

Supplementary Table S3. Summary of functional enrichment in the network generated from initial co-expression network selected genes (for complete details, see Supplementary File 5).

| Description | Observed | Background | Strength | FDR |
|---|----------|------------|----------|----------|
| Biological process (GO) | | | | |
| Immune system process | 14 | 2481 | 0.76 | 3.12E-05 |
| Immune response | 11 | 1588 | 0.85 | 0.00037 |
| Regulation of response to stimulus | 15 | 4114 | 0.57 | 0.00067 |
| Immune response-activating cell surface receptor signaling pathway | 5 | 311 | 1.22 | 0.0448 |
| Regulation of immune system process | 8 | 1514 | 0.74 | 0.0448 |
| Positive regulation of immune system process | 7 | 949 | 0.88 | 0.0448 |
| Signal transduction | 14 | 4876 | 0.47 | 0.0448 |
| Positive regulation of catalytic activity | 8 | 1489 | 0.74 | 0.0448 |
| Positive regulation of GTPase activity | 5 | 407 | 1.1 | 0.0448 |
| Leukocyte activation | 7 | 929 | 0.89 | 0.0448 |
| Regulation of immune response | 7 | 896 | 0.91 | 0.0448 |
| Antigen receptor-mediated signaling pathway | 4 | 199 | 1.32 | 0.0448 |
| Positive regulation of T cell activation | 4 | 209 | 1.29 | 0.0448 |
| Leukocyte migration | 5 | 316 | 1.21 | 0.0448 |
| Local network cluster (STRING) | | | | |
| Mixed, incl. Generation of second messenger molecules, and Antigen activates B Cell Receptor (BCR) leading to generation of second messengers | 6 | 38 | 2.21 | 1.17E-05 |
| Mixed, incl. T cell receptor complex, and CD28 dependent Vav1 pathway | 4 | 22 | 2.27 | 0.0091 |
| KEGG pathway | | | | |
| Natural killer cell mediated cytotoxicity | 4 | 121 | 1.53 | 0.0026 |
| Yersinia infection | 4 | 125 | 1.52 | 0.0026 |
| T cell receptor signaling pathway | 3 | 101 | 1.49 | 0.0201 |
| Reactome pathway | | | | |
| Immune system | 11 | 1956 | 0.76 | 0.0062 |
| Generation of second messenger molecules | 3 | 29 | 2.03 | 0.0328 |
| Protein domains and features (InterPro) | | | | |
| SH2 domain | 4 | 112 | 1.57 | 0.0468 |
| SH3 domain | 5 | 221 | 1.37 | 0.0468 |
| SH3-like domain superfamily | 5 | 211 | 1.39 | 0.0468 |
| SH2 domain superfamily | 4 | 113 | 1.56 | 0.0468 |