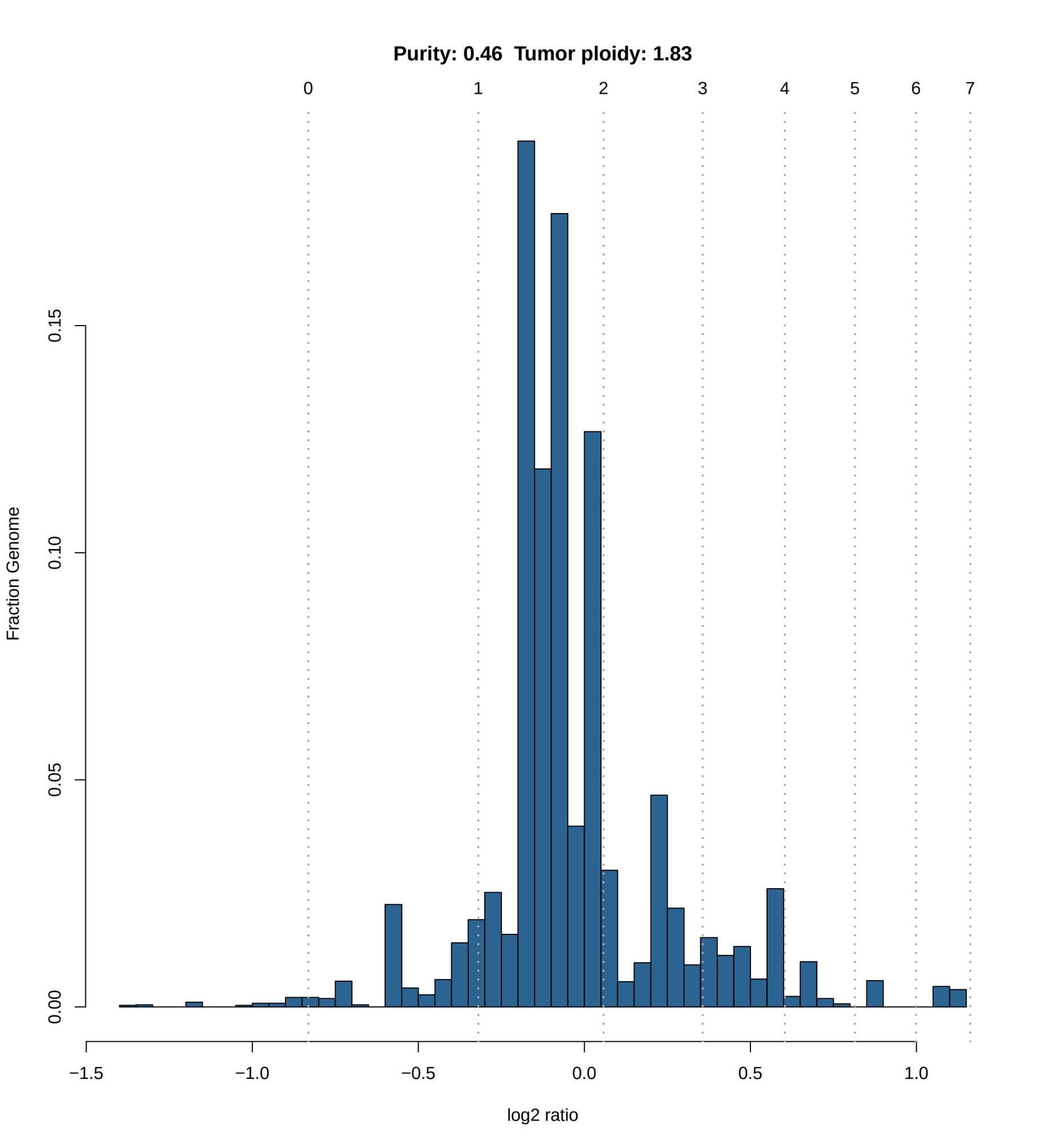
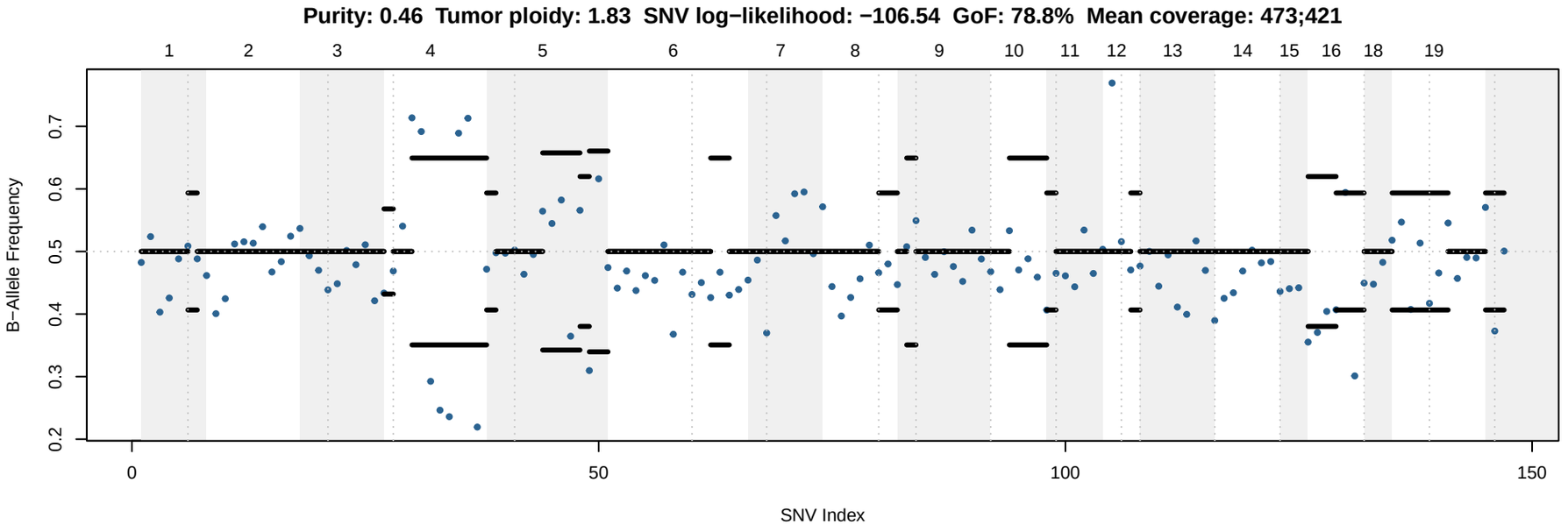
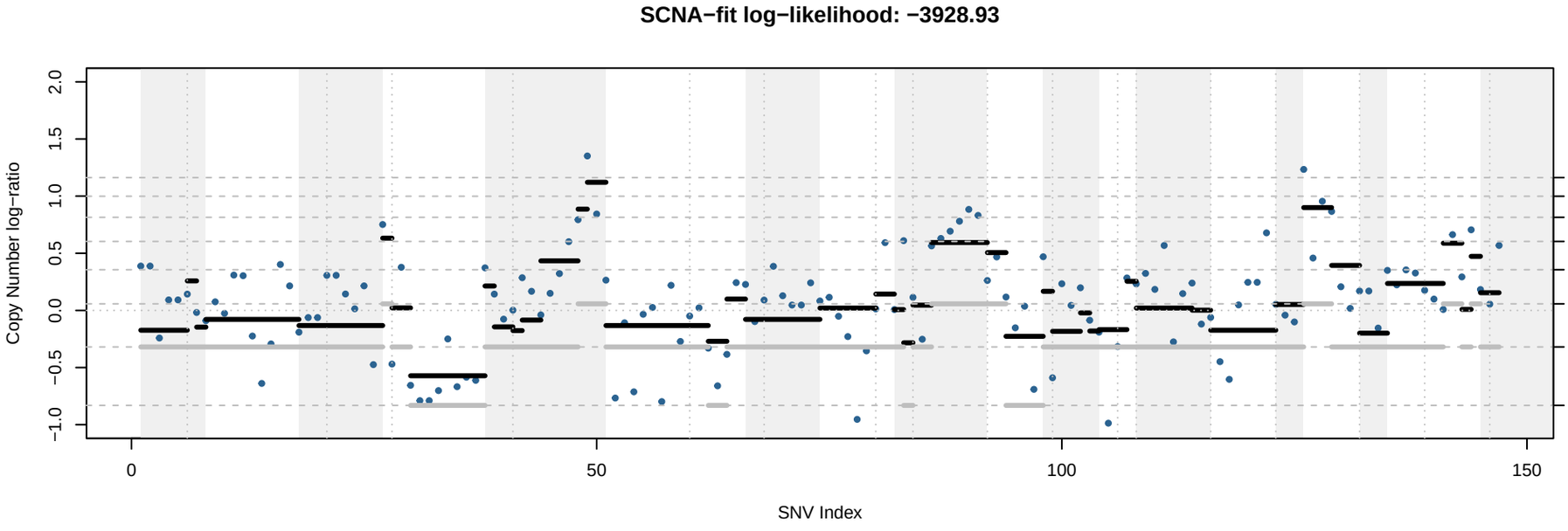
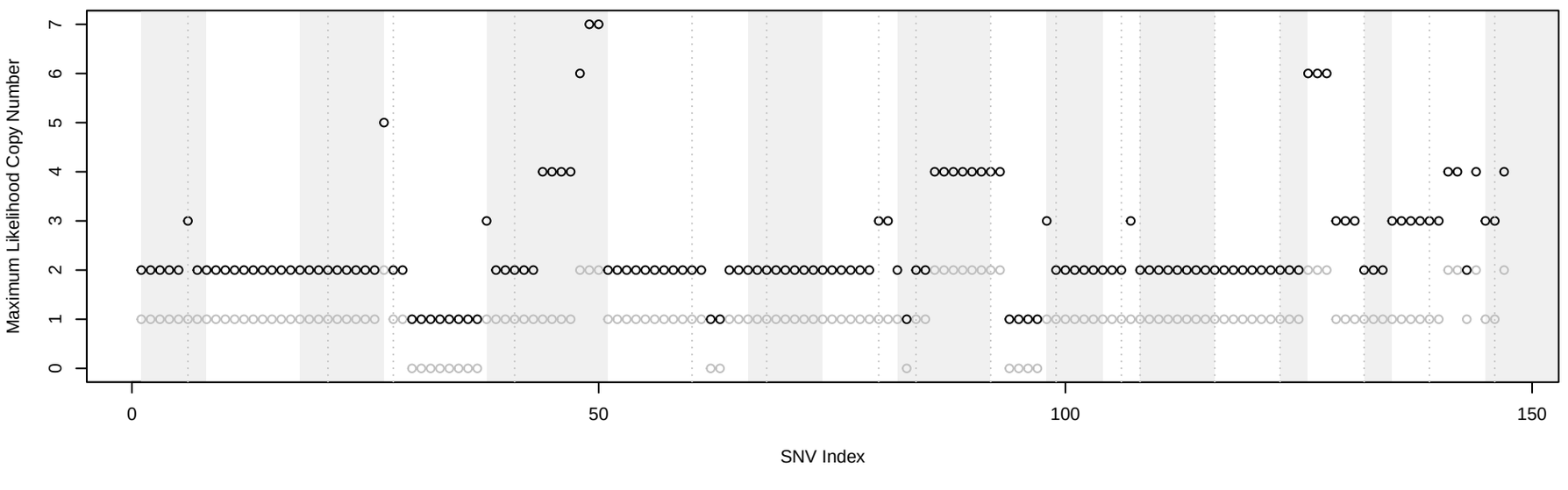
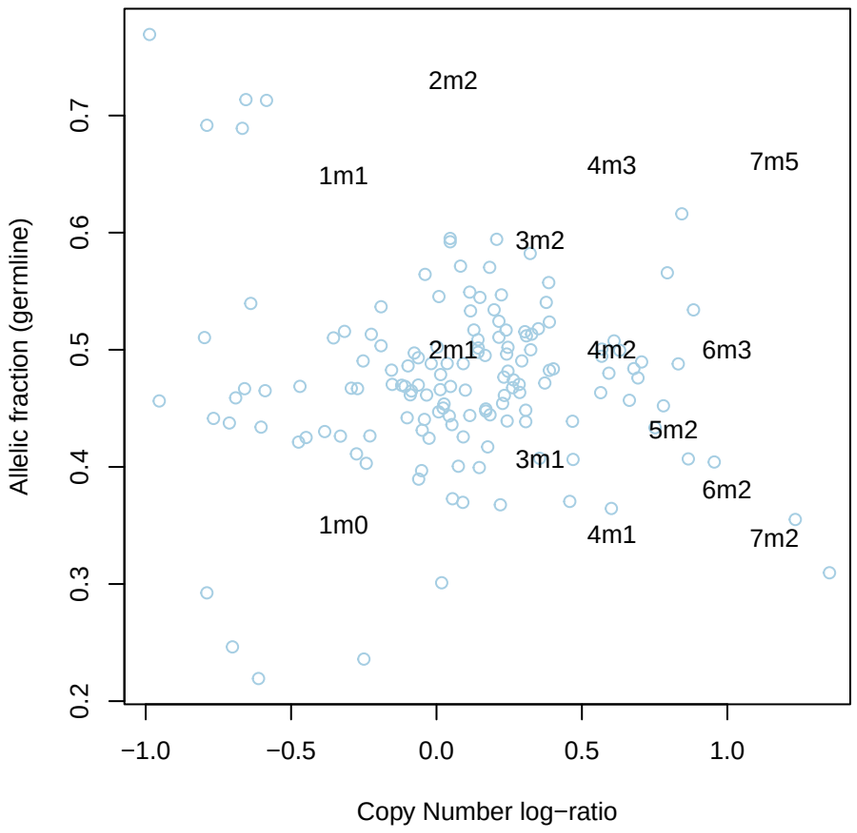
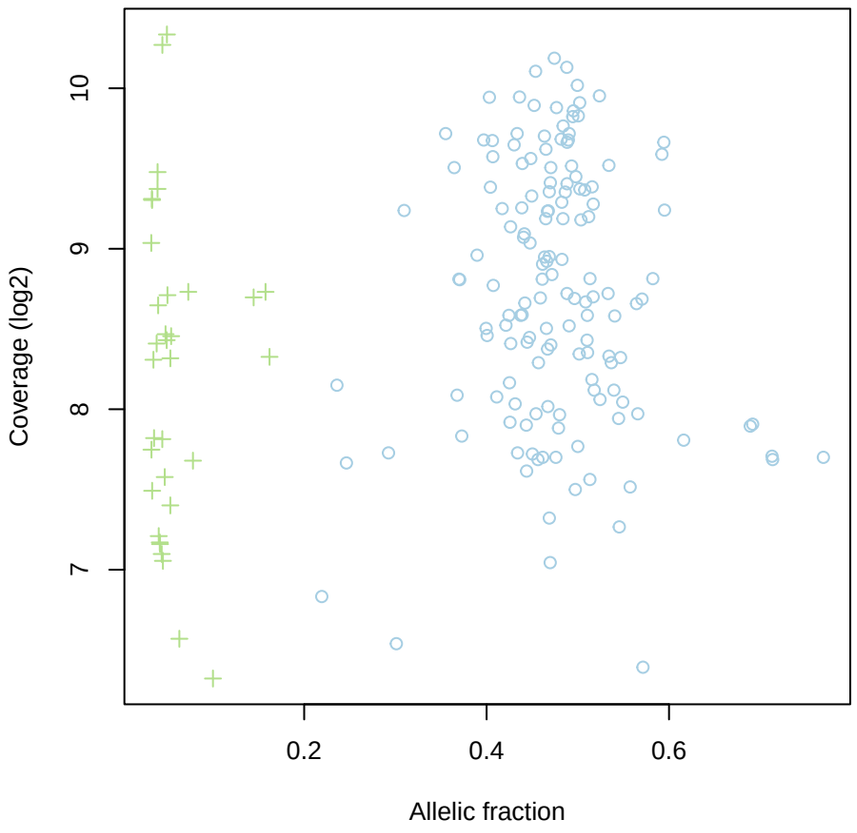

Purity: 0.46 Tumor ploidy: 1.83
0
1
2
3
4
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

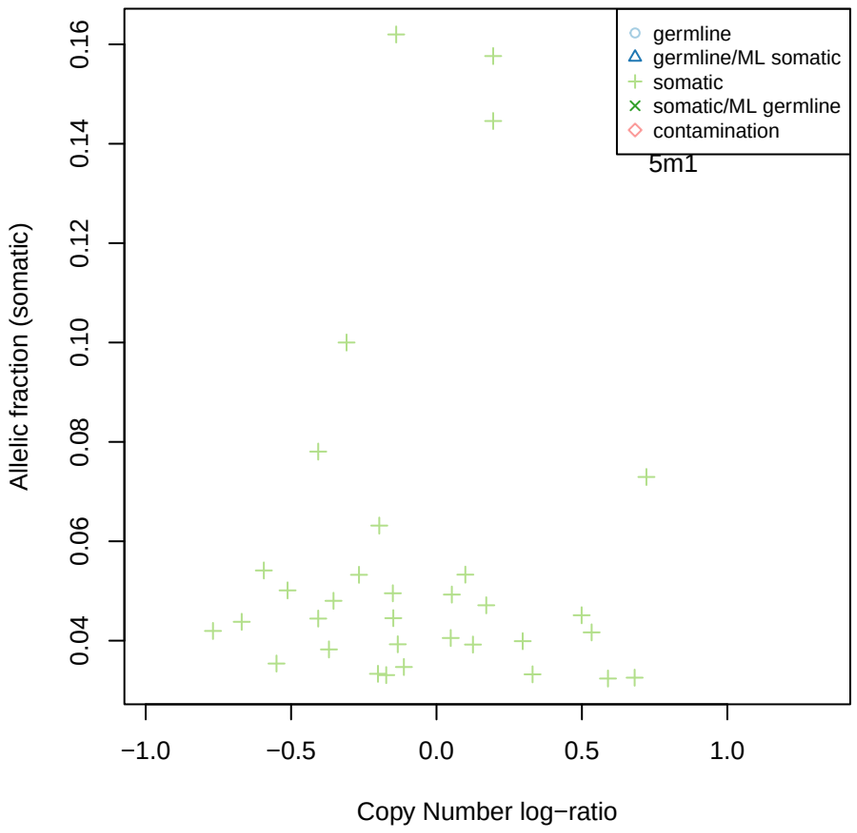

Purity: 0.46 Tumor ploidy: 1.83 SNV log−likelihood: −106.54 GoF: 78.8% Mean coverage: 473;421
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

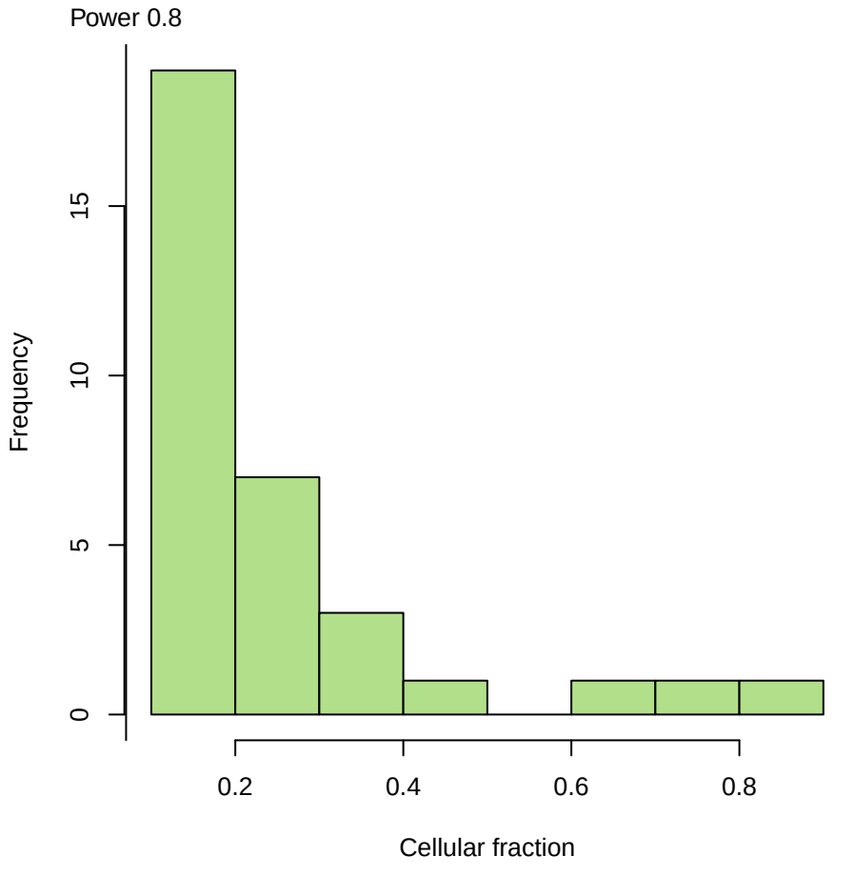

SCNA−fit log−likelihood: −3928.93
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
0 1 2 3 4 6
0 50 100 150
SNV Index

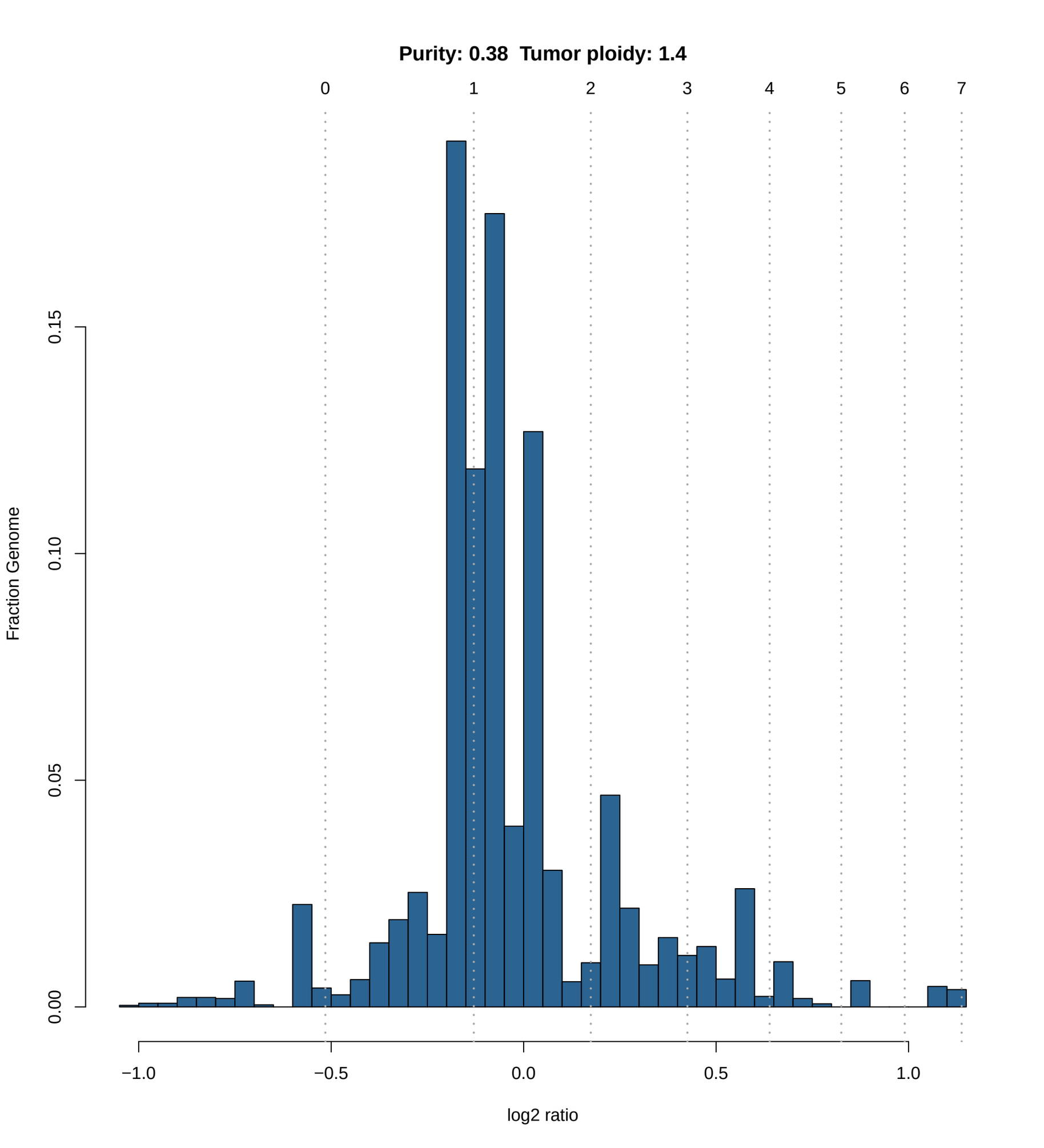

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

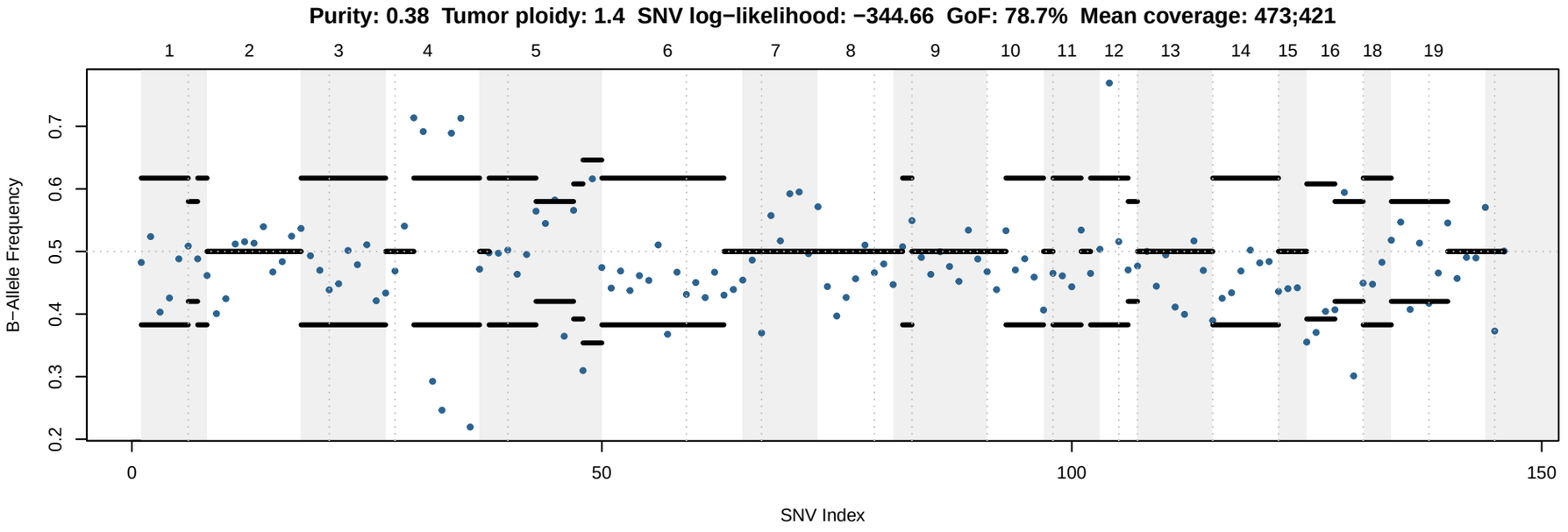

Allelic fraction (germline)
Copy Number log−ratio
2m2
1m1
4m3
7m5
3m2
2m1
4m2
6m3
5m2
3m1
6m2
1m0
4m1
7m2

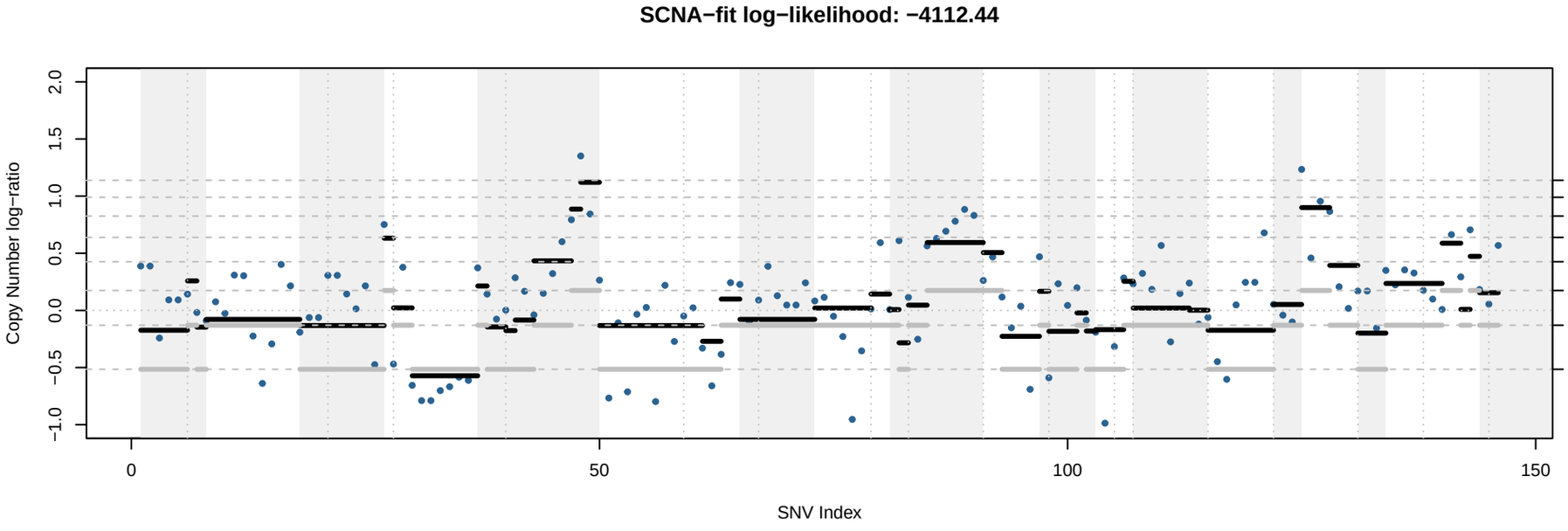

Coverage (log2)
Allelic fraction

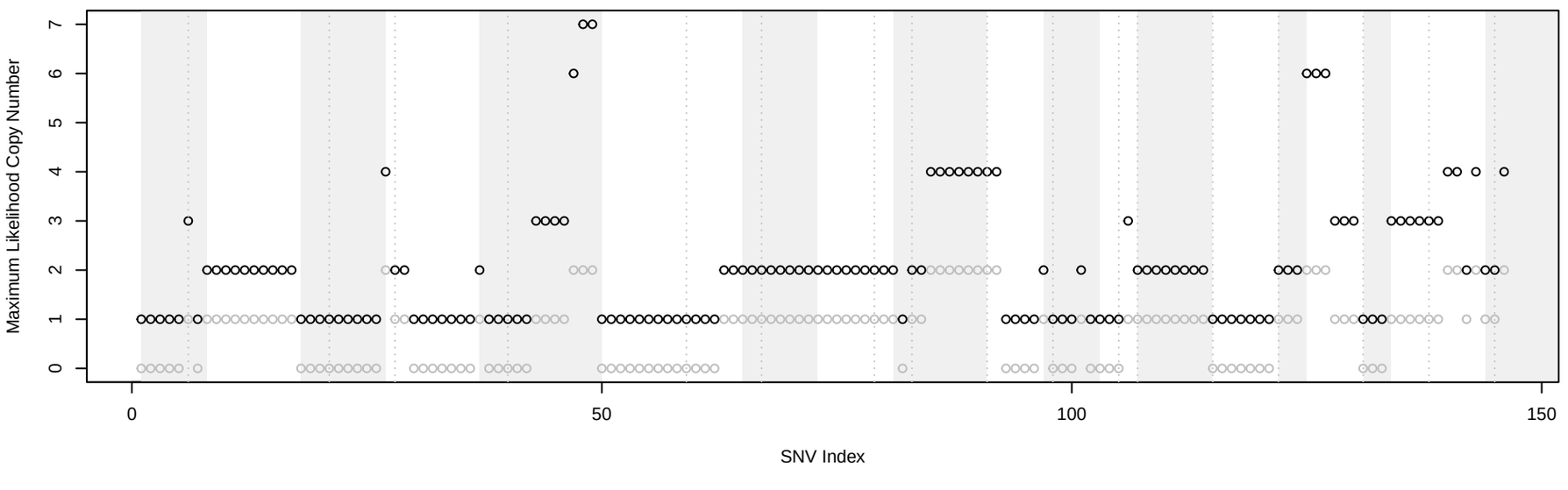

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
Allelic fraction (somatic)
Copy Number log−ratio

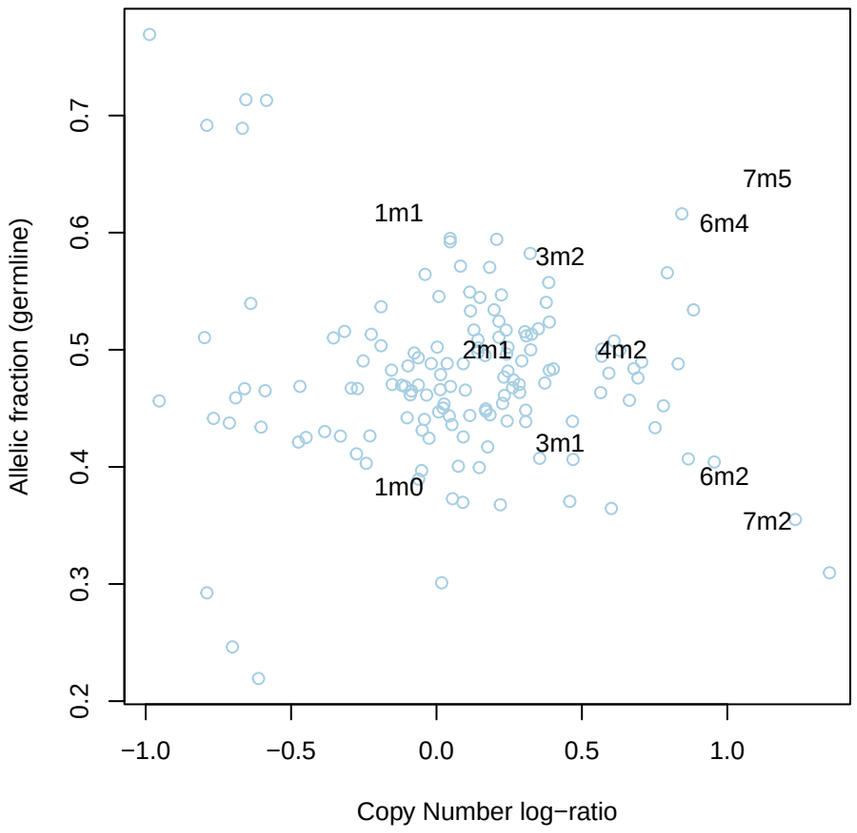

Power 0.8
Frequency
Cellular fraction

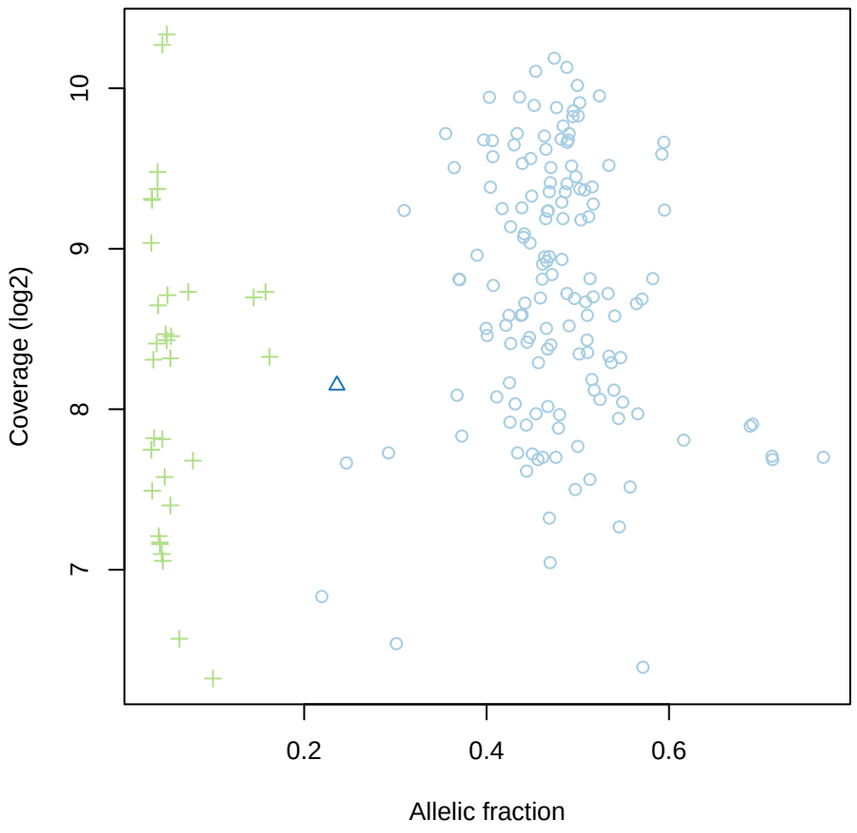

Purity: 0.38 Tumor ploidy: 1.4
0
1
2
3
4
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

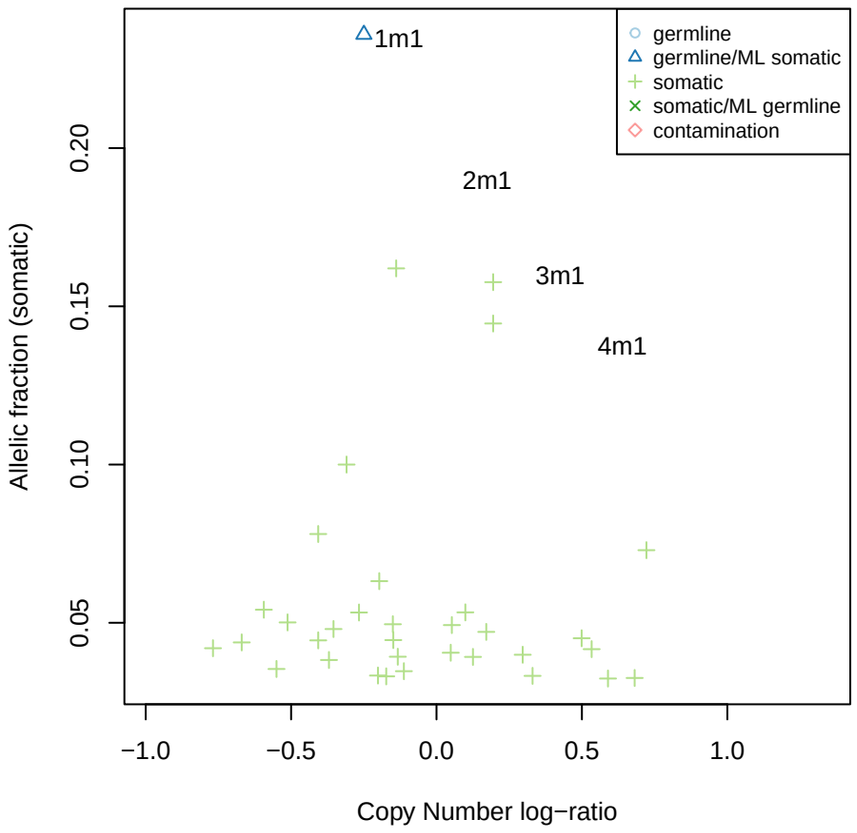

Purity: 0.38 Tumor ploidy: 1.4 SNV log−likelihood: −344.66 GoF: 78.7% Mean coverage: 473;421
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

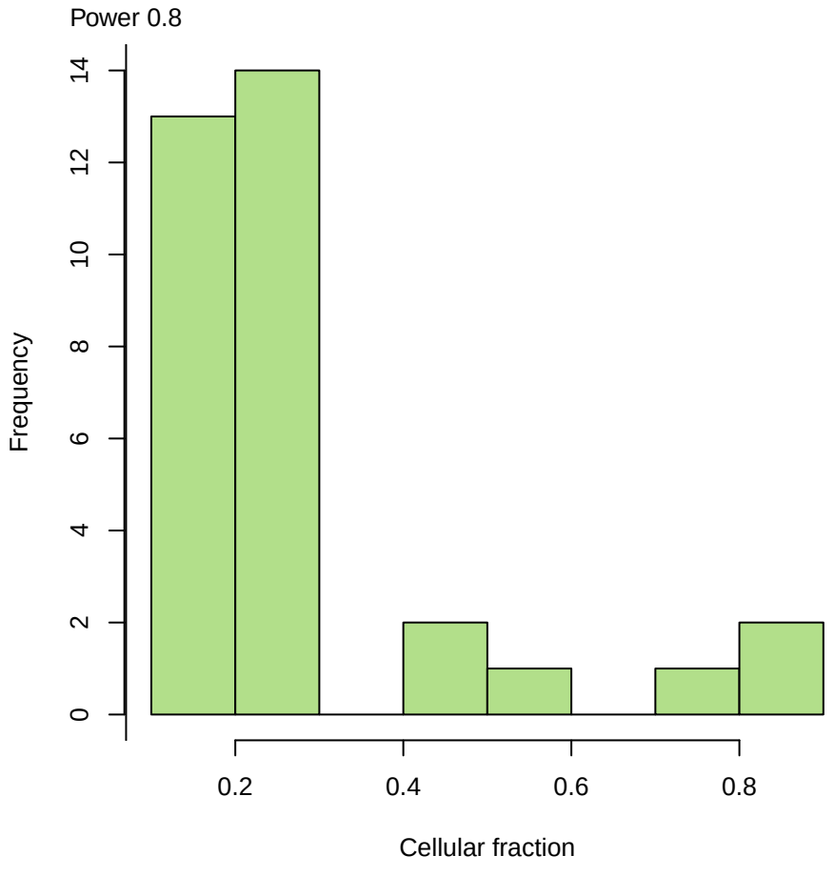

SCNA−fit log−likelihood: −4112.44
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
0 1 2 3 5 7
0 50 100 150
SNV Index


Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index


Allelic fraction (germline)
Copy Number log−ratio
1m1
7m5
6m4
3m2
2m1
4m2
3m1
1m0
6m2
7m2


Coverage (log2)
Allelic fraction


Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
4m1


Power 0.8
Frequency
Cellular fraction