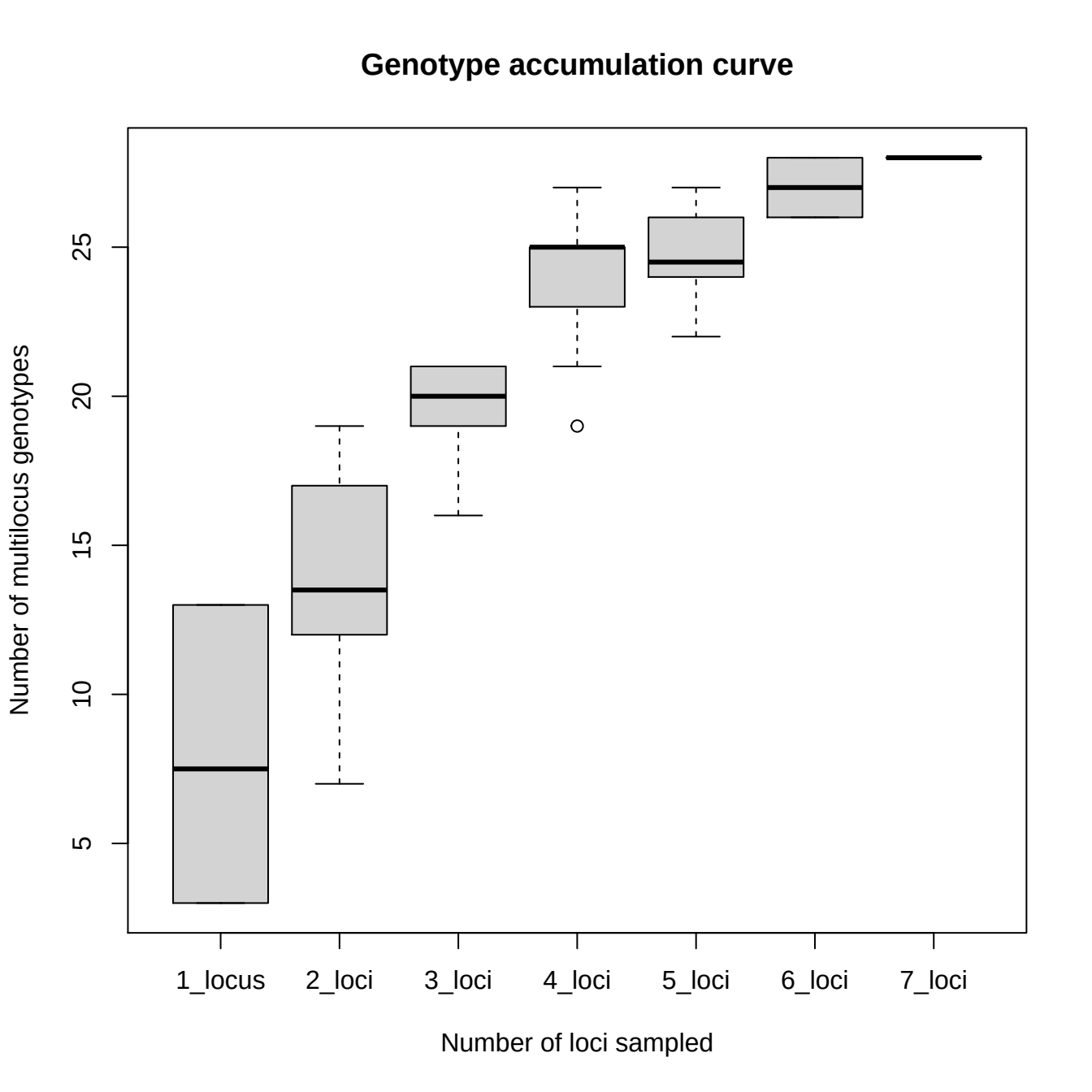
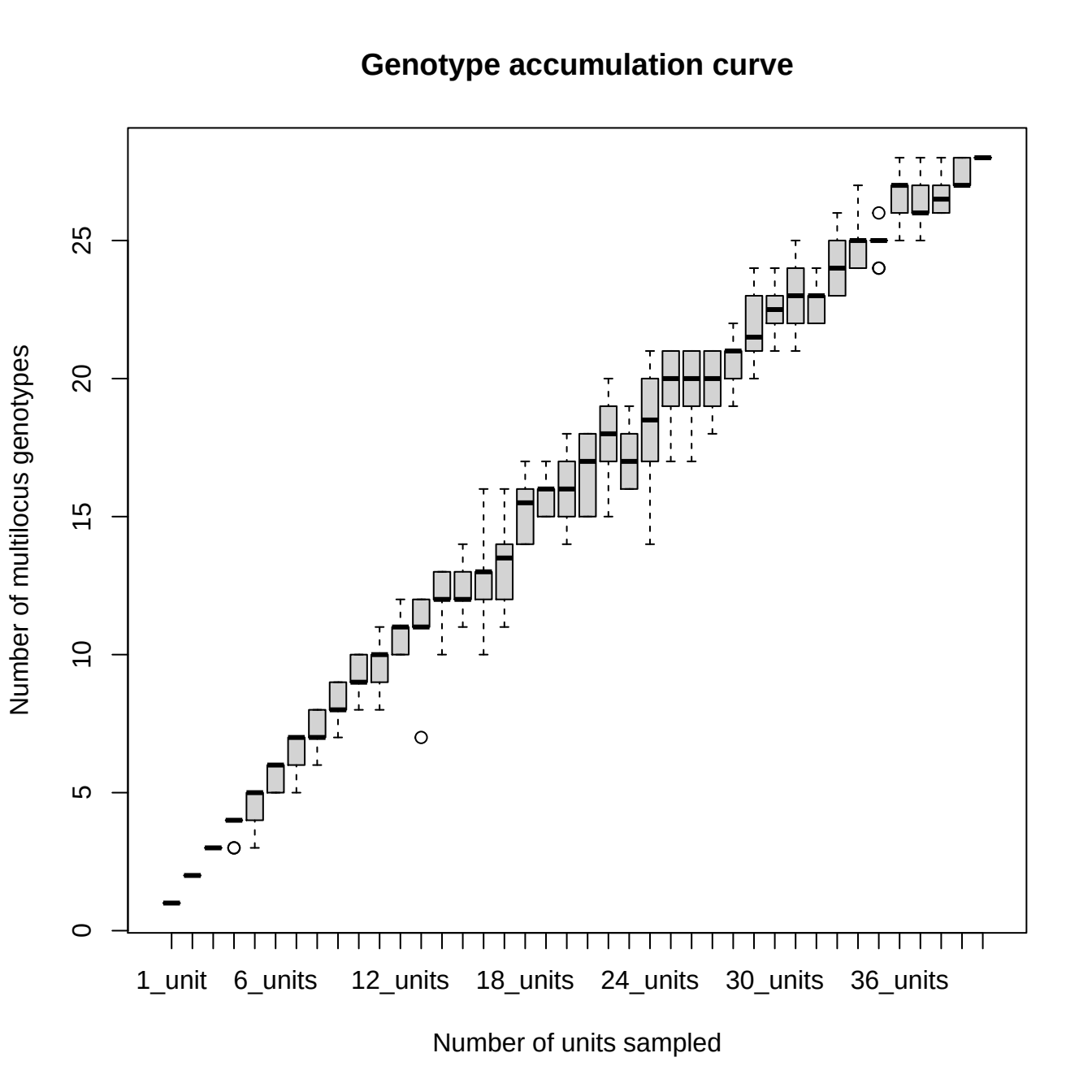
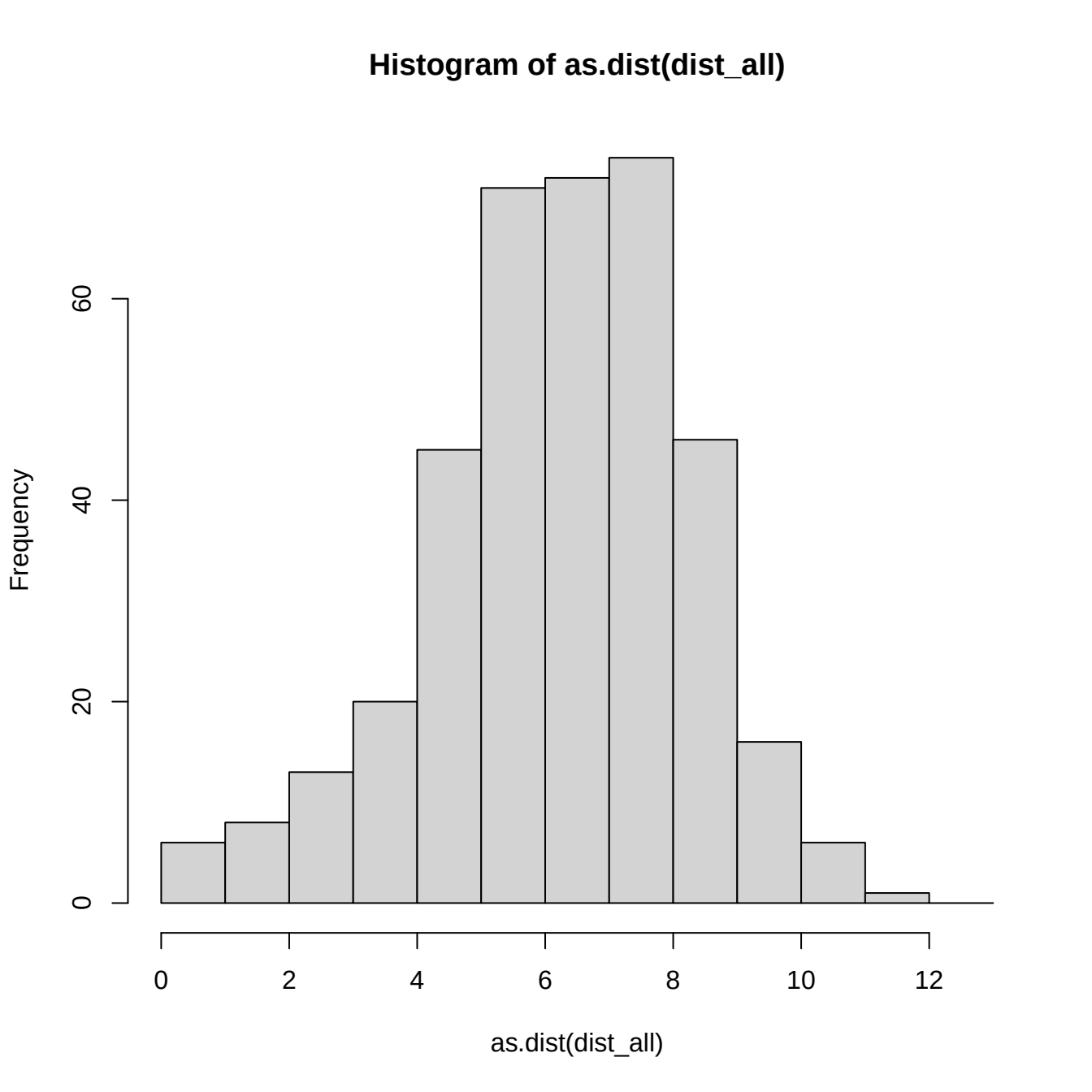
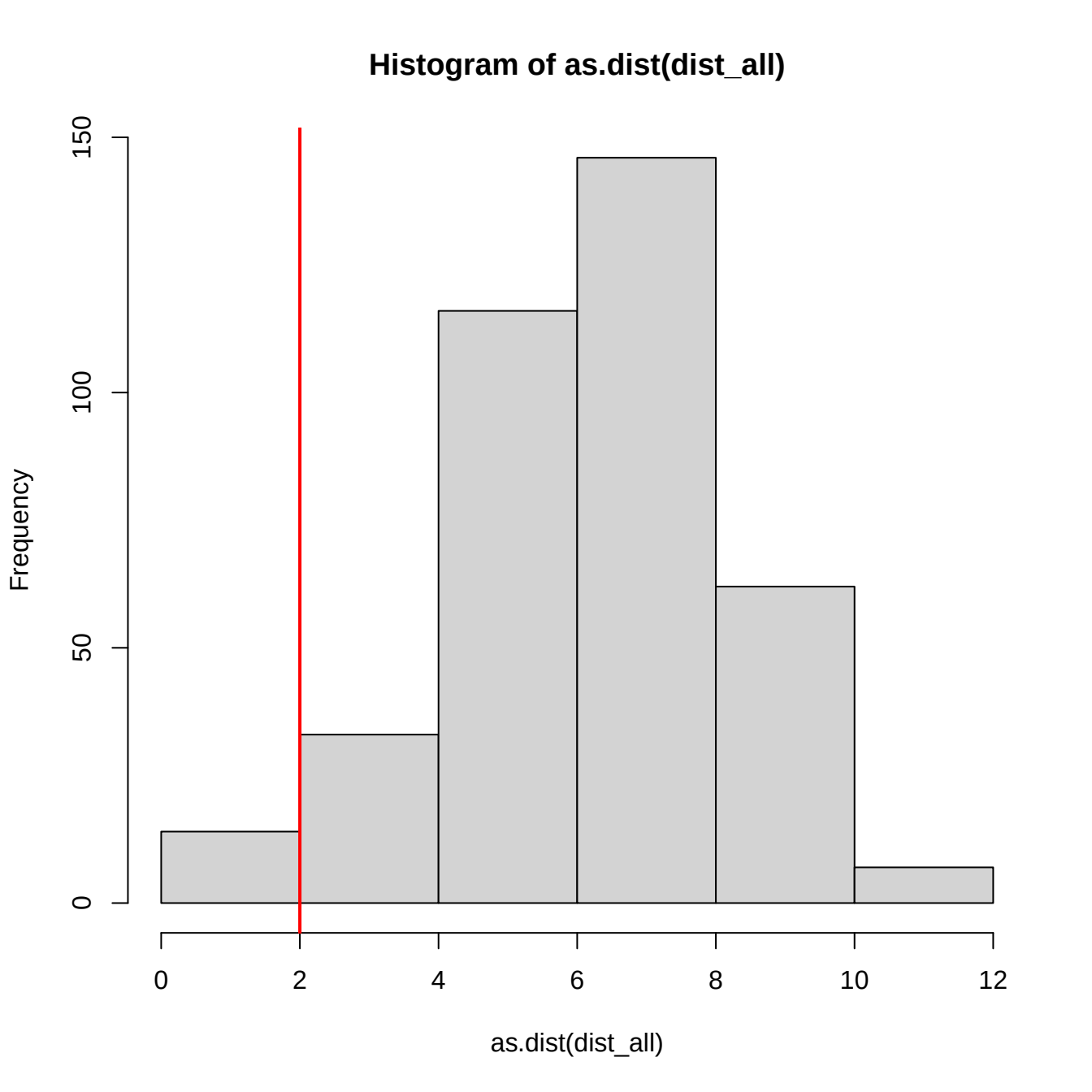
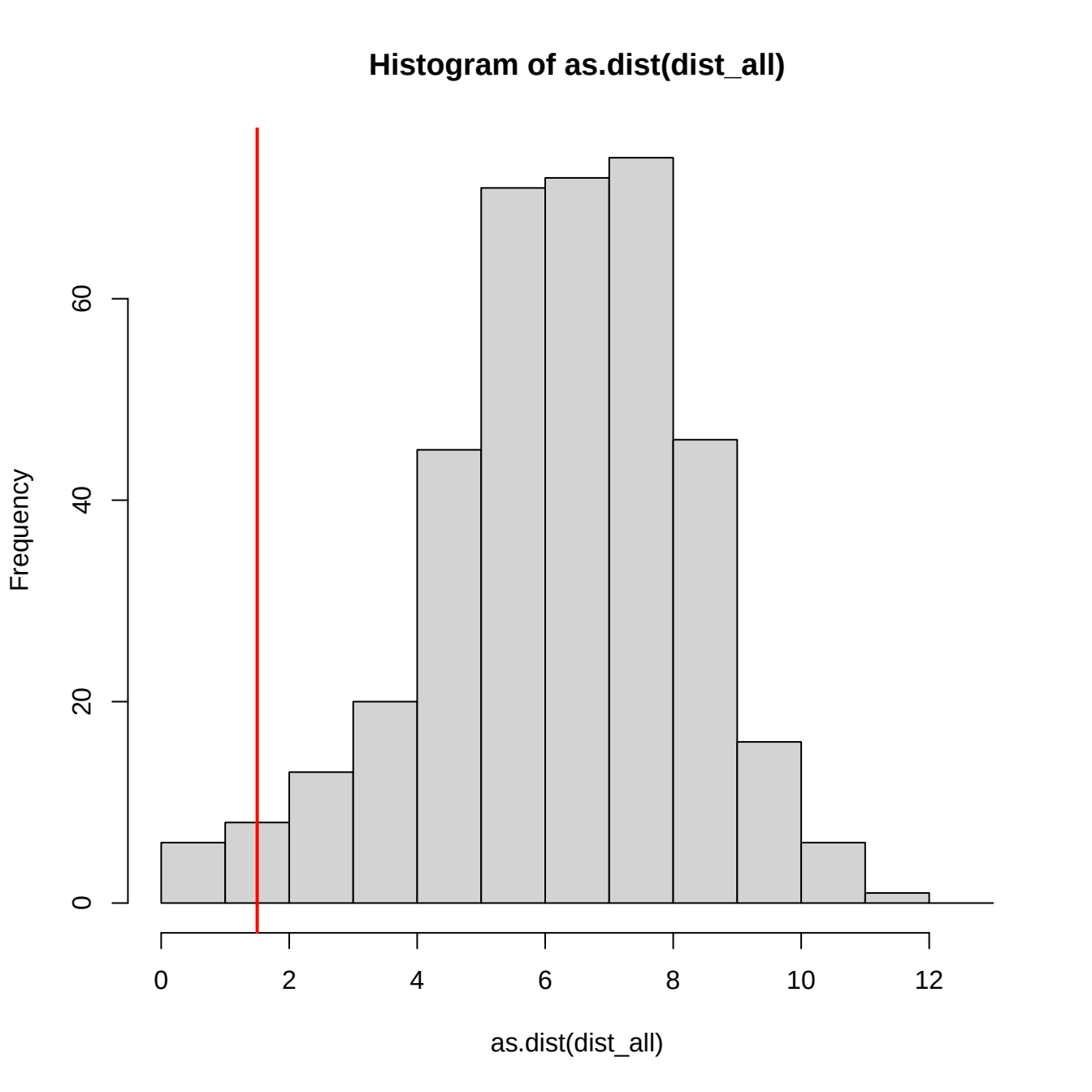
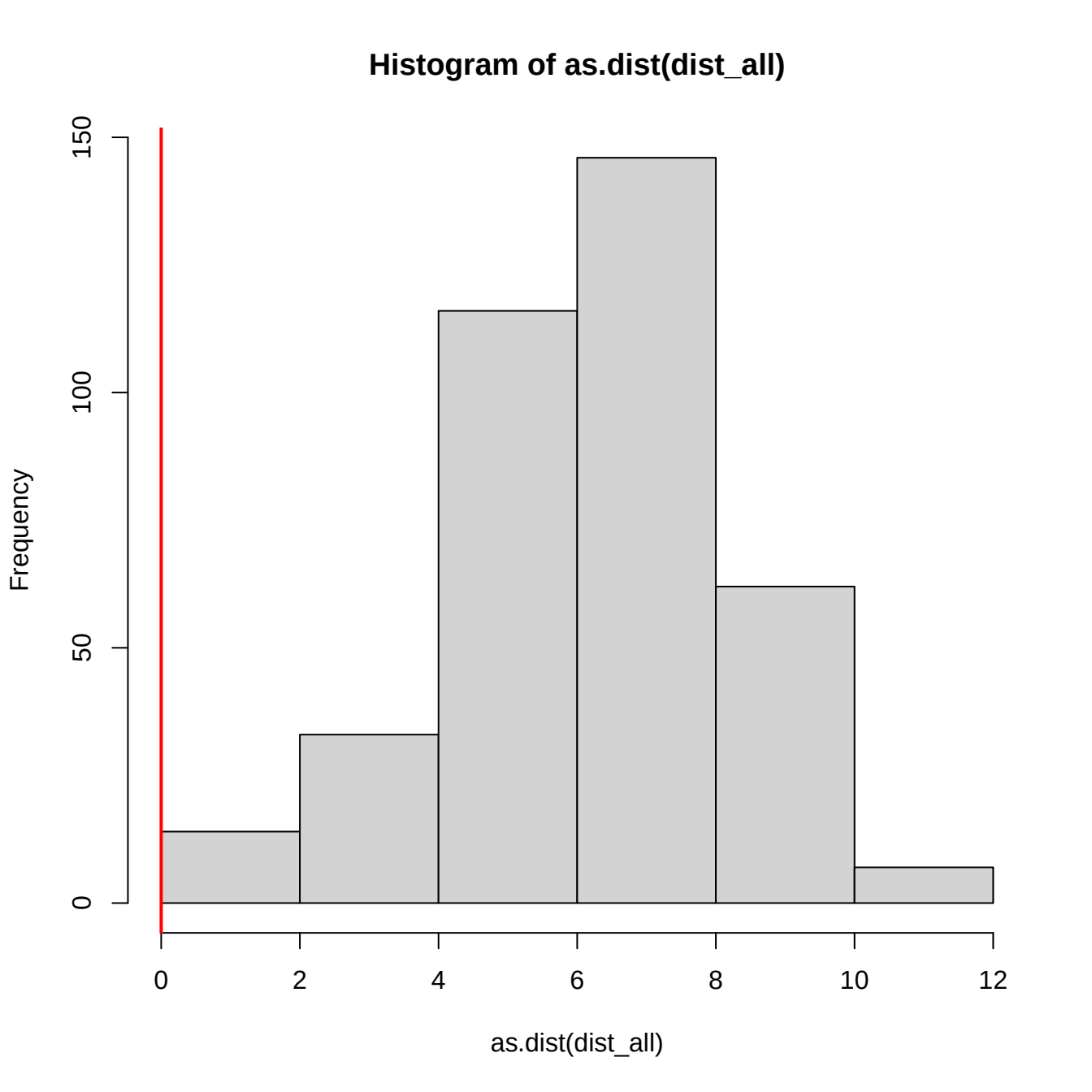

Genotype accumulation curve
Number of multilocus genotypes
5
10
15
20
25
1_locus
2_loci
3_loci
4_loci
5_loci
6_loci
7_loci
Number of loci sampled

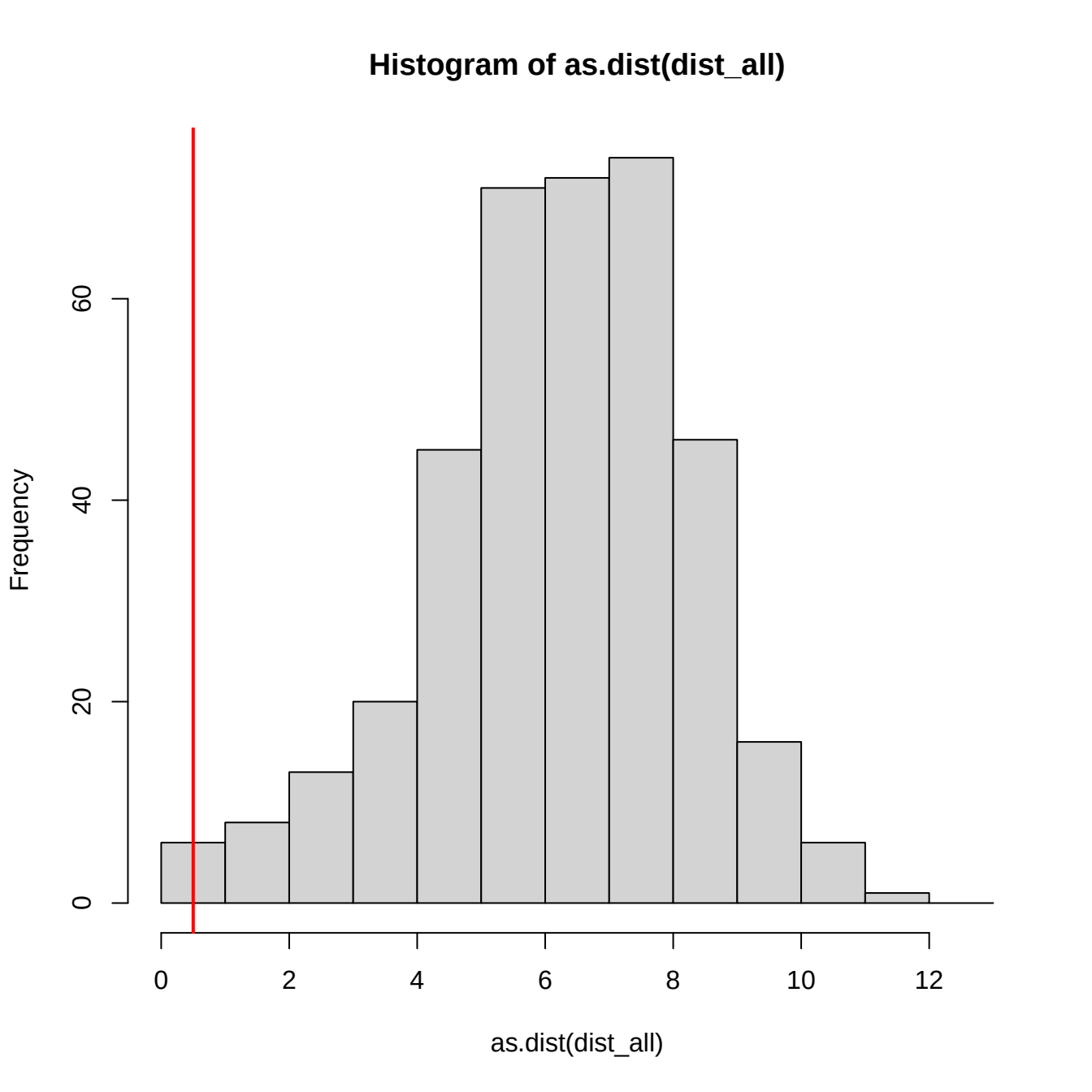

Genotype accumulation curve
Number of multilocus genotypes
0
5
10
15
20
25
1_unit
6_units
12_units
18_units
24_units
30_units
36_units
Number of units sampled

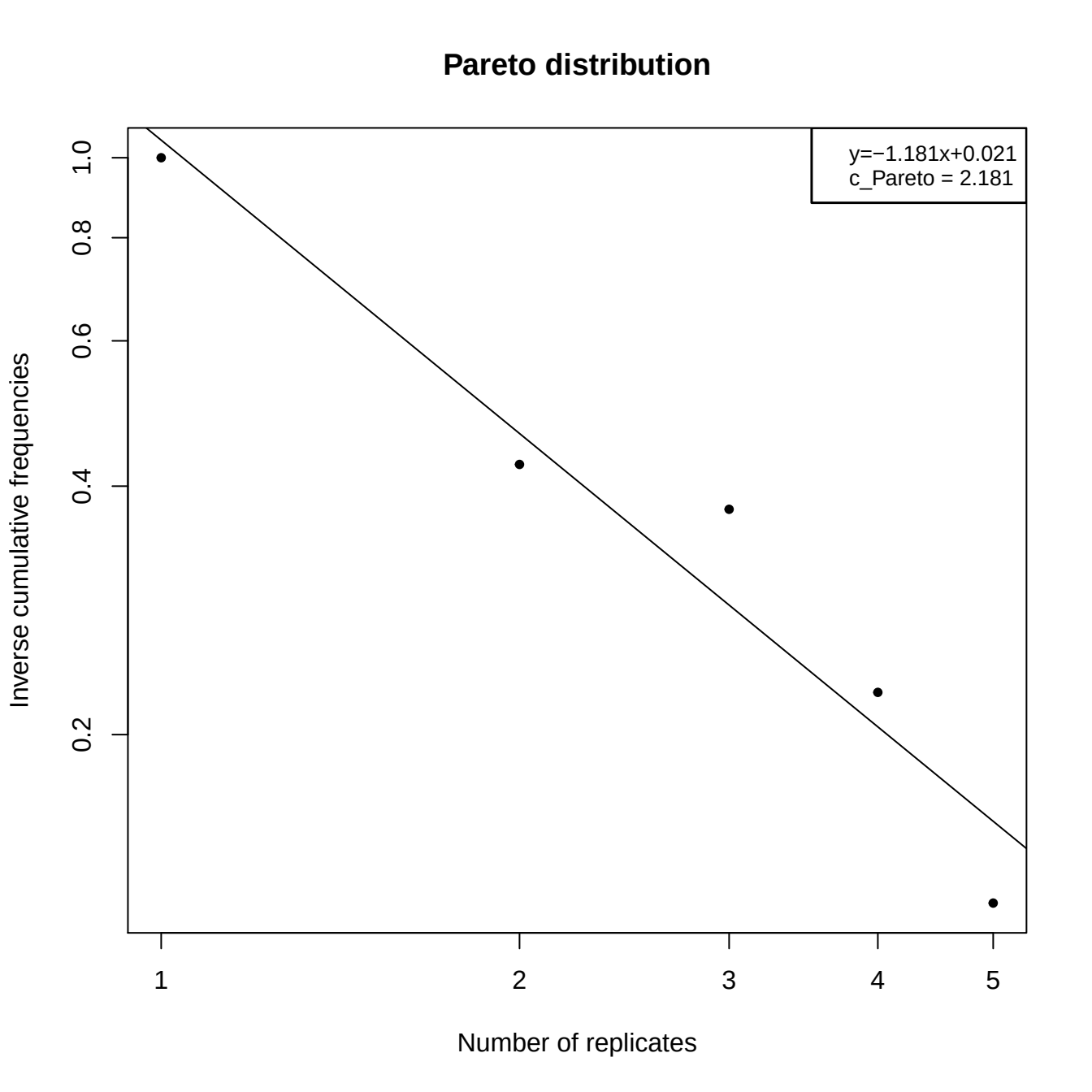

Histogram of as.dist(dist_all)
Frequency
0
20
40
60
0
2
4
6
8
10
12
as.dist(dist_all)

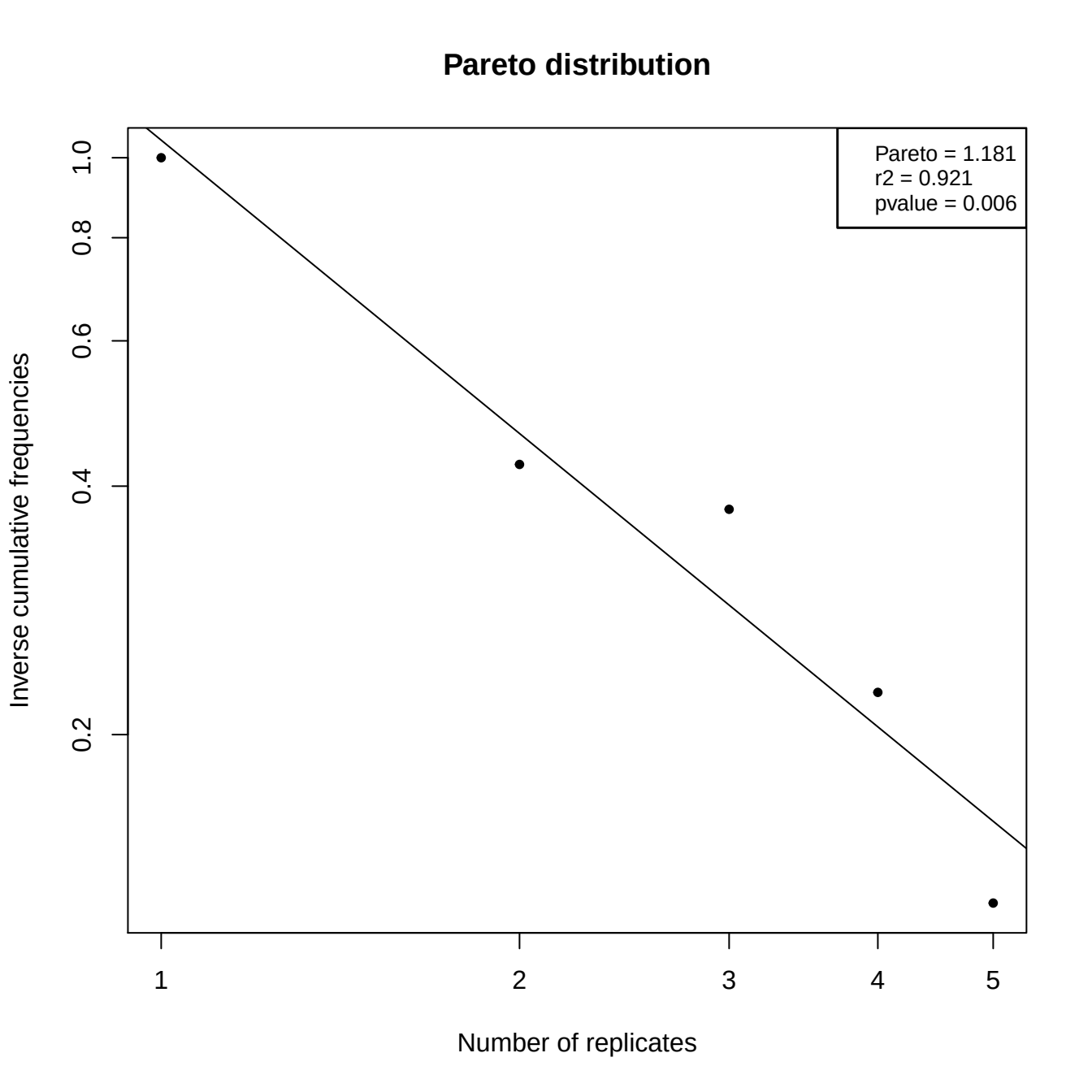

Histogram of as.dist(dist_all)
Frequency
0
50
100
150
0
2
4
6
8
10
12
as.dist(dist_all)

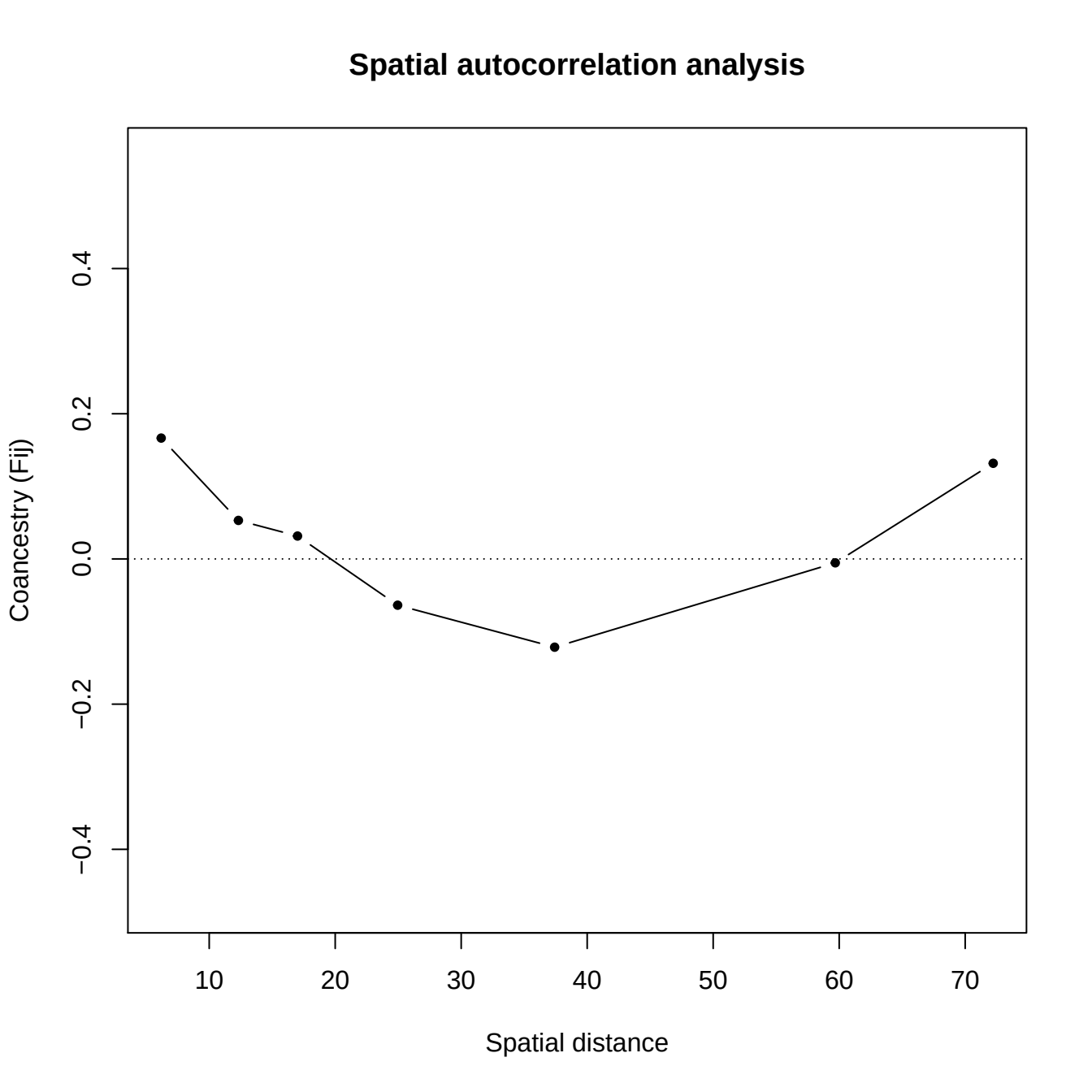

Histogram of as.dist(dist_all)
Frequency
0
20
40
60
0
2
4
6
8
10
12
as.dist(dist_all)

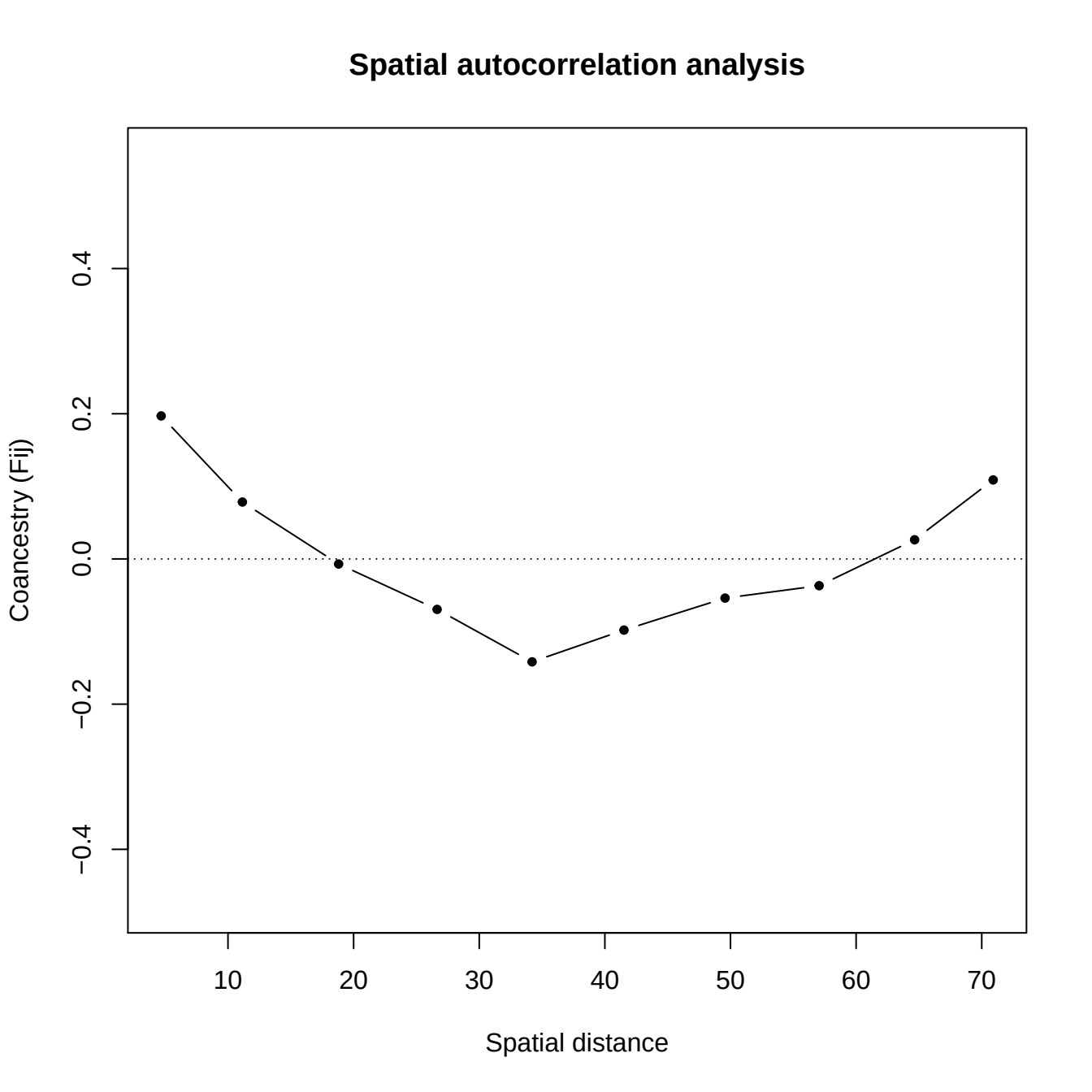

Histogram of as.dist(dist_all)
Frequency
0
50
100
150
0
2
4
6
8
10
12
as.dist(dist_all)


Histogram of as.dist(dist_all)
Frequency
0
20
40
60
0
2
4
6
8
10
12
as.dist(dist_all)


Pareto distribution
y=−1.181x+0.021
c_Pareto = 2.181
Inverse cumulative frequencies
0.2
0.4
0.6
0.8
1.0
1
2
3
4
5
Number of replicates


Pareto distribution
Pareto = 1.181
r2 = 0.921
pvalue = 0.006
Inverse cumulative frequencies
0.2
0.4
0.6
0.8
1.0
1
2
3
4
5
Number of replicates


Spatial autocorrelation analysis
Coancestry (Fij)
0.4
0.2
0.0
−0.2
−0.4
10
20
30
40
50
60
70
Spatial distance


Spatial autocorrelation analysis
Coancestry (Fij)
0.4
0.2
0.0
−0.2
−0.4
10
20
30
40
50
60
70
Spatial distance