**Table S6.** Genes associated with disease-related traits when compared the rust control (R) vs no control (C) treatments in the hybrid. All the significant correlations ranged between |0.74| and |0.94|. A negative correlation indicates an increase in gene expression as the trait value increases, while positive correlations indicate an increase in gene expression as the trait value increases. Stepwise regression data is not shown.

| **Gene annotation (Gene ID (Denoeud et al. 2014))** | **GO description** | **Spearman correlation** |
| --- | --- | --- |
| **Trait**[[1]](#footnote-2) | **Spearman ρ** | **Prob>|ρ|** |
| Putative Small subunit processome component 20 homolog (Cc00\_g24200) | binding  | RI | -0.76 | 0.0062 |
| RE | -0.87 | 0.0005 |
| Putative Disease resistance protein RGA2 (Cc00\_g26280) | defense response  | RI | -0.76 | 0.0062 |
| RE | -0.83 | 0.0017 |
| RE | -0.81 | 0.0025 |
| Putative Myosin-J heavy chain (Cc01\_g17540) | myosin complex  | RE | -0.85 | 0.0008 |
| Oligopeptide transporter 4 (Cc02\_g20620) | transmembrane transport  | RI | -0.76 | 0.0062 |
| RE | -0.75 | 0.0085 |
| Putative Probable 1,4-dihydroxy-2-naphthoate octaprenyltransferase (Cc02\_g21250) | integral component of membrane  | RI | -0.75 | 0.0085 |
| RE | -0.82 | 0.0021 |
| Putative Probable serine/threonine-protein kinase DDB\_G0276461 (Cc02\_g27140) | protein serine/threonine kinase activity  | RE | -0.76 | 0.0062 |
|  |
| Supporting information 6 continued… |
| Putative Aldo-keto reductase yakc (Cc02\_g36130) | oxidation-reduction process  | RI | -0.93 | 0.0000 |
| RS | -0.87 | 0.0005 |
| RE | -0.94 | 0.0000 |
| Putative RING finger and CHY zinc finger domain-containing protein (Cc04\_g15950) | zinc ion binding  | RE | -0.79 | 0.0037 |
| Hypothetical protein (Cc04\_g16980) | DNA helicase activity  | RI | -0.87 | 0.0005 |
| RS | -0.77 | 0.0053 |
| RE | -0.93 | 0.0000 |
| Putative uncharacterized protein (Cc06\_g23510) | nucleic acid binding  | RE | -0.87 | 0.0005 |
| ABC transporter C family member (Cc09\_g08460) | integral component of membrane  | RI | -0.76 | 0.0062 |
| RE | -0.75 | 0.0085 |
| Putative Glycogen synthase (Cc09\_g09040) | biosynthetic process  | RE | -0.79 | 0.0037 |
| Putative pre-mRNA-processing protein 40A (Cc10\_g07620) | protein binding  | RI | -0.75 | 0.0085 |
| RE | -0.83 | 0.0017 |
| Armadillo/beta-catenin-like repeat ; C2 calcium/lipid-binding domain (CaLB) protein (Cc10\_g12190) | binding  | RE | -0.84 | 0.0013 |
| Sodium/hydrogen exchanger 7 (Cc11\_g05270) | cation transport  | RI | -0.85 | 0.0010 |
| RS | -0.75 | 0.0085 |
| RE | -0.91 | 0.0001 |
|  |  |  |  |  |
|  |
| Supporting information 6 continued… |
| Putative Uridine-cytidine kinase C (Cc11\_g08540) | nucleotide binding  | RI | -0.80 | 0.0031 |
| RS | -0.75 | 0.0073 |
| RE | -0.91 | 0.0001 |
| Basic endochitinase (Cc00\_g14300) | chitinase activity  | RE | 0.86 | 0.0006 |
| RING/FYVE/PHD zinc finger superfamily protein (Cc00\_g23100) | zinc ion binding  | RE | 0.87 | 0.0005 |
| UDP-glycosyltransferase 85A3 (Cc00\_g30680) | metabolic process  | RE | 0.86 | 0.0006 |
| Sucrose synthase 2 (Cc01\_g21050) | biosynthetic process  | RE | 0.80 | 0.0031 |
| Carboxylesterase 1 (Cc02\_g03630) | hydrolase activity  | RI | 0.81 | 0.0026 |
| RE | 0.86 | 0.0006 |
| Phosphoenolpyruvate carboxylase kinase 2 (Cc02\_g08980) | protein serine/threonine kinase activity  | RE | 0.75 | 0.0073 |
| Flavoprotein WrbA (Cc02\_g11960) | FMN binding  | RI | 0.78 | 0.0045 |
| RE | 0.88 | 0.0003 |
| Pathogenesis-related genes transcriptional activator PTI5 (Cc02\_g14240) | transcription factor activity, sequence-specific DNA binding | RI | 0.80 | 0.0031 |
| RE | 0.81 | 0.0026 |
| Arginine decarboxylase (Cc02\_g16860) | arginine decarboxylase activity  | RE | 0.74 | 0.0098 |
| phosphate transporter 3;1 (Cc04\_g09390) | membrane  | RI | 0.81 | 0.0026 |
| RS | 0.74 | 0.0098 |
| RE | 0.80 | 0.0031 |
|  |  |  |  |  |
|  |  |  |  |  |
| Supporting information 6 continued… |
| Putative Stellacyanin (Cc06\_g08240) | copper ion binding  | RI | 0.75 | 0.0085 |
| RS | 0.74 | 0.0098 |
| RE | 0.81 | 0.0026 |
| PeroxiRedoxin-2B (Cc06\_g09990) | cell Redox homeostasis  | RE | 0.77 | 0.0053 |
| Nuclear transport factor 2 (Cc07\_g00920) | transport  | RI | 0.75 | 0.0085 |
| RE | 0.91 | 0.0001 |
| Dihydrodipicolinate synthase, chloroplastic (Cc08\_g04960) | lyase activity  | RI | 0.82 | 0.0021 |
| RE | 0.87 | 0.0005 |
| V-type proton ATPase 16 kDa proteolipid subunit (Cc10\_g02030) | ATP synthesis coupled proton transport  | RE | 0.80 | 0.0031 |
| Probable calcium-binding protein CML41 (Cc10\_g03450) | calcium ion binding  | RE | 0.82 | 0.0021 |
| Probable trehalose-phosphate phosphatase E (Cc10\_g07410) | catalytic activity  | RI | 0.87 | 0.0005 |
| RS | 0.84 | 0.0013 |
| RE | 0.94 | 0.0000 |
| Putative LRR receptor-like serine/threonine-protein kinase FLS2 (Cc11\_g06630) | protein binding  | RE | 0.79 | 0.0037 |
| RE | 0.78 | 0.0045 |
| 40S ribosomal protein S27-1 (Cc11\_g14900) | structural constituent of ribosome  | RI | 0.88 | 0.0003 |
| RS | 0.82 | 0.0021 |
| RE | 0.85 | 0.0010 |

1. RI = rust incidence, RS = rust severity, RE = rust sporulation [↑](#footnote-ref-2)