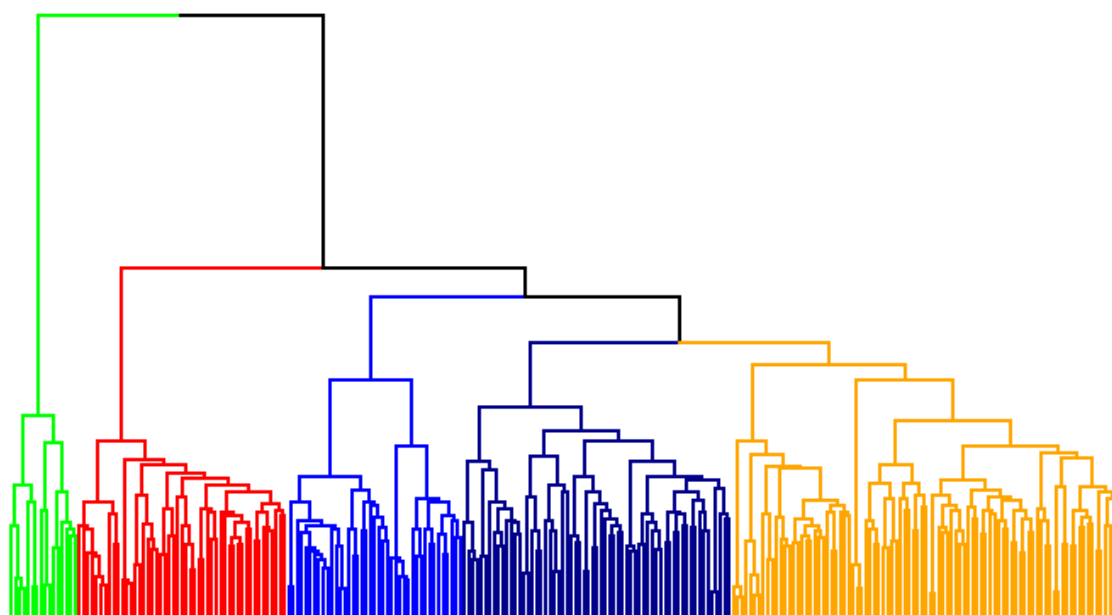**Supplementary Figure S1** SNP quality control steps. (A) Violin plot of read depth per individual. Average read depth was 13. The red ellipse indicates areas where genotypes showed zero reads due to low DNA quality. (B) Missing percentage before filtering for 70% call rate and MAF > 0.05. (C) Percentage of missing markers per individual retained for downstream analysis.

Supplementary Figure S2 Phylogenetic tree of 260 triticale genotypes based on Euclidean distance matrix and Wad.D^2 agglomeration. The clustering did not follow prior winter and spring classification.
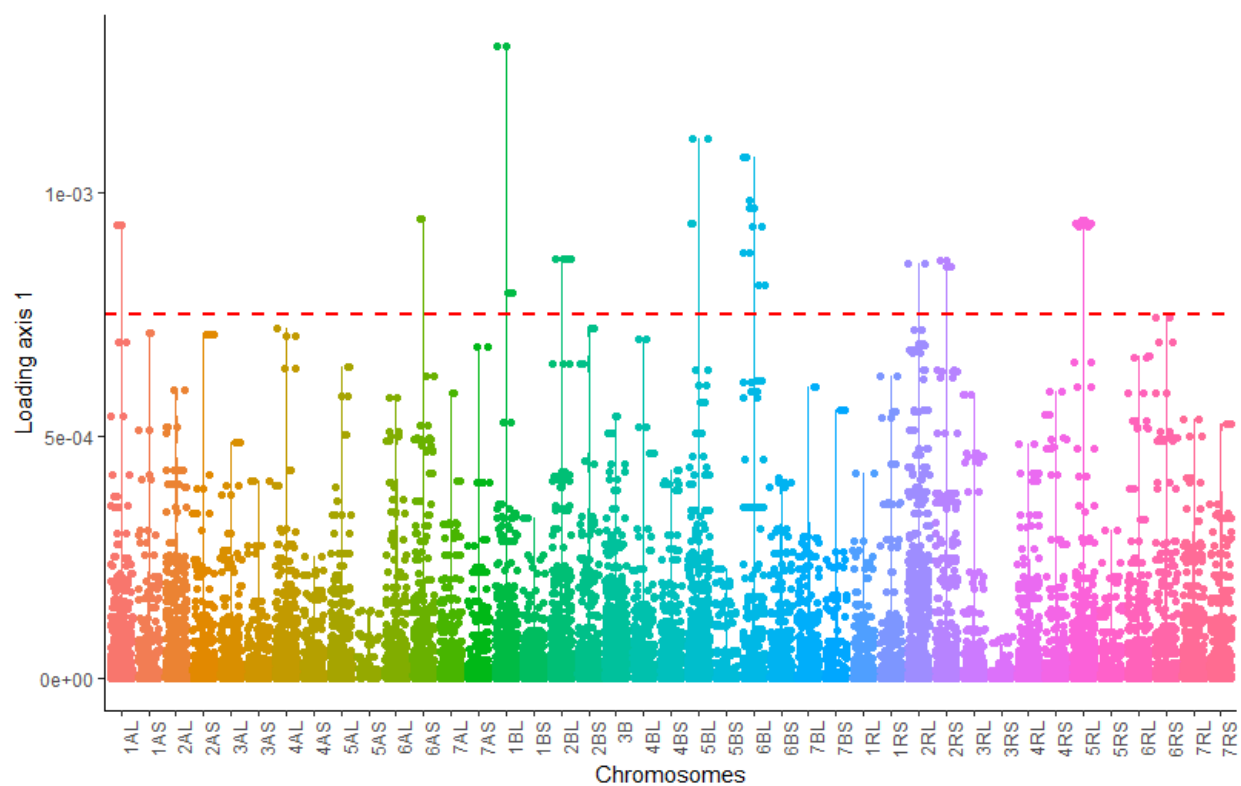
Supplementary Figure S3 Lodgings of markers on the first discriminant axis. Chromosome positions were based on the wheat and rye reference genomes.
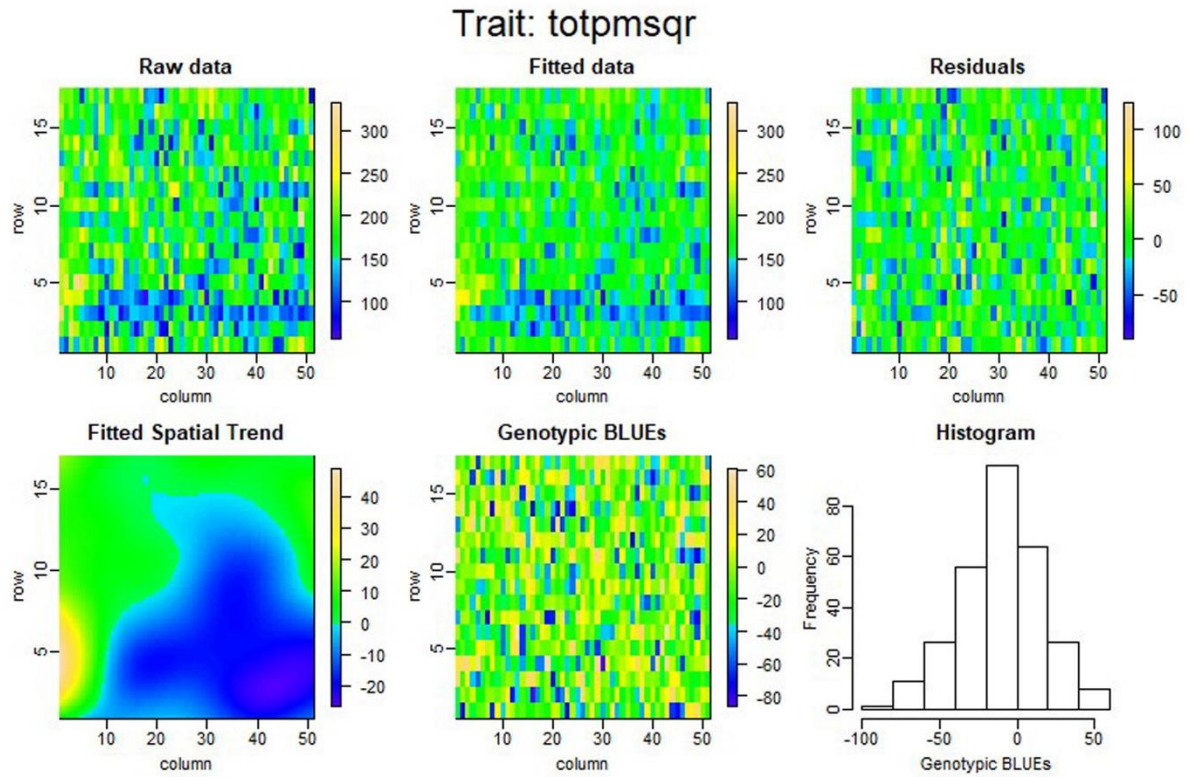
Supplementary Figure S4 Sample spatial trend analysis output of forage yield using 2D tensor product smoothing splines with the SpATS/R package. Rows 1 to 5 showed larger variations at columns 40 to 54 (Fitted spatial trend).