**Supplementary Table 9 Gene ontology enrichment analysis in cluster 1 and cluster 2.**

**Supplementary Table 9a Gene ontology enrichment in cluster 1.**

| GO Term | originalGeneSetSize | actualGeneSetSize | logitNES | p-value | q-value |
|---|---|---|---|---|---|
| NEURON PART | 1265 | 1135 | 0.5592 | 1.88E-27 | 4.43E-24 |
| SYNAPSE | 754 | 693 | 0.7005 | 5.49E-27 | 8.62E-24 |
| SYNAPSE PART | 610 | 558 | 0.7796 | 1.20E-26 | 1.42E-23 |
| NEUROGENESIS | 1402 | 1257 | 0.4780 | 1.68E-22 | 1.32E-19 |
| SYNAPTIC SIGNALING | 424 | 363 | 0.8456 | 1.37E-20 | 9.20E-18 |
| CHROMOSOME ORGANIZATION | 1009 | 822 | 0.5468 | 1.32E-19 | 7.77E-17 |
| POLY A RNA BINDING | 1170 | 1061 | 0.4764 | 4.79E-19 | 2.25E-16 |
| MICROTUBULE CYTOSKELETON | 1068 | 945 | 0.5015 | 6.24E-19 | 2.67E-16 |
| CENTRAL NERVOUS SYSTEM DEVELOPMENT | 872 | 781 | 0.5486 | 7.24E-19 | 2.84E-16 |
| HALLMARK G2M CHECKPOINT | 200 | 192 | 1.1197 | 1.07E-18 | 3.89E-16 |
| CELL CYCLE | 1316 | 1163 | 0.4908 | 1.25E-18 | 4.21E-16 |
| NEURON PROJECTION | 942 | 865 | 0.5108 | 1.19E-18 | 4.38E-16 |
| MITOTIC CELL CYCLE | 766 | 704 | 0.5650 | 3.55E-18 | 1.05E-15 |
| AXON | 418 | 388 | 0.7507 | 4.04E-18 | 1.12E-15 |
| HEAD DEVELOPMENT | 703 | 643 | 0.5878 | 5.10E-18 | 1.34E-15 |
| CELL CYCLE PROCESS | 1081 | 949 | 0.4807 | 1.32E-17 | 3.10E-15 |
| HALLMARK MYC TARGETS V1 | 200 | 193 | 1.0503 | 6.86E-17 | 1.54E-14 |
| CYTOSKELETAL PART | 1436 | 1152 | 0.4257 | 1.11E-16 | 2.37E-14 |
| PRESYNAPSE | 283 | 262 | 0.8660 | 1.85E-16 | 3.79E-14 |
| HALLMARK E2F TARGETS | 200 | 192 | 1.0333 | 2.32E-16 | 4.37E-14 |
| MRNA METABOLIC PROCESS | 611 | 527 | 0.6132 | 2.53E-16 | 4.41E-14 |
| NEURON DIFFERENTIATION | 874 | 774 | 0.4972 | 3.69E-16 | 6.20E-14 |
| SOMATODENDRITIC COMPARTMENT | 650 | 597 | 0.5506 | 2.61E-15 | 4.23E-13 |
| AXON PART | 219 | 201 | 0.9290 | 9.68E-15 | 1.52E-12 |
| TUBULIN BINDING | 273 | 246 | 0.8333 | 3.35E-14 | 4.79E-12 |
| CELL PROJECTION PART | 946 | 830 | 0.4359 | 2.01E-13 | 2.48E-11 |
| CELL CELL SIGNALING | 767 | 611 | 0.5069 | 2.69E-13 | 3.17E-11 |
| NEUROTRANSMITTER TRANSPORT | 150 | 135 | 1.0997 | 2.96E-13 | 3.40E-11 |
| DENDRITE | 451 | 423 | 0.6067 | 3.06E-13 | 3.43E-11 |
| POSTSYNAPSE | 378 | 345 | 0.6697 | 3.75E-13 | 4.10E-11 |
| NUCLEAR TRANSCRIBED MRNA CATABOLIC PROCESS NONSENSE MEDIATED DECAY | 118 | 112 | 1.1978 | 6.82E-13 | 7.14E-11 |
| CHROMOSOME | 880 | 727 | 0.4571 | 7.25E-13 | 7.43E-11 |
| MODULATION OF SYNAPTIC TRANSMISSION | 301 | 275 | 0.7378 | 9.70E-13 | 9.21E-11 |
| MICROTUBULE | 405 | 361 | 0.6424 | 9.70E-13 | 9.21E-11 |
| CELL BODY | 494 | 449 | 0.5685 | 9.92E-13 | 9.21E-11 |
| SUPRAMOLECULAR FIBER | 670 | 481 | 0.5512 | 1.56E-12 | 1.42E-10 |
| MULTI ORGANISM METABOLIC PROCESS | 138 | 134 | 1.0629 | 1.82E-12 | 1.59E-10 |
| RNA SPLICING | 367 | 314 | 0.6679 | 4.49E-12 | 3.78E-10 |
| TRANSLATIONAL INITIATION | 146 | 136 | 0.9869 | 3.13E-11 | 2.44E-09 |
| REGULATION OF NERVOUS SYSTEM DEVELOPMENT | 750 | 689 | 0.4270 | 3.91E-11 | 2.79E-09 |
| EXCITATORY SYNAPSE | 197 | 189 | 0.8254 | 4.08E-11 | 2.86E-09 |
| RNA PROCESSING | 835 | 730 | 0.4188 | 4.21E-11 | 2.91E-09 |
| CELL CYCLE PHASE TRANSITION | 255 | 236 | 0.7344 | 4.41E-11 | 2.97E-09 |
| EXOCYTIC VESICLE MEMBRANE | 56 | 54 | 1.5615 | 4.78E-11 | 3.17E-09 |
| MICROTUBULE BINDING | 201 | 182 | 0.8382 | 4.88E-11 | 3.19E-09 |
| MICROTUBULE BASED PROCESS | 522 | 457 | 0.5242 | 5.14E-11 | 3.27E-09 |
| ESTABLISHMENT OF PROTEIN LOCALIZATION TO ENDOPLASMIC RETICULUM | 104 | 101 | 1.1298 | 9.49E-11 | 5.73E-09 |
| MRNA PROCESSING | 432 | 365 | 0.5635 | 2.67E-10 | 1.48E-08 |
| REGULATION OF CELL CYCLE PROCESS | 558 | 491 | 0.4858 | 2.76E-10 | 1.51E-08 |
| NEURON PROJECTION TERMINUS | 129 | 118 | 1.0034 | 3.47E-10 | 1.86E-08 |
| REGULATION OF NEUROTRANSMITTER LEVELS | 190 | 170 | 0.8245 | 3.90E-10 | 2.04E-08 |
| ORGANELLE FISSION | 496 | 418 | 0.5170 | 5.48E-10 | 2.77E-08 |
| CHROMATIN ORGANIZATION | 663 | 524 | 0.4624 | 5.47E-10 | 2.77E-08 |
| CENTROSOME | 487 | 438 | 0.5029 | 6.48E-10 | 3.25E-08 |
| MYELIN SHEATH | 168 | 162 | 0.8326 | 6.94E-10 | 3.44E-08 |
| PRESYNAPTIC PROCESS INVOLVED IN SYNAPTIC TRANSMISSION | 116 | 105 | 1.0479 | 7.08E-10 | 3.47E-08 |
| RIBONUCLEOPROTEIN COMPLEX | 721 | 654 | 0.4080 | 1.05E-09 | 5.05E-08 |
| NEURON DEVELOPMENT | 687 | 612 | 0.4104 | 1.16E-09 | 5.50E-08 |
| SIGNAL RELEASE | 171 | 149 | 0.8559 | 1.25E-09 | 5.87E-08 |
| REGULATION OF NEURON DIFFERENTIATION | 554 | 515 | 0.4446 | 1.99E-09 | 9.29E-08 |
| MICROTUBULE ORGANIZING CENTER | 623 | 554 | 0.4339 | 2.14E-09 | 9.86E-08 |
| CHROMOSOME SEGREGATION | 272 | 228 | 0.6666 | 3.56E-09 | 1.63E-07 |
| CELLULAR MACROMOLECULAR COMPLEX ASSEMBLY | 727 | 592 | 0.4130 | 3.88E-09 | 1.76E-07 |
| RNA SPLICING VIA TRANSESTERIFICATION REACTIONS | 267 | 240 | 0.6377 | 6.59E-09 | 2.93E-07 |
| REGULATION OF MICROTUBULE BASED PROCESS | 243 | 219 | 0.6646 | 7.88E-09 | 3.37E-07 |
| NITROGEN COMPOUND TRANSPORT | 507 | 416 | 0.4812 | 7.87E-09 | 3.37E-07 |
| SISTER CHROMATID SEGREGATION | 176 | 159 | 0.7779 | 1.01E-08 | 4.20E-07 |
| CELL CYCLE G2 M PHASE TRANSITION | 138 | 130 | 0.8638 | 1.03E-08 | 4.24E-07 |
| PROTEIN LOCALIZATION TO ENDOPLASMIC RETICULUM | 123 | 119 | 0.9005 | 1.26E-08 | 4.82E-07 |
| FOREBRAIN DEVELOPMENT | 357 | 327 | 0.5317 | 1.53E-08 | 6.00E-07 |
| NUCLEAR CHROMOSOME SEGREGATION | 228 | 189 | 0.7005 | 1.65E-08 | 6.42E-07 |
| MITOTIC NUCLEAR DIVISION | 361 | 331 | 0.5271 | 1.67E-08 | 6.44E-07 |
| SYNAPTIC MEMBRANE | 261 | 236 | 0.6192 | 2.25E-08 | 8.56E-07 |
| SPINDLE | 289 | 253 | 0.5932 | 2.86E-08 | 1.07E-06 |
| CYTOSOLIC RIBOSOME | 113 | 102 | 0.9418 | 3.68E-08 | 1.34E-06 |
| REGULATION OF EXOCYTOSIS | 186 | 162 | 0.7355 | 4.22E-08 | 1.52E-06 |
| ATPASE ACTIVITY | 427 | 385 | 0.4725 | 4.79E-08 | 1.70E-06 |
| HALLMARK MITOTIC SPINDLE | 200 | 199 | 0.8582 | 4.92E-08 | 1.73E-06 |
| CHROMOSOMAL REGION | 330 | 272 | 0.5548 | 7.10E-08 | 2.42E-06 |
| MIDBRAIN DEVELOPMENT | 90 | 79 | 1.0510 | 8.05E-08 | 2.71E-06 |
| CHROMATIN BINDING | 435 | 381 | 0.4664 | 8.26E-08 | 2.74E-06 |
| CYTOSOLIC LARGE RIBOSOMAL SUBUNIT | 61 | 56 | 1.2655 | 9.11E-08 | 3.00E-06 |
| REGULATION OF DENDRITE DEVELOPMENT | 120 | 114 | 0.8578 | 9.80E-08 | 3.20E-06 |
| CELL DIVISION | 460 | 424 | 0.4390 | 1.02E-07 | 3.32E-06 |
| CHROMATIN MODIFICATION | 539 | 461 | 0.4207 | 1.06E-07 | 3.43E-06 |
| CELL MORPHOGENESIS INVOLVED IN NEURON DIFFERENTIATION | 368 | 334 | 0.4837 | 1.06E-07 | 3.48E-06 |
| NEURON PROJECTION DEVELOPMENT | 545 | 492 | 0.4004 | 1.13E-07 | 3.59E-06 |
| SYNAPTIC VESICLE CYCLE | 90 | 79 | 1.0371 | 1.15E-07 | 3.64E-06 |
| NUCLEAR CHROMOSOME | 523 | 413 | 0.4422 | 1.26E-07 | 3.77E-06 |
| REGULATION OF MRNA SPLICING VIA SPLICEOSOME | 62 | 44 | 1.4332 | 1.30E-07 | 4.04E-06 |
| GLUTAMATE SECRETION | 28 | 28 | 1.8600 | 1.92E-07 | 5.87E-06 |
| NEURON PROJECTION MORPHOGENESIS | 402 | 364 | 0.4490 | 2.64E-07 | 7.82E-06 |
| LIMBIC SYSTEM DEVELOPMENT | 100 | 91 | 0.9171 | 3.89E-07 | 1.12E-05 |
| ORGANELLE LOCALIZATION | 415 | 372 | 0.4419 | 4.97E-07 | 1.41E-05 |
| HIPPOCAMPUS DEVELOPMENT | 73 | 67 | 1.0702 | 5.01E-07 | 1.41E-05 |
| REGULATION OF MRNA METABOLIC PROCESS | 118 | 95 | 0.8858 | 5.21E-07 | 1.45E-05 |
| PROTEIN TARGETING TO MEMBRANE | 157 | 151 | 0.6957 | 5.18E-07 | 1.45E-05 |
| GLUTAMATE RECEPTOR BINDING | 37 | 35 | 1.5434 | 5.38E-07 | 1.48E-05 |
| RNA CATABOLIC PROCESS | 227 | 208 | 0.5888 | 5.60E-07 | 1.53E-05 |
| REGULATION OF MICROTUBULE POLYMERIZATION OR DEPOLYMERIZATION | 178 | 161 | 0.6700 | 5.82E-07 | 1.58E-05 |
| CALCIUM ION REGULATED EXOCYTOSIS | 81 | 71 | 1.0280 | 6.16E-07 | 1.67E-05 |
| LOCOMOTORY BEHAVIOR | 181 | 158 | 0.6747 | 6.22E-07 | 1.67E-05 |
| REGULATION OF MITOTIC CELL CYCLE | 468 | 425 | 0.4073 | 7.39E-07 | 1.94E-05 |
| EXOCYTIC VESICLE | 142 | 134 | 0.7038 | 7.43E-07 | 1.94E-05 |
| DICARBOXYLIC ACID TRANSPORT | 71 | 64 | 1.0769 | 7.77E-07 | 2.02E-05 |
| TELENCEPHALON DEVELOPMENT | 238 | 216 | 0.5695 | 7.96E-07 | 2.07E-05 |
| ESTABLISHMENT OF PROTEIN LOCALIZATION TO ORGANELLE | 361 | 336 | 0.4552 | 8.42E-07 | 2.17E-05 |
| REGULATION OF CELLULAR PROTEIN CATABOLIC PROCESS | 274 | 261 | 0.5146 | 9.22E-07 | 2.36E-05 |
| CALMODULIN BINDING | 179 | 164 | 0.6466 | 1.10E-06 | 2.79E-05 |
| MITOTIC SISTER CHROMATID SEGREGATION | 91 | 82 | 0.9234 | 1.24E-06 | 3.10E-05 |
| SUBSTANTIA NIGRA DEVELOPMENT | 45 | 43 | 1.3154 | 1.26E-06 | 3.11E-05 |
| NEURON SPINE | 121 | 113 | 0.7793 | 1.26E-06 | 3.11E-05 |
| AMINO ACID TRANSPORT | 124 | 109 | 0.7918 | 1.35E-06 | 3.29E-05 |
| REGULATION OF PROTEIN CATABOLIC PROCESS | 393 | 373 | 0.4228 | 1.44E-06 | 3.47E-05 |
| PROTEIN DNA COMPLEX SUBUNIT ORGANIZATION | 229 | 158 | 0.6486 | 1.60E-06 | 3.85E-05 |
| REGULATION OF CALCIUM ION DEPENDENT EXOCYTOSIS | 86 | 70 | 0.9815 | 2.10E-06 | 4.84E-05 |
| REGULATION OF CHROMOSOME ORGANIZATION | 278 | 246 | 0.5118 | 2.12E-06 | 4.88E-05 |
| NEGATIVE REGULATION OF NERVOUS SYSTEM DEVELOPMENT | 262 | 246 | 0.4912 | 2.98E-06 | 6.60E-05 |
| MRNA BINDING | 335 | 131 | 0.6941 | 3.05E-06 | 6.67E-05 |
| POSITIVE REGULATION OF CELLULAR PROTEIN CATABOLIC PROCESS | 192 | 185 | 0.5787 | 3.41E-06 | 7.37E-05 |
| KINETOCHORE | 110 | 108 | 0.7628 | 3.44E-06 | 7.37E-05 |
| PROTEASOMAL PROTEIN CATABOLIC PROCESS | 271 | 261 | 0.4860 | 3.48E-06 | 7.39E-05 |
| POSTSYNAPTIC MEMBRANE | 205 | 182 | 0.5828 | 3.50E-06 | 7.39E-05 |
| PRESYNAPTIC ACTIVE ZONE | 29 | 28 | 1.6084 | 3.50E-06 | 7.39E-05 |
| MICROTUBULE CYTOSKELETON ORGANIZATION | 348 | 305 | 0.4455 | 4.25E-06 | 8.89E-05 |
| MICROTUBULE BASED MOVEMENT | 205 | 185 | 0.5720 | 4.38E-06 | 9.08E-05 |
| NUCLEAR EXPORT | 147 | 123 | 0.7009 | 4.95E-06 | 1.01E-04 |
| DNA CONFORMATION CHANGE | 273 | 198 | 0.5492 | 5.02E-06 | 1.01E-04 |
| REGULATION OF ESTABLISHMENT OF PLANAR POLARITY | 110 | 106 | 0.7562 | 5.07E-06 | 1.01E-04 |
| NEURAL NUCLEUS DEVELOPMENT | 66 | 61 | 1.0133 | 5.06E-06 | 1.01E-04 |
| NON CANONICAL WNT SIGNALING PATHWAY | 140 | 130 | 0.6798 | 5.18E-06 | 1.02E-04 |
| SINGLE ORGANISM BEHAVIOR | 384 | 328 | 0.4245 | 5.50E-06 | 1.07E-04 |
| EMBRYONIC ORGAN MORPHOGENESIS | 279 | 237 | 0.4970 | 6.09E-06 | 1.17E-04 |
| NEGATIVE REGULATION OF CELL DEVELOPMENT | 303 | 277 | 0.4475 | 6.30E-06 | 1.21E-04 |
| SWI SNF SUPERFAMILY TYPE COMPLEX | 71 | 69 | 0.9355 | 6.64E-06 | 1.27E-04 |
| EPHRIN RECEPTOR SIGNALING PATHWAY | 85 | 84 | 0.8424 | 6.72E-06 | 1.28E-04 |
| ACID SECRETION | 66 | 54 | 1.0620 | 7.37E-06 | 1.38E-04 |
| CHROMOSOME CENTROMERIC REGION | 174 | 158 | 0.6045 | 7.39E-06 | 1.38E-04 |
| REGULATION OF DENDRITE MORPHOGENESIS | 74 | 72 | 0.9052 | 8.12E-06 | 1.49E-04 |
| CENTRAL NERVOUS SYSTEM NEURON DIFFERENTIATION | 166 | 142 | 0.6341 | 8.48E-06 | 1.55E-04 |
| ANAPHASE PROMOTING COMPLEX DEPENDENT CATABOLIC PROCESS | 77 | 74 | 0.8886 | 8.78E-06 | 1.59E-04 |
| RIBONUCLEOPROTEIN COMPLEX LOCALIZATION | 118 | 97 | 0.7679 | 9.44E-06 | 1.70E-04 |
| NEURAL RETINA DEVELOPMENT | 50 | 42 | 1.2021 | 9.71E-06 | 1.74E-04 |
| REGULATION OF CELL CYCLE PHASE TRANSITION | 321 | 299 | 0.4290 | 1.14E-05 | 2.01E-04 |
| REGULATION OF PROTEASOMAL PROTEIN CATABOLIC PROCESS | 181 | 174 | 0.5588 | 1.33E-05 | 2.31E-04 |
| CONDENSED CHROMOSOME | 195 | 167 | 0.5698 | 1.36E-05 | 2.36E-04 |
| TERMINAL BOUTON | 64 | 59 | 0.9770 | 1.43E-05 | 2.45E-04 |
| SPLICEOSOMAL COMPLEX | 172 | 154 | 0.5907 | 1.51E-05 | 2.57E-04 |
| SYNAPTIC VESICLE LOCALIZATION | 106 | 95 | 0.7573 | 1.52E-05 | 2.58E-04 |
| NUCLEOSOME BINDING | 45 | 43 | 1.1564 | 1.54E-05 | 2.60E-04 |
| UBIQUITIN LIKE PROTEIN LIGASE BINDING | 264 | 249 | 0.4629 | 1.54E-05 | 2.60E-04 |
| OLIGODENDROCYTE DIFFERENTIATION | 60 | 57 | 0.9881 | 1.64E-05 | 2.74E-04 |
| NUCLEAR SPECK | 194 | 171 | 0.5554 | 1.77E-05 | 2.92E-04 |
| METENCEPHALON DEVELOPMENT | 100 | 93 | 0.7589 | 1.78E-05 | 2.93E-04 |
| REGULATION OF CELL DIVISION | 272 | 225 | 0.4831 | 1.80E-05 | 2.95E-04 |
| REGULATION OF ALTERNATIVE MRNA SPLICING VIA SPLICEOSOME | 35 | 25 | 1.5614 | 1.88E-05 | 3.07E-04 |
| HISTONE BINDING | 177 | 139 | 0.6146 | 1.91E-05 | 3.10E-04 |
| EAR DEVELOPMENT | 195 | 173 | 0.5495 | 1.93E-05 | 3.12E-04 |
| NEURONAL POSTSYNAPTIC DENSITY | 53 | 51 | 1.0379 | 1.99E-05 | 3.20E-04 |
| REGULATION OF LIGASE ACTIVITY | 130 | 120 | 0.6608 | 2.02E-05 | 3.24E-04 |
| REGULATION OF LONG TERM SYNAPTIC POTENTIATION | 19 | 19 | 1.8437 | 2.03E-05 | 3.24E-04 |
| ORGANIC ACID TRANSPORT | 261 | 211 | 0.4949 | 2.10E-05 | 3.34E-04 |
| REGULATION OF SYNAPTIC PLASTICITY | 140 | 135 | 0.6184 | 2.25E-05 | 3.56E-04 |
| HINDBRAIN DEVELOPMENT | 137 | 125 | 0.6427 | 2.26E-05 | 3.60E-04 |
| MICROTUBULE ASSOCIATED COMPLEX | 145 | 134 | 0.6195 | 2.34E-05 | 3.66E-04 |
| NEURON NEURON SYNAPTIC TRANSMISSION | 56 | 48 | 1.0608 | 2.41E-05 | 3.74E-04 |
| SPINAL CORD DEVELOPMENT | 106 | 87 | 0.7714 | 2.50E-05 | 3.86E-04 |
| PALLIUM DEVELOPMENT | 153 | 142 | 0.5973 | 2.64E-05 | 4.02E-04 |
| PRESYNAPTIC MEMBRANE | 55 | 54 | 0.9884 | 2.71E-05 | 4.12E-04 |
| MICROTUBULE MOTOR ACTIVITY | 77 | 68 | 0.8734 | 2.74E-05 | 4.15E-04 |
| PHOSPHATASE REGULATOR ACTIVITY | 87 | 74 | 0.8339 | 2.83E-05 | 4.26E-04 |
| REGULATION OF RNA STABILITY | 139 | 131 | 0.6196 | 2.87E-05 | 4.30E-04 |
| REGULATION OF SYNAPSE STRUCTURE OR ACTIVITY | 232 | 216 | 0.4803 | 2.92E-05 | 4.36E-04 |
| REGULATION OF RNA SPLICING | 97 | 72 | 0.8439 | 2.95E-05 | 4.39E-04 |
| L AMINO ACID TRANSPORT | 58 | 49 | 1.0361 | 2.98E-05 | 4.41E-04 |
| CATALYTIC STEP 2 SPLICEOSOME | 89 | 86 | 0.7665 | 3.11E-05 | 4.59E-04 |
| RNA LOCALIZATION | 185 | 157 | 0.5621 | 3.14E-05 | 4.62E-04 |
| METHYLTRANSFERASE COMPLEX | 90 | 79 | 0.7943 | 3.62E-05 | 5.27E-04 |
| REGULATION OF PROTEIN COMPLEX DISASSEMBLY | 217 | 195 | 0.4977 | 3.87E-05 | 5.63E-04 |
| L AMINO ACID TRANSMEMBRANE TRANSPORTER ACTIVITY | 54 | 45 | 1.0854 | 4.04E-05 | 5.83E-04 |
| REGULATION OF PROTEIN UBIQUITINATION INVOLVED IN UBIQUITIN DEPENDENT PR | 103 | 98 | 0.7045 | 4.13E-05 | 5.95E-04 |
| MOTOR ACTIVITY | 131 | 113 | 0.6531 | 4.30E-05 | 6.15E-04 |
| POSITIVE REGULATION OF LIGASE ACTIVITY | 110 | 101 | 0.6888 | 4.64E-05 | 6.58E-04 |
| SPINDLE CHECKPOINT | 25 | 24 | 1.5042 | 4.83E-05 | 6.77E-04 |
| NUCLEOBASE CONTAINING COMPOUND TRANSPORT | 199 | 168 | 0.5280 | 5.11E-05 | 7.07E-04 |
| KINESIN COMPLEX | 55 | 50 | 0.9892 | 5.31E-05 | 7.31E-04 |
| NUCLEOSOMAL DNA BINDING | 30 | 29 | 1.3359 | 5.44E-05 | 7.41E-04 |
| SPINDLE MICROTUBULE | 58 | 56 | 0.9289 | 5.50E-05 | 7.44E-04 |
| ADULT BEHAVIOR | 135 | 114 | 0.6386 | 5.80E-05 | 7.73E-04 |
| DNA PACKAGING | 194 | 121 | 0.6174 | 6.11E-05 | 8.13E-04 |
| REGIONALIZATION | 311 | 255 | 0.4226 | 6.32E-05 | 8.37E-04 |
| RIBOSOMAL SUBUNIT | 163 | 153 | 0.5462 | 6.41E-05 | 8.45E-04 |
| NEGATIVE REGULATION OF GLIOGENESIS | 37 | 32 | 1.2443 | 6.81E-05 | 8.93E-04 |
| PEPTIDYL LYSINE MODIFICATION | 312 | 269 | 0.4085 | 7.13E-05 | 9.33E-04 |
| PERIKARYON | 108 | 95 | 0.6922 | 7.20E-05 | 9.39E-04 |
| REGULATION OF RAS PROTEIN SIGNAL TRANSDUCTION | 184 | 169 | 0.5145 | 7.48E-05 | 9.64E-04 |
| SISTER CHROMATID COHESION | 111 | 101 | 0.6682 | 7.64E-05 | 9.81E-04 |