**Supplemental Table 4A**. Results of the similarity search for analogous protein sequences (blastp) for female de novo assembled transcripts and protein annotation (i.e., Molecular function and Biological process) from Uniprot database. Data only shows the most significant hits (<0.001).

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **No.**  | **Category** | **qaccver** | **saccver** | **pident** | **length** | **evalue** | **bitscore** | **Protein** | **Molecular Function** | **Biological Process** |
| 1 | Cell cycle and division | TRINITY\_DN15375\_c0\_g2\_i1 | sp|Q3TZI6|CCNJ\_MOUSE | 46.1 | 254 | 3.59E-68 | 227 | Cyclin-J | Cyclin-dependent protein serine/threonine kinase regulator activity | mitotic cell cycle phase transition |
| 2 | TRINITY\_DN6454\_c0\_g1\_i1 | sp|Q6I6F4|BIRC5\_FELCA | 45.2 | 126 | 7.14E-32 | 117 | Baculoviral IAP repeat-containing protein 5 | cysteine-type endopeptidase inhibitor activitycysteine-type endopeptidase inhibitor activity involved in apoptotic processmicrotubule bindingprotein homodimerization activitytubulin bindingzinc ion binding | apoptotic processcell divisionchromosome segregationestablishment of chromosome localizationG2/M transition of mitotic cell cyclemeiosis Imicrotubule cytoskeleton organizationmitotic cytokinesismitotic spindle assembly checkpoint signalingnegative regulation of apoptotic processnegative regulation of cysteine-type endopeptidase activity involved in apoptotic processnegative regulation of DNA-templated transcriptionnegative regulation of neuron apoptotic processpositive regulation of exit from mitosispositive regulation of mitotic cell cycleprotein phosphorylation |
| 3 | TRINITY\_DN1115\_c0\_g1\_i4 | sp|Q91879|CKS2\_XENLA | 70.3 | 74 | 1.05E-30 | 108 | Cyclin-dependent kinases regulatory subunit 2 | cyclin-dependent protein serine/threonine kinase regulator activity | Cell cycleCell division |
| 4 | TRINITY\_DN3478\_c0\_g1\_i1 | sp|P39963|CCNB3\_CHICK | 45 | 407 | 3.41E-95 | 300 | G2/mitotic-specific cyclin-B3 | cyclin-dependent protein serine/threonine kinase regulator activity | cell divisionmitotic cell cycle phase transition |
| 5 | TRINITY\_DN103939\_c0\_g1\_i7 | sp|P51954|NEK1\_MOUSE | 50.2 | 267 | 3.69E-80 | 281 | Serine/threonine-protein kinase Nek1 | 14-3-3 protein bindingATP bindingkinase activitymetal ion bindingprotein kinase activityprotein serine kinase activityprotein serine/threonine kinase activityprotein tyrosine kinase activity | cell cyclecell divisioncilium assemblyDNA damage responsekidney developmentmulticellular organism growthphosphorylationregulation of DNA damage checkpointresponse to ionizing radiationspermatogenesis |
| 6 | TRINITY\_DN4929\_c1\_g1\_i2 | sp|Q99741|CDC6\_HUMAN | 51.7 | 408 | 2.18E-136 | 419 | Cell division control protein 6 homolog | ATP bindingATP hydrolysis activitykinase bindingnucleotide binding  | cell divisioncellular response to angiotensincellular response to vasopressinDNA replication checkpoint signalingDNA replication initiationmitotic DNA replication checkpoint signalingnegative regulation of cell population proliferationnegative regulation of DNA replicationpositive regulation of chromosome segregationpositive regulation of cytokinesispositive regulation of fibroblast proliferationregulation of cyclin-dependent protein serine/threonine kinase activityregulation of mitotic metaphase/anaphase transitiontraversing start control point of mitotic cell cycle |
| 7 | TRINITY\_DN6986\_c0\_g1\_i1 | sp|P24861|CCNA\_PATVU | 49.2 | 419 | 4.65E-106 | 330 | G2/mitotic-specific cyclin-A | cyclin-dependent protein serine/threonine kinase regulator activity | cell divisionmitotic cell cycle phase transition |
| 8 | TRINITY\_DN726\_c0\_g1\_i1 | sp|P15206|CCNB\_MARGL | 46.8 | 391 | 2.13E-94 | 305 | G2/mitotic-specific cyclin-B | cyclin-dependent protein serine/threonine kinase regulator activity | cell divisionmitotic cell cycle phase transition |
| 9 | TRINITY\_DN992\_c0\_g1\_i3 | sp|P24862|CCNB\_PATVU | 41 | 402 | 2.34E-86 | 280 | G2/mitotic-specific cyclin-B | cyclin-dependent protein serine/threonine kinase regulator activity | cell divisionmitotic cell cycle phase transition |
| 10 | TRINITY\_DN4520\_c0\_g1\_i2 | sp|P15206|CCNB\_MARGL | 44.3 | 393 | 3.34E-82 | 266 | G2/mitotic-specific cyclin-B | cyclin-dependent protein serine/threonine kinase regulator activity | cell divisionmitotic cell cycle phase transition |
| 11 | TRINITY\_DN5786\_c0\_g1\_i1 | sp|P23437|CDK2\_XENLA | 73.6 | 295 | 1.99E-160 | 458 | Cyclin-dependent kinase 2 | ATP bindingcyclin-dependent protein kinase activitycyclin-dependent protein serine/threonine kinase activityprotein serine kinase activity | cell cyclecell divisionprotein phosphorylation |
| 12 | TRINITY\_DN47850\_c0\_g1\_i1 | sp|P56616|UBE2C\_XENLA | 65.1 | 175 | 1.45E-71 | 226 | Ubiquitin-conjugating enzyme E2 C | ATP bindingubiquitin conjugating enzyme activity | anaphase-promoting complex-dependent catabolic processcell divisionexit from mitosisfree ubiquitin chain polymerizationprotein K-linked ubiquitinationubiquitin-dependent protein catabolic process |
| 13 | TRINITY\_DN30869\_c0\_g2\_i1 | sp|E7F6T8|UBP37\_DANRE | 27.3 | 722 | 1.07E-48 | 191 | Ubiquitin carboxyl-terminal hydrolase 37 | cysteine-type deubiquitinase activitycysteine-type endopeptidase activity | cell divisioncentral nervous system morphogenesiscranial skeletal system developmentG/S transition of mitotic cell cycleprotein K-linked deubiquitinationprotein K48-linked deubiquitination |
| 14 | TRINITY\_DN6947\_c0\_g1\_i1 | sp|Q7ZUY3|H2AX\_DANRE | 73.9 | 142 | 1.57E-62 | 198 | Histone H2AX | DNA bindingprotein heterodimerization activitystructural constituent of chromatin | DNA damage responseDNA recombinationDNA repairmeiotic cell cycle |
| 15 | TRINITY\_DN33062\_c0\_g1\_i1 | sp|Q9I9A7|CDT1\_XENLA | 40.2 | 391 | 1.22E-68 | 240 | DNA replication factor Cdt1 | chromatin DNA binding | DNA replication preinitiation complex assemblyregulation of DNA-templated DNA replication initiationterPro |
| 16 | TRINITY\_DN9140\_c0\_g1\_i1 | sp|A6H8I0|UBP22\_DANRE | 57.5 | 534 | 2.38E-208 | 596 | Ubiquitin carboxyl-terminal hydrolase 22 | cysteine-type deubiquitinase activityzinc ion binding | cell cyclechromatin organizationproteolysis |
| 17 | TRINITY\_DN48905\_c0\_g1\_i10 | sp|D3Z3K2|CIP1\_MOUSE | 45.8 | 179 | 4.29E-44 | 159 | E3 ubiquitin-protein ligase CCNB1IP1 | identical protein bindingmetal ion bindingubiquitin protein ligase activityubiquitin-protein transferase activity | blastocyst formationchiasma assemblyprotein ubiquitinationreciprocal meiotic recombinationspermatid developmen |
| 18 | TRINITY\_DN5533\_c0\_g1\_i5 | sp|Q9GRC0|MOS\_PATPE | 45.3 | 267 | 1.81E-69 | 231 | Serine/threonine-protein kinase mos | ATP bindingMAP kinase kinase kinase activityprotein serine kinase activity | female gamete generationfemale meiosis IInegative regulation of mitotic cell cyclephosphorylation |
| 19 | TRINITY\_DN6145\_c1\_g2\_i3 | sp|Q8N9W6|BOLL\_HUMAN | 43.7 | 87 | 1.50E-12 | 71.2 | Protein boule-like | identical protein bindingmRNA 3'-UTR bindingtranslation activator activity | 3'-UTR-mediated mRNA stabilizationcell differentiationmeiotic cell cyclepositive regulation of translational initiationspermatogenesis |
| 20 | TRINITY\_DN11811\_c0\_g1\_i1 | sp|P30740|ILEU\_HUMAN | 42.6 | 296 | 3.20E-73 | 238 | Leukocyte elastase inhibitor | peptidase inhibitor activityserine-type endopeptidase inhibitor activitySerine protease inhibitor | negative regulation of endopeptidase activitynegative regulation of interleukin- beta productiontype B pancreatic cell proliferation |
| 21 | Metabolism and transport | TRINITY\_DN10917\_c0\_g1\_i2 | sp|Q21565|AMT3\_CAEEL | 50.8 | 303 | 6.59E-87 | 291 | Putative ammonium transporter 3 | ammonium transmembrane transporter activity | Ammonium homeostasis Ammonium transmembrane transport |
| 21 | TRINITY\_DN7661\_c0\_g2\_i3 | sp|P54147|Y108\_SYNY3 | 39.8 | 88 | 2.46E-09 | 60.8 | Putative ammonium transporter sll0108 | ammonium transmembrane transporter activity | Ammonium homeostasis Ammonium transmembrane transport |
| 23 | TRINITY\_DN2969\_c2\_g1\_i10 | sp|P12259|FA5\_HUMAN | 39.3 | 150 | 1.28E-20 | 90.9 | Coagulation factor V | copper ion binding | blood circulationblood coagulationresponse to vitamin K |
| 24 | TRINITY\_DN61746\_c0\_g1\_i5 | sp|Q9TU53|CUBN\_CANLF | 53.1 | 32 | 7.35E-05 | 44.3 | Cubilin | calcium ion bindingcobalamin binding | Cholesterol metabolic processprotein transport |
| 25 | TRINITY\_DN12587\_c0\_g1\_i1 | sp|Q1W694|B1Q\_LOXIN | 37 | 289 | 1.45E-57 | 191 | Dermonecrotic toxin LiSicTox-betaID1 | phospholipase activityphosphoric diester hydrolase activitytoxin activity | envenomation resulting in induction of edema in another organismkilling of cells of another organismlipid catabolic processphospholipid metabolic process |
| 26 | TRINITY\_DN7586\_c0\_g1\_i1 | sp|Q98SN9|S61A1\_ONCMY | 80.4 | 51 | 3.06E-23 | 94.7 | Protein transport protein Sec61 subunit alpha isoform A | Developmental protein | pronephric nephron developmentprotein targeting to ER |
| 27 | TRINITY\_DN392408\_c0\_g1\_i1 | sp|P97329|KI20A\_MOUSE | 49.6 | 127 | 6.05E-37 | 137 | Kinesin-like protein KIF20A | ATP bindingATP hydrolysis activitymicrotubule bindingmicrotubule motor activityprotein kinase binding | microtubule bundle formationmicrotubule-based movementmidbody abscissionmitotic cytokinesisprotein transportregulation of cytokinesis |
| 28 | TRINITY\_DN4578\_c0\_g1\_i1 | sp|O35343|IMA3\_MOUSE | 59.2 | 530 | 4.92E-99 | 318 | Importin subunit alpha-3 | nuclear import signal receptor activitynuclear localization sequence binding | dopamine secretiongene expressionNLS-bearing protein import into nucleusprotein import into nucleusresponse to hydrogen peroxide |
| 29 | TRINITY\_DN29796\_c0\_g1\_i1 | sp|P97852|DHB4\_RAT | 41.3 | 126 | 1.69E-24 | 101 | Peroxisomal multifunctional enzyme type | enoyl-CoA hydratase activityestradiol 17-beta-dehydrogenase [NAD(P)] activityidentical protein bindingisomerase activityprotein homodimerization activitytestosterone dehydrogenase [NAD(P)] activity | androgen metabolic processcellular response to organic cyclic compoundcholesterol metabolic processestrogen metabolic processfatty acid beta-oxidationmedium-chain fatty-acyl-CoA metabolic processresponse to organic cyclic compoundresponse to steroid hormoneresponse to xenobiotic stimulusSertoli cell developmentvery long-chain fatty acid metabolic processvery long-chain fatty-acyl-CoA metabolic process |
| 30 | TRINITY\_DN13209\_c0\_g1\_i5 | sp|Q7Z020|TRPA1\_DROME | 24.3 | 321 | 1.57E-05 | 53.1 | Transient receptor potential cation channel subfamily A member 1 | calcium channel activityligand-gated monoatomic ion channel activitymonoatomic cation channel activitytemperature-gated cation channel activity | calcium ion transportcellular response to heatdetection of chemical stimulus involved in sensory perception of bitter tastedetection of chemical stimulus involved in sensory perception of paindetection of temperature stimulus involved in sensory perception of paindetection of temperature stimulus involved in thermoceptionmechanosensory behaviormonoatomic cation transportnegative phototaxisneuronal signal transductionphototransductionpositive regulation of calcium-mediated signalingresponse to heatresponse to light stimulustemperature compensation of the circadian clockthermosensory behaviorthermotaxis |
| 31 | TRINITY\_DN7778\_c0\_g1\_i1 | sp|I6V1W0|BMBL\_DANRE | 36.5 | 384 | 3.02E-72 | 248 | Protein brambleberry |  | karyomere membrane fusionpronuclear fusion |
| 32 | TRINITY\_DN48658\_c0\_g1\_i1 | sp|Q8C5H1|ANO4\_MOUSE | 37 | 864 | 1.25E-154 | 484 | Anoctamin-4 | chloride channel activityphospholipid scramblase activityprotein dimerization activity | calcium activated galactosylceramide scramblingcalcium activated phosphatidylcholine scramblingcalcium activated phosphatidylserine scramblingchloride transmembrane transportchloride transportestablishment of localization in cell |
| 33 | TRINITY\_DN12942\_c1\_g1\_i7 | sp|Q8CFM6|STAB2\_RAT | 54.5 | 44 | 2.51E-04 | 47.4 | Stabilin-2 | calcium ion bindingcargo receptor activityhyaluronic acid bindinglow-density lipoprotein particle bindinglow-density lipoprotein particle receptor activity | cell adhesiondefense response to bacteriumdefense response to Gram-positive bacteriumendocytosishyaluronan catabolic processreceptor-mediated endocytosis |
| 34 | TRINITY\_DN6840\_c0\_g1\_i1 | sp|Q98930|SORL\_CHICK | 55.3 | 38 | 2.07E-05 | 53.1 | Sortilin-related receptor | Receptor | endocytosispost-Golgi vesicle-mediated transportprotein retention in Golgi apparatusprotein targetingprotein targeting to lysosome |
| 35 | TRINITY\_DN3270\_c0\_g1\_i1 | sp|O93477|SAHHB\_XENLA | 78.4 | 125 | 4.34E-64 | 203 | Adenosylhomocysteinase B | adenosylhomocysteinase activityNAD binding | One-carbon metabolism |
| 36 | TRINITY\_DN5075\_c0\_g1\_i6 | sp|P15870|H1D\_STRPU | 41.3 | 104 | 1.90E-09 | 60.5 | Histone H1-delta | double-stranded DNA bindingnucleosomal DNA bindingstructural constituent of chromatin | chromosome condensationnegative regulation of DNA recombinationnucleosome assembly |
| 37 | Genetic Processes | TRINITY\_DN21245\_c0\_g1\_i2 | sp|P35061|H2A\_ACRFO | 89.5 | 124 | 3.70E-67 | 217 | Histone H2A | DNA bindingprotein heterodimerization activitystructural constituent of chromatin |  |
| 38 | TRINITY\_DN25744\_c0\_g1\_i5 | sp|P31509|ESCA\_CRYAO | 55.6 | 27 | 1.72E-04 | 42 | Escargot/snail protein homolog | DNA bindingmetal ion binding |  |
| 39 | TRINITY\_DN23865\_c0\_g1\_i1 | sp|Q9I8B3|RB24B\_XENLA | 46.9 | 143 | 2.13E-31 | 124 | RNA-binding protein 24-B | mRNA 3'-UTR AU-rich region bindingmRNA 3'-UTR bindingmRNA CDS bindingpre-mRNA intronic bindingsequence-specific mRNA binding | 3'-UTR-mediated mRNA destabilizationcell differentiationDNA damage responsemRNA destabilizationmRNA processingmRNA stabilizationnegative regulation of cytoplasmic translationpositive regulation of 3'-UTR-mediated mRNA stabilizationpositive regulation of myoblast differentiationpositive regulation of myotube differentiationpositive regulation of skeletal muscle fiber differentiationpositive regulation of stem cell differentiationregulation of alternative mRNA splicing, via spliceosomeregulation of mRNA stabilityregulation of myotube differentiationRNA splicing |
| 40 | TRINITY\_DN8472\_c0\_g1\_i3 | sp|Q803U7|EXO1\_DANRE | 50.1 | 347 | 5.50E-91 | 311 | Exonuclease 1 | 5'-3' DNA exonuclease activity5'-flap endonuclease activityDNA bindingflap endonuclease activitymetal ion bindingsingle-stranded DNA 5'-3' DNA exonuclease activity | DNA recombinationmismatch repair |
| 41 | TRINITY\_DN10744\_c0\_g1\_i3 | sp|Q1ZZU3|SWI5\_HUMAN | 54.1 | 74 | 2.49E-14 | 73.9 | DNA repair protein SWI5 homolog |  | cellular response to ionizing radiationdouble-strand break repair via homologous recombination |
| 42 | TRINITY\_DN4236\_c0\_g1\_i1 | sp|P04047|KITH\_CHICK | 62.8 | 191 | 3.08E-80 | 252 | Thymidine kinase, cytosolic | ATP bindingidentical protein bindingthymidine kinase activityzinc ion binding | DNA biosynthetic processphosphorylationprotein homotetramerizationthymidine metabolic process |
| 43 | TRINITY\_DN10913\_c0\_g1\_i15 | sp|O00142|KITM\_HUMAN | 49.3 | 209 | 2.29E-66 | 216 | Thymidine kinase 2, mitochondrial | ATP bindingdeoxycytidine kinase activitydeoxynucleoside kinase activitynucleoside kinase activitythymidine kinase activity | deoxycytidine metabolic processDNA biosynthetic processnucleobase-containing compound metabolic processphosphorylationpyrimidine nucleoside salvagethymidine metabolic process |
| 44 | TRINITY\_DN6819\_c0\_g1\_i1 | sp|Q14493|SLBP\_HUMAN | 38.2 | 207 | 9.16E-25 | 106 | Histone RNA hairpin-binding protein | histone pre-mRNA DCP bindinghistone pre-mRNA stem-loop bindingidentical protein bindingmRNA bindingRNA binding | cap-dependent translational initiationmRNA 3'-end processing by stem-loop binding and cleavagemRNA transport |
| 45 | TRINITY\_DN3881\_c0\_g1\_i1 | sp|Q9WV03|FA50A\_MOUSE | 70.7 | 41 | 7.54E-09 | 54.3 | Protein FAM50A |  | chromatin organizationmRNA processingSregulation of RNA splicingRNA splicing |
| 46 | TRINITY\_DN42270\_c0\_g1\_i1 | sp|Q0VDT2|ZN367\_MOUSE | 50.7 | 229 | 1.37E-30 | 126 | Zinc finger protein 367 | DNA-binding transcription factor activityDNA-binding transcription factor activity, RNA polymerase II-specificmetal ion bindingRNA polymerase II cis-regulatory region sequence-specific DNA binding | regulation of transcription by RNA polymerase II |
| 47 | TRINITY\_DN12746\_c0\_g1\_i1 | sp|Q18248|DMD4\_CAEEL | 34.3 | 178 | 7.39E-20 | 92.4 | Doublesex- and mab-3-related transcription factor dmd-4 |  Function DNA-binding transcription factor activity, RNA polymerase II-specificmetal ion bindingRNA polymerase II cis-regulatory region sequence-specific DNA bindingubiquitin binding | regulation of transcription by RNA polymerase IIsex differentiationsynapse pruning |
| 48 | TRINITY\_DN14879\_c0\_g1\_i8 | sp|Q9GKU5|HDA11\_MACFA | 64.1 | 323 | 7.25E-153 | 441 | Histone deacetylase 11 | DNA-binding transcription factor bindinghistone deacetylase activity | Chromatin organization |
| 49 | TRINITY\_DN16128\_c1\_g1\_i6 | sp|Q9QYE3|BC11A\_MOUSE | 60.7 | 28 | 1.64E-05 | 46.2 | B-cell lymphoma/leukemia 11A | DNA-binding transcription factor activityDNA-binding transcription factor bindingDNA-binding transcription repressor activity, RNA polymerase II-specificmetal ion bindingprotein heterodimerization activityprotein homodimerization activityprotein kinase bindingRNA polymerase II cis-regulatory region sequence-specific DNA bindingtranscription coregulator activitytranscription corepressor activitytranscription regulatory region nucleic acid binding | B cell differentiationgene expressionnegative regulation of branching morphogenesis of a nervenegative regulation of collateral sproutingnegative regulation of dendrite developmentnegative regulation of dendrite extensionnegative regulation of gene expressionnegative regulation of neuron projection developmentnegative regulation of neuron remodelingnegative regulation of transcription by RNA polymerase IIpositive regulation of collateral sproutingpositive regulation of gene expressionpositive regulation of neuron projection developmentprotein sumoylationregulation of dendrite developmentregulation of transcription by RNA polymerase IIT cell differentiation |
| 50 | TRINITY\_DN3080\_c1\_g1\_i9 | sp|Q9QYE3|BC11A\_MOUSE | 58.6 | 29 | 1.03E-04 | 45.8 | B-cell lymphoma/leukemia 11A | DNA-binding transcription factor activityDNA-binding transcription factor bindingDNA-binding transcription repressor activity, RNA polymerase II-specificmetal ion bindingprotein heterodimerization activityprotein homodimerization activityprotein kinase bindingRNA polymerase II cis-regulatory region sequence-specific DNA bindingtranscription coregulator activitytranscription corepressor activitytranscription regulatory region nucleic acid binding | B cell differentiationgene expressionnegative regulation of branching morphogenesis of a nervenegative regulation of collateral sproutingnegative regulation of dendrite developmentnegative regulation of dendrite extensionnegative regulation of gene expressionnegative regulation of neuron projection developmentnegative regulation of neuron remodelingnegative regulation of transcription by RNA polymerase IIpositive regulation of collateral sproutingpositive regulation of gene expressionpositive regulation of neuron projection developmentprotein sumoylationregulation of dendrite developmentregulation of transcription by RNA polymerase IIT cell differentiation |
| 51 | TRINITY\_DN353237\_c0\_g1\_i1 | sp|O01727|RS6\_BRAFL | 91.2 | 68 | 6.96E-38 | 128 | Small ribosomal subunit protein eS6 | structural constituent of ribosome | translation |
| 52 | TRINITY\_DN26128\_c1\_g1\_i1 | sp|Q3ZBH8|RS20\_BOVIN | 92.5 | 67 | 3.31E-38 | 125 | Small ribosomal subunit protein uS10 | MDM2/MDM4 family protein bindingRNA bindingstructural constituent of ribosomeubiquitin ligase inhibitor activity | positive regulation of signal transduction by p53 class mediatortranslation |
| 53 | TRINITY\_DN17267\_c5\_g1\_i1 | sp|Q90YU9|RL18A\_ICTPU | 71.4 | 28 | 2.58E-07 | 48.5 | Large ribosomal subunit protein eL20 | structural constituent of ribosome | translation |
| 54 | Cell Signaling and Response | TRINITY\_DN1441\_c0\_g1\_i1 | sp|P08419|CEL2A\_PIG | 45.3 | 247 | 4.05E-54 | 193 | Chymotrypsin-like elastase family member 2A | endopeptidase activityserine-type endopeptidase activity | Insulin catabolic processproteolysisregulation of insulin secretionregulation of platelet aggregationresponse to insulin |
| 55 | TRINITY\_DN16152\_c0\_g1\_i2 | sp|Q28295|VWF\_CANLF | 30.4 | 368 | 7.45E-40 | 157 | von Willebrand factor | collagen bindingidentical protein bindingimmunoglobulin bindingintegrin bindingprotease bindingprotein-folding chaperone binding | blood coagulationcell adhesioncell-substrate adhesionhemostasisplatelet activation |
| 56 | TRINITY\_DN42156\_c0\_g1\_i7 | sp|P80012|VWF\_BOVIN | 32.1 | 140 | 4.26E-15 | 74.7 | von Willebrand factor | collagen bindingidentical protein bindingimmunoglobulin bindingintegrin bindingprotease bindingprotein-folding chaperone binding | blood coagulationcell adhesioncell-substrate adhesionhemostasisplatelet activation |
| 57 | TRINITY\_DN73988\_c0\_g1\_i5 | sp|O43854|EDIL3\_HUMAN | 34.9 | 106 | 4.23E-19 | 84.3 | EGF-like repeat and discoidin I-like domain-containing protein 3 | calcium ion bindingintegrin binding | cell adhesionpositive regulation of cell-substrate adhesion |
| 58 | TRINITY\_DN70086\_c0\_g1\_i6 | sp|O35474|EDIL3\_MOUSE | 38.9 | 149 | 1.22E-19 | 87.8 | EGF-like repeat and discoidin I-like domain-containing protein 3 | calcium ion binding | cell adhesionpositive regulation of cell-substrate adhesion |
| 59 | TRINITY\_DN30556\_c0\_g1\_i2 | sp|O43854|EDIL3\_HUMAN | 37.8 | 74 | 6.99E-11 | 64.7 | EGF-like repeat and discoidin I-like domain-containing protein 3 | calcium ion bindingintegrin binding | cell adhesionpositive regulation of cell-substrate adhesion |
| 60 | TRINITY\_DN29716\_c0\_g1\_i1 | sp|Q96HU8|DIRA2\_HUMAN | 40.3 | 191 | 6.65E-30 | 119 | GTP-binding protein | GTP-bindingNucleotide-binding | Signal transduction |
| 61 | TRINITY\_DN16376\_c0\_g1\_i6 | sp|P78504|JAG1\_HUMAN | 51.3 | 39 | 2.04E-07 | 57 | Protein jagged-1 | calcium ion bindinggrowth factor activity1 molecular adaptor activityNotch binding1 phospholipid bindingstructural molecule activity | angiogenesis aorta morphogenesisaortic valve morphogenesisblood vessel remodelingcardiac neural crest cell development involved in outflow tract morphogenesiscardiac right ventricle morphogenesiscardiac septum morphogenesiscell fate determination ciliary body morphogenesisdistal tubule developmentendocardial cushion cell developmentendothelial cell differentiation hemopoiesis inhibition of neuroepithelial cell differentiationinner ear auditory receptor cell differentiationkeratinocyte differentiation loop of Henle developmentmorphogenesis of an epithelial sheetmyoblast differentiation negative regulation of cell migration negative regulation of cell-cell adhesionnegative regulation of cell-matrix adhesion negative regulation of endothelial cell differentiationnegative regulation of fat cell differentiationnegative regulation of neuron differentiationnegative regulation of stem cell differentiation nephron developmentnervous system development neuroendocrine cell differentiationneuronal stem cell population maintenanceNotch signaling involved in heart developmentSource:BHF-UCLNotch signaling pathwaypodocyte developmentpositive regulation of cardiac epithelial to mesenchymal transitionSource:BHF-UCLpositive regulation of myeloid cell differentiationSource:Ensemblpositive regulation of Notch signaling pathwaypositive regulation of osteoblast differentiationSource:Ensemblpositive regulation of transcription by RNA polymerase IISource:BHF-UCLpulmonary artery morphogenesisSource:BHF-UCLpulmonary valve morphogenesisSource:BHF-UCL2sregulation of cell population proliferationregulation of epithelial cell proliferationSource:Ensemblregulation of reproductive processSource:Ensemblresponse to muramyl dipeptideSource:EnsemblT cell mediated immunity |
| 62 | TRINITY\_DN5741\_c1\_g1\_i2 | sp|Q29RU2|OIT3\_BOVIN | 43.1 | 123 | 1.89E-20 | 99.4 | Oncoprotein-induced transcript 3 protein | calcium ion binding |  |
| 63 | TRINITY\_DN10396\_c0\_g1\_i1 | sp|Q8WUQ7|CATIN\_HUMAN | 94.1 | 17 | 4.61E-04 | 41.6 | Splicing factor Cactin | RNA binding | cellular response to interleukin-cellular response to lipopolysaccharidecellular response to tumor necrosis factorinnate immune responsemRNA cis splicing, via spliceosomemRNA splicing, via spliceosomenegative regulation of canonical NF-kappaB signal transductionnegative regulation of innate immune responsenegative regulation of interferon-beta productionnegative regulation of interleukin-8 productionnegative regulation of lipopolysaccharide-mediated signaling pathway negative regulation of NF-kappaB transcription factor activitynegative regulation of protein phosphorylationnegative regulation of toll-like receptor signaling pathwaynegative regulation of tumor necrosis factor productionnegative regulation of type I interferon-mediated signaling pathway |
| 64 | TRINITY\_DN8282\_c0\_g2\_i1 | sp|O15347|HMGB3\_HUMAN | 41 | 173 | 8.58E-32 | 122 | High mobility group protein B3 | DNA binding, bendingdouble-stranded DNA bindingfour-way junction DNA bindingRNA binding | DNA geometric changeDNA recombinationinnate immune responseregulation of transcription by RNA polymerase II |
| 65 | TRINITY\_DN7791\_c0\_g1\_i1 | sp|P58911|TX60A\_PHYSE | 31.5 | 451 | 1.64E-70 | 239 | DELTA-alicitoxin-Pse2a | toxin activity | killing of cells of another organism |
| 66 | TRINITY\_DN5458\_c0\_g1\_i15 | sp|Q5T700|LRAD1\_HUMAN | 30.3 | 145 | 8.71E-06 | 48.9 | Low-density lipoprotein receptor class A domain-containing protein 1 | receptor |  |
| 67 | TRINITY\_DN16152\_c0\_g2\_i2 | sp|Q98UI9|MUC5B\_CHICK | 43 | 86 | 2.09E-14 | 75.5 | Mucin-5B | Virion binding | cholesterol homeostasisintestinal cholesterol absorption macrophage activation involved in immune response |
| 68 | Cell Structure and Dynamics | TRINITY\_DN3539\_c1\_g1\_i1 | sp|Q7Z6J4|FGD2\_HUMAN | 31.2 | 330 | 1.60E-33 | 140 | FYVE, RhoGEF and PH domain-containing protein 2 | guanyl-nucleotide exchange factor activitymetal ion bindingphosphatidylinositol phosphate bindingsmall GTPase binding | actin cytoskeleton organizationcytoskeleton organizationfilopodium assemblyregulation of cell shaperegulation of GTPase activityregulation of small GTPase mediated signal transduction |
| 69 | TRINITY\_DN14509\_c0\_g1\_i1 | sp|Q0P4I1|CEP44\_XENTR | 45 | 109 | 4.08E-23 | 104 | Centrosomal protein of 44 kDa | microtubule binding | centriole replication, centriole-centriole cohesion and centrosome cycle |
| 70 | TRINITY\_DN6124\_c0\_g1\_i1 | sp|Q557J6|DBNL\_DICDI | 59.5 | 37 | 4.17E-05 | 43.9 | Drebrin-like protein | actin bindingactin filament bindingmyosin I heavy chain bindingprofilin bindingprotein kinase binding | actin filament bundle assemblyaggregation involved in sorocarp developmentcell motilityestablishment or maintenance of cell polaritynegative regulation of phagocytosisphagosome maturationpseudopodium assemblyregulation of actin filament polymerization |
| 71 | TRINITY\_DN11289\_c0\_g1\_i1 | sp|A4QNG1|CC167\_XENTR | 46.7 | 75 | 1.50E-12 | 64.3 | Coiled-coil domain-containing protein | membrane protein |  |
| 72 | TRINITY\_DN32265\_c0\_g2\_i1 | sp|Q68CR1|SE1L3\_HUMAN | 29.5 | 946 | 5.48E-112 | 380 | Protein sel-1 homolog 3 | membrane protein |  |
| 73 | Enzymatic Reactions | TRINITY\_DN52912\_c0\_g1\_i1 | sp|Q07973|CP24A\_HUMAN | 30.3 | 534 | 6.30E-58 | 204 | 1,25-dihydroxyvitamin D(3) 24-hydroxylase, mitochondrial | 1-alpha,25-dihydroxyvitamin D3 23-hydroxylase activity3s1-alpha,25-dihydroxyvitamin D3 24-hydroxylase activity4s25-hydroxycholecalciferol-23-hydroxylase activity3s25-hydroxycholecalciferol-24-hydroxylase activity2sheme binding1 iron ion bindingvitamin D 25-hydroxylase activity | osteoblast differentiationresponse to vitamin Dvitamin D catabolic process5 vitamin D metabolic processvitamin D receptor signaling pathwayvitamin metabolic process |
| 74 | TRINITY\_DN22304\_c0\_g1\_i1 | sp|A6H611|MIPEP\_MOUSE | 47.7 | 654 | 2.48E-202 | 593 | Mitochondrial intermediate peptidase |  Function endopeptidase activitymetal ion bindingmetalloendopeptidase activity | peptide metabolic processprotein processing involved in protein targeting to mitochondrion |
| 75 | Ubiquitin-Related Processes: | TRINITY\_DN9045\_c0\_g1\_i2 | sp|Q9QXP6|MKRN1\_MOUSE | 63 | 27 | 2.68E-04 | 48.1 | E3 ubiquitin-protein ligase makorin-1 | chromatin bindingmetal ion bindingubiquitin protein ligase activity | cellular response to leukemia inhibitory factorSource:MGIprotein ubiquitination |
| 76 | TRINITY\_DN37965\_c1\_g1\_i5 | sp|Q96L50|LLR1\_HUMAN | 31.1 | 415 | 1.17E-39 | 152 | Leucine-rich repeat protein 1 |  | protein ubiquitinationsignal transduction |
| 77 | TRINITY\_DN9305\_c3\_g1\_i1 | sp|G0S9J5|RSP5\_CHATD | 22.6 | 345 | 3.22E-04 | 48.9 | E3 ubiquitin-protein ligase RSP5 | ubiquitin protein ligase activity | protein ubiquitinationubiquitin-dependent protein catabolic process |
| 78 | TRINITY\_DN99502\_c0\_g1\_i3 | sp|Q7ZW16|RNF41\_DANRE | 33.1 | 127 | 5.44E-09 | 59.3 | E3 ubiquitin-protein ligase NRDP1 | ubiquitin protein ligase activityubiquitin-protein transferase activityzinc ion binding | extrinsic apoptotic signaling pathwaymelanocyte differentiationprotein polyubiquitinationprotein ubiquitination |
| 79 | Light Production | TRINITY\_DN3623\_c1\_g1\_i2 | sp|P05938|LBP\_RENRE | 41.3 | 184 | 4.30E-38 | 141 | Luciferin-binding protein | Photoprotein | Luminescence |
| 80 | Growth and development | TRINITY\_DN37579\_c1\_g1\_i1 | sp|P48970|UNIV\_STRPU | 31.7 | 287 | 4.53E-32 | 130 | Univin | CytokineGrowth factor activity |  |
| 81 | TRINITY\_DN36054\_c0\_g1\_i2 | sp|Q9QXP4|DONS\_MOUSE | 33.8 | 284 | 2.76E-47 | 173 | Protein downstream neighbor of Son | Developmental protein |  |
| 82 | Unknown biological process | TRINITY\_DN12116\_c3\_g2\_i4 | sp|Q6INL2|KLH30\_XENLA | 41.1 | 73 | 9.09E-06 | 52.4 | Kelch-like protein 30 |  |  |
| 83 |  | TRINITY\_DN1222\_c0\_g1\_i1 | sp|P0C5Q0|YL54F\_YEAST | 85.2 | 27 | 3.67E-08 | 50.1 | Putative uncharacterized protein YLR154W-F |  |  |
|  |  |  |  |  |  |  |  |  |  |  |
|  | **Min** |  |  | **22.6** | **17** | **2.E-208** | **41.6** |  |  |  |
|  | **Max** |  |  | **94.1** | **946** | **5.E-04** | **596** |  |  |  |
|  | **Average** |  |  | **49.28** | **227.48** | **2.E-05** | **168.87** |  |  |  |
|  | **SD** |  |  | **16.42** | **190.86** | **8.E-05** | **127.80** |  |  |  |