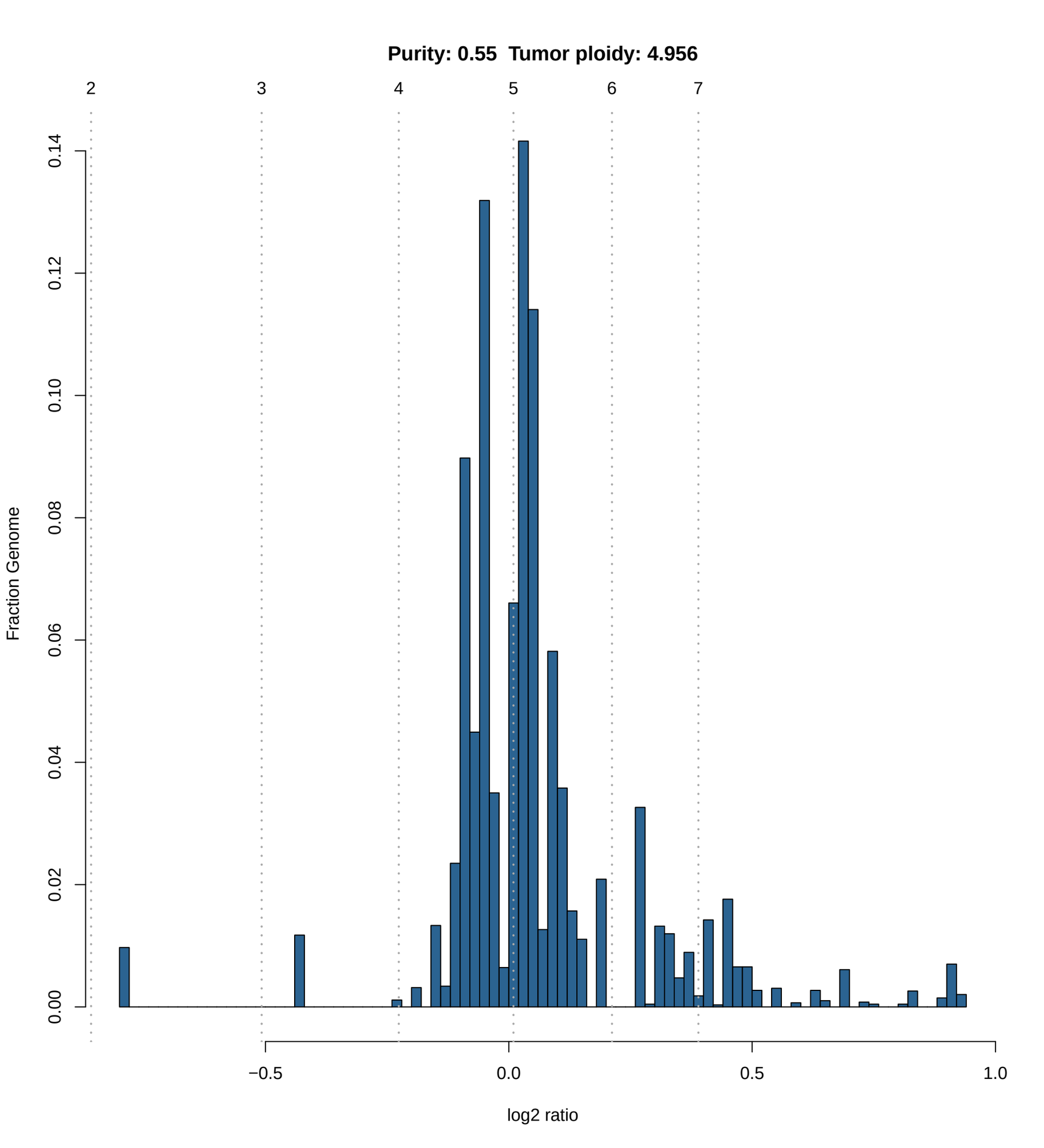
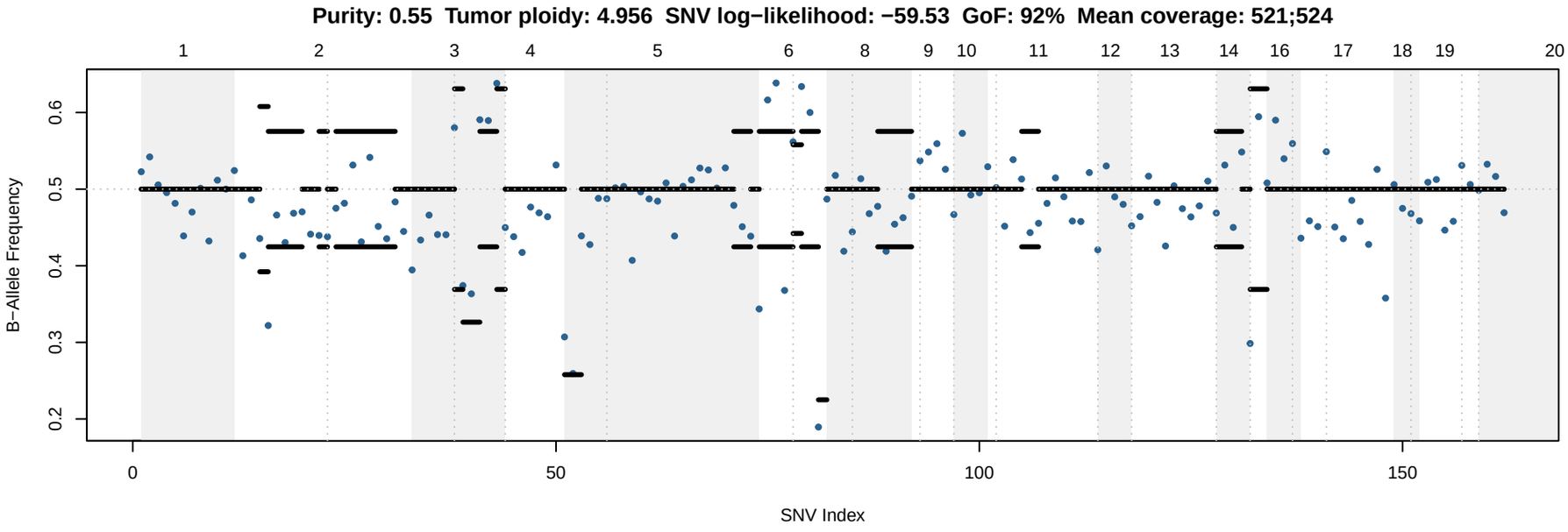
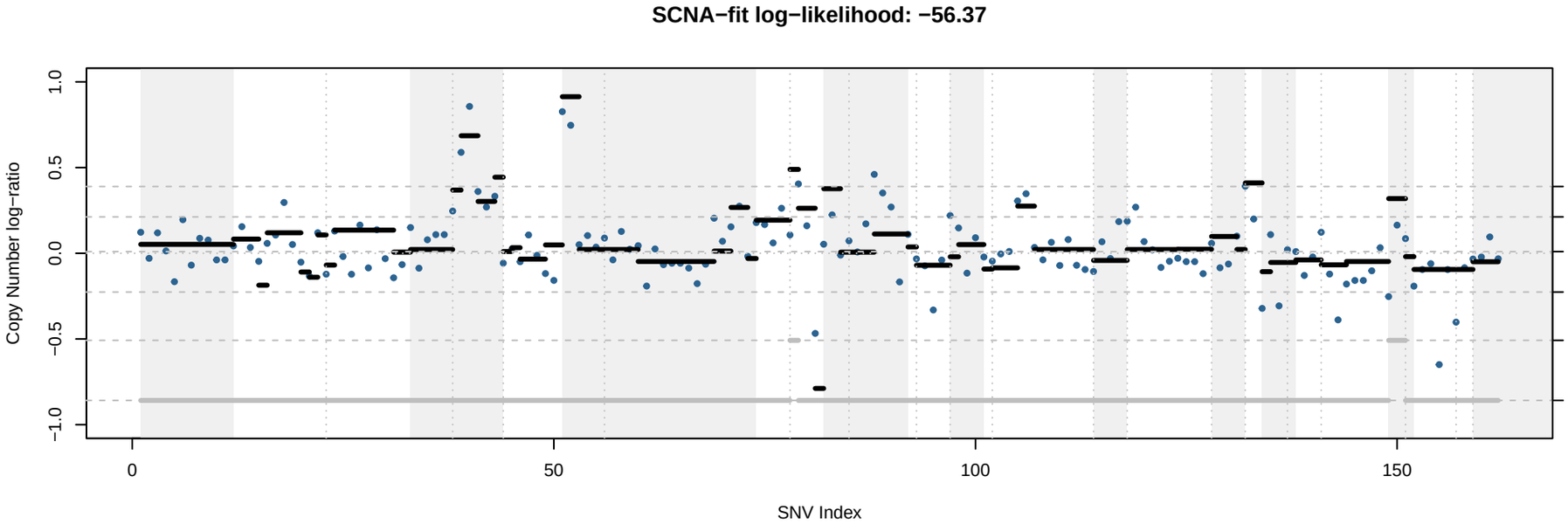
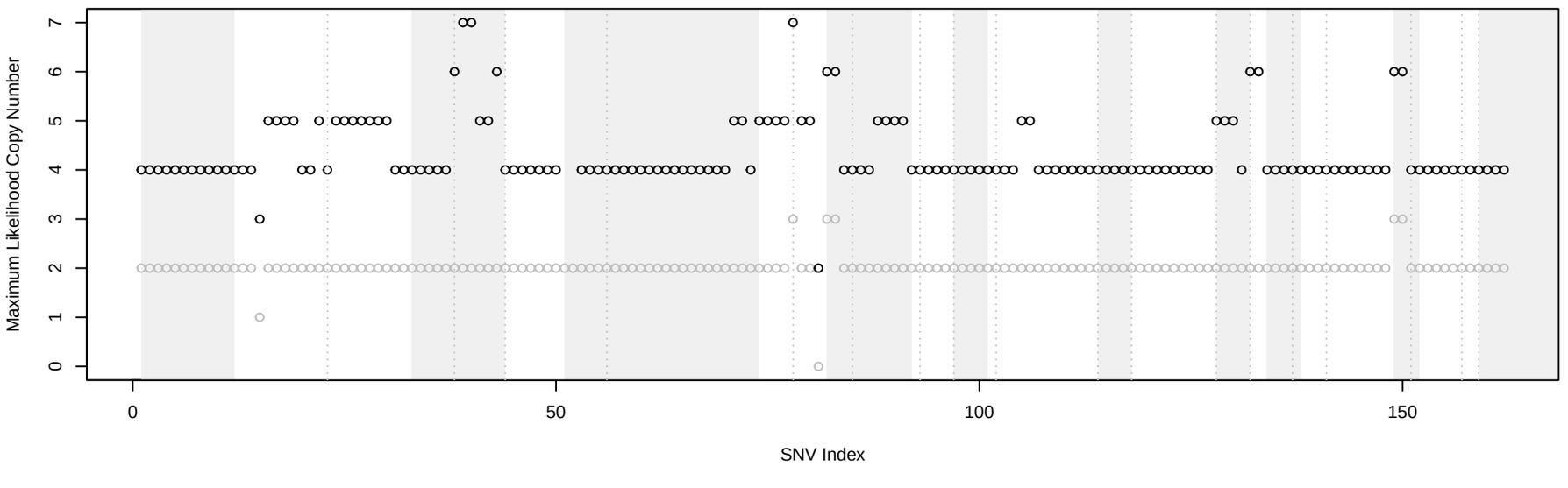
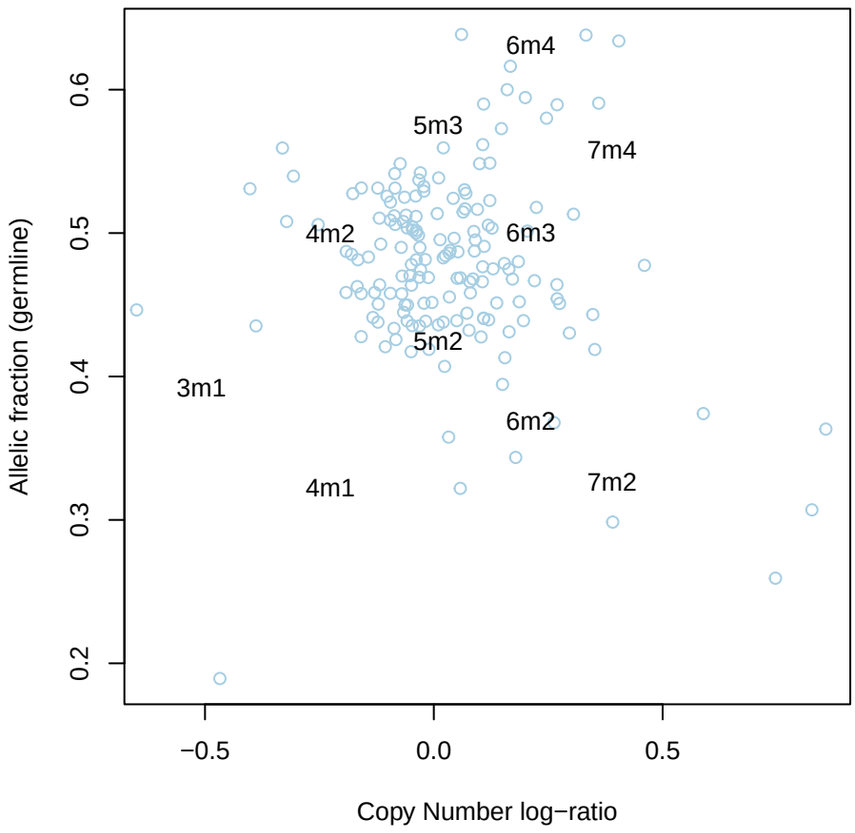
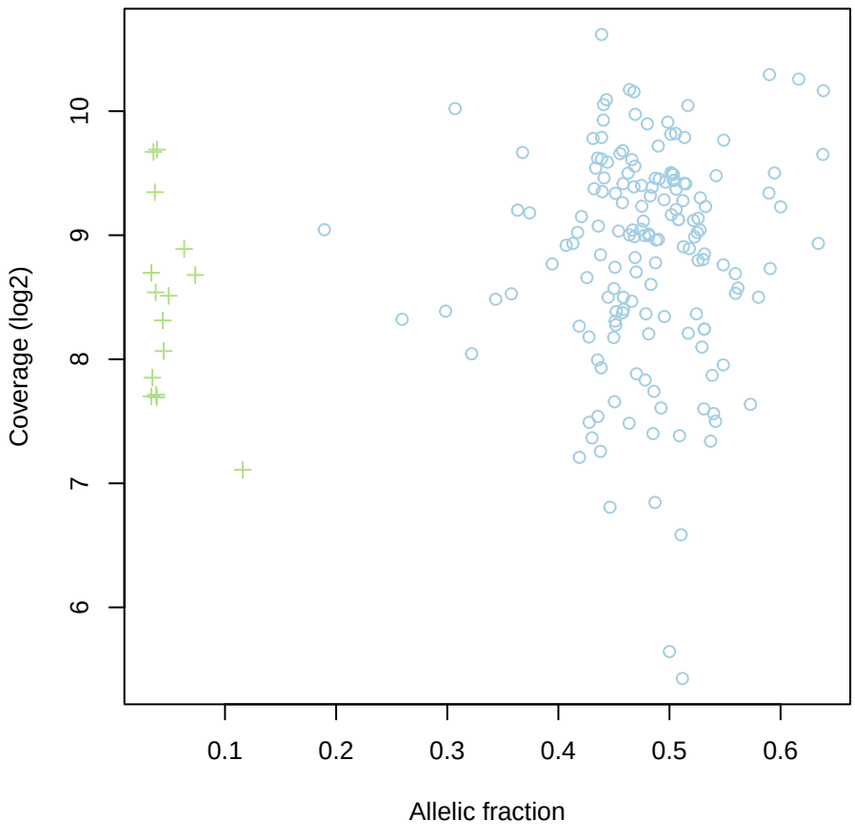

Purity: 0.55 Tumor ploidy: 4.956
2
3
4
5
6
7
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

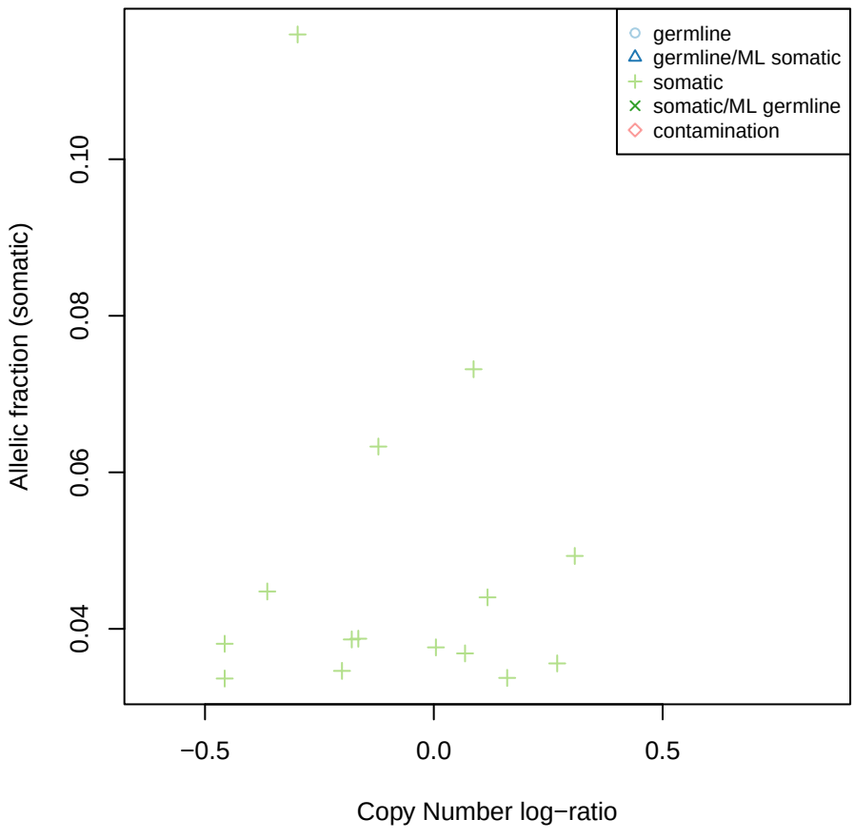

Purity: 0.55 Tumor ploidy: 4.956 SNV log−likelihood: −59.53 GoF: 92% Mean coverage: 521;524
1 2 3 4 5 6 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

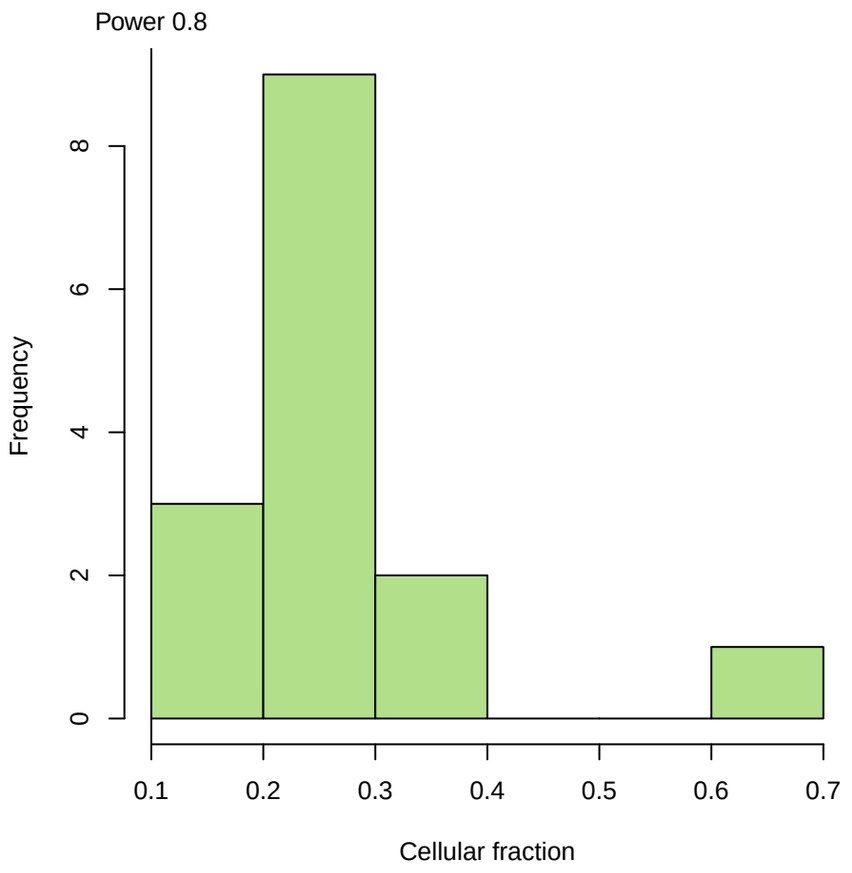

SCNA−fit log−likelihood: −56.37
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 50 100 150
SNV Index

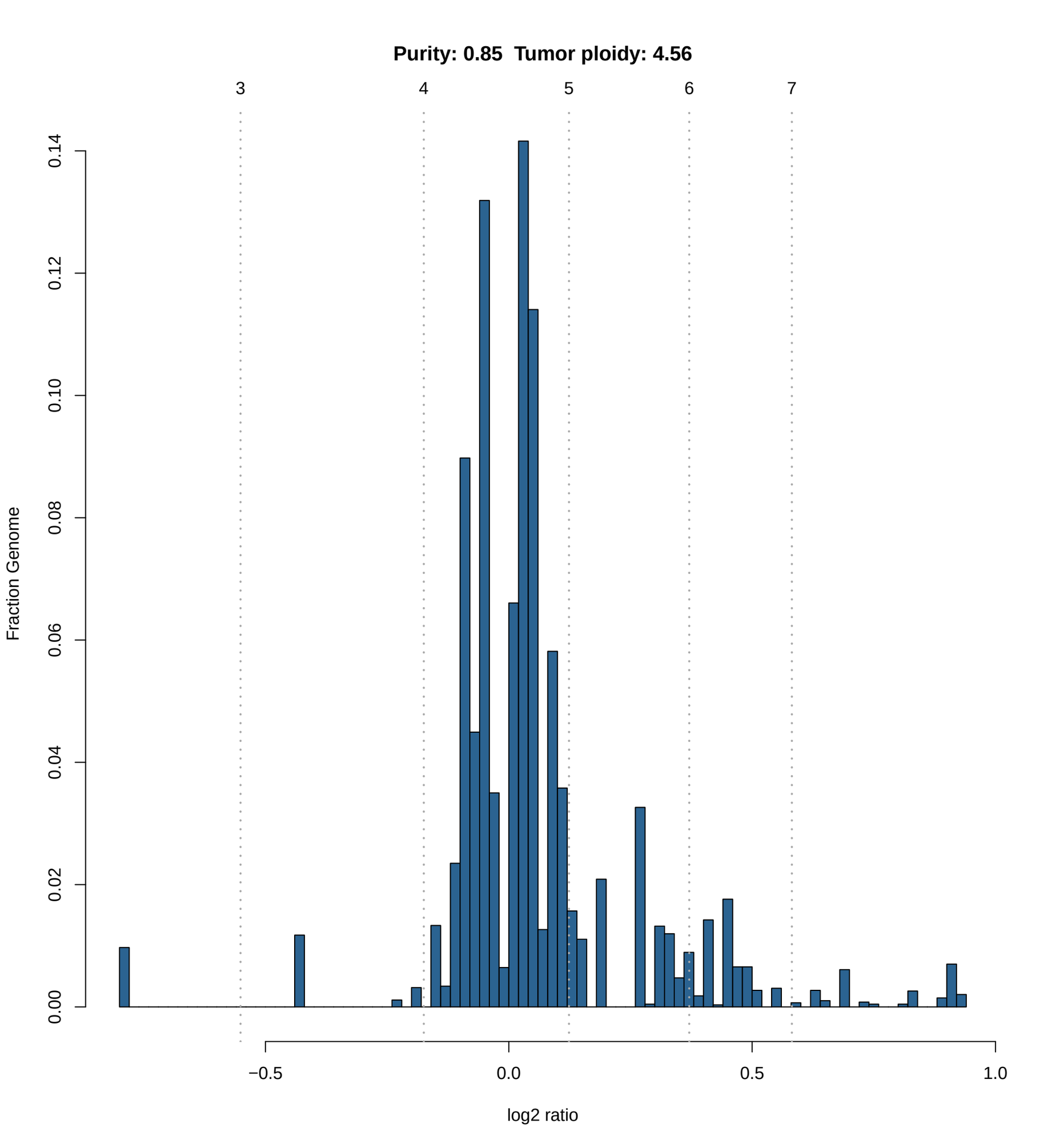

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

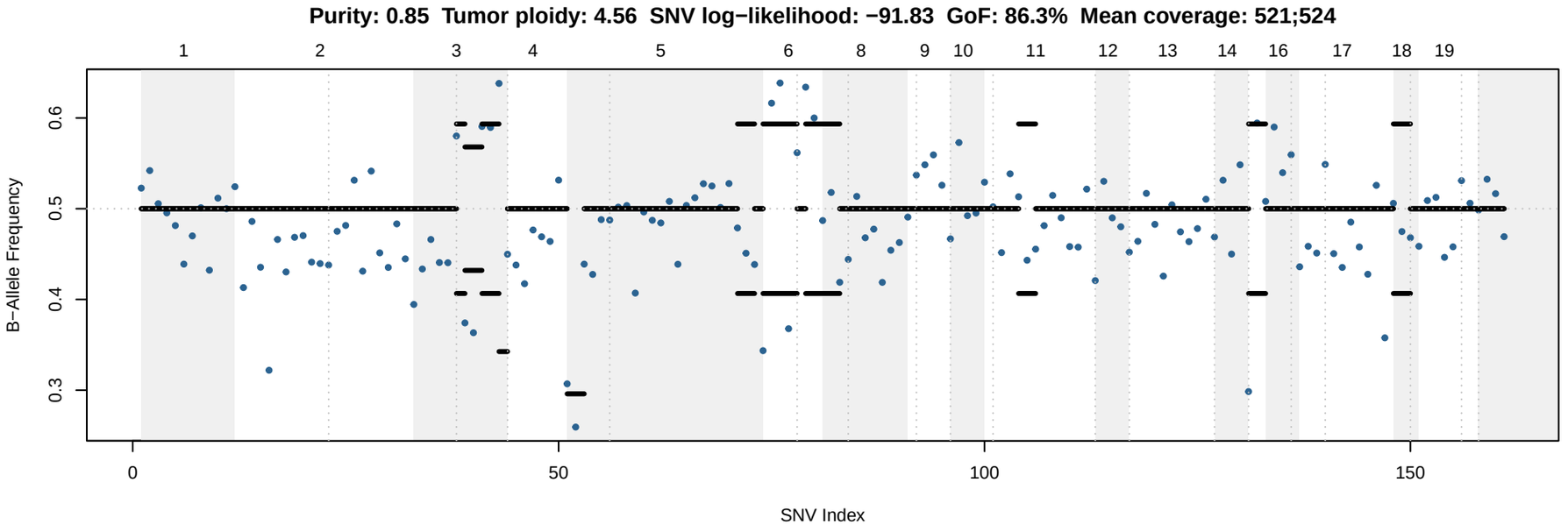

6m4
5m3
7m4
4m2
6m3
5m2
3m1
6m2
4m1
7m2
Allelic fraction (germline)
Copy Number log−ratio
0.2
0.3
0.4
0.5
0.6
−0.5
0.0
0.5

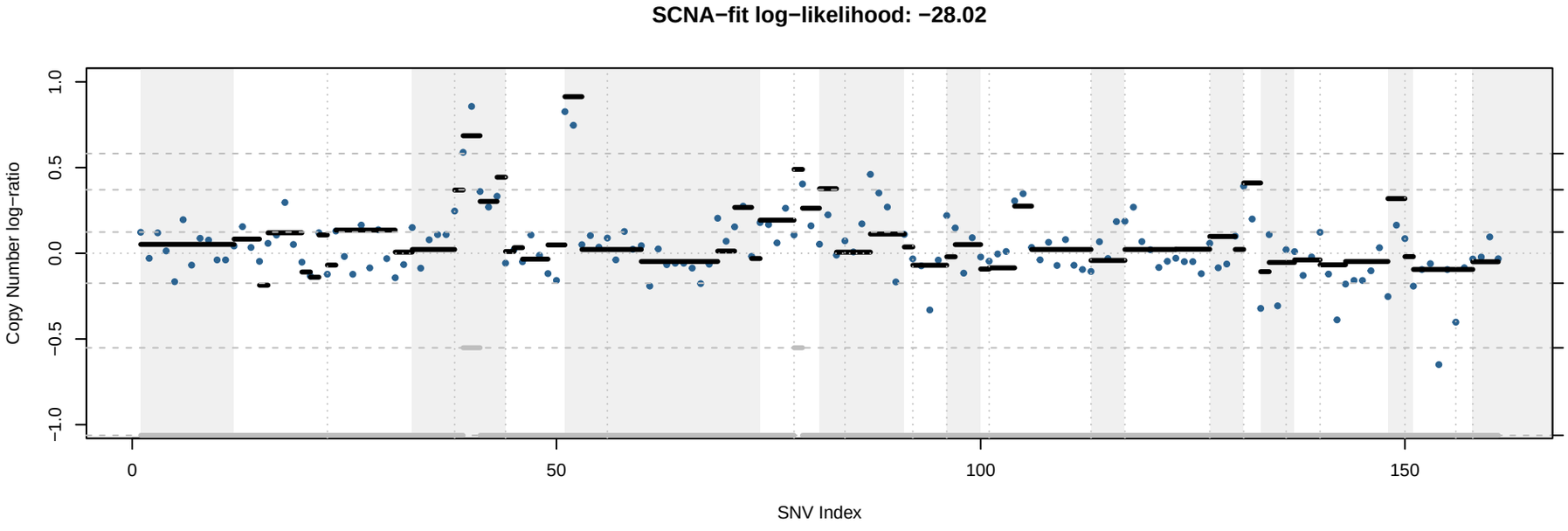

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

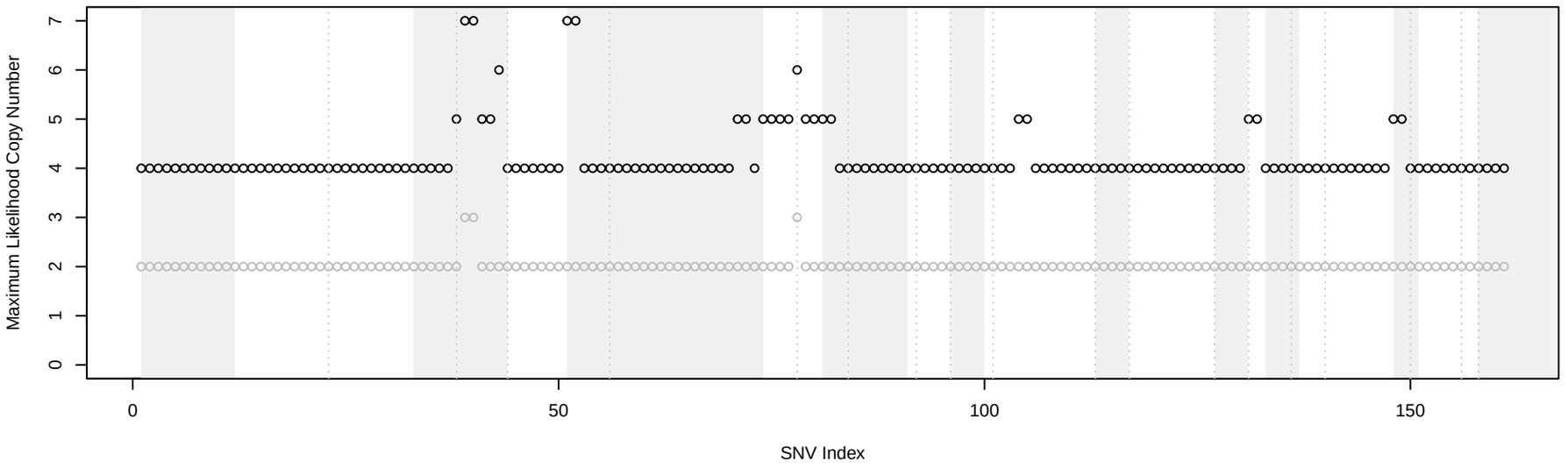

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
−0.5
0.0
0.5

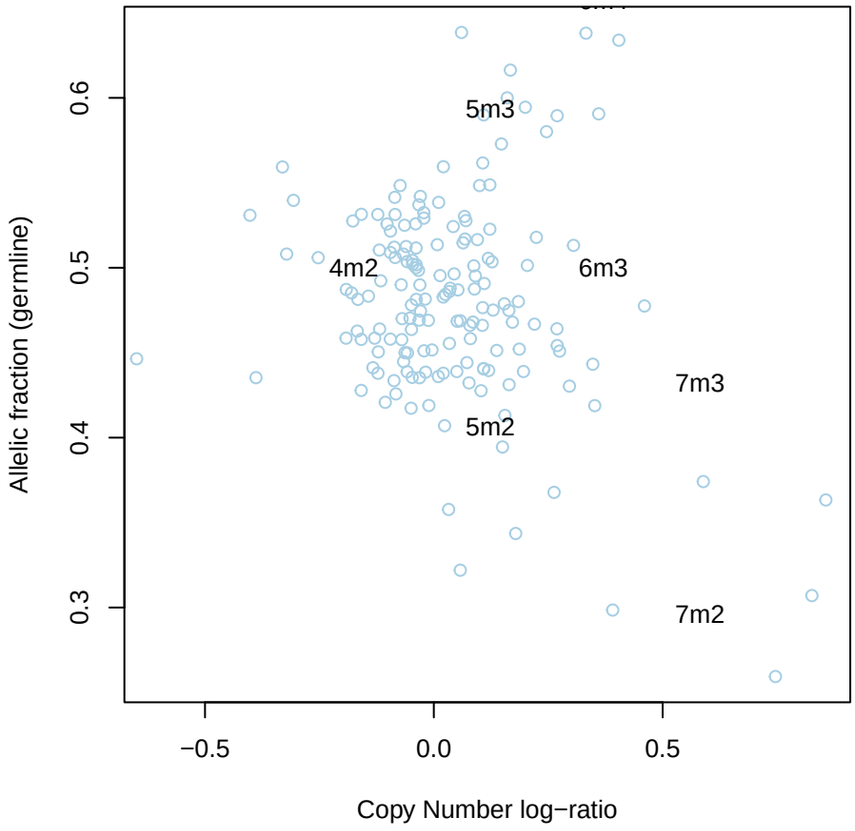

Power 0.8
Frequency
Cellular fraction
0
2
4
6
8
0.1
0.2
0.3
0.4
0.5
0.6
0.7

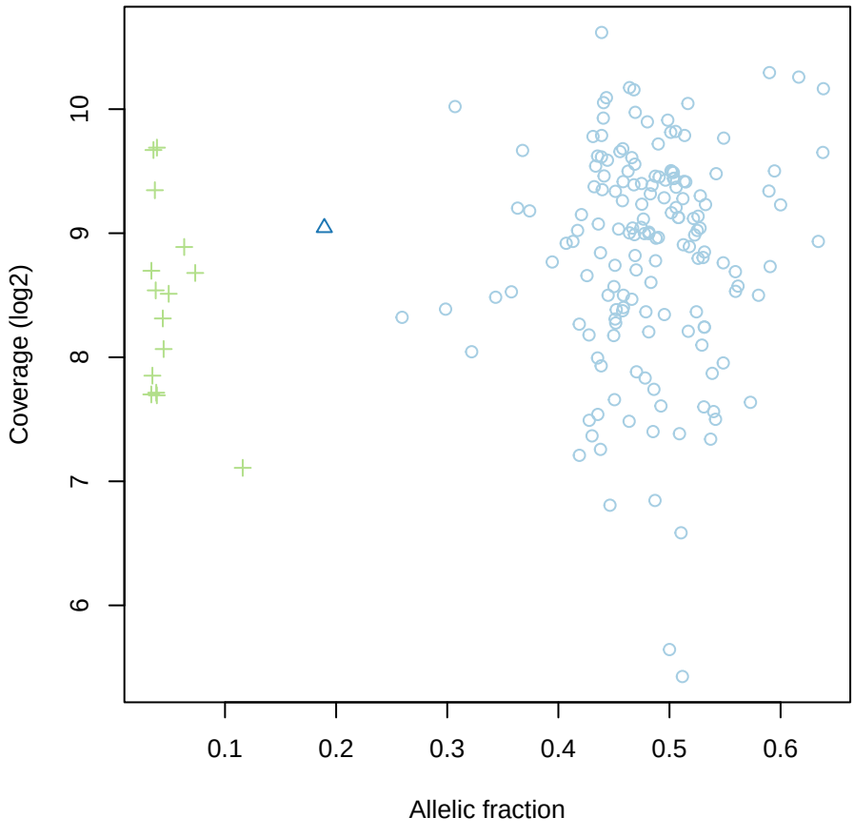

Purity: 0.85 Tumor ploidy: 4.56
3
4
5
6
7
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

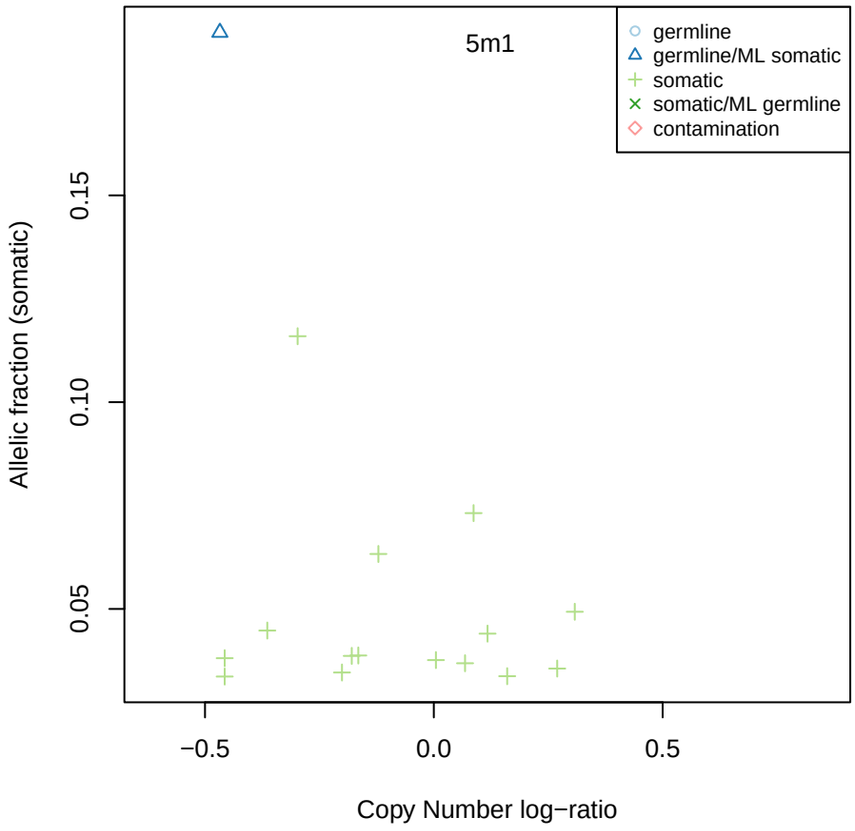

Purity: 0.85 Tumor ploidy: 4.56 SNV log−likelihood: −91.83 GoF: 86.3% Mean coverage: 521;524
1 2 3 4 5 6 8 9 10 11 12 13 14 16 17 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

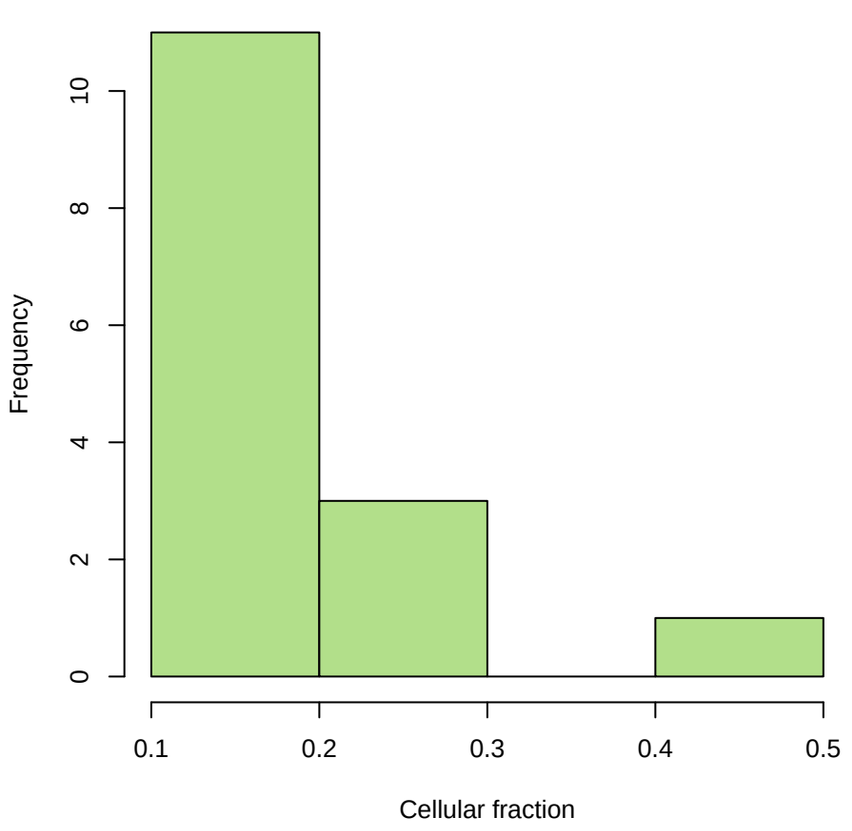

SCNA−fit log−likelihood: −28.02
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 50 100 150
SNV Index

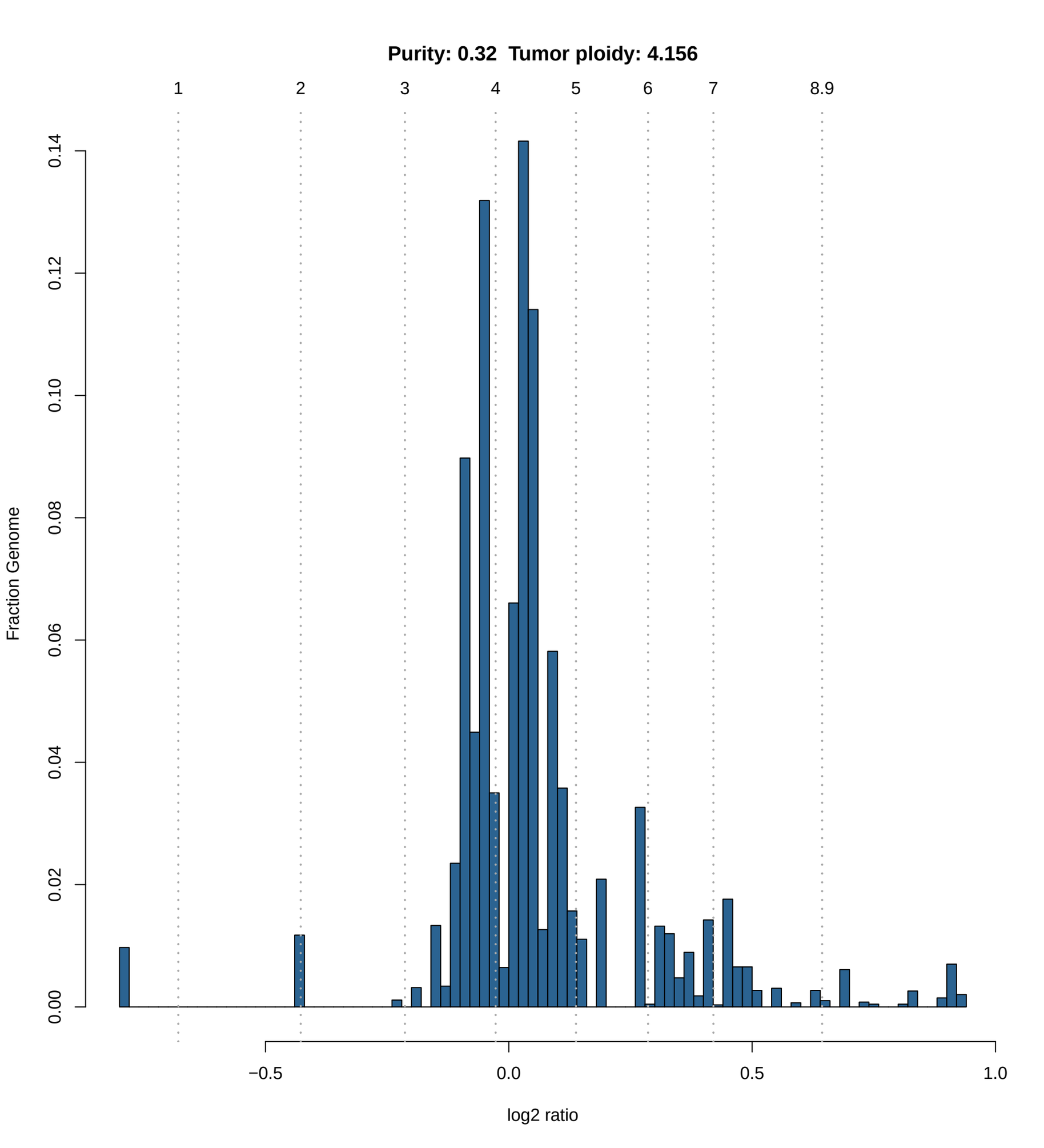

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

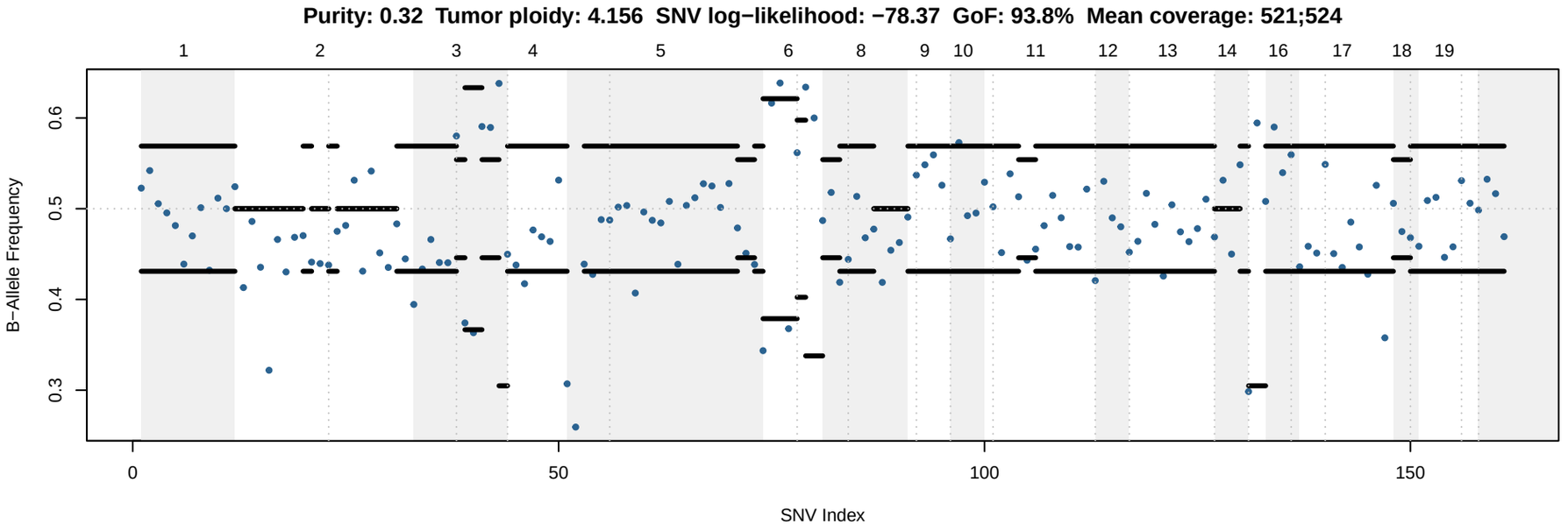

Allelic fraction (germline)
0.3
0.4
0.5
0.6
5m3
4m2
6m3
7m3
5m2
7m2
−0.5
0.0
0.5
Copy Number log−ratio

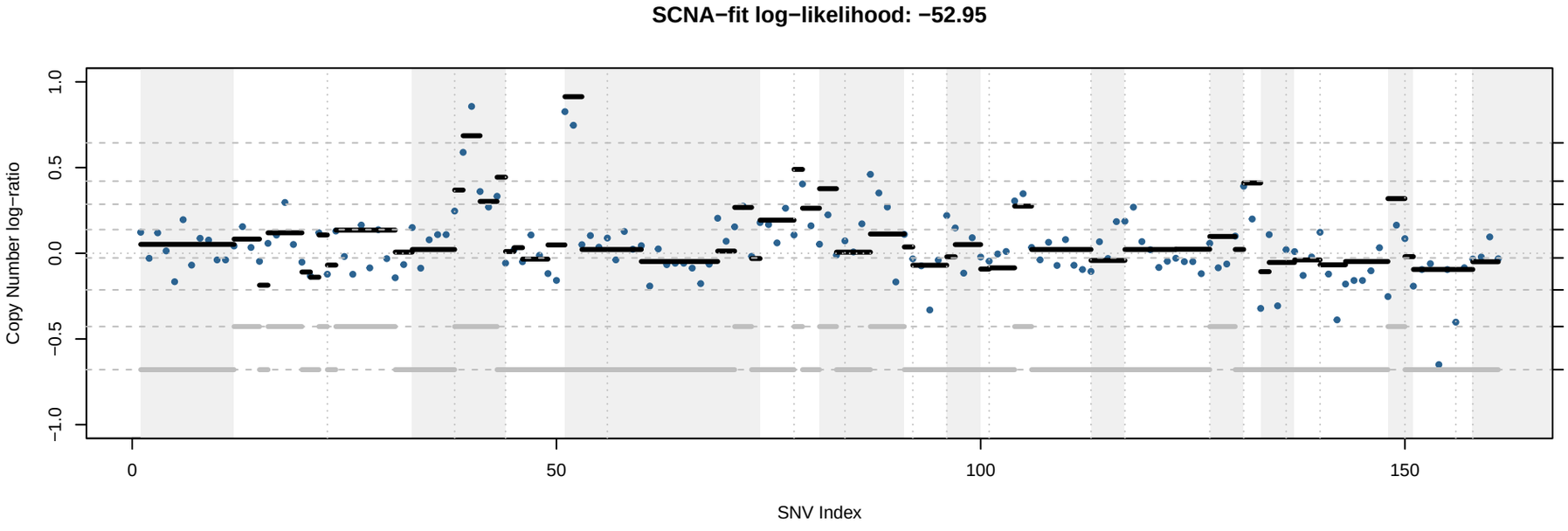

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

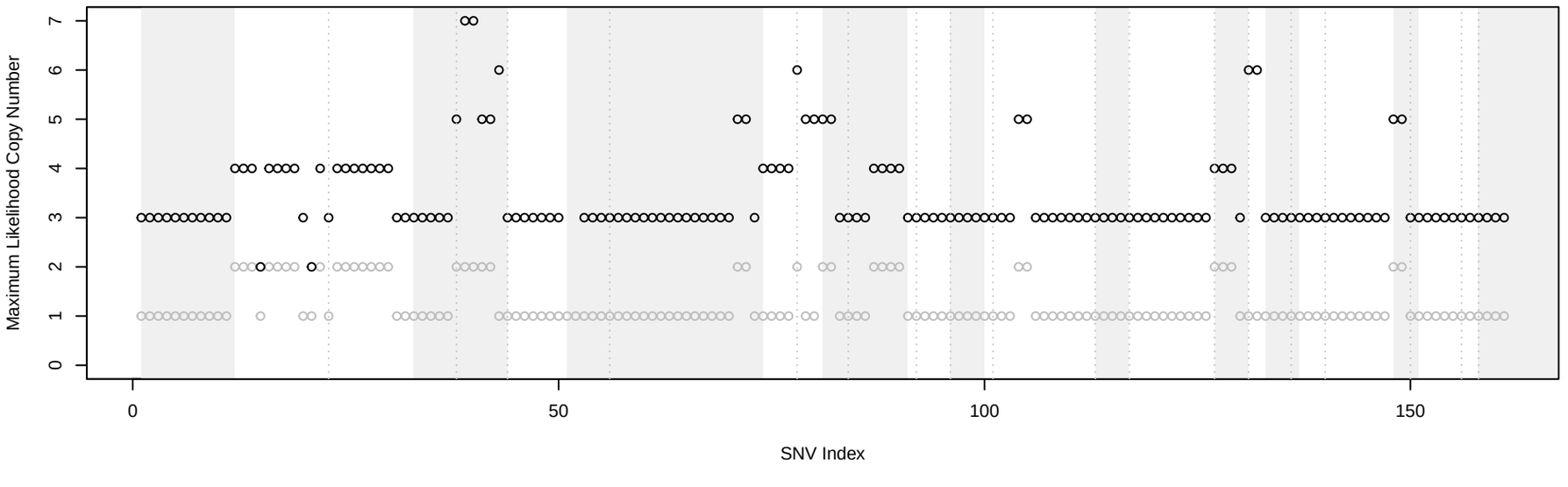

Allelic fraction (somatic)
0.05
0.10
0.15
5m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.5
0.0
0.5
Copy Number log−ratio

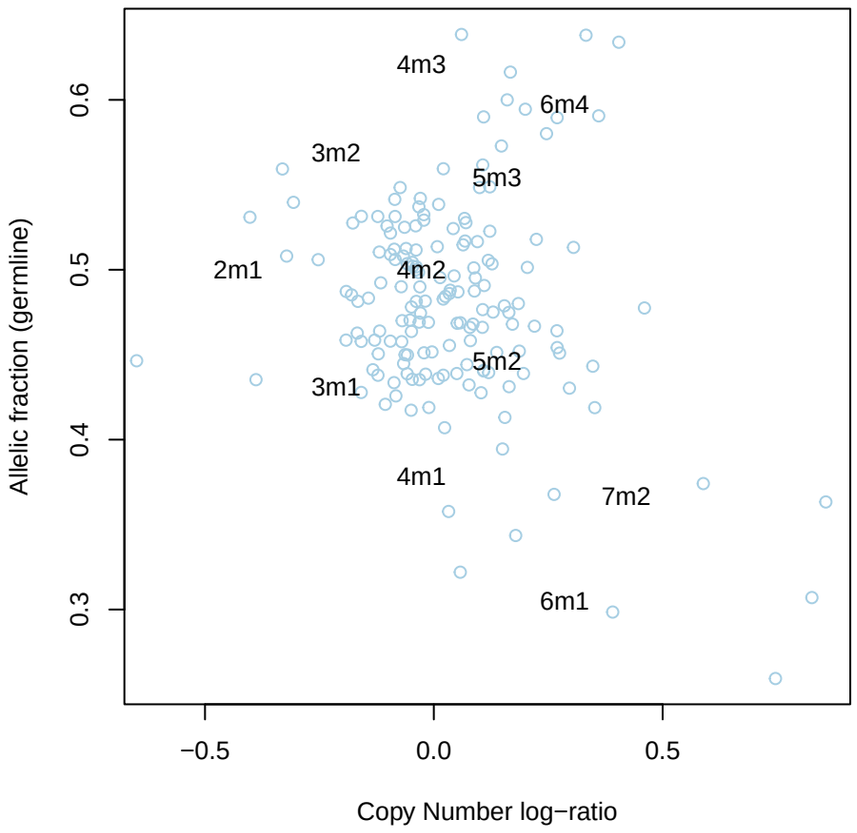

Frequency
0
2
4
6
8
10
0.1
0.2
0.3
0.4
0.5
Cellular fraction

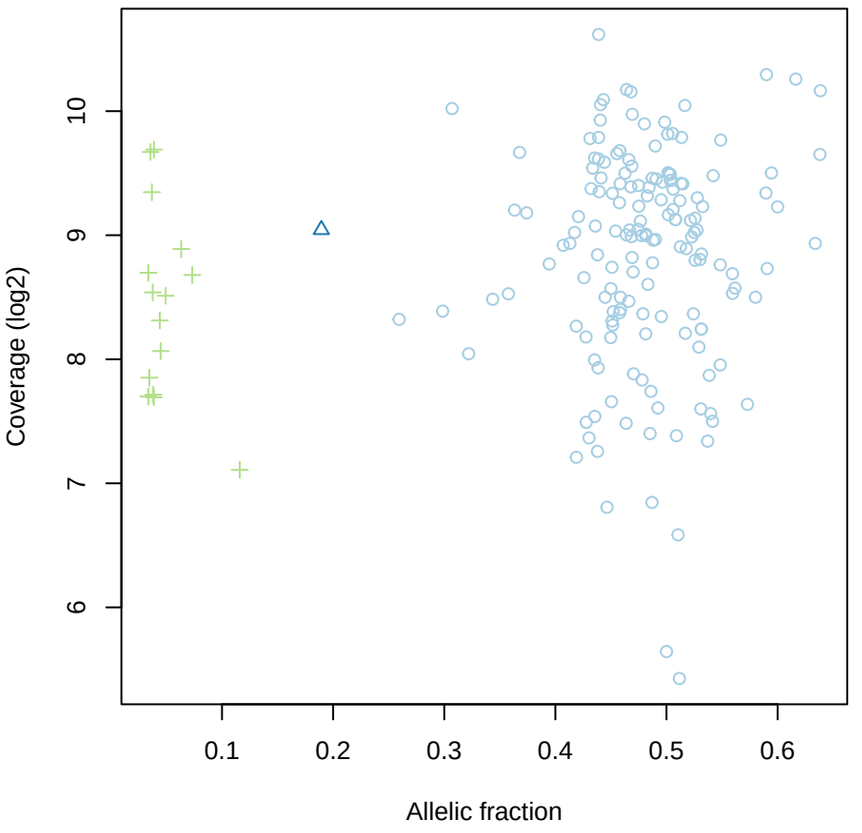

Purity: 0.32 Tumor ploidy: 4.156
1
2
3
4
5
6
7
8.9
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

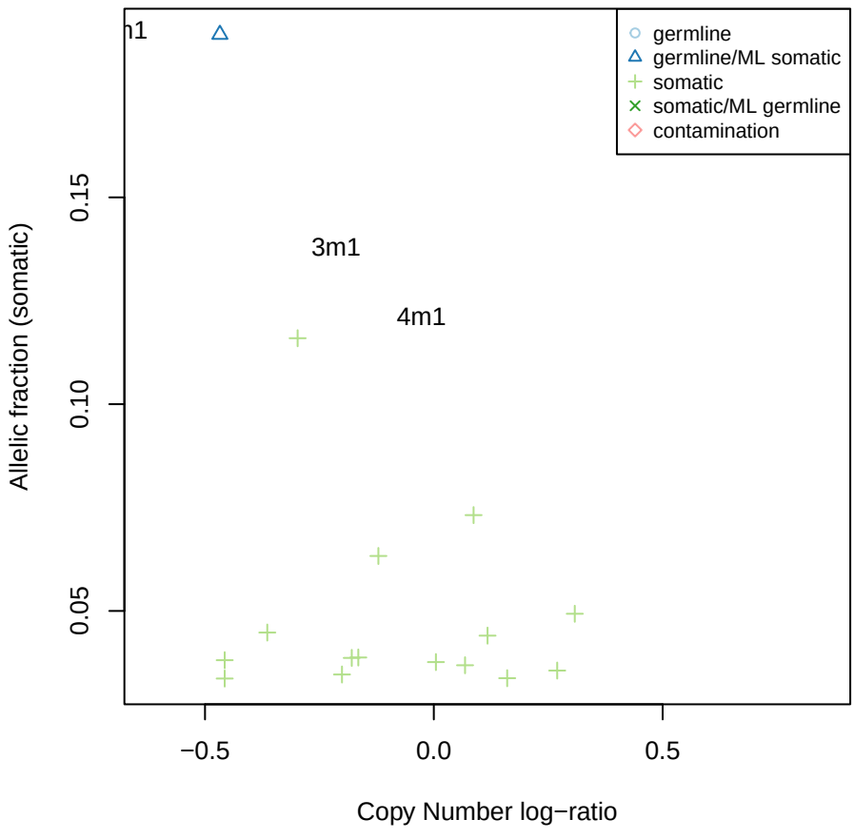

Purity: 0.32 Tumor ploidy: 4.156 SNV log−likelihood: −78.37 GoF: 93.8% Mean coverage: 521;524
1 2 3 4 5 6 8 9 10 11 12 13 14 16 17 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

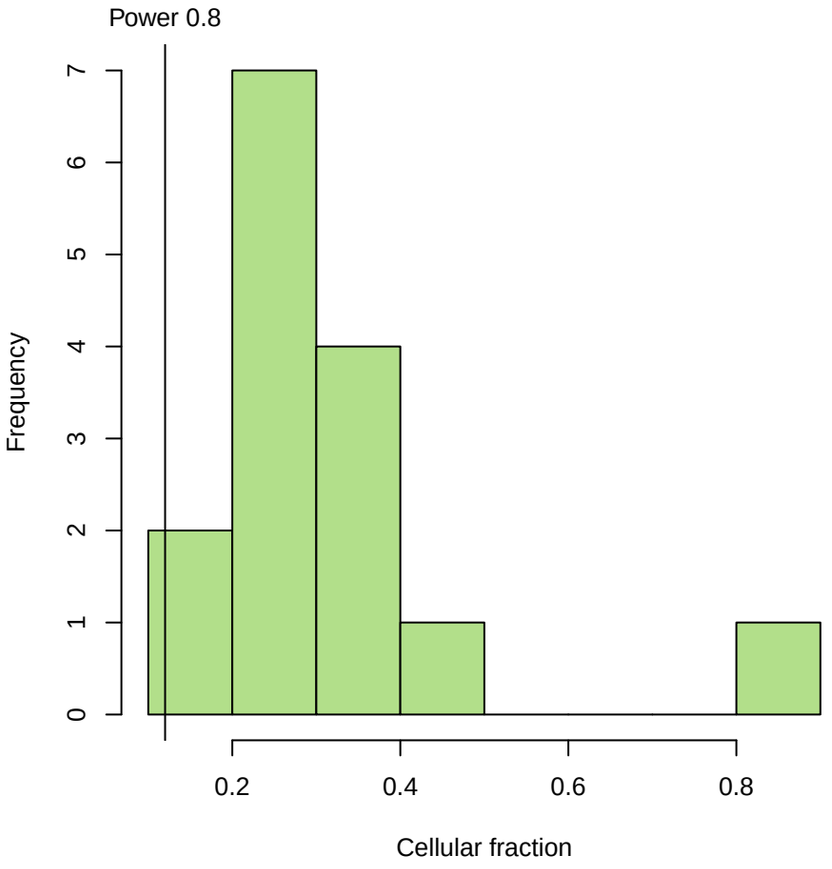

SCNA−fit log−likelihood: −52.95
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6 8.9
0 50 100 150
SNV Index

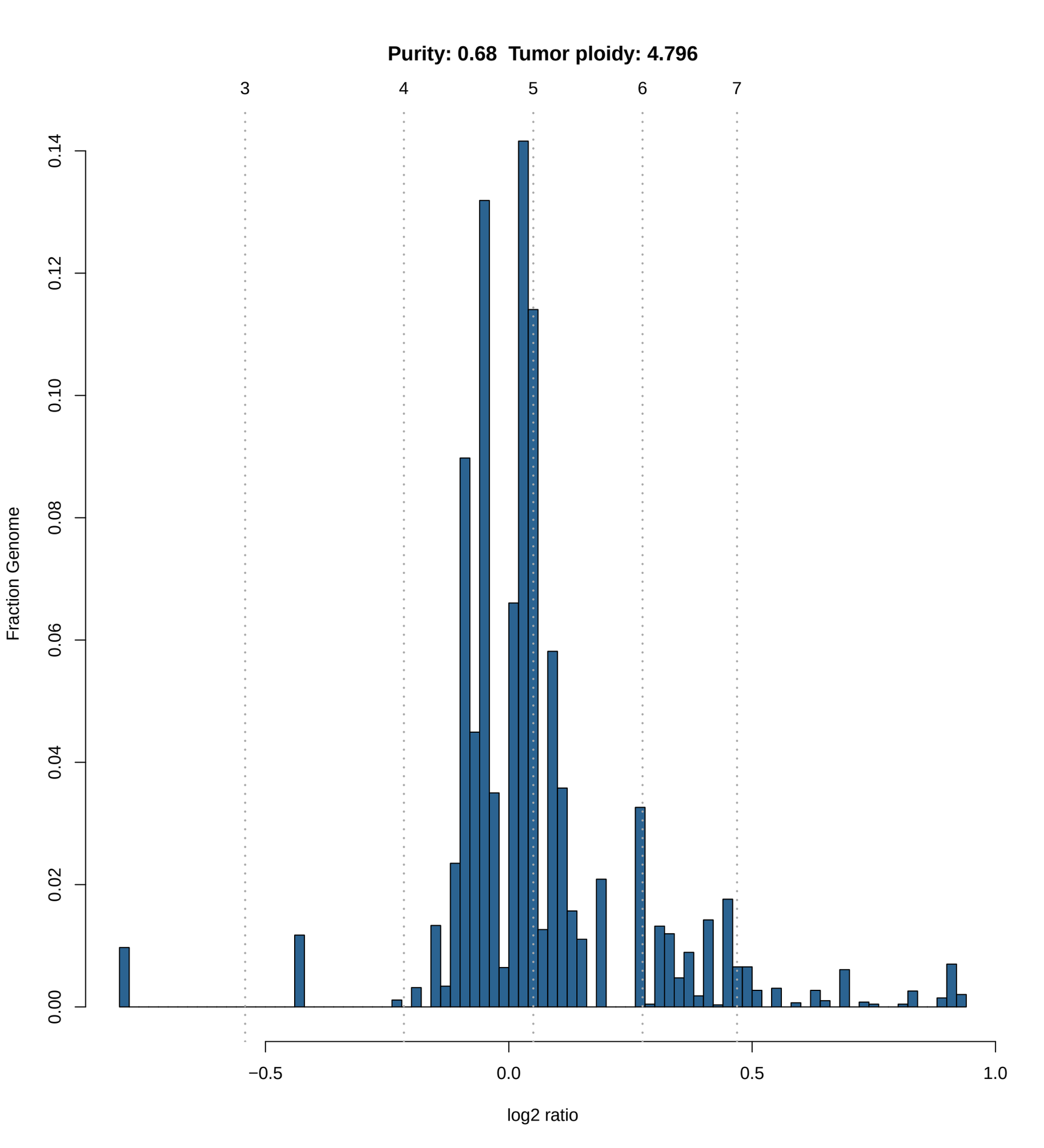

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

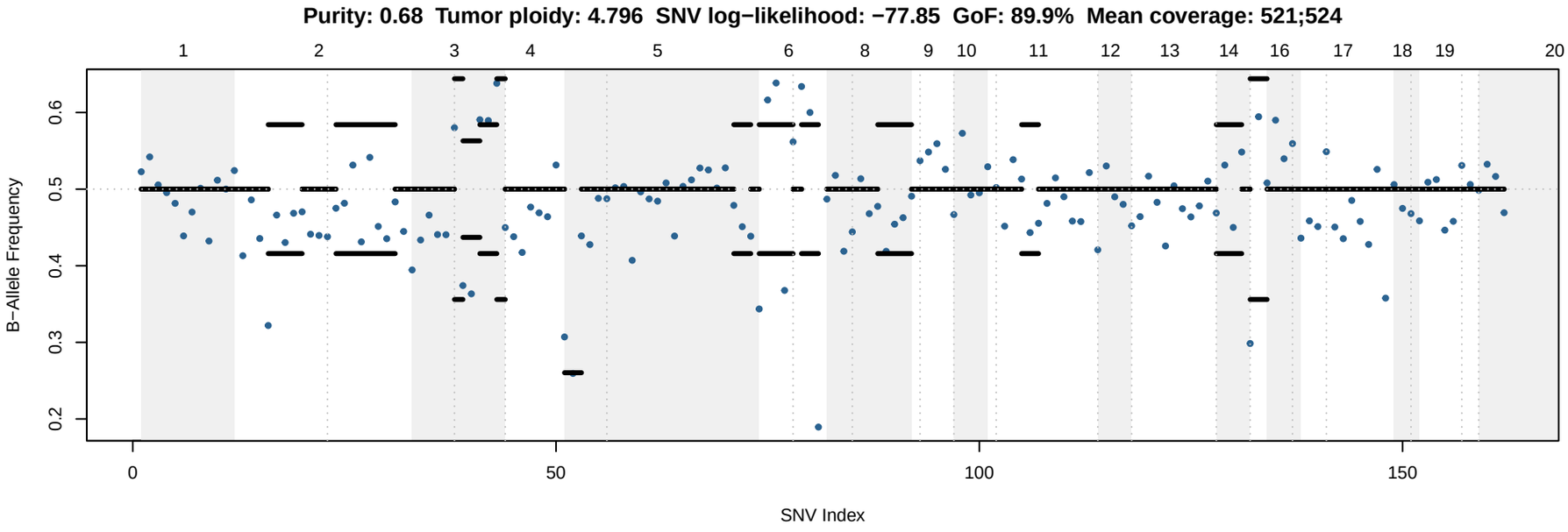

4m3
6m4
3m2
5m3
2m1
4m2
5m2
3m1
4m1
7m2
6m1
Allelic fraction (germline)
Copy Number log−ratio

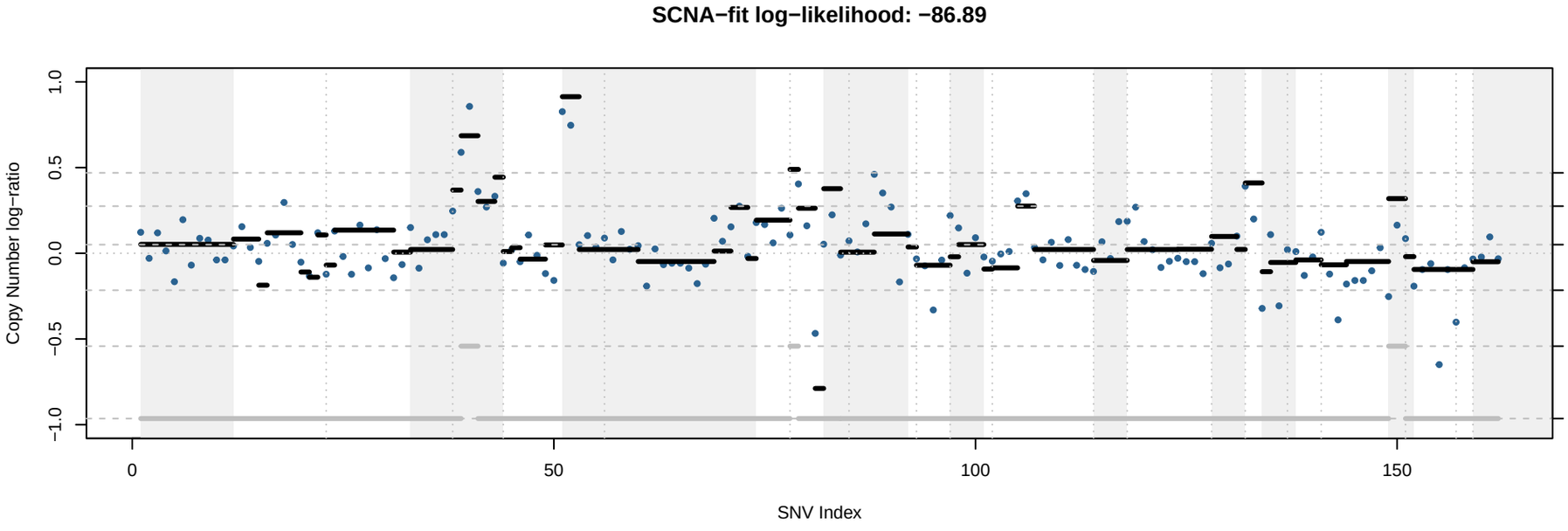

Coverage (log2)
Allelic fraction

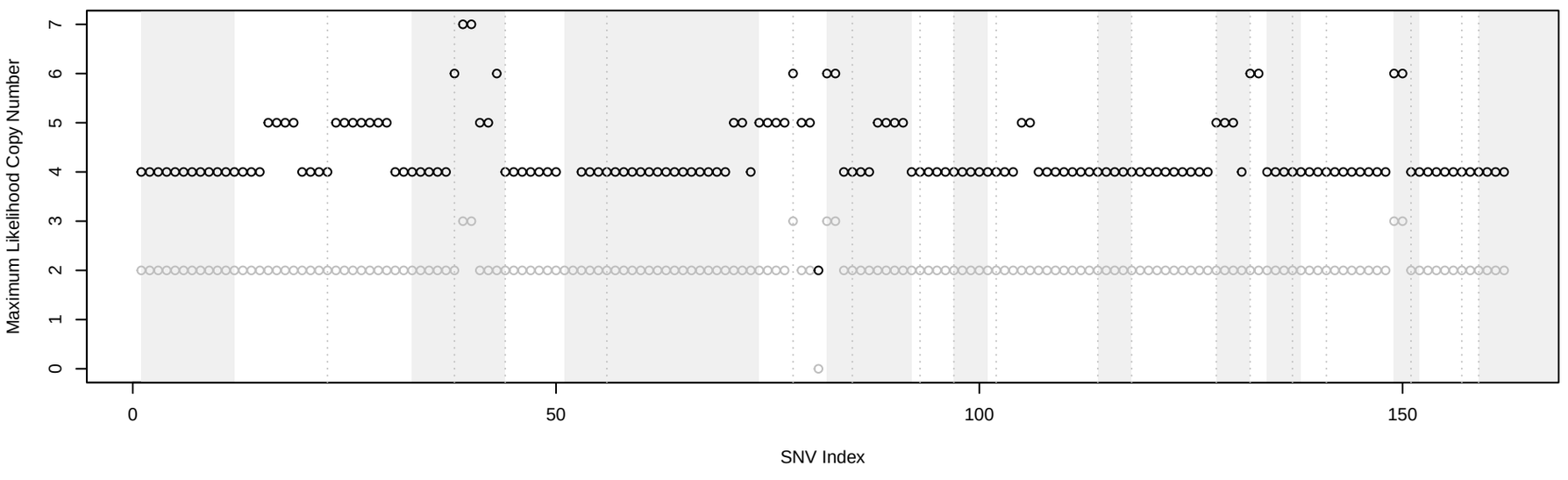

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
Allelic fraction (somatic)
Copy Number log−ratio

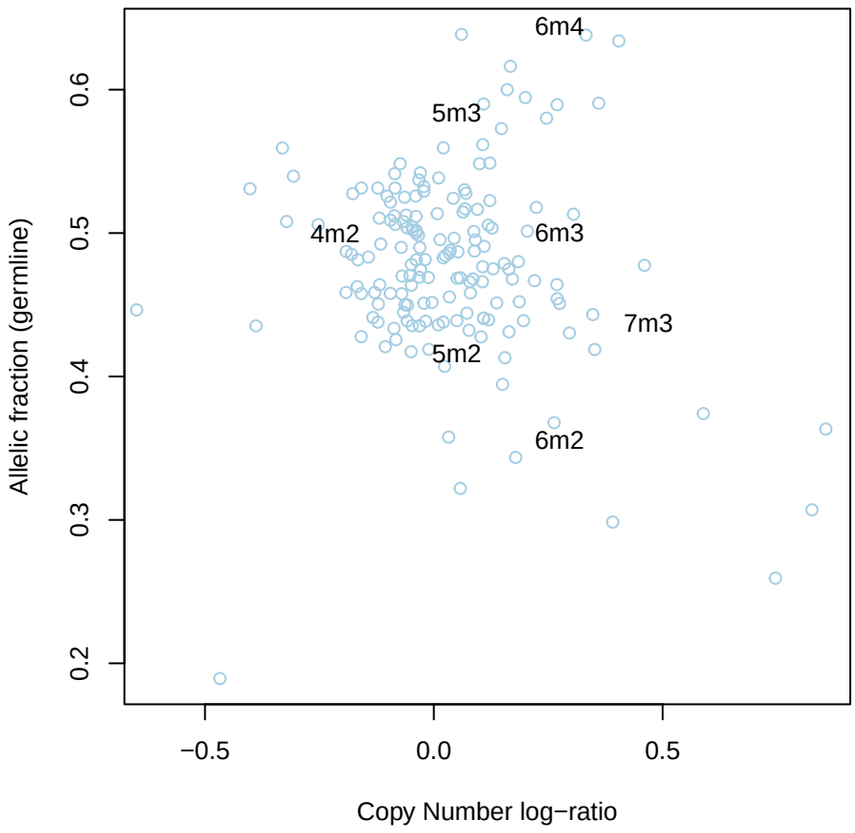

Power 0.8
Frequency
Cellular fraction

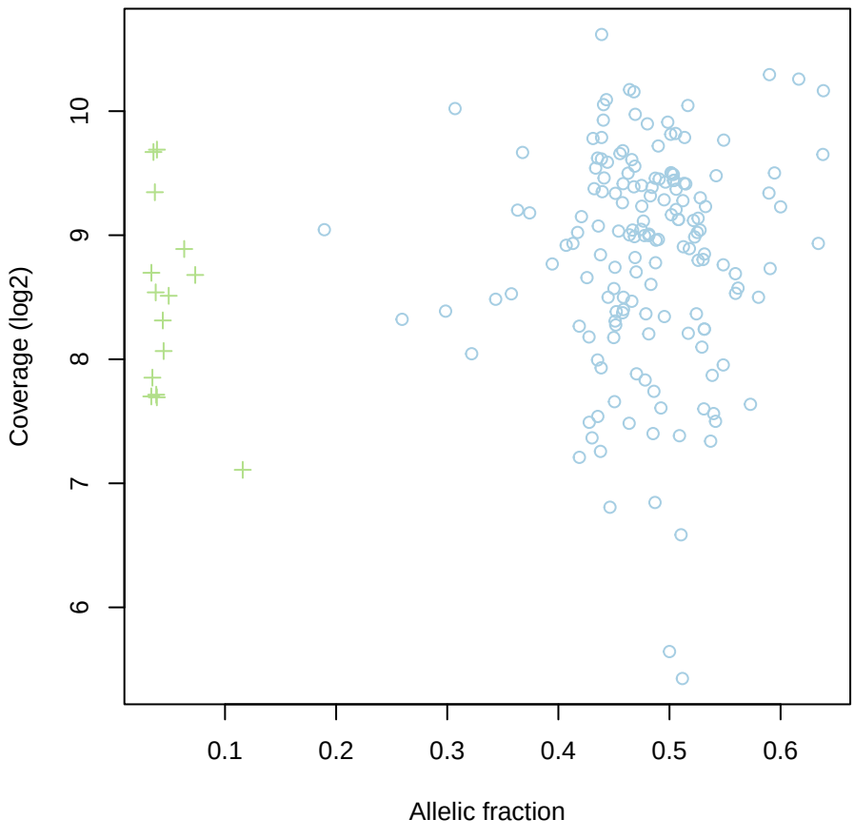

Purity: 0.68 Tumor ploidy: 4.796
3
4
5
6
7
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

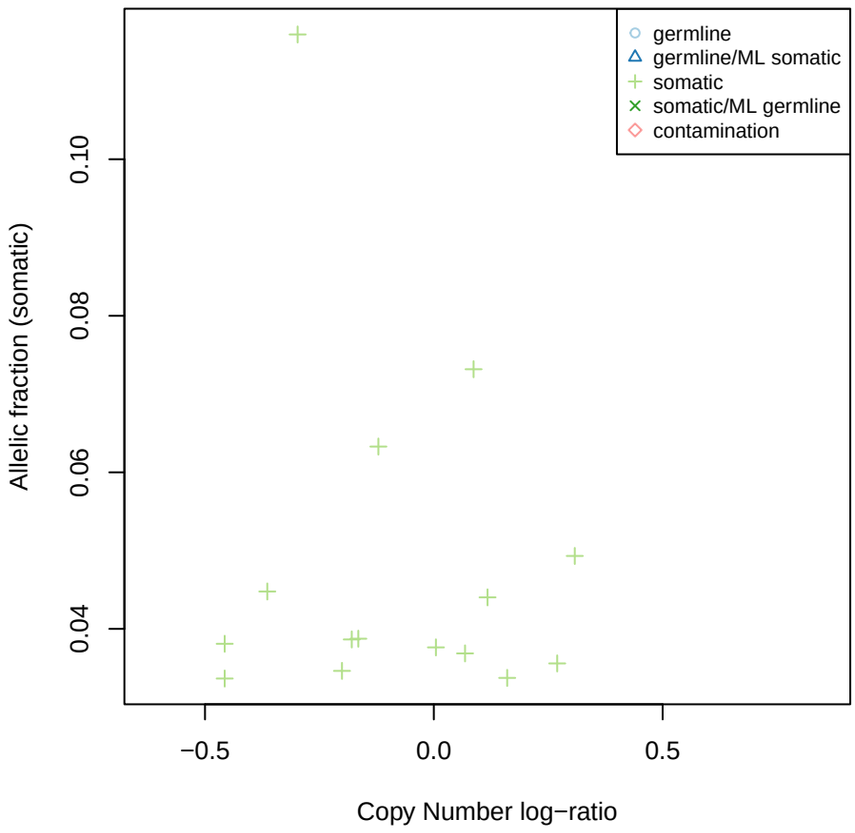

Purity: 0.68 Tumor ploidy: 4.796 SNV log−likelihood: −77.85 GoF: 89.9% Mean coverage: 521;524
1 2 3 4 5 6 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

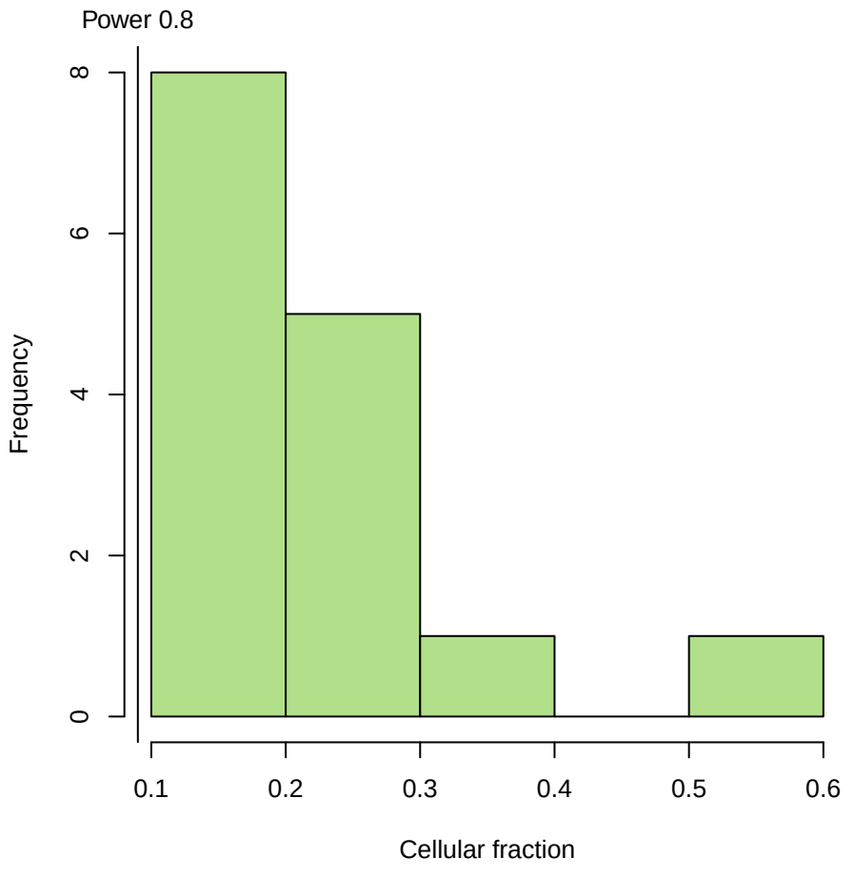

SCNA−fit log−likelihood: −86.89
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 50 100 150
SNV Index

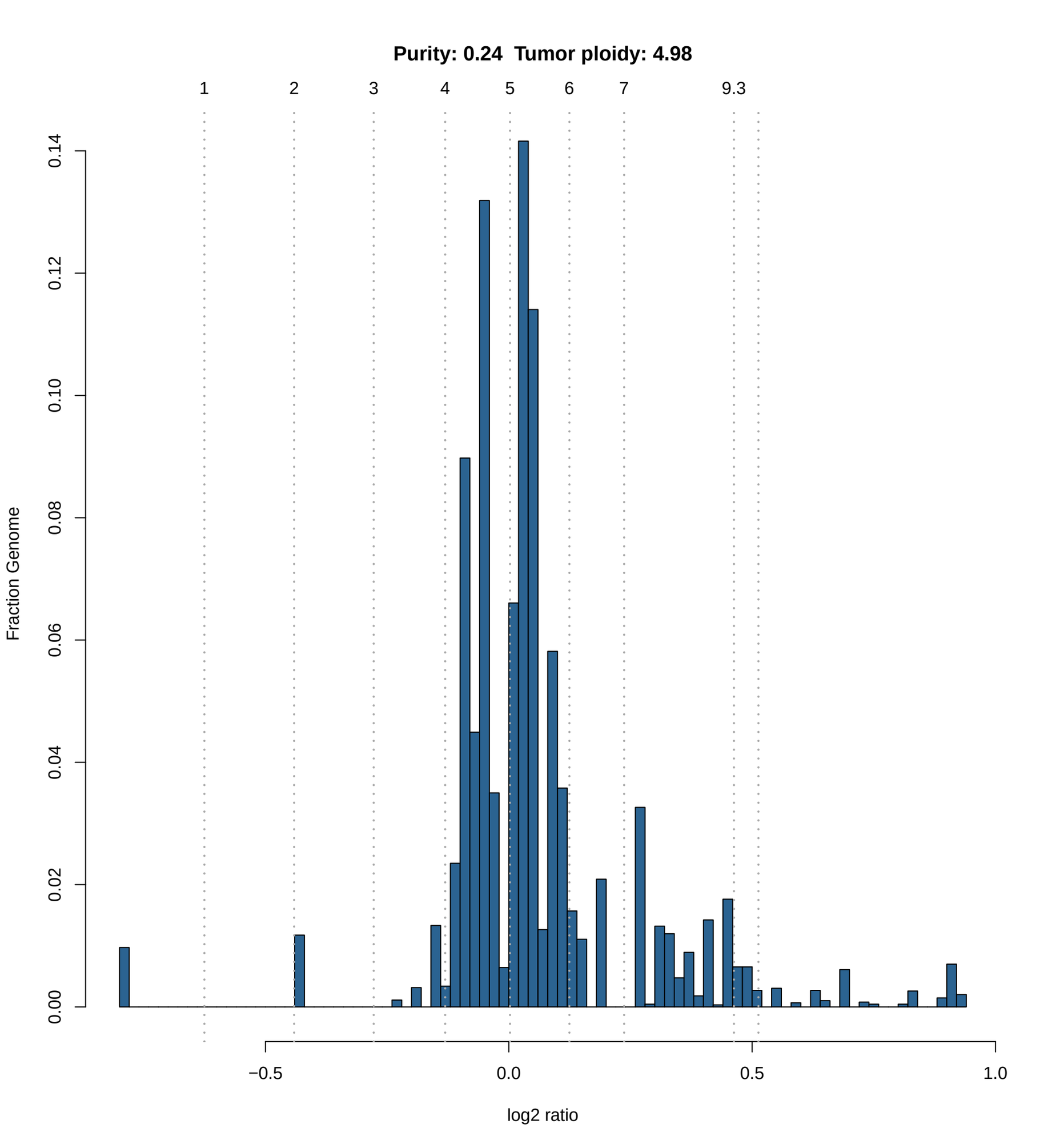

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

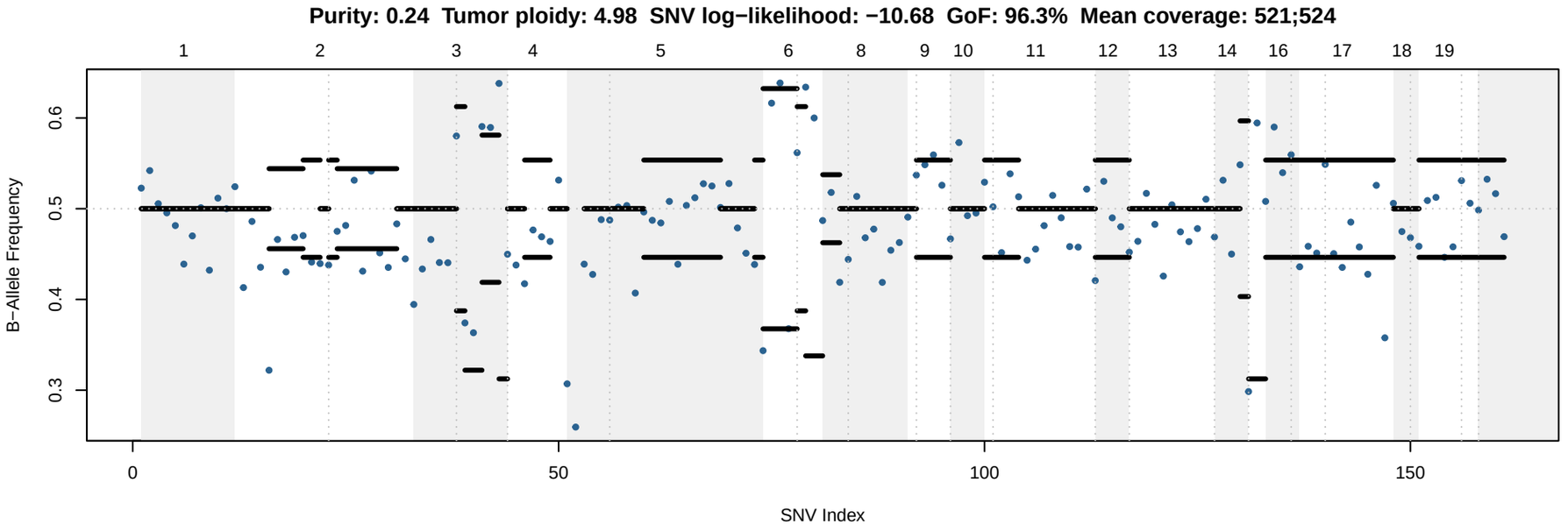

6m4
5m3
4m2
6m3
7m3
5m2
6m2
Allelic fraction (germline)
Copy Number log−ratio

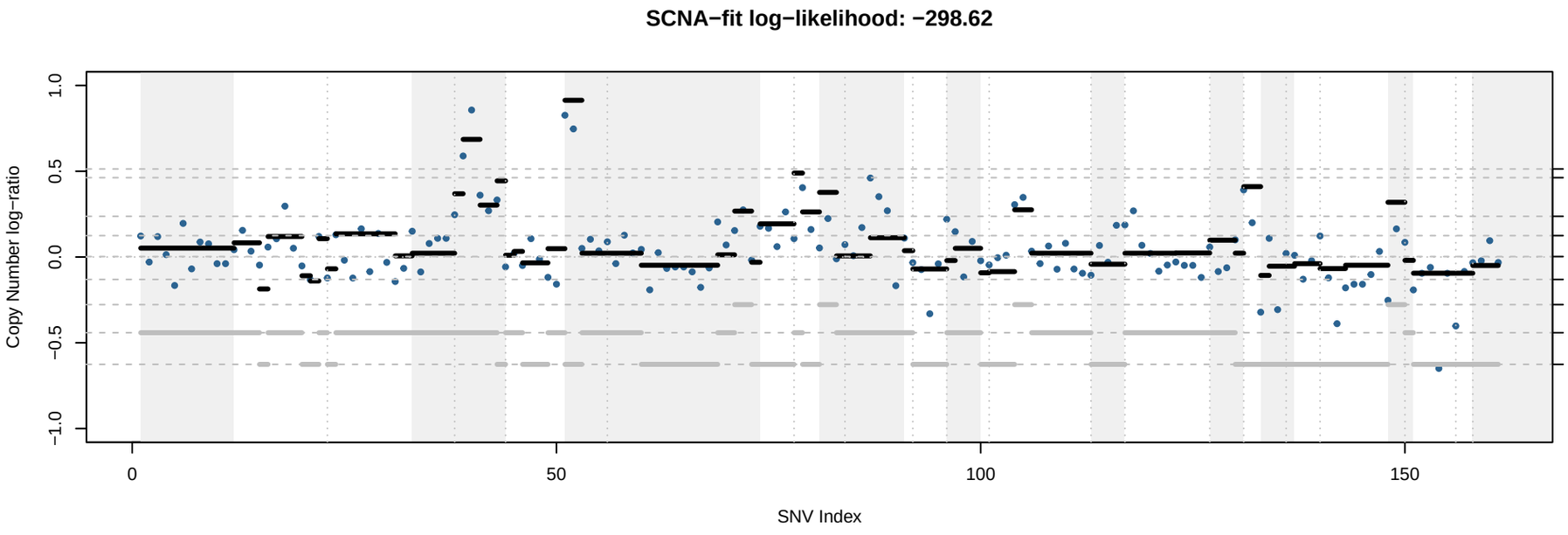

Coverage (log2)
Allelic fraction

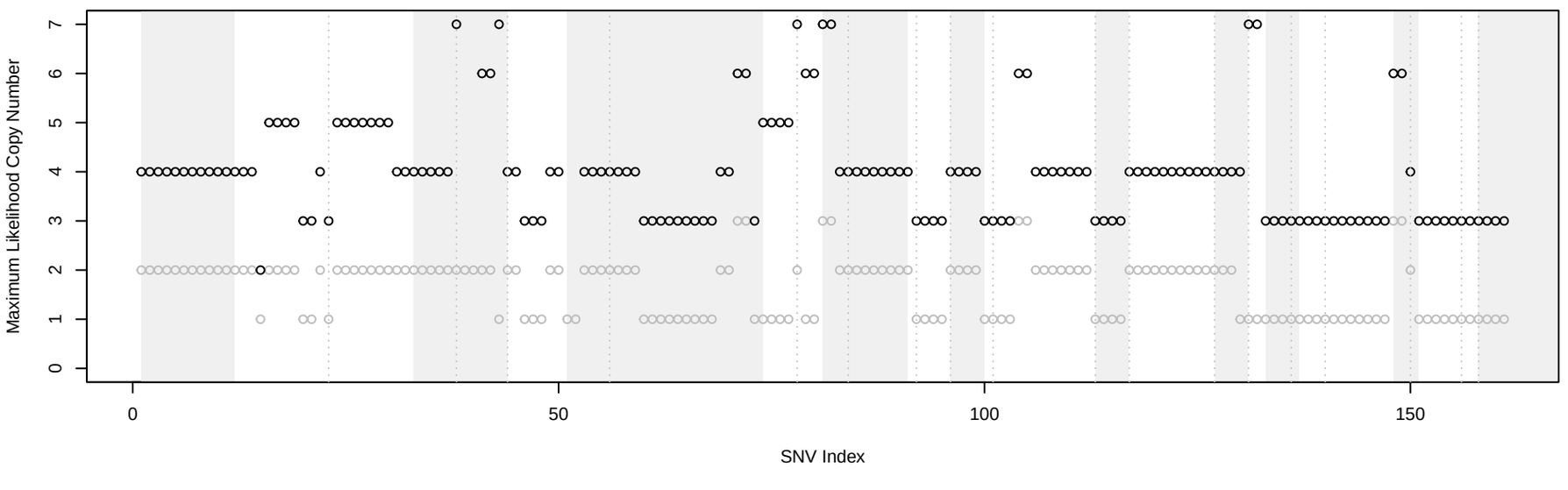

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

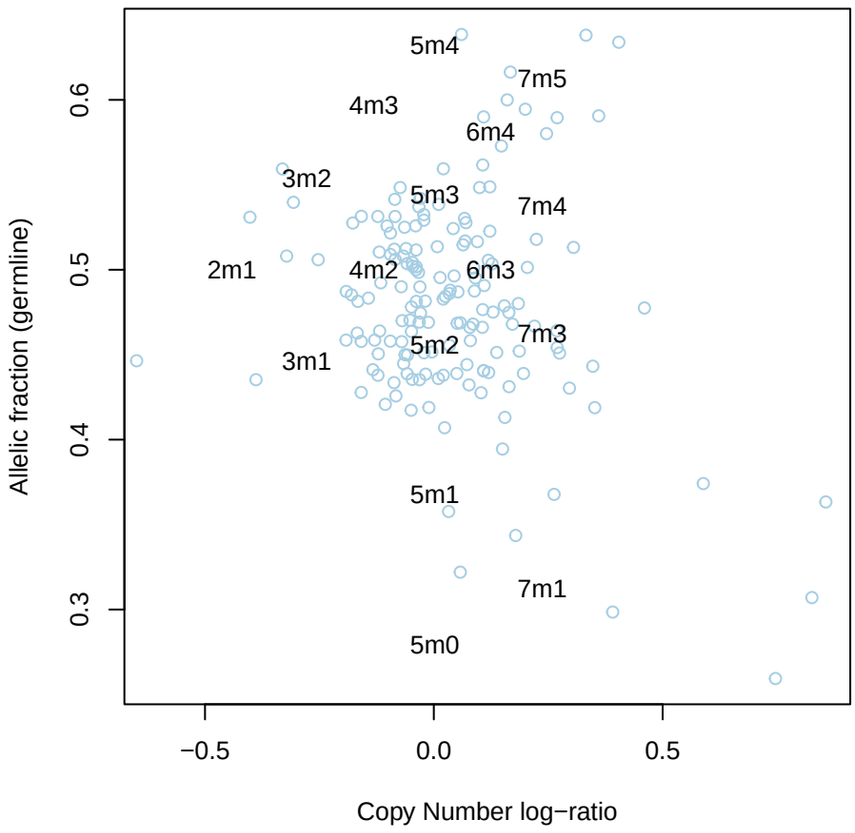

Power 0.8
Frequency
Cellular fraction

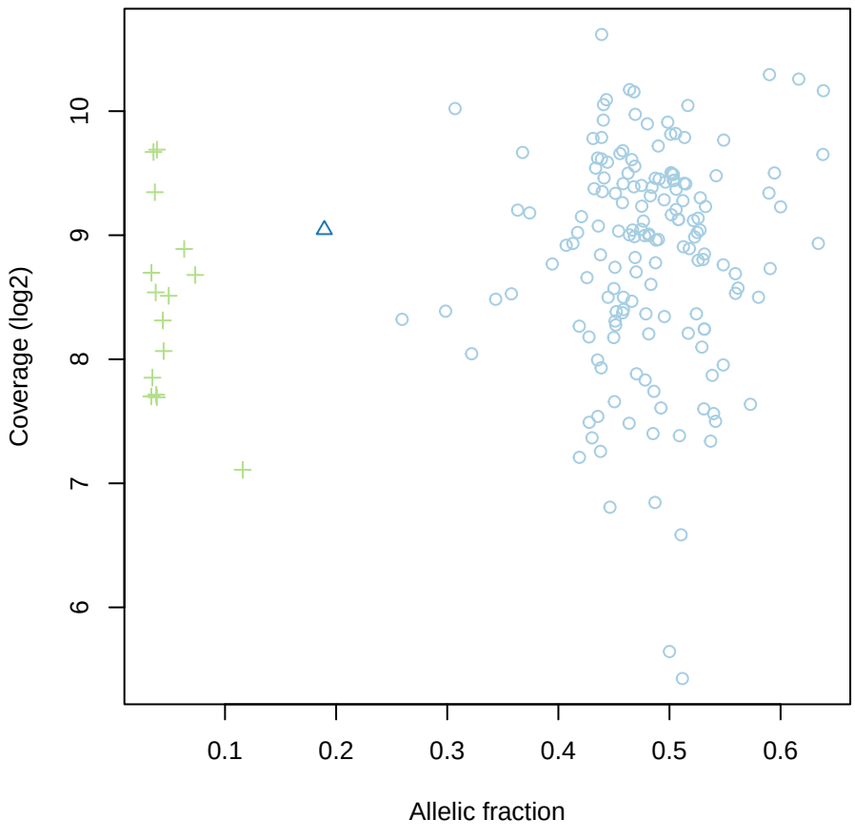

Purity: 0.24 Tumor ploidy: 4.98
1
2
3
4
5
6
7
9.3
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

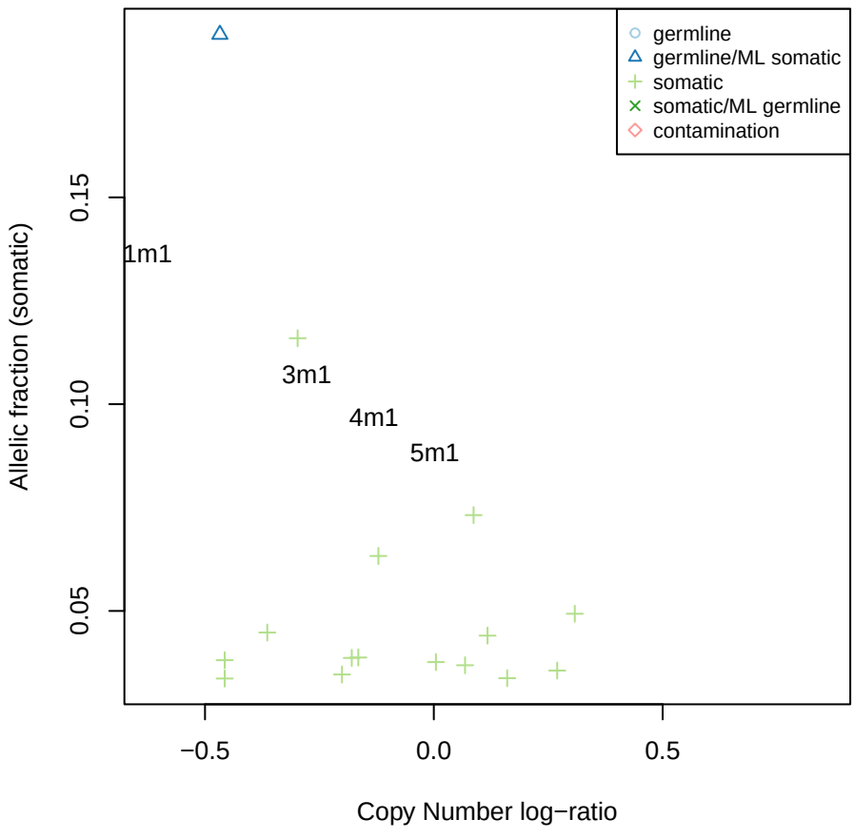

Purity: 0.24 Tumor ploidy: 4.98 SNV log−likelihood: −10.68 GoF: 96.3% Mean coverage: 521;524
1 2 3 4 5 6 8 9 10 11 12 13 14 16 17 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

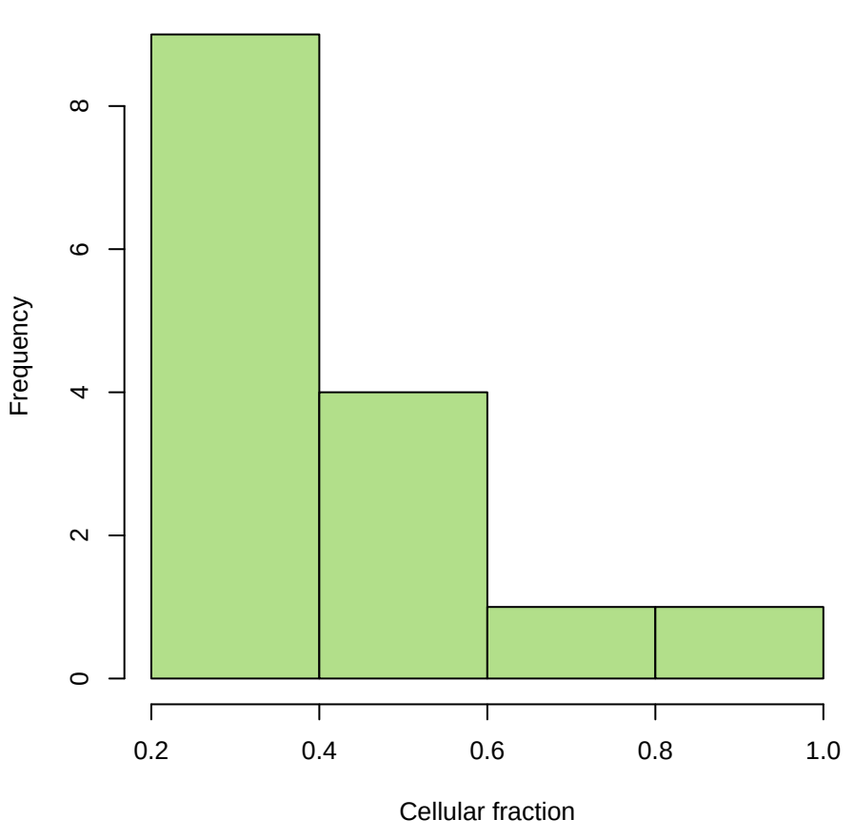

SCNA−fit log−likelihood: −298.62
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 6 9.3
0 50 100 150
SNV Index

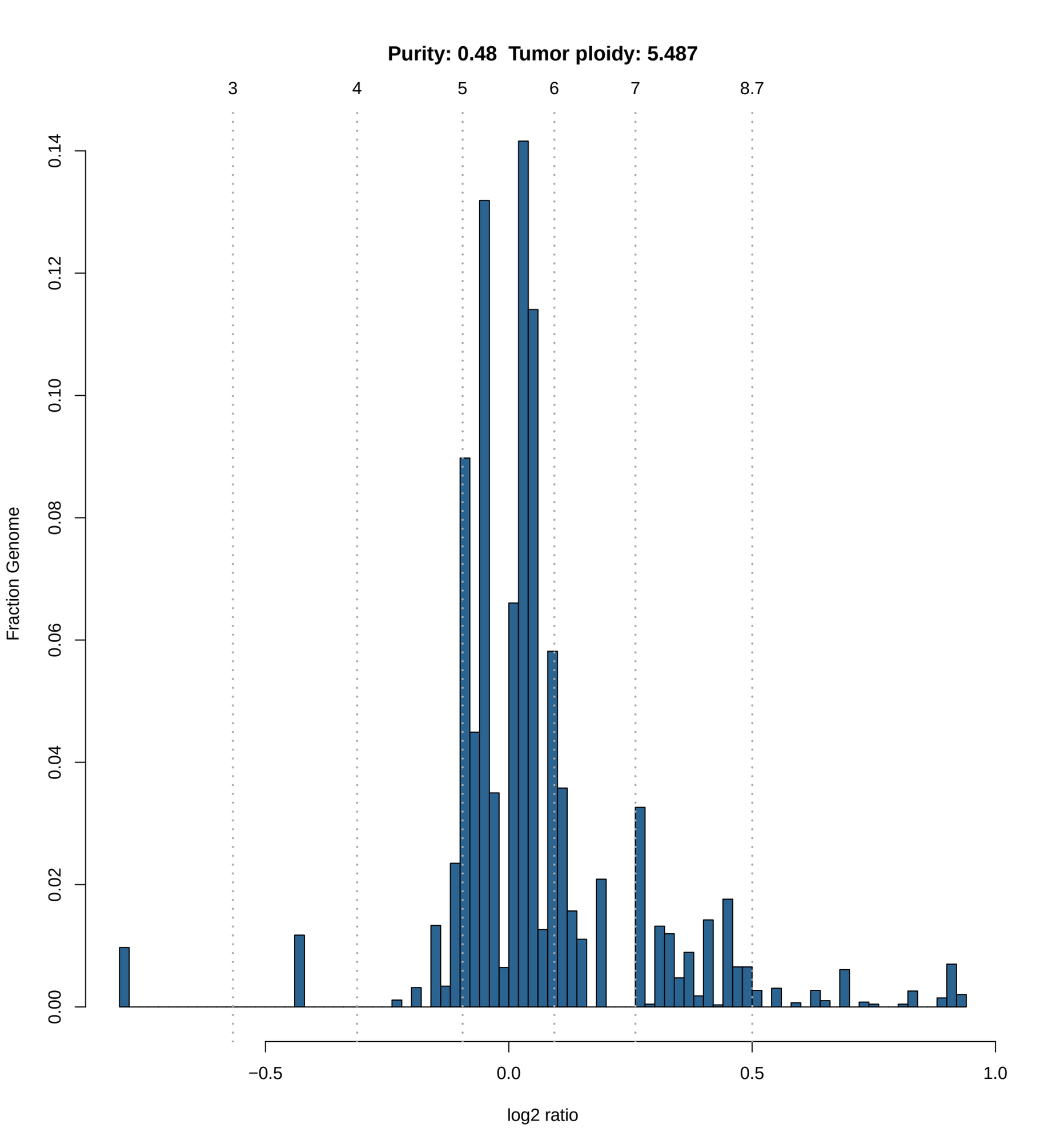

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

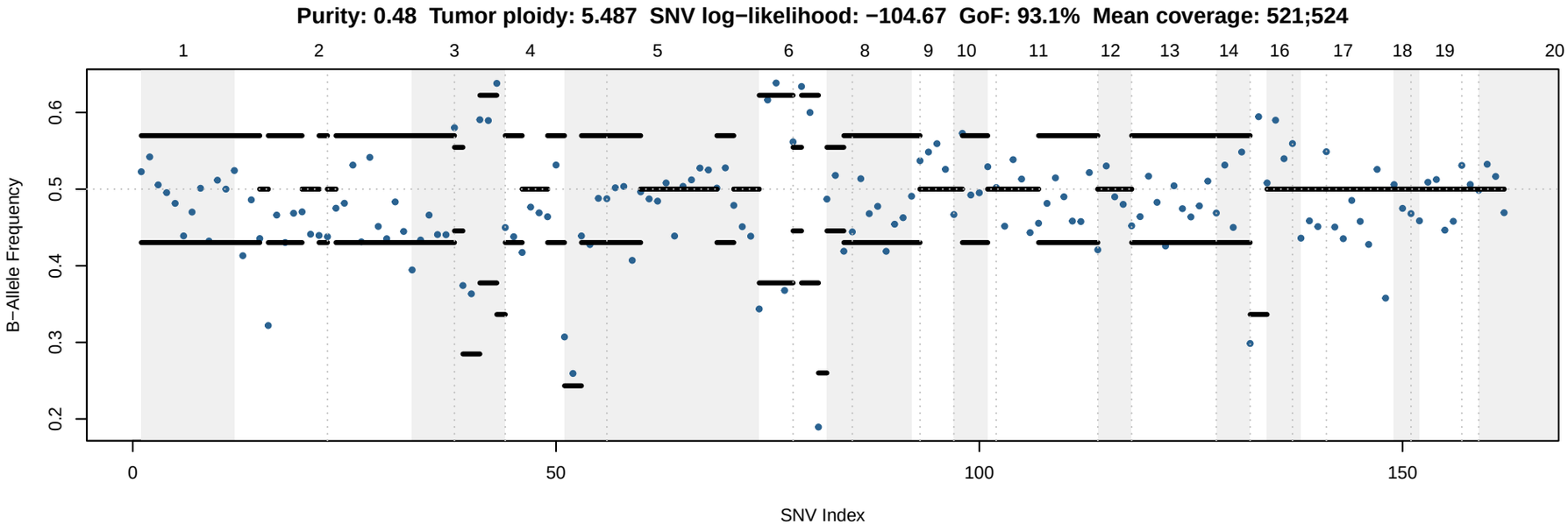

5m4
7m5
4m3
6m4
3m2
5m3
7m4
2m1
4m2
6m3
7m3
5m2
3m1
5m1
7m1
5m0
Allelic fraction (germline)
Copy Number log−ratio
0.3
0.4
0.5
0.6
−0.5
0.0
0.5

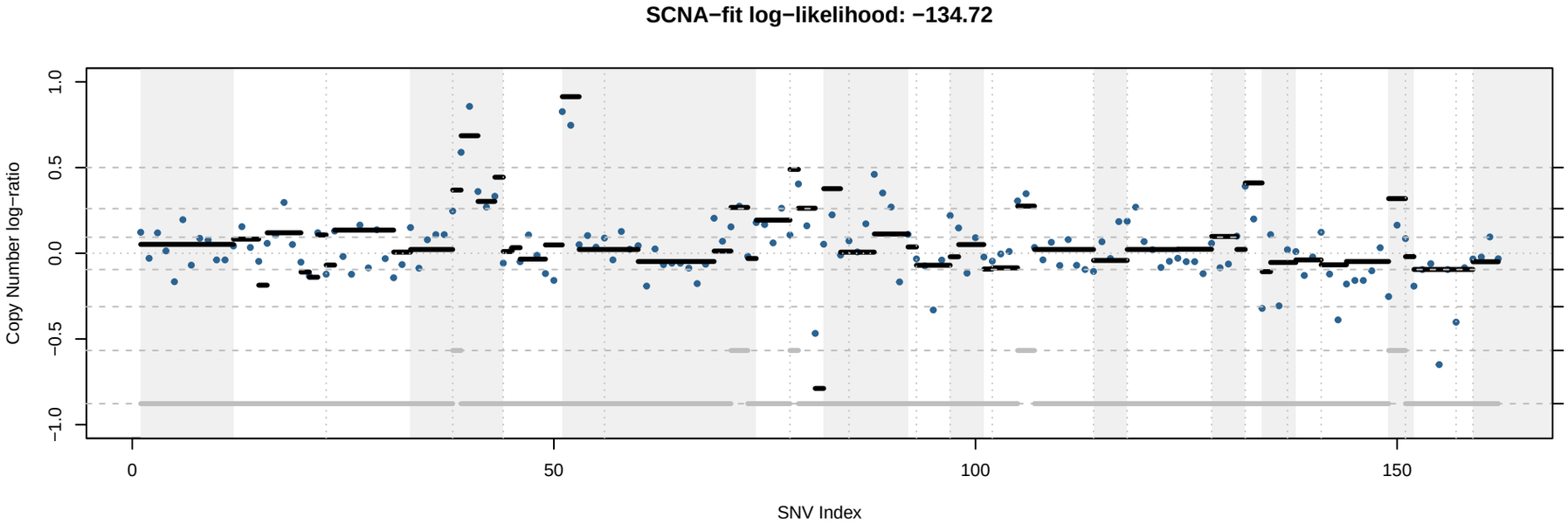

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

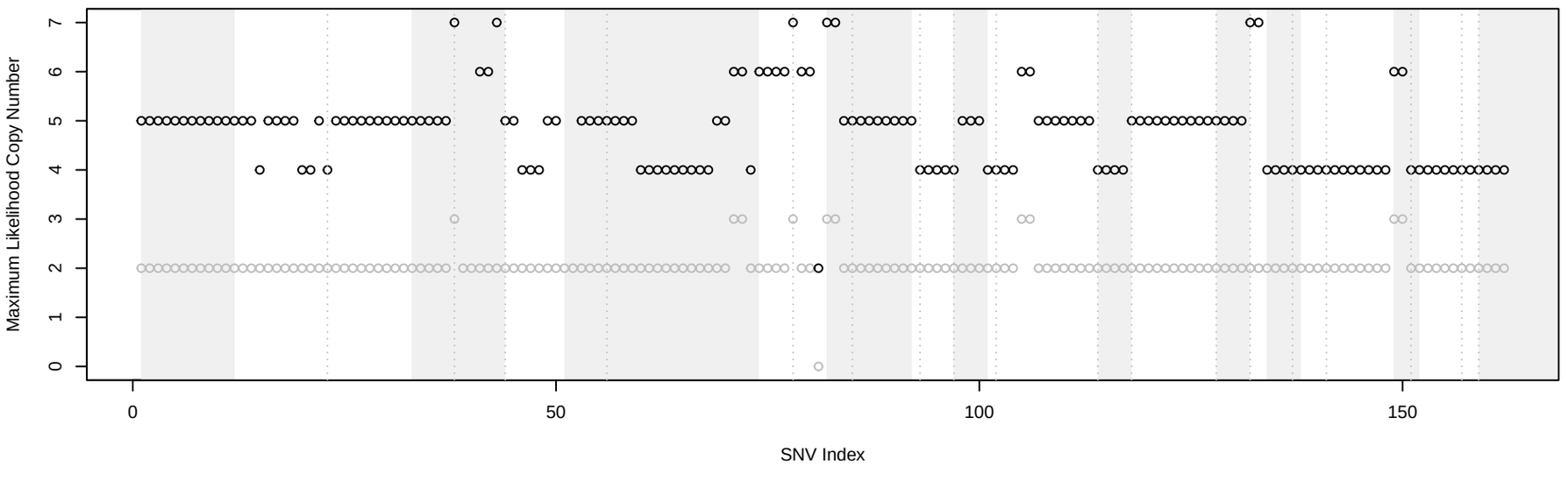

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
3m1
4m1
5m1
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
−0.5
0.0
0.5

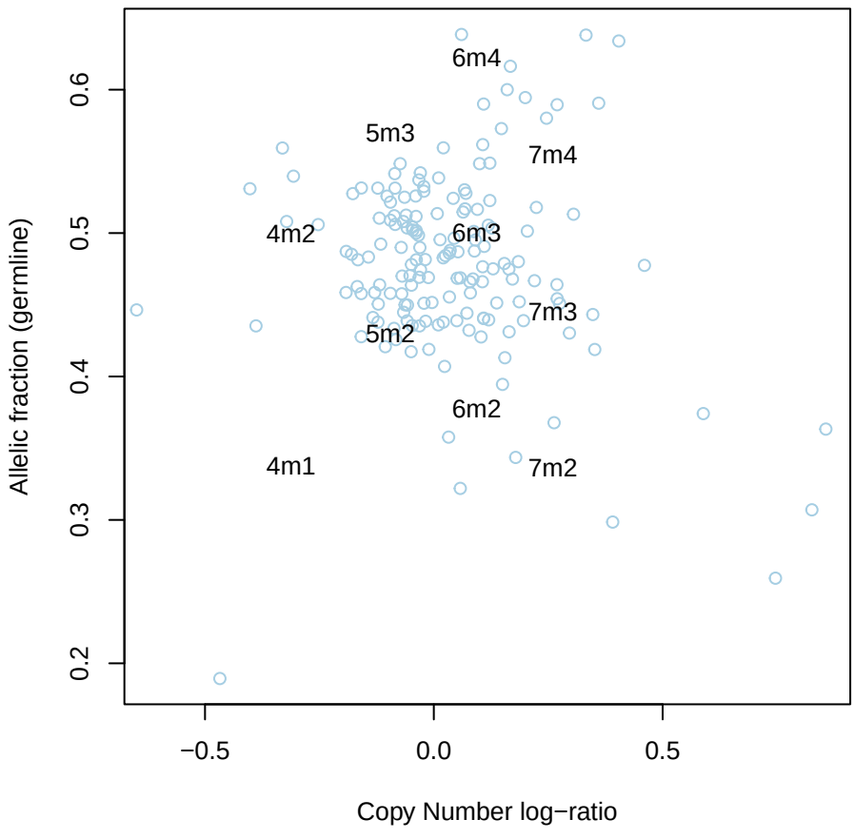

Frequency
Cellular fraction
0
2
4
6
8
0.2
0.4
0.6
0.8
1.0

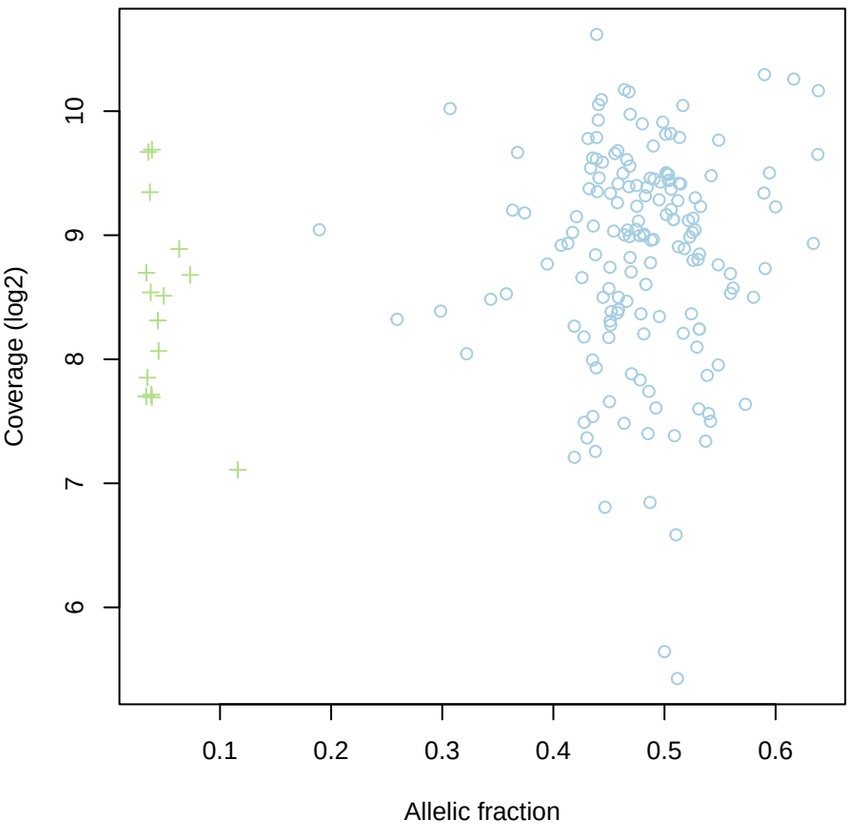

Purity: 0.48 Tumor ploidy: 5.487
3
4
5
6
7
8.7
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

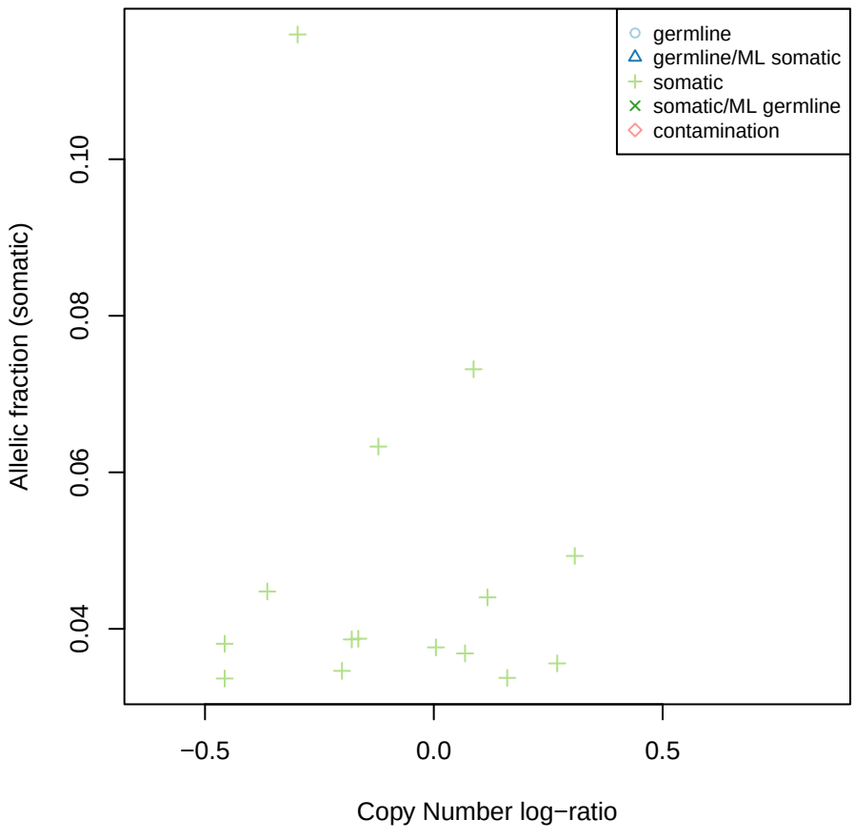

Purity: 0.48 Tumor ploidy: 5.487 SNV log−likelihood: −104.67 GoF: 93.1% Mean coverage: 521;524
1 2 3 4 5 6 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

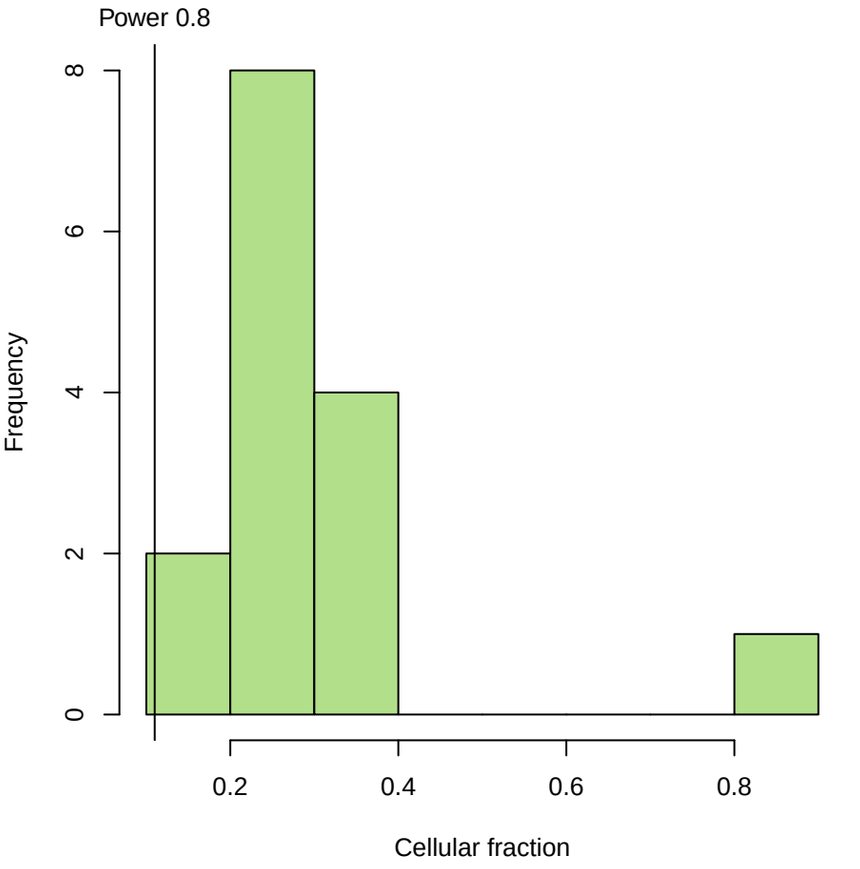

SCNA−fit log−likelihood: −134.72
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7 8.7
0 50 100 150
SNV Index

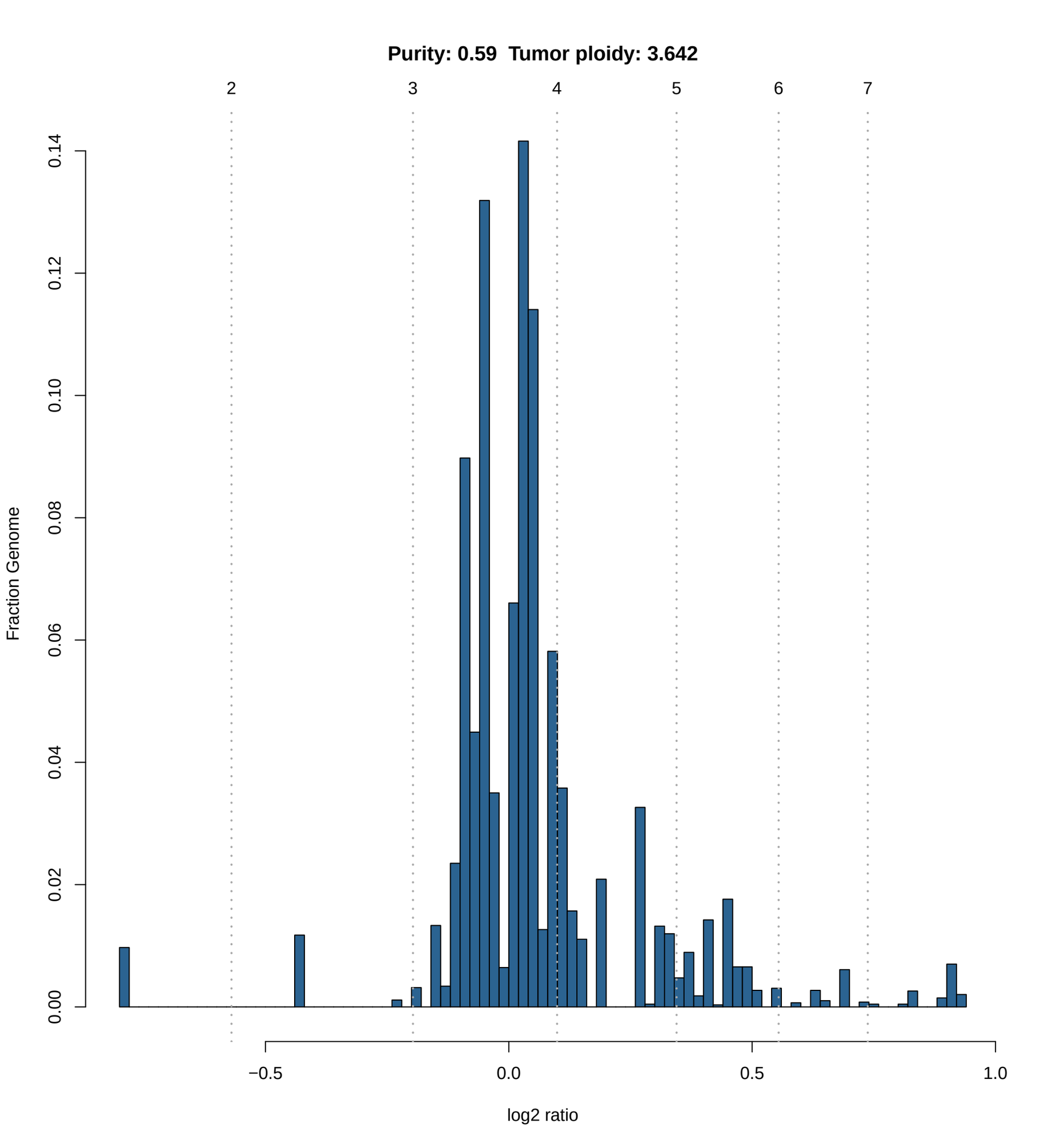

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

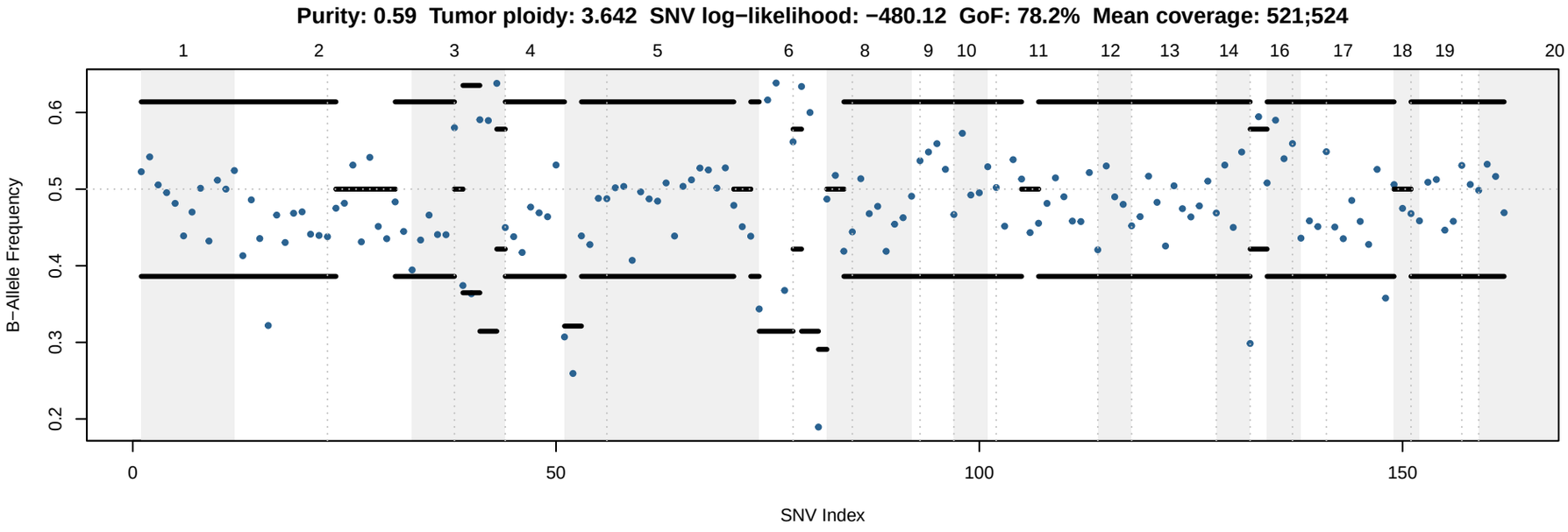

6m4
5m3
7m4
4m2
6m3
7m3
5m2
6m2
4m1
7m2
Allelic fraction (germline)
Copy Number log−ratio
0.2
0.3
0.4
0.5
0.6
−0.5
0.0
0.5

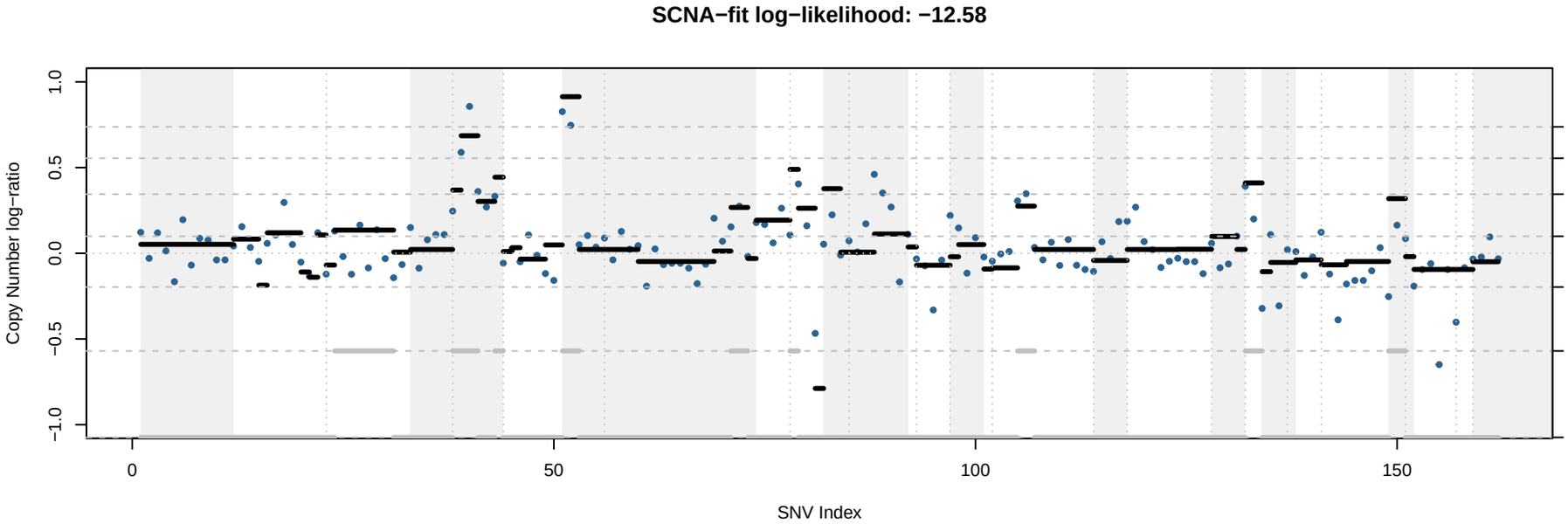

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

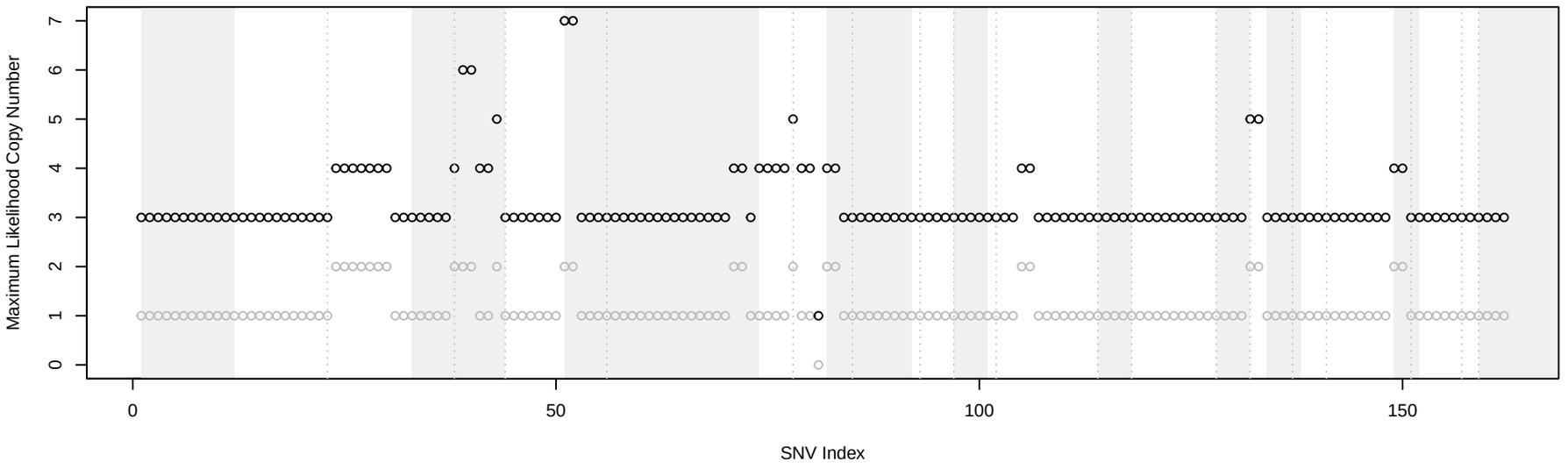

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
−0.5
0.0
0.5

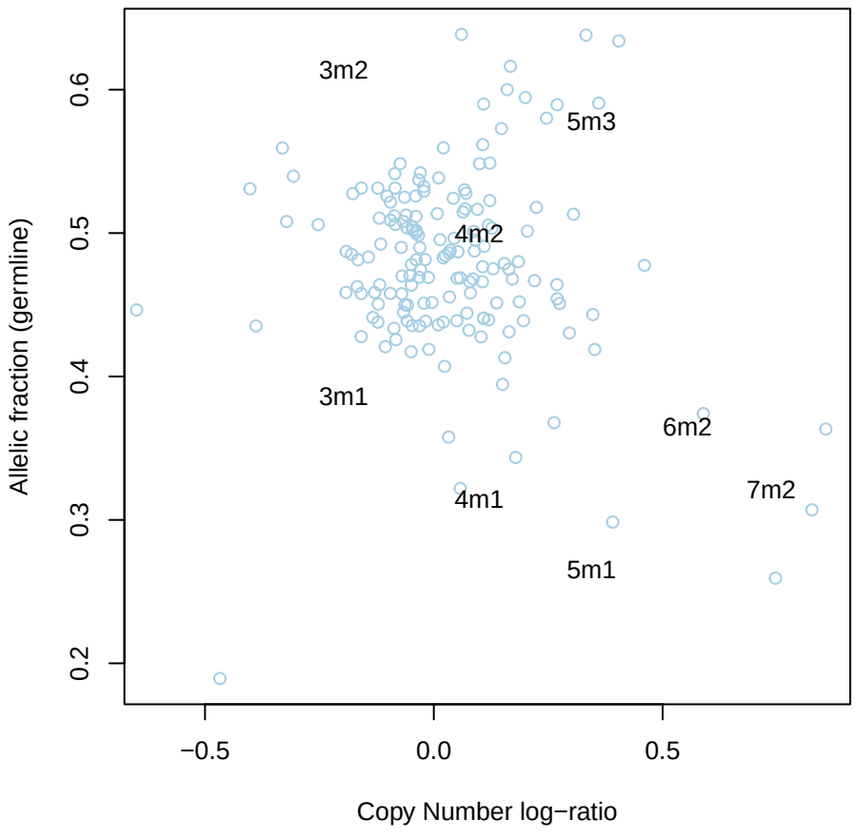

Power 0.8
Frequency
Cellular fraction
0
2
4
6
8
0.2
0.4
0.6
0.8

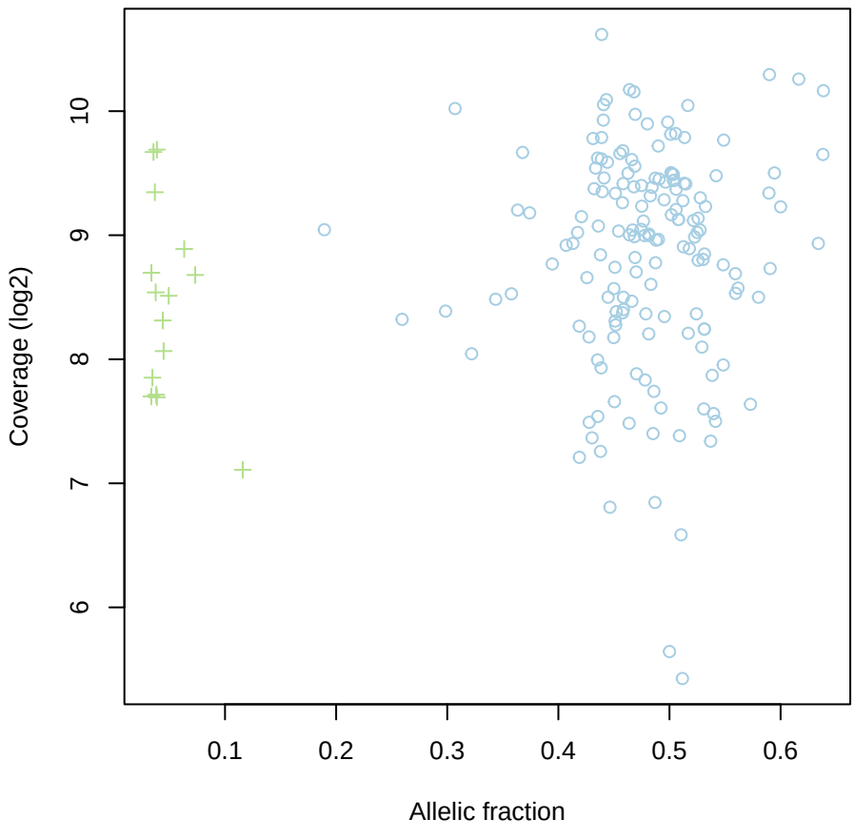

Purity: 0.59 Tumor ploidy: 3.642
2
3
4
5
6
7
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

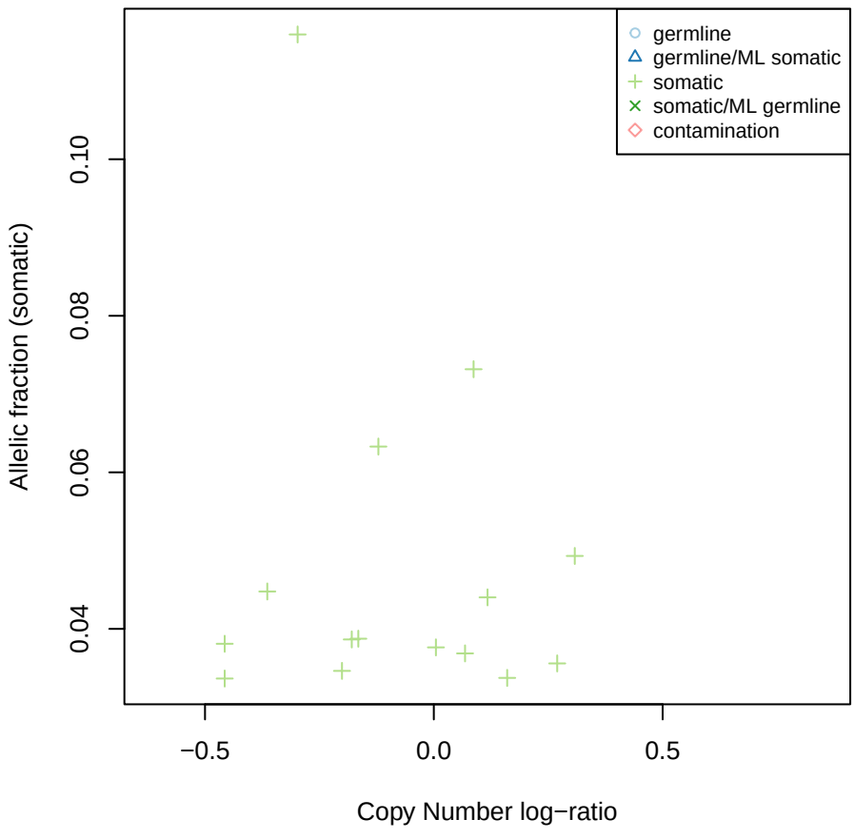

Purity: 0.59 Tumor ploidy: 3.642 SNV log−likelihood: −480.12 GoF: 78.2% Mean coverage: 521;524
1 2 3 4 5 6 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

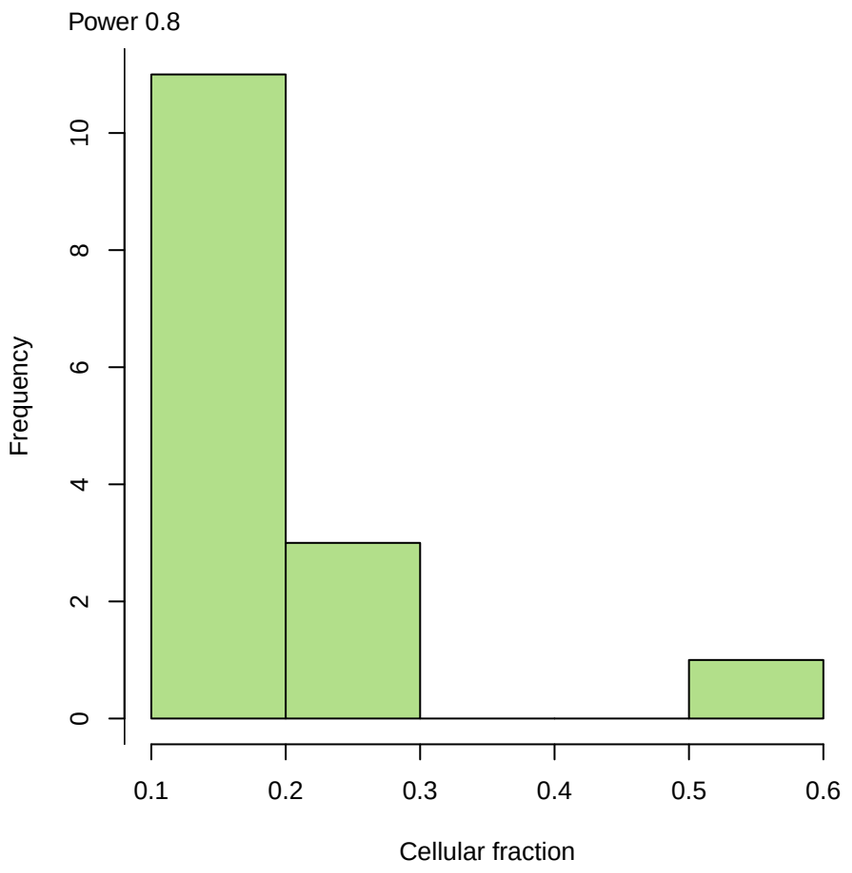

SCNA−fit log−likelihood: −12.58
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6 7
0 50 100 150
SNV Index

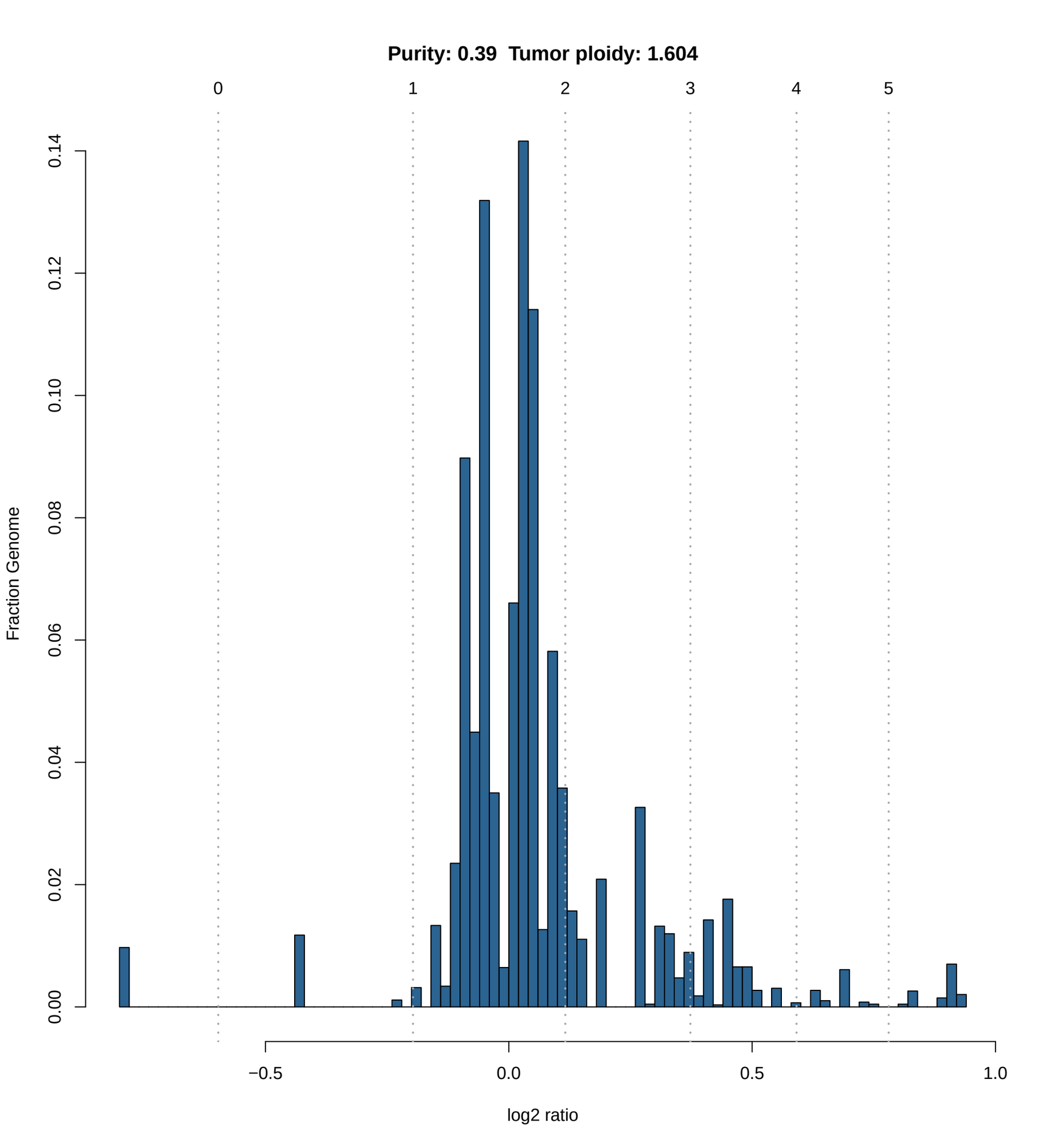

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

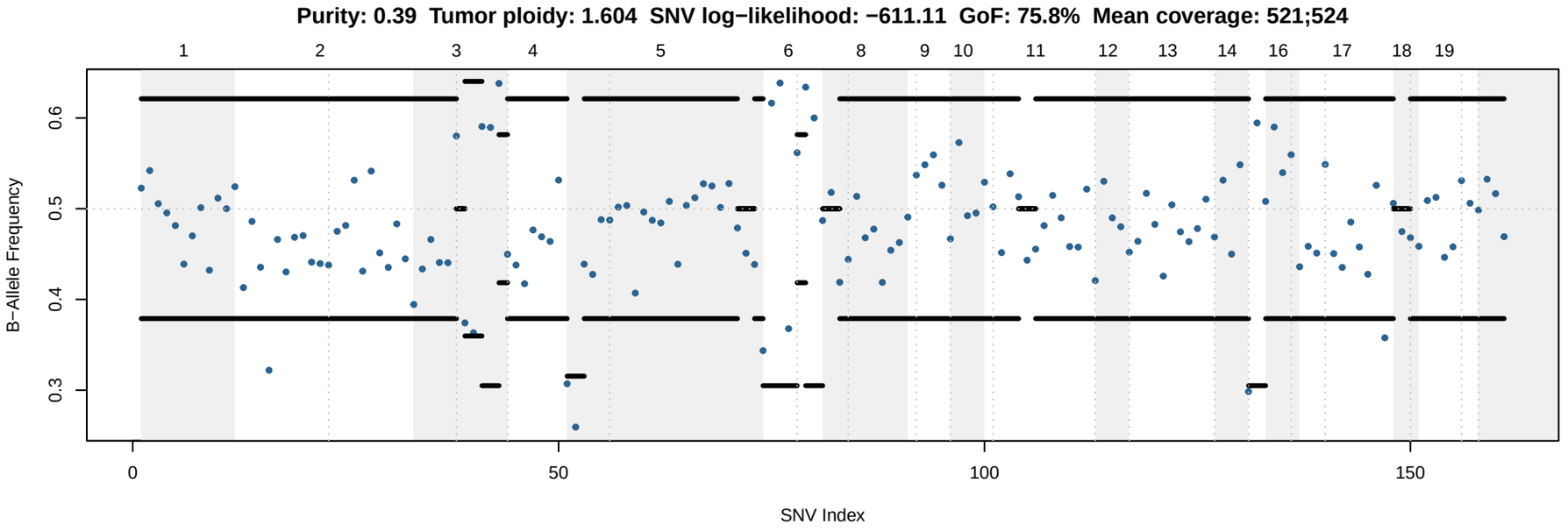

3m2
5m3
4m2
3m1
6m2
4m1
7m2
5m1
Allelic fraction (germline)
Copy Number log−ratio
0.2
0.3
0.4
0.5
0.6
−0.5
0.0
0.5

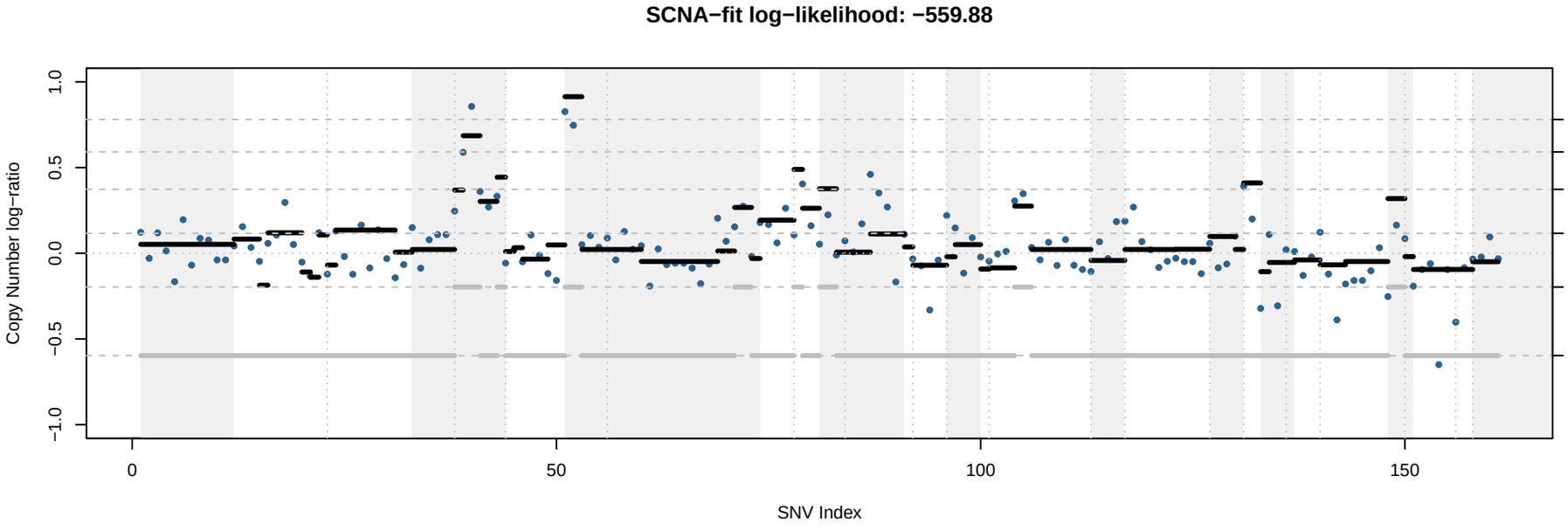

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

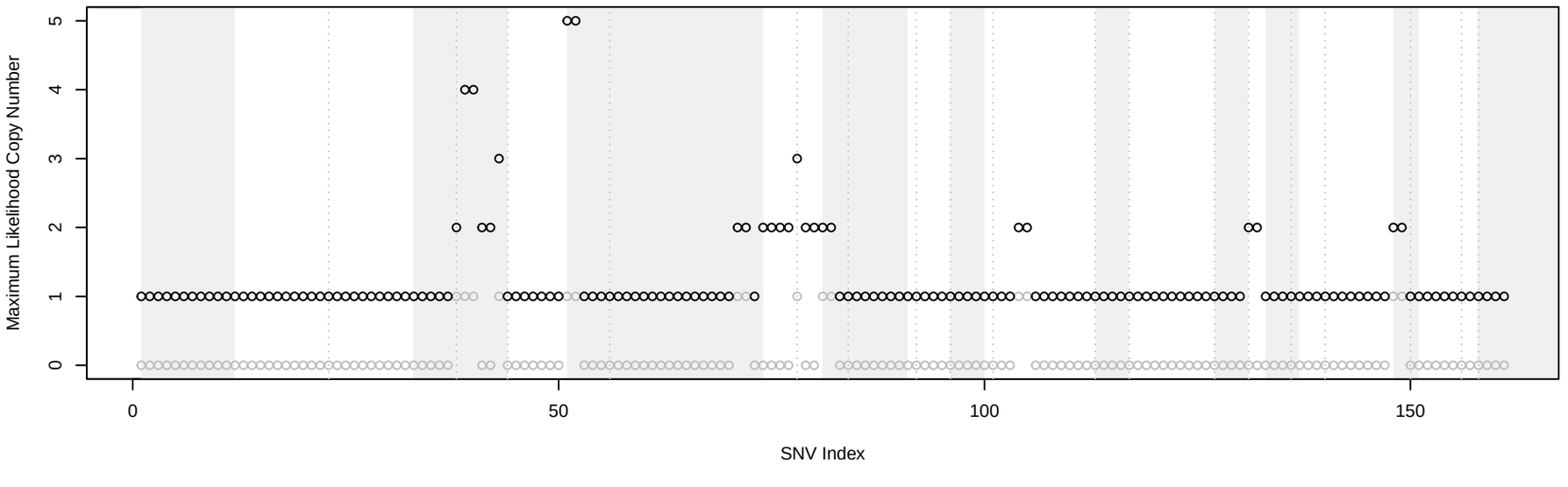

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
−0.5
0.0
0.5

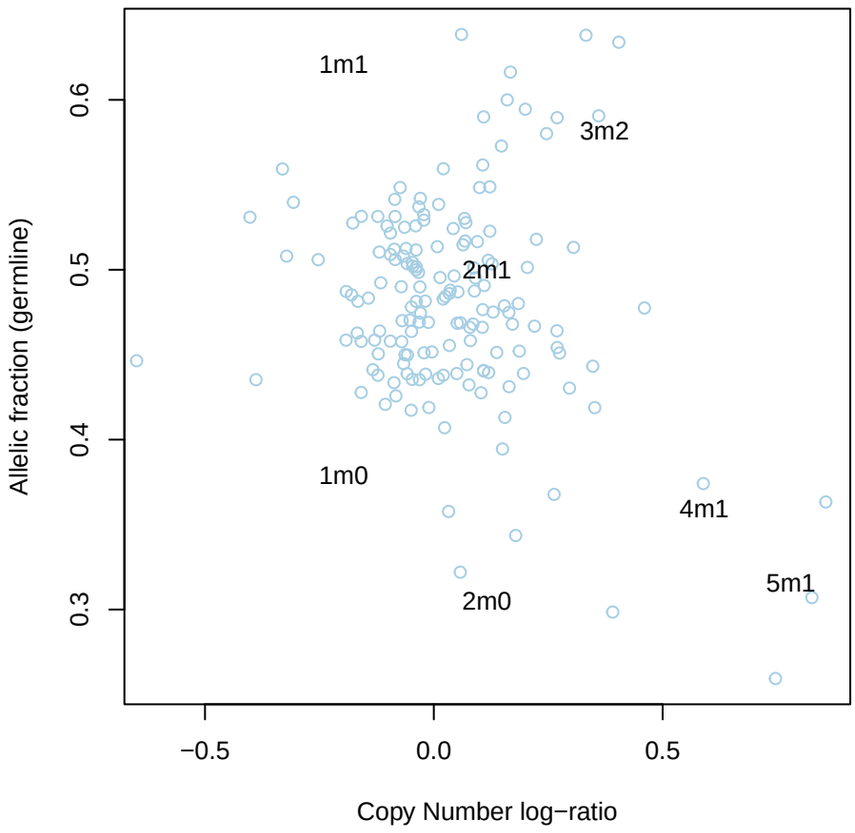

Power 0.8
Frequency
Cellular fraction
0
2
4
6
8
10
0.1
0.2
0.3
0.4
0.5
0.6

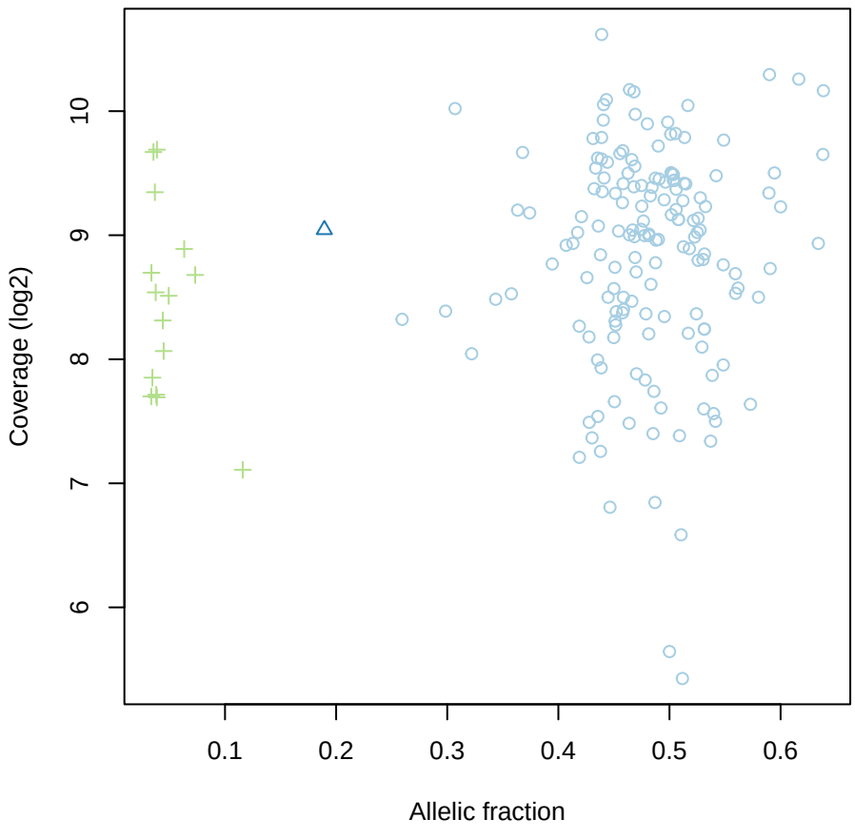

Purity: 0.39 Tumor ploidy: 1.604
0
1
2
3
4
5
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

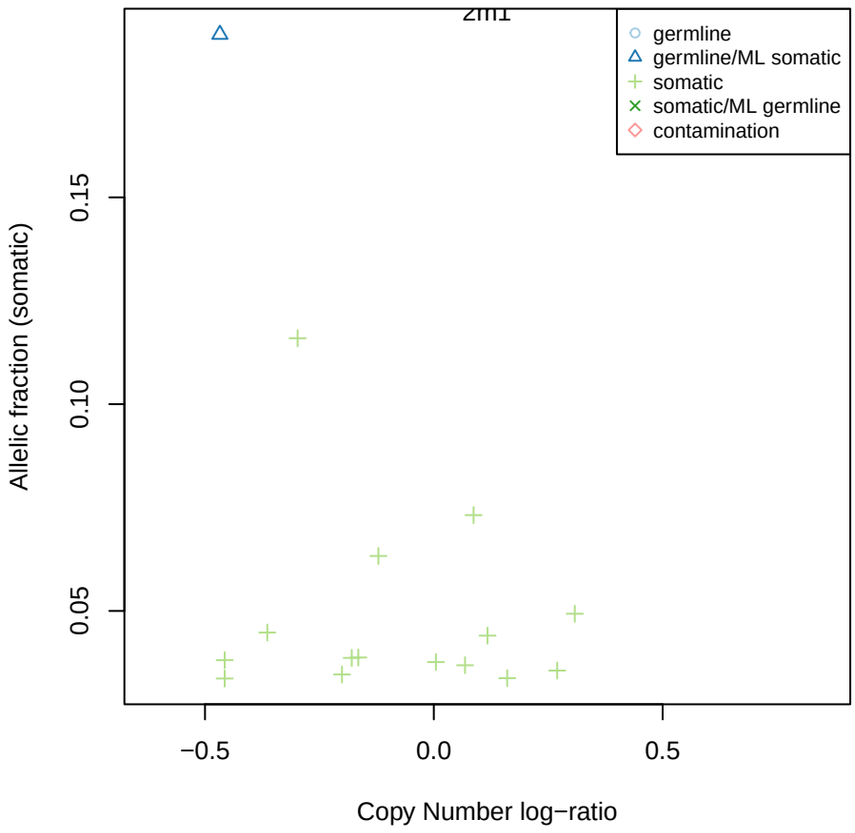

Purity: 0.39 Tumor ploidy: 1.604 SNV log−likelihood: −611.11 GoF: 75.8% Mean coverage: 521;524
1 2 3 4 5 6 8 9 10 11 12 13 14 16 17 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

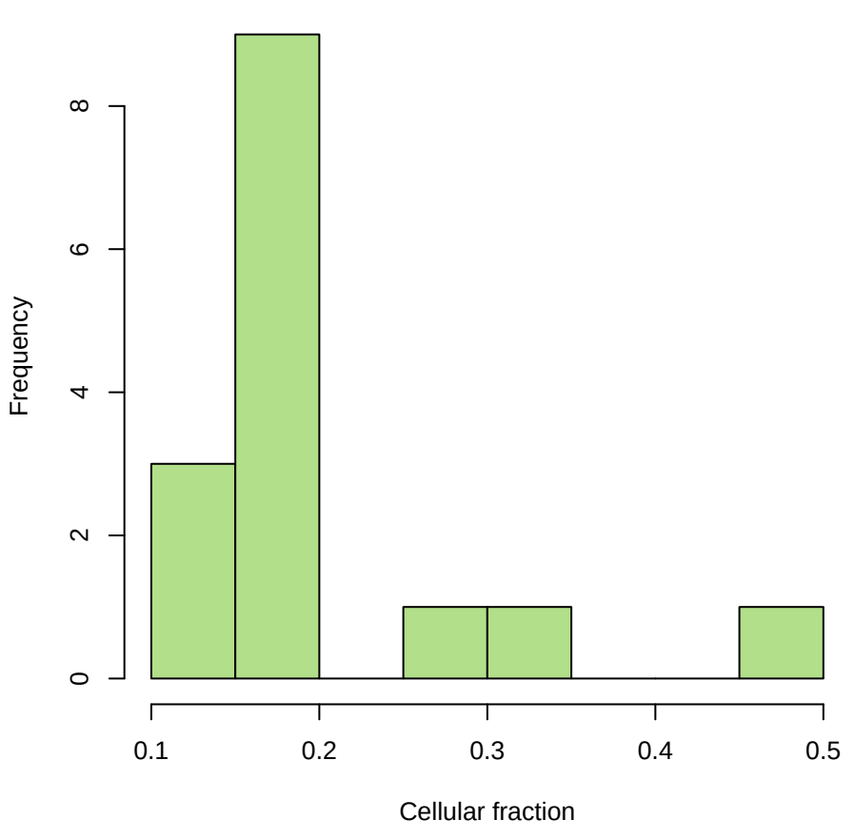

SCNA−fit log−likelihood: −559.88
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5
0 50 100 150
SNV Index

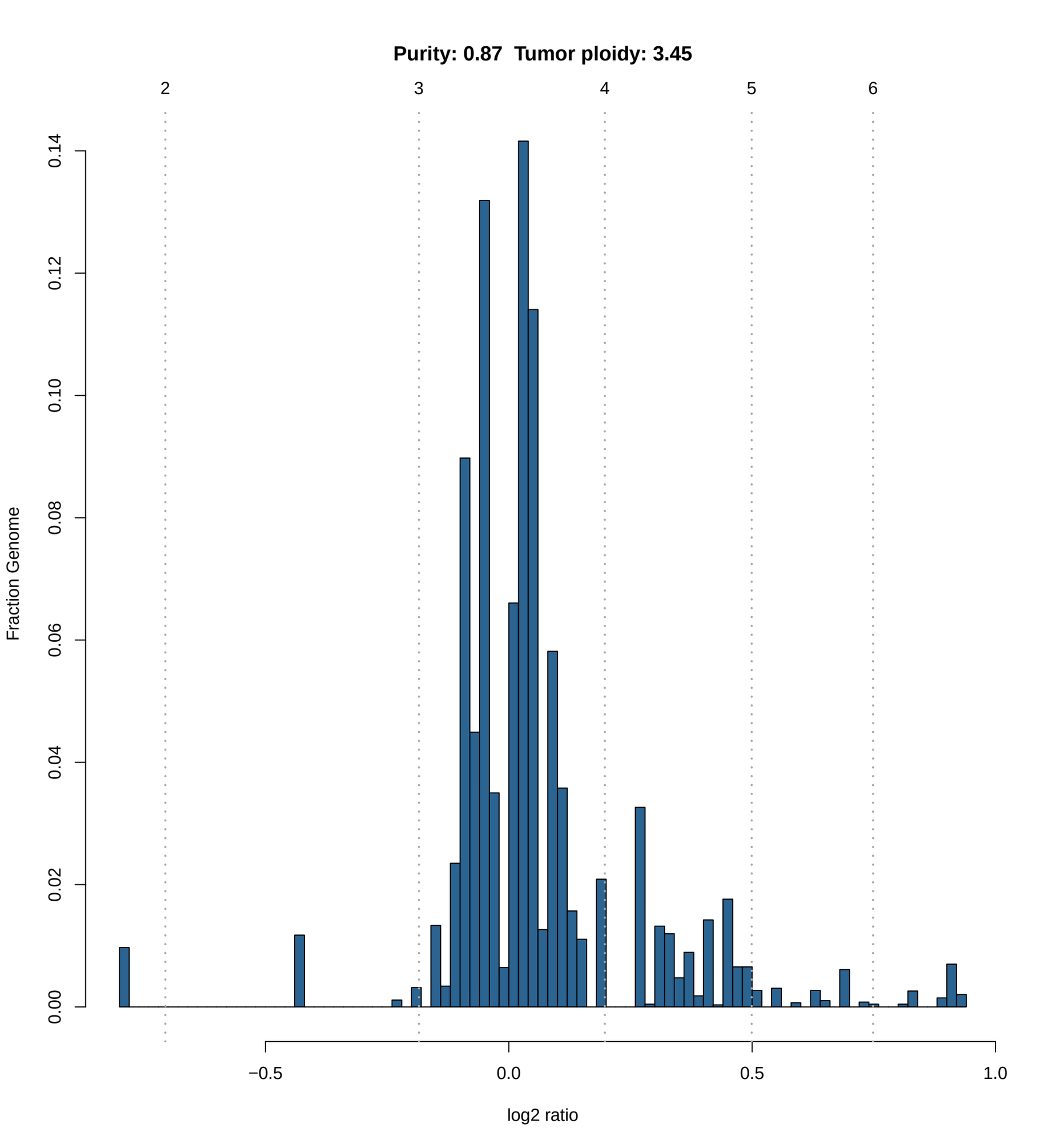

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

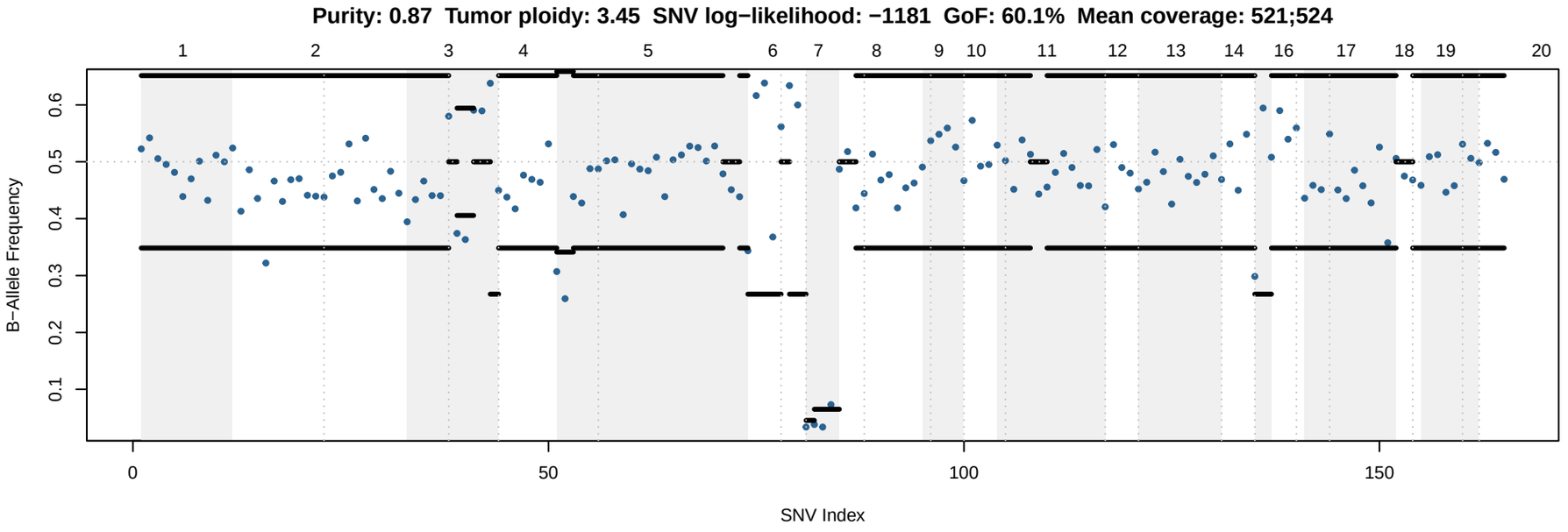

1m1
3m2
2m1
1m0
4m1
5m1
2m0
Allelic fraction (germline)
Copy Number log−ratio

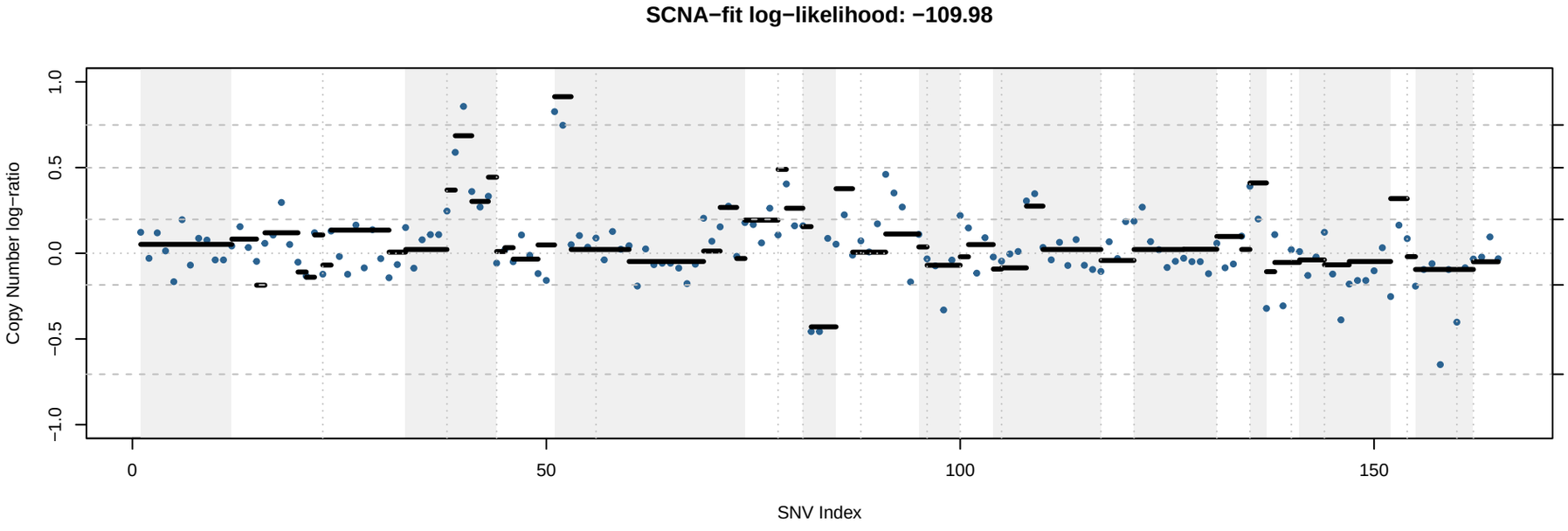

Coverage (log2)
Allelic fraction

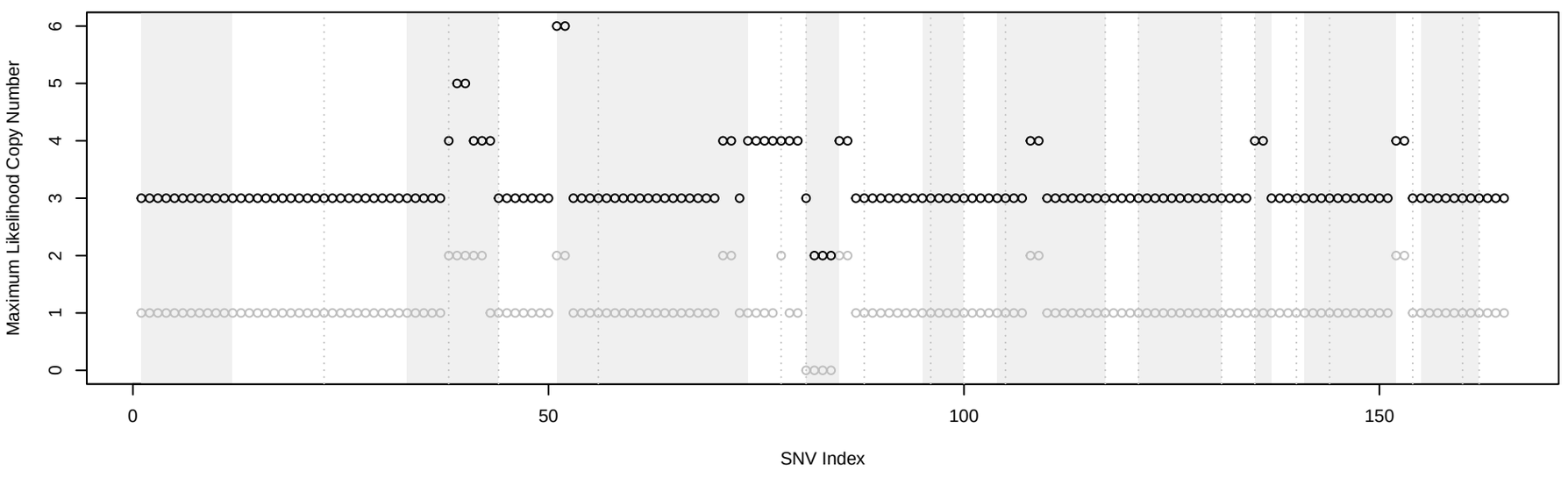

2m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

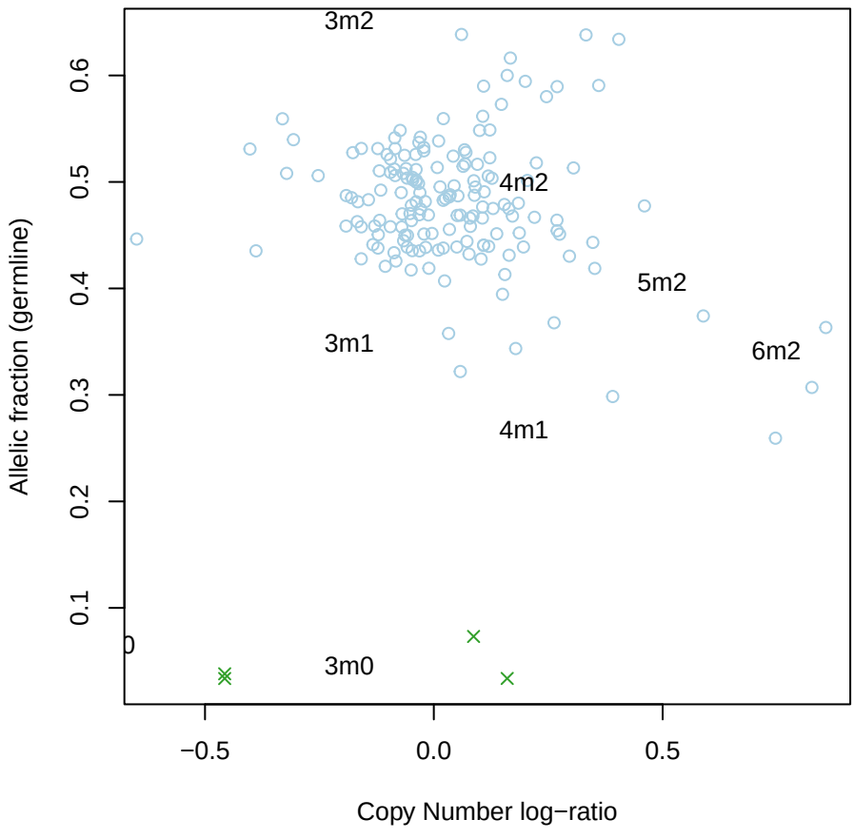

Frequency
Cellular fraction

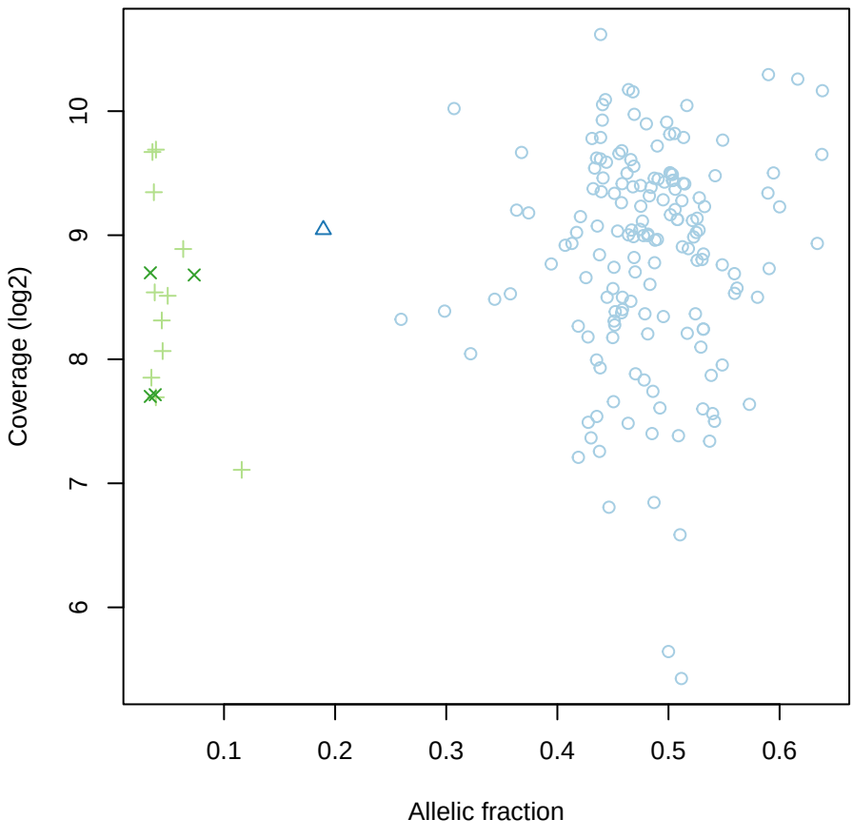

Purity: 0.87 Tumor ploidy: 3.45
2
3
4
5
6
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

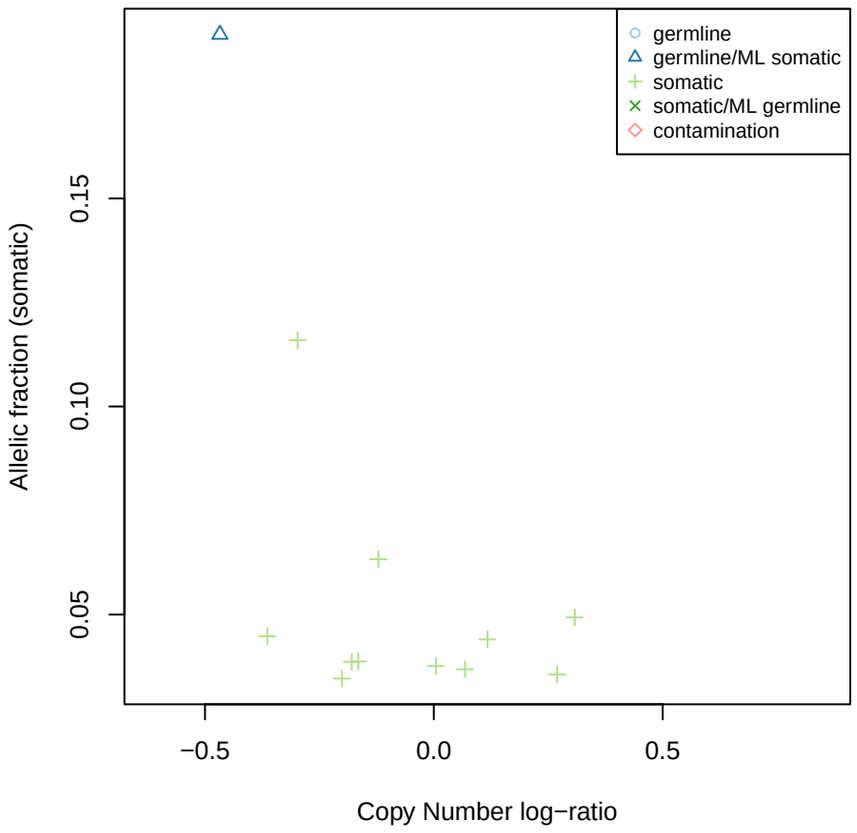

Purity: 0.87 Tumor ploidy: 3.45 SNV log−likelihood: −1181 GoF: 60.1% Mean coverage: 521;524
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

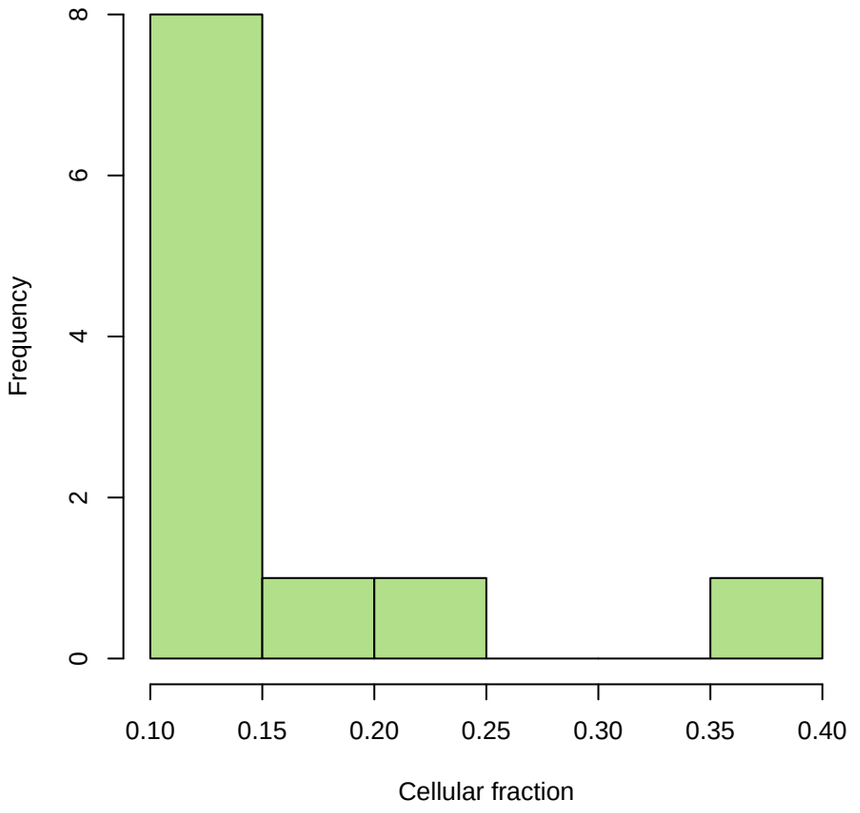

SCNA−fit log−likelihood: −109.98
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6
0 50 100 150
SNV Index


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


3m2
4m2
5m2
3m1
6m2
4m1
3m0
Allelic fraction (germline)
Copy Number log−ratio


Coverage (log2)
Allelic fraction


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


Frequency
Cellular fraction