Table: Gene sets enriched in phenotype **positive correlation with profile**[**[plain text format]**](http://docs.google.com/gsea_report_for_triple_means_peak_pos_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\_PROTEIN\_LOCALIZATION\_TO\_ENDOPLASMIC\_RETICULUM](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM) | [Details ...](http://docs.google.com/GOBP_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM.html) | 38 | 0.71 | 3.37 | 0.000 | 0.000 | 0.000 | 408 | tags=79%, list=27%, signal=105% |
| 2 | [GOBP\_NUCLEAR\_TRANSCRIBED\_MRNA\_CATABOLIC\_PROCESS\_NONSENSE\_MEDIATED\_DECAY](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY) | [Details ...](http://docs.google.com/GOBP_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY.html) | 37 | 0.72 | 3.37 | 0.000 | 0.000 | 0.000 | 408 | tags=81%, list=27%, signal=108% |
| 3 | [GOBP\_COTRANSLATIONAL\_PROTEIN\_TARGETING\_TO\_MEMBRANE](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE) | [Details ...](http://docs.google.com/GOBP_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE.html) | 37 | 0.72 | 3.36 | 0.000 | 0.000 | 0.000 | 408 | tags=81%, list=27%, signal=108% |
| 4 | [GOBP\_ESTABLISHMENT\_OF\_PROTEIN\_LOCALIZATION\_TO\_ENDOPLASMIC\_RETICULUM](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM) | [Details ...](http://docs.google.com/GOBP_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM.html) | 37 | 0.72 | 3.35 | 0.000 | 0.000 | 0.000 | 408 | tags=81%, list=27%, signal=108% |
| 5 | [GOBP\_NUCLEAR\_TRANSCRIBED\_MRNA\_CATABOLIC\_PROCESS](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS) | [Details ...](http://docs.google.com/GOBP_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS.html) | 39 | 0.70 | 3.31 | 0.000 | 0.000 | 0.000 | 393 | tags=77%, list=26%, signal=101% |
| 6 | [GOBP\_VIRAL\_GENE\_EXPRESSION](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_VIRAL_GENE_EXPRESSION) | [Details ...](http://docs.google.com/GOBP_VIRAL_GENE_EXPRESSION.html) | 42 | 0.65 | 3.22 | 0.000 | 0.000 | 0.000 | 393 | tags=74%, list=26%, signal=97% |
| 7 | [GOMF\_STRUCTURAL\_CONSTITUENT\_OF\_RIBOSOME](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOMF_STRUCTURAL_CONSTITUENT_OF_RIBOSOME) | [Details ...](http://docs.google.com/GOMF_STRUCTURAL_CONSTITUENT_OF_RIBOSOME.html) | 39 | 0.64 | 3.07 | 0.000 | 0.000 | 0.000 | 393 | tags=77%, list=26%, signal=101% |
| 8 | [GOBP\_RESPONSE\_TO\_XENOBIOTIC\_STIMULUS](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_RESPONSE_TO_XENOBIOTIC_STIMULUS) | [Details ...](http://docs.google.com/GOBP_RESPONSE_TO_XENOBIOTIC_STIMULUS.html) | 20 | 0.72 | 2.78 | 0.000 | 0.000 | 0.001 | 175 | tags=70%, list=12%, signal=78% |
| 9 | [GOCC\_RIBOSOMAL\_SUBUNIT](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOCC_RIBOSOMAL_SUBUNIT) | [Details ...](http://docs.google.com/GOCC_RIBOSOMAL_SUBUNIT.html) | 42 | 0.57 | 2.76 | 0.000 | 0.000 | 0.001 | 393 | tags=74%, list=26%, signal=97% |
| 10 | [GOBP\_CYTOPLASMIC\_TRANSLATION](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_CYTOPLASMIC_TRANSLATION) | [Details ...](http://docs.google.com/GOBP_CYTOPLASMIC_TRANSLATION.html) | 15 | 0.77 | 2.74 | 0.000 | 0.000 | 0.001 | 322 | tags=87%, list=21%, signal=109% |
| 11 | [GOBP\_RNA\_CATABOLIC\_PROCESS](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_RNA_CATABOLIC_PROCESS) | [Details ...](http://docs.google.com/GOBP_RNA_CATABOLIC_PROCESS.html) | 51 | 0.54 | 2.69 | 0.000 | 0.000 | 0.001 | 393 | tags=65%, list=26%, signal=85% |
| 12 | [GOBP\_TRANSLATIONAL\_INITIATION](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_TRANSLATIONAL_INITIATION) | [Details ...](http://docs.google.com/GOBP_TRANSLATIONAL_INITIATION.html) | 44 | 0.53 | 2.59 | 0.000 | 0.000 | 0.002 | 393 | tags=68%, list=26%, signal=89% |
| 13 | [GOCC\_RIBOSOME](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOCC_RIBOSOME) | [Details ...](http://docs.google.com/GOCC_RIBOSOME.html) | 45 | 0.51 | 2.52 | 0.000 | 0.000 | 0.005 | 393 | tags=71%, list=26%, signal=93% |
| 14 | [GOCC\_CYTOSOLIC\_RIBOSOME](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOCC_CYTOSOLIC_RIBOSOME) | [Details ...](http://docs.google.com/GOCC_CYTOSOLIC_RIBOSOME.html) | 40 | 0.53 | 2.48 | 0.000 | 0.001 | 0.006 | 393 | tags=73%, list=26%, signal=95% |
| 15 | [GOBP\_PROTEIN\_TARGETING\_TO\_MEMBRANE](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_PROTEIN_TARGETING_TO_MEMBRANE) | [Details ...](http://docs.google.com/GOBP_PROTEIN_TARGETING_TO_MEMBRANE.html) | 43 | 0.51 | 2.45 | 0.000 | 0.001 | 0.008 | 393 | tags=72%, list=26%, signal=95% |
| 16 | [GOCC\_LARGE\_RIBOSOMAL\_SUBUNIT](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOCC_LARGE_RIBOSOMAL_SUBUNIT) | [Details ...](http://docs.google.com/GOCC_LARGE_RIBOSOMAL_SUBUNIT.html) | 23 | 0.56 | 2.31 | 0.000 | 0.002 | 0.030 | 408 | tags=78%, list=27%, signal=106% |
| 17 | [GOBP\_AMIDE\_BIOSYNTHETIC\_PROCESS](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_AMIDE_BIOSYNTHETIC_PROCESS) | [Details ...](http://docs.google.com/GOBP_AMIDE_BIOSYNTHETIC_PROCESS.html) | 73 | 0.41 | 2.29 | 0.000 | 0.003 | 0.035 | 362 | tags=53%, list=24%, signal=67% |
| 18 | [GOCC\_CYTOSOLIC\_SMALL\_RIBOSOMAL\_SUBUNIT](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOCC_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT) | [Details ...](http://docs.google.com/GOCC_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT.html) | 18 | 0.58 | 2.25 | 0.000 | 0.003 | 0.048 | 393 | tags=78%, list=26%, signal=104% |
| 19 | [GOCC\_POLYSOME](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOCC_POLYSOME) | [Details ...](http://docs.google.com/GOCC_POLYSOME.html) | 15 | 0.62 | 2.24 | 0.000 | 0.003 | 0.051 | 322 | tags=73%, list=21%, signal=92% |
| 20 | [GOBP\_PEPTIDE\_BIOSYNTHETIC\_PROCESS](http://www.gsea-msigdb.org/gsea/msigdb/cards/GOBP_PEPTIDE_BIOSYNTHETIC_PROCESS) | [Details ...](http://docs.google.com/GOBP_PEPTIDE_BIOSYNTHETIC_PROCESS.html) | 67 | 0.41 | 2.22 | 0.000 | 0.004 | 0.059 | 362 | tags=54%, list=24%, signal=68% |
| 21 | GOCC\_SMALL\_RIBOSOMAL\_SUBUNIT |  | 19 | 0.58 | 2.21 | 0.000 | 0.004 | 0.061 | 393 | tags=74%, list=26%, signal=98% |
| 22 | GOBP\_RIBOSOME\_BIOGENESIS |  | 22 | 0.54 | 2.17 | 0.000 | 0.005 | 0.086 | 391 | tags=64%, list=26%, signal=85% |
| 23 | GOCC\_CYTOSOLIC\_LARGE\_RIBOSOMAL\_SUBUNIT |  | 21 | 0.55 | 2.15 | 0.000 | 0.005 | 0.097 | 408 | tags=76%, list=27%, signal=103% |
| 24 | GOCC\_RIBONUCLEOPROTEIN\_COMPLEX |  | 65 | 0.39 | 2.12 | 0.000 | 0.007 | 0.123 | 362 | tags=52%, list=24%, signal=66% |
| 25 | GOBP\_RIBONUCLEOPROTEIN\_COMPLEX\_BIOGENESIS |  | 26 | 0.49 | 2.11 | 0.000 | 0.007 | 0.133 | 391 | tags=62%, list=26%, signal=82% |
| 26 | GOBP\_MRNA\_METABOLIC\_PROCESS |  | 64 | 0.41 | 2.11 | 0.000 | 0.007 | 0.134 | 362 | tags=48%, list=24%, signal=61% |
| 27 | GOBP\_SULFUR\_COMPOUND\_BIOSYNTHETIC\_PROCESS |  | 18 | 0.54 | 2.11 | 0.000 | 0.006 | 0.135 | 175 | tags=50%, list=12%, signal=56% |
| 28 | GOBP\_SULFUR\_COMPOUND\_METABOLIC\_PROCESS |  | 28 | 0.46 | 1.99 | 0.000 | 0.015 | 0.289 | 192 | tags=43%, list=13%, signal=48% |
| 29 | GOCC\_MITOCHONDRIAL\_PROTEIN\_CONTAINING\_COMPLEX |  | 21 | 0.50 | 1.99 | 0.000 | 0.014 | 0.295 | 365 | tags=71%, list=24%, signal=93% |
| 30 | GOBP\_ORGANIC\_CYCLIC\_COMPOUND\_CATABOLIC\_PROCESS |  | 71 | 0.35 | 1.90 | 0.000 | 0.025 | 0.471 | 362 | tags=49%, list=24%, signal=62% |
| 31 | GOBP\_CELLULAR\_RESPONSE\_TO\_TOXIC\_SUBSTANCE |  | 29 | 0.43 | 1.90 | 0.000 | 0.026 | 0.492 | 175 | tags=41%, list=12%, signal=46% |
| 32 | GOBP\_RRNA\_METABOLIC\_PROCESS |  | 17 | 0.52 | 1.89 | 0.000 | 0.026 | 0.502 | 391 | tags=65%, list=26%, signal=86% |
| 33 | GOMF\_RNA\_BINDING |  | 123 | 0.31 | 1.89 | 0.000 | 0.026 | 0.517 | 315 | tags=38%, list=21%, signal=44% |
| 34 | GOBP\_DETOXIFICATION |  | 32 | 0.42 | 1.89 | 0.005 | 0.025 | 0.517 | 179 | tags=41%, list=12%, signal=45% |
| 35 | GOBP\_PROTEIN\_TARGETING |  | 53 | 0.37 | 1.89 | 0.000 | 0.025 | 0.519 | 393 | tags=64%, list=26%, signal=84% |
| 36 | GOCC\_NEURON\_SPINE |  | 15 | 0.53 | 1.88 | 0.009 | 0.025 | 0.527 | 196 | tags=27%, list=13%, signal=30% |
| 37 | GOBP\_ESTABLISHMENT\_OF\_PROTEIN\_LOCALIZATION\_TO\_ORGANELLE |  | 67 | 0.35 | 1.84 | 0.000 | 0.033 | 0.637 | 393 | tags=58%, list=26%, signal=75% |
| 38 | GOBP\_CELLULAR\_OXIDANT\_DETOXIFICATION |  | 27 | 0.43 | 1.83 | 0.000 | 0.033 | 0.648 | 153 | tags=41%, list=10%, signal=45% |
| 39 | GOCC\_INNER\_MITOCHONDRIAL\_MEMBRANE\_PROTEIN\_COMPLEX |  | 19 | 0.47 | 1.83 | 0.005 | 0.033 | 0.652 | 435 | tags=84%, list=29%, signal=117% |
| 40 | GOBP\_ESTABLISHMENT\_OF\_PROTEIN\_LOCALIZATION\_TO\_MEMBRANE |  | 54 | 0.36 | 1.82 | 0.000 | 0.035 | 0.683 | 393 | tags=63%, list=26%, signal=82% |
| 41 | GOBP\_NEGATIVE\_REGULATION\_OF\_CYTOSKELETON\_ORGANIZATION |  | 18 | 0.46 | 1.79 | 0.016 | 0.040 | 0.742 | 77 | tags=22%, list=5%, signal=23% |
| 42 | GOBP\_SUPEROXIDE\_METABOLIC\_PROCESS |  | 15 | 0.50 | 1.77 | 0.008 | 0.044 | 0.780 | 107 | tags=40%, list=7%, signal=43% |
| 43 | GOMF\_MONOCARBOXYLIC\_ACID\_BINDING |  | 15 | 0.48 | 1.76 | 0.008 | 0.046 | 0.808 | 185 | tags=53%, list=12%, signal=60% |
| 44 | GOBP\_OXIDATIVE\_PHOSPHORYLATION |  | 16 | 0.48 | 1.76 | 0.008 | 0.045 | 0.809 | 435 | tags=88%, list=29%, signal=122% |
| 45 | GOBP\_PROTON\_TRANSMEMBRANE\_TRANSPORT |  | 16 | 0.47 | 1.76 | 0.004 | 0.044 | 0.817 | 435 | tags=81%, list=29%, signal=113% |
| 46 | GOMF\_RRNA\_BINDING |  | 15 | 0.47 | 1.73 | 0.018 | 0.052 | 0.866 | 393 | tags=60%, list=26%, signal=80% |
| 47 | GOBP\_RIBONUCLEOPROTEIN\_COMPLEX\_SUBUNIT\_ORGANIZATION |  | 15 | 0.48 | 1.73 | 0.012 | 0.052 | 0.871 | 375 | tags=60%, list=25%, signal=79% |
| 48 | GOBP\_PEPTIDE\_METABOLIC\_PROCESS |  | 87 | 0.30 | 1.72 | 0.000 | 0.055 | 0.885 | 362 | tags=47%, list=24%, signal=58% |
| 49 | GOCC\_EXTRINSIC\_COMPONENT\_OF\_CYTOPLASMIC\_SIDE\_OF\_PLASMA\_MEMBRANE |  | 15 | 0.49 | 1.72 | 0.027 | 0.054 | 0.886 | 221 | tags=40%, list=15%, signal=46% |
| 50 | GOBP\_REGULATION\_OF\_CATION\_CHANNEL\_ACTIVITY |  | 24 | 0.40 | 1.67 | 0.029 | 0.069 | 0.945 | 202 | tags=29%, list=13%, signal=33% |
| 51 | GOBP\_MONOCARBOXYLIC\_ACID\_METABOLIC\_PROCESS |  | 62 | 0.32 | 1.66 | 0.010 | 0.072 | 0.958 | 185 | tags=32%, list=12%, signal=35% |
| 52 | GOBP\_FATTY\_ACID\_METABOLIC\_PROCESS |  | 34 | 0.37 | 1.66 | 0.019 | 0.071 | 0.961 | 175 | tags=38%, list=12%, signal=42% |
| 53 | GOMF\_PEPTIDE\_BINDING |  | 46 | 0.33 | 1.66 | 0.000 | 0.070 | 0.963 | 178 | tags=30%, list=12%, signal=33% |
| 54 | GOBP\_NCRNA\_PROCESSING |  | 19 | 0.42 | 1.64 | 0.027 | 0.078 | 0.975 | 391 | tags=58%, list=26%, signal=77% |
| 55 | GOMF\_OXIDOREDUCTASE\_ACTIVITY\_ACTING\_ON\_PEROXIDE\_AS\_ACCEPTOR |  | 15 | 0.46 | 1.63 | 0.021 | 0.083 | 0.979 | 153 | tags=47%, list=10%, signal=51% |
| 56 | GOBP\_ORGANONITROGEN\_COMPOUND\_BIOSYNTHETIC\_PROCESS |  | 142 | 0.25 | 1.62 | 0.000 | 0.084 | 0.981 | 282 | tags=33%, list=19%, signal=37% |
| 57 | GOCC\_SECRETORY\_GRANULE\_MEMBRANE |  | 42 | 0.33 | 1.60 | 0.027 | 0.097 | 0.991 | 155 | tags=31%, list=10%, signal=34% |
| 58 | GOBP\_DNA\_CONFORMATION\_CHANGE |  | 19 | 0.40 | 1.59 | 0.023 | 0.100 | 0.993 | 182 | tags=42%, list=12%, signal=47% |
| 59 | GOBP\_POSITIVE\_REGULATION\_OF\_TUMOR\_NECROSIS\_FACTOR\_SUPERFAMILY\_CYTOKINE\_PRODUCTION |  | 19 | 0.41 | 1.59 | 0.033 | 0.101 | 0.994 | 318 | tags=47%, list=21%, signal=59% |
| 60 | GOMF\_ANTIOXIDANT\_ACTIVITY |  | 24 | 0.38 | 1.58 | 0.005 | 0.101 | 0.995 | 153 | tags=38%, list=10%, signal=41% |
| 61 | GOBP\_TUMOR\_NECROSIS\_FACTOR\_SUPERFAMILY\_CYTOKINE\_PRODUCTION |  | 28 | 0.36 | 1.58 | 0.029 | 0.103 | 0.995 | 174 | tags=29%, list=12%, signal=32% |
| 62 | GOBP\_I\_KAPPAB\_KINASE\_NF\_KAPPAB\_SIGNALING |  | 27 | 0.36 | 1.55 | 0.020 | 0.119 | 1.000 | 132 | tags=26%, list=9%, signal=28% |
| 63 | GOCC\_ORGANELLE\_INNER\_MEMBRANE |  | 45 | 0.31 | 1.55 | 0.022 | 0.117 | 1.000 | 365 | tags=53%, list=24%, signal=68% |
| 64 | GOBP\_CELLULAR\_LIPID\_METABOLIC\_PROCESS |  | 83 | 0.27 | 1.54 | 0.012 | 0.120 | 1.000 | 150 | tags=24%, list=10%, signal=25% |
| 65 | GOMF\_AMYLOID\_BETA\_BINDING |  | 18 | 0.41 | 1.54 | 0.052 | 0.125 | 1.000 | 156 | tags=33%, list=10%, signal=37% |
| 66 | GOBP\_NEGATIVE\_REGULATION\_OF\_PROTEIN\_CONTAINING\_COMPLEX\_ASSEMBLY |  | 23 | 0.36 | 1.52 | 0.064 | 0.136 | 1.000 | 346 | tags=43%, list=23%, signal=56% |
| 67 | GOMF\_CATION\_TRANSMEMBRANE\_TRANSPORTER\_ACTIVITY |  | 37 | 0.33 | 1.52 | 0.006 | 0.135 | 1.000 | 280 | tags=41%, list=19%, signal=49% |
| 68 | GOBP\_RESPONSE\_TO\_TOXIC\_SUBSTANCE |  | 51 | 0.29 | 1.50 | 0.016 | 0.148 | 1.000 | 242 | tags=35%, list=16%, signal=41% |
| 69 | GOMF\_CALCIUM\_DEPENDENT\_PROTEIN\_BINDING |  | 16 | 0.41 | 1.50 | 0.028 | 0.147 | 1.000 | 202 | tags=38%, list=13%, signal=43% |
| 70 | GOBP\_CELL\_AGING |  | 18 | 0.38 | 1.50 | 0.028 | 0.146 | 1.000 | 209 | tags=39%, list=14%, signal=45% |
| 71 | GOCC\_NEURON\_TO\_NEURON\_SYNAPSE |  | 32 | 0.32 | 1.49 | 0.040 | 0.151 | 1.000 | 410 | tags=53%, list=27%, signal=71% |
| 72 | GOBP\_POSITIVE\_REGULATION\_OF\_I\_KAPPAB\_KINASE\_NF\_KAPPAB\_SIGNALING |  | 18 | 0.38 | 1.47 | 0.074 | 0.164 | 1.000 | 132 | tags=28%, list=9%, signal=30% |
| 73 | GOBP\_CELLULAR\_AMIDE\_METABOLIC\_PROCESS |  | 104 | 0.25 | 1.46 | 0.014 | 0.170 | 1.000 | 362 | tags=44%, list=24%, signal=54% |
| 74 | GOCC\_NUCLEAR\_OUTER\_MEMBRANE\_ENDOPLASMIC\_RETICULUM\_MEMBRANE\_NETWORK |  | 79 | 0.26 | 1.42 | 0.020 | 0.209 | 1.000 | 177 | tags=25%, list=12%, signal=27% |
| 75 | GOCC\_MICROTUBULE |  | 26 | 0.32 | 1.39 | 0.043 | 0.242 | 1.000 | 1038 | tags=100%, list=69%, signal=314% |
| 76 | GOMF\_AMIDE\_BINDING |  | 50 | 0.27 | 1.39 | 0.041 | 0.241 | 1.000 | 178 | tags=28%, list=12%, signal=31% |
| 77 | GOBP\_ANTIGEN\_PROCESSING\_AND\_PRESENTATION\_OF\_PEPTIDE\_ANTIGEN |  | 26 | 0.33 | 1.38 | 0.118 | 0.249 | 1.000 | 254 | tags=38%, list=17%, signal=45% |
| 78 | GOMF\_ORGANIC\_ACID\_BINDING |  | 19 | 0.35 | 1.38 | 0.074 | 0.252 | 1.000 | 185 | tags=42%, list=12%, signal=47% |
| 79 | GOBP\_CELLULAR\_PROTEIN\_CONTAINING\_COMPLEX\_ASSEMBLY |  | 88 | 0.23 | 1.37 | 0.012 | 0.264 | 1.000 | 310 | tags=32%, list=21%, signal=38% |
| 80 | GOBP\_NIK\_NF\_KAPPAB\_SIGNALING |  | 17 | 0.36 | 1.36 | 0.093 | 0.277 | 1.000 | 93 | tags=24%, list=6%, signal=25% |
| 81 | GOBP\_ORGANIC\_ACID\_METABOLIC\_PROCESS |  | 93 | 0.24 | 1.36 | 0.041 | 0.277 | 1.000 | 185 | tags=27%, list=12%, signal=29% |
| 82 | GOBP\_ICOSANOID\_METABOLIC\_PROCESS |  | 22 | 0.33 | 1.36 | 0.110 | 0.273 | 1.000 | 175 | tags=36%, list=12%, signal=41% |
| 83 | GOMF\_RNA\_POLYMERASE\_II\_SPECIFIC\_DNA\_BINDING\_TRANSCRIPTION\_FACTOR\_BINDING |  | 26 | 0.31 | 1.34 | 0.077 | 0.297 | 1.000 | 116 | tags=27%, list=8%, signal=29% |
| 84 | GOBP\_LONG\_CHAIN\_FATTY\_ACID\_METABOLIC\_PROCESS |  | 15 | 0.38 | 1.34 | 0.126 | 0.294 | 1.000 | 175 | tags=47%, list=12%, signal=52% |
| 85 | GOCC\_ORGANELLE\_SUBCOMPARTMENT |  | 112 | 0.22 | 1.33 | 0.015 | 0.300 | 1.000 | 104 | tags=17%, list=7%, signal=17% |
| 86 | GOBP\_CELLULAR\_MACROMOLECULE\_CATABOLIC\_PROCESS |  | 97 | 0.23 | 1.33 | 0.015 | 0.301 | 1.000 | 395 | tags=49%, list=26%, signal=63% |
| 87 | GOCC\_MITOCHONDRIAL\_ENVELOPE |  | 58 | 0.25 | 1.33 | 0.026 | 0.298 | 1.000 | 365 | tags=52%, list=24%, signal=66% |
| 88 | GOBP\_CELL\_CYCLE\_G2\_M\_PHASE\_TRANSITION |  | 18 | 0.35 | 1.33 | 0.130 | 0.299 | 1.000 | 839 | tags=94%, list=56%, signal=210% |
| 89 | GOBP\_REACTIVE\_OXYGEN\_SPECIES\_METABOLIC\_PROCESS |  | 50 | 0.25 | 1.33 | 0.040 | 0.297 | 1.000 | 156 | tags=26%, list=10%, signal=28% |
| 90 | GOCC\_CYTOPLASMIC\_SIDE\_OF\_MEMBRANE |  | 27 | 0.31 | 1.31 | 0.120 | 0.327 | 1.000 | 337 | tags=41%, list=22%, signal=52% |
| 91 | GOMF\_PROTEIN\_HOMODIMERIZATION\_ACTIVITY |  | 74 | 0.24 | 1.30 | 0.054 | 0.328 | 1.000 | 94 | tags=19%, list=6%, signal=19% |
| 92 | GOCC\_EXTRINSIC\_COMPONENT\_OF\_MEMBRANE |  | 31 | 0.29 | 1.30 | 0.105 | 0.328 | 1.000 | 221 | tags=32%, list=15%, signal=37% |
| 93 | GOBP\_INTRACELLULAR\_PROTEIN\_TRANSPORT |  | 95 | 0.22 | 1.29 | 0.086 | 0.343 | 1.000 | 282 | tags=33%, list=19%, signal=38% |
| 94 | GOBP\_POSITIVE\_REGULATION\_OF\_NEURON\_DEATH |  | 16 | 0.35 | 1.27 | 0.144 | 0.373 | 1.000 | 174 | tags=25%, list=12%, signal=28% |
| 95 | GOBP\_POSITIVE\_REGULATION\_OF\_DEFENSE\_RESPONSE |  | 56 | 0.24 | 1.27 | 0.087 | 0.382 | 1.000 | 174 | tags=23%, list=12%, signal=25% |
| 96 | GOBP\_REGULATION\_OF\_SIGNALING\_RECEPTOR\_ACTIVITY |  | 30 | 0.29 | 1.26 | 0.111 | 0.397 | 1.000 | 142 | tags=20%, list=9%, signal=22% |
| 97 | GOBP\_CELLULAR\_HORMONE\_METABOLIC\_PROCESS |  | 24 | 0.30 | 1.25 | 0.164 | 0.396 | 1.000 | 98 | tags=29%, list=6%, signal=31% |
| 98 | GOCC\_CATALYTIC\_COMPLEX |  | 55 | 0.25 | 1.25 | 0.089 | 0.394 | 1.000 | 354 | tags=42%, list=23%, signal=53% |
| 99 | GOCC\_MEMBRANE\_PROTEIN\_COMPLEX |  | 102 | 0.22 | 1.25 | 0.058 | 0.396 | 1.000 | 263 | tags=29%, list=17%, signal=33% |
| 100 | GOBP\_TERPENOID\_METABOLIC\_PROCESS |  | 21 | 0.31 | 1.24 | 0.171 | 0.403 | 1.000 | 98 | tags=29%, list=6%, signal=30% |
| 101 | GOBP\_PROTEIN\_LOCALIZATION\_TO\_ORGANELLE |  | 92 | 0.22 | 1.24 | 0.049 | 0.399 | 1.000 | 281 | tags=30%, list=19%, signal=35% |
| 102 | GOBP\_MACROPHAGE\_ACTIVATION |  | 23 | 0.30 | 1.23 | 0.169 | 0.430 | 1.000 | 174 | tags=22%, list=12%, signal=24% |
| 103 | GOBP\_ISOPRENOID\_METABOLIC\_PROCESS |  | 24 | 0.30 | 1.22 | 0.162 | 0.434 | 1.000 | 120 | tags=29%, list=8%, signal=31% |
| 104 | GOCC\_AZUROPHIL\_GRANULE |  | 21 | 0.31 | 1.22 | 0.158 | 0.440 | 1.000 | 261 | tags=43%, list=17%, signal=51% |
| 105 | GOBP\_REGULATION\_OF\_CELL\_CYCLE\_G1\_S\_PHASE\_TRANSITION |  | 21 | 0.31 | 1.22 | 0.169 | 0.437 | 1.000 | 209 | tags=29%, list=14%, signal=33% |
| 106 | GOBP\_POSITIVE\_REGULATION\_OF\_CELLULAR\_AMIDE\_METABOLIC\_PROCESS |  | 16 | 0.33 | 1.21 | 0.185 | 0.450 | 1.000 | 301 | tags=44%, list=20%, signal=54% |
| 107 | GOBP\_LIPID\_METABOLIC\_PROCESS |  | 130 | 0.20 | 1.21 | 0.020 | 0.446 | 1.000 | 153 | tags=20%, list=10%, signal=20% |
| 108 | GOMF\_PHOSPHATIDYLINOSITOL\_PHOSPHATE\_BINDING |  | 15 | 0.33 | 1.21 | 0.197 | 0.454 | 1.000 | 111 | tags=20%, list=7%, signal=21% |
| 109 | GOBP\_REGULATION\_OF\_REACTIVE\_OXYGEN\_SPECIES\_METABOLIC\_PROCESS |  | 34 | 0.26 | 1.20 | 0.180 | 0.452 | 1.000 | 156 | tags=26%, list=10%, signal=29% |
| 110 | GOBP\_POSITIVE\_REGULATION\_OF\_INTERLEUKIN\_6\_PRODUCTION |  | 17 | 0.33 | 1.20 | 0.195 | 0.450 | 1.000 | 318 | tags=53%, list=21%, signal=66% |
| 111 | GOBP\_INTERLEUKIN\_1\_BETA\_PRODUCTION |  | 17 | 0.33 | 1.20 | 0.224 | 0.450 | 1.000 | 341 | tags=47%, list=23%, signal=60% |
| 112 | GOBP\_POSITIVE\_REGULATION\_OF\_TRANSPORTER\_ACTIVITY |  | 16 | 0.32 | 1.20 | 0.186 | 0.448 | 1.000 | 202 | tags=38%, list=13%, signal=43% |
| 113 | GOBP\_REGULATION\_OF\_CELL\_CYCLE\_G2\_M\_PHASE\_TRANSITION |  | 15 | 0.33 | 1.19 | 0.240 | 0.479 | 1.000 | 1010 | tags=100%, list=67%, signal=299% |
| 114 | GOMF\_PROTEIN\_DIMERIZATION\_ACTIVITY |  | 111 | 0.20 | 1.18 | 0.103 | 0.477 | 1.000 | 198 | tags=23%, list=13%, signal=24% |
| 115 | GOBP\_NEGATIVE\_REGULATION\_OF\_SUPRAMOLECULAR\_FIBER\_ORGANIZATION |  | 21 | 0.29 | 1.18 | 0.172 | 0.473 | 1.000 | 156 | tags=19%, list=10%, signal=21% |
| 116 | GOBP\_REACTIVE\_OXYGEN\_SPECIES\_BIOSYNTHETIC\_PROCESS |  | 22 | 0.30 | 1.18 | 0.222 | 0.488 | 1.000 | 150 | tags=32%, list=10%, signal=35% |
| 117 | GOBP\_NCRNA\_METABOLIC\_PROCESS |  | 24 | 0.29 | 1.16 | 0.263 | 0.526 | 1.000 | 391 | tags=50%, list=26%, signal=66% |
| 118 | GOMF\_LYASE\_ACTIVITY |  | 21 | 0.29 | 1.15 | 0.245 | 0.540 | 1.000 | 182 | tags=33%, list=12%, signal=37% |
| 119 | GOBP\_INTRACELLULAR\_TRANSPORT |  | 129 | 0.19 | 1.15 | 0.100 | 0.536 | 1.000 | 282 | tags=30%, list=19%, signal=34% |
| 120 | GOBP\_UNSATURATED\_FATTY\_ACID\_METABOLIC\_PROCESS |  | 17 | 0.31 | 1.15 | 0.229 | 0.538 | 1.000 | 175 | tags=35%, list=12%, signal=39% |
| 121 | GOCC\_ENVELOPE |  | 94 | 0.20 | 1.15 | 0.203 | 0.536 | 1.000 | 321 | tags=38%, list=21%, signal=46% |
| 122 | GOBP\_SENSORY\_PERCEPTION\_OF\_PAIN |  | 20 | 0.29 | 1.14 | 0.262 | 0.549 | 1.000 | 217 | tags=35%, list=14%, signal=40% |
| 123 | GOBP\_PROTEIN\_IMPORT |  | 17 | 0.31 | 1.14 | 0.227 | 0.547 | 1.000 | 218 | tags=35%, list=14%, signal=41% |
| 124 | GOBP\_ICOSANOID\_BIOSYNTHETIC\_PROCESS |  | 16 | 0.30 | 1.13 | 0.254 | 0.567 | 1.000 | 153 | tags=31%, list=10%, signal=34% |
| 125 | GOBP\_POSITIVE\_REGULATION\_OF\_LEUKOCYTE\_MEDIATED\_IMMUNITY |  | 18 | 0.29 | 1.13 | 0.298 | 0.567 | 1.000 | 107 | tags=17%, list=7%, signal=18% |
| 126 | GOCC\_SPECIFIC\_GRANULE |  | 31 | 0.24 | 1.13 | 0.257 | 0.567 | 1.000 | 155 | tags=26%, list=10%, signal=28% |
| 127 | GOBP\_REACTIVE\_NITROGEN\_SPECIES\_METABOLIC\_PROCESS |  | 19 | 0.29 | 1.12 | 0.281 | 0.581 | 1.000 | 150 | tags=32%, list=10%, signal=35% |
| 128 | GOCC\_TERTIARY\_GRANULE |  | 34 | 0.24 | 1.12 | 0.246 | 0.589 | 1.000 | 172 | tags=29%, list=11%, signal=32% |
| 129 | GOBP\_POSITIVE\_REGULATION\_OF\_NF\_KAPPAB\_TRANSCRIPTION\_FACTOR\_ACTIVITY |  | 19 | 0.29 | 1.11 | 0.271 | 0.603 | 1.000 | 128 | tags=26%, list=8%, signal=28% |
| 130 | GOBP\_HORMONE\_METABOLIC\_PROCESS |  | 37 | 0.24 | 1.11 | 0.276 | 0.608 | 1.000 | 98 | tags=22%, list=6%, signal=23% |
| 131 | GOBP\_PHAGOCYTOSIS |  | 50 | 0.23 | 1.11 | 0.283 | 0.604 | 1.000 | 139 | tags=20%, list=9%, signal=21% |
| 132 | GOBP\_POSITIVE\_REGULATION\_OF\_INFLAMMATORY\_RESPONSE |  | 29 | 0.25 | 1.10 | 0.288 | 0.607 | 1.000 | 199 | tags=28%, list=13%, signal=31% |
| 133 | GOBP\_RECEPTOR\_MEDIATED\_ENDOCYTOSIS |  | 39 | 0.23 | 1.10 | 0.293 | 0.607 | 1.000 | 142 | tags=23%, list=9%, signal=25% |
| 134 | GOCC\_CELL\_LEADING\_EDGE |  | 37 | 0.23 | 1.10 | 0.307 | 0.605 | 1.000 | 160 | tags=19%, list=11%, signal=21% |
| 135 | GOMF\_UBIQUITIN\_LIKE\_PROTEIN\_LIGASE\_BINDING |  | 27 | 0.26 | 1.10 | 0.293 | 0.608 | 1.000 | 324 | tags=33%, list=21%, signal=42% |
| 136 | GOBP\_NEGATIVE\_REGULATION\_OF\_GENE\_EXPRESSION |  | 146 | 0.17 | 1.09 | 0.220 | 0.618 | 1.000 | 281 | tags=27%, list=19%, signal=30% |
| 137 | GOBP\_ANTIGEN\_PROCESSING\_AND\_PRESENTATION |  | 31 | 0.24 | 1.09 | 0.295 | 0.623 | 1.000 | 254 | tags=32%, list=17%, signal=38% |
| 138 | GOBP\_NEUTROPHIL\_CHEMOTAXIS |  | 32 | 0.24 | 1.08 | 0.318 | 0.636 | 1.000 | 174 | tags=25%, list=12%, signal=28% |
| 139 | GOCC\_SPECIFIC\_GRANULE\_LUMEN |  | 18 | 0.27 | 1.08 | 0.311 | 0.640 | 1.000 | 140 | tags=28%, list=9%, signal=30% |
| 140 | GOMF\_OXIDOREDUCTASE\_ACTIVITY |  | 79 | 0.19 | 1.08 | 0.330 | 0.643 | 1.000 | 166 | tags=20%, list=11%, signal=22% |
| 141 | GOBP\_NEUTROPHIL\_MIGRATION |  | 33 | 0.24 | 1.08 | 0.308 | 0.642 | 1.000 | 174 | tags=24%, list=12%, signal=27% |
| 142 | GOBP\_POSITIVE\_REGULATION\_OF\_CELLULAR\_PROTEIN\_LOCALIZATION |  | 21 | 0.28 | 1.08 | 0.332 | 0.638 | 1.000 | 142 | tags=19%, list=9%, signal=21% |
| 143 | GOBP\_CELL\_CYCLE\_G1\_S\_PHASE\_TRANSITION |  | 24 | 0.25 | 1.07 | 0.337 | 0.652 | 1.000 | 209 | tags=25%, list=14%, signal=29% |
| 144 | GOBP\_ORGANELLE\_MEMBRANE\_FUSION |  | 16 | 0.29 | 1.07 | 0.357 | 0.657 | 1.000 | 1073 | tags=100%, list=71%, signal=342% |
| 145 | GOMF\_ION\_TRANSMEMBRANE\_TRANSPORTER\_ACTIVITY |  | 60 | 0.20 | 1.06 | 0.306 | 0.662 | 1.000 | 263 | tags=32%, list=17%, signal=37% |
| 146 | GOBP\_CATION\_TRANSMEMBRANE\_TRANSPORT |  | 82 | 0.19 | 1.06 | 0.338 | 0.662 | 1.000 | 263 | tags=27%, list=17%, signal=31% |
| 147 | GOCC\_EXTRINSIC\_COMPONENT\_OF\_PLASMA\_MEMBRANE |  | 21 | 0.26 | 1.06 | 0.353 | 0.658 | 1.000 | 145 | tags=24%, list=10%, signal=26% |
| 148 | GOBP\_POSITIVE\_REGULATION\_OF\_CYTOKINE\_PRODUCTION |  | 73 | 0.20 | 1.06 | 0.327 | 0.662 | 1.000 | 150 | tags=19%, list=10%, signal=20% |
| 149 | GOBP\_NEGATIVE\_REGULATION\_OF\_ORGANELLE\_ORGANIZATION |  | 32 | 0.23 | 1.06 | 0.320 | 0.664 | 1.000 | 77 | tags=13%, list=5%, signal=13% |
| 150 | GOBP\_PROTEIN\_COMPLEX\_OLIGOMERIZATION |  | 18 | 0.27 | 1.05 | 0.340 | 0.676 | 1.000 | 180 | tags=28%, list=12%, signal=31% |
| 151 | GOBP\_REGULATION\_OF\_CELL\_CYCLE\_PHASE\_TRANSITION |  | 36 | 0.23 | 1.05 | 0.366 | 0.679 | 1.000 | 209 | tags=22%, list=14%, signal=25% |
| 152 | GOBP\_POSITIVE\_REGULATION\_OF\_CATION\_TRANSMEMBRANE\_TRANSPORT |  | 24 | 0.25 | 1.05 | 0.392 | 0.682 | 1.000 | 202 | tags=29%, list=13%, signal=33% |
| 153 | GOBP\_POSITIVE\_REGULATION\_OF\_RESPONSE\_TO\_BIOTIC\_STIMULUS |  | 30 | 0.23 | 1.04 | 0.357 | 0.709 | 1.000 | 155 | tags=20%, list=10%, signal=22% |
| 154 | GOBP\_CELL\_CYCLE\_PHASE\_TRANSITION |  | 42 | 0.21 | 1.03 | 0.383 | 0.706 | 1.000 | 324 | tags=33%, list=21%, signal=41% |
| 155 | GOCC\_POSTSYNAPSE |  | 54 | 0.20 | 1.03 | 0.407 | 0.704 | 1.000 | 400 | tags=37%, list=26%, signal=49% |
| 156 | GOBP\_MACROMOLECULE\_CATABOLIC\_PROCESS |  | 126 | 0.17 | 1.03 | 0.304 | 0.704 | 1.000 | 396 | tags=45%, list=26%, signal=56% |
| 157 | GOBP\_MONOCYTE\_CHEMOTAXIS |  | 24 | 0.24 | 1.03 | 0.386 | 0.703 | 1.000 | 314 | tags=38%, list=21%, signal=47% |
| 158 | GOBP\_ENDOMEMBRANE\_SYSTEM\_ORGANIZATION |  | 26 | 0.24 | 1.03 | 0.409 | 0.700 | 1.000 | 97 | tags=15%, list=6%, signal=16% |
| 159 | GOBP\_NEGATIVE\_REGULATION\_OF\_BINDING |  | 24 | 0.25 | 1.03 | 0.394 | 0.701 | 1.000 | 209 | tags=25%, list=14%, signal=29% |
| 160 | GOMF\_DNA\_BINDING\_TRANSCRIPTION\_FACTOR\_BINDING |  | 34 | 0.22 | 1.03 | 0.427 | 0.700 | 1.000 | 116 | tags=21%, list=8%, signal=22% |
| 161 | GOBP\_POSITIVE\_REGULATION\_OF\_COLD\_INDUCED\_THERMOGENESIS |  | 16 | 0.28 | 1.02 | 0.385 | 0.709 | 1.000 | 146 | tags=25%, list=10%, signal=27% |
| 162 | GOMF\_CARBOXYLIC\_ACID\_BINDING |  | 23 | 0.25 | 1.02 | 0.393 | 0.715 | 1.000 | 185 | tags=35%, list=12%, signal=39% |
| 163 | GOBP\_ORGANIC\_ACID\_BIOSYNTHETIC\_PROCESS |  | 35 | 0.22 | 1.01 | 0.425 | 0.731 | 1.000 | 175 | tags=26%, list=12%, signal=28% |
| 164 | GOBP\_NEGATIVE\_REGULATION\_OF\_MYELOID\_CELL\_DIFFERENTIATION |  | 15 | 0.28 | 1.00 | 0.424 | 0.753 | 1.000 | 174 | tags=27%, list=12%, signal=30% |
| 165 | GOBP\_NUCLEAR\_TRANSPORT |  | 23 | 0.24 | 1.00 | 0.469 | 0.764 | 1.000 | 138 | tags=22%, list=9%, signal=24% |
| 166 | GOBP\_PROTEIN\_CONTAINING\_COMPLEX\_LOCALIZATION |  | 16 | 0.27 | 1.00 | 0.450 | 0.765 | 1.000 | 23 | tags=13%, list=2%, signal=13% |
| 167 | GOBP\_FATTY\_ACID\_BIOSYNTHETIC\_PROCESS |  | 21 | 0.25 | 1.00 | 0.413 | 0.761 | 1.000 | 175 | tags=29%, list=12%, signal=32% |
| 168 | GOBP\_REGULATION\_OF\_INNATE\_IMMUNE\_RESPONSE |  | 37 | 0.21 | 0.99 | 0.429 | 0.761 | 1.000 | 155 | tags=19%, list=10%, signal=21% |
| 169 | GOMF\_ELECTRON\_TRANSFER\_ACTIVITY |  | 18 | 0.25 | 0.99 | 0.438 | 0.758 | 1.000 | 351 | tags=56%, list=23%, signal=72% |
| 170 | GOMF\_CATION\_CHANNEL\_ACTIVITY |  | 23 | 0.25 | 0.99 | 0.486 | 0.760 | 1.000 | 280 | tags=30%, list=19%, signal=37% |
| 171 | GOBP\_OSTEOCLAST\_DIFFERENTIATION |  | 19 | 0.25 | 0.99 | 0.432 | 0.770 | 1.000 | 174 | tags=26%, list=12%, signal=29% |
| 172 | GOBP\_CARBOHYDRATE\_DERIVATIVE\_BIOSYNTHETIC\_PROCESS |  | 40 | 0.20 | 0.98 | 0.493 | 0.775 | 1.000 | 47 | tags=13%, list=3%, signal=13% |
| 173 | GOBP\_PROTEIN\_LOCALIZATION\_TO\_MEMBRANE |  | 85 | 0.17 | 0.98 | 0.507 | 0.779 | 1.000 | 366 | tags=41%, list=24%, signal=51% |
| 174 | GOBP\_REGULATION\_OF\_MYELOID\_CELL\_DIFFERENTIATION |  | 40 | 0.20 | 0.98 | 0.484 | 0.775 | 1.000 | 174 | tags=23%, list=12%, signal=25% |
| 175 | GOBP\_REGULATION\_OF\_MRNA\_METABOLIC\_PROCESS |  | 18 | 0.26 | 0.98 | 0.449 | 0.780 | 1.000 | 109 | tags=17%, list=7%, signal=18% |
| 176 | GOBP\_RESPONSE\_TO\_ENDOPLASMIC\_RETICULUM\_STRESS |  | 21 | 0.24 | 0.97 | 0.460 | 0.793 | 1.000 | 177 | tags=24%, list=12%, signal=27% |
| 177 | GOBP\_NEGATIVE\_REGULATION\_OF\_CELL\_CYCLE\_PROCESS |  | 29 | 0.23 | 0.97 | 0.500 | 0.799 | 1.000 | 209 | tags=21%, list=14%, signal=24% |
| 178 | GOBP\_POSITIVE\_REGULATION\_OF\_LIPID\_LOCALIZATION |  | 21 | 0.25 | 0.97 | 0.491 | 0.800 | 1.000 | 140 | tags=24%, list=9%, signal=26% |
| 179 | GOMF\_KINASE\_BINDING |  | 70 | 0.17 | 0.96 | 0.539 | 0.809 | 1.000 | 209 | tags=20%, list=14%, signal=22% |
| 180 | GOBP\_CELLULAR\_MODIFIED\_AMINO\_ACID\_METABOLIC\_PROCESS |  | 22 | 0.25 | 0.96 | 0.520 | 0.805 | 1.000 | 175 | tags=32%, list=12%, signal=35% |
| 181 | GOMF\_GTPASE\_ACTIVITY |  | 32 | 0.21 | 0.96 | 0.529 | 0.807 | 1.000 | 337 | tags=34%, list=22%, signal=43% |
| 182 | GOCC\_TRANSPORTER\_COMPLEX |  | 23 | 0.24 | 0.96 | 0.522 | 0.803 | 1.000 | 280 | tags=35%, list=19%, signal=42% |
| 183 | GOBP\_INTERLEUKIN\_1\_PRODUCTION |  | 22 | 0.24 | 0.95 | 0.531 | 0.809 | 1.000 | 341 | tags=41%, list=23%, signal=52% |
| 184 | GOBP\_REGULATION\_OF\_TRANS\_SYNAPTIC\_SIGNALING |  | 46 | 0.19 | 0.95 | 0.571 | 0.816 | 1.000 | 202 | tags=17%, list=13%, signal=19% |
| 185 | GOCC\_TRANSFERASE\_COMPLEX |  | 22 | 0.23 | 0.95 | 0.543 | 0.815 | 1.000 | 370 | tags=36%, list=25%, signal=47% |
| 186 | GOBP\_ACUTE\_INFLAMMATORY\_RESPONSE |  | 25 | 0.23 | 0.95 | 0.516 | 0.813 | 1.000 | 150 | tags=24%, list=10%, signal=26% |
| 187 | GOBP\_REGULATION\_OF\_REGULATED\_SECRETORY\_PATHWAY |  | 15 | 0.26 | 0.94 | 0.514 | 0.822 | 1.000 | 107 | tags=20%, list=7%, signal=21% |
| 188 | GOBP\_REGULATION\_OF\_CELLULAR\_AMIDE\_METABOLIC\_PROCESS |  | 37 | 0.20 | 0.94 | 0.531 | 0.829 | 1.000 | 328 | tags=35%, list=22%, signal=44% |
| 189 | GOCC\_PROTEIN\_DNA\_COMPLEX |  | 21 | 0.24 | 0.94 | 0.553 | 0.830 | 1.000 | 182 | tags=24%, list=12%, signal=27% |
| 190 | GOBP\_PURINE\_CONTAINING\_COMPOUND\_BIOSYNTHETIC\_PROCESS |  | 16 | 0.25 | 0.94 | 0.507 | 0.831 | 1.000 | 219 | tags=25%, list=15%, signal=29% |
| 191 | GOBP\_NEGATIVE\_REGULATION\_OF\_DNA\_METABOLIC\_PROCESS |  | 15 | 0.26 | 0.94 | 0.535 | 0.828 | 1.000 | 251 | tags=40%, list=17%, signal=47% |
| 192 | GOBP\_FC\_RECEPTOR\_MEDIATED\_STIMULATORY\_SIGNALING\_PATHWAY |  | 15 | 0.26 | 0.93 | 0.559 | 0.836 | 1.000 | 108 | tags=20%, list=7%, signal=21% |
| 193 | GOBP\_POSITIVE\_REGULATION\_OF\_REACTIVE\_OXYGEN\_SPECIES\_METABOLIC\_PROCESS |  | 20 | 0.24 | 0.93 | 0.566 | 0.832 | 1.000 | 150 | tags=25%, list=10%, signal=27% |
| 194 | GOMF\_TUBULIN\_BINDING |  | 31 | 0.20 | 0.92 | 0.549 | 0.851 | 1.000 | 1206 | tags=100%, list=80%, signal=487% |
| 195 | GOBP\_REGULATION\_OF\_SYNAPTIC\_PLASTICITY |  | 21 | 0.23 | 0.92 | 0.599 | 0.850 | 1.000 | 23 | tags=10%, list=2%, signal=10% |
| 196 | GOBP\_REGULATION\_OF\_PROTEIN\_MODIFICATION\_BY\_SMALL\_PROTEIN\_CONJUGATION\_OR\_REMOVAL |  | 16 | 0.25 | 0.92 | 0.530 | 0.848 | 1.000 | 393 | tags=50%, list=26%, signal=67% |
| 197 | GOBP\_CHROMATIN\_ORGANIZATION |  | 45 | 0.19 | 0.92 | 0.641 | 0.846 | 1.000 | 182 | tags=20%, list=12%, signal=22% |
| 198 | GOBP\_ALCOHOL\_METABOLIC\_PROCESS |  | 32 | 0.20 | 0.91 | 0.655 | 0.859 | 1.000 | 120 | tags=19%, list=8%, signal=20% |
| 199 | GOBP\_REGULATION\_OF\_DNA\_BINDING |  | 19 | 0.24 | 0.91 | 0.565 | 0.855 | 1.000 | 202 | tags=32%, list=13%, signal=36% |
| 200 | GOBP\_REGULATION\_OF\_HORMONE\_LEVELS |  | 87 | 0.16 | 0.91 | 0.697 | 0.854 | 1.000 | 98 | tags=13%, list=6%, signal=13% |
| 201 | GOBP\_NUCLEOSIDE\_PHOSPHATE\_BIOSYNTHETIC\_PROCESS |  | 20 | 0.23 | 0.91 | 0.601 | 0.855 | 1.000 | 219 | tags=25%, list=15%, signal=29% |
| 202 | GOMF\_GATED\_CHANNEL\_ACTIVITY |  | 21 | 0.23 | 0.91 | 0.587 | 0.852 | 1.000 | 112 | tags=14%, list=7%, signal=15% |
| 203 | GOBP\_FC\_RECEPTOR\_SIGNALING\_PATHWAY |  | 20 | 0.24 | 0.91 | 0.609 | 0.857 | 1.000 | 216 | tags=25%, list=14%, signal=29% |
| 204 | GOBP\_CIRCADIAN\_RHYTHM |  | 25 | 0.21 | 0.90 | 0.638 | 0.859 | 1.000 | 244 | tags=28%, list=16%, signal=33% |
| 205 | GOBP\_ORGANOPHOSPHATE\_BIOSYNTHETIC\_PROCESS |  | 38 | 0.20 | 0.90 | 0.645 | 0.863 | 1.000 | 171 | tags=21%, list=11%, signal=23% |
| 206 | GOBP\_ELECTRON\_TRANSPORT\_CHAIN |  | 19 | 0.24 | 0.90 | 0.610 | 0.860 | 1.000 | 351 | tags=53%, list=23%, signal=68% |
| 207 | GOCC\_NUCLEAR\_PROTEIN\_CONTAINING\_COMPLEX |  | 52 | 0.18 | 0.90 | 0.709 | 0.858 | 1.000 | 229 | tags=23%, list=15%, signal=26% |
| 208 | GOBP\_B\_CELL\_MEDIATED\_IMMUNITY |  | 23 | 0.22 | 0.90 | 0.625 | 0.860 | 1.000 | 108 | tags=17%, list=7%, signal=18% |
| 209 | GOBP\_NEUROPEPTIDE\_SIGNALING\_PATHWAY |  | 25 | 0.22 | 0.89 | 0.602 | 0.866 | 1.000 | 199 | tags=20%, list=13%, signal=23% |
| 210 | GOBP\_PHOSPHOLIPASE\_C\_ACTIVATING\_G\_PROTEIN\_COUPLED\_RECEPTOR\_SIGNALING\_PATHWAY |  | 15 | 0.25 | 0.89 | 0.610 | 0.865 | 1.000 | 24 | tags=13%, list=2%, signal=13% |
| 211 | GOMF\_ENZYME\_INHIBITOR\_ACTIVITY |  | 74 | 0.16 | 0.89 | 0.775 | 0.864 | 1.000 | 141 | tags=15%, list=9%, signal=16% |
| 212 | GOBP\_ANTIGEN\_PROCESSING\_AND\_PRESENTATION\_OF\_PEPTIDE\_OR\_POLYSACCHARIDE\_ANTIGEN\_VIA\_MHC\_CLASS\_II |  | 17 | 0.24 | 0.89 | 0.639 | 0.863 | 1.000 | 254 | tags=41%, list=17%, signal=49% |
| 213 | GOBP\_RNA\_PROCESSING |  | 37 | 0.19 | 0.89 | 0.633 | 0.867 | 1.000 | 253 | tags=24%, list=17%, signal=29% |
| 214 | GOBP\_POSTTRANSCRIPTIONAL\_REGULATION\_OF\_GENE\_EXPRESSION |  | 42 | 0.18 | 0.89 | 0.730 | 0.864 | 1.000 | 328 | tags=33%, list=22%, signal=41% |
| 215 | GOBP\_ATP\_METABOLIC\_PROCESS |  | 28 | 0.21 | 0.88 | 0.655 | 0.865 | 1.000 | 435 | tags=61%, list=29%, signal=84% |
| 216 | GOBP\_NEGATIVE\_REGULATION\_OF\_CELLULAR\_COMPONENT\_ORGANIZATION |  | 75 | 0.16 | 0.87 | 0.787 | 0.884 | 1.000 | 109 | tags=12%, list=7%, signal=12% |
| 217 | GOBP\_ENDOCRINE\_PROCESS |  | 17 | 0.23 | 0.87 | 0.637 | 0.880 | 1.000 | 199 | tags=29%, list=13%, signal=33% |
| 218 | GOBP\_MEMBRANE\_INVAGINATION |  | 19 | 0.22 | 0.87 | 0.673 | 0.892 | 1.000 | 107 | tags=21%, list=7%, signal=22% |
| 219 | GOBP\_POSITIVE\_REGULATION\_OF\_RESPONSE\_TO\_EXTERNAL\_STIMULUS |  | 88 | 0.15 | 0.86 | 0.744 | 0.893 | 1.000 | 155 | tags=16%, list=10%, signal=17% |
| 220 | GOBP\_MONOCARBOXYLIC\_ACID\_BIOSYNTHETIC\_PROCESS |  | 24 | 0.21 | 0.86 | 0.692 | 0.889 | 1.000 | 175 | tags=25%, list=12%, signal=28% |
| 221 | GOBP\_GRANULOCYTE\_MIGRATION |  | 40 | 0.18 | 0.86 | 0.701 | 0.891 | 1.000 | 174 | tags=20%, list=12%, signal=22% |
| 222 | GOMF\_CHROMATIN\_BINDING |  | 43 | 0.18 | 0.86 | 0.725 | 0.897 | 1.000 | 94 | tags=14%, list=6%, signal=14% |
| 223 | GOBP\_INTERLEUKIN\_6\_PRODUCTION |  | 31 | 0.19 | 0.86 | 0.687 | 0.894 | 1.000 | 121 | tags=16%, list=8%, signal=17% |
| 224 | GOBP\_CELLULAR\_RESPONSE\_TO\_LIGHT\_STIMULUS |  | 15 | 0.24 | 0.86 | 0.686 | 0.893 | 1.000 | 209 | tags=33%, list=14%, signal=38% |
| 225 | GOBP\_REGULATION\_OF\_VESICLE\_MEDIATED\_TRANSPORT |  | 59 | 0.16 | 0.86 | 0.798 | 0.891 | 1.000 | 108 | tags=15%, list=7%, signal=16% |
| 226 | GOBP\_REGULATION\_OF\_SYNAPSE\_STRUCTURE\_OR\_ACTIVITY |  | 16 | 0.24 | 0.85 | 0.670 | 0.901 | 1.000 | 297 | tags=31%, list=20%, signal=38% |
| 227 | GOBP\_GLYCOPROTEIN\_METABOLIC\_PROCESS |  | 21 | 0.21 | 0.85 | 0.715 | 0.900 | 1.000 | 119 | tags=19%, list=8%, signal=20% |
| 228 | GOBP\_IMMUNE\_RESPONSE\_REGULATING\_SIGNALING\_PATHWAY |  | 55 | 0.17 | 0.84 | 0.815 | 0.911 | 1.000 | 155 | tags=16%, list=10%, signal=18% |
| 229 | GOBP\_RESPONSE\_TO\_HEAT |  | 21 | 0.21 | 0.84 | 0.695 | 0.908 | 1.000 | 209 | tags=24%, list=14%, signal=27% |
| 230 | GOBP\_AMINE\_METABOLIC\_PROCESS |  | 17 | 0.23 | 0.84 | 0.707 | 0.907 | 1.000 | 166 | tags=24%, list=11%, signal=26% |
| 231 | GOBP\_GRANULOCYTE\_CHEMOTAXIS |  | 39 | 0.18 | 0.83 | 0.749 | 0.913 | 1.000 | 174 | tags=21%, list=12%, signal=23% |
| 232 | GOBP\_REGULATION\_OF\_CELL\_CYCLE\_ARREST |  | 16 | 0.23 | 0.83 | 0.707 | 0.917 | 1.000 | 209 | tags=25%, list=14%, signal=29% |
| 233 | GOBP\_VESICLE\_MEDIATED\_TRANSPORT\_IN\_SYNAPSE |  | 16 | 0.23 | 0.82 | 0.731 | 0.931 | 1.000 | 935 | tags=94%, list=62%, signal=244% |
| 234 | GOMF\_METAL\_ION\_TRANSMEMBRANE\_TRANSPORTER\_ACTIVITY |  | 22 | 0.21 | 0.82 | 0.738 | 0.928 | 1.000 | 280 | tags=36%, list=19%, signal=44% |
| 235 | GOMF\_TRANSCRIPTION\_COREGULATOR\_ACTIVITY |  | 26 | 0.18 | 0.81 | 0.844 | 0.951 | 1.000 | 194 | tags=19%, list=13%, signal=22% |
| 236 | GOBP\_POSITIVE\_REGULATION\_OF\_CHEMOKINE\_PRODUCTION |  | 15 | 0.22 | 0.81 | 0.756 | 0.949 | 1.000 | 1177 | tags=100%, list=78%, signal=449% |
| 237 | GOBP\_REGULATION\_OF\_LYMPHOCYTE\_MEDIATED\_IMMUNITY |  | 19 | 0.22 | 0.80 | 0.794 | 0.948 | 1.000 | 50 | tags=11%, list=3%, signal=11% |
| 238 | GOMF\_MODIFIED\_AMINO\_ACID\_BINDING |  | 17 | 0.21 | 0.80 | 0.751 | 0.948 | 1.000 | 175 | tags=24%, list=12%, signal=26% |
| 239 | GOBP\_PURINE\_CONTAINING\_COMPOUND\_METABOLIC\_PROCESS |  | 36 | 0.17 | 0.80 | 0.828 | 0.946 | 1.000 | 35 | tags=8%, list=2%, signal=8% |
| 240 | GOBP\_HUMORAL\_IMMUNE\_RESPONSE\_MEDIATED\_BY\_CIRCULATING\_IMMUNOGLOBULIN |  | 16 | 0.21 | 0.79 | 0.796 | 0.967 | 1.000 | 50 | tags=13%, list=3%, signal=13% |
| 241 | GOBP\_MAINTENANCE\_OF\_LOCATION |  | 37 | 0.17 | 0.78 | 0.852 | 0.965 | 1.000 | 106 | tags=14%, list=7%, signal=14% |
| 242 | GOBP\_REGULATION\_OF\_LYMPHOCYTE\_MIGRATION |  | 17 | 0.22 | 0.78 | 0.822 | 0.962 | 1.000 | 284 | tags=29%, list=19%, signal=36% |
| 243 | GOBP\_CARBOHYDRATE\_TRANSPORT |  | 15 | 0.22 | 0.78 | 0.791 | 0.959 | 1.000 | 260 | tags=33%, list=17%, signal=40% |
| 244 | GOBP\_NEGATIVE\_REGULATION\_OF\_IMMUNE\_RESPONSE |  | 22 | 0.19 | 0.78 | 0.779 | 0.959 | 1.000 | 103 | tags=14%, list=7%, signal=14% |
| 245 | GOCC\_PHAGOCYTIC\_VESICLE |  | 23 | 0.19 | 0.78 | 0.816 | 0.961 | 1.000 | 195 | tags=22%, list=13%, signal=25% |
| 246 | GOBP\_NEUROTRANSMITTER\_TRANSPORT |  | 22 | 0.20 | 0.78 | 0.777 | 0.960 | 1.000 | 232 | tags=27%, list=15%, signal=32% |
| 247 | GOCC\_SPINDLE |  | 22 | 0.19 | 0.77 | 0.837 | 0.959 | 1.000 | 304 | tags=32%, list=20%, signal=39% |
| 248 | GOMF\_HORMONE\_RECEPTOR\_BINDING |  | 16 | 0.21 | 0.77 | 0.776 | 0.958 | 1.000 | 1200 | tags=100%, list=79%, signal=482% |
| 249 | GOBP\_POSITIVE\_REGULATION\_OF\_SYNAPTIC\_TRANSMISSION |  | 18 | 0.21 | 0.77 | 0.799 | 0.957 | 1.000 | 199 | tags=22%, list=13%, signal=25% |
| 250 | GOMF\_KINASE\_INHIBITOR\_ACTIVITY |  | 16 | 0.20 | 0.76 | 0.813 | 0.960 | 1.000 | 99 | tags=13%, list=7%, signal=13% |
| 251 | GOBP\_CILIUM\_ORGANIZATION |  | 16 | 0.21 | 0.76 | 0.789 | 0.957 | 1.000 | 4 | tags=6%, list=0%, signal=6% |
| 252 | GOBP\_PROTEIN\_LOCALIZATION\_TO\_NUCLEUS |  | 24 | 0.18 | 0.76 | 0.874 | 0.960 | 1.000 | 138 | tags=17%, list=9%, signal=18% |
| 253 | GOBP\_SMALL\_GTPASE\_MEDIATED\_SIGNAL\_TRANSDUCTION |  | 41 | 0.15 | 0.75 | 0.908 | 0.963 | 1.000 | 1283 | tags=100%, list=85%, signal=647% |
| 254 | GOCC\_NUCLEOLUS |  | 60 | 0.14 | 0.75 | 0.934 | 0.961 | 1.000 | 293 | tags=28%, list=19%, signal=34% |
| 255 | GOBP\_REGULATION\_OF\_NERVOUS\_SYSTEM\_PROCESS |  | 16 | 0.21 | 0.75 | 0.808 | 0.960 | 1.000 | 217 | tags=25%, list=14%, signal=29% |
| 256 | GOBP\_MICROTUBULE\_CYTOSKELETON\_ORGANIZATION |  | 36 | 0.16 | 0.75 | 0.899 | 0.963 | 1.000 | 77 | tags=8%, list=5%, signal=9% |
| 257 | GOBP\_PROTEIN\_DEPHOSPHORYLATION |  | 21 | 0.18 | 0.74 | 0.881 | 0.964 | 1.000 | 202 | tags=24%, list=13%, signal=27% |
| 258 | GOBP\_REGULATION\_OF\_CELLULAR\_LOCALIZATION |  | 71 | 0.13 | 0.73 | 1.000 | 0.981 | 1.000 | 156 | tags=13%, list=10%, signal=13% |
| 259 | GOBP\_REGULATION\_OF\_ADAPTIVE\_IMMUNE\_RESPONSE |  | 22 | 0.18 | 0.72 | 0.904 | 0.977 | 1.000 | 50 | tags=9%, list=3%, signal=9% |
| 260 | GOBP\_PROTEIN\_MODIFICATION\_BY\_SMALL\_PROTEIN\_REMOVAL |  | 16 | 0.19 | 0.72 | 0.884 | 0.981 | 1.000 | 104 | tags=13%, list=7%, signal=13% |
| 261 | GOCC\_TRANS\_GOLGI\_NETWORK |  | 20 | 0.18 | 0.72 | 0.903 | 0.978 | 1.000 | 36 | tags=10%, list=2%, signal=10% |
| 262 | GOBP\_LYMPHOCYTE\_MIGRATION |  | 24 | 0.17 | 0.71 | 0.915 | 0.979 | 1.000 | 174 | tags=17%, list=12%, signal=19% |
| 263 | GOBP\_CHROMOSOME\_ORGANIZATION |  | 66 | 0.13 | 0.71 | 0.960 | 0.981 | 1.000 | 115 | tags=12%, list=8%, signal=13% |
| 264 | GOBP\_REGULATION\_OF\_EXOCYTOSIS |  | 22 | 0.17 | 0.69 | 0.932 | 0.991 | 1.000 | 107 | tags=14%, list=7%, signal=14% |
| 265 | GOBP\_RAS\_PROTEIN\_SIGNAL\_TRANSDUCTION |  | 30 | 0.15 | 0.68 | 0.937 | 0.998 | 1.000 | 1283 | tags=100%, list=85%, signal=652% |
| 266 | GOBP\_ACTIVATION\_OF\_CYSTEINE\_TYPE\_ENDOPEPTIDASE\_ACTIVITY\_INVOLVED\_IN\_APOPTOTIC\_PROCESS |  | 15 | 0.19 | 0.68 | 0.938 | 0.996 | 1.000 | 1230 | tags=100%, list=81%, signal=534% |
| 267 | GOCC\_MITOCHONDRIAL\_MATRIX |  | 16 | 0.19 | 0.68 | 0.909 | 0.992 | 1.000 | 393 | tags=56%, list=26%, signal=75% |
| 268 | GOBP\_PROTEIN\_MODIFICATION\_BY\_SMALL\_PROTEIN\_CONJUGATION\_OR\_REMOVAL |  | 55 | 0.13 | 0.67 | 0.982 | 0.996 | 1.000 | 176 | tags=13%, list=12%, signal=14% |
| 269 | GOMF\_GTPASE\_ACTIVATOR\_ACTIVITY |  | 19 | 0.17 | 0.66 | 0.946 | 0.996 | 1.000 | 1002 | tags=95%, list=66%, signal=278% |
| 270 | GOBP\_REGULATION\_OF\_CELLULAR\_PROTEIN\_CATABOLIC\_PROCESS |  | 22 | 0.16 | 0.65 | 0.950 | 0.998 | 1.000 | 389 | tags=36%, list=26%, signal=48% |
| 271 | GOBP\_MONOCARBOXYLIC\_ACID\_TRANSPORT |  | 20 | 0.16 | 0.65 | 0.932 | 0.996 | 1.000 | 149 | tags=15%, list=10%, signal=16% |
| 272 | GOMF\_HYDROLASE\_ACTIVITY\_ACTING\_ON\_ACID\_ANHYDRIDES |  | 58 | 0.13 | 0.64 | 0.972 | 0.996 | 1.000 | 223 | tags=17%, list=15%, signal=19% |
| 273 | GOCC\_SYNAPTIC\_MEMBRANE |  | 27 | 0.15 | 0.64 | 0.932 | 0.994 | 1.000 | 2 | tags=4%, list=0%, signal=4% |
| 274 | GOBP\_REGULATION\_OF\_CALCIUM\_ION\_TRANSPORT\_INTO\_CYTOSOL |  | 16 | 0.17 | 0.61 | 0.976 | 1.000 | 1.000 | 202 | tags=19%, list=13%, signal=21% |
| 275 | GOBP\_REGULATION\_OF\_GTPASE\_ACTIVITY |  | 45 | 0.12 | 0.61 | 1.000 | 1.000 | 1.000 | 337 | tags=29%, list=22%, signal=36% |
| 276 | GOBP\_PROTEIN\_LOCALIZATION\_TO\_CELL\_JUNCTION |  | 15 | 0.17 | 0.58 | 0.979 | 1.000 | 1.000 | 23 | tags=7%, list=2%, signal=7% |
| 277 | GOBP\_POSITIVE\_REGULATION\_OF\_CELLULAR\_PROTEIN\_CATABOLIC\_PROCESS |  | 17 | 0.15 | 0.58 | 0.983 | 1.000 | 1.000 | 1283 | tags=100%, list=85%, signal=658% |
| 278 | GOCC\_DENDRITIC\_TREE |  | 56 | 0.11 | 0.56 | 1.000 | 1.000 | 1.000 | 217 | tags=14%, list=14%, signal=16% |
| 279 | GOBP\_PROTEIN\_MODIFICATION\_BY\_SMALL\_PROTEIN\_CONJUGATION |  | 43 | 0.11 | 0.54 | 1.000 | 1.000 | 1.000 | 393 | tags=35%, list=26%, signal=46% |
| 280 | GOBP\_POSITIVE\_REGULATION\_OF\_GTPASE\_ACTIVITY |  | 37 | 0.11 | 0.50 | 1.000 | 1.000 | 1.000 | 337 | tags=27%, list=22%, signal=34% |
| 281 | GOCC\_CHROMOSOME\_CENTROMERIC\_REGION |  | 15 | 0.13 | 0.46 | 0.996 | 0.999 | 1.000 | 1316 | tags=100%, list=87%, signal=771% |