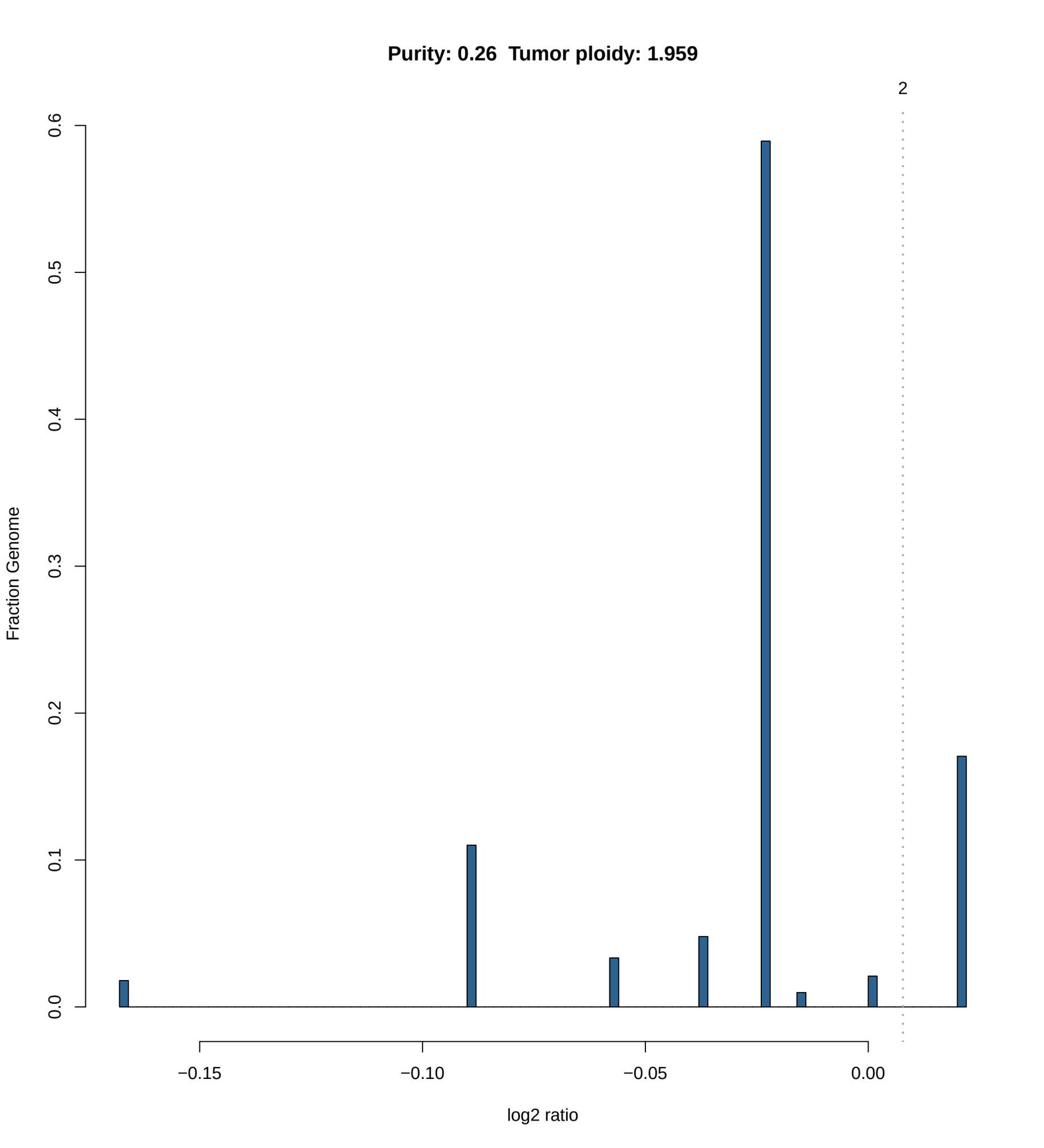
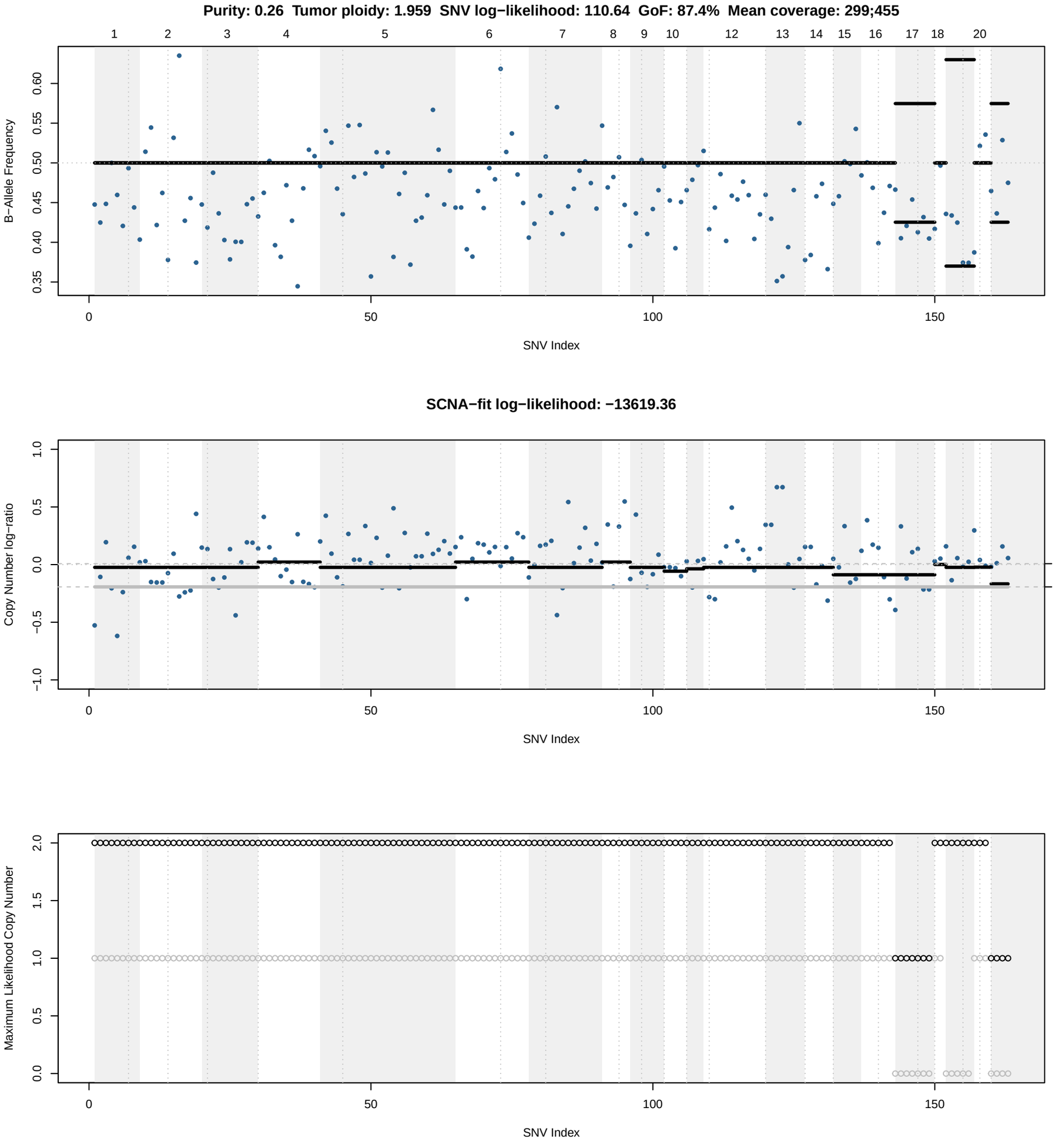
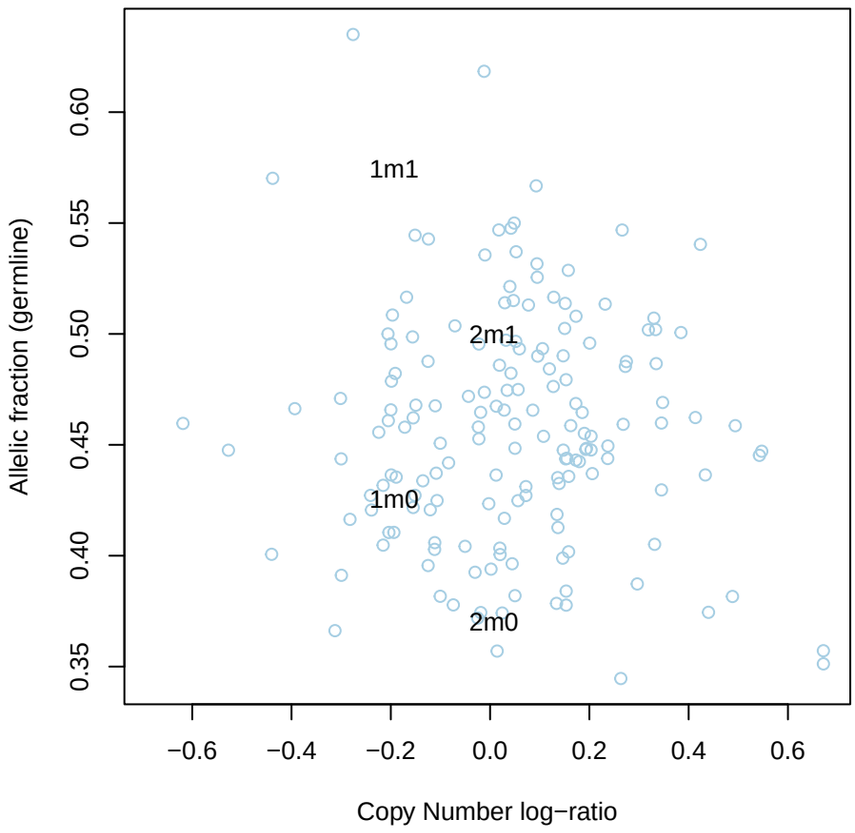
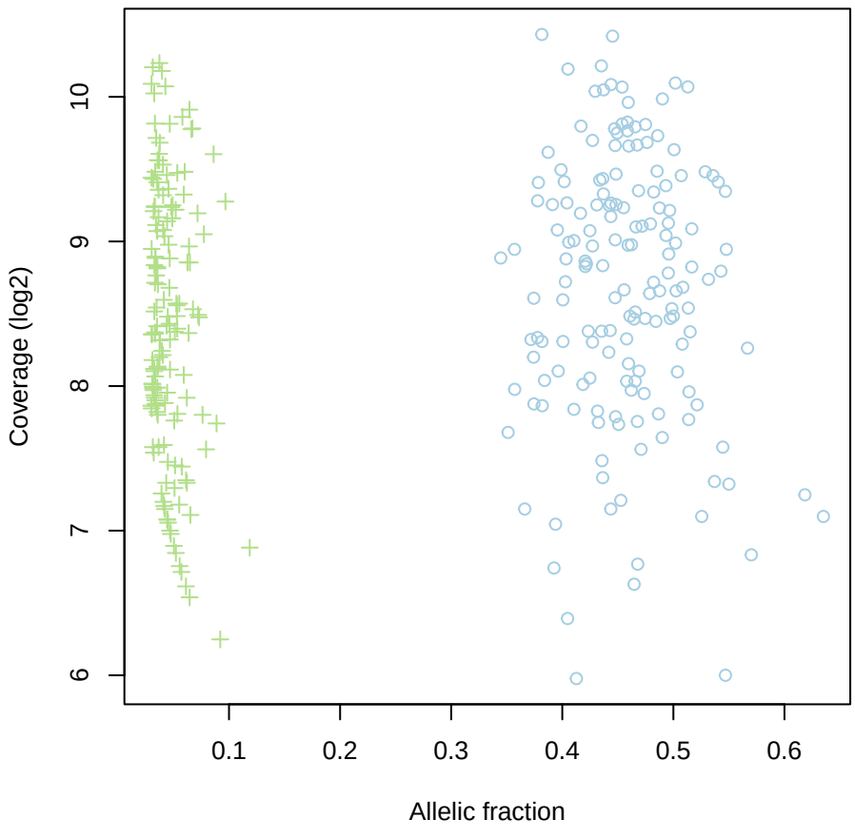
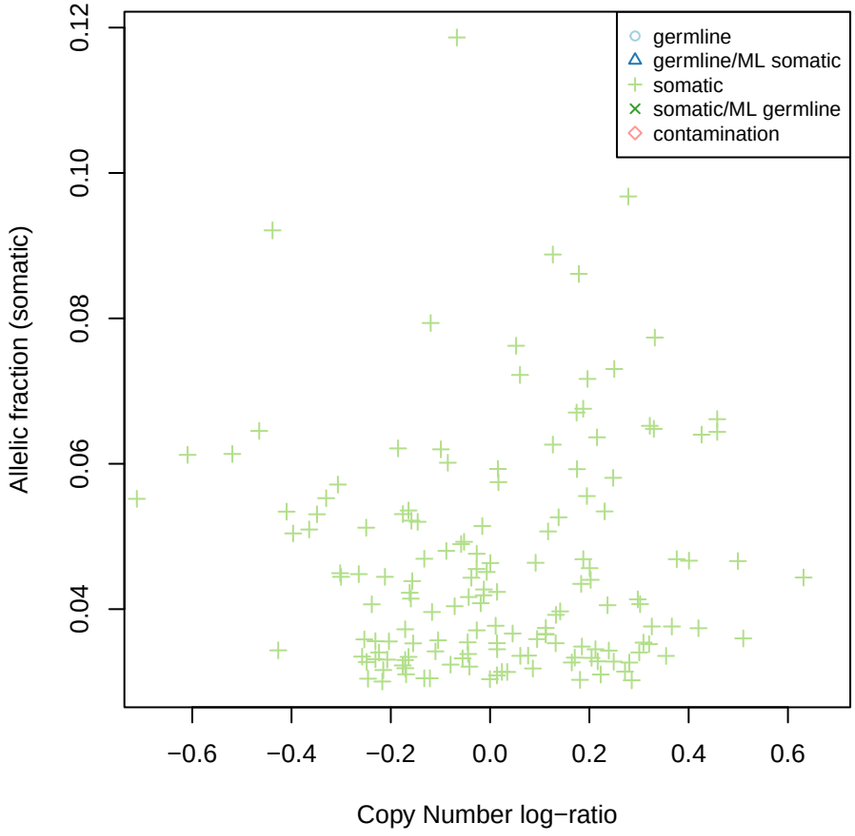
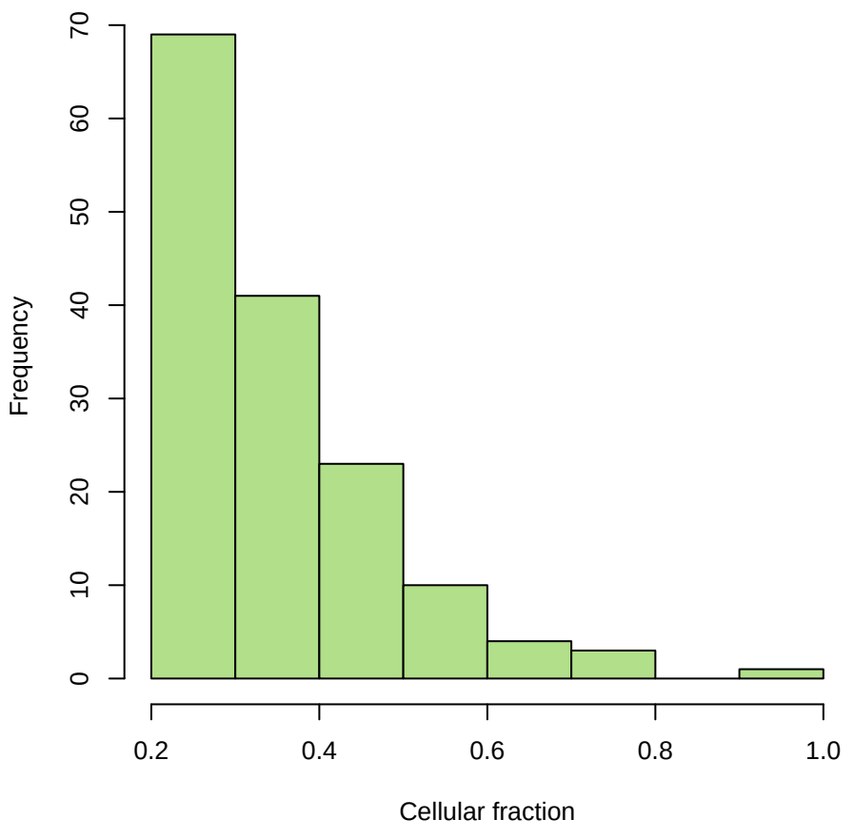

Purity: 0.26 Tumor ploidy: 1.959
2
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.6
−0.15
−0.10
−0.05
0.00
log2 ratio

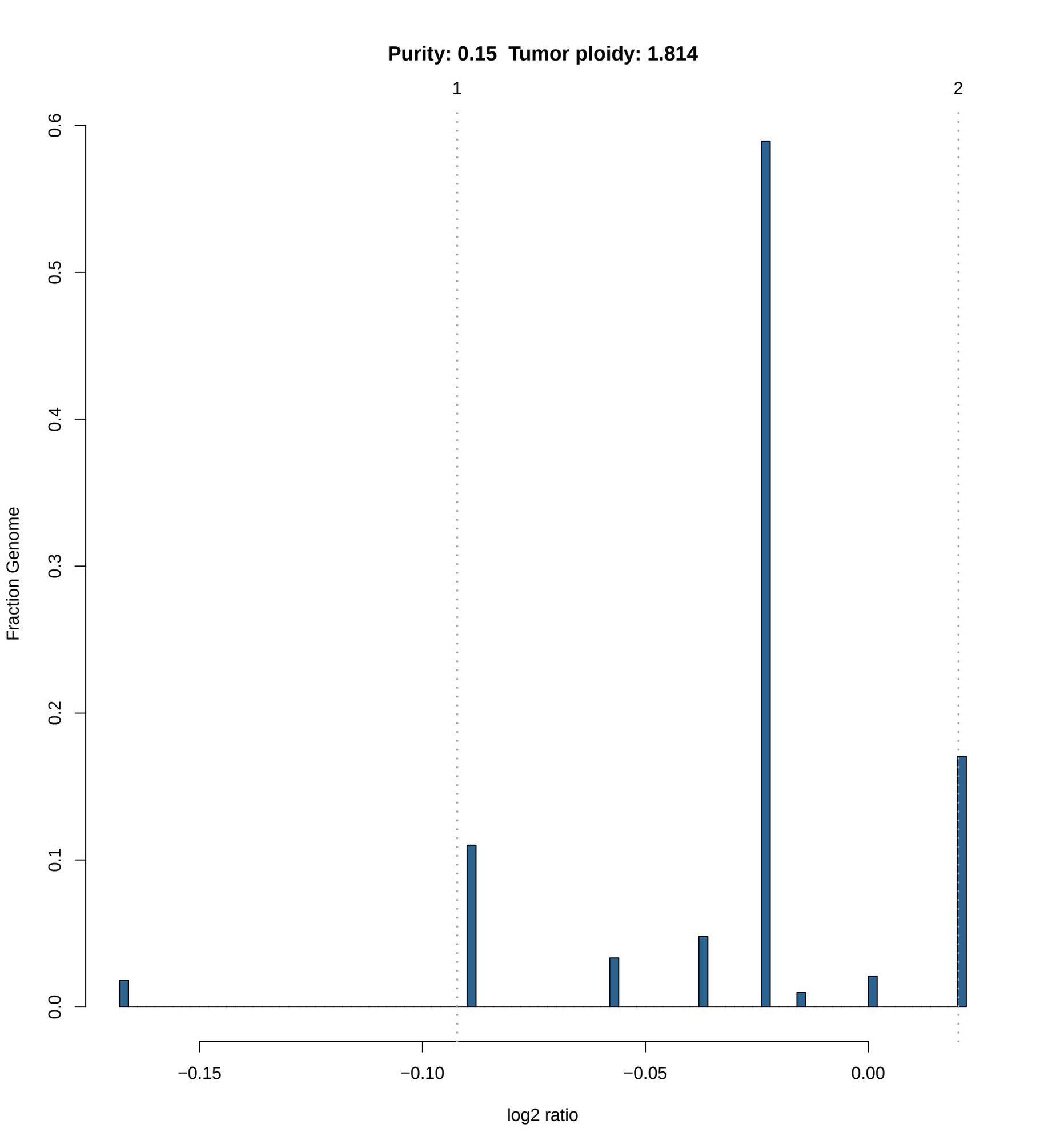

Purity: 0.26 Tumor ploidy: 1.959 SNV log−likelihood: 110.64 GoF: 87.4% Mean coverage: 299;455
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 18 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index
SCNA−fit log−likelihood: −13619.36
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2
0 50 100 150
SNV Index
Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 50 100 150
SNV Index

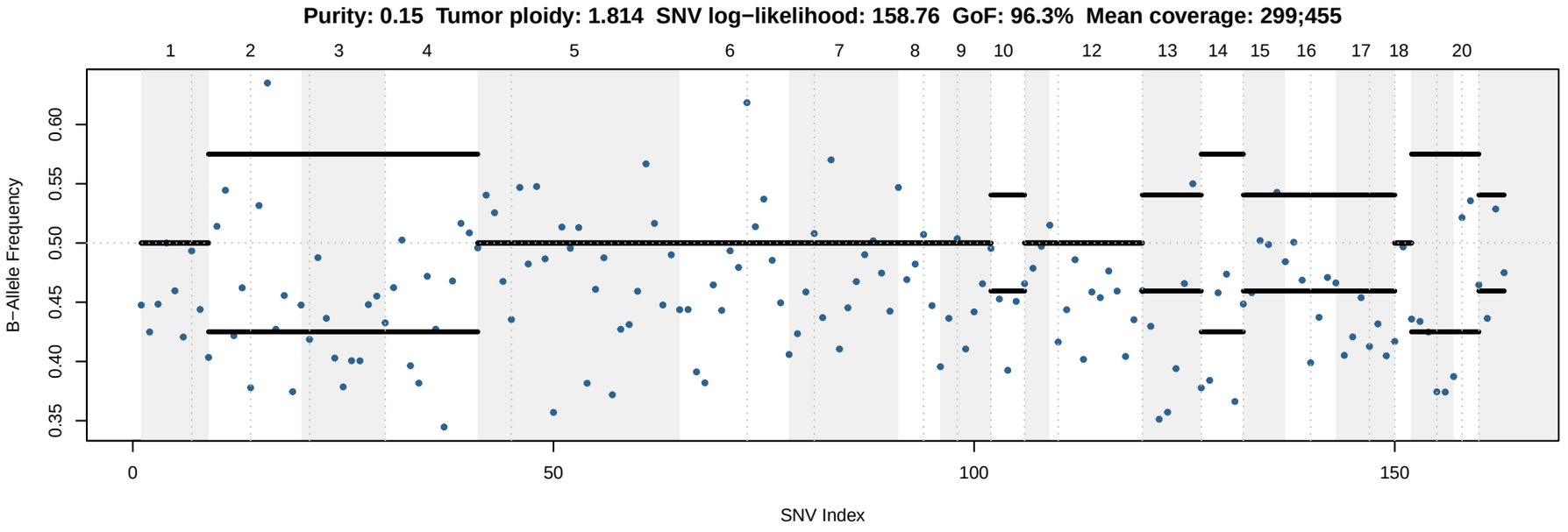

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
1m1
2m1
1m0
2m0
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

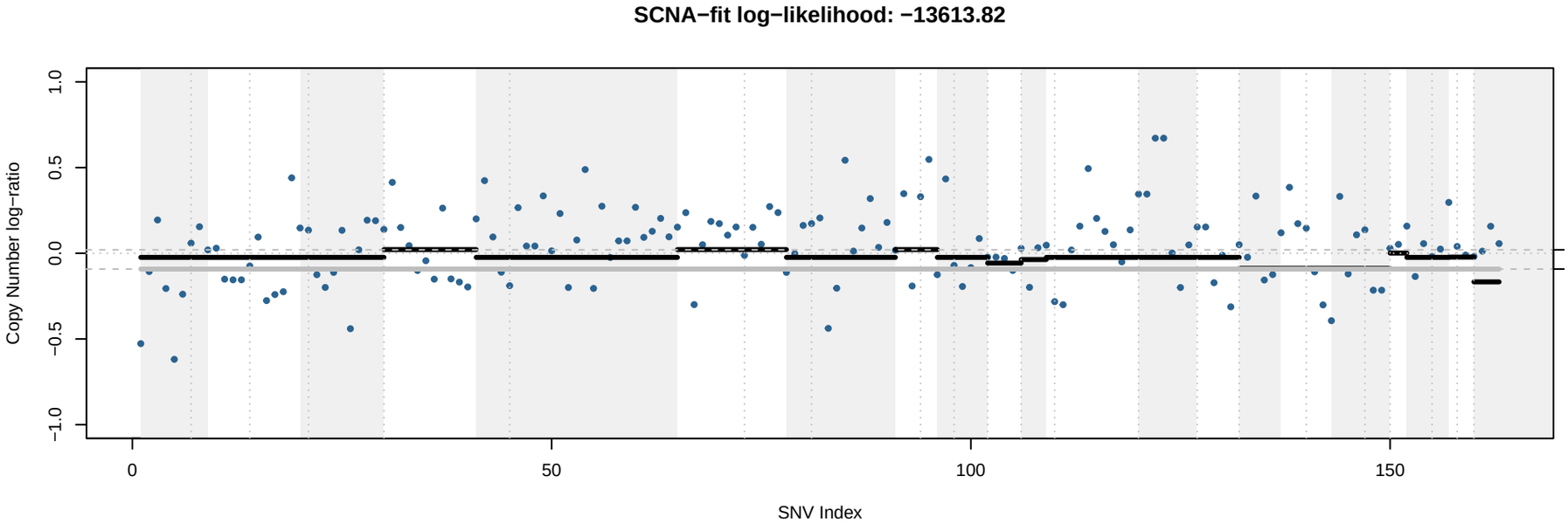

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

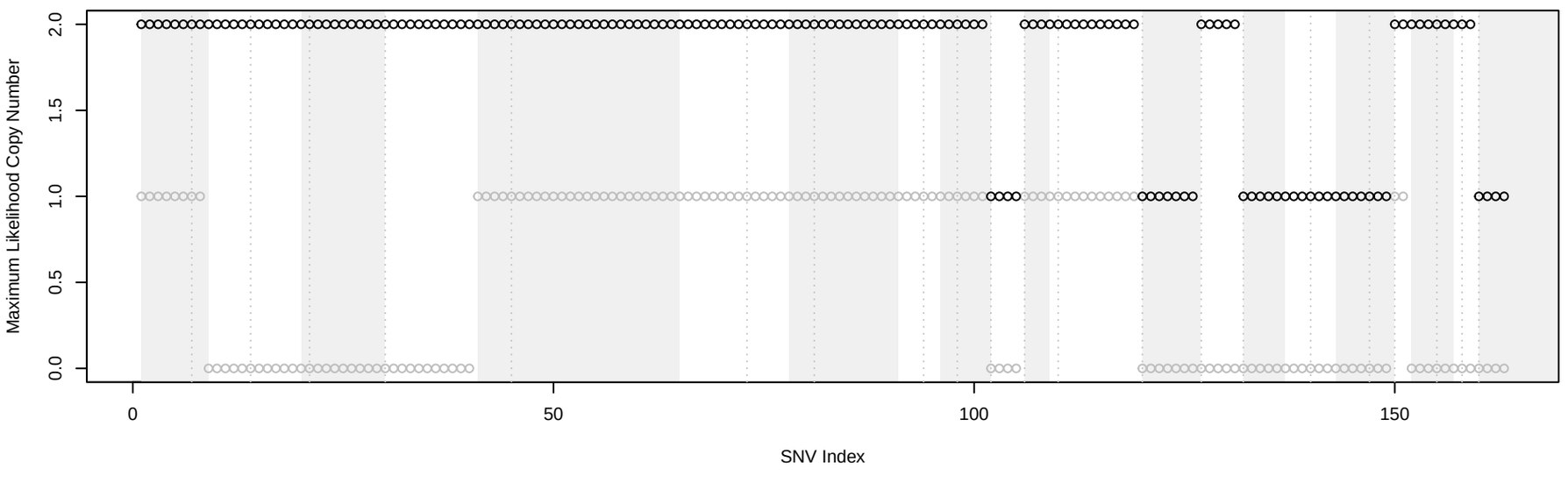

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

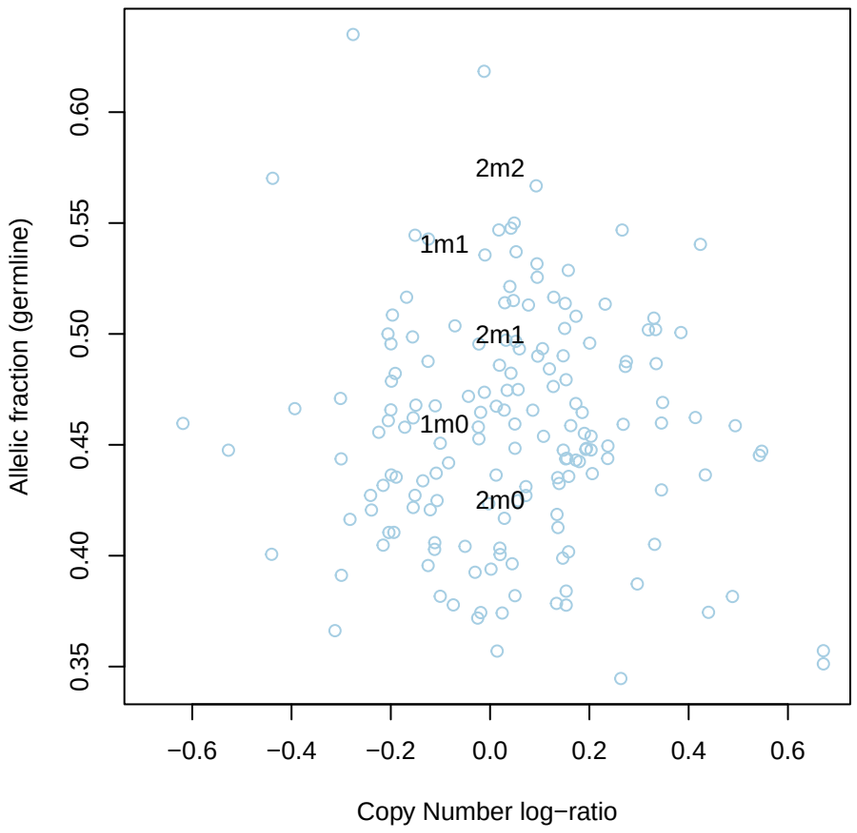

Frequency
0
10
20
30
40
50
60
70
0.2
0.4
0.6
0.8
1.0
Cellular fraction

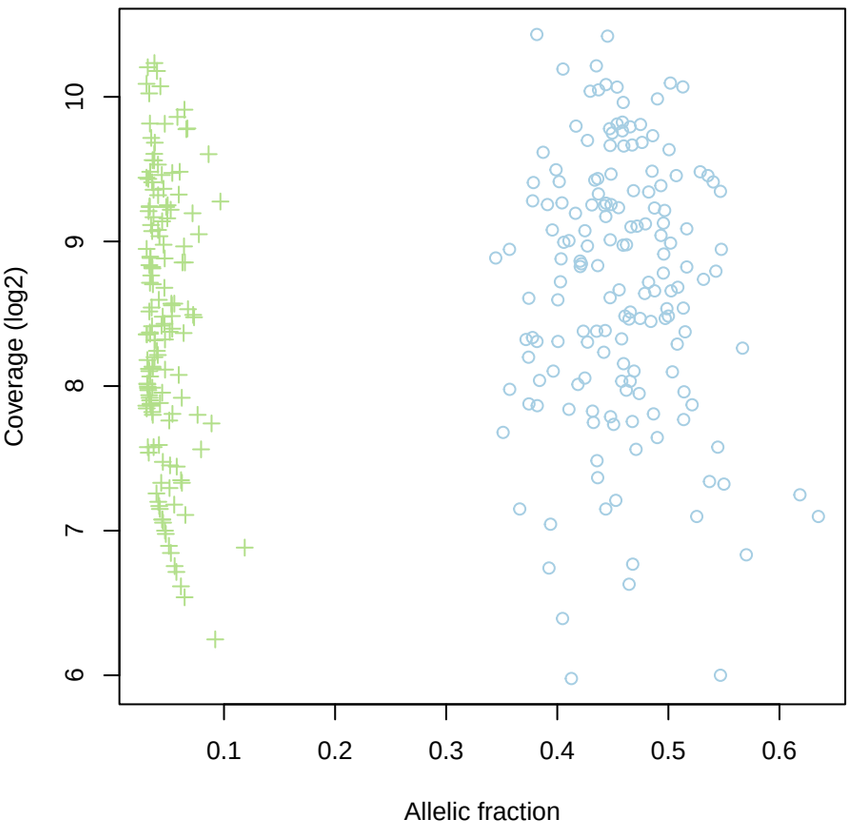

Purity: 0.15 Tumor ploidy: 1.814
1
2
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−0.15
−0.10
−0.05
0.00
log2 ratio

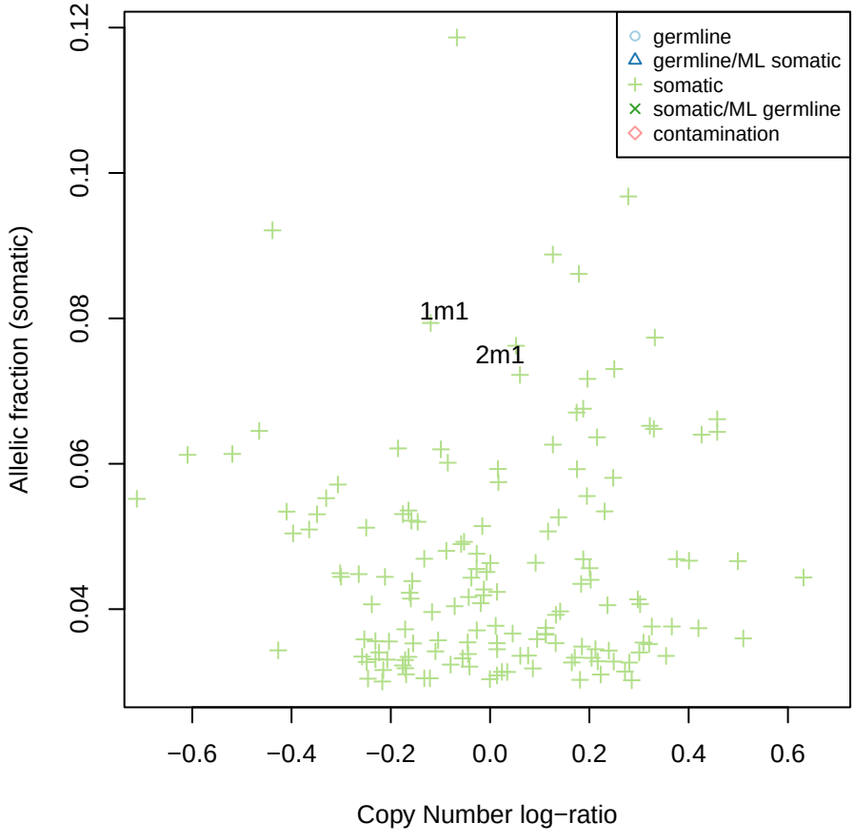

Purity: 0.15 Tumor ploidy: 1.814 SNV log−likelihood: 158.76 GoF: 96.3% Mean coverage: 299;455
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 18 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

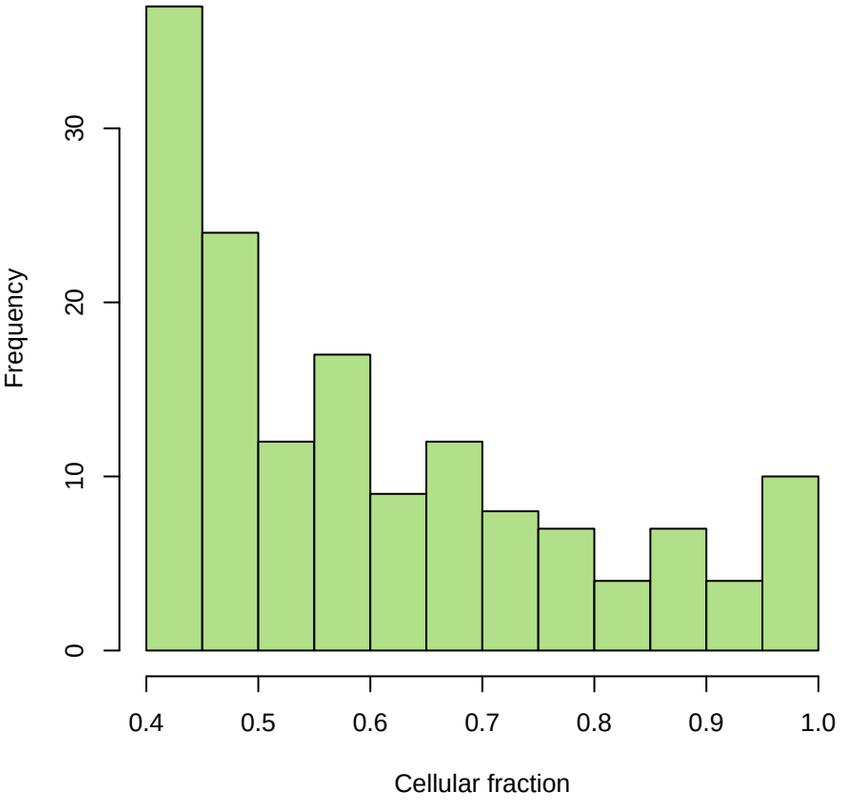

SCNA−fit log−likelihood: −13613.82
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
1
0 50 100 150
SNV Index

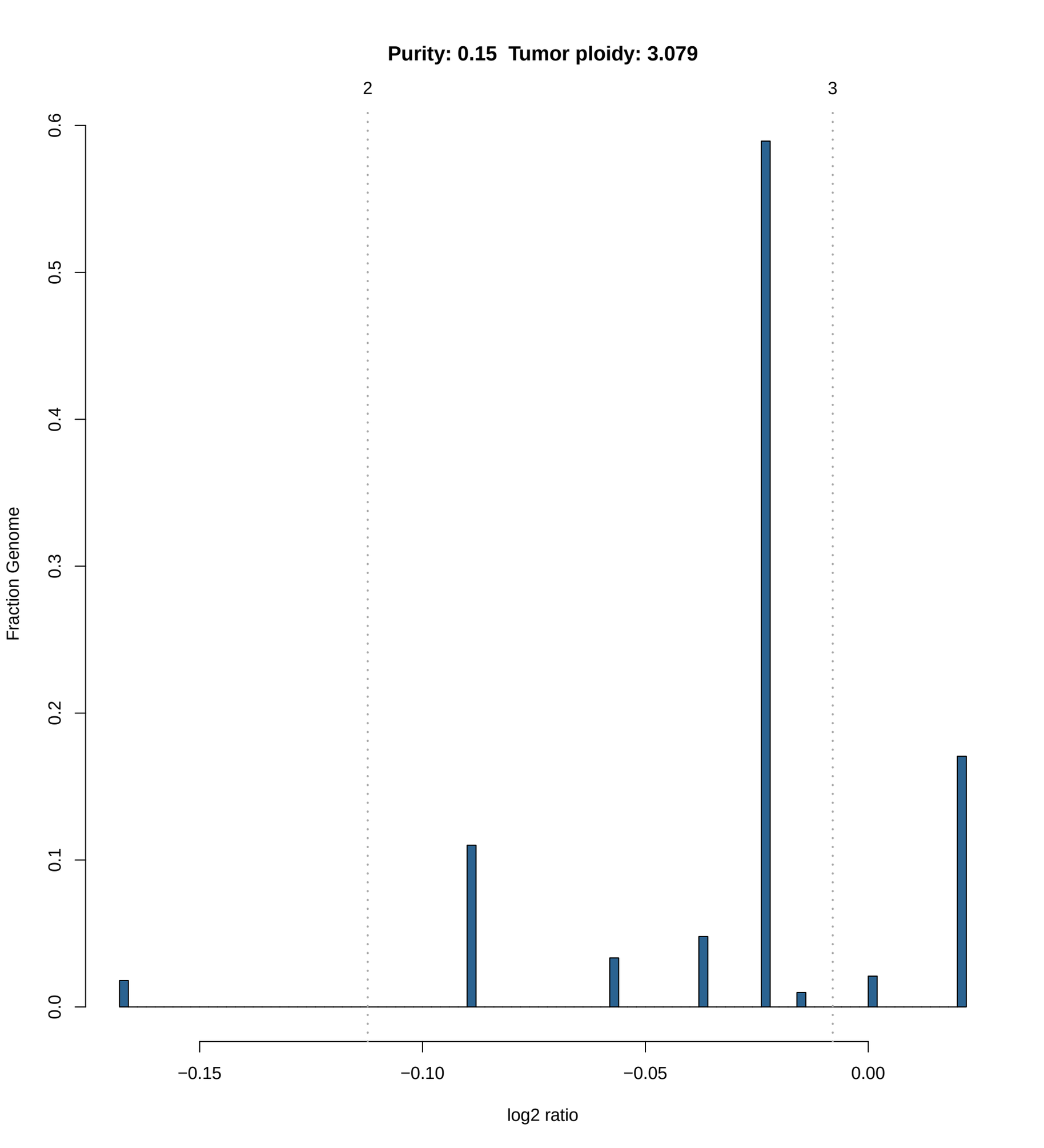

Maximum Likelihood Copy Number
2.0 1.5 1.0 0.5 0.0
0 50 100 150
SNV Index

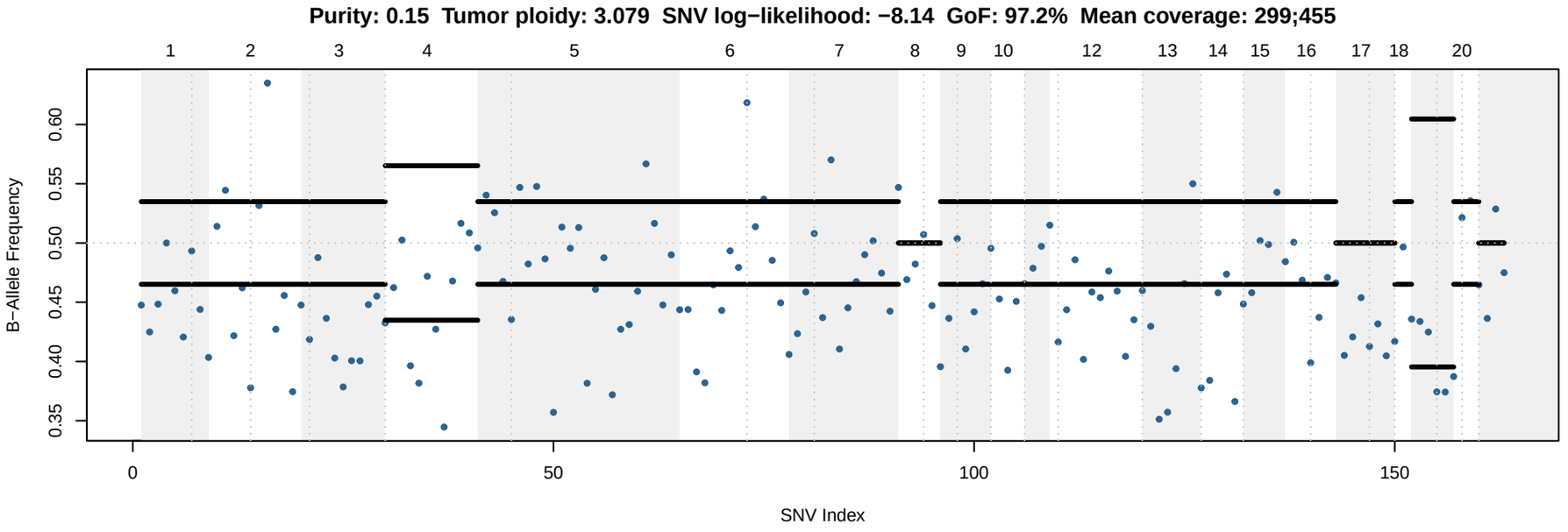

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
2m2
1m1
2m1
1m0
2m0
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

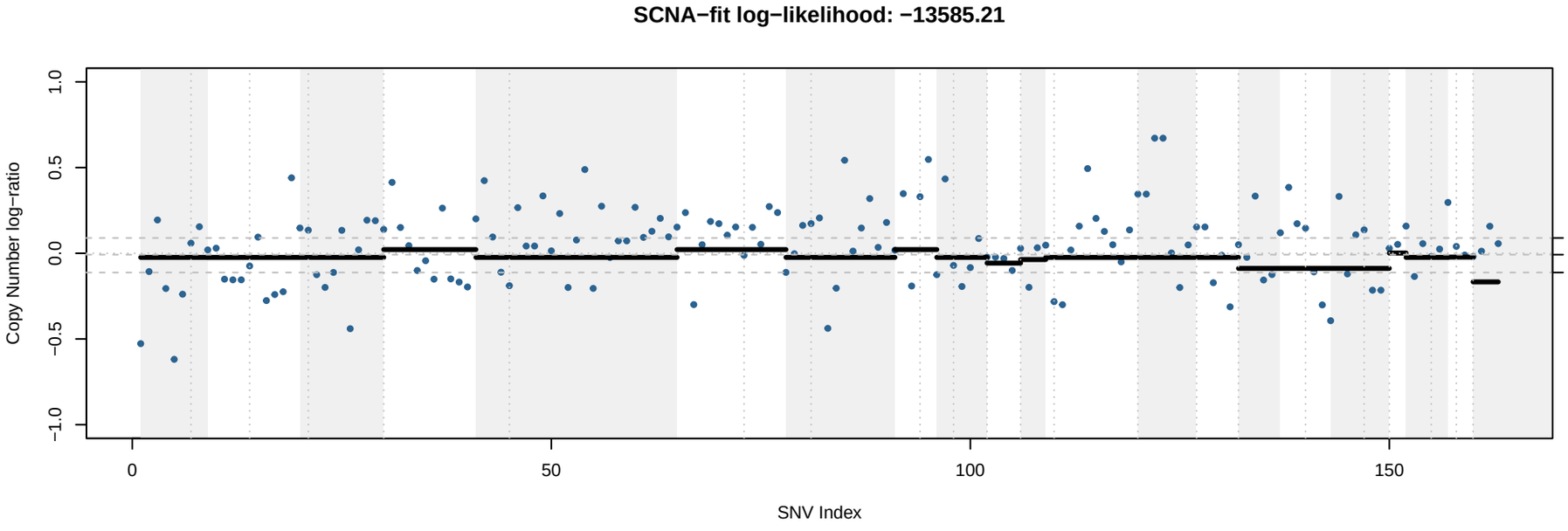

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

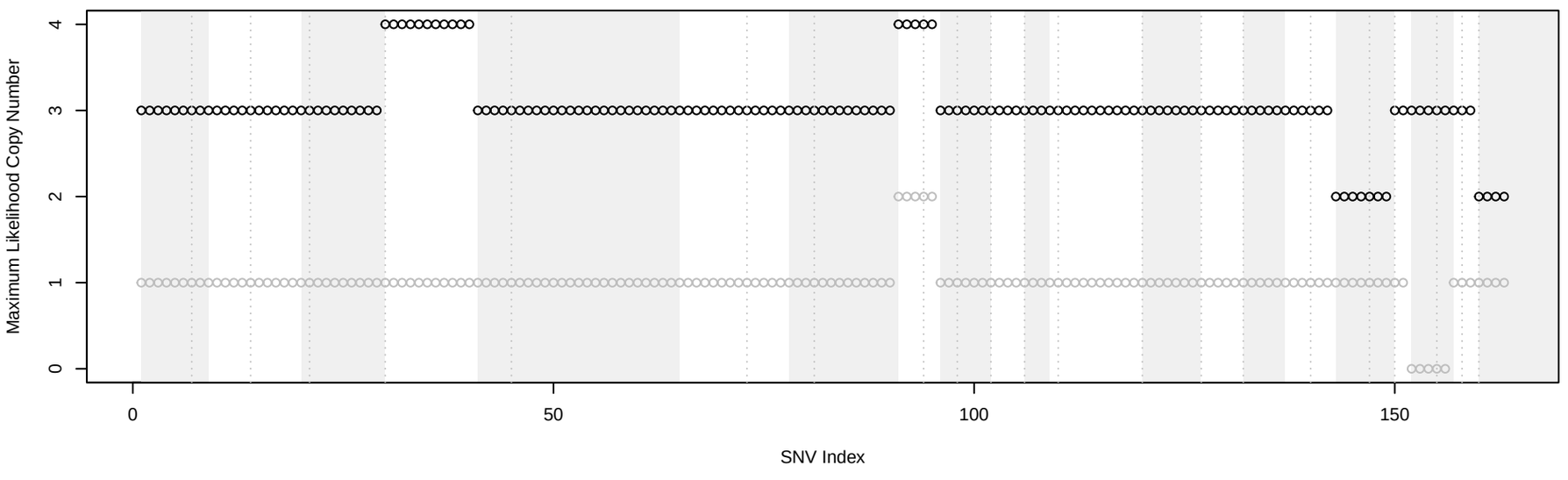

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

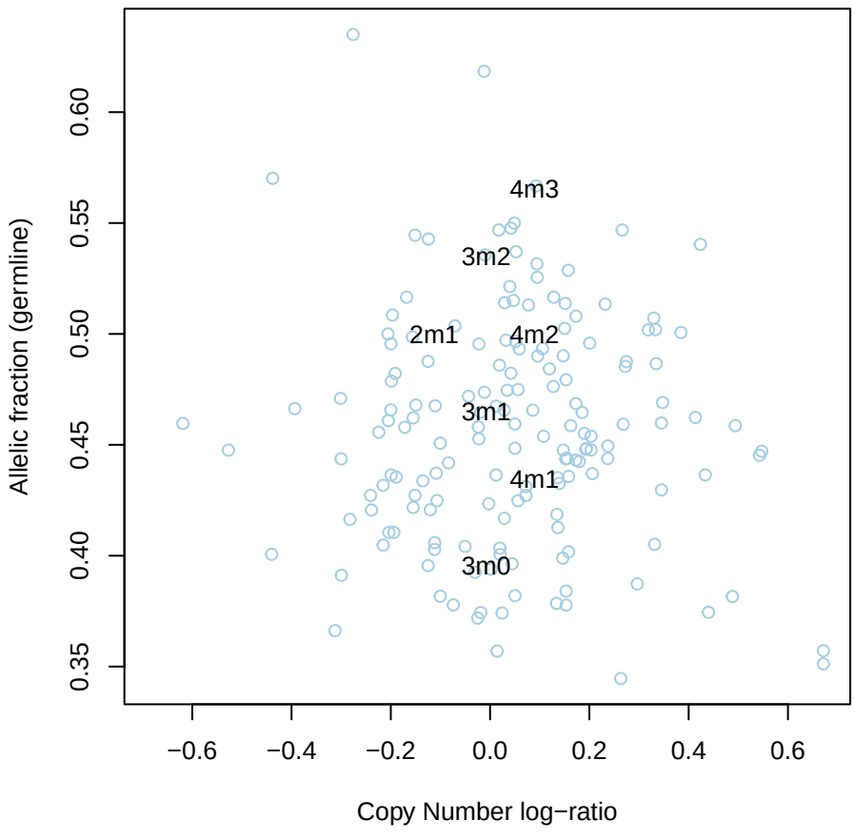

Frequency
0
10
20
30
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

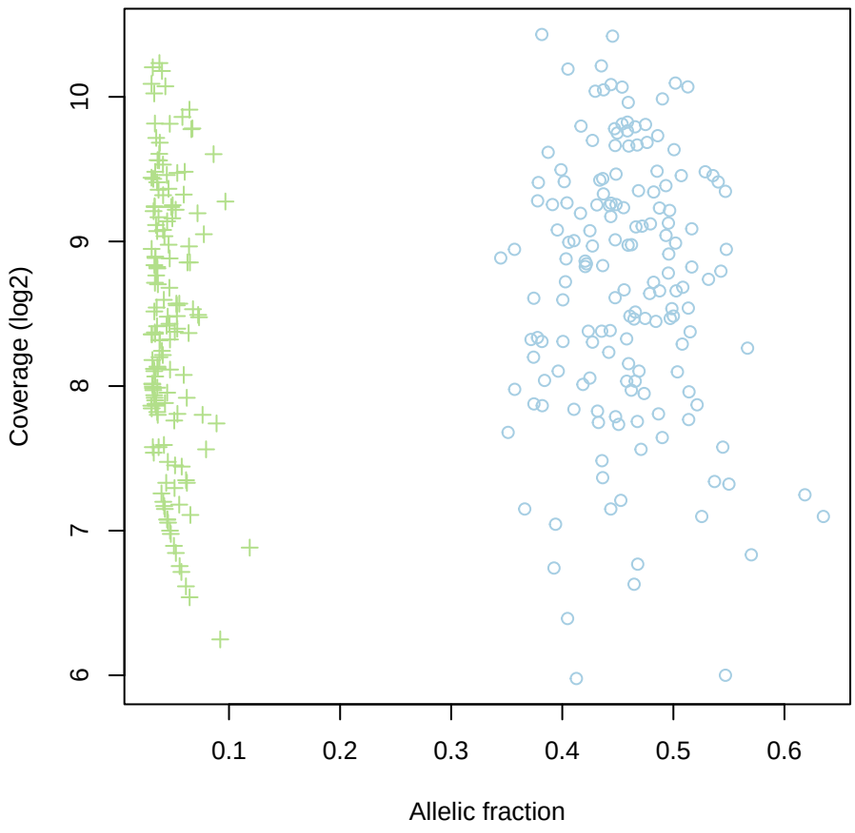

Purity: 0.15 Tumor ploidy: 3.079
2
3
0.6
0.5
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.15
−0.10
−0.05
0.00
log2 ratio

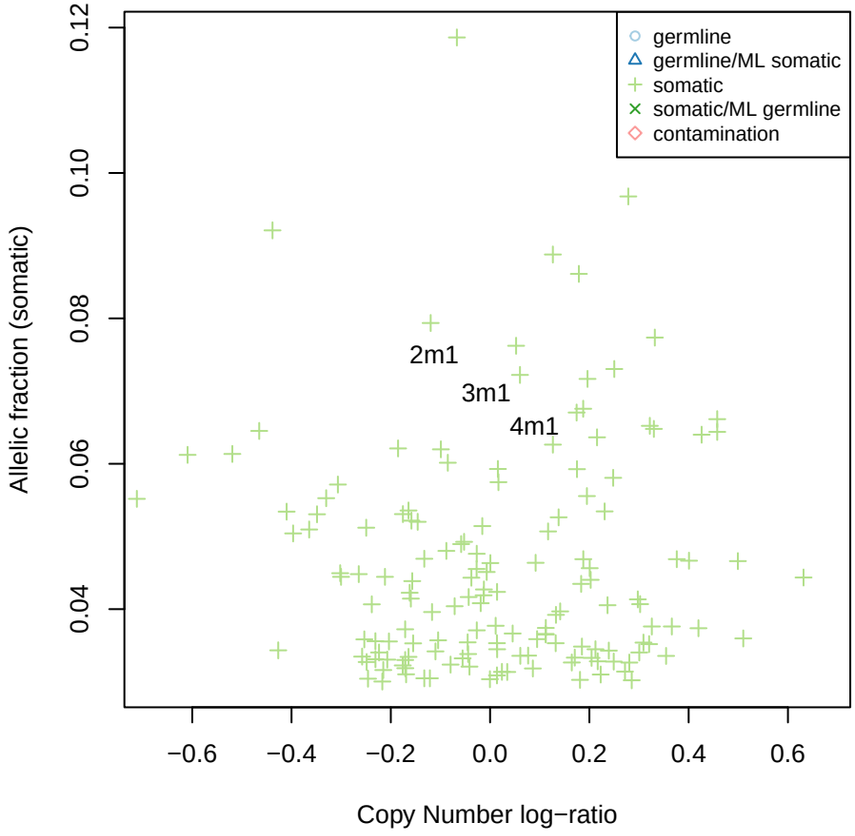

Purity: 0.15 Tumor ploidy: 3.079 SNV log−likelihood: −8.14 GoF: 97.2% Mean coverage: 299;455
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 18 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

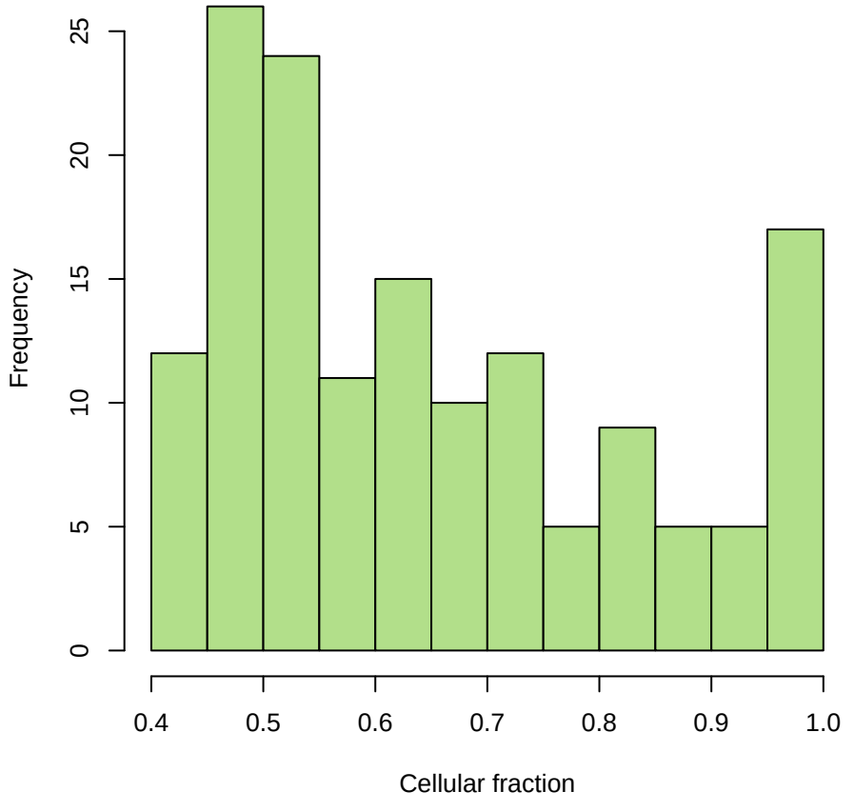

SCNA−fit log−likelihood: −13585.21
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 4
0 50 100 150
SNV Index

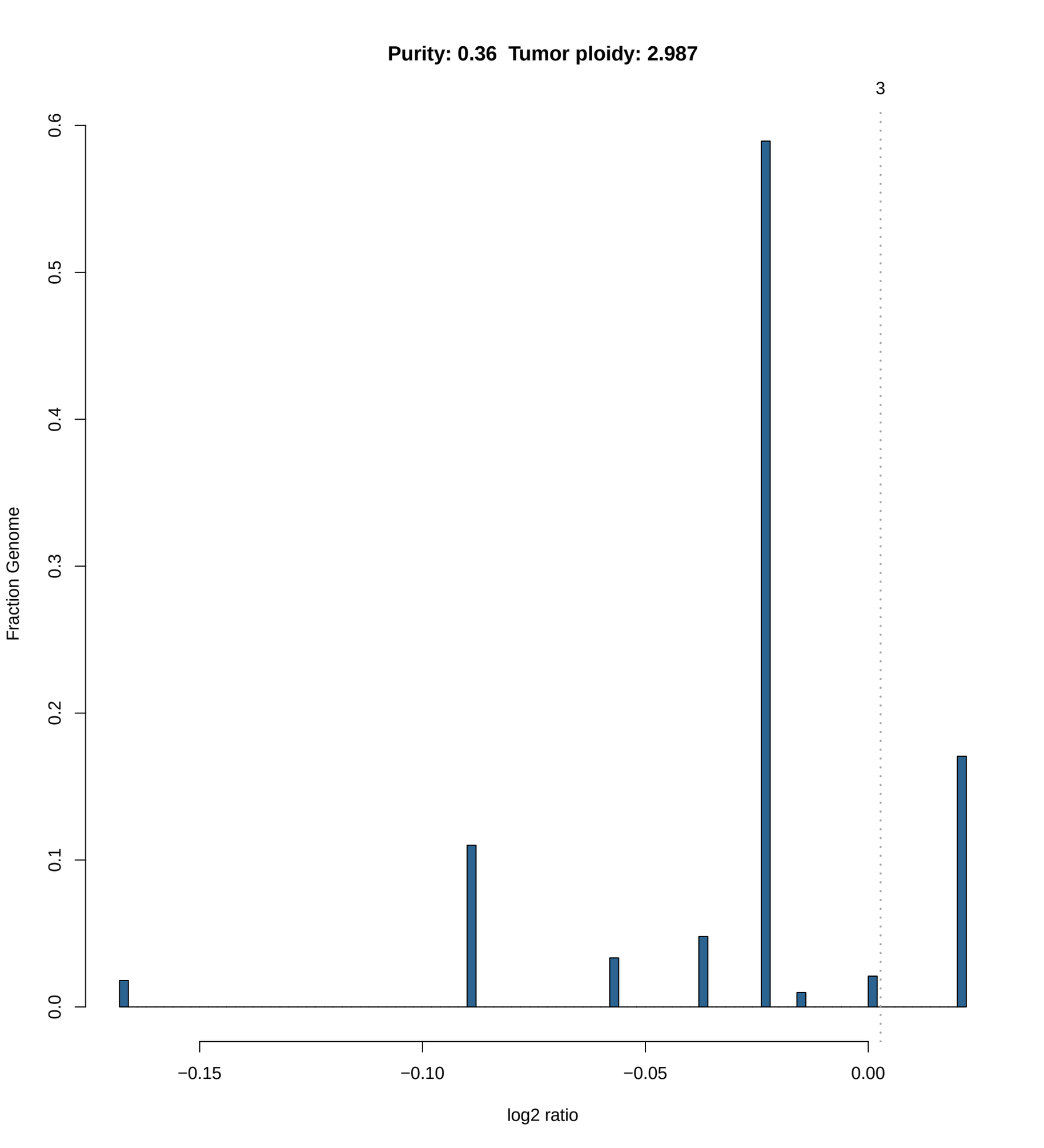

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

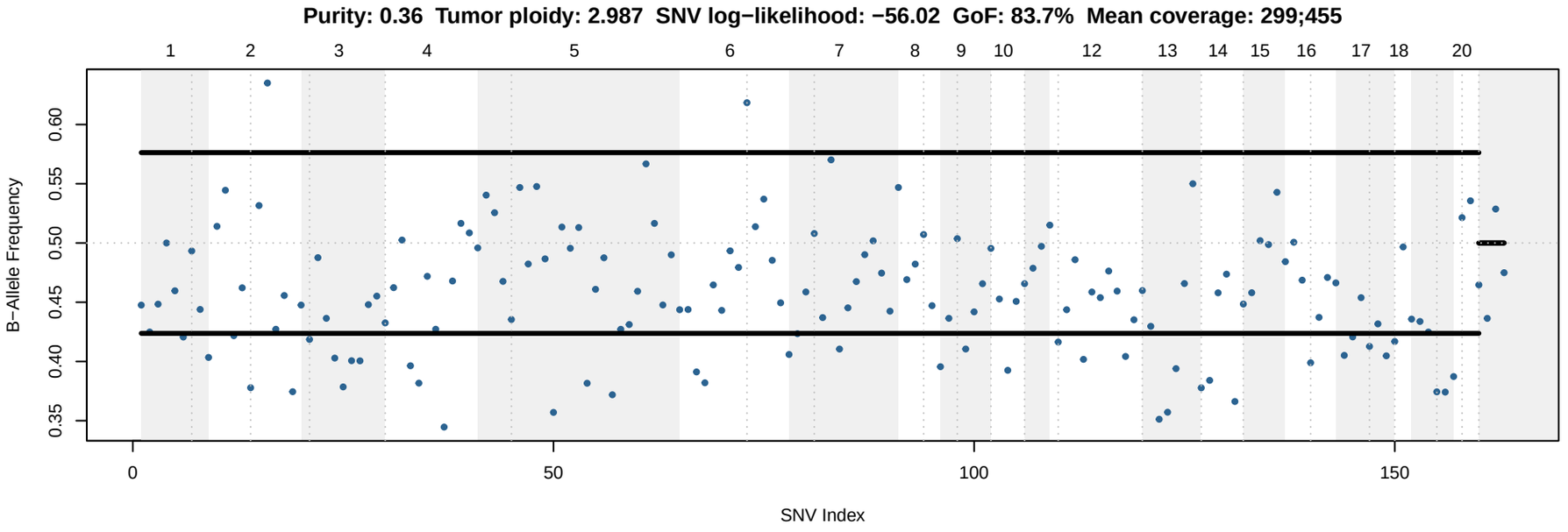

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
4m3
3m2
2m1
4m2
3m1
4m1
3m0
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

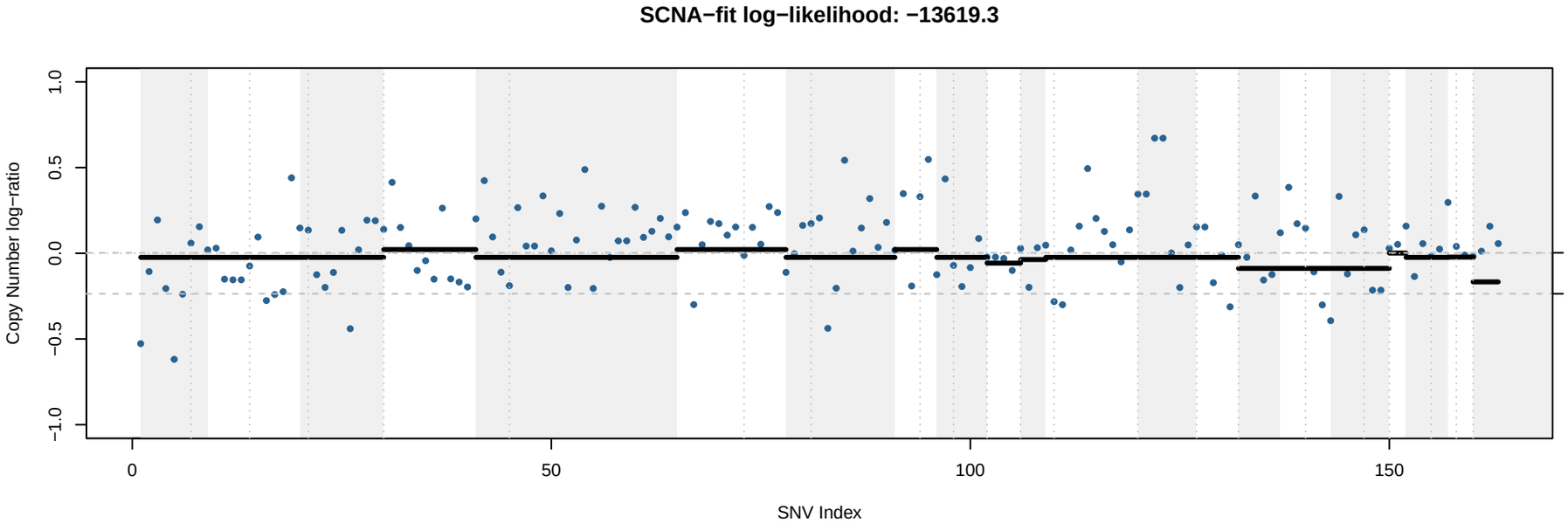

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

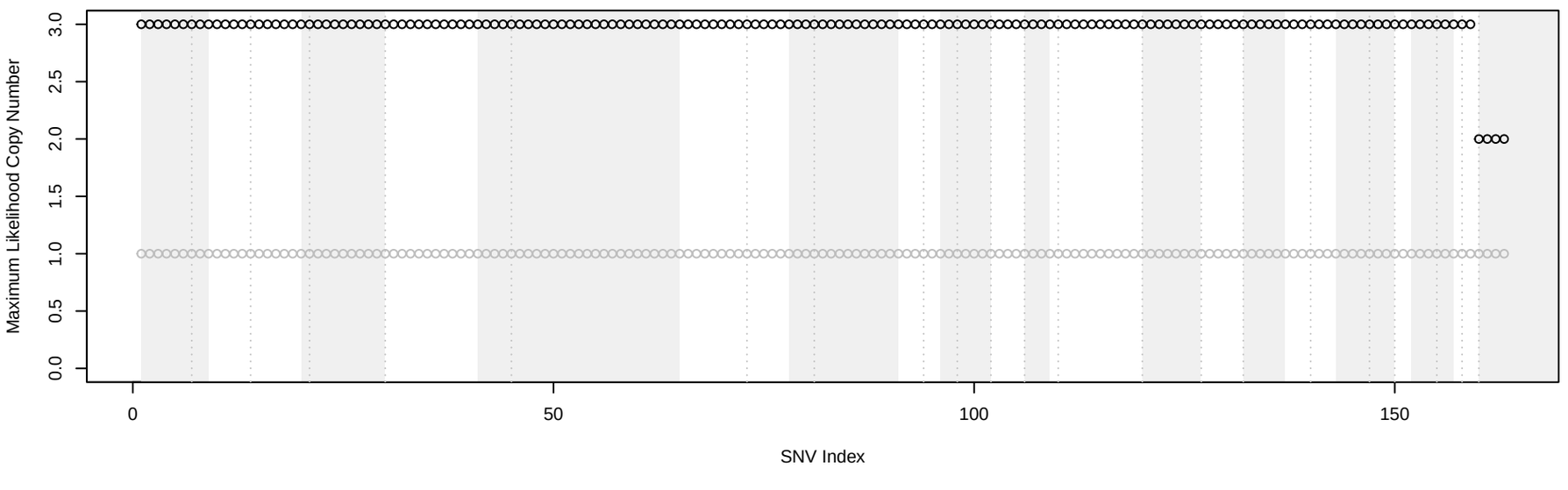

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

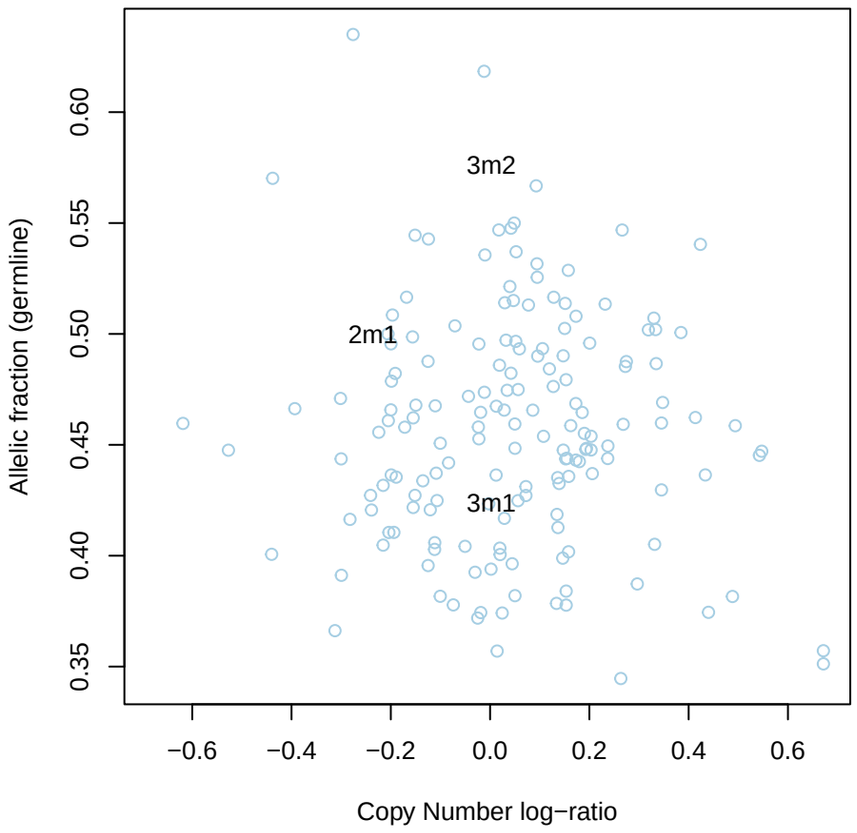

Frequency
0
5
10
15
20
25
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

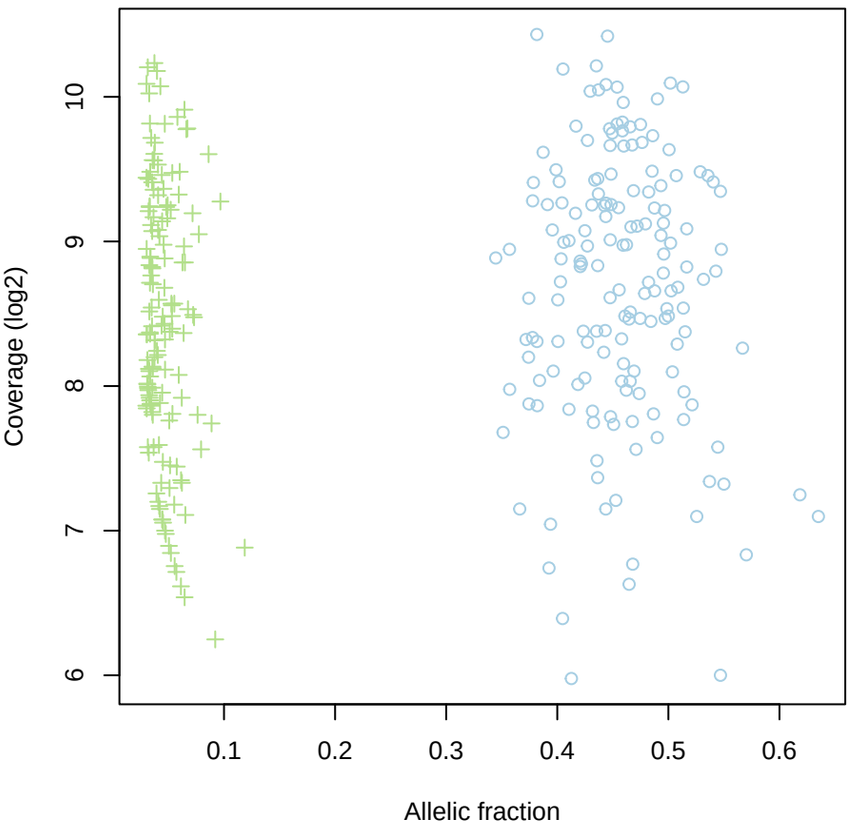

Purity: 0.36 Tumor ploidy: 2.987
3
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.6
−0.15
−0.10
−0.05
0.00
log2 ratio

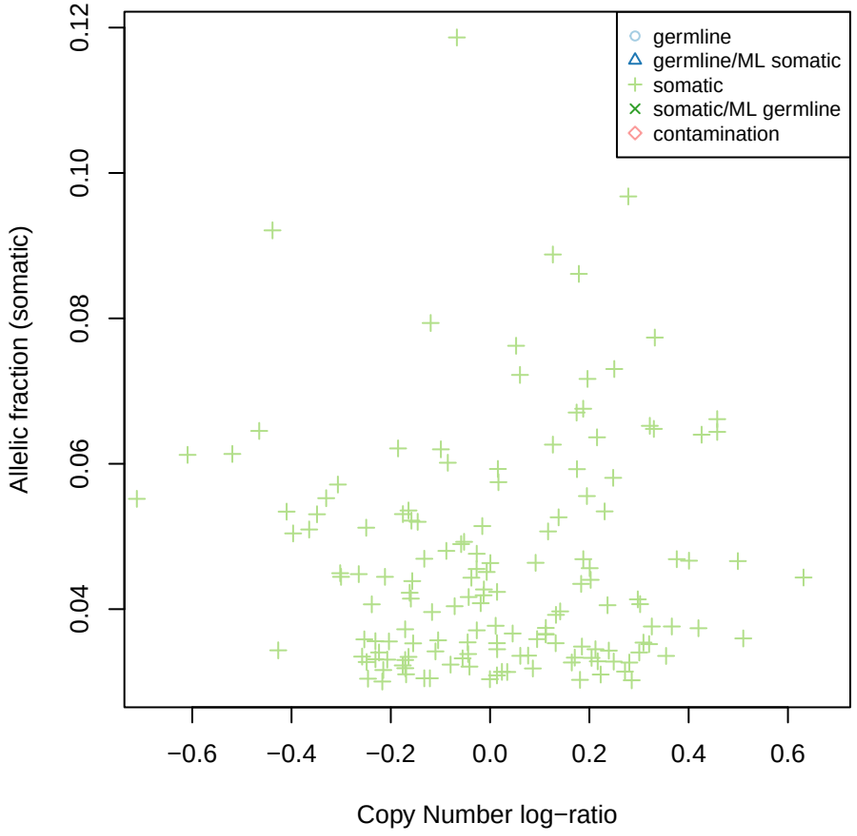

Purity: 0.36 Tumor ploidy: 2.987 SNV log−likelihood: −56.02 GoF: 83.7% Mean coverage: 299;455
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 18 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

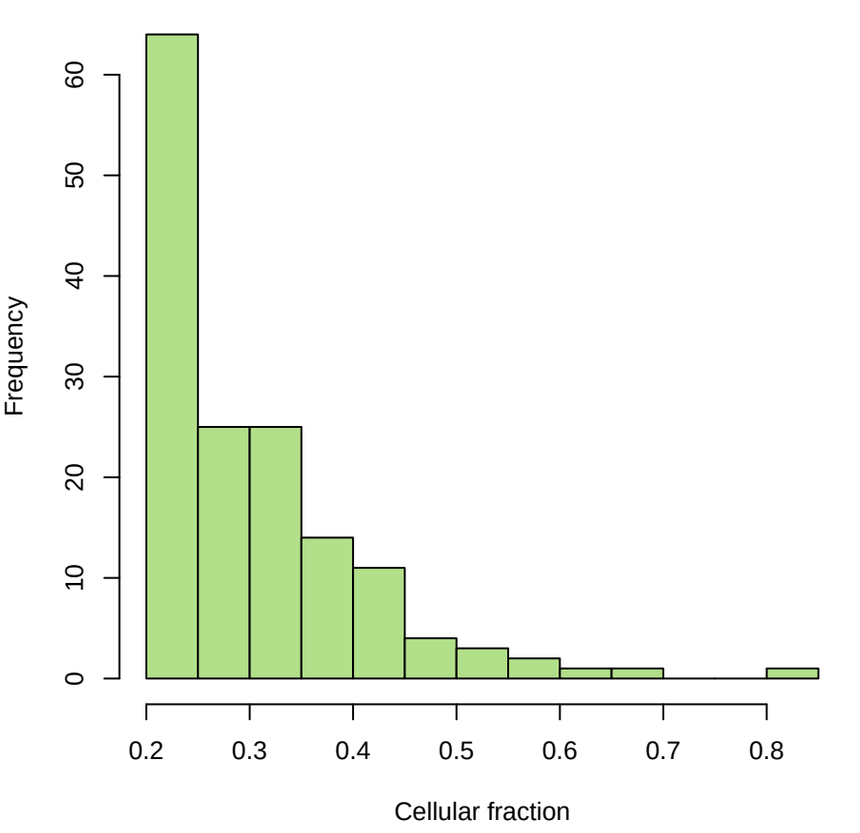

SCNA−fit log−likelihood: −13619.3
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3
0 50 100 150
SNV Index

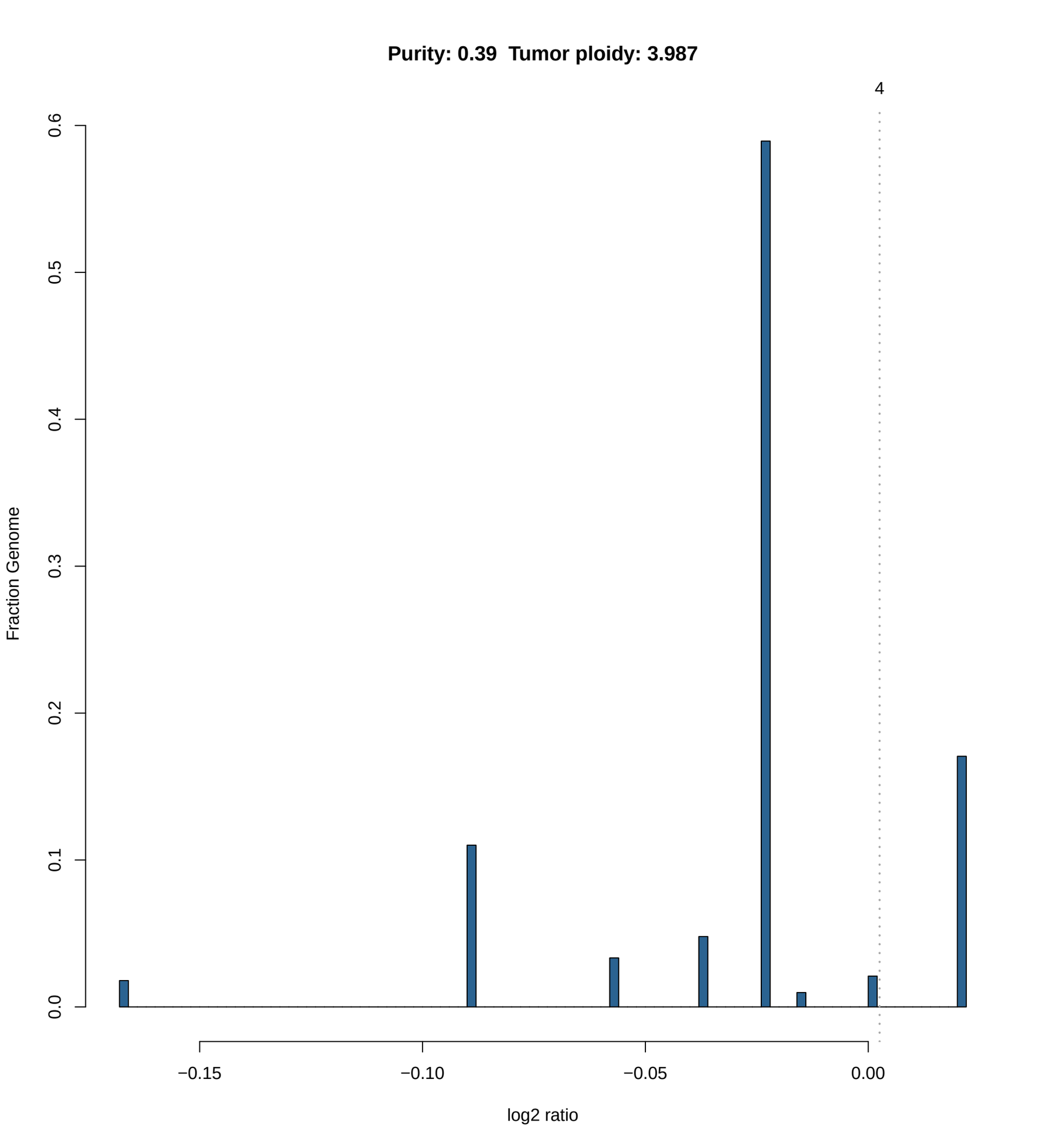

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

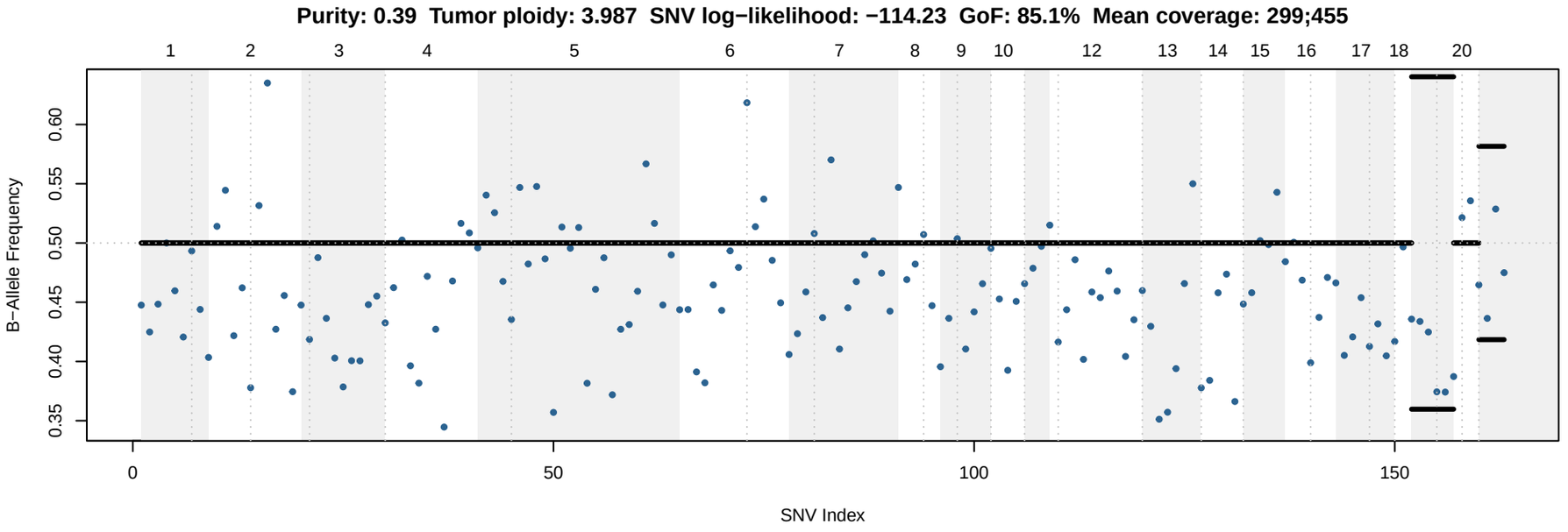

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
3m2
2m1
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

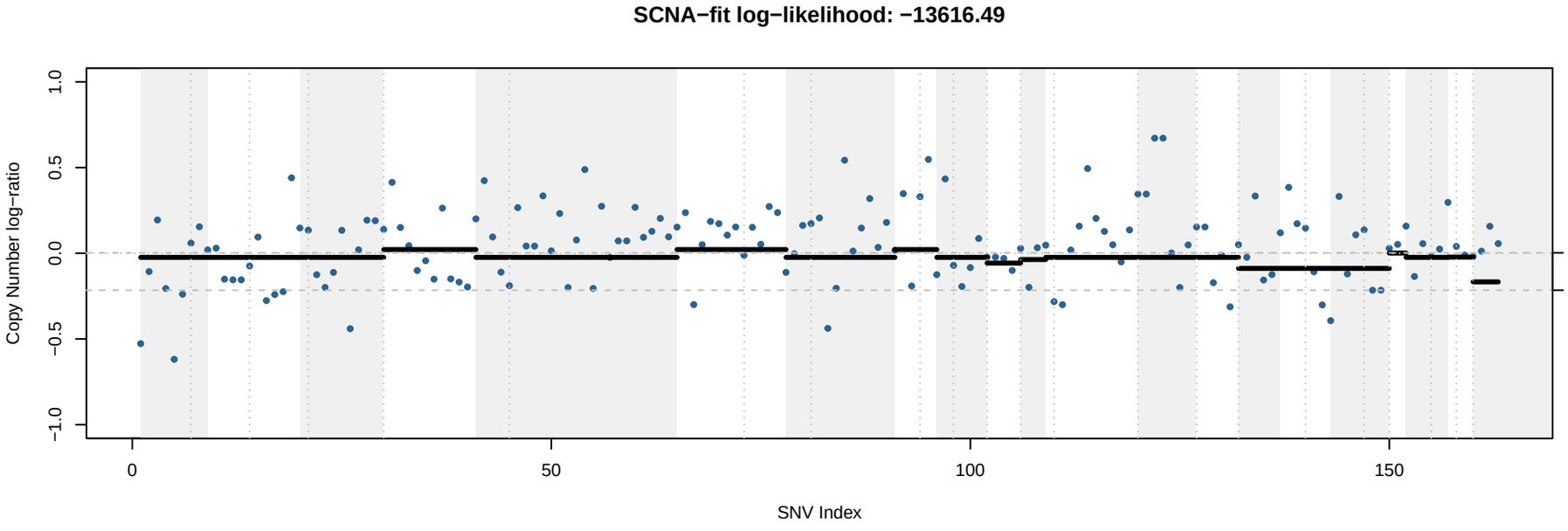

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

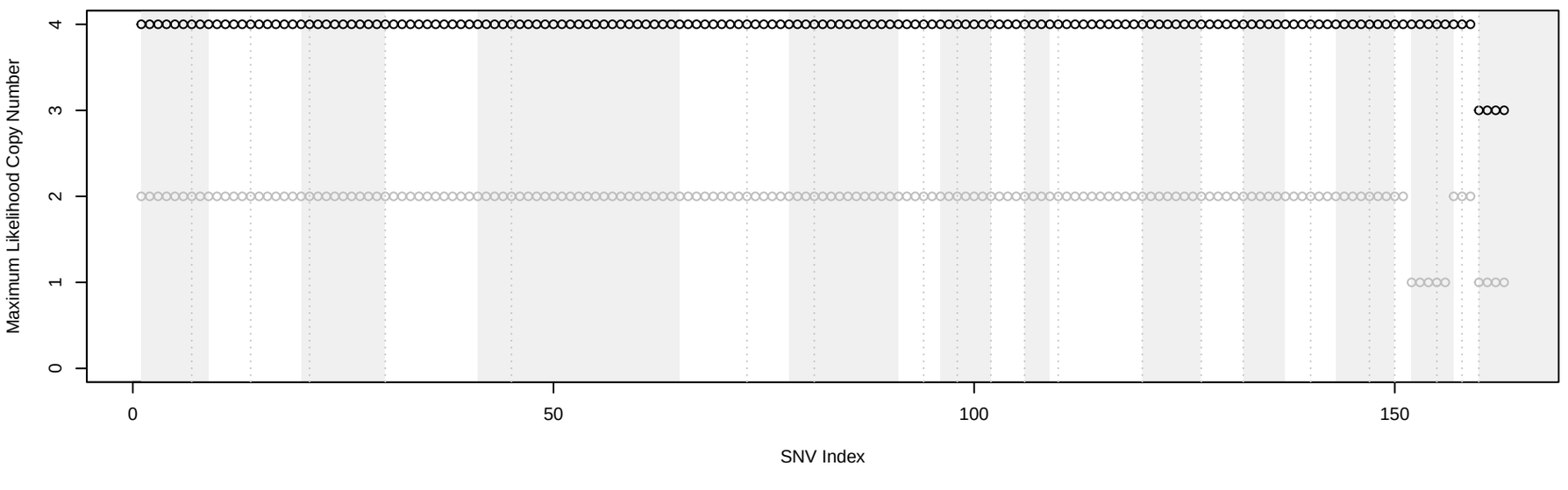

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

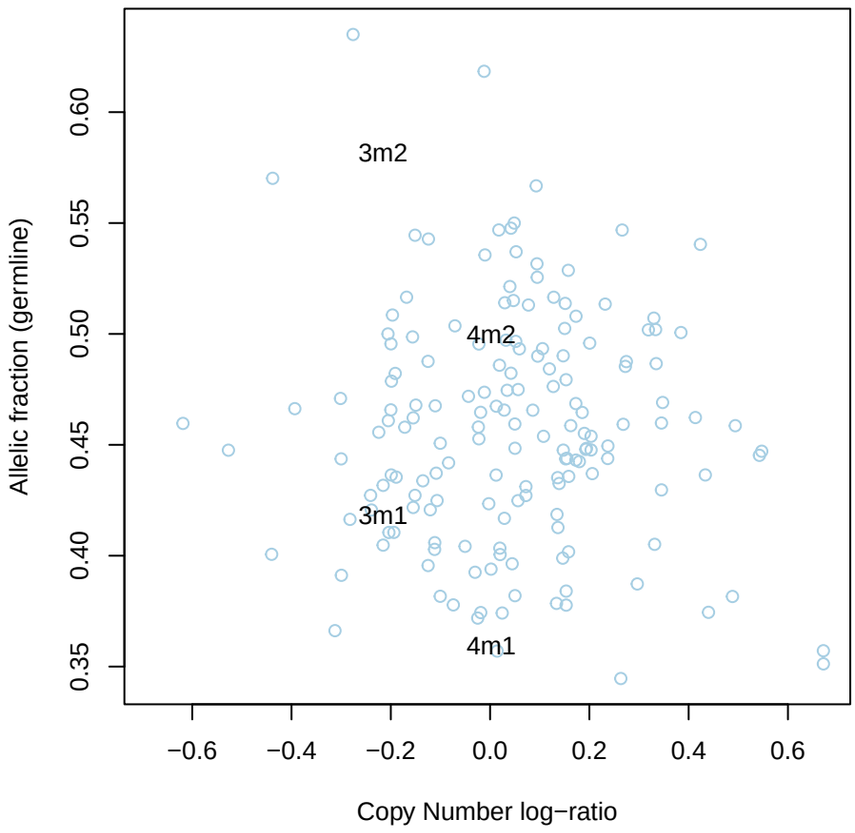

Frequency
0
10
20
30
40
50
60
0.2
0.3
0.4
0.5
0.6
0.7
0.8
Cellular fraction

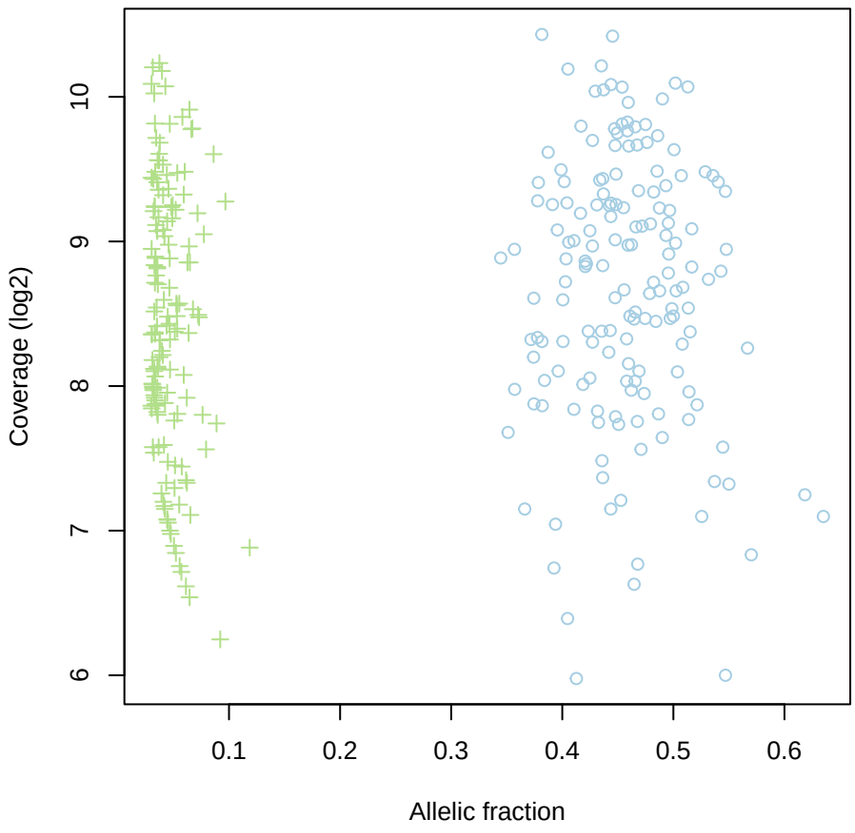

Purity: 0.39 Tumor ploidy: 3.987
4
0.6
0.5
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.15
−0.10
−0.05
0.00
log2 ratio

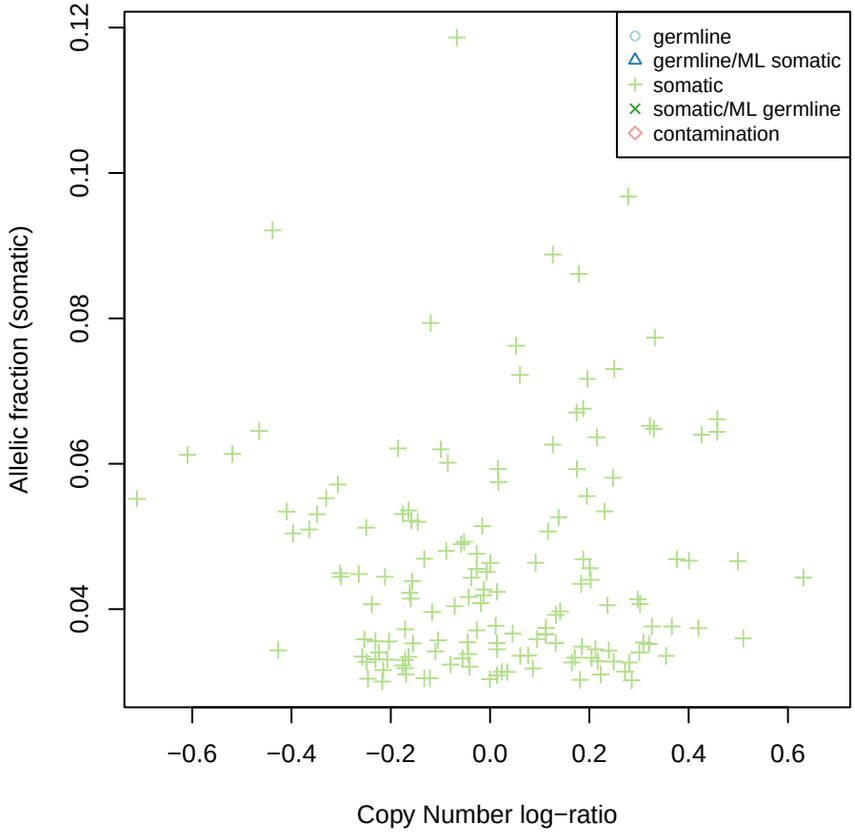

Purity: 0.39 Tumor ploidy: 3.987 SNV log−likelihood: −114.23 GoF: 85.1% Mean coverage: 299;455
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 18 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

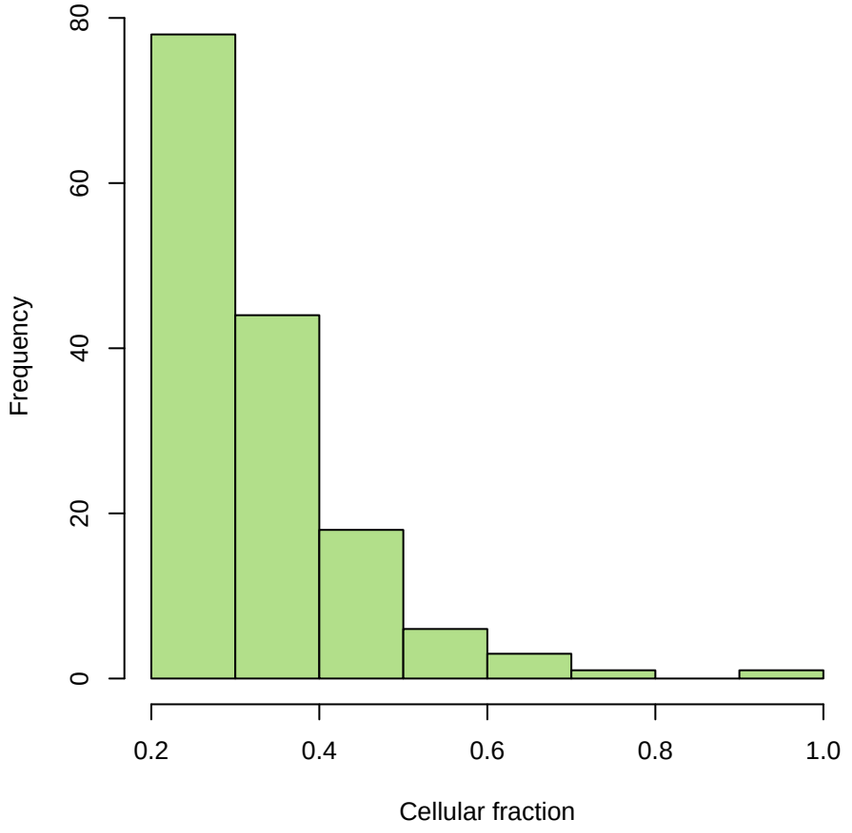

SCNA−fit log−likelihood: −13616.49
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4
3
0 50 100 150
SNV Index

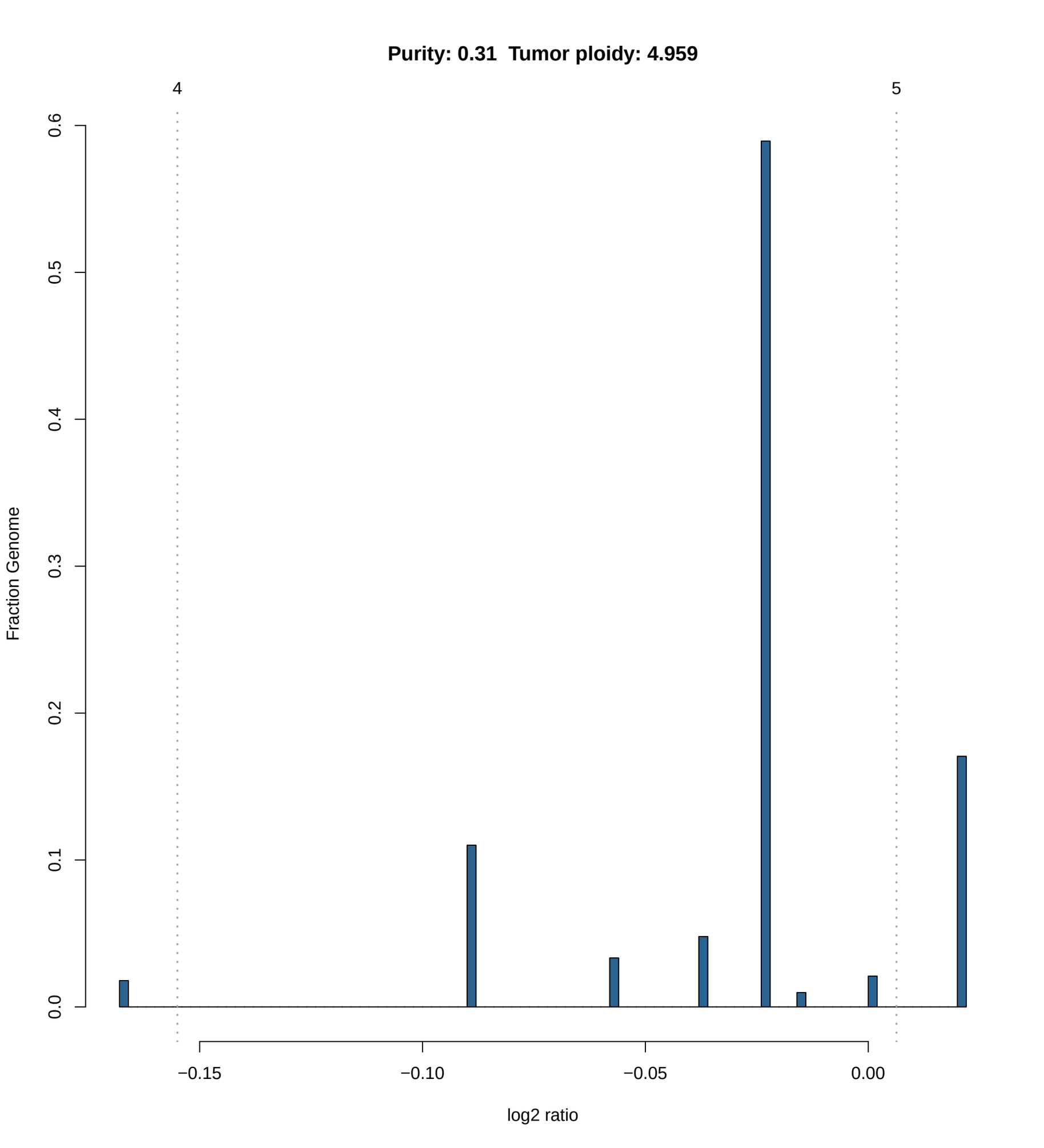

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

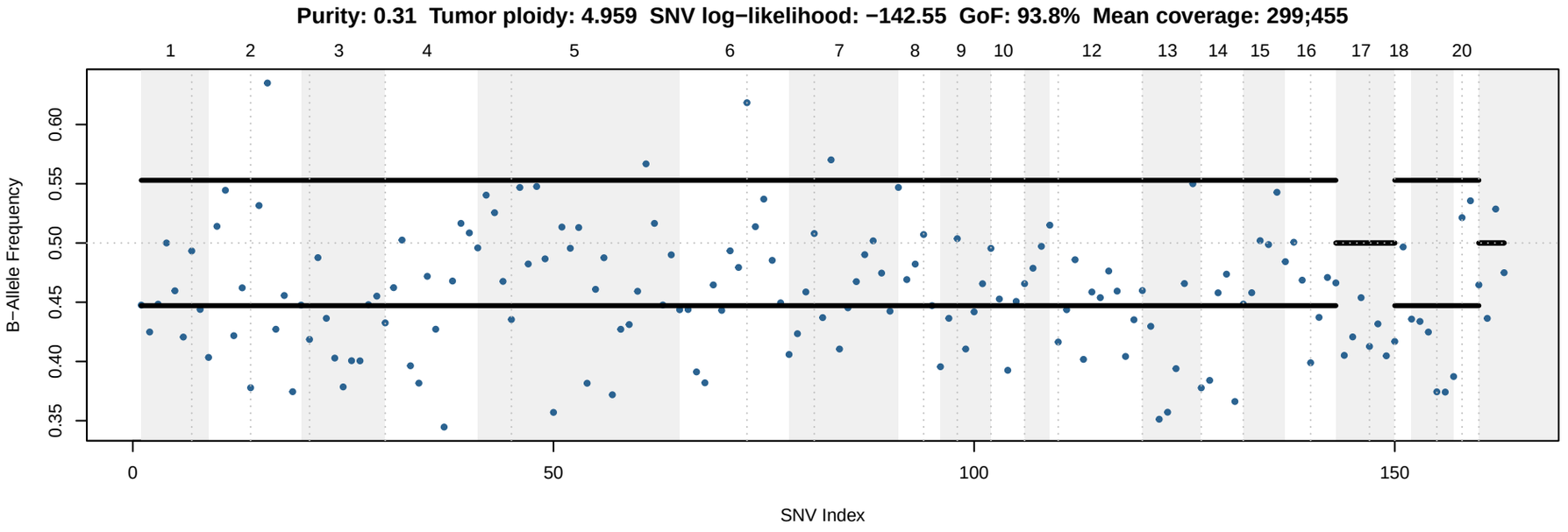

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
3m2
4m2
3m1
4m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

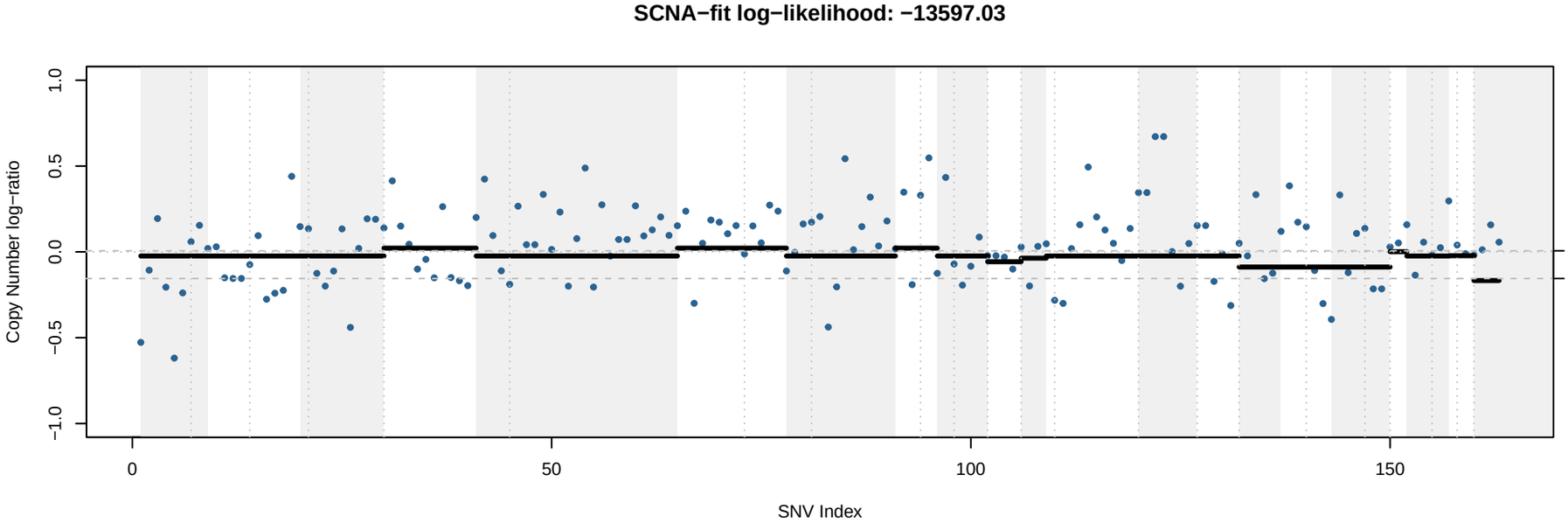

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

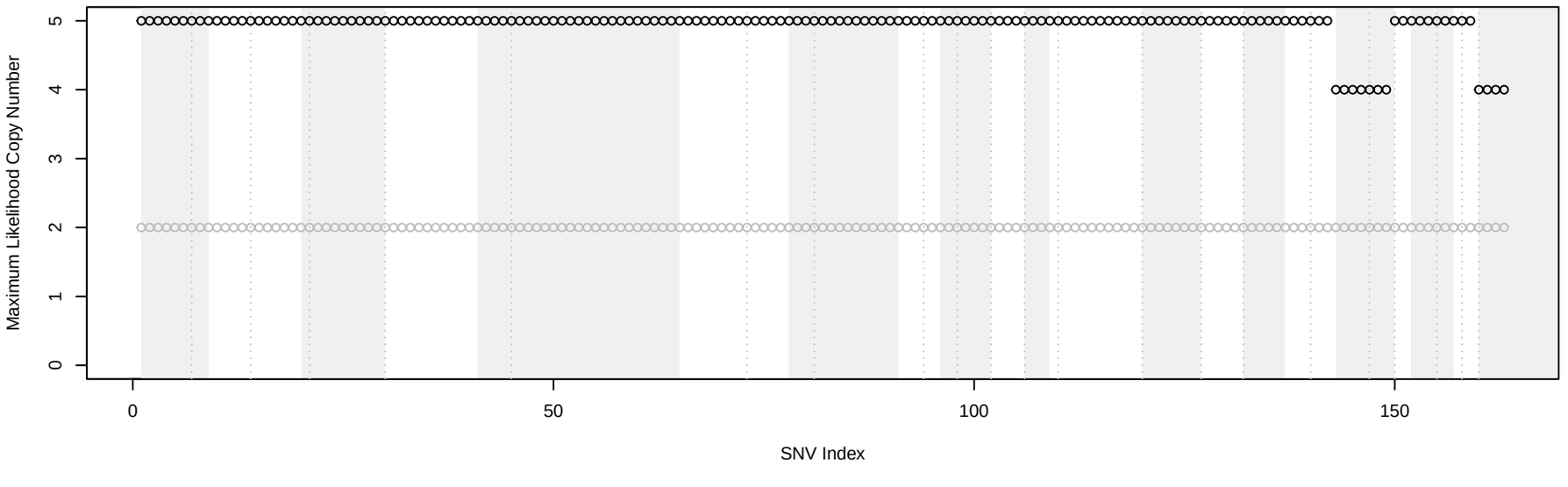

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

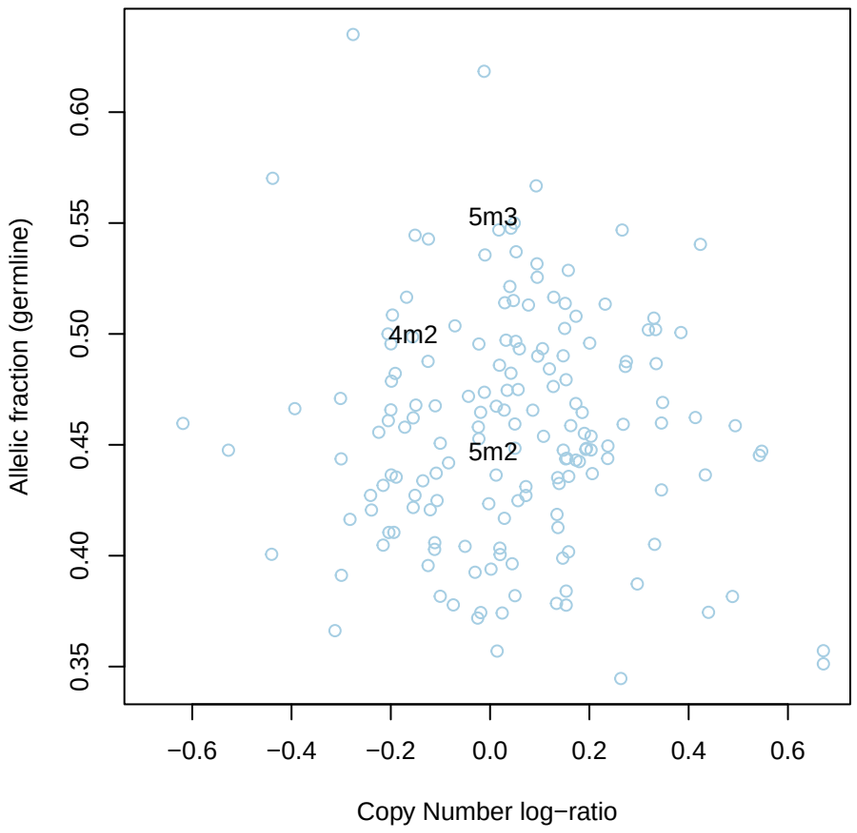

Frequency
0
20
40
60
80
0.2
0.4
0.6
0.8
1.0
Cellular fraction

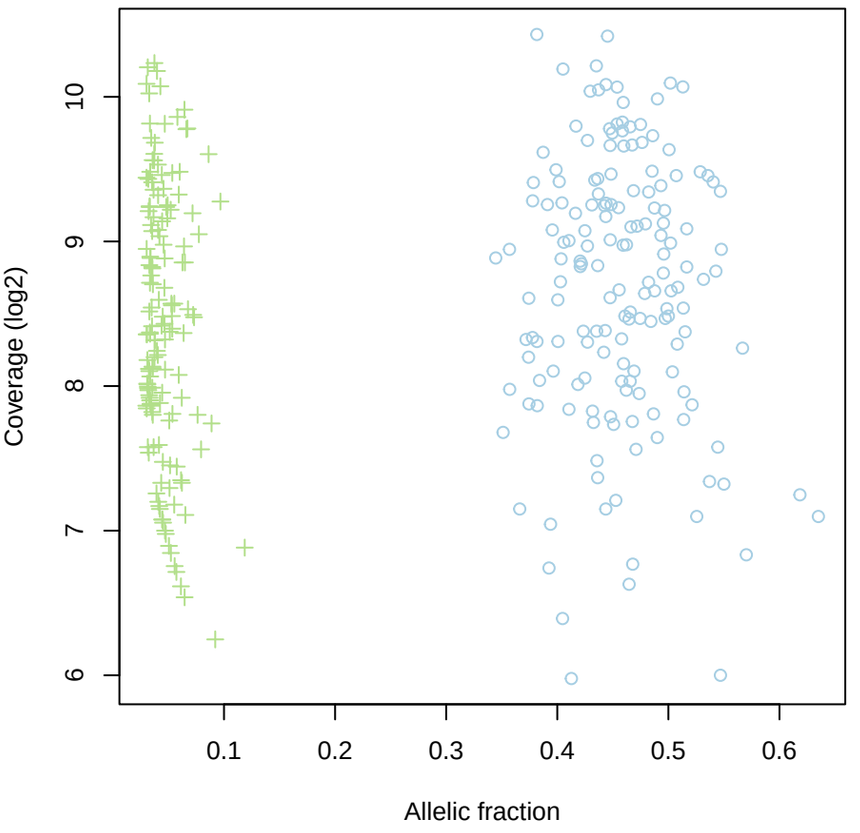

Purity: 0.31 Tumor ploidy: 4.959
4
5
0.6
0.5
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.15
−0.10
−0.05
0.00
log2 ratio

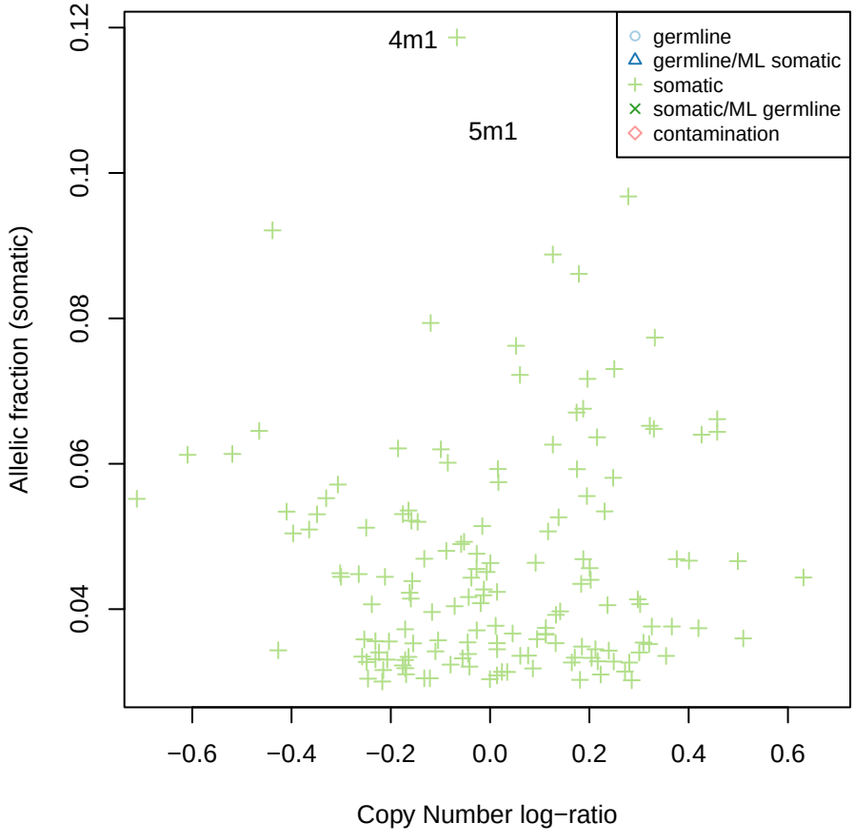

Purity: 0.31 Tumor ploidy: 4.959 SNV log−likelihood: −142.55 GoF: 93.8% Mean coverage: 299;455
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 18 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

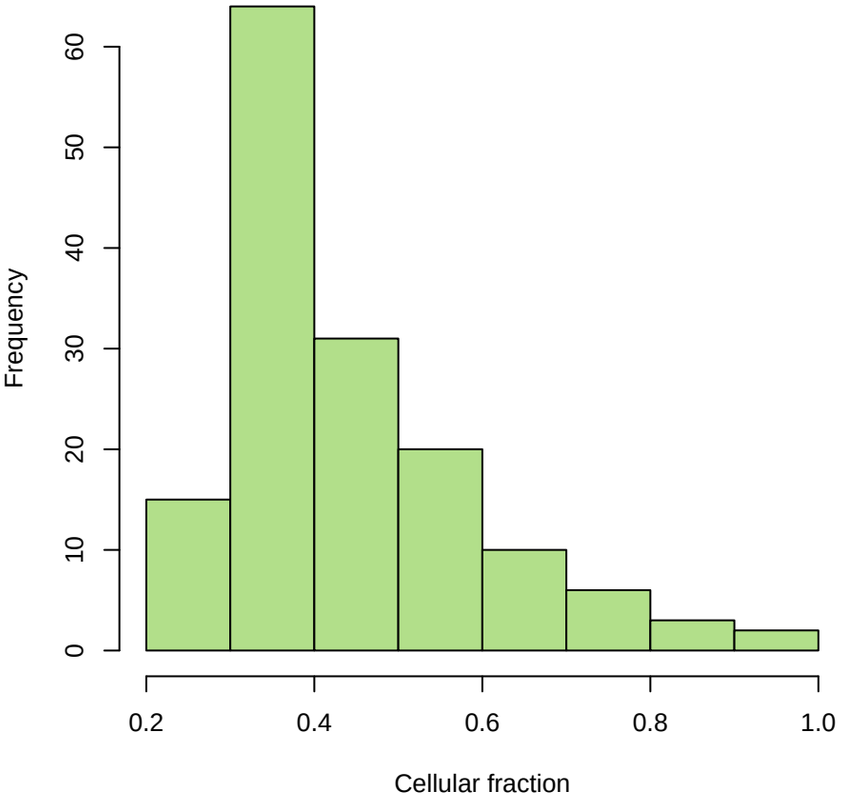

SCNA−fit log−likelihood: −13597.03
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5
0 50 100 150
SNV Index

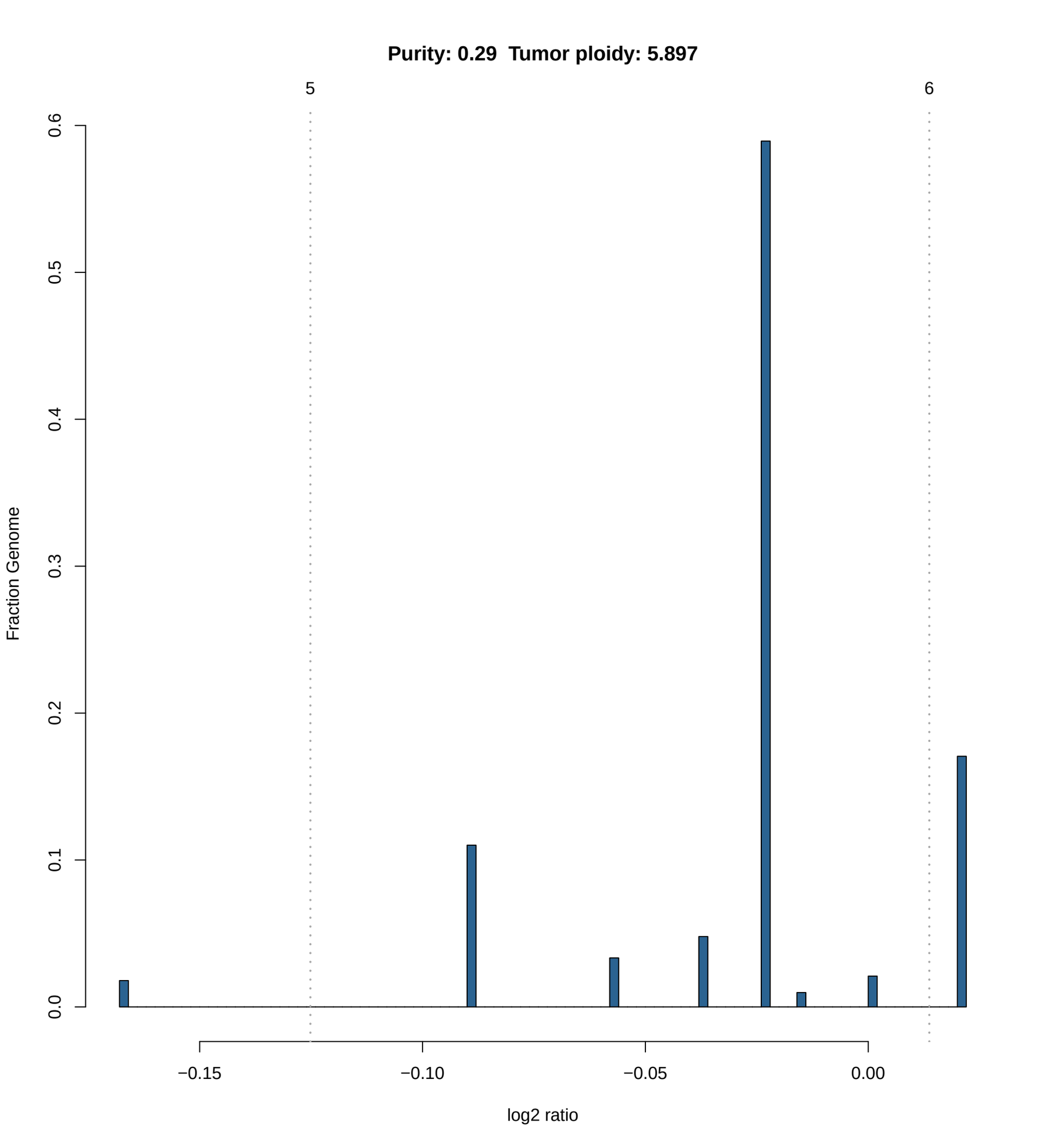

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

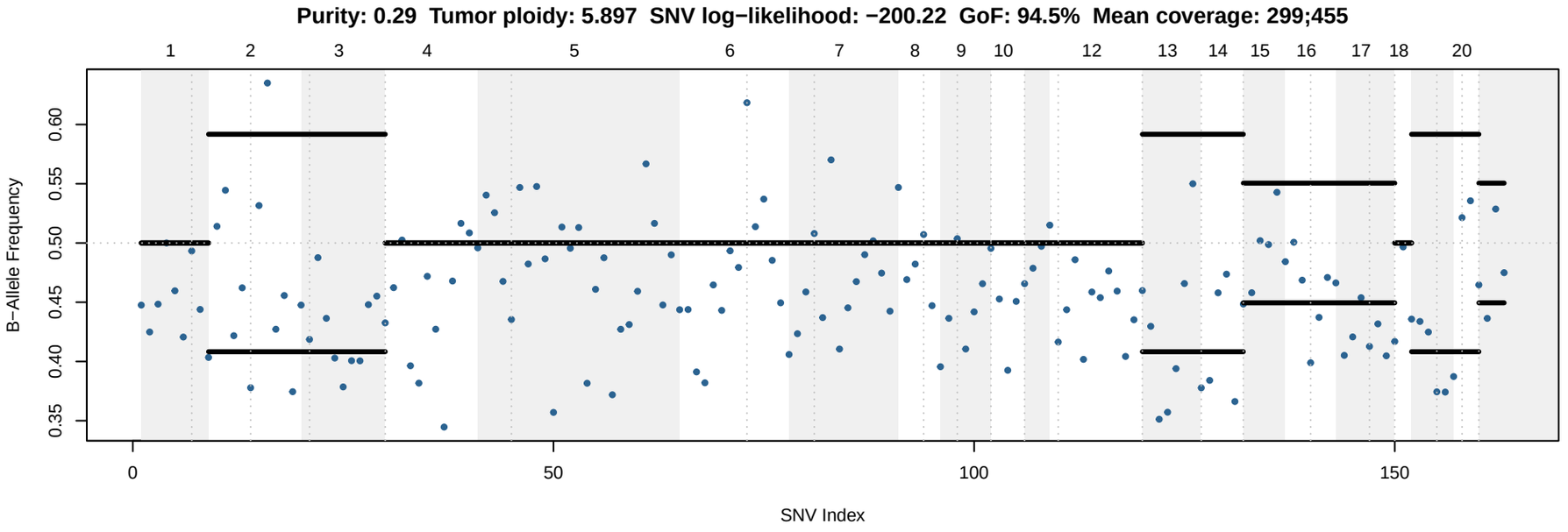

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
5m3
4m2
5m2
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

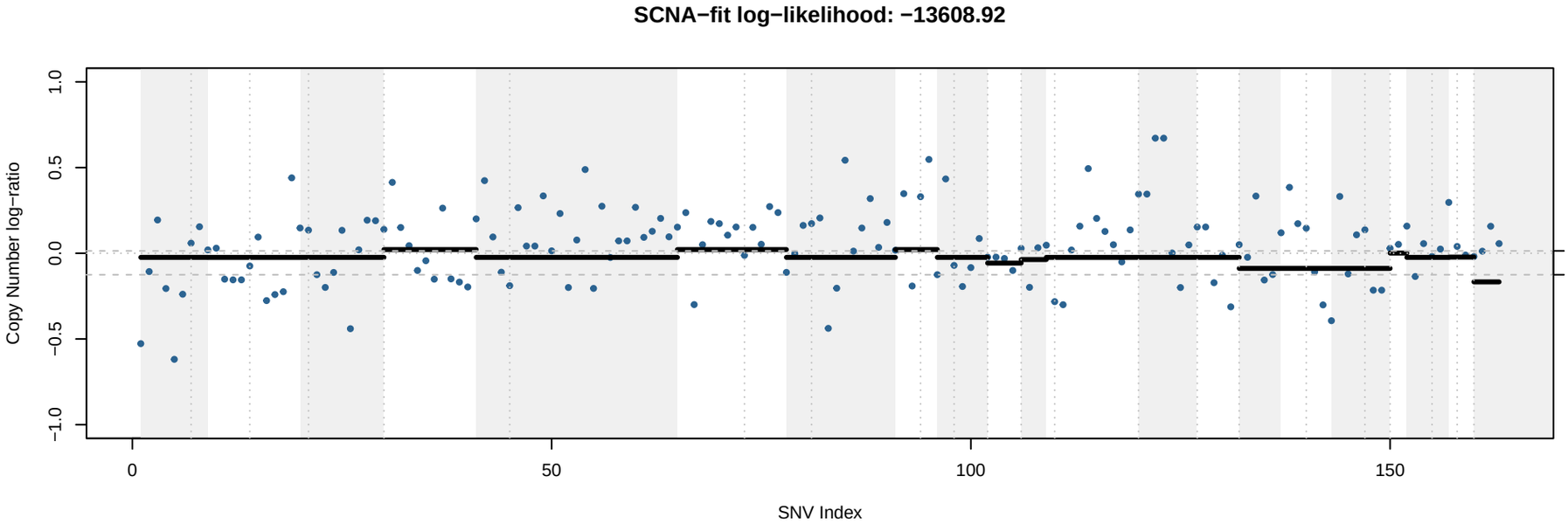

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

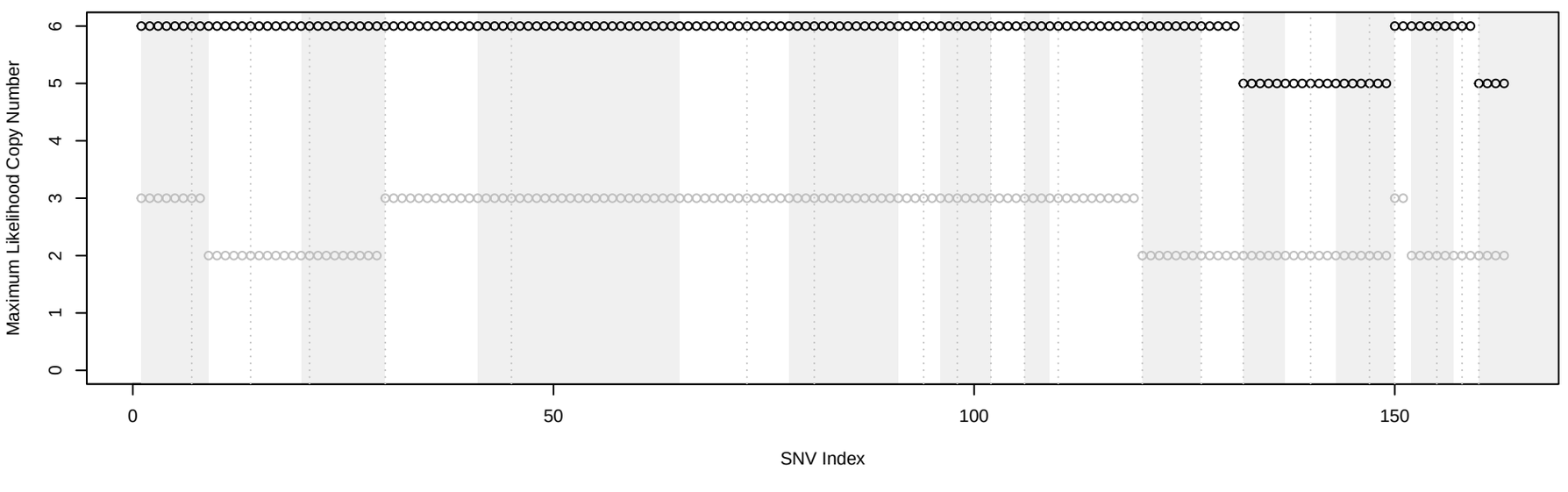

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
4m1
5m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

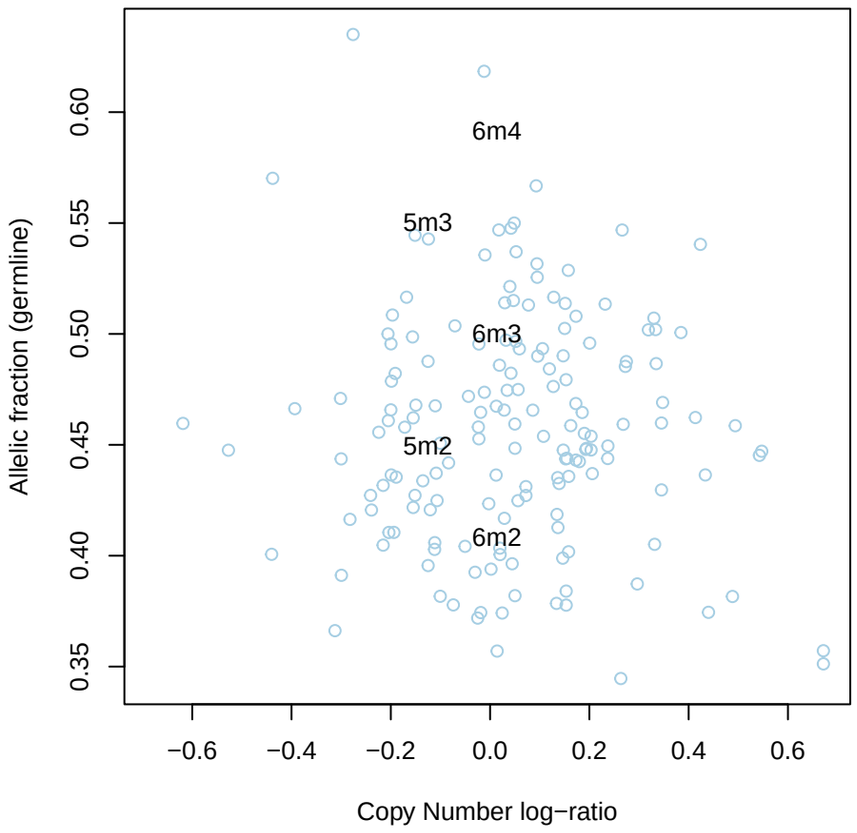

Frequency
0
10
20
30
40
50
60
0.2
0.4
0.6
0.8
1.0
Cellular fraction

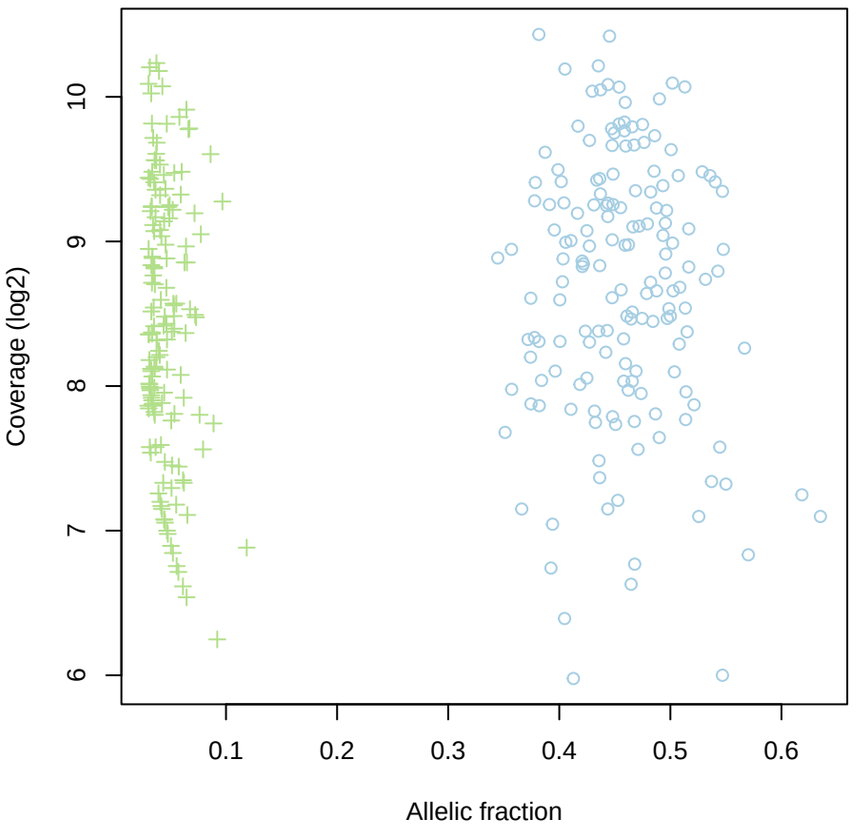

Purity: 0.29 Tumor ploidy: 5.897
5
6
0.6
0.5
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.15
−0.10
−0.05
0.00
log2 ratio

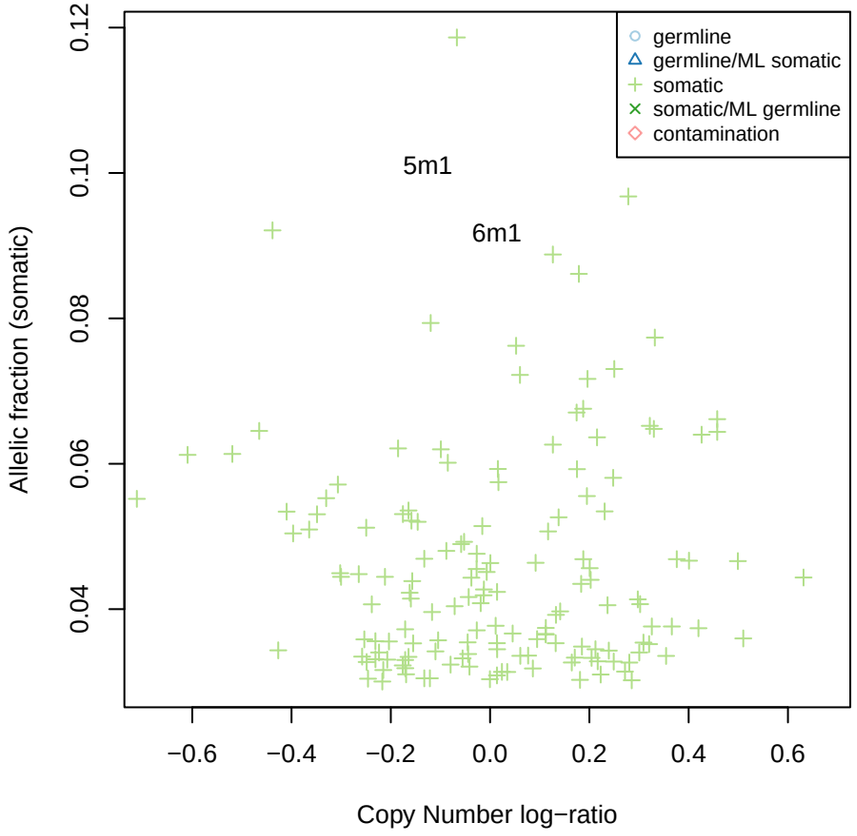

Purity: 0.29 Tumor ploidy: 5.897 SNV log−likelihood: −200.22 GoF: 94.5% Mean coverage: 299;455
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 18 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

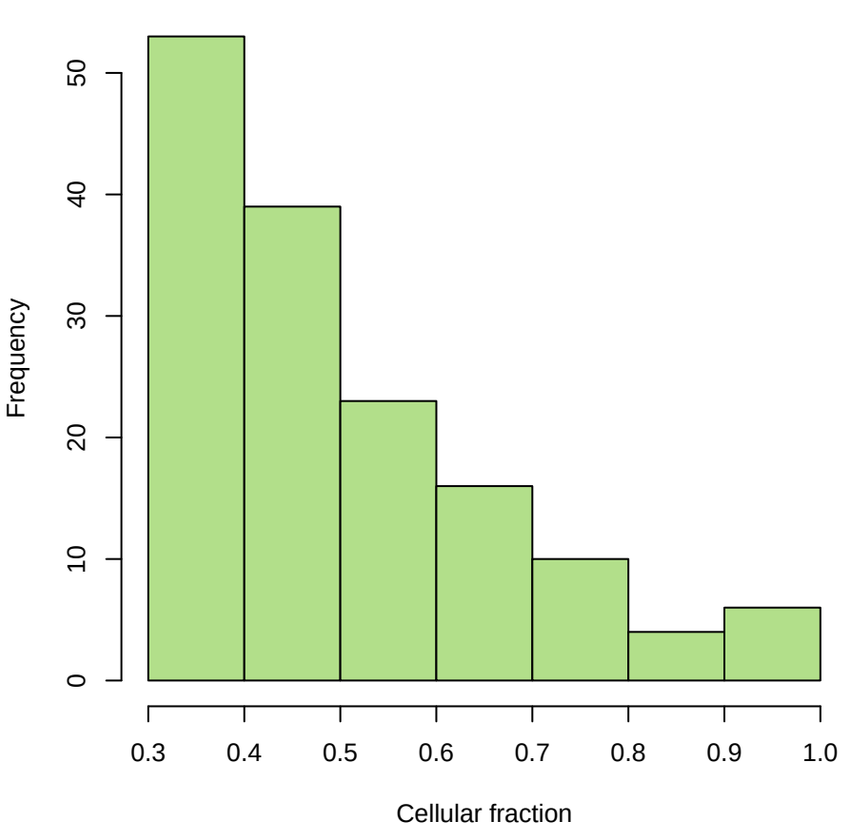

SCNA−fit log−likelihood: −13608.92
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
5
0 50 100 150
SNV Index

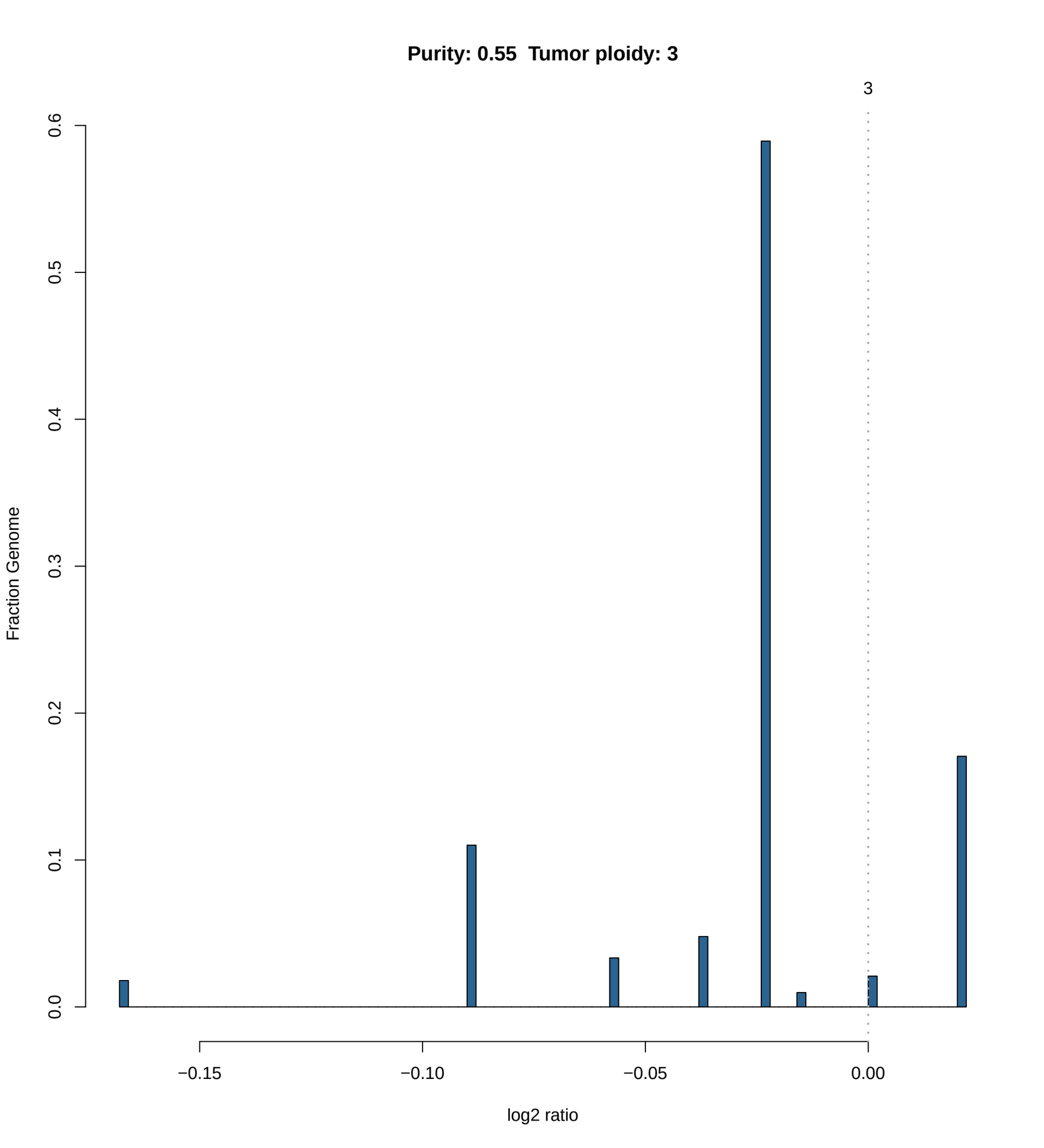

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

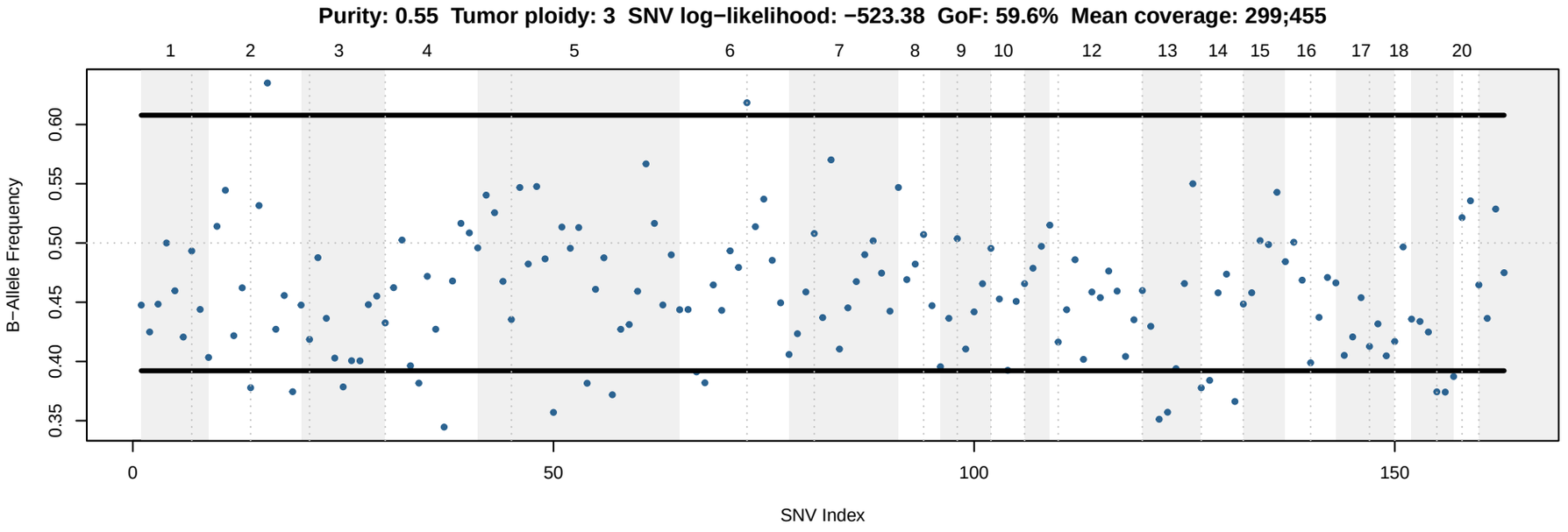

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
6m4
5m3
6m3
5m2
6m2
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

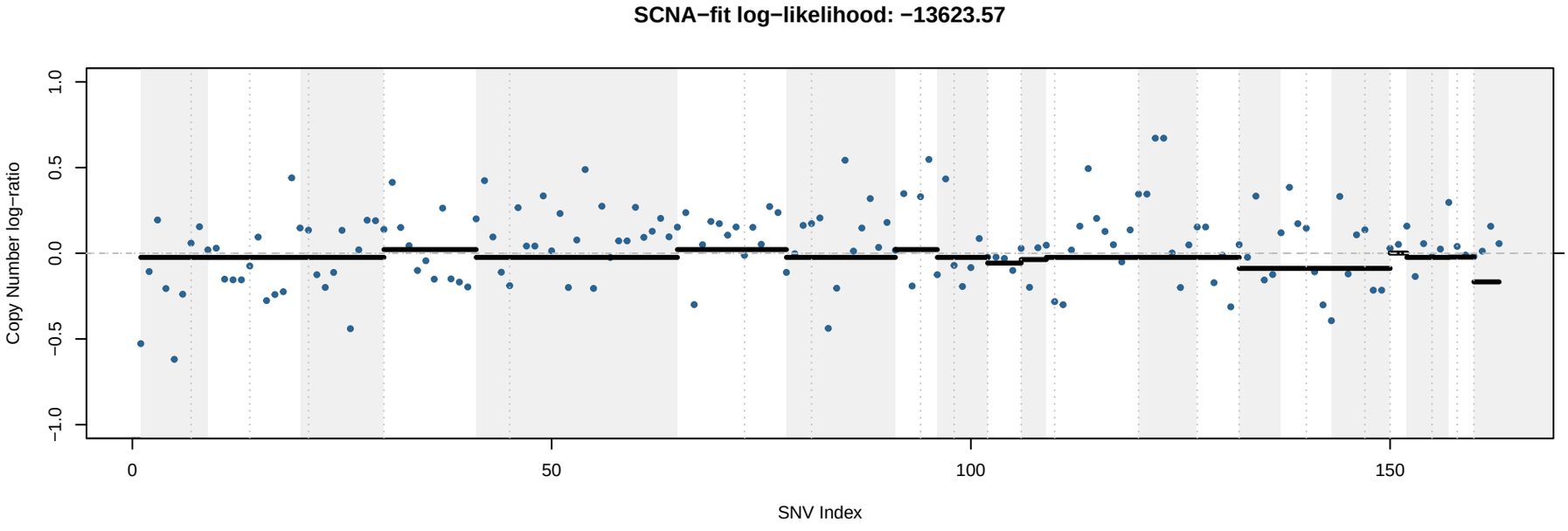

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

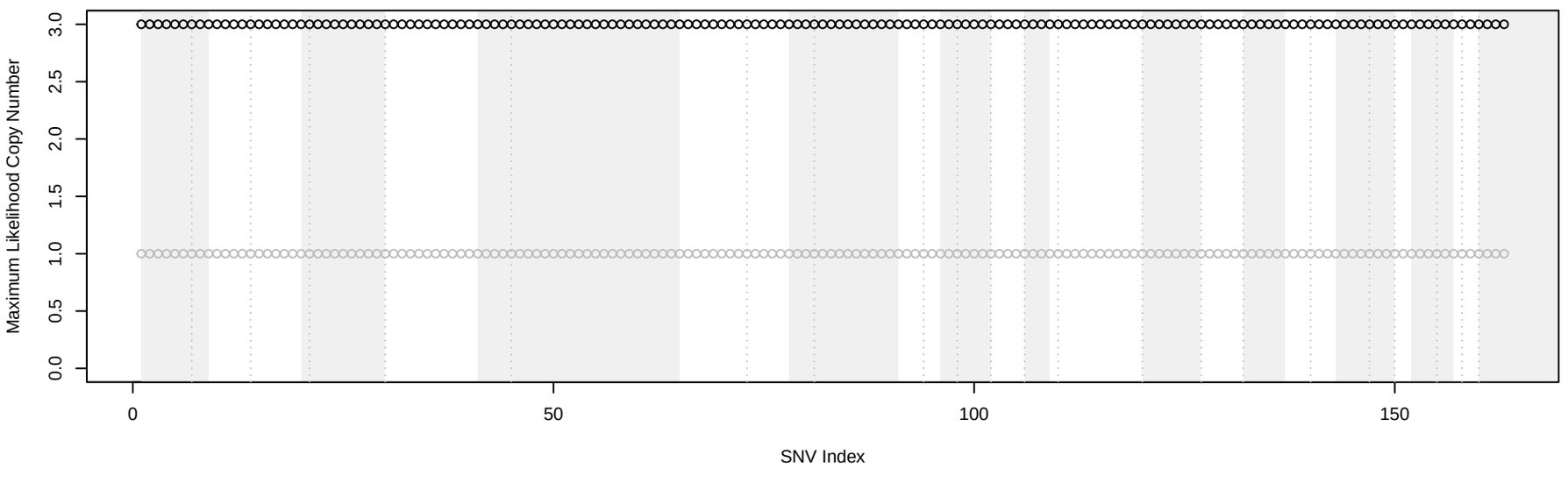

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
6m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

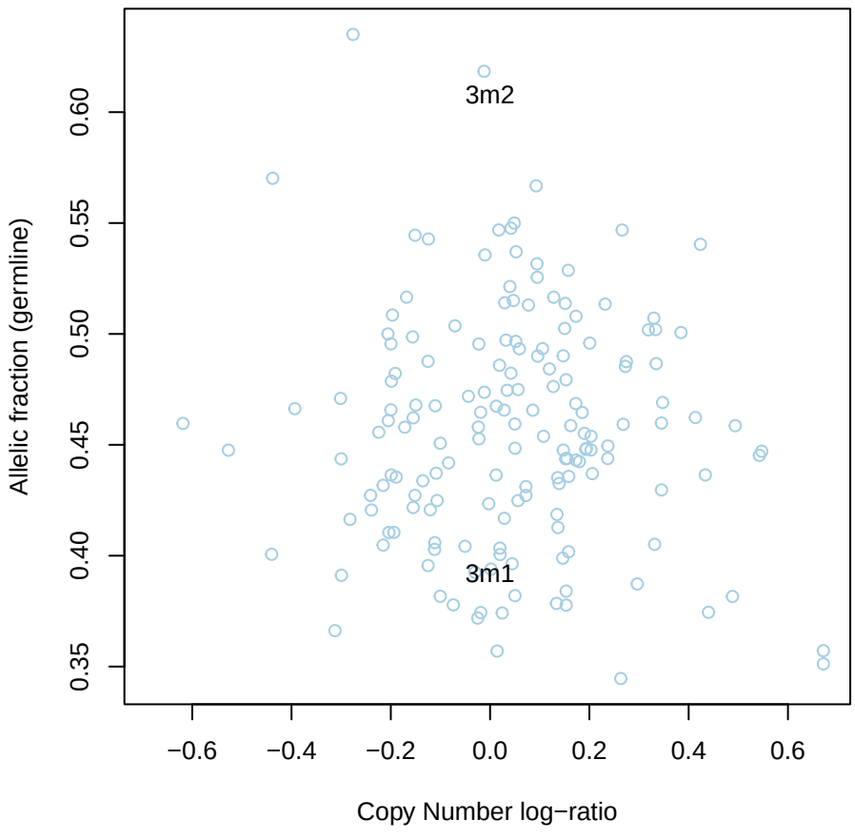

Frequency
0
10
20
30
40
50
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

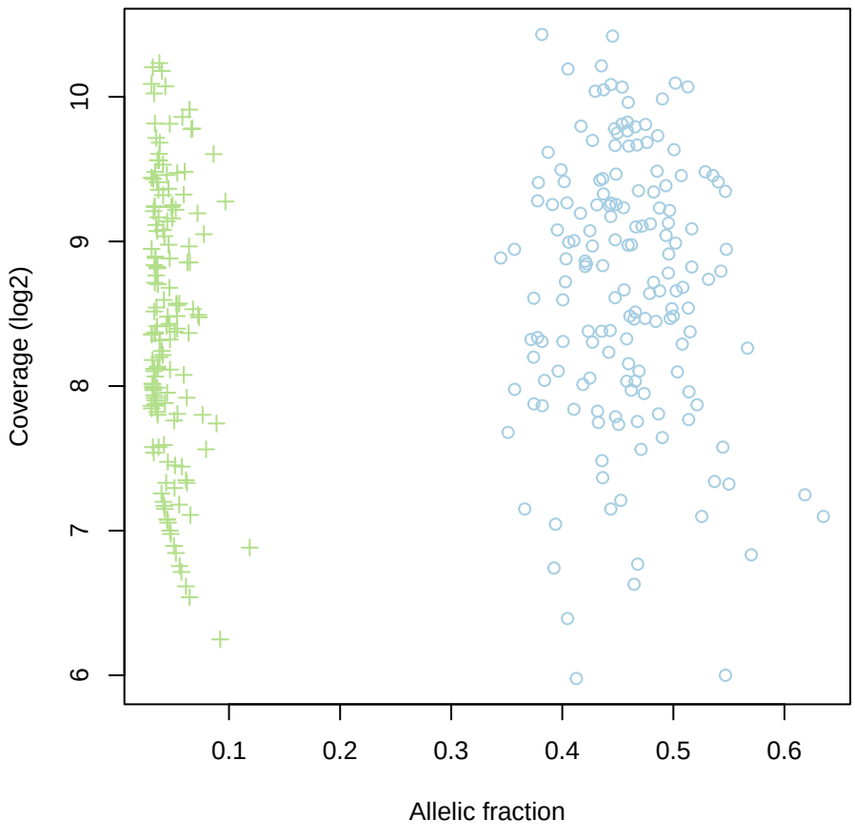

Purity: 0.55 Tumor ploidy: 3
3
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.6
−0.15
−0.10
−0.05
0.00
log2 ratio

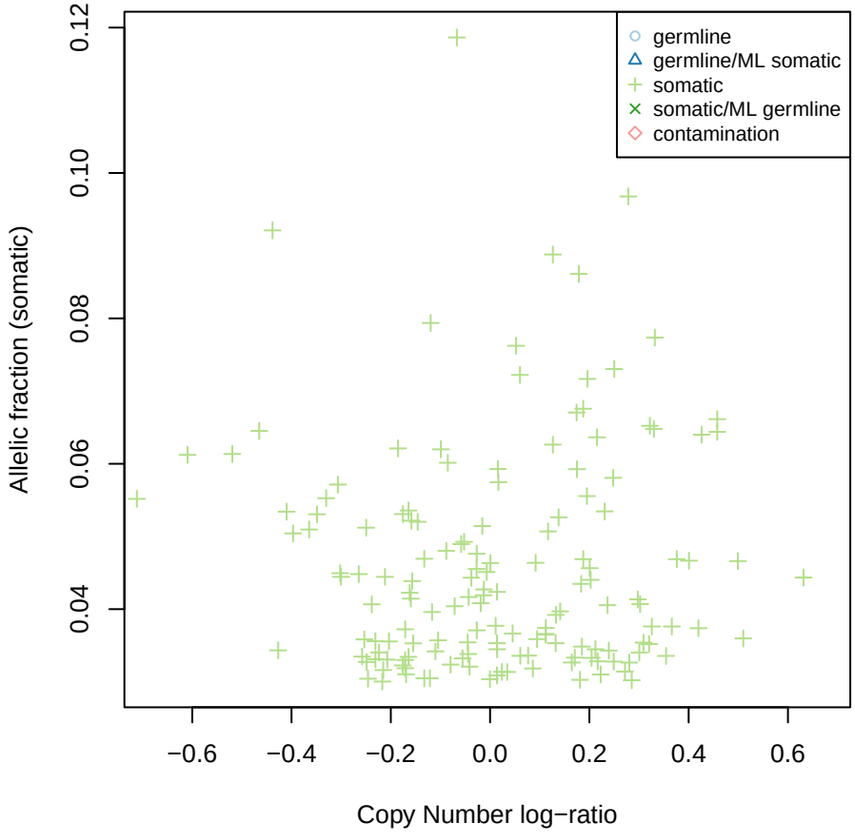

Purity: 0.55 Tumor ploidy: 3 SNV log−likelihood: −523.38 GoF: 59.6% Mean coverage: 299;455
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 18 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

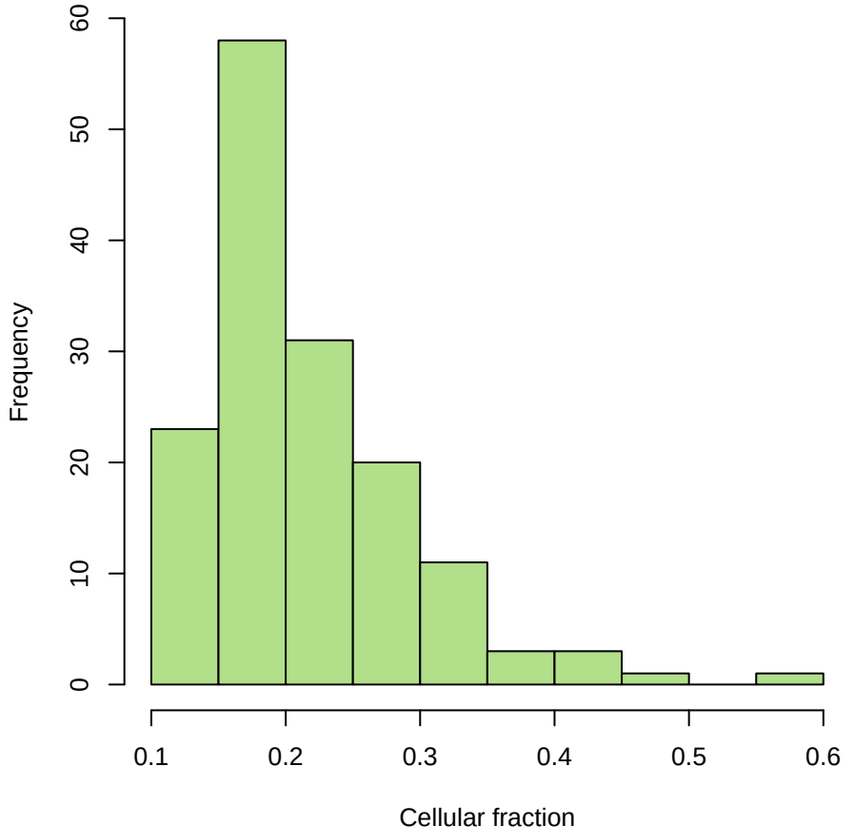

SCNA−fit log−likelihood: −13623.57
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
3
0 50 100 150
SNV Index

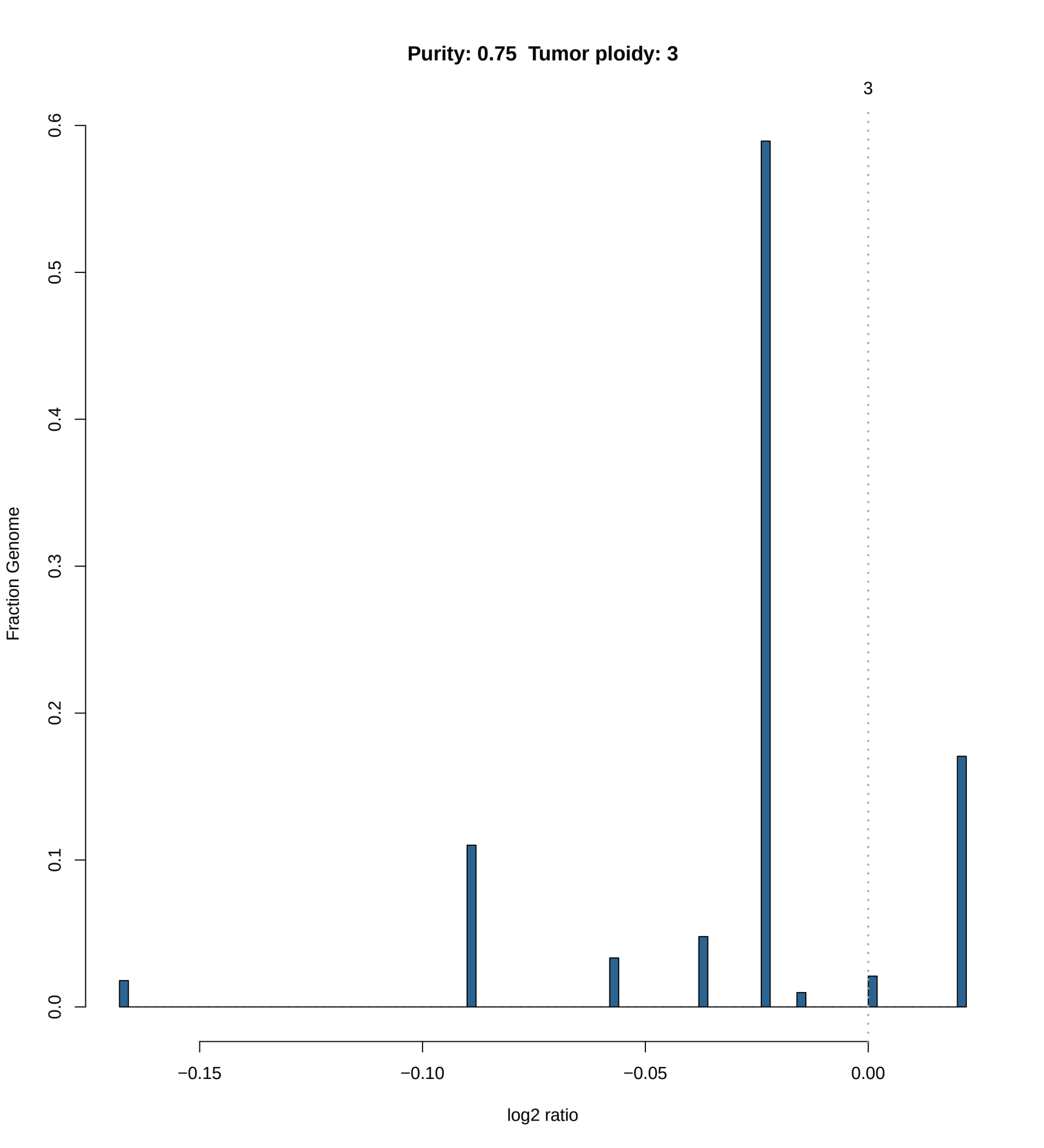

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

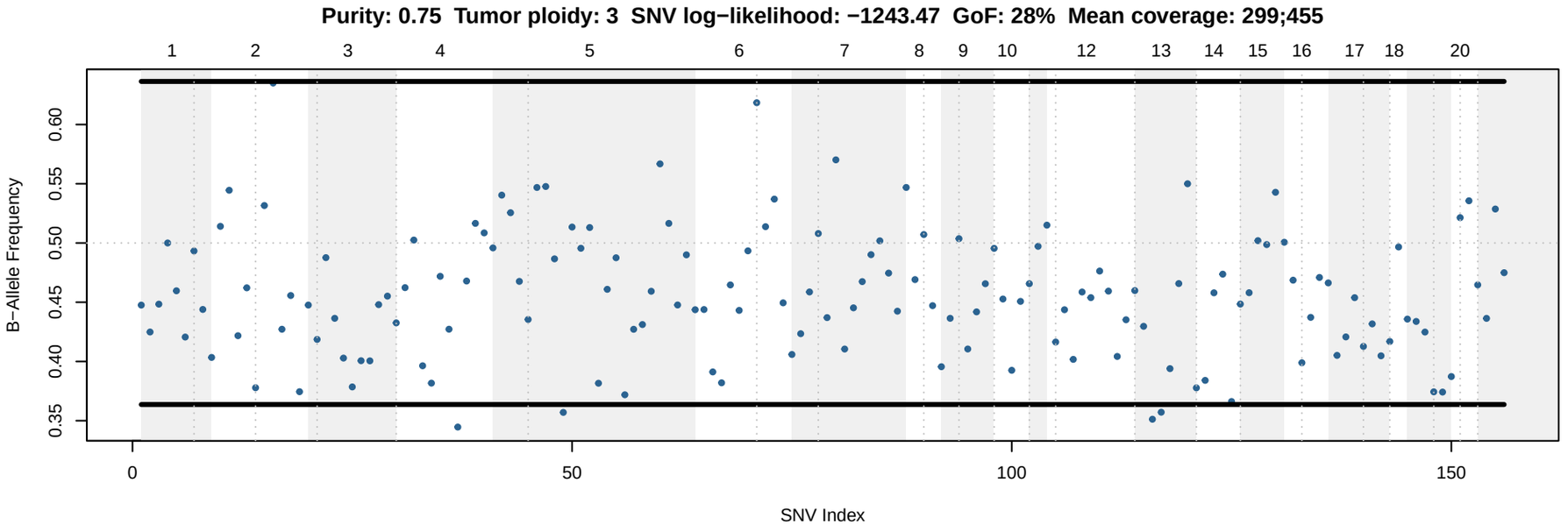

3m2
3m1
Allelic fraction (germline)
Copy Number log−ratio
0.35
0.40
0.45
0.50
0.55
0.60
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6

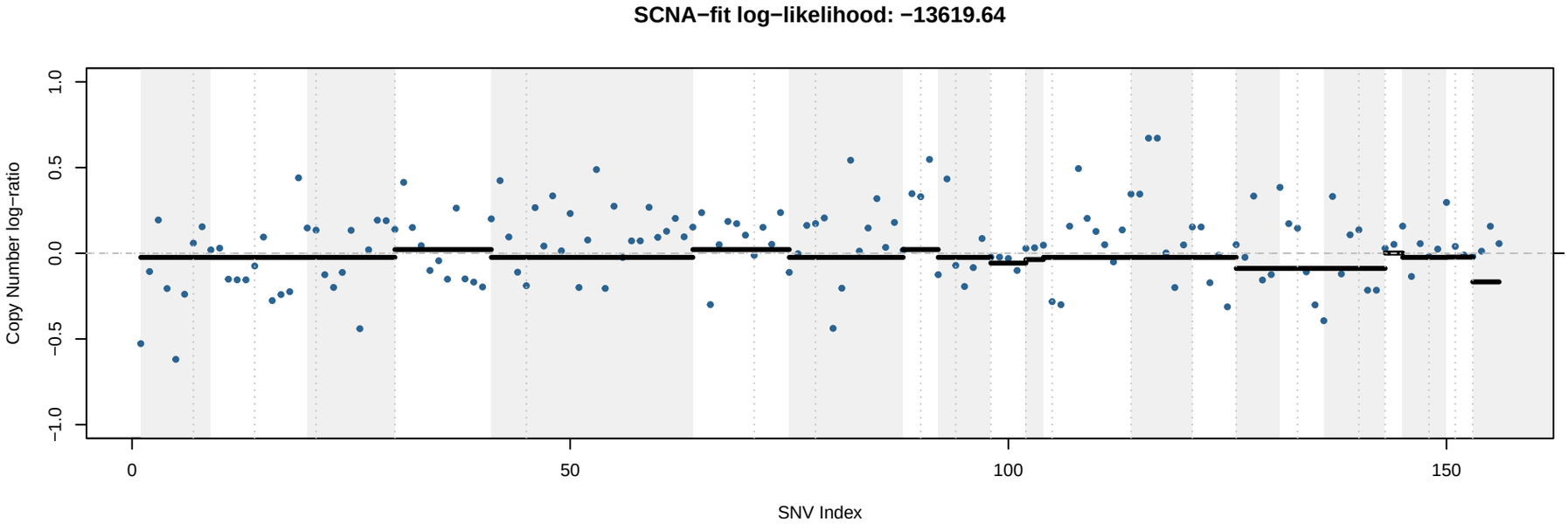

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

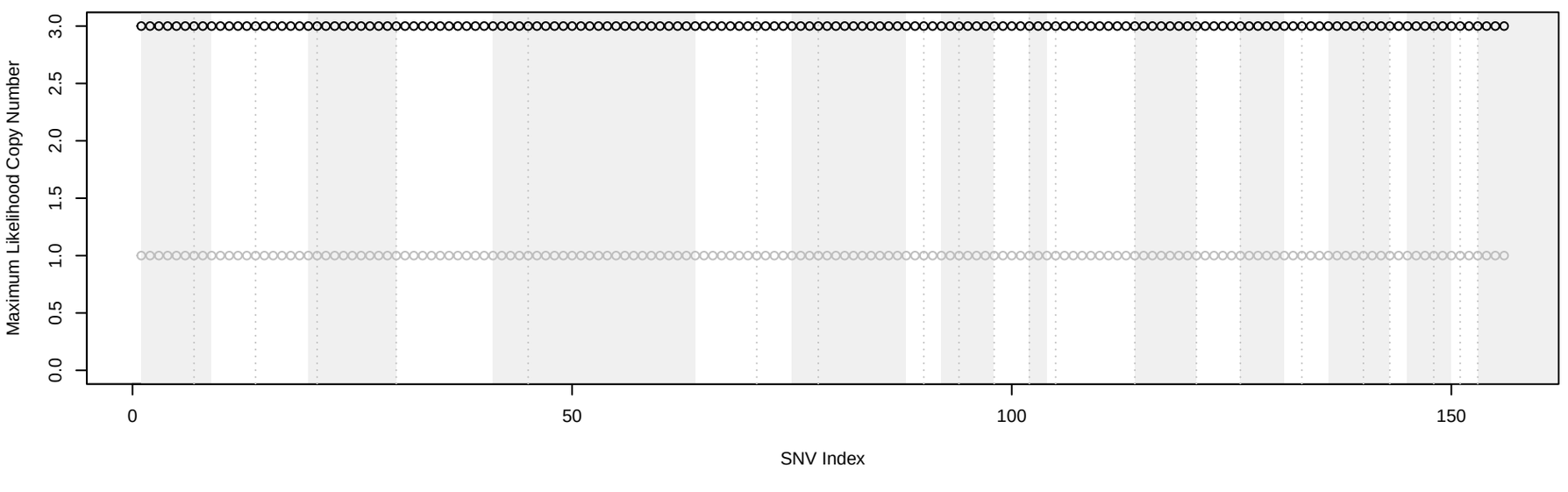

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
0.12
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6

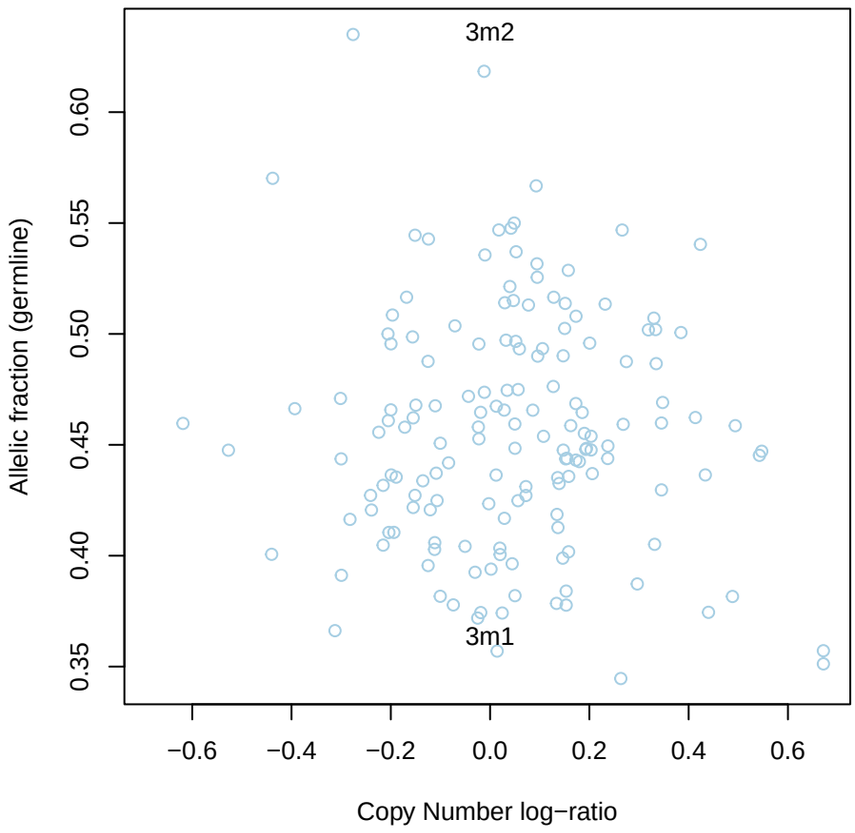

Frequency
Cellular fraction
0
10
20
30
40
50
60
0.1
0.2
0.3
0.4
0.5
0.6

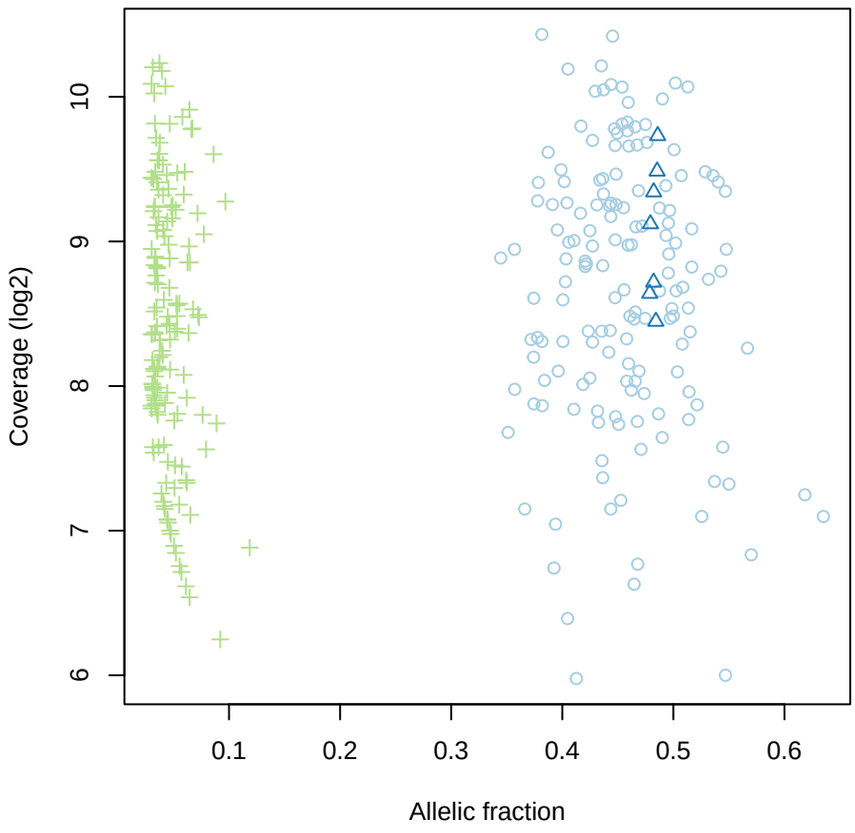

Purity: 0.75 Tumor ploidy: 3
3
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.6
−0.15
−0.10
−0.05
0.00
log2 ratio

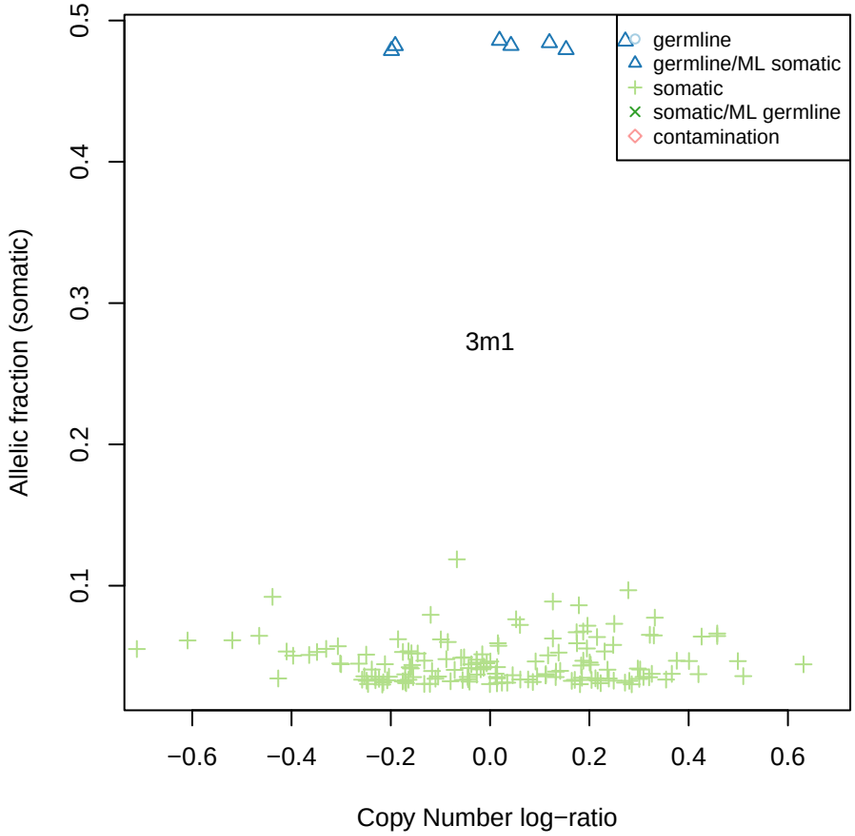

Purity: 0.75 Tumor ploidy: 3 SNV log−likelihood: −1243.47 GoF: 28% Mean coverage: 299;455
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 18 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

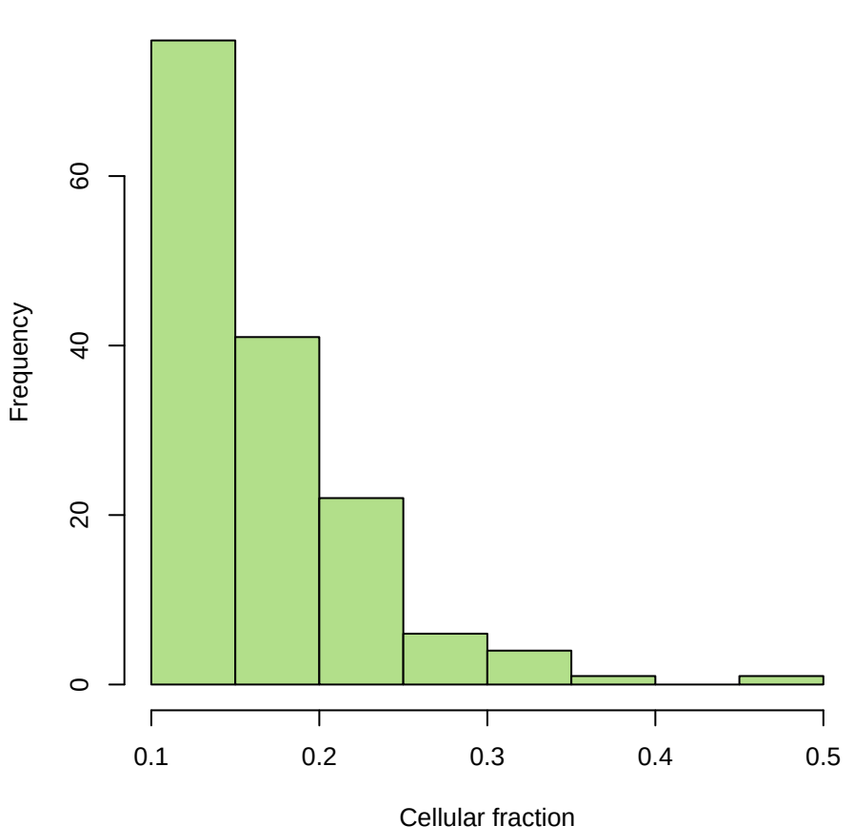

SCNA−fit log−likelihood: −13619.64
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
3
0 50 100 150
SNV Index


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


3m2
3m1
Allelic fraction (germline)
Copy Number log−ratio
0.35
0.40
0.45
0.50
0.55
0.60
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6


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


germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
Allelic fraction (somatic)
Copy Number log−ratio
0.1
0.2
0.3
0.4
0.5
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6


Frequency
Cellular fraction
0
20
40
60
0.1
0.2
0.3
0.4
0.5