

SUPPLEMENTARY MATERIALS

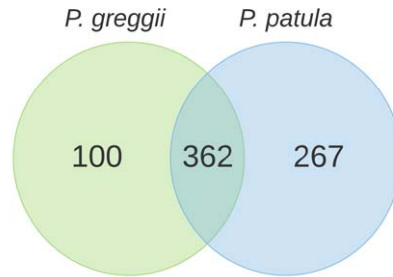


Figure S1. Venn diagram illustrating common and differential proteins identified in the seeds of *P. patula* and *P. greggii* by nLC LTQ Orbitrap using the Sequest/HT search engine. (<http://bioinfop.cnb.csic.es/tools/venny/>).

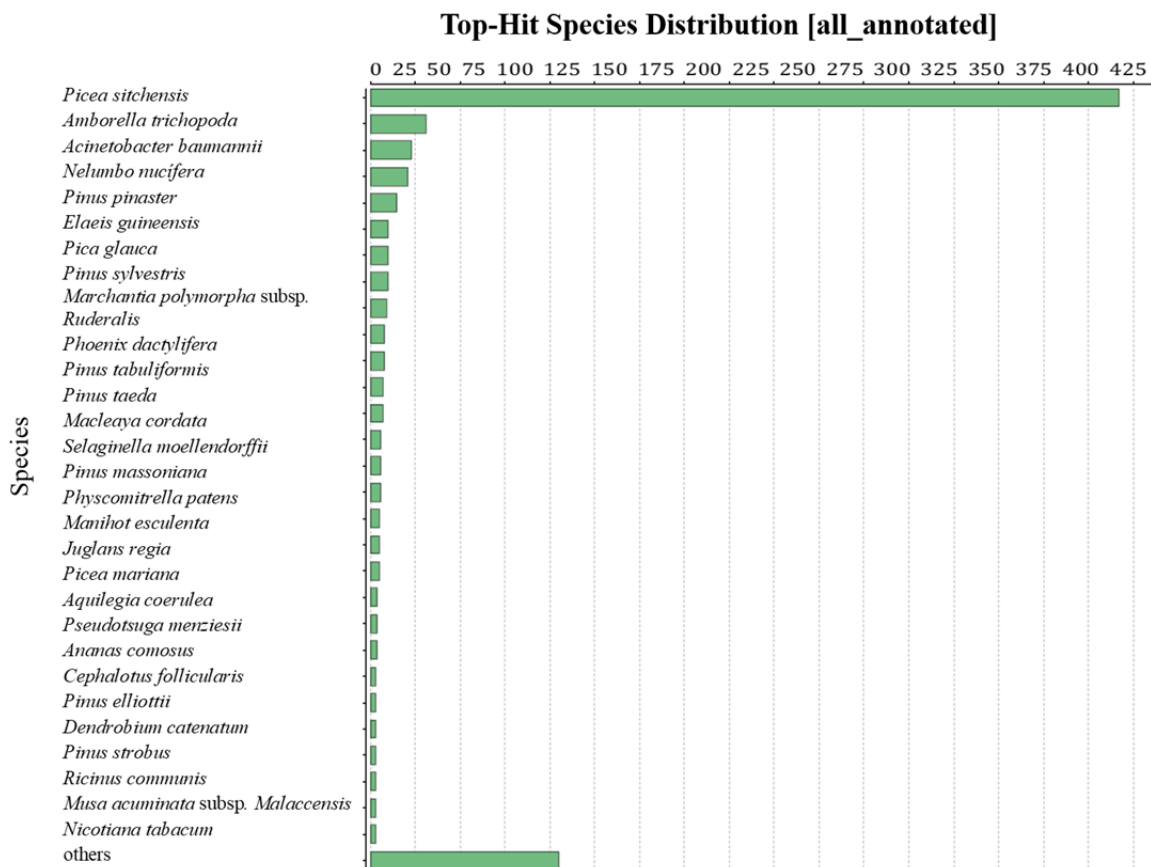


Figure S2. Distribution of the species with the greatest contribution in the annotation of the sequences of the proteins identified in the study. Graph generated by the Blast2GO software (v.4.1.9) against the nr-NCBI database (downloaded on November 18, 2017), keeping up to 20 blast “hits” with an e-value threshold of 1e-5.

Table S1. Characteristics of *Pinus patula* and *Pinus greggii* seeds used in the work.

| Species | Common name | N° seeds/kg | Feasibility of the seeds (years) | Humidity (%) | Germination (%) | Germination time (days) |
|------------------------------------|-------------|-------------|----------------------------------|--------------|-----------------|-------------------------|
| <i>Pinus greggii</i> Englem | palo Prieto | 77,00 | 5 | 5 -7% | 72-86% | 12-15 |
| <i>Pinus patula</i> Schl. et Cham. | pino llorón | 133,06 | > 10 | 6-7% | 85-87% | 12-15 |

Table S2. List of the identified proteins by nLC LTQ Orbitrap in seeds of *P. patula* and *P. greggii*. The functional classification was carried out using Blast2GO software (v.4. 1.9) against nr-NCBI database.

| Accession Numbers ^a | Description ^b | MW [kDa] calc ^c | pI ^d | Coverage (%) | # Unique Peptides | Commons | <i>Pinus greggii</i> | <i>Pinus patula</i> |
|---|--|----------------------------|-----------------|--------------|-------------------|---------|----------------------|---------------------|
| Acyl-CoA metabolic process | | | | | | | | |
| 25186 | peroxisomal acyl-coenzyme A oxidase 1 | 75 | 7 | 3 | 1 | | | X |
| ADP binding | | | | | | | | |
| 6974 | probable disease resistance At4g33300 | 92 | 7 | 3 | 2 | X | | |
| 160983 | NBS-LRR | 12 | 6 | 13 | 1 | | X | |
| Alanine metabolic process | | | | | | | | |
| 7786 | glutamate decarboxylase | 58 | 7 | 4 | 1 | X | | |
| Alpha-amino acid metabolic process | | | | | | | | |
| 29605 | auxin down-regulated | 28 | 5 | 13 | 3 | X | | |
| ATP binding | | | | | | | | |
| 11804 | cell division cycle 48 homolog | 98 | 6 | 33 | 21 | X | | |
| 1494 | ATP synthase subunit mitochondrial-like | 62 | 6 | 44 | 15 | X | | |
| 17291 | heat shock cognate 70 kDa 2-like | 71 | 5 | 22 | 3 | X | | |
| 18113 | actin | 42 | 5 | 58 | 1 | X | | |
| 18234 | ru large subunit-binding subunit chloroplastic | 66 | 6 | 8 | 4 | X | | |
| 1892 | nuclear valosin-containing -like | 85 | 7 | 5 | 2 | X | | |
| 3551 | T-complex 1 subunit beta | 58 | 6 | 9 | 3 | X | | |
| 3604 | chaperonin CPN60- mitochondrial | 64 | 8 | 36 | 9 | X | | |
| 70 | probable mediator of RNA polymerase II transcription subunit 37c | 71 | 5 | 34 | 4 | X | | |
| 6274 | Heat shock 70 kDa mitochondrial | 40 | 5 | 10 | 3 | X | | |
| 7476 | ATPase family AAA domain-containing 3-like | 70 | 9 | 1 | 1 | X | | |
| 7764 | succinyl- ligase [ADP-forming] subunit alpha-mitochondrial | 34 | 9 | 4 | 1 | X | | |
| 7903 | PTI1-like tyrosine- kinase 3 isoform X2 | 40 | 8 | 5 | 1 | X | | |
| 9725 | heat shock 70 kDa mitochondrial | 73 | 6 | 28 | 9 | X | | |
| 1032 | ATP-dependent 6-phosphofructokinase 2 | 52 | 7 | 5 | 1 | | X | |
| 3373 | cysteine mitochondrial | 51 | 8 | 2 | 1 | | X | |
| 5690 | galactokinase | 55 | 5 | 4 | 1 | | X | |
| 103861 | heat shock cognate 70 kDa | 17 | 6 | 32 | 1 | | | X |
| 127555 | heat shock 70 kDa 15-like | 42 | 6 | 21 | 1 | | | X |
| 12998 | pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha | 67 | 7 | 3 | 1 | | | X |
| 17239 | dnaJ homolog | 46 | 6 | 7 | 2 | | | X |
| 18564 | heat shock 70 kDa 15-like | 96 | 5 | 12 | 3 | | | X |
| 202631 | Actin domain containing | 28 | 5 | 17 | 1 | | | X |
| 20608 | ABC transporter F family member 1 | 67 | 7 | 2 | 1 | | | X |
| 3105 | chaperone mitochondrial | 72 | 6 | 16 | 4 | | | X |

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Table S2 Continued

| | | | | | | |
|-----------------------------|---|-----|---|----|----|---|
| Binding | | | | | | |
| 474 | neurofilament heavy polypeptide-like | 109 | 7 | 2 | 1 | X |
| 7484 | programmed cell death 4 | 84 | 5 | 3 | 2 | X |
| Biosynthetic process | | | | | | |
| 11216 | ketol-acid chloroplastic | 64 | 7 | 6 | 2 | X |
| 11837 | serine hydroxymethyltransferase 4 | 52 | 7 | 13 | 3 | X |
| 12050 | cysteine synthase | 35 | 6 | 31 | 6 | X |
| 12125 | UBP1-associated 2C | 47 | 7 | 5 | 2 | X |
| 126671 | enolase | 48 | 6 | 29 | 7 | X |
| 15879 | fluG | 98 | 6 | 1 | 1 | X |
| 16966 | nucleoside diphosphate kinase 1 | 16 | 6 | 46 | 8 | X |
| 17175 | Adenosine kinase 2 | 37 | 5 | 8 | 1 | X |
| 17743 | aspartate mitochondrial | 49 | 8 | 5 | 1 | X |
| 34775 | UDP-sugar pyrophosphorylase | 60 | 7 | 5 | 1 | X |
| 4809 | aspartate | 50 | 8 | 18 | 7 | X |
| 5373 | acetolactate synthase small subunit chloroplastic-like | 55 | 8 | 8 | 4 | X |
| 6921 | 6,7-dimethyl-8-ribityllumazine chloroplastic | 24 | 9 | 11 | 1 | X |
| 7574 | agmatine deiminase | 41 | 5 | 14 | 3 | X |
| 8123 | strictosidine synthase-like 4-like | 40 | 6 | 7 | 2 | X |
| 9637 | homocysteine S-methyltransferase 2-like isoform X1 | 37 | 5 | 16 | 4 | X |
| 17494 | 5methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1 | 85 | 6 | 7 | 4 | X |
| 22555 | enolase | 48 | 6 | 45 | 1 | X |
| 7698 | bifunctional purine biosynthesis | 68 | 7 | 2 | 1 | X |
| 1130 | NADH dehydrogenase [ubiquinone] iron-sulfur mitochondrial | 82 | 8 | 3 | 2 | X |
| 15701 | glutamine synthetase | 39 | 6 | 4 | 1 | X |
| 1638 | inositol-phosphate phosphatase-like | 30 | 5 | 11 | 1 | X |
| 17452 | choline-phosphate cytidylyltransferase 2-like | 39 | 6 | 5 | 1 | X |
| 22340 | farnesyltransferase geranylgeranyltransferase type i alpha subunit | 13 | 4 | 14 | 1 | X |
| 31982 | N-alpha-acetyltransferase auxiliary subunit | 104 | 7 | 3 | 2 | X |
| 3336 | probable glucan 1,3-alpha-glucosidase | 104 | 6 | 2 | 1 | X |
| 34766 | aspartate chloroplastic | 51 | 9 | 3 | 1 | X |
| 5907 | bifunctional D-cysteine desulfhydrase 1-aminocyclopropane-1-carboxylate mitochondrial | 50 | 8 | 2 | 1 | X |
| 6320 | argininosuccinate chloroplastic | 57 | 6 | 3 | 1 | X |
| 6383 | ubiquinone biosynthesis COQ9- mitochondrial | 35 | 7 | 5 | 1 | X |
| Calcium ion binding | | | | | | |
| 11782 | annexin D2 | 37 | 8 | 44 | 11 | X |
| 37393 | EF-hands-containing | 42 | 5 | 8 | 2 | X |
| 12118 | calcium-dependent kinase 1 | 63 | 7 | 2 | 1 | X |
| 127899 | annexin D1 | 36 | 9 | 3 | 1 | X |
| 16914 | probable calcium-binding CML49 | 32 | 8 | 7 | 1 | X |
| 186650 | neurocalcin homolog | 23 | 5 | 4 | 1 | X |
| Carbohydrate binding | | | | | | |
| 12320 | alpha-mannosidase At3g26720 | 79 | 5 | 9 | 4 | X |
| 7948 | beta-galactosidase 9 isoform X1 | 73 | 6 | 3 | 1 | X |

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Table S2 Continued

| | | | | | | | |
|--|--|-----|----|----|----|---|---|
| 193755 | pentatricopeptide repeat-containing At1g19720 | 12 | 7 | 19 | 1 | | X |
| 2476 | beta-galactosidase isoform X1 | 131 | 6 | 1 | 1 | | X |
| 17223 | DNA-damage-repair toleration DRT102 | 39 | 5 | 3 | 1 | X | |
| 18489 | malate glyoxysomal | 37 | 7 | 28 | 5 | X | |
| 1976 | probable lactoylglutathione chloroplastic | 41 | 8 | 7 | 2 | X | |
| 2261 | beta-hexosaminidase 1 | 65 | 5 | 1 | 1 | X | |
| 36134 | DJ-1 homolog D-like | 12 | 4 | 21 | 1 | X | |
| 37912 | cytoplasmic | 64 | 5 | 48 | 25 | X | |
| 5608 | probable alpha-galactosidase B | 74 | 6 | 3 | 3 | X | |
| 1014 | probable 2-oxoglutarate-dependent dioxygenase At3g49630 | 37 | 6 | 3 | 1 | | X |
| 1290 | malate chloroplastic | 48 | 9 | 9 | 1 | | X |
| 15816 | alpha-xylosidase 1 | 105 | 7 | 3 | 2 | | X |
| 2 | alpha-galactosidase-like isoform X3 | 55 | 8 | 2 | 1 | | X |
| 4708 | Lactoylglutathione lyase | 33 | 5 | 4 | 1 | | X |
| Carbohydrate phosphorylation | | | | | | | |
| 99940 | L-arabinokinase-like | 27 | 6 | 5 | 1 | | X |
| Carbon-sulfur lyase activity | | | | | | | |
| 13715 | GFA family | 15 | 6 | 7 | 1 | X | |
| Catabolic process | | | | | | | |
| 10538 | peroxisomal fatty acid beta-oxidation multifunctional AIM1 | 78 | 9 | 15 | 8 | X | |
| 1200 | alpha-glucan H isozyme | 96 | 7 | 16 | 8 | X | |
| 30722 | S-formylglutathione hydrolase | 33 | 7 | 11 | 2 | X | |
| 12496 | probable enoyl- hydratase peroxisomal | 31 | 9 | 3 | 1 | | X |
| 14939 | 26S proteasome non-ATPase regulatory subunit 7 homolog A | 39 | 7 | 4 | 1 | | X |
| 15687 | proteasome subunit alpha type-6 | 28 | 6 | 8 | 2 | | X |
| 16017 | 3-hydroxyisobutyryl- hydrolase mitochondrial isoform X1 | 48 | 6 | 4 | 1 | | X |
| 16112 | aminopeptidase M1 | 26 | 6 | 27 | 1 | | X |
| 17114 | basic endochitinase | 36 | 8 | 6 | 1 | | X |
| 18206 | ubiquitin receptor RAD23d | 42 | 5 | 5 | 1 | | X |
| 20233 | ubiquitin-activating enzyme E1 2 | 117 | 5 | 5 | 3 | | X |
| 20508 | 26S protease regulatory subunit 6A homolog | 50 | 5 | 7 | 2 | | X |
| 2228 | proteasome subunit beta type-7-A-like | 30 | 7 | 3 | 1 | | X |
| 24684 | phospholipase A2 | 17 | 8 | 10 | 1 | | X |
| 29027 | phospholipase D alpha 1 | 92 | 6 | 4 | 2 | | X |
| 3305 | ubiquitin carboxyl-terminal hydrolase 12 isoform X2 | 81 | 6 | 6 | 1 | | X |
| 8881 | ubiquitin carboxyl-terminal hydrolase 12 isoform X2 | 68 | 5 | 7 | 1 | | X |
| Catalytic activity | | | | | | | |
| 10344 | uncharacterized protein LOC18446042 | 21 | 10 | 11 | 1 | | X |
| 17733 | unknown | 26 | 5 | 5 | 1 | | X |
| 17803 | Heat-stress-associated 32 | 33 | 6 | 4 | 1 | | X |
| 5346 | PLP-dependent transferase | 43 | 7 | 3 | 1 | | X |
| Chloroplast ATP binding/organization/envelope | | | | | | | |
| 21245 | ru large subunit-binding subunit alpha | 64 | 6 | 5 | 2 | X | |
| 34549 | spermatogenesis-associated 20 isoform X1 | 96 | 7 | 11 | 5 | X | |
| 34886 | malate dehydrogenase | 37 | 7 | 16 | 3 | X | |

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Table S2 Continued

| | | | | | | | |
|---|--|-----|----|----|----|---|---|
| 47949 | chaperone mitochondrial | 20 | 7 | 28 | 3 | X | |
| 489 | dehydroascorbate reductase | 33 | 8 | 7 | 2 | X | |
| 5747 | alpha-1,4 glucan phosphorylase L chloroplastic amyloplastic | 110 | 6 | 9 | 6 | X | |
| 7150 | V-type proton ATPase catalytic subunit A | 70 | 5 | 9 | 4 | X | |
| 7884 | chaperone chloroplastic | 114 | 7 | 15 | 7 | X | |
| 9530 | aconitate cytoplasmic | 110 | 7 | 40 | 32 | X | |
| 17303 | isocitrate dehydrogenase [NADP] | 50 | 7 | 3 | 1 | | X |
| 2089 | 3-methyl-2-oxobutanoate hydroxymethyltransferase mitochondrial | 43 | 8 | 4 | 1 | | X |
| 34070 | long chain acyl- synthetase chloroplastic-like | 77 | 7 | 3 | 1 | | X |
| 12459 | importin subunit beta-1 | 90 | 5 | 2 | 1 | | X |
| 14666 | probable ATP synthase 24 kDa mitochondrial | 32 | 10 | 11 | 2 | | X |
| 2921 | leucine--tRNA cytoplasmic | 109 | 6 | 4 | 2 | | X |
| 29831 | outer envelope pore chloroplastic | 19 | 10 | 13 | 1 | | X |
| 3736 | 20 kDa chloroplastic | 27 | 9 | 4 | 1 | | X |
| 46723 | probable trans-2-enoyl- mitochondrial | 42 | 9 | 11 | 1 | | X |
| Chromosomal part | | | | | | | |
| 151327 | cohesin subunit SA-3 isoform X1 | 16 | 6 | 5 | 1 | | X |
| Cytoplasm | | | | | | | |
| 20693 | translationally-controlled tumor homolog | 19 | 5 | 5 | 1 | X | |
| Cytoskeleton organization | | | | | | | |
| 21550 | profilin-1 | 15 | 5 | 16 | 2 | X | |
| 126970 | actin-depolymerizing factor 2 | 17 | 7 | 19 | 1 | | X |
| 39916 | cyclase-associated 1-like | 56 | 8 | 2 | 1 | | X |
| 34145 | actin-depolymerizing factor 7 | 16 | 7 | 29 | 2 | | X |
| Defense response | | | | | | | |
| 1843 | anti-microbial | 14 | 8 | 12 | 1 | X | |
| 97763 | late embryogenesis abundant | 17 | 8 | 20 | 2 | X | |
| 35762 | anti-microbial | 13 | 8 | 12 | 1 | | X |
| 17113 | MLP 423 | 17 | 5 | 7 | 1 | | X |
| Dephosphorylation | | | | | | | |
| 20289 | purple acid phosphatase 23 | 60 | 6 | 10 | 2 | | X |
| DNA binding | | | | | | | |
| 18121 | poly [ADP-ribose] polymerase 1 | 45 | 8 | 6 | 2 | X | |
| 22707 | zinc finger GIS2-like | 28 | 8 | 17 | 2 | X | |
| 32133 | cold shock 1-like | 12 | 7 | 45 | 2 | X | |
| 7992 | Glycine-rich 2 | 19 | 7 | 18 | 1 | | X |
| Embryo development ending in seed dormancy | | | | | | | |
| 47723 | 11 kDa late embryogenesis abundant | 13 | 9 | 45 | 3 | | X |
| Enzyme inhibitor | | | | | | | |
| 6686 | probable pectinesterase pectinesterase inhibitor 51 | 59 | 7 | 3 | 1 | | X |
| Extracellular region/transport | | | | | | | |
| 20384 | STS14 -like | 20 | 7 | 22 | 4 | X | |
| 21274 | serpin-ZX | 44 | 6 | 20 | 7 | X | |
| 4419 | embryo-specific ATS3B-like | 19 | 5 | 7 | 1 | | X |
| Fatty acid biosynthetic process | | | | | | | |
| 17755 | acetyl- cytosolic 1 | 43 | 8 | 9 | 1 | X | |
| 25239 | acyl carrier chloroplastic-like | 23 | 5 | 7 | 1 | X | |

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Table S2 Continued

| | | | | | | |
|-----------------------------------|---|-----|----|----|----|---|
| 25548 | 3-hydroxyacyl-[acyl-carrier-] dehydratase -like | 27 | 10 | 6 | 1 | X |
| 26955 | acetyl- cytosolic 1 | 41 | 7 | 19 | 4 | X |
| 36734 | biotin carboxylase chloroplastic | 60 | 7 | 2 | 1 | X |
| Fructose metabolic process | | | | | | |
| 7200 | xylose isomerase | 57 | 6 | 7 | 2 | X |
| Gene expression | | | | | | |
| 1012 | ADR12-2 family | 49 | 9 | 43 | 6 | X |
| 11424 | 60S ribosomal L3 | 45 | 10 | 8 | 4 | X |
| 11756 | 40S ribosomal S11 | 22 | 11 | 7 | 1 | X |
| 126648 | 60S ribosomal L8 | 31 | 10 | 33 | 6 | X |
| 126786 | elongation factor 1-gamma | 50 | 7 | 7 | 2 | X |
| 126834 | eukaryotic translation initiation factor 5A-2-like | 19 | 5 | 7 | 1 | X |
| 126888 | 60S ribosomal L11 | 22 | 10 | 7 | 1 | X |
| 13481 | argonaute 1 | 108 | 9 | 8 | 5 | X |
| 15147 | GTP-binding nuclear Ran-3 | 26 | 7 | 23 | 1 | X |
| 16965 | 60S ribosomal L27a-3 | 18 | 10 | 17 | 2 | X |
| 17138 | 40S ribosomal S8 | 26 | 10 | 8 | 1 | X |
| 17142 | 40S ribosomal S2-3-like | 31 | 11 | 11 | 2 | X |
| 17202 | GTP-binding nuclear Ran-3 | 18 | 5 | 77 | 7 | X |
| 17290 | 40S ribosomal S3-3-like | 31 | 10 | 12 | 3 | X |
| 18060 | 60S ribosomal L35-like | 14 | 11 | 12 | 1 | X |
| 18460 | 40S ribosomal S27-2 | 11 | 10 | 8 | 1 | X |
| 18541 | 40S ribosomal S23 | 16 | 10 | 8 | 1 | X |
| 18823 | eukaryotic initiation factor 4A-11 | 47 | 5 | 31 | 9 | X |
| 19251 | 40S ribosomal S5 | 30 | 10 | 9 | 2 | X |
| 2049 | 40S ribosomal S6 | 29 | 11 | 11 | 2 | X |
| 21427 | translation elongation factor EF-1 subunit alpha | 49 | 9 | 37 | 5 | X |
| 3159 | oil body-associated 1A-like | 29 | 7 | 35 | 6 | X |
| 36305 | 60S ribosomal L7-2-like | 31 | 10 | 8 | 2 | X |
| 6421 | elongation factor mitochondrial | 48 | 7 | 4 | 1 | X |
| 9515 | RNA-binding KH domain-containing PEPPER-like | 47 | 8 | 3 | 1 | X |
| 126677 | elongation factor 2 | 97 | 6 | 18 | 10 | X |
| 152850 | response regulator | 11 | 5 | 7 | 1 | X |
| 11466 | elongation factor 2 | 94 | 6 | 42 | 22 | X |
| 126657 | GTP-binding nuclear Ran-3 | 25 | 7 | 30 | 1 | X |
| 16972 | ras-related RABA1f | 24 | 6 | 12 | 2 | X |
| 1913 | phytochrome | 72 | 5 | 2 | 1 | X |
| 205714 | ras-related rab7 | 13 | 8 | 18 | 1 | X |
| 20987 | eukaryotic translation initiation factor 3 subunit E | 52 | 6 | 3 | 1 | X |
| 29274 | ras-related RABC1 | 24 | 5 | 13 | 1 | X |
| 4786 | exportin-2 | 110 | 6 | 1 | 1 | X |
| 10495 | phosphoglycerate chloroplastic | 53 | 9 | 4 | 1 | X |
| 126855 | glyceraldehyde-3-phosphate dehydrogenase cytosolic | 39 | 8 | 62 | 15 | X |
| 13187 | 2,3-bisphosphoglycerate-independent phosphoglycerate mutase | 61 | 6 | 15 | 6 | X |
| 16504 | pyruvate cytosolic isozyme | 57 | 8 | 5 | 2 | X |
| 16934 | fructose-bisphosphate cytoplasmic isozyme 1 | 42 | 9 | 24 | 5 | X |

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Table S2 Continued

| | | | | | | | |
|--|--|-----|---|----|----|---|---|
| 17023 | fructose-bisphosphate aldolase chloroplastic | 49 | 8 | 5 | 2 | X | |
| 17064 | fructose-bisphosphate aldolase cytosolic | 44 | 8 | 52 | 15 | X | |
| 18227 | glucose-6-phosphate isomerase chloroplastic | 71 | 6 | 12 | 5 | X | |
| 18273 | glucose-6-phosphate cytosolic | 68 | 7 | 7 | 3 | X | |
| 20710 | cytosolic triosephosphate isomerase | 27 | 5 | 30 | 7 | X | |
| 2317 | pyruvate dehydrogenase E1 component subunit alpha- mitochondrial | 44 | 8 | 3 | 1 | X | |
| 9616 | pyruvate decarboxylase 2 | 67 | 6 | 7 | 1 | X | |
| 1069 | dihydrolipoyllysine-residue acetyltransferase component 2 of pyruvate dehydrogenase mitochondrial-like | 62 | 9 | 3 | 1 | | X |
| 18066 | phosphoenolpyruvate carboxykinase [ATP]-like | 49 | 9 | 4 | 1 | | X |
| 72 | pyruvate decarboxylase 2 | 66 | 6 | 5 | 1 | | X |
| 9912 | phosphoenolpyruvate carboxylase | 110 | 6 | 6 | 4 | | X |
| 9318 | glycine--tRNA mitochondrial 1-like | 84 | 6 | 2 | 1 | | X |
| 16736 | late embryogenesis abundant D-34-like | 30 | 5 | 24 | 3 | X | |
| 152850 | response regulator | 11 | 5 | 7 | 1 | | X |
| 11466 | elongation factor 2 | 94 | 6 | 42 | 22 | | X |
| 126657 | GTP-binding nuclear Ran-3 | 25 | 7 | 30 | 1 | | X |
| 16972 | ras-related RABA1f | 24 | 6 | 12 | 2 | | X |
| 1913 | phytochrome | 72 | 5 | 2 | 1 | | X |
| 205714 | ras-related rab7 | 13 | 8 | 18 | 1 | | X |
| 20987 | eukaryotic translation initiation factor 3 subunit E | 52 | 6 | 3 | 1 | | X |
| 29274 | ras-related RABC1 | 24 | 5 | 13 | 1 | | X |
| 4786 | exportin-2 | 110 | 6 | 1 | 1 | | X |
| <i>Gluconeogenesis/glycolytic process</i> | | | | | | | |
| 10495 | phosphoglycerate chloroplastic | 53 | 9 | 4 | 1 | X | |
| 126855 | glyceraldehyde-3-phosphate dehydrogenase cytosolic | 39 | 8 | 62 | 15 | X | |
| 13187 | 2,3-bisphosphoglycerate-independent phosphoglycerate mutase | 61 | 6 | 15 | 6 | X | |
| 16504 | pyruvate cytosolic isozyme | 57 | 8 | 5 | 2 | X | |
| 16934 | fructose-bisphosphate cytoplasmic isozyme 1 | 42 | 9 | 24 | 5 | X | |
| 17023 | fructose-bisphosphate aldolase chloroplastic | 49 | 8 | 5 | 2 | X | |
| 17064 | fructose-bisphosphate aldolase cytosolic | 44 | 8 | 52 | 15 | X | |
| 18227 | glucose-6-phosphate isomerase chloroplastic | 71 | 6 | 12 | 5 | X | |
| 18273 | glucose-6-phosphate cytosolic | 68 | 7 | 7 | 3 | X | |
| 20710 | cytosolic triosephosphate isomerase | 27 | 5 | 30 | 7 | X | |
| 2317 | pyruvate dehydrogenase E1 component subunit alpha- mitochondrial | 44 | 8 | 3 | 1 | X | |
| 9616 | pyruvate decarboxylase 2 | 67 | 6 | 7 | 1 | X | |
| 1069 | dihydrolipoyllysine-residue acetyltransferase component 2 of pyruvate dehydrogenase mitochondrial-like | 62 | 9 | 3 | 1 | | X |
| 18066 | phosphoenolpyruvate carboxykinase [ATP]-like | 49 | 9 | 4 | 1 | | X |
| 72 | pyruvate decarboxylase 2 | 66 | 6 | 5 | 1 | | X |
| 9912 | phosphoenolpyruvate carboxylase | 110 | 6 | 6 | 4 | | X |
| <i>Glycyl-tRNA aminoacylation</i> | | | | | | | |
| 9318 | glycine--tRNA mitochondrial 1-like | 84 | 6 | 2 | 1 | | X |
| 16736 | late embryogenesis abundant D-34-like | 30 | 5 | 24 | 3 | X | |

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Table S2 Continued

| | | | | | | |
|--|---|-----|----|----|----|---|
| 17334 | probable disulfide-isomerase A6 | 39 | 6 | 15 | 3 | X |
| 18279 | copper transport ATX1-like | 12 | 9 | 32 | 2 | X |
| 29553 | thioredoxin-dependent peroxidase | 18 | 6 | 44 | 5 | X |
| 29847 | thioredoxin H-type-like | 13 | 5 | 31 | 1 | X |
| 3137 | Dihydrolipoyl dehydrogenase mitochondrial | 54 | 8 | 16 | 6 | X |
| 39097 | 1-Cys peroxiredoxin | 26 | 8 | 36 | 13 | X |
| 4123 | dihydrolipoyl dehydrogenase chloroplastic | 61 | 7 | 2 | 1 | X |
| 4283 | glutaredoxin | 15 | 7 | 37 | 4 | X |
| 11544 | CBS domain-containing mitochondrial | 23 | 9 | 4 | 1 | X |
| 127370 | disulfide isomerase-like 2-3 | 37 | 9 | 20 | 4 | X |
| <i>Hydrolase</i> | | | | | | |
| 1369 | nudix hydrolase 3 | 98 | 5 | 3 | 1 | X |
| <i>Integral component of membrane/transport</i> | | | | | | |
| 1026 | SNF1-related kinase regulatory subunit gamma-1-like | 52 | 5 | 6 | 2 | X |
| 103759 | bidirectional sugar transporter SWEET3-like | 12 | 10 | 6 | 1 | X |
| 11312 | oleosin 1-like | 16 | 8 | 30 | 4 | X |
| 11673 | cytochrome c1- heme mitochondrial | 39 | 7 | 2 | 1 | X |
| 126790 | Alpha-1,4-glucan- synthase [UDP-forming] | 44 | 6 | 11 | 4 | X |
| 144508 | reticulon B2 | 31 | 8 | 8 | 3 | X |
| 15985 | ADP,ATP carrier mitochondrial | 42 | 10 | 4 | 1 | X |
| 17164 | temperature-induced lipocalin | 21 | 7 | 7 | 1 | X |
| 18096 | Outer envelope pore 16- chloroplastic | 16 | 9 | 64 | 6 | X |
| 18445 | hypothetical protein | 14 | 10 | 12 | 1 | X |
| 18453 | mitochondrial outer membrane porin of 36 kDa-like | 30 | 9 | 11 | 3 | X |
| 21563 | malate mitochondrial | 38 | 9 | 18 | 2 | X |
| 2590 | AWPM-19 domain-containing | 19 | 10 | 12 | 2 | X |
| 29869 | ATP synthase subunit mitochondrial | 27 | 9 | 13 | 2 | X |
| 30099 | luminal-binding 5 | 76 | 5 | 15 | 8 | X |
| 30576 | importin subunit alpha-2 | 59 | 5 | 8 | 3 | X |
| 35282 | mitochondrial outer membrane porin of 36 kDa | 32 | 9 | 18 | 4 | X |
| 36654 | basic blue -like | 17 | 9 | 23 | 3 | X |
| 37512 | probable peroxygenase 3 | 22 | 9 | 8 | 1 | X |
| 37838 | phosphoglycerate kinase | 44 | 8 | 16 | 7 | X |
| 42466 | peroxygenase 2 | 27 | 6 | 53 | 10 | X |
| 46103 | unknown | 15 | 8 | 35 | 3 | X |
| 48178 | UPF0098 CPn_0877 CP_0992 CPj0877 0906 | 25 | 6 | 39 | 4 | X |
| 958 | malate mitochondrial | 36 | 9 | 30 | 7 | X |
| 11133 | probable endopeptidase p60 | 16 | 9 | 12 | 1 | X |
| 11148 | PLAC8 family | 28 | 6 | 3 | 1 | X |
| 11188 | 3-oxoacyl-[acyl-carrier-] synthase chloroplastic | 53 | 7 | 5 | 1 | X |
| 11712 | coatomer subunit beta -2 isoform X1 | 106 | 5 | 3 | 2 | X |
| 1349 | 30099 luminal-binding 5 | 21 | 10 | 19 | 2 | X |
| 2092 | ELC-like | 47 | 6 | 3 | 1 | X |
| 23105 | phosphoglycerate kinase | 52 | 7 | 20 | 1 | X |
| 28912 | stomatatin mitochondrial | 48 | 8 | 4 | 1 | X |
| 34191 | ubiquitin-conjugating enzyme E2 36 | 17 | 7 | 12 | 1 | X |

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Table S2 Continued

| | | | | | | | |
|--|---|-----|----|----|---|---|---|
| 34934 | Mitochondrial ATP synthase subunit G | 14 | 9 | 8 | 1 | | X |
| 49703 | aquaporin TIP1-1 | 22 | 9 | 16 | 1 | | X |
| 513 | unknown | 23 | 6 | 13 | 1 | | X |
| 5702 | apoptosis inhibitor 5 API5 isoform X1 | 61 | 9 | 3 | 1 | | X |
| 7507 | vacuolar-sorting receptor 6-like | 68 | 5 | 3 | 1 | | X |
| 94568 | oleosin-L | 13 | 10 | 19 | 3 | | X |
| 1108 | unknown | 28 | 9 | 5 | 1 | | X |
| 16971 | early nodulin 1 | 26 | 6 | 4 | 1 | | X |
| 17035 | 60S ribosomal L10 | 26 | 10 | 9 | 2 | | X |
| 17078 | pectin methylesterase | 62 | 7 | 4 | 2 | | X |
| 17254 | ribose-5-phosphate isomerase a | 33 | 9 | 5 | 1 | | X |
| 1743 | coatomer subunit beta -2 isoform X1 | 107 | 5 | 5 | 2 | | X |
| 17570 | cytochrome C | 12 | 9 | 7 | 1 | | X |
| 17847 | mitochondrial outer membrane porin 2 | 32 | 8 | 3 | 1 | | X |
| 1811 | outer envelope pore chloroplastic | 23 | 9 | 8 | 1 | | X |
| 2040 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit mitochondrial | 44 | 9 | 3 | 1 | | X |
| 22195 | unknown | 14 | 8 | 9 | 1 | | X |
| 34966 | transmembrane emp24 domain-containing p24beta3 | 25 | 8 | 9 | 2 | | X |
| 37903 | CRAL-TRIO domain | 95 | 5 | 3 | 1 | | X |
| 6072 | cytochrome c oxidase subunit 2 (mitochondrion) | 37 | 6 | 9 | 2 | | X |
| 7879 | transmembrane emp24 domain-containing p24delta9-like | 25 | 5 | 5 | 1 | | X |
| 9180 | ras-related RABB1c | 24 | 7 | 7 | 1 | | X |
| 9374 | probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit mitochondrial | 22 | 5 | 13 | 1 | | X |
| <i>Integral component of mitochondrial inner membrane</i> | | | | | | | |
| 42394 | outer envelope pore 16- chloroplastic | 19 | 9 | 15 | 2 | | X |
| <i>Lipid metabolic process</i> | | | | | | | |
| 100802 | GDSL esterase lipase 5-like | 17 | 9 | 24 | 2 | X | |
| 184134 | GDSL esterase lipase 1-like | 19 | 10 | 10 | 1 | | X |
| 34067 | prosaposin | 48 | 5 | 4 | 1 | | X |
| <i>Lipid storage</i> | | | | | | | |
| 8599 | oleosin 1 | 18 | 10 | 13 | 2 | X | |
| <i>L-phenylalanine metabolic process</i> | | | | | | | |
| 29416 | macrophage migration inhibitory factor homolog isoform X2 | 12 | 8 | 17 | 2 | X | |
| <i>Magnesium ion binding</i> | | | | | | | |
| 34088 | soluble inorganic pyrophosphatase 4 | 26 | 6 | 7 | 1 | X | |
| 6529 | 2-hydroxyacyl- lyase | 61 | 6 | 3 | 1 | X | |
| <i>Membrane</i> | | | | | | | |
| 10950 | prohibitin- mitochondrial | 33 | 10 | 4 | 1 | | X |
| 30782 | EXORDIUM-like 2 | 35 | 8 | 4 | 1 | | X |
| 9131 | prohibitin- mitochondrial | 31 | 8 | 4 | 1 | | X |
| <i>Metabolic process</i> | | | | | | | |
| 1885 | 3-ketoacyl- thiolase peroxisomal | 53 | 8 | 33 | 5 | X | |
| <i>Metal ion binding</i> | | | | | | | |
| 17806 | ribulose-phosphate 3- cytoplasmic isoform | 25 | 5 | 8 | 1 | X | |
| 3477 | zinc finger CCCH domain-containing 37 isoform X1 | 70 | 8 | 5 | 1 | | X |

Continue

Table S2 Continued

| | | | | | | |
|---|---|-----|----|----|----|---|
| Methylation | | | | | | |
| 157004 | arsenite methyltransferase | 11 | 5 | 9 | 1 | X |
| 199819 | hypothetical protein AK830_g5958 | 23 | 6 | 8 | 1 | X |
| 21146 | 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1 | 85 | 6 | 25 | 13 | X |
| 30607 | methyltransferase DDB_G0268948 | 30 | 5 | 26 | 6 | X |
| Mitochondrial matrix/Mitochondrial electron transport/organization | | | | | | |
| 18399 | mitochondrial outer membrane porin of 36 kDa | 33 | 8 | 3 | 1 | X |
| 20337 | Cytochrome c oxidase subunit mitochondrial | 13 | 9 | 12 | 1 | X |
| 7069 | Mitochondrial Rho GTPase 1 | 72 | 6 | 4 | 1 | X |
| 9493 | transferase mitochondrial | 47 | 7 | 6 | 2 | X |
| NADP metabolic process | | | | | | |
| 19530 | S-adenosyl-L-homocysteine hydrolase | 56 | 6 | 20 | 7 | X |
| 23663 | glutathione cytosolic | 58 | 8 | 5 | 1 | X |
| 2037 | glyceraldehyde-3-phosphate cytosolic-like | 40 | 7 | 51 | 1 | X |
| 5845 | ATP-dependent (S)-NAD(P)H-hydrate dehydratase isoform X2 | 48 | 8 | 2 | 1 | X |
| 7132 | isocitrate dehydrogenase [NADP]-like | 55 | 9 | 2 | 1 | X |
| Negative regulation of endopeptidase activity | | | | | | |
| 17034 | cysteine ase inhibitor 12 | 27 | 9 | 7 | 1 | X |
| Nuclear pore/transport | | | | | | |
| 12400 | nuclear pore complex NUP98A isoform X1 | 109 | 9 | 2 | 1 | X |
| Nuclear proteasome complex | | | | | | |
| 11704 | 26S proteasome regulatory subunit 4 homolog B | 52 | 7 | 6 | 2 | X |
| Nucleosome assembly | | | | | | |
| 128994 | histone H4-like | 14 | 11 | 52 | 1 | X |
| 151977 | Histone H4 | 12 | 11 | 44 | 4 | X |
| 18015 | probable histone | 14 | 10 | 60 | 3 | X |
| 18225 | histone H2A | 15 | 10 | 34 | 2 | X |
| 209168 | histone H2B | 18 | 10 | 66 | 4 | X |
| 21477 | histone H4-like | 14 | 11 | 50 | 1 | X |
| 36619 | Histone | 17 | 11 | 36 | 2 | X |
| 46780 | histone -like | 15 | 10 | 63 | 0 | X |
| 144492 | histone H2A | 17 | 10 | 49 | 8 | X |
| 1486 | histone H1 | 25 | 10 | 4 | 1 | X |
| 151962 | Histone | 17 | 11 | 30 | 3 | X |
| 18727 | probable histone | 12 | 10 | 25 | 1 | X |
| 33367 | histone | 17 | 10 | 66 | 2 | X |
| 33776 | probable histone | 16 | 11 | 34 | 1 | X |
| 35961 | histone H3 | 18 | 11 | 8 | 1 | X |
| 4452 | probable histone | 19 | 10 | 38 | 1 | X |
| 1305 | histone H2A | 15 | 11 | 69 | 11 | X |
| 142362 | Histone H2A | 12 | 10 | 11 | 1 | X |
| 15624 | histone -like | 18 | 10 | 25 | 2 | X |
| 1708 | histone H2A-like | 17 | 10 | 10 | 1 | X |
| 17569 | histone H2AX | 15 | 10 | 33 | 1 | X |
| 29880 | histone H2AX | 14 | 10 | 26 | 1 | X |
| 35527 | histone | 22 | 10 | 29 | 3 | X |
| 94788 | histone -like | 18 | 10 | 56 | 1 | X |

Continue

Table S2 Continued

| <i>Nucleotide/binding/phosphorylation</i> | | | | | | |
|---|--|----|----|----|----|---|
| 10839 | polyadenylate-binding RBP47-like isoform X2 | 43 | 6 | 5 | 1 | X |
| 11860 | RNA-binding (RRM RBD RNP motifs) family | 29 | 9 | 10 | 1 | X |
| 11864 | UTP--glucose-1-phosphate uridylyltransferase | 54 | 5 | 22 | 7 | X |
| 17030 | UBP1-associated 2C-like | 27 | 9 | 27 | 4 | X |
| 17181 | oligouridylylate-binding 1-like | 37 | 5 | 33 | 5 | X |
| 20788 | RNA-binding 1 | 29 | 9 | 24 | 3 | X |
| 208468 | glycine-rich RNA-binding | 17 | 9 | 41 | 6 | X |
| 29622 | adenylate kinase 4 | 29 | 7 | 16 | 3 | X |
| 30037 | DNA RNA-binding Alba | 15 | 6 | 20 | 1 | X |
| 34197 | polyadenylate-binding 3 | 72 | 8 | 2 | 1 | X |
| 34895 | heterogeneous nuclear ribonucleo 1 | 41 | 8 | 23 | 4 | X |
| 37895 | RNA-binding Musashi homolog 2 | 44 | 8 | 4 | 1 | X |
| 37907 | heterogeneous nuclear ribonucleo H2 isoform X1 | 29 | 7 | 7 | 1 | X |
| 8514 | heterogeneous nuclear ribonucleo 1-like | 50 | 7 | 4 | 1 | X |
| 10025 | polyadenylate-binding RBP45-like isoform X1 | 48 | 7 | 7 | 3 | X |
| 23100 | aspartate--tRNA ligase cytoplasmic | 64 | 7 | 3 | 1 | X |
| 27035 | binding partner of ACD11 1-like | 37 | 7 | 3 | 1 | X |
| 29499 | UBP1-associated 2C-like | 44 | 9 | 3 | 1 | X |
| 7292 | polyadenylate-binding 8-like | 74 | 7 | 2 | 1 | X |
| 10068 | glycine-rich RNA-binding mitochondrial-like | 24 | 5 | 16 | 2 | X |
| 17592 | RNA-binding glycine-rich | 18 | 7 | 6 | 1 | X |
| 18207 | RNA-binding 1-like isoform X2 | 43 | 7 | 6 | 1 | X |
| 2024 | ras GTPase-activating -binding 1-like | 58 | 6 | 3 | 1 | X |
| 2540 | RNA-binding 1 | 29 | 9 | 21 | 6 | X |
| 34381 | heat shock 70 kDa 15-like | 91 | 6 | 2 | 1 | X |
| 3773 | ribose-phosphate pyrophosphokinase 4 | 47 | 8 | 4 | 1 | X |
| 38616 | Zinc CCHC-type | 33 | 7 | 6 | 1 | X |
| 9786 | polyadenylate-binding RBP47 isoform X2 | 45 | 6 | 2 | 1 | X |
| 98226 | disease resistance RGA1 | 21 | 9 | 5 | 1 | X |
| <i>Nucleus/membrane</i> | | | | | | |
| 4129 | CTL DDB_G0288717 | 64 | 7 | 4 | 1 | X |
| <i>Nucleus/nucleic acid binding</i> | | | | | | |
| 127304 | glycine-rich RNA-binding RZ1C isoform X1 | 30 | 9 | 6 | 1 | X |
| <i>Nutrient reservoir activity</i> | | | | | | |
| 1003 | vicilin-like seed storage At2g28490 | 30 | 9 | 32 | 14 | X |
| 128065 | Cupin_1 domain-containing | 17 | 6 | 71 | 4 | X |
| 20850 | legumin-like storage | 12 | 5 | 48 | 2 | X |
| 40716 | vicilin-like antimicrobial peptides 2-2 | 24 | 8 | 57 | 15 | X |
| 42291 | legumin-like storage | 59 | 9 | 68 | 49 | X |
| 42436 | Cupin 1 | 55 | 7 | 34 | 18 | X |
| 44132 | 11S globulin seed storage 2-like | 15 | 10 | 89 | 15 | X |
| 47854 | legumin-like storage | 24 | 8 | 30 | 8 | X |
| 593 | sucrose-binding -like | 49 | 6 | 19 | 8 | X |
| 66263 | legumin-like storage | 12 | 5 | 54 | 3 | X |
| 70603 | legumin-like storage | 11 | 5 | 69 | 1 | X |
| 74731 | legumin-like storage | 14 | 6 | 40 | 10 | X |
| <i>Oxidation-reduction</i> | | | | | | |
| 11200 | thioredoxin H4-1-like | 13 | 5 | 13 | 1 | X |
| 127205 | alcohol | 51 | 8 | 15 | 1 | X |

Continue

Table S2 Continued

| | | | | | | |
|---------------|---|----|---|----|----|---|
| 16000 | sorbitol dehydrogenase | 39 | 6 | 23 | 6 | X |
| 16901 | glyceraldehyde-3-phosphate dehydrogenase chloroplastic | 50 | 9 | 44 | 11 | X |
| 16925 | glycerate dehydrogenase | 44 | 7 | 2 | 1 | X |
| 16930 | superoxide dismutase [Cu-Zn] chloroplastic | 22 | 7 | 18 | 2 | X |
| 16961 | catalase | 57 | 7 | 4 | 1 | X |
| 16973 | 2-Cys peroxiredoxin chloroplastic | 43 | 8 | 16 | 5 | X |
| 17112 | 2-methylene-furan-3-one reductase-like | 34 | 5 | 6 | 1 | X |
| 17250 | stromal 70 kDa heat shock-related chloroplastic | 39 | 6 | 5 | 1 | X |
| 17595 | catalase isozyme 1 | 57 | 8 | 16 | 5 | X |
| 17911 | aldo-keto reductase family 4 member C9-like | 38 | 6 | 6 | 2 | X |
| 18017 | superoxide dismutase [Mn] mitochondrial | 27 | 8 | 56 | 10 | X |
| 20033 | heat shock 70 kDa 8 | 62 | 5 | 2 | 1 | X |
| 20329 | aldehyde dehydrogenase family 2 member mitochondrial | 63 | 8 | 20 | 6 | X |
| 21445 | heat shock 70 kDa | 72 | 5 | 62 | 32 | X |
| 2308 | betaine aldehyde dehydrogenase mitochondrial | 59 | 6 | 2 | 1 | X |
| 27054 | formate mitochondrial | 43 | 8 | 8 | 3 | X |
| 30025 | glutathione peroxidase | 27 | 9 | 24 | 3 | X |
| 30396 | superoxide dismutase [Cu-Zn]-like | 15 | 6 | 30 | 3 | X |
| 3418 | aldose reductase | 39 | 7 | 44 | 16 | X |
| 3428 | 11-beta-hydroxysteroid dehydrogenase 1B-like | 40 | 9 | 21 | 8 | X |
| 37866 | peroxiredoxin- mitochondrial | 21 | 8 | 12 | 3 | X |
| 41574 | NADP-dependent glyceraldehyde-3-phosphate dehydrogenase | 54 | 7 | 7 | 2 | X |
| 44377 | 6-phosphogluconate decarboxylating chloroplastic | 54 | 6 | 4 | 1 | X |
| 44645 | aldehyde dehydrogenase family 2 member mitochondrial-like | 59 | 7 | 8 | 3 | X |
| 45788 | probable aldo-keto reductase 1 | 43 | 7 | 4 | 1 | X |
| 543 | D-3-phosphoglycerate dehydrogenase chloroplastic-like | 69 | 8 | 2 | 1 | X |
| 6735 | probable mitochondrial saccharopine dehydrogenase-like oxidoreductase At5g39410 | 53 | 9 | 7 | 2 | X |
| 7305 | homogentisate 1,2-dioxygenase | 52 | 7 | 9 | 2 | X |
| 7525 | glucose and ribitol dehydrogenase homolog 1-like | 35 | 8 | 47 | 24 | X |
| 782 | alcohol | 48 | 8 | 25 | 3 | X |
| 8450 | quinone-oxidoreductase chloroplastic | 35 | 9 | 15 | 2 | X |
| 893 | aldehyde dehydrogenase | 47 | 8 | 17 | 4 | X |
| 17126 | quinone oxidoreductase PIG3 | 35 | 7 | 16 | 2 | X |
| 18967 | catalase heme-binding enzyme | 11 | 8 | 13 | 1 | X |
| 21225 | glyceraldehyde-3-phosphate dehydrogenase cytosolic | 40 | 7 | 36 | 1 | X |
| 30306 | thioredoxin H-type-like | 13 | 5 | 50 | 3 | X |
| 3036 | electron transfer flavo -ubiquinone mitochondrial isoform X1 | 44 | 9 | 8 | 1 | X |
| 34390 | short-chain dehydrogenase reductase 2a | 32 | 6 | 7 | 1 | X |
| 4014 | thioredoxin mitochondrial-like | 20 | 9 | 9 | 1 | X |
| 101292 | ketose-bisphosphate aldolase class-II family | 26 | 8 | 7 | 1 | X |
| 10948 | glyoxysomal fatty acid beta-oxidation multifunctional MFP-a | 79 | 9 | 1 | 1 | X |

Continue

Table S2 Continued

| | | | | | | | |
|--|---|----|----|----|----|---|---|
| 11278 | methylmalonate-semialdehyde dehydrogenase [acylating] mitochondrial | 60 | 7 | 2 | 1 | | X |
| 13226 | betaine aldehyde dehydrogenase chloroplastic | 27 | 5 | 6 | 1 | | X |
| 13382 | NADH dehydrogenase subunit 7 (mitochondrion) | 38 | 7 | 10 | 2 | | X |
| 1541 | L-galactono-1,4-lactone mitochondrial | 72 | 8 | 1 | 1 | | X |
| 17080 | pyruvate dehydrogenase E1 component subunit beta- mitochondrial | 41 | 5 | 7 | 1 | | X |
| 17339 | alcohol | 50 | 8 | 22 | 2 | | X |
| 17674 | thioredoxin H-type | 13 | 5 | 30 | 1 | | X |
| 17753 | quinone oxidoreductase 1 | 40 | 9 | 11 | 2 | | X |
| 17910 | guanosine nucleotide diphosphate dissociation inhibitor 2 | 50 | 6 | 11 | 2 | | X |
| 18103 | NADH dehydrogenase [ubiquinone] flavo mitochondrial | 28 | 8 | 6 | 1 | | X |
| 1839 | alcohol | 41 | 6 | 11 | 1 | | X |
| 18864 | cinnamoyl- reductase 1 | 35 | 6 | 6 | 1 | | X |
| 20195 | glutathione peroxidase | 34 | 9 | 10 | 1 | | X |
| 21157 | ATP synthase subunit mitochondrial | 37 | 9 | 4 | 1 | | X |
| 333 | tropinone reductase homolog At5g06060-like | 29 | 6 | 7 | 1 | | X |
| 3363 | probable aldehyde dehydrogenase | 61 | 7 | 5 | 2 | | X |
| 34862 | probable voltage-gated potassium channel subunit beta | 37 | 7 | 5 | 1 | | X |
| 40553 | 2-alkenal reductase (NADP(+)-dependent)-like | 38 | 7 | 10 | 3 | | X |
| 8825 | thioredoxin reductase 2-like | 41 | 8 | 4 | 1 | | X |
| 9092 | 6-phosphogluconate dehydrogenase | 53 | 7 | 4 | 1 | | X |
| 9095 | 3-oxoacyl-[acyl-carrier-] reductase 4 | 36 | 9 | 17 | 4 | | X |
| 9324 | dehydroascorbate reductase | 26 | 6 | 32 | 6 | | X |
| <i>Peptidyl-prolyl cis-trans isomerase activity</i> | | | | | | | |
| 17713 | peptidyl-prolyl cis-trans isomerase Pin1 | 14 | 10 | 15 | 1 | | X |
| <i>Peroxisome</i> | | | | | | | |
| 26891 | Unknown | 35 | 9 | 5 | 1 | | X |
| <i>Phosphorylation</i> | | | | | | | |
| 30842 | ribose-phosphate pyrophosphokinase 4 | 36 | 6 | 21 | 4 | X | |
| 10634 | phosphoenolpyruvate carboxykinase [ATP]-like | 73 | 7 | 4 | 2 | | X |
| <i>Photosynthesis</i> | | | | | | | |
| 585 | ribulose biphosphate carboxylase small chain clone 512-like | 21 | 9 | 11 | 1 | X | |
| 37794 | protochlorophyllide chloroplastic | 44 | 9 | 5 | 1 | | X |
| <i>Plant-type cell wall</i> | | | | | | | |
| 355 | Allergen Act d 3 | 40 | 7 | 4 | 1 | | X |
| <i>Plasmodesma/signal transducer activity</i> | | | | | | | |
| 29858 | RALF-like 33 | 15 | 8 | 7 | 1 | X | |
| <i>Plastid</i> | | | | | | | |
| 1457 | small heat shock chloroplastic | 28 | 6 | 18 | 2 | X | |
| <i>Proteasome assembly/proteolysis</i> | | | | | | | |
| 10255 | leucine aminopeptidase 1-like | 65 | 7 | 4 | 2 | X | |
| 1135 | aspartic ase A1-like | 60 | 5 | 27 | 11 | X | |
| 15158 | probable mitochondrial-processing peptidase subunit mitochondrial | 59 | 7 | 11 | 2 | X | |
| 17210 | cathepsin B-like | 28 | 7 | 28 | 1 | X | |

Continue

Table S2 Continued

| | | | | | | |
|----------------------------------|---|-----|----|----|----|---|
| 17473 | proteasome subunit alpha type-3 | 27 | 6 | 12 | 2 | X |
| 22541 | DJ-1 homolog D | 43 | 6 | 5 | 1 | X |
| 29925 | proteasome subunit alpha type-2-A | 26 | 6 | 15 | 2 | X |
| 34710 | proteasome subunit beta type-3-A | 23 | 6 | 16 | 2 | X |
| 4103 | puromycin-sensitive aminopeptidase isoform X1 | 109 | 6 | 5 | 3 | X |
| 649 | aminopeptidase M1 | 98 | 5 | 18 | 8 | X |
| 7148 | 26S proteasome non-ATPase regulatory subunit 5 | 59 | 5 | 3 | 1 | X |
| 186 | probable aspartyl aminopeptidase | 58 | 7 | 4 | 1 | X |
| 44072 | proline iminopeptidase-like | 52 | 6 | 3 | 1 | X |
| 48138 | serine carboxypeptidase-like 50 | 19 | 8 | 10 | 1 | X |
| 1070 | 26S proteasome non-ATPase regulatory subunit 8 homolog A | 31 | 5 | 8 | 1 | X |
| 17901 | aspartic ase nepenthesin-1 | 53 | 6 | 2 | 1 | X |
| 19099 | cysteine ase RD21A-like | 51 | 5 | 3 | 1 | X |
| 21056 | serine carboxypeptidase-like | 57 | 5 | 3 | 1 | X |
| 3094 | dipeptidyl-peptidase 5 | 76 | 6 | 3 | 1 | X |
| 3379 | probable mitochondrial-processing peptidase subunit mitochondrial | 57 | 6 | 4 | 1 | X |
| 35455 | cysteine protease | 16 | 9 | 13 | 1 | X |
| 37904 | probable Xaa-Pro aminopeptidase P | 75 | 5 | 2 | 1 | X |
| 3936 | proteasome subunit alpha type-5 | 27 | 5 | 9 | 1 | X |
| 4052 | proteasome subunit beta type-1 | 25 | 6 | 6 | 1 | X |
| 4488 | proteasome subunit beta type-6 | 26 | 6 | 18 | 3 | X |
| Protein ADP-ribosylation | | | | | | |
| 15759 | poly [ADP-ribose] polymerase 3 | 47 | 6 | 46 | 16 | X |
| 2451 | poly [ADP-ribose] polymerase 3 | 82 | 7 | 9 | 4 | X |
| Protein binding | | | | | | |
| 11539 | PLAT domain-containing 3-like | 18 | 5 | 11 | 2 | X |
| 12991 | selenium-binding 1-like | 56 | 6 | 11 | 4 | X |
| 15795 | probable gamma-aminobutyrate transaminase mitochondrial | 60 | 8 | 3 | 1 | X |
| 265 | guanine nucleotide-binding subunit beta | 35 | 8 | 25 | 5 | X |
| 3271 | dnaJ P58IPK homolog | 22 | 11 | 25 | 3 | X |
| 34082 | disulfide isomerase-like 2-3 | 50 | 5 | 4 | 2 | X |
| 376 | peptidyl-prolyl cis-trans isomerase FKBP12 | 15 | 10 | 27 | 2 | X |
| 8149 | importin subunit alpha-2 | 60 | 5 | 3 | 1 | X |
| 8202 | T-complex 1 subunit gamma | 61 | 6 | 6 | 2 | X |
| 13520 | actin-interacting 1-2 | 66 | 7 | 3 | 1 | X |
| 34863 | polyubiquitin 11 | 22 | 9 | 62 | 4 | X |
| 2173 | plant UBX domain-containing 11 | 69 | 5 | 3 | 1 | X |
| 2300 | transport SEC31 homolog B-like | 126 | 5 | 3 | 2 | X |
| 2354 | serine threonine- phosphatase BSL1-like | 101 | 7 | 1 | 1 | X |
| 5451 | phospholipase A-2-activating | 86 | 6 | 2 | 1 | X |
| 7589 | plant UBX domain-containing 8 | 70 | 5 | 2 | 1 | X |
| 77544 | cyclophilin 1 | 13 | 9 | 18 | 1 | X |
| 8133 | 70 kDa peptidyl-prolyl isomerase-like | 65 | 5 | 2 | 1 | X |
| 9308 | WD repeat-containing WRAP73 | 53 | 6 | 4 | 1 | X |
| Protein dephosphorylation | | | | | | |
| 10353 | probable phosphatase 2C 76 | 34 | 5 | 5 | 1 | X |

Continue

Table S2 Continued

| | | | | | | |
|--|---|-----|----|----|----|---|
| <i>Protein domain specific binding</i> | | | | | | |
| 18468 | 14-33 | 30 | 5 | 48 | 8 | X |
| 17434 | 14-3-3 GF14 iota | 30 | 5 | 7 | 1 | X |
| <i>Protein folding</i> | | | | | | |
| 11308 | dnaJ homolog subfamily B member 13-like | 38 | 9 | 10 | 2 | X |
| 13792 | Heat shock 70 kDa mitochondrial | 22 | 10 | 32 | 3 | X |
| 17492 | hsp70-Hsp90 organizing 3 | 65 | 6 | 22 | 9 | X |
| 17558 | T-complex 1 subunit epsilon | 59 | 6 | 5 | 1 | X |
| 17694 | tau class glutathione S-transferase | 29 | 5 | 33 | 10 | X |
| 18686 | disulfide isomerase-like 1-4 | 63 | 5 | 2 | 1 | X |
| 20670 | peptidyl-prolyl cis-trans isomerase | 29 | 9 | 15 | 2 | X |
| 2193 | T-complex 1 subunit theta | 59 | 5 | 6 | 2 | X |
| 620 | T-complex 1 subunit alpha | 59 | 6 | 4 | 1 | X |
| 8022 | peptidyl-prolyl cis-trans isomerase | 25 | 9 | 48 | 7 | X |
| 268 | T-complex 1 subunit eta | 67 | 8 | 3 | 1 | X |
| 9383 | T-complex 1 subunit zeta 1 | 59 | 7 | 6 | 2 | X |
| 10287 | probable prefoldin subunit 2 | 16 | 6 | 6 | 1 | X |
| 10394 | T-complex 1 subunit zeta 1 | 59 | 7 | 4 | 1 | X |
| 16755 | Peptidyl-prolyl cis-trans isomerase | 22 | 9 | 6 | 1 | X |
| 16913 | peptidyl-prolyl cis-trans isomerase CYP19-4 | 23 | 9 | 11 | 2 | X |
| 17039 | disulfide-isomerase | 30 | 5 | 13 | 3 | X |
| <i>Protein refolding</i> | | | | | | |
| 10398 | chaperonin CPN60- mitochondrial | 63 | 7 | 19 | 3 | X |
| 1197 | chaperone 1 | 101 | 6 | 41 | 31 | X |
| <i>Pyruvate metabolic process</i> | | | | | | |
| 33344 | 4-hydroxy-4-methyl-2-oxoglutarate aldolase 2 | 23 | 7 | 12 | 2 | X |
| <i>Regulation of transcription/ DNA-templated</i> | | | | | | |
| 23613 | trihelix transcription factor GT-3b-like | 39 | 9 | 2 | 1 | X |
| 3154 | phytochrome | 122 | 6 | 1 | 1 | X |
| 502 | XS domain-containing | 90 | 7 | 2 | 1 | X |
| 5873 | staphylococcal nuclease domain-containing 1-like | 110 | 7 | 5 | 2 | X |
| <i>Regulation of translational elongation</i> | | | | | | |
| 29456 | elongation factor 1-beta 2-like | 25 | 5 | 29 | 4 | X |
| <i>Response to antibiotic</i> | | | | | | |
| 1318 | erythromycin esterase | 48 | 6 | 3 | 1 | X |
| <i>Response to cytokinin</i> | | | | | | |
| 11039 | probable ribose-5-phosphate isomerase chloroplastic | 31 | 6 | 5 | 1 | X |
| 19007 | ERBB-3 BINDING PROTEIN 1 | 40 | 7 | 13 | 3 | X |
| <i>Response to desiccation</i> | | | | | | |
| 26026 | late embryogenesis abundant | 17 | 6 | 15 | 2 | X |
| <i>Response to oxidative stress</i> | | | | | | |
| 3143 | kDa class I heat shock -like | 20 | 5 | 7 | 1 | X |
| 209194 | respiratory burst oxidase homolog A-like | 28 | 9 | 5 | 1 | X |
| <i>Response to stimulus</i> | | | | | | |
| 47933 | HVA22 f | 21 | 7 | 10 | 1 | X |
| <i>Response to stress</i> | | | | | | |
| 11238 | universal stress PHOS34 | 22 | 6 | 7 | 1 | X |
| 17198 | universal stress A | 53 | 9 | 3 | 1 | X |

Continue

Table S2 Continued

| | | | | | | | |
|--|--|----|----|----|----|---|---|
| 2194 | universal stress PHOS34-like | 39 | 6 | 16 | 4 | X | |
| 3825 | dehydrin | 16 | 7 | 5 | 1 | X | |
| 93756 | L-isoadipate O-methyltransferase-like isoform X2 | 32 | 8 | 5 | 1 | X | |
| 29214 | universal stress A | 17 | 7 | 12 | 1 | | X |
| 36599 | universal stress A | 24 | 7 | 4 | 1 | | X |
| 99660 | serine threonine- phosphatase PP1 | 41 | 6 | 3 | 1 | | X |
| 12872 | heat shock 90- mitochondrial | 92 | 5 | 4 | 2 | | X |
| 2429 | heat shock 83 | 84 | 5 | 7 | 3 | | X |
| 3299 | universal stress PHOS32 | 26 | 5 | 5 | 1 | | X |
| 8982 | universal stress A | 18 | 8 | 18 | 3 | | X |
| <i>Ribonuclease inhibitor</i> | | | | | | | |
| 8814 | 4-hydroxy-4-methyl-2-oxoglutarate aldolase 3 | 20 | 6 | 6 | 1 | | X |
| <i>RNA binding</i> | | | | | | | |
| 1508 | heterogeneous nuclear ribonucleo 1 | 44 | 8 | 3 | 1 | X | |
| 16620 | KH domain-containing At4g18375-like isoform X1 | 70 | 9 | 18 | 10 | X | |
| 1733 | flowering locus K homology domain | 53 | 7 | 27 | 7 | X | |
| 19012 | KH domain-containing HEN4 | 75 | 8 | 17 | 7 | X | |
| 37699 | eukaryotic translation initiation factor-like | 94 | 9 | 5 | 3 | X | |
| 6616 | KH domain-containing At4g18375 | 75 | 8 | 19 | 10 | X | |
| 8505 | KH domain-containing At4g18375-like isoform X1 | 69 | 8 | 18 | 8 | X | |
| 8659 | KH domain-containing HEN4 | 70 | 9 | 2 | 2 | X | |
| 2151 | polyadenylate-binding 2-like | 73 | 8 | 3 | 1 | | X |
| 3411 | zinc finger CCCH domain-containing 14-like | 38 | 9 | 6 | 1 | | X |
| 8139 | small nuclear ribonucleo -associated B -like | 33 | 11 | 3 | 1 | | X |
| 10422 | proline--tRNA cytoplasmic-like | 59 | 7 | 5 | 1 | | X |
| 19000 | YTH domain-containing family 1 isoform X1 | 81 | 6 | 2 | 1 | | X |
| 23571 | zinc finger CCCH domain-containing 14-like | 35 | 9 | 17 | 3 | | X |
| 29946 | NHP2 1 | 14 | 7 | 17 | 1 | | X |
| <i>Seed development</i> | | | | | | | |
| 3904 | GEM 5 | 32 | 7 | 11 | 1 | X | |
| 4230 | GEM 5 | 39 | 8 | 8 | 1 | | X |
| <i>Small-subunit processome</i> | | | | | | | |
| 8467 | nucleolar 56 | 65 | 8 | 3 | 1 | | X |
| <i>Structural constituent of ribosome/translation/ribosome biogenesis</i> | | | | | | | |
| 209193 | 60S ribosomal L18a | 21 | 10 | 15 | 3 | X | |
| 209735 | 40S ribosomal S26-3-like | 16 | 11 | 7 | 1 | X | |
| 2765 | 60S ribosomal L17-2 | 23 | 11 | 22 | 3 | X | |
| 29444 | 60S ribosomal L37a | 15 | 10 | 12 | 1 | X | |
| 29881 | 40S ribosomal S7 | 25 | 10 | 18 | 3 | X | |
| 30026 | 60S ribosomal L30 | 16 | 9 | 21 | 2 | X | |
| 30044 | 40S ribosomal S9-2 | 25 | 10 | 5 | 1 | X | |
| 31296 | 60S ribosomal L26-1-like | 19 | 11 | 7 | 1 | X | |
| 32349 | 40S ribosomal S16 | 16 | 10 | 12 | 2 | X | |
| 32661 | 40S ribosomal S18 | 19 | 11 | 14 | 3 | X | |
| 32827 | 40S ribosomal S20-2 | 18 | 10 | 12 | 2 | X | |
| 334 | 60S ribosomal L28-2-like | 17 | 10 | 18 | 1 | X | |
| 34657 | 40S ribosomal S4-3 | 30 | 10 | 19 | 2 | X | |
| 375 | 60S ribosomal L13-1 | 24 | 11 | 27 | 2 | X | |
| 3842 | 40S ribosomal S17 | 16 | 10 | 25 | 2 | X | |

Continue

Table S2 Continued

| | | | | | | | |
|---|--|----|----|----|---|---|---|
| 3895 | 40S ribosomal SA-like | 35 | 5 | 13 | 3 | X | |
| 4931 | 40S ribosomal S15a-1 | 17 | 11 | 31 | 3 | X | |
| 49797 | 60S ribosomal L36-2-like | 16 | 11 | 7 | 1 | X | |
| 5013 | 40S ribosomal S19-3 | 21 | 10 | 31 | 5 | X | |
| 7146 | 40S ribosomal S13 | 17 | 11 | 17 | 2 | X | |
| 8389 | 60S ribosomal L5-like | 34 | 9 | 16 | 3 | X | |
| 11017 | 60S ribosomal L19-3-like | 24 | 11 | 9 | 1 | | X |
| 126788 | 60S ribosomal L12 | 18 | 8 | 11 | 1 | | X |
| 127151 | 60S ribosomal L4 | 45 | 10 | 20 | 7 | | X |
| 128081 | 60S ribosomal L10a | 26 | 10 | 5 | 1 | | X |
| 17165 | 60S ribosomal L35a-3 | 13 | 11 | 24 | 1 | | X |
| 17419 | 60S ribosomal L13a-4 | 24 | 10 | 9 | 2 | | X |
| 17503 | 40S ribosomal S8 | 26 | 10 | 23 | 1 | | X |
| 17539 | 40S ribosomal S6 | 30 | 11 | 12 | 1 | | X |
| 18105 | 60S acidic ribosomal P0 | 34 | 5 | 15 | 3 | | X |
| 30348 | 60S ribosomal L14-1 | 18 | 10 | 9 | 1 | | X |
| 36630 | 60S ribosomal L14-1 | 16 | 10 | 10 | 1 | | X |
| 47432 | 60S ribosomal L10 | 26 | 10 | 21 | 3 | | X |
| 126721 | 40S ribosomal S12 | 19 | 6 | 6 | 1 | | X |
| 126789 | 60S ribosomal L24 | 22 | 11 | 4 | 1 | | X |
| 127521 | 40S ribosomal S21 | 12 | 7 | 14 | 1 | | X |
| 144155 | 60S acidic ribosomal P1 | 13 | 7 | 13 | 1 | | X |
| 1532 | 60S ribosomal L18-2 | 25 | 11 | 5 | 1 | | X |
| 1619 | 40S ribosomal S15 | 19 | 10 | 25 | 2 | | X |
| 16907 | 60S ribosomal L4 | 45 | 10 | 25 | 7 | | X |
| 17136 | 40S ribosomal S4-3 | 30 | 10 | 16 | 1 | | X |
| 17170 | 60S ribosomal L30 | 18 | 5 | 32 | 3 | | X |
| 17396 | 40S ribosomal S3a | 30 | 10 | 15 | 3 | | X |
| 17926 | 60S acidic ribosomal P1-like | 13 | 5 | 13 | 1 | | X |
| 20319 | 60S acidic ribosomal P0 | 36 | 5 | 22 | 6 | | X |
| 20708 | 60S ribosomal L21-1-like | 19 | 10 | 6 | 1 | | X |
| 23575 | 60S acidic ribosomal P3-2 | 28 | 5 | 7 | 1 | | X |
| 24008 | 60S ribosomal L6-1-like | 26 | 10 | 3 | 1 | | X |
| 24579 | 60S ribosomal L12 | 18 | 8 | 25 | 3 | | X |
| 2461 | 60S ribosomal L7a-1 | 29 | 10 | 5 | 1 | | X |
| 27283 | 60S ribosomal L9 | 22 | 10 | 6 | 1 | | X |
| 29567 | 60S ribosomal L23a | 21 | 11 | 11 | 1 | | X |
| 32841 | 60S ribosomal L13-1 | 24 | 11 | 14 | 1 | | X |
| 44394 | 60S ribosomal L23 | 17 | 10 | 17 | 2 | | X |
| 53498 | 40S ribosomal S24-1 | 15 | 10 | 17 | 1 | | X |
| 540 | 60S ribosomal L22-2 | 16 | 10 | 9 | 1 | | X |
| 814 | 60S ribosomal L15 | 27 | 11 | 4 | 1 | | X |
| <i>Sucrose metabolic process</i> | | | | | | | |
| 79458 | probable sucrose-phosphate synthase 3 isoform X1 | 12 | 9 | 22 | 1 | | X |
| <i>Transferase</i> | | | | | | | |
| 148756 | tRNA 2 -phosphotransferase 1-like isoform X3 | 20 | 9 | 22 | 3 | | X |
| 1667 | UDP-rhamnose:rhamnosyltransferase 1 | 54 | 6 | 2 | 1 | | X |
| 1886 | 3-ketoacyl- thiolase peroxisomal | 49 | 7 | 15 | 1 | | X |

Continue

Table S2 Continued

| <i>Transketolase</i> | | | | | | |
|-----------------------------------|--|-----|----|----|----|---|
| 6341 | chloroplastic-like | 63 | 7 | 7 | 2 | X |
| 4464 | chloroplastic | 82 | 7 | 6 | 3 | X |
| 46111 | chloroplastic-like isoform X1 | 11 | 9 | 14 | 1 | X |
| <i>Tricarboxylic acid cycle</i> | | | | | | |
| 12895 | succinate-- ligase [ADP-forming] subunit mitochondrial | 46 | 5 | 2 | 1 | X |
| 17841 | citrate glyoxysomal | 56 | 8 | 12 | 3 | X |
| 19243 | succinate dehydrogenase [ubiquinone] flavo subunit mitochondrial | 70 | 7 | 6 | 3 | X |
| 28548 | 2-oxoglutarate mitochondrial | 116 | 7 | 16 | 10 | X |
| 44435 | isocitrate lyase | 66 | 7 | 40 | 18 | X |
| 9096 | malate synthase | 30 | 7 | 49 | 1 | X |
| 9964 | malate glyoxysomal | 32 | 7 | 45 | 1 | X |
| 11868 | citrate mitochondrial | 53 | 8 | 3 | 1 | X |
| 18344 | dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex mitochondrial-like | 51 | 9 | 3 | 1 | X |
| 7640 | NADP-dependent malic enzyme | 67 | 6 | 2 | 1 | X |
| <i>tRNA binding</i> | | | | | | |
| 1874 | probable methionine--tRNA ligase | 98 | 7 | 3 | 1 | X |
| <i>Tyrosine metabolic process</i> | | | | | | |
| 156701 | dual specificity | 14 | 7 | 25 | 1 | X |
| 32877 | macrophage migration inhibitory factor homolog | 12 | 5 | 10 | 1 | X |
| <i>Unknown</i> | | | | | | |
| 101716 | vicilin-like seed storage At2g28490 | 15 | 7 | 57 | 6 | X |
| 10251 | P-loop containing nucleoside triphosphate hydrolase | 54 | 7 | 9 | 3 | X |
| 10365 | oil body-associated 2B-like | 31 | 5 | 20 | 5 | X |
| 1038 | PREDICTED: uncharacterized protein LOC105049275 | 39 | 5 | 32 | 8 | X |
| 10878 | stress response NST1 isoform X2 | 12 | 10 | 10 | 1 | X |
| 116241 | SNF1-related kinase regulatory subunit gamma-like PV42a | 16 | 6 | 32 | 3 | X |
| 11886 | small heat shock chloroplastic | 26 | 9 | 9 | 1 | X |
| 120781 | kDa class I heat shock -like | 21 | 7 | 15 | 2 | X |
| 12115 | FLX-like 3 | 32 | 9 | 33 | 6 | X |
| 126758 | Development cell death domain | 52 | 9 | 33 | 9 | X |
| 147073 | kDa class I heat shock -like | 18 | 7 | 29 | 2 | X |
| 1534 | kDa class IV heat shock | 20 | 6 | 24 | 3 | X |
| 15893 | phosphatidylglycerol phosphatidylinositol transfer DDB_G0282179 | 17 | 6 | 45 | 5 | X |
| 1694 | kDa class I heat shock -like | 24 | 7 | 6 | 1 | X |
| 17052 | SRC2 homolog | 34 | 5 | 8 | 1 | X |
| 17069 | unknown | 19 | 5 | 13 | 2 | X |
| 17922 | small heat-shock | 18 | 10 | 7 | 1 | X |
| 18038 | desiccation-related PCC13-62-like | 38 | 9 | 17 | 5 | X |
| 18092 | FRIGIDA 3 | 66 | 6 | 5 | 2 | X |
| 18130 | heat shock 22 kDa mitochondrial isoform X2 | 25 | 9 | 8 | 1 | X |
| 18190 | gamma carbonic anhydrase mitochondrial-like | 30 | 7 | 5 | 1 | X |

Continue

Table S2 Continued

| | | | | | | |
|--------|--|----|----|----|----|---|
| 18329 | MFT2 | 22 | 9 | 55 | 6 | X |
| 18529 | Cryptomeria japonica clone: expressed in male strobili | 18 | 9 | 12 | 1 | X |
| 18781 | em GEA6 | 13 | 8 | 13 | 2 | X |
| 19274 | embryonic DC-8-like | 70 | 5 | 61 | 65 | X |
| 20189 | late embryogenesis abundant D-34-like | 17 | 7 | 58 | 14 | X |
| 202170 | late embryogenesis abundant | 17 | 7 | 25 | 4 | X |
| 21617 | kDa class I heat shock -like | 23 | 8 | 9 | 1 | X |
| 23352 | kDa class I heat shock | 16 | 8 | 9 | 1 | X |
| 24056 | Nucleic acid-binding | 17 | 7 | 11 | 1 | X |
| 261 | hypothetical protein | 33 | 5 | 52 | 9 | X |
| 30471 | small heat-shock | 17 | 6 | 35 | 3 | X |
| 3142 | hypothetical protein AXG93_209s1080 | 15 | 11 | 20 | 1 | X |
| 34861 | FLX-like 2 | 40 | 7 | 10 | 2 | X |
| 34879 | hydroxyproline-rich glyco family | 40 | 7 | 63 | 14 | X |
| 37889 | late embryo abundance | 26 | 6 | 4 | 1 | X |
| 3960 | Unknown protein motif | 20 | 5 | 34 | 4 | X |
| 404 | embryonic DC-8 | 43 | 5 | 31 | 10 | X |
| 41431 | kDa class I heat shock -like | 16 | 6 | 60 | 8 | X |
| 4144 | MOTHER of FT and TFL1 | 22 | 6 | 64 | 8 | X |
| 42389 | alpha carbonic anhydrase 7-like | 34 | 6 | 6 | 1 | X |
| 42567 | Glyoxalase-like domain-containing | 16 | 6 | 39 | 7 | X |
| 4426 | kDa class I heat shock -like | 18 | 8 | 32 | 1 | X |
| 44539 | legumin-like storage | 14 | 10 | 28 | 3 | X |
| 47852 | gibberellin-regulated 2-like | 13 | 9 | 18 | 1 | X |
| 5317 | probable glutamate carboxypeptidase 2 | 84 | 6 | 4 | 2 | X |
| 6550 | Xeroderma pigmentosum group G | 25 | 10 | 4 | 1 | X |
| 8896 | DUF2662 domain-containing | 23 | 4 | 7 | 2 | X |
| 95485 | FLX-like 1 | 39 | 7 | 9 | 2 | X |
| 96428 | 2S seed storage precursor | 13 | 6 | 26 | 7 | X |
| 98873 | poly [ADP-ribose] polymerase 3 | 15 | 7 | 20 | 2 | X |
| 11014 | embryonic dc-8 | 43 | 6 | 44 | 13 | X |
| 143203 | acetyltransferase At1g77540 | 13 | 7 | 15 | 1 | X |
| 17591 | peroxisomal small heat shock | 31 | 8 | 10 | 1 | X |
| 33757 | kDa class I heat shock -like | 18 | 6 | 33 | 1 | X |
| 5150 | coilin isoform X2 | 56 | 8 | 6 | 1 | X |
| 7971 | chaperone dnaJ 10-like | 39 | 7 | 4 | 1 | X |
| 8891 | small heat shock chloroplastic | 27 | 8 | 6 | 1 | X |
| 1037 | Nucleic acid- OB-fold | 15 | 5 | 7 | 1 | X |
| 11406 | auxin down-regulated | 28 | 7 | 3 | 1 | X |
| 12545 | DUF4149 domain-containing | 36 | 9 | 3 | 1 | X |
| 127827 | kDa class I heat shock -like | 18 | 7 | 29 | 1 | X |
| 1416 | FLX-like 1 | 34 | 8 | 6 | 1 | X |
| 150952 | thioredoxin Clot | 17 | 6 | 6 | 1 | X |
| 152148 | hypothetical protein AURANDRAFT_64842 | 16 | 5 | 11 | 1 | X |
| 15439 | unknown | 52 | 8 | 4 | 1 | X |
| 157981 | predicted protein | 19 | 4 | 13 | 1 | X |
| 16779 | reactive Intermediate Deaminase chloroplastic | 21 | 9 | 9 | 1 | X |
| 16997 | phenylcoumaran benzylic ether reductase | 34 | 6 | 4 | 1 | X |

Continue

Table S2 Continued

| | | | | | | | |
|---------------|---|----|----|----|----|---|---|
| 172059 | Drosophila busckii chromosome X sequence | 14 | 9 | 6 | 1 | | X |
| 17729 | FLX-like 2 | 35 | 7 | 4 | 1 | | X |
| 18452 | kDa class IV heat shock -like | 21 | 7 | 7 | 1 | | X |
| 190268 | hypothetical protein OXYTRI_15016 (macronuclear) | 17 | 5 | 9 | 1 | | X |
| 196033 | UBN2_3 domain-containing | 17 | 9 | 5 | 1 | | X |
| 19808 | small heat shock chloroplastic | 25 | 8 | 8 | 1 | | X |
| 24924 | kDa class III heat shock | 18 | 7 | 13 | 1 | | X |
| 260 | late embryogenesis abundant | 23 | 8 | 4 | 1 | | X |
| 27113 | Nicotiana tabacum uncharacterized LOC107788454 (LOC107788454) transcript variant mRNA | 12 | 8 | 21 | 1 | | X |
| 28722 | MLP1 isoform X2 | 78 | 5 | 1 | 1 | | X |
| 30701 | small heat-shock | 17 | 6 | 33 | 1 | | X |
| 31195 | phenylcoumaran benzylic ether reductase | 34 | 6 | 5 | 1 | | X |
| 32660 | small heat-shock | 17 | 6 | 33 | 1 | | X |
| 34461 | hypothetical protein BVC80_1833g45 | 17 | 5 | 6 | 1 | | X |
| 3591 | ricin B-like lectin R40G2 | 47 | 5 | 13 | 2 | | X |
| 3745 | embryonic dc-8 | 41 | 6 | 39 | 13 | | X |
| 3978 | gamma-interferon-inducible lysosomal thiol reductase | 27 | 5 | 5 | 1 | | X |
| 45729 | Poplar cDNA sequences | 14 | 10 | 15 | 1 | | X |
| 6881 | WD40-like Beta Propeller | 42 | 6 | 3 | 1 | | X |
| 8193 | Heme-binding 2 | 30 | 7 | 10 | 2 | | X |
| 96481 | (+)-neomenthol dehydrogenase-like isoform X2 | 36 | 6 | 5 | 1 | | X |
| 21240 | GTP-binding SAR1A | 24 | 9 | 14 | 2 | X | |
| 17819 | mitochondrial-processing peptidase subunit alpha | 55 | 6 | 4 | 1 | X | |
| 1792 | ATP synthase subunit mitochondrial | 30 | 10 | 4 | 1 | X | |
| 208477 | alcohol dehydrogenase class-3 | 51 | 8 | 23 | 5 | X | |
| 2160 | LIM domain-containing WLIM1-like | 24 | 9 | 20 | 4 | X | |
| 4135 | ranBP2-type zinc finger At1g67325 | 36 | 9 | 7 | 1 | X | |
| 203431 | unknown preotein motif | 12 | 9 | 16 | 1 | | X |
| 2015 | RING-H2 finger ATL3-like | 41 | 5 | 3 | 1 | | X |

^aPinus_DB *Pinus* sustainpine v3.

^bBlast Description Annotator

^cMolecular weight (KDa) and isoelectric point of protein calculated for each database.