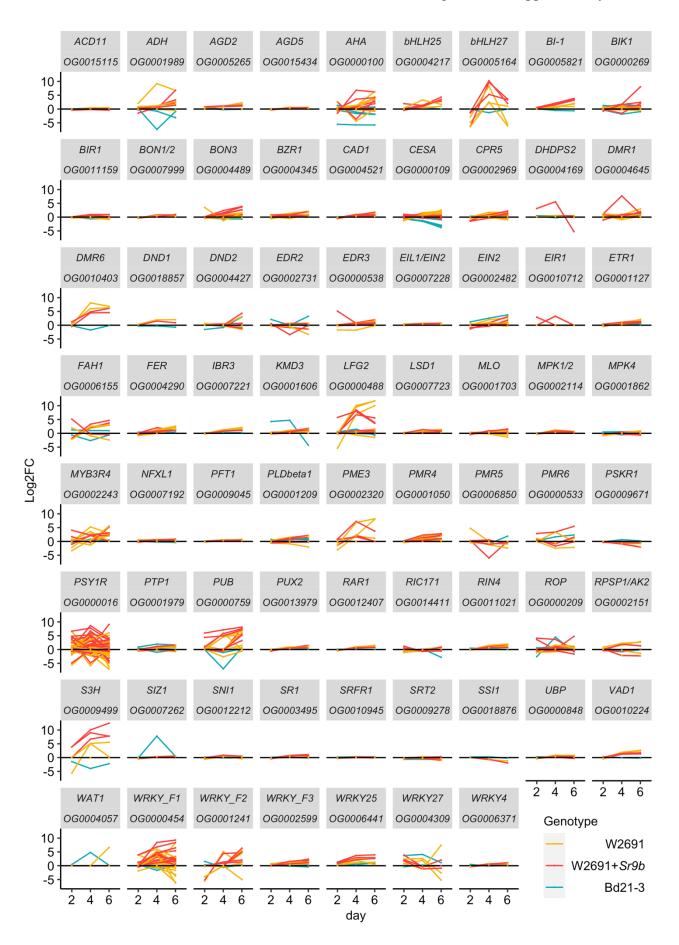
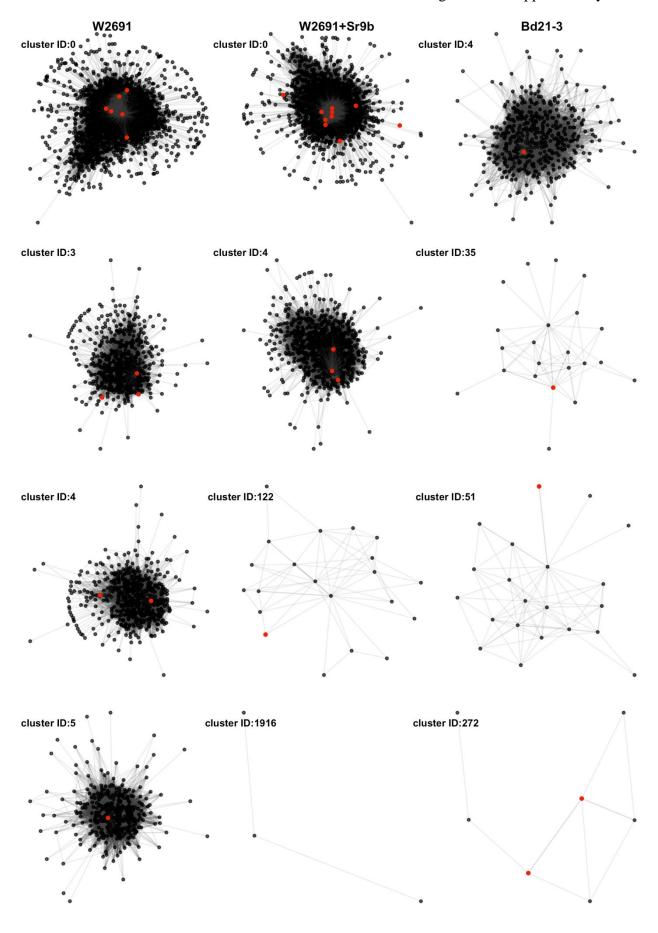
## Henningsen et al. Supplementary Material

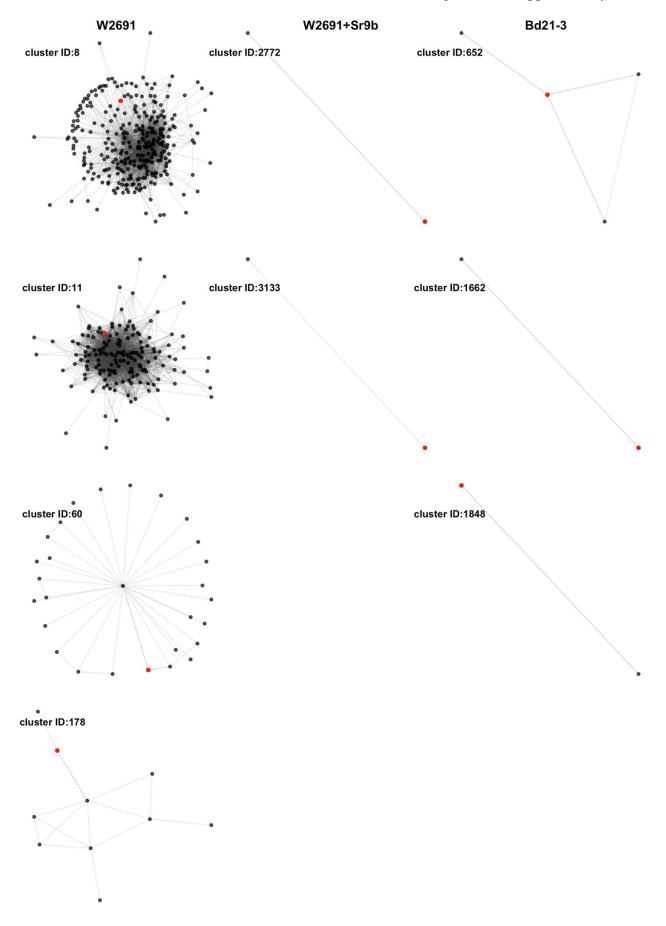


**Supplementary Figure 1.** Expression profile patterns of orthogroups containing candidate *S* genes in *T. aestivum* (W2691 and W2691+*Sr9b*) and *B. distachyon* (Bd21-3) genotypes throughout infection with *P. graminis* f. sp. *tritici*. Log2 fold change values (y-axis) for all gene orthologs are presented per sampling time point (x-axis). Name of *S* gene and orthogroup identifier are shown in each graph.

AGD2 BdiBd21\_3\_1G0280300 BdiBd21\_3\_1G0628300 AT4G33680 CTraesCS4A02G116000 TraesCS4D02G189600 TraesCS7D02G452900 0.02 BI-1 TraesCS6A02G083200 TraesCS6B02G113900 BdiBd21\_3\_3G0030500 HORVU6Hr1G014450 TraesCS6D02G077000 800.0 DMR6 TraesCS4B02G346900 - TraesCS4D02G341800 AT5G24530 BdiBd21\_3\_1G1026800 0.05 FAH1 TraesCS5A02G019200 TraesCS5D02G024600 BdiBd21\_3\_4G0011900 AT2G34770 TraesCS5D02G424200 BdiBd21\_3\_1G0091300 0.04 IBR3 AT3G06810 BdiBd21\_3\_1G0234900 TraesCS2A02G109700 TraesCS2D02G109900 TraesCS2B02G127700 L 0.04 VAD1 TraesCS2A02G231900 LTraesCS2D02G236800 TraesCS2B02G253500 -AT1G02120 BdiBd21\_3\_1G0357000 0.1 WRKY25 - AT2G30250 BdiBd21\_3\_2G0000500 BdiBd21\_3\_4G0022900 TraesCS1A02G070400 TraesCS1D02G072900 TraesCS1B02G088900 0.1

**Supplementary Figure 2.** Molecular phylogenetic analysis of amino acid sequences of orthologous genes for five of the six S genes of interest. The orthogroup for DND1 only included three genes (One *A. thaliana* susceptibility gene, one *T. aestivum* ortholog, and one *B. distachyon* ortholog) and so no phylogenetic tree was generated. Scale bars represent nucleotide substitutions per site.





**Supplementary Figure 3.** All clusters (nodes > 1) containing a *T. aestivum* or *B. distachyon* ortholog of the eight susceptibility candidates. Red points represent *T. aestivum* and *B. distachyon* orthologs of *S* genes. Gene IDs of members in co-expression clusters are presented in Table S9.

Table S1. RNA-seq reads, NCBI accession numbers and mapping statistics (excel file).

**Table S2.** Enriched GO terms (Observed count over expected count) among up- and down-regulated genes at three time points across the two *T. aestivum* genotypes and *B. distachyon* Bd21-3.

Table S3. List of candidate susceptibility genes and orthogroups (excel file).

Table S4. List of orthogroups containing two or more genes including gene IDs (excel file).

Table S5. List of singleton orthogroups and gene IDs (excel file).

**Table S6.** Average gene expression (FPKM), orthogroup, GO terms, and cluster numbers associated with all genes in W2691, W2691+*Sr9b*, Bd21-3 (excel file).

**Table S7.** Average gene expression (FPKM), orthogroup, GO terms, and cluster numbers associated with eight *S* gene candidates in W2691, W2691+*Sr9b*, Bd21-3 (excel file).

**Table S8.** Co-expression network data for W2691, W2691+Sr9b, Bd21-3 genotypes using the mock and infected RNA-seq data (text file, see github page https://github.com/henni164/stem\_rust\_susceptibility).

**Table S9.** Co-expression network data for clusters containing *S* gene candidates (text file, see github page https://github.com/henni164/stem\_rust\_susceptibility).