

Table S1. Primer sequences used in this study

| Gene ID | Sequence(5'-3') |
|------------------|---------------------------------------------------|
| Potri.002G030900 | GGGCAAGGGATGAAGGAGTTTA CTCCAGTCCAATAGCACCCCTT |
| Potri.004G059600 | ATCAGTTCCCCAAGTGGAATCC GACGGGATAGTCTACAGCAAGG |
| Potri.011G153300 | TAGGAGAGGCAATCCCAGAAGA ATGAGCCTTTGGGACTCTCAAG |
| Potri.006G209200 | TGGGTACTGAGATGAGAGCTCA AGCACCATTTCTAATTGCTCCCA |
| Potri.012G067600 | ATCCTCCGCCCAATGAATATCC AGTCCGCAGATTAAGAAAGCCA |
| Potri.013G090300 | CGCAAGTATGAACAAGGTTGCA GGGATGTTTCTGCATGTATGGC |
| Potri.015G033600 | GAAGAGGTAGATCAGCGGGAAG TCACTCATTTGACACACCACCA |
| Potri.017G082900 | GATGGCTGTGGAGAATTCATGC CACGACGGTGGAATTACGATG |

Table S2 The statistic of transcriptome sequence quality pre- and post- processing

| Sample | Raw Data | Valid Data | Valid Ratio (reads)% | Q30% | Mapped reads | Mapping Rate(%) |
|---------|------------------|------------------|-------------------------|-------|-----------------|--------------------|
| CK_Di1 | 40937780(6.14G) | 39151098(5.87G) | 95.64 | 98.12 | 33724066 | 86.14 |
| CK_Di2 | 41709612(6.26G) | 40690354(6.10G) | 97.56 | 98.00 | 35103839 | 86.27 |
| CK_Di3 | 50525036(7.58G) | 49441064(7.42G) | 97.85 | 98.30 | 42762384 | 86.49 |
| CK_Te1 | 43254944(6.49G) | 42966190(6.44G) | 99.33 | 98.54 | 37494494 | 87.27 |
| CK_Te2 | 31076296(4.66G) | 30854578(4.63G) | 99.29 | 98.42 | 26829187 | 86.95 |
| CK_Te3 | 52471146(7.87G) | 52144852(7.82G) | 99.38 | 98.35 | 45309079 | 86.89 |
| Dro_Di1 | 44638308(6.70G) | 44340014(6.65G) | 99.33 | 98.20 | 38456220 | 86.73 |
| Dro_Di2 | 35263734(5.29G) | 35017318(5.25G) | 99.30 | 98.72 | 30431223 | 86.90 |
| Dro_Di3 | 32687338(4.90G) | 32430362(4.86G) | 99.21 | 98.31 | 28024075 | 86.41 |
| Dro_Te1 | 35550550(5.33G) | 34435186(5.17G) | 96.86 | 97.86 | 30053391 | 87.28 |
| Dro_Te2 | 41329582(6.20G) | 40052292(6.01G) | 96.91 | 98.33 | 35209046 | 87.91 |
| Dro_Te3 | 53784504(8.07G) | 51985308(7.80G) | 96.65 | 98.37 | 45873025 | 88.24 |
| Re_Di1 | 38919728(5.84G) | 37922010(5.69G) | 97.44 | 98.09 | 32525493 | 85.77 |
| Re_Di2 | 37712898(5.66G) | 36464632(5.47G) | 96.69 | 98.04 | 31365395 | 86.02 |
| Re_Di3 | 37473760(5.62G) | 35857588(5.38G) | 95.69 | 98.13 | 30996166 | 86.44 |
| Re_Te1 | 46309984(6.95G) | 43773740(6.57G) | 94.52 | 97.92 | 38271237 | 87.43 |
| Re_Te2 | 71430152(10.71G) | 69306878(10.40G) | 97.03 | 98.50 | 60920266 | 87.90 |
| Re_Te3 | 40043120(6.01G) | 37687786(5.65G) | 94.12 | 97.82 | 32748733 | 86.89 |

Note: Raw Data: Raw Data statistics, sequence reads and bases of each sample; Valid Data: The effective data volume statistics, the reads number and proportion of each sample after quality pretreatment, the total number of bases (bases) and the proportion and average length; Q30: The quality score is not less than30 (Single base error rate 0.001) base number and proportion.

Table.S3 The opposite expression co-DEGs on the compared tetraploid with diploid during drought condition

| Gene name | Te | Di | Gene symbol | Annotation |
|------------------|----|------|-------------|-------------------------------------------------------------------------------------|
| Potri.019G088200 | up | down | AT1G17860 | Kunitz family trypsin and protease inhibitor protein |
| Potri.013G080400 | up | down | AT4G24350 | Phosphorylase superfamily protein |
| Potri.013G082800 | up | down | AT4G24340 | Phosphorylase superfamily protein |
| Potri.009G114800 | up | down | AT1G49310 | transmembrane protein |
| Potri.013G080450 | up | down | AT4G24350 | Phosphorylase superfamily protein |
| Potri.013G082700 | up | down | AT4G24340 | Phosphorylase superfamily protein |
| Potri.019G031200 | up | down | APY2 | apyrase 2 |
| Potri.009G042500 | up | down | IRX12 | Laccase/Diphenol oxidase family protein |
| Potri.012G130900 | up | down | ATS3 | Embryo-specific protein 3, (ATS3) |
| Potri.013G103800 | up | down | AT1G75280 | NmrA-like negative transcriptional regulat- or family protein |
| Potri.015G129400 | up | down | FLA11 | FASCICLIN-like arabinogalactan-protein 11 |
| Potri.009G092300 | up | down | AGP18 | arabinogalactan protein 18 |
| Potri.002G111900 | up | down | TUA2 | tubulin alpha-2 chain |
| Potri.002G257900 | up | down | CESA4 | cellulose synthase A4 |
| Potri.018G103900 | up | down | IRX3 | Cellulose synthase family protein |
| Potri.010G141600 | up | down | CTL2 | chitinase-like protein 2 |
| Potri.001G280200 | up | down | MDIS1 | Leucine-rich repeat protein kinase family protein |
| Potri.010G183500 | up | down | LAC12 | laccase 12 |
| Potri.006G277300 | up | down | CHY1 | beta-hydroxyisobutyryl-CoA hydrolase 1 |
| Potri.010G244900 | up | down | FLA17 | FASCICLIN-like arabinogalactan protein 17 precursor |
| Potri.015G060100 | up | down | IRX6 | COBRA-like extracellular glycosylphosph- atidyl inositol-anchored protein family |
| Potri.014G139900 | up | down | AT1G52140 | Avr9/Cf-9 rapidly elicited protein |
| Potri.019G121801 | up | down | AT1G73325 | Kunitz family trypsin and protease inhibitor protein |
| Potri.004G059600 | up | down | IRX1 | cellulose synthase family protein |
| Potri.001G068100 | up | down | GUT1 | Exostosin family protein |
| Potri.005G141300 | up | down | IRX15-L | Protein of unknown function (DUF579) |
| Potri.005G065200 | up | down | AT5G64030 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein |
| Potri.006G181900 | up | down | IRX3 | Cellulose synthase family protein |
| Potri.T029200 | up | down | AT1G73325 | Kunitz family trypsin and protease inhibitor protein |

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|-------------------------|----|------|-----------|---------------------------------------------------------|
| Potri.010G184000 | up | down | TBL33 | TRICHOME BIREFRINGENCE-LIKE 33 |
| Potri.004G211900 | up | down | AT2G28315 | Nucleotide/sugar transporter family protein |
| Potri.019G002100 | up | down | AT2G03200 | Eukaryotic aspartyl protease family protein |
| Potri.016G119100 | up | down | TBL3 | Plant protein of unknown function (DUF828) |
| Potri.006G129200 | up | down | FLA11 | FASCICLIN-like arabinogalactan-protein 11 |
| Potri.005G232400 | up | down | AT1G19715 | Mannose-binding lectin superfamily protein |
| Potri.004G156500 | up | down | MCM4 | Minichromosome maintenance (MCM2/3/5) family protein |
| Potri.T131500 | up | down | PRB1 | basic pathogenesis-related protein 1 |
| Potri.003G173300 | up | down | MAP65-8 | microtubule-associated protein 65-8 |
| Potri.001G416800 | up | down | GAUT12 | galacturonosyltransferase 12 |
| Potri.016G111000 | up | down | PHT4 | phosphate transporter 4 |
| Potri.010G193100 | up | down | IRX12 | Laccase/Diphenol oxidase family protein |
| Potri.007G031700 | up | down | GATL2 | galacturonosyltransferase-like 2 |
| Potri.016G112000 | up | down | IRX12 | Laccase/Diphenol oxidase family protein |
| Potri.014G159800 | up | down | MPL1 | Myzus persicae-induced lipase 1 |
| Potri.009G098966 | up | down | | |
| Potri.001G375700 | up | down | IQD10 | IQ-domain 10 |
| Potri.008G094700 | up | down | KLCR2 | Tetratricopeptide repeat (TPR)-like superfamily protein |
| Potri.014G022600 | up | down | AT3G53010 | Domain of unknown function (DUF303) |
| Potri.008G061700 | up | down | AT3G55646 | TPRXL |
| Potri.001G055100 | up | down | MAP65-8 | microtubule-associated protein 65-8 |
| Potri.001G289500 | up | down | TUA6 | Tubulin/FtsZ family protein |
| Potri.T093800 | up | down | CIPK21 | CBL-interacting protein kinase 21 |
| Potri.002G101600 | up | down | EXI1 | hypothetical protein |
| Potri.011G068300 | up | down | AT1G29200 | O-fucosyltransferase family protein |
| MSTRG.22338 | up | down | | |
| Potri.006G137300 | up | down | RBOHE | Riboflavin synthase-like superfamily protein |
| Potri.014G110400 | up | down | GLP10 | germin-like protein 10 |
| Potri.009G049900 | up | down | HSP17.8 | HSP20-like chaperones superfamily protein |
| Potri.009G011100 | up | down | UXT1 | Nucleotide/sugar transporter family protein |
| Potri.002G261700 | up | down | TRM30 | hypothetical protein |
| Potri.002G082400 | up | down | ILL6 | IAA-leucine resistant (ILR)-like gene 6 |
| Potri.008G026400 | up | down | ATCSLA09 | Nucleotide-diphospho-sugar transferases |

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|-------------------------|----|------|--------------|-------------------------------------------------------------------------------|
| | | | | superfamily protein |
| Potri.003G076000 | up | down | HSP23.6-MITO | mitochondrion-localized small heat shock protein 23.6 |
| Potri.004G187201 | up | down | | |
| Potri.016G086400 | up | down | IRX9 | Nucleotide-diphospho-sugar transferases superfamily protein |
| Potri.004G211600 | up | down | UBL5A | Ubiquitin-like superfamily protein |
| Potri.006G110900 | up | down | AT2G38600 | HAD superfamily, subfamily IIIB acid phosphatase |
| Potri.008G069900 | up | down | ESK1 | Plant protein of unknown function (DUF828) |
| Potri.008G073800 | up | down | LAC12 | laccase 12 |
| Potri.006G120400 | up | down | AT1G63300 | Myosin heavy chain-related protein |
| Potri.009G129900 | up | down | PRP4 | proline-rich protein 4 |
| Potri.014G126000 | up | down | EXL2 | EXORDIUM like 2 |
| Potri.001G191400 | up | down | AT3G16370 | GDSL-like Lipase/Acylhydrolase superfamily protein |
| Potri.004G056500 | up | down | SAG12 | senescence-associated gene 12 |
| Potri.019G101900 | up | down | EXPB3 | expansin B3 |
| Potri.004G185000 | up | down | CER4 | Jojoba acyl CoA reductase-related male sterility protein |
| Potri.011G153300 | up | down | NST1 | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein |
| Potri.008G006500 | up | down | AT1G71070 | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein |
| Potri.014G029900 | up | down | PGSIP3 | plant glycogenin-like starch initiation protein 3 |
| Potri.008G224300 | up | down | SYD | P-loop containing nucleoside triphosphate hydrolases superfamily protein |
| Potri.002G227400 | up | down | APR3 | APS reductase 3 |
| Potri.011G047300 | up | down | LPA1 | tetratricopeptide repeat (TPR)-containing protein |
| Potri.006G188300 | up | down | ChiC | Glycosyl hydrolase family protein with chitinase insertion domain |
| Potri.001G127100 | up | down | AT5G45290 | RING/U-box superfamily protein |
| Potri.002G231350 | up | down | | |
| Potri.001G268600 | up | down | CAD7 | elicitor-activated gene 3-1 |
| MSTRG.6488 | up | down | | |
| Potri.005G134500 | up | down | AT3G19080 | SWIB complex BAF60b domain-containing protein |
| Potri.006G094300 | up | down | AT3G54040 | PAR1 protein |
| Potri.004G187400 | up | down | AT1G07400 | HSP20-like chaperones superfamily protein |

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|-------------------------|----|------|-----------|----------------------------------------------------------------------------|
| Potri.009G009500 | up | down | AT5G60720 | Protein of unknown function, DUF547 |
| Potri.T140850 | up | down | | |
| Potri.004G187400 | up | down | AT1G07400 | HSP20-like chaperones superfamily protein |
| Potri.T117800 | up | down | AT3G14470 | NB-ARC domain-containing disease resistance protein |
| Potri.016G103900 | up | down | AT5G09850 | Transcription elongation factor (TFIIS) family protein |
| Potri.006G149900 | up | down | AT2G26695 | Ran BP2/NZF zinc finger-like superfamily protein |
| MSTRG.21672 | up | down | | |
| Potri.010G195600 | up | down | AT3G55700 | UDP-Glycosyltransferase superfamily protein |
| Potri.008G017100 | up | down | CAT6 | cationic amino acid transporter 6 |
| Potri.010G236700 | up | down | CYP94C1 | cytochrome P450, family 94, subfamily C, polypeptide 1 |
| Potri.004G056000 | up | down | SAG12 | senescence-associated gene 12 |
| Potri.010G236600 | up | down | LAX3 | like AUX1 3 |
| Potri.002G258000 | up | down | MIK2 | Leucine-rich repeat receptor-like protein kinase family protein |
| Potri.010G095200 | up | down | CYCD1 | CYCLIN D1 |
| Potri.010G121800 | up | down | AT1G68390 | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein |
| Potri.002G101800 | up | down | AT1G72220 | RING/U-box superfamily protein |
| Potri.014G113200 | up | down | ABCB21 | P-glycoprotein 21 |
| Potri.006G234300 | up | down | OZF2 | Zinc finger C-x8-C-x5-C-x3-H type family protein |
| Potri.004G056100 | up | down | SAG12 | senescence-associated gene 12 |
| Potri.012G055300 | up | down | AT1G48780 | hypothetical protein |
| Potri.010G072200 | up | down | PRP1 | proline-rich protein 1 |
| Potri.015G033600 | up | down | MYB52 | myb domain protein 52 |
| Potri.009G010400 | up | down | NCRK | Protein kinase superfamily protein |
| Potri.017G135000 | up | down | PUB21 | ARM repeat superfamily protein |
| Potri.010G096400 | up | down | AT1G60060 | Serine/threonine-protein kinase WNK (With No Lysine)-related |
| Potri.010G127600 | up | down | CXE17 | carboxyesterase 17 |
| Potri.015G088400 | up | down | AT1G24480 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein |
| Potri.005G183300 | up | down | AT1G21550 | Calcium-binding EF-hand family protein |
| Potri.013G066200 | up | down | UNE7 | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein |
| Potri.002G258400 | up | down | AT1G35710 | Protein kinase family protein with leucine-rich repeat domain |
| Potri.002G030900 | up | down | BLH11 | BEL1-like homeodomain 11 |

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| Potri.018G117900 | up | down | RLP1 | receptor like protein 1 |
| Potri.009G138900 | up | down | AT2G16990 | Major facilitator superfamily protein |
| Potri.005G246100 | up | down | PETE1 | plastocyanin 1 |
| Potri.004G056100 | up | down | SAG12 | senescence-associated gene 12 |
| Potri.005G095500 | up | down | TPS21 | terpene synthase 21 |
| Potri.001G173700 | down | up | AT3G15650 | alpha/beta-Hydrolases superfamily protein |
| Potri.004G078500 | down | up | AT1G65720 | transmembrane protein |
| Potri.004G044000 | down | up | AT1G53035 | transmembrane protein |
| Potri.010G155150 | down | up | | |
| Potri.002G122900 | down | up | ASPG1 | N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein |
| Potri.004G020500 | down | up | THI1 | thiazole biosynthetic enzyme, chloroplast (ARA6) (THI1) (THI4) |
| Potri.T092101 | down | up | | |
| Potri.001G015300 | down | up | LOX2 | lipoxygenase 2 |
| Potri.002G233200 | down | up | AT5G16740 | Transmembrane amino acid transporter family protein |
| Potri.004G054100 | down | up | PDC2 | pyruvate decarboxylase-2 |
| Potri.001G076800 | down | up | MPB2C | movement protein binding protein 2C |
| Potri.T092101 | down | up | | |
| Potri.016G083500 | down | up | GSTL3 | Glutathione S-transferase family protein |
| Potri.006G262600 | down | up | AT1G13940 | Plant protein of unknown function (DUF863) |
| Potri.011G151100 | down | up | AT4G10550 | Subtilase family protein |
| Potri.019G128200 | down | up | CHAL | allergen-related |
| Potri.012G022600 | down | up | GRF7 | growth-regulating factor 7 |
| Potri.005G103200 | down | up | NAC036 | NAC domain containing protein 36 |
| Potri.005G130100 | down | up | AT5G66590 | CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein |
| Potri.T040800 | down | up | RLP9 | receptor like protein 9 |
| Potri.T143400 | down | up | PDC2 | pyruvate decarboxylase-2 |
| Potri.T092101 | down | up | | |
| Potri.006G034900 | down | up | AT3G10760 | Homeodomain-like superfamily protein |
| Potri.006G191900 | down | up | KHZ2 | KH domain-containing protein / zinc finger (CCCH type) family protein |
| Potri.005G133400 | down | up | AT1G33940 | Serine/Threonine-kinase ULK4-like protein |
| Potri.001G430100 | down | up | AT3G20340 | protein expression protein |
| Potri.010G069700 | down | up | AT3G25400 | dCTP pyrophosphatase-like protein |
| Potri.003G179400 | down | up | AT5G12040 | Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase family protein |
| Potri.019G130100 | down | up | AT5G05280 | RING/U-box superfamily protein |
| Potri.014G055100 | down | up | AT3G58610 | ketol-acid reductoisomerase |

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|-------------------------|------|----|-----------|---------------------------------|-----------------------------|--|
| MSTRG.22028 | down | up | | | | |
| Potri.005G178500 | down | up | AT1G77540 | Acyl-CoA superfamily protein | N-acyltransferases (NAT) | |

Table.S4 The opposite expression co-DEGs on the compared tetraploid with diploid during recovery condition

| Gene name | Te | Di | Gene symbol | Annotation |
|------------------|------|------|-------------|------------------------------------------------------------------------------|
| Potri.017G010900 | up | down | JAL34 | Mannose-binding lectin superfamily protein |
| Potri.001G297466 | up | down | | |
| Potri.017G082900 | up | down | HB34 | homeobox protein 34 |
| Potri.002G235200 | up | down | PDS3 | phytoene desaturase 3 |
| Potri.019G100001 | up | down | | |
| Potri.011G159000 | up | down | AT1G23460 | Pectin lyase-like superfamily protein |
| Potri.005G133400 | up | down | AT1G33940 | Serine/Threonine-kinase ULK4-like protein |
| Potri.008G211900 | up | down | AT1G23460 | Pectin lyase-like superfamily protein |
| Potri.002G124500 | up | down | AT5G67090 | Subtilisin-like serine endopeptidase family protein |
| Potri.005G256000 | up | down | XCP2 | xylem cysteine peptidase 2 |
| Potri.019G047200 | up | down | ITPK1 | Inositol 1,3,4-trisphosphate 5/6-kinase family protein |
| Potri.001G119300 | up | down | AT1G62760 | Plant invertase/pectin methylesterase inhibitor superfamily protein |
| Potri.004G078500 | up | down | AT1G65720 | transmembrane protein |
| Potri.019G058000 | up | down | AT3G56360 | hypothetical protein |
| Potri.002G234400 | up | down | ABCI14 | trigalactosyldiacylglycerol 1 |
| Potri.001G028200 | up | down | AT3G54400 | Eukaryotic aspartyl protease family protein |
| Potri.005G049000 | up | down | AT1G54500 | Rubredoxin-like superfamily protein |
| Potri.008G114100 | up | down | AT4G11610 | C2 calcium/lipid-binding plant phosphorib- osyltransferase family protein |
| Potri.002G026100 | down | up | CYP83B1 | cytochrome P450, family 83, subfamily B, polypeptide 1 |
| Potri.010G142800 | down | up | AT4G16260 | Glycosyl hydrolase superfamily protein |
| Potri.001G127700 | down | up | NUDT2 | nudix hydrolase homolog 2 |
| Potri.T167100 | down | up | AT4G16260 | Glycosyl hydrolase superfamily protein |
| Potri.005G093200 | down | up | GSR2 | hypothetical protein |
| Potri.008G027500 | down | up | AT3-MMP | Matrixin family protein |
| Potri.002G025300 | down | up | CYP83B1 | cytochrome P450, family 83, subfamily B, polypeptide 1 |
| Potri.001G378700 | down | up | AT3G20180 | Copper transport protein family |
| Potri.003G192600 | down | up | CXE17 | carboxyesterase 17 |
| Potri.010G140032 | down | up | | |
| Potri.006G255100 | down | up | AT1G56130 | Leucine-rich repeat transmembrane protein kinase |

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|-------------------------|------|----|-----------|--------------------------------------------------------------------------|
| Potri.007G059300 | down | up | AAE1 | acyl activating enzyme 1 |
| Potri.005G079400 | down | up | AO | Cupredoxin superfamily protein |
| Potri.006G110900 | down | up | AT2G38600 | HAD superfamily, subfamily IIIB acid phosphatase |
| Potri.005G095500 | down | up | TPS21 | terpene synthase 21 |
| Potri.001G304800 | down | up | CCoAOMT1 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein |
| Potri.001G462700 | down | up | MEE23 | FAD-binding Berberine family protein |
| Potri.004G026000 | down | up | CRK25 | cysteine-rich RLK (RECEPTOR-like prot-ein kinase) 25 |
| Potri.009G064900 | down | up | CYP87A2 | cytochrome P450, family 87, subfamily A, polypeptide 2 |
| Potri.013G134500 | down | up | AT1G03670 | ankyrin repeat family protein |
| Potri.014G168400 | down | up | NUDT2 | nudix hydrolase homolog 2 |
| Potri.001G375200 | down | up | GLR2.7 | glutamate receptor 2.7 |
| Potri.010G127600 | down | up | CXE17 | carboxyesterase 17 |
| Potri.007G088400 | down | up | AAT | aspartate aminotransferase |
| Potri.003G216400 | down | up | AT1G58170 | Disease resistance-responsive (dirigent-like protein) family protein |
| Potri.004G024900 | down | up | CRK25 | cysteine-rich RLK (RECEPTOR-like protein kinase) 25 |
| Potri.001G221800 | down | up | AT1G75800 | Pathogenesis-related thaumatin superfamily protein |
| Potri.001G102400 | down | up | OSM34 | osmotin 34 |
| Potri.001G255100 | down | up | AT4G16260 | Glycosyl hydrolase superfamily protein |
| Potri.006G234300 | down | up | OZF2 | Zinc finger C-x8-C-x5-C-x3-H type family protein |
| Potri.016G045000 | down | up | LECRK-S.5 | Concanavalin A-like lectin protein kinase family protein |
| Potri.004G012600 | down | up | CRK10 | cysteine-rich RLK (RECEPTOR-like prot-ein kinase) 10 |
| Potri.013G090300 | down | up | WRKY70 | WRKY DNA-binding protein 70 |
| Potri.004G068000 | down | up | AT5G08350 | GRAM domain-containing protein / ABA-responsive protein-related |
| Potri.003G087000 | down | up | EXPR | expansin-like B1 |
| Potri.017G004300 | down | up | BIR1 | BAK1-interacting receptor-like kinase 1 |
| Potri.017G050200 | down | up | AGP1 | arabinogalactan protein 1 |
| Potri.001G099400 | down | up | ACS6 | 1-aminocyclopropane-1-carboxylic acid (acc) synthase 6 |
| Potri.017G003301 | down | up | | |
| Potri.008G159300 | down | up | CML11 | calmodulin-like 11 |

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|-------------------------|------|----|-----------|----------------------------------------------------------------|
| Potri.011G047300 | down | up | LPA1 | tetratricopeptide repeat (TPR)-containing protein |
| Potri.013G043100 | down | up | AT1G01225 | NC domain-containing protein-related |
| Potri.009G064900 | down | up | CYP87A2 | cytochrome P450, family 87, subfamily A, polypeptide 2 |
| Potri.015G061600 | down | up | NILR1 | Leucine-rich repeat protein kinase family protein |
| Potri.004G025100 | down | up | CRK10 | cysteine-rich RLK (RECEPTOR-like protein kinase) 10 |
| Potri.017G003400 | down | up | BIR1 | BAK1-interacting receptor-like kinase 1 |
| Potri.002G077300 | down | up | AT1G21550 | Calcium-binding EF-hand family protein |
| Potri.001G192100 | down | up | BCB | blue-copper-binding protein |
| Potri.016G116800 | down | up | AT5G55720 | Pectin lyase-like superfamily protein |
| Potri.001G412400 | down | up | RK3 | receptor kinase 3 |
| Potri.016G106800 | down | up | AT3G54040 | PAR1 protein |
| Potri.008G197400 | down | up | NSH3 | inosine-uridine preferring nucleoside hydrolase family protein |
| Potri.016G141900 | down | up | ORP4B | OSBP(oxysterol binding protein)-related protein 4B |
| Potri.007G049900 | down | up | CYP81D8 | cytochrome P450, family 81, subfamily D, polypeptide 8 |
| Potri.002G190800 | down | up | NIMIN-1 | NIM1-interacting 1 |
| Potri.001G413400 | down | up | RK3 | receptor kinase 3 |
| Potri.011G158700 | down | up | MEE23 | FAD-binding Berberine family protein |
| Potri.005G063700 | down | up | PUB25 | plant U-box 25 |
| Potri.T079700 | down | up | AT4G39830 | Cupredoxin superfamily protein |
| Potri.001G228300 | down | up | RLK1 | receptor-like protein kinase 1 |
| Potri.015G044750 | down | up | | |
| Potri.004G091400 | down | up | HTB9 | Histone superfamily protein |
| Potri.001G461700 | down | up | AT4G20820 | FAD-binding Berberine family protein |
| Potri.003G075800 | down | up | AT3G22160 | VQ motif-containing protein |
| Potri.009G094500 | down | up | AT2G15220 | Plant basic secretory protein (BSP) family protein |
| Potri.018G117900 | down | up | RLP1 | receptor like protein 1 |
| Potri.004G180500 | down | up | sks5 | SKU5 similar 5 |
| Potri.015G015800 | down | up | NGA4 | AP2/B3-like transcriptional factor family protein |
| Potri.001G221200 | down | up | AT1G75800 | Pathogenesis-related thaumatin superfamily protein |
| Potri.014G019700 | down | up | VEP1 | NAD(P)-binding Rossmann-fold superfamily protein |
| Potri.002G012900 | down | up | AT1G47670 | Transmembrane amino acid transporter |

| | | | | |
|-------------------------|------|----|-----------|--------------------------------------------------------------------------|
| Potri.T090800 | down | up | CRK25 | family protein cysteine-rich RLK (RECEPTOR-like protein kinase) 25 |
| Potri.011G081701 | down | up | | |
| Potri.004G056000 | down | up | SAG12 | senescence-associated gene 12 |
| Potri.006G218500 | down | up | RGIL6 | Rhamnogalacturonate lyase family protein |
| Potri.006G042200 | down | up | AT2G41380 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein |
| Potri.018G043000 | down | up | CCD1 | carotenoid cleavage dioxygenase 1 |
| Potri.012G054700 | down | up | LRK10L1.2 | Protein kinase superfamily protein |
| Potri.T079500 | down | up | AT4G39830 | Cupredoxin superfamily protein |
| Potri.006G023151 | down | up | | |
| Potri.001G221400 | down | up | AT1G75800 | Pathogenesis-related thaumatin superfamily protein |
| Potri.017G150560 | down | up | | |
| Potri.002G091500 | down | up | ALD1 | AGD2-like defense response protein 1 |
| Potri.011G114600 | down | up | TAX2 | taximin |
| Potri.017G018800 | down | up | ESD4 | Cysteine proteinases superfamily protein |
| Potri.017G005800 | down | up | AT3G59850 | Pectin lyase-like superfamily protein |
| Potri.001G294100 | down | up | VDAC2 | voltage dependent anion channel 2 |
| Potri.010G020200 | down | up | AT4G27290 | S-locus lectin protein kinase family protein |
| Potri.013G041900 | down | up | PR4 | pathogenesis-related 4 |
| Potri.003G013700 | down | up | RLP15 | receptor like protein 15 |
| Potri.012G067600 | down | up | AT1G74360 | Leucine-rich repeat protein kinase family protein |
| Potri.006G036200 | down | up | AAE11 | AMP-dependent synthetase and ligase family protein |
| Potri.017G006200 | down | up | AT3G59850 | Pectin lyase-like superfamily protein |
| Potri.006G209200 | down | up | NAC090 | NAC domain containing protein 90 |
| Potri.001G070700 | down | up | AT1G28190 | hypothetical protein |
| Potri.005G043700 | down | up | AT1G51790 | Leucine-rich repeat protein kinase family protein |

Table S5 Read abundance of various classes of sRNAs sequences in eighteen libranes

| Type | Category | Raw reads | Valid reads | rRNA | tRNA | snoRNA | snRNA | Other Rfam RNA |
|----------------|--------------|-----------|-------------|---------|--------|--------|-------|----------------|
| CK_Di1 | Total reads | 14131837 | 10323827 | 731674 | 114900 | 17816 | 14332 | 21262 |
| | Unique reads | 2012058 | 1186829 | 11778 | 1579 | 1063 | 632 | 1106 |
| CK_Di2 | Total reads | 12772905 | 8527271 | 683660 | 118022 | 17014 | 13493 | 18535 |
| | Unique reads | 1905815 | 1126023 | 10904 | 1648 | 1072 | 624 | 990 |
| CK_Di3 | Total reads | 14094520 | 8281943 | 768616 | 68246 | 18862 | 14496 | 22135 |
| | Unique reads | 1954982 | 1030869 | 12376 | 1319 | 1108 | 543 | 1057 |
| CK_Te1 | Total reads | 13815380 | 9707436 | 652849 | 106981 | 17131 | 12172 | 19893 |
| | Unique reads | 1882722 | 1198106 | 8991 | 1298 | 1006 | 549 | 976 |
| CK_Te2 | Total reads | 10211545 | 7602773 | 481340 | 65645 | 11889 | 9602 | 16337 |
| | Unique reads | 1567928 | 1019539 | 7852 | 977 | 805 | 454 | 871 |
| CK_Te3 | Total reads | 13471409 | 10272776 | 584941 | 105579 | 16039 | 12779 | 18526 |
| | Unique reads | 2126854 | 1450898 | 8098 | 1294 | 1022 | 551 | 994 |
| Dro_Di1 | Total reads | 14024315 | 10278377 | 718732 | 111249 | 22193 | 20198 | 19943 |
| | Unique reads | 1763471 | 1073347 | 10846 | 1645 | 1249 | 721 | 1048 |
| Dro_Di2 | Total reads | 14748966 | 10339159 | 674179 | 101846 | 17897 | 15028 | 23665 |
| | Unique reads | 1792977 | 1072825 | 10722 | 1660 | 1069 | 654 | 1128 |
| Dro_Di3 | Total reads | 18914322 | 13642486 | 662823 | 92536 | 21904 | 20333 | 25621 |
| | Unique reads | 2599613 | 1724704 | 10944 | 1757 | 1205 | 822 | 1221 |
| Dro_Te1 | Total reads | 12622437 | 9874433 | 855291 | 131078 | 30942 | 15176 | 26661 |
| | Unique reads | 1624828 | 1018478 | 10949 | 1806 | 1327 | 575 | 1079 |
| Dro_Te2 | Total reads | 13039587 | 9459234 | 735755 | 137269 | 24546 | 14877 | 34212 |
| | Unique reads | 1963133 | 1049561 | 13477 | 2101 | 1203 | 567 | 1314 |
| Dro_Te3 | Total reads | 14353470 | 11125393 | 1010233 | 161701 | 33180 | 16036 | 37768 |
| | Unique reads | 1842820 | 1037637 | 11966 | 2059 | 1355 | 624 | 1246 |

| | | | | | | | | |
|---------------|--------------|----------|----------|---------|--------|-------|-------|-------|
| Re_Di1 | Total reads | 16115294 | 11119500 | 1445666 | 300898 | 43793 | 30889 | 46109 |
| | Unique reads | 1866059 | 911548 | 16639 | 3429 | 1695 | 891 | 1472 |
| Re_Di2 | Total reads | 11164382 | 8164513 | 763890 | 182356 | 30295 | 18097 | 23750 |
| | Unique reads | 1455943 | 809220 | 10769 | 1747 | 1315 | 568 | 1071 |
| Re_Di3 | Total reads | 15732765 | 11992908 | 813254 | 365505 | 28853 | 23920 | 33186 |
| | Unique reads | 2074777 | 1241489 | 10701 | 2030 | 1342 | 722 | 1264 |
| Re_Te1 | Total reads | 11814243 | 8872001 | 572542 | 163855 | 19900 | 17312 | 40286 |
| | Unique reads | 1858082 | 1083583 | 10251 | 1589 | 1013 | 573 | 1113 |
| Re_Te2 | Total reads | 9747252 | 7743966 | 495190 | 117072 | 16764 | 13068 | 18646 |
| | Unique reads | 1464652 | 932175 | 8694 | 1322 | 898 | 480 | 921 |
| Re_Te3 | Total reads | 12417596 | 9617902 | 591224 | 194520 | 23359 | 19707 | 29323 |
| | Unique reads | 1864821 | 1206938 | 9216 | 1429 | 1141 | 620 | 1078 |

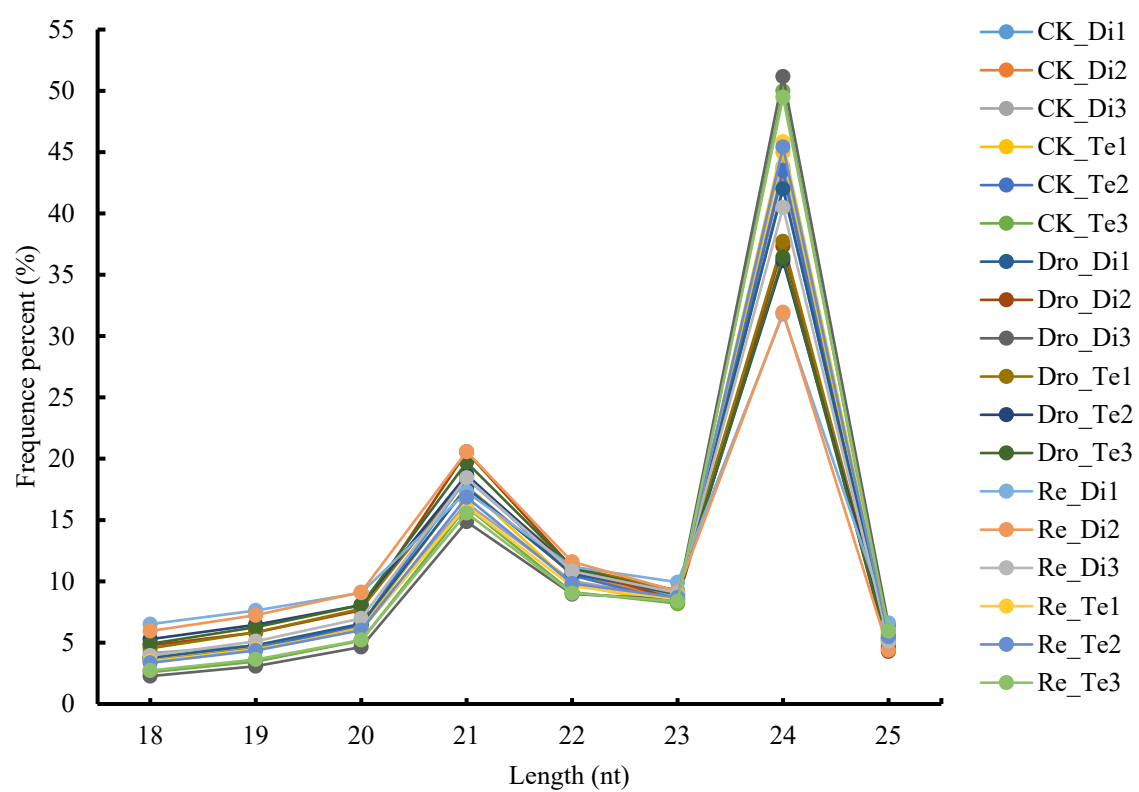


Figure S1 Size distribution of small RNA