

| 20 DAP up (116)  |   |        |       |  |
|--|---|--------|-------|--|
| Seq. ID  | Gene Annotation   | Factor | P     | Function                               |
| <b>PRIMARY &amp; SECONDARY METABOLISM &amp; TRANSPORT (26)</b> |   |        |       |  |
| P00898 (30,35DAP)  | Sucrose-phosphate synthase  | 3.7    | 0.011 | Sucrose metabolism                     |
| P02786   | Sucrose-phosphatase   | 2.1    | 0.018 | Sucrose metabolism                     |
| P01278 (25DAP)   | Sucrose synthase (VfSUS)  | 3.7    | 0.003 | Sucrose metabolism                     |
| P03899   | Glyceraldehyde-3-phosphate dehydrogenase, plastidial                        | 3.8    | 0.012 | Glycolysis                             |
| P01309   | Phosphoglucosyltransferase, cytoplasmic                                     | 2.8    | 0.037 | Glycolysis                             |
| P01595 (25DAP)   | Pyruvate dehydrogenase E1   | 2.4    | 0.007 | Glycolysis                             |
| P02802 (25DAP)   | 2-Oxoglutarate dehydrogenase, E1  | 2.1    | 0.007 | TCA cycle                              |
| P02915 (30DAP)   | NADH dehydrogenase (ubiquinone), mitochondrial complex 1, 75 kDa            | 2.6    | 0.029 | NADH oxidation                         |
| P02543   | ATP citrate lyase B   | 3.2    | 0.030 | CH metabolism, citrate degradation     |
| P01521 (30DAP)   | GDP-mannose 3,5-epimerase 2   | 2.8    | 0.014 | Ascorbate synthesis                    |
| P04257   | Malate dehydrogenase (NADP), chloroplast                                    | 2.8    | 0.030 | CH metabolism                          |
| P01320 (25DAP)   | Acetohydroxy- acid synthase small subunit                                   | 3.6    | 0.002 | Ile, Val biosynthesis                  |
| P00936 (25,30DAP)  | Methionine synthase   | 2.2    | 0.017 | Methionine synthesis                   |
| P02211   | L-allo-threonine acetaldehyde-lyase   | 2.0    | 0.036 | Thr/Gly interconversion                |
| P03092   | Aspartate transaminase  | 2.0    | 0.033 | Amino acid metabolism                  |
| P02005   | L-asparaginase  | 2.0    | 0.019 | Amino acid metabolism                  |
| P01761   | N-carbamoylputrescine amidohydrolase  | 3.2    | 0.030 | Polyamine synthesis                    |
| P02136 (25DAP)   | Putrescine aminopropyltransferase 2 (Spermidine synthase)                   | 2.2    | 0.008 | Polyamine synthesis                    |
| P04530   | S-adenosyl-L-homocysteine hydrolase (AdoHcy)                                | 2.1    | 0.035 | Methylation cycle                      |
| P02413   | O-diphenol-O-methyl transferase   | 2.1    | 0.032 | Methyltransferase, lignin biosynthesis |
| P01419 (30,35DAP)  | DNA (cytosine-5)-methyltransferase  | 2.1    | 0.035 | Methyltransferase, DNA biosynthesis    |
| P03466 (30,35DAP)  | Glycoside hydrolase   | 3.2    | 0.019 | CH metabolism                          |
| P00472   | Esterase/lipase/thioesterase  | 8.2    | 0.018 | Lipid metabolism                       |
| P01851   | Purple acid phosphatase   | 3.4    | 0.028 | Phosphoesterase                        |
| P02042   | Reversibly glycosylated polypeptide   | 2.4    | 0.002 | Cell wall synthesis                    |
| P04316 (25DAP)   | Reversibly glycosylated polypeptide   | 2.3    | 0.025 | Cell wall synthesis                    |
| <b>TRANSPORT (9)</b>   |   |        |       |  |
| P02071 (30DAP)   | Glc-6-phosphate/phosphate-translocator precursor, plastid                   | 5.4    | 0.034 | Metabolite transport, plastidial       |
| P03530   | Hexose transporter  | 4.4    | 0.014 | Sugar transport                        |
| P01343   | Monosaccharid transporter (VfSTP1)  | 4.0    | 0.029 | Sugar transport                        |
| P01679   | Xanthine/uracil permease (plasma membrane)                                  | 3.7    | 0.002 | Transport                              |
| P00853 (35DAP)   | Boron transporter   | 2.3    | 0.036 | Transport                              |
| P01923 (25DAP)   | ATP/ADP-transporter, chloroplast  | 2.2    | 0.047 | Transport                              |
| P01668   | ABC transporter (plasma membrane)   | 2.1    | 0.045 | Transport                              |
| P04427   | ATP synthase, delta (mitochondrion)   | 2.0    | 0.031 | ATP synthesis                          |
| P01272   | Import intermediate associated protein, IAP100 (plastid)                    | 7.4    | 0.025 | Protein import                         |
| <b>ENDOMEMBRANE TRANSPORT &amp; PROTEIN PROCESSING (10)</b>    |   |        |       |  |
| P02117 (25DAP)   | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit ST3B | 2.1    | 0.008 | Glycosylation                          |
| P02026   | Chaperonin 10 (chloroplast)   | 3.1    | 0.047 | Chaperone                              |
| P02333 (25,30,35DAP)   | Chaperonin 10 (chloroplast)   | 2.4    | 0.033 | Chaperone                              |
| P01640   | Chaperonin delta-subunit, cytosolic   | 2.3    | 0.045 | Chaperone                              |
| P00166 (25,30DAP)  | Chaperone PHSP1, mitochondrial  | 2.3    | 0.030 | Chaperone                              |
| P02763 (25,30DAP)  | Chaperone multifunctional (14-3-3 family)                                   | 3.3    | 0.048 | Chaperone                              |
| P00386 (25,30DAP)  | Vesicle transport v-SNARE   | 3.3    | 0.024 | Vesicle trafficking                    |
| P00502 (35DAP)   | SNAP25 (SNARE) Vesicle trafficking protein                                  | 2.0    | 0.012 | Vesicle trafficking                    |
| P00846   | Vacuolar protein sorting-associating protein                                | 2.1    | 0.018 | Vesicle trafficking                    |
| P03208   | Legumain  | 2.3    | 0.017 | Storage protein processing             |
| <b>REGULATED PROTEIN DEGRADATION (10)</b>                      |   |        |       |  |
| P02118   | Ubiquitin   | 2.2    | 0.023 | Ubiquitin mediated protein degradation |
| P02435 (25,30DAP)  | Ubiquitin   | 2.2    | 0.000 | Ubiquitin mediated protein degradation |
| P01166   | Ubiquitin-protein ligase  | 2.4    | 0.048 | Ubiquitin mediated protein degradation |
| P04406   | 20S proteasome alpha subunit  | 2.0    | 0.001 | Ubiquitin mediated protein degradation |
| P01831   | 20S proteasome, beta  | 2.3    | 0.030 | Ubiquitin mediated protein degradation |
| P01006 (25,30DAP)  | N-acyl-L-amino-acid amidohydrolase  | 3.4    | 0.002 | Peptidase                              |
| P02142 (30DAP)   | Peptidase/protease (Insulin degrading enzyme)                               | 5.4    | 0.034 | Proteinase                             |
| P02453 (25,30DAP)  | Serine carboxypeptidase (S10)   | 4.7    | 0.006 | Proteinase                             |
| P02234 (25,30DAP)  | Leucine aminopeptidase  | 123.8  | 0.009 | Proteinase                             |
| P02043 (25DAP)   | Oligopeptidase A  | 4.7    | 0.008 | Proteinase                             |
| <b>CELL PROLIFERATION (9)</b>                                  |   |        |       |  |
| P03116 (25,30,35DAP)   | Annexin   | 3.6    | 0.004 | Cell proliferation                     |
| P00079 (25DAP)   | Annexin   | 2.1    | 0.004 | Cell proliferation                     |
| P00033 (25,35DAP)  | Tubulin beta  | 2.5    | 0.001 | Cell proliferation                     |
| P04421 (25DAP)   | Actin   | 2.1    | 0.038 | Cell proliferation                     |
| P02409   | Actin-depolymerizing factor   | 4.0    | 0.010 | Cell proliferation                     |
| P02077   | Ca(2+)-regulated actin-binding protein                                      | 3.0    | 0.019 | Cell proliferation                     |
| P01979   | Exoribonuclease   | 3.7    | 0.000 | Cell proliferation                     |
| P00843 (30DAP)   | Cell division cycle protein   | 2.1    | 0.031 | Cell proliferation                     |
| P03980   | Flap endonuclease 1a  | 2.3    | 0.018 | DNA synthesis                          |
| <b>STORAGE RELATED (5)</b>                                     |   |        |       |  |
| P02195 (25,30DAP)  | Vicilin   | 3.6    | 0.001 | Storage protein                        |
| P00940 (25,35DAP)  | USP   | 7.4    | 0.005 | Storage protein                        |
| P01844 (30,35DAP)  | USP   | 6.2    | 0.027 | Storage protein                        |
| P01245 (30DAP)   | Ferritin 3  | 4.8    | 0.001 | Storage protein                        |
| P02120 (25,30DAP)  | GDSL-motif lipase/hydrolase   | 2.5    | 0.047 | Lipid metabolism                       |
| <b>DISEASE &amp; STRESS RESPONSE (7)</b>                       |   |        |       |  |
| P00931   | (Benzo)quinone oxidoreductase   | 2.8    | 0.015 | ROS response                           |
| P02086   | Aldo/keto reductase   | 2.1    | 0.004 | Oxidoreductase                         |
| P03401   | Alcohol dehydrogenase class III   | 2.2    | 0.015 | Alcohol dehydrogenase                  |
| P01432 (30DAP)   | Thioredoxin   | 4.4    | 0.004 | Redox regulation                       |
| P00051   | Methionine sulfoxide reductase A  | 3.0    | 0.025 | Oxidoreductase                         |
| P01347   | Pyridoxal biosynthesis protein PDX1   | 2.1    | 0.047 | Photoprotection                        |
| P02655 (25DAP)   | Dehydration-responsive protein RD22   | 2.3    | 0.049 | Drought response                       |
| <b>SIGNALING AND HORMONAL FUNCTIONS (10)</b>                   |   |        |       |  |
| P02122 (25,30DAP)  | MYB-112/50 TF, Tuber-specific and sucrose-responsive element binding factor | 3.1    | 0.001 | Transcription factor                   |
| P01965   | Ser/Thr-protein kinase SAPK7, Osmotic stress/ABA-activated protein kinase 7 | 2.6    | 0.008 | Protein phosphorylation                |
| P02807 (30,35DAP)  | Ca-dependent protein kinase CPK1  | 2.5    | 0.038 | Protein phosphorylation                |
| P00010 (30DAP)   | Receptor-like protein kinase 4 RPK4   | 2.1    | 0.014 | Protein phosphorylation                |
| P01017   | Ser/Thr protein phosphatase   | 2.3    | 0.012 | Protein phosphorylation                |
| P02146   | Protein phosphatase 2A  | 2.1    | 0.004 | Protein phosphorylation                |
| P04716 (25DAP)   | S-adenosyl-L- methionine:jasmonic acid carboxyl methyltransferase           | 2.9    | 0.004 | JA synthesis                           |
| P01789   | Leunig/STYLOSA  | 2.5    | 0.032 | Homeotic functions                     |
| P04005 (30DAP)   | Ent-kaurenoic acid oxidase, CyP450 88A3                                     | 2.4    | 0.050 | GA synthesis                           |
| P01030   | Diacylglycerol kinase   | 2.1    | 0.013 | Lipid signaling                        |
| <b>PHOTOSYNTHESIS (3)</b>                                      |   |        |       |  |
| P01497 (30DAP)   | Ferredoxin-1, plastidial  | 2.0    | 0.003 | Photosynthesis                         |
| P01410 (25DAP)   | PS I reaction center subunit V  | 2.0    | 0.023 | Photosynthesis                         |
| P02149 (25DAP)   | Red chlorophyll catabolite reductase  | 3.1    | 0.007 | Chlorophyll catabolism                 |
| <b>TRANSCRIPTION &amp; TRANSLATION &amp; HISTONES (27)</b>     |   |        |       |  |

|                   |  |     |       |                      |
|-------------------|--|-----|-------|----------------------|
| P01225            | PRP4 pre- mRNA-processing factor 4     | 6.0 | 0.010 | Translation          |
| P01928            | Translation initiation factor IF-3.    | 2.2 | 0.012 | Translation          |
| P01123            | Elongation factor 1-alpha              | 2.0 | 0.038 | Translation          |
| P01558            | Lysyl-tRNA synthetase                  | 3.7 | 0.032 | Translation          |
| P01409            | tRNA (guanine-N(7)-)-methyltransferase | 2.5 | 0.016 | Translation          |
| P00741 (30,35DAP) | Peptidyl-tRNA hydrolase                | 2.3 | 0.005 | Translation          |
| P02316            | Small nuclear ribonucleoprotein        | 3.4 | 0.016 | Ribosomal protein    |
| P02072            | Ribosomal protein 60S acidic           | 3.3 | 0.025 | Ribosomal protein    |
| P02199            | Ribosomal protein L30 (60S)            | 3.2 | 0.018 | Ribosomal protein    |
| P02048            | Ribosomal protein L30 (60S)            | 2.2 | 0.009 | Ribosomal protein    |
| P02139            | Ribosomal protein L23                  | 2.8 | 0.001 | Ribosomal protein    |
| P01096            | Ribosomal protein L24, chloroplast     | 2.3 | 0.013 | Ribosomal protein    |
| P00082            | Ribosomal protein L35, plast.          | 2.1 | 0.014 | Ribosomal protein    |
| P04092            | Ribosomal protein L19                  | 2.0 | 0.002 | Ribosomal protein    |
| P04063            | Histone-lysine N-methyltransferase     | 2.1 | 0.018 | Histone              |
| P01812            | HMG1/Y protein                         | 2.8 | 0.010 | Histone              |
| P01651            | Nucleosome assembly protein            | 2.5 | 0.000 | Chromatin remodeling |
| P02006            | Histone H2A                            | 3.1 | 0.050 | Histone              |
| P02404            | Histone H1                             | 2.9 | 0.034 | Histone              |
| P01296            | Histone H4                             | 2.3 | 0.020 | Histone              |
| P01546            | Histone H2A                            | 2.7 | 0.008 | Histone              |
| P03596            | Histone H2B                            | 2.6 | 0.009 | Histone              |
| P04684            | Histone H2A                            | 2.2 | 0.005 | Histone              |
| P01899            | Histone H2B                            | 2.1 | 0.022 | Histone              |
| P03703            | Histone H2B.                           | 3.0 | 0.011 | Histone              |
| P02138            | Histone H2A                            | 4.9 | 0.033 | Histone              |
| P02173            | Histone H2B1                           | 4.2 | 0.028 | Histone              |

#### Upregulated, no annotation (87)

#### 20 DAP down (72)

| Seq. ID  | Gene Annotation                                       | Factor | P     | Function                               |
|--|---|--------|-------|--|
| <b>PRIMARY &amp; SECONDARY METABOLISM (8)</b>              |   |        |       |  |
| P03795   | Phosphoglycerate mutase                               | 2.3    | 0.043 | Glycolysis                             |
| P05197   | ADP-glucose pyrophosphorylase                         | 5.9    | 0.000 | Starch metabolism                      |
| P04162 (25DAP)   | ADP-glucose pyrophosphorylase                         | 5.1    | 0.001 | Starch metabolism                      |
| P04337   | 6-phosphogluconate dehydrogenase                      | 2.3    | 0.025 | Pentose-P cycle                        |
| P04168   | Chalcone-flavanone isomerase                          | 2.0    | 0.014 | Flavonoid biosynthesis                 |
| P04622   | 3-isopropylmalate dehydratase                         | 7.2    | 0.007 | Branched-chain amino acid biosynthesis |
| P05158 (25DAP)   | Cytochrome P450 (CYP71B2)                             | 3.1    | 0.003 | Broad functions                        |
| P03541   | Cytochrome P450 94A1                                  | 2.3    | 0.048 | Broad functions                        |
| <b>TRANSPORT (7)</b>                                       |   |        |       |  |
| P05196   | Oligopeptide transporter 4 (ATOPT4).                  | 2.1    | 0.002 | Peptide transport                      |
| P01176 (25DAP)   | OEP16.2, amino acid selective channel                 | 2.9    | 0.039 | Plastidial outer membrane protein      |
| P02349   | Plasma membrane H <sup>+</sup> -ATPase                | 5.0    | 0.002 | H <sup>+</sup> transport               |
| P04384   | Tonoplast intrinsic protein alpha (Alpha TIP)         | 2.6    | 0.004 | Vacuolar transport                     |
| P04008   | Vacuolar ATPase subunit H                             | 2.1    | 0.033 | Vacuolar transport                     |
| P00510   | Boron transporter-like protein                        | 3.9    | 0.007 | Metal transport                        |
| P00469 (30DAP)   | Zinc transporter 4, chloroplast                       | 2.9    | 0.018 | Metal transport                        |
| <b>ENDOMEMBRANE TRANSPORT &amp; PROTEIN PROCESSING (5)</b> |   |        |       |  |
| P04129   | Small G-protein ROP3                                  | 2.1    | 0.018 | Vesicle transport                      |
| P05151   | ADP-ribosylation factor GTP binding protein)          | 2.2    | 0.002 | Vesicle transport                      |
| P04986   | Chaperone multifunctional (14-3-3 family)             | 2.0    | 0.001 | Chaperone                              |
| P01559   | Vesicle transport protein /ER/Golgi)                  | 2.3    | 0.011 | Vesicle transport                      |
| P00059 (25,30,35DAP)                                       | Peptidyl-prolyl cis-trans isomerase                   | 2.5    | 0.015 | Protein processing                     |
| P03208   | Legumain  | 2.4    | 0.020 | Storage protein processing             |
| <b>REGULATED PROTEIN DEGRADATION (9)</b>                   |   |        |       |  |
| P02453 (25,30DAP)  | Serine carboxypeptidase 1                             | 3.0    | 0.020 | Proteinase                             |
| P02708 (25,30,35DAP)                                       | Prolyl Oligopeptidase                                 | 2.6    | 0.032 | Proteinase                             |
| P01932 (30,35DAP)  | Ubiquitin-protein ligase/ zinc ion binding            | 2.5    | 0.049 | Ubiquitin mediated protein degradation |
| P01451 (25DAP)   | Cullin 3B   | 2.3    | 0.040 | Ubiquitin mediated protein degradation |
| P02115   | Aspartic protease                                     | 2.1    | 0.048 | Proteinase                             |
| P03124 (25DAP)   | 20S core proteasome subunit alpha 2                   | 2.0    | 0.049 | Ubiquitin mediated protein degradation |
| P03922   | Aminoacylproline aminopeptidase                       | 2.0    | 0.001 | Proteinase                             |
| P02732   | 26S proteasome regulatory subunit                     | 1.9    | 0.003 | Ubiquitin mediated protein degradation |
| P03243 (25,30,35DAP)                                       | Ubiquitin-conjugating enzyme E2                       | 3.0    | 0.007 | Ubiquitin mediated protein degradation |
| <b>CELL PROLIFERATION (5)</b>                              |   |        |       |  |
| P03363 (30DAP)   | Expansin  | 3.3    | 0.003 | Cell expansion                         |
| P05195   | Glucan endo-1,3-beta-glucosidase                      | 2.2    | 0.001 | Cell wall metabolism                   |
| P04715 (25DAP)   | Beta-xylosidase/alpha-L-arabinosidase                 | 2.2    | 0.016 | Cell wall metabolism                   |
| P00443   | Pectinesterase  | 2.7    | 0.033 | Cell wall metabolism                   |
| P05130 (25DAP)   | Tubulin, beta   | 2.6    | 0.008 | Cell proliferation                     |
| <b>STORAGE RELATED (13)</b>                                |   |        |       |  |
| P04998   | Legumin B   | 4.5    | 0.000 | Storage protein                        |
| P04997 (25DAP)   | Legumin B   | 3.8    | 0.003 | Storage protein                        |
| P04448 (25,30DAP)  | Legumin A2  | 3.5    | 0.012 | Storage protein                        |
| P02001 (25DAP)   | Legumin B   | 3.0    | 0.020 | Storage protein                        |
| PCPS13 (35DAP)   | Legumin B   | 2.2    | 0.003 | Storage protein                        |
| P04995   | Legumin K   | 2.0    | 0.004 | Storage protein                        |
| P04441 (25,30DAP)  | Albumin 2   | 23.8   | 0.003 | Storage protein                        |
| P04535 (25DAP)   | Albumin   | 17.7   | 0.001 | Storage protein                        |
| P04532 (25,30DAP)  | Glycinin  | 17.2   | 0.002 | Storage protein                        |
| P00507   | Patatin-like protein                                  | 2.4    | 0.029 | Storage protein                        |
| P04150 (25DAP)   | Oleosin   | 3.9    | 0.000 | Lipid storage                          |
| P04214   | Oleosin   | 2.6    | 0.002 | Lipid storage                          |
| P02768   | Lipoxygenase  | 2.5    | 0.032 | Lipid storage                          |
| <b>DISEASE &amp; STRESS TOLERANCE (8)</b>                  |   |        |       |  |
| P00404 (25DAP)   | Protease inhibitor I3 (Kunitz-type)                   | 3.2    | 0.009 | Disease response                       |
| P04697   | Metallothionein                                       | 2.7    | 0.019 | Detoxification                         |
| P04811 (30DAP)   | Dehydration-responsive protein RD22                   | 3.2    | 0.000 | Drought response                       |
| P04644 (25,30,35DAP)                                       | Disease resistance response protein 206-d             | 8.4    | 0.009 | Disease response                       |
| P04184   | Pathogenesis-related protein PR-1                     | 2.7    | 0.035 | Disease response                       |
| P00761   | Pathogenesis-related protein (MLO-like protein)       | 2.1    | 0.015 | Disease response                       |
| P02520   | Polygalacturonase inhibitor                           | 2.4    | 0.029 | Disease response                       |
| P05133   | Polygalacturonase inhibitor                           | 2.0    | 0.010 | Disease response                       |
| <b>SIGNALING AND HORMONAL FUNCTIONS (10)</b>               |   |        |       |  |
| P02114 (35DAP)   | Two-component response regulator ARR5                 | 10.6   | 0.045 | CK functions                           |
| P03467 (25DAP)   | Indole-3-acetic acid-amido synthetase                 | 5.0    | 0.039 | Auxin degradation                      |
| P00915 (30DAP)   | Protein kinase APK1A, chloroplast                     | 3.2    | 0.040 | Protein phosphorylation                |
| P05015 (25DAP)   | Short-chain dehydrogenase/reductase (tasselseed)      | 2.2    | 0.049 | Broad functions                        |
| PCPS10   | SNF1-related protein kinase regulatory subunit beta-1 | 2.6    | 0.023 | Protein kinase                         |
| P03764   | GSK-3-like protein kinase, Msk4                       | 2.4    | 0.017 | Protein kinase                         |

|   |   |     |       |  |
|---|---|-----|-------|--|
| PCPS04  | Phosphatidylethanolamine-binding protein            | 2.3 | 0.013 | Lipid signaling                        |
| PCPS24 (25DAP)  | UNIFOLIATA  | 2.2 | 0.007 | Development                            |
| P04812  | GRAS family transcription factor / DELLA/ /GAI      | 2.0 | 0.016 | Repressor of GA functions              |
| P04604  | 12-oxophytodienoic acid 10, 11-reductase, OPR1      | 2.4 | 0.000 | JA Biosynthesis                        |
| P04941 (25DAP)  | 26S proteasome regulatory subunit S5A               | 2.5 | 0.001 | Ubiquitin mediated protein degradation |
| <b>PHOTOSYTHESIS (3)</b>                                  |   |     |       |  |
| P04368 (25,30DAP)   | Rubisco   | 3.2 | 0.012 | Photosynthesis                         |
| P05030  | Photosystem II core complex proteins psbY           | 2.5 | 0.036 | Photosynthesis                         |
| P04462 (25,30DAP)   | PS II subunit (22kDa)                               | 2.2 | 0.006 | Photosynthesis                         |
| <b>TRANSCRIPTION &amp; TRANSLATION &amp; HISTONES (4)</b> |   |     |       |  |
| P02752  | Eukaryotic elongation factor 1A                     | 2.5 | 0.013 | Translation                            |
| P01853  | 30S ribosomal protein S9, chloroplast               | 2.3 | 0.001 | Ribosomal protein                      |
| P04315  | Ribosomal protein S27                               | 2.3 | 0.008 | Ribosomal protein                      |
| P04134 (30DAP)  | WD-40 repeat protein MSI1 (Core histone-binding su) | 2.1 | 0.000 | Histone binding protein                |
| <b>Downregulated, no annotation (47)</b>                  |   |     |       |  |

**25 DAP up (273)**

| Seq. ID  | Gene Annotation   | Factor | P     | Function                               |
|--|---|--------|-------|--|
| <b>PRIMARY &amp; SECONDARY METABOLISM &amp; TRANSPORT (41)</b> |   |        |       |  |
| P01278 (20DAP)   | Sucrose synthase  | 10.8   | 0.001 | Sucrose metabolism                     |
| PCPS16   | Sucrose synthase  | 3.0    | 0.003 | Sucrose metabolism                     |
| P03580   | Sucrose synthase  | 2.5    | 0.009 | Sucrose metabolism                     |
| P00908   | Glyceraldehyde-3-phosphate DH (NADP+), chloroplast                          | 3.4    | 0.046 | Glycolysis                             |
| P00460   | Glyceraldehyde-3-phosphate DH (NADP+), chloroplast                          | 2.6    | 0.020 | Glycolysis                             |
| P02370 (30DAP)   | Glucose-6-phosphate isomerase, cytosolic                                    | 2.0    | 0.017 | Glycolysis                             |
| P02459 (30,35DAP)  | Glycerlaldehyde-3-phosphate DH, cytosolic                                   | 2.9    | 0.002 | Glycolysis                             |
| P01595 (20DAP)   | Pyruvate dehydrogenase E1 alpha   | 2.8    | 0.003 | Glycolysis                             |
| P01033   | Pyruvate dehydrogenase E2, dihydrolipoyllysine acetyltransferase            | 2.1    | 0.002 | TCA cycle                              |
| P02802 (20DAP)   | 2-Oxoglutarate dehydrogenase, E1  | 2.3    | 0.006 | TCA cycle                              |
| P01798   | Malate dehydrogenase, plastidial  | 6.2    | 0.007 | CH metabolism                          |
| P01847 (30,35DAP)  | Nudix hydrolase, nucleoside sugar hydratase                                 | 2.3    | 0.008 | Nucleoside sugar catabolism            |
| P01976 (30,35DAP)  | Starch phosphorylase, L chloroplast   | 3.8    | 0.004 | Starch metabolism                      |
| P02064 (30DAP)   | O-acetylserine (Thiol)-lyase (Cys synthase), plastidial (ASTL)              | 7.1    | 0.031 | Cys biosynthesis                       |
| P02204   | Serine acetyltransferase, cytoplasm   | 7.0    | 0.003 | Cys biosynthesis                       |
| P03651   | Serine acetyltransferase, mitochondrial                                     | 2.1    | 0.013 | Cys biosynthesis                       |
| P04298 (30DAP)   | 5'-adenylsulfate reductase 1, chloroplast                                   | 2.1    | 0.009 | Cys biosynthesis                       |
| P00936 (20,30DAP)  | Methionine synthase   | 3.5    | 0.004 | Met biosynthesis                       |
| P04228   | Methionine synthase   | 2.1    | 0.035 | Met biosynthesis                       |
| P02505 (30DAP)   | Ketol-acid reductoisomerase, chloroplast                                    | 3.3    | 0.013 | Leu/Val/Ile biosynthesis               |
| P04292 (30DAP)   | Argininosuccinate synthase, chloroplast                                     | 2.9    | 0.011 | Arg biosynthesis                       |
| P01261 (30DAP)   | Argininosuccinate synthase, chloroplast                                     | 2.3    | 0.022 | Arg biosynthesis                       |
| P00532   | Bifunctional ornithine acetyltransferase/N-acetylglutamate synthase         | 2.0    | 0.048 | Arg biosynthesis                       |
| P01320 (20DAP)   | Acetohydroxy- acid synthase small subunit                                   | 2.7    | 0.049 | Ile, Val biosynthesis                  |
| P02083   | 3-Dehydroquinate synthase   | 2.2    | 0.001 | Aromatic amino acid biosynthesis       |
| P02005   | L-asparaginase  | 2.0    | 0.002 | Amino acid metabolism                  |
| P00938 (30DAP)   | 4-coumaroyl- CoA synthase 3   | 5.6    | 0.018 | Phenylpropanoid metabolism             |
| P04682   | Phenylalanine ammonia-lyase   | 4.9    | 0.018 | Phenylpropanoid metabolism             |
| P02136 (20DAP)   | Putrescine aminopropyltransferase 2, (Spermidine synthase)                  | 2.5    | 0.024 | Polyamine biosynthesis                 |
| P00743   | Copper amine oxidase  | 3.5    | 0.028 | Oxidative deamination of polyamines    |
| P02413   | O-diphenol-O-methyl transferase   | 2.3    | 0.016 | Methyltransferase                      |
| P02713 (35DAP)   | NADH-ubiquinone oxidoreductase, complex 1 75 kDa                            | 2.3    | 0.029 | NADH oxidation                         |
| P01416 (30,35DAP)  | Adenylate kinase (ATP- AMP transphosphorylase), chloroplast                 | 2.0    | 0.014 | Nucleotide metabolism                  |
| P01076 (35DAP)   | FA/sphingolipid desaturase  | 3.4    | 0.023 | FA metabolism                          |
| P01721   | Long-chain-fatty-acid-CoA ligase 3  | 3.2    | 0.008 | FA metabolism                          |
| P02795   | Oleoyl-acyl carrier protein thioesterase, chloroplast                       | 5.5    | 0.006 | FA metabolism                          |
| P01020   | Omega-6 fatty acid desaturase, chloroplast                                  | 2.0    | 0.035 | FA metabolism                          |
| P04316 (20DAP)   | Reversibly glycosylated polypeptide-2                                       | 9.8    | 0.047 | Cell wall metabolism                   |
| P02042   | Reversibly glycosylatable polypeptide (Amylogenin)                          | 4.9    | 0.044 | Cell wall metabolism                   |
| P02328 (30DAP)   | Reversibly glycosylatable polypeptide 1                                     | 2.5    | 0.023 | Cell wall metabolism                   |
| P01258   | Beta-D-glucosidase  | 2.7    | 0.050 | Cell wall metabolism                   |
| <b>TRANSPORT (10)</b>  |   |        |       |  |
| P00784 (30,35DAP)  | Peptide transporter PTR2  | 8.3    | 0.010 | Peptide transport                      |
| P01453   | F1F0 ATP synthase, delta chain, chloroplast                                 | 7.9    | 0.021 | ATP synthesis                          |
| P02609   | F1F0 ATP synthase, delta chain, chloroplast                                 | 2.5    | 0.031 | ATP synthesis                          |
| P04485 (30,35DAP)  | F1F0-ATP synthase, delta chain, mitochondrial                               | 10.0   | 0.005 | ATP synthesis                          |
| P04234   | F1F0 ATP synthase, gamma chain, mitochondrial                               | 2.1    | 0.044 | ATP synthesis                          |
| P03984   | F1F0 ATP synthase, beta chain, mitochondrial                                | 2.0    | 0.000 | ATP synthesis                          |
| P01149   | H+-transporting ATPase, plasma membrane                                     | 5.3    | 0.017 | ATP synthesis                          |
| P02092 (30DAP)   | P-type H+-ATPase, plasma membrane   | 2.2    | 0.033 | H+ transport                           |
| P01923 (20DAP)   | ATP/ADP-transporter, chloroplast  | 3.5    | 0.020 | ADP/ATP transport                      |
| P02225 (30,35DAP)  | Uncoupling protein, mitochondrial   | 4.1    | 0.003 | Respiratory control                    |
| <b>ENDOMEMBRANE TRANSPORT &amp; PROTEIN PROCESSING (25)</b>    |   |        |       |  |
| P00689 (30,35DAP)  | Coatomer subunit gamma  | 19.7   | 0.007 | Vesicle trafficking                    |
| P04006   | Vacuolar protein-sorting protein VPS29                                      | 3.4    | 0.010 | Vesicle trafficking                    |
| P01402   | sec23/sec24 transport family protein  | 2.8    | 0.033 | Vesicle trafficking                    |
| P01573 (30,35DAP)  | Signal peptide peptidase  | 2.3    | 0.001 | Vesicle trafficking                    |
| P01828   | GTP-binding protein   | 2.2    | 0.042 | Vesicle trafficking                    |
| P01677 (30DAP)   | GTP-binding protein ras1  | 13.3   | 0.031 | Vesicle trafficking                    |
| P00781   | ER lumen protein retaining receptor   | 17.9   | 0.003 | Vesicle trafficking                    |
| P00166 (20,30DAP)  | Chaperone PHSP1,mitochondrial   | 3.9    | 0.030 | Chaperone                              |
| P01809   | Chaperone DnaJ  | 2.5    | 0.035 | Chaperone                              |
| P04537   | Chaperonin Cpn60/TCP-1  | 2.0    | 0.007 | Chaperone                              |
| P02333   | Chaperonin 10, chloroplast  | 2.0    | 0.024 | Chaperone                              |
| P02026   | Chaperonin 20kDa, chloroplast   | 2.4    | 0.011 | Chaperone                              |
| P02607   | Chaperonin 60 alpha, chloroplast  | 11.4   | 0.014 | Chaperone                              |
| P03657 (30,35DAP)  | Chaperone (copper)  | 8.6    | 0.015 | Chaperone                              |
| P02763 (20,30DAP)  | Chaperone multifunctional (14-3-3 family)                                   | 2.2    | 0.007 | Chaperone                              |
| P00619   | Heat shock protein Hsp90  | 3.9    | 0.013 | Chaperone                              |
| P01143 (20DAP)   | Heat shock protein DnaJ   | 3.7    | 0.040 | Chaperone                              |
| P02110   | Heat shock protein 17K  | 2.1    | 0.015 | Chaperone                              |
| P04523 (30DAP)   | Calreticulin  | 4.5    | 0.011 | Ca-binding chaperone (ER)              |
| P02258 (30,35DAP)  | Calreticulin  | 14.5   | 0.005 | Ca-binding chaperone(ER)               |
| P04206   | Calnexin  | 3.5    | 0.050 | Ca-binding chaperone(ER)               |
| P02117 (20DAP)   | Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit STT3B | 6.0    | 0.000 | Protein processing                     |
| P04457   | Dolichyl-diphosphooligosaccharide-protein glycosyltransferase               | 3.2    | 0.030 | Protein processing                     |
| P04656   | Disulfide-isomerase   | 3.6    | 0.019 | Protein processing                     |
| P04217 (30DAP)   | Disulfide-isomerase   | 3.4    | 0.001 | Protein processing                     |
| <b>REGULATED PROTEIN DEGRADATION (15)</b>                      |   |        |       |  |
| P02435 (20,30DAP)  | Ubiquitin   | 2.1    | 0.008 | Ubiquitin mediated protein degradation |
| P03243   | Ubiquitin-conjugating enzyme E2   | 3.4    | 0.006 | Ubiquitin mediated protein degradation |
| P00690 (35DAP)   | Ubiquitin-protein ligase E3   | 2.6    | 0.001 | Ubiquitin mediated protein degradation |
| P03124   | 20S core proteasome subunit alpha 2   | 2.8    | 0.025 | Ubiquitin mediated protein degradation |
| P02732   | 26S proteasome regulatory particle non-ATPase subunit                       | 2.4    | 0.014 | Ubiquitin mediated protein degradation |
| P01451   | Cullin 3B   | 5.1    | 0.022 | Ubiquitin mediated protein degradation |
| P01009   | Suppressor of G2 allele of SKP1   | 3.3    | 0.002 | Ubiquitin mediated protein degradation |
| P01877   | Suppressor of G2 allele of SKP1   | 2.5    | 0.028 | Ubiquitin mediated protein degradation |
| P01006 (20,30DAP)  | N-acyl-L-amino-acid amidohydrolase  | 2.9    | 0.001 | Peptidase                              |
| P02234 (20,30DAP)  | Leucine aminopeptidase  | 35.3   | 0.018 | Proteinase                             |

|   |   |      |       |                             |
|---|---|------|-------|-----------------------------|
| P02453 (20,30DAP)   | Serine carboxipeptidase 1   | 4.1  | 0.025 | Proteinase                  |
| P04496 (30DAP)  | Cysteine proteinase 15A (Turgor-responsive protein 15A)                     | 3.5  | 0.018 | Proteinase                  |
| P02043 (20DAP)  | Oligopeptidase A  | 2.8  | 0.021 | Proteinase                  |
| P01338 (30DAP)  | Mitochondrial-processing peptidase  | 2.3  | 0.047 | Proteinase                  |
| P02708  | Prolyl endopeptidase  | 2.0  | 0.036 | Proteinase                  |
| <b>CELL PROLIFERATION (11)</b>                              |   |      |       |                             |
| P03116  | Annexin   | 6.2  | 0.001 | Cell proliferation          |
| P04306 (30DAP)  | Annexin   | 4.1  | 0.002 | Cell proliferation          |
| P00079 (20DAP)  | Annexin   | 2.0  | 0.006 | Cell proliferation          |
| P01280  | Annexin   | 2.5  | 0.027 | Cell proliferation          |
| P00178 (30,35DAP)   | Annexin   | 2.3  | 0.016 | Cell proliferation          |
| P02637  | Tubulin beta-1  | 2.7  | 0.022 | Cell proliferation          |
| P00033 (20,35DAP)   | Tubulin beta-1  | 2.7  | 0.011 | Cell proliferation          |
| P04322 (30DAP)  | Tubulin beta  | 2.0  | 0.017 | Cell proliferation          |
| P04421 (20DAP)  | Actin   | 4.5  | 0.023 | Cell proliferation          |
| P02077  | Ca(2+)-regulated actin-binding protein                                      | 2.3  | 0.005 | Cell proliferation          |
| P04096  | AAA-type ATPase / Cell division control protein                             | 2.0  | 0.013 | Cell proliferation          |
| <b>STORAGE RELATED (6)</b>                                  |   |      |       |                             |
| P04038 (30,35DAP)   | Vicilin A   | 4.4  | 0.005 | Storage protein             |
| P02195 (20,30DAP)   | Vicilin   | 3.9  | 0.004 | Storage protein             |
| P00430  | Albumin 1   | 3.5  | 0.007 | Storage protein             |
| P00940 (20,35DAP)   | USP   | 2.0  | 0.041 | Storage protein             |
| P03007  | GDSL-motif lipase/hydrolase   | 6.4  | 0.039 | Oil body degradation        |
| P02120 (20,30DAP)   | GDSL-motif lipase/hydrolase   | 3.8  | 0.008 | Oil body degradation        |
| <b>DISEASE &amp; STRESS TOLERANCE (20)</b>                  |   |      |       |                             |
| P03234 (20DAP)  | Alcohol dehydrogenase class III   | 6.1  | 0.013 | Alcohol dehydrogenase       |
| P02489 (30,35DAP)   | Alcohol dehydrogenase   | 4.7  | 0.001 | Alcohol dehydrogenase       |
| P03051 (30,35DAP)   | Alcohol dehydrogenase   | 3.9  | 0.001 | Alcohol dehydrogenase       |
| P03230 (30DAP)  | Alcohol dehydrogenase   | 3.8  | 0.001 | Alcohol dehydrogenase       |
| P02861 (30DAP)  | Alcohol dehydrogenase   | 2.1  | 0.013 | Alcohol dehydrogenase       |
| P02104  | Alcohol dehydrogenase   | 2.1  | 0.006 | Alcohol dehydrogenase       |
| P00931  | (Benzo)quinone oxidoreductase   | 2.1  | 0.017 | ROS response                |
| P04797  | Superoxide dismutase  | 13.2 | 0.018 | Detoxification              |
| P01659  | Glutathione reductase (NADH)  | 8.8  | 0.005 | Detoxification              |
| P02406  | Glutathione S-transferase   | 2.0  | 0.008 | Detoxification              |
| P03755 (30,35DAP)   | Phospholipid hydroperoxide glutathione peroxidase                           | 4.2  | 0.008 | Detoxification              |
| P03812  | Peroxioredoxin Q  | 2.1  | 0.031 | Detoxification              |
| P04171 (30,35DAP)   | Metallothionein-like protein 1 (MT-1)                                       | 2.1  | 0.006 | Detoxification              |
| P00886  | Dehydration-responsive protein RD22   | 2.2  | 0.009 | Drought response            |
| P02655 (20DAP)  | Dehydration-responsive protein RD22   | 2.0  | 0.043 | Drought response            |
| P04232  | LEA protein   | 2.0  | 0.003 | Drought response            |
| P02378  | LEA protein   | 5.4  | 0.049 | Drought response            |
| P00798  | Pathogenesis-related protein STH-21   | 7.6  | 0.015 | Defense                     |
| P04050  | Wound-inducible basic protein   | 6.6  | 0.044 | Defense                     |
| P02161  | Class IV chitinase  | 4.0  | 0.001 | Defense                     |
| P01206 (30,35DAP)   | Syntaxin-132 (AtSYP132)   | 2.5  | 0.004 | Vesicle trafficking         |
| <b>SIGNALING &amp; Hormone functions (20)</b>               |   |      |       |                             |
| P02122 (20,30DAP)   | MYB-112/50 TF, Tuber-specific and sucrose-responsive element binding factor | 2.6  | 0.003 | Transcription factor        |
| P01965  | Ser/Thr-protein kinase SAPK7, Osmotic stress/ABA-activated protein kinase 7 | 3.9  | 0.035 | Protein phosphorylation     |
| P00558  | Phosphatidylinositol 3-kinase   | 3.5  | 0.001 | Inositol metabolism         |
| P01051  | Defender against cell death 1 (DAD-1)                                       | 3.3  | 0.039 | Defender against cell death |
| P04412  | Phosphatidylethanolamine binding protein FT / TF1                           | 3.0  | 0.009 | Signaling                   |
| P01377  | Leucine-rich repeat receptor protein kinase EXS                             | 2.6  | 0.009 | Protein phosphorylation     |
| P01224  | Receptor protein kinase TMK1  | 2.4  | 0.019 | Protein phosphorylation     |
| P00642  | Protein kinase  | 2.2  | 0.007 | Protein phosphorylation     |
| P02753  | Protein-Tyrosine-phosphatase  | 2.1  | 0.024 | Protein phosphorylation     |
| P01656 (30DAP)  | Auxin-responsive protein IAA8   | 7.1  | 0.001 | Auxin function repression   |
| P04475  | Gibberellin regulated protein (GAST1)                                       | 2.3  | 0.011 | GA functions                |
| P04716 (20DAP)  | S-adenosyl-L- methionine:jasmonic acid carboxyl methyltransferase           | 2.9  | 0.013 | JA synthesis                |
| P00392  | Allene oxide cyclase 4, chloroplast   | 2.0  | 0.012 | JA synthesis                |
| P04233 (30,35DAP)   | 12-oxophytodienoic acid 10, 11-reductase, OPR2                              | 2.0  | 0.007 | JA biosynthesis             |
| P01268 (20,35DAP)   | EMB2737 (EMBRYO DEFECTIVE 2737)   | 2.3  | 0.016 | Embryogenesis               |
| P01782  | Ethylene-induced calmodulin-binding protein, transcriptional activator      | 2.1  | 0.039 | Ca-signaling                |
| P02191  | Calmodulin 7  | 2.2  | 0.021 | Ca-signaling                |
| P02259 (30,35DAP)   | Homeobox protein  | 4.7  | 0.012 | Homeotic functions          |
| P01367 (20DAP)  | Argonaute 1   | 4.8  | 0.029 | Homeotic functions          |
| P02862  | Argonaute 1   | 2.5  | 0.024 | Homeotic functions          |
| <b>PHOTOSYNTHESIS (9)</b>                                   |   |      |       |                             |
| P00436  | PS I assembly protein   | 2.4  | 0.023 | Photosynthesis              |
| P01196  | PS I assembly protein   | 2.1  | 0.010 | Photosynthesis              |
| P01410 (20DAP)  | PS I reaction center subunit V  | 2.1  | 0.038 | Photosynthesis              |
| P00009 (30DAP)  | PS II D1, reaction center   | 3.1  | 0.000 | Photosynthesis              |
| P01038 (30DAP)  | PS II reaction center protein I (PSII-I)                                    | 4.9  | 0.044 | Photosynthesis              |
| P02826  | PS II oxygen-evolving complex protein 1                                     | 2.1  | 0.001 | Photosynthesis              |
| P02155  | Phytol kinase 1, chloroplast  | 22.7 | 0.001 | Chlorophyll degradation     |
| P02149 (20DAP)  | Red chlorophyll catabolite reductase, chloroplast                           | 2.9  | 0.023 | Chlorophyll degradation     |
| P00854 (30DAP)  | CAB-8   | 2.2  | 0.002 | Chlorophyll binding protein |
| <b>TRANSCRIPTION &amp; TRANSLATION &amp; HISTONES (116)</b> |   |      |       |                             |
| P00844  | Elongation factor EF-2  | 6.2  | 0.001 | Translation                 |
| P01177  | Elongation factor 1-alpha (EF-1-alpha)                                      | 2.3  | 0.001 | Translation                 |
| P02494  | Translation initiation factor 3g  | 6.0  | 0.007 | Translation                 |
| P01643  | Translation initiation factor (eIF-3 zeta)                                  | 7.6  | 0.000 | Translation                 |
| P03971  | Translation initiation factor 5A-2  | 2.2  | 0.041 | Translation                 |
| P01474  | Elongation factor 1-alpha (EF-1-alpha)                                      | 3.3  | 0.000 | Translation                 |
| P02752  | Elongation factor 1A  | 2.4  | 0.007 | Translation                 |
| P01147 (35DAP)  | Transducin family protein / WD-40 repeat                                    | 2.3  | 0.004 | Pre-mRNA splicing           |
| P00528  | RNA polymerase beta subunit   | 3.6  | 0.015 | Transcription               |
| P00457 (30DAP)  | DNA-directed RNA polymerase   | 2.0  | 0.017 | Transcription               |
| P01638  | DEAD-box ATP-dependent RNA helicase   | 2.4  | 0.032 | Transcription               |
| P00629  | DEAD box RNA helicase   | 2.3  | 0.007 | Transcription               |
| P03994  | Glutamyl-tRNA(Gln) amidotransferase   | 4.0  | 0.001 | Translation                 |
| P02221 (30DAP)  | WD repeat protein pop3  | 2.0  | 0.013 | mRNA processing             |
| P02953  | 40S ribosomal protein S17   | 4.7  | 0.002 | Ribosomal protein           |

|                |                                      |       |       |                   |
|----------------|--------------------------------------|-------|-------|-------------------|
| P01384         | Ribosomal protein L28                | 121.9 | 0.000 | Ribosomal protein |
| P01380         | 40S ribosomal protein S25            | 26.3  | 0.010 | Ribosomal protein |
| P01182         | Ribosomal protein L27                | 21.7  | 0.009 | Ribosomal protein |
| P01994         | Ribosomal protein S10, plastid.      | 20.7  | 0.003 | Ribosomal protein |
| P02048         | 60S RIBOSOMAL PROTEIN                | 8.9   | 0.001 | Ribosomal protein |
| P01362         | 60S ribosomal protein L12            | 7.4   | 0.006 | Ribosomal protein |
| P02342         | Ribosomal protein L8, cytosolic      | 6.8   | 0.012 | Ribosomal protein |
| P01388         | Ribosomal protein L36                | 6.3   | 0.028 | Ribosomal protein |
| P00006         | 60S ribosomal protein L38            | 5.7   | 0.007 | Ribosomal protein |
| P04732         | 40S ribosomal protein S4             | 4.9   | 0.047 | Ribosomal protein |
| P04411         | 40S ribosomal protein S19-3          | 4.3   | 0.021 | Ribosomal protein |
| P02097         | 60S ribosomal protein L21            | 4.2   | 0.003 | Ribosomal protein |
| P04287         | 60S ribosomal protein L5             | 4.1   | 0.001 | Ribosomal protein |
| P02076         | 60S ribosomal protein                | 4.0   | 0.049 | Ribosomal protein |
| P04372         | 40S ribosomal protein                | 3.7   | 0.050 | Ribosomal protein |
| P02286         | 40S ribosomal protein S24            | 3.6   | 0.010 | Ribosomal protein |
| P04958         | Acidic ribosomal protein P0          | 3.6   | 0.020 | Ribosomal protein |
| P02854         | Pyruvate dehydrogenase complex E3    | 3.5   | 0.001 | Ribosomal protein |
| P01485         | Ribosomal protein 27a                | 3.4   | 0.005 | Ribosomal protein |
| P03529         | 40S ribosomal protein S7             | 3.4   | 0.001 | Ribosomal protein |
| P04044         | 60S ribosomal protein L6_1,00E-87... | 3.3   | 0.005 | Ribosomal protein |
| P02275         | Ribosomal protein S25                | 3.1   | 0.018 | Ribosomal protein |
| P01317         | 40S ribosomal protein S16            | 2.9   | 0.006 | Ribosomal protein |
| P02780         | Ribosomal protein L33                | 2.9   | 0.006 | Ribosomal protein |
| P04304         | 40S ribosomal protein                | 2.8   | 0.004 | Ribosomal protein |
| P03475         | 40S ribosomal protein S30            | 2.8   | 0.014 | Ribosomal protein |
| P03094         | Ribosomal protein L28                | 2.7   | 0.041 | Ribosomal protein |
| P04290         | 60S ribosomal protein L21            | 2.7   | 0.004 | Ribosomal protein |
| P02984         | 60S ribosomal protein                | 2.7   | 0.005 | Ribosomal protein |
| P04542         | Ribosomal protein L18a               | 2.6   | 0.019 | Ribosomal protein |
| P02959         | 60S ribosomal protein L19            | 2.6   | 0.007 | Ribosomal protein |
| P05074         | Acidic ribosomal protein P0          | 2.6   | 0.002 | Ribosomal protein |
| P01797         | 60S ribosomal protein L21            | 2.5   | 0.014 | Ribosomal protein |
| P04219         | 40S ribosomal protein S10            | 2.5   | 0.019 | Ribosomal protein |
| P02139         | Ribosomal protein L23                | 2.5   | 0.032 | Ribosomal protein |
| P01752         | 60S ribosomal protein L15            | 2.4   | 0.012 | Ribosomal protein |
| P04399         | Ribosomal protein L9                 | 2.4   | 0.002 | Ribosomal protein |
| P04243         | 60S ribosomal protein L24            | 2.4   | 0.037 | Ribosomal protein |
| P04553         | Ribosomal protein S3a                | 2.4   | 0.004 | Ribosomal protein |
| P04495         | 60S ribosomal protein L13a           | 2.3   | 0.039 | Ribosomal protein |
| P03749         | 40S ribosomal protein S6             | 2.3   | 0.041 | Ribosomal protein |
| P02072         | 60S acidic ribosomal protein P1      | 2.2   | 0.005 | Ribosomal protein |
| P04216         | 60S ribosomal protein L10A           | 2.2   | 0.024 | Ribosomal protein |
| P04901         | Ribosomal protein S3a                | 2.2   | 0.013 | Ribosomal protein |
| P02326         | 60S ribosomal protein L7             | 2.2   | 0.017 | Ribosomal protein |
| P04476         | 40S ribosomal protein S6             | 2.2   | 0.001 | Ribosomal protein |
| P01202         | 40S ribosomal protein S30            | 2.1   | 0.000 | Ribosomal protein |
| P01035         | S28 ribosomal protein                | 2.1   | 0.028 | Ribosomal protein |
| P04204         | Ribosomal protein L9, cytosolic      | 2.1   | 0.004 | Ribosomal protein |
| P04103         | 60S RIBOSOMAL PROTEIN L36            | 2.1   | 0.020 | Ribosomal protein |
| P03107         | Ribosomal protein GL41               | 2.0   | 0.024 | Ribosomal protein |
| P04702         | Ribosomal protein L27                | 2.0   | 0.042 | Ribosomal protein |
| P00262         | 40S ribosomal protein SA             | 2.0   | 0.048 | Ribosomal protein |
| P04391         | 40S ribosomal protein SA             | 2.0   | 0.004 | Ribosomal protein |
| P01594         | Nuclear ribonucleoprotein            | 2.2   | 0.006 | Ribosomal protein |
| P04279         | Small nuclear ribonucleoprotein      | 4.0   | 0.026 | Ribosomal protein |
| P01473         | Small nuclear ribonucleoprotein U2B  | 2.2   | 0.003 | Ribosomal protein |
| P02078         | Ribonucleoprotein                    | 2.1   | 0.004 | Ribosomal protein |
| P01325 (30DAP) | Poly A binding protein               | 26.6  | 0.030 | mRNA processing   |
| P01839         | RNA-binding protein                  | 2.0   | 0.022 | mRNA processing   |
| P01229         | Histone deacetylase                  | 2.2   | 0.018 | Histone           |
| P01501         | Histone H4                           | 12.7  | 0.036 | Histone           |
| P01983         | Histone H3                           | 12.1  | 0.002 | Histone           |
| P01207         | Histone H4                           | 14.2  | 0.002 | Histone           |
| P01246         | Histone H4                           | 13.7  | 0.003 | Histone           |
| P01909         | Histone H2B1                         | 10.0  | 0.022 | Histone           |
| P01476         | Histone H4                           | 10.0  | 0.000 | Histone           |
| P01951         | Histone H4                           | 9.7   | 0.018 | Histone           |
| P02173         | Histone H2B1                         | 8.6   | 0.001 | Histone           |
| P02006         | Histone H2A                          | 8.3   | 0.031 | Histone           |
| P01955         | Histone H4                           | 7.2   | 0.001 | Histone           |
| P01115         | Histone H4                           | 6.8   | 0.001 | Histone           |
| P01127         | Histone H4                           | 6.1   | 0.049 | Histone           |
| P04482         | Histone H4                           | 5.1   | 0.001 | Histone           |
| P01927         | Histone H3                           | 4.5   | 0.048 | Histone           |
| P02404         | Histone H1                           | 4.4   | 0.020 | Histone           |
| P03703         | Histone H2B                          | 4.0   | 0.001 | Histone           |
| P02532         | Histone H4                           | 4.0   | 0.001 | Histone           |
| P04195         | Histone H3                           | 3.8   | 0.042 | Histone           |
| P04068         | Histone H2B                          | 3.8   | 0.039 | Histone           |
| P04869         | Histone H2B1                         | 3.6   | 0.035 | Histone           |
| P04684         | Histone H2A                          | 3.5   | 0.005 | Histone           |
| P04858         | Histone H2B1                         | 3.0   | 0.002 | Histone           |
| P00999         | Histone H2B                          | 2.9   | 0.001 | Histone           |
| P03596         | Histone H2B                          | 2.8   | 0.021 | Histone           |
| P01222         | Histone H3                           | 2.5   | 0.013 | Histone           |
| P00150         | Histone H3                           | 2.7   | 0.002 | Histone           |
| P04335         | Histone H4                           | 2.6   | 0.025 | Histone           |
| P04375         | Histone H1B                          | 2.6   | 0.002 | Histone           |
| P02616         | Histone H3                           | 2.4   | 0.001 | Histone           |
| P02318         | Histone H1                           | 2.4   | 0.040 | Histone           |
| P04748         | Histone H3                           | 2.3   | 0.047 | Histone           |
| P02323         | Histone H1                           | 2.3   | 0.028 | Histone           |

|        |              |     |       |         |
|--------|--------------|-----|-------|---------|
| P02138 | Histone H2A  | 2.2 | 0.026 | Histone |
| P04383 | Histone H3   | 2.1 | 0.002 | Histone |
| P01318 | Histone H3   | 2.1 | 0.005 | Histone |
| P03987 | Histone H2A  | 2.1 | 0.000 | Histone |
| P01368 | Histone H2B1 | 2.0 | 0.032 | Histone |
| P04426 | Histone H2B  | 2.1 | 0.008 | Histone |
| P04584 | Histone H4   | 2.1 | 0.005 | Histone |
| P03343 | Histone H2A  | 2.1 | 0.003 | Histone |

#### Upregulated, no annotation (122)

#### 25 DAP down (102)

| Seq. ID  | Gene Annotation                                      | Factor | P     | Function                        |
|--|--|--------|-------|---------------------------------|
| <b>PRIMARY &amp; SECONDARY METABOLISM (26)</b> |  |        |       |                                 |
| PCPS17 (35DAP)                                 | Sucrose synthase isoform 3                           | 2.5    | 0.012 | Sucrose metabolism              |
| PCPS21   | Vacuolar acid invertase Psl-1                        | 2.2    | 0.012 | Sucrose metabolism              |
| P05180   | Neutral invertase                                    | 2.8    | 0.034 | Sucrose metabolism              |
| P03795   | Phosphoglycerate mutase, cytosol                     | 2.2    | 0.013 | Glycolysis                      |
| P03767 (30DAP)                                 | Pyruvate kinase, chloroplast                         | 2.0    | 0.010 | Glycolysis                      |
| P04337   | 6-phosphogluconate dehydrogenase, plastid            | 2.1    | 0.002 | Pentose-P cycle                 |
| P04162 (20DAP)                                 | ADP-glucose pyrophosphorylase, small su              | 6.0    | 0.032 | Starch metabolism               |
| P05197   | ADP-glucose pyrophosphorylase, small su              | 4.8    | 0.001 | Starch metabolism               |
| P00655   | ADP-glucose pyrophosphorylase, small su              | 2.1    | 0.011 | Starch metabolism               |
| PCPS09   | ADP-glucose pyrophosphorylase, large su              | 2.0    | 0.004 | Starch metabolism               |
| P04791   | Beta-amylase, plastidial                             | 2.0    | 0.014 | Starch metabolism               |
| P00615   | UDP-glucose 4-epimerase                              | 2.0    | 0.004 | UDP-Glc/UDP-Gal interconversion |
| P00535   | UDP-glucose 4-epimerase                              | 2.8    | 0.036 | UDP-Glc/UDP-Gal interconversion |
| P04822 (30DAP)                                 | Galactinol synthase                                  | 4.7    | 0.002 | Raffinose sugar metabolism      |
| P01058 (30,35DAP)                              | Adenosine deaminase                                  | 2.5    | 0.023 | Purine metabolism               |
| P04879 (35DAP)                                 | S-adenosylmethionine synthetase                      | 2.2    | 0.004 | Methylation cycle               |
| P03766 (30DAP)                                 | S-adenosylmethionine decarboxylase                   | 2.1    | 0.010 | Methylation cycle               |
| P04479   | Iron/ascorbate family oxidoreductases, cytosol       | 2.2    | 0.023 | Oxidoreductase                  |
| P03631 (30,35DAP)                              | UDP-glucuronosyl/UDP-glucosyltransferase             | 3.2    | 0.016 | CK homeostasis                  |
| P05041   | Isoflavone oxidoreductase                            | 2.2    | 0.031 | Oxidoreductase                  |
| P03951 (30DAP)                                 | Inorganic pyrophosphatase                            | 2.2    | 0.016 | Pyrophosphatase                 |
| P03480 (30DAP)                                 | Cytochrome c oxidase                                 | 2.2    | 0.002 | Oxidase                         |
| P00518 (35DAP)                                 | Glutamine synthetase, GS1, cytosolic                 | 2.1    | 0.014 | Amino acid metabolism           |
| P04838 (35DAP)                                 | Extradiol ring-cleavage dioxygenase                  | 2.1    | 0.029 | Dioxygenase                     |
| P01154 (30DAP)                                 | Phosphatidylinositol-glycan biosynthesis class C, ER | 2.3    | 0.006 | Glycolipid synthesis            |
| P03786 (30,35DAP)                              | Alkaline phytoceramidase                             | 2.6    | 0.006 | FA metabolism                   |

#### TRANSPORT (10)

|                   |  |     |       |                                   |
|-------------------|--|-----|-------|-----------------------------------|
| P01543            | Glucose transporter, plastid               | 2.8 | 0.007 | Plastid sugar transport           |
| P00852 (30DAP)    | OEP16.1, amino acid selective channel      | 5.6 | 0.008 | Plastidial outer membrane protein |
| P01176 (20DAP)    | OEP16.2, amino acid selective channel      | 2.0 | 0.001 | Plastidial outer membrane protein |
| P01612            | Tic32, 3-ketoacyl-CoA synthase, SDR family | 2.5 | 0.022 | Chloroplast translocator          |
| P02762 (30DAP)    | Zinc transporter                           | 2.5 | 0.032 | Metal transport                   |
| P03782 (35DAP)    | K+ channel beta chain                      | 2.5 | 0.008 | K+ transport                      |
| P01893            | Chloride channel protein CLC-d             | 2.4 | 0.010 | CH metabolism                     |
| P03613            | Nitrate/chlorate transporter, related      | 2.1 | 0.008 | Nitrate transport                 |
| P04444 (30DAP)    | Ca-ATPase, IIB (ER)                        | 2.4 | 0.002 | Ca transport                      |
| P04982 (30,35DAP) | Aquaporin, PIP-type 7a, turgor-responsive  | 2.0 | 0.047 | Water transport                   |

#### ENDOMEMBRANE TRANSPORT & PROTEIN PROCESSING (12)

|                   |  |     |       |                            |
|-------------------|--|-----|-------|----------------------------|
| P03208 (20DAP)    | Legumain                                     | 2.4 | 0.020 | Storage protein processing |
| P04764 (30,35DAP) | DnaK-type molecular chaperone HSC71.0        | 2.2 | 0.011 | Chaperone                  |
| P04986            | Chaperone multifunctional (14-3-3 family)    | 2.2 | 0.004 | Chaperone                  |
| P03093            | Coated vesicle membrane protein              | 2.1 | 0.002 | Vesicle trafficking        |
| P02510 (30DAP)    | Alpha-soluble NSF attachment protein         | 2.0 | 0.019 | Vesicle trafficking        |
| P05117            | Signal recognition particle receptor         | 2.1 | 0.007 | Vesicle trafficking        |
| P04914 (30DAP)    | Beta-Ig-H3/fasciclin                         | 2.0 | 0.009 | Vesicle trafficking        |
| P05035 (35DAP)    | Microtubule-associated protein               | 2.9 | 0.001 | Vesicle trafficking        |
| P05151            | ADP-ribosylation factor GTP binding protein) | 2.5 | 0.006 | Vesicle transport          |
| P04309            | ADP-ribosylation factor GTP binding protein) | 2.1 | 0.022 | Vesicle transport          |
| P00059 (30,35DAP) | Peptidyl-prolyl cis-trans isomerase          | 3.0 | 0.003 | Protein processing         |
| P05208 (30DAP)    | Peptidyl-prolyl cis-trans isomerase          | 2.3 | 0.007 | Protein processing         |

#### REGULATED PROTEIN DEGRADATION (12)

|                   |  |     |       |  |
|-------------------|--|-----|-------|--|
| P02453 (20,30DAP) | Serine carboxypeptidase 1                  | 3.0 | 0.020 | Proteinase                             |
| P02708 (30,35DAP) | Prolyl Oligopeptidase                      | 2.6 | 0.032 | Proteinase                             |
| P01932 (30,35DAP) | Ubiquitin-protein ligase/ zinc ion binding | 2.5 | 0.049 | Ubiquitin mediated protein degradation |
| P02115            | Aspartic protease                          | 2.1 | 0.048 | Proteinase                             |
| P03124            | 20S core proteasome subunit alpha 2        | 2.0 | 0.049 | Ubiquitin mediated protein degradation |
| P03922            | Prolyl Oligopeptidase                      | 2.0 | 0.001 | Proteinase                             |
| P02732            | 26S proteasome regulatory subunit          | 1.9 | 0.003 | Ubiquitin mediated protein degradation |
| P01451            | Cullin 3B                                  | 2.3 | 0.040 | Ubiquitin mediated protein degradation |
| P03356 (30DAP)    | Ubiquitin                                  | 2.0 | 0.006 | Ubiquitin mediated protein degradation |
| P04941 (20DAP)    | 26S proteasome regulatory subunit S5A      | 2.1 | 0.008 | Ubiquitin mediated protein degradation |
| P00331            | Subtilisin-like proteinase                 | 2.4 | 0.002 | Proteinase                             |
| P03243 (30,35DAP) | Ubiquitin-conjugating enzyme E2            | 3.0 | 0.007 | Ubiquitin mediated protein degradation |

#### CELL PROLIFERATION (2)

|                |                                       |     |       |                      |
|----------------|---------------------------------------|-----|-------|----------------------|
| P05130 (20DAP) | Beta tubulin                          | 2.1 | 0.013 | Cell proliferation   |
| P04715 (20DAP) | Beta-xylosidase/alpha-L-arabinosidase | 2.1 | 0.011 | Cell wall metabolism |

#### STORAGE RELATED (10)

|                   |                  |      |       |                 |
|-------------------|------------------|------|-------|-----------------|
| P04995            | Legumin K        | 2.7  | 0.001 | Storage protein |
| P04997 (20DAP)    | Legumin B        | 2.0  | 0.001 | Storage protein |
| P02001 (20DAP)    | Legumin B        | 2.1  | 0.009 | Storage protein |
| P04448 (20,30DAP) | Legumin A2       | 2.8  | 0.000 | Storage protein |
| P04535 (20,30DAP) | Albumin          | 6.7  | 0.001 | Storage protein |
| P04441 (20,30DAP) | Albumin 2        | 5.9  | 0.021 | Storage protein |
| P04532 (20,30DAP) | Glycinin subunit | 12.6 | 0.000 | Storage protein |
| P04214            | 15.8 kDa oleosin | 3.4  | 0.038 | Lipid storage   |
| P04150 (20DAP)    | Oleosin          | 2.7  | 0.000 | Lipid storage   |
| P03997            | LEA protein      | 2.6  | 0.001 | LEA protein     |

#### DISEASE & STRESS TOLERANCE (8)

|        |   |     |       |                   |
|--------|---|-----|-------|-------------------|
| P04644 | Disease resistance response protein 206-d | 6.4 | 0.030 | Pathogen response |
|--------|---|-----|-------|-------------------|

|   |  |      |       |                                       |
|---|--|------|-------|---------------------------------------|
| P01681  | Senescence-associated protein (din1)               | 2.2  | 0.002 | Stress response                       |
| P00638 (30,35DAP)   | Trypsin/chymotrypsin inhibitor                     | 4.7  | 0.018 | Pathogen response                     |
| P00404 (20DAP)  | Leguminous Kunitz-type inhibitor                   | 2.2  | 0.010 | Pathogen response                     |
| P00971  | Peroxidase   | 2.4  | 0.013 | Detoxification                        |
| P04867 (35DAP)  | Superoxide dismutase                               | 2.2  | 0.011 | Detoxification                        |
| P04250 (30,35DAP)   | Pathogenesis-related protein 17                    | 2.0  | 0.015 | Pathogen response                     |
| P00685  | Flavin-containing monooxygenase FMO                | 2.5  | 0.004 | Pathogen response                     |
| <b>SIGNALING &amp; HORMONE FUNCTIONS (13)</b>             |  |      |       |                                       |
| P02114 (35DAP)  | Two-component response regulator ARR5              | 10.6 | 0.045 | CK functions                          |
| P05015 (20DAP)  | Short-chain dehydrogenases/reductases (tasselseed) | 2.9  | 0.039 | Short-chain dehydrogenases/reductases |
| P04580  | Short chain dehydrogenase                          | 2.3  | 0.011 | Short-chain dehydrogenases/reductases |
| P05158 (20DAP)  | Cytochrome P450 (CYP71B2)                          | 2.4  | 0.012 | Oxygenase Cyp                         |
| P03467 (20DAP)  | Indole-3-acetic acid-amido synthetase              | 2.0  | 0.014 | Auxin degradation                     |
| P03111  | Serine/Threonine protein kinase                    | 2.7  | 0.003 | Protein kinase                        |
| P05048 (30DAP)  | Phytochrome B                                      | 2.6  | 0.005 | Signaling                             |
| P00932  | Thioredoxin  | 2.3  | 0.037 | Redox regulation                      |
| P03792 (30DAP)  | Thioredoxin h                                      | 2.2  | 0.011 | Redox regulation                      |
| P04464 (20,30DAP)   | Ferredoxin   | 2.2  | 0.019 | Redox regulation                      |
| P04812  | GRAS family transcription factor / DELLA/ /GAI     | 2.2  | 0.005 | Repressor of GA functions             |
| PCPS25  | Stamina pistilloidia                               | 2.2  | 0.003 | Development                           |
| PCPS24 (20DAP)  | UNIFOLIATA protein, TF                             | 2.1  | 0.005 | Development                           |
| <b>PHOTOSYTHESIS (7)</b>                                  |  |      |       |                                       |
| P04559 (35DAP)  | PS II protein PsbX                                 | 2.4  | 0.016 | Photosynthesis                        |
| P00462  | PS II 22K protein                                  | 2.2  | 0.022 | Photosynthesis                        |
| P04462 (20,30DAP)   | PS II subunit (22kDa)                              | 2.1  | 0.005 | Photosynthesis                        |
| P05030  | PS II manganese-binding protein PsbY               | 2.1  | 0.001 | Photosynthesis                        |
| P05083  | Rubisco, small su                                  | 3.1  | 0.003 | Photosynthesis                        |
| P04369  | Rubisco, small su                                  | 2.2  | 0.035 | Photosynthesis                        |
| P04368 (20,30DAP)   | Rubisco, small su                                  | 2.1  | 0.042 | Photosynthesis                        |
| <b>TRANSCRIPTION &amp; TRANSLATION &amp; HISTONES (2)</b> |  |      |       |                                       |
| P05129  | Ribosomal protein L12, chloroplast                 | 2.2  | 0.001 | Ribosomal protein                     |
| P04897  | Histone H2B  | 2.2  | 0.008 | Histone                               |
| <b>Downregulated, no annotation (72)</b>                  |  |      |       |                                       |

| 30 DAP up (201)  |   |        |       |  |
|--|---|--------|-------|--|
| Seq. ID  | Gene Annotation   | Factor | P     | Function                               |
| <b>PRIMARY &amp; SECONDARY METABOLISM &amp; TRANSPORT (39)</b> |   |        |       |  |
| P00898 (20,35DAP)  | Sucrose-phosphate synthase  | 3.2    | 0.012 | Sucrose metabolism                     |
| P02459 (25,35DAP)  | Glyceraldehyde-3-phosphate DH, cytosolic                                  | 4.7    | 0.040 | Glycolysis                             |
| P02370 (25DAP)   | Glucose-6-phosphate isomerase, cytosolic                                  | 2.1    | 0.021 | Glycolysis                             |
| P03836   | Phosphoglucosmutase, chloroplast  | 2.0    | 0.020 | Glycolysis                             |
| P01841 (35DAP)   | Pyruvate dehydrogenase E1, beta subunit                                   | 2.3    | 0.003 | Glycolysis                             |
| P02739   | Pyruvate dehydrogenase E1, beta subunit                                   | 2.0    | 0.010 | Glycolysis                             |
| P01841 (35DAP)   | UDP-glucose pyrophosphorylase   | 2.1    | 0.003 | CH metabolism                          |
| P01521 (20DAP)   | GDP-mannose 3,5-epimerase 2   | 9.3    | 0.034 | CH metabolism                          |
| P04677 (20DAP)   | Invertase/pectin methylesterase inhibitor                                 | 4.9    | 0.008 | CH metabolism                          |
| P03466 (20,35DAP)  | Glycoside hydrolase   | 8.8    | 0.001 | CH metabolism                          |
| P02670 (35DAP)   | Beta3-glucuronyltransferase   | 2.9    | 0.044 | CH metabolism                          |
| P01976 (25,35DAP)  | Starch phosphorylase, L chloroplast                                       | 7.5    | 0.003 | Starch metabolism                      |
| P02446   | Starch debranching enzyme, isoform 2                                      | 3.2    | 0.013 | Starch metabolism                      |
| P04817   | NADP-dependent oxidoreductase P1 (ADH-superfamily)                        | 3.6    | 0.016 | NADH oxidation                         |
| P02915 (20DAP)   | NADH dehydrogenase (ubiquinone), mitochondrial, complex 1 75 kDa          | 2.4    | 0.016 | NADH oxidation                         |
| P02505 (25DAP)   | Ketol-acid reductoisomerase, chloroplast                                  | 4.7    | 0.012 | Leu/Val/Ile biosynthesis               |
| P04292 (25DAP)   | Argininosuccinate synthase, chloroplast                                   | 2.8    | 0.006 | Arg biosynthesis                       |
| P01261 (25DAP)   | Argininosuccinate synthase, chloroplast                                   | 2.7    | 0.008 | Arg biosynthesis                       |
| P04298 (25DAP)   | 5'-adenylylsulfate reductase 1, chloroplast                               | 2.3    | 0.030 | Cys biosynthesis                       |
| P02064 (25DAP)   | O-acetylserine (Thiol)-lyase (Cys synthase), plastid                      | 5.9    | 0.009 | Cys biosynthesis                       |
| P00936 (20,25DAP)  | Methionine synthase   | 2.4    | 0.007 | Met biosynthesis                       |
| P01003   | Methionine synthase   | 2.3    | 0.000 | Met biosynthesis                       |
| P03804   | Phosphoserine phosphatase, chloroplast                                    | 2.1    | 0.021 | Ser biosynthesis                       |
| P01351   | Indole-3-glycerol phosphate synthase, chloroplast                         | 2.0    | 0.023 | Aromatic amino acid biosynthesis       |
| P02005   | L-asparaginase  | 2.1    | 0.042 | Amino acid metabolism                  |
| P02008   | Fumarylacetoacetase   | 2.5    | 0.020 | Phe/Tyr degradation                    |
| P00389   | Flavonol synthase   | 4.5    | 0.039 | Flavonoid biosynthesis                 |
| P04102   | Riboflavin synthase   | 3.6    | 0.016 | Riboflavin biosynthesis                |
| P01821 (35DAP)   | Phytoene synthase (geranylgeranyl-diphosphate geranylgeranyl transferase) | 2.7    | 0.004 | Carotenoid synthesis                   |
| P00938 (25DAP)   | 4-coumaroyl- CoA synthase 3   | 2.7    | 0.042 | Phenylpropanoid metabolism             |
| P01709   | S-adenosylmethionine synthetase   | 12.0   | 0.035 | Methylation cycle                      |
| P01419 (20,35DAP)  | DNA (cytosine-5-)-methyltransferase                                       | 2.8    | 0.033 | Methyltransferase                      |
| P02413   | O-diphenol-O-methyl transferase   | 2.0    | 0.028 | Methyltransferase                      |
| P01416 (25,35DAP)  | Adenylate kinase, (ATP- AMP transphosphorylase) chloroplast               | 2.1    | 0.020 | Nucleotide metabolism                  |
| P01847 (25,35DAP)  | Nudix hydrolase, nucleoside sugar hydratase                               | 2.8    | 0.011 | Nucleoside sugar catabolism            |
| P01648 (35DAP)   | MGDG synthase type A  | 2.6    | 0.022 | FA metabolism                          |
| P01436   | Epoxide hydrolase   | 5.2    | 0.031 | FA metabolism                          |
| P02042   | Reversibly glycosylatable polypeptide                                     | 3.8    | 0.010 | Cell wall metabolism                   |
| P02328 (25DAP)   | Reversibly glycosylatable polypeptide 1                                   | 4.6    | 0.020 | Cell wall metabolism                   |
| <b>TRANSPORT (6)</b>   |   |        |       |  |
| P02071 (20DAP)   | Glc-6-phosphate/phosphate-translocator precursor, plastid                 | 4.4    | 0.034 | Glc-6-P transport                      |
| P00784 (25,35DAP)  | Peptide transporter PTR2  | 7.4    | 0.043 | Peptide transport                      |
| P04485 (25,35DAP)  | ATP synthase delta chain, mitochondrial                                   | 5.1    | 0.015 | ATP synthesis                          |
| P02092 (25DAP)   | P-type H+-ATPase, plasma membrane   | 2.8    | 0.003 | H+ transport                           |
| P00808   | SecA-type chloroplast protein transport factor                            | 3.9    | 0.025 | Chloroplast translocation              |
| P02225 (25,35DAP)  | Uncoupling protein, mitochondrial   | 3.4    | 0.046 | Respiratory control                    |
| <b>ENDOMEMBRANE TRANSPORT &amp; PROTEIN PROCESSING (28)</b>    |   |        |       |  |
| P01677 (25DAP)   | GTP-binding protein ras1  | 35.0   | 0.012 | Vesicle trafficking                    |
| P00676   | G protein beta  | 2.1    | 0.027 | Vesicle trafficking                    |
| P01121   | Rab1  | 3.6    | 0.034 | Vesicle trafficking                    |
| P01988 (35DAP)   | Ras-related protein Rab7D   | 4.1    | 0.008 | Vesicle trafficking                    |
| P00689 (25,35DAP)  | Coatmer subunit gamma   | 10.8   | 0.035 | Vesicle trafficking                    |
| P01526 (35DAP)   | SNF7 protein  | 6.3    | 0.024 | Vesicle trafficking                    |
| P02196   | Clathrin assembly protein AP180   | 6.2    | 0.028 | Vesicle trafficking                    |
| P00386 (20,25DAP)  | Vesicle transport v-SNARE   | 3.4    | 0.005 | Vesicle trafficking                    |
| P02445   | TRF1-interacting ankyrin-related ADP-ribose polymerase                    | 2.1    | 0.011 | Vesicle trafficking                    |
| P03171   | Harpin-induced protein  | 2.8    | 0.020 | Vesicle trafficking                    |
| P02414   | Heat shock protein DnaJ   | 8.9    | 0.030 | Chaperone                              |
| P00619   | Heat shock protein Hsp90  | 2.7    | 0.036 | Chaperone                              |
| P00166 (20,25DAP)  | Chaperone PHSP1, mitochondrial  | 3.1    | 0.018 | Chaperone                              |
| P02333 (20,25,35DAP)   | Chaperonin 10, chloroplast  | 2.0    | 0.010 | Chaperone                              |
| P02055 (35DAP)   | Chaperone HSP20-like  | 2.3    | 0.003 | Chaperone                              |
| P02026   | Chaperonin 20 kDa, chloroplast  | 2.2    | 0.011 | Chaperone                              |
| P03657 (25,35DAP)  | Chaperone (copper)  | 2.3    | 0.004 | Chaperone                              |
| P02763 (20,25DAP)  | Chaperone multifunctional (14-3-3 family)                                 | 2.9    | 0.013 | Chaperone                              |
| P02258 (25,35DAP)  | Calreticulin  | 11.3   | 0.034 | Ca-binding chaperone (ER)              |
| P04523 (25DAP)   | Calreticulin  | 3.1    | 0.024 | Ca-binding chaperone(ER)               |
| P02165 (35DAP)   | Dolichyl-diphosphooligosaccharide-protein glycosyltransferase             | 2.0    | 0.008 | Protein processing                     |
| P02511   | Signal peptide peptidase  | 5.7    | 0.001 | Protein processing                     |
| P01573 (25,35DAP)  | Signal peptide peptidase  | 2.5    | 0.012 | Protein processing                     |
| P01305   | Signal recognition particle receptor beta subunit                         | 2.5    | 0.029 | Protein processing                     |
| P01338 (25DAP)   | Mitochondrial-processing peptidase  | 3.0    | 0.007 | Protein processing                     |
| P04217 (25DAP)   | Protein disulfide-isomerase   | 2.5    | 0.002 | Protein processing                     |
| P01763   | ORMDL protein (protein folding in ER)                                     | 2.8    | 0.007 | Protein processing                     |
| P01279 (35DAP)   | Peptidyl-prolyl cis- trans isomerase                                      | 3.1    | 0.028 | Protein processing                     |
| <b>REGULATED PROTEIN DEGRADATION (12)</b>                      |   |        |       |  |
| P02435 (20,25DAP)  | Ubiquitin   | 2.0    | 0.000 | Ubiquitin mediated protein degradation |
| P02386 (35DAP)   | Ubiquitin fusion degradation protein UFD1                                 | 2.3    | 0.023 | Ubiquitin mediated protein degradation |
| P01932 (20,35DAP)  | Ubiquitin protein ligase  | 2.2    | 0.031 | Ubiquitin mediated protein degradation |
| P03243   | Ubiquitin-conjugating enzyme E2   | 2.0    | 0.012 | Ubiquitin mediated protein degradation |
| P00934   | RING zinc finger protein, Ubiquitin conjugation                           | 16.6   | 0.001 | Ubiquitin mediated protein degradation |
| P02675   | Serine carboxypeptidase   | 76.4   | 0.004 | Proteinase                             |
| P02453 (20,25DAP)  | Serine carboxipeptidase 1   | 2.0    | 0.004 | Proteinase                             |
| P02234 (20,25DAP)  | Leucine aminopeptidase  | 28.0   | 0.003 | Proteinase                             |
| P04496 (25DAP)   | Cysteine proteinase 15A, (Turgor-responsive protein 15A)                  | 2.2    | 0.033 | Proteinase                             |
| P01006 (20,25DAP)  | N-acyl-L-amino-acid amidohydrolase  | 2.1    | 0.000 | Peptidase                              |

|  |   |       |       |                             |
|--|---|-------|-------|-----------------------------|
| P02708 (25,35DAP)  | Prolyl endopeptidase  | 2.1   | 0.003 | Proteinase                  |
| P02142 (20DAP)   | Peptidase/protease (Insulin degrading enzyme)                               | 6.3   | 0.006 | Proteinase                  |
| <b>CELL PROLIFERATION (16)</b>                           |   |       |       |                             |
| P00153   | Cyclin D3   | 3.9   | 0.001 | Cell proliferation          |
| P00657   | Cyclin B  | 2.4   | 0.043 | Cell proliferation          |
| P04306 (25DAP)   | Annexin   | 8.1   | 0.005 | Cell proliferation          |
| P03116   | Annexin   | 5.1   | 0.010 | Cell proliferation          |
| P00178 (25,35DAP)  | Annexin   | 2.7   | 0.000 | Cell proliferation          |
| P02931 (35DAP)   | Annexin   | 2.1   | 0.009 | Cell proliferation          |
| P02837 (35DAP)   | Tubulin alpha   | 2.0   | 0.045 | Cell proliferation          |
| P04322 (25DAP)   | Tubulin beta  | 2.0   | 0.009 | Cell proliferation          |
| P02170   | Tubulin-specific chaperone C  | 4.5   | 0.046 | Cell proliferation          |
| P01817 (35DAP)   | Tubulin-specific chaperone A  | 2.2   | 0.006 | Cell proliferation          |
| P00843 (20DAP)   | Putative cell division control protein 48                                   | 2.8   | 0.005 | Cell proliferation          |
| P01910 (35DAP)   | Prohibitin  | 2.8   | 0.003 | Cell proliferation          |
| P02077   | Ca(2+)-regulated actin-binding protein                                      | 2.5   | 0.027 | Cell proliferation          |
| P02536   | Xyloglucan endotransglycosylase   | 17.4  | 0.013 | Cell wall metabolism        |
| P02774   | Phosphatidylinositol N-acetylglucosaminyltransferase subunit P              | 2.0   | 0.036 | Cell wall metabolism        |
| P04435   | BURP domain-containing protein / polygalacturonase                          | 3.9   | 0.046 | Cell wall metabolism        |
| <b>STORAGE RELATED (8)</b>                               |   |       |       |                             |
| P04038 (25,35DAP)  | Vicilin A   | 10.8  | 0.000 | Storage protein             |
| P04635 (35DAP)   | Vicilin   | 3.8   | 0.000 | Storage protein             |
| P02195 (20,25DAP)  | Vicilin   | 2.2   | 0.006 | Storage protein             |
| P00635 (35DAP)   | USP   | 8.9   | 0.000 | Storage protein             |
| P01844 (20,35DAP)  | USP   | 3.1   | 0.027 | Storage protein             |
| P01146 (35DAP)   | USP   | 2.0   | 0.004 | Storage protein             |
| P01245 (20DAP)   | Ferritin 3  | 2.0   | 0.011 | Ferritin                    |
| P02120 (20,25DAP)  | GDSL-motif lipase/hydrolase   | 3.0   | 0.022 | Oil body degradation        |
| <b>DISEASE &amp; STRESS TOLERANCE (17)</b>               |   |       |       |                             |
| P03051 (25,35DAP)  | Alcohol dehydrogenase   | 3.3   | 0.004 | Alcohol dehydrogenase       |
| P02489 (25,35DAP)  | Alcohol dehydrogenase   | 2.8   | 0.002 | Alcohol dehydrogenase       |
| P03230 (25DAP)   | Alcohol dehydrogenase   | 3.0   | 0.011 | Alcohol dehydrogenase       |
| P02861 (25DAP)   | Alcohol dehydrogenase   | 2.0   | 0.001 | Alcohol dehydrogenase       |
| P04420   | Formate dehydrogenase 1, mitochondrial                                      | 2.1   | 0.017 | Formate dehydrogenase       |
| P00931   | (Benzo)quinone oxidoreductase   | 2.2   | 0.025 | ROS response                |
| P01432 (20DAP)   | Thioredoxin   | 35.5  | 0.000 | Detoxification              |
| P01032   | Glutathione S-transferase   | 2.3   | 0.047 | Detoxification              |
| P03755 (25,35DAP)  | Phospholipid hydroperoxide glutathione peroxidase                           | 2.3   | 0.010 | Detoxification              |
| P02353 (35DAP)   | Cupredoxin  | 23.1  | 0.007 | Detoxification              |
| P01497 (20DAP)   | Ferredoxin 1  | 8.2   | 0.002 | Detoxification              |
| P04171 (25,35DAP)  | Metallothionein-like protein 1 (MT-1)                                       | 3.8   | 0.001 | Detoxification              |
| P02134 (35DAP)   | Dienelactone hydrolase ( $\alpha\beta$ -hydrolase)                          | 2.7   | 0.038 | Detoxification              |
| P02815 (20,35DAP)  | Dehydration-responsive protein RD22   | 28.4  | 0.033 | Drought response            |
| P02219 (35DAP)   | Subtilisin proteinase inhibitor   | 3.2   | 0.041 | Disease response            |
| P01896 (35DAP)   | Disease resistance protein RGA2   | 2.4   | 0.037 | Disease response            |
| P01206 (25,35DAP)  | Syntaxin-132 (AtSYP132)   | 2.0   | 0.001 | Cell proliferation          |
| <b>SIGNALING &amp; HORMONAL FUNCTIONS (16)</b>           |   |       |       |                             |
| P01758 (35DAP)   | WRKY-24/32 transcription factor   | 2.1   | 0.001 | Trancription factor         |
| P01092   | Myb family transcription factor   | 3.0   | 0.013 | Trancription factor         |
| P02122 (20,25DAP)  | MYB-112/50 TF, Tuber-specific and sucrose-responsive element binding factor | 2.0   | 0.010 | Trancription factor         |
| P04334   | FUSCA-3   | 2.5   | 0.018 | Trancription factor         |
| P04065   | Transcriptional coactivator/pterin dehydratase                              | 4.8   | 0.005 | Trancriptional activation   |
| P02441   | MAP kinase PsMAPK2  | 4.5   | 0.040 | Protein phosphorylation     |
| P00766   | MAPKK   | 4.4   | 0.001 | Protein phosphorylation     |
| P01662 (35DAP)   | MAP kinase, Medicago  | 2.1   | 0.000 | Protein phosphorylation     |
| P02825 (35DAP)   | Receptor-like protein kinase 3  | 3.3   | 0.005 | Protein phosphorylation     |
| P00010 (20DAP)   | Ser/Thr-protein kinase receptor (S-receptor kinase, SRK)                    | 2.2   | 0.015 | Protein phosphorylation     |
| P01965   | Ser/Thr-protein kinase SAPK7, Osmotic stress/ABA-activated protein kinase 7 | 2.0   | 0.024 | Protein phosphorylation     |
| P02807 (20,35DAP)  | Ca-dependent protein kinase CPK1  | 2.3   | 0.039 | Protein phosphorylation     |
| P00679   | NAC domain-containing protein 78 (ANAC078)                                  | 2.2   | 0.014 | DNA binding                 |
| P02259 (25,35DAP)  | Homeobox protein  | 3.2   | 0.050 | Homeotic functions          |
| P01656 (25DAP)   | Auxin-responsive protein IAA8   | 2.5   | 0.043 | Auxin function repression   |
| P04005 (20DAP)   | Ent-kaurenic acid oxidase 1 (KAO1, CyP450 88A3)                             | 2.1   | 0.039 | GA functions                |
| <b>PHOTOSYNTHESIS (5)</b>                                |   |       |       |                             |
| P01039   | PS II reaction center protein I (PSII-I)                                    | 2.6   | 0.004 | Photosynthesis              |
| P01038 (25DAP)   | PS II reaction center protein I (PSII-I)                                    | 2.5   | 0.032 | Photosynthesis              |
| P00009 (25DAP)   | PSII D1 reaction center   | 2.3   | 0.000 | Photosynthesis              |
| P01714   | PS II reaction center   | 2.0   | 0.012 | Photosynthesis              |
| P00854 (25DAP)   | CAB-8   | 3.2   | 0.027 | Chlorophyll binding protein |
| <b>TRANCRITION &amp; TRANSLATION &amp; HISTONES (54)</b> |   |       |       |                             |
| P00844   | Elongation factor EF-2  | 11.0  | 0.014 | Translation                 |
| P01177   | Elongation factor 1-alpha (EF-1-alpha)                                      | 2.0   | 0.005 | Translation                 |
| P01474   | Elongation factor 1-alpha   | 2.6   | 0.009 | Translation                 |
| P01687 (35DAP)   | Translation initiation factor   | 2.2   | 0.008 | Translation                 |
| P00741   | Peptidyl-tRNA hydrolase   | 2.0   | 0.023 | Translation                 |
| P01728   | Nascent polypeptide-associated complex NAC                                  | 3.7   | 0.027 | Translation                 |
| P00629   | DEAD box RNA helicase   | 3.3   | 0.015 | Translation                 |
| P00457 (25DAP)   | DNA-directed RNA polymerase   | 2.2   | 0.030 | Translation                 |
| P02221 (25DAP)   | WD repeat protein pop3  | 2.0   | 0.002 | mRNA processing             |
| P01325 (20,25DAP)  | Poly(A)-binding protein   | 18.0  | 0.002 | mRNA processing             |
| P04576   | RNA-binding protein, chloroplast  | 3.0   | 0.030 | mRNA processing             |
| P02581   | 60S ribosomal protein L22-2   | 180.2 | 0.024 | Ribosomal protein           |
| P01384   | Ribosomal protein L28   | 25.4  | 0.002 | Ribosomal protein           |
| P04287   | 40S ribosomal protein S13   | 7.4   | 0.005 | Ribosomal protein           |
| P03529   | 40S ribosomal protein S7  | 5.1   | 0.012 | Ribosomal protein           |
| P01485   | Ribosomal protein 27a   | 4.8   | 0.021 | Ribosomal protein           |
| P01182   | Ribosomal protein L27   | 3.8   | 0.002 | Ribosomal protein           |
| P04216   | 60S ribosomal protein L10A  | 3.5   | 0.021 | Ribosomal protein           |
| P02342   | Ribosomal protein L8, cytosolic   | 3.1   | 0.000 | Ribosomal protein           |
| P02096   | Ribosomal RNA- processing protein   | 3.0   | 0.015 | Ribosomal protein           |

|        |                                       |     |       |                   |
|--------|---------------------------------------|-----|-------|-------------------|
| P04553 | Ribosomal protein S3a                 | 3.0 | 0.000 | Ribosomal protein |
| P02048 | 60S RIBOSOMAL PROTEIN                 | 2.9 | 0.049 | Ribosomal protein |
| P02286 | 40S ribosomal protein S24             | 2.7 | 0.002 | Ribosomal protein |
| P01105 | Ribosomal protein L27a                | 2.7 | 0.036 | Ribosomal protein |
| P02854 | Ribosomal protein L10a                | 2.4 | 0.020 | Ribosomal protein |
| P04304 | 40S ribosomal protein S11             | 2.4 | 0.013 | Ribosomal protein |
| P04387 | Ribosomal protein s19                 | 2.3 | 0.021 | Ribosomal protein |
| P04388 | 40S ribosomal protein S9              | 2.2 | 0.031 | Ribosomal protein |
| P01797 | 60S ribosomal protein L21             | 2.2 | 0.041 | Ribosomal protein |
| P02959 | 60S ribosomal protein L19             | 2.1 | 0.017 | Ribosomal protein |
| P01202 | 40S ribosomal protein S30             | 2.1 | 0.010 | Ribosomal protein |
| P02984 | 60S ribosomal protein                 | 2.1 | 0.008 | Ribosomal protein |
| P00082 | Ribosomal protein L35, chloropl.      | 2.0 | 0.006 | Ribosomal protein |
| P02080 | Ribosomal protein L13                 | 2.0 | 0.022 | Ribosomal protein |
| P02330 | 60S ribosomal protein L13-1           | 2.0 | 0.010 | Ribosomal protein |
| P01081 | 28 kDa ribonucleoprotein, chloroplast | 2.1 | 0.001 | Ribosomal protein |
| P01501 | Histone H4                            | 2.3 | 0.037 | Histone           |
| P04584 | Histone H4                            | 2.3 | 0.008 | Histone           |
| P02017 | Histone H3                            | 2.3 | 0.003 | Histone           |
| P04684 | Histone H2A                           | 2.3 | 0.005 | Histone           |
| P01951 | Histone H4                            | 2.5 | 0.029 | Histone           |
| P02532 | Histone H4                            | 2.5 | 0.012 | Histone           |
| P01924 | Histone H2B                           | 2.5 | 0.042 | Histone           |
| P03703 | Histone H2B                           | 2.7 | 0.006 | Histone           |
| P02006 | Histone H2A                           | 2.9 | 0.011 | Histone           |
| P02444 | Histone H4                            | 3.2 | 0.003 | Histone           |
| P01899 | Histone H2B                           | 3.3 | 0.009 | Histone           |
| P04375 | Histone H1. b                         | 3.5 | 0.006 | Histone           |
| P02404 | Histone H1                            | 2.1 | 0.001 | Histone           |
| P04858 | Histone H2B1                          | 2.1 | 0.021 | Histone           |
| P02173 | Histone H2B1                          | 4.6 | 0.002 | Histone           |
| P03596 | Histone H2B                           | 2.1 | 0.016 | Histone           |
| P02318 | Histone H1                            | 2.1 | 0.019 | Histone           |
| P01983 | Histone H3                            | 3.9 | 0.042 | Histone           |

#### Upregulated, no annotation (99)

#### 30 DAP down (117)

| Seq. ID   | Gene Annotation  | Factor | P     | Function                          |
|---|--|--------|-------|-----------------------------------|
| <b>PRIMARY &amp; SECONDARY METABOLISM (21)</b>              |  |        |       |                                   |
| P03795  | Phosphoglycerate mutase  | 2.3    | 0.008 | Glycolysis                        |
| P04974 (35DAP)  | Fructose-bisphosphate aldolase, cytoplasm                                    | 2.0    | 0.004 | Glycolysis                        |
| P03767 (25DAP)  | Pyruvate kinase, chloroplast   | 2.3    | 0.005 | Glycolysis                        |
| P03214 (35DAP)  | Invertase/pectin methyltransferase inhibitor                                 | 2.5    | 0.001 | CH metabolism                     |
| P05197  | ADP-glucose pyrophosphorylase, small su                                      | 4.0    | 0.022 | Starch metabolism                 |
| P00655  | ADP-glucose pyrophosphorylase, small su                                      | 2.4    | 0.005 | Starch metabolism                 |
| P04822 (25DAP)  | Glycosyl transferase (Galactinol synthase)                                   | 2.8    | 0.002 | Raffinose sugar metabolism        |
| P04337  | 6-Phosphogluconate dehydrogenase, plastid                                    | 2.4    | 0.006 | Ser biosynthesis                  |
| P02864 (35DAP)  | Glutamine synthetase (Cytosolic GS1)   | 2.1    | 0.001 | Glu biosynthesis                  |
| P03631 (25,35DAP)   | UDP-glucuronosyl/UDP-glucosyltransferase                                     | 2.9    | 0.032 | Glucosyltransferase               |
| P05031  | Ferredoxin--NADP reductase, chloroplast                                      | 2.7    | 0.011 | NADH oxidation                    |
| P03480 (25DAP)  | Cytochrome c oxidase   | 2.3    | 0.003 | Respiration                       |
| P05167  | SAM-dependent methyltransferase  | 2.0    | 0.025 | Methylation cycle                 |
| P03766 (25DAP)  | S-adenosylmethionine decarboxylase   | 2.8    | 0.009 | Methylation cycle                 |
| P03506 (35DAP)  | Enoyl-CoA hydratase/isomerase  | 3.0    | 0.002 | FA metabolism                     |
| P03551  | Long-chain acyl-CoA synthetase 5   | 2.4    | 0.019 | FA metabolism                     |
| P02503 (35DAP)  | 3-ketoacyl-CoA synthase 10 (Fiddlehead-like protein)                         | 2.0    | 0.025 | FA metabolism                     |
| P01058 (25,35DAP)   | Adenosine deaminase  | 6.3    | 0.006 | Purine metabolism                 |
| P04410 (35DAP)  | 5-phosphoribosyl-1-pyrophosphate amidotransferase                            | 2.7    | 0.022 | Nucleotide metabolism             |
| P03951 (25DAP)  | Inorganic pyrophosphatase  | 2.5    | 0.005 | Pyrophosphatase                   |
| P01154 (25DAP)  | Phosphatidylinositol-glycan biosynthesis class C                             | 2.1    | 0.038 | Inositol metabolism               |
| <b>TRANSPORT (10)</b>                                       |  |        |       |                                   |
| P00852 (25DAP)  | OEP16.1, amino acid selective channel  | 4.2    | 0.001 | Plastidial outer membrane protein |
| P05186  | Mitochondrial import receptor subunit TOM20                                  | 2.2    | 0.001 | Mitochondrial translocator        |
| P05161 (35DAP)  | Mitochondrial matrix protein frataxin, involved in Fe/S protein biosynthesis | 2.5    | 0.010 | Mitochondrial translocator        |
| P01824  | Acyl carrier protein 4, chloroplast  | 4.0    | 0.017 | Lipid transport                   |
| P03790  | Zinc transporter ZAT-1   | 3.0    | 0.000 | Metal transport                   |
| P02762 (30DAP)  | Zinc transporter 4, chloroplast precursor (ZRT/IRT-like protein 4)           | 2.0    | 0.006 | Metal transport                   |
| P00469 (20DAP)  | Zinc transporter, ZIP4   | 2.0    | 0.018 | Metal transport                   |
| P04444 (25DAP)  | Ca-ATPase, IIB (ER)  | 2.0    | 0.028 | Ca transport                      |
| P03993  | Aquaporin PIP-type 7a (Turgor-responsive protein 7a)                         | 2.2    | 0.005 | Water transport                   |
| P04982 (25,35DAP)   | Aquaporin, PIP-type 7a, turgor-responsive                                    | 2.0    | 0.001 | Water transport                   |
| <b>ENDOMEMBRANE TRANSPORT &amp; PROTEIN PROCESSING (14)</b> |  |        |       |                                   |
| P03208 (20DAP)  | Legumain   | 2.4    | 0.020 | Storage protein processing        |
| P04730  | Ras small GTPase   | 2.2    | 0.014 | Vesicle trafficking               |
| P04603  | GTP-binding protein  | .0     | 0.002 | Vesicle trafficking               |
| P04764 (25,35DAP)   | Chaperone HSC71.0, DnaK  | 2.8    | 0.006 | Chaperone                         |
| P02041  | HSP20-like chaperone   | 2.0    | 0.016 | Chaperone                         |
| P04986  | Chaperone multifunctional (14-3-3 family)                                    | 2.2    | 0.005 | Chaperone                         |
| P04972  | Calreticulin   | 2.4    | 0.002 | Ca-binding chaperone              |
| P03666 (35DAP)  | Nonaspanin (TM9SF)   | 3.0    | 0.002 | Vesicle trafficking               |
| P04914 (25DAP)  | Beta-Ig-H3/fasciclin   | 2.6    | 0.014 | Vesicle trafficking               |
| P02510 (25DAP)  | Alpha-soluble NSF attachment protein   | 2.2    | 0.005 | Vesicle trafficking               |
| P01199  | SNF7 family protein  | 2.1    | 0.010 | Vesicle trafficking               |
| P05151  | ADP-ribosylation factor GTP binding protein                                  | 2.4    | 0.004 | Vesicle trafficking               |
| P00059  | Peptidyl-prolyl cis-trans isomerase  | 2.3    | 0.007 | Protein trafficking               |
| P05208 (25DAP)  | Peptidyl-prolyl cis-trans isomerase  | 2.2    | 0.002 | Protein trafficking               |
| <b>REGULATED PROTEIN DEGRADATION (15)</b>                   |  |        |       |                                   |
| P02453 (20,25DAP)   | Serine carboxypeptidase 1  | 3.0    | 0.020 | Proteinase                        |
| P02708 (25,35DAP)   | Prolyl Oligopeptidase  | 2.6    | 0.032 | Proteinase                        |

|  |   |      |       |  |
|--|---|------|-------|--|
| P01932 (35DAP)   | Ubiquitin-protein ligase/ zinc ion binding                        | 2.5  | 0.049 | Ubiquitin mediated protein degradation       |
| P01451 (25DAP)   | Cullin 3B   | 2.3  | 0.040 | Ubiquitin mediated protein degradation       |
| P02115   | Aspartic protease   | 2.1  | 0.048 | Proteinase                                   |
| P03124 (25DAP)   | 20S core proteasome subunit alpha 2                               | 2.0  | 0.049 | Ubiquitin mediated protein degradation       |
| P03922   | Aminoacylproline aminopeptidase                                   | 2.0  | 0.001 | Proteinase                                   |
| P02732   | 26S proteasome regulatory subunit                                 | 2.0  | 0.003 | Ubiquitin mediated protein degradation       |
| P03243 (25,35DAP)  | Ubiquitin-conjugating enzyme E2                                   | 3.0  | 0.007 | Ubiquitin mediated protein degradation       |
| P02037   | E3 ubiquitin-protein ligase                                       | 2.7  | 0.014 | Ubiquitin mediated protein degradation       |
| P00708   | E3 ubiquitin-protein ligase LRSAM1                                | 2.3  | 0.006 | Ubiquitin mediated protein degradation       |
| P04419   | Ubiquitin-conjugating enzyme, E2                                  | 2.1  | 0.018 | Ubiquitin mediated protein degradation       |
| P03356 (25DAP)   | Ubiquitin   | 2.0  | 0.000 | Ubiquitin mediated protein degradation       |
| P04967   | Thiol protease aleurain   | 2.2  | 0.001 | Proteinase                                   |
| P04140   | Aspartic proteinase   | 2.2  | 0.008 | Proteinase                                   |
| <b>CELL PROLIFERATION (3)</b>                              |   |      |       |  |
| P03363 (20DAP)   | Expansin-like A2  | 2.1  | 0.009 | Cell expansion                               |
| P02936   | Xyloglucan endo-1,4-beta-D-glucanase                              | 2.1  | 0.012 | Cell wall metabolism                         |
| P03595   | NAP1 microtubule regulating factor                                | 2.2  | 0.002 | Cell wall metabolism                         |
| <b>STORAGE RELATED (5)</b>                                 |   |      |       |  |
| P04448 (20,25DAP)  | Legumin A   | 2.0  | 0.007 | Storage protein                              |
| P04995   | Legumin K   | 2.0  | 0.002 | Storage protein                              |
| P04441 (20,25DAP)  | Albumin 2   | 2.3  | 0.000 | Storage protein                              |
| P04532 (20,25DAP)  | Glycinin subunit  | 3.1  | 0.019 | Storage protein                              |
| P03272   | Ferritin-3, chloroplast   | 3.5  | 0.019 | Ferritin                                     |
| <b>DISEASE &amp; STRESS TOLERANCE (15)</b>                 |   |      |       |  |
| P04246   | Plant lipid transfer/seed storage/Trypsin-alpha amylase inhibitor | 5.7  | 0.008 | Pathogen response                            |
| P05016 (35DAP)   | Plant lipid transfer/seed storage/Trypsin-alpha amylase inhibitor | 4.0  | 0.007 | Pathogen response                            |
| P01528 (35DAP)   | Plant lipid transfer/seed storage/Trypsin-alpha amylase inhibitor | 3.6  | 0.001 | Pathogen response                            |
| P04349   | Plant lipid transfer/seed storage/Trypsin-alpha amylase inhibitor | 2.1  | 0.006 | Pathogen response                            |
| P03274   | Plant lipid transfer protein/Par allergen                         | 2.3  | 0.028 | Pathogen response                            |
| P03786 (25,35DAP)  | Alkaline phytoceramidase  | 2.6  | 0.001 | Defense against cell death                   |
| P00638 (25,35DAP)  | Trypsin/chymotrypsin inhibitor                                    | 3.9  | 0.010 | Pathogen response                            |
| P04644   | Disease resistance response protein 206-d                         | 2.7  | 0.000 | Pathogen response                            |
| P04250 (25,35DAP)  | Pathogenesis-related protein 17                                   | 2.4  | 0.003 | Pathogen response                            |
| P03505   | Germin-like protein   | 2.2  | 0.008 | Pathogen response                            |
| P00684 (35DAP)   | NADP-dependent oxidoreductase P1                                  | 2.1  | 0.007 | Defense                                      |
| P04569 (35DAP)   | Glycoside hydrolase, chitinase                                    | 2.2  | 0.033 | Pathogen response                            |
| P04908   | Glycoside hydrolase, chitinase                                    | 2.1  | 0.008 | Pathogen response                            |
| P04811   | Dehydration-responsive protein RD22                               | 2.2  | 0.002 | Drought response                             |
| P01277   | Fibrillin 8   | 2.1  | 0.003 | Lipid binding protein, stress/ABA responsive |
| <b>SIGNALING &amp; HORMONAL FUNCTIONS (14)</b>             |   |      |       |  |
| P02114 (35DAP)   | Two-component response regulator ARR5                             | 10.6 | 0.045 | CK functions                                 |
| P04794   | Short chain dehydrogenase/reductase                               | 3.2  | 0.009 | Short-chain dehydrogenases/reductases        |
| P04123   | 9-cis-epoxycarotenoid dioxygenase (NCED)                          | 2.8  | 0.001 | ABA biosynthesis                             |
| P04812   | DELLA protein GAI   | 2.6  | 0.006 | Repressor of GA functions                    |
| P05048 (25DAP)   | Phytochrome B   | 2.5  | 0.002 | Signaling                                    |
| P03792 (25DAP)   | Thioredoxin h   | 2.5  | 0.030 | Redox regulation                             |
| P04599 (35DAP)   | LEC1, transcription factor  | 2.2  | 0.030 | Transcription factor                         |
| P04407   | BZIP transcription factor ATB2_2                                  | 2.0  | 0.003 | Transcription factor                         |
| P03681   | Receptor-like Serine/Threonine kinase                             | 2.0  | 0.032 | Protein kinase                               |
| P00915 (20DAP)   | Protein kinase APK1A, chloroplast                                 | 2.0  | 0.001 | Protein kinase                               |
| P04464 (25DAP)   | Ferredoxin 3  | 2.2  | 0.024 | Redox regulation                             |
| P01836   | Carbohydrate kinase, PfkB   | 2.2  | 0.048 | Myo-inositol kinase                          |
| P01646 (35DAP)   | Protein-Tyrosine-phosphatase                                      | 2.1  | 0.028 | Protein phosphatase                          |
| P04793   | Trehalose 6-phosphate synthase, class II                          | 2.0  | 0.043 | Trehalose signaling                          |
| <b>PHOTOSYNTHESIS (3)</b>                                  |   |      |       |  |
| P04462 (20,25DAP)  | PS II subunit (22kDa)   | 2.6  | 0.011 | Photosynthesis                               |
| P04368 (20,25DAP)  | Rubisco, small chain  | 2.1  | 0.005 | Photosynthesis                               |
| P05191 (35DAP)   | Thylakoid membrane phosphoprotein 14 kDa                          | 2.4  | 0.012 | Photosynthesis                               |
| <b>TRANSCRIPTION &amp; TRANSLATION &amp; HISTONES (17)</b> |   |      |       |  |
| P04154   | Elongation factor G, chloroplast                                  | 3.3  | 0.014 | Trancription                                 |
| P02152   | DEAD-box ATP-dependent RNA helicase 19                            | 4.9  | 0.013 | Trancription                                 |
| P04861   | RNA polymerase II, RPB4   | 2.5  | 0.000 | Trancription                                 |
| P03465   | DNA-directed RNA polymerase Iib                                   | 2.1  | 0.011 | Trancription                                 |
| P01397   | Translation initiation factor 5A-4                                | 2.2  | 0.003 | Translation                                  |
| P04251   | Elongation factor 1-alpha   | 2.1  | 0.017 | Translation                                  |
| P03599   | Translation initiation factor 4G                                  | 2.0  | 0.024 | Translation                                  |
| P04844   | Ribonuclease (translational inhibitor)                            | 2.0  | 0.010 | Translation                                  |
| P04386   | Ribosomal protein s19   | 3.7  | 0.001 | Ribosomal protein                            |
| P04248   | Ribosomal protein L17, cytosolic                                  | 2.7  | 0.001 | Ribosomal protein                            |
| P05120   | Ribosomal protein S21   | 2.0  | 0.003 | Ribosomal protein                            |
| P03276   | Ribosome recycling factor, chloroplast                            | 2.2  | 0.035 | Ribosomal protein                            |
| P04842   | Small nuclear ribonucleoprotein                                   | 2.0  | 0.009 | Ribosomal protein                            |
| P04510   | Histone H2B1  | 2.1  | 0.015 | Histone                                      |
| P05146   | Histone H2A   | 3.2  | 0.000 | Histone                                      |
| P04348   | Histone H1.41   | 2.2  | 0.015 | Histone                                      |
| P04134 (20,30DAP)  | WD-40 repeat protein MSI1 (Core histone-binding su                | 2.1  | 0.001 | Histone binding protein                      |
| <b>Downregulated, no annotation (90)</b>                   |   |      |       |  |

| <b>35DAP up (134)</b>  |   |        |       |  |
|--|---|--------|-------|--|
| Seq. ID  | Gene Annotation   | Factor | P     | Function                               |
| <b>PRIMARY &amp; SECONDARY METABOLISM &amp; TRANSPORT (29)</b> |   |        |       |  |
| P00898 (20,30DAP)  | Sucrose-phosphate synthase  | 2.7    | 0.003 | Sucrose metabolism                     |
| P00816   | Fructose-bisphosphate aldolase, chloroplast   | 2.1    | 0.011 | Glycolysis                             |
| P01841 (30DAP)   | Pyruvate dehydrogenase E1, beta subunit   | 2.0    | 0.007 | Glycolysis                             |
| P01043   | Enolase (2-phosphoglycerate dehydratase), cytoplasm                                     | 4.4    | 0.019 | Glycolysis                             |
| P02459 (25,30DAP)  | Glyceraldehyde-3-phosphate DH, cytosolic  | 2.4    | 0.006 | Glycolysis                             |
| P03466 (20,30DAP)  | Glycoside hydrolase   | 4.8    | 0.048 | CH metabolism                          |
| P01502 (30DAP)   | UDP-glucose pyrophosphorylase   | 2.3    | 0.001 | CH metabolism                          |
| P04097   | ATP citrate lyase a-subunit, cytosol  | 2.0    | 0.016 | CH metabolism, citrate degradation     |
| P01847 (25,30DAP)  | Nudix hydrolase, nucleoside sugar hydratase   | 3.0    | 0.016 | Nucleoside sugar catabolism            |
| P03815   | Granule-bound starch synthase 1, chloroplast  | 4.5    | 0.001 | Starch metabolism                      |
| P00897   | Phosphoglucan, water dikinase, chloroplast  | 2.0    | 0.001 | Starch metabolism                      |
| P01976 (25,30DAP)  | Starch phosphorylase, L chloroplast   | 2.2    | 0.030 | Starch metabolism                      |
| P02005   | L-asparaginase  | 3.0    | 0.001 | Amino acid metabolism                  |
| P02413   | O-diphenol-O-methyl transferase   | 2.0    | 0.001 | Methyltransferase                      |
| P01419 (20,30DAP)  | DNA (cytosine-5-)-methyltransferase   | 2.6    | 0.049 | Methyltransferase                      |
| P01416 (25,30DAP)  | Adenylate kinase (ATP- AMP transphosphorylase), chloroplast                             | 2.2    | 0.012 | Nucleotide metabolism                  |
| P01821 (30DAP)   | Phytoene synthase (geranylgeranyl-diphosphate geranylgeranyl transferase)               | 2.2    | 0.006 | Carotenoide synthesis                  |
| P02518   | Spermidine synthase 1 (Putrescine aminopropyltransferase 1)                             | 22.9   | 0.038 | Polyamine biosynthesis                 |
| P04233 (25DAP)   | 12-oxophytodienoic acid 10, 11-reductase, OPR2  | 2.0    | 0.039 | NADH oxidation                         |
| P04137   | NADH-ubiquinone oxidoreductase, complex I NDUFS6  | 2.0    | 0.000 | NADH oxidation                         |
| P02713 (25DAP)   | NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial                            | 2.0    | 0.018 | NADH oxidation                         |
| P00048   | Quinolate phosphoribosyltransferase   | 2.0    | 0.017 | NAD(+) biosynthesis                    |
| P02429   | Acetyl-coenzyme A synthetase  | 2.4    | 0.016 | Ac-CoA synthesis                       |
| P01076 (25DAP)   | Delta 8-sphingolipid desaturase   | 3.0    | 0.007 | FA metabolism                          |
| P01949   | 1-acyl-sn-glycerol-3-phosphate acyltransferase PLS1, (Phospholipid synthesis protein 1) | 2.1    | 0.002 | FA metabolism                          |
| P01648 (30DAP)   | MGDG synthase type A  | 2.0    | 0.022 | FA metabolism                          |
| P01223   | Beta-1,3-glucanase  | 2.5    | 0.034 | Cell wall metabolism                   |
| P02670 (30DAP)   | Beta3-glucuronyltransferase   | 2.3    | 0.041 | Cell wall metabolism                   |
| P02042   | Reversibly glycosylatable polypeptide   | 3.0    | 0.037 | Cell wall metabolism                   |
| <b>TRANSPORT (6)</b>   |   |        |       |  |
| P00784 (25,30DAP)  | Peptide transporter PTR2  | 2.4    | 0.004 | Peptide transport                      |
| P04485 (25,30DAP)  | ATP synthase delta chain, mitochondrial   | 3.3    | 0.016 | ATP synthesis                          |
| P01371   | Import inner membrane translocase subunit TIM50, mitochondrial                          | 3.1    | 0.004 | Mitochondrial translocator             |
| P01734   | Chloroplast inner membrane import protein Tic22   | 3.4    | 0.048 | Chloroplast translocator               |
| P02225 (25,30DAP)  | Uncoupling protein, mitochondrial   | 2.9    | 0.028 | Respiratory control                    |
| P00853 (20DAP)   | Boron transporter   | 2.4    | 0.012 | Transport                              |
| <b>ENDOMEMBRANE TRANSPORT &amp; PROTEIN PROCESSING (15)</b>    |   |        |       |  |
| P00689 (25,30DAP)  | Coatomer subunit gamma  | 8.5    | 0.045 | Vesicle trafficking                    |
| P01526 (30DAP)   | SNF7 protein  | 4.6    | 0.045 | Vesicle trafficking                    |
| P00213   | Prenylated rab acceptor PRA1  | 2.7    | 0.044 | Vesicle trafficking                    |
| P00502 (20DAP)   | SNAP25 homologous protein (SNARE)   | 2.0    | 0.024 | Vesicle trafficking                    |
| P02165 (30DAP)   | Dolichyl-diphosphooligosaccharide-protein glycosyltransferase                           | 2.3    | 0.004 | Protein processing                     |
| P01988 (30DAP)   | Ras-related protein Rab7D   | 2.3    | 0.026 | Protein processing                     |
| P01279 (30DAP)   | Peptidyl-prolyl cis- trans isomerase  | 2.4    | 0.009 | Protein processing                     |
| P01573 (25,30DAP)  | Signal peptide peptidase  | 2.3    | 0.032 | Protein processing                     |
| P02026   | Chaperonin 20 kDa, chloroplast  | 2.7    | 0.009 | Chaperone                              |
| P02333   | Chaperonin 10, chloroplast  | 3.4    | 0.043 | Chaperone                              |
| P02055 (30DAP)   | Chaperone HSP20-like  | 2.2    | 0.002 | Chaperone                              |
| P03657 (25,30DAP)  | Chaperone (copper)  | 2.2    | 0.035 | Chaperone                              |
| P01606   | Chaperone blp5, DnaK  | 2.0    | 0.013 | Chaperone                              |
| P00619 (25,30DAP)  | Heat shock protein Hsp90  | 2.3    | 0.002 | Chaperone                              |
| P02258 (25,30DAP)  | Calreticulin  | 4.2    | 0.043 | Ca-binding chaperone (ER)              |
| <b>REGULATED PROTEIN DEGRADATION (7)</b>                       |   |        |       |  |
| P02177   | 26S proteasome regulatory subunit   | 4.9    | 0.006 | Ubiquitin mediated protein degradation |
| P02498   | 26S proteasome subunit S3-a   | 2.0    | 0.024 | Ubiquitin mediated protein degradation |
| P02386 (30DAP)   | Ubiquitin fusion degradation protein UFD1   | 2.3    | 0.025 | Ubiquitin mediated protein degradation |
| P03243 (25,30DAP)  | Ubiquitin-conjugating enzyme E2   | 2.2    | 0.001 | Ubiquitin mediated protein degradation |
| P01932 (30DAP)   | Ubiquitin-protein ligase  | 2.2    | 0.001 | Ubiquitin mediated protein degradation |
| P00690 (25DAP)   | E3 ubiquitin ligase   | 2.1    | 0.008 | Ubiquitin mediated protein degradation |
| P02708 (25,30DAP)  | Prolyl endopeptidase  | 2.5    | 0.001 | Protease                               |
| <b>CELL PROLIFERATION (10)</b>                                 |   |        |       |  |
| P00178 (25,30DAP)  | Annexin   | 2.7    | 0.014 | Cell proliferation                     |
| P03116   | Annexin   | 2.7    | 0.005 | Cell proliferation                     |
| P02931 (30DAP)   | Annexin   | 2.0    | 0.004 | Cell proliferation                     |
| P01817 (30DAP)   | Tubulin-specific chaperone A  | 2.2    | 0.032 | Cell proliferation                     |
| P02837 (30DAP)   | Tubulin alpha   | 2.1    | 0.028 | Cell proliferation                     |
| P00033 (20,25DAP)  | Tubulin beta  | 2.0    | 0.005 | Cell proliferation                     |
| P02077   | Ca(2+)-regulated actin-binding protein  | 2.4    | 0.034 | Cell proliferation                     |
| P02293   | MCM3 (Minichromosome maintenance protein 3)   | 4.1    | 0.046 | Cell proliferation                     |
| P01910 (30DAP)   | Prohibitin  | 3.6    | 0.032 | Cell proliferation                     |
| P00884   | ycf1-protein, chloroplast   | 3.4    | 0.024 | Cell proliferation                     |
| <b>STORAGE RELATED (14)</b>                                    |   |        |       |  |
| P04038 (25,30DAP)  | Vicilin A   | 11.1   | 0.005 | Storage protein                        |
| P04635 (30DAP)   | Vicilin   | 6.0    | 0.018 | Storage protein                        |
| P04533   | Vicilin A   | 4.8    | 0.042 | Storage protein                        |
| P04616   | Vicilin   | 2.5    | 0.014 | Storage protein                        |
| P02231   | Vicilin A   | 2.2    | 0.003 | Storage protein                        |
| P00635 (30DAP)   | USP   | 78.2   | 0.049 | Storage protein                        |
| P01146 (30DAP)   | USP   | 9.5    | 0.002 | Storage protein                        |
| P01292   | USP   | 7.0    | 0.003 | Storage protein                        |
| P01331   | USP   | 6.0    | 0.001 | Storage protein                        |
| P04466   | USP   | 4.4    | 0.001 | Storage protein                        |
| P02121   | USP   | 4.2    | 0.002 | Storage protein                        |
| P00940 (20,25DAP)  | USP   | 3.8    | 0.032 | Storage protein                        |
| P04363   | USP   | 2.0    | 0.002 | Storage protein                        |
| P01844 (20,30DAP)  | USP   | 3.1    | 0.009 | Storage protein                        |
| <b>DISEASE &amp; STRESS TOLERANCE (15)</b>                     |   |        |       |  |
| P03051 (25,30DAP)  | Alcohol dehydrogenase   | 8.0    | 0.024 | Alcohol dehydrogenase                  |
| P02489 (25,30DAP)  | Alcohol dehydrogenase   | 4.2    | 0.029 | Alcohol dehydrogenase                  |
| P00931   | (Benzo)quinone oxidoreductase   | 2.1    | 0.014 | ROS response                           |
| P02428   | (Benzo)quinone oxidoreductase   | 2.0    | 0.035 | ROS response                           |
| P03755 (25,30DAP)  | Phospholipid hydroperoxide glutathione peroxidase                                       | 3.0    | 0.008 | Detoxification                         |
| P01200   | Glutathione S-transferase   | 2.3    | 0.015 | Detoxification                         |
| P02353 (30DAP)   | Cupredoxin  | 2.7    | 0.045 | Detoxification                         |
| P01489   | Cupredoxin  | 2.4    | 0.002 | Detoxification                         |
| P04171 (25,30DAP)  | Metallothionein-like protein 1 (MT-1).  | 3.1    | 0.005 | Detoxification                         |
| P02134 (30DAP)   | Dienelactone hydrolase  | 2.6    | 0.037 | Detoxification                         |
| P02815 (30DAP)   | Dehydration-responsive protein RD22   | 34.8   | 0.000 | Drought response                       |
| P01896 (30DAP)   | Disease resistance protein RGA2   | 2.7    | 0.010 | Disease response                       |
| P03402   | Kunitz inhibitor ST1-like   | 4.7    | 0.026 | Disease response                       |
| P02219 (30DAP)   | Subtilisin proteinase inhibitor   | 4.6    | 0.031 | Disease response                       |
| P01206 (25,30DAP)  | Syntaxin-132 (AtSYP132)   | 2.1    | 0.019 | Cell proliferation                     |
| <b>SIGNALING &amp; HORMONE FUNCTIONS (16)</b>                  |   |        |       |  |

|   |  |               |          |  |
|---|--|---------------|----------|--|
| P01758 (30DAP)  | WRKY-24/32 transcription factor  | 2.5           | 0.003    | Trancription factor                    |
| P01940  | bZIP-TF / Dc3 promoter binding element                                       | 5.3           | 0.006    | Trancription factor                    |
| P00997  | Serine/Threonine-protein phosphatase PP1                                     | 5.6           | 0.021    | Protein phosphorylation                |
| P02807 (20,30DAP)   | Ca-dependent protein kinase CPK1   | 2.1           | 0.019    | Protein phosphorylation                |
| P00484  | Calcium-dependent protein kinase (CDPK)                                      | 2.0           | 0.008    | Protein phosphorylation                |
| P01662 (30DAP)  | MAP kinase, Medicago   | 2.0           | 0.045    | Protein phosphorylation                |
| P01639  | Protein phosphatase 2C   | 2.8           | 0.046    | Protein phosphorylation                |
| P02825 (30DAP)  | Receptor-like protein kinase 3   | 2.8           | 0.018    | Protein phosphorylation                |
| P01965  | Ser/Thr-protein kinase SAPPK7, Osmotic stress/ABA-activated protein kinase 7 | 2.4           | 0.015    | Protein phosphorylation                |
| P01268 (25DAP)  | EMB2737 (EMBRYO DEFECTIVE 2737)  | 2.1           | 0.028    | Embryogenesis                          |
| P02259 (25,30DAP)   | Homeobox protein   | 2.0           | 0.012    | Homeotic functions                     |
| P02114  | Two-component response regulator ARR5  | 4.2           | 0.016    | CK functions                           |
| P01142  | Cytokinin dehydrogenase 5 (Cytokinin oxidase 5)                              | 2.0           | 0.033    | CK degradation                         |
| P01513  | Inner membrane protein PPF-1, chloroplast                                    | 4.9           | 0.042    | Plastid biogenesis                     |
| P01335  | GIANT CHLOROPLAST 1  | 2.0           | 0.020    | Plastid division                       |
| P00791  | NAC domain-containing protein 29   | 3.0           | 0.012    | Cell proliferation                     |
| <b>TRANSCRIPTION &amp; TRANSLATION &amp; HISTONES (22)</b>  |  |               |          |  |
| P02494  | Translation initiation factor 3g   | 2.7           | 0.036    | Translation                            |
| P01687 (30DAP)  | Translation initiation factor  | 2.2           | 0.008    | Translation                            |
| P00844  | Elongation factor EF-2   | 2.1           | 0.039    | Translation                            |
| P01682  | Methionyl-tRNA synthetase  | 2.0           | 0.015    | Translation                            |
| P00741 (20,30DAP)   | Peptidyl-tRNA hydrolase  | 2.0           | 0.014    | Translation                            |
| P01518  | RNA-binding protein RNP-1  | 4.9           | 0.007    | Translation                            |
| P02000  | SNF2 domain-containing protein (helicase)                                    | 2.3           | 0.019    | Translation                            |
| P01384  | Ribosomal protein L28  | 8.1           | 0.006    | Translation                            |
| P01994  | 30S ribosomal protein S10, chloroplast                                       | 2.5           | 0.003    | Ribosomal protein                      |
| P00082  | Ribosomal protein L35, chloroplast   | 2.1           | 0.035    | Ribosomal protein                      |
| P01485  | Ribosomal protein 27a  | 2.1           | 0.028    | Ribosomal protein                      |
| P01594  | Nuclear ribonucleoprotein  | 2.5           | 0.002    | Ribosomal protein                      |
| P01571  | Nuclear ribonucleoprotein  | 2.4           | 0.029    | Ribosomal protein                      |
| P01577  | Small nuclear ribonucleoprotein  | 2.0           | 0.001    | Ribosomal protein                      |
| P01147 (25DAP)  | Transducin family protein / WD-40 repeat                                     | 2.5           | 0.003    | Pre-mRNA splicing                      |
| P02173  | Histone H2B1   | 2.1           | 0.011    | Histone                                |
| P02404  | Histone H1   | 2.0           | 0.043    | Histone                                |
| P04063  | Histone H3-K9 methyltransferase  | 2.0           | 0.017    | Histone                                |
| P02006  | Histone H2A  | 2.2           | 0.039    | Histone                                |
| P00150  | Histone H3   | 2.1           | 0.014    | Histone                                |
| P02532  | Histone H4   | 2.4           | 0.002    | Histone                                |
| P01955  | Histone H4   | 2.8           | 0.029    | Histone                                |
| <b>Upregulated, no annotation (71)</b>                      |  |               |          |  |
| <b>35 DAP down (97)</b>                                     |  |               |          |  |
| <b>Seq. ID</b>  | <b>Gene Annotation</b>   | <b>Factor</b> | <b>P</b> | <b>Function</b>                        |
| <b>PRIMARY &amp; SECONDARY METABOLISM (24)</b>              |  |               |          |  |
| PCPS17 (25DAP)  | Sucrose synthase isoform 3   | 4.9           | 0.001    | Sucrose metabolism                     |
| P04974 (30DAP)  | Fructose-bisphosphate aldolase, cytoplasm                                    | 2.4           | 0.015    | Glycolysis                             |
| P03795  | Phosphoglycerate mutase  | 2.4           | 0.003    | Glycolysis                             |
| P05105 (30DAP)  | D-3-phosphoglycerate dehydrogenase   | 2.1           | 0.020    | Glycolysis                             |
| P03214 (30DAP)  | Invertase/pectin methylesterase inhibitor                                    | 8.7           | 0.026    | CH metabolism                          |
| P05197  | ADP-glucose pyrophosphorylase, small su                                      | 4.2           | 0.016    | Starch metabolism                      |
| P02602 (25DAP)  | Beta-amylase   | 2.0           | 0.026    | Starch metabolism                      |
| P04822 (25,30DAP)   | Glycosyl transferase (Galactinol synthase)                                   | 2.7           | 0.002    | Raffinose sugar metabolism             |
| P03631 (25,30DAP)   | UDP-glucuronosyl/UDP-glucosyltransferase                                     | 2.1           | 0.008    | Glucosyltransferase                    |
| P02222  | Inositol monophosphatase   | 3.1           | 0.025    | Inositol metabolism                    |
| P04337  | 6-phosphogluconate dehydrogenase, plastid                                    | 2.0           | 0.013    | Pentose-P cycle                        |
| P00518 (25DAP)  | Glutamine synthetase, GS1, cytosolic   | 2.0           | 0.039    | Amino acid metabolism                  |
| P02864 (30DAP)  | Glutamine synthetase, GS1, cytosolic   | 2.0           | 0.015    | Amino acid metabolism                  |
| P04556  | Serine-glyoxylate aminotransferase   | 2.5           | 0.038    | Transamination                         |
| P04838 (25DAP)  | Extradial ring-cleavage dioxygenase, class III enzyme                        | 2.2           | 0.002    | Aromatic compound metabolism           |
| P01058 (25,30DAP)   | Adenosine deaminase  | 2.2           | 0.043    | Purine metabolism                      |
| P00512 (30DAP)  | NADPH-cytochrome p450 reductase  | 2.2           | 0.044    | NADH oxidation                         |
| P04410 (30DAP)  | Purine/pyrimidine phosphoribosyl transferase, chloroplast                    | 2.3           | 0.047    | Nucleotide metabolism                  |
| P04705  | Dihydropyrimidinase  | 2.2           | 0.026    | Nucleotide metabolism                  |
| P02503 (30DAP)  | 3-ketoacyl-CoA synthase 10 (Fiddlehead-like protein)                         | 2.1           | 0.007    | FA metabolism                          |
| P03506 (30DAP)  | Enoyl-CoA hydratase/isomerase  | 2.7           | 0.004    | FA metabolism                          |
| P01842  | Cytochrome b5  | 2.4           | 0.045    | FA metabolism                          |
| P04840  | Cytochrome b5  | 2.4           | 0.018    | FA metabolism                          |
| P03786 (25,30DAP)   | Alkaline phytoceramidase   | 2.0           | 0.008    | FA metabolism                          |
| <b>TRANSPORT (6)</b>  |  |               |          |  |
| P05161 (30DAP)  | Mitochondrial matrix protein frataxin, involved in Fe/S protein biosynthesis | 2.7           | 0.012    | Mitochondrial translocator             |
| P04487  | Dicarboxylate/tricarboxylate carrier, mitochondrial                          | 2.5           | 0.017    | Mitochondrial translocator             |
| P04460  | 36 kDa outer mitochondrial membrane protein porin (POM 36)                   | 2.1           | 0.007    | Mitochondrial translocator             |
| P03557  | Vacuolar H+-transporting two-sector ATPase                                   | 2.1           | 0.012    | H+-Transport                           |
| P04982 (25,30DAP)   | Aquaporin, PIP-type 7a, turgor-responsive                                    | 2.1           | 0.007    | Water transport                        |
| P03782 (25DAP)  | K+ channel beta chain KB1  | 2.0           | 0.001    | K+-transport                           |
| <b>ENDOMEMBRANE TRANSPORT &amp; PROTEIN PROCESSING (13)</b> |  |               |          |  |
| P03208 (20DAP)  | Legumain   | 2.4           | 0.020    | Storage protein processing             |
| P04764 (25,30DAP)   | Chaperone HSC71.0, DnaK  | 3.3           | 0.005    | Chaperone                              |
| P04986  | Chaperone multifunctional (14-3-3 family)                                    | 2.2           | 0.005    | Chaperone                              |
| P05151  | ADP-ribosylation factor GTP binding protein)                                 | 2.2           | 0.007    | Vesicle trafficking                    |
| P04646  | GTP-binding protein, ras-like  | 2.0           | 0.008    | Vesicle trafficking                    |
| P00159  | EMB2001 (EMBRYO DEFECTIVE 2001); GTP binding                                 | 2.1           | 0.002    | Vesicle trafficking                    |
| P01402  | Sec23/sec24 transport family protein   | 4.6           | 0.006    | Vesicle trafficking                    |
| P03666 (30DAP)  | Nonaspanin (TM9SF)   | 3.1           | 0.005    | Vesicle trafficking                    |
| P05035 (25DAP)  | Microtubule-associated protein   | 2.5           | 0.009    | Vesicle trafficking                    |
| P04656  | Protein disulfide-isomerase A6 (ER)  | 2.1           | 0.009    | Protein processing                     |
| P04414  | Peptidyl-prolyl isomerase FKBP12   | 2.4           | 0.015    | Protein trafficking                    |
| P00059  | Peptidyl-prolyl cis-trans isomerase  | 2.3           | 0.009    | Protein trafficking                    |
| P04242 (30DAP)  | Peptidyl-prolyl cis-trans isomerase  | 2.0           | 0.003    | Protein trafficking                    |
| <b>REGULATED PROTEIN DEGRADATION (14)</b>                   |  |               |          |  |
| P03205  | Ubiquitin-conjugating enzyme, E2   | 2.8           | 0.027    | Ubiquitin mediated protein degradation |
| P04345  | Ubiquitin-conjugating enzyme, E2   | 2.5           | 0.032    | Ubiquitin mediated protein degradation |
| P00977  | Ubiquitin-protein ligase   | 2.1           | 0.025    | Ubiquitin mediated protein degradation |
| P01398  | Ubiquitin  | 2.6           | 0.027    | Ubiquitin mediated protein degradation |
| P03935  | Skp1 (U3 ubiquitin ligase su)  | 2.5           | 0.010    | Ubiquitin mediated protein degradation |
| P02453 (20,25,30DAP)  | Serine carboxypeptidase 1  | 3.0           | 0.020    | Proteinase                             |
| P02708 (25,30DAP)   | Prolyl Oligopeptidase  | 2.6           | 0.032    | Proteinase                             |
| P01932 (30DAP)  | Ubiquitin-protein ligase/ zinc ion binding                                   | 2.5           | 0.049    | Ubiquitin mediated protein degradation |
| P01451 (25DAP)  | Cullin 3B  | 2.3           | 0.040    | Ubiquitin mediated protein degradation |
| P02115  | Aspartic protease  | 2.1           | 0.048    | Proteinase                             |
| P03124 (25DAP)  | 20S core proteasome subunit alpha 2  | 2.0           | 0.049    | Ubiquitin mediated protein degradation |
| P03922  | Aminoacylproline aminopeptidase  | 2.0           | 0.001    | Proteinase                             |
| P02732  | 26S proteasome regulatory subunit  | 1.9           | 0.003    | Ubiquitin mediated protein degradation |
| P03243 (25,30DAP)   | Ubiquitin-conjugating enzyme E2  | 3.0           | 0.007    | Ubiquitin mediated protein degradation |
| <b>CELL PROLIFERATION (2)</b>                               |  |               |          |  |
| P05156  | Actin-depolymerizing factor 2 (ADF 2).                                       | 2.5           | 0.015    | Cell proliferation                     |
| P04743  | Actin-depolymerizing factor 2 (ADF 2).                                       | 2.1           | 0.025    | Cell proliferation                     |

| <b>STORAGE RELATED (4)</b>                                 |   |      |       |                           |
|--|---|------|-------|---------------------------|
| P04996   | Legumin B   | 4.6  | 0.001 | Storage protein           |
| P04995   | Legumin K   | 3.4  | 0.015 | Storage protein           |
| PCPS13 (20DAP)   | Legumin B   | 2.2  | 0.006 | Storage protein           |
| P05134   | ABA-induced guard cell protein (LEA-like)                         | 7.2  | 0.010 | LEA protein               |
| <b>DISEASE &amp; STRESS TOLERANCE (9)</b>                  |   |      |       |                           |
| P04644   | Disease resistance response protein 206-d                         | 7.5  | 0.001 | Pathogen response         |
| P05016 (30DAP)   | Plant lipid transfer/seed storage/Trypsin-alpha amylase inhibitor | 5.6  | 0.007 | Pathogen response         |
| P01528 (30DAP)   | Plant lipid transfer/seed storage/Trypsin-alpha amylase inhibitor | 2.1  | 0.000 | Pathogen response         |
| P00684 (30DAP)   | NADP-dependent oxidoreductase P1                                  | 2.1  | 0.011 | NADH oxidation            |
| P00638 (25,30DAP)  | Trypsin/chymotrypsin inhibitor                                    | 2.2  | 0.008 | Pathogen response         |
| P04250 (25,30DAP)  | Pathogenesis-related protein 17                                   | 5.4  | 0.000 | Pathogen response         |
| P04569 (30DAP)   | Glycoside hydrolase, chitinase                                    | 2.8  | 0.010 | Pathogen response         |
| P04867 (25DAP)   | Superoxide dismutase  | 3.4  | 0.007 | Detoxification            |
| P02585   | Metallothioneine  | 2.8  | 0.000 | Detoxification            |
| <b>SIGNALING &amp; HORMONAL FUNCTIONS (7)</b>              |   |      |       |                           |
| P02114   | Two-component response regulator ARR5                             | 10.6 | 0.045 | CK functions              |
| P04812   | DELLA protein GAI   | 2.4  | 0.003 | Repressor of GA functions |
| P04341   | Short-chain alcohol dehydrogenase                                 | 3.4  | 0.030 | SDR family                |
| P04599 (30DAP)   | LEC1, transcription factor  | 2.1  | 0.036 | Transcription factor      |
| P02886   | Protein kinase  | 2.3  | 0.034 | Protein kinase            |
| P05090   | Protein phosphatase   | 2.2  | 0.007 | Protein kinase            |
| P01646 (30DAP)   | Protein-tyrosine-phosphatase                                      | 2.1  | 0.026 | Protein kinase            |
| <b>PHOTOSYTHESIS (2)</b>                                   |   |      |       |                           |
| P04559 (25DAP)   | Photosystem II protein PsbX                                       | 2.0  | 0.006 | Photosynthesis            |
| P05191 (30DAP)   | Thylakoid membrane phosphoprotein 14 kDa                          | 2.4  | 0.004 | Photosynthesis            |
| <b>TRANSCRIPTION &amp; TRANSLATION &amp; HISTONES (16)</b> |   |      |       |                           |
| P03634   | Transcription elongation factor                                   | 2.2  | 0.002 | Transcription             |
| P03465   | DNA-directed RNA polymerase Iib                                   | 2.0  | 0.009 | Transcription             |
| P04251   | Elongation factor 1-alpha   | 3.0  | 0.023 | Translation               |
| P04154   | Elongation factor G, chloroplast                                  | 2.9  | 0.030 | Translation               |
| P04741   | Translation elongation factor 2                                   | 2.2  | 0.004 | Translation               |
| PCPS26   | Translation elongation factor EF-1                                | 2.4  | 0.002 | Translation               |
| P04453   | Translation elongation factor 2                                   | 2.1  | 0.020 | Translation               |
| P04886   | Translation initiation factor SU11                                | 2.1  | 0.002 | Translation               |
| P01397   | Translation initiation factor 5A-4                                | 2.0  | 0.019 | Translation               |
| P04844   | Ribonuclease (translational inhibitor)                            | 2.1  | 0.015 | Translation               |
| P00042   | Ribosomal protein L25   | 3.1  | 0.019 | Ribosomal protein         |
| P04315   | Ribosomal protein S27E  | 2.6  | 0.001 | Ribosomal protein         |
| P03181   | 40S ribosomal protein S25   | 2.5  | 0.029 | Ribosomal protein         |
| P04248   | Ribosomal protein L17, cytosolic                                  | 2.0  | 0.004 | Ribosomal protein         |
| P04201   | 40S ribosomal protein S15a-1                                      | 2.2  | 0.008 | Ribosomal protein         |
| P04291   | Ribosomal protein S13, cytosolic                                  | 2.0  | 0.007 | Ribosomal protein         |
| <b>Downregulated, no annotation (60)</b>                   |   |      |       |                           |