Genome-wide association mapping and prediction of adult stage *Septoria tritici* blotch infection in European winter wheat using high density marker arrays

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Supplementary figures

**Figure S1.** Pearson product moment correlation of *Septoria tritici* blotch (STB) infection between flag and first leaves at two time points in years (a) 2009 and (b) 2010. T1 and T2 denote the time-points of STB infection scoring. Color key is given in the figure. The correlation among leaves and times of inoculation was significant ($P < 0.0001$).
Figure S2. Principal component analysis (PCA) on a population of 371 European winter wheat varieties. Two dimensional (a) PC plot on markers from 35k array and (b) markers from 90k array showing the absence of pronounced clustering among the varieties. Different colors represent the Ppd-D1 alleles. $n$ denote the number of varieties used in the analysis.
Figure S3. Population structure analysis of 371 European winter wheat varieties based on 28,228 marker genotypes. (a) Bar plots show the existence of admixed sub-populations. (b) The cross-entropy plot shows that there exists a minimal sub-structuring in the panel.
Figure S4. Linkage disequilibrium (LD) decay over genetic distance (cM) between adjacent markers in a population of 371 European winter wheat varieties. Only those markers mapped according to ITMI map were used to calculate the $r^2$ and genetic distances.