S7 Table. Gene Set Enrichment Analysis (GSEA) categories enriched among transcript isoforms under-expressed (FDR-adjusted P-value < 0.05 and > 10 transcript isoforms) and over- expressed (P-value < 0.01 and > 10 transcript isoforms) in microglia relative to peripheral macrophages in BCG-challenged mice.

|  |  |  |  |
| --- | --- | --- | --- |
| Categories  | NG1  |  P-value | FDR2 |
| Under-expressed in microglia vs macrophages |
| ADAPTIVE\_IMMUNE\_RESPONSE | 21 | 0.00E+00 | 0.00E+00 |
| ADAPTIVE\_IMMUNE\_RESPONSE\_GO\_0002460 | 20 | 0.00E+00 | 0.00E+00 |
| POSITIVE\_REGULATION\_OF\_IMMUNE\_RESPONSE | 20 | 0.00E+00 | 0.00E+00 |
| REGULATION\_OF\_IMMUNE\_RESPONSE | 22 | 0.00E+00 | 0.00E+00 |
| REGULATION\_OF\_IMMUNE\_SYSTEM\_PROCESS | 46 | 0.00E+00 | 1.05E-03 |
| CHEMOKINE\_RECEPTOR\_BINDING | 28 | 0.00E+00 | 1.18E-03 |
| POSITIVE\_REGULATION\_OF\_IMMUNE\_SYSTEM\_PROCESS | 37 | 0.00E+00 | 1.34E-03 |
| POSITIVE\_REGULATION\_OF\_RESPONSE\_TO\_STIMULUS | 27 | 0.00E+00 | 1.57E-03 |
| KEGG\_PRIMARY\_IMMUNODEFICIENCY | 30 | 0.00E+00 | 1.88E-03 |
| KEGG\_RIBOSOME | 81 | 0.00E+00 | 1.90E-03 |
| REGULATION\_OF\_LYMPHOCYTE\_ACTIVATION | 28 | 0.00E+00 | 2.07E-03 |
| CELLULAR\_DEFENSE\_RESPONSE | 38 | 0.00E+00 | 2.28E-03 |
| LYMPHOCYTE\_ACTIVATION | 47 | 0.00E+00 | 3.78E-03 |
| G\_PROTEIN\_COUPLED\_RECEPTOR\_BINDING | 35 | 0.00E+00 | 4.34E-03 |
| CHEMOKINE\_ACTIVITY | 27 | 0.00E+00 | 4.62E-03 |
| POSITIVE\_REGULATION\_OF\_MULTICELLULAR\_ORGANISMAL\_PROCESS | 47 | 0.00E+00 | 4.63E-03 |
| CYTOKINE\_ACTIVITY | 61 | 0.00E+00 | 6.65E-03 |
| B\_CELL\_ACTIVATION | 18 | 0.00E+00 | 7.59E-03 |
| LOCOMOTORY\_BEHAVIOR | 61 | 0.00E+00 | 8.08E-03 |
| LEUKOCYTE\_ACTIVATION | 51 | 0.00E+00 | 8.95E-03 |
| KEGG\_HEMATOPOIETIC\_CELL\_LINEAGE | 52 | 0.00E+00 | 9.40E-03 |
| G1\_S\_TRANSITION\_OF\_MITOTIC\_CELL\_CYCLE | 26 | 0.00E+00 | 1.07E-02 |
| CYTOKINE\_AND\_CHEMOKINE\_MEDIATED\_SIGNALING\_PATHWAY | 15 | 1.45E-02 | 1.35E-02 |
| CELL\_ACTIVATION | 54 | 0.00E+00 | 1.36E-02 |
| REGULATION\_OF\_T\_CELL\_ACTIVATION | 22 | 0.00E+00 | 1.40E-02 |
| T\_CELL\_ACTIVATION | 32 | 0.00E+00 | 1.46E-02 |
| REGULATION\_OF\_RESPONSE\_TO\_STIMULUS | 35 | 0.00E+00 | 1.80E-02 |
| IMMUNE\_EFFECTOR\_PROCESS | 23 | 2.70E-02 | 1.82E-02 |
| POSITIVE\_REGULATION\_OF\_LYMPHOCYTE\_ACTIVATION | 20 | 0.00E+00 | 2.35E-02 |
| CYTOKINE\_METABOLIC\_PROCESS | 31 | 0.00E+00 | 2.40E-02 |
| Over-expressed in microglia vs macrophages |
| BRAIN\_DEVELOPMENT | 25 | 0.00E+00 | 2.73E-02 |
| CENTRAL\_NERVOUS\_SYSTEM\_DEVELOPMENT | 62 | 0.00E+00 | 3.35E-02 |
| POTASSIUM\_ION\_TRANSPORT | 21 | 0.00E+00 | 4.81E-02 |
| PHOSPHATASE\_REGULATOR\_ACTIVITY | 202 | 0.00E+00 | 1.93E-01 |
| POTASSIUM\_CHANNEL\_ACTIVITY | 246 | 0.00E+00 | 3.54E-01 |
| VOLTAGE\_GATED\_CATION\_CHANNEL\_ACTIVITY | 107 | 0.00E+00 | 3.67E-01 |
| PATTERN\_SPECIFICATION\_PROCESS | 146 | 0.00E+00 | 3.84E-01 |
| NERVOUS\_SYSTEM\_DEVELOPMENT | 179 | 0.00E+00 | 3.86E-01 |
| TRANSFORMING\_GROWTH\_FACTOR\_BETA\_RECEPTOR\_SIGNALING\_PATHWAY | 208 | 0.00E+00 | 3.94E-01 |
| VOLTAGE\_GATED\_CHANNEL\_ACTIVITY | 100 | 1.00E-03 | 3.67E-01 |
| KEGG\_TIGHT\_JUNCTION | 88 | 2.00E-03 | 3.51E-01 |
| METAL\_ION\_TRANSMEMBRANE\_TRANSPORTER\_ACTIVITY | 125 | 3.00E-03 | 3.77E-01 |
| SYSTEM\_PROCESS | 23 | 3.17E-03 | 6.77E-02 |
| TRANSMISSION\_OF\_NERVE\_IMPULSE | 29 | 6.20E-03 | 2.55E-01 |
| CATION\_TRANSMEMBRANE\_TRANSPORTER\_ACTIVITY | 27 | 6.24E-03 | 1.88E-01 |
| ENZYME\_LINKED\_RECEPTOR\_PROTEIN\_SIGNALING\_PATHWAY | 64 | 7.04E-03 | 3.53E-01 |
| SYNAPTIC\_TRANSMISSION | 59 | 7.04E-03 | 3.68E-01 |
| KEGG\_AXON\_GUIDANCE | 80 | 8.01E-03 | 3.74E-01 |
| KEGG\_VASCULAR\_SMOOTH\_MUSCLE\_CONTRACTION | 93 | 8.02E-03 | 3.74E-01 |
| ION\_TRANSMEMBRANE\_TRANSPORTER\_ACTIVITY | 69 | 8.04E-03 | 3.65E-01 |
| NEUROLOGICAL\_SYSTEM\_PROCESS | 17 | 8.62E-03 | 7.99E-02 |
| SUBSTRATE\_SPECIFIC\_TRANSMEMBRANE\_TRANSPORTER\_ACTIVITY | 31 | 9.25E-03 | 2.51E-01 |
| SUBSTRATE\_SPECIFIC\_TRANSPORTER\_ACTIVITY | 19 | 9.64E-03 | 1.90E-01 |

 1 NG: number of genes.

 2 FDR: adjusted P-value.