

**Table S1.** Differentially expressed genes. Gene information and annotations are as described in Rigault et al. 2011. Fold change is based on ratios between R and N-R

**A. Genes preferentially expressed in R Trees**

| Clone       | White spruce<br>gene ID | GenBank<br>accession no | Protein families (Pfam release 27)<br>Pfam accession | Pfam description                                   | Annotation of most similar Arabidopsis sequence (Tair v. 10)<br>TAIR accession | TAIR description                                     | Fold<br>change | Adjusted p-<br>value |
|-------------|-------------------------|-------------------------|--|--|--|--|----------------|----------------------|
| GQ03511_F06 | GQ03511_F06             | BT114253                | PF00232.13   | Glycosyl hydrolase family 1                        | AT1G26560.1  | beta glucosidase 40                                  | 773.35         | 3.80E-11             |
| WS0046_N09  | NA                      | BT114253                | PF00232.13   | Glycosyl hydrolase family 1                        | AT1G26560.1  | beta glucosidase 40                                  | 92.50          | 2.77E-04             |
| GQ03123_M16 | GQ03123_M16             | BT108582                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 23.13          | 8.43E-03             |
| GQ03235_M14 | GQ03235_M14             | BT111304                | PF05918.6  | Apoptosis inhibitory protein 5 (API5)              | AT5G13390.1  | no exine formation 1                                 | 14.78          | 3.50E-02             |
| WS0323_L22  | WS0323_L22              | DR554713                | PF04191.8;PF02544.11                                 | Phospholipid methyltransferase;3-oxo-5- $\alpha$ - | AT5G16010.1  | 3-oxo-5- $\alpha$ -steroid 4-dehydrogenase family pr | 14.62          | 2.93E-02             |
| GQ03816_N15 | GQ03816_N15             | BT117306                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 12.86          | 1.07E-02             |
| GQ02014_P22 | GQ02014_P22             | CO485936                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 11.95          | 7.37E-03             |
| GQ03203_P07 | GQ03203_P07             | BT109036                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 10.73          | 6.86E-05             |
| GQ0204_F12  | GQ0204_F12              | BT102979                | PF03181.10   | BURP domain  | AT5G25610.1  | BURP domain-containing protein                       | 10.07          | 3.70E-02             |
| GQ03101_L02 | GQ03101_L02             | BT107001                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 9.50           | 4.47E-03             |
| WS0294_C22  | NA                      | BT102516                | PF00955.16   | HCO3- transporter family                           | AT3G62270.1  | HCO3- transporter family                             | 9.35           | 1.41E-03             |
| GQ0254_P20  | GQ0254_P20              | DV990798                | PF13504.1;PF00560.28                                 | Leucine rich repeat;Leucine Rich Repeat            | AT1G69550.1  | disease resistance protein (TIR-NBS-LRR class)       | 9.26           | 6.86E-05             |
| WS03814_P16 | NA                      | none                    | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 8.85           | 4.85E-02             |
| GQ0184_A05  | GQ0184_A05              | BT102376                | PF13561.1;PF08659.5;PF01073.14;PF001010              | Enoyl-(Acyl carrier protein) reductase;KR dc       | AT3G51680.1  | NAD(P)-binding Rossmann-fold superfamily prote       | 8.58           | 8.08E-03             |
| WS0054_L09  | WS0054_L09              | CO232690                | No significant sequence similarity found             | No significant sequence similarity found           | AT5G13390.1  | no exine formation 1                                 | 8.49           | 2.29E-03             |
| GQ03227_D21 | GQ03227_D21             | BT110739                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 7.57           | 6.86E-05             |
| WS02633_F17 | WS02633_F17             | DR565469                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 7.28           | 7.37E-03             |
| GQ0063_N06  | GQ0063_N06              | BT101013                | PF07714.12;PF00069.20                                | Protein tyrosine kinase;Protein kinase doma        | AT1G67000.1  | Protein kinase superfamily protein                   | 6.19           | 4.55E-03             |
| WS01036_J22 | NA                      | BT119131                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 6.15           | 1.28E-03             |
| GQ04108_B13 | GQ04108_B13             | BT119634                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 5.79           | 4.29E-04             |
| GQ03325_I19 | GQ03325_I19             | BT113093                | PF00891.13   | O-methyltransferase                                | AT5G54160.1  | O-methyltransferase 1                                | 5.64           | 3.44E-02             |
| GQ03516_E18 | GQ03516_E18             | BT114526                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 4.87           | 6.86E-05             |
| GQ03615_I02 | GQ03615_I02             | BT115391                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 4.60           | 8.58E-03             |
| GQ02829_O12 | GQ02829_O12             | BT105904                | PF00560.28   | Leucine Rich Repeat                                | No significant sequence similarity found                                       | No significant sequence similarity found             | 4.40           | 7.37E-03             |
| GQ03114_N23 | GQ03114_N23             | BT107945                | PF13855.1;PF13516.1;PF13504.1;PF12799                | Leucine rich repeat;Leucine Rich repeat;Leu        | AT2G34930.1  | disease resistance family protein / LRR family prc   | 4.39           | 8.58E-03             |
| WS0102_I24  | NA                      | BT105362                | No significant sequence similarity found             | No significant sequence similarity found           | AT5G13390.1  | no exine formation 1                                 | 4.05           | 1.09E-02             |
| WS00731_A19 | WS00731_A19             | DR572109                | No significant sequence similarity found             | No significant sequence similarity found           | AT3G02080.1  | Ribosomal protein S19e family protein                | 3.95           | 4.85E-02             |
| GQ02801_N16 | GQ02801_N16             | BT103797                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 3.79           | 1.28E-03             |
| WS02912_I05 | NA                      | BT112497                | PF00940.14   | DNA-dependent RNA polymerase                       | AT1G68990.2  | male gametophyte defective 3                         | 3.78           | 1.38E-03             |
| GQ02819_P21 | GQ02819_P21             | BT103797                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 3.78           | 5.03E-04             |
| GQ03229_P15 | GQ03229_P15             | EX374262                | PF04570.9;PF03936.11                                 | Protein of unknown function (DUF581);Terp          | AT1G48800.1  | Terpenoid cyclases/Protein prenyltransferases su     | 3.76           | 3.58E-02             |
| WS01048_N06 | NA                      | BT106380                | PF13847.1;PF13659.1;PF13649.1;PF13489                | Methyltransferase domain;Methyltransferase         | AT1G64970.1  | gamma-tocopherol methyltransferase                   | 3.67           | 3.44E-02             |
| GQ03809_B11 | GQ03809_B11             | BT116905                | PF00069.20;PF07714.12                                | Protein kinase domain;Protein tyrosine kina        | AT5G48740.1  | Leucine-rich repeat protein kinase family protein    | 3.66           | 8.58E-03             |
| WS0269_K02  | WS0269_K02              | DR566995                | PF01061.19   | ABC-2 type transporter                             | AT1G66950.1  | pleiotropic drug resistance 11                       | 3.48           | 1.42E-05             |
| WS0322_H02  | WS0322_H02              | DR551147                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 3.45           | 1.44E-02             |
| WS00729_K12 | WS00729_K12             | DR571624                | PF00891.13   | O-methyltransferase                                | AT1G63140.2  | O-methyltransferase family protein                   | 3.39           | 1.40E-02             |
| GQ0165_G03  | GQ0165_G03              | BT102062                | PF07714.12;PF00069.20                                | Protein tyrosine kinase;Protein kinase doma        | AT2G19130.1  | S-locus lectin protein kinase family protein         | 3.28           | 8.44E-06             |
| GQ03411_N02 | GQ02829_L16             | BT105885                | PF14200.1  | Ricin-type beta-trefoil lectin domain-like         | AT2G39050.1  | hydroxyproline-rich glycoprotein family protein      | 3.20           | 1.05E-02             |
| GQ03324_O07 | GQ03324_O07             | BT113047                | PF07714.12;PF00069.20                                | Protein tyrosine kinase;Protein kinase doma        | AT5G48740.1  | Leucine-rich repeat protein kinase family protein    | 3.14           | 1.31E-02             |
| WS0271_D12  | NA                      | EF083454                | PF01077  | Nitrite and sulphite reductase 4Fe-4S doma         | AT2G15620  | nitrite reductase 1                                  | 3.03           | 2.36E-02             |
| GQ0025_G19  | GQ0025_G19              | GE472399                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 2.99           | 8.58E-03             |
| GQ0067_E14  | GQ0067_E14              | BT101094                | PF14368.1  | Probable lipid transfer                            | No significant sequence similarity found                                       | No significant sequence similarity found             | 2.96           | 3.37E-02             |
| GQ04010_H23 | GQ04010_H23             | BT118810                | PF00903.20;PF12681.2                                 | Glyoxalase/Bleomycin resistance protein/Dic        | AT1G80160.1  | Lactoylglutathione lyase / glyoxalase I family prot  | 2.96           | 1.97E-02             |
| GQ03231_L06 | GQ03231_L06             | BT111038                | PF01722.13   | BoIA-like protein                                  | AT5G09830.1  | BoIA-like family protein                             | 2.95           | 2.54E-03             |
| GQ0224_F08  | GQ0224_F08              | BT103290                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 2.89           | 2.36E-02             |
| GQ03702_F21 | GQ03702_F21             | BT111641                | PF04749.12   | PLAC8 family                                       | AT5G35525.1  | PLAC8 family protein                                 | 2.88           | 4.24E-03             |
| WS00725_O14 | WS00725_O14             | CO239495                | PF12695.2;PF07859.8                                  | Alpha/beta hydrolase family;alpha/beta hydr        | AT5G06570.1  | alpha/beta-Hydrolases superfamily protein            | 2.88           | 1.30E-02             |
| GQ03503_H18 | GQ03503_H18             | BT113872                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 2.84           | 1.80E-03             |
| GQ02806_L23 | GQ02806_L23             | EX313805                | No significant sequence similarity found             | No significant sequence similarity found           | AT2G24762.1  | glutamine dumper 4                                   | 2.79           | 2.82E-03             |
| GQ03203_I02 | GQ03606_P20             | BT115003                | PF00027.24;PF00520.26;PF07885.11;PF11                | Cyclic nucleotide-binding domain;Ion transp        | AT4G22200.1  | potassium transport 2/3                              | 2.76           | 2.97E-02             |
| GQ02817_H15 | GQ02817_H15             | BT104993                | PF14543.1;PF14541.1;PF00026.18                       | Xylanase inhibitor N-terminal;Xylanase inhib       | AT1G05840.1  | Eukaryotic aspartyl protease family protein          | 2.70           | 5.18E-03             |
| GQ03224_L18 | GQ03224_L18             | BT110637                | PF09713.5  | Plant protein 1589 of unknown function (A_1        | AT3G55240.1  | Plant protein 1589 of unknown function               | 2.69           | 9.64E-03             |
| WS00746_O02 | WS00746_O02             | DR577653                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 2.57           | 3.70E-02             |
| GQ04101_L12 | GQ04101_L12             | BT119131                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 2.57           | 5.18E-03             |
| GQ03415_H10 | GQ03415_H10             | BT112841                | PF13504.1  | Leucine rich repeat                                | AT5G44510.1  | target of AVR8 operation1                            | 2.57           | 8.08E-03             |
| GQ03239_H15 | GQ03239_H15             | BT111562                | PF13460.1;PF07993.7;PF05368.8;PF02719                | NADH(P)-binding;Male sterility protein;Nmr         | AT1G68540.1  | NAD(P)-binding Rossmann-fold superfamily prote       | 2.56           | 1.37E-03             |
| GQ03901_I04 | GQ03901_I04             | BT117487                | No significant sequence similarity found             | No significant sequence similarity found           | AT2G16070.2  | plastid division2                                    | 2.54           | 8.43E-03             |
| GQ0134_I08  | GQ0134_I08              | CO477838                | PF06830.6  | Root cap   | AT3G19430.1  | late embryogenesis abundant protein-related / LE     | 2.52           | 1.38E-03             |
| GQ03816_H16 | GQ03816_H16             | BT102516                | PF00955.16   | HCO3- transporter family                           | AT3G62270.1  | HCO3- transporter family                             | 2.47           | 4.42E-02             |
| WS0071_E21  | WS0071_E21              | CO236991                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 2.42           | 2.63E-02             |
| GQ03916_O21 | GQ03916_O21             | EX434729                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 2.41           | 2.57E-02             |
| WS0268_P14  | WS0268_P14              | DR566763                | No significant sequence similarity found             | No significant sequence similarity found           | No significant sequence similarity found                                       | No significant sequence similarity found             | 2.39           | 2.72E-02             |
| WS03923_I15 | NA                      | DR586559                | PF00560.28;PF13504.1;PF13855.1                       | Leucine Rich Repeat;Leucine rich repeat;Le         | AT1G69550.1  | disease resistance protein (TIR-NBS-LRR class)       | 2.35           | 8.08E-03             |
| WS01049_K03 | NA                      | BT116840                | PF01596.12;PF13578.1                                 | O-methyltransferase;Methyltransferase dom          | AT4G26220.1  | S-adenosyl-L-methionine-dependent methyltransl       | 2.34           | 8.58E-03             |
| WS02717_L22 | NA                      | BT109614                | PF02668.11   | Taurine catabolism dioxygenase TauD, Tfd           | AT3G21360.1  | 2-oxoglutarate (2OG) and Fe(II)-dependent oxyg       | 2.33           | 2.49E-02             |
| WS04210_O18 | NA                      | GE479334                | PF13855.1;PF13504.1;PF12799.2;PF00560                | Leucine rich repeat;Leucine rich repeat;Leu        | AT1G69550.1  | disease resistance protein (TIR-NBS-LRR class)       | 2.32           | 1.61E-04             |

|             |             |          |  |   |  |   |      |          |
|-------------|-------------|----------|--|---|--|---|------|----------|
| GQ02815_I04 | GQ02815_I04 | BT104822 | No significant sequence similarity found | No significant sequence similarity found      | AT1G21600.1                              | plastid transcriptionally active 6                  | 2.29 | 2.29E-02 |
| WS02745_I16 | NA          | CO234896 | PF02535.17                               | ZIP Zinc transporter                          | AT5G59520.1                              | ZRT/IRT-like protein 2                              | 2.27 | 2.82E-03 |
| GQ03513_L09 | GQ03513_L09 | BT114389 | PF02133.10                               | Permease for cytosine/purines, uracil, thiam  | AT5G03555.1                              | permease, cytosine/purines, uracil, thiamine, alla  | 2.21 | 8.61E-03 |
| GQ03518_O02 | GQ03518_O02 | EX407521 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 2.21 | 3.73E-03 |
| GQ03219_D07 | GQ03219_D07 | BT110285 | PF13450.1;PF01266.19                     | NAD(P)-binding Rossmann-like domain;FAC       | AT2G24580.1                              | FAD-dependent oxidoreductase family protein         | 2.20 | 1.90E-02 |
| WS0343_O05  | WS0343_O05  | DR587036 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 2.16 | 3.36E-02 |
| GQ03224_L02 | GQ03224_L02 | BT110632 | PF08241.7                                | Methyltransferase domain                      | AT4G22530.1                              | S-adenosyl-L-methionine-dependent methyltransf      | 2.14 | 1.56E-02 |
| WS0263_B14  | WS0263_B14  | CO234896 | PF02535.17                               | ZIP Zinc transporter                          | AT5G59520.1                              | ZRT/IRT-like protein 2                              | 2.14 | 1.28E-03 |
| GQ0073_O14  | GQ0073_O14  | BT101220 | PF12697.2;PF12695.2;PF00561.15           | Alpha/beta hydrolase family;Alpha/beta hydr   | AT1G26360.1                              | methyl esterase 13                                  | 2.11 | 4.88E-02 |
| GQ03409_D03 | GQ03409_D03 | BT113455 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 2.10 | 1.90E-02 |
| WS00819_E21 | WS00819_E21 | CO253371 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 2.08 | 9.72E-03 |
| GQ0065_L03  | GQ0065_L03  | BT101047 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 2.08 | 2.26E-02 |
| GQ03317_B01 | GQ03317_B01 | BT112539 | PF05056.7                                | Protein of unknown function (DUF674)          | AT5G43240.1                              | Protein of unknown function (DUF674)                | 2.07 | 3.34E-02 |
| GQ00611_H18 | GQ00611_H18 | BT100935 | PF13456.1                                | Reverse transcriptase-like                    | No significant sequence similarity found | No significant sequence similarity found            | 2.07 | 2.95E-02 |
| GQ03228_K23 | GQ03228_K23 | BT110841 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 2.05 | 6.34E-03 |
| GQ03519_C08 | GQ03519_C08 | BT114673 | PF00107.21                               | Zinc-binding dehydrogenase                    | AT5G43940.2                              | GroES-like zinc-binding dehydrogenase family pr     | 2.04 | 1.51E-02 |
| GQ03507_I24 | GQ03507_I24 | BT114071 | PF08240.7;PF00107.21                     | Alcohol dehydrogenase GroES-like domain;      | AT5G43940.2                              | GroES-like zinc-binding dehydrogenase family pr     | 2.02 | 1.58E-02 |
| GQ04107_M22 | GQ04107_M22 | BT119613 | PF05834.7;PF01494.14;PF00070.22          | Lycopene cyclase protein;FAD binding dom      | AT4G38540.1                              | FAD/NAD(P)-binding oxidoreductase family prote      | 2.01 | 8.32E-03 |
| GQ03239_O14 | GQ03239_O14 | BT111585 | PF00082.17                               | Subtilase family                              | AT1G32940.1                              | Subtilase family protein                            | 2.01 | 2.55E-03 |
| GQ02908_P19 | GQ02908_P19 | EX335170 | PF04765.8                                | Protein of unknown function (DUF616)          | AT5G46220.1                              | Protein of unknown function (DUF616)                | 2.00 | 1.68E-02 |
| GQ03819_G05 | GQ03819_G05 | BT117432 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.99 | 3.77E-02 |
| WS04223_D09 | NA          | DR556040 | PF01357.16;PF03330.13                    | Pollen allergen;Rare lipoprotein A (RlpA)-lik | AT3G55500.1                              | expansin A16  | 1.99 | 8.05E-04 |
| GQ03606_F03 | GQ03606_F03 | BT114973 | PF13417.1;PF13410.1;PF13409.1;PF02798    | Glutathione S-transferase, N-terminal doma    | AT1G78320.1                              | glutathione S-transferase TAU 23                    | 1.99 | 1.85E-03 |
| GQ02808_D22 | GQ02808_D22 | BT104251 | PF14595.1;PF13905.1;PF13098.1;PF00085    | Thioredoxin;Thioredoxin-like;Thioredoxin-lik  | AT3G08710.1                              | thioredoxin H-type 9                                | 1.98 | 1.51E-02 |
| GQ03233_M04 | GQ03233_M04 | BT111167 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.97 | 5.57E-02 |
| GQ02904_F23 | GQ04009_E16 | BT118700 | PF00505.14;PF09011.5                     | HMG (high mobility group) box;HMG-box do      | AT2G34450.2                              | HMG-box (high mobility group) DNA-binding fami      | 1.97 | 2.82E-03 |
| GQ03817_H04 | GQ03817_H04 | BT117337 | PF05978.11;PF07690.11                    | Ion channel regulatory protein UNC-93;Majo    | AT1G18000.1                              | Major facilitator superfamily protein               | 1.96 | 5.24E-03 |
| GQ03009_B07 | GQ03009_B07 | BT106719 | PF13460.1;PF05368.8;PF01370.16;PF0111    | NADH(P)-binding;Nmra-like family;NAD dep      | AT4G39230.1                              | Nmra-like negative transcriptional regulator fami   | 1.95 | 1.46E-02 |
| GQ03711_E11 | GQ03711_E11 | BT116062 | PF13504.1;PF08263.7;PF00560.28           | Leucine rich repeat;Leucine rich repeat N-te  | AT5G66330.1                              | Leucine-rich repeat (LRR) family protein            | 1.94 | 2.35E-02 |
| GQ03308_H11 | GQ03308_H11 | BT111981 | No significant sequence similarity found | No significant sequence similarity found      | AT3G28050.1                              | nodulin MN21 /EamA-like transporter family prot     | 1.93 | 2.57E-02 |
| WS0404_G24  | NA          | BT113456 | PF00274.14                               | Fructose-bisphosphate aldolase class-I        | AT2G36460.1                              | Aldolase superfamily protein                        | 1.92 | 3.83E-02 |
| WS02617_I14 | WS02617_I14 | DR559695 | PF00560.28                               | Leucine Rich Repeat                           | No significant sequence similarity found | No significant sequence similarity found            | 1.92 | 4.47E-03 |
| GQ03606_D15 | GQ03606_D15 | BT114966 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.92 | 2.15E-02 |
| GQ03902_N15 | GQ03902_N15 | BT117545 | PF00149.23;PF14008.1                     | Calcineurin-like phosphoesterase;Iron/zinc    | AT3G52820.1                              | purple acid phosphatase 22                          | 1.91 | 3.53E-02 |
| WS03216_K05 | WS03216_K05 | DR549850 | PF12481.3;PF13522.1;PF13537.1            | Aluminium induced protein;Glutamine amid      | AT5G43830.1                              | Aluminium induced protein with YGL and LRDR r       | 1.91 | 4.75E-03 |
| WS0105_F06  | NA          | CO218828 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.91 | 2.00E-02 |
| WS02719_L03 | NA          | EF085274 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.90 | 7.92E-03 |
| GQ03321_I12 | GQ03321_I12 | BT112832 | PF05129.8                                | Transcription elongation factor Elf1 like     | AT5G46030.1                              | unknown protein@ CONTAINS InterPro DOMAIN           | 1.89 | 2.15E-02 |
| GQ03239_D19 | GQ03239_D19 | BT111546 | PF00125.19                               | Core histone H2A/H2B/H3/H4                    | AT5G22880.1                              | histone B2  | 1.88 | 1.30E-02 |
| WS00824_H12 | WS00824_H12 | CO255201 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.88 | 3.36E-02 |
| GQ04108_J17 | GQ04108_J17 | BT119672 | No significant sequence similarity found | No significant sequence similarity found      | AT4G30110.1                              | heavy metal atpase 2                                | 1.87 | 4.00E-02 |
| WS0347_A16  | WS0347_A16  | DR588070 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.87 | 3.10E-02 |
| GQ03239_I03 | GQ03239_I03 | BT111564 | PF00578.16;PF08534.5                     | AhpC/TSA family;Redoxin                       | AT3G26060.2                              | Thioredoxin superfamily protein                     | 1.86 | 2.57E-02 |
| GQ03009_L20 | GQ03009_L20 | BT106748 | PF07714.12;PF00069.20                    | Protein tyrosine kinase;Protein kinase doma   | AT4G32830.1                              | ataurora1   | 1.86 | 1.33E-04 |
| WS02724_E05 | NA          | BT106742 | PF09439.5;PF08477.8;PF04670.7;PF01926    | Signal recognition particle receptor beta sut | AT3G62290.1                              | ADP-ribosylation factor A1E                         | 1.85 | 8.58E-03 |
| GQ04002_E12 | GQ04002_E12 | BT118093 | PF05804.7;PF00514.18                     | Kinesin-associated protein (KAP);Armadiolo    | AT1G27910.1                              | plant U-box 45                                      | 1.84 | 1.53E-02 |
| WS03211_C11 | WS03211_C11 | DR547895 | PF03330.13;PF01357.16                    | Rare lipoprotein A (RlpA)-like double-psi bei | AT3G55500.1                              | expansin A16  | 1.84 | 1.28E-03 |
| GQ03902_G12 | GQ03902_G12 | BT117530 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.83 | 1.90E-02 |
| WS00752_O20 | WS00752_O20 | DR579796 | No significant sequence similarity found | No significant sequence similarity found      | AT3G24240.1                              | Leucine-rich repeat receptor-like protein kinase fe | 1.83 | 2.93E-02 |
| WS02737_B22 | NA          | BT109931 | No significant sequence similarity found | No significant sequence similarity found      | AT1G23460.1                              | Pectin lyase-like superfamily protein               | 1.82 | 1.11E-02 |
| GQ03307_N13 | GQ03307_N13 | BT111934 | PF00403.21                               | Heavy-metal-associated domain                 | AT5G05365.1                              | Heavy metal transport/detoxification superfamily    | 1.82 | 4.92E-02 |
| GQ03607_J11 | GQ03607_J11 | BT115030 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.81 | 1.05E-02 |
| GQ03321_A06 | GQ03321_A06 | BT112790 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.81 | 1.30E-02 |
| GQ03814_F24 | GQ03814_F24 | BT117173 | PF00931.17                               | NB-ARC domain                                 | AT3G50950.2                              | HOPZ-ACTIVATED RESISTANCE 1                         | 1.81 | 2.63E-02 |
| GQ02825_A02 | GQ02825_A02 | BT102004 | PF00011.16                               | Hsp20/alpha crystallin family                 | AT5G51440.1                              | HSP20-like chaperones superfamily protein           | 1.79 | 8.25E-04 |
| GQ03811_M11 | GQ03811_M11 | BT117048 | PF03035.14                               | Lipoxygenase                                  | AT3G22400.1                              | PLAT/LH2 domain-containing lipoxygenase fami        | 1.79 | 4.43E-03 |
| GQ03009_L20 | GQ03009_L20 | BT106748 | PF07714.12;PF00069.20                    | Protein tyrosine kinase;Protein kinase doma   | AT4G32830.1                              | ataurora1   | 1.78 | 6.61E-03 |
| GQ03512_D14 | GQ03512_D14 | BT114305 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.78 | 1.82E-02 |
| GQ02811_E24 | GQ02811_E24 | BT104512 | PF00931.17                               | NB-ARC domain                                 | AT5G17680.1                              | disease resistance protein (TIR-NBS-LRR class),     | 1.77 | 2.82E-03 |
| GQ04009_J23 | GQ04009_J23 | BT118727 | PF00270.24;PF00271.26                    | DEAD/DEAH box helicase;Helicase conserv       | AT5G19210.2                              | P-loop containing nucleoside triphosphate hydroly   | 1.76 | 7.71E-03 |
| WS00842_A10 | WS00842_A10 | DR594851 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.76 | 1.67E-03 |
| WS00829_C02 | WS00829_C02 | DR590634 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.76 | 1.07E-02 |
| WS01016_C17 | NA          | BT118505 | PF01494.14                               | FAD binding domain                            | AT4G38540.1                              | FAD/NAD(P)-binding oxidoreductase family prote      | 1.75 | 1.56E-02 |
| GQ03308_J03 | GQ03308_J03 | BT111995 | PF14379.1;PF00249.26                     | MYB-CC type transfactor, LHEQLE motif;M       | AT4G28610.1                              | phosphate starvation response 1                     | 1.74 | 2.82E-02 |
| GQ04008_E05 | GQ04008_E05 | BT118619 | PF07714.12;PF00069.20                    | Protein tyrosine kinase;Protein kinase doma   | AT5G65700.1                              | Leucine-rich receptor-like protein kinase family pr | 1.74 | 3.33E-02 |
| WS03939_A12 | NA          | DR548272 | PF13504.1;PF00560.28                     | Leucine rich repeat;Leucine Rich Repeat       | AT3G44400.1                              | Disease resistance protein (TIR-NBS-LRR class)      | 1.73 | 1.30E-02 |
| GQ03214_O21 | GQ03214_O21 | BT110014 | PF01357.16;PF03330.13                    | Pollen allergen;Rare lipoprotein A (RlpA)-lik | AT5G02610.1                              | expansin A9   | 1.73 | 1.38E-03 |
| WS02816_K10 | NA          | CO236539 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.73 | 6.61E-03 |
| GQ03504_I16 | GQ03504_I16 | BT113921 | PF01535.15;PF12854.2;PF13041.1;PF13811   | PPR repeat;PPR repeat;PPR repeat family;      | AT4G13650.1                              | Pentatricopeptide repeat (PPR) superfamily prote    | 1.72 | 4.88E-02 |
| WS03820_L20 | NA          | DR552710 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.72 | 4.69E-02 |
| GQ03712_H23 | GQ03712_H23 | BT116144 | No significant sequence similarity found | No significant sequence similarity found      | AT3G48120.1                              | unknown protein@ Has 22990 Blast hits to 1294;      | 1.71 | 3.47E-02 |

|             |             |          |  |   |  |  |      |          |
|-------------|-------------|----------|--|---|--|--|------|----------|
| GQ04113_C22 | GQ04113_C22 | BT119961 | No significant sequence similarity found | No significant sequence similarity found        | No significant sequence similarity found | No significant sequence similarity found           | 1.71 | 2.31E-02 |
| GQ03315_M15 | GQ03315_M15 | BT112471 | PF07498.7                                | Rho termination factor, N-terminal domain       | No significant sequence similarity found | No significant sequence similarity found           | 1.71 | 1.40E-02 |
| WS03811_O16 | NA          | BT104908 | PF00023.25;PF12796.2;PF13606.1;PF1363    | Ankyrin repeat;Ankyrin repeats (3 copies);A     | AT2G03430.1                              | Ankyrin repeat family protein                      | 1.70 | 6.03E-03 |
| WS01014_G18 | NA          | BT116800 | No significant sequence similarity found | No significant sequence similarity found        | AT1G28100.4                              | unknown protein@ FUNCTIONS IN: molecular_fu        | 1.70 | 4.12E-02 |
| GQ03103_L21 | GQ03103_L21 | BT107172 | No significant sequence similarity found | No significant sequence similarity found        | No significant sequence similarity found | No significant sequence similarity found           | 1.69 | 8.16E-03 |
| GQ03919_B06 | GQ03919_B06 | BT117971 | No significant sequence similarity found | No significant sequence similarity found        | No significant sequence similarity found | No significant sequence similarity found           | 1.69 | 8.78E-03 |
| GQ02905_L17 | GQ02905_L17 | BT106239 | PF01545.16                               | Cation efflux family                            | AT3G58060.1                              | Cation efflux family protein                       | 1.68 | 1.44E-02 |
| WS0023_O13  | WS0023_O13  | C0236539 | No significant sequence similarity found | No significant sequence similarity found        | No significant sequence similarity found | No significant sequence similarity found           | 1.68 | 5.18E-03 |
| GQ02828_M01 | GQ02828_M01 | BT105807 | PF01535.15;PF13041.1;PF13812.1           | PPR repeat;PPR repeat family;Pentatricope       | AT1G10910.1                              | Pentatricopeptide repeat (PPR) superfamily prote   | 1.68 | 8.58E-03 |
| WS0284_L18  | NA          | BT117620 | PF00067.17                               | Cytochrome P450                                 | AT4G36220.1                              | ferulic acid 5-hydroxylase 1                       | 1.68 | 4.12E-02 |
| GQ0044_J22  | GQ03912_J04 | BT117795 | PF06094.7                                | AIG2-like family                                | AT3G02910.1                              | AIG2-like (avirulence induced gene) family protein | 1.68 | 2.63E-02 |
| GQ0168_L24  | GQ0168_L24  | C0481073 | No significant sequence similarity found | No significant sequence similarity found        | AT5G53370.1                              | pectin methylesterase PCR fragment F               | 1.68 | 1.09E-02 |
| GQ03609_F15 | GQ03609_F15 | BT115104 | No significant sequence similarity found | No significant sequence similarity found        | No significant sequence similarity found | No significant sequence similarity found           | 1.68 | 8.58E-03 |
| GQ03808_D18 | GQ03808_D18 | BT116861 | No significant sequence similarity found | No significant sequence similarity found        | No significant sequence similarity found | No significant sequence similarity found           | 1.66 | 2.09E-02 |
| GQ03238_K02 | GQ03238_K02 | BT111504 | PF12697.2;PF05577.7                      | Alpha/beta hydrolase family;Serine carboxy      | AT5G22860.1                              | Serine carboxypeptidase S28 family protein         | 1.64 | 1.56E-02 |
| GQ0209_D21  | GQ0209_D21  | BT103234 | PF00501.23;PF13193.1                     | AMP-binding enzyme;AMP-binding enzyme           | AT3G16910.1                              | acyl-activating enzyme 7                           | 1.64 | 3.60E-02 |
| WS03711_J17 | NA          | ES250621 | No significant sequence similarity found | No significant sequence similarity found        | No significant sequence similarity found | No significant sequence similarity found           | 1.64 | 3.62E-02 |
| WS0283_L05  | NA          | BT109156 | No significant sequence similarity found | No significant sequence similarity found        | AT1G08940.1                              | Phosphoglycerate mutase family protein             | 1.63 | 4.01E-02 |
| GQ03205_K22 | GQ03205_K22 | BT109192 | No significant sequence similarity found | No significant sequence similarity found        | AT4G01050.1                              | thylakoid rhodanese-like                           | 1.62 | 1.58E-02 |
| WS02729_I16 | NA          | BT118328 | PF00582.21                               | Universal stress protein family                 | AT2G47710.1                              | Adenine nucleotide alpha hydrolases-like superfa   | 1.61 | 1.11E-02 |
| WS00738_N24 | WS00738_N24 | BT109688 | PF00646.28                               | F-box domain                                    | AT5G15710.1                              | Galactose oxidase/kelch repeat superfamily prote   | 1.61 | 4.07E-02 |
| WS00841_P06 | WS00841_P06 | DR594825 | No significant sequence similarity found | No significant sequence similarity found        | AT4G33990.1                              | Tetratricopeptide repeat (TPR)-like superfamily p  | 1.61 | 3.36E-02 |
| GQ04013_I22 | GQ04013_I22 | BT119026 | PF13920.1                                | Zinc finger, C3HC4 type (RING finger)           | AT2G21380.1                              | Kinesin motor family protein                       | 1.60 | 4.35E-02 |
| WS00837_B19 | WS00837_B19 | DR593423 | No significant sequence similarity found | No significant sequence similarity found        | AT4G20910.1                              | double-stranded RNA binding protein-related / Ds   | 1.59 | 2.44E-02 |
| WS02621_A21 | GQ03104_A09 | BT107189 | No significant sequence similarity found | No significant sequence similarity found        | No significant sequence similarity found | No significant sequence similarity found           | 1.59 | 4.12E-02 |
| GQ03321_I20 | GQ03321_I20 | BT112833 | PF03407.11                               | Nucleotide-diphospho-sugar transferase          | AT1G70630.1                              | Nucleotide-diphospho-sugar transferase family pr   | 1.59 | 1.79E-02 |
| WS0277_C06  | NA          | BT115174 | PF00657.17                               | GDLS-like Lipase/Acylhydrolase                  | AT4G01130.1                              | GDLS-like Lipase/Acylhydrolase superfamily prot    | 1.59 | 2.24E-02 |
| GQ04110_K11 | GQ04110_K11 | BT119823 | PF00166.16                               | Chaperonin 10 Kd subunit                        | AT5G20720.1                              | chaperonin 20                                      | 1.59 | 8.16E-03 |
| WS02614_N04 | WS02614_N04 | DR558714 | PF04548.11                               | AIG1 family                                     | AT1G33830.1                              | P-loop containing nucleoside triphosphate hydroli  | 1.58 | 2.67E-02 |
| GQ04008_H01 | GQ04008_H01 | BT118641 | PF00459.20                               | Inositol monophosphatase family                 | AT4G39120.1                              | myo-inositol monophosphatase like 2                | 1.58 | 3.64E-02 |
| WS03219_O18 | WS03219_O18 | DR550970 | PF00201.13                               | UDP-glucuronosyl and UDP-glucosyl transfe       | AT1G05560.1                              | UDP-glucosyltransferase 75B1                       | 1.58 | 2.14E-02 |
| GQ03102_K14 | GQ03102_K14 | BT107092 | No significant sequence similarity found | No significant sequence similarity found        | No significant sequence similarity found | No significant sequence similarity found           | 1.57 | 8.39E-03 |
| GQ03517_L16 | GQ03517_L16 | BT114600 | No significant sequence similarity found | No significant sequence similarity found        | AT2G26340.2                              | unknown protein.                                   | 1.57 | 2.28E-03 |
| WS00721_P22 | WS00721_P22 | C0238490 | PF03936.11                               | Terpene synthase family, metal binding dom      | No significant sequence similarity found | No significant sequence similarity found           | 1.57 | 6.34E-03 |
| GQ03205_O12 | GQ03205_O12 | BT109210 | PF00125.19;PF00808.18                    | Core histone H2A/H2B/H3/H4;Histone-like t       | AT1G08880.1                              | Histone superfamily protein                        | 1.55 | 1.87E-02 |
| GQ03609_O18 | GQ03609_O18 | BT100952 | No significant sequence similarity found | No significant sequence similarity found        | AT5G67130.1                              | PLC-like phosphodiesterases superfamily protein    | 1.55 | 3.44E-02 |
| GQ0192_L17  | GQ0192_L17  | GT739991 | No significant sequence similarity found | No significant sequence similarity found        | No significant sequence similarity found | No significant sequence similarity found           | 1.54 | 2.92E-02 |
| GQ03313_I07 | GQ03313_I07 | BT112328 | No significant sequence similarity found | No significant sequence similarity found        | No significant sequence similarity found | No significant sequence similarity found           | 1.54 | 8.58E-03 |
| GQ03209_G12 | GQ03209_G12 | BT109515 | No significant sequence similarity found | No significant sequence similarity found        | AT1G70570.2                              | anthranilate phosphoribosyltransferase, putative   | 1.53 | 6.34E-03 |
| GQ03320_D24 | GQ03320_D24 | BT112738 | PF09835.4                                | Uncharacterized protein conserved in bacte      | AT4G10140.1                              | unknown protein@ FUNCTIONS IN: molecular_fu        | 1.53 | 2.43E-02 |
| GQ0209_M12  | GQ0209_M12  | BT103248 | PF00067.17                               | Cytochrome P450                                 | AT5G07990.1                              | Cytochrome P450 superfamily protein                | 1.52 | 4.52E-02 |
| GQ00412_H24 | GQ00412_H24 | BT100725 | PF00005.22;PF13191.1                     | ABC transporter;AAA ATPase domain               | AT1G27940.1                              | P-glycoprotein 13                                  | 1.52 | 1.68E-02 |
| GQ0026_F21  | GQ0026_F21  | BT100579 | PF00069.20;PF07714.12                    | Protein kinase domain;Protein tyrosine kina     | AT1G51940.1                              | protein kinase family protein / peptidoglycan-bind | 1.52 | 2.82E-02 |
| GQ03604_M07 | GQ03604_M07 | BT114900 | PF01722.13                               | BolA-like protein                               | AT5G09830.1                              | BolA-like family protein                           | 1.50 | 3.65E-02 |
| GQ02808_K07 | GQ02808_K07 | BT104293 | PF00728.17;PF14845.1                     | Glycosyl hydrolase family 20, catalytic doma    | AT1G65590.1                              | beta-hexosaminidase 3                              | 1.50 | 1.46E-02 |
| GQ03214_E01 | GQ03214_E01 | BT109961 | No significant sequence similarity found | No significant sequence similarity found        | AT1G32310.1                              | unknown protein@ Has 28 Blast hits to 28 protein   | 1.50 | 3.37E-02 |
| GQ0047_L17  | GQ0047_L17  | BT100867 | No significant sequence similarity found | No significant sequence similarity found        | No significant sequence similarity found | No significant sequence similarity found           | 1.48 | 2.71E-02 |
| WS02717_D20 | NA          | BT116794 | PF00892.15                               | EamA-like transporter family                    | AT3G02690.1                              | nodulin MtN21 /EamA-like transporter family prot   | 1.48 | 1.38E-03 |
| GQ02902_M01 | GQ02902_M01 | BT106090 | No significant sequence similarity found | No significant sequence similarity found        | AT3G16850.1                              | Pectin lyase-like superfamily protein              | 1.47 | 3.13E-02 |
| GQ03101_E12 | GQ03101_E12 | BT106963 | No significant sequence similarity found | No significant sequence similarity found        | AT1G28520.1                              | vascular plant one zinc finger protein             | 1.47 | 9.35E-03 |
| GQ02902_M01 | GQ02902_M01 | BT106090 | No significant sequence similarity found | No significant sequence similarity found        | AT3G16850.1                              | Pectin lyase-like superfamily protein              | 1.47 | 1.40E-02 |
| GQ02820_P15 | GQ02820_P15 | BT105332 | PF00335.15                               | Tetraspanin family                              | AT4G28770.2                              | Tetraspanin family protein                         | 1.47 | 8.39E-03 |
| GQ03210_M14 | GQ03210_M14 | BT109624 | No significant sequence similarity found | No significant sequence similarity found        | AT2G44090.1                              | Ankyrin repeat family protein                      | 1.47 | 4.69E-02 |
| GQ0173_M21  | GQ0173_M21  | DV979231 | No significant sequence similarity found | No significant sequence similarity found        | AT4G09720.3                              | RAB GTPase homolog G3A                             | 1.46 | 4.18E-02 |
| GQ0069_B02  | GQ0069_B02  | BT101149 | PF03083.11                               | Sugar efflux transporter for intercellular excl | AT1G21460.1                              | Nodulin MtN3 family protein                        | 1.46 | 1.65E-02 |
| GQ03802_J18 | GQ03802_J18 | BT116585 | No significant sequence similarity found | No significant sequence similarity found        | AT1G15750.1                              | Transducin family protein / WD-40 repeat family    | 1.45 | 3.72E-02 |
| GQ03221_F24 | GQ03221_F24 | BT110412 | PF14416.1;PF13839.1                      | PMR5 N terminal Domain;GDLS/SGNH-like           | AT1G48880.1                              | TRICHOME BIREFRINGENCE-LIKE 7                      | 1.45 | 1.87E-02 |
| GQ03207_A13 | GQ03207_A13 | BT109314 | No significant sequence similarity found | No significant sequence similarity found        | AT4G24090.1                              | unknown protein@ FUNCTIONS IN: molecular_fu        | 1.45 | 3.07E-02 |
| GQ03221_D16 | GQ03221_D16 | BT110401 | PF13229.1                                | Right handed beta helix region                  | AT4G20050.1                              | Pectin lyase-like superfamily protein              | 1.45 | 3.58E-02 |
| GQ04109_N06 | GQ04109_N06 | BT119767 | PF00564.19                               | PB1 domain                                      | AT4G24690.1                              | ubiquitin-associated (UBA)/TS-N domain-containi    | 1.44 | 7.92E-03 |
| WS01038_L19 | NA          | DR542446 | No significant sequence similarity found | No significant sequence similarity found        | No significant sequence similarity found | No significant sequence similarity found           | 1.44 | 2.00E-02 |
| GQ03404_H18 | GQ03404_H18 | BT113305 | PF00403.21                               | Heavy-metal-associated domain                   | AT2G28660.1                              | Chloroplast-targeted copper chaperone protein      | 1.44 | 3.53E-02 |
| GQ03418_P01 | GQ03418_P01 | BT113742 | PF00575.18                               | S1 RNA binding domain                           | AT3G03710.1                              | polyribonucleotide nucleotidyltransferase, putativ | 1.44 | 1.37E-03 |
| WS0288_H01  | NA          | BT115230 | PF00069.20                               | Protein kinase domain                           | AT4G24740.1                              | FUS3-complementing gene 2                          | 1.43 | 2.62E-02 |
| WS0389_D09  | NA          | none     | No significant sequence similarity found | No significant sequence similarity found        | No significant sequence similarity found | No significant sequence similarity found           | 1.42 | 2.44E-02 |
| GQ04007_M17 | GQ04007_M17 | BT118571 | PF08547.7                                | Complex I intermediate-associated protein 2     | AT1G72420.1                              | NADH:ubiquinone oxidoreductase intermediate-a      | 1.42 | 4.95E-03 |
| GQ03205_C02 | GQ03205_C02 | BT109145 | No significant sequence similarity found | No significant sequence similarity found        | No significant sequence similarity found | No significant sequence similarity found           | 1.41 | 4.42E-02 |
| GQ04010_E15 | GQ04010_E15 | EX439329 | PF00504.16                               | Chlorophyll A-B binding protein                 | AT3G54890.1                              | photosystem I light harvesting complex gene 1      | 1.41 | 1.12E-02 |
| GQ03239_J03 | GQ03239_J03 | BT100475 | No significant sequence similarity found | No significant sequence similarity found        | No significant sequence similarity found | No significant sequence similarity found           | 1.40 | 4.42E-02 |
| GQ03518_A12 | GQ03518_A12 | BT114624 | PF00249.26                               | Myb-like DNA-binding domain                     | AT5G13820.1                              | telomeric DNA binding protein 1                    | 1.40 | 1.59E-02 |
| GQ03209_N07 | GQ03209_N07 | BT109546 | No significant sequence similarity found | No significant sequence similarity found        | AT5G44650.1                              | Encodes a nucleus-encoded thylakoid protein, co    | 1.40 | 1.44E-02 |

|             |             |          |  |   |  |  |      |          |
|-------------|-------------|----------|--|---|--|--|------|----------|
| GQ04111_B10 | GQ04111_B10 | BT119847 | PF00564.19;PF00571.23                    | PB1 domain;CBS domain                       | AT5G50640.1                              | CBS / octicosapeptide/Phox/Bemp1 (PB1) domai       | 1.40 | 7.92E-03 |
| WS0279_A14  | NA          | BT107091 | PF05042.8                                | Caleosin related protein                    | AT4G26740.1                              | seed gene 1  | 1.40 | 2.29E-02 |
| GQ04113_A22 | GQ04113_A22 | BT119953 | PF11623.3                                | Protein of unknown function (DUF3252)       | AT4G23890.1                              | unknown protein@ FUNCTIONS IN: molecular_ft        | 1.40 | 2.95E-02 |
| GQ03210_A19 | GQ03210_A19 | BT109564 | PF01553.16                               | Acyltransferase                             | AT3G18850.1                              | lysophosphatidyl acyltransferase 5                 | 1.40 | 4.22E-02 |
| GQ04103_B18 | GQ04103_B18 | BT119244 | PF00004.24;PF05496.7;PF07728.9           | ATPase family associated with various cellu | AT4G04180.1                              | P-loop containing nucleoside triphosphate hydroly  | 1.39 | 2.95E-02 |
| GQ03714_G02 | GQ03714_G02 | BT116237 | PF01485.16                               | IBR domain                                  | AT3G14250.1                              | RING/U-box superfamily protein                     | 1.39 | 7.37E-03 |
| GQ03612_C20 | GQ03612_C20 | BT115237 | PF01434.13                               | Peptidase family M41                        | AT4G23940.1                              | FtsH extracellular protease family                 | 1.39 | 3.44E-02 |
| GQ03238_F18 | GQ03238_F18 | BT111486 | PF01546.23                               | Peptidase family M20/M25/M40                | AT1G44820.1                              | Peptidase M20/M25/M40 family protein               | 1.39 | 7.92E-03 |
| GQ02817_O20 | GQ02817_O20 | BT105042 | PF10018.4                                | Vitamin-D-receptor interacting Mediator sub | AT5G02850.1                              | hydroxyproline-rich glycoprotein family protein    | 1.38 | 1.05E-02 |
| GQ03212_C12 | GQ03212_C12 | BT109764 | No significant sequence similarity found | No significant sequence similarity found    | AT2G31840.1                              | Thioredoxin superfamily protein                    | 1.38 | 2.07E-02 |
| WS00737_F13 | WS00737_F13 | DR574287 | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found           | 1.37 | 3.60E-02 |
| WS0101_I05  | NA          | BT115392 | PF01545.16                               | Cation efflux family                        | AT2G39450.1                              | Cation efflux family protein                       | 1.37 | 2.14E-02 |
| WS00740_O07 | WS00740_O07 | DR575548 | No significant sequence similarity found | No significant sequence similarity found    | AT3G53810.1                              | Concanavalin A-like lectin protein kinase family p | 1.36 | 2.82E-02 |
| GQ03418_F09 | GQ03418_F09 | BT113715 | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found           | 1.36 | 3.82E-02 |
| GQ03307_A19 | GQ03307_A19 | BT111894 | PF11493.3                                | Thylakoid soluble phosphoprotein TSP9       | No significant sequence similarity found | No significant sequence similarity found           | 1.34 | 4.10E-02 |
| GQ02804_E24 | GQ02804_E24 | BT103931 | PF00069.20;PF07714.12                    | Protein kinase domain;Protein tyrosine kina | AT2G35620.1                              | Leucine-rich repeat protein kinase family protein  | 1.34 | 8.28E-03 |
| GQ03216_K10 | GQ03216_K10 | BT108873 | PF03652.10                               | Uncharacterised protein family (UPF0081)    | AT1G12244.1                              | Polynucleotidyl transferase, ribonuclease H-like s | 1.33 | 2.82E-02 |
| GQ03611_B22 | GQ03611_B22 | BT115195 | PF00574.18                               | Cip protease                                | AT1G09130.3                              | ATP-dependent caseinolytic (Cip) protease/croto    | 1.32 | 4.88E-02 |
| WS02722_E16 | NA          | C0480383 | PF00005.22                               | ABC transporter                             | AT5G58270.1                              | ABC transporter of the mitochondrion 3             | 1.30 | 3.06E-03 |
| GQ03326_B19 | GQ03326_B19 | BT113130 | PF01933.13                               | Uncharacterised protein family UPF0052      | AT2G34090.2                              | maternal effect embryo arrest 18                   | 1.30 | 2.72E-02 |
| WS02725_K19 | NA          | BT112649 | PF04720.7                                | Protein of unknown function (DUF506)        | AT2G39650.1                              | Protein of unknown function (DUF506)               | 1.29 | 4.43E-02 |
| WS02722_E16 | NA          | C0480383 | PF00005.22                               | ABC transporter                             | AT5G58270.1                              | ABC transporter of the mitochondrion 3             | 1.29 | 1.63E-02 |
| GQ03510_O14 | GQ03510_O14 | BT114231 | PF05421.6                                | Protein of unknown function (DUF751)        | AT4G16410.1                              | unknown protein@ CONTAINS InterPro DOMAIN          | 1.29 | 4.35E-02 |
| GQ04008_C01 | GQ04008_C01 | BT118601 | PF12697.2;PF12695.2;PF00561.15           | Alpha/beta hydrolase family;Alpha/beta hydr | AT1G13820.1                              | alpha/beta-Hydrolases superfamily protein          | 1.28 | 4.10E-02 |
| WS0046_L09  | NA          | BT106187 | PF00682.14                               | HMGL-like                                   | AT2G26800.2                              | Aldolase superfamily protein                       | 1.28 | 2.39E-02 |
| GQ03205_F02 | GQ03205_F02 | BT109158 | PF02922.13                               | Carbohydrate-binding module 48 (Isoamylas   | AT5G03650.1                              | starch branching enzyme 2.2                        | 1.26 | 3.72E-02 |
| WS00738_D06 | WS00738_D06 | DR574591 | PF04539.11                               | Sigma-70 region 3                           | AT1G64860.1                              | sigma factor A                                     | 1.24 | 9.50E-03 |
| GQ04003_H15 | GQ04003_H15 | BT118196 | PF12159.3                                | Protein of unknown function (DUF3593)       | AT1G64355.1                              | unknown protein@ FUNCTIONS IN: molecular_ft        | 1.21 | 4.98E-02 |

B. Genes preferentially expressed in N-R Trees

| Clone       | Cluster_GCAT | GenBank      | Pfam accession                           | Pfam description                             | TAIR accession                           | Tair10   | Fold   | Fold     |
|-------------|--------------|--------------|--|--|--|--|--------|----------|
|             | 3.1          | accession no |  |  |  | TAIR description                                   | change |          |
| GQ03706_F07 | GQ03706_F07  | BT115795     | No significant sequence similarity found | No significant sequence similarity found     | No significant sequence similarity found | No significant sequence similarity found           | 1.16   | 3.36E-02 |
| GQ04011_L18 | GQ04011_L18  | BT118908     | No significant sequence similarity found | No significant sequence similarity found     | AT4G38520.1                              | Protein phosphatase 2C family protein              | 1.22   | 1.29E-02 |
| WS02717_F06 | NA           | BT118322     | PF01169.14                               | Uncharacterized protein family UPF0016       | AT5G36290.1                              | Uncharacterized protein family (UPF0016)           | 1.23   | 2.45E-02 |
| GQ03211_D04 | GQ03211_D04  | BT109662     | PF00069.20;PF07714.12                    | Protein kinase domain;Protein tyrosine kina  | AT1G10210.1                              | mitogen-activated protein kinase 1                 | 1.23   | 1.05E-02 |
| GQ03601_E04 | GQ03601_E04  | BT106829     | PF04857.15                               | CAF1 family ribonuclease                     | AT2G32070.1                              | Polynucleotidyl transferase, ribonuclease H-like s | 1.24   | 1.99E-02 |
| GQ02810_O03 | GQ02810_O03  | BT103634     | PF00069.20;PF07714.12                    | Protein kinase domain;Protein tyrosine kina  | AT1G17830.1                              | somatic embryogenesis receptor-like kinase 1       | 1.25   | 3.58E-02 |
| GQ03811_D01 | GQ03811_D01  | BT117021     | PF00612.22;PF13178.1                     | IQ calmodulin-binding motif;Protein of unkn  | AT5G03040.1                              | IQ-domain 2  | 1.26   | 2.57E-02 |
| GQ04113_L11 | GQ04113_L11  | BT119987     | PF00398.15                               | Ribosomal RNA adenine dimethylase            | AT2G47420.1                              | Ribosomal RNA adenine dimethylase family prote     | 1.27   | 4.35E-02 |
| GQ03004_N24 | GQ03004_N24  | BT106554     | PF04144.8                                | SCAMP family                                 | AT1G03550.1                              | Secretory carrier membrane protein (SCAMP) far     | 1.28   | 3.56E-02 |
| GQ03225_F03 | GQ03225_F03  | BT110659     | No significant sequence similarity found | No significant sequence similarity found     | No significant sequence similarity found | No significant sequence similarity found           | 1.29   | 2.68E-02 |
| GQ03702_H20 | GQ03702_H20  | BT100778     | PF00141.18                               | Peroxidase                                   | AT1G07890.3                              | ascorbate peroxidase 1                             | 1.30   | 2.35E-02 |
| GQ02830_C23 | GQ02830_C23  | BT105925     | PF00071.17;PF08477.8                     | Ras family;Miro-like protein                 | AT1G20090.1                              | RHO-related protein from plants 2                  | 1.30   | 3.93E-02 |
| GQ03313_E14 | GQ03313_E14  | BT112305     | No significant sequence similarity found | No significant sequence similarity found     | AT2G47690.1                              | NADH-ubiquinone oxidoreductase-related             | 1.31   | 4.11E-02 |
| WS02711_F21 | NA           | BT112338     | PF12697.2;PF12695.2;PF12146.3;PF05448    | Alpha/beta hydrolase family;Alpha/beta hydr  | AT5G11650.1                              | alpha/beta-Hydrolases superfamily protein          | 1.32   | 3.36E-02 |
| WS02736_L22 | NA           | BT114582     | PF00311.12                               | Phosphoenolpyruvate carboxylase              | AT1G68750.1                              | phosphoenolpyruvate carboxylase 4                  | 1.32   | 4.85E-02 |
| GQ03711_F07 | GQ03711_F07  | BT116065     | PF01593.19;PF07156.9;PF13450.1           | Flavin containing amine oxidoreductase;Pre   | AT5G63910.1                              | farnesylcysteine lyase                             | 1.33   | 3.72E-02 |
| GQ03118_H12 | GQ03118_H12  | BT108212     | No significant sequence similarity found | No significant sequence similarity found     | No significant sequence similarity found | No significant sequence similarity found           | 1.34   | 4.69E-02 |
| GQ03611_I17 | GQ03611_I17  | BT115211     | No significant sequence similarity found | No significant sequence similarity found     | No significant sequence similarity found | No significant sequence similarity found           | 1.35   | 4.51E-02 |
| WS00748_I21 | WS00748_I21  | DR578254     | No significant sequence similarity found | No significant sequence similarity found     | AT4G03030.1                              | Galactose oxidase/kelch repeat superfamily prote   | 1.35   | 3.44E-02 |
| GQ03702_H20 | GQ03702_H20  | EX415463     | PF00141.18                               | Peroxidase                                   | AT1G07890.3                              | ascorbate peroxidase 1                             | 1.35   | 9.72E-03 |
| GQ03122_L02 | GQ03122_L02  | BT108491     | PF13499.1;PF13405.1;PF13202.1            | EF-hand domain pair;EF-hand domain;EF h      | AT2G44310.1                              | Calcium-binding EF-hand family protein             | 1.36   | 8.60E-03 |
| GQ03325_O19 | GQ03325_O19  | BT111797     | PF03016.10                               | Exostosin family                             | AT4G38040.1                              | Exostosin family protein                           | 1.36   | 2.68E-02 |
| WS00823_A13 | WS00823_A13  | BT102612     | PF00240.18;PF11976.3;PF13019.1;PF1388    | Ubiquitin family;Ubiquitin-2 like Rad60 SUM  | AT5G03240.1                              | polyubiquitin 3                                    | 1.36   | 4.10E-02 |
| GQ03105_A13 | GQ03105_A13  | BT107249     | PF05627.6                                | Cleavage site for pathogenic type III effect | AT2G04410.1                              | RP11-interacting protein 4 (RIN4) family protein   | 1.37   | 2.99E-02 |
| GQ0209_H14  | GQ0209_H14   | DV989427     | No significant sequence similarity found | No significant sequence similarity found     | AT3G33530.3                              | Transducin family protein / WD-40 repeat family    | 1.37   | 2.00E-02 |
| WS03735_N24 | NA           | BT112576     | PF05003.7;PF11961.3                      | Protein of unknown function (DUF668);Dom     | AT5G04550.1                              | Protein of unknown function (DUF668)               | 1.37   | 9.18E-03 |
| GQ04013_O23 | GQ04013_O23  | BT119063     | PF00096.21                               | Zinc finger, C2H2 type                       | AT4G02670.1                              | indeterminate(ID)-domain 12                        | 1.38   | 3.70E-02 |
| GQ03211_G09 | GQ03211_G09  | BT109681     | No significant sequence similarity found | No significant sequence similarity found     | AT3G01140.1                              | myb domain protein 106                             | 1.38   | 4.17E-02 |
| GQ01816_D10 | GQ01816_D10  | BT102342     | No significant sequence similarity found | No significant sequence similarity found     | No significant sequence similarity found | No significant sequence similarity found           | 1.38   | 2.42E-02 |
| GQ03121_B01 | GQ03121_B01  | BT108380     | PF02485.16                               | Core-2/1-Branching enzyme                    | AT4G27480.1                              | Core-2/1-branching beta-1,6-N-acetylglucosaminy    | 1.39   | 1.58E-02 |
| GQ03210_G15 | GQ03210_G15  | BT109596     | PF00550.20                               | Phosphopantetheine attachment site           | AT4G29050.2                              | acyl carrier protein 4                             | 1.40   | 4.12E-02 |
| GQ02809_J22 | GQ02809_J22  | BT104366     | PF05199.8;PF00732.14                     | GMC oxidoreductase;GMC oxidoreductase        | AT4G19380.1                              | Long-chain fatty alcohol dehydrogenase family pr   | 1.40   | 4.88E-02 |
| GQ03206_I13 | GQ03206_I13  | BT109262     | PF12850.2;PF00149.23                     | Calcineurin-like phosphoesterase superfam    | AT5G63140.1                              | purple acid phosphatase 29                         | 1.41   | 5.52E-03 |
| GQ03415_P13 | GQ03415_P13  | BT113641     | No significant sequence similarity found | No significant sequence similarity found     | No significant sequence similarity found | No significant sequence similarity found           | 1.41   | 2.66E-02 |
| GQ03317_N03 | GQ03317_N03  | BT112576     | PF05003.7;PF11961.3                      | Protein of unknown function (DUF668);Dom     | AT5G04550.1                              | Protein of unknown function (DUF668)               | 1.42   | 2.54E-02 |
| WS01043_J11 | NA           | BT101076     | PF14200.1                                | Ricin-type beta-trefoil lectin domain-like   | AT2G39050.1                              | hydroxyproline-rich glycoprotein family protein    | 1.42   | 3.99E-02 |
| GQ03803_G18 | GQ03803_G18  | BT116619     | PF02800.15;PF00044.19                    | Glyceraldehyde 3-phosphate dehydrogenas      | AT1G79530.1                              | glyceraldehyde-3-phosphate dehydrogenase of pl     | 1.42   | 4.59E-02 |
| GQ04008_E02 | GQ04008_E02  | BT118617     | PF05653.9                                | Magnesium transporter NIPA                   | AT3G26670.1                              | Protein of unknown function (DUF803)               | 1.43   | 1.64E-03 |
| GQ03319_F19 | GQ03319_F19  | BT112680     | No significant sequence similarity found | No significant sequence similarity found     | No significant sequence similarity found | No significant sequence similarity found           | 1.43   | 2.63E-02 |
| GQ02904_H08 | GQ02904_H08  | BT106178     | PF00786.23;PF00620.22                    | P21-Rho-binding domain;RhoGAP domain         | AT4G03100.1                              | Rho GTPase activating protein with PAK-box/P21     | 1.44   | 2.02E-02 |

|             |             |           |  |   |  |   |      |          |
|-------------|-------------|-----------|--|---|--|---|------|----------|
| GQ03503_G07 | GQ03503_G07 | BT100580  | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found          | 1.44 | 3.37E-02 |
| WS02732_O13 | NA          | BT118520  | PF01925.14                               | Sulfite exporter TauE/SaE                     | AT2G25737.1                              | Sulfite exporter TauE/SaE family protein          | 1.46 | 1.56E-02 |
| GQ0048_P22  | GQ0048_P22  | BT100885  | PF03145.11                               | Seven in absentia protein family              | AT3G58040.1                              | seven in absentia of Arabidopsis 2                | 1.46 | 1.46E-02 |
| WS01044_L01 | NA          | BT111085  | PF01643.12;PF12590.3                     | Acyl-ACP thioesterase;Acyl-ATP thioesteras    | AT1G08510.1                              | fatty acyl-ACP thioesterases B                    | 1.46 | 4.00E-02 |
| GQ03911_H24 | GQ03911_H24 | BT117761  | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found          | 1.46 | 8.66E-03 |
| GQ03708_A12 | GQ03708_A12 | BT115886  | PF07690.11;PF00083.19                    | Major Facilitator Superfamily;Sugar (and oth  | AT4G02050.1                              | sugar transporter protein 7                       | 1.47 | 4.43E-02 |
| GQ03210_F15 | GQ03210_F15 | BT109592  | PF03982.8                                | Diacylglycerol acyltransferase                | AT3G51520.1                              | diacylglycerol acyltransferase family             | 1.47 | 3.68E-02 |
| GQ03312_L11 | GQ03312_L11 | BT111035  | PF08659.5;PF07993.7;PF05368.8;PF01370    | KR domain;Male sterility protein;NmrA-like f  | AT5G42800.1                              | dihydroflavonol 4-reductase                       | 1.47 | 2.00E-02 |
| WS0284_K02  | NA          | BT106253  | PF00013.24;PF13014.1                     | KH domain;KH domain                           | AT3G62330.1                              | Zinc knuckle (CCHC-type) family protein           | 1.47 | 2.92E-02 |
| GQ02903_E13 | GQ02903_E13 | BT106116  | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found          | 1.47 | 1.38E-03 |
| GQ03511_O06 | GQ03511_O06 | BT114286  | No significant sequence similarity found | No significant sequence similarity found      | AT3G12587.1                              | Oligosaccharyltransferase                         | 1.47 | 6.09E-03 |
| GQ02901_N03 | GQ02901_N03 | BT106038  | PF07228.7;PF00481.16                     | Stage II sporulation protein E (SpolIE);Prote | AT1G22280.3                              | phytochrome-associated protein phosphatase typ    | 1.48 | 3.68E-02 |
| GQ03319_F07 | GQ03319_F07 | BT112676  | No significant sequence similarity found | No significant sequence similarity found      | AT2G25290.1                              | Octicosapeptide/Phox/Bem1p (PB1) domain-cont      | 1.49 | 4.77E-02 |
| GQ02807_J21 | GQ02807_J21 | BT100738  | PF07107.6;PF12680.2;PF14534.1            | Wound-induced protein Wl12;Snoal-like do      | AT5G01740.1                              | Nuclear transport factor 2 (NTF2) family protein  | 1.49 | 2.62E-02 |
| GQ03314_I18 | GQ03314_I18 | BT112400  | PF02485.16                               | Core-2/I-Branching enzyme                     | AT5G15050.1                              | Core-2/I-branching beta-1,6-N-acetylglucosaminy   | 1.49 | 1.58E-02 |
| WS0023_P04  | WS0023_P04  | CO236551  | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found          | 1.49 | 4.88E-02 |
| GQ02808_H12 | GQ02808_H12 | BT104279  | PF00300.17                               | Histidine phosphatase superfamily (branch     | AT1G22170.1                              | Phosphoglycerate mutase family protein            | 1.49 | 3.40E-02 |
| GQ02823_L07 | GQ02823_L07 | BT105525  | PF00620.22                               | RhoGAP domain                                 | AT5G61530.1                              | small G protein family protein / RhoGAP family pr | 1.49 | 1.12E-02 |
| GQ04104_M09 | GQ04104_M09 | BT119371  | PF01852.14                               | START domain                                  | AT4G04890.1                              | protodermal factor 2                              | 1.50 | 1.90E-02 |
| GQ03232_H17 | GQ03232_H17 | BT111085  | PF01643.12;PF12590.3                     | Acyl-ACP thioesterase;Acyl-ATP thioesteras    | AT1G08510.1                              | fatty acyl-ACP thioesterases B                    | 1.51 | 2.64E-02 |
| GQ03206_C05 | GQ03206_C05 | BT109227  | PF12638.2                                | Staygreen protein                             | AT4G22920.1                              | non-yellowing 1                                   | 1.51 | 2.77E-02 |
| WS0322_G20  | WS0322_G20  | DR551141  | PF00501.23;PF13193.1                     | AMP-binding enzyme;AMP-binding enzyme         | AT3G21240.1                              | 4-coumarate:CoA ligase 2                          | 1.51 | 4.59E-02 |
| GQ03705_K13 | GQ03705_K13 | BT115759  | PF03168.8                                | Late embryogenesis abundant protein           | AT3G54200.1                              | Late embryogenesis abundant (LEA) hydroxyproli    | 1.51 | 2.90E-02 |
| GQ03806_P03 | GQ03806_P03 | BT116796  | PF03009.12                               | Glycerophosphoryl diester phosphodiestera     | AT1G74210.1                              | PLC-like phosphodiesterases superfamily protein   | 1.52 | 8.93E-04 |
| GQ03719_G10 | GQ03719_G10 | BT116479  | PF00249.26;PF13921.1                     | Myb-like DNA-binding domain;Myb-like DNA      | AT4G28110.1                              | myb domain protein 41                             | 1.52 | 3.45E-03 |
| GQ03407_K01 | GQ03407_K01 | BT113417  | PF07714.12;PF08263.7                     | Protein tyrosine kinase;Leucine rich repeat   | AT4G28650.1                              | Leucine-rich repeat transmembrane protein kinas   | 1.52 | 4.11E-02 |
| GQ03007_B12 | GQ03007_B12 | BT106644  | PF00487.19                               | Fatty acid desaturase                         | AT3G61580.1                              | Fatty acid/sphingolipid desaturase                | 1.52 | 4.88E-02 |
| GQ03901_C05 | GQ03901_C05 | BT117468  | PF00011.16                               | Hsp20/alpha crystallin family                 | AT5G12020.1                              | 17.6 kDa class II heat shock protein              | 1.52 | 1.61E-02 |
| GQ01816_D03 | GQ01816_D03 | BT102341  | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found          | 1.53 | 4.18E-02 |
| GQ03508_E16 | GQ03508_E16 | BT114110  | PF00622.23                               | SPRY domain                                   | AT4G06536.1                              | SPla/Ryanodine receptor (SPRY) domain-contain     | 1.53 | 2.29E-03 |
| WS00738_F08 | WS00738_F08 | DR574635  | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found          | 1.53 | 2.99E-02 |
| WS02710_O16 | NA          | BT115539  | PF00561.15;PF12695.2;PF12697.2           | alpha/beta hydrolase fold;Alpha/beta hydroli  | AT3G03990.1                              | alpha/beta-Hydrolases superfamily protein         | 1.54 | 4.69E-02 |
| GQ02805_I02 | GQ02805_I02 | BT1104021 | No significant sequence similarity found | No significant sequence similarity found      | AT3G12340.1                              | FKBP-like peptidyl-prolyl cis-trans isomerase fam | 1.54 | 3.56E-02 |
| WS02727_E06 | NA          | BT114001  | No significant sequence similarity found | No significant sequence similarity found      | AT2G33430.1                              | differentiation and greening-like 1               | 1.55 | 4.88E-02 |
| GQ03710_H08 | GQ03710_H08 | BT116015  | PF13602.1;PF08240.7;PF00107.21           | Zinc-binding dehydrogenase;Alcohol dehydr     | AT1G23740.1                              | Oxidoreductase, zinc-binding dehydrogenase fan    | 1.56 | 2.65E-02 |
| GQ03115_I17 | GQ03115_I17 | BT107995  | PF02801.17;PF00109.21                    | Beta-ketoacyl synthase, C-terminal domain;    | AT5G46290.3                              | 3-ketoacyl-acyl carrier protein synthase I        | 1.56 | 2.16E-02 |
| GQ0202_G07  | GQ0202_G07  | BT102884  | PF00378.15                               | Enoyl-CoA hydratase/isomerase family          | AT5G43280.1                              | delta(3,5),delta(2,4)-dienoyl-CoA isomerase 1     | 1.56 | 2.44E-02 |
| GQ04102_I02 | GQ04102_I02 | EX441268  | PF08240.7                                | Alcohol dehydrogenase GroES-like domain       | AT5G63620.1                              | GroES-like zinc-binding alcohol dehydrogenase f;  | 1.59 | 1.53E-02 |
| WS03725_M02 | NA          | ES255294  | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found          | 1.60 | 5.40E-03 |
| WS02627_J09 | WS02627_J09 | DR563387  | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found          | 1.61 | 3.80E-02 |
| GQ03711_F16 | GQ03711_F16 | BT116067  | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found          | 1.62 | 4.11E-02 |
| GQ03601_N08 | GQ03601_N08 | BT114771  | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found          | 1.62 | 4.88E-02 |
| GQ03115_F07 | GQ03115_F07 | BT107981  | PF12804.2;PF00483.18;PF00132.19          | MobA-like NTP transferase domain;Nucleoti     | AT2G39770.1                              | Glucose-1-phosphate adenyltransferase family      | 1.62 | 6.64E-03 |
| GQ01313_E24 | GQ01313_E24 | BT101789  | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found          | 1.64 | 2.55E-03 |
| WS0076_I02  | WS0076_I02  | CO239761  | PF00108.18;PF00109.21;PF02801.17;PF02    | Thiolase, N-terminal domain;Beta-ketoacyl     | AT5G46290.3                              | 3-ketoacyl-acyl carrier protein synthase I        | 1.64 | 7.92E-03 |
| WS01038_J16 | NA          | DR542397  | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found          | 1.64 | 3.30E-02 |
| WS0281_D16  | NA          | BT117017  | PF00450.17                               | Serine carboxypeptidase                       | AT3G07990.1                              | serine carboxypeptidase-like 27                   | 1.64 | 6.27E-03 |
| WS01027_E16 | NA          | BT115089  | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found          | 1.65 | 2.62E-03 |
| GQ03204_C19 | GQ03204_C19 | BT109058  | PF09353.5                                | Domain of unknown function (DUF1995)          | No significant sequence similarity found | No significant sequence similarity found          | 1.66 | 3.37E-02 |
| GQ02614_F04 | GQ02614_F04 | BT103639  | PF01490.13                               | Transmembrane amino acid transporter pro      | AT4G38250.1                              | Transmembrane amino acid transporter family pr    | 1.66 | 1.04E-02 |
| WS0079_N08  | WS0079_N08  | CO241334  | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found          | 1.66 | 3.68E-02 |
| GQ0168_E22  | GQ0168_E22  | BT102191  | PF00069.20;PF07714.12                    | Protein kinase domain;Protein tyrosine kin    | AT1G25390.1                              | Protein kinase superfamily protein                | 1.66 | 1.99E-02 |
| WS02749_E04 | NA          | BT112762  | PF12695.2;PF12697.2                      | Alpha/beta hydrolase family;Alpha/beta hydi   | AT3G10870.1                              | methyl esterase 17                                | 1.66 | 4.15E-02 |
| GQ03228_B11 | GQ03712_B10 | BT116116  | No significant sequence similarity found | No significant sequence similarity found      | AT1G05410.1                              | Protein of unknown function (DUF1423)             | 1.66 | 2.72E-02 |
| GQ03114_H16 | GQ03114_H16 | BT107920  | PF00091.20;PF03953.12                    | Tubulin/FtsZ family, GTPase domain;Tubuli     | AT5G23860.1                              | tubulin beta 8                                    | 1.66 | 2.27E-02 |
| GQ03815_J03 | GQ03815_J03 | BT117237  | PF02817.12;PF00364.17;PF00198.18         | e3 binding domain;Biotin-requiring enzyme;    | AT1G34430.1                              | 2-oxoacid dehydrogenases acyltransferase family   | 1.67 | 2.43E-02 |
| WS00738_H06 | WS00738_H06 | DR574679  | PF01179.15                               | Copper amine oxidase, enzyme domain           | AT1G31690.1                              | Copper amine oxidase family protein               | 1.68 | 1.28E-03 |
| WS00820_D24 | WS00820_D24 | CO253708  | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found          | 1.68 | 2.72E-02 |
| GQ03808_F14 | GQ03808_F14 | BT116870  | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found          | 1.68 | 3.37E-02 |
| GQ03611_D21 | GQ03611_D21 | BT115199  | PF00646.28;PF12937.2                     | F-box domain;F-box-like                       | AT4G24210.1                              | F-box family protein                              | 1.68 | 2.63E-02 |
| GQ04013_G23 | GQ04013_G23 | BT119016  | PF00109.21                               | Beta-ketoacyl synthase, N-terminal domain     | AT5G46290.3                              | 3-ketoacyl-acyl carrier protein synthase I        | 1.68 | 4.99E-02 |
| WS02710_B04 | NA          | BT113523  | PF00504.16                               | Chlorophyll A-B binding protein               | AT1G44575.1                              | Chlorophyll A-B binding family protein            | 1.68 | 1.60E-02 |
| GQ03204_C19 | GQ03204_C19 | BT109058  | PF09353.5                                | Domain of unknown function (DUF1995)          | No significant sequence similarity found | No significant sequence similarity found          | 1.69 | 5.45E-03 |
| WS00723_H07 | WS00723_H07 | CO238992  | PF00106.20;PF08659.5;PF13561.1           | short chain dehydrogenase;KR domain;Eno       | AT4G13180.1                              | NAD(P)-binding Rossmann-fold superfamily prote    | 1.69 | 2.90E-02 |
| WS00755_N17 | WS00755_N17 | BT119066  | PF01061.19                               | ABC-2 type transporter                        | AT2G26910.1                              | pleiotropic drug resistance 4                     | 1.69 | 7.37E-03 |
| GQ03116_I11 | GQ03116_I11 | BT108071  | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found          | 1.69 | 8.16E-03 |
| GQ0209_F13  | GQ0209_F13  | CO486665  | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found          | 1.70 | 3.95E-03 |
| GQ03239_I08 | GQ03239_I08 | BT111565  | No significant sequence similarity found | No significant sequence similarity found      | AT3G11980.1                              | Jojoba acyl CoA reductase-related male sterility  | 1.70 | 3.77E-02 |
| GQ03213_C05 | GQ03213_C05 | BT110483  | PF07714.12;PF08263.7                     | Protein tyrosine kinase;Leucine rich repeat   | AT3G47110.1                              | Leucine-rich repeat protein kinase family protein | 1.70 | 3.68E-02 |
| WS00754_K07 | WS00754_K07 | DR580382  | PF00083.19                               | Sugar (and other) transporter                 | AT2G38940.1                              | phosphate transporter 1@4                         | 1.71 | 2.54E-03 |
| GQ02810_J24 | GQ02810_J24 | BT104460  | PF00498.21                               | FHA domain                                    | AT3G02400.1                              | SMAD/FHA domain-containing protein                | 1.71 | 7.37E-03 |

|             |             |          |  |   |  |   |      |          |
|-------------|-------------|----------|--|---|--|---|------|----------|
| WS00716_P14 | WS00716_P14 | CO241881 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.72 | 2.43E-02 |
| WS02735_G12 | NA          | BT105066 | PF00255.14;PF00578.16;PF08534.5          | Glutathione peroxidase/AhpC/TSA family;Rt     | AT4G11600.1                              | glutathione peroxidase 6                            | 1.72 | 4.12E-02 |
| GQ04108_F24 | GQ04108_F24 | BT119651 | PF00571.23                               | CBS domain                                    | AT1G69800.2                              | Cystathionine beta-synthase (CBS) protein           | 1.73 | 2.72E-02 |
| WS00827_A14 | WS00827_A14 | DR589884 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.73 | 1.12E-02 |
| WS00110_A11 | WS00110_A11 | CO229801 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.75 | 1.40E-02 |
| GQ03617_N20 | GQ03617_N20 | BT115490 | PF04707.9                                | PRELI-like family                             | AT5G13070.1                              | MSF1-like family protein                            | 1.76 | 3.53E-02 |
| GQ03126_K16 | GQ03126_K16 | BT108758 | PF00026.18;PF14541.1                     | Eukaryotic aspartyl protease;Xylanase inhib   | AT3G25700.1                              | Eukaryotic aspartyl protease family protein         | 1.77 | 3.34E-02 |
| GQ03316_K19 | GQ03316_K19 | BT112517 | PF13561.1;PF08659.5;PF00106.20           | Enoyl-(Acyl carrier protein) reductase;KR     | dr AT3G06060.1                           | NAD(P)-binding Rossmann-fold superfamily prote      | 1.77 | 1.38E-03 |
| GQ03816_E16 | GQ03816_E16 | BT117268 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.78 | 2.36E-02 |
| GQ03238_G19 | GQ03238_G19 | BT111488 | No significant sequence similarity found | No significant sequence similarity found      | AT2G39080.1                              | NAD(P)-binding Rossmann-fold superfamily prote      | 1.79 | 1.48E-02 |
| WS0022_M04  | WS0022_M04  | CO236109 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.80 | 4.85E-02 |
| GQ02824_J22 | GQ02824_J22 | BT105574 | PF00450.17                               | Serine carboxypeptidase                       | AT1G15000.1                              | serine carboxypeptidase-like 50                     | 1.80 | 6.11E-03 |
| GQ03114_L04 | GQ03114_L04 | BT118472 | No significant sequence similarity found | No significant sequence similarity found      | AT4G24220.1                              | NAD(P)-binding Rossmann-fold superfamily prote      | 1.80 | 9.52E-03 |
| GQ03236_K17 | GQ03236_K17 | BT111375 | No significant sequence similarity found | No significant sequence similarity found      | AT1G31130.1                              | unknown protein@ FUNCTIONS IN: molecular_fu         | 1.80 | 1.90E-02 |
| GQ03502_I17 | GQ03502_I17 | BT113837 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.83 | 4.71E-02 |
| WS03733_I21 | NA          | BT111163 | PF03798.11                               | TLC domain                                    | AT1G35180.1                              | TRAM, LAG1 and CLN8 (TLC) lipid-sensing dom;        | 1.84 | 1.38E-03 |
| GQ03801_M13 | GQ03801_M13 | BT116549 | No significant sequence similarity found | No significant sequence similarity found      | AT2G16760.1                              | Calcium-dependent phosphotriesterase superfar       | 1.84 | 1.30E-02 |
| GQ04013_P22 | GQ04013_P22 | BT119066 | PF01061.19                               | ABC-2 type transporter                        | AT2G26910.1                              | pleiotropic drug resistance 4                       | 1.84 | 2.54E-03 |
| GQ01310_H20 | GQ01310_H20 | BT101673 | PF00403.21                               | Heavy-metal-associated domain                 | No significant sequence similarity found |   | 1.85 | 2.86E-02 |
| GQ01307_L15 | GQ01307_L15 | EX308322 | No significant sequence similarity found | No significant sequence similarity found      | AT3G48090.1                              | alpha/beta-Hydrolases superfamily protein           | 1.85 | 1.48E-02 |
| WS00753_K12 | WS00753_K12 | DR580043 | PF00450.17                               | Serine carboxypeptidase                       | AT4G12910.1                              | serine carboxypeptidase-like 20                     | 1.85 | 2.95E-02 |
| GQ03603_F13 | GQ03603_F13 | BT114835 | No significant sequence similarity found | No significant sequence similarity found      | AT4G13970.1                              | zinc ion binding                                    | 1.85 | 3.47E-02 |
| WS03215_C01 | WS03215_C01 | DR549317 | PF00046.24                               | Homeobox domain                               | AT4G04890.1                              | protodermal factor 2                                | 1.88 | 2.55E-03 |
| GQ03211_N18 | GQ03211_N18 | BT109732 | No significant sequence similarity found | No significant sequence similarity found      | AT1G26761.1                              | Arabinanase/levansucrase/invertase                  | 1.88 | 1.25E-02 |
| WS00726_M14 | WS00726_M14 | DR570621 | PF01657.12                               | Salt stress response/antifungal               | AT3G22060.1                              | Receptor-like protein kinase-related family protei  | 1.88 | 1.05E-02 |
| WS03946_L19 | NA          | BT102416 | PF01764.20                               | Lipase (class 3)                              | AT4G10955.1                              | alpha/beta-Hydrolases superfamily protein           | 1.89 | 4.02E-03 |
| WS02723_J11 | NA          | BT101673 | PF00403.21                               | Heavy-metal-associated domain                 | No significant sequence similarity found | No significant sequence similarity found            | 1.89 | 4.27E-02 |
| WS02716_J03 | NA          | BT105066 | PF00255.14;PF00578.16;PF08534.5          | Glutathione peroxidase/AhpC/TSA family;Rt     | AT4G11600.1                              | glutathione peroxidase 6                            | 1.91 | 3.22E-03 |
| GQ0194_I21  | GQ0194_I21  | DV982363 | PF00153.22                               | Mitochondrial carrier protein                 | AT3G48850.1                              | phosphate transporter 3@2                           | 1.92 | 1.05E-02 |
| WS0087_D10  | WS0087_D10  | CO258001 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.92 | 2.35E-02 |
| GQ03310_G15 | GQ03310_G15 | BT112126 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 1.93 | 1.65E-02 |
| GQ03202_M18 | GQ03202_M18 | GT739032 | PF00108.18;PF00109.21;PF02801.17;PF02    | Thiolase, N-terminal domain;Beta-ketoacyl s   | AT5G46290.3                              | 3-ketoacyl-acyl carrier protein synthase I          | 1.93 | 3.39E-03 |
| GQ03617_F05 | GQ03617_F05 | BT103156 | PF00195.14;PF02797.10;PF08392.7;PF085    | Chalcone and stilbene synthases, N-termin     | AT5G13930.1                              | Chalcone and stilbene synthase family protein       | 2.00 | 2.63E-02 |
| GQ03807_F09 | GQ03807_F09 | BT116822 | PF13460.1;PF05368.8;PF01370.16;PF0111    | NADH(P)-binding;NmrA-like family;NAD dep      | AT4G39230.1                              | NmrA-like negative transcriptional regulator fami   | 2.00 | 1.11E-02 |
| GQ03211_I16 | GQ03211_I16 | BT109692 | PF14634.1;PF13923.1;PF13920.1;PF13639    | zinc-RING finger domain;Zinc finger, C3HC     | AT3G61460.1                              | brassinosteroid-responsive RING-H2                  | 2.00 | 3.00E-02 |
| WS0023_D24  | WS0023_D24  | CO236333 | PF00232.13                               | Glycosyl hydrolase family 1                   | AT5G42260.1                              | beta glucosidase 12                                 | 2.01 | 6.47E-04 |
| GQ03222_H20 | GQ03222_H20 | BT110482 | PF13855.1;PF13516.1;PF13504.1;PF12799    | Leucine rich repeat;Leucine Rich repeat;Leu   | AT5G46330.1                              | Leucine-rich receptor-like protein kinase family pr | 2.02 | 3.70E-02 |
| WS03220_J13 | WS03220_J13 | DR551528 | PF13912.1                                | C2H2-type zinc finger                         | AT2G45120.1                              | C2H2-like zinc finger protein                       | 2.03 | 4.95E-03 |
| GQ02815_C18 | GQ02815_C18 | BT104795 | PF11721.3                                | Di-glucose binding within endoplasmic reticu  | AT1G56145.2                              | Leucine-rich repeat transmembrane protein kinas     | 2.03 | 9.64E-03 |
| GQ0191_L12  | GQ0191_L12  | BT102416 | PF01764.20                               | Lipase (class 3)                              | AT4G10955.1                              | alpha/beta-Hydrolases superfamily protein           | 2.04 | 8.05E-04 |
| GQ04112_D24 | GQ04112_D24 | BT119913 | PF14008.1;PF00149.23                     | Iron/zinc purple acid phosphatase-like prote  | AT2G16430.2                              | purple acid phosphatase 10                          | 2.05 | 8.43E-03 |
| WS0328_C01  | WS0328_C01  | DR556219 | PF00305.14                               | Lipoxygenase                                  | AT3G22400.1                              | PLAT/LH2 domain-containing lipoxygenase family      | 2.05 | 8.58E-03 |
| GQ02806_H09 | GQ02806_H09 | BT104102 | PF05623.7                                | Protein of unknown function (DUF789)          | AT4G03420.1                              | Protein of unknown function (DUF789)                | 2.05 | 1.65E-02 |
| WS00838_H23 | WS00838_H23 | DR593647 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 2.05 | 8.05E-04 |
| GQ03512_I20 | GQ03512_I20 | BT114330 | PF14634.1;PF13923.1;PF13920.1;PF13639    | zinc-RING finger domain;Zinc finger, C3HC     | AT3G61460.1                              | brassinosteroid-responsive RING-H2                  | 2.06 | 2.63E-02 |
| GQ03705_B12 | GQ03705_B12 | BT115726 | PF03330.13;PF01357.16                    | Rare lipoprotein A (RlpA)-like double-psi bet | AT4G38400.1                              | expansin-like A2                                    | 2.06 | 3.60E-02 |
| GQ03325_L19 | GQ03325_L19 | BT113105 | PF14368.1                                | Probable lipid transfer                       | No significant sequence similarity found | No significant sequence similarity found            | 2.08 | 8.22E-03 |
| GQ03237_P23 | GQ03237_P23 | BT111466 | No significant sequence similarity found | No significant sequence similarity found      | AT4G18910.1                              | NOD26-like intrinsic protein 1 @2                   | 2.09 | 6.86E-05 |
| GQ04005_M02 | GQ04005_M02 | BT118376 | No significant sequence similarity found | No significant sequence similarity found      | AT1G19170.1                              | Pectin lyase-like superfamily protein               | 2.09 | 4.19E-02 |
| WS01024_N10 | NA          | EX401877 | PF03283.8                                | Pectinacetyl esterase                         | AT3G62060.1                              | Pectinacetyl esterase family protein                | 2.10 | 3.45E-03 |
| WS00721_K17 | WS00721_K17 | CO242456 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 2.10 | 7.49E-03 |
| GQ03208_M02 | GQ03208_M02 | BT109463 | PF00378.15                               | Enoyl-CoA hydratase/isomerase family          | AT4G14430.1                              | indole-3-butyric acid response 10                   | 2.11 | 2.67E-02 |
| GQ02813_C15 | GQ02813_C15 | BT104660 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 2.11 | 4.47E-03 |
| WS03720_K01 | NA          | BT108424 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 2.12 | 3.00E-02 |
| GQ03223_D13 | GQ03223_D13 | BT110541 | PF00560.28;PF12799.2;PF13504.1;PF1351    | Leucine Rich Repeat;Leucine Rich repeats      | AT1G34420.1                              | leucine-rich repeat transmembrane protein kinas     | 2.12 | 4.76E-03 |
| GQ03701_M23 | GQ03701_M23 | BT115574 | No significant sequence similarity found | No significant sequence similarity found      | AT2G20515.1                              | unknown protein@ FUNCTIONS IN: molecular_fu         | 2.13 | 4.49E-02 |
| GQ03704_E09 | GQ03704_E09 | BT115684 | PF12681.2;PF00903.20                     | Glyoxalase-like domain;Glyoxalase/Bleomyc     | AT1G80160.1                              | Lactoylglutathione lyase / glyoxalase I family prot | 2.14 | 2.29E-03 |
| GQ03610_B16 | GQ03610_B16 | BT115145 | PF00266.14                               | Aminotransferase class-V                      | AT5G26600.2                              | Pyridoxal phosphate (PLP)-dependent transferas      | 2.16 | 3.46E-02 |
| GQ0069_J22  | GQ0069_J22  | BT101161 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 2.20 | 6.34E-03 |
| GQ03201_L13 | GQ03201_L13 | BT108846 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 2.20 | 3.60E-02 |
| WS0072_K23  | WS0072_K23  | CO237447 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 2.22 | 4.77E-02 |
| GQ03411_M23 | GQ03411_M23 | BT113512 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 2.22 | 2.00E-02 |
| WS0072_B18  | WS0072_B18  | CO237250 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 2.23 | 1.67E-03 |
| GQ0198_B06  | GQ0198_B06  | BT102617 | PF06521.6                                | PAR1 protein                                  | AT5G52390.1                              | PAR1 protein  | 2.24 | 2.56E-02 |
| GQ02012_N20 | GQ02012_N20 | CO486458 | No significant sequence similarity found | No significant sequence similarity found      | AT4G37050.1                              | PATATIN-like protein 4                              | 2.27 | 7.37E-03 |
| GQ04013_B01 | GQ04013_B01 | BT118991 | PF01544.13                               | CorA-like Mg2+ transporter protein            | AT3G19640.1                              | magnesium transporter 4                             | 2.28 | 2.69E-02 |
| WS03226_G01 | WS03226_G01 | DR553546 | PF00560.28;PF13516.1                     | Leucine Rich Repeat;Leucine Rich repeat       | AT3G28450.1                              | Leucine-rich repeat protein kinase family protein   | 2.30 | 3.00E-02 |
| GQ02805_I01 | GQ02805_I01 | BT104020 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 2.31 | 4.56E-02 |
| GQ0069_F12  | GQ0069_I08  | BT103569 | No significant sequence similarity found | No significant sequence similarity found      | AT5G52390.1                              | PAR1 protein  | 2.32 | 2.36E-02 |
| GQ04013_I04 | GQ04013_I04 | BT119022 | No significant sequence similarity found | No significant sequence similarity found      | No significant sequence similarity found | No significant sequence similarity found            | 2.33 | 1.73E-02 |
| GQ04103_J03 | GQ04103_J03 | BT119280 | PF03106.10                               | WRKY DNA-binding domain                       | AT2G38470.1                              | WRKY DNA-binding protein 33                         | 2.35 | 1.66E-02 |

|             |             |            |  |   |  |   |       |          |
|-------------|-------------|------------|--|---|--|---|-------|----------|
| GQ03313_D05 | GQ03313_D05 | BT112299   | PF03492.10                               | SAM dependent carboxyl methyltransferase    | AT1G68040.1                              | S-adenosyl-L-methionine-dependent methyltransf      | 2.41  | 2.95E-02 |
| WS02735_A13 | NA          | DR531295.1 | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 2.42  | 3.37E-02 |
| GQ03604_M11 | GQ03604_M11 | BT103156   | PF00195.14;PF02797.10;PF08392.7;PF085    | Chalcone and stilbene synthases, N-termin   | AT5G13930.1                              | Chalcone and stilbene synthase family protein       | 2.46  | 2.04E-02 |
| WS0294_O08  | NA          | BT111697   | No significant sequence similarity found | No significant sequence similarity found    | AT5G42070.1                              | unknown protein@ FUNCTIONS IN: molecular_fu         | 2.49  | 3.84E-02 |
| WS00740_P05 | WS00740_P05 | DR575567   | PF00909.16                               | Ammonium Transporter Family                 | AT2G38290.1                              | ammonium transporter 2                              | 2.51  | 1.61E-04 |
| GQ04008_C02 | GQ04008_C02 | BT118602   | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 2.52  | 4.77E-02 |
| WS02628_A07 | WS02628_A07 | DR563548   | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 2.53  | 1.11E-02 |
| WS04215_E12 | NA          | BT102191   | PF00069.20;PF07714.12                    | Protein kinase domain;Protein tyrosine kin  | AT1G25390.1                              | Protein kinase superfamily protein                  | 2.55  | 1.71E-02 |
| WS01043_O06 | NA          | BT108891   | PF05910.7                                | Plant protein of unknown function (DUF868)  | AT3G04860.1                              | Plant protein of unknown function (DUF868)          | 2.59  | 1.58E-02 |
| GQ0192_L04  | GQ0192_L04  | BT102437   | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 2.59  | 4.20E-03 |
| GQ03302_F07 | GQ03302_F07 | BT111697   | No significant sequence similarity found | No significant sequence similarity found    | AT5G42070.1                              | unknown protein@ FUNCTIONS IN: molecular_fu         | 2.60  | 2.93E-02 |
| GQ0131_I01  | GQ0131_I01  | CO477558   | No significant sequence similarity found | No significant sequence similarity found    | AT5G23050.1                              | acyl-activating enzyme 17                           | 2.60  | 4.72E-02 |
| GQ01304_P06 | GQ01304_P06 | BT101457   | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 2.68  | 3.88E-02 |
| GQ03236_L18 | GQ03236_L18 | BT111380   | PF03936.11                               | Terpene synthase family, metal binding dom  | AT4G16730.1                              | terpene synthase 02                                 | 2.72  | 1.46E-02 |
| GQ03206_K20 | GQ03206_K20 | BT109278   | PF05050.7;PF13383.1                      | Methyltransferase FkbM domain;Methyltran    | No significant sequence similarity found | No significant sequence similarity found            | 2.72  | 4.43E-02 |
| GQ03614_F12 | GQ03614_F12 | BT115331   | PF01554.13                               | Mate  | AT3G26590.1                              | MATE efflux family protein                          | 2.73  | 4.96E-02 |
| GQ02010_C09 | GQ02010_C09 | BT102653   | No significant sequence similarity found | No significant sequence similarity found    | AT4G23180.1                              | cysteine-rich RLK (RECEPTOR-like protein kinas      | 2.74  | 1.90E-02 |
| GQ03321_J10 | GQ03321_J10 | BT112835   | PF00248.16                               | Aldo/keto reductase family                  | AT1G60710.1                              | NAD(P)-linked oxidoreductase superfamily protei     | 2.74  | 9.58E-02 |
| GQ03506_O14 | GQ03506_O14 | BT114040   | PF00201.13                               | UDP-glucuronosyl and UDP-glucosyl transfe   | AT2G15490.1                              | UDP-glycosyltransferase 73B4                        | 2.74  | 2.14E-02 |
| WS01016_C13 | NA          | CO233173   | No significant sequence similarity found | No significant sequence similarity found    | AT5G38240.1                              | Protein kinase family protein                       | 2.79  | 1.58E-02 |
| WS0278_G08  | NA          | BT106498   | PF00141.18                               | Peroxidase                                  | AT1G71695.1                              | Peroxidase superfamily protein                      | 2.83  | 4.71E-02 |
| GQ03313_C08 | GQ03313_C08 | BT112296   | PF01476.15                               | LysM domain                                 | AT2G23770.1                              | protein kinase family protein / peptidoglycan-bind  | 2.84  | 1.35E-02 |
| GQ03505_M10 | GQ03505_M10 | BT113980   | PF00069.20;PF07714.12                    | Protein kinase domain;Protein tyrosine kin  | AT1G25390.1                              | Protein kinase superfamily protein                  | 2.86  | 2.51E-03 |
| WS03210_C23 | WS03210_C23 | DR547551   | PF00067.17                               | Cytochrome P450                             | AT3G52970.2                              | cytochrome P450, family 76, subfamily G, polype     | 2.89  | 3.11E-02 |
| GQ0024_D06  | GQ0024_D06  | BT100532   | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 2.93  | 1.28E-03 |
| GQ03312_B21 | GQ02810_H14 | BT104446   | PF05050.7                                | Methyltransferase FkbM domain               | No significant sequence similarity found | No significant sequence similarity found            | .297  | 2.29E-02 |
| WS0276_K19  | NA          | CO486458   | No significant sequence similarity found | No significant sequence similarity found    | AT4G37050.1                              | PATATIN-like protein 4                              | 3.00  | 1.38E-03 |
| WS01038_P01 | NA          | BT118485   | PF04749.12                               | PLAC8 family                                | AT1G49030.1                              | PLAC8 family protein                                | 3.05  | 2.69E-02 |
| WS00748_B17 | WS00748_B17 | DR578092   | PF01095.14                               | Pectinesterase                              | AT5G47500.1                              | Pectin lyase-like superfamily protein               | 3.13  | 1.51E-02 |
| GQ0164_N20  | GQ0164_N20  | BT102042   | PF02365.10                               | No apical meristem (NAM) protein            | AT1G52890.1                              | NAC domain containing protein 19                    | 3.16  | 1.77E-02 |
| GQ03322_M11 | GQ03322_M11 | BT112921   | PF06200.9                                | tify domain                                 | No significant sequence similarity found | No significant sequence similarity found            | 3.19  | 8.58E-03 |
| GQ0013_C19  | GQ0013_C19  | BT100392   | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 3.21  | 3.58E-02 |
| WS00824_B11 | WS00824_B11 | CO255068   | No significant sequence similarity found | No significant sequence similarity found    | AT3G05660.1                              | receptor like protein 33                            | 3.22  | 1.29E-02 |
| WS0089_N20  | WS0089_N20  | CO258571   | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 3.24  | 1.54E-02 |
| GQ0256_J06  | GQ0256_J06  | BT103542   | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 3.30  | 8.05E-04 |
| WS01034_N04 | NA          | BT111157   | PF00903.20;PF12681.2                     | Glyoxalase/Bleomycin resistance protein/Di  | AT1G80160.1                              | Lactoylglutathione lyase / glyoxalase I family prot | 3.33  | 2.06E-02 |
| WS02713_I23 | NA          | EX418143   | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 3.33  | 3.60E-02 |
| GQ03316_D20 | GQ03316_D20 | BT112493   | PF01694.17                               | Rhomboid family                             | AT3G17611.1                              | RHOMBOLD-like protein 14                            | 3.35  | 4.42E-02 |
| WS01025_P08 | NA          | BT111380   | PF03936.11                               | Terpene synthase family, metal binding dom  | AT4G16730.1                              | terpene synthase 02                                 | 3.44  | 1.24E-02 |
| GQ03126_N20 | GQ03126_N20 | BT108771   | PF00394.17;PF07731.9                     | Multicopper oxidase;Multicopper oxidase     | AT1G23010.1                              | Cupredoxin superfamily protein                      | 3.50  | 1.46E-02 |
| GQ03901_K02 | GQ03901_K02 | BT117493   | PF00067.17                               | Cytochrome P450                             | AT3G48280.1                              | cytochrome P450, family 71, subfamily A, polype     | 3.51  | 8.58E-03 |
| GQ03206_N16 | GQ03206_N16 | BT109298   | PF00538.14                               | linker histone H1 and H5 family             | No significant sequence similarity found | No significant sequence similarity found            | 3.54  | 6.27E-03 |
| WS00713_M03 | WS00713_M03 | CO240470   | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 3.58  | 3.77E-02 |
| GQ03516_I23 | GQ03516_I23 | BT114539   | PF01734.17                               | Patatin-like phospholipase                  | AT4G37070.2                              | Acyl transferase/acyl hydrolase/lysophospholip      | 3.68  | 4.12E-04 |
| GQ03204_K15 | GQ03204_K15 | BT109102   | No significant sequence similarity found | No significant sequence similarity found    | AT1G69550.1                              | disease resistance protein (TIR-NBS-LRR class)      | 3.72  | 1.09E-02 |
| WS01034_N11 | NA          | BT104795   | PF11721.3                                | Di-glucose binding within endoplasmic retic | AT1G56145.2                              | Leucine-rich repeat transmembrane protein kinas     | 3.92  | 4.62E-04 |
| GQ04109_N20 | GQ04109_N20 | BT119772   | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 3.96  | 2.39E-02 |
| WS0324_C03  | WS0324_C03  | DR554845   | PF00067.17                               | Cytochrome P450                             | AT3G53280.1                              | cytochrome p450 71b5                                | 3.99  | 4.15E-02 |
| GQ03237_G19 | GQ03237_G19 | BT104516   | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 4.22  | 8.58E-03 |
| WS00733_B19 | WS00733_B19 | DR573094   | PF06955.7;PF00722.16                     | Xyloglucan endo-transglycosylase (XET) C-1  | AT5G13870.1                              | xyloglucan endotransglucosylase/hydrolase 5         | 4.34  | 4.51E-03 |
| GQ03602_G21 | GQ03602_G21 | BT114799   | PF00257.14                               | Dehydrin                                    | No significant sequence similarity found | No significant sequence similarity found            | 4.60  | 9.45E-03 |
| WS01029_M07 | NA          | CO226469   | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 4.63  | 4.24E-03 |
| GQ0252_P15  | GQ0252_P15  | CO487774   | PF00067.17                               | Cytochrome P450                             | AT4G36220.1                              | ferulic acid 5-hydroxylase 1                        | 4.68  | 1.67E-03 |
| GQ04004_I14 | GQ04004_I14 | EX437174   | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 4.70  | 1.28E-03 |
| WS00720_P10 | WS00720_P10 | CO242218   | PF00201.13                               | UDP-glucuronosyl and UDP-glucosyl transfe   | AT2G28080.1                              | UDP-Glycosyltransferase superfamily protein         | 4.77  | 9.64E-03 |
| GQ0033_D11  | GQ0033_D11  | BT100631   | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 4.82  | 1.11E-02 |
| WS00743_P13 | WS00743_P13 | DR576621   | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 5.57  | 2.77E-04 |
| GQ03712_I20 | GQ03712_I20 | BT116148   | PF06521.6                                | PAR1 protein                                | AT5G52390.1                              | PAR1 protein  | 5.96  | 4.47E-03 |
| GQ03907_J01 | GQ0256_A12  | BT103518   | PF14555.1;PF00789.15                     | UBA-like domain;UBX domain                  | AT1G14570.2                              | UBX domain-containing protein                       | 6.58  | 2.35E-02 |
| GQ03909_M24 | GQ03909_M24 | EX432133   | PF00082.17;PF02225.17                    | Subtilase family;PA domain                  | AT1G20160.1                              | Subtilisin-like serine endopeptidase family protein | 9.24  | 2.14E-02 |
| GQ03008_N03 | GQ03008_N03 | BT106714   | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 10.26 | 2.68E-02 |
| WS00831_E16 | WS00831_E16 | DR591433   | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 14.09 | 2.26E-02 |
| WS0024_K05  | WS0024_K05  | CO236779   | No significant sequence similarity found | No significant sequence similarity found    | No significant sequence similarity found | No significant sequence similarity found            | 17.68 | 6.34E-03 |

A. Genes up-regulated in R trees, B. Genes up-regulated in N-R trees