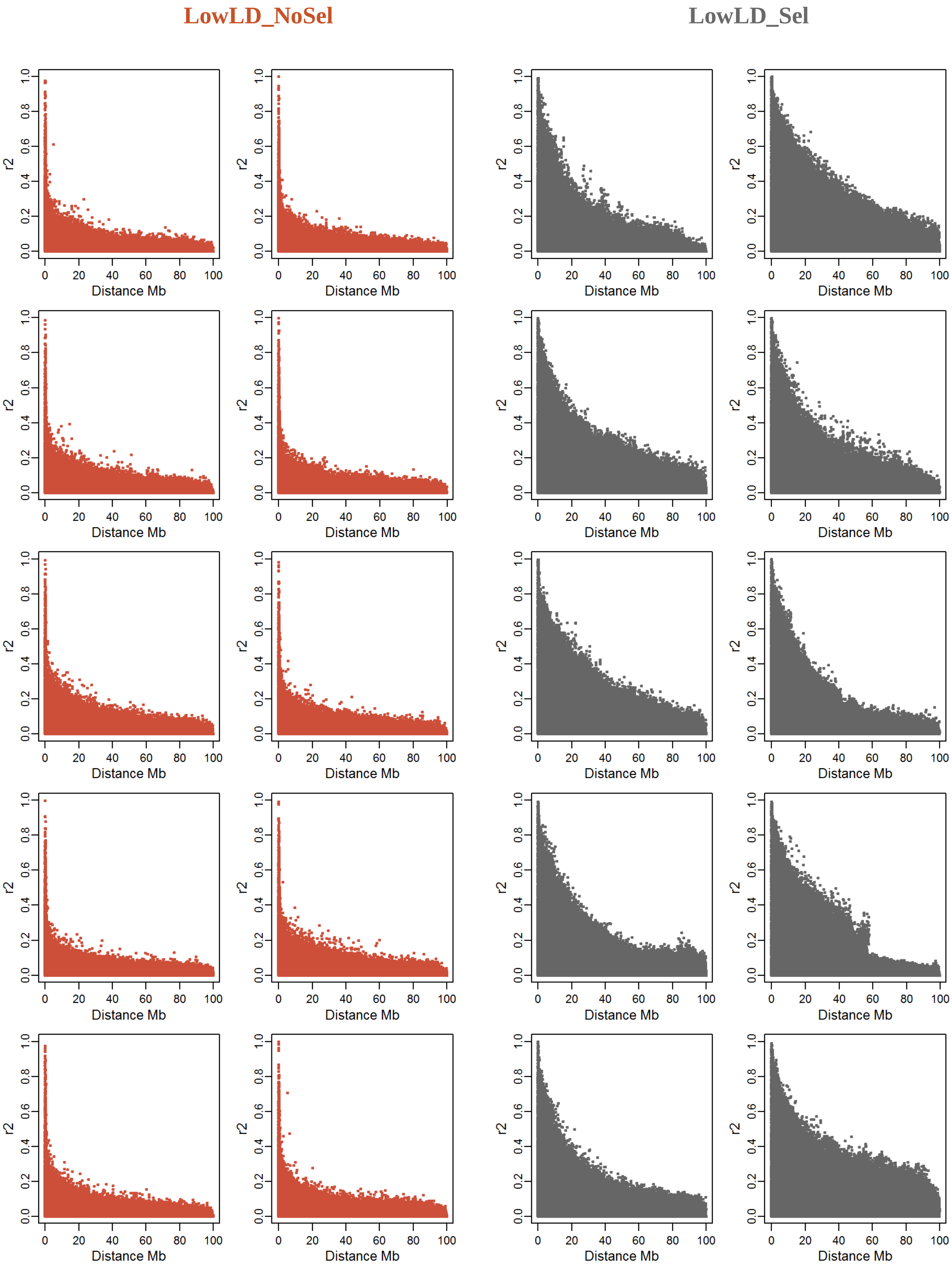
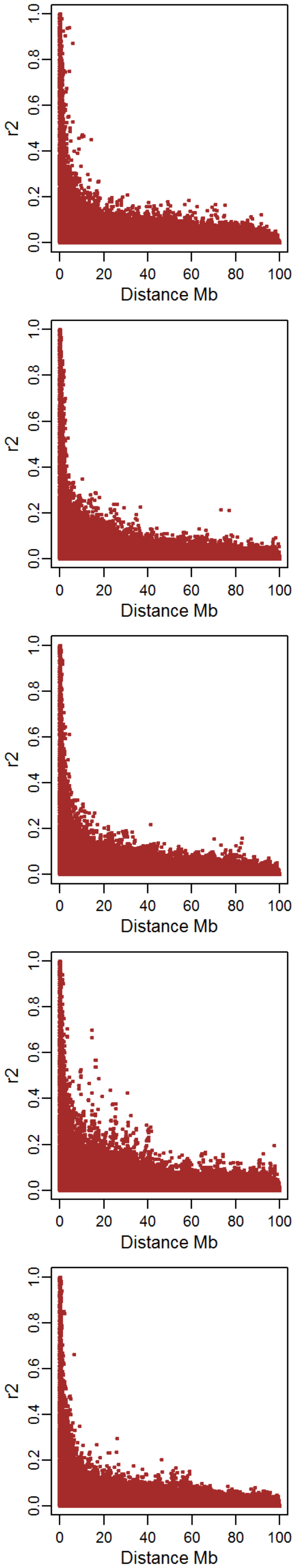
**Figure S1.** Pair-wise values of r2 against inter-marker distance for all replicates of the four scenarios.


LowLD_NoSel
LowLD_Sel
r2
0.0
0.2
0.4
0.6
0.8
1.0
Distance Mb
0
20
40
60
80
100


**HighLD_NoSel**

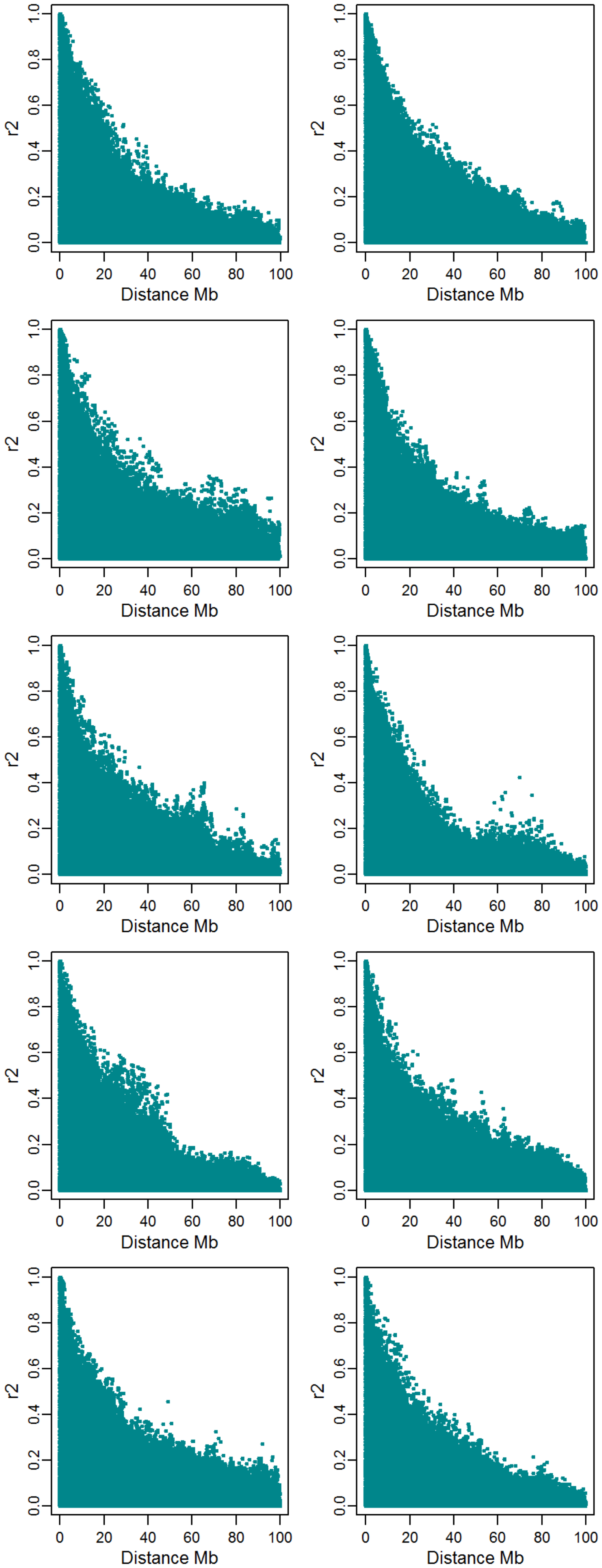
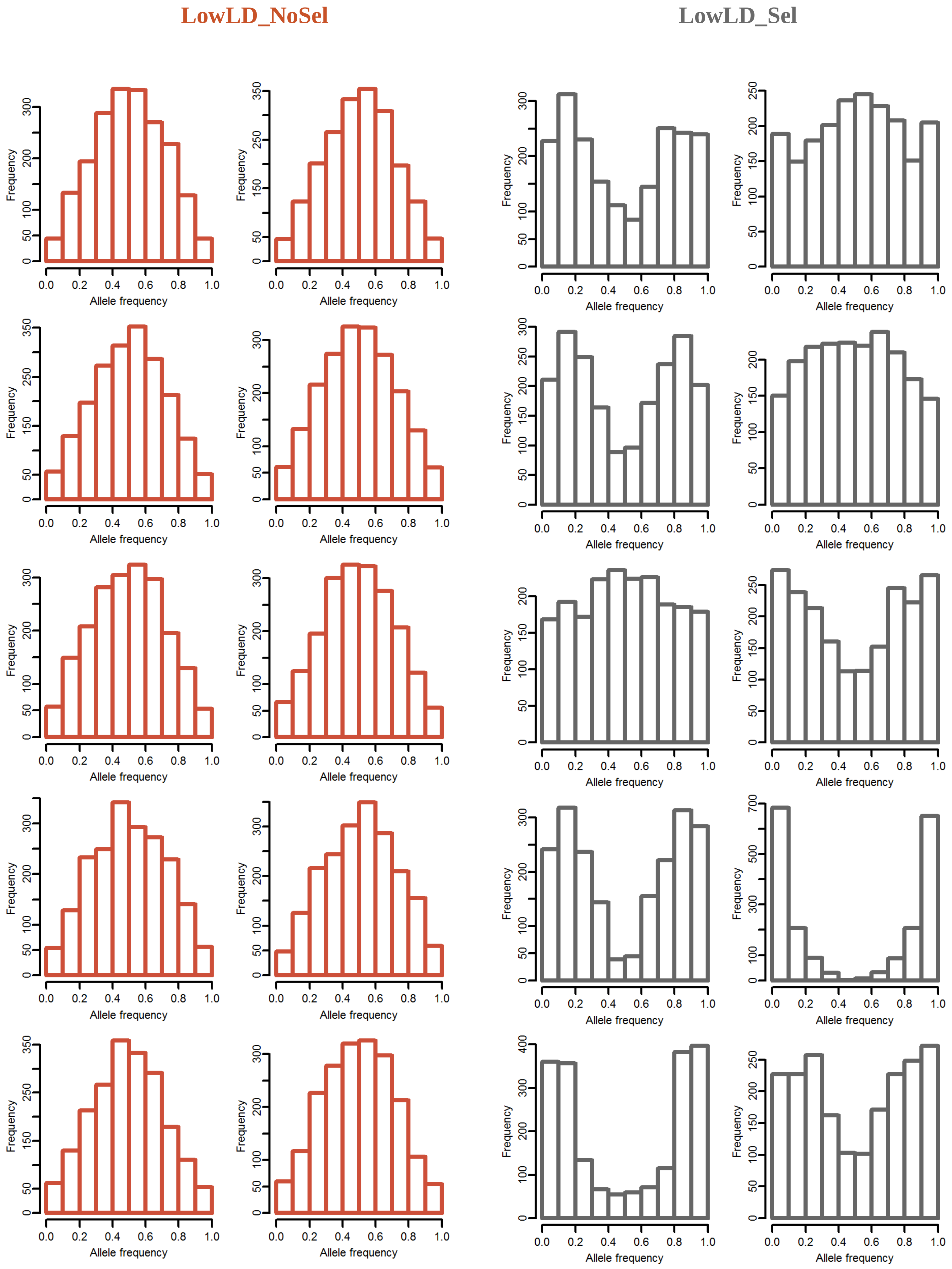
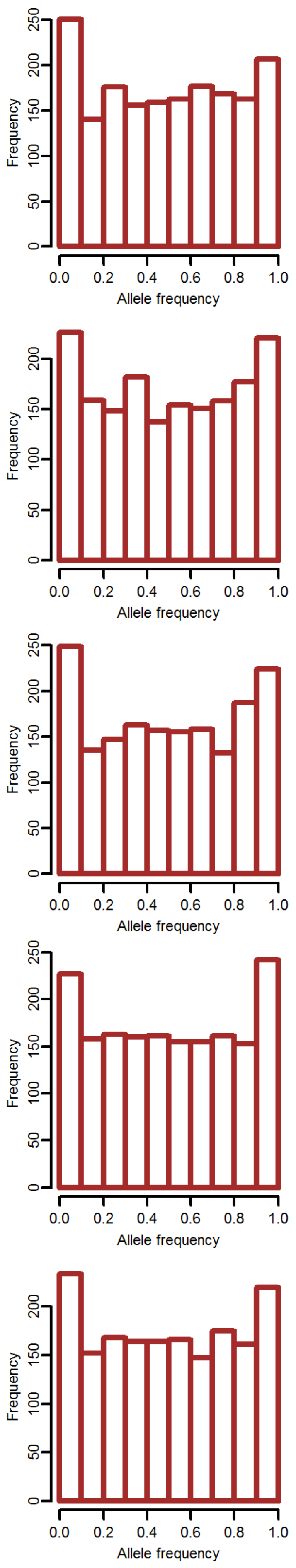

**HighLD_Sel**

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


LowLD_NoSel
LowLD_Sel
Frequency
Allele frequency
0.0
0.2
0.4
0.6
0.8
1.0
0
50
100
150
200
250
300
350
400
500
700

**HighLD_NoSel**



**HighLD_Sel**

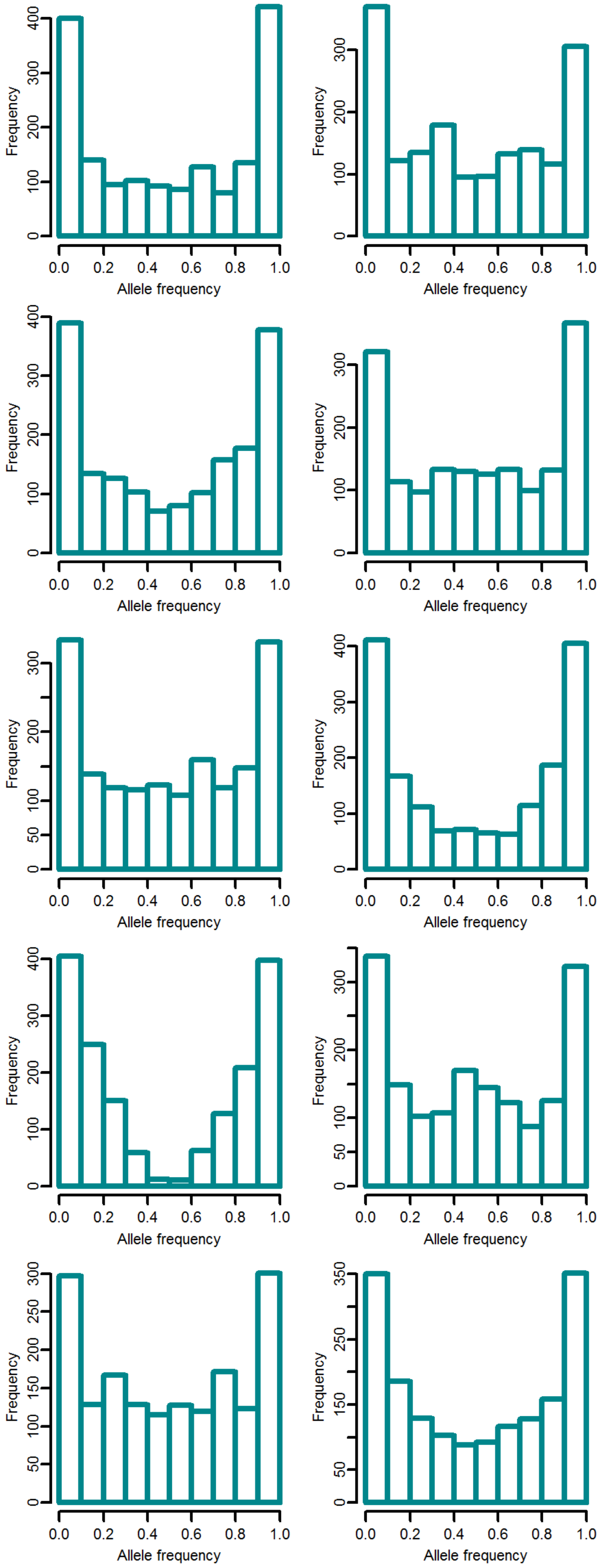
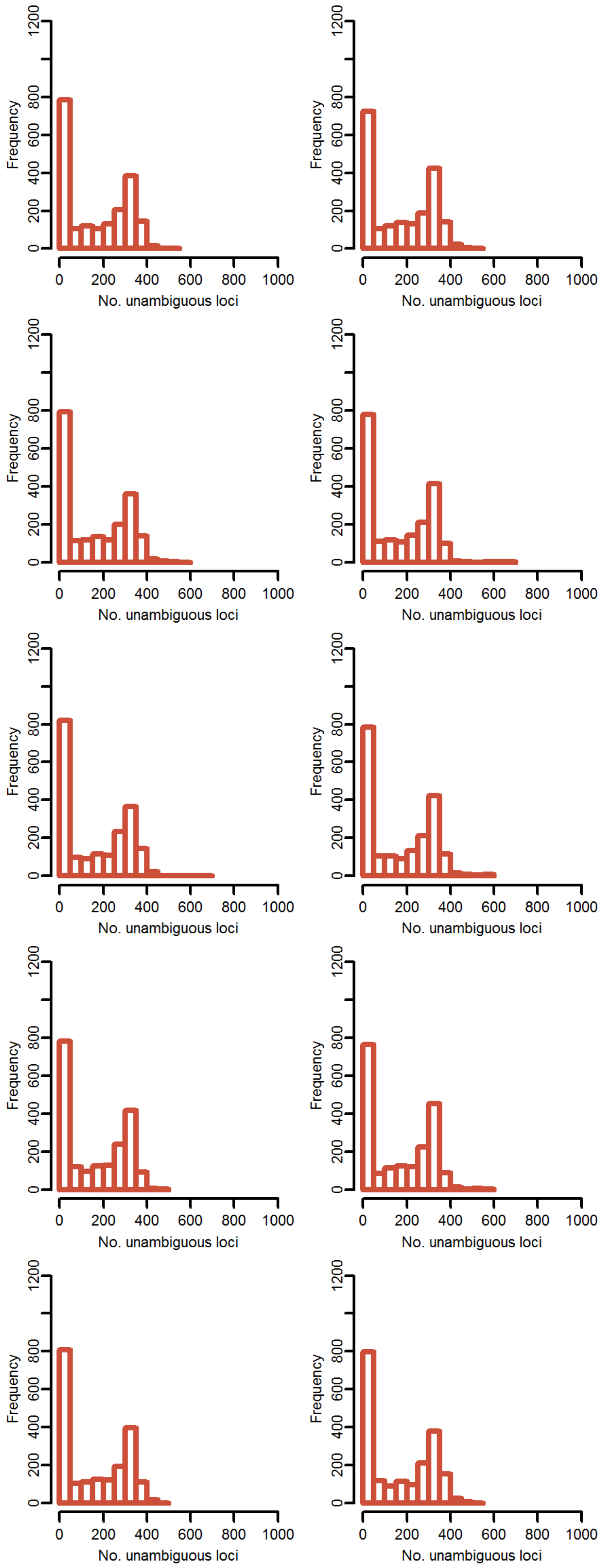
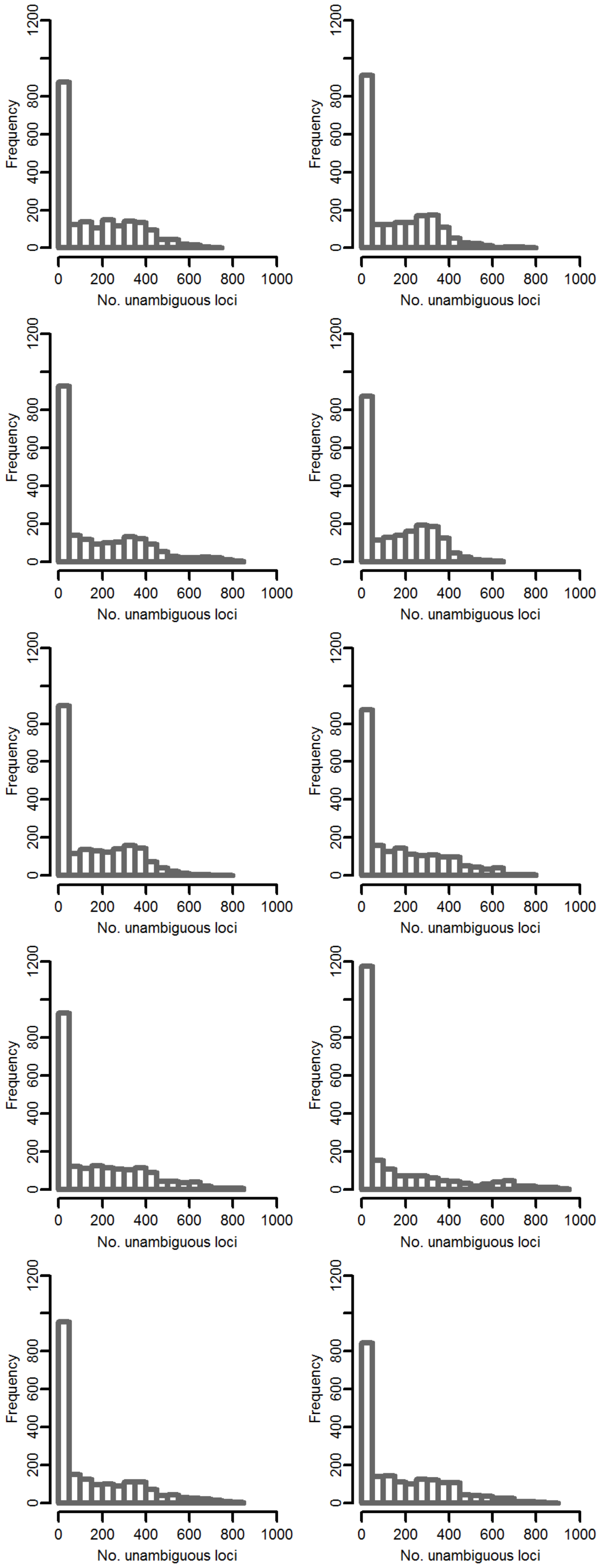


**Figure S3.** Distributions of the number of unambiguously imputed loci per Dam for all replicates of the four scenarios.

## LowLD_NoSel



## LowLD_Sel



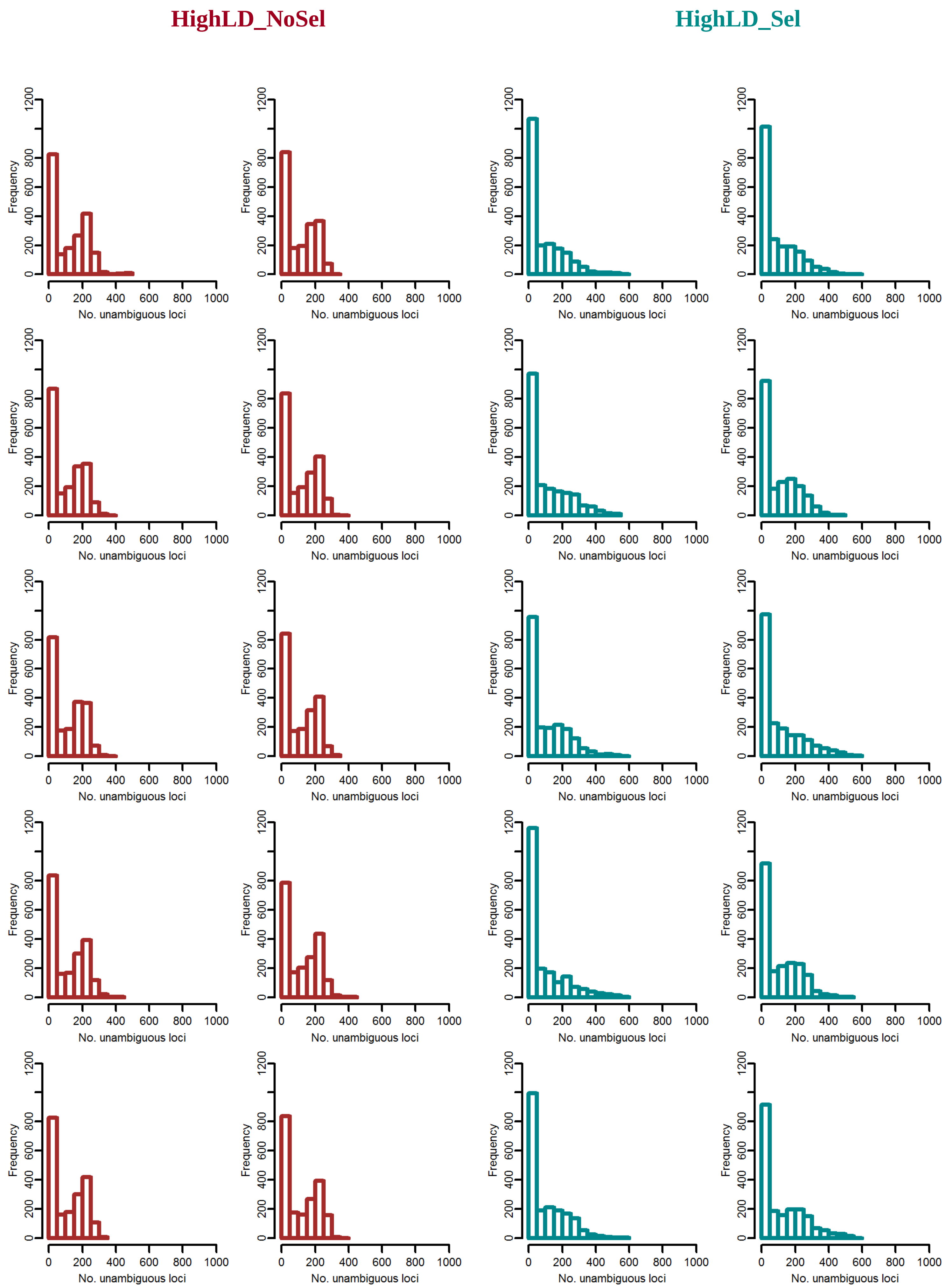
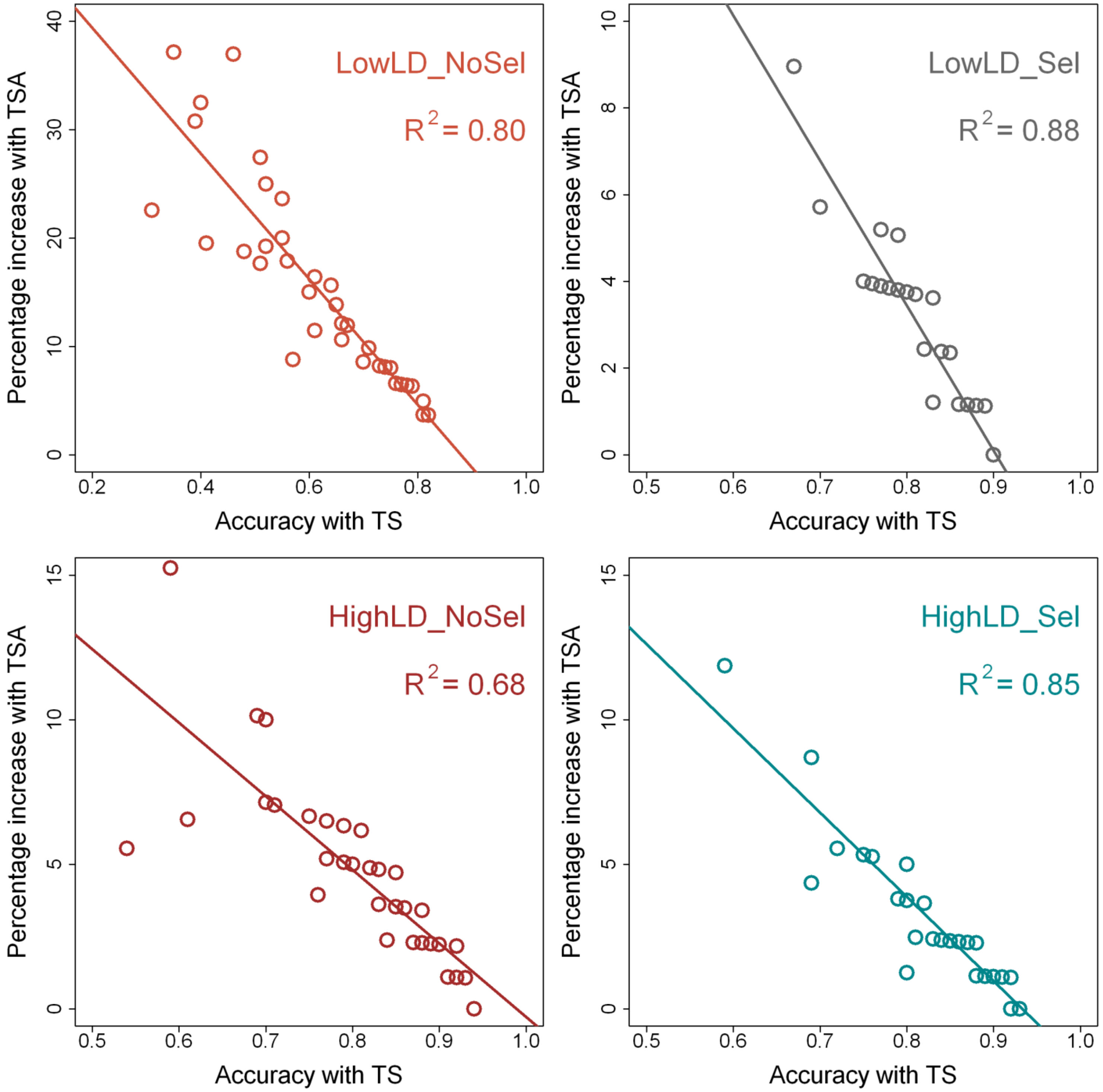

HighLD_NoSel
HighLD_Sel
Frequency
0
200
400
600
800
1200
No. unambiguous loci
0
200
400
600
800
1000

**Figure S4.** Regression analyses of the percentage increase in accuracy obtained with TSA against the accuracy already obtained with TS across all h2 and numbers of offspring for the four scenarios.


LowLD_NoSel
R² = 0.80
LowLD_Sel
R² = 0.88
HighLD_NoSel
R² = 0.68
HighLD_Sel
R² = 0.85
Percentage increase with TSA
Accuracy with TS
0
10
20
30
40
2
4
6
8
5
15
0.2
0.4
0.6
0.8
1.0
0.5
0.7
0.9