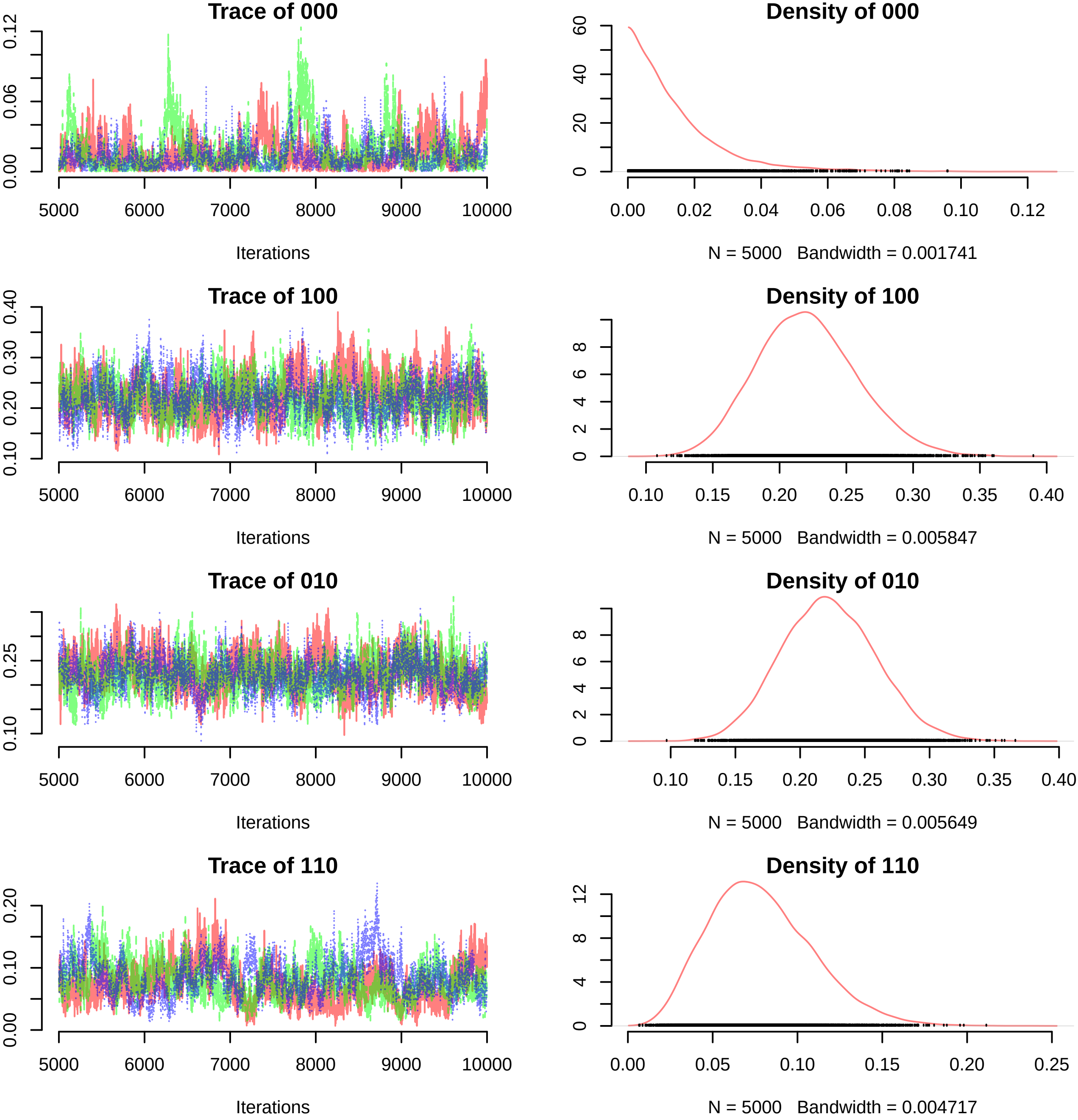
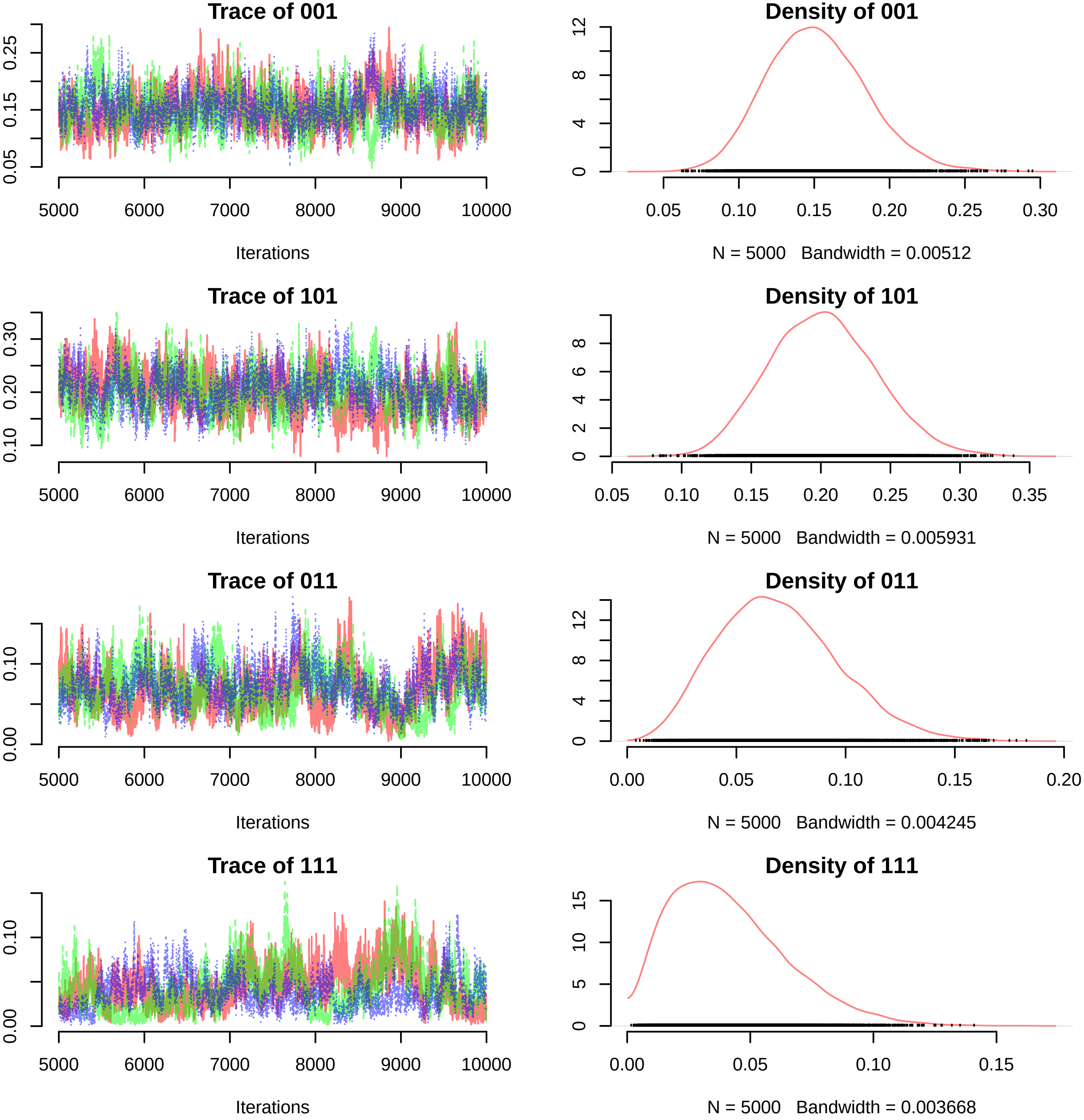
	Value
No. marker loci	3
No. children	100
No. blood samples	100
No. partial observations	0
No. mcmc iterations overall	10000
Thinning interval	1
Burn in overall	5000

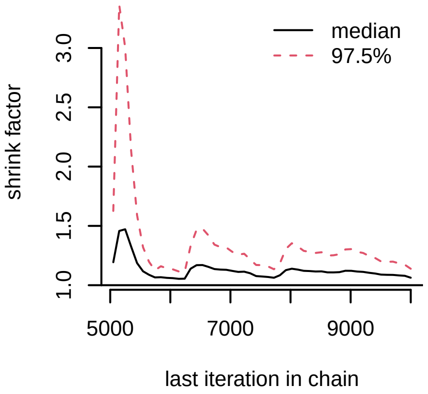
	Effective posterior sample size
000	246
100	336
010	357
110	175
001	345
101	286
011	169
111	129

	No of observations
0 0 1	3
0 0.5 0.5	5
0 1 0	3
0 1 0.5	2
0.5 0 0.5	5
0.5 0 1	3
0.5 0.5 0	8
0.5 0.5 0.5	44
0.5 0.5 1	3
0.5 1 0.5	2
1 0 0	5
1 0 0.5	3
1 0 1	7
1 0.5 0	3
1 0.5 0.5	3
1 1 0.5	1

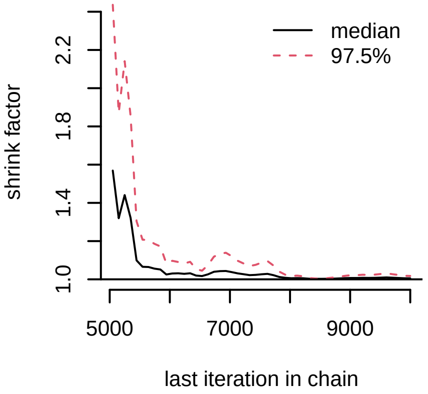

Trace of 000
0.00
0.06
0.12
5000
6000
7000
8000
9000
10000
Iterations
Density of 000
0
20
40
60
0.00
0.02
0.04
0.06
0.08
0.10
0.12
N = 5000 Bandwidth = 0.001741
Trace of 100
0.10
0.20
0.30
0.40
5000
6000
7000
8000
9000
10000
Iterations
Density of 100
0
2
4
6
8
0.10
0.15
0.20
0.25
0.30
0.35
0.40
N = 5000 Bandwidth = 0.005847
Trace of 010
0.10
0.25
5000
6000
7000
8000
9000
10000
Iterations
Density of 010
0
2
4
6
8
0.10
0.15
0.20
0.25
0.30
0.35
0.40
N = 5000 Bandwidth = 0.005649
Trace of 110
0.00
0.10
0.20
5000
6000
7000
8000
9000
10000
Iterations
Density of 110
0
4
8
12
0.00
0.05
0.10
0.15
0.20
0.25
N = 5000 Bandwidth = 0.004717


Trace of 001
0.05
0.15
0.25
5000
6000
7000
8000
9000
10000
Iterations
Density of 001
0
4
8
12
0.05
0.10
0.15
0.20
0.25
0.30
N = 5000 Bandwidth = 0.00512
Trace of 101
0.10
0.20
0.30
5000
6000
7000
8000
9000
10000
Iterations
Density of 101
0
2
4
6
8
0.05
0.10
0.15
0.20
0.25
0.30
0.35
N = 5000 Bandwidth = 0.005931
Trace of 011
0.00
0.10
5000
6000
7000
8000
9000
10000
Iterations
Density of 011
0
4
8
12
0.00
0.05
0.10
0.15
0.20
N = 5000 Bandwidth = 0.004245
Trace of 111
0.00
0.10
5000
6000
7000
8000
9000
10000
Iterations
Density of 111
0
5
10
15
0.00
0.05
0.10
0.15
N = 5000 Bandwidth = 0.003668

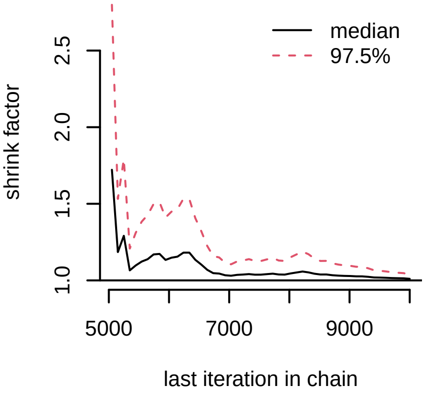
000



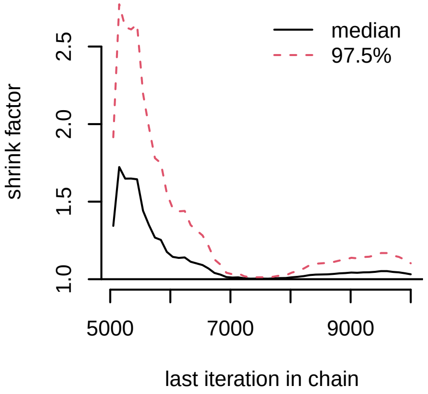
100



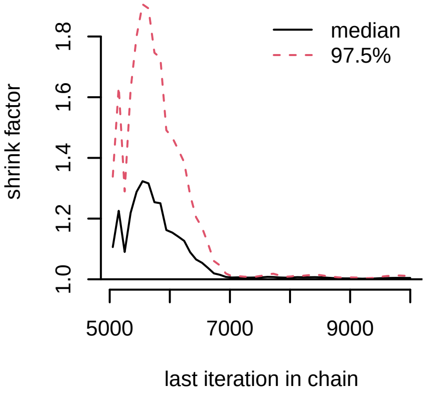
010



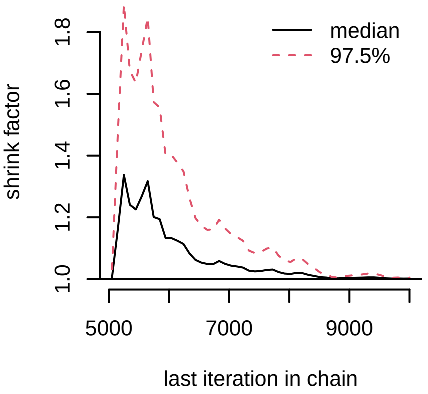
110



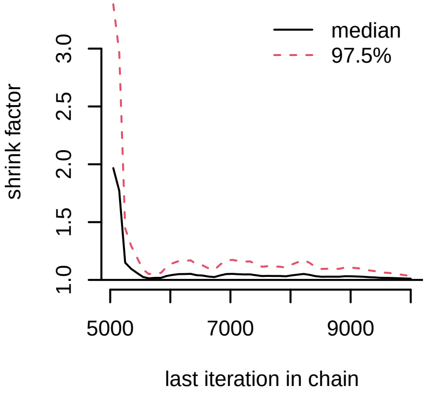
001



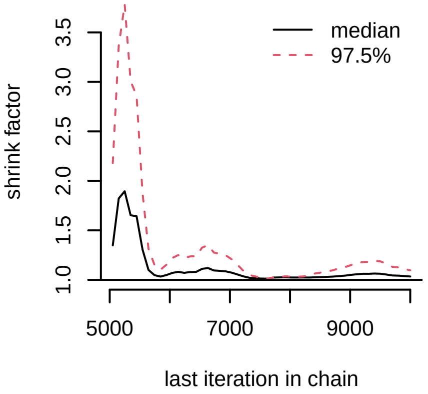
101

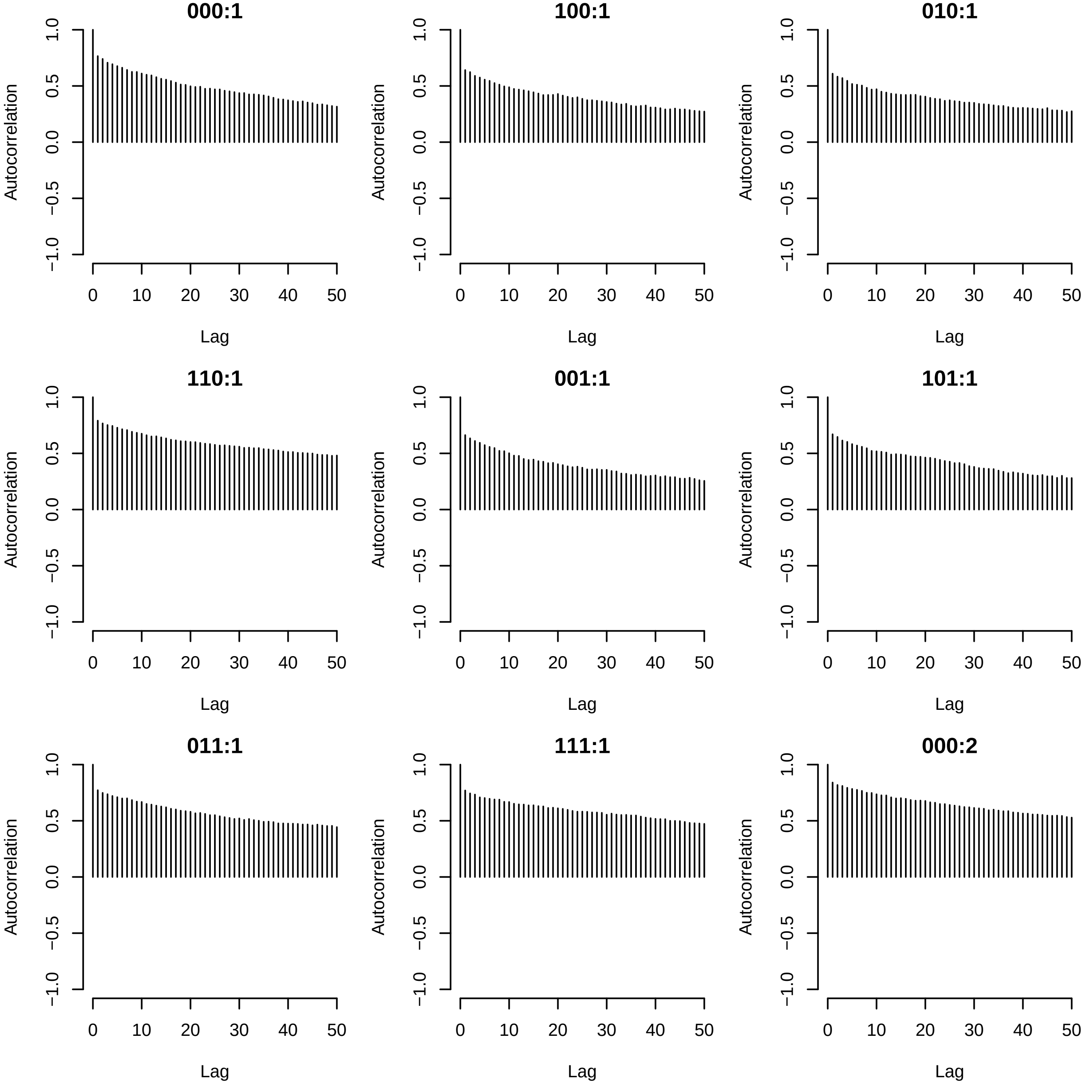


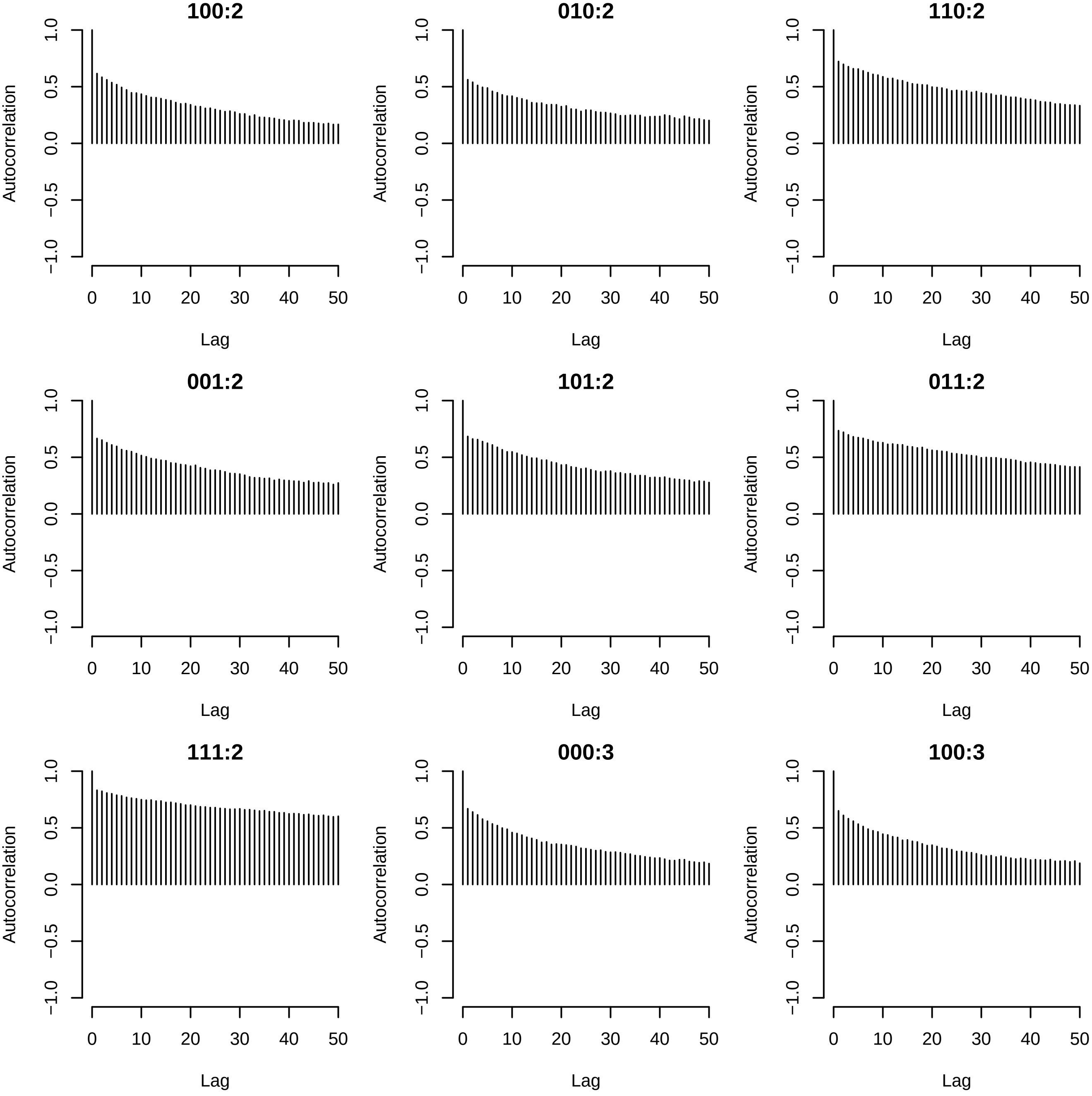
011

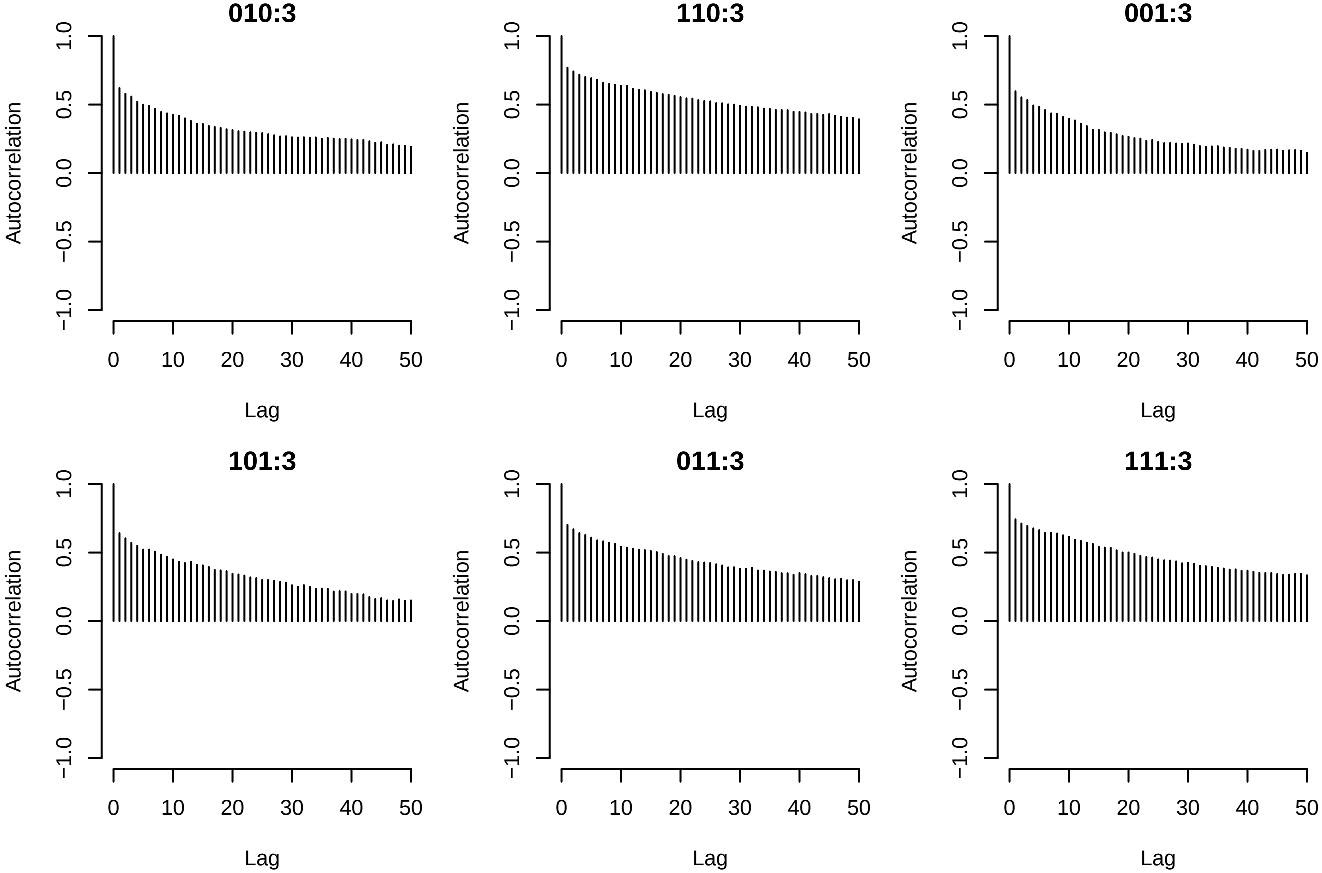


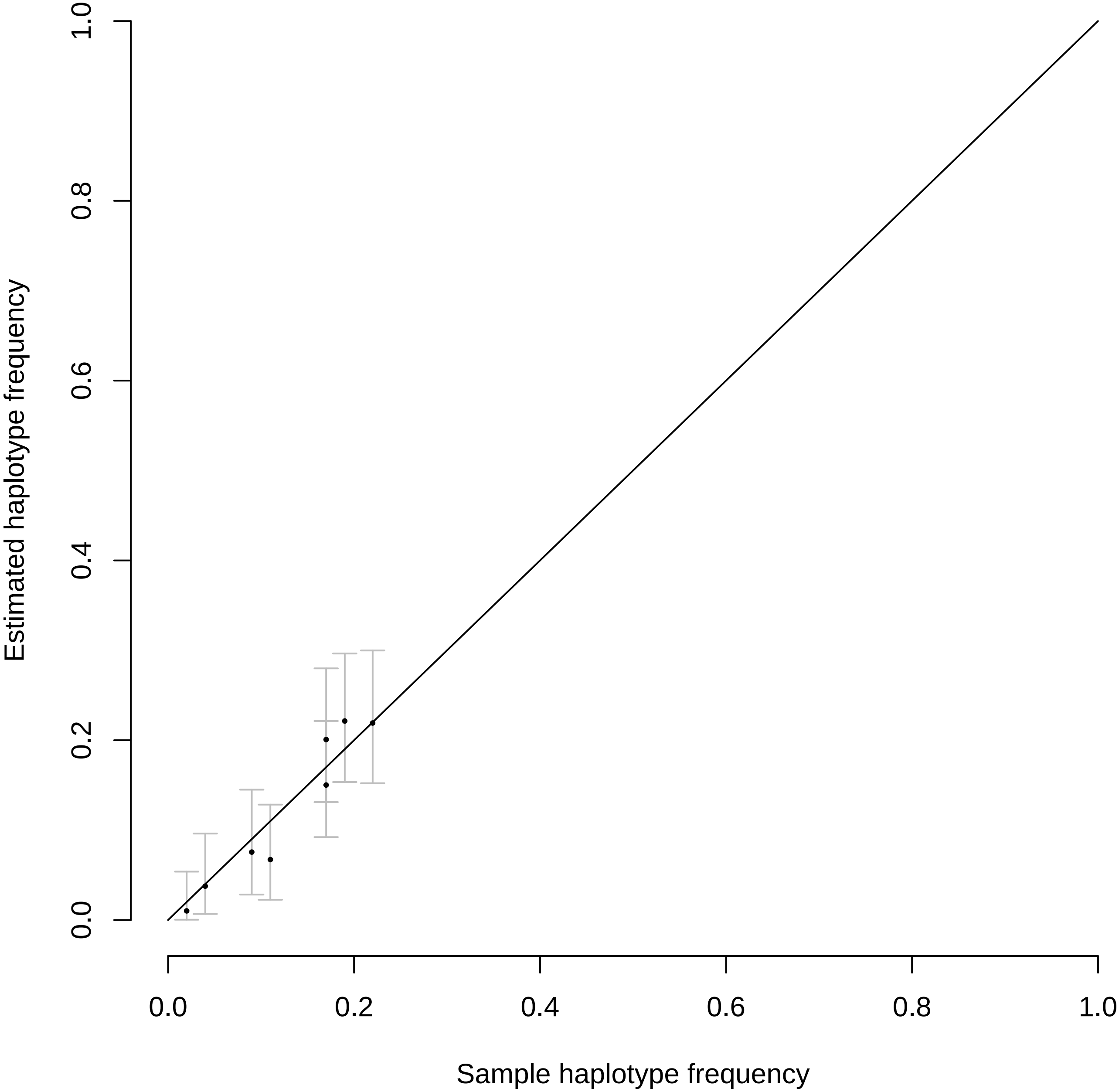
111

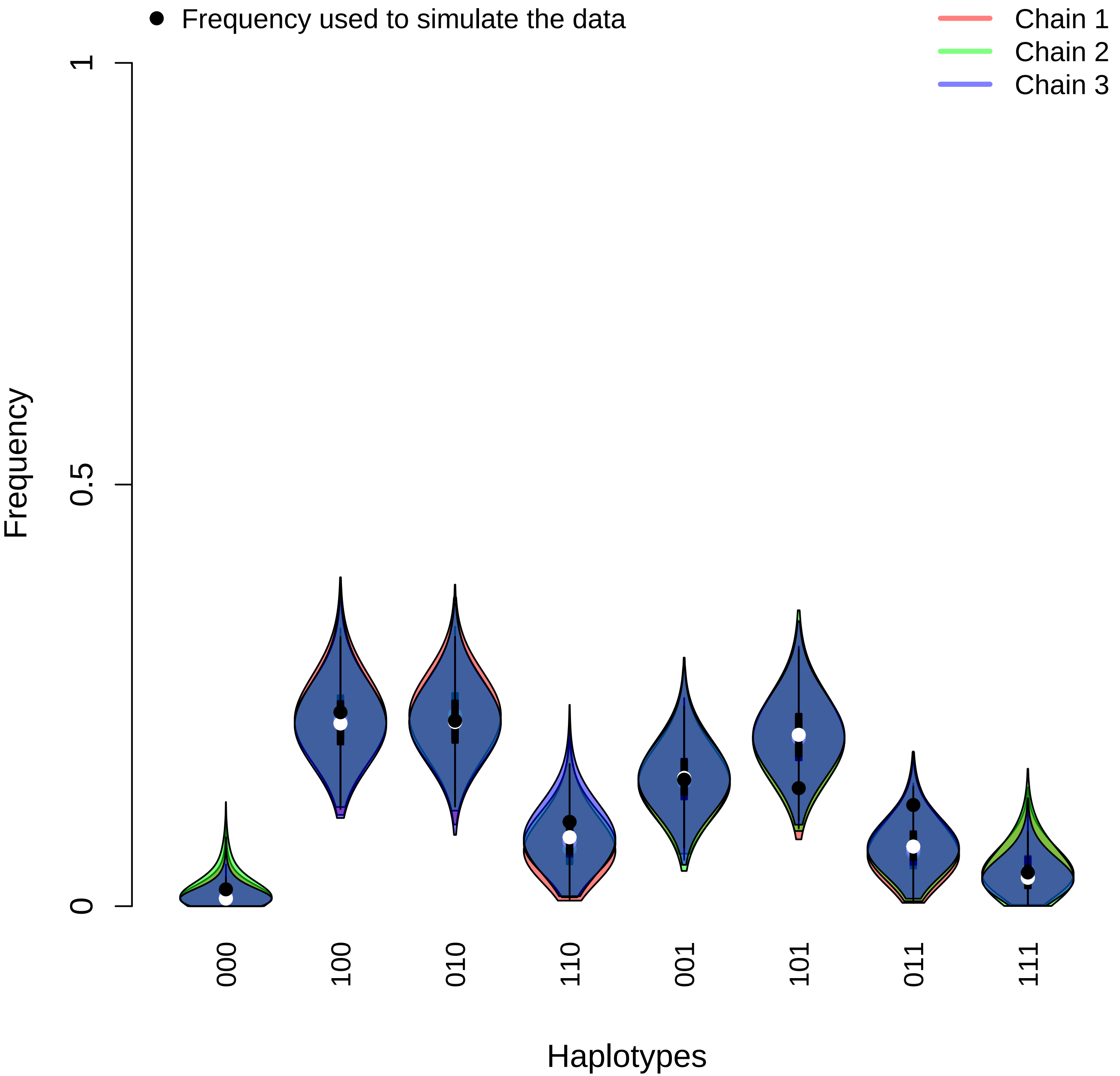


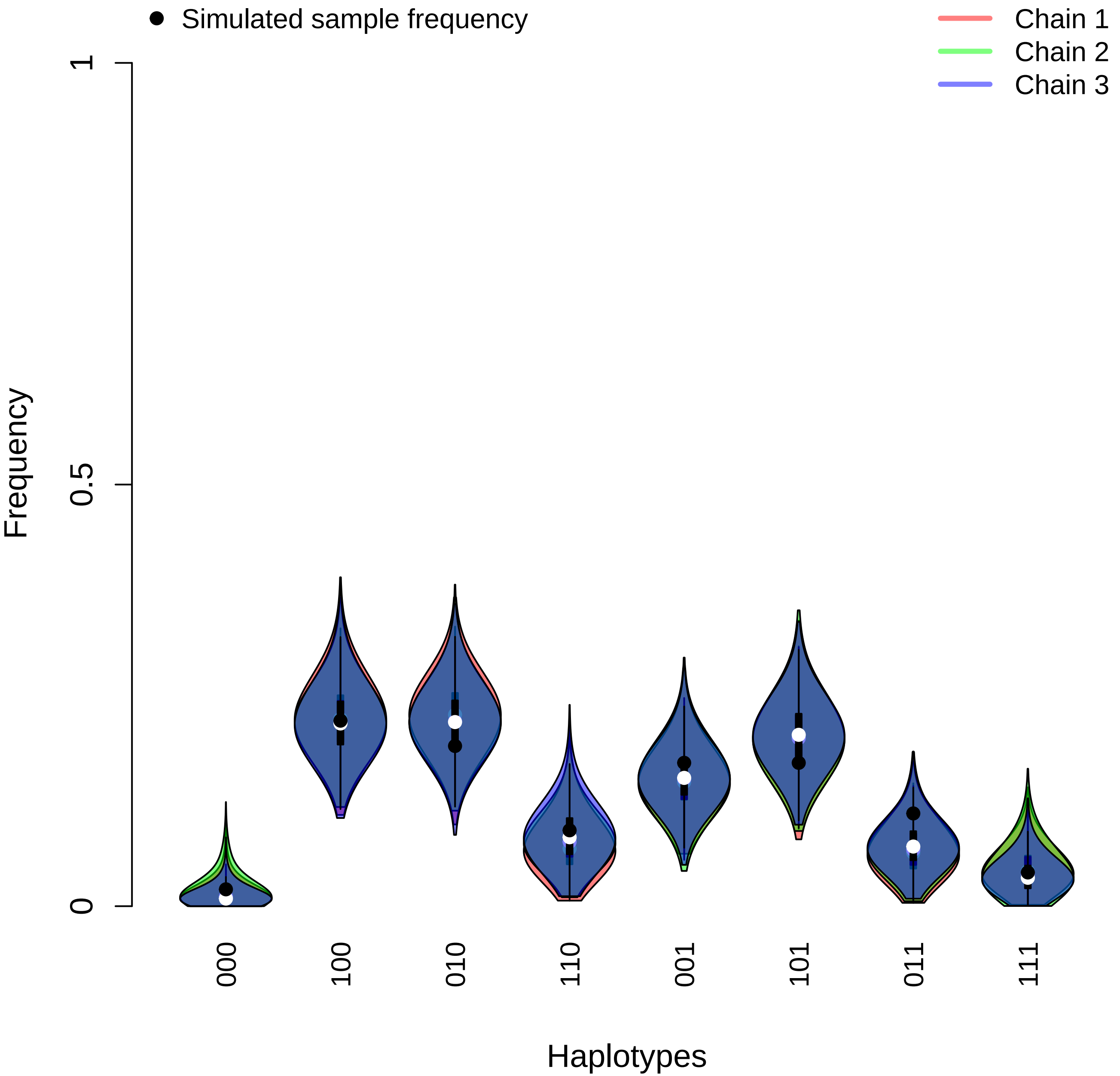

000:1
100:1
010:1
110:1
001:1
101:1
011:1
111:1
000:2
Autocorrelation
1.0
0.5
0.0
−0.5
−1.0
Lag
0
10
20
30
40
50

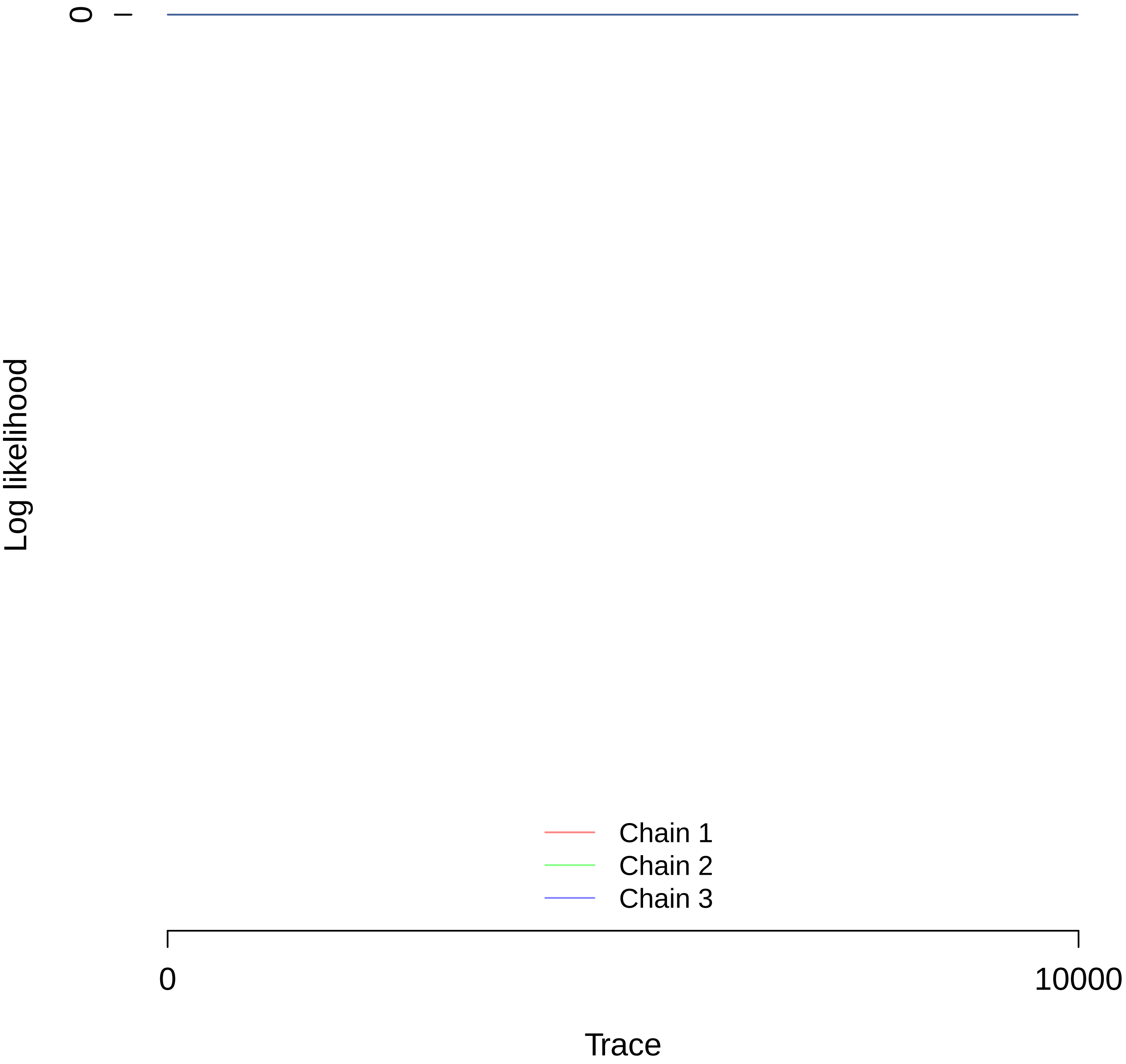

100:2
010:2
110:2
001:2
101:2
011:2
111:2
000:3
100:3
Autocorrelation
−1.0
−0.5
0.0
0.5
1.0
Lag
0
10
20
30
40
50


010:3
110:3
001:3
101:3
011:3
111:3
Autocorrelation
1.0
0.5
0.0
−0.5
−1.0
Lag
0
10
20
30
40
50

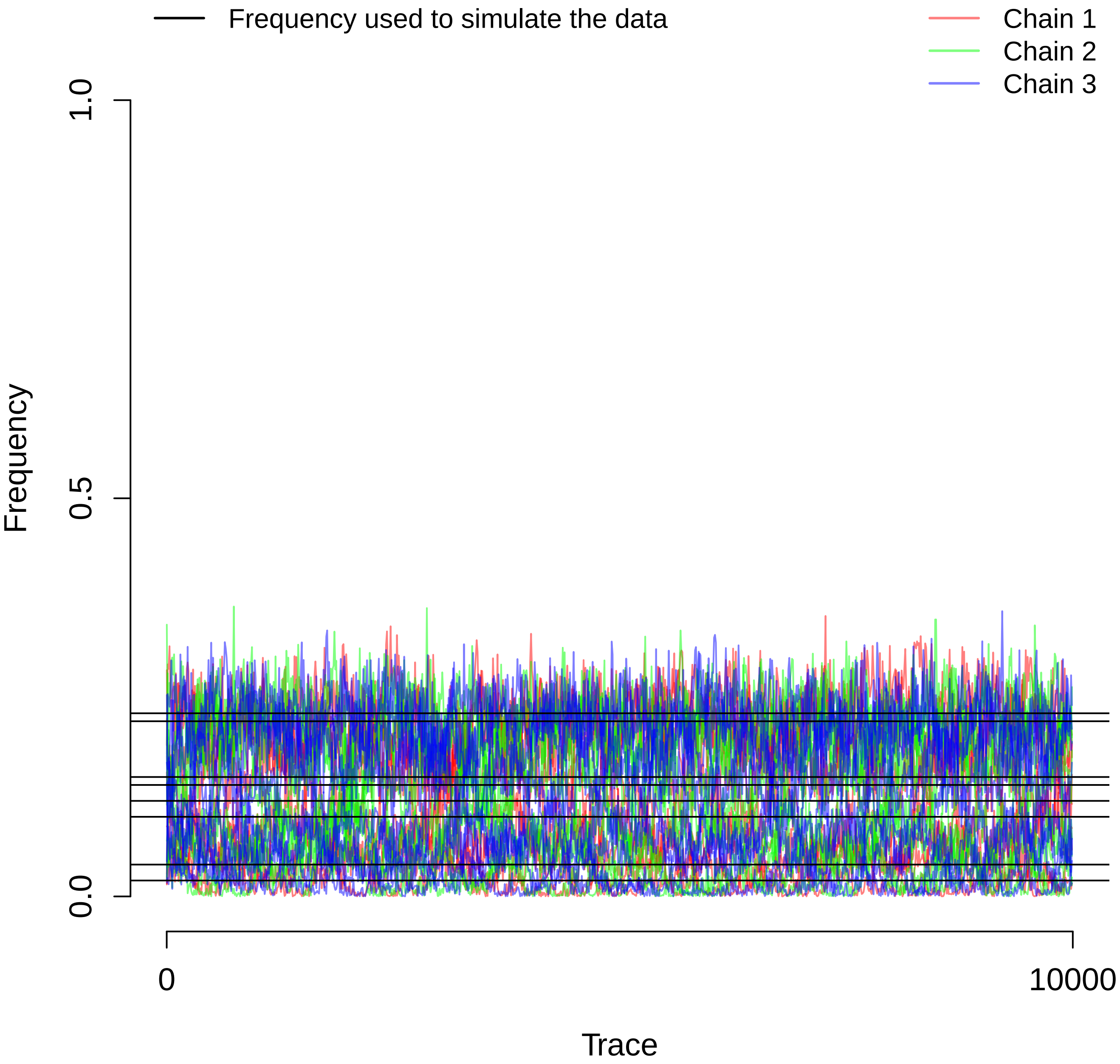

Estimated haplotype frequency
0.0
0.2
0.4
0.6
0.8
1.0
Sample haplotype frequency
0.0
0.2
0.4
0.6
0.8
1.0


● Frequency used to simulate the data
Chain 1
Chain 2
Chain 3
Frequency
1
0.5
0
000
100
010
110
001
101
011
111
Haplotypes

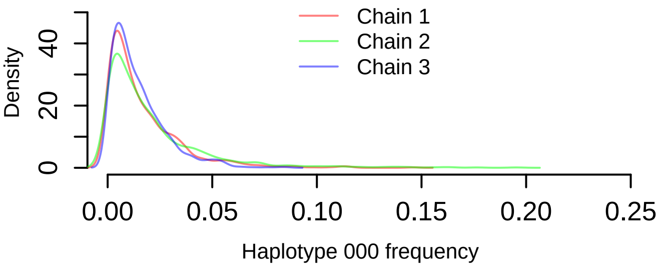

● Simulated sample frequency
Chain 1
Chain 2
Chain 3
Frequency
1
0.5
0
000
100
010
110
001
101
011
111
Haplotypes



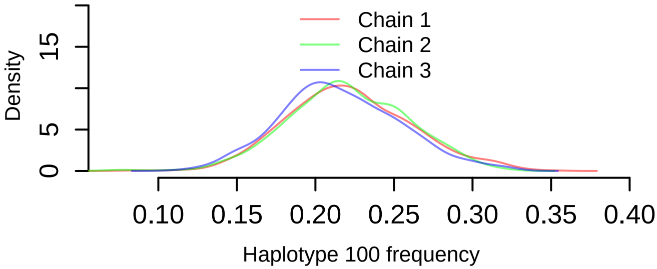
In addition to the thinning interval used to generate results, thinned by 10



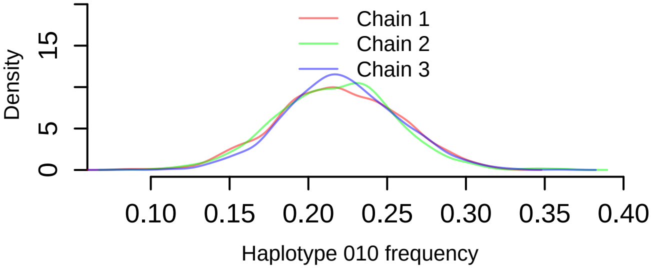
In addition to the thinning interval used to generate results, thinned by 10



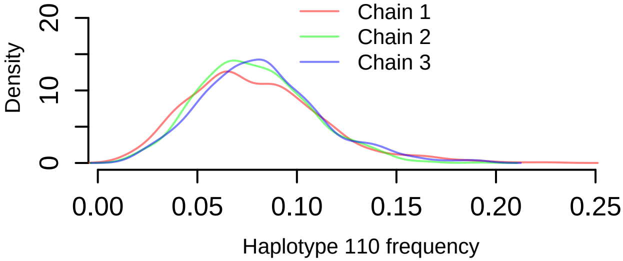
In addition to the thinning interval used to generate results, thinned by 10



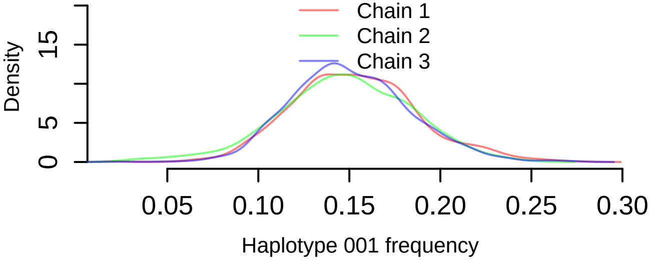
In addition to the thinning interval used to generate results, thinned by 10



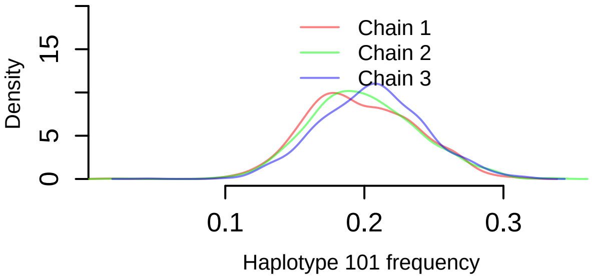
In addition to the thinning interval used to generate results, thinned by 10



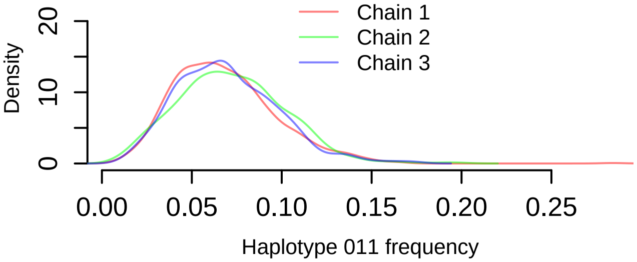
In addition to the thinning interval used to generate results, thinned by 10



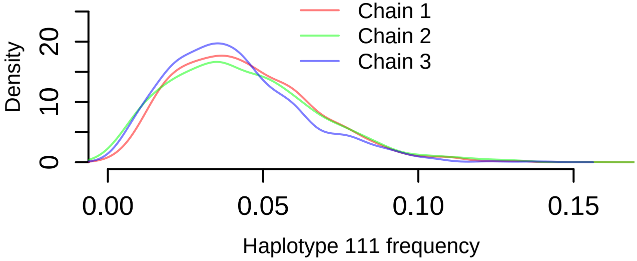
In addition to the thinning interval used to generate results, thinned by 10



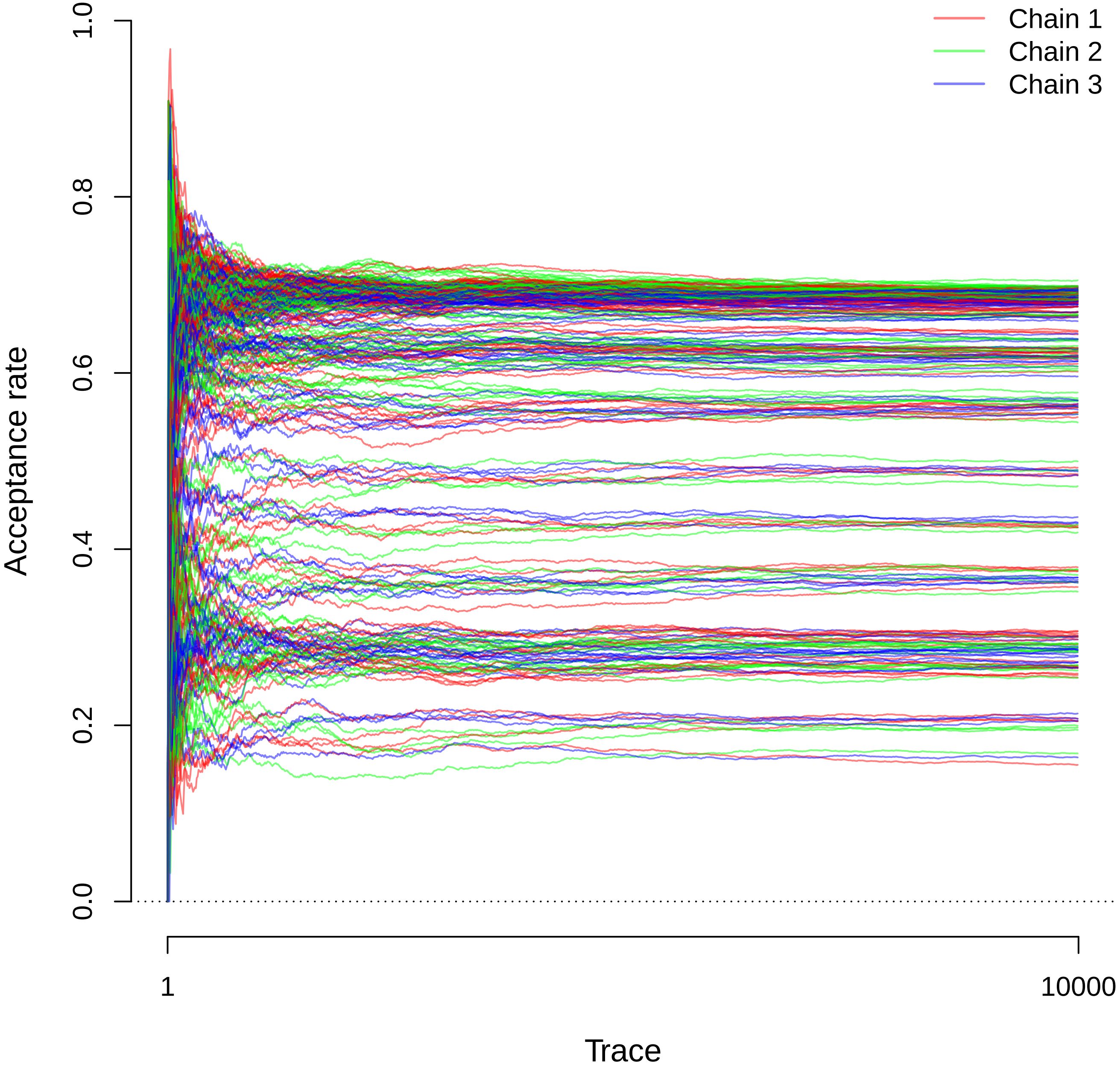
In addition to the thinning interval used to generate results, thinned by 10



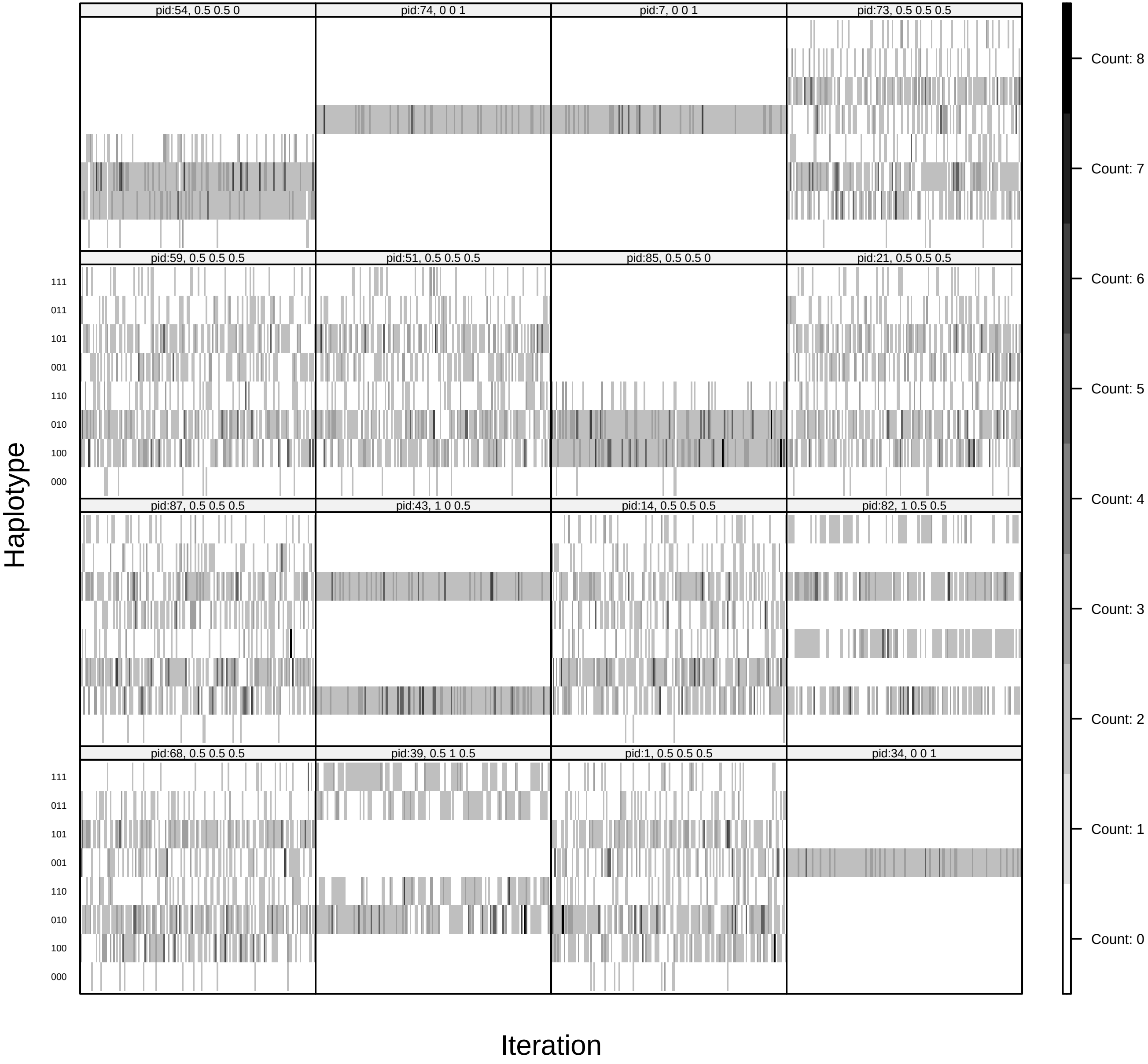
In addition to the thinning interval used to generate results, thinned by 10



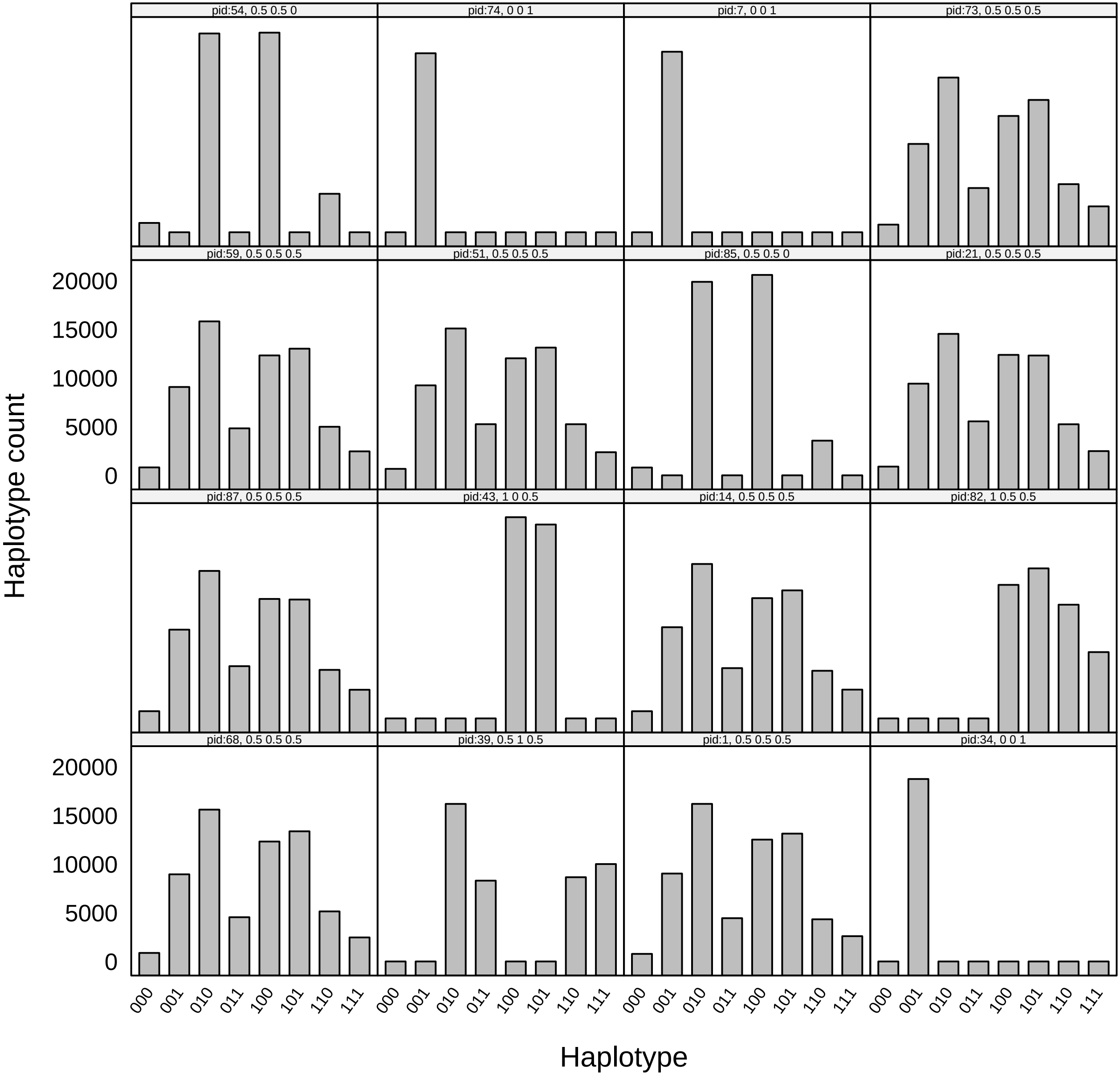
In addition to the thinning interval used to generate results, thinned by 10



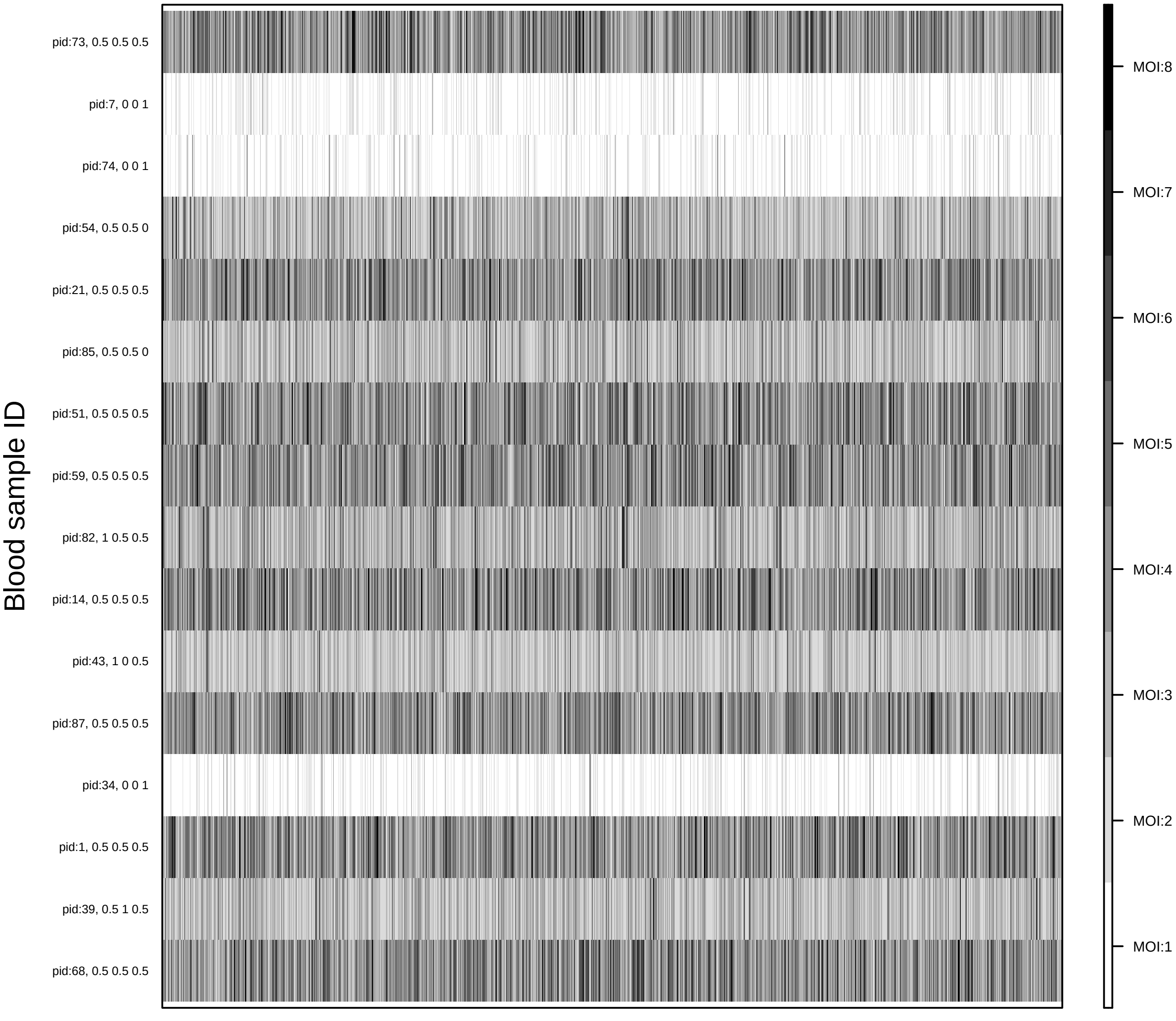
In addition to the thinning interval used to generate results, thinned by 10



Posterior for 16 random blood samples, additionally thinned by 100, post burnin

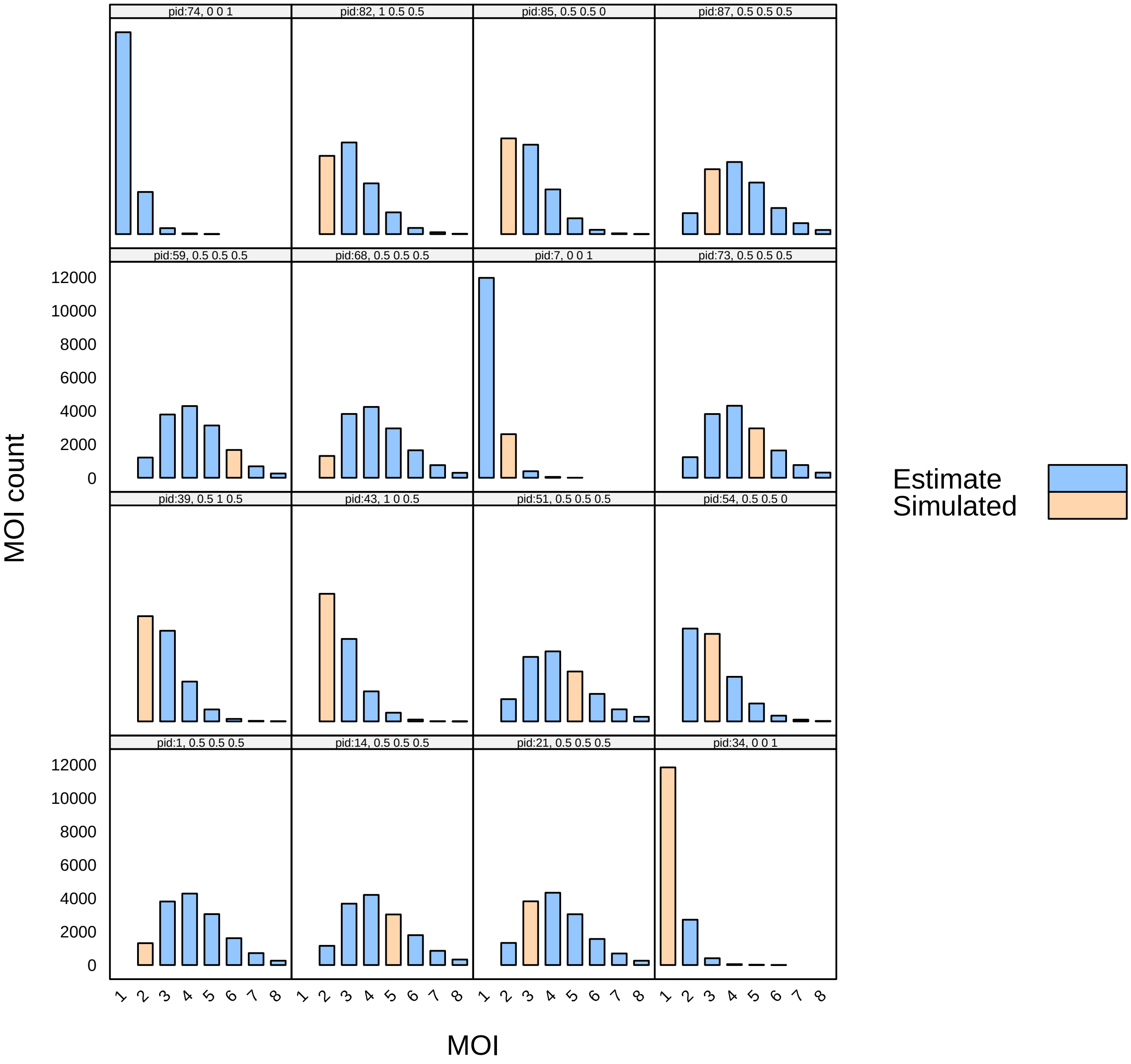


Haplotype barchart, 16 randomly selected blood samples, post burnin



Traces (burnin removed, chains collapsed, then further thinned (by 10))

MOI posterior, 16 blood samples, post burnin, additionally thinned by 10



MOI barchart, 16 blood samples, post burnin, chains combined