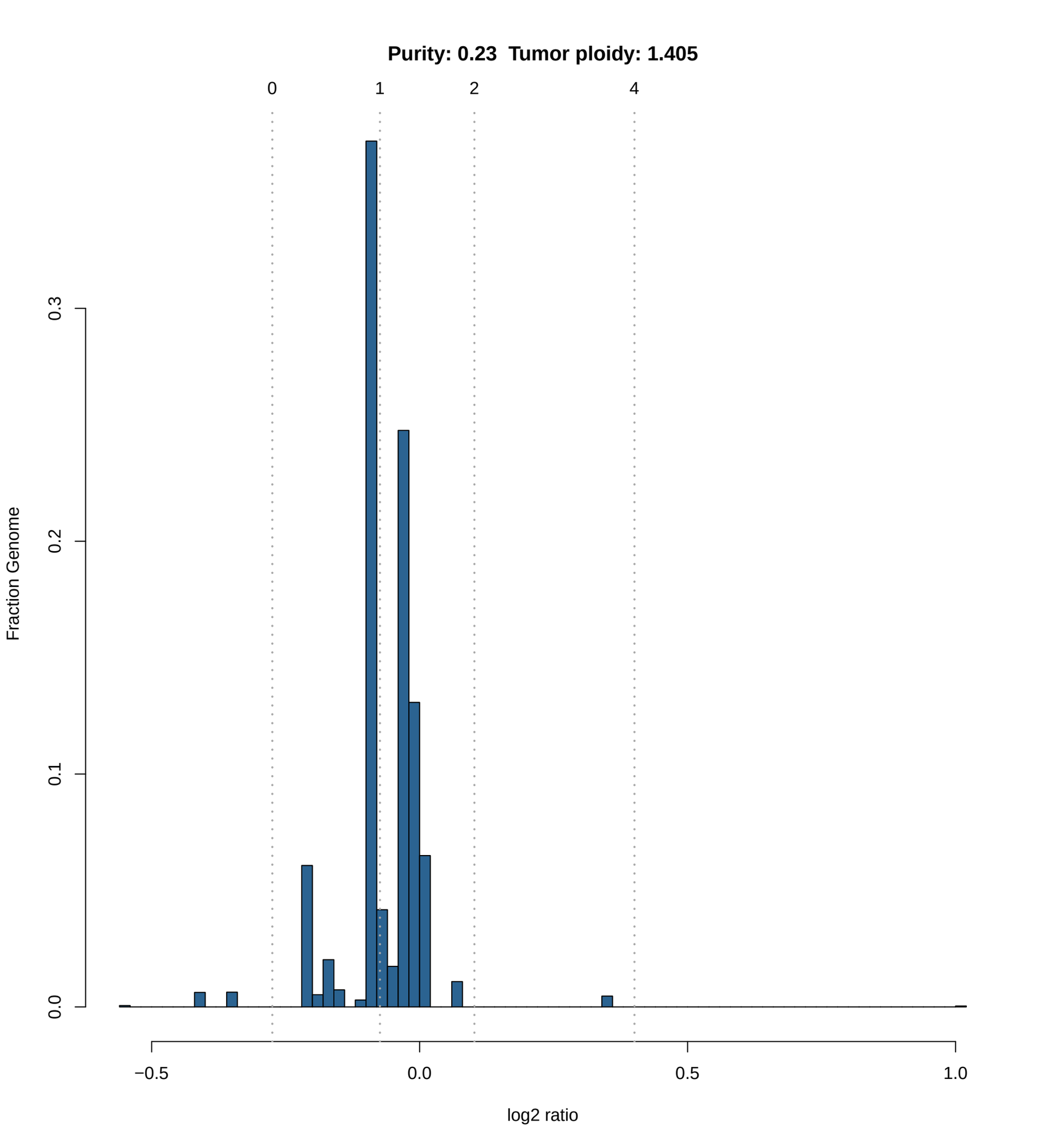
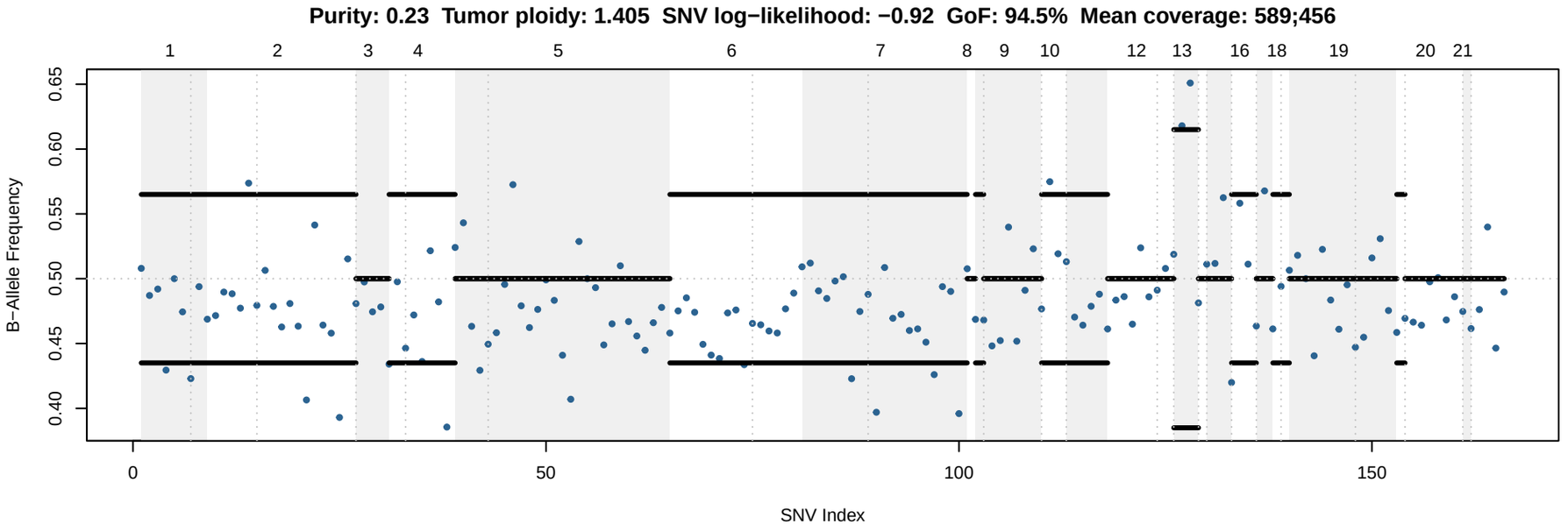
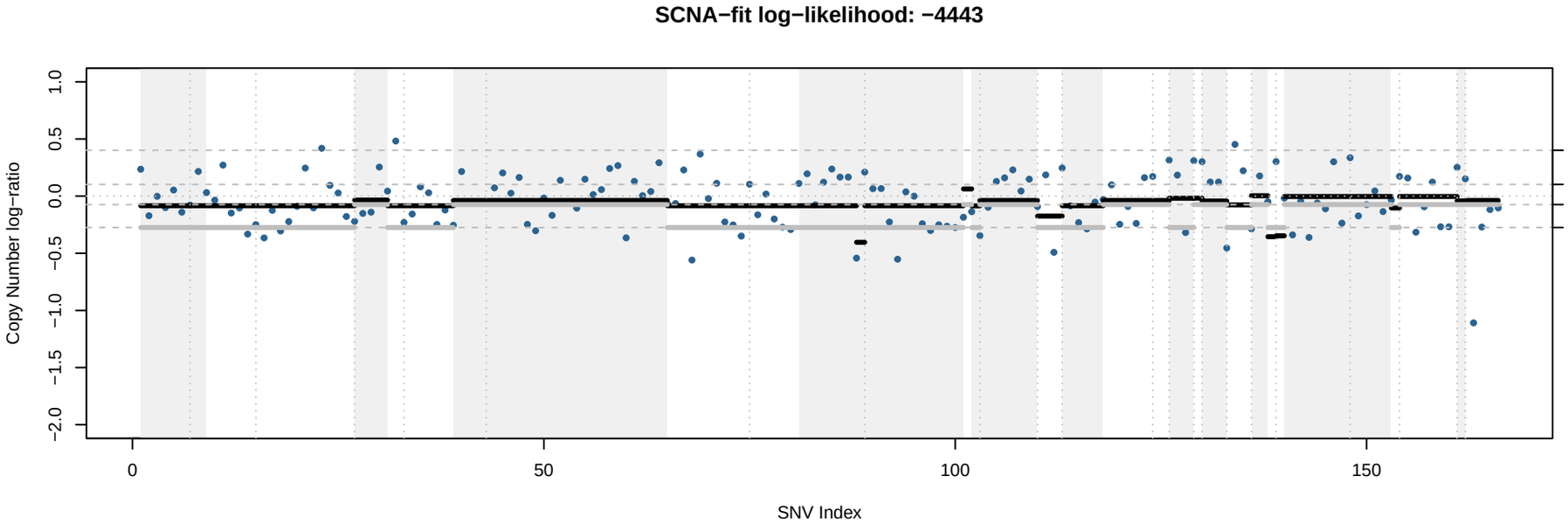
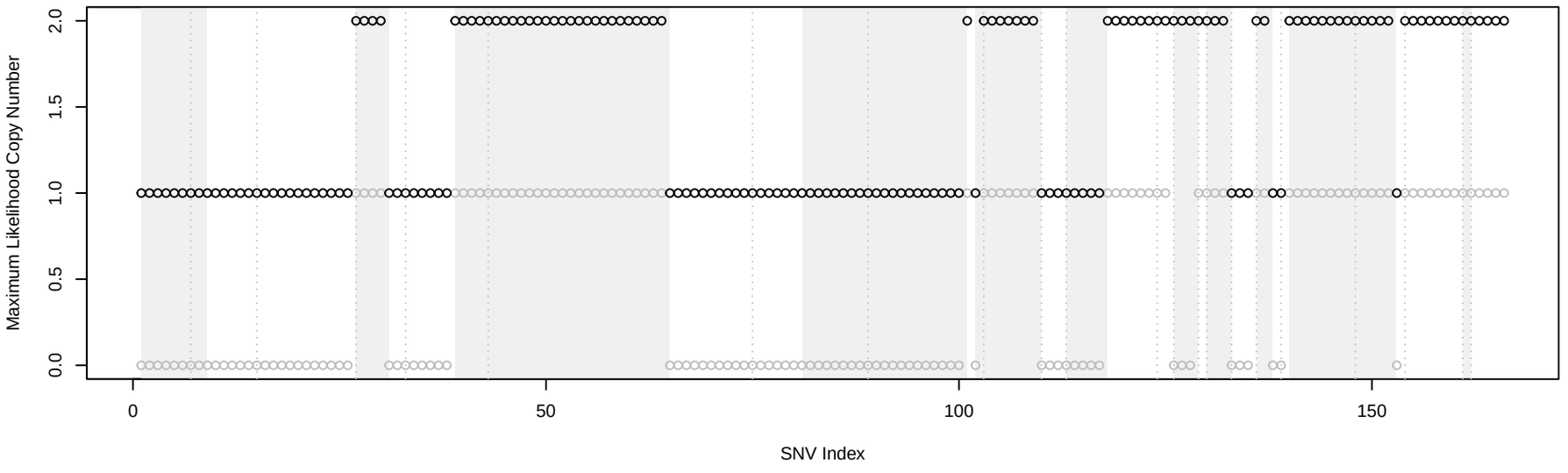
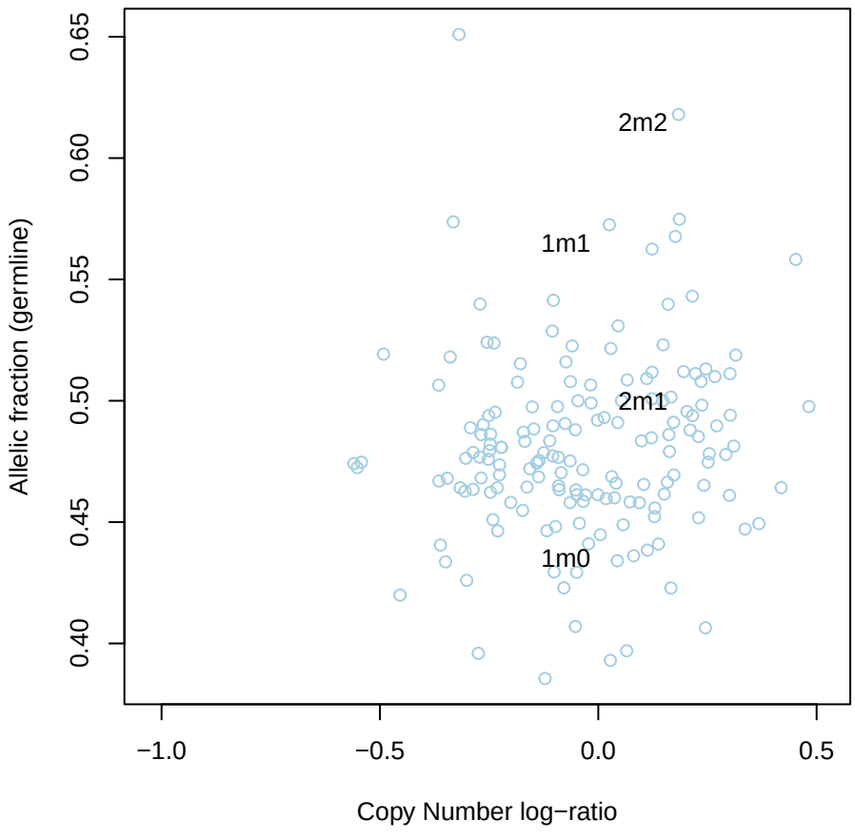
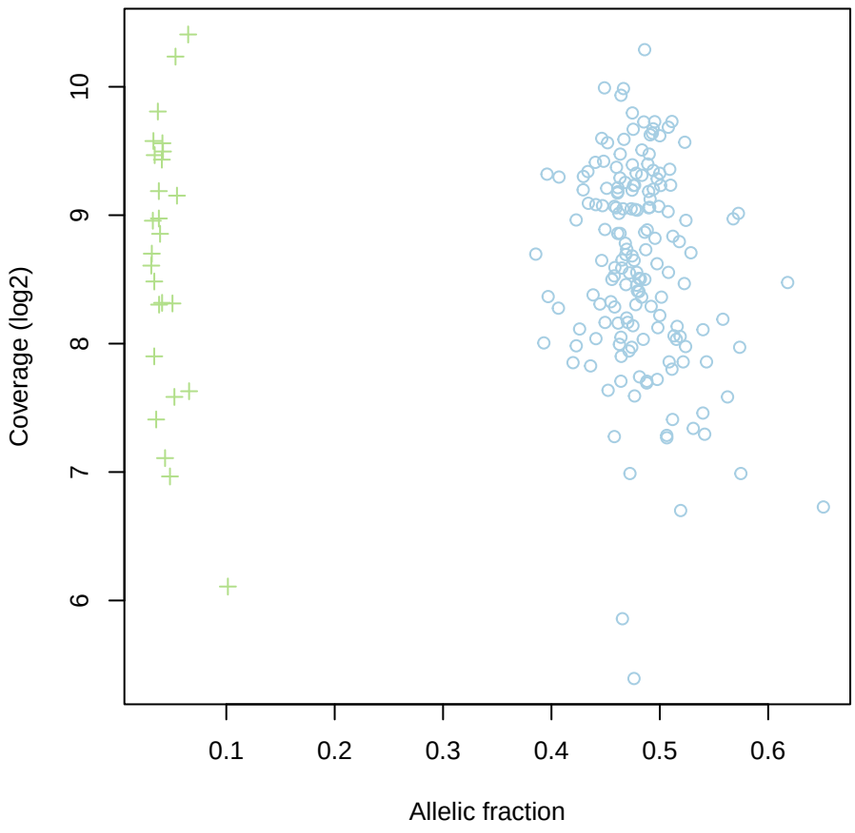

Purity: 0.23 Tumor ploidy: 1.405
0
1
2
4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

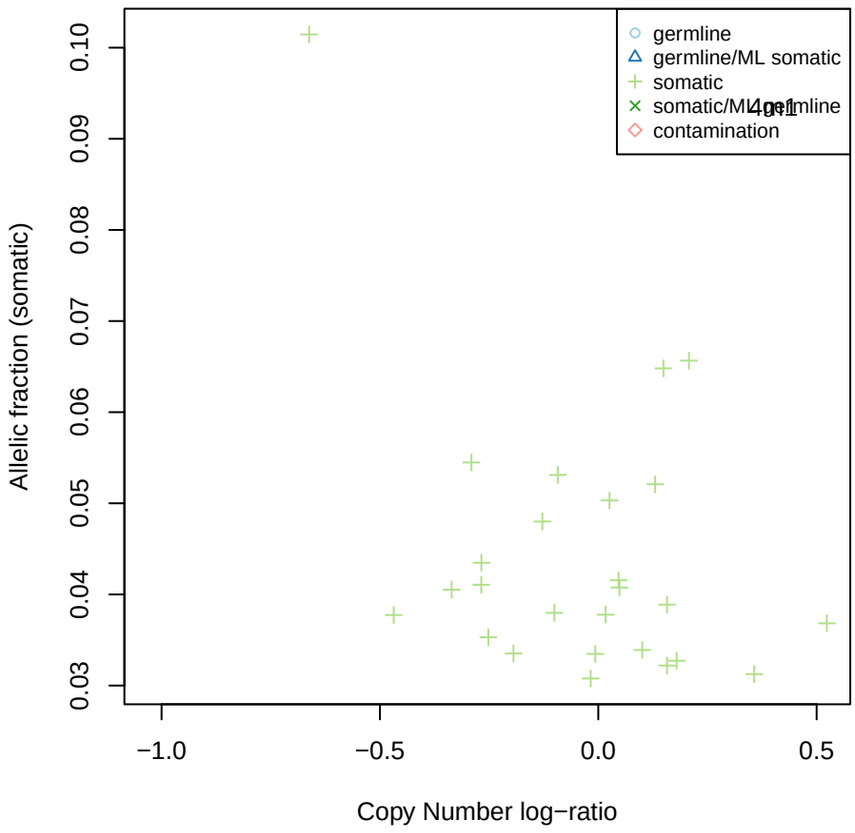

Purity: 0.23 Tumor ploidy: 1.405 SNV log−likelihood: −0.92 GoF: 94.5% Mean coverage: 589;456
1 2 3 4 5 6 7 8 9 10 12 13 16 18 19 20 21
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60 0.65
0 50 100 150
SNV Index

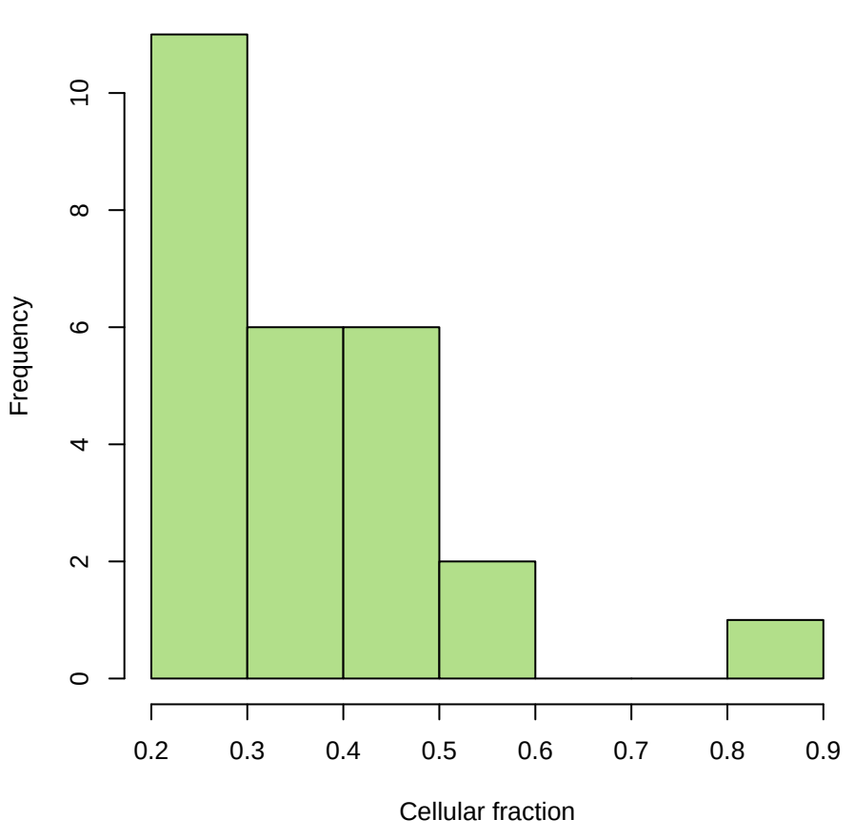

SCNA−fit log−likelihood: −4443
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
0 2 4
0 50 100 150
SNV Index

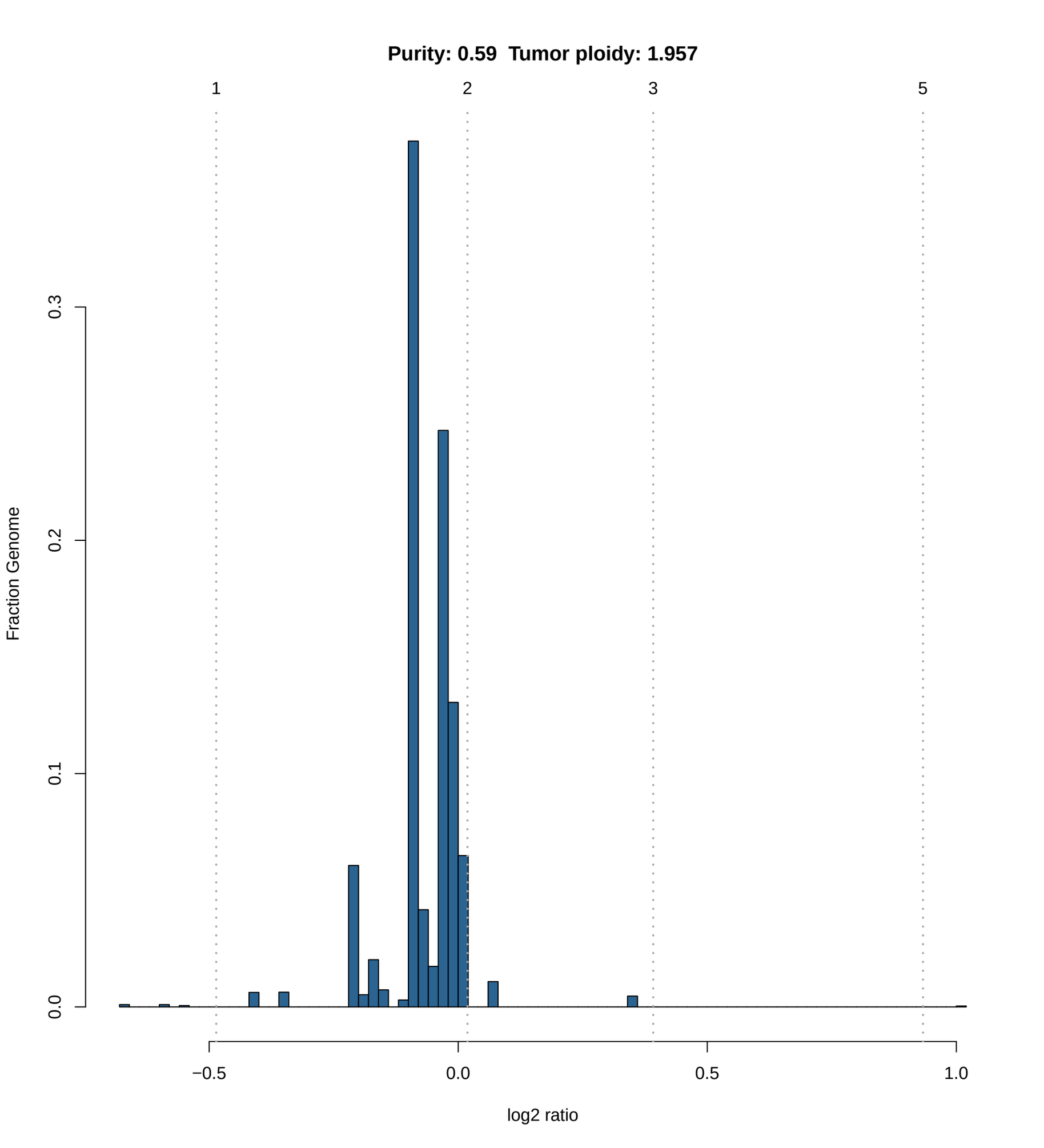

Maximum Likelihood Copy Number
2.0 1.5 1.0 0.5 0.0
0 50 100 150
SNV Index

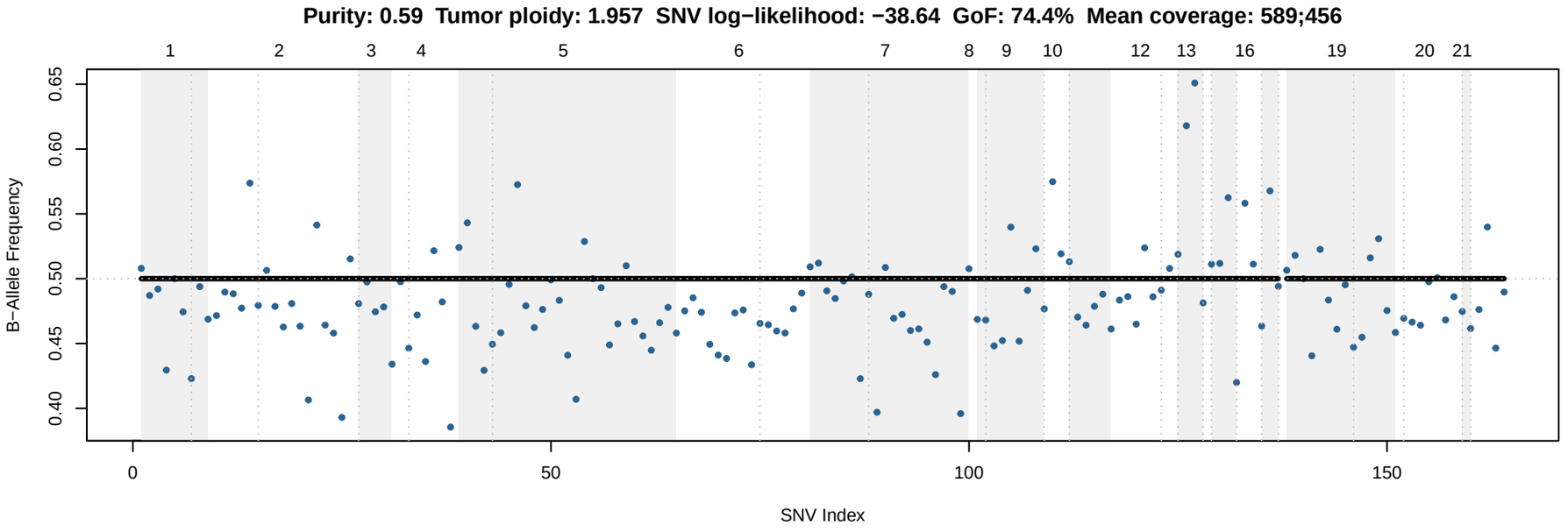

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
2m2
1m1
2m1
1m0
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

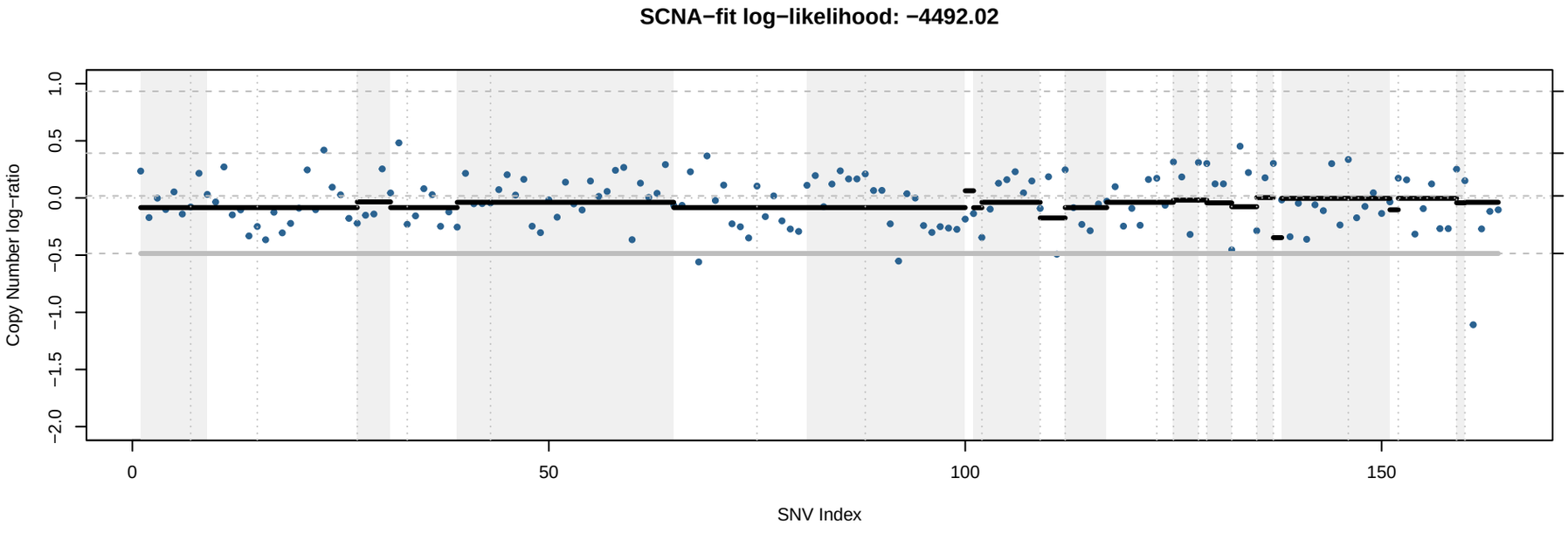

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

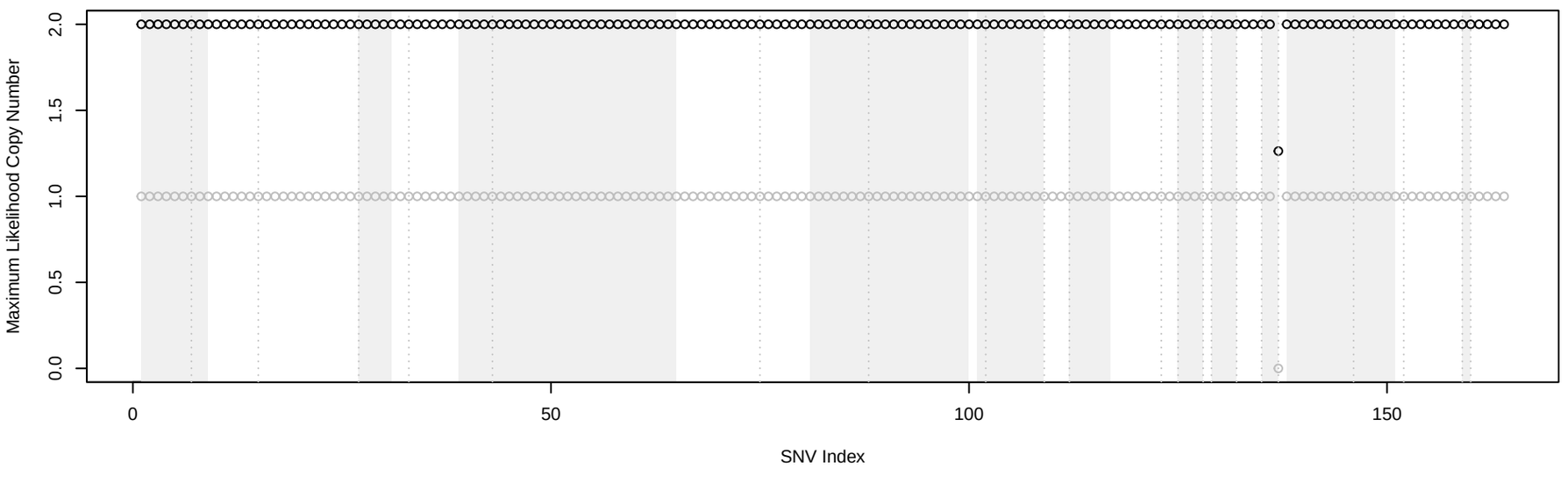

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
Allelic fraction (somatic)
0.03
0.04
0.05
0.06
0.07
0.08
0.09
0.10
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

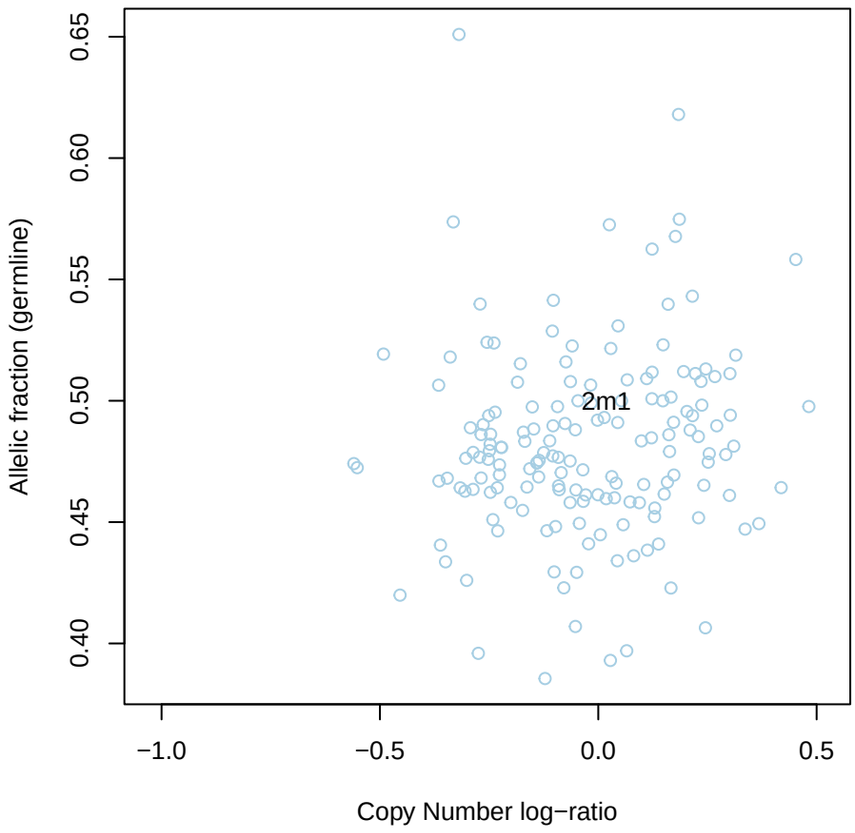

Frequency
0
2
4
6
8
10
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
Cellular fraction

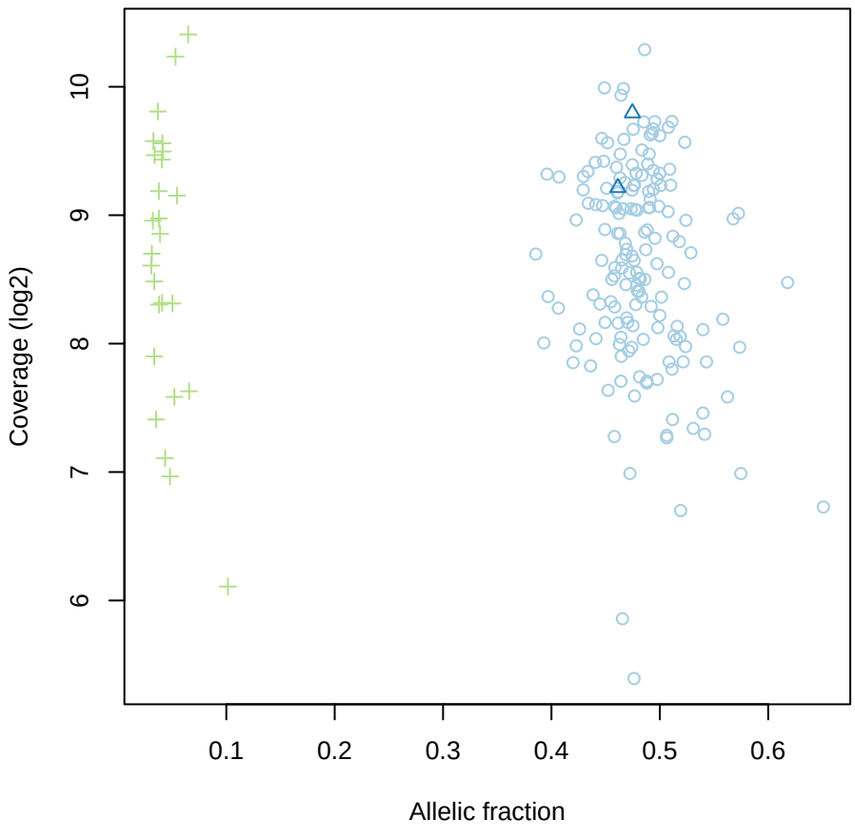

Purity: 0.59 Tumor ploidy: 1.957
1
2
3
5
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

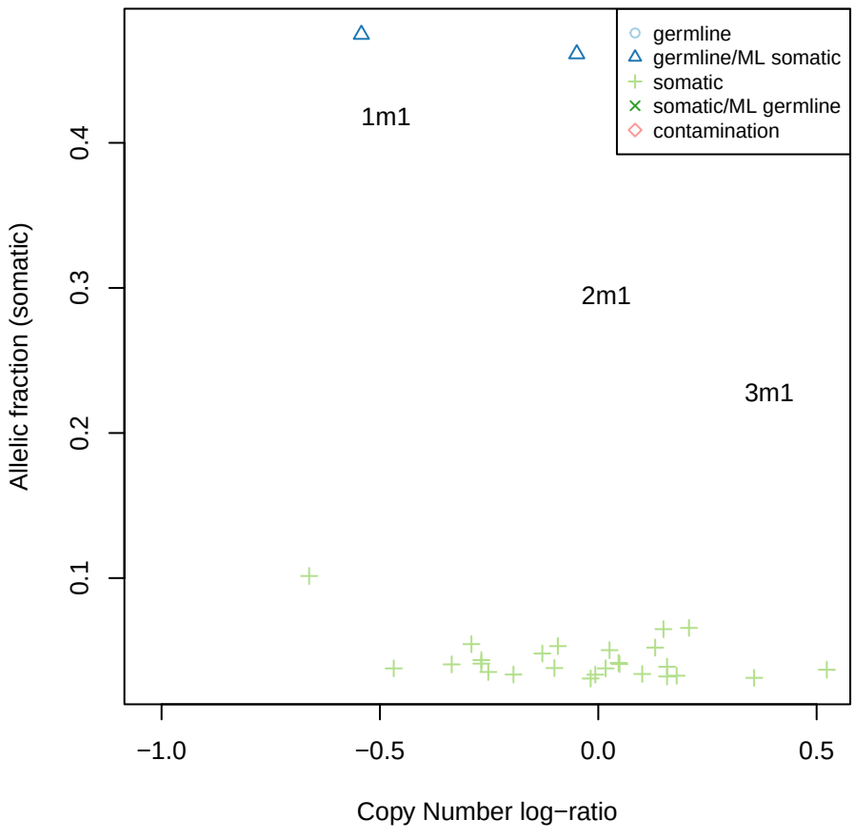

Purity: 0.59 Tumor ploidy: 1.957 SNV log−likelihood: −38.64 GoF: 74.4% Mean coverage: 589;456
1 2 3 4 5 6 7 8 9 10 12 13 16 19 20 21
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60 0.65
0 50 100 150
SNV Index

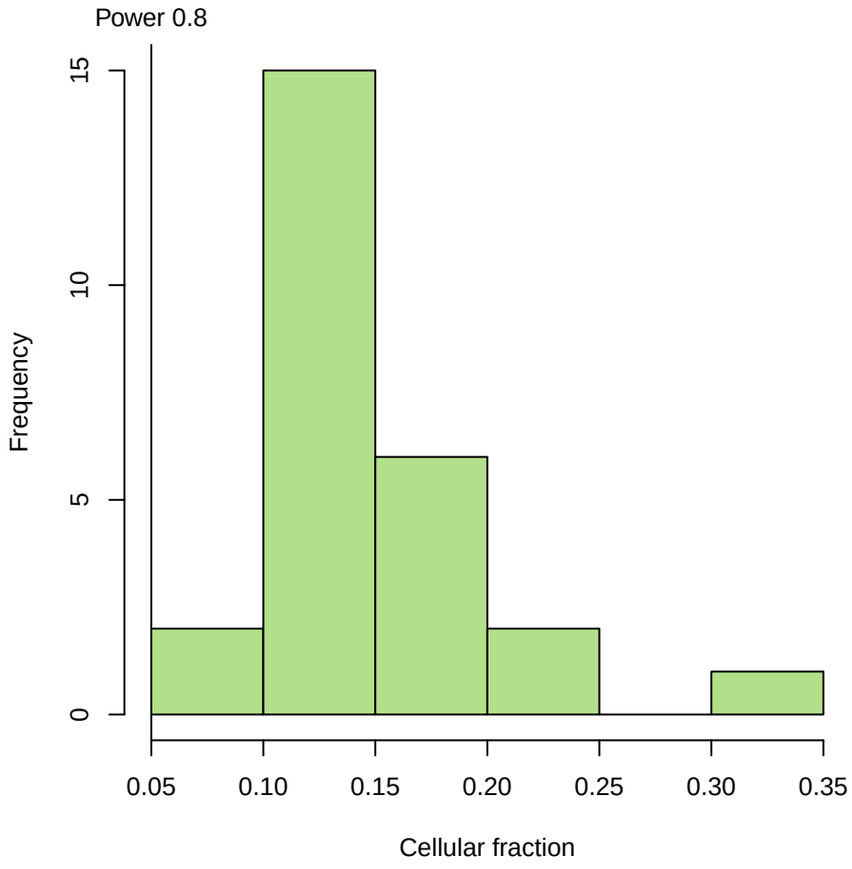

SCNA−fit log−likelihood: −4492.02
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
1 2 3 5
0 50 100 150
SNV Index

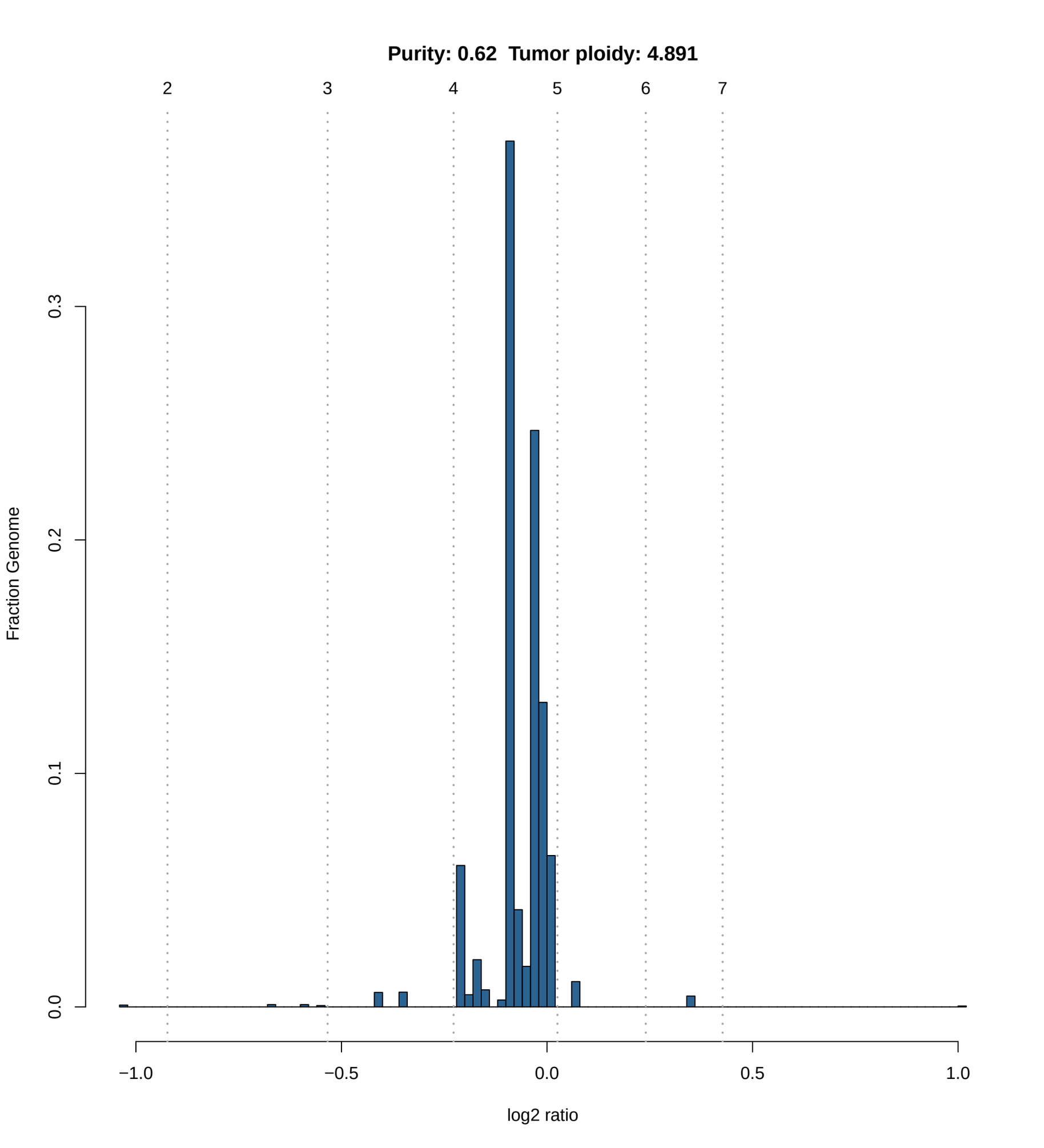

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 50 100 150
SNV Index

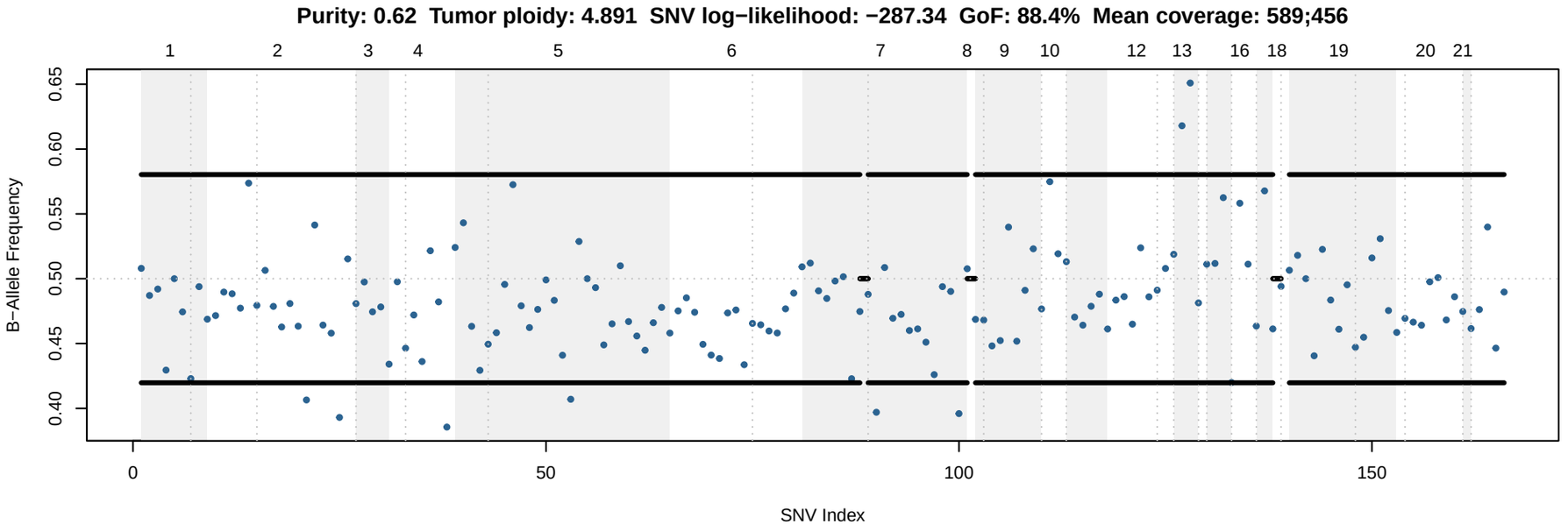

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
2m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

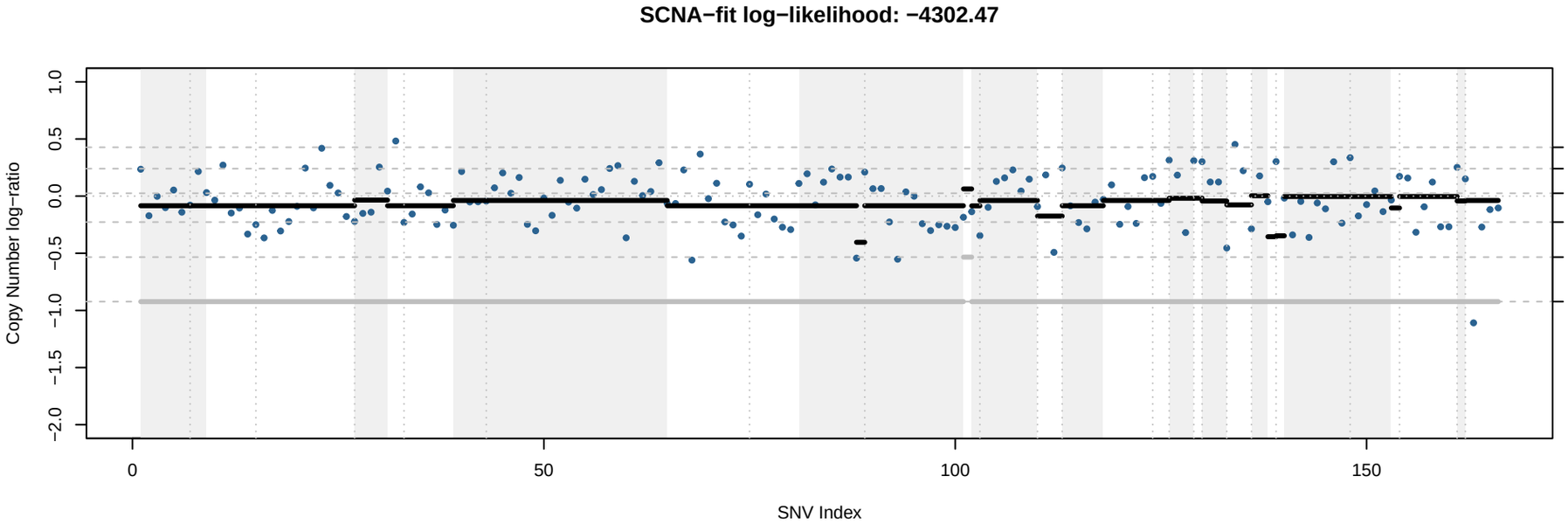

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

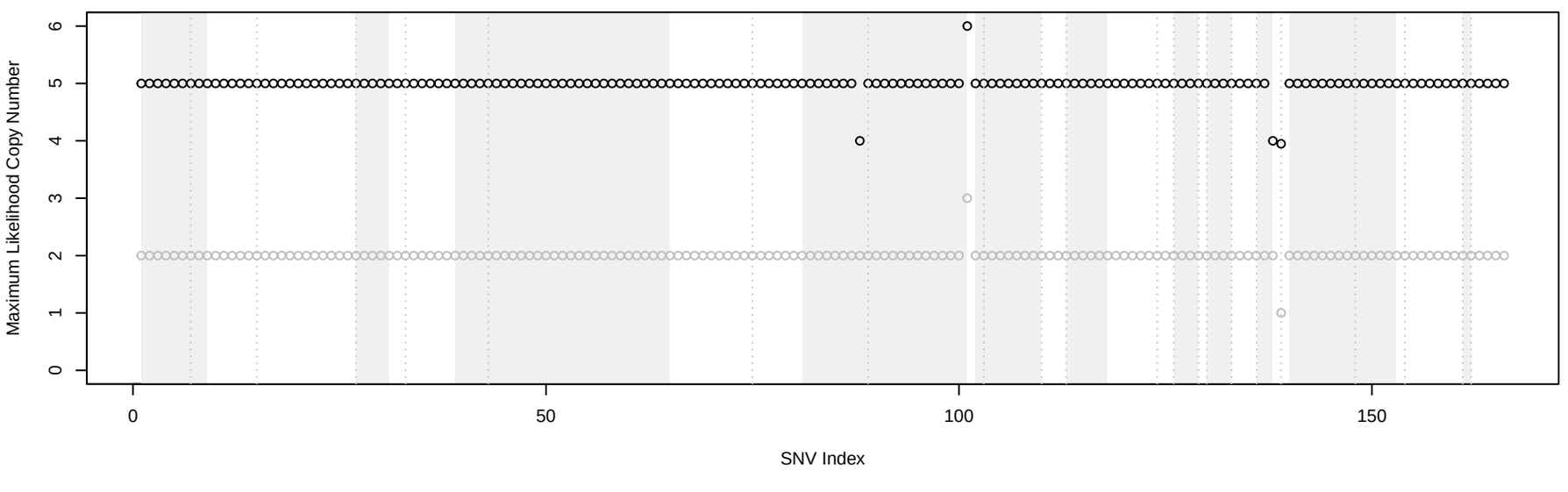

Allelic fraction (somatic)
0.1
0.2
0.3
0.4
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

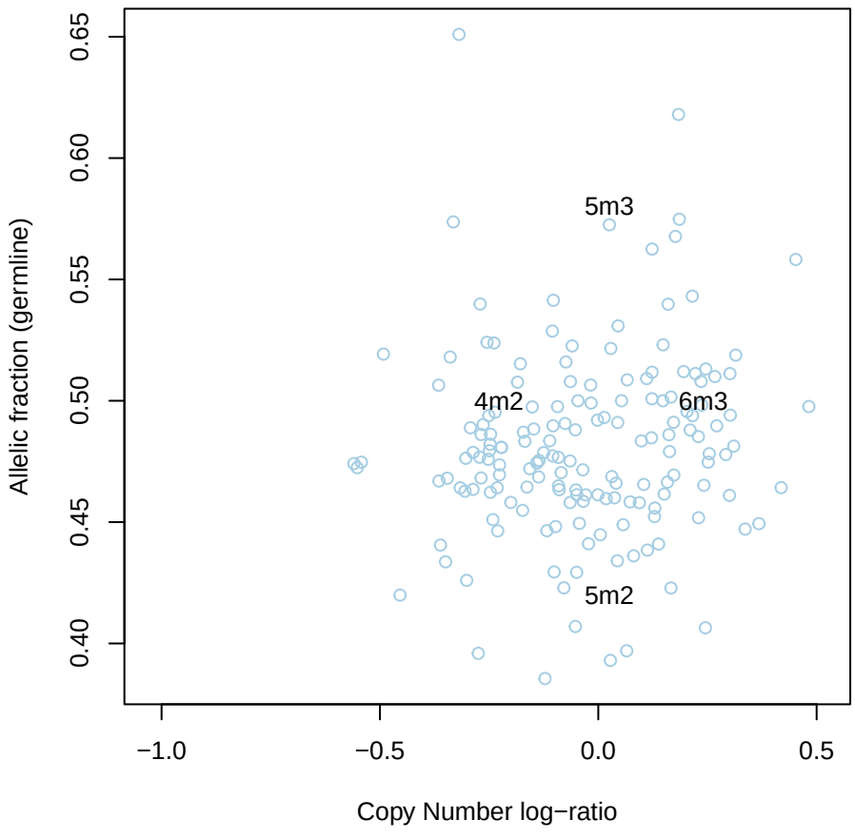

Power 0.8
Frequency
0
5
10
15
0.05
0.10
0.15
0.20
0.25
0.30
0.35
Cellular fraction

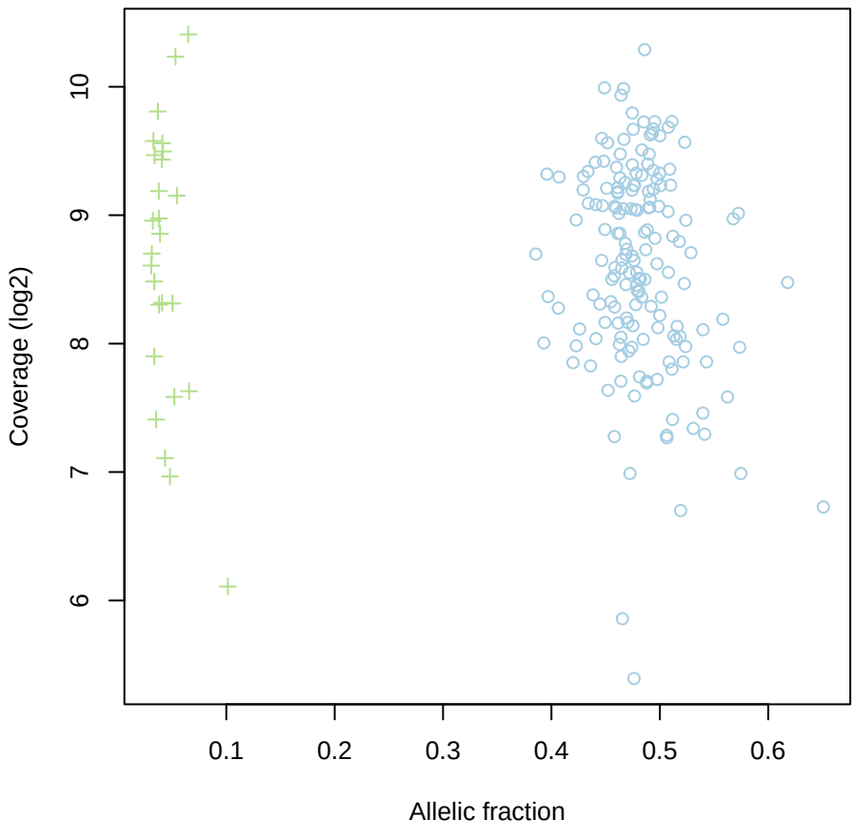

Purity: 0.62 Tumor ploidy: 4.891
2
3
4
5
6
7
0.0
0.1
0.2
0.3
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

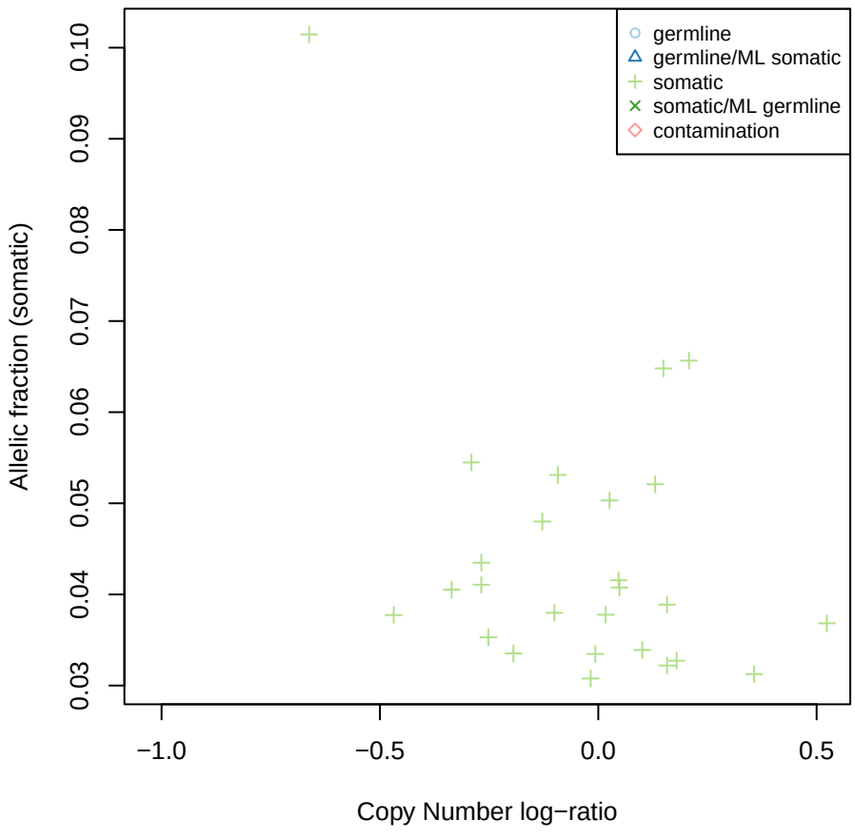

Purity: 0.62 Tumor ploidy: 4.891 SNV log−likelihood: −287.34 GoF: 88.4% Mean coverage: 589;456
1 2 3 4 5 6 7 8 9 10 12 13 16 18 19 20 21
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60 0.65
0 50 100 150
SNV Index

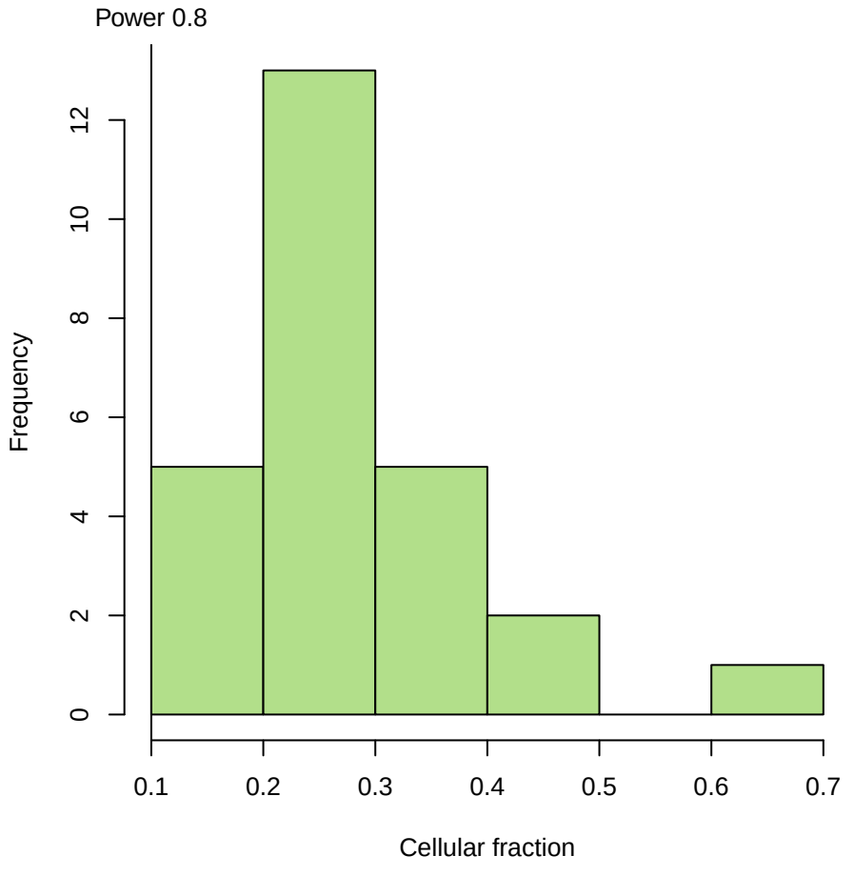

SCNA−fit log−likelihood: −4302.47
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
2 3 4 5 7
0 50 100 150
SNV Index

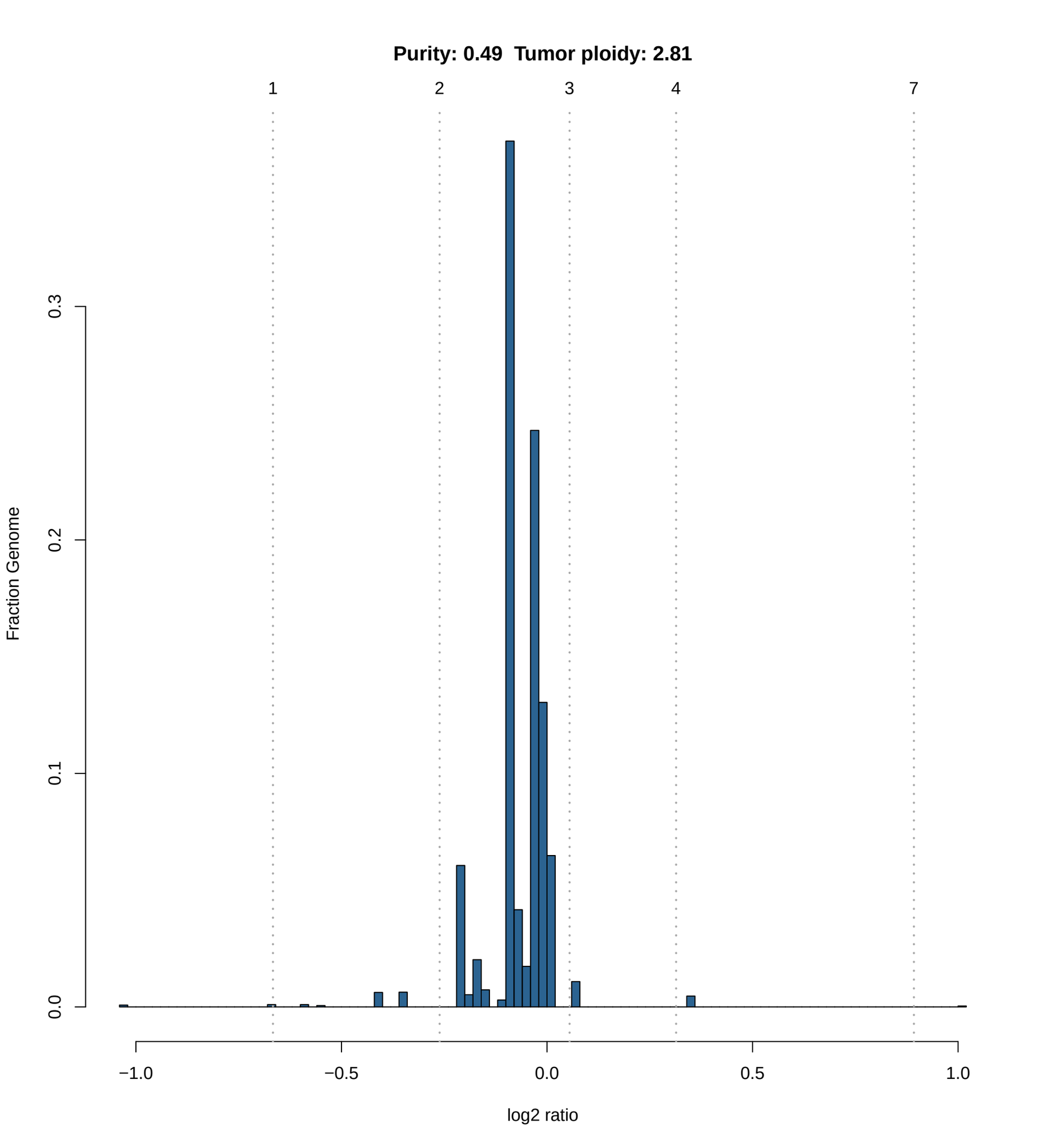

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

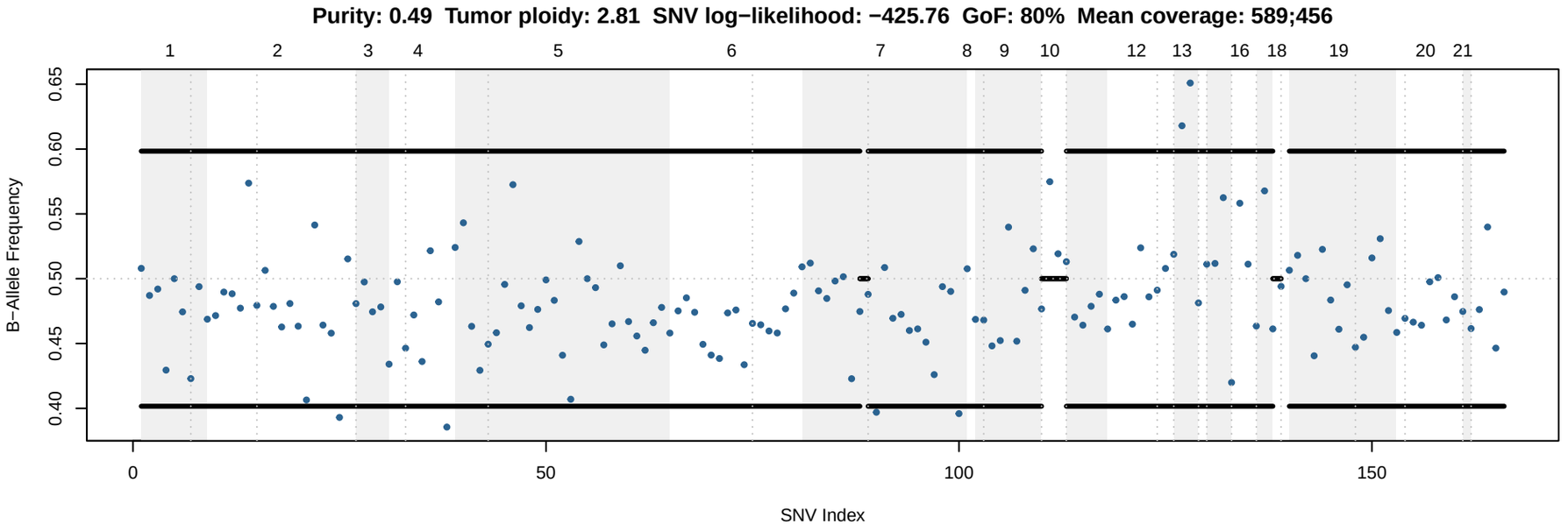

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
5m3
4m2
6m3
5m2
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

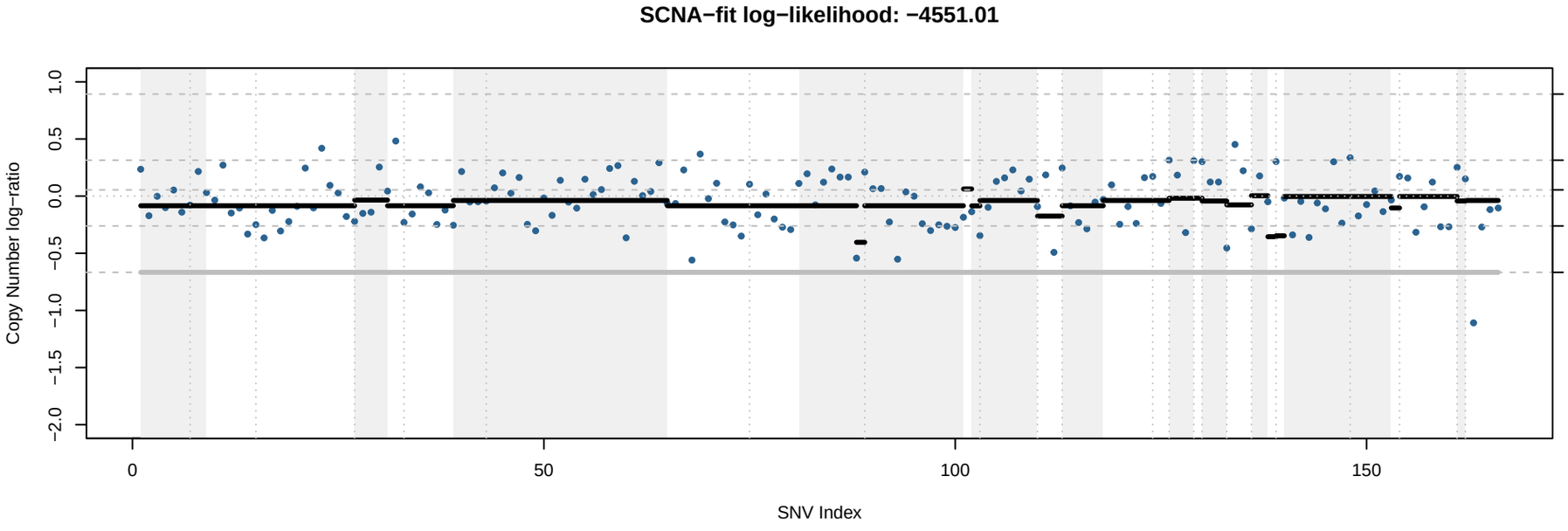

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

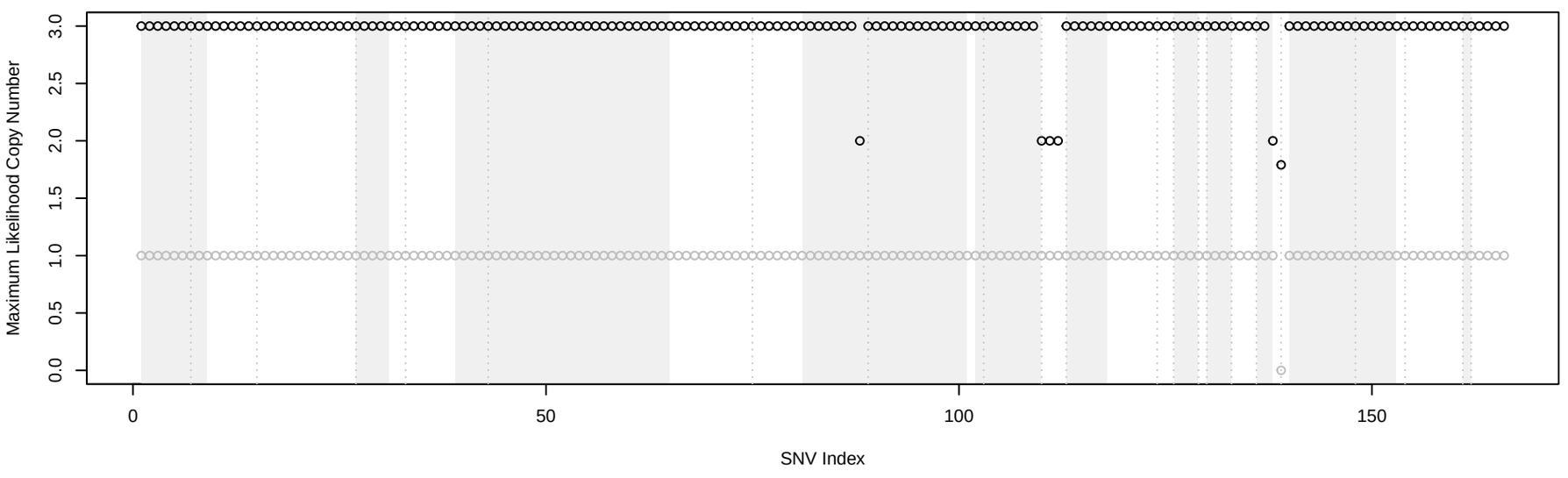

Allelic fraction (somatic)
0.03
0.04
0.05
0.06
0.07
0.08
0.09
0.10
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

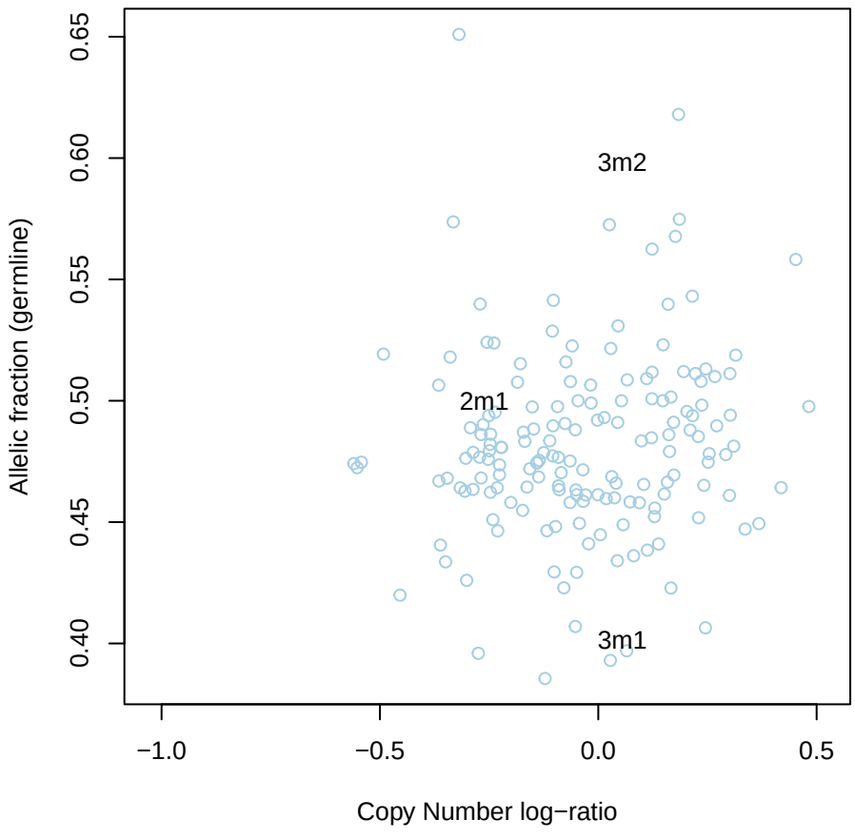

Power 0.8
Frequency
0
2
4
6
8
10
12
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Cellular fraction

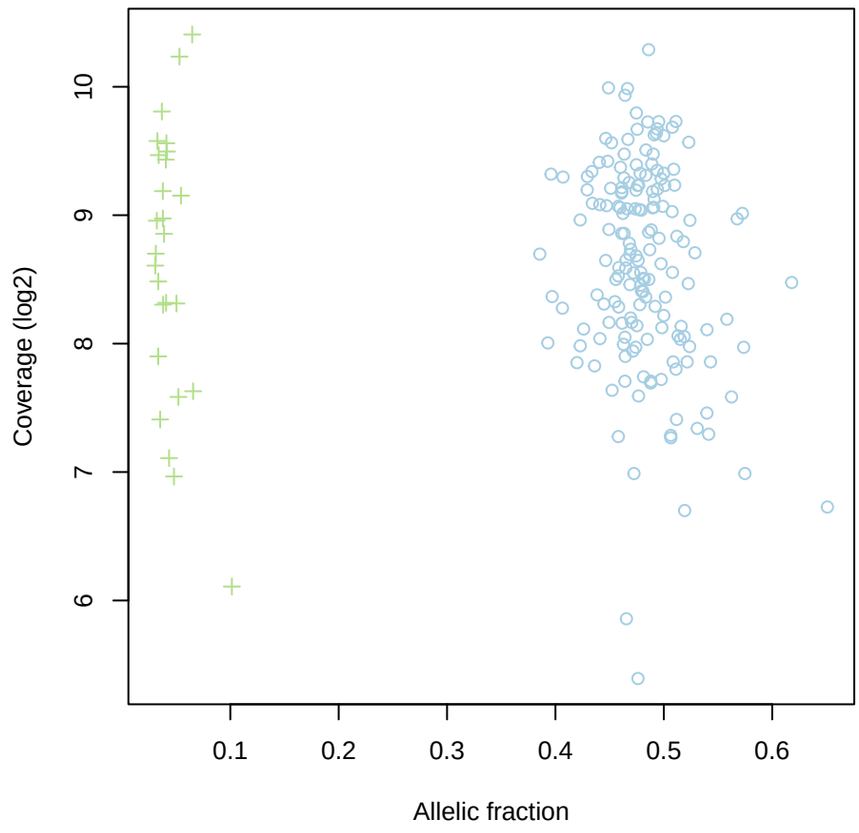

Purity: 0.49 Tumor ploidy: 2.81
1
2
3
4
7
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

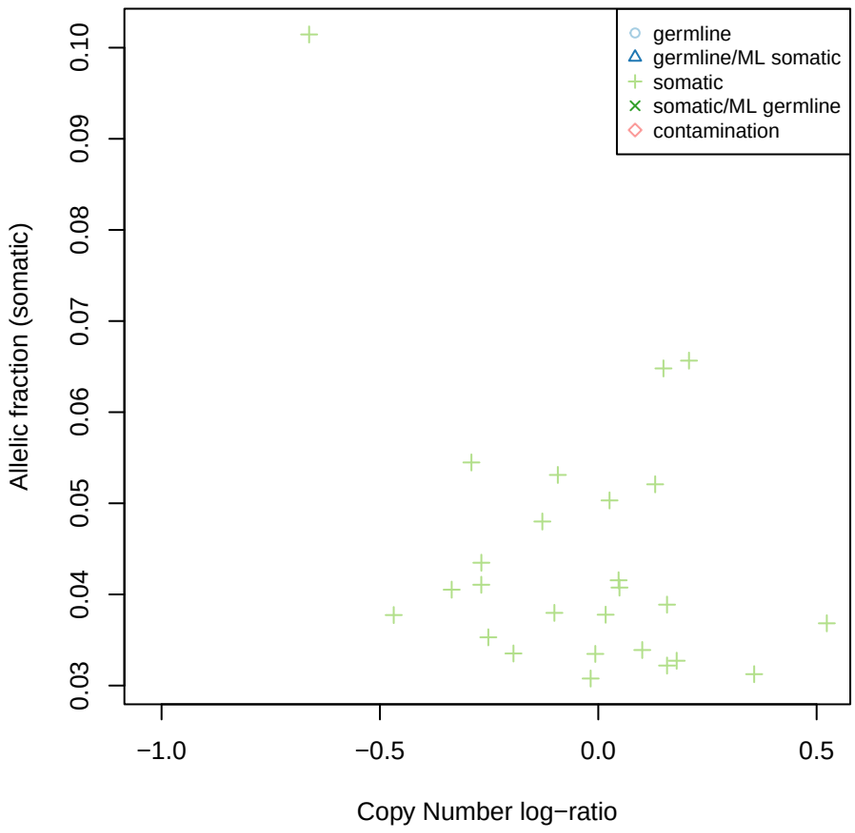

Purity: 0.49 Tumor ploidy: 2.81 SNV log−likelihood: −425.76 GoF: 80% Mean coverage: 589;456
1 2 3 4 5 6 7 8 9 10 12 13 16 18 19 20 21
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60 0.65
0 50 100 150
SNV Index

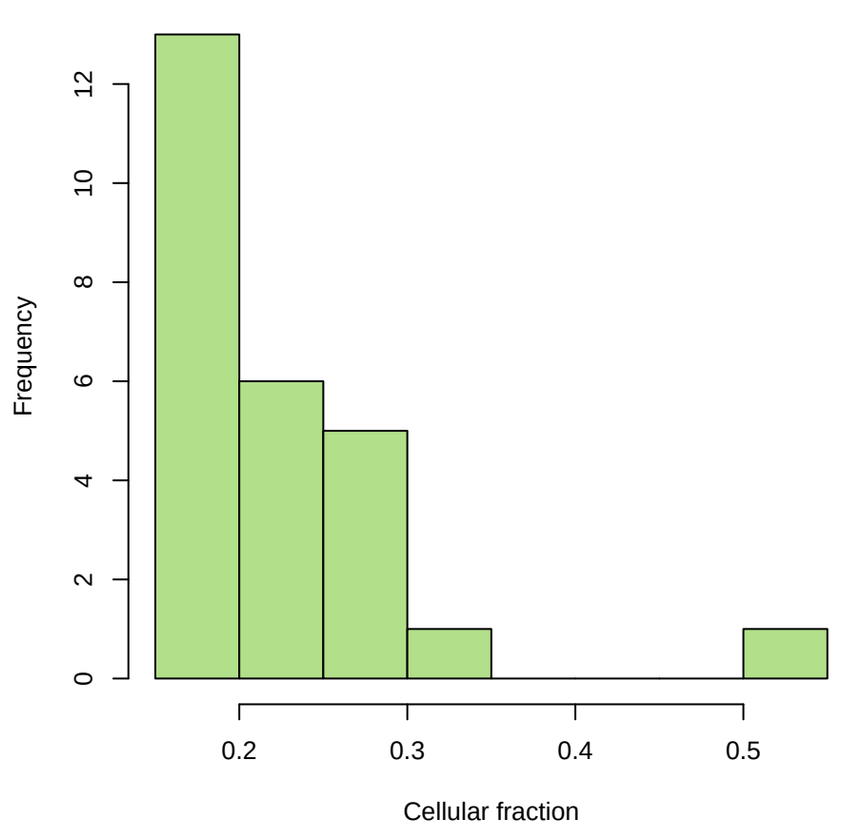

SCNA−fit log−likelihood: −4551.01
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
1 2 3 4 7
0 50 100 150
SNV Index

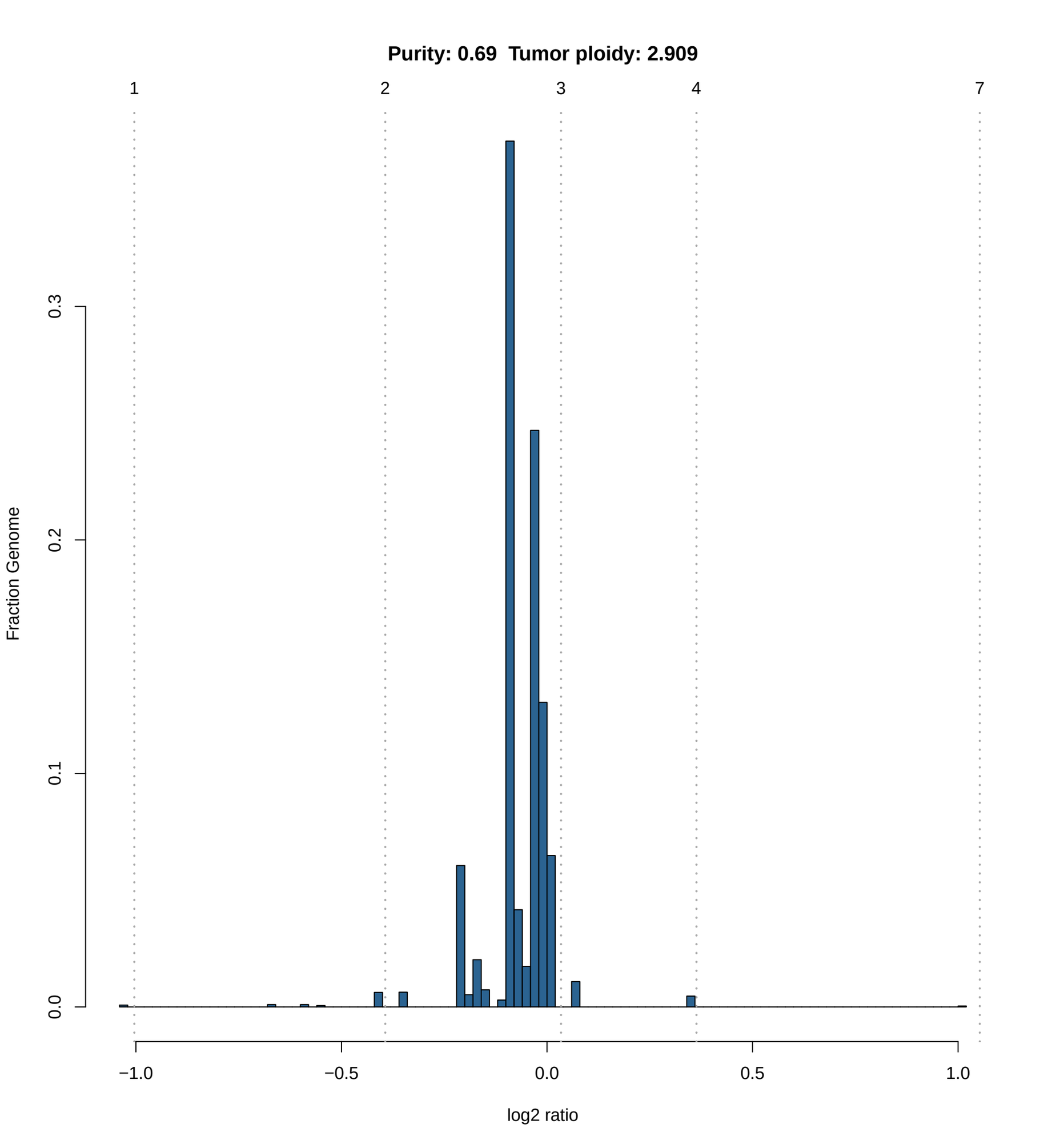

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

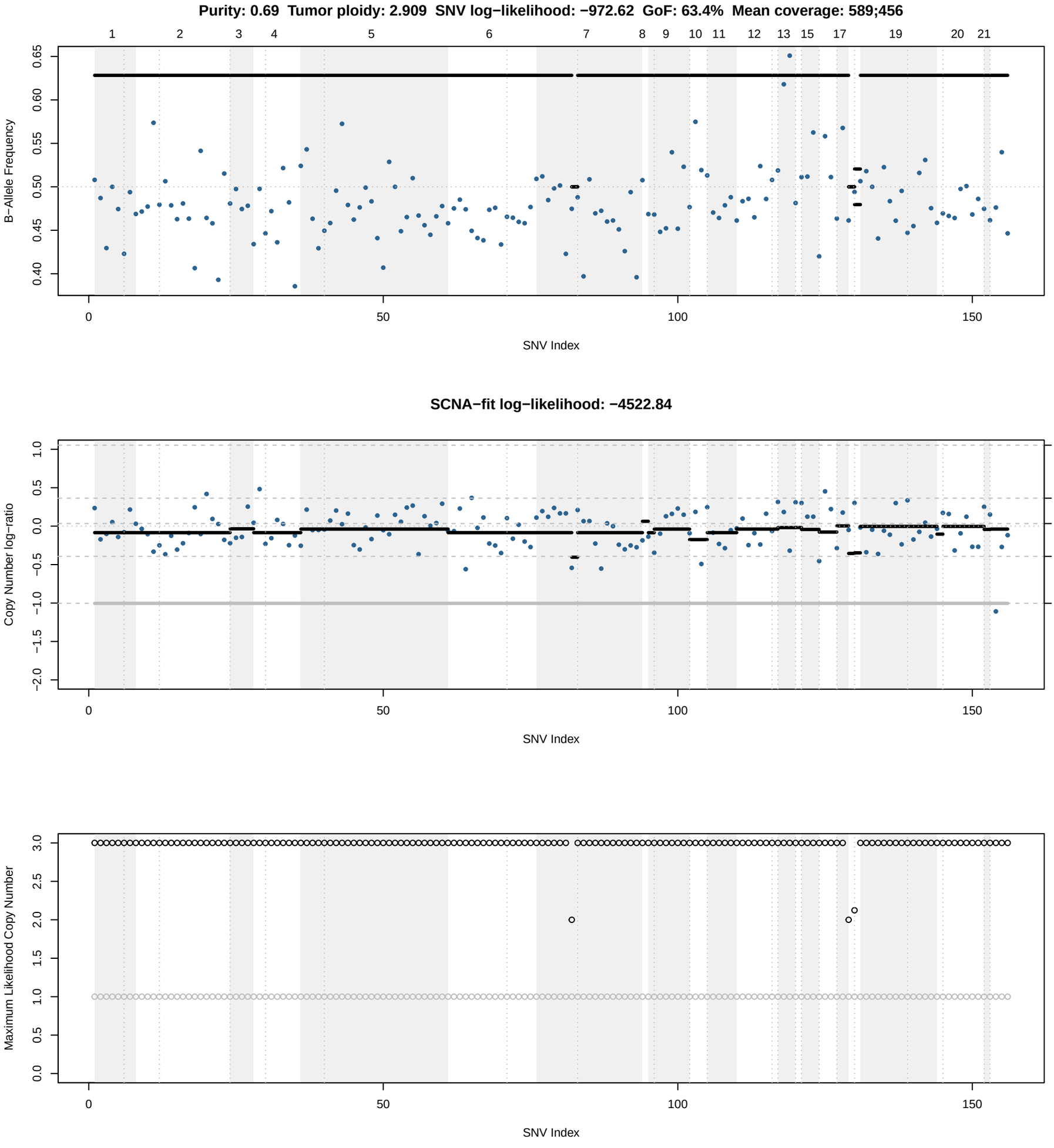

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
3m2
2m1
3m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

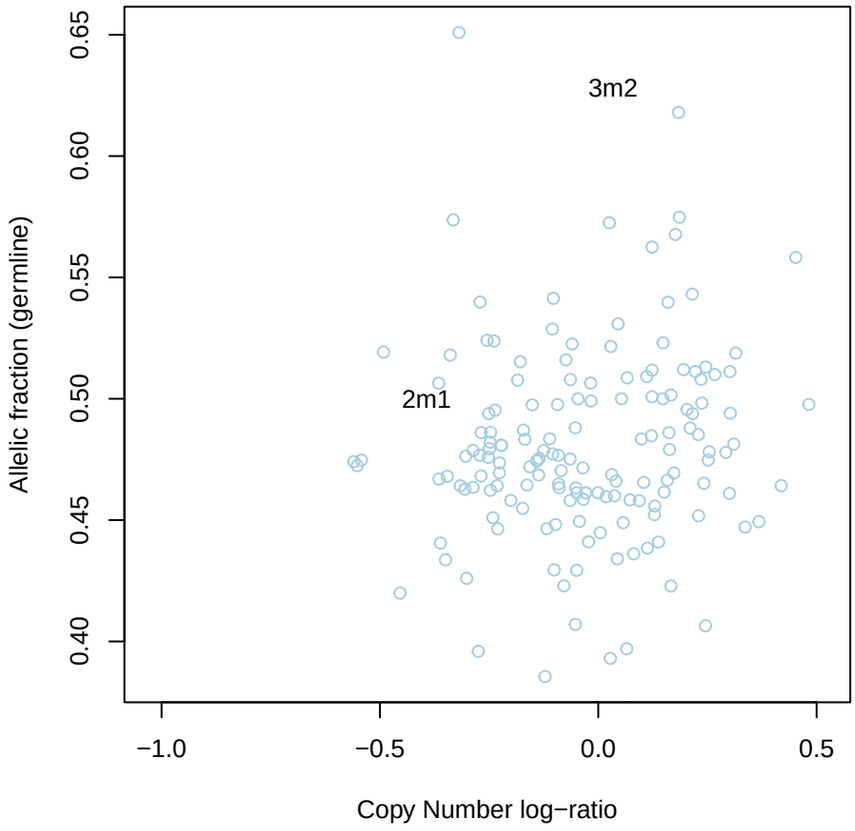

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

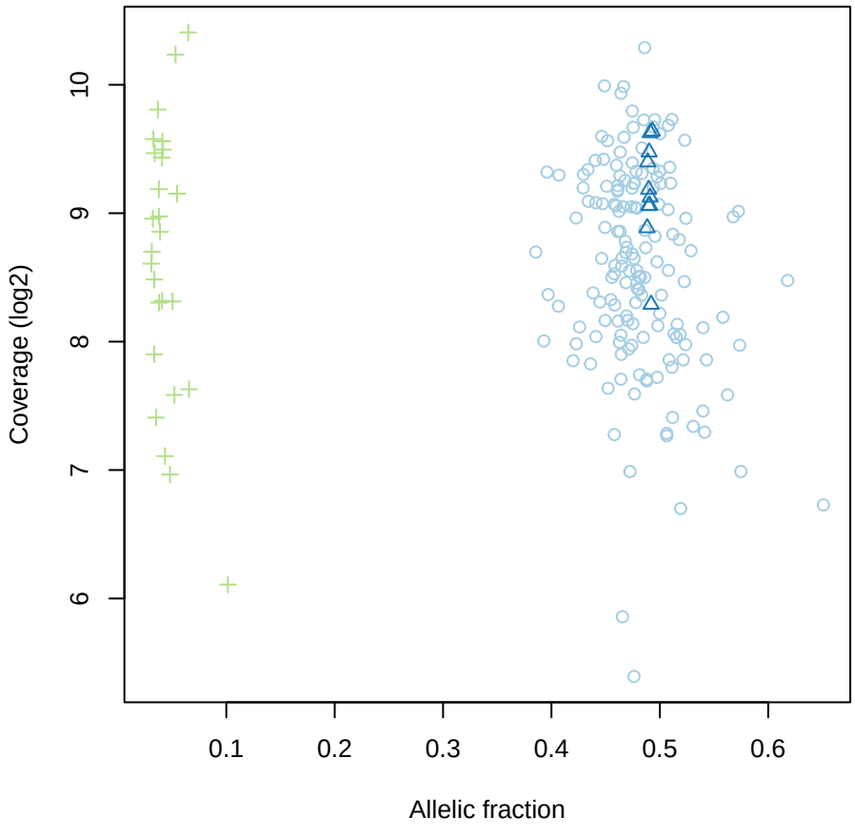

Allelic fraction (somatic)
0.03
0.04
0.05
0.06
0.07
0.08
0.09
0.10
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

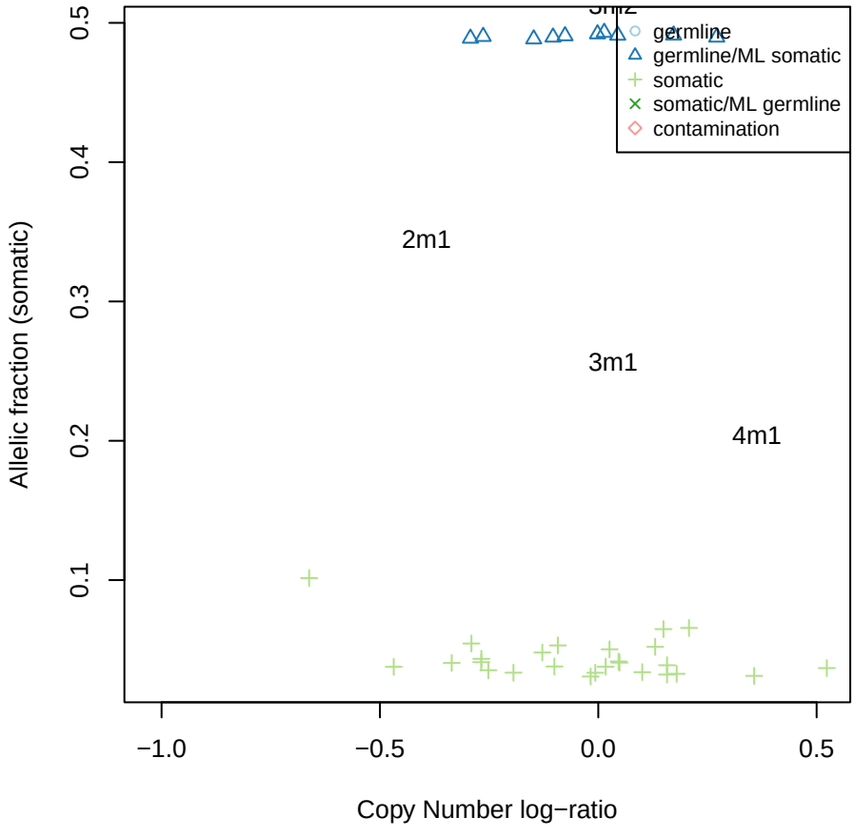

Frequency
0
2
4
6
8
10
12
0.2
0.3
0.4
0.5
Cellular fraction

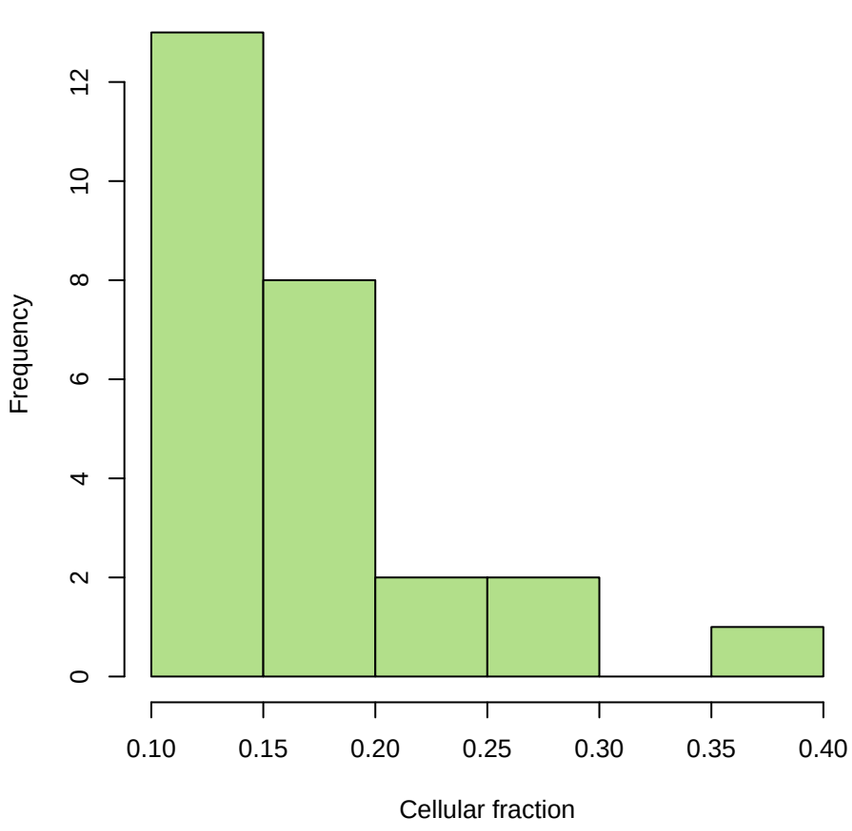

Purity: 0.69 Tumor ploidy: 2.909
1
2
3
4
7
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio


Purity: 0.69 Tumor ploidy: 2.909 SNV log−likelihood: −972.62 GoF: 63.4% Mean coverage: 589;456
1 2 3 4 5 6 7 8 9 10 11 12 13 15 17 19 20 21
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60 0.65
0 50 100 150
SNV Index
SCNA−fit log−likelihood: −4522.84
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
1 2 3 4 7
0 50 100 150
SNV Index
Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index


Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
3m2
2m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio


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


Allelic fraction (somatic)
0.1
0.2
0.3
0.4
0.5
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio


Frequency
0
2
4
6
8
10
12
0.10
0.15
0.20
0.25
0.30
0.35
0.40
Cellular fraction