**SUPPLEMENTARY TABLE LEGENDS**

**Supplementary Table 1.** Passport data for the 470 wheat accessions in the association mapping panel. ID = accession identification number. SHW = synthetic hexaploid wheat (0 = no, 1 = yes). NA = missing data.

**Supplementary Table 2.** Phenotypic data used for genome wide association scans (GWAS). ID = accession identification number, as used in Supplementary Table 1. NA = missing data. For the awn phenotype, 0 = absence, 1 = presence.

**Supplementary Table 3.** Genotypic data derived from the use of the wheat 90k Illumina iSelect single nucleotide polymorphism (SNP) array (Wang *et al*. 2014) across the association mapping panel of 470 accessions. Chromosome and genetic position (cM) of the subset of 18,895 SNPs located on the previously published wheat consensus map (Wang *et al*. 2014) are indicated. NA = not on the Wang *et al.* (2014) genetic map.

**Supplementary Table 4.** Genotype calls for 26 KASP markers (open access via CerealsDB website, and further described by Rasheed *et al*. 2016) genotyped across 349 accessions of the association mapping panel.

**SUPPLEMENTARY FIGURE LEGENDS**

**Supplementary Figure 1.** Venn diagram illustrating the overlap in accessions of the association mapping panel for the three Fusarium disease trials held in the seasons 2011, 2012 and 2013.

**Supplementary Figure 2.** Kinship matrix generated using the subset of 4,313 SNPs, as generated by the software GAPIT (Lipka *et al*. 2012).

**Supplementary Figure 3.** Intra-chromosomal linkage disequilibrium (LD) in the association mapping panel, as measured chromosome-by-chromosome by *r2* between genetically mapped marker pairs. A LOWESS curve is fitted to the data, indicated in red.