

167 david id matched

Annotation Cluster 2 Enrichment Score: 6.170111838016615

Annotation Cluster 3 Enrichment Score: 4.295846146513621

Annotation Cluster 4 Enrichment Score: 3.4703660898619857

Annotation Cluster 5 Enrichment Score: 3.3033187139944187

| Category        | Term                     | Count | %          | PValue            | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR               |
|-----------------|--------------------------|-------|------------|-------------------|-------------|------------|----------|-----------|--------------|------------|------------|-------------------|
| GOTERM_MF_FAT   | GO:0004857~enzyme        | 12    | 7.18562874 | <b>9.61E-06</b>   | KNG1, CDKN  | 118        | 243      | 13288     | 5.56099602   | 0.00266856 | 0.00133517 | <b>0.01269442</b> |
| GOTERM_MF_FAT   | GO:0004866~endopeptidase | 9     | 5.38922156 | <b>8.70E-05</b>   | KNG1, NGP,  | 118        | 161      | 13288     | 6.29497842   | 0.02389302 | 0.00482494 | 0.11482746        |
| INTERPRO        | IPR000010:Proteinase     | 5     | 2.99401198 | <b>9.94E-05</b>   | KNG1, NGP,  | 157        | 28       | 17763     | 20.2035942   | 0.03420696 | 0.03420696 | 0.13591622        |
| SMART           | SM00043:CY               | 5     | 2.99401198 | <b>1.21E-04</b>   | KNG1, NGP,  | 86         | 28       | 9131      | 18.9597176   | 0.0091367  | 0.0091367  | 0.12700807        |
| GOTERM_MF_FAT   | GO:0030414~peptidase     | 9     | 5.38922156 | <b>1.61E-04</b>   | KNG1, NGP,  | 118        | 176      | 13288     | 5.75847458   | 0.04390512 | 0.00745509 | 0.21308287        |
| GOTERM_MF_FAT   | GO:0004869~cysteine      | 5     | 2.99401198 | <b>3.70E-04</b>   | KNG1, NGP,  | 118        | 39       | 13288     | 14.4372012   | 0.09779676 | 0.01459466 | 0.48775619        |
| INTERPRO        | IPR018073:Proteinase     | 4     | 2.39520958 | <b>5.81E-04</b>   | KNG1, STFA1 | 157        | 19       | 17763     | 23.8189742   | 0.1839561  | 0.0655175  | 0.79122895        |
| SP_PIR_KEYWORDS | thiol protease inhibitor | 4     | 2.39520958 | <b>8.92E-04</b>   | KNG1, STFA1 | 157        | 22       | 17854     | 20.6763173   | 0.22386215 | 0.01930546 | 1.17550453        |
| UP_SEQ_FEATURE  | site:Reactive site       | 3     | 1.79640719 | <b>0.0022884</b>  | STFA1, BC10 | 149        | 8        | 16021     | 40.3213087   | 0.67232366 | 0.24340883 | 3.23351533        |
| UP_PIR_KEYWORDS | protease inhibitor       | 6     | 3.59281437 | <b>0.00269049</b> | KNG1, SERP1 | 157        | 109      | 17854     | 6.25980249   | 0.53472567 | 0.03946985 | 3.50707337        |
| UP_SEQ_FEATURE  | short sequence motif:    | 3     | 1.79640719 | <b>0.00292443</b> | STFA1, BC10 | 149        | 9        | 16021     | 35.8411633   | 0.75980028 | 0.24817892 | 4.11479424        |

|                 |                      |   |            |            |             |     |    |       |            |            |            |            |
|-----------------|----------------------|---|------------|------------|-------------|-----|----|-------|------------|------------|------------|------------|
| INTERPRO        | IPR001713:Proteinase | 3 | 1.79640719 | 0.00400142 | STFA1, BC10 | 157 | 11 | 17763 | 30.8563984 | 0.75421688 | 0.13092911 | 5.33599345 |
| PIR_SUPERFAMILY | PIRSF001638:cystatin | 3 | 1.79640719 | 0.00509003 | STFA1, BC10 | 101 | 9  | 8136  | 26.8514851 | 0.42370031 | 0.24085595 | 5.58404919 |

#### Annotation Cluster 6 Enrichment Score: 2.571421951575464

| Category        | Term                  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|-----------------------|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT   | GO:0002526--acute in  | 10    | 5.98802395 | 5.65E-08   | C8A, C9, LO  | 127        | 81       | 13588     | 13.2089044   | 5.13E-05   | 2.57E-05   | 8.82E-05   |
| KEGG_PATHWAY    | mmu05322:Systemic I   | 9     | 5.38922156 | 1.99E-05   | C9, HIST1H2  | 67         | 103      | 5738      | 7.4832633    | 0.00201016 | 0.00201016 | 0.02215176 |
| GOTERM_BP_FAT   | GO:0002252--immune    | 9     | 5.38922156 | 2.20E-05   | C8A, C9, LO  | 127        | 126      | 13588     | 7.64229471   | 0.01978609 | 0.00221803 | 0.03434029 |
| GOTERM_BP_FAT   | GO:0006955--immune    | 16    | 9.58083832 | 3.02E-05   | CXCL1, C9, F | 127        | 471      | 13588     | 3.63455205   | 0.02704115 | 0.00273759 | 0.04710297 |
| GOTERM_BP_FAT   | GO:0051605--protein   | 6     | 3.59281437 | 3.35E-04   | C8A, C9, LO  | 127        | 65       | 13588     | 9.87619624   | 0.2624065  | 0.01884286 | 0.5217254  |
| SP_PIR_KEYWORDS | immune response       | 8     | 4.79041916 | 0.00117957 | C8A, C9, LO  | 157        | 184      | 17854     | 4.94433675   | 0.28480094 | 0.02365811 | 1.55183215 |
| GOTERM_BP_FAT   | GO:0002443--leukocyt  | 6     | 3.59281437 | 0.00141137 | C8A, C9, LO  | 127        | 89       | 13588     | 7.21295231   | 0.72263692 | 0.06210886 | 2.1799276  |
| GOTERM_BP_FAT   | GO:0016485--protein   | 6     | 3.59281437 | 0.00148345 | C8A, C9, LO  | 127        | 90       | 13588     | 7.1328084    | 0.74023423 | 0.06217253 | 2.29006199 |
| KEGG_PATHWAY    | mmu04610:Complem      | 6     | 3.59281437 | 0.00160223 | C8A, KNG1,   | 67         | 75       | 5738      | 6.85134328   | 0.14952036 | 0.07778547 | 1.76732524 |
| GOTERM_BP_FAT   | GO:0050778--positive  | 7     | 4.19161677 | 0.00166119 | C8A, C9, LO  | 127        | 136      | 13588     | 5.50694766   | 0.77900578 | 0.06352795 | 2.56113172 |
| GOTERM_BP_FAT   | GO:0048584--positive  | 8     | 4.79041916 | 0.00172774 | C8A, C9, LO  | 127        | 186      | 13588     | 4.60181187   | 0.79198442 | 0.06332845 | 2.66243353 |
| GOTERM_BP_FAT   | GO:0051604--protein   | 6     | 3.59281437 | 0.00197426 | C8A, C9, LO  | 127        | 96       | 13588     | 6.68700787   | 0.83377297 | 0.06926067 | 3.03687077 |
| GOTERM_BP_FAT   | GO:0002684--positive  | 8     | 4.79041916 | 0.00306874 | C8A, CORO1   | 127        | 206      | 13588     | 4.15503402   | 0.93862197 | 0.09486211 | 4.68302804 |
| GOTERM_BP_FAT   | GO:0006956--compler   | 4     | 2.39520958 | 0.00444644 | C8A, C9, LO  | 127        | 36       | 13588     | 11.888014    | 0.98251434 | 0.1302332  | 6.71798271 |
| GOTERM_BP_FAT   | GO:0002541--activatio | 4     | 2.39520958 | 0.00444644 | C8A, C9, LO  | 127        | 36       | 13588     | 11.888014    | 0.98251434 | 0.1302332  | 6.71798271 |
| GOTERM_BP_FAT   | GO:0006959--humoral   | 4     | 2.39520958 | 0.01369271 | C8A, C9, LO  | 127        | 54       | 13588     | 7.92534267   | 0.99999634 | 0.26872978 | 19.3583837 |
| GOTERM_BP_FAT   | GO:0016064--immunc    | 4     | 2.39520958 | 0.02064726 | C8A, C9, LO  | 127        | 63       | 13588     | 6.79315086   | 0.99999999 | 0.34359473 | 27.7891258 |
| SP_PIR_KEYWORDS | complement pathway    | 3     | 1.79640719 | 0.02149087 | C8A, C9, LO  | 157        | 26       | 17854     | 13.1215091   | 0.99790865 | 0.19164729 | 25.0153268 |
| GOTERM_BP_FAT   | GO:0019724--B cell m  | 4     | 2.39520958 | 0.02241131 | C8A, C9, LO  | 127        | 65       | 13588     | 6.58413083   | 1          | 0.36071972 | 29.7924176 |
| SP_PIR_KEYWORDS | innate immunity       | 4     | 2.39520958 | 0.02796084 | C8A, C9, LO  | 157        | 75       | 17854     | 6.06505308   | 0.99968218 | 0.21656008 | 31.3257458 |
| GOTERM_BP_FAT   | GO:0006958--compler   | 3     | 1.79640719 | 0.03133262 | C8A, C9, LO  | 127        | 30       | 13588     | 10.6992126   | 1          | 0.4264272  | 39.1512559 |
| GOTERM_BP_FAT   | GO:0002449--lymphoc   | 4     | 2.39520958 | 0.03353649 | C8A, C9, LO  | 127        | 76       | 13588     | 5.63116453   | 1          | 0.44256246 | 41.2761327 |
| GOTERM_BP_FAT   | GO:0002455--humoral   | 3     | 1.79640719 | 0.0415969  | C8A, C9, LO  | 127        | 35       | 13588     | 9.17075366   | 1          | 0.49176307 | 48.4707005 |
| GOTERM_BP_FAT   | GO:0002250--adaptive  | 4     | 2.39520958 | 0.04312082 | C8A, C9, LO  | 127        | 84       | 13588     | 5.09486314   | 1          | 0.49844948 | 49.7345767 |
| GOTERM_BP_FAT   | GO:0002460--adaptive  | 4     | 2.39520958 | 0.04312082 | C8A, C9, LO  | 127        | 84       | 13588     | 5.09486314   | 1          | 0.49844948 | 49.7345767 |
| GOTERM_BP_FAT   | GO:0002253--activatio | 4     | 2.39520958 | 0.04570906 | C8A, C9, LO  | 127        | 86       | 13588     | 4.97637795   | 1          | 0.50739053 | 51.8149045 |
| GOTERM_BP_FAT   | GO:0045087--innate ir | 4     | 2.39520958 | 0.07727972 | C8A, C9, LO  | 127        | 107      | 13588     | 3.99970564   | 1          | 0.62726494 | 71.4958695 |

#### Annotation Cluster 7 Enrichment Score: 2.484785242230664

| Category      | Term                 | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|----------------------|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_CC_FAT | GO:0016023--cytoplas | 12    | 7.18562874 | 0.00209316 | EGFR, CORO   | 121        | 414      | 12504     | 2.99532878   | 0.2773133  | 0.1026056  | 2.48498816 |
| GOTERM_CC_FAT | GO:0031988--membra   | 12    | 7.18562874 | 0.00234134 | EGFR, CORO   | 121        | 420      | 12504     | 2.95253837   | 0.30464515 | 0.07008919 | 2.77584242 |
| GOTERM_CC_FAT | GO:0031410--cytoplas | 13    | 7.78443114 | 0.00348234 | EGFR, NGP, ( | 121        | 508      | 12504     | 2.64449795   | 0.41766221 | 0.07433559 | 4.10282761 |
| GOTERM_CC_FAT | GO:0031982--vesicle  | 13    | 7.78443114 | 0.00413345 | EGFR, NGP, ( | 121        | 519      | 12504     | 2.58844886   | 0.47376777 | 0.07711586 | 4.85260954 |
| GOTERM_CC_FAT | GO:0030141--secretor | 6     | 3.59281437 | 0.00534101 | CAMP, EAR6   | 121        | 117      | 12504     | 5.29942784   | 0.56398381 | 0.08810521 | 6.22896035 |

#### Annotation Cluster 8 Enrichment Score: 2.251937441120359

| Category        | Term                   | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|------------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| SP_PIR_KEYWORDS | heme                   | 9     | 5.38922156 | 3.54E-05   | CYP17A1, HF | 157        | 142      | 17854     | 7.20758949   | 0.01000187 | 0.00200843 | 0.04689215 |
| GOTERM_MF_FAT   | GO:0020037--heme bi    | 9     | 5.38922156 | 3.95E-05   | CYP17A1, HF | 118        | 144      | 13288     | 7.03813559   | 0.01091406 | 0.00365134 | 0.05212395 |
| COG_ONTOLOGY    | Secondary metabolite   | 7     | 4.19161677 | 4.29E-05   | CYP17A1, LC | 15         | 109      | 2040      | 8.73394495   | 2.58E-04   | 2.58E-04   | 0.02054853 |
| GOTERM_MF_FAT   | GO:0046906--tetrapyr   | 9     | 5.38922156 | 5.54E-05   | CYP17A1, HF | 118        | 151      | 13288     | 6.71186441   | 0.01527025 | 0.00383962 | 0.07308161 |
| SP_PIR_KEYWORDS | metalloprotein         | 6     | 3.59281437 | 1.27E-04   | CYP17A1, LC | 157        | 56       | 17854     | 12.1842584   | 0.03552749 | 0.00515438 | 0.16864336 |
| INTERPRO        | IPR002401:Cytochrom    | 6     | 3.59281437 | 3.74E-04   | CYP17A1, LC | 157        | 70       | 17763     | 9.6977252    | 0.1228492  | 0.06343671 | 0.51089152 |
| SP_PIR_KEYWORDS | chromoprotein          | 5     | 2.99401198 | 4.01E-04   | CYP17A1, LC | 157        | 40       | 17854     | 14.2149682   | 0.10770889 | 0.0125827  | 0.53033328 |
| INTERPRO        | IPR017973:Cytochrom    | 6     | 3.59281437 | 7.34E-04   | CYP17A1, LC | 157        | 81       | 17763     | 8.38075018   | 0.22654492 | 0.05008003 | 0.99880673 |
| INTERPRO        | IPR001128:Cytochrom    | 6     | 3.59281437 | 0.00101447 | CYP17A1, LC | 157        | 87       | 17763     | 7.80276741   | 0.29899821 | 0.04948303 | 1.37858327 |
| INTERPRO        | IPR017972:Cytochrom    | 6     | 3.59281437 | 0.00112374 | CYP17A1, LC | 157        | 89       | 17763     | 7.62742432   | 0.32532841 | 0.0427833  | 1.5260128  |
| GOTERM_BP_FAT   | GO:0055114--oxidatio   | 16    | 9.58083832 | 0.00138694 | NDUFB10, K  | 127        | 672      | 13588     | 2.54743157   | 0.17640594 | 0.06417512 | 2.14257059 |
| GOTERM_MF_FAT   | GO:0009055--electron   | 8     | 4.79041916 | 0.00204845 | CYP17A1, LC | 118        | 202      | 13288     | 4.45980869   | 0.43450416 | 0.05541087 | 2.67196308 |
| SP_PIR_KEYWORDS | iron                   | 10    | 5.98802395 | 0.00208114 | CYP17A1, HF | 157        | 321      | 17854     | 3.54267119   | 0.44659152 | 0.03630332 | 2.72289129 |
| UP_SEQ_FEATURE  | metal ion-binding site | 6     | 3.59281437 | 0.00224133 | CYP17A1, LC | 149        | 99       | 16021     | 6.51657515   | 0.66470737 | 0.30528288 | 3.16799056 |

|                 |                        |    |            |            |             |     |      |       |            |            |            |            |
|-----------------|------------------------|----|------------|------------|-------------|-----|------|-------|------------|------------|------------|------------|
| SP_PIR_KEYWORDS | Monoxygenase           | 6  | 3.59281437 | 0.00258497 | CYP17A1, LC | 157 | 108  | 17854 | 6.31776362 | 0.5205339  | 0.04001526 | 3.37170122 |
| GOTERM_MF_FAT   | GO:0005506--iron ion   | 10 | 5.98802395 | 0.00328341 | CYP17A1, HF | 118 | 343  | 13288 | 3.28309532 | 0.59919902 | 0.0797568  | 4.25078679 |
| SP_PIR_KEYWORDS | oxidoreductase         | 13 | 7.78443114 | 0.00447872 | LOC1000442  | 157 | 572  | 17854 | 2.58453966 | 0.72051683 | 0.06175171 | 5.77476061 |
| KEGG_PATHWAY    | mmu00830:Retinol m     | 5  | 2.99401198 | 0.00749136 | LOC1000442  | 67  | 68   | 5738  | 6.29719052 | 0.53208847 | 0.17293253 | 8.02180216 |
| PIR_SUPERFAMILY | PIRSF000050:cytochro   | 3  | 1.79640719 | 0.00911031 | LOC1000442  | 101 | 12   | 8136  | 20.1386139 | 0.62783681 | 0.28069822 | 9.79201725 |
| SP_PIR_KEYWORDS | microsome              | 5  | 2.99401198 | 0.01150167 | LOC1000442  | 157 | 100  | 17854 | 5.68598726 | 0.96257452 | 0.1231472  | 14.212355  |
| SP_PIR_KEYWORDS | endoplasmic reticulum  | 13 | 7.78443114 | 0.01598305 | LOC1000442  | 157 | 678  | 17854 | 2.18046709 | 0.98970248 | 0.15589299 | 19.2253357 |
| SP_PIR_KEYWORDS | electron transfer      | 3  | 1.79640719 | 0.02307888 | CYP17A1, CY | 157 | 27   | 17854 | 12.6355272 | 0.99868145 | 0.19257922 | 26.6119606 |
| GOTERM_CC_FAT   | GO:0005792--microso    | 6  | 3.59281437 | 0.02721972 | LOC1000442  | 121 | 176  | 12504 | 3.5229151  | 0.98612327 | 0.34802834 | 28.2098654 |
| GOTERM_CC_FAT   | GO:0042598--vesicular  | 6  | 3.59281437 | 0.03084011 | LOC1000442  | 121 | 182  | 12504 | 3.40677504 | 0.9922144  | 0.35686922 | 31.3536066 |
| GOTERM_CC_FAT   | GO:0005783--endopla    | 14 | 8.38323353 | 0.05827162 | LOC1000442  | 121 | 838  | 12504 | 1.72642458 | 0.99990912 | 0.5395246  | 51.3745559 |
| KEGG_PATHWAY    | mmu00590:Arachidon     | 4  | 2.39520958 | 0.06974514 | LOC1000442  | 67  | 83   | 5738  | 4.12731523 | 0.99932579 | 0.6476527  | 55.2442095 |
| PIR_SUPERFAMILY | PIRSF000045:cytochro   | 3  | 1.79640719 | 0.07194221 | CYP17A1, CY | 101 | 36   | 8136  | 6.71287129 | 0.99968515 | 0.73917429 | 56.8585593 |
| GOTERM_CC_FAT   | GO:0005624--membra     | 9  | 5.38922156 | 0.11713973 | RAC2, LOC10 | 121 | 510  | 12504 | 1.82362664 | 1          | 0.70089169 | 77.6026492 |
| GOTERM_CC_FAT   | GO:0005626--insolubl   | 9  | 5.38922156 | 0.13495041 | RAC2, LOC10 | 121 | 528  | 12504 | 1.76145755 | 1          | 0.67486195 | 82.4651474 |
| GOTERM_CC_FAT   | GO:0000267--cell fract | 9  | 5.38922156 | 0.21342953 | RAC2, LOC10 | 121 | 596  | 12504 | 1.56048588 | 1          | 0.77427828 | 94.4040393 |
| GOTERM_CC_FAT   | GO:0019898--extrinsic  | 4  | 2.39520958 | 0.83641803 | LOC1000442  | 121 | 472  | 12504 | 0.87575291 | 1          | 0.9974473  | 100        |
| SP_PIR_KEYWORDS | metal-binding          | 19 | 11.3772455 | 0.91307395 | S100A6, APC | 157 | 2682 | 17854 | 0.80562086 | 1          | 0.99965565 | 100        |
| GOTERM_MF_FAT   | GO:0046914--transitio  | 15 | 8.98203593 | 0.9900629  | S100A6, LOC | 118 | 2608 | 13288 | 0.64768119 | 1          | 1          | 100        |

#### Annotation Cluster 9 Enrichment Score: 2.116135966901011

| Category      | Term                 | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|----------------------|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0006022--aminogl  | 6     | 3.59281437 | 1.16E-04   | PGLYRP1, ITI | 127        | 52       | 13588     | 12.3452453   | 0.10004345 | 0.00750093 | 0.18099638 |
| GOTERM_BP_FAT | GO:0005976--polysacc | 6     | 3.59281437 | 0.00163571 | PGLYRP1, ITI | 127        | 92       | 13588     | 6.97774735   | 0.77382365 | 0.06533347 | 2.52230865 |
| GOTERM_BP_FAT | GO:0006026--aminogl  | 3     | 1.79640719 | 0.01184435 | PGLYRP1, C   | 127        | 18       | 13588     | 17.832021    | 0.99997998 | 0.25353146 | 16.9674913 |
| GOTERM_BP_FAT | GO:0000272--polysacc | 3     | 1.79640719 | 0.01596558 | PGLYRP1, C   | 127        | 21       | 13588     | 15.2845894   | 0.99999955 | 0.29386275 | 22.2100558 |
| GOTERM_BP_FAT | GO:0009057--macrom   | 6     | 3.59281437 | 0.73139553 | UHRF1, SO    | 127        | 654      | 13588     | 0.98157914   | 1          | 0.99959075 | 99.999999  |

#### Annotation Cluster 10 Enrichment Score: 2.0569934354400283

| Category     | Term                  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|--------------|-----------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| KEGG_PATHWAY | mmu04610:Compleme     | 6     | 3.59281437 | 0.00160223 | C8A, KNG1,  | 67         | 75       | 5738      | 6.85134328   | 0.14952036 | 0.07778547 | 1.76732524 |
| BIOCARTA     | m_classicPathway:Clas | 3     | 1.79640719 | 0.01251241 | C9, LOC1000 | 17         | 13       | 1171      | 15.8959276   | 0.44666604 | 0.44666604 | 11.2720512 |
| BIOCARTA     | m_lectinPathway:Lecti | 3     | 1.79640719 | 0.01251241 | C9, LOC1000 | 17         | 13       | 1171      | 15.8959276   | 0.44666604 | 0.44666604 | 11.2720512 |
| BIOCARTA     | m_compPathway:Com     | 3     | 1.79640719 | 0.02358413 | C9, LOC1000 | 17         | 18       | 1171      | 11.4803922   | 0.67428555 | 0.42928602 | 20.2832679 |

#### Annotation Cluster 11 Enrichment Score: 1.9600886784789286

| Category        | Term                  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|-----------------------|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| INTERPRO        | IPR002172:Low densit  | 5     | 2.99401198 | 7.01E-04   | C8A, C9, C6, | 157        | 46       | 17763     | 12.2978399   | 0.21764697 | 0.05951756 | 0.95454561 |
| SMART           | SM00192:LDLa          | 5     | 2.99401198 | 8.47E-04   | C8A, C9, C6, | 86         | 46       | 9131      | 11.5406977   | 0.06239835 | 0.03170167 | 0.88813562 |
| KEGG_PATHWAY    | mmu04610:Compleme     | 6     | 3.59281437 | 0.00160223 | C8A, KNG1,   | 67         | 75       | 5738      | 6.85134328   | 0.14952036 | 0.07778547 | 1.76732524 |
| INTERPRO        | IPR001862:Membrane    | 3     | 1.79640719 | 0.00477412 | C8A, C9, C6  | 157        | 12       | 17763     | 28.2850318   | 0.81268105 | 0.14124147 | 6.33550226 |
| SMART           | SM00457:MACPF         | 3     | 1.79640719 | 0.00532023 | C8A, C9, C6  | 86         | 12       | 9131      | 26.5436047   | 0.33330133 | 0.12640556 | 5.45878397 |
| KEGG_PATHWAY    | mmu05020:Prion dise   | 4     | 2.39520958 | 0.0073162  | C8A, C9, C6, | 67         | 35       | 5738      | 9.78763326   | 0.52367384 | 0.21902917 | 7.84112845 |
| UP_SEQ_FEATURE  | domain:EGF-like       | 4     | 2.39520958 | 0.0250163  | C8A, C9, SEL | 149        | 68       | 16021     | 6.32491117   | 0.99999562 | 0.70881358 | 30.4744745 |
| SP_PIR_KEYWORDS | egf-like domain       | 6     | 3.59281437 | 0.04551278 | C8A, C9, SEL | 157        | 222      | 17854     | 3.07350663   | 0.9999982  | 0.30751763 | 46.0578804 |
| INTERPRO        | IPR000884:Thrombos    | 3     | 1.79640719 | 0.09484593 | C8A, C9, C6  | 157        | 59       | 17763     | 5.75288783   | 1          | 0.84049178 | 74.4080806 |
| SMART           | SM00209:TSP1          | 3     | 1.79640719 | 0.10433367 | C8A, C9, C6  | 86         | 59       | 9131      | 5.39869925   | 0.99976926 | 0.69769525 | 68.6357671 |
| INTERPRO        | IPR013032:EGF-like re | 6     | 3.59281437 | 0.1378983  | C8A, C9, SEL | 157        | 310      | 17763     | 2.18980892   | 1          | 0.8851243  | 86.8584315 |

#### Annotation Cluster 12 Enrichment Score: 1.9142102102993352

| Category      | Term                  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|-----------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_CC_FAT | GO:0032994--protein-  | 4     | 2.39520958 | 0.00213119 | SAA1, SORL1 | 121        | 27       | 12504     | 15.3094582   | 0.28156988 | 0.07934666 | 2.52961066 |
| GOTERM_CC_FAT | GO:0034358--plasma l  | 4     | 2.39520958 | 0.00213119 | SAA1, SORL1 | 121        | 27       | 12504     | 15.3094582   | 0.28156988 | 0.07934666 | 2.52961066 |
| GOTERM_BP_FAT | GO:0008203--choleste  | 4     | 2.39520958 | 0.02717037 | SAA1, SORL1 | 127        | 70       | 13588     | 6.11383577   | 1          | 0.39977455 | 34.9405327 |
| GOTERM_BP_FAT | GO:0016125--sterol m  | 4     | 2.39520958 | 0.03466649 | SAA1, SORL1 | 127        | 77       | 13588     | 5.55803252   | 1          | 0.44747366 | 42.3385067 |
| GOTERM_BP_FAT | GO:0008202--steroid r | 5     | 2.99401198 | 0.06276239 | CYP17A1, SA | 127        | 161      | 13588     | 3.32273683   | 1          | 0.57385394 | 63.6331078 |

Annotation Cluster 13 Enrichment Score: 1.6532053527757617

| Category        | Term                  | Count | %          | PValue            | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|-----------------------|-------|------------|-------------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| PIR_SUPERFAMILY | PIRSF002353:S-100 pr  | 4     | 2.39520958 | <b>3.66E-04</b>   | S100A6, S10 | 101        | 12       | 8136      | 26.8514851   | 0.03873604 | 0.03873604 | 0.41104214 |
| INTERPRO        | IPR013787:S100/CaBP   | 4     | 2.39520958 | <b>7.87E-04</b>   | S100A6, S10 | 157        | 21       | 17763     | 21.5505005   | 0.24079185 | 0.04487515 | 1.07070454 |
| INTERPRO        | IPR001751:S100/CaBP   | 4     | 2.39520958 | <b>0.00103426</b> | S100A6, S10 | 157        | 23       | 17763     | 19.6765439   | 0.30384073 | 0.04426261 | 1.40529398 |
| UP_SEQ_FEATURE  | calcium-binding regic | 3     | 1.79640719 | <b>0.00526488</b> | S100A8, S10 | 149        | 12       | 16021     | 26.8808725   | 0.92352322 | 0.34848923 | 7.29382322 |
| UP_SEQ_FEATURE  | calcium-binding regic | 3     | 1.79640719 | <b>0.00526488</b> | S100A8, S10 | 149        | 12       | 16021     | 26.8808725   | 0.92352322 | 0.34848923 | 7.29382322 |
| SP_PIR_KEYWORDS | calcium binding       | 4     | 2.39520958 | <b>0.00800906</b> | S100A6, S10 | 157        | 47       | 17854     | 9.67827619   | 0.89809666 | 0.0945223  | 10.1076781 |
| SP_PIR_KEYWORDS | EF hand               | 3     | 1.79640719 | <b>0.02471372</b> | S100A6, S10 | 157        | 28       | 17854     | 12.1842584   | 0.99918055 | 0.19915674 | 28.2227979 |
| SP_PIR_KEYWORDS | calcium               | 11    | 6.58682635 | 0.10769659        | S100A6, APC | 157        | 731      | 17854     | 1.71124104   | 1          | 0.49769273 | 77.9083816 |
| INTERPRO        | IPR018248:EF hand     | 4     | 2.39520958 | 0.11034671        | S100A6, S10 | 157        | 132      | 17763     | 3.42848871   | 1          | 0.85754429 | 79.792926  |
| INTERPRO        | IPR011992:EF-Hand ty  | 5     | 2.99401198 | 0.14063021        | S100A6, S10 | 157        | 227      | 17763     | 2.49207329   | 1          | 0.88018225 | 87.4166914 |
| UP_SEQ_FEATURE  | domain:EF-hand 2      | 4     | 2.39520958 | 0.18465777        | S100A6, S10 | 149        | 160      | 16021     | 2.68808725   | 1          | 0.99466048 | 94.6545036 |
| UP_SEQ_FEATURE  | domain:EF-hand 1      | 4     | 2.39520958 | 0.1866924         | S100A6, S10 | 149        | 161      | 16021     | 2.67139105   | 1          | 0.99351823 | 94.8637591 |
| INTERPRO        | IPR018249:EF-HAND 2   | 4     | 2.39520958 | 0.26992824        | S100A6, S10 | 157        | 205      | 17763     | 2.20761224   | 1          | 0.97453572 | 98.6470575 |
| INTERPRO        | IPR018247:EF-HAND 1   | 4     | 2.39520958 | 0.28175247        | S100A6, S10 | 157        | 211      | 17763     | 2.14483654   | 1          | 0.97320841 | 98.9178395 |

Annotation Cluster 14 Enrichment Score: 1.5454828304805655

| Category        | Term                  | Count | %          | PValue            | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|-----------------------|-------|------------|-------------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| SP_PIR_KEYWORDS | Lectin                | 8     | 4.79041916 | <b>6.70E-04</b>   | APCS, KLRA1  | 157        | 167      | 17854     | 5.44765247   | 0.17326121 | 0.0157305  | 0.88384421 |
| GOTERM_MF_FAT   | GO:0005529--sugar bi  | 8     | 4.79041916 | <b>0.00109111</b> | APCS, KLRA1  | 118        | 181      | 13288     | 4.97724506   | 0.26176643 | 0.03315943 | 1.43155404 |
| INTERPRO        | IPR001304:C-type lect | 3     | 1.79640719 | 0.27768581        | KLRA17, SELI | 157        | 118      | 17763     | 2.87644392   | 1          | 0.97459188 | 98.8309659 |
| SMART           | SM00034:CLECT         | 3     | 1.79640719 | 0.30078125        | KLRA17, SELI | 86         | 118      | 9131      | 2.69934963   | 1          | 0.93407361 | 97.6833396 |
| INTERPRO        | IPR016186:C-type lect | 3     | 1.79640719 | 0.30691152        | KLRA17, SELI | 157        | 127      | 17763     | 2.67260143   | 1          | 0.97703535 | 99.335492  |

Annotation Cluster 15 Enrichment Score: 1.53039354271653

| Category        | Term                  | Count | %          | PValue            | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|-----------------------|-------|------------|-------------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT   | GO:0016052--carbohy   | 7     | 4.19161677 | <b>1.04E-04</b>   | TP11, HK3, PI | 127        | 81       | 13588     | 9.24623311   | 0.08988916 | 0.00781835 | 0.16174637 |
| GOTERM_BP_FAT   | GO:0006007--glucose   | 4     | 2.39520958 | <b>0.01236391</b> | TP11, HK3, PI | 127        | 52       | 13588     | 8.23016354   | 0.99998758 | 0.25715948 | 17.6461707 |
| GOTERM_BP_FAT   | GO:0019320--hexose    | 4     | 2.39520958 | <b>0.01236391</b> | TP11, HK3, PI | 127        | 52       | 13588     | 8.23016354   | 0.99998758 | 0.25715948 | 17.6461707 |
| GOTERM_BP_FAT   | GO:0046365--monosa    | 4     | 2.39520958 | <b>0.01369271</b> | TP11, HK3, PI | 127        | 54       | 13588     | 7.92534267   | 0.99999634 | 0.26872978 | 19.3583837 |
| GOTERM_BP_FAT   | GO:0044275--cellular  | 4     | 2.39520958 | <b>0.01815063</b> | TP11, HK3, PI | 127        | 60       | 13588     | 7.1328084    | 0.99999994 | 0.32076958 | 24.8623346 |
| GOTERM_BP_FAT   | GO:0046164--alcohol   | 4     | 2.39520958 | <b>0.02241131</b> | TP11, HK3, PI | 127        | 65       | 13588     | 6.58413083   | 1          | 0.36071972 | 29.7924176 |
| KEGG_PATHWAY    | mmu00010:Glycolysis   | 4     | 2.39520958 | <b>0.04288933</b> | TP11, HK3, PI | 67         | 68       | 5738      | 5.03775241   | 0.98805522 | 0.58748894 | 38.5818796 |
| SP_PIR_KEYWORDS | glycolysis            | 3     | 1.79640719 | 0.05202088        | TP11, HK3, PI | 157        | 42       | 17854     | 8.12283894   | 0.99999974 | 0.3291872  | 50.7332625 |
| GOTERM_BP_FAT   | GO:0006096--glycolysi | 3     | 1.79640719 | 0.06269399        | TP11, HK3, PI | 127        | 44       | 13588     | 7.29491768   | 1          | 0.57875574 | 63.5916704 |
| KEGG_PATHWAY    | mmu00051:Fructose a   | 3     | 1.79640719 | 0.06708109        | TP11, PFKFB4  | 67         | 37       | 5738      | 6.943929     | 0.99910002 | 0.68927783 | 53.7980958 |
| GOTERM_BP_FAT   | GO:0019318--hexose    | 5     | 2.99401198 | 0.07224799        | TP11, PFKFB4  | 127        | 169      | 13588     | 3.16544751   | 1          | 0.61159918 | 68.971196  |
| GOTERM_BP_FAT   | GO:0005996--monosa    | 5     | 2.99401198 | 0.10182577        | TP11, PFKFB4  | 127        | 191      | 13588     | 2.80084099   | 1          | 0.7135364  | 81.2855133 |
| GOTERM_BP_FAT   | GO:0006006--glucose   | 4     | 2.39520958 | 0.14086588        | TP11, HK3, PI | 127        | 140      | 13588     | 3.05691789   | 1          | 0.80247777 | 90.645912  |
| GOTERM_BP_FAT   | GO:0006091--generati  | 4     | 2.39520958 | 0.43711589        | TP11, NDUFB   | 127        | 261      | 13588     | 1.63972607   | 1          | 0.98303575 | 99.9872587 |

Annotation Cluster 16 Enrichment Score: 1.470063004288343

| Category      | Term                 | Count | %          | PValue            | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|----------------------|-------|------------|-------------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0050778--positive | 7     | 4.19161677 | <b>0.00166119</b> | C8A, C9, LOC | 127        | 136      | 13588     | 5.50694766   | 0.77900578 | 0.06352795 | 2.56113172 |
| GOTERM_BP_FAT | GO:0048584--positive | 8     | 4.79041916 | <b>0.00172774</b> | C8A, C9, LOC | 127        | 186      | 13588     | 4.60181187   | 0.79198442 | 0.06332845 | 2.66243353 |
| GOTERM_BP_FAT | GO:0002684--positive | 8     | 4.79041916 | <b>0.00306874</b> | C8A, CORO1   | 127        | 206      | 13588     | 4.15503402   | 0.93862197 | 0.09486211 | 4.68302804 |
| GOTERM_BP_FAT | GO:0002824--positive | 3     | 1.79640719 | <b>0.03945441</b> | HPX, H2-Q8,  | 127        | 34       | 13588     | 9.4404817    | 1          | 0.48549719 | 46.6434426 |
| GOTERM_BP_FAT | GO:0002821--positive | 3     | 1.79640719 | <b>0.03945441</b> | HPX, H2-Q8,  | 127        | 34       | 13588     | 9.4404817    | 1          | 0.48549719 | 46.6434426 |
| GOTERM_BP_FAT | GO:0002705--positive | 3     | 1.79640719 | 0.05293277        | HPX, H2-Q8,  | 127        | 40       | 13588     | 8.02440945   | 1          | 0.53772255 | 57.2027992 |
| GOTERM_BP_FAT | GO:0002708--positive | 3     | 1.79640719 | 0.05293277        | HPX, H2-Q8,  | 127        | 40       | 13588     | 8.02440945   | 1          | 0.53772255 | 57.2027992 |
| GOTERM_BP_FAT | GO:0002699--positive | 3     | 1.79640719 | 0.06778593        | HPX, H2-Q8,  | 127        | 46       | 13588     | 6.97774735   | 1          | 0.59248475 | 66.5587439 |
| GOTERM_BP_FAT | GO:0002822--regulati | 3     | 1.79640719 | 0.09509617        | HPX, H2-Q8,  | 127        | 56       | 13588     | 5.73172103   | 1          | 0.69221545 | 78.973462  |
| GOTERM_BP_FAT | GO:0002819--regulati | 3     | 1.79640719 | 0.09509617        | HPX, H2-Q8,  | 127        | 56       | 13588     | 5.73172103   | 1          | 0.69221545 | 78.973462  |
| GOTERM_BP_FAT | GO:0002706--regulati | 3     | 1.79640719 | 0.1218649         | HPX, H2-Q8,  | 127        | 65       | 13588     | 4.93809812   | 1          | 0.76701413 | 86.8399472 |
| GOTERM_BP_FAT | GO:0002703--regulati | 3     | 1.79640719 | 0.13744305        | HPX, H2-Q8,  | 127        | 70       | 13588     | 4.58537683   | 1          | 0.80160362 | 90.0471184 |
| GOTERM_BP_FAT | GO:0002697--regulati | 3     | 1.79640719 | 0.1964331         | HPX, H2-Q8,  | 127        | 88       | 13588     | 3.64745884   | 1          | 0.86817429 | 96.7051154 |

Annotation Cluster 17 Enrichment Score: 1.35121892328476

| Category        | Term                  | Count | %          | PValue            | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR               |
|-----------------|-----------------------|-------|------------|-------------------|--------------|------------|----------|-----------|--------------|------------|------------|-------------------|
| GOTERM_MF_FAT   | GO:0030246--carbohy   | 14    | 8.38323353 | <b>4.23E-06</b>   | KLRA17, APC  | 118        | 317      | 13288     | 4.97331979   | 0.00117604 | 0.00117604 | <b>0.00559046</b> |
| GOTERM_BP_FAT   | GO:0006022--aminogl   | 6     | 3.59281437 | <b>1.16E-04</b>   | PGLYRP1, ITI | 127        | 52       | 13588     | 12.3452453   | 0.10004345 | 0.00750093 | 0.18099638        |
| GOTERM_MF_FAT   | GO:0001871--pattern   | 7     | 4.19161677 | <b>9.29E-04</b>   | PGLYRP1, ITI | 118        | 128      | 13288     | 6.15836864   | 0.22762419 | 0.03176989 | 1.21960486        |
| GOTERM_MF_FAT   | GO:0030247--polysacc  | 7     | 4.19161677 | <b>9.29E-04</b>   | PGLYRP1, ITI | 118        | 128      | 13288     | 6.15836864   | 0.22762419 | 0.03176989 | 1.21960486        |
| GOTERM_BP_FAT   | GO:0005976--polysacc  | 6     | 3.59281437 | <b>0.00163571</b> | PGLYRP1, ITI | 127        | 92       | 13588     | 6.97774735   | 0.77382365 | 0.06533347 | 2.52230865        |
| GOTERM_MF_FAT   | GO:0005539--glycosar  | 6     | 3.59281437 | <b>0.00332672</b> | PGLYRP1, ITI | 118        | 114      | 13288     | 5.92685103   | 0.60401176 | 0.07429305 | 4.30572547        |
| GOTERM_BP_FAT   | GO:0030203--glycosar  | 4     | 2.39520958 | <b>0.00598968</b> | PGLYRP1, ITI | 127        | 40       | 13588     | 10.6992126   | 0.99572503 | 0.16135438 | 8.94912283        |
| GOTERM_MF_FAT   | GO:0008201--heparin   | 4     | 2.39520958 | <b>0.03676527</b> | MPO, LTF, PI | 118        | 83       | 13288     | 5.42699612   | 0.99996997 | 0.45803339 | 39.0268869        |
| SP_PIR_KEYWORDS | zymogen               | 4     | 2.39520958 | 0.25221558        | PRTN3, MMI   | 157        | 199      | 17854     | 2.28582402   | 1          | 0.74157407 | 97.8749225        |
| GOTERM_MF_FAT   | GO:0008236--serine-ty | 4     | 2.39520958 | 0.28680628        | PRTN3, LTF,  | 118        | 212      | 13288     | 2.12472018   | 1          | 0.96084233 | 98.8486586        |
| GOTERM_MF_FAT   | GO:0017171--serine h  | 4     | 2.39520958 | 0.28920723        | PRTN3, LTF,  | 118        | 213      | 13288     | 2.11474497   | 1          | 0.95317589 | 98.8988126        |
| INTERPRO        | IPR001314:Peptidase f | 3     | 1.79640719 | 0.35701734        | PRTN3, PRSS  | 157        | 143      | 17763     | 2.37356911   | 1          | 0.98792207 | 99.7618878        |
| GOTERM_BP_FAT   | GO:0006508--proteoly  | 12    | 7.18562874 | 0.36316069        | C8A, UHRF1,  | 127        | 1034     | 13588     | 1.24168812   | 1          | 0.96616126 | 99.9125365        |
| INTERPRO        | IPR018114:Peptidase f | 3     | 1.79640719 | 0.38335202        | PRTN3, PRSS  | 157        | 151      | 17763     | 2.2478171    | 1          | 0.99090723 | 99.8656046        |
| INTERPRO        | IPR001254:Peptidase f | 3     | 1.79640719 | 0.4081005         | PRTN3, PRSS  | 157        | 159      | 17763     | 2.13471938   | 1          | 0.99299208 | 99.9232491        |
| SP_PIR_KEYWORDS | Serine protease       | 3     | 1.79640719 | 0.42079768        | PRTN3, LTF,  | 157        | 164      | 17854     | 2.08023924   | 1          | 0.8909141  | 99.9280227        |
| SMART           | SM00020:Tryp_SPc      | 3     | 1.79640719 | 0.43765542        | PRTN3, PRSS  | 86         | 159      | 9131      | 2.00329092   | 1          | 0.97389747 | 99.7659682        |
| SP_PIR_KEYWORDS | Protease              | 6     | 3.59281437 | 0.45947268        | PRTN3, MMI   | 157        | 509      | 17854     | 1.3405078    | 1          | 0.90868317 | 99.9711936        |
| GOTERM_MF_FAT   | GO:0004252--serine-ty | 3     | 1.79640719 | 0.49794573        | PRTN3, PRSS  | 118        | 189      | 13288     | 1.78746301   | 1          | 0.9926398  | 99.9888418        |
| GOTERM_MF_FAT   | GO:0004175--endopep   | 5     | 2.99401198 | 0.51028736        | PRTN3, MMI   | 118        | 421      | 13288     | 1.33741294   | 1          | 0.99113443 | 99.9919679        |
| GOTERM_MF_FAT   | GO:0070011--peptidas  | 6     | 3.59281437 | 0.61794469        | PRTN3, MMI   | 118        | 603      | 13288     | 1.1204992    | 1          | 0.99737899 | 99.9996974        |
| GOTERM_MF_FAT   | GO:0008233--peptidas  | 6     | 3.59281437 | 0.65521988        | PRTN3, MMI   | 118        | 629      | 13288     | 1.07418286   | 1          | 0.997903   | 99.999922         |

Annotation Cluster 18 Enrichment Score: 1.3337468841134212

| Category        | Term                  | Count | %          | PValue            | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|-----------------------|-------|------------|-------------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT   | GO:0032956--regulati  | 5     | 2.99401198 | <b>0.00230204</b> | ACTR3, ARPC  | 127        | 60       | 13588     | 8.9160105    | 0.87664137 | 0.07733301 | 3.53263294 |
| GOTERM_BP_FAT   | GO:0032970--regulati  | 5     | 2.99401198 | <b>0.00244614</b> | ACTR3, ARPC  | 127        | 61       | 13588     | 8.76984639   | 0.89180424 | 0.07906282 | 3.74983196 |
| GOTERM_BP_FAT   | GO:0030833--regulati  | 4     | 2.39520958 | <b>0.00831901</b> | ACTR3, ARPC  | 127        | 45       | 13588     | 9.5104112    | 0.99949212 | 0.20535224 | 12.2223893 |
| GOTERM_BP_FAT   | GO:0008064--regulati  | 4     | 2.39520958 | <b>0.01111272</b> | ACTR3, ARPC  | 127        | 50       | 13588     | 8.55937008   | 0.9999608  | 0.25166884 | 16.0029242 |
| GOTERM_BP_FAT   | GO:0030832--regulati  | 4     | 2.39520958 | <b>0.01172866</b> | ACTR3, ARPC  | 127        | 51       | 13588     | 8.39153929   | 0.99997774 | 0.2573804  | 16.815661  |
| GOTERM_BP_FAT   | GO:0051493--regulati  | 5     | 2.99401198 | <b>0.01348915</b> | ACTR3, ARPC  | 127        | 99       | 13588     | 5.40364273   | 0.99999559 | 0.27108081 | 19.0982599 |
| SP_PIR_KEYWORDS | actin-binding         | 7     | 4.19161677 | <b>0.01456052</b> | ACTR3, ARPC  | 157        | 226      | 17854     | 3.52229299   | 0.9844794  | 0.14803932 | 17.6641928 |
| GOTERM_BP_FAT   | GO:0032271--regulati  | 4     | 2.39520958 | <b>0.01583282</b> | ACTR3, ARPC  | 127        | 57       | 13588     | 7.50821937   | 0.99999949 | 0.297735   | 22.0461156 |
| GOTERM_BP_FAT   | GO:0043254--regulati  | 4     | 2.39520958 | <b>0.02241131</b> | ACTR3, ARPC  | 127        | 65       | 13588     | 6.58413083   | 1          | 0.36071972 | 29.7924176 |
| GOTERM_MF_FAT   | GO:0003779--actin bir | 7     | 4.19161677 | <b>0.04185486</b> | ACTR3, ARPC  | 118        | 288      | 13288     | 2.73705273   | 0.99999312 | 0.48332578 | 43.1474932 |
| GOTERM_BP_FAT   | GO:0044087--regulati  | 4     | 2.39520958 | <b>0.04973279</b> | ACTR3, ARPC  | 127        | 89       | 13588     | 4.80863488   | 1          | 0.52625202 | 54.8896537 |
| GOTERM_BP_FAT   | GO:0033043--regulati  | 5     | 2.99401198 | 0.05504206        | ACTR3, ARPC  | 127        | 154      | 13588     | 3.47377032   | 1          | 0.54108175 | 58.6662972 |
| GOTERM_MF_FAT   | GO:0008092--cytoskel  | 8     | 4.79041916 | 0.07301192        | ACTR3, ARPC  | 118        | 414      | 13288     | 2.17604192   | 1          | 0.67020597 | 63.261269  |
| GOTERM_CC_FAT   | GO:0031252--cell lead | 4     | 2.39520958 | 0.09285946        | ACTR3, COR   | 121        | 112      | 12504     | 3.69067296   | 0.99999972 | 0.66006405 | 68.975963  |
| GOTERM_CC_FAT   | GO:0015629--actin cyt | 5     | 2.99401198 | 0.13461221        | ARPC1B, CO   | 121        | 205      | 12504     | 2.52045958   | 1          | 0.69255175 | 82.3826405 |
| SP_PIR_KEYWORDS | cytoskeleton          | 9     | 5.38922156 | 0.13899728        | ACTR3, ARPC  | 157        | 583      | 17854     | 1.75553638   | 1          | 0.55840444 | 86.2365875 |
| GOTERM_BP_FAT   | GO:0032535--regulati  | 4     | 2.39520958 | 0.18800817        | ACTR3, ARPC  | 127        | 161      | 13588     | 2.65818947   | 1          | 0.86624578 | 96.122728  |
| GOTERM_CC_FAT   | GO:0005856--cytoskel  | 13    | 7.78443114 | 0.39141545        | KIF23, PRC1, | 121        | 1122     | 12504     | 1.19733062   | 1          | 0.91651574 | 99.743061  |
| GOTERM_CC_FAT   | GO:0044430--cytoskel  | 9     | 5.38922156 | 0.46705804        | KIF23, ARPC  | 121        | 774      | 12504     | 1.20161445   | 1          | 0.94324789 | 99.9478087 |
| GOTERM_CC_FAT   | GO:0043228--non-me    | 18    | 10.7784431 | 0.67905922        | KIF23, HMGM  | 121        | 1919     | 12504     | 0.9693065    | 1          | 0.98777084 | 99.9998818 |
| GOTERM_CC_FAT   | GO:0043232--intracell | 18    | 10.7784431 | 0.67905922        | KIF23, HMGM  | 121        | 1919     | 12504     | 0.9693065    | 1          | 0.98777084 | 99.9998818 |

Annotation Cluster 19 Enrichment Score: 1.2875736646536076

| Category        | Term                  | Count | %          | PValue            | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|-----------------------|-------|------------|-------------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| INTERPRO        | IPR001427:Pancreatic  | 3     | 1.79640719 | <b>0.01312652</b> | EAR4, EAR3, | 157        | 20       | 17763     | 16.9710191   | 0.99019342 | 0.3198159  | 16.5328747 |
| GOTERM_MF_FAT   | GO:0004522--pancrea   | 3     | 1.79640719 | <b>0.01316833</b> | EAR4, EAR3, | 118        | 20       | 13288     | 16.8915254   | 0.97490568 | 0.24683449 | 16.0609391 |
| SMART           | SM00092:RNAse_Pc      | 3     | 1.79640719 | <b>0.01459533</b> | EAR4, EAR3, | 86         | 20       | 9131      | 15.9261628   | 0.67287728 | 0.2437286  | 14.3343824 |
| GOTERM_MF_FAT   | GO:0016892--endoribi  | 3     | 1.79640719 | <b>0.01723674</b> | EAR4, EAR3, | 118        | 23       | 13288     | 14.688283    | 0.99204212 | 0.29196134 | 20.5182809 |
| PIR_SUPERFAMILY | PIRSF001015:pyrimidir | 3     | 1.79640719 | <b>0.01803901</b> | EAR4, EAR3, | 101        | 17       | 8136      | 14.2154921   | 0.85998413 | 0.32510618 | 18.5331266 |

|                 |                      |   |            |                   |             |     |     |       |            |            |            |            |
|-----------------|----------------------|---|------------|-------------------|-------------|-----|-----|-------|------------|------------|------------|------------|
| GOTERM_MF_FAT   | GO:0016894--endonuc  | 3 | 1.79640719 | <b>0.02176662</b> | EAR4, EAR3, | 118 | 26  | 13288 | 12.9934811 | 0.99779703 | 0.33493018 | 25.2232138 |
| GOTERM_MF_FAT   | GO:0004521--endorib  | 3 | 1.79640719 | 0.07669187        | EAR4, EAR3, | 118 | 52  | 13288 | 6.49674055 | 1          | 0.6522591  | 65.1415604 |
| SP_PIR_KEYWORDS | Endonuclease         | 3 | 1.79640719 | 0.11058703        | EAR4, EAR3, | 157 | 65  | 17854 | 5.24860363 | 1          | 0.50012419 | 78.8380735 |
| GOTERM_MF_FAT   | GO:0004540--ribonucl | 3 | 1.79640719 | 0.12054887        | EAR4, EAR3, | 118 | 68  | 13288 | 4.96809571 | 1          | 0.80274005 | 81.6699672 |
| SP_PIR_KEYWORDS | nuclease             | 3 | 1.79640719 | 0.22400749        | EAR4, EAR3, | 157 | 102 | 17854 | 3.34469839 | 1          | 0.7111438  | 96.5288748 |
| GOTERM_MF_FAT   | GO:0004519--endonuc  | 3 | 1.79640719 | 0.22974474        | EAR4, EAR3, | 118 | 103 | 13288 | 3.27990785 | 1          | 0.93864315 | 96.8179933 |
| GOTERM_MF_FAT   | GO:0004518--nuclease | 3 | 1.79640719 | 0.39412857        | EAR4, EAR3, | 118 | 154 | 13288 | 2.1937046  | 1          | 0.97913138 | 99.8664206 |

Annotation Cluster 20 Enrichment Score: 1.2807548560221207

| Category        | Term                  | Count | %          | PValue            | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|-----------------------|-------|------------|-------------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| UP_SEQ_FEATURE  | short sequence motif  | 3     | 1.79640719 | <b>0.00717187</b> | SORL1, SORL | 149        | 14       | 16021     | 23.0407478   | 0.96996175 | 0.35477775 | 9.81129624 |
| GOTERM_BP_FAT   | GO:0010324--membra    | 6     | 3.59281437 | <b>0.03069904</b> | CEBPE, SORL | 127        | 188      | 13588     | 3.41464232   | 1          | 0.42600148 | 38.5271911 |
| GOTERM_BP_FAT   | GO:0006897--endocyt   | 6     | 3.59281437 | <b>0.03069904</b> | CEBPE, SORL | 127        | 188      | 13588     | 3.41464232   | 1          | 0.42600148 | 38.5271911 |
| GOTERM_BP_FAT   | GO:0016044--membra    | 7     | 4.19161677 | <b>0.04104313</b> | CEBPE, SORL | 127        | 272      | 13588     | 2.75347383   | 1          | 0.49314352 | 48.0041038 |
| GOTERM_BP_FAT   | GO:0006909--phagocy   | 3     | 1.79640719 | 0.07566903        | CEBPE, SIRP | 127        | 49       | 13588     | 6.55053833   | 1          | 0.6242056  | 70.7094288 |
| SP_PIR_KEYWORDS | Endocytosis           | 3     | 1.79640719 | 0.1952543         | SORL1, SORL | 157        | 93       | 17854     | 3.66837888   | 1          | 0.66768139 | 94.3784545 |
| GOTERM_BP_FAT   | GO:0016192--vesicle-r | 7     | 4.19161677 | 0.26428658        | CEBPE, SORL | 127        | 466      | 13588     | 1.60717786   | 1          | 0.92243843 | 99.1683346 |

Annotation Cluster 21 Enrichment Score: 1.1768576146264627

| Category        | Term                | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|---------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| UP_SEQ_FEATURE  | domain:SH2          | 4     | 2.39520958 | 0.05073083 | FGR, SOCS3, | 149        | 90       | 16021     | 4.77882177   | 1          | 0.87911135 | 52.619042  |
| SP_PIR_KEYWORDS | SH2 domain          | 4     | 2.39520958 | 0.06152872 | FGR, SOCS3, | 157        | 103      | 17854     | 4.41630079   | 0.99999999 | 0.36292731 | 56.8935264 |
| INTERPRO        | IPR000980:SH2 motif | 4     | 2.39520958 | 0.07433863 | FGR, SOCS3, | 157        | 111      | 17763     | 4.07712171   | 1          | 0.79615091 | 65.232539  |
| SMART           | SM00252:SH2         | 4     | 2.39520958 | 0.08452888 | FGR, SOCS3, | 86         | 111      | 9131      | 3.82610517   | 0.99878383 | 0.67328765 | 60.5191582 |

Annotation Cluster 22 Enrichment Score: 1.1430923142442477

| Category      | Term                  | Count | %          | PValue            | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|-----------------------|-------|------------|-------------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0006631--fatty aci | 6     | 3.59281437 | <b>0.02834112</b> | TP11, LOC10   | 127        | 184      | 13588     | 3.48887367   | 1          | 0.40673181 | 36.151681  |
| GOTERM_BP_FAT | GO:0051186--cofactor  | 5     | 2.99401198 | 0.08912481        | TP11, HPX, PI | 127        | 182      | 13588     | 2.93934412   | 1          | 0.6721764  | 76.7006687 |
| GOTERM_BP_FAT | GO:0006732--coenzym   | 4     | 2.39520958 | 0.14733552        | TP11, PGD, A  | 127        | 143      | 13588     | 2.99278674   | 1          | 0.8105272  | 91.6867198 |

Annotation Cluster 23 Enrichment Score: 1.105002108033453

| Category      | Term                 | Count | %          | PValue            | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|----------------------|-------|------------|-------------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0042325--regulati | 9     | 5.38922156 | <b>0.00559923</b> | CDKN1C, EG   | 127        | 290      | 13588     | 3.32044529   | 0.9938934  | 0.15628977 | 8.3893978  |
| GOTERM_BP_FAT | GO:0019220--regulati | 9     | 5.38922156 | <b>0.0069597</b>  | CDKN1C, EG   | 127        | 301      | 13588     | 3.19910011   | 0.99823834 | 0.17977115 | 10.3258754 |
| GOTERM_BP_FAT | GO:0051174--regulati | 9     | 5.38922156 | <b>0.0069597</b>  | CDKN1C, EG   | 127        | 301      | 13588     | 3.19910011   | 0.99823834 | 0.17977115 | 10.3258754 |
| GOTERM_BP_FAT | GO:0001932--regulati | 4     | 2.39520958 | 0.10240085        | EGFR, HPX, S | 127        | 121      | 13588     | 3.53692978   | 1          | 0.71110173 | 81.4716302 |
| GOTERM_BP_FAT | GO:0043405--regulati | 3     | 1.79640719 | 0.1830219         | PROK1, IL1B, | 127        | 84       | 13588     | 3.82114736   | 1          | 0.86104583 | 95.7340376 |
| GOTERM_BP_FAT | GO:0031399--regulati | 4     | 2.39520958 | 0.19741876        | EGFR, HPX, S | 127        | 165      | 13588     | 2.59374851   | 1          | 0.86695451 | 96.7676228 |
| GOTERM_BP_FAT | GO:0045859--regulati | 4     | 2.39520958 | 0.24845481        | PROK1, IL1B, | 127        | 186      | 13588     | 2.30090594   | 1          | 0.91141559 | 98.8405771 |
| GOTERM_BP_FAT | GO:0043549--regulati | 4     | 2.39520958 | 0.26341528        | PROK1, IL1B, | 127        | 192      | 13588     | 2.22900262   | 1          | 0.92349547 | 99.1528308 |
| GOTERM_BP_FAT | GO:0051338--regulati | 4     | 2.39520958 | 0.28100933        | PROK1, IL1B, | 127        | 199      | 13588     | 2.1505955    | 1          | 0.92941469 | 99.4190709 |
| GOTERM_BP_FAT | GO:0032268--regulati | 4     | 2.39520958 | 0.48290942        | EGFR, HPX, S | 127        | 280      | 13588     | 1.52845894   | 1          | 0.98929256 | 99.9966106 |

Annotation Cluster 24 Enrichment Score: 1.1042554885097877

| Category      | Term                 | Count | %          | PValue            | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|----------------------|-------|------------|-------------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| KEGG_PATHWAY  | mmu04610:Compleme    | 6     | 3.59281437 | <b>0.00160223</b> | C8A, KNG1,  | 67         | 75       | 5738      | 6.85134328   | 0.14952036 | 0.07778547 | 1.76732524 |
| GOTERM_BP_FAT | GO:0050817--coagula  | 3     | 1.79640719 | 0.13744305        | KNG1, C9, F | 127        | 70       | 13588     | 4.58537683   | 1          | 0.80160362 | 90.0471184 |
| GOTERM_BP_FAT | GO:0007596--blood c  | 3     | 1.79640719 | 0.13744305        | KNG1, C9, F | 127        | 70       | 13588     | 4.58537683   | 1          | 0.80160362 | 90.0471184 |
| GOTERM_BP_FAT | GO:0007599--hemosta  | 3     | 1.79640719 | 0.14061005        | KNG1, C9, F | 127        | 71       | 13588     | 4.52079406   | 1          | 0.80563047 | 90.6023489 |
| GOTERM_BP_FAT | GO:0050878--regulati | 3     | 1.79640719 | 0.19980552        | KNG1, C9, F | 127        | 89       | 13588     | 3.60647616   | 1          | 0.86786569 | 96.9144165 |
| GOTERM_BP_FAT | GO:0042060--wound h  | 3     | 1.79640719 | 0.27853087        | KNG1, C9, F | 127        | 112      | 13588     | 2.86586052   | 1          | 0.92911553 | 99.3870215 |

Annotation Cluster 25 Enrichment Score: 1.091359055884475

| Category        | Term                | Count | %          | PValue            | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|---------------------|-------|------------|-------------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| SP_PIR_KEYWORDS | lysosome            | 5     | 2.99401198 | <b>0.03766133</b> | EAR4, LAPTM | 157        | 144      | 17854     | 3.94860226   | 0.99998159 | 0.26765098 | 39.8724297 |
| GOTERM_CC_FAT   | GO:0005764--lysosom | 5     | 2.99401198 | 0.09208285        | EAR4, LAPTM | 121        | 178      | 12504     | 2.90277649   | 0.99999969 | 0.68393103 | 68.6554872 |

|               |                       |   |            |            |             |     |     |       |            |            |            |            |
|---------------|-----------------------|---|------------|------------|-------------|-----|-----|-------|------------|------------|------------|------------|
| GOTERM_CC_FAT | GO:0000323--lytic vac | 5 | 2.99401198 | 0.09352488 | EAR4, LAPTM | 121 | 179 | 12504 | 2.88655986 | 0.99999975 | 0.6374698  | 69.2481621 |
| GOTERM_CC_FAT | GO:0005773--vacuole   | 5 | 2.99401198 | 0.13291138 | EAR4, LAPTM | 121 | 204 | 12504 | 2.53281478 | 1          | 0.70714153 | 81.9622879 |

Annotation Cluster 26 Enrichment Score: 1.0576281710510596

| Category        | Term                | Count | %          | PValue            | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|---------------------|-------|------------|-------------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| UP_SEQ_FEATURE  | propeptide:Removed  | 7     | 4.19161677 | <b>0.01648493</b> | LY6C1, RAC2 | 149        | 220      | 16021     | 3.42120195   | 0.99969496 | 0.59320753 | 21.2176766 |
| GOTERM_CC_FAT   | GO:0031225--anchore | 5     | 2.99401198 | 0.13804072        | LY6C1, GLPF | 121        | 207      | 12504     | 2.49610732   | 1          | 0.66593515 | 83.2028154 |
| SP_PIR_KEYWORDS | gpi-anchor          | 3     | 1.79640719 | 0.29513531        | LY6C1, CD17 | 157        | 124      | 17854     | 2.75128416   | 1          | 0.77797879 | 99.0290307 |

Annotation Cluster 27 Enrichment Score: 0.9974825582896878

| Category        | Term                 | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|----------------------|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| UP_SEQ_FEATURE  | domain:SH3           | 5     | 2.99401198 | 0.06452593 | FGR, NCF4, ↑ | 149        | 163      | 16021     | 3.29826656   | 1          | 0.91781264 | 61.5947469 |
| SP_PIR_KEYWORDS | sh3 domain           | 5     | 2.99401198 | 0.10345389 | FGR, NCF4, ↑ | 157        | 204      | 17854     | 2.78724866   | 1          | 0.49044915 | 76.4751865 |
| INTERPRO        | IPR001452:Src homolo | 5     | 2.99401198 | 0.11490549 | FGR, NCF4, ↑ | 157        | 211      | 17763     | 2.68104567   | 1          | 0.84392954 | 81.1640063 |
| SMART           | SM00326:SH3          | 5     | 2.99401198 | 0.13342828 | FGR, NCF4, ↑ | 86         | 211      | 9131      | 2.51598148   | 0.99998124 | 0.74346723 | 77.8427177 |

Annotation Cluster 28 Enrichment Score: 0.8191659182334934

| Category      | Term                | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|---------------------|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0043434--respons | 4     | 2.39520958 | 0.05827915 | SERPINA1C, | 127        | 95       | 13588     | 4.50493162   | 1          | 0.55681275 | 60.8214961 |
| GOTERM_BP_FAT | GO:0010033--respons | 8     | 4.79041916 | 0.18877269 | CORO1A, AP | 127        | 505      | 13588     | 1.69492477   | 1          | 0.86460763 | 96.1793062 |
| GOTERM_BP_FAT | GO:0009725--respons | 4     | 2.39520958 | 0.19741876 | SERPINA1C, | 127        | 165      | 13588     | 2.59374851   | 1          | 0.86695451 | 96.7676228 |
| GOTERM_BP_FAT | GO:0009719--respons | 4     | 2.39520958 | 0.24349809 | SERPINA1C, | 127        | 184      | 13588     | 2.32591578   | 1          | 0.90840281 | 98.7153232 |

Annotation Cluster 29 Enrichment Score: 0.7519615970238339

| Category        | Term                  | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|-----------------------|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT   | GO:0030198--extracell | 4     | 2.39520958 | 0.06747047 | LGALS3, MM | 127        | 101      | 13588     | 4.23731192   | 1          | 0.59590779 | 66.3817137 |
| GOTERM_BP_FAT   | GO:0043062--extracell | 4     | 2.39520958 | 0.16055747 | LGALS3, MM | 127        | 149      | 13588     | 2.87227184   | 1          | 0.82558646 | 93.4858754 |
| GOTERM_CC_FAT   | GO:0031012--extracell | 6     | 3.59281437 | 0.17593975 | LGALS3, MM | 121        | 309      | 12504     | 2.00657948   | 1          | 0.72858335 | 90.2114118 |
| SP_PIR_KEYWORDS | extracellular matrix  | 4     | 2.39520958 | 0.28625455 | MMP9, TGFE | 157        | 213      | 17854     | 2.13558207   | 1          | 0.77607704 | 98.8537994 |
| GOTERM_CC_FAT   | GO:0005578--proteina  | 5     | 2.99401198 | 0.31866278 | LGALS3, MM | 121        | 297      | 12504     | 1.73971116   | 1          | 0.88949674 | 99.0027963 |

Annotation Cluster 30 Enrichment Score: 0.748646146245307

| Category      | Term                   | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|------------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0034754--cellular l | 3     | 1.79640719 | 0.08382706 | CYP17A1, RE | 127        | 52       | 13588     | 6.17262265   | 1          | 0.65352352 | 74.4937426 |
| GOTERM_BP_FAT | GO:0042445--hormon     | 3     | 1.79640719 | 0.20318493 | CYP17A1, RE | 127        | 90       | 13588     | 3.5664042    | 1          | 0.86759979 | 97.1116186 |
| GOTERM_BP_FAT | GO:0010817--regulati   | 3     | 1.79640719 | 0.333262   | CYP17A1, RE | 127        | 128      | 13588     | 2.50762795   | 1          | 0.95696993 | 99.8210351 |

Annotation Cluster 31 Enrichment Score: 0.7352306803883413

| Category        | Term                     | Count | %          | PValue            | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|--------------------------|-------|------------|-------------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| SP_PIR_KEYWORDS | citrullination           | 3     | 1.79640719 | <b>0.00840001</b> | HIST1H2AF,  | 157        | 16       | 17854     | 21.3224522   | 0.90888916 | 0.09499964 | 10.5760002 |
| PIR_SUPERFAMILY | PIRSF002048:histone H    | 3     | 1.79640719 | <b>0.01068105</b> | HIST1H2AF,  | 101        | 13       | 8136      | 18.5894897   | 0.68643818 | 0.2516913  | 11.3891274 |
| INTERPRO        | IPR002119:Histone H2     | 3     | 1.79640719 | <b>0.02014206</b> | HIST1H2AF,  | 157        | 25       | 17763     | 13.5768153   | 0.9991926  | 0.42179228 | 24.2923454 |
| SMART           | SM00414:H2A              | 3     | 1.79640719 | <b>0.02236469</b> | HIST1H2AF,  | 86         | 25       | 9131      | 12.7409302   | 0.82075681 | 0.29093095 | 21.180946  |
| INTERPRO        | IPR007125:Histone co     | 3     | 1.79640719 | 0.05249472        | HIST1H2AF,  | 157        | 42       | 17763     | 8.08143767   | 0.99999999 | 0.7402587  | 52.1687178 |
| SP_PIR_KEYWORDS | nucleosome core          | 3     | 1.79640719 | 0.05651952        | HIST1H2AF,  | 157        | 44       | 17854     | 7.75361899   | 0.99999993 | 0.34535805 | 53.7428755 |
| UP_SEQ_FEATURE  | cross-link:Glycyl lysine | 5     | 2.99401198 | 0.07045009        | EGFR, UHRF1 | 149        | 168      | 16021     | 3.20010387   | 1          | 0.9066916  | 64.9404419 |
| SP_PIR_KEYWORDS | isopeptide bond          | 6     | 3.59281437 | 0.09596988        | EGFR, UHRF1 | 157        | 277      | 17854     | 2.46324358   | 1          | 0.47098812 | 73.7356311 |
| INTERPRO        | IPR009072:Histone-fo     | 3     | 1.79640719 | 0.10032079        | HIST1H2AF,  | 157        | 61       | 17763     | 5.56426856   | 1          | 0.84277032 | 76.4458767 |
| SP_PIR_KEYWORDS | chromosomal protein      | 4     | 2.39520958 | 0.11652045        | HMG2, HIS   | 157        | 136      | 17854     | 3.34469839   | 1          | 0.51229265 | 80.6342526 |
| GOTERM_CC_FAT   | GO:0000786--nucleos      | 3     | 1.79640719 | 0.11927454        | HIST1H2AF,  | 121        | 62       | 12504     | 5.0002666    | 1          | 0.68589446 | 78.2444675 |
| SP_PIR_KEYWORDS | methylation              | 5     | 2.99401198 | 0.12852312        | RAC2, HIST1 | 157        | 221      | 17854     | 2.57284491   | 1          | 0.53515603 | 83.8447651 |
| GOTERM_BP_FAT   | GO:0006334--nucleos      | 3     | 1.79640719 | 0.14699079        | HIST1H2AF,  | 127        | 73       | 13588     | 4.39693668   | 1          | 0.81336215 | 91.6341145 |
| GOTERM_BP_FAT   | GO:0031497--chromat      | 3     | 1.79640719 | 0.15343022        | HIST1H2AF,  | 127        | 75       | 13588     | 4.27968504   | 1          | 0.82068722 | 92.567147  |
| GOTERM_BP_FAT   | GO:0065004--protein-     | 3     | 1.79640719 | 0.15667059        | HIST1H2AF,  | 127        | 76       | 13588     | 4.22337339   | 1          | 0.82077671 | 92.998926  |
| GOTERM_BP_FAT   | GO:0034728--nucleos      | 3     | 1.79640719 | 0.15667059        | HIST1H2AF,  | 127        | 76       | 13588     | 4.22337339   | 1          | 0.82077671 | 92.998926  |
| GOTERM_CC_FAT   | GO:0032993--protein-     | 3     | 1.79640719 | 0.16191882        | HIST1H2AF,  | 121        | 75       | 12504     | 4.13355372   | 1          | 0.71191834 | 88.0128978 |
| GOTERM_CC_FAT   | GO:0000785--chromat      | 4     | 2.39520958 | 0.2111266         | HMG2, HIS   | 121        | 165      | 12504     | 2.50518407   | 1          | 0.78380836 | 94.2040762 |

|                 |                        |    |            |            |             |     |      |       |            |   |            |            |
|-----------------|------------------------|----|------------|------------|-------------|-----|------|-------|------------|---|------------|------------|
| GOTERM_BP_FAT   | GO:0006323--DNA pa     | 3  | 1.79640719 | 0.24070606 | HIST1H2AF,  | 127 | 101  | 13588 | 3.17798394 | 1 | 0.90756623 | 98.6393048 |
| GOTERM_BP_FAT   | GO:0006333--chromat    | 3  | 1.79640719 | 0.2682099  | HIST1H2AF,  | 127 | 109  | 13588 | 2.94473741 | 1 | 0.92404219 | 99.2349131 |
| GOTERM_CC_FAT   | GO:0044427--chromo:    | 5  | 2.99401198 | 0.36454258 | HMG2, HIS   | 121 | 318  | 12504 | 1.62482458 | 1 | 0.90392434 | 99.5682898 |
| SP_PIR_KEYWORDS | ubl conjugation        | 6  | 3.59281437 | 0.48480181 | EGFR, UHRF1 | 157 | 524  | 17854 | 1.30213449 | 1 | 0.92154797 | 99.9847493 |
| GOTERM_CC_FAT   | GO:0005694--chromo:    | 5  | 2.99401198 | 0.49329837 | HMG2, HIS   | 121 | 378  | 12504 | 1.36691591 | 1 | 0.95074226 | 99.9715383 |
| GOTERM_BP_FAT   | GO:0034622--cellular i | 3  | 1.79640719 | 0.60074101 | HIST1H2AF,  | 127 | 217  | 13588 | 1.47915382 | 1 | 0.99729484 | 99.9999401 |
| GOTERM_BP_FAT   | GO:0034621--cellular i | 3  | 1.79640719 | 0.66669214 | HIST1H2AF,  | 127 | 245  | 13588 | 1.31010767 | 1 | 0.99897192 | 99.9999964 |
| GOTERM_BP_FAT   | GO:0006325--chromat    | 3  | 1.79640719 | 0.79365978 | HIST1H2AF,  | 127 | 315  | 13588 | 1.01897263 | 1 | 0.99986372 | 100        |
| GOTERM_BP_FAT   | GO:0065003--macrom     | 3  | 1.79640719 | 0.8250157  | HIST1H2AF,  | 127 | 338  | 13588 | 0.94963425 | 1 | 0.99994284 | 100        |
| GOTERM_BP_FAT   | GO:0043933--macrom     | 3  | 1.79640719 | 0.85846361 | HIST1H2AF,  | 127 | 367  | 13588 | 0.87459504 | 1 | 0.99997876 | 100        |
| GOTERM_BP_FAT   | GO:0051276--chromo:    | 3  | 1.79640719 | 0.8926984  | HIST1H2AF,  | 127 | 404  | 13588 | 0.79449599 | 1 | 0.99999336 | 100        |
| SP_PIR_KEYWORDS | dna-binding            | 8  | 4.79041916 | 0.96654579 | NFE2, HMG2  | 157 | 1404 | 17854 | 0.64797576 | 1 | 0.99997793 | 100        |
| GOTERM_MF_FAT   | GO:0003677--DNA bir    | 9  | 5.38922156 | 0.99198331 | NFE2, HMG2  | 118 | 1781 | 13288 | 0.56905757 | 1 | 1          | 100        |
| SP_PIR_KEYWORDS | nucleus                | 22 | 13.1736527 | 0.99573075 | S100A6, HM  | 157 | 3808 | 17854 | 0.65699433 | 1 | 0.99999994 | 100        |

Annotation Cluster 32 Enrichment Score: 0.7167445343276986

| Category      | Term                 | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|----------------------|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0001525--angioge  | 4     | 2.39520958 | 0.12616727 | PROK2, PRO | 127        | 133      | 13588     | 3.2178083    | 1          | 0.77539177 | 87.8109167 |
| GOTERM_BP_FAT | GO:0001568--blood ve | 5     | 2.99401198 | 0.19102231 | PROK2, SOC | 127        | 244      | 13588     | 2.1924616    | 1          | 0.86534169 | 96.3413408 |
| GOTERM_BP_FAT | GO:0001944--vasculat | 5     | 2.99401198 | 0.20238774 | PROK2, SOC | 127        | 250      | 13588     | 2.13984252   | 1          | 0.86905203 | 97.0661919 |
| GOTERM_BP_FAT | GO:0048514--blood ve | 4     | 2.39520958 | 0.27848825 | PROK2, PRO | 127        | 198      | 13588     | 2.16145709   | 1          | 0.93075227 | 99.3864563 |

Annotation Cluster 33 Enrichment Score: 0.6765487319051727

| Category       | Term                  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|----------------|-----------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| UP_SEQ_FEATURE | domain:Fibronectin ty | 3     | 1.79640719 | 0.04798607 | SORL1, CSF3 | 149        | 38       | 16021     | 8.48869657   | 1          | 0.88663455 | 50.6151217 |
| UP_SEQ_FEATURE | domain:Fibronectin ty | 3     | 1.79640719 | 0.09453931 | SORL1, CSF3 | 149        | 56       | 16021     | 5.76018696   | 1          | 0.9513348  | 75.9450071 |
| UP_SEQ_FEATURE | domain:Fibronectin ty | 3     | 1.79640719 | 0.14935243 | SORL1, CSF3 | 149        | 74       | 16021     | 4.3590604    | 1          | 0.99028295 | 90.1799501 |
| INTERPRO       | IPR008957:Fibronectin | 4     | 2.39520958 | 0.22791274 | F13A1, SORL | 157        | 187      | 17763     | 2.42010968   | 1          | 0.9559192  | 97.0917164 |
| UP_SEQ_FEATURE | domain:Fibronectin ty | 3     | 1.79640719 | 0.30441662 | SORL1, CSF3 | 149        | 120      | 16021     | 2.68808725   | 1          | 0.99954089 | 99.4527659 |
| UP_SEQ_FEATURE | domain:Fibronectin ty | 3     | 1.79640719 | 0.3078243  | SORL1, CSF3 | 149        | 121      | 16021     | 2.66587165   | 1          | 0.99942757 | 99.4899966 |
| INTERPRO       | IPR003961:Fibronectin | 3     | 1.79640719 | 0.50058649 | SORL1, CSF3 | 157        | 191      | 17763     | 1.77707006   | 1          | 0.99803268 | 99.9924854 |
| SMART          | SM00060:FN3           | 3     | 1.79640719 | 0.53413524 | SORL1, CSF3 | 86         | 191      | 9131      | 1.66766103   | 1          | 0.98850269 | 99.9677079 |

Annotation Cluster 34 Enrichment Score: 0.6387954498973422

| Category | Term                | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|----------|---------------------|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| INTERPRO | IPR003597:Immunoglc | 3     | 1.79640719 | 0.16526479 | AZGP1, SIRP, | 157        | 83       | 17763     | 4.08940219   | 1          | 0.91211288 | 91.5464623 |
| SMART    | SM00407:IGc1        | 3     | 1.79640719 | 0.18063503 | AZGP1, SIRP, | 86         | 83       | 9131      | 3.83762959   | 0.99999973 | 0.81406349 | 87.7108427 |
| INTERPRO | IPR003006:Immunoglc | 3     | 1.79640719 | 0.21278285 | AZGP1, SIRP, | 157        | 98       | 17763     | 3.46347329   | 1          | 0.9497447  | 96.2076627 |
| INTERPRO | IPR007110:Immunoglc | 7     | 4.19161677 | 0.438429   | AZGP1, GP4   | 157        | 604      | 17763     | 1.31122664   | 1          | 0.99508091 | 99.9626182 |

Annotation Cluster 35 Enrichment Score: 0.6175275604625841

| Category      | Term                  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|-----------------------|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0019835--cytolysis | 3     | 1.79640719 | 0.01900463 | C8A, LY2Z, C | 127        | 23       | 13588     | 13.9554947   | 0.99999997 | 0.32696705 | 25.8757407 |
| GOTERM_BP_FAT | GO:0008219--cell deat | 4     | 2.39520958 | 0.85419253 | C8A, LY2Z, C | 127        | 507      | 13588     | 0.84411934   | 1          | 0.99997803 | 100        |
| GOTERM_BP_FAT | GO:0016265--death     | 4     | 2.39520958 | 0.86497224 | C8A, LY2Z, C | 127        | 519      | 13588     | 0.82460213   | 1          | 0.99998129 | 100        |

Annotation Cluster 36 Enrichment Score: 0.5289806299463069

| Category      | Term                  | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|-----------------------|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0030036--actin cyt | 4     | 2.39520958 | 0.19741876 | CORO1A, RA | 127        | 165      | 13588     | 2.59374851   | 1          | 0.86695451 | 96.7676228 |
| GOTERM_BP_FAT | GO:0030029--actin fil | 4     | 2.39520958 | 0.22385201 | CORO1A, RA | 127        | 176      | 13588     | 2.43163923   | 1          | 0.89057133 | 98.083313  |
| GOTERM_BP_FAT | GO:0007010--cytoskel  | 4     | 2.39520958 | 0.58574513 | CORO1A, RA | 127        | 326      | 13588     | 1.31278682   | 1          | 0.99683882 | 99.9989935 |

Annotation Cluster 37 Enrichment Score: 0.5106601105603661

| Category | Term                | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|----------|---------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| INTERPRO | IPR013783:Immunoglc | 10    | 5.98802395 | 0.11443332 | AZGP1, GP4  | 157        | 644      | 17763     | 1.75683428   | 1          | 0.85534338 | 81.0261114 |
| INTERPRO | IPR013151:Immunoglc | 4     | 2.39520958 | 0.20611214 | GP49A, EMB, | 157        | 178      | 17763     | 2.54247477   | 1          | 0.9498141  | 95.7437499 |
| INTERPRO | IPR003599:Immunoglc | 5     | 2.99401198 | 0.2959374  | EMB, SIRPA, | 157        | 313      | 17763     | 1.80735028   | 1          | 0.97580331 | 99.1762196 |



|                 |                       |   |            |            |             |     |     |       |            |   |            |            |
|-----------------|-----------------------|---|------------|------------|-------------|-----|-----|-------|------------|---|------------|------------|
| SMART           | SM00409:IG            | 5 | 2.99401198 | 0.33294823 | EMB, SIRPA, | 86  | 313 | 9131  | 1.69607697 | 1 | 0.93903195 | 98.5886661 |
| UP_SEQ_FEATURE  | domain:lg-like C2-typ | 3 | 1.79640719 | 0.33832465 | GP49A, CEA  | 149 | 130 | 16021 | 2.48131131 | 1 | 0.99956294 | 99.7328341 |
| UP_SEQ_FEATURE  | domain:lg-like C2-typ | 3 | 1.79640719 | 0.3416909  | GP49A, CEA  | 149 | 131 | 16021 | 2.46237    | 1 | 0.9994691  | 99.7516862 |
| SP_PIR_KEYWORDS | Immunoglobulin dom    | 6 | 3.59281437 | 0.34546156 | GP49A, CSF3 | 157 | 443 | 17854 | 1.54022228 | 1 | 0.82968276 | 99.6361657 |
| INTERPRO        | IPR007110:Immunogl    | 7 | 4.19161677 | 0.438429   | AZGP1, GP49 | 157 | 604 | 17763 | 1.31122664 | 1 | 0.99508091 | 99.9626182 |
| INTERPRO        | IPR013106:Immunogl    | 4 | 2.39520958 | 0.62310368 | EMB, SIRPA, | 157 | 364 | 17763 | 1.2432981  | 1 | 0.99964466 | 99.99984   |

Annotation Cluster 38 Enrichment Score: 0.4714487995125752

| Category      | Term                 | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|----------------------|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0045859--regulati | 4     | 2.39520958 | 0.24845481 | PROK1, IL1B, | 127        | 186      | 13588     | 2.30090594   | 1          | 0.91141559 | 98.8405771 |
| GOTERM_BP_FAT | GO:0043549--regulati | 4     | 2.39520958 | 0.26341528 | PROK1, IL1B, | 127        | 192      | 13588     | 2.22900262   | 1          | 0.92349547 | 99.1528308 |
| GOTERM_BP_FAT | GO:0051338--regulati | 4     | 2.39520958 | 0.28100933 | PROK1, IL1B, | 127        | 199      | 13588     | 2.1505955    | 1          | 0.92941469 | 99.4190709 |
| GOTERM_BP_FAT | GO:0045860--positive | 3     | 1.79640719 | 0.31965857 | PROK1, CEA   | 127        | 124      | 13588     | 2.58851918   | 1          | 0.95221738 | 99.7547251 |
| GOTERM_BP_FAT | GO:0033674--positive | 3     | 1.79640719 | 0.34003582 | PROK1, CEA   | 127        | 130      | 13588     | 2.46904906   | 1          | 0.95914695 | 99.8473978 |
| GOTERM_BP_FAT | GO:0051347--positive | 3     | 1.79640719 | 0.35687624 | PROK1, CEA   | 127        | 135      | 13588     | 2.3776028    | 1          | 0.9645653  | 99.898052  |
| GOTERM_BP_FAT | GO:0043085--positive | 4     | 2.39520958 | 0.43711589 | C9, PROK1, C | 127        | 261      | 13588     | 1.63972607   | 1          | 0.98303575 | 99.9872587 |
| GOTERM_BP_FAT | GO:0044093--positive | 4     | 2.39520958 | 0.54259434 | C9, PROK1, C | 127        | 306      | 13588     | 1.39858988   | 1          | 0.9943951  | 99.9995001 |

Annotation Cluster 39 Enrichment Score: 0.457466784163882

| Category        | Term                 | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|----------------------|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| SP_PIR_KEYWORDS | cell adhesion        | 6     | 3.59281437 | 0.23918783 | SELL, TGFB1, | 157        | 380      | 17854     | 1.79557492   | 1          | 0.73176097 | 97.3283891 |
| GOTERM_BP_FAT   | GO:0007155--cell adh | 7     | 4.19161677 | 0.4203127  | AZGP1, SELL, | 127        | 561      | 13588     | 1.33501761   | 1          | 0.98095243 | 99.9798364 |
| GOTERM_BP_FAT   | GO:0022610--biologic | 7     | 4.19161677 | 0.4219763  | AZGP1, SELL, | 127        | 562      | 13588     | 1.33264214   | 1          | 0.98074705 | 99.9807208 |

Annotation Cluster 40 Enrichment Score: 0.301200468919087

| Category      | Term                 | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|----------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_MF_FAT | GO:0008047--enzyme   | 5     | 2.99401198 | 0.1769276  | ALOX5AP, R  | 118        | 249      | 13288     | 2.26124838   | 1          | 0.88527158 | 92.3593862 |
| GOTERM_MF_FAT | GO:0005096--GTPase   | 3     | 1.79640719 | 0.50631989 | RGS16, IQGA | 118        | 192      | 13288     | 1.7595339    | 1          | 0.99165528 | 99.9910646 |
| GOTERM_MF_FAT | GO:0030695--GTPase   | 3     | 1.79640719 | 0.83119355 | RGS16, IQGA | 118        | 361      | 13288     | 0.93581858   | 1          | 0.99992595 | 100        |
| GOTERM_MF_FAT | GO:0060589--nucleosi | 3     | 1.79640719 | 0.83806052 | RGS16, IQGA | 118        | 367      | 13288     | 0.9205191    | 1          | 0.99991496 | 100        |

Annotation Cluster 41 Enrichment Score: 0.28554980872746516

| Category        | Term                  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|-----------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_MF_FAT   | GO:0005509--calcium   | 14    | 8.38323353 | 0.03330314 | S100A6, APC | 118        | 840      | 13288     | 1.87683616   | 0.99991858 | 0.44483883 | 36.0679971 |
| GOTERM_MF_FAT   | GO:0043169--cation b  | 31    | 18.5628743 | 0.83149092 | S100A6, S10 | 118        | 3885     | 13288     | 0.89856249   | 1          | 0.99991221 | 100        |
| GOTERM_MF_FAT   | GO:0043167--ion bind  | 31    | 18.5628743 | 0.85242273 | S100A6, S10 | 118        | 3934     | 13288     | 0.88737043   | 1          | 0.99993694 | 100        |
| GOTERM_MF_FAT   | GO:0046872--metal io  | 29    | 17.3652695 | 0.90684834 | S100A6, S10 | 118        | 3850     | 13288     | 0.84823245   | 1          | 0.99999061 | 100        |
| SP_PIR_KEYWORDS | metal-binding         | 19    | 11.3772455 | 0.91307395 | S100A6, APC | 157        | 2682     | 17854     | 0.80562086   | 1          | 0.99965565 | 100        |
| GOTERM_MF_FAT   | GO:0046914--transitio | 15    | 8.98203593 | 0.9900629  | S100A6, LOC | 118        | 2608     | 13288     | 0.64768119   | 1          | 1          | 100        |

Annotation Cluster 42 Enrichment Score: 0.19937427682504422

| Category        | Term                 | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|----------------------|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| SP_PIR_KEYWORDS | kinase               | 9     | 5.38922156 | 0.27785059 | CDKN1C, EG   | 157        | 707      | 17854     | 1.44763466   | 1          | 0.77487655 | 98.6614754 |
| GOTERM_MF_FAT   | GO:0030554--adenyl r | 15    | 8.98203593 | 0.48707158 | KIF23, EGFR, | 118        | 1535     | 13288     | 1.10042511   | 1          | 0.99243452 | 99.9851916 |
| GOTERM_MF_FAT   | GO:0001883--purine n | 15    | 8.98203593 | 0.50036388 | KIF23, EGFR, | 118        | 1548     | 13288     | 1.09118381   | 1          | 0.99195281 | 99.9895311 |
| GOTERM_MF_FAT   | GO:0001882--nucleosi | 15    | 8.98203593 | 0.51054503 | KIF23, EGFR, | 118        | 1558     | 13288     | 1.08418007   | 1          | 0.99013819 | 99.9920236 |
| SP_PIR_KEYWORDS | transferase          | 13    | 7.78443114 | 0.55556474 | EGFR, PKF    | 157        | 1385     | 17854     | 1.06740555   | 1          | 0.95170346 | 99.9978472 |
| GOTERM_MF_FAT   | GO:0005524--ATP bin  | 13    | 7.78443114 | 0.627578   | KIF23, EGFR, | 118        | 1443     | 13288     | 1.01450603   | 1          | 0.997444   | 99.9997841 |
| GOTERM_MF_FAT   | GO:0032559--adenyl r | 13    | 7.78443114 | 0.64414177 | KIF23, EGFR, | 118        | 1460     | 13288     | 1.00269329   | 1          | 0.99778256 | 99.9998816 |
| GOTERM_MF_FAT   | GO:0017076--purine n | 16    | 9.58083832 | 0.69272521 | KIF23, EGFR, | 118        | 1871     | 13288     | 0.9629945    | 1          | 0.99876263 | 99.999983  |
| SP_PIR_KEYWORDS | atp-binding          | 11    | 6.58682635 | 0.69525124 | ACTR3, EGFF  | 157        | 1287     | 17854     | 0.97196363   | 1          | 0.98527708 | 99.9999855 |
| GOTERM_MF_FAT   | GO:0032555--purine r | 14    | 8.38323353 | 0.81446894 | KIF23, EGFR, | 118        | 1796     | 13288     | 0.87780756   | 1          | 0.99991442 | 100        |
| GOTERM_MF_FAT   | GO:0032553--ribonucl | 14    | 8.38323353 | 0.81446894 | KIF23, EGFR, | 118        | 1796     | 13288     | 0.87780756   | 1          | 0.99991442 | 100        |
| GOTERM_MF_FAT   | GO:0000166--nucleoti | 17    | 10.1796407 | 0.82371032 | KIF23, EGFR, | 118        | 2183     | 13288     | 0.87694589   | 1          | 0.99992216 | 100        |
| SP_PIR_KEYWORDS | nucleotide-binding   | 12    | 7.18562874 | 0.85387312 | ACTR3, EGFF  | 157        | 1631     | 17854     | 0.83668727   | 1          | 0.99872028 | 100        |
| UP_SEQ_FEATURE  | nucleotide phosphate | 6     | 3.59281437 | 0.92689919 | EGFR, PKF    | 149        | 907      | 16021     | 0.711291     | 1          | 1          | 100        |

Annotation Cluster 43 Enrichment Score: 0.19594501059387362

| Category        | Term                | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|---------------------|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| UP_SEQ_FEATURE  | repeat:WD 5         | 3     | 1.79640719 | 0.55926381 | ARPC1B, CO | 149        | 202      | 16021     | 1.59688351   | 1          | 0.99999743 | 99.9992148 |
| INTERPRO        | IPR019782:WD40 repe | 3     | 1.79640719 | 0.56368848 | ARPC1B, CO | 157        | 214      | 17763     | 1.58607655   | 1          | 0.99929495 | 99.9988154 |
| INTERPRO        | IPR017986:WD40 repe | 3     | 1.79640719 | 0.59757173 | ARPC1B, CO | 157        | 228      | 17763     | 1.48868589   | 1          | 0.99957793 | 99.9996079 |
| UP_SEQ_FEATURE  | repeat:WD 4         | 3     | 1.79640719 | 0.60085473 | ARPC1B, CO | 149        | 218      | 16021     | 1.47968105   | 1          | 0.99999806 | 99.9998106 |
| INTERPRO        | IPR019781:WD40 repe | 3     | 1.79640719 | 0.61407637 | ARPC1B, CO | 157        | 235      | 17763     | 1.44434205   | 1          | 0.99964176 | 99.9997789 |
| UP_SEQ_FEATURE  | repeat:WD 3         | 3     | 1.79640719 | 0.63243836 | ARPC1B, CO | 149        | 231      | 16021     | 1.39640896   | 1          | 0.9999991  | 99.999942  |
| UP_SEQ_FEATURE  | repeat:WD 2         | 3     | 1.79640719 | 0.64175931 | ARPC1B, CO | 149        | 235      | 16021     | 1.3726403    | 1          | 0.99999907 | 99.9999598 |
| UP_SEQ_FEATURE  | repeat:WD 1         | 3     | 1.79640719 | 0.64175931 | ARPC1B, CO | 149        | 235      | 16021     | 1.3726403    | 1          | 0.99999907 | 99.9999598 |
| INTERPRO        | IPR019775:WD40 repe | 3     | 1.79640719 | 0.66467171 | ARPC1B, CO | 157        | 258      | 17763     | 1.31558288   | 1          | 0.99983199 | 99.9999676 |
| INTERPRO        | IPR001680:WD40 repe | 3     | 1.79640719 | 0.66674652 | ARPC1B, CO | 157        | 259      | 17763     | 1.31050341   | 1          | 0.9998058  | 99.9999703 |
| SP_PIR_KEYWORDS | wd repeat           | 3     | 1.79640719 | 0.67220777 | ARPC1B, CO | 157        | 263      | 17854     | 1.29718341   | 1          | 0.98186123 | 99.9999619 |
| SMART           | SM00320:WD40        | 3     | 1.79640719 | 0.69974795 | ARPC1B, CO | 86         | 259      | 9131      | 1.22981952   | 1          | 0.99854288 | 99.9996826 |
| INTERPRO        | IPR015943:WD40/YVT  | 3     | 1.79640719 | 0.75145227 | ARPC1B, CO | 157        | 305      | 17763     | 1.11285371   | 1          | 0.99997489 | 99.9999995 |

Annotation Cluster 44 Enrichment Score: 0.1842739646897345

| Category      | Term                 | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|----------------------|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_CC_FAT | GO:0005635--nuclear  | 3     | 1.79640719 | 0.4332424  | RAC2, ALOX | 121        | 153      | 12504     | 2.02625182   | 1          | 0.93609741 | 99.8907409 |
| GOTERM_CC_FAT | GO:0012505--endome   | 6     | 3.59281437 | 0.58791533 | CORO1A, RA | 121        | 535      | 12504     | 1.1589403    | 1          | 0.97800607 | 99.9976219 |
| GOTERM_CC_FAT | GO:0031967--organell | 5     | 2.99401198 | 0.76725765 | NDUFB10, R | 121        | 540      | 12504     | 0.95684114   | 1          | 0.99539246 | 99.9999975 |
| GOTERM_CC_FAT | GO:0031975--envelop  | 5     | 2.99401198 | 0.76977513 | NDUFB10, R | 121        | 542      | 12504     | 0.95331036   | 1          | 0.9949791  | 99.9999978 |
| GOTERM_CC_FAT | GO:0031090--organell | 7     | 4.19161677 | 0.79667159 | CORO1A, N[ | 121        | 809      | 12504     | 0.89415563   | 1          | 0.9958588  | 99.9999995 |

Annotation Cluster 45 Enrichment Score: 0.17884116355633026

| Category        | Term                  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|-----------------------|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| SP_PIR_KEYWORDS | membrane              | 54    | 32.3353293 | 0.22138904 | S100A6, S10  | 157        | 5507     | 17854     | 1.11510191   | 1          | 0.71258514 | 96.3704174 |
| UP_SEQ_FEATURE  | topological domain:Ex | 22    | 13.1736527 | 0.44867074 | EGFR, PTPRE  | 149        | 2174     | 16021     | 1.08809419   | 1          | 0.99995455 | 99.9805013 |
| UP_SEQ_FEATURE  | topological domain:C[ | 26    | 15.5688623 | 0.59307493 | LRTM1, SOR   | 149        | 2780     | 16021     | 1.00561537   | 1          | 0.99999827 | 99.9997502 |
| UP_SEQ_FEATURE  | transmembrane regio   | 36    | 21.5568862 | 0.74281778 | C9, LRTM1, S | 149        | 4113     | 16021     | 0.94112464   | 1          | 0.99999996 | 99.9999997 |
| SP_PIR_KEYWORDS | transmembrane         | 40    | 23.9520958 | 0.90161572 | C9, KLRA17,  | 157        | 5237     | 17854     | 0.86858694   | 1          | 0.9995683  | 100        |
| GOTERM_CC_FAT   | GO:0031224--intrinsic | 48    | 28.742515  | 0.97074653 | C9, KLRA17,  | 121        | 5914     | 12504     | 0.83873258   | 1          | 0.9999782  | 100        |
| SP_PIR_KEYWORDS | receptor              | 15    | 8.98203593 | 0.97502854 | EGFR, KLRA1  | 157        | 2465     | 17854     | 0.69200656   | 1          | 0.99999003 | 100        |
| GOTERM_CC_FAT   | GO:0016021--integral  | 43    | 25.748503  | 0.99323112 | C9, KLRA17,  | 121        | 5709     | 12504     | 0.77834476   | 1          | 0.99999966 | 100        |

Annotation Cluster 46 Enrichment Score: 0.146664792421245

| Category        | Term                 | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|----------------------|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| SP_PIR_KEYWORDS | microtubule          | 3     | 1.79640719 | 0.57687186 | KIF23, PRC1, | 157        | 221      | 17854     | 1.54370695   | 1          | 0.95809055 | 99.9988773 |
| GOTERM_CC_FAT   | GO:0005874--microtul | 3     | 1.79640719 | 0.67423824 | KIF23, PRC1, | 121        | 240      | 12504     | 1.29173554   | 1          | 0.98840982 | 99.9998587 |
| GOTERM_CC_FAT   | GO:0015630--microtul | 3     | 1.79640719 | 0.93349692 | KIF23, PRC1, | 121        | 450      | 12504     | 0.68892562   | 1          | 0.99981105 | 100        |

Annotation Cluster 47 Enrichment Score: 0.1422658193029558

| Category      | Term                 | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|----------------------|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0043065--positive | 3     | 1.79640719 | 0.67321675 | C9, MMP9, F  | 127        | 248      | 13588     | 1.29425959   | 1          | 0.99900082 | 99.9999974 |
| GOTERM_BP_FAT | GO:0043068--positive | 3     | 1.79640719 | 0.6775093  | C9, MMP9, F  | 127        | 250      | 13588     | 1.28390551   | 1          | 0.9989886  | 99.9999979 |
| GOTERM_BP_FAT | GO:0010942--positive | 3     | 1.79640719 | 0.68175631 | C9, MMP9, F  | 127        | 252      | 13588     | 1.27371579   | 1          | 0.99902267 | 99.9999983 |
| GOTERM_BP_FAT | GO:0042981--regulati | 5     | 2.99401198 | 0.75965799 | PROK2, C9, I | 127        | 553      | 13588     | 0.96737908   | 1          | 0.99973754 | 100        |
| GOTERM_BP_FAT | GO:0043067--regulati | 5     | 2.99401198 | 0.76828458 | PROK2, C9, I | 127        | 560      | 13588     | 0.95528684   | 1          | 0.99977587 | 100        |
| GOTERM_BP_FAT | GO:0010941--regulati | 5     | 2.99401198 | 0.77190797 | PROK2, C9, I | 127        | 563      | 13588     | 0.9501965    | 1          | 0.99978404 | 100        |

Annotation Cluster 48 Enrichment Score: 0.13002255844042354

| Category      | Term                 | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|----------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0001701--in utero | 3     | 1.79640719 | 0.71217926 | EGFR, SOCS3 | 127        | 267      | 13588     | 1.20215872   | 1          | 0.9994408  | 99.9999996 |
| GOTERM_BP_FAT | GO:0043009--chordate | 4     | 2.39520958 | 0.75341728 | EGFR, IFTM1 | 127        | 421      | 13588     | 1.01655227   | 1          | 0.99972579 | 100        |
| GOTERM_BP_FAT | GO:0009792--embryon  | 4     | 2.39520958 | 0.75911474 | EGFR, IFTM1 | 127        | 425      | 13588     | 1.00698472   | 1          | 0.99974776 | 100        |

Annotation Cluster 49 Enrichment Score: 0.12759471237788161

| Category        | Term                   | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|------------------------|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT   | GO:0015674--di-, tri-v | 3     | 1.79640719 | 0.44154894 | CORO1A, AT | 127        | 161      | 13588     | 1.9936421    | 1          | 0.98343891 | 99.9887377 |
| GOTERM_BP_FAT   | GO:0030001--metal io   | 4     | 2.39520958 | 0.78216371 | CORO1A, KC | 127        | 442      | 13588     | 0.96825453   | 1          | 0.99982466 | 100        |
| SP_PIR_KEYWORDS | ion transport          | 4     | 2.39520958 | 0.85739625 | KCNAB2, AT | 157        | 543      | 17854     | 0.83771451   | 1          | 0.99872444 | 100        |
| GOTERM_BP_FAT   | GO:0006812--cation tr  | 4     | 2.39520958 | 0.86145848 | CORO1A, KC | 127        | 515      | 13588     | 0.8310068    | 1          | 0.99997984 | 100        |
| GOTERM_BP_FAT   | GO:0006811--ion tran   | 5     | 2.99401198 | 0.90226476 | CORO1A, KC | 127        | 712      | 13588     | 0.7513492    | 1          | 0.99999566 | 100        |

Annotation Cluster 50 Enrichment Score: 0.025492400164834415

| Category        | Term                    | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|-------------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_MF_FAT   | GO:0046983--protein     | 4     | 2.39520958 | 0.57925949 | PTPRE, NFE2 | 118        | 340      | 13288     | 1.32482552   | 1          | 0.99578833 | 99.9989184 |
| SP_PIR_KEYWORDS | activator               | 3     | 1.79640719 | 0.92738144 | NFE2, CEBPE | 157        | 484      | 17854     | 0.70487445   | 1          | 0.99976795 | 100        |
| GOTERM_MF_FAT   | GO:0043565--sequenc     | 3     | 1.79640719 | 0.95947649 | NFE2, CEBPE | 118        | 556      | 13288     | 0.60760883   | 1          | 0.99999799 | 100        |
| SP_PIR_KEYWORDS | dna-binding             | 8     | 4.79041916 | 0.96654579 | NFE2, HMGN  | 157        | 1404     | 17854     | 0.64797576   | 1          | 0.99997793 | 100        |
| GOTERM_MF_FAT   | GO:0003700--transcrip   | 3     | 1.79640719 | 0.99293745 | NFE2, CEBPE | 118        | 776      | 13288     | 0.43534859   | 1          | 1          | 100        |
| GOTERM_MF_FAT   | GO:0030528--transcrip   | 3     | 1.79640719 | 0.99982212 | NFE2, CEBPE | 118        | 1206     | 13288     | 0.2801248    | 1          | 1          | 100        |
| SP_PIR_KEYWORDS | transcription regulatic | 4     | 2.39520958 | 0.99991327 | UHRF1, NFE2 | 157        | 1546     | 17854     | 0.29422961   | 1          | 1          | 100        |
| SP_PIR_KEYWORDS | Transcription           | 5     | 2.99401198 | 0.99991962 | UHRF1, NFE2 | 157        | 1769     | 17854     | 0.32142381   | 1          | 1          | 100        |
| GOTERM_BP_FAT   | GO:0006355--regulatio   | 4     | 2.39520958 | 0.99992875 | CDKN1C, NF  | 127        | 1465     | 13588     | 0.29212867   | 1          | 1          | 100        |
| GOTERM_BP_FAT   | GO:0051252--regulatio   | 4     | 2.39520958 | 0.99994211 | CDKN1C, NF  | 127        | 1488     | 13588     | 0.28761324   | 1          | 1          | 100        |
| GOTERM_BP_FAT   | GO:0006350--transcrip   | 5     | 2.99401198 | 0.99997244 | UHRF1, NFE2 | 127        | 1772     | 13588     | 0.30189652   | 1          | 1          | 100        |
| GOTERM_BP_FAT   | GO:0045449--regulatio   | 6     | 3.59281437 | 0.99999739 | CDKN1C, UH  | 127        | 2227     | 13588     | 0.28825898   | 1          | 1          | 100        |

Annotation Cluster 51 Enrichment Score: 0.01872958839405146

| Category      | Term                 | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR |
|---------------|----------------------|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|-----|
| GOTERM_BP_FAT | GO:0010604--positive | 4     | 2.39520958 | 0.93719611 | HPX, IL1B, ST | 127        | 633      | 13588     | 0.67609558   | 1          | 0.99999951 | 100 |
| GOTERM_BP_FAT | GO:0010557--positive | 3     | 1.79640719 | 0.95996764 | IL1B, STAT3,  | 127        | 530      | 13588     | 0.60561581   | 1          | 0.99999994 | 100 |
| GOTERM_BP_FAT | GO:0031328--positive | 3     | 1.79640719 | 0.96649078 | IL1B, STAT3,  | 127        | 552      | 13588     | 0.58147895   | 1          | 0.99999997 | 100 |
| GOTERM_BP_FAT | GO:0009891--positive | 3     | 1.79640719 | 0.96782505 | IL1B, STAT3,  | 127        | 557      | 13588     | 0.57625921   | 1          | 0.99999998 | 100 |

Annotation Cluster 52 Enrichment Score: 0.012925643429738315

| Category      | Term                | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR |
|---------------|---------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|-----|
| GOTERM_BP_FAT | GO:0006468--protein | 4     | 2.39520958 | 0.94019401 | EGFR, PTPRE | 127        | 640      | 13588     | 0.66870079   | 1          | 0.99999959 | 100 |
| GOTERM_BP_FAT | GO:0016310--phospho | 4     | 2.39520958 | 0.96577055 | EGFR, PTPRE | 127        | 718      | 13588     | 0.59605641   | 1          | 0.99999997 | 100 |
| GOTERM_BP_FAT | GO:0006796--phospho | 4     | 2.39520958 | 0.98878756 | EGFR, PTPRE | 127        | 866      | 13588     | 0.49418996   | 1          | 1          | 100 |
| GOTERM_BP_FAT | GO:0006793--phospho | 4     | 2.39520958 | 0.98878756 | EGFR, PTPRE | 127        | 866      | 13588     | 0.49418996   | 1          | 1          | 100 |

Annotation Cluster 53 Enrichment Score: 5.301682331445533E-5

| Category      | Term                  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini | FDR |
|---------------|-----------------------|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|-----------|-----|
| GOTERM_CC_FAT | GO:0070013--intracell | 3     | 1.79640719 | 0.99986139 | MKI67, PPIB, | 121        | 1133     | 12504     | 0.27362447   | 1          | 1         | 100 |
| GOTERM_CC_FAT | GO:0043233--organell  | 3     | 1.79640719 | 0.99986537 | MKI67, PPIB, | 121        | 1136     | 12504     | 0.27290187   | 1          | 1         | 100 |
| GOTERM_CC_FAT | GO:0031974--membra    | 3     | 1.79640719 | 0.99990704 | MKI67, PPIB, | 121        | 1174     | 12504     | 0.26406859   | 1          | 1         | 100 |

| Common ge | Category        | Term                  | Count | %  | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------|-----------------|-----------------------|-------|----|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Liver     | GOTERM_BP_FAT   | GO:0008610--lipid bio | 4     | 40 | 1.74E-04   | SCD1, CYP17 | 7          | 285      | 13588     | 27.2441103   | 0.01418855 | 0.01418855 | 0.18600258 |
| CH/C      | GOTERM_BP_FAT   | GO:0006631--fatty aci | 3     | 30 | 0.0026395  | SCD1, ACAC  | 7          | 184      | 13588     | 31.6490683   | 0.19484899 | 0.10269793 | 2.78406114 |
| NH/NC     | SP_PIR_KEYWORDS | steroidogenesis       | 2     | 20 | 0.00625714 | CYP17A1, H  | 9          | 14       | 17854     | 283.396825   | 0.27847871 | 0.27847871 | 5.91608977 |
|           | SP_PIR_KEYWORDS | oxidoreductase        | 3     | 30 | 0.02523826 | SCD1, CYP17 | 9          | 572      | 17854     | 10.4044289   | 0.73532027 | 0.48552966 | 21.9915792 |
|           | GOTERM_BP_FAT   | GO:0006694--steroid t | 2     | 20 | 0.03095011 | CYP17A1, H  | 7          | 71       | 13588     | 54.6800805   | 0.92407531 | 0.5765576  | 28.5283802 |
|           | GOTERM_BP_FAT   | GO:0055114--oxidatio  | 3     | 30 | 0.03207776 | SCD1, CYP17 | 7          | 672      | 13588     | 8.66581633   | 0.93098899 | 0.48745784 | 29.4118973 |
|           | KEGG_PATHWAY    | mmu01040:Biosynthes   | 2     | 20 | 0.03249372 | SCD1, ACOT  | 8          | 27       | 5738      | 53.1296296   | 0.50027662 | 0.50027662 | 22.5131936 |
|           | GOTERM_BP_FAT   | GO:0006633--fatty aci | 2     | 20 | 0.03524443 | SCD1, ACAC  | 7          | 81       | 13588     | 47.9294533   | 0.94725053 | 0.44480746 | 31.8403234 |
|           | KEGG_PATHWAY    | mmu00140:Steroid hc   | 2     | 20 | 0.05364974 | CYP17A1, H  | 8          | 45       | 5738      | 31.8777778   | 0.68588402 | 0.43953949 | 34.6736908 |
|           | GOTERM_BP_FAT   | GO:0016053--organic   | 2     | 20 | 0.0606787  | SCD1, ACAC  | 7          | 141      | 13588     | 27.5339412   | 0.99410122 | 0.57493011 | 48.7646683 |
|           | GOTERM_BP_FAT   | GO:0046394--carboxyl  | 2     | 20 | 0.0606787  | SCD1, ACAC  | 7          | 141      | 13588     | 27.5339412   | 0.99410122 | 0.57493011 | 48.7646683 |
|           | GOTERM_BP_FAT   | GO:0008202--steroid r | 2     | 20 | 0.06903157 | CYP17A1, H  | 7          | 161      | 13588     | 24.1135759   | 0.99716426 | 0.56739137 | 53.4277452 |
|           | GOTERM_CC_FAT   | GO:0005783--endopla   | 3     | 30 | 0.09594157 | SCD1, CYP17 | 9          | 838      | 12504     | 4.97374702   | 0.98400234 | 0.98400234 | 60.4733454 |

## Unique Liver Annotation

89 david id matched

| UNIQUE TH/SH | Annotation Cluster 1 | Enrichment Score: 2.4326697067761396              | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|--------------|----------------------|---|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| LIVER        | GOTERM_BP_FAT        | GO:0002526~acute inflammatory response            | 7     | 7.86516854 | 4.61E-06   | ORM1, C4BP    | 74         | 81       | 13588     | 15.8685352   | 0.00352182 | 0.00352182 | 0.00702932 |
|              | GOTERM_BP_FAT        | GO:0006955~immune response                        | 12    | 13.4831461 | 3.94E-05   | APOA4, C4BP   | 74         | 471      | 13588     | 4.67825788   | 0.0297383  | 0.01498137 | 0.06013396 |
|              | GOTERM_BP_FAT        | GO:0002250~adaptive immune response               | 6     | 6.74157303 | 8.65E-05   | C4BP, CFB, G  | 74         | 84       | 13588     | 13.1158301   | 0.06409353 | 0.02183794 | 0.13189466 |
|              | GOTERM_BP_FAT        | GO:0002460~adaptive immune response based on      | 6     | 6.74157303 | 8.65E-05   | C4BP, CFB, G  | 74         | 84       | 13588     | 13.1158301   | 0.06409353 | 0.02183794 | 0.13189466 |
|              | INTERPRO             | IPR016060:Complement control module               | 5     | 5.61797753 | 1.12E-04   | C4BP, CFB, H  | 83         | 54       | 17763     | 19.8159304   | 0.02552242 | 0.02552242 | 0.14348385 |
|              | GOTERM_BP_FAT        | GO:0006953~acute-phase response                   | 4     | 4.49438202 | 5.44E-04   | ORM1, SERP    | 74         | 30       | 13588     | 24.4828829   | 0.34097665 | 0.09899915 | 0.82741704 |
|              | GOTERM_BP_FAT        | GO:0006952~defense response                       | 10    | 11.2359551 | 6.35E-04   | APOA4, ORN    | 74         | 448      | 13588     | 4.09869691   | 0.38513411 | 0.0926892  | 0.96436741 |
|              | GOTERM_BP_FAT        | GO:0002455~humoral immune response mediated       | 4     | 4.49438202 | 8.61E-04   | C4BP, CFB, IC | 74         | 35       | 13588     | 20.9853282   | 0.48289925 | 0.08991456 | 1.30548288 |
|              | GOTERM_BP_FAT        | GO:0006954~inflammatory response                  | 7     | 7.86516854 | 0.00130272 | ORM1, C4BP    | 74         | 225      | 13588     | 5.71267267   | 0.63158001 | 0.11734111 | 1.9698989  |
|              | SP_PIR_KEYWORDS      | sushi   | 4     | 4.49438202 | 0.00131794 | C4BP, CFB, H  | 85         | 46       | 17854     | 18.2649616   | 0.24390508 | 0.13046281 | 1.6549116  |
|              | SMART                | SM00032:CCP                                       | 4     | 4.49438202 | 0.0016846  | C4BP, CFB, H  | 42         | 53       | 9131      | 16.4079066   | 0.08239394 | 0.08239394 | 1.61782205 |
|              | SP_PIR_KEYWORDS      | immune response                                   | 6     | 6.74157303 | 0.00176117 | C4BP, LST1, : | 85         | 184      | 17854     | 6.84936061   | 0.31181512 | 0.11711994 | 2.20577109 |
|              | INTERPRO             | IPR000436:Sushi/SCR/CCP                           | 4     | 4.49438202 | 0.00188092 | C4BP, CFB, H  | 83         | 53       | 17763     | 16.1518527   | 0.35267151 | 0.19543273 | 2.38642266 |
|              | GOTERM_BP_FAT        | GO:0045087~innate immune response                 | 5     | 5.61797753 | 0.00260743 | APOA4, C4BP   | 74         | 107      | 13588     | 8.58044961   | 0.86465066 | 0.19925335 | 3.90641652 |
|              | GOTERM_BP_FAT        | GO:0006959~humoral immune response                | 4     | 4.49438202 | 0.00303209 | C4BP, CFB, IC | 74         | 54       | 13588     | 13.6016016   | 0.90232506 | 0.20753824 | 4.52897727 |
|              | GOTERM_BP_FAT        | GO:0002252~immune effector process                | 5     | 5.61797753 | 0.00468554 | C4BP, CFB, IC | 74         | 126      | 13588     | 7.28657229   | 0.97260944 | 0.27895276 | 6.91720338 |
|              | GOTERM_BP_FAT        | GO:0016064~immunoglobulin mediated immune r       | 4     | 4.49438202 | 0.00468997 | C4BP, CFB, IC | 74         | 63       | 13588     | 11.6585157   | 0.97270274 | 0.2592416  | 6.92353145 |
|              | GOTERM_BP_FAT        | GO:0002684~positive regulation of immune system   | 6     | 6.74157303 | 0.00497496 | C4BP, CFB, B  | 74         | 206      | 13588     | 5.34820257   | 0.97807946 | 0.25462783 | 7.32945866 |
|              | GOTERM_BP_FAT        | GO:0019724~B cell mediated immunity               | 4     | 4.49438202 | 0.00511943 | C4BP, CFB, IC | 74         | 65       | 13588     | 11.2997921   | 0.98038681 | 0.24483969 | 7.53459639 |
|              | SP_PIR_KEYWORDS      | acute phase                                       | 3     | 3.37078652 | 0.00564447 | ORM1, SERP    | 85         | 24       | 17854     | 26.2558824   | 0.69881093 | 0.25918494 | 6.9119648  |
|              | GOTERM_BP_FAT        | GO:0050778~positive regulation of immune respon   | 5     | 5.61797753 | 0.00613154 | C4BP, CFB, IC | 74         | 136      | 13588     | 6.75079491   | 0.99100616 | 0.26954015 | 8.95991521 |
|              | SP_PIR_KEYWORDS      | complement pathway                                | 3     | 3.37078652 | 0.00660624 | C4BP, CFB, C  | 85         | 26       | 17854     | 24.2361991   | 0.75467433 | 0.18187356 | 8.04485269 |
|              | GOTERM_BP_FAT        | GO:0002449~lymphocyte mediated immunity           | 4     | 4.49438202 | 0.00790054 | C4BP, CFB, IC | 74         | 76       | 13588     | 9.66429587   | 0.99770229 | 0.30050914 | 11.401947  |
|              | GOTERM_BP_FAT        | GO:0009611~response to wounding                   | 7     | 7.86516854 | 0.01076381 | ORM1, C4BP    | 74         | 347      | 13588     | 3.70418257   | 0.99974893 | 0.36905899 | 15.2252559 |
|              | GOTERM_BP_FAT        | GO:0002253~activation of immune response          | 4     | 4.49438202 | 0.01107149 | C4BP, CFB, IC | 74         | 86       | 13588     | 8.54054054   | 0.99980216 | 0.36163517 | 15.6268015 |
|              | GOTERM_BP_FAT        | GO:0006958~complement activation, classical path  | 3     | 3.37078652 | 0.01123691 | C4BP, CFB, C  | 74         | 30       | 13588     | 18.3621622   | 0.99982595 | 0.35131613 | 15.8419368 |
|              | UP_SEQ_FEATURE       | domain:Sushi 2                                    | 3     | 3.37078652 | 0.01148217 | C4BP, CFB, C  | 80         | 33       | 16021     | 18.2056818   | 0.97837996 | 0.97837996 | 14.5045922 |
|              | UP_SEQ_FEATURE       | domain:Sushi 1                                    | 3     | 3.37078652 | 0.01148217 | C4BP, CFB, C  | 80         | 33       | 16021     | 18.2056818   | 0.97837996 | 0.97837996 | 14.5045922 |
|              | KEGG_PATHWAY         | mmu04610:Complement and coagulation cascades      | 4     | 4.49438202 | 0.0121193  | C4BP, SERPIN  | 38         | 75       | 5738      | 8.05333333   | 0.51886147 | 0.51886147 | 11.5026402 |
|              | GOTERM_BP_FAT        | GO:0002443~leukocyte mediated immunity            | 4     | 4.49438202 | 0.01214638 | C4BP, CFB, IC | 74         | 89       | 13588     | 8.25265715   | 0.99991399 | 0.35966657 | 17.0156703 |
|              | GOTERM_BP_FAT        | GO:0002541~activation of plasma proteins involve  | 3     | 3.37078652 | 0.01594085 | C4BP, CFB, C  | 74         | 36       | 13588     | 15.3018018   | 0.99999549 | 0.42850693 | 21.7496065 |
|              | GOTERM_BP_FAT        | GO:0006956~complement activation                  | 3     | 3.37078652 | 0.01594085 | C4BP, CFB, C  | 74         | 36       | 13588     | 15.3018018   | 0.99999549 | 0.42850693 | 21.7496065 |
|              | GOTERM_BP_FAT        | GO:0048584~positive regulation of response to sti | 5     | 5.61797753 | 0.0177829  | C4BP, CFB, IC | 74         | 186      | 13588     | 4.9360651    | 0.99999893 | 0.44985695 | 23.9555835 |
|              | GOTERM_BP_FAT        | GO:0051605~protein maturation by peptide bond     | 3     | 3.37078652 | 0.0476548  | C4BP, CFB, C  | 74         | 65       | 13588     | 8.47484407   | 1          | 0.68926453 | 52.5374862 |
|              | SP_PIR_KEYWORDS      | innate immunity                                   | 3     | 3.37078652 | 0.04865931 | C4BP, CFB, C  | 85         | 75       | 17854     | 8.40188235   | 0.99997446 | 0.58574231 | 46.8043932 |
|              | GOTERM_BP_FAT        | GO:0016485~protein processing                     | 3     | 3.37078652 | 0.08431083 | C4BP, CFB, C  | 74         | 90       | 13588     | 6.12072072   | 1          | 0.79175143 | 73.92752   |
|              | GOTERM_BP_FAT        | GO:0051604~protein maturation                     | 3     | 3.37078652 | 0.0940765  | C4BP, CFB, C  | 74         | 96       | 13588     | 5.73817568   | 1          | 0.7798888  | 77.863346  |
|              | GOTERM_BP_FAT        | GO:0006508~proteolysis                            | 7     | 7.86516854 | 0.48445516 | C4BP, CFB, H  | 74         | 1034     | 13588     | 1.24308641   | 1          | 0.99597927 | 99.9959404 |
|              |                      |   |       |            |            |               |            |          |           |              |            |            |            |
|              | Annotation Cluster 2 | Enrichment Score: 1.781568957744204               | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|              | GOTERM_CC_FAT        | GO:0044449~contractile fiber part                 | 4     | 4.49438202 | 0.00926951 | SRI, KRT8, LN | 64         | 86       | 12504     | 9.0872093    | 0.76168483 | 0.38001113 | 10.5701492 |
|              | GOTERM_CC_FAT        | GO:0030016~myofibril                              | 4     | 4.49438202 | 0.01081007 | SRI, KRT8, LN | 64         | 91       | 12504     | 8.58791209   | 0.81246955 | 0.34193628 | 12.2241422 |
|              | GOTERM_CC_FAT        | GO:0043292~contractile fiber                      | 4     | 4.49438202 | 0.01214312 | SRI, KRT8, LN | 64         | 95       | 12504     | 8.22631579   | 0.84763669 | 0.31360189 | 13.6326651 |
|              | GOTERM_CC_FAT        | GO:0030017~sarcomere                              | 3     | 3.37078652 | 0.06144815 | SRI, KRT8, LN | 64         | 80       | 12504     | 7.3265625    | 0.99994264 | 0.66214494 | 53.2685585 |
|              |                      |   |       |            |            |               |            |          |           |              |            |            |            |
|              | Annotation Cluster 3 | Enrichment Score: 1.6039460640800736              | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|              | SP_PIR_KEYWORDS      | cell shape  | 3     | 3.37078652 | 0.00611665 | LST1, MYH9,   | 85         | 25       | 17854     | 25.2056471   | 0.72766191 | 0.22905805 | 7.46975027 |
|              | GOTERM_BP_FAT        | GO:0008360~regulation of cell shape               | 3     | 3.37078652 | 0.02633769 | LST1, MYH9,   | 74         | 47       | 13588     | 11.720529    | 1          | 0.55860022 | 33.4599266 |
|              | GOTERM_BP_FAT        | GO:0022604~regulation of cell morphogenesis       | 3     | 3.37078652 | 0.09573501 | LST1, MYH9,   | 74         | 97       | 13588     | 5.67901923   | 1          | 0.77941355 | 78.4738653 |

|                      |  |       |            |                   |              |            |          |           |              |            |            |                   |
|----------------------|--|-------|------------|-------------------|--------------|------------|----------|-----------|--------------|------------|------------|-------------------|
| Annotation Cluster 4 | Enrichment Score: 1.4732814924862054             |       |            |                   |              |            |          |           |              |            |            |                   |
| Category             | Term   | Count | %          | PValue            | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR               |
| GOTERM_BP_FAT        | GO:0006952~defense response                      | 10    | 11.2359551 | <b>6.35E-04</b>   | APOA4, ORN   | 74         | 448      | 13588     | 4.09869691   | 0.38513411 | 0.0926892  | 0.96436741        |
| SP_PIR_KEYWORDS      | Secreted   | 15    | 16.8539326 | <b>0.00621329</b> | HAMP2, OLF   | 85         | 1420     | 17854     | 2.21880696   | 0.73321912 | 0.19765876 | 7.58354133        |
| GOTERM_CC_FAT        | GO:0005576~extracellular region                  | 17    | 19.1011236 | <b>0.00778839</b> | ALDOA, HAN   | 64         | 1680     | 12504     | 1.97700893   | 0.7000405  | 0.7000405  | 8.95309559        |
| GOTERM_CC_FAT        | GO:0005615~extracellular space                   | 8     | 8.98876404 | <b>0.01399331</b> | APOA4, ORN   | 64         | 511      | 12504     | 3.05870841   | 0.88584399 | 0.30350746 | 15.5532824        |
| SP_PIR_KEYWORDS      | signal   | 22    | 24.7191011 | <b>0.03233689</b> | HAMP2, OLF   | 85         | 2970     | 17854     | 1.55590414   | 0.99905914 | 0.5018585  | 34.0277687        |
| GOTERM_CC_FAT        | GO:0044421~extracellular region part             | 9     | 10.1123596 | <b>0.03959809</b> | APOA4, ORN   | 64         | 774      | 12504     | 2.27180233   | 0.99801498 | 0.58888217 | 38.4105682        |
| UP_SEQ_FEATURE       | signal peptide                                   | 22    | 24.7191011 | <b>0.04808989</b> | HAMP2, OLF   | 80         | 2963     | 16021     | 1.48693048   | 0.99999992 | 0.99972015 | 48.7658197        |
| SP_PIR_KEYWORDS      | disulfide bond                                   | 17    | 19.1011236 | 0.11201746        | HAMP2, IGK   | 85         | 2469     | 17854     | 1.44625354   | 1          | 0.75321498 | 77.7599318        |
| UP_SEQ_FEATURE       | disulfide bond                                   | 17    | 19.1011236 | 0.11822811        | HAMP2, IGK   | 80         | 2379     | 16021     | 1.43104771   | 1          | 0.99976468 | 81.865016         |
| SP_PIR_KEYWORDS      | glycoprotein                                     | 20    | 22.4719101 | 0.32721231        | OLFM4, GAN   | 85         | 3600     | 17854     | 1.1669281    | 1          | 0.96982903 | 99.3361697        |
| UP_SEQ_FEATURE       | glycosylation site:N-linked (GlcNAc...)          | 18    | 20.2247191 | 0.54245994        | OLFM4, GAN   | 80         | 3444     | 16021     | 1.04666812   | 1          | 1          | 99.9975327        |
| Annotation Cluster 5 | Enrichment Score: 1.168650165494244              |       |            |                   |              |            |          |           |              |            |            |                   |
| Category             | Term   | Count | %          | PValue            | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR               |
| KEGG_PATHWAY         | mmu03010:Ribosome                                | 4     | 4.49438202 | <b>0.01916619</b> | RPL18A, LOC  | 38         | 89       | 5738      | 6.78651685   | 0.68686921 | 0.44041909 | 17.6293979        |
| GOTERM_MF_FAT        | GO:0005198~structural molecule activity          | 7     | 7.86516854 | <b>0.02907212</b> | RPL18A, LOC  | 70         | 450      | 13288     | 2.95288889   | 0.99682708 | 0.99682708 | 30.8060824        |
| GOTERM_MF_FAT        | GO:0003735~structural constituent of ribosome    | 4     | 4.49438202 | <b>0.04374202</b> | RPL18A, LOC  | 70         | 151      | 13288     | 5.02857143   | 0.99983702 | 0.94537647 | 42.7812623        |
| SP_PIR_KEYWORDS      | ribosomal protein                                | 4     | 4.49438202 | 0.05095305        | RPL18A, LOC  | 85         | 177      | 17854     | 4.74682619   | 0.99998469 | 0.57379869 | 48.4046924        |
| GOTERM_CC_FAT        | GO:0005840~ribosome                              | 4     | 4.49438202 | 0.07250174        | RPL18A, LOC  | 64         | 192      | 12504     | 4.0703125    | 0.99999075 | 0.651355   | 59.4596324        |
| GOTERM_BP_FAT        | GO:0006412~translation                           | 5     | 5.61797753 | 0.09240848        | EEF1B2, RPL1 | 74         | 319      | 13588     | 2.87808184   | 1          | 0.78718537 | 77.2330287        |
| SP_PIR_KEYWORDS      | ribonucleoprotein                                | 4     | 4.49438202 | 0.13019177        | RPL18A, LOC  | 85         | 266      | 17854     | 3.15860239   | 1          | 0.78909157 | 82.8802956        |
| GOTERM_CC_FAT        | GO:0030529~ribonucleoprotein complex             | 4     | 4.49438202 | 0.4131174         | RPL18A, LOC  | 64         | 462      | 12504     | 1.69155844   | 1          | 0.9672757  | 99.8326836        |
| Annotation Cluster 6 | Enrichment Score: 1.1680916531289633             |       |            |                   |              |            |          |           |              |            |            |                   |
| Category             | Term   | Count | %          | PValue            | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR               |
| SMART                | SM00407:IGc1                                     | 4     | 4.49438202 | <b>0.00602032</b> | IGK-C, H2-Q  | 42         | 83       | 9131      | 10.4773379   | 0.26505854 | 0.14271273 | 5.67429226        |
| INTERPRO             | IPR003597:Immunoglobulin C1-set                  | 4     | 4.49438202 | <b>0.00668158</b> | IGK-C, H2-Q  | 83         | 83       | 17763     | 10.3138336   | 0.78746002 | 0.40322098 | 8.24128112        |
| INTERPRO             | IPR003006:Immunoglobulin/major histocompatibilit | 4     | 4.49438202 | <b>0.01052828</b> | IGK-C, H2-Q  | 83         | 98       | 17763     | 8.73518564   | 0.91326749 | 0.45731792 | 12.6971023        |
| GOTERM_BP_FAT        | GO:0019882~antigen processing and presentation   | 3     | 3.37078652 | 0.07955351        | H2-Q5, H2-C  | 74         | 87       | 13588     | 6.33178006   | 1          | 0.80371167 | 71.7817577        |
| GOTERM_CC_FAT        | GO:0009897~external side of plasma membrane      | 3     | 3.37078652 | 0.27831081        | H2-Q5, H2-C  | 64         | 206      | 12504     | 2.84526699   | 1          | 0.92889648 | 98.0012075        |
| INTERPRO             | IPR007110:Immunoglobulin-like                    | 5     | 5.61797753 | 0.30447938        | IGK-C, H2-Q  | 83         | 604      | 17763     | 1.77162292   | 1          | 0.99999374 | 99.0516945        |
| INTERPRO             | IPR013783:Immunoglobulin-like fold               | 5     | 5.61797753 | 0.346529          | IGK-C, H2-Q  | 83         | 644      | 17763     | 1.66158423   | 1          | 0.99999538 | 99.5739275        |
| GOTERM_CC_FAT        | GO:0009986~cell surface                          | 3     | 3.37078652 | 0.45700731        | H2-Q5, H2-C  | 64         | 305      | 12504     | 1.92172131   | 1          | 0.9692855  | 99.9341454        |
| Annotation Cluster 7 | Enrichment Score: 1.1632749465217602             |       |            |                   |              |            |          |           |              |            |            |                   |
| Category             | Term   | Count | %          | PValue            | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR               |
| GOTERM_BP_FAT        | GO:0006006~glucose metabolic process             | 4     | 4.49438202 | <b>0.03948014</b> | ALDOA, ATF4  | 74         | 140      | 13588     | 5.24633205   | 1          | 0.64245662 | 45.9240462        |
| GOTERM_BP_FAT        | GO:0019318~hexose metabolic process              | 4     | 4.49438202 | 0.0625377         | ALDOA, ATF4  | 74         | 169      | 13588     | 4.34607388   | 1          | 0.77664872 | 62.6795624        |
| GOTERM_BP_FAT        | GO:0005996~monosaccharide metabolic process      | 4     | 4.49438202 | 0.08336072        | ALDOA, ATF4  | 74         | 191      | 13588     | 3.84547899   | 1          | 0.79555711 | 73.5115606        |
| UP_SEQ_FEATURE       | active site:Proton acceptor                      | 7     | 7.86516854 | 0.1079986         | ALDOA, CPT.  | 80         | 662      | 16021     | 2.11757931   | 1          | 0.99992408 | 78.7924661        |
| Annotation Cluster 8 | Enrichment Score: 1.1522947914347288             |       |            |                   |              |            |          |           |              |            |            |                   |
| Category             | Term   | Count | %          | PValue            | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR               |
| GOTERM_BP_FAT        | GO:0006487~protein amino acid N-linked glycosyl. | 3     | 3.37078652 | <b>0.00788468</b> | GANAB, SER   | 74         | 25       | 13588     | 22.0345946   | 0.99767398 | 0.31543721 | 11.3803283        |
| GOTERM_BP_FAT        | GO:0006486~protein amino acid glycosylation      | 3     | 3.37078652 | 0.08591568        | GANAB, SER   | 74         | 91       | 13588     | 6.05346005   | 1          | 0.78327977 | 74.6162862        |
| GOTERM_BP_FAT        | GO:0070085~glycosylation                         | 3     | 3.37078652 | 0.08591568        | GANAB, SER   | 74         | 91       | 13588     | 6.05346005   | 1          | 0.78327977 | 74.6162862        |
| GOTERM_BP_FAT        | GO:0043413~biopolymer glycosylation              | 3     | 3.37078652 | 0.08591568        | GANAB, SER   | 74         | 91       | 13588     | 6.05346005   | 1          | 0.78327977 | 74.6162862        |
| GOTERM_BP_FAT        | GO:0009101~glycoprotein biosynthetic process     | 3     | 3.37078652 | 0.13050749        | GANAB, SER   | 74         | 117      | 13588     | 4.70824671   | 1          | 0.84730733 | 88.16826          |
| GOTERM_BP_FAT        | GO:0009100~glycoprotein metabolic process        | 3     | 3.37078652 | 0.1868937         | GANAB, SER   | 74         | 147      | 13588     | 3.74738003   | 1          | 0.90608627 | 95.7476504        |
| Annotation Cluster 9 | Enrichment Score: 1.1235513467794078             |       |            |                   |              |            |          |           |              |            |            |                   |
| Category             | Term   | Count | %          | PValue            | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR               |
| INTERPRO             | IPR016060:Complement control module              | 5     | 5.61797753 | <b>1.12E-04</b>   | C4BP, CFB, H | 83         | 54       | 17763     | 19.8159304   | 0.02552242 | 0.02552242 | <b>0.14348385</b> |
| SP_PIR_KEYWORDS      | sushi  | 4     | 4.49438202 | <b>0.00131794</b> | C4BP, CFB, H | 85         | 46       | 17854     | 18.2649616   | 0.24390508 | 0.13046281 | 1.6549116         |
| SMART                | SM00032:CCP                                      | 4     | 4.49438202 | <b>0.0016846</b>  | C4BP, CFB, H | 42         | 53       | 9131      | 16.4079066   | 0.08239394 | 0.08239394 | 1.61782205        |

|                 |  |   |            |            |               |    |      |       |            |            |            |            |
|-----------------|--|---|------------|------------|---------------|----|------|-------|------------|------------|------------|------------|
| INTERPRO        | IPR000436:Sushi/SCR/CCP                          | 4 | 4.49438202 | 0.00188092 | C4BP, CFB, H  | 83 | 53   | 17763 | 16.1518527 | 0.35267151 | 0.19543273 | 2.38642266 |
| UP_SEQ_FEATURE  | domain:Peptidase S1                              | 3 | 3.37078652 | 0.10402364 | CFB, HP, C1S  | 80 | 111  | 16021 | 5.4125     | 1          | 0.99999474 | 77.4735435 |
| INTERPRO        | IPR001314:Peptidase S1A, chymotrypsin            | 3 | 3.37078652 | 0.14132477 | CFB, HP, C1S  | 83 | 143  | 17763 | 4.48976325 | 1          | 0.99912321 | 85.8397232 |
| SMART           | SM00020:Tryp_SPc                                 | 3 | 3.37078652 | 0.15952956 | CFB, HP, C1S  | 42 | 159  | 9131  | 4.10197664 | 0.99985854 | 0.94789475 | 81.3863005 |
| INTERPRO        | IPR001254:Peptidase S1 and S6, chymotrypsin/Hap  | 3 | 3.37078652 | 0.16705354 | CFB, HP, C1S  | 83 | 159  | 17763 | 4.03796317 | 1          | 0.99912147 | 90.4154224 |
| GOTERM_MF_FAT   | GO:0004252~serine-type endopeptidase activity    | 3 | 3.37078652 | 0.25731523 | CFB, HP, C1S  | 70 | 189  | 13288 | 3.01315193 | 1          | 0.99929065 | 97.5600361 |
| GOTERM_MF_FAT   | GO:0008236~serine-type peptidase activity        | 3 | 3.37078652 | 0.3016512  | CFB, HP, C1S  | 70 | 212  | 13288 | 2.68625337 | 1          | 0.99958162 | 98.8683469 |
| GOTERM_MF_FAT   | GO:0017171~serine hydrolase activity             | 3 | 3.37078652 | 0.30357348 | CFB, HP, C1S  | 70 | 213  | 13288 | 2.67364185 | 1          | 0.99913689 | 98.9066197 |
| GOTERM_MF_FAT   | GO:0004175~endopeptidase activity                | 4 | 4.49438202 | 0.37445758 | CFB, HP, C1S  | 70 | 421  | 13288 | 1.80359688 | 1          | 0.99854739 | 99.7136619 |
| GOTERM_MF_FAT   | GO:0008233~peptidase activity                    | 5 | 5.61797753 | 0.41371543 | CFB, SLPI, HF | 70 | 629  | 13288 | 1.50897116 | 1          | 0.9978119  | 99.8724935 |
| SP_PIR_KEYWORDS | Protease   | 4 | 4.49438202 | 0.43063743 | CFB, SLPI, C1 | 85 | 509  | 17854 | 1.65066451 | 1          | 0.98987305 | 99.9196812 |
| GOTERM_BP_FAT   | GO:0006508~proteolysis                           | 7 | 7.86516854 | 0.48445516 | C4BP, CFB, H  | 74 | 1034 | 13588 | 1.24308641 | 1          | 0.99597927 | 99.9959404 |
| GOTERM_MF_FAT   | GO:0070011~peptidase activity, acting on L-amino | 4 | 4.49438202 | 0.61179415 | CFB, HP, C1S  | 70 | 603  | 13288 | 1.25922767 | 1          | 0.99917212 | 99.9992575 |
| SP_PIR_KEYWORDS | hydrolase  | 5 | 5.61797753 | 0.93029097 | GANAB, CFB,   | 85 | 1500 | 17854 | 0.70015686 | 1          | 0.99999896 | 100        |

|                       |  |       |            |            |            |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 10 | Enrichment Score: 0.9910735999220784             |       |            |            |            |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_MF_FAT         | GO:0004857~enzyme inhibitor activity             | 5     | 5.61797753 | 0.03743758 | SERPINA3G, | 70         | 243      | 13288     | 3.90593768   | 0.999413   | 0.97577199 | 37.8902582 |
| SP_PIR_KEYWORDS       | Serine protease inhibitor                        | 3     | 3.37078652 | 0.05702943 | SERPINA3G, | 85         | 82       | 17854     | 7.68464849   | 0.99999608 | 0.56391245 | 52.4322576 |
| SP_PIR_KEYWORDS       | protease inhibitor                               | 3     | 3.37078652 | 0.0932997  | SERPINA3G, | 85         | 109      | 17854     | 5.78111171   | 1          | 0.72685404 | 71.042022  |
| GOTERM_MF_FAT         | GO:0004867~serine-type endopeptidase inhibitor a | 3     | 3.37078652 | 0.12003172 | SERPINA3G, | 70         | 115      | 13288     | 4.95204969   | 1          | 0.99803769 | 79.7307395 |
| GOTERM_MF_FAT         | GO:0004866~endopeptidase inhibitor activity      | 3     | 3.37078652 | 0.20367222 | SERPINA3G, | 70         | 161      | 13288     | 3.53717835   | 1          | 0.99938978 | 94.1732048 |
| GOTERM_MF_FAT         | GO:0030414~peptidase inhibitor activity          | 3     | 3.37078652 | 0.23229692 | SERPINA3G, | 70         | 176      | 13288     | 3.23571429   | 1          | 0.9993664  | 96.3103612 |

|                       |   |       |            |            |            |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 11 | Enrichment Score: 0.9704375904575754              |       |            |            |            |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0044057~regulation of system process           | 4     | 4.49438202 | 0.09369501 | APOA4, YWH | 74         | 201      | 13588     | 3.65416162   | 1          | 0.78517488 | 77.7206424 |
| GOTERM_BP_FAT         | GO:0050804~regulation of synaptic transmission    | 3     | 3.37078652 | 0.10076071 | YWHAG, LST | 74         | 100      | 13588     | 5.50864865   | 1          | 0.79080693 | 80.2292039 |
| GOTERM_BP_FAT         | GO:0051969~regulation of transmission of nerve ir | 3     | 3.37078652 | 0.11276316 | YWHAG, LST | 74         | 107      | 13588     | 5.14826977   | 1          | 0.82257097 | 83.8951368 |
| GOTERM_BP_FAT         | GO:0031644~regulation of neurological system prc  | 3     | 3.37078652 | 0.1233317  | YWHAG, LST | 74         | 113      | 13588     | 4.87491031   | 1          | 0.84009882 | 86.5869583 |

|                       |   |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 12 | Enrichment Score: 0.8573178879260404          |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0001775~cell activation                    | 5     | 5.61797753 | 0.04324923 | LST1, GADD4 | 74         | 246      | 13588     | 3.73214678   | 1          | 0.66461395 | 49.0735827 |
| GOTERM_BP_FAT         | GO:0030099~myeloid cell differentiation       | 3     | 3.37078652 | 0.0940765  | G6PDX, BCL6 | 74         | 96       | 13588     | 5.73817568   | 1          | 0.77988888 | 77.863346  |
| GOTERM_BP_FAT         | GO:0045321~leukocyte activation               | 4     | 4.49438202 | 0.11354615 | GADD45G, B  | 74         | 219      | 13588     | 3.35381957   | 1          | 0.81907753 | 84.110697  |
| GOTERM_BP_FAT         | GO:0030097~hemopoiesis                        | 4     | 4.49438202 | 0.15231358 | GADD45G, G  | 74         | 251      | 13588     | 2.92624098   | 1          | 0.87017517 | 91.9703899 |
| GOTERM_BP_FAT         | GO:0002521~leukocyte differentiation          | 3     | 3.37078652 | 0.17724283 | GADD45G, B  | 74         | 142      | 13588     | 3.87933003   | 1          | 0.89965187 | 94.9085783 |
| GOTERM_BP_FAT         | GO:0048534~hemopoietic or lymphoid organ deve | 4     | 4.49438202 | 0.19191866 | GADD45G, G  | 74         | 281      | 13588     | 2.61383091   | 1          | 0.90932059 | 96.1315344 |
| GOTERM_BP_FAT         | GO:0002520~immune system development          | 4     | 4.49438202 | 0.21123658 | GADD45G, G  | 74         | 295      | 13588     | 2.4897847    | 1          | 0.91708238 | 97.3260322 |
| GOTERM_BP_FAT         | GO:0046649~lymphocyte activation              | 3     | 3.37078652 | 0.27392473 | GADD45G, B  | 74         | 191      | 13588     | 2.88410924   | 1          | 0.95154567 | 99.244489  |

|                       |   |       |            |            |               |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 13 | Enrichment Score: 0.8450782384944543        |       |            |            |               |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0001775~cell activation                  | 5     | 5.61797753 | 0.04324923 | LST1, GADD4   | 74         | 246      | 13588     | 3.73214678   | 1          | 0.66461395 | 49.0735827 |
| GOTERM_BP_FAT         | GO:0000902~cell morphogenesis               | 4     | 4.49438202 | 0.23097134 | LST1, KRT8, I | 74         | 309      | 13588     | 2.37697892   | 1          | 0.92913681 | 98.1836285 |
| GOTERM_BP_FAT         | GO:0032989~cellular component morphogenesis | 4     | 4.49438202 | 0.29189641 | LST1, KRT8, I | 74         | 351      | 13588     | 2.09255409   | 1          | 0.95864234 | 99.4846392 |

|                       |  |       |            |            |            |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 14 | Enrichment Score: 0.7524315242149725               |       |            |            |            |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0045860~positive regulation of protein kinase   | 4     | 4.49438202 | 0.02905303 | GNAI2, GAD | 74         | 124      | 13588     | 5.92327812   | 1          | 0.58047281 | 36.2364792 |
| GOTERM_BP_FAT         | GO:0032147~activation of protein kinase activity   | 3     | 3.37078652 | 0.03064149 | GNAI2, GAD | 74         | 51       | 13588     | 10.8012719   | 1          | 0.58642121 | 37.8101623 |
| GOTERM_BP_FAT         | GO:0033674~positive regulation of kinase activity  | 4     | 4.49438202 | 0.03276652 | GNAI2, GAD | 74         | 130      | 13588     | 5.64989605   | 1          | 0.59804418 | 39.8587173 |
| GOTERM_BP_FAT         | GO:0051347~positive regulation of transferase acti | 4     | 4.49438202 | 0.03604186 | GNAI2, GAD | 74         | 135      | 13588     | 5.44064064   | 1          | 0.62075843 | 42.8930634 |
| GOTERM_BP_FAT         | GO:0045859~regulation of protein kinase activity   | 4     | 4.49438202 | 0.07839151 | GNAI2, GAD | 74         | 186      | 13588     | 3.94885208   | 1          | 0.80710036 | 71.2331305 |
| GOTERM_BP_FAT         | GO:0043549~regulation of kinase activity           | 4     | 4.49438202 | 0.08437065 | GNAI2, GAD | 74         | 192      | 13588     | 3.82545045   | 1          | 0.78443666 | 73.9535018 |
| GOTERM_BP_FAT         | GO:0051338~regulation of transferase activity      | 4     | 4.49438202 | 0.09158691 | GNAI2, GAD | 74         | 199      | 13588     | 3.69088687   | 1          | 0.79101848 | 76.9164476 |

|                 |  |   |            |            |              |    |      |       |            |   |            |            |
|-----------------|--|---|------------|------------|--------------|----|------|-------|------------|---|------------|------------|
| GOTERM_BP_FAT   | GO:000165~MAPKKK cascade                             | 3 | 3.37078652 | 0.12511631 | GNAI2, GAD   | 74 | 114  | 13588 | 4.83214794 | 1 | 0.83931944 | 86.9976962 |
| GOTERM_BP_FAT   | GO:0043085~positive regulation of catalytic activity | 4 | 4.49438202 | 0.16520886 | GNAI2, GAD   | 74 | 261  | 13588 | 2.81412447 | 1 | 0.88870235 | 93.6454272 |
| GOTERM_BP_FAT   | GO:0042325~regulation of phosphorylation             | 4 | 4.49438202 | 0.20428524 | GNAI2, GAD   | 74 | 290  | 13588 | 2.53271202 | 1 | 0.91796436 | 96.942855  |
| GOTERM_BP_FAT   | GO:0019220~regulation of phosphate metabolic pr      | 4 | 4.49438202 | 0.21964801 | GNAI2, GAD   | 74 | 301  | 13588 | 2.44015444 | 1 | 0.92325298 | 97.72966   |
| GOTERM_BP_FAT   | GO:0051174~regulation of phosphorus metabolic p      | 4 | 4.49438202 | 0.21964801 | GNAI2, GAD   | 74 | 301  | 13588 | 2.44015444 | 1 | 0.92325298 | 97.72966   |
| GOTERM_BP_FAT   | GO:0044093~positive regulation of molecular functi   | 4 | 4.49438202 | 0.22671141 | GNAI2, GAD   | 74 | 306  | 13588 | 2.40028264 | 1 | 0.92762384 | 98.0238477 |
| GOTERM_BP_FAT   | GO:0007243~protein kinase cascade                    | 3 | 3.37078652 | 0.36283338 | GNAI2, GAD   | 74 | 236  | 13588 | 2.33417316 | 1 | 0.98194963 | 99.8970981 |
| GOTERM_BP_FAT   | GO:0007242~intracellular signaling cascade           | 7 | 7.86516854 | 0.36858604 | LST1, GNAI2, | 74 | 915  | 13588 | 1.40475558 | 1 | 0.98254794 | 99.9104002 |
| GOTERM_BP_FAT   | GO:0006468~protein amino acid phosphorylation        | 5 | 5.61797753 | 0.45252709 | GNAI2, PLK1, | 74 | 640  | 13588 | 1.43454392 | 1 | 0.99406835 | 99.9898428 |
| GOTERM_BP_FAT   | GO:0006796~phosphate metabolic process               | 6 | 6.74157303 | 0.5008801  | GNAI2, PLK1, | 74 | 866  | 13588 | 1.27220523 | 1 | 0.99652711 | 99.9975233 |
| GOTERM_BP_FAT   | GO:0006793~phosphorus metabolic process              | 6 | 6.74157303 | 0.5008801  | GNAI2, PLK1, | 74 | 866  | 13588 | 1.27220523 | 1 | 0.99652711 | 99.9975233 |
| GOTERM_BP_FAT   | GO:0016310~phosphorylation                           | 5 | 5.61797753 | 0.54334297 | GNAI2, PLK1, | 74 | 718  | 13588 | 1.2787021  | 1 | 0.99807774 | 99.9993624 |
| SP_PIR_KEYWORDS | kinase   | 4 | 4.49438202 | 0.65177142 | PLK1, ADPGK  | 85 | 707  | 17854 | 1.18838506 | 1 | 0.99926389 | 99.9998404 |
| GOTERM_BP_FAT   | GO:0007166~cell surface receptor linked signal tra   | 5 | 5.61797753 | 0.99969088 | GNAI2, ITGB  | 74 | 2495 | 13588 | 0.3679792  | 1 | 1          | 100        |

#### Annotation Cluster 15 Enrichment Score: 0.7366280007934504

| Category      | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|---|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0032944~regulation of mononuclear cell prolifi   | 3     | 3.37078652 | 0.06880595 | LST1, BCL6, I | 74         | 80       | 13588     | 6.88581081   | 1          | 0.78990173 | 66.311801  |
| GOTERM_BP_FAT | GO:0050670~regulation of lymphocyte proliferation   | 3     | 3.37078652 | 0.06880595 | LST1, BCL6, I | 74         | 80       | 13588     | 6.88581081   | 1          | 0.78990173 | 66.311801  |
| GOTERM_BP_FAT | GO:0070663~regulation of leukocyte proliferation    | 3     | 3.37078652 | 0.07182426 | LST1, BCL6, I | 74         | 82       | 13588     | 6.71786421   | 1          | 0.78627372 | 67.9404007 |
| GOTERM_BP_FAT | GO:0051249~regulation of lymphocyte activation      | 3     | 3.37078652 | 0.18109359 | LST1, BCL6, I | 74         | 144      | 13588     | 3.82545045   | 1          | 0.90160077 | 95.260382  |
| GOTERM_BP_FAT | GO:0002694~regulation of leukocyte activation       | 3     | 3.37078652 | 0.20052711 | LST1, BCL6, I | 74         | 154      | 13588     | 3.57704458   | 1          | 0.9166356  | 96.7149049 |
| GOTERM_BP_FAT | GO:0050865~regulation of cell activation            | 3     | 3.37078652 | 0.20444502 | LST1, BCL6, I | 74         | 156      | 13588     | 3.53118503   | 1          | 0.91520751 | 96.9522106 |
| GOTERM_BP_FAT | GO:0007242~intracellular signaling cascade          | 7     | 7.86516854 | 0.36858604 | LST1, GNAI2,  | 74         | 915      | 13588     | 1.40475558   | 1          | 0.98254794 | 99.9104002 |
| GOTERM_BP_FAT | GO:0008284~positive regulation of cell proliferatio | 3     | 3.37078652 | 0.4530561  | GNAI2, BCL6   | 74         | 284      | 13588     | 1.93966502   | 1          | 0.9937754  | 99.9899915 |
| GOTERM_BP_FAT | GO:0042127~regulation of cell proliferation         | 4     | 4.49438202 | 0.55652061 | LST1, GNAI2,  | 74         | 538      | 13588     | 1.36521652   | 1          | 0.99837298 | 99.9995922 |

#### Annotation Cluster 16 Enrichment Score: 0.7119658528681817

| Category        | Term                           | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|--------------------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| SP_PIR_KEYWORDS | oxidoreductase                 | 7     | 7.86516854 | 0.05260419 | CYBA, CYP2C | 85         | 572      | 17854     | 2.57050596   | 0.99998942 | 0.55881654 | 49.5290913 |
| SP_PIR_KEYWORDS | nadp                           | 3     | 3.37078652 | 0.14405698 | CYBA, G6PD  | 85         | 142      | 17854     | 4.43761392   | 1          | 0.80772826 | 86.0301455 |
| GOTERM_BP_FAT   | GO:0051114~oxidation reduction | 7     | 7.86516854 | 0.15180843 | CYBA, CYP2C | 74         | 672      | 13588     | 1.91272523   | 1          | 0.87350552 | 91.8970485 |
| SP_PIR_KEYWORDS | iron                           | 3     | 3.37078652 | 0.44753334 | CYBA, CYP2C | 85         | 321      | 17854     | 1.96305662   | 1          | 0.99052399 | 99.9451378 |
| GOTERM_MF_FAT   | GO:0005506~iron ion binding    | 3     | 3.37078652 | 0.5351737  | CYBA, CYP2C | 70         | 343      | 13288     | 1.6603082    | 1          | 0.99801967 | 99.9929672 |

#### Annotation Cluster 17 Enrichment Score: 0.6979576725617672

| Category        | Term                                      | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|---|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT   | GO:0007155~cell adhesion                  | 7     | 7.86516854 | 0.08050274 | OLFM4, LGA    | 74         | 561      | 13588     | 2.29117888   | 1          | 0.79955698 | 72.2226507 |
| GOTERM_BP_FAT   | GO:0022610~biological adhesion            | 7     | 7.86516854 | 0.08103796 | OLFM4, LGA    | 74         | 562      | 13588     | 2.28710205   | 1          | 0.79379877 | 72.4684009 |
| SP_PIR_KEYWORDS | cell adhesion                             | 5     | 5.61797753 | 0.10420753 | OLFM4, PSTI   | 85         | 380      | 17854     | 2.76377709   | 1          | 0.74648814 | 75.1539637 |
| KEGG_PATHWAY    | mmu04810:Regulation of actin cytoskeleton | 4     | 4.49438202 | 0.16295743 | ITGB5, MYH9   | 38         | 217      | 5738      | 2.78341014   | 0.99997683 | 0.83115997 | 83.1809278 |
| GOTERM_MF_FAT   | GO:0003779~actin binding                  | 4     | 4.49438202 | 0.18826828 | YWHAQ, PST    | 70         | 288      | 13288     | 2.63650794   | 1          | 0.99970685 | 92.5990408 |
| GOTERM_CC_FAT   | GO:0015629~actin cytoskeleton             | 3     | 3.37078652 | 0.27643789 | PSTPIP1, MY   | 64         | 205      | 12504     | 2.85914634   | 1          | 0.93723211 | 97.9380856 |
| GOTERM_MF_FAT   | GO:0008092~cytoskeletal protein binding   | 4     | 4.49438202 | 0.36449225 | YWHAQ, PST    | 70         | 414      | 13288     | 1.83409248   | 1          | 0.999368   | 99.6512159 |
| KEGG_PATHWAY    | mmu04510:Focal adhesion                   | 3     | 3.37078652 | 0.36691794 | ITGB5, VCL, I | 38         | 198      | 5738      | 2.28787879   | 1          | 0.96756977 | 98.9760013 |
| GOTERM_CC_FAT   | GO:0005856~cytoskeleton                   | 6     | 6.74157303 | 0.67807318 | KRT8, VIM, P  | 64         | 1122     | 12504     | 1.0447861    | 1          | 0.99410574 | 99.9998755 |

#### Annotation Cluster 18 Enrichment Score: 0.6900004978158222

| Category      | Term   | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_CC_FAT | GO:0048770~pigment granule                   | 3     | 3.37078652 | 0.06833144 | HSP90AB1, C | 64         | 85       | 12504     | 6.89558824   | 0.99998154 | 0.66377796 | 57.2181111 |
| GOTERM_CC_FAT | GO:0042470~melanosome                        | 3     | 3.37078652 | 0.06833144 | HSP90AB1, C | 64         | 85       | 12504     | 6.89558824   | 0.99998154 | 0.66377796 | 57.2181111 |
| GOTERM_CC_FAT | GO:0031982~vesicle                           | 5     | 5.61797753 | 0.26517297 | ALDOA, HSP  | 64         | 519      | 12504     | 1.88222543   | 1          | 0.94847336 | 97.5182641 |
| GOTERM_CC_FAT | GO:0016023~cytoplasmic membrane-bounded vesi | 4     | 4.49438202 | 0.34696383 | ALDOA, HSP  | 64         | 414      | 12504     | 1.88768116   | 1          | 0.96241481 | 99.3974606 |
| GOTERM_CC_FAT | GO:0031988~membrane-bounded vesicle          | 4     | 4.49438202 | 0.35529203 | ALDOA, HSP  | 64         | 420      | 12504     | 1.86071429   | 1          | 0.95370424 | 99.4834442 |
| GOTERM_CC_FAT | GO:0031410~cytoplasmic vesicle               | 4     | 4.49438202 | 0.47463193 | ALDOA, HSP  | 64         | 508      | 12504     | 1.53838583   | 1          | 0.96722326 | 99.9556718 |

#### Annotation Cluster 19 Enrichment Score: 0.5350752225873454

| Category              | Term  | Count | %          | PValue            | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------------|---|-------|------------|-------------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_CC_FAT         | GO:0005624~membrane fraction                  | 5     | 5.61797753 | 0.25513574        | GNAI2, SQLE   | 64         | 510      | 12504     | 1.91544118   | 1          | 0.9513975  | 97.0796414 |
| GOTERM_CC_FAT         | GO:0005626~insoluble fraction                 | 5     | 5.61797753 | 0.2752884         | GNAI2, SQLE   | 64         | 528      | 12504     | 1.85014205   | 1          | 0.94589202 | 97.8984455 |
| GOTERM_CC_FAT         | GO:0000267~cell fraction                      | 5     | 5.61797753 | 0.35335816        | GNAI2, SQLE   | 64         | 596      | 12504     | 1.63905201   | 1          | 0.95911777 | 99.4645471 |
| Annotation Cluster 20 |   |       |            |                   |               |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue            | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0005783~endoplasmic reticulum              | 11    | 12.3595506 | <b>0.00866463</b> | SRI, GANAB,   | 64         | 838      | 12504     | 2.56458831   | 0.738198   | 0.48833409 | 9.91295802 |
| SP_PIR_KEYWORDS       | endoplasmic reticulum                         | 9     | 10.1123596 | <b>0.01435486</b> | GANAB, SQL    | 85         | 678      | 17854     | 2.78823529   | 0.95335941 | 0.31829653 | 16.7194647 |
| UP_SEQ_FEATURE        | topological domain:Luminal                    | 4     | 4.49438202 | 0.33468278        | LRMP, LMAN    | 80         | 414      | 16021     | 1.93490338   | 1          | 1          | 99.6031679 |
| SP_PIR_KEYWORDS       | membrane                                      | 25    | 28.0898876 | 0.71224056        | SRI, CPT2, LS | 85         | 5507     | 17854     | 0.95354575   | 1          | 0.99966529 | 99.9999857 |
| UP_SEQ_FEATURE        | transmembrane region                          | 19    | 21.3483146 | 0.76041002        | LST1, MCL1,   | 80         | 4113     | 16021     | 0.92511245   | 1          | 1          | 99.9999996 |
| SP_PIR_KEYWORDS       | transmembrane                                 | 20    | 22.4719101 | 0.93291989        | LST1, H2-Q5,  | 85         | 5237     | 17854     | 0.80216559   | 1          | 0.99999881 | 100        |
| UP_SEQ_FEATURE        | topological domain:Cytoplasmic                | 9     | 10.1123596 | 0.97454331        | H2-D1, LRMI   | 80         | 2780     | 16021     | 0.64833183   | 1          | 1          | 100        |
| GOTERM_CC_FAT         | GO:0016021~integral to membrane               | 20    | 22.4719101 | 0.99592855        | LST1, H2-Q5,  | 64         | 5709     | 12504     | 0.68444561   | 1          | 1          | 100        |
| GOTERM_CC_FAT         | GO:0031224~intrinsic to membrane              | 20    | 22.4719101 | 0.9981569         | LST1, H2-Q5,  | 64         | 5914     | 12504     | 0.66072032   | 1          | 1          | 100        |
| Annotation Cluster 21 |   |       |            |                   |               |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue            | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0006915~apoptosis                          | 5     | 5.61797753 | 0.23980865        | LST1, MCL1,   | 74         | 465      | 13588     | 1.97442604   | 1          | 0.93462449 | 98.4773736 |
| GOTERM_BP_FAT         | GO:0012501~programmed cell death              | 5     | 5.61797753 | 0.24916867        | LST1, MCL1,   | 74         | 473      | 13588     | 1.94103194   | 1          | 0.94005369 | 98.739702  |
| GOTERM_BP_FAT         | GO:0008219~cell death                         | 5     | 5.61797753 | 0.28977           | LST1, MCL1,   | 74         | 507      | 13588     | 1.81086412   | 1          | 0.95908813 | 99.4605062 |
| GOTERM_BP_FAT         | GO:0016265~death                              | 5     | 5.61797753 | 0.3043449         | LST1, MCL1,   | 74         | 519      | 13588     | 1.76899443   | 1          | 0.96345877 | 99.6068597 |
| SP_PIR_KEYWORDS       | Apoptosis                                     | 3     | 3.37078652 | 0.47263128        | MCL1, SERPI   | 85         | 337      | 17854     | 1.86985512   | 1          | 0.99212938 | 99.9695366 |
| Annotation Cluster 22 |   |       |            |                   |               |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue            | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS       | ATP   | 4     | 4.49438202 | <b>0.03436779</b> | PLK1, FES, TC | 85         | 151      | 17854     | 5.5641605    | 0.99939732 | 0.4903396  | 35.7585082 |
| GOTERM_BP_FAT         | GO:0051301~cell division                      | 5     | 5.61797753 | 0.06436944        | PLK1, PSTPIP  | 74         | 281      | 13588     | 3.26728864   | 1          | 0.77664325 | 63.7771499 |
| SP_PIR_KEYWORDS       | atp-binding                                   | 9     | 10.1123596 | 0.25823145        | HSP90AB1, F   | 85         | 1287     | 17854     | 1.46886055   | 1          | 0.95098503 | 97.7173299 |
| SP_PIR_KEYWORDS       | nucleotide-binding                            | 10    | 11.2359551 | 0.35951677        | HSP90AB1, C   | 85         | 1631     | 17854     | 1.28784218   | 1          | 0.97713423 | 99.6438371 |
| GOTERM_MF_FAT         | GO:0030554~adenyl nucleotide binding          | 10    | 11.2359551 | 0.40287549        | HSP90AB1, F   | 70         | 1535     | 13288     | 1.23666822   | 1          | 0.998773   | 99.8397329 |
| GOTERM_MF_FAT         | GO:0001883~purine nucleoside binding          | 10    | 11.2359551 | 0.41292163        | HSP90AB1, F   | 70         | 1548     | 13288     | 1.22628276   | 1          | 0.99848301 | 99.8703218 |
| GOTERM_MF_FAT         | GO:0001882~nucleoside binding                 | 10    | 11.2359551 | 0.42065488        | HSP90AB1, F   | 70         | 1558     | 13288     | 1.21841188   | 1          | 0.99729715 | 99.8901028 |
| GOTERM_MF_FAT         | GO:0005524~ATP binding                        | 9     | 10.1123596 | 0.47860901        | HSP90AB1, F   | 70         | 1443     | 13288     | 1.18396198   | 1          | 0.99874915 | 99.9705125 |
| GOTERM_MF_FAT         | GO:0032559~adenyl ribonucleotide binding      | 9     | 10.1123596 | 0.49233399        | HSP90AB1, F   | 70         | 1460     | 13288     | 1.17017613   | 1          | 0.99865294 | 99.9788637 |
| GOTERM_MF_FAT         | GO:0017076~purine nucleotide binding          | 11    | 12.3595506 | 0.51319638        | HSP90AB1, C   | 70         | 1871     | 13288     | 1.11604184   | 1          | 0.99830637 | 99.9874815 |
| GOTERM_MF_FAT         | GO:0032553~ribonucleotide binding             | 10    | 11.2359551 | 0.59920365        | HSP90AB1, C   | 70         | 1796     | 13288     | 1.05695196   | 1          | 0.99920052 | 99.9988941 |
| GOTERM_MF_FAT         | GO:0032555~purine ribonucleotide binding      | 10    | 11.2359551 | 0.59920365        | HSP90AB1, C   | 70         | 1796     | 13288     | 1.05695196   | 1          | 0.99920052 | 99.9988941 |
| UP_SEQ_FEATURE        | nucleotide phosphate-binding region:ATP       | 5     | 5.61797753 | 0.66095995        | PLK1, MYH9,   | 80         | 907      | 16021     | 1.10398291   | 1          | 1          | 99.9999578 |
| GOTERM_MF_FAT         | GO:0000166~nucleotide binding                 | 11    | 12.3595506 | 0.71689387        | HSP90AB1, C   | 70         | 2183     | 13288     | 0.95653426   | 1          | 0.99988988 | 99.9999856 |
| UP_SEQ_FEATURE        | binding site:ATP                              | 3     | 3.37078652 | 0.75512163        | PLK1, FES, TC | 80         | 545      | 16021     | 1.10236239   | 1          | 1          | 99.9999995 |
| Annotation Cluster 23 |   |       |            |                   |               |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue            | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0031252~cell leading edge                  | 3     | 3.37078652 | 0.10929539        | VIM, PSTPIP   | 64         | 112      | 12504     | 5.23325893   | 0.99999998 | 0.77357946 | 75.0537652 |
| GOTERM_CC_FAT         | GO:0043228~non-membrane-bounded organelle     | 12    | 13.4831461 | 0.37153923        | HMG2, RPI     | 64         | 1919     | 12504     | 1.22173007   | 1          | 0.95539939 | 99.6196853 |
| GOTERM_CC_FAT         | GO:0043232~intracellular non-membrane-bounded | 12    | 13.4831461 | 0.37153923        | HMG2, RPI     | 64         | 1919     | 12504     | 1.22173007   | 1          | 0.95539939 | 99.6196853 |
| GOTERM_CC_FAT         | GO:0044430~cytoskeletal part                  | 5     | 5.61797753 | 0.55290018        | KRT8, VIM, P  | 64         | 774      | 12504     | 1.2621124    | 1          | 0.98166421 | 99.993599  |
| GOTERM_CC_FAT         | GO:0042995~cell projection                    | 4     | 4.49438202 | 0.55876562        | ALDOA, PSTI   | 64         | 575      | 12504     | 1.35913043   | 1          | 0.98050285 | 99.9945368 |
| GOTERM_CC_FAT         | GO:0005856~cytoskeleton                       | 6     | 6.74157303 | 0.67807318        | KRT8, VIM, P  | 64         | 1122     | 12504     | 1.0447861    | 1          | 0.99410574 | 99.9998755 |
| SP_PIR_KEYWORDS       | coiled coil                                   | 7     | 7.86516854 | 0.83636974        | OLFM4, CCD    | 85         | 1732     | 17854     | 0.84891998   | 1          | 0.99995887 | 100        |
| Annotation Cluster 24 |   |       |            |                   |               |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue            | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0030054~cell junction                      | 4     | 4.49438202 | 0.42398395        | MYH9, CAMI    | 64         | 470      | 12504     | 1.66276596   | 1          | 0.96655917 | 99.8662878 |
| GOTERM_CC_FAT         | GO:0044459~plasma membrane part               | 10    | 11.2359551 | 0.44131194        | H2-Q5, H2-C   | 64         | 1633     | 12504     | 1.19641764   | 1          | 0.96819724 | 99.9073081 |



|                 |                            |    |            |            |               |    |      |       |            |   |            |            |
|-----------------|----------------------------|----|------------|------------|---------------|----|------|-------|------------|---|------------|------------|
| GOTERM_CC_FAT   | GO:0005886~plasma membrane | 16 | 17.9775281 | 0.50623047 | SRI, H2-Q5, ( | 64 | 2906 | 12504 | 1.07570544 | 1 | 0.97328483 | 99.9789373 |
| SP_PIR_KEYWORDS | cell junction              | 3  | 3.37078652 | 0.55351781 | CAMK2N1, v    | 85 | 392  | 17854 | 1.607503   | 1 | 0.9972461  | 99.9962949 |
| SP_PIR_KEYWORDS | cell membrane              | 7  | 7.86516854 | 0.82843845 | ATF4, H2-D1   | 85 | 1713 | 17854 | 0.85833591 | 1 | 0.99995894 | 100        |

|                       |  |       |            |            |            |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 25 | Enrichment Score: 0.23671676062303326            |       |            |            |            |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0046907~intracellular transport               | 4     | 4.49438202 | 0.40960844 | YWHAG, IGH | 74         | 431      | 13588     | 1.70414498   | 1          | 0.98981692 | 99.9678604 |
| GOTERM_BP_FAT         | GO:0008104~protein localization                  | 5     | 5.61797753 | 0.58164954 | YWHAG, BCL | 74         | 753      | 13588     | 1.21926708   | 1          | 0.99889888 | 99.9998326 |
| GOTERM_BP_FAT         | GO:0015031~protein transport                     | 4     | 4.49438202 | 0.68621577 | YWHAG, MY  | 74         | 651      | 13588     | 1.12824345   | 1          | 0.99984782 | 99.9999979 |
| GOTERM_BP_FAT         | GO:0045184~establishment of protein localization | 4     | 4.49438202 | 0.69126087 | YWHAG, MY  | 74         | 656      | 13588     | 1.11964403   | 1          | 0.99985313 | 99.9999984 |

|                       |                                      |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|--------------------------------------|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 26 | Enrichment Score: 0.1673663251140142 |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term                                 | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0019866~organelle inner membrane  | 3     | 3.37078652 | 0.46878463 | CPT2, SLC25, | 64         | 312      | 12504     | 1.87860577   | 1          | 0.96916894 | 99.9493774 |
| GOTERM_CC_FAT         | GO:0031967~organelle envelope        | 3     | 3.37078652 | 0.76261274 | CPT2, SLC25, | 64         | 540      | 12504     | 1.08541667   | 1          | 0.99821346 | 99.9999968 |
| GOTERM_CC_FAT         | GO:0031975~envelope                  | 3     | 3.37078652 | 0.76443248 | CPT2, SLC25, | 64         | 542      | 12504     | 1.08141144   | 1          | 0.99793914 | 99.9999971 |
| GOTERM_CC_FAT         | GO:0031090~organelle membrane        | 4     | 4.49438202 | 0.78328201 | CPT2, SLC25, | 64         | 809      | 12504     | 0.96600742   | 1          | 0.99827858 | 99.9999989 |

|                       |  |       |            |            |             |            |          |           |              |            |            |     |
|-----------------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|-----|
| Annotation Cluster 27 | Enrichment Score: 0.09886753683186479              |       |            |            |             |            |          |           |              |            |            |     |
| Category              | Term   | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR |
| GOTERM_BP_FAT         | GO:0051173~positive regulation of nitrogen comp    | 3     | 3.37078652 | 0.78010766 | HSP90AB1, A | 74         | 526      | 13588     | 1.04727161   | 1          | 0.9999841  | 100 |
| GOTERM_BP_FAT         | GO:0031328~positive regulation of cellular biosynt | 3     | 3.37078652 | 0.80263241 | HSP90AB1, A | 74         | 552      | 13588     | 0.9979436    | 1          | 0.99999192 | 100 |
| GOTERM_BP_FAT         | GO:0009891~positive regulation of biosynthetic pr  | 3     | 3.37078652 | 0.8067262  | HSP90AB1, A | 74         | 557      | 13588     | 0.98898539   | 1          | 0.99999135 | 100 |

|                       |  |       |            |            |             |            |          |           |              |            |            |     |
|-----------------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|-----|
| Annotation Cluster 28 | Enrichment Score: 0.0925665711147286           |       |            |            |             |            |          |           |              |            |            |     |
| Category              | Term   | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR |
| GOTERM_BP_FAT         | GO:0042981~regulation of apoptosis             | 3     | 3.37078652 | 0.80345716 | LST1, MCL1, | 74         | 553      | 13588     | 0.996139     | 1          | 0.99999125 | 100 |
| GOTERM_BP_FAT         | GO:0043067~regulation of programmed cell death | 3     | 3.37078652 | 0.80914671 | LST1, MCL1, | 74         | 560      | 13588     | 0.98368726   | 1          | 0.99999119 | 100 |
| GOTERM_BP_FAT         | GO:0010941~regulation of cell death            | 3     | 3.37078652 | 0.81154067 | LST1, MCL1, | 74         | 563      | 13588     | 0.97844559   | 1          | 0.99999103 | 100 |

|                       |  |       |            |            |               |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 29 | Enrichment Score: 0.03750725724640617            |       |            |            |               |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS       | dna-binding                                      | 7     | 7.86516854 | 0.65600963 | ATF4, HMGN    | 85         | 1404     | 17854     | 1.04724317   | 1          | 0.99914961 | 99.9998633 |
| GOTERM_CC_FAT         | GO:0031981~nuclear lumen                         | 4     | 4.49438202 | 0.83153905 | ATF4, MCL1,   | 64         | 883      | 12504     | 0.88505096   | 1          | 0.99926669 | 99.9999999 |
| GOTERM_CC_FAT         | GO:0043233~organelle lumen                       | 5     | 5.61797753 | 0.8361155  | ALDOA, ATF4,  | 64         | 1136     | 12504     | 0.85992518   | 1          | 0.99920854 | 100        |
| GOTERM_BP_FAT         | GO:0006357~regulation of transcription from RNA  | 3     | 3.37078652 | 0.84968655 | ATF4, BCL6, ' | 74         | 616      | 13588     | 0.89426114   | 1          | 0.99999765 | 100        |
| GOTERM_CC_FAT         | GO:0031974~membrane-enclosed lumen               | 5     | 5.61797753 | 0.85485011 | ALDOA, ATF4,  | 64         | 1174     | 12504     | 0.83209114   | 1          | 0.99940708 | 100        |
| GOTERM_MF_FAT         | GO:0003677~DNA binding                           | 7     | 7.86516854 | 0.91498977 | ATF4, HMGN    | 70         | 1781     | 13288     | 0.7460977    | 1          | 0.99999996 | 100        |
| GOTERM_CC_FAT         | GO:0070013~intracellular organelle lumen         | 4     | 4.49438202 | 0.93330027 | ATF4, MCL1,   | 64         | 1133     | 12504     | 0.68976169   | 1          | 0.9999512  | 100        |
| GOTERM_MF_FAT         | GO:0030528~transcription regulator activity      | 3     | 3.37078652 | 0.98902862 | ATF4, PPP1R   | 70         | 1206     | 13288     | 0.47221038   | 1          | 1          | 100        |
| SP_PIR_KEYWORDS       | nucleus  | 11    | 12.3595506 | 0.99144768 | ATF4, HMGN    | 85         | 3808     | 17854     | 0.60675358   | 1          | 1          | 100        |
| SP_PIR_KEYWORDS       | transcription regulation                         | 3     | 3.37078652 | 0.99561225 | ATF4, BCL6,   | 85         | 1546     | 17854     | 0.40759455   | 1          | 1          | 100        |
| GOTERM_BP_FAT         | GO:0006350~transcription                         | 4     | 4.49438202 | 0.99740876 | ATF4, PPP1R   | 74         | 1772     | 13588     | 0.41449576   | 1          | 1          | 100        |
| GOTERM_BP_FAT         | GO:0006355~regulation of transcription, DNA-depi | 3     | 3.37078652 | 0.99766921 | ATF4, BCL6, ' | 74         | 1465     | 13588     | 0.37601697   | 1          | 1          | 100        |
| GOTERM_BP_FAT         | GO:0051252~regulation of RNA metabolic process   | 3     | 3.37078652 | 0.99793961 | ATF4, BCL6, ' | 74         | 1488     | 13588     | 0.37020488   | 1          | 1          | 100        |
| SP_PIR_KEYWORDS       | Transcription                                    | 3     | 3.37078652 | 0.99842791 | ATF4, BCL6,   | 85         | 1769     | 17854     | 0.35621321   | 1          | 1          | 100        |
| GOTERM_BP_FAT         | GO:0045449~regulation of transcription           | 4     | 4.49438202 | 0.99976067 | ATF4, BCL6, ' | 74         | 2227     | 13588     | 0.32980983   | 1          | 1          | 100        |

|                       |   |       |            |            |              |            |          |           |              |            |            |     |
|-----------------------|---|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|-----|
| Annotation Cluster 30 | Enrichment Score: 0.007014895955419285  |       |            |            |              |            |          |           |              |            |            |     |
| Category              | Term                                    | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR |
| SP_PIR_KEYWORDS       | metal-binding                           | 9     | 10.1123596 | 0.94885486 | CYBA, CYP2C  | 85         | 2682     | 17854     | 0.7048559    | 1          | 0.99999957 | 100 |
| GOTERM_MF_FAT         | GO:0043169~cation binding               | 14    | 15.7303371 | 0.98261132 | SRI, CYP2C4, | 70         | 3885     | 13288     | 0.68406692   | 1          | 1          | 100 |
| GOTERM_MF_FAT         | GO:0043167~ion binding                  | 14    | 15.7303371 | 0.98520466 | SRI, CYP2C4, | 70         | 3934     | 13288     | 0.67554652   | 1          | 1          | 100 |
| GOTERM_MF_FAT         | GO:0046914~transition metal ion binding | 8     | 8.98876404 | 0.9890466  | CYBA, CYP2C  | 70         | 2608     | 13288     | 0.58229623   | 1          | 1          | 100 |
| GOTERM_MF_FAT         | GO:0046872~metal ion binding            | 13    | 14.6067416 | 0.99089558 | SRI, CYP2C4, | 70         | 3850     | 13288     | 0.64097959   | 1          | 1          | 100 |
| SP_PIR_KEYWORDS       | zinc                                    | 4     | 4.49438202 | 0.99503441 | PRICKLE3, PF | 85         | 1886     | 17854     | 0.44548687   | 1          | 1          | 100 |
| GOTERM_MF_FAT         | GO:0008270~zinc ion binding             | 5     | 5.61797753 | 0.99702253 | PRICKLE3, PF | 70         | 2105     | 13288     | 0.45089922   | 1          | 1          | 100 |

| Category        | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|---|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT   | GO:0002526~acute inflammatory response            | 7     | 7.86516854 | 4.61E-06   | ORM1, C4BP    | 74         | 81       | 13588     | 15.8685352   | 0.00352182 | 0.00352182 | 0.00702932 |
| GOTERM_BP_FAT   | GO:0006955~immune response                        | 12    | 13.4831461 | 3.94E-05   | APOA4, C4BP   | 74         | 471      | 13588     | 4.67825788   | 0.0297383  | 0.01498137 | 0.06013396 |
| GOTERM_BP_FAT   | GO:0002460~adaptive immune response based on      | 6     | 6.74157303 | 8.65E-05   | C4BP, CFB, G  | 74         | 84       | 13588     | 13.1158301   | 0.06409353 | 0.02183794 | 0.13189466 |
| GOTERM_BP_FAT   | GO:0002250~adaptive immune response               | 6     | 6.74157303 | 8.65E-05   | C4BP, CFB, G  | 74         | 84       | 13588     | 13.1158301   | 0.06409353 | 0.02183794 | 0.13189466 |
| INTERPRO        | IPR016060:Complement control module               | 5     | 5.61797753 | 1.12E-04   | C4BP, CFB, H  | 83         | 54       | 17763     | 19.8159304   | 0.02552242 | 0.02552242 | 0.14348385 |
| SP_PIR_KEYWORDS | acetylation                                       | 25    | 28.0898876 | 1.24E-04   | HSP90A1, A    | 85         | 2325     | 17854     | 2.25857052   | 0.02594436 | 0.02594436 | 0.15677333 |
| GOTERM_BP_FAT   | GO:0006953~acute-phase response                   | 4     | 4.49438202 | 5.44E-04   | ORM1, SERP    | 74         | 30       | 13588     | 24.4828829   | 0.34097665 | 0.09899915 | 0.82741704 |
| GOTERM_BP_FAT   | GO:0006952~defense response                       | 10    | 11.2359551 | 6.35E-04   | APOA4, ORN    | 74         | 448      | 13588     | 4.09869691   | 0.38513411 | 0.0926892  | 0.96436741 |
| GOTERM_BP_FAT   | GO:0034097~response to cytokine stimulus          | 4     | 4.49438202 | 6.60E-04   | MCL1, SERP    | 74         | 32       | 13588     | 22.9527027   | 0.39682943 | 0.08080704 | 1.00225514 |
| GOTERM_BP_FAT   | GO:0002455~humoral immune response mediated       | 4     | 4.49438202 | 8.61E-04   | C4BP, CFB, IC | 74         | 35       | 13588     | 20.9853282   | 0.48289925 | 0.08991456 | 1.30548288 |
| GOTERM_BP_FAT   | GO:0006954~inflammatory response                  | 7     | 7.86516854 | 0.00130272 | ORM1, C4BP    | 74         | 225      | 13588     | 5.71267267   | 0.63158001 | 0.11734111 | 1.9698989  |
| SP_PIR_KEYWORDS | sushi   | 4     | 4.49438202 | 0.00131794 | C4BP, CFB, H  | 85         | 46       | 17854     | 18.2649616   | 0.24390508 | 0.13046281 | 1.6549116  |
| SMART           | SM00032:CCP                                       | 4     | 4.49438202 | 0.0016846  | C4BP, CFB, H  | 42         | 53       | 9131      | 16.4079066   | 0.08239394 | 0.08239394 | 1.61782205 |
| SP_PIR_KEYWORDS | immune response                                   | 6     | 6.74157303 | 0.00176117 | C4BP, LST1, I | 85         | 184      | 17854     | 6.84936061   | 0.31181512 | 0.11711994 | 2.20577109 |
| INTERPRO        | IPR00436:Sushi/SCR/CCP                            | 4     | 4.49438202 | 0.00188092 | C4BP, CFB, H  | 83         | 53       | 17763     | 16.1518527   | 0.35267151 | 0.19543273 | 2.38642266 |
| GOTERM_BP_FAT   | GO:0045087~innate immune response                 | 5     | 5.61797753 | 0.00260743 | APOA4, C4BP   | 74         | 107      | 13588     | 8.58044961   | 0.86465066 | 0.19925335 | 3.90641652 |
| GOTERM_BP_FAT   | GO:0006959~humoral immune response                | 4     | 4.49438202 | 0.00303209 | C4BP, CFB, IC | 74         | 54       | 13588     | 13.6016016   | 0.90232506 | 0.20753824 | 4.52897727 |
| GOTERM_BP_FAT   | GO:0002252~immune effector process                | 5     | 5.61797753 | 0.00468554 | C4BP, CFB, IC | 74         | 126      | 13588     | 7.28657229   | 0.97260944 | 0.27895276 | 6.91720338 |
| GOTERM_BP_FAT   | GO:0016064~immunoglobulin mediated immune r       | 4     | 4.49438202 | 0.00468997 | C4BP, CFB, IC | 74         | 63       | 13588     | 11.6585157   | 0.97270274 | 0.2592416  | 6.92353145 |
| GOTERM_BP_FAT   | GO:0002684~positive regulation of immune system   | 6     | 6.74157303 | 0.00497496 | C4BP, CFB, B  | 74         | 206      | 13588     | 5.34820257   | 0.97807946 | 0.25462783 | 7.32945866 |
| GOTERM_BP_FAT   | GO:0019724~B cell mediated immunity               | 4     | 4.49438202 | 0.00511943 | C4BP, CFB, IC | 74         | 65       | 13588     | 11.2997921   | 0.98038681 | 0.24483969 | 7.53459639 |
| SP_PIR_KEYWORDS | acute phase                                       | 3     | 3.37078652 | 0.00564447 | ORM1, SERP    | 85         | 24       | 17854     | 26.2558824   | 0.69881093 | 0.25918494 | 6.9119648  |
| SMART           | SM00407:IGc1                                      | 4     | 4.49438202 | 0.00602032 | IGK-C, H2-Q   | 42         | 83       | 9131      | 10.4773379   | 0.26505854 | 0.14271273 | 5.67429226 |
| SP_PIR_KEYWORDS | cell shape  | 3     | 3.37078652 | 0.00611665 | LST1, MYH9,   | 85         | 25       | 17854     | 25.2056471   | 0.72766191 | 0.22905805 | 7.46975027 |
| GOTERM_BP_FAT   | GO:0050778~positive regulation of immune respor   | 5     | 5.61797753 | 0.00613154 | C4BP, CFB, IC | 74         | 136      | 13588     | 6.75079491   | 0.99100616 | 0.26954015 | 8.95991521 |
| SP_PIR_KEYWORDS | Secreted  | 15    | 16.8539326 | 0.00621329 | HAMP2, OLF    | 85         | 1420     | 17854     | 2.21880696   | 0.73321912 | 0.19765876 | 7.58354133 |
| SP_PIR_KEYWORDS | complement pathway                                | 3     | 3.37078652 | 0.00660624 | C4BP, CFB, C  | 85         | 26       | 17854     | 24.2361991   | 0.75467433 | 0.18187356 | 8.04485269 |
| INTERPRO        | IPR003597:Immunoglobulin C1-set                   | 4     | 4.49438202 | 0.00668158 | IGK-C, H2-Q   | 83         | 83       | 17763     | 10.3138336   | 0.78746002 | 0.40322098 | 8.24128112 |
| GOTERM_CC_FAT   | GO:0005576~extracellular region                   | 17    | 19.1011236 | 0.00778839 | ALDOA, HAN    | 64         | 1680     | 12504     | 1.97700893   | 0.7000405  | 0.7000405  | 8.95309559 |
| GOTERM_BP_FAT   | GO:0006487~protein amino acid N-linked glycosyl   | 3     | 3.37078652 | 0.00788468 | GANAB, SER    | 74         | 25       | 13588     | 22.0345946   | 0.99767398 | 0.31543721 | 11.3803283 |
| GOTERM_BP_FAT   | GO:0002449~lymphocyte mediated immunity           | 4     | 4.49438202 | 0.00790054 | C4BP, CFB, IC | 74         | 76       | 13588     | 9.66429587   | 0.99770229 | 0.30050914 | 11.401947  |
| GOTERM_CC_FAT   | GO:0005783~endoplasmic reticulum                  | 11    | 12.3595506 | 0.00866463 | SRI, GANAB,   | 64         | 838      | 12504     | 2.56458831   | 0.738198   | 0.48833409 | 9.91295802 |
| GOTERM_CC_FAT   | GO:0044449~contractile fiber part                 | 4     | 4.49438202 | 0.00926951 | SRI, KRT8, LM | 64         | 86       | 12504     | 9.0872093    | 0.76168483 | 0.38001113 | 10.5701492 |
| INTERPRO        | IPR003006:Immunoglobulin/major histocompatibilit  | 4     | 4.49438202 | 0.01052828 | IGK-C, H2-Q   | 83         | 98       | 17763     | 8.73518564   | 0.91326749 | 0.45731792 | 12.6971023 |
| GOTERM_BP_FAT   | GO:0009611~response to wounding                   | 7     | 7.86516854 | 0.01076381 | ORM1, C4BP    | 74         | 347      | 13588     | 3.70418257   | 0.99974893 | 0.36905899 | 15.2252559 |
| GOTERM_CC_FAT   | GO:0030016~myofibril                              | 4     | 4.49438202 | 0.01081007 | SRI, KRT8, LM | 64         | 91       | 12504     | 8.58791209   | 0.81246955 | 0.34193628 | 12.2241422 |
| GOTERM_BP_FAT   | GO:0002253~activation of immune response          | 4     | 4.49438202 | 0.01107149 | C4BP, CFB, IC | 74         | 86       | 13588     | 8.54054054   | 0.99980216 | 0.36163517 | 15.6268015 |
| GOTERM_BP_FAT   | GO:0006958~complement activation, classical path  | 3     | 3.37078652 | 0.01123691 | C4BP, CFB, C  | 74         | 30       | 13588     | 18.3621622   | 0.99982595 | 0.35131613 | 15.8419368 |
| UP_SEQ_FEATURE  | domain:Sushi 1                                    | 3     | 3.37078652 | 0.01148217 | C4BP, CFB, C  | 80         | 33       | 16021     | 18.2056818   | 0.97837996 | 0.97837996 | 14.5045922 |
| UP_SEQ_FEATURE  | domain:Sushi 2                                    | 3     | 3.37078652 | 0.01148217 | C4BP, CFB, C  | 80         | 33       | 16021     | 18.2056818   | 0.97837996 | 0.97837996 | 14.5045922 |
| KEGG_PATHWAY    | mmu04610:Complement and coagulation cascades      | 4     | 4.49438202 | 0.01211193 | C4BP, SERP    | 38         | 75       | 5738      | 8.05333333   | 0.51886147 | 0.51886147 | 11.5026402 |
| GOTERM_CC_FAT   | GO:0043292~contractile fiber                      | 4     | 4.49438202 | 0.01214312 | SRI, KRT8, LM | 64         | 95       | 12504     | 8.22631579   | 0.84763669 | 0.31360189 | 13.6326651 |
| GOTERM_BP_FAT   | GO:0002443~leukocyte mediated immunity            | 4     | 4.49438202 | 0.01214638 | C4BP, CFB, IC | 74         | 89       | 13588     | 8.25265715   | 0.99991399 | 0.35966657 | 17.0156703 |
| GOTERM_CC_FAT   | GO:0005615~extracellular space                    | 8     | 8.98876404 | 0.01399331 | APOA4, ORN    | 64         | 511      | 12504     | 3.05870841   | 0.88584399 | 0.30350746 | 15.5532824 |
| SP_PIR_KEYWORDS | endoplasmic reticulum                             | 9     | 10.1123596 | 0.01435486 | GANAB, SQL    | 85         | 678      | 17854     | 2.78823529   | 0.95335941 | 0.31829653 | 16.7194647 |
| GOTERM_BP_FAT   | GO:0006956~complement activation                  | 3     | 3.37078652 | 0.01594085 | C4BP, CFB, C  | 74         | 36       | 13588     | 15.3018018   | 0.99999549 | 0.42850693 | 21.7496065 |
| GOTERM_BP_FAT   | GO:0002541~activation of plasma proteins involve  | 3     | 3.37078652 | 0.01594085 | C4BP, CFB, C  | 74         | 36       | 13588     | 15.3018018   | 0.99999549 | 0.42850693 | 21.7496065 |
| GOTERM_BP_FAT   | GO:0048584~positive regulation of response to sti | 5     | 5.61797753 | 0.0177829  | C4BP, CFB, IC | 74         | 186      | 13588     | 4.9360651    | 0.99999893 | 0.44985695 | 23.9555835 |
| SP_PIR_KEYWORDS | pentose phosphate pathway                         | 2     | 2.24719101 | 0.01868847 | ALDOA, G6P    | 85         | 4        | 17854     | 105.023529   | 0.98167421 | 0.35878014 | 21.2358275 |
| SP_PIR_KEYWORDS | duplication                                       | 4     | 4.49438202 | 0.01901972 | APOA4, CFB,   | 85         | 120      | 17854     | 7.00156863   | 0.98294002 | 0.33442368 | 21.5715876 |
| KEGG_PATHWAY    | mmu03010:Ribosome                                 | 4     | 4.49438202 | 0.01916619 | RPL18A, LOC   | 38         | 89       | 5738      | 6.78651685   | 0.68686921 | 0.44041909 | 17.6293979 |
| GOTERM_BP_FAT   | GO:0001816~cytokine production                    | 3     | 3.37078652 | 0.02230498 | GADD45G, G    | 74         | 43       | 13588     | 12.8108108   | 0.99999997 | 0.51322834 | 29.1271279 |
| GOTERM_CC_FAT   | GO:0005826~contractile ring                       | 2     | 2.24719101 | 0.02494331 | PSTPIP1, MY   | 64         | 5        | 12504     | 78.15        | 0.97955442 | 0.42633672 | 26.1412123 |
| GOTERM_BP_FAT   | GO:0008360~regulation of cell shape               | 3     | 3.37078652 | 0.02633769 | LST1, MYH9,   | 74         | 47       | 13588     | 11.720529    | 1          | 0.55860022 | 33.4599266 |
| GOTERM_BP_FAT   | GO:0045860~positive regulation of protein kinase  | 4     | 4.49438202 | 0.02905303 | GNAI2, GAD    | 74         | 124      | 13588     | 5.92327812   | 1          | 0.58047281 | 36.2364792 |

|                 |  |    |            |            |               |    |      |       |            |            |            |            |
|-----------------|--|----|------------|------------|---------------|----|------|-------|------------|------------|------------|------------|
| GOTERM_MF_FAT   | GO:0005198~structural molecule activity            | 7  | 7.86516854 | 0.02907212 | RPL18A, LOC   | 70 | 450  | 13288 | 2.95288889 | 0.99682708 | 0.99682708 | 30.8060824 |
| GOTERM_BP_FAT   | GO:0032147~activation of protein kinase activity   | 3  | 3.37078652 | 0.03064149 | GNAI2, GAD    | 74 | 51   | 13588 | 10.8012719 | 1          | 0.58642121 | 37.8101623 |
| SP_PIR_KEYWORDS | signal   | 22 | 24.7191011 | 0.03233689 | HAMP2, OLF    | 85 | 2970 | 17854 | 1.55590414 | 0.99905914 | 0.46927919 | 34.0277687 |
| GOTERM_BP_FAT   | GO:0033674~positive regulation of kinase activity  | 4  | 4.49438202 | 0.03276652 | GNAI2, GAD    | 74 | 130  | 13588 | 5.64989605 | 1          | 0.59804418 | 39.8587173 |
| SP_PIR_KEYWORDS | ATP  | 4  | 4.49438202 | 0.03436779 | PLK1, FES, TC | 85 | 151  | 17854 | 5.5641605  | 0.99939732 | 0.46089402 | 35.7585082 |
| GOTERM_CC_FAT   | GO:0032155~cell division site part                 | 2  | 2.24719101 | 0.03474829 | PSTPIP1, MY   | 64 | 7    | 12504 | 55.8214286 | 0.99568829 | 0.49378947 | 34.5743167 |
| GOTERM_CC_FAT   | GO:0032153~cell division site                      | 2  | 2.24719101 | 0.03474829 | PSTPIP1, MY   | 64 | 7    | 12504 | 55.8214286 | 0.99568829 | 0.49378947 | 34.5743167 |
| GOTERM_BP_FAT   | GO:0051347~positive regulation of transferase acti | 4  | 4.49438202 | 0.03604186 | GNAI2, GAD    | 74 | 135  | 13588 | 5.44064064 | 1          | 0.62075843 | 42.8930634 |
| GOTERM_MF_FAT   | GO:0004857~enzyme inhibitor activity               | 5  | 5.61797753 | 0.03743758 | SERPINA3G,    | 70 | 243  | 13288 | 3.90593768 | 0.999413   | 0.97577199 | 37.8902582 |
| GOTERM_BP_FAT   | GO:0006006~glucose metabolic process               | 4  | 4.49438202 | 0.03948014 | ALDOA, ATF4   | 74 | 140  | 13588 | 5.24633205 | 1          | 0.64245662 | 45.9240462 |
| GOTERM_CC_FAT   | GO:0044421~extracellular region part               | 9  | 10.1123596 | 0.03959809 | APOA4, ORN    | 64 | 774  | 12504 | 2.27180233 | 0.99801498 | 0.49909938 | 38.4105682 |
| GOTERM_BP_FAT   | GO:0001775~cell activation                         | 5  | 5.61797753 | 0.04324923 | LST1, GADD4   | 74 | 246  | 13588 | 3.73214678 | 1          | 0.66461395 | 49.0735827 |
| GOTERM_MF_FAT   | GO:0003735~structural constituent of ribosome      | 4  | 4.49438202 | 0.04374202 | RPL18A, LOC   | 70 | 151  | 13288 | 5.02857143 | 0.99983702 | 0.94537647 | 42.7812623 |
| GOTERM_BP_FAT   | GO:0051605~protein maturation by peptide bond      | 3  | 3.37078652 | 0.0476548  | C4BP, CFB, C  | 74 | 65   | 13588 | 8.47484407 | 1          | 0.68926453 | 52.5374862 |
| UP_SEQ_FEATURE  | signal peptide                                     | 22 | 24.7191011 | 0.04808989 | HAMP2, OLF    | 80 | 2963 | 16021 | 1.48693048 | 0.99999992 | 0.99972015 | 48.7658197 |
| KEGG_PATHWAY    | mmu04110:Cell cycle                                | 4  | 4.49438202 | 0.04858564 | YWHAG, PLK    | 38 | 128  | 5738  | 4.71875    | 0.9496288  | 0.63068743 | 39.2944358 |
| SP_PIR_KEYWORDS | innate immunity                                    | 3  | 3.37078652 | 0.04865931 | C4BP, CFB, C  | 85 | 75   | 17854 | 8.40188235 | 0.99997446 | 0.55668614 | 46.8043932 |
| SP_PIR_KEYWORDS | immunoglobulin c region                            | 2  | 2.24719101 | 0.05056652 | IGK-C, IGH-6  | 85 | 11   | 17854 | 38.1903743 | 0.99998331 | 0.54422677 | 48.13816   |
| SP_PIR_KEYWORDS | ribosomal protein                                  | 4  | 4.49438202 | 0.05095305 | RPL18A, LOC   | 85 | 177  | 17854 | 4.74682619 | 0.99998469 | 0.5224713  | 48.4046924 |
| SP_PIR_KEYWORDS | oxidoreductase                                     | 7  | 7.86516854 | 0.05260419 | CYBA, CYP2C   | 85 | 572  | 17854 | 2.57050596 | 0.99998942 | 0.51130059 | 49.5290913 |
| SP_PIR_KEYWORDS | Serine protease inhibitor                          | 3  | 3.37078652 | 0.05702943 | SERPINA3G,    | 85 | 82   | 17854 | 7.68464849 | 0.99999608 | 0.51918636 | 52.4322576 |
| GOTERM_CC_FAT   | GO:0005829~cytosol                                 | 7  | 7.86516854 | 0.05746577 | GNAI2, CFB,   | 64 | 549  | 12504 | 2.49112022 | 0.99988991 | 0.59804647 | 50.8336269 |
| GOTERM_CC_FAT   | GO:0030017~sarcomere                               | 3  | 3.37078652 | 0.06144815 | SRI, KRT8, LM | 64 | 80   | 12504 | 7.3265625  | 0.99994264 | 0.58845645 | 53.2685585 |
| UP_SEQ_FEATURE  | region of interest:RCL                             | 2  | 2.24719101 | 0.0622633  | SERPINA3G,    | 80 | 13   | 16021 | 30.8096154 | 1          | 0.99918663 | 58.2020679 |
| GOTERM_BP_FAT   | GO:0019318~hexose metabolic process                | 4  | 4.49438202 | 0.0625377  | ALDOA, ATF4   | 74 | 169  | 13588 | 4.34607388 | 1          | 0.77664872 | 62.6795624 |
| GOTERM_BP_FAT   | GO:0051301~cell division                           | 5  | 5.61797753 | 0.06436944 | PLK1, PSTPIP  | 74 | 281  | 13588 | 3.26728864 | 1          | 0.77664325 | 63.7771499 |
| GOTERM_CC_FAT   | GO:0048770~pigment granule                         | 3  | 3.37078652 | 0.06833144 | HSP90A1, C    | 64 | 85   | 12504 | 6.89558824 | 0.99998154 | 0.5967988  | 57.2181111 |
| GOTERM_CC_FAT   | GO:0042470~melanosome                              | 3  | 3.37078652 | 0.06833144 | HSP90A1, C    | 64 | 85   | 12504 | 6.89558824 | 0.99998154 | 0.5967988  | 57.2181111 |
| GOTERM_BP_FAT   | GO:0050670~regulation of lymphocyte proliferatio   | 3  | 3.37078652 | 0.06880595 | LST1, BCL6, I | 74 | 80   | 13588 | 6.88581081 | 1          | 0.78990173 | 66.311801  |
| GOTERM_BP_FAT   | GO:0032944~regulation of mononuclear cell prolifi  | 3  | 3.37078652 | 0.06880595 | LST1, BCL6, I | 74 | 80   | 13588 | 6.88581081 | 1          | 0.78990173 | 66.311801  |
| GOTERM_BP_FAT   | GO:0016052~carbohydrate catabolic process          | 3  | 3.37078652 | 0.07030971 | ALDOA, ADP    | 74 | 81   | 13588 | 6.8008008  | 1          | 0.78801297 | 67.132615  |
| GOTERM_BP_FAT   | GO:0070663~regulation of leukocyte proliferation   | 3  | 3.37078652 | 0.07182426 | LST1, BCL6, I | 74 | 82   | 13588 | 6.71786421 | 1          | 0.78627372 | 67.9404007 |
| GOTERM_CC_FAT   | GO:0005840~ribosome                                | 4  | 4.49438202 | 0.07250174 | RPL18A, LOC   | 64 | 192  | 12504 | 4.0703125  | 0.99999075 | 0.58999799 | 59.4596324 |
| GOTERM_BP_FAT   | GO:0000186~activation of MAPKK activity            | 2  | 2.24719101 | 0.0776632  | GNAI2, GAD    | 74 | 15   | 13588 | 24.4828829 | 1          | 0.8040041  | 70.8842023 |
| GOTERM_BP_FAT   | GO:0045859~regulation of protein kinase activity   | 4  | 4.49438202 | 0.07839151 | GNAI2, GAD    | 74 | 186  | 13588 | 3.94885208 | 1          | 0.7987869  | 71.2331305 |
| GOTERM_BP_FAT   | GO:0019882~antigen processing and presentation     | 3  | 3.37078652 | 0.07955351 | H2-Q5, H2-E   | 74 | 87   | 13588 | 6.33178006 | 1          | 0.79555706 | 71.7817577 |
| GOTERM_BP_FAT   | GO:0007155~cell adhesion                           | 7  | 7.86516854 | 0.08050274 | OLFM4, LGA    | 74 | 561  | 13588 | 2.29117888 | 1          | 0.79154345 | 72.2226507 |
| GOTERM_BP_FAT   | GO:0022610~biological adhesion                     | 7  | 7.86516854 | 0.08103796 | OLFM4, LGA    | 74 | 562  | 13588 | 2.28710205 | 1          | 0.78589952 | 72.4684009 |
| GOTERM_BP_FAT   | GO:0048821~erythrocyte development                 | 2  | 2.24719101 | 0.08262382 | G6PDX, BCL6   | 74 | 16   | 13588 | 22.9527027 | 1          | 0.78480997 | 73.1846895 |
| GOTERM_BP_FAT   | GO:0005996~monosaccharide metabolic process        | 4  | 4.49438202 | 0.08336072 | ALDOA, ATF4   | 74 | 191  | 13588 | 3.84547899 | 1          | 0.78025973 | 73.5115606 |
| GOTERM_BP_FAT   | GO:0016485~protein processing                      | 3  | 3.37078652 | 0.08431083 | C4BP, CFB, C  | 74 | 90   | 13588 | 6.12072072 | 1          | 0.77671103 | 73.92752   |
| GOTERM_BP_FAT   | GO:0043549~regulation of kinase activity           | 4  | 4.49438202 | 0.08437065 | GNAI2, GAD    | 74 | 192  | 13588 | 3.82545045 | 1          | 0.76956423 | 73.9535018 |
| GOTERM_BP_FAT   | GO:0070085~glycosylation                           | 3  | 3.37078652 | 0.08591568 | GANAB, SER    | 74 | 91   | 13588 | 6.05346005 | 1          | 0.76870883 | 74.6162862 |
| GOTERM_BP_FAT   | GO:0043413~biopolymer glycosylation                | 3  | 3.37078652 | 0.08591568 | GANAB, SER    | 74 | 91   | 13588 | 6.05346005 | 1          | 0.76870883 | 74.6162862 |
| GOTERM_BP_FAT   | GO:0006486~protein amino acid glycosylation        | 3  | 3.37078652 | 0.08591568 | GANAB, SER    | 74 | 91   | 13588 | 6.05346005 | 1          | 0.76870883 | 74.6162862 |
| SMART           | SM00387:HATPase_c                                  | 2  | 2.24719101 | 0.08616037 | HSP90A1, T    | 42 | 20   | 9131  | 21.7404762 | 0.98989888 | 0.78383278 | 58.1729123 |
| INTERPRO        | IPR003594:ATP-binding region, ATPase-like          | 2  | 2.24719101 | 0.08843297 | HSP90A1, T    | 83 | 20   | 17763 | 21.4012048 | 1          | 0.98612498 | 69.5129022 |
| UP_SEQ_FEATURE  | domain:FCH   | 2  | 2.24719101 | 0.08969377 | PSTPIP1, FES  | 80 | 19   | 16021 | 21.0802632 | 1          | 0.99959021 | 72.0617543 |
| SMART           | SM00055:FCH  | 2  | 2.24719101 | 0.09027269 | PSTPIP1, FES  | 42 | 21   | 9131  | 20.7052154 | 0.99197449 | 0.70069209 | 59.9586552 |
| GOTERM_BP_FAT   | GO:0006790~sulfur metabolic process                | 3  | 3.37078652 | 0.09078542 | G6PDX, GSTP   | 74 | 94   | 13588 | 5.86026452 | 1          | 0.78103006 | 76.6036395 |
| GOTERM_BP_FAT   | GO:0051338~regulation of transferase activity      | 4  | 4.49438202 | 0.09158691 | GNAI2, GAD    | 74 | 199  | 13588 | 3.69088687 | 1          | 0.77722903 | 76.9164476 |
| GOTERM_BP_FAT   | GO:0006412~translation                             | 5  | 5.61797753 | 0.09240848 | EEF1B2, RPL1  | 74 | 319  | 13588 | 2.87808184 | 1          | 0.7735974  | 77.2330287 |
| INTERPRO        | IPR001060:Fps/Fes/Fer/CIP4 homology                | 2  | 2.24719101 | 0.09264582 | PSTPIP1, FES  | 83 | 21   | 17763 | 20.3820998 | 1          | 0.97631854 | 71.2719207 |
| SP_PIR_KEYWORDS | protease inhibitor                                 | 3  | 3.37078652 | 0.0932997  | SERPINA3G,    | 85 | 109  | 17854 | 5.78111171 | 1          | 0.68448676 | 71.042022  |
| GOTERM_BP_FAT   | GO:0044057~regulation of system process            | 4  | 4.49438202 | 0.09369501 | APOA4, YWH    | 74 | 201  | 13588 | 3.65416162 | 1          | 0.77181988 | 77.7206424 |
| GOTERM_BP_FAT   | GO:0051604~protein maturation                      | 3  | 3.37078652 | 0.0940765  | C4BP, CFB, C  | 74 | 96   | 13588 | 5.73817568 | 1          | 0.76669441 | 77.863346  |
| GOTERM_BP_FAT   | GO:0030099~myeloid cell differentiation            | 3  | 3.37078652 | 0.0940765  | G6PDX, BCL6   | 74 | 96   | 13588 | 5.73817568 | 1          | 0.76669441 | 77.863346  |

|               |   |   |            |            |             |    |    |       |            |   |            |            |
|---------------|---|---|------------|------------|-------------|----|----|-------|------------|---|------------|------------|
| GOTERM_BP_FAT | GO:0022604~regulation of cell morphogenesis     | 3 | 3.37078652 | 0.09573501 | LST1, MYH9, | 74 | 97 | 13588 | 5.67901923 | 1 | 0.76646636 | 78.4738653 |
| GOTERM_BP_FAT | GO:0043271~negative regulation of ion transport | 2 | 2.24719101 | 0.09734836 | LST1, GNAI2 | 74 | 19 | 13588 | 19.3285917 | 1 | 0.76609179 | 79.0526354 |

Unique Liver Up&Down Annotation

| UNIQUE       | Category        | Term           | Count | %          | PValue            | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|--------------|-----------------|----------------|-------|------------|-------------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Liver        | SP_PIR_KEYWORDS | acetylation    | 9     | 39.1304348 | <b>0.00162477</b> | HMGB2, DOI  | 20         | 2325     | 17854     | 3.4556129    | 0.1133731  | 0.1133731  | 1.68758082 |
| TC/SC.fc     | KEGG_PATHWAY    | mmu05322:5     | 3     | 13.0434783 | <b>0.00308055</b> | C8B, HIST1H | 6          | 103      | 5738      | 27.8543689   | 0.01834154 | 0.01834154 | 1.46573985 |
| Up-regulated | SP_PIR_KEYWORDS | chromosome     | 3     | 13.0434783 | <b>0.00904814</b> | HMGB2, HIS  | 20         | 136      | 17854     | 19.6919118   | 0.48962522 | 0.28559481 | 9.07499315 |
|              | SP_PIR_KEYWORDS | citrullination | 2     | 8.69565217 | <b>0.01689881</b> | HIST1H2AD,  | 20         | 16       | 17854     | 111.5875     | 0.71668582 | 0.34321569 | 16.3380702 |
|              | PIR_SUPERFAMILY | PIRSF002048    | 2     | 8.69565217 | <b>0.02058894</b> | HIST1H2AD,  | 14         | 13       | 8136      | 89.4065934   | 0.28313059 | 0.28313059 | 13.7340553 |
|              | SP_PIR_KEYWORDS | methylation    | 3     | 13.0434783 | <b>0.02271022</b> | HIST1H2AD,  | 20         | 221      | 17854     | 12.1180995   | 0.81730427 | 0.3462193  | 21.3719361 |
|              | INTERPRO        | IPR002119:H    | 2     | 8.69565217 | <b>0.02778987</b> | HIST1H2AD,  | 21         | 25       | 17763     | 67.6685714   | 0.72649417 | 0.72649417 | 23.3854571 |
|              | SMART           | SM00414:H2     | 2     | 8.69565217 | <b>0.03238406</b> | HIST1H2AD,  | 13         | 25       | 9131      | 56.1907692   | 0.3692719  | 0.3692719  | 20.0383228 |
|              | SP_PIR_KEYWORDS | phosphopro     | 12    | 52.173913  | <b>0.0372295</b>  | C8B, HMGB2  | 20         | 6311     | 17854     | 1.69741721   | 0.9396489  | 0.42965579 | 32.7738878 |
|              | SP_PIR_KEYWORDS | nucleosome     | 2     | 8.69565217 | <b>0.04582264</b> | HIST1H2AD,  | 20         | 44       | 17854     | 40.5772727   | 0.96891478 | 0.43926328 | 38.7953778 |
|              | INTERPRO        | IPR007125:H    | 2     | 8.69565217 | <b>0.04626619</b> | HIST1H2AD,  | 21         | 42       | 17763     | 40.2789116   | 0.88685114 | 0.66362394 | 36.0928253 |
|              | GOTERM_BP_FAT   | GO:0006334     | 2     | 8.69565217 | <b>0.06262203</b> | HIST1H2AD,  | 13         | 73       | 13588     | 28.6364594   | 0.99999856 | 0.99999856 | 55.7696398 |
|              | GOTERM_BP_FAT   | GO:0031497     | 2     | 8.69565217 | <b>0.06428596</b> | HIST1H2AD,  | 13         | 75       | 13588     | 27.8728205   | 0.99999901 | 0.99900256 | 56.749885  |
|              | INTERPRO        | IPR000884:TI   | 2     | 8.69565217 | <b>0.06440862</b> | C8B, SPON2  | 21         | 59       | 17763     | 28.6731235   | 0.95323018 | 0.6397075  | 46.701819  |
|              | GOTERM_BP_FAT   | GO:0065004     | 2     | 8.69565217 | <b>0.0651169</b>  | HIST1H2AD,  | 13         | 76       | 13588     | 27.5060729   | 0.99999917 | 0.99061343 | 57.2318838 |
|              | GOTERM_BP_FAT   | GO:0034728     | 2     | 8.69565217 | <b>0.0651169</b>  | HIST1H2AD,  | 13         | 76       | 13588     | 27.5060729   | 0.99999917 | 0.99061343 | 57.2318838 |
|              | GOTERM_CC_FAT   | GO:0000786     | 2     | 8.69565217 | <b>0.0718882</b>  | HIST1H2AD,  | 16         | 62       | 12504     | 25.2096774   | 0.99460464 | 0.99460464 | 53.7948148 |
|              | GOTERM_CC_FAT   | GO:0005694     | 3     | 13.0434783 | <b>0.07385294</b> | HMGB2, HIS  | 16         | 378      | 12504     | 6.20238095   | 0.99534846 | 0.9317978  | 54.7971318 |
|              | SMART           | SM00209:TSI    | 2     | 8.69565217 | <b>0.07488451</b> | C8B, SPON2  | 13         | 59       | 9131      | 23.809648    | 0.66368725 | 0.42007522 | 41.065141  |
|              | GOTERM_BP_FAT   | GO:0006323     | 2     | 8.69565217 | <b>0.08567199</b> | HIST1H2AD,  | 13         | 101      | 13588     | 20.697639    | 0.99999999 | 0.99050915 | 67.6909469 |
|              | GOTERM_CC_FAT   | GO:0032993     | 2     | 8.69565217 | <b>0.0863364</b>  | HIST1H2AD,  | 16         | 75       | 12504     | 20.84        | 0.99820095 | 0.87837743 | 60.7199588 |
|              | GOTERM_BP_FAT   | GO:0006333     | 2     | 8.69565217 | <b>0.09216159</b> | HIST1H2AD,  | 13         | 109      | 13588     | 19.1785462   | 1          | 0.98208752 | 70.4673894 |
|              | GOTERM_MF_FAT   | GO:0032403     | 2     | 8.69565217 | <b>0.09529269</b> | GNAT1, DOK  | 18         | 78       | 13288     | 18.9287749   | 0.9972837  | 0.9972837  | 63.2127289 |

| UNIQUE         | Category        | Term           | Count | %          | PValue            | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|----------------|-----------------|----------------|-------|------------|-------------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Liver          | SP_PIR_KEYWORDS | peroxisome     | 4     | 11.4285714 | <b>7.31E-04</b>   | PEX11A, DEC  | 34         | 96       | 17854     | 21.879902    | 0.06507803 | 0.06507803 | 0.79589835 |
| TC/SC.fc       | GOTERM_CC_FAT   | GO:0005777     | 4     | 11.4285714 | <b>8.77E-04</b>   | PEX11A, DEC  | 24         | 104      | 12504     | 20.0384615   | 0.06860602 | 0.06860602 | 0.93076137 |
| Down-regulated | GOTERM_CC_FAT   | GO:0042579     | 4     | 11.4285714 | <b>8.77E-04</b>   | PEX11A, DEC  | 24         | 104      | 12504     | 20.0384615   | 0.06860602 | 0.06860602 | 0.93076137 |
|                | GOTERM_BP_FAT   | GO:0006631     | 4     | 11.4285714 | <b>0.00505034</b> | ACSM3, CYP   | 27         | 184      | 13588     | 10.9404187   | 0.63303977 | 0.63303977 | 6.13914574 |
|                | SP_PIR_KEYWORDS | fatty acid me  | 3     | 8.57142857 | <b>0.0056634</b>  | ACSM3, LPIA  | 34         | 61       | 17854     | 25.8254581   | 0.40697215 | 0.22991699 | 6.01618102 |
|                | UP_SEQ_FEATURE  | nucleotide p   | 3     | 8.57142857 | <b>0.00697903</b> | HSD17B11, C  | 34         | 61       | 16021     | 23.1740598   | 0.58039196 | 0.58039196 | 7.76887298 |
|                | SP_PIR_KEYWORDS | oxidoreducta   | 5     | 14.2857143 | <b>0.02043891</b> | HSD17B11, C  | 34         | 572      | 17854     | 4.59018922   | 0.85041069 | 0.46915608 | 20.1966772 |
|                | SP_PIR_KEYWORDS | alternative sp | 15    | 42.8571429 | <b>0.02195037</b> | TXNIP, HSD1  | 34         | 4481     | 17854     | 1.75781404   | 0.87022169 | 0.39979373 | 21.5316719 |
|                | GOTERM_CC_FAT   | GO:0030667     | 2     | 5.71428571 | <b>0.0254592</b>  | PCSK4, DMB   | 24         | 14       | 12504     | 74.4285714   | 0.87617678 | 0.64811476 | 24.0306833 |
|                | SP_PIR_KEYWORDS | lipid metabo   | 3     | 8.57142857 | <b>0.02606892</b> | ACSM3, LPIA  | 34         | 136      | 17854     | 11.5834775   | 0.91197687 | 0.38493734 | 25.0670496 |
|                | SP_PIR_KEYWORDS | nadp           | 3     | 8.57142857 | <b>0.02823472</b> | HSD17B11, C  | 34         | 142      | 17854     | 11.0940348   | 0.92827892 | 0.3554235  | 26.8675398 |
|                | GOTERM_BP_FAT   | GO:0006732     | 3     | 8.57142857 | <b>0.03030763</b> | PDK4, BC016  | 27         | 143      | 13588     | 10.5578866   | 0.99774302 | 0.9524923  | 31.9627881 |
|                | GOTERM_BP_FAT   | GO:0055114     | 5     | 14.2857143 | <b>0.03728362</b> | HSD17B11, C  | 27         | 672      | 13588     | 3.74448854   | 0.99945965 | 0.91854985 | 37.8402197 |
|                | UP_SEQ_FEATURE  | composition    | 4     | 11.4285714 | <b>0.04273849</b> | GM129, FAM   | 34         | 380      | 16021     | 4.96006192   | 0.99555579 | 0.93333512 | 39.6118123 |
|                | KEGG_PATHWAY    | mmu01040:E     | 2     | 5.71428571 | <b>0.04610616</b> | ACAA1B, AC   | 11         | 27       | 5738      | 38.6397306   | 0.69274351 | 0.69274351 | 31.816502  |
|                | GOTERM_BP_FAT   | GO:0051186     | 3     | 8.57142857 | <b>0.04699273</b> | PDK4, BC016  | 27         | 182      | 13588     | 8.2954823    | 0.99992738 | 0.90768704 | 45.2449807 |
|                | GOTERM_MF_FAT   | GO:0009055     | 3     | 8.57142857 | <b>0.04719852</b> | CYP2G1, CYF  | 24         | 202      | 13288     | 8.22277228   | 0.99124538 | 0.99124538 | 41.4094548 |
|                | SP_PIR_KEYWORDS | transit pepti  | 4     | 11.4285714 | <b>0.05158349</b> | ACSM3, PDK   | 34         | 457      | 17854     | 4.59621573   | 0.99234549 | 0.50145712 | 43.931472  |
|                | GOTERM_BP_FAT   | GO:0050873     | 2     | 5.71428571 | <b>0.05408319</b> | PEX11A, LAN  | 27         | 29       | 13588     | 34.7075351   | 0.99998345 | 0.88939456 | 50.1299556 |
|                | GOTERM_MF_FAT   | GO:0004857     | 3     | 8.57142857 | <b>0.06551902</b> | TXNIP, SERPI | 24         | 243      | 13288     | 6.83539095   | 0.99869411 | 0.96386293 | 52.7290301 |
|                | KEGG_PATHWAY    | mmu00071:F     | 2     | 5.71428571 | <b>0.07577131</b> | CYP4A31, AC  | 11         | 45       | 5738      | 23.1838384   | 0.86052827 | 0.62654086 | 47.2331666 |
|                | UP_SEQ_FEATURE  | short sequen   | 2     | 5.71428571 | <b>0.08684223</b> | DEC2, ACO    | 34         | 44       | 16021     | 21.4184492   | 0.99998719 | 0.97659939 | 64.9728146 |
|                | INTERPRO        | IPR002347:G    | 2     | 5.71428571 | <b>0.09332254</b> | HSD17B11, C  | 32         | 56       | 17763     | 19.8247768   | 0.99980121 | 0.99980121 | 65.3129416 |
|                | SP_PIR_KEYWORDS | cytoplasm      | 10    | 28.5714286 | <b>0.09382144</b> | HSD17B11, T  | 34         | 3029     | 17854     | 1.7336337    | 0.99988421 | 0.67792389 | 65.9146387 |
|                | UP_SEQ_FEATURE  | splice varian  | 14    | 40         | <b>0.09957131</b> | HSD17B11, T  | 34         | 4448     | 16021     | 1.48311204   | 0.99999775 | 0.96128056 | 70.2143979 |

| UNIQUE | Category | Term | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini | FDR |
|--------|----------|------|-------|---|--------|-------|------------|----------|-----------|--------------|------------|-----------|-----|
|--------|----------|------|-------|---|--------|-------|------------|----------|-----------|--------------|------------|-----------|-----|

|                                   |                 |              |    |            |            |               |    |      |       |            |            |            |            |
|-----------------------------------|-----------------|--------------|----|------------|------------|---------------|----|------|-------|------------|------------|------------|------------|
| Liver<br>TH/SH.fc<br>Up-regulated | GOTERM_BP_FAT   | GO:0002526   | 7  | 8.86075949 | 2.54E-06   | ORM1, C4BP    | 67 | 81   | 13588 | 17.5264419 | 0.00169348 | 0.00169348 | 0.00380729 |
|                                   | INTERPRO        | IPR016060:CI | 5  | 6.32911392 | 7.50E-05   | C4BP, CFB, H  | 75 | 54   | 17763 | 21.9296296 | 0.01502819 | 0.01502819 | 0.09406549 |
|                                   | GOTERM_BP_FAT   | GO:0006955   | 11 | 13.9240506 | 8.41E-05   | APOA4, C4BI   | 67 | 471  | 13588 | 4.73644516 | 0.05455402 | 0.02765953 | 0.12593724 |
|                                   | SP_PIR_KEYWORDS | acetylation  | 23 | 29.1139241 | 1.54E-04   | HSP90AB1, A   | 76 | 2325 | 17854 | 2.3239502  | 0.03115352 | 0.03115352 | 0.19331211 |
|                                   | GOTERM_BP_FAT   | GO:0006953   | 4  | 5.06329114 | 4.05E-04   | ORM1, SERP    | 67 | 30   | 13588 | 27.040796  | 0.23656402 | 0.08604627 | 0.60451218 |
|                                   | GOTERM_BP_FAT   | GO:0034097   | 4  | 5.06329114 | 4.91E-04   | MCL1, SERP    | 67 | 32   | 13588 | 25.3507463 | 0.27927468 | 0.07861223 | 0.732972   |
|                                   | GOTERM_BP_FAT   | GO:0002455   | 4  | 5.06329114 | 6.41E-04   | C4BP, CFB, IC | 67 | 35   | 13588 | 23.1778252 | 0.34800178 | 0.08198605 | 0.95619082 |
|                                   | GOTERM_BP_FAT   | GO:0002250   | 5  | 6.32911392 | 7.32E-04   | C4BP, CFB, G  | 67 | 84   | 13588 | 12.0717839 | 0.38631627 | 0.078156   | 1.09084179 |
|                                   | GOTERM_BP_FAT   | GO:0002460   | 5  | 6.32911392 | 7.32E-04   | C4BP, CFB, G  | 67 | 84   | 13588 | 12.0717839 | 0.38631627 | 0.078156   | 1.09084179 |
|                                   | GOTERM_BP_FAT   | GO:0006954   | 7  | 8.86075949 | 7.65E-04   | ORM1, C4BP    | 67 | 225  | 13588 | 6.30951907 | 0.39987464 | 0.07034827 | 1.14046776 |
|                                   | SP_PIR_KEYWORDS | sushi        | 4  | 5.06329114 | 9.49E-04   | C4BP, CFB, H  | 76 | 46   | 17854 | 20.4279176 | 0.17768544 | 0.09318438 | 1.18894969 |
|                                   | SP_PIR_KEYWORDS | immune resp  | 6  | 7.59493671 | 0.0010606  | C4BP, LST1, I | 76 | 184  | 17854 | 7.66046911 | 0.19635668 | 0.07027513 | 1.32760333 |
|                                   | INTERPRO        | IPR000436:Si | 4  | 5.06329114 | 0.0014001  | C4BP, CFB, H  | 75 | 53   | 17763 | 17.874717  | 0.24649333 | 0.13195238 | 1.74358564 |
|                                   | GOTERM_BP_FAT   | GO:0006952   | 9  | 11.3924051 | 0.00140908 | APOA4, ORM    | 67 | 448  | 13588 | 4.07422708 | 0.60957516 | 0.11091726 | 2.09056949 |
|                                   | SMART           | SM00032:CC   | 4  | 5.06329114 | 0.00145609 | C4BP, CFB, H  | 40 | 53   | 9131  | 17.2283019 | 0.06755338 | 0.06755338 | 1.38102102 |
|                                   | GOTERM_BP_FAT   | GO:0045087   | 5  | 6.32911392 | 0.00180064 | APOA4, C4BI   | 67 | 107  | 13588 | 9.47691449 | 0.6994399  | 0.1250316  | 2.66421405 |
|                                   | GOTERM_BP_FAT   | GO:0006959   | 4  | 5.06329114 | 0.00227489 | C4BP, CFB, IC | 67 | 54   | 13588 | 15.0226645 | 0.7810874  | 0.14093292 | 3.35481768 |
|                                   | GOTERM_BP_FAT   | GO:0002252   | 5  | 6.32911392 | 0.00326045 | C4BP, CFB, IC | 67 | 126  | 13588 | 8.04785596 | 0.88676297 | 0.17965043 | 4.77536341 |
|                                   | GOTERM_BP_FAT   | GO:0016064   | 4  | 5.06329114 | 0.00353075 | C4BP, CFB, IC | 67 | 63   | 13588 | 12.8765695 | 0.90550223 | 0.17847939 | 5.16155157 |
|                                   | GOTERM_BP_FAT   | GO:0019724   | 4  | 5.06329114 | 0.00385697 | C4BP, CFB, IC | 67 | 65   | 13588 | 12.4803674 | 0.92404173 | 0.17985548 | 5.62567446 |
|                                   | GOTERM_BP_FAT   | GO:0050778   | 5  | 6.32911392 | 0.00428368 | C4BP, CFB, IC | 67 | 136  | 13588 | 7.45610184 | 0.94292302 | 0.18496589 | 6.22958625 |
|                                   | SP_PIR_KEYWORDS | acute phase  | 3  | 3.79746835 | 0.00452643 | ORM1, SERP    | 76 | 24   | 17854 | 29.3651316 | 0.60724184 | 0.20835349 | 5.55363188 |
|                                   | SP_PIR_KEYWORDS | cell shape   | 3  | 3.79746835 | 0.00490671 | LST1, MYH9,   | 76 | 25   | 17854 | 28.1905263 | 0.63697007 | 0.18343927 | 6.00703175 |
|                                   | INTERPRO        | IPR003597:In | 4  | 5.06329114 | 0.00502307 | IGK-C, H2-Q   | 75 | 83   | 17763 | 11.4139759 | 0.63840022 | 0.28756915 | 6.12635223 |
|                                   | SMART           | SM00407:IGc  | 4  | 5.06329114 | 0.00522892 | IGK-C, H2-Q   | 40 | 83   | 9131  | 11.0012048 | 0.22248068 | 0.11822944 | 4.88024926 |
|                                   | SP_PIR_KEYWORDS | complement   | 3  | 3.79746835 | 0.00530121 | C4BP, CFB, C  | 76 | 26   | 17854 | 27.1062753 | 0.66544513 | 0.16680902 | 6.47527121 |
|                                   | GOTERM_CC_FAT   | GO:0005783   | 11 | 13.9240506 | 0.00541864 | SRI, GANAB,   | 60 | 838  | 12504 | 2.73556086 | 0.56687982 | 0.56687982 | 6.31001048 |
|                                   | SP_PIR_KEYWORDS | Secreted     | 14 | 17.721519  | 0.00587001 | OLF4, ADP     | 76 | 1420 | 17854 | 2.31612305 | 0.70263237 | 0.15907698 | 7.14661176 |
|                                   | GOTERM_BP_FAT   | GO:0002449   | 4  | 5.06329114 | 0.00597692 | C4BP, CFB, IC | 67 | 76   | 13588 | 10.6739984 | 0.98165806 | 0.23399838 | 8.59056976 |
|                                   | GOTERM_BP_FAT   | GO:0006487   | 3  | 3.79746835 | 0.00648632 | GANAB, SER    | 67 | 25   | 13588 | 24.3367164 | 0.98696958 | 0.23759648 | 9.28993635 |
|                                   | GOTERM_BP_FAT   | GO:0009611   | 7  | 8.86075949 | 0.00666021 | ORM1, C4BP    | 67 | 347  | 13588 | 4.09118672 | 0.98840541 | 0.23063458 | 9.52751727 |
|                                   | SP_PIR_KEYWORDS | endoplasmic  | 9  | 11.3924051 | 0.00746032 | GANAB, SQL    | 76 | 678  | 17854 | 3.11842105 | 0.78617263 | 0.17537231 | 9.00012263 |
|                                   | GOTERM_CC_FAT   | GO:0044449   | 4  | 5.06329114 | 0.00773891 | SRI, KRT8, LN | 60 | 86   | 12504 | 9.69302326 | 0.69772801 | 0.45020732 | 8.89861266 |
|                                   | INTERPRO        | IPR003006:In | 4  | 5.06329114 | 0.00795386 | IGK-C, H2-Q   | 75 | 98   | 17763 | 9.66693878 | 0.80073165 | 0.33187214 | 9.53933055 |
|                                   | GOTERM_BP_FAT   | GO:0002253   | 4  | 5.06329114 | 0.00840719 | C4BP, CFB, IC | 67 | 86   | 13588 | 9.43283582 | 0.9964161  | 0.26864049 | 11.8824478 |
|                                   | GOTERM_CC_FAT   | GO:0030016   | 4  | 5.06329114 | 0.00903557 | SRI, KRT8, LN | 60 | 91   | 12504 | 9.16043956 | 0.75286047 | 0.37245134 | 10.3165042 |
|                                   | GOTERM_BP_FAT   | GO:0002443   | 4  | 5.06329114 | 0.00923373 | C4BP, CFB, IC | 67 | 89   | 13588 | 9.11487506 | 0.99794506 | 0.27794813 | 12.9765644 |
|                                   | GOTERM_BP_FAT   | GO:0006958   | 3  | 3.79746835 | 0.00925966 | C4BP, CFB, C  | 67 | 30   | 13588 | 20.280597  | 0.99798062 | 0.26673507 | 13.0106824 |
|                                   | UP_SEQ_FEATURE  | domain:Sush  | 3  | 3.79746835 | 0.00961134 | C4BP, CFB, C  | 73 | 33   | 16021 | 19.9514321 | 0.94990966 | 0.94990966 | 12.1643683 |
|                                   | UP_SEQ_FEATURE  | domain:Sush  | 3  | 3.79746835 | 0.00961134 | C4BP, CFB, C  | 73 | 33   | 16021 | 19.9514321 | 0.94990966 | 0.94990966 | 12.1643683 |
|                                   | GOTERM_CC_FAT   | GO:0005576   | 16 | 20.2531646 | 0.0097038  | ALDOA, OLF    | 60 | 1680 | 12504 | 1.9847619  | 0.77724489 | 0.31299972 | 11.0392823 |
|                                   | GOTERM_CC_FAT   | GO:0005615   | 8  | 10.1265823 | 0.00991337 | APOA4, ORM    | 60 | 511  | 12504 | 3.26262231 | 0.78438821 | 0.26424283 | 11.2648587 |
|                                   | GOTERM_CC_FAT   | GO:0043292   | 4  | 5.06329114 | 0.0101592  | SRI, KRT8, LN | 60 | 95   | 12504 | 8.77473684 | 0.79247802 | 0.23055541 | 11.5288007 |
|                                   | KEGG_PATHWAY    | mmu04610:C   | 4  | 5.06329114 | 0.01124067 | C4BP, SERP    | 37 | 75   | 5738  | 8.27099099 | 0.46298948 | 0.46298948 | 10.522895  |
|                                   | GOTERM_BP_FAT   | GO:0048584   | 5  | 6.32911392 | 0.01267098 | C4BP, CFB, IC | 67 | 186  | 13588 | 5.45177339 | 0.99979766 | 0.33304052 | 17.3920153 |
|                                   | GOTERM_BP_FAT   | GO:0006956   | 3  | 3.79746835 | 0.01316243 | C4BP, CFB, C  | 67 | 36   | 13588 | 16.9004975 | 0.99985483 | 0.33082555 | 18.0059597 |
|                                   | GOTERM_BP_FAT   | GO:0002541   | 3  | 3.79746835 | 0.01316243 | C4BP, CFB, C  | 67 | 36   | 13588 | 16.9004975 | 0.99985483 | 0.33082555 | 18.0059597 |
|                                   | SP_PIR_KEYWORDS | duplication  | 4  | 5.06329114 | 0.01407565 | APOA4, CFB,   | 76 | 120  | 17854 | 7.83070175 | 0.94607621 | 0.27708587 | 16.3506731 |
|                                   | SP_PIR_KEYWORDS | pentose pho  | 2  | 2.53164557 | 0.01669877 | ALDOA, G6P    | 76 | 4    | 17854 | 117.460526 | 0.96885159 | 0.29312342 | 19.1108391 |
|                                   | GOTERM_BP_FAT   | GO:0002684   | 5  | 6.32911392 | 0.0178027  | C4BP, CFB, IC | 67 | 206  | 13588 | 4.922475   | 0.99999374 | 0.40603154 | 23.5965844 |
|                                   | KEGG_PATHWAY    | mmu03010:F   | 4  | 5.06329114 | 0.0178081  | RPL18A, LOC   | 37 | 89   | 5738  | 6.96993623 | 0.62778057 | 0.38990212 | 16.1998948 |
|                                   | GOTERM_MF_FAT   | GO:0005198   | 7  | 8.86075949 | 0.01812628 | RPL18A, LOC   | 63 | 450  | 13288 | 3.28098765 | 0.96146074 | 0.96146074 | 20.1402302 |
|                                   | GOTERM_BP_FAT   | GO:0001816   | 3  | 3.79746835 | 0.01846049 | GADD45G, G    | 67 | 43   | 13588 | 14.1492537 | 0.999996   | 0.4041953  | 24.3596665 |
|                                   | SP_PIR_KEYWORDS | signal       | 21 | 26.5822785 | 0.01866752 | OLF4, GAN     | 76 | 2970 | 17854 | 1.66105795 | 0.97938746 | 0.29734972 | 21.1270924 |
|                                   | GOTERM_BP_FAT   | GO:0008360   | 3  | 3.79746835 | 0.02182717 | LST1, MYH9,   | 67 | 47   | 13588 | 12.9450619 | 0.9999996  | 0.44500619 | 28.1551275 |
|                                   | GOTERM_BP_FAT   | GO:0045860   | 4  | 5.06329114 | 0.02237332 | GNAI2, GAD    | 67 | 124  | 13588 | 6.54212807 | 0.99999972 | 0.44037021 | 28.7538181 |
|                                   | GOTERM_CC_FAT   | GO:0005826   | 2  | 2.53164557 | 0.02337456 | PSTPIP1, MY   | 60 | 5    | 12504 | 83.36      | 0.97381111 | 0.40568496 | 24.7030497 |

|                 |               |    |            |            |               |    |      |       |            |            |            |            |
|-----------------|---------------|----|------------|------------|---------------|----|------|-------|------------|------------|------------|------------|
| GOTERM_BP_FAT   | GO:0033674    | 4  | 5.06329114 | 0.02528833 | GNAI2, GAD    | 67 | 130  | 13588 | 6.2401837  | 0.99999996 | 0.46887085 | 31.8712657 |
| GOTERM_BP_FAT   | GO:0032147    | 3  | 3.79746835 | 0.02542763 | GNAI2, GAD    | 67 | 51   | 13588 | 11.9297629 | 0.99999997 | 0.45857814 | 32.0170051 |
| SP_PIR_KEYWORDS | ATP           | 4  | 5.06329114 | 0.02571802 | PLK1, FES, TC | 76 | 151  | 17854 | 6.22307424 | 0.99533295 | 0.36062816 | 27.9742487 |
| GOTERM_MF_FAT   | GO:0004857    | 5  | 6.32911392 | 0.02663642 | SERPINA3G,    | 63 | 243  | 13288 | 4.33993076 | 0.99181599 | 0.90953447 | 28.2456643 |
| GOTERM_BP_FAT   | GO:0051347    | 4  | 5.06329114 | 0.02786678 | GNAI2, GAD    | 67 | 135  | 13588 | 6.00906578 | 0.99999999 | 0.47797297 | 34.5222171 |
| GOTERM_CC_FAT   | GO:0044421    | 9  | 11.3924051 | 0.02807542 | APOA4, ORM    | 60 | 774  | 12504 | 2.42325581 | 0.98754294 | 0.42200122 | 28.9375514 |
| GOTERM_BP_FAT   | GO:0006006    | 4  | 5.06329114 | 0.0305806  | ALDOA, ATF    | 67 | 140  | 13588 | 5.79445629 | 1          | 0.49868547 | 37.2081416 |
| GOTERM_CC_FAT   | GO:0032155    | 2  | 2.53164557 | 0.03257325 | PSTPIP1, MY   | 60 | 7    | 12504 | 59.5428571 | 0.99390202 | 0.43257354 | 32.7837148 |
| GOTERM_CC_FAT   | GO:0032153    | 2  | 2.53164557 | 0.03257325 | PSTPIP1, MY   | 60 | 7    | 12504 | 59.5428571 | 0.99390202 | 0.43257354 | 32.7837148 |
| GOTERM_MF_FAT   | GO:0003735    | 4  | 5.06329114 | 0.03341877 | RPL18A, LOC   | 63 | 151  | 13288 | 5.58730159 | 0.99764263 | 0.86691086 | 34.1564793 |
| UP_SEQ_FEATURE  | signal peptic | 21 | 26.5822785 | 0.03458943 | OLFM4, GAN    | 73 | 2963 | 16021 | 1.55544408 | 0.99998177 | 0.99573059 | 37.671664  |
| SP_PIR_KEYWORDS | ribosomal pr  | 4  | 5.06329114 | 0.0384807  | RPL18A, LOC   | 76 | 177  | 17854 | 5.30895034 | 0.99969143 | 0.46303007 | 38.9953844 |
| SP_PIR_KEYWORDS | innate immu   | 3  | 3.79746835 | 0.03967503 | C4BP, CFB, C  | 76 | 75   | 17854 | 9.39684211 | 0.99976113 | 0.44881587 | 39.9429068 |
| GOTERM_BP_FAT   | GO:0051605    | 3  | 3.79746835 | 0.0397287  | C4BP, CFB, C  | 67 | 65   | 13588 | 9.36027555 | 1          | 0.58199071 | 45.5238407 |
| GOTERM_CC_FAT   | GO:0005829    | 7  | 8.86075949 | 0.04401357 | GNAI2, CFB,   | 60 | 549  | 12504 | 2.6571949  | 0.99902374 | 0.50001542 | 41.7227901 |
| SP_PIR_KEYWORDS | immunoglob    | 2  | 2.53164557 | 0.04526213 | IGK-C, IGH-6  | 76 | 11   | 17854 | 42.7129187 | 0.9999282  | 0.47065074 | 44.1981462 |
| KEGG_PATHWAY    | mmu04110:C    | 4  | 5.06329114 | 0.04536219 | YWHAG, PLK    | 37 | 128  | 5738  | 4.84628378 | 0.92217398 | 0.57305204 | 36.6573596 |
| SP_PIR_KEYWORDS | Serine prote  | 3  | 3.79746835 | 0.04660359 | SERPINA3G,    | 76 | 82   | 17854 | 8.59467266 | 0.99994625 | 0.4590633  | 45.1776215 |
| GOTERM_BP_FAT   | GO:0051301    | 5  | 6.32911392 | 0.04756571 | PLK1, PSTPIP  | 67 | 281  | 13588 | 3.60864716 | 1          | 0.63788831 | 51.8182349 |
| GOTERM_BP_FAT   | GO:0019318    | 4  | 5.06329114 | 0.04894768 | ALDOA, ATF    | 67 | 169  | 13588 | 4.80014131 | 1          | 0.63736906 | 52.8551665 |
| GOTERM_BP_FAT   | GO:0007155    | 7  | 8.86075949 | 0.0543782  | OLFM4, LGA    | 67 | 561  | 13588 | 2.53055578 | 1          | 0.66608648 | 56.731474  |
| GOTERM_CC_FAT   | GO:0030017    | 3  | 3.79746835 | 0.05471344 | SRI, KR18, LN | 60 | 80   | 12504 | 7.815      | 0.99982751 | 0.54512847 | 49.0834096 |
| GOTERM_BP_FAT   | GO:0022610    | 7  | 8.86075949 | 0.0547615  | OLFM4, LGA    | 67 | 562  | 13588 | 2.52605301 | 1          | 0.65810792 | 56.9935099 |
| UP_SEQ_FEATURE  | region of int | 2  | 2.53164557 | 0.05689437 | SERPINA3G,    | 73 | 13   | 16021 | 33.7639621 | 0.99999999 | 0.9976491  | 54.645257  |
| GOTERM_BP_FAT   | GO:0016052    | 3  | 3.79746835 | 0.05892103 | ALDOA, ADP    | 67 | 81   | 13588 | 7.51133223 | 1          | 0.67539916 | 59.7434741 |
| GOTERM_CC_FAT   | GO:0042470    | 3  | 3.79746835 | 0.06090345 | HSP90AB1, C   | 60 | 85   | 12504 | 7.35529412 | 0.99993728 | 0.5535411  | 52.9421741 |
| GOTERM_CC_FAT   | GO:0048770    | 3  | 3.79746835 | 0.06090345 | HSP90AB1, C   | 60 | 85   | 12504 | 7.35529412 | 0.99993728 | 0.5535411  | 52.9421741 |
| GOTERM_BP_FAT   | GO:0045859    | 4  | 5.06329114 | 0.06172683 | GNAI2, GAD    | 67 | 186  | 13588 | 4.36141871 | 1          | 0.68291221 | 61.5047936 |
| GOTERM_CC_FAT   | GO:0005840    | 4  | 5.06329114 | 0.06199809 | RPL18A, LOC   | 60 | 192  | 12504 | 4.34166667 | 0.99994759 | 0.53148765 | 53.5959775 |
| GOTERM_BP_FAT   | GO:0005996    | 4  | 5.06329114 | 0.0657552  | ALDOA, ATF    | 67 | 191  | 13588 | 4.24724545 | 1          | 0.69695486 | 63.9081597 |
| GOTERM_BP_FAT   | GO:0043549    | 4  | 5.06329114 | 0.06657521 | GNAI2, GAD    | 67 | 192  | 13588 | 4.22512438 | 1          | 0.69219204 | 64.3799006 |
| GOTERM_BP_FAT   | GO:0019882    | 3  | 3.79746835 | 0.06679632 | H2-Q5, H2-C   | 67 | 87   | 13588 | 6.99330932 | 1          | 0.68423993 | 64.5061125 |
| GOTERM_BP_FAT   | GO:0006412    | 5  | 6.32911392 | 0.06925714 | EEF1B2, RPL1  | 67 | 319  | 13588 | 3.17877696 | 1          | 0.68889094 | 65.8829114 |
| GOTERM_BP_FAT   | GO:0000186    | 2  | 2.53164557 | 0.07046765 | GNAI2, GAD    | 67 | 15   | 13588 | 27.040796  | 1          | 0.68666408 | 66.5417334 |
| GOTERM_BP_FAT   | GO:0016485    | 3  | 3.79746835 | 0.07085881 | C4BP, CFB, C  | 67 | 90   | 13588 | 6.760199   | 1          | 0.68018749 | 66.7520692 |
| GOTERM_BP_FAT   | GO:0070085    | 3  | 3.79746835 | 0.07223068 | GANAB, SER    | 67 | 91   | 13588 | 6.6859111  | 1          | 0.67906278 | 67.4800544 |
| GOTERM_BP_FAT   | GO:0006486    | 3  | 3.79746835 | 0.07223068 | GANAB, SER    | 67 | 91   | 13588 | 6.6859111  | 1          | 0.67906278 | 67.4800544 |
| GOTERM_BP_FAT   | GO:0043413    | 3  | 3.79746835 | 0.07223068 | GANAB, SER    | 67 | 91   | 13588 | 6.6859111  | 1          | 0.67906278 | 67.4800544 |
| GOTERM_BP_FAT   | GO:0051338    | 4  | 5.06329114 | 0.07244678 | GNAI2, GAD    | 67 | 199  | 13588 | 4.07650191 | 1          | 0.67198856 | 67.5933612 |
| GOTERM_BP_FAT   | GO:0044057    | 4  | 5.06329114 | 0.07416609 | APOA4, YWH    | 67 | 201  | 13588 | 4.0359397  | 1          | 0.67286298 | 68.4818103 |
| SP_PIR_KEYWORDS | cell adhesior | 5  | 6.32911392 | 0.0758096  | OLFM4, PSTI   | 76 | 380  | 17854 | 3.09106648 | 0.99999991 | 0.61531133 | 62.9508061 |
| SP_PIR_KEYWORDS | protease inh  | 3  | 3.79746835 | 0.07689328 | SERPINA3G,    | 76 | 109  | 17854 | 6.46571704 | 0.99999993 | 0.59975357 | 63.4942484 |
| GOTERM_BP_FAT   | GO:0051604    | 3  | 3.79746835 | 0.0792178  | C4BP, CFB, C  | 67 | 96   | 13588 | 6.33768657 | 1          | 0.69002028 | 70.9625206 |
| INTERPRO        | IPR003594:A   | 2  | 2.53164557 | 0.08014394 | HSP90AB1, T   | 75 | 20   | 17763 | 23.684     | 0.99999995 | 0.96577977 | 64.9631267 |
| GOTERM_BP_FAT   | GO:0022604    | 3  | 3.79746835 | 0.08063998 | LST1, MYH9    | 67 | 97   | 13588 | 6.27234959 | 1          | 0.68911328 | 71.6272986 |
| UP_SEQ_FEATURE  | domain:FC-H   | 2  | 2.53164557 | 0.08206491 | PSTPIP1, FES  | 73 | 19   | 16021 | 23.1016583 | 1          | 0.99868802 | 68.3355908 |
| SMART           | SM00387:HA    | 2  | 2.53164557 | 0.08212643 | HSP90AB1, T   | 40 | 20   | 9131  | 22.8275    | 0.98364775 | 0.74617999 | 55.8617204 |
| INTERPRO        | IPR001060:F   | 2  | 2.53164557 | 0.08398034 | PSTPIP1, FES  | 75 | 21   | 17763 | 22.5561905 | 0.99999998 | 0.94782513 | 66.754099  |
| GOTERM_BP_FAT   | GO:0050804    | 3  | 3.79746835 | 0.08495409 | YWHAG, LST    | 67 | 100  | 13588 | 6.0841791  | 1          | 0.70135785 | 73.5580034 |
| SMART           | SM00055:FC    | 2  | 2.53164557 | 0.08605542 | PSTPIP1, FES  | 40 | 21   | 9131  | 21.7404762 | 0.98669076 | 0.66034475 | 57.6322239 |
| GOTERM_BP_FAT   | GO:0043271    | 2  | 2.53164557 | 0.08841793 | LST1, GNAI2   | 67 | 19   | 13588 | 21.3479969 | 1          | 0.70914561 | 75.0186795 |
| UP_SEQ_FEATURE  | domain:Pept   | 3  | 3.79746835 | 0.08897578 | CFB, HP, C1S  | 73 | 111  | 16021 | 5.93150685 | 1          | 0.99690361 | 71.3915694 |
| GOTERM_BP_FAT   | GO:0051969    | 3  | 3.79746835 | 0.09528408 | YWHAG, LST    | 67 | 107  | 13588 | 5.6861487  | 1          | 0.73007184 | 77.6942061 |
| SP_PIR_KEYWORDS | plasma        | 2  | 2.53164557 | 0.09615316 | APOA4, CFB    | 76 | 24   | 17854 | 19.5767544 | 1          | 0.66582369 | 72.0081563 |
| GOTERM_CC_FAT   | GO:0031252    | 3  | 3.79746835 | 0.09793666 | VIM, PSTPIP1  | 60 | 112  | 12504 | 5.58214286 | 0.99999987 | 0.67818418 | 70.9582305 |
| GOTERM_BP_FAT   | GO:0010033    | 6  | 7.59493671 | 0.09828846 | MCCL1, SERPI  | 67 | 505  | 13588 | 2.40957588 | 1          | 0.73474968 | 78.7786488 |
| KEGG_PATHWAY    | mmu04914:F    | 3  | 3.79746835 | 0.09888164 | HSP90AB1, C   | 37 | 85   | 5738  | 5.47344992 | 0.99674162 | 0.76108123 | 64.0878251 |

| UNIQUE         | Annotation Cluster 1 | Enrichment Score: 0.3369359825543763 |       |    |            |             |            |          |           |              |            |            |            |  |
|----------------|----------------------|--------------------------------------|-------|----|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|--|
| Liver          | Category             | Term                                 | Count | %  | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |  |
| TH/SH.fc       | GOTERM_MF_FAT        | GO:0046914                           | 3     | 30 | 0.33546548 | CYP2C44, BC | 7          | 2608     | 13288     | 2.18361087   | 0.99998927 | 0.99998927 | 96.7247357 |  |
| Down-regulated | SP_PIR_KEYWORDS      | metal-bindin                         | 3     | 30 | 0.34351353 | CYP2C44, BC | 9          | 2682     | 17854     | 2.2189908    | 0.99999989 | 0.99999989 | 97.7705083 |  |
|                | GOTERM_MF_FAT        | GO:0046872                           | 3     | 30 | 0.55741535 | CYP2C44, BC | 7          | 3850     | 13288     | 1.47918367   | 1          | 0.99998894 | 99.8907216 |  |
|                | GOTERM_MF_FAT        | GO:0043169                           | 3     | 30 | 0.56322595 | CYP2C44, BC | 7          | 3885     | 13288     | 1.46585769   | 1          | 0.99956107 | 99.9021593 |  |
|                | GOTERM_MF_FAT        | GO:0043167                           | 3     | 30 | 0.57130342 | CYP2C44, BC | 7          | 3934     | 13288     | 1.44759968   | 1          | 0.99733897 | 99.9163047 |  |



## Common Lung Annotation

472 david id matched

| COMM     | Annotation Cluster 1 | Enrichment Score: 10.99580979061693                  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|----------|----------------------|--|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| lung     | Category             | Term   |       |            |            |               |            |          |           |              |            |            |            |
| TC/SC.fc | GOTERM_BP_FAT        | GO:0006952--defense response                         | 49    | 10.3813559 | 6.77E-18   | RARRES2, A    | 341        | 448      | 13588     | 4.35832111   | 1.30E-14   | 6.52E-15   | 1.16E-14   |
| TH/SH.fc | GOTERM_BP_FAT        | GO:0009611--response to wounding                     | 35    | 7.41525424 | 8.98E-12   | F2RL2, ADOF   | 341        | 347      | 13588     | 4.01920103   | 1.73E-08   | 4.33E-09   | 1.54E-08   |
|          | GOTERM_BP_FAT        | GO:0006954--inflammatory response                    | 26    | 5.50847458 | 4.16E-10   | ADORA3, NF    | 341        | 225      | 13588     | 4.60460085   | 8.01E-07   | 1.60E-07   | 7.12E-07   |
|          | SP_PIR_KEYWORDS      | inflammatory response                                | 13    | 2.75423729 | 4.11E-07   | NFKBID, TLR   | 439        | 78       | 17854     | 6.77828398   | 1.56E-04   | 3.12E-05   | 5.68E-04   |
|          | Annotation Cluster 2 | Enrichment Score: 7.290062913487951                  |       |            |            |               |            |          |           |              |            |            |            |
|          | Category             | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|          | SP_PIR_KEYWORDS      | signal   | 129   | 27.3305085 | 2.22E-11   | F2RL2, MPZL   | 439        | 2970     | 17854     | 1.76646189   | 8.44E-09   | 8.44E-09   | 3.08E-08   |
|          | UP_SEQ_FEATURE       | signal peptide                                       | 129   | 27.3305085 | 2.43E-09   | F2RL2, MPZL   | 425        | 2963     | 16021     | 1.64118957   | 2.94E-06   | 2.94E-06   | 3.94E-06   |
|          | SP_PIR_KEYWORDS      | disulfide bond                                       | 106   | 22.4576271 | 5.83E-09   | MPZL3, F2RL   | 439        | 2469     | 17854     | 1.74604642   | 2.22E-06   | 7.39E-07   | 8.08E-06   |
|          | UP_SEQ_FEATURE       | disulfide bond                                       | 101   | 21.3983051 | 9.78E-07   | MPZL3, F2RL   | 425        | 2379     | 16021     | 1.60039661   | 0.00117973 | 5.90E-04   | 0.0015822  |
|          | SP_PIR_KEYWORDS      | glycoprotein   | 131   | 27.7542373 | 1.04E-06   | F2RL2, MPZL   | 439        | 3600     | 17854     | 1.47992534   | 3.95E-04   | 6.58E-05   | 0.00143865 |
|          | UP_SEQ_FEATURE       | glycosylation site:N-linked (GlcNAc...)              | 126   | 26.6949153 | 5.67E-05   | F2RL2, MPZL   | 425        | 3444     | 16021     | 1.37913917   | 0.06617039 | 0.01696969 | 0.09172203 |
|          | Annotation Cluster 3 | Enrichment Score: 5.985495700600087                  |       |            |            |               |            |          |           |              |            |            |            |
|          | Category             | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|          | SP_PIR_KEYWORDS      | immune response                                      | 22    | 4.66101695 | 5.22E-09   | TNFAIP8L2, I  | 439        | 184      | 17854     | 4.86268198   | 1.98E-06   | 9.92E-07   | 7.23E-06   |
|          | GOTERM_BP_FAT        | GO:0045087--innate immune response                   | 15    | 3.1779661  | 4.29E-07   | TNFAIP8L2, I  | 341        | 107      | 13588     | 5.58609916   | 8.27E-04   | 8.27E-05   | 7.35E-04   |
|          | SP_PIR_KEYWORDS      | innate immunity                                      | 9     | 1.90677966 | 4.93E-04   | TNFAIP8L2, C  | 439        | 75       | 17854     | 4.88036446   | 0.17093743 | 0.01241954 | 0.68061397 |
|          | Annotation Cluster 4 | Enrichment Score: 5.463311857114418                  |       |            |            |               |            |          |           |              |            |            |            |
|          | Category             | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|          | GOTERM_BP_FAT        | GO:0001775--cell activation                          | 26    | 5.50847458 | 2.71E-09   | ITGAL, SBNC   | 341        | 246      | 13588     | 4.21152517   | 5.23E-06   | 8.71E-07   | 4.65E-06   |
|          | GOTERM_BP_FAT        | GO:0002274--myeloid leukocyte activation             | 10    | 2.11864407 | 1.38E-07   | FYB, SLC11A   | 341        | 35       | 13588     | 11.3850021   | 2.65E-04   | 3.31E-05   | 2.36E-04   |
|          | GOTERM_BP_FAT        | GO:0045321--leukocyte activation                     | 22    | 4.66101695 | 1.42E-07   | FYB, ITGAL, S | 341        | 219      | 13588     | 4.00294594   | 2.74E-04   | 3.05E-05   | 2.44E-04   |
|          | GOTERM_BP_FAT        | GO:0046649--lymphocyte activation                    | 14    | 2.96610169 | 0.00104666 | ITGAL, PIK3C  | 341        | 191      | 13588     | 2.9207597    | 0.86693687 | 0.04200569 | 1.77659682 |
|          | GOTERM_BP_FAT        | GO:0042110--T cell activation                        | 9     | 1.90677966 | 0.00867084 | ITGAL, SLC11  | 341        | 116      | 13588     | 3.09161695   | 0.99999995 | 0.17719277 | 13.849162  |
|          | Annotation Cluster 5 | Enrichment Score: 3.9178190277876666                 |       |            |            |               |            |          |           |              |            |            |            |
|          | Category             | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|          | GOTERM_BP_FAT        | GO:0002237--response to molecule of bacterial origin | 10    | 2.11864407 | 2.94E-06   | SLC11A1, TH   | 341        | 49       | 13588     | 8.13214435   | 0.00564626 | 4.35E-04   | 0.00503226 |
|          | GOTERM_BP_FAT        | GO:0032496--response to lipopolysaccharide           | 8     | 1.69491525 | 3.74E-05   | SLC11A1, TH   | 341        | 38       | 13588     | 8.38894891   | 0.06941715 | 0.00326485 | 0.06392065 |
|          | GOTERM_BP_FAT        | GO:0010033--response to organic substance            | 22    | 4.66101695 | 0.01606493 | HMGB2, MA     | 341        | 505      | 13588     | 1.73593101   | 1          | 0.25287042 | 24.2115629 |
|          | Annotation Cluster 6 | Enrichment Score: 3.8869306481835086                 |       |            |            |               |            |          |           |              |            |            |            |
|          | Category             | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|          | GOTERM_BP_FAT        | GO:0001906--cell killing                             | 6     | 1.27118644 | 3.31E-05   | PTPN6, HAM    | 341        | 16       | 13588     | 14.9428152   | 0.06184833 | 0.00303556 | 0.05672557 |
|          | GOTERM_BP_FAT        | GO:0002443--leukocyte mediated immunity              | 11    | 2.33050847 | 7.42E-05   | PTPN6, SLC1   | 341        | 89       | 13588     | 4.92497282   | 0.13322614 | 0.00570276 | 0.12699166 |
|          | GOTERM_BP_FAT        | GO:0001909--leukocyte mediated cytotoxicity          | 5     | 1.05932203 | 1.63E-04   | PTPN6, NCF    | 341        | 12       | 13588     | 16.6031281   | 0.26890869 | 0.0100529  | 0.2779875  |
|          | GOTERM_BP_FAT        | GO:0002444--myeloid leukocyte mediated immunity      | 5     | 1.05932203 | 7.08E-04   | ADORA3, NC    | 341        | 17       | 13588     | 11.7198551   | 0.74442082 | 0.03437535 | 1.20514582 |
|          | Annotation Cluster 7 | Enrichment Score: 3.6507166319155293                 |       |            |            |               |            |          |           |              |            |            |            |
|          | Category             | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|          | INTERPRO             | IPR000980:SH2 motif                                  | 12    | 2.54237288 | 7.00E-05   | TNS4, PTPN    | 425        | 111      | 17763     | 4.51841017   | 0.05474659 | 0.0185924  | 0.1075053  |
|          | SP_PIR_KEYWORDS      | SH2 domain   | 11    | 2.33050847 | 2.20E-04   | TNS4, PTPN    | 439        | 103      | 17854     | 4.34336643   | 0.08018211 | 0.00756935 | 0.30402852 |
|          | SMART                | SM00252:SH2  | 12    | 2.54237288 | 2.61E-04   | TNS4, PTPN    | 256        | 111      | 9131      | 3.85599662   | 0.0458239  | 0.02318062 | 0.32047238 |
|          | UP_SEQ_FEATURE       | domain:SH2   | 10    | 2.11864407 | 6.22E-04   | TNS4, FGR, S  | 425        | 90       | 16021     | 4.18849673   | 0.52802713 | 0.13943554 | 1.00135506 |
|          | Annotation Cluster 8 | Enrichment Score: 3.4979037972827625                 |       |            |            |               |            |          |           |              |            |            |            |
|          | Category             | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|          | GOTERM_CC_FAT        | GO:0005576--extracellular region                     | 69    | 14.6186441 | 1.54E-04   | RARRES2, F1   | 330        | 1680     | 12504     | 1.55623377   | 0.04129247 | 0.04129247 | 0.20260939 |
|          | GOTERM_CC_FAT        | GO:0005615--extracellular space                      | 29    | 6.1440678  | 1.99E-04   | OLFM4, MM     | 330        | 511      | 12504     | 2.1503647    | 0.05297969 | 0.02685032 | 0.26146408 |

|                       |  |       |            |            |               |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| SP_PIR_KEYWORDS       | Secreted   | 57    | 12.0762712 | 2.79E-04   | RARRES2, S1   | 439        | 1420     | 17854     | 1.63251628   | 0.10050433 | 0.00753724 | 0.38514102 |
| GOTERM_CC_FAT         | GO:0044421--extracellular region part                  | 36    | 7.62711864 | 0.00119661 | OLFM4, MM     | 330        | 774      | 12504     | 1.76236786   | 0.27968553 | 0.05320994 | 1.56547285 |
| Annotation Cluster 9  |  |       |            |            |               |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0002366--leukocyte activation during immune resp    | 8     | 1.69491525 | 9.05E-06   | SLC11A1, SB   | 341        | 31       | 13588     | 10.2832277   | 0.017275   | 0.00102453 | 0.01548629 |
| GOTERM_BP_FAT         | GO:0002263--cell activation during immune response     | 8     | 1.69491525 | 9.05E-06   | SLC11A1, SB   | 341        | 31       | 13588     | 10.2832277   | 0.017275   | 0.00102453 | 0.01548629 |
| GOTERM_BP_FAT         | GO:0002285--lymphocyte activation during immune re     | 5     | 1.05932203 | 0.00110844 | SLC11A1, PL   | 341        | 19       | 13588     | 10.4861861   | 0.88187849 | 0.04352523 | 1.88052112 |
| GOTERM_BP_FAT         | GO:0002286--T cell activation during immune respons    | 4     | 0.84745763 | 0.00460428 | SLC11A1, BC   | 341        | 14       | 13588     | 11.3850021   | 0.99986201 | 0.12086439 | 7.59561401 |
| GOTERM_BP_FAT         | GO:0042110--T cell activation                          | 9     | 1.90677966 | 0.00867084 | ITGAL, SLC11  | 341        | 116      | 13588     | 3.09161695   | 0.99999995 | 0.17719277 | 13.849162  |
| Annotation Cluster 10 |  |       |            |            |               |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0001817--regulation of cytokine production          | 14    | 2.96610169 | 4.58E-05   | FCER1A, H2-   | 341        | 139      | 13588     | 4.013418     | 0.08437681 | 0.00382529 | 0.07831382 |
| GOTERM_BP_FAT         | GO:0048584--positive regulation of response to stimu   | 14    | 2.96610169 | 8.19E-04   | FCER1A, PTP   | 341        | 186      | 13588     | 2.99927475   | 0.79370476 | 0.03869272 | 1.39306595 |
| GOTERM_BP_FAT         | GO:0051240--positive regulation of multicellular organ | 13    | 2.75423729 | 8.20E-04   | ADORA3, LST   | 341        | 163      | 13588     | 3.17802206   | 0.79394489 | 0.03779438 | 1.39408662 |
| GOTERM_BP_FAT         | GO:0001819--positive regulation of cytokine productio  | 8     | 1.69491525 | 8.71E-04   | SLC11A1, M    | 341        | 62       | 13588     | 5.14161385   | 0.81332723 | 0.03828056 | 1.48062212 |
| Annotation Cluster 11 |  |       |            |            |               |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS       | sh3 domain   | 16    | 3.38983051 | 1.61E-04   | FYB, NCF2, F  | 439        | 204      | 17854     | 3.1897807    | 0.0593007  | 0.0067694  | 0.22246334 |
| INTERPRO              | IPR001452:Src homology-3 domain                        | 16    | 3.38983051 | 1.73E-04   | FYB, NCF2, F  | 425        | 211      | 17763     | 3.1693114    | 0.12961984 | 0.03411094 | 0.26486851 |
| SMART                 | SM00326:SH3  | 16    | 3.38983051 | 8.22E-04   | FYB, NCF2, F  | 256        | 211      | 9131      | 2.70468009   | 0.13757351 | 0.03632516 | 1.00769595 |
| UP_SEQ_FEATURE        | domain:SH3   | 12    | 2.54237288 | 0.00412198 | FYB, FGR, PR  | 425        | 163      | 16021     | 2.77520029   | 0.99316375 | 0.42532247 | 6.46409765 |
| Annotation Cluster 12 |  |       |            |            |               |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| INTERPRO              | IPR001849:Pleckstrin homology                          | 18    | 3.81355932 | 1.88E-04   | FERMT3, CYT   | 425        | 261      | 17763     | 2.88243408   | 0.14030586 | 0.02978319 | 0.2884039  |
| INTERPRO              | IPR011993:Pleckstrin homology-type                     | 18    | 3.81355932 | 6.11E-04   | FERMT3, CYT   | 425        | 289      | 17763     | 2.60316711   | 0.38832557 | 0.05959476 | 0.93470038 |
| UP_SEQ_FEATURE        | domain:PH  | 15    | 3.1779661  | 9.95E-04   | FERMT3, CYT   | 425        | 202      | 16021     | 2.79924287   | 0.69942269 | 0.18154897 | 1.5982933  |
| SMART                 | SM00233:PH   | 18    | 3.81355932 | 0.00100472 | FERMT3, CYT   | 256        | 261      | 9131      | 2.45985991   | 0.16551553 | 0.03554126 | 1.23055463 |
| Annotation Cluster 13 |  |       |            |            |               |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_MF_FAT         | GO:0030246--carbohydrate binding                       | 23    | 4.87288136 | 2.04E-05   | SELP, KLRA1   | 339        | 317      | 13288     | 2.84399282   | 0.01052906 | 0.00527846 | 0.02956793 |
| INTERPRO              | IPR016186:C-type lectin-like                           | 12    | 2.54237288 | 2.34E-04   | SELP, THBD,   | 425        | 127      | 17763     | 3.94916165   | 0.17168249 | 0.03090547 | 0.35920502 |
| SP_PIR_KEYWORDS       | Lectin   | 14    | 2.96610169 | 2.49E-04   | SELP, KLRA1   | 439        | 167      | 17854     | 3.40943625   | 0.0904385  | 0.00786827 | 0.34474679 |
| INTERPRO              | IPR001304:C-type lectin                                | 11    | 2.33050847 | 5.31E-04   | SELP, THBD,   | 425        | 118      | 17763     | 3.89617149   | 0.34760559 | 0.059191   | 0.81264867 |
| GOTERM_MF_FAT         | GO:0005529--sugar binding                              | 14    | 2.96610169 | 7.39E-04   | SELP, KLRA1   | 339        | 181      | 13288     | 3.03186167   | 0.31799518 | 0.07368758 | 1.06355241 |
| SMART                 | SM00034:CLECT  | 11    | 2.33050847 | 0.0016705  | SELP, THBD,   | 256        | 118      | 9131      | 3.32498014   | 0.25987926 | 0.0489199  | 2.03829964 |
| UP_SEQ_FEATURE        | domain:C-type lectin                                   | 9     | 1.90677966 | 0.00263052 | SELP, THBD,   | 425        | 90       | 16021     | 3.76964706   | 0.95838174 | 0.32793623 | 4.1718372  |
| INTERPRO              | IPR018378:C-type lectin, conserved site                | 8     | 1.69491525 | 0.01231016 | SELP, CLEC4I  | 425        | 104      | 17763     | 3.21502262   | 0.99995269 | 0.40793988 | 17.3254802 |
| Annotation Cluster 14 |  |       |            |            |               |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0042108--positive regulation of cytokine biosynthe  | 9     | 1.90677966 | 7.95E-06   | FCER1A, APC   | 341        | 42       | 13588     | 8.53875157   | 0.01519038 | 9.56E-04   | 0.01360326 |
| GOTERM_BP_FAT         | GO:0001817--regulation of cytokine production          | 14    | 2.96610169 | 4.58E-05   | FCER1A, H2-   | 341        | 139      | 13588     | 4.013418     | 0.08437681 | 0.00382529 | 0.07831382 |
| GOTERM_BP_FAT         | GO:0042035--regulation of cytokine biosynthetic proc   | 9     | 1.90677966 | 1.85E-04   | FCER1A, APC   | 341        | 64       | 13588     | 5.60355572   | 0.29942848 | 0.01105898 | 0.3157734  |
| GOTERM_BP_FAT         | GO:0032680--regulation of tumor necrosis factor proc   | 6     | 1.27118644 | 4.89E-04   | MYD88, TLR:   | 341        | 27       | 13588     | 8.85500163   | 0.60981881 | 0.02580412 | 0.83296247 |
| GOTERM_BP_FAT         | GO:0032675--regulation of interleukin-6 production     | 5     | 1.05932203 | 0.0079666  | MYD88, TLR:   | 341        | 32       | 13588     | 6.22617302   | 0.99999998 | 0.17127535 | 12.7955233 |
| GOTERM_BP_FAT         | GO:0045410--positive regulation of interleukin-6 biosy | 3     | 0.63559322 | 0.01206292 | TLR1, IL1B, T | 341        | 7        | 13588     | 17.0775031   | 1          | 0.21610783 | 18.7583931 |
| GOTERM_BP_FAT         | GO:0042534--regulation of tumor necrosis factor bios   | 3     | 0.63559322 | 0.01581989 | TLR1, BCL3,   | 341        | 8        | 13588     | 14.9428152   | 1          | 0.25154356 | 23.8878257 |
| GOTERM_BP_FAT         | GO:0045408--regulation of interleukin-6 biosynthetic p | 3     | 0.63559322 | 0.0405912  | TLR1, IL1B, T | 341        | 13       | 13588     | 9.19557861   | 1          | 0.41681699 | 50.8019333 |
| Annotation Cluster 15 |  |       |            |            |               |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_MF_FAT         | GO:0003779--actin binding                              | 22    | 4.66101695 | 1.51E-05   | FMNL1, PAR    | 339        | 288      | 13288     | 2.99426418   | 0.00778272 | 0.00778272 | 0.02182623 |

|                 |   |    |            |            |               |     |      |       |            |            |            |            |
|-----------------|---|----|------------|------------|---------------|-----|------|-------|------------|------------|------------|------------|
| GOTERM_MF_FAT   | GO:0008092--cytoskeletal protein binding          | 27 | 5.7203898  | 2.12E-05   | LMO7, ANLN    | 339 | 414  | 13288 | 2.55636783 | 0.01093708 | 0.00365907 | 0.0307199  |
| SP_PIR_KEYWORDS | actin-binding                                     | 18 | 3.81355932 | 4.51E-05   | PARVG, TWF    | 439 | 226  | 17854 | 3.23917995 | 0.01697859 | 0.00213826 | 0.06236697 |
| SP_PIR_KEYWORDS | cytoskeleton                                      | 30 | 6.3559322  | 2.65E-04   | PRC1, S100A   | 439 | 583  | 17854 | 2.09278065 | 0.09572982 | 0.00771066 | 0.3659269  |
| GOTERM_CC_FAT   | GO:0015629--actin cytoskeleton                    | 15 | 3.1779661  | 0.00106165 | MYL7, FERM    | 330 | 205  | 12504 | 2.77250554 | 0.25251878 | 0.05654746 | 1.39004847 |
| GOTERM_CC_FAT   | GO:0005856--cytoskeleton                          | 44 | 9.3220339  | 0.00769878 | KIF23, KIF22, | 330 | 1122 | 12504 | 1.485918   | 0.87968325 | 0.16177752 | 9.683345   |
| GOTERM_CC_FAT   | GO:0044430--cytoskeletal part                     | 30 | 6.3559322  | 0.03446362 | KIF23, KIF22, | 330 | 774  | 12504 | 1.46863989 | 0.99993292 | 0.35389907 | 37.0089677 |
| GOTERM_CC_FAT   | GO:0043232--intracellular non-membrane-bounded or | 62 | 13.1355932 | 0.06300308 | KIF23, KIF22, | 330 | 1919 | 12504 | 1.22419821 | 0.99999998 | 0.48335208 | 57.5809477 |
| GOTERM_CC_FAT   | GO:0043228--non-membrane-bounded organelle        | 62 | 13.1355932 | 0.06300308 | KIF23, KIF22, | 330 | 1919 | 12504 | 1.22419821 | 0.99999998 | 0.48335208 | 57.5809477 |

|                       |  |       |            |            |               |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 16 | Enrichment Score: 2.839625333426206              |       |            |            |               |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0031982--vesicle                              | 28    | 5.93220339 | 5.78E-04   | TLR1, TLR2, 1 | 330        | 519      | 12504     | 2.0442109    | 0.14661047 | 0.0514743  | 0.75960209 |
| GOTERM_CC_FAT         | GO:0030141--secretory granule                    | 11    | 2.33050847 | 0.00102572 | SELP, ECE1, I | 330        | 117      | 12504     | 3.56239316   | 0.24511667 | 0.06788401 | 1.34330275 |
| GOTERM_CC_FAT         | GO:0031988--membrane-bounded vesicle             | 23    | 4.87288136 | 0.00170031 | SELP, CLN3,   | 330        | 420      | 12504     | 2.07497835   | 0.37266911 | 0.06444149 | 2.217642   |
| GOTERM_CC_FAT         | GO:0031410--cytoplasmic vesicle                  | 26    | 5.50847458 | 0.00199371 | TLR1, TLR2, 1 | 330        | 508      | 12504     | 1.9392985    | 0.42121305 | 0.06606889 | 2.59567859 |
| GOTERM_CC_FAT         | GO:0016023--cytoplasmic membrane-bounded vesicle | 22    | 4.66101695 | 0.00315061 | SELP, CLN3,   | 330        | 414      | 12504     | 2.01352657   | 0.57879225 | 0.09159948 | 4.07319652 |

|                       |                                      |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|--------------------------------------|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 17 | Enrichment Score: 2.8306527808655573 |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term                                 | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0006935--chemotaxis               | 14    | 2.96610169 | 3.22E-06   | S100A8, S10  | 341        | 109      | 13588     | 5.11802846   | 0.00618864 | 4.43E-04   | 0.00551716 |
| GOTERM_BP_FAT         | GO:0042330--taxis                    | 14    | 2.96610169 | 3.22E-06   | S100A8, S10  | 341        | 109      | 13588     | 5.11802846   | 0.00618864 | 4.43E-04   | 0.00551716 |
| GOTERM_BP_FAT         | GO:0050900--leukocyte migration      | 8     | 1.69491525 | 8.57E-05   | SELP, CORO1  | 341        | 43       | 13588     | 7.41348974   | 0.1521132  | 0.00632637 | 0.14654512 |
| GOTERM_BP_FAT         | GO:0007626--locomotory behavior      | 18    | 3.81355932 | 1.10E-04   | S100A8, S10  | 341        | 239      | 13588     | 3.0010675    | 0.19040892 | 0.00725719 | 0.18755307 |
| GOTERM_BP_FAT         | GO:0030595--leukocyte chemotaxis     | 6     | 1.27118644 | 4.89E-04   | CORO1A, S1   | 341        | 27       | 13588     | 8.85500163   | 0.60981881 | 0.02580412 | 0.83296247 |
| GOTERM_BP_FAT         | GO:0060326--cell chemotaxis          | 6     | 1.27118644 | 4.89E-04   | CORO1A, S1   | 341        | 27       | 13588     | 8.85500163   | 0.60981881 | 0.02580412 | 0.83296247 |
| SP_PIR_KEYWORDS       | chemotaxis                           | 7     | 1.48305085 | 0.00406195 | S100A8, ROE  | 439        | 62       | 17854     | 4.59174076   | 0.78704695 | 0.07441951 | 5.47896306 |
| GOTERM_BP_FAT         | GO:0007610--behavior                 | 20    | 4.23728814 | 0.00655868 | CLN3, S100A  | 341        | 405      | 13588     | 1.96777814   | 0.99999687 | 0.15176065 | 10.6525972 |
| GOTERM_BP_FAT         | GO:0030593--neutrophil chemotaxis    | 4     | 0.84745763 | 0.00813704 | IL1B, CSF3R, | 341        | 17       | 13588     | 9.37588408   | 0.99999985 | 0.17270261 | 13.0516344 |
| GOTERM_BP_FAT         | GO:0016477--cell migration           | 12    | 2.54237288 | 0.03926178 | WNT2, FMN    | 341        | 240      | 13588     | 1.99237537   | 1          | 0.40831457 | 49.6218757 |
| GOTERM_BP_FAT         | GO:0006928--cell motion              | 15    | 3.1779661  | 0.07847926 | FMNL1, SELF  | 341        | 367      | 13588     | 1.62864471   | 1          | 0.56905521 | 75.3159865 |
| GOTERM_BP_FAT         | GO:0051674--localization of cell     | 12    | 2.54237288 | 0.10110147 | WNT2, FMN    | 341        | 284      | 13588     | 1.68369749   | 1          | 0.63262796 | 83.8697254 |
| GOTERM_BP_FAT         | GO:0048870--cell motility            | 12    | 2.54237288 | 0.10110147 | WNT2, FMN    | 341        | 284      | 13588     | 1.68369749   | 1          | 0.63262796 | 83.8697254 |

|                       |                                     |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|-------------------------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 18 | Enrichment Score: 2.782556353947907 |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term                                | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS       | cell adhesion                       | 21    | 4.44915254 | 0.00119783 | MPZL3, PAR  | 439        | 380      | 17854     | 2.24753627   | 0.36583597 | 0.02643534 | 1.64556717 |
| GOTERM_BP_FAT         | GO:0007155--cell adhesion           | 27    | 5.7203898  | 0.00191405 | MPZL3, ITGA | 341        | 561      | 13588     | 1.91779447   | 0.97502785 | 0.06376873 | 3.22632538 |
| GOTERM_BP_FAT         | GO:0022610--biological adhesion     | 27    | 5.7203898  | 0.00195877 | MPZL3, ITGA | 341        | 562      | 13588     | 1.91438202   | 0.97709238 | 0.06410373 | 3.30051495 |

|                       |   |       |            |            |               |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 19 | Enrichment Score: 2.619429484094543                   |       |            |            |               |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0010627--regulation of protein kinase cascade      | 16    | 3.38983051 | 7.94E-06   | FCER1A, PTP   | 341        | 155      | 13588     | 4.11329108   | 0.01516852 | 0.00101846 | 0.01358354 |
| GOTERM_BP_FAT         | GO:0043122--regulation of I-kappaB kinase/NF-kappa    | 8     | 1.69491525 | 5.29E-05   | LST1, MYD8    | 341        | 40       | 13588     | 7.96950147   | 0.09680189 | 0.00423324 | 0.09044669 |
| GOTERM_BP_FAT         | GO:0043123--positive regulation of I-kappaB kinase/N  | 6     | 1.27118644 | 0.0012702  | LST1, MYD8    | 341        | 33       | 13588     | 7.24500133   | 0.91352999 | 0.04777998 | 2.15214987 |
| GOTERM_BP_FAT         | GO:0009967--positive regulation of signal transductor | 13    | 2.75423729 | 0.00130851 | FCER1A, ITG   | 341        | 172      | 13588     | 3.01173021   | 0.9196887  | 0.0482453  | 2.21638359 |
| GOTERM_BP_FAT         | GO:0010740--positive regulation of protein kinase cas | 9     | 1.90677966 | 0.00159782 | OSM, ADO      | 341        | 88       | 13588     | 4.07531325   | 0.95403481 | 0.05750841 | 2.7001418  |
| GOTERM_BP_FAT         | GO:0010647--positive regulation of cell communicatio  | 13    | 2.75423729 | 0.00288271 | FCER1A, ITG   | 341        | 189      | 13588     | 2.74083384   | 0.9961517  | 0.08447348 | 4.82150426 |
| GOTERM_BP_FAT         | GO:0010829--negative regulation of glucose transport  | 3     | 0.63559322 | 0.03491338 | LST1, IL1B, L | 341        | 12       | 13588     | 9.96187683   | 1          | 0.38884862 | 45.5731336 |
| GOTERM_BP_FAT         | GO:0010827--regulation of glucose transport           | 3     | 0.63559322 | 0.08825819 | LST1, IL1B, L | 341        | 20       | 13588     | 5.9771261    | 1          | 0.59478888 | 79.4360647 |
| GOTERM_BP_FAT         | GO:0051051--negative regulation of transport          | 4     | 0.84745763 | 0.26894945 | OSM, LST1, I  | 341        | 72       | 13588     | 2.21375041   | 1          | 0.87872098 | 99.5310593 |

|                       |                                      |       |            |            |            |            |          |           |              |            |            |            |
|-----------------------|--------------------------------------|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 20 | Enrichment Score: 2.6110541148731934 |       |            |            |            |            |          |           |              |            |            |            |
| Category              | Term                                 | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0005615--extracellular space      | 29    | 6.1440678  | 1.99E-04   | OLFM4, MM  | 330        | 511      | 12504     | 2.1503647    | 0.05297969 | 0.02685032 | 0.26146408 |
| SP_PIR_KEYWORDS       | cytokine                             | 12    | 2.54237288 | 0.00438064 | OSM, S100A | 439        | 177      | 17854     | 2.75726806   | 0.81143251 | 0.07636917 | 5.89682385 |
| GOTERM_MF_FAT         | GO:0005125--cytokine activity        | 11    | 2.33050847 | 0.01687399 | OSM, PGLYR | 339        | 180      | 13288     | 2.39541134   | 0.99985156 | 0.44438936 | 21.8300113 |

|                       |   |                                      |            |            |              |            |          |           |              |            |            |            |
|-----------------------|---|--------------------------------------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 21 |   | Enrichment Score: 2.549234926763092  |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count                                | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0032680--regulation of tumor necrosis factor prod  | 6                                    | 1.27118644 | 4.89E-04   | MYD88, TLR:  | 341        | 27       | 13588     | 8.85500163   | 0.60981881 | 0.02580412 | 0.83296247 |
| GOTERM_BP_FAT         | GO:0001819--positive regulation of cytokine productio | 8                                    | 1.69491525 | 8.71E-04   | SLC11A1, M   | 341        | 62       | 13588     | 5.14161385   | 0.81332723 | 0.03828056 | 1.48062212 |
| GOTERM_BP_FAT         | GO:0032760--positive regulation of tumor necrosis fac | 3                                    | 0.63559322 | 0.05288738 | MYD88, TLR:  | 341        | 15       | 13588     | 7.96950147   | 1          | 0.46764421 | 60.5493202 |
| Annotation Cluster 22 |   | Enrichment Score: 2.29540207526642   |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count                                | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0016052--carbohydrate catabolic process            | 10                                   | 2.11864407 | 1.85E-04   | OVGP1, BCL1  | 341        | 81       | 13588     | 4.91944535   | 0.29967337 | 0.01073615 | 0.31608314 |
| GOTERM_BP_FAT         | GO:0005996--monosaccharide metabolic process          | 14                                   | 2.96610169 | 0.00104666 | PTGES3, TAL  | 341        | 191      | 13588     | 2.9207597    | 0.86693687 | 0.04200569 | 1.77659682 |
| GOTERM_BP_FAT         | GO:0006007--glucose catabolic process                 | 7                                    | 1.48305085 | 0.00181265 | TALDO1, AD   | 341        | 52       | 13588     | 5.36408753   | 0.96963077 | 0.06155703 | 3.05788713 |
| GOTERM_BP_FAT         | GO:0019320--hexose catabolic process                  | 7                                    | 1.48305085 | 0.00181265 | TALDO1, AD   | 341        | 52       | 13588     | 5.36408753   | 0.96963077 | 0.06155703 | 3.05788713 |
| GOTERM_BP_FAT         | GO:0046365--monosaccharide catabolic process          | 7                                    | 1.48305085 | 0.00220554 | TALDO1, AD   | 341        | 54       | 13588     | 5.16541762   | 0.98577217 | 0.07069652 | 3.70896853 |
| GOTERM_BP_FAT         | GO:0006006--glucose metabolic process                 | 11                                   | 2.33050847 | 0.00273178 | PTGES3, TAL  | 341        | 140      | 13588     | 3.13087558   | 0.99484925 | 0.08274585 | 4.57459154 |
| GOTERM_BP_FAT         | GO:0019318--hexose metabolic process                  | 12                                   | 2.54237288 | 0.00352518 | PTGES3, TAL  | 341        | 169      | 13588     | 2.8294088    | 0.99888788 | 0.09934976 | 5.86581243 |
| GOTERM_BP_FAT         | GO:0044275--cellular carbohydrate catabolic process   | 7                                    | 1.48305085 | 0.00377297 | TALDO1, AD   | 341        | 60       | 13588     | 4.64887586   | 0.99931114 | 0.10444378 | 6.26569638 |
| GOTERM_BP_FAT         | GO:0046164--alcohol catabolic process                 | 7                                    | 1.48305085 | 0.00561084 | TALDO1, AD   | 341        | 65       | 13588     | 4.29127002   | 0.99998034 | 0.14155497 | 9.18213404 |
| SP_PIR_KEYWORDS       | glycolysis  | 5                                    | 1.05932203 | 0.01918282 | ADPGK, HK3,  | 439        | 42       | 17854     | 4.84163141   | 0.99936399 | 0.19991659 | 23.5203514 |
| GOTERM_BP_FAT         | GO:0006096--glycolysis                                | 5                                    | 1.05932203 | 0.02382407 | ADPGK, HK3,  | 341        | 44       | 13588     | 4.52812583   | 1          | 0.31659012 | 33.8169101 |
| GOTERM_BP_FAT         | GO:0006091--generation of precursor metabolites and   | 13                                   | 2.75423729 | 0.03156517 | PTGES3, ADF  | 341        | 261      | 13588     | 1.98474174   | 1          | 0.37374032 | 42.2489538 |
| KEGG_PATHWAY          | mmu00010:Glycolysis / Gluconeogenesis                 | 4                                    | 0.84745763 | 0.35022086 | HK3, PKM2,   | 178        | 68       | 5738      | 1.89623265   | 1          | 0.76858631 | 99.3353938 |
| Annotation Cluster 23 |   | Enrichment Score: 2.2826134641419413 |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count                                | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| INTERPRO              | IPR003599:Immunoglobulin subtype                      | 21                                   | 4.44915254 | 6.85E-05   | MPZL3, IL1R, | 425        | 313      | 17763     | 2.80415711   | 0.05361841 | 0.02717854 | 0.10522891 |
| SMART                 | SM00409:IG  | 21                                   | 4.44915254 | 4.73E-04   | MPZL3, IL1R, | 256        | 313      | 9131      | 2.39305861   | 0.08156867 | 0.02796427 | 0.58057023 |
| SP_PIR_KEYWORDS       | Immunoglobulin domain                                 | 23                                   | 4.87288136 | 0.0014451  | MPZL3, FCF   | 439        | 443      | 17854     | 2.11151961   | 0.42278299 | 0.02850873 | 1.98212949 |
| INTERPRO              | IPR013783:Immunoglobulin-like fold                    | 29                                   | 6.1440678  | 0.00175986 | MPZL3, IL1R, | 425        | 644      | 17763     | 1.88208623   | 0.75735982 | 0.12080032 | 2.66927413 |
| UP_SEQ_FEATURE        | domain:lg-like C2-type 1                              | 10                                   | 2.11864407 | 0.00771642 | IGSF10, ALC# | 425        | 130      | 16021     | 2.89972851   | 0.99991302 | 0.60740773 | 11.7788373 |
| UP_SEQ_FEATURE        | domain:lg-like C2-type 2                              | 10                                   | 2.11864407 | 0.00809825 | IGSF10, ALC# | 425        | 131      | 16021     | 2.87759317   | 0.99994534 | 0.5902533  | 12.326449  |
| INTERPRO              | IPR013151:Immunoglobulin                              | 10                                   | 2.11864407 | 0.02735872 | FCER1A, IL1F | 425        | 178      | 17763     | 2.34805023   | 1          | 0.53655425 | 34.6941196 |
| INTERPRO              | IPR007110:Immunoglobulin-like                         | 22                                   | 4.66101695 | 0.05547677 | MPZL3, IL1R, | 425        | 604      | 17763     | 1.52234515   | 1          | 0.71068068 | 58.383661  |
| INTERPRO              | IPR013106:Immunoglobulin V-set                        | 11                                   | 2.33050847 | 0.36613252 | MPZL3, ALC#  | 425        | 364      | 17763     | 1.2630446    | 1          | 0.99612759 | 99.9090761 |
| Annotation Cluster 24 |   | Enrichment Score: 2.1830534325015787 |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count                                | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| BIOCARTA              | m_monocytePathway:Monocyte and its Surface Molec      | 5                                    | 1.05932203 | 0.00104951 | ITGAL, SELP, | 55         | 11       | 1171      | 9.67768595   | 0.09778815 | 0.09778815 | 1.15434873 |
| BIOCARTA              | m_neutrophilPathway:Neutrophil and Its Surface Mole   | 4                                    | 0.84745763 | 0.00440795 | ITGAL, CD44, | 55         | 8        | 1171      | 10.6454545   | 0.35139687 | 0.194641   | 4.76731234 |
| BIOCARTA              | m_lymphocytePathway:Adhesion Molecules on Lymph       | 3                                    | 0.63559322 | 0.06104027 | ITGAL, CD44, | 55         | 9        | 1171      | 7.0969697    | 0.99791358 | 0.87221863 | 50.1626942 |
| Annotation Cluster 25 |   | Enrichment Score: 2.055134663035264  |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count                                | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0002526--acute inflammatory response               | 9                                    | 1.90677966 | 9.30E-04   | CFP, ORM1,   | 341        | 81       | 13588     | 4.42750081   | 0.8332674  | 0.03989518 | 1.57948547 |
| GOTERM_BP_FAT         | GO:0006953--acute-phase response                      | 5                                    | 1.05932203 | 0.00631331 | ORM1, SAA3   | 341        | 30       | 13588     | 6.64125122   | 0.99999496 | 0.14828203 | 10.2741076 |
| SP_PIR_KEYWORDS       | acute phase   | 3                                    | 0.63559322 | 0.11641611 | ORM1, SAA3   | 439        | 24       | 17854     | 5.08371298   | 1          | 0.57477274 | 81.9756675 |
| Annotation Cluster 26 |   | Enrichment Score: 2.0194376300871975 |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count                                | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_MF_FAT         | GO:0030246--carbohydrate binding                      | 23                                   | 4.87288136 | 2.04E-05   | SELP, KLRA1  | 339        | 317      | 13288     | 2.84399282   | 0.01052906 | 0.00527846 | 0.02956793 |
| GOTERM_MF_FAT         | GO:0005539--glycosaminoglycan binding                 | 9                                    | 1.90677966 | 0.00860559 | CD44, PGLYF  | 339        | 114      | 13288     | 3.09455054   | 0.98863242 | 0.42857594 | 11.7573024 |
| GOTERM_MF_FAT         | GO:0030247--polysaccharide binding                    | 9                                    | 1.90677966 | 0.01652068 | CD44, PGLYF  | 339        | 128      | 13288     | 2.75608407   | 0.99982119 | 0.48510071 | 21.422476  |
| GOTERM_MF_FAT         | GO:0001871--pattern binding                           | 9                                    | 1.90677966 | 0.01652068 | CD44, PGLYF  | 339        | 128      | 13288     | 2.75608407   | 0.99982119 | 0.48510071 | 21.422476  |
| GOTERM_MF_FAT         | GO:0008201--heparin binding                           | 6                                    | 1.27118644 | 0.06021424 | MPO, LTF, PI | 339        | 83       | 13288     | 2.83356435   | 1          | 0.67020837 | 59.2926034 |
| GOTERM_BP_FAT         | GO:0030203--glycosaminoglycan metabolic process       | 3                                    | 0.63559322 | 0.26453696 | PGLYRP1, PR  | 341        | 40       | 13588     | 2.98856305   | 1          | 0.87553219 | 99.4801793 |
| Annotation Cluster 27 |   | Enrichment Score: 1.9586994780206821 |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count                                | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |

|                 |  |     |            |            |             |     |      |       |            |            |            |            |
|-----------------|--|-----|------------|------------|-------------|-----|------|-------|------------|------------|------------|------------|
| SP_PIR_KEYWORDS | glycoprotein                           | 131 | 27.7542373 | 1.04E-06   | F2RL2, MPZL | 439 | 3600 | 17854 | 1.47992534 | 3.95E-04   | 6.58E-05   | 0.00143865 |
| UP_SEQ_FEATURE  | glycosylation site:N-linked (GlcNAc..) | 126 | 26.6949153 | 5.67E-05   | F2RL2, MPZL | 425 | 3444 | 16021 | 1.37913917 | 0.06617039 | 0.01696969 | 0.09172203 |
| SP_PIR_KEYWORDS | membrane                               | 171 | 36.2288136 | 2.01E-04   | F2RL2, MPZL | 439 | 5507 | 17854 | 1.2628508  | 0.0736287  | 0.00761884 | 0.27823969 |
| UP_SEQ_FEATURE  | topological domain:Extracellular       | 81  | 17.1610169 | 0.00124129 | F2RL2, MPZL | 425 | 2174 | 16021 | 1.40451431 | 0.7766832  | 0.19278584 | 1.98939395 |
| UP_SEQ_FEATURE  | topological domain:Cytoplasmic         | 88  | 18.6440678 | 0.04883971 | F2RL2, MPZL | 425 | 2780 | 16021 | 1.19326957 | 1          | 0.94375212 | 55.5184178 |
| UP_SEQ_FEATURE  | transmembrane region                   | 121 | 25.6355932 | 0.11578228 | F2RL2, MPZL | 425 | 4113 | 16021 | 1.10898929 | 1          | 0.97559807 | 86.3411386 |
| SP_PIR_KEYWORDS | transmembrane                          | 131 | 27.7542373 | 0.45394499 | F2RL2, MPZL | 439 | 5237 | 17854 | 1.01732503 | 1          | 0.92006345 | 99.9769684 |
| SP_PIR_KEYWORDS | receptor                               | 56  | 11.8644068 | 0.79752959 | F2RL2, GPR8 | 439 | 2465 | 17854 | 0.92393648 | 1          | 0.9933682  | 100        |
| GOTERM_CC_FAT   | GO:0031224~intrinsic to membrane       | 146 | 30.9322034 | 0.89317723 | F2RL2, MPZL | 330 | 5914 | 12504 | 0.93541981 | 1          | 0.99852545 | 100        |
| GOTERM_CC_FAT   | GO:0016021~integral to membrane        | 136 | 28.8135593 | 0.96135597 | F2RL2, MPZL | 330 | 5709 | 12504 | 0.90263858 | 1          | 0.99982567 | 100        |

|                       |  |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 28 | Enrichment Score: 1.9423900004454913               |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0009620~response to fungus                      | 7     | 1.48305085 | 2.30E-06   | HAMP2, MYI  | 341        | 17       | 13588     | 16.4077971   | 0.00442444 | 3.69E-04   | 0.00394091 |
| GOTERM_BP_FAT         | GO:0043901~negative regulation of multi-organism p | 3     | 0.63559322 | 0.01206292 | MYD88, TLR: | 341        | 7        | 13588     | 17.0775031   | 1          | 0.21610783 | 18.7583931 |
| GOTERM_BP_FAT         | GO:0043903~regulation of symbiosis, encompassing r | 3     | 0.63559322 | 0.01206292 | MYD88, TLR: | 341        | 7        | 13588     | 17.0775031   | 1          | 0.21610783 | 18.7583931 |
| GOTERM_BP_FAT         | GO:0043900~regulation of multi-organism process    | 3     | 0.63559322 | 0.0405912  | MYD88, TLR: | 341        | 13       | 13588     | 9.19557861   | 1          | 0.41681699 | 50.8019333 |
| GOTERM_BP_FAT         | GO:0045926~negative regulation of growth           | 4     | 0.84745763 | 0.26215908 | MYD88, TLR: | 341        | 71       | 13588     | 2.24492999   | 1          | 0.87370095 | 99.4506485 |
| GOTERM_BP_FAT         | GO:0040008~regulation of growth                    | 7     | 1.48305085 | 0.62171955 | OSM, MYD8:  | 341        | 256      | 13588     | 1.08958028   | 1          | 0.99303124 | 99.9999941 |

|                       |   |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 29 | Enrichment Score: 1.9260943112703237                |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0002252~immune effector process                  | 16    | 3.38983051 | 5.78E-07   | PTPN6, ADO  | 341        | 126      | 13588     | 5.06000093   | 0.00111259 | 1.01E-04   | 9.89E-04   |
| GOTERM_BP_FAT         | GO:0002443~leukocyte mediated immunity              | 11    | 2.33050847 | 7.42E-05   | PTPN6, SLC1 | 341        | 89       | 13588     | 4.92497282   | 0.13322614 | 0.00570276 | 0.12699166 |
| GOTERM_BP_FAT         | GO:0051050~positive regulation of transport         | 10    | 2.11864407 | 0.00593626 | FCER1A, SLC | 341        | 132      | 13588     | 3.01875056   | 0.99998953 | 0.14355361 | 9.68952943 |
| GOTERM_BP_FAT         | GO:0006909~phagocytosis                             | 6     | 1.27118644 | 0.00737161 | SLC11A1, CE | 341        | 49       | 13588     | 4.87928661   | 0.99999935 | 0.16316551 | 11.8958977 |
| GOTERM_BP_FAT         | GO:0048002~antigen processing and presentation of   | 5     | 1.05932203 | 0.01094083 | SLC11A1, FC | 341        | 35       | 13588     | 5.69250105   | 1          | 0.20771728 | 17.1643695 |
| GOTERM_BP_FAT         | GO:0002449~lymphocyte mediated immunity             | 7     | 1.48305085 | 0.01182864 | PTPN6, SLC1 | 341        | 76       | 13588     | 3.67016515   | 1          | 0.21636038 | 18.4279822 |
| GOTERM_BP_FAT         | GO:0002822~regulation of adaptive immune response   | 6     | 1.27118644 | 0.01282194 | FCER1A, PTP | 341        | 56       | 13588     | 4.26937579   | 1          | 0.22401317 | 19.820224  |
| GOTERM_BP_FAT         | GO:0002819~regulation of adaptive immune response   | 6     | 1.27118644 | 0.01282194 | FCER1A, PTP | 341        | 56       | 13588     | 4.26937579   | 1          | 0.22401317 | 19.820224  |
| GOTERM_BP_FAT         | GO:0050727~regulation of inflammatory response      | 6     | 1.27118644 | 0.01377491 | FCER1A, SBN | 341        | 57       | 13588     | 4.19447446   | 1          | 0.23241337 | 21.1348906 |
| GOTERM_BP_FAT         | GO:0060627~regulation of vesicle-mediated transport | 7     | 1.48305085 | 0.01768234 | FCER1A, SLC | 341        | 83       | 13588     | 3.36063315   | 1          | 0.27038438 | 26.3160873 |
| GOTERM_BP_FAT         | GO:0002250~adaptive immune response                 | 7     | 1.48305085 | 0.01865552 | SLC11A1, M^ | 341        | 84       | 13588     | 3.32062561   | 1          | 0.27874023 | 27.5557113 |
| GOTERM_BP_FAT         | GO:0002460~adaptive immune response based on so     | 7     | 1.48305085 | 0.01865552 | SLC11A1, M^ | 341        | 84       | 13588     | 3.32062561   | 1          | 0.27874023 | 27.5557113 |
| GOTERM_BP_FAT         | GO:0050766~positive regulation of phagocytosis      | 4     | 0.84745763 | 0.01897831 | SLC11A1, FC | 341        | 23       | 13588     | 6.93000128   | 1          | 0.27861322 | 27.9625212 |
| GOTERM_BP_FAT         | GO:0050764~regulation of phagocytosis               | 4     | 0.84745763 | 0.02376182 | SLC11A1, FC | 341        | 25       | 13588     | 6.37560117   | 1          | 0.31804493 | 33.7446345 |
| GOTERM_BP_FAT         | GO:0045807~positive regulation of endocytosis       | 4     | 0.84745763 | 0.0525045  | SLC11A1, FC | 341        | 34       | 13588     | 4.68794204   | 1          | 0.46716648 | 60.2754345 |
| GOTERM_BP_FAT         | GO:0019882~antigen processing and presentation      | 6     | 1.27118644 | 0.06694784 | SLC11A1, FC | 341        | 87       | 13588     | 2.74810395   | 1          | 0.52752882 | 69.4603384 |
| GOTERM_BP_FAT         | GO:0051130~positive regulation of cellular componen | 7     | 1.48305085 | 0.08582241 | WNT2, SLC1: | 341        | 122      | 13588     | 2.28633239   | 1          | 0.58780573 | 78.4751434 |
| GOTERM_BP_FAT         | GO:0030100~regulation of endocytosis                | 4     | 0.84745763 | 0.1407615  | SLC11A1, FC | 341        | 52       | 13588     | 3.06519287   | 1          | 0.71006475 | 92.5494067 |
| GOTERM_BP_FAT         | GO:0016064~immunoglobulin mediated immune resp      | 4     | 0.84745763 | 0.20888341 | MYD88, FCG  | 341        | 63       | 13588     | 2.53000047   | 1          | 0.81902518 | 98.1881165 |
| GOTERM_BP_FAT         | GO:0019724~B cell mediated immunity                 | 4     | 0.84745763 | 0.22198766 | MYD88, FCG  | 341        | 65       | 13588     | 2.4521543    | 1          | 0.8320269  | 98.6386817 |

|                       |  |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 30 | Enrichment Score: 1.917343165259976                  |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0001819~positive regulation of cytokine productic | 8     | 1.69491525 | 8.71E-04   | SLC11A1, M^ | 341        | 62       | 13588     | 5.14161385   | 0.81332723 | 0.03828056 | 1.48062212 |
| GOTERM_BP_FAT         | GO:0032729~positive regulation of interferon-gamma   | 4     | 0.84745763 | 0.00813704 | SLC11A1, H2 | 341        | 17       | 13588     | 9.37588408   | 0.99999985 | 0.17270261 | 13.0516344 |
| GOTERM_BP_FAT         | GO:0032649~regulation of interferon-gamma product    | 4     | 0.84745763 | 0.04512057 | SLC11A1, H2 | 341        | 32       | 13588     | 4.98093842   | 1          | 0.43656427 | 54.6299992 |
| GOTERM_BP_FAT         | GO:0019882~antigen processing and presentation       | 6     | 1.27118644 | 0.06694784 | SLC11A1, FC | 341        | 87       | 13588     | 2.74810395   | 1          | 0.52752882 | 69.4603384 |

|                       |   |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 31 | Enrichment Score: 1.8604289577141517                |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| PIR_SUPERFAMILY       | PIRSF001980:Fc gamma receptor III                   | 4     | 0.84745763 | 9.68E-05   | FCER1A, FCG | 239        | 4        | 8136      | 34.041841    | 0.02635439 | 0.02635439 | 0.12758423 |
| GOTERM_BP_FAT         | GO:0002697~regulation of immune effector process    | 9     | 1.90677966 | 0.00159782 | FCER1A, PTP | 341        | 88       | 13588     | 4.07531325   | 0.95403481 | 0.05750841 | 2.7001418  |
| GOTERM_BP_FAT         | GO:0002703~regulation of leukocyte mediated immur   | 8     | 1.69491525 | 0.00179105 | FCER1A, PTP | 341        | 70       | 13588     | 4.55400084   | 0.96833829 | 0.06193676 | 3.02197125 |
| GOTERM_BP_FAT         | GO:0032796~regulation of response to external stimu | 9     | 1.90677966 | 0.00428359 | FCER1A, CLN | 341        | 103      | 13588     | 3.48182103   | 0.99974338 | 0.11448599 | 7.08470504 |
| GOTERM_BP_FAT         | GO:0002699~positive regulation of immune effector p | 6     | 1.27118644 | 0.00563082 | FCER1A, CD: | 341        | 46       | 13588     | 5.19750096   | 0.99998109 | 0.14019545 | 9.21336234 |

|                 |   |   |            |            |             |     |    |       |            |            |            |            |
|-----------------|---|---|------------|------------|-------------|-----|----|-------|------------|------------|------------|------------|
| SP_PIR_KEYWORDS | immunoglobulin receptor                             | 3 | 0.63559322 | 0.01162057 | FCER1A, FCG | 439 | 7  | 17854 | 17.4298731 | 0.98822379 | 0.146689   | 14.9402425 |
| GOTERM_BP_FAT   | GO:0002822~regulation of adaptive immune response   | 6 | 1.27118644 | 0.01282194 | FCER1A, PTP | 341 | 56 | 13588 | 4.26937579 | 1          | 0.22401317 | 19.820224  |
| GOTERM_BP_FAT   | GO:0002819~regulation of adaptive immune response   | 6 | 1.27118644 | 0.01282194 | FCER1A, PTP | 341 | 56 | 13588 | 4.26937579 | 1          | 0.22401317 | 19.820224  |
| GOTERM_BP_FAT   | GO:0050727~regulation of inflammatory response      | 6 | 1.27118644 | 0.01377491 | FCER1A, SBN | 341 | 57 | 13588 | 4.19447446 | 1          | 0.23241337 | 21.1348906 |
| GOTERM_BP_FAT   | GO:0031349~positive regulation of defense response  | 6 | 1.27118644 | 0.01377491 | FCER1A, ADC | 341 | 57 | 13588 | 4.19447446 | 1          | 0.23241337 | 21.1348906 |
| GOTERM_BP_FAT   | GO:0001810~regulation of type I hypersensitivity    | 3 | 0.63559322 | 0.01581989 | FCER1A, FCG | 341 | 8  | 13588 | 14.9428152 | 1          | 0.25154356 | 23.8878257 |
| GOTERM_BP_FAT   | GO:0060627~regulation of vesicle-mediated transport | 7 | 1.48305085 | 0.01768234 | FCER1A, SLC | 341 | 83 | 13588 | 3.36063315 | 1          | 0.27038438 | 26.3160873 |
| GOTERM_BP_FAT   | GO:0002706~regulation of lymphocyte mediated imm    | 6 | 1.27118644 | 0.02314652 | FCER1A, PTP | 341 | 65 | 13588 | 3.67823145 | 1          | 0.31330744 | 33.0261728 |
| GOTERM_MF_FAT   | GO:0019865~immunoglobulin binding                   | 3 | 0.63559322 | 0.0304878  | FCER1A, FCG | 339 | 11 | 13288 | 10.6902655 | 0.99999989 | 0.57006789 | 36.1150044 |
| GOTERM_BP_FAT   | GO:0002712~regulation of B cell mediated immunity   | 4 | 0.84745763 | 0.03829586 | FCER1A, PTP | 341 | 30 | 13588 | 5.31300098 | 1          | 0.4046887  | 48.7478159 |
| GOTERM_BP_FAT   | GO:0002889~regulation of immunoglobulin mediated    | 4 | 0.84745763 | 0.03829586 | FCER1A, PTP | 341 | 30 | 13588 | 5.31300098 | 1          | 0.4046887  | 48.7478159 |
| GOTERM_BP_FAT   | GO:0002864~regulation of acute inflammatory respon  | 3 | 0.63559322 | 0.0405912  | FCER1A, FCG | 341 | 13 | 13588 | 9.19557861 | 1          | 0.41681699 | 50.8019333 |
| GOTERM_BP_FAT   | GO:0002883~regulation of hypersensitivity           | 3 | 0.63559322 | 0.0405912  | FCER1A, FCG | 341 | 13 | 13588 | 9.19557861 | 1          | 0.41681699 | 50.8019333 |
| GOTERM_BP_FAT   | GO:0002673~regulation of acute inflammatory respon  | 3 | 0.63559322 | 0.07340235 | FCER1A, FCG | 341 | 18 | 13588 | 6.64125122 | 1          | 0.55172616 | 72.8818797 |
| GOTERM_BP_FAT   | GO:0002861~regulation of inflammatory response to   | 3 | 0.63559322 | 0.07340235 | FCER1A, FCG | 341 | 18 | 13588 | 6.64125122 | 1          | 0.55172616 | 72.8818797 |
| GOTERM_MF_FAT   | GO:0032403~protein complex binding                  | 5 | 1.05932203 | 0.13709211 | FCER1A, DOI | 339 | 78 | 13288 | 2.51266924 | 1          | 0.79631944 | 88.1620473 |

|                       |   |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 32 | Enrichment Score: 1.8030766048576599                    |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_MF_FAT         | GO:0004869~cysteine-type endopeptidase inhibitor ac     | 7     | 1.48305085 | 4.16E-04   | NGP, TNFSF:  | 339        | 39       | 13288     | 7.03547387   | 0.19388634 | 0.05245669 | 0.60034522 |
| INTERPRO              | IPR000010:Proteinase inhibitor I25, cystatin            | 5     | 1.05932203 | 0.00416219 | NGP, STFA1,  | 425        | 28       | 17763     | 7.46344538   | 0.96503411 | 0.18908042 | 6.2055976  |
| SMART                 | SM00043:CY  | 5     | 1.05932203 | 0.00717525 | NGP, STFA1,  | 256        | 28       | 9131      | 6.36928013   | 0.72643108 | 0.16903838 | 8.48796391 |
| GOTERM_MF_FAT         | GO:0030414~peptidase inhibitor activity                 | 11    | 2.33050847 | 0.01462932 | NGP, SERPIN  | 339        | 176      | 13288     | 2.44985251   | 0.99951626 | 0.50042475 | 19.2069848 |
| SP_PIR_KEYWORDS       | thiol protease inhibitor                                | 4     | 0.84745763 | 0.01597061 | BIRC5, STFA: | 439        | 22       | 17854     | 7.39449161   | 0.99779674 | 0.17401756 | 19.9789354 |
| UP_SEQ_FEATURE        | site:Reactive site                                      | 3     | 0.63559322 | 0.01760345 | STFA1, BC10  | 425        | 8        | 16021     | 14.1361765   | 1          | 0.78372101 | 24.9737321 |
| GOTERM_MF_FAT         | GO:0004857~enzyme inhibitor activity                    | 13    | 2.75423729 | 0.02130371 | NGP, SERPIN  | 339        | 243      | 13288     | 2.09699309   | 0.99998569 | 0.50200253 | 26.7754169 |
| UP_SEQ_FEATURE        | short sequence motif:Secondary area of contact          | 3     | 0.63559322 | 0.02224079 | STFA1, BC10  | 425        | 9        | 16021     | 12.5654902   | 1          | 0.83632026 | 30.5026546 |
| PIR_SUPERFAMILY       | PIRSF001638:cystatin                                    | 3     | 0.63559322 | 0.02678616 | STFA1, BC10  | 239        | 9        | 8136      | 11.3472803   | 0.99944348 | 0.77659294 | 30.1073049 |
| INTERPRO              | IPR001713:Proteinase inhibitor I25A, stefin A           | 3     | 0.63559322 | 0.0271114  | STFA1, BC10  | 425        | 11       | 17763     | 11.3987166   | 1          | 0.54580654 | 34.4385838 |
| SP_PIR_KEYWORDS       | protease inhibitor                                      | 7     | 1.48305085 | 0.05184863 | SERPINB1A,   | 439        | 109      | 17854     | 2.61181585   | 1          | 0.38227095 | 52.1483837 |
| GOTERM_MF_FAT         | GO:0004866~endopeptidase inhibitor activity             | 9     | 1.90677966 | 0.05351708 | NGP, SERPIN  | 339        | 161      | 13288     | 2.19117243   | 1          | 0.65188777 | 54.8867749 |
| INTERPRO              | IPR018073:Proteinase inhibitor I25, cystatin, conserved | 3     | 0.63559322 | 0.07442441 | STFA1, BC10  | 425        | 19       | 17763     | 6.59925697   | 1          | 0.79696622 | 69.5151861 |

|                       |   |       |            |            |               |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 33 | Enrichment Score: 1.765543439464521                     |       |            |            |               |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS       | inflammatory response                                   | 13    | 2.75423729 | 4.11E-07   | NFKBID, TLR:  | 439        | 78       | 17854     | 6.77828398   | 1.56E-04   | 3.12E-05   | 5.68E-04   |
| GOTERM_BP_FAT         | GO:0045087~innate immune response                       | 15    | 3.1779661  | 4.29E-07   | TNFAIP8L2, I  | 341        | 107      | 13588     | 5.58609916   | 8.27E-04   | 8.27E-05   | 7.35E-04   |
| INTERPRO              | IPR000157:Toll-Interleukin receptor                     | 7     | 1.48305085 | 1.67E-05   | IL18RAP, MY   | 425        | 24       | 17763     | 12.1902941   | 0.01332307 | 0.01332307 | 0.02562098 |
| UP_SEQ_FEATURE        | domain:TIR  | 7     | 1.48305085 | 3.83E-05   | IL18RAP, MY   | 425        | 25       | 16021     | 10.5550118   | 0.045186   | 0.01529474 | 0.06195824 |
| SMART                 | SM00255:TIR   | 7     | 1.48305085 | 3.94E-05   | IL18RAP, MY   | 256        | 24       | 9131      | 10.4031576   | 0.00707186 | 0.00707186 | 0.04855322 |
| KEGG_PATHWAY          | mmu04620:Toll-like receptor signaling pathway           | 12    | 2.54237288 | 2.10E-04   | PIK3CG, IRAI  | 178        | 99       | 5738      | 3.90738849   | 0.0266971  | 0.00674215 | 0.24365063 |
| INTERPRO              | IPR004075:Interleukin-1 receptor, type I/Toll precursor | 4     | 0.84745763 | 0.00253036 | IL18RAP, TLR  | 425        | 12       | 17763     | 13.9317647   | 0.8695788  | 0.15612326 | 3.81683016 |
| INTERPRO              | IPR017241:Toll-like receptor                            | 3     | 0.63559322 | 0.00330365 | TLR1, TLR2, 1 | 425        | 4        | 17763     | 31.3464706   | 0.93008918 | 0.17307246 | 4.95582842 |
| PIR_SUPERFAMILY       | PIRSF037595:Toll-like_receptor                          | 3     | 0.63559322 | 0.00491771 | TLR1, TLR2, 1 | 239        | 4        | 8136      | 25.5313808   | 0.74350251 | 0.49354419 | 6.29694671 |
| GOTERM_BP_FAT         | GO:0032675~regulation of interleukin-6 production       | 5     | 1.05932203 | 0.0079666  | MYD88, TLR:   | 341        | 32       | 13588     | 6.22617302   | 0.99999998 | 0.17127535 | 12.7955233 |
| UP_SEQ_FEATURE        | repeat:LRR 11   | 7     | 1.48305085 | 0.02918798 | IGSF10, LRR   | 425        | 88       | 16021     | 2.99858289   | 1          | 0.87793388 | 38.0748001 |
| INTERPRO              | IPR003591:Leucine-rich repeat, typical subtype          | 8     | 1.69491525 | 0.03518806 | IGSF10, OGN   | 425        | 129      | 17763     | 2.59195622   | 1          | 0.6050764  | 42.3183163 |
| UP_SEQ_FEATURE        | repeat:LRR 9  | 8     | 1.69491525 | 0.04343875 | IGSF10, LRR   | 425        | 122      | 16021     | 2.47189971   | 1          | 0.94910385 | 51.2511898 |
| INTERPRO              | IPR001611:Leucine-rich repeat                           | 10    | 2.11864407 | 0.05372443 | IGSF10, OGN   | 425        | 202      | 17763     | 2.06907397   | 1          | 0.70866433 | 57.1817915 |
| UP_SEQ_FEATURE        | repeat:LRR 10   | 7     | 1.48305085 | 0.05574001 | IGSF10, LRR   | 425        | 103      | 16021     | 2.56189606   | 1          | 0.95700341 | 60.4613175 |
| UP_SEQ_FEATURE        | repeat:LRR 7  | 9     | 1.90677966 | 0.05745452 | IGSF10, OGN   | 425        | 157      | 16021     | 2.16094417   | 1          | 0.95518429 | 61.606911  |
| UP_SEQ_FEATURE        | repeat:LRR 12   | 6     | 1.27118644 | 0.0582296  | IGSF10, LRR   | 425        | 79       | 16021     | 2.86302308   | 1          | 0.95106129 | 62.1145149 |
| UP_SEQ_FEATURE        | repeat:LRR 8  | 8     | 1.69491525 | 0.06343199 | IGSF10, LRR   | 425        | 133      | 16021     | 2.26745688   | 1          | 0.94658021 | 65.3620478 |
| SMART                 | SM00369:LRR_TYP   | 8     | 1.69491525 | 0.06927313 | IGSF10, OGN   | 256        | 129      | 9131      | 2.21196705   | 0.99999756 | 0.53239123 | 58.6982368 |
| UP_SEQ_FEATURE        | repeat:LRR 13   | 5     | 1.05932203 | 0.09321328 | IGSF10, LRR   | 425        | 65       | 16021     | 2.89972851   | 1          | 0.9623953  | 79.464651  |
| UP_SEQ_FEATURE        | repeat:LRR 6  | 9     | 1.90677966 | 0.11867561 | IGSF10, OGN   | 425        | 185      | 16021     | 1.83388235   | 1          | 0.97349626 | 87.0465385 |
| UP_SEQ_FEATURE        | repeat:LRR 4  | 10    | 2.11864407 | 0.13317527 | IGSF10, OGN   | 425        | 221      | 16021     | 1.70572265   | 1          | 0.9801691  | 90.095588  |

|                 |   |    |            |            |              |     |     |       |            |   |            |            |
|-----------------|---|----|------------|------------|--------------|-----|-----|-------|------------|---|------------|------------|
| INTERPRO        | IPR000483:Cysteine-rich flanking region, C-terminal     | 5  | 1.05932203 | 0.13684133 | IGSF10, LRG: | 425 | 83  | 17763 | 2.5177888  | 1 | 0.90171489 | 89.5685133 |
| SP_PIR_KEYWORDS | leucine-rich repeat                                     | 11 | 2.33050847 | 0.14080581 | IGSF10, OGN  | 439 | 275 | 17854 | 1.62678815 | 1 | 0.62372662 | 87.7660628 |
| UP_SEQ_FEATURE  | repeat:LRR 5  | 9  | 1.90677966 | 0.17124098 | IGSF10, OGN  | 425 | 203 | 16021 | 1.6712721  | 1 | 0.99111186 | 95.2103768 |
| UP_SEQ_FEATURE  | repeat:LRR 14   | 4  | 0.84745763 | 0.17801041 | LRRC33, TLR: | 425 | 55  | 16021 | 2.7415615  | 1 | 0.99033572 | 95.805553  |
| SMART           | SM00082:LRRCT   | 5  | 1.05932203 | 0.20163265 | IGSF10, LRG: | 256 | 83  | 9131  | 2.14867282 | 1 | 0.86822746 | 93.7571306 |
| UP_SEQ_FEATURE  | repeat:LRR 3  | 10 | 2.11864407 | 0.20310565 | IGSF10, OGN  | 425 | 245 | 16021 | 1.53863145 | 1 | 0.99314204 | 97.4600592 |
| UP_SEQ_FEATURE  | repeat:LRR 1  | 10 | 2.11864407 | 0.27347941 | IGSF10, OGN  | 425 | 266 | 16021 | 1.41716055 | 1 | 0.99734857 | 99.4308643 |
| UP_SEQ_FEATURE  | repeat:LRR 2  | 10 | 2.11864407 | 0.27347941 | IGSF10, OGN  | 425 | 266 | 16021 | 1.41716055 | 1 | 0.99734857 | 99.4308643 |
| UP_SEQ_FEATURE  | repeat:LRR 16   | 3  | 0.63559322 | 0.29593113 | LRRC33, TLR: | 425 | 41  | 16021 | 2.75827834 | 1 | 0.99784042 | 99.6575009 |
| UP_SEQ_FEATURE  | repeat:LRR 15   | 3  | 0.63559322 | 0.364047   | LRRC33, TLR: | 425 | 48  | 16021 | 2.35602941 | 1 | 0.99937813 | 99.933971  |
| INTERPRO        | IPR000372:Leucine-rich repeat, cysteine-rich flanking r | 4  | 0.84745763 | 0.38345849 | IGSF10, OGN  | 425 | 93  | 17763 | 1.79764706 | 1 | 0.99698319 | 99.9405979 |
| SMART           | SM00013:LRNT  | 4  | 0.84745763 | 0.4837332  | IGSF10, OGN  | 256 | 93  | 9131  | 1.53410618 | 1 | 0.98781493 | 99.9709375 |
| SP_PIR_KEYWORDS | cytoplasmic vesicle                                     | 7  | 1.48305085 | 0.50632386 | OVGP1, COR   | 439 | 232 | 17854 | 1.22710313 | 1 | 0.93524009 | 99.9942978 |

|                       |  |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 34 | Enrichment Score: 1.762631969127945              |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| BIOCARTA              | m_monocytePathway:Monocyte and its Surface Molec | 5     | 1.05932203 | 0.00104951 | ITGAL, SELP, | 55         | 11       | 1171      | 9.67768595   | 0.09778815 | 0.09778815 | 1.15434873 |
| GOTERM_BP_FAT         | GO:0007159~leukocyte adhesion                    | 4     | 0.84745763 | 0.00460428 | ITGAL, SELP, | 341        | 14       | 13588     | 11.3850021   | 0.99986201 | 0.12086439 | 7.59561401 |
| GOTERM_CC_FAT         | GO:0009897~external side of plasma membrane      | 13    | 2.75423729 | 0.00842936 | FCER1A, ITG, | 330        | 206      | 12504     | 2.39117387   | 0.90167072 | 0.16340731 | 10.5557142 |
| GOTERM_BP_FAT         | GO:0045123~cellular extravasation                | 3     | 0.63559322 | 0.00876047 | SELP, SELPLG | 341        | 6        | 13588     | 19.9237537   | 0.99999996 | 0.1769951  | 13.9823894 |
| KEGG_PATHWAY          | mmu04514:Cell adhesion molecules (CAMs)          | 8     | 1.69491525 | 0.19713639 | ALCAM, ITG,  | 178        | 154      | 5738      | 1.67459507   | 1          | 0.6497327  | 92.219025  |
| GOTERM_BP_FAT         | GO:0016337~cell-cell adhesion                    | 8     | 1.69491525 | 0.3775479  | ITGAL, SELP, | 341        | 236      | 13588     | 1.35076296   | 1          | 0.93924488 | 99.9701045 |

|                       |  |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 35 | Enrichment Score: 1.754286323965046                      |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| INTERPRO              | IPR006117:2'-5'-oligoadenylate synthetase, conserved s   | 4     | 0.84745763 | 6.92E-04   | OASL1, OAS: | 425        | 8        | 17763     | 20.8976471   | 0.42664914 | 0.05993512 | 1.05708046 |
| INTERPRO              | IPR018952:2'-5'-oligoadenylate synthetase 1, domain ;    | 4     | 0.84745763 | 0.00323161 | OASL1, OAS: | 425        | 13       | 17763     | 12.8600905   | 0.92590579 | 0.18142151 | 4.85024222 |
| INTERPRO              | IPR006116:2'-5'-oligoadenylate synthetase, ubiquitin-lik | 4     | 0.84745763 | 0.0040407  | OASL1, OAS: | 425        | 14       | 17763     | 11.9415126   | 0.96143077 | 0.19508615 | 6.02967962 |
| INTERPRO              | IPR002934:Nucleotidyltransferase                         | 3     | 0.63559322 | 0.03202761 | OAS3, OAS2, | 425        | 12       | 17763     | 10.4488235   | 1          | 0.58204682 | 39.3467731 |
| GOTERM_MF_FAT         | GO:0016779~nucleotidyltransferase activity               | 7     | 1.48305085 | 0.10525671 | POLR2G, LO  | 339        | 127      | 13288     | 2.16049985   | 1          | 0.76313824 | 80.0023297 |
| GOTERM_MF_FAT         | GO:0003723~RNA binding                                   | 11    | 2.33050847 | 0.97895748 | POLR2G, MC  | 339        | 672      | 13288     | 0.64162804   | 1          | 0.99999999 | 100        |

|                       |  |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 36 | Enrichment Score: 1.7219103210495543               |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| KEGG_PATHWAY          | mmu04670:Leukocyte transendothelial migration      | 17    | 3.60169492 | 5.74E-07   | PIK3CG, ITG, | 178        | 119      | 5738      | 4.60513644   | 7.40E-05   | 7.40E-05   | 6.67E-04   |
| KEGG_PATHWAY          | mmu04650:Natural killer cell mediated cytotoxicity | 17    | 3.60169492 | 8.10E-07   | PIK3CG, BLD, | 178        | 122      | 5738      | 4.49189538   | 1.04E-04   | 5.22E-05   | 9.42E-04   |
| KEGG_PATHWAY          | mmu04666:Fc gamma R-mediated phagocytosis          | 12    | 2.54237288 | 1.91E-04   | PIK3CG, ARP  | 178        | 98       | 5738      | 3.9472598    | 0.0244028  | 0.00820135 | 0.22247446 |
| KEGG_PATHWAY          | mmu04662:B cell receptor signaling pathway         | 10    | 2.11864407 | 7.26E-04   | PIK3CG, PTPI | 178        | 80       | 5738      | 4.02949438   | 0.08940012 | 0.01855602 | 0.84072495 |
| KEGG_PATHWAY          | mmu04664:Fc epsilon RI signaling pathway           | 10    | 2.11864407 | 8.70E-04   | FCER1A, PIK: | 178        | 82       | 5738      | 3.93121403   | 0.10619168 | 0.0185367  | 1.00696591 |
| KEGG_PATHWAY          | mmu05223:Non-small cell lung cancer                | 5     | 1.05932203 | 0.08413343 | PIK3CG, RAC  | 178        | 54       | 5738      | 2.98481065   | 0.99998808 | 0.48669702 | 64.0144103 |
| KEGG_PATHWAY          | mmu04370:VEGF signaling pathway                    | 6     | 1.27118644 | 0.08453316 | PIK3CG, RAC  | 178        | 76       | 5738      | 2.54494382   | 0.99998873 | 0.46898667 | 64.1966376 |
| KEGG_PATHWAY          | mmu04070:Phosphatidylinositol signaling system     | 5     | 1.05932203 | 0.20019853 | PIK3CG, DGK  | 178        | 75       | 5738      | 2.14906367   | 1          | 0.6427065  | 92.5572403 |
| KEGG_PATHWAY          | mmu00562:Inositol phosphate metabolism             | 4     | 0.84745763 | 0.23188943 | PIK3CG, ALD  | 178        | 54       | 5738      | 2.38784852   | 1          | 0.69073327 | 95.3490849 |
| KEGG_PATHWAY          | mmu04510:Focal adhesion                            | 9     | 1.90677966 | 0.26666331 | PARVG, PIK3  | 178        | 198      | 5738      | 1.46527068   | 1          | 0.72490139 | 97.2863766 |
| KEGG_PATHWAY          | mmu04914:Progesterone-mediated oocyte maturation   | 5     | 1.05932203 | 0.26678707 | CCNB1, PIK3  | 178        | 85       | 5738      | 1.89623265   | 1          | 0.71377412 | 97.2916977 |
| KEGG_PATHWAY          | mmu04012:ErbB signaling pathway                    | 5     | 1.05932203 | 0.28059749 | PIK3CG, EIF4 | 178        | 87       | 5738      | 1.85026411   | 1          | 0.72401191 | 97.829004  |
| KEGG_PATHWAY          | mmu05214:Glioma                                    | 4     | 0.84745763 | 0.31611965 | PIK3CG, PLC  | 178        | 64       | 5738      | 2.01474719   | 1          | 0.73413544 | 98.7952257 |
| KEGG_PATHWAY          | mmu04722:Neurotrophin signaling pathway            | 6     | 1.27118644 | 0.37309752 | PIK3CG, IRA  | 178        | 130      | 5738      | 1.48781331   | 1          | 0.76989719 | 99.5619309 |
| KEGG_PATHWAY          | mmu04960:Aldosterone-regulated sodium reabsorptio  | 3     | 0.63559322 | 0.37358931 | PIK3CG, PIK3 | 178        | 42       | 5738      | 2.30256822   | 1          | 0.76227906 | 99.5659108 |
| KEGG_PATHWAY          | mmu05210:Colorectal cancer                         | 4     | 0.84745763 | 0.49847296 | PIK3CG, RAC  | 178        | 86       | 5738      | 1.49934675   | 1          | 0.83745298 | 99.9672975 |
| KEGG_PATHWAY          | mmu05212:Pancreatic cancer                         | 3     | 0.63559322 | 0.65695672 | PIK3CG, RAC  | 178        | 72       | 5738      | 1.34316479   | 1          | 0.90360201 | 99.9996052 |

|                       |  |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 37 | Enrichment Score: 1.7087545531605406                 |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0001819~positive regulation of cytokine productio | 8     | 1.69491525 | 8.71E-04   | SLC11A1, M  | 341        | 62       | 13588     | 5.14161385   | 0.81332723 | 0.03828056 | 1.48062212 |
| GOTERM_BP_FAT         | GO:0032675~regulation of interleukin-6 production    | 5     | 1.05932203 | 0.0079666  | MYD88, TLR: | 341        | 32       | 13588     | 6.22617302   | 0.99999998 | 0.17127535 | 12.7955233 |
| GOTERM_BP_FAT         | GO:0032755~positive regulation of interleukin-6 prod | 3     | 0.63559322 | 0.07340235 | MYD88, TLR: | 341        | 18       | 13588     | 6.64125122   | 1          | 0.55172616 | 72.8818797 |

BIOCARTA m\_nthiPathway:NfKb activation by Nontypeable Hemo 3 0.63559322 0.2870445 MYD88, TLR: 55 23 1171 2.7770751 1 0.99601875 97.6270125

Annotation Cluster 38 Enrichment Score: 1.66247420461649

| Category      | Term   | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0010627~regulation of protein kinase cascade        | 16    | 3.38983051 | 7.94E-06   | FCER1A, PTP | 341        | 155      | 13588     | 4.11329108   | 0.01516852 | 0.00101846 | 0.01358354 |
| GOTERM_BP_FAT | GO:0080135~regulation of cellular response to stress   | 10    | 2.11864407 | 1.02E-04   | FCER1A, CLN | 341        | 75       | 13588     | 5.31300098   | 0.17761374 | 0.00695942 | 0.17364169 |
| GOTERM_BP_FAT | GO:0046328~regulation of JNK cascade                   | 7     | 1.48305085 | 8.40E-04   | FCER1A, MYI | 341        | 45       | 13588     | 6.19850114   | 0.80164168 | 0.03778388 | 1.42744314 |
| GOTERM_BP_FAT | GO:0070302~regulation of stress-activated protein kin  | 7     | 1.48305085 | 9.45E-04   | FCER1A, MYI | 341        | 46       | 13588     | 6.06375112   | 0.8382758  | 0.03967724 | 1.60615991 |
| GOTERM_BP_FAT | GO:0043408~regulation of MAPKKK cascade                | 9     | 1.90677966 | 0.00227362 | OSM, FCER1  | 341        | 93       | 13588     | 3.85621039   | 0.98752441 | 0.07161129 | 3.82137674 |
| GOTERM_BP_FAT | GO:0001932~regulation of protein amino acid phospho    | 10    | 2.11864407 | 0.00335274 | OSM, FCER1  | 341        | 121      | 13588     | 3.29318242   | 0.99844803 | 0.09612674 | 5.58658778 |
| GOTERM_BP_FAT | GO:0043507~positive regulation of JUN kinase activity  | 4     | 0.84745763 | 0.00682605 | FCER1A, MDP | 341        | 16       | 13588     | 9.96187683   | 0.99999813 | 0.15559985 | 11.0633257 |
| GOTERM_BP_FAT | GO:0042325~regulation of phosphorylation               | 15    | 3.1779661  | 0.01445987 | FCER1A, PTP | 341        | 290      | 13588     | 2.06107797   | 1          | 0.2404504  | 22.0672568 |
| GOTERM_BP_FAT | GO:0043506~regulation of JUN kinase activity           | 4     | 0.84745763 | 0.01478498 | FCER1A, MD  | 341        | 21       | 13588     | 7.5900014    | 1          | 0.24107382 | 22.5061555 |
| GOTERM_BP_FAT | GO:0051174~regulation of phosphorus metabolic pro      | 15    | 3.1779661  | 0.01949427 | FCER1A, PTP | 341        | 301      | 13588     | 1.98575618   | 1          | 0.28086847 | 28.6083279 |
| GOTERM_BP_FAT | GO:0019220~regulation of phosphate metabolic pro       | 15    | 3.1779661  | 0.01949427 | FCER1A, PTP | 341        | 301      | 13588     | 1.98575618   | 1          | 0.28086847 | 28.6083279 |
| GOTERM_BP_FAT | GO:0031399~regulation of protein modification proce    | 10    | 2.11864407 | 0.02305072 | OSM, FCER1  | 341        | 165      | 13588     | 2.41500044   | 1          | 0.31438565 | 32.9136535 |
| GOTERM_BP_FAT | GO:0007243~protein kinase cascade                      | 12    | 2.54237288 | 0.03545687 | OSM, FCER1  | 341        | 236      | 13588     | 2.02614444   | 1          | 0.38928236 | 46.0954165 |
| GOTERM_BP_FAT | GO:0007257~activation of JUN kinase activity           | 3     | 0.63559322 | 0.0405912  | FCER1A, MD  | 341        | 13       | 13588     | 9.19557861   | 1          | 0.41681699 | 50.8019333 |
| GOTERM_BP_FAT | GO:0045859~regulation of protein kinase activity       | 10    | 2.11864407 | 0.0444007  | FCER1A, PTP | 341        | 186      | 13588     | 2.1423391    | 1          | 0.43334371 | 54.0409403 |
| GOTERM_BP_FAT | GO:0007254~JNK cascade                                 | 4     | 0.84745763 | 0.04512057 | FCER1A, MYI | 341        | 32       | 13588     | 4.98093842   | 1          | 0.43656427 | 54.6299992 |
| GOTERM_BP_FAT | GO:0032268~regulation of cellular protein metabolic p  | 13    | 2.75423729 | 0.04940545 | FCER1A, CLN | 341        | 280      | 13588     | 1.85006284   | 1          | 0.46078028 | 57.9917461 |
| GOTERM_BP_FAT | GO:0043549~regulation of kinase activity               | 10    | 2.11864407 | 0.05240837 | FCER1A, PTP | 341        | 192      | 13588     | 2.07539101   | 1          | 0.46857519 | 60.2063917 |
| GOTERM_BP_FAT | GO:0031098~stress-activated protein kinase signaling   | 4     | 0.84745763 | 0.05640109 | FCER1A, MYI | 341        | 35       | 13588     | 4.55400084   | 1          | 0.48398039 | 62.9811028 |
| GOTERM_BP_FAT | GO:0043405~regulation of MAP kinase activity           | 6     | 1.27118644 | 0.05933595 | FCER1A, PTP | 341        | 84       | 13588     | 2.84625052   | 1          | 0.49993203 | 64.9033644 |
| GOTERM_BP_FAT | GO:0051338~regulation of transferase activity          | 10    | 2.11864407 | 0.0628488  | FCER1A, PTP | 341        | 199      | 13588     | 2.0023873    | 1          | 0.51050839 | 67.0806242 |
| GOTERM_BP_FAT | GO:0044093~positive regulation of molecular functio    | 13    | 2.75423729 | 0.08355056 | FCER1A, HM  | 341        | 306      | 13588     | 1.69286796   | 1          | 0.57944816 | 77.5409231 |
| GOTERM_BP_FAT | GO:0045860~positive regulation of protein kinase acti  | 7     | 1.48305085 | 0.09109059 | FCER1A, SLC | 341        | 124      | 13588     | 2.24945606   | 1          | 0.60507142 | 80.5026402 |
| GOTERM_BP_FAT | GO:0033674~positive regulation of kinase activity      | 7     | 1.48305085 | 0.10791748 | FCER1A, SLC | 341        | 130      | 13588     | 2.14563501   | 1          | 0.64913241 | 85.8401911 |
| GOTERM_BP_FAT | GO:0051347~positive regulation of transferase activity | 7     | 1.48305085 | 0.12307705 | FCER1A, SLC | 341        | 135      | 13588     | 2.06616705   | 1          | 0.67186569 | 89.4405432 |
| GOTERM_BP_FAT | GO:0032147~activation of protein kinase activity       | 4     | 0.84745763 | 0.13499092 | SLC11A1, DC | 341        | 51       | 13588     | 3.12529469   | 1          | 0.69841699 | 91.6449243 |
| GOTERM_BP_FAT | GO:0043406~positive regulation of MAP kinase activit   | 4     | 0.84745763 | 0.18324882 | FCER1A, MD  | 341        | 59       | 13588     | 2.70152592   | 1          | 0.78452092 | 96.8725133 |
| GOTERM_BP_FAT | GO:0000165~MAPKKK cascade                              | 5     | 1.05932203 | 0.31916848 | FCER1A, SLC | 341        | 114      | 13588     | 1.74769769   | 1          | 0.90823194 | 99.8613072 |
| GOTERM_BP_FAT | GO:0000187~activation of MAPK activity                 | 3     | 0.63559322 | 0.35704099 | FCER1A, MD  | 341        | 50       | 13588     | 2.39085044   | 1          | 0.92935203 | 99.9479315 |
| GOTERM_BP_FAT | GO:0043085~positive regulation of catalytic activity   | 8     | 1.69491525 | 0.47904401 | FCER1A, SLC | 341        | 261      | 13588     | 1.22137954   | 1          | 0.97207222 | 99.9985798 |

Annotation Cluster 39 Enrichment Score: 1.616124082267183

| Category      | Term   | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0006739~NADP metabolic process                  | 5     | 1.05932203 | 3.16E-04   | TALDO1, NC  | 341        | 14       | 13588     | 14.2312526   | 0.45599006 | 0.01774617 | 0.53960495 |
| GOTERM_BP_FAT | GO:0043603~cellular amide metabolic process        | 6     | 1.27118644 | 0.00272645 | TALDO1, NC  | 341        | 39       | 13588     | 6.13038574   | 0.99479593 | 0.08390809 | 4.56585791 |
| GOTERM_BP_FAT | GO:0009820~alkaloid metabolic process              | 5     | 1.05932203 | 0.00275362 | TALDO1, NC  | 341        | 24       | 13588     | 8.30156403   | 0.99506194 | 0.08209169 | 4.61034933 |
| GOTERM_BP_FAT | GO:0046496~nicotinamide nucleotide metabolic proce | 5     | 1.05932203 | 0.00275362 | TALDO1, NC  | 341        | 24       | 13588     | 8.30156403   | 0.99506194 | 0.08209169 | 4.61034933 |
| GOTERM_BP_FAT | GO:0006769~nicotinamide metabolic process          | 5     | 1.05932203 | 0.00275362 | TALDO1, NC  | 341        | 24       | 13588     | 8.30156403   | 0.99506194 | 0.08209169 | 4.61034933 |
| GOTERM_BP_FAT | GO:0019362~pyridine nucleotide metabolic process   | 5     | 1.05932203 | 0.0049052  | TALDO1, NC  | 341        | 28       | 13588     | 7.11562631   | 0.99992292 | 0.12654186 | 8.07262953 |
| GOTERM_BP_FAT | GO:0019748~secondary metabolic process             | 7     | 1.48305085 | 0.00749538 | RDH12, ALD  | 341        | 69       | 13588     | 4.04250074   | 0.99999949 | 0.16380606 | 12.0837456 |
| GOTERM_BP_FAT | GO:0006733~oxidoreduction coenzyme metabolic pro   | 5     | 1.05932203 | 0.01455003 | TALDO1, NC  | 341        | 38       | 13588     | 5.24309307   | 1          | 0.23972121 | 22.1891997 |
| GOTERM_BP_FAT | GO:0006766~vitamin metabolic process               | 5     | 1.05932203 | 0.09421548 | RDH12, ALD  | 341        | 69       | 13588     | 2.88750053   | 1          | 0.61255622 | 81.6188342 |
| GOTERM_BP_FAT | GO:0006732~coenzyme metabolic process              | 7     | 1.48305085 | 0.14936073 | MOCOS, TAL  | 341        | 143      | 13588     | 1.95057728   | 1          | 0.72993438 | 93.7278503 |
| GOTERM_BP_FAT | GO:0009109~coenzyme catabolic process              | 3     | 0.63559322 | 0.16339684 | NCF2, NCF1  | 341        | 29       | 13588     | 4.12215593   | 1          | 0.75542496 | 95.2823411 |
| GOTERM_BP_FAT | GO:0051186~cofactor metabolic process              | 8     | 1.69491525 | 0.17222228 | ISCA1, MOC  | 341        | 182      | 13588     | 1.75153878   | 1          | 0.77095199 | 96.0655213 |
| GOTERM_BP_FAT | GO:0051187~cofactor catabolic process              | 3     | 0.63559322 | 0.19042778 | NCF2, NCF1  | 341        | 32       | 13588     | 3.73570381   | 1          | 0.79466999 | 97.3111666 |
| KEGG_PATHWAY  | mmu00030:Pentose phosphate pathway                 | 3     | 0.63559322 | 0.19058354 | TALDO1, PGI | 178        | 26       | 5738      | 3.71953328   | 1          | 0.66413273 | 91.4475792 |
| GOTERM_BP_FAT | GO:0006763~water-soluble vitamin metabolic process | 3     | 0.63559322 | 0.20876021 | NCF2, NCF1  | 341        | 34       | 13588     | 3.51595653   | 1          | 0.81999249 | 98.1832807 |
| KEGG_PATHWAY  | mmu00480:Glutathione metabolism                    | 3     | 0.63559322 | 0.48028234 | PGD, G6PDX  | 178        | 52       | 5738      | 1.85976664   | 1          | 0.82776354 | 99.9505091 |

Annotation Cluster 40 Enrichment Score: 1.6018273983056266

| Category      | Term   | Count | %          | PValue   | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|--|-------|------------|----------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0002366~leukocyte activation during immune resp | 8     | 1.69491525 | 9.05E-06 | SLC11A1, SB | 341        | 31       | 13588     | 10.2832277   | 0.017275   | 0.00102453 | 0.01548629 |



|               |   |   |            |            |             |     |     |       |            |          |            |            |
|---------------|---|---|------------|------------|-------------|-----|-----|-------|------------|----------|------------|------------|
| GOTERM_BP_FAT | GO:0002263~cell activation during immune response     | 8 | 1.69491525 | 9.05E-06   | SLC11A1, SB | 341 | 31  | 13588 | 10.2832277 | 0.017275 | 0.00102453 | 0.01548629 |
| GOTERM_BP_FAT | GO:0043299~leukocyte degranulation                    | 3 | 0.63559322 | 0.02459962 | ADORA3, M   | 341 | 10  | 13588 | 11.9542522 | 1        | 0.3208177  | 34.711224  |
| GOTERM_BP_FAT | GO:0002275~myeloid cell activation during immune r    | 3 | 0.63559322 | 0.03491338 | SBNO2, ADC  | 341 | 12  | 13588 | 9.96187683 | 1        | 0.38884862 | 45.5731336 |
| GOTERM_BP_FAT | GO:0045055~regulated secretory pathway                | 3 | 0.63559322 | 0.0405912  | ADORA3, M   | 341 | 13  | 13588 | 9.19557861 | 1        | 0.41681699 | 50.8019333 |
| GOTERM_BP_FAT | GO:0050729~positive regulation of inflammatory resp   | 3 | 0.63559322 | 0.12024516 | FCER1A, ADC | 341 | 24  | 13588 | 4.98093842 | 1        | 0.6676393  | 88.8413918 |
| GOTERM_BP_FAT | GO:0032103~positive regulation of response to exterr  | 3 | 0.63559322 | 0.25520182 | FCER1A, ADC | 341 | 39  | 13588 | 3.06519287 | 1        | 0.86823247 | 99.3549118 |
| GOTERM_BP_FAT | GO:0046903~secretion                                  | 7 | 1.69491525 | 0.31643663 | FCER1A, ADC | 341 | 221 | 13588 | 1.4424437  | 1        | 0.90663705 | 99.8514668 |
| GOTERM_BP_FAT | GO:0032940~secretion by cell                          | 8 | 1.48305085 | 0.32170792 | FCER1A, ADC | 341 | 186 | 13588 | 1.49963737 | 1        | 0.90894106 | 99.869901  |
| GOTERM_BP_FAT | GO:0003001~generation of a signal involved in cell-ce | 4 | 0.84745763 | 0.35127073 | FCER1A, ADC | 341 | 84  | 13588 | 1.89750035 | 1        | 0.9260638  | 99.9393272 |
| GOTERM_BP_FAT | GO:0006887~exocytosis                                 | 3 | 0.63559322 | 0.76582215 | ADORA3, M   | 341 | 110 | 13588 | 1.0867502  | 1        | 0.99875524 | 100        |

|                       |   |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 41 | Enrichment Score: 1.5586695542329367                |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| INTERPRO              | IPR000198:RhoGAP                                    | 7     | 1.48305085 | 0.00522341 | ARHGAP30, , | 425        | 67       | 17763     | 4.36667252   | 0.98516291 | 0.21939329 | 7.72918444 |
| SMART                 | SM00324:RhoGAP                                      | 7     | 1.48305085 | 0.01076181 | ARHGAP30, , | 256        | 67       | 9131      | 3.7265042    | 0.85738748 | 0.21608368 | 12.4777212 |
| GOTERM_MF_FAT         | GO:0008047~enzyme activator activity                | 14    | 2.96610169 | 0.01132043 | GPSM3, 110  | 339        | 249      | 13288     | 2.20388338   | 0.9972535  | 0.44553012 | 15.1906001 |
| GOTERM_MF_FAT         | GO:0005096~GTPase activator activity                | 11    | 2.33050847 | 0.02497952 | ARHGAP30, , | 339        | 192      | 13288     | 2.24569813   | 0.99999796 | 0.53736105 | 30.656348  |
| SP_PIR_KEYWORDS       | GTPase activation                                   | 8     | 1.69491525 | 0.05047922 | ARHGAP30, , | 439        | 136      | 17854     | 2.39233552   | 1          | 0.38864639 | 51.182683  |
| UP_SEQ_FEATURE        | domain:Rho-GAP                                      | 5     | 1.05932203 | 0.06383659 | ARHGAP30, , | 425        | 57       | 16021     | 3.30670795   | 1          | 0.9417827  | 65.6033431 |
| GOTERM_MF_FAT         | GO:0030695~GTPase regulator activity                | 15    | 3.1779661  | 0.07745588 | GPSM3, CYT  | 339        | 361      | 13288     | 1.62871081   | 1          | 0.71789923 | 68.8617985 |
| GOTERM_MF_FAT         | GO:0060589~nucleoside-triphosphatase regulator acti | 15    | 3.1779661  | 0.08553046 | GPSM3, CYT  | 339        | 367      | 13288     | 1.60208338   | 1          | 0.72377146 | 72.5816818 |

|                       |  |       |            |            |               |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 42 | Enrichment Score: 1.545788765883106      |       |            |            |               |            |          |           |              |            |            |            |
| Category              | Term                                     | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS       | cell cycle                               | 21    | 4.44915254 | 0.00749983 | PRC1, ANLN, , | 439        | 447      | 17854     | 1.91065723   | 0.94276992 | 0.11236514 | 9.89713841 |
| GOTERM_BP_FAT         | GO:0000278~mitotic cell cycle            | 14    | 2.96610169 | 0.0085489  | ANLN, CDC2    | 341        | 244      | 13588     | 2.28633239   | 0.99999993 | 0.17678732 | 13.6675764 |
| SP_PIR_KEYWORDS       | cell division                            | 14    | 2.96610169 | 0.01087779 | PRC1, ANLN, , | 439        | 256      | 17854     | 2.22412443   | 0.98433315 | 0.14773193 | 14.051015  |
| GOTERM_BP_FAT         | GO:0051301~cell division                 | 15    | 3.1779661  | 0.01132825 | PRC1, ANLN, , | 341        | 281      | 13588     | 2.12709114   | 1          | 0.21017459 | 17.7180305 |
| SP_PIR_KEYWORDS       | mitosis                                  | 11    | 2.33050847 | 0.01309546 | CCNB1, KIF2   | 439        | 179      | 17854     | 2.49925555   | 0.9933234  | 0.15377632 | 16.6806988 |
| KEGG_PATHWAY          | mmu04110:Cell cycle                      | 10    | 2.11864407 | 0.01691204 | CCNB1, CCN    | 178        | 128      | 5738      | 2.51843399   | 0.88923137 | 0.18129244 | 17.9925596 |
| GOTERM_BP_FAT         | GO:0007049~cell cycle                    | 25    | 5.29661017 | 0.01952523 | PRC1, ANLN, , | 341        | 611      | 13588     | 1.63042174   | 1          | 0.27919943 | 28.6468942 |
| GOTERM_BP_FAT         | GO:0007067~mitosis                       | 10    | 2.11864407 | 0.04963041 | CCNB1, CDC    | 341        | 190      | 13588     | 2.09723723   | 1          | 0.46023135 | 58.1615949 |
| GOTERM_BP_FAT         | GO:0000280~nuclear division              | 10    | 2.11864407 | 0.04963041 | CCNB1, CDC    | 341        | 190      | 13588     | 2.09723723   | 1          | 0.46023135 | 58.1615949 |
| GOTERM_BP_FAT         | GO:0000087~M phase of mitotic cell cycle | 10    | 2.11864407 | 0.05517142 | CCNB1, CDC    | 341        | 194      | 13588     | 2.05399522   | 1          | 0.47827698 | 62.1465891 |
| GOTERM_BP_FAT         | GO:0048285~organelle fission             | 10    | 2.11864407 | 0.05967686 | CCNB1, CDC    | 341        | 197      | 13588     | 2.02271611   | 1          | 0.49792808 | 65.1204554 |
| GOTERM_BP_FAT         | GO:0022402~cell cycle process            | 16    | 3.38983051 | 0.06913881 | MKI67, ANLN   | 341        | 393      | 13588     | 1.62229037   | 1          | 0.53541125 | 70.6649206 |
| GOTERM_BP_FAT         | GO:0022403~cell cycle phase              | 14    | 2.96610169 | 0.06917817 | MKI67, ANLN   | 341        | 328      | 13588     | 1.70080824   | 1          | 0.53364925 | 70.6861461 |
| GOTERM_BP_FAT         | GO:0000279~M phase                       | 11    | 2.33050847 | 0.1724537  | CCNB1, CDC    | 341        | 283      | 13588     | 1.54884304   | 1          | 0.76872515 | 96.0843071 |

|                       |  |       |            |            |            |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 43 | Enrichment Score: 1.523408682389824                  |       |            |            |            |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0051493~regulation of cytoskeleton organization   | 8     | 1.69491525 | 0.01205946 | WNT2, ARPC | 341        | 99       | 13588     | 3.22000059   | 1          | 0.21805893 | 18.7535302 |
| GOTERM_BP_FAT         | GO:0032271~regulation of protein polymerization      | 6     | 1.27118644 | 0.01377491 | WNT2, ARPC | 341        | 57       | 13588     | 4.19447446   | 1          | 0.23241337 | 21.1348906 |
| GOTERM_BP_FAT         | GO:0033043~regulation of organelle organization      | 10    | 2.11864407 | 0.0154234  | WNT2, ARPC | 341        | 154      | 13588     | 2.58750048   | 1          | 0.24807115 | 23.361249  |
| GOTERM_BP_FAT         | GO:0032956~regulation of actin cytoskeleton organiz  | 6     | 1.27118644 | 0.01691672 | ARPC1B, CO | 341        | 60       | 13588     | 3.98475073   | 1          | 0.26233276 | 25.3268446 |
| GOTERM_BP_FAT         | GO:0032970~regulation of actin filament-based proce  | 6     | 1.27118644 | 0.01806121 | ARPC1B, CO | 341        | 61       | 13588     | 3.91942695   | 1          | 0.27321607 | 26.8010453 |
| GOTERM_BP_FAT         | GO:0043254~regulation of protein complex assembly    | 6     | 1.27118644 | 0.02314652 | WNT2, ARPC | 341        | 65       | 13588     | 3.67823145   | 1          | 0.31330744 | 33.0261728 |
| GOTERM_BP_FAT         | GO:0030833~regulation of actin filament polymerizati | 5     | 1.05932203 | 0.0256487  | ARPC1B, CO | 341        | 45       | 13588     | 4.42750081   | 1          | 0.32778317 | 35.9028723 |
| GOTERM_BP_FAT         | GO:0008064~regulation of actin polymerization or de  | 5     | 1.05932203 | 0.03600945 | ARPC1B, CO | 341        | 50       | 13588     | 3.98475073   | 1          | 0.39190282 | 46.6216057 |
| GOTERM_BP_FAT         | GO:0030832~regulation of actin filament length       | 5     | 1.05932203 | 0.03833185 | ARPC1B, CO | 341        | 51       | 13588     | 3.90661837   | 1          | 0.40286493 | 48.7806373 |
| GOTERM_BP_FAT         | GO:0044087~regulation of cellular component biogen   | 6     | 1.27118644 | 0.07231052 | WNT2, ARPC | 341        | 89       | 13588     | 2.68634881   | 1          | 0.54810136 | 72.3296849 |
| GOTERM_BP_FAT         | GO:0032535~regulation of cellular component size     | 6     | 1.27118644 | 0.37680421 | ARPC1B, CO | 341        | 161      | 13588     | 1.48500027   | 1          | 0.93933849 | 99.9694872 |

|                       |   |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 44 | Enrichment Score: 1.4940027615675058                  |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0048585~negative regulation of response to stimu   | 8     | 1.69491525 | 0.00115679 | CLN3, PTPN   | 341        | 65       | 13588     | 4.90430859   | 0.89239301 | 0.04447591 | 1.96178681 |
| GOTERM_BP_FAT         | GO:0046627~negative regulation of insulin receptor si | 3     | 0.63559322 | 0.01206292 | SOC3S, IL1B, | 341        | 7        | 13588     | 17.0775031   | 1          | 0.21610783 | 18.7583931 |

|               |  |   |            |            |              |     |     |       |            |   |            |            |
|---------------|--|---|------------|------------|--------------|-----|-----|-------|------------|---|------------|------------|
| GOTERM_BP_FAT | GO:0046626--regulation of insulin receptor signaling p | 3 | 0.63559322 | 0.02459962 | SOCS3, IL1B, | 341 | 10  | 13588 | 11.9542522 | 1 | 0.3208177  | 34.711224  |
| GOTERM_BP_FAT | GO:0010648--negative regulation of cell communicati    | 9 | 1.90677966 | 0.09555015 | CLN3, PTPNF  | 341 | 186 | 13588 | 1.92810519 | 1 | 0.61616796 | 82.0769913 |
| GOTERM_BP_FAT | GO:0010741--negative regulation of protein kinase ca   | 3 | 0.63559322 | 0.12863502 | PTPN6, NFKF  | 341 | 25  | 13588 | 4.78170088 | 1 | 0.68432451 | 90.5294663 |
| GOTERM_BP_FAT | GO:0009968--negative regulation of signal transductio  | 7 | 1.48305085 | 0.2574881  | PTPN6, NFKF  | 341 | 171 | 13588 | 1.63118451 | 1 | 0.86910235 | 99.3879823 |

|                       |   |       |            |            |               |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 45 | Enrichment Score: 1.4571898693177692            |       |            |            |               |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0005856--cytoskeleton                        | 44    | 9.3220339  | 0.00769878 | KIF23, KIF22, | 330        | 1122     | 12504     | 1.485918     | 0.87968325 | 0.1617752  | 9.683345   |
| GOTERM_MF_FAT         | GO:0003774--motor activity                      | 10    | 2.11864407 | 0.00871676 | KIF1C, KIF23, | 339        | 138      | 13288     | 2.8404087    | 0.98927391 | 0.3958286  | 11.9003901 |
| SP_PIR_KEYWORDS       | motor protein                                   | 9     | 1.90677966 | 0.01093298 | KIF1C, KIF23, | 439        | 123      | 17854     | 2.97583199   | 0.98466181 | 0.14334403 | 14.1173752 |
| INTERPRO              | IPR019821:Kinesin, motor region, conserved site | 5     | 1.05932203 | 0.0175309  | KIF1C, KIF23, | 425        | 42       | 17763     | 4.97563025   | 0.99999933 | 0.49192988 | 23.7890095 |
| INTERPRO              | IPR001752:Kinesin, motor region                 | 5     | 1.05932203 | 0.02048995 | KIF1C, KIF23, | 425        | 44       | 17763     | 4.74946524   | 0.99999994 | 0.53073731 | 27.2394786 |
| SMART                 | SM00129:KiSc                                    | 5     | 1.05932203 | 0.03367664 | KIF1C, KIF23, | 256        | 44       | 9131      | 4.05317827   | 0.99790084 | 0.40181272 | 34.4237801 |
| GOTERM_CC_FAT         | GO:0044430--cytoskeletal part                   | 30    | 6.3559322  | 0.03446362 | KIF23, KIF22, | 330        | 774      | 12504     | 1.46863989   | 0.99993292 | 0.35389907 | 37.0089677 |
| GOTERM_BP_FAT         | GO:0007018--microtubule-based movement          | 7     | 1.48305085 | 0.041104   | KIF1C, KIF23, | 341        | 101      | 13588     | 2.76170843   | 1          | 0.41454139 | 51.2501197 |
| SP_PIR_KEYWORDS       | microtubule                                     | 11    | 2.33050847 | 0.04676936 | KIF1C, KIF23, | 439        | 221      | 17854     | 2.0242839    | 0.99999999 | 0.37293324 | 48.4748972 |
| GOTERM_CC_FAT         | GO:0005874--microtubule                         | 12    | 2.54237288 | 0.05292293 | KIF1C, KIF23, | 330        | 240      | 12504     | 1.89454545   | 0.99999966 | 0.4361837  | 51.1570393 |
| UP_SEQ_FEATURE        | domain:Kinesin-motor                            | 4     | 0.84745763 | 0.06458288 | KIF1C, KIF2C, | 425        | 35       | 16021     | 4.30816807   | 1          | 0.93788146 | 66.044283  |
| GOTERM_BP_FAT         | GO:0007017--microtubule-based process           | 10    | 2.11864407 | 0.08269647 | WNT2, KIF1C   | 341        | 211      | 13588     | 1.88850746   | 1          | 0.57742131 | 77.1799336 |
| GOTERM_MF_FAT         | GO:0003777--microtubule motor activity          | 5     | 1.05932203 | 0.11500378 | KIF1C, KIF23, | 339        | 73       | 13288     | 2.68476987   | 1          | 0.77837906 | 82.9338515 |
| GOTERM_CC_FAT         | GO:0015630--microtubule cytoskeleton            | 16    | 3.38983051 | 0.20796293 | KIF23, KIF22, | 330        | 450      | 12504     | 1.34723232   | 1          | 0.68698257 | 95.3692427 |

|                       |   |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 46 | Enrichment Score: 1.4412062708986788              |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0046649--lymphocyte activation                 | 14    | 2.96610169 | 0.00104666 | ITGAL, PIK3C | 341        | 191      | 13588     | 2.9207597    | 0.86693687 | 0.04200569 | 1.77659682 |
| GOTERM_BP_FAT         | GO:0030097--hemopoiesis                           | 13    | 2.75423729 | 0.02430708 | CEBPE, HCLS  | 341        | 251      | 13588     | 2.06381512   | 1          | 0.31976398 | 34.3752348 |
| GOTERM_BP_FAT         | GO:0048534--hemopoietic or lymphoid organ develop | 14    | 2.96610169 | 0.02478802 | CEBPE, HCLS  | 341        | 281      | 13588     | 1.98528506   | 1          | 0.32073724 | 34.9267581 |
| GOTERM_BP_FAT         | GO:0030099--myeloid cell differentiation          | 7     | 1.48305085 | 0.03328711 | CEBPE, HCLS  | 341        | 96       | 13588     | 2.90554741   | 1          | 0.37869249 | 43.9816993 |
| GOTERM_BP_FAT         | GO:0002520--immune system development             | 14    | 2.96610169 | 0.03473804 | CEBPE, HCLS  | 341        | 295      | 13588     | 1.89106814   | 1          | 0.38947945 | 45.4036178 |
| GOTERM_BP_FAT         | GO:0002521--leukocyte differentiation             | 8     | 1.69491525 | 0.06596158 | CEBPE, PLCG  | 341        | 142      | 13588     | 2.24492999   | 1          | 0.52608992 | 68.9030345 |
| GOTERM_BP_FAT         | GO:0030183--B cell differentiation                | 4     | 0.84745763 | 0.10747592 | PLCG2, BCL3  | 341        | 46       | 13588     | 3.46500064   | 1          | 0.64929061 | 85.7197385 |
| GOTERM_BP_FAT         | GO:0042113--B cell activation                     | 5     | 1.05932203 | 0.13136675 | PLCG2, PIK3C | 341        | 78       | 13588     | 2.55432739   | 1          | 0.69094273 | 91.0250488 |
| GOTERM_BP_FAT         | GO:0030098--lymphocyte differentiation            | 6     | 1.27118644 | 0.157468   | PLCG2, BCL3  | 341        | 114      | 13588     | 2.09723723   | 1          | 0.74284003 | 94.6761686 |

|                       |  |       |            |            |            |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 47 | Enrichment Score: 1.4067836544000516         |       |            |            |            |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0005976--polysaccharide metabolic process | 8     | 1.69491525 | 0.00822088 | PTGES3, OV | 341        | 92       | 13588     | 3.46500064   | 0.99999988 | 0.17243862 | 13.1773428 |
| GOTERM_BP_FAT         | GO:0006022--aminoglycan metabolic process    | 5     | 1.05932203 | 0.04073815 | OVGP1, BCL | 341        | 52       | 13588     | 3.83149109   | 1          | 0.4158603  | 50.9307659 |
| GOTERM_BP_FAT         | GO:0006026--aminoglycan catabolic process    | 3     | 0.63559322 | 0.07340235 | OVGP1, BCL | 341        | 18       | 13588     | 6.64125122   | 1          | 0.55172616 | 72.8818797 |
| GOTERM_BP_FAT         | GO:0000272--polysaccharide catabolic process | 3     | 0.63559322 | 0.09599221 | OVGP1, BCL | 341        | 21       | 13588     | 5.69250105   | 1          | 0.61613775 | 82.2263516 |

|                       |   |       |            |            |            |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 48 | Enrichment Score: 1.3955830074494209        |       |            |            |            |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0030036--actin cytoskeleton organization | 10    | 2.11864407 | 0.02305072 | FMNL1, COR | 341        | 165      | 13588     | 2.41500044   | 1          | 0.31438565 | 32.9136535 |
| GOTERM_BP_FAT         | GO:0030029--actin filament-based process    | 10    | 2.11864407 | 0.03305845 | FMNL1, COR | 341        | 176      | 13588     | 2.26406292   | 1          | 0.37878575 | 43.7544541 |
| GOTERM_BP_FAT         | GO:0007015--actin filament organization     | 5     | 1.05932203 | 0.05120182 | CORO1A, EV | 341        | 56       | 13588     | 3.5781315    | 1          | 0.46466902 | 59.3301115 |
| GOTERM_BP_FAT         | GO:0007010--cytoskeleton organization       | 14    | 2.96610169 | 0.06705262 | FMNL1, S10 | 341        | 326      | 13588     | 1.71124265   | 1          | 0.52611858 | 69.5189891 |

|                       |   |       |            |            |            |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 49 | Enrichment Score: 1.3793928801860769                  |       |            |            |            |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0002687--positive regulation of leukocyte migratio | 3     | 0.63559322 | 0.00593819 | SELP, ADOR | 341        | 5        | 13588     | 23.9085044   | 0.99998957 | 0.14182508 | 9.69253695 |
| GOTERM_BP_FAT         | GO:0030325--positive regulation of cell migration     | 5     | 1.05932203 | 0.01327379 | SELP, CORO | 341        | 37       | 13588     | 5.38479829   | 1          | 0.22892126 | 20.4461302 |
| GOTERM_BP_FAT         | GO:0002685--regulation of leukocyte migration         | 3     | 0.63559322 | 0.01581989 | SELP, ADOR | 341        | 8        | 13588     | 14.9428152   | 1          | 0.25154356 | 23.8878257 |
| GOTERM_BP_FAT         | GO:0051272--positive regulation of cell motion        | 5     | 1.05932203 | 0.0188339  | SELP, CORO | 341        | 41       | 13588     | 4.85945211   | 1          | 0.27889075 | 27.7807944 |
| GOTERM_BP_FAT         | GO:0040017--positive regulation of locomotion         | 5     | 1.05932203 | 0.02382407 | SELP, CORO | 341        | 44       | 13588     | 4.52812583   | 1          | 0.31659012 | 33.8169101 |
| GOTERM_BP_FAT         | GO:0030334--regulation of cell migration              | 5     | 1.05932203 | 0.19873828 | SELP, CORO | 341        | 92       | 13588     | 2.1656254    | 1          | 0.80627293 | 97.7465036 |
| GOTERM_BP_FAT         | GO:0051270--regulation of cell motion                 | 5     | 1.05932203 | 0.27969836 | SELP, CORO | 341        | 107      | 13588     | 1.86203305   | 1          | 0.88428539 | 99.6360842 |

|               |                                     |   |            |            |              |     |     |       |            |   |            |            |
|---------------|-------------------------------------|---|------------|------------|--------------|-----|-----|-------|------------|---|------------|------------|
| GOTERM_BP_FAT | GO:0040012~regulation of locomotion | 5 | 1.05932203 | 0.29653551 | SELP, CORO1A | 341 | 110 | 13588 | 1.81125033 | 1 | 0.89388189 | 99.7572463 |
|---------------|-------------------------------------|---|------------|------------|--------------|-----|-----|-------|------------|---|------------|------------|

Annotation Cluster 50 Enrichment Score: 1.3771402085997995

| Category      | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini  | FDR        |
|---------------|---|-------|------------|------------|--------------|------------|----------|-----------|-----------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0002697~regulation of immune effector process                      | 9     | 1.90677966 | 0.00159782 | FCER1A, PTP  | 341        | 88       | 13588     | 4.07531325      | 0.95403481 | 0.05750841 | 2.7001418  |
| GOTERM_BP_FAT | GO:0002703~regulation of leukocyte mediated immunity                  | 8     | 1.69491525 | 0.00179105 | FCER1A, PTP  | 341        | 70       | 13588     | 4.55400084      | 0.96833829 | 0.06193676 | 3.02197125 |
| GOTERM_BP_FAT | GO:0002699~positive regulation of immune effector process             | 6     | 1.27118644 | 0.00563082 | FCER1A, CD3E | 341        | 46       | 13588     | 5.19750096      | 0.99998109 | 0.14019545 | 9.21336234 |
| GOTERM_BP_FAT | GO:0002886~regulation of myeloid leukocyte mediated immunity          | 4     | 0.84745763 | 0.00564972 | FCER1A, ADC  | 341        | 15       | 13588     | 10.626002       | 0.99998177 | 0.13884637 | 9.24288844 |
| GOTERM_BP_FAT | GO:0048002~antigen processing and presentation of peptide antigen     | 5     | 1.05932203 | 0.01094083 | SLC11A1, FC  | 341        | 35       | 13588     | 5.69250105      | 1          | 0.20771728 | 17.1643695 |
| GOTERM_BP_FAT | GO:0002822~regulation of adaptive immune response                     | 6     | 1.27118644 | 0.01282194 | FCER1A, PTP  | 341        | 56       | 13588     | 4.26937579      | 1          | 0.22401317 | 19.820224  |
| GOTERM_BP_FAT | GO:0002819~regulation of adaptive immune response                     | 6     | 1.27118644 | 0.01282194 | FCER1A, PTP  | 341        | 56       | 13588     | 4.26937579      | 1          | 0.22401317 | 19.820224  |
| GOTERM_BP_FAT | GO:0050727~regulation of inflammatory response                        | 6     | 1.27118644 | 0.01377491 | FCER1A, SBN  | 341        | 57       | 13588     | 4.19447446      | 1          | 0.23241337 | 21.1348906 |
| GOTERM_BP_FAT | GO:0031349~positive regulation of defense response                    | 6     | 1.27118644 | 0.01377491 | FCER1A, ADC  | 341        | 57       | 13588     | 4.19447446      | 1          | 0.23241337 | 21.1348906 |
| GOTERM_BP_FAT | GO:0043300~regulation of leukocyte degranulation                      | 6     | 0.63559322 | 0.01581989 | FCER1A, ADC  | 341        | 8        | 13588     | 14.9428152      | 1          | 0.25154356 | 23.8878257 |
| GOTERM_BP_FAT | GO:0060627~regulation of vesicle-mediated transport                   | 7     | 1.48305085 | 0.01768234 | FCER1A, SLC  | 341        | 83       | 13588     | 3.36063315      | 1          | 0.27038438 | 26.3160873 |
| GOTERM_BP_FAT | GO:0002706~regulation of lymphocyte mediated immunity                 | 6     | 1.27118644 | 0.02314652 | FCER1A, PTP  | 341        | 65       | 13588     | 3.67823145      | 1          | 0.31330744 | 33.0261728 |
| GOTERM_BP_FAT | GO:0002824~positive regulation of adaptive immune response            | 4     | 0.84745763 | 0.0525045  | FCER1A, SLC  | 341        | 34       | 13588     | 4.68794204      | 1          | 0.46716648 | 60.2754345 |
| GOTERM_BP_FAT | GO:0002821~positive regulation of adaptive immune response            | 4     | 0.84745763 | 0.0525045  | FCER1A, SLC  | 341        | 34       | 13588     | 4.68794204      | 1          | 0.46716648 | 60.2754345 |
| GOTERM_BP_FAT | GO:0019882~antigen processing and presentation                        | 6     | 1.27118644 | 0.06694784 | SLC11A1, FC  | 341        | 87       | 13588     | 2.74810395      | 1          | 0.52752882 | 69.4603384 |
| GOTERM_BP_FAT | GO:0002708~positive regulation of lymphocyte mediated immunity        | 4     | 0.84745763 | 0.07783424 | FCER1A, H2-  | 341        | 40       | 13588     | 3.98475073      | 1          | 0.56788156 | 75.0185604 |
| GOTERM_BP_FAT | GO:0002705~positive regulation of leukocyte mediated immunity         | 4     | 0.84745763 | 0.07783424 | FCER1A, H2-  | 341        | 40       | 13588     | 3.98475073      | 1          | 0.56788156 | 75.0185604 |
| GOTERM_BP_FAT | GO:0015837~amine transport  | 6     | 1.27118644 | 0.0807821  | FCER1A, CLN  | 341        | 92       | 13588     | 2.59875048      | 1          | 0.57231866 | 76.3508684 |
| GOTERM_BP_FAT | GO:0060341~regulation of cellular localization                        | 8     | 1.69491525 | 0.10976718 | OSM, FCER1A  | 341        | 161      | 13588     | 1.98000036      | 1          | 0.65226773 | 86.334446  |
| GOTERM_BP_FAT | GO:0002478~antigen processing and presentation of peptide antigen     | 3     | 0.63559322 | 0.11199941 | FCGR2B, CTS  | 341        | 23       | 13588     | 5.19750096      | 1          | 0.65495261 | 86.9092901 |
| GOTERM_BP_FAT | GO:0050729~positive regulation of inflammatory response               | 3     | 0.63559322 | 0.12024516 | FCER1A, ADC  | 341        | 24       | 13588     | 4.98093842      | 1          | 0.6676393  | 88.8413918 |
| GOTERM_BP_FAT | GO:0019884~antigen processing and presentation of peptide antigen     | 3     | 0.63559322 | 0.15454861 | FCGR2B, CTS  | 341        | 28       | 13588     | 4.26937579      | 1          | 0.73714152 | 94.351426  |
| GOTERM_BP_FAT | GO:0017157~regulation of exocytosis                                   | 3     | 0.63559322 | 0.19042778 | FCER1A, ADC  | 341        | 32       | 13588     | 3.73570381      | 1          | 0.79466999 | 97.3111666 |
| GOTERM_BP_FAT | GO:0032103~positive regulation of response to external stimulus       | 3     | 0.63559322 | 0.25520182 | FCER1A, ADC  | 341        | 39       | 13588     | 3.06519287      | 1          | 0.86823247 | 99.3549118 |
| GOTERM_BP_FAT | GO:0046903~secretion  | 8     | 1.69491525 | 0.31643663 | FCER1A, ADC  | 341        | 221      | 13588     | 1.4424437       | 1          | 0.90663705 | 99.8514668 |
| GOTERM_BP_FAT | GO:0032940~secretion by cell  | 7     | 1.48305085 | 0.32170792 | FCER1A, ADC  | 341        | 186      | 13588     | 1.49963737      | 1          | 0.90894106 | 99.869901  |
| GOTERM_BP_FAT | GO:0003001~generation of a signal involved in cell-cell communication | 4     | 0.84745763 | 0.35127073 | FCER1A, ADC  | 341        | 84       | 13588     | 1.89750035      | 1          | 0.9260638  | 99.9393272 |
| GOTERM_BP_FAT | GO:0051046~regulation of secretion                                    | 5     | 1.05932203 | 0.38182501 | OSM, FCER1A  | 341        | 125      | 13588     | 1.59390029      | 1          | 0.94116097 | 99.9734327 |

Annotation Cluster 51 Enrichment Score: 1.3695252818830936

| Category | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini  | FDR        |
|----------|---|-------|------------|------------|--------------|------------|----------|-----------|-----------------|------------|------------|------------|
| INTERPRO | IPR018244:Allergen V5/Tpx-1 related, conserved site | 3     | 0.63559322 | 0.03202761 | GLUPR2, GLUP | 425        | 12       | 17763     | 10.4488235      | 1          | 0.58204682 | 39.3467731 |
| INTERPRO | IPR014044:SCP-like extracellular                    | 3     | 0.63559322 | 0.04280033 | GLUPR2, GLUP | 425        | 14       | 17763     | 8.95613445      | 1          | 0.64456033 | 48.9263143 |
| INTERPRO | IPR001283:Allergen V5/Tpx-1 related                 | 3     | 0.63559322 | 0.04280033 | GLUPR2, GLUP | 425        | 14       | 17763     | 8.95613445      | 1          | 0.64456033 | 48.9263143 |
| SMART    | SM00198:SCP   | 3     | 0.63559322 | 0.05668655 | GLUPR2, GLUP | 256        | 14       | 9131      | 7.64313616      | 0.99997258 | 0.50355367 | 51.2666781 |

Annotation Cluster 52 Enrichment Score: 1.354726796413791

| Category      | Term   | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini  | FDR        |
|---------------|--|-------|------------|------------|-------------|------------|----------|-----------|-----------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0031349~positive regulation of defense response       | 6     | 1.27118644 | 0.01377491 | FCER1A, ADC | 341        | 57       | 13588     | 4.19447446      | 1          | 0.23241337 | 21.1348906 |
| GOTERM_BP_FAT | GO:0045088~regulation of innate immune response          | 5     | 1.05932203 | 0.02755517 | MYD88, TLR1 | 341        | 46       | 13588     | 4.3312508       | 1          | 0.34541205 | 38.0161571 |
| GOTERM_BP_FAT | GO:0045089~positive regulation of innate immune response | 3     | 0.63559322 | 0.22726251 | MYD88, TLR1 | 341        | 36       | 13588     | 3.32062561      | 1          | 0.83887325 | 98.7883256 |

Annotation Cluster 53 Enrichment Score: 1.3435869431985736

| Category        | Term   | Count | %          | PValue     | Genes          | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini  | FDR        |
|-----------------|--|-------|------------|------------|----------------|------------|----------|-----------|-----------------|------------|------------|------------|
| GOTERM_BP_FAT   | GO:0042060~wound healing                     | 9     | 1.90677966 | 0.00706753 | F2RL2, SLC11A1 | 341        | 112      | 13588     | 3.20203184      | 0.99999883 | 0.15879193 | 11.4327462 |
| GOTERM_BP_FAT   | GO:0050817~coagulation                       | 6     | 1.27118644 | 0.03069554 | F2RL2, THBD    | 341        | 70       | 13588     | 3.41550063      | 1          | 0.36768415 | 41.3548031 |
| GOTERM_BP_FAT   | GO:0007596~blood coagulation                 | 6     | 1.27118644 | 0.03069554 | F2RL2, THBD    | 341        | 70       | 13588     | 3.41550063      | 1          | 0.36768415 | 41.3548031 |
| GOTERM_BP_FAT   | GO:0007599~hemostasis                        | 6     | 1.27118644 | 0.03237007 | F2RL2, THBD    | 341        | 71       | 13588     | 3.36739499      | 1          | 0.37465559 | 43.0650872 |
| SP_PIR_KEYWORDS | blood coagulation                            | 4     | 0.84745763 | 0.06166663 | F2RL2, THBD    | 439        | 37       | 17854     | 4.39672474      | 1          | 0.40892022 | 58.5699956 |
| GOTERM_BP_FAT   | GO:0050878~regulation of body fluid levels   | 6     | 1.27118644 | 0.07231052 | F2RL2, THBD    | 341        | 89       | 13588     | 2.68634881      | 1          | 0.54810136 | 72.3296849 |
| KEGG_PATHWAY    | mmu04610:Complement and coagulation cascades | 4     | 0.84745763 | 0.40933422 | THBD, F5, F1   | 178        | 75       | 5738      | 1.71925094      | 1          | 0.79392495 | 99.7808076 |

Annotation Cluster 54 Enrichment Score: 1.3236833145430504

| Category        | Term   | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|--|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_MF_FAT   | GO:0008289~lipid binding                               | 17    | 3.60169492 | 0.01535484 | PLUNC, NCF | 339        | 345      | 13288     | 1.93147792   | 0.9996697  | 0.48724588 | 20.063626  |
| GOTERM_MF_FAT   | GO:0019992~diacylglycerol binding                      | 6     | 1.27118644 | 0.0168655  | HMHA1, RA  | 339        | 59       | 13288     | 3.98620069   | 0.99985089 | 0.46705966 | 21.8202448 |
| INTERPRO        | IPR002219:Protein kinase C-like, phorbol ester/diacylg | 6     | 1.27118644 | 0.02058162 | HMHA1, RA  | 425        | 66       | 17763     | 3.79957219   | 0.99999995 | 0.5166281  | 27.3440048 |
| INTERPRO        | IPR002219:Protein kinase C, phorbol ester/diacylglycer | 5     | 1.05932203 | 0.0352688  | HMHA1, RA  | 425        | 52       | 17763     | 4.01877828   | 1          | 0.59429635 | 42.3924131 |
| SMART           | SM00109:C1   | 6     | 1.27118644 | 0.03671424 | HMHA1, RA  | 256        | 66       | 9131      | 3.24254261   | 0.99880896 | 0.40424022 | 36.9181797 |
| UP_SEQ_FEATURE  | zinc finger region:Phorbol-ester/DAG-type              | 4     | 0.84745763 | 0.07863344 | HMHA1, RA  | 425        | 38       | 16021     | 3.96804954   | 1          | 0.94064907 | 73.4188036 |
| SP_PIR_KEYWORDS | zinc-finger  | 16    | 3.38983051 | 0.99921753 | MELA, BMX, | 439        | 1204     | 17854     | 0.54046118   | 1          | 0.99999999 | 100        |

| Annotation Cluster 55 |                                       | Enrichment Score: 1.2875541575542382 |            |            |              |            |          |           |              |            |            |            |
|-----------------------|---------------------------------------|--------------------------------------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Category              | Term                                  | Count                                | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0006909~phagocytosis               | 6                                    | 1.27118644 | 0.00737161 | SLC11A1, CE  | 341        | 49       | 13588     | 4.87928661   | 0.99999935 | 0.16316551 | 11.8958977 |
| GOTERM_BP_FAT         | GO:0010324~membrane invagination      | 10                                   | 2.11864407 | 0.04695993 | CLN3, SLC11  | 341        | 188      | 13588     | 2.11954826   | 1          | 0.44779138 | 56.1029824 |
| GOTERM_BP_FAT         | GO:0006897~endocytosis                | 10                                   | 2.11864407 | 0.04695993 | CLN3, SLC11  | 341        | 188      | 13588     | 2.11954826   | 1          | 0.44779138 | 56.1029824 |
| GOTERM_BP_FAT         | GO:0016044~membrane organization      | 12                                   | 2.54237288 | 0.08045362 | BLD, CLN3, S | 341        | 272      | 13588     | 1.75797826   | 1          | 0.57459948 | 76.2057927 |
| GOTERM_BP_FAT         | GO:0016192~vesicle-mediated transport | 15                                   | 3.1779661  | 0.2790398  | CLN3, ADOR   | 341        | 466      | 13588     | 1.28264509   | 1          | 0.88444241 | 99.6303467 |

| Annotation Cluster 56 |   | Enrichment Score: 1.2869801864205108 |            |            |              |            |          |           |              |            |            |            |
|-----------------------|---|--------------------------------------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Category              | Term                                      | Count                                | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0042110~T cell activation              | 9                                    | 1.90677966 | 0.00867084 | ITGAL, SLC11 | 341        | 116      | 13588     | 3.09161695   | 0.99999995 | 0.17719277 | 13.849162  |
| GOTERM_BP_FAT         | GO:0042098~T cell proliferation           | 4                                    | 0.84745763 | 0.03204403 | ITGAL, SLC11 | 341        | 28       | 13588     | 5.69250105   | 1          | 0.37381783 | 42.735812  |
| GOTERM_BP_FAT         | GO:0046651~lymphocyte proliferation       | 4                                    | 0.84745763 | 0.08726714 | ITGAL, SLC11 | 341        | 42       | 13588     | 3.7950007    | 1          | 0.59232316 | 79.0500715 |
| GOTERM_BP_FAT         | GO:0008283~cell proliferation             | 11                                   | 2.33050847 | 0.09213217 | PTGES3, ITG  | 341        | 247      | 13588     | 1.77458535   | 1          | 0.60760223 | 80.8815914 |
| GOTERM_BP_FAT         | GO:0070661~leukocyte proliferation        | 4                                    | 0.84745763 | 0.09215613 | ITGAL, SLC11 | 341        | 43       | 13588     | 3.70674487   | 1          | 0.6058627  | 80.8902247 |
| GOTERM_BP_FAT         | GO:0032943~mononuclear cell proliferation | 4                                    | 0.84745763 | 0.09215613 | ITGAL, SLC11 | 341        | 43       | 13588     | 3.70674487   | 1          | 0.6058627  | 80.8902247 |

| Annotation Cluster 57 |   | Enrichment Score: 1.2776309923365277 |            |            |            |            |          |           |              |            |            |            |
|-----------------------|---|--------------------------------------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Category              | Term  | Count                                | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0030055~cell-substrate junction          | 7                                    | 1.48305085 | 0.00765427 | WNT2, TNS4 | 330        | 66       | 12504     | 4.01873278   | 0.87819531 | 0.17419303 | 9.62993939 |
| GOTERM_CC_FAT         | GO:0016323~basolateral plasma membrane      | 10                                   | 2.11864407 | 0.01220686 | WNT2, TNS4 | 330        | 141      | 12504     | 2.68729852   | 0.96544702 | 0.21366771 | 14.9434497 |
| GOTERM_CC_FAT         | GO:0005925~focal adhesion                   | 6                                    | 1.27118644 | 0.01676349 | WNT2, TNS4 | 330        | 57       | 12504     | 3.98851675   | 0.99026601 | 0.26567882 | 19.9712769 |
| GOTERM_CC_FAT         | GO:0005912~adherens junction                | 8                                    | 1.69491525 | 0.02174525 | WNT2, TNS4 | 330        | 106      | 12504     | 2.85969125   | 0.99757987 | 0.31373811 | 25.1529913 |
| GOTERM_CC_FAT         | GO:0005924~cell-substrate adherens junction | 6                                    | 1.27118644 | 0.02189241 | WNT2, TNS4 | 330        | 61       | 12504     | 3.72697466   | 0.9976776  | 0.30006923 | 25.3012292 |
| GOTERM_CC_FAT         | GO:0070161~anchoring junction               | 8                                    | 1.69491525 | 0.0437239  | WNT2, TNS4 | 330        | 123      | 12504     | 2.46444937   | 0.99999522 | 0.41293252 | 44.5216388 |
| GOTERM_CC_FAT         | GO:06355932~cell-cell adherens junction     | 3                                    | 0.63559322 | 0.19583271 | TGM1, LMO  | 330        | 31       | 12504     | 3.66686217   | 1          | 0.67591512 | 94.3423029 |
| GOTERM_CC_FAT         | GO:0030054~cell junction                    | 13                                   | 2.75423729 | 0.58450627 | PARVG, TAN | 330        | 470      | 12504     | 1.04804642   | 1          | 0.95428218 | 99.9990595 |
| SP_PIR_KEYWORDS       | cell junction                               | 8                                    | 1.69491525 | 0.84995857 | TNS4, PARV | 439        | 392      | 17854     | 0.82999396   | 1          | 0.99686901 | 100        |

| Annotation Cluster 58 |  | Enrichment Score: 1.242197009978523 |            |            |             |            |          |           |              |            |            |            |
|-----------------------|--|-------------------------------------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Category              | Term   | Count                               | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0006690~icosanoid metabolic process               | 5                                   | 1.05932203 | 0.00988107 | PTGES3, FCE | 341        | 34       | 13588     | 5.85992755   | 1          | 0.19337318 | 15.6318692 |
| GOTERM_BP_FAT         | GO:0006691~leukotriene metabolic process             | 4                                   | 0.84745763 | 0.01117548 | FCER1A, NCI | 341        | 19       | 13588     | 8.38894891   | 1          | 0.20964514 | 17.5001153 |
| GOTERM_BP_FAT         | GO:0033559~unsaturated fatty acid metabolic process  | 5                                   | 1.05932203 | 0.01207122 | PTGES3, FCE | 341        | 36       | 13588     | 5.53437602   | 1          | 0.21426878 | 18.7700777 |
| GOTERM_BP_FAT         | GO:0043449~cellular alkene metabolic process         | 4                                   | 0.84745763 | 0.01478498 | FCER1A, NCI | 341        | 21       | 13588     | 7.5900014    | 1          | 0.24107382 | 22.5061555 |
| GOTERM_BP_FAT         | GO:0046456~icosanoid biosynthetic process            | 4                                   | 0.84745763 | 0.0291363  | PTGES3, FCE | 341        | 27       | 13588     | 5.90333442   | 1          | 0.35912693 | 39.7188634 |
| GOTERM_BP_FAT         | GO:0006636~unsaturated fatty acid biosynthetic proci | 4                                   | 0.84745763 | 0.03204403 | PTGES3, FCE | 341        | 28       | 13588     | 5.69250105   | 1          | 0.37381783 | 42.735812  |
| GOTERM_BP_FAT         | GO:0006631~fatty acid metabolic process              | 10                                  | 2.11864407 | 0.04194274 | PTGES3, FCE | 341        | 184      | 13588     | 2.1656254    | 1          | 0.41688875 | 51.9749085 |
| GOTERM_BP_FAT         | GO:0043450~alkene biosynthetic process               | 3                                   | 0.63559322 | 0.06631164 | FCER1A, ALC | 341        | 17       | 13588     | 7.03191306   | 1          | 0.52602354 | 69.1019261 |
| GOTERM_BP_FAT         | GO:0019370~leukotriene biosynthetic process          | 3                                   | 0.63559322 | 0.06631164 | FCER1A, ALC | 341        | 17       | 13588     | 7.03191306   | 1          | 0.52602354 | 69.1019261 |
| GOTERM_BP_FAT         | GO:0008610~lipid biosynthetic process                | 10                                  | 2.11864407 | 0.28482304 | PTGES3, ALD | 341        | 285      | 13588     | 1.39815815   | 1          | 0.88792907 | 99.6779514 |
| GOTERM_BP_FAT         | GO:0006633~fatty acid biosynthetic process           | 4                                   | 0.84745763 | 0.3306528  | PTGES3, FCE | 341        | 81       | 13588     | 1.96777814   | 1          | 0.91410198 | 99.8963459 |
| GOTERM_BP_FAT         | GO:0016053~organic acid biosynthetic process         | 5                                   | 1.05932203 | 0.47142879 | PTGES3, FCE | 341        | 141      | 13588     | 1.41303217   | 1          | 0.97035768 | 99.9981794 |
| GOTERM_BP_FAT         | GO:0046394~carboxylic acid biosynthetic process      | 5                                   | 1.05932203 | 0.47142879 | PTGES3, FCE | 341        | 141      | 13588     | 1.41303217   | 1          | 0.97035768 | 99.9981794 |

| Annotation Cluster 59 |   | Enrichment Score: 1.1978119093054524 |            |           |              |            |          |           |              |            |            |            |
|-----------------------|---|--------------------------------------|------------|-----------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Category              | Term                                      | Count                                | %          | PValue    | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| INTERPRO              | IPR001969:Peptidase aspartic, active site | 4                                    | 0.84745763 | 0.0113835 | MELA, HK3, I | 425        | 20       | 17763     | 8.35905882   | 0.99989945 | 0.40033213 | 16.1259993 |

|               |   |   |            |            |             |     |    |       |            |   |            |            |
|---------------|---|---|------------|------------|-------------|-----|----|-------|------------|---|------------|------------|
| GOTERM_MF_FAT | GO:0070001~aspartic-type peptidase activity     | 3 | 0.63559322 | 0.14967324 | MELA, CTSE, | 339 | 27 | 13288 | 4.35529335 | 1 | 0.80733045 | 90.4288202 |
| GOTERM_MF_FAT | GO:0004190~aspartic-type endopeptidase activity | 3 | 0.63559322 | 0.14967324 | MELA, CTSE, | 339 | 27 | 13288 | 4.35529335 | 1 | 0.80733045 | 90.4288202 |

|                       |   |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 60 | Enrichment Score: 1.1629205625866685                  |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| UP_SEQ_FEATURE        | domain:CH 2   | 4     | 0.84745763 | 0.01717975 | PARVG, DST,  | 425        | 21       | 16021     | 7.18028011   | 1          | 0.82500746 | 24.4485069 |
| UP_SEQ_FEATURE        | domain:CH 1   | 4     | 0.84745763 | 0.01717975 | PARVG, DST,  | 425        | 21       | 16021     | 7.18028011   | 1          | 0.82500746 | 24.4485069 |
| INTERPRO              | IPR001715:Calponin-like actin-binding                 | 6     | 1.27118644 | 0.0231062  | PARVG, LMC   | 425        | 68       | 17763     | 3.68782007   | 0.99999999 | 0.51465689 | 30.1680187 |
| SMART                 | SM00033:CH  | 6     | 1.27118644 | 0.04097161 | PARVG, LMC   | 256        | 68       | 9131      | 3.14717371   | 0.99946338 | 0.41601117 | 40.2676822 |
| INTERPRO              | IPR002048:Calcium-binding EF-hand                     | 8     | 1.69491525 | 0.04622578 | MYL7, DGKG   | 425        | 137      | 17763     | 2.44060112   | 1          | 0.66284032 | 51.662722  |
| INTERPRO              | IPR018249:EF-HAND 2                                   | 10    | 2.11864407 | 0.057902   | MYL7, S100A  | 425        | 205      | 17763     | 2.03879484   | 1          | 0.71690796 | 59.9950797 |
| SP_PIR_KEYWORDS       | calcium   | 26    | 5.50847458 | 0.0605095  | ITGAL, MYL7  | 439        | 731      | 17854     | 1.44652846   | 1          | 0.41670418 | 57.8570703 |
| UP_SEQ_FEATURE        | domain:EF-hand 2                                      | 9     | 1.90677966 | 0.06277149 | MYL7, S100A  | 425        | 160      | 16021     | 2.12042647   | 1          | 0.95068477 | 64.9647217 |
| UP_SEQ_FEATURE        | domain:EF-hand 1                                      | 9     | 1.90677966 | 0.06460986 | MYL7, S100A  | 425        | 161      | 16021     | 2.10725612   | 1          | 0.93193198 | 66.0601285 |
| GOTERM_MF_FAT         | GO:0005509~calcium ion binding                        | 29    | 6.1440678  | 0.08576909 | ITGAL, MYL7  | 339        | 840      | 13288     | 1.35325186   | 1          | 0.71504085 | 72.6850432 |
| SMART                 | SM00054:EFh   | 8     | 1.69491525 | 0.08884511 | MYL7, DGKG   | 256        | 137      | 9131      | 2.08280109   | 0.99999995 | 0.60561345 | 68.2109372 |
| INTERPRO              | IPR011992:EF-Hand type                                | 10    | 2.11864407 | 0.0962106  | PLCL2, MYL7  | 425        | 227      | 17763     | 1.84120238   | 1          | 0.85578796 | 78.8559229 |
| INTERPRO              | IPR018248:EF hand                                     | 7     | 1.48305085 | 0.09662703 | MYL7, S100A  | 425        | 132      | 17763     | 2.21641711   | 1          | 0.85043939 | 79.0050735 |
| INTERPRO              | IPR001589:Actinin-type, actin-binding, conserved site | 3     | 0.63559322 | 0.12707228 | DST, LCPI, P | 425        | 26       | 17763     | 4.82253394   | 1          | 0.90219705 | 87.6000216 |
| INTERPRO              | IPR018247:EF-HAND 1                                   | 9     | 1.90677966 | 0.132954   | MYL7, S100A  | 425        | 211      | 17763     | 1.78273766   | 1          | 0.89914032 | 88.8230989 |
| SP_PIR_KEYWORDS       | EF hand   | 3     | 0.63559322 | 0.14979561 | S100A8, S10  | 439        | 28       | 17854     | 4.35746827   | 1          | 0.63013239 | 89.423854  |
| UP_SEQ_FEATURE        | calcium-binding region:2                              | 6     | 1.27118644 | 0.16700797 | DGKG, LPCA   | 425        | 110      | 16021     | 2.05617112   | 1          | 0.99083802 | 94.798876  |
| UP_SEQ_FEATURE        | calcium-binding region:1                              | 6     | 1.27118644 | 0.2125434  | DGKG, LPCA   | 425        | 120      | 16021     | 1.88482353   | 1          | 0.99365322 | 97.9053345 |

|                       |   |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 61 | Enrichment Score: 1.1622166760103947                  |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0002684~positive regulation of immune system pr    | 18    | 3.81355932 | 1.68E-05   | FCER1A, SEL  | 341        | 206      | 13588     | 3.48182103   | 0.0318992  | 0.00161964 | 0.02880861 |
| GOTERM_BP_FAT         | GO:0050865~regulation of cell activation              | 14    | 2.96610169 | 1.50E-04   | FCER1A, ITG, | 341        | 156      | 13588     | 3.57605835   | 0.25031356 | 0.00955738 | 0.25572438 |
| GOTERM_BP_FAT         | GO:0002694~regulation of leukocyte activation         | 13    | 2.75423729 | 4.94E-04   | FCER1A, ITG, | 341        | 154      | 13588     | 3.36375062   | 0.61389065 | 0.02539192 | 0.84220801 |
| GOTERM_BP_FAT         | GO:0051249~regulation of lymphocyte activation        | 10    | 2.11864407 | 0.01027182 | ITGAL, PTPN  | 341        | 144      | 13588     | 2.76718801   | 1          | 0.19824617 | 16.2000065 |
| GOTERM_BP_FAT         | GO:0050867~positive regulation of cell activation     | 8     | 1.69491525 | 0.01336067 | FCER1A, ITG, | 341        | 101      | 13588     | 3.1562382    | 1          | 0.22822401 | 20.5659401 |
| GOTERM_BP_FAT         | GO:0002696~positive regulation of leukocyte activati  | 7     | 1.48305085 | 0.03785041 | FCER1A, ITG, | 341        | 99       | 13588     | 2.81750052   | 1          | 0.40314372 | 48.3399324 |
| GOTERM_BP_FAT         | GO:0032944~regulation of mononuclear cell proliferat  | 6     | 1.27118644 | 0.04999867 | ITGAL, PTPN  | 341        | 80       | 13588     | 2.98856305   | 1          | 0.46066692 | 58.4382403 |
| GOTERM_BP_FAT         | GO:0050670~regulation of lymphocyte proliferation     | 6     | 1.27118644 | 0.04999867 | ITGAL, PTPN  | 341        | 80       | 13588     | 2.98856305   | 1          | 0.46066692 | 58.4382403 |
| GOTERM_BP_FAT         | GO:0070663~regulation of leukocyte proliferation      | 6     | 1.27118644 | 0.05455111 | ITGAL, PTPN  | 341        | 82       | 13588     | 2.91567127   | 1          | 0.47635701 | 61.7189297 |
| GOTERM_BP_FAT         | GO:0050850~positive regulation of calcium-mediated    | 3     | 0.63559322 | 0.05946757 | FCER1A, ITG, | 341        | 16       | 13588     | 7.47140762   | 1          | 0.498692   | 64.9873283 |
| GOTERM_BP_FAT         | GO:0050848~regulation of calcium-mediated signaling   | 3     | 0.63559322 | 0.07340235 | FCER1A, ITG, | 341        | 18       | 13588     | 6.64125122   | 1          | 0.55172616 | 72.8818797 |
| GOTERM_BP_FAT         | GO:0051250~negative regulation of lymphocyte activ    | 4     | 0.84745763 | 0.1407615  | PTPN6, LST1  | 341        | 52       | 13588     | 3.06519287   | 1          | 0.71006475 | 92.5494067 |
| GOTERM_BP_FAT         | GO:0002695~negative regulation of leukocyte activati  | 4     | 0.84745763 | 0.14661349 | PTPN6, LST1  | 341        | 53       | 13588     | 3.00735904   | 1          | 0.72429129 | 93.3719331 |
| GOTERM_BP_FAT         | GO:0050866~negative regulation of cell activation     | 4     | 0.84745763 | 0.14661349 | PTPN6, LST1  | 341        | 53       | 13588     | 3.00735904   | 1          | 0.72429129 | 93.3719331 |
| GOTERM_BP_FAT         | GO:0051251~positive regulation of lymphocyte activa   | 5     | 1.05932203 | 0.20911643 | ITGAL, CORC  | 341        | 94       | 13588     | 2.11954826   | 1          | 0.81824359 | 98.1972303 |
| GOTERM_BP_FAT         | GO:0070664~negative regulation of leukocyte prolifer  | 3     | 0.63559322 | 0.2179941  | PTPN6, LST1  | 341        | 35       | 13588     | 3.41550063   | 1          | 0.8303037  | 98.5139916 |
| GOTERM_BP_FAT         | GO:0032945~negative regulation of mononuclear cell    | 3     | 0.63559322 | 0.2179941  | PTPN6, LST1  | 341        | 35       | 13588     | 3.41550063   | 1          | 0.8303037  | 98.5139916 |
| GOTERM_BP_FAT         | GO:0050672~negative regulation of lymphocyte prolif   | 3     | 0.63559322 | 0.2179941  | PTPN6, LST1  | 341        | 35       | 13588     | 3.41550063   | 1          | 0.8303037  | 98.5139916 |
| GOTERM_BP_FAT         | GO:0050863~regulation of T cell activation            | 5     | 1.05932203 | 0.28529481 | ITGAL, PTPN  | 341        | 108      | 13588     | 1.84479201   | 1          | 0.88758107 | 99.6815686 |
| GOTERM_BP_FAT         | GO:0002683~negative regulation of immune system p     | 4     | 0.84745763 | 0.29628358 | PTPN6, LST1  | 341        | 76       | 13588     | 2.09723723   | 1          | 0.89442819 | 99.7557538 |
| GOTERM_BP_FAT         | GO:0032946~positive regulation of mononuclear cell    | 3     | 0.63559322 | 0.35704099 | ITGAL, CORC  | 341        | 50       | 13588     | 2.39085044   | 1          | 0.92935203 | 99.9479315 |
| GOTERM_BP_FAT         | GO:0050671~positive regulation of lymphocyte prolife  | 3     | 0.63559322 | 0.35704099 | ITGAL, CORC  | 341        | 50       | 13588     | 2.39085044   | 1          | 0.92935203 | 99.9479315 |
| GOTERM_BP_FAT         | GO:0042127~regulation of cell proliferation           | 16    | 3.38983051 | 0.37041399 | ITGAL, PTPN  | 341        | 538      | 13588     | 1.18505598   | 1          | 0.93664282 | 99.9636652 |
| GOTERM_BP_FAT         | GO:0070665~positive regulation of leukocyte prolifera | 3     | 0.63559322 | 0.37511797 | ITGAL, CORC  | 341        | 52       | 13588     | 2.29889465   | 1          | 0.93888712 | 99.9680427 |
| GOTERM_BP_FAT         | GO:0042129~regulation of T cell proliferation         | 3     | 0.63559322 | 0.43658115 | ITGAL, PTPN  | 341        | 59       | 13588     | 2.02614444   | 1          | 0.96122668 | 99.9945693 |
| GOTERM_BP_FAT         | GO:0008285~negative regulation of cell proliferation  | 7     | 1.48305085 | 0.49003359 | WNT2, PTPN   | 341        | 224      | 13588     | 1.2452346    | 1          | 0.97463001 | 99.9990141 |
| GOTERM_BP_FAT         | GO:0050870~positive regulation of T cell activation   | 3     | 0.63559322 | 0.49463336 | ITGAL, CORC  | 341        | 66       | 13588     | 1.81125033   | 1          | 0.97559837 | 99.9991557 |
| GOTERM_BP_FAT         | GO:0008284~positive regulation of cell proliferation  | 7     | 1.48305085 | 0.71870904 | ITGAL, CORC  | 341        | 284      | 13588     | 0.98215687   | 1          | 0.99763438 | 100        |

|                       |                                      |       |   |        |       |            |          |           |              |            |           |     |
|-----------------------|--------------------------------------|-------|---|--------|-------|------------|----------|-----------|--------------|------------|-----------|-----|
| Annotation Cluster 62 | Enrichment Score: 1.1524561813617786 |       |   |        |       |            |          |           |              |            |           |     |
| Category              | Term                                 | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini | FDR |

|                 |                                   |    |            |            |             |     |     |       |            |            |            |            |
|-----------------|-----------------------------------|----|------------|------------|-------------|-----|-----|-------|------------|------------|------------|------------|
| SP_PIR_KEYWORDS | lipoprotein                       | 24 | 5.08474576 | 0.01965582 | SELP, ADOR  | 439 | 589 | 17854 | 1.6571696  | 0.99947051 | 0.19898083 | 24.0293614 |
| UP_SEQ_FEATURE  | propeptide:Removed in mature form | 11 | 2.33050847 | 0.06823401 | RAC2, CD17  | 425 | 220 | 16021 | 1.88482353 | 1          | 0.93618136 | 68.1261475 |
| GOTERM_CC_FAT   | GO:0031225~anchored to membrane   | 10 | 2.11864407 | 0.09677053 | GLIPR2, RAC | 330 | 207 | 12504 | 1.8304787  | 1          | 0.55966349 | 73.8482795 |
| SP_PIR_KEYWORDS | gpi-anchor                        | 6  | 1.27118644 | 0.1892083  | CD177, CD5  | 439 | 124 | 17854 | 1.9678889  | 1          | 0.69028396 | 94.5178826 |

|                       |   |       |            |            |            |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 63 | Enrichment Score: 1.1225650397173565                |       |            |            |            |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| INTERPRO              | IPR002345:Lipocalin                                 | 5     | 1.05932203 | 0.02373824 | LCN2, ORM1 | 425        | 46       | 17763     | 4.54296675   | 1          | 0.51100207 | 30.8587719 |
| PIR_SUPERFAMILY       | PIRSF002514:lipocalin                               | 3     | 0.63559322 | 0.09594317 | LCN2, MUP3 | 239        | 18       | 8136      | 5.67364017   | 1          | 0.98125609 | 73.5704222 |
| INTERPRO              | IPR000566:Lipocalin-related protein and Bos/Can/Equ | 4     | 0.84745763 | 0.11158669 | LCN2, ORM1 | 425        | 49       | 17763     | 3.41186074   | 1          | 0.8792402  | 83.754897  |
| INTERPRO              | IPR012674:Calycin                                   | 4     | 0.84745763 | 0.1272521  | LCN2, ORM1 | 425        | 52       | 17763     | 3.21502262   | 1          | 0.89769718 | 87.6391992 |

|                       |   |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 64 | Enrichment Score: 1.115717638776693             |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_MF_FAT         | GO:0004896~cytokine receptor activity           | 7     | 1.48305085 | 0.00262987 | IL1R2, IL18R | 339        | 55       | 13288     | 4.98879056   | 0.74438059 | 0.20335353 | 3.73925694 |
| GOTERM_MF_FAT         | GO:0019955~cytokine binding                     | 8     | 1.69491525 | 0.00706455 | IL1R2, PLP2, | 339        | 88       | 13288     | 3.56342183   | 0.97458519 | 0.40822684 | 9.75130688 |
| UP_SEQ_FEATURE        | short sequence motif:Box 1 motif                | 4     | 0.84745763 | 0.02749325 | CSF3R, CSF2  | 425        | 25       | 16021     | 6.03143529   | 1          | 0.87791854 | 36.3025254 |
| KEGG_PATHWAY          | mmu04060:Cytokine-cytokine receptor interaction | 14    | 2.96610169 | 0.0376174  | IL1R2, IL18R | 178        | 244      | 5738      | 1.84960398   | 0.99289014 | 0.31646847 | 35.9759386 |
| KEGG_PATHWAY          | mmu04630:Jak-STAT signaling pathway             | 10    | 2.11864407 | 0.04460845 | OSM, PIK3C   | 178        | 152      | 5738      | 2.12078652   | 0.99722412 | 0.34327173 | 41.1806728 |
| UP_SEQ_FEATURE        | short sequence motif:WSXWS motif                | 4     | 0.84745763 | 0.04787417 | CSF3R, CSF2  | 425        | 31       | 16021     | 4.86406072   | 1          | 0.94821501 | 54.7822427 |
| INTERPRO              | IPR008957:Fibronectin, type III-like fold       | 9     | 1.90677966 | 0.07996177 | ROBO1, FL3   | 425        | 187      | 17763     | 2.01153822   | 1          | 0.81271711 | 72.1993561 |
| INTERPRO              | IPR003961:Fibronectin, type III                 | 7     | 1.48305085 | 0.30535659 | ROBO1, SOR   | 425        | 191      | 17763     | 1.53176471   | 1          | 0.99112825 | 99.6289365 |
| UP_SEQ_FEATURE        | domain:Fibronectin type-III 2                   | 5     | 1.05932203 | 0.39273885 | ROBO1, SOR   | 425        | 120      | 16021     | 1.57068627   | 1          | 0.99963721 | 99.9687129 |
| UP_SEQ_FEATURE        | domain:Fibronectin type-III 1                   | 5     | 1.05932203 | 0.39873666 | ROBO1, SOR   | 425        | 121      | 16021     | 1.55777054   | 1          | 0.99961879 | 99.9733545 |
| SMART                 | SM00060:FN3                                     | 7     | 1.48305085 | 0.44389564 | ROBO1, SOR   | 256        | 191      | 9131      | 1.30720304   | 1          | 0.98537401 | 99.9273949 |
| UP_SEQ_FEATURE        | domain:Fibronectin type-III 3                   | 3     | 0.63559322 | 0.58678124 | ROBO1, SOR   | 425        | 74       | 16021     | 1.52823529   | 1          | 0.99999288 | 99.999383  |

|                       |                                     |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|-------------------------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 65 | Enrichment Score: 1.061734433110695 |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term                                | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0006869~lipid transport          | 8     | 1.69491525 | 0.02988928 | APOB48R, AI | 341        | 119      | 13588     | 2.67882402   | 1          | 0.36431935 | 40.5141763 |
| GOTERM_BP_FAT         | GO:0010876~lipid localization       | 8     | 1.69491525 | 0.04185341 | APOB48R, AI | 341        | 128      | 13588     | 2.49046921   | 1          | 0.41826746 | 51.8982048 |
| GOTERM_BP_FAT         | GO:0055092~sterol homeostasis       | 3     | 0.63559322 | 0.13715666 | APOA2, NPC  | 341        | 26       | 13588     | 4.59778931   | 1          | 0.70152041 | 91.9958663 |
| GOTERM_BP_FAT         | GO:0042632~cholesterol homeostasis  | 3     | 0.63559322 | 0.13715666 | APOA2, NPC  | 341        | 26       | 13588     | 4.59778931   | 1          | 0.70152041 | 91.9958663 |
| GOTERM_BP_FAT         | GO:0055088~lipid homeostasis        | 3     | 0.63559322 | 0.20876021 | APOA2, NPC  | 341        | 34       | 13588     | 3.51595653   | 1          | 0.81999249 | 98.1832807 |

|                       |   |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 66 | Enrichment Score: 1.0376256693655401                  |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| KEGG_PATHWAY          | mmu00830:Retinol metabolism                           | 7     | 1.48305085 | 0.0178194  | RDH12, ALD  | 178        | 68       | 5738      | 3.31840714   | 0.90167035 | 0.17575363 | 18.8684933 |
| SP_PIR_KEYWORDS       | iron  | 15    | 3.1779661  | 0.02769782 | CYP2C37, LC | 439        | 321      | 17854     | 1.90045345   | 0.99997685 | 0.25657784 | 32.2168569 |
| GOTERM_MF_FAT         | GO:0005506~iron ion binding                           | 16    | 3.38983051 | 0.02965255 | CYP2C37, LC | 339        | 343      | 13288     | 1.82846135   | 0.99999983 | 0.57947111 | 35.3138554 |
| GOTERM_MF_FAT         | GO:0020037~heme binding                               | 9     | 1.90677966 | 0.03083058 | CYBA, CYP2C | 339        | 144      | 13288     | 2.44985251   | 0.99999991 | 0.55562229 | 36.4411087 |
| GOTERM_MF_FAT         | GO:0009055~electron carrier activity                  | 11    | 2.33050847 | 0.03375025 | ACADSB, CY  | 339        | 202      | 13288     | 2.13452496   | 0.99999998 | 0.57124913 | 39.1565953 |
| COG_ONTOLOGY          | Secondary metabolites biosynthesis, transport, and ca | 6     | 1.27118644 | 0.03575809 | CYP2C37, Cy | 36         | 109      | 2040      | 3.11926606   | 0.37710037 | 0.37710037 | 21.4218955 |
| SP_PIR_KEYWORDS       | microsome   | 7     | 1.48305085 | 0.03652135 | CYP2C37, Cy | 439        | 100      | 17854     | 2.84687927   | 0.99999928 | 0.3106799  | 40.2536482 |
| GOTERM_MF_FAT         | GO:0046906~tetrapyrrole binding                       | 9     | 1.90677966 | 0.03917277 | CYBA, CYP2C | 339        | 151      | 13288     | 2.33628319   | 1          | 0.60972046 | 43.9155297 |
| PIR_SUPERFAMILY       | PIRSF000050:cytochrome P450 CYP4B1                    | 3     | 0.63559322 | 0.04636596 | CYP4F18, LO | 239        | 12       | 8136      | 8.51046025   | 0.99999796 | 0.88739435 | 46.5456176 |
| UP_SEQ_FEATURE        | metal ion-binding site:Iron (heme axial ligand)       | 7     | 1.48305085 | 0.04759871 | CYBA, CYP2C | 425        | 99       | 16021     | 2.66540701   | 1          | 0.95486524 | 54.5701321 |
| GOTERM_CC_FAT         | GO:0005624~membrane fraction                          | 21    | 4.44915254 | 0.04872609 | SOAT2, SELP | 330        | 510      | 12504     | 1.5602139    | 0.99999886 | 0.4346439  | 48.2265033 |
| SP_PIR_KEYWORDS       | heme  | 8     | 1.69491525 | 0.06089367 | CYBA, CYP2C | 439        | 142      | 17854     | 2.29125092   | 1          | 0.41171011 | 58.0950152 |
| GOTERM_CC_FAT         | GO:0005626~insoluble fraction                         | 21    | 4.44915254 | 0.06525311 | SOAT2, SELP | 330        | 528      | 12504     | 1.50702479   | 0.99999999 | 0.48332179 | 58.903843  |
| GOTERM_CC_FAT         | GO:0000267~cell fraction                              | 23    | 4.87288136 | 0.06867698 | SOAT2, SELP | 330        | 596      | 12504     | 1.46223307   | 1          | 0.48943448 | 60.8439107 |
| GOTERM_BP_FAT         | GO:0055114~oxidation reduction                        | 24    | 5.08474576 | 0.07871341 | SEPX1, ACAT | 341        | 672      | 13588     | 1.42312526   | 1          | 0.56824681 | 75.4231278 |
| INTERPRO              | IPR002401:Cytochrome P450, E-class, group I           | 5     | 1.05932203 | 0.08613344 | CYP2C37, Cy | 425        | 70       | 17763     | 2.98537815   | 1          | 0.82902956 | 74.9299066 |
| GOTERM_CC_FAT         | GO:0005792~microsome                                  | 9     | 1.90677966 | 0.09347071 | CYP2C37, Cy | 330        | 176      | 12504     | 1.93760331   | 1          | 0.5572688  | 72.5608257 |
| GOTERM_CC_FAT         | GO:0042598~vesicular fraction                         | 9     | 1.90677966 | 0.1078757  | CYP2C37, Cy | 330        | 182      | 12504     | 1.87372627   | 1          | 0.56092287 | 77.7823795 |
| SP_PIR_KEYWORDS       | oxidoreductase  | 20    | 4.23728814 | 0.11238079 | ALDH6A1, SI | 439        | 572      | 17854     | 1.42201762   | 1          | 0.56781537 | 80.8020468 |
| KEGG_PATHWAY          | mmu00590:Arachidonic acid metabolism                  | 6     | 1.27118644 | 0.11239688 | CYP2C37, Cy | 178        | 83       | 5738      | 2.33031      | 0.99999979 | 0.53654093 | 75.0073613 |

|                 |  |    |            |            |             |     |     |       |            |   |            |            |
|-----------------|--|----|------------|------------|-------------|-----|-----|-------|------------|---|------------|------------|
| INTERPRO        | IPR017973:Cytochrome P450, C-terminal region     | 5  | 1.05932203 | 0.12837308 | CYP2C37, CY | 425 | 81  | 17763 | 2.57995643 | 1 | 0.89506139 | 87.8808283 |
| INTERPRO        | IPR001128:Cytochrome P450                        | 5  | 1.05932203 | 0.15442508 | CYP2C37, CY | 425 | 87  | 17763 | 2.4020284  | 1 | 0.92524172 | 92.3958736 |
| INTERPRO        | IPR017972:Cytochrome P450, conserved site        | 5  | 1.05932203 | 0.16352017 | CYP2C37, CY | 425 | 89  | 17763 | 2.34805023 | 1 | 0.92994354 | 93.5596601 |
| SP_PIR_KEYWORDS | chromoprotein                                    | 3  | 0.63559322 | 0.25723602 | LOC1000442  | 439 | 40  | 17854 | 3.05022779 | 1 | 0.77836199 | 98.3704396 |
| SP_PIR_KEYWORDS | Monooxygenase                                    | 5  | 1.05932203 | 0.27357974 | CYP2C37, CY | 439 | 108 | 17854 | 1.88285666 | 1 | 0.78926524 | 98.8024372 |
| KEGG_PATHWAY    | mmu00980:Metabolism of xenobiotics by cytochrome | 3  | 0.63559322 | 0.60950691 | CYP2C37, UC | 178 | 66  | 5738  | 1.46527068 | 1 | 0.88538217 | 99.9982189 |
| GOTERM_CC_FAT   | GO:0005783--endoplasmic reticulum                | 22 | 4.66101695 | 0.62502758 | SOAT2, CLN: | 330 | 838 | 12504 | 0.9947494  | 1 | 0.96669736 | 99.9997567 |
| KEGG_PATHWAY    | mmu00982:Drug metabolism                         | 3  | 0.63559322 | 0.67891054 | CYP2C37, UC | 178 | 75  | 5738  | 1.2894382  | 1 | 0.91305472 | 99.998171  |
| SP_PIR_KEYWORDS | endoplasmic reticulum                            | 16 | 3.38983051 | 0.69600915 | SOAT2, CYP: | 439 | 678 | 17854 | 0.95975702 | 1 | 0.98111132 | 99.9999931 |

|                       |   |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 67 | Enrichment Score: 1.0372743993536089                    |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0002253--activation of immune response               | 7     | 1.48305085 | 0.02071043 | CFP, PTPN6, | 341        | 86       | 13588     | 3.24340176   | 1          | 0.29142924 | 30.1090159 |
| GOTERM_BP_FAT         | GO:0002757--immune response-activating signal trans     | 5     | 1.05932203 | 0.0316158  | PTPN6, MYD  | 341        | 48       | 13588     | 4.15078201   | 1          | 0.3720084  | 42.3006094 |
| GOTERM_BP_FAT         | GO:0002764--immune response-regulating signal tran      | 5     | 1.05932203 | 0.04073815 | PTPN6, MYD  | 341        | 52       | 13588     | 3.83149109   | 1          | 0.4158603  | 50.9307659 |
| GOTERM_BP_FAT         | GO:0002429--immune response-activating cell surface     | 4     | 0.84745763 | 0.08249216 | PTPN6, PLCG | 341        | 41       | 13588     | 3.88756169   | 1          | 0.57837205 | 77.092776  |
| GOTERM_BP_FAT         | GO:0043388--positive regulation of DNA binding          | 4     | 0.84745763 | 0.08726714 | HMGB2, MYI  | 341        | 42       | 13588     | 3.7950007    | 1          | 0.59232316 | 79.0500715 |
| GOTERM_BP_FAT         | GO:0002768--immune response-regulating cell surface     | 4     | 0.84745763 | 0.09715603 | PTPN6, PLCG | 341        | 44       | 13588     | 3.62250067   | 1          | 0.61899413 | 82.6139954 |
| GOTERM_BP_FAT         | GO:0051099--positive regulation of binding              | 4     | 0.84745763 | 0.1022637  | HMGB2, MYI  | 341        | 45       | 13588     | 3.54200065   | 1          | 0.63527638 | 84.2230259 |
| GOTERM_BP_FAT         | GO:0051101--regulation of DNA binding                   | 5     | 1.05932203 | 0.11417614 | HMGB2, MYI  | 341        | 74       | 13588     | 2.69239914   | 1          | 0.65906025 | 87.4478536 |
| GOTERM_BP_FAT         | GO:0051090--regulation of transcription factor activity | 4     | 0.84745763 | 0.18324882 | MYD88, NFK  | 341        | 59       | 13588     | 2.70152592   | 1          | 0.78452092 | 96.8725133 |
| GOTERM_BP_FAT         | GO:0051098--regulation of binding                       | 5     | 1.05932203 | 0.18852368 | HMGB2, MYI  | 341        | 90       | 13588     | 2.21375041   | 1          | 0.79357332 | 97.2008374 |
| GOTERM_BP_FAT         | GO:0051091--positive regulation of transcription facto  | 3     | 0.63559322 | 0.20876021 | MYD88, TLR: | 341        | 34       | 13588     | 3.51595653   | 1          | 0.81999249 | 98.1832807 |
| GOTERM_BP_FAT         | GO:0050851--antigen receptor-mediated signaling pat     | 3     | 0.63559322 | 0.22726251 | PTPN6, PLCG | 341        | 36       | 13588     | 3.32062561   | 1          | 0.83887325 | 98.7883256 |

|                       |  |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 68 | Enrichment Score: 1.0221880093293618       |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term                                       | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0030099--myeloid cell differentiation   | 7     | 1.48305085 | 0.03328711 | CEBPE, HCLS | 341        | 96       | 13588     | 2.90554741   | 1          | 0.37869249 | 43.9816993 |
| GOTERM_BP_FAT         | GO:0030218--erythrocyte differentiation    | 4     | 0.84745763 | 0.11820104 | HCLS1, G6PT | 341        | 48       | 13588     | 3.32062561   | 1          | 0.66754296 | 88.3891745 |
| GOTERM_BP_FAT         | GO:0034101--erythrocyte homeostasis        | 4     | 0.84745763 | 0.13499092 | HCLS1, G6PT | 341        | 51       | 13588     | 3.12529469   | 1          | 0.69841699 | 91.6449243 |
| GOTERM_BP_FAT         | GO:0048872--homeostasis of number of cells | 6     | 1.27118644 | 0.15347797 | CORO1A, HC  | 341        | 113      | 13588     | 2.11579685   | 1          | 0.73739857 | 94.2277248 |

|                       |  |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 69 | Enrichment Score: 1.000532217220348                      |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0030005--cellular di-, tri-valent inorganic cation ho | 9     | 1.90677966 | 0.01940489 | CLN3, SLC11 | 341        | 134      | 13588     | 2.67632512   | 1          | 0.28184015 | 28.4968406 |
| GOTERM_BP_FAT         | GO:0042592--homeostatic process                          | 24    | 5.08474576 | 0.02118115 | CLN3, HAMF  | 341        | 584      | 13588     | 1.63756879   | 1          | 0.29491251 | 30.6818609 |
| GOTERM_BP_FAT         | GO:0055066--di-, tri-valent inorganic cation homeosta    | 9     | 1.90677966 | 0.03045288 | CLN3, SLC11 | 341        | 146      | 13588     | 2.45635319   | 1          | 0.36756861 | 41.1029765 |
| GOTERM_BP_FAT         | GO:0006879--cellular iron ion homeostasis                | 4     | 0.84745763 | 0.03509761 | SLC11A1, HA | 341        | 29       | 13588     | 5.49620791   | 1          | 0.38830394 | 45.750705  |
| GOTERM_BP_FAT         | GO:0030003--cellular cation homeostasis                  | 9     | 1.90677966 | 0.03733912 | CLN3, SLC11 | 341        | 152      | 13588     | 2.35939188   | 1          | 0.40102328 | 47.8679985 |
| GOTERM_BP_FAT         | GO:0055080--cation homeostasis                           | 10    | 2.11864407 | 0.04194274 | CLN3, EDNR  | 341        | 184      | 13588     | 2.1656254    | 1          | 0.41688875 | 51.9749085 |
| GOTERM_BP_FAT         | GO:0055072--iron ion homeostasis                         | 4     | 0.84745763 | 0.05640109 | SLC11A1, HA | 341        | 35       | 13588     | 4.55400084   | 1          | 0.48398039 | 62.9811028 |
| GOTERM_BP_FAT         | GO:0048878--chemical homeostasis                         | 15    | 3.1779661  | 0.07538265 | CLN3, HAMF  | 341        | 365      | 13588     | 1.63756879   | 1          | 0.5577812  | 73.8570435 |
| GOTERM_BP_FAT         | GO:0050801--ion homeostasis                              | 12    | 2.54237288 | 0.11837837 | CLN3, EDNR  | 341        | 293      | 13588     | 1.63197982   | 1          | 0.66481357 | 88.4290785 |
| GOTERM_BP_FAT         | GO:0006873--cellular ion homeostasis                     | 11    | 2.33050847 | 0.12023422 | CLN3, SLC11 | 341        | 261      | 13588     | 1.67939686   | 1          | 0.66924147 | 88.8390168 |
| GOTERM_BP_FAT         | GO:0055082--cellular chemical homeostasis                | 11    | 2.33050847 | 0.13590982 | CLN3, SLC11 | 341        | 268      | 13588     | 1.63553202   | 1          | 0.69950838 | 91.795558  |
| GOTERM_BP_FAT         | GO:0019725--cellular homeostasis                         | 13    | 2.75423729 | 0.15151907 | CLN3, HAMF  | 341        | 343      | 13588     | 1.51025538   | 1          | 0.733954   | 93.9947656 |
| GOTERM_BP_FAT         | GO:0006874--cellular calcium ion homeostasis             | 5     | 1.05932203 | 0.19360975 | CLN3, ATP2A | 341        | 91       | 13588     | 2.18942348   | 1          | 0.7993914  | 97.4864512 |
| GOTERM_BP_FAT         | GO:0055074--calcium ion homeostasis                      | 5     | 1.05932203 | 0.21436291 | CLN3, ATP2A | 341        | 95       | 13588     | 2.09723723   | 1          | 0.82568124 | 98.3913527 |
| GOTERM_BP_FAT         | GO:0006875--cellular metal ion homeostasis               | 5     | 1.05932203 | 0.24110662 | CLN3, ATP2A | 341        | 100      | 13588     | 1.99237537   | 1          | 0.85416219 | 99.110814  |
| GOTERM_BP_FAT         | GO:0055065--metal ion homeostasis                        | 5     | 1.05932203 | 0.27411978 | CLN3, ATP2A | 341        | 106      | 13588     | 1.8795994    | 1          | 0.88263613 | 99.5847075 |
| GOTERM_BP_FAT         | GO:0006816--calcium ion transport                        | 4     | 0.84745763 | 0.58688119 | CORO1A, AT  | 341        | 121      | 13588     | 1.31727297   | 1          | 0.99008943 | 99.9999732 |
| KEGG_PATHWAY          | mmu04020:Calcium signaling pathway                       | 6     | 1.27118644 | 0.70872641 | EDNRB, ATP: | 178        | 191      | 5738      | 1.0126478    | 1          | 0.91677919 | 99.9999411 |

|                       |   |       |            |            |            |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 70 | Enrichment Score: 0.9932727066924716                  |       |            |            |            |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| UP_SEQ_FEATURE        | metal ion-binding site:Calcium 2                      | 5     | 1.05932203 | 0.06056421 | ATP2A2, MN | 425        | 56       | 16021     | 3.3657563    | 1          | 0.95101944 | 63.6056793 |
| UP_SEQ_FEATURE        | metal ion-binding site:Calcium 2; via carbonyl oxygen | 4     | 0.84745763 | 0.07381155 | ATP2A2, MN | 425        | 37       | 16021     | 4.07529412   | 1          | 0.94454491 | 71.0765903 |

|                |   |   |            |            |            |     |    |       |            |   |            |            |
|----------------|---|---|------------|------------|------------|-----|----|-------|------------|---|------------|------------|
| UP_SEQ_FEATURE | metal ion-binding site:Calcium 3; via carbonyl oxygen | 3 | 0.63559322 | 0.10551938 | MMP9, PADI | 425 | 21 | 16021 | 5.38521008 | 1 | 0.97104391 | 83.5374908 |
| UP_SEQ_FEATURE | metal ion-binding site:Calcium 1                      | 4 | 0.84745763 | 0.11592968 | ATP2A2, MN | 425 | 45 | 16021 | 3.35079739 | 1 | 0.97341578 | 86.3779294 |
| UP_SEQ_FEATURE | metal ion-binding site:Calcium 3                      | 3 | 0.63559322 | 0.19759193 | MMP9, PADI | 425 | 31 | 16021 | 3.64804554 | 1 | 0.99335128 | 97.1603135 |

|                       |  |       |            |            |               |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 71 | Enrichment Score: 0.9578501287373892     |       |            |            |               |            |          |           |              |            |            |            |
| Category              | Term                                     | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_MF_FAT         | GO:0005524~ATP binding                   | 48    | 10.1694915 | 0.04495537 | KIF23, KIF22, | 339        | 1443     | 13288     | 1.3038716    | 1          | 0.62945225 | 48.607199  |
| GOTERM_MF_FAT         | GO:0001882~nucleoside binding            | 51    | 10.8050847 | 0.04846187 | KIF23, KIF22, | 339        | 1558     | 13288     | 1.28310632   | 1          | 0.64273474 | 51.271432  |
| GOTERM_MF_FAT         | GO:0032559~adenyl ribonucleotide binding | 48    | 10.1694915 | 0.05221542 | KIF23, KIF22, | 339        | 1460     | 13288     | 1.28868954   | 1          | 0.65645441 | 53.980528  |
| GOTERM_MF_FAT         | GO:0030554~adenyl nucleotide binding     | 50    | 10.5932203 | 0.05419348 | KIF23, KIF22, | 339        | 1535     | 13288     | 1.2767961    | 1          | 0.64326752 | 55.3511094 |
| GOTERM_MF_FAT         | GO:0001883~purine nucleoside binding     | 50    | 10.5932203 | 0.06222132 | KIF23, KIF22, | 339        | 1548     | 13288     | 1.26607365   | 1          | 0.65817332 | 60.5328274 |
| SP_PIR_KEYWORDS       | kinase                                   | 25    | 5.29661017 | 0.06942628 | FGR, PFKFB4,  | 439        | 707      | 17854     | 1.43810834   | 1          | 0.42765338 | 63.0692097 |
| SP_PIR_KEYWORDS       | atp-binding                              | 39    | 8.26271186 | 0.1341739  | KIF23, KIF22, | 439        | 1287     | 17854     | 1.23241527   | 1          | 0.61089838 | 86.3919524 |
| GOTERM_MF_FAT         | GO:0032555~purine ribonucleotide binding | 54    | 11.440678  | 0.1366704  | KIF23, KIF22, | 339        | 1796     | 13288     | 1.1785482    | 1          | 0.80203656 | 88.0780467 |
| GOTERM_MF_FAT         | GO:0032553~ribonucleotide binding        | 54    | 11.440678  | 0.1366704  | KIF23, KIF22, | 339        | 1796     | 13288     | 1.1785482    | 1          | 0.80203656 | 88.0780467 |
| GOTERM_MF_FAT         | GO:0017076~purine nucleotide binding     | 56    | 11.8644068 | 0.13751939 | KIF23, KIF22, | 339        | 1871     | 13288     | 1.17320569   | 1          | 0.79069541 | 88.2465957 |
| SP_PIR_KEYWORDS       | nucleotide-binding                       | 47    | 9.95762712 | 0.17725109 | KIF23, KIF22, | 439        | 1631     | 17854     | 1.17196572   | 1          | 0.67480403 | 93.2862024 |
| SP_PIR_KEYWORDS       | transferase                              | 39    | 8.26271186 | 0.25590243 | POLR2G, GC    | 439        | 1385     | 17854     | 1.14521188   | 1          | 0.7808194  | 98.3294652 |
| UP_SEQ_FEATURE        | nucleotide phosphate-binding region:ATP  | 28    | 5.93220339 | 0.2878483  | KIF22, FGR, F | 425        | 907      | 16021     | 1.16372787   | 1          | 0.99758364 | 99.5880337 |
| GOTERM_MF_FAT         | GO:0000166~nucleotide binding            | 60    | 12.7118644 | 0.32471303 | KIF23, KIF22, | 339        | 2183     | 13288     | 1.07735154   | 1          | 0.96435088 | 99.6593145 |

|                       |   |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 72 | Enrichment Score: 0.9566679698523817                      |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| PIR_SUPERFAMILY       | PIRSF002048:histone H2A                                   | 4     | 0.84745763 | 0.00568835 | HIST1H2AF,   | 239        | 13       | 8136      | 10.4744126   | 0.79288194 | 0.40833939 | 7.24982863 |
| SP_PIR_KEYWORDS       | chromosomal protein                                       | 10    | 2.11864407 | 0.00641081 | HMGB2, HIS   | 439        | 136      | 17854     | 2.9904194    | 0.91318262 | 0.10514051 | 8.51876608 |
| SP_PIR_KEYWORDS       | citruination  | 4     | 0.84745763 | 0.00647327 | HIST1H2AF,   | 439        | 16       | 17854     | 10.167426    | 0.91523228 | 0.10174152 | 8.59835841 |
| KEGG_PATHWAY          | mmu05322:Systemic lupus erythematosus                     | 9     | 1.90677966 | 0.01376175 | HIST1H2AF,   | 178        | 103      | 5738      | 2.81673394   | 0.83263775 | 0.18013995 | 14.8838483 |
| INTERPRO              | IPR007125:Histone core                                    | 5     | 1.05932203 | 0.0175309  | HIST1H2AF,   | 425        | 42       | 17763     | 4.97563025   | 0.99999933 | 0.49192988 | 23.7890095 |
| INTERPRO              | IPR002119:Histone H2A                                     | 4     | 0.84745763 | 0.02104009 | HIST1H2AF,   | 425        | 25       | 17763     | 6.68724706   | 0.99999996 | 0.50951644 | 27.864651  |
| SP_PIR_KEYWORDS       | nucleosome core   | 5     | 1.05932203 | 0.02239815 | HIST1H2AF,   | 439        | 44       | 17854     | 4.62155726   | 0.99981737 | 0.21803454 | 26.9191173 |
| SMART                 | SM00414:H2A   | 4     | 0.84745763 | 0.03146362 | HIST1H2AF,   | 256        | 25       | 9131      | 5.706875     | 0.99683139 | 0.40733911 | 32.5497895 |
| SP_PIR_KEYWORDS       | ubl conjugation   | 21    | 4.44915254 | 0.03441062 | KIF22, HIST1 | 439        | 524      | 17854     | 1.62989271   | 0.99999834 | 0.30206549 | 38.4159198 |
| SP_PIR_KEYWORDS       | methylation   | 11    | 2.33050847 | 0.04676936 | HIST1H2AF,   | 439        | 221      | 17854     | 2.0242839    | 0.99999999 | 0.37293324 | 48.4748972 |
| UP_SEQ_FEATURE        | cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain | 9     | 1.90677966 | 0.07840929 | HIST1H2AF,   | 425        | 168      | 16021     | 2.01945378   | 1          | 0.94490627 | 73.313991  |
| GOTERM_CC_FAT         | GO:0000786~nucleosome                                     | 5     | 1.05932203 | 0.08010334 | HIST1H2AF,   | 330        | 62       | 12504     | 3.05571848   | 1          | 0.52192073 | 66.7227627 |
| GOTERM_BP_FAT         | GO:0006323~DNA packaging                                  | 6     | 1.27118644 | 0.10918385 | HIST1H2AF,   | 341        | 101      | 13588     | 2.36717865   | 1          | 0.65192926 | 86.1803571 |
| GOTERM_BP_FAT         | GO:0006334~nucleosome assembly                            | 5     | 1.05932203 | 0.11004397 | HIST1H2AF,   | 341        | 73       | 13588     | 2.72928132   | 1          | 0.65152022 | 86.4069958 |
| GOTERM_BP_FAT         | GO:0031497~chromatin assembly                             | 5     | 1.05932203 | 0.11837582 | HIST1H2AF,   | 341        | 75       | 13588     | 2.65650049   | 1          | 0.6664589  | 88.4285054 |
| GOTERM_BP_FAT         | GO:0065004~protein-DNA complex assembly                   | 5     | 1.05932203 | 0.12264171 | HIST1H2AF,   | 341        | 76       | 13588     | 2.62154653   | 1          | 0.67209563 | 89.3504506 |
| GOTERM_BP_FAT         | GO:0034728~nucleosome organization                        | 5     | 1.05932203 | 0.12264171 | HIST1H2AF,   | 341        | 76       | 13588     | 2.62154653   | 1          | 0.67209563 | 89.3504506 |
| GOTERM_CC_FAT         | GO:0005694~chromosome                                     | 15    | 3.1779661  | 0.12521279 | KIF22, HMGB  | 330        | 378      | 12504     | 1.5036075    | 1          | 0.60002613 | 82.8453904 |
| GOTERM_CC_FAT         | GO:0044427~chromosomal part                               | 13    | 2.75423729 | 0.13498174 | KIF22, MKI67 | 330        | 318      | 12504     | 1.54899943   | 1          | 0.62055877 | 85.2052054 |
| GOTERM_CC_FAT         | GO:0032993~protein-DNA complex                            | 5     | 1.05932203 | 0.13507589 | HIST1H2AF,   | 330        | 75       | 12504     | 2.52606061   | 1          | 0.61197786 | 85.226411  |
| SP_PIR_KEYWORDS       | isopeptide bond   | 11    | 2.33050847 | 0.14511531 | NFE2, HIST1  | 439        | 277      | 17854     | 1.61504239   | 1          | 0.6234545  | 88.5887284 |
| GOTERM_CC_FAT         | GO:0000785~chromatin                                      | 8     | 1.69491525 | 0.14512932 | KIF22, HIST1 | 330        | 165      | 12504     | 1.83713499   | 1          | 0.62336095 | 87.3359449 |
| INTERPRO              | IPR009072:Histone-fold                                    | 4     | 0.84745763 | 0.17831426 | HIST1H2AF,   | 425        | 61       | 17763     | 2.74067502   | 1          | 0.93735273 | 95.1036515 |
| GOTERM_BP_FAT         | GO:0051258~protein polymerization                         | 3     | 0.63559322 | 0.26453696 | WNT2, TUBA   | 341        | 40       | 13588     | 2.98856305   | 1          | 0.87553219 | 99.4801793 |
| GOTERM_BP_FAT         | GO:0034621~cellular macromolecular complex subuni         | 9     | 1.90677966 | 0.27274324 | HIST1H2AF,   | 341        | 245      | 13588     | 1.46378598   | 1          | 0.88201845 | 99.5710186 |
| GOTERM_BP_FAT         | GO:0006333~chromatin assembly or disassembly              | 5     | 1.05932203 | 0.29090767 | HIST1H2AF,   | 341        | 109      | 13588     | 1.82987631   | 1          | 0.89077897 | 99.7217707 |
| GOTERM_BP_FAT         | GO:0034622~cellular macromolecular complex assem          | 8     | 1.69491525 | 0.29924137 | HIST1H2AF,   | 341        | 217      | 13588     | 1.46903253   | 1          | 0.89412272 | 99.7727437 |
| GOTERM_BP_FAT         | GO:0043933~macromolecular complex subunit organi          | 9     | 1.90677966 | 0.70356773 | HIST1H2AF,   | 341        | 367      | 13588     | 0.97718683   | 1          | 0.99700602 | 99.9999999 |
| GOTERM_BP_FAT         | GO:0065003~macromolecular complex assembly                | 8     | 1.69491525 | 0.74595003 | HIST1H2AF,   | 341        | 338      | 13588     | 0.94313627   | 1          | 0.99826918 | 100        |
| GOTERM_BP_FAT         | GO:0043623~cellular protein complex assembly              | 3     | 0.63559322 | 0.75688937 | WNT2, TUBA   | 341        | 108      | 13588     | 1.1068752    | 1          | 0.99854384 | 100        |
| GOTERM_BP_FAT         | GO:0051276~chromosome organization                        | 8     | 1.69491525 | 0.88338221 | HIST1H2AF,   | 341        | 404      | 13588     | 0.78905955   | 1          | 0.99991952 | 100        |
| GOTERM_BP_FAT         | GO:0006325~chromatin organization                         | 6     | 1.27118644 | 0.89908246 | HIST1H2AF,   | 341        | 315      | 13588     | 0.75900014   | 1          | 0.99995533 | 100        |
| GOTERM_BP_FAT         | GO:0070271~protein complex biogenesis                     | 3     | 0.63559322 | 0.97905535 | WNT2, TUBA   | 341        | 227      | 13588     | 0.52661904   | 1          | 0.99999992 | 100        |
| GOTERM_BP_FAT         | GO:0006461~protein complex assembly                       | 3     | 0.63559322 | 0.97905535 | WNT2, TUBA   | 341        | 227      | 13588     | 0.52661904   | 1          | 0.99999992 | 100        |



|                       |   |                                      |            |            |              |            |          |           |              |            |            |            |
|-----------------------|---|--------------------------------------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 73 |   | Enrichment Score: 0.9172861398951649 |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count                                | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0031252~cell leading edge                        | 8                                    | 1.69491525 | 0.0283458  | CORO1A, TI   | 330        | 112      | 12504     | 2.70649351   | 0.99962137 | 0.32561064 | 31.5414685 |
| GOTERM_CC_FAT         | GO:0030027~lamellipodium                            | 5                                    | 1.05932203 | 0.08385269 | TIAM2, PSTP  | 330        | 63       | 12504     | 3.00721501   | 1          | 0.52758032 | 68.4664576 |
| SP_PIR_KEYWORDS       | cell projection                                     | 8                                    | 1.69491525 | 0.20749256 | TIAM2, FERN  | 439        | 196      | 17854     | 1.65998791   | 1          | 0.71703518 | 96.0022899 |
| GOTERM_CC_FAT         | GO:0042995~cell projection                          | 17                                   | 3.60169492 | 0.43435731 | CLN3, MYL7,  | 330        | 575      | 12504     | 1.12025296   | 1          | 0.90272342 | 99.9451772 |
| Annotation Cluster 74 |   | Enrichment Score: 0.8907200617815311 |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count                                | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS       | lysosome  | 8                                    | 1.69491525 | 0.0646368  | CLN3, NPC1,  | 439        | 144      | 17854     | 2.25942799   | 1          | 0.410803   | 60.3490556 |
| GOTERM_CC_FAT         | GO:0005764~lysosome                                 | 9                                    | 1.90677966 | 0.09814259 | CLN3, SLC11  | 330        | 178      | 12504     | 1.91583248   | 1          | 0.55455542 | 74.366981  |
| GOTERM_CC_FAT         | GO:0000323~lytic vacuole                            | 9                                    | 1.90677966 | 0.10052736 | CLN3, SLC11  | 330        | 179      | 12504     | 1.90512951   | 1          | 0.55352492 | 75.2459709 |
| GOTERM_CC_FAT         | GO:0005773~vacuole                                  | 9                                    | 1.90677966 | 0.17090162 | CLN3, SLC11  | 330        | 204      | 12504     | 1.67165775   | 1          | 0.65693508 | 91.5398574 |
| GOTERM_CC_FAT         | GO:0005770~late endosome                            | 3                                    | 0.63559322 | 0.32287309 | CLN3, SLC11  | 330        | 44       | 12504     | 2.58347107   | 1          | 0.8165367  | 99.4131285 |
| Annotation Cluster 75 |   | Enrichment Score: 0.8885094126339086 |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count                                | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| INTERPRO              | IPR003663:Sugar/inositol transporter                | 3                                    | 0.63559322 | 0.0271114  | SLC2A6, SLC  | 425        | 11       | 17763     | 11.3987166   | 1          | 0.54580654 | 34.4385838 |
| INTERPRO              | IPR005828:General substrate transporter             | 3                                    | 0.63559322 | 0.04280033 | SLC2A6, SLC  | 425        | 14       | 17763     | 8.95613445   | 1          | 0.64456033 | 48.9263143 |
| GOTERM_MF_FAT         | GO:0005351~sugar:hydrogen symporter activity        | 3                                    | 0.63559322 | 0.06121991 | SLC2A6, SLC  | 339        | 16       | 13288     | 7.34955752   | 1          | 0.66405398 | 59.918497  |
| GOTERM_MF_FAT         | GO:0005402~cation:sugar symporter activity          | 3                                    | 0.63559322 | 0.06121991 | SLC2A6, SLC  | 339        | 16       | 13288     | 7.34955752   | 1          | 0.66405398 | 59.918497  |
| GOTERM_MF_FAT         | GO:0015295~solute:hydrogen symporter activity       | 3                                    | 0.63559322 | 0.08303689 | SLC2A6, SLC  | 339        | 19       | 13288     | 6.18910107   | 1          | 0.72279084 | 71.4795938 |
| GOTERM_MF_FAT         | GO:0051119~sugar transmembrane transporter activit  | 3                                    | 0.63559322 | 0.12353375 | SLC2A6, SLC  | 339        | 24       | 13288     | 4.89970501   | 1          | 0.78081113 | 85.1658355 |
| INTERPRO              | IPR005829:Sugar transporter, conserved site         | 3                                    | 0.63559322 | 0.16858199 | SLC2A6, SLC  | 425        | 31       | 17763     | 4.04470588   | 1          | 0.92939491 | 94.1329628 |
| GOTERM_BP_FAT         | GO:0008643~carbohydrate transport                   | 4                                    | 0.84745763 | 0.18957791 | APOA2, SLC2  | 341        | 60       | 13588     | 2.65650049   | 1          | 0.79431864 | 97.2624385 |
| SP_PIR_KEYWORDS       | sugar transport                                     | 3                                    | 0.63559322 | 0.2207557  | SLC2A6, SLC  | 439        | 36       | 17854     | 3.38914199   | 1          | 0.72703352 | 96.8352501 |
| GOTERM_MF_FAT         | GO:0015293~symporter activity                       | 6                                    | 1.27118644 | 0.24580198 | SLC2A6, SLC  | 339        | 132      | 13288     | 1.78171091   | 1          | 0.92297679 | 98.313575  |
| GOTERM_MF_FAT         | GO:0015294~solute:cation symporter activity         | 4                                    | 0.84745763 | 0.28400611 | SLC2A6, SLC  | 339        | 73       | 13288     | 2.1478159    | 1          | 0.94939539 | 99.2052219 |
| GOTERM_BP_FAT         | GO:0055085~transmembrane transport                  | 6                                    | 1.27118644 | 0.99088208 | LOC1000476   | 341        | 460      | 13588     | 0.5197501    | 1          | 1          | 100        |
| Annotation Cluster 76 |   | Enrichment Score: 0.8668362658133669 |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count                                | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0034358~plasma lipoprotein particle              | 4                                    | 0.84745763 | 0.03310998 | APOB48R, AI  | 330        | 27       | 12504     | 5.61346801   | 0.99990153 | 0.35552561 | 35.8352122 |
| GOTERM_CC_FAT         | GO:0022994~protein-lipid complex                    | 4                                    | 0.84745763 | 0.03310998 | APOB48R, AI  | 330        | 27       | 12504     | 5.61346801   | 0.99990153 | 0.35552561 | 35.8352122 |
| SP_PIR_KEYWORDS       | steroid metabolism                                  | 4                                    | 0.84745763 | 0.07002027 | APOB48R, SC  | 439        | 39       | 17854     | 4.17125168   | 1          | 0.42403184 | 63.3942165 |
| SP_PIR_KEYWORDS       | lipid metabolism                                    | 7                                    | 1.48305085 | 0.11820722 | APOB48R, SC  | 439        | 136      | 17854     | 2.09329358   | 1          | 0.57413404 | 82.474953  |
| SP_PIR_KEYWORDS       | cholesterol metabolism                              | 3                                    | 0.63559322 | 0.16712537 | APOB48R, SC  | 439        | 30       | 17854     | 4.06697039   | 1          | 0.66236958 | 92.0473572 |
| GOTERM_BP_FAT         | GO:0008203~cholesterol metabolic process            | 4                                    | 0.84745763 | 0.25539126 | APOB48R, SC  | 341        | 70       | 13588     | 2.27700042   | 1          | 0.86750986 | 99.3577147 |
| GOTERM_BP_FAT         | GO:0016125~sterol metabolic process                 | 4                                    | 0.84745763 | 0.30314755 | APOB48R, SC  | 341        | 77       | 13588     | 2.07000038   | 1          | 0.89703018 | 99.7934805 |
| SP_PIR_KEYWORDS       | lipid transport                                     | 3                                    | 0.63559322 | 0.35700121 | APOB48R, AI  | 439        | 51       | 17854     | 2.39233552   | 1          | 0.86436266 | 99.7787525 |
| GOTERM_BP_FAT         | GO:0008202~steroid metabolic process                | 6                                    | 1.27118644 | 0.37680421 | APOB48R, SC  | 341        | 161      | 13588     | 1.48500027   | 1          | 0.93933849 | 99.9694872 |
| Annotation Cluster 77 |   | Enrichment Score: 0.8457520523302436 |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count                                | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0043065~positive regulation of apoptosis         | 12                                   | 2.54237288 | 0.04755364 | ALDH1A1, BI  | 341        | 248      | 13588     | 1.92810519   | 1          | 0.44992006 | 56.568742  |
| GOTERM_BP_FAT         | GO:0043068~positive regulation of programmed cell d | 12                                   | 2.54237288 | 0.05005311 | ALDH1A1, BI  | 341        | 250      | 13588     | 1.91268035   | 1          | 0.45896798 | 58.4789937 |
| GOTERM_BP_FAT         | GO:0010942~positive regulation of cell death        | 12                                   | 2.54237288 | 0.05214754 | ALDH1A1, BI  | 341        | 252      | 13588     | 1.89750035   | 1          | 0.46890802 | 60.0184781 |
| GOTERM_BP_FAT         | GO:0043067~regulation of programmed cell death      | 20                                   | 4.23728814 | 0.11056789 | PIK3CG, BID, | 341        | 560      | 13588     | 1.42312526   | 1          | 0.65165046 | 86.5433258 |
| GOTERM_BP_FAT         | GO:0010941~regulation of cell death                 | 20                                   | 4.23728814 | 0.11382789 | PIK3CG, BID, | 341        | 563      | 13588     | 1.415542     | 1          | 0.65956345 | 87.3631172 |
| GOTERM_BP_FAT         | GO:0006917~induction of apoptosis                   | 8                                    | 1.69491525 | 0.12619015 | PTPN6, CASF  | 341        | 167      | 13588     | 1.90886263   | 1          | 0.67842056 | 90.0641832 |
| GOTERM_BP_FAT         | GO:0012502~induction of programmed cell death       | 8                                    | 1.69491525 | 0.12619015 | PTPN6, CASF  | 341        | 167      | 13588     | 1.90886263   | 1          | 0.67842056 | 90.0641832 |
| GOTERM_BP_FAT         | GO:0042981~regulation of apoptosis                  | 19                                   | 4.02542373 | 0.15403411 | PIK3CG, BID, | 341        | 553      | 13588     | 1.36908253   | 1          | 0.73732079 | 94.2922957 |
| GOTERM_BP_FAT         | GO:0043069~negative regulation of programmed cell   | 9                                    | 1.90677966 | 0.26734943 | PIK3CG, CLN  | 341        | 244      | 13588     | 1.46978511   | 1          | 0.87782358 | 99.5131774 |
| GOTERM_BP_FAT         | GO:0060548~negative regulation of cell death        | 9                                    | 1.90677966 | 0.27274324 | PIK3CG, CLN  | 341        | 245      | 13588     | 1.46378598   | 1          | 0.88201845 | 99.5710186 |
| GOTERM_BP_FAT         | GO:0043066~negative regulation of apoptosis         | 8                                    | 1.69491525 | 0.39036113 | PIK3CG, CLN  | 341        | 239      | 13588     | 1.33380778   | 1          | 0.94433197 | 99.9790599 |
| GOTERM_BP_FAT         | GO:0006916~anti-apoptosis                           | 3                                    | 0.63559322 | 0.65055091 | PROK2, HSP,  | 341        | 88       | 13588     | 1.35843775   | 1          | 0.99480323 | 99.9999985 |

|                       |  |       |            |            |              |            |          |           |              |            |            |            |            |
|-----------------------|--|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|------------|
| Annotation Cluster 78 | Enrichment Score: 0.8183799807790646                 |       |            |            |              |            |          |           |              |            |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |            |
| UP_SEQ_FEATURE        | domain:SH2   | 10    | 2.11864407 | 6.22E-04   | TNSA, FGR, S | 425        | 90       | 16021     | 4.18849673   | 0.52802713 | 0.13943554 | 1.00135506 |            |
| GOTERM_MF_FAT         | GO:0004715--non-membrane spanning protein tyrosir    | 4     | 0.84745763 | 0.08086507 | FGR, BMX, F  | 339        | 40       | 13288     | 3.91976401   |            | 1          | 0.72325968 | 70.4862507 |
| GOTERM_MF_FAT         | GO:0004713--protein tyrosine kinase activity         | 6     | 1.27118644 | 0.40524452 | IGSF10, WNT1 | 339        | 164      | 13288     | 1.43406      |            | 1          | 0.97861523 | 99.945772  |
| INTERPRO              | IPR008266:Tyrosine protein kinase, active site       | 4     | 0.84745763 | 0.4347065  | FGR, BMX, F  | 425        | 101      | 17763     | 1.65525917   |            | 1          | 0.99857213 | 99.9843359 |
| SP_PIR_KEYWORDS       | tyrosine-protein kinase                              | 4     | 0.84745763 | 0.5444898  | FGR, BMX, F  | 439        | 116      | 17854     | 1.40240358   |            | 1          | 0.94347968 | 99.9981281 |
| INTERPRO              | IPR001245Tyrosine protein kinase                     | 4     | 0.84745763 | 0.57114469 | FGR, BMX, F  | 425        | 124      | 17763     | 1.34823529   |            | 1          | 0.99977595 | 99.999775  |
| SMART                 | SM00219:TyrKc  | 4     | 0.84745763 | 0.6779982  | FGR, BMX, F  | 256        | 124      | 9131      | 1.15057964   |            | 1          | 0.99829508 | 99.9999133 |
| Annotation Cluster 79 | Enrichment Score: 0.8161261963973913                 |       |            |            |              |            |          |           |              |            |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |            |
| GOTERM_BP_FAT         | GO:0007229--integrin-mediated signaling pathway      | 7     | 1.48305085 | 0.01182864 | ITGAL, ITGB2 | 341        | 76       | 13588     | 3.67016515   |            | 1          | 0.21636038 | 18.4279822 |
| SP_PIR_KEYWORDS       | integrin   | 5     | 1.05932203 | 0.06253411 | ITGAL, ITGB2 | 439        | 61       | 17854     | 3.33358228   |            | 1          | 0.40672365 | 59.0971005 |
| GOTERM_CC_FAT         | GO:0008305--integrin complex                         | 3     | 0.63559322 | 0.16727559 | ITGAL, ITGB2 | 330        | 28       | 12504     | 4.05974026   |            | 1          | 0.6639033  | 91.0390651 |
| UP_SEQ_FEATURE        | domain:VWFA  | 4     | 0.84745763 | 0.17143076 | ITGAL, ITGB2 | 425        | 54       | 16021     | 2.79233115   |            | 1          | 0.99026756 | 95.2280905 |
| GOTERM_CC_FAT         | GO:0043235--receptor complex                         | 5     | 1.05932203 | 0.17477671 | ITGAL, PTPN  | 330        | 83       | 12504     | 2.288258488  |            | 1          | 0.65842875 | 92.0463683 |
| INTERPRO              | IPR002035: von Willebrand factor, type A             | 4     | 0.84745763 | 0.35088511 | ITGAL, ITGB2 | 425        | 88       | 17763     | 1.8997861    |            | 1          | 0.99561177 | 99.8690089 |
| SMART                 | SM00327:VWA  | 4     | 0.84745763 | 0.44747371 | ITGAL, ITGB2 | 256        | 88       | 9131      | 1.62127131   |            | 1          | 0.98354531 | 99.9329441 |
| INTERPRO              | IPR013111:EGF, extracellular                         | 3     | 0.63559322 | 0.5081611  | ITGB2L, ADA  | 425        | 71       | 17763     | 1.76599834   |            | 1          | 0.99950302 | 99.9981534 |
| Annotation Cluster 80 | Enrichment Score: 0.8136603464583088                 |       |            |            |              |            |          |           |              |            |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |            |
| GOTERM_BP_FAT         | GO:0005976--polysaccharide metabolic process         | 8     | 1.69491525 | 0.00822088 | PTGES3, OVC  | 341        | 92       | 13588     | 3.46500064   | 0.99999988 | 0.17243862 | 13.1773428 |            |
| GOTERM_BP_FAT         | GO:0006073--cellular glucan metabolic process        | 3     | 0.63559322 | 0.1995687  | PTGES3, PPP  | 341        | 33       | 13588     | 3.62250067   |            | 1          | 0.80653685 | 97.7861492 |
| GOTERM_BP_FAT         | GO:0044042--glucan metabolic process                 | 3     | 0.63559322 | 0.1995687  | PTGES3, PPP  | 341        | 33       | 13588     | 3.62250067   |            | 1          | 0.80653685 | 97.7861492 |
| GOTERM_BP_FAT         | GO:0005977--glycogen metabolic process               | 3     | 0.63559322 | 0.1995687  | PTGES3, PPP  | 341        | 33       | 13588     | 3.62250067   |            | 1          | 0.80653685 | 97.7861492 |
| GOTERM_BP_FAT         | GO:0006112--energy reserve metabolic process         | 3     | 0.63559322 | 0.23655797 | PTGES3, PPP  | 341        | 37       | 13588     | 3.23087897   |            | 1          | 0.85002811 | 99.0150419 |
| GOTERM_BP_FAT         | GO:0044264--cellular polysaccharide metabolic proces | 3     | 0.63559322 | 0.29252221 | PTGES3, PPP  | 341        | 43       | 13588     | 2.78005865   |            | 1          | 0.89156831 | 99.732418  |
| GOTERM_BP_FAT         | GO:0015980--energy derivation by oxidation of organ  | 4     | 0.84745763 | 0.44574427 | PTGES3, PPP  | 341        | 98       | 13588     | 1.62642887   |            | 1          | 0.96361758 | 99.9958984 |
| Annotation Cluster 81 | Enrichment Score: 0.7928055859775247                 |       |            |            |              |            |          |           |              |            |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |            |
| GOTERM_MF_FAT         | GO:0046983--protein dimerization activity            | 14    | 2.96610169 | 0.09475802 | NFE2, FOXL2  | 339        | 340      | 13288     | 1.61402048   |            | 1          | 0.74258467 | 76.3245628 |
| GOTERM_MF_FAT         | GO:0042802--identical protein binding                | 12    | 2.54237288 | 0.12124228 | RASSF5, COF  | 339        | 290      | 13288     | 1.62197132   |            | 1          | 0.78163307 | 84.594574  |
| GOTERM_MF_FAT         | GO:0042803--protein homodimerization activity        | 7     | 1.48305085 | 0.36417756 | OLFML2B, G   | 339        | 193      | 13288     | 1.42167607   |            | 1          | 0.9713922  | 99.8574806 |
| Annotation Cluster 82 | Enrichment Score: 0.747528960232035                  |       |            |            |              |            |          |           |              |            |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |            |
| GOTERM_BP_FAT         | GO:0008015--blood circulation                        | 7     | 1.48305085 | 0.05997531 | WNT2, EDNF   | 341        | 111      | 13588     | 2.51290587   |            | 1          | 0.49770275 | 65.3094684 |
| GOTERM_BP_FAT         | GO:0003013--circulatory system process               | 7     | 1.48305085 | 0.05997531 | WNT2, EDNF   | 341        | 111      | 13588     | 2.51290587   |            | 1          | 0.49770275 | 65.3094684 |
| GOTERM_BP_FAT         | GO:0008217--regulation of blood pressure             | 4     | 0.84745763 | 0.22198766 | EDNRB, G6P   | 341        | 65       | 13588     | 2.4521543    |            | 1          | 0.8320269  | 98.6386817 |
| GOTERM_BP_FAT         | GO:0035150--regulation of tube size                  | 3     | 0.63559322 | 0.33877955 | WNT2, G6PC   | 341        | 48       | 13588     | 2.49046921   |            | 1          | 0.91964333 | 99.9159041 |
| GOTERM_BP_FAT         | GO:0050880--regulation of blood vessel size          | 3     | 0.63559322 | 0.33877955 | WNT2, G6PC   | 341        | 48       | 13588     | 2.49046921   |            | 1          | 0.91964333 | 99.9159041 |
| GOTERM_BP_FAT         | GO:0003018--vascular process in circulatory system   | 3     | 0.63559322 | 0.35704099 | WNT2, G6PC   | 341        | 50       | 13588     | 2.39085044   |            | 1          | 0.92935203 | 99.9479315 |
| Annotation Cluster 83 | Enrichment Score: 0.7239855356308065                 |       |            |            |              |            |          |           |              |            |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |            |
| GOTERM_CC_FAT         | GO:0044433--cytoplasmic vesicle part                 | 6     | 1.27118644 | 0.10530549 | WNT2, CLN3   | 330        | 95       | 12504     | 2.39311005   |            | 1          | 0.5613359  | 76.9239017 |
| GOTERM_CC_FAT         | GO:0012506--vesicle membrane                         | 6     | 1.27118644 | 0.11244213 | WNT2, SELP,  | 330        | 97       | 12504     | 2.34376757   |            | 1          | 0.56743791 | 79.2352125 |
| GOTERM_CC_FAT         | GO:0030659--cytoplasmic vesicle membrane             | 5     | 1.05932203 | 0.1959681  | WNT2, SELP,  | 330        | 87       | 12504     | 2.17763845   |            | 1          | 0.66936441 | 94.3548428 |
| GOTERM_CC_FAT         | GO:0012505--endomembrane system                      | 15    | 3.1779661  | 0.54763649 | CLN3, SELP,  | 330        | 535      | 12504     | 1.06236194   |            | 1          | 0.94487086 | 99.9971162 |
| Annotation Cluster 84 | Enrichment Score: 0.6792113502245118                 |       |            |            |              |            |          |           |              |            |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |            |
| GOTERM_MF_FAT         | GO:0005164--tumor necrosis factor receptor binding   | 3     | 0.63559322 | 0.1150916  | LST1, TNFSF: | 339        | 23       | 13288     | 5.11273567   |            | 1          | 0.77074966 | 82.9583424 |

|               |  |   |            |            |              |     |    |       |            |   |            |            |
|---------------|--|---|------------|------------|--------------|-----|----|-------|------------|---|------------|------------|
| GOTERM_MF_FAT | GO:0032813~tumor necrosis factor receptor superfam   | 3 | 0.63559322 | 0.14083702 | LST1, TNFSF: | 339 | 26 | 13288 | 4.52280463 | 1 | 0.79249778 | 88.8842027 |
| GOTERM_BP_FAT | GO:0051223~regulation of protein transport           | 4 | 0.84745763 | 0.22198766 | LST1, TNFSF: | 341 | 65 | 13588 | 2.4521543  | 1 | 0.8320269  | 98.6386817 |
| GOTERM_BP_FAT | GO:0051222~positive regulation of protein transport  | 3 | 0.63559322 | 0.22726251 | LST1, TNFSF: | 341 | 36 | 13588 | 3.32062561 | 1 | 0.83887325 | 98.7883256 |
| GOTERM_BP_FAT | GO:0070201~regulation of establishment of protein lc | 4 | 0.84745763 | 0.26215908 | LST1, TNFSF: | 341 | 71 | 13588 | 2.24492999 | 1 | 0.87370095 | 99.4506485 |
| GOTERM_BP_FAT | GO:0032880~regulation of protein localization        | 4 | 0.84745763 | 0.39223822 | LST1, TNFSF: | 341 | 90 | 13588 | 1.77100033 | 1 | 0.94484274 | 99.9801366 |

|                       |   |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 85 | Enrichment Score: 0.6788609458437971              |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0016485~protein processing                     | 5     | 1.05932203 | 0.18852368 | CFP, CLN3, E | 341        | 90       | 13588     | 2.21375041   | 1          | 0.79357332 | 97.2008374 |
| GOTERM_BP_FAT         | GO:0051604~protein maturation                     | 5     | 1.05932203 | 0.21964555 | CFP, CLN3, E | 341        | 96       | 13588     | 2.07539101   | 1          | 0.83063406 | 98.566805  |
| GOTERM_BP_FAT         | GO:0051605~protein maturation by peptide bond cle | 4     | 0.84745763 | 0.22198766 | CFP, ECE1, F | 341        | 65       | 13588     | 2.4521543    | 1          | 0.8320269  | 98.6386817 |

|                       |                                      |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|--------------------------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 86 | Enrichment Score: 0.6527043255312192 |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term                                 | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0015837~amine transport           | 6     | 1.27118644 | 0.0807821  | FCER1A, CLN | 341        | 92       | 13588     | 2.59875048   | 1          | 0.57231866 | 76.3508684 |
| GOTERM_BP_FAT         | GO:0046942~carboxylic acid transport | 5     | 1.05932203 | 0.2356949  | CLN3, SLC11 | 341        | 99       | 13588     | 2.01250037   | 1          | 0.84987487 | 98.995807  |
| GOTERM_BP_FAT         | GO:0015849~organic acid transport    | 5     | 1.05932203 | 0.24110662 | CLN3, SLC11 | 341        | 100      | 13588     | 1.99237537   | 1          | 0.85416219 | 99.110814  |
| GOTERM_BP_FAT         | GO:0006865~amino acid transport      | 3     | 0.63559322 | 0.53371356 | CLN3, SLC11 | 341        | 71       | 13588     | 1.68369749   | 1          | 0.98312311 | 99.9997871 |

|                       |   |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 87 | Enrichment Score: 0.6440846467938851                |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0009166~nucleotide catabolic process             | 3     | 0.63559322 | 0.18134608 | NCF2, NCF1, | 341        | 31       | 13588     | 3.85621039   | 1          | 0.78199649 | 96.7454275 |
| GOTERM_BP_FAT         | GO:0034655~nucleobase, nucleoside, nucleotide and i | 3     | 0.63559322 | 0.22726251 | NCF2, NCF1, | 341        | 36       | 13588     | 3.32062561   | 1          | 0.83887325 | 98.7883256 |
| GOTERM_BP_FAT         | GO:0034656~nucleobase, nucleoside and nucleotide c  | 3     | 0.63559322 | 0.22726251 | NCF2, NCF1, | 341        | 36       | 13588     | 3.32062561   | 1          | 0.83887325 | 98.7883256 |
| GOTERM_BP_FAT         | GO:0044270~nitrogen compound catabolic process      | 3     | 0.63559322 | 0.28320286 | NCF2, NCF1, | 341        | 42       | 13588     | 2.84625052   | 1          | 0.88709895 | 99.6652323 |

|                       |   |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 88 | Enrichment Score: 0.6374316120034745            |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS       | kinetochore                                     | 5     | 1.05932203 | 0.06253411 | KIF2C, PLK1, | 439        | 61       | 17854     | 3.33358228   | 1          | 0.40672365 | 59.0971005 |
| GOTERM_CC_FAT         | GO:0000793~condensed chromosome                 | 6     | 1.27118644 | 0.1514024  | HMGB2, MKI   | 330        | 107      | 12504     | 2.12472387   | 1          | 0.63197852 | 88.5073328 |
| GOTERM_CC_FAT         | GO:0000775~chromosome, centromeric region       | 6     | 1.27118644 | 0.16838718 | CDCA8, MKI   | 330        | 111      | 12504     | 2.04815725   | 1          | 0.65868334 | 91.1954255 |
| GOTERM_CC_FAT         | GO:0000777~condensed chromosome kinetochore     | 3     | 0.63559322 | 0.40835995 | CENPA, SPA   | 330        | 53       | 12504     | 2.14476844   | 1          | 0.88683985 | 99.9008853 |
| GOTERM_CC_FAT         | GO:0000779~condensed chromosome, centromeric re | 3     | 0.63559322 | 0.47110963 | CENPA, SPA   | 330        | 60       | 12504     | 1.89454545   | 1          | 0.92029583 | 99.9773813 |
| GOTERM_CC_FAT         | GO:0000776~kinetochore                          | 3     | 0.63559322 | 0.48829969 | CENPA, SPA   | 330        | 62       | 12504     | 1.83343109   | 1          | 0.92190144 | 99.985366  |

|                       |   |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 89 | Enrichment Score: 0.6373495105453898            |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0009725~response to hormone stimulus         | 8     | 1.69491525 | 0.12058311 | WNT2, HMG   | 341        | 165      | 13588     | 1.93200036   | 1          | 0.66710481 | 88.9145383 |
| GOTERM_BP_FAT         | GO:0009719~response to endogenous stimulus      | 8     | 1.69491525 | 0.17855533 | WNT2, HMG   | 341        | 184      | 13588     | 1.73250032   | 1          | 0.77760027 | 96.5502062 |
| GOTERM_BP_FAT         | GO:0048545~response to steroid hormone stimulus | 4     | 0.84745763 | 0.18957791 | WNT2, HMG   | 341        | 60       | 13588     | 2.65650049   | 1          | 0.79431864 | 97.2624385 |
| GOTERM_BP_FAT         | GO:0043434~response to peptide hormone stimulus | 3     | 0.63559322 | 0.69144067 | WNT2, EIF4E | 341        | 95       | 13588     | 1.25834234   | 1          | 0.9965723  | 99.9999998 |

|                       |   |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 90 | Enrichment Score: 0.6241667762578328                |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0034637~cellular carbohydrate biosynthetic proce | 4     | 0.84745763 | 0.16462456 | PTGES3, PGE | 341        | 56       | 13588     | 2.84625052   | 1          | 0.75683865 | 95.3994579 |
| GOTERM_BP_FAT         | GO:0046165~alcohol biosynthetic process             | 3     | 0.63559322 | 0.23655797 | PGD, PLCG2, | 341        | 37       | 13588     | 3.23087897   | 1          | 0.85002811 | 99.0150419 |
| GOTERM_BP_FAT         | GO:0016051~carbohydrate biosynthetic process        | 4     | 0.84745763 | 0.34440343 | PTGES3, PGE | 341        | 83       | 13588     | 1.9203618    | 1          | 0.92185119 | 99.9273433 |

|                       |  |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 91 | Enrichment Score: 0.6118945775322034         |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0006644~phospholipid metabolic process    | 7     | 1.69491525 | 0.11510816 | PIK3CG, CLN | 341        | 163      | 13588     | 1.95570588   | 1          | 0.65886624 | 87.6720138 |
| SP_PIR_KEYWORDS       | Acyltransferase                              | 8     | 1.48305085 | 0.18180327 | SOAT2, LOC: | 439        | 155      | 17854     | 1.8366963    | 1          | 0.67954997 | 93.7825786 |
| SP_PIR_KEYWORDS       | phospholipid biosynthesis                    | 3     | 0.63559322 | 0.27553081 | LOC1000445  | 439        | 42       | 17854     | 2.90497885   | 1          | 0.78783288 | 98.8462063 |
| GOTERM_BP_FAT         | GO:0008654~phospholipid biosynthetic process | 3     | 0.63559322 | 0.61879063 | LOC1000445  | 341        | 83       | 13588     | 1.44027135   | 1          | 0.99284553 | 99.9999932 |

|                       |                                      |       |   |        |       |            |          |           |              |            |           |     |
|-----------------------|--------------------------------------|-------|---|--------|-------|------------|----------|-----------|--------------|------------|-----------|-----|
| Annotation Cluster 92 | Enrichment Score: 0.6006685242686174 |       |   |        |       |            |          |           |              |            |           |     |
| Category              | Term                                 | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini | FDR |

|               |  |   |            |            |               |     |     |       |            |   |            |            |
|---------------|--|---|------------|------------|---------------|-----|-----|-------|------------|---|------------|------------|
| GOTERM_BP_FAT | GO:0051130~positive regulation of cellular componen  | 7 | 1.48305085 | 0.08582241 | WNT2, SLC11A1 | 341 | 122 | 13588 | 2.28633239 | 1 | 0.58780573 | 78.4751434 |
| GOTERM_BP_FAT | GO:0010638~positive regulation of organelle organiz  | 3 | 0.63559322 | 0.37511797 | WNT2, LST1,   | 341 | 52  | 13588 | 2.29889465 | 1 | 0.93888712 | 99.9680427 |
| GOTERM_BP_FAT | GO:0008285~negative regulation of cell proliferation | 7 | 1.48305085 | 0.49003359 | WNT2, PTPN    | 341 | 224 | 13588 | 1.2452346  | 1 | 0.97463001 | 99.9990141 |

|                       |                                      |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|--------------------------------------|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 93 | Enrichment Score: 0.6003398124487961 |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term                                 | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0043588~skin development          | 3     | 0.63559322 | 0.17233262 | PTGES3, LTB, | 341        | 30       | 13588     | 3.98475073   | 1          | 0.76982516 | 96.0744888 |
| GOTERM_BP_FAT         | GO:0007398~ectoderm development      | 6     | 1.27118644 | 0.2402972  | PTGES3, LHX  | 341        | 133      | 13588     | 1.79763191   | 1          | 0.85409436 | 99.0944396 |
| GOTERM_BP_FAT         | GO:0008544~epidermis development     | 5     | 1.05932203 | 0.38182501 | PTGES3, TGN  | 341        | 125      | 13588     | 1.59390029   | 1          | 0.94116097 | 99.9734327 |

|                       |   |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 94 | Enrichment Score: 0.5933563721426269                    |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| INTERPRO              | IPR004827:Basic-leucine zipper (bZIP) transcription fac | 5     | 1.05932203 | 0.03971801 | FOSL2, NFE2 | 425        | 54       | 17763     | 3.86993464   | 1          | 0.62746216 | 46.3408639 |
| SMART                 | SM00338:BRLZ  | 5     | 1.05932203 | 0.06341139 | FOSL2, NFE2 | 256        | 54       | 9131      | 3.3025897    | 0.99999244 | 0.52145279 | 55.3775224 |
| GOTERM_MF_FAT         | GO:0046983~protein dimerization activity                | 14    | 2.96610169 | 0.09475802 | NFE2, FOSL2 | 339        | 340      | 13288     | 1.61402048   | 1          | 0.74258467 | 76.3245628 |
| INTERPRO              | IPR011616:bZIP transcription factor, bZIP-1             | 3     | 0.63559322 | 0.16009567 | FOSL2, NFE2 | 425        | 30       | 17763     | 4.17952941   | 1          | 0.9291107  | 93.1425455 |
| UP_SEQ_FEATURE        | domain:Leucine-zipper                                   | 5     | 1.05932203 | 0.31447253 | FOSL2, NFE2 | 425        | 107      | 16021     | 1.76151732   | 1          | 0.99821705 | 99.7775935 |
| UP_SEQ_FEATURE        | DNA-binding region:Basic motif                          | 6     | 1.27118644 | 0.38617281 | FOSL2, NFE2 | 425        | 154      | 16021     | 1.46869366   | 1          | 0.99961189 | 99.9627669 |
| GOTERM_MF_FAT         | GO:0043565~sequence-specific DNA binding                | 8     | 1.69491525 | 0.98906171 | FOSL2, NFE2 | 339        | 556      | 13288     | 0.56399482   | 1          | 1          | 100        |
| GOTERM_MF_FAT         | GO:0003700~transcription factor activity                | 11    | 2.33050847 | 0.99558278 | FOSL2, NFE2 | 339        | 776      | 13288     | 0.55563665   | 1          | 1          | 100        |
| GOTERM_MF_FAT         | GO:0030528~transcription regulator activity             | 14    | 2.96610169 | 0.9999474  | SBNO2, NFE  | 339        | 1206     | 13288     | 0.45503065   | 1          | 1          | 100        |

|                       |  |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 95 | Enrichment Score: 0.5931529171973309             |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0006644~phospholipid metabolic process        | 8     | 1.69491525 | 0.11510816 | PIK3CG, CLN  | 341        | 163      | 13588     | 1.95570588   | 1          | 0.65886624 | 87.6720138 |
| GOTERM_BP_FAT         | GO:0046486~glycerolipid metabolic process        | 6     | 1.27118644 | 0.22189824 | APOB48R, PI  | 341        | 129      | 13588     | 1.85337243   | 1          | 0.83299622 | 98.6360011 |
| GOTERM_BP_FAT         | GO:0006650~glycerophospholipid metabolic process | 3     | 0.63559322 | 0.65055091 | PIK3CG, PIK3 | 341        | 88       | 13588     | 1.35843775   | 1          | 0.99480323 | 99.9999985 |

|                       |                                      |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|--------------------------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 96 | Enrichment Score: 0.5498567243383871 |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term                                 | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| UP_SEQ_FEATURE        | domain:Ras-associating               | 3     | 0.63559322 | 0.22688203 | RASSF5, RIN | 425        | 34       | 16021     | 3.32615917   | 1          | 0.99435223 | 98.4440441 |
| INTERPRO              | IPR000159:Ras-association            | 3     | 0.63559322 | 0.28294741 | RASSF5, RIN | 425        | 44       | 17763     | 2.84967914   | 1          | 0.98840199 | 99.3957037 |
| SMART                 | SM00314:RA                           | 3     | 0.63559322 | 0.34907923 | RASSF5, RIN | 256        | 44       | 9131      | 2.43190696   | 1          | 0.97019281 | 99.4951808 |

|                       |   |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 97 | Enrichment Score: 0.5401305586397369                  |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS       | iron transport  | 4     | 0.84745763 | 0.01225677 | SLC11A1, LTI | 439        | 20       | 17854     | 8.13394077   | 0.99077974 | 0.14921714 | 15.6950916 |
| GOTERM_BP_FAT         | GO:0006826~iron ion transport                         | 4     | 0.84745763 | 0.04512057 | SLC11A1, LTI | 341        | 32       | 13588     | 4.98093842   | 1          | 0.43656427 | 54.6299992 |
| GOTERM_BP_FAT         | GO:0015674~di-, tri-valent inorganic cation transport | 8     | 1.69491525 | 0.10976718 | SLC11A1, CC  | 341        | 161      | 13588     | 1.98000036   | 1          | 0.65226773 | 86.334446  |
| GOTERM_MF_FAT         | GO:0015082~di-, tri-valent inorganic cation transmem  | 3     | 0.63559322 | 0.19524939 | SLC11A1, AT  | 339        | 32       | 13288     | 3.67477876   | 1          | 0.88033342 | 95.6874969 |
| GOTERM_BP_FAT         | GO:0000041~transition metal ion transport             | 4     | 0.84745763 | 0.25539126 | SLC11A1, LTI | 341        | 70       | 13588     | 2.27700042   | 1          | 0.86750986 | 99.3577147 |
| GOTERM_BP_FAT         | GO:0030001~metal ion transport                        | 11    | 2.33050847 | 0.67240281 | SHKBP1, SLC  | 341        | 442      | 13588     | 0.99168005   | 1          | 0.99566666 | 99.9999995 |
| GOTERM_BP_FAT         | GO:0006812~cation transport                           | 11    | 2.33050847 | 0.83499763 | SHKBP1, SLC  | 341        | 515      | 13588     | 0.85111181   | 1          | 0.99968142 | 100        |
| GOTERM_MF_FAT         | GO:0022890~inorganic cation transmembrane transp      | 3     | 0.63559322 | 0.83772902 | SLC11A1, AT  | 339        | 127      | 13288     | 0.92592851   | 1          | 0.99997152 | 100        |
| GOTERM_MF_FAT         | GO:0046873~metal ion transmembrane transporter ac     | 6     | 1.27118644 | 0.86485446 | SHKBP1, SLC  | 339        | 290      | 13288     | 0.81098566   | 1          | 0.99998378 | 100        |
| GOTERM_BP_FAT         | GO:0006811~ion transport                              | 13    | 2.75423729 | 0.94729489 | KCTD20, FX   | 341        | 712      | 13588     | 0.7275528    | 1          | 0.9999968  | 100        |
| SP_PIR_KEYWORDS       | ion transport   | 8     | 1.69491525 | 0.98106644 | SLC11A1, AT  | 439        | 543      | 17854     | 0.59918532   | 1          | 0.99998464 | 100        |

|                       |   |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 98 | Enrichment Score: 0.5343899380907865        |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0046486~glycerolipid metabolic process   | 6     | 1.27118644 | 0.22189824 | APOB48R, PI | 341        | 129      | 13588     | 1.85337243   | 1          | 0.83299622 | 98.6360011 |
| GOTERM_BP_FAT         | GO:0006639~acylglycerol metabolic process   | 3     | 0.63559322 | 0.29252221 | APOB48R, A  | 341        | 43       | 13588     | 2.78005865   | 1          | 0.89156831 | 99.732418  |
| GOTERM_BP_FAT         | GO:0006662~glycerol ether metabolic process | 3     | 0.63559322 | 0.3111073  | APOB48R, A  | 341        | 45       | 13588     | 2.65650049   | 1          | 0.90347824 | 99.8303486 |
| GOTERM_BP_FAT         | GO:0006638~neutral lipid metabolic process  | 3     | 0.63559322 | 0.3111073  | APOB48R, A  | 341        | 45       | 13588     | 2.65650049   | 1          | 0.90347824 | 99.8303486 |
| GOTERM_BP_FAT         | GO:0018904~organic ether metabolic process  | 3     | 0.63559322 | 0.33877955 | APOB48R, A  | 341        | 48       | 13588     | 2.49046921   | 1          | 0.91964333 | 99.9159041 |

Annotation Cluster 99 Enrichment Score: 0.5321474163451122

| Category               | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|------------------------|---|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| UP_SEQ_FEATURE         | metal ion-binding site:Magnesium                      | 6     | 1.27118644 | 0.13774425 | MAT2A, ATP    | 425        | 103      | 16021     | 2.19591091   | 1          | 0.98122339 | 90.90723   |
| SP_PIR_KEYWORDS        | magnesium   | 12    | 2.54237288 | 0.40111684 | ITGAL, MAT2   | 439        | 403      | 17854     | 1.21100855   | 1          | 0.89620826 | 99.9172927 |
| GOTERM_MF_FAT          | GO:0000287~magnesium ion binding                      | 12    | 2.54237288 | 0.45836704 | ITGAL, MAT2   | 339        | 409      | 13288     | 1.15005301   | 1          | 0.98710562 | 99.9859984 |
| Annotation Cluster 100 |   |       |            |            |               |            |          |           |              |            |            |            |
| Category               | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT          | GO:0031012~extracellular matrix                       | 12    | 2.54237288 | 0.19289488 | WNT2, OGN,    | 330        | 309      | 12504     | 1.47149162   | 1          | 0.67670928 | 94.0637804 |
| SP_PIR_KEYWORDS        | extracellular matrix                                  | 8     | 1.69491525 | 0.27302269 | WNT2, OGN,    | 439        | 213      | 17854     | 1.52750061   | 1          | 0.79270138 | 98.7896611 |
| GOTERM_CC_FAT          | GO:0005578~proteinaceous extracellular matrix         | 9     | 1.90677966 | 0.52554307 | WNT2, OGN,    | 330        | 297      | 12504     | 1.14820937   | 1          | 0.9367511  | 99.9945941 |
| Annotation Cluster 101 |   |       |            |            |               |            |          |           |              |            |            |            |
| Category               | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT          | GO:0051336~regulation of hydrolase activity           | 8     | 1.69491525 | 0.2192594  | APOA2, NLR    | 341        | 196      | 13588     | 1.62642887   | 1          | 0.83115328 | 98.5546167 |
| GOTERM_BP_FAT          | GO:0043281~regulation of caspase activity             | 3     | 0.63559322 | 0.35704099 | NLRP12, HSF   | 341        | 50       | 13588     | 2.39085044   | 1          | 0.92935203 | 99.9479315 |
| GOTERM_BP_FAT          | GO:0052548~regulation of endopeptidase activity       | 3     | 0.63559322 | 0.35704099 | NLRP12, HSF   | 341        | 50       | 13588     | 2.39085044   | 1          | 0.92935203 | 99.9479315 |
| GOTERM_BP_FAT          | GO:0052547~regulation of peptidase activity           | 3     | 0.63559322 | 0.36610426 | NLRP12, HSF   | 341        | 51       | 13588     | 2.34397102   | 1          | 0.93456711 | 99.9591645 |
| Annotation Cluster 102 |   |       |            |            |               |            |          |           |              |            |            |            |
| Category               | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT          | GO:0045787~positive regulation of cell cycle          | 3     | 0.63559322 | 0.20876021 | LST1, BIRC5,  | 341        | 34       | 13588     | 3.51595653   | 1          | 0.81999249 | 98.1832807 |
| GOTERM_BP_FAT          | GO:0010564~regulation of cell cycle process           | 4     | 0.84745763 | 0.27575969 | OSM, LST1, I  | 341        | 73       | 13588     | 2.18342506   | 1          | 0.88353167 | 99.6004785 |
| GOTERM_BP_FAT          | GO:0051726~regulation of cell cycle                   | 8     | 1.69491525 | 0.2887706  | OSM, LST1, I  | 341        | 214      | 13588     | 1.48962644   | 1          | 0.88945839 | 99.7070631 |
| GOTERM_BP_FAT          | GO:0043523~regulation of neuron apoptosis             | 4     | 0.84745763 | 0.32377368 | CLN3, LST1,   | 341        | 80       | 13588     | 1.99237537   | 1          | 0.9099474  | 99.8765194 |
| GOTERM_BP_FAT          | GO:0007346~regulation of mitotic cell cycle           | 3     | 0.63559322 | 0.69694951 | LST1, BIRC5,  | 341        | 96       | 13588     | 1.2452346    | 1          | 0.99681217 | 99.9999999 |
| Annotation Cluster 103 |   |       |            |            |               |            |          |           |              |            |            |            |
| Category               | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| KEGG_PATHWAY           | mmu05221:Acute myeloid leukemia                       | 4     | 0.84745763 | 0.25682216 | PIK3CG, EIF4  | 178        | 57       | 5738      | 2.26217228   | 1          | 0.72093921 | 96.8313338 |
| KEGG_PATHWAY           | mmu04012:ErbB signaling pathway                       | 5     | 1.05932203 | 0.28059749 | PIK3CG, EIF4  | 178        | 87       | 5738      | 1.8526411    | 1          | 0.72401191 | 97.829004  |
| KEGG_PATHWAY           | mmu04150:mTOR signaling pathway                       | 3     | 0.63559322 | 0.50028575 | PIK3CG, EIF4  | 178        | 54       | 5738      | 1.79088639   | 1          | 0.83300554 | 99.968646  |
| Annotation Cluster 104 |   |       |            |            |               |            |          |           |              |            |            |            |
| Category               | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT          | GO:0006915~apoptosis                                  | 15    | 3.1779661  | 0.27612584 | BID, LST1, LI | 341        | 465      | 13588     | 1.28540346   | 1          | 0.88305834 | 99.6039219 |
| GOTERM_BP_FAT          | GO:0008219~cell death                                 | 16    | 3.38983051 | 0.28792876 | BID, LST1, LY | 341        | 507      | 13588     | 1.25751502   | 1          | 0.88943011 | 99.701071  |
| GOTERM_BP_FAT          | GO:0012501~programmed cell death                      | 15    | 3.1779661  | 0.29730198 | BID, LST1, LI | 341        | 473      | 13588     | 1.26366302   | 1          | 0.89383159 | 99.7617342 |
| GOTERM_BP_FAT          | GO:0016265~death                                      | 16    | 3.38983051 | 0.32163633 | BID, LST1, LY | 341        | 519      | 13588     | 1.22843953   | 1          | 0.90958089 | 99.8696658 |
| SP_PIR_KEYWORDS        | Apoptosis   | 9     | 1.90677966 | 0.5874348  | TNS4, BID, R  | 439        | 337      | 17854     | 1.08613452   | 1          | 0.95816139 | 99.9995248 |
| Annotation Cluster 105 |   |       |            |            |               |            |          |           |              |            |            |            |
| Category               | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT          | GO:0033673~negative regulation of kinase activity     | 3     | 0.63559322 | 0.36610426 | PTPN6, ILL1B, | 341        | 51       | 13588     | 2.34397102   | 1          | 0.93456711 | 99.9591645 |
| GOTERM_BP_FAT          | GO:0006469~negative regulation of protein kinase act  | 3     | 0.63559322 | 0.36610426 | PTPN6, ILL1B, | 341        | 51       | 13588     | 2.34397102   | 1          | 0.93456711 | 99.9591645 |
| GOTERM_BP_FAT          | GO:0051348~negative regulation of transferase activit | 3     | 0.63559322 | 0.38407893 | PTPN6, ILL1B, | 341        | 53       | 13588     | 2.25551928   | 1          | 0.94190999 | 99.975043  |
| Annotation Cluster 106 |   |       |            |            |               |            |          |           |              |            |            |            |
| Category               | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT          | GO:0009891~positive regulation of biosynthetic proce  | 22    | 4.66101695 | 0.0408297  | FCER1A, HM    | 341        | 557      | 13588     | 1.57386923   | 1          | 0.41448084 | 51.010859  |
| GOTERM_BP_FAT          | GO:0031328~positive regulation of cellular biosynthes | 21    | 4.44915254 | 0.06263356 | FCER1A, HM    | 341        | 552      | 13588     | 1.51593778   | 1          | 0.51127325 | 66.9509662 |
| GOTERM_BP_FAT          | GO:0010557~positive regulation of macromolecule bi    | 20    | 4.23728814 | 0.07412427 | FCER1A, HM    | 341        | 530      | 13588     | 1.50367952   | 1          | 0.5534254  | 73.2412773 |
| GOTERM_BP_FAT          | GO:0010604~positive regulation of macromolecule m     | 22    | 4.66101695 | 0.11507324 | FCER1A, HM    | 341        | 633      | 13588     | 1.38490547   | 1          | 0.6604267  | 87.6636853 |
| GOTERM_BP_FAT          | GO:0051173~positive regulation of nitrogen compour    | 14    | 2.96610169 | 0.5586211  | HMGB2, TLR    | 341        | 526      | 13588     | 1.06058004   | 1          | 0.98695493 | 99.9999168 |
| GOTERM_BP_FAT          | GO:0045893~positive regulation of transcription, DNA  | 11    | 2.33050847 | 0.5968454  | OSM, INHBA    | 341        | 416      | 13588     | 1.05366005   | 1          | 0.9911627  | 99.9999824 |
| GOTERM_BP_FAT          | GO:0051254~positive regulation of RNA metabolic pr    | 11    | 2.33050847 | 0.60597129 | OSM, INHBA    | 341        | 419      | 13588     | 1.04611594   | 1          | 0.99184371 | 99.9999881 |
| GOTERM_BP_FAT          | GO:0045941~positive regulation of transcription       | 12    | 2.54237288 | 0.64679472 | OSM, INHBA    | 341        | 475      | 13588     | 1.00667387   | 1          | 0.99459154 | 99.9999982 |
| GOTERM_BP_FAT          | GO:0010628~positive regulation of gene expression     | 12    | 2.54237288 | 0.68139999 | OSM, INHBA    | 341        | 488      | 13588     | 0.97985674   | 1          | 0.99610907 | 99.9999997 |

|               |  |    |            |            |            |     |      |       |            |   |            |     |
|---------------|--|----|------------|------------|------------|-----|------|-------|------------|---|------------|-----|
| GOTERM_BP_FAT | GO:0045935~positive regulation of nucleobase, nucleoside, or nucleotide metabolism | 12 | 2.54237288 | 0.73521011 | OSM, INHBA | 341 | 510  | 13588 | 0.93758841 | 1 | 0.99802467 | 100 |
| GOTERM_BP_FAT | GO:0045944~positive regulation of transcription from RNA polymerase II promoter    | 8  | 1.69491525 | 0.79644083 | OSM, INHBA | 341 | 358  | 13588 | 0.89044709 | 1 | 0.99927596 | 100 |
| GOTERM_BP_FAT | GO:0006357~regulation of transcription from RNA polymerase II promoter             | 9  | 1.90677966 | 0.98819043 | OSM, SAP30 | 341 | 616  | 13588 | 0.58218761 | 1 | 0.99999999 | 100 |
| GOTERM_BP_FAT | GO:0051252~regulation of RNA metabolic process                                     | 21 | 4.44915254 | 0.99961962 | HMG2, SBN  | 341 | 1488 | 13588 | 0.56236401 | 1 | 1          | 100 |
| GOTERM_BP_FAT | GO:0006355~regulation of transcription, DNA-dependent                              | 20 | 4.23728814 | 0.99975571 | HMG2, SBN  | 341 | 1465 | 13588 | 0.54399327 | 1 | 1          | 100 |

|                        |                                       |       |            |            |            |            |          |           |                 |            |            |            |
|------------------------|---------------------------------------|-------|------------|------------|------------|------------|----------|-----------|-----------------|------------|------------|------------|
| Annotation Cluster 107 | Enrichment Score: 0.42489433965418927 |       |            |            |            |            |          |           |                 |            |            |            |
| Category               | Term                                  | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini  | FDR        |
| GOTERM_MF_FAT          | GO:0005179~hormone activity           | 5     | 1.05932203 | 0.32411171 | INHBA, HAM | 339        | 113      | 13288     | 1.73440885      | 1          | 0.96601764 | 99.6548977 |
| SP_PIR_KEYWORDS        | cleavage on pair of basic residues    | 8     | 1.69491525 | 0.36760387 | INHBA, APO | 439        | 238      | 17854     | 1.36704887      | 1          | 0.87108464 | 99.8242432 |
| SP_PIR_KEYWORDS        | hormone                               | 4     | 0.84745763 | 0.44590484 | INHBA, HAM | 439        | 100      | 17854     | 1.62678815      | 1          | 0.91961193 | 99.9718029 |

|                        |  |       |            |            |            |            |          |           |                 |            |            |            |
|------------------------|--|-------|------------|------------|------------|------------|----------|-----------|-----------------|------------|------------|------------|
| Annotation Cluster 108 | Enrichment Score: 0.41811071739545125                                |       |            |            |            |            |          |           |                 |            |            |            |
| Category               | Term   | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT          | GO:0050730~regulation of peptidyl-tyrosine phosphorylation           | 4     | 0.84745763 | 0.14661349 | OSM, FCER1 | 341        | 53       | 13588     | 3.00735904      | 1          | 0.72429129 | 93.3719331 |
| GOTERM_BP_FAT          | GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation  | 3     | 0.63559322 | 0.2179941  | OSM, FCER1 | 341        | 35       | 13588     | 3.41550063      | 1          | 0.8303037  | 98.5139916 |
| GOTERM_BP_FAT          | GO:0001934~positive regulation of protein amino acid phosphorylation | 3     | 0.63559322 | 0.41061619 | OSM, FCER1 | 341        | 56       | 13588     | 2.13468789      | 1          | 0.95170639 | 99.9882568 |
| GOTERM_BP_FAT          | GO:0042327~positive regulation of phosphorylation                    | 3     | 0.63559322 | 0.44509851 | OSM, FCER1 | 341        | 60       | 13588     | 1.99237537      | 1          | 0.96373133 | 99.9958158 |
| GOTERM_BP_FAT          | GO:0032270~positive regulation of cellular protein metabolic process | 4     | 0.84745763 | 0.45884033 | OSM, FCER1 | 341        | 100      | 13588     | 1.59390029      | 1          | 0.96722347 | 99.9972761 |
| GOTERM_BP_FAT          | GO:0010562~positive regulation of phosphorus metabolic process       | 3     | 0.63559322 | 0.46191532 | OSM, FCER1 | 341        | 62       | 13588     | 1.92810519      | 1          | 0.96792958 | 99.9975292 |
| GOTERM_BP_FAT          | GO:0045937~positive regulation of phosphate metabolic process        | 3     | 0.63559322 | 0.46191532 | OSM, FCER1 | 341        | 62       | 13588     | 1.92810519      | 1          | 0.96792958 | 99.9975292 |
| GOTERM_BP_FAT          | GO:0051247~positive regulation of protein metabolic process          | 4     | 0.84745763 | 0.51600467 | OSM, FCER1 | 341        | 109      | 13588     | 1.46229385      | 1          | 0.97984046 | 99.999597  |
| GOTERM_BP_FAT          | GO:0031401~positive regulation of protein modification               | 3     | 0.63559322 | 0.5848611  | OSM, FCER1 | 341        | 78       | 13588     | 1.53259644      | 1          | 0.98995984 | 99.9999709 |

|                        |   |       |            |            |             |            |          |           |                 |            |            |            |
|------------------------|---|-------|------------|------------|-------------|------------|----------|-----------|-----------------|------------|------------|------------|
| Annotation Cluster 109 | Enrichment Score: 0.39784409781701285   |       |            |            |             |            |          |           |                 |            |            |            |
| Category               | Term  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini  | FDR        |
| GOTERM_MF_FAT          | GO:0016620~oxidoreductase activity, acting on the aldehyde or oxo group of substrates | 3     | 0.63559322 | 0.16765663 | ALDH1A1, A  | 339        | 29       | 13288     | 4.05492829      | 1          | 0.83927237 | 92.9754716 |
| UP_SEQ_FEATURE         | active site:Nucleophile   | 7     | 1.48305085 | 0.28609323 | ALDH1A1, SI | 425        | 168      | 16021     | 1.57068627      | 1          | 0.99769133 | 99.5712973 |
| UP_SEQ_FEATURE         | nucleotide phosphate-binding region:NAD   | 3     | 0.63559322 | 0.57935097 | ALDH1A1, A  | 425        | 73       | 16021     | 1.54917002      | 1          | 0.99999206 | 99.9999177 |
| SP_PIR_KEYWORDS        | nad   | 3     | 0.63559322 | 0.92204808 | ALDH1A1, A  | 439        | 169      | 17854     | 0.72194741      | 1          | 0.99938983 | 100        |

|                        |                                      |       |            |            |            |            |          |           |                 |            |            |            |
|------------------------|--------------------------------------|-------|------------|------------|------------|------------|----------|-----------|-----------------|------------|------------|------------|
| Annotation Cluster 110 | Enrichment Score: 0.3837030714237871 |       |            |            |            |            |          |           |                 |            |            |            |
| Category               | Term                                 | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini  | FDR        |
| UP_SEQ_FEATURE         | domain:PX                            | 3     | 0.63559322 | 0.30576652 | NCF1, NCF4 | 425        | 42       | 16021     | 2.69260504      | 1          | 0.99797887 | 99.7272177 |
| INTERPRO               | IPR001683:Phox-like                  | 3     | 0.63559322 | 0.30954783 | NCF1, NCF4 | 425        | 47       | 17763     | 2.66778473      | 1          | 0.99114806 | 99.6618753 |
| SMART                  | SM00312:PX                           | 3     | 0.63559322 | 0.37943943 | NCF1, NCF4 | 256        | 47       | 9131      | 2.27667886      | 1          | 0.97208219 | 99.7197003 |
| GOTERM_MF_FAT          | GO:0035091~phosphoinositide binding  | 3     | 0.63559322 | 0.57247368 | NCF1, NCF4 | 339        | 75       | 13288     | 1.5679056       | 1          | 0.995635   | 99.9995437 |
| GOTERM_MF_FAT          | GO:0005543~phospholipid binding      | 4     | 0.84745763 | 0.58677142 | NCF1, NCF4 | 339        | 119      | 13288     | 1.31756774      | 1          | 0.995976   | 99.9997211 |

|                        |  |       |            |            |            |            |          |           |                 |            |            |            |
|------------------------|--|-------|------------|------------|------------|------------|----------|-----------|-----------------|------------|------------|------------|
| Annotation Cluster 111 | Enrichment Score: 0.3814279282471711   |       |            |            |            |            |          |           |                 |            |            |            |
| Category               | Term                                   | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini  | FDR        |
| GOTERM_MF_FAT          | GO:0048037~cofactor binding            | 9     | 1.90677966 | 0.21671589 | MOCOS, AC  | 339        | 226      | 13288     | 1.56096797      | 1          | 0.89978959 | 97.0839227 |
| GOTERM_MF_FAT          | GO:0070279~vitamin B6 binding          | 3     | 0.63559322 | 0.40092745 | MOCOS, PYC | 339        | 54       | 13288     | 2.17764667      | 1          | 0.97864581 | 99.9397885 |
| GOTERM_MF_FAT          | GO:0030170~pyridoxal phosphate binding | 3     | 0.63559322 | 0.40092745 | MOCOS, PYC | 339        | 54       | 13288     | 2.17764667      | 1          | 0.97864581 | 99.9397885 |
| SP_PIR_KEYWORDS        | pyridoxal phosphate                    | 3     | 0.63559322 | 0.43497441 | MOCOS, PYC | 439        | 60       | 17854     | 2.03348519      | 1          | 0.91738115 | 99.9630467 |
| GOTERM_MF_FAT          | GO:0019842~vitamin binding             | 3     | 0.63559322 | 0.81728645 | MOCOS, PYC | 339        | 121      | 13288     | 0.97184232      | 1          | 0.99994949 | 100        |

|                        |   |       |            |            |               |            |          |           |                 |            |            |            |
|------------------------|---|-------|------------|------------|---------------|------------|----------|-----------|-----------------|------------|------------|------------|
| Annotation Cluster 112 | Enrichment Score: 0.3535472957721118          |       |            |            |               |            |          |           |                 |            |            |            |
| Category               | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichment | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS        | kinase  | 25    | 5.29661017 | 0.06942628 | FGR, PFKFB4   | 439        | 707      | 17854     | 1.43810834      | 1          | 0.42765338 | 63.0692097 |
| SP_PIR_KEYWORDS        | phosphotransferase                            | 6     | 1.27118644 | 0.1892083  | FGR, PLK1, P  | 439        | 124      | 17854     | 1.9678889       | 1          | 0.69028396 | 94.5178826 |
| UP_SEQ_FEATURE         | active site:Proton acceptor                   | 22    | 4.66101695 | 0.22415008 | ACADS, FG     | 425        | 662      | 16021     | 1.2527528       | 1          | 0.9944395  | 98.3526654 |
| GOTERM_BP_FAT          | GO:0006468~protein amino acid phosphorylation | 20    | 4.23728814 | 0.25281441 | FCER1A, PIK   | 341        | 640      | 13588     | 1.2452346       | 1          | 0.86626401 | 99.3185869 |
| UP_SEQ_FEATURE         | nucleotide phosphate-binding region:ATP       | 28    | 5.93220339 | 0.2878483  | KIF22, FGR, F | 425        | 907      | 16021     | 1.16372787      | 1          | 0.99758364 | 99.5880337 |
| GOTERM_BP_FAT          | GO:0016310~phosphorylation                    | 21    | 4.44915254 | 0.34367737 | FCER1A, PIK   | 341        | 718      | 13588     | 1.16545634      | 1          | 0.92195368 | 99.9259536 |
| GOTERM_BP_FAT          | GO:0006793~phosphorus metabolic process       | 24    | 5.08474576 | 0.41387723 | FCER1A, PIK   | 341        | 866      | 13588     | 1.10431891      | 1          | 0.9527911  | 99.9893207 |
| GOTERM_BP_FAT          | GO:0006796~phosphate metabolic process        | 24    | 5.08474576 | 0.41387723 | FCER1A, PIK   | 341        | 866      | 13588     | 1.10431891      | 1          | 0.9527911  | 99.9893207 |

|                 |  |    |            |            |              |     |     |       |            |   |            |            |
|-----------------|--|----|------------|------------|--------------|-----|-----|-------|------------|---|------------|------------|
| GOTERM_MF_FAT   | GO:0004672~protein kinase activity                     | 17 | 3.60169492 | 0.41409786 | POLR2G, FGI  | 339 | 583 | 13288 | 1.14298436 | 1 | 0.97863856 | 99.9563523 |
| INTERPRO        | IPR017441:Protein kinase, ATP binding site             | 13 | 2.75423729 | 0.43622658 | FGR, BMX, S  | 425 | 467 | 17763 | 1.16346643 | 1 | 0.99848112 | 99.9849705 |
| UP_SEQ_FEATURE  | binding site:ATP                                       | 16 | 3.38983051 | 0.47373215 | MAT2A, FGR   | 425 | 545 | 16021 | 1.10668538 | 1 | 0.99991174 | 99.9969127 |
| INTERPRO        | IPR000719:Protein kinase, core                         | 12 | 2.54237288 | 0.62767896 | IRAK4, FGR,  | 425 | 491 | 17763 | 1.02147358 | 1 | 0.99990026 | 99.9999743 |
| UP_SEQ_FEATURE  | domain:Protein kinase                                  | 12 | 2.54237288 | 0.71910021 | IRAK4, FGR,  | 425 | 476 | 16021 | 0.95033119 | 1 | 0.99999993 | 99.9999999 |
| INTERPRO        | IPR008271:Serine/threonine protein kinase, active site | 8  | 1.69491525 | 0.75960207 | IRAK4, PLK1, | 425 | 360 | 17763 | 0.92878431 | 1 | 0.99999779 | 100        |
| SP_PIR_KEYWORDS | serine/threonine-protein kinase                        | 8  | 1.69491525 | 0.83511142 | IRAK4, PLK1, | 439 | 384 | 17854 | 0.8472855  | 1 | 0.99618439 | 100        |
| GOTERM_MF_FAT   | GO:0004674~protein serine/threonine kinase activity    | 9  | 1.90677966 | 0.84462649 | IRAK4, CCNC  | 339 | 421 | 13288 | 0.84379543 | 1 | 0.999972   | 100        |
| INTERPRO        | IPR002290:Serine/threonine protein kinase              | 5  | 1.05932203 | 0.88044114 | PLK1, MAPK   | 425 | 265 | 17763 | 0.78859046 | 1 | 0.99999999 | 100        |
| INTERPRO        | IPR017442:Serine/threonine protein kinase-related      | 7  | 1.48305085 | 0.88536298 | IRAK4, PLK1, | 425 | 374 | 17763 | 0.78226486 | 1 | 0.99999999 | 100        |
| SMART           | SM00220:S_TKc  | 5  | 1.05932203 | 0.94199151 | PLK1, MAPK   | 256 | 265 | 9131  | 0.67298054 | 1 | 0.99999903 | 100        |

|                        |  |       |            |            |             |            |          |           |              |            |            |            |
|------------------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 113 | Enrichment Score: 0.34426897499993503      |       |            |            |             |            |          |           |              |            |            |            |
| Category               | Term                                       | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT          | GO:0044057~regulation of system process    | 9     | 1.90677966 | 0.13166982 | PROK2, APO  | 341        | 201      | 13588     | 1.78421675   | 1          | 0.69027309 | 91.0784994 |
| GOTERM_BP_FAT          | GO:0008016~regulation of heart contraction | 3     | 0.63559322 | 0.35704099 | ATP2A2, RYF | 341        | 50       | 13588     | 2.39085044   | 1          | 0.92935203 | 99.9479315 |
| KEGG_PATHWAY           | mmu04260:Cardiac muscle contraction        | 3     | 0.63559322 | 0.69971271 | ATP2A2, RYF | 178        | 78       | 5738      | 1.23984443   | 1          | 0.91484803 | 99.999916  |
| KEGG_PATHWAY           | mmu05410:Hypertrophic cardiomyopathy (HCM) | 3     | 0.63559322 | 0.73798093 | ATP2A2, RYF | 178        | 84       | 5738      | 1.15128411   | 1          | 0.9299167  | 99.9999828 |
| KEGG_PATHWAY           | mmu05414:Dilated cardiomyopathy            | 3     | 0.63559322 | 0.78250283 | ATP2A2, RYF | 178        | 92       | 5738      | 1.05117245   | 1          | 0.94699083 | 99.999998  |

|                        |                                      |       |            |            |             |            |          |           |              |            |            |            |
|------------------------|--------------------------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 114 | Enrichment Score: 0.3382891074791464 |       |            |            |             |            |          |           |              |            |            |            |
| Category               | Term                                 | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| UP_SEQ_FEATURE         | repeat:ANK 4                         | 6     | 1.27118644 | 0.24157332 | ANKRD46, N  | 425        | 126      | 16021     | 1.79507003   | 1          | 0.99579405 | 98.8592348 |
| UP_SEQ_FEATURE         | repeat:ANK 1                         | 7     | 1.48305085 | 0.39401189 | ANKRD46, N  | 425        | 191      | 16021     | 1.38154604   | 1          | 0.99961091 | 99.9697573 |
| UP_SEQ_FEATURE         | repeat:ANK 2                         | 7     | 1.48305085 | 0.39401189 | ANKRD46, N  | 425        | 191      | 16021     | 1.38154604   | 1          | 0.99961091 | 99.9697573 |
| UP_SEQ_FEATURE         | repeat:ANK 3                         | 6     | 1.27118644 | 0.41243551 | ANKRD46, N  | 425        | 159      | 16021     | 1.42250832   | 1          | 0.99970384 | 99.9816476 |
| INTERPRO               | IPR002110:Ankyrin                    | 7     | 1.48305085 | 0.44070598 | ANKRD46, N  | 425        | 223      | 17763     | 1.31195991   | 1          | 0.99847952 | 99.9867037 |
| SP_PIR_KEYWORDS        | ank repeat                           | 7     | 1.48305085 | 0.4636503  | ANKRD46, N  | 439        | 222      | 17854     | 1.28237805   | 1          | 0.92370382 | 99.9820319 |
| SMART                  | SM00248:ANK                          | 7     | 1.48305085 | 0.59516978 | ANKRD46, N  | 256        | 223      | 9131      | 1.11962234   | 1          | 0.99634924 | 99.9985459 |
| UP_SEQ_FEATURE         | repeat:ANK 6                         | 3     | 0.63559322 | 0.61552681 | NFKBID, TAN | 425        | 78       | 16021     | 1.44986425   | 1          | 0.99999688 | 99.9999808 |
| UP_SEQ_FEATURE         | repeat:ANK 5                         | 3     | 0.63559322 | 0.779376   | NFKBID, TAN | 425        | 107      | 16021     | 1.05691039   | 1          | 1          | 100        |

|                        |  |       |            |            |              |            |          |           |              |            |            |            |
|------------------------|--|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 115 | Enrichment Score: 0.3353418515269346                 |       |            |            |              |            |          |           |              |            |            |            |
| Category               | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| INTERPRO               | IPR006025:Peptidase M, neutral zinc metallopeptidase | 5     | 1.05932203 | 0.15442508 | ECE1, MMP9   | 425        | 87       | 17763     | 2.4020284    | 1          | 0.92524172 | 92.3958736 |
| UP_SEQ_FEATURE         | metal ion-binding site:Zinc; catalytic               | 6     | 1.27118644 | 0.20312776 | ECE1, APOB   | 425        | 118      | 16021     | 1.91676969   | 1          | 0.99250841 | 97.4611994 |
| SP_PIR_KEYWORDS        | zymogen  | 8     | 1.69491525 | 0.21820713 | CASP4, F5, P | 439        | 199      | 17854     | 1.63496297   | 1          | 0.72725187 | 96.6889095 |
| GOTERM_MF_FAT          | GO:0004222~metalloendopeptidase activity             | 5     | 1.05932203 | 0.32989496 | ECE1, MMP9   | 339        | 114      | 13288     | 1.71919474   | 1          | 0.96280298 | 99.6952542 |
| SP_PIR_KEYWORDS        | metalloprotease                                      | 5     | 1.05932203 | 0.48292623 | ECE1, MMP9   | 439        | 146      | 17854     | 1.39279808   | 1          | 0.92652403 | 99.9891745 |
| GOTERM_MF_FAT          | GO:0004175~endopeptidase activity                    | 12    | 2.54237288 | 0.51509717 | CASP4, ECE1  | 339        | 421      | 13288     | 1.1172724    | 1          | 0.99279741 | 99.9971765 |
| GOTERM_MF_FAT          | GO:0008237~metallopeptidase activity                 | 5     | 1.05932203 | 0.70453365 | ECE1, MMP9   | 339        | 187      | 13288     | 1.04806524   | 1          | 0.99940678 | 99.9999978 |
| SP_PIR_KEYWORDS        | Protease   | 12    | 2.54237288 | 0.70809154 | CASP4, ECE1  | 439        | 509      | 17854     | 0.95881424   | 1          | 0.98290028 | 99.999996  |
| GOTERM_MF_FAT          | GO:0070011~peptidase activity, acting on L-amino aci | 13    | 2.75423729 | 0.84605302 | MELA, PRTN   | 339        | 603      | 13288     | 0.84505692   | 1          | 0.99997023 | 100        |
| GOTERM_MF_FAT          | GO:0008233~peptidase activity                        | 13    | 2.75423729 | 0.88206893 | MELA, PRTN   | 339        | 629      | 13288     | 0.81012611   | 1          | 0.99999133 | 100        |
| GOTERM_BP_FAT          | GO:0006508~proteolysis                               | 18    | 3.81355932 | 0.97914427 | SOCS3, MEL   | 341        | 1034     | 13588     | 0.69367034   | 1          | 0.99999992 | 100        |

|                        |  |       |            |            |             |            |          |           |              |            |            |            |
|------------------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 116 | Enrichment Score: 0.32018927202175984                |       |            |            |             |            |          |           |              |            |            |            |
| Category               | Term   | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_MF_FAT          | GO:0042277~peptide binding                           | 6     | 1.27118644 | 0.38502152 | F2RL2, EDNR | 339        | 160      | 13288     | 1.4699115    | 1          | 0.97536178 | 99.9120212 |
| GOTERM_MF_FAT          | GO:0001653~peptide receptor activity                 | 4     | 0.84745763 | 0.53330246 | F2RL2, EDNR | 339        | 110      | 13288     | 1.42536873   | 1          | 0.99406376 | 99.9983772 |
| GOTERM_MF_FAT          | GO:0008528~peptide receptor activity, G-protein coup | 4     | 0.84745763 | 0.53330246 | F2RL2, EDNR | 339        | 110      | 13288     | 1.42536873   | 1          | 0.99406376 | 99.9983772 |

|                        |  |       |            |            |            |            |          |           |              |            |            |            |
|------------------------|--|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 117 | Enrichment Score: 0.3127149946912622     |       |            |            |            |            |          |           |              |            |            |            |
| Category               | Term                                     | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| INTERPRO               | IPR011510:Sterile alpha motif homology 2 | 3     | 0.63559322 | 0.23848498 | SAMHD1, SA | 425        | 39       | 17763     | 3.21502262   | 1          | 0.97710088 | 98.4774547 |
| UP_SEQ_FEATURE         | domain:SAM                               | 3     | 0.63559322 | 0.54074395 | SAMHD1, SA | 425        | 68       | 16021     | 1.66307958   | 1          | 0.99997951 | 99.9996591 |
| INTERPRO               | IPR001660:Sterile alpha motif SAM        | 3     | 0.63559322 | 0.61841596 | SAMHD1, SA | 425        | 87       | 17763     | 1.44121704   | 1          | 0.99988976 | 99.9999626 |

|                        |  |       |            |            |               |            |          |           |              |            |            |            |
|------------------------|--|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| SMART                  | SM00454:SAM  | 3     | 0.63559322 | 0.70373091 | SAMHD1, SA    | 256        | 87       | 9131      | 1.22992996   | 1          | 0.99868693 | 99.9999689 |
| Annotation Cluster 118 | Enrichment Score: 0.2973118472595731                 |       |            |            |               |            |          |           |              |            |            |            |
| Category               | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| UP_SEQ_FEATURE         | domain:EGF-like                                      | 4     | 0.84745763 | 0.26840843 | SELP, SELL, S | 425        | 68       | 16021     | 2.21743945   | 1          | 0.99724455 | 99.3630769 |
| SP_PIR_KEYWORDS        | egf-like domain                                      | 7     | 1.48305085 | 0.4636503  | SELP, THBD,   | 439        | 222      | 17854     | 1.28237805   | 1          | 0.92370382 | 99.9820319 |
| INTERPRO               | IPR000742:EGF-like, type 3                           | 6     | 1.27118644 | 0.51640112 | SELP, THBD,   | 425        | 199      | 17763     | 1.26015962   | 1          | 0.9995406  | 99.9985755 |
| INTERPRO               | IPR006210:EGF-like                                   | 6     | 1.27118644 | 0.52747748 | SELP, THBD,   | 425        | 203      | 17763     | 1.23532889   | 1          | 0.99960147 | 99.9990021 |
| INTERPRO               | IPR006209:EGF  | 4     | 0.84745763 | 0.59272813 | SELP, THBD,   | 425        | 128      | 17763     | 1.30610294   | 1          | 0.99985039 | 99.9998982 |
| INTERPRO               | IPR013032:EGF-like region, conserved site            | 8     | 1.69491525 | 0.61206051 | SELP, ITGB2L  | 425        | 310      | 17763     | 1.07858824   | 1          | 0.99988415 | 99.9999518 |
| SMART                  | SM00181:EGF  | 6     | 1.27118644 | 0.67451151 | SELP, THBD,   | 256        | 203      | 9131      | 1.05422568   | 1          | 0.99852238 | 99.999901  |
| Annotation Cluster 119 | Enrichment Score: 0.27168992674963605                |       |            |            |               |            |          |           |              |            |            |            |
| Category               | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| UP_SEQ_FEATURE         | domain:lg-like C2-type 3                             | 5     | 1.05932203 | 0.19882167 | IGSF10, ALC/  | 425        | 87       | 16021     | 2.16646383   | 1          | 0.99295032 | 97.229909  |
| UP_SEQ_FEATURE         | domain:lg-like C2-type 5                             | 3     | 0.63559322 | 0.364047   | IGSF10, ROB   | 425        | 48       | 16021     | 2.35602941   | 1          | 0.99937813 | 99.933971  |
| UP_SEQ_FEATURE         | domain:lg-like C2-type 4                             | 3     | 0.63559322 | 0.43859705 | IGSF10, ROB   | 425        | 56       | 16021     | 2.01945378   | 1          | 0.9998164  | 99.9912165 |
| INTERPRO               | IPR013098:Immunoglobulin I-set                       | 3     | 0.63559322 | 0.81013284 | IGSF10, ROB   | 425        | 127      | 17763     | 0.98729041   | 1          | 0.9999997  | 100        |
| INTERPRO               | IPR003598:Immunoglobulin subtype 2                   | 3     | 0.63559322 | 0.94010434 | IGSF10, ROB   | 425        | 187      | 17763     | 0.67051274   | 1          | 1          | 100        |
| SMART                  | SM00408:IGc2   | 3     | 0.63559322 | 0.96926215 | IGSF10, ROB   | 256        | 187      | 9131      | 0.5722134    | 1          | 0.9999999  | 100        |
| Annotation Cluster 120 | Enrichment Score: 0.26824551983223294                |       |            |            |               |            |          |           |              |            |            |            |
| Category               | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT          | GO:0060674--placenta blood vessel development        | 3     | 0.63559322 | 0.07340235 | WNT2, SOCS    | 341        | 18       | 13588     | 6.64125122   | 1          | 0.55172616 | 72.8818797 |
| GOTERM_BP_FAT          | GO:0060711--labyrinthine layer development           | 3     | 0.63559322 | 0.2179941  | WNT2, SOCS    | 341        | 35       | 13588     | 3.41550063   | 1          | 0.8303037  | 98.5139916 |
| GOTERM_BP_FAT          | GO:0001892--embryonic placenta development           | 3     | 0.63559322 | 0.45354381 | WNT2, SOCS    | 341        | 61       | 13588     | 1.95971348   | 1          | 0.96573315 | 99.9967819 |
| GOTERM_BP_FAT          | GO:0001568--blood vessel development                 | 7     | 1.48305085 | 0.57487294 | WNT2, PROK    | 341        | 244      | 13588     | 1.14316619   | 1          | 0.98890427 | 99.9999562 |
| GOTERM_BP_FAT          | GO:0001944--vasculature development                  | 7     | 1.48305085 | 0.5986584  | WNT2, PROK    | 341        | 250      | 13588     | 1.11573021   | 1          | 0.99125633 | 99.9999837 |
| GOTERM_BP_FAT          | GO:0001890--placenta development                     | 3     | 0.63559322 | 0.64437111 | WNT2, SOCS    | 341        | 87       | 13588     | 1.37405198   | 1          | 0.99447809 | 99.9999979 |
| GOTERM_BP_FAT          | GO:0001525--angiogenesis                             | 4     | 0.84745763 | 0.65078249 | PROK2, IL1B,  | 341        | 133      | 13588     | 1.19842127   | 1          | 0.99474933 | 99.9999985 |
| GOTERM_BP_FAT          | GO:0001701--in utero embryonic development           | 7     | 1.48305085 | 0.66197861 | CCNB1, WN     | 341        | 267      | 13588     | 1.0446912    | 1          | 0.99534705 | 99.9999991 |
| GOTERM_BP_FAT          | GO:0048514--blood vessel morphogenesis               | 5     | 1.05932203 | 0.73408678 | PROK2, IL1B,  | 341        | 198      | 13588     | 1.00625019   | 1          | 0.99801536 | 100        |
| GOTERM_BP_FAT          | GO:0043009--chordate embryonic development           | 9     | 1.90677966 | 0.83169509 | CCNB1, WN     | 341        | 421      | 13588     | 0.85184695   | 1          | 0.99965831 | 100        |
| GOTERM_BP_FAT          | GO:0009792--embryonic development ending in birth    | 9     | 1.90677966 | 0.83916493 | CCNB1, WN     | 341        | 425      | 13588     | 0.84382957   | 1          | 0.99971041 | 100        |
| GOTERM_BP_FAT          | GO:0048568--embryonic organ development              | 4     | 0.84745763 | 0.94310794 | WNT2, ALDH    | 341        | 241      | 13588     | 0.66136942   | 1          | 0.99999568 | 100        |
| GOTERM_BP_FAT          | GO:0051094--positive regulation of developmental pro | 3     | 0.63559322 | 0.97218119 | SOC33, IL1B,  | 341        | 214      | 13588     | 0.55860992   | 1          | 0.99999976 | 100        |
| Annotation Cluster 121 | Enrichment Score: 0.25316527653735293                |       |            |            |               |            |          |           |              |            |            |            |
| Category               | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT          | GO:0007409--axonogenesis                             | 6     | 1.27118644 | 0.38676202 | ALCAM, ROE    | 341        | 163      | 13588     | 1.46677941   | 1          | 0.94288391 | 99.9768401 |
| GOTERM_BP_FAT          | GO:0030030--cell projection organization             | 10    | 2.11864407 | 0.40387243 | ALCAM, COF    | 341        | 319      | 13588     | 1.24913816   | 1          | 0.94890621 | 99.9857319 |
| GOTERM_BP_FAT          | GO:0007411--axon guidance                            | 4     | 0.84745763 | 0.44574427 | ALCAM, ROE    | 341        | 98       | 13588     | 1.62642887   | 1          | 0.96361758 | 99.9958984 |
| GOTERM_BP_FAT          | GO:0048812--neuron projection morphogenesis          | 6     | 1.27118644 | 0.45101725 | ALCAM, ROE    | 341        | 176      | 13588     | 1.35843775   | 1          | 0.96517978 | 99.9965175 |
| GOTERM_BP_FAT          | GO:0031175--neuron projection development            | 7     | 1.48305085 | 0.4639844  | ALCAM, LST:   | 341        | 218      | 13588     | 1.27950712   | 1          | 0.96829431 | 99.9976869 |
| GOTERM_BP_FAT          | GO:0048667--cell morphogenesis involved in neuron c  | 6     | 1.27118644 | 0.48012193 | ALCAM, ROE    | 341        | 182      | 13588     | 1.31365409   | 1          | 0.97210482 | 99.9986293 |
| GOTERM_BP_FAT          | GO:0048858--cell projection morphogenesis            | 6     | 1.27118644 | 0.57268725 | ALCAM, ROE    | 341        | 202      | 13588     | 1.18358933   | 1          | 0.98873964 | 99.9999522 |
| GOTERM_BP_FAT          | GO:0032990--cell part morphogenesis                  | 6     | 1.27118644 | 0.61563295 | ALCAM, ROE    | 341        | 212      | 13588     | 1.12775964   | 1          | 0.99263358 | 99.9999922 |
| GOTERM_BP_FAT          | GO:0000904--cell morphogenesis involved in different | 6     | 1.27118644 | 0.61563295 | ALCAM, ROE    | 341        | 212      | 13588     | 1.12775964   | 1          | 0.99263358 | 99.9999922 |
| GOTERM_BP_FAT          | GO:0032989--cellular component morphogenesis         | 9     | 1.90677966 | 0.6556853  | ALCAM, LST:   | 341        | 351      | 13588     | 1.02173096   | 1          | 0.99503926 | 99.9999988 |
| GOTERM_BP_FAT          | GO:0048666--neuron development                       | 7     | 1.48305085 | 0.74301818 | ALCAM, LST:   | 341        | 292      | 13588     | 0.95524846   | 1          | 0.99820211 | 100        |
| GOTERM_BP_FAT          | GO:0000902--cell morphogenesis                       | 7     | 1.48305085 | 0.78959121 | ALCAM, LST:   | 341        | 309      | 13588     | 0.90269434   | 1          | 0.99917248 | 100        |
| GOTERM_BP_FAT          | GO:0030182--neuron differentiation                   | 8     | 1.69491525 | 0.87573178 | ALCAM, LST:   | 341        | 399      | 13588     | 0.79894752   | 1          | 0.99989585 | 100        |
| Annotation Cluster 122 | Enrichment Score: 0.2528276633873335                 |       |            |            |               |            |          |           |              |            |            |            |
| Category               | Term   | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT          | GO:0008584--male gonad development                   | 3     | 0.63559322 | 0.25520182 | HMGB2, NK     | 341        | 39       | 13588     | 3.06519287   | 1          | 0.86823247 | 99.3549118 |
| GOTERM_BP_FAT          | GO:0046546--development of primary male sexual ch    | 3     | 0.63559322 | 0.38407893 | HMGB2, NK     | 341        | 53       | 13588     | 2.25551928   | 1          | 0.94190999 | 99.975043  |



|               |   |   |            |            |            |     |     |       |            |   |            |            |
|---------------|---|---|------------|------------|------------|-----|-----|-------|------------|---|------------|------------|
| GOTERM_BP_FAT | GO:0046661~male sex differentiation               | 3 | 0.63559322 | 0.41933791 | HMGB2, NK  | 341 | 57  | 13588 | 2.09723723 | 1 | 0.95483699 | 99.9909018 |
| GOTERM_BP_FAT | GO:0048608~reproductive structure development     | 4 | 0.84745763 | 0.63549036 | HMGB2, CD4 | 341 | 130 | 13588 | 1.22607715 | 1 | 0.9940749  | 99.9999969 |
| GOTERM_BP_FAT | GO:0008406~gonad development                      | 3 | 0.63559322 | 0.65055091 | HMGB2, NK  | 341 | 88  | 13588 | 1.35843775 | 1 | 0.99480323 | 99.9999985 |
| GOTERM_BP_FAT | GO:0045137~development of primary sexual characte | 3 | 0.63559322 | 0.73814126 | HMGB2, NK  | 341 | 104 | 13588 | 1.14944733 | 1 | 0.99806718 | 100        |
| GOTERM_BP_FAT | GO:0007548~sex differentiation                    | 3 | 0.63559322 | 0.84048671 | HMGB2, NK  | 341 | 130 | 13588 | 0.91955786 | 1 | 0.99971555 | 100        |
| GOTERM_BP_FAT | GO:0003006~reproductive developmental process     | 5 | 1.05932203 | 0.90042952 | HMGB2, CD4 | 341 | 264 | 13588 | 0.75468764 | 1 | 0.99995691 | 100        |

|                        |                                       |       |            |           |             |            |          |           |              |            |            |            |
|------------------------|---------------------------------------|-------|------------|-----------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 123 | Enrichment Score: 0.25154626983069783 |       |            |           |             |            |          |           |              |            |            |            |
| Category               | Term                                  | Count | %          | PValue    | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| INTERPRO               | IPR001781:Zinc finger, LIM-type       | 3     | 0.63559322 | 0.5303521 | LHX1, LMO7, | 425        | 74       | 17763     | 1.69440382   | 1          | 0.99958626 | 99.9990914 |
| SP_PIR_KEYWORDS        | LIM domain                            | 3     | 0.63559322 | 0.5378481 | LHX1, LMO7, | 439        | 73       | 17854     | 1.67135769   | 1          | 0.94361562 | 99.9977128 |
| SMART                  | SM00132:LIM                           | 3     | 0.63559322 | 0.6167899 | LHX1, LMO7, | 256        | 74       | 9131      | 1.44599873   | 1          | 0.99683319 | 99.9992604 |

|                        |   |       |            |            |              |            |          |           |              |            |            |            |
|------------------------|---|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 124 | Enrichment Score: 0.2420568247094855                  |       |            |            |              |            |          |           |              |            |            |            |
| Category               | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| INTERPRO               | IPR001331:Guanine-nucleotide dissociation stimulator, | 3     | 0.63559322 | 0.36203033 | PLEKHG3, TI/ | 425        | 53       | 17763     | 2.36577137   | 1          | 0.99614942 | 99.8996054 |
| UP_SEQ_FEATURE         | domain:DH   | 3     | 0.63559322 | 0.43859705 | PLEKHG3, TI/ | 425        | 56       | 16021     | 2.01945378   | 1          | 0.9998164  | 99.9912165 |
| INTERPRO               | IPR000219:Dbl homology (DH) domain                    | 3     | 0.63559322 | 0.46178601 | PLEKHG3, TI/ | 425        | 65       | 17763     | 1.92901357   | 1          | 0.99891152 | 99.9926304 |
| GOTERM_MF_FAT          | GO:0005083~small GTPase regulator activity            | 7     | 1.48305085 | 0.49753275 | PLEKHG3, TI/ | 339        | 223      | 13288     | 1.2304192    | 1          | 0.99137715 | 99.9952747 |
| GOTERM_MF_FAT          | GO:0005089~Rho guanyl-nucleotide exchange factor      | 3     | 0.63559322 | 0.54265427 | PLEKHG3, TI/ | 339        | 71       | 13288     | 1.65623831   | 1          | 0.99408116 | 99.9987892 |
| SMART                  | SM00325:RhoGEF  | 3     | 0.63559322 | 0.5459404  | PLEKHG3, TI/ | 256        | 65       | 9131      | 1.64621394   | 1          | 0.99375222 | 99.9940229 |
| GOTERM_MF_FAT          | GO:0005088~Ras guanyl-nucleotide exchange factor a    | 3     | 0.63559322 | 0.62780287 | PLEKHG3, TI/ | 339        | 83       | 13288     | 1.41678217   | 1          | 0.99774524 | 99.9999386 |
| GOTERM_BP_FAT          | GO:0035023~regulation of Rho protein signal transdu   | 3     | 0.63559322 | 0.63810549 | PLEKHG3, TI/ | 341        | 86       | 13588     | 1.39002933   | 1          | 0.99413079 | 99.9999972 |
| GOTERM_BP_FAT          | GO:0046578~regulation of Ras protein signal transdu   | 5     | 1.05932203 | 0.66751411 | PLEKHG3, TI/ | 341        | 181      | 13588     | 1.10075987   | 1          | 0.99559105 | 99.9999993 |
| SP_PIR_KEYWORDS        | guanine-nucleotide releasing factor                   | 3     | 0.63559322 | 0.71786485 | TIAM2, CYTH  | 439        | 102      | 17854     | 1.19616776   | 1          | 0.98415933 | 99.9999975 |
| GOTERM_MF_FAT          | GO:0005085~guanyl-nucleotide exchange factor activi   | 4     | 0.84745763 | 0.72645139 | PLEKHG3, TI/ | 339        | 147      | 13288     | 1.06660245   | 1          | 0.99959345 | 99.9999993 |
| GOTERM_BP_FAT          | GO:0051056~regulation of small GTPase mediated sig    | 5     | 1.05932203 | 0.82632536 | PLEKHG3, TI/ | 341        | 228      | 13588     | 0.87384884   | 1          | 0.99962085 | 100        |

|                        |   |       |            |            |             |            |          |           |              |            |            |            |
|------------------------|---|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 125 | Enrichment Score: 0.24193501311298787             |       |            |            |             |            |          |           |              |            |            |            |
| Category               | Term  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| INTERPRO               | IPR018029:C2 membrane targeting protein           | 4     | 0.84745763 | 0.46593321 | PLCL2, PLCG | 425        | 106      | 17763     | 1.57718091   | 1          | 0.99890261 | 99.993456  |
| UP_SEQ_FEATURE         | domain:C2   | 3     | 0.63559322 | 0.54074395 | PLCL2, PLCG | 425        | 68       | 16021     | 1.66307958   | 1          | 0.99997951 | 99.9996591 |
| INTERPRO               | IPR000008:C2 calcium-dependent membrane targeting | 4     | 0.84745763 | 0.60325321 | PLCL2, PLCG | 425        | 130      | 17763     | 1.28600905   | 1          | 0.99987091 | 99.9999319 |
| SMART                  | SM00239:C2  | 4     | 0.84745763 | 0.70867151 | PLCL2, PLCG | 256        | 130      | 9131      | 1.09747596   | 1          | 0.99853991 | 99.9999747 |

|                        |   |       |            |            |              |            |          |           |              |            |            |            |
|------------------------|---|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 126 | Enrichment Score: 0.2321544815311004                  |       |            |            |              |            |          |           |              |            |            |            |
| Category               | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| UP_SEQ_FEATURE         | lipid moiety-binding region:S-geranylgeranyl cysteine | 5     | 1.05932203 | 0.24371171 | RAB32, RAC1, | 425        | 95       | 16021     | 1.98402477   | 1          | 0.99565172 | 98.9101721 |
| SP_PIR_KEYWORDS        | prenylation   | 6     | 1.27118644 | 0.28396293 | RAB32, RAC1, | 439        | 145      | 17854     | 1.6828843    | 1          | 0.79538208 | 99.0188395 |
| GOTERM_MF_FAT          | GO:0003924~GTPase activity                            | 5     | 1.05932203 | 0.41086813 | RAC2, GNG2   | 339        | 128      | 13288     | 1.53115782   | 1          | 0.9789369  | 99.9527379 |
| UP_SEQ_FEATURE         | short sequence motif:Effector region                  | 4     | 0.84745763 | 0.44117765 | RAB32, RAC1, | 425        | 92       | 16021     | 1.63897698   | 1          | 0.99980946 | 99.9918474 |
| INTERPRO               | IPR005225:Small GTP-binding protein                   | 5     | 1.05932203 | 0.55272093 | RAB32, ARL1  | 425        | 164      | 17763     | 1.27424677   | 1          | 0.99972212 | 99.9995706 |
| INTERPRO               | IPR013753:Ras   | 4     | 0.84745763 | 0.55450138 | RAB32, RAC1, | 425        | 121      | 17763     | 1.38166262   | 1          | 0.99970426 | 99.9995961 |
| INTERPRO               | IPR001806:Ras GTPase                                  | 4     | 0.84745763 | 0.60325321 | RAB32, RAC1, | 425        | 130      | 17763     | 1.28600905   | 1          | 0.99987091 | 99.9999319 |
| GOTERM_BP_FAT          | GO:0007264~small GTPase mediated signal transducti    | 7     | 1.48305085 | 0.62923786 | RAB32, ARL1  | 341        | 258      | 13588     | 1.08113392   | 1          | 0.99362561 | 99.9999958 |
| UP_SEQ_FEATURE         | nucleotide phosphate-binding region:GTP               | 6     | 1.27118644 | 0.85454913 | RAB32, ARL1  | 425        | 274      | 16021     | 0.82547016   | 1          | 1          | 100        |
| SP_PIR_KEYWORDS        | gtp-binding   | 6     | 1.27118644 | 0.88561903 | RAB32, ARL1  | 439        | 313      | 17854     | 0.77961094   | 1          | 0.99839864 | 100        |
| GOTERM_MF_FAT          | GO:0005525~GTP binding                                | 6     | 1.27118644 | 0.94952508 | RAB32, ARL1  | 339        | 354      | 13288     | 0.66436678   | 1          | 0.99999978 | 100        |
| GOTERM_MF_FAT          | GO:0019001~guanyl nucleotide binding                  | 6     | 1.27118644 | 0.95644972 | RAB32, ARL1  | 339        | 363      | 13288     | 0.64789488   | 1          | 0.99999986 | 100        |
| GOTERM_MF_FAT          | GO:0032561~guanyl ribonucleotide binding              | 6     | 1.27118644 | 0.95644972 | RAB32, ARL1  | 339        | 363      | 13288     | 0.64789488   | 1          | 0.99999986 | 100        |

|                        |   |       |            |            |             |            |          |           |              |            |            |            |
|------------------------|---|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 127 | Enrichment Score: 0.2247395227233975        |       |            |            |             |            |          |           |              |            |            |            |
| Category               | Term  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT          | GO:0001508~regulation of action potential   | 3     | 0.63559322 | 0.39298414 | CLN3, UGT8, | 341        | 54       | 13588     | 2.21375041   | 1          | 0.94475423 | 99.9805498 |
| GOTERM_BP_FAT          | GO:0019226~transmission of nerve impulse    | 6     | 1.27118644 | 0.67130738 | WNT2, CLN3  | 341        | 226      | 13588     | 1.05789842   | 1          | 0.99565577 | 99.9999995 |
| GOTERM_BP_FAT          | GO:0042391~regulation of membrane potential | 3     | 0.63559322 | 0.80257382 | CLN3, UGT8, | 341        | 119      | 13588     | 1.00455901   | 1          | 0.99935888 | 100        |

|                        |  |       |            |            |              |            |          |           |              |            |            |            |
|------------------------|--|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 128 | Enrichment Score: 0.21652189442976819                |       |            |            |              |            |          |           |              |            |            |            |
| Category               | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT          | GO:0033554~cellular response to stress               | 13    | 2.75423729 | 0.31554758 | FCER1A, CLN  | 341        | 404      | 13588     | 1.28222177   | 1          | 0.90659701 | 99.8481251 |
| GOTERM_BP_FAT          | GO:0006974~response to DNA damage stimulus           | 7     | 1.48305085 | 0.72800541 | KIF22, PNKP, | 341        | 287      | 13588     | 0.97189042   | 1          | 0.99789024 | 100        |
| GOTERM_BP_FAT          | GO:0006259~DNA metabolic process                     | 10    | 2.11864407 | 0.73123572 | KIF22, PNKP, | 341        | 421      | 13588     | 0.94649661   | 1          | 0.99794466 | 100        |
| GOTERM_BP_FAT          | GO:0006281~DNA repair                                | 5     | 1.05932203 | 0.81031814 | KIF22, PNKP, | 341        | 222      | 13588     | 0.89746638   | 1          | 0.99945567 | 100        |
| Annotation Cluster 129 | Enrichment Score: 0.19491076729900406                |       |            |            |              |            |          |           |              |            |            |            |
| Category               | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT          | GO:0044271~nitrogen compound biosynthetic proces     | 10    | 2.11864407 | 0.34354343 | MOCOS, MA    | 341        | 302      | 13588     | 1.31945389   | 1          | 0.92248305 | 99.9256945 |
| GOTERM_BP_FAT          | GO:0009152~purine ribonucleotide biosynthetic proce  | 4     | 0.84745763 | 0.50357282 | ATP2A2, AM   | 341        | 107      | 13588     | 1.48962644   | 1          | 0.9773773  | 99.999378  |
| GOTERM_BP_FAT          | GO:0009260~ribonucleotide biosynthetic process       | 4     | 0.84745763 | 0.5282686  | ATP2A2, AM   | 341        | 111      | 13588     | 1.43594621   | 1          | 0.98224158 | 99.9997403 |
| GOTERM_BP_FAT          | GO:0009150~purine ribonucleotide metabolic process   | 4     | 0.84745763 | 0.57553466 | ATP2A2, AM   | 341        | 119      | 13588     | 1.33941201   | 1          | 0.98885879 | 99.9999574 |
| GOTERM_BP_FAT          | GO:0009259~ribonucleotide metabolic process          | 4     | 0.84745763 | 0.60898607 | ATP2A2, AM   | 341        | 125      | 13588     | 1.27512023   | 1          | 0.99205856 | 99.9999895 |
| GOTERM_BP_FAT          | GO:0009165~nucleotide biosynthetic process           | 5     | 1.05932203 | 0.6370162  | ATP2A2, G6f  | 341        | 174      | 13588     | 1.14504331   | 1          | 0.99412073 | 99.9999971 |
| GOTERM_BP_FAT          | GO:0034654~nucleobase, nucleoside, nucleotide and i  | 5     | 1.05932203 | 0.6589821  | ATP2A2, G6f  | 341        | 179      | 13588     | 1.11305886   | 1          | 0.99520549 | 99.999999  |
| GOTERM_BP_FAT          | GO:0034404~nucleobase, nucleoside and nucleotide b   | 5     | 1.05932203 | 0.6589821  | ATP2A2, G6f  | 341        | 179      | 13588     | 1.11305886   | 1          | 0.99520549 | 99.999999  |
| GOTERM_BP_FAT          | GO:0006164~purine nucleotide biosynthetic process    | 4     | 0.84745763 | 0.67045412 | ATP2A2, AM   | 341        | 137      | 13588     | 1.16343087   | 1          | 0.9956607  | 99.9999994 |
| GOTERM_BP_FAT          | GO:0009206~purine ribonucleoside triphosphate biosy  | 3     | 0.63559322 | 0.68017622 | ATP2A2, NM   | 341        | 93       | 13588     | 1.28540346   | 1          | 0.996091   | 99.9999997 |
| GOTERM_BP_FAT          | GO:0009201~ribonucleoside triphosphate biosynthetic  | 3     | 0.63559322 | 0.68017622 | ATP2A2, NM   | 341        | 93       | 13588     | 1.28540346   | 1          | 0.996091   | 99.9999997 |
| GOTERM_BP_FAT          | GO:0009145~purine nucleoside triphosphate biosynth   | 3     | 0.63559322 | 0.68584976 | ATP2A2, NM   | 341        | 94       | 13588     | 1.27172896   | 1          | 0.99631405 | 99.9999998 |
| GOTERM_BP_FAT          | GO:0009142~nucleoside triphosphate biosynthetic prc  | 3     | 0.63559322 | 0.69144067 | ATP2A2, NM   | 341        | 95       | 13588     | 1.25834234   | 1          | 0.9965723  | 99.9999998 |
| GOTERM_BP_FAT          | GO:0009205~purine ribonucleoside triphosphate metz   | 3     | 0.63559322 | 0.72328423 | ATP2A2, NM   | 341        | 101      | 13588     | 1.18358933   | 1          | 0.99774526 | 100        |
| GOTERM_BP_FAT          | GO:0009199~ribonucleoside triphosphate metabolic p   | 3     | 0.63559322 | 0.72831384 | ATP2A2, NM   | 341        | 102      | 13588     | 1.17198551   | 1          | 0.99786958 | 100        |
| GOTERM_BP_FAT          | GO:0009144~purine nucleoside triphosphate metaboli   | 3     | 0.63559322 | 0.74766445 | ATP2A2, NM   | 341        | 106      | 13588     | 1.12775964   | 1          | 0.99829676 | 100        |
| GOTERM_BP_FAT          | GO:0006163~purine nucleotide metabolic process       | 4     | 0.84745763 | 0.76784176 | ATP2A2, AM   | 341        | 160      | 13588     | 0.99618768   | 1          | 0.99878458 | 100        |
| GOTERM_BP_FAT          | GO:0009141~nucleoside triphosphate metabolic proce   | 3     | 0.63559322 | 0.78691717 | ATP2A2, NM   | 341        | 115      | 13588     | 1.03950019   | 1          | 0.999138   | 100        |
| Annotation Cluster 130 | Enrichment Score: 0.1931570167324535                 |       |            |            |              |            |          |           |              |            |            |            |
| Category               | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT          | GO:0001503~ossification                              | 4     | 0.84745763 | 0.49729597 | IGSF10, NAB  | 341        | 106      | 13588     | 1.50367952   | 1          | 0.97603848 | 99.9992287 |
| GOTERM_BP_FAT          | GO:0060348~bone development                          | 4     | 0.84745763 | 0.5697892  | IGSF10, NAB  | 341        | 118      | 13588     | 1.35076296   | 1          | 0.9884726  | 99.9999464 |
| GOTERM_BP_FAT          | GO:0001501~skeletal system development               | 5     | 1.05932203 | 0.92939386 | IGSF10, MMI  | 341        | 285      | 13588     | 0.69907908   | 1          | 0.99998958 | 100        |
| Annotation Cluster 131 | Enrichment Score: 0.17525223966280346                |       |            |            |              |            |          |           |              |            |            |            |
| Category               | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT          | GO:0032269~negative regulation of cellular protein m | 3     | 0.63559322 | 0.54127825 | CLN3, PTPNF  | 341        | 72       | 13588     | 1.66031281   | 1          | 0.98417685 | 99.9998391 |
| GOTERM_BP_FAT          | GO:0051248~negative regulation of protein metabolic  | 3     | 0.63559322 | 0.5848611  | CLN3, PTPNF  | 341        | 78       | 13588     | 1.53259644   | 1          | 0.98995984 | 99.9999709 |
| GOTERM_BP_FAT          | GO:0010605~negative regulation of macromolecule m    | 9     | 1.90677966 | 0.94139083 | SAP30, CLN3  | 341        | 506      | 13588     | 0.70875013   | 1          | 0.99999522 | 100        |
| Annotation Cluster 132 | Enrichment Score: 0.15451147864421547                |       |            |            |              |            |          |           |              |            |            |            |
| Category               | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS        | Intermediate filament                                | 3     | 0.63559322 | 0.5452119  | LMNB1, KRT;  | 439        | 74       | 17854     | 1.64877178   | 1          | 0.9422443  | 99.9981688 |
| GOTERM_CC_FAT          | GO:0045111~intermediate filament cytoskeleton        | 4     | 0.84745763 | 0.71721311 | LMNB1, DST   | 330        | 140      | 12504     | 1.0825974    | 1          | 0.98454195 | 99.9999941 |
| GOTERM_CC_FAT          | GO:0005882~intermediate filament                     | 3     | 0.63559322 | 0.87953276 | LMNB1, KRT;  | 330        | 137      | 12504     | 0.82972794   | 1          | 0.99816942 | 100        |
| Annotation Cluster 133 | Enrichment Score: 0.12833456295938792                |       |            |            |              |            |          |           |              |            |            |            |
| Category               | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS        | neurogenesis   | 5     | 1.05932203 | 0.47226335 | LOC1000476   | 439        | 144      | 17854     | 1.4121425    | 1          | 0.92451564 | 99.9856395 |
| SP_PIR_KEYWORDS        | differentiation                                      | 9     | 1.90677966 | 0.88054619 | LOC1000476   | 439        | 460      | 17854     | 0.7957116    | 1          | 0.99835202 | 100        |
| SP_PIR_KEYWORDS        | developmental protein                                | 12    | 2.54237288 | 0.99096868 | WNT2, LOC1   | 439        | 814      | 17854     | 0.59955337   | 1          | 0.99999963 | 100        |
| Annotation Cluster 134 | Enrichment Score: 0.12444360986386376                |       |            |            |              |            |          |           |              |            |            |            |
| Category               | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT          | GO:0031980~mitochondrial lumen                       | 5     | 1.05932203 | 0.62544293 | ACADSB, ETI  | 330        | 163      | 12504     | 1.16229782   | 1          | 0.96538223 | 99.9997603 |
| GOTERM_CC_FAT          | GO:0005759~mitochondrial matrix                      | 5     | 1.05932203 | 0.62544293 | ACADSB, ETI  | 330        | 163      | 12504     | 1.16229782   | 1          | 0.96538223 | 99.9997603 |
| SP_PIR_KEYWORDS        | mitochondrion  | 19    | 4.02542373 | 0.66072803 | BID, ALDH6A  | 439        | 790      | 17854     | 0.97813212   | 1          | 0.97446027 | 99.9999683 |

|                        |   |       |            |            |               |            |          |           |              |            |            |            |
|------------------------|---|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| SP_PIR_KEYWORDS        | transit peptide                                     | 10    | 2.11864407 | 0.79303954 | ISCA1, ALDH   | 439        | 457      | 17854     | 0.88992787   | 1          | 0.99318221 | 100        |
| UP_SEQ_FEATURE         | transit peptide:Mitochondrion                       | 10    | 2.11864407 | 0.84440525 | ISCA1, ALDH   | 425        | 449      | 16021     | 0.83956505   | 1          | 1          | 100        |
| GOTERM_CC_FAT          | GO:0005739~mitochondrion                            | 30    | 6.3559322  | 0.87496527 | BID, ACADSF   | 330        | 1322     | 12504     | 0.85985422   | 1          | 0.9980894  | 100        |
| GOTERM_CC_FAT          | GO:0044429~mitochondrial part                       | 11    | 2.33050847 | 0.88850535 | BID, ACADSF   | 330        | 524      | 12504     | 0.79541985   | 1          | 0.9984405  | 100        |
| Annotation Cluster 135 |   |       |            |            |               |            |          |           |              |            |            |            |
| Category               | Enrichment Score: 0.0883517723369116                |       |            |            |               |            |          |           |              |            |            |            |
|                        | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT          | GO:0030324~lung development                         | 3     | 0.63559322 | 0.77018093 | WNT2, PTGE    | 341        | 111      | 13588     | 1.07695966   | 1          | 0.99882104 | 100        |
| GOTERM_BP_FAT          | GO:0030323~respiratory tube development             | 3     | 0.63559322 | 0.77868723 | WNT2, PTGE    | 341        | 113      | 13588     | 1.05789842   | 1          | 0.99899186 | 100        |
| GOTERM_BP_FAT          | GO:0060541~respiratory system development           | 3     | 0.63559322 | 0.82070556 | WNT2, PTGE    | 341        | 124      | 13588     | 0.9640526    | 1          | 0.99957028 | 100        |
| GOTERM_BP_FAT          | GO:0035295~tube development                         | 5     | 1.05932203 | 0.90042952 | WNT2, PTGE    | 341        | 264      | 13588     | 0.75468764   | 1          | 0.99995691 | 100        |
| Annotation Cluster 136 |   |       |            |            |               |            |          |           |              |            |            |            |
| Category               | Enrichment Score: 0.08083006877527528               |       |            |            |               |            |          |           |              |            |            |            |
|                        | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT          | GO:0005635~nuclear envelope                         | 5     | 1.05932203 | 0.57539709 | NPC1, RAC2,   | 330        | 153      | 12504     | 1.238265     | 1          | 0.95255405 | 99.9987483 |
| GOTERM_CC_FAT          | GO:0031090~organelle membrane                       | 20    | 4.23728814 | 0.73030286 | BID, SELP, CI | 330        | 809      | 12504     | 0.93673446   | 1          | 0.98608213 | 99.9999968 |
| GOTERM_CC_FAT          | GO:0031975~envelope                                 | 13    | 2.75423729 | 0.77055542 | BID, LMNB1,   | 330        | 542      | 12504     | 0.90882254   | 1          | 0.99081478 | 99.9999996 |
| GOTERM_CC_FAT          | GO:0031967~organelle envelope                       | 12    | 2.54237288 | 0.84693499 | BID, NPC1, L  | 330        | 540      | 12504     | 0.8420202    | 1          | 0.99670087 | 100        |
| GOTERM_CC_FAT          | GO:0044429~mitochondrial part                       | 11    | 2.33050847 | 0.88850535 | BID, ACADSF   | 330        | 524      | 12504     | 0.79541985   | 1          | 0.9984405  | 100        |
| GOTERM_CC_FAT          | GO:0019866~organelle inner membrane                 | 6     | 1.27118644 | 0.91727114 | UGT1A7C, LI   | 330        | 312      | 12504     | 0.72867133   | 1          | 0.99924439 | 100        |
| GOTERM_CC_FAT          | GO:0031966~mitochondrial membrane                   | 7     | 1.48305085 | 0.92565625 | BID, UGT1A7   | 330        | 368      | 12504     | 0.72075099   | 1          | 0.99935203 | 100        |
| GOTERM_CC_FAT          | GO:0005740~mitochondrial envelope                   | 7     | 1.48305085 | 0.94797041 | BID, UGT1A7   | 330        | 391      | 12504     | 0.67835387   | 1          | 0.99967088 | 100        |
| GOTERM_CC_FAT          | GO:0005743~mitochondrial inner membrane             | 5     | 1.05932203 | 0.95499802 | UGT1A7C, IC   | 330        | 296      | 12504     | 0.64004914   | 1          | 0.99975889 | 100        |
| Annotation Cluster 137 |   |       |            |            |               |            |          |           |              |            |            |            |
| Category               | Enrichment Score: 0.07934832063552757               |       |            |            |               |            |          |           |              |            |            |            |
|                        | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT          | GO:0005789~endoplasmic reticulum membrane           | 4     | 0.84745763 | 0.76747947 | CLN3, 11100   | 330        | 152      | 12504     | 0.99712919   | 1          | 0.99092661 | 99.9999996 |
| GOTERM_CC_FAT          | GO:0042175~nuclear envelope-endoplasmic reticulum   | 4     | 0.84745763 | 0.79678187 | CLN3, 11100   | 330        | 160      | 12504     | 0.94727273   | 1          | 0.9929976  | 99.9999999 |
| GOTERM_CC_FAT          | GO:0044432~endoplasmic reticulum part               | 4     | 0.84745763 | 0.94525466 | CLN3, 11100   | 330        | 231      | 12504     | 0.65611964   | 1          | 0.99967778 | 100        |
| Annotation Cluster 138 |   |       |            |            |               |            |          |           |              |            |            |            |
| Category               | Enrichment Score: 0.058688301180663364              |       |            |            |               |            |          |           |              |            |            |            |
|                        | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT          | GO:0007601~visual perception                        | 3     | 0.63559322 | 0.72328423 | RDH12, UNC    | 341        | 101      | 13588     | 1.18358933   | 1          | 0.99774526 | 100        |
| GOTERM_BP_FAT          | GO:0050953~sensory perception of light stimulus     | 3     | 0.63559322 | 0.72831384 | RDH12, UNC    | 341        | 102      | 13588     | 1.17198551   | 1          | 0.99786958 | 100        |
| SP_PIR_KEYWORDS        | sensory perception                                  | 3     | 0.63559322 | 0.96589727 | RDH12, UNC    | 439        | 209      | 17854     | 0.58377565   | 1          | 0.99992586 | 100        |
| GOTERM_BP_FAT          | GO:0050890~cognition                                | 7     | 1.48305085 | 1          | RDH12, CLN3   | 341        | 1480     | 13588     | 0.18846794   | 1          | 1          | 100        |
| GOTERM_BP_FAT          | GO:0007600~sensory perception                       | 5     | 1.05932203 | 1          | RDH12, UNC    | 341        | 1402     | 13588     | 0.14210951   | 1          | 1          | 100        |
| Annotation Cluster 139 |   |       |            |            |               |            |          |           |              |            |            |            |
| Category               | Enrichment Score: 0.04215939478459952               |       |            |            |               |            |          |           |              |            |            |            |
|                        | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| INTERPRO               | IPR001314:Peptidase S1A, chymotrypsin               | 3     | 0.63559322 | 0.85900913 | PRTN3, PRSS   | 425        | 143      | 17763     | 0.87682435   | 1          | 0.99999997 | 100        |
| INTERPRO               | IPR018114:Peptidase S1/S6, chymotrypsin/Hap, active | 3     | 0.63559322 | 0.87887539 | PRTN3, PRSS   | 425        | 151      | 17763     | 0.83037008   | 1          | 0.99999999 | 100        |
| INTERPRO               | IPR001254:Peptidase S1 and S6, chymotrypsin/Hap     | 3     | 0.63559322 | 0.89613235 | PRTN3, PRSS   | 425        | 159      | 17763     | 0.78859046   | 1          | 0.99999999 | 100        |
| GOTERM_MF_FAT          | GO:0008236~serine-type peptidase activity           | 4     | 0.84745763 | 0.90938376 | PRTN3, LTF,   | 339        | 212      | 13288     | 0.73957812   | 1          | 0.9999965  | 100        |
| GOTERM_MF_FAT          | GO:0017171~serine hydrolase activity                | 4     | 0.84745763 | 0.91102118 | PRTN3, LTF,   | 339        | 213      | 13288     | 0.73610592   | 1          | 0.99999639 | 100        |
| SP_PIR_KEYWORDS        | Serine protease                                     | 3     | 0.63559322 | 0.9137765  | PRTN3, LTF,   | 439        | 164      | 17854     | 0.743958     | 1          | 0.99922598 | 100        |
| SMART                  | SM00020:Tryp_SPc                                    | 3     | 0.63559322 | 0.93990073 | PRTN3, PRSS   | 256        | 159      | 9131      | 0.67298054   | 1          | 0.99999922 | 100        |
| GOTERM_MF_FAT          | GO:0004252~serine-type endopeptidase activity       | 3     | 0.63559322 | 0.9554984  | PRTN3, PRSS   | 339        | 189      | 13288     | 0.62218476   | 1          | 0.99999986 | 100        |
| Annotation Cluster 140 |   |       |            |            |               |            |          |           |              |            |            |            |
| Category               | Enrichment Score: 0.035533174892259246              |       |            |            |               |            |          |           |              |            |            |            |
|                        | Term  | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT          | GO:0005730~nucleolus                                | 8     | 1.69491525 | 0.71191865 | BCAS2, CDC,   | 330        | 310      | 12504     | 0.97782991   | 1          | 0.9843689  | 99.9999925 |
| GOTERM_CC_FAT          | GO:0031981~nuclear lumen                            | 16    | 3.38983051 | 0.97732344 | BCAS2, POLF   | 330        | 883      | 12504     | 0.68658499   | 1          | 0.99994385 | 100        |
| GOTERM_CC_FAT          | GO:0070013~intracellular organelle lumen            | 21    | 4.44915254 | 0.98211995 | BCAS2, POLF   | 330        | 1133     | 12504     | 0.70230282   | 1          | 0.99996652 | 100        |
| GOTERM_CC_FAT          | GO:0043233~organelle lumen                          | 21    | 4.44915254 | 0.98274674 | BCAS2, POLF   | 330        | 1136     | 12504     | 0.70044814   | 1          | 0.99996636 | 100        |
| GOTERM_CC_FAT          | GO:0031974~membrane-enclosed lumen                  | 21    | 4.44915254 | 0.98914349 | BCAS2, POLF   | 330        | 1174     | 12504     | 0.67777606   | 1          | 0.9999872  | 100        |

|                        |  |  |            |            |              |            |          |           |              |            |            |            |  |
|------------------------|--|--|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|--|
| Annotation Cluster 141 |  | Enrichment Score: 0.03193274302375379  |            |            |              |            |          |           |              |            |            |            |  |
| Category               | Term   | Count                                  | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |  |
| KEGG_PATHWAY           | mmu04080:Neuroactive ligand-receptor interaction       | 9                                      | 1.90677966 | 0.55534206 | F2RL2, P2RY: | 178        | 260      | 5738      | 1.11585998   | 1          | 0.86608357 | 99.9919327 |  |
| GOTERM_BP_FAT          | GO:0007166--cell surface receptor linked signal transd | 38                                     | 8.05084746 | 0.99995263 | F2RL2, ITGA1 | 341        | 2495     | 13588     | 0.6068959    | 1          | 1          | 100        |  |
| SP_PIR_KEYWORDS        | transducer   | 15                                     | 3.1779661  | 0.99999586 | F2RL2, GPR9  | 439        | 1467     | 17854     | 0.41584564   | 1          | 1          | 100        |  |
| SP_PIR_KEYWORDS        | g-protein coupled receptor                             | 12                                     | 2.54237288 | 0.99999967 | F2RL2, P2RY: | 439        | 1411     | 17854     | 0.34587983   | 1          | 1          | 100        |  |
| INTERPRO               | IPR000276:7TM GPCR, rhodopsin-like                     | 9                                      | 1.90677966 | 1          | F2RL2, P2RY: | 425        | 1458     | 17763     | 0.25799564   | 1          | 1          | 100        |  |
| GOTERM_BP_FAT          | GO:0007186--G-protein coupled receptor protein sign    | 16                                     | 3.38983051 | 1          | F2RL2, GPR9  | 341        | 1877     | 13588     | 0.33966975   | 1          | 1          | 100        |  |
| INTERPRO               | IPR017452:GPCR, rhodopsin-like superfamily             | 9                                      | 1.90677966 | 1          | F2RL2, P2RY: | 425        | 1575     | 17763     | 0.23883025   | 1          | 1          | 100        |  |
| PIR_SUPERFAMILY        | PIRSF000006:rhodopsin-like G protein-coupled recept    | 8                                      | 1.69491525 | 1          | F2RL2, P2RY: | 239        | 1200     | 8136      | 0.22694561   | 1          | 1          | 100        |  |
| Annotation Cluster 142 |  | Enrichment Score: 0.02635705189680636  |            |            |              |            |          |           |              |            |            |            |  |
| Category               | Term   | Count                                  | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |  |
| GOTERM_MF_FAT          | GO:0005198--structural molecule activity               | 9                                      | 1.90677966 | 0.89058245 | ISCA1, RPL18 | 339        | 450      | 13288     | 0.7839528    | 1          | 0.99999347 | 100        |  |
| GOTERM_MF_FAT          | GO:0003735--structural constituent of ribosome         | 3                                      | 0.63559322 | 0.90035247 | RPL18A, LOC  | 339        | 151      | 13288     | 0.77876106   | 1          | 0.99999552 | 100        |  |
| GOTERM_BP_FAT          | GO:0006412--translation                                | 5                                      | 1.05932203 | 0.96055145 | RPL18A, F13, | 341        | 319      | 13588     | 0.62456908   | 1          | 0.99999902 | 100        |  |
| GOTERM_CC_FAT          | GO:0005840--ribosome                                   | 3                                      | 0.63559322 | 0.96397616 | RPL18A, LOC  | 330        | 192      | 12504     | 0.59204545   | 1          | 0.99982885 | 100        |  |
| GOTERM_CC_FAT          | GO:0030529--ribonucleoprotein complex                  | 6                                      | 1.27118644 | 0.99435423 | BCAS2, MOV   | 330        | 462      | 12504     | 0.49208973   | 1          | 0.99999646 | 100        |  |
| Annotation Cluster 143 |  | Enrichment Score: 0.026023367416938413 |            |            |              |            |          |           |              |            |            |            |  |
| Category               | Term   | Count                                  | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |  |
| INTERPRO               | IPR011333:BTB/POZ fold                                 | 3                                      | 0.63559322 | 0.93115141 | SHKBP1, ABT  | 425        | 180      | 17763     | 0.69658824   | 1          | 1          | 100        |  |
| INTERPRO               | IPR000210:BTB/POZ-like                                 | 3                                      | 0.63559322 | 0.93115141 | SHKBP1, ABT  | 425        | 180      | 17763     | 0.69658824   | 1          | 1          | 100        |  |
| SMART                  | SM00225:BTB  | 3                                      | 0.63559322 | 0.96358334 | SHKBP1, ABT  | 256        | 180      | 9131      | 0.59446615   | 1          | 0.99999985 | 100        |  |
| Annotation Cluster 144 |  | Enrichment Score: 0.024634359349020526 |            |            |              |            |          |           |              |            |            |            |  |
| Category               | Term   | Count                                  | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |  |
| INTERPRO               | IPR015943:WD40/YVTN repeat-like                        | 6                                      | 1.27118644 | 0.85652566 | SHKBP1, ARF  | 425        | 305      | 17763     | 0.82220251   | 1          | 0.99999997 | 100        |  |
| UP_SEQ_FEATURE         | repeat:WD 5  | 4                                      | 0.84745763 | 0.90607166 | SHKBP1, ARF  | 425        | 202      | 16021     | 0.74646476   | 1          | 1          | 100        |  |
| UP_SEQ_FEATURE         | repeat:WD 4  | 4                                      | 0.84745763 | 0.93082165 | SHKBP1, ARF  | 425        | 218      | 16021     | 0.69167836   | 1          | 1          | 100        |  |
| UP_SEQ_FEATURE         | repeat:WD 3  | 4                                      | 0.84745763 | 0.94635685 | SHKBP1, ARF  | 425        | 231      | 16021     | 0.65275274   | 1          | 1          | 100        |  |
| INTERPRO               | IPR019775:WD40 repeat, conserved site                  | 4                                      | 0.84745763 | 0.94791488 | SHKBP1, ARF  | 425        | 258      | 17763     | 0.64798906   | 1          | 1          | 100        |  |
| INTERPRO               | IPR001680:WD40 repeat                                  | 4                                      | 0.84745763 | 0.94883586 | SHKBP1, ARF  | 425        | 259      | 17763     | 0.64548717   | 1          | 1          | 100        |  |
| UP_SEQ_FEATURE         | repeat:WD 2  | 4                                      | 0.84745763 | 0.95044311 | SHKBP1, ARF  | 425        | 235      | 16021     | 0.64164205   | 1          | 1          | 100        |  |
| UP_SEQ_FEATURE         | repeat:WD 1  | 4                                      | 0.84745763 | 0.95044311 | SHKBP1, ARF  | 425        | 235      | 16021     | 0.64164205   | 1          | 1          | 100        |  |
| SP_PIR_KEYWORDS        | wd repeat  | 4                                      | 0.84745763 | 0.95825347 | SHKBP1, ARF  | 439        | 263      | 17854     | 0.61855063   | 1          | 0.99987745 | 100        |  |
| INTERPRO               | IPR019782:WD40 repeat 2                                | 3                                      | 0.63559322 | 0.965316   | ARPC1B, CO   | 425        | 214      | 17763     | 0.58591534   | 1          | 1          | 100        |  |
| INTERPRO               | IPR017986:WD40 repeat, region                          | 3                                      | 0.63559322 | 0.97400222 | ARPC1B, CO   | 425        | 228      | 17763     | 0.54993808   | 1          | 1          | 100        |  |
| INTERPRO               | IPR019781:WD40 repeat, subgroup                        | 3                                      | 0.63559322 | 0.97751746 | ARPC1B, CO   | 425        | 235      | 17763     | 0.53355695   | 1          | 1          | 100        |  |
| SMART                  | SM00320:WD40   | 4                                      | 0.84745763 | 0.97787184 | SHKBP1, ARF  | 256        | 259      | 9131      | 0.55085666   | 1          | 0.99999996 | 100        |  |
| Annotation Cluster 145 |  | Enrichment Score: 0.013712591923804413 |            |            |              |            |          |           |              |            |            |            |  |
| Category               | Term   | Count                                  | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |  |
| SP_PIR_KEYWORDS        | activator  | 11                                     | 2.33050847 | 0.75316481 | AKNA, NFE2,  | 439        | 484      | 17854     | 0.92431145   | 1          | 0.98852409 | 99.9999996 |  |
| SP_PIR_KEYWORDS        | dna-binding  | 28                                     | 5.93220339 | 0.92741196 | AKNA, KIF22  | 439        | 1404     | 17854     | 0.81107672   | 1          | 0.99947438 | 100        |  |
| GOTERM_MF_FAT          | GO:0043565--sequence-specific DNA binding              | 8                                      | 1.69491525 | 0.98906171 | FOSL2, NFE2  | 339        | 556      | 13288     | 0.56399482   | 1          | 1          | 100        |  |
| GOTERM_MF_FAT          | GO:0003700--transcription factor activity              | 11                                     | 2.33050847 | 0.99558278 | FOSL2, NFE2  | 339        | 776      | 13288     | 0.55563665   | 1          | 1          | 100        |  |
| GOTERM_MF_FAT          | GO:0003677--DNA binding                                | 30                                     | 6.3559322  | 0.99790783 | AKNA, KIF22  | 339        | 1781     | 13288     | 0.66026345   | 1          | 1          | 100        |  |
| SP_PIR_KEYWORDS        | transcription regulation                               | 23                                     | 4.87288136 | 0.99875904 | AKNA, SBNC   | 439        | 1546     | 17854     | 0.60504734   | 1          | 0.99999997 | 100        |  |
| GOTERM_BP_FAT          | GO:0051252--regulation of RNA metabolic process        | 21                                     | 4.44915254 | 0.99961962 | HMGB2, SBN   | 341        | 1488     | 13588     | 0.56236401   | 1          | 1          | 100        |  |
| SP_PIR_KEYWORDS        | Transcription  | 25                                     | 5.29661017 | 0.99974015 | AKNA, POLR   | 439        | 1769     | 17854     | 0.57475557   | 1          | 1          | 100        |  |
| GOTERM_BP_FAT          | GO:0006355--regulation of transcription, DNA-depend    | 20                                     | 4.23728814 | 0.99975571 | HMGB2, SBN   | 341        | 1465     | 13588     | 0.54399327   | 1          | 1          | 100        |  |
| GOTERM_BP_FAT          | GO:0045449--regulation of transcription                | 35                                     | 7.41525424 | 0.99976031 | AKNA, HMG    | 341        | 2227     | 13588     | 0.6262518    | 1          | 1          | 100        |  |
| GOTERM_BP_FAT          | GO:0006350--transcription                              | 25                                     | 5.29661017 | 0.99987433 | AKNA, POLR   | 341        | 1772     | 13588     | 0.56218267   | 1          | 1          | 100        |  |
| GOTERM_MF_FAT          | GO:0030528--transcription regulator activity           | 14                                     | 2.96610169 | 0.9999474  | SBN02, NFE,  | 339        | 1206     | 13288     | 0.45503065   | 1          | 1          | 100        |  |
| Annotation Cluster 146 |  | Enrichment Score: 0.013530130050849017 |            |            |              |            |          |           |              |            |            |            |  |

| Category               | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR |
|------------------------|--|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|-----|
| SP_PIR_KEYWORDS        | metal-binding  | 60    | 12.7118644 | 0.83838244 | SEPX1, APOE  | 439        | 2682     | 17854     | 0.90983678   | 1          | 0.99624681 | 100 |
| GOTERM_MF_FAT          | GO:0043169~cation binding                            | 82    | 17.3728814 | 0.98791988 | MOCOS, SEF   | 339        | 3885     | 13288     | 0.82733758   | 1          | 1          | 100 |
| GOTERM_MF_FAT          | GO:0043167~ion binding                               | 83    | 17.5847458 | 0.98858755 | MOCOS, SEF   | 339        | 3934     | 13288     | 0.82699647   | 1          | 1          | 100 |
| GOTERM_MF_FAT          | GO:0046872~metal ion binding                         | 80    | 16.9491525 | 0.99184733 | MOCOS, SEF   | 339        | 3850     | 13288     | 0.81449642   | 1          | 1          | 100 |
| GOTERM_MF_FAT          | GO:0046914~transition metal ion binding              | 50    | 10.5932203 | 0.99467647 | MOCOS, SEF   | 339        | 2608     | 13288     | 0.7514885    | 1          | 1          | 100 |
| SP_PIR_KEYWORDS        | zinc   | 32    | 6.77966102 | 0.99539161 | SEPX1, APOE  | 439        | 1886     | 17854     | 0.690048     | 1          | 0.99999925 | 100 |
| GOTERM_MF_FAT          | GO:0008270~zinc ion binding                          | 30    | 6.3559322  | 0.99997561 | SEPX1, APOE  | 339        | 2105     | 13288     | 0.5586362    | 1          | 1          | 100 |
| Annotation Cluster 147 |  |       |            |            |              |            |          |           |              |            |            |     |
| Category               | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR |
| GOTERM_BP_FAT          | GO:0006605~protein targeting                         | 3     | 0.63559322 | 0.84961897 | BID, SLC11A1 | 341        | 133      | 13588     | 0.89881595   | 1          | 0.99977687 | 100 |
| GOTERM_BP_FAT          | GO:0006886~intracellular protein transport           | 3     | 0.63559322 | 0.99297605 | BID, SLC11A1 | 341        | 276      | 13588     | 0.43312508   | 1          | 1          | 100 |
| GOTERM_BP_FAT          | GO:0034613~cellular protein localization             | 3     | 0.63559322 | 0.99583805 | BID, SLC11A1 | 341        | 299      | 13588     | 0.39980777   | 1          | 1          | 100 |
| GOTERM_BP_FAT          | GO:0070727~cellular macromolecule localization       | 3     | 0.63559322 | 0.99602431 | BID, SLC11A1 | 341        | 301      | 13588     | 0.39715124   | 1          | 1          | 100 |
| GOTERM_BP_FAT          | GO:0015031~protein transport                         | 8     | 1.69491525 | 0.99744448 | BID, RAB32,  | 341        | 651      | 13588     | 0.48967751   | 1          | 1          | 100 |
| GOTERM_BP_FAT          | GO:0045184~establishment of protein localization     | 8     | 1.69491525 | 0.99766025 | BID, RAB32,  | 341        | 656      | 13588     | 0.48594521   | 1          | 1          | 100 |
| GOTERM_BP_FAT          | GO:0008104~protein localization                      | 8     | 1.69491525 | 0.9996035  | BID, RAB32,  | 341        | 753      | 13588     | 0.42334669   | 1          | 1          | 100 |
| Annotation Cluster 148 |  |       |            |            |              |            |          |           |              |            |            |     |
| Category               | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR |
| GOTERM_MF_FAT          | GO:0046873~metal ion transmembrane transporter ac    | 6     | 1.27118644 | 0.86485446 | SHKBP1, SLC  | 339        | 290      | 13288     | 0.81098566   | 1          | 0.99998378 | 100 |
| GOTERM_MF_FAT          | GO:0005261~cation channel activity                   | 3     | 0.63559322 | 0.98799951 | SHKBP1, KCT  | 339        | 248      | 13288     | 0.474165     | 1          | 1          | 100 |
| GOTERM_MF_FAT          | GO:0005216~ion channel activity                      | 4     | 0.84745763 | 0.99406127 | SHKBP1, KCT  | 339        | 349      | 13288     | 0.44925662   | 1          | 1          | 100 |
| GOTERM_MF_FAT          | GO:0022836~gated channel activity                    | 3     | 0.63559322 | 0.99436575 | SHKBP1, KCT  | 339        | 281      | 13288     | 0.41848014   | 1          | 1          | 100 |
| GOTERM_MF_FAT          | GO:0022838~substrate specific channel activity       | 4     | 0.84745763 | 0.99530041 | SHKBP1, KCT  | 339        | 360      | 13288     | 0.43552933   | 1          | 1          | 100 |
| SP_PIR_KEYWORDS        | ionic channel  | 3     | 0.63559322 | 0.99537842 | KCTD20, RYF  | 439        | 301      | 17854     | 0.40534589   | 1          | 0.99999931 | 100 |
| GOTERM_MF_FAT          | GO:0022803~passive transmembrane transporter activ   | 4     | 0.84745763 | 0.99577709 | SHKBP1, KCT  | 339        | 365      | 13288     | 0.42956318   | 1          | 1          | 100 |
| GOTERM_MF_FAT          | GO:0015267~channel activity                          | 4     | 0.84745763 | 0.99577709 | SHKBP1, KCT  | 339        | 365      | 13288     | 0.42956318   | 1          | 1          | 100 |
| Annotation Cluster 149 |  |       |            |            |              |            |          |           |              |            |            |     |
| Category               | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR |
| GOTERM_BP_FAT          | GO:0032504~multicellular organism reproduction       | 6     | 1.27118644 | 0.97762762 | WNT2, PROK2  | 341        | 409      | 13588     | 0.58456001   | 1          | 0.99999999 | 100 |
| GOTERM_BP_FAT          | GO:0048609~reproductive process in a multicellular o | 6     | 1.27118644 | 0.97762762 | WNT2, PROK2  | 341        | 409      | 13588     | 0.58456001   | 1          | 0.99999999 | 100 |
| GOTERM_BP_FAT          | GO:0019953~sexual reproduction                       | 5     | 1.05932203 | 0.98839551 | PROK2, OVG   | 341        | 386      | 13588     | 0.51615942   | 1          | 0.99999999 | 100 |
| GOTERM_BP_FAT          | GO:0007283~spermatogenesis                           | 3     | 0.63559322 | 0.98873607 | PROK2, HMC   | 341        | 255      | 13588     | 0.4687942    | 1          | 0.99999999 | 100 |
| GOTERM_BP_FAT          | GO:0048232~male gamete generation                    | 3     | 0.63559322 | 0.98873607 | PROK2, HMC   | 341        | 255      | 13588     | 0.4687942    | 1          | 0.99999999 | 100 |
| GOTERM_BP_FAT          | GO:0007276~gamete generation                         | 3     | 0.63559322 | 0.9980092  | PROK2, HMC   | 341        | 331      | 13588     | 0.36115566   | 1          | 1          | 100 |
| Annotation Cluster 150 |  |       |            |            |              |            |          |           |              |            |            |     |
| Category               | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR |
| GOTERM_BP_FAT          | GO:0010605~negative regulation of macromolecule r    | 9     | 1.90677966 | 0.94139083 | SAP30, CLNE  | 341        | 506      | 13588     | 0.70875013   | 1          | 0.99999522 | 100 |
| GOTERM_BP_FAT          | GO:0010558~negative regulation of macromolecule b    | 6     | 1.27118644 | 0.98083628 | SAP30, SBNC  | 341        | 418      | 13588     | 0.57197379   | 1          | 0.99999994 | 100 |
| GOTERM_BP_FAT          | GO:0031327~negative regulation of cellular biosynthe | 6     | 1.27118644 | 0.9844489  | SAP30, SBNC  | 341        | 430      | 13588     | 0.55601173   | 1          | 0.99999998 | 100 |
| GOTERM_BP_FAT          | GO:0009890~negative regulation of biosynthetic proc  | 6     | 1.27118644 | 0.98550373 | SAP30, SBNC  | 341        | 434      | 13588     | 0.5508872    | 1          | 0.99999998 | 100 |
| SP_PIR_KEYWORDS        | repressor  | 5     | 1.05932203 | 0.98758789 | SAP30, SBNC  | 439        | 391      | 17854     | 0.52007294   | 1          | 0.99999436 | 100 |
| GOTERM_BP_FAT          | GO:0010629~negative regulation of gene expression    | 5     | 1.05932203 | 0.99266624 | SAP30, SBNC  | 341        | 410      | 13588     | 0.48594521   | 1          | 1          | 100 |
| GOTERM_BP_FAT          | GO:0016481~negative regulation of transcription      | 4     | 0.84745763 | 0.99585378 | SAP30, SBNC  | 341        | 372      | 13588     | 0.42846782   | 1          | 1          | 100 |
| GOTERM_BP_FAT          | GO:0045892~negative regulation of transcription, DN  | 3     | 0.63559322 | 0.9966141  | SAP30, SBNC  | 341        | 308      | 13588     | 0.38812507   | 1          | 1          | 100 |
| GOTERM_BP_FAT          | GO:0051253~negative regulation of RNA metabolic pi   | 3     | 0.63559322 | 0.99676624 | SAP30, SBNC  | 341        | 310      | 13588     | 0.38562104   | 1          | 1          | 100 |
| GOTERM_BP_FAT          | GO:0045934~negative regulation of nucleobase, nucle  | 4     | 0.84745763 | 0.99756222 | SAP30, SBNC  | 341        | 397      | 13588     | 0.40148622   | 1          | 1          | 100 |
| GOTERM_BP_FAT          | GO:0051172~negative regulation of nitrogen compou    | 4     | 0.84745763 | 0.99776246 | SAP30, SBNC  | 341        | 401      | 13588     | 0.39748137   | 1          | 1          | 100 |
| Annotation Cluster 151 |  |       |            |            |              |            |          |           |              |            |            |     |
| Category               | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR |
| GOTERM_BP_FAT          | GO:0016071~mRNA metabolic process                    | 4     | 0.84745763 | 0.98251795 | BCAS2, SLC1  | 341        | 302      | 13588     | 0.52778155   | 1          | 0.99999996 | 100 |
| GOTERM_BP_FAT          | GO:0006397~mRNA processing                           | 3     | 0.63559322 | 0.99037073 | BCAS2, MOV   | 341        | 262      | 13588     | 0.45626917   | 1          | 1          | 100 |

|                        |   |       |            |            |             |            |          |           |              |            |            |     |
|------------------------|---|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|-----|
| GOTERM_BP_FAT          | GO:0006396~RNA processing                             | 3     | 0.63559322 | 0.99983741 | BCAS2, MOV  | 341        | 437      | 13588     | 0.27355268   | 1          | 1          | 100 |
| Annotation Cluster 152 | Enrichment Score: 0.0027746641498543876               |       |            |            |             |            |          |           |              |            |            |     |
| Category               | Term  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR |
| GOTERM_CC_FAT          | GO:0005667~transcription factor complex               | 3     | 0.63559322 | 0.98631235 | NKX2-1, SFP | 330        | 234      | 12504     | 0.48578089   | 1          | 0.99997934 | 100 |
| GOTERM_MF_FAT          | GO:0016563~transcription activator activity           | 3     | 0.63559322 | 0.99065816 | NKX2-1, SFP | 339        | 259      | 13288     | 0.45402672   | 1          | 1          | 100 |
| GOTERM_CC_FAT          | GO:0044451~nucleoplasm part                           | 6     | 1.27118644 | 0.99795372 | SAP30, POLF | 330        | 513      | 12504     | 0.44316853   | 1          | 0.99999966 | 100 |
| GOTERM_CC_FAT          | GO:0005654~nucleoplasm                                | 6     | 1.27118644 | 0.99966077 | SAP30, POLF | 330        | 599      | 12504     | 0.37954166   | 1          | 0.99999999 | 100 |
| Annotation Cluster 153 | Enrichment Score: 4.2260219991200113E-4               |       |            |            |             |            |          |           |              |            |            |     |
| Category               | Term  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR |
| GOTERM_BP_FAT          | GO:0009057~macromolecule catabolic process            | 9     | 1.90677966 | 0.99354527 | CLN3, OVGP  | 341        | 654      | 13588     | 0.54836019   | 1          | 1          | 100 |
| SP_PIR_KEYWORDS        | ubl conjugation pathway                               | 4     | 0.84745763 | 0.99953461 | UHRF1, SOC  | 439        | 484      | 17854     | 0.33611326   | 1          | 1          | 100 |
| GOTERM_BP_FAT          | GO:0019941~modification-dependent protein cataboli    | 4     | 0.84745763 | 0.99978806 | UHRF1, SOC  | 341        | 508      | 13588     | 0.3137599    | 1          | 1          | 100 |
| GOTERM_BP_FAT          | GO:0043632~modification-dependent macromolecule       | 4     | 0.84745763 | 0.99978806 | UHRF1, SOC  | 341        | 508      | 13588     | 0.3137599    | 1          | 1          | 100 |
| GOTERM_BP_FAT          | GO:0044265~cellular macromolecule catabolic proces    | 5     | 1.05932203 | 0.9998791  | UHRF1, SOC  | 341        | 609      | 13588     | 0.32715523   | 1          | 1          | 100 |
| GOTERM_BP_FAT          | GO:0051603~proteolysis involved in cellular protein c | 4     | 0.84745763 | 0.99988238 | UHRF1, SOC  | 341        | 534      | 13588     | 0.2984832    | 1          | 1          | 100 |
| GOTERM_BP_FAT          | GO:0044257~cellular protein catabolic process         | 4     | 0.84745763 | 0.99989015 | UHRF1, SOC  | 341        | 537      | 13588     | 0.2968157    | 1          | 1          | 100 |
| GOTERM_BP_FAT          | GO:0030163~protein catabolic process                  | 4     | 0.84745763 | 0.99992884 | UHRF1, SOC  | 341        | 556      | 13588     | 0.28667271   | 1          | 1          | 100 |

# Unique Lung Annotation

104 david id matched

| UNIQUE TH/SH | Annotation Category | Cluster 1                               | Enrichment Score: 3.31493721559225 | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|--------------|---------------------|---|------------------------------------|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| lung         | GOTERM_MF_FAT       | GO:0008092~cytoskeletal protein binding |                                    | 12    | 11.5384615 | 4.50E-05   | TNS4, KIF1B, | 83         | 414      | 13288     | 4.64047494   | 0.00922972 | 0.00922972 | 0.05667544 |
|              | SP_PIR_KEYWORDS     | actin-binding                           |                                    | 8     | 7.69230769 | 2.80E-04   | TNS4, TWf2,  | 101        | 226      | 17854     | 6.25742574   | 0.05502661 | 0.01404999 | 0.35114418 |
|              | GOTERM_MF_FAT       | GO:0003779~actin binding                |                                    | 9     | 8.65384615 | 3.93E-04   | TNS4, TWf2,  | 83         | 288      | 13288     | 5.00301205   | 0.0777155  | 0.03964356 | 0.49340184 |
|              | GOTERM_CC_FAT       | GO:0015629~actin cytoskeleton           |                                    | 6     | 5.76923077 | 0.01110531 | MYL7, CGN,   | 83         | 205      | 12504     | 4.40928592   | 0.86300399 | 0.32804284 | 12.8289579 |

| Annotation Category | Cluster 2                                | Enrichment Score: 2.6093134365398596 | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------------|--|--------------------------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| SP_PIR_KEYWORDS     | cell cycle                               |                                      | 12    | 11.5384615 | 4.09E-05   | CCNB1, KIF2 | 101        | 447      | 17854     | 4.74556449   | 0.00823646 | 0.00823646 | 0.05138873 |
| SP_PIR_KEYWORDS     | cell division                            |                                      | 9     | 8.65384615 | 9.56E-05   | CCNB1, KIF2 | 101        | 256      | 17854     | 6.21465037   | 0.01912873 | 0.00961055 | 0.11996564 |
| SP_PIR_KEYWORDS     | mitosis                                  |                                      | 7     | 6.73076923 | 5.11E-04   | CCNB1, KIF2 | 101        | 179      | 17854     | 6.91288235   | 0.09804072 | 0.02042569 | 0.63925274 |
| GOTERM_BP_FAT       | GO:0007049~cell cycle                    |                                      | 12    | 11.5384615 | 0.00106578 | CCNB1, UHR  | 83         | 611      | 13588     | 3.21527025   | 0.57070653 | 0.57070653 | 1.62166618 |
| KEGG_PATHWAY        | mmu04110:Cell cycle                      |                                      | 6     | 5.76923077 | 0.00125569 | CCNB1, BUB  | 38         | 128      | 5738      | 7.078125     | 0.07610596 | 0.07610596 | 1.26419008 |
| GOTERM_BP_FAT       | GO:0051301~cell division                 |                                      | 8     | 7.69230769 | 0.00152043 | CCNB1, PRC  | 83         | 281      | 13588     | 4.66080693   | 0.70079347 | 0.45300225 | 2.30594699 |
| GOTERM_BP_FAT       | GO:0000278~mitotic cell cycle            |                                      | 7     | 6.73076923 | 0.00354007 | CCNB1, SPA  | 83         | 244      | 13588     | 4.69662256   | 0.9399309  | 0.50493437 | 5.29220021 |
| GOTERM_BP_FAT       | GO:0007067~mitosis                       |                                      | 6     | 5.76923077 | 0.0058032  | CCNB1, SPA  | 83         | 190      | 13588     | 5.16981611   | 0.99010123 | 0.48280485 | 8.53700302 |
| GOTERM_BP_FAT       | GO:0000280~nuclear division              |                                      | 6     | 5.76923077 | 0.0058032  | CCNB1, SPA  | 83         | 190      | 13588     | 5.16981611   | 0.99010123 | 0.48280485 | 8.53700302 |
| GOTERM_BP_FAT       | GO:0000087~M phase of mitotic cell cycle |                                      | 6     | 5.76923077 | 0.00632846 | CCNB1, SPA  | 83         | 194      | 13588     | 5.06322196   | 0.99349001 | 0.46703638 | 9.27509438 |
| GOTERM_BP_FAT       | GO:0048285~organelle fission             |                                      | 6     | 5.76923077 | 0.00674376 | CCNB1, SPA  | 83         | 197      | 13588     | 4.98611706   | 0.99532683 | 0.44910617 | 9.85473085 |
| SP_PIR_KEYWORDS     | ubl conjugation                          |                                      | 9     | 8.65384615 | 0.00918903 | CCNB1, UHR  | 101        | 524      | 17854     | 3.03616507   | 0.84506744 | 0.14392485 | 10.9432119 |
| GOTERM_BP_FAT       | GO:0022402~cell cycle process            |                                      | 8     | 7.69230769 | 0.00949895 | CCNB1, SPA  | 83         | 393      | 13588     | 3.33253625   | 0.99948362 | 0.49745052 | 13.6133483 |
| GOTERM_BP_FAT       | GO:0022403~cell cycle phase              |                                      | 7     | 6.73076923 | 0.01425994 | CCNB1, SPA  | 83         | 328      | 13588     | 3.49382897   | 0.99998869 | 0.55671317 | 19.7651112 |
| GOTERM_BP_FAT       | GO:0000279~M phase                       |                                      | 6     | 5.76923077 | 0.02814079 | CCNB1, SPA  | 83         | 283      | 13588     | 3.47090127   | 1          | 0.75700845 | 35.444873  |

| Annotation Category | Cluster 3                                | Enrichment Score: 2.488501618146076 | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------------|--|-------------------------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_CC_FAT       | GO:0043232~intracellular non-membrane-bo |                                     | 27    | 25.9615385 | 1.51E-04   | MYL7, PRC1, | 83         | 1919     | 12504     | 2.11962807   | 0.02646248 | 0.02646248 | 0.18506733 |
| GOTERM_CC_FAT       | GO:0043228~non-membrane-bounded orgar    |                                     | 27    | 25.9615385 | 1.51E-04   | MYL7, PRC1, | 83         | 1919     | 12504     | 2.11962807   | 0.02646248 | 0.02646248 | 0.18506733 |
| SP_PIR_KEYWORDS     | cytoskeleton                             |                                     | 11    | 10.5769231 | 0.00158249 | CCNB1, TNS  | 101        | 583      | 17854     | 3.33532599   | 0.27379013 | 0.0446737  | 1.96865664 |
| GOTERM_CC_FAT       | GO:0005856~cytoskeleton                  |                                     | 17    | 16.3461538 | 0.0022766  | MYL7, TWf2, | 83         | 1122     | 12504     | 2.28258488   | 0.33348818 | 0.18359825 | 2.76326405 |
| GOTERM_CC_FAT       | GO:0044430~cytoskeletal part             |                                     | 13    | 12.5       | 0.004405   | MYL7, PRC1, | 83         | 774      | 12504     | 2.53030728   | 0.54425527 | 0.23044343 | 5.28302187 |
| GOTERM_CC_FAT       | GO:0015630~microtubule cytoskeleton      |                                     | 8     | 7.69230769 | 0.02799928 | CCNB1, KIF1 | 83         | 450      | 12504     | 2.67823293   | 0.99362247 | 0.42974055 | 29.4711364 |
| SP_PIR_KEYWORDS     | coiled coil                              |                                     | 12    | 11.5384615 | 0.37738993 | KIF1C, BCAS | 101        | 1732     | 17854     | 1.22475019   | 1          | 0.94500118 | 99.7390783 |

| Annotation Category | Cluster 4                                  | Enrichment Score: 1.7598544880438483 | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------------|--|--------------------------------------|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_MF_FAT       | GO:0003774~motor activity                  |                                      | 6     | 5.76923077 | 0.00161566 | KIF1C, MYL7,  | 83         | 138      | 13288     | 6.96071241   | 0.28329735 | 0.10508936 | 2.0159049  |
| GOTERM_BP_FAT       | GO:0007018~microtubule-based movement      |                                      | 5     | 4.80769231 | 0.0032277  | KIF1C, KIF2C, | 83         | 101      | 13588     | 8.1044972    | 0.92298101 | 0.57453293 | 4.83596433 |
| GOTERM_CC_FAT       | GO:0044430~cytoskeletal part               |                                      | 13    | 12.5       | 0.004405   | MYL7, PRC1,   | 83         | 774      | 12504     | 2.53030728   | 0.54425527 | 0.23044343 | 5.28302187 |
| SP_PIR_KEYWORDS     | motor protein                              |                                      | 5     | 4.80769231 | 0.0050569  | KIF1C, MYL7,  | 101        | 123      | 17854     | 7.18586493   | 0.64087523 | 0.10755221 | 6.16641431 |
| SP_PIR_KEYWORDS     | microtubule                                |                                      | 6     | 5.76923077 | 0.00808178 | KIF1C, KIF2C, | 101        | 221      | 17854     | 4.79924735   | 0.80585523 | 0.15118593 | 9.68565997 |
| GOTERM_BP_FAT       | GO:0007017~microtubule-based process       |                                      | 6     | 5.76923077 | 0.00893704 | WNT2, KIF1C   | 83         | 211      | 13588     | 4.65528465   | 0.99919037 | 0.50928576 | 12.8588958 |
| UP_SEQ_FEATURE      | domain:Kinesin-motor                       |                                      | 3     | 2.88461538 | 0.01896037 | KIF1C, KIF2C, | 98         | 35       | 16021     | 14.0125364   | 0.99940518 | 0.97561117 | 23.3419765 |
| INTERPRO            | IPR019821:Kinesin, motor region, conserved |                                      | 3     | 2.88461538 | 0.0203836  | KIF1C, KIF2C, | 94         | 42       | 17763     | 13.4977204   | 0.99607286 | 0.99607286 | 23.7093486 |
| GOTERM_CC_FAT       | GO:0005874~microtubule                     |                                      | 6     | 5.76923077 | 0.02062769 | KIF1C, KIF2C, | 83         | 240      | 12504     | 3.76626506   | 0.9755256  | 0.41140577 | 22.6058731 |
| INTERPRO            | IPR001752:Kinesin, motor region            |                                      | 3     | 2.88461538 | 0.02224562 | KIF1C, KIF2C, | 94         | 44       | 17763     | 12.8841876   | 0.99764599 | 0.95148184 | 25.5930325 |
| GOTERM_CC_FAT       | GO:0015630~microtubule cytoskeleton        |                                      | 8     | 7.69230769 | 0.02799928 | CCNB1, KIF1   | 83         | 450      | 12504     | 2.67823293   | 0.99362247 | 0.42974055 | 29.4711364 |
| SMART               | SM00129:KISc                               |                                      | 3     | 2.88461538 | 0.02867611 | KIF1C, KIF2C, | 56         | 44       | 9131      | 11.117289    | 0.85763843 | 0.85763843 | 25.8003172 |
| GOTERM_MF_FAT       | GO:0003777~microtubule motor activity      |                                      | 3     | 2.88461538 | 0.07464631 | KIF1C, KIF2C, | 83         | 73       | 13288     | 6.57930352   | 0.99999989 | 0.86434842 | 62.3591626 |
| GOTERM_BP_FAT       | GO:0046907~intracellular transport         |                                      | 6     | 5.76923077 | 0.11888349 | KIF1C, NPC1,  | 83         | 431      | 13588     | 2.27903726   | 1          | 0.97893716 | 85.6373676 |
| SP_PIR_KEYWORDS     | coiled coil                                |                                      | 12    | 11.5384615 | 0.37738993 | KIF1C, BCAS   | 101        | 1732     | 17854     | 1.22475019   | 1          | 0.94500118 | 99.7390783 |

Annotation Cluster 5 Enrichment Score: 1.6572540102901863

| Category              | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm   | Bonferroni | Benjamini  | FDR        |
|-----------------------|---|-------|------------|------------|--------------|------------|----------|-----------|--|------------|------------|------------|
| GOTERM_MF_FAT         | GO:0003774~motor activity                         | 6     | 5.76923077 | 0.00161566 | KIF1C, MYL7, | 83         | 138      | 13288     | 6.96071241   | 0.28329735 | 0.10508936 | 2.0159049  |
| GOTERM_CC_FAT         | GO:0015629~actin cytoskeleton                     | 6     | 5.76923077 | 0.01110531 | MYL7, CGN,   | 83         | 205      | 12504     | 4.40928592   | 0.86300399 | 0.32804284 | 12.8289579 |
| GOTERM_CC_FAT         | GO:0016459~myosin complex                         | 3     | 2.88461538 | 0.06063093 | MYL7, CGN,   | 83         | 61       | 12504     | 7.40904602   | 0.99998538 | 0.41148854 | 53.6515283 |
| KEGG_PATHWAY          | mmu04530:Tight junction                           | 3     | 2.88461538 | 0.21597832 | MYL7, CGN,   | 38         | 135      | 5738      | 3.35555556   | 0.99999978 | 0.95338414 | 91.4883455 |
| Annotation Cluster 6  |   |       |            |            |              |            |          |           |  |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm <td>Bonferroni</td> <td>Benjamini</td> <td>FDR</td> | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS       | ubl conjugation                                   | 9     | 8.65384615 | 0.00918903 | CCNB1, UHR   | 101        | 524      | 17854     | 3.03616507   | 0.84506744 | 0.14392485 | 10.9432119 |
| UP_SEQ_FEATURE        | cross-link:Glycyl lysine isopeptide (Lys-Gly) (ir | 5     | 4.80769231 | 0.01902466 | UHRF1, HIST  | 98         | 168      | 16021     | 4.86546404   | 0.99942012 | 0.91661023 | 23.4117104 |
| SP_PIR_KEYWORDS       | isopeptide bond                                   | 5     | 4.80769231 | 0.07023201 | UHRF1, HIST  | 101        | 277      | 17854     | 3.19083533   | 0.99999959 | 0.52072656 | 59.9167962 |
| Annotation Cluster 7  |   |       |            |            |              |            |          |           |  |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm <td>Bonferroni</td> <td>Benjamini</td> <td>FDR</td> | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS       | Secreted  | 19    | 18.2692308 | 8.39E-04   | HAMP2, RAR   | 101        | 1420     | 17854     | 2.36526286   | 0.15589558 | 0.02785131 | 1.04779154 |
| GOTERM_CC_FAT         | GO:0005576~extracellular region                   | 20    | 19.2307692 | 0.01113596 | HAMP2, RAR   | 83         | 1680     | 12504     | 1.79345955   | 0.8637577  | 0.28267055 | 12.8621686 |
| SP_PIR_KEYWORDS       | disulfide bond                                    | 23    | 22.1153846 | 0.01698693 | LOC1000476   | 101        | 2469     | 17854     | 1.64672433   | 0.96859658 | 0.23372819 | 19.3533208 |
| SP_PIR_KEYWORDS       | signal  | 26    | 25         | 0.0209344  | HAMP2, RAR   | 101        | 2970     | 17854     | 1.54750142   | 0.98606901 | 0.26306821 | 23.3260731 |
| UP_SEQ_FEATURE        | disulfide bond                                    | 22    | 21.1538462 | 0.04541643 | HAMP2, LYZ   | 98         | 2379     | 16021     | 1.5117911  | 0.99999999 | 0.98898578 | 47.5564446 |
| UP_SEQ_FEATURE        | signal peptide                                    | 26    | 25         | 0.04679389 | HAMP2, RAR   | 98         | 2963     | 16021     | 1.43451549   | 0.99999999 | 0.97573965 | 48.597582  |
| SP_PIR_KEYWORDS       | glycoprotein                                      | 23    | 22.1153846 | 0.36105425 | LOC1000476   | 101        | 3600     | 17854     | 1.12937844   | 1          | 0.94600193 | 99.6388231 |
| UP_SEQ_FEATURE        | glycosylation site:N-linked (GlcNAc...)           | 22    | 21.1538462 | 0.52545794 | LOC1000476   | 98         | 3444     | 16021     | 1.04429472   | 1          | 0.99999996 | 99.9968035 |
| Annotation Cluster 8  |   |       |            |            |              |            |          |           |  |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm <td>Bonferroni</td> <td>Benjamini</td> <td>FDR</td> | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0006952~defense response                       | 9     | 8.65384615 | 0.00554211 | ORM1, HAM    | 83         | 448      | 13588     | 3.28883391   | 0.9878097  | 0.52026387 | 8.1680261  |
| GOTERM_BP_FAT         | GO:0006953~acute-phase response                   | 3     | 2.88461538 | 0.01402699 | ORM1, REG3   | 83         | 30       | 13588     | 16.3710843   | 0.99998636 | 0.57755855 | 19.4739032 |
| GOTERM_BP_FAT         | GO:0006954~inflammatory response                  | 5     | 4.80769231 | 0.04708076 | ORM1, TIRAI  | 83         | 225      | 13588     | 3.63801874   | 1          | 0.89455438 | 52.2600952 |
| GOTERM_BP_FAT         | GO:0009611~response to wounding                   | 6     | 5.76923077 | 0.05853674 | ORM1, TIRAI  | 83         | 347      | 13588     | 2.83073504   | 1          | 0.92987171 | 60.3406834 |
| SP_PIR_KEYWORDS       | inflammatory response                             | 3     | 2.88461538 | 0.07090414 | TIRAP, REG3  | 101        | 78       | 17854     | 6.79893374   | 0.99999965 | 0.50708429 | 60.2790593 |
| GOTERM_BP_FAT         | GO:0002526~acute inflammatory response            | 3     | 2.88461538 | 0.08589938 | ORM1, REG3   | 83         | 81       | 13588     | 6.06336457   | 1          | 0.9607345  | 74.7682187 |
| Annotation Cluster 9  |   |       |            |            |              |            |          |           |  |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm <td>Bonferroni</td> <td>Benjamini</td> <td>FDR</td> | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0003013~circulatory system process             | 5     | 4.80769231 | 0.00452452 | WNT2, EDNF   | 83         | 111      | 13588     | 7.37436231   | 0.97256905 | 0.51286632 | 6.71666564 |
| GOTERM_BP_FAT         | GO:0008015~blood circulation                      | 5     | 4.80769231 | 0.00452452 | WNT2, EDNF   | 83         | 111      | 13588     | 7.37436231   | 0.97256905 | 0.51286632 | 6.71666564 |
| GOTERM_BP_FAT         | GO:0008217~regulation of blood pressure           | 3     | 2.88461538 | 0.05860864 | EDNRB, MYH   | 83         | 65       | 13588     | 7.55588508   | 1          | 0.91960086 | 60.3870966 |
| GOTERM_BP_FAT         | GO:0007166~cell surface receptor linked signr     | 5     | 4.80769231 | 0.99993128 | WNT2, EDNF   | 83         | 2495     | 13588     | 0.32807784   | 1          | 1          | 100        |
| Annotation Cluster 10 |   |       |            |            |              |            |          |           |  |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm <td>Bonferroni</td> <td>Benjamini</td> <td>FDR</td> | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0030055~cell-substrate junction                | 4     | 3.84615385 | 0.00924496 | WNT2, TNS4   | 83         | 66       | 12504     | 9.13033954   | 0.80857448 | 0.33854552 | 10.7912241 |
| GOTERM_CC_FAT         | GO:0005912~adherens junction                      | 4     | 3.84615385 | 0.0323682  | WNT2, TNS4   | 83         | 106      | 12504     | 5.68492839   | 0.99713975 | 0.38619042 | 33.2712037 |
| GOTERM_CC_FAT         | GO:0070161~anchoring junction                     | 4     | 3.84615385 | 0.04695131 | WNT2, TNS4   | 83         | 123      | 12504     | 4.89920658   | 0.99980836 | 0.43484738 | 44.635606  |
| GOTERM_CC_FAT         | GO:0005925~focal adhesion                         | 3     | 2.88461538 | 0.05376452 | WNT2, TNS4   | 83         | 57       | 12504     | 7.92897907   | 0.99994656 | 0.42102602 | 49.3099644 |
| GOTERM_CC_FAT         | GO:0005924~cell-substrate adherens junctor        | 3     | 2.88461538 | 0.06063093 | WNT2, TNS4   | 83         | 61       | 12504     | 7.40904602   | 0.99998538 | 0.41148854 | 53.6515283 |
| GOTERM_CC_FAT         | GO:0016323~basolateral plasma membrane            | 4     | 3.84615385 | 0.06533808 | WNT2, TNS4   | 83         | 141      | 12504     | 4.27377595   | 0.99999402 | 0.40722247 | 56.4275031 |
| GOTERM_CC_FAT         | GO:0030054~cell junction                          | 7     | 6.73076923 | 0.08783356 | WNT2, TNS4   | 83         | 470      | 12504     | 2.24373238   | 0.99999992 | 0.49431177 | 67.7053161 |
| Annotation Cluster 11 |   |       |            |            |              |            |          |           |  |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm <td>Bonferroni</td> <td>Benjamini</td> <td>FDR</td> | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0015630~microtubule cytoskeleton               | 8     | 7.69230769 | 0.02799928 | CCNB1, KIF1  | 83         | 450      | 12504     | 2.67823293   | 0.99362247 | 0.42974055 | 29.4711364 |
| GOTERM_MF_FAT         | GO:0008017~microtubule binding                    | 3     | 2.88461538 | 0.05447131 | KIF1B, SPAG1 | 83         | 61       | 13288     | 7.87359273   | 0.99999025 | 0.80762816 | 50.6107545 |
| GOTERM_MF_FAT         | GO:0015631~tubulin binding                        | 3     | 2.88461538 | 0.08001352 | KIF1B, SPAG1 | 83         | 76       | 13288     | 6.31959417   | 0.99999997 | 0.85174905 | 65.0182695 |
| Annotation Cluster 12 |   |       |            |            |              |            |          |           |  |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm <td>Bonferroni</td> <td>Benjamini</td> <td>FDR</td> | Bonferroni | Benjamini  | FDR        |



|                 |  |    |            |            |            |     |     |       |            |            |            |            |
|-----------------|--|----|------------|------------|------------|-----|-----|-------|------------|------------|------------|------------|
| GOTERM_CC_FAT   | GO:0044421~extracellular region part       | 11 | 10.5769231 | 0.02949745 | WNT2, ORM  | 83  | 774 | 12504 | 2.14102923 | 0.99515371 | 0.41313133 | 30.796073  |
| SP_PIR_KEYWORDS | extracellular matrix                       | 5  | 4.80769231 | 0.03180637 | WNT2, OGN, | 101 | 213 | 17854 | 4.14958397 | 0.99853995 | 0.30423127 | 33.3555026 |
| GOTERM_CC_FAT   | GO:0031012~extracellular matrix            | 6  | 5.76923077 | 0.05218442 | WNT2, OGN, | 83  | 309 | 12504 | 2.92525442 | 0.99992808 | 0.42946149 | 48.2594091 |
| GOTERM_CC_FAT   | GO:0005578~proteinaceous extracellular mat | 5  | 4.80769231 | 0.13069971 | WNT2, OGN, | 83  | 297 | 12504 | 2.53620543 | 1          | 0.61669254 | 82.1300385 |

|                       |  |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 13 | Enrichment Score: 1.2527036651344312     |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term                                     | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0070013~intracellular organelle lumen | 14    | 13.4615385 | 0.03234672 | BCAS2, POLF | 83         | 1133     | 12504     | 1.86152554   | 0.99712843 | 0.41261893 | 33.2529952 |
| GOTERM_CC_FAT         | GO:0043233~organelle lumen               | 14    | 13.4615385 | 0.03295363 | BCAS2, POLF | 83         | 1136     | 12504     | 1.85660954   | 0.99743186 | 0.36796671 | 33.7658643 |
| GOTERM_CC_FAT         | GO:0031974~membrane-enclosed lumen       | 14    | 13.4615385 | 0.04137923 | BCAS2, POLF | 83         | 1174     | 12504     | 1.79651485   | 0.99945908 | 0.41567754 | 40.521907  |
| GOTERM_CC_FAT         | GO:0031981~nuclear lumen                 | 9     | 8.65384615 | 0.22114105 | BCAS2, SAP3 | 83         | 883      | 12504     | 1.5355101    | 1          | 0.72975668 | 95.3704292 |

|                       |                                      |       |            |            |            |            |          |           |              |            |            |            |
|-----------------------|--------------------------------------|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 14 | Enrichment Score: 1.0780946039253037 |       |            |            |            |            |          |           |              |            |            |            |
| Category              | Term                                 | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0006260~DNA replication           | 4     | 3.84615385 | 0.06415112 | MELA, MCM  | 83         | 152      | 13588     | 4.30818009   | 1          | 0.92783825 | 63.8159462 |
| SP_PIR_KEYWORDS       | dna replication                      | 3     | 2.88461538 | 0.08222816 | MCM10, MC  | 101        | 85       | 17854     | 6.23902155   | 0.99999997 | 0.52933306 | 65.9468392 |
| GOTERM_BP_FAT         | GO:0006259~DNA metabolic process     | 6     | 5.76923077 | 0.11053286 | UHRF1, MEL | 83         | 421      | 13588     | 2.33317116   | 1          | 0.97565551 | 83.4024528 |

|                       |  |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 15 | Enrichment Score: 1.0702000756543102     |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term                                     | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS       | kinetochore                              | 4     | 3.84615385 | 0.00484988 | KIF2C, CENP, | 101        | 61       | 17854     | 11.5916247   | 0.62546078 | 0.11552174 | 5.92100316 |
| GOTERM_CC_FAT         | GO:0000777~condensed chromosome kineto   | 3     | 2.88461538 | 0.04720053 | CENPA, SPA   | 83         | 53       | 12504     | 8.52739259   | 0.99981708 | 0.41602837 | 44.8133442 |
| GOTERM_CC_FAT         | GO:0000779~condensed chromosome, centr   | 3     | 2.88461538 | 0.05888707 | CENPA, SPA   | 83         | 60       | 12504     | 7.53253012   | 0.99997967 | 0.43367631 | 52.5825208 |
| GOTERM_CC_FAT         | GO:0000776~kinetochore                   | 3     | 2.88461538 | 0.06239246 | CENPA, SPA   | 83         | 62       | 12504     | 7.28954528   | 0.99998953 | 0.40622053 | 54.7088476 |
| GOTERM_CC_FAT         | GO:0000793~condensed chromosome          | 3     | 2.88461538 | 0.15559046 | CENPA, SPA   | 83         | 107      | 12504     | 4.22384867   | 1          | 0.63338076 | 87.4971877 |
| GOTERM_CC_FAT         | GO:0044427~chromosomal part              | 5     | 4.80769231 | 0.15578702 | SAP30, HIST  | 83         | 318      | 12504     | 2.36872016   | 1          | 0.62182547 | 87.5329225 |
| GOTERM_CC_FAT         | GO:0000775~chromosome, centromeric regio | 3     | 2.88461538 | 0.16481    | CENPA, SPA   | 83         | 111      | 12504     | 4.0716379    | 1          | 0.63277635 | 89.0758056 |
| GOTERM_CC_FAT         | GO:0005694~chromosome                    | 5     | 4.80769231 | 0.23579358 | SAP30, HIST  | 83         | 378      | 12504     | 1.99273284   | 1          | 0.74529182 | 96.3344927 |
| GOTERM_CC_FAT         | GO:0000785~chromatin                     | 3     | 2.88461538 | 0.29467259 | SAP30, HIST  | 83         | 165      | 12504     | 2.73910186   | 1          | 0.78031822 | 98.6321431 |

|                       |  |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 16 | Enrichment Score: 1.0322641874379634     |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term                                     | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_MF_FAT         | GO:0030554~adenyl nucleotide binding     | 16    | 15.3846154 | 0.04714747 | ACADSB, TW   | 83         | 1535     | 13288     | 1.66875711   | 0.99995221 | 0.91685751 | 45.5702086 |
| UP_SEQ_FEATURE        | nucleotide phosphate-binding region:ATP  | 11    | 10.5769231 | 0.04759643 | KIF1C, IRAK4 | 98         | 907      | 16021     | 1.98266319   | 0.99999999 | 0.95730022 | 49.1952972 |
| GOTERM_MF_FAT         | GO:0001883~purine nucleoside binding     | 16    | 15.3846154 | 0.05015317 | ACADSB, TW   | 83         | 1548     | 13288     | 1.654743     | 0.99997507 | 0.87995959 | 47.695225  |
| GOTERM_MF_FAT         | GO:0001882~nucleoside binding            | 16    | 15.3846154 | 0.05255647 | ACADSB, TW   | 83         | 1558     | 13288     | 1.64412206   | 0.99998521 | 0.84332565 | 49.3361326 |
| SP_PIR_KEYWORDS       | atp-binding                              | 13    | 12.5       | 0.05571758 | MAT2A, PIF1  | 101        | 1287     | 17854     | 1.78557856   | 0.99999065 | 0.45638186 | 51.3122469 |
| GOTERM_MF_FAT         | GO:0005524~ATP binding                   | 14    | 13.4615385 | 0.10409524 | TWF2, MAT2   | 83         | 1443     | 13288     | 1.55325669   | 1          | 0.87235772 | 74.9529614 |
| GOTERM_MF_FAT         | GO:0017076~purine nucleotide binding     | 17    | 16.3461538 | 0.10702308 | ACADSB, TW   | 83         | 1871     | 13288     | 1.4546438    | 1          | 0.8567513  | 75.9645779 |
| GOTERM_MF_FAT         | GO:0032559~adenyl ribonucleotide binding | 14    | 13.4615385 | 0.11140666 | TWF2, MAT2   | 83         | 1460     | 13288     | 1.53517082   | 1          | 0.8461347  | 77.4090352 |
| SP_PIR_KEYWORDS       | nucleotide-binding                       | 14    | 13.4615385 | 0.12311283 | MAT2A, PIF1  | 101        | 1631     | 17854     | 1.5173586    | 1          | 0.65407239 | 80.7826525 |
| GOTERM_MF_FAT         | GO:0000166~nucleotide binding            | 18    | 17.3076923 | 0.18078208 | ACADSB, TW   | 83         | 2183     | 13288     | 1.32008014   | 1          | 0.94682167 | 91.8847954 |
| GOTERM_MF_FAT         | GO:0032553~ribonucleotide binding        | 15    | 14.4230769 | 0.21222719 | TWF2, MAT2   | 83         | 1796     | 13288     | 1.3371079    | 1          | 0.96222189 | 95.0430962 |
| GOTERM_MF_FAT         | GO:0032555~purine ribonucleotide binding | 15    | 14.4230769 | 0.21222719 | TWF2, MAT2   | 83         | 1796     | 13288     | 1.3371079    | 1          | 0.96222189 | 95.0430962 |

|                       |  |       |            |            |           |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|-----------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 17 | Enrichment Score: 0.9441826607161281     |       |            |            |           |            |          |           |              |            |            |            |
| Category              | Term                                     | Count | %          | PValue     | Genes     | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0009725~response to hormone stimulus  | 4     | 3.84615385 | 0.07782753 | WNT2, MAT | 83         | 165      | 13588     | 3.96874772   | 1          | 0.95309276 | 71.1271953 |
| GOTERM_BP_FAT         | GO:0009719~response to endogenous stimu  | 4     | 3.84615385 | 0.09989109 | WNT2, MAT | 83         | 184      | 13588     | 3.55893138   | 1          | 0.97344335 | 80.082371  |
| GOTERM_BP_FAT         | GO:0010033~response to organic substance | 6     | 5.76923077 | 0.18914377 | WNT2, MAT | 83         | 505      | 13588     | 1.94507933   | 1          | 0.99135176 | 95.9830279 |

|                       |                                      |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|--------------------------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 18 | Enrichment Score: 0.8344870419104118 |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term                                 | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0005759~mitochondrial matrix      | 5     | 4.80769231 | 0.02219304 | ACADSB, ETH | 83         | 163      | 12504     | 4.62118412   | 0.98158991 | 0.39307925 | 24.1130583 |
| GOTERM_CC_FAT         | GO:0031980~mitochondrial lumen       | 5     | 4.80769231 | 0.02219304 | ACADSB, ETH | 83         | 163      | 12504     | 4.62118412   | 0.98158991 | 0.39307925 | 24.1130583 |
| SP_PIR_KEYWORDS       | mitochondrion                        | 9     | 8.65384615 | 0.07535282 | ISCA1, ACAC | 101        | 790      | 17854     | 2.01386139   | 0.99999987 | 0.51292229 | 62.6018426 |
| SP_PIR_KEYWORDS       | transit peptide                      | 6     | 5.76923077 | 0.11376421 | ISCA1, ACAC | 101        | 457      | 17854     | 2.32086141   | 1          | 0.63814065 | 78.0460075 |

|                |                                |    |            |            |             |    |      |       |            |   |            |            |
|----------------|--------------------------------|----|------------|------------|-------------|----|------|-------|------------|---|------------|------------|
| UP_SEQ_FEATURE | transit peptide:Mitochondrion  | 6  | 5.76923077 | 0.13649932 | ISCA1, ACAD | 98 | 449  | 16021 | 2.18458252 | 1 | 0.99918952 | 86.9704475 |
| GOTERM_MF_FAT  | GO:0050662~coenzyme binding    | 3  | 2.88461538 | 0.25952785 | ACADSB, IDH | 83 | 160  | 13288 | 3.00180723 | 1 | 0.97911065 | 97.7274531 |
| GOTERM_CC_FAT  | GO:0044429~mitochondrial part  | 6  | 5.76923077 | 0.25990017 | ACADSB, ETH | 83 | 524  | 12504 | 1.7250069  | 1 | 0.7742056  | 97.5283324 |
| GOTERM_CC_FAT  | GO:0005739~mitochondrion       | 11 | 10.5769231 | 0.36631522 | WNT2, ISCA1 | 83 | 1322 | 12504 | 1.25352241 | 1 | 0.82886623 | 99.6334514 |
| GOTERM_MF_FAT  | GO:0048037~cofactor binding    | 3  | 2.88461538 | 0.40789224 | ACADSB, IDH | 83 | 226  | 13288 | 2.12517326 | 1 | 0.99751542 | 99.8640199 |
| GOTERM_BP_FAT  | GO:0055114~oxidation reduction | 4  | 3.84615385 | 0.77816059 | ACADSB, IDH | 83 | 672  | 13588 | 0.97446931 | 1 | 0.999998   | 100        |

#### Annotation Cluster 19 Enrichment Score: 0.7687343753049075

| Category      | Term                                       | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0007017~microtubule-based process       | 6     | 5.76923077 | 0.00893704 | WNT2, KIF1C | 83         | 211      | 13588     | 4.65528465   | 0.99919037 | 0.50928576 | 12.8588958 |
| GOTERM_BP_FAT | GO:0051493~regulation of cytoskeleton orga | 3     | 2.88461538 | 0.12016159 | WNT2, CAPC  | 83         | 99       | 13588     | 4.96093465   | 1          | 0.9767141  | 85.9534982 |
| GOTERM_BP_FAT | GO:0033043~regulation of organelle organiz | 3     | 2.88461538 | 0.23802734 | WNT2, CAPC  | 83         | 154      | 13588     | 3.18917227   | 1          | 0.99705101 | 98.4516901 |
| GOTERM_CC_FAT | GO:0016023~cytoplasmic membrane-bounde     | 5     | 4.80769231 | 0.28788377 | WNT2, KIF1B | 83         | 414      | 12504     | 1.81945172   | 1          | 0.77927505 | 98.4611819 |
| GOTERM_CC_FAT | GO:0031988~membrane-bounded vesicle        | 5     | 4.80769231 | 0.29674729 | WNT2, KIF1B | 83         | 420      | 12504     | 1.79345955   | 1          | 0.77507195 | 98.6807965 |
| GOTERM_CC_FAT | GO:0031410~cytoplasmic vesicle             | 5     | 4.80769231 | 0.42830648 | WNT2, KIF1B | 83         | 508      | 12504     | 1.48278152   | 1          | 0.87968481 | 99.8966181 |
| GOTERM_CC_FAT | GO:0031982~vesicle                         | 5     | 4.80769231 | 0.4445437  | WNT2, KIF1B | 83         | 519      | 12504     | 1.45135455   | 1          | 0.87670268 | 99.9274564 |

#### Annotation Cluster 20 Enrichment Score: 0.7408358974967068

| Category        | Term                              | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|-----------------------------------|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| INTERPRO        | IPR002048:Calcium-binding EF-hand | 4     | 3.84615385 | 0.03523241 | MYL7, RYR2,  | 94         | 137      | 17763     | 5.51731635   | 0.99993548 | 0.95989153 | 37.5826333 |
| SMART           | SM00054:EFh                       | 4     | 3.84615385 | 0.04925684 | MYL7, RYR2,  | 56         | 137      | 9131      | 4.76068822   | 0.96609724 | 0.81587298 | 40.4324736 |
| INTERPRO        | IPR018249:EF-HAND 2               | 4     | 3.84615385 | 0.09271688 | MYL7, RYR2,  | 94         | 205      | 17763     | 3.68718215   | 1          | 0.98725117 | 72.1569659 |
| INTERPRO        | IPR011992:EF-Hand type            | 4     | 3.84615385 | 0.11642829 | MYL7, RYR2,  | 94         | 227      | 17763     | 3.3298341    | 1          | 0.99140691 | 80.3398652 |
| INTERPRO        | IPR018248:EF hand                 | 3     | 2.88461538 | 0.15202564 | MYL7, DST, I | 94         | 132      | 17763     | 4.29472921   | 1          | 0.99609277 | 88.5472987 |
| UP_SEQ_FEATURE  | domain:EF-hand 2                  | 3     | 2.88461538 | 0.25263035 | MYL7, DST, I | 98         | 160      | 16021     | 3.06524235   | 1          | 0.99996589 | 98.2465824 |
| UP_SEQ_FEATURE  | domain:EF-hand 1                  | 3     | 2.88461538 | 0.2548744  | MYL7, DST, I | 98         | 161      | 16021     | 3.04620357   | 1          | 0.99992608 | 98.3182929 |
| INTERPRO        | IPR018247:EF-HAND 1               | 3     | 2.88461538 | 0.30301052 | MYL7, DST, I | 94         | 211      | 17763     | 2.68675003   | 1          | 0.99997938 | 99.1292315 |
| SP_PIR_KEYWORDS | calcium                           | 4     | 3.84615385 | 0.78229584 | MYL7, DST, I | 101        | 731      | 17854     | 0.96729016   | 1          | 0.99857362 | 99.9999995 |
| GOTERM_MF_FAT   | GO:0005509~calcium ion binding    | 4     | 3.84615385 | 0.89837475 | MYL7, RYR2,  | 83         | 840      | 13288     | 0.76236374   | 1          | 0.99999959 | 100        |

#### Annotation Cluster 21 Enrichment Score: 0.6813280536546339

| Category      | Term  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|---|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0080135~regulation of cellular response  | 4     | 3.84615385 | 0.01047084 | NPC1, MDFIC | 83         | 75       | 13588     | 8.73124498   | 0.99976293 | 0.50122306 | 14.9038712 |
| GOTERM_BP_FAT | GO:0001932~regulation of protein amino aci  | 3     | 2.88461538 | 0.16564084 | MDFIC, TIRA | 83         | 121      | 13588     | 4.05894653   | 1          | 0.99026894 | 93.7747006 |
| GOTERM_BP_FAT | GO:0032268~regulation of cellular protein m | 4     | 3.84615385 | 0.2389331  | MDFIC, TIRA | 83         | 280      | 13588     | 2.33872633   | 1          | 0.99664663 | 98.4796699 |
| GOTERM_BP_FAT | GO:0031399~regulation of protein modificati | 3     | 2.88461538 | 0.2626371  | MDFIC, TIRA | 83         | 165      | 13588     | 2.97656079   | 1          | 0.99724093 | 99.0640598 |
| GOTERM_BP_FAT | GO:0042325~regulation of phosphorylation    | 3     | 2.88461538 | 0.52528358 | MDFIC, TIRA | 83         | 290      | 13588     | 1.69356045   | 1          | 0.99985198 | 99.9989061 |
| GOTERM_BP_FAT | GO:0051174~regulation of phosphorus meta    | 3     | 2.88461538 | 0.54546159 | MDFIC, TIRA | 83         | 301      | 13588     | 1.63166954   | 1          | 0.99983075 | 99.999438  |
| GOTERM_BP_FAT | GO:0019220~regulation of phosphate metab    | 3     | 2.88461538 | 0.54546159 | MDFIC, TIRA | 83         | 301      | 13588     | 1.63166954   | 1          | 0.99983075 | 99.999438  |

#### Annotation Cluster 22 Enrichment Score: 0.6180671550942028

| Category      | Term                                     | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0034622~cellular macromolecular compl | 4     | 3.84615385 | 0.14329442 | WNT2, HIST1 | 83         | 217      | 13588     | 3.0177114    | 1          | 0.98543564 | 90.6641671 |
| GOTERM_BP_FAT | GO:0034621~cellular macromolecular compl | 4     | 3.84615385 | 0.18417184 | WNT2, HIST1 | 83         | 245      | 13588     | 2.6728301    | 1          | 0.99248914 | 95.5883245 |
| GOTERM_BP_FAT | GO:0065003~macromolecular complex assem  | 4     | 3.84615385 | 0.33421271 | WNT2, HIST1 | 83         | 338      | 13588     | 1.93740643   | 1          | 0.99820923 | 99.8044198 |
| GOTERM_BP_FAT | GO:0043933~macromolecular complex subur  | 4     | 3.84615385 | 0.3821694  | WNT2, HIST1 | 83         | 367      | 13588     | 1.78431437   | 1          | 0.99903458 | 99.9378352 |

#### Annotation Cluster 23 Enrichment Score: 0.5977019787647363

| Category      | Term                            | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|---------------------------------|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0042592~homeostatic process  | 7     | 6.73076923 | 0.14061585 | EDNRB, HAN | 83         | 584      | 13588     | 1.96228751   | 1          | 0.98631983 | 90.2064588 |
| GOTERM_BP_FAT | GO:0048878~chemical homeostasis | 5     | 4.80769231 | 0.17851466 | EDNRB, HAN | 83         | 365      | 13588     | 2.24261429   | 1          | 0.99234973 | 95.0952399 |
| GOTERM_BP_FAT | GO:0055080~cation homeostasis   | 3     | 2.88461538 | 0.30515207 | EDNRB, HAN | 83         | 184      | 13588     | 2.66919853   | 1          | 0.99785063 | 99.6234657 |
| GOTERM_BP_FAT | GO:0050801~ion homeostasis      | 3     | 2.88461538 | 0.53084483 | EDNRB, HAN | 83         | 293      | 13588     | 1.67622024   | 1          | 0.99983307 | 99.9990869 |

#### Annotation Cluster 24 Enrichment Score: 0.449879119431194

| Category      | Term                                    | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|---|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0032989~cellular component morphogen | 5     | 4.80769231 | 0.16205877 | ALCAM, MEL | 83         | 351      | 13588     | 2.3320633    | 1          | 0.99066147 | 93.3520718 |

|               |   |   |            |            |            |    |     |       |            |   |            |            |
|---------------|---|---|------------|------------|------------|----|-----|-------|------------|---|------------|------------|
| GOTERM_BP_FAT | GO:0007409~axonogenesis                   | 3 | 2.88461538 | 0.25815718 | ALCAM, NKX | 83 | 163 | 13588 | 3.01308301 | 1 | 0.99731507 | 98.9729737 |
| GOTERM_BP_FAT | GO:0048812~neuron projection morphogene   | 3 | 2.88461538 | 0.28727551 | ALCAM, NKX | 83 | 176 | 13588 | 2.79052574 | 1 | 0.99776515 | 99.4441606 |
| GOTERM_BP_FAT | GO:0048667~cell morphogenesis involved in | 3 | 2.88461538 | 0.30068875 | ALCAM, NKX | 83 | 182 | 13588 | 2.69853039 | 1 | 0.99816874 | 99.5846254 |
| GOTERM_BP_FAT | GO:0030030~cell projection organization   | 4 | 3.84615385 | 0.30271732 | ALCAM, CAP | 83 | 319 | 13588 | 2.05280054 | 1 | 0.99800242 | 99.6027206 |
| GOTERM_BP_FAT | GO:0048858~cell projection morphogenesis  | 3 | 2.88461538 | 0.34504612 | ALCAM, NKX | 83 | 202 | 13588 | 2.43134916 | 1 | 0.99842524 | 99.8479153 |
| GOTERM_BP_FAT | GO:0000904~cell morphogenesis involved in | 3 | 2.88461538 | 0.36691368 | ALCAM, NKX | 83 | 212 | 13588 | 2.31666288 | 1 | 0.99892987 | 99.9096418 |
| GOTERM_BP_FAT | GO:0032990~cell part morphogenesis        | 3 | 2.88461538 | 0.36691368 | ALCAM, NKX | 83 | 212 | 13588 | 2.31666288 | 1 | 0.99892987 | 99.9096418 |
| GOTERM_BP_FAT | GO:0031175~neuron projection development  | 3 | 2.88461538 | 0.37990478 | ALCAM, NKX | 83 | 218 | 13588 | 2.25290151 | 1 | 0.99910421 | 99.9342483 |
| GOTERM_BP_FAT | GO:0048666~neuron development             | 3 | 2.88461538 | 0.5289959  | ALCAM, NKX | 83 | 292 | 13588 | 1.68196072 | 1 | 0.99984622 | 99.9990301 |
| GOTERM_BP_FAT | GO:0000902~cell morphogenesis             | 3 | 2.88461538 | 0.55976478 | ALCAM, NKX | 83 | 309 | 13588 | 1.58942566 | 1 | 0.99984807 | 99.9996558 |
| GOTERM_BP_FAT | GO:0030182~neuron differentiation         | 3 | 2.88461538 | 0.69871997 | ALCAM, NKX | 83 | 399 | 13588 | 1.2309086  | 1 | 0.99999316 | 99.999999  |

#### Annotation Cluster 25 Enrichment Score: 0.43759377034078767

| Category      | Term                                    | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|---|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0001701~in utero embryonic developme | 4     | 3.84615385 | 0.21822204 | CCNB1, WNT | 83         | 267      | 13588     | 2.4525969    | 1          | 0.99558546 | 97.7052483 |
| GOTERM_BP_FAT | GO:0043009~chordate embryonic developme | 4     | 3.84615385 | 0.46912512 | CCNB1, WNT | 83         | 421      | 13588     | 1.55544744   | 1          | 0.99969622 | 99.9939257 |
| GOTERM_BP_FAT | GO:0009792~embryonic development endin  | 4     | 3.84615385 | 0.47537317 | CCNB1, WNT | 83         | 425      | 13588     | 1.54080794   | 1          | 0.99966211 | 99.9949341 |

#### Annotation Cluster 26 Enrichment Score: 0.41477405165693537

| Category      | Term                                    | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|---|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_CC_FAT | GO:0005789~endoplasmic reticulum membra | 3     | 2.88461538 | 0.26303243 | 1110002B05I | 83         | 152      | 12504     | 2.97336715   | 1          | 0.76968659 | 97.6539109 |
| GOTERM_CC_FAT | GO:0012505~endomembrane system          | 6     | 5.76923077 | 0.27372951 | WNT2, NPC1  | 83         | 535      | 12504     | 1.68953947   | 1          | 0.77645979 | 98.039916  |
| GOTERM_CC_FAT | GO:0042175~nuclear envelope-endoplasmic | 3     | 2.88461538 | 0.28251257 | 1110002B05I | 83         | 160      | 12504     | 2.8246988    | 1          | 0.78025365 | 98.3122453 |
| GOTERM_CC_FAT | GO:0031090~organelle membrane           | 7     | 6.73076923 | 0.43934179 | WNT2, KIF1B | 83         | 809      | 12504     | 1.30352808   | 1          | 0.87778973 | 99.9186475 |
| GOTERM_CC_FAT | GO:0044332~endoplasmic reticulum part   | 3     | 2.88461538 | 0.44928812 | 1110002B05I | 83         | 231      | 12504     | 1.95650133   | 1          | 0.87532611 | 99.9347176 |
| GOTERM_CC_FAT | GO:0005783~endoplasmic reticulum        | 5     | 4.80769231 | 0.80846189 | NPC1, 1110C | 83         | 838      | 12504     | 0.89886994   | 1          | 0.9925751  | 99.9999999 |

#### Annotation Cluster 27 Enrichment Score: 0.3984501506673375

| Category        | Term                               | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|------------------------------------|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| UP_SEQ_FEATURE  | domain:lg-like C2-type 1           | 3     | 2.88461538 | 0.18601883 | ALCAM, FCR | 98         | 130      | 16021     | 3.77260597   | 1          | 0.99985988 | 94.2618591 |
| UP_SEQ_FEATURE  | domain:lg-like C2-type 2           | 3     | 2.88461538 | 0.18820183 | ALCAM, FCR | 98         | 131      | 16021     | 3.74380745   | 1          | 0.99969339 | 94.4719011 |
| INTERPRO        | IPR007110:Immunoglobulin-like      | 4     | 3.84615385 | 0.61706884 | ALCAM, H2- | 94         | 604      | 17763     | 1.25144427   | 1          | 1          | 99.9996674 |
| INTERPRO        | IPR013783:Immunoglobulin-like fold | 4     | 3.84615385 | 0.66041284 | ALCAM, H2- | 94         | 644      | 17763     | 1.17371481   | 1          | 1          | 99.9999314 |
| SP_PIR_KEYWORDS | Immunoglobulin domain              | 3     | 2.88461538 | 0.71354172 | ALCAM, FCR | 101        | 443      | 17854     | 1.19710346   | 1          | 0.99718518 | 99.9999847 |

#### Annotation Cluster 28 Enrichment Score: 0.3857363849857757

| Category      | Term                          | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|-------------------------------|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_CC_FAT | GO:0000267~cell fraction      | 6     | 5.76923077 | 0.35272169 | CCNB1, WNT | 83         | 596      | 12504     | 1.5166168    | 1          | 0.82103827 | 99.5241615 |
| GOTERM_CC_FAT | GO:0005624~membrane fraction  | 5     | 4.80769231 | 0.43126738 | CCNB1, WNT | 83         | 510      | 12504     | 1.47696669   | 1          | 0.8766561  | 99.9030118 |
| GOTERM_CC_FAT | GO:0005626~insoluble fraction | 5     | 4.80769231 | 0.45773284 | CCNB1, WNT | 83         | 528      | 12504     | 1.42661555   | 1          | 0.87691881 | 99.9460134 |

#### Annotation Cluster 29 Enrichment Score: 0.3844136165309649

| Category       | Term                               | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|----------------|------------------------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| UP_SEQ_FEATURE | domain:PH                          | 3     | 2.88461538 | 0.34641435 | PLEKHG3, KI | 98         | 202      | 16021     | 2.42791473   | 1          | 0.99999693 | 99.7275732 |
| INTERPRO       | IPR001849:Pleckstrin homology      | 3     | 2.88461538 | 0.39781245 | PLEKHG3, KI | 94         | 261      | 17763     | 2.17204696   | 1          | 0.99999881 | 99.8724885 |
| INTERPRO       | IPR011993:Pleckstrin homology-type | 3     | 2.88461538 | 0.44838591 | PLEKHG3, KI | 94         | 289      | 17763     | 1.96160642   | 1          | 0.99999952 | 99.9597338 |
| SMART          | SM00233:PH                         | 3     | 2.88461538 | 0.46926626 | PLEKHG3, KI | 56         | 261      | 9131      | 1.87417898   | 1          | 0.99997536 | 99.8492521 |

#### Annotation Cluster 30 Enrichment Score: 0.34145040100093715

| Category      | Term                            | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|---------------------------------|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0006928~cell motion          | 4     | 3.84615385 | 0.3821694  | WNT2, ALCA | 83         | 367      | 13588     | 1.78431437   | 1          | 0.99903458 | 99.9378352 |
| GOTERM_BP_FAT | GO:0016477~cell migration       | 3     | 2.88461538 | 0.4265428  | WNT2, EDNF | 83         | 240      | 13588     | 2.04638554   | 1          | 0.99956328 | 99.9801728 |
| GOTERM_BP_FAT | GO:0048870~cell motility        | 3     | 2.88461538 | 0.51403174 | WNT2, EDNF | 83         | 284      | 13588     | 1.72933989   | 1          | 0.99982839 | 99.9984333 |
| GOTERM_BP_FAT | GO:0051674~localization of cell | 3     | 2.88461538 | 0.51403174 | WNT2, EDNF | 83         | 284      | 13588     | 1.72933989   | 1          | 0.99982839 | 99.9984333 |

#### Annotation Cluster 31 Enrichment Score: 0.3162757961828146

| Category | Term | Count | % | PValue | Genes | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini | FDR |
|----------|------|-------|---|--------|-------|------------|----------|-----------|--------------|------------|-----------|-----|
|----------|------|-------|---|--------|-------|------------|----------|-----------|--------------|------------|-----------|-----|

|                 |  |   |            |            |              |     |      |       |            |   |            |            |
|-----------------|--|---|------------|------------|--------------|-----|------|-------|------------|---|------------|------------|
| GOTERM_BP_FAT   | GO:0006468~protein amino acid phosphoryl     | 7 | 6.73076923 | 0.18897167 | CCNB1, WN1   | 83  | 640  | 13588 | 1.79058735 | 1 | 0.99244214 | 95.9699357 |
| GOTERM_BP_FAT   | GO:0016310~phosphorylation                   | 7 | 6.73076923 | 0.26534286 | CCNB1, WN1   | 83  | 718  | 13588 | 1.59606672 | 1 | 0.99703823 | 99.1153552 |
| GOTERM_BP_FAT   | GO:0006796~phosphate metabolic process       | 8 | 7.69230769 | 0.26717073 | CCNB1, WN1   | 83  | 866  | 13588 | 1.51234035 | 1 | 0.99676108 | 99.1485072 |
| GOTERM_BP_FAT   | GO:0006793~phosphorus metabolic process      | 8 | 7.69230769 | 0.26717073 | CCNB1, WN1   | 83  | 866  | 13588 | 1.51234035 | 1 | 0.99676108 | 99.1485072 |
| UP_SEQ_FEATURE  | active site:Proton acceptor                  | 6 | 5.76923077 | 0.3727325  | IRAK4, ACAC  | 98  | 662  | 16021 | 1.48168814 | 1 | 0.99999756 | 99.8460483 |
| UP_SEQ_FEATURE  | binding site:ATP                             | 5 | 4.80769231 | 0.42091898 | IRAK4, KIF2C | 98  | 545  | 16021 | 1.49981277 | 1 | 0.99999824 | 99.9492605 |
| GOTERM_MF_FAT   | GO:0004672~protein kinase activity           | 5 | 4.80769231 | 0.48751118 | WNT2, IRAK4  | 83  | 583  | 13288 | 1.37303933 | 1 | 0.99897731 | 99.9779413 |
| INTERPRO        | IPR008271:Serine/threonine protein kinase, a | 3 | 2.88461538 | 0.56517035 | IRAK4, BUB1  | 94  | 360  | 17763 | 1.57473404 | 1 | 0.99999999 | 99.9982327 |
| SP_PIR_KEYWORDS | serine/threonine-protein kinase              | 3 | 2.88461538 | 0.63720236 | IRAK4, BUB1  | 101 | 384  | 17854 | 1.38103342 | 1 | 0.99476053 | 99.9997036 |
| INTERPRO        | IPR017441:Protein kinase, ATP binding site   | 3 | 2.88461538 | 0.7061062  | IRAK4, BUB1  | 94  | 467  | 17763 | 1.21392774 | 1 | 1          | 99.9999897 |
| INTERPRO        | IPR000719:Protein kinase, core               | 3 | 2.88461538 | 0.7320233  | IRAK4, BUB1  | 94  | 491  | 17763 | 1.15459115 | 1 | 1          | 99.9999969 |
| GOTERM_MF_FAT   | GO:0004674~protein serine/threonine kinase   | 3 | 2.88461538 | 0.73813132 | IRAK4, BUB1  | 83  | 421  | 13288 | 1.14082935 | 1 | 0.99997549 | 99.9999953 |
| SP_PIR_KEYWORDS | kinase                                       | 4 | 3.84615385 | 0.76267541 | IRAK4, BUB1  | 101 | 707  | 17854 | 1.00012604 | 1 | 0.99819308 | 99.9999986 |
| UP_SEQ_FEATURE  | domain:Protein kinase                        | 3 | 2.88461538 | 0.78799064 | IRAK4, BUB1  | 98  | 476  | 16021 | 1.03033356 | 1 | 1          | 100        |
| SP_PIR_KEYWORDS | transferase                                  | 7 | 6.73076923 | 0.79735957 | IRAK4, POLR  | 101 | 1385 | 17854 | 0.89343389 | 1 | 0.99879087 | 99.9999998 |

|                       |  |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 32 | Enrichment Score: 0.3044807207541374     |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term                                     | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0030097~hemopoiesis                   | 3     | 2.88461538 | 0.44919137 | TIRAP, HBB-I | 83         | 251      | 13588     | 1.95670331   | 1          | 0.99957045 | 99.9893109 |
| GOTERM_BP_FAT         | GO:0048534~hemopoietic or lymphoid organ | 3     | 2.88461538 | 0.50834179 | TIRAP, HBB-I | 83         | 281      | 13588     | 1.7478026    | 1          | 0.9998269  | 99.9981272 |
| GOTERM_BP_FAT         | GO:0002520~immune system development     | 3     | 2.88461538 | 0.5345282  | TIRAP, HBB-I | 83         | 295      | 13588     | 1.66485603   | 1          | 0.99982714 | 99.9991908 |

|                       |                                       |       |            |            |            |            |          |           |              |            |            |            |
|-----------------------|---------------------------------------|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 33 | Enrichment Score: 0.30348800451916147 |       |            |            |            |            |          |           |              |            |            |            |
| Category              | Term                                  | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0007155~cell adhesion              | 5     | 4.80769231 | 0.44046887 | ALCAM, LGA | 83         | 561      | 13588     | 1.45909843   | 1          | 0.99964343 | 99.9863993 |
| GOTERM_BP_FAT         | GO:0022610~biological adhesion        | 5     | 4.80769231 | 0.44182397 | ALCAM, LGA | 83         | 562      | 13588     | 1.45650217   | 1          | 0.99960515 | 99.9868956 |
| SP_PIR_KEYWORDS       | cell adhesion                         | 3     | 2.88461538 | 0.63149729 | ALCAM, ZYX | 101        | 380      | 17854     | 1.39557061   | 1          | 0.99504219 | 99.9996395 |

|                       |  |       |            |            |              |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 34 | Enrichment Score: 0.23565480719926         |       |            |            |              |            |          |           |              |            |            |            |
| Category              | Term                                       | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS       | dna-binding                                | 12    | 11.5384615 | 0.16169482 | SAP30, UHRF1 | 101        | 1404     | 17854     | 1.51087416   | 1          | 0.74596495 | 89.0765172 |
| GOTERM_CC_FAT         | GO:0031981~nuclear lumen                   | 9     | 8.65384615 | 0.22114105 | BCAS2, SAP3  | 83         | 883      | 12504     | 1.5355101    | 1          | 0.72975668 | 95.3704292 |
| SP_PIR_KEYWORDS       | activator                                  | 4     | 3.84615385 | 0.51189911 | MDFIC, NKX   | 101        | 484      | 17854     | 1.46092791   | 1          | 0.98406855 | 99.9877135 |
| GOTERM_MF_FAT         | GO:0003677~DNA binding                     | 12    | 11.5384615 | 0.54792303 | UHRF1, FOSL  | 83         | 1781     | 13288     | 1.07869547   | 1          | 0.99958524 | 99.995455  |
| SP_PIR_KEYWORDS       | transcription regulation                   | 9     | 8.65384615 | 0.64478572 | SAP30, UHRF1 | 101        | 1546     | 17854     | 1.02907535   | 1          | 0.99462997 | 99.9997727 |
| GOTERM_CC_FAT         | GO:0044451~nucleoplasm part                | 4     | 3.84615385 | 0.65976587 | SAP30, POLR  | 83         | 513      | 12504     | 1.17466357   | 1          | 0.96751203 | 99.9998248 |
| SP_PIR_KEYWORDS       | Transcription                              | 10    | 9.61538462 | 0.66884876 | SAP30, POLR  | 101        | 1769     | 17854     | 0.99927799   | 1          | 0.99508464 | 99.9999058 |
| GOTERM_BP_FAT         | GO:0006350~transcription                   | 10    | 9.61538462 | 0.75857014 | SAP30, POLR  | 83         | 1772     | 13588     | 0.92387609   | 1          | 0.99999726 | 100        |
| GOTERM_CC_FAT         | GO:0005654~nucleoplasm                     | 4     | 3.84615385 | 0.75929471 | SAP30, POLR  | 83         | 599      | 12504     | 1.00601404   | 1          | 0.98638638 | 99.9999975 |
| GOTERM_BP_FAT         | GO:0045449~regulation of transcription     | 10    | 9.61538462 | 0.9367747  | SAP30, UHRF1 | 83         | 2227     | 13588     | 0.73511829   | 1          | 1          | 100        |
| GOTERM_BP_FAT         | GO:0006355~regulation of transcription, DN | 5     | 4.80769231 | 0.98158357 | SAP30, FOSL  | 83         | 1465     | 13588     | 0.55874008   | 1          | 1          | 100        |
| GOTERM_BP_FAT         | GO:0051252~regulation of RNA metabolic pr  | 5     | 4.80769231 | 0.98349282 | SAP30, FOSL  | 83         | 1488     | 13588     | 0.55010364   | 1          | 1          | 100        |

|                       |   |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 35 | Enrichment Score: 0.22514182487637777         |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0043085~positive regulation of catalytic i | 3     | 2.88461538 | 0.46934935 | MDFIC, TIRA | 83         | 261      | 13588     | 1.88173383   | 1          | 0.99965638 | 99.9939649 |
| GOTERM_BP_FAT         | GO:0044093~positive regulation of molecular   | 3     | 2.88461538 | 0.55443806 | MDFIC, TIRA | 83         | 306      | 13588     | 1.60500827   | 1          | 0.99984651 | 99.999586  |
| GOTERM_BP_FAT         | GO:0007242~intracellular signaling cascade    | 5     | 4.80769231 | 0.81138181 | PLEKHG3, TV | 83         | 915      | 13588     | 0.89459477   | 1          | 0.99999896 | 100        |

|                       |                                       |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|---------------------------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 36 | Enrichment Score: 0.16368709052793085 |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term                                  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0008219~cell death                 | 4     | 3.84615385 | 0.59515165 | TNS4, LYZ1  | 83         | 507      | 13588     | 1.29160429   | 1          | 0.99992957 | 99.9999047 |
| GOTERM_BP_FAT         | GO:0016265~death                      | 4     | 3.84615385 | 0.61117338 | TNS4, LYZ1  | 83         | 519      | 13588     | 1.2617406    | 1          | 0.99994759 | 99.9999487 |
| GOTERM_BP_FAT         | GO:0006915~apoptosis                  | 3     | 2.88461538 | 0.77619276 | TNS4, BUB1F | 83         | 465      | 13588     | 1.05619899   | 1          | 0.99999839 | 100        |
| GOTERM_BP_FAT         | GO:0012501~programmed cell death      | 3     | 2.88461538 | 0.78431402 | TNS4, BUB1F | 83         | 473      | 13588     | 1.03833516   | 1          | 0.99999819 | 100        |

Annotation Cluster 37 Enrichment Score: 0.11196744977318468

| Category        | Term   | Count | % | PValue     | Genes      | List Total  | Pop Hits | Pop Total | Fold Enrichr | Bonferroni | Benjamini | FDR        |            |
|-----------------|--|-------|---|------------|------------|-------------|----------|-----------|--------------|------------|-----------|------------|------------|
| SP_PIR_KEYWORDS | activator                                    |       | 4 | 3.84615385 | 0.51189911 | MDFIC, NKX. | 101      | 484       | 1.7854       | 1.46092791 | 1         | 0.98406855 | 99.9877135 |
| GOTERM_BP_FAT   | GO:0051173~positive regulation of nitrogen   |       | 4 | 3.84615385 | 0.6203269  | MDFIC, NKX. | 83       | 526       | 1.3588       | 1.24494938 | 1         | 0.99995339 | 99.9999644 |
| GOTERM_BP_FAT   | GO:0031328~positive regulation of cellular b |       | 4 | 3.84615385 | 0.6530619  | MDFIC, NKX. | 83       | 552       | 1.3588       | 1.18631046 | 1         | 0.99997882 | 99.9999911 |
| GOTERM_BP_FAT   | GO:0009891~positive regulation of biosynthe  |       | 4 | 3.84615385 | 0.65912647 | MDFIC, NKX. | 83       | 557       | 1.3588       | 1.17566135 | 1         | 0.99997967 | 99.9999932 |
| GOTERM_BP_FAT   | GO:0045893~positive regulation of transcript |       | 3 | 2.88461538 | 0.72054113 | MDFIC, NKX. | 83       | 416       | 1.3588       | 1.18060704 | 1         | 0.99999407 | 99.9999997 |
| GOTERM_BP_FAT   | GO:0051254~positive regulation of RNA met    |       | 3 | 2.88461538 | 0.72425313 | MDFIC, NKX. | 83       | 419       | 1.3588       | 1.17215401 | 1         | 0.99999397 | 99.9999997 |
| GOTERM_BP_FAT   | GO:0010604~positive regulation of macromc    |       | 4 | 3.84615385 | 0.74211413 | MDFIC, NKX. | 83       | 633       | 1.3588       | 1.0345077  | 1         | 0.99999626 | 99.9999999 |
| GOTERM_BP_FAT   | GO:0045941~positive regulation of transcript |       | 3 | 2.88461538 | 0.78630413 | MDFIC, NKX. | 83       | 475       | 1.3588       | 1.03396322 | 1         | 0.99999807 | 100        |
| GOTERM_BP_FAT   | GO:0010628~positive regulation of gene exp   |       | 3 | 2.88461538 | 0.79885613 | MDFIC, NKX. | 83       | 488       | 1.3588       | 1.00641912 | 1         | 0.99999867 | 100        |
| GOTERM_BP_FAT   | GO:0045935~positive regulation of nucleoba   |       | 3 | 2.88461538 | 0.81863601 | MDFIC, NKX. | 83       | 510       | 1.3588       | 0.96300496 | 1         | 0.99999913 | 100        |
| GOTERM_BP_FAT   | GO:0010557~positive regulation of macromc    |       | 3 | 2.88461538 | 0.83510933 | MDFIC, NKX. | 83       | 530       | 1.3588       | 0.92666515 | 1         | 0.99999946 | 100        |
| GOTERM_MF_FAT   | GO:0003700~transcription factor activity     |       | 3 | 2.88461538 | 0.95664785 | FOSL2, NKX2 | 83       | 776       | 1.3288       | 0.61892933 | 1         | 0.99999999 | 100        |
| GOTERM_BP_FAT   | GO:0006355~regulation of transcription, DN/  |       | 5 | 4.80769231 | 0.98158357 | SAP30, FOSL | 83       | 1465      | 1.3588       | 0.55874008 | 1         | 1          | 100        |
| GOTERM_BP_FAT   | GO:0051252~regulation of RNA metabolic pr    |       | 5 | 4.80769231 | 0.98349282 | SAP30, FOSL | 83       | 1488      | 1.3588       | 0.55010364 | 1         | 1          | 100        |
| GOTERM_MF_FAT   | GO:0030528~transcription regulator activity  |       | 3 | 2.88461538 | 0.99631446 | FOSL2, NKX2 | 83       | 1206      | 1.3288       | 0.39824972 | 1         | 1          | 100        |

#### Annotation Cluster 38 Enrichment Score: 0.11069637994706268

| Category        | Term                                    | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|---|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|------------|------------|
| SP_PIR_KEYWORDS | metal-binding                           | 16    | 15.3846154 | 0.54547236 | MAT2A, MEL   | 101        | 2682     | 17854     | 1.05456989   | 1          | 0.9880179  | 99.994978  |
| SP_PIR_KEYWORDS | zinc                                    | 11    | 10.5769231 | 0.6210885  | SAP30, UHRF1 | 101        | 1886     | 17854     | 1.0310154    | 1          | 0.99499915 | 99.9994886 |
| GOTERM_MF_FAT   | GO:0046914~transition metal ion binding | 15    | 14.4230769 | 0.76105363 | MAT2A, MEL   | 83         | 2608     | 13288     | 0.92079976   | 1          | 0.99998194 | 99.9999985 |
| GOTERM_MF_FAT   | GO:0043167~ion binding                  | 22    | 21.1538462 | 0.81959321 | MYL7, MAT2   | 83         | 3934     | 13288     | 0.89530261   | 1          | 0.99999479 | 100        |
| GOTERM_MF_FAT   | GO:0046872~metal ion binding            | 21    | 20.1923077 | 0.8512345  | MYL7, MAT2   | 83         | 3850     | 13288     | 0.87325301   | 1          | 0.99999792 | 100        |
| GOTERM_MF_FAT   | GO:0043169~cation binding               | 21    | 20.1923077 | 0.86292558 | MYL7, MAT2   | 83         | 3885     | 13288     | 0.86538587   | 1          | 0.99999816 | 100        |
| SP_PIR_KEYWORDS | zinc-finger                             | 5     | 4.80769231 | 0.91214329 | SAP30, UHRF1 | 101        | 1204     | 17854     | 0.73410414   | 1          | 0.99990573 | 100        |
| GOTERM_MF_FAT   | GO:0008270~zinc ion binding             | 10    | 9.61538462 | 0.91918618 | UHRF1, MEL   | 83         | 2105     | 13288     | 0.7605529    | 1          | 0.99999985 | 100        |

#### Annotation Cluster 39 Enrichment Score: 0.09996406706782997

| Category      | Term                           | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini | FDR        |            |
|---------------|--------------------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|-----------|------------|------------|
| GOTERM_BP_FAT | GO:0030001~metal ion transport | 3     | 2.88461538 | 0.75136817 | KCTD20, RYF | 83         | 442      | 13588     | 1.11115957   |            | 1         | 0.99999691 | 99.9999999 |
| GOTERM_BP_FAT | GO:0006811~ion transport       | 4     | 3.84615385 | 0.81080374 | WNT2, KCTD  | 83         | 712      | 13588     | 0.91972384   |            | 1         | 0.99999908 | 100        |
| GOTERM_BP_FAT | GO:0006812~cation transport    | 3     | 2.88461538 | 0.82288522 | KCTD20, RYF | 83         | 515      | 13588     | 0.9536554    |            | 1         | 0.99999917 | 100        |

#### Annotation Cluster 40 Enrichment Score: 0.0014761171842190355

| Category        | Term                             | Count | %  | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini | FDR |     |
|-----------------|----------------------------------|-------|----|------------|------------|------------|----------|-----------|--------------|------------|-----------|-----|-----|
| UP_SEQ_FEATURE  | topological domain:Extracellular |       | 8  | 7.69230769 | 0.98317039 | ALCAM, EDN | 98       | 2174      | 1.6021       | 0.60158083 | 1         | 1   | 100 |
| SP_PIR_KEYWORDS | membrane                         |       | 20 | 19.2307692 | 0.99739205 | LOC1000476 | 101      | 5507      | 1.7854       | 0.6419912  | 1         | 1   | 100 |
| UP_SEQ_FEATURE  | transmembrane region             |       | 15 | 14.4230769 | 0.99753137 | LOC1000476 | 98       | 4113      | 1.6021       | 0.59620566 | 1         | 1   | 100 |
| UP_SEQ_FEATURE  | topological domain:Cytoplasmic   |       | 8  | 7.69230769 | 0.99891218 | ALCAM, EDN | 98       | 2780      | 1.6021       | 0.47044487 | 1         | 1   | 100 |
| SP_PIR_KEYWORDS | transmembrane                    |       | 17 | 16.3461538 | 0.99935833 | LOC1000476 | 101      | 5237      | 1.7854       | 0.57382637 | 1         | 1   | 100 |
| GOTERM_CC_FAT   | GO:0031224~intrinsic to membrane |       | 21 | 20.1923077 | 0.99999459 | LOC1000476 | 83       | 5914      | 1.2504       | 0.53494465 | 1         | 1   | 100 |
| GOTERM_CC_FAT   | GO:0016021~integral to membrane  |       | 18 | 17.3076923 | 0.99999937 | LOC1000476 | 83       | 5709      | 1.2504       | 0.47498876 | 1         | 1   | 100 |

[illegible]

|                      |  |       |            |            |             |            |          |           |              |            |            |            |
|----------------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 6 | Enrichment Score: 1.689093031417033              |       |            |            |             |            |          |           |              |            |            |            |
| Category             | Term   | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS      | ubl conjugation                                  | 7     | 15.9090909 | 0.00102051 | CCNB1, UHR  | 41         | 524      | 17854     | 5.81725936   | 0.09429324 | 0.01094408 | 1.12044638 |
| UP_SEQ_FEATURE       | cross-link:Glycyl lysine isopeptide (Lys-Gly) (i | 3     | 6.81818182 | 0.06578748 | UHRF1, HIST | 41         | 168      | 16021     | 6.97778746   | 0.9999837  | 0.99596262 | 56.1087434 |
| SP_PIR_KEYWORDS      | isopeptide bond                                  | 3     | 6.81818182 | 0.12757389 | UHRF1, HIST | 41         | 277      | 17854     | 4.71621027   | 0.99999822 | 0.50179947 | 77.8230385 |

|                      |  |       |            |            |             |            |          |           |              |            |              |            |
|----------------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|--------------|------------|
| Annotation Cluster 7 | Enrichment Score: 0.9841340497764857   |       |            |            |             |            |          |           |              |            |              |            |
| Category             | Term                                   | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini    | FDR        |
| SP_PIR_KEYWORDS      | dna-binding                            | 10    | 22.7272727 | 0.0032915  | SAP30, UHR  | 41         | 1404     | 17854     | 3.10159127   | 0.27370694 | 0.03147421   | 3.57297811 |
| GOTERM_MF_FAT        | GO:0003677~DNA binding                 | 10    | 22.7272727 | 0.01395134 | UHRF1, FOSI | 31         | 1781     | 13288     | 2.40676677   | 0.74043791 | 0.49052764   | 14.3363479 |
| GOTERM_BP_FAT        | GO:0006259~DNA metabolic process       | 5     | 11.3636364 | 0.02228703 | UHRF1, MEL  | 36         | 421      | 13588     | 4.48271312   | 0.99867522 | 0.45250923   | 25.9376549 |
| SP_PIR_KEYWORDS      | transcription regulation               | 5     | 11.3636364 | 0.46011902 | SAP30, UHR  | 41         | 1546     | 17854     | 1.40835516   |            | 1 0.89079164 | 99.8888949 |
| SP_PIR_KEYWORDS      | Transcription                          | 5     | 11.3636364 | 0.56947144 | SAP30, UHR  | 41         | 1769     | 17854     | 1.23081802   |            | 1 0.94603922 | 99.9908594 |
| GOTERM_BP_FAT        | GO:0006350~transcription               | 5     | 11.3636364 | 0.68684393 | SAP30, UHR  | 36         | 1772     | 13588     | 1.06502383   |            | 1 0.99999982 | 99.9999808 |
| GOTERM_BP_FAT        | GO:0045449~regulation of transcription | 6     | 13.6363636 | 0.70113235 | SAP30, UHR  | 36         | 2227     | 13588     | 1.01691364   |            | 1 0.99999962 | 99.9999897 |

|                      |  |       |            |            |              |            |          |           |              |            |              |            |
|----------------------|--|-------|------------|------------|--------------|------------|----------|-----------|--------------|------------|--------------|------------|
| Annotation Cluster 8 | Enrichment Score: 0.8742700494286476         |       |            |            |              |            |          |           |              |            |              |            |
| Category             | Term   | Count | %          | PValue     | Genes        | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini    | FDR        |
| UP_SEQ_FEATURE       | nucleotide phosphate-binding region:ATP      | 7     | 15.9090909 | 0.02392446 | IRAK4, KIF2C | 41         | 907      | 16021     | 3.0157582    | 0.98021595 | 0.98021595   | 25.3990713 |
| GOTERM_MF_FAT        | GO:0005524~ATP binding                       | 8     | 18.1818182 | 0.03818063 | IRAK4, KIF2C | 31         | 1443     | 13288     | 2.37641115   | 0.97617802 | 0.607134     | 34.8682778 |
| GOTERM_MF_FAT        | GO:0032559~adenyl ribonucleotide binding     | 8     | 18.1818182 | 0.04034168 | IRAK4, KIF2C | 31         | 1460     | 13288     | 2.34874061   | 0.98080462 | 0.54643519   | 36.4620537 |
| GOTERM_MF_FAT        | GO:0030554~adenyl nucleotide binding         | 8     | 18.1818182 | 0.05085989 | IRAK4, KIF2C | 31         | 1535     | 13288     | 2.2339813    | 0.99333636 | 0.56620433   | 43.7248132 |
| GOTERM_MF_FAT        | GO:0001883~purine nucleoside binding         | 8     | 18.1818182 | 0.05285016 | IRAK4, KIF2C | 31         | 1548     | 13288     | 2.21522047   | 0.99455254 | 0.52510328   | 45.0109504 |
| GOTERM_MF_FAT        | GO:0001882~nucleoside binding                | 8     | 18.1818182 | 0.05441539 | IRAK4, KIF2C | 31         | 1558     | 13288     | 2.20100211   | 0.9953523  | 0.48901903   | 46.0035851 |
| SP_PIR_KEYWORDS      | atp-binding                                  | 7     | 15.9090909 | 0.065023   | IRAK4, KIF2C | 41         | 1287     | 17854     | 2.36848788   | 0.99852874 | 0.35259013   | 52.3822177 |
| GOTERM_BP_FAT        | GO:0006468~protein amino acid phosphory      | 5     | 11.3636364 | 0.08064715 | CCNB1, IRAK  | 36         | 640      | 13588     | 2.94878472   |            | 1 0.87255574 | 67.3776055 |
| GOTERM_MF_FAT        | GO:0032553~ribonucleotide binding            | 8     | 18.1818182 | 0.10073233 | IRAK4, KIF2C | 31         | 1796     | 13288     | 1.90933257   | 0.99996256 | 0.67778249   | 68.9447706 |
| GOTERM_MF_FAT        | GO:0032555~purine ribonucleotide binding     | 8     | 18.1818182 | 0.10073233 | IRAK4, KIF2C | 31         | 1796     | 13288     | 1.90933257   | 0.99996256 | 0.67778249   | 68.9447706 |
| GOTERM_BP_FAT        | GO:0016310~phosphorylation                   | 5     | 11.3636364 | 0.11124382 | CCNB1, IRAK  | 36         | 718      | 13588     | 2.62844321   |            | 1 0.93054563 | 79.2178682 |
| GOTERM_MF_FAT        | GO:0017076~purine nucleotide binding         | 8     | 18.1818182 | 0.11897676 | IRAK4, KIF2C | 31         | 1871     | 13288     | 1.83279599   | 0.99999477 | 0.70359964   | 75.2204942 |
| SP_PIR_KEYWORDS      | nucleotide-binding                           | 7     | 15.9090909 | 0.15383686 | IRAK4, KIF2C | 41         | 1631     | 17854     | 1.86894169   | 0.99999991 | 0.55521269   | 84.1726329 |
| UP_SEQ_FEATURE       | binding site:ATP                             | 4     | 9.09090909 | 0.15420815 | IRAK4, KIF2C | 41         | 545      | 16021     | 2.86793466   |            | 1 0.99988191 | 86.8219216 |
| INTERPRO             | IPR008271:Serine/threonine protein kinase, c | 3     | 6.81818182 | 0.15788914 | IRAK4, BUB1  | 36         | 360      | 17763     | 4.11180556   |            | 1 1          | 85.9648129 |
| GOTERM_BP_FAT        | GO:0006793~phosphorus metabolic process      | 5     | 11.3636364 | 0.18128666 | CCNB1, IRAK  | 36         | 866      | 13588     | 2.17924044   |            | 1 0.98501112 | 93.0376477 |
| GOTERM_BP_FAT        | GO:0006796~phosphate metabolic process       | 5     | 11.3636364 | 0.18128666 | CCNB1, IRAK  | 36         | 866      | 13588     | 2.17924044   |            | 1 0.98501112 | 93.0376477 |
| SP_PIR_KEYWORDS      | kinase                                       | 4     | 9.09090909 | 0.21014207 | IRAK4, BUB1  | 41         | 707      | 17854     | 2.46372512   |            | 1 0.6636636  | 92.5973674 |
| GOTERM_MF_FAT        | GO:0000166~nucleotide binding                | 8     | 18.1818182 | 0.21237681 | IRAK4, KIF2C | 31         | 2183     | 13288     | 1.57084805   |            | 1 0.87550749 | 92.7880073 |
| SP_PIR_KEYWORDS      | serine/threonine-protein kinase              | 3     | 6.81818182 | 0.21239281 | IRAK4, BUB1  | 41         | 384      | 17854     | 3.40205793   |            | 1 0.65100442 | 92.8268551 |
| INTERPRO             | IPR017441:Protein kinase, ATP binding site   | 3     | 6.81818182 | 0.23445106 | IRAK4, BUB1  | 36         | 467      | 17763     | 3.16970021   |            | 1 0.99999984 | 95.2772421 |
| GOTERM_MF_FAT        | GO:0004674~protein serine/threonine kinase   | 3     | 6.81818182 | 0.24566886 | IRAK4, BUB1  | 31         | 421      | 13288     | 3.05447858   |            | 1 0.89516742 | 95.5179959 |
| INTERPRO             | IPR000719:Protein kinase, core               | 3     | 6.81818182 | 0.25205662 | IRAK4, BUB1  | 36         | 491      | 17763     | 3.01476578   |            | 1 0.99998795 | 96.3797565 |
| UP_SEQ_FEATURE       | domain:Protein kinase                        | 3     | 6.81818182 | 0.33427679 | IRAK4, BUB1  | 41         | 476      | 16021     | 2.46274851   |            | 1 0.99999993 | 99.2726128 |
| GOTERM_MF_FAT        | GO:0004672~protein kinase activity           | 3     | 6.81818182 | 0.38150867 | IRAK4, BUB1  | 31         | 583      | 13288     | 2.20572124   |            | 1 0.97122078 | 99.4967831 |
| UP_SEQ_FEATURE       | active site:Proton acceptor                  | 3     | 6.81818182 | 0.49657192 | IRAK4, BUB1  | 41         | 662      | 16021     | 1.77079803   |            | 1 1          | 99.975266  |
| SP_PIR_KEYWORDS      | transferase                                  | 4     | 9.09090909 | 0.60938148 | IRAK4, AGPA  | 41         | 1385     | 17854     | 1.25765607   |            | 1 0.95689937 | 99.9968759 |

|                      |                                      |       |            |            |             |            |          |           |              |            |              |            |
|----------------------|--------------------------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|--------------|------------|
| Annotation Cluster 9 | Enrichment Score: 0.4416282205834825 |       |            |            |             |            |          |           |              |            |              |            |
| Category             | Term                                 | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini    | FDR        |
| GOTERM_BP_FAT        | GO:0006915~apoptosis                 | 3     | 6.81818182 | 0.33786064 | TNS4, BUB1f | 36         | 465      | 13588     | 2.43512545   |            | 1 0.99919929 | 99.5881725 |
| GOTERM_BP_FAT        | GO:0012501~programmed cell death     | 3     | 6.81818182 | 0.34545716 | TNS4, BUB1f | 36         | 473      | 13588     | 2.39393939   |            | 1 0.99858132 | 99.6468533 |
| GOTERM_BP_FAT        | GO:0008219~cell death                | 3     | 6.81818182 | 0.3774444  | TNS4, BUB1f | 36         | 507      | 13588     | 2.23339908   |            | 1 0.9990572  | 99.8188357 |
| GOTERM_BP_FAT        | GO:0016265~death                     | 3     | 6.81818182 | 0.38859959 | TNS4, BUB1f | 36         | 519      | 13588     | 2.18175979   |            | 1 0.99898009 | 99.8576151 |

|                       |                                       |       |            |           |            |            |          |           |              |            |            |            |
|-----------------------|---------------------------------------|-------|------------|-----------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 10 | Enrichment Score: 0.29975387150830163 |       |            |           |            |            |          |           |              |            |            |            |
| Category              | Term                                  | Count | %          | PValue    | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS       | zinc                                  | 8     | 18.1818182 | 0.1234795 | SAP30, UHR | 41         | 1886     | 17854     | 1.84714068   | 0.9999972  | 0.50846867 | 76.6470256 |

|                 |   |   |            |            |             |    |      |       |            |   |            |            |
|-----------------|---|---|------------|------------|-------------|----|------|-------|------------|---|------------|------------|
| SP_PIR_KEYWORDS | zinc-finger                             | 5 | 11.3636364 | 0.28277892 | SAP30, UHRI | 41 | 1204 | 17854 | 1.80840288 | 1 | 0.75383154 | 97.4470801 |
| SP_PIR_KEYWORDS | metal-binding                           | 8 | 18.1818182 | 0.39483768 | SAP30, UHRI | 41 | 2682 | 17854 | 1.29892145 | 1 | 0.85754986 | 99.608426  |
| GOTERM_MF_FAT   | GO:0008270~zinc ion binding             | 6 | 13.6363636 | 0.52713669 | UHRF1, MEL  | 31 | 2105 | 13288 | 1.22179143 | 1 | 0.99411677 | 99.9738454 |
| GOTERM_MF_FAT   | GO:0046914~transition metal ion binding | 6 | 13.6363636 | 0.72863917 | UHRF1, MEL  | 31 | 2608 | 13288 | 0.98614684 | 1 | 0.99976303 | 99.9999423 |
| GOTERM_MF_FAT   | GO:0046872~metal ion binding            | 7 | 15.9090909 | 0.90503265 | IRAK4, UHRF | 31 | 3850 | 13288 | 0.77935484 | 1 | 0.99999927 | 100        |
| GOTERM_MF_FAT   | GO:0043169~cation binding               | 7 | 15.9090909 | 0.91012052 | IRAK4, UHRF | 31 | 3885 | 13288 | 0.77233362 | 1 | 0.99999877 | 100        |
| GOTERM_MF_FAT   | GO:0043167~ion binding                  | 7 | 15.9090909 | 0.91687394 | IRAK4, UHRF | 31 | 3934 | 13288 | 0.76271381 | 1 | 0.99999827 | 100        |

|                       |                                       |       |            |            |            |            |          |           |              |            |            |            |
|-----------------------|---------------------------------------|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 11 | Enrichment Score: 0.24593981726737843 |       |            |            |            |            |          |           |              |            |            |            |
| Category              | Term                                  | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS       | Secreted                              | 5     | 11.3636364 | 0.39494385 | ORM1, LGAL | 41         | 1420     | 17854     | 1.53332188   | 1          | 0.84656302 | 99.6091834 |
| GOTERM_CC_FAT         | GO:0044421~extracellular region part  | 3     | 6.81818182 | 0.54354748 | ORM1, LGAL | 30         | 774      | 12504     | 1.61550388   | 1          | 0.9949775  | 99.9853852 |
| GOTERM_CC_FAT         | GO:0005576~extracellular region       | 5     | 11.3636364 | 0.55924011 | ORM1, LGAL | 30         | 1680     | 12504     | 1.24047619   | 1          | 0.99450919 | 99.9901437 |
| UP_SEQ_FEATURE        | disulfide bond                        | 5     | 11.3636364 | 0.8647082  | ORM1, H2-C | 41         | 2379     | 16021     | 0.82126124   | 1          | 1          | 100        |

|                       |  |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 12 | Enrichment Score: 0.1196320804083633     |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term                                     | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0070013~intracellular organelle lumen | 3     | 6.81818182 | 0.75281155 | SAP30, ETHE | 30         | 1133     | 12504     | 1.10361871   | 1          | 0.99977188 | 99.9999854 |
| GOTERM_CC_FAT         | GO:0043233~organelle lumen               | 3     | 6.81818182 | 0.75416694 | SAP30, ETHE | 30         | 1136     | 12504     | 1.10070423   | 1          | 0.99965623 | 99.9999862 |
| GOTERM_CC_FAT         | GO:0031974~membrane-enclosed lumen       | 3     | 6.81818182 | 0.77081471 | SAP30, ETHE | 30         | 1174     | 12504     | 1.06507666   | 1          | 0.99964924 | 99.9999938 |

|                       |  |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|--|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 13 | Enrichment Score: 0.07989282143390561      |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term                                       | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0045449~regulation of transcription     | 6     | 13.6363636 | 0.70113235 | SAP30, UHRI | 36         | 2227     | 13588     | 1.01691364   | 1          | 0.99999962 | 99.9999897 |
| GOTERM_BP_FAT         | GO:0006355~regulation of transcription, DN | 3     | 6.81818182 | 0.90382553 | SAP30, FOSL | 36         | 1465     | 13588     | 0.77292378   | 1          | 1          | 100        |
| GOTERM_BP_FAT         | GO:0051252~regulation of RNA metabolic p   | 3     | 6.81818182 | 0.90873431 | SAP30, FOSL | 36         | 1488     | 13588     | 0.7609767    | 1          | 1          | 100        |

|                       |   |       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|---|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 14 | Enrichment Score: 0.07774263050212354   |       |            |            |             |            |          |           |              |            |            |            |
| Category              | Term                                    | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0005886~plasma membrane              | 9     | 20.4545455 | 0.35611793 | TNS4, PLP2, | 30         | 2906     | 12504     | 1.29084652   | 1          | 0.96649749 | 99.2966708 |
| SP_PIR_KEYWORDS       | disulfide bond                          | 6     | 13.6363636 | 0.66534558 | ORM1, LOC1  | 41         | 2469     | 17854     | 1.0582343    | 1          | 0.97096898 | 99.999433  |
| SP_PIR_KEYWORDS       | cell membrane                           | 4     | 9.09090909 | 0.75208521 | LOC1000476  | 41         | 1713     | 17854     | 1.01684393   | 1          | 0.98727222 | 99.9999793 |
| SP_PIR_KEYWORDS       | signal                                  | 6     | 13.6363636 | 0.81831759 | TNS4, ORM1  | 41         | 2970     | 17854     | 0.87972407   | 1          | 0.99431419 | 99.9999993 |
| UP_SEQ_FEATURE        | disulfide bond                          | 5     | 11.3636364 | 0.8647082  | ORM1, H2-C  | 41         | 2379     | 16021     | 0.82126124   | 1          | 1          | 100        |
| UP_SEQ_FEATURE        | signal peptide                          | 6     | 13.6363636 | 0.88599001 | TNS4, ORM1  | 41         | 2963     | 16021     | 0.79127121   | 1          | 1          | 100        |
| SP_PIR_KEYWORDS       | glycoprotein                            | 6     | 13.6363636 | 0.92773293 | ORM1, LOC1  | 41         | 3600     | 17854     | 0.72577236   | 1          | 0.99944458 | 100        |
| UP_SEQ_FEATURE        | glycosylation site:N-linked (GlcNAc...) | 6     | 13.6363636 | 0.95104661 | ORM1, LOC1  | 41         | 3444     | 16021     | 0.68075975   | 1          | 1          | 100        |
| SP_PIR_KEYWORDS       | membrane                                | 7     | 15.9090909 | 0.99366645 | PLP2, LOC10 | 41         | 5507     | 17854     | 0.55352168   | 1          | 0.99999919 | 100        |
| GOTERM_CC_FAT         | GO:0031224~intrinsic to membrane        | 8     | 18.1818182 | 0.9971484  | PLP2, LOC10 | 30         | 5914     | 12504     | 0.56381468   | 1          | 1          | 100        |
| UP_SEQ_FEATURE        | transmembrane region                    | 4     | 9.09090909 | 0.99925171 | PLP2, LOC10 | 41         | 4113     | 16021     | 0.38002052   | 1          | 1          | 100        |
| SP_PIR_KEYWORDS       | transmembrane                           | 4     | 9.09090909 | 0.99986031 | PLP2, LOC10 | 41         | 5237     | 17854     | 0.33260524   | 1          | 1          | 100        |
| GOTERM_CC_FAT         | GO:0016021~integral to membrane         | 5     | 11.3636364 | 0.99994916 | PLP2, LOC10 | 30         | 5709     | 12504     | 0.36503766   | 1          | 1          | 100        |

|                 |  |       |            |          |             |            |          |           |              |            |            |            |
|-----------------|--|-------|------------|----------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Category        | Term                                     | Count | %          | PValue   | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS | cell cycle                               | 12    | 27.2727273 | 2.58E-09 | CCNB1, KIF2 | 41         | 447      | 17854     | 11.690293    | 2.50E-07   | 2.50E-07   | 2.84E-06   |
| SP_PIR_KEYWORDS | cell division                            | 9     | 20.4545455 | 8.28E-08 | CCNB1, KIF2 | 41         | 256      | 17854     | 15.3092607   | 8.04E-06   | 4.02E-06   | 9.14E-05   |
| GOTERM_BP_FAT   | GO:0007049~cell cycle                    | 11    | 25         | 2.08E-06 | CCNB1, UHR  | 36         | 611      | 13588     | 6.7952355    | 6.11E-04   | 6.11E-04   | 0.00276846 |
| SP_PIR_KEYWORDS | mitosis                                  | 7     | 15.9090909 | 2.70E-06 | CCNB1, KIF2 | 41         | 179      | 17854     | 17.0292955   | 2.62E-04   | 8.73E-05   | 0.00298064 |
| KEGG_PATHWAY    | mmu04110:Cell cycle                      | 6     | 13.6363636 | 5.70E-06 | CCNB1, BUB  | 14         | 128      | 5738      | 19.2120536   | 1.25E-04   | 1.25E-04   | 0.00445864 |
| GOTERM_BP_FAT   | GO:0051301~cell division                 | 8     | 18.1818182 | 6.15E-06 | CCNB1, PRC  | 36         | 281      | 13588     | 10.7457493   | 0.00180519 | 9.03E-04   | 0.00818681 |
| SP_PIR_KEYWORDS | phosphoprotein                           | 29    | 65.9090909 | 8.43E-06 | LOC1000476  | 41         | 6311     | 17854     | 2.00102029   | 8.18E-04   | 2.04E-04   | 0.00930435 |
| GOTERM_BP_FAT   | GO:0000278~mitotic cell cycle            | 7     | 15.9090909 | 3.31E-05 | CCNB1, SPA  | 36         | 244      | 13588     | 10.8283242   | 0.00967593 | 0.00323577 | 0.04404774 |
| SP_PIR_KEYWORDS | nucleus                                  | 21    | 47.7272727 | 5.64E-05 | FOSL2, PRC1 | 41         | 3808     | 17854     | 2.40145265   | 0.00545394 | 0.00109318 | 0.06219972 |
| GOTERM_BP_FAT   | GO:0000280~nuclear division              | 6     | 13.6363636 | 1.17E-04 | CCNB1, SPA  | 36         | 190      | 13588     | 11.9192982   | 0.03384148 | 0.00856991 | 0.15587702 |
| GOTERM_BP_FAT   | GO:0007067~mitosis                       | 6     | 13.6363636 | 1.17E-04 | CCNB1, SPA  | 36         | 190      | 13588     | 11.9192982   | 0.03384148 | 0.00856991 | 0.15587702 |
| GOTERM_BP_FAT   | GO:0000087~M phase of mitotic cell cycle | 6     | 13.6363636 | 1.29E-04 | CCNB1, SPA  | 36         | 194      | 13588     | 11.6735395   | 0.03725652 | 0.0075649  | 0.17189548 |
| GOTERM_BP_FAT   | GO:0048285~organelle fission             | 6     | 13.6363636 | 1.39E-04 | CCNB1, SPA  | 36         | 197      | 13588     | 11.4957699   | 0.0399814  | 0.00677737 | 0.18471567 |



|                 |  |    |            |            |              |    |      |       |            |            |            |            |
|-----------------|--|----|------------|------------|--------------|----|------|-------|------------|------------|------------|------------|
| GOTERM_BP_FAT   | GO:0022403~cell cycle phase                      | 7  | 15.9090909 | 1.70E-04   | CCNB1, SPA   | 36 | 328  | 13588 | 8.0552168  | 0.04870798 | 0.00710807 | 0.22600807 |
| SP_PIR_KEYWORDS | cytoskeleton                                     | 8  | 18.1818182 | 2.79E-04   | CCNB1, TNS   | 41 | 583  | 17854 | 5.97548425 | 0.02668115 | 0.00449712 | 0.30720064 |
| SP_PIR_KEYWORDS | acetylation                                      | 15 | 34.0909091 | 3.26E-04   | TWF2, HIST1  | 41 | 2325 | 17854 | 2.80944138 | 0.03117923 | 0.00451487 | 0.35972408 |
| SP_PIR_KEYWORDS | kinetochore                                      | 4  | 9.09090909 | 3.43E-04   | KIF2C, CENP  | 41 | 61   | 17854 | 28.554978  | 0.03269517 | 0.00414658 | 0.37747415 |
| GOTERM_BP_FAT   | GO:0022402~cell cycle process                    | 7  | 15.9090909 | 4.49E-04   | CCNB1, SPA   | 36 | 393  | 13588 | 6.72292904 | 0.12370914 | 0.01637165 | 0.59659624 |
| GOTERM_BP_FAT   | GO:0000279~M phase                               | 6  | 13.6363636 | 7.36E-04   | CCNB1, SPA   | 36 | 283  | 13588 | 8.00235571 | 0.19460006 | 0.02375945 | 0.97584179 |
| SP_PIR_KEYWORDS | ub1 conjugation                                  | 7  | 15.9090909 | 0.00102051 | CCNB1, UHRF  | 41 | 524  | 17854 | 5.81725936 | 0.09429324 | 0.01094408 | 1.12044638 |
| GOTERM_CC_FAT   | GO:0043228~non-membrane-bounded orga             | 12 | 27.2727273 | 0.0025633  | CCNB1, TNS   | 30 | 1919 | 12504 | 2.60635748 | 0.24209099 | 0.24209099 | 2.84862287 |
| GOTERM_CC_FAT   | GO:0043232~intracellular non-membrane-b          | 12 | 27.2727273 | 0.0025633  | CCNB1, TNS   | 30 | 1919 | 12504 | 2.60635748 | 0.24209099 | 0.24209099 | 2.84862287 |
| SP_PIR_KEYWORDS | dna-binding                                      | 10 | 22.7272727 | 0.0032915  | SAP30, UHRF  | 41 | 1404 | 17854 | 3.10159127 | 0.27370694 | 0.03147421 | 3.57297811 |
| GOTERM_CC_FAT   | GO:0044427~chromosomal part                      | 5  | 11.3636364 | 0.00590141 | SAP30, HIST  | 30 | 318  | 12504 | 6.55345912 | 0.47230696 | 0.27357517 | 6.44743946 |
| GOTERM_CC_FAT   | GO:0000777~condensed chromosome kinet            | 3  | 6.81818182 | 0.00665161 | CENPA, SPA   | 30 | 53   | 12504 | 23.5924528 | 0.51362427 | 0.21357502 | 7.23932244 |
| GOTERM_BP_FAT   | GO:0006260~DNA replication                       | 4  | 9.09090909 | 0.00691133 | MEL1, MCM    | 36 | 152  | 13588 | 9.93274854 | 0.86983943 | 0.18445497 | 8.82517597 |
| GOTERM_CC_FAT   | GO:0000779~condensed chromosome, cent            | 3  | 6.81818182 | 0.00845863 | CENPA, SPA   | 30 | 60   | 12504 | 20.84      | 0.60045034 | 0.2049532  | 9.12172981 |
| GOTERM_CC_FAT   | GO:0000776~kinetochore                           | 3  | 6.81818182 | 0.00901106 | CENPA, SPA   | 30 | 62   | 12504 | 20.1677419 | 0.62378905 | 0.17759397 | 9.69022023 |
| GOTERM_CC_FAT   | GO:0005694~chromosome                            | 5  | 11.3636364 | 0.01073736 | SAP30, HIST  | 30 | 378  | 12504 | 5.51322751 | 0.6883598  | 0.1766037  | 11.4459005 |
| SP_PIR_KEYWORDS | cytoplasm  | 14 | 31.8181818 | 0.01214537 | LOC1000476   | 41 | 3029 | 17854 | 2.01270644 | 0.69434974 | 0.10215317 | 12.6155369 |
| GOTERM_CC_FAT   | GO:0005856~cytoskeleton                          | 8  | 18.1818182 | 0.01235698 | CCNB1, TNS   | 30 | 1122 | 12504 | 2.97183601 | 0.7389043  | 0.17455969 | 13.0647409 |
| GOTERM_MF_FAT   | GO:0008092~cytoskeletal protein binding          | 5  | 11.3636364 | 0.01340576 | TNS4, TWF2   | 31 | 414  | 13288 | 5.17687393 | 0.72628202 | 0.72628202 | 13.8128599 |
| GOTERM_MF_FAT   | GO:0003677~DNA binding                           | 10 | 22.7272727 | 0.01395134 | UHRF1, FOSI  | 31 | 1781 | 13288 | 2.40676677 | 0.74043791 | 0.49052764 | 14.3363479 |
| SP_PIR_KEYWORDS | actin-binding                                    | 4  | 9.09090909 | 0.01401357 | TNS4, TWF2   | 41 | 226  | 17854 | 7.70731707 | 0.74562106 | 0.10781121 | 14.4220612 |
| SP_PIR_KEYWORDS | dna replication                                  | 3  | 6.81818182 | 0.01553985 | MCM10, MC    | 41 | 85   | 17854 | 15.369297  | 0.78111305 | 0.11029162 | 15.8726769 |
| INTERPRO        | IPR001208:DNA-dependent ATPase MCM               | 2  | 4.54545455 | 0.01565789 | MCM5, MCM    | 36 | 8    | 17763 | 123.354167 | 0.84220628 | 0.84220628 | 16.5008099 |
| INTERPRO        | IPR018525:DNA-dependent ATPase MCM, c            | 2  | 4.54545455 | 0.01565789 | MCM5, MCM    | 36 | 8    | 17763 | 123.354167 | 0.84220628 | 0.84220628 | 16.5008099 |
| UP_SEQ_FEATURE  | domain:MCM                                       | 2  | 4.54545455 | 0.0198044  | MCM5, MCM    | 41 | 8    | 16021 | 97.6890244 | 0.960856   | 0.960856   | 21.4981438 |
| COG_ONTOLOGY    | Signal transduction mechanisms                   | 2  | 4.54545455 | 0.02045723 | UHRF1, BUB   | 4  | 14   | 2040  | 72.8571429 | 0.06012475 | 0.06012475 | 6.29939229 |
| SMART           | SM00350:MCM                                      | 2  | 4.54545455 | 0.0217029  | MCM5, MCM    | 26 | 8    | 9131  | 87.7980769 | 0.48224653 | 0.48224653 | 17.0482141 |
| GOTERM_BP_FAT   | GO:0006259~DNA metabolic process                 | 5  | 11.3636364 | 0.02228703 | UHRF1, MEL   | 36 | 421  | 13588 | 4.48271312 | 0.99867522 | 0.45250923 | 25.9376549 |
| UP_SEQ_FEATURE  | nucleotide phosphate-binding region:ATP          | 7  | 15.9090909 | 0.02392446 | IRAK4, KIF2C | 41 | 907  | 16021 | 3.0157582  | 0.98021595 | 0.8593442  | 25.3990713 |
| GOTERM_CC_FAT   | GO:0000793~condensed chromosome                  | 3  | 6.81818182 | 0.02534387 | CENPA, SPA   | 30 | 107  | 12504 | 11.6859813 | 0.93748944 | 0.29287829 | 25.1025632 |
| GOTERM_BP_FAT   | GO:0006270~DNA replication initiation            | 2  | 4.54545455 | 0.02546984 | MCM5, MCM    | 36 | 10   | 13588 | 75.4888889 | 0.99949206 | 0.46852298 | 29.085915  |
| GOTERM_MF_FAT   | GO:0003779~actin binding                         | 4  | 9.09090909 | 0.02656698 | TNS4, TWF2   | 31 | 288  | 13288 | 5.95340502 | 0.92459794 | 0.57753142 | 25.663263  |
| GOTERM_CC_FAT   | GO:0000775~chromosome, centromeric regi          | 3  | 6.81818182 | 0.02712873 | CENPA, SPA   | 30 | 111  | 12504 | 11.2648649 | 0.9487161  | 0.28110649 | 26.6325298 |
| SP_PIR_KEYWORDS | chromosomal protein                              | 3  | 6.81818182 | 0.03720866 | KIF2C, HIST1 | 41 | 136  | 17854 | 9.60581062 | 0.97472909 | 0.231044   | 34.1938024 |
| GOTERM_MF_FAT   | GO:0005524~ATP binding                           | 8  | 18.1818182 | 0.03818063 | IRAK4, KIF2C | 31 | 1443 | 13288 | 2.37641115 | 0.97617802 | 0.607134   | 34.8682778 |
| GOTERM_MF_FAT   | GO:0032559~adenyl ribonucleotide binding         | 8  | 18.1818182 | 0.04034168 | IRAK4, KIF2C | 31 | 1460 | 13288 | 2.34874061 | 0.98080462 | 0.54643519 | 36.4620537 |
| GOTERM_BP_FAT   | GO:0032729~positive regulation of interfero      | 2  | 4.54545455 | 0.04292259 | H2-Q1, RAET  | 36 | 17   | 13588 | 44.4052288 | 0.9999975  | 0.62922486 | 44.2583591 |
| GOTERM_MF_FAT   | GO:0030554~adenyl nucleotide binding             | 8  | 18.1818182 | 0.05085989 | IRAK4, KIF2C | 31 | 1535 | 13288 | 2.2339813  | 0.99333636 | 0.56620433 | 43.7248132 |
| GOTERM_MF_FAT   | GO:0001883~purine nucleoside binding             | 8  | 18.1818182 | 0.05285016 | IRAK4, KIF2C | 31 | 1548 | 13288 | 2.21522047 | 0.99455254 | 0.52510328 | 45.0109504 |
| GOTERM_MF_FAT   | GO:0001882~nucleoside binding                    | 8  | 18.1818182 | 0.05441539 | IRAK4, KIF2C | 31 | 1558 | 13288 | 2.20100211 | 0.99535523 | 0.48901903 | 46.0035851 |
| GOTERM_CC_FAT   | GO:0000785~chromatin                             | 3  | 6.81818182 | 0.05569715 | SAP30, HIST  | 30 | 165  | 12504 | 7.57818182 | 0.99794874 | 0.46147976 | 47.549075  |
| GOTERM_BP_FAT   | GO:0031343~positive regulation of cell killin    | 2  | 4.54545455 | 0.0576401  | H2-Q1, RAET  | 36 | 23   | 13588 | 32.821256  | 0.99999997 | 0.71255633 | 54.6559699 |
| GOTERM_BP_FAT   | GO:0001912~positive regulation of leukocyt       | 2  | 4.54545455 | 0.0576401  | H2-Q1, RAET  | 36 | 23   | 13588 | 32.821256  | 0.99999997 | 0.71255633 | 54.6559699 |
| SP_PIR_KEYWORDS | atp-binding                                      | 7  | 15.9090909 | 0.065023   | IRAK4, KIF2C | 41 | 1287 | 17854 | 2.36848788 | 0.99852874 | 0.35259013 | 52.3822177 |
| UP_SEQ_FEATURE  | cross-link:Glycyl lysine isopeptide (Lys-Gly) (i | 3  | 6.81818182 | 0.06578748 | UHRF1, HIST  | 41 | 168  | 16021 | 6.97778746 | 0.9999837  | 0.97464482 | 56.1087434 |
| GOTERM_BP_FAT   | GO:0000910~cytokinesis                           | 2  | 4.54545455 | 0.06732938 | PRC1, ANLN   | 36 | 27   | 13588 | 27.9588477 | 1          | 0.74492108 | 60.4883682 |
| GOTERM_BP_FAT   | GO:0031341~regulation of cell killing            | 2  | 4.54545455 | 0.07453277 | H2-Q1, RAET  | 36 | 30   | 13588 | 25.162963  | 1          | 0.75907368 | 64.3658001 |
| GOTERM_BP_FAT   | GO:0001910~regulation of leukocyte mediat        | 2  | 4.54545455 | 0.07453277 | H2-Q1, RAET  | 36 | 30   | 13588 | 25.162963  | 1          | 0.75907368 | 64.3658001 |
| KEGG_PATHWAY    | mmu03030:DNA replication                         | 2  | 4.54545455 | 0.07653492 | MCM5, MCM    | 14 | 35   | 5738  | 23.4204082 | 0.82651958 | 0.58349019 | 46.3748138 |
| GOTERM_BP_FAT   | GO:0032649~regulation of interferon-gamm         | 2  | 4.54545455 | 0.07930497 | H2-Q1, RAET  | 36 | 32   | 13588 | 23.5902778 | 1          | 0.76043992 | 66.7374004 |
| INTERPRO        | IPR007125:Histone core                           | 2  | 4.54545455 | 0.0795879  | HIST1H2AG,   | 36 | 42   | 17763 | 23.4960317 | 0.99993892 | 0.99218434 | 61.2352181 |
| GOTERM_BP_FAT   | GO:0006468~protein amino acid phosphory          | 5  | 11.3636364 | 0.08064715 | CCNB1, IRAK  | 36 | 640  | 13588 | 2.94878472 | 1          | 0.74675372 | 67.3776055 |
| GOTERM_BP_FAT   | GO:0006261~DNA-dependent DNA replicati           | 2  | 4.54545455 | 0.08405326 | MCM5, MCM    | 36 | 34   | 13588 | 22.2026144 | 1          | 0.74296523 | 68.951477  |
| GOTERM_CC_FAT   | GO:0015630~microtubule cytoskeleton              | 4  | 9.09090909 | 0.08487282 | CCNB1, KIF2  | 30 | 450  | 12504 | 3.70488889 | 0.99993082 | 0.58138199 | 63.1632719 |
| SP_PIR_KEYWORDS | centromere                                       | 2  | 4.54545455 | 0.08589931 | KIF2C, CENP  | 41 | 40   | 17854 | 21.7731707 | 0.9998354  | 0.41986864 | 62.8854896 |
| INTERPRO        | IPR002345:Lipocalin                              | 2  | 4.54545455 | 0.08683847 | ORM1, UHRF   | 36 | 46   | 17763 | 21.4528986 | 0.99997579 | 0.97106945 | 64.584776  |
| SP_PIR_KEYWORDS | microtubule                                      | 3  | 6.81818182 | 0.0875959  | KIF2C, PRC1, | 41 | 221  | 17854 | 5.91126807 | 0.99986254 | 0.40730261 | 63.6386417 |

|             |                      |   |       |             |            |               |            |          |           |              |            |            |            |
|-------------|----------------------|---|-------|-------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
|             | INTERPRO             | IPR011161:MHC class I-like antigen recognit | 2     | 4.54545455  | 0.09223995 | H2-Q1, RAET   | 36         | 49       | 17763     | 20.1394558   | 0.9999879  | 0.94102694 | 66.9060461 |
|             | SP_PIR_KEYWORDS      | nucleosome core                             | 2     | 4.54545455  | 0.09408257 | HIST1H2AG,    | 41         | 44       | 17854     | 19.7937916   | 0.9999312  | 0.41284153 | 66.3918271 |
|             | GOTERM_BP_FAT        | GO:0002708~positive regulation of lymphoc   | 2     | 4.54545455  | 0.09815584 | H2-Q1, RAET   | 36         | 40       | 13588     | 18.8722222   | 1          | 0.78100559 | 74.749575  |
|             | GOTERM_BP_FAT        | GO:0002705~positive regulation of leukocyt  | 2     | 4.54545455  | 0.09815584 | H2-Q1, RAET   | 36         | 40       | 13588     | 18.8722222   | 1          | 0.78100559 | 74.749575  |
| UNIQUE      | 60 david id matched  |   |       |             |            |               |            |          |           |              |            |            |            |
| lung        | Annotation Cluster 1 | Enrichment Score: 2.0618505698464653        |       |             |            |               |            |          |           |              |            |            |            |
| TH/SH       | Category             | Term  | Count | %           | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| down-regula | GOTERM_BP_FAT        | GO:0003013~circulatory system process       | 5     | 8.33333333  | 5.28E-04   | WNT2, EDNF    | 47         | 111      | 13588     | 13.02281     | 0.28323867 | 0.28323867 | 0.78282059 |
|             | GOTERM_BP_FAT        | GO:0008015~blood circulation                | 5     | 8.33333333  | 5.28E-04   | WNT2, EDNF    | 47         | 111      | 13588     | 13.02281     | 0.28323867 | 0.28323867 | 0.78282059 |
|             | GOTERM_BP_FAT        | GO:0008217~regulation of blood pressure     | 3     | 5           | 0.02037131 | EDNRB, MYH    | 47         | 65       | 13588     | 13.3433715   | 0.99999766 | 0.80226073 | 26.3616961 |
|             | GOTERM_BP_FAT        | GO:0007166~cell surface receptor linked sig | 4     | 6.66666667  | 0.99441758 | WNT2, EDNF    | 47         | 2495     | 13588     | 0.46349721   | 1          | 1          | 100        |
|             | Annotation Cluster 2 | Enrichment Score: 2.052868642711485         |       |             |            |               |            |          |           |              |            |            |            |
|             | Category             | Term  | Count | %           | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|             | SP_PIR_KEYWORDS      | Secreted                                    | 14    | 23.3333333  | 6.14E-04   | HAMP2, RAF    | 60         | 1420     | 17854     | 2.93375587   | 0.0924119  | 0.0924119  | 0.73671606 |
|             | SP_PIR_KEYWORDS      | signal                                      | 20    | 33.3333333  | 0.00243589 | HAMP2, RAF    | 60         | 2970     | 17854     | 2.00381594   | 0.31978106 | 0.17524613 | 2.89581465 |
|             | UP_SEQ_FEATURE       | signal peptide                              | 20    | 33.3333333  | 0.00428574 | HAMP2, RAF    | 57         | 2963     | 16021     | 1.89719997   | 0.64935026 | 0.40784315 | 5.40657455 |
|             | SP_PIR_KEYWORDS      | disulfide bond                              | 17    | 28.3333333  | 0.0052566  | HAMP2, LYZ    | 60         | 2469     | 17854     | 2.04885919   | 0.56514105 | 0.24238342 | 6.15291428 |
|             | UP_SEQ_FEATURE       | disulfide bond                              | 17    | 28.3333333  | 0.00608461 | HAMP2, LYZ    | 57         | 2379     | 16021     | 2.00848801   | 0.77444253 | 0.3912779  | 7.59446489 |
|             | GOTERM_CC_FAT        | GO:0005576~extracellular region             | 15    | 25          | 0.00723341 | HAMP2, RAF    | 53         | 1680     | 12504     | 2.106469     | 0.61922262 | 0.61922262 | 8.1383109  |
|             | SP_PIR_KEYWORDS      | glycoprotein                                | 17    | 28.3333333  | 0.12252358 | PLUNC, DCN    | 60         | 3600     | 17854     | 1.40517593   | 1          | 0.87319972 | 79.2963015 |
|             | UP_SEQ_FEATURE       | glycosylation site:N-linked (GlcNAc...)     | 16    | 26.6666667  | 0.20799032 | PLUNC, DCN    | 57         | 3444     | 16021     | 1.30578479   | 1          | 0.99432902 | 95.1085117 |
|             | Annotation Cluster 3 | Enrichment Score: 1.9066902341847056        |       |             |            |               |            |          |           |              |            |            |            |
|             | Category             | Term  | Count | %           | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|             | GOTERM_MF_FAT        | GO:0008092~cytoskeletal protein binding     | 7     | 11.6666667  | 0.00485595 | KIF1B, CGN,   | 52         | 414      | 13288     | 4.32069863   | 0.54991363 | 0.32911523 | 5.73174513 |
|             | SMART                | SM00033:CH                                  | 3     | 5           | 0.0194921  | LMO7, DST,    | 30         | 68       | 9131      | 13.4279412   | 0.56253215 | 0.33858648 | 16.654901  |
|             | INTERPRO             | IPR001715:Calponin-like actin-binding       | 3     | 5           | 0.02012781 | LMO7, DST,    | 58         | 68       | 17763     | 13.5114097   | 0.96437236 | 0.81124715 | 21.8511922 |
|             | Annotation Cluster 4 | Enrichment Score: 1.640061697964257         |       |             |            |               |            |          |           |              |            |            |            |
|             | Category             | Term  | Count | %           | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|             | GOTERM_BP_FAT        | GO:0009725~response to hormone stimulus     | 4     | 6.66666667  | 0.01822353 | WNT2, MAT:    | 47         | 165      | 13588     | 7.00863959   | 0.99999071 | 0.80895505 | 23.9244899 |
|             | GOTERM_BP_FAT        | GO:0009719~response to endogenous stimuli   | 4     | 6.66666667  | 0.02422237 | WNT2, MAT:    | 47         | 184      | 13588     | 6.28492137   | 0.9999998  | 0.820295   | 30.503148  |
|             | GOTERM_BP_FAT        | GO:0010033~response to organic substance    | 6     | 10          | 0.02722486 | WNT2, MAT:    | 47         | 505      | 13588     | 3.43492732   | 0.99999997 | 0.79420209 | 33.6606531 |
|             | Annotation Cluster 5 | Enrichment Score: 1.5260338034703365        |       |             |            |               |            |          |           |              |            |            |            |
|             | Category             | Term  | Count | %           | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|             | GOTERM_MF_FAT        | GO:0003774~motor activity                   | 5     | 8.33333333  | 0.00190679 | KIF1C, MYL7,  | 52         | 138      | 13288     | 9.25863991   | 0.26875901 | 0.26875901 | 2.28776711 |
|             | GOTERM_MF_FAT        | GO:0008092~cytoskeletal protein binding     | 7     | 11.66666667 | 0.00485595 | KIF1B, CGN,   | 52         | 414      | 13288     | 4.32069863   | 0.54991363 | 0.32911523 | 5.73174513 |
|             | GOTERM_BP_FAT        | GO:0030705~cytoskeleton-dependent intrac    | 3     | 5           | 0.00553759 | KIF1B, MYH6   | 47         | 33       | 13588     | 26.2823985   | 0.9697535  | 0.68842804 | 7.92445069 |
|             | SP_PIR_KEYWORDS      | motor protein                               | 4     | 6.66666667  | 0.00783454 | KIF1C, MYL7,  | 60         | 123      | 17854     | 9.67696477   | 0.71140532 | 0.26705383 | 9.04174997 |
|             | GOTERM_CC_FAT        | GO:0015629~actin cytoskeleton               | 5     | 8.33333333  | 0.01028202 | MYL7, CGN,    | 53         | 205      | 12504     | 5.75425679   | 0.74705619 | 0.49706487 | 11.3831177 |
|             | GOTERM_BP_FAT        | GO:0046907~intracellular transport          | 6     | 10          | 0.01477415 | KIF1C, NPC1,  | 47         | 431      | 13588     | 4.02468283   | 0.99991536 | 0.84671117 | 19.852261  |
|             | GOTERM_CC_FAT        | GO:0043232~intracellular non-membrane-bu    | 15    | 25          | 0.02209217 | BCAS2, MYL    | 53         | 1919     | 12504     | 1.84412086   | 0.94875827 | 0.3905511  | 22.9884747 |
|             | GOTERM_CC_FAT        | GO:0043228~non-membrane-bounded orga        | 15    | 25          | 0.02209217 | BCAS2, MYL    | 53         | 1919     | 12504     | 1.84412086   | 0.94875827 | 0.3905511  | 22.9884747 |
|             | GOTERM_MF_FAT        | GO:0003779~actin binding                    | 5     | 8.33333333  | 0.04363648 | CGN, MYH6,    | 52         | 288      | 13288     | 4.43643162   | 0.98241223 | 0.73994199 | 25.8254731 |
|             | GOTERM_CC_FAT        | GO:0016459~myosin complex                   | 3     | 5           | 0.02655259 | MYL7, CGN,    | 53         | 61       | 12504     | 11.6028457   | 0.97210274 | 0.40029542 | 26.9970316 |
|             | SP_PIR_KEYWORDS      | actin-binding                               | 4     | 6.66666667  | 0.03875632 | MYH6, PALLI   | 60         | 226      | 17854     | 5.26666667   | 0.99806049 | 0.64685851 | 37.889935  |
|             | GOTERM_CC_FAT        | GO:0044430~cytoskeletal part                | 8     | 13.3333333  | 0.0400081  | KIF1C, MYL7,  | 53         | 774      | 12504     | 2.43849642   | 0.99561887 | 0.41902341 | 37.9618966 |
|             | GOTERM_CC_FAT        | GO:0005856~cytoskeleton                     | 9     | 15          | 0.09049991 | KIF1C, MYL7,  | 53         | 1122     | 12504     | 1.89244274   | 0.99999668 | 0.6505403  | 67.0170526 |
|             | GOTERM_BP_FAT        | GO:0007010~cytoskeleton organization        | 4     | 6.66666667  | 0.09777695 | WNT2, MYH     | 47         | 326      | 13588     | 3.54731758   | 1          | 0.98672041 | 78.3421917 |
|             | KEGG_PATHWAY         | mmu04530:Tight junction                     | 3     | 5           | 0.10086065 | MYL7, CGN,    | 24         | 135      | 5738      | 5.93126296   | 0.9939229  | 0.92204425 | 63.7469577 |
|             | UP_SEQ_FEATURE       | nucleotide phosphate-binding region:ATP     | 4     | 6.66666667  | 0.62149975 | KIF1C, KIF1B, | 57         | 907      | 16021     | 1.23955976   | 1          | 1          | 99.9996536 |
|             | SP_PIR_KEYWORDS      | coiled coil                                 | 6     | 10          | 0.6895304  | KIF1C, BCAS   | 60         | 1732     | 17854     | 1.03083141   | 1          | 0.99967611 | 99.9999243 |
|             | Annotation Cluster 6 | Enrichment Score: 1.2509433613814636        |       |             |            |               |            |          |           |              |            |            |            |

| Category              | Term                                     | Count | %           | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------------|--|-------|-------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT         | GO:0010033~response to organic substance | 6     | 10          | 0.02722486 | WNT2, MAT:    | 47         | 505      | 13588     | 3.43492732   | 0.99999997 | 0.79420209 | 33.6606531 |
| GOTERM_CC_FAT         | GO:0044421~extracellular region part     | 8     | 13.33333333 | 0.0400081  | WNT2, OGN,    | 53         | 774      | 12504     | 2.43849642   | 0.99561887 | 0.41902341 | 37.9618966 |
| GOTERM_CC_FAT         | GO:0005615~extracellular space           | 5     | 8.33333333  | 0.162202   | SEPP1, CCL5,  | 53         | 511      | 12504     | 2.30845918   | 1          | 0.7495747  | 87.3734482 |
| Annotation Cluster 7  |  |       |             |            |               |            |          |           |              |            |            |            |
| Category              | Term                                     | Count | %           | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0070013~intracellular organelle lumen | 11    | 18.33333333 | 0.01688201 | BCAS2, POLF   | 53         | 1133     | 12504     | 2.2905294    | 0.89611562 | 0.52990739 | 18.0518094 |
| GOTERM_CC_FAT         | GO:0043233~organelle lumen               | 11    | 18.33333333 | 0.01717109 | BCAS2, POLF   | 53         | 1136     | 12504     | 2.28448047   | 0.90010034 | 0.43779979 | 18.333111  |
| GOTERM_CC_FAT         | GO:0031974~membrane-enclosed lumen       | 11    | 18.33333333 | 0.02116331 | BCAS2, POLF   | 53         | 1174     | 12504     | 2.21053647   | 0.94186172 | 0.43390094 | 22.1287983 |
| GOTERM_CC_FAT         | GO:0005730~nucleolus                     | 5     | 8.33333333  | 0.03956687 | BCAS2, DNA    | 53         | 310      | 12504     | 3.80523433   | 0.99534276 | 0.44931505 | 37.6276632 |
| GOTERM_CC_FAT         | GO:0031981~nuclear lumen                 | 7     | 11.66666667 | 0.1584875  | BCAS2, POLF   | 53         | 883      | 12504     | 1.87029637   | 1          | 0.76173186 | 86.7031268 |
| SP_PIR_KEYWORDS       | nucleus                                  | 10    | 16.66666667 | 0.90771261 | BCAS2, POLF   | 60         | 3808     | 17854     | 0.78142507   | 1          | 0.99999645 | 100        |
| Annotation Cluster 8  |  |       |             |            |               |            |          |           |              |            |            |            |
| Category              | Term                                     | Count | %           | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| SMART                 | SM00054:EFh                              | 4     | 6.66666667  | 0.00907808 | MYL7, RYR2,   | 30         | 137      | 9131      | 8.886618     | 0.31820101 | 0.31820101 | 8.09374733 |
| INTERPRO              | IPR002048:Calcium-binding EF-hand        | 4     | 6.66666667  | 0.00969445 | MYL7, RYR2,   | 58         | 137      | 17763     | 8.94185754   | 0.79762771 | 0.79762771 | 11.1416279 |
| INTERPRO              | IPR018249:EF-HAND 2                      | 4     | 6.66666667  | 0.0281     | MYL7, RYR2,   | 58         | 205      | 17763     | 5.97577796   | 0.99066875 | 0.78947036 | 29.2214174 |
| INTERPRO              | IPR01992:EF-Hand type                    | 4     | 6.66666667  | 0.03638163 | MYL7, RYR2,   | 58         | 227      | 17763     | 5.39662768   | 0.99770686 | 0.78116952 | 36.1977256 |
| INTERPRO              | IPR018248:EF hand                        | 3     | 5           | 0.06712339 | MYL7, DST, I  | 58         | 132      | 17763     | 6.9604232    | 0.99998875 | 0.89761556 | 56.9379694 |
| UP_SEQ_FEATURE        | domain:EF-hand 2                         | 3     | 5           | 0.10771273 | MYL7, DST, I  | 57         | 160      | 16021     | 5.27006579   | 1          | 0.96906905 | 77.1194481 |
| UP_SEQ_FEATURE        | domain:EF-hand 1                         | 3     | 5           | 0.10883214 | MYL7, DST, I  | 57         | 161      | 16021     | 5.23733246   | 1          | 0.95601072 | 77.4881524 |
| INTERPRO              | IPR018247:EF-HAND 1                      | 3     | 5           | 0.14702087 | MYL7, DST, I  | 58         | 211      | 17763     | 4.35438797   | 1          | 0.98704861 | 85.4597038 |
| SP_PIR_KEYWORDS       | calcium                                  | 4     | 6.66666667  | 0.43679311 | MYL7, DST, I  | 60         | 731      | 17854     | 1.62827177   | 1          | 0.99352233 | 99.9009589 |
| GOTERM_MF_FAT         | GO:0005509~calcium ion binding           | 4     | 6.66666667  | 0.63382495 | MYL7, RYR2,   | 52         | 840      | 13288     | 1.21684982   | 1          | 0.99999226 | 99.9994879 |
| Annotation Cluster 9  |  |       |             |            |               |            |          |           |              |            |            |            |
| Category              | Term                                     | Count | %           | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0048878~chemical homeostasis          | 5     | 8.33333333  | 0.03448514 | EDNRB, HAN    | 47         | 365      | 13588     | 3.96036141   | 1          | 0.84156706 | 40.6530128 |
| GOTERM_BP_FAT         | GO:0042592~homeostatic process           | 6     | 10          | 0.04639888 | EDNRB, HAN    | 47         | 584      | 13588     | 2.97027106   | 1          | 0.88210267 | 50.6566978 |
| GOTERM_BP_FAT         | GO:0055080~cation homeostasis            | 3     | 5           | 0.12840666 | EDNRB, HAN    | 47         | 184      | 13588     | 4.71369103   | 1          | 0.98380365 | 87.0402488 |
| GOTERM_BP_FAT         | GO:0050801~ion homeostasis               | 3     | 5           | 0.26119664 | EDNRB, HAN    | 47         | 293      | 13588     | 2.96013361   | 1          | 0.99569949 | 98.890038  |
| Annotation Cluster 10 |  |       |             |            |               |            |          |           |              |            |            |            |
| Category              | Term                                     | Count | %           | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0005759~mitochondrial matrix          | 4     | 6.66666667  | 0.03017321 | ACADSB, HS    | 53         | 163      | 12504     | 5.78955898   | 0.98300482 | 0.3991159  | 30.1095369 |
| GOTERM_CC_FAT         | GO:0031980~mitochondrial lumen           | 4     | 6.66666667  | 0.03017321 | ACADSB, HS    | 53         | 163      | 12504     | 5.78955898   | 0.98300482 | 0.3991159  | 30.1095369 |
| SP_PIR_KEYWORDS       | mitochondrion                            | 7     | 11.66666667 | 0.04554059 | ISCA1, ACAC   | 60         | 790      | 17854     | 2.63666667   | 0.9993666  | 0.65078169 | 42.9705665 |
| SP_PIR_KEYWORDS       | transit peptide                          | 5     | 8.33333333  | 0.06415594 | ISCA1, ACAC   | 60         | 457      | 17854     | 3.25565281   | 0.99997181 | 0.73005897 | 55.0186149 |
| UP_SEQ_FEATURE        | transit peptide:Mitochondrion            | 5     | 8.33333333  | 0.07157763 | ISCA1, ACAC   | 57         | 449      | 16021     | 3.12995741   | 0.99999999 | 0.97333234 | 61.7539925 |
| GOTERM_MF_FAT         | GO:0050662~coenzyme binding              | 3     | 5           | 0.12552079 | ACADSB, IDH   | 52         | 160      | 13288     | 4.79134615   | 1          | 0.99590995 | 80.3362545 |
| GOTERM_CC_FAT         | GO:0044429~mitochondrial part            | 5     | 8.33333333  | 0.17270869 | ACADSB, IDH   | 53         | 524      | 12504     | 2.25118825   | 1          | 0.75363016 | 89.1057256 |
| GOTERM_CC_FAT         | GO:0005739~mitochondrion                 | 9     | 15          | 0.17910495 | WNT2, ISCA:   | 53         | 1322     | 12504     | 1.60614278   | 1          | 0.74880356 | 90.0508953 |
| GOTERM_MF_FAT         | GO:0048037~cofactor binding              | 3     | 5           | 0.21508013 | ACADSB, IDH   | 52         | 226      | 13288     | 3.39210347   | 1          | 0.99964497 | 94.6951464 |
| GOTERM_BP_FAT         | GO:0055114~oxidation reduction           | 4     | 6.66666667  | 0.39923859 | ACADSB, IDH   | 47         | 672      | 13588     | 1.72087133   | 1          | 0.99967299 | 99.9487402 |
| Annotation Cluster 11 |  |       |             |            |               |            |          |           |              |            |            |            |
| Category              | Term                                     | Count | %           | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0006952~defense response              | 6     | 10          | 0.01719775 | HAMP2, RAF    | 47         | 448      | 13588     | 3.87196049   | 0.99998207 | 0.83821247 | 22.7341077 |
| GOTERM_BP_FAT         | GO:0006954~inflammatory response         | 3     | 5           | 0.17663559 | REG3G, CCL5   | 47         | 225      | 13588     | 3.85475177   | 1          | 0.9892729  | 94.4404871 |
| GOTERM_BP_FAT         | GO:0009611~response to wounding          | 3     | 5           | 0.32911525 | REG3G, CCL5   | 47         | 347      | 13588     | 2.49947882   | 1          | 0.99866339 | 99.7353761 |
| Annotation Cluster 12 |  |       |             |            |               |            |          |           |              |            |            |            |
| Category              | Term                                     | Count | %           | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0007018~microtubule-based movement    | 4     | 6.66666667  | 0.00479966 | KIF1C, KIF1B, | 47         | 101      | 13588     | 11.4497577   | 0.95173575 | 0.78030874 | 6.90338342 |
| GOTERM_BP_FAT         | GO:0007017~microtubule-based process     | 5     | 8.33333333  | 0.00553879 | WNT2, KIF1C   | 47         | 211      | 13588     | 6.85086216   | 0.96977656 | 0.58304807 | 7.9261075  |

|                 |  |   |             |            |               |    |      |       |            |   |            |            |
|-----------------|--|---|-------------|------------|---------------|----|------|-------|------------|---|------------|------------|
| SP_PIR_KEYWORDS | microtubule                              | 3 | 5           | 0.16564301 | KIF1C, KIF1B, | 60 | 221  | 17854 | 4.03936652 | 1 | 0.88930622 | 88.7182991 |
| GOTERM_CC_FAT   | GO:0005874~microtubule                   | 3 | 5           | 0.26349973 | KIF1C, KIF1B, | 53 | 240  | 12504 | 2.9490566  | 1 | 0.79081124 | 97.2017808 |
| GOTERM_CC_FAT   | GO:0015630~microtubule cytoskeleton      | 4 | 6.66666667  | 0.28779733 | KIF1C, KIF1B, | 53 | 450  | 12504 | 2.09710692 | 1 | 0.81209591 | 98.1097209 |
| SP_PIR_KEYWORDS | nucleotide-binding                       | 7 | 11.66666667 | 0.45537049 | KIF1C, KIF1B, | 60 | 1631 | 17854 | 1.27711016 | 1 | 0.99361041 | 99.9338848 |
| GOTERM_MF_FAT   | GO:0032555~purine ribonucleotide binding | 7 | 11.66666667 | 0.70407402 | KIF1C, KIF1B, | 52 | 1796 | 13288 | 0.99597396 | 1 | 0.9999848  | 99.9999613 |
| GOTERM_MF_FAT   | GO:0032553~ribonucleotide binding        | 7 | 11.66666667 | 0.70407402 | KIF1C, KIF1B, | 52 | 1796 | 13288 | 0.99597396 | 1 | 0.9999848  | 99.9999613 |

#### Annotation Cluster 13 Enrichment Score: 0.8803492561843432

| Category        | Term                                      | Count | %           | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|---|-------|-------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_CC_FAT   | GO:0044421~extracellular region part      | 8     | 13.33333333 | 0.0400081  | WNT2, OGN, | 53         | 774      | 12504     | 2.43849642   | 0.99561887 | 0.41902341 | 37.9618966 |
| GOTERM_CC_FAT   | GO:0031012~extracellular matrix           | 4     | 6.66666667  | 0.13702907 | WNT2, OGN, | 53         | 309      | 12504     | 3.0540392    | 1          | 0.72929308 | 82.1508675 |
| SP_PIR_KEYWORDS | extracellular matrix                      | 3     | 5           | 0.15634825 | WNT2, OGN, | 60         | 213      | 17854     | 4.19107981   | 1          | 0.89338566 | 87.1072473 |
| GOTERM_CC_FAT   | GO:0005578~proteinaceous extracellular ma | 3     | 5           | 0.35119578 | WNT2, OGN, | 53         | 297      | 12504     | 2.38307604   | 1          | 0.87190272 | 99.3645433 |

#### Annotation Cluster 14 Enrichment Score: 0.8690204092887235

| Category      | Term                                  | Count | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|---------------------------------------|-------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0007017~microtubule-based process  | 5     | 8.33333333 | 0.00553879 | WNT2, KIF1C | 47         | 211      | 13588     | 6.85086216   | 0.96977656 | 0.58304807 | 7.9261075  |
| GOTERM_CC_FAT | GO:0016023~cytoplasmic membrane-bound | 4     | 6.66666667 | 0.24705696 | WNT2, KIF1E | 53         | 414      | 12504     | 2.27946404   | 1          | 0.79248152 | 96.3775173 |
| GOTERM_CC_FAT | GO:0031988~membrane-bounded vesicle   | 4     | 6.66666667 | 0.2537841  | WNT2, KIF1E | 53         | 420      | 12504     | 2.24690027   | 1          | 0.78931232 | 96.7383883 |
| GOTERM_CC_FAT | GO:0031410~cytoplasmic vesicle        | 4     | 6.66666667 | 0.35441188 | WNT2, KIF1E | 53         | 508      | 12504     | 1.85767345   | 1          | 0.8655946  | 99.4004143 |
| GOTERM_CC_FAT | GO:0031982~vesicle                    | 4     | 6.66666667 | 0.36703989 | WNT2, KIF1E | 53         | 519      | 12504     | 1.8183008    | 1          | 0.8594469  | 99.524077  |

#### Annotation Cluster 15 Enrichment Score: 0.7498262226370075

| Category      | Term                                      | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|---|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0007409~axonogenesis                   | 3     | 5          | 0.1051855  | ALCAM, NKX | 47         | 163      | 13588     | 5.32097637   | 1          | 0.9874256  | 80.8409405 |
| GOTERM_BP_FAT | GO:0032989~cellular component morphoge    | 4     | 6.66666667 | 0.11535472 | ALCAM, NKX | 47         | 351      | 13588     | 3.29465964   | 1          | 0.98935053 | 83.8351197 |
| GOTERM_BP_FAT | GO:0048812~neuron projection morphogen    | 3     | 5          | 0.1194182  | ALCAM, NKX | 47         | 176      | 13588     | 4.92794971   | 1          | 0.98833353 | 84.9045945 |
| GOTERM_BP_FAT | GO:0048667~cell morphogenesis involved in | 3     | 5          | 0.12614426 | ALCAM, NKX | 47         | 182      | 13588     | 4.76548983   | 1          | 0.98856424 | 86.5309969 |
| GOTERM_BP_FAT | GO:0048858~cell projection morphogenesis  | 3     | 5          | 0.1491825  | ALCAM, NKX | 47         | 202      | 13588     | 4.29365915   | 1          | 0.98560519 | 90.9464476 |
| GOTERM_BP_FAT | GO:0000904~cell morphogenesis involved in | 3     | 5          | 0.1610091  | ALCAM, NKX | 47         | 212      | 13588     | 4.09112806   | 1          | 0.98801377 | 92.6475008 |
| GOTERM_BP_FAT | GO:0032990~cell part morphogenesis        | 3     | 5          | 0.1610091  | ALCAM, NKX | 47         | 212      | 13588     | 4.09112806   | 1          | 0.98801377 | 92.6475008 |
| GOTERM_BP_FAT | GO:0031175~neuron projection developmer   | 3     | 5          | 0.16818865 | ALCAM, NKX | 47         | 218      | 13588     | 3.97852821   | 1          | 0.98846174 | 93.5294356 |
| GOTERM_BP_FAT | GO:0048666~neuron development             | 3     | 5          | 0.25993578 | ALCAM, NKX | 47         | 292      | 13588     | 2.97027106   | 1          | 0.99621872 | 98.8615382 |
| GOTERM_BP_FAT | GO:0000902~cell morphogenesis             | 3     | 5          | 0.28137824 | ALCAM, NKX | 47         | 309      | 13588     | 2.80685809   | 1          | 0.99691854 | 99.2646901 |
| GOTERM_BP_FAT | GO:0030030~cell projection organization   | 3     | 5          | 0.29398274 | ALCAM, NKX | 47         | 319      | 13588     | 2.71886881   | 1          | 0.99733453 | 99.4347894 |
| GOTERM_BP_FAT | GO:0030182~neuron differentiation         | 3     | 5          | 0.39306305 | ALCAM, NKX | 47         | 399      | 13588     | 2.1737322    | 1          | 0.999686   | 99.9403221 |

#### Annotation Cluster 16 Enrichment Score: 0.702550472140257

| Category      | Term                            | Count | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|---------------|---------------------------------|-------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT | GO:0006928~cell motion          | 4     | 6.66666667 | 0.12719797 | WNT2, ALCA | 47         | 367      | 13588     | 3.15102325   | 1          | 0.98623279 | 86.7704583 |
| GOTERM_BP_FAT | GO:0016477~cell migration       | 3     | 5          | 0.19495766 | WNT2, EDNF | 47         | 240      | 13588     | 3.61382979   | 1          | 0.99100517 | 96.021422  |
| GOTERM_BP_FAT | GO:0048870~cell motility        | 3     | 5          | 0.24985545 | WNT2, EDNF | 47         | 284      | 13588     | 3.05394067   | 1          | 0.9965173  | 98.6078845 |
| GOTERM_BP_FAT | GO:0051674~localization of cell | 3     | 5          | 0.24985545 | WNT2, EDNF | 47         | 284      | 13588     | 3.05394067   | 1          | 0.9965173  | 98.6078845 |

#### Annotation Cluster 17 Enrichment Score: 0.6196064912791557

| Category        | Term                                    | Count | %           | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|---|-------|-------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_MF_FAT   | GO:0003774~motor activity               | 5     | 8.33333333  | 0.00190679 | KIF1C, MYL7,  | 52         | 138      | 13288     | 9.25863991   | 0.26875901 | 0.26875901 | 2.28776711 |
| SP_PIR_KEYWORDS | motor protein                           | 4     | 6.66666667  | 0.00783454 | KIF1C, MYL7,  | 60         | 123      | 17854     | 9.67696477   | 0.71140532 | 0.26705383 | 9.04174997 |
| GOTERM_CC_FAT   | GO:0044430~cytoskeletal part            | 8     | 13.33333333 | 0.0400081  | KIF1C, MYL7,  | 53         | 774      | 12504     | 2.43849642   | 0.99561887 | 0.41902341 | 37.9618966 |
| GOTERM_MF_FAT   | GO:0030554~adenyl nucleotide binding    | 8     | 13.33333333 | 0.37487794 | KIF1C, ACAD   | 52         | 1535     | 13288     | 1.33179654   | 1          | 0.99998341 | 99.664331  |
| GOTERM_MF_FAT   | GO:0001883~purine nucleoside binding    | 8     | 13.33333333 | 0.38340215 | KIF1C, ACAD   | 52         | 1548     | 13288     | 1.3206122    | 1          | 0.99964022 | 99.715811  |
| GOTERM_MF_FAT   | GO:0001882~nucleoside binding           | 8     | 13.33333333 | 0.38996916 | KIF1C, ACAD   | 52         | 1558     | 13288     | 1.31213587   | 1          | 0.99936935 | 99.7504142 |
| SP_PIR_KEYWORDS | atp-binding                             | 6     | 10          | 0.4223064  | KIF1C, KIF1B, | 60         | 1287     | 17854     | 1.38725719   | 1          | 0.99556633 | 99.8655037 |
| GOTERM_MF_FAT   | GO:0017076~purine nucleotide binding    | 9     | 15          | 0.4300881  | KIF1C, ACAD   | 52         | 1871     | 13288     | 1.22920692   | 1          | 0.99954006 | 99.8906108 |
| SP_PIR_KEYWORDS | nucleotide-binding                      | 7     | 11.66666667 | 0.45537049 | KIF1C, KIF1B, | 60         | 1631     | 17854     | 1.27711016   | 1          | 0.99361041 | 99.9338848 |
| GOTERM_MF_FAT   | GO:000166~nucleotide binding            | 10    | 16.66666667 | 0.46474582 | KIF1C, ACAD   | 52         | 2183     | 13288     | 1.17058388   | 1          | 0.99962357 | 99.9488819 |
| UP_SEQ_FEATURE  | nucleotide phosphate-binding region:ATP | 4     | 6.66666667  | 0.62149975 | KIF1C, KIF1B, | 57         | 907      | 16021     | 1.23955976   | 1          | 1          | 99.9996536 |

|                 |   |   |            |            |               |    |      |       |            |   |            |            |
|-----------------|---|---|------------|------------|---------------|----|------|-------|------------|---|------------|------------|
| GOTERM_MF_FAT   | GO:0005524 ~ATP binding                   | 6 | 10         | 0.66256152 | KIF1C, KIF1B, | 52 | 1443 | 13288 | 1.06252999 | 1 | 0.99999306 | 99.9998099 |
| GOTERM_MF_FAT   | GO:0032559 ~adenyl ribonucleotide binding | 6 | 10         | 0.67302957 | KIF1C, KIF1B, | 52 | 1460 | 13288 | 1.05015806 | 1 | 0.99998944 | 99.9998703 |
| SP_PIR_KEYWORDS | coiled coil                               | 6 | 10         | 0.6895304  | KIF1C, BCAS.  | 60 | 1732 | 17854 | 1.03083141 | 1 | 0.99967611 | 99.9999243 |
| GOTERM_MF_FAT   | GO:0032555 ~purine ribonucleotide binding | 7 | 11.6666667 | 0.70407402 | KIF1C, KIF1B, | 52 | 1796 | 13288 | 0.99597396 | 1 | 0.9999848  | 99.9999613 |
| GOTERM_MF_FAT   | GO:0032553 ~ribonucleotide binding        | 7 | 11.6666667 | 0.70407402 | KIF1C, KIF1B, | 52 | 1796 | 13288 | 0.99597396 | 1 | 0.9999848  | 99.9999613 |

|                       |                                    |                                     |   |            |            |            |          |           |              |            |            |            |
|-----------------------|------------------------------------|-------------------------------------|---|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 18 |                                    | Enrichment Score: 0.608805987421836 |   |            |            |            |          |           |              |            |            |            |
| Category              | Term                               | Count                               | % | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| UP_SEQ_FEATURE        | domainIg-like C2-type 1            | 3                                   | 5 | 0.075781   | ALCAM, FCR | 57         | 130      | 16021     | 6.48623482   | 1          | 0.95943244 | 63.935273  |
| UP_SEQ_FEATURE        | domainIg-like C2-type 2            | 3                                   | 5 | 0.07678841 | ALCAM, FCR | 57         | 131      | 16021     | 6.43672157   | 1          | 0.93826938 | 64.4407092 |
| SP_PIR_KEYWORDS       | Immunoglobulin domain              | 3                                   | 5 | 0.4322509  | ALCAM, FCR | 60         | 443      | 17854     | 2.01512415   | 1          | 0.99481079 | 99.8908941 |
| INTERPRO              | IPR007110:Immunoglobulin-like      | 3                                   | 5 | 0.5819461  | ALCAM, FCR | 58         | 604      | 17763     | 1.52115209   | 1          | 1          | 99.9974465 |
| INTERPRO              | IPR013783:Immunoglobulin-like fold | 3                                   | 5 | 0.6172987  | ALCAM, FCR | 58         | 644      | 17763     | 1.42667059   | 1          | 1          | 99.9991253 |

|                       |                                 |                                      |            |            |            |            |          |           |              |            |            |            |
|-----------------------|---------------------------------|--------------------------------------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 19 |                                 | Enrichment Score: 0.5379238773457455 |            |            |            |            |          |           |              |            |            |            |
| Category              | Term                            | Count                                | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0030054 ~cell junction       | 5                                    | 8.33333333 | 0.13079304 | WNT2, CGN, | 53         | 470      | 12504     | 2.50983541   | 0.99999999 | 0.73595961 | 80.5830612 |
| GOTERM_CC_FAT         | GO:004459 ~plasma membrane part | 10                                   | 16.6666667 | 0.23251466 | WNT2, ALCA | 53         | 1633     | 12504     | 1.44473073   | 1          | 0.81288416 | 95.4694648 |
| GOTERM_CC_FAT         | GO:0005886 ~plasma membrane     | 11                                   | 18.3333333 | 0.8001905  | WNT2, ALCA | 53         | 2906     | 12504     | 0.89303848   | 1          | 0.9952734  | 99.9999993 |

|                       |                                |                                     |            |            |            |            |          |           |              |            |            |            |
|-----------------------|--------------------------------|-------------------------------------|------------|------------|------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 20 |                                | Enrichment Score: 0.500080412526188 |            |            |            |            |          |           |              |            |            |            |
| Category              | Term                           | Count                               | %          | PValue     | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_CC_FAT         | GO:0000267 ~cell fraction      | 5                                   | 8.33333333 | 0.23480187 | WNT2, PGRN | 53         | 596      | 12504     | 1.97923262   | 1          | 0.8016828  | 95.6248447 |
| GOTERM_CC_FAT         | GO:0005624 ~membrane fraction  | 4                                   | 6.66666667 | 0.35670978 | WNT2, PGRN | 53         | 510      | 12504     | 1.85038846   | 1          | 0.85854961 | 99.424899  |
| GOTERM_CC_FAT         | GO:0005626 ~insoluble fraction | 4                                   | 6.66666667 | 0.37734812 | WNT2, PGRN | 53         | 528      | 12504     | 1.78730703   | 1          | 0.86041716 | 99.6072149 |

|                       |  |                                      |   |            |           |            |          |           |              |            |            |            |
|-----------------------|--|--------------------------------------|---|------------|-----------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 21 |  | Enrichment Score: 0.4636856487157493 |   |            |           |            |          |           |              |            |            |            |
| Category              | Term                                     | Count                                | % | PValue     | Genes     | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_BP_FAT         | GO:0001701 ~in utero embryonic developme | 3                                    | 5 | 0.22850268 | WNT2, MYH | 47         | 267      | 13588     | 3.24838633   | 1          | 0.99569451 | 97.8869673 |
| GOTERM_BP_FAT         | GO:0043009 ~chordate embryonic developm  | 3                                    | 5 | 0.41936593 | WNT2, MYH | 47         | 421      | 13588     | 2.0601405    | 1          | 0.99965255 | 99.9691155 |
| GOTERM_BP_FAT         | GO:0009792 ~embryonic development endin  | 3                                    | 5 | 0.42409056 | WNT2, MYH | 47         | 425      | 13588     | 2.04075094   | 1          | 0.99962957 | 99.9726483 |

|                       |  |                                       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|--|---------------------------------------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 22 |  | Enrichment Score: 0.11773862909639404 |            |            |             |            |          |           |              |            |            |            |
| Category              | Term                                     | Count                                 | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| GOTERM_MF_FAT         | GO:0043167 ~ion binding                  | 15                                    | 25         | 0.68248984 | MYL7, MAT2  | 52         | 3934     | 13288     | 0.97434594   | 1          | 0.99998439 | 99.9999091 |
| GOTERM_MF_FAT         | GO:0046872 ~metal ion binding            | 14                                    | 23.3333333 | 0.75565794 | MYL7, MAT2  | 52         | 3850     | 13288     | 0.92923077   | 1          | 0.99999478 | 99.9999962 |
| GOTERM_MF_FAT         | GO:0043169 ~cation binding               | 14                                    | 23.3333333 | 0.76835438 | MYL7, MAT2  | 52         | 3885     | 13288     | 0.92085932   | 1          | 0.99999381 | 99.999998  |
| SP_PIR_KEYWORDS       | metal-binding                            | 8                                     | 13.3333333 | 0.80288238 | ISCA1, MAT2 | 60         | 2682     | 17854     | 0.88759632   | 1          | 0.99996511 | 99.9999997 |
| GOTERM_MF_FAT         | GO:0046914 ~transition metal ion binding | 9                                     | 15         | 0.81034866 | ISCA1, MAT2 | 52         | 2608     | 13288     | 0.88184285   | 1          | 0.9999977  | 99.9999998 |

|                       |   |                                       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|---|---------------------------------------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 23 |   | Enrichment Score: 0.09156628758122415 |            |            |             |            |          |           |              |            |            |            |
| Category              | Term                                    | Count                                 | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| SP_PIR_KEYWORDS       | activator                               | 3                                     | 5          | 0.47785241 | MDFIC, NKX. | 60         | 484      | 17854     | 1.84442149   | 1          | 0.99410387 | 99.9602158 |
| SP_PIR_KEYWORDS       | Transcription                           | 5                                     | 8.33333333 | 0.84897417 | POLR2G, MC  | 60         | 1769     | 17854     | 0.84105898   | 1          | 0.99998974 | 100        |
| GOTERM_BP_FAT         | GO:0006350 ~transcription               | 5                                     | 8.33333333 | 0.86730299 | POLR2G, MC  | 47         | 1772     | 13588     | 0.81576293   | 1          | 1          | 100        |
| SP_PIR_KEYWORDS       | transcription regulation                | 4                                     | 6.66666667 | 0.89541558 | MDFIC, NKX. | 60         | 1546     | 17854     | 0.76990082   | 1          | 0.99999817 | 100        |
| SP_PIR_KEYWORDS       | nucleus                                 | 10                                    | 16.6666667 | 0.90771261 | BCAS2, POLI | 60         | 3808     | 17854     | 0.78142507   | 1          | 0.99999645 | 100        |
| GOTERM_BP_FAT         | GO:0045449 ~regulation of transcription | 4                                     | 6.66666667 | 0.98689322 | MDFIC, NKX. | 47         | 2227     | 13588     | 0.51927505   | 1          | 1          | 100        |

|                       |                                  |                                       |            |            |             |            |          |           |              |            |            |            |
|-----------------------|----------------------------------|---------------------------------------|------------|------------|-------------|------------|----------|-----------|--------------|------------|------------|------------|
| Annotation Cluster 24 |                                  | Enrichment Score: 0.03132099349081887 |            |            |             |            |          |           |              |            |            |            |
| Category              | Term                             | Count                                 | %          | PValue     | Genes       | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
| UP_SEQ_FEATURE        | topological domain:Extracellular | 7                                     | 11.6666667 | 0.78958664 | ALCAM, EDN  | 57         | 2174     | 16021     | 0.90500976   | 1          | 1          | 99.9999998 |
| UP_SEQ_FEATURE        | topological domain:Cytoplasmic   | 8                                     | 13.3333333 | 0.87553424 | ALCAM, EDN  | 57         | 2780     | 16021     | 0.80883504   | 1          | 1          | 100        |
| UP_SEQ_FEATURE        | transmembrane region             | 11                                    | 18.3333333 | 0.93737637 | ALCAM, EDN  | 57         | 4113     | 16021     | 0.75170725   | 1          | 1          | 100        |
| SP_PIR_KEYWORDS       | transmembrane                    | 13                                    | 21.6666667 | 0.95609892 | TSPAN8, NP  | 60         | 5237     | 17854     | 0.73866081   | 1          | 0.9999998  | 100        |
| SP_PIR_KEYWORDS       | membrane                         | 13                                    | 21.6666667 | 0.97451984 | TANC1, TSP/ | 60         | 5507     | 17854     | 0.70244537   | 1          | 0.99999998 | 100        |
| GOTERM_CC_FAT         | GO:0016021 ~integral to membrane | 13                                    | 21.6666667 | 0.99979168 | TSPAN8, NP  | 53         | 5709     | 12504     | 0.53722524   | 1          | 1          | 100        |

|               |                                  |    |            |            |            |    |      |       |            |   |   |     |
|---------------|----------------------------------|----|------------|------------|------------|----|------|-------|------------|---|---|-----|
| GOTERM_CC_FAT | GO:0031224~intrinsic to membrane | 13 | 21.6666667 | 0.99991502 | TSPAN8, NP | 53 | 5914 | 12504 | 0.51860312 | 1 | 1 | 100 |
|---------------|----------------------------------|----|------------|------------|------------|----|------|-------|------------|---|---|-----|

| Category        | Term                                       | Count | %          | PValue     | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichm | Bonferroni | Benjamini  | FDR        |
|-----------------|--|-------|------------|------------|---------------|------------|----------|-----------|--------------|------------|------------|------------|
| GOTERM_BP_FAT   | GO:0003013~circulatory system process      | 5     | 8.33333333 | 5.28E-04   | WNT2, EDNF    | 47         | 111      | 13588     | 13.02281     | 0.28323867 | 0.28323867 | 0.78282059 |
| GOTERM_BP_FAT   | GO:0008015~blood circulation               | 5     | 8.33333333 | 5.28E-04   | WNT2, EDNF    | 47         | 111      | 13588     | 13.02281     | 0.28323867 | 0.28323867 | 0.78282059 |
| SP_PIR_KEYWORDS | Secreted                                   | 14    | 23.3333333 | 6.14E-04   | HAMP2, RAF    | 60         | 1420     | 17854     | 2.93375587   | 0.0924119  | 0.0924119  | 0.73671606 |
| UP_SEQ_FEATURE  | compositionally biased region:Cys-rich     | 5     | 8.33333333 | 0.00122732 | OGN, MDFIC    | 57         | 134      | 16021     | 10.4876931   | 0.25892303 | 0.25892303 | 1.57672845 |
| GOTERM_MF_FAT   | GO:0003774~motor activity                  | 5     | 8.33333333 | 0.00190679 | KIF1C, MYL7   | 52         | 138      | 13288     | 9.25863991   | 0.26875901 | 0.26875901 | 2.28776711 |
| SP_PIR_KEYWORDS | signal                                     | 20    | 33.3333333 | 0.00243589 | HAMP2, RAF    | 60         | 2970     | 17854     | 2.00381594   | 0.31978106 | 0.17524613 | 2.89581465 |
| UP_SEQ_FEATURE  | signal peptide                             | 20    | 33.3333333 | 0.00428574 | HAMP2, RAF    | 57         | 2963     | 16021     | 1.89719997   | 0.64935026 | 0.40784315 | 5.40657455 |
| GOTERM_BP_FAT   | GO:0007018~microtubule-based movement      | 4     | 6.66666667 | 0.00479966 | KIF1C, KIF1B, | 47         | 101      | 13588     | 11.4497577   | 0.95173575 | 0.78030874 | 6.90338342 |
| GOTERM_MF_FAT   | GO:0008092~cytoskeletal protein binding    | 7     | 11.6666667 | 4.86E-03   | KIF1B, CGN,   | 52         | 414      | 13288     | 4.32069863   | 0.54991363 | 0.32911523 | 5.73174513 |
| SP_PIR_KEYWORDS | disulfide bond                             | 17    | 28.3333333 | 0.0052566  | HAMP2, LYZ    | 60         | 2469     | 17854     | 2.04885919   | 0.56514105 | 0.24238342 | 6.15291428 |
| GOTERM_BP_FAT   | GO:0030705~cytoskeleton-dependent intrac   | 3     | 5          | 0.00553759 | KIF1B, MYH6   | 47         | 33       | 13588     | 26.2823985   | 0.9697535  | 0.68842804 | 7.92445069 |
| GOTERM_BP_FAT   | GO:0007017~microtubule-based process       | 5     | 8.33333333 | 0.00553879 | WNT2, KIF1C   | 47         | 211      | 13588     | 6.85086216   | 0.96977656 | 0.58304807 | 7.9261075  |
| UP_SEQ_FEATURE  | disulfide bond                             | 17    | 28.3333333 | 0.00608461 | HAMP2, LYZ    | 57         | 2379     | 16021     | 2.00848801   | 0.77444253 | 0.3912779  | 7.59446489 |
| GOTERM_CC_FAT   | GO:0005576~extracellular region            | 15    | 25         | 0.00723341 | HAMP2, RAF    | 53         | 1680     | 12504     | 2.106469     | 0.61922262 | 0.61922262 | 8.1383109  |
| SP_PIR_KEYWORDS | motor protein                              | 4     | 6.66666667 | 0.00783454 | KIF1C, MYL7   | 60         | 123      | 17854     | 9.67696477   | 0.71140532 | 0.26705383 | 9.04174997 |
| PIR_SUPERFAMILY | PIRSF002322:kinesin-related protein KIF1B  | 2     | 3.33333333 | 0.00883052 | KIF1C, KIF1B  | 37         | 2        | 8136      | 219.891892   | 0.31709453 | 0.31709453 | 7.92269091 |
| SMART           | SM00054:EFh                                | 4     | 6.66666667 | 0.00907808 | MYL7, RYR2,   | 30         | 137      | 9131      | 8.886618     | 0.31820101 | 0.31820101 | 8.09374733 |
| INTERPRO        | IPR002048:Calcium-binding EF-hand          | 4     | 6.66666667 | 0.00969445 | MYL7, RYR2,   | 58         | 137      | 17763     | 8.94185754   | 0.79762771 | 0.79762771 | 11.1416279 |
| SP_PIR_KEYWORDS | stress response                            | 3     | 5          | 0.00970208 | IDH2, HSPA1   | 60         | 45       | 17854     | 19.8377778   | 0.78570745 | 0.2651454  | 11.0833217 |
| GOTERM_CC_FAT   | GO:0015629~actin cytoskeleton              | 5     | 8.33333333 | 0.01028202 | MYL7, CGN,    | 53         | 205      | 12504     | 5.75425679   | 0.74705619 | 0.4970648  | 11.3831177 |
| GOTERM_BP_FAT   | GO:0046907~intracellular transport         | 6     | 10         | 0.01477415 | KIF1C, NPC1,  | 47         | 431      | 13588     | 4.02468283   | 0.99991536 | 0.84671117 | 19.852261  |
| GOTERM_CC_FAT   | GO:0070013~intracellular organelle lumen   | 11    | 18.3333333 | 0.01688201 | BCAS2, POLF   | 53         | 1133     | 12504     | 2.2905294    | 0.89611562 | 0.52990739 | 18.0518094 |
| GOTERM_CC_FAT   | GO:0043233~organelle lumen                 | 11    | 18.3333333 | 0.01717109 | BCAS2, POLF   | 53         | 1136     | 12504     | 2.28448047   | 0.90010034 | 0.43779979 | 18.333111  |
| GOTERM_BP_FAT   | GO:0006952~defense response                | 6     | 10         | 0.01719775 | HAMP2, RAF    | 47         | 448      | 13588     | 3.87196409   | 0.99998207 | 0.83821247 | 22.7341077 |
| GOTERM_BP_FAT   | GO:0009725~response to hormone stimulus    | 4     | 6.66666667 | 0.01822353 | WNT2, MAT:    | 47         | 165      | 13588     | 7.00863959   | 0.99999071 | 0.80895505 | 23.9244899 |
| SMART           | SM00033:CH                                 | 3     | 5          | 0.0194921  | LMO7, DST,    | 30         | 68       | 9131      | 13.4279412   | 0.56253215 | 0.33858648 | 16.654901  |
| INTERPRO        | IPR001715:Calponin-like actin-binding      | 3     | 5          | 0.02012781 | LMO7, DST,    | 58         | 68       | 17763     | 13.5114097   | 0.96437236 | 0.81124715 | 21.8511922 |
| GOTERM_BP_FAT   | GO:0008217~regulation of blood pressure    | 3     | 5          | 0.02037131 | EDNRB, MYH    | 47         | 65       | 13588     | 13.3433715   | 0.99999766 | 0.80226073 | 26.3616961 |
| GOTERM_CC_FAT   | GO:0031974~membrane-enclosed lumen         | 11    | 18.3333333 | 0.02116331 | BCAS2, POLF   | 53         | 1174     | 12504     | 2.21053647   | 0.94186172 | 0.43390094 | 22.1287983 |
| GOTERM_CC_FAT   | GO:0043228~non-membrane-bounded orga       | 15    | 25         | 0.02209217 | BCAS2, MYL    | 53         | 1919     | 12504     | 1.84412086   | 0.94875827 | 0.3905511  | 22.9884747 |
| GOTERM_CC_FAT   | GO:0043232~intracellular non-membrane-bi   | 15    | 25         | 0.02209217 | BCAS2, MYL    | 53         | 1919     | 12504     | 1.84412086   | 0.94875827 | 0.3905511  | 22.9884747 |
| GOTERM_BP_FAT   | GO:0009719~response to endogenous stimuli  | 4     | 6.66666667 | 0.02422237 | WNT2, MAT:    | 47         | 184      | 13588     | 6.28492137   | 0.9999998  | 0.820295   | 30.5503148 |
| GOTERM_MF_FAT   | GO:0003779~actin binding                   | 5     | 8.33333333 | 0.02433648 | CGN, MYH6,    | 52         | 288      | 13288     | 4.43643162   | 0.98241223 | 0.73994199 | 25.8254731 |
| GOTERM_CC_FAT   | GO:0016459~myosin complex                  | 3     | 5          | 0.02655259 | MYL7, CGN,    | 53         | 61       | 12504     | 11.6028457   | 0.97210274 | 0.40029542 | 26.9970316 |
| GOTERM_BP_FAT   | GO:0080135~regulation of cellular response | 3     | 5          | 0.02660553 | NPC1, MDFIC   | 47         | 75       | 13588     | 11.5642553   | 0.99999996 | 0.81710621 | 33.029918  |
| GOTERM_BP_FAT   | GO:0010033~response to organic substance   | 6     | 10         | 0.02722486 | WNT2, MAT:    | 47         | 505      | 13588     | 3.43492732   | 0.99999997 | 0.79420209 | 33.6606531 |
| INTERPRO        | IPR018249:EF-HAND 2                        | 4     | 6.66666667 | 0.0281     | MYL7, RYR2,   | 58         | 205      | 17763     | 5.97577796   | 0.99066875 | 0.78947036 | 29.2214174 |
| UP_SEQ_FEATURE  | compositionally biased region:Poly-Pro     | 5     | 8.33333333 | 0.02972565 | NPC1, RIN2,   | 57         | 336      | 16021     | 4.1825919    | 0.99936573 | 0.84130337 | 32.3296387 |
| GOTERM_CC_FAT   | GO:0005759~mitochondrial matrix            | 4     | 6.66666667 | 0.03017321 | ACADSB, HS    | 53         | 163      | 12504     | 5.78955898   | 0.98300482 | 0.3991159  | 30.1095369 |
| GOTERM_CC_FAT   | GO:0031980~mitochondrial lumen             | 4     | 6.66666667 | 0.03017321 | ACADSB, HS    | 53         | 163      | 12504     | 5.78955898   | 0.98300482 | 0.3991159  | 30.1095369 |
| GOTERM_BP_FAT   | GO:0048878~chemical homeostasis            | 5     | 8.33333333 | 0.03448514 | EDNRB, HAN    | 47         | 365      | 13588     | 3.96036141   | 1          | 0.84156706 | 40.6530128 |
| INTERPRO        | IPR013126:Heat shock protein 70            | 2     | 3.33333333 | 0.03474679 | HSPA1A, HS    | 58         | 11       | 17763     | 55.6833856   | 0.99697193 | 0.76541976 | 34.8727117 |
| INTERPRO        | IPR001023:Heat shock protein Hsp70         | 2     | 3.33333333 | 0.03474679 | HSPA1A, HS    | 58         | 11       | 17763     | 55.6833856   | 0.99697193 | 0.76541976 | 34.8727117 |
| PIR_SUPERFAMILY | PIRSF002581:chaperone HSP70                | 2     | 3.33333333 | 0.03486962 | HSPA1A, HS    | 37         | 8        | 8136      | 54.972973    | 0.78263113 | 0.53377165 | 28.1283771 |
| INTERPRO        | IPR011992:EF-Hand type                     | 4     | 6.66666667 | 0.03638163 | MYL7, RYR2,   | 58         | 227      | 17763     | 5.39662768   | 0.99770686 | 0.70345797 | 36.1977256 |
| GOTERM_BP_FAT   | GO:0008088~axon cargo transport            | 2     | 3.33333333 | 0.03662802 | KIF1B, DST    | 47         | 11       | 13588     | 52.5647969   | 1          | 0.83607969 | 42.5814887 |
| SP_PIR_KEYWORDS | actin-binding                              | 4     | 6.66666667 | 0.03875632 | MYH6, PALLI   | 60         | 226      | 17854     | 5.26666667   | 0.99806049 | 0.64685851 | 37.889935  |
| GOTERM_CC_FAT   | GO:0005730~nucleolus                       | 5     | 8.33333333 | 0.03956687 | BCAS2, DNA    | 53         | 310      | 12504     | 3.80523433   | 0.99534276 | 0.44931505 | 37.6276632 |
| GOTERM_CC_FAT   | GO:0044430~cytoskeletal part               | 8     | 13.3333333 | 0.0400081  | KIF1C, MYL7,  | 53         | 774      | 12504     | 2.43849642   | 0.99561887 | 0.41902341 | 37.9618966 |
| GOTERM_CC_FAT   | GO:0044421~extracellular region part       | 8     | 13.3333333 | 0.0400081  | WNT2, OGN,    | 53         | 774      | 12504     | 2.43849642   | 0.99561887 | 0.41902341 | 37.9618966 |
| GOTERM_BP_FAT   | GO:0006790~sulfur metabolic process        | 3     | 5          | 0.04025137 | MAT2A, SEPI   | 47         | 94       | 13588     | 9.22679946   | 1          | 0.84256998 | 45.7099071 |
| INTERPRO        | IPR018181:Heat shock protein 70, conserved | 2     | 3.33333333 | 0.04093569 | HSPA1A, HS    | 58         | 13       | 17763     | 47.1167109   | 0.99894555 | 0.68096526 | 39.7593978 |
| INTERPRO        | IPR002928:Myosin tail                      | 2     | 3.33333333 | 0.0440155  | CGN, MYH6     | 58         | 14       | 17763     | 43.7512315   | 0.99937779 | 0.65166961 | 42.0636641 |
| SP_PIR_KEYWORDS | mitochondrion                              | 7     | 11.6666667 | 0.04554059 | ISCA1, ACAC   | 60         | 790      | 17854     | 2.63666667   | 0.9993666  | 0.65078169 | 42.9705665 |

|                 |   |   |            |            |              |    |      |       |            |            |            |            |
|-----------------|---|---|------------|------------|--------------|----|------|-------|------------|------------|------------|------------|
| GOTERM_BP_FAT   | GO:0042592~homeostatic process                      | 6 | 10         | 0.04639888 | EDNRB, HAN   | 47 | 584  | 13588 | 2.97027106 | 1          | 0.86404234 | 50.6566978 |
| GOTERM_BP_FAT   | GO:0016998~cell wall macromolecule catabolism       | 2 | 3.33333333 | 0.0528401  | LYZ1, OXR1   | 47 | 16   | 13588 | 36.1382979 | 1          | 0.88205826 | 55.3865889 |
| GOTERM_BP_FAT   | GO:0044036~cell wall macromolecule metabolism       | 2 | 3.33333333 | 0.0528401  | LYZ1, OXR1   | 47 | 16   | 13588 | 36.1382979 | 1          | 0.88205826 | 55.3865889 |
| GOTERM_BP_FAT   | GO:0010970~microtubule-based transport              | 2 | 3.33333333 | 0.05924993 | KIF1B, DST   | 47 | 18   | 13588 | 32.1229314 | 1          | 0.89601105 | 59.6708093 |
| GOTERM_MF_FAT   | GO:0016408~C-acyltransferase activity               | 2 | 3.33333333 | 0.05970513 | 1110002B05I  | 52 | 16   | 13288 | 31.9423077 | 0.99995876 | 0.91986416 | 52.5970283 |
| GOTERM_CC_FAT   | GO:0016324~apical plasma membrane                   | 3 | 5          | 0.0637382  | WNT2, LMO    | 53 | 99   | 12504 | 7.14922813 | 0.99984302 | 0.54900951 | 53.7027841 |
| SP_PIR_KEYWORDS | transit peptide                                     | 5 | 8.33333333 | 0.06415594 | ISCA1, ACAC  | 60 | 457  | 17854 | 3.25565281 | 0.99997181 | 0.73005897 | 55.0186149 |
| INTERPRO        | IPR018248:EF hand                                   | 3 | 5          | 0.06712339 | MYL7, DST, I | 58 | 132  | 17763 | 6.9604232  | 0.99998875 | 0.75934426 | 56.9379694 |
| UP_SEQ_FEATURE  | domain:CH 1   | 2 | 3.33333333 | 0.07093657 | DST, PLS3    | 57 | 21   | 16021 | 26.7685881 | 0.99999998 | 0.97241875 | 61.4108196 |
| UP_SEQ_FEATURE  | domain:CH 2   | 2 | 3.33333333 | 0.07093657 | DST, PLS3    | 57 | 21   | 16021 | 26.7685881 | 0.99999998 | 0.97241875 | 61.4108196 |
| UP_SEQ_FEATURE  | transit peptide:Mitochondrion                       | 5 | 8.33333333 | 0.07157763 | ISCA1, ACAC  | 57 | 449  | 16021 | 3.12995741 | 0.99999999 | 0.95121112 | 61.7539925 |
| GOTERM_BP_FAT   | GO:0030301~cholesterol transport                    | 2 | 3.33333333 | 0.07508943 | NPC1, NPC2   | 47 | 23   | 13588 | 25.1396855 | 1          | 0.9349135  | 68.6688472 |
| GOTERM_BP_FAT   | GO:0015918~sterol transport                         | 2 | 3.33333333 | 0.07508943 | NPC1, NPC2   | 47 | 23   | 13588 | 25.1396855 | 1          | 0.9349135  | 68.6688472 |
| GOTERM_BP_FAT   | GO:0031329~regulation of cellular catabolic process | 2 | 3.33333333 | 0.07508943 | NPC1, ADAM   | 47 | 23   | 13588 | 25.1396855 | 1          | 0.9349135  | 68.6688472 |
| UP_SEQ_FEATURE  | domainIg-like C2-type 1                             | 3 | 5          | 0.075781   | ALCAM, FCR   | 57 | 130  | 16021 | 6.48623482 | 1          | 0.9358775  | 63.935273  |
| UP_SEQ_FEATURE  | domainIg-like C2-type 2                             | 3 | 5          | 0.07678841 | ALCAM, FCR   | 57 | 131  | 16021 | 6.43672157 | 1          | 0.91256445 | 64.4407092 |
| INTERPRO        | IPR001589:Actinin-type, actin-binding, conserved    | 2 | 3.33333333 | 0.08022386 | DST, PLS3    | 58 | 26   | 17763 | 23.5583554 | 0.99999889 | 0.78212475 | 63.7241926 |
| GOTERM_BP_FAT   | GO:0055092~sterol homeostasis                       | 2 | 3.33333333 | 0.08446759 | NPC1, NPC2   | 47 | 26   | 13588 | 22.2389525 | 1          | 0.94639795 | 73.0740483 |
| GOTERM_BP_FAT   | GO:0042632~cholesterol homeostasis                  | 2 | 3.33333333 | 0.08446759 | NPC1, NPC2   | 47 | 26   | 13588 | 22.2389525 | 1          | 0.94639795 | 73.0740483 |
| UP_SEQ_FEATURE  | domain:FHA  | 2 | 3.33333333 | 0.08708377 | KIF1C, KIF1B | 57 | 26   | 16021 | 21.6207827 | 1          | 0.91542568 | 69.2443552 |
| KEGG_PATHWAY    | mmu03040:Spliceosome                                | 3 | 5          | 0.08729618 | BCAS2, HSP   | 24 | 124  | 5738  | 5.78427419 | 0.98753094 | 0.98753094 | 58.1779792 |
| SP_PIR_KEYWORDS | Chaperone   | 3 | 5          | 0.08799547 | DNAJB9, HSP  | 60 | 150  | 17854 | 5.95133333 | 0.99999952 | 0.80151623 | 67.0385327 |
| GOTERM_CC_FAT   | GO:0005856~cytoskeleton                             | 9 | 15         | 0.09049991 | KIF1C, MYL7  | 53 | 1122 | 12504 | 1.89244274 | 0.99999668 | 0.6505403  | 67.0170526 |
| GOTERM_BP_FAT   | GO:0031110~regulation of microtubule polymerization | 2 | 3.33333333 | 0.09066794 | WNT2, DST    | 47 | 28   | 13588 | 20.6504559 | 1          | 0.94990911 | 75.6615592 |
| SMART           | SM00240:FHA   | 2 | 3.33333333 | 0.09405357 | KIF1C, KIF1B | 30 | 31   | 9131  | 19.6365591 | 0.98421278 | 0.7491378  | 59.9147552 |
| INTERPRO        | IPR000253:Forkhead-associated                       | 2 | 3.33333333 | 0.09490988 | KIF1C, KIF1B | 58 | 31   | 17763 | 19.7586207 | 0.99999992 | 0.80512958 | 70.1562121 |
| GOTERM_BP_FAT   | GO:0006953~acute-phase response                     | 2 | 3.33333333 | 0.09682722 | REG3G, AHS   | 47 | 30   | 13588 | 19.2737589 | 1          | 0.95288868 | 78.0007457 |
| GOTERM_BP_FAT   | GO:0007010~cytoskeleton organization                | 4 | 6.66666667 | 0.09777695 | WNT2, MYH    | 47 | 326  | 13588 | 3.54731758 | 1          | 0.94747656 | 78.3421917 |