### Supplementary Table S3 - Cluster analysis in 5hmC sites unique to males

| GO Term                                                   | expected | observed | p-value (fdr) | enrichment |
|-----------------------------------------------------------|----------|----------|---------------|------------|
| olfactory receptor activity                               | 146.187  | 22       | 1.11E-04      | down       |
| sensory perception of smell                               | 153.39   | 31       | 7.22E-04      | down       |
| sensory perception of chemical stimulus                   | 169.916  | 44       | 6.31E-04      | down       |
| protein binding                                           | 3343.23  | 3701     | 3.14E-02      | up         |
| G-protein coupled receptor activity binding               | 321.187  | 189      | 1.51E-02      | down       |
| biological regulation                                     | 2838.14  | 3152     | 7.53E-02      | up         |
| regulation of biological process                          | 2675.43  | 2977     | 1.22E-01      | up         |
| signaling                                                 | 1477.12  | 1729     | 2.06E-01      | up         |
| regulation of cellular process                            | 2542.8   | 2836     | 5.23E-01      | up         |
| cellular process                                          | 4714.42  | 4981     | 2.30E-01      | up         |
| signaling process                                         | 1069.07  | 1269     | 1.24E-01      | up         |
| signal transmission                                       | 1066.53  | 1265     | 1.86E-01      | up         |
| sensory perception                                        | 315.679  | 209      | 5.00E-02      | down       |
| multicellular organismal development                      | 1291.95  | 1488     | 7.15E-13      | up         |
| developmental process                                     | 1417.38  | 1619     | 1.03E-12      | up         |
| anatomical structure development                          | 1184.32  | 1372     | 1.16E-12      | up         |
| system development                                        | 1069.07  | 1247     | 2.33E-12      | up         |
| signaling pathway                                         | 1055.93  | 1229     | 8.49E-12      | up         |
| nervous system development                                | 488.984  | 612      | 1.06E-11      | up         |
| signal transduction                                       | 925.002  | 1078     | 3.14E-10      | up         |
| adenyl ribonucleotide binding                             | 613.137  | 740      | 4.54E-10      | up         |
| cytoskeletal protein binding                               | 208.475  | 285      | 4.54E-10      | up         |
| ATP binding                                               | 603.391  | 729      | 4.77E-10      | up         |
| cellular developmental process                             | 798.731  | 939      | 8.78E-10      | up         |
| neurogenesis                                              | 269.492  | 354      | 1.28E-09      | up         |
| cell communication                                        | 696.188  | 827      | 1.30E-09      | up         |
| cognition                                                 | 355.933  | 262      | 1.43E-09      | down       |
| phosphotransferase activity, alcohol group as acceptor    | 294.916  | 382      | 2.03E-09      | up         |
| neuron differentiation                                     | 227.967  | 305      | 2.03E-09      | up         |
| regulation of cellular biosynthetic process               | 1227.55  | 1391     | 2.26E-09      | up         |
| cellular component organization                           | 1149.16  | 1308     | 2.47E-09      | up         |
| regulation of cellular metabolic process                  | 1521.19  | 1697     | 3.02E-09      | up         |
| cell differentiation                                      | 761.019  | 893      | 4.13E-09      | up         |
| regulation of primary metabolic process                   | 1446.19  | 1615     | 7.66E-09      | up         |
| regulation of biosynthetic process                        | 1236.44  | 1395     | 7.97E-09      | up         |
| regulation of metabolic process                           | 1596.61  | 1771     | 7.97E-09      | up         |
| adenyl nucleotide binding                                 | 645.341  | 766      | 7.97E-09      | up         |
| organ development                                         | 804.239  | 937      | 7.97E-09      | up         |
| regulation of macromolecule biosynthetic process          | 1165.26  | 1320     | 8.08E-09      | up         |
| generation of neurons                                     | 250.848  | 328      | 1.06E-08      | up         |
| protein amino acid phosphorylation                        | 335.17   | 423      | 1.44E-08      | up         |
| anatomical structure morphogenesis                        | 580.51   | 693      | 1.81E-08      | up         |
| purine nucleoside binding                                 | 660.171  | 779      | 1.98E-08      | up         |
| regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 1223.31  | 1377     | 2.14E-08      | up         |
| regulation of nitrogen compound metabolic process         | 1233.9   | 1388     | 2.16E-08      | up         |
| regulation of gene expression                             | 1188.99  | 1340     | 2.60E-08      | up         |
| regulation of macromolecule metabolic process             | 1377.12  | 1537     | 2.60E-08      | up         |
| nucleoside binding                                        | 664.408  | 782      | 3.00E-08      | up         |
| kinase activity                                           | 319.069  | 403      | 3.00E-08      | up         |
| regulation of transcription                               | 1061.02  | 1204     | 3.51E-08      | up         |
| negative regulation of cellular process                  | 783.476  | 909      | 3.80E-08      | up         |
| transcription                                             | 1100.43  | 1245     | 3.91E-08      | up         |
| enzyme linked receptor protein signaling pathway          | 197.882  | 264      | 4.27E-08      | up         |
| intracellular                                             | 4577.55  | 4765     | 4.42E-08      | up         |
| negative regulation of biological process                | 855.511  | 985      | 4.59E-08      | up         |
| transferase activity, transferring phosphorus-containing groups | 368.645  | 457      | 5.05E-08      | up         |
| protein kinase activity                                   | 247.458  | 320      | 6.96E-08      | up         |
| regulation of signaling pathway                          | 419.069  | 512      | 6.96E-08      | up         |
| regulation of cell communication                          | 481.357  | 580      | 8.05E-08      | up         |
| protein tyrosine kinase activity                          | 58.4747  | 94       | 9.69E-08      | up         |
| cell development                                          | 336.018  | 419      | 9.69E-08      | up         |
| cell surface receptor linked signaling pathway            | 622.883  | 733      | 9.89E-08      | up         |
| nucleoside-triphosphatase regulator activity             | 175      | 235      | 1.53E-07      | up         |
| cell projection                                           | 318.221  | 398      | 1.54E-07      | up         |
| primary metabolic process                                 | 3091.53  | 3280     | 1.66E-07      | up         |
cellular macromolecule metabolic process
down
ribonucleotide binding
down
purine ribonucleotide binding
down
cellular component morphogenesis
down
GTPase regulator activity
down
macromolecule metabolic process
down
cell junction
down
neuron development
down
plasma membrane part
down
intracellular signaling pathway
down
protein modification process
down
protein domain specific binding
down
small GTPase regulator activity
down
actin cytoskeleton
down
transmembrane receptor protein tyrosine kinase signaling pathway
down
cellular biosynthetic process
down
actin binding
down
macromolecule modification
down
phosphorylation
down
intermediate filament cytoskeleton
down
cell morphogenesis
down
synapse
down
biosynthetic process
down
cell projection organization
down
transcription regulator activity
down
neuron projection
down
nucleotide binding
down
purine nucleotide binding
down
intermediate filament
down
cellular macromolecule biosynthetic process
down
negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
down
macromolecule biosynthetic process
down
transmembrane receptor activity
down
negative regulation of nitrogen compound metabolic process
down
cytoskeleton organization
down
transmembrane receptor protein kinase activity
down
actin cytoskeleton organization
down
intracellular part
down
negative regulation of gene expression
down
phosphorus metabolic process
down
phosphate metabolic process
down
negative regulation of transcription
down
negative regulation of macromolecule biosynthetic process
down
negative regulation of cellular biosynthetic process
down
negative regulation of biosynthetic process
down
actin filament-based process
down
intracellular signal transduction
down
central nervous system development
down
cellular metabolic process
down
positive regulation of cellular process
down
neuron projection development
down
transmembrane receptor protein tyrosine kinase activity
down
transcription repressor activity
down
positive regulation of biological process
down
neuron projection morphogenesis
down
receptor activity
down
cytoskeleton
down
cell morphogenesis involved in differentiation
down
molecular function
down
localization
down
cation binding
down
ion binding
down
transferase activity
down
post-translational protein modification
down
enzyme binding
down
guanyl-nucleotide exchange factor activity
down
keratin filament
down
transmission of nerve impulse
down

1.83E-07
1.90E-07
1.90E-07
1.93E-07
2.32E-07
2.62E-07
4.82E-07
5.49E-07
6.33E-07
6.47E-07
6.47E-07
6.57E-07
9.14E-07
9.48E-07
9.48E-07
9.63E-07
9.68E-07
1.04E-06
down
1.07E-06
up
1.11E-06
up
1.12E-06
up
1.59E-06
up
1.97E-06
up
1.97E-06
up
1.98E-06
up
2.06E-06
up
2.06E-06
up
2.26E-06
down
2.38E-06
up
2.38E-06
up
2.57E-06
up
3.45E-06
down
3.45E-06
up
3.91E-06
up
3.91E-06
up
3.99E-06
up
4.47E-06
up
4.50E-06
up
5.17E-06
up
5.17E-06
up
5.17E-06
up
5.17E-06
up
5.62E-06
up
5.62E-06
up
6.23E-06
up
7.07E-06
up
7.75E-06
up
1.19E-05
up
1.36E-05
up
1.40E-05
up
1.54E-05
up
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up
1.87E-05
down
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up
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up
2.61E-05
down
2.71E-05
up
2.87E-05
up
3.15E-05
up
3.65E-05
up
3.72E-05
up
3.95E-05
up
4.10E-05
up
4.31E-05
up
5.07E-05
up
5.12E-05
down
5.41E-05
up
| Process/Activity                                                                 | Metabolite Type | Molecule Type | Regulation Status |
|--------------------------------------------------------------------------------|----------------|---------------|-------------------|
| Ras protein signal transduction                                                | cytoplasm      | Ras protein   | up                |
| Metabolic process                                                             | TCA cycle      | NADH          | up                |
| Regulation of developmental process                                           | ATP            | GTP           | up                |
| Negative regulation of metabolic process                                      | glucose        | 6-phosphogluconate | up                |
| Regulation of signaling process                                               | calcium        | Ca^{2+}       | up                |
| Negative regulation of cellular metabolic process                             | sodium         | Na^{+}        | up                |
| Structural constituent of ribosome                                            | nucleobase      | nucleoside    | down              |
| Cell part morphogenesis                                                       | protein         | SH3 domain    | up                |
| Synaptic transmission                                                         | neurotransmitter| GABA          | up                |
| Regulation of signal transduction                                             | protein         | protein kinase| down              |
| Synapse part                                                                  | metal ion      | zinc ion      | up                |
| Cell morphology involved in neuron differentiation                            | nucleobase      | nucleoside    | down              |
| Negative regulation of transcription from RNA polymerase II promoter          | RNA             | RNA polymerase| down              |
| Negative regulation of macromolecule metabolic process                        | protein         | Rho protein   | up                |
| Chemokine activity                                                           | tissue          | cytokine      | up                |
| Regulation of small GTPase mediated signal transduction                       | GTPase          | GTP           | up                |
| Regulation of transcription from RNA polymerase II promoter                   | RNA             | RNA polymerase| up                |
| Axonogenesis                                                                  | RNA             | RNA polymerase| up                |
| Regulation of multicellular organismal process                                | RNA             | RNA polymerase| up                |
| Negative regulation of RNA metabolic process                                  | RNA             | RNA polymerase| up                |
| Regulation of cellular component organization                                 | RNA             | RNA polymerase| up                |
| Negative regulation of transcription, DNA-dependent                           | RNA             | RNA polymerase| up                |
| Nitrogen compound metabolic process                                           | amino acid      | nitrate       | up                |
| Cell projection morphogenesis                                                  | protein         | Rho protein   | up                |
| Transcription from RNA polymerase II promoter                                 | RNA             | RNA polymerase| up                |
| Cellular nitrogen compound metabolic process                                  | RNA             | RNA polymerase| up                |
| Ribosome                                                                      | RNA             | RNA polymerase| up                |
| Growth factor binding                                                         | protein         | protein kinase| down              |
| Cytokine activity                                                             | protein         | protein kinase| up                |
| Transition metal ion binding                                                  | metal ion       | metal ion     | up                |
| Intracellular organelle                                                       | organelle       | organelle     | up                |
| Rho protein signal transduction                                               | protein         | Rho protein   | up                |
| Regulation of biological quality                                              | protein         | protein kinase| up                |
| Protein serine/threonine kinase activity                                       | protein         | protein kinase| up                |
| Nuclear                                                                      | protein         | nuclear protein| up                |
| Nucleic acid metabolic process                                                | nucleic acid    | DNA            | up                |
| Cell leading edge                                                             | protein         | SH3 domain    | up                |
| Organ morphogenesis                                                           | protein         | Rho protein   | up                |
| Neurological system process                                                   | protein         | Rho protein   | up                |
| DNA binding                                                                  | DNA             | DNA            | up                |
| Cellular component movement                                                   | protein         | Rho protein   | up                |
| Rho guanyl-nucleotide exchange factor activity                               | protein         | Rho protein   | up                |
| Regulation of cell proliferation                                              | protein         | Rho protein   | up                |
| Protein metabolic process                                                     | protein         | Rho protein   | up                |
| Brain development                                                             | protein         | Rho protein   | up                |
| Lamellodium                                                                  | protein         | Rho protein   | up                |
| SH3 domain binding                                                            | protein         | SH3 domain    | up                |
| Cell proliferation                                                            | protein         | Rho protein   | up                |
| Postsynaptic membrane                                                         | protein         | Rho protein   | up                |
| Defense response                                                             | protein         | Rho protein   | up                |
| Regulation of Ras protein signal transduction                                 | protein         | Rho protein   | down              |
| Keratinization                                                               | protein         | keratin       | up                |
| Microspike assembly                                                           | protein         | microspike    | up                |
| Positive regulation of gene expression                                        | protein         | Rho protein   | up                |
| Generation of a signal involved in cell-cell signaling                       | protein         | Rho protein   | up                |
| Signal release                                                               | protein         | Rho protein   | up                |
| Positive regulation of transcription                                         | protein         | Rho protein   | up                |
| Ribonucleoprotein complex                                                     | protein         | Rho protein   | up                |
| Ras guanyl-nucleotide exchange factor activity                               | protein         | Rho protein   | down              |
| Regulation of localization                                                    | protein         | Rho protein   | up                |
| Establishment of localization                                                | protein         | Rho protein   | up                |
| Gene Name                                           | Log2FoldChange | p-value   | Status |
|-----------------------------------------------------|----------------|-----------|--------|
| transcription factor activity                       | 389.831        | 446       | up     |
| cytosol                                             | 542.798        | 608       | up     |
| Golgi apparatus part                                | 222.034        | 265       | up     |
| cell part                                           | 6024.17        | 610       | up     |
| cell                                                | 6024.59        | 610       | up     |
| programmed cell death                              | 468.645        | 529       | up     |
| postsynaptic density                                | 33.0509        | 50        | up     |
| filopodium assembly                                 | 9.74579        | 19        | up     |
| apoptosis                                           | 465.255        | 525       | up     |
| transcription factor binding                       | 218.221        | 260       | up     |
| sensory organ development                           | 104.661        | 134       | up     |
| positive regulation of cellular biosynthetic process| 309.747        | 359       | up     |
| skeletal muscle fiber development                   | 19.9153        | 33        | up     |
| vasculature development                             | 144.916        | 179       | up     |
| regulation of transcription, DNA-dependent          | 725.849        | 798       | up     |
| cellular component assembly                         | 420.764        | 477       | up     |
| gene expression                                     | 1531.78        | 1629      | up     |
| polysaccharide biosynthetic process                 | 25.4238        | 40        | up     |
| transport                                           | 1175.43        | 1263      | up     |
| transcription activator activity                    | 179.661        | 217       | up     |
| intracellular membrane-bounded organelle            | 3388.57        | 3505      | up     |
| cell death                                          | 513.137        | 574       | up     |
| response to stimulus                                | 1492.8         | 1398      | down   |
| digestive system development                        | 27.1187        | 42        | up     |
| regulation of cellular component biogenesis         | 63.5595        | 86        | up     |
| calmodulin binding                                  | 59.3222        | 81        | up     |
| death                                               | 514.408        | 575       | up     |
| muscle cell differentiation                         | 60.1696        | 82        | up     |
| positive regulation of nitrogen compound metabolic process | 291.526    | 338       | up     |
| cellular protein metabolic process                  | 1005.51        | 1086      | up     |
| transcription, DNA-dependent                        | 780.087        | 852       | up     |
| blood vessel development                            | 141.526        | 174       | up     |
| non-membrane spanning protein tyrosine kinase activity| 16.5255        | 28        | up     |
| enzyme regulator activity                           | 353.814        | 404       | up     |
| membrane-bounded organelle                          | 3391.53        | 3505      | up     |
| Golgi membrane                                      | 184.322        | 221       | up     |
| ribosomal subunit                                   | 48.7289        | 30        | down   |
| regulation of Rho protein signal transduction       | 45.3391        | 64        | up     |
| regulation of peptide secretion                     | 25.8475        | 40        | up     |
| cytokine receptor binding                           | 77.5426        | 54        | down   |
| endocytosis                                         | 113.983        | 143       | up     |
| membrane invagination                               | 113.983        | 143       | up     |
| RNA biosynthetic process                            | 781.782        | 853       | up     |
| regulation of RNA metabolic process                 | 746.188        | 816       | up     |
| regulation of peptide transport                     | 25.8475        | 40        | up     |
| Golgi apparatus                                     | 365.679        | 416       | up     |
| regulation of cell differentiation                  | 234.323        | 275       | up     |
| enzyme activator activity                           | 141.102        | 173       | up     |
| camera-type eye morphogenesis                        | 22.034         | 35        | up     |
| cell-cell signaling                                 | 299.577        | 345       | up     |
| positive regulation of transcription, DNA-dependent | 213.56         | 252       | down   |
| cation channel activity                             | 111.865        | 140       | up     |
| adherens junction                                   | 61.0171        | 82        | up     |
| heart development                                   | 102.119        | 129       | up     |
| GTPase activator activity                           | 91.5256        | 117       | up     |
| nuclear membrane                                    | 53.39          | 73        | up     |
| mitochondrial inner membrane                        | 118.221        | 90        | down   |
| positive regulation of macromolecule biosynthetic process | 291.95      | 336       | up     |
| positive regulation of biosynthetic process         | 314.408        | 360       | up     |
| muscle structure development                        | 128.39         | 158       | up     |
| identical protein binding                           | 289.407        | 333       | up     |
| regulation of cell morphogenesis                    | 66.5256        | 88        | up     |
| catalytic activity                                  | 2111.87        | 2211      | up     |
| peptide secretion                                   | 37.712         | 54        | up     |
| positive regulation of cellular metabolic process   | 414.832        | 466       | up     |
| mitochondrial part                                  | 246.611        | 207       | down   |
| MAPKXX cascade                                      | 124.153        | 153       | up     |
| motor activity                                      | 58.8984        | 79        | up     |
cell projection part
renal system development
response to hormone stimulus
cytosolic membrane-bounded vesicle
muscle fiber development
positive regulation of metabolic process
regulation of cellular component movement
cell maturation
positive regulation of RNA metabolic process
multicellular organismal process
membrane raft
positive regulation of protein kinase activity
electron carrier activity
regulation of peptide hormone secretion
peptide hormone secretion
signal complex assembly
myosin complex
cell-cell adherens junction
axon	net retina development in camera-type eye
ion channel activity
positive regulation of macromolecule metabolic process
kinesin binding
developmental maturation
positive regulation of kinase activity
sequence-specific DNA binding
nucleus localization
actin filament bundle
negative regulation of cell proliferation
large ribosomal subunit
neurotransmitter secretion
cytoplasmic vesicle
positive regulation of transcription from RNA polymerase II promoter
cell migration
positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
 gated channel activity
voltage-gated ion channel activity
voltage-gated channel activity
mitochondrial membrane part
cell motility
localization of cell
dendrite
membrane-bounded vesicle
regulation of phosphorylation
regulation of insulin secretion
cation channel complex
positive regulation of signaling pathway
muscle organ development
nucleosome
integral to Golgi membrane
axon guidance
mitochondrion
basolateral plasma membrane
regulation of cellular component size
regulation of locomotion
nucleosome assembly
gland development
anatomical structure formation involved in morphogenesis
actin filament organization
exocrine system development
presynaptic membrane
muscle cell development
regulation of phosphate metabolic process
regulation of phosphorus metabolic process
receptor signaling protein tyrosine kinase activity
cytoskeletal adaptor activity
peptide transport
| Gene Expression | Score   | p-value | Significance |
|-----------------|---------|---------|--------------|
| vesicle-mediated transport | 277.543 | 0.025333 | up |
| synaptosome | 38.9831 | 0.025333 | up |
| cell projection assembly | 41.5255 | 0.025333 | up |
| response to oxygen levels | 64.8307 | 0.025333 | up |
| epidermal cell differentiation | 34.7458 | 0.025725 | up |
| digestive tract development | 23.3051 | 0.025725 | down |
| protein-DNA complex assembly | 34.7458 | 0.025725 | down |
| negative regulation of cellular component organization | 74.5765 | 0.026103 | up |
| regulation of cell migration | 92.3731 | 0.0261597 | up |
| keratinocyte differentiation | 30.9323 | 0.0264359 | up |
| vesicle | 296.611 | 0.0266344 | up |
| adenylate cyclase activity | 4.66103 | 0.0268905 | up |
| positive regulation of glycogen metabolic process | 4.66103 | 0.0268905 | up |
| negative regulation of protein complex disassembly | 17.7967 | 0.0270883 | up |
| cellular membrane organization | 183.051 | 0.0297167 | up |
| BMP signaling pathway | 27.5424 | 0.0298263 | up |
| substrate-specific channel activity | 161.865 | 0.0300338 | up |
| transcription cofactor activity | 150.848 | 0.0300451 | up |
| regulation of protein kinase activity | 156.356 | 0.0300451 | up |
| intrinsic to Golgi membrane | 19.4916 | 0.0307745 | up |
| SMAD binding | 19.4916 | 0.0307745 | up |
| oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, | 11.8644 | 0.0308427 | down |
| striated muscle cell development | 30.0848 | 0.0311685 | up |
| positive regulation of transferase activity | 106.356 | 0.0317232 | up |
| growth | 223.306 | 0.0317522 | up |
| protein depolymerization | 20.339 | 0.0322542 | up |
| urogenital system development | 61.8646 | 0.0322108 | up |
| G-protein signaling, coupled to CAMP nucleotide second messenger | 36.017 | 0.0322108 | up |
| carbohydrate transport | 38.5594 | 0.0323318 | up |
| regulation of hormone levels | 97.4579 | 0.0323318 | up |
| channel activity | 168.644 | 0.0323318 | up |
| gland morphogenesis | 36.017 | 0.0323318 | up |
| passive transmembrane transporter activity | 168.644 | 0.0323318 | up |
| chromatin assembly | 30.5085 | 0.0323318 | down |
| melanosome | 38.5594 | 0.0323318 | up |
| pigment granule | 38.5594 | 0.0323318 | up |
| canonical Wnt receptor signaling pathway | 33.4747 | 0.0323318 | up |
| membrane organization | 183.475 | 0.0323318 | up |
| response to other organism | 152.543 | 0.0325138 | down |
| respiratory chain | 26.695 | 0.0325138 | down |
| extracellular structure organization | 71.6103 | 0.0327608 | up |
| regulation of kinase activity | 162.289 | 0.0327608 | up |
| neuron recognition | 8.89833 | 0.0333232 | up |
| regulation of cytoskeleton organization | 57.6273 | 0.0333232 | up |
| positive regulation of cell differentiation | 108.475 | 0.0344912 | up |
| stress fiber | 11.8644 | 0.034567 | up |
| myelinated sheath | 6.77968 | 0.034567 | up |
| cellular component maintenance | 11.8644 | 0.034567 | up |
| anchoring junction | 68.2205 | 0.034955 | up |
| cell adhesion | 333.052 | 0.0353505 | up |
| cellular localization | 497.035 | 0.0359784 | up |
| mitochondrial envelope | 175 | 0.036354 | down |
| regulation of anatomical structure morphogenesis | 130.509 | 0.036584 | up |
| regulation of neuron differentiation | 75.4239 | 0.036767 | up |
| response to endogenous stimulus | 211.017 | 0.0372812 | up |
| biological adhesion | 333.475 | 0.0386452 | up |
| blood vessel morphogenesis | 122.458 | 0.0388013 | up |
| positive regulation of peptide secretion | 12.7119 | 0.0388679 | up |
| nucleosome organization | 32.6272 | 0.0389177 | down |
| regulation of molecular function | 444.069 | 0.0399146 | up |
| regulation of anatomical structure size | 169.492 | 0.0408487 | up |
| protein homooligomerization | 44.0679 | 0.0408582 | up |
| positive regulation of cell communication | 174.153 | 0.0408582 | up |
| glycosaminoglycan biosynthetic process | 9.74579 | 0.0408582 | up |
| voltage-gated cation channel activity | 59.7459 | 0.0408582 | up |
| ear development | 42.373 | 0.0408697 | up |
| term                                                      | score | rank | p-value | status |
|-----------------------------------------------------------|-------|------|---------|--------|
| ruffle                                                    | 31.356| 44   | 0.0412167| up     |
| insulin secretion                                        | 31.356| 44   | 0.0412167| up     |
| focal adhesion                                            | 36.4408| 50   | 0.0416032| up     |
| cell junction organization                                | 33.8984| 47   | 0.0416032| up     |
| tube development                                          | 141.949| 168  | 0.0416032| up     |
| eye morphogenesis                                         | 34.7458| 48   | 0.0416032| up     |
| negative regulation of signaling pathway                 | 112.712| 136  | 0.0418743| up     |
| organelle organization                                   | 610.595| 662  | 0.0420762| up     |
| filopodium                                                | 13.5594| 22   | 0.0420762| up     |
| neuronal cell body                                       | 75.8476| 95   | 0.04353  | up     |
| cell body                                                 | 75.8476| 95   | 0.04353  | up     |
| semaphorin receptor activity                              | 2.96611| 7    | 0.0441824| up     |
| retina morphogenesis in camera-type eye                   | 7.62714| 14   | 0.0445754| up     |
| microtubule                                               | 115.678| 139  | 0.0454255| up     |
| actin filament binding                                    | 20.7628| 31   | 0.0455415| up     |
| nuclear envelope                                          | 95.7629| 117  | 0.0463311| up     |
| protein complex assembly                                  | 241.95| 275  | 0.0463311| up     |
| protein complex biogenesis                                | 241.95| 275  | 0.0463311| up     |
| aminoglycan biosynthetic process                          | 10.5932| 18   | 0.0465744| up     |
| cytochrome-c oxidase activity                             | 9.74579| 3    | 0.0468106| down   |
| response to biotic stimulus                               | 188.984| 160  | 0.0468106| down   |
| heme-copper terminal oxidase activity                     | 9.74579| 3    | 0.0468106| down   |
| oxidoreductase activity, acting on heme group of donors   | 9.74579| 3    | 0.0468106| down   |
| oxidoreductase activity, acting on heme group of donors, oxygen as acceptor | 9.74579| 3    | 0.0468106| down   |
| ion channel complex                                       | 87.7121| 108  | 0.0469103| up     |
| extracellular region                                      | 799.578| 743  | 0.0472259| down   |
| clathrin coat of coated pit                               | 4.2373| 9    | 0.0472259| up     |
| positive regulation of glycogen biosynthetic process      | 4.2373| 9    | 0.0472259| up     |
| regulation of cell death                                  | 373.73| 414  | 0.0477704| up     |
| transcription corepressor activity                        | 61.0171| 78   | 0.0478799| up     |
| embryonic development                                     | 261.018| 295  | 0.0481942| up     |
| GTPase binding                                            | 45.3391| 60   | 0.0496326| up     |