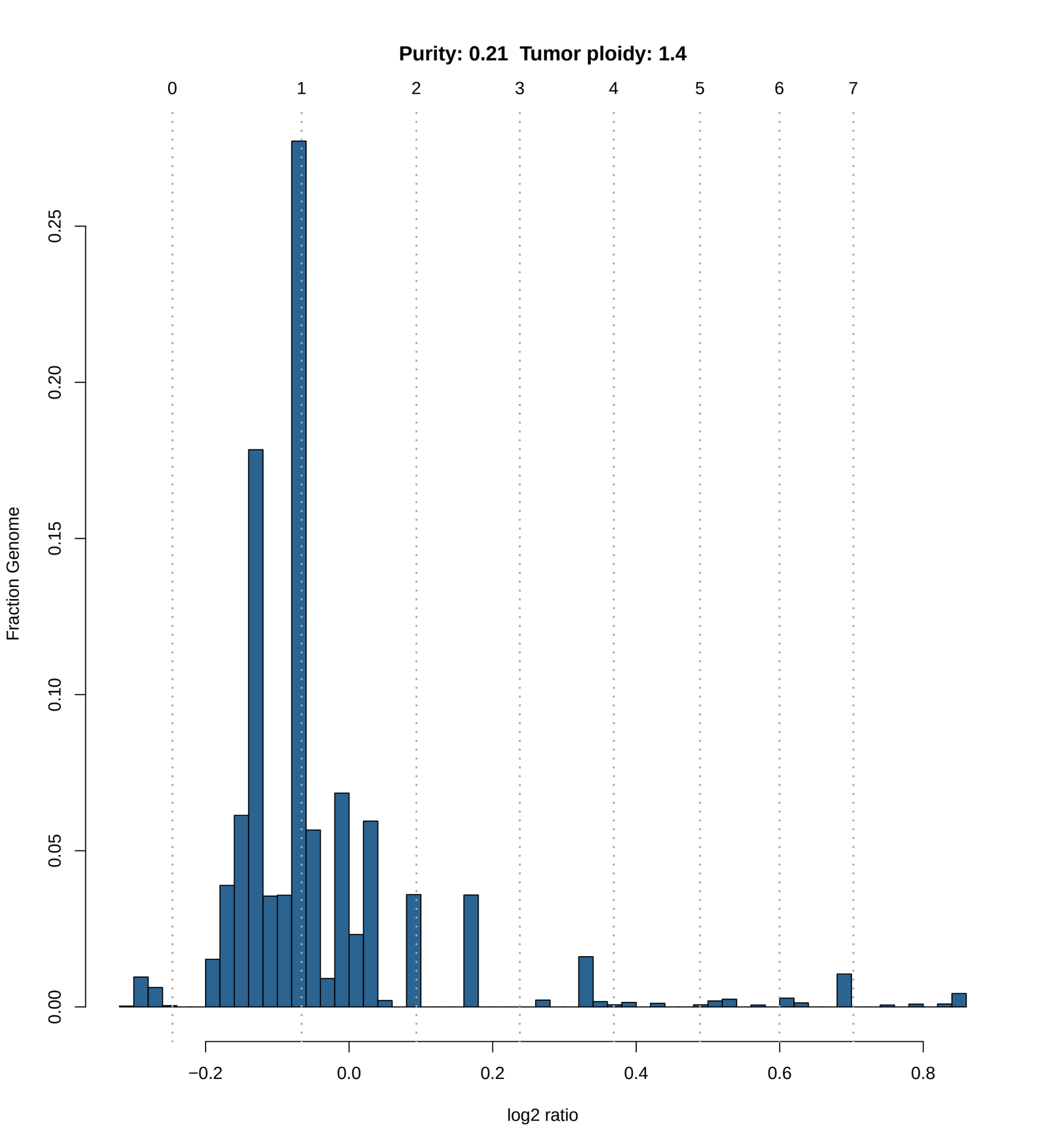
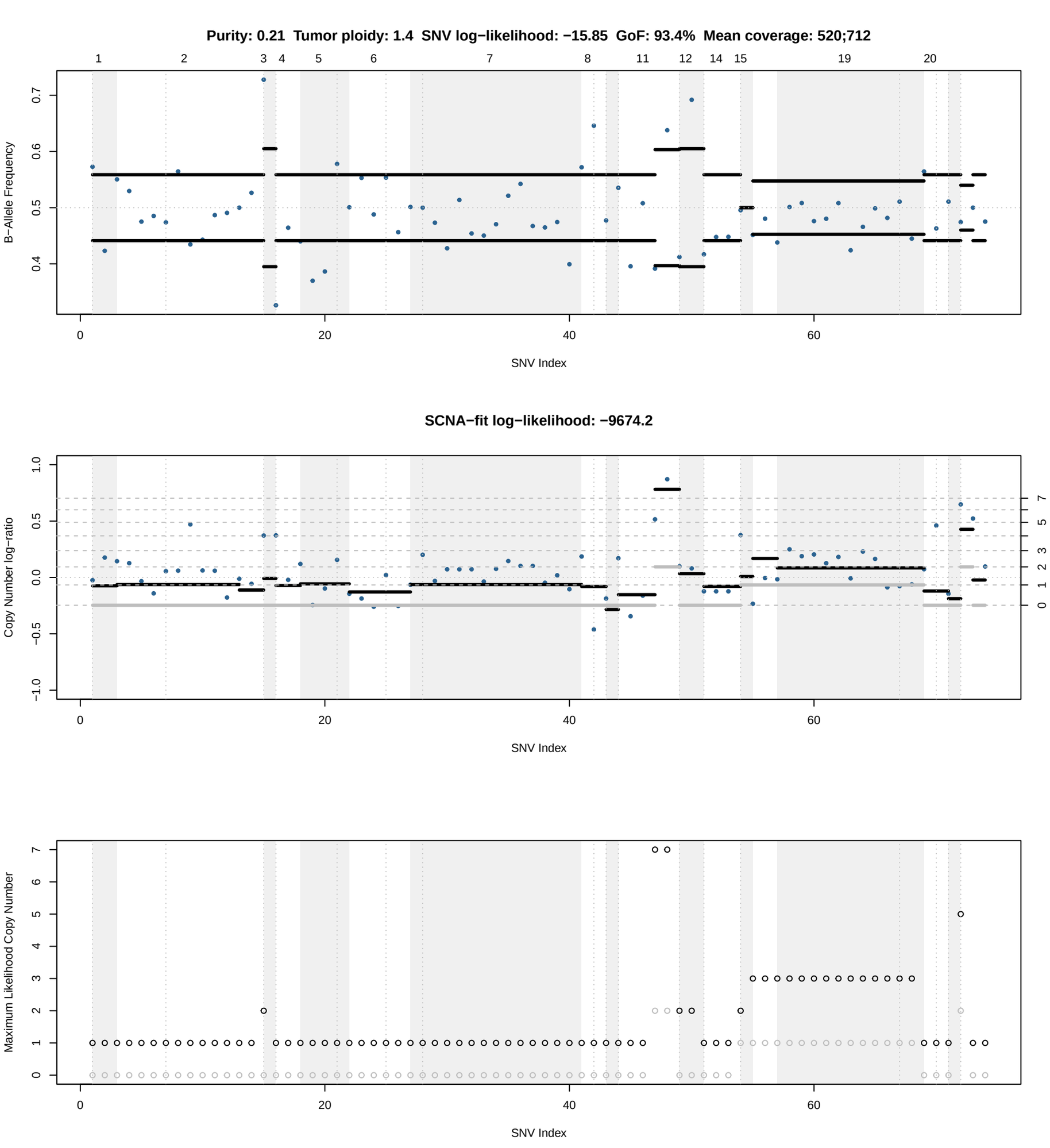
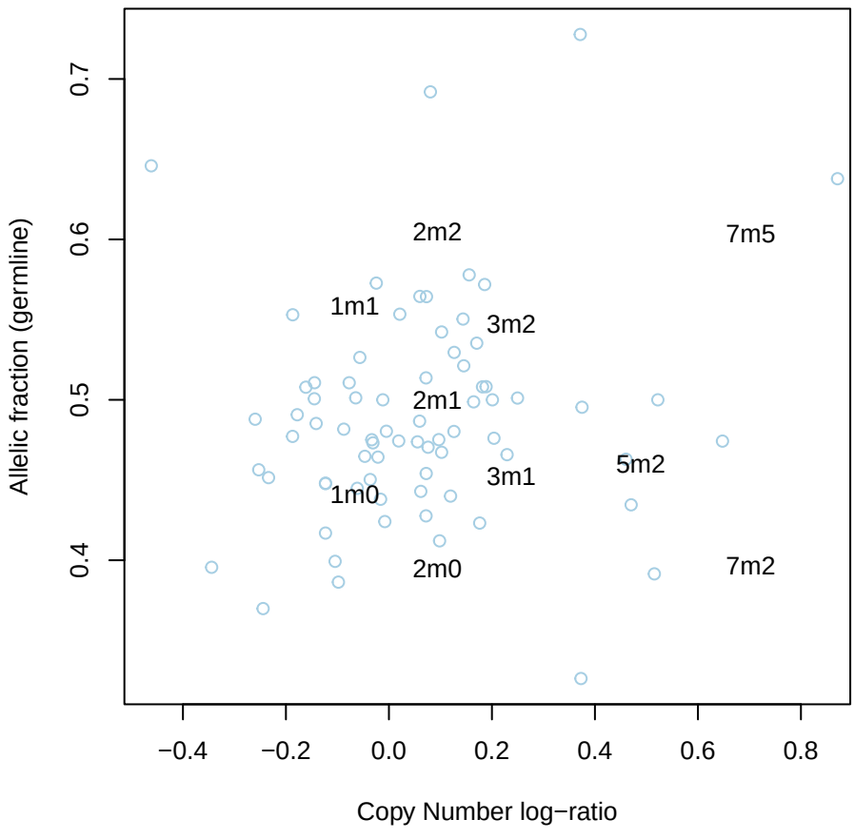
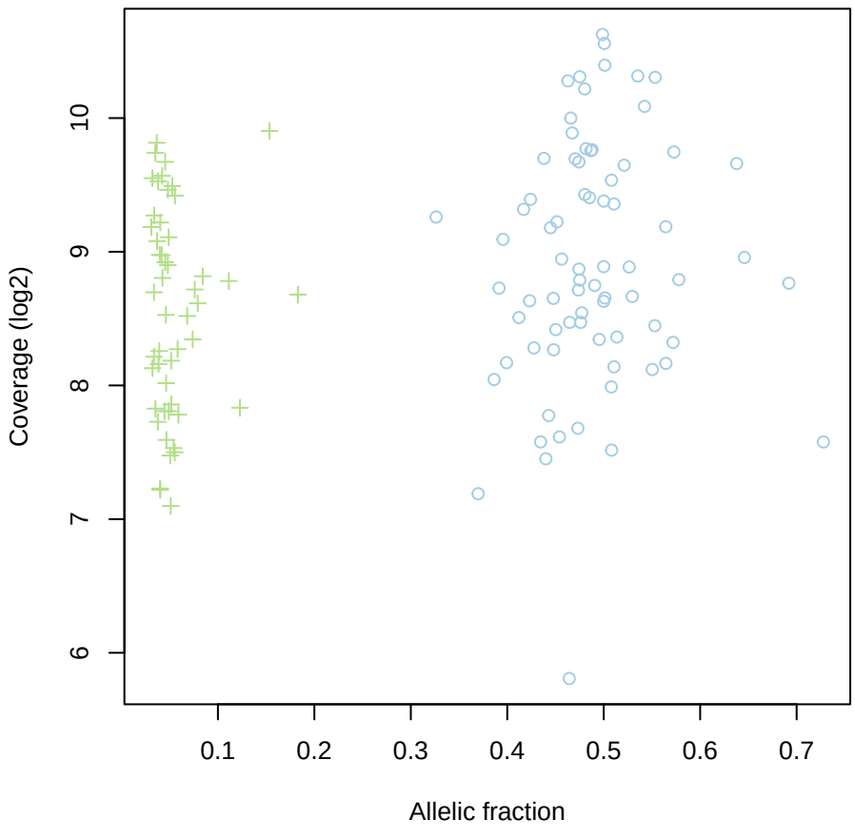
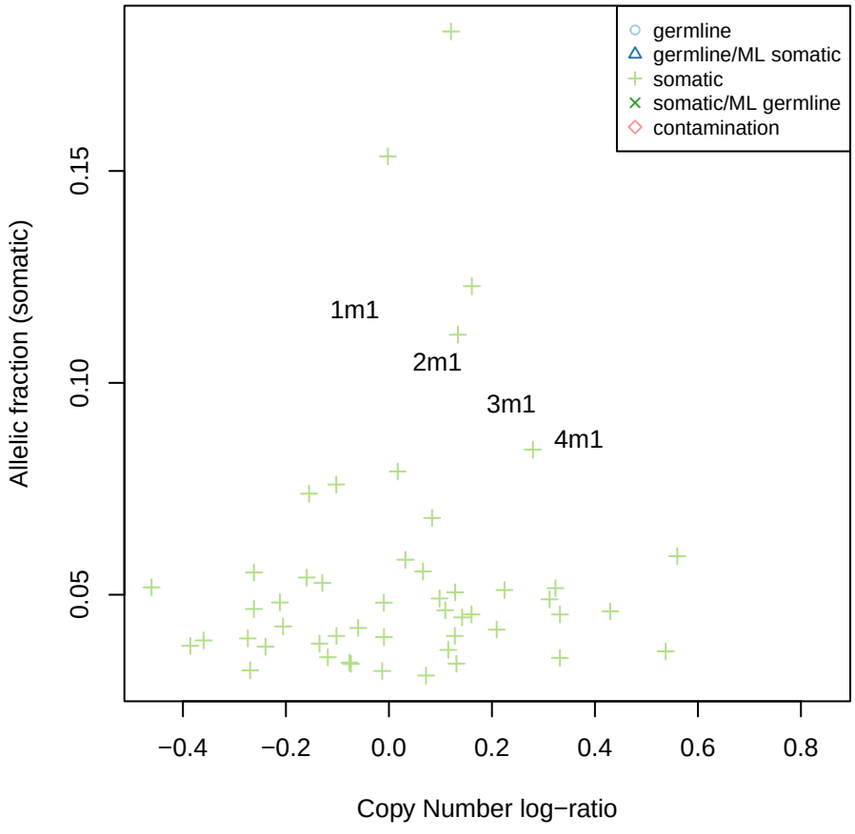
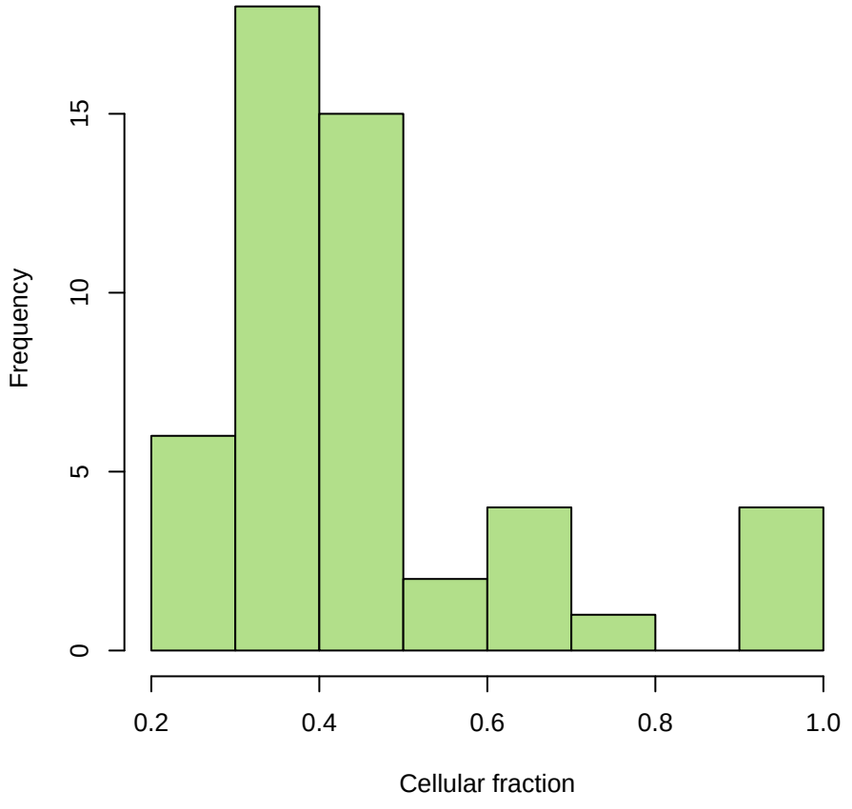

Purity: 0.21 Tumor ploidy: 1.4
0
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.2
0.0
0.2
0.4
0.6
0.8
log2 ratio

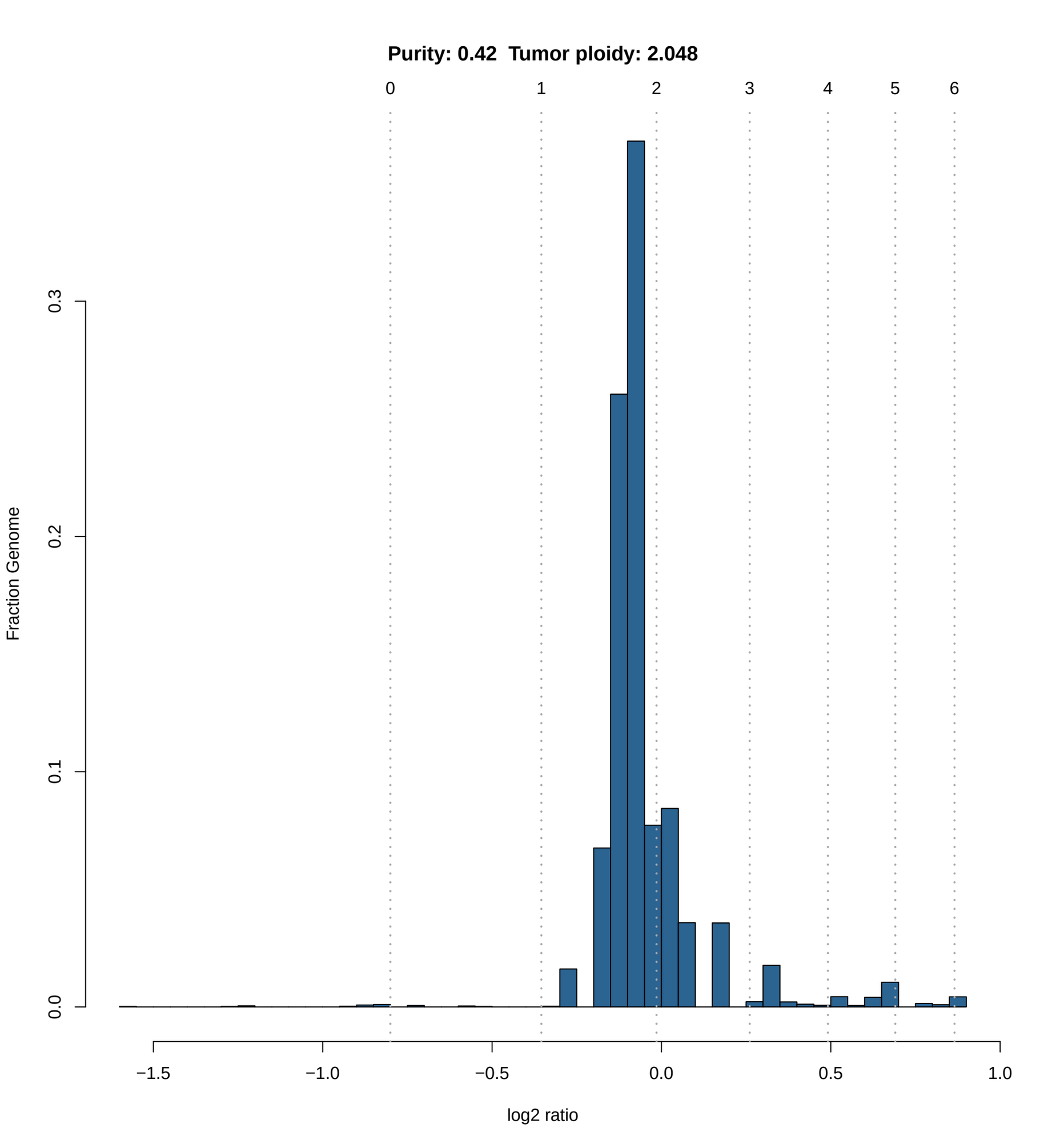

Purity: 0.21 Tumor ploidy: 1.4 SNV log−likelihood: −15.85 GoF: 93.4% Mean coverage: 520;712
1 2 3 4 5 6 7 8 11 12 14 15 19 20
B−Allele Frequency
0.4 0.5 0.6 0.7
0 20 40 60
SNV Index
SCNA−fit log−likelihood: −9674.2
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 5 7
0 20 40 60
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60
SNV Index

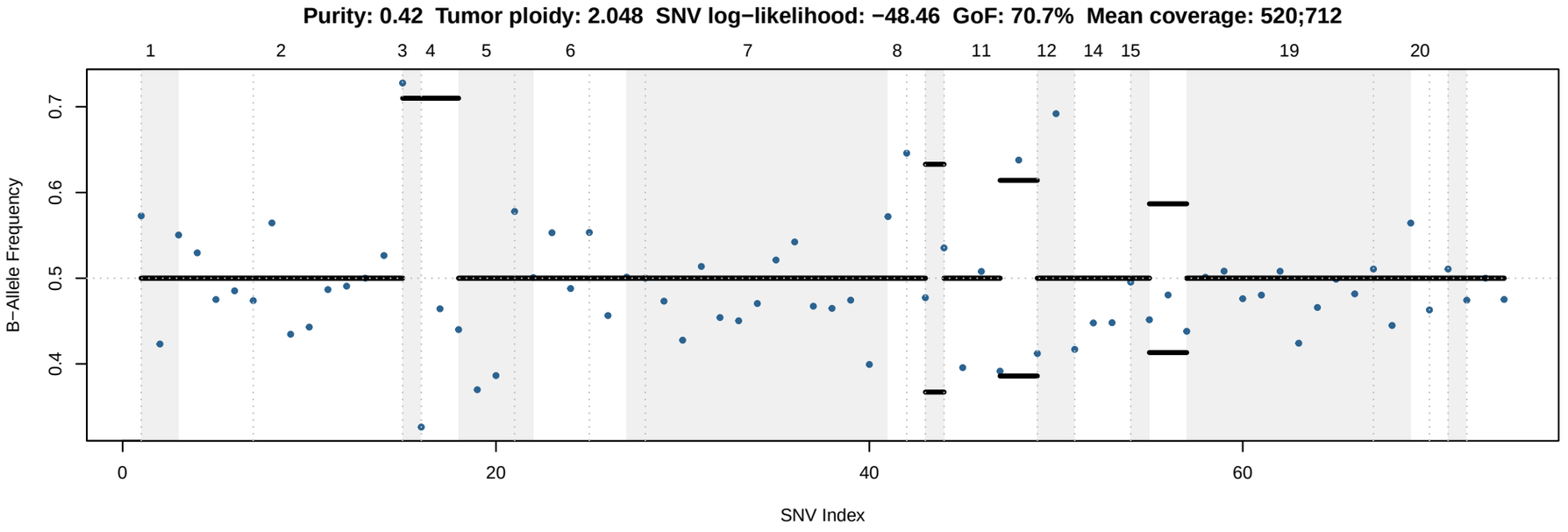

Allelic fraction (germline)
Copy Number log−ratio
2m2
7m5
1m1
3m2
2m1
5m2
3m1
1m0
2m0
7m2

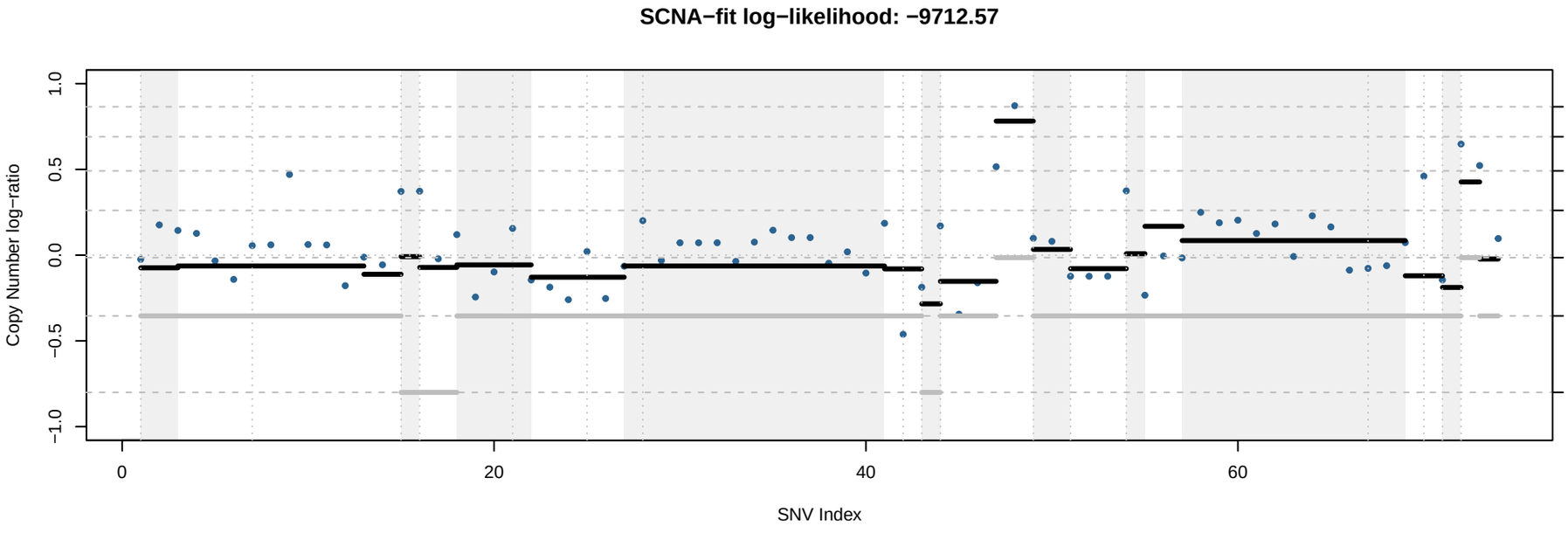

Coverage (log2)
Allelic fraction

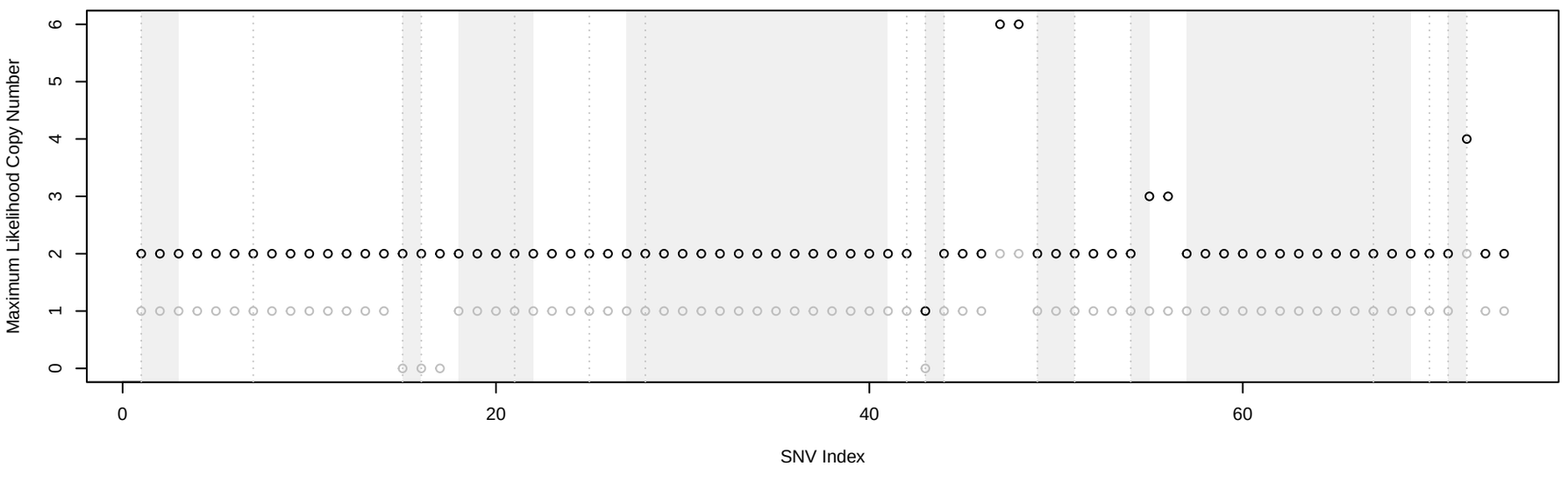

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1
3m1
4m1

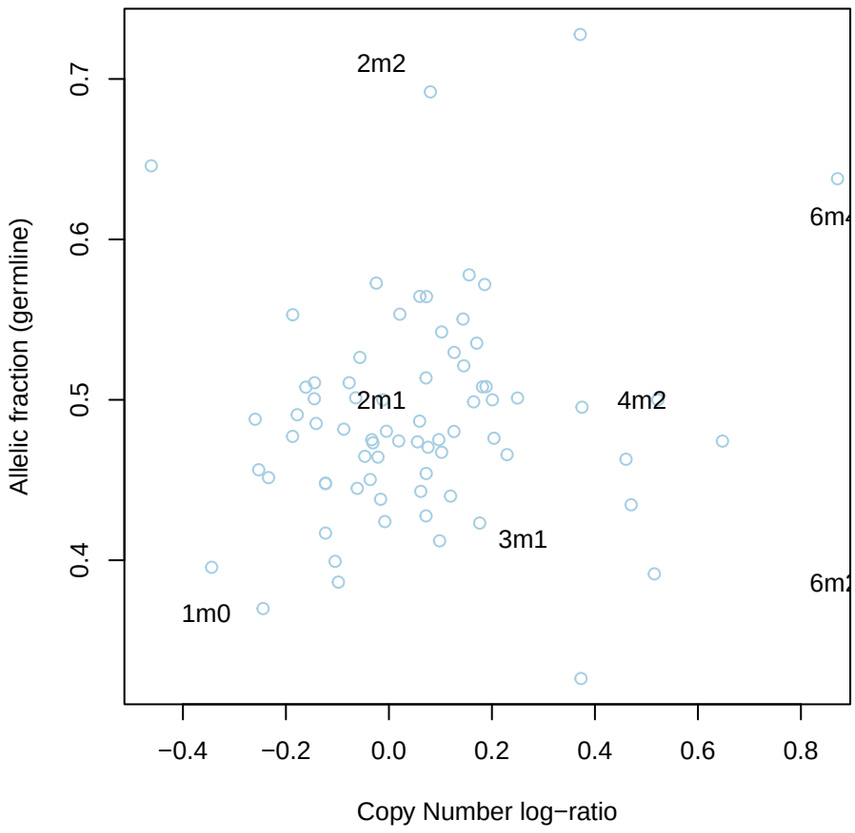

Frequency
Cellular fraction

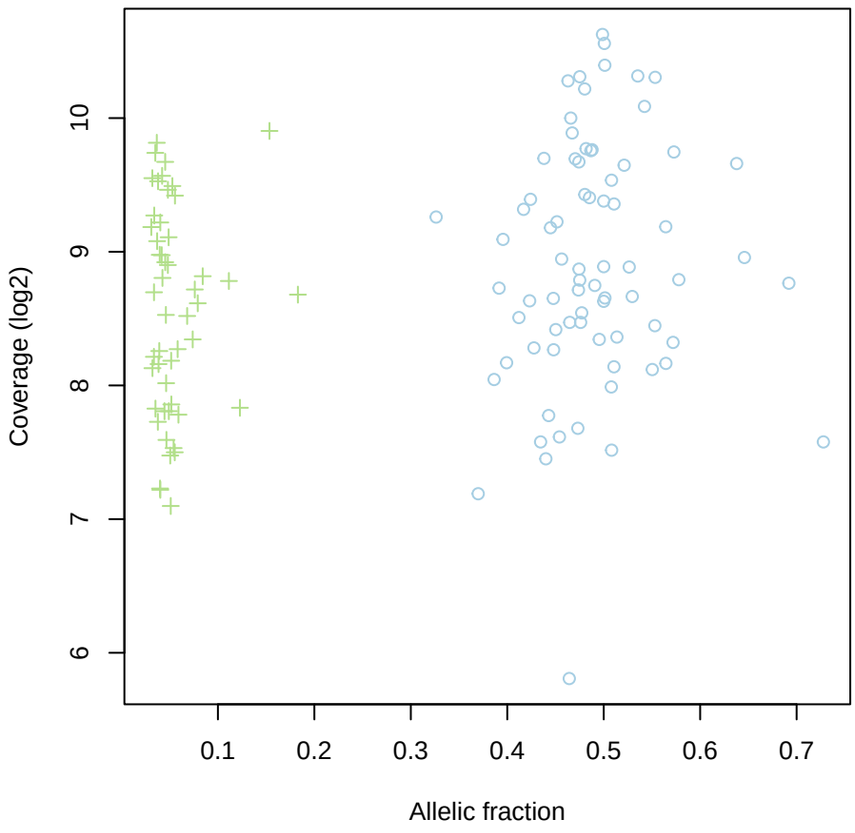

Purity: 0.42 Tumor ploidy: 2.048
0
1
2
3
4
5
6
0.3
0.2
0.1
0.0
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

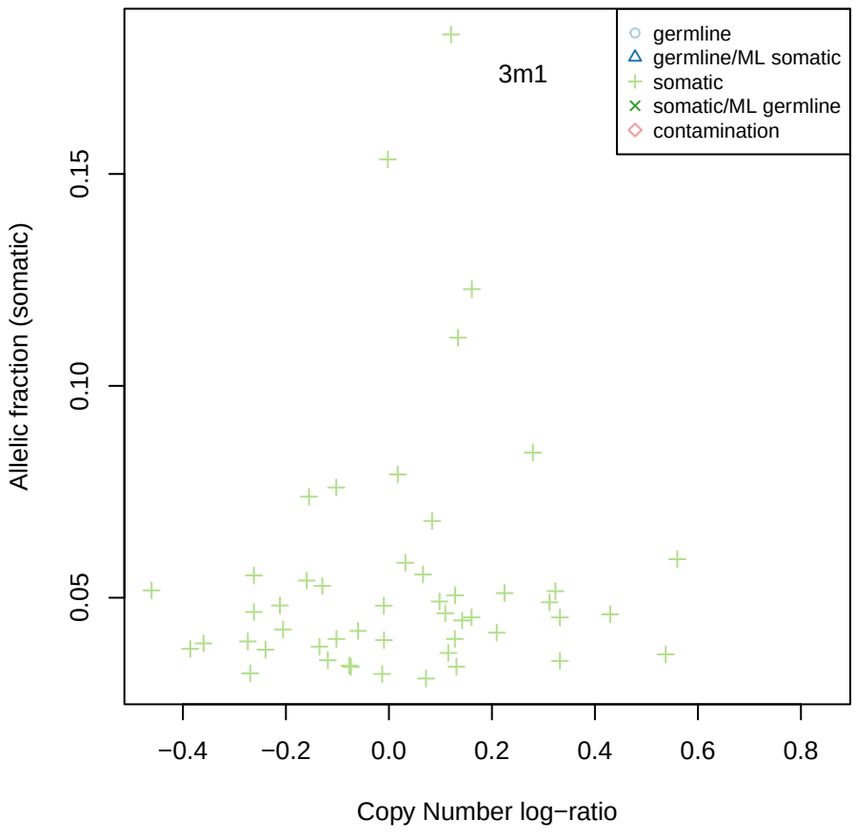

Purity: 0.42 Tumor ploidy: 2.048 SNV log−likelihood: −48.46 GoF: 70.7% Mean coverage: 520;712
1 2 3 4 5 6 7 8 11 12 14 15 19 20
B−Allele Frequency
0.4 0.5 0.6 0.7
0 20 40 60
SNV Index

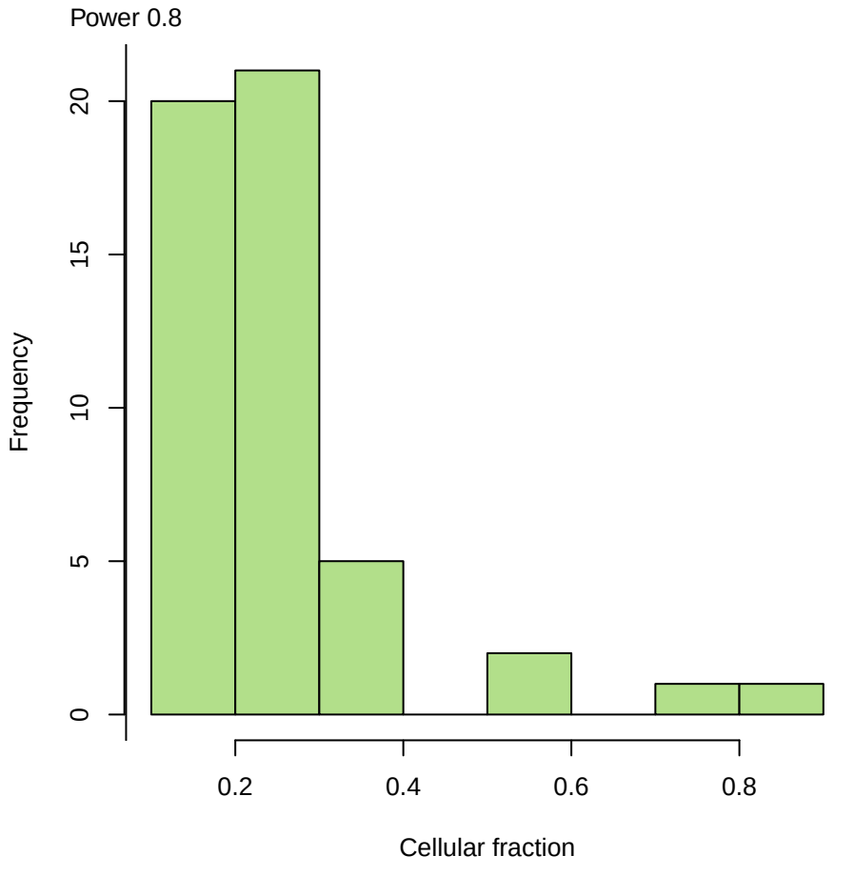

SCNA−fit log−likelihood: −9712.57
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 6
0 20 40 60
SNV Index

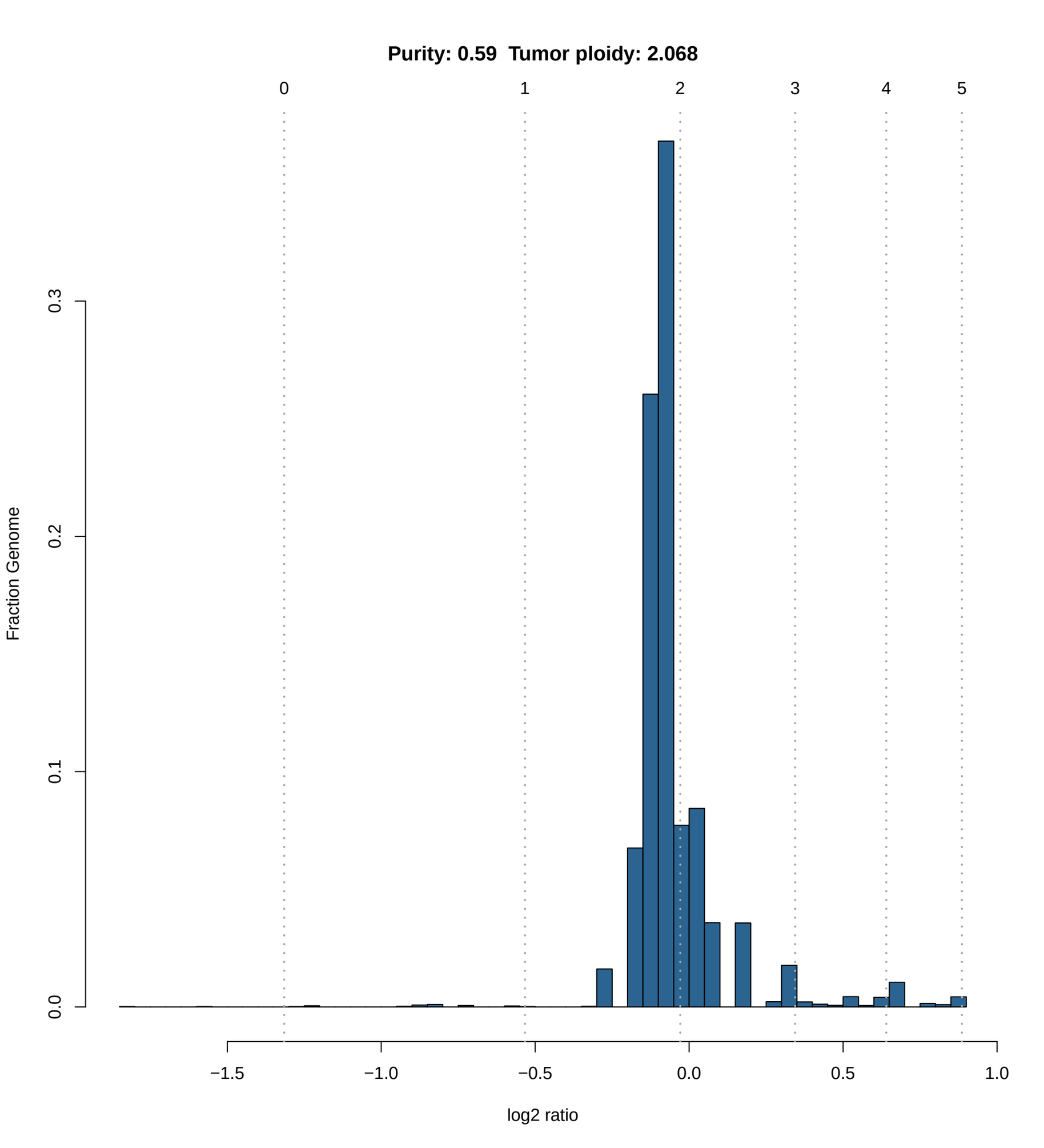

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60
SNV Index

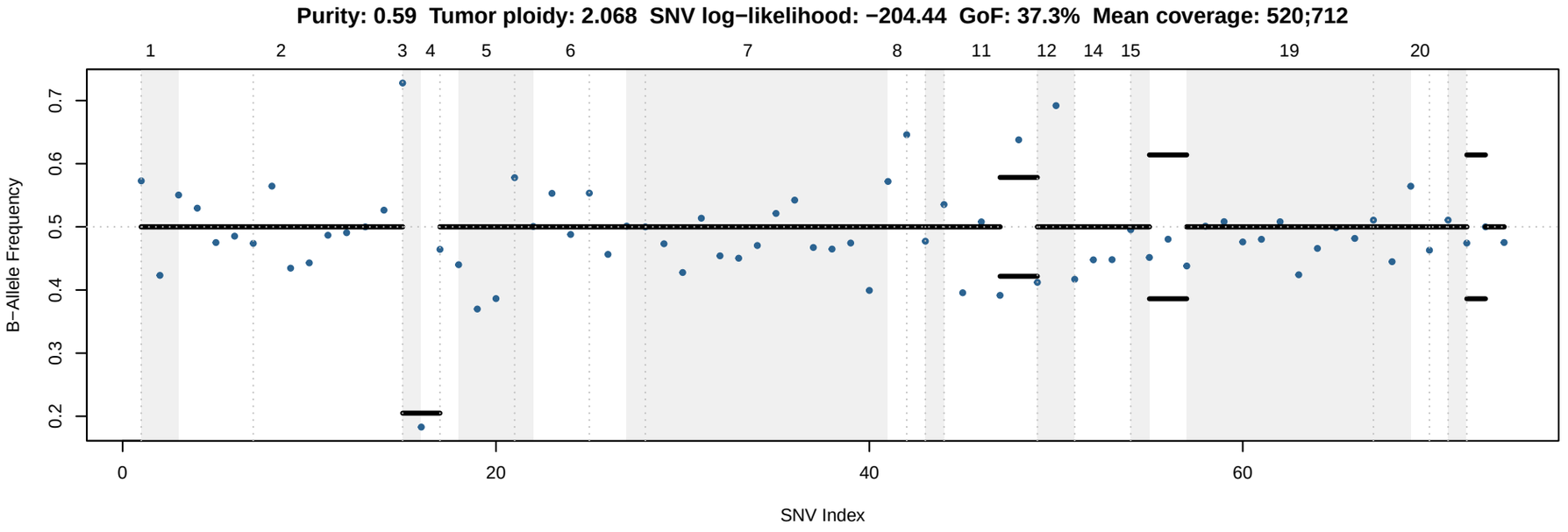

2m2
6m4
2m1
4m2
3m1
6m2
1m0
Allelic fraction (germline)
Copy Number log−ratio
0.4
0.5
0.6
0.7
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8

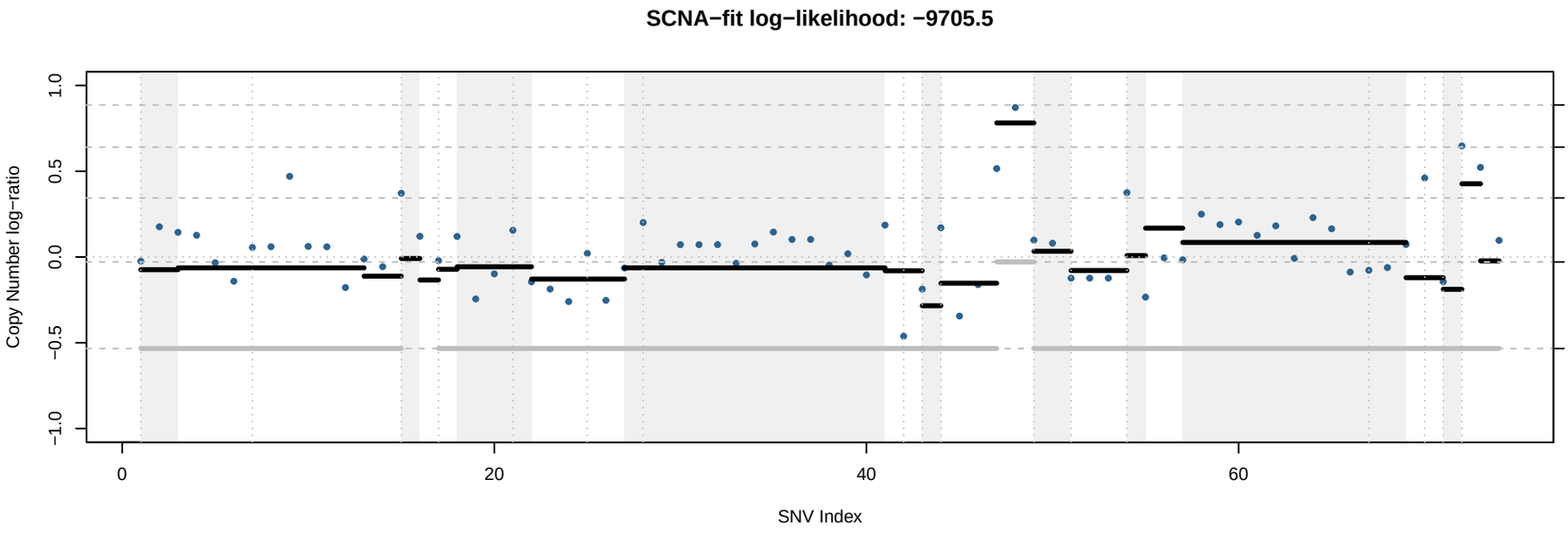

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7

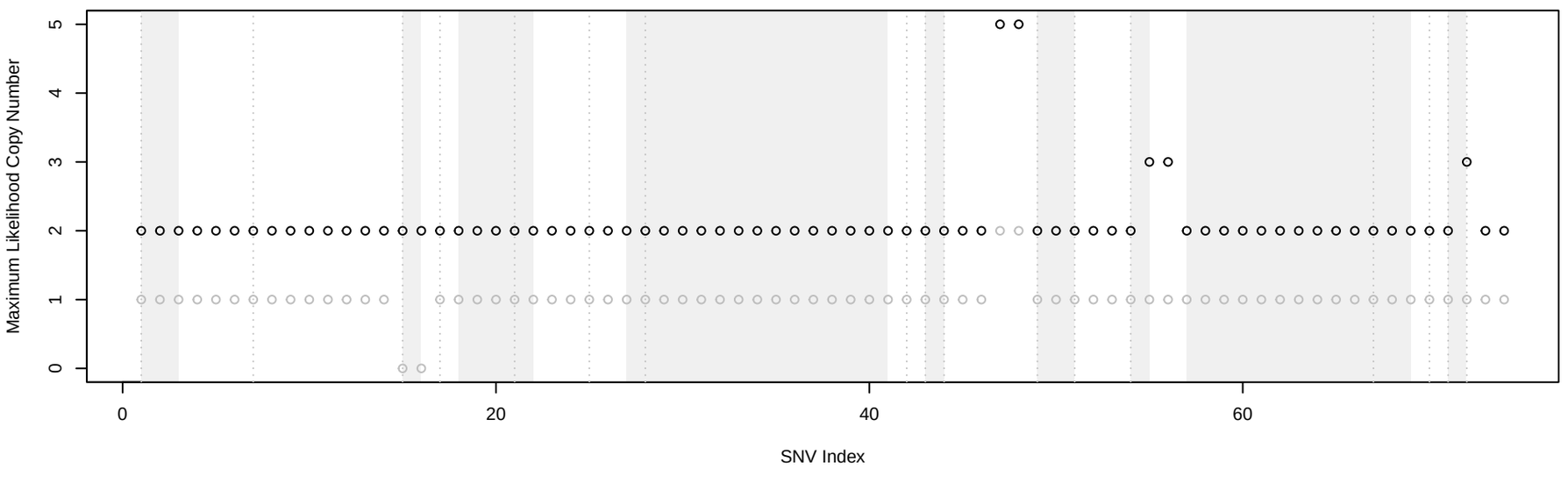

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8

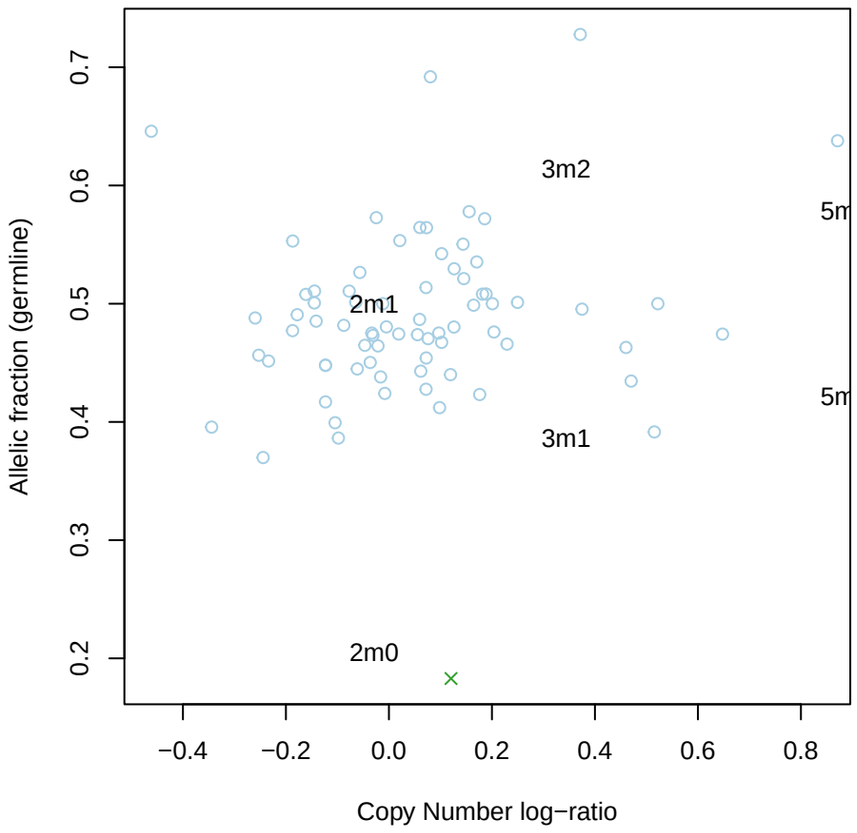

Power 0.8
Frequency
Cellular fraction
0
5
10
15
20
0.2
0.4
0.6
0.8

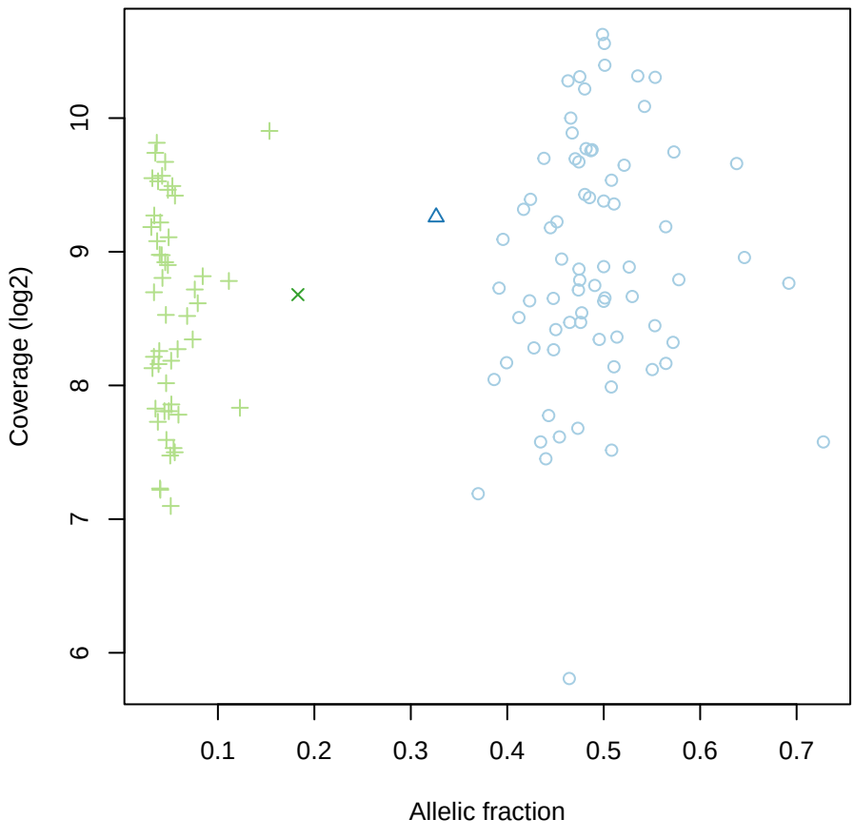

Purity: 0.59 Tumor ploidy: 2.068
0
1
2
3
4
5
0.3
0.2
0.1
0.0
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

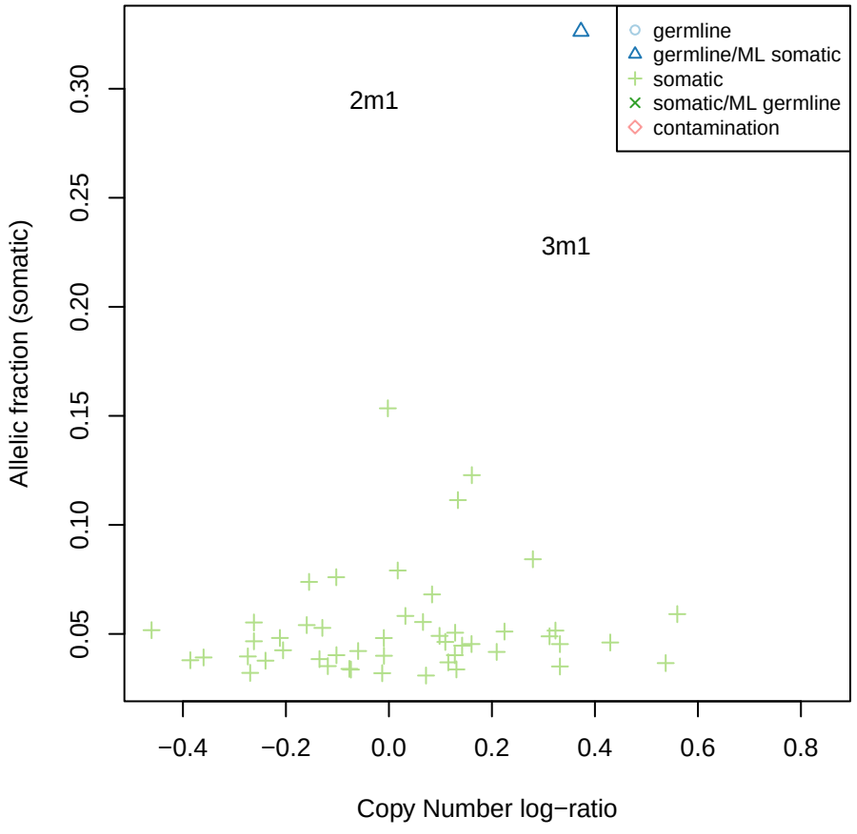

Purity: 0.59 Tumor ploidy: 2.068 SNV log−likelihood: −204.44 GoF: 37.3% Mean coverage: 520;712
1 2 3 4 5 6 7 8 11 12 14 15 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60
SNV Index

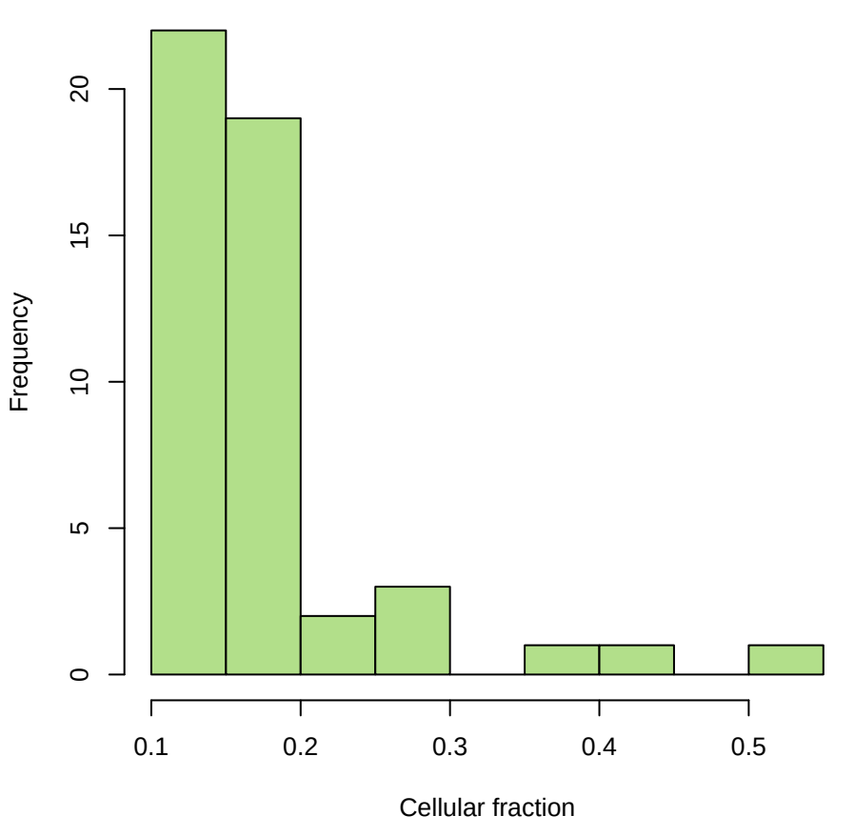

SCNA−fit log−likelihood: −9705.5
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5
0 20 40 60
SNV Index

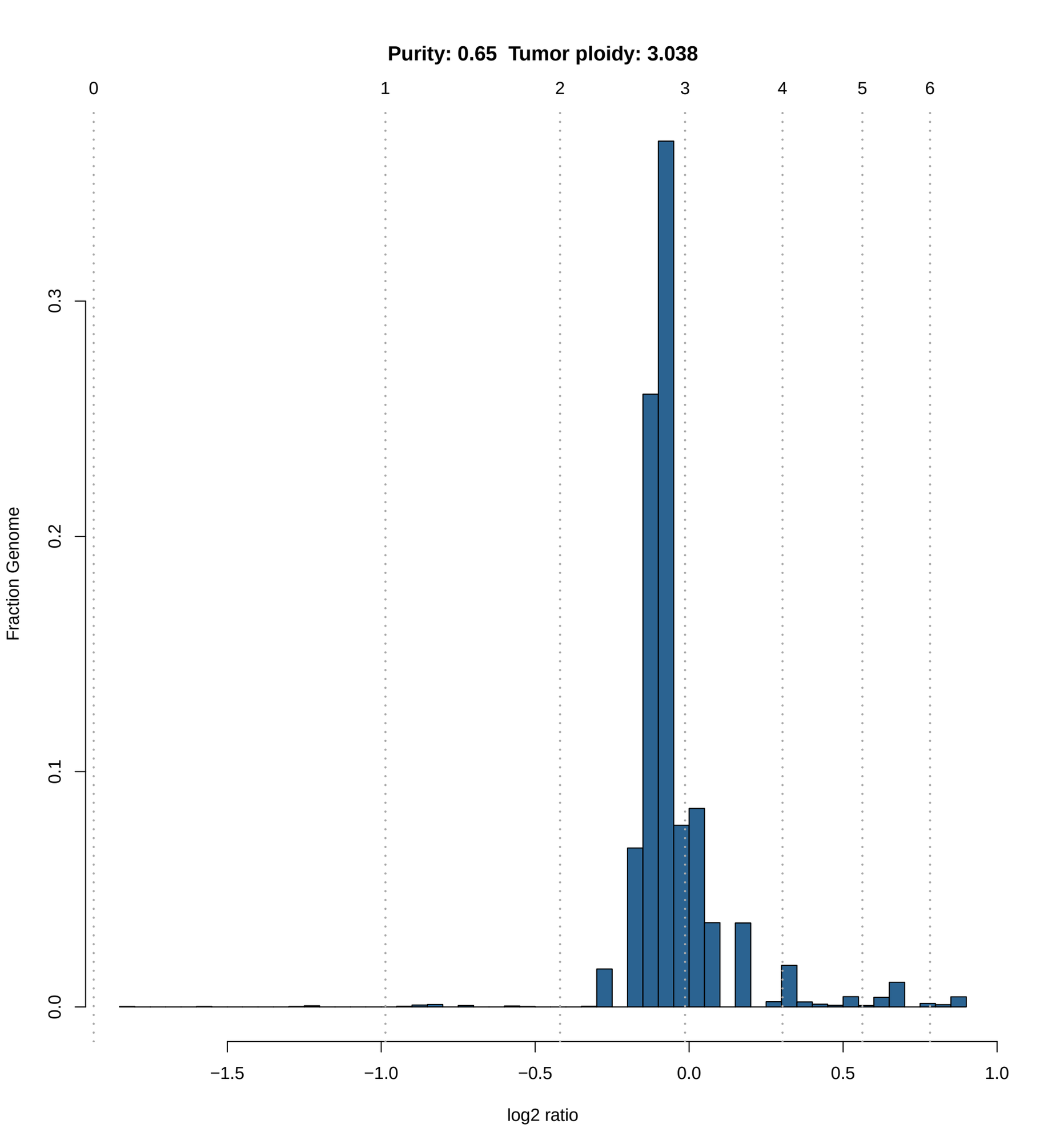

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60
SNV Index

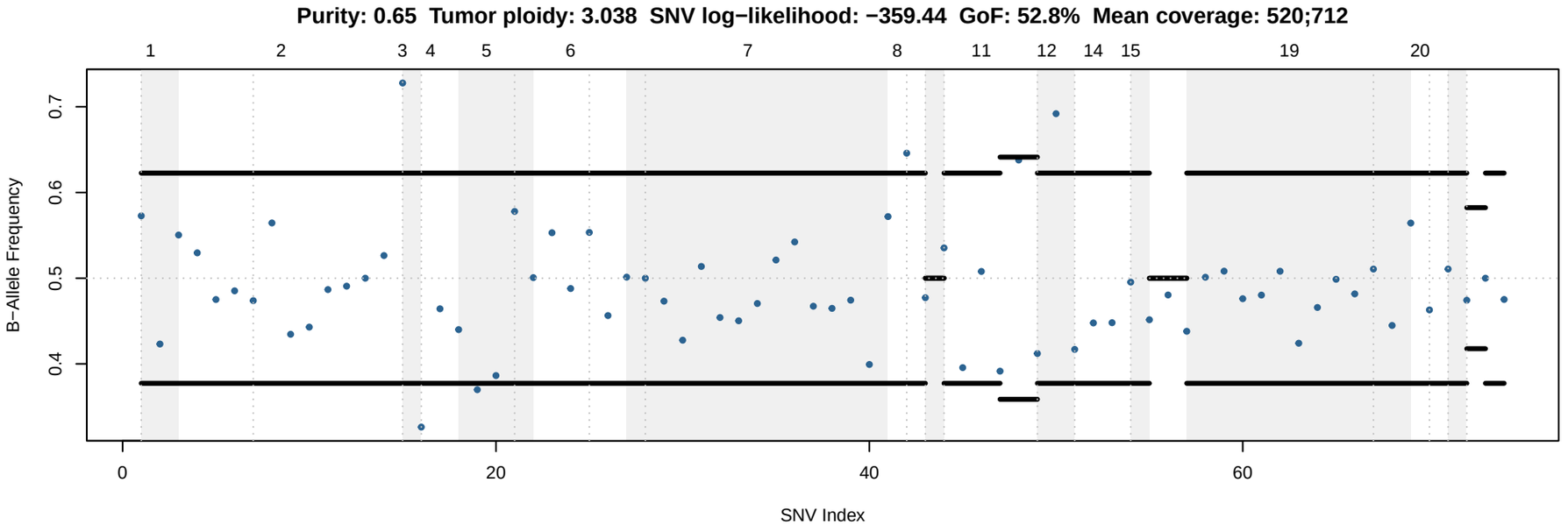

Allelic fraction (germline)
Copy Number log−ratio
2m0
2m1
3m1
3m2
5m
5m

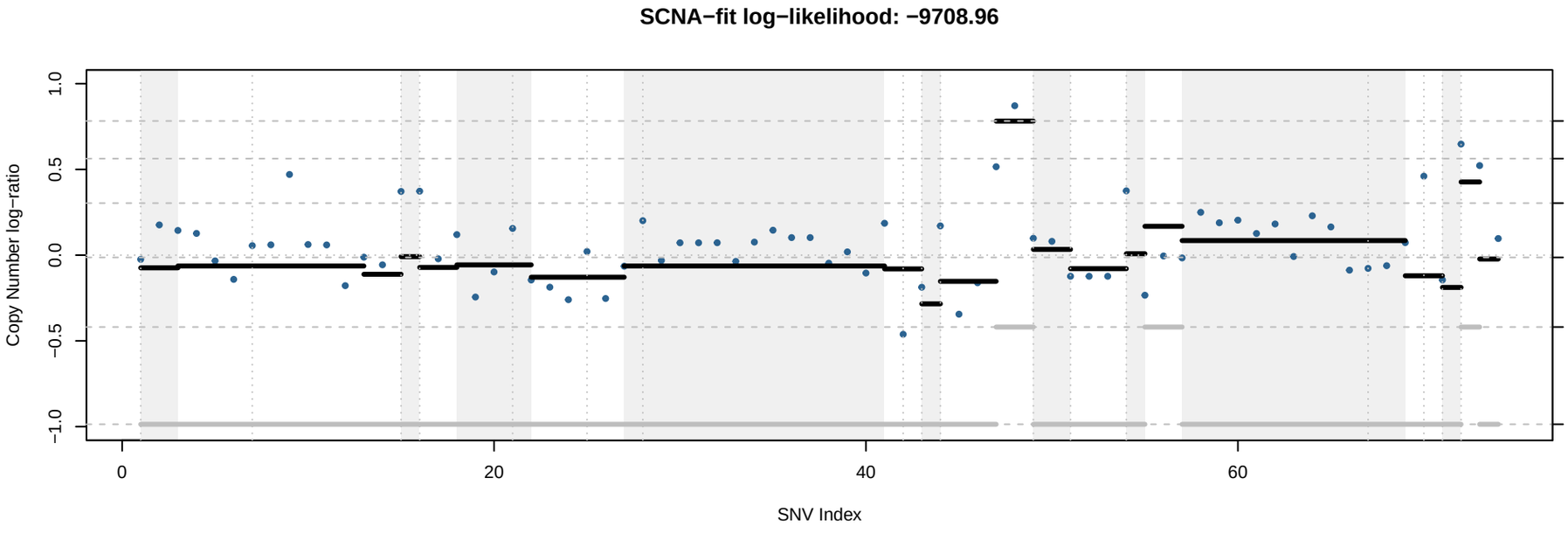

Coverage (log2)
Allelic fraction

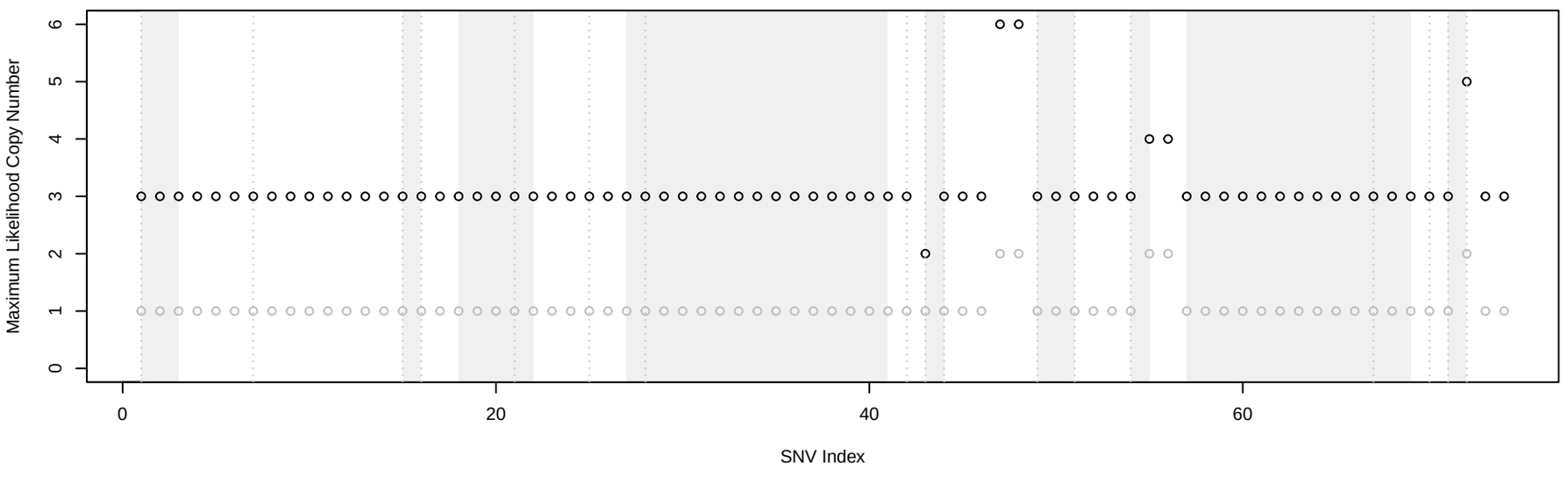

Allelic fraction (somatic)
Copy Number log−ratio
2m1
3m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

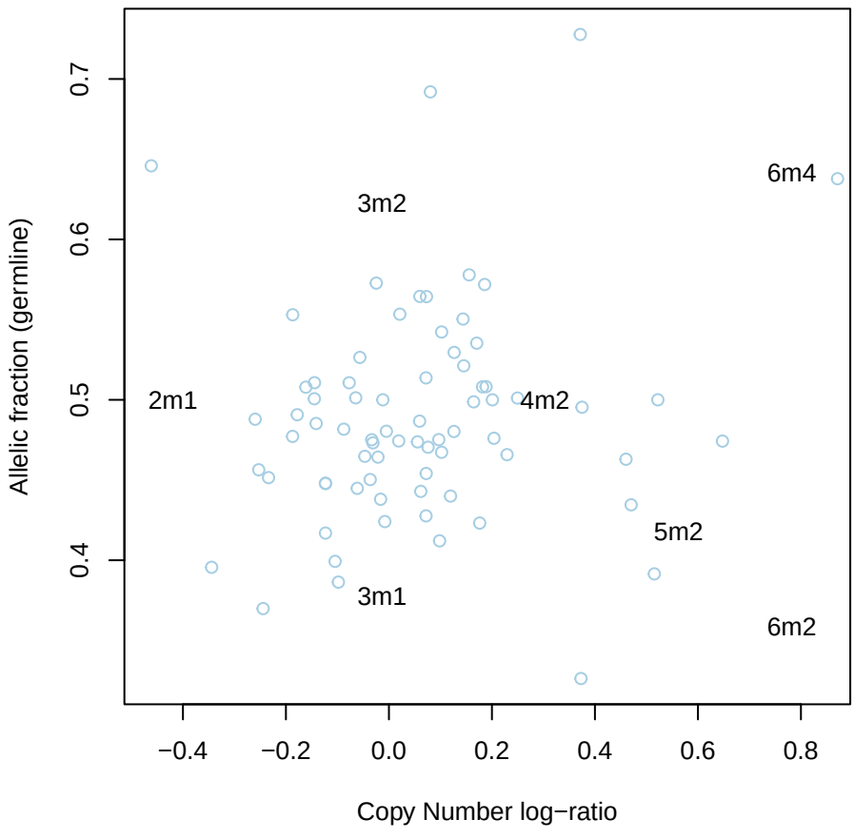

Frequency
Cellular fraction

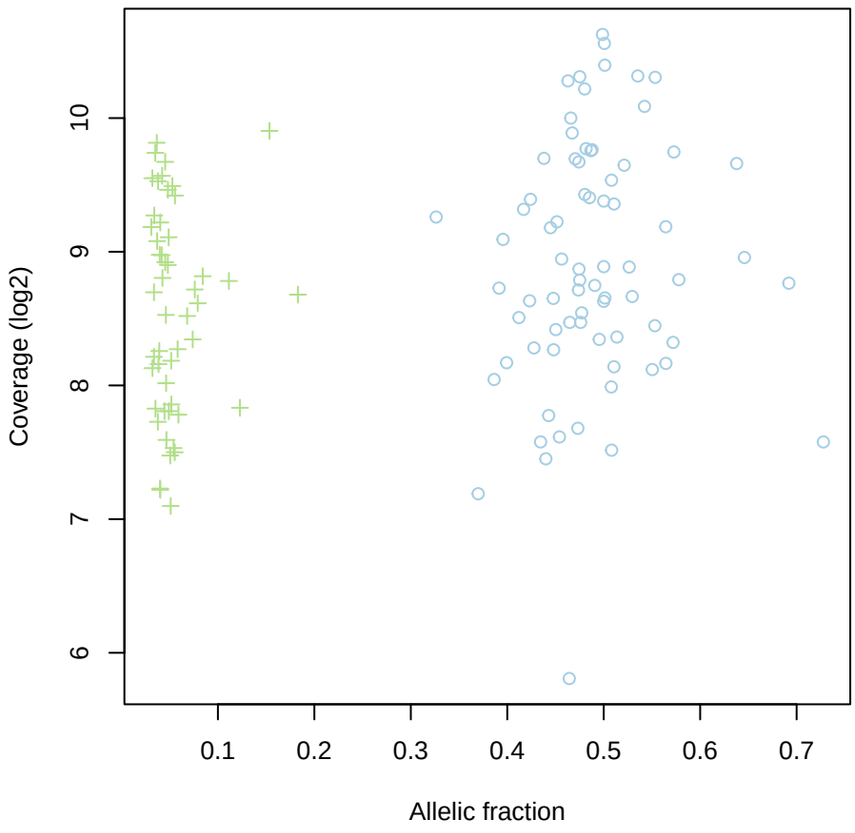

Purity: 0.65 Tumor ploidy: 3.038
0
1
2
3
4
5
6
0.0
0.1
0.2
0.3
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

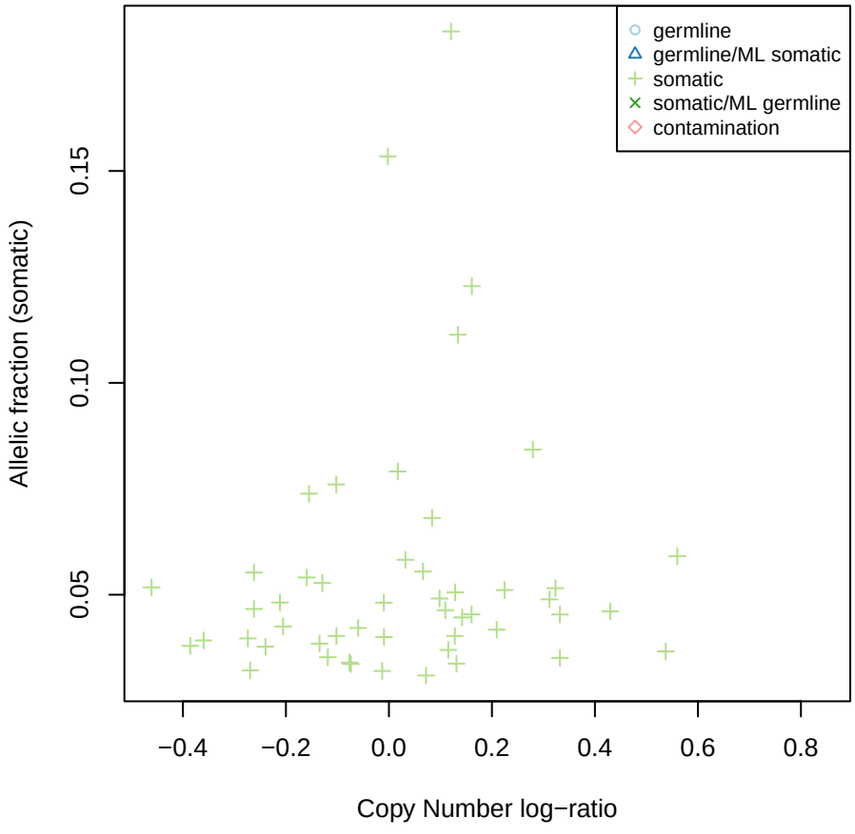

Purity: 0.65 Tumor ploidy: 3.038 SNV log−likelihood: −359.44 GoF: 52.8% Mean coverage: 520;712
1
2
3
4
5
6
7
8
11
12
14
15
19
20
B−Allele Frequency
0.4
0.5
0.6
0.7
0
20
40
60
SNV Index

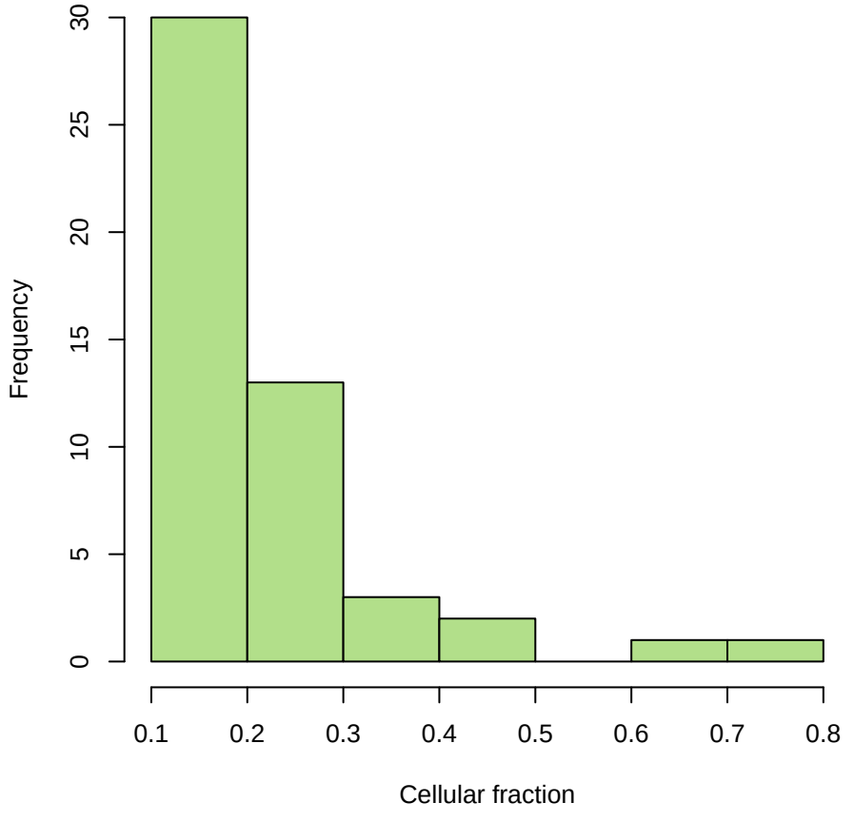

SCNA−fit log−likelihood: −9708.96
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1
2
3
4
5
6
0
20
40
60
SNV Index


Maximum Likelihood Copy Number
0
1
2
3
4
5
6
0
20
40
60
SNV Index


Allelic fraction (germline)
Copy Number log−ratio
2m1
3m2
4m2
5m2
6m4
3m1
6m2


Coverage (log2)
Allelic fraction


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


Frequency
Cellular fraction