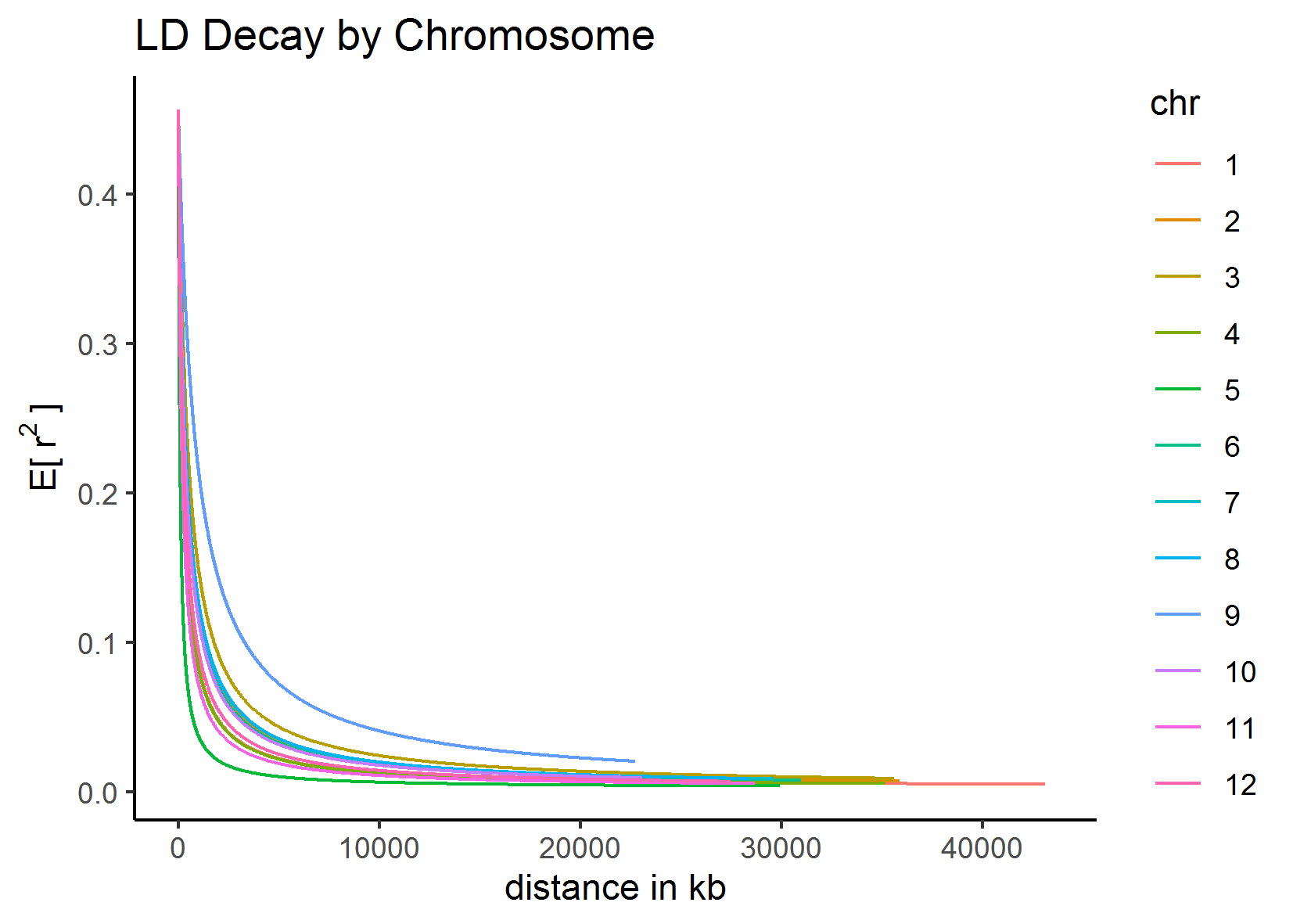


**Figure S1.** Density of SNP markers in the calibration set (334 S0 plants) in the 12-chromosome R package Synbreed (Wimmer et al., 2012)



**Figure S2.** MAF distribution among the population of 334 S0 plants.



**Figure S3.** Linkage disequilibrium, measured as r2 between all pairs of markers considered in a 50 variants window (PLINK1.09). R2 values plotted against distances between markers in kb as a nonlinear regression model based on Hill and Weir’s (1988) equation.

![](data:None;base64,) **Figure S4.** Neighbor joining tree of Euclidean distance between the 334 S0 plants (Darwin)