**Table S4.** Genes found to be differentially expressed and associated to a trait according to the stepwise regression when compared the rust control treatment with no rust control. The regulation represents if the gene expression was upregulated (increased with an increase in the trait), or was downregulated (decreased with an increase of the trait). GO terms with several pathways, are referred to as “Several”, rather than a specific GO term code.

| **Cultivar** | **Trait** | **Regulation** | **Annotation (Gene ID (Denoeud et al. 2014))** | **Std Error** | **Prob>|*t*|** | **GO term** |
| --- | --- | --- | --- | --- | --- | --- |
| Inbred | TH | Down | Putative BON1-associated protein 2 (Cc00\_g30940) | 9.42E-06 | 0.0002 | Several |
| Inbred | OC | Down | Putative uncharacterized protein (Cc00\_g03090) | 5.64E-05 | 0.0033 | Several |
| Inbred | TH | Down | Beta-fructofuranosidase, insoluble isoenzyme 1 (Cc06\_g06090) | 3.23E-06 | 0.0007 | GO:0005975 |
| Hybrid | TL | Down | 40S ribosomal protein S27-1 (Cc11\_g14900) | 2.32E-07 | 0.0001 | GO:0003735 |
| Hybrid | TL | Down | 40S ribosomal protein S27-1 (Cc11\_g14900) | 2.32E-07 | 0.0001 | GO:0003735 |
| Inbred | RI | Down | Putative Cytochrome P450 87A3 (Cc02\_g08960) | 3.11E-10 | <.0001 | GO:0004497 |
| Inbred | RI | Down | Cytochrome P450 87A3 (Cc00\_g06850) | 4.16E-10 | <.0001 | GO:0004497 |
| Hybrid | RI | Down | Putative Calcium-dependent lipid-binding (CaLB domain) family protein (Cc00\_g10550) | 1.55E-09 | <.0001 | Several |
| Hybrid | TH | Up | Putative Disease resistance protein RGA2 (Cc00\_g26280) | 3.45E-06 | <.0001 | GO:0006952 |
| Hybrid | TL | Down | Sucrose synthase 2 (Cc04\_g08870) | 1.12E-07 | 0.0015 | GO:0009058 |
| Hybrid | TL | Down | Hypothetical protein (Cc00\_g07620) | 1.67E-07 | 0.0004 | Several |
| Hybrid | RS | Up | Putative uncharacterized protein (Cc00\_g03090) | 3.76E-06 | <.0001 | Several |
| Hybrid | RI | Up | Putative Aldo-keto reductase yakc (Cc02\_g36130) | 4.93E-06 | <.0001 | GO:0055114 |
| Hybrid | TL | Up | Hypothetical protein (Cc00\_g07620) | 1.45E-05 | <.0001 | Several |
| Hybrid | RI | Up | Hypothetical protein (Cc00\_g07620) | 5.55E-07 | <.0001 | Several |
| Hybrid | RE | Down | Putative Monoglyceride lipase (Cc00\_g15700) | 1.71E-08 | <.0001 | Several |
| Hybrid | OC | Up | Putative Disease resistance protein RGA2 (Cc00\_g26280) | 2.09E-09 | <.0001 | GO:0006952 |
| Hybrid | TL | Up | Putative ABC transporter A family member 12 (Cc00\_g22610) | 8.17E-06 | <.0001 | Several |
| Hybrid | OC | Up | Putative ABC transporter A family member 12 (Cc00\_g22610) | 1.28E-09 | <.0001 | Several |
|  |  |  |  |  |  |  |
| Supporting information 4 continued… | | | | | | |
| Hybrid | RI | Up | Putative ABC transporter A family member 12 (Cc00\_g22610) | 5.66E-07 | <.0001 | Several |
| Hybrid | RE | Down | UDP-glycosyltransferase 85A3 (Cc00\_g30680) | 6.25E-08 | 0.0003 | GO:0008152 |
| Hybrid | OC | Up | Putative Small subunit processome component 20 homolog (Cc00\_g24200) | 2.76E-09 | <.0001 | GO:0005488 |
| Inbred | RE | Down | Putative BON1-associated protein 2 (Cc00\_g30940) | 3.99E-05 | 0.0004 | Several |
| Hybrid | RI | Down | Small nuclear ribonucleoprotein family protein (Cc02\_g33830) | 7.41E-09 | <.0001 | Several |
| Inbred | RI | Down | Major allergen Pru ar 1 (Cc03\_g01290) | 1.07E-09 | <.0001 | GO:0006952 |
| Hybrid | TH | Down | Putative unknown protein; INVOLVED IN (Cc08\_g08670) | 0.001706 | 0.0009 | Several |
| Hybrid | RE | Down | RING/FYVE/PHD zinc finger superfamily protein (Cc00\_g23100) | 1.46E-08 | 0.0002 | GO:0008270 |
| Hybrid | TL | Down | Hypothetical protein (Cc00\_g07620) | 1.25E-06 | <.0001 | Several |
| Hybrid | TH | Down | Basic endochitinase (Cc00\_g14300) | 0.000259 | 0.0008 | GO:0004568 |
| Hybrid | TL | Down | Mannan endo-1,4-beta-mannosidase 5 (Cc00\_g30210) | 0.000888 | <.0001 | GO:0003824 |
| Inbred | TH | Down | Mannan endo-1,4-beta-mannosidase 5 (Cc00\_g30210) | 1.26E-05 | 0.0003 | GO:0003824 |
| Hybrid | TL | Down | Hypothetical protein (Cc00\_g07620) | 5.33E-06 | 0.0002 | Several |
| Hybrid | RS | Up | Putative pentatricopeptide repeat-containing protein At1g12700, mitochondrial (Cc00\_g04090) | 2.21E-06 | <.0001 | Several |
| Hybrid | RE | Down | Pathogenesis-related genes transcriptional activator PTI5 (Cc02\_g14240) | 9.26E-08 | 0.0007 | GO:0003700 |
| Hybrid | RS | Down | Arginine decarboxylase (Cc02\_g16860) | 8.77E-09 | 0.0018 | GO:0008792 |
| Hybrid | TL | Up | Oligopeptide transporter 4 (Cc02\_g20620) | 8.25E-06 | <.0001 | GO:0055085 |
| Hybrid | RI | Up | Putative Probable 1,4-dihydroxy-2-naphthoate octaprenyltransferase (Cc02\_g21250) | 2.77E-07 | 0.0007 | GO:0016021 |
| Hybrid | TL | Down | Pectinesterase 2 (Cc02\_g24210) | 0.000249 | <.0001 | GO:0005618 |
| Hybrid | RS | Down | Putative Receptor-like protein 12 (Cc11\_g00880) | 6.42E-08 | <.0001 | GO:0005515 |
|  |  |  |  |  |  |  |
| Supporting information 4 continued… | | | | | | |
| Hybrid | RE | Down | Putative Receptor-like protein 12 (Cc01\_g08260) | 7.18E-09 | 0.0002 | GO:0005515 |
| Hybrid | TL | Down | Putative Basic 7S globulin (Cc00\_g13300) | 0.000199 | <.0001 | GO:0006508 |
| Hybrid | RE | Up | Putative Myosin-J heavy chain (Cc01\_g17540) | 1.27E-06 | <.0001 | GO:0016459 |
| Hybrid | OC | Up | Pentatricopeptide repeat-containing protein At5g48730, chloroplastic (Cc01\_g16930) | 2.45E-09 | <.0001 | Several |
| Inbred | RS | Down | Tyrosine aminotransferase (Cc05\_g07600) | 6.64E-05 | 0.0008 | GO:0016847 |
| Inbred | OC | Down | Hypothetical protein (Cc00\_g07620) | 3.13E-06 | <.0001 | Several |
| Inbred | RI | Down | Hypothetical protein (Cc00\_g07620) | 2.36E-10 | <.0001 | Several |
| Hybrid | TH | Up | Hypothetical protein (Cc00\_g07620) | 1.83E-06 | <.0001 | Several |
| Hybrid | TL | Up | Protein of unknown function (DUF707) (Cc09\_g03510) | 3.51E-06 | 0.0078 | Several |
| Inbred | TH | Down | Pathogenesis-related protein R major form (Cc11\_g07800) | 1.54E-08 | <.0001 | Several |
| Hybrid | RI | Down | Ammonium transporter 3 member 1 (Cc07\_g19370) | 5.38E-09 | 0.0002 | GO:0016020 |
| Hybrid | RE | Down | Nuclear transport factor 2 (Cc07\_g00920) | 2.15E-08 | <.0001 | GO:0006810 |
| Hybrid | RE | Up | Putative unknown protein; Has 50 Blast hits to 45 proteins in 14 species (Cc03\_g11440) | 9.79E-06 | <.0001 | Several |
| Hybrid | TH | Down | Acidic endochitinase SE2 (Cc05\_g00810) | 0.000144 | 0.002 | GO:0003824 |
| Hybrid | RE | Down | 40S ribosomal protein S10 (Cc02\_g02340) | 4.82E-09 | <.0001 | Several |
| Hybrid | RE | Down | Carboxylesterase 1 (Cc02\_g03630) | 2.72E-08 | <.0001 | GO:0016787 |
| Hybrid | TL | Up | Sodium/hydrogen exchanger 7 (Cc11\_g05270) | 2.06E-05 | <.0001 | GO:0006812 |
| Hybrid | RI | Down | Putative LRR receptor-like serine/threonine-protein kinase FLS2 (Cc11\_g06630) | 5.22E-08 | <.0001 | GO:0005515 |
| Hybrid | TH | Down | Putative Leucine-rich repeat receptor-like protein kinase PXL1 (Cc11\_g06760) | 0.001395 | 0.0038 | GO:0005515 |
| Hybrid | RI | Down | Putative Leucine-rich repeat receptor-like protein kinase TDR (Cc00\_g31890) | 7.57E-09 | <.0001 | GO:0005515 |
| Hybrid | RS | Up | ABC transporter C family member 1 (Cc09\_g08460) | 6.31E-07 | <.0001 | GO:0016021 |
| Inbred | RS | Down | 1-aminocyclopropane-1-carboxylate oxidase 3 (Cc05\_g02900) | 1.06E-06 | <.0001 | GO:0016491 |
|  |  |  |  |  |  |  |
| Supporting information 4 continued… | | | | | | |
| Inbred | RE | Down | Putative Hyoscyamine 6-dioxygenase (Cc05\_g10390) | 3.57E-06 | 0.0001 | GO:0016491 |
| Inbred | RS | Down | Probable glutathione S-transferase parC (Cc07\_g20060) | 1.71E-05 | 0.0001 | Several |
| Inbred | OC | Down | Probable glutathione S-transferase (Cc05\_g10080) | 4.32E-05 | <.0001 | Several |
| Hybrid | TL | Down | Tubulin beta-2 chain (Cc04\_g06320) | 1.39E-07 | <.0001 | GO:0051258 |
| Hybrid | TH | Down | Purple acid phosphatase 17 (Cc04\_g09270) | 3.86E-05 | 0.0005 | GO:0016787 |
| Inbred | RI | Down | phosphate transporter 3;1 (Cc04\_g09390) | 2.00E-09 | <.0001 | GO:0016020 |
| Hybrid | OC | Up | Putative Glycogen synthase (Cc09\_g09040) | 6.09E-10 | <.0001 | GO:0009058 |
| Hybrid | OC | Up | Putative Glycogen synthase (Cc09\_g09040) | 6.09E-10 | <.0001 | GO:0009058 |
| Hybrid | RE | Up | Putative Glycogen synthase (Cc09\_g09040) | 8.49E-07 | <.0001 | GO:0009058 |
| Hybrid | RE | Up | Putative Glycosyl transferase, family 8 (Cc06\_g00020) | 2.92E-05 | <.0001 | Several |
| Hybrid | OC | Up | Putative uncharacterized protein Sb01g036200 (Cc06\_g00350) | 7.16E-09 | <.0001 | GO:0016020 |
| Inbred | OC | Down | Probable anion transporter 3, chloroplastic (Cc06\_g01670) | 5.24E-06 | 0.0071 | GO:0055085 |
| Hybrid | RS | Down | PAR1 protein (Cc06\_g01870) | 1.27E-07 | <.0001 | Several |
| Inbred | RI | Down | PAR1 protein (Cc06\_g01870) | 2.62E-10 | <.0001 | Several |
| Inbred | TH | Down | PAR1 protein (Cc06\_g01870) | 4.84E-07 | 0.0005 | Several |
| Hybrid | RI | Down | Probable glutathione S-transferase (Cc05\_g10080) | 1.90E-09 | 0.0016 | Several |
| Hybrid | TL | Down | V-type proton ATPase 16 kDa proteolipid subunit (Cc10\_g02030) | 1.04E-07 | <.0001 | GO:0015986 |
| Hybrid | TL | Down | V-type proton ATPase 16 kDa proteolipid subunit (Cc10\_g02030) | 1.04E-07 | <.0001 | GO:0015986 |
| Inbred | RE | Down | Putative Anthocyanidin 3-O-glucosyltransferase 5 (Cc10\_g03270) | 1.54E-05 | 0.001 | GO:0008152 |
| Inbred | TL | Down | Probable calcium-binding protein CML41 (Cc10\_g03450) | 0.000955 | <.0001 | GO:0005509 |
| Inbred | OC | Down | Probable calcium-binding protein CML41 (Cc10\_g03450) | 0.000127 | 0.0008 | GO:0005509 |
|  |  |  |  |  |  |  |
| Supporting information 4 continued… | | | | | | |
| Inbred | RE | Down | Probable calcium-binding protein CML41 (Cc10\_g03450) | 6.15E-05 | 0.0014 | GO:0005509 |
| Hybrid | TL | Up | Putative Probable serine/threonine-protein kinase DDB\_G0276461 (Cc02\_g27140) | 0.000027 | <.0001 | GO:0004674 |
| Hybrid | RE | Up | Putative Probable serine/threonine-protein kinase DDB\_G0276461 (Cc02\_g27140) | 7.23E-06 | <.0001 | GO:0004674 |
| Hybrid | RE | Up | Putative uncharacterized protein (Cc00\_g03090) | 1.94E-06 | 0.0015 | Several |
| Inbred | RS | Down | Putative Vetispiradiene synthase 1 (Cc08\_g06960) | 2.85E-05 | <.0001 | GO:0016829 |
| Hybrid | OC | Up | Remorin family protein (Cc11\_g03240) | 1.71E-09 | <.0001 | Several |
| Hybrid | OC | Up | Remorin family protein (Cc11\_g03240) | 1.71E-09 | <.0001 | Several |
| Hybrid | TH | Up | Remorin family protein (Cc11\_g03240) | 6.88E-07 | <.0001 | Several |
| Hybrid | TL | Down | Beta-D-xylosidase 1 (Cc03\_g01070) | 3.22E-05 | <.0001 | GO:0005975 |
| Hybrid | OC | Up | Hypothetical protein (Cc00\_g07620) | 2.60E-09 | 0.0004 | Several |
| Hybrid | RE | Up | Hypothetical protein (Cc00\_g07620) | 5.35E-06 | <.0001 | Several |
| Hybrid | OC | Up | Putative Non-lysosomal glucosylceramidase (Cc03\_g07570) | 2.26E-09 | <.0001 | Several |
| Hybrid | RS | Up | Putative Non-lysosomal glucosylceramidase (Cc03\_g07570) | 5.12E-07 | 0.0032 | Several |
| Inbred | TH | Down | Putative Reticuline oxidase-like protein (Cc03\_g15300) | 1.21E-06 | 0.0062 | GO:0050660 |
| Inbred | RI | Down | 1-aminocyclopropane-1-carboxylate synthase (Cc02\_g38530) | 2.21E-09 | 0.0002 | GO:0003824 |
| Hybrid | TH | Down | Chitinase 2 (Cc03\_g12410) | 0.000318 | 0.001 | GO:0003824 |
| Hybrid | RI | Up | Putative Pentatricopeptide repeat-containing protein At3g48810 (Cc01\_g05040) | 1.56E-06 | <.0001 | Several |
| Hybrid | RI | Up | Protein of unknown function (DUF581) (Cc04\_g00800) | 8.06E-08 | <.0001 | Several |
| Hybrid | RS | Down | Flavoprotein WrbA (Cc02\_g11960) | 2.11E-07 | 0.0008 | GO:0010181 |
| Inbred | RE | Down | Putative Probable E3 ubiquitin-protein ligase ARI7 (Cc02\_g10790) | 2.04E-05 | <.0001 | GO:0008270 |
| Hybrid | RE | Down | Phosphoenolpyruvate carboxylase kinase 2 (Cc02\_g08980) | 7.09E-09 | 0.0077 | GO:0004674 |
| Hybrid | RS | Down | Thaumatin-like protein (Cc08\_g14230) | 5.09E-08 | <.0001 | Several |
| Supporting information 4 continued… | | | | | | |
| Inbred | RE | Down | Putative Acidic mammalian chitinase (Cc06\_g15430) | 3.23E-05 | 0.0005 | GO:0003824 |
| Inbred | OC | Down | Putative Stellacyanin (Cc06\_g08240) | 3.47E-06 | <.0001 | GO:0005507 |
| Inbred | RI | Down | Putative Stellacyanin (Cc06\_g08240) | 1.30E-10 | <.0001 | GO:0005507 |
| Inbred | TH | Down | serine-type endopeptidase inhibitors (Cc10\_g10180) | 5.38E-07 | 0.0002 | GO:0004867 |
| Hybrid | TL | Down | Putative Strictosidine synthase 1 (Cc05\_g04400) | 2.25E-06 | 0.0005 | GO:0016844 |
| Inbred | TH | Down | 1-aminocyclopropane-1-carboxylate synthase (Cc02\_g38530) | 3.22E-06 | 0.0028 | GO:0003824 |
| Inbred | RE | Down | Tabersonine 16-hydroxylase (Fragment) (Cc03\_g14110) | 0.000015 | 0.0003 | GO:0004497 |
| Hybrid | TL | Up | Armadillo/beta-catenin-like repeat ; C2 calcium/lipid-binding domain (CaLB) protein (Cc10\_g12190) | 1.76E-05 | <.0001 | GO:0005488 |
| Inbred | OC | Down | Metal transporter Nramp5 (Cc00\_g20930) | 0.00021 | 0.0014 | GO:0005215 |
| Inbred | OC | Down | Hypothetical protein (Cc00\_g07620) | 0.000112 | 0.0001 | Several |
| Inbred | RI | Down | Hypothetical protein (Cc00\_g07620) | 2.68E-09 | <.0001 | Several |
| Hybrid | TH | Up | Phosphate transporter PHO1 homolog 1 (Cc11\_g10900) | 9.13E-07 | 0.0002 | Several |
| Hybrid | TH | Up | Phosphate transporter PHO1 homolog 1 (Cc11\_g10900) | 9.13E-07 | 0.0002 | Several |
| Hybrid | TH | Up | Putative Uridine-cytidine kinase C (Cc11\_g08540) | 1.57E-06 | <.0001 | GO:0000166 |
| Hybrid | TH | Up | Putative Uridine-cytidine kinase C (Cc11\_g08540) | 1.57E-06 | <.0001 | GO:0000166 |
| Inbred | TH | Down | Hypothetical protein (Cc00\_g07620) | 2.35E-06 | <.0001 | Several |
| Hybrid | RS | Down | Putative uncharacterized protein (Cc00\_g03090) | 6.48E-07 | <.0001 | Several |
| Hybrid | RI | Up | Putative pre-mRNA-processing protein 40A (Cc02\_g20050) | 5.62E-07 | <.0001 | GO:0005515 |
| Inbred | RI | Down | Probable trehalose-phosphate phosphatase E (Cc10\_g07410) | 1.44E-09 | <.0001 | GO:0003824 |
| Inbred | TL | Down | Putative uncharacterized protein (Cc00\_g03090) | 0.001399 | 0.0011 | Several |
| Hybrid | RI | Down | Putative Uncharacterized endoplasmic reticulum membrane protein C16E8.02 (Cc04\_g16310) | 1.18E-09 | <.0001 | Several |
| Supporting information 4 continued… | | | | | | |
| Hybrid | TL | Up | Hypothetical protein (Cc00\_g07620) | 3.23E-05 | 0.0002 | GO:0003678 |
| Hybrid | TH | Up | Putative U-box domain-containing protein 50 (Cc07\_g14020) | 6.54E-08 | <.0001 | GO:0006468 |
| Inbred | OC | Down | Benzoate--CoA ligase, peroxisomal (Cc07\_g12710) | 5.65E-05 | 0.0002 | GO:0003824 |
| Hybrid | TL | Down | Pathogenesis-related leaf protein 6 (Cc02\_g20280) | 1.94E-08 | <.0001 | GO:0005576 |
| Hybrid | RS | Down | Pathogenesis-related leaf protein 6 (Cc02\_g20280) | 3.82E-09 | <.0001 | GO:0005576 |
| Inbred | TH | Down | Thioesterase superfamily protein (Cc04\_g11880) | 2.57E-06 | 0.0002 | Several |
| Hybrid | RS | Up | Developmentally-regulated GTP-binding protein 1 (Cc07\_g16280) | 1.59E-06 | <.0001 | Several |
| Inbred | RE | Down | Putative Probable carboxylesterase 6 (Cc07\_g16100) | 5.47E-06 | 0.001 | GO:0016787 |
| Hybrid | RS | Down | EIN3-binding F-box protein 1 (Cc06\_g08370) | 1.28E-08 | <.0001 | Several |
| Hybrid | TH | Down | EIN3-binding F-box protein 1 (Cc06\_g08370) | 0.000134 | 0.0018 | Several |
| Inbred | RS | Down | 1-aminocyclopropane-1-carboxylate synthase 3 (Cc07\_g07490) | 8.96E-05 | <.0001 | GO:0003824 |
| Hybrid | RS | Up | Hypothetical protein (Cc00\_g07620) | 2.74E-07 | <.0001 | Several |
| Inbred | TL | Down | Putative methyltransferase DDB\_G0268948 (Cc06\_g18640) | 0.002042 | 0.0012 | GO:0008168 |
| Hybrid | RS | Up | Putative uncharacterized protein (Cc00\_g03090) | 6.16E-07 | <.0001 | GO:0003676 |
| Hybrid | TH | Up | Golgin candidate 1 (Cc06\_g10330) | 5.38E-07 | <.0001 | Several |
| Hybrid | RI | Down | PeroxiRedoxin-2B (Cc06\_g09990) | 1.56E-09 | <.0001 | GO:0045454 |
| Inbred | RE | Down | Putative Ankyrin repeat-containing protein At5g02620 (Cc05\_g06990) | 0.000154 | 0.0006 | Several |
| Hybrid | TH | Up | Putative RING finger and CHY zinc finger domain-containing protein 1 (Cc04\_g15950) | 6.41E-07 | <.0001 | GO:0008270 |
| Hybrid | RI | Down | Dihydrodipicolinate synthase, chloroplastic (Cc08\_g04960) | 8.52E-08 | <.0001 | GO:0016829 |