**Supplementary Table 3. Results of the GO enrichment analysis**

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| --- | --- | --- | --- | --- | --- |
| Category | Term | Count | % | *P*-Value | FDR |
| BP | GO:0032755~positive regulation of interleukin-6 production | 14 | 14.43 | 3.32E-15 | 1.47E-12 |
| BP | GO:0016310~phosphorylation | 24 | 24.74 | 3.37E-14 | 1.19E-11 |
| BP | GO:0006935~chemotaxis | 14 | 14.43 | 6.73E-14 | 1.98E-11 |
| BP | GO:0032757~positive regulation of interleukin-8 production | 11 | 11.34 | 7.12E-13 | 1.57E-10 |
| BP | GO:0032760~positive regulation of tumor necrosis factor production | 12 | 12.37 | 8.25E-12 | 1.46E-09 |
| BP | GO:0007204~positive regulation of cytosolic calcium ion concentration | 13 | 13.40 | 7.62E-12 | 1.46E-09 |
| BP | GO:0032731~positive regulation of interleukin-1 beta production | 9 | 9.28 | 1.13E-09 | 1.54E-07 |
| BP | GO:1901224~positive regulation of NIK/NF-kappaB signaling | 9 | 9.28 | 1.45E-09 | 1.83E-07 |
| BP | GO:0009410~response to xenobiotic stimulus | 13 | 13.40 | 4.19E-09 | 3.86E-07 |
| BP | GO:1902894~negative regulation of pri-miRNA transcription from RNA polymerase II promoter | 7 | 7.22 | 4.52E-09 | 3.86E-07 |
| BP | GO:0003376~sphingosine-1-phosphate signaling pathway | 6 | 6.19 | 8.00E-09 | 6.15E-07 |
| BP | GO:1902895~positive regulation of pri-miRNA transcription from RNA polymerase II promoter | 8 | 8.25 | 1.91E-08 | 1.25E-06 |
| BP | GO:0006468~protein phosphorylation | 14 | 14.43 | 5.00E-08 | 2.95E-06 |
| BP | GO:0019722~calcium-mediated signaling | 9 | 9.28 | 4.94E-08 | 2.95E-06 |
| BP | GO:0018105~peptidyl-serine phosphorylation | 10 | 10.31 | 1.05E-07 | 5.48E-06 |
| BP | GO:0045893~positive regulation of transcription, DNA-templated | 17 | 17.53 | 4.85E-07 | 2.20E-05 |
| BP | GO:0051092~positive regulation of NF-kappaB transcription factor activity | 9 | 9.28 | 5.22E-07 | 2.30E-05 |
| BP | GO:0071276~cellular response to cadmium ion | 6 | 6.19 | 6.88E-07 | 2.96E-05 |
| BP | GO:0002407~dendritic cell chemotaxis | 5 | 5.15 | 1.01E-06 | 4.14E-05 |
| BP | GO:0032733~positive regulation of interleukin-10 production | 6 | 6.19 | 2.04E-06 | 7.50E-05 |
| BP | GO:0032733~positive regulation of interleukin-10 production | 6 | 6.19 | 2.04E-06 | 7.50E-05 |
| BP | GO:0032735~positive regulation of interleukin-12 production | 6 | 6.19 | 2.58E-06 | 9.12E-05 |
| BP | GO:0032735~positive regulation of interleukin-12 production | 6 | 6.19 | 2.58E-06 | 9.12E-05 |
| BP | GO:0006979~response to oxidative stress | 8 | 8.25 | 2.72E-06 | 9.43E-05 |
| BP | GO:0043491~protein kinase B signaling | 7 | 7.22 | 4.47E-06 | 1.39E-04 |
| BP | GO:0018108~peptidyl-tyrosine phosphorylation | 6 | 6.19 | 4.92E-06 | 1.47E-04 |
| BP | GO:0032740~positive regulation of interleukin-17 production | 5 | 5.15 | 7.97E-06 | 2.20E-04 |
| BP | GO:0007200~phospholipase C-activating G-protein coupled receptor signaling pathway | 7 | 7.22 | 8.47E-06 | 2.27E-04 |
| BP | GO:1900017~positive regulation of cytokine production involved in inflammatory response | 5 | 5.15 | 1.65E-05 | 4.04E-04 |
| BP | GO:0010595~positive regulation of endothelial cell migration | 6 | 6.19 | 1.95E-05 | 4.41E-04 |
| BP | GO:0007166~cell surface receptor signaling pathway | 10 | 10.31 | 3.47E-05 | 7.14E-04 |
| BP | GO:0032722~positive regulation of chemokine production | 5 | 5.15 | 6.17E-05 | 0.001210854 |
| BP | GO:0050728~negative regulation of inflammatory response | 7 | 7.22 | 9.07E-05 | 0.001673335 |
| BP | GO:0008283~cell proliferation | 7 | 7.22 | 9.78E-05 | 0.001744812 |
| BP | GO:0070371~ERK1 and ERK2 cascade | 5 | 5.15 | 1.03E-04 | 0.001810562 |
| BP | GO:0046330~positive regulation of JNK cascade | 6 | 6.19 | 1.24E-04 | 0.002134026 |
| BP | GO:0034614~cellular response to reactive oxygen species | 5 | 5.15 | 1.31E-04 | 0.002158911 |
| BP | GO:0018107~peptidyl-threonine phosphorylation | 5 | 5.15 | 1.63E-04 | 0.002663974 |
| BP | GO:0036092~phosphatidylinositol-3-phosphate biosynthetic process | 4 | 4.12 | 1.73E-04 | 0.002798525 |
| BP | GO:0007254~JNK cascade | 5 | 5.15 | 2.44E-04 | 0.00384189 |
| BP | GO:0048015~phosphatidylinositol-mediated signaling | 4 | 4.12 | 2.55E-04 | 0.003988182 |
| BP | GO:0097421~liver regeneration | 4 | 4.12 | 4.88E-04 | 0.00695062 |
| BP | GO:0060326~cell chemotaxis | 5 | 5.15 | 5.11E-04 | 0.007166677 |
| BP | GO:0050829~defense response to Gram-negative bacterium | 5 | 5.15 | 9.01E-04 | 0.011455832 |
| BP | GO:0035094~response to nicotine | 4 | 4.12 | 9.63E-04 | 0.012160679 |
| BP | GO:0016477~cell migration | 7 | 7.22 | 0.001282395 | 0.015208 |
| BP | GO:0032689~negative regulation of interferon-gamma production | 4 | 4.12 | 0.001560549 | 0.017905781 |
| BP | GO:0046718~viral entry into host cell | 5 | 5.15 | 0.001759244 | 0.01937483 |
| BP | GO:0046854~phosphatidylinositol phosphorylation | 4 | 4.12 | 0.002348417 | 0.024266974 |
| BP | GO:0007186~G-protein coupled receptor signaling pathway | 13 | 13.40 | 0.002734447 | 0.027144761 |
| BP | GO:1904019~epithelial cell apoptotic process | 3 | 3.09 | 0.004856171 | 0.042063012 |
| BP | GO:0070098~chemokine-mediated signaling pathway | 4 | 4.12 | 0.00516309 | 0.043861444 |
| CC | GO:0005943~phosphatidylinositol 3-kinase complex, class IA | 4 | 4.12 | 8.17E-06 | 1.76E-04 |
| CC | GO:0005942~phosphatidylinositol 3-kinase complex | 3 | 3.09 | 0.004707073 | 0.044000904 |
| MF | GO:0005524~ATP binding | 31 | 31.96 | 5.73E-11 | 5.21E-09 |
| MF | GO:0004672~protein kinase activity | 17 | 17.53 | 9.81E-11 | 7.14E-09 |
| MF | GO:0004674~protein serine/threonine kinase activity | 15 | 15.46 | 9.52E-09 | 5.77E-07 |
| MF | GO:0001223~transcription coactivator binding | 7 | 7.22 | 1.52E-07 | 6.16E-06 |
| MF | GO:0016301~kinase activity | 11 | 11.34 | 3.66E-07 | 1.33E-05 |
| MF | GO:0046934~phosphatidylinositol-4,5-bisphosphate 3-kinase activity | 4 | 4.12 | 4.39E-06 | 1.23E-04 |
| MF | GO:0035005~1-phosphatidylinositol-4-phosphate 3-kinase activity | 4 | 4.12 | 4.39E-06 | 1.23E-04 |
| MF | GO:0019957~C-C chemokine binding | 5 | 5.15 | 5.16E-06 | 1.25E-04 |
| MF | GO:0016493~C-C chemokine receptor activity | 5 | 5.15 | 5.16E-06 | 1.25E-04 |
| MF | GO:0016494~C-X-C chemokine receptor activity | 4 | 4.12 | 7.00E-06 | 1.59E-04 |
| MF | GO:0016303~1-phosphatidylinositol-3-kinase activity | 4 | 4.12 | 1.49E-05 | 3.19E-04 |
| MF | GO:0004713~protein tyrosine kinase activity | 7 | 7.22 | 2.40E-05 | 4.61E-04 |
| MF | GO:0004715~non-membrane spanning protein tyrosine kinase activity | 5 | 5.15 | 8.69E-05 | 0.001506434 |
| MF | GO:0004950~chemokine receptor activity | 4 | 4.12 | 1.16E-04 | 0.001924431 |
| MF | GO:0004879~RNA polymerase II transcription factor activity, ligand-activated sequence-specific DNA binding | 5 | 5.15 | 1.63E-04 | 0.002584033 |
| MF | GO:0000976~transcription regulatory region sequence-specific DNA binding | 8 | 8.25 | 2.02E-04 | 0.002942517 |
| MF | GO:0038036~sphingosine-1-phosphate receptor activity | 3 | 3.09 | 7.02E-04 | 0.008518423 |
| MF | GO:0001618~virus receptor activity | 5 | 5.15 | 7.38E-04 | 0.008668824 |
| MF | GO:0005178~integrin binding | 6 | 6.19 | 0.001240143 | 0.014106629 |
| MF | GO:0005125~cytokine activity | 6 | 6.19 | 0.00305448 | 0.030884186 |
| MF | GO:0005125~cytokine activity | 6 | 6.19 | 0.00305448 | 0.030884186 |
| MF | GO:0003682~chromatin binding | 9 | 9.28 | 0.003375775 | 0.033210324 |

BP, biological process; CC, cellular component; FDR, false discovery rate; GO, gene ontology; MF, molecular function; miRNA, microRNA.