**Supplementary Table 4.** Top 20 KEGG gene sets correlate with up-regulated mRNAs by GSEA

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Pathway Name | SIZE | ES | NES | NOM p-val | FDR q-val |
| KEGG\_NATURAL\_KILLER\_CELL\_MEDIATED\_CYTOTOXICITY | 33 | 0.6 | 2.87 | <0.001 | <0.001 |
| KEGG\_AUTOIMMUNE\_THYROID\_DISEASE | 19 | 0.62 | 2.49 | <0.001 | <0.001 |
| KEGG\_CYTOKINE\_CYTOKINE\_RECEPTOR\_INTERACTION | 71 | 0.41 | 2.43 | <0.001 | <0.001 |
| KEGG\_LEISHMANIA\_INFECTION | 19 | 0.6 | 2.39 | <0.001 | <0.001 |
| KEGG\_GRAFT\_VERSUS\_HOST\_DISEASE | 17 | 0.62 | 2.39 | <0.001 | <0.001 |
| KEGG\_SYSTEMIC\_LUPUS\_ERYTHEMATOSUS | 26 | 0.54 | 2.39 | <0.001 | <0.001 |
| KEGG\_HEMATOPOIETIC\_CELL\_LINEAGE | 28 | 0.53 | 2.38 | <0.001 | <0.001 |
| KEGG\_CHEMOKINE\_SIGNALING\_PATHWAY | 37 | 0.49 | 2.37 | <0.001 | <0.001 |
| KEGG\_TOLL\_LIKE\_RECEPTOR\_SIGNALING\_PATHWAY | 13 | 0.65 | 2.31 | <0.001 | <0.001 |
| KEGG\_ANTIGEN\_PROCESSING\_AND\_PRESENTATION | 22 | 0.56 | 2.26 | <0.001 | <0.001 |
| KEGG\_INTESTINAL\_IMMUNE\_NETWORK\_FOR\_IGA\_PRODUCTION | 17 | 0.58 | 2.24 | <0.001 | <0.001 |
| KEGG\_ALLOGRAFT\_REJECTION | 17 | 0.59 | 2.24 | <0.001 | <0.001 |
| KEGG\_TYPE\_I\_DIABETES\_MELLITUS | 17 | 0.59 | 2.21 | 0.002 | 0.001 |
| KEGG\_PRIMARY\_IMMUNODEFICIENCY | 20 | 0.52 | 2.11 | 0.002 | 0.002 |
| KEGG\_VIRAL\_MYOCARDITIS | 22 | 0.5 | 2.1 | 0.005 | 0.002 |
| KEGG\_NOD\_LIKE\_RECEPTOR\_SIGNALING\_PATHWAY | 10 | 0.66 | 2.03 | 0.002 | 0.004 |
| KEGG\_FC\_EPSILON\_RI\_SIGNALING\_PATHWAY | 12 | 0.59 | 1.96 | 0.004 | 0.006 |
| KEGG\_CELL\_CYCLE | 17 | 0.47 | 1.78 | 0.009 | 0.024 |
| KEGG\_ASTHMA | 13 | 0.51 | 1.77 | 0.021 | 0.024 |
| KEGG\_B\_CELL\_RECEPTOR\_SIGNALING\_PATHWAY | 12 | 0.52 | 1.77 | 0.018 | 0.024 |