Table: Gene sets enriched in phenotype **negative correlation with profile**[**[plain text format]**](http://docs.google.com/gsea_report_for_triple_means_peak_neg_1620771247543.tsv)

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GS  follow link to MSigDB | GS DETAILS | SIZE | ES | NES | NOM p-val | FDR q-val | FWER p-val | RANK AT MAX | LEADING EDGE |
| 1 | [GOBP\_CANONICAL\_WNT\_SIGNALING\_PATHWAY](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_CANONICAL_WNT_SIGNALING_PATHWAY) | [Details ...](http://docs.google.com/GOBP_CANONICAL_WNT_SIGNALING_PATHWAY.html) | 41 | -0.59 | -2.18 | 0.000 | 0.007 | 0.007 | 339 | tags=59%, list=22%, signal=73% |
| 2 | [GOBP\_EYE\_MORPHOGENESIS](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_EYE_MORPHOGENESIS) | [Details ...](http://docs.google.com/GOBP_EYE_MORPHOGENESIS.html) | 21 | -0.66 | -2.11 | 0.000 | 0.007 | 0.015 | 188 | tags=52%, list=12%, signal=59% |
| 3 | [GOBP\_REGULATION\_OF\_WNT\_SIGNALING\_PATHWAY](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_REGULATION_OF_WNT_SIGNALING_PATHWAY) | [Details ...](http://docs.google.com/GOBP_REGULATION_OF_WNT_SIGNALING_PATHWAY.html) | 43 | -0.54 | -2.02 | 0.000 | 0.025 | 0.074 | 254 | tags=47%, list=17%, signal=54% |
| 4 | [GOBP\_NEGATIVE\_REGULATION\_OF\_CANONICAL\_WNT\_SIGNALING\_PATHWAY](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_NEGATIVE_REGULATION_OF_CANONICAL_WNT_SIGNALING_PATHWAY) | [Details ...](http://docs.google.com/GOBP_NEGATIVE_REGULATION_OF_CANONICAL_WNT_SIGNALING_PATHWAY.html) | 30 | -0.57 | -2.01 | 0.000 | 0.020 | 0.081 | 254 | tags=50%, list=17%, signal=59% |
| 5 | [GOBP\_RESPONSE\_TO\_RETINOIC\_ACID](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_RESPONSE_TO_RETINOIC_ACID) | [Details ...](http://docs.google.com/GOBP_RESPONSE_TO_RETINOIC_ACID.html) | 19 | -0.64 | -2.00 | 0.000 | 0.021 | 0.102 | 460 | tags=79%, list=30%, signal=112% |
| 6 | [GOBP\_NEGATIVE\_REGULATION\_OF\_WNT\_SIGNALING\_PATHWAY](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_NEGATIVE_REGULATION_OF_WNT_SIGNALING_PATHWAY) | [Details ...](http://docs.google.com/GOBP_NEGATIVE_REGULATION_OF_WNT_SIGNALING_PATHWAY.html) | 32 | -0.56 | -1.96 | 0.001 | 0.027 | 0.158 | 254 | tags=47%, list=17%, signal=55% |
| 7 | [GOBP\_CELL\_CELL\_SIGNALING\_BY\_WNT](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_CELL_CELL_SIGNALING_BY_WNT) | [Details ...](http://docs.google.com/GOBP_CELL_CELL_SIGNALING_BY_WNT.html) | 52 | -0.49 | -1.89 | 0.000 | 0.066 | 0.376 | 339 | tags=46%, list=22%, signal=57% |
| 8 | [GOBP\_EMBRYO\_DEVELOPMENT\_ENDING\_IN\_BIRTH\_OR\_EGG\_HATCHING](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_EMBRYO_DEVELOPMENT_ENDING_IN_BIRTH_OR_EGG_HATCHING) | [Details ...](http://docs.google.com/GOBP_EMBRYO_DEVELOPMENT_ENDING_IN_BIRTH_OR_EGG_HATCHING.html) | 70 | -0.45 | -1.87 | 0.000 | 0.073 | 0.442 | 654 | tags=66%, list=43%, signal=111% |
| 9 | [GOBP\_ARTERY\_DEVELOPMENT](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_ARTERY_DEVELOPMENT) | [Details ...](http://docs.google.com/GOBP_ARTERY_DEVELOPMENT.html) | 18 | -0.60 | -1.84 | 0.000 | 0.095 | 0.572 | 301 | tags=50%, list=20%, signal=62% |
| 10 | [GOBP\_CELLULAR\_RESPONSE\_TO\_KETONE](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_CELLULAR_RESPONSE_TO_KETONE) | [Details ...](http://docs.google.com/GOBP_CELLULAR_RESPONSE_TO_KETONE.html) | 16 | -0.61 | -1.84 | 0.001 | 0.093 | 0.599 | 254 | tags=50%, list=17%, signal=59% |
| 11 | [GOMF\_EXTRACELLULAR\_MATRIX\_STRUCTURAL\_CONSTITUENT](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOMF_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT) | [Details ...](http://docs.google.com/GOMF_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT.html) | 66 | -0.45 | -1.83 | 0.000 | 0.092 | 0.634 | 645 | tags=73%, list=43%, signal=121% |
| 12 | [GOBP\_RESPIRATORY\_SYSTEM\_DEVELOPMENT](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_RESPIRATORY_SYSTEM_DEVELOPMENT) | [Details ...](http://docs.google.com/GOBP_RESPIRATORY_SYSTEM_DEVELOPMENT.html) | 38 | -0.50 | -1.83 | 0.000 | 0.086 | 0.643 | 395 | tags=50%, list=26%, signal=66% |
| 13 | [GOBP\_REGULATION\_OF\_LYMPHOCYTE\_DIFFERENTIATION](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION) | [Details ...](http://docs.google.com/GOBP_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION.html) | 25 | -0.54 | -1.80 | 0.001 | 0.109 | 0.763 | 595 | tags=68%, list=39%, signal=110% |
| 14 | [GOBP\_ODONTOGENESIS](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_ODONTOGENESIS) | [Details ...](http://docs.google.com/GOBP_ODONTOGENESIS.html) | 38 | -0.49 | -1.80 | 0.000 | 0.102 | 0.763 | 536 | tags=68%, list=35%, signal=103% |
| 15 | [GOBP\_NEGATIVE\_REGULATION\_OF\_DEVELOPMENTAL\_GROWTH](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_NEGATIVE_REGULATION_OF_DEVELOPMENTAL_GROWTH) | [Details ...](http://docs.google.com/GOBP_NEGATIVE_REGULATION_OF_DEVELOPMENTAL_GROWTH.html) | 15 | -0.62 | -1.80 | 0.004 | 0.096 | 0.765 | 144 | tags=40%, list=10%, signal=44% |
| 16 | [GOBP\_EXTERNAL\_ENCAPSULATING\_STRUCTURE\_ORGANIZATION](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_EXTERNAL_ENCAPSULATING_STRUCTURE_ORGANIZATION) | [Details ...](http://docs.google.com/GOBP_EXTERNAL_ENCAPSULATING_STRUCTURE_ORGANIZATION.html) | 111 | -0.42 | -1.80 | 0.000 | 0.094 | 0.783 | 645 | tags=67%, list=43%, signal=108% |
| 17 | [GOBP\_SENSORY\_ORGAN\_MORPHOGENESIS](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_SENSORY_ORGAN_MORPHOGENESIS) | [Details ...](http://docs.google.com/GOBP_SENSORY_ORGAN_MORPHOGENESIS.html) | 36 | -0.49 | -1.78 | 0.002 | 0.109 | 0.861 | 355 | tags=47%, list=24%, signal=60% |
| 18 | [GOBP\_SODIUM\_ION\_TRANSPORT](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_SODIUM_ION_TRANSPORT) | [Details ...](http://docs.google.com/GOBP_SODIUM_ION_TRANSPORT.html) | 17 | -0.59 | -1.78 | 0.001 | 0.106 | 0.866 | 477 | tags=76%, list=32%, signal=111% |
| 19 | [GOCC\_COLLAGEN\_CONTAINING\_EXTRACELLULAR\_MATRIX](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOCC_COLLAGEN_CONTAINING_EXTRACELLULAR_MATRIX) | [Details ...](http://docs.google.com/GOCC_COLLAGEN_CONTAINING_EXTRACELLULAR_MATRIX.html) | 147 | -0.40 | -1.78 | 0.000 | 0.103 | 0.876 | 645 | tags=63%, list=43%, signal=100% |
| 20 | [GOBP\_EMBRYO\_DEVELOPMENT](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_EMBRYO_DEVELOPMENT) | [Details ...](http://docs.google.com/GOBP_EMBRYO_DEVELOPMENT.html) | 144 | -0.40 | -1.77 | 0.000 | 0.099 | 0.879 | 377 | tags=42%, list=25%, signal=50% |
| 21 | GOBP\_CELL\_SURFACE\_RECEPTOR\_SIGNALING\_PATHWAY\_INVOLVED\_IN\_CELL\_CELL\_SIGNALING |  | 59 | -0.45 | -1.77 | 0.000 | 0.095 | 0.880 | 339 | tags=42%, list=22%, signal=53% |
| 22 | GOCC\_EXTERNAL\_ENCAPSULATING\_STRUCTURE |  | 167 | -0.39 | -1.77 | 0.000 | 0.091 | 0.880 | 580 | tags=57%, list=38%, signal=83% |
| 23 | GOBP\_POSITIVE\_REGULATION\_OF\_CANONICAL\_WNT\_SIGNALING\_PATHWAY |  | 16 | -0.58 | -1.77 | 0.004 | 0.093 | 0.898 | 300 | tags=50%, list=20%, signal=62% |
| 24 | GOBP\_AXIS\_SPECIFICATION |  | 16 | -0.59 | -1.77 | 0.003 | 0.092 | 0.905 | 401 | tags=63%, list=27%, signal=84% |
| 25 | GOBP\_EMBRYONIC\_ORGAN\_DEVELOPMENT |  | 65 | -0.43 | -1.76 | 0.000 | 0.095 | 0.922 | 401 | tags=45%, list=27%, signal=58% |
| 26 | GOBP\_MULTI\_MULTICELLULAR\_ORGANISM\_PROCESS |  | 47 | -0.46 | -1.75 | 0.001 | 0.103 | 0.942 | 336 | tags=47%, list=22%, signal=58% |
| 27 | GOBP\_REPRODUCTION |  | 165 | -0.39 | -1.75 | 0.000 | 0.102 | 0.949 | 369 | tags=42%, list=24%, signal=49% |
| 28 | GOBP\_ANIMAL\_ORGAN\_MORPHOGENESIS |  | 170 | -0.39 | -1.74 | 0.000 | 0.108 | 0.964 | 401 | tags=42%, list=27%, signal=50% |
| 29 | GOBP\_CELL\_FATE\_COMMITMENT |  | 41 | -0.46 | -1.73 | 0.005 | 0.109 | 0.971 | 553 | tags=66%, list=37%, signal=101% |
| 30 | GOBP\_ODONTOGENESIS\_OF\_DENTIN\_CONTAINING\_TOOTH |  | 21 | -0.55 | -1.73 | 0.008 | 0.106 | 0.973 | 395 | tags=67%, list=26%, signal=89% |
| 31 | GOBP\_RESPONSE\_TO\_PEPTIDE\_HORMONE |  | 61 | -0.44 | -1.73 | 0.002 | 0.105 | 0.975 | 336 | tags=41%, list=22%, signal=51% |
| 32 | GOBP\_COLLAGEN\_FIBRIL\_ORGANIZATION |  | 19 | -0.56 | -1.73 | 0.001 | 0.108 | 0.982 | 645 | tags=89%, list=43%, signal=154% |
| 33 | GOBP\_RESPONSE\_TO\_STEROID\_HORMONE |  | 67 | -0.42 | -1.73 | 0.001 | 0.105 | 0.982 | 324 | tags=43%, list=21%, signal=53% |
| 34 | GOBP\_MORPHOGENESIS\_OF\_EMBRYONIC\_EPITHELIUM |  | 17 | -0.57 | -1.72 | 0.007 | 0.105 | 0.983 | 273 | tags=59%, list=18%, signal=71% |
| 35 | GOBP\_SENSORY\_SYSTEM\_DEVELOPMENT |  | 50 | -0.45 | -1.72 | 0.001 | 0.111 | 0.987 | 297 | tags=38%, list=20%, signal=46% |
| 36 | GOBP\_EMBRYONIC\_MORPHOGENESIS |  | 97 | -0.41 | -1.72 | 0.000 | 0.110 | 0.988 | 476 | tags=52%, list=32%, signal=70% |
| 37 | GOBP\_RESPONSE\_TO\_ACID\_CHEMICAL |  | 18 | -0.57 | -1.71 | 0.005 | 0.113 | 0.989 | 263 | tags=50%, list=17%, signal=60% |
| 38 | GOBP\_TUBE\_FORMATION |  | 17 | -0.57 | -1.71 | 0.004 | 0.112 | 0.991 | 273 | tags=59%, list=18%, signal=71% |
| 39 | GOBP\_EMBRYONIC\_ORGAN\_MORPHOGENESIS |  | 41 | -0.45 | -1.71 | 0.007 | 0.112 | 0.994 | 401 | tags=49%, list=27%, signal=65% |
| 40 | GOBP\_FAT\_CELL\_DIFFERENTIATION |  | 29 | -0.49 | -1.70 | 0.002 | 0.117 | 0.996 | 365 | tags=55%, list=24%, signal=71% |
| 41 | GOBP\_RESPONSE\_TO\_HORMONE |  | 136 | -0.38 | -1.70 | 0.000 | 0.116 | 0.998 | 395 | tags=41%, list=26%, signal=51% |
| 42 | GOBP\_CELLULAR\_RESPONSE\_TO\_HORMONE\_STIMULUS |  | 80 | -0.41 | -1.69 | 0.000 | 0.128 | 0.999 | 505 | tags=48%, list=33%, signal=68% |
| 43 | GOBP\_ENDOCRINE\_SYSTEM\_DEVELOPMENT |  | 20 | -0.54 | -1.69 | 0.006 | 0.127 | 0.999 | 536 | tags=70%, list=35%, signal=107% |
| 44 | GOMF\_INTEGRIN\_BINDING |  | 46 | -0.44 | -1.68 | 0.005 | 0.133 | 0.999 | 567 | tags=59%, list=38%, signal=91% |
| 45 | GOBP\_SENSORY\_PERCEPTION\_OF\_LIGHT\_STIMULUS |  | 19 | -0.55 | -1.68 | 0.008 | 0.131 | 0.999 | 208 | tags=42%, list=14%, signal=48% |
| 46 | GOBP\_SENSORY\_ORGAN\_DEVELOPMENT |  | 70 | -0.41 | -1.68 | 0.002 | 0.130 | 0.999 | 355 | tags=40%, list=24%, signal=50% |
| 47 | GOBP\_NEURAL\_CREST\_CELL\_DIFFERENTIATION |  | 15 | -0.58 | -1.67 | 0.004 | 0.137 | 0.999 | 254 | tags=47%, list=17%, signal=56% |
| 48 | GOBP\_POSITIVE\_REGULATION\_OF\_EPITHELIAL\_CELL\_PROLIFERATION |  | 31 | -0.48 | -1.67 | 0.005 | 0.137 | 1.000 | 281 | tags=39%, list=19%, signal=47% |
| 49 | GOBP\_POSITIVE\_REGULATION\_OF\_ENDOTHELIAL\_CELL\_PROLIFERATION |  | 17 | -0.54 | -1.66 | 0.014 | 0.147 | 1.000 | 281 | tags=41%, list=19%, signal=50% |
| 50 | GOBP\_DIENCEPHALON\_DEVELOPMENT |  | 16 | -0.55 | -1.66 | 0.017 | 0.145 | 1.000 | 567 | tags=75%, list=38%, signal=119% |
| 51 | GOBP\_MESENCHYMAL\_CELL\_DIFFERENTIATION |  | 37 | -0.45 | -1.66 | 0.004 | 0.143 | 1.000 | 254 | tags=38%, list=17%, signal=44% |
| 52 | GOMF\_GROWTH\_FACTOR\_ACTIVITY |  | 35 | -0.46 | -1.65 | 0.005 | 0.145 | 1.000 | 588 | tags=63%, list=39%, signal=101% |
| 53 | GOBP\_OSTEOBLAST\_DIFFERENTIATION |  | 35 | -0.46 | -1.65 | 0.011 | 0.146 | 1.000 | 174 | tags=37%, list=12%, signal=41% |
| 54 | GOBP\_RESPONSE\_TO\_OSMOTIC\_STRESS |  | 16 | -0.55 | -1.65 | 0.011 | 0.148 | 1.000 | 297 | tags=38%, list=20%, signal=46% |
| 55 | GOBP\_POSITIVE\_REGULATION\_OF\_WNT\_SIGNALING\_PATHWAY |  | 19 | -0.53 | -1.65 | 0.015 | 0.149 | 1.000 | 300 | tags=47%, list=20%, signal=58% |
| 56 | GOMF\_CHANNEL\_REGULATOR\_ACTIVITY |  | 18 | -0.54 | -1.65 | 0.010 | 0.147 | 1.000 | 124 | tags=33%, list=8%, signal=36% |
| 57 | GOBP\_BONE\_MORPHOGENESIS |  | 24 | -0.50 | -1.64 | 0.018 | 0.149 | 1.000 | 174 | tags=38%, list=12%, signal=42% |
| 58 | GOCC\_CILIUM |  | 29 | -0.47 | -1.63 | 0.012 | 0.160 | 1.000 | 350 | tags=38%, list=23%, signal=48% |
| 59 | GOBP\_DIGESTIVE\_SYSTEM\_DEVELOPMENT |  | 24 | -0.49 | -1.63 | 0.018 | 0.166 | 1.000 | 493 | tags=63%, list=33%, signal=91% |
| 60 | GOMF\_CELL\_ADHESION\_MOLECULE\_BINDING |  | 82 | -0.39 | -1.62 | 0.003 | 0.175 | 1.000 | 516 | tags=49%, list=34%, signal=70% |
| 61 | GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_DIFFERENTIATION |  | 119 | -0.37 | -1.62 | 0.001 | 0.174 | 1.000 | 580 | tags=52%, list=38%, signal=78% |
| 62 | GOBP\_CELL\_MIGRATION |  | 240 | -0.35 | -1.62 | 0.000 | 0.175 | 1.000 | 615 | tags=52%, list=41%, signal=74% |
| 63 | GOBP\_EPITHELIAL\_TUBE\_FORMATION |  | 16 | -0.54 | -1.62 | 0.011 | 0.174 | 1.000 | 273 | tags=56%, list=18%, signal=68% |
| 64 | GOCC\_APICAL\_PART\_OF\_CELL |  | 55 | -0.41 | -1.62 | 0.009 | 0.173 | 1.000 | 447 | tags=51%, list=30%, signal=70% |
| 65 | GOCC\_APICAL\_PLASMA\_MEMBRANE |  | 44 | -0.43 | -1.61 | 0.004 | 0.181 | 1.000 | 447 | tags=52%, list=30%, signal=72% |
| 66 | GOMF\_ION\_CHANNEL\_REGULATOR\_ACTIVITY |  | 16 | -0.54 | -1.60 | 0.023 | 0.192 | 1.000 | 124 | tags=31%, list=8%, signal=34% |
| 67 | GOCC\_BASOLATERAL\_PLASMA\_MEMBRANE |  | 30 | -0.46 | -1.60 | 0.016 | 0.193 | 1.000 | 257 | tags=33%, list=17%, signal=39% |
| 68 | GOBP\_BIOLOGICAL\_ADHESION |  | 225 | -0.34 | -1.60 | 0.000 | 0.198 | 1.000 | 580 | tags=48%, list=38%, signal=67% |
| 69 | GOBP\_RESPONSE\_TO\_KETONE |  | 35 | -0.44 | -1.59 | 0.012 | 0.197 | 1.000 | 254 | tags=37%, list=17%, signal=44% |
| 70 | GOBP\_SUBSTRATE\_ADHESION\_DEPENDENT\_CELL\_SPREADING |  | 17 | -0.52 | -1.59 | 0.016 | 0.199 | 1.000 | 513 | tags=59%, list=34%, signal=88% |
| 71 | GOBP\_RETINA\_DEVELOPMENT\_IN\_CAMERA\_TYPE\_EYE |  | 16 | -0.53 | -1.59 | 0.020 | 0.200 | 1.000 | 60 | tags=25%, list=4%, signal=26% |
| 72 | GOBP\_IN\_UTERO\_EMBRYONIC\_DEVELOPMENT |  | 33 | -0.45 | -1.59 | 0.011 | 0.201 | 1.000 | 654 | tags=64%, list=43%, signal=110% |
| 73 | GOBP\_REGULATION\_OF\_CELL\_DIVISION |  | 20 | -0.51 | -1.58 | 0.035 | 0.207 | 1.000 | 567 | tags=65%, list=38%, signal=103% |
| 74 | GOCC\_ENDOPLASMIC\_RETICULUM\_LUMEN |  | 70 | -0.38 | -1.58 | 0.004 | 0.206 | 1.000 | 645 | tags=61%, list=43%, signal=102% |
| 75 | GOBP\_REGULATION\_OF\_EPITHELIAL\_CELL\_DIFFERENTIATION |  | 22 | -0.49 | -1.58 | 0.025 | 0.214 | 1.000 | 372 | tags=50%, list=25%, signal=65% |
| 76 | GOBP\_NEURAL\_TUBE\_DEVELOPMENT |  | 16 | -0.54 | -1.58 | 0.026 | 0.212 | 1.000 | 339 | tags=63%, list=22%, signal=80% |
| 77 | GOBP\_MESENCHYME\_DEVELOPMENT |  | 48 | -0.41 | -1.57 | 0.009 | 0.212 | 1.000 | 254 | tags=35%, list=17%, signal=41% |
| 78 | GOBP\_SKELETAL\_SYSTEM\_MORPHOGENESIS |  | 49 | -0.41 | -1.57 | 0.010 | 0.217 | 1.000 | 654 | tags=65%, list=43%, signal=111% |
| 79 | GOBP\_GLAND\_MORPHOGENESIS |  | 22 | -0.49 | -1.57 | 0.017 | 0.223 | 1.000 | 294 | tags=50%, list=19%, signal=61% |
| 80 | GOBP\_NON\_CANONICAL\_WNT\_SIGNALING\_PATHWAY |  | 15 | -0.54 | -1.57 | 0.021 | 0.220 | 1.000 | 326 | tags=53%, list=22%, signal=67% |
| 81 | GOBP\_REGULATION\_OF\_T\_CELL\_DIFFERENTIATION |  | 19 | -0.51 | -1.57 | 0.024 | 0.219 | 1.000 | 595 | tags=58%, list=39%, signal=94% |
| 82 | GOBP\_REGULATION\_OF\_BMP\_SIGNALING\_PATHWAY |  | 19 | -0.50 | -1.56 | 0.019 | 0.220 | 1.000 | 326 | tags=58%, list=22%, signal=73% |
| 83 | GOBP\_CELL\_ADHESION\_MEDIATED\_BY\_INTEGRIN |  | 16 | -0.52 | -1.56 | 0.027 | 0.218 | 1.000 | 460 | tags=69%, list=30%, signal=98% |
| 84 | GOCC\_NUCLEAR\_SPECK |  | 17 | -0.51 | -1.56 | 0.029 | 0.220 | 1.000 | 501 | tags=53%, list=33%, signal=78% |
| 85 | GOBP\_RESPONSE\_TO\_EXTRACELLULAR\_STIMULUS |  | 84 | -0.37 | -1.56 | 0.008 | 0.218 | 1.000 | 573 | tags=54%, list=38%, signal=82% |
| 86 | GOBP\_INTEGRIN\_MEDIATED\_SIGNALING\_PATHWAY |  | 22 | -0.48 | -1.56 | 0.028 | 0.217 | 1.000 | 567 | tags=68%, list=38%, signal=108% |
| 87 | GOCC\_COLLAGEN\_TRIMER |  | 29 | -0.45 | -1.56 | 0.017 | 0.218 | 1.000 | 713 | tags=69%, list=47%, signal=128% |
| 88 | GOBP\_RESPONSE\_TO\_BMP |  | 32 | -0.44 | -1.54 | 0.019 | 0.259 | 1.000 | 272 | tags=41%, list=18%, signal=49% |
| 89 | GOBP\_CAMERA\_TYPE\_EYE\_DEVELOPMENT |  | 36 | -0.42 | -1.53 | 0.027 | 0.265 | 1.000 | 350 | tags=36%, list=23%, signal=46% |
| 90 | GOBP\_ACTIN\_FILAMENT\_ORGANIZATION |  | 56 | -0.40 | -1.53 | 0.009 | 0.264 | 1.000 | 263 | tags=32%, list=17%, signal=37% |
| 91 | GOCC\_BASEMENT\_MEMBRANE |  | 33 | -0.44 | -1.53 | 0.027 | 0.275 | 1.000 | 629 | tags=61%, list=42%, signal=102% |
| 92 | GOCC\_BASAL\_PART\_OF\_CELL |  | 40 | -0.41 | -1.52 | 0.012 | 0.276 | 1.000 | 324 | tags=35%, list=21%, signal=43% |
| 93 | GOBP\_TUBE\_DEVELOPMENT |  | 192 | -0.33 | -1.52 | 0.001 | 0.274 | 1.000 | 339 | tags=34%, list=22%, signal=39% |
| 94 | GOMF\_COLLAGEN\_BINDING |  | 25 | -0.46 | -1.52 | 0.027 | 0.276 | 1.000 | 640 | tags=80%, list=42%, signal=137% |
| 95 | GOBP\_DEVELOPMENTAL\_GROWTH |  | 83 | -0.36 | -1.52 | 0.012 | 0.274 | 1.000 | 611 | tags=51%, list=40%, signal=80% |
| 96 | GOBP\_REGULATION\_OF\_FAT\_CELL\_DIFFERENTIATION |  | 17 | -0.51 | -1.52 | 0.027 | 0.274 | 1.000 | 365 | tags=65%, list=24%, signal=84% |
| 97 | GOBP\_EPITHELIAL\_TUBE\_MORPHOGENESIS |  | 43 | -0.40 | -1.52 | 0.023 | 0.283 | 1.000 | 419 | tags=47%, list=28%, signal=63% |
| 98 | GOBP\_OUTFLOW\_TRACT\_MORPHOGENESIS |  | 16 | -0.51 | -1.52 | 0.034 | 0.281 | 1.000 | 174 | tags=31%, list=12%, signal=35% |
| 99 | GOBP\_MORPHOGENESIS\_OF\_A\_BRANCHING\_STRUCTURE |  | 35 | -0.42 | -1.51 | 0.024 | 0.280 | 1.000 | 395 | tags=49%, list=26%, signal=64% |
| 100 | GOBP\_PLACENTA\_DEVELOPMENT |  | 30 | -0.43 | -1.51 | 0.032 | 0.278 | 1.000 | 343 | tags=47%, list=23%, signal=59% |
| 101 | GOBP\_NEGATIVE\_REGULATION\_OF\_CELLULAR\_RESPONSE\_TO\_GROWTH\_FACTOR\_STIMULUS |  | 21 | -0.47 | -1.51 | 0.040 | 0.283 | 1.000 | 545 | tags=62%, list=36%, signal=96% |
| 102 | GOBP\_CELLULAR\_RESPONSE\_TO\_STEROID\_HORMONE\_STIMULUS |  | 31 | -0.42 | -1.51 | 0.024 | 0.281 | 1.000 | 493 | tags=48%, list=33%, signal=70% |
| 103 | GOBP\_RESPONSE\_TO\_PEPTIDE |  | 83 | -0.36 | -1.51 | 0.012 | 0.281 | 1.000 | 336 | tags=37%, list=22%, signal=45% |
| 104 | GOBP\_TISSUE\_REMODELING |  | 36 | -0.42 | -1.50 | 0.031 | 0.290 | 1.000 | 254 | tags=36%, list=17%, signal=42% |
| 105 | GOBP\_MEMORY |  | 19 | -0.48 | -1.50 | 0.042 | 0.297 | 1.000 | 253 | tags=37%, list=17%, signal=44% |
| 106 | GOBP\_BONE\_DEVELOPMENT |  | 37 | -0.41 | -1.49 | 0.036 | 0.308 | 1.000 | 401 | tags=49%, list=27%, signal=65% |
| 107 | GOBP\_GLAND\_DEVELOPMENT |  | 60 | -0.37 | -1.49 | 0.026 | 0.315 | 1.000 | 497 | tags=50%, list=33%, signal=72% |
| 108 | GOBP\_NEGATIVE\_REGULATION\_OF\_INTRACELLULAR\_SIGNAL\_TRANSDUCTION |  | 72 | -0.36 | -1.49 | 0.012 | 0.313 | 1.000 | 544 | tags=46%, list=36%, signal=68% |
| 109 | GOBP\_EMBRYONIC\_PLACENTA\_DEVELOPMENT |  | 18 | -0.48 | -1.49 | 0.046 | 0.318 | 1.000 | 232 | tags=39%, list=15%, signal=45% |
| 110 | GOBP\_B\_CELL\_DIFFERENTIATION |  | 23 | -0.45 | -1.48 | 0.044 | 0.324 | 1.000 | 705 | tags=87%, list=47%, signal=161% |
| 111 | GOBP\_SKIN\_DEVELOPMENT |  | 53 | -0.37 | -1.48 | 0.029 | 0.325 | 1.000 | 554 | tags=55%, list=37%, signal=83% |
| 112 | GOBP\_DEVELOPMENTAL\_PROCESS\_INVOLVED\_IN\_REPRODUCTION |  | 104 | -0.34 | -1.48 | 0.012 | 0.324 | 1.000 | 622 | tags=58%, list=41%, signal=91% |
| 113 | GOBP\_CELL\_JUNCTION\_ASSEMBLY |  | 49 | -0.38 | -1.48 | 0.018 | 0.323 | 1.000 | 535 | tags=47%, list=35%, signal=70% |
| 114 | GOBP\_FORMATION\_OF\_PRIMARY\_GERM\_LAYER |  | 34 | -0.41 | -1.48 | 0.041 | 0.328 | 1.000 | 376 | tags=53%, list=25%, signal=69% |
| 115 | GOBP\_REGULATION\_OF\_CELL\_ADHESION |  | 127 | -0.34 | -1.48 | 0.008 | 0.327 | 1.000 | 596 | tags=50%, list=39%, signal=75% |
| 116 | GOBP\_POST\_TRANSLATIONAL\_PROTEIN\_MODIFICATION |  | 45 | -0.39 | -1.47 | 0.018 | 0.333 | 1.000 | 228 | tags=31%, list=15%, signal=36% |
| 117 | GOBP\_POSITIVE\_REGULATION\_OF\_DEVELOPMENTAL\_PROCESS |  | 177 | -0.32 | -1.47 | 0.004 | 0.330 | 1.000 | 519 | tags=44%, list=34%, signal=59% |
| 118 | GOBP\_RESPONSE\_TO\_TRANSFORMING\_GROWTH\_FACTOR\_BETA |  | 51 | -0.38 | -1.47 | 0.014 | 0.329 | 1.000 | 632 | tags=59%, list=42%, signal=98% |
| 119 | GOBP\_LOCOMOTION |  | 269 | -0.31 | -1.47 | 0.001 | 0.335 | 1.000 | 615 | tags=49%, list=41%, signal=68% |
| 120 | GOBP\_ENDODERM\_DEVELOPMENT |  | 30 | -0.42 | -1.47 | 0.053 | 0.333 | 1.000 | 672 | tags=80%, list=45%, signal=141% |
| 121 | GOBP\_REGULATION\_OF\_CELLULAR\_RESPONSE\_TO\_GROWTH\_FACTOR\_STIMULUS |  | 58 | -0.37 | -1.47 | 0.029 | 0.336 | 1.000 | 292 | tags=36%, list=19%, signal=43% |
| 122 | GOBP\_EPIDERMIS\_DEVELOPMENT |  | 56 | -0.38 | -1.47 | 0.029 | 0.334 | 1.000 | 412 | tags=45%, list=27%, signal=59% |
| 123 | GOBP\_EMBRYONIC\_SKELETAL\_SYSTEM\_DEVELOPMENT |  | 23 | -0.45 | -1.47 | 0.043 | 0.332 | 1.000 | 652 | tags=65%, list=43%, signal=113% |
| 124 | GOBP\_OSSIFICATION |  | 72 | -0.35 | -1.47 | 0.032 | 0.334 | 1.000 | 294 | tags=36%, list=19%, signal=43% |
| 125 | GOBP\_REGULATION\_OF\_DEVELOPMENTAL\_GROWTH |  | 44 | -0.38 | -1.46 | 0.031 | 0.336 | 1.000 | 497 | tags=43%, list=33%, signal=62% |
| 126 | GOBP\_REPRODUCTIVE\_SYSTEM\_DEVELOPMENT |  | 68 | -0.36 | -1.46 | 0.024 | 0.334 | 1.000 | 622 | tags=62%, list=41%, signal=100% |
| 127 | GOMF\_GROWTH\_FACTOR\_BINDING |  | 42 | -0.39 | -1.46 | 0.041 | 0.337 | 1.000 | 263 | tags=36%, list=17%, signal=42% |
| 128 | GOBP\_POSITIVE\_REGULATION\_OF\_LYMPHOCYTE\_DIFFERENTIATION |  | 15 | -0.50 | -1.46 | 0.055 | 0.341 | 1.000 | 575 | tags=60%, list=38%, signal=96% |
| 129 | GOBP\_ENZYME\_LINKED\_RECEPTOR\_PROTEIN\_SIGNALING\_PATHWAY |  | 159 | -0.33 | -1.46 | 0.009 | 0.340 | 1.000 | 661 | tags=52%, list=44%, signal=83% |
| 130 | GOCC\_APICAL\_JUNCTION\_COMPLEX |  | 18 | -0.47 | -1.46 | 0.072 | 0.339 | 1.000 | 633 | tags=61%, list=42%, signal=104% |
| 131 | GOBP\_TRANSMEMBRANE\_RECEPTOR\_PROTEIN\_SERINE\_THREONINE\_KINASE\_SIGNALING\_PATHWAY |  | 62 | -0.37 | -1.46 | 0.026 | 0.337 | 1.000 | 292 | tags=35%, list=19%, signal=42% |
| 132 | GOCC\_FICOLIN\_1\_RICH\_GRANULE\_LUMEN |  | 20 | -0.46 | -1.46 | 0.053 | 0.337 | 1.000 | 112 | tags=25%, list=7%, signal=27% |
| 133 | GOBP\_NEGATIVE\_REGULATION\_OF\_MAPK\_CASCADE |  | 30 | -0.42 | -1.46 | 0.056 | 0.335 | 1.000 | 544 | tags=53%, list=36%, signal=82% |
| 134 | GOBP\_ORGANONITROGEN\_COMPOUND\_CATABOLIC\_PROCESS |  | 106 | -0.34 | -1.46 | 0.013 | 0.333 | 1.000 | 339 | tags=33%, list=22%, signal=40% |
| 135 | GOBP\_POSITIVE\_REGULATION\_OF\_PROTEIN\_KINASE\_B\_SIGNALING |  | 29 | -0.42 | -1.45 | 0.062 | 0.335 | 1.000 | 536 | tags=55%, list=35%, signal=84% |
| 136 | GOBP\_NEURON\_MIGRATION |  | 22 | -0.45 | -1.45 | 0.054 | 0.335 | 1.000 | 719 | tags=64%, list=48%, signal=120% |
| 137 | GOBP\_GROWTH |  | 123 | -0.33 | -1.45 | 0.012 | 0.334 | 1.000 | 611 | tags=49%, list=40%, signal=75% |
| 138 | GOBP\_EPIDERMAL\_CELL\_DIFFERENTIATION |  | 36 | -0.40 | -1.45 | 0.041 | 0.336 | 1.000 | 412 | tags=50%, list=27%, signal=67% |
| 139 | GOBP\_STEM\_CELL\_DIFFERENTIATION |  | 34 | -0.41 | -1.45 | 0.052 | 0.336 | 1.000 | 611 | tags=59%, list=40%, signal=97% |
| 140 | GOMF\_PROTEOGLYCAN\_BINDING |  | 16 | -0.48 | -1.45 | 0.063 | 0.342 | 1.000 | 629 | tags=75%, list=42%, signal=127% |
| 141 | GOBP\_RESPONSE\_TO\_HYDROGEN\_PEROXIDE |  | 17 | -0.48 | -1.45 | 0.057 | 0.343 | 1.000 | 145 | tags=29%, list=10%, signal=32% |
| 142 | GOBP\_MONONUCLEAR\_CELL\_DIFFERENTIATION |  | 67 | -0.36 | -1.45 | 0.020 | 0.340 | 1.000 | 595 | tags=54%, list=39%, signal=85% |
| 143 | GOBP\_ANTIMICROBIAL\_HUMORAL\_IMMUNE\_RESPONSE\_MEDIATED\_BY\_ANTIMICROBIAL\_PEPTIDE |  | 19 | -0.47 | -1.44 | 0.055 | 0.346 | 1.000 | 366 | tags=53%, list=24%, signal=69% |
| 144 | GOCC\_NUCLEAR\_BODY |  | 41 | -0.39 | -1.44 | 0.049 | 0.345 | 1.000 | 542 | tags=46%, list=36%, signal=70% |
| 145 | GOBP\_POSITIVE\_REGULATION\_OF\_LIPID\_METABOLIC\_PROCESS |  | 21 | -0.45 | -1.44 | 0.055 | 0.344 | 1.000 | 491 | tags=52%, list=33%, signal=77% |
| 146 | GOBP\_FOREBRAIN\_DEVELOPMENT |  | 48 | -0.38 | -1.44 | 0.031 | 0.348 | 1.000 | 660 | tags=63%, list=44%, signal=107% |
| 147 | GOMF\_DNA\_BINDING\_TRANSCRIPTION\_FACTOR\_ACTIVITY |  | 104 | -0.33 | -1.44 | 0.028 | 0.345 | 1.000 | 665 | tags=60%, list=44%, signal=99% |
| 148 | GOBP\_NEGATIVE\_REGULATION\_OF\_CELL\_ADHESION |  | 50 | -0.37 | -1.44 | 0.047 | 0.346 | 1.000 | 525 | tags=54%, list=35%, signal=80% |
| 149 | GOBP\_REGULATION\_OF\_NEURON\_DIFFERENTIATION |  | 27 | -0.43 | -1.44 | 0.054 | 0.344 | 1.000 | 419 | tags=41%, list=28%, signal=55% |
| 150 | GOCC\_EXTERNAL\_SIDE\_OF\_PLASMA\_MEMBRANE |  | 64 | -0.35 | -1.44 | 0.034 | 0.342 | 1.000 | 536 | tags=55%, list=35%, signal=81% |
| 151 | GOBP\_POSITIVE\_REGULATION\_OF\_PEPTIDASE\_ACTIVITY |  | 34 | -0.40 | -1.44 | 0.045 | 0.340 | 1.000 | 363 | tags=38%, list=24%, signal=49% |
| 152 | GOBP\_RESPONSE\_TO\_CORTICOSTEROID |  | 46 | -0.38 | -1.44 | 0.036 | 0.341 | 1.000 | 263 | tags=35%, list=17%, signal=41% |
| 153 | GOBP\_NEGATIVE\_REGULATION\_OF\_TRANSMEMBRANE\_RECEPTOR\_PROTEIN\_SERINE\_THREONINE\_KINASE\_SIGNALING\_PATHWAY |  | 21 | -0.46 | -1.44 | 0.047 | 0.339 | 1.000 | 326 | tags=48%, list=22%, signal=60% |
| 154 | GOCC\_ACTIN\_BASED\_CELL\_PROJECTION |  | 17 | -0.47 | -1.44 | 0.058 | 0.340 | 1.000 | 142 | tags=29%, list=9%, signal=32% |
| 155 | GOMF\_INSULIN\_LIKE\_GROWTH\_FACTOR\_BINDING |  | 16 | -0.48 | -1.43 | 0.061 | 0.341 | 1.000 | 263 | tags=44%, list=17%, signal=52% |
| 156 | GOMF\_HEPARIN\_BINDING |  | 55 | -0.37 | -1.43 | 0.043 | 0.340 | 1.000 | 516 | tags=53%, list=34%, signal=77% |
| 157 | GOBP\_HEART\_MORPHOGENESIS |  | 38 | -0.39 | -1.43 | 0.048 | 0.344 | 1.000 | 232 | tags=29%, list=15%, signal=33% |
| 158 | GOBP\_MULTI\_ORGANISM\_PROCESS |  | 116 | -0.33 | -1.43 | 0.023 | 0.343 | 1.000 | 372 | tags=38%, list=25%, signal=46% |
| 159 | GOBP\_CELLULAR\_RESPONSE\_TO\_PEPTIDE\_HORMONE\_STIMULUS |  | 33 | -0.40 | -1.43 | 0.056 | 0.343 | 1.000 | 336 | tags=36%, list=22%, signal=46% |
| 160 | GOBP\_REGULATION\_OF\_BONE\_MINERALIZATION |  | 17 | -0.47 | -1.43 | 0.072 | 0.346 | 1.000 | 157 | tags=35%, list=10%, signal=39% |
| 161 | GOBP\_SUPRAMOLECULAR\_FIBER\_ORGANIZATION |  | 110 | -0.33 | -1.43 | 0.019 | 0.349 | 1.000 | 267 | tags=29%, list=18%, signal=33% |
| 162 | GOBP\_T\_CELL\_DIFFERENTIATION |  | 31 | -0.41 | -1.42 | 0.059 | 0.352 | 1.000 | 595 | tags=52%, list=39%, signal=83% |
| 163 | GOBP\_CELL\_SUBSTRATE\_ADHESION |  | 67 | -0.35 | -1.42 | 0.030 | 0.357 | 1.000 | 567 | tags=54%, list=38%, signal=82% |
| 164 | GOBP\_GASTRULATION |  | 42 | -0.38 | -1.42 | 0.054 | 0.355 | 1.000 | 645 | tags=69%, list=43%, signal=117% |
| 165 | GOMF\_GLYCOSAMINOGLYCAN\_BINDING |  | 66 | -0.35 | -1.42 | 0.034 | 0.356 | 1.000 | 579 | tags=55%, list=38%, signal=85% |
| 166 | GOBP\_PEPTIDYL\_TYROSINE\_MODIFICATION |  | 55 | -0.36 | -1.42 | 0.041 | 0.354 | 1.000 | 559 | tags=45%, list=37%, signal=70% |
| 167 | GOBP\_POSITIVE\_REGULATION\_OF\_GROWTH |  | 33 | -0.40 | -1.42 | 0.067 | 0.352 | 1.000 | 536 | tags=52%, list=35%, signal=78% |
| 168 | GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_ADHESION |  | 74 | -0.34 | -1.42 | 0.031 | 0.355 | 1.000 | 575 | tags=46%, list=38%, signal=71% |
| 169 | GOBP\_PROTEIN\_KINASE\_B\_SIGNALING |  | 42 | -0.38 | -1.42 | 0.042 | 0.353 | 1.000 | 559 | tags=50%, list=37%, signal=77% |
| 170 | GOMF\_COPPER\_ION\_BINDING |  | 16 | -0.49 | -1.42 | 0.077 | 0.353 | 1.000 | 580 | tags=56%, list=38%, signal=90% |
| 171 | GOBP\_ACTIN\_FILAMENT\_BUNDLE\_ORGANIZATION |  | 22 | -0.44 | -1.41 | 0.064 | 0.359 | 1.000 | 263 | tags=36%, list=17%, signal=43% |
| 172 | GOBP\_REGULATION\_OF\_ANIMAL\_ORGAN\_MORPHOGENESIS |  | 25 | -0.43 | -1.41 | 0.050 | 0.358 | 1.000 | 382 | tags=44%, list=25%, signal=58% |
| 173 | GOBP\_REGULATION\_OF\_MAP\_KINASE\_ACTIVITY |  | 40 | -0.39 | -1.41 | 0.053 | 0.357 | 1.000 | 457 | tags=45%, list=30%, signal=63% |
| 174 | GOBP\_REGULATION\_OF\_ACTIN\_FILAMENT\_LENGTH |  | 26 | -0.42 | -1.41 | 0.072 | 0.357 | 1.000 | 229 | tags=31%, list=15%, signal=36% |
| 175 | GOBP\_CELLULAR\_RESPONSE\_TO\_EXTERNAL\_STIMULUS |  | 44 | -0.38 | -1.41 | 0.047 | 0.355 | 1.000 | 707 | tags=66%, list=47%, signal=120% |
| 176 | GOBP\_ENDODERM\_FORMATION |  | 26 | -0.42 | -1.41 | 0.053 | 0.362 | 1.000 | 672 | tags=81%, list=45%, signal=143% |
| 177 | GOBP\_NEGATIVE\_REGULATION\_OF\_MAP\_KINASE\_ACTIVITY |  | 18 | -0.46 | -1.41 | 0.068 | 0.361 | 1.000 | 382 | tags=50%, list=25%, signal=66% |
| 178 | GOBP\_REGULATION\_OF\_CELL\_DIFFERENTIATION |  | 212 | -0.31 | -1.41 | 0.014 | 0.359 | 1.000 | 624 | tags=50%, list=41%, signal=73% |
| 179 | GOBP\_MULTICELLULAR\_ORGANISM\_REPRODUCTION |  | 77 | -0.34 | -1.41 | 0.038 | 0.358 | 1.000 | 612 | tags=55%, list=41%, signal=87% |
| 180 | GOBP\_EPITHELIUM\_DEVELOPMENT |  | 165 | -0.31 | -1.41 | 0.015 | 0.357 | 1.000 | 440 | tags=38%, list=29%, signal=48% |
| 181 | GOCC\_TIGHT\_JUNCTION |  | 17 | -0.46 | -1.41 | 0.081 | 0.355 | 1.000 | 633 | tags=59%, list=42%, signal=100% |
| 182 | GOBP\_EPITHELIAL\_CELL\_APOPTOTIC\_PROCESS |  | 19 | -0.45 | -1.41 | 0.084 | 0.354 | 1.000 | 519 | tags=63%, list=34%, signal=95% |
| 183 | GOBP\_REGULATION\_OF\_CELLULAR\_COMPONENT\_MOVEMENT |  | 171 | -0.31 | -1.40 | 0.008 | 0.360 | 1.000 | 567 | tags=44%, list=38%, signal=62% |
| 184 | GOCC\_CELL\_CELL\_JUNCTION |  | 56 | -0.36 | -1.40 | 0.042 | 0.358 | 1.000 | 512 | tags=41%, list=34%, signal=60% |
| 185 | GOBP\_PEPTIDYL\_AMINO\_ACID\_MODIFICATION |  | 117 | -0.32 | -1.40 | 0.020 | 0.358 | 1.000 | 588 | tags=44%, list=39%, signal=67% |
| 186 | GOBP\_REGULATION\_OF\_REPRODUCTIVE\_PROCESS |  | 23 | -0.43 | -1.40 | 0.086 | 0.356 | 1.000 | 654 | tags=65%, list=43%, signal=113% |
| 187 | GOBP\_MORPHOGENESIS\_OF\_A\_POLARIZED\_EPITHELIUM |  | 18 | -0.46 | -1.40 | 0.089 | 0.355 | 1.000 | 326 | tags=39%, list=22%, signal=49% |
| 188 | GOBP\_POSITIVE\_REGULATION\_OF\_PROTEIN\_BINDING |  | 15 | -0.49 | -1.40 | 0.077 | 0.354 | 1.000 | 228 | tags=40%, list=15%, signal=47% |
| 189 | GOBP\_ORGANIC\_ACID\_CATABOLIC\_PROCESS |  | 16 | -0.47 | -1.40 | 0.078 | 0.358 | 1.000 | 296 | tags=44%, list=20%, signal=54% |
| 190 | GOBP\_NEGATIVE\_REGULATION\_OF\_ERK1\_AND\_ERK2\_CASCADE |  | 17 | -0.46 | -1.40 | 0.089 | 0.357 | 1.000 | 544 | tags=53%, list=36%, signal=82% |
| 191 | GOBP\_CARTILAGE\_DEVELOPMENT |  | 38 | -0.38 | -1.40 | 0.063 | 0.359 | 1.000 | 680 | tags=68%, list=45%, signal=121% |
| 192 | GOCC\_PIGMENT\_GRANULE |  | 17 | -0.46 | -1.40 | 0.073 | 0.362 | 1.000 | 320 | tags=53%, list=21%, signal=66% |
| 193 | GOBP\_SKELETAL\_SYSTEM\_DEVELOPMENT |  | 95 | -0.33 | -1.40 | 0.030 | 0.361 | 1.000 | 665 | tags=61%, list=44%, signal=102% |
| 194 | GOMF\_EXTRACELLULAR\_MATRIX\_STRUCTURAL\_CONSTITUENT\_CONFERRING\_TENSILE\_STRENGTH |  | 18 | -0.46 | -1.39 | 0.083 | 0.368 | 1.000 | 645 | tags=67%, list=43%, signal=115% |
| 195 | GOBP\_POSITIVE\_REGULATION\_OF\_RESPONSE\_TO\_WOUNDING |  | 18 | -0.46 | -1.39 | 0.094 | 0.367 | 1.000 | 614 | tags=72%, list=41%, signal=120% |
| 196 | GOBP\_POSITIVE\_REGULATION\_OF\_LOCOMOTION |  | 107 | -0.32 | -1.39 | 0.025 | 0.365 | 1.000 | 567 | tags=46%, list=38%, signal=68% |
| 197 | GOBP\_POSITIVE\_REGULATION\_OF\_B\_CELL\_ACTIVATION |  | 17 | -0.45 | -1.39 | 0.092 | 0.365 | 1.000 | 575 | tags=65%, list=38%, signal=103% |
| 198 | GOBP\_RESPONSE\_TO\_ENDOGENOUS\_STIMULUS |  | 248 | -0.30 | -1.39 | 0.008 | 0.364 | 1.000 | 326 | tags=31%, list=22%, signal=33% |
| 199 | GOBP\_ENDODERMAL\_CELL\_DIFFERENTIATION |  | 23 | -0.42 | -1.39 | 0.080 | 0.365 | 1.000 | 672 | tags=83%, list=45%, signal=147% |
| 200 | GOBP\_PROTEIN\_CATABOLIC\_PROCESS |  | 68 | -0.34 | -1.39 | 0.049 | 0.368 | 1.000 | 339 | tags=31%, list=22%, signal=38% |
| 201 | GOBP\_REGULATION\_OF\_CELL\_SUBSTRATE\_ADHESION |  | 41 | -0.37 | -1.39 | 0.065 | 0.375 | 1.000 | 525 | tags=56%, list=35%, signal=84% |
| 202 | GOBP\_NEGATIVE\_REGULATION\_OF\_DEVELOPMENTAL\_PROCESS |  | 144 | -0.31 | -1.39 | 0.020 | 0.374 | 1.000 | 681 | tags=56%, list=45%, signal=92% |
| 203 | GOBP\_CELLULAR\_RESPONSE\_TO\_REACTIVE\_OXYGEN\_SPECIES |  | 22 | -0.43 | -1.38 | 0.097 | 0.373 | 1.000 | 168 | tags=27%, list=11%, signal=30% |
| 204 | GOBP\_LEUKOCYTE\_MIGRATION |  | 107 | -0.32 | -1.38 | 0.033 | 0.376 | 1.000 | 615 | tags=52%, list=41%, signal=82% |
| 205 | GOBP\_GLUCOSE\_METABOLIC\_PROCESS |  | 25 | -0.41 | -1.38 | 0.072 | 0.382 | 1.000 | 121 | tags=24%, list=8%, signal=26% |
| 206 | GOBP\_REGULATION\_OF\_EPITHELIAL\_CELL\_APOPTOTIC\_PROCESS |  | 16 | -0.46 | -1.38 | 0.102 | 0.384 | 1.000 | 519 | tags=69%, list=34%, signal=104% |
| 207 | GOBP\_CALCIUM\_MEDIATED\_SIGNALING |  | 26 | -0.40 | -1.38 | 0.084 | 0.383 | 1.000 | 524 | tags=50%, list=35%, signal=75% |
| 208 | GOBP\_RESPONSE\_TO\_GROWTH\_FACTOR |  | 130 | -0.31 | -1.38 | 0.031 | 0.382 | 1.000 | 632 | tags=52%, list=42%, signal=81% |
| 209 | GOCC\_CONTRACTILE\_FIBER |  | 31 | -0.39 | -1.38 | 0.081 | 0.383 | 1.000 | 548 | tags=52%, list=36%, signal=79% |
| 210 | GOBP\_REGULATION\_OF\_TRANSMEMBRANE\_RECEPTOR\_PROTEIN\_SERINE\_THREONINE\_KINASE\_SIGNALING\_PATHWAY |  | 45 | -0.37 | -1.38 | 0.056 | 0.385 | 1.000 | 654 | tags=62%, list=43%, signal=106% |
| 211 | GOBP\_MUSCLE\_CONTRACTION |  | 53 | -0.35 | -1.37 | 0.062 | 0.389 | 1.000 | 508 | tags=45%, list=34%, signal=66% |
| 212 | GOBP\_CARDIOCYTE\_DIFFERENTIATION |  | 17 | -0.45 | -1.37 | 0.095 | 0.388 | 1.000 | 670 | tags=71%, list=44%, signal=125% |
| 213 | GOBP\_NEGATIVE\_REGULATION\_OF\_CELL\_DIFFERENTIATION |  | 92 | -0.33 | -1.37 | 0.030 | 0.390 | 1.000 | 656 | tags=57%, list=43%, signal=94% |
| 214 | GOBP\_REGULATION\_OF\_ACTIN\_FILAMENT\_ORGANIZATION |  | 41 | -0.37 | -1.37 | 0.063 | 0.390 | 1.000 | 263 | tags=29%, list=17%, signal=34% |
| 215 | GOBP\_REGULATION\_OF\_CELLULAR\_RESPONSE\_TO\_TRANSFORMING\_GROWTH\_FACTOR\_BETA\_STIMULUS |  | 24 | -0.42 | -1.37 | 0.093 | 0.391 | 1.000 | 326 | tags=38%, list=22%, signal=47% |
| 216 | GOBP\_MUSCLE\_SYSTEM\_PROCESS |  | 63 | -0.34 | -1.37 | 0.069 | 0.392 | 1.000 | 508 | tags=44%, list=34%, signal=64% |
| 217 | GOBP\_POSITIVE\_REGULATION\_OF\_PROTEOLYSIS |  | 47 | -0.36 | -1.37 | 0.069 | 0.391 | 1.000 | 363 | tags=34%, list=24%, signal=43% |
| 218 | GOBP\_UROGENITAL\_SYSTEM\_DEVELOPMENT |  | 53 | -0.35 | -1.37 | 0.079 | 0.390 | 1.000 | 447 | tags=42%, list=30%, signal=57% |
| 219 | GOBP\_EMBRYONIC\_SKELETAL\_SYSTEM\_MORPHOGENESIS |  | 21 | -0.43 | -1.37 | 0.096 | 0.390 | 1.000 | 652 | tags=62%, list=43%, signal=107% |
| 220 | GOBP\_B\_CELL\_ACTIVATION |  | 49 | -0.36 | -1.37 | 0.069 | 0.391 | 1.000 | 575 | tags=61%, list=38%, signal=96% |
| 221 | GOBP\_MITOCHONDRIAL\_TRANSPORT |  | 16 | -0.46 | -1.36 | 0.103 | 0.395 | 1.000 | 267 | tags=31%, list=18%, signal=38% |
| 222 | GOBP\_EXTRACELLULAR\_MATRIX\_DISASSEMBLY |  | 21 | -0.43 | -1.36 | 0.096 | 0.393 | 1.000 | 407 | tags=57%, list=27%, signal=77% |
| 223 | GOBP\_RESPONSE\_TO\_VITAMIN |  | 24 | -0.42 | -1.36 | 0.093 | 0.394 | 1.000 | 573 | tags=63%, list=38%, signal=99% |
| 224 | GOBP\_POSITIVE\_REGULATION\_OF\_WOUND\_HEALING |  | 15 | -0.47 | -1.36 | 0.100 | 0.392 | 1.000 | 516 | tags=67%, list=34%, signal=100% |
| 225 | GOBP\_POSITIVE\_REGULATION\_OF\_ORGANELLE\_ORGANIZATION |  | 60 | -0.34 | -1.36 | 0.057 | 0.392 | 1.000 | 267 | tags=30%, list=18%, signal=35% |
| 226 | GOBP\_REGULATION\_OF\_PROTEIN\_SERINE\_THREONINE\_KINASE\_ACTIVITY |  | 62 | -0.34 | -1.36 | 0.063 | 0.393 | 1.000 | 319 | tags=34%, list=21%, signal=41% |
| 227 | GOBP\_VITAMIN\_METABOLIC\_PROCESS |  | 17 | -0.45 | -1.36 | 0.101 | 0.396 | 1.000 | 291 | tags=53%, list=19%, signal=65% |
| 228 | GOBP\_CELLULAR\_RESPONSE\_TO\_CHEMICAL\_STRESS |  | 49 | -0.35 | -1.36 | 0.080 | 0.397 | 1.000 | 326 | tags=35%, list=22%, signal=43% |
| 229 | GOCC\_ACTIN\_CYTOSKELETON |  | 63 | -0.33 | -1.36 | 0.068 | 0.397 | 1.000 | 327 | tags=32%, list=22%, signal=39% |
| 230 | GOBP\_CELL\_CELL\_JUNCTION\_ASSEMBLY |  | 20 | -0.44 | -1.36 | 0.093 | 0.396 | 1.000 | 633 | tags=55%, list=42%, signal=93% |
| 231 | GOBP\_SEXUAL\_REPRODUCTION |  | 68 | -0.33 | -1.36 | 0.048 | 0.397 | 1.000 | 673 | tags=60%, list=45%, signal=104% |
| 232 | GOBP\_TRANSFORMING\_GROWTH\_FACTOR\_BETA\_RECEPTOR\_SIGNALING\_PATHWAY |  | 40 | -0.37 | -1.36 | 0.082 | 0.401 | 1.000 | 632 | tags=55%, list=42%, signal=92% |
| 233 | GOBP\_MUSCLE\_CELL\_DEVELOPMENT |  | 27 | -0.39 | -1.35 | 0.094 | 0.401 | 1.000 | 784 | tags=74%, list=52%, signal=151% |
| 234 | GOBP\_CELL\_FATE\_SPECIFICATION |  | 16 | -0.45 | -1.35 | 0.110 | 0.419 | 1.000 | 373 | tags=56%, list=25%, signal=74% |
| 235 | GOBP\_REGULATION\_OF\_GROWTH |  | 91 | -0.32 | -1.35 | 0.057 | 0.420 | 1.000 | 536 | tags=42%, list=35%, signal=61% |
| 236 | GOBP\_ALPHA\_AMINO\_ACID\_METABOLIC\_PROCESS |  | 15 | -0.45 | -1.35 | 0.113 | 0.420 | 1.000 | 296 | tags=47%, list=20%, signal=57% |
| 237 | GOBP\_ANTERIOR\_POSTERIOR\_PATTERN\_SPECIFICATION |  | 32 | -0.39 | -1.35 | 0.084 | 0.418 | 1.000 | 665 | tags=66%, list=44%, signal=115% |
| 238 | GOBP\_ANATOMICAL\_STRUCTURE\_MATURATION |  | 24 | -0.41 | -1.35 | 0.101 | 0.417 | 1.000 | 512 | tags=54%, list=34%, signal=81% |
| 239 | GOBP\_CELL\_CELL\_JUNCTION\_ORGANIZATION |  | 25 | -0.40 | -1.34 | 0.111 | 0.417 | 1.000 | 512 | tags=44%, list=34%, signal=65% |
| 240 | GOBP\_RESPONSE\_TO\_LIPID |  | 155 | -0.30 | -1.34 | 0.035 | 0.429 | 1.000 | 363 | tags=36%, list=24%, signal=43% |
| 241 | GOBP\_POSITIVE\_REGULATION\_OF\_NEUROGENESIS |  | 29 | -0.39 | -1.34 | 0.093 | 0.429 | 1.000 | 619 | tags=48%, list=41%, signal=80% |
| 242 | GOMF\_GTPASE\_BINDING |  | 18 | -0.44 | -1.34 | 0.119 | 0.427 | 1.000 | 192 | tags=17%, list=13%, signal=19% |
| 243 | GOBP\_TELENCEPHALON\_DEVELOPMENT |  | 27 | -0.39 | -1.34 | 0.090 | 0.432 | 1.000 | 850 | tags=93%, list=56%, signal=208% |
| 244 | GOBP\_CELL\_CELL\_ADHESION |  | 124 | -0.30 | -1.34 | 0.050 | 0.431 | 1.000 | 512 | tags=39%, list=34%, signal=54% |
| 245 | GOBP\_CELLULAR\_PROTEIN\_CATABOLIC\_PROCESS |  | 49 | -0.35 | -1.34 | 0.092 | 0.433 | 1.000 | 326 | tags=29%, list=22%, signal=35% |
| 246 | GOBP\_REGULATION\_OF\_SUPRAMOLECULAR\_FIBER\_ORGANIZATION |  | 54 | -0.34 | -1.33 | 0.081 | 0.434 | 1.000 | 267 | tags=28%, list=18%, signal=33% |
| 247 | GOBP\_POSITIVE\_REGULATION\_OF\_MAP\_KINASE\_ACTIVITY |  | 26 | -0.39 | -1.33 | 0.110 | 0.432 | 1.000 | 516 | tags=50%, list=34%, signal=75% |
| 248 | GOBP\_CELL\_PROJECTION\_ASSEMBLY |  | 36 | -0.37 | -1.33 | 0.092 | 0.433 | 1.000 | 170 | tags=22%, list=11%, signal=24% |
| 249 | GOBP\_TRANSMEMBRANE\_RECEPTOR\_PROTEIN\_TYROSINE\_KINASE\_SIGNALING\_PATHWAY |  | 99 | -0.31 | -1.33 | 0.054 | 0.432 | 1.000 | 545 | tags=40%, list=36%, signal=59% |
| 250 | GOBP\_ERYTHROCYTE\_HOMEOSTASIS |  | 18 | -0.44 | -1.33 | 0.136 | 0.432 | 1.000 | 85 | tags=22%, list=6%, signal=23% |
| 251 | GOBP\_REGULATION\_OF\_CELL\_DEVELOPMENT |  | 63 | -0.34 | -1.33 | 0.073 | 0.446 | 1.000 | 622 | tags=51%, list=41%, signal=83% |
| 252 | GOBP\_SECOND\_MESSENGER\_MEDIATED\_SIGNALING |  | 48 | -0.34 | -1.33 | 0.090 | 0.445 | 1.000 | 524 | tags=46%, list=35%, signal=68% |
| 253 | GOBP\_REGULATION\_OF\_RESPONSE\_TO\_WOUNDING |  | 34 | -0.37 | -1.33 | 0.111 | 0.444 | 1.000 | 455 | tags=50%, list=30%, signal=70% |
| 254 | GOBP\_RESPONSE\_TO\_FIBROBLAST\_GROWTH\_FACTOR |  | 19 | -0.42 | -1.33 | 0.122 | 0.443 | 1.000 | 614 | tags=68%, list=41%, signal=114% |
| 255 | GOMF\_PROTEASE\_BINDING |  | 19 | -0.43 | -1.33 | 0.119 | 0.442 | 1.000 | 554 | tags=63%, list=37%, signal=99% |
| 256 | GOBP\_CIRCULATORY\_SYSTEM\_PROCESS |  | 99 | -0.31 | -1.33 | 0.058 | 0.441 | 1.000 | 519 | tags=45%, list=34%, signal=65% |
| 257 | GOBP\_MONOSACCHARIDE\_METABOLIC\_PROCESS |  | 28 | -0.39 | -1.32 | 0.124 | 0.452 | 1.000 | 135 | tags=25%, list=9%, signal=27% |
| 258 | GOBP\_POSITIVE\_REGULATION\_OF\_DEVELOPMENTAL\_GROWTH |  | 23 | -0.41 | -1.32 | 0.128 | 0.454 | 1.000 | 536 | tags=48%, list=35%, signal=73% |
| 259 | GOBP\_REGULATION\_OF\_PEPTIDYL\_TYROSINE\_PHOSPHORYLATION |  | 47 | -0.34 | -1.32 | 0.103 | 0.453 | 1.000 | 559 | tags=45%, list=37%, signal=69% |
| 260 | GOBP\_REGULATION\_OF\_SMALL\_MOLECULE\_METABOLIC\_PROCESS |  | 42 | -0.35 | -1.32 | 0.104 | 0.452 | 1.000 | 578 | tags=50%, list=38%, signal=79% |
| 261 | GOBP\_REGULATION\_OF\_MULTICELLULAR\_ORGANISMAL\_DEVELOPMENT |  | 226 | -0.29 | -1.32 | 0.027 | 0.452 | 1.000 | 624 | tags=48%, list=41%, signal=69% |
| 262 | GOBP\_NEGATIVE\_REGULATION\_OF\_MULTICELLULAR\_ORGANISMAL\_PROCESS |  | 176 | -0.29 | -1.32 | 0.037 | 0.454 | 1.000 | 688 | tags=53%, list=46%, signal=86% |
| 263 | GOBP\_REGULATION\_OF\_CELL\_SIZE |  | 20 | -0.42 | -1.32 | 0.128 | 0.453 | 1.000 | 442 | tags=40%, list=29%, signal=56% |
| 264 | GOBP\_STRIATED\_MUSCLE\_CELL\_DEVELOPMENT |  | 17 | -0.44 | -1.32 | 0.135 | 0.452 | 1.000 | 328 | tags=41%, list=22%, signal=52% |
| 265 | GOBP\_SMALL\_MOLECULE\_CATABOLIC\_PROCESS |  | 29 | -0.38 | -1.32 | 0.124 | 0.452 | 1.000 | 365 | tags=38%, list=24%, signal=49% |
| 266 | GOMF\_ANION\_TRANSMEMBRANE\_TRANSPORTER\_ACTIVITY |  | 29 | -0.38 | -1.32 | 0.109 | 0.451 | 1.000 | 438 | tags=52%, list=29%, signal=71% |
| 267 | GOMF\_SIGNALING\_RECEPTOR\_BINDING |  | 261 | -0.28 | -1.32 | 0.016 | 0.450 | 1.000 | 589 | tags=46%, list=39%, signal=62% |
| 268 | GOBP\_NEGATIVE\_REGULATION\_OF\_RESPONSE\_TO\_EXTERNAL\_STIMULUS |  | 55 | -0.33 | -1.32 | 0.093 | 0.449 | 1.000 | 516 | tags=45%, list=34%, signal=67% |
| 269 | GOBP\_EPITHELIAL\_TO\_MESENCHYMAL\_TRANSITION |  | 25 | -0.40 | -1.32 | 0.130 | 0.449 | 1.000 | 254 | tags=36%, list=17%, signal=43% |
| 270 | GOBP\_MORPHOGENESIS\_OF\_AN\_EPITHELIUM |  | 74 | -0.32 | -1.31 | 0.085 | 0.450 | 1.000 | 440 | tags=39%, list=29%, signal=53% |
| 271 | GOBP\_AMEBOIDAL\_TYPE\_CELL\_MIGRATION |  | 64 | -0.33 | -1.31 | 0.081 | 0.449 | 1.000 | 627 | tags=55%, list=42%, signal=90% |
| 272 | GOBP\_REGULATION\_OF\_TUBE\_SIZE |  | 21 | -0.41 | -1.31 | 0.126 | 0.447 | 1.000 | 382 | tags=43%, list=25%, signal=57% |
| 273 | GOBP\_NEGATIVE\_REGULATION\_OF\_CELL\_DEVELOPMENT |  | 24 | -0.40 | -1.31 | 0.126 | 0.450 | 1.000 | 644 | tags=63%, list=43%, signal=107% |
| 274 | GOCC\_BLOOD\_MICROPARTICLE |  | 34 | -0.37 | -1.31 | 0.109 | 0.451 | 1.000 | 500 | tags=53%, list=33%, signal=77% |
| 275 | GOMF\_SULFUR\_COMPOUND\_BINDING |  | 65 | -0.33 | -1.31 | 0.090 | 0.451 | 1.000 | 533 | tags=51%, list=35%, signal=75% |
| 276 | GOBP\_CELLULAR\_AMINO\_ACID\_METABOLIC\_PROCESS |  | 21 | -0.42 | -1.31 | 0.123 | 0.451 | 1.000 | 299 | tags=38%, list=20%, signal=47% |
| 277 | GOBP\_ACTIN\_POLYMERIZATION\_OR\_DEPOLYMERIZATION |  | 28 | -0.38 | -1.31 | 0.139 | 0.450 | 1.000 | 229 | tags=29%, list=15%, signal=33% |
| 278 | GOBP\_ACTIVATION\_OF\_PROTEIN\_KINASE\_ACTIVITY |  | 36 | -0.36 | -1.31 | 0.116 | 0.449 | 1.000 | 559 | tags=47%, list=37%, signal=73% |
| 279 | GOBP\_REGULATION\_OF\_MITOCHONDRION\_ORGANIZATION |  | 18 | -0.43 | -1.31 | 0.141 | 0.453 | 1.000 | 267 | tags=33%, list=18%, signal=40% |
| 280 | GOBP\_RESPONSE\_TO\_OXYGEN\_CONTAINING\_COMPOUND |  | 250 | -0.28 | -1.31 | 0.022 | 0.455 | 1.000 | 579 | tags=46%, list=38%, signal=62% |
| 281 | GOBP\_HEART\_DEVELOPMENT |  | 68 | -0.32 | -1.31 | 0.095 | 0.455 | 1.000 | 670 | tags=53%, list=44%, signal=91% |
| 282 | GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_POPULATION\_PROLIFERATION |  | 155 | -0.29 | -1.31 | 0.064 | 0.456 | 1.000 | 519 | tags=40%, list=34%, signal=55% |
| 283 | GOBP\_ACTIN\_FILAMENT\_BASED\_PROCESS |  | 91 | -0.31 | -1.30 | 0.084 | 0.456 | 1.000 | 327 | tags=27%, list=22%, signal=33% |
| 284 | GOBP\_DEFENSE\_RESPONSE\_TO\_VIRUS |  | 25 | -0.39 | -1.30 | 0.133 | 0.457 | 1.000 | 466 | tags=44%, list=31%, signal=63% |
| 285 | GOBP\_REGULATION\_OF\_B\_CELL\_ACTIVATION |  | 31 | -0.38 | -1.30 | 0.119 | 0.457 | 1.000 | 575 | tags=61%, list=38%, signal=97% |
| 286 | GOBP\_LEUKOCYTE\_DIFFERENTIATION |  | 88 | -0.31 | -1.30 | 0.065 | 0.458 | 1.000 | 636 | tags=55%, list=42%, signal=89% |
| 287 | GOBP\_ENDOTHELIAL\_CELL\_PROLIFERATION |  | 37 | -0.36 | -1.30 | 0.116 | 0.457 | 1.000 | 336 | tags=35%, list=22%, signal=44% |
| 288 | GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_SUBSTRATE\_ADHESION |  | 22 | -0.41 | -1.30 | 0.141 | 0.460 | 1.000 | 453 | tags=55%, list=30%, signal=77% |
| 289 | GOBP\_TUBE\_MORPHOGENESIS |  | 151 | -0.29 | -1.30 | 0.064 | 0.460 | 1.000 | 339 | tags=32%, list=22%, signal=38% |
| 290 | GOBP\_CELL\_POPULATION\_PROLIFERATION |  | 303 | -0.28 | -1.30 | 0.019 | 0.460 | 1.000 | 525 | tags=41%, list=35%, signal=50% |
| 291 | GOCC\_SARCOLEMMA |  | 24 | -0.40 | -1.30 | 0.138 | 0.461 | 1.000 | 328 | tags=33%, list=22%, signal=42% |
| 292 | GOBP\_REGULATION\_OF\_WOUND\_HEALING |  | 29 | -0.38 | -1.30 | 0.155 | 0.461 | 1.000 | 455 | tags=52%, list=30%, signal=73% |
| 293 | GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_DEVELOPMENT |  | 39 | -0.36 | -1.30 | 0.113 | 0.463 | 1.000 | 577 | tags=49%, list=38%, signal=77% |
| 294 | GOBP\_CELLULAR\_PROCESS\_INVOLVED\_IN\_REPRODUCTION\_IN\_MULTICELLULAR\_ORGANISM |  | 25 | -0.39 | -1.30 | 0.152 | 0.462 | 1.000 | 644 | tags=68%, list=43%, signal=117% |
| 295 | GOBP\_REGULATION\_OF\_PROTEIN\_PHOSPHORYLATION |  | 158 | -0.29 | -1.30 | 0.052 | 0.464 | 1.000 | 559 | tags=42%, list=37%, signal=59% |
| 296 | GOBP\_MOVEMENT\_IN\_HOST\_ENVIRONMENT |  | 25 | -0.38 | -1.29 | 0.145 | 0.465 | 1.000 | 715 | tags=72%, list=47%, signal=134% |
| 297 | GOBP\_COLLAGEN\_METABOLIC\_PROCESS |  | 30 | -0.37 | -1.29 | 0.150 | 0.464 | 1.000 | 534 | tags=57%, list=35%, signal=86% |
| 298 | GOBP\_REGULATION\_OF\_PROTEIN\_BINDING |  | 27 | -0.39 | -1.29 | 0.137 | 0.463 | 1.000 | 228 | tags=30%, list=15%, signal=34% |
| 299 | GOBP\_NEGATIVE\_REGULATION\_OF\_NEURON\_DEATH |  | 35 | -0.36 | -1.29 | 0.148 | 0.462 | 1.000 | 359 | tags=34%, list=24%, signal=44% |
| 300 | GOBP\_BIOMINERALIZATION |  | 35 | -0.36 | -1.29 | 0.127 | 0.462 | 1.000 | 292 | tags=37%, list=19%, signal=45% |
| 301 | GOCC\_FICOLIN\_1\_RICH\_GRANULE |  | 28 | -0.38 | -1.29 | 0.134 | 0.461 | 1.000 | 135 | tags=25%, list=9%, signal=27% |
| 302 | GOBP\_STRIATED\_MUSCLE\_CELL\_DIFFERENTIATION |  | 40 | -0.35 | -1.29 | 0.141 | 0.461 | 1.000 | 784 | tags=65%, list=52%, signal=132% |
| 303 | GOBP\_REGULATION\_OF\_PHOSPHORUS\_METABOLIC\_PROCESS |  | 184 | -0.28 | -1.29 | 0.055 | 0.463 | 1.000 | 567 | tags=42%, list=38%, signal=59% |
| 304 | GOBP\_ACTIN\_FILAMENT\_BASED\_MOVEMENT |  | 20 | -0.41 | -1.29 | 0.139 | 0.461 | 1.000 | 508 | tags=45%, list=34%, signal=67% |
| 305 | GOBP\_ANATOMICAL\_STRUCTURE\_FORMATION\_INVOLVED\_IN\_MORPHOGENESIS |  | 195 | -0.28 | -1.29 | 0.044 | 0.462 | 1.000 | 681 | tags=53%, list=45%, signal=85% |
| 306 | GOBP\_NEGATIVE\_REGULATION\_OF\_CELL\_POPULATION\_PROLIFERATION |  | 132 | -0.29 | -1.29 | 0.072 | 0.462 | 1.000 | 627 | tags=48%, list=42%, signal=76% |
| 307 | GOBP\_ACTOMYOSIN\_STRUCTURE\_ORGANIZATION |  | 26 | -0.39 | -1.29 | 0.157 | 0.469 | 1.000 | 327 | tags=35%, list=22%, signal=43% |
| 308 | GOBP\_BONE\_REMODELING |  | 19 | -0.41 | -1.29 | 0.156 | 0.472 | 1.000 | 254 | tags=37%, list=17%, signal=44% |
| 309 | GOBP\_MUSCLE\_STRUCTURE\_DEVELOPMENT |  | 93 | -0.30 | -1.28 | 0.091 | 0.474 | 1.000 | 734 | tags=56%, list=49%, signal=102% |
| 310 | GOBP\_GAMETE\_GENERATION |  | 48 | -0.34 | -1.28 | 0.112 | 0.473 | 1.000 | 670 | tags=63%, list=44%, signal=109% |
| 311 | GOBP\_POSITIVE\_REGULATION\_OF\_PHOSPHORUS\_METABOLIC\_PROCESS |  | 129 | -0.29 | -1.28 | 0.079 | 0.473 | 1.000 | 559 | tags=41%, list=37%, signal=60% |
| 312 | GOBP\_REGULATION\_OF\_ANATOMICAL\_STRUCTURE\_SIZE |  | 66 | -0.32 | -1.28 | 0.099 | 0.471 | 1.000 | 229 | tags=24%, list=15%, signal=27% |
| 313 | GOBP\_NEGATIVE\_REGULATION\_OF\_RESPONSE\_TO\_STIMULUS |  | 226 | -0.28 | -1.28 | 0.047 | 0.475 | 1.000 | 682 | tags=50%, list=45%, signal=78% |
| 314 | GOBP\_RESPONSE\_TO\_STARVATION |  | 24 | -0.39 | -1.28 | 0.150 | 0.483 | 1.000 | 543 | tags=58%, list=36%, signal=90% |
| 315 | GOBP\_EAR\_MORPHOGENESIS |  | 15 | -0.43 | -1.28 | 0.176 | 0.483 | 1.000 | 654 | tags=67%, list=43%, signal=116% |
| 316 | GOBP\_MUSCLE\_ORGAN\_DEVELOPMENT |  | 53 | -0.33 | -1.28 | 0.128 | 0.485 | 1.000 | 817 | tags=70%, list=54%, signal=147% |
| 317 | GOBP\_VASCULATURE\_DEVELOPMENT |  | 138 | -0.29 | -1.28 | 0.075 | 0.486 | 1.000 | 339 | tags=31%, list=22%, signal=37% |
| 318 | GOMF\_TRANSITION\_METAL\_ION\_BINDING |  | 95 | -0.30 | -1.28 | 0.104 | 0.485 | 1.000 | 497 | tags=43%, list=33%, signal=60% |
| 319 | GOBP\_DEVELOPMENTAL\_GROWTH\_INVOLVED\_IN\_MORPHOGENESIS |  | 35 | -0.35 | -1.27 | 0.152 | 0.493 | 1.000 | 611 | tags=43%, list=40%, signal=70% |
| 320 | GOBP\_BIOLOGICAL\_PROCESS\_INVOLVED\_IN\_INTERACTION\_WITH\_HOST |  | 28 | -0.37 | -1.27 | 0.134 | 0.492 | 1.000 | 634 | tags=64%, list=42%, signal=109% |
| 321 | GOBP\_HEAD\_DEVELOPMENT |  | 93 | -0.30 | -1.27 | 0.100 | 0.492 | 1.000 | 738 | tags=58%, list=49%, signal=107% |
| 322 | GOBP\_PROTEIN\_PHOSPHORYLATION |  | 185 | -0.28 | -1.27 | 0.068 | 0.491 | 1.000 | 559 | tags=41%, list=37%, signal=56% |
| 323 | GOBP\_CELLULAR\_RESPONSE\_TO\_PEPTIDE |  | 47 | -0.34 | -1.27 | 0.143 | 0.491 | 1.000 | 336 | tags=34%, list=22%, signal=42% |
| 324 | GOBP\_SENSORY\_PERCEPTION\_OF\_MECHANICAL\_STIMULUS |  | 22 | -0.40 | -1.27 | 0.167 | 0.490 | 1.000 | 673 | tags=73%, list=45%, signal=129% |
| 325 | GOBP\_NEGATIVE\_REGULATION\_OF\_DEFENSE\_RESPONSE |  | 32 | -0.36 | -1.27 | 0.159 | 0.489 | 1.000 | 512 | tags=47%, list=34%, signal=69% |
| 326 | GOBP\_ANATOMICAL\_STRUCTURE\_HOMEOSTASIS |  | 60 | -0.32 | -1.27 | 0.135 | 0.488 | 1.000 | 542 | tags=43%, list=36%, signal=65% |
| 327 | GOBP\_CELL\_SUBSTRATE\_JUNCTION\_ORGANIZATION |  | 17 | -0.43 | -1.27 | 0.185 | 0.497 | 1.000 | 535 | tags=59%, list=35%, signal=90% |
| 328 | GOBP\_REGULATION\_OF\_MACROPHAGE\_MIGRATION |  | 16 | -0.42 | -1.27 | 0.174 | 0.496 | 1.000 | 559 | tags=56%, list=37%, signal=88% |
| 329 | GOBP\_VIRAL\_LIFE\_CYCLE |  | 37 | -0.35 | -1.26 | 0.153 | 0.500 | 1.000 | 744 | tags=70%, list=49%, signal=135% |
| 330 | GOBP\_CARDIAC\_MUSCLE\_TISSUE\_DEVELOPMENT |  | 20 | -0.41 | -1.26 | 0.164 | 0.503 | 1.000 | 784 | tags=80%, list=52%, signal=164% |
| 331 | GOBP\_REGULATION\_OF\_AUTOPHAGY |  | 22 | -0.38 | -1.26 | 0.162 | 0.502 | 1.000 | 192 | tags=27%, list=13%, signal=31% |
| 332 | GOBP\_RESPONSE\_TO\_INSULIN |  | 30 | -0.37 | -1.26 | 0.170 | 0.501 | 1.000 | 307 | tags=33%, list=20%, signal=41% |
| 333 | GOBP\_PATTERN\_SPECIFICATION\_PROCESS |  | 59 | -0.32 | -1.26 | 0.131 | 0.502 | 1.000 | 665 | tags=58%, list=44%, signal=99% |
| 334 | GOBP\_POSITIVE\_REGULATION\_OF\_PROTEIN\_PHOSPHORYLATION |  | 113 | -0.29 | -1.26 | 0.103 | 0.500 | 1.000 | 588 | tags=42%, list=39%, signal=64% |
| 335 | GOCC\_CELL\_SURFACE |  | 122 | -0.29 | -1.26 | 0.090 | 0.501 | 1.000 | 538 | tags=45%, list=36%, signal=64% |
| 336 | GOBP\_CELL\_MATRIX\_ADHESION |  | 40 | -0.34 | -1.26 | 0.151 | 0.500 | 1.000 | 554 | tags=55%, list=37%, signal=85% |
| 337 | GOBP\_CELLULAR\_KETONE\_METABOLIC\_PROCESS |  | 20 | -0.40 | -1.26 | 0.173 | 0.501 | 1.000 | 485 | tags=50%, list=32%, signal=73% |
| 338 | GOBP\_EPITHELIAL\_CELL\_PROLIFERATION |  | 81 | -0.30 | -1.26 | 0.101 | 0.500 | 1.000 | 281 | tags=28%, list=19%, signal=33% |
| 339 | GOMF\_RECEPTOR\_REGULATOR\_ACTIVITY |  | 119 | -0.29 | -1.26 | 0.106 | 0.499 | 1.000 | 605 | tags=47%, list=40%, signal=72% |
| 340 | GOBP\_ENTRY\_INTO\_HOST |  | 25 | -0.38 | -1.26 | 0.171 | 0.498 | 1.000 | 715 | tags=72%, list=47%, signal=134% |
| 341 | GOCC\_COATED\_VESICLE |  | 23 | -0.39 | -1.26 | 0.168 | 0.497 | 1.000 | 457 | tags=39%, list=30%, signal=55% |
| 342 | GOBP\_CONNECTIVE\_TISSUE\_DEVELOPMENT |  | 47 | -0.34 | -1.26 | 0.165 | 0.496 | 1.000 | 680 | tags=66%, list=45%, signal=116% |
| 343 | GOBP\_CELLULAR\_RESPONSE\_TO\_LIPID |  | 85 | -0.30 | -1.26 | 0.133 | 0.495 | 1.000 | 573 | tags=52%, list=38%, signal=79% |
| 344 | GOBP\_REGULATION\_OF\_INTRINSIC\_APOPTOTIC\_SIGNALING\_PATHWAY |  | 26 | -0.38 | -1.26 | 0.183 | 0.494 | 1.000 | 539 | tags=46%, list=36%, signal=71% |
| 345 | GOBP\_NEGATIVE\_REGULATION\_OF\_SIGNALING |  | 193 | -0.28 | -1.26 | 0.079 | 0.493 | 1.000 | 688 | tags=51%, list=46%, signal=81% |
| 346 | GOBP\_REGULATION\_OF\_ACTIN\_FILAMENT\_BASED\_PROCESS |  | 53 | -0.32 | -1.26 | 0.139 | 0.498 | 1.000 | 263 | tags=25%, list=17%, signal=29% |
| 347 | GOCC\_ENDOCYTIC\_VESICLE\_MEMBRANE |  | 24 | -0.38 | -1.26 | 0.179 | 0.497 | 1.000 | 468 | tags=42%, list=31%, signal=59% |
| 348 | GOBP\_HOMOTYPIC\_CELL\_CELL\_ADHESION |  | 17 | -0.42 | -1.26 | 0.191 | 0.497 | 1.000 | 682 | tags=59%, list=45%, signal=106% |
| 349 | GOCC\_ANCHORED\_COMPONENT\_OF\_MEMBRANE |  | 31 | -0.36 | -1.25 | 0.150 | 0.498 | 1.000 | 743 | tags=71%, list=49%, signal=137% |
| 350 | GOBP\_NEGATIVE\_REGULATION\_OF\_EPITHELIAL\_CELL\_PROLIFERATION |  | 33 | -0.35 | -1.25 | 0.155 | 0.500 | 1.000 | 516 | tags=45%, list=34%, signal=68% |
| 351 | GOBP\_EAR\_DEVELOPMENT |  | 28 | -0.37 | -1.25 | 0.180 | 0.499 | 1.000 | 401 | tags=39%, list=27%, signal=52% |
| 352 | GOMF\_EXTRACELLULAR\_MATRIX\_BINDING |  | 25 | -0.38 | -1.25 | 0.177 | 0.501 | 1.000 | 198 | tags=36%, list=13%, signal=41% |
| 353 | GOCC\_CYTOPLASMIC\_REGION |  | 21 | -0.39 | -1.25 | 0.168 | 0.501 | 1.000 | 529 | tags=43%, list=35%, signal=65% |
| 354 | GOBP\_POSITIVE\_REGULATION\_OF\_NERVOUS\_SYSTEM\_DEVELOPMENT |  | 31 | -0.36 | -1.25 | 0.164 | 0.501 | 1.000 | 619 | tags=45%, list=41%, signal=75% |
| 355 | GOBP\_WOUND\_HEALING |  | 82 | -0.30 | -1.25 | 0.113 | 0.500 | 1.000 | 530 | tags=49%, list=35%, signal=71% |
| 356 | GOBP\_RESPONSE\_TO\_WOUNDING |  | 112 | -0.29 | -1.25 | 0.116 | 0.501 | 1.000 | 554 | tags=48%, list=37%, signal=71% |
| 357 | GOBP\_BLOOD\_VESSEL\_MORPHOGENESIS |  | 125 | -0.29 | -1.25 | 0.100 | 0.499 | 1.000 | 339 | tags=31%, list=22%, signal=37% |
| 358 | GOBP\_NEGATIVE\_REGULATION\_OF\_PROTEIN\_SERINE\_THREONINE\_KINASE\_ACTIVITY |  | 28 | -0.37 | -1.25 | 0.182 | 0.510 | 1.000 | 382 | tags=43%, list=25%, signal=56% |
| 359 | GOBP\_REGULATION\_OF\_OSSIFICATION |  | 26 | -0.37 | -1.25 | 0.187 | 0.510 | 1.000 | 294 | tags=35%, list=19%, signal=42% |
| 360 | GOBP\_GLIOGENESIS |  | 46 | -0.32 | -1.24 | 0.161 | 0.520 | 1.000 | 632 | tags=54%, list=42%, signal=91% |
| 361 | GOMF\_SEQUENCE\_SPECIFIC\_DNA\_BINDING |  | 111 | -0.29 | -1.24 | 0.118 | 0.528 | 1.000 | 672 | tags=56%, list=45%, signal=93% |
| 362 | GOMF\_PROTEIN\_SERINE\_THREONINE\_KINASE\_ACTIVITY |  | 20 | -0.40 | -1.24 | 0.191 | 0.527 | 1.000 | 261 | tags=30%, list=17%, signal=36% |
| 363 | GOBP\_REGULATION\_OF\_LYMPHOCYTE\_ACTIVATION |  | 84 | -0.29 | -1.24 | 0.147 | 0.526 | 1.000 | 575 | tags=44%, list=38%, signal=67% |
| 364 | GOMF\_PEPTIDASE\_ACTIVITY |  | 58 | -0.31 | -1.24 | 0.171 | 0.525 | 1.000 | 487 | tags=50%, list=32%, signal=71% |
| 365 | GOBP\_NEGATIVE\_REGULATION\_OF\_RESPONSE\_TO\_WOUNDING |  | 20 | -0.39 | -1.24 | 0.172 | 0.526 | 1.000 | 413 | tags=50%, list=27%, signal=68% |
| 366 | GOBP\_CELLULAR\_RESPONSE\_TO\_ABIOTIC\_STIMULUS |  | 41 | -0.34 | -1.24 | 0.180 | 0.526 | 1.000 | 297 | tags=37%, list=20%, signal=44% |
| 367 | GOCC\_PLATELET\_ALPHA\_GRANULE\_LUMEN |  | 23 | -0.38 | -1.24 | 0.179 | 0.525 | 1.000 | 375 | tags=43%, list=25%, signal=57% |
| 368 | GOMF\_HORMONE\_ACTIVITY |  | 43 | -0.33 | -1.24 | 0.171 | 0.524 | 1.000 | 731 | tags=58%, list=48%, signal=109% |
| 369 | GOBP\_CELLULAR\_RESPONSE\_TO\_EXTRACELLULAR\_STIMULUS |  | 37 | -0.34 | -1.24 | 0.182 | 0.524 | 1.000 | 707 | tags=62%, list=47%, signal=114% |
| 370 | GOBP\_INTRACELLULAR\_RECEPTOR\_SIGNALING\_PATHWAY |  | 22 | -0.38 | -1.24 | 0.189 | 0.524 | 1.000 | 362 | tags=41%, list=24%, signal=53% |
| 371 | GOMF\_PROTEIN\_CONTAINING\_COMPLEX\_BINDING |  | 168 | -0.27 | -1.24 | 0.099 | 0.523 | 1.000 | 567 | tags=45%, list=38%, signal=64% |
| 372 | GOCC\_CENTROSOME |  | 31 | -0.35 | -1.24 | 0.188 | 0.522 | 1.000 | 749 | tags=74%, list=50%, signal=144% |
| 373 | GOMF\_TRANSCRIPTION\_REGULATOR\_ACTIVITY |  | 133 | -0.28 | -1.23 | 0.113 | 0.523 | 1.000 | 654 | tags=53%, list=43%, signal=85% |
| 374 | GOBP\_INOSITOL\_LIPID\_MEDIATED\_SIGNALING |  | 16 | -0.42 | -1.23 | 0.194 | 0.523 | 1.000 | 783 | tags=75%, list=52%, signal=154% |
| 375 | GOBP\_RESPONSE\_TO\_REACTIVE\_OXYGEN\_SPECIES |  | 32 | -0.35 | -1.23 | 0.191 | 0.522 | 1.000 | 228 | tags=28%, list=15%, signal=32% |
| 376 | GOBP\_CENTRAL\_NERVOUS\_SYSTEM\_DEVELOPMENT |  | 124 | -0.28 | -1.23 | 0.133 | 0.525 | 1.000 | 738 | tags=55%, list=49%, signal=98% |
| 377 | GOBP\_BIOLOGICAL\_PROCESS\_INVOLVED\_IN\_INTERACTION\_WITH\_SYMBIONT |  | 18 | -0.40 | -1.23 | 0.203 | 0.524 | 1.000 | 228 | tags=39%, list=15%, signal=45% |
| 378 | GOMF\_ACTIN\_FILAMENT\_BINDING |  | 21 | -0.39 | -1.23 | 0.196 | 0.523 | 1.000 | 508 | tags=52%, list=34%, signal=78% |
| 379 | GOBP\_CIRCULATORY\_SYSTEM\_DEVELOPMENT |  | 178 | -0.27 | -1.23 | 0.100 | 0.524 | 1.000 | 681 | tags=51%, list=45%, signal=81% |
| 380 | GOBP\_MYELOID\_CELL\_HOMEOSTASIS |  | 20 | -0.39 | -1.23 | 0.186 | 0.525 | 1.000 | 85 | tags=20%, list=6%, signal=21% |
| 381 | GOBP\_NEGATIVE\_REGULATION\_OF\_GROWTH |  | 37 | -0.34 | -1.23 | 0.171 | 0.526 | 1.000 | 267 | tags=27%, list=18%, signal=32% |
| 382 | GOBP\_NERVOUS\_SYSTEM\_PROCESS |  | 115 | -0.28 | -1.23 | 0.130 | 0.525 | 1.000 | 253 | tags=25%, list=17%, signal=28% |
| 383 | GOBP\_REGULATION\_OF\_SYSTEMIC\_ARTERIAL\_BLOOD\_PRESSURE |  | 19 | -0.39 | -1.23 | 0.203 | 0.527 | 1.000 | 519 | tags=47%, list=34%, signal=71% |
| 384 | GOCC\_ACTIN\_FILAMENT |  | 21 | -0.39 | -1.23 | 0.205 | 0.530 | 1.000 | 451 | tags=43%, list=30%, signal=60% |
| 385 | GOBP\_RENAL\_SYSTEM\_PROCESS |  | 24 | -0.37 | -1.23 | 0.198 | 0.529 | 1.000 | 223 | tags=29%, list=15%, signal=34% |
| 386 | GOBP\_NEGATIVE\_REGULATION\_OF\_LEUKOCYTE\_CELL\_CELL\_ADHESION |  | 22 | -0.37 | -1.23 | 0.209 | 0.529 | 1.000 | 334 | tags=36%, list=22%, signal=46% |
| 387 | GOCC\_MICROTUBULE\_ORGANIZING\_CENTER |  | 36 | -0.34 | -1.23 | 0.188 | 0.528 | 1.000 | 749 | tags=69%, list=50%, signal=135% |
| 388 | GOBP\_POSITIVE\_REGULATION\_OF\_LEUKOCYTE\_MIGRATION |  | 42 | -0.33 | -1.23 | 0.179 | 0.527 | 1.000 | 589 | tags=48%, list=39%, signal=76% |
| 389 | GOBP\_REGULATION\_OF\_CELLULAR\_COMPONENT\_SIZE |  | 47 | -0.32 | -1.22 | 0.189 | 0.534 | 1.000 | 229 | tags=23%, list=15%, signal=27% |
| 390 | GOBP\_POSITIVE\_REGULATION\_OF\_PROTEIN\_SERINE\_THREONINE\_KINASE\_ACTIVITY |  | 36 | -0.34 | -1.22 | 0.194 | 0.533 | 1.000 | 588 | tags=50%, list=39%, signal=80% |
| 391 | GOBP\_DEFENSE\_RESPONSE\_TO\_GRAM\_NEGATIVE\_BACTERIUM |  | 16 | -0.41 | -1.22 | 0.227 | 0.534 | 1.000 | 366 | tags=44%, list=24%, signal=57% |
| 392 | GOBP\_ESTABLISHMENT\_OF\_ORGANELLE\_LOCALIZATION |  | 31 | -0.35 | -1.22 | 0.204 | 0.537 | 1.000 | 166 | tags=23%, list=11%, signal=25% |
| 393 | GOBP\_STEROID\_BIOSYNTHETIC\_PROCESS |  | 17 | -0.40 | -1.22 | 0.216 | 0.543 | 1.000 | 485 | tags=59%, list=32%, signal=86% |
| 394 | GOBP\_CHONDROCYTE\_DIFFERENTIATION |  | 22 | -0.37 | -1.22 | 0.207 | 0.543 | 1.000 | 680 | tags=68%, list=45%, signal=122% |
| 395 | GOBP\_REGULATION\_OF\_INTRACELLULAR\_SIGNAL\_TRANSDUCTION |  | 204 | -0.27 | -1.22 | 0.114 | 0.544 | 1.000 | 559 | tags=41%, list=37%, signal=57% |
| 396 | GOBP\_CARBOHYDRATE\_DERIVATIVE\_CATABOLIC\_PROCESS |  | 26 | -0.36 | -1.22 | 0.210 | 0.544 | 1.000 | 410 | tags=42%, list=27%, signal=57% |
| 397 | GOMF\_CYTOKINE\_ACTIVITY |  | 46 | -0.32 | -1.22 | 0.194 | 0.546 | 1.000 | 340 | tags=37%, list=23%, signal=46% |
| 398 | GOMF\_PROTEIN\_DOMAIN\_SPECIFIC\_BINDING |  | 63 | -0.31 | -1.21 | 0.177 | 0.546 | 1.000 | 432 | tags=33%, list=29%, signal=45% |
| 399 | GOBP\_REGULATION\_OF\_CELLULAR\_CARBOHYDRATE\_METABOLIC\_PROCESS |  | 17 | -0.40 | -1.21 | 0.221 | 0.545 | 1.000 | 99 | tags=24%, list=7%, signal=25% |
| 400 | GOBP\_NEGATIVE\_REGULATION\_OF\_INFLAMMATORY\_RESPONSE |  | 23 | -0.38 | -1.21 | 0.205 | 0.544 | 1.000 | 512 | tags=48%, list=34%, signal=71% |
| 401 | GOBP\_REGULATION\_OF\_PROTEIN\_MODIFICATION\_PROCESS |  | 185 | -0.27 | -1.21 | 0.102 | 0.544 | 1.000 | 588 | tags=42%, list=39%, signal=60% |
| 402 | GOBP\_INTERLEUKIN\_8\_PRODUCTION |  | 16 | -0.40 | -1.21 | 0.213 | 0.545 | 1.000 | 531 | tags=69%, list=35%, signal=105% |
| 403 | GOBP\_CELLULAR\_CARBOHYDRATE\_METABOLIC\_PROCESS |  | 24 | -0.38 | -1.21 | 0.216 | 0.550 | 1.000 | 578 | tags=54%, list=38%, signal=86% |
| 404 | GOBP\_BONE\_MINERALIZATION |  | 25 | -0.36 | -1.21 | 0.212 | 0.550 | 1.000 | 157 | tags=28%, list=10%, signal=31% |
| 405 | GOBP\_NEGATIVE\_REGULATION\_OF\_HEMOPOIESIS |  | 20 | -0.39 | -1.21 | 0.225 | 0.548 | 1.000 | 656 | tags=60%, list=43%, signal=105% |
| 406 | GOBP\_IMMUNE\_SYSTEM\_DEVELOPMENT |  | 133 | -0.27 | -1.21 | 0.146 | 0.549 | 1.000 | 636 | tags=51%, list=42%, signal=81% |
| 407 | GOBP\_CELLULAR\_RESPONSE\_TO\_OXYGEN\_CONTAINING\_COMPOUND |  | 161 | -0.27 | -1.21 | 0.118 | 0.548 | 1.000 | 579 | tags=45%, list=38%, signal=66% |
| 408 | GOBP\_MUSCLE\_TISSUE\_DEVELOPMENT |  | 49 | -0.32 | -1.21 | 0.204 | 0.547 | 1.000 | 817 | tags=71%, list=54%, signal=151% |
| 409 | GOBP\_POSITIVE\_REGULATION\_OF\_PROTEIN\_KINASE\_ACTIVITY |  | 61 | -0.30 | -1.21 | 0.174 | 0.547 | 1.000 | 588 | tags=43%, list=39%, signal=67% |
| 410 | GOBP\_HUMORAL\_IMMUNE\_RESPONSE |  | 60 | -0.30 | -1.21 | 0.178 | 0.546 | 1.000 | 615 | tags=53%, list=41%, signal=86% |
| 411 | GOBP\_NEURON\_PROJECTION\_REGENERATION |  | 16 | -0.40 | -1.21 | 0.220 | 0.548 | 1.000 | 116 | tags=25%, list=8%, signal=27% |
| 412 | GOBP\_POSITIVE\_REGULATION\_OF\_PEPTIDYL\_TYROSINE\_PHOSPHORYLATION |  | 36 | -0.33 | -1.21 | 0.191 | 0.548 | 1.000 | 559 | tags=44%, list=37%, signal=69% |
| 413 | GOBP\_REGULATION\_OF\_BODY\_FLUID\_LEVELS |  | 75 | -0.30 | -1.21 | 0.168 | 0.550 | 1.000 | 530 | tags=48%, list=35%, signal=70% |
| 414 | GOMF\_ACTIN\_BINDING |  | 41 | -0.32 | -1.21 | 0.195 | 0.550 | 1.000 | 328 | tags=32%, list=22%, signal=39% |
| 415 | GOBP\_REGULATION\_OF\_ORGANELLE\_ORGANIZATION |  | 111 | -0.28 | -1.20 | 0.161 | 0.552 | 1.000 | 267 | tags=23%, list=18%, signal=26% |
| 416 | GOBP\_MUSCLE\_CELL\_DIFFERENTIATION |  | 49 | -0.32 | -1.20 | 0.188 | 0.552 | 1.000 | 670 | tags=51%, list=44%, signal=89% |
| 417 | GOBP\_REGULATION\_OF\_PROTEIN\_KINASE\_ACTIVITY |  | 96 | -0.28 | -1.20 | 0.172 | 0.553 | 1.000 | 588 | tags=41%, list=39%, signal=62% |
| 418 | GOBP\_MUSCLE\_CELL\_PROLIFERATION |  | 35 | -0.33 | -1.20 | 0.206 | 0.553 | 1.000 | 644 | tags=57%, list=43%, signal=97% |
| 419 | GOMF\_CYTOKINE\_BINDING |  | 20 | -0.38 | -1.20 | 0.235 | 0.556 | 1.000 | 240 | tags=35%, list=16%, signal=41% |
| 420 | GOBP\_REGULATION\_OF\_NEUROGENESIS |  | 44 | -0.32 | -1.20 | 0.207 | 0.556 | 1.000 | 622 | tags=45%, list=41%, signal=75% |
| 421 | GOBP\_REGULATION\_OF\_EPITHELIAL\_CELL\_MIGRATION |  | 37 | -0.33 | -1.20 | 0.220 | 0.555 | 1.000 | 237 | tags=32%, list=16%, signal=38% |
| 422 | GOBP\_DEVELOPMENTAL\_MATURATION |  | 32 | -0.34 | -1.20 | 0.209 | 0.558 | 1.000 | 512 | tags=44%, list=34%, signal=65% |
| 423 | GOBP\_MAMMARY\_GLAND\_DEVELOPMENT |  | 24 | -0.36 | -1.20 | 0.217 | 0.558 | 1.000 | 136 | tags=25%, list=9%, signal=27% |
| 424 | GOBP\_ACTIVATION\_OF\_MAPK\_ACTIVITY |  | 19 | -0.38 | -1.20 | 0.249 | 0.559 | 1.000 | 516 | tags=53%, list=34%, signal=79% |
| 425 | GOBP\_PROTEASOMAL\_PROTEIN\_CATABOLIC\_PROCESS |  | 29 | -0.35 | -1.20 | 0.211 | 0.566 | 1.000 | 300 | tags=24%, list=20%, signal=30% |
| 426 | GOBP\_PROTEIN\_PROCESSING |  | 33 | -0.34 | -1.19 | 0.224 | 0.573 | 1.000 | 708 | tags=70%, list=47%, signal=128% |
| 427 | GOBP\_PROTEOLYSIS |  | 180 | -0.26 | -1.19 | 0.138 | 0.574 | 1.000 | 382 | tags=32%, list=25%, signal=38% |
| 428 | GOBP\_PROTEIN\_ACYLATION |  | 16 | -0.40 | -1.19 | 0.238 | 0.574 | 1.000 | 604 | tags=44%, list=40%, signal=72% |
| 429 | GOBP\_ANTIMICROBIAL\_HUMORAL\_RESPONSE |  | 32 | -0.34 | -1.19 | 0.220 | 0.575 | 1.000 | 366 | tags=38%, list=24%, signal=48% |
| 430 | GOMF\_SERINE\_HYDROLASE\_ACTIVITY |  | 24 | -0.36 | -1.19 | 0.252 | 0.577 | 1.000 | 446 | tags=54%, list=30%, signal=76% |
| 431 | GOCC\_I\_BAND |  | 16 | -0.39 | -1.19 | 0.237 | 0.579 | 1.000 | 548 | tags=50%, list=36%, signal=78% |
| 432 | GOBP\_NEURAL\_PRECURSOR\_CELL\_PROLIFERATION |  | 20 | -0.38 | -1.19 | 0.247 | 0.578 | 1.000 | 649 | tags=60%, list=43%, signal=104% |
| 433 | GOBP\_REGULATION\_OF\_ANATOMICAL\_STRUCTURE\_MORPHOGENESIS |  | 152 | -0.26 | -1.19 | 0.173 | 0.578 | 1.000 | 516 | tags=38%, list=34%, signal=51% |
| 434 | GOBP\_BRANCHING\_MORPHOGENESIS\_OF\_AN\_EPITHELIAL\_TUBE |  | 26 | -0.36 | -1.19 | 0.259 | 0.580 | 1.000 | 395 | tags=42%, list=26%, signal=56% |
| 435 | GOCC\_SUPRAMOLECULAR\_POLYMER |  | 117 | -0.27 | -1.19 | 0.180 | 0.580 | 1.000 | 806 | tags=60%, list=53%, signal=118% |
| 436 | GOBP\_STRESS\_FIBER\_ASSEMBLY |  | 16 | -0.40 | -1.19 | 0.244 | 0.579 | 1.000 | 479 | tags=44%, list=32%, signal=63% |
| 437 | GOBP\_REGIONALIZATION |  | 45 | -0.32 | -1.18 | 0.220 | 0.583 | 1.000 | 401 | tags=38%, list=27%, signal=50% |
| 438 | GOBP\_SMOOTH\_MUSCLE\_CELL\_PROLIFERATION |  | 33 | -0.33 | -1.18 | 0.239 | 0.583 | 1.000 | 644 | tags=58%, list=43%, signal=98% |
| 439 | GOBP\_CARDIAC\_CHAMBER\_MORPHOGENESIS |  | 21 | -0.37 | -1.18 | 0.240 | 0.583 | 1.000 | 232 | tags=24%, list=15%, signal=28% |
| 440 | GOMF\_ENDOPEPTIDASE\_ACTIVITY |  | 51 | -0.31 | -1.18 | 0.223 | 0.582 | 1.000 | 600 | tags=59%, list=40%, signal=94% |
| 441 | GOMF\_NEUROPEPTIDE\_HORMONE\_ACTIVITY |  | 18 | -0.38 | -1.18 | 0.250 | 0.582 | 1.000 | 637 | tags=44%, list=42%, signal=76% |
| 442 | GOBP\_RESPONSE\_TO\_MECHANICAL\_STIMULUS |  | 40 | -0.32 | -1.18 | 0.219 | 0.582 | 1.000 | 645 | tags=58%, list=43%, signal=98% |
| 443 | GOBP\_REGULATION\_OF\_CARBOHYDRATE\_METABOLIC\_PROCESS |  | 18 | -0.39 | -1.18 | 0.257 | 0.584 | 1.000 | 99 | tags=22%, list=7%, signal=23% |
| 444 | GOBP\_MESONEPHROS\_DEVELOPMENT |  | 21 | -0.37 | -1.18 | 0.262 | 0.585 | 1.000 | 419 | tags=43%, list=28%, signal=58% |
| 445 | GOBP\_REGULATION\_OF\_NEURAL\_PRECURSOR\_CELL\_PROLIFERATION |  | 15 | -0.41 | -1.18 | 0.251 | 0.585 | 1.000 | 619 | tags=60%, list=41%, signal=101% |
| 446 | GOBP\_PROTEIN\_MATURATION |  | 42 | -0.32 | -1.18 | 0.225 | 0.584 | 1.000 | 556 | tags=50%, list=37%, signal=77% |
| 447 | GOMF\_SERINE\_TYPE\_ENDOPEPTIDASE\_INHIBITOR\_ACTIVITY |  | 26 | -0.35 | -1.18 | 0.237 | 0.583 | 1.000 | 413 | tags=38%, list=27%, signal=52% |
| 448 | GOBP\_RESPONSE\_TO\_MONOSACCHARIDE |  | 28 | -0.35 | -1.18 | 0.252 | 0.585 | 1.000 | 578 | tags=46%, list=38%, signal=74% |
| 449 | GOBP\_REGULATION\_OF\_IMMUNE\_SYSTEM\_PROCESS |  | 231 | -0.26 | -1.18 | 0.123 | 0.584 | 1.000 | 575 | tags=43%, list=38%, signal=59% |
| 450 | GOBP\_LEUKOCYTE\_CELL\_CELL\_ADHESION |  | 64 | -0.30 | -1.18 | 0.216 | 0.583 | 1.000 | 363 | tags=30%, list=24%, signal=37% |
| 451 | GOBP\_TISSUE\_HOMEOSTASIS |  | 47 | -0.31 | -1.18 | 0.226 | 0.585 | 1.000 | 540 | tags=45%, list=36%, signal=67% |
| 452 | GOBP\_RESPONSE\_TO\_ESTRADIOL |  | 24 | -0.36 | -1.18 | 0.243 | 0.584 | 1.000 | 611 | tags=63%, list=40%, signal=103% |
| 453 | GOBP\_ORGANELLE\_FISSION |  | 33 | -0.33 | -1.18 | 0.228 | 0.589 | 1.000 | 681 | tags=61%, list=45%, signal=108% |
| 454 | GOBP\_CELLULAR\_RESPONSE\_TO\_CORTICOSTEROID\_STIMULUS |  | 20 | -0.37 | -1.17 | 0.268 | 0.588 | 1.000 | 114 | tags=20%, list=8%, signal=21% |
| 455 | GOBP\_LYMPHOCYTE\_ACTIVATION |  | 118 | -0.27 | -1.17 | 0.201 | 0.589 | 1.000 | 575 | tags=46%, list=38%, signal=68% |
| 456 | GOBP\_APOPTOTIC\_PROCESS |  | 256 | -0.25 | -1.17 | 0.128 | 0.592 | 1.000 | 595 | tags=43%, list=39%, signal=58% |
| 457 | GOBP\_ACTIN\_MEDIATED\_CELL\_CONTRACTION |  | 19 | -0.38 | -1.17 | 0.260 | 0.593 | 1.000 | 508 | tags=42%, list=34%, signal=63% |
| 458 | GOBP\_SIGNAL\_TRANSDUCTION\_IN\_RESPONSE\_TO\_DNA\_DAMAGE |  | 16 | -0.40 | -1.17 | 0.269 | 0.594 | 1.000 | 548 | tags=50%, list=36%, signal=78% |
| 459 | GOBP\_POSITIVE\_REGULATION\_OF\_APOPTOTIC\_SIGNALING\_PATHWAY |  | 23 | -0.35 | -1.17 | 0.257 | 0.597 | 1.000 | 558 | tags=52%, list=37%, signal=81% |
| 460 | GOBP\_HORMONE\_MEDIATED\_SIGNALING\_PATHWAY |  | 17 | -0.38 | -1.17 | 0.264 | 0.596 | 1.000 | 362 | tags=35%, list=24%, signal=46% |
| 461 | GOBP\_POSITIVE\_REGULATION\_OF\_PROTEIN\_MODIFICATION\_PROCESS |  | 128 | -0.26 | -1.17 | 0.186 | 0.596 | 1.000 | 588 | tags=41%, list=39%, signal=61% |
| 462 | GOBP\_REGULATION\_OF\_PEPTIDYL\_SERINE\_PHOSPHORYLATION |  | 23 | -0.36 | -1.17 | 0.258 | 0.597 | 1.000 | 588 | tags=39%, list=39%, signal=63% |
| 463 | GOBP\_NEURON\_APOPTOTIC\_PROCESS |  | 34 | -0.33 | -1.17 | 0.250 | 0.597 | 1.000 | 240 | tags=26%, list=16%, signal=31% |
| 464 | GOBP\_RESPONSE\_TO\_NUTRIENT |  | 39 | -0.32 | -1.17 | 0.239 | 0.596 | 1.000 | 573 | tags=54%, list=38%, signal=85% |
| 465 | GOBP\_COAGULATION |  | 50 | -0.30 | -1.17 | 0.244 | 0.595 | 1.000 | 554 | tags=54%, list=37%, signal=82% |
| 466 | GOCC\_PERINUCLEAR\_REGION\_OF\_CYTOPLASM |  | 85 | -0.27 | -1.17 | 0.217 | 0.595 | 1.000 | 615 | tags=46%, list=41%, signal=73% |
| 467 | GOCC\_PLASMA\_MEMBRANE\_REGION |  | 128 | -0.27 | -1.17 | 0.194 | 0.597 | 1.000 | 460 | tags=33%, list=30%, signal=43% |
| 468 | GOBP\_REGULATION\_OF\_PEPTIDE\_TRANSPORT |  | 66 | -0.29 | -1.17 | 0.228 | 0.596 | 1.000 | 644 | tags=48%, list=43%, signal=81% |
| 469 | GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_GROWTH |  | 24 | -0.35 | -1.17 | 0.260 | 0.596 | 1.000 | 497 | tags=46%, list=33%, signal=67% |
| 470 | GOBP\_ANTIGEN\_RECEPTOR\_MEDIATED\_SIGNALING\_PATHWAY |  | 37 | -0.32 | -1.17 | 0.247 | 0.596 | 1.000 | 507 | tags=46%, list=34%, signal=67% |
| 471 | GOBP\_COGNITION |  | 35 | -0.32 | -1.16 | 0.256 | 0.595 | 1.000 | 253 | tags=23%, list=17%, signal=27% |
| 472 | GOBP\_B\_CELL\_RECEPTOR\_SIGNALING\_PATHWAY |  | 21 | -0.36 | -1.16 | 0.276 | 0.594 | 1.000 | 705 | tags=76%, list=47%, signal=141% |
| 473 | GOMF\_CYSTEINE\_TYPE\_PEPTIDASE\_ACTIVITY |  | 15 | -0.40 | -1.16 | 0.276 | 0.594 | 1.000 | 264 | tags=40%, list=17%, signal=48% |
| 474 | GOBP\_POSITIVE\_REGULATION\_OF\_PROTEIN\_METABOLIC\_PROCESS |  | 176 | -0.26 | -1.16 | 0.173 | 0.594 | 1.000 | 339 | tags=28%, list=22%, signal=32% |
| 475 | GOBP\_RESPONSE\_TO\_ESTROGEN |  | 20 | -0.37 | -1.16 | 0.258 | 0.594 | 1.000 | 718 | tags=60%, list=48%, signal=113% |
| 476 | GOBP\_REGULATION\_OF\_TRANSPORTER\_ACTIVITY |  | 33 | -0.33 | -1.16 | 0.246 | 0.598 | 1.000 | 118 | tags=18%, list=8%, signal=19% |
| 477 | GOBP\_REGULATION\_OF\_PEPTIDASE\_ACTIVITY |  | 86 | -0.28 | -1.16 | 0.222 | 0.600 | 1.000 | 382 | tags=33%, list=25%, signal=41% |
| 478 | GOMF\_G\_PROTEIN\_COUPLED\_RECEPTOR\_BINDING |  | 62 | -0.29 | -1.16 | 0.243 | 0.602 | 1.000 | 589 | tags=50%, list=39%, signal=79% |
| 479 | GOBP\_POSITIVE\_REGULATION\_OF\_SMOOTH\_MUSCLE\_CELL\_PROLIFERATION |  | 20 | -0.37 | -1.16 | 0.274 | 0.602 | 1.000 | 688 | tags=70%, list=46%, signal=127% |
| 480 | GOCC\_GOLGI\_LUMEN |  | 18 | -0.38 | -1.16 | 0.266 | 0.601 | 1.000 | 697 | tags=78%, list=46%, signal=143% |
| 481 | GOBP\_AMINE\_TRANSPORT |  | 24 | -0.35 | -1.16 | 0.264 | 0.603 | 1.000 | 896 | tags=83%, list=59%, signal=202% |
| 482 | GOMF\_VITAMIN\_BINDING |  | 16 | -0.39 | -1.16 | 0.282 | 0.608 | 1.000 | 159 | tags=25%, list=11%, signal=28% |
| 483 | GOBP\_REGULATION\_OF\_ENDOTHELIAL\_CELL\_MIGRATION |  | 29 | -0.34 | -1.16 | 0.268 | 0.609 | 1.000 | 715 | tags=69%, list=47%, signal=128% |
| 484 | GOBP\_REGULATION\_OF\_OSTEOBLAST\_DIFFERENTIATION |  | 20 | -0.36 | -1.15 | 0.270 | 0.611 | 1.000 | 254 | tags=30%, list=17%, signal=36% |
| 485 | GOBP\_NEGATIVE\_REGULATION\_OF\_IMMUNE\_SYSTEM\_PROCESS |  | 69 | -0.29 | -1.15 | 0.252 | 0.612 | 1.000 | 688 | tags=52%, list=46%, signal=91% |
| 486 | GOMF\_CYTOKINE\_RECEPTOR\_BINDING |  | 42 | -0.31 | -1.15 | 0.260 | 0.611 | 1.000 | 340 | tags=36%, list=23%, signal=45% |
| 487 | GOBP\_DEFENSE\_RESPONSE\_TO\_BACTERIUM |  | 56 | -0.29 | -1.15 | 0.259 | 0.613 | 1.000 | 615 | tags=54%, list=41%, signal=87% |
| 488 | GOBP\_SPROUTING\_ANGIOGENESIS |  | 22 | -0.35 | -1.15 | 0.272 | 0.612 | 1.000 | 253 | tags=27%, list=17%, signal=32% |
| 489 | GOBP\_REGULATION\_OF\_APOPTOTIC\_SIGNALING\_PATHWAY |  | 55 | -0.29 | -1.15 | 0.256 | 0.611 | 1.000 | 558 | tags=45%, list=37%, signal=69% |
| 490 | GOBP\_PEPTIDYL\_SERINE\_MODIFICATION |  | 35 | -0.32 | -1.15 | 0.264 | 0.612 | 1.000 | 216 | tags=23%, list=14%, signal=26% |
| 491 | GOBP\_CARDIAC\_CONDUCTION |  | 18 | -0.38 | -1.15 | 0.291 | 0.612 | 1.000 | 118 | tags=22%, list=8%, signal=24% |
| 492 | GOBP\_RESPONSE\_TO\_ABIOTIC\_STIMULUS |  | 172 | -0.26 | -1.15 | 0.203 | 0.611 | 1.000 | 321 | tags=27%, list=21%, signal=30% |
| 493 | GOBP\_NEGATIVE\_REGULATION\_OF\_CELL\_DEATH |  | 145 | -0.26 | -1.15 | 0.220 | 0.610 | 1.000 | 359 | tags=30%, list=24%, signal=35% |
| 494 | GOBP\_PALLIUM\_DEVELOPMENT |  | 20 | -0.37 | -1.15 | 0.279 | 0.609 | 1.000 | 819 | tags=85%, list=54%, signal=183% |
| 495 | GOBP\_ENDOTHELIAL\_CELL\_MIGRATION |  | 36 | -0.32 | -1.15 | 0.282 | 0.610 | 1.000 | 614 | tags=58%, list=41%, signal=96% |
| 496 | GOBP\_REGULATION\_OF\_AXONOGENESIS |  | 19 | -0.37 | -1.15 | 0.286 | 0.612 | 1.000 | 419 | tags=32%, list=28%, signal=43% |
| 497 | GOBP\_MULTICELLULAR\_ORGANISMAL\_SIGNALING |  | 21 | -0.36 | -1.15 | 0.283 | 0.612 | 1.000 | 638 | tags=52%, list=42%, signal=89% |
| 498 | GOMF\_CIS\_REGULATORY\_REGION\_SEQUENCE\_SPECIFIC\_DNA\_BINDING |  | 85 | -0.27 | -1.15 | 0.246 | 0.611 | 1.000 | 665 | tags=56%, list=44%, signal=95% |
| 499 | GOBP\_REGULATION\_OF\_TISSUE\_REMODELING |  | 16 | -0.39 | -1.15 | 0.288 | 0.614 | 1.000 | 254 | tags=31%, list=17%, signal=37% |
| 500 | GOBP\_TRANSITION\_METAL\_ION\_HOMEOSTASIS |  | 17 | -0.37 | -1.15 | 0.284 | 0.615 | 1.000 | 497 | tags=41%, list=33%, signal=61% |
| 501 | GOBP\_POSITIVE\_REGULATION\_OF\_NUCLEOBASE\_CONTAINING\_COMPOUND\_METABOLIC\_PROCESS |  | 175 | -0.25 | -1.14 | 0.217 | 0.616 | 1.000 | 665 | tags=49%, list=44%, signal=77% |
| 502 | GOBP\_SENSORY\_PERCEPTION |  | 64 | -0.28 | -1.14 | 0.267 | 0.617 | 1.000 | 234 | tags=27%, list=15%, signal=30% |
| 503 | GOBP\_TISSUE\_MORPHOGENESIS |  | 94 | -0.27 | -1.14 | 0.244 | 0.617 | 1.000 | 440 | tags=35%, list=29%, signal=46% |
| 504 | GOBP\_NEGATIVE\_REGULATION\_OF\_NEURON\_APOPTOTIC\_PROCESS |  | 24 | -0.35 | -1.14 | 0.281 | 0.618 | 1.000 | 240 | tags=29%, list=16%, signal=34% |
| 505 | GOBP\_NEGATIVE\_REGULATION\_OF\_IMMUNE\_EFFECTOR\_PROCESS |  | 17 | -0.37 | -1.14 | 0.287 | 0.619 | 1.000 | 453 | tags=47%, list=30%, signal=66% |
| 506 | GOCC\_VESICLE\_LUMEN |  | 73 | -0.28 | -1.14 | 0.260 | 0.617 | 1.000 | 375 | tags=33%, list=25%, signal=42% |
| 507 | GOBP\_DEFENSE\_RESPONSE |  | 273 | -0.25 | -1.14 | 0.185 | 0.620 | 1.000 | 567 | tags=42%, list=38%, signal=55% |
| 508 | GOBP\_REGULATION\_OF\_CELL\_CELL\_ADHESION |  | 73 | -0.28 | -1.14 | 0.293 | 0.619 | 1.000 | 649 | tags=45%, list=43%, signal=75% |
| 509 | GOMF\_STRUCTURAL\_MOLECULE\_ACTIVITY |  | 161 | -0.25 | -1.14 | 0.215 | 0.618 | 1.000 | 444 | tags=34%, list=29%, signal=42% |
| 510 | GOBP\_REGULATION\_OF\_LEUKOCYTE\_DIFFERENTIATION |  | 48 | -0.30 | -1.14 | 0.276 | 0.619 | 1.000 | 656 | tags=54%, list=43%, signal=93% |
| 511 | GOBP\_HOMEOSTATIC\_PROCESS |  | 239 | -0.25 | -1.14 | 0.189 | 0.617 | 1.000 | 598 | tags=42%, list=40%, signal=58% |
| 512 | GOBP\_EPITHELIAL\_CELL\_DIFFERENTIATION |  | 94 | -0.27 | -1.14 | 0.252 | 0.616 | 1.000 | 412 | tags=34%, list=27%, signal=44% |
| 513 | GOBP\_REGULATION\_OF\_LEUKOCYTE\_APOPTOTIC\_PROCESS |  | 17 | -0.37 | -1.14 | 0.297 | 0.620 | 1.000 | 575 | tags=59%, list=38%, signal=94% |
| 514 | GOBP\_NEGATIVE\_REGULATION\_OF\_TRANSCRIPTION\_BY\_RNA\_POLYMERASE\_II |  | 85 | -0.27 | -1.14 | 0.244 | 0.620 | 1.000 | 588 | tags=42%, list=39%, signal=65% |
| 515 | GOBP\_CELL\_CELL\_SIGNALING |  | 207 | -0.25 | -1.14 | 0.200 | 0.619 | 1.000 | 459 | tags=33%, list=30%, signal=41% |
| 516 | GOBP\_LIPID\_CATABOLIC\_PROCESS |  | 27 | -0.34 | -1.14 | 0.282 | 0.623 | 1.000 | 453 | tags=41%, list=30%, signal=57% |
| 517 | GOBP\_CEREBRAL\_CORTEX\_DEVELOPMENT |  | 16 | -0.38 | -1.14 | 0.296 | 0.622 | 1.000 | 696 | tags=69%, list=46%, signal=126% |
| 518 | GOMF\_ZINC\_ION\_BINDING |  | 61 | -0.28 | -1.14 | 0.268 | 0.622 | 1.000 | 168 | tags=23%, list=11%, signal=25% |
| 519 | GOBP\_RESPONSE\_TO\_OXYGEN\_LEVELS |  | 68 | -0.28 | -1.13 | 0.282 | 0.622 | 1.000 | 622 | tags=47%, list=41%, signal=76% |
| 520 | GOBP\_POSITIVE\_REGULATION\_OF\_INTRACELLULAR\_SIGNAL\_TRANSDUCTION |  | 132 | -0.26 | -1.13 | 0.224 | 0.623 | 1.000 | 588 | tags=44%, list=39%, signal=66% |
| 521 | GOMF\_DNA\_BINDING\_TRANSCRIPTION\_REPRESSOR\_ACTIVITY |  | 24 | -0.34 | -1.13 | 0.296 | 0.626 | 1.000 | 411 | tags=38%, list=27%, signal=51% |
| 522 | GOBP\_MALE\_GAMETE\_GENERATION |  | 34 | -0.32 | -1.13 | 0.300 | 0.627 | 1.000 | 409 | tags=38%, list=27%, signal=51% |
| 523 | GOBP\_REGULATION\_OF\_GRANULOCYTE\_CHEMOTAXIS |  | 15 | -0.39 | -1.13 | 0.323 | 0.627 | 1.000 | 805 | tags=80%, list=53%, signal=170% |
| 524 | GOBP\_POSITIVE\_REGULATION\_OF\_CELLULAR\_COMPONENT\_ORGANIZATION |  | 127 | -0.26 | -1.13 | 0.242 | 0.628 | 1.000 | 686 | tags=50%, list=45%, signal=85% |
| 525 | GOBP\_REGULATION\_OF\_CELLULAR\_KETONE\_METABOLIC\_PROCESS |  | 18 | -0.37 | -1.13 | 0.312 | 0.631 | 1.000 | 179 | tags=28%, list=12%, signal=31% |
| 526 | GOBP\_NEGATIVE\_REGULATION\_OF\_PHOSPHORUS\_METABOLIC\_PROCESS |  | 64 | -0.28 | -1.13 | 0.293 | 0.631 | 1.000 | 588 | tags=44%, list=39%, signal=69% |
| 527 | GOBP\_POSITIVE\_REGULATION\_OF\_CYTOSKELETON\_ORGANIZATION |  | 30 | -0.33 | -1.13 | 0.298 | 0.631 | 1.000 | 508 | tags=40%, list=34%, signal=59% |
| 528 | GOBP\_NEGATIVE\_REGULATION\_OF\_LOCOMOTION |  | 50 | -0.30 | -1.13 | 0.299 | 0.634 | 1.000 | 567 | tags=46%, list=38%, signal=71% |
| 529 | GOBP\_REGULATION\_OF\_BIOMINERALIZATION |  | 23 | -0.35 | -1.13 | 0.310 | 0.633 | 1.000 | 292 | tags=35%, list=19%, signal=42% |
| 530 | GOBP\_RESPONSE\_TO\_ORGANIC\_CYCLIC\_COMPOUND |  | 145 | -0.25 | -1.13 | 0.253 | 0.633 | 1.000 | 579 | tags=46%, list=38%, signal=67% |
| 531 | GOBP\_NEGATIVE\_REGULATION\_OF\_TRANSFERASE\_ACTIVITY |  | 44 | -0.30 | -1.12 | 0.307 | 0.637 | 1.000 | 545 | tags=41%, list=36%, signal=62% |
| 532 | GOBP\_KIDNEY\_EPITHELIUM\_DEVELOPMENT |  | 25 | -0.33 | -1.12 | 0.301 | 0.637 | 1.000 | 419 | tags=40%, list=28%, signal=54% |
| 533 | GOBP\_NEGATIVE\_REGULATION\_OF\_KINASE\_ACTIVITY |  | 43 | -0.30 | -1.12 | 0.309 | 0.639 | 1.000 | 545 | tags=42%, list=36%, signal=64% |
| 534 | GOBP\_ORGANELLE\_LOCALIZATION |  | 43 | -0.31 | -1.12 | 0.298 | 0.642 | 1.000 | 801 | tags=60%, list=53%, signal=125% |
| 535 | GOCC\_SUPRAMOLECULAR\_COMPLEX |  | 133 | -0.25 | -1.12 | 0.271 | 0.641 | 1.000 | 649 | tags=43%, list=43%, signal=69% |
| 536 | GOBP\_POSITIVE\_REGULATION\_OF\_SIGNALING |  | 228 | -0.24 | -1.12 | 0.233 | 0.642 | 1.000 | 578 | tags=42%, list=38%, signal=57% |
| 537 | GOBP\_POSITIVE\_REGULATION\_OF\_TRANSCRIPTION\_BY\_RNA\_POLYMERASE\_II |  | 122 | -0.25 | -1.12 | 0.273 | 0.647 | 1.000 | 685 | tags=51%, list=45%, signal=86% |
| 538 | GOBP\_REGULATION\_OF\_MAPK\_CASCADE |  | 99 | -0.27 | -1.12 | 0.283 | 0.646 | 1.000 | 588 | tags=43%, list=39%, signal=66% |
| 539 | GOBP\_CELL\_DIVISION |  | 41 | -0.30 | -1.12 | 0.316 | 0.646 | 1.000 | 571 | tags=44%, list=38%, signal=69% |
| 540 | GOCC\_PLASMA\_MEMBRANE\_BOUNDED\_CELL\_PROJECTION\_CYTOPLASM |  | 17 | -0.37 | -1.12 | 0.325 | 0.645 | 1.000 | 529 | tags=35%, list=35%, signal=54% |
| 541 | GOBP\_CELLULAR\_COMPONENT\_DISASSEMBLY |  | 51 | -0.29 | -1.12 | 0.309 | 0.644 | 1.000 | 407 | tags=37%, list=27%, signal=49% |
| 542 | GOBP\_REGULATION\_OF\_IMMUNE\_EFFECTOR\_PROCESS |  | 65 | -0.28 | -1.12 | 0.296 | 0.643 | 1.000 | 556 | tags=43%, list=37%, signal=65% |
| 543 | GOBP\_CELL\_CELL\_ADHESION\_VIA\_PLASMA\_MEMBRANE\_ADHESION\_MOLECULES |  | 27 | -0.33 | -1.12 | 0.301 | 0.646 | 1.000 | 512 | tags=44%, list=34%, signal=66% |
| 544 | GOBP\_CHEMICAL\_HOMEOSTASIS |  | 152 | -0.25 | -1.12 | 0.275 | 0.647 | 1.000 | 638 | tags=44%, list=42%, signal=69% |
| 545 | GOBP\_CARBOHYDRATE\_BIOSYNTHETIC\_PROCESS |  | 20 | -0.35 | -1.12 | 0.341 | 0.646 | 1.000 | 121 | tags=20%, list=8%, signal=21% |
| 546 | GOBP\_CELLULAR\_RESPONSE\_TO\_BIOTIC\_STIMULUS |  | 42 | -0.30 | -1.11 | 0.305 | 0.648 | 1.000 | 340 | tags=40%, list=23%, signal=51% |
| 547 | GOBP\_POSITIVE\_REGULATION\_OF\_VASCULATURE\_DEVELOPMENT |  | 31 | -0.32 | -1.11 | 0.326 | 0.648 | 1.000 | 516 | tags=52%, list=34%, signal=77% |
| 548 | GOBP\_GLIAL\_CELL\_DIFFERENTIATION |  | 30 | -0.32 | -1.11 | 0.311 | 0.649 | 1.000 | 632 | tags=50%, list=42%, signal=84% |
| 549 | GOBP\_RESPONSE\_TO\_CYTOKINE |  | 186 | -0.24 | -1.11 | 0.251 | 0.648 | 1.000 | 631 | tags=47%, list=42%, signal=71% |
| 550 | GOBP\_DNA\_DAMAGE\_RESPONSE\_SIGNAL\_TRANSDUCTION\_BY\_P53\_CLASS\_MEDIATOR |  | 15 | -0.38 | -1.11 | 0.339 | 0.647 | 1.000 | 548 | tags=47%, list=36%, signal=73% |
| 551 | GOBP\_HOMEOSTASIS\_OF\_NUMBER\_OF\_CELLS |  | 35 | -0.31 | -1.11 | 0.333 | 0.646 | 1.000 | 594 | tags=46%, list=39%, signal=74% |
| 552 | GOBP\_RESPONSE\_TO\_ORGANOPHOSPHORUS |  | 25 | -0.34 | -1.11 | 0.322 | 0.646 | 1.000 | 712 | tags=68%, list=47%, signal=127% |
| 553 | GOBP\_POSITIVE\_REGULATION\_OF\_EPITHELIAL\_CELL\_MIGRATION |  | 23 | -0.34 | -1.11 | 0.334 | 0.647 | 1.000 | 516 | tags=52%, list=34%, signal=78% |
| 554 | GOBP\_IMMUNE\_EFFECTOR\_PROCESS |  | 179 | -0.24 | -1.11 | 0.267 | 0.646 | 1.000 | 575 | tags=42%, list=38%, signal=60% |
| 555 | GOBP\_CELL\_JUNCTION\_ORGANIZATION |  | 85 | -0.27 | -1.11 | 0.318 | 0.645 | 1.000 | 535 | tags=36%, list=35%, signal=53% |
| 556 | GOBP\_RESPONSE\_TO\_PURINE\_CONTAINING\_COMPOUND |  | 25 | -0.34 | -1.11 | 0.323 | 0.647 | 1.000 | 712 | tags=68%, list=47%, signal=127% |
| 557 | GOBP\_REGULATION\_OF\_PROTEOLYSIS |  | 104 | -0.26 | -1.11 | 0.289 | 0.646 | 1.000 | 382 | tags=31%, list=25%, signal=38% |
| 558 | GOBP\_REGULATION\_OF\_GENE\_EXPRESSION\_EPIGENETIC |  | 16 | -0.37 | -1.11 | 0.324 | 0.645 | 1.000 | 40 | tags=19%, list=3%, signal=19% |
| 559 | GOBP\_TISSUE\_MIGRATION |  | 51 | -0.29 | -1.11 | 0.296 | 0.644 | 1.000 | 614 | tags=55%, list=41%, signal=89% |
| 560 | GOBP\_REGULATION\_OF\_CELL\_DEATH |  | 245 | -0.24 | -1.11 | 0.240 | 0.645 | 1.000 | 578 | tags=40%, list=38%, signal=55% |
| 561 | GOBP\_REGULATION\_OF\_LEUKOCYTE\_MIGRATION |  | 59 | -0.28 | -1.11 | 0.312 | 0.648 | 1.000 | 589 | tags=42%, list=39%, signal=67% |
| 562 | GOBP\_APOPTOTIC\_SIGNALING\_PATHWAY |  | 81 | -0.26 | -1.10 | 0.297 | 0.656 | 1.000 | 575 | tags=44%, list=38%, signal=68% |
| 563 | GOBP\_CELLULAR\_RESPONSE\_TO\_NITROGEN\_COMPOUND |  | 89 | -0.26 | -1.10 | 0.295 | 0.657 | 1.000 | 510 | tags=38%, list=34%, signal=54% |
| 564 | GOBP\_POSITIVE\_REGULATION\_OF\_LEUKOCYTE\_CHEMOTAXIS |  | 28 | -0.32 | -1.10 | 0.332 | 0.657 | 1.000 | 589 | tags=50%, list=39%, signal=80% |
| 565 | GOBP\_REGULATION\_OF\_COAGULATION |  | 19 | -0.36 | -1.10 | 0.331 | 0.658 | 1.000 | 376 | tags=47%, list=25%, signal=62% |
| 566 | GOBP\_NEUROGENESIS |  | 198 | -0.24 | -1.10 | 0.268 | 0.658 | 1.000 | 673 | tags=45%, list=45%, signal=70% |
| 567 | GOBP\_RESPONSE\_TO\_NITROGEN\_COMPOUND |  | 148 | -0.25 | -1.10 | 0.293 | 0.660 | 1.000 | 336 | tags=29%, list=22%, signal=34% |
| 568 | GOBP\_SMOOTH\_MUSCLE\_CONTRACTION |  | 17 | -0.36 | -1.10 | 0.338 | 0.660 | 1.000 | 401 | tags=35%, list=27%, signal=48% |
| 569 | GOBP\_GERM\_CELL\_DEVELOPMENT |  | 15 | -0.38 | -1.10 | 0.339 | 0.660 | 1.000 | 644 | tags=67%, list=43%, signal=115% |
| 570 | GOBP\_NEGATIVE\_REGULATION\_OF\_ENDOTHELIAL\_CELL\_PROLIFERATION |  | 15 | -0.38 | -1.10 | 0.347 | 0.663 | 1.000 | 516 | tags=47%, list=34%, signal=70% |
| 571 | GOBP\_PROTEIN\_PHOSPHOPANTETHEINYLATION |  | 16 | -0.37 | -1.10 | 0.345 | 0.667 | 1.000 | 301 | tags=38%, list=20%, signal=46% |
| 572 | GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_PROJECTION\_ORGANIZATION |  | 38 | -0.30 | -1.09 | 0.340 | 0.672 | 1.000 | 577 | tags=42%, list=38%, signal=66% |
| 573 | GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_CELL\_ADHESION |  | 47 | -0.29 | -1.09 | 0.358 | 0.682 | 1.000 | 644 | tags=40%, list=43%, signal=68% |
| 574 | GOBP\_REGULATION\_OF\_GENERATION\_OF\_PRECURSOR\_METABOLITES\_AND\_ENERGY |  | 15 | -0.37 | -1.09 | 0.362 | 0.681 | 1.000 | 99 | tags=20%, list=7%, signal=21% |
| 575 | GOBP\_REGULATION\_OF\_RESPONSE\_TO\_STRESS |  | 190 | -0.24 | -1.09 | 0.309 | 0.681 | 1.000 | 575 | tags=41%, list=38%, signal=58% |
| 576 | GOBP\_CELL\_GROWTH |  | 65 | -0.28 | -1.09 | 0.321 | 0.680 | 1.000 | 513 | tags=37%, list=34%, signal=54% |
| 577 | GOBP\_NEGATIVE\_REGULATION\_OF\_COAGULATION |  | 15 | -0.37 | -1.09 | 0.364 | 0.680 | 1.000 | 376 | tags=47%, list=25%, signal=62% |
| 578 | GOBP\_RESPONSE\_TO\_CHEMOKINE |  | 24 | -0.33 | -1.09 | 0.348 | 0.679 | 1.000 | 315 | tags=38%, list=21%, signal=47% |
| 579 | GOMF\_PHOSPHATASE\_ACTIVITY |  | 19 | -0.35 | -1.09 | 0.323 | 0.679 | 1.000 | 574 | tags=53%, list=38%, signal=84% |
| 580 | GOBP\_NEURON\_PROJECTION\_EXTENSION |  | 21 | -0.35 | -1.09 | 0.351 | 0.680 | 1.000 | 954 | tags=90%, list=63%, signal=242% |
| 581 | GOBP\_NEGATIVE\_REGULATION\_OF\_CELL\_CELL\_ADHESION |  | 32 | -0.30 | -1.09 | 0.356 | 0.680 | 1.000 | 479 | tags=41%, list=32%, signal=58% |
| 582 | GOBP\_DEVELOPMENTAL\_CELL\_GROWTH |  | 29 | -0.32 | -1.09 | 0.355 | 0.680 | 1.000 | 766 | tags=55%, list=51%, signal=110% |
| 583 | GOBP\_POSITIVE\_REGULATION\_OF\_TRANSFERASE\_ACTIVITY |  | 75 | -0.27 | -1.09 | 0.334 | 0.679 | 1.000 | 588 | tags=39%, list=39%, signal=60% |
| 584 | GOCC\_ANCHORING\_JUNCTION |  | 112 | -0.25 | -1.09 | 0.335 | 0.678 | 1.000 | 512 | tags=35%, list=34%, signal=49% |
| 585 | GOBP\_CARBOHYDRATE\_HOMEOSTASIS |  | 31 | -0.31 | -1.08 | 0.357 | 0.684 | 1.000 | 636 | tags=48%, list=42%, signal=82% |
| 586 | GOBP\_NEPHRON\_MORPHOGENESIS |  | 15 | -0.36 | -1.08 | 0.375 | 0.685 | 1.000 | 627 | tags=67%, list=42%, signal=113% |
| 587 | GOBP\_MALE\_SEX\_DIFFERENTIATION |  | 19 | -0.34 | -1.08 | 0.374 | 0.685 | 1.000 | 611 | tags=63%, list=40%, signal=105% |
| 588 | GOBP\_MODIFICATION\_DEPENDENT\_MACROMOLECULE\_CATABOLIC\_PROCESS |  | 34 | -0.30 | -1.08 | 0.370 | 0.693 | 1.000 | 326 | tags=24%, list=22%, signal=29% |
| 589 | GOBP\_REGULATION\_OF\_HEMOPOIESIS |  | 64 | -0.27 | -1.08 | 0.361 | 0.692 | 1.000 | 595 | tags=50%, list=39%, signal=79% |
| 590 | GOCC\_SIDE\_OF\_MEMBRANE |  | 94 | -0.26 | -1.08 | 0.346 | 0.693 | 1.000 | 536 | tags=43%, list=35%, signal=62% |
| 591 | GOMF\_PROTEIN\_C\_TERMINUS\_BINDING |  | 23 | -0.33 | -1.08 | 0.349 | 0.694 | 1.000 | 786 | tags=65%, list=52%, signal=134% |
| 592 | GOBP\_CELLULAR\_RESPONSE\_TO\_MOLECULE\_OF\_BACTERIAL\_ORIGIN |  | 40 | -0.29 | -1.08 | 0.383 | 0.696 | 1.000 | 340 | tags=40%, list=23%, signal=50% |
| 593 | GOBP\_NEGATIVE\_REGULATION\_OF\_CYSTEINE\_TYPE\_ENDOPEPTIDASE\_ACTIVITY |  | 16 | -0.36 | -1.08 | 0.362 | 0.696 | 1.000 | 181 | tags=25%, list=12%, signal=28% |
| 594 | GOBP\_CARBOHYDRATE\_METABOLIC\_PROCESS |  | 44 | -0.29 | -1.08 | 0.361 | 0.697 | 1.000 | 164 | tags=20%, list=11%, signal=22% |
| 595 | GOBP\_POTASSIUM\_ION\_TRANSPORT |  | 22 | -0.33 | -1.07 | 0.362 | 0.700 | 1.000 | 151 | tags=18%, list=10%, signal=20% |
| 596 | GOBP\_AUTONOMIC\_NERVOUS\_SYSTEM\_DEVELOPMENT |  | 16 | -0.36 | -1.07 | 0.377 | 0.701 | 1.000 | 493 | tags=44%, list=33%, signal=64% |
| 597 | GOBP\_CELLULAR\_RESPONSE\_TO\_STARVATION |  | 17 | -0.35 | -1.07 | 0.384 | 0.700 | 1.000 | 543 | tags=53%, list=36%, signal=82% |
| 598 | GOBP\_CELLULAR\_RESPONSE\_TO\_INSULIN\_STIMULUS |  | 17 | -0.35 | -1.07 | 0.377 | 0.700 | 1.000 | 504 | tags=41%, list=33%, signal=61% |
| 599 | GOCC\_TRANSPORT\_VESICLE |  | 38 | -0.29 | -1.07 | 0.373 | 0.700 | 1.000 | 673 | tags=47%, list=45%, signal=83% |
| 600 | GOBP\_NEGATIVE\_REGULATION\_OF\_WOUND\_HEALING |  | 17 | -0.36 | -1.07 | 0.381 | 0.702 | 1.000 | 413 | tags=47%, list=27%, signal=64% |
| 601 | GOBP\_CELL\_CHEMOTAXIS |  | 72 | -0.26 | -1.07 | 0.344 | 0.701 | 1.000 | 615 | tags=49%, list=41%, signal=78% |
| 602 | GOMF\_PHOSPHOLIPID\_BINDING |  | 41 | -0.29 | -1.07 | 0.396 | 0.701 | 1.000 | 281 | tags=27%, list=19%, signal=32% |
| 603 | GOBP\_CELLULAR\_RESPONSE\_TO\_ORGANIC\_CYCLIC\_COMPOUND |  | 80 | -0.26 | -1.07 | 0.357 | 0.702 | 1.000 | 579 | tags=45%, list=38%, signal=69% |
| 604 | GOCC\_OUTER\_MEMBRANE |  | 18 | -0.35 | -1.07 | 0.387 | 0.702 | 1.000 | 225 | tags=33%, list=15%, signal=39% |
| 605 | GOBP\_LEUKOCYTE\_APOPTOTIC\_PROCESS |  | 19 | -0.34 | -1.07 | 0.384 | 0.704 | 1.000 | 575 | tags=58%, list=38%, signal=92% |
| 606 | GOBP\_RESPONSE\_TO\_METAL\_ION |  | 61 | -0.26 | -1.07 | 0.365 | 0.704 | 1.000 | 145 | tags=20%, list=10%, signal=21% |
| 607 | GOCC\_VACUOLAR\_MEMBRANE |  | 33 | -0.30 | -1.07 | 0.386 | 0.705 | 1.000 | 590 | tags=55%, list=39%, signal=88% |
| 608 | GOBP\_VASCULAR\_PROCESS\_IN\_CIRCULATORY\_SYSTEM |  | 36 | -0.30 | -1.07 | 0.382 | 0.704 | 1.000 | 422 | tags=39%, list=28%, signal=53% |
| 609 | GOBP\_CENTRAL\_NERVOUS\_SYSTEM\_NEURON\_DIFFERENTIATION |  | 27 | -0.32 | -1.07 | 0.375 | 0.704 | 1.000 | 536 | tags=41%, list=35%, signal=62% |
| 610 | GOBP\_REGULATION\_OF\_NERVOUS\_SYSTEM\_DEVELOPMENT |  | 50 | -0.28 | -1.07 | 0.378 | 0.703 | 1.000 | 622 | tags=40%, list=41%, signal=66% |
| 611 | GOBP\_POSITIVE\_REGULATION\_OF\_HEMOPOIESIS |  | 25 | -0.32 | -1.07 | 0.395 | 0.702 | 1.000 | 624 | tags=52%, list=41%, signal=87% |
| 612 | GOBP\_BLOOD\_VESSEL\_ENDOTHELIAL\_CELL\_MIGRATION |  | 18 | -0.35 | -1.07 | 0.377 | 0.702 | 1.000 | 516 | tags=56%, list=34%, signal=83% |
| 613 | GOBP\_REGULATION\_OF\_TRANSFERASE\_ACTIVITY |  | 114 | -0.24 | -1.07 | 0.377 | 0.703 | 1.000 | 588 | tags=38%, list=39%, signal=57% |
| 614 | GOBP\_APPENDAGE\_DEVELOPMENT |  | 25 | -0.32 | -1.06 | 0.376 | 0.710 | 1.000 | 174 | tags=20%, list=12%, signal=22% |
| 615 | GOBP\_REGULATION\_OF\_DNA\_TEMPLATED\_TRANSCRIPTION\_IN\_RESPONSE\_TO\_STRESS |  | 17 | -0.36 | -1.06 | 0.404 | 0.713 | 1.000 | 25 | tags=12%, list=2%, signal=12% |
| 616 | GOBP\_POSITIVE\_REGULATION\_OF\_TRANSPORT |  | 125 | -0.24 | -1.06 | 0.388 | 0.718 | 1.000 | 103 | tags=15%, list=7%, signal=15% |
| 617 | GOBP\_REGULATION\_OF\_BLOOD\_CIRCULATION |  | 44 | -0.28 | -1.06 | 0.387 | 0.719 | 1.000 | 118 | tags=18%, list=8%, signal=19% |
| 618 | GOBP\_REGULATION\_OF\_VASCULATURE\_DEVELOPMENT |  | 68 | -0.26 | -1.06 | 0.391 | 0.721 | 1.000 | 516 | tags=43%, list=34%, signal=62% |
| 619 | GOBP\_INTRINSIC\_APOPTOTIC\_SIGNALING\_PATHWAY |  | 35 | -0.29 | -1.06 | 0.389 | 0.722 | 1.000 | 489 | tags=37%, list=32%, signal=54% |
| 620 | GOBP\_POSITIVE\_REGULATION\_OF\_ANION\_TRANSPORT |  | 60 | -0.27 | -1.06 | 0.398 | 0.724 | 1.000 | 644 | tags=50%, list=43%, signal=84% |
| 621 | GOBP\_RESPONSE\_TO\_MOLECULE\_OF\_BACTERIAL\_ORIGIN |  | 76 | -0.25 | -1.06 | 0.381 | 0.724 | 1.000 | 363 | tags=36%, list=24%, signal=44% |
| 622 | GOBP\_REGULATION\_OF\_RECEPTOR\_MEDIATED\_ENDOCYTOSIS |  | 15 | -0.36 | -1.05 | 0.401 | 0.726 | 1.000 | 376 | tags=40%, list=25%, signal=53% |
| 623 | GOBP\_NEGATIVE\_REGULATION\_OF\_PHOSPHORYLATION |  | 56 | -0.27 | -1.05 | 0.406 | 0.729 | 1.000 | 545 | tags=39%, list=36%, signal=59% |
| 624 | GOBP\_PEPTIDE\_SECRETION |  | 60 | -0.26 | -1.05 | 0.398 | 0.739 | 1.000 | 679 | tags=50%, list=45%, signal=87% |
| 625 | GOBP\_NEGATIVE\_REGULATION\_OF\_APOPTOTIC\_SIGNALING\_PATHWAY |  | 34 | -0.29 | -1.05 | 0.412 | 0.738 | 1.000 | 539 | tags=44%, list=36%, signal=67% |
| 626 | GOBP\_REGULATION\_OF\_LIPID\_BIOSYNTHETIC\_PROCESS |  | 24 | -0.32 | -1.05 | 0.418 | 0.737 | 1.000 | 485 | tags=46%, list=32%, signal=66% |
| 627 | GOBP\_REGULATION\_OF\_CELL\_ACTIVATION |  | 110 | -0.24 | -1.05 | 0.402 | 0.736 | 1.000 | 575 | tags=41%, list=38%, signal=61% |
| 628 | GOBP\_ORGAN\_GROWTH |  | 26 | -0.32 | -1.05 | 0.409 | 0.738 | 1.000 | 766 | tags=65%, list=51%, signal=130% |
| 629 | GOBP\_POSITIVE\_REGULATION\_OF\_ESTABLISHMENT\_OF\_PROTEIN\_LOCALIZATION |  | 30 | -0.30 | -1.05 | 0.407 | 0.737 | 1.000 | 644 | tags=47%, list=43%, signal=80% |
| 630 | GOBP\_POSITIVE\_REGULATION\_OF\_MYELOID\_CELL\_DIFFERENTIATION |  | 19 | -0.33 | -1.05 | 0.413 | 0.741 | 1.000 | 624 | tags=58%, list=41%, signal=97% |
| 631 | GOBP\_POSITIVE\_REGULATION\_OF\_PROTEIN\_POLYMERIZATION |  | 19 | -0.33 | -1.04 | 0.409 | 0.742 | 1.000 | 267 | tags=26%, list=18%, signal=32% |
| 632 | GOBP\_POSITIVE\_REGULATION\_OF\_PEPTIDE\_SECRETION |  | 21 | -0.33 | -1.04 | 0.396 | 0.741 | 1.000 | 578 | tags=48%, list=38%, signal=76% |
| 633 | GOBP\_PLATELET\_DEGRANULATION |  | 39 | -0.29 | -1.04 | 0.412 | 0.741 | 1.000 | 375 | tags=36%, list=25%, signal=47% |
| 634 | GOBP\_HEART\_PROCESS |  | 44 | -0.28 | -1.04 | 0.418 | 0.742 | 1.000 | 123 | tags=18%, list=8%, signal=19% |
| 635 | GOBP\_MIDBRAIN\_DEVELOPMENT |  | 16 | -0.35 | -1.04 | 0.419 | 0.742 | 1.000 | 669 | tags=56%, list=44%, signal=100% |
| 636 | GOBP\_RESPONSE\_TO\_IONIZING\_RADIATION |  | 20 | -0.33 | -1.04 | 0.420 | 0.741 | 1.000 | 304 | tags=35%, list=20%, signal=43% |
| 637 | GOBP\_RESPONSE\_TO\_CARBOHYDRATE |  | 31 | -0.30 | -1.04 | 0.411 | 0.740 | 1.000 | 578 | tags=42%, list=38%, signal=67% |
| 638 | GOBP\_REGULATION\_OF\_ACTIN\_FILAMENT\_BUNDLE\_ASSEMBLY |  | 15 | -0.36 | -1.04 | 0.421 | 0.740 | 1.000 | 479 | tags=40%, list=32%, signal=58% |
| 639 | GOBP\_RESPONSE\_TO\_VIRUS |  | 45 | -0.28 | -1.04 | 0.410 | 0.742 | 1.000 | 595 | tags=44%, list=39%, signal=71% |
| 640 | GOCC\_NUCLEAR\_ENVELOPE |  | 38 | -0.28 | -1.04 | 0.428 | 0.741 | 1.000 | 107 | tags=18%, list=7%, signal=19% |
| 641 | GOBP\_STRESS\_ACTIVATED\_PROTEIN\_KINASE\_SIGNALING\_CASCADE |  | 27 | -0.30 | -1.04 | 0.409 | 0.741 | 1.000 | 334 | tags=33%, list=22%, signal=42% |
| 642 | GOBP\_POSITIVE\_REGULATION\_OF\_BIOSYNTHETIC\_PROCESS |  | 198 | -0.23 | -1.04 | 0.412 | 0.748 | 1.000 | 654 | tags=46%, list=43%, signal=71% |
| 643 | GOBP\_NEGATIVE\_REGULATION\_OF\_NUCLEOBASE\_CONTAINING\_COMPOUND\_METABOLIC\_PROCESS |  | 134 | -0.24 | -1.04 | 0.433 | 0.748 | 1.000 | 622 | tags=42%, list=41%, signal=65% |
| 644 | GOBP\_CELL\_ACTIVATION |  | 243 | -0.22 | -1.04 | 0.412 | 0.749 | 1.000 | 575 | tags=42%, list=38%, signal=57% |
| 645 | GOBP\_EXTRINSIC\_APOPTOTIC\_SIGNALING\_PATHWAY |  | 36 | -0.28 | -1.03 | 0.410 | 0.752 | 1.000 | 575 | tags=53%, list=38%, signal=83% |
| 646 | GOBP\_INFLAMMATORY\_RESPONSE |  | 153 | -0.23 | -1.03 | 0.402 | 0.753 | 1.000 | 567 | tags=41%, list=38%, signal=59% |
| 647 | GOBP\_REGULATION\_OF\_CYTOSKELETON\_ORGANIZATION |  | 63 | -0.25 | -1.03 | 0.426 | 0.752 | 1.000 | 267 | tags=22%, list=18%, signal=26% |
| 648 | GOBP\_ERK1\_AND\_ERK2\_CASCADE |  | 57 | -0.26 | -1.03 | 0.428 | 0.752 | 1.000 | 578 | tags=42%, list=38%, signal=66% |
| 649 | GOBP\_KERATINOCYTE\_DIFFERENTIATION |  | 29 | -0.30 | -1.03 | 0.420 | 0.751 | 1.000 | 412 | tags=41%, list=27%, signal=56% |
| 650 | GOBP\_NEURON\_DIFFERENTIATION |  | 163 | -0.23 | -1.03 | 0.417 | 0.754 | 1.000 | 673 | tags=43%, list=45%, signal=69% |
| 651 | GOBP\_REGULATION\_OF\_LEUKOCYTE\_MEDIATED\_CYTOTOXICITY |  | 17 | -0.34 | -1.03 | 0.435 | 0.753 | 1.000 | 334 | tags=35%, list=22%, signal=45% |
| 652 | GOBP\_REGULATION\_OF\_BINDING |  | 47 | -0.27 | -1.03 | 0.428 | 0.752 | 1.000 | 232 | tags=23%, list=15%, signal=27% |
| 653 | GOBP\_CELLULAR\_GLUCOSE\_HOMEOSTASIS |  | 19 | -0.33 | -1.03 | 0.435 | 0.751 | 1.000 | 636 | tags=53%, list=42%, signal=90% |
| 654 | GOBP\_REGULATION\_OF\_SYSTEM\_PROCESS |  | 86 | -0.25 | -1.03 | 0.427 | 0.755 | 1.000 | 679 | tags=48%, list=45%, signal=82% |
| 655 | GOBP\_FIBROBLAST\_PROLIFERATION |  | 17 | -0.34 | -1.03 | 0.426 | 0.754 | 1.000 | 644 | tags=59%, list=43%, signal=101% |
| 656 | GOMF\_ACTIVE\_TRANSMEMBRANE\_TRANSPORTER\_ACTIVITY |  | 17 | -0.34 | -1.03 | 0.447 | 0.755 | 1.000 | 438 | tags=47%, list=29%, signal=66% |
| 657 | GOBP\_MOLTING\_CYCLE |  | 15 | -0.35 | -1.03 | 0.442 | 0.754 | 1.000 | 535 | tags=47%, list=35%, signal=72% |
| 658 | GOBP\_ION\_HOMEOSTASIS |  | 102 | -0.24 | -1.03 | 0.428 | 0.755 | 1.000 | 512 | tags=33%, list=34%, signal=47% |
| 659 | GOBP\_FEMALE\_SEX\_DIFFERENTIATION |  | 16 | -0.34 | -1.02 | 0.434 | 0.762 | 1.000 | 611 | tags=69%, list=40%, signal=114% |
| 660 | GOBP\_SKELETAL\_MUSCLE\_ORGAN\_DEVELOPMENT |  | 27 | -0.30 | -1.02 | 0.439 | 0.761 | 1.000 | 817 | tags=63%, list=54%, signal=135% |
| 661 | GOBP\_POSITIVE\_REGULATION\_OF\_ENDOTHELIAL\_CELL\_MIGRATION |  | 17 | -0.34 | -1.02 | 0.454 | 0.761 | 1.000 | 516 | tags=53%, list=34%, signal=80% |
| 662 | GOMF\_PEPTIDASE\_REGULATOR\_ACTIVITY |  | 56 | -0.26 | -1.02 | 0.446 | 0.760 | 1.000 | 413 | tags=32%, list=27%, signal=43% |
| 663 | GOBP\_POSITIVE\_REGULATION\_OF\_LEUKOCYTE\_CELL\_CELL\_ADHESION |  | 41 | -0.27 | -1.02 | 0.432 | 0.762 | 1.000 | 644 | tags=39%, list=43%, signal=66% |
| 664 | GOBP\_RESPONSE\_TO\_OXIDATIVE\_STRESS |  | 62 | -0.25 | -1.02 | 0.426 | 0.764 | 1.000 | 326 | tags=27%, list=22%, signal=34% |
| 665 | GOBP\_B\_CELL\_PROLIFERATION |  | 23 | -0.31 | -1.02 | 0.452 | 0.763 | 1.000 | 499 | tags=52%, list=33%, signal=77% |
| 666 | GOBP\_NEGATIVE\_REGULATION\_OF\_BIOSYNTHETIC\_PROCESS |  | 151 | -0.23 | -1.02 | 0.452 | 0.763 | 1.000 | 622 | tags=42%, list=41%, signal=65% |
| 667 | GOBP\_REGULATION\_OF\_LEUKOCYTE\_CHEMOTAXIS |  | 35 | -0.29 | -1.02 | 0.461 | 0.765 | 1.000 | 589 | tags=46%, list=39%, signal=73% |
| 668 | GOBP\_REGULATION\_OF\_CELL\_JUNCTION\_ASSEMBLY |  | 20 | -0.32 | -1.02 | 0.438 | 0.767 | 1.000 | 861 | tags=80%, list=57%, signal=184% |
| 669 | GOCC\_PERIKARYON |  | 32 | -0.29 | -1.02 | 0.458 | 0.767 | 1.000 | 693 | tags=44%, list=46%, signal=79% |
| 670 | GOBP\_KIDNEY\_MORPHOGENESIS |  | 18 | -0.34 | -1.02 | 0.465 | 0.766 | 1.000 | 382 | tags=39%, list=25%, signal=51% |
| 671 | GOBP\_POSITIVE\_REGULATION\_OF\_PEPTIDYL\_SERINE\_PHOSPHORYLATION |  | 18 | -0.33 | -1.02 | 0.456 | 0.767 | 1.000 | 578 | tags=39%, list=38%, signal=62% |
| 672 | GOBP\_RENAL\_TUBULE\_DEVELOPMENT |  | 19 | -0.32 | -1.02 | 0.461 | 0.766 | 1.000 | 382 | tags=37%, list=25%, signal=49% |
| 673 | GOBP\_T\_CELL\_ACTIVATION |  | 73 | -0.25 | -1.02 | 0.442 | 0.765 | 1.000 | 644 | tags=44%, list=43%, signal=73% |
| 674 | GOBP\_PROTEIN\_LOCALIZATION\_TO\_PLASMA\_MEMBRANE |  | 28 | -0.30 | -1.02 | 0.466 | 0.765 | 1.000 | 673 | tags=46%, list=45%, signal=82% |
| 675 | GOCC\_MEMBRANE\_MICRODOMAIN |  | 52 | -0.26 | -1.02 | 0.466 | 0.766 | 1.000 | 75 | tags=17%, list=5%, signal=18% |
| 676 | GOCC\_PLASMA\_MEMBRANE\_RAFT |  | 20 | -0.32 | -1.01 | 0.454 | 0.769 | 1.000 | 65 | tags=20%, list=4%, signal=21% |
| 677 | GOBP\_DIGESTION |  | 19 | -0.32 | -1.01 | 0.445 | 0.768 | 1.000 | 497 | tags=53%, list=33%, signal=77% |
| 678 | GOBP\_POSITIVE\_REGULATION\_OF\_CHEMOTAXIS |  | 38 | -0.28 | -1.01 | 0.453 | 0.767 | 1.000 | 614 | tags=50%, list=41%, signal=82% |
| 679 | GOBP\_ADULT\_BEHAVIOR |  | 15 | -0.35 | -1.01 | 0.452 | 0.769 | 1.000 | 749 | tags=47%, list=50%, signal=92% |
| 680 | GOBP\_DNA\_BIOSYNTHETIC\_PROCESS |  | 24 | -0.31 | -1.01 | 0.454 | 0.770 | 1.000 | 614 | tags=46%, list=41%, signal=76% |
| 681 | GOCC\_CHROMOSOME |  | 137 | -0.23 | -1.01 | 0.455 | 0.769 | 1.000 | 674 | tags=51%, list=45%, signal=84% |
| 682 | GOBP\_NEGATIVE\_REGULATION\_OF\_PROTEIN\_MODIFICATION\_PROCESS |  | 67 | -0.25 | -1.01 | 0.449 | 0.769 | 1.000 | 588 | tags=40%, list=39%, signal=63% |
| 683 | GOBP\_NEGATIVE\_REGULATION\_OF\_VASCULATURE\_DEVELOPMENT |  | 33 | -0.29 | -1.01 | 0.462 | 0.767 | 1.000 | 567 | tags=45%, list=38%, signal=71% |
| 684 | GOBP\_DEFENSE\_RESPONSE\_TO\_OTHER\_ORGANISM |  | 165 | -0.22 | -1.01 | 0.466 | 0.769 | 1.000 | 565 | tags=41%, list=37%, signal=58% |
| 685 | GOMF\_IRON\_ION\_BINDING |  | 19 | -0.32 | -1.01 | 0.465 | 0.768 | 1.000 | 448 | tags=42%, list=30%, signal=59% |
| 686 | GOBP\_RESPONSE\_TO\_CAMP |  | 22 | -0.31 | -1.01 | 0.446 | 0.767 | 1.000 | 712 | tags=64%, list=47%, signal=119% |
| 687 | GOBP\_REGULATION\_OF\_T\_CELL\_ACTIVATION |  | 58 | -0.26 | -1.01 | 0.463 | 0.768 | 1.000 | 644 | tags=41%, list=43%, signal=69% |
| 688 | GOCC\_ENDOPLASMIC\_RETICULUM |  | 207 | -0.22 | -1.01 | 0.457 | 0.767 | 1.000 | 648 | tags=48%, list=43%, signal=73% |
| 689 | GOMF\_OXIDOREDUCTASE\_ACTIVITY\_ACTING\_ON\_PAIRED\_DONORS\_WITH\_INCORPORATION\_OR\_REDUCTION\_OF\_MOLECULAR\_OXYGEN |  | 15 | -0.35 | -1.01 | 0.444 | 0.766 | 1.000 | 369 | tags=47%, list=24%, signal=61% |
| 690 | GOBP\_REGULATION\_OF\_RESPONSE\_TO\_DNA\_DAMAGE\_STIMULUS |  | 22 | -0.31 | -1.01 | 0.467 | 0.768 | 1.000 | 214 | tags=23%, list=14%, signal=26% |
| 691 | GOMF\_METALLOPEPTIDASE\_ACTIVITY |  | 18 | -0.33 | -1.01 | 0.467 | 0.768 | 1.000 | 534 | tags=56%, list=35%, signal=85% |
| 692 | GOBP\_REGULATION\_OF\_EXTRINSIC\_APOPTOTIC\_SIGNALING\_PATHWAY |  | 27 | -0.30 | -1.01 | 0.473 | 0.768 | 1.000 | 558 | tags=56%, list=37%, signal=87% |
| 693 | GOBP\_REGULATION\_OF\_HEART\_CONTRACTION |  | 40 | -0.27 | -1.01 | 0.457 | 0.767 | 1.000 | 118 | tags=18%, list=8%, signal=18% |
| 694 | GOCC\_INTRINSIC\_COMPONENT\_OF\_PLASMA\_MEMBRANE |  | 177 | -0.22 | -1.01 | 0.478 | 0.766 | 1.000 | 492 | tags=36%, list=33%, signal=47% |
| 695 | GOBP\_JNK\_CASCADE |  | 19 | -0.32 | -1.01 | 0.439 | 0.768 | 1.000 | 310 | tags=37%, list=21%, signal=46% |
| 696 | GOBP\_RESPONSE\_TO\_BACTERIUM |  | 137 | -0.23 | -1.01 | 0.484 | 0.767 | 1.000 | 627 | tags=48%, list=42%, signal=75% |
| 697 | GOBP\_NOTCH\_SIGNALING\_PATHWAY |  | 22 | -0.31 | -1.01 | 0.440 | 0.769 | 1.000 | 355 | tags=32%, list=24%, signal=41% |
| 698 | GOBP\_REGULATION\_OF\_INTRACELLULAR\_PROTEIN\_TRANSPORT |  | 18 | -0.33 | -1.00 | 0.454 | 0.771 | 1.000 | 607 | tags=56%, list=40%, signal=92% |
| 699 | GOBP\_RESPONSE\_TO\_DRUG |  | 61 | -0.25 | -1.00 | 0.475 | 0.773 | 1.000 | 567 | tags=48%, list=38%, signal=73% |
| 700 | GOBP\_LEARNING |  | 17 | -0.33 | -1.00 | 0.462 | 0.772 | 1.000 | 144 | tags=18%, list=10%, signal=19% |
| 701 | GOBP\_REGENERATION |  | 39 | -0.27 | -1.00 | 0.476 | 0.774 | 1.000 | 707 | tags=56%, list=47%, signal=103% |
| 702 | GOBP\_MACROPHAGE\_MIGRATION |  | 20 | -0.32 | -1.00 | 0.460 | 0.775 | 1.000 | 559 | tags=50%, list=37%, signal=78% |
| 703 | GOMF\_ADENYL\_NUCLEOTIDE\_BINDING |  | 74 | -0.24 | -1.00 | 0.486 | 0.774 | 1.000 | 597 | tags=41%, list=40%, signal=64% |
| 704 | GOBP\_HEMATOPOIETIC\_PROGENITOR\_CELL\_DIFFERENTIATION |  | 16 | -0.34 | -1.00 | 0.472 | 0.775 | 1.000 | 265 | tags=31%, list=18%, signal=38% |
| 705 | GOBP\_STRIATED\_MUSCLE\_CONTRACTION |  | 28 | -0.29 | -1.00 | 0.480 | 0.775 | 1.000 | 508 | tags=36%, list=34%, signal=53% |
| 706 | GOMF\_PHOSPHORIC\_ESTER\_HYDROLASE\_ACTIVITY |  | 30 | -0.29 | -1.00 | 0.470 | 0.774 | 1.000 | 695 | tags=60%, list=46%, signal=109% |
| 707 | GOBP\_LEUKOCYTE\_MEDIATED\_CYTOTOXICITY |  | 18 | -0.32 | -1.00 | 0.464 | 0.774 | 1.000 | 334 | tags=33%, list=22%, signal=42% |
| 708 | GOBP\_GLIAL\_CELL\_DEVELOPMENT |  | 22 | -0.31 | -1.00 | 0.477 | 0.777 | 1.000 | 632 | tags=50%, list=42%, signal=85% |
| 709 | GOBP\_NEPHRON\_DEVELOPMENT |  | 26 | -0.30 | -1.00 | 0.476 | 0.778 | 1.000 | 447 | tags=38%, list=30%, signal=54% |
| 710 | GOBP\_SEX\_DIFFERENTIATION |  | 33 | -0.28 | -1.00 | 0.500 | 0.780 | 1.000 | 611 | tags=61%, list=40%, signal=100% |
| 711 | GOBP\_RESPONSE\_TO\_BIOTIC\_STIMULUS |  | 237 | -0.21 | -0.99 | 0.496 | 0.781 | 1.000 | 566 | tags=40%, list=37%, signal=53% |
| 712 | GOBP\_PROCESS\_UTILIZING\_AUTOPHAGIC\_MECHANISM |  | 35 | -0.28 | -0.99 | 0.488 | 0.781 | 1.000 | 192 | tags=17%, list=13%, signal=19% |
| 713 | GOBP\_RESPONSE\_TO\_INORGANIC\_SUBSTANCE |  | 81 | -0.24 | -0.99 | 0.489 | 0.782 | 1.000 | 145 | tags=17%, list=10%, signal=18% |
| 714 | GOBP\_CARDIAC\_MUSCLE\_CONTRACTION |  | 23 | -0.30 | -0.99 | 0.484 | 0.784 | 1.000 | 123 | tags=17%, list=8%, signal=19% |
| 715 | GOBP\_CELL\_PROJECTION\_ORGANIZATION |  | 148 | -0.22 | -0.99 | 0.524 | 0.785 | 1.000 | 585 | tags=35%, list=39%, signal=52% |
| 716 | GOBP\_AXON\_EXTENSION |  | 15 | -0.34 | -0.99 | 0.492 | 0.784 | 1.000 | 415 | tags=27%, list=27%, signal=36% |
| 717 | GOBP\_SMALL\_MOLECULE\_METABOLIC\_PROCESS |  | 169 | -0.22 | -0.99 | 0.522 | 0.784 | 1.000 | 299 | tags=25%, list=20%, signal=28% |
| 718 | GOBP\_MODULATION\_OF\_PROCESS\_OF\_OTHER\_ORGANISM |  | 24 | -0.30 | -0.99 | 0.471 | 0.783 | 1.000 | 363 | tags=38%, list=24%, signal=49% |
| 719 | GOBP\_CELL\_MATURATION |  | 16 | -0.33 | -0.99 | 0.482 | 0.782 | 1.000 | 47 | tags=19%, list=3%, signal=19% |
| 720 | GOBP\_CYTOSKELETON\_ORGANIZATION |  | 136 | -0.22 | -0.99 | 0.513 | 0.781 | 1.000 | 327 | tags=24%, list=22%, signal=27% |
| 721 | GOBP\_POSITIVE\_REGULATION\_OF\_IMMUNE\_SYSTEM\_PROCESS |  | 162 | -0.22 | -0.99 | 0.508 | 0.780 | 1.000 | 575 | tags=40%, list=38%, signal=58% |
| 722 | GOBP\_REGULATION\_OF\_TRANSPORT |  | 206 | -0.21 | -0.99 | 0.521 | 0.784 | 1.000 | 588 | tags=40%, list=39%, signal=56% |
| 723 | GOBP\_ENDOTHELIUM\_DEVELOPMENT |  | 20 | -0.31 | -0.99 | 0.486 | 0.783 | 1.000 | 715 | tags=50%, list=47%, signal=94% |
| 724 | GOBP\_COMPLEMENT\_ACTIVATION |  | 20 | -0.31 | -0.99 | 0.479 | 0.786 | 1.000 | 556 | tags=50%, list=37%, signal=78% |
| 725 | GOBP\_NEGATIVE\_REGULATION\_OF\_SECRETION |  | 27 | -0.29 | -0.99 | 0.495 | 0.787 | 1.000 | 766 | tags=63%, list=51%, signal=126% |
| 726 | GOMF\_TRANSFERASE\_ACTIVITY\_TRANSFERRING\_PHOSPHORUS\_CONTAINING\_GROUPS |  | 45 | -0.26 | -0.99 | 0.477 | 0.787 | 1.000 | 586 | tags=38%, list=39%, signal=60% |
| 727 | GOBP\_REGULATION\_OF\_PEPTIDE\_SECRETION |  | 45 | -0.26 | -0.98 | 0.497 | 0.792 | 1.000 | 644 | tags=47%, list=43%, signal=79% |
| 728 | GOBP\_CELL\_CYCLE\_CHECKPOINT |  | 19 | -0.31 | -0.98 | 0.508 | 0.791 | 1.000 | 826 | tags=74%, list=55%, signal=161% |
| 729 | GOMF\_MOLECULAR\_TRANSDUCER\_ACTIVITY |  | 108 | -0.23 | -0.98 | 0.521 | 0.792 | 1.000 | 618 | tags=44%, list=41%, signal=68% |
| 730 | GOBP\_POSITIVE\_REGULATION\_OF\_MULTICELLULAR\_ORGANISMAL\_PROCESS |  | 220 | -0.21 | -0.98 | 0.525 | 0.791 | 1.000 | 644 | tags=45%, list=43%, signal=66% |
| 731 | GOBP\_RECEPTOR\_INTERNALIZATION |  | 18 | -0.32 | -0.98 | 0.504 | 0.792 | 1.000 | 151 | tags=22%, list=10%, signal=24% |
| 732 | GOBP\_REGULATION\_OF\_CHEMOTAXIS |  | 46 | -0.26 | -0.98 | 0.496 | 0.792 | 1.000 | 614 | tags=46%, list=41%, signal=75% |
| 733 | GOBP\_REGULATION\_OF\_CELL\_PROJECTION\_ORGANIZATION |  | 65 | -0.24 | -0.98 | 0.509 | 0.792 | 1.000 | 577 | tags=37%, list=38%, signal=57% |
| 734 | GOBP\_NEGATIVE\_REGULATION\_OF\_PROTEIN\_METABOLIC\_PROCESS |  | 142 | -0.22 | -0.98 | 0.521 | 0.791 | 1.000 | 627 | tags=42%, list=42%, signal=64% |
| 735 | GOMF\_ENZYME\_ACTIVATOR\_ACTIVITY |  | 58 | -0.25 | -0.98 | 0.519 | 0.791 | 1.000 | 284 | tags=22%, list=19%, signal=27% |
| 736 | GOMF\_PASSIVE\_TRANSMEMBRANE\_TRANSPORTER\_ACTIVITY |  | 38 | -0.27 | -0.98 | 0.496 | 0.792 | 1.000 | 477 | tags=37%, list=32%, signal=52% |
| 737 | GOBP\_PROTEIN\_LOCALIZATION\_TO\_CELL\_PERIPHERY |  | 31 | -0.28 | -0.98 | 0.497 | 0.793 | 1.000 | 673 | tags=45%, list=45%, signal=80% |
| 738 | GOBP\_CELLULAR\_HOMEOSTASIS |  | 123 | -0.22 | -0.98 | 0.526 | 0.794 | 1.000 | 519 | tags=34%, list=34%, signal=48% |
| 739 | GOBP\_RESPONSE\_TO\_TYPE\_I\_INTERFERON |  | 19 | -0.32 | -0.98 | 0.501 | 0.793 | 1.000 | 595 | tags=47%, list=39%, signal=77% |
| 740 | GOBP\_POSITIVE\_REGULATION\_OF\_MAPK\_CASCADE |  | 72 | -0.24 | -0.98 | 0.526 | 0.793 | 1.000 | 588 | tags=42%, list=39%, signal=65% |
| 741 | GOCC\_LYSOSOMAL\_LUMEN |  | 17 | -0.32 | -0.98 | 0.510 | 0.796 | 1.000 | 681 | tags=65%, list=45%, signal=117% |
| 742 | GOMF\_PHOSPHATIDYLINOSITOL\_BINDING |  | 16 | -0.33 | -0.98 | 0.511 | 0.796 | 1.000 | 99 | tags=19%, list=7%, signal=20% |
| 743 | GOBP\_NEGATIVE\_REGULATION\_OF\_HYDROLASE\_ACTIVITY |  | 74 | -0.24 | -0.97 | 0.534 | 0.797 | 1.000 | 684 | tags=50%, list=45%, signal=87% |
| 744 | GOBP\_CARDIAC\_CHAMBER\_DEVELOPMENT |  | 25 | -0.29 | -0.97 | 0.508 | 0.797 | 1.000 | 232 | tags=20%, list=15%, signal=23% |
| 745 | GOBP\_NEGATIVE\_REGULATION\_OF\_CELLULAR\_AMIDE\_METABOLIC\_PROCESS |  | 16 | -0.33 | -0.97 | 0.512 | 0.796 | 1.000 | 846 | tags=63%, list=56%, signal=141% |
| 746 | GOBP\_SMALL\_MOLECULE\_BIOSYNTHETIC\_PROCESS |  | 67 | -0.24 | -0.97 | 0.520 | 0.796 | 1.000 | 485 | tags=37%, list=32%, signal=53% |
| 747 | GOBP\_LIPID\_MODIFICATION |  | 15 | -0.33 | -0.97 | 0.524 | 0.798 | 1.000 | 574 | tags=53%, list=38%, signal=85% |
| 748 | GOMF\_IDENTICAL\_PROTEIN\_BINDING |  | 220 | -0.21 | -0.97 | 0.553 | 0.799 | 1.000 | 516 | tags=37%, list=34%, signal=48% |
| 749 | GOBP\_RECEPTOR\_METABOLIC\_PROCESS |  | 23 | -0.30 | -0.97 | 0.525 | 0.798 | 1.000 | 228 | tags=26%, list=15%, signal=30% |
| 750 | GOCC\_PLATELET\_ALPHA\_GRANULE |  | 31 | -0.28 | -0.97 | 0.528 | 0.797 | 1.000 | 375 | tags=35%, list=25%, signal=46% |
| 751 | GOBP\_CATION\_TRANSPORT |  | 127 | -0.22 | -0.97 | 0.554 | 0.796 | 1.000 | 151 | tags=15%, list=10%, signal=15% |
| 752 | GOBP\_NEGATIVE\_REGULATION\_OF\_CELL\_ACTIVATION |  | 41 | -0.26 | -0.97 | 0.533 | 0.796 | 1.000 | 595 | tags=41%, list=39%, signal=67% |
| 753 | GOBP\_REGULATION\_OF\_CELL\_MORPHOGENESIS |  | 43 | -0.26 | -0.97 | 0.529 | 0.802 | 1.000 | 567 | tags=37%, list=38%, signal=58% |
| 754 | GOBP\_POSITIVE\_REGULATION\_OF\_SECRETION |  | 48 | -0.25 | -0.96 | 0.546 | 0.808 | 1.000 | 644 | tags=46%, list=43%, signal=77% |
| 755 | GOBP\_REGULATION\_OF\_CELL\_MATRIX\_ADHESION |  | 18 | -0.31 | -0.96 | 0.527 | 0.807 | 1.000 | 525 | tags=56%, list=35%, signal=84% |
| 756 | GOBP\_CORNIFICATION |  | 17 | -0.32 | -0.96 | 0.514 | 0.808 | 1.000 | 535 | tags=53%, list=35%, signal=81% |
| 757 | GOMF\_ENDOPEPTIDASE\_REGULATOR\_ACTIVITY |  | 45 | -0.26 | -0.96 | 0.516 | 0.807 | 1.000 | 619 | tags=44%, list=41%, signal=73% |
| 758 | GOMF\_TRANSPORTER\_ACTIVITY |  | 85 | -0.23 | -0.96 | 0.544 | 0.806 | 1.000 | 477 | tags=36%, list=32%, signal=50% |
| 759 | GOBP\_RESPONSE\_TO\_AXON\_INJURY |  | 21 | -0.30 | -0.96 | 0.534 | 0.805 | 1.000 | 114 | tags=19%, list=8%, signal=20% |
| 760 | GOBP\_MULTICELLULAR\_ORGANISMAL\_HOMEOSTASIS |  | 86 | -0.23 | -0.96 | 0.558 | 0.806 | 1.000 | 541 | tags=38%, list=36%, signal=56% |
| 761 | GOBP\_NEGATIVE\_REGULATION\_OF\_EXTRINSIC\_APOPTOTIC\_SIGNALING\_PATHWAY |  | 16 | -0.32 | -0.96 | 0.519 | 0.806 | 1.000 | 688 | tags=75%, list=46%, signal=136% |
| 762 | GOMF\_RIBONUCLEOTIDE\_BINDING |  | 100 | -0.22 | -0.96 | 0.550 | 0.806 | 1.000 | 597 | tags=40%, list=40%, signal=62% |
| 763 | GOBP\_MYELOID\_LEUKOCYTE\_MIGRATION |  | 61 | -0.24 | -0.96 | 0.551 | 0.808 | 1.000 | 477 | tags=36%, list=32%, signal=51% |
| 764 | GOBP\_POSITIVE\_REGULATION\_OF\_CATABOLIC\_PROCESS |  | 33 | -0.27 | -0.96 | 0.529 | 0.809 | 1.000 | 497 | tags=33%, list=33%, signal=49% |
| 765 | GOCC\_CLATHRIN\_COATED\_VESICLE |  | 16 | -0.33 | -0.96 | 0.519 | 0.808 | 1.000 | 550 | tags=38%, list=36%, signal=58% |
| 766 | GOCC\_INTERMEDIATE\_FILAMENT\_CYTOSKELETON |  | 23 | -0.29 | -0.96 | 0.520 | 0.807 | 1.000 | 535 | tags=43%, list=35%, signal=66% |
| 767 | GOBP\_NEGATIVE\_REGULATION\_OF\_PROTEOLYSIS |  | 62 | -0.24 | -0.96 | 0.540 | 0.806 | 1.000 | 627 | tags=45%, list=42%, signal=74% |
| 768 | GOCC\_COATED\_VESICLE\_MEMBRANE |  | 19 | -0.31 | -0.96 | 0.541 | 0.808 | 1.000 | 550 | tags=37%, list=36%, signal=57% |
| 769 | GOBP\_POSITIVE\_REGULATION\_OF\_NEURON\_PROJECTION\_DEVELOPMENT |  | 21 | -0.30 | -0.96 | 0.520 | 0.808 | 1.000 | 567 | tags=43%, list=38%, signal=68% |
| 770 | GOCC\_EARLY\_ENDOSOME |  | 33 | -0.27 | -0.96 | 0.554 | 0.810 | 1.000 | 870 | tags=70%, list=58%, signal=161% |
| 771 | GOBP\_MITOTIC\_CELL\_CYCLE\_CHECKPOINT |  | 16 | -0.32 | -0.95 | 0.533 | 0.816 | 1.000 | 826 | tags=75%, list=55%, signal=164% |
| 772 | GOBP\_REGULATION\_OF\_RESPONSE\_TO\_EXTERNAL\_STIMULUS |  | 157 | -0.21 | -0.95 | 0.595 | 0.815 | 1.000 | 526 | tags=37%, list=35%, signal=51% |
| 773 | GOBP\_NEGATIVE\_REGULATION\_OF\_LYMPHOCYTE\_ACTIVATION |  | 31 | -0.27 | -0.95 | 0.546 | 0.819 | 1.000 | 595 | tags=45%, list=39%, signal=73% |
| 774 | GOBP\_LEUKOCYTE\_CHEMOTAXIS |  | 62 | -0.24 | -0.95 | 0.573 | 0.820 | 1.000 | 615 | tags=45%, list=41%, signal=73% |
| 775 | GOBP\_DEVELOPMENT\_OF\_PRIMARY\_SEXUAL\_CHARACTERISTICS |  | 29 | -0.28 | -0.95 | 0.558 | 0.822 | 1.000 | 611 | tags=59%, list=40%, signal=97% |
| 776 | GOBP\_REGULATION\_OF\_CELLULAR\_RESPONSE\_TO\_STRESS |  | 74 | -0.23 | -0.95 | 0.576 | 0.822 | 1.000 | 326 | tags=24%, list=22%, signal=30% |
| 777 | GOBP\_RESPONSE\_TO\_TOPOLOGICALLY\_INCORRECT\_PROTEIN |  | 16 | -0.32 | -0.95 | 0.528 | 0.823 | 1.000 | 516 | tags=38%, list=34%, signal=56% |
| 778 | GOMF\_PROTEIN\_KINASE\_ACTIVITY |  | 39 | -0.26 | -0.95 | 0.548 | 0.823 | 1.000 | 323 | tags=23%, list=21%, signal=29% |
| 779 | GOBP\_CELLULAR\_ION\_HOMEOSTASIS |  | 87 | -0.23 | -0.95 | 0.582 | 0.823 | 1.000 | 512 | tags=33%, list=34%, signal=48% |
| 780 | GOBP\_PLATELET\_ACTIVATION |  | 27 | -0.28 | -0.95 | 0.550 | 0.826 | 1.000 | 554 | tags=48%, list=37%, signal=75% |
| 781 | GOBP\_REGULATION\_OF\_PRODUCTION\_OF\_MOLECULAR\_MEDIATOR\_OF\_IMMUNE\_RESPONSE |  | 20 | -0.30 | -0.94 | 0.554 | 0.826 | 1.000 | 531 | tags=45%, list=35%, signal=68% |
| 782 | GOBP\_REGULATION\_OF\_PROTEIN\_CONTAINING\_COMPLEX\_ASSEMBLY |  | 58 | -0.24 | -0.94 | 0.560 | 0.825 | 1.000 | 267 | tags=22%, list=18%, signal=26% |
| 783 | GOBP\_REGULATION\_OF\_ANION\_TRANSPORT |  | 112 | -0.22 | -0.94 | 0.620 | 0.826 | 1.000 | 644 | tags=45%, list=43%, signal=72% |
| 784 | GOBP\_ORGANOPHOSPHATE\_CATABOLIC\_PROCESS |  | 15 | -0.32 | -0.94 | 0.549 | 0.827 | 1.000 | 410 | tags=40%, list=27%, signal=54% |
| 785 | GOBP\_MAPK\_CASCADE |  | 119 | -0.22 | -0.94 | 0.600 | 0.832 | 1.000 | 588 | tags=38%, list=39%, signal=57% |
| 786 | GOCC\_CELL\_PROJECTION\_MEMBRANE |  | 29 | -0.27 | -0.94 | 0.560 | 0.832 | 1.000 | 524 | tags=34%, list=35%, signal=52% |
| 787 | GOBP\_REGULATION\_OF\_PHAGOCYTOSIS |  | 16 | -0.32 | -0.94 | 0.583 | 0.833 | 1.000 | 51 | tags=19%, list=3%, signal=19% |
| 788 | GOCC\_TRANSCRIPTION\_REGULATOR\_COMPLEX |  | 27 | -0.28 | -0.94 | 0.556 | 0.832 | 1.000 | 624 | tags=52%, list=41%, signal=87% |
| 789 | GOBP\_REGULATION\_OF\_CYSTEINE\_TYPE\_ENDOPEPTIDASE\_ACTIVITY |  | 35 | -0.26 | -0.94 | 0.572 | 0.833 | 1.000 | 682 | tags=49%, list=45%, signal=87% |
| 790 | GOBP\_CELLULAR\_RESPONSE\_TO\_INORGANIC\_SUBSTANCE |  | 28 | -0.27 | -0.94 | 0.560 | 0.832 | 1.000 | 144 | tags=18%, list=10%, signal=19% |
| 791 | GOBP\_REGULATION\_OF\_RESPONSE\_TO\_CYTOKINE\_STIMULUS |  | 23 | -0.29 | -0.94 | 0.568 | 0.832 | 1.000 | 559 | tags=43%, list=37%, signal=68% |
| 792 | GOBP\_REGULATION\_OF\_STRESS\_ACTIVATED\_PROTEIN\_KINASE\_SIGNALING\_CASCADE |  | 18 | -0.30 | -0.94 | 0.540 | 0.833 | 1.000 | 303 | tags=33%, list=20%, signal=41% |
| 793 | GOBP\_POSITIVE\_REGULATION\_OF\_BINDING |  | 24 | -0.28 | -0.94 | 0.553 | 0.832 | 1.000 | 228 | tags=25%, list=15%, signal=29% |
| 794 | GOBP\_REGULATION\_OF\_METAL\_ION\_TRANSPORT |  | 40 | -0.26 | -0.94 | 0.558 | 0.831 | 1.000 | 103 | tags=15%, list=7%, signal=16% |
| 795 | GOBP\_CELL\_KILLING |  | 28 | -0.28 | -0.94 | 0.592 | 0.834 | 1.000 | 133 | tags=21%, list=9%, signal=23% |
| 796 | GOBP\_ADENYLATE\_CYCLASE\_ACTIVATING\_G\_PROTEIN\_COUPLED\_RECEPTOR\_SIGNALING\_PATHWAY |  | 24 | -0.29 | -0.93 | 0.571 | 0.838 | 1.000 | 615 | tags=46%, list=41%, signal=76% |
| 797 | GOBP\_RESPONSE\_TO\_TUMOR\_NECROSIS\_FACTOR |  | 50 | -0.24 | -0.93 | 0.581 | 0.840 | 1.000 | 575 | tags=48%, list=38%, signal=75% |
| 798 | GOBP\_POSITIVE\_REGULATION\_OF\_HORMONE\_SECRETION |  | 23 | -0.29 | -0.93 | 0.574 | 0.846 | 1.000 | 505 | tags=39%, list=33%, signal=58% |
| 799 | GOBP\_RESPONSE\_TO\_ALCOHOL |  | 51 | -0.24 | -0.93 | 0.592 | 0.846 | 1.000 | 254 | tags=24%, list=17%, signal=27% |
| 800 | GOBP\_SIGNAL\_TRANSDUCTION\_BY\_P53\_CLASS\_MEDIATOR |  | 19 | -0.30 | -0.93 | 0.578 | 0.847 | 1.000 | 548 | tags=37%, list=36%, signal=57% |
| 801 | GOCC\_VACUOLAR\_LUMEN |  | 30 | -0.27 | -0.93 | 0.581 | 0.848 | 1.000 | 252 | tags=27%, list=17%, signal=31% |
| 802 | GOBP\_REGULATION\_OF\_BLOOD\_PRESSURE |  | 40 | -0.25 | -0.93 | 0.606 | 0.849 | 1.000 | 551 | tags=45%, list=36%, signal=69% |
| 803 | GOBP\_NEGATIVE\_REGULATION\_OF\_MITOTIC\_CELL\_CYCLE |  | 27 | -0.27 | -0.92 | 0.579 | 0.850 | 1.000 | 553 | tags=37%, list=37%, signal=57% |
| 804 | GOMF\_KINASE\_ACTIVITY |  | 42 | -0.24 | -0.92 | 0.605 | 0.849 | 1.000 | 586 | tags=36%, list=39%, signal=57% |
| 805 | GOBP\_NEGATIVE\_REGULATION\_OF\_CATALYTIC\_ACTIVITY |  | 120 | -0.21 | -0.92 | 0.630 | 0.849 | 1.000 | 575 | tags=39%, list=38%, signal=58% |
| 806 | GOBP\_NEPHRON\_EPITHELIUM\_DEVELOPMENT |  | 20 | -0.29 | -0.92 | 0.593 | 0.848 | 1.000 | 382 | tags=35%, list=25%, signal=46% |
| 807 | GOMF\_GROWTH\_FACTOR\_RECEPTOR\_BINDING |  | 19 | -0.29 | -0.92 | 0.577 | 0.848 | 1.000 | 536 | tags=42%, list=35%, signal=64% |
| 808 | GOCC\_VACUOLE |  | 83 | -0.22 | -0.92 | 0.625 | 0.847 | 1.000 | 372 | tags=30%, list=25%, signal=38% |
| 809 | GOBP\_REGULATION\_OF\_CELL\_KILLING |  | 18 | -0.30 | -0.92 | 0.584 | 0.847 | 1.000 | 334 | tags=33%, list=22%, signal=42% |
| 810 | GOBP\_ADAPTIVE\_IMMUNE\_RESPONSE |  | 68 | -0.23 | -0.92 | 0.604 | 0.846 | 1.000 | 595 | tags=46%, list=39%, signal=72% |
| 811 | GOBP\_REGULATION\_OF\_B\_CELL\_PROLIFERATION |  | 17 | -0.31 | -0.92 | 0.576 | 0.846 | 1.000 | 574 | tags=53%, list=38%, signal=84% |
| 812 | GOBP\_CELLULAR\_RESPONSE\_TO\_DNA\_DAMAGE\_STIMULUS |  | 61 | -0.23 | -0.92 | 0.604 | 0.850 | 1.000 | 660 | tags=43%, list=44%, signal=73% |
| 813 | GOBP\_POSITIVE\_REGULATION\_OF\_CATALYTIC\_ACTIVITY |  | 158 | -0.20 | -0.92 | 0.652 | 0.849 | 1.000 | 524 | tags=32%, list=35%, signal=44% |
| 814 | GOBP\_MONOAMINE\_TRANSPORT |  | 15 | -0.32 | -0.92 | 0.576 | 0.850 | 1.000 | 766 | tags=60%, list=51%, signal=121% |
| 815 | GOCC\_INTRINSIC\_COMPONENT\_OF\_ORGANELLE\_MEMBRANE |  | 30 | -0.27 | -0.92 | 0.590 | 0.850 | 1.000 | 262 | tags=23%, list=17%, signal=28% |
| 816 | GOBP\_CYTOKINE\_MEDIATED\_SIGNALING\_PATHWAY |  | 126 | -0.21 | -0.92 | 0.647 | 0.852 | 1.000 | 624 | tags=44%, list=41%, signal=69% |
| 817 | GOCC\_CHROMATIN |  | 116 | -0.21 | -0.92 | 0.663 | 0.854 | 1.000 | 683 | tags=52%, list=45%, signal=87% |
| 818 | GOBP\_STEROID\_METABOLIC\_PROCESS |  | 38 | -0.25 | -0.91 | 0.596 | 0.855 | 1.000 | 485 | tags=45%, list=32%, signal=64% |
| 819 | GOBP\_PEPTIDYL\_LYSINE\_MODIFICATION |  | 29 | -0.27 | -0.91 | 0.595 | 0.855 | 1.000 | 580 | tags=38%, list=38%, signal=60% |
| 820 | GOBP\_REGULATION\_OF\_PROTEIN\_LOCALIZATION |  | 84 | -0.22 | -0.91 | 0.622 | 0.855 | 1.000 | 644 | tags=42%, list=43%, signal=69% |
| 821 | GOBP\_NEGATIVE\_REGULATION\_OF\_PEPTIDASE\_ACTIVITY |  | 56 | -0.23 | -0.91 | 0.616 | 0.854 | 1.000 | 627 | tags=45%, list=42%, signal=74% |
| 822 | GOBP\_ORGANIC\_HYDROXY\_COMPOUND\_TRANSPORT |  | 35 | -0.25 | -0.91 | 0.597 | 0.855 | 1.000 | 228 | tags=20%, list=15%, signal=23% |
| 823 | GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_DEATH |  | 115 | -0.21 | -0.91 | 0.641 | 0.854 | 1.000 | 334 | tags=23%, list=22%, signal=28% |
| 824 | GOMF\_G\_PROTEIN\_COUPLED\_RECEPTOR\_ACTIVITY |  | 31 | -0.26 | -0.91 | 0.613 | 0.853 | 1.000 | 598 | tags=42%, list=40%, signal=68% |
| 825 | GOBP\_REGULATION\_OF\_MUSCLE\_SYSTEM\_PROCESS |  | 34 | -0.26 | -0.91 | 0.591 | 0.853 | 1.000 | 508 | tags=35%, list=34%, signal=52% |
| 826 | GOBP\_NEGATIVE\_REGULATION\_OF\_NERVOUS\_SYSTEM\_DEVELOPMENT |  | 17 | -0.30 | -0.91 | 0.609 | 0.856 | 1.000 | 622 | tags=47%, list=41%, signal=79% |
| 827 | GOBP\_REGULATION\_OF\_DNA\_BINDING\_TRANSCRIPTION\_FACTOR\_ACTIVITY |  | 56 | -0.23 | -0.91 | 0.620 | 0.855 | 1.000 | 401 | tags=34%, list=27%, signal=44% |
| 828 | GOMF\_CYTOSKELETAL\_PROTEIN\_BINDING |  | 90 | -0.22 | -0.91 | 0.645 | 0.855 | 1.000 | 673 | tags=46%, list=45%, signal=77% |
| 829 | GOBP\_POSITIVE\_REGULATION\_OF\_ION\_TRANSPORT |  | 92 | -0.22 | -0.91 | 0.661 | 0.857 | 1.000 | 587 | tags=41%, list=39%, signal=63% |
| 830 | GOBP\_LIPID\_EXPORT\_FROM\_CELL |  | 20 | -0.29 | -0.91 | 0.595 | 0.857 | 1.000 | 851 | tags=75%, list=56%, signal=170% |
| 831 | GOBP\_REGULATION\_OF\_LEUKOCYTE\_MEDIATED\_IMMUNITY |  | 30 | -0.26 | -0.91 | 0.622 | 0.857 | 1.000 | 334 | tags=27%, list=22%, signal=34% |
| 832 | GOMF\_DNA\_BINDING\_TRANSCRIPTION\_ACTIVATOR\_ACTIVITY |  | 56 | -0.23 | -0.91 | 0.616 | 0.857 | 1.000 | 665 | tags=50%, list=44%, signal=86% |
| 833 | GOCC\_TRANSPORT\_VESICLE\_MEMBRANE |  | 19 | -0.29 | -0.91 | 0.598 | 0.857 | 1.000 | 457 | tags=37%, list=30%, signal=52% |
| 834 | GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_ACTIVATION |  | 67 | -0.22 | -0.91 | 0.640 | 0.856 | 1.000 | 575 | tags=39%, list=38%, signal=60% |
| 835 | GOBP\_ZYMOGEN\_ACTIVATION |  | 15 | -0.31 | -0.91 | 0.598 | 0.857 | 1.000 | 708 | tags=73%, list=47%, signal=137% |
| 836 | GOBP\_CELLULAR\_LIPID\_CATABOLIC\_PROCESS |  | 17 | -0.30 | -0.90 | 0.614 | 0.859 | 1.000 | 275 | tags=24%, list=18%, signal=28% |
| 837 | GOBP\_POSITIVE\_REGULATION\_OF\_HYDROLASE\_ACTIVITY |  | 88 | -0.22 | -0.90 | 0.646 | 0.859 | 1.000 | 334 | tags=23%, list=22%, signal=27% |
| 838 | GOBP\_METAL\_ION\_HOMEOSTASIS |  | 92 | -0.21 | -0.90 | 0.653 | 0.858 | 1.000 | 512 | tags=33%, list=34%, signal=46% |
| 839 | GOBP\_DEVELOPMENT\_OF\_PRIMARY\_FEMALE\_SEXUAL\_CHARACTERISTICS |  | 15 | -0.31 | -0.90 | 0.615 | 0.860 | 1.000 | 611 | tags=67%, list=40%, signal=111% |
| 840 | GOBP\_REGULATION\_OF\_SECRETION |  | 91 | -0.21 | -0.90 | 0.658 | 0.860 | 1.000 | 644 | tags=43%, list=43%, signal=70% |
| 841 | GOBP\_NEGATIVE\_REGULATION\_OF\_PEPTIDE\_SECRETION |  | 15 | -0.32 | -0.90 | 0.615 | 0.860 | 1.000 | 744 | tags=53%, list=49%, signal=104% |
| 842 | GOBP\_NEGATIVE\_REGULATION\_OF\_LEUKOCYTE\_PROLIFERATION |  | 20 | -0.29 | -0.90 | 0.616 | 0.860 | 1.000 | 334 | tags=25%, list=22%, signal=32% |
| 843 | GOBP\_NEURON\_DEATH |  | 55 | -0.23 | -0.90 | 0.629 | 0.860 | 1.000 | 240 | tags=20%, list=16%, signal=23% |
| 844 | GOBP\_RESPONSE\_TO\_AMYLOID\_BETA |  | 15 | -0.31 | -0.90 | 0.606 | 0.862 | 1.000 | 168 | tags=27%, list=11%, signal=30% |
| 845 | GOBP\_RHYTHMIC\_PROCESS |  | 39 | -0.25 | -0.90 | 0.618 | 0.861 | 1.000 | 636 | tags=49%, list=42%, signal=82% |
| 846 | GOBP\_NEGATIVE\_REGULATION\_OF\_DNA\_BINDING\_TRANSCRIPTION\_FACTOR\_ACTIVITY |  | 24 | -0.27 | -0.90 | 0.615 | 0.863 | 1.000 | 384 | tags=38%, list=25%, signal=49% |
| 847 | GOBP\_REGULATION\_OF\_LIPID\_TRANSPORT |  | 24 | -0.27 | -0.90 | 0.627 | 0.862 | 1.000 | 551 | tags=46%, list=36%, signal=71% |
| 848 | GOCC\_GOLGI\_APPARATUS |  | 142 | -0.20 | -0.90 | 0.680 | 0.861 | 1.000 | 700 | tags=49%, list=46%, signal=83% |
| 849 | GOBP\_RESPONSE\_TO\_INTERLEUKIN\_1 |  | 33 | -0.25 | -0.89 | 0.632 | 0.866 | 1.000 | 357 | tags=30%, list=24%, signal=39% |
| 850 | GOBP\_MYELOID\_LEUKOCYTE\_DIFFERENTIATION |  | 38 | -0.24 | -0.89 | 0.652 | 0.866 | 1.000 | 636 | tags=50%, list=42%, signal=84% |
| 851 | GOCC\_ENDOSOME |  | 85 | -0.21 | -0.89 | 0.664 | 0.868 | 1.000 | 588 | tags=41%, list=39%, signal=64% |
| 852 | GOBP\_REGULATION\_OF\_CATABOLIC\_PROCESS |  | 73 | -0.22 | -0.89 | 0.660 | 0.872 | 1.000 | 497 | tags=32%, list=33%, signal=45% |
| 853 | GOBP\_REGULATION\_OF\_DEFENSE\_RESPONSE |  | 102 | -0.21 | -0.89 | 0.688 | 0.874 | 1.000 | 649 | tags=47%, list=43%, signal=77% |
| 854 | GOCC\_CELL\_SUBSTRATE\_JUNCTION |  | 62 | -0.22 | -0.89 | 0.657 | 0.873 | 1.000 | 328 | tags=24%, list=22%, signal=30% |
| 855 | GOBP\_REGULATION\_OF\_ION\_TRANSPORT |  | 163 | -0.20 | -0.89 | 0.711 | 0.872 | 1.000 | 644 | tags=43%, list=43%, signal=67% |
| 856 | GOBP\_MEMBRANE\_ORGANIZATION |  | 94 | -0.21 | -0.89 | 0.707 | 0.872 | 1.000 | 590 | tags=37%, list=39%, signal=57% |
| 857 | GOBP\_REGULATION\_OF\_NEURON\_PROJECTION\_DEVELOPMENT |  | 51 | -0.23 | -0.88 | 0.652 | 0.879 | 1.000 | 254 | tags=20%, list=17%, signal=23% |
| 858 | GOBP\_CARDIAC\_SEPTUM\_MORPHOGENESIS |  | 15 | -0.31 | -0.88 | 0.635 | 0.879 | 1.000 | 855 | tags=67%, list=57%, signal=152% |
| 859 | GOBP\_MYELOID\_LEUKOCYTE\_MEDIATED\_IMMUNITY |  | 94 | -0.21 | -0.88 | 0.703 | 0.880 | 1.000 | 384 | tags=30%, list=25%, signal=37% |
| 860 | GOBP\_POSITIVE\_REGULATION\_OF\_TRANSMEMBRANE\_RECEPTOR\_PROTEIN\_SERINE\_THREONINE\_KINASE\_SIGNALING\_PATHWAY |  | 19 | -0.29 | -0.88 | 0.640 | 0.879 | 1.000 | 654 | tags=58%, list=43%, signal=101% |
| 861 | GOBP\_MITOTIC\_NUCLEAR\_DIVISION |  | 22 | -0.28 | -0.88 | 0.641 | 0.879 | 1.000 | 678 | tags=55%, list=45%, signal=98% |
| 862 | GOBP\_POSITIVE\_REGULATION\_OF\_PEPTIDE\_HORMONE\_SECRETION |  | 16 | -0.29 | -0.88 | 0.643 | 0.884 | 1.000 | 578 | tags=44%, list=38%, signal=70% |
| 863 | GOBP\_POSITIVE\_CHEMOTAXIS |  | 15 | -0.30 | -0.88 | 0.658 | 0.888 | 1.000 | 605 | tags=47%, list=40%, signal=77% |
| 864 | GOBP\_KERATINIZATION |  | 22 | -0.27 | -0.88 | 0.662 | 0.889 | 1.000 | 535 | tags=50%, list=35%, signal=76% |
| 865 | GOBP\_ANION\_TRANSMEMBRANE\_TRANSPORT |  | 44 | -0.23 | -0.87 | 0.683 | 0.889 | 1.000 | 324 | tags=30%, list=21%, signal=37% |
| 866 | GOBP\_REGULATION\_OF\_PROTEIN\_POLYMERIZATION |  | 35 | -0.24 | -0.87 | 0.660 | 0.888 | 1.000 | 267 | tags=20%, list=18%, signal=24% |
| 867 | GOBP\_REGULATION\_OF\_CELL\_CYCLE |  | 94 | -0.21 | -0.87 | 0.721 | 0.889 | 1.000 | 672 | tags=43%, list=45%, signal=72% |
| 868 | GOBP\_INTERFERON\_GAMMA\_PRODUCTION |  | 20 | -0.27 | -0.87 | 0.659 | 0.889 | 1.000 | 531 | tags=35%, list=35%, signal=53% |
| 869 | GOMF\_CALMODULIN\_BINDING |  | 25 | -0.26 | -0.87 | 0.674 | 0.888 | 1.000 | 74 | tags=12%, list=5%, signal=12% |
| 870 | GOBP\_PRODUCTION\_OF\_MOLECULAR\_MEDIATOR\_OF\_IMMUNE\_RESPONSE |  | 26 | -0.26 | -0.87 | 0.639 | 0.887 | 1.000 | 615 | tags=50%, list=41%, signal=83% |
| 871 | GOBP\_T\_CELL\_PROLIFERATION |  | 34 | -0.25 | -0.87 | 0.676 | 0.887 | 1.000 | 184 | tags=15%, list=12%, signal=16% |
| 872 | GOBP\_POSITIVE\_REGULATION\_OF\_LEUKOCYTE\_PROLIFERATION |  | 29 | -0.25 | -0.87 | 0.657 | 0.887 | 1.000 | 559 | tags=34%, list=37%, signal=54% |
| 873 | GOCC\_INTERMEDIATE\_FILAMENT |  | 22 | -0.27 | -0.87 | 0.643 | 0.886 | 1.000 | 535 | tags=41%, list=35%, signal=62% |
| 874 | GOBP\_REGULATION\_OF\_INFLAMMATORY\_RESPONSE |  | 67 | -0.22 | -0.87 | 0.686 | 0.887 | 1.000 | 526 | tags=39%, list=35%, signal=57% |
| 875 | GOBP\_REGULATION\_OF\_NITRIC\_OXIDE\_METABOLIC\_PROCESS |  | 16 | -0.29 | -0.87 | 0.646 | 0.887 | 1.000 | 75 | tags=19%, list=5%, signal=20% |
| 876 | GOBP\_REGULATION\_OF\_IMMUNE\_RESPONSE |  | 121 | -0.20 | -0.87 | 0.712 | 0.889 | 1.000 | 560 | tags=38%, list=37%, signal=56% |
| 877 | GOBP\_CYCLIC\_NUCLEOTIDE\_MEDIATED\_SIGNALING |  | 19 | -0.28 | -0.87 | 0.661 | 0.889 | 1.000 | 834 | tags=74%, list=55%, signal=163% |
| 878 | GOBP\_ADAPTIVE\_IMMUNE\_RESPONSE\_BASED\_ON\_SOMATIC\_RECOMBINATION\_OF\_IMMUNE\_RECEPTORS\_BUILT\_FROM\_IMMUNOGLOBULIN\_SUPERFAMILY\_DOMAINS |  | 43 | -0.23 | -0.87 | 0.692 | 0.892 | 1.000 | 643 | tags=47%, list=43%, signal=79% |
| 879 | GOBP\_CHEMOKINE\_PRODUCTION |  | 21 | -0.27 | -0.87 | 0.647 | 0.892 | 1.000 | 738 | tags=57%, list=49%, signal=110% |
| 880 | GOBP\_REGULATION\_OF\_VIRAL\_LIFE\_CYCLE |  | 16 | -0.29 | -0.87 | 0.650 | 0.892 | 1.000 | 744 | tags=63%, list=49%, signal=122% |
| 881 | GOBP\_NEURON\_DEVELOPMENT |  | 130 | -0.20 | -0.87 | 0.740 | 0.892 | 1.000 | 673 | tags=40%, list=45%, signal=66% |
| 882 | GOBP\_REGULATION\_OF\_RAS\_PROTEIN\_SIGNAL\_TRANSDUCTION |  | 18 | -0.28 | -0.86 | 0.668 | 0.893 | 1.000 | 715 | tags=50%, list=47%, signal=94% |
| 883 | GOBP\_REGULATION\_OF\_HORMONE\_SECRETION |  | 45 | -0.23 | -0.86 | 0.701 | 0.900 | 1.000 | 636 | tags=44%, list=42%, signal=74% |
| 884 | GOBP\_LEUKOCYTE\_PROLIFERATION |  | 63 | -0.22 | -0.86 | 0.706 | 0.900 | 1.000 | 595 | tags=38%, list=39%, signal=60% |
| 885 | GOBP\_LYMPHOCYTE\_ACTIVATION\_INVOLVED\_IN\_IMMUNE\_RESPONSE |  | 27 | -0.25 | -0.86 | 0.673 | 0.901 | 1.000 | 634 | tags=56%, list=42%, signal=94% |
| 886 | GOBP\_TAXIS |  | 111 | -0.20 | -0.86 | 0.743 | 0.905 | 1.000 | 615 | tags=40%, list=41%, signal=62% |
| 887 | GOBP\_SMOOTH\_MUSCLE\_CELL\_MIGRATION |  | 17 | -0.28 | -0.86 | 0.681 | 0.906 | 1.000 | 805 | tags=76%, list=53%, signal=162% |
| 888 | GOBP\_NUCLEOBASE\_CONTAINING\_SMALL\_MOLECULE\_METABOLIC\_PROCESS |  | 43 | -0.23 | -0.85 | 0.699 | 0.906 | 1.000 | 410 | tags=28%, list=27%, signal=37% |
| 889 | GOBP\_SECRETION |  | 223 | -0.18 | -0.85 | 0.797 | 0.906 | 1.000 | 590 | tags=39%, list=39%, signal=55% |
| 890 | GOBP\_REGULATION\_OF\_LEUKOCYTE\_PROLIFERATION |  | 55 | -0.22 | -0.85 | 0.712 | 0.907 | 1.000 | 595 | tags=36%, list=39%, signal=58% |
| 891 | GOMF\_MRNA\_BINDING |  | 18 | -0.27 | -0.85 | 0.694 | 0.909 | 1.000 | 100 | tags=11%, list=7%, signal=12% |
| 892 | GOBP\_REGULATION\_OF\_CYTOSOLIC\_CALCIUM\_ION\_CONCENTRATION |  | 51 | -0.22 | -0.85 | 0.723 | 0.910 | 1.000 | 491 | tags=31%, list=33%, signal=45% |
| 893 | GOBP\_REGULATION\_OF\_MUSCLE\_CELL\_DIFFERENTIATION |  | 18 | -0.28 | -0.85 | 0.697 | 0.910 | 1.000 | 670 | tags=61%, list=44%, signal=109% |
| 894 | GOBP\_INNATE\_IMMUNE\_RESPONSE |  | 130 | -0.19 | -0.85 | 0.781 | 0.910 | 1.000 | 561 | tags=38%, list=37%, signal=56% |
| 895 | GOBP\_RECEPTOR\_SIGNALING\_PATHWAY\_VIA\_STAT |  | 23 | -0.26 | -0.85 | 0.692 | 0.909 | 1.000 | 559 | tags=43%, list=37%, signal=68% |
| 896 | GOBP\_REGULATION\_OF\_CATION\_TRANSMEMBRANE\_TRANSPORT |  | 46 | -0.23 | -0.85 | 0.726 | 0.911 | 1.000 | 151 | tags=15%, list=10%, signal=16% |
| 897 | GOBP\_DEPHOSPHORYLATION |  | 29 | -0.25 | -0.85 | 0.688 | 0.911 | 1.000 | 574 | tags=45%, list=38%, signal=71% |
| 898 | GOMF\_ION\_CHANNEL\_BINDING |  | 15 | -0.29 | -0.85 | 0.687 | 0.911 | 1.000 | 52 | tags=13%, list=3%, signal=14% |
| 899 | GOBP\_CELL\_MORPHOGENESIS |  | 118 | -0.20 | -0.85 | 0.777 | 0.911 | 1.000 | 585 | tags=33%, list=39%, signal=50% |
| 900 | GOBP\_REGULATION\_OF\_MEMBRANE\_POTENTIAL |  | 38 | -0.23 | -0.85 | 0.723 | 0.910 | 1.000 | 52 | tags=11%, list=3%, signal=11% |
| 901 | GOBP\_EPITHELIAL\_CELL\_DEVELOPMENT |  | 20 | -0.27 | -0.85 | 0.705 | 0.909 | 1.000 | 181 | tags=20%, list=12%, signal=22% |
| 902 | GOCC\_CELL\_CORTEX |  | 33 | -0.23 | -0.85 | 0.711 | 0.908 | 1.000 | 361 | tags=24%, list=24%, signal=31% |
| 903 | GOBP\_POSITIVE\_REGULATION\_OF\_CELLULAR\_COMPONENT\_BIOGENESIS |  | 57 | -0.21 | -0.84 | 0.738 | 0.909 | 1.000 | 637 | tags=44%, list=42%, signal=73% |
| 904 | GOBP\_PATTERN\_RECOGNITION\_RECEPTOR\_SIGNALING\_PATHWAY |  | 28 | -0.25 | -0.84 | 0.711 | 0.908 | 1.000 | 611 | tags=54%, list=40%, signal=88% |
| 905 | GOBP\_ESTABLISHMENT\_OR\_MAINTENANCE\_OF\_CELL\_POLARITY |  | 20 | -0.27 | -0.84 | 0.691 | 0.908 | 1.000 | 265 | tags=15%, list=18%, signal=18% |
| 906 | GOBP\_REGULATION\_OF\_LIPID\_METABOLIC\_PROCESS |  | 54 | -0.22 | -0.84 | 0.725 | 0.911 | 1.000 | 548 | tags=43%, list=36%, signal=64% |
| 907 | GOCC\_SECRETORY\_VESICLE |  | 163 | -0.19 | -0.84 | 0.813 | 0.916 | 1.000 | 384 | tags=27%, list=25%, signal=32% |
| 908 | GOBP\_BEHAVIOR |  | 73 | -0.20 | -0.84 | 0.733 | 0.916 | 1.000 | 637 | tags=37%, list=42%, signal=61% |
| 909 | GOBP\_PLASMA\_MEMBRANE\_ORGANIZATION |  | 17 | -0.28 | -0.84 | 0.698 | 0.917 | 1.000 | 694 | tags=47%, list=46%, signal=86% |
| 910 | GOBP\_RESPONSE\_TO\_RADIATION |  | 52 | -0.22 | -0.84 | 0.748 | 0.916 | 1.000 | 304 | tags=25%, list=20%, signal=30% |
| 911 | GOMF\_CHEMOKINE\_ACTIVITY |  | 18 | -0.27 | -0.83 | 0.718 | 0.922 | 1.000 | 315 | tags=33%, list=21%, signal=42% |
| 912 | GOBP\_REGULATION\_OF\_BIOLOGICAL\_PROCESS\_INVOLVED\_IN\_SYMBIOTIC\_INTERACTION |  | 20 | -0.26 | -0.83 | 0.688 | 0.922 | 1.000 | 634 | tags=50%, list=42%, signal=85% |
| 913 | GOBP\_POSITIVE\_REGULATION\_OF\_TRANSMEMBRANE\_TRANSPORT |  | 30 | -0.24 | -0.83 | 0.710 | 0.922 | 1.000 | 60 | tags=13%, list=4%, signal=14% |
| 914 | GOBP\_NEGATIVE\_REGULATION\_OF\_CELL\_PROJECTION\_ORGANIZATION |  | 19 | -0.27 | -0.83 | 0.701 | 0.922 | 1.000 | 90 | tags=16%, list=6%, signal=17% |
| 915 | GOBP\_ORGANIC\_HYDROXY\_COMPOUND\_BIOSYNTHETIC\_PROCESS |  | 18 | -0.27 | -0.83 | 0.689 | 0.921 | 1.000 | 766 | tags=78%, list=51%, signal=156% |
| 916 | GOCC\_ENDOCYTIC\_VESICLE |  | 43 | -0.22 | -0.83 | 0.734 | 0.920 | 1.000 | 468 | tags=33%, list=31%, signal=46% |
| 917 | GOBP\_CELL\_RECOGNITION |  | 23 | -0.25 | -0.83 | 0.702 | 0.920 | 1.000 | 585 | tags=48%, list=39%, signal=77% |
| 918 | GOBP\_TISSUE\_REGENERATION |  | 15 | -0.28 | -0.83 | 0.708 | 0.921 | 1.000 | 644 | tags=53%, list=43%, signal=92% |
| 919 | GOCC\_RECEPTOR\_COMPLEX |  | 44 | -0.22 | -0.83 | 0.753 | 0.923 | 1.000 | 546 | tags=39%, list=36%, signal=59% |
| 920 | GOBP\_REGULATION\_OF\_HUMORAL\_IMMUNE\_RESPONSE |  | 17 | -0.27 | -0.83 | 0.687 | 0.922 | 1.000 | 556 | tags=47%, list=37%, signal=74% |
| 921 | GOBP\_HEPATICOBILIARY\_SYSTEM\_DEVELOPMENT |  | 17 | -0.27 | -0.83 | 0.708 | 0.924 | 1.000 | 339 | tags=35%, list=22%, signal=45% |
| 922 | GOBP\_REGULATION\_OF\_REACTIVE\_OXYGEN\_SPECIES\_BIOSYNTHETIC\_PROCESS |  | 18 | -0.27 | -0.83 | 0.733 | 0.924 | 1.000 | 75 | tags=17%, list=5%, signal=17% |
| 923 | GOBP\_PROTEIN\_POLYUBIQUITINATION |  | 15 | -0.28 | -0.82 | 0.722 | 0.926 | 1.000 | 203 | tags=20%, list=13%, signal=23% |
| 924 | GOCC\_SECRETORY\_GRANULE |  | 151 | -0.18 | -0.82 | 0.827 | 0.927 | 1.000 | 407 | tags=28%, list=27%, signal=35% |
| 925 | GOMF\_MOLECULAR\_ADAPTOR\_ACTIVITY |  | 20 | -0.26 | -0.82 | 0.733 | 0.928 | 1.000 | 831 | tags=55%, list=55%, signal=121% |
| 926 | GOBP\_NEGATIVE\_REGULATION\_OF\_CYTOKINE\_PRODUCTION |  | 44 | -0.22 | -0.82 | 0.762 | 0.928 | 1.000 | 574 | tags=41%, list=38%, signal=64% |
| 927 | GOMF\_HYDROLASE\_ACTIVITY\_ACTING\_ON\_ESTER\_BONDS |  | 45 | -0.22 | -0.82 | 0.745 | 0.929 | 1.000 | 574 | tags=42%, list=38%, signal=66% |
| 928 | GOBP\_CELL\_CYCLE\_ARREST |  | 28 | -0.24 | -0.82 | 0.733 | 0.932 | 1.000 | 595 | tags=43%, list=39%, signal=69% |
| 929 | GOCC\_EARLY\_ENDOSOME\_MEMBRANE |  | 16 | -0.28 | -0.81 | 0.745 | 0.937 | 1.000 | 349 | tags=25%, list=23%, signal=32% |
| 930 | GOBP\_ORGANIC\_ACID\_TRANSPORT |  | 32 | -0.23 | -0.81 | 0.745 | 0.938 | 1.000 | 247 | tags=22%, list=16%, signal=26% |
| 931 | GOBP\_MYELOID\_CELL\_DIFFERENTIATION |  | 59 | -0.20 | -0.81 | 0.784 | 0.938 | 1.000 | 636 | tags=46%, list=42%, signal=76% |
| 932 | GOBP\_LIPID\_BIOSYNTHETIC\_PROCESS |  | 57 | -0.21 | -0.81 | 0.769 | 0.939 | 1.000 | 485 | tags=39%, list=32%, signal=55% |
| 933 | GOBP\_EMBRYONIC\_APPENDAGE\_MORPHOGENESIS |  | 15 | -0.28 | -0.81 | 0.744 | 0.940 | 1.000 | 729 | tags=60%, list=48%, signal=115% |
| 934 | GOBP\_POSITIVE\_REGULATION\_OF\_MOLECULAR\_FUNCTION |  | 202 | -0.18 | -0.81 | 0.864 | 0.941 | 1.000 | 524 | tags=31%, list=35%, signal=41% |
| 935 | GOBP\_MYOTUBE\_DIFFERENTIATION |  | 17 | -0.27 | -0.81 | 0.736 | 0.940 | 1.000 | 719 | tags=47%, list=48%, signal=89% |
| 936 | GOBP\_REGULATION\_OF\_MONONUCLEAR\_CELL\_MIGRATION |  | 35 | -0.22 | -0.81 | 0.748 | 0.943 | 1.000 | 589 | tags=40%, list=39%, signal=64% |
| 937 | GOBP\_MONONUCLEAR\_CELL\_MIGRATION |  | 45 | -0.21 | -0.81 | 0.766 | 0.943 | 1.000 | 334 | tags=24%, list=22%, signal=30% |
| 938 | GOBP\_REGULATION\_OF\_PEPTIDE\_HORMONE\_SECRETION |  | 33 | -0.23 | -0.81 | 0.754 | 0.942 | 1.000 | 707 | tags=52%, list=47%, signal=95% |
| 939 | GOBP\_REGULATION\_OF\_ANTIGEN\_RECEPTOR\_MEDIATED\_SIGNALING\_PATHWAY |  | 15 | -0.28 | -0.80 | 0.714 | 0.947 | 1.000 | 491 | tags=47%, list=33%, signal=68% |
| 940 | GOBP\_NEGATIVE\_REGULATION\_OF\_CELL\_GROWTH |  | 26 | -0.24 | -0.80 | 0.757 | 0.946 | 1.000 | 766 | tags=58%, list=51%, signal=115% |
| 941 | GOCC\_VESICLE\_MEMBRANE |  | 89 | -0.19 | -0.80 | 0.823 | 0.949 | 1.000 | 468 | tags=35%, list=31%, signal=48% |
| 942 | GOBP\_CELL\_CYCLE |  | 125 | -0.18 | -0.80 | 0.815 | 0.948 | 1.000 | 678 | tags=41%, list=45%, signal=68% |
| 943 | GOBP\_POSITIVE\_REGULATION\_OF\_PROTEIN\_CONTAINING\_COMPLEX\_ASSEMBLY |  | 31 | -0.23 | -0.80 | 0.759 | 0.949 | 1.000 | 267 | tags=23%, list=18%, signal=27% |
| 944 | GOBP\_LOCOMOTORY\_BEHAVIOR |  | 17 | -0.26 | -0.80 | 0.732 | 0.948 | 1.000 | 345 | tags=24%, list=23%, signal=30% |
| 945 | GOBP\_T\_CELL\_ACTIVATION\_INVOLVED\_IN\_IMMUNE\_RESPONSE |  | 16 | -0.26 | -0.80 | 0.761 | 0.949 | 1.000 | 607 | tags=56%, list=40%, signal=93% |
| 946 | GOBP\_METAL\_ION\_TRANSPORT |  | 57 | -0.20 | -0.80 | 0.791 | 0.950 | 1.000 | 141 | tags=14%, list=9%, signal=15% |
| 947 | GOBP\_DIVALENT\_INORGANIC\_CATION\_HOMEOSTASIS |  | 76 | -0.19 | -0.80 | 0.819 | 0.949 | 1.000 | 291 | tags=20%, list=19%, signal=23% |
| 948 | GOBP\_REGULATION\_OF\_HYDROLASE\_ACTIVITY |  | 162 | -0.17 | -0.79 | 0.849 | 0.949 | 1.000 | 684 | tags=42%, list=45%, signal=69% |
| 949 | GOBP\_NEGATIVE\_REGULATION\_OF\_ANION\_TRANSPORT |  | 34 | -0.22 | -0.79 | 0.785 | 0.950 | 1.000 | 766 | tags=59%, list=51%, signal=117% |
| 950 | GOMF\_MICROTUBULE\_BINDING |  | 18 | -0.26 | -0.79 | 0.763 | 0.949 | 1.000 | 793 | tags=56%, list=53%, signal=116% |
| 951 | GOBP\_AGING |  | 65 | -0.20 | -0.79 | 0.833 | 0.952 | 1.000 | 326 | tags=26%, list=22%, signal=32% |
| 952 | GOBP\_IMPORT\_ACROSS\_PLASMA\_MEMBRANE |  | 16 | -0.26 | -0.79 | 0.760 | 0.952 | 1.000 | 516 | tags=44%, list=34%, signal=66% |
| 953 | GOBP\_CELLULAR\_RESPONSE\_TO\_CARBOHYDRATE\_STIMULUS |  | 18 | -0.26 | -0.79 | 0.758 | 0.952 | 1.000 | 634 | tags=50%, list=42%, signal=85% |
| 954 | GOBP\_REGULATION\_OF\_PROTEIN\_CATABOLIC\_PROCESS |  | 37 | -0.22 | -0.79 | 0.788 | 0.953 | 1.000 | 339 | tags=22%, list=22%, signal=27% |
| 955 | GOBP\_TEMPERATURE\_HOMEOSTASIS |  | 25 | -0.24 | -0.79 | 0.784 | 0.952 | 1.000 | 95 | tags=16%, list=6%, signal=17% |
| 956 | GOBP\_NEGATIVE\_REGULATION\_OF\_CELL\_CYCLE |  | 51 | -0.20 | -0.79 | 0.801 | 0.951 | 1.000 | 602 | tags=39%, list=40%, signal=63% |
| 957 | GOBP\_PROTEIN\_CONTAINING\_COMPLEX\_DISASSEMBLY |  | 18 | -0.25 | -0.79 | 0.765 | 0.952 | 1.000 | 132 | tags=17%, list=9%, signal=18% |
| 958 | GOBP\_LYMPHOCYTE\_MEDIATED\_IMMUNITY |  | 39 | -0.21 | -0.79 | 0.811 | 0.952 | 1.000 | 575 | tags=38%, list=38%, signal=61% |
| 959 | GOBP\_RESPONSE\_TO\_INTERFERON\_GAMMA |  | 42 | -0.21 | -0.79 | 0.795 | 0.954 | 1.000 | 334 | tags=26%, list=22%, signal=33% |
| 960 | GOBP\_POSITIVE\_REGULATION\_OF\_CALCIUM\_ION\_TRANSPORT |  | 27 | -0.23 | -0.78 | 0.801 | 0.955 | 1.000 | 103 | tags=15%, list=7%, signal=16% |
| 961 | GOBP\_CYTOKINE\_PRODUCTION |  | 116 | -0.18 | -0.78 | 0.859 | 0.954 | 1.000 | 644 | tags=44%, list=43%, signal=71% |
| 962 | GOBP\_T\_CELL\_RECEPTOR\_SIGNALING\_PATHWAY |  | 19 | -0.25 | -0.78 | 0.766 | 0.955 | 1.000 | 321 | tags=21%, list=21%, signal=26% |
| 963 | GOBP\_LEUKOCYTE\_MEDIATED\_IMMUNITY |  | 126 | -0.18 | -0.78 | 0.867 | 0.961 | 1.000 | 575 | tags=38%, list=38%, signal=56% |
| 964 | GOBP\_MAINTENANCE\_OF\_LOCATION\_IN\_CELL |  | 27 | -0.23 | -0.78 | 0.777 | 0.960 | 1.000 | 550 | tags=37%, list=36%, signal=57% |
| 965 | GOBP\_GLYCEROPHOSPHOLIPID\_METABOLIC\_PROCESS |  | 18 | -0.25 | -0.78 | 0.776 | 0.960 | 1.000 | 738 | tags=61%, list=49%, signal=118% |
| 966 | GOBP\_CELL\_MORPHOGENESIS\_INVOLVED\_IN\_DIFFERENTIATION |  | 83 | -0.19 | -0.78 | 0.849 | 0.960 | 1.000 | 585 | tags=31%, list=39%, signal=48% |
| 967 | GOBP\_REGULATION\_OF\_INTRACELLULAR\_TRANSPORT |  | 23 | -0.24 | -0.78 | 0.801 | 0.960 | 1.000 | 607 | tags=48%, list=40%, signal=79% |
| 968 | GOBP\_REGULATION\_OF\_ENDOCYTOSIS |  | 29 | -0.22 | -0.78 | 0.801 | 0.960 | 1.000 | 393 | tags=31%, list=26%, signal=41% |
| 969 | GOBP\_MUSCLE\_CELL\_MIGRATION |  | 19 | -0.24 | -0.77 | 0.775 | 0.960 | 1.000 | 805 | tags=68%, list=53%, signal=145% |
| 970 | GOBP\_ENDOCYTOSIS |  | 75 | -0.19 | -0.77 | 0.827 | 0.960 | 1.000 | 588 | tags=40%, list=39%, signal=62% |
| 971 | GOBP\_RESPONSE\_TO\_ETHANOL |  | 36 | -0.21 | -0.77 | 0.807 | 0.959 | 1.000 | 249 | tags=22%, list=16%, signal=26% |
| 972 | GOMF\_IMMUNE\_RECEPTOR\_ACTIVITY |  | 18 | -0.25 | -0.77 | 0.744 | 0.959 | 1.000 | 457 | tags=39%, list=30%, signal=55% |
| 973 | GOBP\_POSITIVE\_REGULATION\_OF\_CYSTEINE\_TYPE\_ENDOPEPTIDASE\_ACTIVITY |  | 22 | -0.24 | -0.77 | 0.804 | 0.958 | 1.000 | 363 | tags=27%, list=24%, signal=35% |
| 974 | GOCC\_PRESYNAPSE |  | 55 | -0.20 | -0.77 | 0.838 | 0.958 | 1.000 | 772 | tags=51%, list=51%, signal=100% |
| 975 | GOBP\_DNA\_REPAIR |  | 27 | -0.23 | -0.77 | 0.803 | 0.957 | 1.000 | 214 | tags=19%, list=14%, signal=21% |
| 976 | GOBP\_POSITIVE\_REGULATION\_OF\_LIPID\_TRANSPORT |  | 17 | -0.25 | -0.77 | 0.788 | 0.958 | 1.000 | 477 | tags=41%, list=32%, signal=60% |
| 977 | GOBP\_NEGATIVE\_REGULATION\_OF\_ION\_TRANSPORT |  | 47 | -0.20 | -0.77 | 0.817 | 0.957 | 1.000 | 766 | tags=55%, list=51%, signal=109% |
| 978 | GOBP\_BIOLOGICAL\_PROCESS\_INVOLVED\_IN\_SYMBIOTIC\_INTERACTION |  | 139 | -0.17 | -0.77 | 0.881 | 0.957 | 1.000 | 287 | tags=19%, list=19%, signal=22% |
| 979 | GOBP\_POSITIVE\_REGULATION\_OF\_T\_CELL\_PROLIFERATION |  | 19 | -0.25 | -0.77 | 0.799 | 0.960 | 1.000 | 644 | tags=37%, list=43%, signal=63% |
| 980 | GOMF\_CHEMOKINE\_RECEPTOR\_BINDING |  | 19 | -0.25 | -0.77 | 0.785 | 0.959 | 1.000 | 315 | tags=32%, list=21%, signal=39% |
| 981 | GOCC\_POLYMERIC\_CYTOSKELETAL\_FIBER |  | 70 | -0.19 | -0.77 | 0.851 | 0.958 | 1.000 | 142 | tags=11%, list=9%, signal=12% |
| 982 | GOCC\_CELL\_BODY |  | 90 | -0.18 | -0.77 | 0.863 | 0.958 | 1.000 | 764 | tags=47%, list=51%, signal=89% |
| 983 | GOBP\_TUMOR\_NECROSIS\_FACTOR\_MEDIATED\_SIGNALING\_PATHWAY |  | 21 | -0.24 | -0.77 | 0.806 | 0.959 | 1.000 | 267 | tags=29%, list=18%, signal=34% |
| 984 | GOBP\_REGULATION\_OF\_CELLULAR\_CATABOLIC\_PROCESS |  | 62 | -0.19 | -0.77 | 0.838 | 0.958 | 1.000 | 267 | tags=18%, list=18%, signal=21% |
| 985 | GOMF\_LIPID\_BINDING |  | 86 | -0.18 | -0.76 | 0.864 | 0.959 | 1.000 | 281 | tags=22%, list=19%, signal=26% |
| 986 | GOCC\_PLASMA\_MEMBRANE\_PROTEIN\_COMPLEX |  | 64 | -0.19 | -0.76 | 0.836 | 0.958 | 1.000 | 512 | tags=34%, list=34%, signal=50% |
| 987 | GOBP\_REGULATION\_OF\_LIPASE\_ACTIVITY |  | 16 | -0.26 | -0.76 | 0.788 | 0.958 | 1.000 | 771 | tags=69%, list=51%, signal=139% |
| 988 | GOBP\_TYROSINE\_PHOSPHORYLATION\_OF\_STAT\_PROTEIN |  | 15 | -0.26 | -0.76 | 0.789 | 0.960 | 1.000 | 265 | tags=20%, list=18%, signal=24% |
| 989 | GOCC\_LEADING\_EDGE\_MEMBRANE |  | 18 | -0.25 | -0.76 | 0.790 | 0.959 | 1.000 | 460 | tags=28%, list=30%, signal=39% |
| 990 | GOBP\_T\_CELL\_MIGRATION |  | 15 | -0.26 | -0.76 | 0.797 | 0.959 | 1.000 | 237 | tags=20%, list=16%, signal=23% |
| 991 | GOBP\_POSITIVE\_REGULATION\_OF\_IMMUNE\_RESPONSE |  | 89 | -0.18 | -0.76 | 0.854 | 0.959 | 1.000 | 574 | tags=38%, list=38%, signal=58% |
| 992 | GOBP\_DETECTION\_OF\_STIMULUS |  | 32 | -0.21 | -0.76 | 0.831 | 0.960 | 1.000 | 103 | tags=13%, list=7%, signal=13% |
| 993 | GOBP\_SEQUESTERING\_OF\_CALCIUM\_ION |  | 16 | -0.26 | -0.76 | 0.798 | 0.959 | 1.000 | 60 | tags=13%, list=4%, signal=13% |
| 994 | GOBP\_ADAPTIVE\_THERMOGENESIS |  | 21 | -0.24 | -0.76 | 0.806 | 0.960 | 1.000 | 541 | tags=43%, list=36%, signal=66% |
| 995 | GOMF\_CALCIUM\_ION\_BINDING |  | 97 | -0.18 | -0.76 | 0.902 | 0.960 | 1.000 | 614 | tags=41%, list=41%, signal=65% |
| 996 | GOBP\_EXOCYTOSIS |  | 137 | -0.17 | -0.76 | 0.904 | 0.960 | 1.000 | 210 | tags=17%, list=14%, signal=18% |
| 997 | GOBP\_DNA\_METABOLIC\_PROCESS |  | 55 | -0.19 | -0.76 | 0.864 | 0.959 | 1.000 | 624 | tags=42%, list=41%, signal=69% |
| 998 | GOBP\_POSITIVE\_REGULATION\_OF\_GENE\_EXPRESSION |  | 160 | -0.17 | -0.75 | 0.909 | 0.960 | 1.000 | 546 | tags=36%, list=36%, signal=50% |
| 999 | GOBP\_NEGATIVE\_REGULATION\_OF\_MOLECULAR\_FUNCTION |  | 168 | -0.17 | -0.75 | 0.913 | 0.961 | 1.000 | 384 | tags=24%, list=25%, signal=29% |
| 1000 | GOBP\_PEPTIDE\_HORMONE\_SECRETION |  | 40 | -0.20 | -0.75 | 0.842 | 0.963 | 1.000 | 636 | tags=43%, list=42%, signal=71% |
| 1001 | GOCC\_LAMELLIPODIUM |  | 16 | -0.25 | -0.75 | 0.817 | 0.963 | 1.000 | 142 | tags=19%, list=9%, signal=20% |
| 1002 | GOBP\_CELL\_ACTIVATION\_INVOLVED\_IN\_IMMUNE\_RESPONSE |  | 117 | -0.17 | -0.75 | 0.901 | 0.963 | 1.000 | 566 | tags=38%, list=37%, signal=57% |
| 1003 | GOBP\_PROTEIN\_POLYMERIZATION |  | 42 | -0.20 | -0.75 | 0.858 | 0.964 | 1.000 | 357 | tags=21%, list=24%, signal=27% |
| 1004 | GOMF\_CARBOHYDRATE\_BINDING |  | 32 | -0.21 | -0.75 | 0.839 | 0.963 | 1.000 | 634 | tags=53%, list=42%, signal=90% |
| 1005 | GOBP\_REGULATION\_OF\_CELLULAR\_COMPONENT\_BIOGENESIS |  | 99 | -0.17 | -0.75 | 0.872 | 0.962 | 1.000 | 525 | tags=31%, list=35%, signal=45% |
| 1006 | GOCC\_POSTSYNAPTIC\_MEMBRANE |  | 15 | -0.25 | -0.75 | 0.796 | 0.962 | 1.000 | 167 | tags=13%, list=11%, signal=15% |
| 1007 | GOCC\_MITOCHONDRION |  | 102 | -0.17 | -0.75 | 0.910 | 0.961 | 1.000 | 267 | tags=19%, list=18%, signal=21% |
| 1008 | GOBP\_POSITIVE\_REGULATION\_OF\_SMALL\_MOLECULE\_METABOLIC\_PROCESS |  | 15 | -0.26 | -0.75 | 0.802 | 0.962 | 1.000 | 644 | tags=53%, list=43%, signal=92% |
| 1009 | GOBP\_POSTSYNAPSE\_ORGANIZATION |  | 18 | -0.24 | -0.75 | 0.821 | 0.961 | 1.000 | 228 | tags=17%, list=15%, signal=19% |
| 1010 | GOBP\_POSITIVE\_REGULATION\_OF\_ENDOCYTOSIS |  | 18 | -0.24 | -0.74 | 0.807 | 0.962 | 1.000 | 376 | tags=33%, list=25%, signal=44% |
| 1011 | GOBP\_NEGATIVE\_REGULATION\_OF\_NEURON\_PROJECTION\_DEVELOPMENT |  | 15 | -0.26 | -0.74 | 0.773 | 0.962 | 1.000 | 60 | tags=13%, list=4%, signal=14% |
| 1012 | GOBP\_CELLULAR\_COMPONENT\_MORPHOGENESIS |  | 89 | -0.18 | -0.74 | 0.893 | 0.962 | 1.000 | 915 | tags=65%, list=61%, signal=156% |
| 1013 | GOBP\_PHOSPHOLIPID\_METABOLIC\_PROCESS |  | 26 | -0.22 | -0.74 | 0.830 | 0.961 | 1.000 | 468 | tags=35%, list=31%, signal=49% |
| 1014 | GOBP\_DEFENSE\_RESPONSE\_TO\_GRAM\_POSITIVE\_BACTERIUM |  | 16 | -0.25 | -0.74 | 0.821 | 0.960 | 1.000 | 322 | tags=31%, list=21%, signal=39% |
| 1015 | GOBP\_APPENDAGE\_MORPHOGENESIS |  | 21 | -0.23 | -0.74 | 0.826 | 0.960 | 1.000 | 841 | tags=67%, list=56%, signal=148% |
| 1016 | GOBP\_RESPONSE\_TO\_LIGHT\_STIMULUS |  | 28 | -0.22 | -0.74 | 0.858 | 0.962 | 1.000 | 214 | tags=21%, list=14%, signal=25% |
| 1017 | GOBP\_MEMBRANE\_FUSION |  | 21 | -0.23 | -0.74 | 0.832 | 0.962 | 1.000 | 901 | tags=76%, list=60%, signal=186% |
| 1018 | GOBP\_CELLULAR\_RESPONSE\_TO\_RADIATION |  | 26 | -0.22 | -0.74 | 0.845 | 0.963 | 1.000 | 279 | tags=27%, list=18%, signal=32% |
| 1019 | GOBP\_REGULATION\_OF\_SMALL\_GTPASE\_MEDIATED\_SIGNAL\_TRANSDUCTION |  | 30 | -0.21 | -0.74 | 0.852 | 0.962 | 1.000 | 894 | tags=60%, list=59%, signal=144% |
| 1020 | GOBP\_CALCIUM\_ION\_TRANSPORT |  | 52 | -0.19 | -0.73 | 0.857 | 0.968 | 1.000 | 103 | tags=12%, list=7%, signal=12% |
| 1021 | GOBP\_ALPHA\_BETA\_T\_CELL\_ACTIVATION |  | 20 | -0.24 | -0.73 | 0.831 | 0.968 | 1.000 | 595 | tags=40%, list=39%, signal=65% |
| 1022 | GOBP\_CARDIAC\_VENTRICLE\_DEVELOPMENT |  | 17 | -0.24 | -0.73 | 0.831 | 0.971 | 1.000 | 232 | tags=18%, list=15%, signal=21% |
| 1023 | GOBP\_REGULATION\_OF\_MITOTIC\_CELL\_CYCLE |  | 50 | -0.19 | -0.73 | 0.885 | 0.970 | 1.000 | 181 | tags=14%, list=12%, signal=15% |
| 1024 | GOBP\_PHENOL\_CONTAINING\_COMPOUND\_METABOLIC\_PROCESS |  | 17 | -0.24 | -0.73 | 0.826 | 0.970 | 1.000 | 109 | tags=18%, list=7%, signal=19% |
| 1025 | GOBP\_HORMONE\_TRANSPORT |  | 58 | -0.18 | -0.72 | 0.871 | 0.974 | 1.000 | 578 | tags=38%, list=38%, signal=59% |
| 1026 | GOBP\_ORGANIC\_HYDROXY\_COMPOUND\_METABOLIC\_PROCESS |  | 54 | -0.18 | -0.72 | 0.896 | 0.973 | 1.000 | 275 | tags=22%, list=18%, signal=26% |
| 1027 | GOBP\_CALCIUM\_ION\_TRANSMEMBRANE\_TRANSPORT |  | 32 | -0.21 | -0.72 | 0.871 | 0.973 | 1.000 | 638 | tags=41%, list=42%, signal=69% |
| 1028 | GOBP\_REGULATION\_OF\_LIPID\_LOCALIZATION |  | 28 | -0.21 | -0.72 | 0.853 | 0.972 | 1.000 | 551 | tags=43%, list=36%, signal=66% |
| 1029 | GOCC\_NUCLEAR\_MEMBRANE |  | 22 | -0.22 | -0.71 | 0.846 | 0.981 | 1.000 | 512 | tags=36%, list=34%, signal=54% |
| 1030 | GOBP\_POSITIVE\_REGULATION\_OF\_ERK1\_AND\_ERK2\_CASCADE |  | 37 | -0.20 | -0.71 | 0.879 | 0.981 | 1.000 | 578 | tags=38%, list=38%, signal=60% |
| 1031 | GOBP\_ACTIVATION\_OF\_IMMUNE\_RESPONSE |  | 66 | -0.18 | -0.71 | 0.909 | 0.981 | 1.000 | 507 | tags=35%, list=34%, signal=50% |
| 1032 | GOBP\_AXON\_DEVELOPMENT |  | 69 | -0.18 | -0.71 | 0.907 | 0.981 | 1.000 | 585 | tags=30%, list=39%, signal=47% |
| 1033 | GOBP\_MYELOID\_LEUKOCYTE\_ACTIVATION |  | 120 | -0.16 | -0.71 | 0.944 | 0.982 | 1.000 | 566 | tags=37%, list=37%, signal=54% |
| 1034 | GOCC\_DISTAL\_AXON |  | 49 | -0.18 | -0.71 | 0.907 | 0.982 | 1.000 | 772 | tags=49%, list=51%, signal=97% |
| 1035 | GOBP\_COVALENT\_CHROMATIN\_MODIFICATION |  | 21 | -0.22 | -0.71 | 0.881 | 0.981 | 1.000 | 581 | tags=38%, list=38%, signal=61% |
| 1036 | GOBP\_REGULATION\_OF\_CALCIUM\_ION\_TRANSMEMBRANE\_TRANSPORT |  | 20 | -0.22 | -0.71 | 0.862 | 0.981 | 1.000 | 60 | tags=10%, list=4%, signal=10% |
| 1037 | GOBP\_ENERGY\_DERIVATION\_BY\_OXIDATION\_OF\_ORGANIC\_COMPOUNDS |  | 28 | -0.21 | -0.70 | 0.875 | 0.983 | 1.000 | 99 | tags=11%, list=7%, signal=11% |
| 1038 | GOBP\_INSULIN\_SECRETION |  | 32 | -0.20 | -0.70 | 0.876 | 0.982 | 1.000 | 636 | tags=44%, list=42%, signal=74% |
| 1039 | GOBP\_POSITIVE\_REGULATION\_OF\_IMMUNE\_EFFECTOR\_PROCESS |  | 36 | -0.19 | -0.70 | 0.873 | 0.983 | 1.000 | 531 | tags=33%, list=35%, signal=50% |
| 1040 | GOBP\_CARBOHYDRATE\_DERIVATIVE\_METABOLIC\_PROCESS |  | 74 | -0.17 | -0.70 | 0.915 | 0.983 | 1.000 | 711 | tags=46%, list=47%, signal=83% |
| 1041 | GOBP\_GENERATION\_OF\_PRECURSOR\_METABOLITES\_AND\_ENERGY |  | 54 | -0.18 | -0.70 | 0.898 | 0.982 | 1.000 | 204 | tags=13%, list=14%, signal=14% |
| 1042 | GOMF\_ATPASE\_ACTIVITY |  | 21 | -0.22 | -0.70 | 0.858 | 0.982 | 1.000 | 267 | tags=24%, list=18%, signal=29% |
| 1043 | GOBP\_NEGATIVE\_REGULATION\_OF\_CATABOLIC\_PROCESS |  | 26 | -0.21 | -0.70 | 0.876 | 0.982 | 1.000 | 326 | tags=19%, list=22%, signal=24% |
| 1044 | GOBP\_POSITIVE\_REGULATION\_OF\_DNA\_BINDING\_TRANSCRIPTION\_FACTOR\_ACTIVITY |  | 33 | -0.20 | -0.70 | 0.878 | 0.982 | 1.000 | 504 | tags=36%, list=33%, signal=53% |
| 1045 | GOBP\_CARDIAC\_SEPTUM\_DEVELOPMENT |  | 18 | -0.23 | -0.70 | 0.860 | 0.981 | 1.000 | 855 | tags=61%, list=57%, signal=139% |
| 1046 | GOBP\_MITOCHONDRION\_ORGANIZATION |  | 40 | -0.19 | -0.70 | 0.895 | 0.981 | 1.000 | 267 | tags=18%, list=18%, signal=21% |
| 1047 | GOCC\_CHROMOSOMAL\_REGION |  | 20 | -0.22 | -0.70 | 0.868 | 0.980 | 1.000 | 728 | tags=55%, list=48%, signal=105% |
| 1048 | GOBP\_AMINOGLYCAN\_METABOLIC\_PROCESS |  | 16 | -0.23 | -0.70 | 0.855 | 0.979 | 1.000 | 697 | tags=63%, list=46%, signal=115% |
| 1049 | GOBP\_INORGANIC\_ION\_TRANSMEMBRANE\_TRANSPORT |  | 76 | -0.17 | -0.70 | 0.917 | 0.978 | 1.000 | 167 | tags=13%, list=11%, signal=14% |
| 1050 | GOBP\_REGULATION\_OF\_MUSCLE\_CONTRACTION |  | 26 | -0.21 | -0.70 | 0.864 | 0.978 | 1.000 | 327 | tags=23%, list=22%, signal=29% |
| 1051 | GOMF\_TRANSCRIPTION\_FACTOR\_BINDING |  | 57 | -0.18 | -0.70 | 0.919 | 0.979 | 1.000 | 642 | tags=44%, list=43%, signal=73% |
| 1052 | GOBP\_PROTEIN\_CONTAINING\_COMPLEX\_SUBUNIT\_ORGANIZATION |  | 153 | -0.15 | -0.69 | 0.956 | 0.979 | 1.000 | 307 | tags=20%, list=20%, signal=22% |
| 1053 | GOBP\_TRANSMEMBRANE\_TRANSPORT |  | 143 | -0.15 | -0.69 | 0.961 | 0.983 | 1.000 | 519 | tags=31%, list=34%, signal=42% |
| 1054 | GOBP\_SIGNAL\_RELEASE |  | 70 | -0.17 | -0.69 | 0.940 | 0.983 | 1.000 | 578 | tags=36%, list=38%, signal=55% |
| 1055 | GOCC\_TERTIARY\_GRANULE\_LUMEN |  | 21 | -0.21 | -0.69 | 0.882 | 0.982 | 1.000 | 600 | tags=48%, list=40%, signal=78% |
| 1056 | GOCC\_MICROTUBULE\_CYTOSKELETON |  | 74 | -0.17 | -0.69 | 0.934 | 0.981 | 1.000 | 679 | tags=39%, list=45%, signal=68% |
| 1057 | GOBP\_REGULATION\_OF\_TRANSMEMBRANE\_TRANSPORT |  | 63 | -0.17 | -0.69 | 0.930 | 0.982 | 1.000 | 151 | tags=13%, list=10%, signal=14% |
| 1058 | GOBP\_CELL\_CYCLE\_PROCESS |  | 91 | -0.16 | -0.68 | 0.954 | 0.986 | 1.000 | 604 | tags=36%, list=40%, signal=57% |
| 1059 | GOBP\_RESPONSE\_TO\_TEMPERATURE\_STIMULUS |  | 33 | -0.19 | -0.68 | 0.904 | 0.987 | 1.000 | 267 | tags=21%, list=18%, signal=25% |
| 1060 | GOBP\_VIRAL\_GENOME\_REPLICATION |  | 16 | -0.22 | -0.68 | 0.866 | 0.990 | 1.000 | 187 | tags=19%, list=12%, signal=21% |
| 1061 | GOMF\_ACTIVATING\_TRANSCRIPTION\_FACTOR\_BINDING |  | 16 | -0.23 | -0.67 | 0.896 | 0.990 | 1.000 | 642 | tags=50%, list=43%, signal=86% |
| 1062 | GOBP\_TOLL\_LIKE\_RECEPTOR\_SIGNALING\_PATHWAY |  | 23 | -0.20 | -0.67 | 0.900 | 0.994 | 1.000 | 611 | tags=52%, list=40%, signal=86% |
| 1063 | GOBP\_ORGANELLE\_ASSEMBLY |  | 58 | -0.17 | -0.67 | 0.940 | 0.995 | 1.000 | 329 | tags=19%, list=22%, signal=23% |
| 1064 | GOBP\_RESPONSE\_TO\_CALCIUM\_ION |  | 20 | -0.21 | -0.67 | 0.904 | 0.994 | 1.000 | 757 | tags=60%, list=50%, signal=119% |
| 1065 | GOBP\_IMPORT\_INTO\_CELL |  | 24 | -0.20 | -0.67 | 0.920 | 0.993 | 1.000 | 597 | tags=42%, list=40%, signal=68% |
| 1066 | GOCC\_GOLGI\_APPARATUS\_SUBCOMPARTMENT |  | 52 | -0.17 | -0.66 | 0.944 | 0.994 | 1.000 | 700 | tags=48%, list=46%, signal=87% |
| 1067 | GOBP\_G\_PROTEIN\_COUPLED\_RECEPTOR\_SIGNALING\_PATHWAY |  | 130 | -0.15 | -0.66 | 0.969 | 0.995 | 1.000 | 637 | tags=38%, list=42%, signal=61% |
| 1068 | GOBP\_REGULATION\_OF\_DNA\_METABOLIC\_PROCESS |  | 28 | -0.19 | -0.66 | 0.926 | 0.995 | 1.000 | 614 | tags=43%, list=41%, signal=71% |
| 1069 | GOBP\_GENE\_SILENCING |  | 16 | -0.22 | -0.66 | 0.904 | 0.996 | 1.000 | 187 | tags=19%, list=12%, signal=21% |
| 1070 | GOMF\_ENZYME\_REGULATOR\_ACTIVITY |  | 139 | -0.15 | -0.66 | 0.974 | 0.997 | 1.000 | 290 | tags=17%, list=19%, signal=19% |
| 1071 | GOBP\_NEGATIVE\_REGULATION\_OF\_TRANSPORT |  | 58 | -0.17 | -0.65 | 0.949 | 0.997 | 1.000 | 766 | tags=53%, list=51%, signal=104% |
| 1072 | GOCC\_LATE\_ENDOSOME |  | 24 | -0.20 | -0.65 | 0.921 | 0.996 | 1.000 | 540 | tags=42%, list=36%, signal=64% |
| 1073 | GOBP\_CELLULAR\_RESPONSE\_TO\_OXYGEN\_LEVELS |  | 34 | -0.18 | -0.65 | 0.938 | 0.996 | 1.000 | 156 | tags=12%, list=10%, signal=13% |
| 1074 | GOBP\_POSITIVE\_REGULATION\_OF\_MONONUCLEAR\_CELL\_MIGRATION |  | 21 | -0.20 | -0.65 | 0.897 | 0.996 | 1.000 | 589 | tags=38%, list=39%, signal=62% |
| 1075 | GOBP\_HINDBRAIN\_DEVELOPMENT |  | 16 | -0.22 | -0.65 | 0.915 | 0.995 | 1.000 | 593 | tags=38%, list=39%, signal=61% |
| 1076 | GOMF\_NUCLEOSIDE\_TRIPHOSPHATASE\_REGULATOR\_ACTIVITY |  | 32 | -0.18 | -0.65 | 0.936 | 0.995 | 1.000 | 60 | tags=6%, list=4%, signal=6% |
| 1077 | GOBP\_VASCULAR\_ENDOTHELIAL\_GROWTH\_FACTOR\_RECEPTOR\_SIGNALING\_PATHWAY |  | 19 | -0.21 | -0.65 | 0.909 | 0.995 | 1.000 | 715 | tags=53%, list=47%, signal=99% |
| 1078 | GOBP\_REGULATION\_OF\_RESPONSE\_TO\_BIOTIC\_STIMULUS |  | 48 | -0.17 | -0.65 | 0.953 | 0.995 | 1.000 | 334 | tags=23%, list=22%, signal=28% |
| 1079 | GOCC\_ADHERENS\_JUNCTION |  | 17 | -0.21 | -0.64 | 0.923 | 0.998 | 1.000 | 512 | tags=29%, list=34%, signal=44% |
| 1080 | GOMF\_KINASE\_REGULATOR\_ACTIVITY |  | 28 | -0.19 | -0.64 | 0.922 | 0.997 | 1.000 | 181 | tags=14%, list=12%, signal=16% |
| 1081 | GOMF\_PROTEIN\_HETERODIMERIZATION\_ACTIVITY |  | 28 | -0.18 | -0.64 | 0.941 | 0.998 | 1.000 | 125 | tags=11%, list=8%, signal=11% |
| 1082 | GOBP\_ORGANIC\_ANION\_TRANSPORT |  | 34 | -0.18 | -0.64 | 0.942 | 0.999 | 1.000 | 296 | tags=21%, list=20%, signal=25% |
| 1083 | GOBP\_CELLULAR\_MACROMOLECULE\_LOCALIZATION |  | 166 | -0.14 | -0.64 | 0.987 | 0.998 | 1.000 | 238 | tags=14%, list=16%, signal=15% |
| 1084 | GOMF\_GUANYL\_NUCLEOTIDE\_BINDING |  | 28 | -0.18 | -0.64 | 0.931 | 0.998 | 1.000 | 483 | tags=32%, list=32%, signal=46% |
| 1085 | GOBP\_LIPID\_LOCALIZATION |  | 50 | -0.17 | -0.63 | 0.951 | 0.999 | 1.000 | 576 | tags=36%, list=38%, signal=56% |
| 1086 | GOMF\_ENZYME\_BINDING |  | 174 | -0.14 | -0.63 | 0.988 | 0.999 | 1.000 | 290 | tags=18%, list=19%, signal=20% |
| 1087 | GOMF\_CADHERIN\_BINDING |  | 27 | -0.19 | -0.63 | 0.935 | 0.999 | 1.000 | 512 | tags=33%, list=34%, signal=50% |
| 1088 | GOCC\_EXOCYTIC\_VESICLE |  | 20 | -0.20 | -0.63 | 0.934 | 0.998 | 1.000 | 772 | tags=55%, list=51%, signal=111% |
| 1089 | GOBP\_FATTY\_ACID\_TRANSPORT |  | 21 | -0.20 | -0.63 | 0.921 | 0.997 | 1.000 | 851 | tags=67%, list=56%, signal=151% |
| 1090 | GOBP\_REGULATION\_OF\_PROTEIN\_LOCALIZATION\_TO\_MEMBRANE |  | 17 | -0.21 | -0.63 | 0.936 | 0.997 | 1.000 | 627 | tags=41%, list=42%, signal=70% |
| 1091 | GOBP\_NEGATIVE\_REGULATION\_OF\_CELL\_CYCLE\_PHASE\_TRANSITION |  | 21 | -0.20 | -0.63 | 0.943 | 0.996 | 1.000 | 181 | tags=14%, list=12%, signal=16% |
| 1092 | GOBP\_REGULATION\_OF\_MYELOID\_LEUKOCYTE\_DIFFERENTIATION |  | 25 | -0.19 | -0.63 | 0.940 | 0.996 | 1.000 | 636 | tags=44%, list=42%, signal=75% |
| 1093 | GOCC\_NEURON\_PROJECTION\_TERMINUS |  | 28 | -0.18 | -0.63 | 0.939 | 0.996 | 1.000 | 764 | tags=57%, list=51%, signal=114% |
| 1094 | GOBP\_REGULATION\_OF\_CELL\_SHAPE |  | 21 | -0.20 | -0.62 | 0.938 | 0.997 | 1.000 | 176 | tags=14%, list=12%, signal=16% |
| 1095 | GOBP\_MICROTUBULE\_BASED\_PROCESS |  | 45 | -0.17 | -0.62 | 0.960 | 0.996 | 1.000 | 286 | tags=18%, list=19%, signal=21% |
| 1096 | GOBP\_MESODERM\_DEVELOPMENT |  | 19 | -0.20 | -0.62 | 0.933 | 0.998 | 1.000 | 731 | tags=58%, list=48%, signal=111% |
| 1097 | GOBP\_VESICLE\_ORGANIZATION |  | 26 | -0.18 | -0.62 | 0.939 | 0.997 | 1.000 | 109 | tags=12%, list=7%, signal=12% |
| 1098 | GOCC\_ENDOSOME\_MEMBRANE |  | 37 | -0.17 | -0.62 | 0.968 | 0.997 | 1.000 | 473 | tags=30%, list=31%, signal=42% |
| 1099 | GOBP\_CALCIUM\_ION\_TRANSPORT\_INTO\_CYTOSOL |  | 23 | -0.19 | -0.62 | 0.931 | 0.997 | 1.000 | 817 | tags=57%, list=54%, signal=121% |
| 1100 | GOBP\_ORGANOPHOSPHATE\_METABOLIC\_PROCESS |  | 74 | -0.15 | -0.61 | 0.983 | 0.998 | 1.000 | 533 | tags=31%, list=35%, signal=46% |
| 1101 | GOBP\_REGULATION\_OF\_PROTEIN\_STABILITY |  | 31 | -0.18 | -0.61 | 0.954 | 0.997 | 1.000 | 850 | tags=61%, list=56%, signal=137% |
| 1102 | GOBP\_FEEDING\_BEHAVIOR |  | 17 | -0.20 | -0.61 | 0.946 | 0.998 | 1.000 | 637 | tags=35%, list=42%, signal=60% |
| 1103 | GOBP\_MACROMOLECULE\_METHYLATION |  | 18 | -0.20 | -0.61 | 0.941 | 0.997 | 1.000 | 284 | tags=22%, list=19%, signal=27% |
| 1104 | GOBP\_SYNAPSE\_ORGANIZATION |  | 48 | -0.16 | -0.61 | 0.972 | 0.997 | 1.000 | 794 | tags=46%, list=53%, signal=94% |
| 1105 | GOCC\_AXON |  | 88 | -0.14 | -0.61 | 0.981 | 0.996 | 1.000 | 772 | tags=43%, list=51%, signal=83% |
| 1106 | GOBP\_CELL\_PART\_MORPHOGENESIS |  | 75 | -0.15 | -0.60 | 0.976 | 0.998 | 1.000 | 915 | tags=64%, list=61%, signal=154% |
| 1107 | GOBP\_METANEPHROS\_DEVELOPMENT |  | 16 | -0.20 | -0.60 | 0.947 | 0.997 | 1.000 | 627 | tags=44%, list=42%, signal=74% |
| 1108 | GOCC\_GLUTAMATERGIC\_SYNAPSE |  | 27 | -0.18 | -0.60 | 0.960 | 0.997 | 1.000 | 879 | tags=56%, list=58%, signal=131% |
| 1109 | GOBP\_ADENYLATE\_CYCLASE\_MODULATING\_G\_PROTEIN\_COUPLED\_RECEPTOR\_SIGNALING\_PATHWAY |  | 34 | -0.17 | -0.60 | 0.964 | 0.997 | 1.000 | 615 | tags=38%, list=41%, signal=63% |
| 1110 | GOBP\_REGULATION\_OF\_PROTEASOMAL\_PROTEIN\_CATABOLIC\_PROCESS |  | 15 | -0.20 | -0.60 | 0.955 | 0.998 | 1.000 | 267 | tags=13%, list=18%, signal=16% |
| 1111 | GOBP\_MRNA\_PROCESSING |  | 15 | -0.20 | -0.60 | 0.936 | 0.997 | 1.000 | 706 | tags=40%, list=47%, signal=74% |
| 1112 | GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_CYCLE\_PROCESS |  | 34 | -0.17 | -0.59 | 0.968 | 0.997 | 1.000 | 672 | tags=47%, list=45%, signal=83% |
| 1113 | GOBP\_REGULATION\_OF\_NEUROTRANSMITTER\_LEVELS |  | 18 | -0.19 | -0.59 | 0.957 | 0.999 | 1.000 | 896 | tags=83%, list=59%, signal=202% |
| 1114 | GOBP\_REGULATION\_OF\_CELLULAR\_PROTEIN\_LOCALIZATION |  | 39 | -0.16 | -0.58 | 0.975 | 1.000 | 1.000 | 627 | tags=36%, list=42%, signal=60% |
| 1115 | GOBP\_ESTABLISHMENT\_OF\_PROTEIN\_LOCALIZATION |  | 182 | -0.13 | -0.58 | 0.999 | 1.000 | 1.000 | 587 | tags=31%, list=39%, signal=44% |
| 1116 | GOBP\_NEGATIVE\_REGULATION\_OF\_CELLULAR\_CATABOLIC\_PROCESS |  | 23 | -0.18 | -0.58 | 0.966 | 1.000 | 1.000 | 326 | tags=17%, list=22%, signal=22% |
| 1117 | GOBP\_ENSHEATHMENT\_OF\_NEURONS |  | 23 | -0.17 | -0.58 | 0.969 | 0.999 | 1.000 | 567 | tags=39%, list=38%, signal=62% |
| 1118 | GOBP\_RESPONSE\_TO\_UV |  | 16 | -0.20 | -0.57 | 0.957 | 0.999 | 1.000 | 403 | tags=31%, list=27%, signal=42% |
| 1119 | GOBP\_GLYCEROLIPID\_METABOLIC\_PROCESS |  | 27 | -0.17 | -0.57 | 0.961 | 0.999 | 1.000 | 468 | tags=33%, list=31%, signal=47% |
| 1120 | GOBP\_POSITIVE\_REGULATION\_OF\_PROTEIN\_CATABOLIC\_PROCESS |  | 22 | -0.18 | -0.57 | 0.969 | 0.999 | 1.000 | 339 | tags=18%, list=22%, signal=23% |
| 1121 | GOBP\_ORGANELLE\_FUSION |  | 18 | -0.18 | -0.56 | 0.979 | 1.000 | 1.000 | 901 | tags=72%, list=60%, signal=177% |
| 1122 | GOBP\_REGULATION\_OF\_HEART\_RATE |  | 17 | -0.18 | -0.56 | 0.973 | 1.000 | 1.000 | 116 | tags=12%, list=8%, signal=13% |
| 1123 | GOBP\_METHYLATION |  | 21 | -0.18 | -0.56 | 0.968 | 0.999 | 1.000 | 672 | tags=48%, list=45%, signal=85% |
| 1124 | GOBP\_REGULATION\_OF\_STRIATED\_MUSCLE\_CONTRACTION |  | 15 | -0.19 | -0.56 | 0.977 | 0.998 | 1.000 | 670 | tags=40%, list=44%, signal=71% |
| 1125 | GOBP\_PROTEIN\_STABILIZATION |  | 25 | -0.17 | -0.56 | 0.979 | 0.999 | 1.000 | 850 | tags=60%, list=56%, signal=135% |
| 1126 | GOBP\_CYTOSOLIC\_CALCIUM\_ION\_TRANSPORT |  | 26 | -0.16 | -0.56 | 0.975 | 0.999 | 1.000 | 705 | tags=42%, list=47%, signal=78% |
| 1127 | GOBP\_CARBOXYLIC\_ACID\_TRANSPORT |  | 26 | -0.17 | -0.55 | 0.970 | 0.998 | 1.000 | 114 | tags=12%, list=8%, signal=12% |
| 1128 | GOBP\_RNA\_SPLICING |  | 16 | -0.18 | -0.55 | 0.970 | 0.998 | 1.000 | 706 | tags=44%, list=47%, signal=81% |
| 1129 | GOBP\_SYNAPTIC\_SIGNALING |  | 72 | -0.13 | -0.55 | 0.997 | 0.998 | 1.000 | 679 | tags=39%, list=45%, signal=67% |
| 1130 | GOCC\_PLASMA\_MEMBRANE\_SIGNALING\_RECEPTOR\_COMPLEX |  | 23 | -0.17 | -0.54 | 0.982 | 0.998 | 1.000 | 546 | tags=35%, list=36%, signal=54% |
| 1131 | GOBP\_REGULATION\_OF\_G\_PROTEIN\_COUPLED\_RECEPTOR\_SIGNALING\_PATHWAY |  | 22 | -0.17 | -0.53 | 0.989 | 1.000 | 1.000 | 800 | tags=59%, list=53%, signal=124% |
| 1132 | GOCC\_SOMATODENDRITIC\_COMPARTMENT |  | 96 | -0.12 | -0.53 | 0.999 | 1.000 | 1.000 | 240 | tags=13%, list=16%, signal=14% |
| 1133 | GOBP\_MITOTIC\_CELL\_CYCLE |  | 69 | -0.13 | -0.52 | 1.000 | 1.000 | 1.000 | 195 | tags=12%, list=13%, signal=13% |
| 1134 | GOBP\_POSITIVE\_REGULATION\_OF\_CELL\_CYCLE |  | 43 | -0.14 | -0.51 | 0.995 | 1.000 | 1.000 | 672 | tags=42%, list=45%, signal=73% |
| 1135 | GOCC\_SITE\_OF\_POLARIZED\_GROWTH |  | 28 | -0.15 | -0.51 | 0.995 | 1.000 | 1.000 | 932 | tags=68%, list=62%, signal=174% |
| 1136 | GOCC\_NEURON\_PROJECTION |  | 137 | -0.11 | -0.51 | 1.000 | 1.000 | 1.000 | 167 | tags=9%, list=11%, signal=10% |
| 1137 | GOBP\_CELL\_MORPHOGENESIS\_INVOLVED\_IN\_NEURON\_DIFFERENTIATION |  | 64 | -0.13 | -0.50 | 0.994 | 1.000 | 1.000 | 257 | tags=13%, list=17%, signal=14% |
| 1138 | GOBP\_REGULATION\_OF\_CELL\_CYCLE\_PROCESS |  | 59 | -0.12 | -0.47 | 1.000 | 1.000 | 1.000 | 536 | tags=29%, list=35%, signal=43% |
| 1139 | GOCC\_SYNAPSE |  | 131 | -0.11 | -0.47 | 1.000 | 1.000 | 1.000 | 679 | tags=34%, list=45%, signal=56% |
| 1140 | GOCC\_CONDENSED\_CHROMOSOME |  | 17 | -0.15 | -0.46 | 0.996 | 1.000 | 1.000 | 782 | tags=53%, list=52%, signal=109% |
| 1141 | GOBP\_NEURON\_PROJECTION\_GUIDANCE |  | 34 | -0.12 | -0.44 | 1.000 | 1.000 | 1.000 | 536 | tags=24%, list=35%, signal=36% |
| 1142 | GOCC\_INTRACELLULAR\_PROTEIN\_CONTAINING\_COMPLEX |  | 26 | -0.13 | -0.44 | 0.997 | 1.000 | 1.000 | 753 | tags=38%, list=50%, signal=75% |
| 1143 | GOMF\_STRUCTURAL\_CONSTITUENT\_OF\_CYTOSKELETON |  | 20 | -0.14 | -0.44 | 0.999 | 1.000 | 1.000 | 142 | tags=10%, list=9%, signal=11% |
| 1144 | GOBP\_CHROMOSOME\_SEGREGATION |  | 16 | -0.14 | -0.42 | 0.999 | 0.999 | 1.000 | 728 | tags=44%, list=48%, signal=84% |