

Table S1. Significantly enriched KEGG pathways identified from GSE119296

| Term ID       | Term description                                | ES    | p-value | FDR   | Classification level |
|---------------|-------------------------------------------------|-------|---------|-------|----------------------|
| path:hsa05144 | Malaria                                         | 5.316 | 0.000   | 0.000 | Human Diseases       |
| path:hsa05150 | Staphylococcus aureus infection                 | 4.781 | 0.000   | 0.000 | Human Diseases       |
| path:hsa00524 | Neomycin, kanamycin and gentamicin biosynthesis | 4.736 | 0.060   | 0.233 | Metabolism           |
| path:hsa05143 | African trypanosomiasis                         | 4.179 | 0.000   | 0.000 | Human Diseases       |
| path:hsa05323 | Rheumatoid arthritis                            | 3.993 | 0.000   | 0.000 | Human Diseases       |
| path:hsa04657 | IL-17 signaling pathway                         | 3.947 | 0.000   | 0.000 | Organismal Systems   |
| path:hsa05134 | Legionellosis                                   | 3.660 | 0.000   | 0.000 | Human Diseases       |
| path:hsa04380 | Osteoclast differentiation                      | 3.599 | 0.000   | 0.000 | Organismal Systems   |
| path:hsa05140 | Leishmaniasis                                   | 3.552 | 0.000   | 0.000 | Human Diseases       |
| path:hsa05020 | Prion diseases                                  | 3.482 | 0.000   | 0.003 | Human Diseases       |

\*ES: Enrichment score.

Table S2. The significantly enriched KEGG pathway from GSEA

| Pathway                                           | Size | ES    | NES   | p-value | FDR   |
|---------------------------------------------------|------|-------|-------|---------|-------|
| KEGG_PATHWAYS_IN_CANCER                           | 313  | 0.537 | 1.930 | 0.000   | 0.001 |
| KEGG_MAPK_SIGNALING_PATHWAY                       | 249  | 0.549 | 1.950 | 0.000   | 0.001 |
| KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION       | 222  | 0.722 | 2.550 | 0.000   | 0.001 |
| KEGG_FOCAL_ADHESION                               | 197  | 0.527 | 1.846 | 0.000   | 0.001 |
| KEGG_CHEMOKINE_SIGNALING_PATHWAY                  | 173  | 0.638 | 2.218 | 0.000   | 0.001 |
| KEGG_JAK_STAT_SIGNALING_PATHWAY                   | 127  | 0.641 | 2.167 | 0.000   | 0.001 |
| KEGG_CELL_CYCLE                                   | 124  | 0.648 | 2.187 | 0.000   | 0.001 |
| KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY    | 115  | 0.602 | 2.018 | 0.000   | 0.001 |
| KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS                 | 111  | 0.658 | 2.198 | 0.000   | 0.001 |
| KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY            | 103  | 0.660 | 2.183 | 0.000   | 0.001 |
| KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY         | 89   | 0.697 | 2.270 | 0.000   | 0.001 |
| KEGG_ECM_RECEPTOR_INTERACTION                     | 83   | 0.655 | 2.110 | 0.000   | 0.001 |
| KEGG_HEMATOPOIETIC_CELL_LINEAGE                   | 81   | 0.756 | 2.426 | 0.000   | 0.001 |
| KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY            | 73   | 0.634 | 2.004 | 0.000   | 0.001 |
| KEGG_P53_SIGNALING_PATHWAY                        | 68   | 0.703 | 2.204 | 0.000   | 0.001 |
| KEGG_LEISHMANIA_INFECTION                         | 67   | 0.752 | 2.351 | 0.000   | 0.001 |
| KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY          | 61   | 0.759 | 2.335 | 0.000   | 0.001 |
| KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION | 40   | 0.728 | 2.090 | 0.000   | 0.001 |
| KEGG_GRAFT_VERSUS_HOST_DISEASE                    | 34   | 0.738 | 2.057 | 0.000   | 0.001 |
| KEGG_ASTHMA                                       | 22   | 0.773 | 1.977 | 0.000   | 0.001 |
| KEGG_CELL_ADHESION_MOLECULES_CAMS                 | 124  | 0.534 | 1.801 | 0.000   | 0.001 |
| KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY              | 71   | 0.598 | 1.888 | 0.000   | 0.001 |
| KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY                | 41   | 0.702 | 2.023 | 0.000   | 0.001 |

|                                                                 |     |       |       |       |       |
|-----------------------------------------------------------------|-----|-------|-------|-------|-------|
| KEGG_PRION_DISEASES                                             | 35  | 0.734 | 2.057 | 0.000 | 0.001 |
| KEGG_WNT_SIGNALING_PATHWAY                                      | 145 | 0.499 | 1.710 | 0.000 | 0.002 |
| KEGG_SMALL_CELL_LUNG_CANCER                                     | 83  | 0.572 | 1.842 | 0.000 | 0.002 |
| KEGG_BLADDER_CANCER                                             | 42  | 0.689 | 1.994 | 0.000 | 0.002 |
| KEGG_PRIMARY_IMMUNODEFICIENCY                                   | 33  | 0.698 | 1.937 | 0.000 | 0.002 |
| KEGG_COLORECTAL_CANCER                                          | 61  | 0.610 | 1.877 | 0.001 | 0.002 |
| KEGG_ALLOGRAFT_REJECTION                                        | 32  | 0.692 | 1.908 | 0.001 | 0.002 |
| KEGG_APOPTOSIS                                                  | 85  | 0.567 | 1.833 | 0.001 | 0.002 |
| KEGG_COMPLEMENT_AND_COAGULATION_CASCADES                        | 67  | 0.590 | 1.845 | 0.001 | 0.002 |
| KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION                       | 109 | 0.516 | 1.720 | 0.001 | 0.003 |
| KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION                        | 66  | 0.577 | 1.803 | 0.001 | 0.003 |
| KEGG_TYPE_I_DIABETES_MELLITUS                                   | 38  | 0.656 | 1.865 | 0.001 | 0.004 |
| KEGG_ERBB_SIGNALING_PATHWAY                                     | 84  | 0.534 | 1.725 | 0.002 | 0.007 |
| KEGG_AXON_GUIDANCE                                              | 127 | 0.483 | 1.634 | 0.002 | 0.007 |
| KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION | 67  | 0.553 | 1.729 | 0.002 | 0.007 |
| KEGG_VEGF_SIGNALING_PATHWAY                                     | 70  | 0.549 | 1.731 | 0.003 | 0.007 |
| KEGG_AUTOIMMUNE_THYROID_DISEASE                                 | 35  | 0.626 | 1.754 | 0.004 | 0.010 |
| KEGG_PANCREATIC_CANCER                                          | 69  | 0.539 | 1.697 | 0.004 | 0.010 |
| KEGG_TGF_BETA_SIGNALING_PATHWAY                                 | 83  | 0.519 | 1.674 | 0.004 | 0.011 |
| KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION                      | 53  | 0.569 | 1.715 | 0.004 | 0.011 |
| KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS                           | 94  | 0.495 | 1.623 | 0.006 | 0.014 |
| KEGG_PROSTATE_CANCER                                            | 86  | 0.505 | 1.636 | 0.006 | 0.015 |
| KEGG_SULFUR_METABOLISM                                          | 11  | 0.777 | 1.720 | 0.008 | 0.018 |
| KEGG_ENDOCYTOSIS                                                | 178 | 0.424 | 1.475 | 0.009 | 0.020 |
| KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY                      | 58  | 0.528 | 1.612 | 0.010 | 0.024 |
| KEGG_CHRONIC_MYELOID_LEUKEMIA                                   | 70  | 0.504 | 1.587 | 0.013 | 0.028 |

|                                       |     |       |       |       |       |
|---------------------------------------|-----|-------|-------|-------|-------|
| KEGG_REGULATION_OF_ACTIN_CYTOSKELETON | 202 | 0.401 | 1.406 | 0.015 | 0.031 |
|---------------------------------------|-----|-------|-------|-------|-------|

\* |NES|>1, p-value<0.05, FDR <0.05. ES: Enrichment Score; NES: Normalized Enrichment Score.

Table S3. The Differentially Expressed immune-related Genes identified from GSE39488

| Gene symbol | log <sub>2</sub> FC | p-value  | adjusted p-value |
|-------------|---------------------|----------|------------------|
| RXFP1       | -4.7766248          | 1.07E-08 | 0.000475         |
| INHBA       | -2.8706021          | 3.21E-07 | 0.001311         |
| THBS1       | -2.3760704          | 1.80E-06 | 0.004207         |
| NR4A3       | -5.2127667          | 5.58E-06 | 0.011084         |
| NR4A2       | -3.8415928          | 1.53E-05 | 0.01796          |
| OLR1        | -3.4160306          | 2.16E-05 | 0.020621         |
| TNFRSF12A   | -3.1166232          | 1.87E-05 | 0.020621         |
| SEMA7A      | -2.458311           | 3.20E-05 | 0.025897         |
| NR4A1       | -4.5912152          | 6.03E-05 | 0.029007         |
| CCL3        | -3.9904548          | 7.69E-05 | 0.029007         |
| CCL4        | -3.7178843          | 5.56E-05 | 0.029007         |
| FGF1        | -3.6000121          | 5.71E-05 | 0.029007         |
| TNFRSF11B   | -2.7638094          | 6.70E-05 | 0.029007         |
| CXCR4       | -2.3881324          | 6.03E-05 | 0.029007         |
| COLEC10     | -2.3644935          | 4.76E-05 | 0.029007         |
| SEMA6A      | 2.2601163           | 6.14E-05 | 0.029007         |
| APOD        | 2.8287472           | 4.70E-05 | 0.029007         |
| SEMA3E      | 2.855126            | 5.25E-05 | 0.029007         |
| NR0B1       | 3.6520038           | 6.08E-05 | 0.029007         |
| IL1RL1      | -3.7121008          | 9.03E-05 | 0.030862         |
| DUOX1       | -2.1943481          | 1.23E-04 | 0.033925         |
| FOS         | -5.2871904          | 2.20E-04 | 0.047366         |
| CRABP1      | -5.0200705          | 2.66E-04 | 0.051549         |
| SHC4        | -1.9991193          | 3.23E-04 | 0.058679         |
| CCL3L3      | -2.5973182          | 3.99E-04 | 0.064609         |
| TUBB3       | -3.4364145          | 4.29E-04 | 0.065792         |
| ADIPOQ      | 3.5256836           | 5.01E-04 | 0.069396         |
| JUN         | -2.4152134          | 5.09E-04 | 0.069916         |
| IL6         | -4.9159673          | 5.46E-04 | 0.072476         |
| S100B       | 2.8308815           | 5.51E-04 | 0.072951         |
| HSPA8       | -2.7939115          | 5.92E-04 | 0.076321         |
| OSM         | -3.3344492          | 7.12E-04 | 0.084763         |
| OXTR        | -3.2593101          | 7.35E-04 | 0.085346         |
| OASL        | -1.5995352          | 7.33E-04 | 0.085346         |
| PCSK2       | 3.5280364           | 7.86E-04 | 0.089014         |
| PTGS2       | -2.5668869          | 8.25E-04 | 0.091969         |
| IL1B        | -3.8062436          | 8.55E-04 | 0.094113         |