**Table S1:** Filtered reads data volume and statistical table of quality

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Sample | Clean Bases | Clean Reads | Q20% | Q30% | GC% |
| CUR0-1 | 6412546931 | 43599460 | 97.98 | 94.32 | 43.00 |
| CUR0-2 | 6390338026 | 43376374 | 98.04 | 94.5 | 42.97 |
| CUR0-3 | 6128863841 | 41613048 | 98.18 | 94.87 | 43.23 |
| CUR200-1 | 7543524604 | 51431526 | 98.08 | 94.64 | 43.33 |
| CUR200-2 | 6015299140 | 40788978 | 98.07 | 94.54 | 43.17 |
| CUR200-3 | 6700001527 | 45256000 | 98.03 | 94.43 | 43.49 |
| Control-1 | 6452067836 | 43747844 | 98.17 | 94.78 | 44.06 |
| Control-2 | 6542979049 | 44398334 | 98.17 | 94.87 | 44.15 |

**Note:** Clean bases is the total number of sequencing reads after quality control (The number of Clean reads multiplied by the length of the reads); Clean reads is the total number of sequencing reads after quality control;（7）Q20 %、Q30 % means the quality assessment of sequencing data after quality control, where Q20 and Q30 refer to the percentage of bases with sequencing quality above 99% and 99.9% respectively, generally Q20 above 85% and Q30 above 80%. (8) GC% % means the percentage of G and C bases in the total bases of quality-controlled data.

**Table S2:** Table of comparison statistics with assembly results

|  |  |  |  |
| --- | --- | --- | --- |
| Sample | Clean Reads | Mapped reads | Mapped ratio |
| CUR0-1 | 21799730 | 18301974 | 83.96% |
| CUR0-2 | 21688187 | 18173622 | 83.80% |
| CUR0-3 | 20806524 | 17482787 | 84.03% |
| CUR200-1 | 25715763 | 21751145 | 84.58% |
| CUR200-2 | 20394489 | 17163321 | 84.16% |
| CUR200-3 | 22628000 | 19070306 | 84.28% |
| Control-1 | 22199167 | 18748253 | 84.45% |
| Control-2 | 21873922 | 18501716 | 84.58% |

**Note:** Clean reads means the number of filtered sequencing reads; Mapped reads implies the number of Clean reads that can be aligned to the assembled transcriptome; Mapped ratio means the percentage of Clean reads that can be located on the assembled transcriptome.

**Table S3:** KEGG metabolic pathway functional annotation analysis results of differentially expressed unigenes

|  |  |  |
| --- | --- | --- |
| KEGG Pathway | Unigene number | Gene id |
| Plant hormone signal transduction | 8 | TRINITY\_DN4666\_c0\_g1; TRINITY\_DN8281\_c0\_g1; TRINITY\_DN5683\_c0\_g1; TRINITY\_DN7510\_c0\_g1; TRINITY\_DN13178\_c0\_g1; TRINITY\_DN5433\_c0\_g1; TRINITY\_DN3919\_c0\_g1; TRINITY\_DN4687\_c0\_g1; |
| Glutathione metabolism | 8 | TRINITY\_DN2438\_c0\_g1; TRINITY\_DN4732\_c0\_g1; TRINITY\_DN6564\_c0\_g1; TRINITY\_DN56492\_c0\_g1; TRINITY\_DN10678\_c0\_g1; TRINITY\_DN3690\_c1\_g2; TRINITY\_DN8963\_c0\_g1; TRINITY\_DN11350\_c1\_g2 |
| Oxidative phosphorylation | 7 | TRINITY\_DN9948\_c0\_g5; TRINITY\_DN9948\_c0\_g6; TRINITY\_DN2571\_c0\_g12; TRINITY\_DN501\_c1\_g3; TRINITY\_DN501\_c1\_g1; TRINITY\_DN860\_c0\_g8;TRINITY\_DN871\_c0\_g2 |
| Starch and sucrose metabolism | 6 | TRINITY\_DN605\_c0\_g1; TRINITY\_DN44347\_c0\_g2; TRINITY\_DN9167\_c1\_g2; TRINITY\_DN4980\_c0\_g1; TRINITY\_DN873\_c0\_g1; TRINITY\_DN27\_c0\_g2 |
| Phagosome | 5 | TRINITY\_DN11486\_c0\_g2; TRINITY\_DN2142\_c0\_g1; TRINITY\_DN11486\_c0\_g1; TRINITY\_DN809\_c0\_g2; TRINITY\_DN16326\_c0\_g1 |
| Plant-pathogen interaction | 5 | TRINITY\_DN1627\_c1\_g1; TRINITY\_DN59454\_c0\_g1; TRINITY\_DN2102\_c0\_g2; TRINITY\_DN6154\_c0\_g1; TRINITY\_DN18928\_c1\_g1 |
| Amino sugar and nucleotide sugar metabolism | 5 | TRINITY\_DN7388\_c0\_g1; TRINITY\_DN9167\_c1\_g2; TRINITY\_DN27\_c0\_g2; TRINITY\_DN7742\_c0\_g2; TRINITY\_DN2879\_c0\_g2 |
| Biosynthesis of cofactors | 4 | TRINITY\_DN4203\_c0\_g1; TRINITY\_DN10923\_c1\_g2; TRINITY\_DN7742\_c0\_g2; TRINITY\_DN1961\_c2\_g2 |
| Brassinosteroid biosynthesis | 4 | TRINITY\_DN19463\_c0\_g1; TRINITY\_DN513\_c1\_g1; TRINITY\_DN12571\_c1\_g1; TRINITY\_DN6461\_c0\_g1 |
| Cysteine and methionine metaboli | 3 | TRINITY\_DN4965\_c0\_g3; TRINITY\_DN1261\_c0\_g1; TRINITY\_DN40192\_c0\_g1 |
| MAPK signaling pathway - plant | 3 | TRINITY\_DN10923\_c1\_g2; TRINITY\_DN18928\_c1\_g1; TRINITY\_DN13755\_c0\_g1; |
| Porphyrin and chlorophyll metabo | 3 | TRINITY\_DN702\_c0\_g1; TRINITY\_DN4203\_c0\_g1; TRINITY\_DN1961\_c2\_g2 |
| Ribosome | 2 | TRINITY\_DN10491\_c0\_g2; TRINITY\_DN5851\_c1\_g1 |
| Flavone and flavonol biosynthesis | 2 | TRINITY\_DN7547\_c0\_g1; TRINITY\_DN10801\_c0\_g1 |
| Tryptophan metabolism | 2 | TRINITY\_DN21612\_c0\_g1; TRINITY\_DN13646\_c0\_g1 |
| Pentose and glucuronate intercon | 2 | TRINITY\_DN7754\_c0\_g1; TRINITY\_DN5793\_c0\_g1 |
| Glycerophospholipid metabolism | 2 | TRINITY\_DN4584\_c0\_g1; TRINITY\_DN18835\_c0\_g1 |
| Glycerolipid metabolism | 2 | TRINITY\_DN4584\_c0\_g1; TRINITY\_DN2363\_c0\_g1 |
| Tyrosine metabolism | 2 | TRINITY\_DN30264\_c0\_g2; TRINITY\_DN10116\_c0\_g1 |
| Selenocompound metabolism | 2 | TRINITY\_DN4965\_c0\_g3; TRINITY\_DN1261\_c0\_g1 |
| Sesquiterpenoid and triterpenoid b | 2 | TRINITY\_DN12850\_c0\_g1; TRINITY\_DN8282\_c0\_g1 |
| Phenylalanine metabolism | 1 | TRINITY\_DN30264\_c0\_g2 |
| Carotenoid biosynthesis | 1 | TRINITY\_DN1375\_c1\_g1 |
| Terpenoid backbone biosynthesis | 1 | TRINITY\_DN2087\_c0\_g3 |
| Glyoxylate and dicarboxylate metabolism | 1 | TRINITY\_DN15081\_c0\_g1 |
| Sulfur metabolism | 1 | TRINITY\_DN7029\_c0\_g1 |
| Ubiquitin mediated proteolysis | 1 | TRINITY\_DN5851\_c1\_g1 |
| RNA degradation | 1 | TRINITY\_DN6937\_c0\_g2 |
| Protein processing in endoplasm | 1 | TRINITY\_DN20404\_c1\_g1 |
| Homologous recombination | 1 | TRINITY\_DN54984\_c0\_g1 |
| ABC transporters | 1 | TRINITY\_DN7829\_c0\_g1 |
| Ether lipid metabolism | 1 | TRINITY\_DN18835\_c0\_g1 |
| Carbon fixation in photosynthetic | 1 | TRINITY\_DN15081\_c0\_g1 |
| Phenylpropanoid biosynthesis | 1 | TRINITY\_DN5436\_c0\_g1 |
| Fatty acid elongation | 1 | TRINITY\_DN2102\_c0\_g2; |
| Fructose and mannose metabolism | 1 | TRINITY\_DN9167\_c1\_g2 |
| Ascorbate and aldarate metabolism | 1 | TRINITY\_DN7742\_c0\_g2 |
| Galactose metabolism | 1 | TRINITY\_DN44347\_c0\_g2 |
| Riboflavin metabolism | 1 | TRINITY\_DN5826\_c0\_g2 |
| Purine metabolism | 1 | TRINITY\_DN10923\_c1\_g2 |
| Arginine and proline metabolism | 1 | TRINITY\_DN56492\_c0\_g1 |
| Thiamine metabolism | 1 | TRINITY\_DN2087\_c0\_g3 |
| Pyrimidine metabolism | 1 | TRINITY\_DN10923\_c1\_g2 |
| Isoquinoline alkaloid biosynthesis | 1 | TRINITY\_DN10116\_c0\_g1 |
| Base excision repair | 1 | TRINITY\_DN6502\_c0\_g1 |
| Nucleocytoplasmic transport | 1 | TRINITY\_DN11637\_c0\_g1 |
| Phosphatidylinositol signaling sys | 1 | TRINITY\_DN18928\_c1\_g1 |
| Endocytosis | 1 | TRINITY\_DN18835\_c0\_g1 |
| Circadian rhythm - plant | 1 | TRINITY\_DN5430\_c0\_g1 |

**Table S4:** 29 differentially expressed unigenes obtained in TFs Analysis

|  |  |  |
| --- | --- | --- |
| Family | Unigene number | Gene id |
| MYB | 6 | TRINITY\_DN10830\_c1\_g1; TRINITY\_DN10830\_c0\_g1; TRINITY\_DN8763\_c1\_g2; TRINITY\_DN2444\_c0\_g1; TRINITY\_DN1138\_c0\_g1; TRINITY\_DN3202\_c0\_g5 |
| AP2/ERF | 6 | TRINITY\_DN8959\_c0\_g1; TRINITY\_DN5338\_c0\_g1; TRINITY\_DN17085\_c0\_g1; TRINITY\_DN7675\_c0\_g1; TRINITY\_DN6154\_c0\_g1; TRINITY\_DN3300\_c0\_g1 |
| NAC | 5 | TRINITY\_DN14696\_c1\_g1; TRINITY\_DN15035\_c0\_g1; TRINITY\_DN1125\_c0\_g1; TRINITY\_DN51735\_c1\_g1; TRINITY\_DN21556\_c0\_g2 |
| bHLH | 4 | TRINITY\_DN3463\_c0\_g1; TRINITY\_DN3176\_c0\_g1; TRINITY\_DN5012\_c0\_g1; TRINITY\_DN2312\_c0\_g1 |
| C2C2 | 3 | TRINITY\_DN7157\_c0\_g1; TRINITY\_DN7157\_c0\_g2; TRINITY\_DN3957\_c1\_g2 |
| bZIP | 1 | TRINITY\_DN25587\_c0\_g4 |
| LBD (AS2/LOB) | 1 | TRINITY\_DN34582\_c0\_g1 |
| B3 | 1 | TRINITY\_DN5877\_c0\_g1 |
| HSF | 1 | TRINITY\_DN30885\_c1\_g1 |
| GRAS | 1 | TRINITY\_DN1329\_c4\_g1 |



**Fig S1:** Functional annotation analysis of differentially expressed unigenes in the 7 major KEGG metabolic pathways