

| Category ID | Category Name | #Genes Category | #Genes Assigned | #Genes Expected | #Genes Enriched | p-value | Corrected p-value |
|-------------|--------------------------------------------|-----------------|-----------------|-----------------|-----------------|----------|-------------------|
| GO:0044424 | intracellular part | 13399 | 716 | 590.5 | 125.5 | 2.40E-17 | <0.001 |
| GO:0005622 | intracellular | 13868 | 728 | 611.2 | 116.8 | 1.50E-15 | <0.001 |
| GO:0005634 | nucleus | 6445 | 397 | 284 | 113 | 2.60E-15 | <0.001 |
| GO:0043231 | intracellular membrane-bounded organelle | 10278 | 556 | 453 | 103 | 1.50E-11 | <0.001 |
| GO:0043227 | membrane-bounded organelle | 10291 | 556 | 453.5 | 102.5 | 2.00E-11 | <0.001 |
| GO:0007049 | cell cycle | 1120 | 97 | 49.4 | 47.6 | 1.30E-10 | <0.001 |
| GO:0000278 | mitotic cell cycle | 484 | 53 | 21.3 | 31.7 | 1.10E-09 | <0.001 |
| GO:0043229 | intracellular organelle | 11513 | 599 | 507.4 | 91.6 | 1.70E-09 | <0.001 |
| GO:0016071 | mRNA metabolic process | 507 | 51 | 22.3 | 28.7 | 3.90E-08 | <0.001 |
| GO:0000087 | M phase of mitotic cell cycle | 314 | 37 | 13.8 | 23.2 | 5.70E-08 | <0.001 |
| GO:0044428 | nuclear part | 1762 | 125 | 77.7 | 47.3 | 6.60E-08 | <0.001 |
| GO:0000956 | nuclear-transcribed mRNA catabolic process | 34 | 11 | 1.5 | 9.5 | 1.30E-07 | <0.001 |
| GO:0007067 | mitosis | 311 | 36 | 13.7 | 22.3 | 1.30E-07 | <0.001 |
| GO:0006402 | mRNA catabolic process | 36 | 11 | 1.6 | 9.4 | 2.50E-07 | <0.001 |
| GO:0003723 | RNA binding | 1019 | 80 | 44.9 | 35.1 | 4.00E-07 | 0.002 |
| GO:0022403 | cell cycle phase | 549 | 51 | 24.2 | 26.8 | 4.70E-07 | 0.002 |
| GO:0006401 | RNA catabolic process | 39 | 11 | 1.7 | 9.3 | 6.20E-07 | 0.002 |
| GO:0006396 | RNA processing | 689 | 59 | 30.4 | 28.6 | 9.20E-07 | 0.002 |
| GO:0008380 | RNA splicing | 380 | 39 | 16.7 | 22.3 | 9.40E-07 | 0.002 |
| GO:0043285 | biopolymer catabolic process | 905 | 72 | 39.9 | 32.1 | 9.50E-07 | 0.002 |
| GO:0006397 | mRNA processing | 464 | 44 | 20.4 | 23.6 | 1.70E-06 | 0.002 |
| GO:0022402 | cell cycle process | 655 | 56 | 28.9 | 27.1 | 1.80E-06 | 0.002 |
| GO:0009057 | macromolecule catabolic process | 1025 | 78 | 45.2 | 32.8 | 1.80E-06 | 0.002 |
| GO:0043283 | biopolymer metabolic process | 7835 | 414 | 345.3 | 68.7 | 2.30E-06 | 0.002 |
| GO:0043170 | macromolecule metabolic process | 8106 | 426 | 357.2 | 68.8 | 2.60E-06 | 0.004 |
| GO:0000279 | M phase | 432 | 41 | 19 | 22 | 3.70E-06 | 0.006 |
| GO:0051726 | regulation of cell cycle | 463 | 43 | 20.4 | 22.6 | 3.70E-06 | 0.006 |
| GO:0051301 | cell division | 405 | 39 | 17.8 | 21.2 | 4.40E-06 | 0.006 |
| GO:0044260 | cellular macromolecule metabolic process | 7947 | 417 | 350.2 | 66.8 | 4.50E-06 | 0.006 |
| GO:0008026 | ATP-dependent helicase activity | 131 | 19 | 5.8 | 13.2 | 4.80E-06 | 0.006 |
| GO:0070035 | purine NTP-dependent helicase activity | 131 | 19 | 5.8 | 13.2 | 4.80E-06 | 0.006 |
| GO:0044265 | cellular macromolecule catabolic process | 966 | 73 | 42.6 | 30.4 | 5.10E-06 | 0.008 |
| GO:0034960 | cellular biopolymer metabolic process | 7783 | 409 | 343 | 66 | 5.20E-06 | 0.008 |

Table 1. Gene Ontology analysis of transcripts of top 1000 ranked probe sets for stabilization by IL-3.