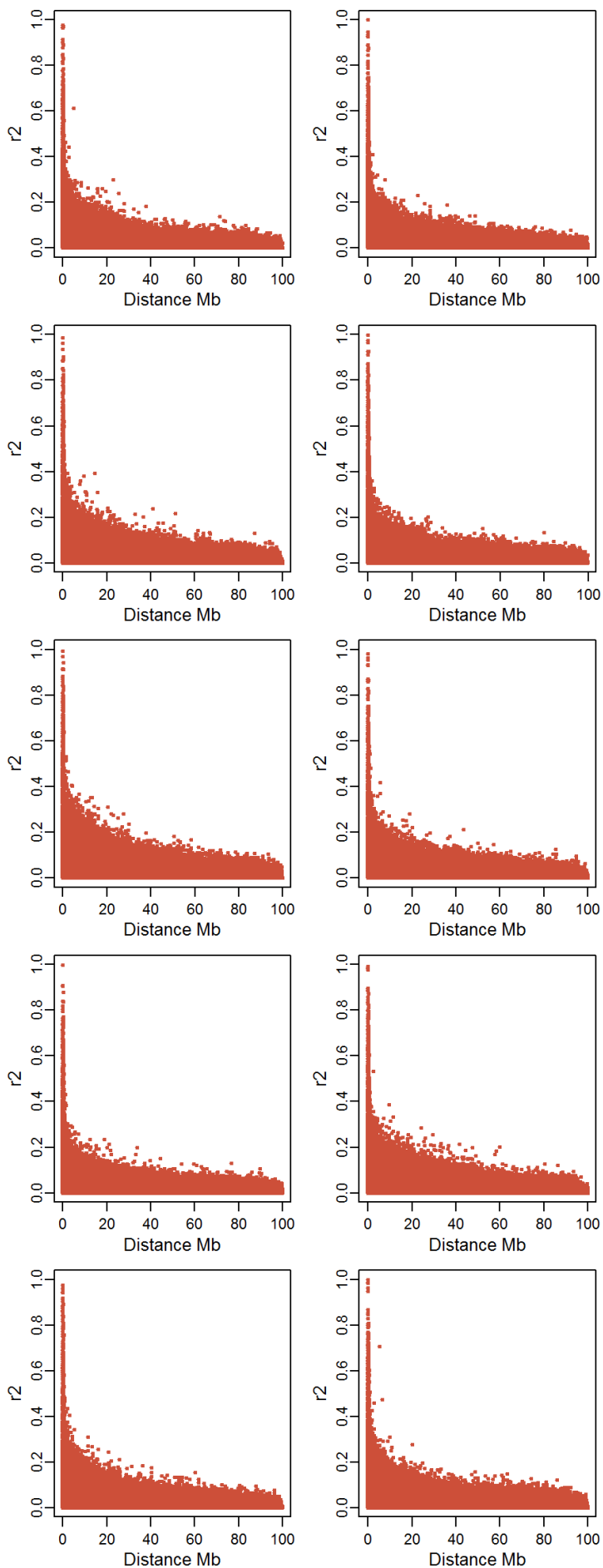
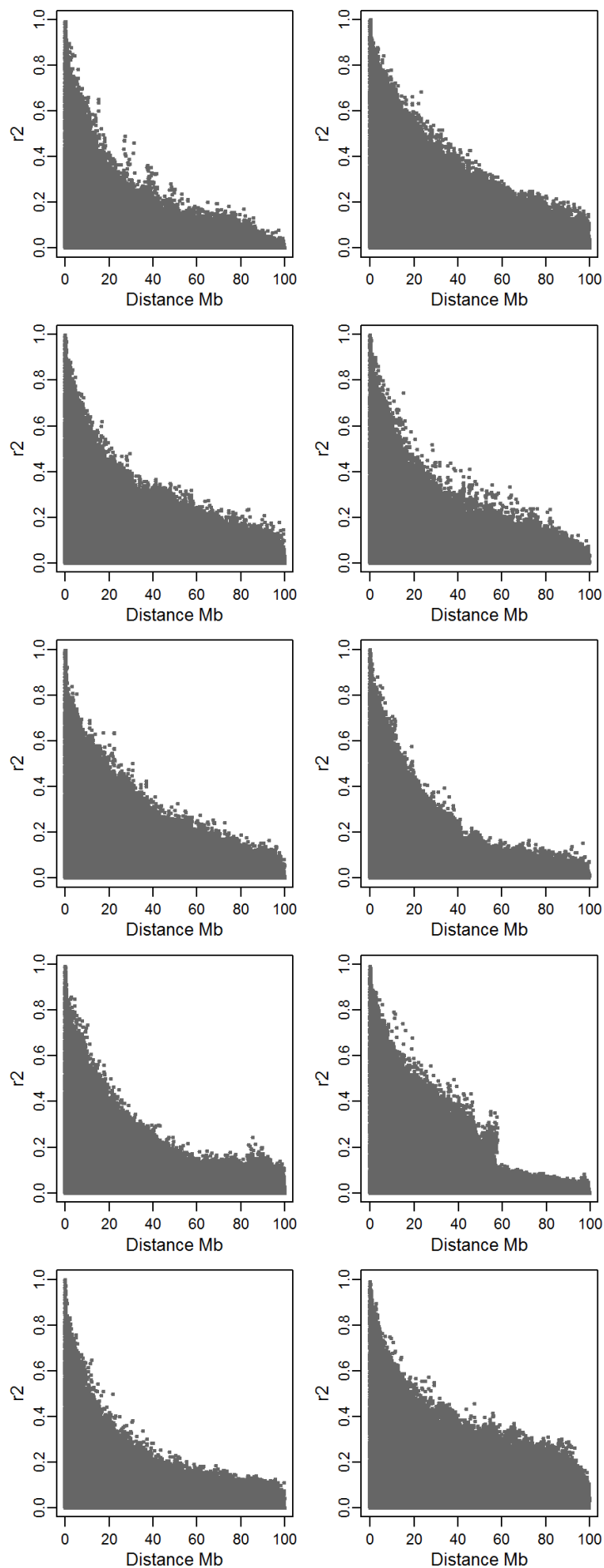


Figure S1. Pair-wise values of r^2 against inter-marker distance for all replicates of the four scenarios.

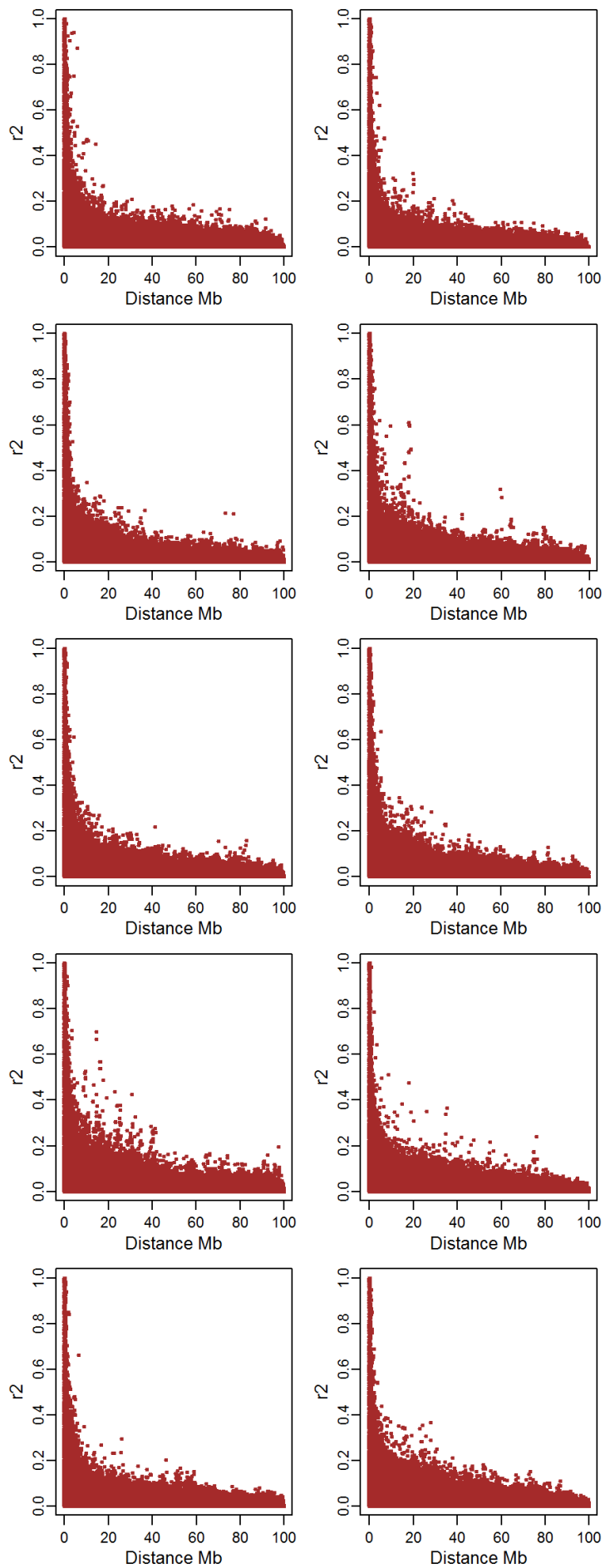
LowLD_NoSel



LowLD_Sel



HighLD_NoSel



HighLD_Sel

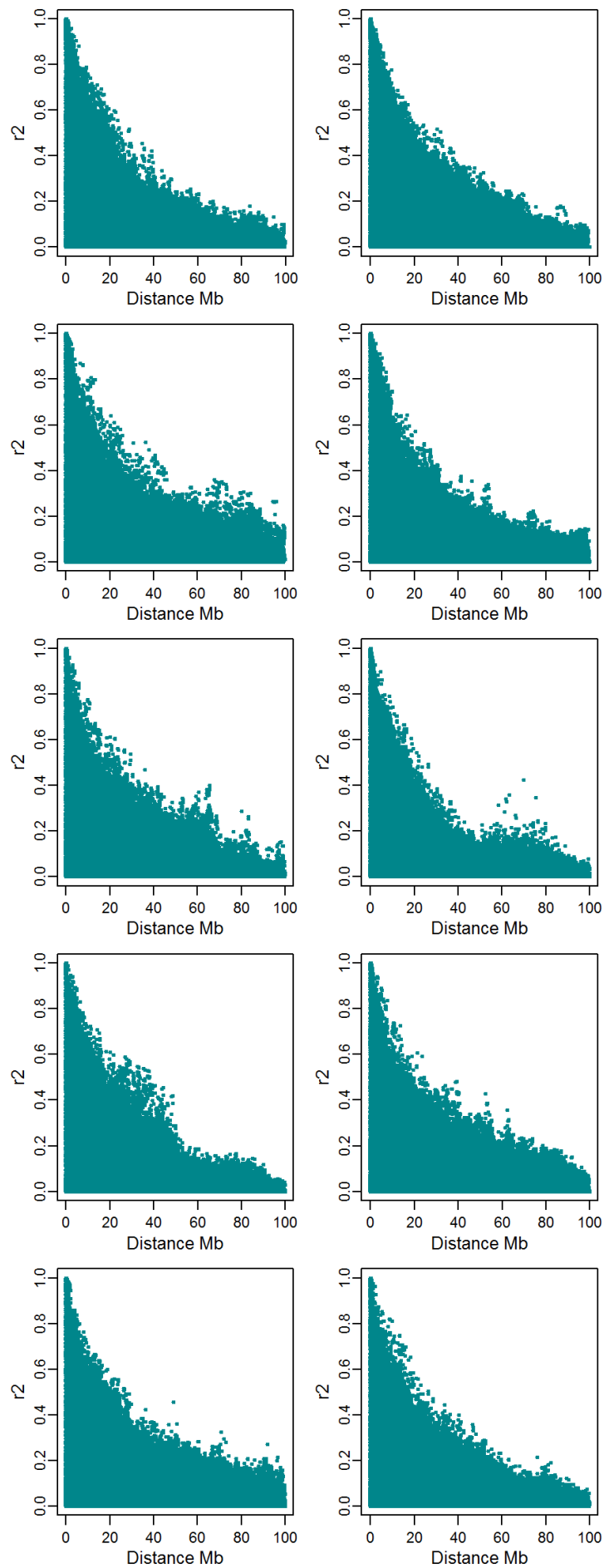
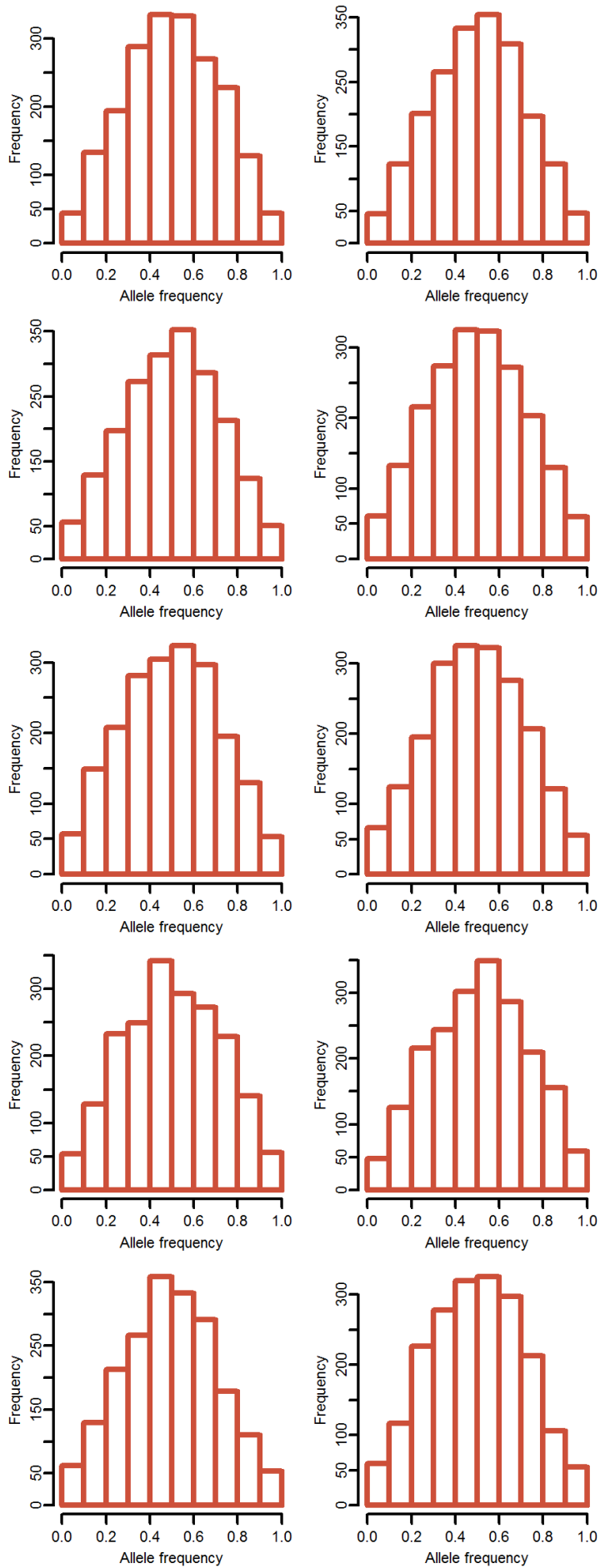
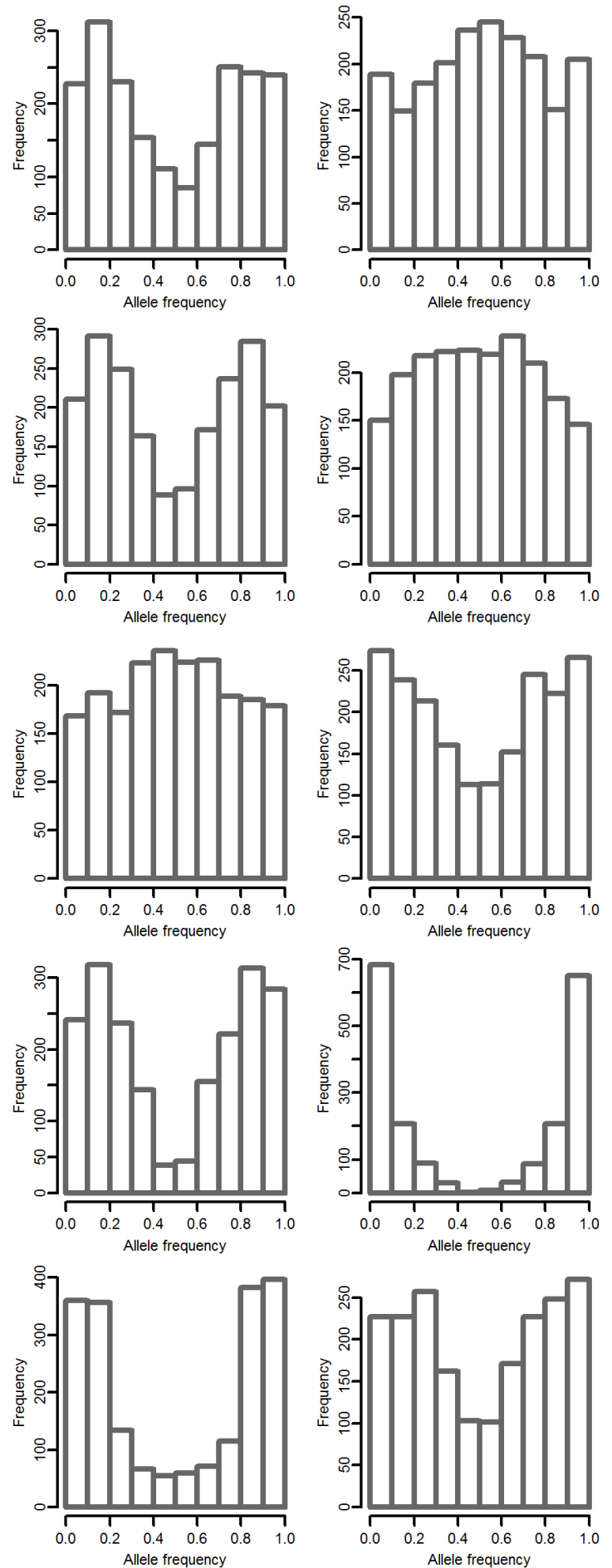


Figure S2. Histograms of the frequencies of allele 2 for all replicates of the four scenarios.

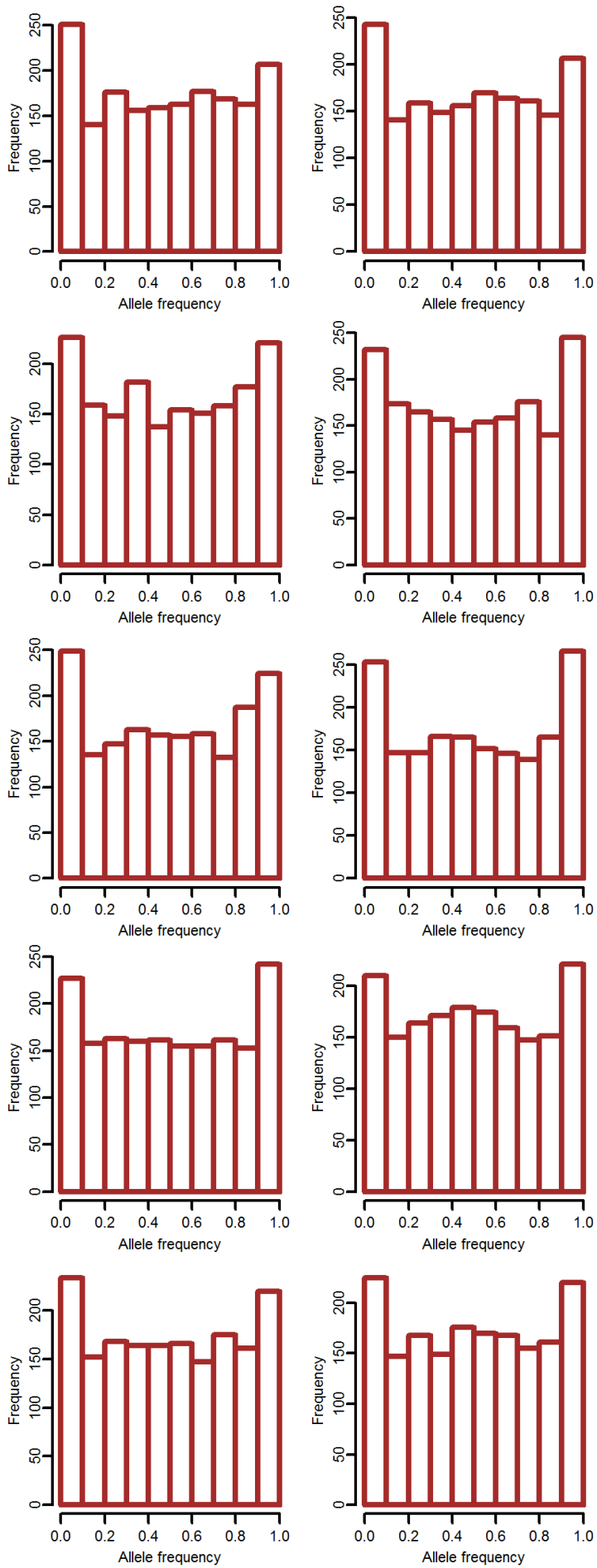
LowLD_NoSel



LowLD_Sel



HighLD_NoSel



HighLD_Sel

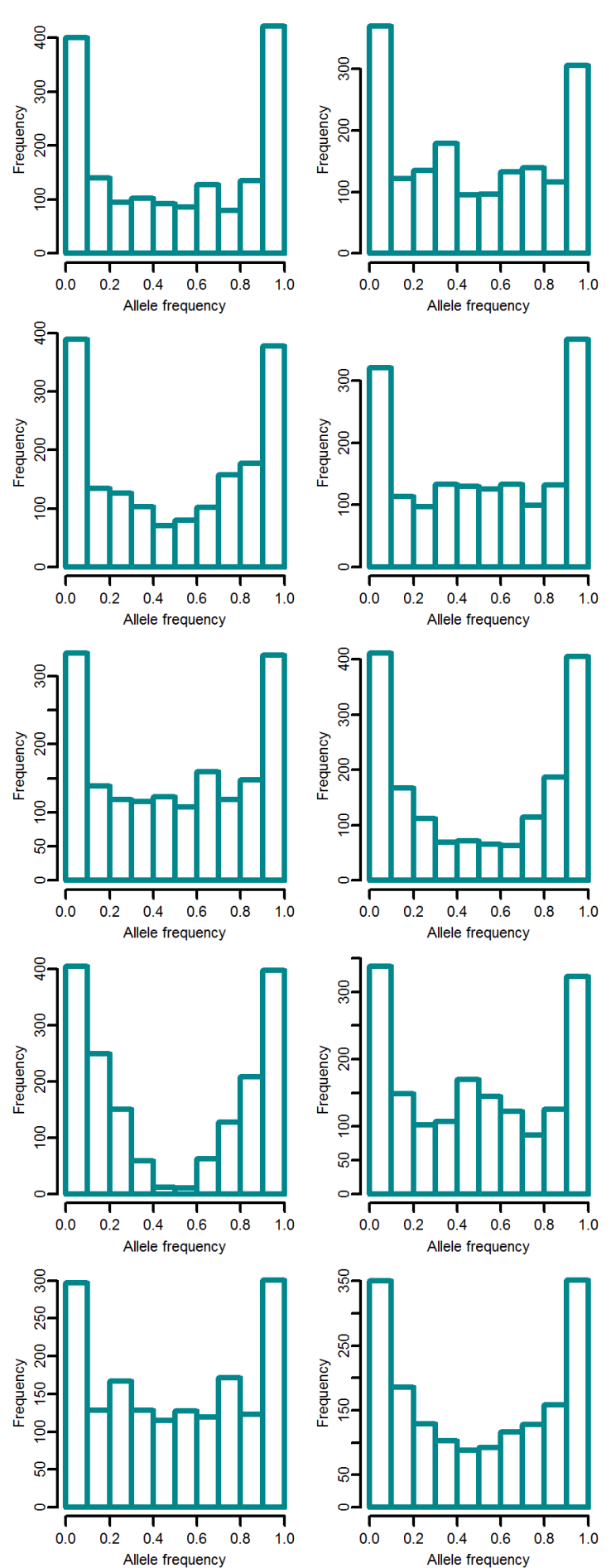
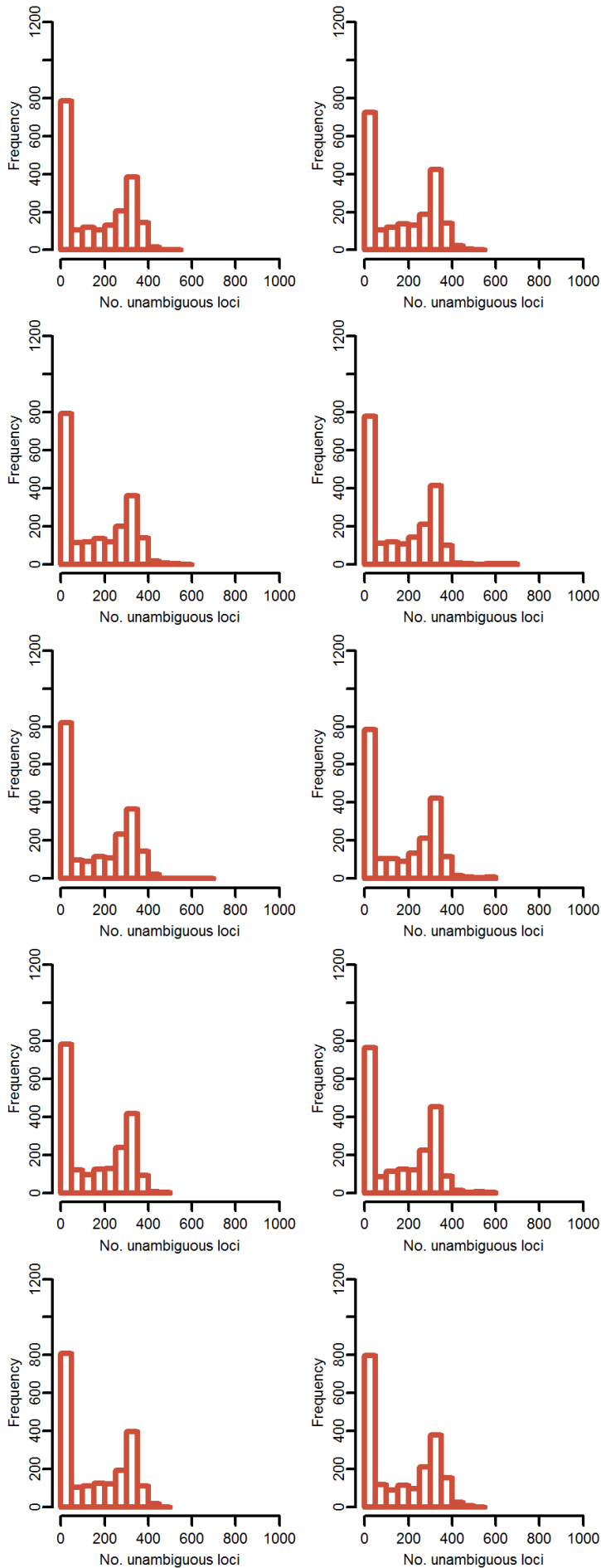
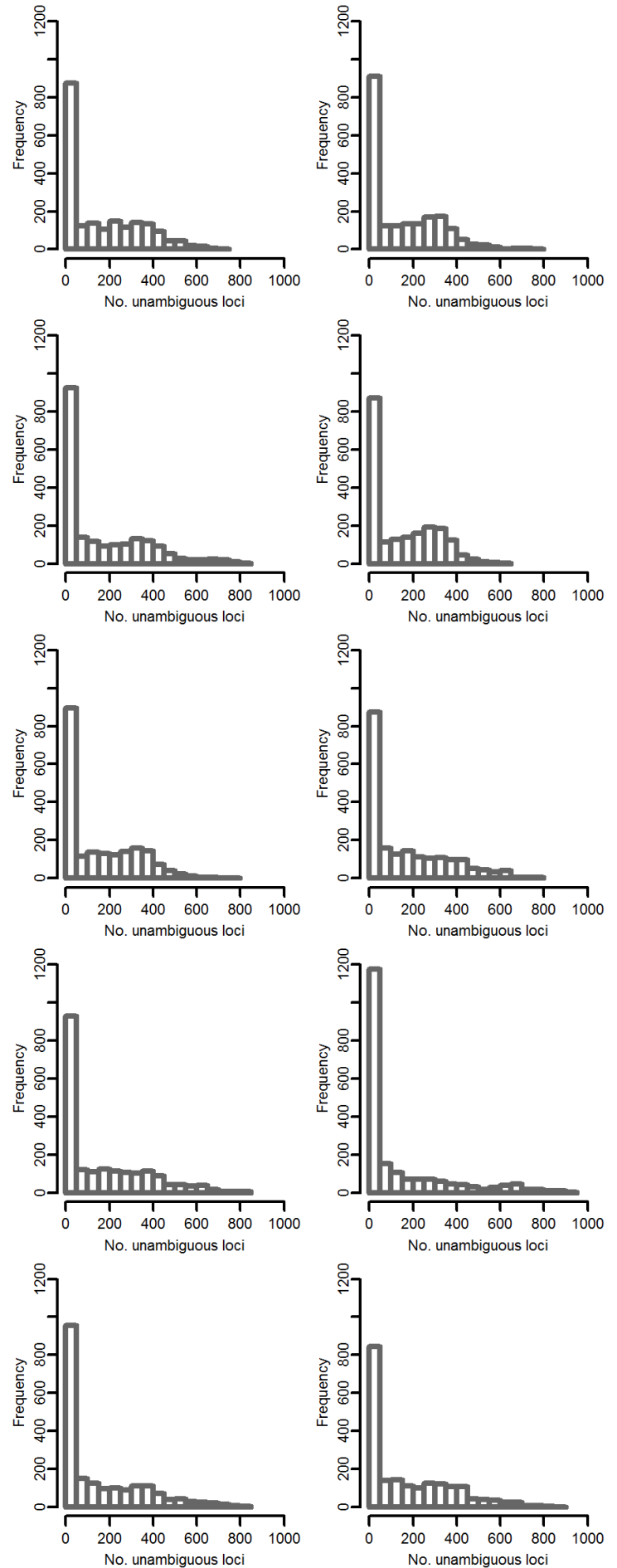


Figure S3. Distributions of the number of unambiguously imputed loci per Dam for all replicates of the four scenarios.

LowLD_NoSel



LowLD_Sel



HighLD_NoSel

HighLD_Sel

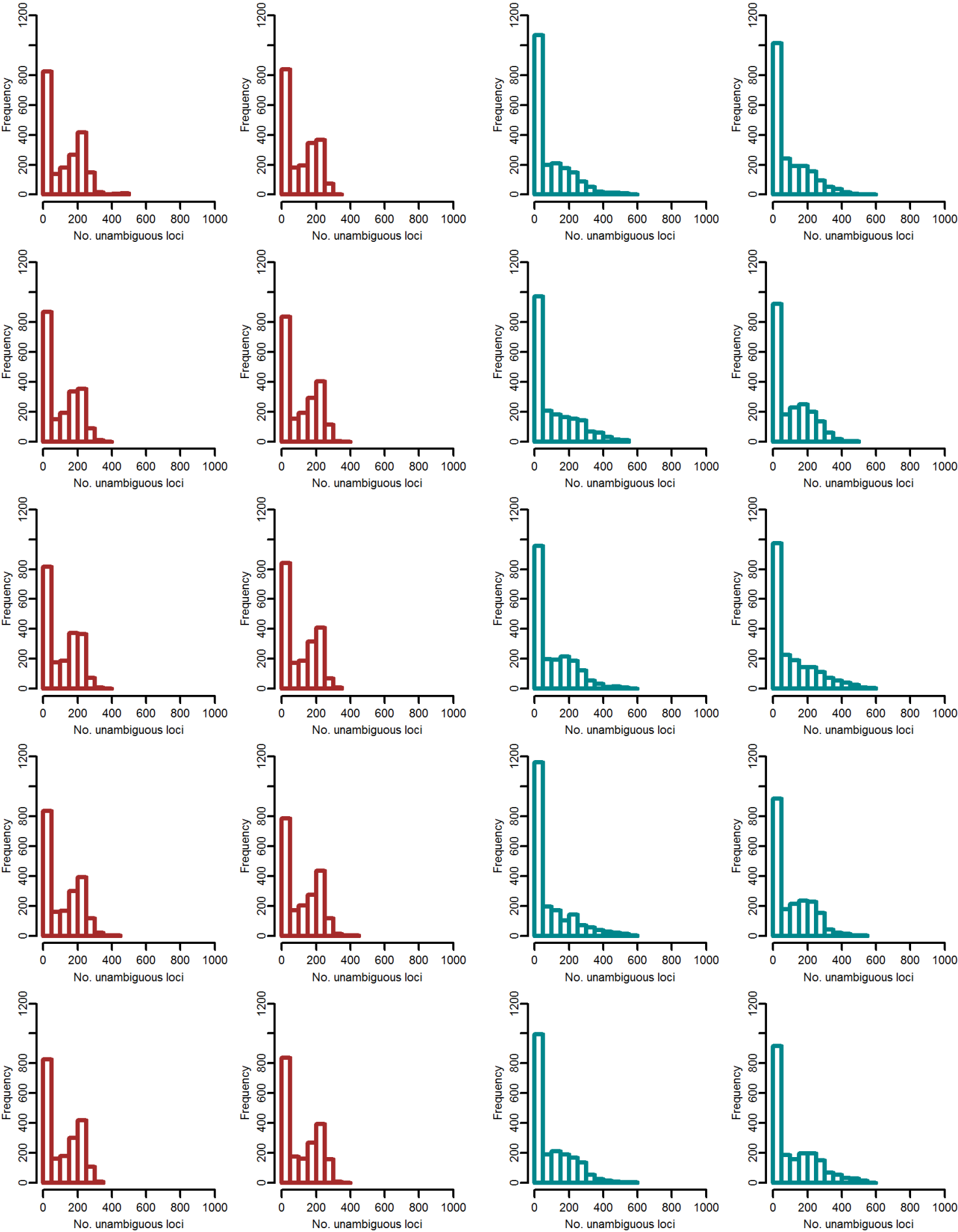


Figure S4. Regression analyses of the percentage increase in accuracy obtained with TSA against the accuracy already obtained with TS across all h^2 and numbers of offspring for the four scenarios.

