Table S1. Go analysis of 303 overlapping DEGs.

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| --- | --- | --- | --- |
| Category | Term | Count | FDR |
| MF | receptor activity | 19 | <0.001 |
| transmembrane signaling receptor activity | 17 | <0.001 |
| chemokine activity | 8 | 0.014 |
| C-C chemokine receptor activity | 5 | 0.036 |
| CC | integral component of plasma membrane | 71 | <0.001 |
| external side of plasma membrane | 29 | <0.001 |
| extracellular region | 69 | <0.001 |
| extracellular space | 55 | <0.001 |
| plasma membrane | 111 | <0.001 |
| extracellular exosome | 76 | 0.004 |
| BP | immune response | 49 | <0.001 |
| inflammatory response | 40 | <0.001 |
| adaptive immune response | 24 | <0.001 |
| innate immune response | 35 | <0.001 |
| cell surface receptor signaling pathway | 27 | <0.001 |
| chemotaxis | 18 | <0.001 |
| regulation of immune response | 20 | <0.001 |
| positive regulation of T cell proliferation | 13 | <0.001 |
| signal transduction | 50 | <0.001 |
| chemokine-mediated signaling pathway | 13 | <0.001 |
| cellular defense response | 12 | <0.001 |
| B cell receptor signaling pathway | 11 | <0.001 |
| positive regulation of ERK1 and ERK2 cascade | 16 | <0.001 |
| cell-cell signaling | 19 | <0.001 |
| dendritic cell chemotaxis | 7 | <0.001 |
| positive regulation of cytosolic calcium ion concentration | 14 | <0.001 |
| T cell costimulation | 10 | 0.007 |
| leukocyte migration | 12 | 0.007 |
| positive regulation of interferon-gamma production | 8 | 0.014 |
| cellular response to lipopolysaccharide | 11 | 0.025 |
| negative regulation of T cell proliferation | 7 | 0.043 |
| positive regulation of interleukin-2 biosynthetic process | 5 | 0.049 |
| receptor activity | 19 | <0.001 |
| transmembrane signaling receptor activity | 17 | <0.001 |
| chemokine activity | 8 | 0.014 |