(a)

(b)

1

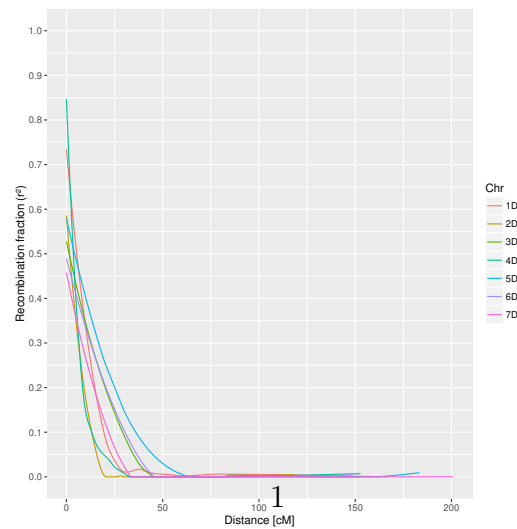**(c)**

Supplementary Figure 1 LD decay plot for the individual chromosomes of the three sub genomes A (a), B (b) and D (c) of the B22 population.

(a)

(b)

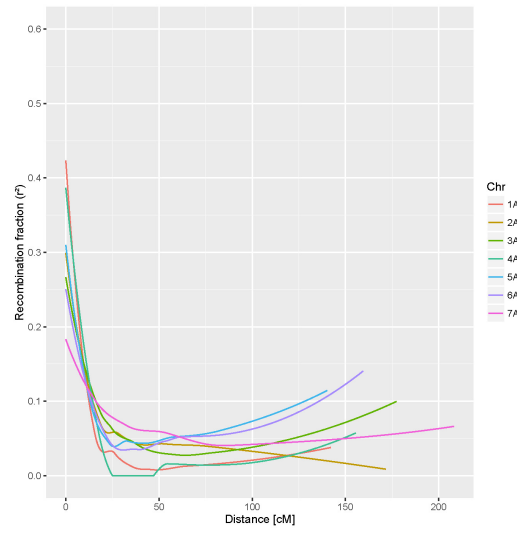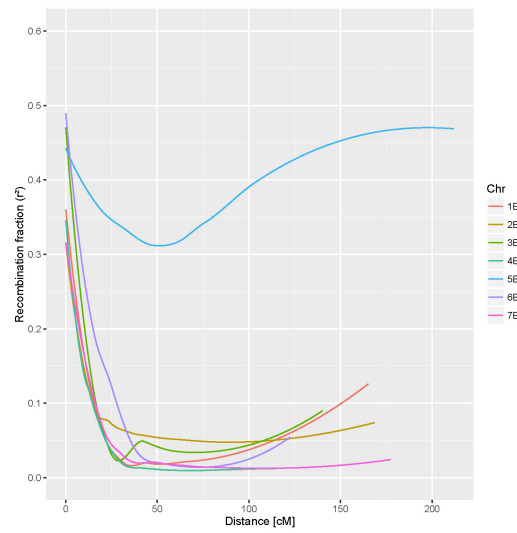**(c)**

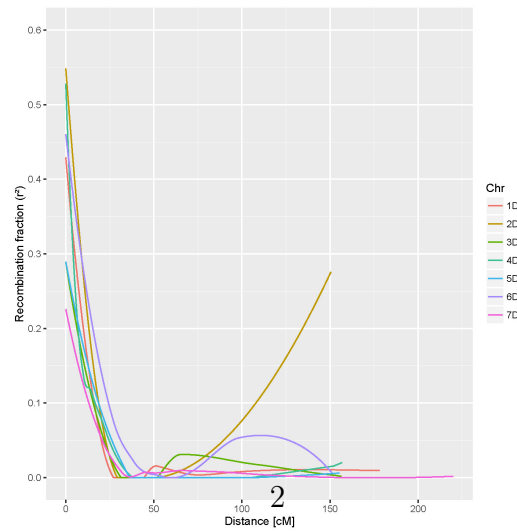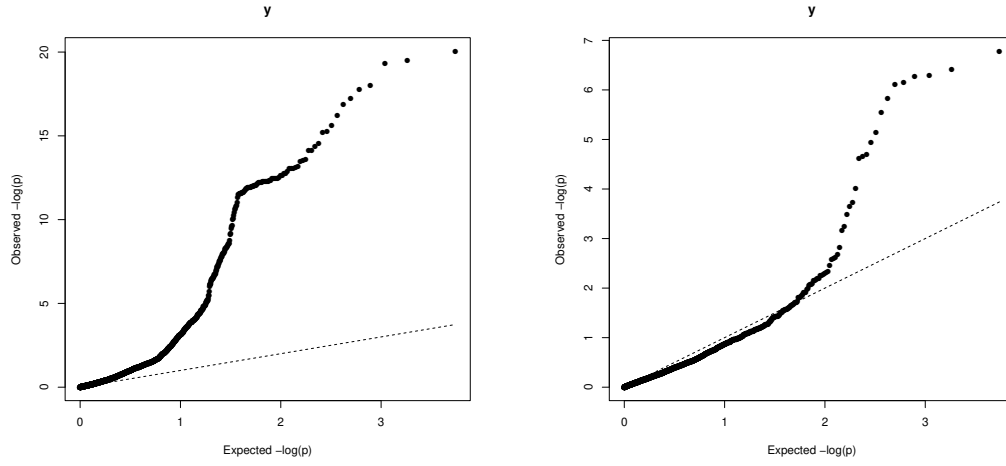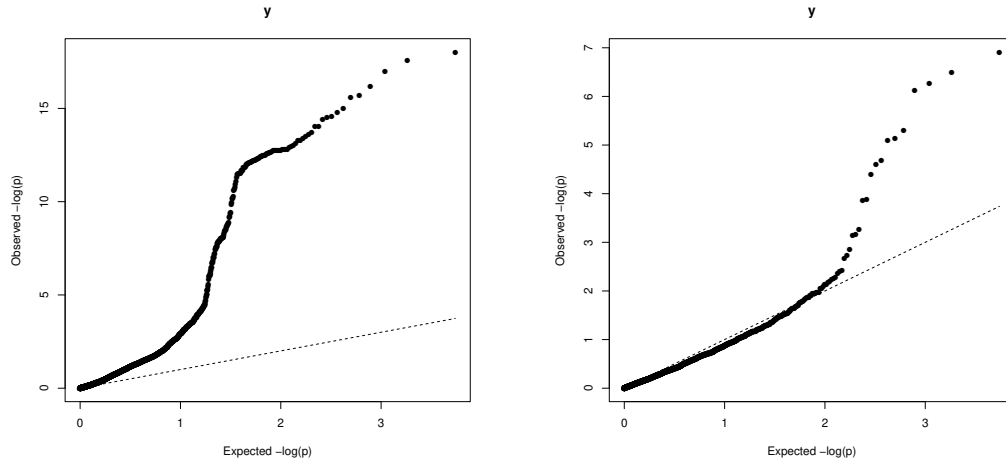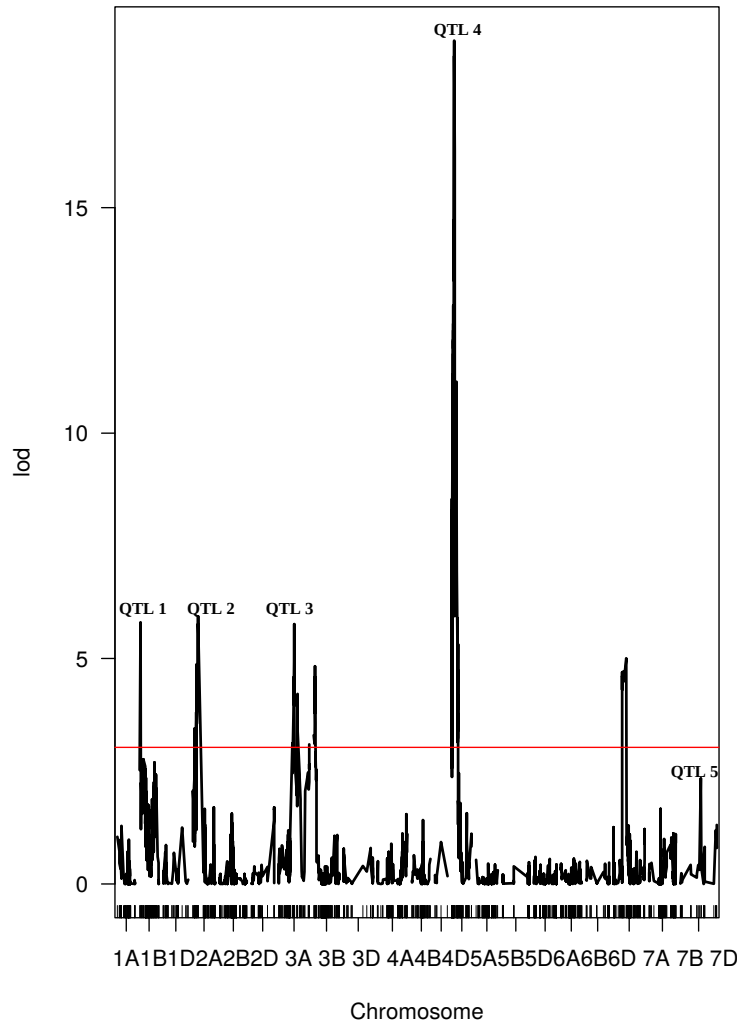**Supplementary Figure 2** LD decay plot for the individual chromosomes of the three sub genomes A (a), B (b) and D (c) of the Z86 population.

Supplementary Figure 3 Q-Q plots based on the single-locus model without the polygenic effect (a) and with the polygenic effect in the model (b) using the Simulation 1 data set.

Supplementary Figure 4 Q-Q plots based on the single-locus model without the polygenic effect (a) and with the polygenic effect in the model (b) using the Simulation 2 data set.

Supplementary Figure 5 LOD scores based on the interval mapping approach using the simulated data without the polygenic effect (Simulation 1). The red line show a LOD threshold for the siginificant QTL determined with r/qtl using 1000 permutations at p = 0.05. Additionally, the simulated QTLs are also shown.