Supplementary Material

# Supplementary Tables

Supplementary Table 1 Summary of the patient data sets

|  |  |  |
| --- | --- | --- |
| **Variable** | **TCGA set (n=571)** | **ICGC set (n=411)** |
| Age |  |  |
| <=55 years | 112 | 146 |
| >55 years | 457 | 265 |
| Gender |  |  |
| Female | 271 | 154 |
| Male | 298 | 257 |
| TNM stage |  |  |
| I/II | 316 | 137 |
| III/IV | 241 | 192 |
| Family history |  |  |
| No | N/A | 172 |
| Yes | N/A | 23 |

Supplementary Table 2 Clinical characteristics of patients

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| No | Surgery time | sex | age | Distant metastasis | grade | Survival status |
| 1 | 2019.08 | M | 47 | No | II | Alive |
| 2 | 2019.07 | F | 56 | No | III | Alive |
| 3 | 2020.02 | M | 75 | No | II | Alive |
| 4 | 2021.01 | M | 65 | No | II | Alive |
| 5 | 2021.01 | M | 66 | No | II | Alive |
| 6 | 2021.01 | M | 78 | No | II-III | Alive |
| 7 | 2021.03 | F | 56 | No | II | Alive |
| 8 | 2021.03 | F | 75 | No | II | Alive |
| 9 | 2021.03 | F | 49 | No | III | Alive |
| 10 | 2021.03 | F | 56 | No | II | Alive |
| 11 | 2021.03 | F | 54 | No | II | Alive |
| 12 | 2021.04 | F | 55 | No | II | Alive |
| 13 | 2021.04 | M | 65 | No | III | Alive |
| 14 | 2021.04 | M | 61 | No | II-III | Alive |
| 15 | 2021.04 | M | 57 | No | II | Alive |
| 16 | 2021.04 | M | 71 | No | II | Alive |
| 17 | 2021.05 | F | 78 | No | II | Alive |
| 18 | 2021.05 | F | 86 | No | II | Alive |
| 19 | 2021.05 | F | 75 | No | III | Alive |
| 20 | 2021.05 | F | 68 | No | III | Alive |
| 21 | 2021.05 | M | 77 | No | II-III | Alive |
| 22 | 2021.05 | M | 67 | No | II | Alive |
| 23 | 2021.06 | M | 87 | No | II | Alive |
| 24 | 2021.06 | F | 65 | No | II | Alive |
| 25 | 2021.06 | F | 47 | No | III | Alive |
| 26 | 2021.06 | M | 39 | No | II | Alive |
| 27 | 2021.06 | F | 76 | No | II | Alive |
| 28 | 2021.06 | M | 65 | No | III | Alive |
| 29 | 2021.09 | M | 55 | No | II-III | Alive |
| 30 | 2021.09 | M | 43 | No | II | Alive |

Supplementary Table 3 Gene ontology (GO) enrichment analysis results

|  |  |  |  |
| --- | --- | --- | --- |
| **ONTOLOGY** | **ID** | **Description** | **pvalue** |
| BP | GO:0060579 | ventral spinal cord interneuron fate commitment | 4.19E-05 |
| BP | GO:0060581 | cell fate commitment involved in pattern specification | 4.19E-05 |
| BP | GO:0021514 | ventral spinal cord interneuron differentiation | 5.93E-05 |
| BP | GO:0021513 | spinal cord dorsal/ventral patterning | 0.000103158 |
| BP | GO:0021511 | spinal cord patterning | 0.000129568 |
| BP | GO:0048665 | neuron fate specification | 0.00026483 |
| BP | GO:0021517 | ventral spinal cord development | 0.000675563 |
| BP | GO:0021515 | cell differentiation in spinal cord | 0.00087701 |
| BP | GO:0048663 | neuron fate commitment | 0.00126925 |
| BP | GO:0019731 | antibacterial humoral response | 0.00135609 |
| BP | GO:0009953 | dorsal/ventral pattern formation | 0.002149973 |
| BP | GO:0001708 | cell fate specification | 0.00279642 |
| BP | GO:0021510 | spinal cord development | 0.003523176 |
| BP | GO:0019730 | antimicrobial humoral response | 0.007107361 |
| BP | GO:0072503 | cellular divalent inorganic cation homeostasis | 0.008537753 |
| BP | GO:1900003 | regulation of serine-type endopeptidase activity | 0.008978497 |
| BP | GO:1902571 | regulation of serine-type peptidase activity | 0.008978497 |
| BP | GO:0072507 | divalent inorganic cation homeostasis | 0.009493425 |
| BP | GO:0051673 | membrane disruption in other organism | 0.009872162 |
| BP | GO:0021953 | central nervous system neuron differentiation | 0.010973333 |
| BP | GO:0010950 | positive regulation of endopeptidase activity | 0.011449289 |
| BP | GO:0010469 | regulation of signaling receptor activity | 0.012180162 |
| BP | GO:0045986 | negative regulation of smooth muscle contraction | 0.012548607 |
| BP | GO:0010273 | detoxification of copper ion | 0.013439241 |
| BP | GO:0050965 | detection of temperature stimulus involved in sensory perception of pain | 0.013439241 |
| BP | GO:1990169 | stress response to copper ion | 0.013439241 |
| BP | GO:0010952 | positive regulation of peptidase activity | 0.013702114 |
| BP | GO:0045779 | negative regulation of bone resorption | 0.01432912 |
| BP | GO:0098962 | regulation of postsynaptic neurotransmitter receptor activity | 0.01432912 |
| BP | GO:0003085 | negative regulation of systemic arterial blood pressure | 0.015218242 |
| BP | GO:0050961 | detection of temperature stimulus involved in sensory perception | 0.015218242 |
| BP | GO:0061687 | detoxification of inorganic compound | 0.015218242 |
| BP | GO:0046851 | negative regulation of bone remodeling | 0.01610661 |
| BP | GO:0097501 | stress response to metal ion | 0.01610661 |
| BP | GO:1901317 | regulation of flagellated sperm motility | 0.01610661 |
| BP | GO:0002089 | lens morphogenesis in camera-type eye | 0.016994223 |
| BP | GO:0030595 | leukocyte chemotaxis | 0.017268016 |
| BP | GO:0098657 | import into cell | 0.017848403 |
| BP | GO:0034104 | negative regulation of tissue remodeling | 0.017881083 |
| BP | GO:0098703 | calcium ion import across plasma membrane | 0.017881083 |
| BP | GO:0016048 | detection of temperature stimulus | 0.01876719 |
| BP | GO:0099633 | protein localization to postsynaptic specialization membrane | 0.01876719 |
| BP | GO:0099645 | neurotransmitter receptor localization to postsynaptic specialization membrane | 0.01876719 |
| BP | GO:1902656 | calcium ion import into cytosol | 0.01876719 |
| BP | GO:0045932 | negative regulation of muscle contraction | 0.019652544 |
| ...... | ...... | ...... | ...... |
| MF | GO:0005245 | voltage-gated calcium channel activity | 0.040035247 |
| MF | GO:0005246 | calcium channel regulator activity | 0.040927359 |

Supplementary Table 4 Kyoto encyclopedia of genes and genomes (KEGG) pathway enrichment analysis results

|  |  |  |  |
| --- | --- | --- | --- |
| **ONTOLOGY** | **ID** | **Description** | **pvalue** |
| KEGG | hsa04978 | Mineral absorption | 0.001107509 |

Supplementary Table 5 Gene set enrichment analysis (GSEA) results

|  |  |  |  |
| --- | --- | --- | --- |
| **ID** | **Description** | **ES** | **pvalue** |
| GOBP\_ACTIVATION\_OF\_IMMUNE\_RESPONSE | GOBP\_ACTIVATION\_OF\_IMMUNE\_RESPONSE | 0.481040126 | 1.00E-10 |
| GOBP\_ADAPTIVE\_IMMUNE\_RESPONSE | GOBP\_ADAPTIVE\_IMMUNE\_RESPONSE | 0.587030859 | 1.00E-10 |
| GOBP\_CELLULAR\_RESPONSE\_TO\_BIOTIC\_STIMULUS | GOBP\_CELLULAR\_RESPONSE\_TO\_BIOTIC\_STIMULUS | 0.548753591 | 1.00E-10 |
| GOBP\_CELLULAR\_RESPONSE\_TO\_MOLECULE\_OF\_BACTERIAL\_ORIGIN | GOBP\_CELLULAR\_RESPONSE\_TO\_MOLECULE\_OF\_BACTERIAL\_ORIGIN | 0.571637353 | 1.00E-10 |
| GOBP\_DEFENSE\_RESPONSE\_TO\_VIRUS | GOBP\_DEFENSE\_RESPONSE\_TO\_VIRUS | 0.561784184 | 1.00E-10 |
| GOBP\_IMMUNE\_RESPONSE\_REGULATING\_SIGNALING\_PATHWAY | GOBP\_IMMUNE\_RESPONSE\_REGULATING\_SIGNALING\_PATHWAY | 0.540155261 | 1.00E-10 |
| GOBP\_LEUKOCYTE\_CELL\_CELL\_ADHESION | GOBP\_LEUKOCYTE\_CELL\_CELL\_ADHESION | 0.519606562 | 1.00E-10 |
| GOBP\_LYMPHOCYTE\_MEDIATED\_IMMUNITY | GOBP\_LYMPHOCYTE\_MEDIATED\_IMMUNITY | 0.543857772 | 1.00E-10 |
| GOBP\_MONONUCLEAR\_CELL\_DIFFERENTIATION | GOBP\_MONONUCLEAR\_CELL\_DIFFERENTIATION | 0.471540255 | 1.00E-10 |
| GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_ACTIVATION | GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_ACTIVATION | 0.540004301 | 1.00E-10 |
| GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_KILLING | GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_KILLING | 0.769125456 | 1.00E-10 |
| GOBP\_POSITIVE\_REGULATION\_OF\_CYTOKINE\_PRODUCTION | GOBP\_POSITIVE\_REGULATION\_OF\_CYTOKINE\_PRODUCTION | 0.536088881 | 1.00E-10 |
| GOBP\_POSITIVE\_REGULATION\_OF\_DEFENSE\_RESPONSE | GOBP\_POSITIVE\_REGULATION\_OF\_DEFENSE\_RESPONSE | 0.510039364 | 1.00E-10 |
| GOBP\_POSITIVE\_REGULATION\_OF\_IMMUNE\_EFFECTOR\_PROCESS | GOBP\_POSITIVE\_REGULATION\_OF\_IMMUNE\_EFFECTOR\_PROCESS | 0.615469149 | 1.00E-10 |
| GOBP\_POSITIVE\_REGULATION\_OF\_LEUKOCYTE\_CELL\_CELL\_ADHESION | GOBP\_POSITIVE\_REGULATION\_OF\_LEUKOCYTE\_CELL\_CELL\_ADHESION | 0.564403241 | 1.00E-10 |
| GOBP\_POSITIVE\_REGULATION\_OF\_LEUKOCYTE\_MEDIATED\_IMMUNITY | GOBP\_POSITIVE\_REGULATION\_OF\_LEUKOCYTE\_MEDIATED\_IMMUNITY | 0.667432752 | 1.00E-10 |
| GOBP\_POSITIVE\_REGULATION\_OF\_RESPONSE\_TO\_EXTERNAL\_STIMULUS | GOBP\_POSITIVE\_REGULATION\_OF\_RESPONSE\_TO\_EXTERNAL\_STIMULUS | 0.446023446 | 1.00E-10 |
| GOBP\_REGULATION\_OF\_CELL\_KILLING | GOBP\_REGULATION\_OF\_CELL\_KILLING | 0.727449803 | 1.00E-10 |
| GOBP\_REGULATION\_OF\_IMMUNE\_EFFECTOR\_PROCESS | GOBP\_REGULATION\_OF\_IMMUNE\_EFFECTOR\_PROCESS | 0.52518087 | 1.00E-10 |
| GOBP\_REGULATION\_OF\_INNATE\_IMMUNE\_RESPONSE | GOBP\_REGULATION\_OF\_INNATE\_IMMUNE\_RESPONSE | 0.505032349 | 1.00E-10 |
| GOBP\_REGULATION\_OF\_LEUKOCYTE\_MEDIATED\_CYTOTOXICITY | GOBP\_REGULATION\_OF\_LEUKOCYTE\_MEDIATED\_CYTOTOXICITY | 0.725373256 | 1.00E-10 |
| GOBP\_REGULATION\_OF\_LEUKOCYTE\_MEDIATED\_IMMUNITY | GOBP\_REGULATION\_OF\_LEUKOCYTE\_MEDIATED\_IMMUNITY | 0.627244932 | 1.00E-10 |
| GOBP\_REGULATION\_OF\_LYMPHOCYTE\_ACTIVATION | GOBP\_REGULATION\_OF\_LYMPHOCYTE\_ACTIVATION | 0.515211802 | 1.00E-10 |
| GOBP\_REGULATION\_OF\_LYMPHOCYTE\_MEDIATED\_IMMUNITY | GOBP\_REGULATION\_OF\_LYMPHOCYTE\_MEDIATED\_IMMUNITY | 0.628974716 | 1.00E-10 |
| GOBP\_REGULATION\_OF\_RESPONSE\_TO\_BIOTIC\_STIMULUS | GOBP\_REGULATION\_OF\_RESPONSE\_TO\_BIOTIC\_STIMULUS | 0.50038285 | 1.00E-10 |
| GOBP\_REGULATION\_OF\_T\_CELL\_ACTIVATION | GOBP\_REGULATION\_OF\_T\_CELL\_ACTIVATION | 0.550177305 | 1.00E-10 |
| GOBP\_RESPONSE\_TO\_INTERFERON\_GAMMA | GOBP\_RESPONSE\_TO\_INTERFERON\_GAMMA | 0.635122975 | 1.00E-10 |
| GOBP\_RESPONSE\_TO\_VIRUS | GOBP\_RESPONSE\_TO\_VIRUS | 0.528741345 | 1.00E-10 |
| GOBP\_T\_CELL\_ACTIVATION | GOBP\_T\_CELL\_ACTIVATION | 0.512581995 | 1.00E-10 |
| GOMF\_CYTOKINE\_RECEPTOR\_BINDING | GOMF\_CYTOKINE\_RECEPTOR\_BINDING | 0.573447303 | 1.00E-10 |
| GOBP\_LEUKOCYTE\_PROLIFERATION | GOBP\_LEUKOCYTE\_PROLIFERATION | 0.501712504 | 1.57E-10 |
| GOBP\_GRANULOCYTE\_CHEMOTAXIS | GOBP\_GRANULOCYTE\_CHEMOTAXIS | 0.647050719 | 2.41E-10 |
| GOBP\_REGULATION\_OF\_LEUKOCYTE\_DIFFERENTIATION | GOBP\_REGULATION\_OF\_LEUKOCYTE\_DIFFERENTIATION | 0.499161209 | 4.79E-10 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_IMMUNE\_SYSTEM\_PROCESS | GOBP\_NEGATIVE\_REGULATION\_OF\_IMMUNE\_SYSTEM\_PROCESS | 0.454912593 | 6.12E-10 |
| GOBP\_ANTIGEN\_RECEPTOR\_MEDIATED\_SIGNALING\_PATHWAY | GOBP\_ANTIGEN\_RECEPTOR\_MEDIATED\_SIGNALING\_PATHWAY | 0.520105704 | 1.02E-09 |
| GOBP\_T\_CELL\_ACTIVATION\_INVOLVED\_IN\_IMMUNE\_RESPONSE | GOBP\_T\_CELL\_ACTIVATION\_INVOLVED\_IN\_IMMUNE\_RESPONSE | 0.648171635 | 1.08E-09 |
| GOBP\_REGULATION\_OF\_CELL\_CELL\_ADHESION | GOBP\_REGULATION\_OF\_CELL\_CELL\_ADHESION | 0.439340174 | 1.35E-09 |
| GOBP\_LEUKOCYTE\_MEDIATED\_CYTOTOXICITY | GOBP\_LEUKOCYTE\_MEDIATED\_CYTOTOXICITY | 0.645960608 | 1.41E-09 |
| GOBP\_T\_CELL\_PROLIFERATION | GOBP\_T\_CELL\_PROLIFERATION | 0.552886532 | 1.51E-09 |
| GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_CELL\_ADHESION | GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_CELL\_ADHESION | 0.499802691 | 1.65E-09 |
| GOBP\_POSITIVE\_REGULATION\_OF\_RESPONSE\_TO\_BIOTIC\_STIMULUS | GOBP\_POSITIVE\_REGULATION\_OF\_RESPONSE\_TO\_BIOTIC\_STIMULUS | 0.512332465 | 1.74E-09 |
| GOBP\_NEUTROPHIL\_CHEMOTAXIS | GOBP\_NEUTROPHIL\_CHEMOTAXIS | 0.659590885 | 1.81E-09 |
| GOBP\_GRANULOCYTE\_MIGRATION | GOBP\_GRANULOCYTE\_MIGRATION | 0.595305731 | 1.90E-09 |
| GOBP\_RESPONSE\_TO\_MOLECULE\_OF\_BACTERIAL\_ORIGIN | GOBP\_RESPONSE\_TO\_MOLECULE\_OF\_BACTERIAL\_ORIGIN | 0.476131546 | 2.23E-09 |
| GOBP\_T\_CELL\_DIFFERENTIATION | GOBP\_T\_CELL\_DIFFERENTIATION | 0.507608769 | 2.35E-09 |
| GOBP\_LYMPHOCYTE\_ACTIVATION\_INVOLVED\_IN\_IMMUNE\_RESPONSE | GOBP\_LYMPHOCYTE\_ACTIVATION\_INVOLVED\_IN\_IMMUNE\_RESPONSE | 0.551275411 | 2.45E-09 |
| GOBP\_CELL\_KILLING | GOBP\_CELL\_KILLING | 0.558031567 | 2.61E-09 |
| GOBP\_REGULATION\_OF\_ADAPTIVE\_IMMUNE\_RESPONSE | GOBP\_REGULATION\_OF\_ADAPTIVE\_IMMUNE\_RESPONSE | 0.575885277 | 2.73E-09 |
| GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_ADHESION | GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_ADHESION | 0.438472412 | 4.39E-09 |
| GOBP\_ADAPTIVE\_IMMUNE\_RESPONSE\_BASED\_ON\_SOMATIC\_RECOMBINATION\_OF\_IMMUNE\_RECEPTORS\_BUILT\_FROM\_IMMUNOGLOBULIN\_SUPERFAMILY\_DOMAINS | GOBP\_ADAPTIVE\_IMMUNE\_RESPONSE\_BASED\_ON\_SOMATIC\_RECOMBINATION\_OF\_IMMUNE\_RECEPTORS\_BUILT\_FROM\_IMMUNOGLOBULIN\_SUPERFAMILY\_DOMAINS | 0.502223515 | 4.80E-09 |
| GOBP\_REGULATION\_OF\_NATURAL\_KILLER\_CELL\_MEDIATED\_IMMUNITY | GOBP\_REGULATION\_OF\_NATURAL\_KILLER\_CELL\_MEDIATED\_IMMUNITY | 0.774983187 | 5.05E-09 |
| GOBP\_REGULATION\_OF\_LEUKOCYTE\_PROLIFERATION | GOBP\_REGULATION\_OF\_LEUKOCYTE\_PROLIFERATION | 0.515621737 | 6.08E-09 |
| GOCC\_TERTIARY\_GRANULE\_MEMBRANE | GOCC\_TERTIARY\_GRANULE\_MEMBRANE | 0.700972623 | 6.61E-09 |
| GOBP\_MYELOID\_LEUKOCYTE\_MIGRATION | GOBP\_MYELOID\_LEUKOCYTE\_MIGRATION | 0.518414977 | 7.06E-09 |
| GOBP\_MACROPHAGE\_ACTIVATION | GOBP\_MACROPHAGE\_ACTIVATION | 0.645537183 | 1.01E-08 |
| GOBP\_REGULATION\_OF\_LYMPHOCYTE\_DIFFERENTIATION | GOBP\_REGULATION\_OF\_LYMPHOCYTE\_DIFFERENTIATION | 0.542082813 | 1.42E-08 |
| GOBP\_REGULATION\_OF\_T\_CELL\_MEDIATED\_IMMUNITY | GOBP\_REGULATION\_OF\_T\_CELL\_MEDIATED\_IMMUNITY | 0.683170682 | 1.58E-08 |
| GOBP\_REGULATION\_OF\_HEMOPOIESIS | GOBP\_REGULATION\_OF\_HEMOPOIESIS | 0.443674334 | 2.00E-08 |
| GOMF\_CYTOKINE\_ACTIVITY | GOMF\_CYTOKINE\_ACTIVITY | 0.503491276 | 2.08E-08 |
| GOBP\_NATURAL\_KILLER\_CELL\_MEDIATED\_IMMUNITY | GOBP\_NATURAL\_KILLER\_CELL\_MEDIATED\_IMMUNITY | 0.706699416 | 2.27E-08 |
| GOBP\_REGULATION\_OF\_INFLAMMATORY\_RESPONSE | GOBP\_REGULATION\_OF\_INFLAMMATORY\_RESPONSE | 0.457251793 | 2.72E-08 |
| GOBP\_POSITIVE\_REGULATION\_OF\_T\_CELL\_PROLIFERATION | GOBP\_POSITIVE\_REGULATION\_OF\_T\_CELL\_PROLIFERATION | 0.637992047 | 2.73E-08 |
| GOBP\_NEUTROPHIL\_MIGRATION | GOBP\_NEUTROPHIL\_MIGRATION | 0.594461044 | 3.46E-08 |
| GOBP\_T\_CELL\_RECEPTOR\_SIGNALING\_PATHWAY | GOBP\_T\_CELL\_RECEPTOR\_SIGNALING\_PATHWAY | 0.519746664 | 4.62E-08 |
| GOBP\_RESPONSE\_TO\_CHEMOKINE | GOBP\_RESPONSE\_TO\_CHEMOKINE | 0.643650361 | 4.89E-08 |
| GOBP\_ALPHA\_BETA\_T\_CELL\_ACTIVATION | GOBP\_ALPHA\_BETA\_T\_CELL\_ACTIVATION | 0.551481005 | 5.73E-08 |
| GOBP\_LYMPHOCYTE\_COSTIMULATION | GOBP\_LYMPHOCYTE\_COSTIMULATION | 0.702661195 | 6.69E-08 |
| GOBP\_CELL\_CHEMOTAXIS | GOBP\_CELL\_CHEMOTAXIS | 0.461064107 | 7.01E-08 |
| GOCC\_TERTIARY\_GRANULE | GOCC\_TERTIARY\_GRANULE | 0.540452316 | 7.90E-08 |
| GOMF\_CARBOHYDRATE\_BINDING | GOMF\_CARBOHYDRATE\_BINDING | 0.475012466 | 8.22E-08 |
| GOBP\_T\_CELL\_MEDIATED\_IMMUNITY | GOBP\_T\_CELL\_MEDIATED\_IMMUNITY | 0.620861717 | 8.37E-08 |
| GOBP\_POSITIVE\_REGULATION\_OF\_LEUKOCYTE\_PROLIFERATION | GOBP\_POSITIVE\_REGULATION\_OF\_LEUKOCYTE\_PROLIFERATION | 0.557450306 | 8.50E-08 |
| GOCC\_SPECIFIC\_GRANULE | GOCC\_SPECIFIC\_GRANULE | 0.543575877 | 8.57E-08 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_CYTOKINE\_PRODUCTION | GOBP\_NEGATIVE\_REGULATION\_OF\_CYTOKINE\_PRODUCTION | 0.458848787 | 1.13E-07 |
| GOBP\_INTERLEUKIN\_10\_PRODUCTION | GOBP\_INTERLEUKIN\_10\_PRODUCTION | 0.71693402 | 1.31E-07 |
| GOBP\_NEGATIVE\_REGULATION\_OF\_LYMPHOCYTE\_ACTIVATION | GOBP\_NEGATIVE\_REGULATION\_OF\_LYMPHOCYTE\_ACTIVATION | 0.547922545 | 1.47E-07 |
| GOBP\_REGULATION\_OF\_PRODUCTION\_OF\_MOLECULAR\_MEDIATOR\_OF\_IMMUNE\_RESPONSE | GOBP\_REGULATION\_OF\_PRODUCTION\_OF\_MOLECULAR\_MEDIATOR\_OF\_IMMUNE\_RESPONSE | 0.558045472 | 1.79E-07 |
| GOBP\_ANTIGEN\_PROCESSING\_AND\_PRESENTATION | GOBP\_ANTIGEN\_PROCESSING\_AND\_PRESENTATION | 0.474672287 | 1.96E-07 |
| GOBP\_T\_CELL\_DIFFERENTIATION\_INVOLVED\_IN\_IMMUNE\_RESPONSE | GOBP\_T\_CELL\_DIFFERENTIATION\_INVOLVED\_IN\_IMMUNE\_RESPONSE | 0.665250864 | 2.10E-07 |
| GOBP\_RESPONSE\_TO\_INTERLEUKIN\_1 | GOBP\_RESPONSE\_TO\_INTERLEUKIN\_1 | 0.502553968 | 2.14E-07 |
| GOBP\_LEUKOCYTE\_CHEMOTAXIS | GOBP\_LEUKOCYTE\_CHEMOTAXIS | 0.487535083 | 2.58E-07 |
| KEGG\_CYTOKINE\_CYTOKINE\_RECEPTOR\_INTERACTION | KEGG\_CYTOKINE\_CYTOKINE\_RECEPTOR\_INTERACTION | 0.608427149 | 1.00E-10 |
| KEGG\_GRAFT\_VERSUS\_HOST\_DISEASE | KEGG\_GRAFT\_VERSUS\_HOST\_DISEASE | 0.862923716 | 1.00E-10 |
| KEGG\_LEISHMANIA\_INFECTION | KEGG\_LEISHMANIA\_INFECTION | 0.758405915 | 1.00E-10 |
| KEGG\_NATURAL\_KILLER\_CELL\_MEDIATED\_CYTOTOXICITY | KEGG\_NATURAL\_KILLER\_CELL\_MEDIATED\_CYTOTOXICITY | 0.657605486 | 1.00E-10 |
| KEGG\_AUTOIMMUNE\_THYROID\_DISEASE | KEGG\_AUTOIMMUNE\_THYROID\_DISEASE | 0.784756822 | 2.81E-10 |
| KEGG\_ANTIGEN\_PROCESSING\_AND\_PRESENTATION | KEGG\_ANTIGEN\_PROCESSING\_AND\_PRESENTATION | 0.709700093 | 3.44E-10 |
| KEGG\_ALLOGRAFT\_REJECTION | KEGG\_ALLOGRAFT\_REJECTION | 0.817545161 | 8.57E-09 |
| KEGG\_JAK\_STAT\_SIGNALING\_PATHWAY | KEGG\_JAK\_STAT\_SIGNALING\_PATHWAY | 0.557752819 | 4.84E-08 |
| KEGG\_TYPE\_I\_DIABETES\_MELLITUS | KEGG\_TYPE\_I\_DIABETES\_MELLITUS | 0.767252821 | 1.38E-07 |
| KEGG\_HEMATOPOIETIC\_CELL\_LINEAGE | KEGG\_HEMATOPOIETIC\_CELL\_LINEAGE | 0.640939891 | 2.58E-07 |
| KEGG\_TOLL\_LIKE\_RECEPTOR\_SIGNALING\_PATHWAY | KEGG\_TOLL\_LIKE\_RECEPTOR\_SIGNALING\_PATHWAY | 0.590851081 | 1.57E-06 |
| KEGG\_INTESTINAL\_IMMUNE\_NETWORK\_FOR\_IGA\_PRODUCTION | KEGG\_INTESTINAL\_IMMUNE\_NETWORK\_FOR\_IGA\_PRODUCTION | 0.710031497 | 4.27E-06 |
| KEGG\_T\_CELL\_RECEPTOR\_SIGNALING\_PATHWAY | KEGG\_T\_CELL\_RECEPTOR\_SIGNALING\_PATHWAY | 0.562096607 | 5.30E-06 |
| KEGG\_NOD\_LIKE\_RECEPTOR\_SIGNALING\_PATHWAY | KEGG\_NOD\_LIKE\_RECEPTOR\_SIGNALING\_PATHWAY | 0.644651389 | 6.23E-06 |
| KEGG\_CHEMOKINE\_SIGNALING\_PATHWAY | KEGG\_CHEMOKINE\_SIGNALING\_PATHWAY | 0.47920795 | 9.82E-06 |
| KEGG\_VIRAL\_MYOCARDITIS | KEGG\_VIRAL\_MYOCARDITIS | 0.588697799 | 0.000127359 |
| KEGG\_CYTOSOLIC\_DNA\_SENSING\_PATHWAY | KEGG\_CYTOSOLIC\_DNA\_SENSING\_PATHWAY | 0.610343228 | 0.000314609 |
| KEGG\_SYSTEMIC\_LUPUS\_ERYTHEMATOSUS | KEGG\_SYSTEMIC\_LUPUS\_ERYTHEMATOSUS | 0.468892976 | 0.000544072 |
| KEGG\_ASTHMA | KEGG\_ASTHMA | 0.701699002 | 0.000803964 |
| KEGG\_PROTEASOME | KEGG\_PROTEASOME | 0.566365784 | 0.005889591 |
| KEGG\_APOPTOSIS | KEGG\_APOPTOSIS | 0.439162267 | 0.012496112 |
| KEGG\_CELL\_ADHESION\_MOLECULES\_CAMS | KEGG\_CELL\_ADHESION\_MOLECULES\_CAMS | 0.39265717 | 0.015860685 |
| KEGG\_DRUG\_METABOLISM\_CYTOCHROME\_P450 | KEGG\_DRUG\_METABOLISM\_CYTOCHROME\_P450 | -0.516236023 | 0.01894448 |
| KEGG\_AMINO\_SUGAR\_AND\_NUCLEOTIDE\_SUGAR\_METABOLISM | KEGG\_AMINO\_SUGAR\_AND\_NUCLEOTIDE\_SUGAR\_METABOLISM | 0.525229807 | 0.019942025 |
| KEGG\_BETA\_ALANINE\_METABOLISM | KEGG\_BETA\_ALANINE\_METABOLISM | 0.604589484 | 0.020544798 |
| KEGG\_CARDIAC\_MUSCLE\_CONTRACTION | KEGG\_CARDIAC\_MUSCLE\_CONTRACTION | -0.500445004 | 0.023749889 |
| KEGG\_CALCIUM\_SIGNALING\_PATHWAY | KEGG\_CALCIUM\_SIGNALING\_PATHWAY | -0.429804361 | 0.024273753 |
| KEGG\_TASTE\_TRANSDUCTION | KEGG\_TASTE\_TRANSDUCTION | -0.55177169 | 0.025171261 |
| KEGG\_CELL\_CYCLE | KEGG\_CELL\_CYCLE | 0.405760594 | 0.025283159 |
| KEGG\_METABOLISM\_OF\_XENOBIOTICS\_BY\_CYTOCHROME\_P450 | KEGG\_METABOLISM\_OF\_XENOBIOTICS\_BY\_CYTOCHROME\_P450 | -0.509572164 | 0.032618241 |
| KEGG\_TYROSINE\_METABOLISM | KEGG\_TYROSINE\_METABOLISM | -0.558891966 | 0.033488385 |
| KEGG\_DILATED\_CARDIOMYOPATHY | KEGG\_DILATED\_CARDIOMYOPATHY | -0.479294048 | 0.034626039 |
| KEGG\_FC\_GAMMA\_R\_MEDIATED\_PHAGOCYTOSIS | KEGG\_FC\_GAMMA\_R\_MEDIATED\_PHAGOCYTOSIS | 0.40238421 | 0.039209455 |
| KEGG\_NEUROACTIVE\_LIGAND\_RECEPTOR\_INTERACTION | KEGG\_NEUROACTIVE\_LIGAND\_RECEPTOR\_INTERACTION | -0.391981772 | 0.041176471 |