

**Table S1**

| Annotation Cluster 1 |                                                               | Enrichment Score: 33.29 |       |          |                 |            |           |          |  |
|----------------------|---------------------------------------------------------------|-------------------------|-------|----------|-----------------|------------|-----------|----------|--|
| Category             | Term                                                          | Count                   | %     | PValue   | Fold Enrichment | Bonferroni | Benjamini | FDR      |  |
| UP_SEQ_FEATURE       | DNA-binding region:Homeobox                                   | 64                      | 17.93 | 2.23E-67 | 21.75           | 1.52E-64   | 1.52E-64  | 3.35E-64 |  |
| INTERPRO             | IPR017970:Homeobox, conserved site                            | 66                      | 18.49 | 5.25E-64 | 18.02           | 1.33E-61   | 6.66E-62  | 6.83E-61 |  |
| INTERPRO             | IPR001356:Homeobox                                            | 66                      | 18.49 | 1.34E-63 | 17.79           | 3.41E-61   | 1.14E-61  | 1.75E-60 |  |
| SP_PIR_KEYWORDS      | Homeobox                                                      | 66                      | 18.49 | 9.89E-63 | 17.60           | 1.94E-60   | 1.94E-60  | 1.24E-59 |  |
| INTERPRO             | IPR012287:Homeodomain-related                                 | 64                      | 17.93 | 3.09E-60 | 17.03           | 7.85E-58   | 1.96E-58  | 4.03E-57 |  |
| SMART                | SM00389:HOX                                                   | 66                      | 18.49 | 3.82E-53 | 11.75           | 2.91E-51   | 2.91E-51  | 4.02E-50 |  |
| SP_PIR_KEYWORDS      | dna-binding                                                   | 125                     | 35.01 | 7.45E-49 | 4.32            | 1.46E-46   | 7.30E-47  | 9.31E-46 |  |
| GOTERM_MF_FAT        | GO:0043565~sequence-specific DNA binding                      | 82                      | 22.97 | 1.82E-48 | 7.31            | 3.42E-46   | 3.42E-46  | 2.26E-45 |  |
| GOTERM_MF_FAT        | GO:0003700~transcription factor activity                      | 94                      | 26.33 | 1.53E-43 | 5.22            | 2.87E-41   | 1.43E-41  | 1.89E-40 |  |
| GOTERM_BP_FAT        | GO:0007389~pattern specification process                      | 52                      | 14.57 | 1.47E-39 | 11.46           | 1.58E-36   | 7.91E-37  | 2.34E-36 |  |
| SP_PIR_KEYWORDS      | DNA binding                                                   | 55                      | 15.41 | 6.28E-39 | 10.44           | 1.23E-36   | 4.11E-37  | 7.85E-36 |  |
| SP_PIR_KEYWORDS      | developmental protein                                         | 75                      | 21.01 | 8.83E-38 | 6.21            | 1.73E-35   | 4.33E-36  | 1.10E-34 |  |
| GOTERM_MF_FAT        | GO:0003677~DNA binding                                        | 131                     | 36.69 | 1.14E-37 | 3.04            | 2.14E-35   | 7.15E-36  | 1.42E-34 |  |
| GOTERM_BP_FAT        | GO:0003002~regionalization                                    | 45                      | 12.61 | 3.30E-37 | 13.44           | 3.56E-34   | 1.19E-34  | 5.27E-34 |  |
| GOTERM_BP_FAT        | GO:0048598~embryonic morphogenesis                            | 50                      | 14.01 | 4.35E-34 | 9.58            | 4.68E-31   | 1.17E-31  | 6.93E-31 |  |
| GOTERM_MF_FAT        | GO:0030528~transcription regulator activity                   | 102                     | 28.57 | 6.20E-34 | 3.65            | 1.16E-31   | 2.91E-32  | 7.69E-31 |  |
| INTERPRO             | IPR001827:Homeobox protein, antennapedia type, conserved site | 21                      | 5.88  | 4.13E-33 | 55.42           | 1.05E-30   | 1.75E-31  | 5.38E-30 |  |
| GOTERM_BP_FAT        | GO:0009952~anterior/posterior pattern formation               | 37                      | 10.36 | 7.60E-33 | 15.54           | 8.18E-30   | 1.64E-30  | 1.21E-29 |  |
| GOTERM_BP_FAT        | GO:0006355~regulation of transcription, DNA-dependent         | 103                     | 28.85 | 3.63E-32 | 3.42            | 3.91E-29   | 6.52E-30  | 5.79E-29 |  |
| UP_SEQ_FEATURE       | short sequence motif:Antp-type hexapeptide                    | 20                      | 5.60  | 1.78E-31 | 56.15           | 1.21E-28   | 2.02E-29  | 2.67E-28 |  |
| GOTERM_BP_FAT        | GO:0051252~regulation of RNA metabolic process                | 103                     | 28.85 | 2.44E-31 | 3.34            | 2.63E-28   | 3.76E-29  | 3.90E-28 |  |
| GOTERM_BP_FAT        | GO:0048706~embryonic skeletal system development              | 29                      | 8.12  | 1.74E-30 | 22.15           | 1.87E-27   | 2.08E-28  | 2.77E-27 |  |
| GOTERM_BP_FAT        | GO:0001501~skeletal system development                        | 47                      | 13.17 | 5.71E-30 | 8.67            | 6.15E-27   | 6.15E-28  | 9.11E-27 |  |
| GOTERM_BP_FAT        | GO:0048562~embryonic organ morphogenesis                      | 32                      | 8.96  | 6.24E-27 | 14.15           | 6.72E-24   | 6.11E-25  | 9.95E-24 |  |
| SP_PIR_KEYWORDS      | nucleus                                                       | 147                     | 41.18 | 7.48E-25 | 2.22            | 1.47E-22   | 2.45E-23  | 9.35E-22 |  |
| SP_PIR_KEYWORDS      | transcription regulation                                      | 96                      | 26.89 | 2.68E-24 | 3.06            | 5.25E-22   | 7.50E-23  | 3.35E-21 |  |
| GOTERM_BP_FAT        | GO:0048705~skeletal system morphogenesis                      | 28                      | 7.84  | 5.51E-24 | 14.70           | 5.93E-21   | 4.94E-22  | 8.79E-21 |  |
| SP_PIR_KEYWORDS      | Transcription                                                 | 96                      | 26.89 | 1.33E-23 | 2.99            | 2.61E-21   | 3.27E-22  | 1.67E-20 |  |
| GOTERM_BP_FAT        | GO:0045449~regulation of transcription                        | 111                     | 31.09 | 2.10E-23 | 2.51            | 2.27E-20   | 1.74E-21  | 3.35E-20 |  |
| GOTERM_BP_FAT        | GO:0048568~embryonic organ development                        | 32                      | 8.96  | 2.53E-23 | 10.94           | 2.73E-20   | 1.95E-21  | 4.04E-20 |  |
| GOTERM_BP_FAT        | GO:0048704~embryonic skeletal system                          | 22                      | 6.16  | 3.04E-23 | 22.70           | 3.27E-20   | 2.18E-21  | 4.85E-20 |  |

|                 |                                                                  |               |       |          |       |            |            |            |  |
|-----------------|------------------------------------------------------------------|---------------|-------|----------|-------|------------|------------|------------|--|
|                 |                                                                  |               |       |          |       |            |            |            |  |
|                 |                                                                  | morphogenesis |       |          |       |            |            |            |  |
| GOTERM_BP_FAT   | GO:0006350~transcription                                         | 95            | 26.61 | 5.23E-21 | 2.66  | 5.64E-18   | 3.52E-19   | 8.35E-18   |  |
| GOTERM_BP_FAT   | GO:0009792~embryonic development ending in birth or egg hatching | 38            | 10.64 | 4.12E-20 | 6.69  | 4.43E-17   | 2.61E-18   | 6.56E-17   |  |
| GOTERM_BP_FAT   | GO:0043009~chordate embryonic development                        | 37            | 10.36 | 2.55E-19 | 6.57  | 2.75E-16   | 1.53E-17   | 4.07E-16   |  |
| INTERPRO        | IPR017995:Homeobox protein, antennapedia type                    | 11            | 3.08  | 4.99E-17 | 58.06 | 1.27E-14   | 1.41E-15   | 6.50E-14   |  |
| PIR_SUPERFAMILY | PIRSF002612:homeotic protein Hox A5/D4                           | 10            | 2.80  | 6.40E-17 | 77.04 | 7.66E-15   | 7.66E-15   | 1.11E-13   |  |
| PIR_SUPERFAMILY | PIRSF500606:homeotic protein Hox D4                              | 5             | 1.40  | 1.27E-07 | 77.04 | 8.73E-06   | 2.91E-06   | 1.31E-04   |  |
| SP_PIR_KEYWORDS | embryo                                                           | 4             | 1.12  | 2.86E-04 | 28.69 | 0.05447035 | 0.00372704 | 0.35635585 |  |
|                 |                                                                  |               |       |          |       | 4          |            | 7          |  |

## Annotation Cluster 2

Enrichment Score: 20.44

| Category        | Term                                | Count | %     | PValue   | Fold Enrichment | Bonferroni | Benjamini | FDR      |
|-----------------|-------------------------------------|-------|-------|----------|-----------------|------------|-----------|----------|
| INTERPRO        | IPR013164:Cadherin, N-terminal      | 45    | 12.61 | 8.72E-69 | 49.14           | 2.21E-66   | 2.21E-66  | 1.14E-65 |
| UP_SEQ_FEATURE  | domain:Cadherin 6                   | 44    | 12.32 | 9.99E-60 | 38.92           | 6.79E-57   | 3.40E-57  | 1.50E-56 |
| UP_SEQ_FEATURE  | domain:Cadherin 5                   | 44    | 12.32 | 5.66E-53 | 29.91           | 3.85E-50   | 1.28E-50  | 8.51E-50 |
| INTERPRO        | IPR002126:Cadherin                  | 45    | 12.61 | 1.74E-51 | 26.39           | 4.42E-49   | 8.84E-50  | 2.27E-48 |
| UP_SEQ_FEATURE  | domain:Cadherin 3                   | 44    | 12.32 | 2.79E-51 | 27.85           | 1.90E-48   | 4.75E-49  | 4.19E-48 |
| UP_SEQ_FEATURE  | domain:Cadherin 4                   | 44    | 12.32 | 2.79E-51 | 27.85           | 1.90E-48   | 4.75E-49  | 4.19E-48 |
| UP_SEQ_FEATURE  | domain:Cadherin 1                   | 44    | 12.32 | 1.33E-50 | 27.06           | 9.04E-48   | 1.81E-48  | 2.00E-47 |
| UP_SEQ_FEATURE  | domain:Cadherin 2                   | 44    | 12.32 | 1.33E-50 | 27.06           | 9.04E-48   | 1.81E-48  | 2.00E-47 |
| GOTERM_BP_FAT   | GO:0007156~homophilic cell adhesion | 45    | 12.61 | 6.68E-46 | 20.20           | 7.20E-43   | 7.20E-43  | 1.07E-42 |
| SMART           | SM00112:CA                          | 45    | 12.61 | 4.18E-44 | 17.43           | 3.18E-42   | 1.59E-42  | 4.40E-41 |
| INTERPRO        | IPR015492:Protocadherin gamma       | 19    | 5.32  | 3.60E-32 | 63.34           | 9.15E-30   | 1.31E-30  | 4.69E-29 |
| GOTERM_BP_FAT   | GO:0016337~cell-cell adhesion       | 45    | 12.61 | 1.47E-30 | 9.59            | 1.58E-27   | 1.98E-28  | 2.34E-27 |
| SP_PIR_KEYWORDS | cell adhesion                       | 46    | 12.89 | 6.38E-25 | 7.04            | 1.25E-22   | 2.50E-23  | 7.97E-22 |
| GOTERM_BP_FAT   | GO:0007155~cell adhesion            | 48    | 13.45 | 1.75E-16 | 4.03            | 2.39E-13   | 1.25E-14  | 3.55E-13 |
| GOTERM_BP_FAT   | GO:0022610~biological adhesion      | 48    | 13.45 | 1.85E-16 | 4.03            | 2.39E-13   | 1.20E-14  | 3.55E-13 |
| SP_PIR_KEYWORDS | calcium                             | 47    | 13.17 | 1.26E-14 | 3.78            | 2.48E-12   | 2.76E-13  | 1.58E-11 |
| GOTERM_MF_FAT   | GO:0005509~calcium ion binding      | 47    | 13.17 | 3.47E-10 | 2.77            | 6.52E-08   | 1.30E-08  | 4.30E-07 |
| GOTERM_CC_FAT   | GO:0005886~plasma membrane          | 65    | 18.21 | 9.94E-05 | 1.52            | 0.02       | 0.00      | 0.12     |
| SP_PIR_KEYWORDS | cell membrane                       | 53    | 14.85 | 0.00     | 1.56            | 0.19       | 0.01      | 1.35     |
| GOTERM_CC_FAT   | GO:0016021~integral to membrane     | 73    | 20.45 | 0.02     | 1.21            | 0.98       | 0.29      | 24.26    |
| UP_SEQ_FEATURE  | topological domain:Extracellular    | 54    | 15.13 | 0.04     | 1.28            | 1          | 0.67      | 47.14    |
| GOTERM_CC_FAT   | GO:0031224~intrinsic to membrane    | 73    | 20.45 | 0.05     | 1.17            | 1.00       | 0.45      | 46.68    |
| UP_SEQ_FEATURE  | topological domain:Cytoplasmic      | 58    | 16.25 | 0.25     | 1.11            | 1          | 0.99      | 98.54    |
| GOTERM_MF_FAT   | GO:0046872~metal ion binding        | 82    | 22.97 | 0.27     | 1.07            | 1          | 0.96      | 98.06    |

|                 |                                         |    |       |      |      |   |      |       |
|-----------------|-----------------------------------------|----|-------|------|------|---|------|-------|
| UP_SEQ_FEATURE  | signal peptide                          | 55 | 15.41 | 0.30 | 1.09 | 1 | 1.00 | 99.50 |
| SP_PIR_KEYWORDS | signal                                  | 55 | 15.41 | 0.30 | 1.09 | 1 | 0.90 | 98.80 |
| GOTERM_MF_FAT   | GO:0043169~cation binding               | 82 | 22.97 | 0.31 | 1.06 | 1 | 0.97 | 98.94 |
| GOTERM_MF_FAT   | GO:0043167~ion binding                  | 82 | 22.97 | 0.37 | 1.05 | 1 | 0.98 | 99.64 |
| UP_SEQ_FEATURE  | glycosylation site:N-linked (GlcNAc...) | 58 | 16.25 | 0.85 | 0.91 | 1 | 1    | 100   |
| SP_PIR_KEYWORDS | transmembrane                           | 68 | 19.05 | 0.92 | 0.88 | 1 | 1.00 | 100   |
| UP_SEQ_FEATURE  | transmembrane region                    | 67 | 18.77 | 0.92 | 0.88 | 1 | 1    | 100   |
| SP_PIR_KEYWORDS | glycoprotein                            | 58 | 16.25 | 0.93 | 0.87 | 1 | 1.00 | 100   |
| SP_PIR_KEYWORDS | membrane                                | 72 | 20.17 | 1.00 | 0.74 | 1 | 1    | 100   |

#### Annotation Cluster 3

Enrichment Score: 12.57

| Category      | Term                                         | Count | %    | PValue   | Fold Enrichment | Bonferroni | Benjamini | FDR         |
|---------------|----------------------------------------------|-------|------|----------|-----------------|------------|-----------|-------------|
| GOTERM_BP_FAT | GO:0048736~appendage development             | 20    | 5.60 | 7.24E-15 | 11.42           | 7.77E-12   | 3.38E-13  | 1.15E-11    |
| GOTERM_BP_FAT | GO:0060173~limb development                  | 20    | 5.60 | 7.24E-15 | 11.42           | 7.77E-12   | 3.38E-13  | 1.15E-11    |
| GOTERM_BP_FAT | GO:0009954~proximal/distal pattern formation | 12    | 3.36 | 2.91E-14 | 30.69           | 3.13E-11   | 1.25E-12  | 4.64E-11    |
| GOTERM_BP_FAT | GO:0035107~appendage morphogenesis           | 19    | 5.32 | 4.98E-14 | 11.29           | 5.36E-11   | 2.06E-12  | 7.93E-11    |
| GOTERM_BP_FAT | GO:0035108~limb morphogenesis                | 19    | 5.32 | 4.98E-14 | 11.29           | 5.36E-11   | 2.06E-12  | 7.93E-11    |
| GOTERM_BP_FAT | GO:0030326~embryonic limb morphogenesis      | 18    | 5.04 | 7.35E-14 | 12.17           | 7.92E-11   | 2.93E-12  | 1.17E-10    |
| GOTERM_BP_FAT | GO:0035113~embryonic appendage morphogenesis | 18    | 5.04 | 7.35E-14 | 12.17           | 7.92E-11   | 2.93E-12  | 1.17E-10    |
| GOTERM_BP_FAT | GO:0035136~forelimb morphogenesis            | 7     | 1.96 | 1.31E-06 | 18.71           | 0.00141056 | 2.02E-05  | 0.002090321 |

#### Annotation Cluster 4

Enrichment Score: 7.63

| Category        | Term                                    | Count | %    | PValue   | Fold Enrichment | Bonferroni | Benjamini | FDR      |
|-----------------|-----------------------------------------|-------|------|----------|-----------------|------------|-----------|----------|
| GOTERM_CC_FAT   | GO:0000786~nucleosome                   | 17    | 4.76 | 6.52E-18 | 23.79           | 1.06E-15   | 1.06E-15  | 7.89E-15 |
| GOTERM_CC_FAT   | GO:0032993~protein-DNA complex          | 17    | 4.76 | 1.47E-15 | 17.43           | 2.34E-13   | 1.17E-13  | 1.74E-12 |
| INTERPRO        | IPR007125:Histone core                  | 14    | 3.92 | 1.25E-13 | 19.71           | 3.17E-11   | 3.17E-12  | 1.63E-10 |
| SP_PIR_KEYWORDS | nucleosome core                         | 14    | 3.92 | 2.59E-13 | 18.83           | 5.09E-11   | 5.09E-12  | 3.24E-10 |
| GOTERM_BP_FAT   | GO:0006334~nucleosome assembly          | 17    | 4.76 | 6.20E-13 | 11.90           | 6.68E-10   | 2.38E-11  | 9.89E-10 |
| GOTERM_BP_FAT   | GO:0031497~chromatin assembly           | 17    | 4.76 | 1.10E-12 | 11.49           | 1.18E-09   | 4.08E-11  | 1.75E-09 |
| KEGG_PATHWAY    | hsa05322:Systemic lupus erythematosus   | 14    | 3.92 | 2.11E-12 | 14.98           | 1.01E-10   | 1.01E-10  | 2.01E-09 |
| GOTERM_BP_FAT   | GO:0065004~protein-DNA complex assembly | 17    | 4.76 | 2.28E-12 | 10.99           | 2.45E-09   | 8.17E-11  | 3.63E-09 |
| GOTERM_BP_FAT   | GO:0034728~nucleosome organization      | 17    | 4.76 | 3.23E-12 | 10.75           | 3.48E-09   | 1.09E-10  | 5.15E-09 |
| GOTERM_CC_FAT   | GO:0000785~chromatin                    | 19    | 5.32 | 9.54E-12 | 8.37            | 1.55E-09   | 5.15E-10  | 1.15E-08 |
| INTERPRO        | IPR009072:Histone-fold                  | 13    | 3.64 | 3.40E-11 | 15.25           | 8.63E-09   | 7.85E-10  | 4.43E-08 |
| GOTERM_BP_FAT   | GO:0006323~DNA packaging                | 17    | 4.76 | 1.19E-10 | 8.55            | 1.28E-07   | 3.78E-09  | 1.90E-07 |

|                 |                                                                                        |    |       |          |       |          |          |          |
|-----------------|----------------------------------------------------------------------------------------|----|-------|----------|-------|----------|----------|----------|
| PIR_SUPERFAMILY | PIRSF002050:histone H2B                                                                | 8  | 2.24  | 2.73E-10 | 41.09 | 1.88E-08 | 9.42E-09 | 2.82E-07 |
| GOTERM_BP_FAT   | GO:0006333~chromatin assembly or disassembly                                           | 17 | 4.76  | 4.16E-10 | 7.87  | 4.48E-07 | 1.25E-08 | 6.64E-07 |
| SP_PIR_KEYWORDS | chromosomal protein                                                                    | 17 | 4.76  | 9.01E-10 | 7.57  | 1.77E-07 | 1.61E-08 | 1.13E-06 |
| INTERPRO        | IPR000558:Histone H2B                                                                  | 8  | 2.24  | 6.03E-09 | 28.15 | 1.53E-06 | 1.18E-07 | 7.85E-06 |
| GOTERM_CC_FAT   | GO:0044427~chromosomal part                                                            | 21 | 5.88  | 1.20E-08 | 4.80  | 1.94E-06 | 4.84E-07 | 1.45E-05 |
| GOTERM_CC_FAT   | GO:0005694~chromosome                                                                  | 22 | 6.16  | 4.50E-08 | 4.22  | 7.30E-06 | 1.22E-06 | 5.45E-05 |
| SMART           | SM00427:H2B                                                                            | 8  | 2.24  | 9.97E-08 | 18.59 | 7.58E-06 | 2.53E-06 | 1.05E-04 |
| SP_PIR_KEYWORDS | isopeptide bond                                                                        | 19 | 5.32  | 2.56E-06 | 3.84  | 5.02E-04 | 4.18E-05 | 0.00     |
| UP_SEQ_FEATURE  | cross-link:Glycyl lysine isopeptide (Lys-Gly)<br>(interchain with G-Cter in ubiquitin) | 15 | 4.20  | 2.74E-06 | 4.87  | 0.00     | 1.55E-04 | 0.00     |
| GOTERM_BP_FAT   | GO:0034622~cellular macromolecular complex<br>assembly                                 | 19 | 5.32  | 7.89E-06 | 3.51  | 0.01     | 1.05E-04 | 0.01     |
| GOTERM_BP_FAT   | GO:0034621~cellular macromolecular complex<br>subunit organization                     | 19 | 5.32  | 3.74E-05 | 3.13  | 0.04     | 4.68E-04 | 0.06     |
| GOTERM_BP_FAT   | GO:0006325~chromatin organization                                                      | 19 | 5.32  | 7.84E-05 | 2.96  | 0.08     | 9.28E-04 | 0.12     |
| SP_PIR_KEYWORDS | methylation                                                                            | 14 | 3.92  | 1.05E-04 | 3.73  | 0.02     | 0.00     | 0.13     |
| SP_PIR_KEYWORDS | ubl conjugation                                                                        | 23 | 6.44  | 1.29E-04 | 2.52  | 0.02     | 0.00     | 0.16     |
| SP_PIR_KEYWORDS | citrullination                                                                         | 5  | 1.40  | 3.27E-04 | 14.67 | 0.06     | 0.00     | 0.41     |
| GOTERM_BP_FAT   | GO:0051276~chromosome organization                                                     | 20 | 5.60  | 5.98E-04 | 2.43  | 0.47     | 0.01     | 0.95     |
| GOTERM_BP_FAT   | GO:0065003~macromolecular complex assembly                                             | 21 | 5.88  | 0.01     | 1.86  | 1.00     | 0.07     | 13.73    |
| GOTERM_BP_FAT   | GO:0043933~macromolecular complex subunit<br>organization                              | 21 | 5.88  | 0.02     | 1.74  | 1.00     | 0.11     | 24.85    |
| GOTERM_CC_FAT   | GO:0043232~intracellular non-membrane-bounded<br>organelle                             | 38 | 10.64 | 0.07     | 1.29  | 1.00     | 0.51     | 57.50    |
| GOTERM_CC_FAT   | GO:0043228~non-membrane-bounded organelle                                              | 38 | 10.64 | 0.07     | 1.29  | 1.00     | 0.51     | 57.50    |
| SP_PIR_KEYWORDS | acetylation                                                                            | 36 | 10.08 | 0.85     | 0.88  | 1.00     | 1.00     | 100      |

| Annotation Cluster 68 |                                                            | Enrichment Score: 0.0066 |      |                 |                    |            |                 |     |  |
|-----------------------|------------------------------------------------------------|--------------------------|------|-----------------|--------------------|------------|-----------------|-----|--|
| Category              | Term                                                       | Count                    | %    | PValue          | Fold<br>Enrichment | Bonferroni | Benjamini       | FDR |  |
| GOTERM_BP_FAT         | GO:0043066~negative regulation of apoptosis                | 3                        | 0.84 | 0.9841102<br>27 | 0.50               | 1          | 0.99999966<br>9 | 100 |  |
| GOTERM_BP_FAT         | GO:0043069~negative regulation of programmed<br>cell death | 3                        | 0.84 | 0.9852620<br>79 | 0.49               | 1          | 0.99999972      | 100 |  |
| GOTERM_BP_FAT         | GO:0060548~negative regulation of cell death               | 3                        | 0.84 | 0.9854825<br>39 | 0.49               | 1          | 0.99999972<br>1 | 100 |  |

| Annotation Cluster 69 |      | Enrichment Score: 0.0060 |   |        |      |            |           |     |  |
|-----------------------|------|--------------------------|---|--------|------|------------|-----------|-----|--|
| Category              | Term | Count                    | % | PValue | Fold | Bonferroni | Benjamini | FDR |  |

|                       |                                          |                           |      |             | Enrichment      |            |             |     |
|-----------------------|------------------------------------------|---------------------------|------|-------------|-----------------|------------|-------------|-----|
| GOTERM_CC_FAT         | GO:0005615~extracellular space           | 5                         | 1.40 | 0.95393026  | 0.64            | 1          | 0.999999829 | 100 |
| GOTERM_CC_FAT         | GO:0044421~extracellular region part     | 5                         | 1.40 | 0.995682095 | 0.46            | 1          | 1           | 100 |
| GOTERM_CC_FAT         | GO:0005576~extracellular region          | 13                        | 3.64 | 0.997089406 | 0.57            | 1          | 1           | 100 |
| GOTERM_BP_FAT         | GO:0009611~response to wounding          | 3                         | 0.84 | 0.998971915 | 0.33            | 1          | 1           | 100 |
| Annotation Cluster 70 |                                          | Enrichment Score: 1.80E-7 |      |             |                 |            |             |     |
| Category              | Term                                     | Count                     | %    | PValue      | Fold Enrichment | Bonferroni | Benjamini   | FDR |
| UP_SEQ_FEATURE        | nucleotide phosphate-binding region:ATP  | 3                         | 0.84 | 0.999996381 | 0.20            | 1          | 1           | 100 |
| SP_PIR_KEYWORDS       | atp-binding                              | 5                         | 1.40 | 0.99999891  | 0.24            | 1          | 1           | 100 |
| SP_PIR_KEYWORDS       | nucleotide-binding                       | 7                         | 1.96 | 0.999999767 | 0.27            | 1          | 1           | 100 |
| GOTERM_MF_FAT         | GO:0005524~ATP binding                   | 6                         | 1.68 | 0.99999999  | 0.22            | 1          | 1           | 100 |
| GOTERM_MF_FAT         | GO:0032559~adenyl ribonucleotide binding | 6                         | 1.68 | 0.999999993 | 0.22            | 1          | 1           | 100 |
| GOTERM_MF_FAT         | GO:0032555~purine ribonucleotide binding | 9                         | 2.52 | 0.999999996 | 0.27            | 1          | 1           | 100 |
| GOTERM_MF_FAT         | GO:0032553~ribonucleotide binding        | 9                         | 2.52 | 0.999999996 | 0.27            | 1          | 1           | 100 |
| GOTERM_MF_FAT         | GO:0030554~adenyl nucleotide binding     | 6                         | 1.68 | 0.999999998 | 0.21            | 1          | 1           | 100 |
| GOTERM_MF_FAT         | GO:0001883~purine nucleoside binding     | 6                         | 1.68 | 0.999999999 | 0.20            | 1          | 1           | 100 |
| GOTERM_MF_FAT         | GO:0017076~purine nucleotide binding     | 9                         | 2.52 | 0.999999999 | 0.25            | 1          | 1           | 100 |
| GOTERM_MF_FAT         | GO:0001882~nucleoside binding            | 6                         | 1.68 | 0.999999999 | 0.20            | 1          | 1           | 100 |
| GOTERM_MF_FAT         | GO:0000166~nucleotide binding            | 12                        | 3.36 | 1           | 0.29            | 1          | 1           | 100 |