Supplementary Table S1. Classification results for biological process by GO analysis.

Term	Count	*p*-value
immune response	30	2.34E-14
inflammatory response	21	3.06E-08
cellular response to lipopolysaccharide	12	1.10E-07
response to drug	18	1.54E-07
platelet degranulation	11	4.33E-07
positive regulation of T cell proliferation	9	5.50E-07
folic acid metabolic process	6	1.76E-06
cytokine-mediated signalling pathway	11	3.96E-06
acute-phase response	7	6.41E-06
response to estrogen	8	1.23E-05
positive regulation of osteoclast differentiation	5	6.71E-05
positive regulation of gene expression	13	7.75E-05
tumor necrosis factor-mediated signalling pathway	9	8.71E-05
leukocyte migration	9	1.10E-04
positive regulation of JAK-STAT cascade	5	1.23E-04
positive regulation of nitric oxide biosynthetic process	6	1.56E-04
positive regulation of cell proliferation	17	1.60E-04
apoptotic process	19	1.65E-04
leukocyte cell-cell adhesion	5	2.07E-04
response to ethanol	8	2.68E-04
signal transduction	29	3.04E-04
negative regulation of inflammatory response	7	3.67E-04
cell surface receptor signalling pathway	12	4.76E-04
cellular protein metabolic process	8	5.45E-04
humoral immune response	6	5.91E-04
glucose transport	5	6.21E-04
positive regulation of transcription from RNA polymerase II promoter	25	6.91E-04
negative regulation of extrinsic apoptotic signalling pathway in absence of ligand	5	9.66E-04
positive regulation of tyrosine phosphorylation of Stat3 protein	5	1.07E-03
response to glucocorticoid	6	1.08E-03
positive regulation of phosphatidylinositol 3-kinase signalling	6	1.08E-03
negative regulation of apoptotic process	15	1.18E-03
positive regulation of B cell proliferation	5	1.18E-03
glucose metabolic process	6	1.24E-03
regulation of immune response	9	1.38E-03
positive regulation of DNA replication	5	1.56E-03
interferon-gamma-mediated signalling pathway	6	1.61E-03
positive regulation of sequence-specific DNA binding transcription factor activity	7	1.65E-03
blood coagulation	9	1.70E-03
negative regulation of catalytic activity	6	2.05E-03
phagocytosis	5	2.57E-03
positive regulation of peptidyl-tyrosine phosphorylation	6	3.03E-03
negative regulation of endopeptidase activity	7	3.36E-03
aging	8	3.76E-03
positive regulation of fibroblast proliferation	5	3.95E-03
MAPK cascade	10	4.39E-03
cellular defense response	5	6.47E-03
integrin-mediated signalling pathway	6	6.74E-03
neutrophil chemotaxis	5	8.06E-03
adaptive immune response	7	8.84E-03
extracellular matrix organisation	8	9.39E-03
cellular response to mechanical stimulus	5	1.04E-02
circadian rhythm	5	1.25E-02
cellular response to DNA damage stimulus	8	1.28E-02
negative regulation of transcription from RNA polymerase II promoter	17	1.30E-02
cellular response to insulin stimulus	5	1.37E-02
response to lipopolysaccharide	7	1.42E-02
defense response to virus	7	1.46E-02

Term	Count	*p*-value
viral entry into host cell	5	1.55E-02
wound healing	5	1.55E-02
negative regulation of transcription, DNA-templated	13	1.72E-02
positive regulation of protein kinase B signalling	5	1.83E-02
defense response to Gram-positive bacterium	5	1.90E-02
response to estradiol	5	2.38E-02
regulation of cell proliferation	7	2.41E-02
transforming growth factor beta receptor signalling pathway	5	2.46E-02
cell cycle arrest	6	2.74E-02
viral process	9	2.79E-02
defense response to bacterium	6	3.04E-02
G1/S transition of mitotic cell cycle	5	3.42E-02
activation of MAPK activity	5	3.97E-02
cell cycle	7	4.67E-02
negative regulation of cell proliferation	10	4.92E-02
positive regulation of angiogenesis	5	4.94E-02
cell adhesion	11	5.01E-02
angiogenesis	7	5.20E-02
response to hypoxia	6	5.60E-02
positive regulation of protein phosphorylation	5	6.63E-02
receptor-mediated endocytosis	6	7.31E-02
cell proliferation	9	7.32E-02
innate immune response	10	7.45E-02
positive regulation of NF-kappa B transcription factor activity	5	7.58E-02
negative regulation of gene expression	5	8.24E-02
cell-cell signalling	7	8.48E-02
transcription from RNA polymerase II promoter	11	8.89E-02

Supplementary Table S2. Classification results for cellular component by GO analysis.

Term	Count	*p*-value
extracellular space	57	1.51E-18
external side of plasma membrane	19	2.97E-11
extracellular region	47	1.87E-09
extracellular exosome	64	1.52E-08
plasma membrane	76	2.44E-06
integral component of plasma membrane	36	6.35E-06
cell surface	20	1.08E-05
platelet alpha granule lumen	7	3.27E-05
membrane	44	1.53E-04
cytosol	57	6.04E-04
collagen trimer	6	3.67E-03
caveola	5	5.96E-03
blood microparticle	7	7.18E-03
proteinaceous extracellular matrix	9	1.04E-02
receptor complex	6	1.39E-02
basolateral plasma membrane	7	1.56E-02
focal adhesion	10	3.14E-02
intermediate filament	5	3.77E-02
perinuclear region of cytoplasm	12	8.79E-02
protein complex	9	9.02E-02
cytoplasm	68	9.79E-02

Supplementary Table S3. Classification results for molecular function by GO analysis.

Term	Count	*p*-value
cytokine activity	22	1.95E-15
protease binding	10	3.13E-06
enzyme binding	15	4.48E-05
glycoprotein binding	7	1.19E-04
protein binding	129	3.92E-04
growth factor activity	9	7.04E-04
identical protein binding	20	1.49E-03
protein phosphatase binding	5	6.61E-03
virus receptor activity	5	9.54E-03
Ras guanyl-nucleotide exchange factor activity	6	1.19E-02
transmembrane signalling receptor activity	8	1.40E-02
receptor activity	8	1.50E-02
transcription factor binding	9	2.01E-02
protein tyrosine kinase activity	6	2.11E-02
transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	8	2.26E-02
RNA polymerase II core promoter proximal region sequence-specific DNA binding	10	2.58E-02
serine-type endopeptidase inhibitor activity	5	2.82E-02
carbohydrate binding	7	2.95E-02
histone deacetylase binding	5	3.31E-02
protein complex binding	7	3.60E-02
receptor binding	9	5.96E-02
kinase activity	7	6.75E-02
hydrolase activity	6	7.72E-02
protein homodimerisation activity	14	9.42E-02

Supplementary Table S4. Gene pathway enrichment analysis.

Term	Count	*p*-value
Cytokine-cytokine receptor interaction	32	1.81E-16
Jak-STAT signalling pathway	22	1.94E-12
Osteoclast differentiation	18	1.68E-09
Haematopoietic cell lineage	15	2.88E-09
Pertussis	14	4.25E-09
Tuberculosis	20	4.51E-09
Leishmaniasis	13	2.32E-08
Rheumatoid arthritis	12	2.13E-06
Influenza A	16	3.59E-06
Measles	14	4.17E-06
Inflammatory bowel disease (IBD)	10	6.96E-06
Malaria	9	7.34E-06
TNF signalling pathway	12	1.46E-05
Non-alcoholic fatty liver disease (NAFLD)	14	1.68E-05
Chagas disease (American trypanosomiasis)	11	6.47E-05
Toll-like receptor signalling pathway	11	7.61E-05
Transcriptional misregulation in cancer	13	2.07E-04
Salmonella infection	9	3.49E-04
Amoebiasis	10	3.90E-04
Hepatitis C	11	4.95E-04
Prolactin signalling pathway	8	7.18E-04
One carbon pool by folate	5	7.24E-04
Hepatitis B	11	9.74E-04
Epstein-Barr virus infection	10	1.09E-03
T cell receptor signalling pathway	9	1.22E-03
Herpes simplex infection	12	1.69E-03
Colorectal cancer	7	1.91E-03
Toxoplasmosis	9	2.25E-03
PI3K-Akt signalling pathway	17	2.53E-03
Prostate cancer	8	2.54E-03
HTLV-I infection	14	2.78E-03
Fc epsilon RI signalling pathway	7	3.06E-03
Adipocytokine signalling pathway	7	3.54E-03
Natural killer cell mediated cytotoxicity	9	4.26E-03
Phagosome	10	4.48E-03
African trypanosomiasis	5	4.94E-03
Staphylococcus aureus infection	6	5.51E-03
NF-kappa B signalling pathway	7	1.02E-02
Cell adhesion molecules (CAMs)	9	1.04E-02
Bladder cancer	5	1.07E-02
Type I diabetes mellitus	5	1.17E-02
Pancreatic cancer	6	1.20E-02
Sphingolipid signalling pathway	8	1.36E-02
RIG-I-like receptor signalling pathway	6	1.61E-02
MAPK signalling pathway	12	1.84E-02
Endometrial cancer	5	2.40E-02
Legionellosis	5	2.71E-02
NOD-like receptor signalling pathway	5	3.05E-02
ErbB signalling pathway	6	3.71E-02
Pathways in cancer	15	3.88E-02
Neurotrophin signalling pathway	7	4.19E-02
Shigellosis	5	4.64E-02
Glioma	5	4.87E-02
HIF-1 signalling pathway	6	5.29E-02
Bile secretion	5	5.83E-02
Proteoglycans in cancer	9	6.21E-02
Melanoma	5	6.35E-02
FoxO signalling pathway	7	6.50E-02
Chronic myeloid leukaemia	5	6.62E-02
Rap1 signalling pathway	9	7.77E-02