**Table S1. The DEGs (differentially expressed genes) involved in dominant KEGG pathways.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Contig no.** | **Predicted genes** | **Full gene name** | **E-value** | **Group** | **KEGG pathway** |
| TRINITY\_DN6795\_c0\_g1 | *Acat1* | *Acetyl-CoA acetyltransferase 1* | 2.24E-185 | 1 | 11, 12, 16, 19 |
| TRINITY\_DN9305\_c1\_g1 | *Hadha* | *Hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit alpha* | 0.00E+00 | 1 | 11, 12, 16, 19, 20 |
| TRINITY\_DN4409\_c0\_g2 | *Hadh* | *Hydroxyacyl-CoA dehydrogenase* | 1.11E-149 | 1 | 11, 12, 19, 20 |
| TRINITY\_DN2407\_c0\_g1 | *Hsd17b10* | *Hydroxysteroid 17-beta dehydrogenase 10* | 5.89E-135 | 1 | 11 |
| TRINITY\_DN153694\_c1\_g1 | *Aldh7a1* | *Aldehyde dehydrogenase 7 family member A1* | 1.83E-292 | 1 | 11, 12 |
| TRINITY\_DN19229\_c0\_g1 | *Abat* | *4-aminobutyrate aminotransferase* | 1.87E-182 | 1 | 11, 16, 19 |
| TRINITY\_DN3031\_c1\_g1 | *Acaa2* | *Acetyl-CoA acyltransferase 2* | 4.91E-194 | 1 | 11, 12, 20 |
| TRINITY\_DN1449\_c0\_g1 | *Acat2* | *Acetyl-CoA acetyltransferase 2* | 2.71E-192 | 1 | 11, 12, 16, 19 |
| TRINITY\_DN3427\_c0\_g1 | *Xdh* | *Xanthine dehydrogenase* | 0.00E+00 | 1 | 11, 14 |
| TRINITY\_DN13239\_c0\_g1 | *Pccb* | *Propionyl-CoA carboxylase subunit beta* | 9.17E-308 | 1 | 11, 16 |
| TRINITY\_DN8804\_c0\_g1 | *Auh* | *AU RNA binding methylglutaconyl-CoA hydratase* | 1.41E-127 | 1 | 11 |
| TRINITY\_DN1654\_c6\_g1 | *Hadhb* | *Hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit beta* | 1.51E-242 | 1 | 11, 12, 20 |
| TRINITY\_DN2391\_c4\_g1 | *Acadm* | *Acyl-CoA dehydrogenase medium chain* | 4.71E-226 | 1 | 11, 12 |
| TRINITY\_DN11380\_c0\_g1 | *Cpt1a* | *Carnitine palmitoyltransferase 1A* | 0.00E+00 | 1 | 12 |
| TRINITY\_DN2446\_c0\_g1 | *Eci2* | *Enoyl-CoA delta isomerase 2* | 7.14E-141 | 1 | 12 |
| TRINITY\_DN5617\_c0\_g2 | *Got2* | *Glutamic-oxaloacetic transaminase 2* | 4.77E-229 | 1 | 13, 14 |
| TRINITY\_DN1638\_c0\_g1 | *Rpia* | *Ribose 5-phosphate isomerase A* | 6.70E-108 | 1 | 13 |
| TRINITY\_DN3794\_c1\_g1 | *Tpi1* | *Triosephosphate isomerase 1* | 2.69E-58 | 1 | 13 |
| TRINITY\_DN6415\_c0\_g1 | *Gapdh* | *Glyceraldehyde-3-phosphate dehydrogenase* | 1.56E-115 | 1 | 13 |
| TRINITY\_DN9646\_c0\_g1 | *Pgk1* | *Phosphoglycerate kinase 1* | 4.29E-225 | 1 | 13 |
| TRINITY\_DN2075\_c2\_g2 | *Gpt2* | *Glutamic--pyruvic transaminase 2* | 6.51E-233 | 1 | 13 |
| TRINITY\_DN121421\_c0\_g1 | *Fbp1* | *Fructose-bisphosphatase 1* | 3.02E-183 | 1 | 13 |
| TRINITY\_DN23287\_c0\_g1 | *Maoa* | *Monoamine oxidase A* | 2.95E-69 | 1 | 14 |
| TRINITY\_DN714\_c0\_g2 | *Fah* | *Fumarylacetoacetate hydrolase* | 1.37E-239 | 1 | 14 |
| TRINITY\_DN1860\_c2\_g1 | *Hpd* | *4-hydroxyphenylpyruvate dioxygenase* | 2.43E-205 | 1 | 14 |
| TRINITY\_DN4393\_c1\_g1 | *Mif* | *Macrophage migration inhibitory factor* | 6.26E-35 | 1 | 14 |
| TRINITY\_DN11223\_c0\_g1 | *Adcy1* | *Adenylate cyclase 1* | 5.74E-97 | 1 | 15 |
| TRINITY\_DN15855\_c0\_g1 | *Oxt* | *Oxytocin/neurophysin I prepropeptide* | 9.15E-14 | 1 | 15 |
| TRINITY\_DN6893\_c1\_g1 | *Dync1li1* | *Dynein cytoplasmic 1 light intermediate chain 1* | 4.83E-106 | 1 | 15 |
| TRINITY\_DN1325\_c0\_g1 | *Prkacb* | *Protein kinase cAMP-activated catalytic subunit beta* | 9.53E-243 | 1 | 15 |
| TRINITY\_DN830\_c19\_g1 | *Dync1i2* | *Dynein cytoplasmic 1 intermediate chain 2* | 4.03E-268 | 1 | 15 |
| TRINITY\_DN6812\_c0\_g1 | *Rab5a* | *RAB5A, member RAS oncogene family* | 2.86E-71 | 1 | 15 |
| TRINITY\_DN3126\_c1\_g1 | *Aqp2* | *Aquaporin 2* | 2.32E-61 | 1 | 15 |
| TRINITY\_DN29097\_c0\_g1 | *Creb3l2* | *cAMP responsive element binding protein 3 like 2* | 3.01E-76 | 1 | 15 |
| TRINITY\_DN57755\_c0\_g2 | *Suclg1* | *Succinate-CoA ligase GDP/ADP-forming subunit alpha* | 3.21E-181 | 1 | 16 |
| TRINITY\_DN2453\_c1\_g3 | *Suclg2* | *Succinate-CoA ligase GDP-forming subunit beta* | 1.40E-76 | 1 | 16 |
| TRINITY\_DN1500\_c0\_g1 | *Dhpr* | *Dihydropteridine reductase* | 9.74E-104 | 1 | 17 |
| TRINITY\_DN4741\_c0\_g1 | *Gsto1* | *Glutathione S-transferase omega 1* | 1.02E-59 | 1 | 17 |
| TRINITY\_DN2416\_c0\_g1 | *Trmt1* | *tRNA methyltransferase 1* | 3.17E-218 | 1 | 17 |
| TRINITY\_DN12649\_c0\_g1 | *Pcbd1* | *Pterin-4 alpha-carbinolamine dehydratase 1* | 3.80E-50 | 1 | 17 |
| TRINITY\_DN30822\_c0\_g1 | *Cbr1* | *Carbonyl reductase 1* | 2.49E-117 | 1 | 17 |
| TRINITY\_DN9173\_c0\_g1 | *Akr1b10* | *Aldo-keto reductase family 1 member B10* | 2.16E-90 | 1 | 17 |
| TRINITY\_DN4068\_c0\_g1 | *Abcc2* | *ATP binding cassette subfamily C member 2* | 0.00E+00 | 1 | 18 |
| TRINITY\_DN6\_c2\_g1 | *Abcb8* | *ATP binding cassette subfamily B member 8* | 9.64E-258 | 1 | 18 |
| TRINITY\_DN6446\_c0\_g1 | *Abcd2* | *ATP binding cassette subfamily D member 2* | 0.00E+00 | 1 | 18 |
| TRINITY\_DN4264\_c1\_g1 | *Abcd4* | *ATP binding cassette subfamily D member 4* | 1.58E-167 | 1 | 18 |
| TRINITY\_DN1632\_c0\_g1 | *Abcc5* | *ATP binding cassette subfamily C member 5* | 0.00E+00 | 1 | 18 |
| TRINITY\_DN6385\_c2\_g1 | *Abcc1* | *ATP binding cassette subfamily C member 1* | 0.00E+00 | 1 | 18 |
| TRINITY\_DN1094\_c0\_g1 | *Gad1* | *Glutamate decarboxylase 1* | 6.20E-38 | 1 | 19 |
| TRINITY\_DN8068\_c0\_g1 | *Med20* | *Mediator complex subunit 20* | 3.86E-79 | 1 | 20 |
| TRINITY\_DN3836\_c0\_g1 | *Elovl5* | *ELOVL fatty acid elongase 5* | 5.11E-126 | 1 | 20 |
| TRINITY\_DN2107\_c1\_g1 | *Rfng* | *RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase* | 3.30E-125 | 4 | 1 |
| TRINITY\_DN924\_c0\_g1 | *Dtx3l* | *Deltex E3 ubiquitin ligase 3L* | 5.78E-47 | 4 | 1 |
| TRINITY\_DN22773\_c0\_g1 | *Baz1b* | *Bromodomain adjacent to zinc finger domain 1B* | 9.86E-125 | 4 | 1 |
| TRINITY\_DN1857\_c0\_g1 | *Hes1* | *Hes family bHLH transcription factor 1* | 1.17E-21 | 4 | 1 |
| TRINITY\_DN78\_c2\_g1 | *Casp8* | *Caspase 8* | 3.68E-41 | 4 | 2, 3, 4, 5, 6, 7, 8, 9 |
| TRINITY\_DN1598\_c0\_g1 | *Casp3* | *Caspase 3* | 5.06E-51 | 4 | 2, 3, 4, 5, 6, 7, 8, 9 |
| TRINITY\_DN2259\_c0\_g1 | *Casp8l* | *Caspase 8-like* | 8.62E-28 | 4 | 2, 3, 4, 5, 6, 7, 8, 9 |
| TRINITY\_DN44\_c5\_g1 | *Ddx58* | *RNA Sensor RIG-I* | 3.60E-41 | 4 | 2, 10 |
| TRINITY\_DN17222\_c0\_g1 | *Chuk* | *Component of inhibitor of nuclear factor kappa B kinase complex* | 1.12E-117 | 4 | 2, 3, 4, 8, 9, 10 |
| TRINITY\_DN1185\_c15\_g1 | *Tbk1* | *TANK-binding kinase 1* | 1.45E-54 | 4 | 2, 3, 4 |
| TRINITY\_DN2217\_c1\_g1 | *Fosl2* | *FOS like 2, AP-1 transcription factor subunit* | 4.88E-15 | 4 | 3, 8 |
| TRINITY\_DN21630\_c1\_g1 | *Casp3l* | *Caspase 3-like* | 1.76E-29 | 4 | 3, 5, 6, 7, 9 |
| TRINITY\_DN17859\_c0\_g1 | *Myd88* | *Myeloid differentiation factor 88* | 6.21E-55 | 4 | 4, 8, 10 |
| TRINITY\_DN3163\_c0\_g1 | *Bcl2* | *BCL2 apoptosis regulator* | 6.23E-27 | 4 | 5, 6, 10 |
| TRINITY\_DN260\_c0\_g1 | *Adgrb1* | *Adhesion G protein-coupled receptor B1* | 1.05E-53 | 4 | 6 |
| TRINITY\_DN451\_c1\_g1 | *Plcg1* | *1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 isoform* | 0.00E+00 | 4 | 7, 10 |
| TRINITY\_DN7257\_c0\_g2 | *Mmp2l* | *Matrix metallopeptidase 2-like* | 8.72E-96 | 4 | 9 |
| TRINITY\_DN2804\_c0\_g1 | *Mmp19l* | *Matrix metallopeptidase 19-like* | 2.85E-57 | 4 | 9 |

1, Notch signaling pathway; 2, RIG-I-like receptor signaling pathway; 3, IL-17 signaling pathway; 4, Toll-like receptor signaling pathway; 5, Apoptosis - multiple species; 6, p53 signaling pathway; 7, Natural killer cell mediated cytotoxicity; 8, Toll and Imd signaling pathway; 9, TNF signaling pathway; 10, NF-kappa B signaling pathway; 11, Valine, leucine and isoleucine degradation; 12, Fatty acid degradation; 13, Carbon fixation in photosynthetic organisms; 14, Tyrosine metabolism; 15, Vasopressin-regulated water reabsorption; 16, Propanoate metabolism; 17, Folate biosynthesis; 18, ABC transporters; 19, Butanoate metabolism; 20, Fatty acid elongation.

**Table S2. The DEGs (differentially expressed genes) of immune-related genes.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Contig no.** | **Predicted genes** | **Full gene name** | **E-value** | **Group** |
| TRINITY\_DN830\_c9\_g1 | *Akirin2* | *Akirin 2* | 1.59E-59 | 1 |
| TRINITY\_DN217\_c10\_g1 | *Arg1* | *Arginase 1* | 1.68E-93 | 1 |
| TRINITY\_DN2680\_c0\_g1 | *Asl* | *Argininosuccinate lyase* | 1.44E-226 | 1 |
| TRINITY\_DN10478\_c0\_g1 | *C19orf66* | *Shiftless antiviral inhibitor of ribosomal frameshifting* | 1.12E-38 | 1 |
| TRINITY\_DN16638\_c0\_g1 | *Camk2a* | *Calcium/calmodulin-dependent protein kinase type II alpha chain* | 5.80E-291 | 1 |
| TRINITY\_DN2582\_c0\_g1 | *Eprs* | *Bifunctional glutamate/proline--tRNA ligase* | 4.42E-285 | 1 |
| TRINITY\_DN6415\_c0\_g1 | *Gapdh* | *Glyceraldehyde-3-phosphate dehydrogenase* | 1.56E-115 | 1 |
| TRINITY\_DN318\_c3\_g1 | *Hsp90b* | *Heat shock protein 90 beta* | 0 | 1 |
| TRINITY\_DN27005\_c0\_g1 | *Mapre1* | *Microtubule-associated protein RP/EB family member 1* | 1.44E-98 | 1 |
| TRINITY\_DN595\_c0\_g1 | *Ncoa7* | *Nuclear receptor coactivator 7* | 2.59E-85 | 1 |
| TRINITY\_DN643\_c2\_g1 | *Otud7b* | *OTU domain-containing protein 7B* | 2.64E-182 | 1 |
| TRINITY\_DN2762\_c0\_g1 | *Pgrp2* | *Peptidoglycan recognition protein 2* | 9.32E-58 | 1 |
| TRINITY\_DN338\_c2\_g2 | *Pgrp3l* | *Peptidoglycan recognition protein 3 like* | 3.13E-55 | 1 |
| TRINITY\_DN1132\_c0\_g1 | *Polr3b* | *DNA-directed RNA polymerase III subunit RPC2* | 0 | 1 |
| TRINITY\_DN1325\_c0\_g1 | *Prkacb* | *cAMP-dependent protein kinase catalytic subunit beta* | 9.53E-243 | 1 |
| TRINITY\_DN1168\_c0\_g2 | *Prkd1* | *Serine/threonine-protein kinase D1-like* | 0 | 1 |
| TRINITY\_DN88490\_c0\_g1 | *Skp1* | *S-phase kinase-associated protein 1* | 5.10E-94 | 1 |
| TRINITY\_DN1667\_c87\_g1 | *Tep1* | *Thioester-containing protein 1* | 1.18E-58 | 1 |
| TRINITY\_DN1009\_c8\_g1 | *Tmed7* | *Transmembrane emp24 domain-containing protein 7* | 1.83E-88 | 1 |
| TRINITY\_DN409\_c4\_g1 | *Ube2n* | *Ubiquitin-conjugating enzyme E2 N* | 4.22E-96 | 1 |
| TRINITY\_DN10\_c10\_g1 | *Wwp1* | *WW domain containing E3 ubiquitin protein ligase 1* | 0 | 1 |
| TRINITY\_DN11056\_c0\_g1 | *Alp2* | *Alkaline phosphatase 2* | 1.84E-166 | 2 |
| TRINITY\_DN5019\_c1\_g1 | *Cnpy3* | *Canopy FGF signaling regulator 3* | 2.64E-66 | 2 |
| TRINITY\_DN9434\_c0\_g1 | *Dak* | *Dihydroxyacetone kinase* | 1.98E-183 | 2 |
| TRINITY\_DN14016\_c0\_g1 | *Gch1* | *GTP cyclohydrolase 1* | 6.53E-101 | 2 |
| TRINITY\_DN6490\_c0\_g1 | *Hspa1* | *Heat shock protein family A (Hsp70) member 1* | 1.89E-41 | 2 |
| TRINITY\_DN3878\_c1\_g1 | *Hspd1* | *Heat shock protein family D (Hsp60) member 1* | 7.24E-306 | 2 |
| TRINITY\_DN13987\_c0\_g1 | *Mmp14* | *Matrix metallopeptidase 14* | 7.59E-34 | 2 |
| TRINITY\_DN8644\_c0\_g1 | *Slc26a6l* | *Solute carrier family 26 member 6 like* | 2.52E-37 | 2 |
| TRINITY\_DN595\_c13\_g1 | *Vim* | *Vimentin* | 6.34E-40 | 2 |
| TRINITY\_DN378\_c5\_g1 | *Vnn1* | *Vanin 1* | 1.18E-51 | 2 |
| TRINITY\_DN4047\_c0\_g1 | *Arhgef26* | *Rho guanine nucleotide exchange factor 26* | 5.93E-137 | 4 |
| TRINITY\_DN1598\_c0\_g1 | *Casp3* | *Caspase 3* | 5.06E-51 | 4 |
| TRINITY\_DN78\_c2\_g1 | *Casp8* | *Caspase 8* | 3.68E-41 | 4 |
| TRINITY\_DN2259\_c0\_g1 | *Casp8l* | *Caspase 8-like* | 8.62E-28 | 4 |
| TRINITY\_DN17222\_c0\_g1 | *Chuk* | *Inhibitor of nuclear factor kappa-B kinase subunit alpha* | 1.12E-117 | 4 |
| TRINITY\_DN44\_c5\_g1 | *Ddx58* | *RNA Sensor RIG-I* | 3.60E-41 | 4 |
| TRINITY\_DN361\_c1\_g2 | *Dmbt1* | *Deleted in malignant brain tumors 1* | 1.68E-24 | 4 |
| TRINITY\_DN1185\_c15\_g1 | *Tbk1* | *TANK-binding kinase 1* | 1.45E-54 | 4 |
| TRINITY\_DN14712\_c0\_g1 | *Irf2* | *Interferon regulatory factor 2* | 4.70E-32 | 4 |
| TRINITY\_DN7257\_c0\_g2 | *Mmp2l* | *Matrix metallopeptidase 2-like* | 8.72E-96 | 4 |
| TRINITY\_DN17859\_c0\_g1 | *Myd88* | *Myeloid differentiation factor 88* | 6.21E-55 | 4 |
| TRINITY\_DN93801\_c0\_g2 | *Parp14* | *Poly(adp-ribose) polymerase family member 14* | 1.41E-16 | 4 |
| TRINITY\_DN451\_c1\_g1 | *Plcg1* | *1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 isoform* | 0.00E+00 | 4 |
| TRINITY\_DN120\_c2\_g1 | *Prkci* | *Protein kinase C iota type* | 2.53E-306 | 4 |
| TRINITY\_DN1028\_c0\_g1 | *Samhd1* | *SAM and HD domain containing deoxynucleoside triphosphate triphosphohydrolase 1* | 2.29E-139 | 4 |
| TRINITY\_DN1742\_c0\_g1 | *Sin3a* | *SIN3 transcription regulator family member A* | 0 | 4 |
| TRINITY\_DN792\_c17\_g1 | *Wnt5b* | Wingless-type MMTV integration site family, member 5B | 2.86E-182 | 4 |
| TRINITY\_DN167\_c2\_g1 | *Parp12* | *Poly(adp-ribose) polymerase family member 12* | 9.37E-49 | 4 |
| TRINITY\_DN5232\_c0\_g2 | *Crisp2* | *Cysteine rich secretory protein 2* | 1.25E-29 | 5 |
| TRINITY\_DN6001\_c0\_g1 | *Hsp90a* | *Heat shock protein 90 alpha* | 2.92E-154 | 5 |
| TRINITY\_DN6242\_c1\_g1 | *Irf1* | *Interferon regulatory factor 1* | 1.82E-33 | 5 |
| TRINITY\_DN826\_c0\_g1 | *Mapkapk2* | *MAP kinase-activated protein kinase 2* | 2.30E-166 | 5 |
| TRINITY\_DN1589\_c0\_g1 | *Nos2* | *Nitric oxide synthase, brain 2* | 0 | 5 |
| TRINITY\_DN15174\_c0\_g1 | *Rps6ka2* | *Ribosomal protein S6 kinase 2* | 0 | 5 |

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**FigS1. Expression-dependant N50 (ExN50) as calculated against a fraction of the total expressed data (Ex).**

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**FigS2. Functional annotation of DEGs in the GO database.**

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**FigS3. KEGG enrichment analysis of DEGs.**