**Table S2.** Identification of 128 DEGs at a read depth >0.5X when comparing the inbred vs hybrid that had known annotated descriptions. Gene ID and annotation are displayed according to the reference genome (Denoeud et al. 2014). A positive fold change (FC) represents upregulated expression in the hybrid as compared to the inbred, while a negative FC represents upregulated expression in the inbred as compared to the hybrid. Average sequencing depth was calculated by averaging all samples and treatments as described by (Dugas et al. 2011). The GO term number is presented for known genes using AgriGO 2.0 (Tian et al. 2017). Any GO term with N/A represents unknown GO term. Statistical significance using Bonferroni and FDR are not shown since were lesser than 0.01. Additional GO description of some GO terms can be seen in Table S6.

| **Gene ID**  **(Denoeud et al. 2014)** | **Annotation description** | **DESeq2 FC** | **Average sequencing depth** | **GO term** |
| --- | --- | --- | --- | --- |
| Cc08\_g16300 | Putative Glutaredoxin family protein | 11.74 | 1.800 | GO:0045454 |
| Cc00\_g20080 | ABC transporter G family member 11 | 8.88 | 4.592 | GO:0016020 |
| Cc02\_g05510 | unknown protein; Has 39 Blast hits to 39 proteins in 15 species | 6.89 | 2.926 | N/A |
| Cc05\_g05180 | Putative B-box type zinc finger family protein | 5.19 | 0.914 | GO:0008270 |
| Cc04\_g10750 | BTB/POZ and TAZ domain-containing protein 2 | 5.34 | 1.486 | GO:0005634 |
| Cc02\_g36770 | Ferric reduction oxidase 7, chloroplastic | 5.33 | 6.880 | GO:0050660 |
| Cc06\_g18960 | Putative N-acylneuraminate-9-phosphatase | 4.68 | 6.767 | GO:0008967 |
| Cc08\_g08370 | Caffeic acid 3-O-methyltransferase | 4.21 | 0.547 | GO:0046983 |
| Cc06\_g13690 | Putative Zinc finger protein CONSTANS-LIKE 4 | 4.15 | 1.029 | GO:0008270 |
| Cc01\_g20020 | Histone H2AX | 3.96 | 0.575 | GO:0005634 |
| Cc05\_g12000 | Protein SPA1-RELATED 4 | 3.50 | 0.598 | N/A |
| Cc07\_g11750 | Undecaprenyl diphosphate synthase, putative | 3.47 | 1.563 | N/A |
| Cc02\_g39100 | Hydroquinone glucosyltransferase | 3.40 | 4.202 | GO:0008152 |
| Cc05\_g02850 | Putative Glucan endo-1,3-beta-glucosidase 3 | 3.29 | 0.530 | GO:0003824 |
| Cc07\_g02190 | Putative L-aspartate oxidase | 3.54 | 2.068 | GO:0005737 |
| Cc04\_g09270 | Purple acid phosphatase 17 | 3.46 | 2.182 | GO:0016787 |
| Cc10\_g11980 | Chlorophyllide a oxygenase, chloroplastic | 3.21 | 0.775 | GO:0005506 |
| Cc07\_g01090 | Putative Glycerophosphodiester phosphodiesterase gde1 | 3.22 | 2.746 | GO:0008889 |
| Cc10\_g02310 | ATP-dependent protease La (LON) domain protein | 3.31 | 1.973 | GO:0004176 |
| Cc02\_g03440 | Putative Post-GPI attachment to proteins factor 3 | 2.99 | 0.663 | N/A |
| Cc11\_g05930 | Putative Probable transmembrane ascorbate ferrireductase 3 | 2.96 | 1.840 | GO:0016021 |
| Cc02\_g38130 | Glycerol-3-phosphate acyltransferase 4 | 2.88 | 0.601 | GO:0008415 |
| Cc02\_g00820 | Putative Two-component response regulator-like APRR5 | 2.98 | 3.399 | GO:0000160 |
| Cc06\_g08450 | SPX domain-containing protein 2 | 2.88 | 2.340 | N/A |
| Cc07\_g10470 | Putative Probable salt tolerance-like protein At1g78600 | 2.84 | 1.072 | GO:0008270 |
| Cc11\_g13920 | Putative Transcription factor MYB1R1 | 2.71 | 0.769 | GO:0003677 |
| Cc10\_g13610 | Putative Probable calcium-binding protein CML44 | 2.72 | 2.397 | GO:0005509 |
| Cc02\_g09170 | Putative Trans-2,3-enoyl-CoA reductase | 2.79 | 0.769 | GO:0005737 |
| Cc07\_g02110 | NAD(P)-binding Rossmann-fold superfamily protein | 2.72 | 1.148 | GO:0003824 |
| Cc05\_g13590 | fatty acid desaturase A | 2.75 | 2.250 | N/A |
| Cc00\_g18980 | Putative Probable receptor-like protein kinase At5g39020 | 2.53 | 0.660 | GO:0004674 |
| Cc05\_g07810 | Glutaredoxin-C9 | 2.64 | 0.909 | GO:0045454 |
| Cc03\_g15890 | F-box/ankyrin repeat protein SKIP35 | 2.59 | 1.624 | N/A |
| Cc02\_g24440 | SPX domain-containing protein 3 | 2.61 | 0.841 | N/A |
| Cc02\_g04050 | DNA photolyases;DNA photolyases | 2.61 | 1.042 | GO:0003913 |
| Cc03\_g06030 | Protein PROTON GRADIENT REGULATION 5, chloroplastic | 2.61 | 5.380 | N/A |
| Cc10\_g00330 | plastid movement impaired1 | 2.45 | 0.716 | N/A |
| Cc00\_g16400 | (+)-neomenthol dehydrogenase | 2.50 | 1.517 | GO:0055114 |
| Cc00\_g05460 | Pathogenesis-related protein 5 | 2.56 | 1.065 | N/A |
| Cc10\_g01850 | ATP sulfurylase 2 | 2.47 | 0.518 | GO:0004781 |
| Cc03\_g00700 | Putative Ca2+-binding protein 1 | 2.41 | 2.435 | GO:0005509 |
| Cc10\_g02730 | RAD-like 1 | 2.35 | 0.853 | GO:0003677 |
| Cc00\_g26120 | SC35-like splicing factor 33 | 2.31 | 0.519 | GO:0003676 |
| Cc05\_g07890 | 8-hydroxyquercetin 8-O-methyltransferase | 2.31 | 2.474 | GO:0046983 |
| Cc04\_g16990 | Putative Pectinesterase | 2.35 | 0.671 | GO:0004857 |
| Cc02\_g39110 | Putative Dihydroflavonol-4-reductase | 2.38 | 0.829 | GO:0003824 |
| Cc06\_g07500 | Probable protein phosphatase 2C 27 | 2.33 | 1.137 | GO:0003824 |
| Cc01\_g09970 | Putative Bifunctional polymyxin resistance protein ArnA | 2.34 | 4.006 | GO:0003824 |
| Cc05\_g09930 | Chlorophyll a-b binding protein 8, chloroplastic | 2.39 | 18.224 | GO:0016020 |
| Cc10\_g08170 | Glutamyl-tRNA reductase 1, chloroplastic | 2.39 | 2.887 | GO:0005737 |
| Cc02\_g20030 | Putative phytosulfokine 4 precursor | 2.28 | 0.682 | GO:0005576 |
| Cc07\_g08970 | Putative Rhomboid-related intramembrane serine protease family protein | 2.27 | 0.605 | GO:0004252 |
| Cc02\_g26830 | Putative Uncharacterized GPI-anchored protein At1g27950 | 2.28 | 0.885 | GO:0008289 |
| Cc00\_g24160 | Putative dihydrodipicolinate reductase 3, chloroplastic | 2.21 | 0.519 | GO:0005737 |
| Cc11\_g15740 | Inorganic phosphate transporter 2-1, chloroplastic | 2.27 | 1.528 | GO:0006817 |
| Cc02\_g07890 | Actin | 2.26 | 4.722 | GO:0005524 |
| Cc06\_g15890 | Actin-97 | 2.26 | 1.632 | GO:0005515 |
| Cc11\_g14720 | Carbonic anhydrase, chloroplastic | 2.31 | 4.534 | GO:0015976 |
| Cc04\_g08250 | Putative Dof zinc finger protein DOF5.4 | 2.28 | 0.534 | GO:0045449 |
| Cc00\_g28800 | Putative Isoflavone 7-O-methyltransferase | 2.20 | 1.758 | GO:0046983 |
| Cc07\_g00260 | Chlorophyll a-b binding protein 13, chloroplastic | 2.21 | 3.158 | GO:0016020 |
| Cc06\_g04970 | Sulfite exporter TauE/SafE family protein | 2.23 | 0.562 | GO:0016021 |
| Cc05\_g12720 | Chlorophyll a-b binding protein 13, chloroplastic | 2.21 | 8.688 | GO:0016020 |
| Cc02\_g24580 | Probable plastid-lipid-associated protein 11, chloroplastic | 2.23 | 0.938 | GO:0009507 |
| Cc02\_g37510 | (+)-neomenthol dehydrogenase | 2.20 | 15.768 | GO:0055114 |
| Cc03\_g15090 | UDP-glycosyltransferase 74F2 | 2.11 | 1.149 | GO:0008152 |
| Cc11\_g13590 | Nitrate transporter 1.7 | 2.11 | 0.571 | GO:0006857 |
| Cc11\_g10250 | Probable nitrite transporter At1g68570 | 2.15 | 2.600 | GO:0006857 |
| Cc01\_g17770 | Photosystem II reaction center PSB28 protein, chloroplastic | 2.14 | 1.372 | GO:0016020 |
| Cc02\_g06400 | Omega-3 fatty acid desaturase, chloroplastic | 2.10 | 3.968 | GO:0006629 |
| Cc02\_g39990 | Putative Protein LHY | 2.10 | 1.531 | GO:0003677 |
| Cc06\_g11160 | Serine acetyltransferase 5 | 2.05 | 0.687 | GO:0005737 |
| Cc00\_g05390 | Putative Cation transport regulator-like protein 2 | 2.04 | 1.072 | N/A |
| Cc01\_g11710 | Putative DDB1- and CUL4-associated factor 8 | 2.04 | 1.175 | N/A |
| Cc07\_g13520 | NTA15 protein | 2.02 | 0.604 | N/A |
| Cc08\_g15910 | Putative Probable WRKY transcription factor 41 | -2.12 | 0.566 | GO:0003700 |
| Cc01\_g21030 | Putative Epoxide hydrolase 2 | -2.13 | 0.512 | GO:0003824 |
| Cc06\_g06600 | BEL1-like homeodomain protein 1 | -2.16 | 3.032 | GO:0003700 |
| Cc09\_g06130 | Putative Uncharacterized protein yqjG | -2.15 | 0.833 | N/A |
| Cc07\_g09950 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | -2.17 | 0.569 | GO:0017111 |
| Cc11\_g05610 | NAD(P)H-dependent 6'-deoxychalcone synthase | -2.28 | 0.730 | GO:0055114 |
| Cc02\_g28890 | Serine carboxypeptidase-like 40 | -2.25 | 1.259 | GO:0006508 |
| Cc06\_g22450 | Putative Cytochrome P450 83B1 | -2.37 | 0.746 | GO:0004497 |
| Cc03\_g02380 | Inactive beta-amylase 9 | -2.27 | 1.250 | GO:0003824 |
| Cc02\_g25540 | Protein of unknown function (DUF581) | -2.39 | 1.454 | N/A |
| Cc09\_g10500 | Lysine histidine transporter-like 8 | -2.41 | 0.710 | N/A |
| Cc05\_g08830 | Secologanin synthase | -2.38 | 0.540 | GO:0004497 |
| Cc04\_g17250 | AAA-ATPase 1 | -2.34 | 0.534 | GO:0017111 |
| Cc06\_g23270 | Putative F-box/kelch-repeat protein At1g15670 | -2.39 | 1.550 | N/A |
| Cc10\_g04940 | Putative Transcription factor MYB44 | -2.40 | 1.047 | GO:0045449 |
| Cc00\_g30530 | Putative Cytochrome P450 83B1 | -2.53 | 0.816 | GO:0004497 |
| Cc02\_g20290 | Pathogenesis-related protein 1B | -2.59 | 24.425 | GO:0005576 |
| Cc02\_g12240 | Major facilitator superfamily protein | -2.56 | 1.893 | GO:0016020 |
| Cc04\_g01330 | Nodulation-signaling pathway 1 protein | -2.53 | 1.121 | N/A |
| Cc04\_g11510 | Tropinone reductase homolog At1g07440 | -2.56 | 0.889 | GO:0005488 |
| Cc07\_g08550 | Probable non-specific lipid-transfer protein AKCS9 | -2.49 | 2.188 | GO:0006869 |
| Cc07\_g11550 | Basic endochitinase A | -2.56 | 1.062 | GO:0004568 |
| Cc06\_g18240 | Glucan endo-1,3-beta-glucosidase, acidic isoform PR-Q' | -2.57 | 6.225 | GO:0003824 |
| Cc06\_g13940 | EG45-like domain containing protein | -2.59 | 4.617 | N/A |
| Cc03\_g00450 | galactinol synthase 2 | -2.55 | 2.128 | N/A |
| Cc08\_g09450 | Putative UPF0481 protein At3g02645 | -2.60 | 0.538 | N/A |
| Cc06\_g07210 | Putative Lysosomal beta glucosidase | -2.59 | 0.685 | GO:0005975 |
| Cc00\_g14270 | NAC domain containing protein 36 | -2.84 | 1.043 | GO:0045449 |
| Cc11\_g07780 | Pathogenesis-related protein R major form | -2.63 | 5.451 | N/A |
| Cc00\_g13890 | Double WRKY type transfactor | -2.94 | 0.570 | GO:0003700 |
| Cc10\_g03880 | Protein of unknown function, DUF617 | -2.92 | 0.570 | N/A |
| Cc04\_g05080 | Probable WRKY transcription factor 40 | -2.94 | 0.516 | GO:0003700 |
| Cc07\_g13290 | Glutamine synthetase cytosolic isozyme 2 | -2.89 | 1.947 | GO:0004356 |
| Cc07\_g07790 | Uncharacterized protein At5g65660 | -3.07 | 0.726 | N/A |
| Cc00\_g14300 | Basic endochitinase | -3.04 | 12.307 | GO:0004568 |
| Cc10\_g11110 | Putative Vinorine synthase | -3.12 | 1.291 | N/A |
| Cc03\_g03550 | Sugar transport protein 13 | -3.22 | 1.514 | GO:0022891 |
| Cc04\_g03730 | Pleiotropic drug resistance protein 1 | -3.18 | 2.748 | GO:0016020 |
| Cc00\_g34980 | UDP-glucose flavonoid 3-O-glucosyltransferase 6 | -3.26 | 0.805 | GO:0008152 |
| Cc00\_g34570 | CYP71AT2v1 | -3.26 | 1.318 | GO:0004497 |
| Cc11\_g00410 | Putative Acidic endochitinase | -3.23 | 40.277 | GO:0003824 |
| Cc07\_g13880 | Probable 1-deoxy-D-xylulose-5-phosphate synthase 2, chloroplastic | -3.27 | 0.903 | GO:0003824 |
| Cc09\_g01430 | WRKY transcription factor 6 | -3.39 | 0.586 | GO:0003700 |
| Cc00\_g33180 | Endochitinase B | -3.42 | 8.574 | GO:0004568 |
| Cc06\_g18280 | Glucan endo-1,3-beta-glucosidase, acidic isoform PR-Q' | -3.82 | 7.356 | GO:0003824 |
| Cc08\_g14230 | Thaumatin-like protein | -3.72 | 1.818 | N/A |
| Cc10\_g10180 | serine-type endopeptidase inhibitors | -3.82 | 0.903 | GO:0004867 |
| Cc00\_g11200 | Probable LRR receptor-like serine/threonine-protein kinase At4g08850 | -4.21 | 0.791 | GO:0006468 |
| Cc03\_g09010 | Putative CYC02 protein | -5.27 | 5.003 | N/A |
| Cc08\_g01530 | Beta-amylase 3, chloroplastic | -7.76 | 0.931 | GO:0003824 |
| Cc05\_g12500 | NAC domain-containing protein 72 | -5.59 | 0.825 | GO:0045449 |
| Cc11\_g12740 | NAC domain-containing protein 29 | -7.70 | 2.419 | GO:0045449 |
| Cc04\_g10600 | Putative Cytochrome P450 82A3 | -43.08 | 0.602 | GO:0004497 |