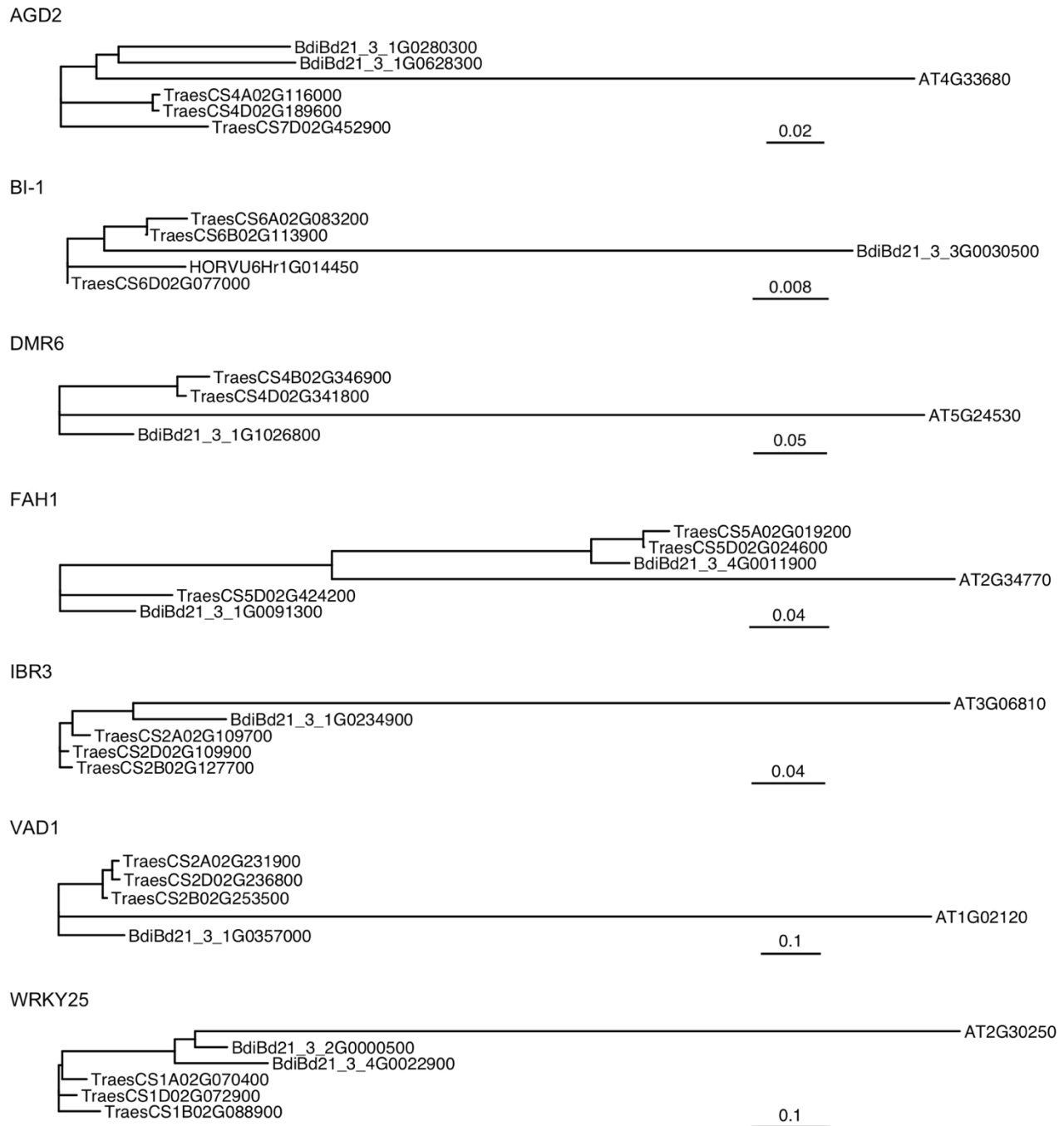
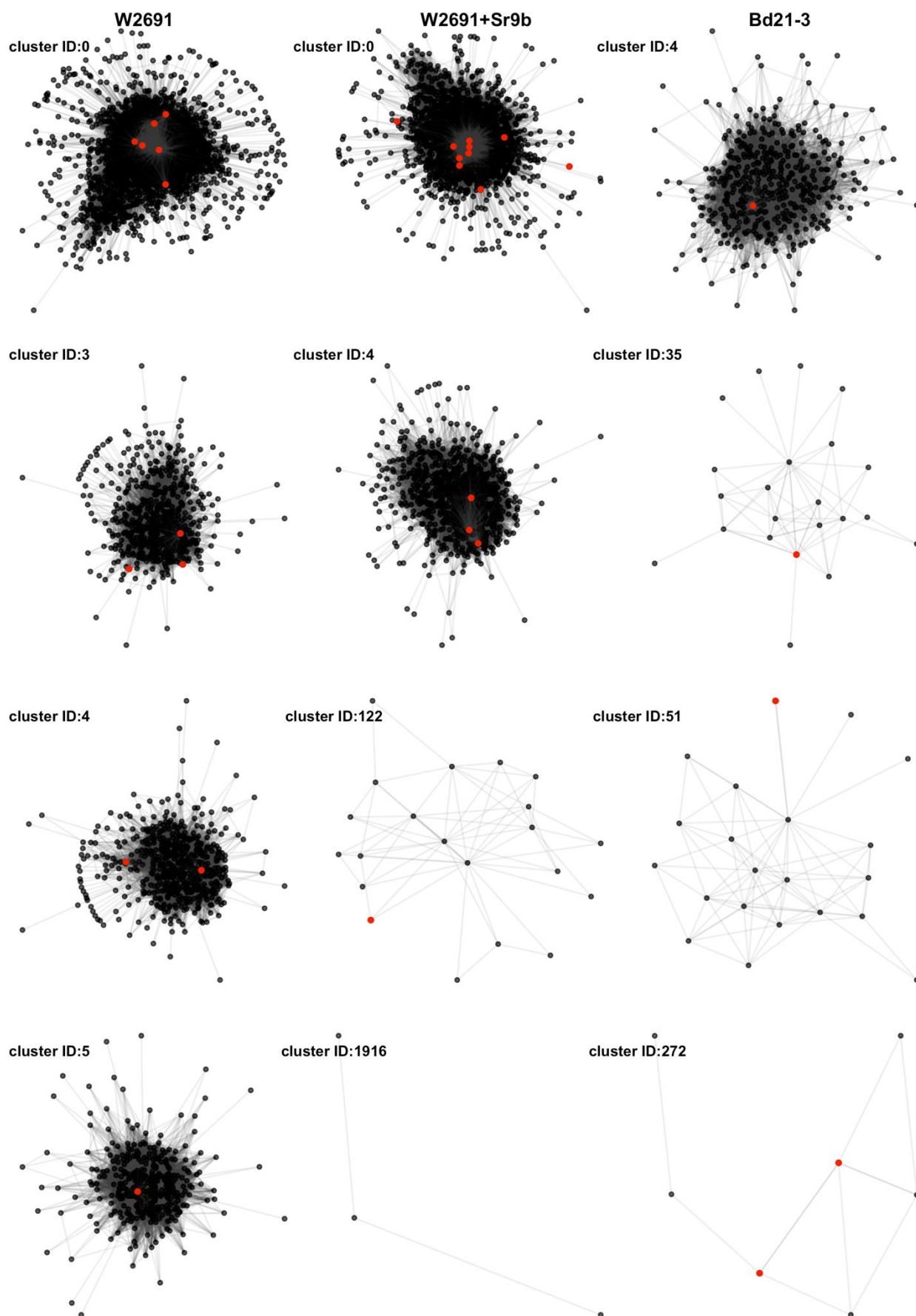
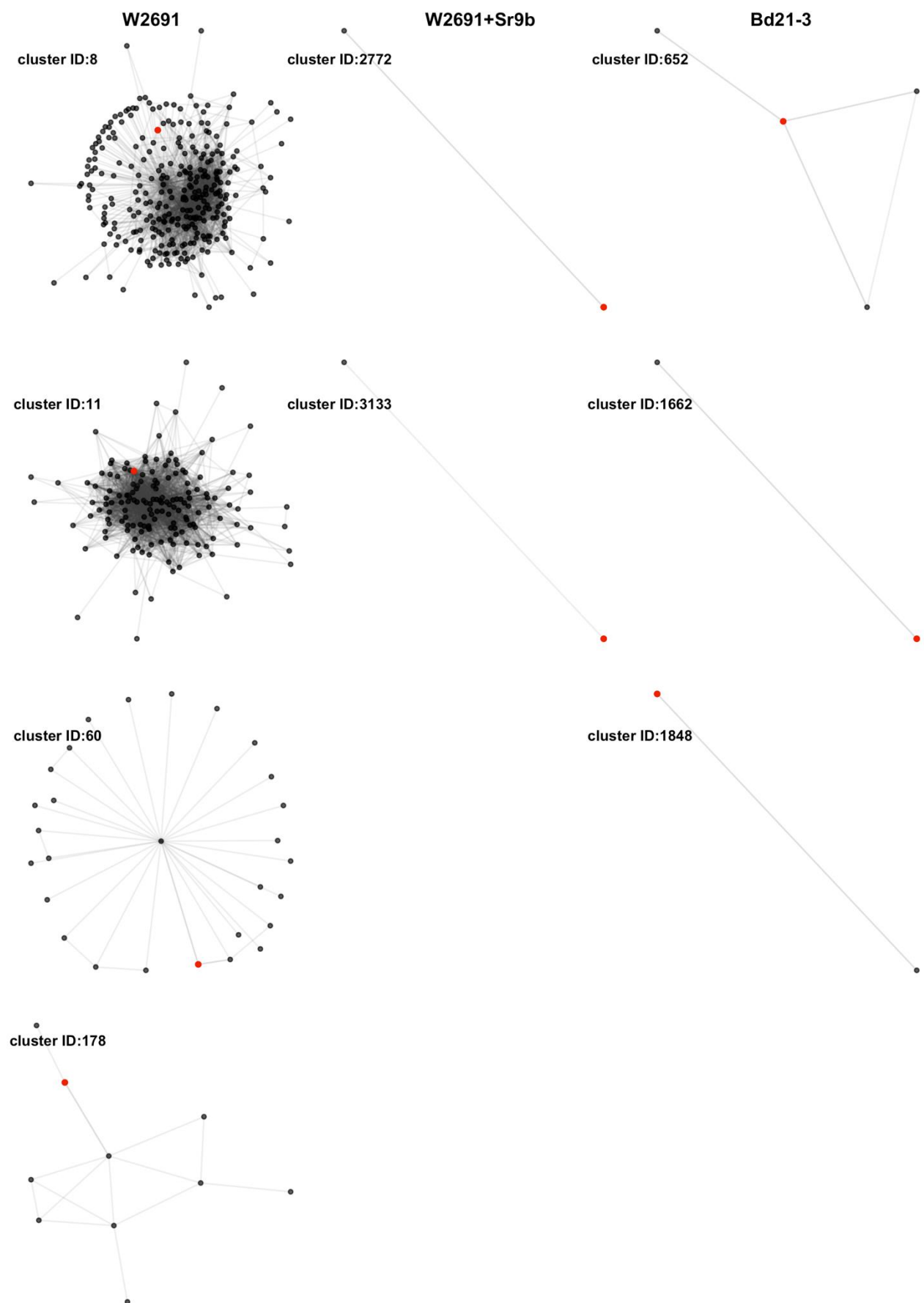


Supplementary Figure 1. Expression profile patterns of orthogroups containing candidate *S* genes in *T. aestivum* (W2691 and W2691+*Sr9b*) and *B. distachyon* (Bd21-3) genotypes throughout infection with *P. graminis* f. sp. *tritici*. Log2 fold change values (y-axis) for all gene orthologs are presented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



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).