**Supplementary Tables**

Table S1. Five qRT-PCR primers used in this study and gene expression analysed by qRT-PCR and RNA-Seq.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Unigene ID** | **Primer name** | **Primer sequence (5´→3´)** | **Fold change (HV:CS)** | |
| **RNA-Seq** | **qRT-PCR** |
| TRINITY\_DN409\_c0\_g1\_i3 | Actin-F | ACGGATATCTACGTCGCACT | IS | IS |
| Actin-P | TCCTTCCTGGGTCTGGAAAA |
| TRINITY\_DN17219\_c0\_g1\_i7 | AADAT-F | TACATCTCGTCATATCCGCT | 4.9696254 | 3.7038574 |
| AADAT-P | CGAGGCGAAAAGTAGAACGA |
| TRINITY\_DN3926\_c0\_g2\_i3 | CHSTC-F | TAGAGCTGCTTGTGGTTTGG | 1.2586507 | 1.8845979 |
| CHSTC-R | ACCAGACAATGCCACACAAA |
| TRINITY\_DN2035\_c0\_g1\_i12 | MORF-F | TGGATGCCCTTCCTTTGATG | 1.2828827 | 2.2032012 |
| MORF-R | ATTATTGGGATGCGAGGCTG |
| TRINITY\_DN2307\_c1\_g1\_i3 | IGFs-F | AGGTGTGAGAGTACGGTCTG | 0.4892081 | 1.4276062 |
| IGFs-R | TGGGCACATATTTCACAGCA |

IS means internal standard used in this study.

Table S2. Summary statistics of Illumina raw reads size and clean reads size for transcriptome assembly.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Individual** | **Tissue** | **Raw reads** | **Raw reads (Gb)** | **Clean reads** | **Clean reads (Gb)** |
| OT\_1 | Gill | 2,697,548 | 2.57 | 2,037,476 | 1.94 |
| Hepatopancreas | 3,155,808 | 3.01 | 2,495,020 | 2.38 |
| Ovary | 3,469,872 | 3.31 | 2,760,092 | 2.63 |
| Abdominal muscle | 2,594,664 | 2.47 | 2,046,920 | 1.95 |
| OT\_2 | Testis | 2,806,192 | 2.68 | 2,165,204 | 2.06 |
|  | **Average** | 2,944,817 | 2.81 | 2,300,942 | 2.19 |
|  | **Total** | 14,724,084 | 14.04 | 11,504,712 | 10.96 |

Table S3. Illumina raw reads size and clean reads size statistics of abdomen muscle from each individual.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **No.** | **Location** | **Sample** | **Raw reads** | **Raw reads (Gb)** | **Clean reads** | **Clean reads (Gb)** |
| 1 | SCS | SCS\_1 | 4,126,812 | 3.94 | 3,635,388 | 3.47 |
| 2 | SCS\_2 | 3,699,788 | 3.53 | 3,232,128 | 3.08 |
| 3 | SCS\_3 | 4,644,908 | 4.43 | 4,116,564 | 3.93 |
| 4 | SCS\_4 | 3,922,996 | 3.74 | 3,474,560 | 3.31 |
| 5 | SCS\_5 | 3,740,068 | 3.57 | 3,425,300 | 3.27 |
| 6 | SCS\_6 | 4,039,960 | 3.85 | 3,717,604 | 3.55 |
| 7 | SCS\_7 | 3,779,240 | 3.60 | 3,417,560 | 3.30 |
| 8 | SCS\_8 | 3,954,980 | 3.77 | 3,476,620 | 3.32 |
| 9 | SCS\_9 | 3,526,632 | 3.36 | 3,066,496 | 2.92 |
| 10 | SCS\_10 | 3,744,828 | 3.57 | 3,425,536 | 3.27 |
| 11 | SCS\_11 | 3,240,036 | 3.09 | 2,648,584 | 2.53 |
| 12 | SCS\_12 | 2,431,740 | 2.32 | 1,958,556 | 1.87 |
| 13 | SCS\_13 | 2,780,816 | 2.65 | 2,248,520 | 2.14 |
| 14 | SCS\_14 | 2,919,044 | 2.78 | 2,163,852 | 2.06 |
| 15 | SCS\_15 | 3,170,728 | 3.02 | 2,540,764 | 2.42 |
| 16 | SCS\_16 | 2,790,428 | 2.66 | 2,198,492 | 2.10 |
| 17 | SCS\_17 | 3,082,992 | 2.94 | 2,409,412 | 2.30 |
| 18 | SCS\_18 | 3,004,336 | 2.87 | 2,314,032 | 2.21 |
| 19 | SCS\_19 | 2,857,200 | 2.72 | 2,235,764 | 2.13 |
| 20 | SCS\_20 | 3,164,996 | 3.02 | 2,442,260 | 2.33 |
| 21 | OT | OT\_1 | 2,594,664 | 2.47 | 2,046,920 | 1.95 |
| 22 | OT\_2 | 2,818,020 | 2.69 | 2,260,224 | 2.16 |
| 23 | OT\_3 | 3,082,912 | 2.94 | 2,462,752 | 2.35 |
| 24 | OT\_4 | 3,038,368 | 2.90 | 2,414,832 | 2.30 |
| 25 | OT\_5 | 2,926,884 | 2.79 | 2,358,452 | 2.25 |
| 26 | OT\_6 | 2,893,732 | 2.76 | 2,346,624 | 2.24 |
| 27 | OT\_7 | 2,698,380 | 2.57 | 2,170,836 | 2.07 |
| 28 | OT\_8 | 2,930,208 | 2.79 | 2,359,188 | 2.25 |
| 29 | OT\_9 | 2,799,520 | 2.67 | 2,225,564 | 2.12 |
| 30 | OT\_10 | 3,432,112 | 3.27 | 2,739,144 | 2.61 |
| 31 | OT\_11 | 3,482,584 | 3.32 | 2,785,516 | 2.66 |
| 32 | OT\_12 | 2,782,076 | 2.65 | 2,248,484 | 2.14 |
| 33 | OT\_13 | 2,606,212 | 2.49 | 2,066,480 | 1.97 |
| 34 | OT\_14 | 2,809,780 | 2.68 | 2,236,188 | 2.13 |
| 35 | OT\_15 | 2,359,416 | 2.25 | 1,849,200 | 1.76 |
| 36 | OT\_16 | 2,702,040 | 2.58 | 2,128,144 | 2.03 |
| 37 | OT\_17 | 3,028,376 | 2.89 | 2,423,740 | 2.31 |
| 38 | OT\_18 | 3,109,036 | 2.97 | 2,458,460 | 2.34 |
| 39 | OT\_19 | 3,103,096 | 2.96 | 2,475,256 | 2.36 |
| 40 | OT\_20 | 2,846,516 | 2.71 | 2,279,132 | 2.17 |
| 41 | OT\_21 | 3,177,700 | 3.03 | 2,560,296 | 2.44 |
| 42 | OT\_22 | 3,659,336 | 3.49 | 2,958,300 | 2.82 |
| 43 | OT\_23 | 3,732,412 | 3.56 | 2,979,692 | 2.84 |
| 44 | OT\_24 | 2,851,632 | 2.72 | 2,272,448 | 2.17 |
| **Average** |  |  | 3183808 | 3.04 | 2619406 | 2.50 |
| **Total** |  |  | 140,087,540 | 133.58 | 115,253,864 | 109.95 |

Table S4. Data statistics of individually assembled transcripts.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **No.** | **Location** | **Sample** | **Sequence number** | **Data size (Kb)** |
| 1 | SCS | SCS\_1 | 41,689 | 42536 |
| 2 | SCS\_2 | 42,721 | 44128 |
| 3 | SCS\_3 | 43,971 | 46620 |
| 4 | SCS\_4 | 41,128 | 43128 |
| 5 | SCS\_5 | 38,043 | 37612 |
| 6 | SCS\_6 | 37,699 | 38168 |
| 7 | SCS\_7 | 38,176 | 37952 |
| 8 | SCS\_10 | 36,072 | 36368 |
| 9 | SCS\_11 | 36,471 | 37548 |
| 10 | SCS\_12 | 35,886 | 34504 |
| 11 | SCS\_15 | 44,551 | 43424 |
| 12 | SCS\_16 | 36,173 | 34340 |
| 13 | SCS\_17 | 41,512 | 39820 |
| 14 | SCS\_18 | 33,395 | 28384 |
| 15 | SCS\_19 | 35,206 | 32872 |
| 16 | SCS\_20 | 48,530 | 45188 |
| 17 | SCS\_21 | 34,670 | 31904 |
| 18 | SCS\_22 | 36,567 | 33032 |
| 19 | SCS\_23 | 36,378 | 32956 |
| 20 | SCS\_24 | 34,519 | 30280 |
| 21 | OT | OT\_1 | 29,940 | 28360 |
| 22 | OT\_2 | 27,662 | 25572 |
| 23 | OT\_3 | 31,661 | 31336 |
| 24 | OT\_4 | 34,536 | 32032 |
| 25 | OT\_6 | 40,828 | 37940 |
| 26 | OT\_7 | 30,551 | 28952 |
| 27 | OT\_8 | 39,714 | 37340 |
| 28 | OT\_9 | 38,516 | 36692 |
| 29 | OT\_10 | 42,564 | 40144 |
| 30 | OT\_12 | 42,257 | 40504 |
| 31 | OT\_13 | 43,768 | 41916 |
| 32 | OT\_14 | 40,615 | 39092 |
| 33 | OT\_15 | 41,008 | 38352 |
| 34 | OT\_16 | 40,574 | 37820 |
| 35 | OT\_17 | 40,248 | 36996 |
| 36 | OT\_18 | 38,963 | 35748 |
| 37 | OT\_19 | 42,755 | 40908 |
| 38 | OT\_21 | 42,560 | 39952 |
| 39 | OT\_23 | 45,267 | 43724 |
| 40 | OT\_24 | 40,954 | 38356 |
| 41 | OT\_25 | 44,630 | 43060 |
| 42 | OT\_26 | 45,805 | 43908 |
| 43 | OT\_27 | 43,323 | 41596 |
| 44 | OT\_28 | 38,839 | 35496 |
| **Average** |  |  | 38707 | 37209 |
| **Total** |  |  | 1,548,298 | 1525560 |

Table S5. Annotation of population-specific genes.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Site** | **Gene number** | **KEGG number** | **KEGG annotation** | **NR annotation** |
| OT | OT\_PSG\_1 |  |  |  |
| OT\_PSG\_2 |  |  |  |
| OT\_PSG\_3 |  |  |  |
| OT\_PSG\_4 |  |  |  |
| OT\_PSG\_5 | K00274 | MAO, aofH; monoamine oxidase | probable flavin-containing monoamine oxidase A [*Penaeus vannamei*] |
| OT\_PSG\_6 |  |  |  |
| OT\_PSG\_7 |  |  |  |
| OT\_PSG\_8 |  |  |  |
| OT\_PSG\_9 |  |  |  |
| OT\_PSG\_10 |  |  |  |
| OT\_PSG\_11 | K00306 | PIPOX; sarcosine oxidase / L-pipecolate oxidase | peroxisomal sarcosine oxidase-like [*Penaeus vannamei*] |
| OT\_PSG\_12 |  |  |  |
| OT\_PSG\_13 |  |  |  |
| OT\_PSG\_14 |  |  |  |
| OT\_PSG\_15 |  |  |  |
| OT\_PSG\_16 | K00825 | AADAT, KAT2; kynurenine/2-aminoadipate aminotransferase | kynurenine/alpha-aminoadipate aminotransferase, mitochondrial-like [*Penaeus* *vannamei*] |
| OT\_PSG\_17 |  |  |  |
| OT\_PSG\_18 | K17461 | RECK, ST15; reversion-inducing-cysteine-rich protein with kazal motifs | reversion-inducing cysteine-rich protein with Kazal motifs-like [*Parasteatoda tepidariorum*] |
| OT\_PSG\_19 |  |  |  |
| OT\_PSG\_20 |  |  |  |
| OT\_PSG\_21 |  |  |  |
| OT\_PSG\_22 | K11363 | SGF11; SAGA-associated factor 11 | putative SAGA-associated factor 11-like [*Penaeus vannamei*] |
| OT\_PSG\_23 |  |  |  |
| OT\_PSG\_24 |  |  |  |
| OT\_PSG\_25 |  |  |  |
| OT\_PSG\_26 | K10694 | ZNRF1\_2; E3 ubiquitin-protein ligase ZNRF1/2 | E3 ubiquitin-protein ligase ZNRF2-like, partial [*Penaeus vannamei*] |
| OT\_PSG\_27 |  |  |  |
| OT\_PSG\_28 |  |  |  |
| OT\_PSG\_29 |  |  |  |
| OT\_PSG\_30 |  |  |  |
| OT\_PSG\_31 |  |  | prophenoloxidase [*Cherax quadricarinatus*] |
| OT\_PSG\_32 | K14805 | DDX24, MAK5; ATP-dependent RNA helicase DDX24/MAK5 | ATP-dependent RNA helicase DDX24 isoform X2 [*Lingula anatina*] |
| OT\_PSG\_33 |  |  |  |
| OT\_PSG\_34 |  |  |  |
| OT\_PSG\_35 |  |  |  |
| OT\_PSG\_36 |  |  |  |
| OT\_PSG\_37 |  |  |  |
| OT\_PSG\_38 | K10660 | MARCH5; E3 ubiquitin-protein ligase MARCH5 | putative E3 ubiquitin-protein ligase MARCH5-like isoform X2 [*Penaeus* *vannamei*] |
| OT\_PSG\_39 |  |  |  |
| OT\_PSG\_40 |  |  |  |
| OT\_PSG\_41 | K11593 | ELF2C, AGO; eukaryotic translation initiation factor 2C | argonaute-2 [*Macrobrachium rosenbergii*] |
| OT\_PSG\_42 |  |  |  |
| OT\_PSG\_43 | K08343 | ATG3; ubiquitin-like-conjugating enzyme ATG3 | autophagy related protein Atg3-like protein [*Penaeus vannamei*] |
| OT\_PSG\_44 | K20631 | ARHGAP6; Rho GTPase-activating protein 6 | LOC113813208 – rho GTPase-activating protein 6-like |
| OT\_PSG\_45 | K20631 | ARHGAP6; Rho GTPase-activating protein 6 | hypothetical protein C7M84\_011091 [*Penaeus vannamei*] |
| OT\_PSG\_46 |  |  | hypothetical protein C7M84\_001778 [*Penaeus vannamei*] |
| OT\_PSG\_47 |  |  | ERAD-associated E3 ubiquitin-protein ligase hrd1-like isoform X1 [*Zootermopsis nevadensis*] |
| OT\_PSG\_48 |  |  | hypothetical protein C7M84\_005291 [*Penaeus vannamei*] |
| OT\_PSG\_49 | K01017 | CHST11; chondroitin 4-sulfotransferase 11 | Carbohydrate sulfotransferase 11 [*Penaeus vannamei*] |
| OT\_PSG\_50 |  |  |  |
| OT\_PSG\_51 |  |  |  |
| SCS | SCS\_PSG\_1 |  |  |  |
| SCS\_PSG\_2 |  |  |  |
| SCS\_PSG\_3 | K01908 | prpE; propionyl-CoA synthetase | acyl-CoA synthetase short-chain family member 3, mitochondrial-like [*Penaeus* *vannamei*] |
| SCS\_PSG\_4 |  |  | notch-regulated ankyrin repeat-containing protein-like [*Penaeus vannamei*] |
| SCS\_PSG\_5 |  |  |  |
| SCS\_PSG\_6 | K14640 | SLC20A, PIT; solute carrier family 20 (sodium-dependent phosphate transporter) |  |
| SCS\_PSG\_7 | K12566 | SGCB; beta-sarcoglycan | beta-sarcoglycan-like [*Penaeus vannamei*] |
| SCS\_PSG\_8 |  |  |  |
| SCS\_PSG\_9 |  |  |  |
| SCS\_PSG\_10 |  |  |  |
| SCS\_PSG\_11 | K01940 | argG, ASS1; argininosuccinate synthase | argininosuccinate synthase 1, partial [*Procambarus clarkii*] |
| SCS\_PSG\_12 |  |  |  |
| SCS\_PSG\_13 |  |  |  |
| SCS\_PSG\_14 |  |  |  |
| SCS\_PSG\_15 |  |  | uncharacterized protein LOC113808556 isoform X1 [*Penaeus vannamei*] |
| SCS\_PSG\_16 | K19719 | COL2A; collagen, type II, alpha | PREDICTED: collagen alpha-1(I) chain-like isoform X1 [*Hyalella azteca*] |
| SCS\_PSG\_17 |  |  |  |
| SCS\_PSG\_18 |  |  |  |
| SCS\_PSG\_19 |  |  |  |
| SCS\_PSG\_20 |  |  |  |
| SCS\_PSG\_21 |  |  |  |
| SCS\_PSG\_22 |  |  |  |
| SCS\_PSG\_23 |  |  |  |
| SCS\_PSG\_24 |  |  |  |
| SCS\_PSG\_25 |  |  |  |
| SCS\_PSG\_26 |  |  |  |
| SCS\_PSG\_27 |  |  |  |
| SCS\_PSG\_28 |  |  |  |
| SCS\_PSG\_29 |  |  |  |
| SCS\_PSG\_30 |  |  |  |
| SCS\_PSG\_31 | K17198 | RERGL; Ras-related and estrogen-regulated growth inhibitor-like protein | ras-related and estrogen-regulated growth inhibitor-like protein [*Penaeus* *vannamei*] |
| SCS\_PSG\_32 |  |  |  |
| SCS\_PSG\_33 |  |  |  |
| SCS\_PSG\_34 |  |  | longitudinals lacking protein-like [*Penaeus vannamei*] |
| SCS\_PSG\_35 |  |  | hypothetical protein C7M84\_016301, partial [*Penaeus vannamei*] |
| SCS\_PSG\_36 |  |  |  |
| SCS\_PSG\_37 |  |  |  |
| SCS\_PSG\_38 |  |  |  |
| SCS\_PSG\_39 |  |  |  |
| SCS\_PSG\_40 | K17916 | KIF16B, SNX23; kinesin family member 16B | putative stAR-related lipid transfer protein 9 [*Penaeus vannamei*] |
| SCS\_PSG\_41 |  |  |  |
| SCS\_PSG\_42 |  |  |  |
| SCS\_PSG\_43 |  |  |  |
| SCS\_PSG\_44 |  |  |  |
| SCS\_PSG\_45 | K00314 | SARDH; sarcosine dehydrogenase [EC:1.5.8.3] | putative sarcosine dehydrogenase, mitochondrial isoform 1 [*Penaeus vannamei*] |
| SCS\_PSG\_46 |  |  | uncharacterized protein LOC113812017 [*Penaeus vannamei*] |
| SCS\_PSG\_47 |  |  |  |
| SCS\_PSG\_48 |  |  |  |
| SCS\_PSG\_49 |  |  |  |
| SCS\_PSG\_50 |  |  |  |
| SCS\_PSG\_51 |  |  |  |
| SCS\_PSG\_52 | K11665 | INO80, INOC1; DNA helicase INO80 [EC:3.6.4.12] | chromatin-remodeling ATPase INO80-like, partial [*Penaeus vannamei*] |
| SCS\_PSG\_53 |  |  |  |
| SCS\_PSG\_54 |  |  |  |
| SCS\_PSG\_55 |  |  |  |
| SCS\_PSG\_56 |  |  |  |
| SCS\_PSG\_57 |  |  |  |
| SCS\_PSG\_58 |  |  | uncharacterized protein LOC113815544 [*Penaeus vannamei*] |
| SCS\_PSG\_59 |  |  |  |
| SCS\_PSG\_60 | K12866 | WBP11, NPWBP; WW domain-binding protein 11 | WW domain-binding protein 11 [*Hyposmocoma kahamanoa*] |
| SCS\_PSG\_61 |  |  |  |

Table S6. Information of DEGs involved in hierarchical clustering analysis.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gene name** | **Mean Expression level** | | **Annotation** | **Function** |
| **SCS** | **OT** |
| CYP | 299.6244 | 113.8614 | Cytochrome P450 2L1-like | Oxidoreductase activity |
| IYD1 | 16.39613 | 1.714703 | Iodotyrosine deiodinase 1 | Oxidoreductase activity |
| PRDX6 | 802.1481 | 368.4071 | Peroxiredoxin 6 | Oxidoreductase activity |
| BDH1 | 134.5952 | 43.86836 | D-beta-hydroxybutyrate dehydrogenase, mitochondrial | Oxidoreductase activity |
| DCXR | 446.9645 | 160.9548 | L-xylulose reductase | Oxidoreductase activity |
| CBR1 | 627.2717 | 196.0291 | Carbonyl reductase 1 | Metabolism of xenobiotics by cytochrome P450 |
| UQCRB | 1441.091 | 635.4685 | Cytochrome b-c1 complex subunit 7 | Oxidoreductase activity |
| GLO1 | 99.33149 | 36.95365 | Lactoylglutathione lyase | Carbon-sulfur lyase activity |
| HAAO | 259.452 | 93.57559 | 3-hydroxyanthranilate 3,4-dioxygenase | Oxidoreductase activity |
| GST | 3806.613 | 524.5651 | Glutathione S-transferase | Metabolism of xenobiotics by cytochrome P450 |
| CRYM | 26.14382 | 6.197359 | Ketimine reductase mu-crystallin | Oxidoreductase activity |
| HSD17B12 | 250.5439 | 107.4343 | Very-long-chain 3-oxoacyl-CoA reductase; very-long-chain 3-oxoacyl- reductase | Oxidoreductase activity |
| DHCR24 | 247.2955 | 94.79837 | Delta(24)-sterol reductase-like | Oxidoreductase activity |
| ALDH16A1 | 204.3789 | 73.01886 | Aldehyde dehydrogenase family 16 member A1-like | Oxidoreductase activity |
| CTU1 | 73.77116 | 26.13554 | Cytoplasmic tRNA 2-thiolation protein 1 | Sulfur relay system |
| CENPV | 73.44353 | 22.44942 | Centromere protein V | Carbon-sulfur lyase activity |
| EPHX1 | 41.70642 | 18.0709 | Microsomal epoxide hydrolase | Metabolism of xenobiotics by cytochrome P450 |
| DHDH | 21.69703 | 1.48632 | Dihydrodiol dehydrogenase / D-xylose 1-dehydrogenase (NADP) | Metabolism of xenobiotics by cytochrome P450 |
| ETHE1 | 4438.87 | 2165.007 | Sulfur dioxygenase | Sulfur metabolism |
| ALDH5A1 | 9.487787 | 3.560396 | Succinate-semialdehyde dehydrogenase, mitochondrial | Oxidoreductase activity |
| PHGDH | 38.90798 | 11.57097 | D-3-phosphoglycerate dehydrogenase / 2-oxoglutarate reductase | Methane metabolism |
| DAK | 10.67231 | 4.552981 | Triose/dihydroxyacetone kinase / FAD-AMP lyase (cyclizing) | Methane metabolism |
| CRYL1 | 14.45513 | 5.130357 | Lambda-crystallin homolog | Oxidoreductase activity |
| UGT | 73.50544 | 20.19949 | Glucuronosyltransferase | Metabolism of xenobiotics by cytochrome P450 |
| TDO2 | 43.30862 | 108.1919 | Tryptophan 2,3-dioxygenase | Dioxygenase activity |
| CDO1 | 1383.229 | 3763.235 | Cysteine dioxygenase type 1 | Dioxygenase activity |
| CD29 | 9.0065 | 84.93304 | Integrin beta 1 | Bacterial invasion of epithelial cells |
| ITGA8 | 0.620438 | 12.14748 | Integrin alpha 8 | Bacterial invasion of epithelial cells |
| CBL | 3.406816 | 7.602773 | E3 ubiquitin-protein ligase CBL | Bacterial invasion of epithelial cells |

Table S7. Information of 74 unigenes which were both found in the DEGs and the outlier SNP dataset.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **Gene ID** | **Expression level** | | **Fold change** | **FDR** | **Annotation** |
| **SCS** | **OT** |
| outlier SNP overlapped DEGs in SCS | TRINITY\_DN6650\_c0\_g1\_i5 | 173.2 | 1.31 | 131.93 | 5.74E-93 | Argininosuccinate synthase |
| TRINITY\_DN2248\_c1\_g3\_i1 | 83.22 | 0.85 | 97.58 | 2.87E-93 |  |
| TRINITY\_DN55850\_c0\_g1\_i1 | 8.18 | 0.49 | 16.64 | 4.05E-15 | Ubiquitin-40S ribosomal protein S27a |
| TRINITY\_DN4130\_c0\_g1\_i1 | 21.7 | 1.49 | 14.6 | 1.17E-16 | Dihydrodiol dehydrogenase |
| TRINITY\_DN55850\_c0\_g2\_i2 | 21.65 | 1.49 | 14.51 | 1.28E-26 | Ubiquitin C |
| TRINITY\_DN2920\_c0\_g1\_i1 | 405.19 | 29.82 | 13.59 | 1.28E-22 | Sarcosine dehydrogenase |
| TRINITY\_DN6599\_c0\_g1\_i1 | 260161.19 | 38217.25 | 6.81 | 1.97E-21 | Plastin-2 |
| TRINITY\_DN38864\_c0\_g1\_i1 | 89.85 | 13.68 | 6.57 | 1.35E-25 |  |
| TRINITY\_DN105\_c1\_g4\_i2 | 4457.31 | 689.08 | 6.47 | 2.71E-12 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein |
| TRINITY\_DN850\_c2\_g1\_i1 | 59.18 | 9.31 | 6.36 | 6.07E-61 |  |
| TRINITY\_DN8231\_c0\_g2\_i1 | 149.41 | 24.25 | 6.16 | 2.33E-23 |  |
| TRINITY\_DN40461\_c0\_g1\_i1 | 145.25 | 25.72 | 5.65 | 1.52E-31 |  |
| TRINITY\_DN52516\_c0\_g3\_i2 | 716.02 | 127.9 | 5.6 | 1.55E-62 |  |
| TRINITY\_DN16203\_c0\_g2\_i1 | 103.21 | 19.84 | 5.2 | 2.91E-34 |  |
| TRINITY\_DN3149\_c0\_g1\_i3 | 141.58 | 33.27 | 4.26 | 3.44E-55 | Non-histone protein 10 |
| TRINITY\_DN3262\_c0\_g1\_i1 | 403.73 | 99.54 | 4.06 | 5.44E-33 | Putative reverse transcriptase |
| TRINITY\_DN1300\_c2\_g1\_i4 | 622.9 | 158.63 | 3.93 | 7.42E-10 | Tenascin |
| TRINITY\_DN1883\_c0\_g1\_i1 | 746.01 | 204.64 | 3.65 | 4.65E-28 | Alanine-glyoxylate transaminase |
| TRINITY\_DN34995\_c0\_g1\_i5 | 314.51 | 90.7 | 3.47 | 7.07E-17 | Organic cation transporter protein-like |
| TRINITY\_DN3\_c0\_g1\_i7 | 2170.77 | 704.6 | 3.08 | 4.78E-02 | Alpha-2-macroglobulin |
| TRINITY\_DN333\_c1\_g1\_i10 | 227802.92 | 76872.27 | 2.96 | 4.94E-10 | Retrovirus-related Pol polyprotein from type-2 retrotransposable element |
| TRINITY\_DN2955\_c0\_g2\_i4 | 208.2 | 73.31 | 2.84 | 3.47E-22 | Probable tRNA N6-adenosine threonylcarbamoyltransferase |
| TRINITY\_DN8435\_c0\_g1\_i9 | 959.75 | 352.47 | 2.72 | 3.70E-52 | Apoptosis-stimulating of p53 protein 1 |
| TRINITY\_DN48284\_c0\_g1\_i5 | 39.55 | 15.4 | 2.57 | 4.20E-05 | Hypothetical protein |
| TRINITY\_DN7759\_c0\_g2\_i1 | 134.15 | 53.34 | 2.52 | 5.31E-07 | Lachesin |
| TRINITY\_DN5603\_c0\_g1\_i1 | 3759.25 | 1504.62 | 2.5 | 3.77E-12 |  |
| TRINITY\_DN228\_c2\_g1\_i1 | 404.92 | 164.25 | 2.47 | 1.72E-08 |  |
| TRINITY\_DN1712\_c0\_g1\_i3 | 9904.54 | 4070.22 | 2.43 | 7.74E-10 | Kynurenine formamidase |
| TRINITY\_DN790\_c0\_g1\_i1 | 357.01 | 148.82 | 2.4 | 1.57E-19 | Sideroflexin-1-like |
| TRINITY\_DN13587\_c0\_g2\_i4 | 9406.01 | 3943.09 | 2.39 | 5.15E-14 | Urate oxidase |
| TRINITY\_DN9337\_c0\_g1\_i9 | 733.03 | 311.48 | 2.35 | 3.86E-20 | Solute carrier family 5 (high affinity choline transporter), member 7 |
| TRINITY\_DN3165\_c0\_g2\_i1 | 460.83 | 196.27 | 2.35 | 1.23E-10 | Adducin |
| TRINITY\_DN541\_c0\_g1\_i4 | 35776.35 | 15487.59 | 2.31 | 4.33E-18 |  |
| TRINITY\_DN3003\_c0\_g1\_i5 | 567.59 | 252.88 | 2.24 | 6.93E-07 | 4-aminobutyrate aminotransferase |
| TRINITY\_DN25024\_c0\_g1\_i2 | 31.45 | 14.03 | 2.24 | 7.44E-06 | Predicted protein |
| TRINITY\_DN9870\_c0\_g1\_i4 | 142.87 | 64.12 | 2.23 | 2.74E-16 | Set1/Ash2 histone methyltransferase complex subunit |
| TRINITY\_DN6742\_c0\_g2\_i5 | 46.62 | 22.66 | 2.06 | 2.51E-07 | WD repeat and HMG-box DNA-binding protein 1-like |
| TRINITY\_DN45489\_c0\_g2\_i2 | 170.53 | 82.97 | 2.06 | 8.91E-09 | 28S ribosomal protein S14 |
| TRINITY\_DN595\_c1\_g1\_i9 | 4438.87 | 2165.01 | 2.05 | 4.23E-06 | Sulfur dioxygenase |
| TRINITY\_DN1681\_c0\_g1\_i14 | 338.72 | 166.57 | 2.03 | 4.98E-18 | Tigger transposable element-derived protein 1 |
| TRINITY\_DN650\_c0\_g1\_i5 | 200.49 | 98.71 | 2.03 | 5.36E-26 | Gamma-secretase subunit pen-2 |
| TRINITY\_DN91578\_c0\_g1\_i1 | 1154.75 | 572.68 | 2.02 | 1.09E-16 | Protein LTV1 |
| outlier SNP overlapped DEGs in OT | TRINITY\_DN1677\_c0\_g1\_i5 | 32.25 | 1436.39 | 0.02 | 4.67E-32 | Venom carboxylesterase-6-like |
| TRINITY\_DN32241\_c0\_g1\_i5 | 8 | 82.15 | 0.1 | 1.94E-35 |  |
| TRINITY\_DN11995\_c0\_g1\_i1 | 9.66 | 76.86 | 0.13 | 1.75E-09 |  |
| TRINITY\_DN4640\_c0\_g1\_i2 | 27.21 | 179.07 | 0.15 | 1.08E-08 | Neuroblast differentiation-associated protein AHNAK-like |
| TRINITY\_DN1459\_c0\_g1\_i2 | 75.12 | 422.7 | 0.18 | 7.11E-23 | Myosin heavy chain |
| TRINITY\_DN46066\_c0\_g1\_i1 | 0.3 | 1.6 | 0.19 | 7.12E-03 | Hypothetical protein |
| TRINITY\_DN7604\_c0\_g1\_i2 | 128.08 | 677.64 | 0.19 | 4.25E-50 | N-acetylated-alpha-linked acidic dipeptidase 2 |
| TRINITY\_DN14884\_c0\_g1\_i4 | 26.56 | 126.63 | 0.21 | 5.14E-46 |  |
| TRINITY\_DN10987\_c0\_g1\_i1 | 135.11 | 627.99 | 0.22 | 2.75E-46 |  |
| TRINITY\_DN2270\_c0\_g1\_i5 | 181.51 | 675.52 | 0.27 | 3.71E-83 | Replication protein A 70 kDa DNA-binding subunit |
| TRINITY\_DN6807\_c0\_g1\_i5 | 90.74 | 319.57 | 0.28 | 8.26E-14 | 52 kDa repressor of the inhibitor of the protein kinase |
| TRINITY\_DN15013\_c0\_g1\_i11 | 12.82 | 43.5 | 0.29 | 9.08E-32 |  |
| TRINITY\_DN911\_c0\_g1\_i14 | 146.68 | 496.57 | 0.3 | 5.48E-12 | TatD DNase family protein |
| TRINITY\_DN15667\_c0\_g1\_i2 | 19.08 | 61.45 | 0.31 | 3.60E-07 | Myosin heavy chain |
| TRINITY\_DN6207\_c0\_g1\_i2 | 253.27 | 737.16 | 0.34 | 2.10E-04 | Neuroblast differentiation-associated protein AHNAK |
| TRINITY\_DN1248\_c0\_g2\_i1 | 25.24 | 73.36 | 0.34 | 1.85E-12 | Ribosome biogenesis protein |
| TRINITY\_DN148\_c0\_g1\_i2 | 3348.4 | 9492.72 | 0.35 | 7.62E-13 | Myosin heavy chain |
| TRINITY\_DN31417\_c0\_g2\_i1 | 243.66 | 683.7 | 0.36 | 9.73E-15 | Serine hydroxymethyltransferase |
| TRINITY\_DN1227\_c0\_g2\_i2 | 339.38 | 906.11 | 0.37 | 5.05E-26 | Protein unc-45 homolog B |
| TRINITY\_DN7055\_c0\_g2\_i1 | 3431.77 | 9102.52 | 0.38 | 1.50E-12 | 4-hydroxyphenylpyruvate dioxygenase |
| TRINITY\_DN5306\_c0\_g1\_i1 | 4.66 | 12.25 | 0.38 | 1.79E-04 |  |
| TRINITY\_DN5758\_c0\_g1\_i9 | 207.73 | 540.62 | 0.38 | 5.82E-15 | RNA-binding protein NOB1 |
| TRINITY\_DN1650\_c4\_g1\_i6 | 135.15 | 320.13 | 0.42 | 1.16E-12 | Signal transducer and activator of transcription 5B |
| TRINITY\_DN26415\_c0\_g1\_i1 | 36.33 | 84.41 | 0.43 | 2.65E-17 | Protein ZBED8-like |
| TRINITY\_DN238\_c0\_g3\_i2 | 68.89 | 158.02 | 0.44 | 1.33E-22 |  |
| TRINITY\_DN3655\_c0\_g1\_i10 | 133.71 | 296.79 | 0.45 | 1.06E-20 | Tigger transposable element-derived protein 1 |
| TRINITY\_DN9147\_c0\_g1\_i2 | 102 | 221.11 | 0.46 | 4.38E-22 | WD repeat-containing protein 37 |
| TRINITY\_DN10889\_c0\_g1\_i8 | 143.95 | 306.19 | 0.47 | 4.23E-12 | Maltase A2-like |
| TRINITY\_DN3497\_c0\_g1\_i2 | 1712.57 | 3549.77 | 0.48 | 6.00E-15 |  |
| TRINITY\_DN2893\_c0\_g1\_i5 | 129.17 | 264.34 | 0.49 | 1.88E-06 | Leucine zipper putative tumor suppressor 2 |
| TRINITY\_DN3615\_c0\_g2\_i5 | 118.73 | 242.36 | 0.49 | 1.92E-13 |  |
| TRINITY\_DN9210\_c0\_g1\_i2 | 15.06 | 30.36 | 0.5 | 1.79E-09 | RNA-directed DNA polymerase from mobile element jockey-like |

**Supplementary Figures**

****Supplementary Figure S1. **(A)** Sequence number in different GO categories of all unigenes. **(B)** Sequence number in the top 30 KEGG categories of all unigenes.

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Supplementary Figure S2.The correlation analysis of real-time PCR and RNA-Seq data.

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Supplementary Figure S3. **(A)** Sequence number in different GO categories of DEGs. **(B)** Sequence number in different GO categories of outlier SNPs