

Figure S1: Heatmap for the distribution of linkage disequilibrium (LD) across the genome in the VIR-LTT panel estimated as r^2 using 5,813 SNP markers. The number of SNP markers for each chromosome and average adjacent marker LD for each chromosome are included.

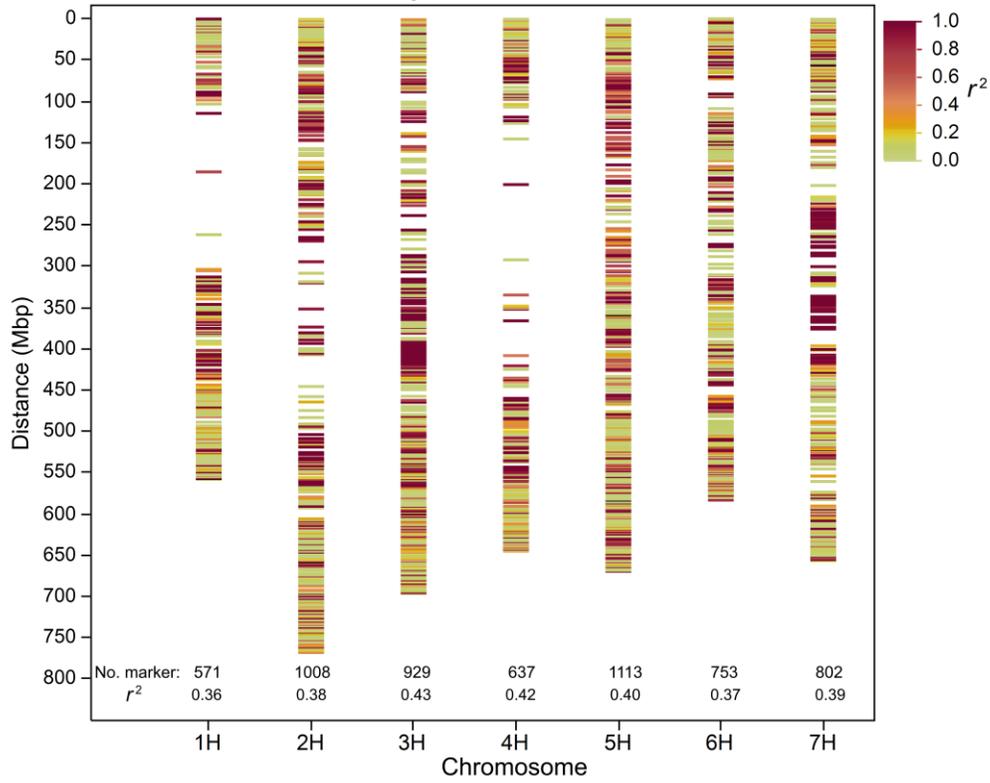


Figure S2: Heatmap matrix displaying the genomic additive relationship matrix for the 267 barley accessions of the VIR-LTT panel based on 5,813 SNP markers.

