2; NOTCH3; SFRP2; EPHA2; ADD1; CCR1; MCL1; JUNB; TIE1; KDR; IGFBP5; GADD45G; WNT3A; ADRB3; COL11A2
GO:0042981	7.90E-14	1.50E-10	32911	172	653	24	BP	regulation of apoptosis	BID; BCL3; TEK; PTGS2; DNJC5; MYC; RBCK1; STAT1; JUN; IRS2; HK1; HIF1A; TGFB1; TRAF5; NOTCH2; SFRP2; MCL1; TIMP1; KDR; HMOX1; WNT3A; GCLC; IL1B; HSPA1B
GO:0045893	8.50E-14	1.70E-10	32911	172	473	21	BP	positive regulation of transcription, DNA-dependent	EGR1; SP1; ATF4; RELA; BCL3; GATA5; CEBPD; MYC; FOS; JUN; HOXA5; EGR2; MYD88; HIF1A; TGFB1; SMAD1; JUNB; WNT2; WNT3A; IL1B; ETS2
GO:0051254	9.70E-14	1.90E-10	32911	172	476	21	BP	positive regulation of RNA metabolic process	EGR1; SP1; ATF4; RELA; BCL3; GATA5; CEBPD; MYC; FOS; JUN; HOXA5; EGR2; MYD88; HIF1A; TGFB1; SMAD1; JUNB; WNT2; WNT3A; IL1B; ETS2
GO:0043067	1.00E-13	2.10E-10	32911	172	662	24	BP	regulation of programmed cell death	BID; BCL3; TEK; PTGS2; DNJC5; MYC; RBCK1; STAT1; JUN; IRS2; HK1; HIF1A; TGFB1; TRAF5; NOTCH2; SFRP2; MCL1; TIMP1; KDR; HMOX1; WNT3A; GCLC; IL1B; HSPA1B
GO:0042127	1.30E-13	2.70E-10	32911	172	670	24	BP	regulation of cell proliferation	RELA; ALDH3A1; TEK; CAV2; PTGS2; MYC; CXCL12; STAT1; JUN; IRS2; CCL2; HOXA5; MYD88; CCND3; HIF1A; TGFB1; TRAF5; SMAD1; SFRP2; WNT2; KDR; CDKN2B; HMOX1; WNT3A
GO:0010604	1.40E-13	2.80E-10	32911	172	808	26	BP	positive regulation of macromolecule metabolic process	EGR1; SP1; ATF4; RELA; BCL3; MAPK3; TEK; GATA5; CEBPD; MYC; FOS; JUN; HOXA5; EGR2; MYD88; HIF1A; TGFB1; HSPA5; SMAD1; EIF3C; JUNB; WNT2; WNT3A; GCLC; IL1B; ETS2

GO:0010941	1.60E-13	3.20E-10	32911	172	675	24	BP	regulation of cell death	BID; BCL3; TEK; PTGS2; DNAJC5; MYC; RBCK1; STAT1; JUN; IRS2; HK1; HIF1A; TGFB1; TRAF5; NOTCH2; SFRP2; MCL1; TIMP1; KDR; HMOX1; WNT3A; GCLC; IL1B; HSPA1B
GO:0006950	2.60E-13	5.30E-10	32911	172	1137	30	BP	response to stress	GPX2; RELA; BCL3; ALDH3A1; THBS1; MAPK3; PTGS2; CCKAR; JUN; CCL2; HSPB1; GADD45A; MYD88; CXCL1; MKNK1; HIF1A; TGFB1; HSPA5; HSPA8; SMAD1; NOTCH2; CCR1; HSPA1A; KDR; HMOX1; PLA2G7; GCLC; ADRB3; IL1B; HSPA1B
GO:0031328	2.60E-13	5.30E-10	32911	172	691	24	BP	positive regulation of cellular biosynthetic process	EGR1; SP1; ATF4; RELA; BCL3; MAPK3; PTGS2; GATA5; CEBPD; MYC; FOS; JUN; HOXA5; EGR2; MYD88; HIF1A; TGFB1; SMAD1; EIF3C; JUNB; WNT2; WNT3A; IL1B; ETS2
GO:0023052	2.90E-13	5.90E-10	32911	172	3239	51	BP	signaling	EGR1; FYN; RGS3; RELA; BCL3; MAPK3; TEK; CAV2; FZD2; FZD4; IL10RB; SOCS6; SOCS3; CCKAR; DLL4; STAT1; CERK; IRS2; CCL2; ADCY6; PPAP2B; ADCY2; ADCY8; ADCY9; HOXA5; OSMR; MYD88; PTGFR; MKNK1; MT1; TGFB1; HSPA5; SMAD1; NOTCH2; NOTCH3; YWHAQ; SFRP2; EPHA2; CCR1; SENP2; CBL; WNT2; TIE1; KDR; TBXA2R; HMOX1; WNT3A; PRKCI; ADRB3; BCR; GUCY1B3
GO:0006807	3.40E-13	6.90E-10	32911	172	3023	49	BP	nitrogen compound metabolic process	EGR1; NR1P1; SP1; ATF4; RELA; BCL3; GATA5; CEBPD; ARG2; MYC; NT5C2; FOS; GATM; STAT1; JUN; ADCY6; ADCY2; TALDO1; ADCY8; ADCY9; SRM; HOXA5; PDE4B; MYB; ADSS; EGR2; CCND3; HIF1A; ACADL; HSPA8; SMAD1; NOTCH2; NOTCH3; HSPA1A; JUNB; IVD; CTPS; ALDH4A1; AMPD3; SENP2; HMOX1; CD01; MYBBP1A; SETD8; ASNS; PRPS1; ALAS1; HSPA1B; GUCY1B3
GO:0009891	4.20E-13	8.40E-10	32911	172	706	24	BP	positive regulation of biosynthetic process	EGR1; SP1; ATF4; RELA; BCL3; MAPK3; PTGS2; GATA5; CEBPD; MYC; FOS; JUN; HOXA5; EGR2; MYD88; HIF1A; TGFB1; SMAD1; EIF3C; JUNB; WNT2; WNT3A; IL1B; ETS2
GO:0034641	4.80E-13	9.70E-10	32911	172	2937	48	BP	cellular nitrogen compound metabolic process	EGR1; NR1P1; SP1; ATF4; RELA; BCL3; GATA5; CEBPD; ARG2; MYC; NT5C2; FOS; GATM; STAT1; JUN; ADCY6; ADCY2; TALDO1; ADCY8; ADCY9; SRM; HOXA5; PDE4B; MYB; ADSS; EGR2; HIF1A; ACADL; HSPA8; SMAD1; NOTCH2; NOTCH3; HSPA1A; JUNB; IVD; CTPS; ALDH4A1; AMPD3; SENP2; HMOX1; CD01; MYBBP1A; SETD8; ASNS; PRPS1; ALAS1; HSPA1B; GUCY1B3
GO:0080090	6.20E-13	1.20E-09	32911	172	2625	45	BP	regulation of primary metabolic process	EGR1; NR1P1; AGFG2; SP1; ATF4; RELA; BCL3; MAPK3; TEK; GATA5; CEBPD; MYC; SOCS3; FOS; STAT1; JUN; ADCY6; PPAP2B; ADCY2; ADCY9; HOXA5; MYB; EGR2; MYD88; MKNK1; HIF1A; ACADL; TGFB1; HSPA5; SMAD1; NOTCH2; NOTCH3; SFRP2; EIF3C; JUNB; SENP2; WNT2; HMOX1; WNT3A; MYBBP1A; SETD8; GCLC; ADRB3; TIE1; ETS2
GO:0010557	6.30E-13	1.20E-09	32911	172	652	23	BP	positive regulation of macromolecule biosynthetic process	EGR1; SP1; ATF4; RELA; BCL3; MAPK3; GATA5; CEBPD; MYC; FOS; JUN; HOXA5; EGR2; MYD88; HIF1A; TGFB1; SMAD1; EIF3C; JUNB; WNT2; WNT3A; IL1B; ETS2
GO:0044283	8.80E-13	1.70E-09	32911	172	417	19	BP	small molecule biosynthetic process	ATF4; GSTO1; PTGS2; GATM; ADCY6; ADCY2; ADCY8; ADCY9; SRM; ADSS; CH25H; CTPS; ALDH4A1; AMPD3; ACS1; ASNS; PRPS1; GCLC; GUCY1B3
GO:0045944	8.80E-13	1.70E-09	32911	172	417	19	BP	positive regulation of transcription from RNA polymerase II promoter	EGR1; SP1; ATF4; BCL3; GATA5; CEBPD; MYC; FOS; JUN; HOXA5; EGR2; MYD88; HIF1A; TGFB1; SMAD1; JUNB; WNT2; IL1B; ETS2
GO:0023033	1.20E-12	2.50E-09	32911	172	3130	49	BP	signaling pathway	EGR1; FYN; RGS3; RELA; BCL3; MAPK3; TEK; FZD2; FZD4; IL10RB; SOCS6; SOCS3; CCKAR; DLL4; STAT1; CERK; IRS2; CCL2; ADCY6; PPAP2B; ADCY2; ADCY8; ADCY9; OSMR; MYD88; PTGFR; MKNK1; MT1; TGFB1; HSPA5; SMAD1; NOTCH2; NOTCH3; YWHAQ; SFRP2; EPHA2; CCR1; SENP2; CBL; WNT2; TIE1; KDR; TBXA2R; HMOX1; WNT3A; PRKCI; ADRB3; BCR; GUCY1B3
GO:0022603	3.40E-12	6.90E-09	32911	172	290	16	BP	regulation of anatomical structure morphogenesis	FYN; THBS1; TEK; PTGS2; MYC; CXCL12; CCL2; TGFB1; SFRP2; EPHA2; WNT2; TIE1; KDR; TBXA2R; WNT3A; IL1B
GO:0045941	3.50E-12	7.10E-09	32911	172	575	21	BP	positive regulation of transcription	EGR1; SP1; ATF4; RELA; BCL3; GATA5; CEBPD; MYC; FOS; JUN; HOXA5; EGR2; MYD88; HIF1A; TGFB1; SMAD1; JUNB; WNT2; WNT3A; IL1B; ETS2
GO:0051173	4.80E-12	9.60E-09	32911	172	651	22	BP	positive regulation of nitrogen compound metabolic process	EGR1; SP1; ATF4; RELA; BCL3; PTGS2; GATA5; CEBPD; MYC; FOS; JUN; HOXA5; EGR2; MYD88; HIF1A; TGFB1; SMAD1; JUNB; WNT2; WNT3A; IL1B; ETS2

GO:0044260	6.00E-12	1.20E-08	32911	172	3875	54	BP	cellular macromolecule metabolic process	SPNB2; EGR1; NRIP1; FYN; SP1; ATF4; RELA; BCL3; EIF2S2; MAPK3; TEK; GATA5; CEBPD; DNAJC5; MYC; FOS; MYLK; STAT1; JUN; TGM1; EIF1A; HOXA5; CCT6A; MYB; EGR2; HK1; CCT5; MKNK1; HIF1A; TGFB1; HSPA8; SMAD1; NOTCH2; NOTCH3; EPHA2; ADD1; EIF3A; EIF3C; EIF3E; HSPA1A; JUNB; PIM1; SENP2; TIE1; KDR; ST3GAL2; GADD45G; MYBBP1A; SETD8; PRKCI; EIF5; BCR; HSPA1B; GBE1
GO:0031326	8.10E-12	1.60E-08	32911	172	2279	40	BP	regulation of cellular biosynthetic process	EGR1; NRIP1; SP1; ATF4; RELA; BCL3; MAPK3; PTGS2; GATA5; CEBPD; MYC; FOS; STAT1; JUN; ADCY6; PPAP2B; ADCY2; ADCY9; HOXA5; MYB; EGR2; MYD88; MKNK1; HIF1A; ACADL; TGFB1; SMAD1; NOTCH2; NOTCH3; EIF3C; JUNB; SENP2; WNT2; HMOX1; WNT3A; MYBBP1A; SETD8; ADRB3; IL1B; ETS2
GO:0009889	1.00E-11	2.10E-08	32911	172	2301	40	BP	regulation of biosynthetic process	EGR1; NRIP1; SP1; ATF4; RELA; BCL3; MAPK3; PTGS2; GATA5; CEBPD; MYC; FOS; STAT1; JUN; ADCY6; PPAP2B; ADCY2; ADCY9; HOXA5; MYB; EGR2; MYD88; MKNK1; HIF1A; ACADL; TGFB1; SMAD1; NOTCH2; NOTCH3; EIF3C; JUNB; SENP2; WNT2; HMOX1; WNT3A; MYBBP1A; SETD8; ADRB3; IL1B; ETS2
GO:0009605	1.00E-11	2.20E-08	32911	172	313	16	BP	response to external stimulus	FYN; TEK; MYC; CXCL12; FOS; CCKAR; STAT1; JUN; CCL2; CXCL1; SFRP2; CCR1; TIE1; ARSA; CSF3R; IL1B
GO:0010628	1.20E-11	2.40E-08	32911	172	614	21	BP	positive regulation of gene expression	EGR1; SP1; ATF4; RELA; BCL3; GATA5; CEBPD; MYC; FOS; JUN; HOXA5; EGR2; MYD88; HIF1A; TGFB1; SMAD1; JUNB; WNT2; WNT3A; IL1B; ETS2
GO:0042592	1.20E-11	2.60E-08	32911	172	616	21	BP	homeostatic process	GPX2; FZD2; EPOR; SOCS6; CCKAR; GSR; JUN; CCL2; MT1; HIF1A; ACADL; TGFB1; SMAD1; ADD1; HSPA1A; KDR; TBXA2R; ADRB3; IL1B; COL11A2; HSPA1B
GO:0045935	1.90E-11	3.90E-08	32911	172	630	21	BP	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	EGR1; SP1; ATF4; RELA; BCL3; GATA5; CEBPD; MYC; FOS; JUN; HOXA5; EGR2; MYD88; HIF1A; TGFB1; SMAD1; JUNB; WNT2; WNT3A; IL1B; ETS2
GO:0044093	2.00E-11	4.10E-08	32911	172	381	17	BP	positive regulation of molecular function	RELA; MYC; CXCL12; CCKAR; CERK; ADCY6; PPAP2B; ADCY2; ADCY9; MYD88; TGFB1; HSPA5; SFRP2; GADD45G; WNT3A; ADRB3; IL1B
GO:0043170	2.20E-11	4.50E-08	32911	172	4397	57	BP	macromolecule metabolic process	SPNB2; EGR1; NRIP1; FYN; SP1; ATF4; RELA; BCL3; EIF2S2; MAPK3; TEK; GATA5; CEBPD; DNAJC5; MYC; FOS; MYLK; STAT1; JUN; TGM1; EIF1A; HOXA5; CCT6A; MYB; EGR2; HK1; CCT5; MYD88; MKNK1; CCND3; HIF1A; TGFB1; HSPA5; HSPA8; SMAD1; NOTCH2; NOTCH3; EPHA2; ADD1; EIF3A; EIF3C; EIF3E; HSPA1A; JUNB; PIM1; SENP2; TIE1; KDR; ST3GAL2; GADD45G; MYBBP1A; SETD8; PRKCI; EIF5; BCR; HSPA1B; GBE1
GO:0008284	2.40E-11	4.80E-08	32911	172	385	17	BP	positive regulation of cell proliferation	RELA; ALDH3A1; PTGS2; MYC; CXCL12; STAT1; JUN; IRS2; CCL2; MYD88; CCND3; HIF1A; TGFB1; TRAF5; WNT2; KDR; WNT3A
GO:0045765	5.80E-11	1.10E-07	32911	172	65	9	BP	regulation of angiogenesis	THBS1; TEK; PTGS2; CCL2; EPHA2; TIE1; KDR; TBXA2R; IL1B
GO:0006357	7.40E-11	1.40E-07	32911	172	677	21	BP	regulation of transcription from RNA polymerase II promoter	EGR1; NRIP1; SP1; ATF4; BCL3; GATA5; CEBPD; MYC; FOS; JUN; HOXA5; EGR2; MYD88; HIF1A; TGFB1; SMAD1; JUNB; WNT2; HMOX1; IL1B; ETS2
GO:0051171	9.60E-11	1.90E-07	32911	172	2253	38	BP	regulation of nitrogen compound metabolic process	EGR1; NRIP1; AGFG2; SP1; ATF4; RELA; BCL3; MAPK3; PTGS2; GATA5; CEBPD; MYC; FOS; STAT1; JUN; ADCY6; PPAP2B; ADCY2; ADCY9; HOXA5; MYB; EGR2; MYD88; HIF1A; TGFB1; SMAD1; NOTCH2; NOTCH3; JUNB; SENP2; WNT2; HMOX1; WNT3A; MYBBP1A; SETD8; ADRB3; IL1B; ETS2
GO:0009124	1.00E-10	2.00E-07	32911	172	46	8	BP	nucleoside monophosphate biosynthetic process	ADCY6; ADCY2; ADCY8; ADCY9; ADSS; AMPD3; PRPS1; GUCY1B3
GO:0009123	1.10E-10	2.30E-07	32911	172	70	9	BP	nucleoside monophosphate metabolic process	ADCY6; ADCY2; ADCY8; ADCY9; PDE4B; ADSS; AMPD3; PRPS1; GUCY1B3
GO:0032501	1.50E-10	3.10E-07	32911	172	3092	45	BP	multicellular organismal process	EGR1; NRIP1; FYN; SP1; GPX2; RELA; MAPK3; PTGS2; FZD2; FZD4; ARG2; MYC; CXCL12; SOCS3; CCKAR; GSR; DLL4; AFP; GAMT; STAT1; JUN; PPAP2B; ADCY8; HOXA5; PDE4B; HIF1A; ACADL; TGFB1; SMAD1; NOTCH2; NOTCH3; SFRP2; ADD1; MCL1; JUNB; F3; WNT2; KDR; CD01; GADD45G; WNT3A; HMG1A; ADRB3; IL1B; COL11A2

GO:0060255	1.90E-10	3.80E-07	32911	172	2531	40	BP	regulation of macromolecule metabolic process	EGR1; NR1P1; SP1; ATF4; RELA; BCL3; MAPK3; TEK; GATA5; CEBPD; MYC; SOCS3; FOS; STAT1; IL2RG; JUN; PPAP2B; HOXA5; MYB; EGR2; MYD88; MKNK1; HIF1A; TGFB1; HSPA5; SMAD1; NOTCH2; NOTCH3; SFRP2; EIF3C; JUNB; SENP2; WNT2; HMOX1; WNT3A; MYBBP1A; SETD8; GCLC; IL1B; ETS2
GO:0051270	2.00E-10	4.10E-07	32911	172	179	12	BP	regulation of cellular component movement	TEK; PTGS2; CXCL12; DLL4; IRS2; CCL2; HIF1A; EPHA2; F3; TIE1; KDR; WNT3A
GO:0019219	2.70E-10	5.40E-07	32911	172	2226	37	BP	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	EGR1; NR1P1; AGFG2; SP1; ATF4; RELA; BCL3; MAPK3; GATA5; CEBPD; MYC; FOS; STAT1; JUN; ADCY6; PPAP2B; ADCY2; ADCY9; HOXA5; MYB; EGR2; MYD88; HIF1A; TGFB1; SMAD1; NOTCH2; NOTCH3; JUNB; SENP2; WNT2; HMOX1; WNT3A; MYBBP1A; SETD8; ADRB3; IL1B; ETS2
GO:0019752	3.40E-10	6.80E-07	32911	172	522	18	BP	carboxylic acid metabolic process	ATF4; GSTO1; PTGS2; ARG2; GAMT; CH25H; HIF1A; ACADL; CYP4A12A; IVD; CTPS; ALDH4A1; ACS1; CD01; SUCLG2; ASNS; GCLC; MTHFD2
GO:0043436	3.40E-10	6.80E-07	32911	172	522	18	BP	oxoacid metabolic process	ATF4; GSTO1; PTGS2; ARG2; GAMT; CH25H; HIF1A; ACADL; CYP4A12A; IVD; CTPS; ALDH4A1; ACS1; CD01; SUCLG2; ASNS; GCLC; MTHFD2
GO:0006082	3.50E-10	7.00E-07	32911	172	523	18	BP	organic acid metabolic process	ATF4; GSTO1; PTGS2; ARG2; GAMT; CH25H; HIF1A; ACADL; CYP4A12A; IVD; CTPS; ALDH4A1; ACS1; CD01; SUCLG2; ASNS; GCLC; MTHFD2
GO:0023034	3.70E-10	7.50E-07	32911	172	818	22	BP	intracellular signaling pathway	BCL3; MAPK3; TEK; FZD2; SOCS6; SOCS3; STAT1; ADCY6; ADCY2; ADCY8; ADCY9; MYD88; MKNK1; HSPA5; SMAD1; YWHAQ; TBXA2R; HMOX1; PRKCI; ADRB3; BCR; GUCY1B3
GO:0042180	5.20E-10	1.00E-06	32911	172	536	18	BP	cellular ketone metabolic process	ATF4; GSTO1; PTGS2; ARG2; GAMT; CH25H; HIF1A; ACADL; CYP4A12A; IVD; CTPS; ALDH4A1; ACS1; CD01; SUCLG2; ASNS; GCLC; MTHFD2
GO:0044271	5.60E-10	1.10E-06	32911	172	294	14	BP	cellular nitrogen compound biosynthetic process	ARG2; ADCY6; ADCY2; ADCY8; ADCY9; SRM; ADSS; CTPS; ALDH4A1; AMPD3; ASNS; PRPS1; ALAS1; GUCY1B3
GO:0030334	6.40E-10	1.30E-06	32911	172	155	11	BP	regulation of cell migration	TEK; PTGS2; CXCL12; DLL4; IRS2; CCL2; HIF1A; EPHA2; F3; TIE1; KDR
GO:0006355	7.50E-10	1.50E-06	32911	172	1193	26	BP	regulation of transcription, DNA-dependent	EGR1; NR1P1; SP1; ATF4; RELA; BCL3; GATA5; CEBPD; MYC; FOS; STAT1; JUN; HOXA5; MYB; EGR2; MYD88; HIF1A; TGFB1; SMAD1; NOTCH3; JUNB; WNT2; HMOX1; WNT3A; IL1B; ETS2
GO:0050790	1.00E-09	2.00E-06	32911	172	705	20	BP	regulation of catalytic activity	AGFG2; RGS3; ARG2; MYC; CERK; IRS2; ADCY6; ADCY2; ADCY9; GADD45A; HIF1A; HSPA5; DUSP16; SFRP2; GADD45G; WNT3A; ADRB3; IL1B; BCR; HSPA1B
GO:0051252	1.00E-09	2.10E-06	32911	172	1213	26	BP	regulation of RNA metabolic process	EGR1; NR1P1; SP1; ATF4; RELA; BCL3; GATA5; CEBPD; MYC; FOS; STAT1; JUN; HOXA5; MYB; EGR2; MYD88; HIF1A; TGFB1; SMAD1; NOTCH3; JUNB; WNT2; HMOX1; WNT3A; IL1B; ETS2
GO:0009653	1.90E-09	3.80E-06	32911	172	893	22	BP	anatomical structure morphogenesis	SP1; RELA; MAPK3; FZD4; MYC; CXCL12; SOCS3; CCKAR; GAMT; TGM1; PPAP2B; HOXA5; HIF1A; TGFB1; NOTCH2; SFRP2; EPHA2; ADD1; WNT2; KDR; WNT3A; COL11A2
GO:0032879	1.90E-09	3.90E-06	32911	172	656	19	BP	regulation of localization	TEK; PTGS2; CXCL12; CCKAR; DLL4; RBCK1; IRS2; CCL2; HK1; HIF1A; TGFB1; EPHA2; F3; TIE1; KDR; HMOX1; WNT3A; PRKCI; TIE1
GO:0040012	2.20E-09	4.40E-06	32911	172	174	11	BP	regulation of locomotion	TEK; PTGS2; CXCL12; DLL4; IRS2; CCL2; HIF1A; EPHA2; F3; TIE1; KDR
GO:0010646	2.50E-09	5.00E-06	32911	172	824	21	BP	regulation of cell communication	EGR1; RGS3; RELA; CAV2; PTGS2; CXCL12; SOCS6; SOCS3; CCKAR; RBCK1; IRS2; CCL2; MYD88; HIF1A; HSPA5; DUSP16; SFRP2; KDR; WNT3A; IL1B; BCR
GO:0044267	2.50E-09	5.10E-06	32911	172	1556	29	BP	cellular protein metabolic process	SPNB2; FYN; EIF2S2; MAPK3; TEK; DNAJC5; MYLK; TGM1; EIF1A; CCT6A; HK1; CCT5; MKNK1; TGFB1; HSPA8; SMAD1; EPHA2; EIF3A; EIF3C; EIF3E; PIM1; SENP2; TIE1; KDR; ST3GAL2; GADD45G; PRKCI; EIF5; BCR
GO:0046483	2.60E-09	5.20E-06	32911	172	391	15	BP	heterocycle metabolic process	ADCY6; ADCY2; ADCY8; ADCY9; PDE4B; ADSS; HSPA8; CTPS; ALDH4A1; AMPD3; HMOX1; PRPS1; ALAS1; MTHFD2; GUCY1B3
GO:0010468	4.00E-09	8.10E-06	32911	172	2231	35	BP	regulation of gene expression	EGR1; NR1P1; SP1; ATF4; RELA; BCL3; MAPK3; GATA5; CEBPD; MYC; FOS; STAT1; IL2RG; JUN; PPAP2B; HOXA5; MYB; EGR2; MYD88; MKNK1; HIF1A; TGFB1; SMAD1; NOTCH2; NOTCH3; EIF3C; JUNB; SENP2; WNT2; HMOX1; WNT3A; MYBBP1A; SETD8; IL1B; ETS2

GO:0006139	4.80E-09	9.60E-06	32911	172	2708	39	BP	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	EGR1; NRIP1; SP1; ATF4; RELA; BCL3; GATA5; CEBPD; MYC; NT5C2; FOS; GATM; STAT1; JUN; ADCY6; ADCY2; TALDO1; ADCY8; ADCY9; HOXA5; PDE4B; MYB; ADSS; EGR2; HIF1A; HSPA8; SMAD1; NOTCH2; NOTCH3; HSPA1A; JUNB; CTPS; AMPD3; SENP2; MYBBP1A; SETD8; PRPS1; HSPA1B; GUCY1B3
GO:0010556	7.00E-09	1.40E-05	32911	172	2166	34	BP	regulation of macromolecule biosynthetic process	EGR1; NRIP1; SP1; ATF4; RELA; BCL3; MAPK3; GATA5; CEBPD; MYC; FOS; STAT1; JUN; PPAP2B; HOXA5; MYB; EGR2; MYD88; MKNK1; HIF1A; TGFB1; SMAD1; NOTCH2; NOTCH3; EIF3C; JUNB; SENP2; WNT2; HMOX1; WNT3A; MYBBP1A; SETD8; IL1B; ETS2
GO:0055114	7.70E-09	1.50E-05	32911	172	637	18	BP	oxidation reduction	CYP51; GPX2; ALDH3A1; PTGS2; CYP2J9; GSR; CH25H; CYP2F2; ACADL; SQLE; IVD; ALDH4A1; ALDH3B1; HMOX1; CD01; MYBBP1A; AKR1B8; MTHFD2
GO:0006796	8.20E-09	1.60E-05	32911	172	882	21	BP	phosphate metabolic process	SPNB2; FYN; MAPK3; TEK; MYLK; CERK; PPAP2B; HK1; MKNK1; CCND3; TGFB1; SMAD1; DUSP16; EPHA2; PIM1; TIE1; KDR; GADD45G; PRKCI; PPA1; BCR
GO:0006793	8.60E-09	1.70E-05	32911	172	884	21	BP	phosphorus metabolic process	SPNB2; FYN; MAPK3; TEK; MYLK; CERK; PPAP2B; HK1; MKNK1; CCND3; TGFB1; SMAD1; DUSP16; EPHA2; PIM1; TIE1; KDR; GADD45G; PRKCI; PPA1; BCR
GO:0045449	1.00E-08	2.00E-05	32911	172	1978	32	BP	regulation of transcription	EGR1; NRIP1; SP1; ATF4; RELA; BCL3; MAPK3; GATA5; CEBPD; MYC; FOS; STAT1; JUN; PPAP2B; HOXA5; MYB; EGR2; MYD88; HIF1A; TGFB1; SMAD1; NOTCH2; NOTCH3; JUNB; SENP2; WNT2; HMOX1; WNT3A; MYBBP1A; SETD8; IL1B; ETS2
GO:0009719	1.10E-08	2.20E-05	32911	172	255	12	BP	response to endogenous stimulus	ALDH3A1; TEK; STAT1; IRS2; EGR2; CCND3; TGFB1; HMGC1; HMOX1; CD01; ARSA; PRKCI
GO:0007167	1.30E-08	2.60E-05	32911	172	258	12	BP	enzyme linked receptor protein signaling pathway	EGR1; TEK; IRS2; CCL2; MYD88; TGFB1; SMAD1; EPHA2; TIE1; KDR; WNT3A; BCR
GO:0016477	1.30E-08	2.70E-05	32911	172	259	12	BP	cell migration	FYN; CXCL12; CCKAR; CCL2; HOXA5; CXCL1; HIF1A; TGFB1; CCR1; KDR; CSF3R; IL1B
GO:0019538	1.40E-08	2.80E-05	32911	172	2117	33	BP	protein metabolic process	SPNB2; FYN; EIF2S2; MAPK3; TEK; DNAJC5; MYC; MYLK; TGM1; EIF1A; CCT6A; HK1; CCT5; MKNK1; HIF1A; TGFB1; HSPA5; HSPA8; SMAD1; EPHA2; ADD1; EIF3A; EIF3C; EIF3E; PIM1; SENP2; TIE1; KDR; ST3GAL2; GADD45G; PRKCI; EIF5; BCR
GO:0055086	1.40E-08	3.00E-05	32911	172	380	14	BP	nucleobase, nucleoside and nucleotide metabolic process	NT5C2; GATM; ADCY6; ADCY2; TALDO1; ADCY8; ADCY9; PDE4B; ADSS; HSPA8; CTPS; AMPD3; PRPS1; GUCY1B3
GO:0045597	1.50E-08	3.00E-05	32911	172	262	12	BP	positive regulation of cell differentiation	RELA; CXCL12; SOCS3; IL2RG; JUN; HIF1A; TGFB1; SMAD1; SFRP2; JUNB; KDR; WNT3A
GO:0009607	1.90E-08	3.80E-05	32911	172	325	13	BP	response to biotic stimulus	GPX2; RELA; BCL3; MAPK3; PTGS2; STAT1; MYD88; TGFB1; HSPA5; CCR1; HSPA1A; IL1B; HSPA1B
GO:0022414	2.10E-08	4.40E-05	32911	172	604	17	BP	reproductive process	NRIP1; SP1; PTGS2; FZD4; CXCL12; EPOR; GSR; AFP; GATM; TGFB1; SMAD1; SFRP2; JUNB; KDR; CD01; ARSA; HMGAI
GO:0009887	2.20E-08	4.50E-05	32911	172	330	13	BP	organ morphogenesis	SP1; RELA; MAPK3; MYC; CXCL12; GATM; TGM1; HOXA5; TGFB1; NOTCH2; EPHA2; WNT3A; COL11A2
GO:0019725	2.20E-08	4.50E-05	32911	172	393	14	BP	cellular homeostasis	FZD2; EPOR; SOCS6; CCKAR; GSR; JUN; CCL2; MT1; HIF1A; TGFB1; ADD1; KDR; TBXA2R; IL1B
GO:0006928	2.50E-08	5.00E-05	32911	172	396	14	BP	cellular component movement	FYN; CXCL12; CCKAR; CCL2; HOXA5; EGR2; CXCL1; HIF1A; TGFB1; CCR1; KDR; WNT3A; CSF3R; IL1B
GO:0009725	2.90E-08	5.80E-05	32911	172	223	11	BP	response to hormone stimulus	ALDH3A1; TEK; STAT1; IRS2; EGR2; CCND3; TGFB1; HMOX1; CD01; ARSA; PRKCI
GO:0051789	3.20E-08	6.60E-05	32911	172	93	8	BP	response to protein stimulus	EGR1; MYC; FOS; TGFB1; HMGC1; HSPA1A; WNT3A; HSPA1B
GO:0009059	3.60E-08	7.20E-05	32911	172	1974	31	BP	macromolecule biosynthetic process	EGR1; NRIP1; SP1; ATF4; RELA; BCL3; EIF2S2; GATA5; CEBPD; MYC; FOS; STAT1; JUN; EIF1A; HOXA5; MYB; EGR2; CCND3; HIF1A; SMAD1; NOTCH2; NOTCH3; EIF3A; EIF3C; EIF3E; JUNB; SENP2; MYBBP1A; SETD8; EIF5; GBE1
GO:0006753	4.10E-08	8.20E-05	32911	172	347	13	BP	nucleoside phosphate metabolic process	NT5C2; ADCY6; ADCY2; TALDO1; ADCY8; ADCY9; PDE4B; ADSS; HSPA8; CTPS; AMPD3; PRPS1; GUCY1B3
GO:0009117	4.10E-08	8.20E-05	32911	172	347	13	BP	nucleotide metabolic process	NT5C2; ADCY6; ADCY2; TALDO1; ADCY8; ADCY9; PDE4B; ADSS; HSPA8; CTPS; AMPD3; PRPS1; GUCY1B3

GO:0016310	4.20E-08	8.40E-05	32911	172	712	18	BP	phosphorylation	SPNB2; FYN; MAPK3; TEK; MYLK; CERK; HK1; MKNK1; CCND3; TGFBI; SMAD1; EPHA2; PIM1; TIE1; KDR; GADD45G; PRKCI; BCR
GO:0006954	4.60E-08	9.20E-05	32911	172	182	10	BP	inflammatory response	THBS1; PTGS2; CCL2; MYD88; CXCL1; TGFB1; SMAD1; CCR1; PLA2G7; IL1B
GO:0016043	5.10E-08	1.00E-04	32911	172	1894	30	BP	cellular component organization	TUBA4A; BID; BCL3; MAPK3; CAV2; FZD4; MYC; CCKAR; LGALS3; JUN; GADD45A; HIF1A; ACADL; TUBB2C; TGFB1; JUP; SFRP2; ADD1; EIF3A; HSPA1A; COL3A1; WNT2; TIE1; KDR; WNT3A; SETD8; PRKCI; COL11A2; HSPA1B; ANAPC11
GO:0009611	6.10E-08	1.20E-04	32911	172	240	11	BP	response to wounding	THBS1; PTGS2; CCL2; MYD88; CXCL1; TGFB1; SMAD1; NOTCH2; CCR1; PLA2G7; IL1B
GO:0048870	6.50E-08	1.30E-04	32911	172	299	12	BP	cell motility	FYN; CXCL12; CCKAR; CCL2; HOXA5; CXCL1; HIF1A; TGFB1; CCR1; KDR; CSF3R; IL1B
GO:0044092	7.20E-08	1.40E-04	32911	172	191	10	BP	negative regulation of molecular function	ARG2; MYC; IRS2; GADD45A; DUSP16; SFRP2; HMOX1; GADD45G; IL1B; HSPA1B
GO:0009991	7.30E-08	1.40E-04	32911	172	103	8	BP	response to extracellular stimulus	TEK; FOS; CCKAR; STAT1; JUN; SFRP2; TIE1; ARSA
GO:0007166	9.40E-08	1.90E-04	32911	172	2530	35	BP	cell surface receptor linked signaling pathway	EGR1; FYN; RGS3; MAPK3; TEK; FZD2; FZD4; IL10RB; CCKAR; DLL4; STAT1; CERK; IRS2; CCL2; PPAP2B; ADCY2; OSMR; MYD88; PTGFR; TGFB1; SMAD1; NOTCH2; NOTCH3; SFRP2; EPHA2; CCR1; SENP2; CBL; WNT2; TIE1; KDR; TBXA2R; WNT3A; ADRB3; BCR
GO:0040011	1.00E-07	2.00E-04	32911	172	375	13	BP	locomotion	FYN; FZD4; CXCL12; CCKAR; CCL2; HOXA5; CXCL1; HIF1A; TGFB1; CCR1; KDR; CSF3R; IL1B
GO:0034645	1.00E-07	2.10E-04	32911	172	1960	30	BP	cellular macromolecule biosynthetic process	EGR1; NRIP1; SP1; ATF4; RELA; BCL3; EIF2S2; GATA5; CEBPD; MYC; FOS; STAT1; JUN; EIF1A; HOXA5; MYB; EGR2; HIF1A; SMAD1; NOTCH2; NOTCH3; EIF3A; EIF3C; EIF3E; JUNB; SENP2; MYBBP1A; SETD8; EIF5; GBE1
GO:0071310	1.10E-07	2.20E-04	32911	172	151	9	BP	cellular response to organic substance	EGR1; MYC; STAT1; IRS2; TGFB1; SMAD1; HMGS1; WNT3A; PRKCI
GO:0009187	1.20E-07	2.50E-04	32911	172	45	6	BP	cyclic nucleotide metabolic process	ADCY6; ADCY2; ADCY8; ADCY9; PDE4B; GUCY1B3
GO:0009888	1.40E-07	2.80E-04	32911	172	321	12	BP	tissue development	RELA; THBS1; MAPK3; PTGS2; EPOR; HOXA5; HIF1A; TGFB1; JUP; SFRP2; JUNB; WNT3A
GO:0001659	1.40E-07	2.80E-04	32911	172	24	5	BP	temperature homeostasis	GPX2; CCKAR; ACADL; ADRB3; IL1B
GO:0055082	1.40E-07	2.90E-04	32911	172	322	12	BP	cellular chemical homeostasis	FZD2; EPOR; SOCS6; CCKAR; JUN; CCL2; MT1; HIF1A; TGFB1; KDR; TBXA2R; IL1B
GO:0030005	1.50E-07	3.00E-04	32911	172	207	10	BP	cellular di-, tri-valent inorganic cation homeostasis	FZD2; EPOR; CCKAR; CCL2; MT1; HIF1A; TGFB1; KDR; TBXA2R; IL1B
GO:0051240	1.60E-07	3.30E-04	32911	172	265	11	BP	positive regulation of multicellular organismal process	BCL3; PTGS2; MYC; CCL2; MYD88; TGFB1; WNT2; KDR; TBXA2R; ADRB3; IL1B
GO:0048513	2.00E-07	4.10E-04	32911	172	707	17	BP	organ development	SP1; RELA; BCL3; TEK; CXCL12; EPOR; IRS2; HOXA5; MYB; HIF1A; TGFB1; SFRP2; JUNB; WNT2; KDR; WNT3A; BCR
GO:0006468	2.00E-07	4.20E-04	32911	172	625	16	BP	protein amino acid phosphorylation	SPNB2; FYN; MAPK3; TEK; MYLK; HK1; MKNK1; TGFB1; SMAD1; EPHA2; PIM1; TIE1; KDR; GADD45G; PRKCI; BCR
GO:0009165	2.10E-07	4.20E-04	32911	172	163	9	BP	nucleotide biosynthetic process	ADCY6; ADCY2; ADCY8; ADCY9; ADSS; CTPS; AMPD3; PRPS1; GUCY1B3
GO:0002237	2.10E-07	4.30E-04	32911	172	80	7	BP	response to molecule of bacterial origin	RELA; MAPK3; PTGS2; STAT1; MYD88; CCR1; IL1B
GO:0046058	2.20E-07	4.40E-04	32911	172	26	5	BP	cAMP metabolic process	ADCY6; ADCY2; ADCY8; ADCY9; PDE4B
GO:0009190	2.20E-07	4.40E-04	32911	172	26	5	BP	cyclic nucleotide biosynthetic process	ADCY6; ADCY2; ADCY8; ADCY9; GUCY1B3

GO:0055066	2.70E-07	5.40E-04	32911	172	220	10	BP	di-, tri-valent inorganic cation homeostasis	FZD2; EPOR; CCKAR; CCL2; MT1; HIF1A; TGFBI; KDR; TBXA2R; IL1B
GO:0034404	2.80E-07	5.70E-04	32911	172	169	9	BP	nucleobase, nucleoside and nucleotide biosynthetic process	ADCY6; ADCY2; ADCY8; ADCY9; ADSS; CTPS; AMPD3; PRPS1; GUCY1B3
GO:0034654	2.80E-07	5.70E-04	32911	172	169	9	BP	nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	ADCY6; ADCY2; ADCY8; ADCY9; ADSS; CTPS; AMPD3; PRPS1; GUCY1B3
GO:0002376	3.10E-07	6.30E-04	32911	172	564	15	BP	immune system process	EGR1; FYN; RELA; BCL3; CXCL12; FCGRT; CCL2; MYD88; CXCL1; CCND3; TGFBI; CCR1; GADD45G; CSF3R; IL1B
GO:0048871	3.20E-07	6.50E-04	32911	172	28	5	BP	multicellular organismal homeostasis	GPX2; CCKAR; ACADL; ADRB3; IL1B
GO:0030003	3.70E-07	7.50E-04	32911	172	228	10	BP	cellular cation homeostasis	FZD2; EPOR; CCKAR; CCL2; MT1; HIF1A; TGFBI; KDR; TBXA2R; IL1B
GO:0006413	3.90E-07	7.90E-04	32911	172	29	5	BP	translational initiation	EIF2S2; EIF1A; EIF3C; EIF3E; EIF5
GO:0043065	3.90E-07	8.00E-04	32911	172	289	11	BP	positive regulation of apoptosis	BID; BCL3; PTGS2; MYC; RBCK1; STAT1; JUN; TGFBI; NOTCH2; HMOX1; IL1B
GO:0006164	4.20E-07	8.40E-04	32911	172	129	8	BP	purine nucleotide biosynthetic process	ADCY6; ADCY2; ADCY8; ADCY9; ADSS; AMPD3; PRPS1; GUCY1B3
GO:0043068	4.40E-07	8.80E-04	32911	172	292	11	BP	positive regulation of programmed cell death	BID; BCL3; PTGS2; MYC; RBCK1; STAT1; JUN; TGFBI; NOTCH2; HMOX1; IL1B
GO:0051246	4.50E-07	9.10E-04	32911	172	428	13	BP	regulation of protein metabolic process	RELA; MAPK3; TEK; SOCS3; JUN; PPAP2B; MKNK1; TGFBI; HSPA5; SFRP2; EIF3C; GCLC; IL1B
GO:0006952	4.50E-07	9.10E-04	32911	172	428	13	BP	defense response	RELA; BCL3; THBS1; PTGS2; CCL2; MYD88; CXCL1; TGFBI; SMAD1; CCR1; PLA2G7; IL1B; HSPA1B
GO:0030595	4.70E-07	9.40E-04	32911	172	30	5	BP	leukocyte chemotaxis	CCL2; CXCL1; CCR1; CSF3R; IL1B
GO:0001525	4.70E-07	9.40E-04	32911	172	131	8	BP	angiogenesis	TEK; DLL4; JUN; HIF1A; EPHA2; KDR; HMOX1; IL1B
GO:0030335	4.80E-07	9.70E-04	32911	172	90	7	BP	positive regulation of cell migration	PTGS2; CXCL12; IRS2; CCL2; HIF1A; F3; KDR
GO:0006171	4.90E-07	9.90E-04	32911	172	13	4	BP	cAMP biosynthetic process	ADCY6; ADCY2; ADCY8; ADCY9
GO:0032268	4.90E-07	9.90E-04	32911	172	361	12	BP	regulation of cellular protein metabolic process	MAPK3; TEK; SOCS3; JUN; PPAP2B; MKNK1; TGFBI; HSPA5; SFRP2; EIF3C; GCLC; IL1B
GO:0010942	5.40E-07	0.001	32911	172	298	11	BP	positive regulation of cell death	BID; BCL3; PTGS2; MYC; RBCK1; STAT1; JUN; TGFBI; NOTCH2; HMOX1; IL1B
GO:0006875	5.60E-07	0.0011	32911	172	183	9	BP	cellular metal ion homeostasis	FZD2; EPOR; CCKAR; CCL2; MT1; TGFBI; KDR; TBXA2R; IL1B
GO:0048583	6.00E-07	0.0012	32911	172	439	13	BP	regulation of response to stimulus	GPX2; RELA; PTGS2; CXCL12; SOCS3; CCL2; MYD88; TGFBI; SFRP2; CCR1; HMOX1; IL1B; HSPA1B
GO:0006519	6.50E-07	0.0013	32911	172	304	11	BP	cellular amino acid and derivative metabolic process	ARG2; GSR; GAMT; SRM; ACADL; IVD; CTPS; ALDH4A1; CD01; ASNS; GCLC
GO:0060326	6.60E-07	0.0013	32911	172	32	5	BP	cell chemotaxis	CCL2; CXCL1; CCR1; CSF3R; IL1B
GO:0042325	6.60E-07	0.0013	32911	172	371	12	BP	regulation of phosphorylation	TEK; SOCS3; CERK; JUN; IRS2; PPAP2B; GADD45A; HSPA5; DUSP16; SFRP2; GADD45G; IL1B

GO:0033673	6. 60E-07	0. 0013	32911	172	59	6	BP	negative regulation of kinase activity	IRS2; GADD45A; DUSP16; SFRP2; GADD45G; IL1B
GO:0006066	7. 20E-07	0. 0014	32911	172	374	12	BP	alcohol metabolic process	CYP51; ATF4; IDI1; MYC; TALDO1; HK1; CH25H; SQLE; HMGCS1; PRPS1; ALDOA; GBE1
GO:0043066	7. 20E-07	0. 0014	32911	172	307	11	BP	negative regulation of apoptosis	BCL3; TEK; DNAJC5; MYC; IRS2; HK1; SFRP2; MCL1; TIMP1; GCLC; HSPA1B
GO:0055065	7. 30E-07	0. 0014	32911	172	189	9	BP	metal ion homeostasis	FZD2; EPOR; CCKAR; CCL2; MT1; TGFBI; KDR; TBXA2R; IL1B
GO:0002682	7. 40E-07	0. 0014	32911	172	375	12	BP	regulation of immune system process	GPX2; RELA; IL2RG; JUN; IRS2; CCL2; MYD88; HIF1A; TGFBI; LMO2; HMOX1; HSPA1B
GO:0045766	7. 70E-07	0. 0015	32911	172	33	5	BP	positive regulation of angiogenesis	TEK; PTGS2; KDR; TBXA2R; IL1B
GO:0040017	8. 10E-07	0. 0016	32911	172	97	7	BP	positive regulation of locomotion	PTGS2; CXCL12; IRS2; CCL2; HIF1A; F3; KDR
GO:0051272	8. 10E-07	0. 0016	32911	172	97	7	BP	positive regulation of cellular component movement	PTGS2; CXCL12; IRS2; CCL2; HIF1A; F3; KDR
GO:0043069	8. 40E-07	0. 0017	32911	172	312	11	BP	negative regulation of programmed cell death	BCL3; TEK; DNAJC5; MYC; IRS2; HK1; SFRP2; MCL1; TIMP1; GCLC; HSPA1B
GO:0051348	9. 00E-07	0. 0018	32911	172	62	6	BP	negative regulation of transferase activity	IRS2; GADD45A; DUSP16; SFRP2; GADD45G; IL1B
GO:0006873	9. 00E-07	0. 0018	32911	172	314	11	BP	cellular ion homeostasis	FZD2; EPOR; CCKAR; JUN; CCL2; MT1; HIF1A; TGFBI; KDR; TBXA2R; IL1B
GO:0048661	9. 00E-07	0. 0018	32911	172	34	5	BP	positive regulation of smooth muscle cell proliferation	PTGS2; STAT1; JUN; MYD88; HIF1A
GO:0035466	9. 10E-07	0. 0018	32911	172	614	15	BP	regulation of signaling pathway	RELA; CAV2; FZD4; SOCS3; RBCK1; PPAP2B; MYD88; HIF1A; HSPA5; DUSP16; SFRP2; KDR; WNT3A; IL1B; BCR
GO:0019220	1. 00E-06	0. 002	32911	172	386	12	BP	regulation of phosphate metabolic process	TEK; SOCS3; CERK; JUN; IRS2; PPAP2B; GADD45A; HSPA5; DUSP16; SFRP2; GADD45G; IL1B
GO:0051174	1. 00E-06	0. 002	32911	172	386	12	BP	regulation of phosphorus metabolic process	TEK; SOCS3; CERK; JUN; IRS2; PPAP2B; GADD45A; HSPA5; DUSP16; SFRP2; GADD45G; IL1B
GO:0006163	1. 00E-06	0. 002	32911	172	254	10	BP	purine nucleotide metabolic process	ADCY6; ADCY2; ADCY8; ADCY9; PDE4B; ADSS; HSPA8; AMPD3; PRPS1; GUCY1B3
GO:0043085	1. 00E-06	0. 002	32911	172	318	11	BP	positive regulation of catalytic activity	MYC; CERK; ADCY6; ADCY2; ADCY9; HSPA5; SFRP2; GADD45G; WNT3A; ADRB3; IL1B
GO:0055080	1. 10E-06	0. 0022	32911	172	257	10	BP	cation homeostasis	FZD2; EPOR; CCKAR; CCL2; MT1; HIF1A; TGFBI; KDR; TBXA2R; IL1B
GO:0060548	1. 10E-06	0. 0023	32911	172	322	11	BP	negative regulation of cell death	BCL3; TEK; DNAJC5; MYC; IRS2; HK1; SFRP2; MCL1; TIMP1; GCLC; HSPA1B
GO:0032496	1. 10E-06	0. 0023	32911	172	65	6	BP	response to lipopolysaccharide	MAPK3; PTGS2; STAT1; MYD88; CCR1; IL1B
GO:0007610	1. 30E-06	0. 0027	32911	172	473	13	BP	behavior	EGR1; PTGS2; CXCL12; CCKAR; JUN; CCL2; ADCY8; EGR2; CXCL1; CCR1; CSF3R; ADRB3; IL1B

GO:0045595	1.40E-06	0.0029	32911	172	554	14	BP	regulation of cell differentiation	RELA; CXCL12; SOCS3; IL2RG; JUN; HIF1A; TGFB1; LMO2; SMAD1; NOTCH3; SFRP2; JUNB; KDR; WNT3A
GO:0032844	1.40E-06	0.0029	32911	172	106	7	BP	regulation of homeostatic process	PTGS2; HIF1A; TGFB1; LMO2; CCR1; GCLC; IL1B
GO:0042110	1.40E-06	0.0029	32911	172	106	7	BP	T cell activation	EGR1; FYN; BCL3; CXCL12; CCND3; TGFB1; GADD45G
GO:0043086	1.50E-06	0.003	32911	172	153	8	BP	negative regulation of catalytic activity	ARG2; IRS2; GADD45A; DUSP16; SFRP2; GADD45G; IL1B; HSPA1B
GO:0010647	1.50E-06	0.0031	32911	172	267	10	BP	positive regulation of cell communication	CAV2; PTGS2; RBCK1; CCL2; MYD88; HIF1A; SFRP2; KDR; WNT3A; IL1B
GO:0051098	1.50E-06	0.0031	32911	172	107	7	BP	regulation of binding	RELA; MAPK3; MYC; PPAP2B; MYD88; TGFB1; HMOX1
GO:0001568	1.70E-06	0.0034	32911	172	69	6	BP	blood vessel development	SOCS3; PPAP2B; EPHA2; JUNB; COL3A1; WNT2
GO:0009266	1.80E-06	0.0037	32911	172	70	6	BP	response to temperature stimulus	CCKAR; CCL2; HSPB1; HSPA1A; ADRB3; HSPA1B
GO:0009628	1.80E-06	0.0037	32911	172	272	10	BP	response to abiotic stimulus	FYN; MYC; CCKAR; STAT1; CCL2; HSPB1; HSPA1A; ARSA; ADRB3; HSPA1B
GO:0051090	2.10E-06	0.0043	32911	172	72	6	BP	regulation of transcription factor activity	RELA; MAPK3; PPAP2B; MYD88; TGFB1; HMOX1
GO:0090046	2.10E-06	0.0043	32911	172	72	6	BP	regulation of transcription regulator activity	RELA; MAPK3; PPAP2B; MYD88; TGFB1; HMOX1
GO:0050801	2.20E-06	0.0045	32911	172	345	11	BP	ion homeostasis	FZD2; EPOR; CCKAR; JUN; CCL2; MT1; HIF1A; TGFB1; KDR; TBXA2R; IL1B
GO:0007178	2.30E-06	0.0047	32911	172	73	6	BP	transmembrane receptor protein serine/threonine kinase signaling pathway	EGR1; CCL2; MYD88; TGFB1; SMAD1; WNT3A
GO:0031399	2.60E-06	0.0053	32911	172	221	9	BP	regulation of protein modification process	TEK; SOCS3; JUN; PPAP2B; TGFB1; HSPA5; SFRP2; GCLC; IL1B
GO:0001936	3.20E-06	0.0065	32911	172	20	4	BP	regulation of endothelial cell proliferation	CAV2; CXCL12; CCL2; WNT2
GO:0030593	3.20E-06	0.0065	32911	172	20	4	BP	neutrophil chemotaxis	CCL2; CXCL1; CSF3R; IL1B
GO:0048878	3.30E-06	0.0067	32911	172	434	12	BP	chemical homeostasis	FZD2; EPOR; SOCS6; CCKAR; JUN; CCL2; MT1; HIF1A; TGFB1; KDR; TBXA2R; IL1B
GO:0006874	3.30E-06	0.0067	32911	172	170	8	BP	cellular calcium ion homeostasis	FZD2; EPOR; CCKAR; CCL2; TGFB1; KDR; TBXA2R; IL1B
GO:0048646	3.60E-06	0.0073	32911	172	363	11	BP	anatomical structure formation involved in morphogenesis	TEK; DLL4; JUN; EGR2; HIF1A; SFRP2; EPHA2; KDR; HMOX1; WNT3A; IL1B
GO:0050900	3.70E-06	0.0076	32911	172	45	5	BP	leukocyte migration	CCL2; CXCL1; CCR1; CSF3R; IL1B
GO:0055074	4.00E-06	0.008	32911	172	174	8	BP	calcium ion homeostasis	FZD2; EPOR; CCKAR; CCL2; TGFB1; KDR; TBXA2R; IL1B
GO:0009408	4.70E-06	0.0094	32911	172	47	5	BP	response to heat	CCKAR; CCL2; HSPB1; HSPA1A; HSPA1B
GO:0046697	4.80E-06	0.0096	32911	172	7	3	BP	decidualization	PTGS2; EPOR; JUNB
GO:0035556	4.90E-06	0.0098	32911	172	531	13	BP	intracellular signal transduction	MAPK3; FZD2; SOCS3; STAT1; ADCY2; ADCY8; MYD88; MKNK1; SMAD1; YWHAQ; TBXA2R; HMOX1; ADRB3
GO:0051726	5.00E-06	0.0101	32911	172	239	9	BP	regulation of cell cycle	MYC; JUN; GADD45A; CCND3; TGFB1; HSPAS; JUNB; GADD45G; BCR

GO:0048534	5.50E-06	0.011	32911	172	129	7	BP	hemopoietic or lymphoid organ development	SP1; BCL3; TEK; HIF1A; TGFB1; KDR; WNT3A
GO:0043687	5.90E-06	0.0119	32911	172	1005	18	BP	post-translational protein modification	SPNB2; FYN; MAPK3; TEK; MYLK; TGM1; HK1; MKNK1; TGFB1; SMAD1; EPHA2; PIM1; SENP2; TIE1; KDR; GADD45G; PRKCI; BCR
GO:0031667	6.20E-06	0.0124	32911	172	86	6	BP	response to nutrient levels	TEK; CCKAR; STAT1; JUN; TIE1; ARSA
GO:0048545	6.20E-06	0.0124	32911	172	86	6	BP	response to steroid hormone stimulus	ALDH3A1; TEK; TGFB1; HMOX1; CD01; ARSA
GO:0040008	6.20E-06	0.0125	32911	172	312	10	BP	regulation of growth	CXCL12; SOCS6; SOCS3; GAMT; MYD88; HIF1A; WNT2; IGFBP5; WNT3A; ADRB3
GO:0001570	6.40E-06	0.0129	32911	172	50	5	BP	vasculogenesis	FZD4; EPHA2; JUNB; TIE1; KDR
GO:0048660	6.40E-06	0.0129	32911	172	50	5	BP	regulation of smooth muscle cell proliferation	PTGS2; STAT1; JUN; MYD88; HIF1A
GO:0030855	6.60E-06	0.0133	32911	172	87	6	BP	epithelial cell differentiation	PTGS2; FZD2; GATA5; JUN; HOXA5; KDR
GO:0051101	6.60E-06	0.0133	32911	172	87	6	BP	regulation of DNA binding	RELA; MAPK3; PPAP2B; MYD88; TGFB1; HMOX1
GO:0006350	7.30E-06	0.0147	32911	172	1561	23	BP	transcription	EGR1; NRIP1; SP1; ATF4; RELA; BCL3; GATA5; CEBPD; MYC; FOS; STAT1; JUN; HOXA5; MYB; EGR2; HIF1A; SMAD1; NOTCH2; NOTCH3; JUNB; SENP2; MYBBP1A; SETD8
GO:0010574	7.70E-06	0.0154	32911	172	8	3	BP	regulation of vascular endothelial growth factor production	PTGS2; CCL2; IL1B
GO:0043535	7.70E-06	0.0154	32911	172	8	3	BP	regulation of blood vessel endothelial cell migration	PTGS2; DLL4; EPHA2
GO:0035239	9.40E-06	0.0189	32911	172	140	7	BP	tube morphogenesis	MYC; CXCL12; HOXA5; HIF1A; TGFB1; KDR; WNT3A
GO:0060249	1.00E-05	0.0208	32911	172	94	6	BP	anatomical structure homeostasis	HIF1A; ADD1; HSPA1A; KDR; COL11A2; HSPA1B
GO:0048609	1.00E-05	0.0216	32911	172	332	10	BP	reproductive process in a multicellular organism	NRIP1; SP1; PTGS2; GSR; AFP; GAMT; SMAD1; JUNB; CD01; HMGA1
GO:0009308	1.00E-05	0.0216	32911	172	332	10	BP	amine metabolic process	ARG2; GAMT; SRM; CCND3; ACADL; IVD; CTPS; ALDH4A1; CD01; ASNS
GO:0023046	1.10E-05	0.022	32911	172	2845	33	BP	signaling process	RGS3; MAPK3; TEK; FZD2; FZD4; IL10RB; CXCL16; EPOR; SOCS3; PPP2R2A; CCKAR; AFP; STAT1; IRS2; CCL2; ADCY2; ADCY8; OSMR; MYD88; PTGFR; MKNK1; CCND3; HIF1A; TRAF5; SMAD1; YWHAQ; CCR1; KDR; TBXA2R; HMOX1; WNT3A; ADRB3; BCR
GO:0010594	1.10E-05	0.023	32911	172	9	3	BP	regulation of endothelial cell migration	PTGS2; DLL4; EPHA2
GO:0006469	1.20E-05	0.0247	32911	172	57	5	BP	negative regulation of protein kinase activity	GADD45A; DUSP16; SFRP2; GADD45G; IL1B
GO:0016055	1.20E-05	0.026	32911	172	147	7	BP	Wnt receptor signaling pathway	FZD2; FZD4; PPAP2B; SFRP2; SENP2; WNT2; WNT3A
GO:0051186	1.40E-05	0.0296	32911	172	208	8	BP	cofactor metabolic process	GSR; TALD01; ACSS1; HMOX1; SUCLG2; GCLC; ALAS1; MTHFD2
GO:0006464	1.50E-05	0.0313	32911	172	1186	19	BP	protein modification process	SPNB2; FYN; MAPK3; TEK; MYLK; TGM1; HK1; MKNK1; TGFB1; SMAD1; EPHA2; PIM1; SENP2; TIE1; KDR; ST3GAL2; GADD45G; PRKCI; BCR
GO:0007204	1.50E-05	0.0314	32911	172	101	6	BP	elevation of cytosolic calcium ion concentration	FZD2; EPOR; CCKAR; KDR; TBXA2R; IL1B

GO:0031620	1.60E-05	0.0328	32911	172	10	3	BP	regulation of fever	PTGS2; CCR1; IL1B
GO:0001817	1.70E-05	0.0351	32911	172	154	7	BP	regulation of cytokine production	RELA; BCL3; PTGS2; CCL2; MYD88; HMOX1; IL1B
GO:0016126	1.70E-05	0.0355	32911	172	30	4	BP	sterol biosynthetic process	CYP51; IDI1; CH25H; HMGCS1
GO:0002053	1.70E-05	0.0355	32911	172	30	4	BP	positive regulation of mesenchymal cell proliferation	MYC; IRS2; WNT2; KDR
GO:0071445	1.70E-05	0.0355	32911	172	30	4	BP	cellular response to protein stimulus	EGR1; MYC; HMGCS1; WNT3A
GO:0030198	1.90E-05	0.0392	32911	172	105	6	BP	extracellular matrix organization	BCL3; LGALS3; SFRP2; COL3A1; WNT3A; COL11A2
GO:0035468	2.10E-05	0.0429	32911	172	219	8	BP	positive regulation of signaling pathway	CAV2; RBCK1; MYD88; HIF1A; SFRP2; KDR; WNT3A; IL1B
GO:0010464	2.30E-05	0.0463	32911	172	32	4	BP	regulation of mesenchymal cell proliferation	MYC; IRS2; WNT2; KDR
GO:0043434	2.40E-05	0.0485	32911	172	109	6	BP	response to peptide hormone stimulus	STAT1; IRS2; EGR2; CCND3; CD01; PRKCI
GO:0042330	2.50E-05	0.0511	32911	172	110	6	BP	taxis	CXCL12; CCL2; CXCL1; CCR1; CSF3R; IL1B
GO:0006935	2.50E-05	0.0511	32911	172	110	6	BP	chemotaxis	CXCL12; CCL2; CXCL1; CCR1; CSF3R; IL1B
GO:0051480	2.80E-05	0.0566	32911	172	112	6	BP	cytosolic calcium ion homeostasis	FZD2; EPOR; CCKAR; KDR; TBXA2R; IL1B
GO:0043549	2.80E-05	0.0572	32911	172	228	8	BP	regulation of kinase activity	CERK; IRS2; GADD45A; HSPA5; DUSP16; SFRP2; GADD45G; IL1B
GO:0043412	2.90E-05	0.0595	32911	172	1243	19	BP	macromolecule modification	SPNB2; FYN; MAPK3; TEK; MYLK; TGM1; HK1; MKNK1; TGFB1; SMAD1; EPHA2; PIM1; SENP2; TIE1; KDR; ST3GAL2; GADD45G; PRKCT; RCR
GO:0031650	2.90E-05	0.0597	32911	172	12	3	BP	regulation of heat generation	PTGS2; CCR1; IL1B
GO:0051338	3.60E-05	0.073	32911	172	236	8	BP	regulation of transferase activity	CERK; IRS2; GADD45A; HSPA5; DUSP16; SFRP2; GADD45G; IL1B
GO:0032989	3.70E-05	0.0753	32911	172	237	8	BP	cellular component morphogenesis	FZD4; CCKAR; HIF1A; TGFB1; ADD1; WNT2; KDR; WNT3A
GO:0031663	3.80E-05	0.0773	32911	172	13	3	BP	lipopolysaccharide-mediated signaling pathway	MAPK3; STAT1; MYD88
GO:0046627	3.80E-05	0.0773	32911	172	13	3	BP	negative regulation of insulin receptor signaling pathway	RELA; SOCS3; IL1B
GO:0008203	3.80E-05	0.0777	32911	172	72	5	BP	cholesterol metabolic process	CYP51; IDI1; CH25H; SQLE; HMGCS1
GO:0032101	4.10E-05	0.0828	32911	172	176	7	BP	regulation of response to external stimulus	GPX2; PTGS2; CXCL12; CCL2; MYD88; CCR1; IL1B
GO:0030097	4.10E-05	0.0831	32911	172	73	5	BP	hemopoiesis	SP1; TEK; HIF1A; KDR; WNT3A
GO:0001775	4.40E-05	0.0898	32911	172	243	8	BP	cell activation	EGR1; FYN; BCL3; CXCL12; CCND3; TGFB1; TIMP1; GADD45G
GO:0048568	4.70E-05	0.0946	32911	172	75	5	BP	embryonic organ development	SP1; MYB; HIF1A; JUNB; WNT2

GO:0010648	4.80E-05	0.0979	32911	172	246	8	BP	negative regulation of cell communication	RGS3; RELA; PTGS2; SOCS6; SOCS3; HSPA5; SFRP2; IL1B
GO:0042108	5.10E-05	0.1029	32911	172	39	4	BP	positive regulation of cytokine biosynthetic process	RELA; BCL3; MYD88; IL1B
GO:0060070	5.10E-05	0.1029	32911	172	39	4	BP	canonical Wnt receptor signaling pathway	FZD4; PPAP2B; WNT2; WNT3A
GO:0046649	5.20E-05	0.106	32911	172	183	7	BP	lymphocyte activation	EGR1; FYN; BCL3; CXCL12; CCND3; TGFB1; GADD45G
GO:0007169	5.20E-05	0.106	32911	172	183	7	BP	transmembrane receptor protein tyrosine kinase signaling pathway	TEK; IRS2; CCL2; EPHA2; TIE1; KDR; BCR
GO:0007154	5.60E-05	0.1124	32911	172	324	9	BP	cell communication	CAV2; FZD2; FOS; DLL4; JUN; HOXA5; SFRP2; WNT2; WNT3A
GO:0044106	5.60E-05	0.1128	32911	172	251	8	BP	cellular amine metabolic process	ARG2; SRM; ACADL; IVD; CTPS; ALDH4A1; CD01; ASNS
GO:0008283	5.70E-05	0.116	32911	172	252	8	BP	cell proliferation	EGR1; FYN; CXCL12; IRS2; CCND3; TGFB1; JUNB; WNT3A
GO:0016125	6.00E-05	0.1215	32911	172	79	5	BP	sterol metabolic process	CYP51; IDI1; CH25H; SQLE; HMGCS1
GO:0030099	6.00E-05	0.1215	32911	172	79	5	BP	myeloid cell differentiation	SP1; TGFB1; ADD1; CCR1; JUNB
GO:0030728	6.00E-05	0.1221	32911	172	15	3	BP	ovulation	NRIP1; PTGS2; AFP
GO:0035121	6.00E-05	0.1221	32911	172	15	3	BP	tail morphogenesis	SFRP2; EPHA2; WNT3A
GO:0009064	6.20E-05	0.1257	32911	172	41	4	BP	glutamine family amino acid metabolic process	ARG2; CTPS; ALDH4A1; ASNS
GO:0019221	6.40E-05	0.1291	32911	172	80	5	BP	cytokine-mediated signaling pathway	IL10RB; STAT1; CCL2; OSMR; MYD88
GO:0023036	6.40E-05	0.1291	32911	172	80	5	BP	initiation of signal transduction	IL10RB; STAT1; CCL2; OSMR; MYD88
GO:0023038	6.40E-05	0.1291	32911	172	80	5	BP	signal initiation by diffusible mediator	IL10RB; STAT1; CCL2; OSMR; MYD88
GO:0023049	6.40E-05	0.1291	32911	172	80	5	BP	signal initiation by protein/peptide mediator	IL10RB; STAT1; CCL2; OSMR; MYD88
GO:0001763	7.30E-05	0.1483	32911	172	133	6	BP	morphogenesis of a branching structure	MYC; CXCL12; SOCS3; HOXA5; TGFB1; KDR
GO:0009056	7.40E-05	0.1496	32911	172	789	14	BP	catabolic process	MYC; TALD01; PDE4B; HK1; ACADL; HSPA8; IVD; HMOX1; CD01; SUCLG2; PLA2G7; ARSA; ALDOA; GSTA2
GO:0001938	7.40E-05	0.1498	32911	172	16	3	BP	positive regulation of endothelial cell proliferation	CXCL12; CCL2; WNT2
GO:0009127	7.40E-05	0.1498	32911	172	16	3	BP	purine nucleoside monophosphate biosynthetic process	ADSS; AMPD3; PRPS1

GO:0009168	7.40E-05	0.1498	32911	172	16	3	BP	purine ribonucleoside monophosphate biosynthetic process	ADSS; AMPD3; PRPS1
GO:0033554	7.70E-05	0.1547	32911	172	419	10	BP	cellular response to stress	BCL3; MAPK3; JUN; GADD45A; MYD88; HIF1A; HSPA5; HSPA1A; HMOX1; HSPA1B
GO:0048729	8.00E-05	0.1604	32911	172	264	8	BP	tissue morphogenesis	MYC; CXCL12; SOCS3; HOXA5; TGFB1; NOTCH2; SFRP2; WNT2
GO:0007165	8.40E-05	0.1691	32911	172	2738	30	BP	signal transduction	RGS3; MAPK3; TEK; FZD2; FZD4; CXCL16; EPOR; SOCS3; PPP2R2A; CCKAR; AFP; STAT1; IRS2; ADCY2; ADCY8; MYD88; PTGFR; MKNK1; CCND3; HIF1A; TRAF5; SMAD1; YWHAQ; CCR1; KDR; TBXA2R; HMOX1; WNT3A; ADRB3; BCR
GO:0005996	8.60E-05	0.1739	32911	172	198	7	BP	monosaccharide metabolic process	ATF4; MYC; TALDO1; HK1; PRPS1; ALDOA; GBE1
GO:0023060	8.70E-05	0.1759	32911	172	2744	30	BP	signal transmission	RGS3; MAPK3; TEK; FZD2; FZD4; CXCL16; EPOR; SOCS3; PPP2R2A; CCKAR; AFP; STAT1; IRS2; ADCY2; ADCY8; MYD88; PTGFR; MKNK1; CCND3; HIF1A; TRAF5; SMAD1; YWHAQ; CCR1; KDR; TBXA2R; HMOX1; WNT3A; ADRB3; BCR
GO:0006629	9.50E-05	0.1911	32911	172	707	13	BP	lipid metabolic process	CYP51; PTDS2; IDI1; PTGS2; AFP; CERK; PPAP2B; CH25H; ACADL; SQLE; CYP4A12A; HMGCS1; PLA2G7
GO:0032943	9.90E-05	0.1985	32911	172	46	4	BP	mononuclear cell proliferation	FYN; CXCL12; CCND3; TGFB1
GO:0006006	1.00E-04	0.2048	32911	172	141	6	BP	glucose metabolic process	ATF4; MYC; TALDO1; HK1; ALDOA; GBE1
GO:0051091	1.00E-04	0.2161	32911	172	47	4	BP	positive regulation of transcription factor activity	RELA; PPAP2B; MYD88; TGFB1
GO:0070661	1.00E-04	0.2161	32911	172	47	4	BP	leukocyte proliferation	FYN; CXCL12; CCND3; TGFB1
GO:0090047	1.00E-04	0.2161	32911	172	47	4	BP	positive regulation of transcription regulator activity	RELA; PPAP2B; MYD88; TGFB1
GO:0046626	1.00E-04	0.2166	32911	172	18	3	BP	regulation of insulin receptor signaling pathway	RELA; SOCS3; IL1B
GO:0009156	1.00E-04	0.2166	32911	172	18	3	BP	ribonucleoside monophosphate biosynthetic process	ADSS; AMPD3; PRPS1
GO:0032583	1.10E-04	0.2213	32911	172	143	6	BP	regulation of gene-specific transcription	GATA5; MYC; TGFB1; SMAD1; WNT3A; IL1B
GO:0051093	1.20E-04	0.2469	32911	172	281	8	BP	negative regulation of developmental process	THBS1; CCL2; TGFB1; LM02; NOTCH3; SFRP2; TIE1; WNT3A
GO:0001836	1.20E-04	0.2562	32911	172	19	3	BP	release of cytochrome c from mitochondria	BID; MYC; JUN
GO:0001837	1.20E-04	0.2562	32911	172	19	3	BP	epithelial to mesenchymal transition	HIF1A; TGFB1; WNT2
GO:0051591	1.20E-04	0.2562	32911	172	19	3	BP	response to cAMP	ALDH3A1; STAT1; CD01
GO:0060674	1.20E-04	0.2562	32911	172	19	3	BP	placenta blood vessel development	SOCS3; JUNB; WNT2
GO:0009126	1.20E-04	0.2562	32911	172	19	3	BP	purine nucleoside monophosphate metabolic process	ADSS; AMPD3; PRPS1

GO:0009167	1. 20E-04	0. 2562	32911	172	19	3	BP	purine ribonucleoside monophosphate metabolic process	ADSS; AMPD3; PRPS1
GO:0071216	1. 30E-04	0. 2757	32911	172	50	4	BP	cellular response to biotic stimulus	MAPK3; STAT1; MYD88; HSPA5
GO:0007190	1. 30E-04	0. 2757	32911	172	50	4	BP	activation of adenylate cyclase activity	ADCY6; ADCY2; ADCY9; ADRB3
GO:0031347	1. 30E-04	0. 2772	32911	172	149	6	BP	regulation of defense response	GPX2; RELA; PTGS2; MYD88; CCR1; IL1B
GO:0048598	1. 30E-04	0. 2775	32911	172	365	9	BP	embryonic morphogenesis	SP1; MYC; SOCS3; PPAP2B; HOXA5; NOTCH2; SFRP2; EPHA2; WNT3A
GO:0051704	1. 40E-04	0. 2853	32911	172	287	8	BP	multi-organism process	GPX2; RELA; BCL3; EPOR; STAT1; MYD88; TGFB1; IL1B
GO:0007275	1. 40E-04	0. 2915	32911	172	841	14	BP	multicellular organismal development	FYN; FZD2; FZD4; DLL4; PPAP2B; HOXA5; NOTCH2; NOTCH3; SFRP2; MCL1; WNT2; KDR; GADD45G; WNT3A
GO:0042493	1. 40E-04	0. 2922	32911	172	95	5	BP	response to drug transcription from RNA polymerase II promoter	ALDH3A1; FOS; STAT1; JUN; SMAD1
GO:0006366	1. 40E-04	0. 2979	32911	172	51	4	BP	organic acid biosynthetic process	MYC; FOS; JUN; JUNB
GO:0016053	1. 40E-04	0. 2981	32911	172	151	6	BP	positive regulation of cellular protein metabolic process	GSTO1; PTGS2; CH25H; ALDH4A1; ACS1; ASNS
GO:0032270	1. 40E-04	0. 2981	32911	172	151	6	BP	carboxylic acid biosynthetic process	MAPK3; TEK; TGFB1; HSPA5; EIF3C; GCLC
GO:0046394	1. 40E-04	0. 2981	32911	172	151	6	BP	protein import into nucleus, translocation	GSTO1; PTGS2; CH25H; ALDH4A1; ACS1; ASNS
GO:0000060	1. 40E-04	0. 3003	32911	172	20	3	BP	cellular aldehyde metabolic process	SPNB2; MAPK3; TGFB1
GO:0006081	1. 40E-04	0. 3003	32911	172	20	3	BP	Wnt receptor signaling pathway, calcium modulating pathway	ALDH3A1; TALDO1; ALDH3B1
GO:0007223	1. 40E-04	0. 3003	32911	172	20	3	BP	immune response regulation of protein kinase activity	FZD2; WNT2; WNT3A
GO:0006955	1. 50E-04	0. 3064	32911	172	290	8	BP	response to cytokine stimulus	BCL3; CXCL12; FCGRT; CCL2; MYD88; CXCL1; TGFB1; IL1B
GO:0045859	1. 50E-04	0. 3159	32911	172	218	7	BP	positive regulation of adenylate cyclase activity	CERK; GADD45A; HSPA5; DUSP16; SFRP2; GADD45G; IL1B
GO:0034097	1. 60E-04	0. 3215	32911	172	52	4	BP	CD4-positive, alpha-beta T cell	PTGS2; STAT1; MCL1; PRKCI
GO:0045762	1. 60E-04	0. 3215	32911	172	52	4	BP	differentiation involved in immune response	ADCY6; ADCY2; ADCY9; ADRB3
GO:0002294	1. 60E-04	0. 3244	32911	172	4	2	BP	T-helper cell differentiation	BCL3; GADD45G
GO:0042093	1. 60E-04	0. 3244	32911	172	4	2	BP		BCL3; GADD45G

GO:0043618	1.60E-04	0.3244	32911	172	4	2	BP	regulation of transcription from RNA polymerase II promoter in response to stress	HIF1A; HMOX1
GO:0043619	1.60E-04	0.3244	32911	172	4	2	BP	regulation of transcription from RNA polymerase II promoter in response to oxidative stress	HIF1A; HMOX1
GO:0006167	1.60E-04	0.3244	32911	172	4	2	BP	AMP biosynthetic process	ADSS; PRPS1
GO:0010720	1.60E-04	0.3382	32911	172	98	5	BP	positive regulation of cell development	RELA; CXCL12; TGFB1; KDR; WNT3A
GO:0043193	1.60E-04	0.3382	32911	172	98	5	BP	positive regulation of gene-specific transcription	GATA5; TGFB1; SMAD1; WNT3A; IL1B
GO:0009966	1.70E-04	0.3427	32911	172	462	10	BP	regulation of signal transduction	RGS3; SOCS6; SOCS3; RBCK1; MYD88; DUSP16; SFRP2; KDR; IL1B; BCR
GO:0045321	1.70E-04	0.3435	32911	172	221	7	BP	leukocyte activation	EGR1; FYN; BCL3; CXCL12; CCND3; TGFB1; GADD45G
GO:0031281	1.70E-04	0.3463	32911	172	53	4	BP	positive regulation of cyclase activity	ADCY6; ADCY2; ADCY9; ADRB3
GO:0051349	1.70E-04	0.3463	32911	172	53	4	BP	positive regulation of lyase activity	ADCY6; ADCY2; ADCY9; ADRB3
GO:0030199	1.70E-04	0.349	32911	172	21	3	BP	collagen fibril organization	SFRP2; COL3A1; COL11A2
GO:0071222	1.70E-04	0.349	32911	172	21	3	BP	cellular response to lipopolysaccharide	MAPK3; STAT1; MYD88
GO:0009161	1.70E-04	0.349	32911	172	21	3	BP	ribonucleoside monophosphate metabolic process	ADSS; AMPD3; PRPS1
GO:0001501	1.70E-04	0.3547	32911	172	99	5	BP	skeletal system development	SP1; LGALS3; HOXA5; TGFB1; EPHA2
GO:0006575	1.80E-04	0.3685	32911	172	157	6	BP	cellular amino acid derivative metabolic process	GSR; GAMT; SRM; ACADL; CD01; GCLC
GO:0050776	1.80E-04	0.3731	32911	172	224	7	BP	regulation of immune response	GPX2; RELA; CCL2; MYD88; TGFB1; HMOX1; HSPA1B
GO:0009892	1.80E-04	0.3733	32911	172	656	12	BP	negative regulation of metabolic process	EGR1; NRIP1; RELA; BCL3; MYC; JUN; PPAP2B; ACADL; TGFB1; MYBBP1A; GCLC; IL1B
GO:0050727	1.90E-04	0.3895	32911	172	101	5	BP	regulation of inflammatory response	GPX2; PTGS2; MYD88; CCR1; IL1B
GO:0023051	1.90E-04	0.3934	32911	172	470	10	BP	regulation of signaling process	RGS3; SOCS6; SOCS3; RBCK1; MYD88; DUSP16; SFRP2; KDR; IL1B; BCR
GO:0032787	2.00E-04	0.4036	32911	172	302	8	BP	monocarboxylic acid metabolic process	ATF4; PTGS2; CH25H; HIF1A; ACADL; CYP4A12A; ACS1; MTHFD2
GO:0043062	2.00E-04	0.4083	32911	172	160	6	BP	extracellular structure organization	BCL3; LGALS3; SFRP2; COL3A1; WNT3A; COL11A2

GO:0000902	2.10E-04	0.4269	32911	172	103	5	BP	cell morphogenesis	FZD4; HIF1A; TGFB1; ADD1; WNT2
GO:0043388	2.10E-04	0.4291	32911	172	56	4	BP	positive regulation of DNA binding	RELA; PPAP2B; MYD88; TGFB1
GO:0048584	2.10E-04	0.4385	32911	172	230	7	BP	positive regulation of response to stimulus	RELA; PTGS2; CXCL12; CCL2; MYD88; IL1B; HSPA1B
GO:0002009	2.40E-04	0.487	32911	172	234	7	BP	morphogenesis of an epithelium	MYC; CXCL12; SOCS3; HOXA5; TGFB1; NOTCH2; SFRP2
GO:0051216	2.40E-04	0.4917	32911	172	58	4	BP	cartilage development	THBS1; MAPK3; HIF1A; SFRP2
GO:0051247	2.40E-04	0.498	32911	172	166	6	BP	positive regulation of protein metabolic process	MAPK3; TEK; TGFB1; HSPA5; EIF3C; GCLC
GO:0048754	2.50E-04	0.5098	32911	172	107	5	BP	branching morphogenesis of a tube	MYC; CXCL12; HOXA5; TGFB1; KDR
GO:0006695	2.60E-04	0.525	32911	172	24	3	BP	cholesterol biosynthetic process	CYP51; IDI1; HMGCS1
GO:0008202	2.60E-04	0.5312	32911	172	168	6	BP	steroid metabolic process	CYP51; IDI1; AFP; CH25H; SQLE; HMGCS1
GO:0006979	2.60E-04	0.5324	32911	172	108	5	BP	response to oxidative stress	GPX2; PTGS2; HIF1A; HMOX1; GCLC
GO:0001710	2.60E-04	0.5388	32911	172	5	2	BP	mesodermal cell fate commitment	SMAD1; WNT3A
GO:0019852	2.60E-04	0.5388	32911	172	5	2	BP	L-ascorbic acid metabolic process	GSTO1; GCLC
GO:0002292	2.60E-04	0.5388	32911	172	5	2	BP	T cell differentiation involved in immune response	BCL3; GADD45G
GO:0002293	2.60E-04	0.5388	32911	172	5	2	BP	alpha-beta T cell differentiation involved in immune response	BCL3; GADD45G
GO:0043620	2.60E-04	0.5388	32911	172	5	2	BP	regulation of transcription in response to stress	HIF1A; HMOX1
GO:0045080	2.60E-04	0.5388	32911	172	5	2	BP	positive regulation of chemokine biosynthetic process	MYD88; IL1B
GO:0007184	2.60E-04	0.5388	32911	172	5	2	BP	SMAD protein nuclear translocation	SPNB2; TGFB1
GO:0051049	2.70E-04	0.5481	32911	172	490	10	BP	regulation of transport	PTGS2; CXCL12; CCKAR; RBCK1; IRS2; HK1; TGFB1; HMOX1; PRKCI; IL1B
GO:0061138	2.70E-04	0.5556	32911	172	109	5	BP	morphogenesis of a branching epithelium	MYC; CXCL12; SOCS3; HOXA5; TGFB1
GO:0030217	2.70E-04	0.5606	32911	172	60	4	BP	T cell differentiation	EGR1; BCL3; TGFB1; GADD45G
GO:0042035	2.70E-04	0.5606	32911	172	60	4	BP	regulation of cytokine biosynthetic process	RELA; BCL3; MYD88; IL1B
GO:0043281	2.70E-04	0.5606	32911	172	60	4	BP	regulation of caspase activity	MYC; SFRP2; WNT3A; HSPA1B

GO:0000904	2.70E-04	0.5606	32911	172	60	4	BP	cell morphogenesis involved in differentiation	FZD4; HIF1A; TGFB1; WNT2
GO:0019318	2.80E-04	0.566	32911	172	170	6	BP	hexose metabolic process	ATF4; MYC; TALD01; HK1; ALDOA; GBE1
GO:0023014	2.80E-04	0.566	32911	172	170	6	BP	signal transmission via phosphorylation event	MAPK3; SOCS3; STAT1; MYD88; MKNK1; SMAD1
GO:0007243	2.80E-04	0.566	32911	172	170	6	BP	intracellular protein kinase cascade	MAPK3; SOCS3; STAT1; MYD88; MKNK1; SMAD1
GO:0006732	2.90E-04	0.5841	32911	172	171	6	BP	coenzyme metabolic process	GSR; TALD01; ACSS1; SUCLG2; GCLC; MTHFD2
GO:0007584	2.90E-04	0.5975	32911	172	61	4	BP	response to nutrient	TEK; STAT1; TIE1; ARSA
GO:0002684	3.10E-04	0.6273	32911	172	244	7	BP	positive regulation of immune system process	RELA; IL2RG; IRS2; CCL2; MYD88; TGFB1; HSPA1B
GO:0044262	3.10E-04	0.634	32911	172	323	8	BP	cellular carbohydrate metabolic process	ATF4; MYC; TALD01; HK1; ST3GAL2; PRPS1; ALDOA; GBE1
GO:0048585	3.20E-04	0.6565	32911	172	113	5	BP	negative regulation of response to stimulus	GPX2; RELA; SOCS3; TGFB1; IL1B
GO:0016525	3.30E-04	0.6693	32911	172	26	3	BP	negative regulation of angiogenesis	THBS1; CCL2; TIE1
GO:0044057	3.30E-04	0.6743	32911	172	326	8	BP	regulation of system process	EGR1; PTGS2; ARG2; CCL2; KDR; TBXA2R; IL1B; HSPA1B
GO:0051099	3.30E-04	0.6765	32911	172	63	4	BP	positive regulation of binding	RELA; PPAP2B; MYD88; TGFB1
GO:0080134	3.50E-04	0.7088	32911	172	249	7	BP	regulation of response to stress	GPX2; RELA; PTGS2; MYD88; SFRP2; CCR1; IL1B
GO:0003006	3.60E-04	0.726	32911	172	250	7	BP	reproductive developmental process	PTGS2; CXCL12; EPOR; TGFB1; SFRP2; JUNB; KDR
GO:0001932	3.70E-04	0.7456	32911	172	179	6	BP	regulation of protein amino acid phosphorylation	TEK; SOCS3; JUN; PPAP2B; SFRP2; IL1B
GO:0030509	3.70E-04	0.75	32911	172	27	3	BP	BMP signaling pathway	EGR1; SMAD1; WNT3A
GO:0035567	3.70E-04	0.75	32911	172	27	3	BP	non-canonical Wnt receptor signaling pathway	FZD2; WNT2; WNT3A
GO:0043407	3.70E-04	0.75	32911	172	27	3	BP	negative regulation of MAP kinase activity	DUSP16; SFRP2; IL1B
GO:0071219	3.70E-04	0.75	32911	172	27	3	BP	cellular response to molecule of bacterial origin	MAPK3; STAT1; MYD88
GO:0008637	3.70E-04	0.75	32911	172	27	3	BP	apoptotic mitochondrial changes	BID; MYC; JUN
GO:0022602	3.80E-04	0.7627	32911	172	65	4	BP	ovulation cycle process	NRIP1; FZD4; AFP; KDR

GO:0010551	3.80E-04	0.7706	32911	172	117	5	BP	regulation of gene-specific transcription from RNA polymerase II promoter	GATA5; MYC; TGFB1; SMAD1; IL1B
GO:0010575	4.00E-04	0.8055	32911	172	6	2	BP	positive regulation of vascular endothelial growth factor production	PTGS2; IL1B
GO:0002287	4.00E-04	0.8055	32911	172	6	2	BP	alpha-beta T cell activation involved in immune response	BCL3; GADD45G
GO:0046033	4.00E-04	0.8055	32911	172	6	2	BP	AMP metabolic process	ADSS; PRPS1
GO:0051929	4.00E-04	0.8055	32911	172	6	2	BP	positive regulation of calcium ion transport via voltage-gated calcium channel activity	CXCL12; CCKAR
GO:0060795	4.00E-04	0.8055	32911	172	6	2	BP	cell fate commitment involved in the formation of primary germ layers	SMAD1; WNT3A
GO:0007263	4.00E-04	0.8055	32911	172	6	2	BP	nitric oxide mediated signal transduction	MT1; GUCY1B3
GO:0006520	4.10E-04	0.8384	32911	172	183	6	BP	cellular amino acid metabolic process	ARG2; IVD; CTPS; ALDH4A1; CD01; ASNS
GO:0044282	4.40E-04	0.8909	32911	172	340	8	BP	small molecule catabolic process	TALD01; PDE4B; HK1; ACADL; HSPA8; IVD; CD01; ALDOA
GO:0008285	4.50E-04	0.9178	32911	172	260	7	BP	negative regulation of cell proliferation	CAV2; PTGS2; JUN; TGFB1; SMAD1; CDKN2B; HMOX1
GO:0090304	4.50E-04	0.9189	32911	172	2322	25	BP	nucleic acid metabolic process	EGR1; NRIP1; SP1; ATF4; RELA; BCL3; GATA5; CEBPD; MYC; FOS; STAT1; JUN; HOXA5; MYB; EGR2; HIF1A; SMAD1; NOTCH2; NOTCH3; HSPA1A; JUNB; SENP2; MYBBP1A; SETD8; HSPA1B
GO:0030879	4.60E-04	0.9298	32911	172	29	3	BP	mammary gland development	IRS2; TGFB1; WNT3A
GO:0043123	4.60E-04	0.9298	32911	172	29	3	BP	positive regulation of I-kappaB kinase/NF-kappaB cascade	RBCK1; MYD88; IL1B
GO:0051092	4.60E-04	0.9298	32911	172	29	3	BP	positive regulation of NF-kappaB transcription factor activity	RELA; MYD88; TGFB1
GO:0005975	5.00E-04	1	32911	172	436	9	BP	carbohydrate metabolic process	ATF4; MYC; TALD01; HK1; CCND3; ST3GAL2; PRPS1; ALDOA; GBE1
GO:0002521	5.20E-04	1	32911	172	125	5	BP	leukocyte differentiation	EGR1; BCL3; TGFB1; JUNB; GADD45G
GO:0007611	5.20E-04	1	32911	172	125	5	BP	learning or memory	EGR1; PTGS2; JUN; ADCY8; IL1B
GO:0032868	5.30E-04	1	32911	172	71	4	BP	response to insulin stimulus	STAT1; IRS2; EGR2; PRKCI

GO:0009790	5.30E-04	1	32911	172	267	7	BP	embryo development	SP1; EPOR; MYB; ADD1; JUNB; TIE1; WNT3A
GO:0031649	5.60E-04	1	32911	172	7	2	BP	heat generation	ADRB3; IL1B
GO:0045073	5.60E-04	1	32911	172	7	2	BP	regulation of chemokine biosynthetic process	MYD88; IL1B
GO:0008354	5.60E-04	1	32911	172	7	2	BP	germ cell migration	CXCL12; TGFB1
GO:0009617	5.70E-04	1	32911	172	128	5	BP	response to bacterium	GPX2; RELA; BCL3; STAT1; MYD88
GO:0001819	5.90E-04	1	32911	172	73	4	BP	positive regulation of cytokine production	BCL3; PTGS2; MYD88; IL1B
GO:0032103	5.90E-04	1	32911	172	73	4	BP	positive regulation of response to external stimulus	PTGS2; CXCL12; CCL2; IL1B
GO:0006694	5.90E-04	1	32911	172	73	4	BP	steroid biosynthetic process	CYP51; IDI1; CH25H; HMGCS1
GO:0042098	6.20E-04	1	32911	172	32	3	BP	T cell proliferation	FYN; CXCL12; CCND3
GO:0060341	6.20E-04	1	32911	172	274	7	BP	regulation of cellular localization in utero	CXCL12; CCKAR; RBCK1; IRS2; TGFB1; HMOX1; IL1B
GO:0001701	6.30E-04	1	32911	172	198	6	BP	embryonic development	SP1; MYB; ADD1; JUNB; TIE1; WNT3A
GO:0006351	6.50E-04	1	32911	172	75	4	BP	transcription, DNA-dependent	MYC; FOS; JUN; JUNB
GO:0045995	6.80E-04	1	32911	172	33	3	BP	regulation of embryonic development	HSPA5; SFRP2; WNT2
GO:0051384	6.80E-04	1	32911	172	33	3	BP	response to glucocorticoid stimulus	ALDH3A1; TGFB1; CD01
GO:0030278	6.80E-04	1	32911	172	76	4	BP	regulation of ossification	EGR2; TGFB1; SMAD1; SFRP2
GO:0007420	6.80E-04	1	32911	172	76	4	BP	brain development	CXCL12; EPOR; IRS2; BCR
GO:0043009	7.00E-04	1	32911	172	202	6	BP	chordate embryonic development	SP1; MYB; ADD1; JUNB; TIE1; WNT3A
GO:0006725	7.10E-04	1	32911	172	134	5	BP	cellular aromatic compound metabolic process	GAMT; CYP2F2; SQLE; AMPD3; MTHFD2
GO:0002902	7.40E-04	1	32911	172	8	2	BP	regulation of B cell apoptosis	MYC; IRS2
GO:0048532	7.40E-04	1	32911	172	8	2	BP	anatomical structure arrangement	EGR2; HSPA5
GO:0060136	7.40E-04	1	32911	172	8	2	BP	embryonic process involved in female pregnancy	SP1; JUNB
GO:0031960	7.40E-04	1	32911	172	34	3	BP	response to corticosteroid stimulus	ALDH3A1; TGFB1; CD01
GO:0008629	7.40E-04	1	32911	172	34	3	BP	induction of apoptosis by intracellular signals	BCL3; MYC; HMOX1

GO:0050678	7.60E-04	1	32911	172	78	4	BP	regulation of epithelial cell proliferation	HOXA5; TGFB1; WNT2; KDR
GO:0009792	7.70E-04	1	32911	172	206	6	BP	embryo development ending in birth or egg hatching	SP1; MYB; ADD1; JUNB; TIE1; WNT3A
GO:0019932	7.80E-04	1	32911	172	137	5	BP	second-messenger-mediated signaling	FZD2; ADCY2; ADCY8; TBXA2R; ADRB3
GO:0032774	7.90E-04	1	32911	172	79	4	BP	RNA biosynthetic process	MYC; FOS; JUN; JUNB
GO:0045761	7.90E-04	1	32911	172	79	4	BP	regulation of adenylate cyclase activity	ADCY6; ADCY2; ADCY9; ADRB3
GO:0051924	7.90E-04	1	32911	172	79	4	BP	regulation of calcium ion transport	PTGS2; CXCL12; CCKAR; TGFB1
GO:0019229	8.10E-04	1	32911	172	35	3	BP	regulation of vasoconstriction	PTGS2; TBXA2R; HSPA1B
GO:0031668	8.10E-04	1	32911	172	35	3	BP	cellular response to extracellular stimulus	FOS; JUN; SFRP2
GO:0048511	8.40E-04	1	32911	172	139	5	BP	rhythmic process	NR1P1; FZD4; AFP; EGR2; KDR
GO:0065003	8.40E-04	1	32911	172	375	8	BP	macromolecular complex assembly	TUBA4A; MAPK3; CAV2; MYC; ACADL; TUBB2C; JUP; EIF3A
GO:0007049	8.50E-04	1	32911	172	469	9	BP	cell cycle	MAPK3; CALM3; GADD45A; CCND3; PARD6B; PIMI; CDKN2B; SETD8; ANAPC11
GO:0043269	8.60E-04	1	32911	172	140	5	BP	regulation of ion transport	PTGS2; CXCL12; CCKAR; HK1; TGFB1
GO:0031279	8.70E-04	1	32911	172	81	4	BP	regulation of cyclase activity	ADCY6; ADCY2; ADCY9; ADRB3
GO:0051339	8.70E-04	1	32911	172	81	4	BP	regulation of lyase activity	ADCY6; ADCY2; ADCY9; ADRB3
GO:0007005	8.70E-04	1	32911	172	81	4	BP	mitochondrion organization	BID; CAV2; MYC; JUN
GO:0071496	8.80E-04	1	32911	172	36	3	BP	cellular response to external stimulus	FOS; JUN; SFRP2
GO:0051707	9.00E-04	1	32911	172	212	6	BP	response to other organism	GPX2; RELA; BCL3; STAT1; MYD88; TGFB1
GO:0010552	9.10E-04	1	32911	172	82	4	BP	positive regulation of gene-specific transcription from RNA polymerase II promoter	GATA5; TGFB1; SMAD1; IL1B
GO:0046777	9.10E-04	1	32911	172	82	4	BP	protein amino acid autophosphorylation	FYN; HK1; KDR; BCR
GO:0031622	9.50E-04	1	32911	172	9	2	BP	positive regulation of fever	PTGS2; IL1B
GO:0032414	9.50E-04	1	32911	172	9	2	BP	positive regulation of ion transmembrane transporter activity	CXCL12; CCKAR
GO:0043367	9.50E-04	1	32911	172	9	2	BP	CD4-positive, alpha beta T cell differentiation	BCL3; GADD45G
GO:0042552	9.50E-04	1	32911	172	37	3	BP	myelination	FYN; EGR2; TGFB1

GO:0043122	9.50E-04	1	32911	172	37	3	BP	regulation of I-kappaB kinase/NF-kappaB cascade	RBCK1; MYD88; IL1B
GO:0045471	9.50E-04	1	32911	172	37	3	BP	response to ethanol	FYN; CD01; ARSA
GO:0032870	9.50E-04	1	32911	172	83	4	BP	cellular response to hormone stimulus	STAT1; IRS2; TGFB1; PRKCI
GO:0052548	9.50E-04	1	32911	172	83	4	BP	regulation of endopeptidase activity	MYC; SFRP2; WNT3A; HSPA1B
GO:0006461	9.80E-04	1	32911	172	296	7	BP	protein complex assembly	TUBA4A; MAPK3; CAV2; MYC; ACADL; TUBB2C; JUP
GO:0031349	0.001	1	32911	172	84	4	BP	positive regulation of defense response	RELA; PTGS2; MYD88; IL1B
GO:0006767	0.001	1	32911	172	38	3	BP	water-soluble vitamin metabolic process	GSTO1; ACADL; GCLC
GO:0031324	0.001	1	32911	172	586	10	BP	negative regulation of cellular metabolic process	EGR1; NRIP1; BCL3; MYC; JUN; PPAP2B; ACADL; TGFB1; MYBBP1A; GCLC
GO:0071495	0.001	1	32911	172	86	4	BP	cellular response to endogenous stimulus	STAT1; IRS2; TGFB1; PRKCI
GO:0002673	0.0011	1	32911	172	39	3	BP	regulation of acute inflammatory response	PTGS2; CCR1; IL1B
GO:0042440	0.0011	1	32911	172	39	3	BP	pigment metabolic process	IDI1; HMOX1; ALAS1
GO:0043627	0.0011	1	32911	172	39	3	BP	response to estrogen stimulus	TEK; HMOX1; ARSA
GO:0030817	0.0011	1	32911	172	87	4	BP	regulation of cAMP biosynthetic process	ADCY6; ADCY2; ADCY9; ADRB3
GO:0044248	0.0011	1	32911	172	592	10	BP	cellular catabolic process	MYC; PDE4B; ACADL; HSPA8; IVD; HMOX1; CD01; SUCLG2; ARSA; GSTA2
GO:0020027	0.0011	1	32911	172	10	2	BP	hemoglobin metabolic process	HIF1A; ADD1
GO:0031100	0.0011	1	32911	172	10	2	BP	organ regeneration	CXCL12; TGFB1
GO:0032411	0.0011	1	32911	172	10	2	BP	positive regulation of transporter activity	CXCL12; CCKAR
GO:0050679	0.0012	1	32911	172	40	3	BP	positive regulation of epithelial cell proliferation	TGFB1; WNT2; KDR
GO:0007272	0.0012	1	32911	172	40	3	BP	ensheathment of neurons	FYN; EGR2; TGFB1
GO:0008366	0.0012	1	32911	172	40	3	BP	axon ensheathment	FYN; EGR2; TGFB1
GO:0009612	0.0012	1	32911	172	40	3	BP	response to mechanical stimulus	FYN; MYC; STAT1

GO:0051241	0.0012	1	32911	172	151	5	BP	negative regulation of multicellular organismal process	PTGS2; ARG2; HMOX1; ADRB3; HSPA1B
GO:0030814	0.0012	1	32911	172	89	4	BP	regulation of cAMP metabolic process	ADCY6; ADCY2; ADCY9; ADRB3
GO:0050769	0.0012	1	32911	172	89	4	BP	positive regulation of neurogenesis	RELA; CXCL12; KDR; WNT3A
GO:0044255	0.0012	1	32911	172	496	9	BP	cellular lipid metabolic process	PTDSS2; IDI1; PTGS2; CERK; PPAP2B; CH25H; ACADL; CYP4A12A; HMGCS1
GO:0022898	0.0012	1	32911	172	41	3	BP	regulation of transmembrane transporter activity	CXCL12; CCKAR; HK1
GO:0032412	0.0012	1	32911	172	41	3	BP	regulation of ion transmembrane transporter activity	CXCL12; CCKAR; HK1
GO:0052547	0.0012	1	32911	172	90	4	BP	regulation of peptidase activity	MYC; SFRP2; WNT3A; HSPA1B
GO:0019935	0.0013	1	32911	172	91	4	BP	cyclic-nucleotide-mediated signaling	FZD2; ADCY2; ADCY8; ADRB3
GO:0043933	0.0013	1	32911	172	404	8	BP	macromolecular complex subunit organization	TUBA4A; MAPK3; CAV2; MYC; ACADL; TUBB2C; JUP; EIF3A
GO:0050871	0.0013	1	32911	172	42	3	BP	positive regulation of B cell activation	IL2RG; IRS2; TGFB1
GO:0009636	0.0013	1	32911	172	42	3	BP	response to toxin	MAPK3; CYP2F2; MT1
GO:0045926	0.0014	1	32911	172	92	4	BP	negative regulation of growth	MYD88; HIF1A; WNT3A; ADRB3
GO:0008217	0.0014	1	32911	172	92	4	BP	regulation of blood pressure	PTGS2; TBXA2R; HMOX1; ADRB3
GO:0051050	0.0014	1	32911	172	232	6	BP	positive regulation of transport	CXCL12; CCKAR; RBCK1; IRS2; PRKCI; IL1B
GO:0010605	0.0014	1	32911	172	609	10	BP	negative regulation of macromolecule metabolic process	EGR1; NRIP1; RELA; BCL3; MYC; JUN; PPAP2B; TGFB1; MYBBP1A; GLCL
GO:0030947	0.0014	1	32911	172	11	2	BP	regulation of vascular endothelial growth factor receptor signaling pathway	FZD4; HIF1A
GO:0031652	0.0014	1	32911	172	11	2	BP	positive regulation of heat generation	PTGS2; IL1B
GO:0032494	0.0014	1	32911	172	11	2	BP	response to peptidoglycan	RELA; MYD88
GO:0045646	0.0014	1	32911	172	11	2	BP	regulation of erythrocyte differentiation	HIF1A; LMO2

GO:0048841	0.0014	1	32911	172	11	2	BP	regulation of axon extension involved in axon guidance	CXCL12; WNT3A
GO:0048732	0.0014	1	32911	172	93	4	BP	gland development	IRS2; HOXA5; TGFB1; WNT3A
GO:0051188	0.0014	1	32911	172	93	4	BP	cofactor biosynthetic process	ACSS1; GCLC; ALAS1; MTHFD2
GO:0032409	0.0014	1	32911	172	43	3	BP	regulation of transporter activity	CXCL12; CCKAR; HK1
GO:0030802	0.0015	1	32911	172	95	4	BP	regulation of cyclic nucleotide biosynthetic process	ADCY6; ADCY2; ADCY9; ADRB3
GO:0030808	0.0015	1	32911	172	95	4	BP	regulation of nucleotide biosynthetic process	ADCY6; ADCY2; ADCY9; ADRB3
GO:0010952	0.0015	1	32911	172	44	3	BP	positive regulation of peptidase activity	MYC; SFRP2; WNT3A
GO:0007179	0.0015	1	32911	172	44	3	BP	transforming growth factor beta receptor signaling pathway	CCL2; TGFB1; SMAD1
GO:0030098	0.0016	1	32911	172	96	4	BP	lymphocyte differentiation	EGR1; BCL3; TGFB1; GADD45G
GO:0008219	0.0016	1	32911	172	516	9	BP	cell death	BID; MYC; TGFB1; TRAF5; SFRP2; EPHA2; MCL1; HMOX1; GADD45G
GO:0046651	0.0016	1	32911	172	45	3	BP	lymphocyte proliferation	FYN; CXCL12; CCND3
GO:0045165	0.0017	1	32911	172	97	4	BP	cell fate commitment	SMAD1; NOTCH3; KDR; WNT3A
GO:0002286	0.0017	1	32911	172	12	2	BP	T cell activation involved in immune response	BCL3; GADD45G
GO:0042089	0.0017	1	32911	172	12	2	BP	cytokine biosynthetic process	MYD88; GADD45G
GO:0043330	0.0017	1	32911	172	12	2	BP	response to exogenous dsRNA	MAPK3; STAT1
GO:0090263	0.0017	1	32911	172	12	2	BP	positive regulation of canonical Wnt receptor signaling pathway	SFRP2; WNT3A
GO:0030799	0.0017	1	32911	172	98	4	BP	regulation of cyclic nucleotide metabolic process	ADCY6; ADCY2; ADCY9; ADRB3
GO:0016265	0.0019	1	32911	172	527	9	BP	death	BID; MYC; TGFB1; TRAF5; SFRP2; EPHA2; MCL1; HMOX1; GADD45G
GO:0006790	0.0019	1	32911	172	101	4	BP	sulfur metabolic process	GSR; GAMT; CD01; GCLC
GO:0051336	0.002	1	32911	172	248	6	BP	regulation of hydrolase activity	AGFG2; MYC; HSPA5; SFRP2; WNT3A; HSPA1B
GO:0001829	0.002	1	32911	172	13	2	BP	trophectodermal cell differentiation	SP1; JUNB
GO:0042107	0.002	1	32911	172	13	2	BP	cytokine metabolic process	MYD88; GADD45G

GO:0042398	0.002	1	32911	172	48	3	BP	cellular amino acid derivative biosynthetic process	GAMT; SRM; GCLC
GO:0007626	0.002	1	32911	172	249	6	BP	locomotory behavior	CXCL12; CCL2; CXCL1; CCR1; CSF3R; IL1B
GO:0002694	0.0021	1	32911	172	172	5	BP	regulation of leukocyte activation	IL2RG; IRS2; MYD88; TGFBI; HMOX1
GO:0032869	0.0021	1	32911	172	49	3	BP	cellular response to insulin stimulus	STAT1; IRS2; PRKCI
GO:0035282	0.0021	1	32911	172	49	3	BP	segmentation	EGR2; SFRP2; WNT3A
GO:0006412	0.0022	1	32911	172	253	6	BP	translation	EIF2S2; EIF1A; EIF3A; EIF3C; EIF3E; EIF5
GO:0071375	0.0022	1	32911	172	50	3	BP	cellular response to peptide hormone stimulus	STAT1; IRS2; PRKCI
GO:0050767	0.0023	1	32911	172	255	6	BP	regulation of neurogenesis	RELA; CXCL12; TGFBI; NOTCH3; KDR; WNT3A
GO:0010959	0.0023	1	32911	172	106	4	BP	regulation of metal ion transport	PTGS2; CXCL12; CCKAR; TGFBI
GO:0051251	0.0023	1	32911	172	106	4	BP	positive regulation of lymphocyte activation	IL2RG; IRS2; MYD88; TGFBI
GO:0048010	0.0023	1	32911	172	14	2	BP	vascular endothelial growth factor receptor signaling pathway	CCL2; KDR
GO:0051248	0.0024	1	32911	172	107	4	BP	negative regulation of protein metabolic process	RELA; JUN; PPAP2B; GCLC
GO:0051345	0.0024	1	32911	172	107	4	BP	positive regulation of hydrolase activity	MYC; HSPA5; SFRP2; WNT3A
GO:0050865	0.0025	1	32911	172	178	5	BP	regulation of cell activation	IL2RG; IRS2; MYD88; TGFBI; HMOX1
GO:0006886	0.0025	1	32911	172	260	6	BP	intracellular protein transport	SPNB2; BID; MAPK3; TGFBI; YWHAQ; PRICKLE1
GO:0007219	0.0025	1	32911	172	52	3	BP	Notch signaling pathway	DLL4; NOTCH2; NOTCH3
GO:0035467	0.0026	1	32911	172	181	5	BP	negative regulation of signaling pathway	RELA; SOCS3; HSPA5; SFRP2; IL1B
GO:0031400	0.0027	1	32911	172	53	3	BP	negative regulation of protein modification process	JUN; PPAP2B; GCLC
GO:0006007	0.0027	1	32911	172	53	3	BP	glucose catabolic process	TALDO1; HK1; ALDOA
GO:0019321	0.0027	1	32911	172	15	2	BP	pentose metabolic process	TALDO1; PRPS1
GO:0032642	0.0027	1	32911	172	15	2	BP	regulation of chemokine production	MYD88; IL1B
GO:0043331	0.0027	1	32911	172	15	2	BP	response to dsRNA	MAPK3; STAT1

GO:0045833	0.0027	1	32911	172	15	2	BP	negative regulation of lipid metabolic process	ACADL; IL1B
GO:0046632	0.0027	1	32911	172	15	2	BP	alpha-beta T cell differentiation	BCL3; GADD45G
GO:0060716	0.0027	1	32911	172	15	2	BP	labyrinthine layer blood vessel development	JUNB; WNT2
GO:0070228	0.0027	1	32911	172	15	2	BP	regulation of lymphocyte apoptosis	MYC; IRS2
GO:0090183	0.0027	1	32911	172	15	2	BP	regulation of kidney development	MYC; TGFB1
GO:0002697	0.0027	1	32911	172	111	4	BP	regulation of immune effector process	CCL2; TGFB1; HMOX1; HSPA1B
GO:0019320	0.0028	1	32911	172	54	3	BP	hexose catabolic process	TALD01; HK1; ALDOA
GO:0002696	0.0029	1	32911	172	113	4	BP	positive regulation of leukocyte activation	IL2RG; IRS2; MYD88; TGFB1
GO:0046365	0.003	1	32911	172	55	3	BP	monosaccharide catabolic process	TALD01; HK1; ALDOA
GO:0051926	0.0031	1	32911	172	16	2	BP	negative regulation of calcium ion transport	PTGS2; TGFB1
GO:0007613	0.0031	1	32911	172	56	3	BP	memory	PTGS2; ADCY8; IL1B
GO:0051960	0.0034	1	32911	172	276	6	BP	regulation of nervous system development	RELA; CXCL12; TGFB1; NOTCH3; KDR; WNT3A
GO:0043523	0.0034	1	32911	172	118	4	BP	regulation of neuron apoptosis	DNAJC5; JUN; KDR; GCLC
GO:0050867	0.0034	1	32911	172	118	4	BP	positive regulation of cell activation	IL2RG; IRS2; MYD88; TGFB1
GO:0006457	0.0034	1	32911	172	118	4	BP	protein folding	DNAJC5; CCT6A; CCT5; HSPA8
GO:0046328	0.0035	1	32911	172	58	3	BP	regulation of JNK cascade	MYD88; SFRP2; IL1B
GO:0050864	0.0035	1	32911	172	58	3	BP	regulation of B cell activation	IL2RG; IRS2; TGFB1
GO:0042594	0.0035	1	32911	172	17	2	BP	response to starvation	CCKAR; JUN
GO:0045637	0.0036	1	32911	172	59	3	BP	regulation of myeloid cell differentiation	JUN; HIF1A; LMO2
GO:0006140	0.0037	1	32911	172	196	5	BP	regulation of nucleotide metabolic process	AGFG2; ADCY6; ADCY2; ADCY9; ADRB3
GO:0051047	0.0039	1	32911	172	122	4	BP	positive regulation of secretion	CXCL12; CCKAR; IRS2; IL1B
GO:0002285	0.0039	1	32911	172	18	2	BP	lymphocyte activation involved in immune response	BCL3; GADD45G
GO:0043154	0.0039	1	32911	172	18	2	BP	negative regulation of caspase activity	SFRP2; HSPA1B

GO:0045987	0.0039	1	32911	172	18	2	BP	positive regulation of smooth muscle contraction	PTGS2; TBXA2R
GO:0050974	0.0039	1	32911	172	18	2	BP	detection of mechanical stimulus involved in sensory perception	FYN; MYC
GO:0006541	0.0039	1	32911	172	18	2	BP	glutamine metabolic process	CTPS; ASNS
GO:0051649	0.0039	1	32911	172	589	9	BP	establishment of localization in cell	SPNB2; BID; MAPK3; FZD4; CCKAR; TGFB1; YWHAQ; PRICKLE1; MYBBP1A
GO:0034762	0.004	1	32911	172	61	3	BP	regulation of transmembrane transport	CXCL12; CCKAR; HK1
GO:0034765	0.004	1	32911	172	61	3	BP	regulation of ion transmembrane transport	CXCL12; CCKAR; HK1
GO:0070302	0.0042	1	32911	172	62	3	BP	regulation of stress-activated protein kinase signaling cascade	MYD88; SFRP2; IL1B
GO:0030177	0.0043	1	32911	172	19	2	BP	positive regulation of Wnt receptor signaling pathway	SFRP2; WNT3A
GO:0048565	0.0043	1	32911	172	19	2	BP	digestive tract development	MYB; COL3A1
GO:0007259	0.0043	1	32911	172	19	2	BP	JAK-STAT cascade	SOCS3; STAT1
GO:0048638	0.0044	1	32911	172	63	3	BP	regulation of developmental growth	CXCL12; WNT2; WNT3A
GO:0006937	0.0044	1	32911	172	63	3	BP	regulation of muscle contraction	PTGS2; ARG2; TBXA2R
GO:0060284	0.0044	1	32911	172	292	6	BP	regulation of cell development	RELA; CXCL12; TGFB1; NOTCH3; KDR; WNT3A
GO:0006974	0.0044	1	32911	172	292	6	BP	response to DNA damage stimulus	BCL3; MAPK3; GADD45A; HSPA1A; HMOX1; HSPA1B
GO:0001894	0.0046	1	32911	172	64	3	BP	tissue homeostasis	ADD1; KDR; COL11A2
GO:0044275	0.0046	1	32911	172	64	3	BP	cellular carbohydrate catabolic process	TALDO1; HK1; ALDOA
GO:0007389	0.0047	1	32911	172	296	6	BP	pattern specification process	CXCL12; HOXA5; EGR2; NOTCH2; SFRP2; WNT3A
GO:0051051	0.0047	1	32911	172	129	4	BP	negative regulation of transport	PTGS2; TGFB1; HMOX1; IL1B
GO:0000165	0.0048	1	32911	172	65	3	BP	MAPKKK cascade	MAPK3; MYD88; SMAD1
GO:0030111	0.0048	1	32911	172	65	3	BP	regulation of Wnt receptor signaling pathway	PPAP2B; SFRP2; WNT3A
GO:0032200	0.0048	1	32911	172	20	2	BP	telomere organization	HSPA1A; HSPA1B
GO:0045669	0.0048	1	32911	172	20	2	BP	positive regulation of osteoblast differentiation	SMAD1; SFRP2

GO:0046330	0.0048	1	32911	172	20	2	BP	positive regulation of JNK cascade	MYD88; IL1B
GO:0046631	0.0048	1	32911	172	20	2	BP	alpha-beta T cell activation	BCL3; GADD45G
GO:0050982	0.0048	1	32911	172	20	2	BP	detection of mechanical stimulus	FYN; MYC
GO:0000723	0.0048	1	32911	172	20	2	BP	telomere maintenance	HSPA1A; HSPA1B
GO:0008045	0.0048	1	32911	172	20	2	BP	motor axon guidance	CXCL12; EGR2
GO:0008610	0.005	1	32911	172	299	6	BP	lipid biosynthetic process	CYP51; PTDSS2; IDI1; PTGS2; CH25H; HMGCS1
GO:0010359	0.0052	1	32911	172	1	1	BP	regulation of anion channel activity	HK1
GO:0014038	0.0052	1	32911	172	1	1	BP	regulation of Schwann cell differentiation	RELA
GO:0014040	0.0052	1	32911	172	1	1	BP	positive regulation of Schwann cell differentiation	RELA
GO:0016109	0.0052	1	32911	172	1	1	BP	tetraterpenoid biosynthetic process	IDI1
GO:0016114	0.0052	1	32911	172	1	1	BP	terpenoid biosynthetic process	IDI1
GO:0016117	0.0052	1	32911	172	1	1	BP	carotenoid biosynthetic process	IDI1
GO:0001765	0.0052	1	32911	172	1	1	BP	membrane raft assembly	CAV2
GO:0018931	0.0052	1	32911	172	1	1	BP	naphthalene metabolic process	CYP2F2
GO:0018979	0.0052	1	32911	172	1	1	BP	trichloroethylene metabolic process	CYP2F2
GO:0002159	0.0052	1	32911	172	1	1	BP	desmosome assembly	JUP
GO:0021594	0.0052	1	32911	172	1	1	BP	rhombomere formation	EGR2
GO:0021660	0.0052	1	32911	172	1	1	BP	rhombomere 3 formation	EGR2
GO:0021666	0.0052	1	32911	172	1	1	BP	rhombomere 5 formation	EGR2
GO:0021874	0.0052	1	32911	172	1	1	BP	Wnt receptor signaling pathway involved in forebrain neuroblast division	WNT3A
GO:0002248	0.0052	1	32911	172	1	1	BP	connective tissue replacement involved in inflammatory response wound healing	HIF1A
GO:0002315	0.0052	1	32911	172	1	1	BP	marginal zone B cell differentiation	BCL3

GO:0032008	0.0052	1	32911	172	1	1	BP	positive regulation of TOR signaling cascade	KDR
GO:0032069	0.0052	1	32911	172	1	1	BP	regulation of nuclease activity	HSPA5
GO:0032075	0.0052	1	32911	172	1	1	BP	positive regulation of nuclease activity	HSPA5
GO:0032740	0.0052	1	32911	172	1	1	BP	positive regulation of interleukin-17 production	MYD88
GO:0032747	0.0052	1	32911	172	1	1	BP	positive regulation of interleukin-23 production	MYD88
GO:0033488	0.0052	1	32911	172	1	1	BP	cholesterol biosynthetic process via 24, 25-dihydrolanosterol	CYP51
GO:0035026	0.0052	1	32911	172	1	1	BP	leading edge cell differentiation	JUN
GO:0042413	0.0052	1	32911	172	1	1	BP	carnitine catabolic process	ACADL
GO:0042701	0.0052	1	32911	172	1	1	BP	progesterone secretion	FZD4
GO:0042758	0.0052	1	32911	172	1	1	BP	long-chain fatty acid catabolic process	ACADL
GO:0045064	0.0052	1	32911	172	1	1	BP	T-helper 2 cell differentiation	BCL3
GO:0045074	0.0052	1	32911	172	1	1	BP	regulation of interleukin-10 biosynthetic process	BCL3
GO:0045082	0.0052	1	32911	172	1	1	BP	positive regulation of interleukin-10 biosynthetic process	BCL3
GO:0048194	0.0052	1	32911	172	1	1	BP	Golgi vesicle budding	PRKCI
GO:0060035	0.0052	1	32911	172	1	1	BP	notochord cell development	EPHA2
GO:0060480	0.0052	1	32911	172	1	1	BP	lung goblet cell differentiation	HOXA5
GO:0060481	0.0052	1	32911	172	1	1	BP	lobar bronchus epithelium development	HOXA5
GO:0060574	0.0052	1	32911	172	1	1	BP	intestinal epithelial cell maturation	HOXA5
GO:0060751	0.0052	1	32911	172	1	1	BP	branch elongation involved in mammary gland duct branching	TGFB1
GO:0060764	0.0052	1	32911	172	1	1	BP	cell-cell signaling involved in mammary gland development	HOXA5

GO:0061056	0.0052	1	32911	172	1	1	BP	sclerotome development	SFRP2
GO:0006552	0.0052	1	32911	172	1	1	BP	leucine catabolic process	IVD
GO:0006579	0.0052	1	32911	172	1	1	BP	betaine catabolic process	ACADL
GO:0006987	0.0052	1	32911	172	1	1	BP	activation of signaling protein activity involved in unfolded protein response	HSPA5
GO:0070164	0.0052	1	32911	172	1	1	BP	negative regulation of adiponectin secretion	IL1B
GO:0070836	0.0052	1	32911	172	1	1	BP	caveola assembly	CAV2
GO:0071503	0.0052	1	32911	172	1	1	BP	response to heparin	EGR1
GO:0071504	0.0052	1	32911	172	1	1	BP	cellular response to heparin	EGR1
GO:0072110	0.0052	1	32911	172	1	1	BP	glomerular mesangial cell proliferation	EGR1
GO:0008063	0.0052	1	32911	172	1	1	BP	Toll signaling pathway	MYD88
GO:0090095	0.0052	1	32911	172	1	1	BP	regulation of metanephric cap mesenchymal cell proliferation	MYC
GO:0090096	0.0052	1	32911	172	1	1	BP	positive regulation of metanephric cap mesenchymal cell proliferation	MYC
GO:0090271	0.0052	1	32911	172	1	1	BP	regulation of fibroblast growth factor production	PTGS2
GO:0009814	0.0052	1	32911	172	1	1	BP	defense response, incompatible interaction	TGFB1
GO:0009817	0.0052	1	32911	172	1	1	BP	defense response to fungus, incompatible interaction	TGFB1
GO:0007267	0.0052	1	32911	172	212	5	BP	cell-cell signaling	CAV2; FZD2; HOXA5; WNT2; WNT3A
GO:0046164	0.0052	1	32911	172	67	3	BP	alcohol catabolic process	TALDO1; HK1; ALDOA
GO:0009108	0.0052	1	32911	172	67	3	BP	coenzyme biosynthetic process	ACSS1; GCLC; MTHFD2
GO:0001676	0.0053	1	32911	172	21	2	BP	long-chain fatty acid metabolic process	ACADL; CYP4A12A
GO:0042168	0.0053	1	32911	172	21	2	BP	heme metabolic process	HMOX1; ALAS1
GO:0045933	0.0053	1	32911	172	21	2	BP	positive regulation of muscle contraction	PTGS2; TBXA2R

GO:0050921	0.0053	1	32911	172	21	2	BP	positive regulation of chemotaxis	CXCL12; CCL2
GO:0006805	0.0053	1	32911	172	21	2	BP	xenobiotic metabolic process	CYP2F2; GSTA2
GO:0008299	0.0053	1	32911	172	21	2	BP	isoprenoid biosynthetic process	ID11; HMGCS1
GO:0008630	0.0053	1	32911	172	21	2	BP	DNA damage response, signal transduction resulting in induction of apoptosis	BCL3; HMOX1
GO:0001666	0.0054	1	32911	172	68	3	BP	response to hypoxia	ALDH3A1; HIF1A; KDR
GO:0030900	0.0054	1	32911	172	68	3	BP	forebrain development	FYN; CCKAR; NOTCH3
GO:0046907	0.0056	1	32911	172	405	7	BP	intracellular transport	SPNB2; BID; MAPK3; TGFB1; YWHAQ; PRICKLE1; MYBBP1A
GO:0001764	0.0057	1	32911	172	69	3	BP	neuron migration	FYN; CXCL12; CCKAR
GO:0009310	0.0057	1	32911	172	69	3	BP	amine catabolic process	ACADL; IVD; CD01
GO:0001892	0.0058	1	32911	172	22	2	BP	embryonic placenta development	SP1; HIF1A
GO:0002221	0.0058	1	32911	172	22	2	BP	pattern recognition receptor signaling pathway	RELA; MYD88
GO:0031396	0.0058	1	32911	172	22	2	BP	regulation of protein ubiquitination	HSPA5; GCLC
GO:0045907	0.0058	1	32911	172	22	2	BP	positive regulation of vasoconstriction	PTGS2; TBXA2R
GO:0070304	0.0058	1	32911	172	22	2	BP	positive regulation of stress-activated protein kinase signaling cascade	MYD88; IL1B
GO:0070482	0.0059	1	32911	172	70	3	BP	response to oxygen levels	ALDH3A1; HIF1A; KDR
GO:0009309	0.0059	1	32911	172	70	3	BP	amine biosynthetic process	SRM; ALDH4A1; ASNS
GO:0048167	0.0061	1	32911	172	71	3	BP	regulation of synaptic plasticity	EGR1; PTGS2; KDR
GO:0048731	0.0062	1	32911	172	413	7	BP	system development	SP1; FOS; LGALS3; HOXA5; TGFB1; EPHA2; ARSA
GO:0032755	0.0063	1	32911	172	23	2	BP	positive regulation of interleukin-6 production	MYD88; IL1B
GO:0006766	0.0066	1	32911	172	73	3	BP	vitamin metabolic process	GSTO1; ACADL; GCLC
GO:0016064	0.0069	1	32911	172	24	2	BP	immunoglobulin mediated immune response	BCL3; MYD88
GO:0002675	0.0069	1	32911	172	24	2	BP	positive regulation of acute inflammatory response	PTGS2; IL1B

GO:0002758	0.0069	1	32911	172	24	2	BP	innate immune response-activating signal transduction	RELA; MYD88
GO:0090257	0.0071	1	32911	172	75	3	BP	regulation of muscle system process	PTGS2; ARG2; TBXA2R
GO:0045596	0.0072	1	32911	172	229	5	BP	negative regulation of cell differentiation	TGFB1; LMO2; NOTCH3; SFRP2; WNT3A
GO:0022604	0.0073	1	32911	172	146	4	BP	regulation of cell morphogenesis	FYN; CXCL12; TGFB1; WNT3A
GO:0010827	0.0075	1	32911	172	25	2	BP	regulation of glucose transport	PRKCI; IL1B
GO:0002218	0.0075	1	32911	172	25	2	BP	activation of innate immune response	RELA; MYD88
GO:0045727	0.0075	1	32911	172	25	2	BP	positive regulation of translation	MAPK3; EIF3C
GO:0050920	0.0075	1	32911	172	25	2	BP	regulation of chemotaxis	CXCL12; CCL2
GO:0021915	0.0081	1	32911	172	26	2	BP	neural tube development	SFRP2; EPHA2
GO:0022607	0.0081	1	32911	172	545	8	BP	cellular component assembly	TUBA4A; MAPK3; CAV2; MYC; ACADL; TUBB2C; JUP; EIF3A
GO:0045860	0.0082	1	32911	172	151	4	BP	positive regulation of protein kinase activity	CERK; HSPA5; GADD45G; IL1B
GO:0048469	0.0082	1	32911	172	79	3	BP	cell maturation	HOXA5; TIMP1; KDR
GO:0019724	0.0087	1	32911	172	27	2	BP	B cell mediated immunity	BCL3; MYD88
GO:0045639	0.0087	1	32911	172	27	2	BP	positive regulation of myeloid cell differentiation	JUN; HIF1A
GO:0048639	0.0087	1	32911	172	27	2	BP	positive regulation of developmental growth	CXCL12; WNT3A
GO:0051258	0.0087	1	32911	172	27	2	BP	protein polymerization	TUBA4A; TUBB2C
GO:0061035	0.0087	1	32911	172	27	2	BP	regulation of cartilage development	RELA; SMAD1
GO:0051249	0.009	1	32911	172	155	4	BP	regulation of lymphocyte activation	IL2RG; IRS2; MYD88; TGFB1
GO:0002703	0.0091	1	32911	172	82	3	BP	regulation of leukocyte mediated immunity	TGFB1; HMOX1; HSPA1B
GO:0051046	0.0092	1	32911	172	243	5	BP	regulation of secretion	CXCL12; CCKAR; IRS2; HMOX1; IL1B
GO:0050804	0.0092	1	32911	172	156	4	BP	regulation of synaptic transmission	EGR1; PTGS2; CCL2; KDR
GO:0034599	0.0093	1	32911	172	28	2	BP	cellular response to oxidative stress	HIF1A; HMOX1
GO:0042060	0.0093	1	32911	172	28	2	BP	wound healing	TGFB1; NOTCH2

GO:0048520	0.0093	1	32911	172	28	2	BP	positive regulation of behavior	CXCL12; CCL2
GO:0009967	0.0094	1	32911	172	157	4	BP	positive regulation of signal transduction	RBCK1; MYD88; KDR; IL1B
GO:0006917	0.0096	1	32911	172	158	4	BP	induction of apoptosis	BCL3; MYC; STAT1; HMOX1
GO:0014070	0.0098	1	32911	172	84	3	BP	response to organic cyclic substance	ALDH3A1; PPP2R2A; SMAD1
GO:0007187	0.0098	1	32911	172	84	3	BP	G-protein signaling, coupled to cyclic nucleotide second messenger	FZD2; ADCY2; ADRB3
GO:0012502	0.0098	1	32911	172	159	4	BP	induction of programmed cell death	BCL3; MYC; STAT1; HMOX1
GO:0048169	0.01	1	32911	172	29	2	BP	regulation of long-term neuronal synaptic plasticity	EGR1; KDR
GO:0048286	0.01	1	32911	172	29	2	BP	lung alveolus development	HOXA5; KDR
GO:0010608	0.01	1	32911	172	160	4	BP	posttranscriptional regulation of gene expression	MAPK3; PPAP2B; MKNK1; EIF3C
GO:0023056	0.01	1	32911	172	160	4	BP	positive regulation of signaling process	RBCK1; MYD88; KDR; IL1B
GO:0033674	0.01	1	32911	172	160	4	BP	positive regulation of kinase activity	CERK; HSPA5; GADD45G; IL1B
GO:0016052	0.0101	1	32911	172	85	3	BP	carbohydrate catabolic process	TALD01; HK1; ALDOA
GO:0019933	0.0101	1	32911	172	85	3	BP	cAMP-mediated signaling	ADCY2; ADCY8; ADRB3
GO:0030324	0.0101	1	32911	172	85	3	BP	lung development	SP1; HOXA5; KDR
GO:0010596	0.0104	1	32911	172	2	1	BP	negative regulation of endothelial cell migration	DLL4
GO:0014028	0.0104	1	32911	172	2	1	BP	notochord formation	EPHA2
GO:0016108	0.0104	1	32911	172	2	1	BP	tetraterpenoid metabolic process	ID11
GO:0016116	0.0104	1	32911	172	2	1	BP	carotenoid metabolic process	ID11
GO:0016926	0.0104	1	32911	172	2	1	BP	protein desumoylation	SENP2
GO:0001732	0.0104	1	32911	172	2	1	BP	formation of translation initiation complex	EIF3A
GO:0019254	0.0104	1	32911	172	2	1	BP	carnitine metabolic process, CoA-linked	ACADL

GO:0019413	0.0104	1	32911	172	2	1	BP	acetate biosynthetic process	ACSS1
GO:0019448	0.0104	1	32911	172	2	1	BP	L-cysteine catabolic process	CD01
GO:0019452	0.0104	1	32911	172	2	1	BP	L-cysteine catabolic process to taurine	CD01
GO:0019542	0.0104	1	32911	172	2	1	BP	propionate biosynthetic process	ACSS1
GO:0019682	0.0104	1	32911	172	2	1	BP	glyceraldehyde-3-phosphate metabolic process	TALD01
GO:0002069	0.0104	1	32911	172	2	1	BP	columnar/cuboidal epithelial cell maturation	HOXA5
GO:0021589	0.0104	1	32911	172	2	1	BP	cerebellum structural organization	HSPA5
GO:0002266	0.0104	1	32911	172	2	1	BP	follicular dendritic cell activation	BCL3
GO:0002268	0.0104	1	32911	172	2	1	BP	follicular dendritic cell differentiation	BCL3
GO:0002513	0.0104	1	32911	172	2	1	BP	tolerance induction to self antigen	TGFB1
GO:0002755	0.0104	1	32911	172	2	1	BP	MyD88-dependent toll-like receptor signaling pathway	MYD88
GO:0030213	0.0104	1	32911	172	2	1	BP	hyaluronan biosynthetic process	CCND3
GO:0031536	0.0104	1	32911	172	2	1	BP	positive regulation of exit from mitosis	TGFB1
GO:0031915	0.0104	1	32911	172	2	1	BP	positive regulation of synaptic plasticity	PTGS2
GO:0031953	0.0104	1	32911	172	2	1	BP	negative regulation of protein amino acid autophosphorylation	JUN
GO:0032667	0.0104	1	32911	172	2	1	BP	regulation of interleukin-23 production	MYD88
GO:0032764	0.0104	1	32911	172	2	1	BP	negative regulation of mast cell cytokine production	HMOX1
GO:0033007	0.0104	1	32911	172	2	1	BP	negative regulation of mast cell activation involved in immune response	HMOX1

GO:0033015	0.0104	1	32911	172	2	1	BP	tetrapyrrole catabolic process	HMOX1
GO:0033762	0.0104	1	32911	172	2	1	BP	response to glucagon stimulus	CD01
GO:0035066	0.0104	1	32911	172	2	1	BP	positive regulation of histone acetylation	TGFB1
GO:0042095	0.0104	1	32911	172	2	1	BP	interferon-gamma biosynthetic process	GADD45G
GO:0042167	0.0104	1	32911	172	2	1	BP	heme catabolic process	HMOX1
GO:0042196	0.0104	1	32911	172	2	1	BP	chlorinated hydrocarbon metabolic process	CYP2F2
GO:0042197	0.0104	1	32911	172	2	1	BP	halogenated hydrocarbon metabolic process	CYP2F2
GO:0042536	0.0104	1	32911	172	2	1	BP	negative regulation of tumor necrosis factor biosynthetic process	BCL3
GO:0042662	0.0104	1	32911	172	2	1	BP	negative regulation of mesodermal cell fate specification	SFRP2
GO:0042908	0.0104	1	32911	172	2	1	BP	xenobiotic transport	SLC2A1
GO:0043301	0.0104	1	32911	172	2	1	BP	negative regulation of leukocyte degranulation	HMOX1
GO:0043305	0.0104	1	32911	172	2	1	BP	negative regulation of mast cell degranulation	HMOX1
GO:0043537	0.0104	1	32911	172	2	1	BP	negative regulation of blood vessel endothelial cell migration	DLL4
GO:0045063	0.0104	1	32911	172	2	1	BP	T-helper 1 cell differentiation	GADD45G
GO:0045657	0.0104	1	32911	172	2	1	BP	positive regulation of monocyte differentiation	JUN
GO:0046149	0.0104	1	32911	172	2	1	BP	pigment catabolic process	HMOX1
GO:0046439	0.0104	1	32911	172	2	1	BP	L-cysteine metabolic process	CD01
GO:0048252	0.0104	1	32911	172	2	1	BP	lauric acid metabolic process	CYP4A12A
GO:0048296	0.0104	1	32911	172	2	1	BP	regulation of isotype switching to IgA isotypes	TGFB1

GO:0048298	0.0104	1	32911	172	2	1	BP	positive regulation of isotype switching to IgA isotypes	TGFB1
GO:0048320	0.0104	1	32911	172	2	1	BP	axial mesoderm formation	EPHA2
GO:0048343	0.0104	1	32911	172	2	1	BP	paraxial mesodermal cell fate commitment	WNT3A
GO:0048672	0.0104	1	32911	172	2	1	BP	positive regulation of collateral sprouting	WNT3A
GO:0048696	0.0104	1	32911	172	2	1	BP	regulation of collateral sprouting in the absence of injury	WNT3A
GO:0048697	0.0104	1	32911	172	2	1	BP	positive regulation of collateral sprouting in the absence of injury	WNT3A
GO:0048842	0.0104	1	32911	172	2	1	BP	positive regulation of axon extension involved in axon guidance	CXCL12
GO:0051280	0.0104	1	32911	172	2	1	BP	negative regulation of release of sequestered calcium ion into cytosol	TGFB1
GO:0051365	0.0104	1	32911	172	2	1	BP	cellular response to potassium ion starvation	JUN
GO:0051541	0.0104	1	32911	172	2	1	BP	elastin metabolic process	HIF1A
GO:0051597	0.0104	1	32911	172	2	1	BP	response to methylmercury	ARSA
GO:0060161	0.0104	1	32911	172	2	1	BP	positive regulation of dopamine receptor signaling pathway	CAV2
GO:0060435	0.0104	1	32911	172	2	1	BP	bronchiole development	HOXA5
GO:0060535	0.0104	1	32911	172	2	1	BP	trachea cartilage morphogenesis	HOXA5
GO:0060536	0.0104	1	32911	172	2	1	BP	cartilage morphogenesis	HOXA5
GO:0061054	0.0104	1	32911	172	2	1	BP	dermatome development	SFRP2
GO:0006529	0.0104	1	32911	172	2	1	BP	asparagine biosynthetic process	ASNS
GO:0006601	0.0104	1	32911	172	2	1	BP	creatine biosynthetic process	GAMT
GO:0006659	0.0104	1	32911	172	2	1	BP	phosphatidylserine biosynthetic process	PTDSS2

GO:0006787	0.0104	1	32911	172	2	1	BP	porphyrin catabolic process	HMOX1
GO:0006788	0.0104	1	32911	172	2	1	BP	heme oxidation	HMOX1
GO:0070098	0.0104	1	32911	172	2	1	BP	chemokine-mediated signaling pathway	CCL2
GO:0070163	0.0104	1	32911	172	2	1	BP	regulation of adiponectin secretion	IL1B
GO:0007098	0.0104	1	32911	172	2	1	BP	centrosome cycle	GADD45A
GO:0071398	0.0104	1	32911	172	2	1	BP	cellular response to fatty acid	EGR1
GO:0071505	0.0104	1	32911	172	2	1	BP	response to mycophenolic acid	EGR1
GO:0071506	0.0104	1	32911	172	2	1	BP	cellular response to mycophenolic acid	EGR1
GO:0072111	0.0104	1	32911	172	2	1	BP	cell proliferation involved in kidney development	EGR1
GO:0072215	0.0104	1	32911	172	2	1	BP	regulation of metanephros development	MYC
GO:0008633	0.0104	1	32911	172	2	1	BP	activation of pro-apoptotic gene products	MYC
GO:0008634	0.0104	1	32911	172	2	1	BP	negative regulation of survival gene product expression	MYC
GO:0090004	0.0104	1	32911	172	2	1	BP	positive regulation of establishment of protein localization in plasma membrane	PRKCI
GO:0090049	0.0104	1	32911	172	2	1	BP	regulation of cell migration involved in sprouting angiogenesis	PTGS2
GO:0090050	0.0104	1	32911	172	2	1	BP	positive regulation of cell migration involved in sprouting angiogenesis	PTGS2
GO:0090264	0.0104	1	32911	172	2	1	BP	regulation of immune complex clearance by monocytes and macrophages	CCL2
GO:0090265	0.0104	1	32911	172	2	1	BP	positive regulation of immune complex clearance by monocytes and macrophages	CCL2
GO:0009093	0.0104	1	32911	172	2	1	BP	cysteine catabolic process	CD01

GO:0009608	0.0104	1	32911	172	2	1	BP	response to symbiont	GPX2
GO:0009609	0.0104	1	32911	172	2	1	BP	response to symbiotic bacterium	GPX2
GO:0070201	0.0104	1	32911	172	86	3	BP	regulation of establishment of protein localization	RBCK1; TGFB1; PRKCI
GO:0009968	0.0104	1	32911	172	86	3	BP	negative regulation of signal transduction	RGS3; SOCS6; SOCS3
GO:0010243	0.0107	1	32911	172	30	2	BP	response to organic nitrogen	HMGCS1; CD01
GO:0001947	0.0107	1	32911	172	30	2	BP	heart looping	HIF1A; WNT3A
GO:0043271	0.0107	1	32911	172	30	2	BP	negative regulation of ion transport	PTGS2; TGFB1
GO:0050873	0.0107	1	32911	172	30	2	BP	brown fat cell differentiation	PTGS2; ADRB3
GO:0051928	0.0107	1	32911	172	30	2	BP	positive regulation of calcium ion transport	CXCL12; CCKAR
GO:0060828	0.0107	1	32911	172	30	2	BP	regulation of canonical Wnt receptor signaling pathway	SFRP2; WNT3A
GO:0006749	0.0107	1	32911	172	30	2	BP	glutathione metabolic process	GSR; GCLC
GO:0023057	0.0107	1	32911	172	87	3	BP	negative regulation of signaling process	RGS3; SOCS6; SOCS3
GO:0006915	0.0111	1	32911	172	462	7	BP	apoptosis	BID; MYC; TRAF5; SFRP2; EPHA2; MCL1; GADD45G
GO:0051347	0.0111	1	32911	172	165	4	BP	positive regulation of transferase activity	CERK; HSPA5; GADD45G; IL1B
GO:0001649	0.0114	1	32911	172	31	2	BP	osteoblast differentiation	JUNB; IGFBP5
GO:0000271	0.0114	1	32911	172	31	2	BP	polysaccharide biosynthetic process	CCND3; GBE1
GO:0033013	0.0114	1	32911	172	31	2	BP	tetrapyrrole metabolic process	HMOX1; ALAS1
GO:0048706	0.0114	1	32911	172	31	2	BP	embryonic skeletal system development	SP1; HOXA5
GO:0051100	0.0114	1	32911	172	31	2	BP	negative regulation of binding	MYC; HMOX1
GO:0051187	0.0114	1	32911	172	31	2	BP	cofactor catabolic process	HMOX1; SUCLG2
GO:0006778	0.0114	1	32911	172	31	2	BP	porphyrin metabolic process	HMOX1; ALAS1
GO:0002683	0.0114	1	32911	172	89	3	BP	negative regulation of immune system process	GPX2; TGFB1; HMOX1

GO:0080135	0.0114	1	32911	172	89	3	BP	regulation of cellular response to stress	MYD88; SFRP2; IL1B
GO:0051969	0.0116	1	32911	172	167	4	BP	regulation of transmission of nerve impulse	EGR1; PTGS2; CCL2; KDR
GO:0016051	0.0118	1	32911	172	90	3	BP	carbohydrate biosynthetic process	ATF4; CCND3; GBE1
GO:0012501	0.0121	1	32911	172	470	7	BP	programmed cell death	BID; MYC; TRAF5; SFRP2; EPHA2; MCL1; GADD45G
GO:0030516	0.0121	1	32911	172	32	2	BP	regulation of axon extension	CXCL12; WNT3A
GO:0032680	0.0121	1	32911	172	32	2	BP	regulation of tumor necrosis factor production	BCL3; MYD88
GO:0042755	0.0121	1	32911	172	32	2	BP	eating behavior	CCKAR; ADRB3
GO:0043506	0.0121	1	32911	172	32	2	BP	regulation of JUN kinase activity	SFRP2; IL1B
GO:0045598	0.0121	1	32911	172	32	2	BP	regulation of fat cell differentiation	SFRP2; WNT3A
GO:0046148	0.0121	1	32911	172	32	2	BP	pigment biosynthetic process	ID1; ALAS1
GO:0050772	0.0121	1	32911	172	32	2	BP	positive regulation of axonogenesis	CXCL12; WNT3A
GO:0051925	0.0121	1	32911	172	32	2	BP	regulation of calcium ion transport via voltage-gated calcium channel activity	CXCL12; CCKAR
GO:0021700	0.0121	1	32911	172	91	3	BP	developmental maturation	HOXA5; TIMP1; KDR
GO:0032944	0.0121	1	32911	172	91	3	BP	regulation of mononuclear cell proliferation	IRS2; MYD88; TGFB1
GO:0050670	0.0121	1	32911	172	91	3	BP	regulation of lymphocyte proliferation	IRS2; MYD88; TGFB1
GO:0030218	0.0128	1	32911	172	33	2	BP	erythrocyte differentiation	SP1; ADD1
GO:0042306	0.0128	1	32911	172	33	2	BP	regulation of protein import into nucleus	RBCK1; TGFB1
GO:0044419	0.0128	1	32911	172	33	2	BP	interspecies interaction between organisms	GPX2; EPOR
GO:0016054	0.0129	1	32911	172	93	3	BP	organic acid catabolic process	ACADL; IVD; CD01
GO:0046395	0.0129	1	32911	172	93	3	BP	carboxylic acid catabolic process	ACADL; IVD; CD01
GO:0070663	0.0129	1	32911	172	93	3	BP	regulation of leukocyte proliferation	IRS2; MYD88; TGFB1
GO:0031099	0.0136	1	32911	172	34	2	BP	regeneration	CXCL12; TGFB1
GO:0032526	0.0136	1	32911	172	34	2	BP	response to retinoic acid	TEK; TIE1

GO:0032269	0.0136	1	32911	172	95	3	BP	negative regulation of cellular protein metabolic process	JUN; PPAP2B; GCLC
GO:0010769	0.014	1	32911	172	96	3	BP	regulation of cell morphogenesis involved in differentiation	CXCL12; TGFB1; WNT3A
GO:0048562	0.014	1	32911	172	96	3	BP	embryonic organ morphogenesis	SP1; HOXA5; EPHA2
GO:0048468	0.0142	1	32911	172	271	5	BP	cell development	CAV2; CXCL12; SFRP2; EPHA2; PRKCI
GO:0009894	0.0144	1	32911	172	178	4	BP	regulation of catabolic process	AGFG2; RELA; GCLC; IL1B
GO:0001933	0.0144	1	32911	172	35	2	BP	negative regulation of protein amino acid phosphorylation	JUN; PPAP2B
GO:0043280	0.0144	1	32911	172	35	2	BP	positive regulation of caspase activity	MYC; WNT3A
GO:0060688	0.0144	1	32911	172	35	2	BP	regulation of morphogenesis of a branching structure	TGFB1; WNT2
GO:0048705	0.0144	1	32911	172	97	3	BP	skeletal system morphogenesis	MYC; HOXA5; COL11A2
GO:0046883	0.0148	1	32911	172	98	3	BP	regulation of hormone secretion	CCKAR; IRS2; IL1B
GO:0002573	0.0152	1	32911	172	36	2	BP	myeloid leukocyte differentiation	TGFB1; JUNB
GO:0032675	0.0152	1	32911	172	36	2	BP	regulation of interleukin-6 production	MYD88; IL1B
GO:0033189	0.0152	1	32911	172	36	2	BP	response to vitamin A	TEK; TIE1
GO:0061025	0.0152	1	32911	172	36	2	BP	membrane fusion	CAV2; TIE1
GO:0006944	0.0152	1	32911	172	36	2	BP	cellular membrane fusion	CAV2; TIE1
GO:0090101	0.0152	1	32911	172	36	2	BP	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	HSPA5; SFRP2
GO:0006916	0.0152	1	32911	172	99	3	BP	anti-apoptosis	TEK; MYC; HSPA1B
GO:0009152	0.0152	1	32911	172	99	3	BP	purine ribonucleotide biosynthetic process	ADSS; AMPD3; PRPS1
GO:0031327	0.0155	1	32911	172	494	7	BP	negative regulation of cellular biosynthetic process	EGR1; NRIP1; BCL3; MYC; ACADL; TGFB1; MYBBP1A
GO:0010273	0.0155	1	32911	172	3	1	BP	detoxification of copper ion	MT1
GO:0010523	0.0155	1	32911	172	3	1	BP	negative regulation of calcium ion transport into cytosol	TGFB1

GO:0010950	0.0155	1	32911	172	3	1	BP	positive regulation of endopeptidase activity	SFRP2
GO:0014850	0.0155	1	32911	172	3	1	BP	response to muscle activity	HIF1A
GO:0001543	0.0155	1	32911	172	3	1	BP	ovarian follicle rupture	NRIP1
GO:0000189	0.0155	1	32911	172	3	1	BP	nuclear translocation of MAPK	MAPK3
GO:0019541	0.0155	1	32911	172	3	1	BP	propionate metabolic process	ACSS1
GO:0019853	0.0155	1	32911	172	3	1	BP	L-ascorbic acid biosynthetic process	GSTO1
GO:0002023	0.0155	1	32911	172	3	1	BP	reduction of food intake in response to dietary excess	CCKAR
GO:0002025	0.0155	1	32911	172	3	1	BP	vasodilation by norepinephrine-epinephrine involved in regulation of systemic arterial blood pressure	ADRB3
GO:0002719	0.0155	1	32911	172	3	1	BP	negative regulation of cytokine production involved in immune response	HMOX1
GO:0002903	0.0155	1	32911	172	3	1	BP	regulation of B cell apoptosis	IRS2
GO:0030157	0.0155	1	32911	172	3	1	BP	pancreatic juice secretion	CCKAR
GO:0030219	0.0155	1	32911	172	3	1	BP	megakaryocyte differentiation	SP1
GO:0031987	0.0155	1	32911	172	3	1	BP	locomotion involved in locomotory behavior	FZD4
GO:0032091	0.0155	1	32911	172	3	1	BP	negative regulation of protein binding	MYC
GO:0032227	0.0155	1	32911	172	3	1	BP	negative regulation of synaptic transmission, dopaminergic	PTGS2
GO:0032660	0.0155	1	32911	172	3	1	BP	regulation of interleukin-17 production	MYD88
GO:0032763	0.0155	1	32911	172	3	1	BP	regulation of mast cell cytokine production	HMOX1
GO:0032829	0.0155	1	32911	172	3	1	BP	regulation of CD4-positive, CD25-positive, alpha-beta regulatory T cell differentiation	IL2RG

GO:0032831	0.0155	1	32911	172	3	1	BP	positive regulation of CD4-positive, CD25-positive, alpha-beta regulatory T cell differentiation	IL2RG
GO:0033687	0.0155	1	32911	172	3	1	BP	osteoblast proliferation	JUNB
GO:0035284	0.0155	1	32911	172	3	1	BP	brain segmentation	EGR2
GO:0040019	0.0155	1	32911	172	3	1	BP	positive regulation of embryonic development	HSPA5
GO:0042396	0.0155	1	32911	172	3	1	BP	phosphagen biosynthetic process	GAMT
GO:0045066	0.0155	1	32911	172	3	1	BP	regulatory T cell differentiation	TGFB1
GO:0045137	0.0155	1	32911	172	3	1	BP	development of primary sexual characteristics	SFRP2
GO:0045655	0.0155	1	32911	172	3	1	BP	regulation of monocyte differentiation	JUN
GO:0045988	0.0155	1	32911	172	3	1	BP	negative regulation of striated muscle contraction	ARG2
GO:0046546	0.0155	1	32911	172	3	1	BP	development of primary male sexual characteristics	SFRP2
GO:0048247	0.0155	1	32911	172	3	1	BP	lymphocyte chemotaxis	CCL2
GO:0048570	0.0155	1	32911	172	3	1	BP	notochord morphogenesis	EPHA2
GO:0051409	0.0155	1	32911	172	3	1	BP	response to nitrosative stress	GCLC
GO:0060028	0.0155	1	32911	172	3	1	BP	convergent extension involved in axis elongation	SFRP2
GO:0060492	0.0155	1	32911	172	3	1	BP	lung induction	WNT2
GO:0060575	0.0155	1	32911	172	3	1	BP	intestinal epithelial cell differentiation	GATA5
GO:0060986	0.0155	1	32911	172	3	1	BP	endocrine hormone secretion	FZD4
GO:0066551	0.0155	1	32911	172	3	1	BP	leucine metabolic process	IVD
GO:0066900	0.0155	1	32911	172	3	1	BP	membrane budding	PRKCI
GO:0070837	0.0155	1	32911	172	3	1	BP	dehydroascorbic acid transport	SLC2A1
GO:0007096	0.0155	1	32911	172	3	1	BP	regulation of exit from mitosis	TGFB1
GO:0008295	0.0155	1	32911	172	3	1	BP	spermidine biosynthetic process	SRM

GO:0090003	0.0155	1	32911	172	3	1	BP	regulation of establishment of protein localization in plasma membrane	PRKCI
GO:0090270	0.0155	1	32911	172	3	1	BP	regulation of fibroblast growth factor production	PTGS2
GO:0090274	0.0155	1	32911	172	3	1	BP	positive regulation of somatostatin secretion	CCKAR
GO:0000098	0.0155	1	32911	172	3	1	BP	sulfur amino acid catabolic process	CD01
GO:0043405	0.0156	1	32911	172	100	3	BP	regulation of MAP kinase activity	DUSP16; SFRP2; IL1B
GO:0006605	0.0156	1	32911	172	100	3	BP	protein targeting	BID; YWHAQ; PRICKLE1
GO:0002263	0.016	1	32911	172	37	2	BP	cell activation involved in immune response	BCL3; GADD45G
GO:0002366	0.016	1	32911	172	37	2	BP	leukocyte activation involved in immune response	BCL3; GADD45G
GO:0002449	0.016	1	32911	172	37	2	BP	lymphocyte mediated immunity	BCL3; MYD88
GO:0090277	0.016	1	32911	172	37	2	BP	positive regulation of peptide hormone secretion	CCKAR; IRS2
GO:0006996	0.016	1	32911	172	997	11	BP	organelle organization	BID; CAV2; MYC; CCKAR; JUN; GADD45A; HSPA1A; SETD8; PRKCI; HSPA1B; ANAPC11
GO:0009260	0.016	1	32911	172	101	3	BP	ribonucleotide biosynthetic process	ADSS; AMPD3; PRPS1
GO:0031644	0.0161	1	32911	172	184	4	BP	regulation of neurological system process	EGR1; PTGS2; CCL2; KDR
GO:0009890	0.0166	1	32911	172	501	7	BP	negative regulation of biosynthetic process	EGR1; NRIP1; BCL3; MYC; ACADL; TGFB1; MYBBP1A
GO:2000021	0.0168	1	32911	172	38	2	BP	regulation of ion homeostasis	TGFB1; GCLC
GO:0051781	0.0168	1	32911	172	38	2	BP	positive regulation of cell division	TGFB1; IL1B
GO:0006940	0.0168	1	32911	172	38	2	BP	regulation of smooth muscle contraction	PTGS2; TBXA2R
GO:0008584	0.0168	1	32911	172	38	2	BP	male gonad development	SFRP2; KDR
GO:0040007	0.0169	1	32911	172	187	4	BP	growth	PTGS2; HOXA5; TGFB1; ADD1
GO:0048610	0.0172	1	32911	172	188	4	BP	reproductive cellular process	FZD4; CXCL12; TGFB1; ARSA
GO:0002700	0.0177	1	32911	172	39	2	BP	regulation of production of molecular mediator of immune response	TGFB1; HMOX1
GO:0002793	0.0177	1	32911	172	39	2	BP	positive regulation of peptide secretion	CCKAR; IRS2

GO:0030336	0.0177	1	32911	172	39	2	BP	negative regulation of cell migration	DLL4; TIE1
GO:0043279	0.0177	1	32911	172	39	2	BP	response to alkaloid	MYC; PPP2R2A
GO:0051130	0.0178	1	32911	172	190	4	BP	positive regulation of cellular component organization	CXCL12; TGFB1; WNT3A; PRKCI
GO:0010466	0.0185	1	32911	172	40	2	BP	negative regulation of peptidase activity	SFRP2; HSPA1B
GO:0016050	0.0185	1	32911	172	40	2	BP	vesicle organization	CAV2; PRKCI
GO:0032846	0.0185	1	32911	172	40	2	BP	positive regulation of homeostatic process	PTGS2; IL1B
GO:0048168	0.0185	1	32911	172	40	2	BP	regulation of neuronal synaptic plasticity	EGR1; KDR
GO:0050777	0.0185	1	32911	172	40	2	BP	negative regulation of immune response	GPX2; TGFB1
GO:0033157	0.0194	1	32911	172	41	2	BP	regulation of intracellular protein transport	RBCK1; TGFB1
GO:0033273	0.0194	1	32911	172	41	2	BP	response to vitamin	TEK; TIE1
GO:0045089	0.0194	1	32911	172	41	2	BP	positive regulation of innate immune response	RELA; MYD88
GO:0045667	0.0194	1	32911	172	41	2	BP	regulation of osteoblast differentiation	SMAD1; SFRP2
GO:0006084	0.0194	1	32911	172	41	2	BP	acetyl-CoA metabolic process	ACSS1; SUCLG2
GO:0006096	0.0194	1	32911	172	41	2	BP	glycolysis	HK1; ALDOA
GO:0051301	0.0199	1	32911	172	296	5	BP	cell division	CCND3; PARD6B; WNT3A; SETD8; ANAPC11
GO:0010627	0.0201	1	32911	172	197	4	BP	regulation of intracellular protein kinase cascade	RBCK1; MYD88; SFRP2; IL1B
GO:0001657	0.0203	1	32911	172	42	2	BP	ureteric bud development	ARG2; SMAD1
GO:0002443	0.0203	1	32911	172	42	2	BP	leukocyte mediated immunity	BCL3; MYD88
GO:0035264	0.0203	1	32911	172	42	2	BP	multicellular organism growth	HOXA5; ADD1
GO:0042770	0.0203	1	32911	172	42	2	BP	DNA damage response, signal transduction	BCL3; HMOX1
GO:0007589	0.0203	1	32911	172	42	2	BP	body fluid secretion	CCKAR; CD01
GO:0008652	0.0203	1	32911	172	42	2	BP	cellular amino acid biosynthetic process	ALDH4A1; ASNS
GO:0009896	0.0203	1	32911	172	42	2	BP	positive regulation of catabolic process	GCLC; IL1B

GO:0010740	0.0206	1	32911	172	111	3	BP	positive regulation of intracellular protein kinase cascade	RBCK1; MYD88; IL1B
GO:0010656	0.0207	1	32911	172	4	1	BP	negative regulation of muscle cell apoptosis	SFRP2
GO:0010662	0.0207	1	32911	172	4	1	BP	regulation of striated muscle cell apoptosis	SFRP2
GO:0010664	0.0207	1	32911	172	4	1	BP	negative regulation of striated muscle cell apoptosis	SFRP2
GO:0010665	0.0207	1	32911	172	4	1	BP	regulation of cardiac muscle cell apoptosis	SFRP2
GO:0010667	0.0207	1	32911	172	4	1	BP	negative regulation of cardiac muscle cell apoptosis	SFRP2
GO:0010758	0.0207	1	32911	172	4	1	BP	regulation of macrophage chemotaxis	CCL2
GO:0010759	0.0207	1	32911	172	4	1	BP	positive regulation of macrophage chemotaxis	CCL2
GO:0001660	0.0207	1	32911	172	4	1	BP	fever	IL1B
GO:0001696	0.0207	1	32911	172	4	1	BP	gastric acid secretion	CCKAR
GO:0001937	0.0207	1	32911	172	4	1	BP	negative regulation of endothelial cell proliferation	CAV2
GO:0019730	0.0207	1	32911	172	4	1	BP	antimicrobial humoral response	BCL3
GO:0021569	0.0207	1	32911	172	4	1	BP	rhombomere 3 development	EGR2
GO:0021612	0.0207	1	32911	172	4	1	BP	facial nerve structural organization	EGR2
GO:0002238	0.0207	1	32911	172	4	1	BP	response to molecule of fungal origin	MYD88
GO:0002507	0.0207	1	32911	172	4	1	BP	tolerance induction	TGFB1
GO:0002701	0.0207	1	32911	172	4	1	BP	negative regulation of production of molecular mediator of immune response	HMOX1
GO:0002904	0.0207	1	32911	172	4	1	BP	positive regulation of B cell apoptosis	MYC
GO:0030949	0.0207	1	32911	172	4	1	BP	positive regulation of vascular endothelial growth factor receptor signaling pathway	HIF1A
GO:0031063	0.0207	1	32911	172	4	1	BP	regulation of histone deacetylation	TGFB1

GO:0031065	0.0207	1	32911	172	4	1	BP	positive regulation of histone deacetylation	TGFB1
GO:0031579	0.0207	1	32911	172	4	1	BP	membrane raft organization	CAV2
GO:0032006	0.0207	1	32911	172	4	1	BP	regulation of TOR signaling cascade	KDR
GO:0032769	0.0207	1	32911	172	4	1	BP	negative regulation of monooxygenase activity	ARG2
GO:0033004	0.0207	1	32911	172	4	1	BP	negative regulation of mast cell activation	HMOX1
GO:0033089	0.0207	1	32911	172	4	1	BP	positive regulation of T cell differentiation in the thymus	IL2RG
GO:0033539	0.0207	1	32911	172	4	1	BP	fatty acid beta-oxidation using acyl-CoA dehydrogenase	ACADL
GO:0003417	0.0207	1	32911	172	4	1	BP	growth plate cartilage development	THBS1
GO:0042448	0.0207	1	32911	172	4	1	BP	progesterone metabolic process	AFP
GO:0042482	0.0207	1	32911	172	4	1	BP	positive regulation of odontogenesis	TGFB1
GO:0042541	0.0207	1	32911	172	4	1	BP	hemoglobin biosynthetic process	HIF1A
GO:0042661	0.0207	1	32911	172	4	1	BP	regulation of mesodermal cell fate specification	SFRP2
GO:0043536	0.0207	1	32911	172	4	1	BP	positive regulation of blood vessel endothelial cell migration	PTGS2
GO:0044273	0.0207	1	32911	172	4	1	BP	sulfur compound catabolic process	CD01
GO:0045589	0.0207	1	32911	172	4	1	BP	regulation of regulatory T cell differentiation	IL2RG
GO:0045591	0.0207	1	32911	172	4	1	BP	positive regulation of regulatory T cell differentiation	IL2RG
GO:0045647	0.0207	1	32911	172	4	1	BP	negative regulation of erythrocyte differentiation	LM02
GO:0045896	0.0207	1	32911	172	4	1	BP	regulation of transcription, mitotic	JUNB

GO:0045897	0.0207	1	32911	172	4	1	BP	positive regulation of transcription, mitotic	JUNB
GO:0045906	0.0207	1	32911	172	4	1	BP	negative regulation of vasoconstriction	HSPA1B
GO:0046021	0.0207	1	32911	172	4	1	BP	regulation of transcription from RNA polymerase II promoter, mitotic	JUNB
GO:0046022	0.0207	1	32911	172	4	1	BP	positive regulation of transcription from RNA polymerase II promoter, mitotic	JUNB
GO:0046322	0.0207	1	32911	172	4	1	BP	negative regulation of fatty acid oxidation	ACADL
GO:0046685	0.0207	1	32911	172	4	1	BP	response to arsenic	GCLC
GO:0048246	0.0207	1	32911	172	4	1	BP	macrophage chemotaxis	CCL2
GO:0050765	0.0207	1	32911	172	4	1	BP	negative regulation of phagocytosis	TGFB1
GO:0051001	0.0207	1	32911	172	4	1	BP	negative regulation of nitric-oxide synthase activity	ARG2
GO:0051152	0.0207	1	32911	172	4	1	BP	positive regulation of smooth muscle cell differentiation	TGFB1
GO:0051354	0.0207	1	32911	172	4	1	BP	negative regulation of oxidoreductase activity	ARG2
GO:0060159	0.0207	1	32911	172	4	1	BP	regulation of dopamine receptor signaling pathway	CAV2
GO:0060317	0.0207	1	32911	172	4	1	BP	cardiac epithelial to mesenchymal transition	WNT2
GO:0060439	0.0207	1	32911	172	4	1	BP	trachea morphogenesis	HOXA5
GO:0060501	0.0207	1	32911	172	4	1	BP	positive regulation of epithelial cell proliferation	WNT2
GO:0060708	0.0207	1	32911	172	4	1	BP	involved in lung morphogenesis	SOCS3
GO:0060708	0.0207	1	32911	172	4	1	BP	spongiotrophoblast differentiation	SOCS3
GO:0006083	0.0207	1	32911	172	4	1	BP	acetate metabolic process	ACSS1

GO:0061046	0.0207	1	32911	172	4	1	BP	regulation of branching involved in lung morphogenesis	WNT2
GO:0006528	0.0207	1	32911	172	4	1	BP	asparagine metabolic process	ASNS
GO:0006600	0.0207	1	32911	172	4	1	BP	creatine metabolic process	GAMT
GO:0070423	0.0207	1	32911	172	4	1	BP	nucleotide-binding oligomerization domain containing signaling pathway	RELA
GO:0070431	0.0207	1	32911	172	4	1	BP	nucleotide-binding oligomerization domain containing 2 signaling pathway	RELA
GO:0070555	0.0207	1	32911	172	4	1	BP	response to interleukin-1	PRKCI
GO:0071156	0.0207	1	32911	172	4	1	BP	regulation of cell cycle arrest	TGFB1
GO:0071158	0.0207	1	32911	172	4	1	BP	positive regulation of cell cycle arrest	TGFB1
GO:0071622	0.0207	1	32911	172	4	1	BP	regulation of granulocyte chemotaxis	CCL2
GO:0071675	0.0207	1	32911	172	4	1	BP	regulation of mononuclear cell migration	CCL2
GO:0007182	0.0207	1	32911	172	4	1	BP	common-partner SMAD protein phosphorylation	SPNB2
GO:0090184	0.0207	1	32911	172	4	1	BP	positive regulation of kidney development	MYC
GO:0090273	0.0207	1	32911	172	4	1	BP	regulation of somatostatin secretion	CCKAR
GO:0090311	0.0207	1	32911	172	4	1	BP	regulation of protein amino acid deacetylation	TGFB1
GO:0090312	0.0207	1	32911	172	4	1	BP	positive regulation of protein amino acid deacetylation	TGFB1
GO:0009052	0.0207	1	32911	172	4	1	BP	pentose-phosphate shunt, non-oxidative branch	TALD01
GO:0009996	0.0207	1	32911	172	4	1	BP	negative regulation of cell fate specification	SFRP2
GO:0032880	0.0211	1	32911	172	112	3	BP	regulation of protein localization	RBCK1; TGFB1; PRKCI

G0:0002250	0.0213	1	32911	172	43	2	BP	adaptive immune response	BCL3; MYD88
G0:0002460	0.0213	1	32911	172	43	2	BP	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	BCL3; MYD88
G0:0040013	0.0213	1	32911	172	43	2	BP	negative regulation of locomotion	DLL4; TIE1
G0:0050806	0.0213	1	32911	172	43	2	BP	positive regulation of synaptic transmission	PTGS2; CCL2
G0:0051054	0.0213	1	32911	172	43	2	BP	regulation of DNA metabolic process	JUN; TGFB1
G0:0051271	0.0213	1	32911	172	43	2	BP	negative regulation of cellular component movement	DLL4; TIE1
G0:0051302	0.0213	1	32911	172	43	2	BP	regulation of cell division	TGFB1; IL1B
G0:0006690	0.0213	1	32911	172	43	2	BP	icosanoid metabolic process	PTGS2; CYP4A12A
G0:0006986	0.0213	1	32911	172	43	2	BP	response to unfolded protein	HSPA1A; HSPA1B
G0:0007368	0.0213	1	32911	172	43	2	BP	determination of left/right symmetry	NOTCH2; WNT3A
G0:0009150	0.0221	1	32911	172	203	4	BP	purine ribonucleotide metabolic process	ADSS; HSPA8; AMPD3; PRPS1
G0:0018108	0.0222	1	32911	172	44	2	BP	peptidyl-tyrosine phosphorylation	FYN; HK1
G0:0018212	0.0222	1	32911	172	44	2	BP	peptidyl-tyrosine modification	FYN; HK1
G0:0033559	0.0222	1	32911	172	44	2	BP	unsaturated fatty acid metabolic process	PTGS2; CYP4A12A
G0:0046822	0.0222	1	32911	172	44	2	BP	regulation of nucleocytoplasmic transport	RBCK1; TGFB1
G0:0009799	0.0222	1	32911	172	44	2	BP	specification of symmetry	NOTCH2; WNT3A
G0:0009855	0.0222	1	32911	172	44	2	BP	determination of bilateral symmetry	NOTCH2; WNT3A
G0:0006091	0.0225	1	32911	172	204	4	BP	generation of precursor metabolites and energy	HK1; MYBBP1A; ALDOA; GBE1
G0:0006631	0.0225	1	32911	172	204	4	BP	fatty acid metabolic process	PTGS2; CH25H; ACADL; CYP4A12A
G0:0050878	0.0226	1	32911	172	115	3	BP	regulation of body fluid levels	CCKAR; F3; CD01

GO:0007411	0.0226	1	32911	172	115	3	BP	axon guidance	CXCL12; EGR2; WNT3A
								positive	
GO:0031401	0.0231	1	32911	172	116	3	BP	regulation of protein modification process	TEK; TGFB1; HSPA5
GO:0006417	0.0231	1	32911	172	116	3	BP	regulation of translation	MAPK3; MKNK1; EIF3C
GO:0001756	0.0232	1	32911	172	45	2	BP	somitogenesis	SFRP2; WNT3A
GO:0042176	0.0232	1	32911	172	45	2	BP	regulation of protein catabolic process	RELA; GCLC
GO:0009259	0.0236	1	32911	172	207	4	BP	ribonucleotide metabolic process	ADSS; HSPA8; AMPD3; PRPS1
								negative	
GO:0051129	0.0241	1	32911	172	118	3	BP	regulation of cellular component organization	SPNB2; TGFB1; WNT3A
								positive	
GO:0051971	0.0241	1	32911	172	46	2	BP	regulation of transmission of nerve impulse	PTGS2; CCL2
GO:0006518	0.0241	1	32911	172	46	2	BP	peptide metabolic process	GSR; GCLC
GO:0001667	0.0251	1	32911	172	47	2	BP	ameboidal cell migration	CXCL12; HIF1A
GO:0043270	0.0251	1	32911	172	47	2	BP	positive regulation of ion transport	CXCL12; CCKAR
GO:0050729	0.0251	1	32911	172	47	2	BP	positive regulation of inflammatory response	PTGS2; IL1B
GO:0050795	0.0251	1	32911	172	47	2	BP	regulation of behavior	CXCL12; CCL2
								negative	
GO:0010454	0.0258	1	32911	172	5	1	BP	regulation of cell fate commitment	SFRP2
								positive	
GO:0010595	0.0258	1	32911	172	5	1	BP	regulation of endothelial cell migration	PTGS2
GO:0014037	0.0258	1	32911	172	5	1	BP	Schwann cell differentiation	EGR2
GO:0019530	0.0258	1	32911	172	5	1	BP	taurine metabolic process	CD01
GO:0019693	0.0258	1	32911	172	5	1	BP	ribose phosphate metabolic process	PRPS1
GO:0019934	0.0258	1	32911	172	5	1	BP	cGMP-mediated signaling	FZD2
GO:0002024	0.0258	1	32911	172	5	1	BP	diet induced thermogenesis	ADRB3
GO:0002051	0.0258	1	32911	172	5	1	BP	osteoblast fate commitment	SMAD1
GO:0021604	0.0258	1	32911	172	5	1	BP	cranial nerve structural organization	EGR2
GO:0002312	0.0258	1	32911	172	5	1	BP	B cell activation involved in immune response	BCL3

GO:0002313	0.0258	1	32911	172	5	1	BP	mature B cell differentiation involved in immune response	BCL3
GO:0032495	0.0258	1	32911	172	5	1	BP	response to muramyl dipeptide	RELA
GO:0042088	0.0258	1	32911	172	5	1	BP	T-helper 1 type immune response	BCL3
GO:0042346	0.0258	1	32911	172	5	1	BP	positive regulation of NF-kappaB import into nucleus	RBCK1
GO:0045351	0.0258	1	32911	172	5	1	BP	type I interferon biosynthetic process	MYD88
GO:0045920	0.0258	1	32911	172	5	1	BP	negative regulation of exocytosis	HMOX1
GO:0045948	0.0258	1	32911	172	5	1	BP	positive regulation of translational initiation	EIF3C
GO:0048170	0.0258	1	32911	172	5	1	BP	positive regulation of long-term neuronal synaptic plasticity	KDR
GO:0048670	0.0258	1	32911	172	5	1	BP	regulation of collateral sprouting	WNT3A
GO:0055009	0.0258	1	32911	172	5	1	BP	atrial cardiac muscle tissue morphogenesis	WNT2
GO:0060428	0.0258	1	32911	172	5	1	BP	lung epithelium development	HOXA5
GO:0060762	0.0258	1	32911	172	5	1	BP	regulation of branching involved in mammary gland duct morphogenesis	TGFB1
GO:0061036	0.0258	1	32911	172	5	1	BP	positive regulation of cartilage development	SMAD1
GO:0006561	0.0258	1	32911	172	5	1	BP	proline biosynthetic process	ALDH4A1
GO:0070542	0.0258	1	32911	172	5	1	BP	response to fatty acid	EGR1
GO:0071396	0.0258	1	32911	172	5	1	BP	cellular response to lipid	EGR1
GO:0007199	0.0258	1	32911	172	5	1	BP	G-protein signaling, coupled to cGMP nucleotide second messenger	FZD2
GO:0008216	0.0258	1	32911	172	5	1	BP	spermidine metabolic process	SRM
GO:0009410	0.0258	1	32911	172	5	1	BP	response to xenobiotic stimulus	GCLC
GO:0001889	0.0261	1	32911	172	48	2	BP	liver development	SP1; RELA

GO:0030307	0.0261	1	32911	172	48	2	BP	positive regulation of cell growth	CXCL12; WNT3A
GO:0033500	0.0261	1	32911	172	48	2	BP	carbohydrate homeostasis	SOCS6; HIF1A
GO:0042593	0.0261	1	32911	172	48	2	BP	glucose homeostasis	SOCS6; HIF1A
GO:0050906	0.0261	1	32911	172	48	2	BP	detection of stimulus involved in sensory perception	FYN; MYC
GO:0003002	0.0266	1	32911	172	215	4	BP	regionalization	HOXA5; EGR2; SFRP2; WNT3A
GO:0031646	0.0271	1	32911	172	49	2	BP	positive regulation of neurological system process	PTGS2; CCL2
GO:0006720	0.0271	1	32911	172	49	2	BP	isoprenoid metabolic process	IDI1; HMGCS1
GO:0048812	0.0274	1	32911	172	124	3	BP	neuron projection morphogenesis	CCKAR; KDR; WNT3A
GO:0042326	0.0282	1	32911	172	50	2	BP	negative regulation of phosphorylation	JUN; PPAP2B
GO:0051128	0.0291	1	32911	172	442	6	BP	regulation of cellular component organization	SPNB2; FYN; CXCL12; TGFB1; WNT3A; PRKCI
GO:0008406	0.0292	1	32911	172	51	2	BP	gonad development	SFRP2; KDR
GO:0017038	0.0303	1	32911	172	52	2	BP	protein import	BID; PRICKLE1
GO:0032386	0.0303	1	32911	172	52	2	BP	regulation of intracellular transport	RBCK1; TGFB1
GO:0045088	0.0303	1	32911	172	52	2	BP	regulation of innate immune response	RELA; MYD88
GO:0046879	0.0303	1	32911	172	52	2	BP	hormone secretion	FZD4; CCKAR
GO:0046887	0.0303	1	32911	172	52	2	BP	positive regulation of hormone secretion	CCKAR; IRS2
GO:0010660	0.0309	1	32911	172	6	1	BP	regulation of muscle cell apoptosis	SFRP2
GO:0010718	0.0309	1	32911	172	6	1	BP	positive regulation of epithelial to mesenchymal transition	TGFB1
GO:0010829	0.0309	1	32911	172	6	1	BP	negative regulation of glucose transport	IL1B
GO:0001678	0.0309	1	32911	172	6	1	BP	cellular glucose homeostasis	SOCS6
GO:0001783	0.0309	1	32911	172	6	1	BP	B cell apoptosis	MYC
GO:0019953	0.0309	1	32911	172	6	1	BP	sexual reproduction	AFP
GO:0002467	0.0309	1	32911	172	6	1	BP	germinal center formation	BCL3
GO:0002690	0.0309	1	32911	172	6	1	BP	positive regulation of leukocyte chemotaxis	CCL2

GO:0000003	0.0309	1	32911	172	6	1	BP	reproduction	AFP
GO:0003085	0.0309	1	32911	172	6	1	BP	negative regulation of systemic arterial blood pressure	ADRB3
GO:0031952	0.0309	1	32911	172	6	1	BP	regulation of protein amino acid autophosphorylation	JUN
GO:0032768	0.0309	1	32911	172	6	1	BP	regulation of monooxygenase activity	ARG2
GO:0033033	0.0309	1	32911	172	6	1	BP	negative regulation of myeloid cell apoptosis	HSPA1B
GO:0033603	0.0309	1	32911	172	6	1	BP	positive regulation of dopamine secretion	CXCL12
GO:0042993	0.0309	1	32911	172	6	1	BP	positive regulation of transcription factor import into nucleus	RBCK1
GO:0043353	0.0309	1	32911	172	6	1	BP	enucleate erythrocyte differentiation	SP1
GO:0043508	0.0309	1	32911	172	6	1	BP	negative regulation of JUN kinase activity	SFRP2
GO:0044070	0.0309	1	32911	172	6	1	BP	regulation of anion transport	HK1
GO:0045084	0.0309	1	32911	172	6	1	BP	positive regulation of interleukin-12 biosynthetic process	RELA
GO:0045410	0.0309	1	32911	172	6	1	BP	positive regulation of interleukin-6 biosynthetic process	IL1B
GO:0045446	0.0309	1	32911	172	6	1	BP	endothelial cell differentiation	KDR
GO:0045717	0.0309	1	32911	172	6	1	BP	negative regulation of fatty acid biosynthetic process	ACADL
GO:0048013	0.0309	1	32911	172	6	1	BP	ephrin receptor signaling pathway	EPHA2
GO:0050999	0.0309	1	32911	172	6	1	BP	regulation of nitric-oxide synthase activity	ARG2
GO:0051414	0.0309	1	32911	172	6	1	BP	response to cortisol stimulus	TGFB1
GO:0006014	0.0309	1	32911	172	6	1	BP	D-ribose metabolic process	PRPS1
GO:0060707	0.0309	1	32911	172	6	1	BP	trophoblast giant cell differentiation	SOCS3

GO:0060744	0.0309	1	32911	172	6	1	BP	mammary gland branching involved in thelarche	TGFB1
GO:0006089	0.0309	1	32911	172	6	1	BP	lactate metabolic process	HIF1A
GO:0006104	0.0309	1	32911	172	6	1	BP	succinyl-CoA metabolic process	SUCLG2
GO:0006534	0.0309	1	32911	172	6	1	BP	cysteine metabolic process	CD01
GO:0006599	0.0309	1	32911	172	6	1	BP	phosphagen metabolic process	GAMT
GO:0006658	0.0309	1	32911	172	6	1	BP	phosphatidylserine metabolic process	PTDSS2
GO:0070230	0.0309	1	32911	172	6	1	BP	positive regulation of lymphocyte apoptosis	MYC
GO:0007029	0.0309	1	32911	172	6	1	BP	endoplasmic reticulum organization	CAV2
GO:0071548	0.0309	1	32911	172	6	1	BP	response to dexamethasone stimulus	TGFB1
GO:0071549	0.0309	1	32911	172	6	1	BP	cellular response to dexamethasone stimulus	TGFB1
GO:0010563	0.0314	1	32911	172	53	2	BP	negative regulation of phosphorus metabolic process	JUN; PPAP2B
GO:0016202	0.0314	1	32911	172	53	2	BP	regulation of striated muscle tissue development	TGFB1; WNT2
GO:0045936	0.0314	1	32911	172	53	2	BP	negative regulation of phosphate metabolic process	JUN; PPAP2B
GO:0051346	0.0314	1	32911	172	53	2	BP	negative regulation of hydrolase activity	SFRP2; HSPA1B
GO:0018130	0.0325	1	32911	172	54	2	BP	heterocycle biosynthetic process	ALDH4A1; ALAS1
GO:0002695	0.0325	1	32911	172	54	2	BP	negative regulation of leukocyte activation	TGFB1; HMOX1
GO:0010035	0.0328	1	32911	172	133	3	BP	response to inorganic substance	MT1; HMOX1; GCLC
GO:0048858	0.0328	1	32911	172	133	3	BP	cell projection morphogenesis	CCKAR; KDR; WNT3A
GO:0031589	0.0336	1	32911	172	55	2	BP	cell-substrate adhesion	TEK; FZD4
GO:0048634	0.0336	1	32911	172	55	2	BP	regulation of muscle organ development	TGFB1; WNT2

GO:0050866	0.0336	1	32911	172	55	2	BP	negative regulation of cell activation	TGFB1; HMOX1
GO:0009582	0.0347	1	32911	172	56	2	BP	detection of abiotic stimulus	FYN; MYC
GO:0009914	0.0347	1	32911	172	56	2	BP	hormone transport	FZD4; CCKAR
GO:0001558	0.0353	1	32911	172	137	3	BP	regulation of cell growth	CXCL12; IGFBP5; WNT3A
GO:0043408	0.0353	1	32911	172	137	3	BP	regulation of MAPKKK cascade	MYD88; SFRP2; IL1B
GO:0022404	0.0359	1	32911	172	57	2	BP	molting cycle process	RELA; PTGS2
GO:0022405	0.0359	1	32911	172	57	2	BP	hair cycle process	RELA; PTGS2
GO:0009063	0.0359	1	32911	172	57	2	BP	cellular amino acid catabolic process	IVD; CD01
GO:0010470	0.036	1	32911	172	7	1	BP	regulation of gastrulation	SFRP2
GO:0010717	0.036	1	32911	172	7	1	BP	regulation of epithelial to mesenchymal transition	TGFB1
GO:0010770	0.036	1	32911	172	7	1	BP	positive regulation of cell morphogenesis involved in differentiation	TGFB1
GO:0021546	0.036	1	32911	172	7	1	BP	rhombomere development	EGR2
GO:0021680	0.036	1	32911	172	7	1	BP	cerebellar Purkinje cell layer development	HSPA5
GO:0002335	0.036	1	32911	172	7	1	BP	mature B cell differentiation	BCL3
GO:0031023	0.036	1	32911	172	7	1	BP	microtubule organizing center organization	GADD45A
GO:0031397	0.036	1	32911	172	7	1	BP	negative regulation of protein ubiquitination	GCLC
GO:0032303	0.036	1	32911	172	7	1	BP	regulation of icosanoid secretion	IL1B
GO:0032305	0.036	1	32911	172	7	1	BP	positive regulation of icosanoid secretion	IL1B
GO:0032306	0.036	1	32911	172	7	1	BP	regulation of prostaglandin secretion	IL1B
GO:0032308	0.036	1	32911	172	7	1	BP	positive regulation of prostaglandin secretion	IL1B
GO:0033599	0.036	1	32911	172	7	1	BP	regulation of mammary gland epithelial cell proliferation	HOXA5
GO:0034446	0.036	1	32911	172	7	1	BP	substrate adhesion-dependent cell spreading	FZD4

GO:0035065	0.036	1	32911	172	7	1	BP	regulation of histone acetylation	TGFB1
GO:0035089	0.036	1	32911	172	7	1	BP	establishment of apical/basal cell polarity	PRKCI
GO:0035428	0.036	1	32911	172	7	1	BP	hexose transmembrane transport	SLC2A1
GO:0042178	0.036	1	32911	172	7	1	BP	xenobiotic catabolic process	GSTA2
GO:0043129	0.036	1	32911	172	7	1	BP	surfactant homeostasis	KDR
GO:0043200	0.036	1	32911	172	7	1	BP	response to amino acid stimulus	CD01
GO:0043249	0.036	1	32911	172	7	1	BP	erythrocyte maturation	TIMP1
GO:0045648	0.036	1	32911	172	7	1	BP	positive regulation of erythrocyte differentiation	HIF1A
GO:0048875	0.036	1	32911	172	7	1	BP	chemical homeostasis within a tissue	KDR
GO:0050798	0.036	1	32911	172	7	1	BP	activated T cell proliferation	FYN
GO:0050966	0.036	1	32911	172	7	1	BP	detection of mechanical stimulus	FYN
GO:0050966	0.036	1	32911	172	7	1	BP	involved in sensory perception of pain	FYN
GO:0050996	0.036	1	32911	172	7	1	BP	positive regulation of lipid catabolic process	IL1B
GO:0051297	0.036	1	32911	172	7	1	BP	centrosome organization	GADD45A
GO:0051900	0.036	1	32911	172	7	1	BP	regulation of mitochondrial depolarization	GCLC
GO:0006002	0.036	1	32911	172	7	1	BP	fructose 6-phosphate metabolic process	TALD01
GO:0060484	0.036	1	32911	172	7	1	BP	lung-associated mesenchyme development	HOXA5
GO:0061162	0.036	1	32911	172	7	1	BP	establishment of monopolar cell polarity	PRKCI
GO:0006560	0.036	1	32911	172	7	1	BP	proline metabolic process	ALDH4A1
GO:0006596	0.036	1	32911	172	7	1	BP	polyamine biosynthetic process	SRM
GO:0006882	0.036	1	32911	172	7	1	BP	cellular zinc ion homeostasis	MT1
GO:0006983	0.036	1	32911	172	7	1	BP	ER overload response	HSPA5
GO:0070306	0.036	1	32911	172	7	1	BP	lens fiber cell differentiation	TGFB1

GO:0071636	0.036	1	32911	172	7	1	BP	positive regulation of transforming growth factor-beta production	PTGS2
GO:0007406	0.036	1	32911	172	7	1	BP	negative regulation of neuroblast proliferation	TGFB1
GO:0008015	0.036	1	32911	172	7	1	BP	blood circulation	STAT1
GO:0009396	0.036	1	32911	172	7	1	BP	folic acid and derivative biosynthetic process	MTHFD2
GO:0003013	0.037	1	32911	172	58	2	BP	circulatory system process	STAT1; ADRB3
GO:0034622	0.0386	1	32911	172	142	3	BP	cellular macromolecular complex assembly	TUBA4A; TUBB2C; EIF3A
GO:0050768	0.0394	1	32911	172	60	2	BP	negative regulation of neurogenesis	TGFB1; WNT3A
GO:0090092	0.0394	1	32911	172	60	2	BP	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	HSPA5; SFRP2
GO:0009581	0.0394	1	32911	172	60	2	BP	detection of external stimulus	FYN; MYC
GO:0032990	0.04	1	32911	172	144	3	BP	cell part morphogenesis	CCKAR; KDR; WNT3A
GO:0002699	0.0406	1	32911	172	61	2	BP	positive regulation of immune effector process	CCL2; HSPA1B
GO:0032946	0.0406	1	32911	172	61	2	BP	regulation of mononuclear cell proliferation	IRS2; MYD88
GO:0042303	0.0406	1	32911	172	61	2	BP	molting cycle	RELA; PTGS2
GO:0045785	0.0406	1	32911	172	61	2	BP	positive regulation of cell adhesion	THBS1; TEK
GO:0048872	0.0406	1	32911	172	61	2	BP	homeostasis of number of cells	TGFB1; ADD1
GO:0050671	0.0406	1	32911	172	61	2	BP	positive regulation of lymphocyte proliferation	IRS2; MYD88
GO:0009952	0.0407	1	32911	172	145	3	BP	anterior/posterior or pattern formation	HOXA5; SFRP2; WNT3A
GO:0014050	0.041	1	32911	172	8	1	BP	negative regulation of glutamate secretion	IL1B
GO:0014072	0.041	1	32911	172	8	1	BP	response to isoquinoline alkaloid	PPP2R2A
GO:0001553	0.041	1	32911	172	8	1	BP	luteinization	FZD4
GO:0000188	0.041	1	32911	172	8	1	BP	inactivation of MAPK activity	DUSP16
GO:0021527	0.041	1	32911	172	8	1	BP	spinal cord association neuron differentiation	WNT3A

G0:0003016	0.041	1	32911	172	8	1	BP	respiratory system process	HOXA5
G0:0031058	0.041	1	32911	172	8	1	BP	positive regulation of histone modification	TGFB1
G0:0032225	0.041	1	32911	172	8	1	BP	regulation of synaptic transmission, dopaminergic	PTGS2
G0:0042177	0.041	1	32911	172	8	1	BP	negative regulation of protein catabolic process	RELA
G0:0042832	0.041	1	32911	172	8	1	BP	defense response to protozoan	BCL3
G0:0043278	0.041	1	32911	172	8	1	BP	response to morphine	PPP2R2A
G0:0045075	0.041	1	32911	172	8	1	BP	regulation of interleukin-12 biosynthetic process	RELA
G0:0045579	0.041	1	32911	172	8	1	BP	positive regulation of B cell differentiation	IL2RG
G0:0045745	0.041	1	32911	172	8	1	BP	positive regulation of G-protein coupled receptor protein signaling pathway	CAV2
G0:0045806	0.041	1	32911	172	8	1	BP	negative regulation of endocytosis	TGFB1
G0:0045922	0.041	1	32911	172	8	1	BP	negative regulation of fatty acid metabolic process	ACADL
G0:0046500	0.041	1	32911	172	8	1	BP	S-adenosylmethionine metabolic process	GAMT
G0:0046902	0.041	1	32911	172	8	1	BP	regulation of mitochondrial membrane permeability	BID
G0:0048596	0.041	1	32911	172	8	1	BP	embryonic camera-type eye morphogenesis	SP1
G0:0050832	0.041	1	32911	172	8	1	BP	defense response to fungus	TGFB1
G0:0050930	0.041	1	32911	172	8	1	BP	induction of positive chemotaxis	CXCL12
G0:0051055	0.041	1	32911	172	8	1	BP	negative regulation of lipid biosynthetic process	ACADL
G0:0051341	0.041	1	32911	172	8	1	BP	regulation of oxidoreductase activity	ARG2
G0:0051702	0.041	1	32911	172	8	1	BP	interaction with symbiont	GPX2
G0:0055069	0.041	1	32911	172	8	1	BP	zinc ion homeostasis	MT1

GO:0060395	0.041	1	32911	172	8	1	BP	SMAD protein signal transduction branch	AFP
GO:0060602	0.041	1	32911	172	8	1	BP	elongation of an epithelium branching involved in	TGFB1
GO:0060670	0.041	1	32911	172	8	1	BP	embryonic placenta morphogenesis	SOCS3
GO:0006750	0.041	1	32911	172	8	1	BP	glutathione biosynthetic process	GCLC
GO:0070229	0.041	1	32911	172	8	1	BP	negative regulation of lymphocyte apoptosis	IRS2
GO:0071634	0.041	1	32911	172	8	1	BP	regulation of transforming growth factor- beta production	PTGS2
GO:0009083	0.041	1	32911	172	8	1	BP	branched chain family amino acid catabolic process	IVD
GO:0009437	0.041	1	32911	172	8	1	BP	carnitine metabolic process	ACADL
GO:0010558	0.0412	1	32911	172	481	6	BP	negative regulation of macromolecule biosynthetic process	EGR1; NRIP1; BCL3; MYC; TGFB1; MYBBP1A
GO:0002757	0.0418	1	32911	172	62	2	BP	immune response- activating signal transduction	RELA; MYD88
GO:0034637	0.0418	1	32911	172	62	2	BP	cellular carbohydrate biosynthetic process	ATF4; GBE1
GO:0043524	0.0418	1	32911	172	62	2	BP	negative regulation of neuron apoptosis	DNAJC5; GCLC
GO:0070665	0.043	1	32911	172	63	2	BP	positive regulation of leukocyte proliferation	IRS2; MYD88
GO:0007276	0.0431	1	32911	172	251	4	BP	gamete generation	GSR; GAMT; SMAD1; HMGA1
GO:0003008	0.0438	1	32911	172	1764	15	BP	system process	EGR1; MAPK3; PTGS2; FZD4; ARG2; MYC; CCKAR; STAT1; JUN; ADCY8; HOXA5; PDE4B; ADRB3; IL1B; COL11A2
GO:0050778	0.0443	1	32911	172	150	3	BP	positive regulation of immune response	RELA; MYD88; HSPA1B
GO:0002819	0.0443	1	32911	172	64	2	BP	regulation of adaptive immune response	TGFB1; HSPA1B
GO:0002822	0.0443	1	32911	172	64	2	BP	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	TGFB1; HSPA1B

GO:0030258	0.0443	1	32911	172	64	2	BP	lipid modification	CERK; ACADL
GO:0045444	0.0443	1	32911	172	64	2	BP	fat cell differentiation	PTGS2; ADRB3
GO:0010721	0.0455	1	32911	172	65	2	BP	negative regulation of cell development	TGFB1; WNT3A
GO:0043623	0.0455	1	32911	172	65	2	BP	cellular protein complex assembly	TUBA4A; TUBB2C
GO:0050770	0.0455	1	32911	172	65	2	BP	regulation of axonogenesis	CXCL12; WNT3A
GO:0001773	0.046	1	32911	172	9	1	BP	myeloid dendritic cell activation	TGFB1
GO:0019627	0.046	1	32911	172	9	1	BP	urea metabolic process	ARG2
GO:0002011	0.046	1	32911	172	9	1	BP	morphogenesis of an epithelial sheet	NOTCH2
GO:0002063	0.046	1	32911	172	9	1	BP	chondrocyte development	SFRP2
GO:0002065	0.046	1	32911	172	9	1	BP	columnar/cuboidal epithelial cell differentiation	GATA5
GO:0021846	0.046	1	32911	172	9	1	BP	proliferation in forebrain	WNT3A
GO:0002688	0.046	1	32911	172	9	1	BP	regulation of leukocyte chemotaxis	CCL2
GO:0030212	0.046	1	32911	172	9	1	BP	hyaluronan metabolic process	CCND3
GO:0003254	0.046	1	32911	172	9	1	BP	regulation of membrane depolarization	GCLC
GO:0032874	0.046	1	32911	172	9	1	BP	positive regulation of stress-activated MAPK cascade	IL1B
GO:0034219	0.046	1	32911	172	9	1	BP	carbohydrate transmembrane transport	SLC2A1
GO:0035162	0.046	1	32911	172	9	1	BP	embryonic hemopoiesis	HIF1A
GO:0042345	0.046	1	32911	172	9	1	BP	regulation of NF-kappaB import into nucleus	RBCK1
GO:0042534	0.046	1	32911	172	9	1	BP	regulation of tumor necrosis factor biosynthetic process	BCL3
GO:0043011	0.046	1	32911	172	9	1	BP	myeloid dendritic cell differentiation	TGFB1
GO:0044060	0.046	1	32911	172	9	1	BP	regulation of endocrine process	IL1B
GO:0045026	0.046	1	32911	172	9	1	BP	plasma membrane fusion	TIE1
GO:0048843	0.046	1	32911	172	9	1	BP	negative regulation of axon extension	WNT3A
GO:0000050	0.046	1	32911	172	9	1	BP	involved in axon guidance	ARG2
								urea cycle	ARG2

GO:0050910	0.046	1	32911	172	9	1	BP	detection of mechanical stimulus involved in sensory perception of sound	MYC
GO:0060045	0.046	1	32911	172	9	1	BP	positive regulation of cardiac muscle cell proliferation	WNT2
GO:0060216	0.046	1	32911	172	9	1	BP	definitive hemopoiesis	SP1
GO:0060349	0.046	1	32911	172	9	1	BP	bone morphogenesis	SFRP2
GO:0060487	0.046	1	32911	172	9	1	BP	lung epithelial cell differentiation	HOXA5
GO:0060638	0.046	1	32911	172	9	1	BP	mesenchymal-epithelial cell signaling	HOXA5
GO:0060644	0.046	1	32911	172	9	1	BP	mammary gland epithelial cell differentiation	HOXA5
GO:0006105	0.046	1	32911	172	9	1	BP	succinate metabolic process	SUCLG2
GO:0006577	0.046	1	32911	172	9	1	BP	betaine metabolic process	ACADL
GO:0071384	0.046	1	32911	172	9	1	BP	cellular response to corticosteroid stimulus	TGFB1
GO:0071385	0.046	1	32911	172	9	1	BP	cellular response to glucocorticoid stimulus	TGFB1
GO:0090190	0.046	1	32911	172	9	1	BP	positive regulation of branching involved in ureteric bud morphogenesis	TGFB1
GO:0002764	0.0468	1	32911	172	66	2	BP	immune response-regulating signaling pathway	RELA; MYD88
GO:0010817	0.048	1	32911	172	155	3	BP	regulation of hormone levels	FZD4; CCKAR; AFP
GO:0032147	0.0494	1	32911	172	68	2	BP	activation of protein kinase activity	CERK; GADD45G
GO:0040014	0.0494	1	32911	172	68	2	BP	regulation of multicellular organism growth	GAMT; ADRB3
GO:0006936	0.0494	1	32911	172	68	2	BP	muscle contraction	ARG2; PDE4B

GO:0044464	1. 10E-38	1. 90E-36	33355	167	####	152	CC	cell part	SPNB2; EGR1; JAM2; CYP51; NRIP1; TUBA4A; BID; FYN; SP1; GPX2; RGS3; ATF4; RELA; RNF5; BCL3; PTSS2; GSTO1; IDI1; ALDH3A1; SLC2A1; MAPK3; TEK; CAV2; CLDN7; PTGS2; FZD2; GATA5; FZD4; CEBPD; DNAJC5; ARG2; ZFP111; MYC; CXCL12; EPOR; NT5C2; SOCS3; FOS; PPP2R2A; MYLK; CCKAR; GSR; DLL4; RBCK1; LGALS3; AFP; GALT; STAT1; CERK; IL2RG; JUN; IRS2; FCGR2; CCL2; TGM1; ADCY6; PPAP2B; ADCY2; TALDO1; ADCY8; ADCY9; HOXA5; OSMR; PDE4B; CCT6A; IL1R2; MYB; ADSS; HSPB1; EGR2; GADD45A; HK1; CCT5; MYD88; CH25H; PTGFR; CYP2F2; CCND3; MT1; PARD6B; HIF1A; ACADL; TUBB2C; TGFBI; SQLE; TRAF5; HSPA5; CYP4A12A; LM02; HSPA8; SMAD1; NOTCH2; NOTCH3; JUP; DUSP16; YWHAQ; HMGCS1; EPHA2; ADD1; EIF3A; EIF3C; EIF3E; SH3GLB2; H2-T24; CCR1; HSPA1A; MCL1; JUNB; PIM1; IVD; PRICKLE1; F3; ALDH4A1; ACSS1; SENP2; CBL; WNT2; TIE1; KDR; TBXA2R; SLC20A1; ST3GAL2; HMOX1; CDO1; NCR1; SUCLG2; GADD45G; ARSA; WNT3A; MYBBP1A; SETD8; AKR1B8; CSF3R; RNF19A; PRKCI; ASNS; PRPS1; GCLC; ALAS1; ADRB3; PPA1; ALDOA; IL1B; BCR; MTHFD2; HSPA1B; GSTA4; ANAPC11; GSTA2; ETS2; GBE1; GUCY1B3
GO:0044424	2. 40E-28	4. 10E-26	33355	167	9777	118	CC	intracellular part	SPNB2; EGR1; CYP51; NRIP1; TUBA4A; BID; FYN; SP1; GPX2; RGS3; ATF4; RELA; RNF5; BCL3; GSTO1; IDI1; ALDH3A1; SLC2A1; MAPK3; CAV2; PTGS2; GATA5; CEBPD; ARG2; ZFP111; MYC; NT5C2; SOCS3; FOS; PPP2R2A; MYLK; CCKAR; GSR; LGALS3; AFP; STAT1; CERK; JUN; IRS2; CCL2; ADCY6; PPAP2B; TALDO1; HOXA5; PDE4B; CCT6A; MYB; ADSS; HSPB1; EGR2; GADD45A; HK1; CCT5; MYD88; CH25H; CYP2F2; CCND3; MT1; PARD6B; HIF1A; ACADL; TUBB2C; TGFBI; SQLE; TRAF5; HSPA5; LM02; HSPA8; SMAD1; NOTCH2; NOTCH3; JUP; DUSP16; YWHAQ; HMGCS1; ADD1; EIF3A; EIF3C; EIF3E; SH3GLB2; HSPA1A; MCL1; JUNB; PIM1; IVD; PRICKLE1; F3; ALDH4A1; ACSS1; SENP2; CBL; WNT2; KDR; TBXA2R; ST3GAL2; HMOX1; CDO1; SUCLG2; GADD45G; ARSA; MYBBP1A; SETD8; AKR1B8; RNF19A; PRKCI; GCLC; ALAS1; PPA1; ALDOA; IL1B; BCR; MTHFD2; HSPA1B; GSTA4; ANAPC11; GSTA2; ETS2; GUCY1B3
GO:0005737	1. 80E-22	3. 20E-20	33355	167	3897	69	CC	cytoplasm	SPNB2; EGR1; BID; SP1; GPX2; RGS3; ATF4; RELA; BCL3; GSTO1; ALDH3A1; SLC2A1; MAPK3; CAV2; PTGS2; MYC; NT5C2; SOCS3; MYLK; CCKAR; GSR; LGALS3; AFP; STAT1; CERK; IRS2; CCL2; TALDO1; PDE4B; CCT6A; ADSS; HSPB1; CCT5; MYD88; CCND3; PARD6B; HIF1A; TGFBI; TRAF5; HSPA8; SMAD1; JUP; DUSP16; YWHAQ; HMGCS1; ADD1; EIF3A; EIF3C; EIF3E; SH3GLB2; MCL1; PIM1; PRICKLE1; F3; SENP2; CBL; WNT2; KDR; ARSA; MYBBP1A; AKR1B8; RNF19A; PRKCI; PPA1; ALDOA; BCR; GSTA4; ANAPC11; GUCY1B3
GO:0044444	2. 80E-15	4. 90E-13	33355	167	4223	61	CC	cytoplasmic part	SPNB2; CYP51; BID; FYN; GPX2; RELA; RNF5; IDI1; ALDH3A1; MAPK3; CAV2; PTGS2; ARG2; CCKAR; GSR; CERK; JUN; IRS2; ADCY6; PPAP2B; TALDO1; PDE4B; CCT6A; HSPB1; HK1; CCT5; CH25H; CYP2F2; MT1; PARD6B; ACADL; TGFBI; SQLE; HSPA5; HSPA8; JUP; HMGCS1; EIF3A; EIF3C; EIF3E; HSPA1A; MCL1; IVD; ALDH4A1; ACSS1; SENP2; TBXA2R; ST3GAL2; HMOX1; CDO1; SUCLG2; ARSA; PRKCI; GCLC; ALAS1; ALDOA; IL1B; MTHFD2; HSPA1B; GSTA2; GUCY1B3
GO:0043227	7. 80E-15	1. 30E-12	33355	167	7147	81	CC	membrane-bounded organelle	SPNB2; EGR1; CYP51; NRIP1; BID; SP1; RGS3; ATF4; RELA; RNF5; BCL3; IDI1; MAPK3; CAV2; PTGS2; GATA5; CEBPD; ARG2; ZFP111; MYC; FOS; CCKAR; GSR; LGALS3; STAT1; CERK; JUN; ADCY6; PPAP2B; HOXA5; PDE4B; MYB; HSPB1; EGR2; GADD45A; HK1; CH25H; CYP2F2; CCND3; MT1; PARD6B; HIF1A; ACADL; TGFBI; SQLE; HSPA5; LM02; HSPA8; SMAD1; NOTCH2; NOTCH3; DUSP16; EIF3A; EIF3E; HSPA1A; MCL1; JUNB; PIM1; IVD; PRICKLE1; ALDH4A1; ACSS1; SENP2; CBL; TBXA2R; ST3GAL2; HMOX1; SUCLG2; GADD45G; ARSA; MYBBP1A; SETD8; PRKCI; ALAS1; ALDOA; IL1B; MTHFD2; HSPA1B; ANAPC11; GSTA2; ETS2
GO:0005829	8. 40E-15	1. 40E-12	33355	167	495	22	CC	cytosol	BID; FYN; GPX2; RELA; ALDH3A1; MAPK3; CAV2; GSR; JUN; IRS2; TALDO1; PDE4B; HK1; MT1; HSPA8; JUP; HMGCS1; HMOX1; CDO1; GCLC; HSPA1B; GSTA2
GO:0043226	1. 80E-14	3. 20E-12	33355	167	7883	85	CC	organelle	SPNB2; EGR1; CYP51; NRIP1; BID; SP1; RGS3; ATF4; RELA; RNF5; BCL3; IDI1; MAPK3; CAV2; PTGS2; GATA5; CEBPD; ARG2; ZFP111; MYC; FOS; CCKAR; GSR; LGALS3; STAT1; CERK; JUN; ADCY6; PPAP2B; HOXA5; PDE4B; MYB; HSPB1; EGR2; GADD45A; HK1; CCT5; CH25H; CYP2F2; CCND3; MT1; PARD6B; HIF1A; ACADL; TGFBI; SQLE; HSPA5; LM02; HSPA8; SMAD1; NOTCH2; NOTCH3; JUP; DUSP16; ADD1; EIF3A; EIF3E; HSPA1A; MCL1; JUNB; PIM1; IVD; PRICKLE1; ALDH4A1; ACSS1; SENP2; CBL; TBXA2R; ST3GAL2; HMOX1; SUCLG2; GADD45G; ARSA; MYBBP1A; SETD8; RNF19A; PRKCI; ALAS1; ALDOA; IL1B; MTHFD2; HSPA1B; ANAPC11; GSTA2; ETS2
GO:0043231	2. 60E-14	4. 50E-12	33355	167	7142	80	CC	intracellular membrane-bounded organelle	SPNB2; EGR1; CYP51; NRIP1; BID; SP1; RGS3; ATF4; RELA; RNF5; BCL3; IDI1; MAPK3; CAV2; PTGS2; GATA5; CEBPD; ARG2; ZFP111; MYC; FOS; CCKAR; GSR; LGALS3; STAT1; CERK; JUN; ADCY6; PPAP2B; HOXA5; PDE4B; MYB; HSPB1; EGR2; GADD45A; HK1; CH25H; CYP2F2; CCND3; MT1; PARD6B; HIF1A; ACADL; TGFBI; SQLE; HSPA5; LM02; HSPA8; SMAD1; NOTCH2; NOTCH3; JUP; DUSP16; ADD1; EIF3A; EIF3E; HSPA1A; MCL1; JUNB; PIM1; IVD; PRICKLE1; ALDH4A1; ACSS1; SENP2; CBL; TBXA2R; ST3GAL2; HMOX1; SUCLG2; GADD45G; ARSA; MYBBP1A; SETD8; PRKCI; ALAS1; ALDOA; IL1B; MTHFD2; HSPA1B; ANAPC11; GSTA2; ETS2

GO:0043229	5.50E-14	9.50E-12	33355	167	7865	84	CC	intracellular organelle	SPNB2; EGR1; CYP51; NRIP1; BID; SP1; RGS3; ATF4; RELA; RNF5; BCL3; ID1; MAPK3; CAV2; PTGS2; GATA5; CEBPD; ARG2; ZFP111; MYC; FOS; CCKAR; GSR; LGALS3; STAT1; CERK; JUN; ADCY6; PPAP2B; HOXA5; PDE4B; MYB; HSPB1; EGR2; GADD45A; HK1; CCT5; CH25H; CYP2F2; CCND3; MT1; PARD6B; HIF1A; ACADL; TGFB1; SQLE; HSPA5; LMO2; SMAD1; NOTCH2; NOTCH3; JUP; DUSP16; ADD1; EIF3A; EIF3E; HSPA1A; MCL1; JUNB; PIM1; IVD; PRICKLE1; ALDH4A1; ACSS1; SENP2; CBL; TBXA2R; ST3GAL2; HMOX1; SUCLG2; GADD45G; ARSA; MYBBP1A; SETD8; RNF19A; PRKCI; ALAS1; ALDOA; IL1B; MTHFD2; HSPA1B; ANAPC11; GSTA2; ETS2
GO:0000267	1.00E-11	1.80E-09	33355	167	1024	26	CC	cell fraction	CYP51; FYN; MAPK3; CAV2; PTGS2; FOS; GSR; CERK; ADCY6; ADCY2; TALD01; ADCY8; PDE4B; HSPB1; CYP2F2; SQLE; CYP4A12A; YWHAQ; KDR; HMOX1; ARSA; PRKCI; ASNS; PRPS1; ANAPC11; GSTA2; ETS2
GO:0043234	5.30E-10	9.20E-08	33355	167	2047	34	CC	protein complex	SPNB2; NRIP1; TUBA4A; ATF4; RELA; MAPK3; CAV2; PTGS2; FOS; PPP2R2A; JUN; FCGRT; ADCY2; CCT6A; HSPB1; CCT5; HIF1A; TUBB2C; LMO2; HSPA8; SMAD1; YWHAQ; EIF3A; EIF3C; EIF3E; SENP2; CBL; SUCLG2; IGF1BP5; MYBBP1A; PRPS1; GCLC; HSPA1B; ANAPC11; GSTA2; ETS2
GO:0016020	5.40E-10	9.40E-08	33355	167	5875	63	CC	membrane	SPNB2; JAM2; CYP51; BID; FYN; RGS3; ATF4; RNF5; PTDSS2; SLC2A1; TEK; CAV2; CLDN7; PTGS2; FZD2; FZD4; DNAJC5; CXCL12; EPOR; CCKAR; DLL4; CERK; FCGRT; TGM1; ADCY6; PPAP2B; ADCY2; ADCY8; ADCY9; OSMR; IL1R2; HSPB1; HK1; CH25H; PTGFR; CYP2F2; PARD6B; ACADL; SQLE; NOTCH2; NOTCH3; JUP; EPHA2; ADD1; CCR1; MCL1; IVD; PRICKLE1; F3; SENP2; TIE1; KDR; TBXA2R; SLC20A1; ST3GAL2; CD01; NCR1; ARSA; CSF3R; RNF19A; PRKCI; ADRB3; GSTA2
GO:0005626	8.30E-10	1.40E-07	33355	167	809	21	CC	insoluble fraction	CYP51; FYN; MAPK3; CAV2; PTGS2; FOS; CERK; ADCY6; ADCY2; TALD01; ADCY8; PDE4B; HSPB1; CYP2F2; SQLE; CYP4A12A; KDR; HMOX1; ARSA; PRKCI; ADRB3
GO:0005634	3.40E-09	5.90E-07	33355	167	4243	50	CC	nucleus	SPNB2; EGR1; NRIP1; SP1; RGS3; ATF4; RELA; BCL3; MAPK3; CAV2; PTGS2; GATA5; CEBPD; ZFP111; MYC; FOS; LGALS3; STAT1; JUN; HOXA5; PDE4B; MYB; HSPB1; EGR2; GADD45A; CCND3; PARD6B; HIF1A; LMO2; SMAD1; NOTCH2; NOTCH3; DUSP16; EIF3A; EIF3E; MCL1; JUNB; PIM1; PRICKLE1; SENP2; CBL; HMOX1; GADD45G; MYBBP1A; SETD8; PRKCI; HSPA1B; ANAPC11; GSTA2; ETS2
GO:0005759	1.10E-08	2.00E-06	33355	167	32	6	CC	mitochondrial matrix	ACADL; IVD; ALDH4A1; ACSS1; ALAS1; HSPA1B
GO:0032991	3.80E-08	6.60E-06	33355	167	2550	35	CC	macromolecular complex	SPNB2; NRIP1; TUBA4A; SP1; ATF4; RELA; MAPK3; CAV2; PTGS2; FOS; PPP2R2A; JUN; FCGRT; ADCY2; CCT6A; HSPB1; CCT5; HIF1A; TUBB2C; LMO2; HSPA8; SMAD1; YWHAQ; EIF3A; EIF3C; EIF3E; SENP2; CBL; SUCLG2; IGF1BP5; MYBBP1A; PRPS1; GCLC; HSPA1B; ANAPC11; GSTA2; ETS2
GO:0044459	7.30E-08	1.20E-05	33355	167	1454	25	CC	plasma membrane part	JAM2; SLC2A1; TEK; CAV2; CLDN7; PTGS2; GSR; DLL4; IL2RG; FCGRT; TGM1; ADCY6; OSMR; HK1; PARD6B; NOTCH2; NOTCH3; JUP; EPHA2; CBL; KDR; HMOX1; ARSA; PRKCI; HSPA1B
GO:0005624	7.30E-08	1.20E-05	33355	167	772	18	CC	membrane fraction	CYP51; FYN; CAV2; PTGS2; FOS; CERK; ADCY6; ADCY2; TALD01; ADCY8; CYP2F2; SQLE; CYP4A12A; KDR; HMOX1; ARSA; PRKCI; ANAPC11; GSTA2; ETS2
GO:0005886	1.40E-07	2.50E-05	33355	167	2198	31	CC	plasma membrane	SPNB2; JAM2; FYN; RGS3; ATF4; SLC2A1; TEK; CAV2; CLDN7; FZD4; CXCL12; EPOR; CCKAR; FCGRT; ADCY6; ADCY2; ADCY9; HSPB1; PTGFR; PARD6B; NOTCH2; NOTCH3; ADD1; CCR1; TIE1; KDR; TBXA2R; CD01; NCR1; ARSA; ADRB3
GO:0044421	3.10E-07	5.40E-05	33355	167	852	18	CC	extracellular region part	THBS1; CXCL12; LGALS3; AFP; CCL2; CXCL1; TGFB1; HSPA8; SFRP2; COL3A1; F3; TIMP1; WNT2; IGF1BP5; ARSA; WNT3A; IL1B; COL11A2
GO:0005901	2.10E-06	3.70E-04	33355	167	42	5	CC	caveola	SLC2A1; CAV2; PTGS2; HK1; HMOX1
GO:0005625	4.40E-06	7.60E-04	33355	167	313	10	CC	soluble fraction	MAPK3; GSR; TALD01; PDE4B; HSPB1; YWHAQ; PRKCI; ASNS; PRPS1; GBE1
GO:0044425	1.70E-05	0.003	33355	167	6245	54	CC	membrane part	JAM2; CYP51; RNF5; PTDSS2; SLC2A1; TEK; CAV2; CLDN7; PTGS2; FZD2; FZD4; EPOR; CCKAR; GSR; DLL4; IL2RG; FCGRT; TGM1; ADCY6; PPAP2B; ADCY2; ADCY8; ADCY9; OSMR; IL1R2; HK1; MYD88; CH25H; PTGFR; PARD6B; SQLE; NOTCH2; NOTCH3; JUP; EPHA2; H2-T24; CCR1; MCL1; F3; CBL; TIE1; KDR; TBXA2R; SLC20A1; ST3GAL2; HMOX1; NCR1; ARSA; CSF3R; RNF19A; PRKCI; ADRB3; HSPA1B; GSTA2
GO:0005852	1.90E-05	0.0034	33355	167	11	3	CC	eukaryotic translation initiation factor 3 complex	EIF3A; EIF3C; EIF3E
GO:0005911	4.90E-05	0.0085	33355	167	189	7	CC	cell-cell junction	JAM2; SLC2A1; CLDN7; TGM1; PARD6B; JUP; PRKCI
GO:0005792	8.70E-05	0.015	33355	167	279	8	CC	microsome	CYP51; FYN; PTGS2; TALD01; CYP2F2; SQLE; CYP4A12A; HMOX1
GO:0042598	1.00E-04	0.0178	33355	167	286	8	CC	vesicular fraction	CYP51; FYN; PTGS2; TALD01; CYP2F2; SQLE; CYP4A12A; HMOX1
GO:0045121	1.00E-04	0.0189	33355	167	149	6	CC	membrane raft	SLC2A1; CAV2; PTGS2; ADCY6; HK1; HMOX1
GO:0005615	1.20E-04	0.022	33355	167	559	11	CC	extracellular space	THBS1; CXCL12; AFP; CCL2; CXCL1; TGFB1; SFRP2; F3; ARSA; WNT3A; IL1B
GO:0005739	1.60E-04	0.0283	33355	167	1355	18	CC	mitochondrion	BID; RNF5; ID1; ARG2; GSR; CERK; HK1; ACADL; HSPA1A; MCL1; IVD; ALDH4A1; ACSS1; SUCLG2; ALAS1; ALDOA; MTHFD2
GO:0044422	2.60E-04	0.045	33355	167	2761	28	CC	organelle part	SPNB2; NRIP1; TUBA4A; ATF4; MAPK3; MYC; FOS; JUN; PPAP2B; HSPB1; HK1; HIF1A; ACADL; TUBB2C; HSPA5; SMAD1; JUP; IVD; ALDH4A1; ACSS1; SENP2; ST3GAL2; HMOX1; SUCLG2; MYBBP1A; ALAS1; HSPA1B; GSTA2

GO:0009986	2.70E-04	0.0467	33355	167	176	6	CC	cell surface	CAV2; IL2RG; TGFBI; HSPA5; F3; WNT3A
GO:0005578	3.20E-04	0.0558	33355	167	256	7	CC	proteinaceous extracellular matrix	LGALS3; TGFBI; COL3A1; TIMP1; WNT2; WNT3A; COL11A2
GO:0005576	4.40E-04	0.0772	33355	167	1473	18	CC	extracellular region	THBS1; CXCL12; EPOR; AFP; CCL2; CXCL1; TGFBI; HSPA5; SFRP2; COL3A1; TIMP1; WNT2; ST3GAL2; PLA2G7; IGFBP5; WNT3A; IL1B; COL11A2
GO:0005832	5.10E-04	0.089	33355	167	7	2	CC	chaperonin-containing T-complex	CCT6A; CCT5
GO:0005923	5.50E-04	0.0966	33355	167	75	4	CC	tight junction	JAM2; CLDN7; PARD6B; PRKCI
GO:0070160	5.50E-04	0.0966	33355	167	75	4	CC	occluding junction	JAM2; CLDN7; PARD6B; PRKCI
GO:0031012	5.70E-04	0.0993	33355	167	282	7	CC	extracellular matrix	LGALS3; TGFBI; COL3A1; TIMP1; WNT2; WNT3A; COL11A2
GO:0005887	8.20E-04	0.1419	33355	167	390	8	CC	integral to plasma membrane	TEK; CAV2; DLL4; OSMR; NOTCH2; NOTCH3; EPHA2; KDR
GO:0005583	8.70E-04	0.1516	33355	167	9	2	CC	fibrillar collagen	COL3A1; COL11A2
GO:0044446	8.80E-04	0.1524	33355	167	2685	26	CC	intracellular organelle part	SPNB2; NRIP1; TUBA4A; ATF4; MAPK3; MYC; FOS; JUN; PPAP2B; HK1; HIF1A; ACADL; TUBB2C; HSPA5; SMAD1; IVD; ALDH4A1; ACSS1; SENP2; ST3GAL2; HMOX1; SUCLG2; MYBBP1A; ALAS1; HSPA1B
GO:0031226	0.0011	0.1955	33355	167	410	8	CC	intrinsic to plasma membrane	TEK; CAV2; DLL4; OSMR; NOTCH2; NOTCH3; EPHA2; KDR
GO:0044429	0.0023	0.4066	33355	167	461	8	CC	mitochondrial part	HK1; ACADL; IVD; ALDH4A1; ACSS1; SUCLG2; ALAS1; HSPA1B
GO:0044428	0.0024	0.4156	33355	167	920	12	CC	nuclear part	NRIP1; ATF4; MAPK3; MYC; FOS; JUN; HIF1A; SMAD1; SENP2; HMOX1; MYBBP1A; GSTA2
GO:0044451	0.0028	0.4919	33355	167	373	7	CC	nucleoplasm part	NRIP1; ATF4; MYC; FOS; JUN; HIF1A; SMAD1
GO:0005581	0.0049	0.8503	33355	167	21	2	CC	collagen	COL3A1; COL11A2
GO:0005667	0.0049	0.8539	33355	167	218	5	CC	transcription factor complex	ATF4; FOS; JUN; HIF1A; SMAD1
GO:0031074	0.005	0.8661	33355	167	1	1	CC	nucleocytoplasmic shuttling complex	MYBBP1A
GO:0042564	0.005	0.8661	33355	167	1	1	CC	NLS-dependent protein nuclear import complex	MYBBP1A
GO:0045298	0.005	0.8661	33355	167	1	1	CC	tubulin complex	TUBB2C
GO:0005586	0.005	0.8661	33355	167	1	1	CC	collagen type III	COL3A1
GO:0005592	0.005	0.8661	33355	167	1	1	CC	collagen type XI	COL11A2
GO:0030141	0.0052	0.9018	33355	167	138	4	CC	stored secretory granule	TGFBI; TBXA2R; ARSA; IL1B
GO:0031224	0.0058	1	33355	167	5562	41	CC	intrinsic to membrane	JAM2; CYP51; RNF5; PTDSS2; SLC2A1; TEK; CAV2; CLDN7; FZD2; FZD4; EPOR; CCKAR; DLL4; FCGRT; ADCY6; PPAP2B; ADCY2; ADCY8; ADCY9; OSMR; IL1R2; MYD88; CH25H; PTGFR; SQLE; NOTCH2; NOTCH3; EPHA2; H2-T24; CCR1; MCL1; F3; TIE1; KDR; TBXA2R; SLC20A1; ST3GAL2; NCR1; CSF3R; RNF19A; ADRB3
GO:0016021	0.0067	1	33355	167	5439	40	CC	integral to membrane	JAM2; CYP51; RNF5; PTDSS2; SLC2A1; TEK; CAV2; CLDN7; FZD2; FZD4; EPOR; CCKAR; DLL4; FCGRT; ADCY6; PPAP2B; ADCY2; ADCY8; ADCY9; OSMR; IL1R2; CH25H; PTGFR; SQLE; NOTCH2; NOTCH3; EPHA2; H2-T24; CCR1; MCL1; F3; TIE1; KDR; TBXA2R; SLC20A1; ST3GAL2; NCR1; CSF3R; RNF19A; ADRB3
GO:0005783	0.0093	1	33355	167	831	10	CC	endoplasmic reticulum	CYP51; RNF5; PTGS2; CCKAR; PPAP2B; CH25H; CYP2F2; SQLE; HSPA5; HMOX1
GO:0044445	0.0099	1	33355	167	88	3	CC	cytosolic part	CCT6A; CCT5; GUCY1B3
GO:0017109	0.0099	1	33355	167	2	1	CC	glutamate-cysteine ligase complex	GCLC
GO:0031232	0.0099	1	33355	167	2	1	CC	extrinsic to external side of plasma membrane	ARSA
GO:0042709	0.0099	1	33355	167	2	1	CC	succinate-CoA ligase complex	SUCLG2
GO:0045244	0.0099	1	33355	167	2	1	CC	succinate-CoA ligase complex (GDP-forming)	SUCLG2

GO:0008074	0.0099	1	33355	167	2	1	CC	guanylate cyclase complex, soluble	GUCY1B3
GO:0030054	0.0146	1	33355	167	510	7	CC	cell junction	JAM2; SLC2A1; CLDN7; TGM1; PARD6B; JUP; PRKCI
GO:0016942	0.0149	1	33355	167	3	1	CC	insulin-like growth factor binding protein complex	IGFBP5
GO:0030062	0.0149	1	33355	167	3	1	CC	mitochondrial tricarboxylic acid cycle enzyme complex	SUCLG2
GO:0032437	0.0149	1	33355	167	3	1	CC	cuticular plate	SPNB2
GO:0008091	0.0149	1	33355	167	3	1	CC	spectrin	SPNB2
GO:0044420	0.0151	1	33355	167	103	3	CC	extracellular matrix part	COL3A1; TIMP1; COL11A2
GO:0043005	0.0152	1	33355	167	397	6	CC	neuron projection	MYC; STAT1; ADCY2; TGFB1; ADD1; KDR
GO:0005913	0.0155	1	33355	167	38	2	CC	cell-cell adherens junction	TGM1; JUP
GO:0042995	0.0177	1	33355	167	785	9	CC	cell projection	MYC; GAMT; STAT1; ADCY2; HIF1A; TGFB1; ADD1; KDR; ALDOA
GO:0001669	0.0188	1	33355	167	42	2	CC	acrosomal vesicle	TBXA2R; ARSA
GO:0016327	0.0198	1	33355	167	4	1	CC	apicolateral plasma membrane	JUP
GO:0031234	0.0198	1	33355	167	4	1	CC	extrinsic to internal side of plasma membrane	CAV2
GO:0045239	0.0198	1	33355	167	4	1	CC	tricarboxylic acid cycle enzyme complex	SUCLG2
GO:0043230	0.0247	1	33355	167	5	1	CC	extracellular organelle	HSPA8
GO:0065010	0.0247	1	33355	167	5	1	CC	extracellular membrane-bounded organelle	HSPA8
GO:0070062	0.0247	1	33355	167	5	1	CC	extracellular vesicular exosome	HSPA8
GO:0019861	0.0251	1	33355	167	49	2	CC	flagellum	HIF1A; ALDOA
GO:0030018	0.0251	1	33355	167	49	2	CC	Z disc	HSPB1; JUP
GO:0005730	0.0266	1	33355	167	128	3	CC	nucleolus	MYC; HMOX1; MYBBP1A
GO:0031988	0.0292	1	33355	167	342	5	CC	membrane-bounded vesicle	TGFB1; HSPA8; TBXA2R; ARSA; IL1B
GO:0019897	0.03	1	33355	167	54	2	CC	extrinsic to plasma membrane	CAV2; ARSA
GO:0005622	0.0316	1	33355	167	1157	11	CC	intracellular	EGR1; SP1; PTDSS2; SLC2A1; RBCK1; HSPB1; EGR2; HSPA8; SMAD1; BCR; HSPA1B
GO:0016600	0.0345	1	33355	167	7	1	CC	flotillin complex	CBL
GO:0031528	0.0393	1	33355	167	8	1	CC	microvillus membrane	ADCY6
GO:0005640	0.0393	1	33355	167	8	1	CC	nuclear outer membrane	GSTA2
GO:0045177	0.0398	1	33355	167	63	2	CC	apical part of cell	PARD6B; PRKCI
GO:0042612	0.0441	1	33355	167	9	1	CC	MHC class I protein complex	FCGRT
GO:0005916	0.0441	1	33355	167	9	1	CC	fascia adherens	JUP
GO:0030424	0.0446	1	33355	167	157	3	CC	axon protein	MYC; STAT1; TGFB1
GO:0000159	0.0489	1	33355	167	10	1	CC	phosphatase type 2A complex	PPP2R2A

GO:0005488	1.10E-46	5.20E-44	32949	176	####	147	MF	binding	SPNB2; EGR1; CYP51; NRIP1; TUBA4A; AGFG2; BID; FYN; SP1; RGS3; ATF4; RELA; RNF5; BCL3; EIF2S2; IDI1; SLC2A1; THBS1; MAPK3; TEK; CAV2; CLDN7; PTGS2; FZD2; GATA5; FZD4; IL10RB; CEBPD; DNJC5; ARG2; CYP2J9; ZFP111; MYC; CXCL12; CXCL16; EPOR; SOCS6; NT5C2; SOCS3; FOS; MYLK; CCKAR; GSR; DLL4; RBCK1; LGALS3; AFP; CALM3; GAMT; STAT1; CERK; IL2RG; JUN; IRS2; FCGRT; CCL2; TGM1; ADCY6; EIF1A; ADCY2; TALD01; ADCY8; ADCY9; HOXA5; OSMR; PDE4B; CCT6A; ILIR2; MYB; ADSS; HSPB1; EGR2; GADD45A; HK1; CCT5; MYD88; CH25H; CXCL1; MKNK1; CYP2F2; CCND3; MT1; PARD6B; HIF1A; ACADL; TUBB2C; TGFB1; SQLE; TRAF5; HSPA5; LMO2; HSPA8; SMAD1; NOTCH2; NOTCH3; JUP; DUSP16; YWHAQ; SFRP2; HMGCS1; EPHA2; ADD1; EIF3A; EIF3C; EIF3E; SH3GLB2; CCR1; MCL1; JUNB; COL3A1; PIM1; IVD; PRICKLE1; CTPS; F3; TIMP1; ACSS1; CBL; TIE1; KDR; HMOX1; CDO1; SUCLG2; IGFBP5; GADD45G; ARSA; WNT3A; MYBBP1A; CSF3R; RNF19A; PRKCI; ASNS; PRPS1; EIF5; GCLC; ALAS1; ADRB3; PPA1; IL1B; BCR; HSPA1B; ANAPC11; GSTA2; ETS2; GDA; GBE1; GUCY1B3
GO:0005515	2.00E-34	9.10E-32	32949	176	5383	100	MF	protein binding	SPNB2; NRIP1; BID; FYN; SP1; RGS3; ATF4; RELA; RNF5; BCL3; SLC2A1; MAPK3; TEK; CAV2; CLDN7; FZD2; FZD4; IL10RB; CEBPD; DNJC5; ARG2; MYC; CXCL12; CXCL16; EPOR; SOCS6; SOCS3; FOS; MYLK; GSR; DLL4; RBCK1; LGALS3; GAMT; STAT1; IL2RG; JUN; IRS2; FCGRT; CCL2; ADCY6; ADCY2; OSMR; CCT6A; ILIR2; HSPB1; EGR2; GADD45A; HK1; CCT5; MYD88; CXCL1; MKNK1; CCND3; PARD6B; HIF1A; TGFB1; TRAF5; HSPA5; LMO2; HSPA8; SMAD1; NOTCH2; NOTCH3; JUP; DUSP16; YWHAQ; SFRP2; HMGCS1; EPHA2; ADD1; EIF3A; SH3GLB2; CCR1; MCL1; JUNB; COL3A1; PRICKLE1; F3; TIMP1; CBL; TIE1; KDR; HMOX1; SUCLG2; IGFBP5; GADD45G; WNT3A; MYBBP1A; CSF3R; RNF19A; ASNS; GCLC; ADRB3; IL1B; HSPA1B; ANAPC11; ETS2; GDA; GUCY1B3
GO:0003824	5.30E-23	2.40E-20	32949	176	4892	81	MF	catalytic activity	CYP51; TUBA4A; FYN; GPX2; RNF5; PTDSS2; GSTO1; IDI1; ALDH3A1; MAPK3; TEK; PTGS2; ARG2; CYP2J9; NT5C2; MYLK; GSR; RBCK1; AFP; GAMT; CERK; TGM1; ADCY6; PPAP2B; ADCY2; TALD01; ADCY8; ADCY9; SRM; PDE4B; ADSS; HK1; CH25H; MKNK1; CYP2F2; CCND3; ACADL; TUBB2C; SQLE; CYP41A2; HSPA8; DUSP16; YWHAQ; HMGCS1; EPHA2; PIM1; IVD; CTPS; ALDH4A1; AMPD3; ACSS1; SENP2; CBL; TIE1; KDR; CDKN2B; ALDH3B1; ST3GAL2; HMOX1; CDO1; SUCLG2; PLA2G7; ARSA; MYBBP1A; SETD8; AKR1B8; RNF19A; PRKCI; ASNS; PRPS1; GCLC; ALAS1; PPA1; ALDOA; BCR; MTHFD2; GSTA4; GSTA2; GDA; GBE1; GUCY1B3
GO:0043169	3.00E-14	1.30E-11	32949	176	3201	53	MF	cation binding	EGR1; CYP51; AGFG2; FYN; SP1; RNF5; EIF2S2; IDI1; THBS1; PTGS2; GATA5; ARG2; CYP2J9; ZFP111; NT5C2; MYLK; DLL4; RBCK1; AFP; CALM3; STAT1; TGM1; ADCY6; ADCY2; ADCY8; ADCY9; PDE4B; ADSS; EGR2; CH25H; CYP2F2; MT1; TRAF5; LMO2; NOTCH2; NOTCH3; ADD1; PIM1; PRICKLE1; TIMP1; CBL; HMOX1; CDO1; ARSA; MYBBP1A; RNF19A; PRKCI; PRPS1; PPA1; ANAPC11; GDA; GBE1; GUCY1B3
GO:0043167	3.30E-14	1.50E-11	32949	176	3210	53	MF	ion binding	EGR1; CYP51; AGFG2; FYN; SP1; RNF5; EIF2S2; IDI1; THBS1; PTGS2; GATA5; ARG2; CYP2J9; ZFP111; NT5C2; MYLK; DLL4; RBCK1; AFP; CALM3; STAT1; TGM1; ADCY6; ADCY2; ADCY8; ADCY9; PDE4B; ADSS; EGR2; CH25H; CYP2F2; MT1; TRAF5; LMO2; NOTCH2; NOTCH3; ADD1; PIM1; PRICKLE1; TIMP1; CBL; HMOX1; CDO1; ARSA; MYBBP1A; RNF19A; PRKCI; PRPS1; PPA1; ANAPC11; GDA; GBE1; GUCY1B3
GO:0046872	7.90E-14	3.50E-11	32949	176	3166	52	MF	metal ion binding	EGR1; CYP51; AGFG2; FYN; SP1; RNF5; EIF2S2; IDI1; THBS1; PTGS2; GATA5; ARG2; CYP2J9; ZFP111; NT5C2; MYLK; DLL4; RBCK1; AFP; CALM3; STAT1; TGM1; ADCY6; ADCY2; ADCY8; ADCY9; PDE4B; ADSS; EGR2; CH25H; CYP2F2; MT1; TRAF5; LMO2; NOTCH2; NOTCH3; ADD1; PIM1; PRICKLE1; TIMP1; CBL; HMOX1; CDO1; ARSA; MYBBP1A; RNF19A; PRKCI; PRPS1; PPA1; ANAPC11; GDA; GUCY1B3
GO:0017076	3.80E-12	1.70E-09	32949	176	1776	36	MF	purine nucleotide binding	TUBA4A; FYN; MAPK3; TEK; MYLK; GSR; CERK; ADCY6; ADCY2; ADCY8; ADCY9; CCT6A; ADSS; HK1; CCT5; MKNK1; ACADL; TUBB2C; SQLE; HSPA5; HSPA8; EPHA2; PIM1; IVD; CTPS; ACSS1; TIE1; KDR; SUCLG2; PRKCI; ASNS; PRPS1; EIF5; GCLC; BCR; GUCY1B3
GO:0046983	1.80E-11	8.30E-09	32949	176	426	18	MF	protein dimerization activity	ATF4; CAV2; CEBPD; MYC; FOS; GSR; GAMT; JUN; HK1; HIF1A; TGFB1; HMGCS1; MCL1; JUNB; SUCLG2; ASNS; GCLC; GUCY1B3
GO:0000166	4.90E-11	2.20E-08	32949	176	2046	37	MF	nucleotide binding	TUBA4A; FYN; MAPK3; TEK; NT5C2; MYLK; GSR; CERK; ADCY6; ADCY2; ADCY8; ADCY9; CCT6A; ADSS; HK1; CCT5; MKNK1; ACADL; TUBB2C; SQLE; HSPA5; HSPA8; EPHA2; PIM1; IVD; CTPS; ACSS1; TIE1; KDR; SUCLG2; PRKCI; ASNS; PRPS1; EIF5; GCLC; BCR; GUCY1B3
GO:0030554	6.20E-11	2.80E-08	32949	176	1475	31	MF	adenyl nucleotide binding	FYN; MAPK3; TEK; MYLK; GSR; CERK; ADCY6; ADCY2; ADCY8; ADCY9; CCT6A; HK1; CCT5; MKNK1; ACADL; SQLE; HSPA5; HSPA8; EPHA2; PIM1; IVD; CTPS; ACSS1; TIE1; KDR; SUCLG2; PRKCI; ASNS; PRPS1; GCLC; BCR
GO:0001883	8.80E-11	3.90E-08	32949	176	1496	31	MF	purine nucleoside binding	FYN; MAPK3; TEK; MYLK; GSR; CERK; ADCY6; ADCY2; ADCY8; ADCY9; CCT6A; HK1; CCT5; MKNK1; ACADL; SQLE; HSPA5; HSPA8; EPHA2; PIM1; IVD; CTPS; ACSS1; TIE1; KDR; SUCLG2; PRKCI; ASNS; PRPS1; GCLC; BCR
GO:0001882	9.70E-11	4.30E-08	32949	176	1502	31	MF	nucleoside binding	FYN; MAPK3; TEK; MYLK; GSR; CERK; ADCY6; ADCY2; ADCY8; ADCY9; CCT6A; HK1; CCT5; MKNK1; ACADL; SQLE; HSPA5; HSPA8; EPHA2; PIM1; IVD; CTPS; ACSS1; TIE1; KDR; SUCLG2; PRKCI; ASNS; PRPS1; GCLC; BCR

GO:0032555	4.80E-10	2.20E-07	32949	176	1703	32	MF	purine ribonucleotide binding	TUBA4A; FYN; MAPK3; TEK; MYLK; CERK; ADCY6; ADCY2; ADCY8; ADCY9; CCT6A; ADSS; HK1; CCT5; MKNK1; TUBB2C; HSPA5; HSPA8; EPHA2; PIM1; CTPS; ACSS1; TIE1; KDR; SUCLG2; PRKCI; ASNS; PRPS1; EIF5; GCLC; BCR; GUCY1B3
GO:0032553	4.90E-10	2.20E-07	32949	176	1704	32	MF	ribonucleotide binding	TUBA4A; FYN; MAPK3; TEK; MYLK; CERK; ADCY6; ADCY2; ADCY8; ADCY9; CCT6A; ADSS; HK1; CCT5; MKNK1; TUBB2C; HSPA5; HSPA8; EPHA2; PIM1; CTPS; ACSS1; TIE1; KDR; SUCLG2; PRKCI; ASNS; PRPS1; EIF5; GCLC; BCR; GUCY1B3
GO:0016740	7.60E-10	3.40E-07	32949	176	1635	31	MF	transferase activity	FYN; PTDSS2; GSTO1; MAPK3; TEK; MYLK; GALT; CERK; TGM1; TALDO1; SRM; HK1; MKNK1; CCND3; DUSP16; HMGCS1; EPHA2; PIM1; TIE1; KDR; CDKN2B; ST3GAL2; MYBBP1A; SETD8; PRKCI; PRPS1; ALAS1; BCR; GSTA4; GSTA2; GBE1
GO:0016491	7.80E-10	3.50E-07	32949	176	679	20	MF	oxidoreductase activity	CYP51; GPX2; ALDH3A1; PTGS2; CYP2J9; GSR; CH25H; CYP2F2; ACADL; SQLE; CYP4A12A; YWHAQ; IVD; ALDH4A1; ALDH3B1; HMOX1; CD01; SUCLG2; AKR1B8; MTHFD2
GO:0030528	5.10E-09	2.30E-06	32949	176	1096	24	MF	transcription regulator activity	EGR1; NRIP1; SP1; ATF4; RELA; BCL3; MAPK3; GATA5; CEBPD; ZFP111; MYC; FOS; RBCK1; STAT1; JUN; HOXA5; MYB; EGR2; HIF1A; TGFBI; SMAD1; JUNB; MYBBP1A; ETS2
GO:0005524	5.30E-09	2.40E-06	32949	176	1376	27	MF	ATP binding	FYN; MAPK3; TEK; MYLK; CERK; ADCY6; ADCY2; ADCY8; ADCY9; CCT6A; HK1; CCT5; MKNK1; HSPA5; HSPA8; EPHA2; PIM1; CTPS; ACSS1; TIE1; KDR; SUCLG2; PRKCI; ASNS; PRPS1; GCLC; BCR
GO:0032559	7.90E-09	3.50E-06	32949	176	1402	27	MF	adenyl ribonucleotide binding	FYN; MAPK3; TEK; MYLK; CERK; ADCY6; ADCY2; ADCY8; ADCY9; CCT6A; HK1; CCT5; MKNK1; HSPA5; HSPA8; EPHA2; PIM1; CTPS; ACSS1; TIE1; KDR; SUCLG2; PRKCI; ASNS; PRPS1; GCLC; BCR
GO:0005102	2.00E-08	9.10E-06	32949	176	742	19	MF	receptor binding	NRIP1; FYN; ATF4; CAV2; CXCL12; CXCL16; DLL4; IRS2; CCL2; ADCY6; MYD88; CXCL1; TGFBI; HSPA8; ADD1; WNT3A; ADRB3;
GO:0019899	3.50E-08	1.50E-05	32949	176	398	14	MF	enzyme binding	NRIP1; BID; FYN; SP1; SLC2A1; ARG2; RBCK1; IRS2; CCND3; HIF1A; JUP; F3; HMOX1; HSPA1B
GO:0003700	4.00E-08	1.80E-05	32949	176	694	18	MF	transcription factor activity	EGR1; SP1; ATF4; RELA; BCL3; GATA5; CEBPD; MYC; FOS; STAT1; JUN; HOXA5; MYB; EGR2; HIF1A; SMAD1; JUNB; ETS2
GO:0046982	8.40E-08	3.80E-05	32949	176	190	10	MF	protein heterodimerization activity	CEBPD; MYC; FOS; JUN; HIF1A; TGFBI; MCL1; SUCLG2; GCLC; GUCY1B3
GO:0016849	1.60E-07	7.20E-05	32949	176	24	5	MF	phosphorus-oxygen lyase activity	ADCY6; ADCY2; ADCY8; ADCY9; GUCY1B3
GO:0009975	2.00E-07	9.00E-05	32949	176	25	5	MF	cyclase activity	ADCY6; ADCY2; ADCY8; ADCY9; GUCY1B3
GO:0019838	2.10E-07	9.50E-05	32949	176	78	7	MF	growth factor binding	TEK; IL10RB; IL2RG; IL1R2; COL3A1; KDR; IGF1BP5
GO:0004016	2.50E-07	1.10E-04	32949	176	11	4	MF	adenylate cyclase activity	ADCY6; ADCY2; ADCY8; ADCY9
GO:0019955	3.20E-07	1.40E-04	32949	176	83	7	MF	cytokine binding	IL10RB; EPOR; IL2RG; OSMR; IL1R2; CCR1; CSF3R
GO:0016772	4.20E-07	1.90E-04	32949	176	904	19	MF	transferase activity, transferring phosphorus-containing groups	FYN; PTDSS2; MAPK3; TEK; MYLK; CERK; HK1; MKNK1; CCND3; DUSP16; EPHA2; PIM1; TIE1; KDR; CDKN2B; MYBBP1A; PRKCI; PRPS1; BCR
GO:0046914	8.00E-07	3.60E-04	32949	176	1546	25	MF	transition metal ion binding	EGR1; CYP51; AGFG2; SP1; RNF5; PTGS2; GATA5; RBCK1; EGR2; CH25H; CYP2F2; MT1; TRAF5; LMO2; PIM1; PRICKLE1; CBL; HMOX1; CD01; MYBBP1A; RNF19A; PRKCI; ANAPC11; GDA; GUCY1B3
GO:0003743	8.40E-07	3.70E-04	32949	176	60	6	MF	translation initiation factor activity	EIF2S2; EIF1A; EIF3A; EIF3C; EIF3E; EIF5
GO:0043565	1.60E-06	7.30E-04	32949	176	547	14	MF	sequence-specific DNA binding	EGR1; SP1; ATF4; RELA; GATA5; CEBPD; MYC; FOS; STAT1; JUN; HOXA5; HIF1A; JUNB; ETS2
GO:0016563	1.60E-06	7.50E-04	32949	176	263	10	MF	transcription activator activity	EGR1; SP1; ATF4; RELA; GATA5; MYC; RBCK1; TGFBI; JUNB; ETS2
GO:0001664	1.80E-06	8.20E-04	32949	176	107	7	MF	G-protein-coupled receptor binding	CAV2; CXCL12; CXCL16; CCL2; CXCL1; WNT3A; ADRB3
GO:0008294	2.90E-06	0.0013	32949	176	6	3	MF	calcium- and calmodulin-responsive adenylate cyclase activity	ADCY6; ADCY2; ADCY8
GO:0003702	3.30E-06	0.0015	32949	176	117	7	MF	RNA polymerase II transcription factor activity	ATF4; RELA; GATA5; CEBPD; JUN; HIF1A; SMAD1

GO:0003690	3.90E-06	0.0018	32949	176	78	6	MF	double-stranded DNA binding	EGR1; SP1; MYC; FOS; JUN; JUNB
GO:0004497	4.60E-06	0.002	32949	176	123	7	MF	monooxygenase activity	CYP51; CYP2J9; CH25H; CYP2F2; SQLE; CYP4A12A; YWHAQ
GO:0032403	4.90E-06	0.0022	32949	176	233	9	MF	protein complex binding	SPNB2; FYN; RELA; LGALS3; IRS2; FCGRT; ADCY2; HIF1A; ADD1
GO:0016301	4.90E-06	0.0022	32949	176	780	16	MF	kinase activity	FYN; MAPK3; TEK; MYLK; CERK; HK1; MKNK1; CCND3; DUSP16; EPHA2; PIM1; TIE1; KDR; CDKN2B; PRKCI; BCR
GO:0004896	6.40E-06	0.0029	32949	176	49	5	MF	cytokine receptor activity	IL10RB; EPOR; OSMR; IL1R2; CSF3R
GO:0042803	7.60E-06	0.0034	32949	176	246	9	MF	protein homodimerization activity	CAV2; CEBPD; GSR; GAMT; JUN; HK1; TGFB1; HMGC1; ASNS
GO:0004672	9.50E-06	0.0043	32949	176	553	13	MF	protein kinase activity	FYN; MAPK3; TEK; MYLK; HK1; MKNK1; CCND3; EPHA2; PIM1; TIE1; KDR; PRKCI; BCR
GO:0008135	1.10E-05	0.0053	32949	176	94	6	MF	translation factor activity, nucleic acid binding	EIF2S2; EIF1A; EIF3A; EIF3C; EIF3E; EIF5
GO:0004871	1.20E-05	0.0054	32949	176	2793	33	MF	signal transducer activity	NRIP1; RGS3; MAPK3; TEK; FZD2; FZD4; IL10RB; CXCL16; EPOR; CCKAR; STAT1; IRS2; FCGRT; OSMR; IL1R2; MYD88; PTGFR; HIF1A; TRAF5; NOTCH2; NOTCH3; EPHA2; CCR1; CBL; WNT2; TIE1; KDR; TBXA2R; SLC20A1; NCRI; WNT3A; CSF3R; ADRB3
GO:0060089	1.20E-05	0.0054	32949	176	2793	33	MF	molecular transducer activity	NRIP1; RGS3; MAPK3; TEK; FZD2; FZD4; IL10RB; CXCL16; EPOR; CCKAR; STAT1; IRS2; FCGRT; OSMR; IL1R2; MYD88; PTGFR; HIF1A; TRAF5; NOTCH2; NOTCH3; EPHA2; CCR1; CBL; WNT2; TIE1; KDR; TBXA2R; SLC20A1; NCRI; WNT3A; CSF3R; ADRB3
GO:0016773	1.30E-05	0.006	32949	176	658	14	MF	phosphotransferase activity, alcohol group as acceptor	FYN; MAPK3; TEK; MYLK; CERK; HK1; MKNK1; CCND3; EPHA2; PIM1; TIE1; KDR; PRKCI; BCR
GO:0016620	1.40E-05	0.0065	32949	176	28	4	MF	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	ALDH3A1; ALDH4A1; ALDH3B1; SUCLG2
GO:0016874	2.70E-05	0.0126	32949	176	363	10	MF	ligase activity	RNF5; RBCK1; ADSS; CTPS; ACSS1; CBL; SUCLG2; RNF19A; ASNS; GRI1
GO:0042608	2.80E-05	0.0128	32949	176	2	2	MF	T cell receptor binding	FYN; ADD1
GO:0008009	2.80E-05	0.0128	32949	176	33	4	MF	chemokine activity	CXCL12; CXCL16; CCL2; CXCL1
GO:0042379	3.20E-05	0.0145	32949	176	34	4	MF	chemokine receptor binding	CXCL12; CXCL16; CCL2; CXCL1
GO:0005506	3.90E-05	0.0178	32949	176	171	7	MF	iron ion binding	CYP51; PTGS2; CH25H; CYP2F2; HMOX1; CD01; GUCY1B3
GO:0043566	4.40E-05	0.0203	32949	176	119	6	MF	structure-specific DNA binding	EGR1; SP1; MYC; FOS; JUN; JUNB
GO:0016903	4.50E-05	0.0204	32949	176	37	4	MF	oxidoreductase activity, acting on the aldehyde or oxo group of donors	ALDH3A1; ALDH4A1; ALDH3B1; SUCLG2
GO:0005126	9.00E-05	0.0409	32949	176	135	6	MF	cytokine receptor binding	CXCL12; CXCL16; CCL2; CXCL1; TGFB1; IL1B
GO:0005198	1.20E-04	0.055	32949	176	351	9	MF	structural molecule activity	SPNB2; TUBA4A; THBS1; CLDN7; TUBB2C; JUP; ADD1; COL3A1; COL11A2
GO:0003704	1.30E-04	0.0616	32949	176	19	3	MF	specific RNA polymerase II transcription factor activity	ATF4; CEBPD; HIF1A
GO:0042802	1.50E-04	0.0693	32949	176	362	9	MF	identical protein binding	CAV2; CEBPD; GSR; GAMT; JUN; HK1; TGFB1; HMGC1; ASNS
GO:0016829	1.90E-04	0.0872	32949	176	155	6	MF	lyase activity	ADCY6; ADCY2; ADCY8; ADCY9; ALDOA; GUCY1B3

GO:0016765	2.00E-04	0.0913	32949	176	54	4	MF	transferase activity, transferring alkyl or aryl (other than methyl) groups	GSTO1; SRM; GSTA4; GSTA2
GO:0020037	2.40E-04	0.1114	32949	176	104	5	MF	heme binding	CYP51; PTGS2; CYP2F2; HMOX1; GUCY1B3
GO:0003676	2.60E-04	0.1188	32949	176	2450	27	MF	nucleic acid binding	EGR1; SP1; ATF4; RELA; BCL3; EIF2S2; GATA5; CEBPD; MYC; FOS; RBCK1; STAT1; JUN; EIF1A; HOXA5; MYB; EGR2; HIF1A; LMO2; SMAD1; EIF3A; EIF3C; EIF3E; JUNB; MYBBP1A; EIF5; ETS2
GO:0003677	2.60E-04	0.1194	32949	176	1680	21	MF	DNA binding	EGR1; SP1; ATF4; RELA; BCL3; GATA5; CEBPD; MYC; FOS; RBCK1; STAT1; JUN; HOXA5; MYB; EGR2; HIF1A; LMO2; SMAD1; JUNB; MYBBP1A; ETS2
GO:0004030	2.80E-04	0.1268	32949	176	5	2	MF	aldehyde dehydrogenase [NAD(P)+] activity	ALDH3A1; ALDH3B1
GO:0004714	2.80E-04	0.1286	32949	176	59	4	MF	transmembrane receptor protein tyrosine kinase activity	TEK; EPHA2; TIE1; KDR
GO:0019900	3.00E-04	0.1389	32949	176	169	6	MF	kinase binding	FYN; SLC2A1; RBCK1; IRS2; CCND3; JUP
GO:0051082	3.20E-04	0.1463	32949	176	61	4	MF	unfolded protein binding	DNAJC5; CCT6A; CCT5; HSPA8
GO:0046906	3.30E-04	0.1506	32949	176	111	5	MF	tetrapyrrole binding	CYP51; PTGS2; CYP2F2; HMOX1; GUCY1B3
GO:0016814	3.90E-04	0.1802	32949	176	27	3	MF	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines	AMPD3; MTHFD2; GDA
GO:0004364	3.90E-04	0.1802	32949	176	27	3	MF	glutathione transferase activity	GSTO1; GSTA4; GSTA2
GO:0050660	4.90E-04	0.2218	32949	176	68	4	MF	FAD binding	GSR; ACADL; SQLE; IVD
GO:0042813	5.80E-04	0.2645	32949	176	7	2	MF	Wnt receptor activity	FZD2; FZD4
GO:0019199	6.00E-04	0.2756	32949	176	72	4	MF	transmembrane receptor protein kinase activity	TEK; EPHA2; TIE1; KDR
GO:0004713	6.60E-04	0.2995	32949	176	129	5	MF	protein tyrosine kinase activity	FYN; TEK; EPHA2; TIE1; KDR
GO:0008270	7.30E-04	0.3334	32949	176	1318	17	MF	zinc ion binding	EGR1; AGFG2; SP1; RNF5; GATA5; RBCK1; EGR2; MT1; TRAF5; LMO2; PRICKLE1; CBL; MYBBP1A; RNF19A; PRKCI; ANAPC11; GDA
GO:0016405	7.70E-04	0.3515	32949	176	8	2	MF	CoA-ligase activity	ACSS1; SUCLG2
GO:0016705	8.10E-04	0.3677	32949	176	135	5	MF	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	CYP51; PTGS2; CH25H; SQLE; HMOX1
GO:0043295	9.90E-04	0.4504	32949	176	9	2	MF	glutathione binding	GSR; GSTA2
GO:0004953	9.90E-04	0.4504	32949	176	9	2	MF	icosanoid receptor activity	PTGFR; TBXA2R
GO:0004954	9.90E-04	0.4504	32949	176	9	2	MF	prostanoid receptor activity	PTGFR; TBXA2R
GO:0035326	0.0011	0.4979	32949	176	38	3	MF	enhancer binding	SP1; RELA; GATA5
GO:0004872	0.0011	0.5322	32949	176	2563	26	MF	receptor activity	NR1P1; TEK; FZD2; FZD4; IL10RB; CXCL16; EPOR; CCKAR; IRS2; FCGRT; OSMR; IL1R2; MYD88; PTGFR; TRAF5; NOTCH2; NOTCH3; EPHA2; CCR1; TIE1; KDR; TBXA2R; SLC20A1; NCR1; CSF3R; ETS2
GO:0016209	0.0011	0.5373	32949	176	39	3	MF	antioxidant activity	GPX2; PTGS2; GSR

GO:0051427	0.0011	0.5373	32949	176	39	3	MF	hormone receptor binding	NRIP1; FYN; ETS2
GO:0010576	0.0012	0.561	32949	176	10	2	MF	metalloenzyme regulator activity	SFRP2; TIMP1
GO:0019865	0.0012	0.561	32949	176	10	2	MF	immunoglobulin binding	LGALS3; FCGRT
GO:0004029	0.0012	0.561	32949	176	10	2	MF	aldehyde dehydrogenase (NAD) activity	ALDH3A1; ALDH4A1
GO:0004926	0.0015	0.6833	32949	176	11	2	MF	non-G-protein coupled 7TM receptor activity	FZD2; FZD4
GO:0048037	0.0016	0.7239	32949	176	232	6	MF	cofactor binding	GSR; ACADL; SQLE; IVD; ASNS; ALAS1
GO:0017147	0.0021	0.9622	32949	176	13	2	MF	Wnt-protein binding	FZD4; SFRP2
GO:0019003	0.0021	0.9622	32949	176	13	2	MF	GDP binding	SUCLG2; PRPS1
GO:0019001	0.0021	0.9821	32949	176	333	7	MF	guanyl nucleotide binding	TUBA4A; ADSS; TUBB2C; SUCLG2; PRPS1; EIF5; GUCY1B3
GO:0032561	0.0021	0.9821	32949	176	333	7	MF	guanyl ribonucleotide binding	TUBA4A; ADSS; TUBB2C; SUCLG2; PRPS1; EIF5; GUCY1B3
GO:0016646	0.0024	1	32949	176	14	2	MF	oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor	ALDH4A1; MTHFD2
GO:0002020	0.0024	1	32949	176	14	2	MF	protease binding	F3; HSPA1B
GO:0003995	0.0024	1	32949	176	14	2	MF	acyl-CoA dehydrogenase activity	ACADL; IVD
GO:0005125	0.0024	1	32949	176	174	5	MF	cytokine activity	CXCL12; CXCL16; CCL2; CXCL1; IL1B
GO:0016810	0.0027	1	32949	176	108	4	MF	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	ARG2; AMPD3; MTHFD2; GDA
GO:0016878	0.0028	1	32949	176	15	2	MF	acid-thiol ligase activity	ACSS1; SUCLG2
GO:0042826	0.0028	1	32949	176	15	2	MF	histone deacetylase binding	NRIP1; HIF1A
GO:0043022	0.0028	1	32949	176	15	2	MF	ribosome binding	HSPA5; EIF3C
GO:0030246	0.0028	1	32949	176	350	7	MF	carbohydrate binding	THBS1; LGALS3; CCL2; TALDO1; HK1; PRPS1; GBE1
GO:0043531	0.0036	1	32949	176	17	2	MF	ADP binding	HSPA8; PRPS1
GO:0043548	0.0036	1	32949	176	17	2	MF	phosphoinositide 3-kinase binding	FYN; IRS2
GO:0015038	0.0053	1	32949	176	1	1	MF	glutathione disulfide oxidoreductase activity	GSR
GO:0001567	0.0053	1	32949	176	1	1	MF	cholesterol 25-hydroxylase activity	CH25H
GO:0017172	0.0053	1	32949	176	1	1	MF	cysteine dioxygenase activity	CD01
GO:0019969	0.0053	1	32949	176	1	1	MF	interleukin-10 binding	IL10RB
GO:0019982	0.0053	1	32949	176	1	1	MF	interleukin-7 binding	IL2RG

GO:0030731	0.0053	1	32949	176	1	1	MF	guanidinoacetate N- methyltransferase activity	GAMT
GO:0030881	0.0053	1	32949	176	1	1	MF	beta-2- microglobulin binding	FCGRT
GO:0031699	0.0053	1	32949	176	1	1	MF	beta-3 adrenergic receptor binding	ADRB3
GO:0031748	0.0053	1	32949	176	1	1	MF	D1 dopamine receptor binding	CAV2
GO:0003842	0.0053	1	32949	176	1	1	MF	1-pyrroline-5- carboxylate dehydrogenase activity	ALDH4A1
GO:0003844	0.0053	1	32949	176	1	1	MF	1,4-alpha-glucan branching enzyme activity	GBE1
GO:0003882	0.0053	1	32949	176	1	1	MF	CDP- diacylglycerol- serine O- phosphatidyltran- sferase activity	PTDSS2
GO:0004098	0.0053	1	32949	176	1	1	MF	cerebroside- sulfatase activity	ARSA
GO:0042609	0.0053	1	32949	176	1	1	MF	CD4 receptor binding	FYN
GO:0042610	0.0053	1	32949	176	1	1	MF	CD8 receptor binding	FYN
GO:0004362	0.0053	1	32949	176	1	1	MF	glutathione- disulfide reductase activity	GSR
GO:0004452	0.0053	1	32949	176	1	1	MF	isopentenyl- diphosphate delta-isomerase activity	ID11
GO:0004487	0.0053	1	32949	176	1	1	MF	methylenetetrahy- drofolate dehydrogenase (NAD+) activity	MTHFD2
GO:0004506	0.0053	1	32949	176	1	1	MF	squalene monooxygenase activity	SQLE
GO:0004766	0.0053	1	32949	176	1	1	MF	spermidine synthase activity	SRM
GO:0004801	0.0053	1	32949	176	1	1	MF	transaldolase activity	TALDO1
GO:0004900	0.0053	1	32949	176	1	1	MF	erythropoietin receptor activity	EPOR
GO:0004920	0.0053	1	32949	176	1	1	MF	interleukin-10 receptor activity	IL10RB
GO:0004924	0.0053	1	32949	176	1	1	MF	oncostatin-M receptor activity	OSMR
GO:0004960	0.0053	1	32949	176	1	1	MF	thromboxane receptor activity	TBXA2R
GO:0005121	0.0053	1	32949	176	1	1	MF	Toll binding high affinity inorganic	MYD88
GO:0005316	0.0053	1	32949	176	1	1	MF	phosphate:sodium symporter activity	SLC20A1

GO:0008398	0.0053	1	32949	176	1	1	MF	sterol 14-demethylase activity	CYP51
GO:0008470	0.0053	1	32949	176	1	1	MF	isovaleryl-CoA dehydrogenase activity	IVD
GO:0008892	0.0053	1	32949	176	1	1	MF	guanine deaminase activity	GDA
GO:0005529	0.0054	1	32949	176	209	5	MF	sugar binding	LGALS3; TALD01; HK1; PRPS1; GBE1
GO:0008083	0.006	1	32949	176	135	4	MF	growth factor activity	CXCL12; CXCL1; TGFB1; IL1B
GO:0019239	0.0061	1	32949	176	22	2	MF	deaminase activity	AMPD3; GDA
GO:0004674	0.0064	1	32949	176	407	7	MF	serine/threonine kinase activity	MAPK3; MYLK; MKNK1; CCND3; PIM1; PRKCI; BCR
GO:0016645	0.0066	1	32949	176	23	2	MF	oxidoreductase activity, acting on the CH-NH group of donors	ALDH4A1; MTHFD2
GO:0005525	0.0073	1	32949	176	317	6	MF	GTP binding	TUBA4A; ADSS; TUBB2C; SUCLG2; EIF5; GUCY1B3
GO:0005201	0.0078	1	32949	176	25	2	MF	extracellular matrix structural constituent	COL3A1; COL11A2
GO:0019901	0.0081	1	32949	176	147	4	MF	protein kinase binding	RBCK1; IRS2; CCND3; JUP
GO:0016877	0.0084	1	32949	176	26	2	MF	ligase activity, forming carbon-sulfur bonds	ACSS1; SUCLG2
GO:0035257	0.0097	1	32949	176	28	2	MF	nuclear hormone receptor binding	NRIP1; ETS2
GO:0008134	0.0103	1	32949	176	245	5	MF	transcription factor binding	NRIP1; RELA; PRICKLE1; MYBBP1A; HSPA1B
GO:0016684	0.0104	1	32949	176	29	2	MF	oxidoreductase activity, acting on peroxide as acceptor	GPX2; PTGS2
GO:0004601	0.0104	1	32949	176	29	2	MF	peroxidase activity	GPX2; PTGS2
GO:0010577	0.0106	1	32949	176	2	1	MF	metalloenzyme activator activity	SFRP2
GO:0015037	0.0106	1	32949	176	2	1	MF	peptide disulfide oxidoreductase activity	GSR
GO:0016401	0.0106	1	32949	176	2	1	MF	palmitoyl-CoA oxidase activity	ACADL
GO:0016749	0.0106	1	32949	176	2	1	MF	N-succinyltransferase activity	ALAS1
GO:0001729	0.0106	1	32949	176	2	1	MF	ceramide kinase activity	CERK
GO:0031690	0.0106	1	32949	176	2	1	MF	adrenergic receptor binding	ADRB3
GO:0031727	0.0106	1	32949	176	2	1	MF	CCR2 chemokine receptor binding	CCL2
GO:0003836	0.0106	1	32949	176	2	1	MF	beta-galactoside alpha-2,3-sialyltransferase activity	ST3GAL2
GO:0003870	0.0106	1	32949	176	2	1	MF	5-aminolevulinate synthase activity	ALAS1
GO:0003883	0.0106	1	32949	176	2	1	MF	CTP synthase activity	CTPS

GO:0004019	0.0106	1	32949	176	2	1	MF	adenylosuccinate synthase activity	ADSS
GO:0004053	0.0106	1	32949	176	2	1	MF	arginase activity	ARG2
GO:0004066	0.0106	1	32949	176	2	1	MF	asparagine synthase (glutamine-hydrolyzing) activity	ASNS
GO:0043177	0.0106	1	32949	176	2	1	MF	organic acid binding	HMGCS1
GO:0004340	0.0106	1	32949	176	2	1	MF	glucokinase activity	HK1
GO:0004357	0.0106	1	32949	176	2	1	MF	glutamate-cysteine ligase activity	GCLC
GO:0004392	0.0106	1	32949	176	2	1	MF	heme oxygenase (decyclizing) activity	HMOX1
GO:0004421	0.0106	1	32949	176	2	1	MF	hydroxymethylglutaryl-CoA synthase activity	HMGCS1
GO:0004466	0.0106	1	32949	176	2	1	MF	long-chain-acyl-CoA dehydrogenase activity	ACADL
GO:0004477	0.0106	1	32949	176	2	1	MF	methenyltetrahydrofolate cyclohydrolase activity	MTHFD2
GO:0004486	0.0106	1	32949	176	2	1	MF	methylenetetrahydrofolate dehydrogenase activity	MTHFD2
GO:0004488	0.0106	1	32949	176	2	1	MF	methylenetetrahydrofolate dehydrogenase (NADP+) activity	MTHFD2
GO:0004666	0.0106	1	32949	176	2	1	MF	prostaglandin-endoperoxide synthase activity	PTGS2
GO:0004776	0.0106	1	32949	176	2	1	MF	succinate-CoA ligase (GDP-forming) activity	SUCLG2
GO:0004777	0.0106	1	32949	176	2	1	MF	succinate-semialdehyde dehydrogenase activity	SUCLG2
GO:0048020	0.0106	1	32949	176	2	1	MF	CCR chemokine receptor binding	CCL2
GO:0004910	0.0106	1	32949	176	2	1	MF	interleukin-1, Type II, blocking receptor activity	IL1R2
GO:0004951	0.0106	1	32949	176	2	1	MF	cholecystokinin receptor activity	CCKAR
GO:0004958	0.0106	1	32949	176	2	1	MF	prostaglandin F receptor activity	PTGFR
GO:0005110	0.0106	1	32949	176	2	1	MF	frizzled-2 binding	WNT3A
GO:0016208	0.0119	1	32949	176	31	2	MF	AMP binding	ACSS1; PRPS1

GO:0005509	0.0122	1	32949	176	461	7	MF	calcium ion binding	THBS1; DLL4; CALM3; STAT1; NOTCH2; NOTCH3; CBL
GO:0050662	0.0122	1	32949	176	166	4	MF	coenzyme binding	GSR; ACADL; SQLE; IVD
GO:0043021	0.0142	1	32949	176	34	2	MF	ribonucleoprotein binding	HSPA5; EIF3C
GO:0051219	0.0142	1	32949	176	34	2	MF	phosphoprotein binding	MAPK3; CAV2
GO:0016879	0.0149	1	32949	176	176	4	MF	ligase activity, forming carbon-nitrogen bonds	ADSS; CTPS; ASNS; GCLC
GO:0003705	0.0158	1	32949	176	36	2	MF	RNA polymerase II transcription factor activity, enhancer binding	RELA; GATA5
GO:0016748	0.0159	1	32949	176	3	1	MF	succinyltransferase activity	ALAS1
GO:0019976	0.0159	1	32949	176	3	1	MF	interleukin-2 binding	IL2RG
GO:0033300	0.0159	1	32949	176	3	1	MF	dehydroascorbic acid transporter activity	SLC2A1
GO:0003876	0.0159	1	32949	176	3	1	MF	AMP deaminase activity	AMPD3
GO:0003987	0.0159	1	32949	176	3	1	MF	acetate-CoA ligase activity	ACSS1
GO:0004566	0.0159	1	32949	176	3	1	MF	beta-glucuronidase activity	AFP
GO:0004687	0.0159	1	32949	176	3	1	MF	myosin light chain kinase activity	MYLK
GO:0004939	0.0159	1	32949	176	3	1	MF	beta-adrenergic receptor activity	ADRB3
GO:0051379	0.0159	1	32949	176	3	1	MF	epinephrine binding	ADRB3
GO:0051380	0.0159	1	32949	176	3	1	MF	norepinephrine binding	ADRB3
GO:0051787	0.0159	1	32949	176	3	1	MF	misfolded protein binding	HSPA5
GO:0005315	0.0159	1	32949	176	3	1	MF	inorganic phosphate transmembrane transporter activity	SLC20A1
GO:0005436	0.0159	1	32949	176	3	1	MF	sodium:phosphate symporter activity	SLC20A1
GO:0061133	0.0159	1	32949	176	3	1	MF	endopeptidase activator activity	SFRP2
GO:0016787	0.0171	1	32949	176	2099	19	MF	hydrolase activity	TUBA4A; IDI1; ARG2; NT5C2; AFP; PPAP2B; PDE4B; TUBB2C; HSPA8; DUSP16; AMPD3; SENP2; HMOX1; PLA2G7; ARSA; PPA1; MTHFD2; GDA; GBE1
GO:0004888	0.0182	1	32949	176	1967	18	MF	transmembrane receptor activity	TEK; FZD2; FZD4; IL10RB; CXCL16; EPOR; CCKAR; OSMR; IL1R2; MYD88; PTGFR; EPHA2; CCR1; TIE1; KDR; TBXA2R; CSF3R; ADRB3
GO:0016744	0.0211	1	32949	176	4	1	MF	transferase activity, transferring aldehyde or ketonic groups	TALD01
GO:0004065	0.0211	1	32949	176	4	1	MF	arylsulfatase activity	ARSA
GO:0042910	0.0211	1	32949	176	4	1	MF	xenobiotic transporter activity	SLC2A1

GO:0004427	0.0211	1	32949	176	4	1	MF	inorganic diphosphatase activity	PPA1
GO:0004749	0.0211	1	32949	176	4	1	MF	ribose phosphate diphosphokinase activity	PRPS1
GO:0004774	0.0211	1	32949	176	4	1	MF	succinate-CoA ligase activity	SUCLG2
GO:0055056	0.0211	1	32949	176	4	1	MF	D-glucose transmembrane transporter activity	SLC2A1
GO:0008198	0.0211	1	32949	176	4	1	MF	ferrous iron binding	CD01
GO:0000287	0.0239	1	32949	176	115	3	MF	magnesium ion binding	ADSS; PRPS1; PPA1
GO:0005516	0.0239	1	32949	176	115	3	MF	calmodulin binding	SPNB2; MYLK; ADD1
GO:0016627	0.0251	1	32949	176	46	2	MF	oxidoreductase activity, acting on the CH-CH group of donors phosphoric ester hydrolase activity	ACADL; IVD
GO:0042578	0.0255	1	32949	176	309	5	MF	diphosphotransferase activity	NT5C2; PPAP2B; PDE4B; DUSP16; HMOX1
GO:0016778	0.0264	1	32949	176	5	1	MF	cyclohydrolase activity	PRPS1
GO:0019238	0.0264	1	32949	176	5	1	MF	IgE binding	MTHFD2
GO:0019863	0.0264	1	32949	176	5	1	MF	IgG binding	LGALS3
GO:0019864	0.0264	1	32949	176	5	1	MF	1-alkyl-2-acetylglycerophosphocholine esterase activity	FCGRT
GO:0003847	0.0264	1	32949	176	5	1	MF	acyl-CoA oxidase activity	PLA2G7
GO:0003997	0.0264	1	32949	176	5	1	MF	RPTP-like protein binding	ACADL
GO:0042153	0.0264	1	32949	176	5	1	MF	fructose-bisphosphate aldolase activity	JUP
GO:0004332	0.0264	1	32949	176	5	1	MF	transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	ALDOA
GO:0046912	0.0264	1	32949	176	5	1	MF	nitric-oxide synthase binding	HMGCS1
GO:0050998	0.0264	1	32949	176	5	1	MF	Notch binding	ARG2
GO:0005112	0.0264	1	32949	176	5	1	MF	Hsp90 protein binding	DLL4
GO:0051879	0.0264	1	32949	176	5	1	MF	peptide binding	GUCY1B3
GO:0042277	0.0277	1	32949	176	213	4	MF	monosaccharide binding	CCKAR; GSR; CCR1; GSTA2
GO:0048029	0.0315	1	32949	176	52	2	MF	oxidoreductase activity, acting on sulfur group of donors, NAD or NADP as acceptor	TALDO1; HK1
GO:0016668	0.0316	1	32949	176	6	1	MF		GSR

GO:0017169	0.0316	1	32949	176	6	1	MF	CDP-alcohol phosphatidyltran sferase activity	PTDSS2
GO:0035035	0.0316	1	32949	176	6	1	MF	histone acetyltransferas e binding	SP1
GO:0035259	0.0316	1	32949	176	6	1	MF	glucocorticoid receptor binding	ETS2
GO:0042577	0.0316	1	32949	176	6	1	MF	lipid phosphatase activity	PPAP2B
GO:0043130	0.0316	1	32949	176	6	1	MF	ubiquitin binding	HSPB1
GO:0004396	0.0316	1	32949	176	6	1	MF	hexokinase activity	HK1
GO:0051059	0.0316	1	32949	176	6	1	MF	NF-kappaB binding	HSPA1B
GO:0019966	0.0368	1	32949	176	7	1	MF	interleukin-1 binding	IL1R2
GO:0004028	0.0368	1	32949	176	7	1	MF	3-chloroallyl aldehyde dehydrogenase activity	ALDH3A1
GO:0004630	0.0368	1	32949	176	7	1	MF	phospholipase D activity	HMOX1
GO:0004908	0.0368	1	32949	176	7	1	MF	interleukin-1 receptor activity	IL1R2
GO:0005021	0.0368	1	32949	176	7	1	MF	vascular endothelial growth factor receptor activity	KDR
GO:0005041	0.0368	1	32949	176	7	1	MF	low-density lipoprotein receptor activity	CXCL16
GO:0050811	0.0368	1	32949	176	7	1	MF	GABA receptor binding	ATF4
GO:0005149	0.0368	1	32949	176	7	1	MF	interleukin-1 receptor binding	IL1B
GO:0008144	0.0397	1	32949	176	59	2	MF	drug binding	HMGCS1; GSTA2
GO:0031683	0.0419	1	32949	176	8	1	MF	G-protein beta/gamma- subunit binding	ADCY2
GO:0032182	0.0419	1	32949	176	8	1	MF	small conjugating protein binding	HSPB1
GO:0003810	0.0419	1	32949	176	8	1	MF	protein- glutamine gamma- glutamyltransfer ase activity	TGM1
GO:0048551	0.0419	1	32949	176	8	1	MF	metalloenzyme inhibitor activity	TIMP1
GO:0004955	0.0419	1	32949	176	8	1	MF	prostaglandin receptor activity	PTGFR
GO:0051428	0.0419	1	32949	176	8	1	MF	peptide hormone receptor binding	FYN
GO:0008191	0.0419	1	32949	176	8	1	MF	metalloendopepti dase inhibitor activity	TIMP1
GO:0008601	0.0419	1	32949	176	8	1	MF	protein phosphatase type 2A regulator activity	PPP2R2A
GO:0008047	0.0428	1	32949	176	245	4	MF	enzyme activator activity	AGFG2; RGS3; SFRP2; BCR

GO:0015114	0.047	1	32949	176	9	1	MF	phosphate transmembrane transporter activity	SLC20A1
GO:0016832	0.047	1	32949	176	9	1	MF	aldehyde-lyase activity	ALDOA
GO:0016884	0.047	1	32949	176	9	1	MF	carbon-nitrogen ligase activity, with glutamine as amido-N-donor	ASNS
GO:0004032	0.047	1	32949	176	9	1	MF	aldehyde reductase activity	AKR1B8
GO:0046965	0.047	1	32949	176	9	1	MF	retinoid X receptor binding	NR1P1
GO:0004935	0.047	1	32949	176	9	1	MF	adrenoceptor activity	ADRB3
GO:0008253	0.047	1	32949	176	9	1	MF	5'-nucleotidase activity	NT5C2

Supplementary Table `KEGG Enrichment analysis'

HBC pathway enrichment

HCV-induced HCC							
Pathway ID	Pathway Term	P-value	T	Q	Q&T	Q&T/Q	Q&T/T
KEGG:05200	Pathways in cancer	3.65E-17	332	599	66	0.166	0.199
KEGG:04310	Wnt signaling pathway	2.61E-06	156	599	29	0.073	0.186
KEGG:05202	Transcriptional misregulation in cancer	9.98E-06	185	598	31	0.078	0.168
KEGG:05217	Basal cell carcinoma	3.78E-05	55	599	15	0.038	0.273
KEGG:04350	TGF-beta signaling pathway	7.75E-05	91	484	17	0.054	0.187
KEGG:05166	HTLV-I infection	1.42E-04	381	609	47	0.117	0.123
KEGG:05221	Acute myeloid leukemia	1.78E-04	57	566	14	0.037	0.246
KEGG:05160	Hepatitis C	2.25E-04	141	560	23	0.062	0.163
KEGG:04916	Melanogenesis	4.60E-04	101	538	18	0.05	0.178
KEGG:04722	Neurotrophin signaling pathway	5.80E-04	126	573	21	0.056	0.167
KEGG:04620	Toll-like receptor signaling pathway	6.33E-04	109	417	16	0.059	0.147
KEGG:05210	Colorectal cancer	1.03E-03	62	599	14	0.035	0.226
KEGG:04114	Oocyte meiosis	1.18E-03	112	519	18	0.052	0.161
KEGG:05212	Pancreatic cancer	2.24E-03	70	498	13	0.04	0.186
KEGG:00230	Purine metabolism	2.89E-03	171	575	24	0.063	0.14
KEGG:05142	Chagas disease (American trypanosomiasis)	4.92E-03	111	484	16	0.051	0.144
KEGG:00740	Riboflavin metabolism	1.56E-02	12	101	3	0.045	0.25
KEGG:05216	Thyroid cancer	2.18E-02	34	398	7	0.027	0.206
KEGG:05215	Prostate cancer	2.68E-02	88	560	14	0.038	0.159
KEGG:04012	ErbB signaling pathway	2.99E-02	88	566	14	0.037	0.159
KEGG:05162	Measles	3.11E-02	154	566	20	0.053	0.13
KEGG:04912	GnRH signaling pathway	3.57E-02	101	560	15	0.04	0.149
KEGG:04010	MAPK signaling pathway	3.70E-02	296	609	33	0.082	0.111

Lung injury pathway enrichment

Phosgene-induced Lung Injury							
Pathway ID	Pathway Term	P-value	T	Q	Q&T	Q&T/Q	Q&T/T
KEGG:05166	HTLV-I infection	1.29E-07	277	169	24	0.167	0.087
KEGG:05200	Pathways in cancer	8.16E-05	323	162	21	0.153	0.065
KEGG:04725	Cholinergic synapse	1.03E-04	110	67	8	0.151	0.073
KEGG:05140	Leishmaniasis	3.20E-04	66	161	9	0.066	0.136
KEGG:04912	GnRH signaling pathway	5.16E-04	97	67	7	0.132	0.072
KEGG:04062	Chemokine signaling pathway	5.79E-04	186	114	12	0.125	0.065
KEGG:04010	MAPK signaling pathway	1.79E-03	269	165	17	0.121	0.063
KEGG:05020	Prion diseases	3.47E-03	35	161	6	0.044	0.171
KEGG:04916	Melanogenesis	3.96E-03	99	146	9	0.073	0.091
KEGG:04723	Retrograde endocannabinoid signaling	5.80E-03	97	67	6	0.113	0.062
KEGG:04380	Osteoclast differentiation	6.13E-03	117	161	10	0.074	0.085
KEGG:05134	Legionellosis	8.99E-03	57	165	7	0.05	0.123
KEGG:04976	Bile secretion	1.28E-02	71	67	5	0.094	0.07
KEGG:04971	Gastric acid secretion	1.36E-02	72	67	5	0.094	0.069
KEGG:04310	Wnt signaling pathway	2.20E-02	151	146	10	0.081	0.066
KEGG:04350	TGF-beta signaling pathway	2.59E-02	84	133	7	0.062	0.083
KEGG:04540	Gap junction	3.22E-02	87	172	8	0.054	0.092
KEGG:00480	Glutathione metabolism	3.49E-02	50	168	6	0.042	0.12
KEGG:05210	Colorectal cancer	4.25E-02	64	93	5	0.066	0.078
KEGG:05132	Salmonella infection	4.92E-02	77	161	7	0.051	0.091
KEGG:05219	Bladder cancer	4.96E-02	42	37	3	0.1	0.071