

Figure S1. QQ-plot determined by MLM+K and MLM+K+Q statistical models for stem rust seedling experiments (6 races) for A: Whole collection, B: Durum sub-sample, C: Q2.

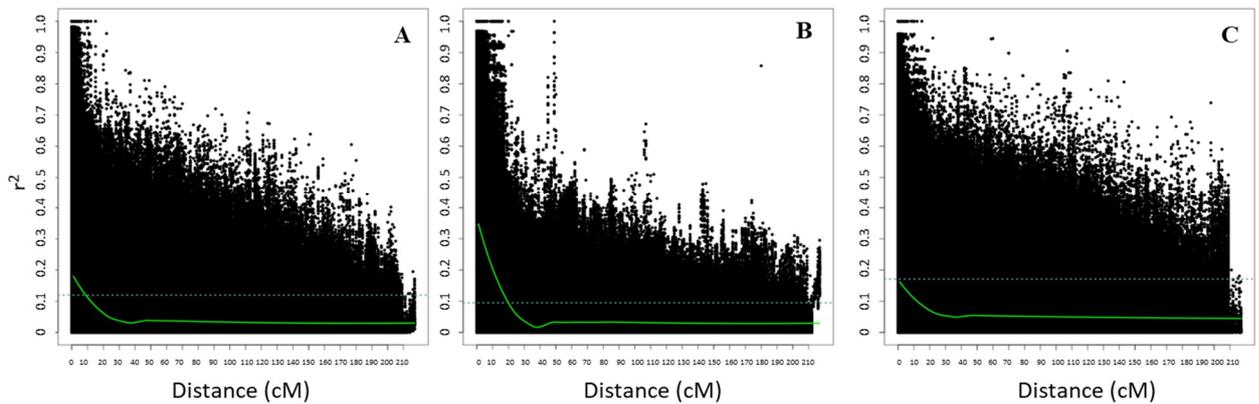


Figure S2. Overview of the LD parameter r^2 for the whole genome of the intrachromosomal pairs in the whole collection (A), in the durum sub-sample (B), and in Q2 group (C). The scatterplots show the distributions of the LD parameter r^2 according to the genetic distance. The horizontal line indicates the 95% percentile of the distribution of the unlinked r^2 , which gives the critical value of r^2 .