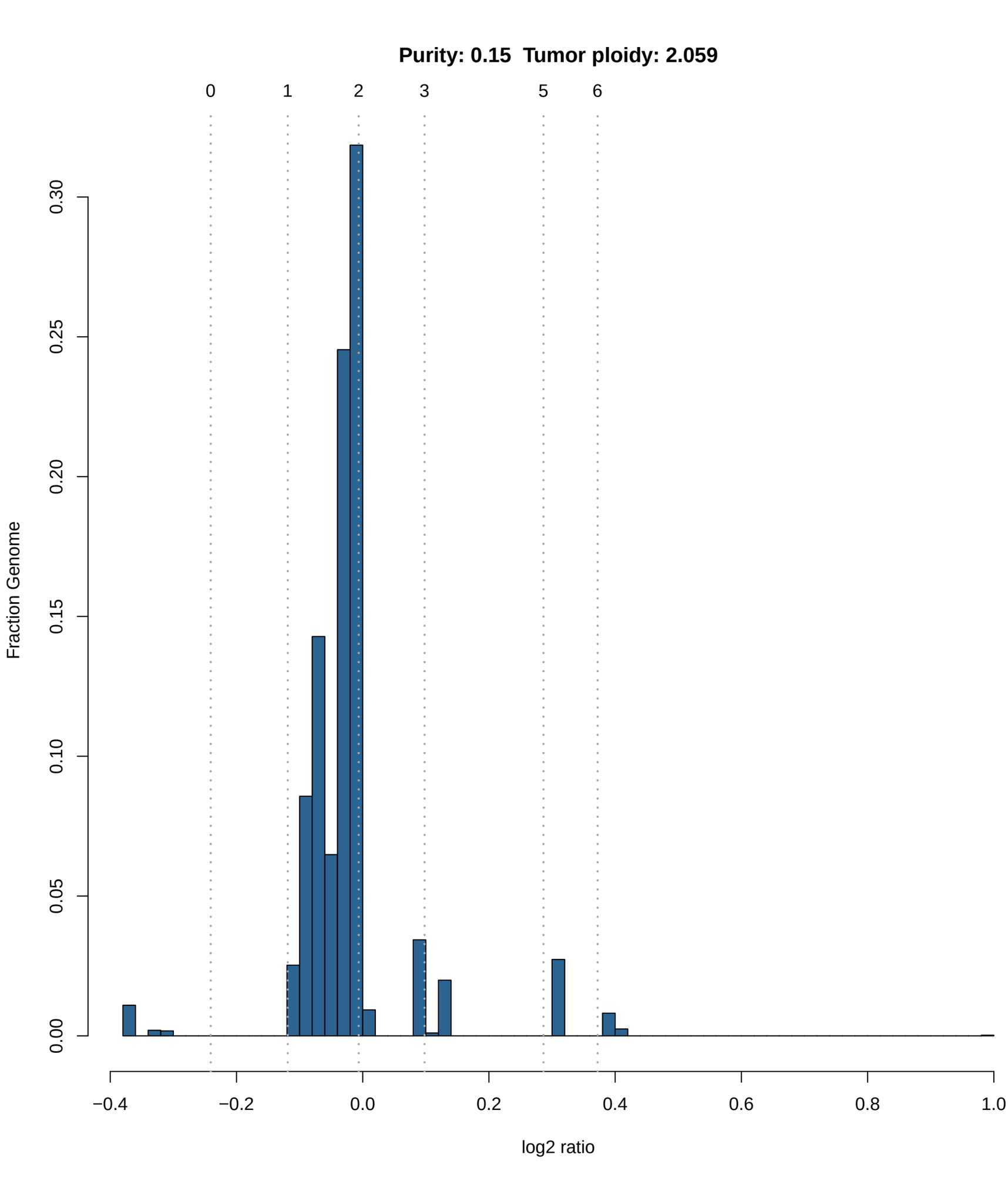
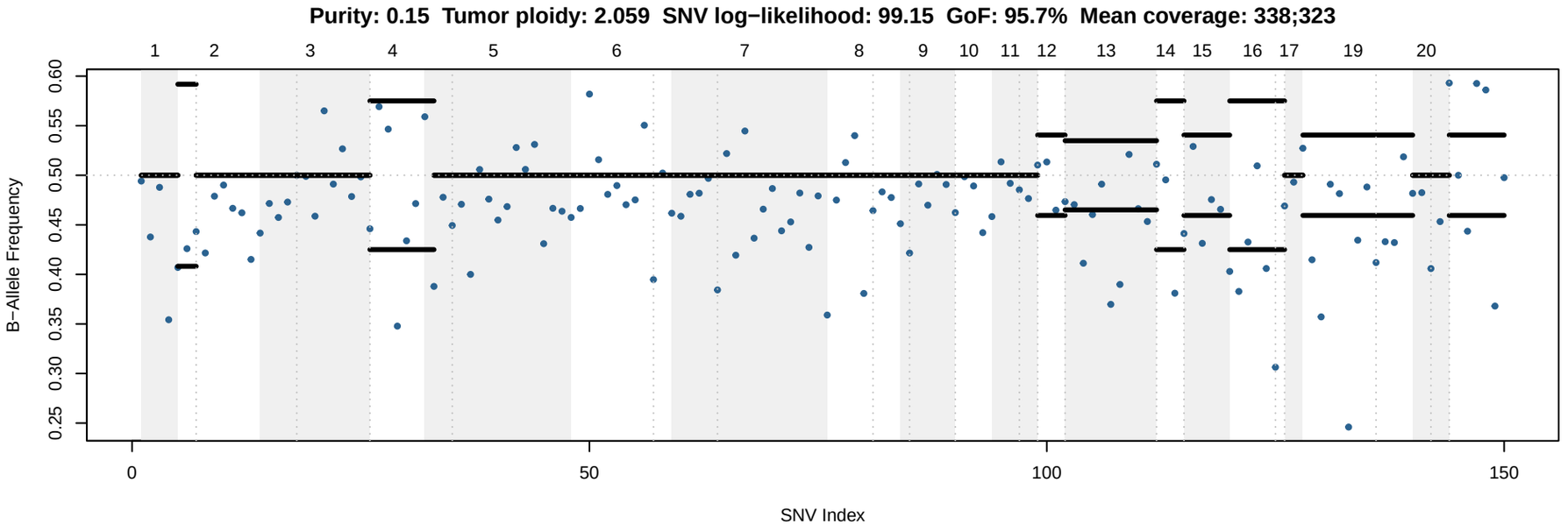
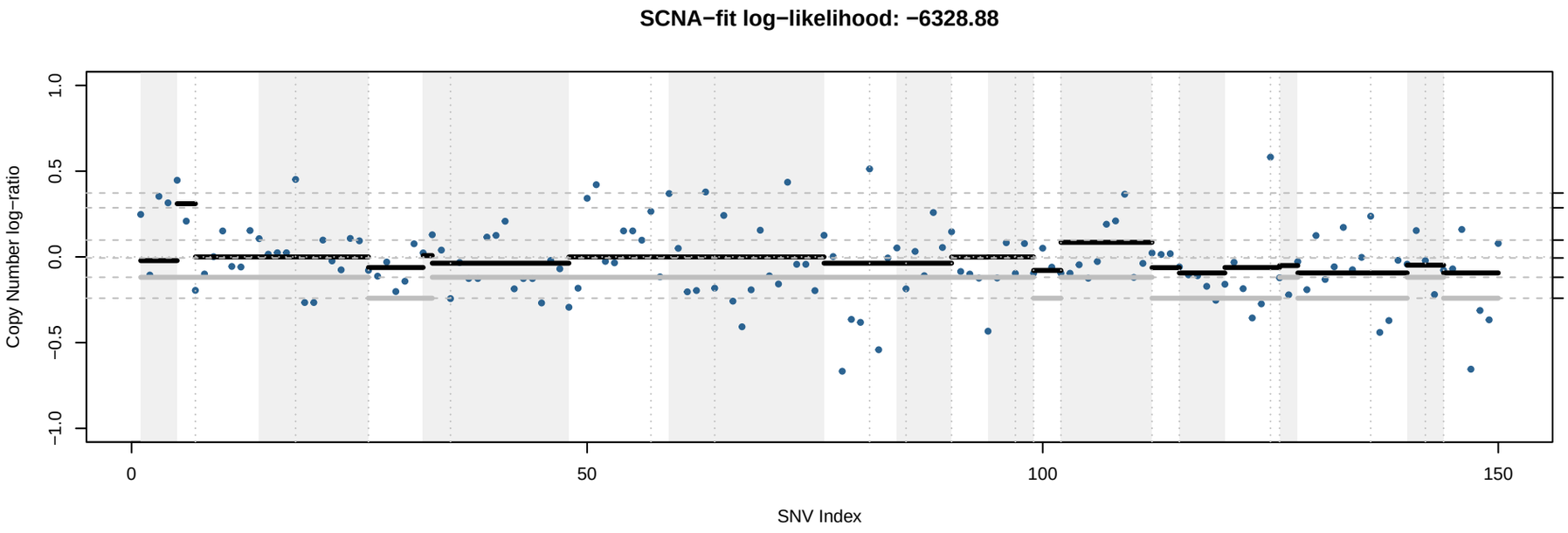
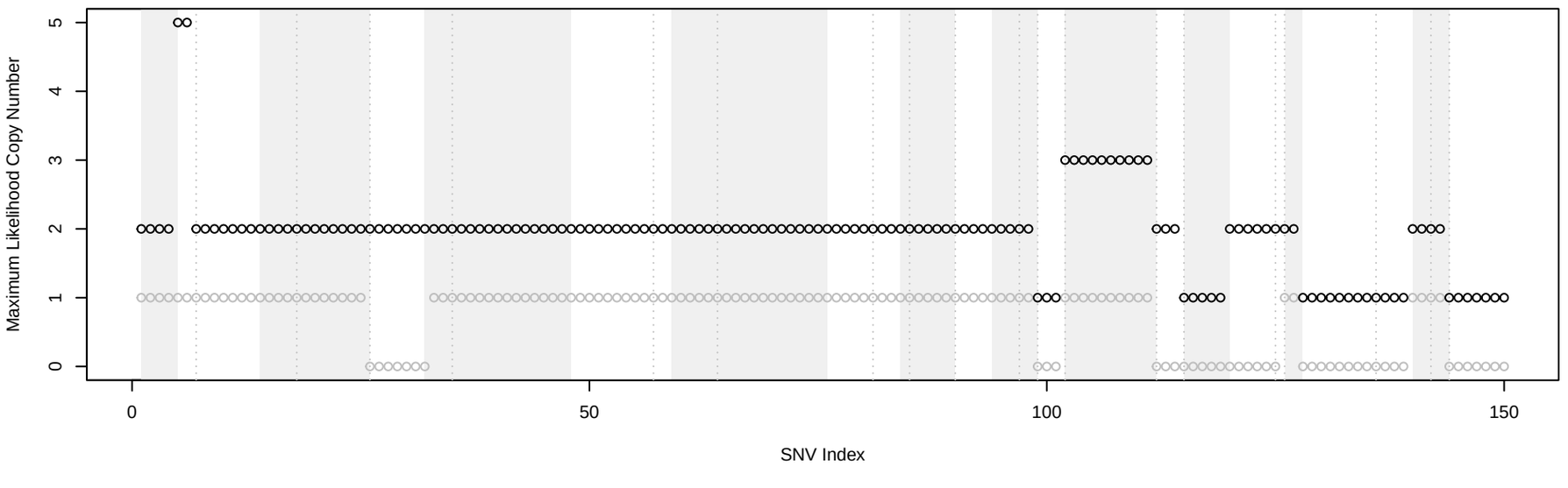
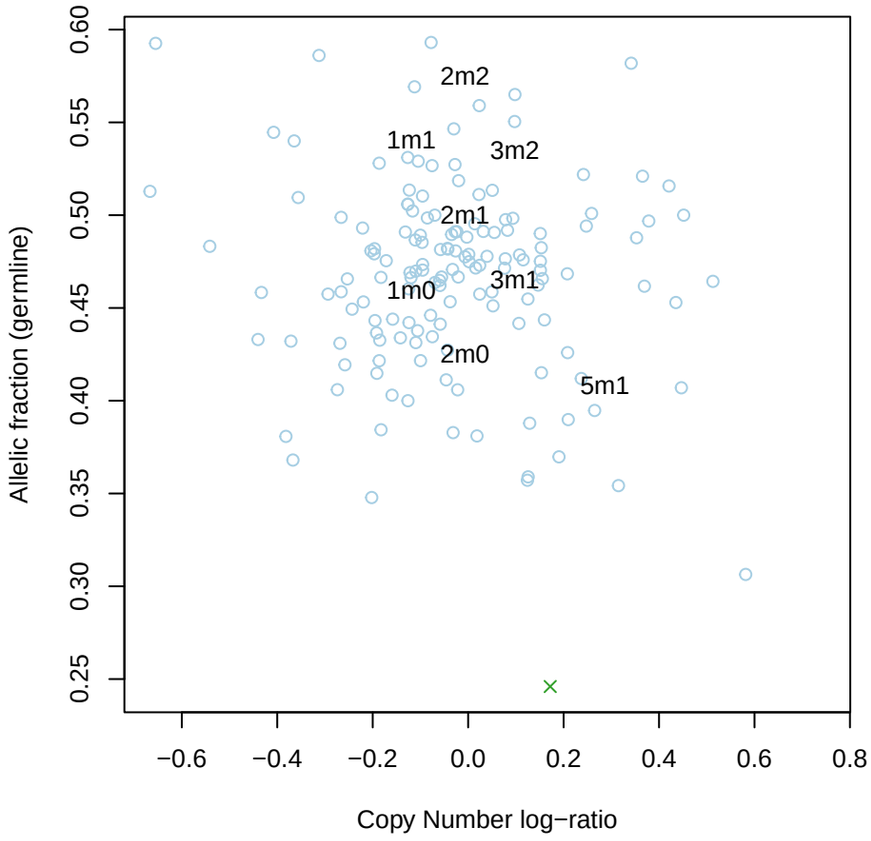
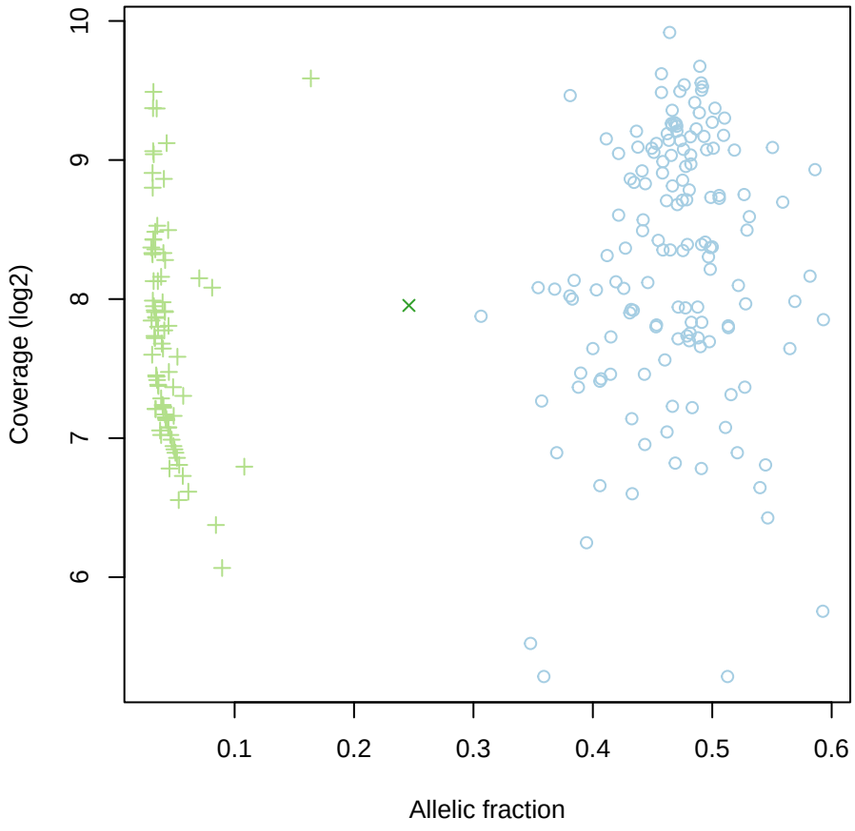

Purity: 0.15 Tumor ploidy: 2.059
0
1
2
3
5
6
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
1.0
log2 ratio

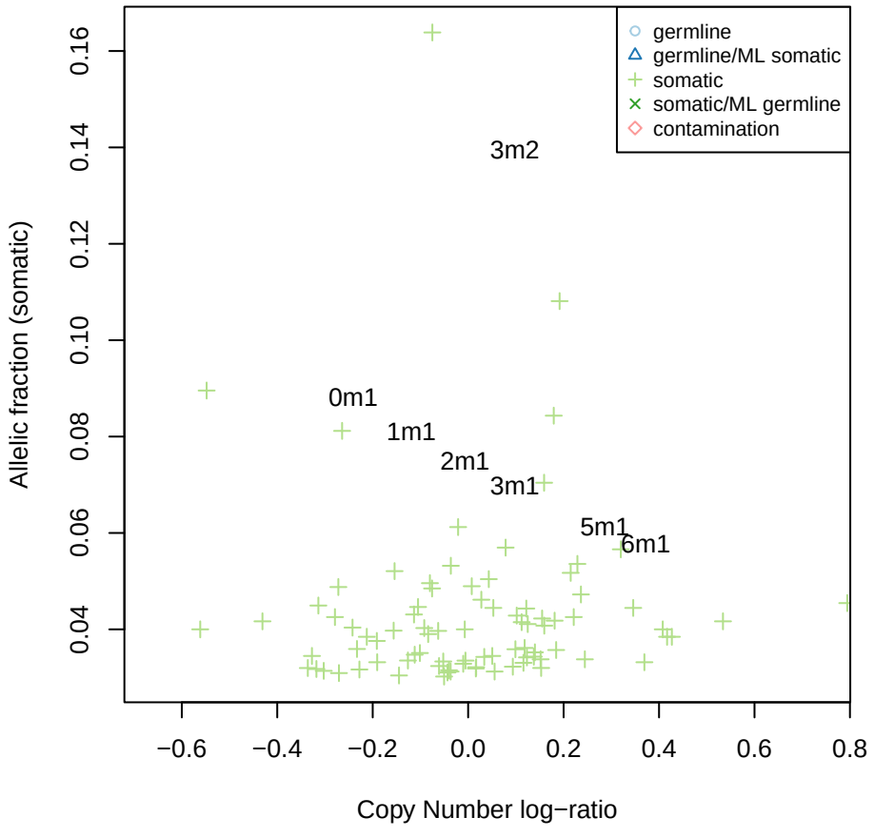

Purity: 0.15 Tumor ploidy: 2.059 SNV log−likelihood: 99.15 GoF: 95.7% Mean coverage: 338;323
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.25 0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

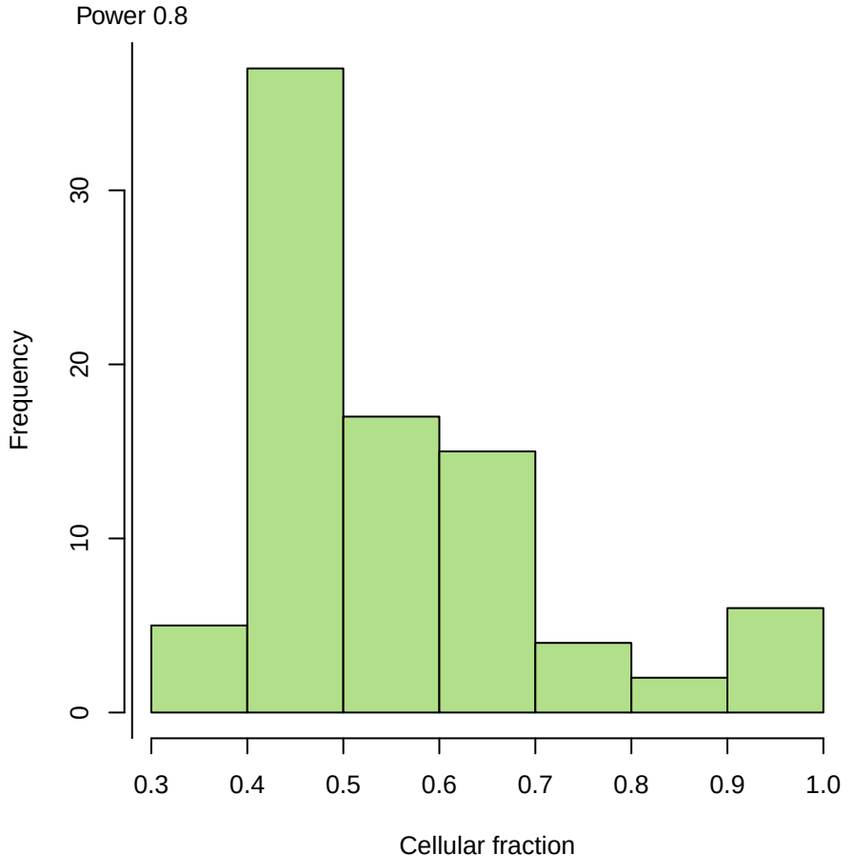

SCNA−fit log−likelihood: −6328.88
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
0 2 5
0 50 100 150
SNV Index

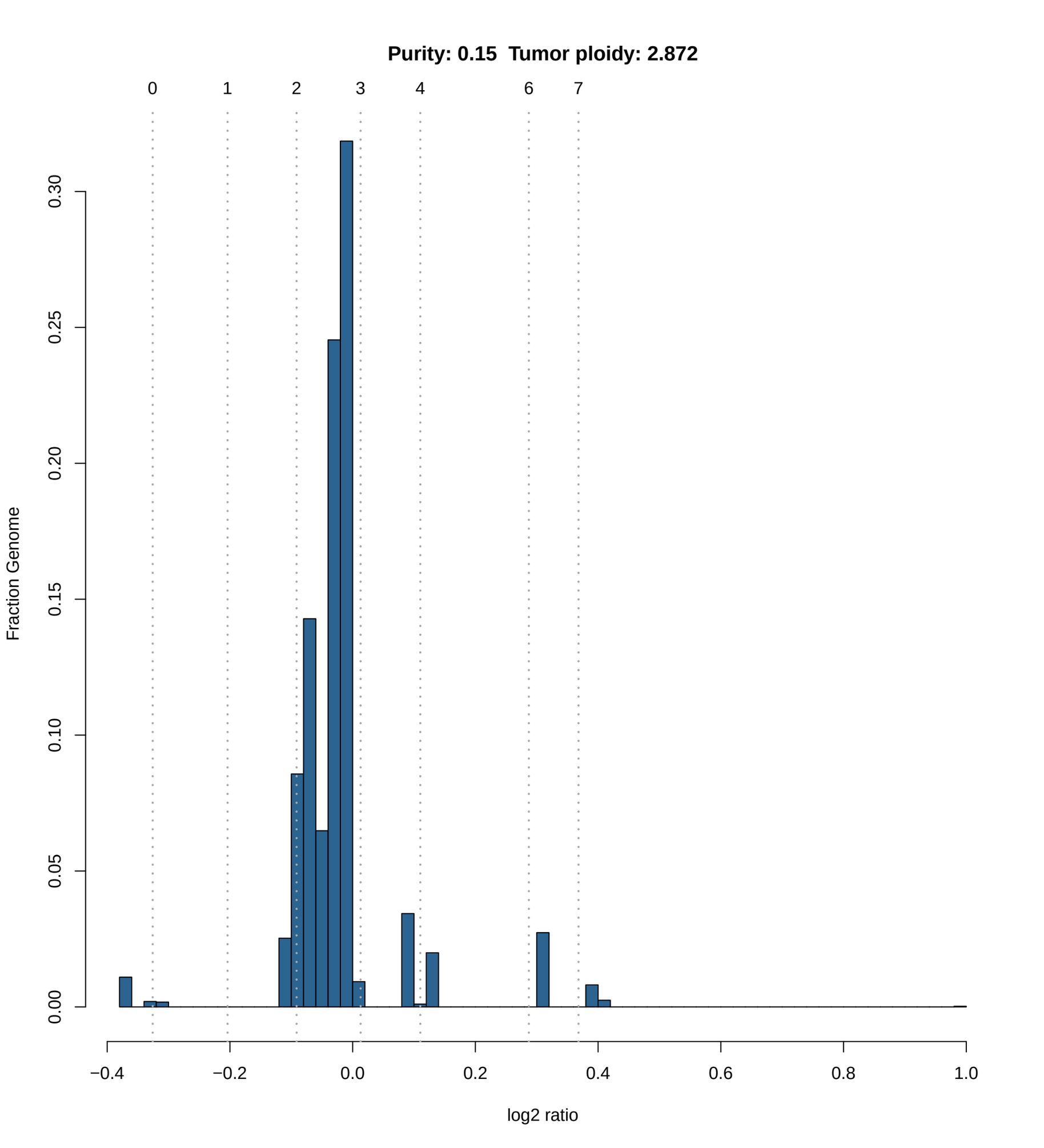

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

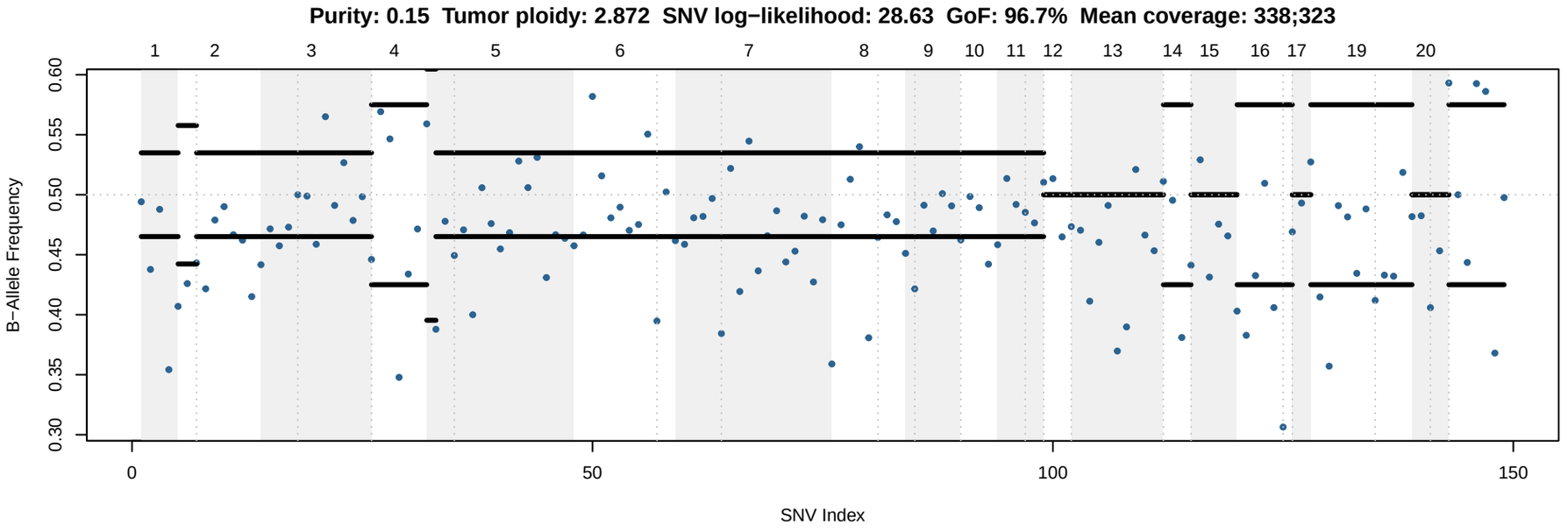

Allelic fraction (germline)
Copy Number log−ratio
2m2
1m1
3m2
2m1
3m1
1m0
2m0
5m1

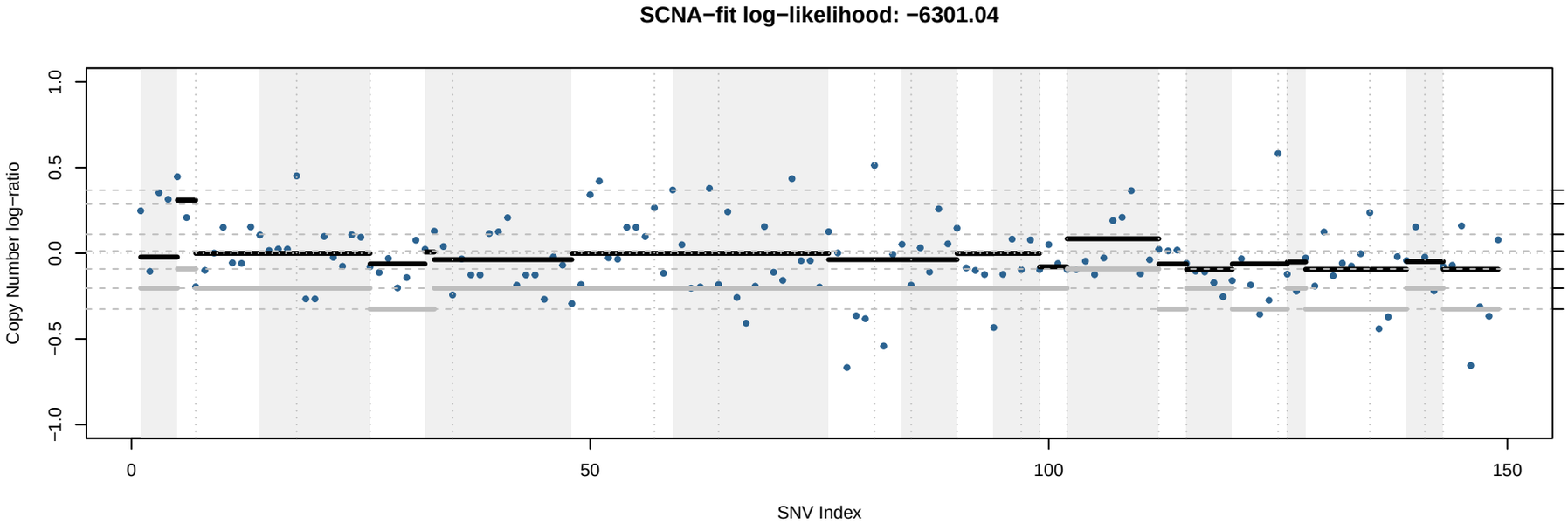

Coverage (log2)
Allelic fraction

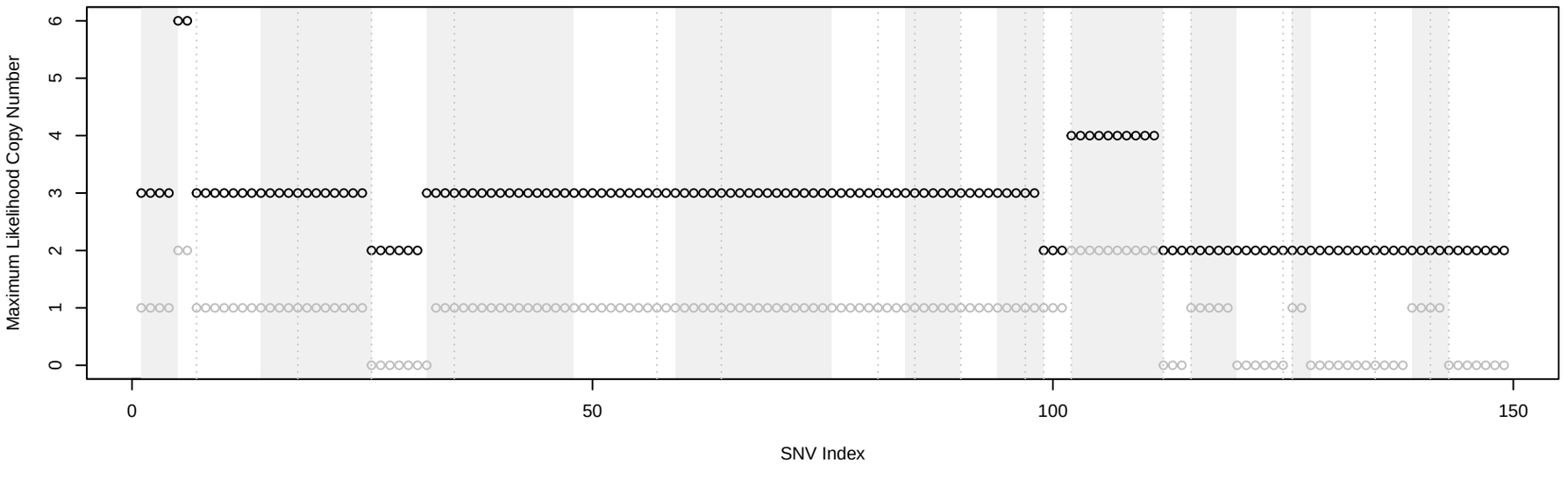

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m2
0m1
1m1
2m1
3m1
5m1
6m1

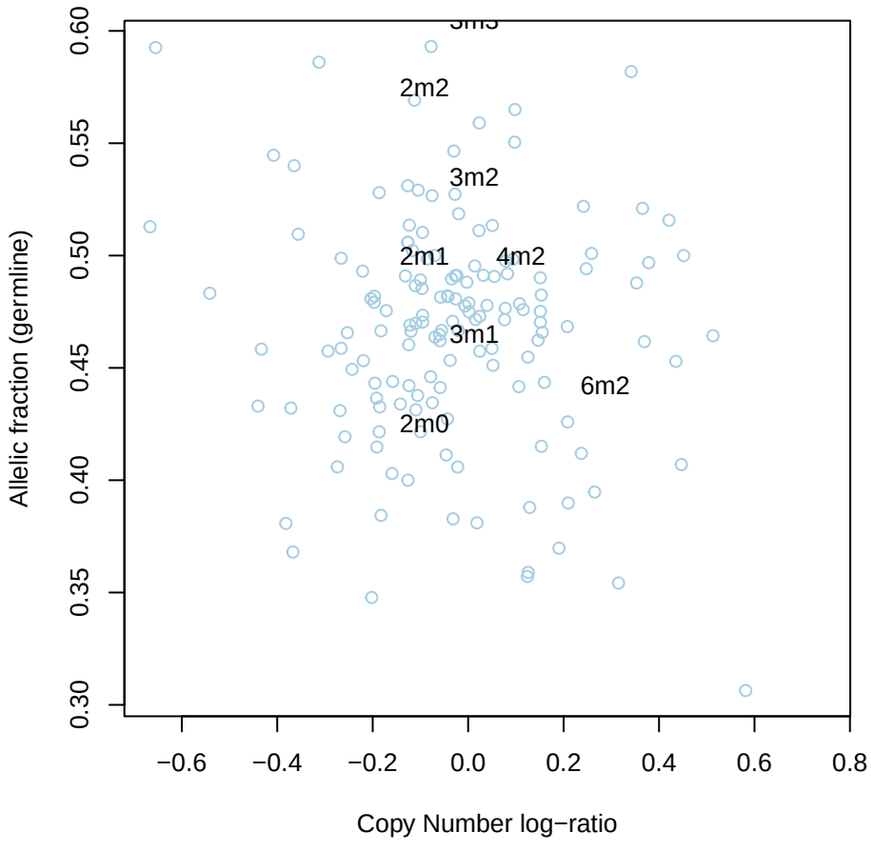

Power 0.8
Frequency
Cellular fraction

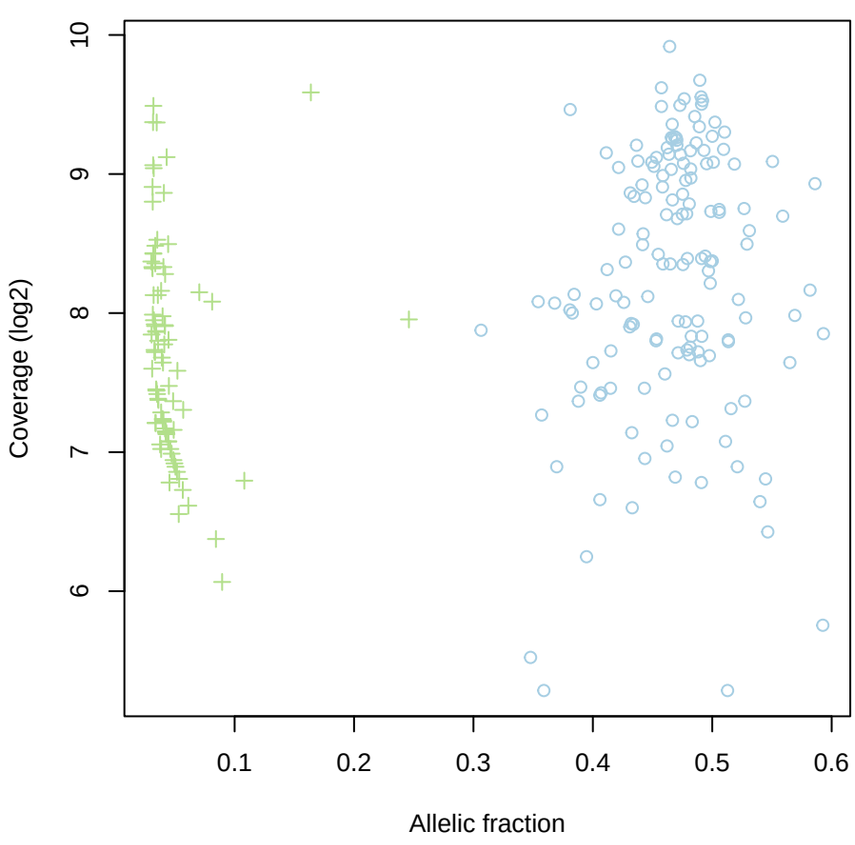

Purity: 0.15 Tumor ploidy: 2.872
0
1
2
3
4
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
1.0
log2 ratio

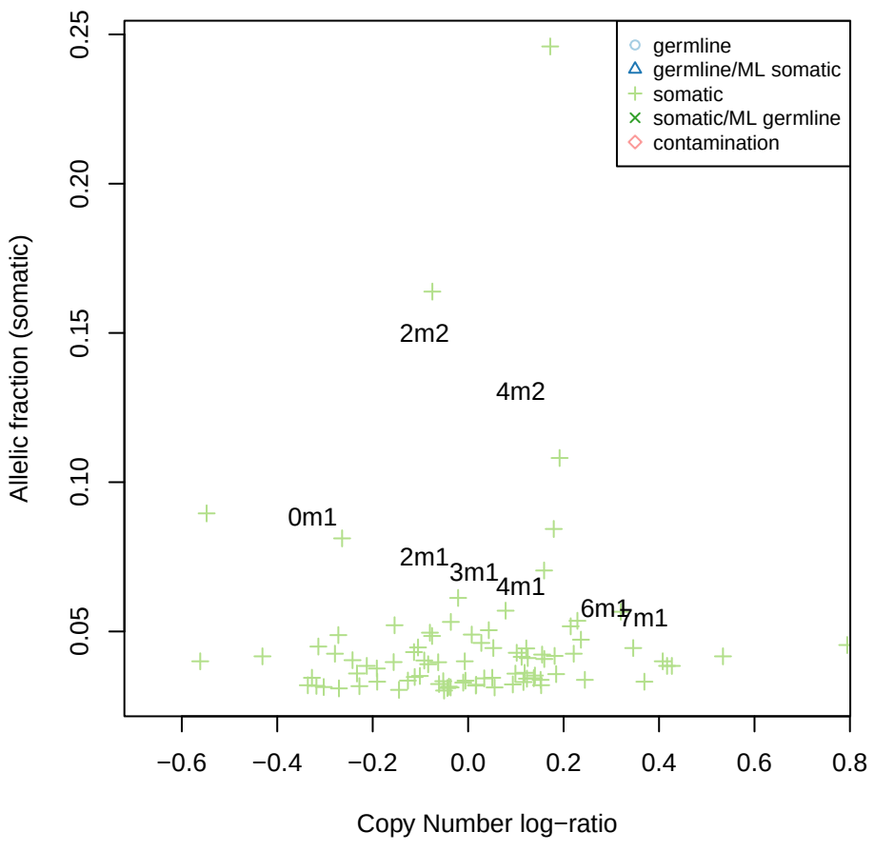

Purity: 0.15 Tumor ploidy: 2.872 SNV log−likelihood: 28.63 GoF: 96.7% Mean coverage: 338;323
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

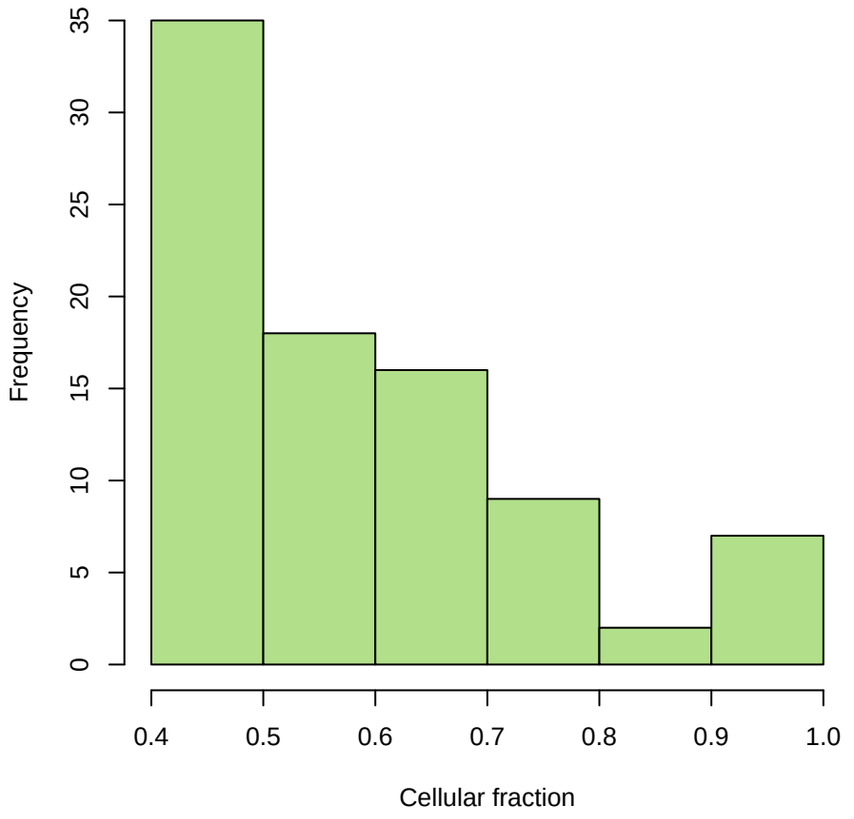

SCNA−fit log−likelihood: −6301.04
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4 6
0 50 100 150
SNV Index

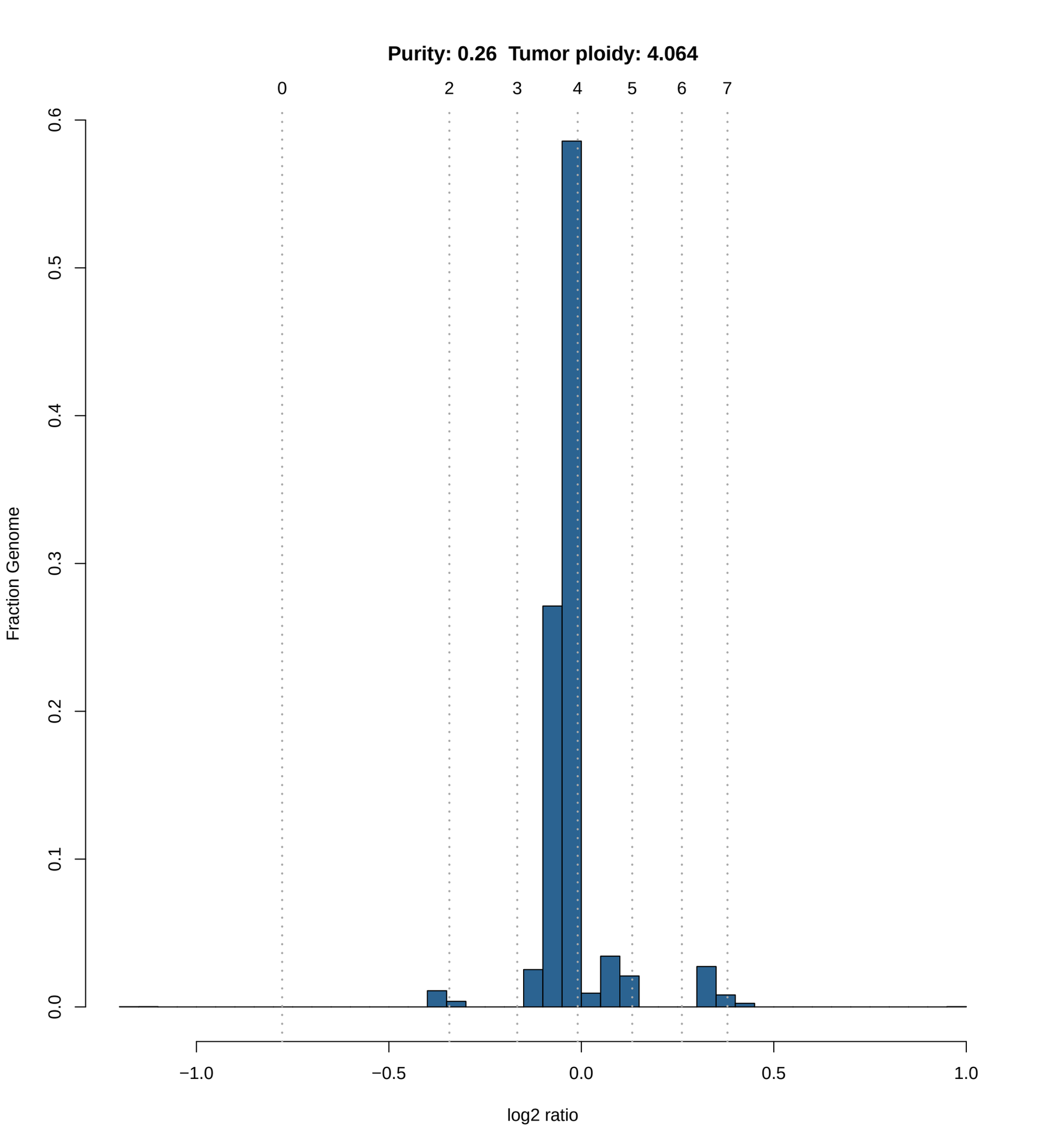

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

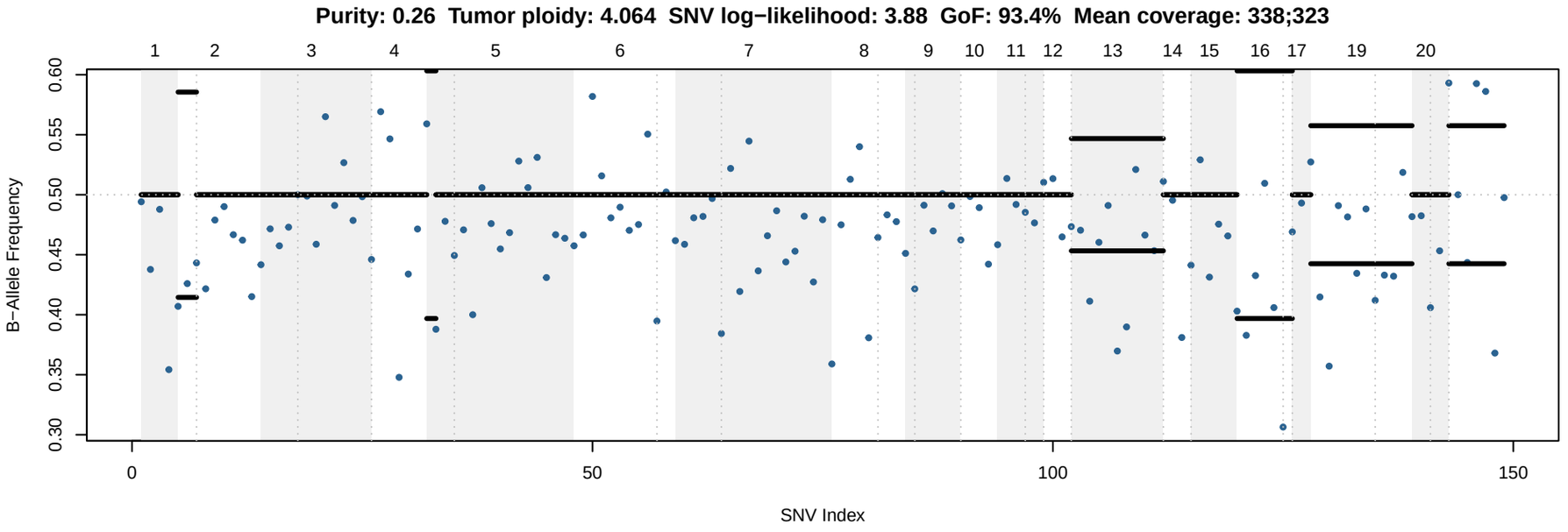

Allelic fraction (germline)
Copy Number log−ratio
2m2
3m2
2m1
4m2
3m1
6m2
2m0

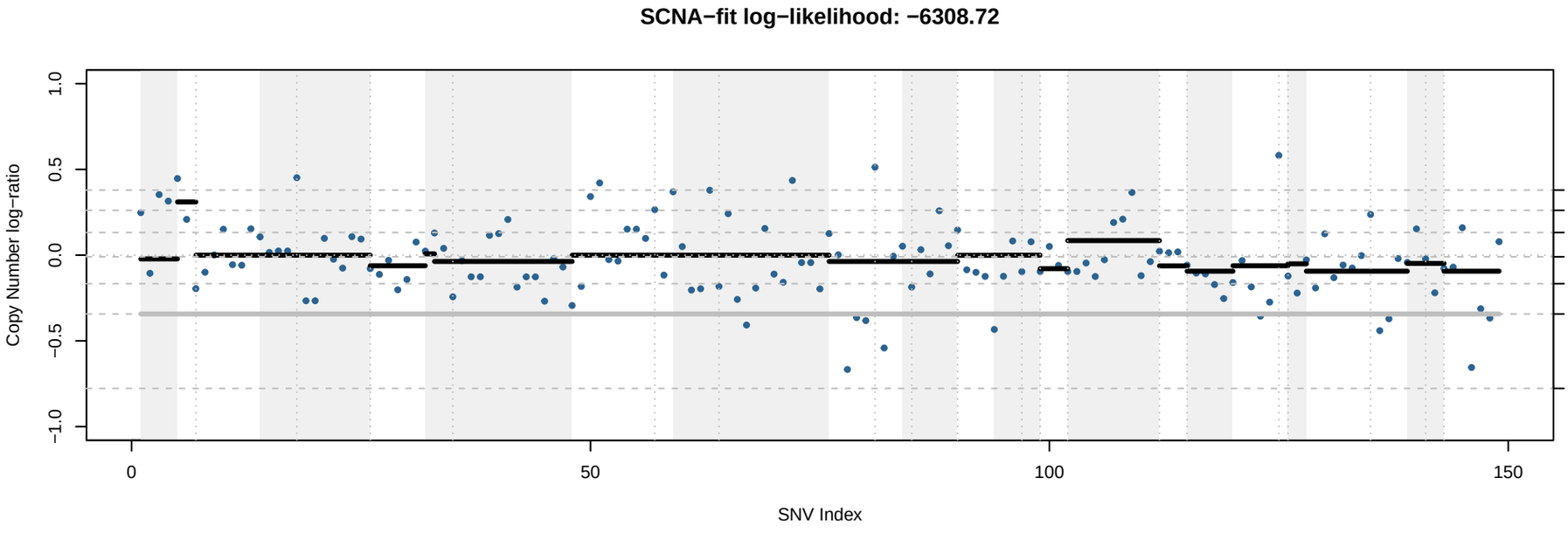

Coverage (log2)
Allelic fraction

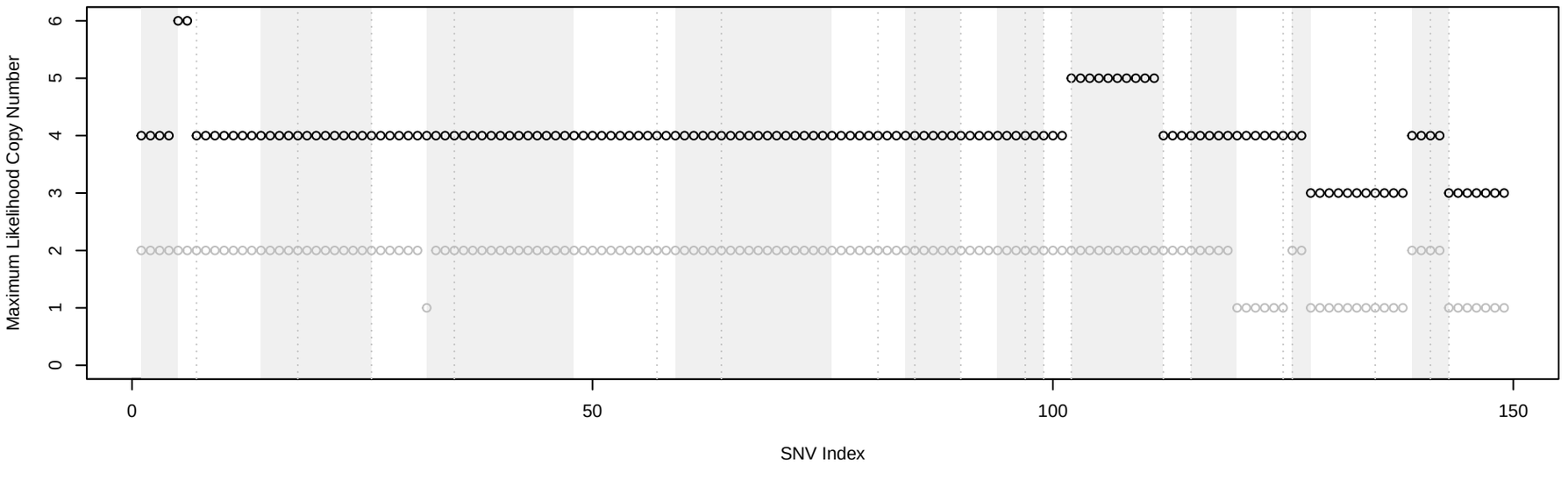

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m2
4m2
0m1
2m1
3m1
4m1
6m1
7m1

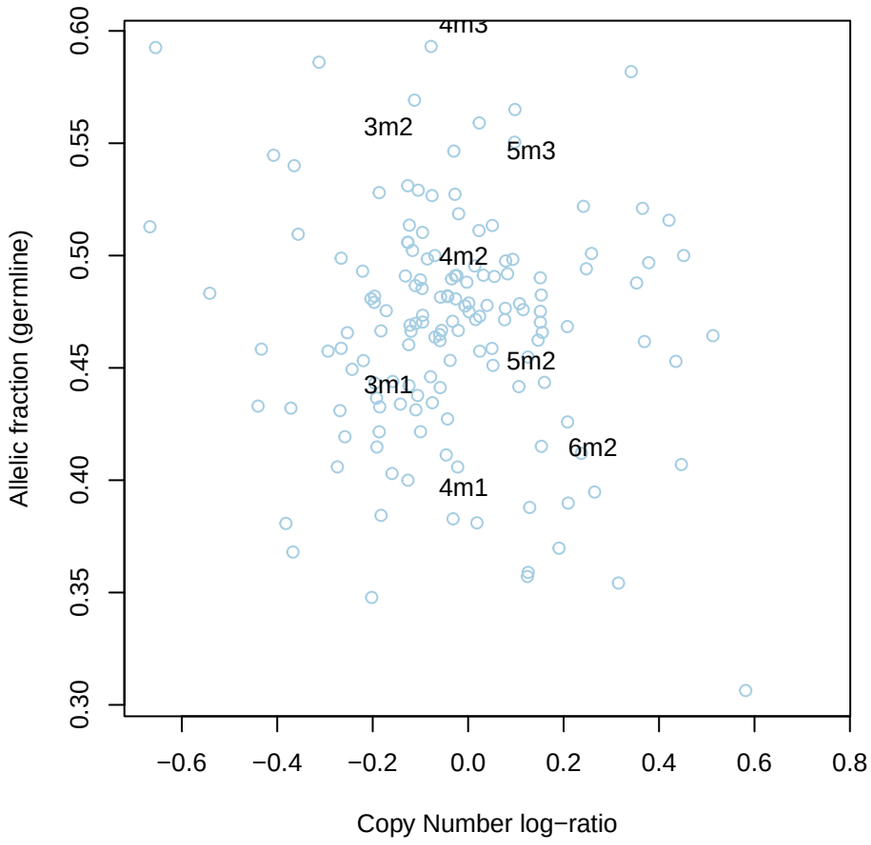

Frequency
Cellular fraction

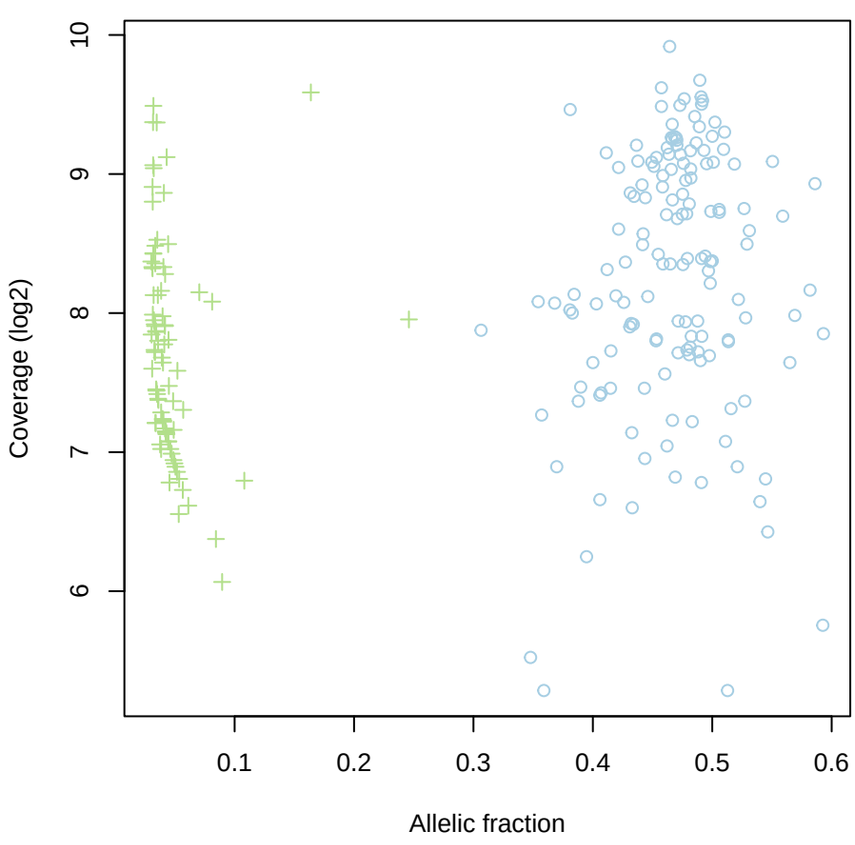

Purity: 0.26 Tumor ploidy: 4.064
0
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

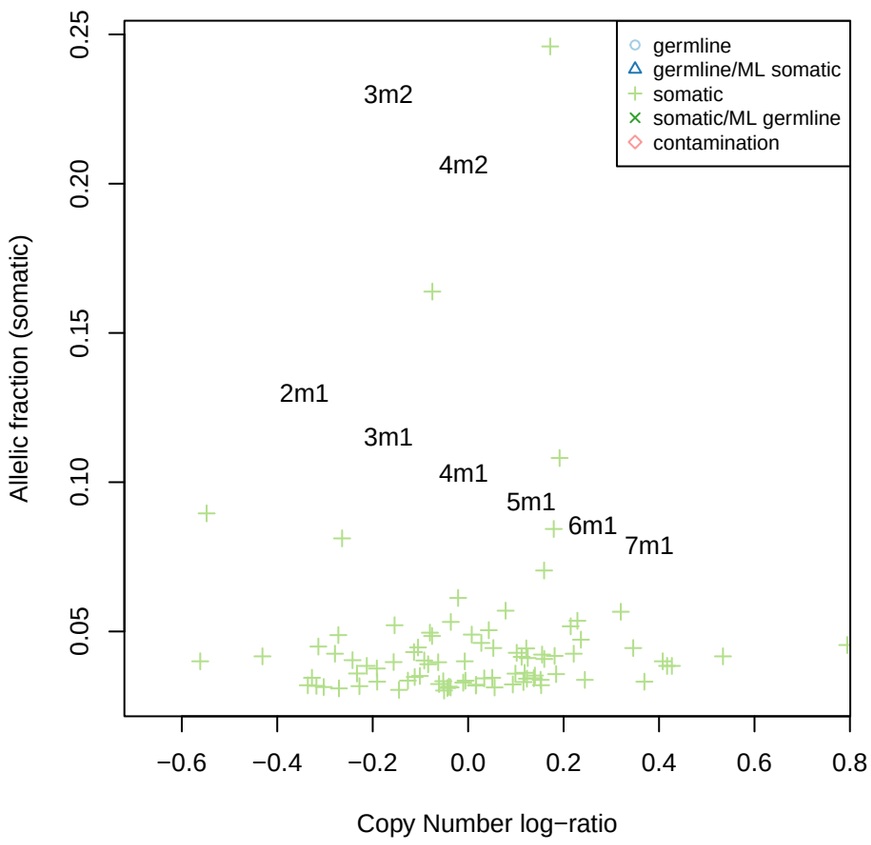

Purity: 0.26 Tumor ploidy: 4.064 SNV log−likelihood: 3.88 GoF: 93.4% Mean coverage: 338;323
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

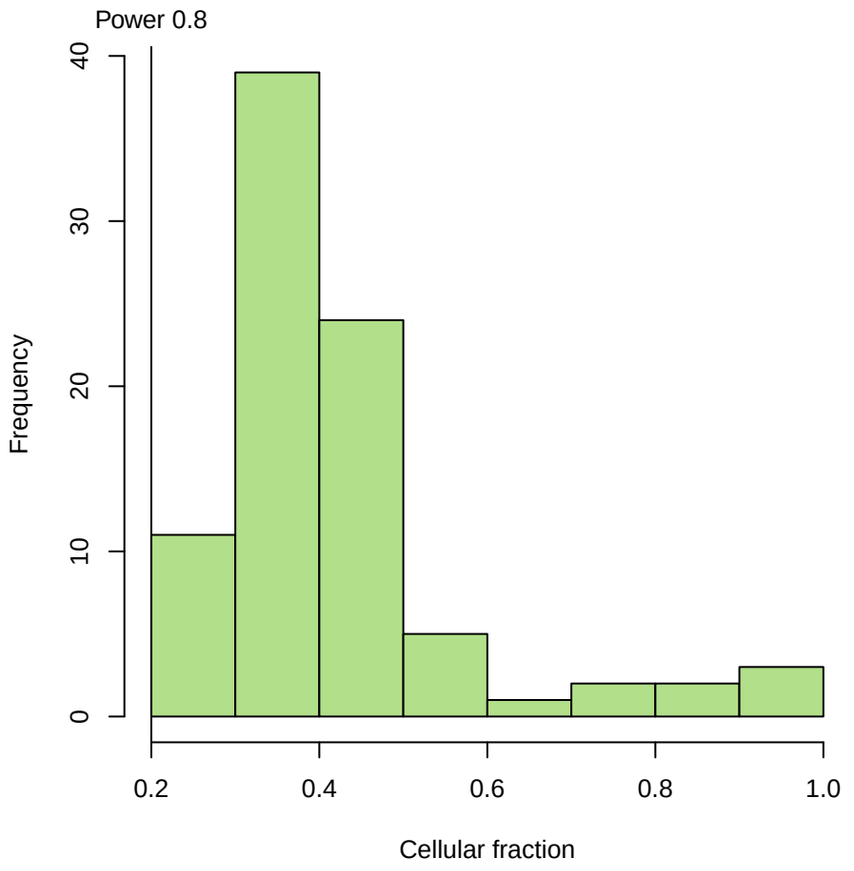

SCNA−fit log−likelihood: −6308.72
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 3 4 6
0 50 100 150
SNV Index

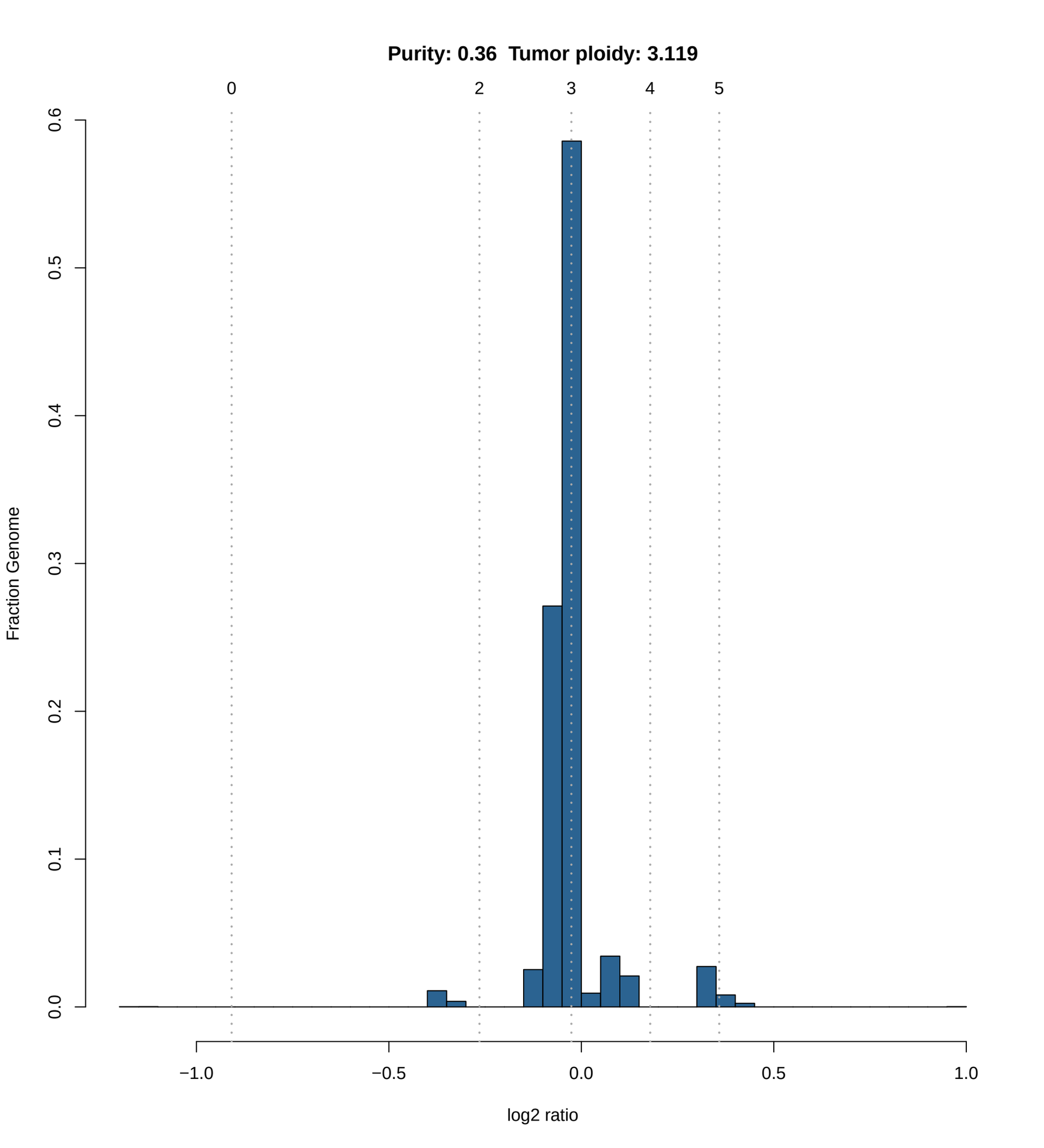

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

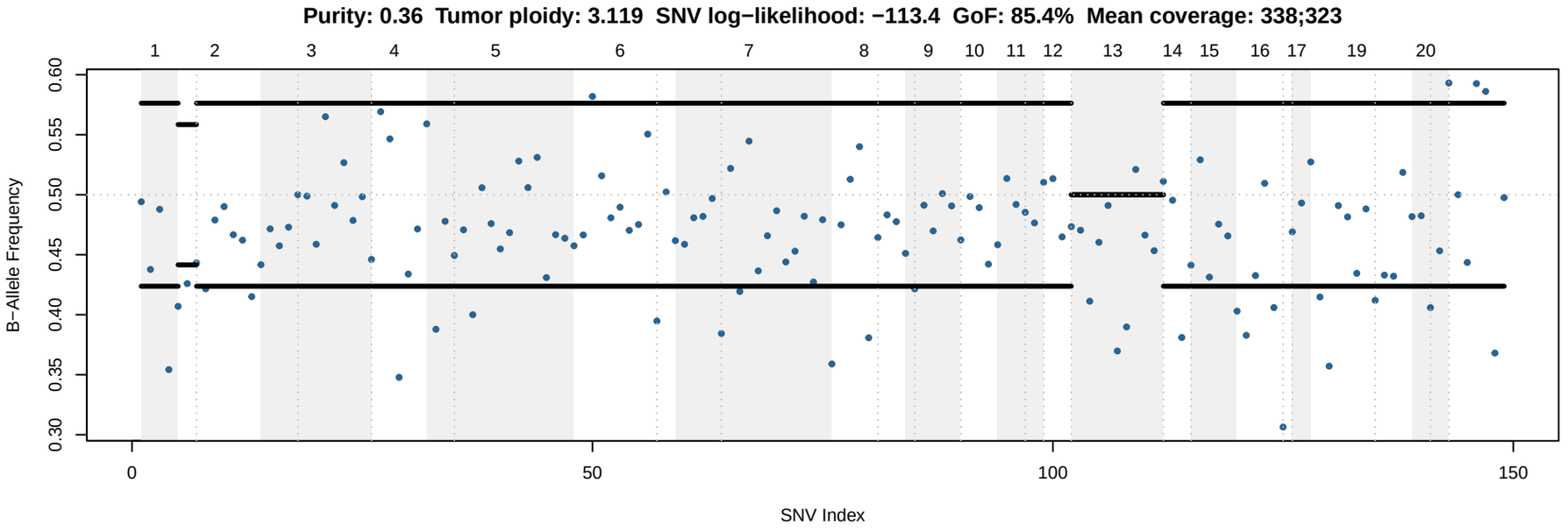

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
5m3
4m2
5m2
3m1
6m2
4m1

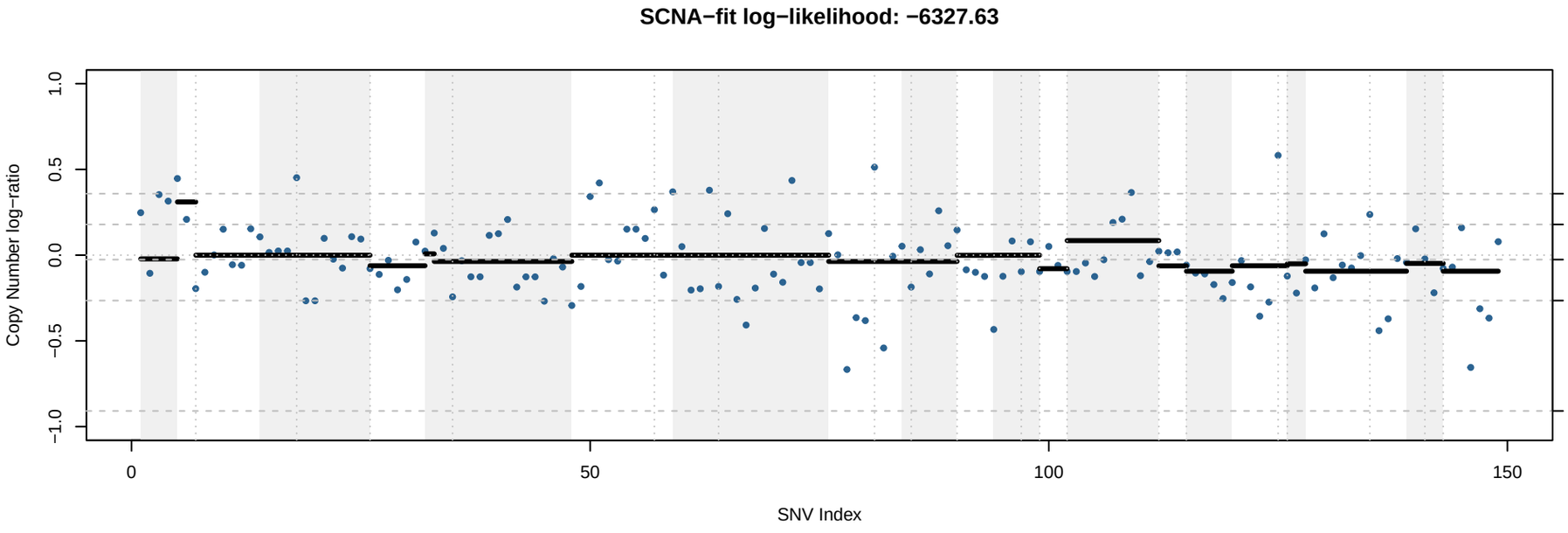

Coverage (log2)
Allelic fraction

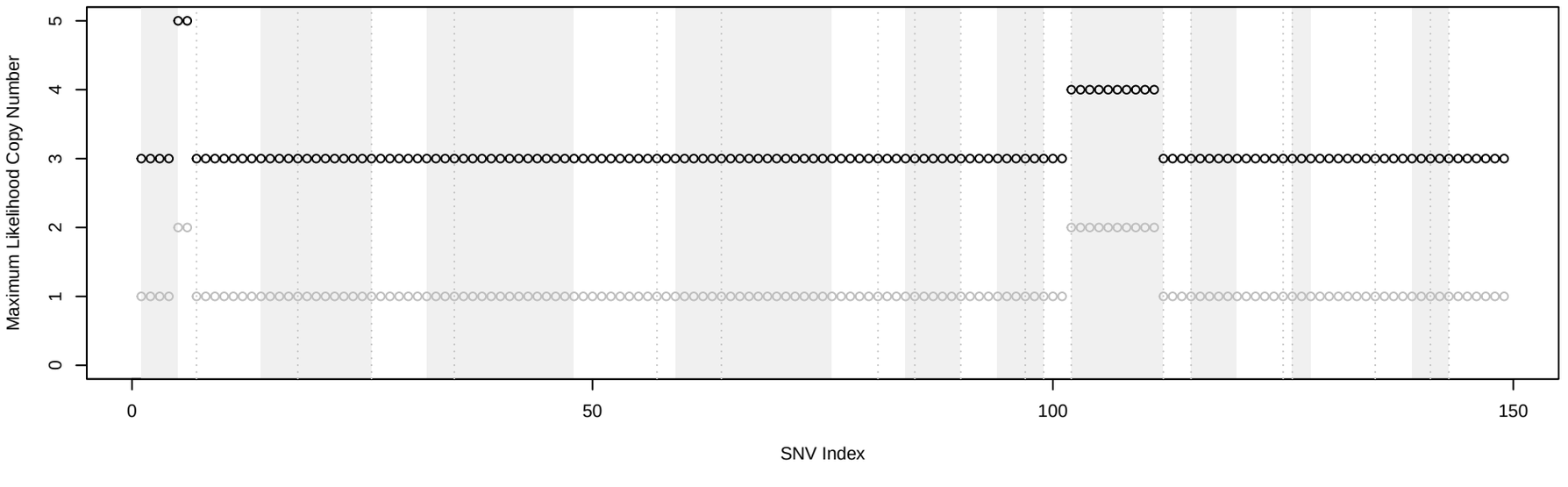

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m2
4m2
2m1
3m1
4m1
5m1
6m1
7m1

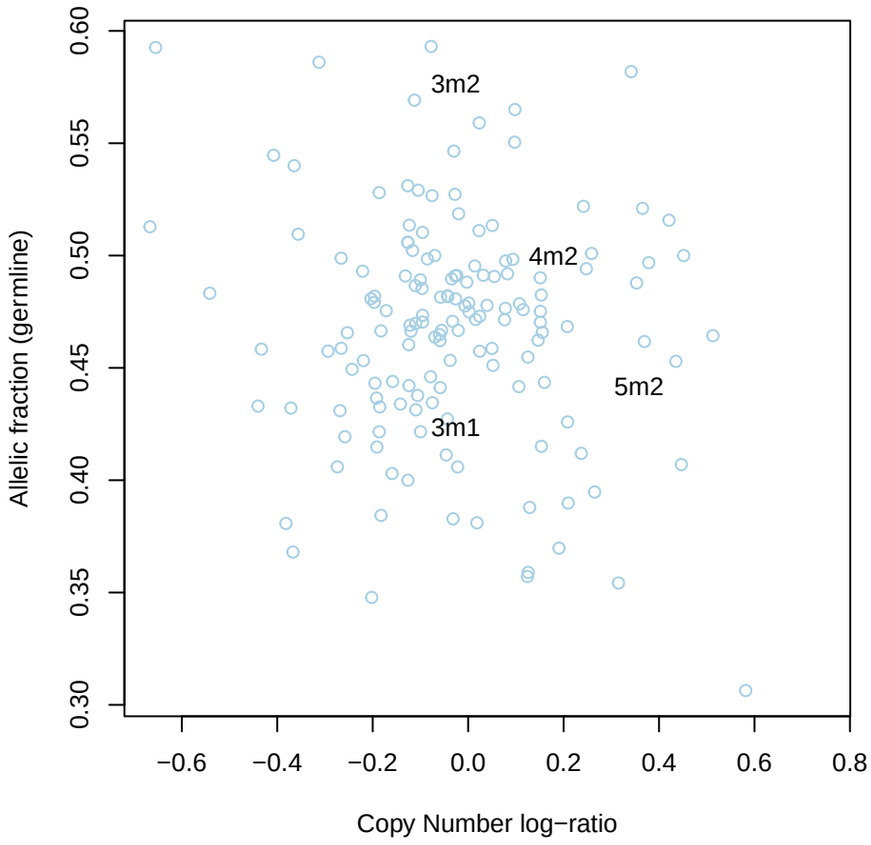

Power 0.8
Frequency
Cellular fraction

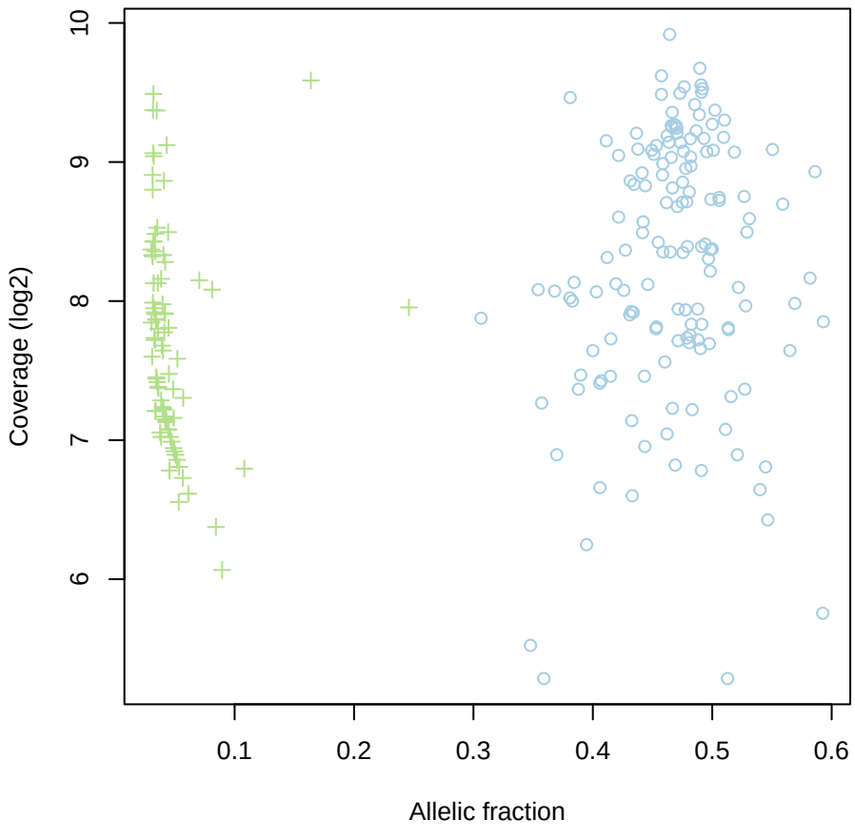

Purity: 0.36 Tumor ploidy: 3.119
0
2
3
4
5
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

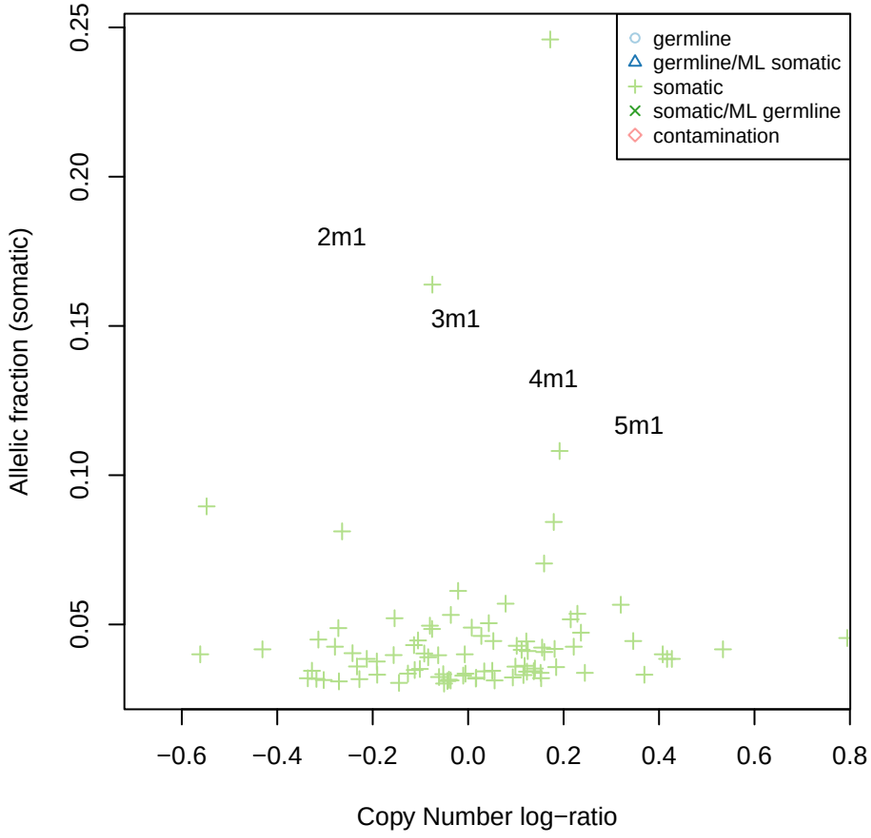

Purity: 0.36 Tumor ploidy: 3.119 SNV log−likelihood: −113.4 GoF: 85.4% Mean coverage: 338;323
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

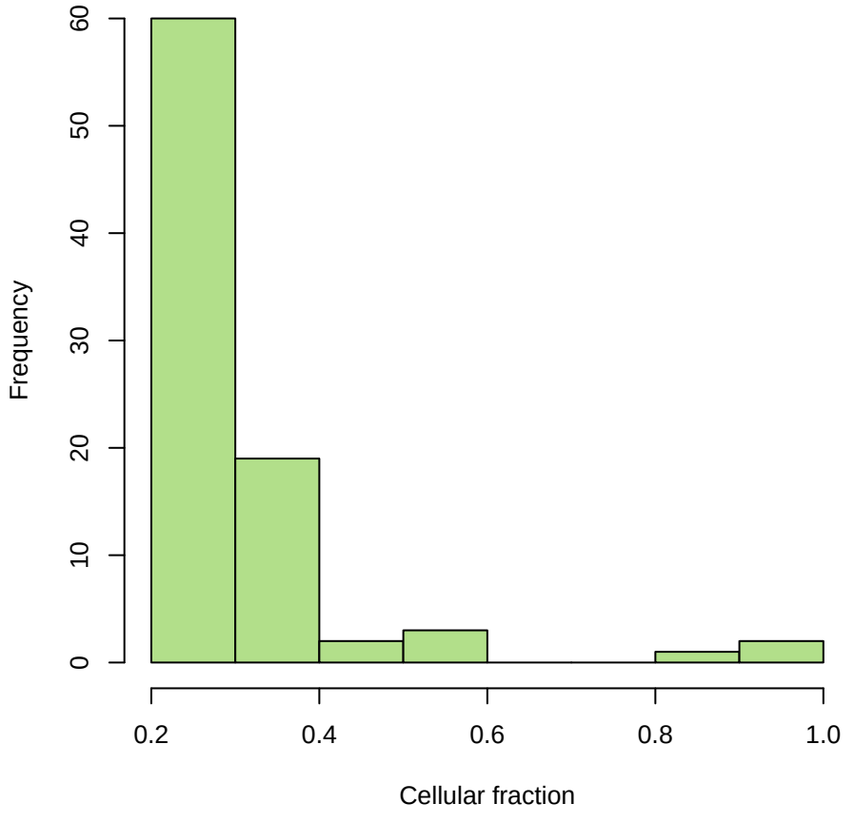

SCNA−fit log−likelihood: −6327.63
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5
0 50 100 150
SNV Index

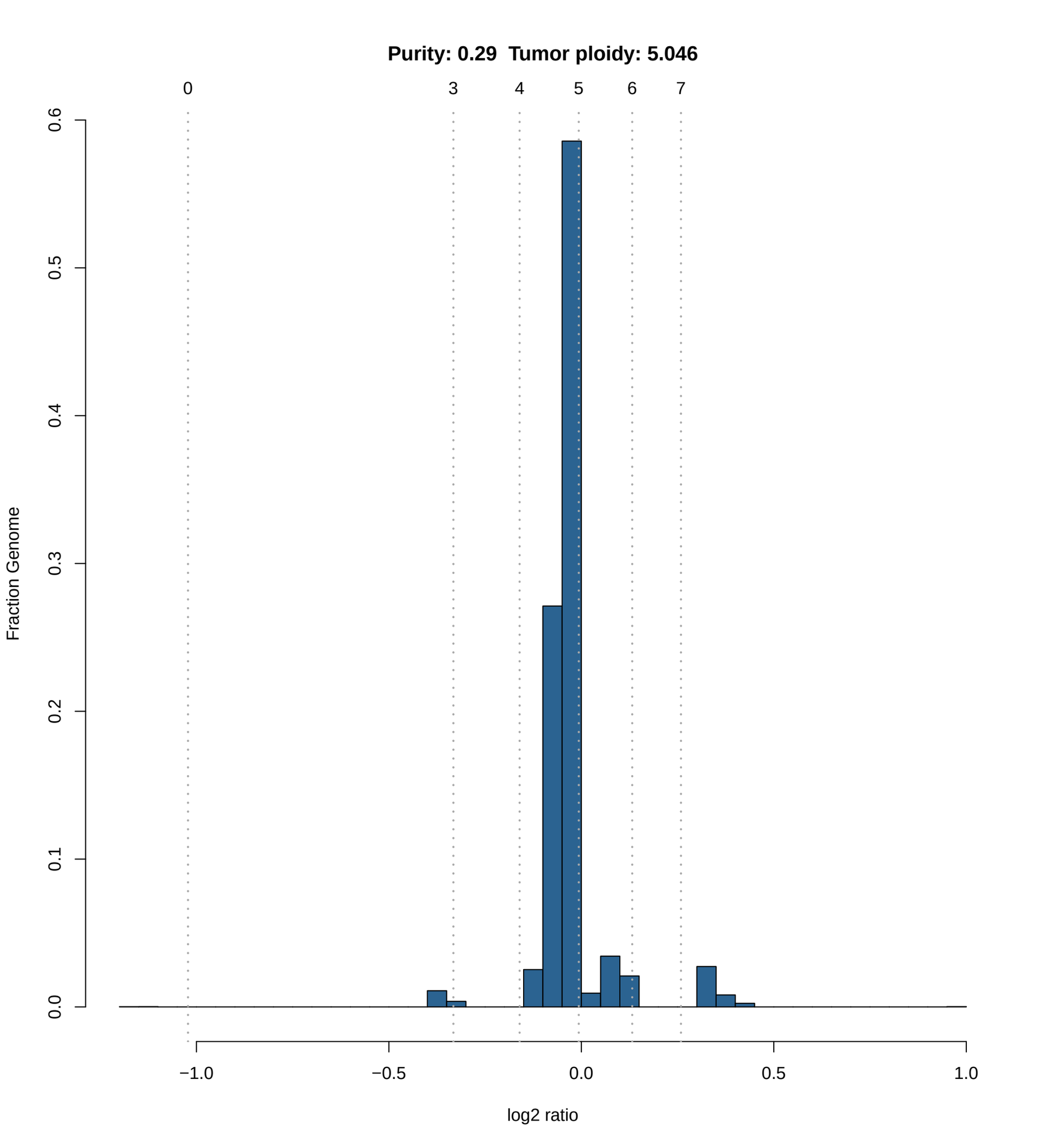

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

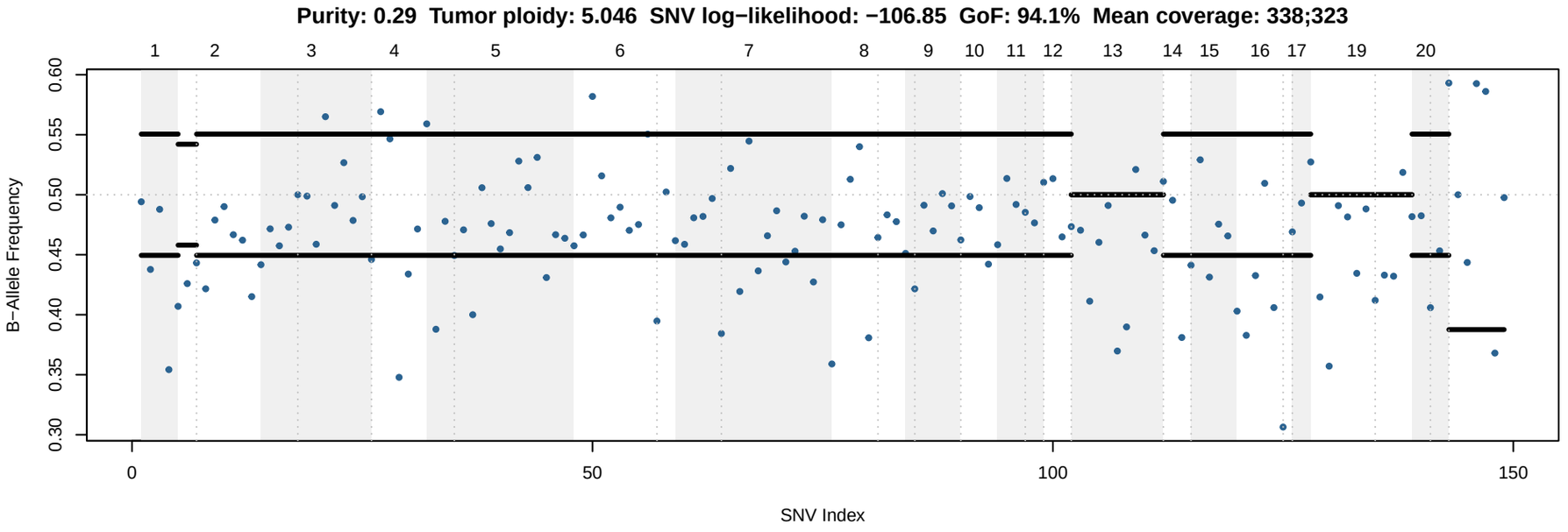

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
3m2
4m2
5m2
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

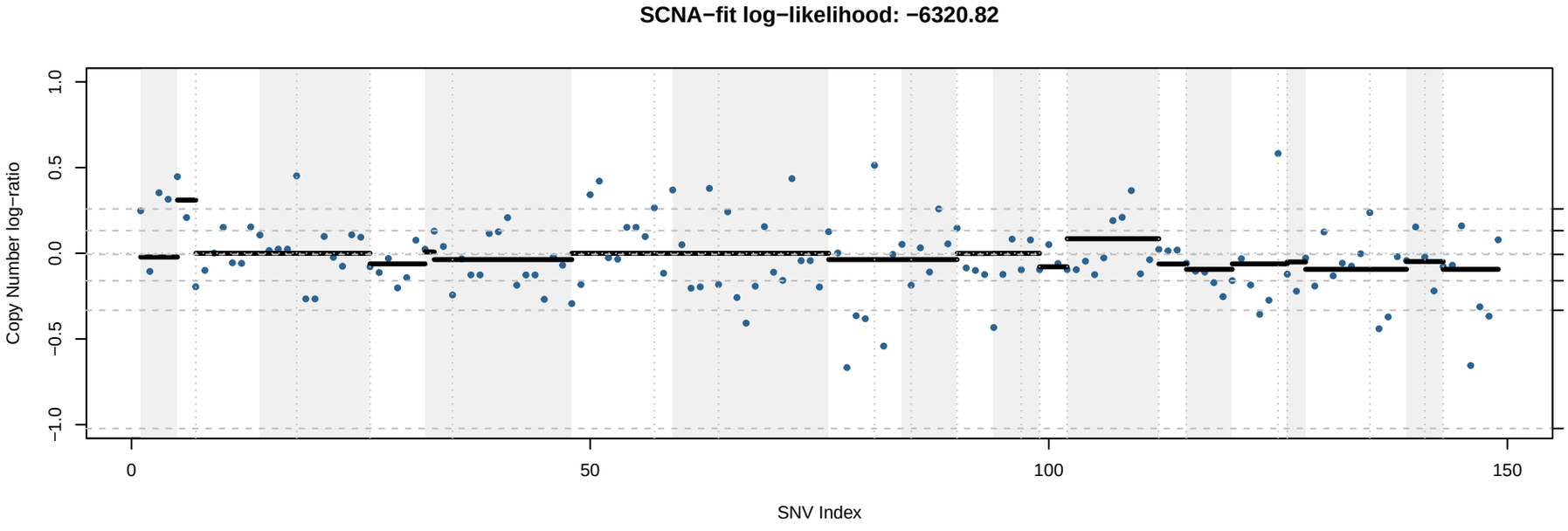

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

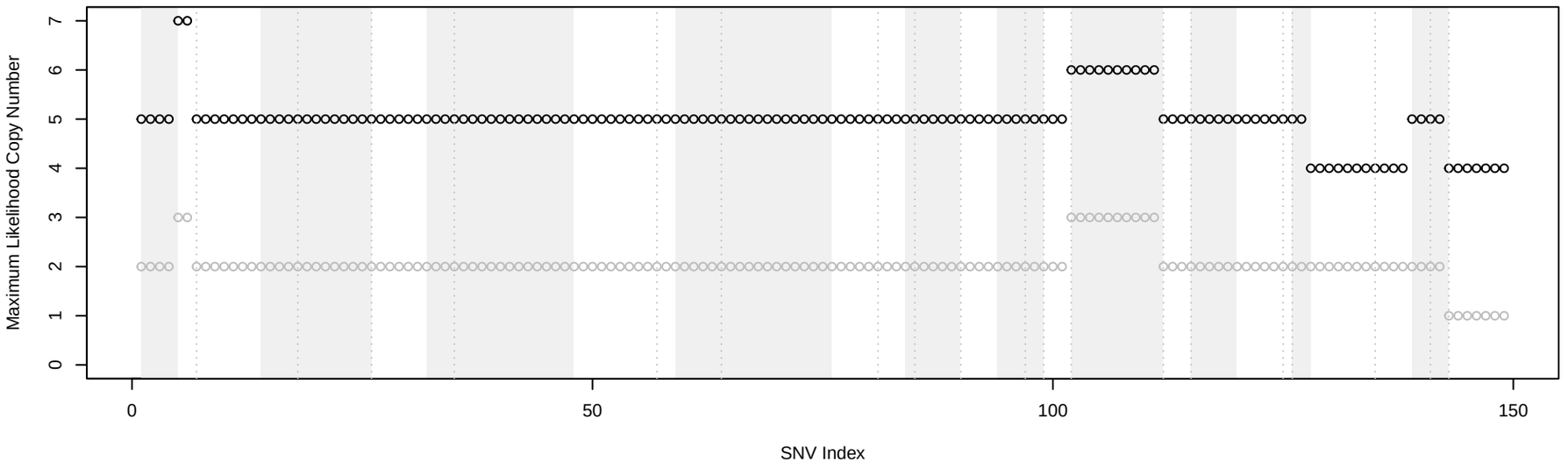

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1
5m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

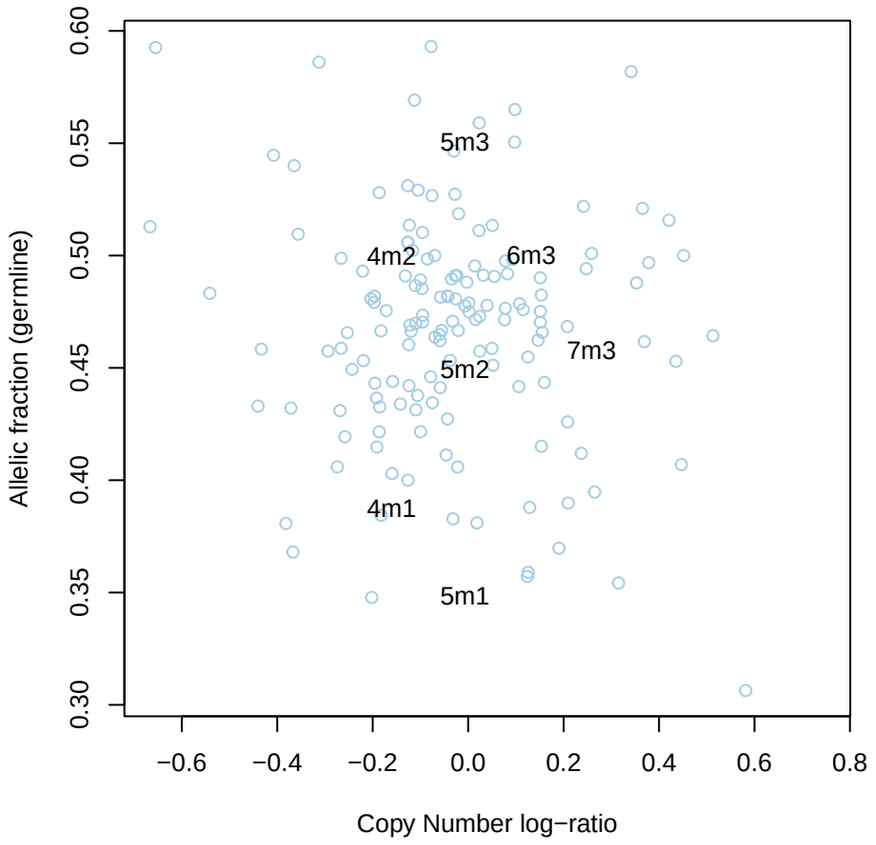

Frequency
0
10
20
30
40
50
60
0.2
0.4
0.6
0.8
1.0
Cellular fraction

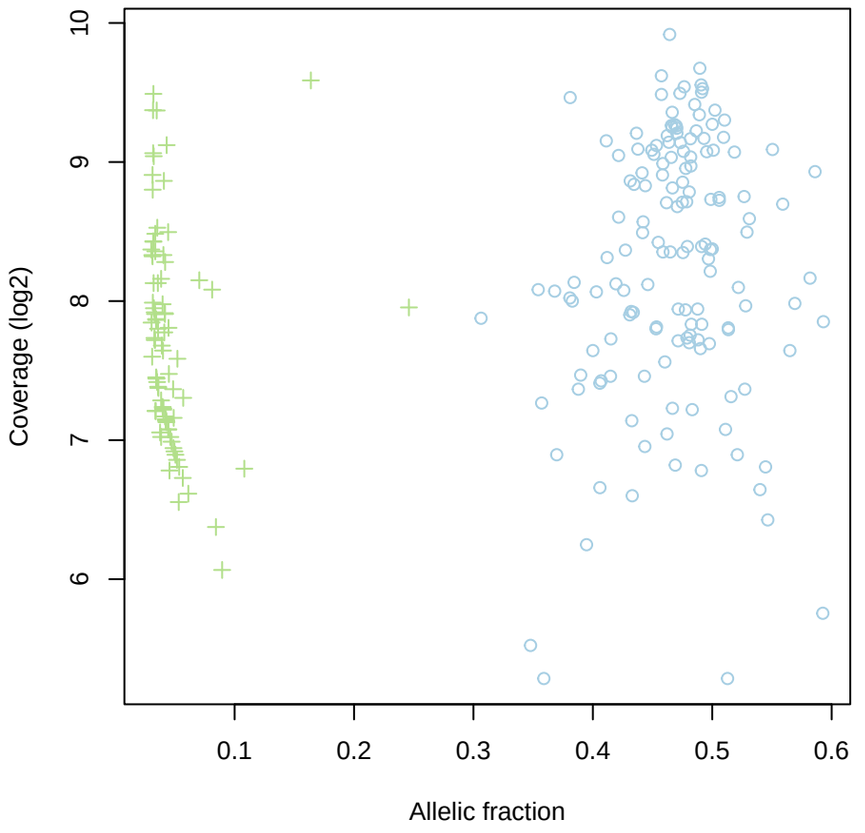

Purity: 0.29 Tumor ploidy: 5.046
0
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

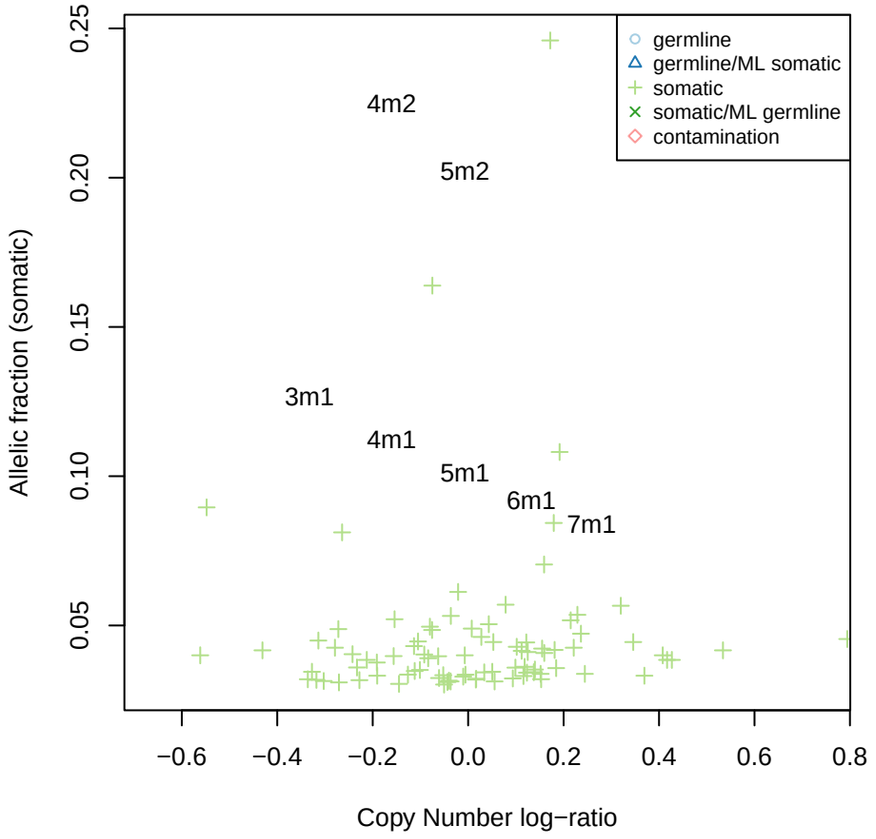

Purity: 0.29 Tumor ploidy: 5.046 SNV log−likelihood: −106.85 GoF: 94.1% Mean coverage: 338;323
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

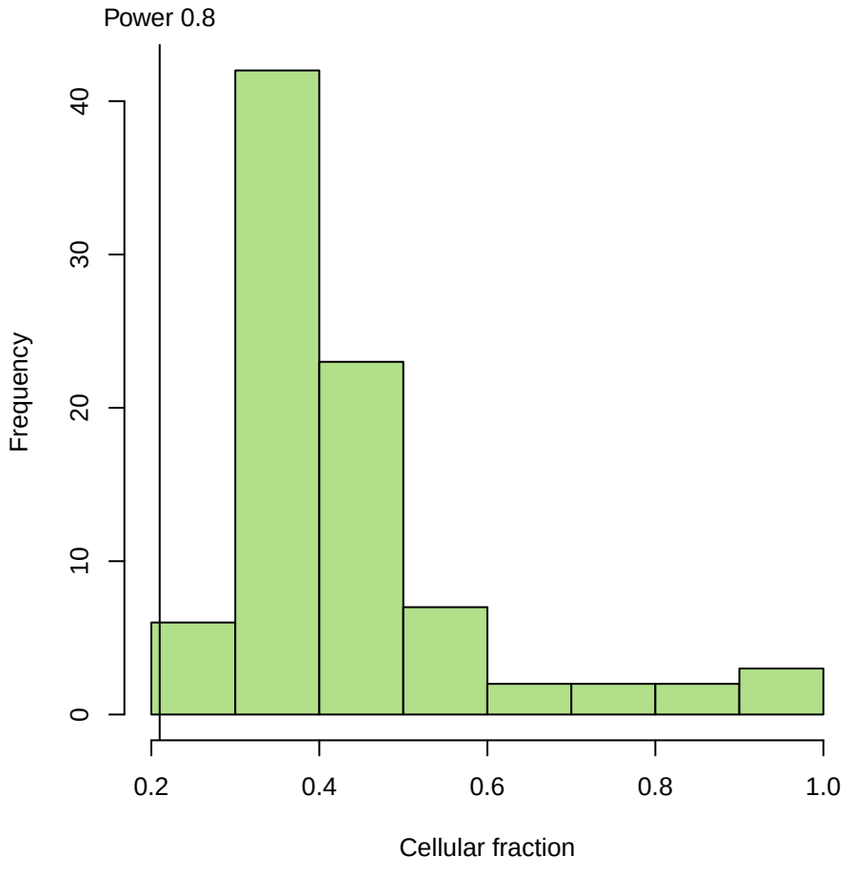

SCNA−fit log−likelihood: −6320.82
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 3 4 5 7
0 50 100 150
SNV Index

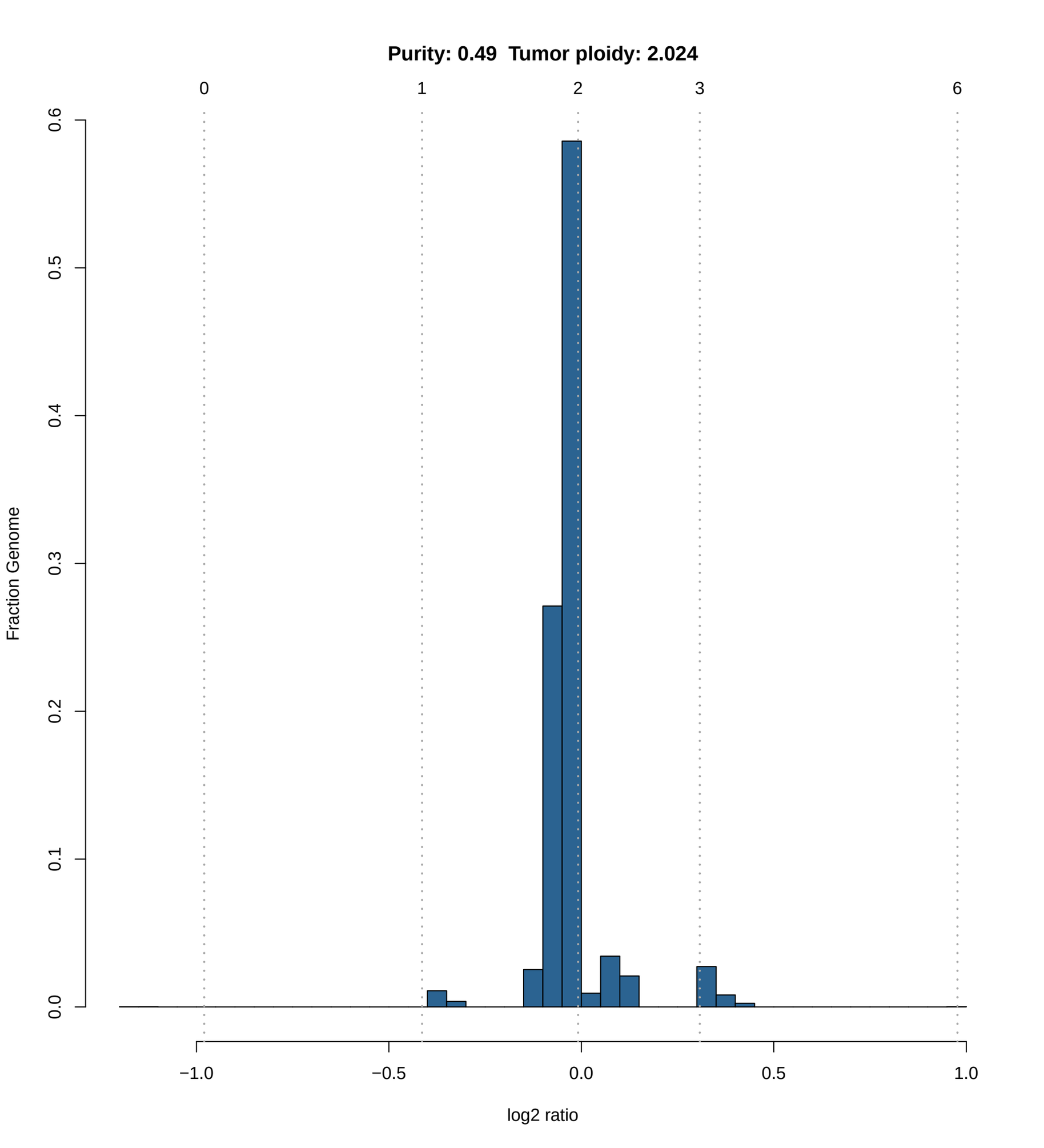

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

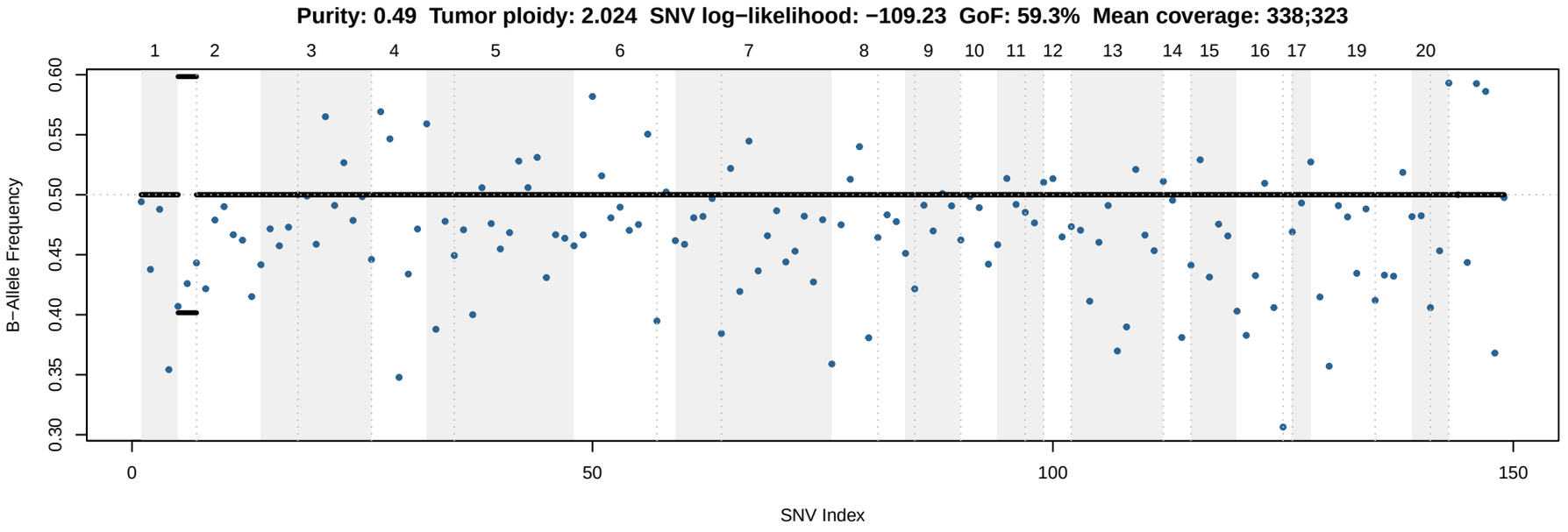

Allelic fraction (germline)
Copy Number log−ratio
5m3
4m2
6m3
7m3
5m2
4m1
5m1

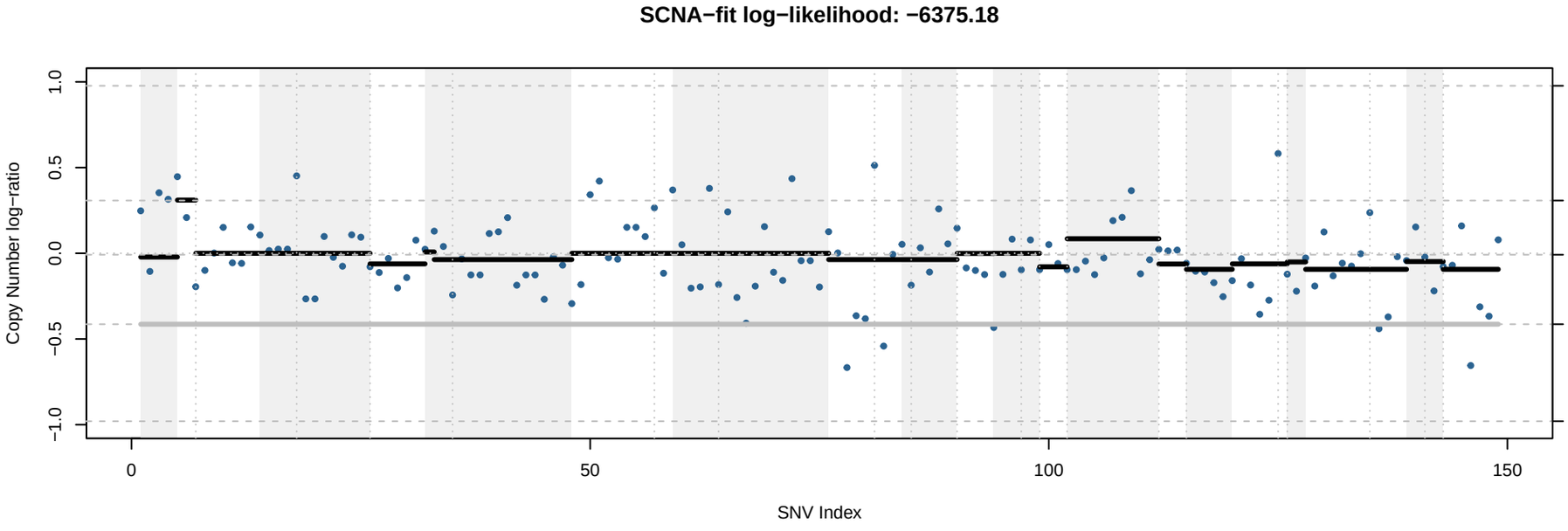

Coverage (log2)
Allelic fraction

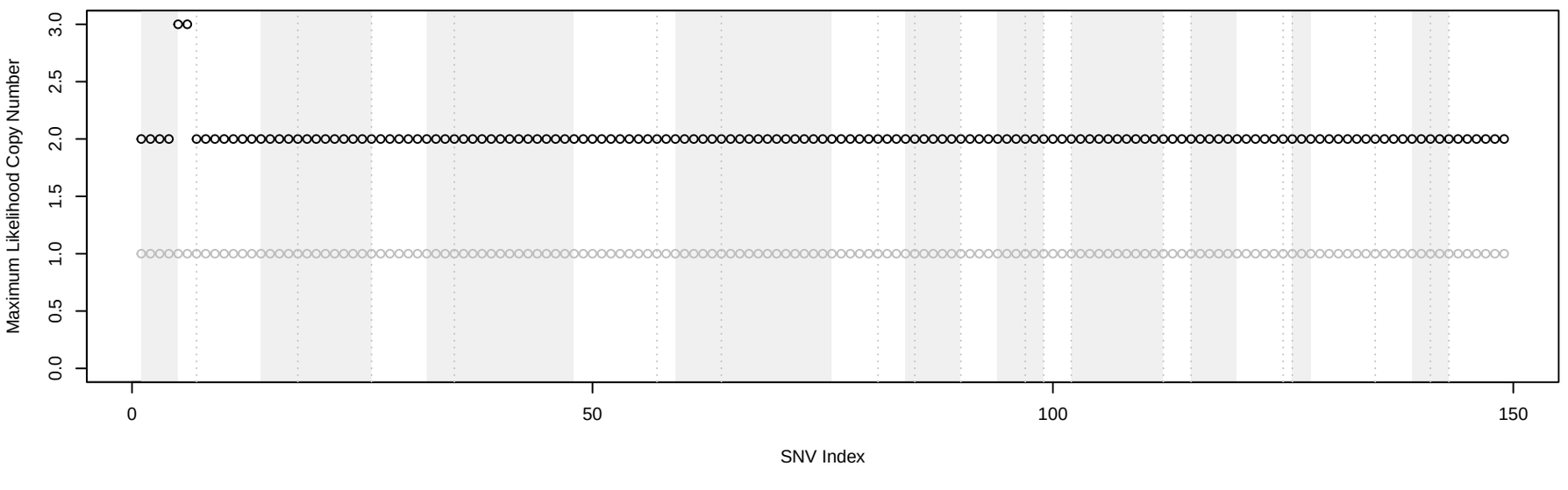

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m2
5m2
3m1
4m1
5m1
6m1
7m1

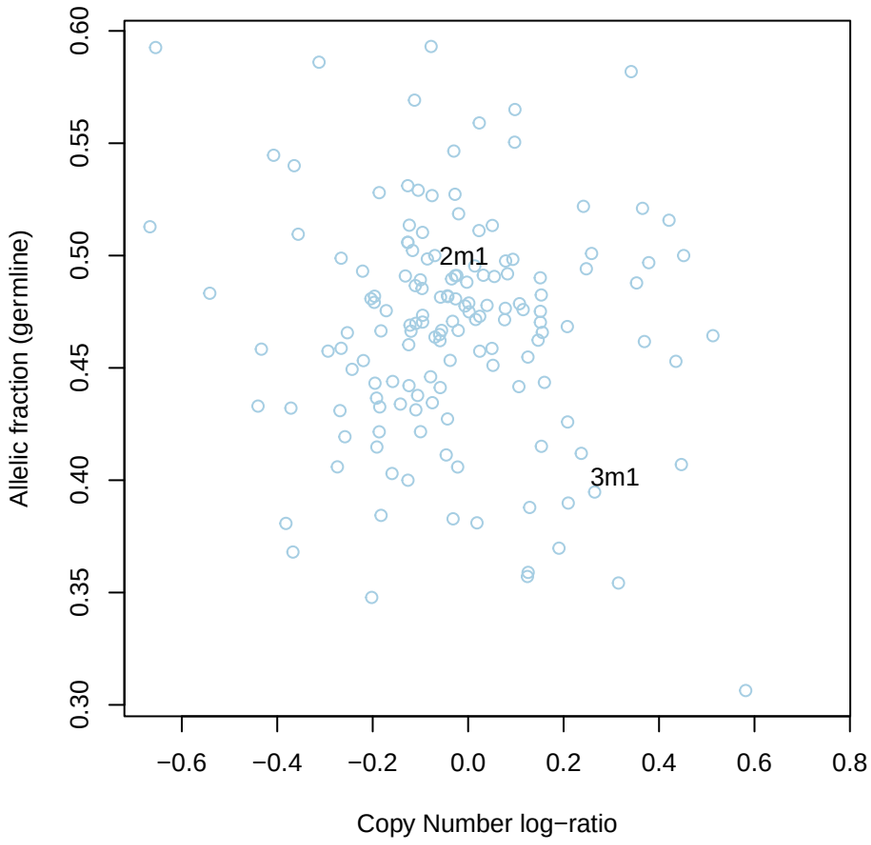

Power 0.8
Frequency
Cellular fraction

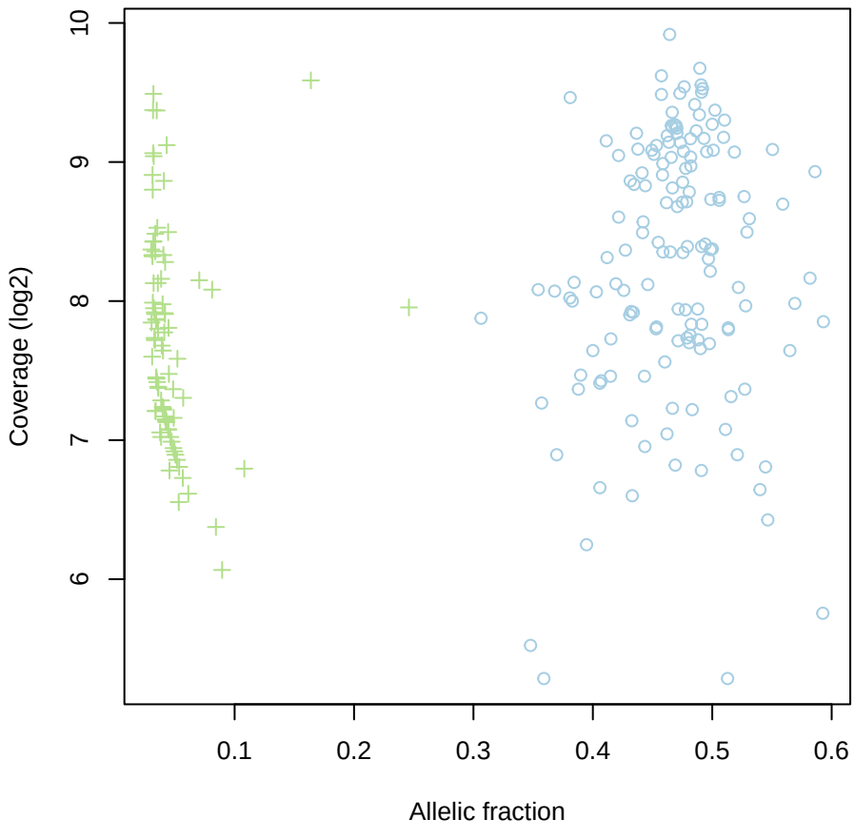

Purity: 0.49 Tumor ploidy: 2.024
0
1
2
3
6
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

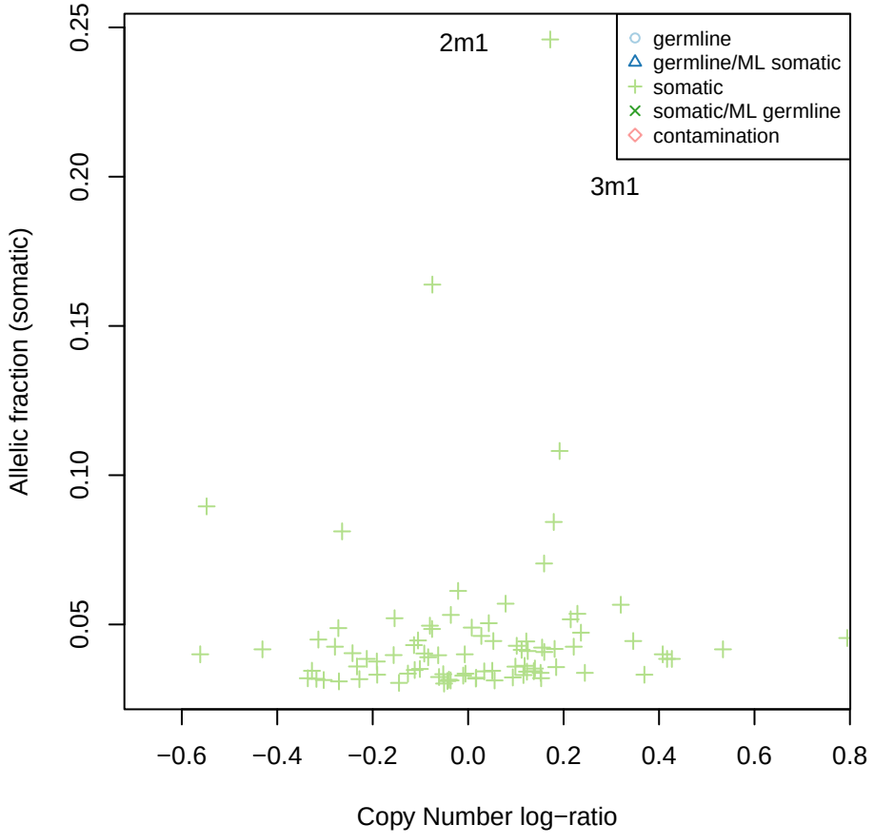

Purity: 0.49 Tumor ploidy: 2.024 SNV log−likelihood: −109.23 GoF: 59.3% Mean coverage: 338;323
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

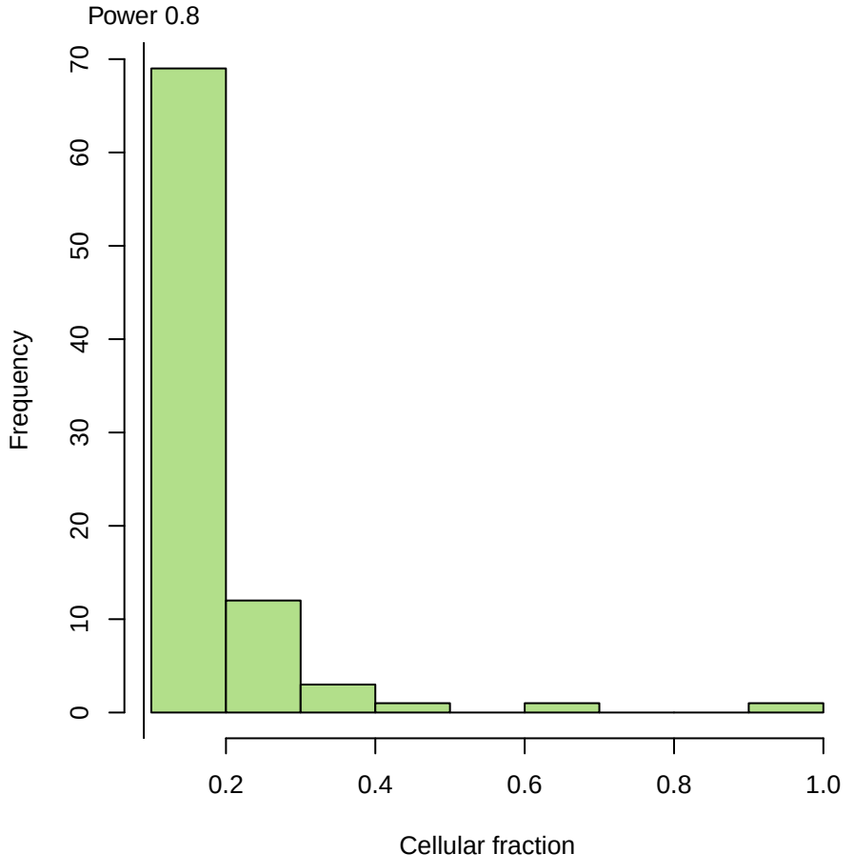

SCNA−fit log−likelihood: −6375.18
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 6
0 50 100 150
SNV Index

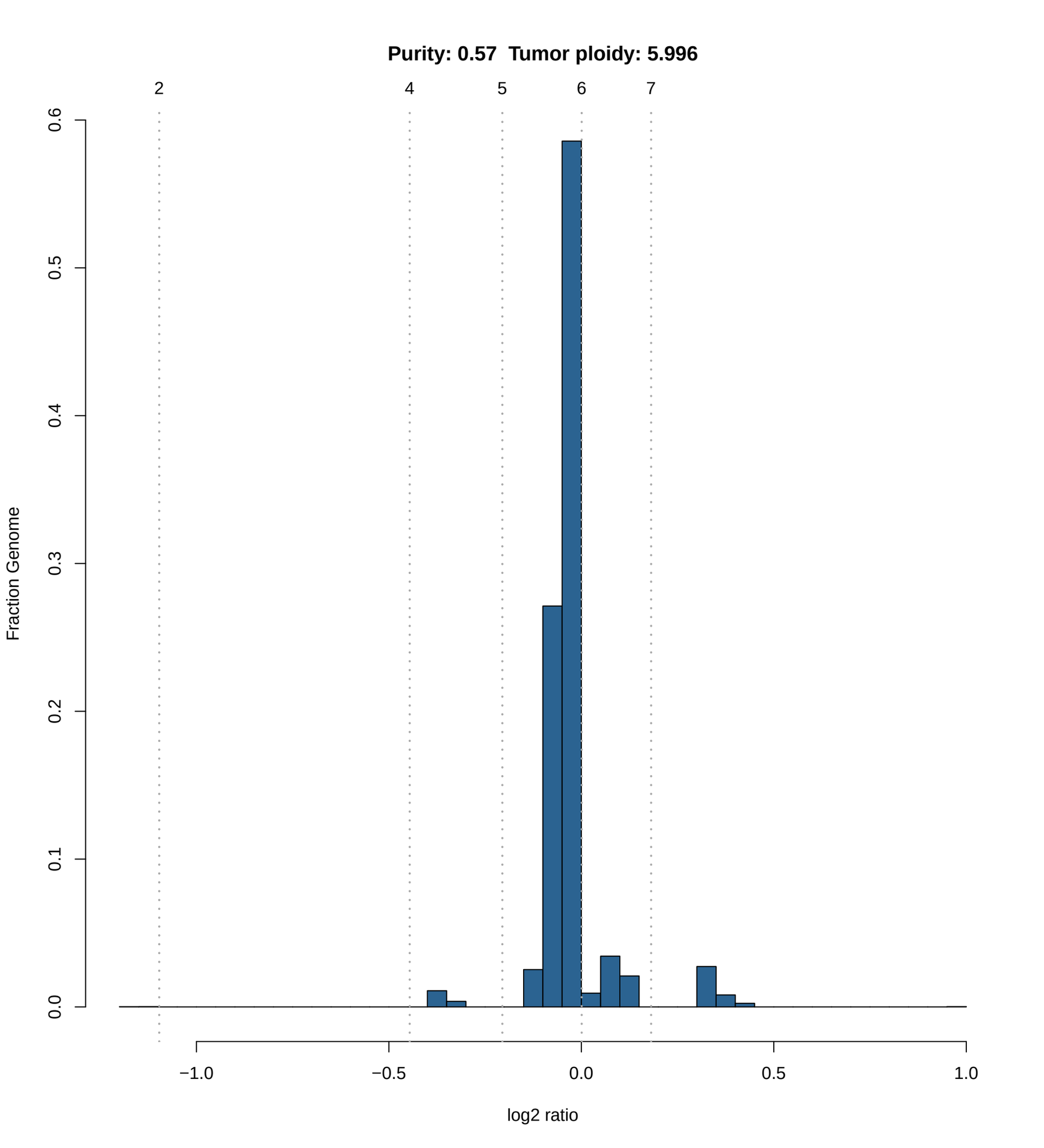

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
∞
0 50 100 150
SNV Index

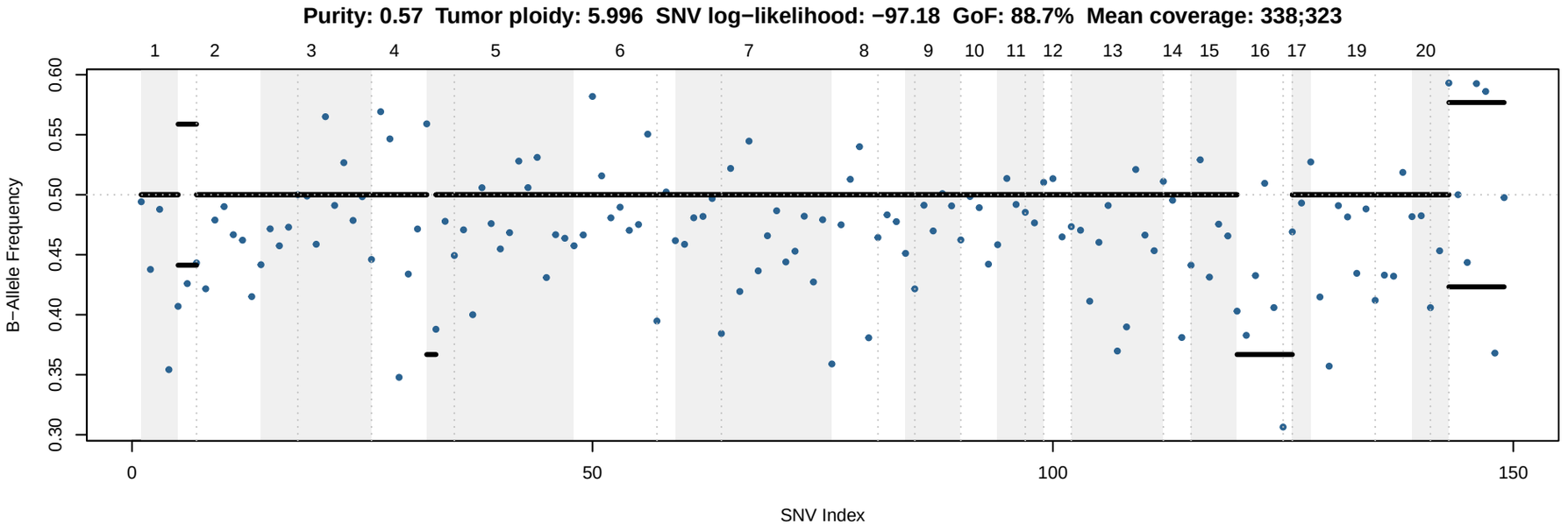

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
2m1
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

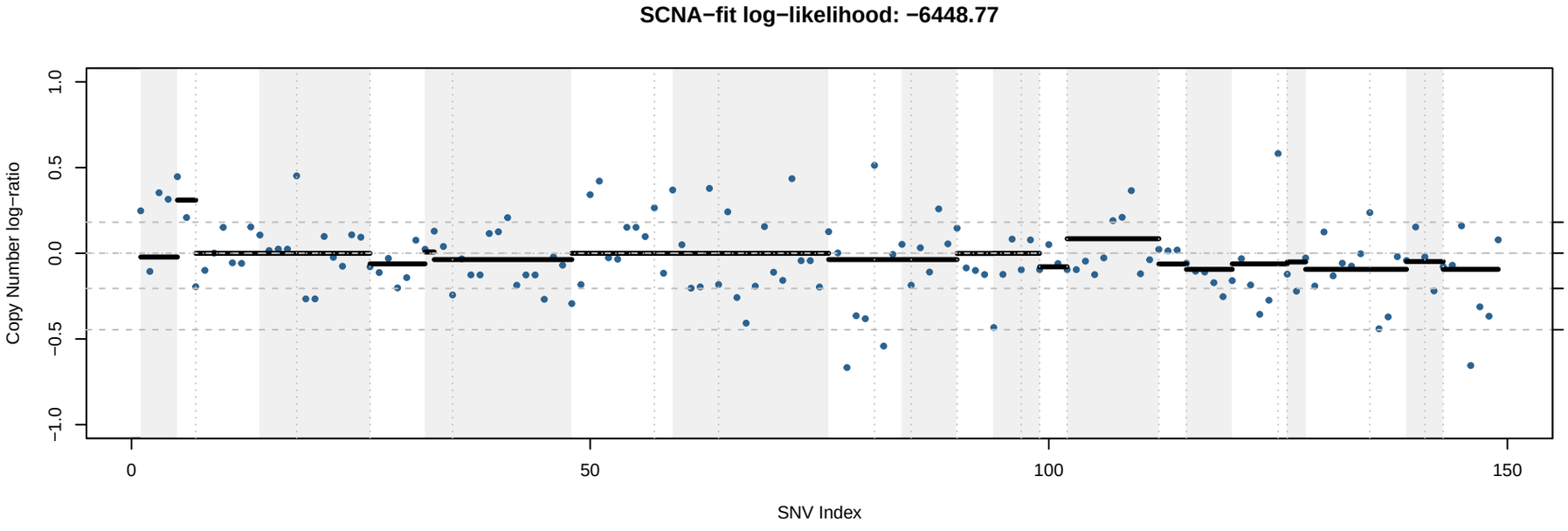

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

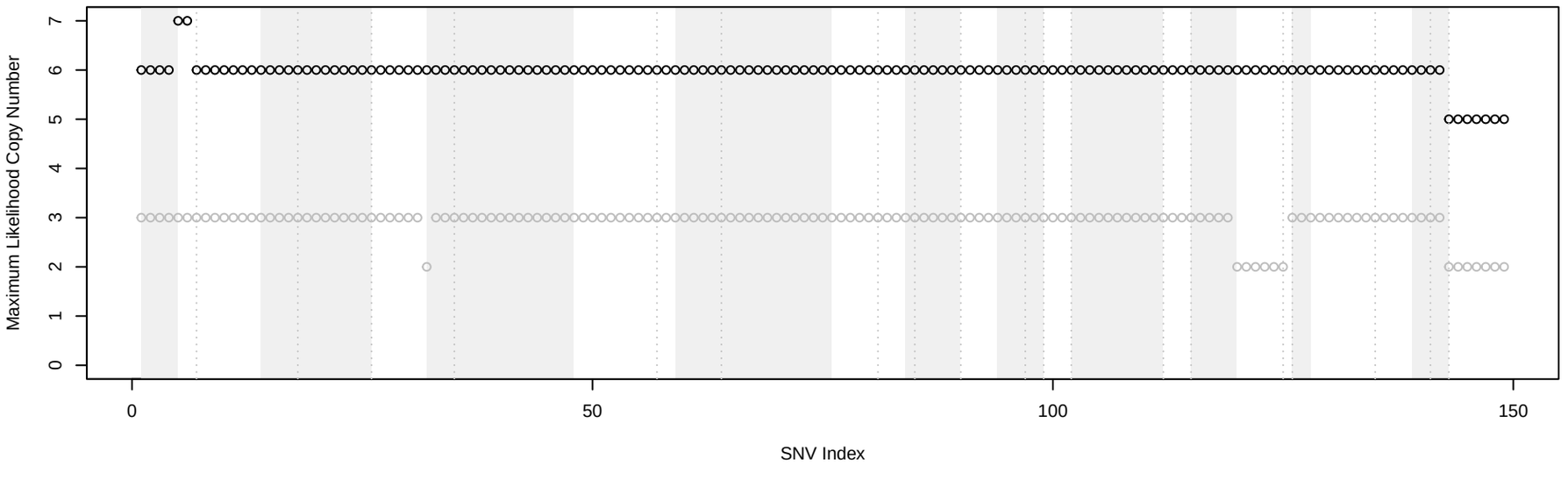

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
2m1
3m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

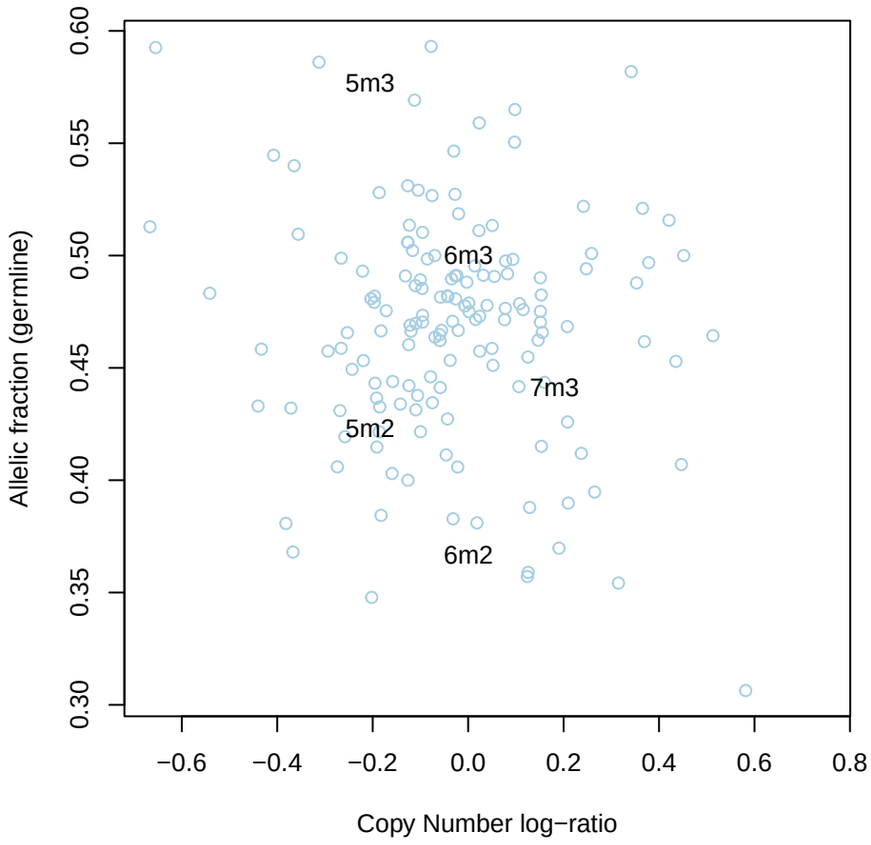

Power 0.8
Frequency
0
10
20
30
40
50
60
70
0.2
0.4
0.6
0.8
1.0
Cellular fraction

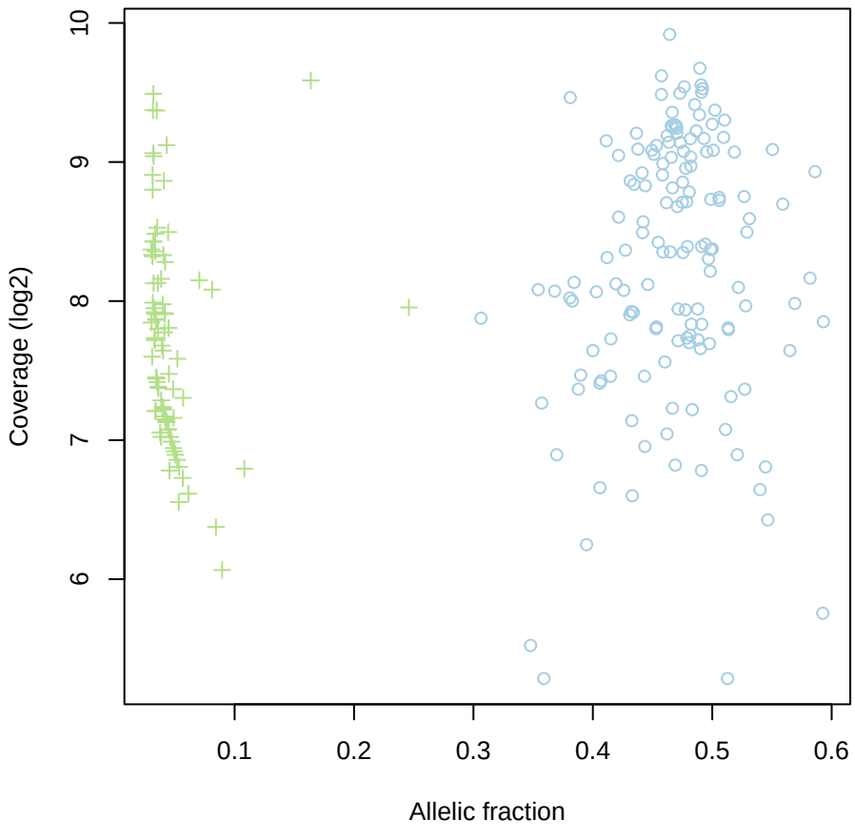

Purity: 0.57 Tumor ploidy: 5.996
2
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

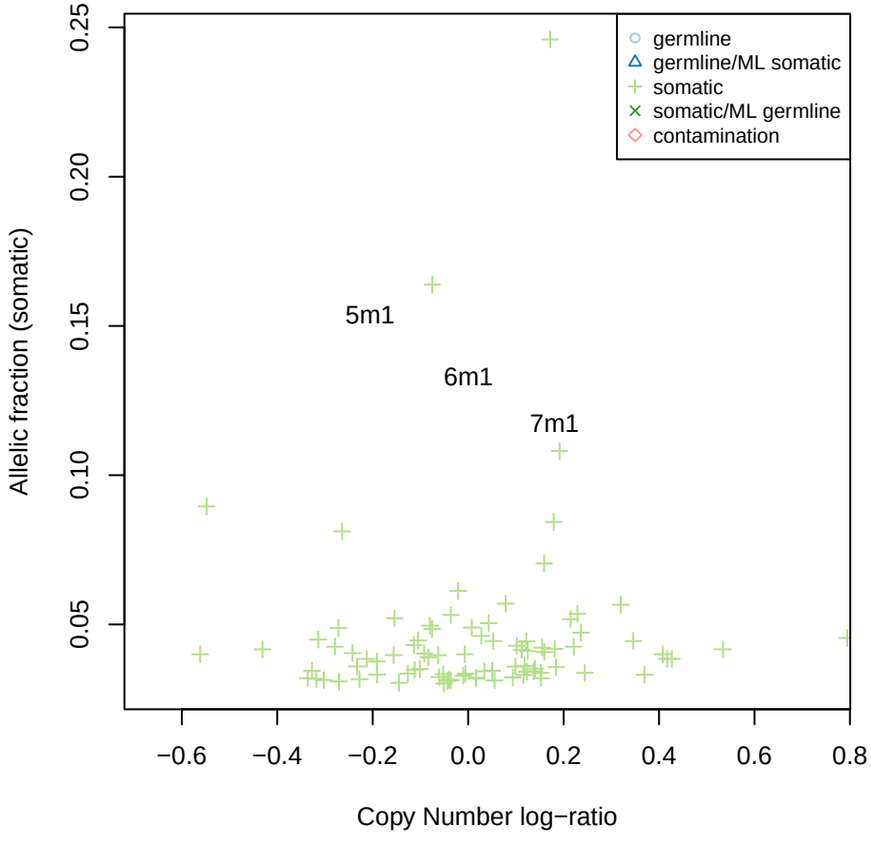

Purity: 0.57 Tumor ploidy: 5.996 SNV log−likelihood: −97.18 GoF: 88.7% Mean coverage: 338;323
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

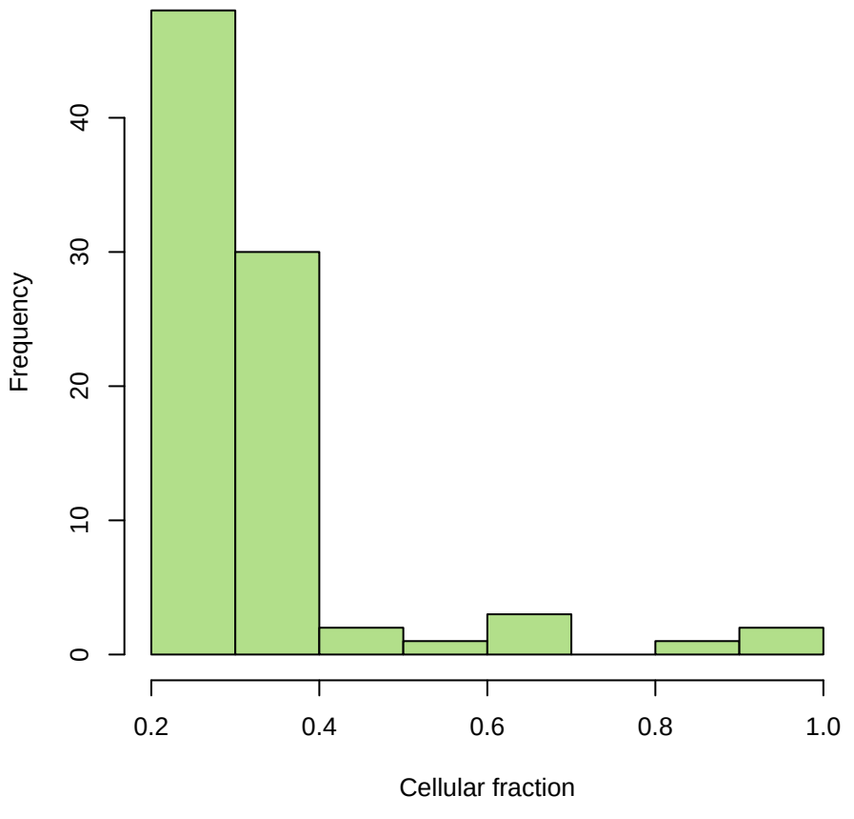

SCNA−fit log−likelihood: −6448.77
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
4 5 6 7
0 50 100 150
SNV Index

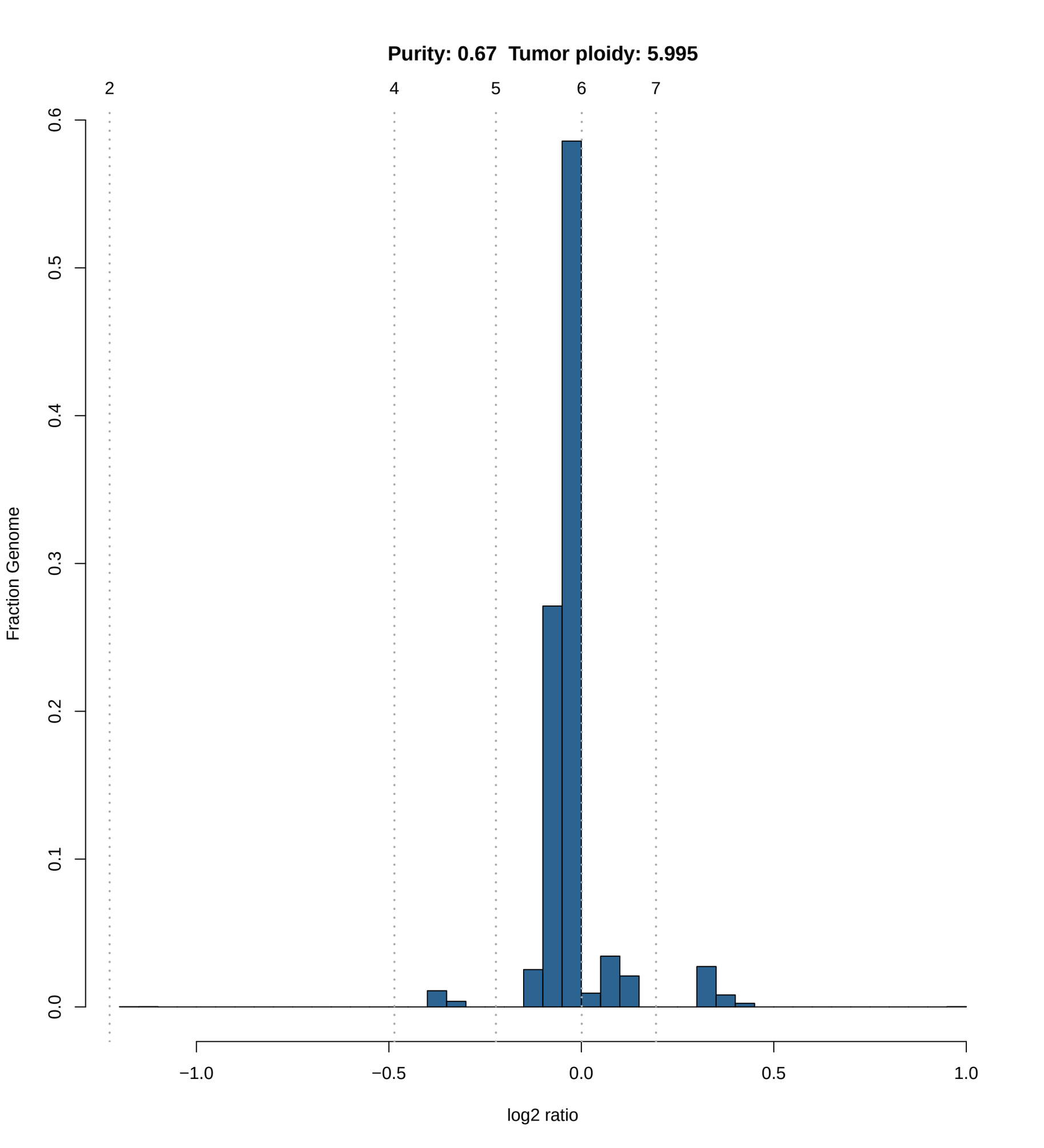

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

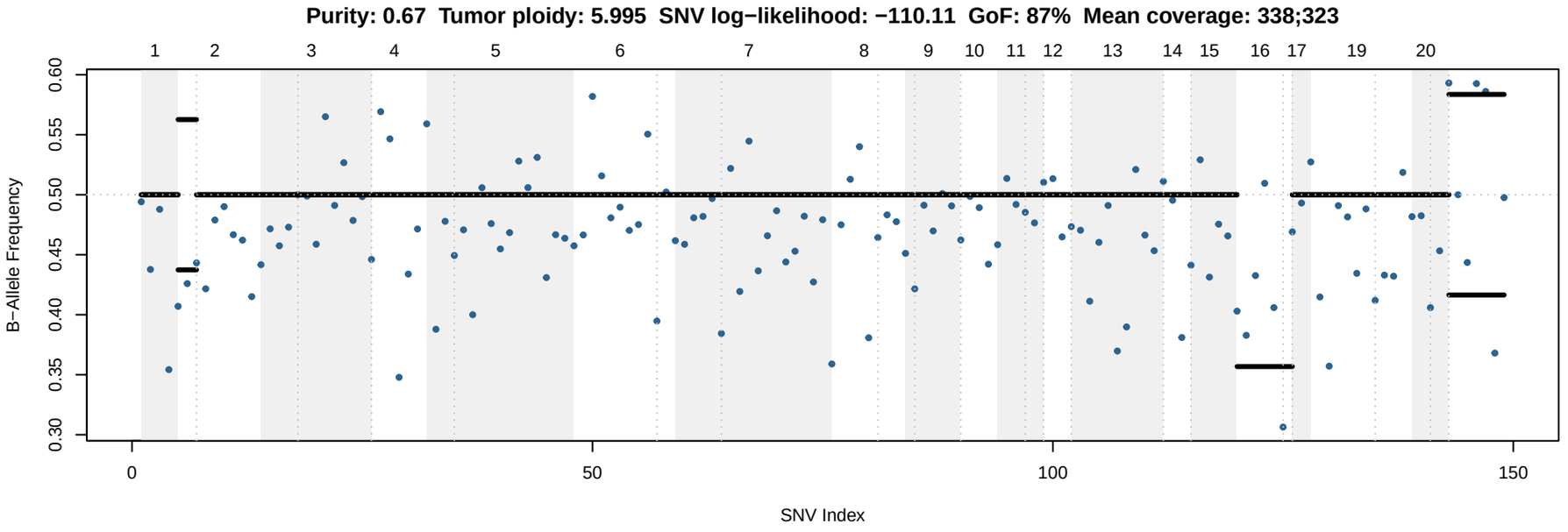

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
5m3
6m3
7m3
5m2
6m2
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

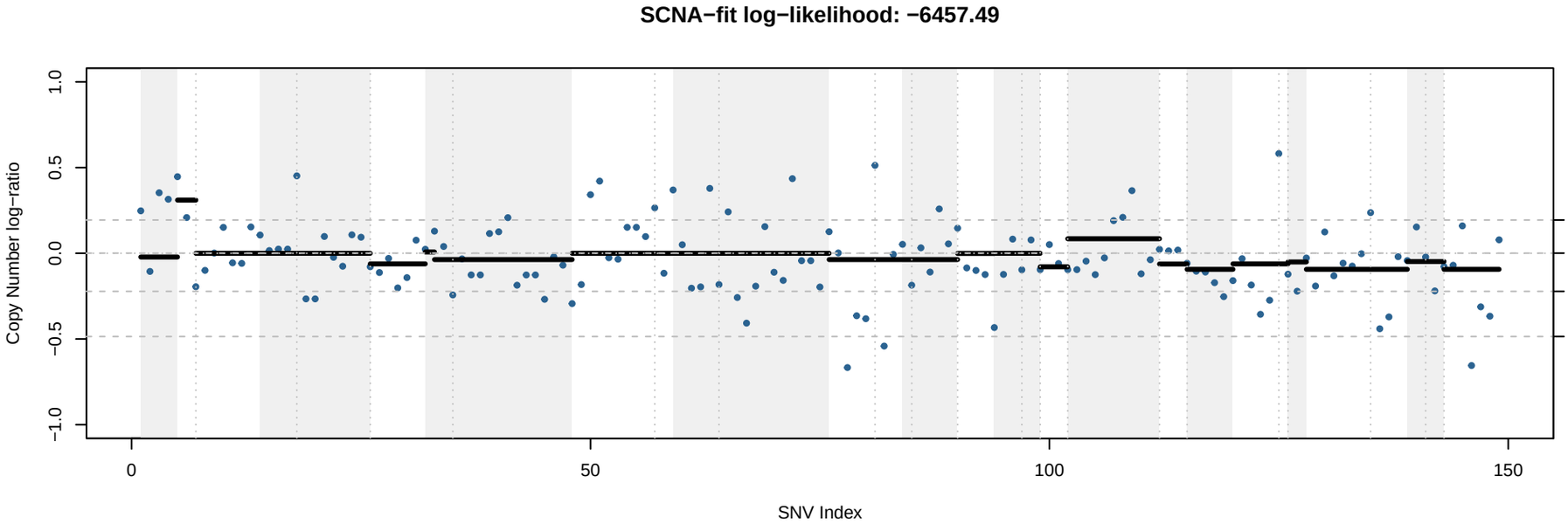

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

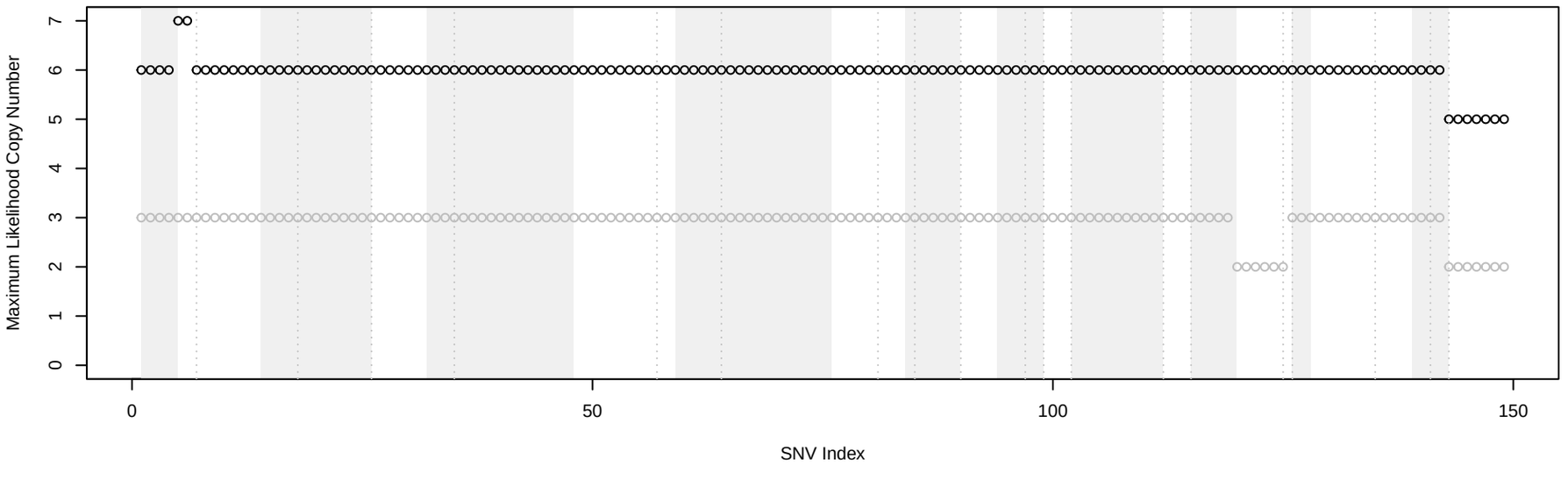

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
6m1
7m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

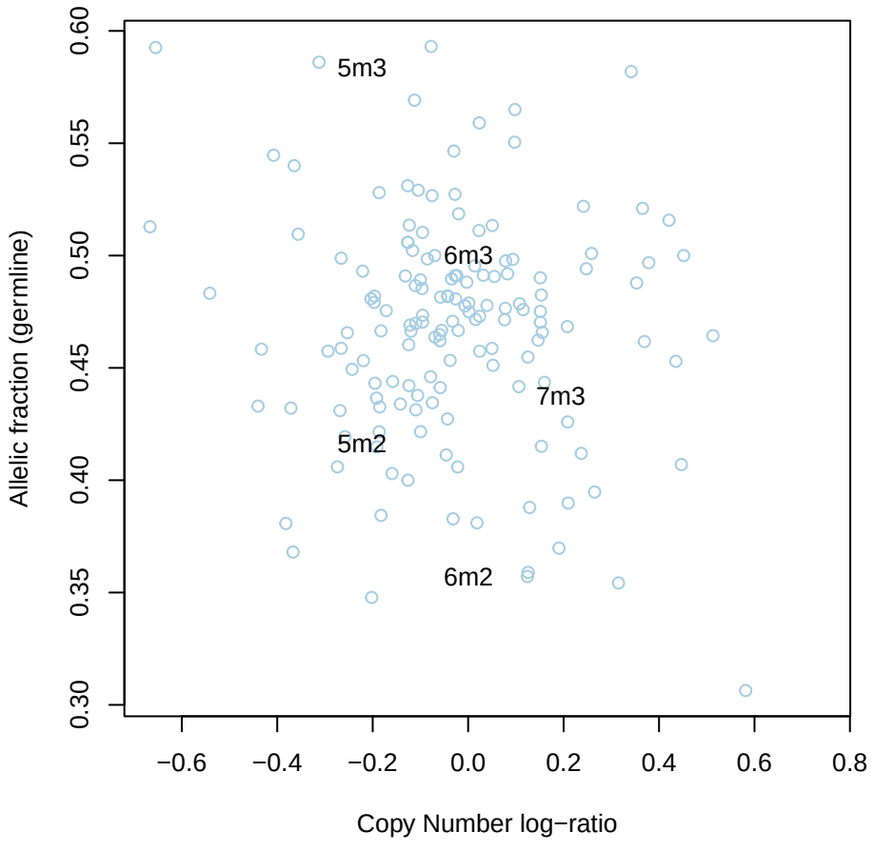

Frequency
0
10
20
30
40
0.2
0.4
0.6
0.8
1.0
Cellular fraction

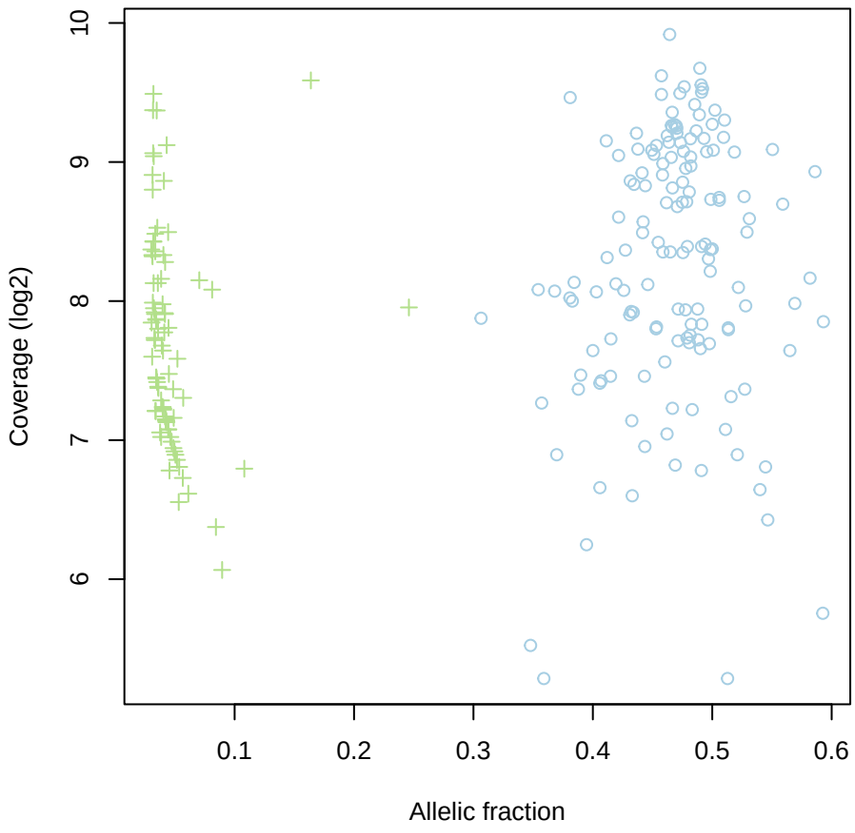

Purity: 0.67 Tumor ploidy: 5.995
2
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

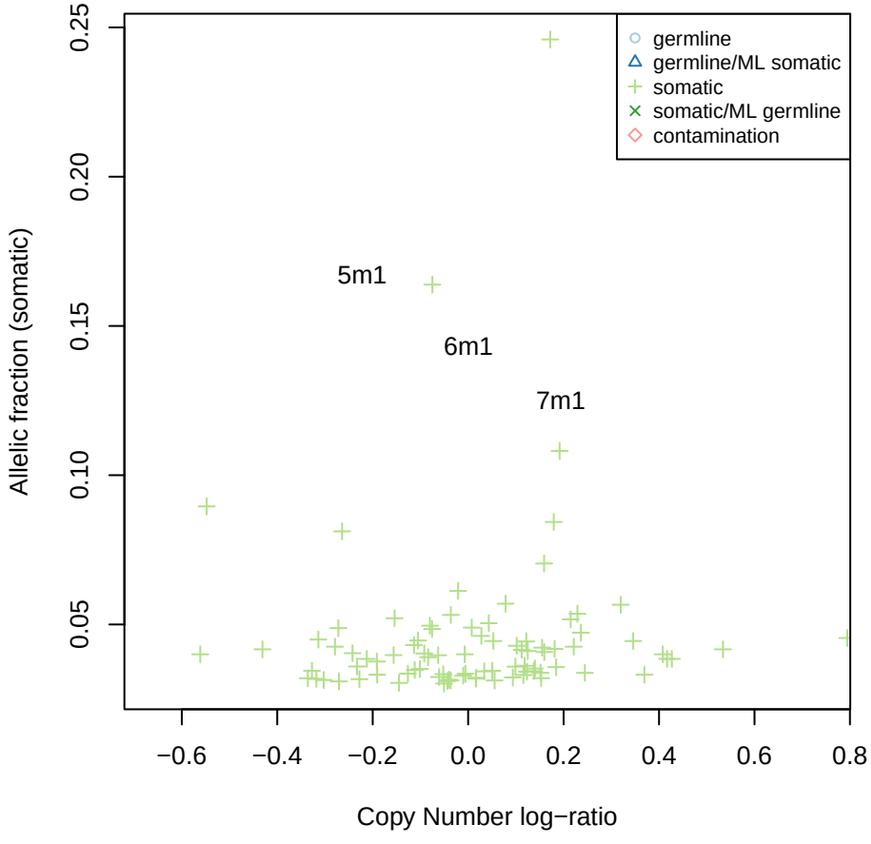

Purity: 0.67 Tumor ploidy: 5.995 SNV log−likelihood: −110.11 GoF: 87% Mean coverage: 338;323
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

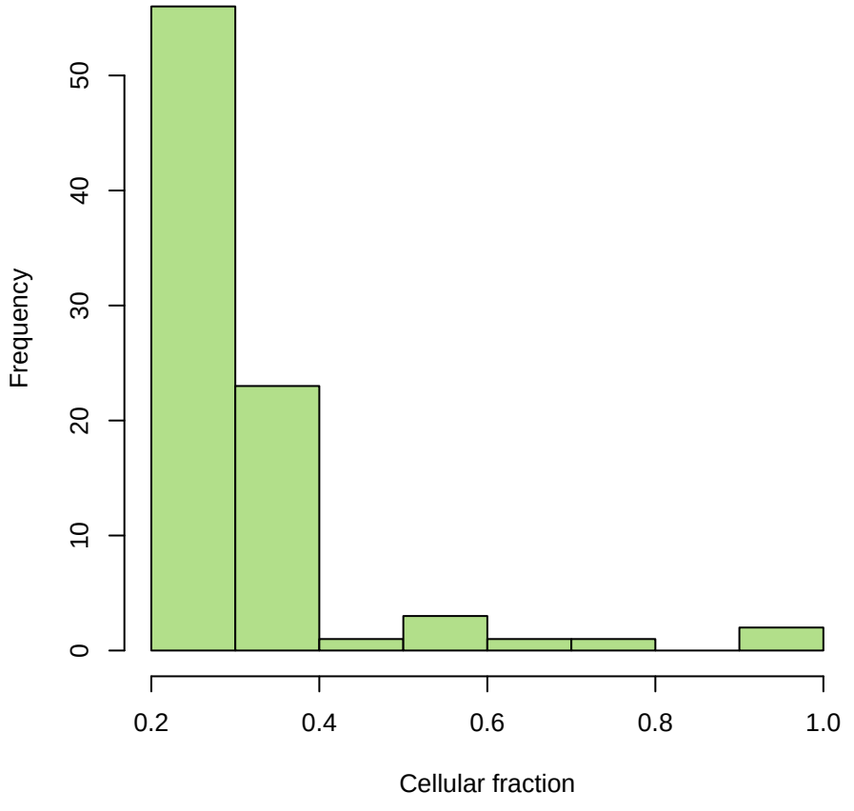

SCNA−fit log−likelihood: −6457.49
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
4 5 6 7
0 50 100 150
SNV Index

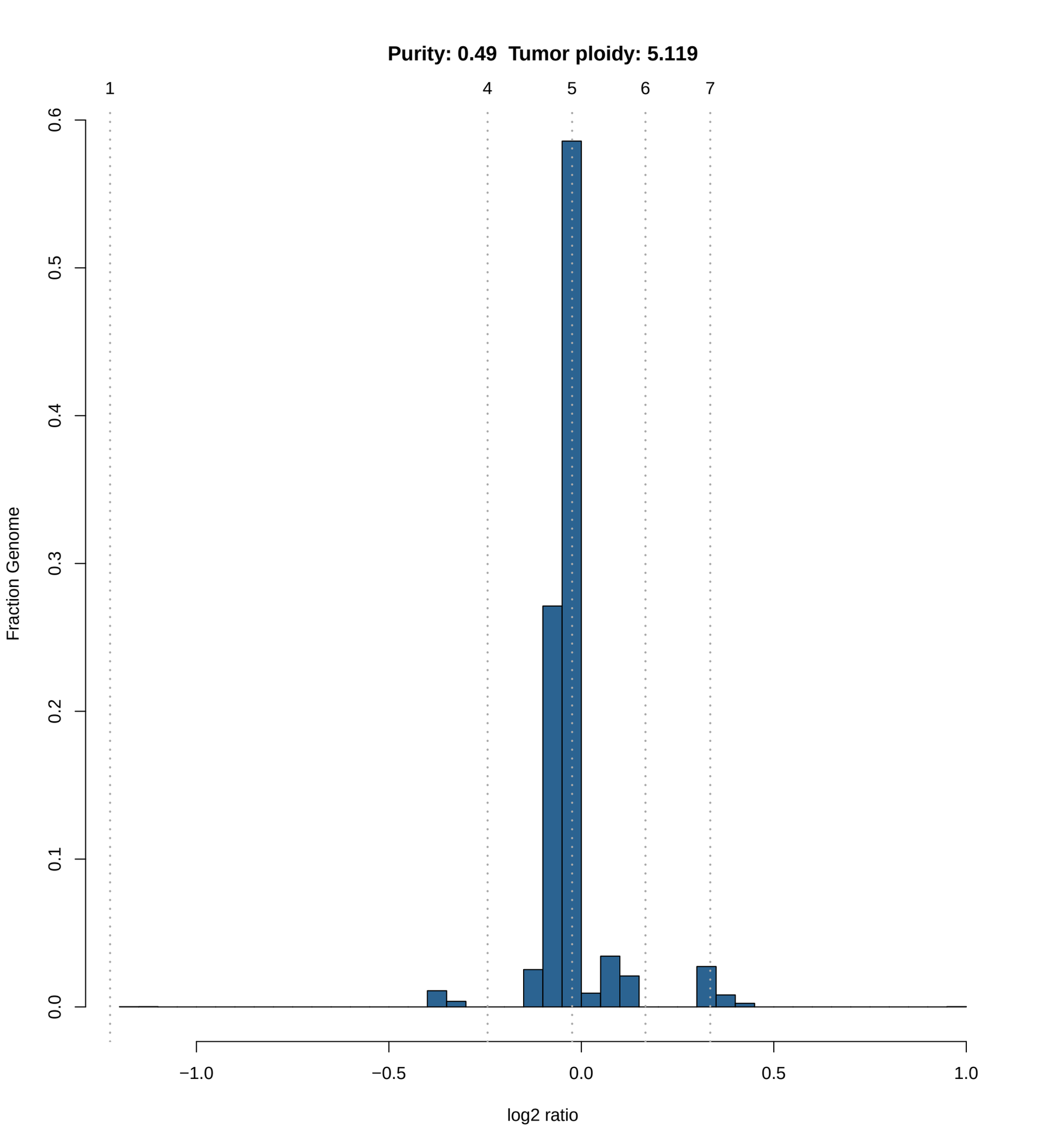

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

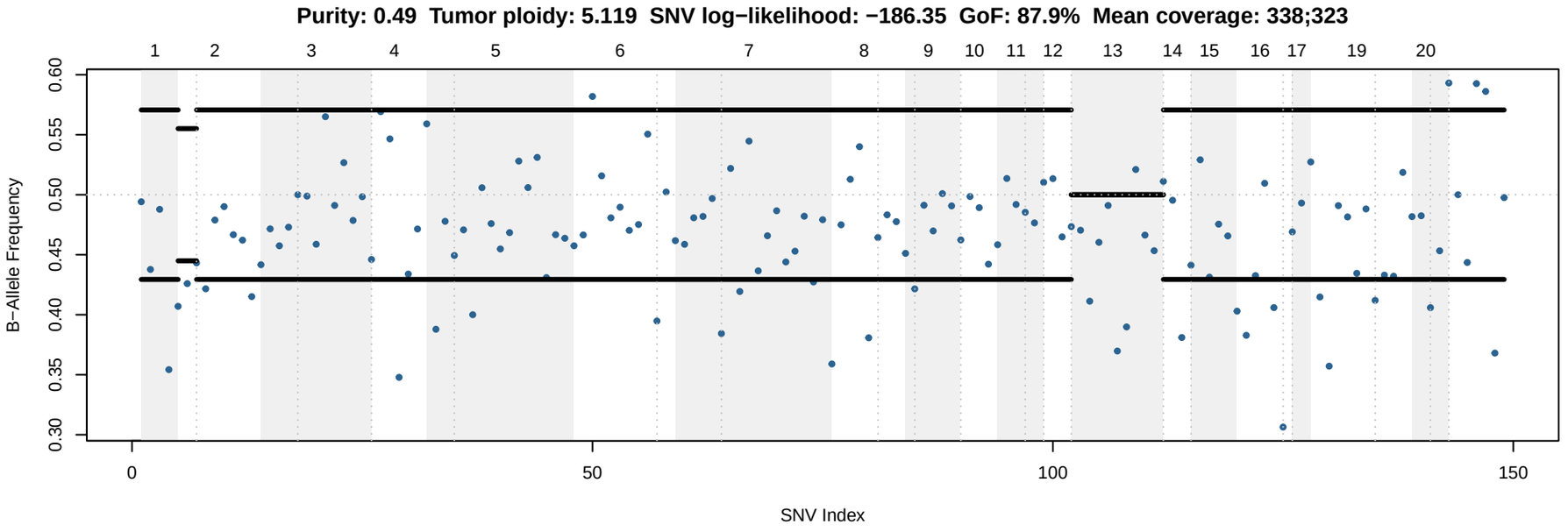

Allelic fraction (germline)
Copy Number log−ratio
5m3
6m3
7m3
5m2
6m2

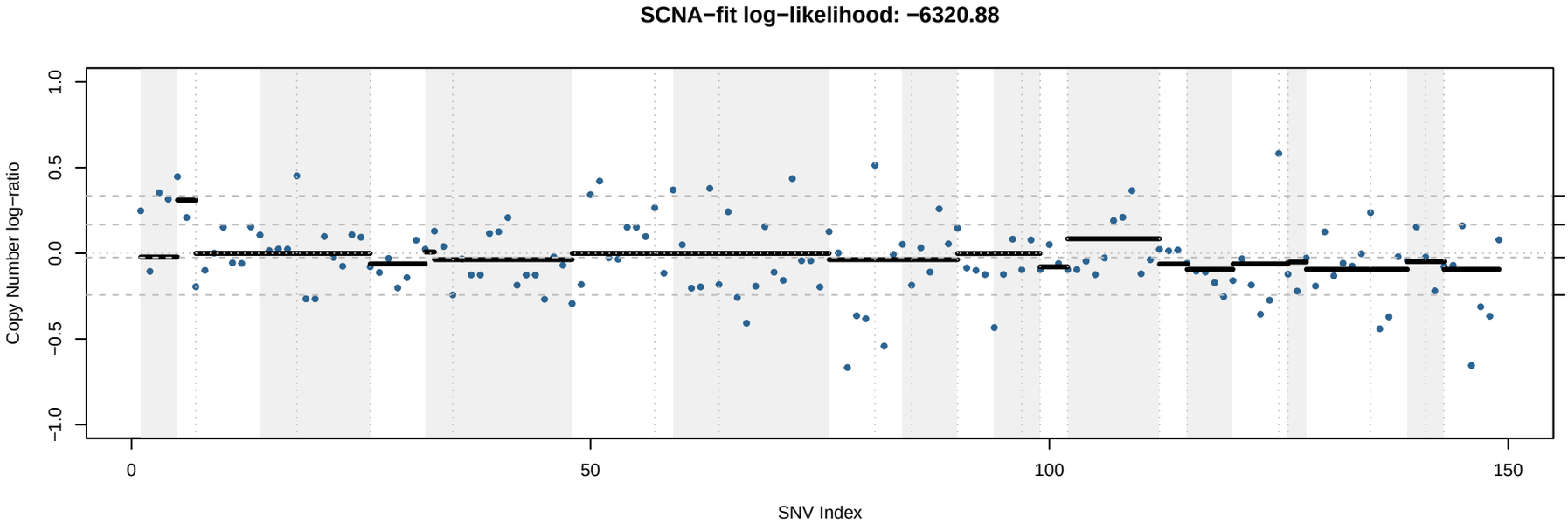

Coverage (log2)
Allelic fraction

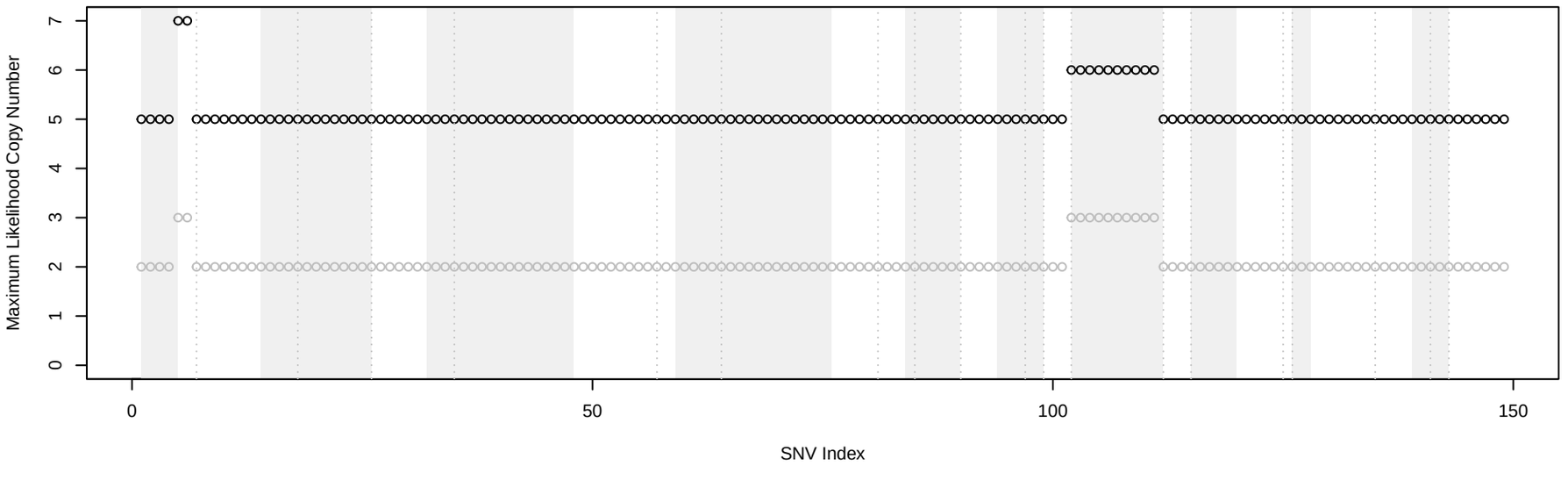

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
6m1
7m1

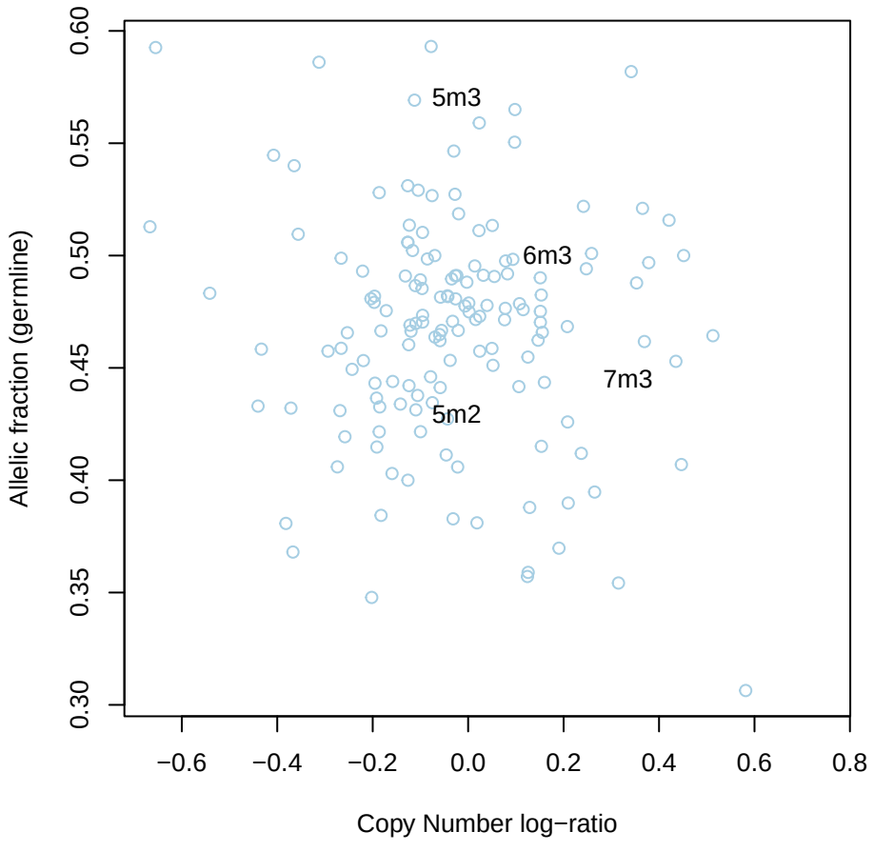

Frequency
Cellular fraction

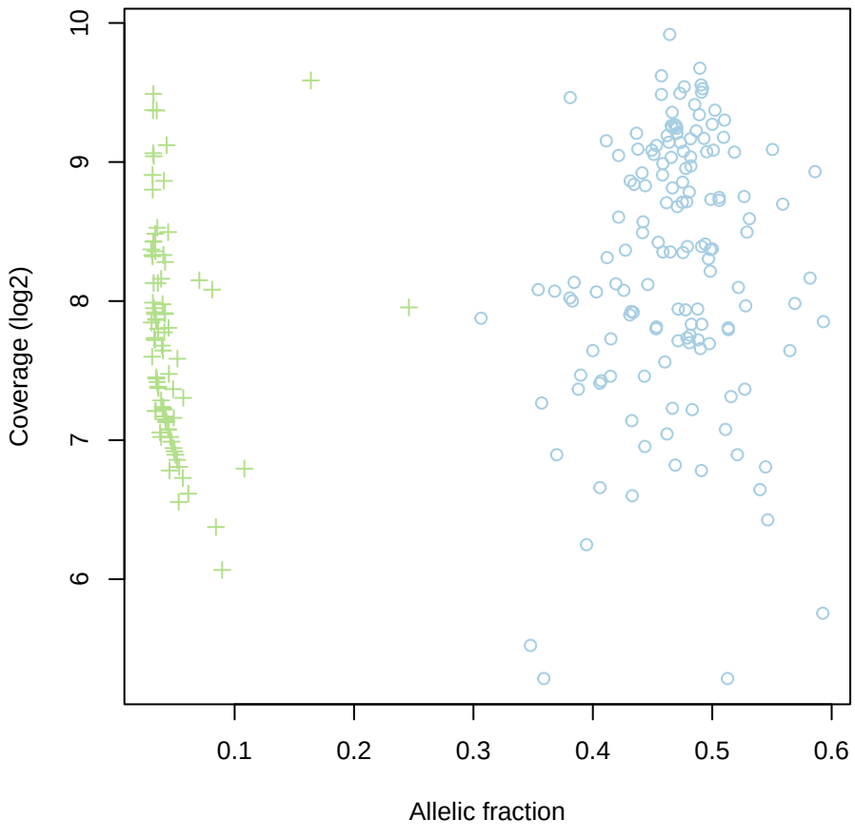

Purity: 0.49 Tumor ploidy: 5.119
1
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

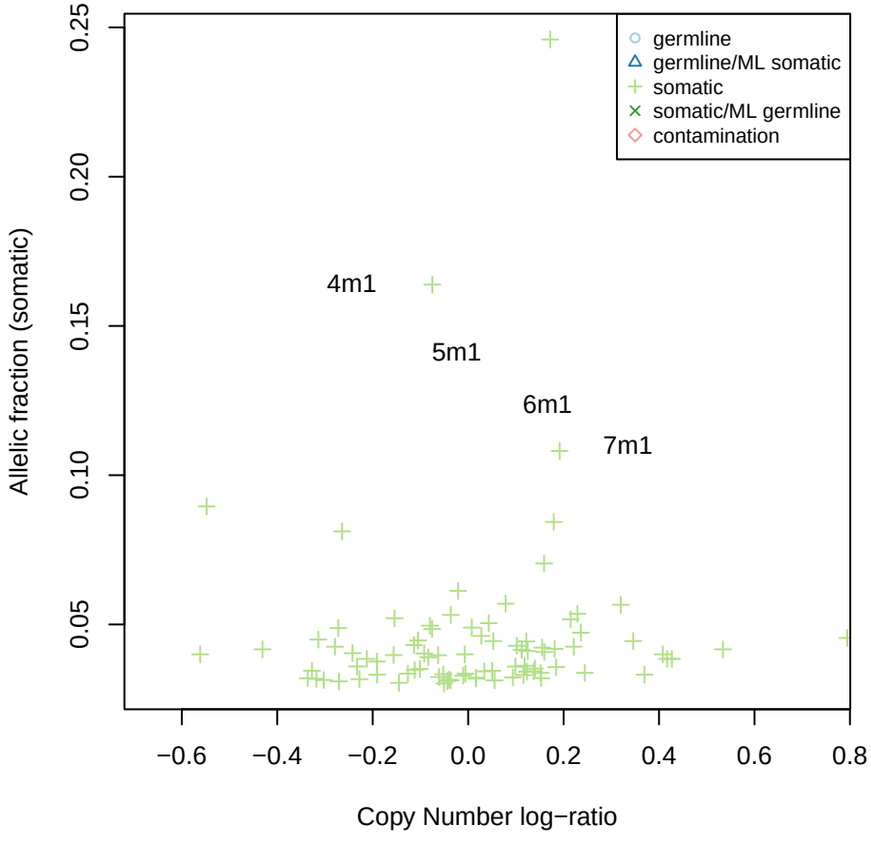

Purity: 0.49 Tumor ploidy: 5.119 SNV log−likelihood: −186.35 GoF: 87.9% Mean coverage: 338;323
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

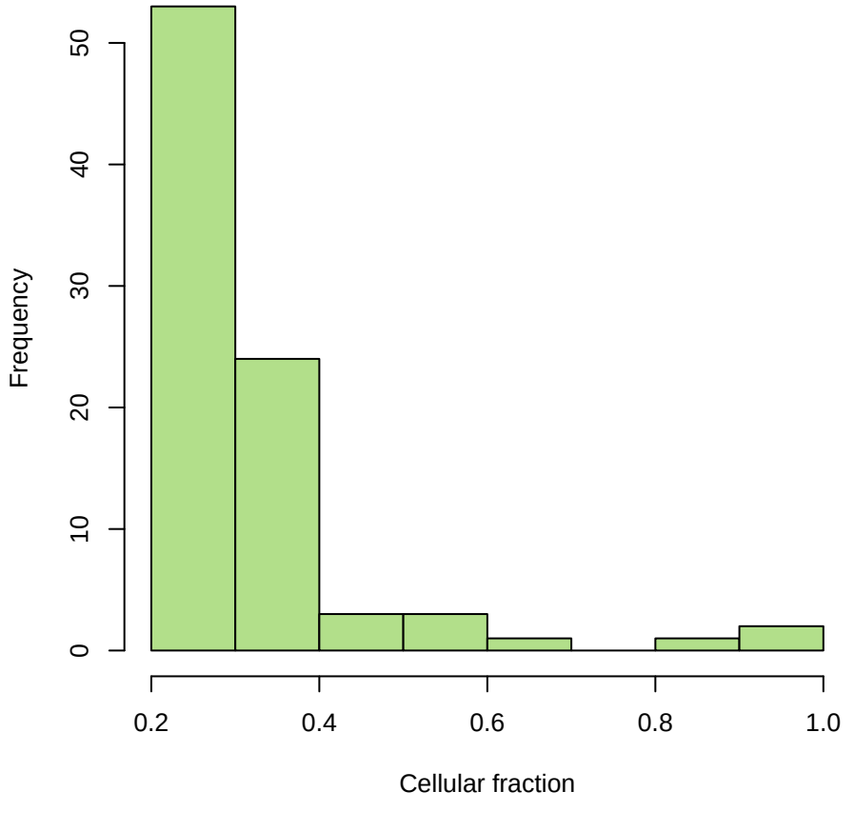

SCNA−fit log−likelihood: −6320.88
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
4 5 6 7
0 50 100 150
SNV Index

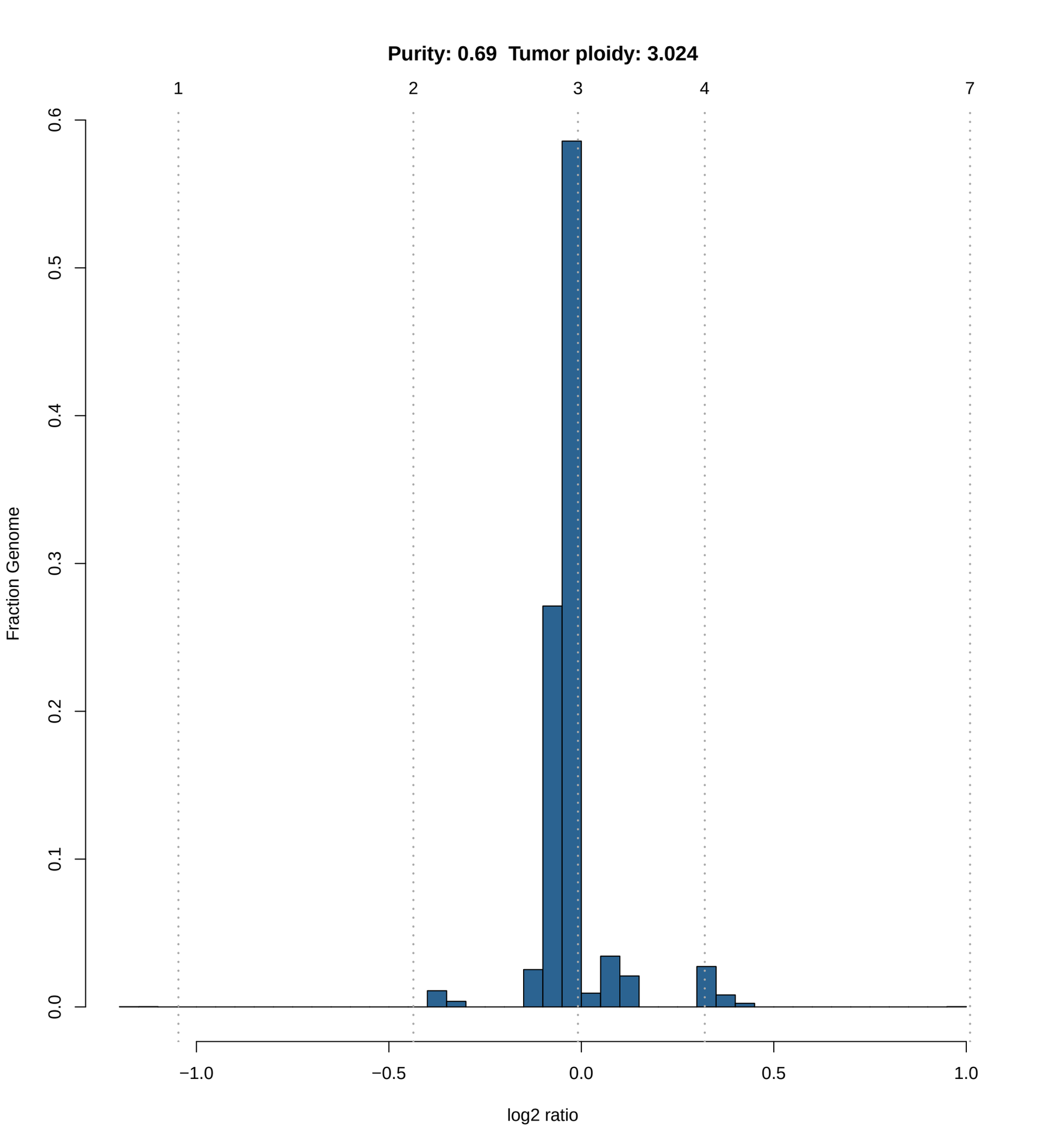

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

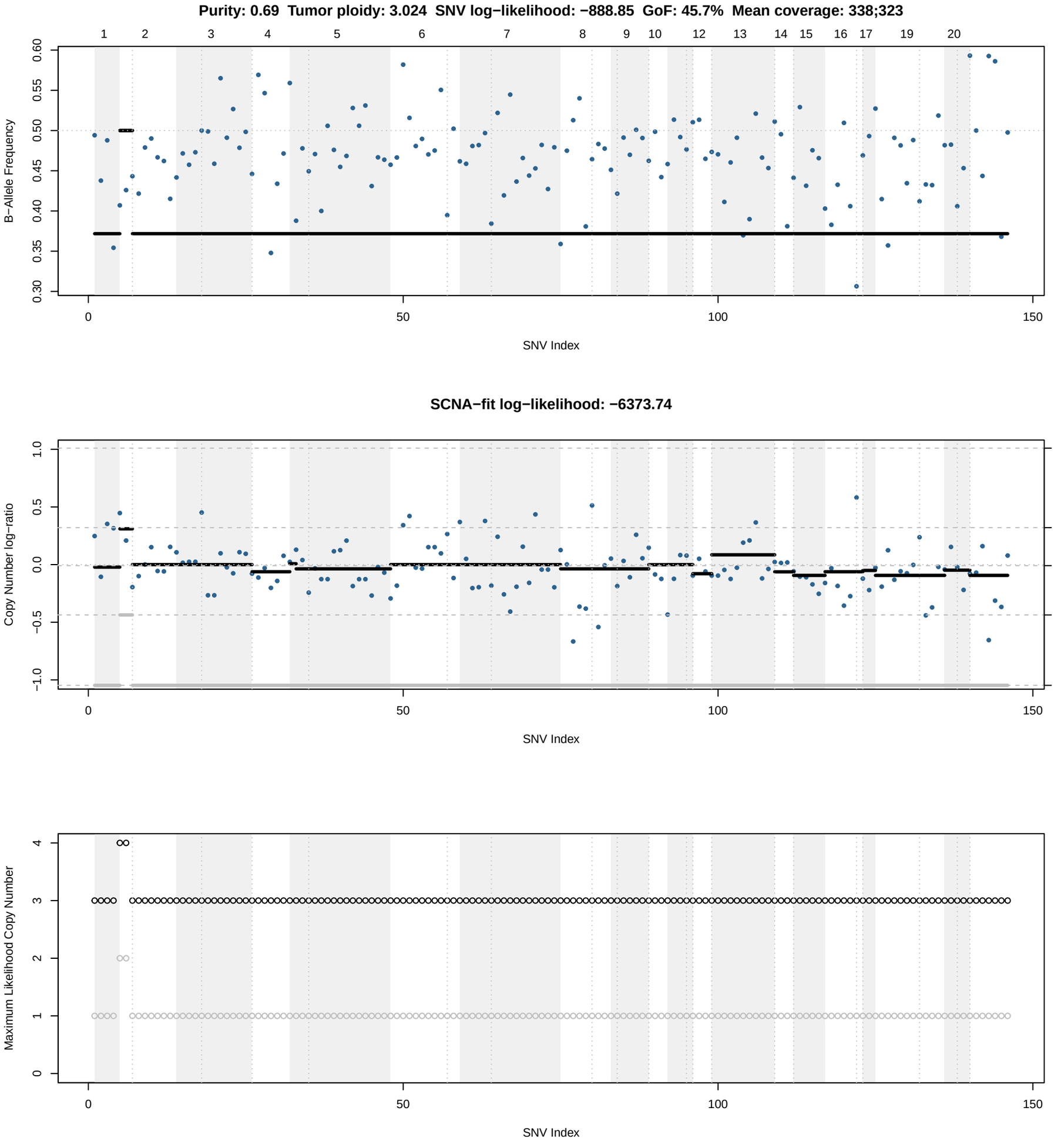

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
5m3
6m3
7m3
5m2
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

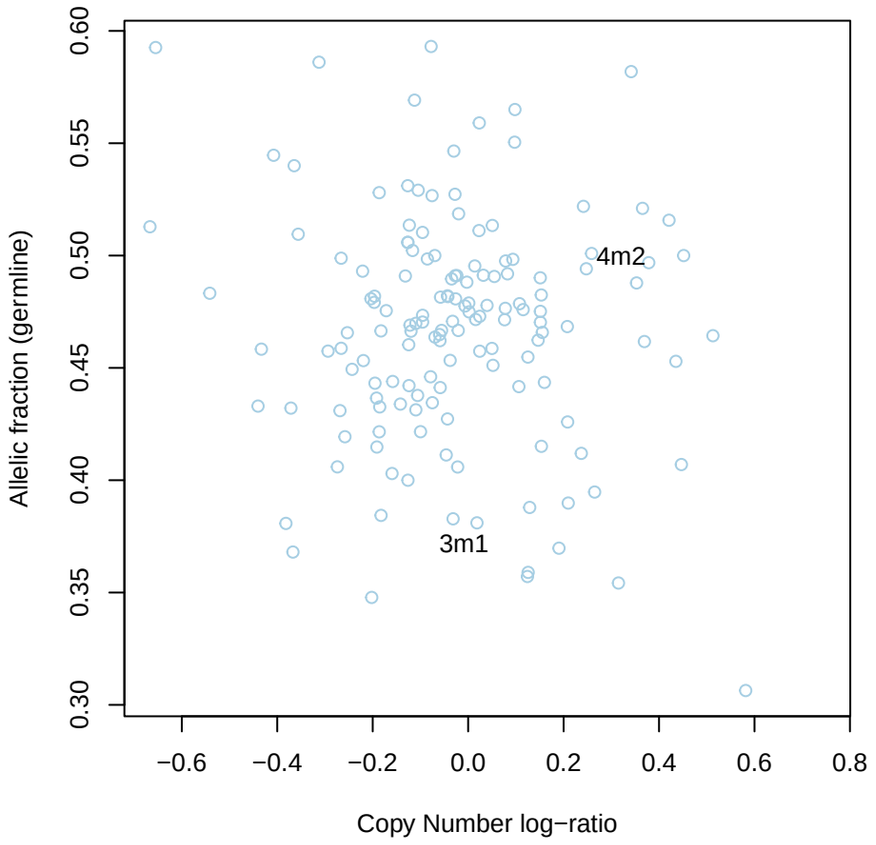

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

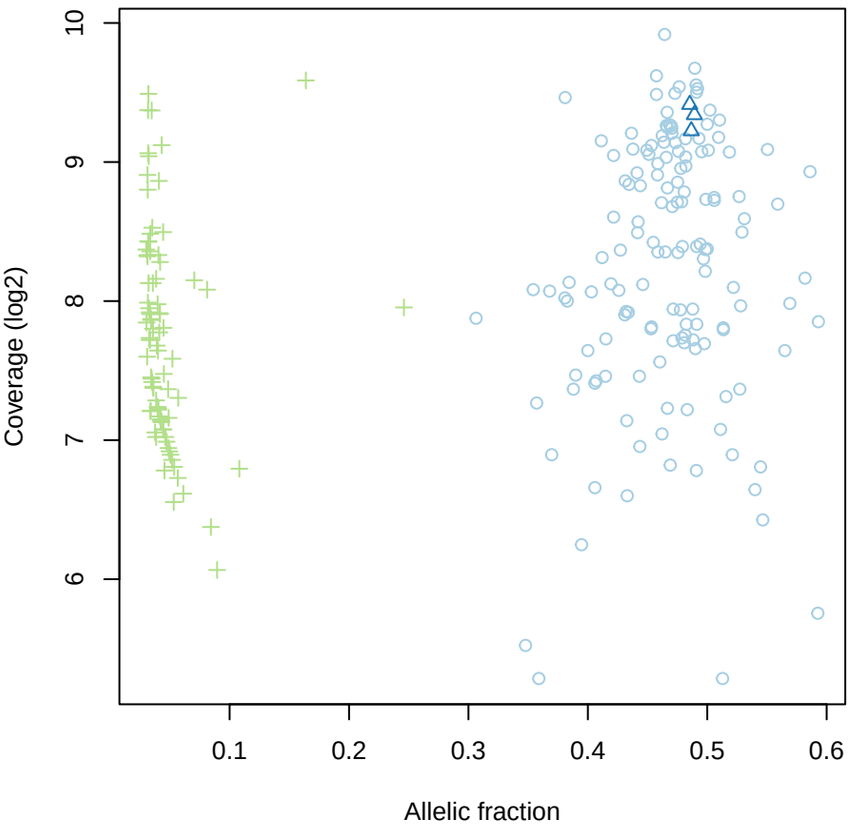

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
7m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

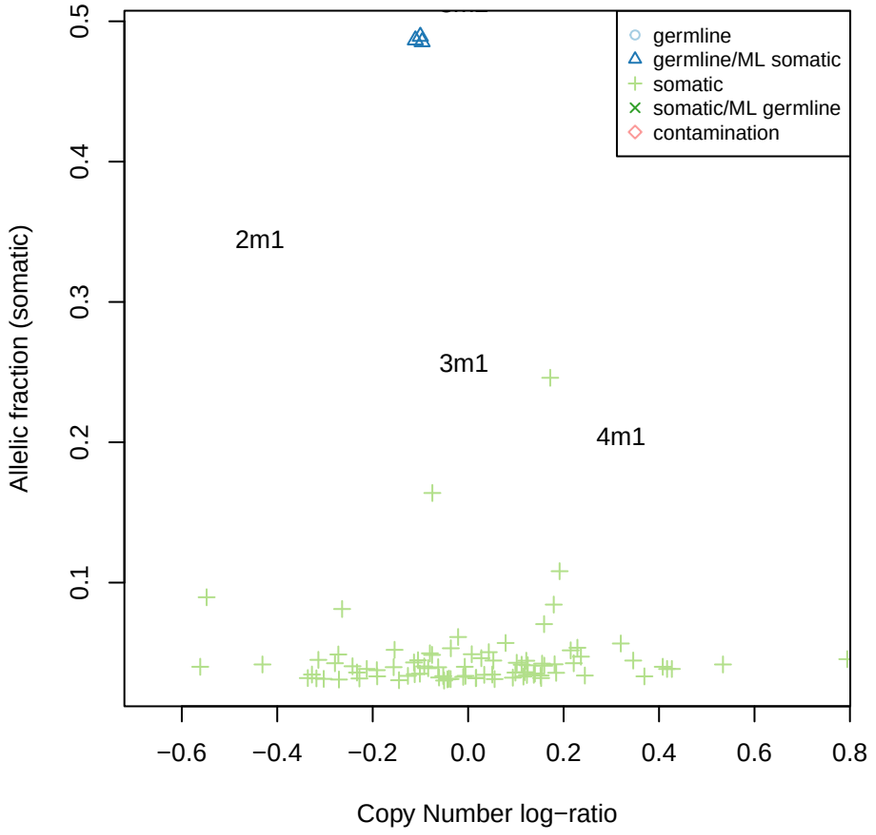

Frequency
0
10
20
30
40
50
0.2
0.4
0.6
0.8
1.0
Cellular fraction

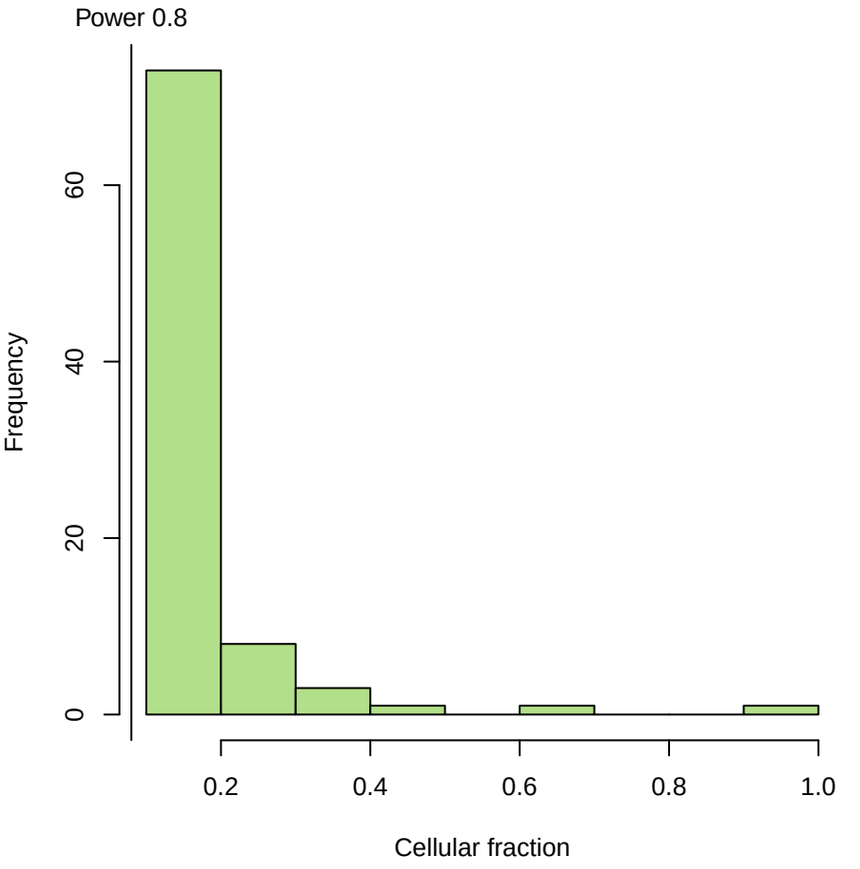

Purity: 0.69 Tumor ploidy: 3.024
1
2
3
4
7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

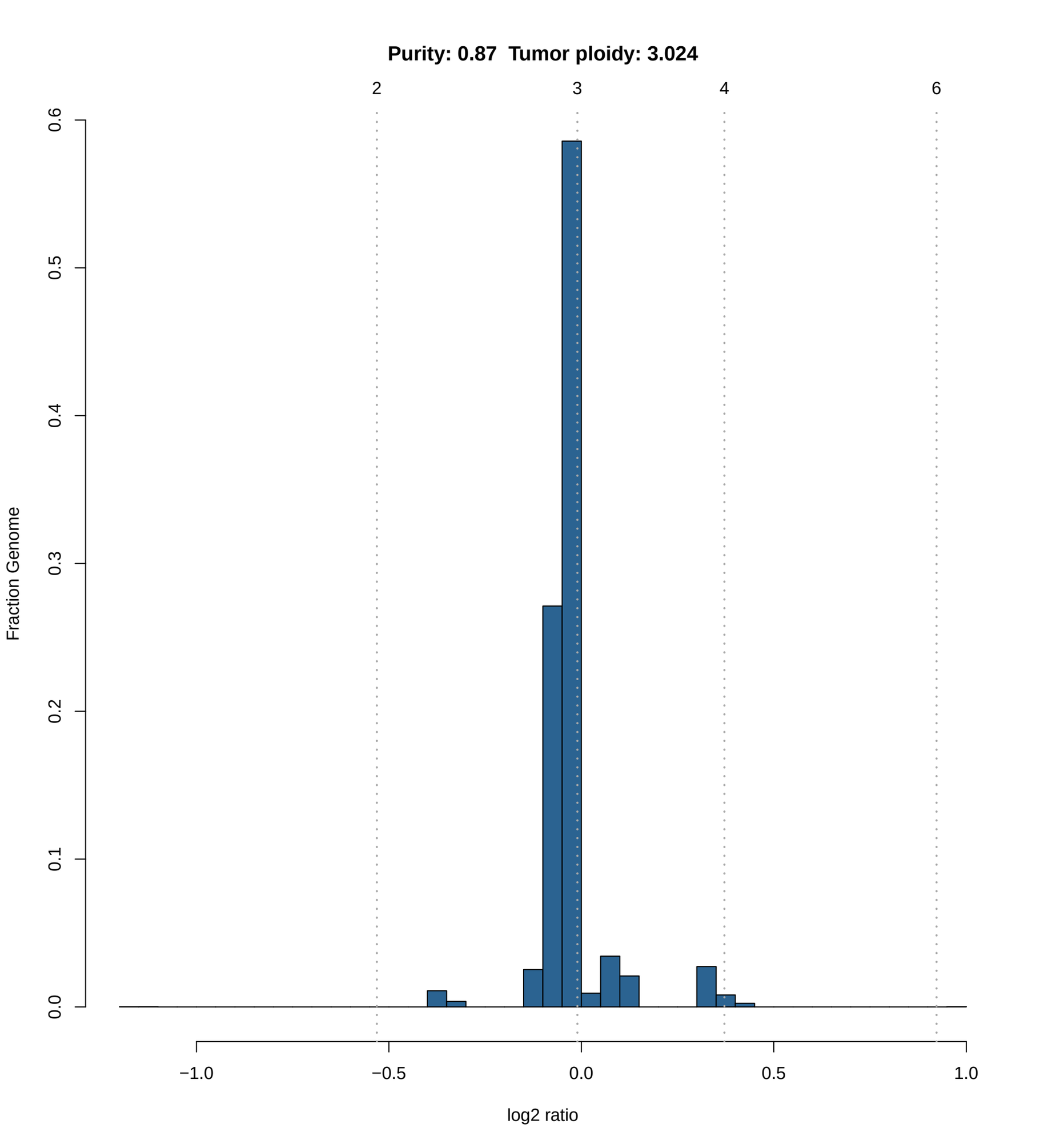

Purity: 0.69 Tumor ploidy: 3.024 SNV log−likelihood: −888.85 GoF: 45.7% Mean coverage: 338;323
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index
SCNA−fit log−likelihood: −6373.74
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 7
0 50 100 150
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

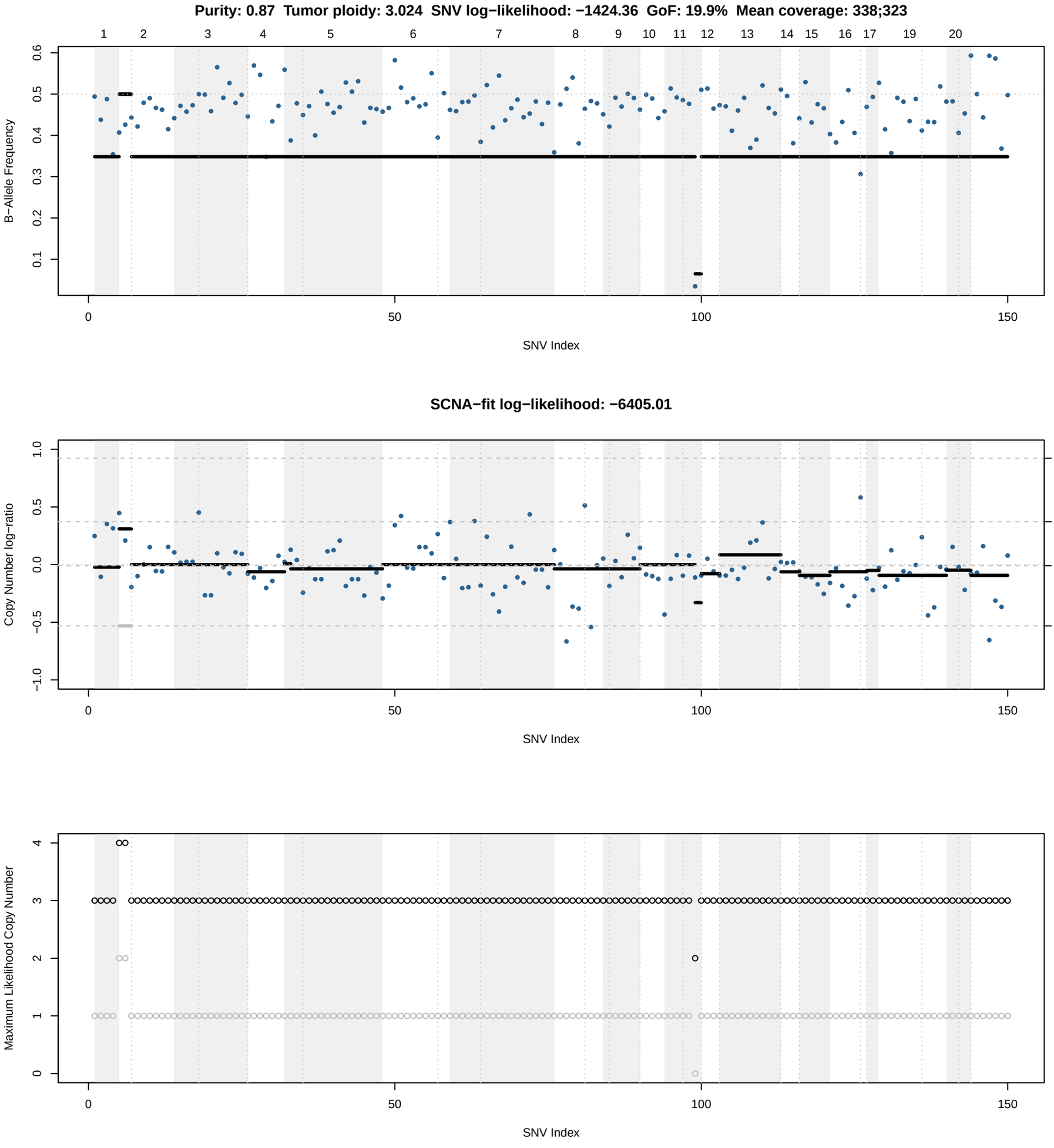

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
4m2
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

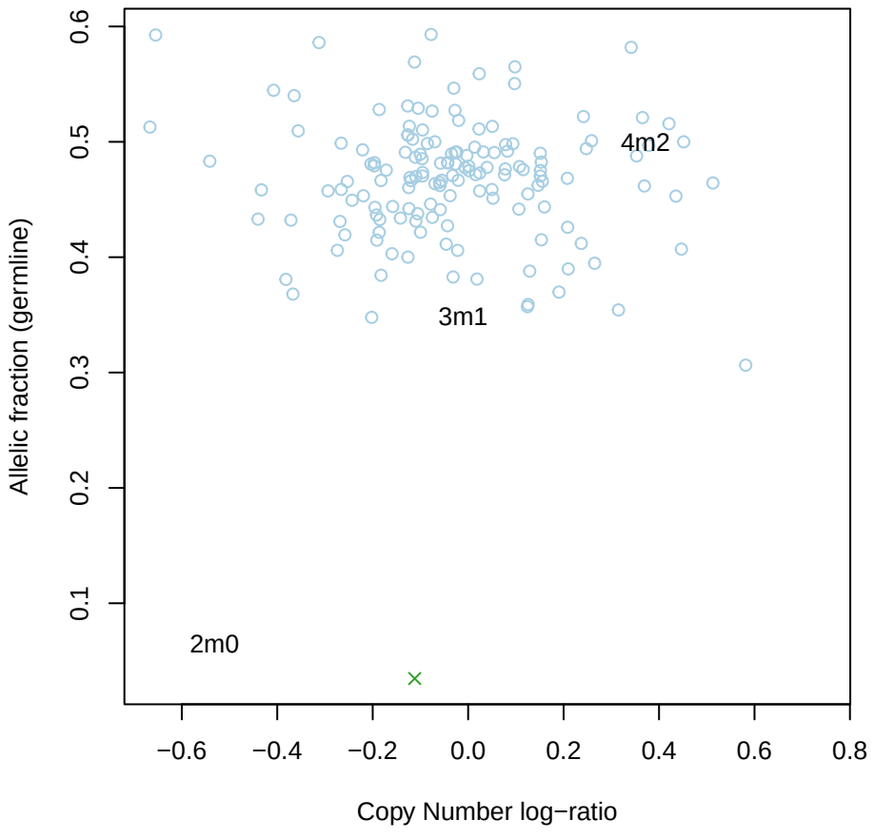

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

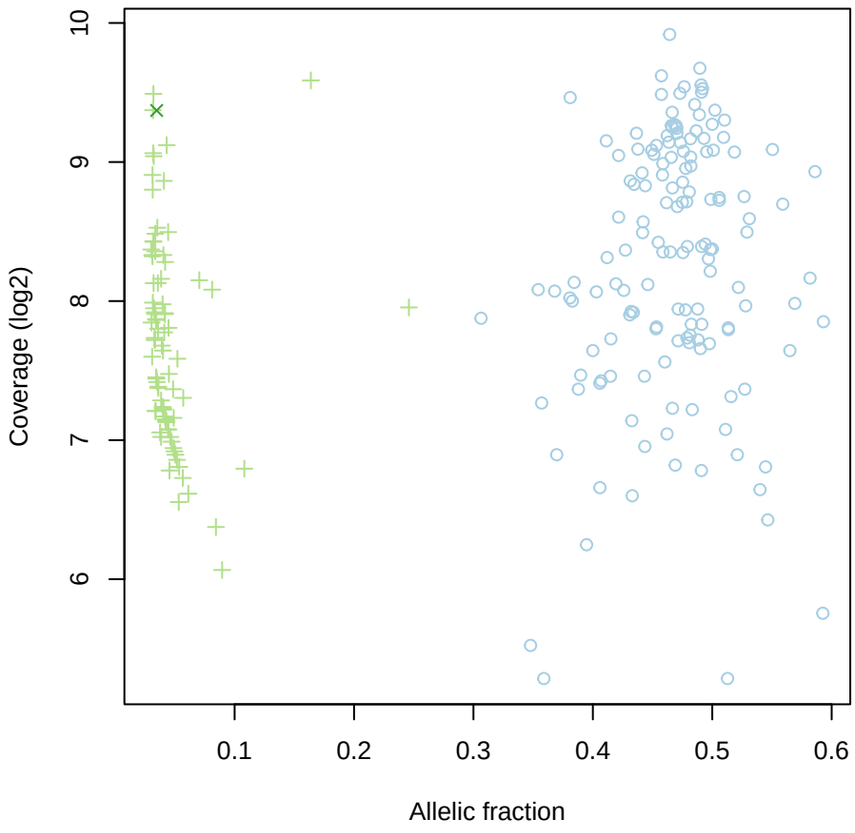

Allelic fraction (somatic)
0.1
0.2
0.3
0.4
0.5
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

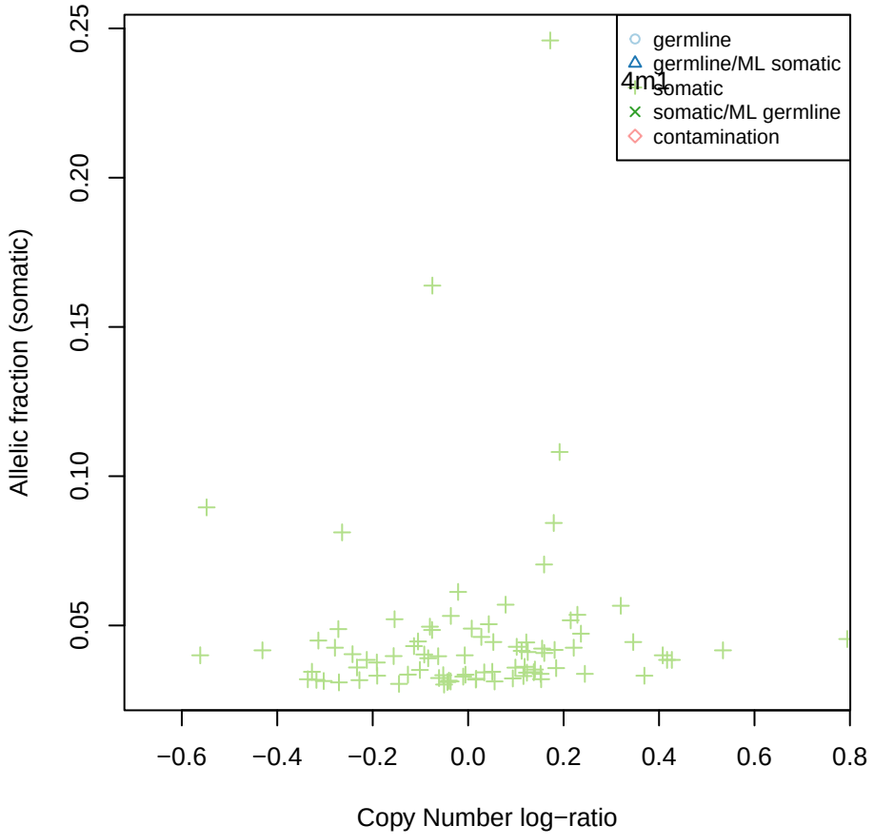

Power 0.8
Frequency
0
20
40
60
0.2
0.4
0.6
0.8
1.0
Cellular fraction

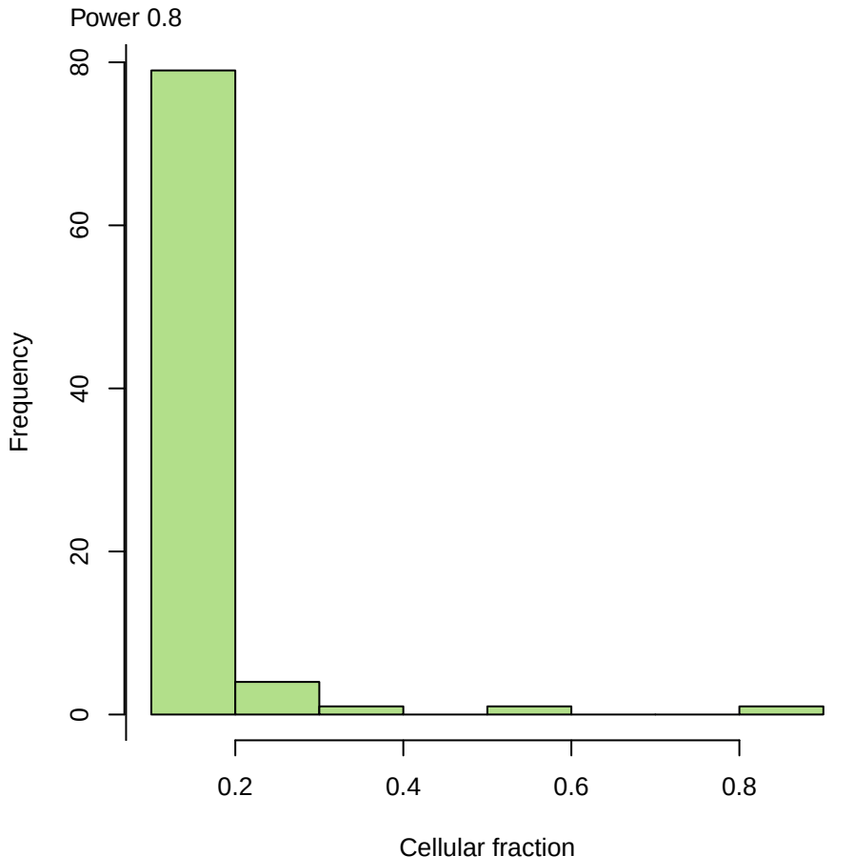

Purity: 0.87 Tumor ploidy: 3.024
2
3
4
6
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio


Purity: 0.87 Tumor ploidy: 3.024 SNV log−likelihood: −1424.36 GoF: 19.9% Mean coverage: 338;323
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index
SCNA−fit log−likelihood: −6405.01
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 6
0 50 100 150
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index


Allelic fraction (germline)
Copy Number log−ratio
4m2
3m1
2m0


Coverage (log2)
Allelic fraction


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


Power 0.8
Frequency
Cellular fraction