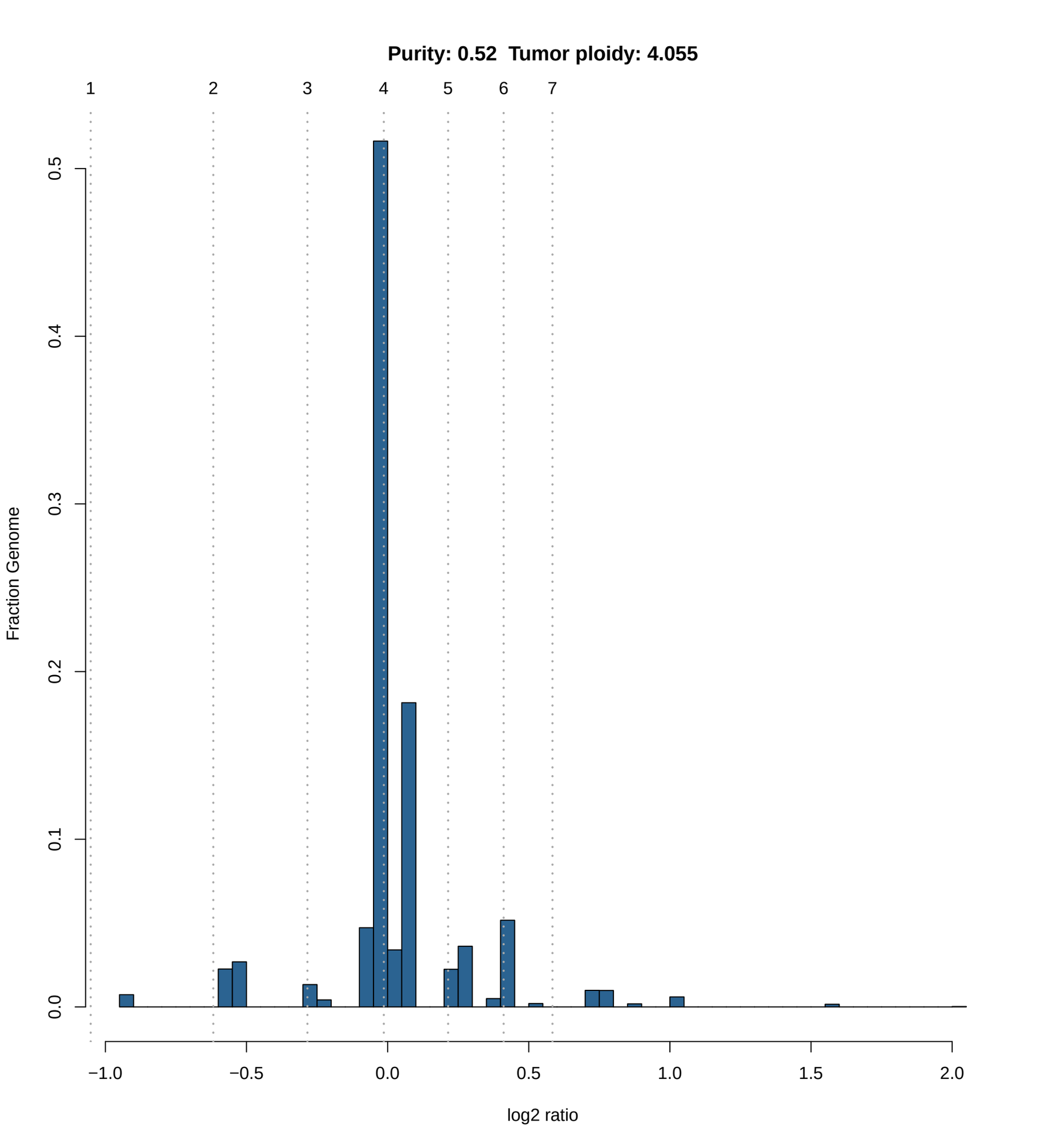
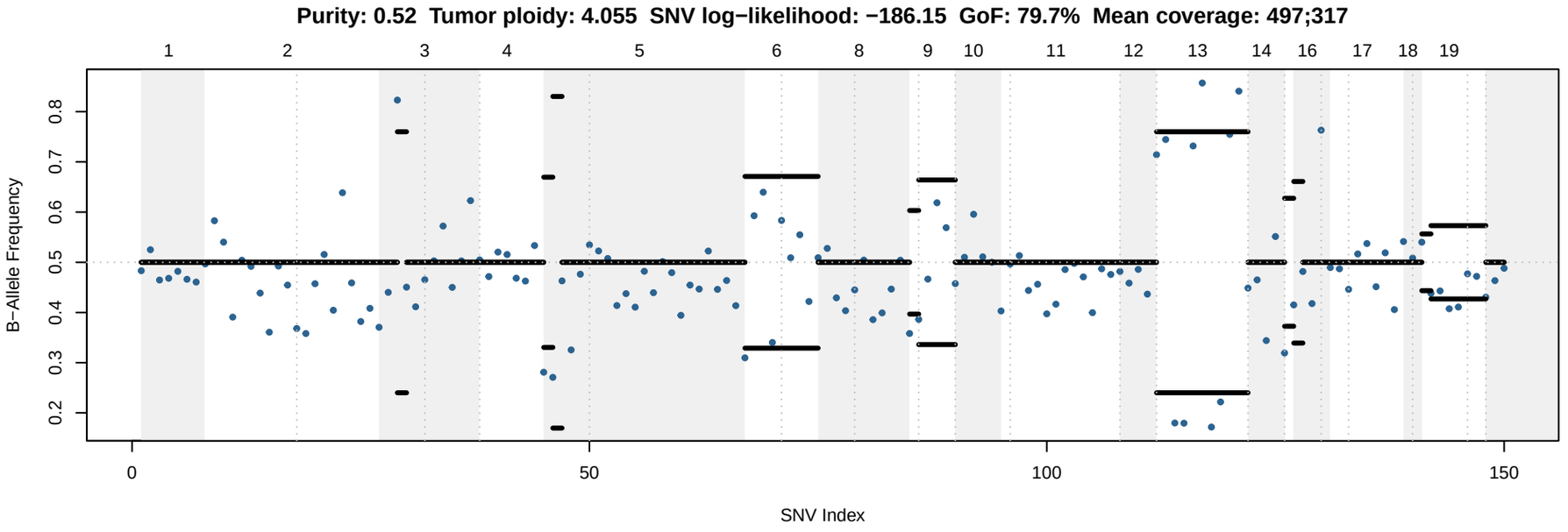
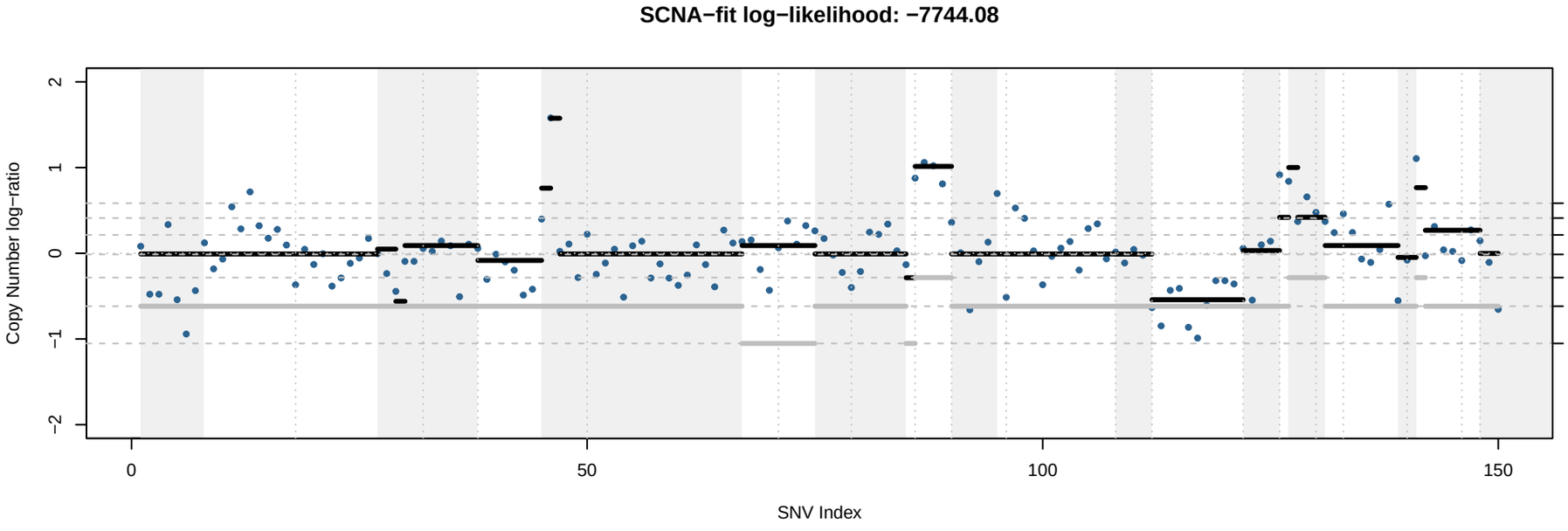
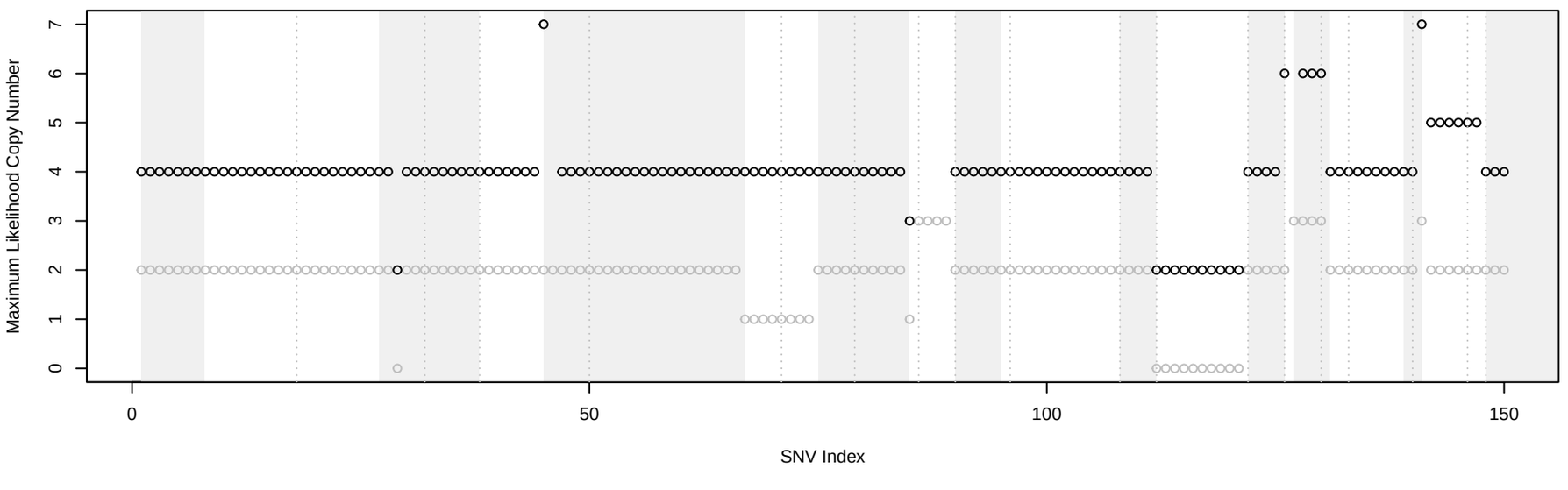
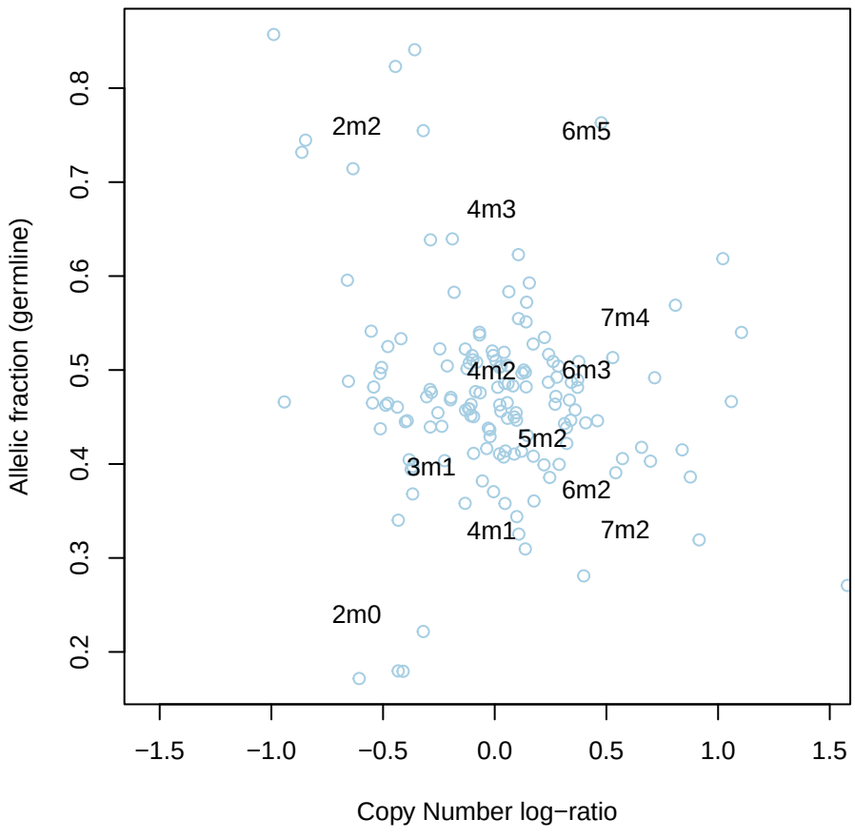
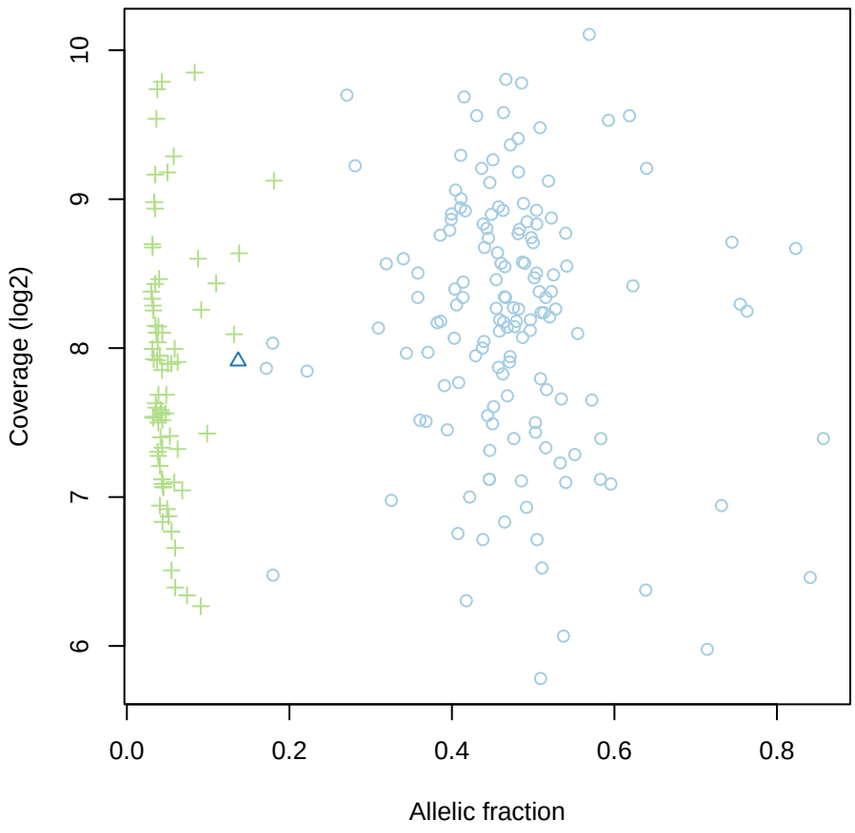

Purity: 0.52 Tumor ploidy: 4.055
1
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

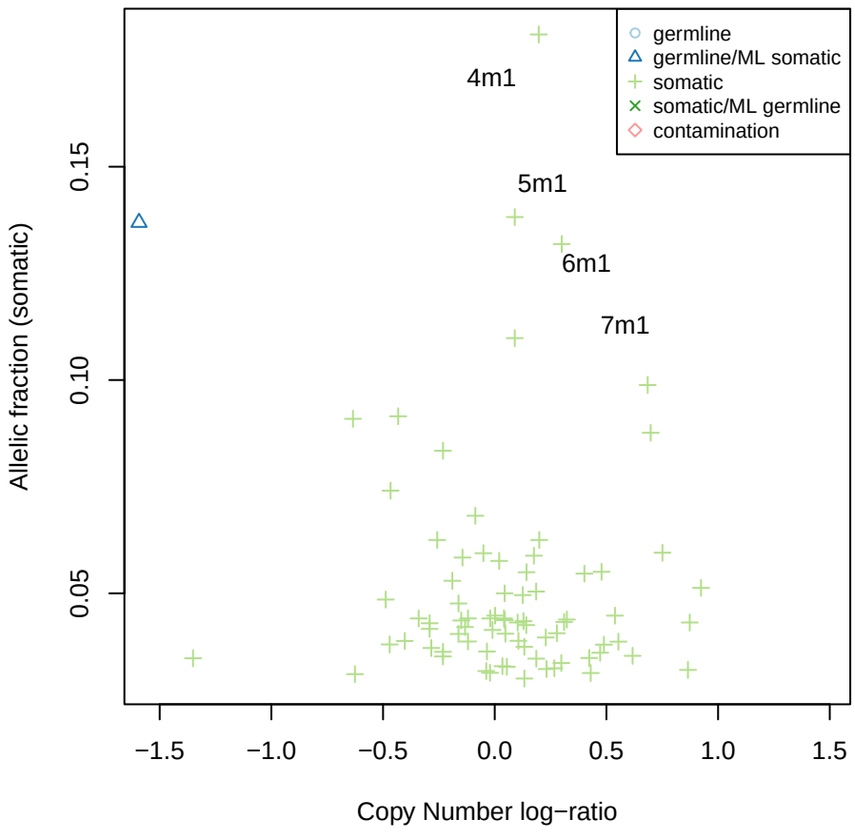

Purity: 0.52 Tumor ploidy: 4.055 SNV log−likelihood: −186.15 GoF: 79.7% Mean coverage: 497;317
1 2 3 4 5 6 8 9 10 11 12 13 14 16 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

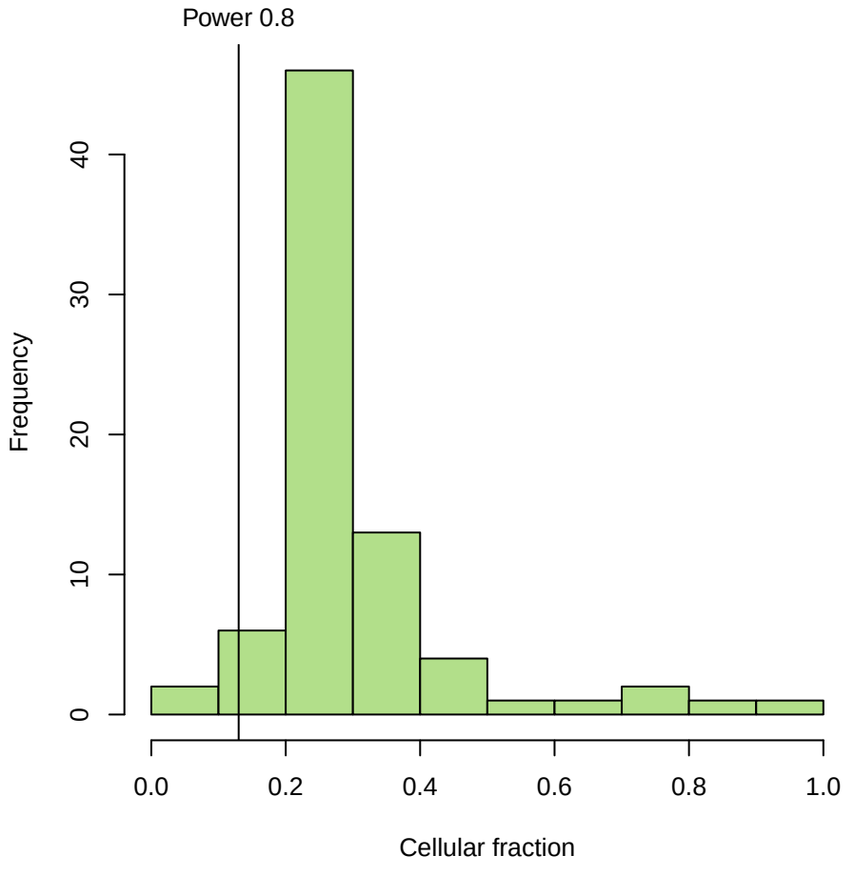

SCNA−fit log−likelihood: −7744.08
Copy Number log−ratio
−2 −1 0 1 2
1 2 3 5 7
0 50 100 150
SNV Index

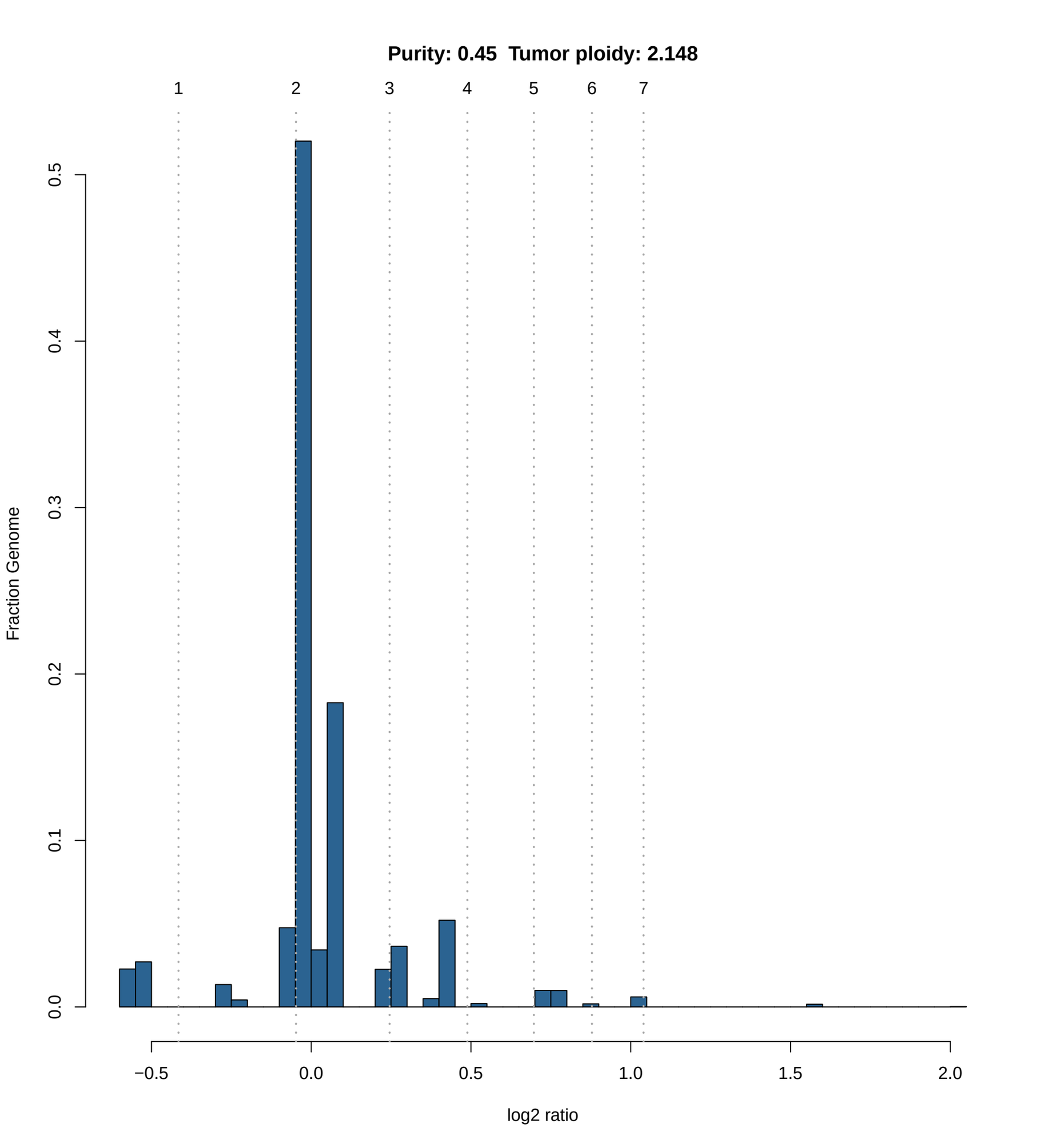

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

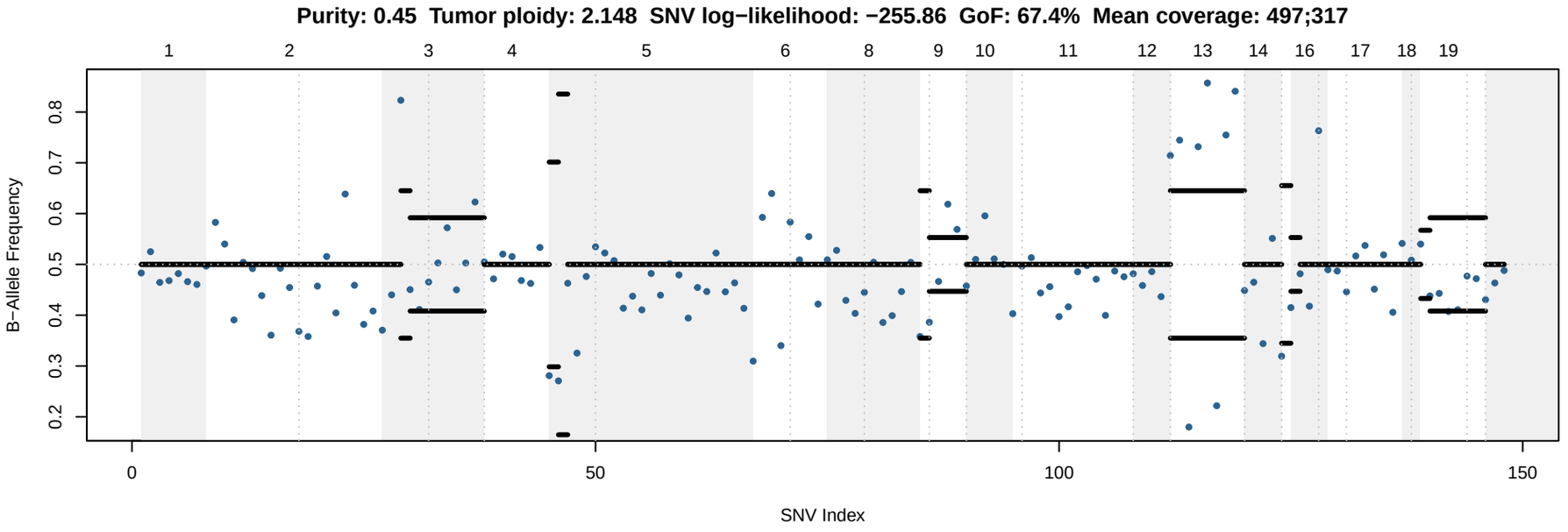

Allelic fraction (germline)
Copy Number log−ratio
2m2
6m5
4m3
7m4
4m2
6m3
5m2
3m1
6m2
4m1
7m2
2m0

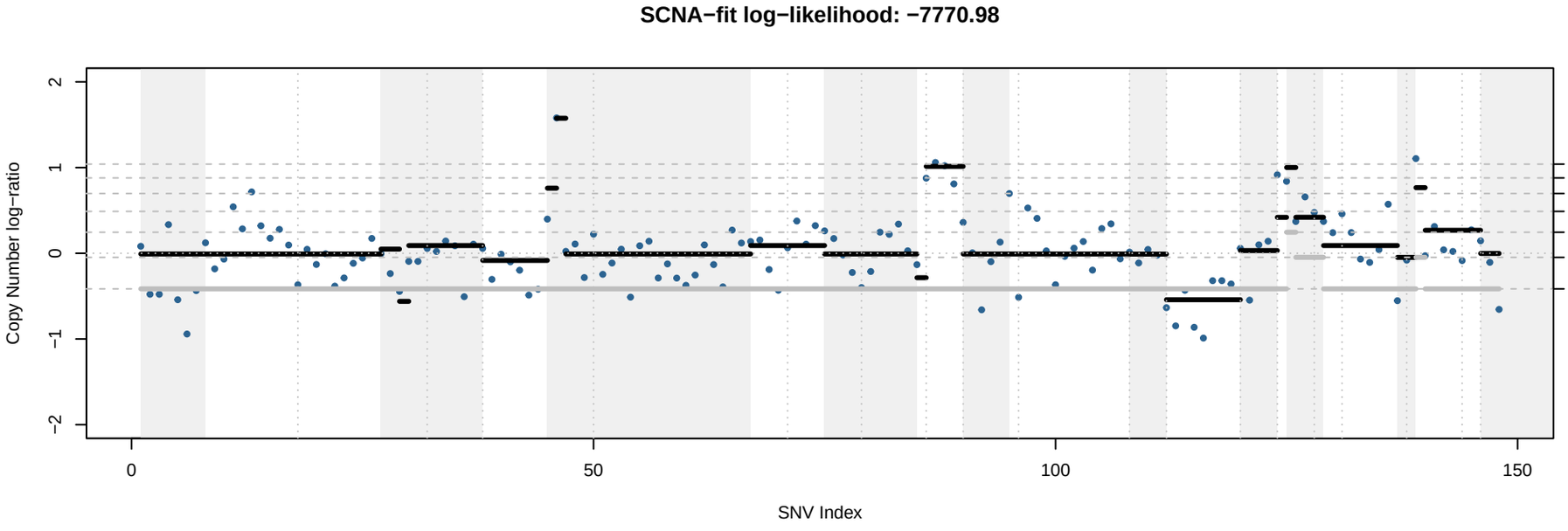

Coverage (log2)
Allelic fraction

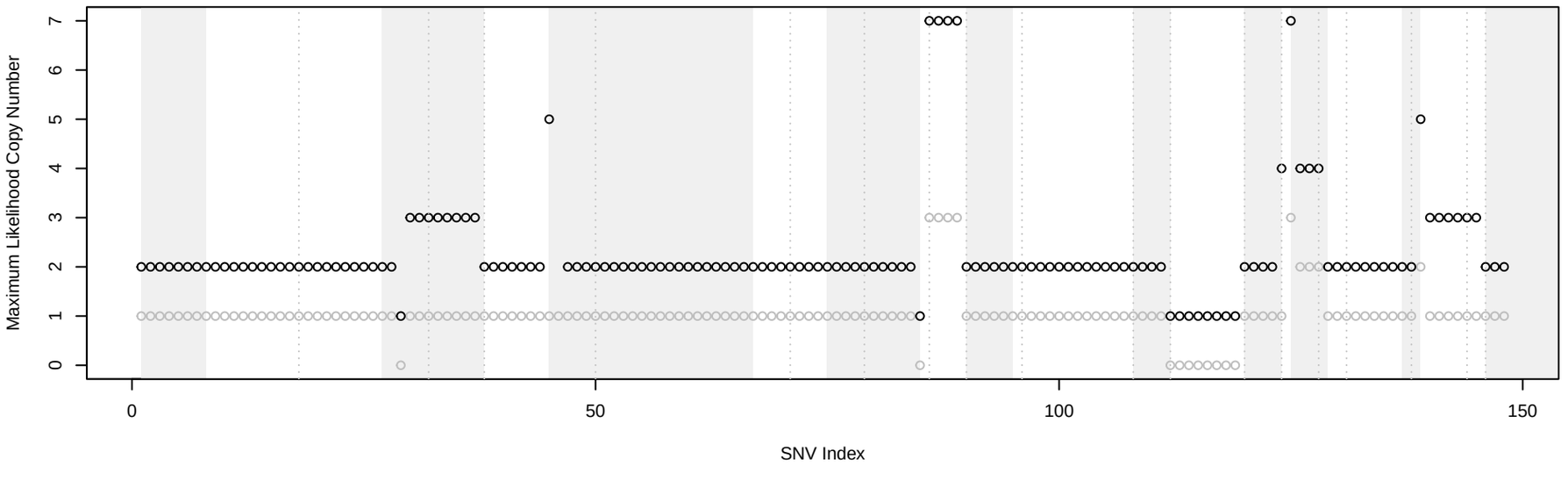

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
4m1
5m1
6m1
7m1

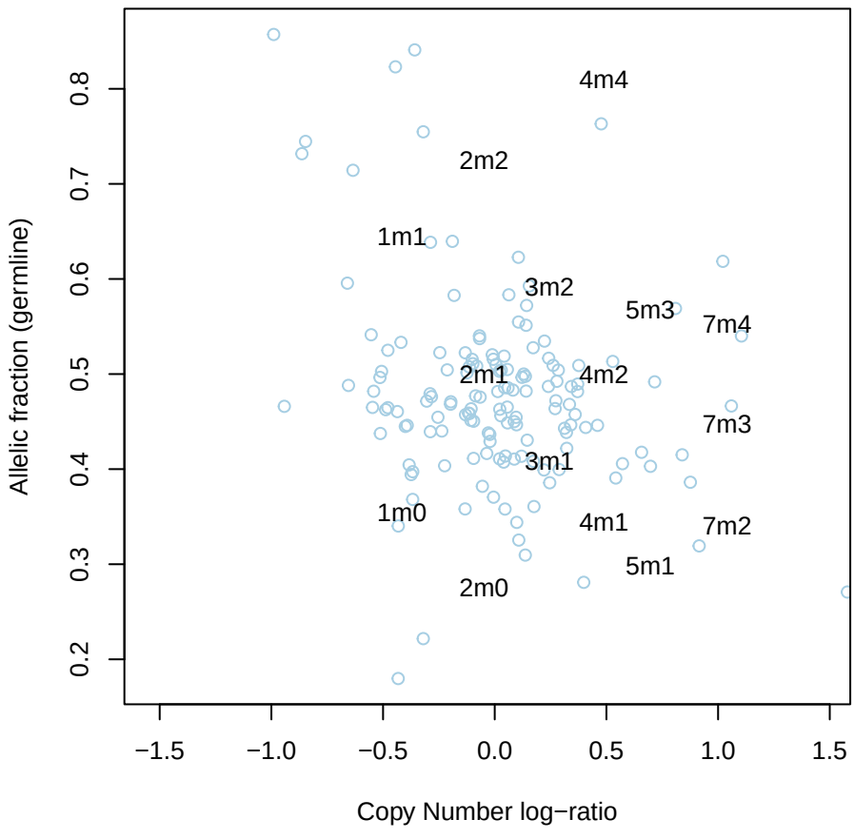

Power 0.8
Frequency
Cellular fraction

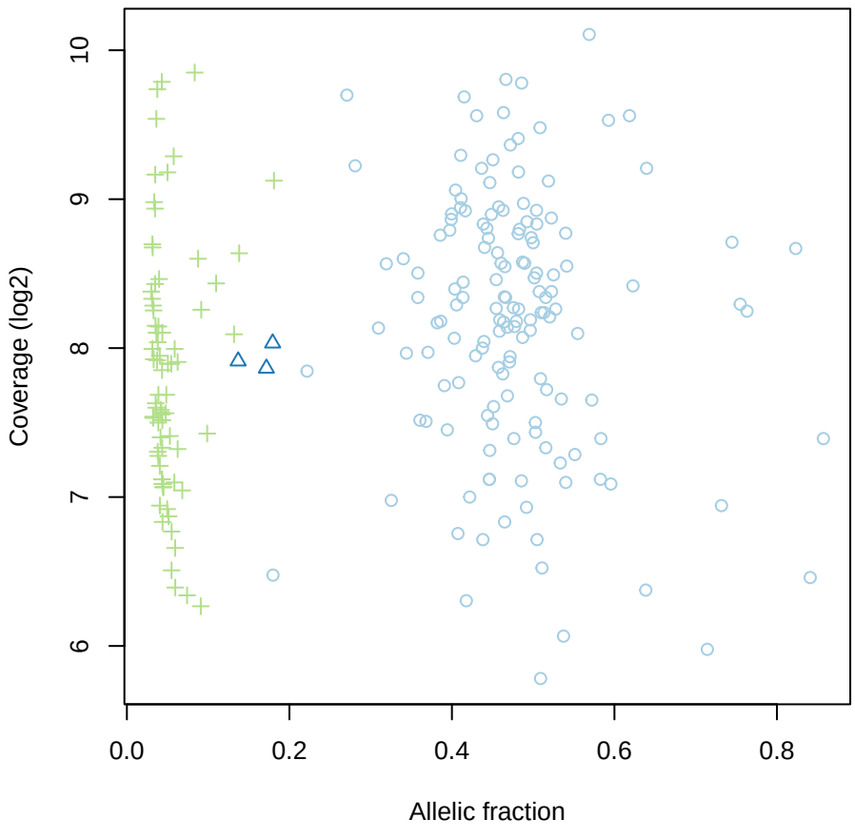

Purity: 0.45 Tumor ploidy: 2.148
1
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

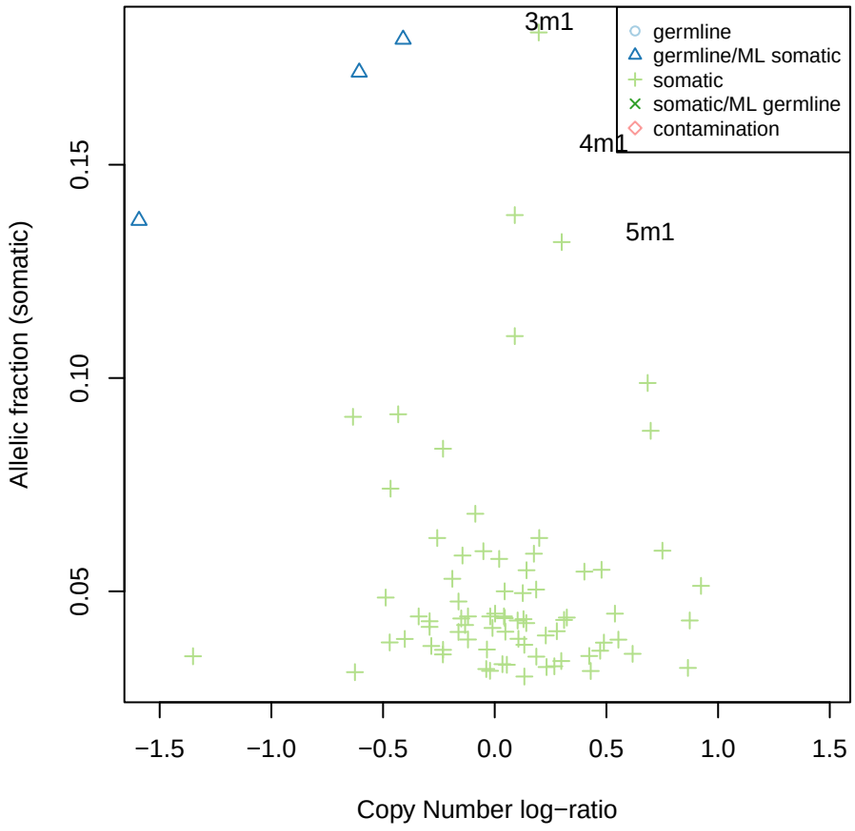

Purity: 0.45 Tumor ploidy: 2.148 SNV log−likelihood: −255.86 GoF: 67.4% Mean coverage: 497;317
1 2 3 4 5 6 8 9 10 11 12 13 14 16 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

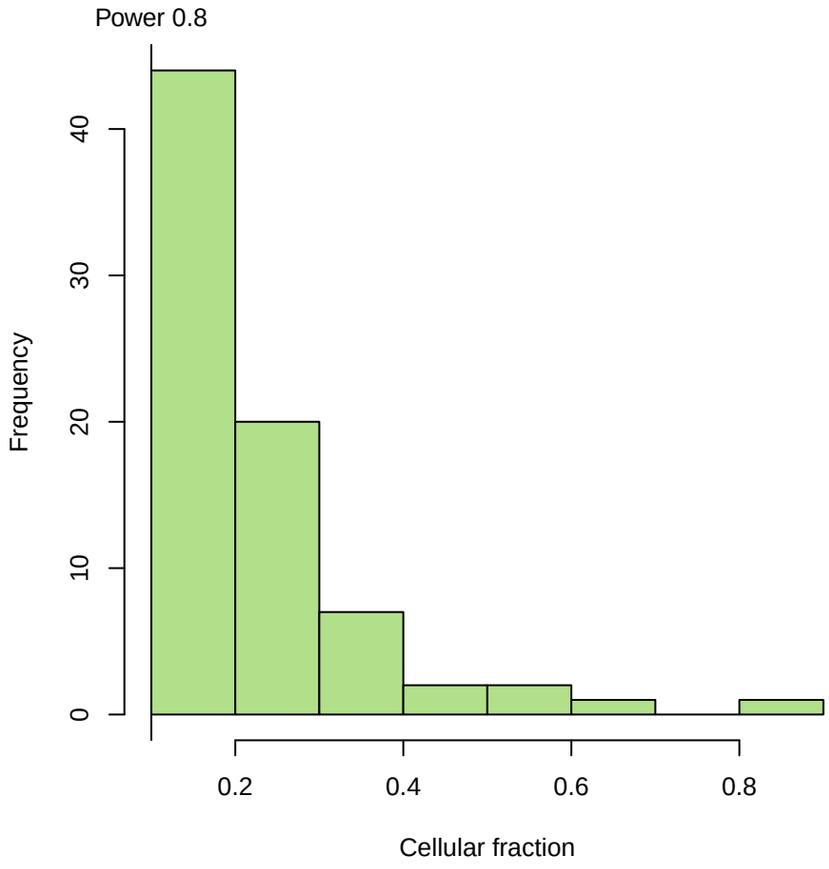

SCNA−fit log−likelihood: −7770.98
Copy Number log−ratio
−2 −1 0 1 2
1 2 3 5 7
0 50 100 150
SNV Index

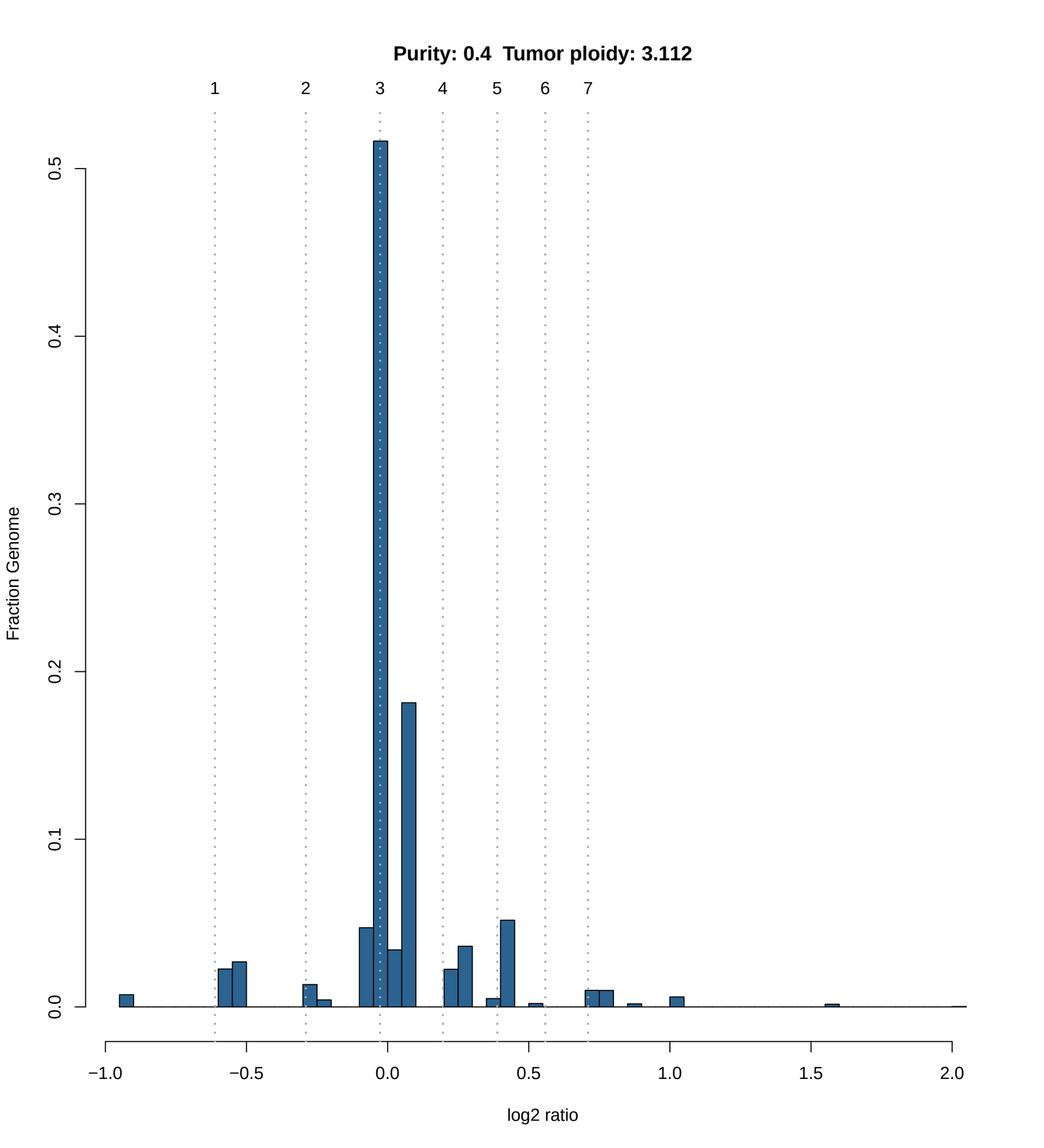

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

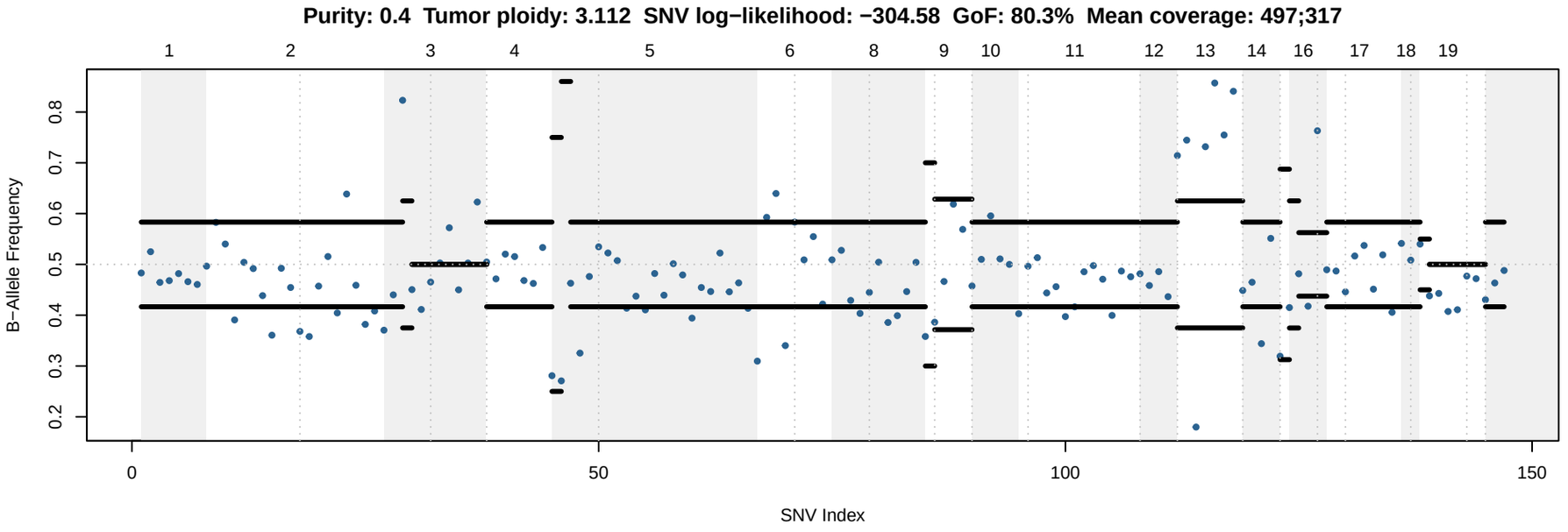

Allelic fraction (germline)
Copy Number log−ratio
4m4
2m2
1m1
3m2
5m3
7m4
2m1
4m2
7m3
3m1
1m0
4m1
7m2
5m1
2m0

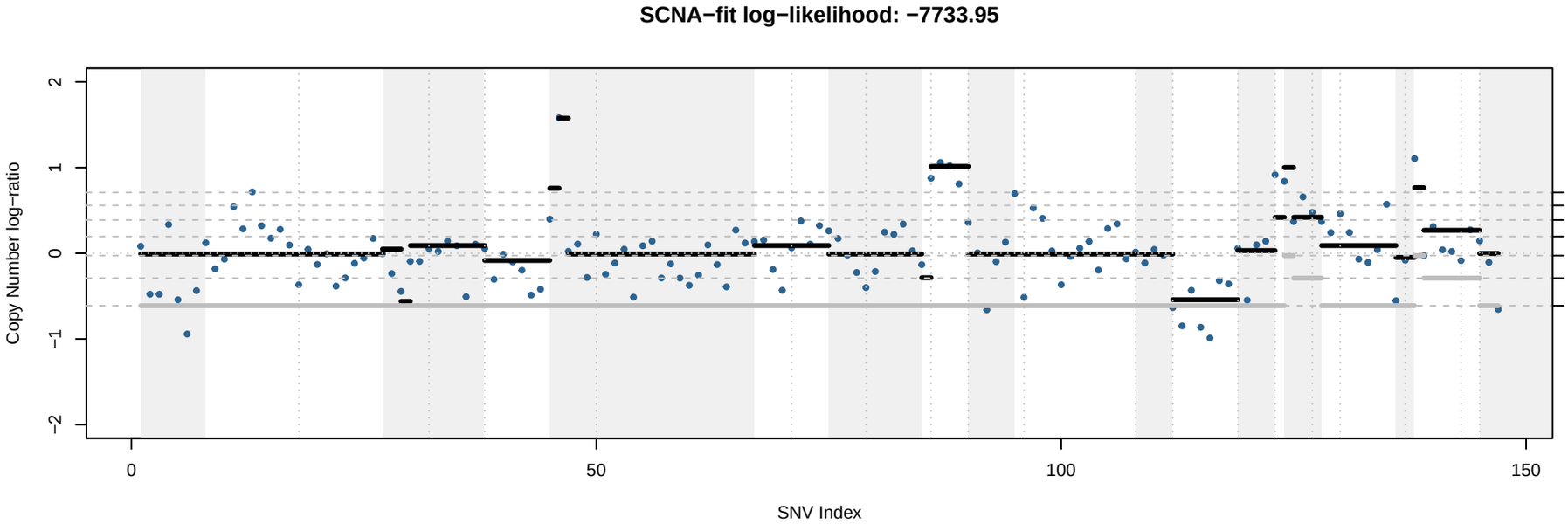

Coverage (log2)
Allelic fraction

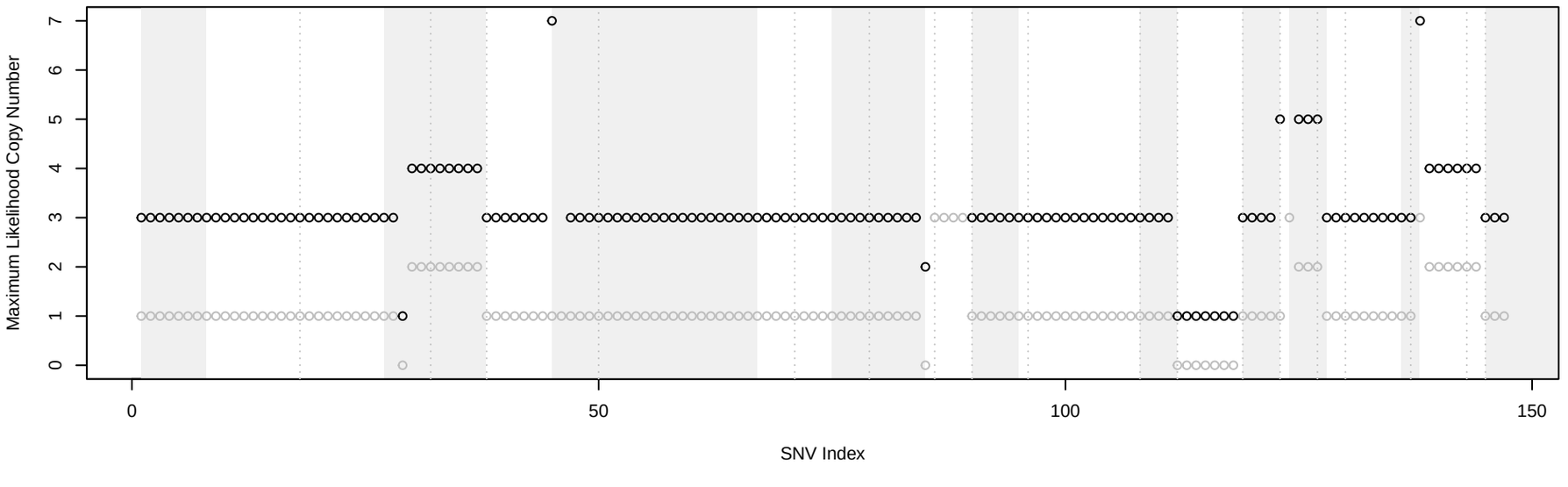

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1


Power 0.8
Frequency
Cellular fraction

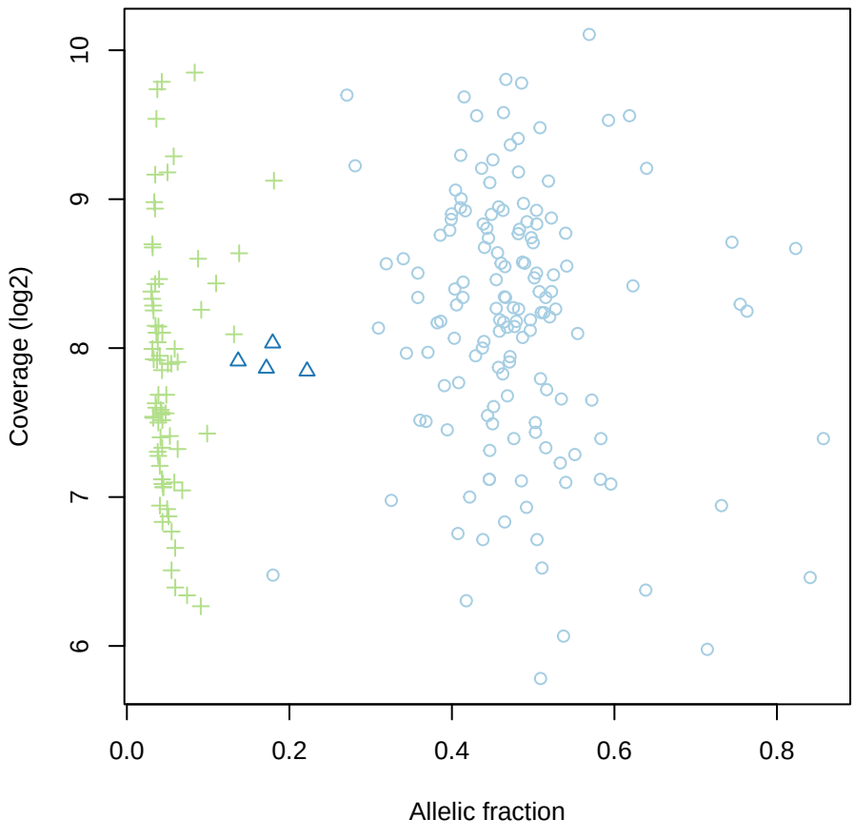

Purity: 0.4 Tumor ploidy: 3.112
1
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

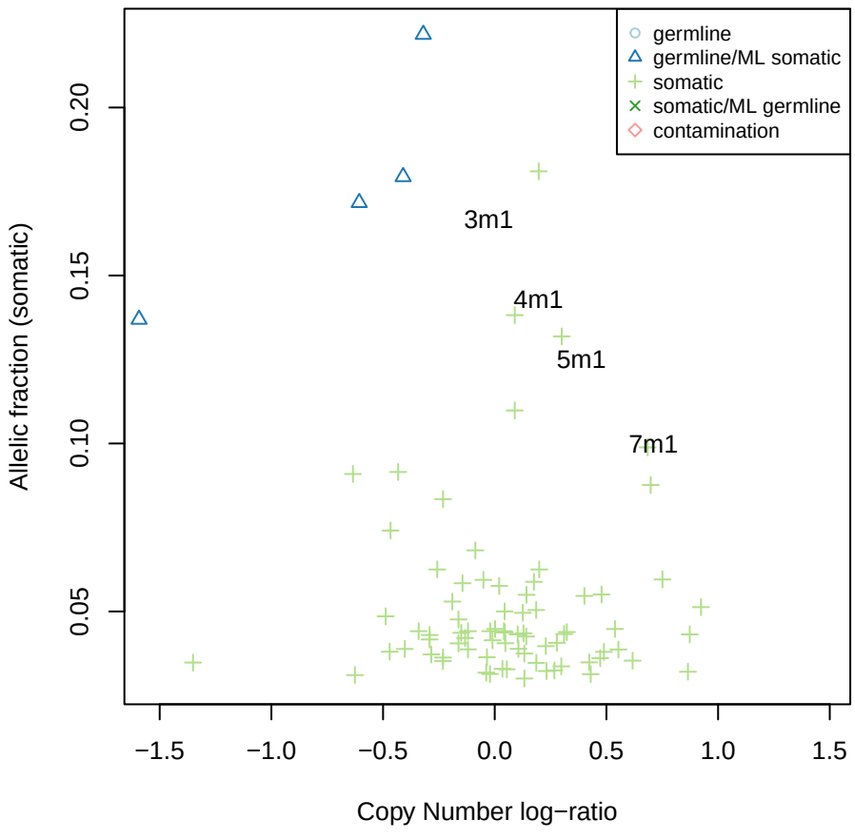

Purity: 0.4 Tumor ploidy: 3.112 SNV log−likelihood: −304.58 GoF: 80.3% Mean coverage: 497;317
1 2 3 4 5 6 8 9 10 11 12 13 14 16 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

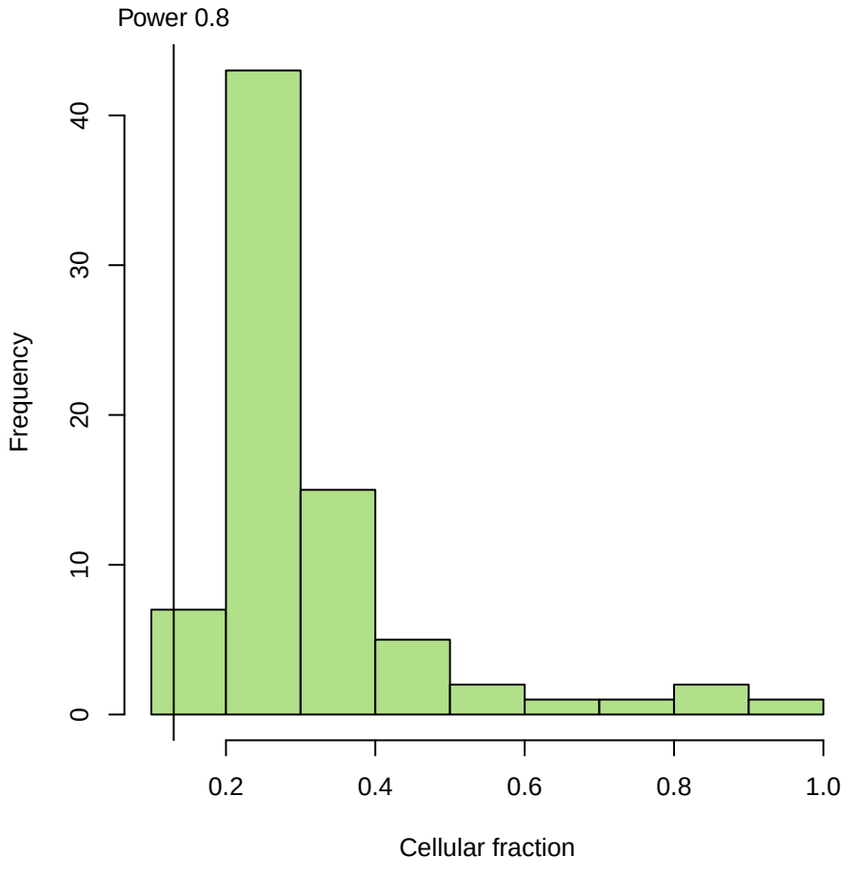

SCNA−fit log−likelihood: −7733.95
Copy Number log−ratio
−2 −1 0 1 2
1 2 4 6
0 50 100 150
SNV Index

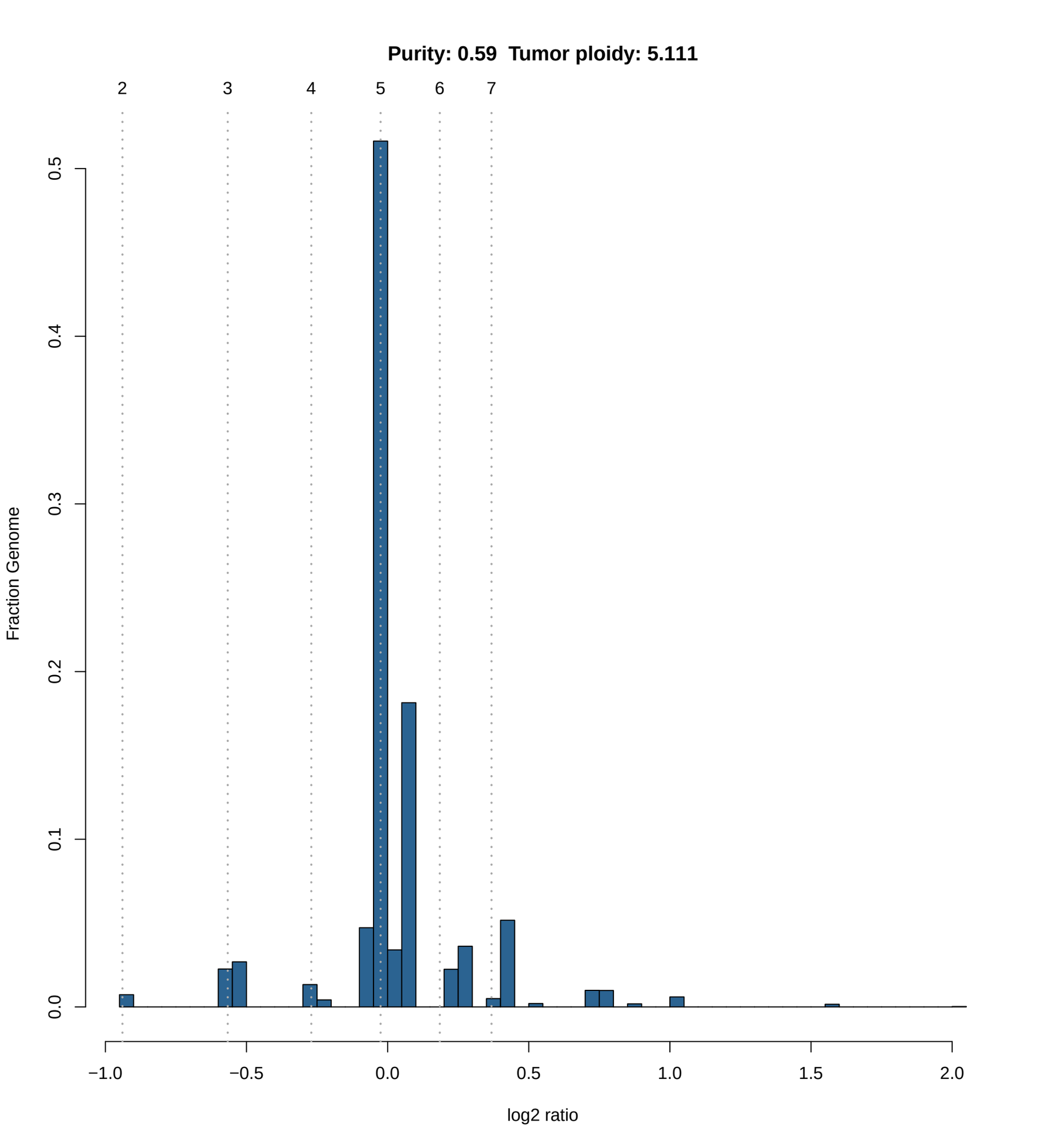

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

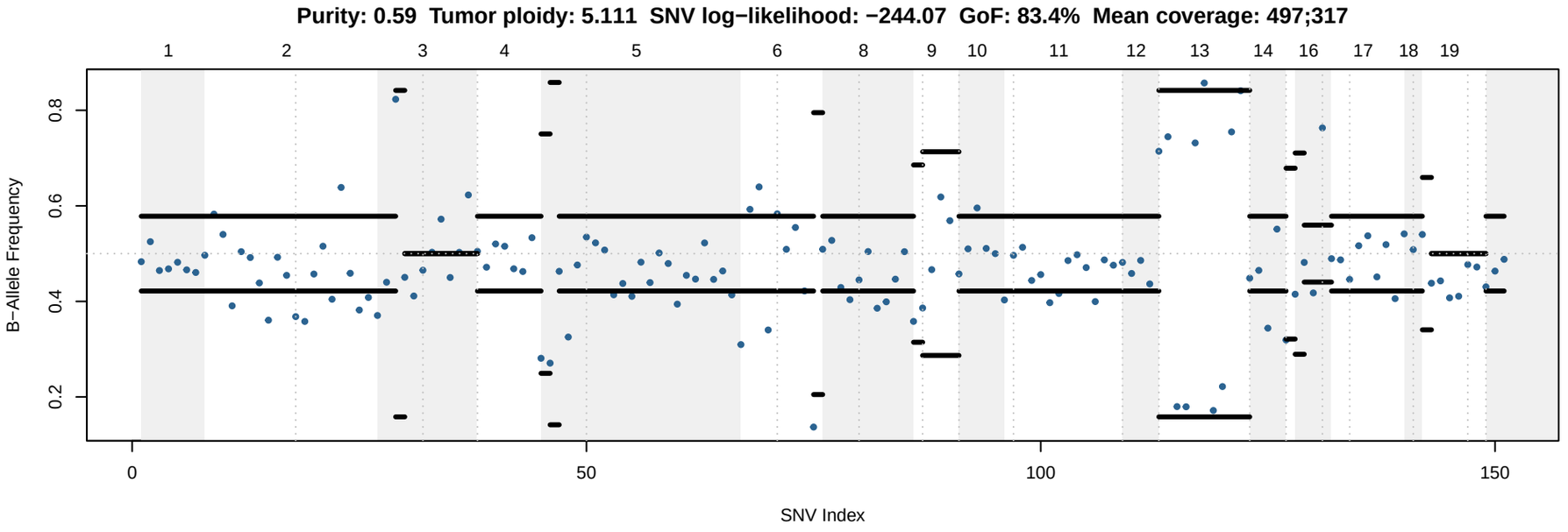
Allelic fraction (germline)
Copy Number log−ratio
5m5
1m1
3m2
7m4
4m2
5m2
3m1
1m0
2m0
5m1
7m1

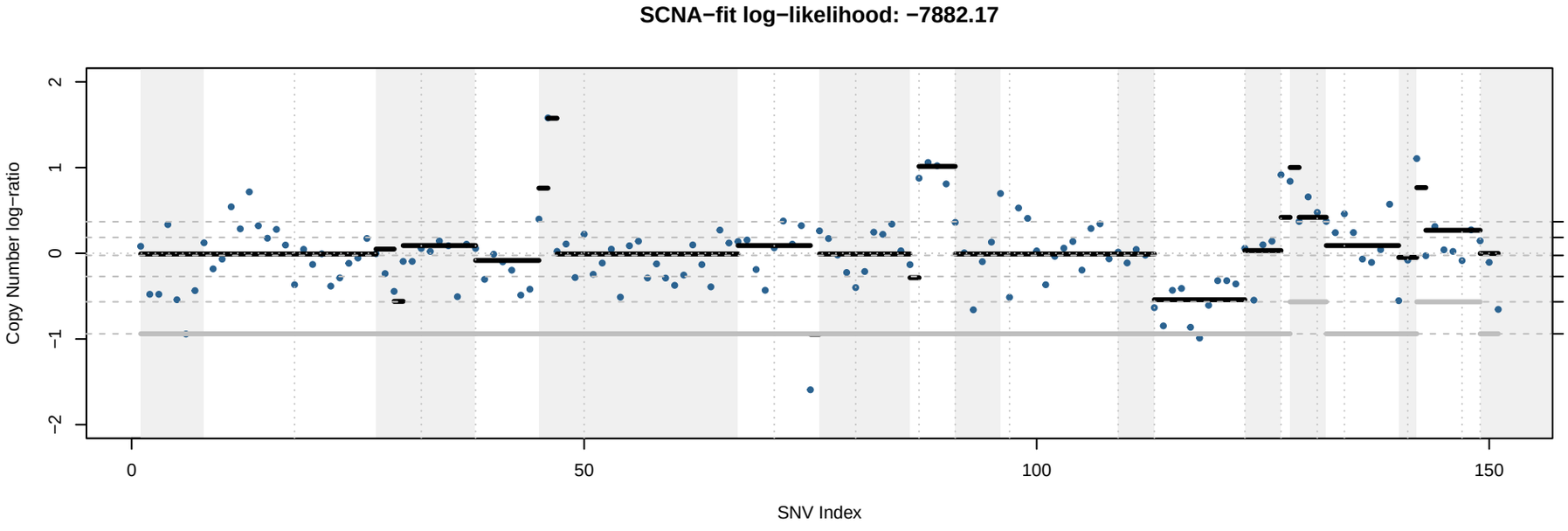

Coverage (log2)
Allelic fraction

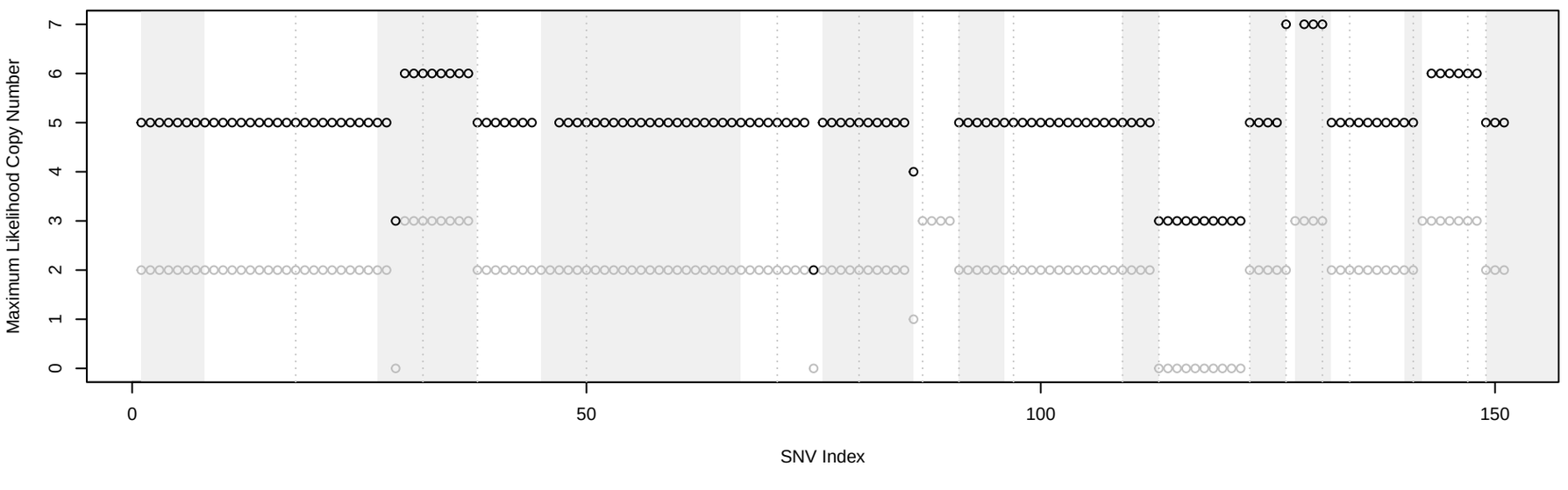

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m1
4m1
5m1
7m1

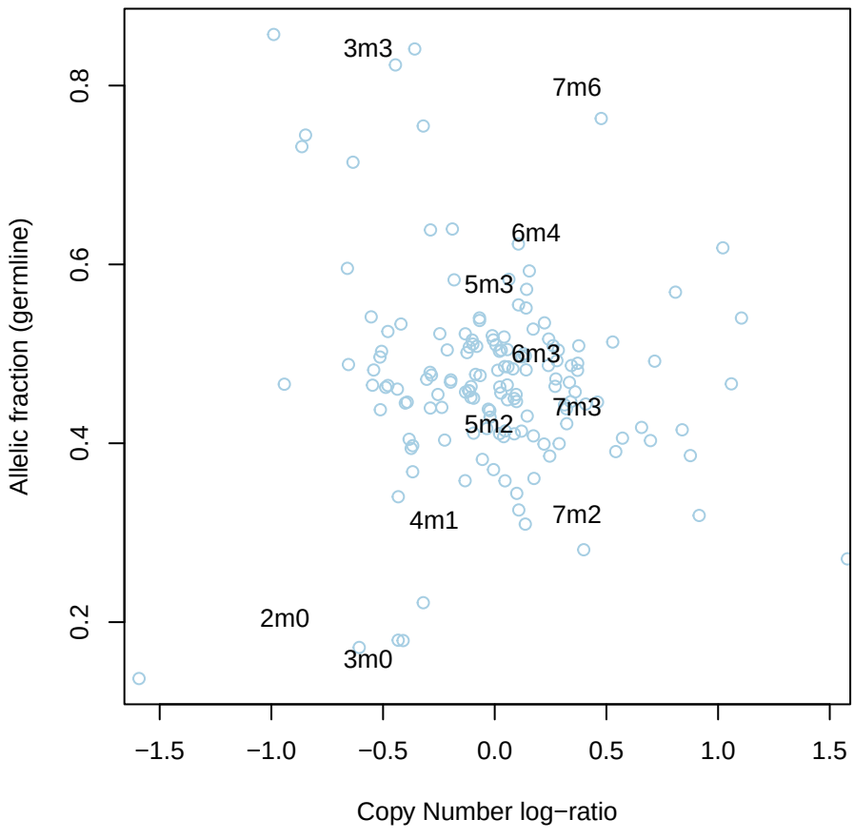

Power 0.8
Frequency
Cellular fraction

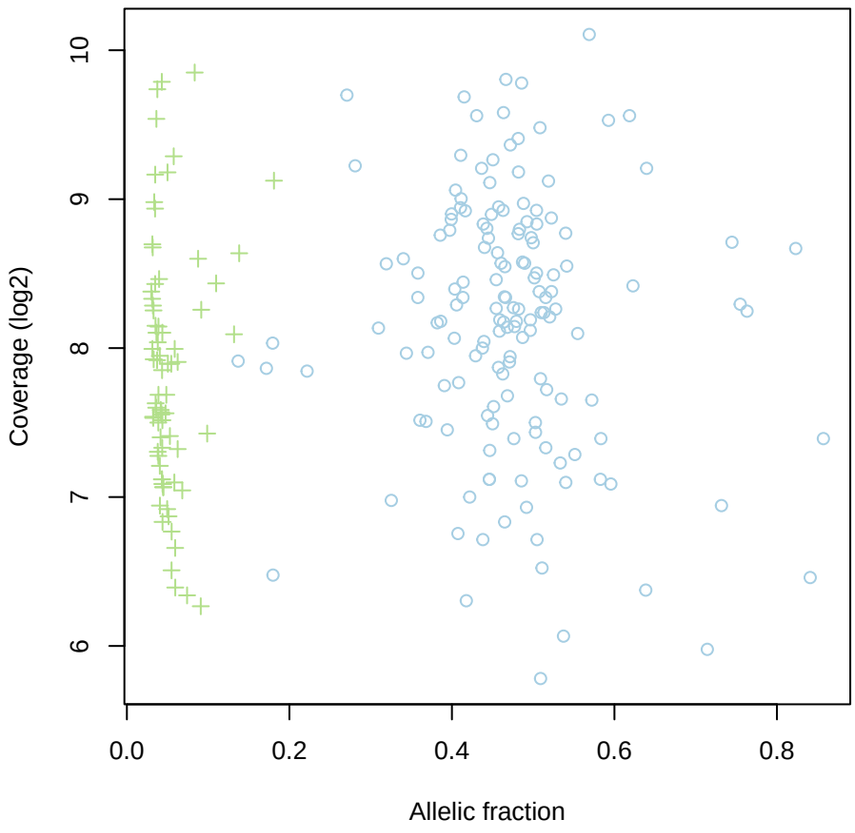

Purity: 0.59 Tumor ploidy: 5.111
2
3
4
5
6
7
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

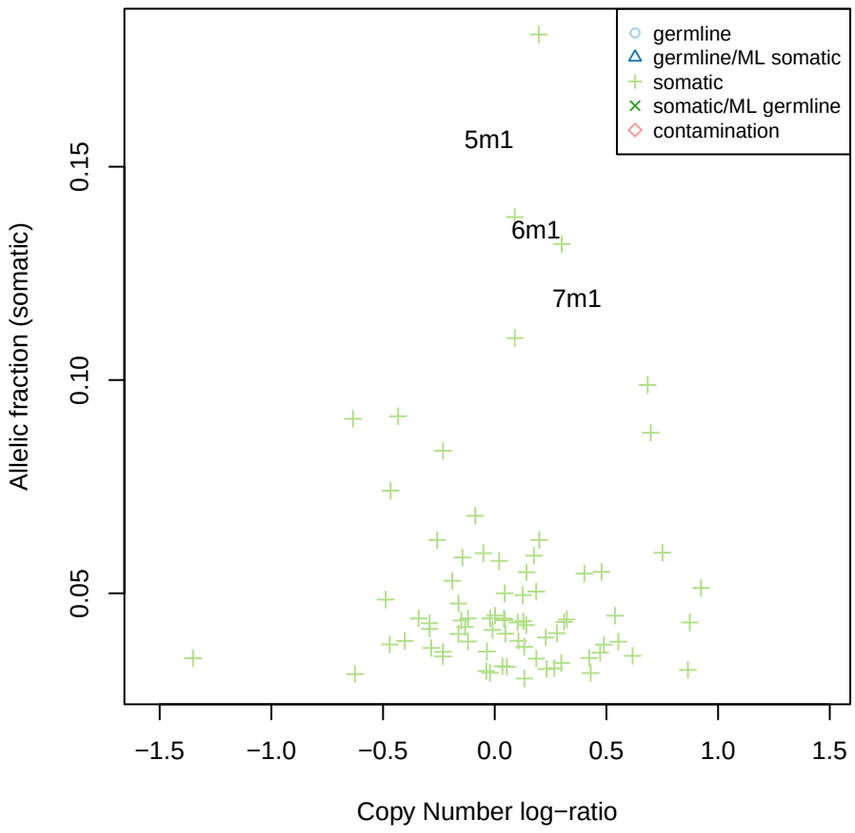

Purity: 0.59 Tumor ploidy: 5.111 SNV log−likelihood: −244.07 GoF: 83.4% Mean coverage: 497;317
1 2 3 4 5 6 8 9 10 11 12 13 14 16 17 18 19
B−Allele Frequency
0.2 0.4 0.6 0.8
0 50 100 150
SNV Index

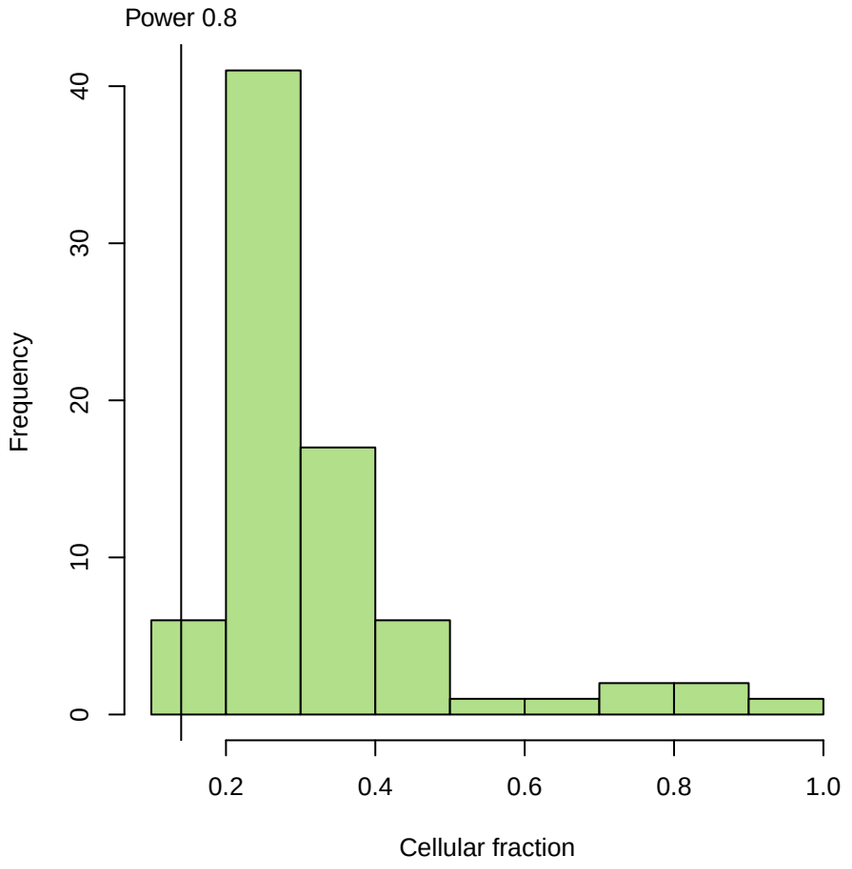

SCNA−fit log−likelihood: −7882.17
Copy Number log−ratio
−2 −1 0 1 2
2 3 4 6
0 50 100 150
SNV Index

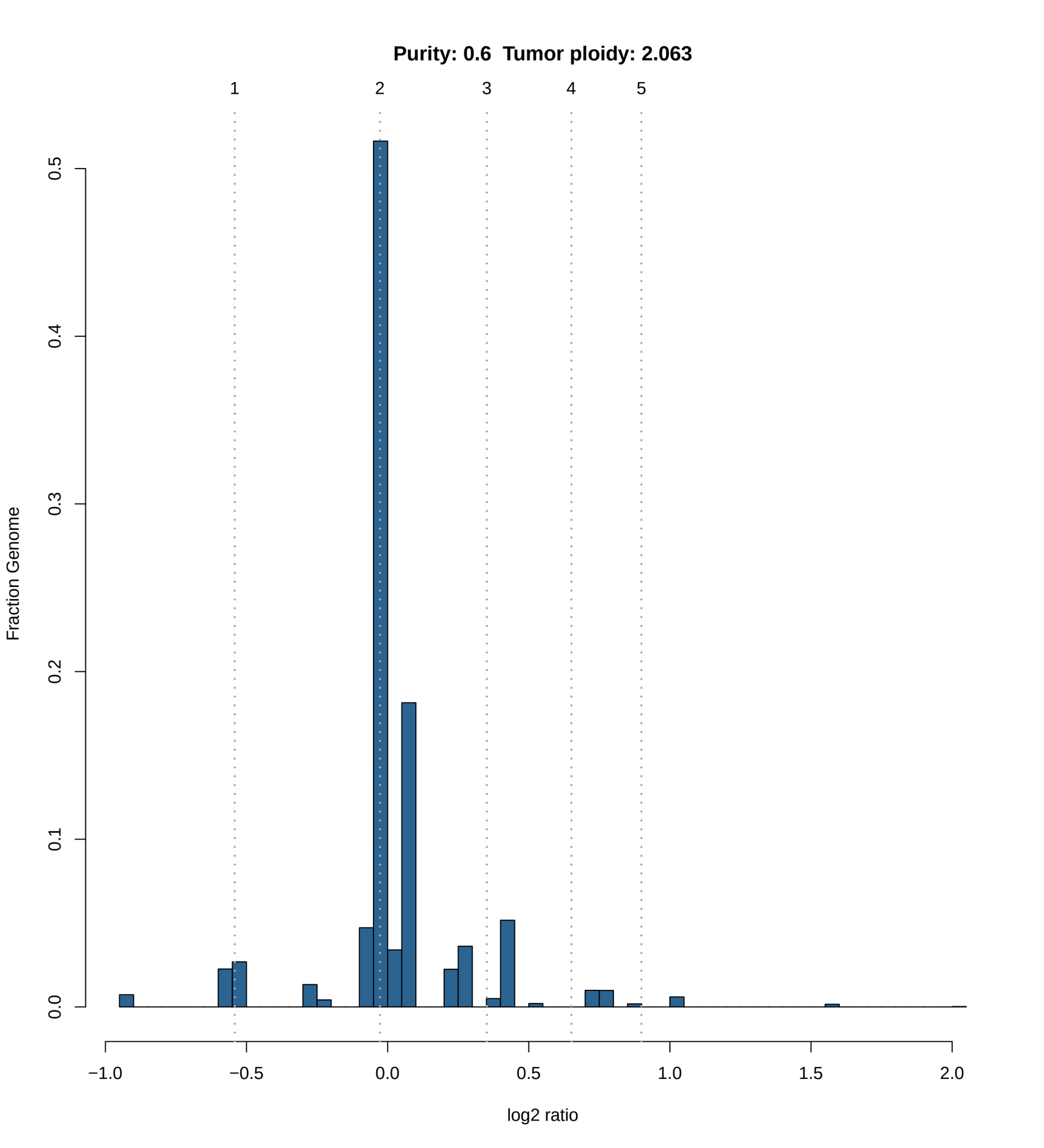

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

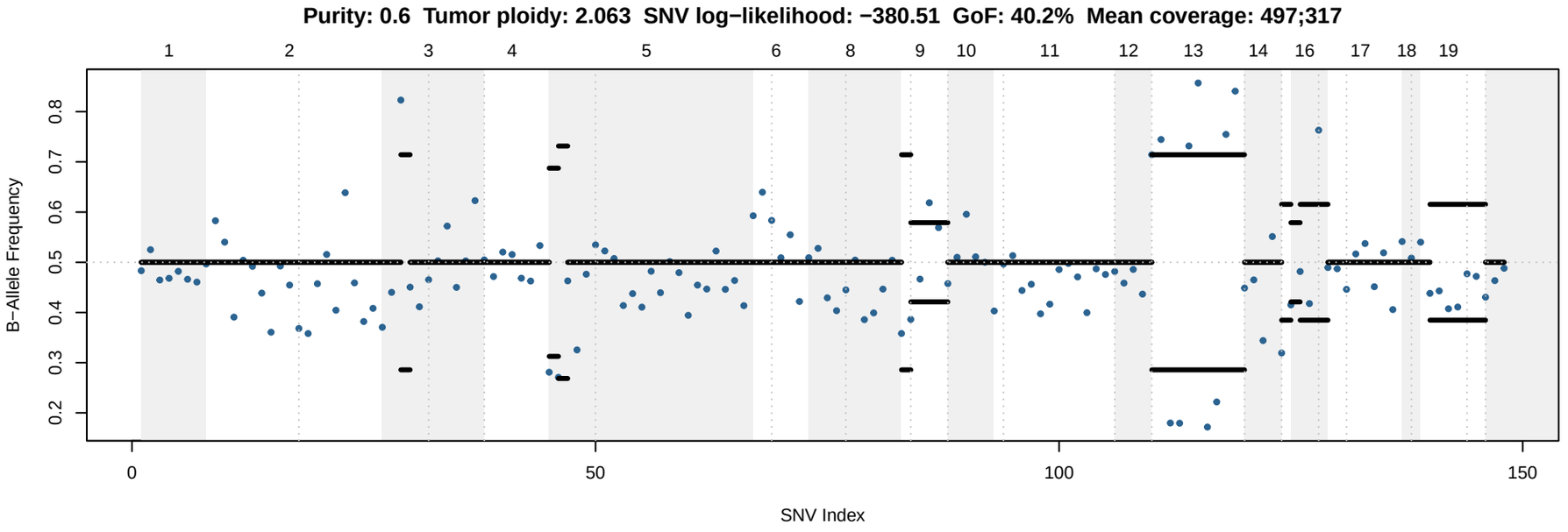

3m3
7m6
6m4
5m3
6m3
7m3
5m2
4m1
7m2
2m0
3m0
Allelic fraction (germline)
Copy Number log−ratio

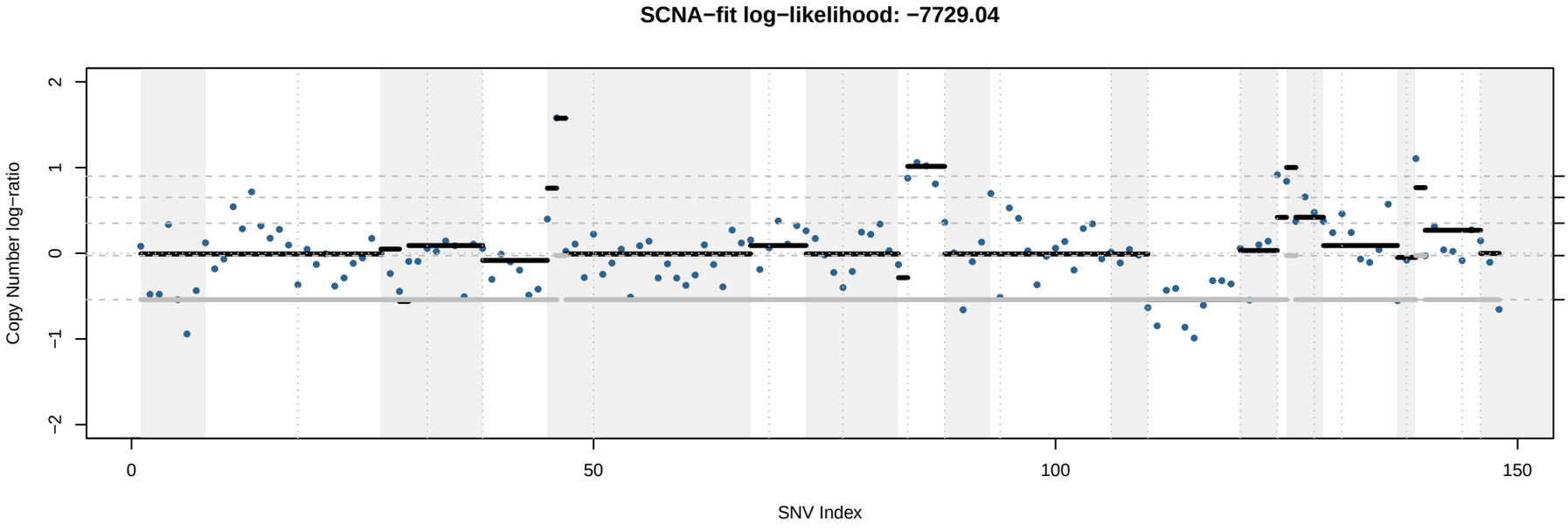

Coverage (log2)
Allelic fraction

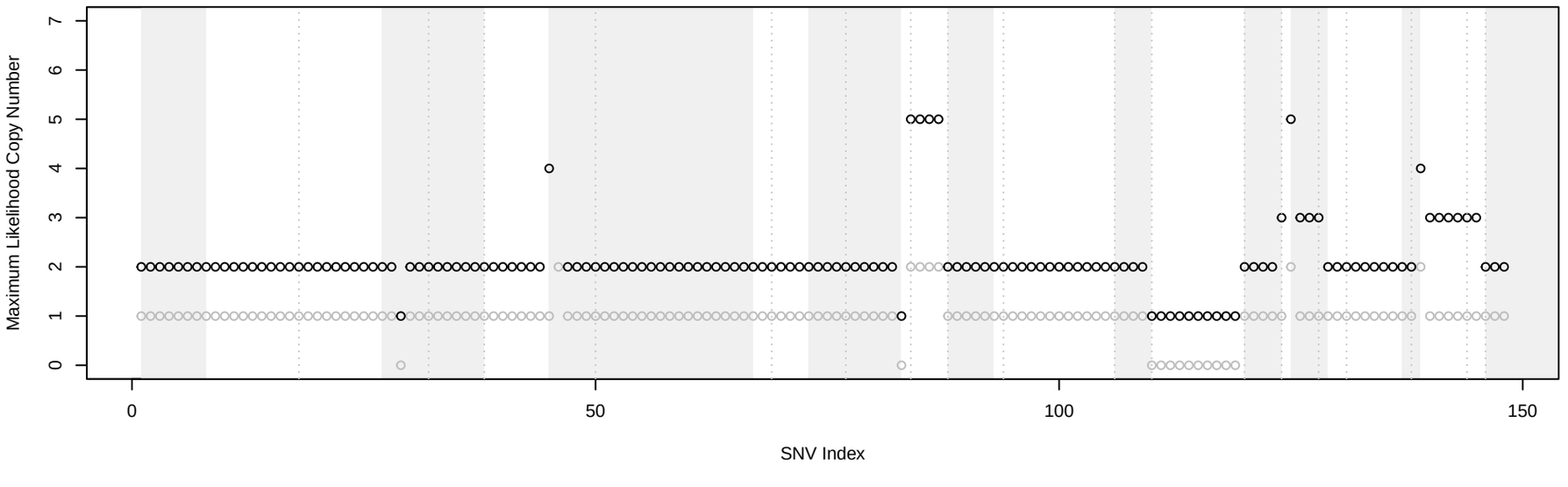

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

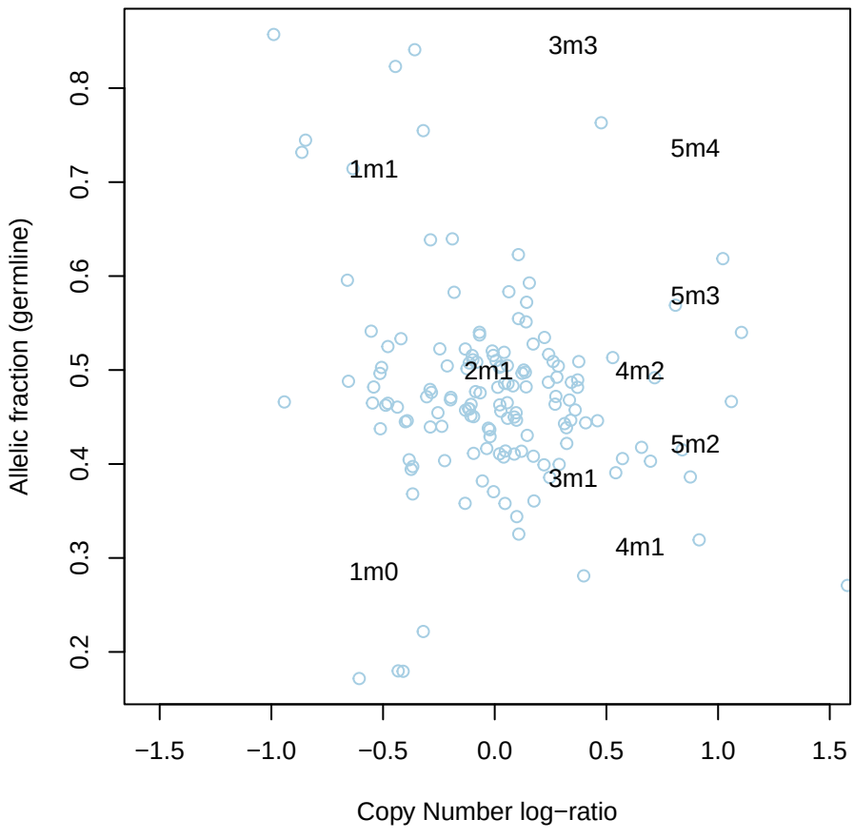

Power 0.8
Frequency
Cellular fraction

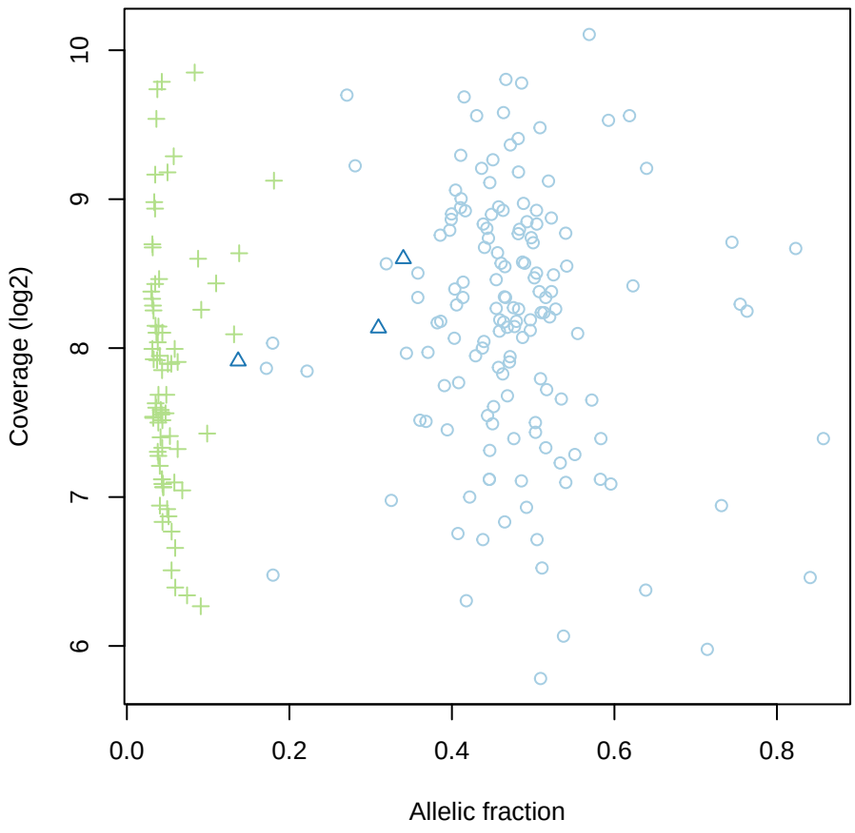

Purity: 0.6 Tumor ploidy: 2.063
1
2
3
4
5
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

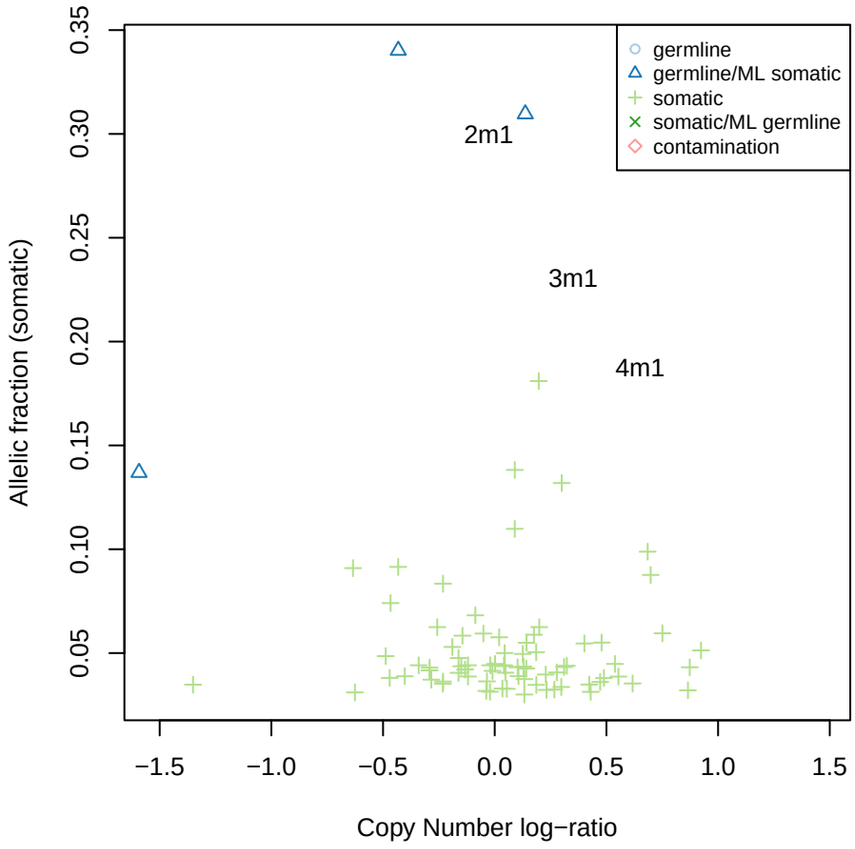

Purity: 0.6 Tumor ploidy: 2.063 SNV log−likelihood: −380.51 GoF: 40.2% Mean coverage: 497;317
1 2 3 4 5 6 8 9 10 11 12 13 14 16 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

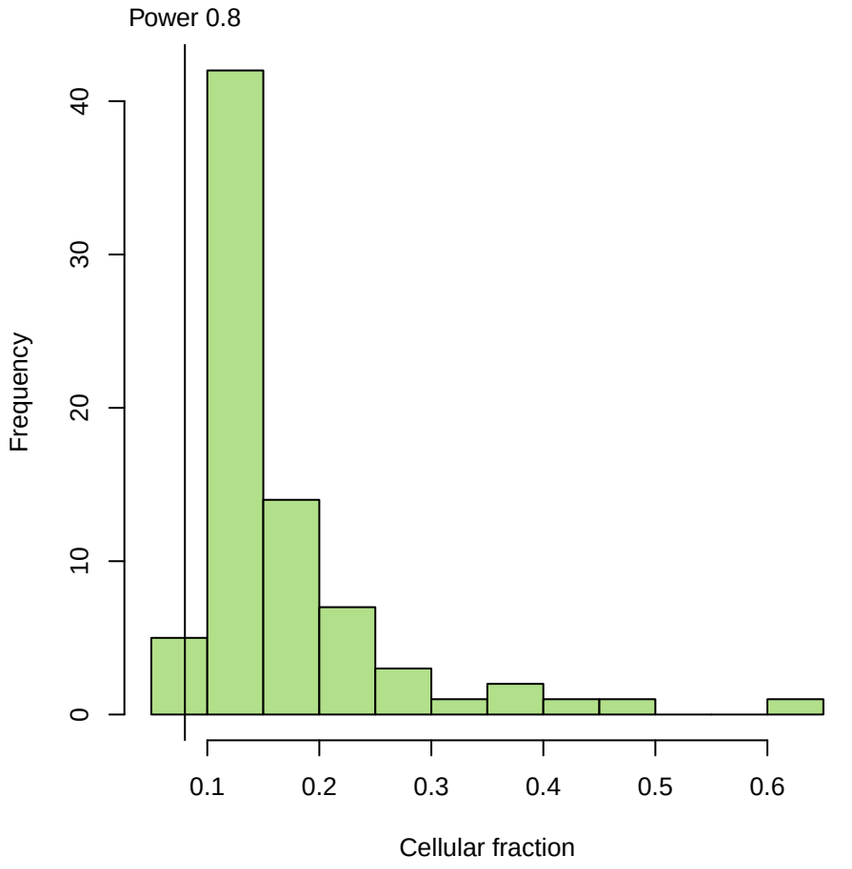

SCNA−fit log−likelihood: −7729.04
Copy Number log−ratio
−2 −1 0 1 2
1 2 3 4
0 50 100 150
SNV Index

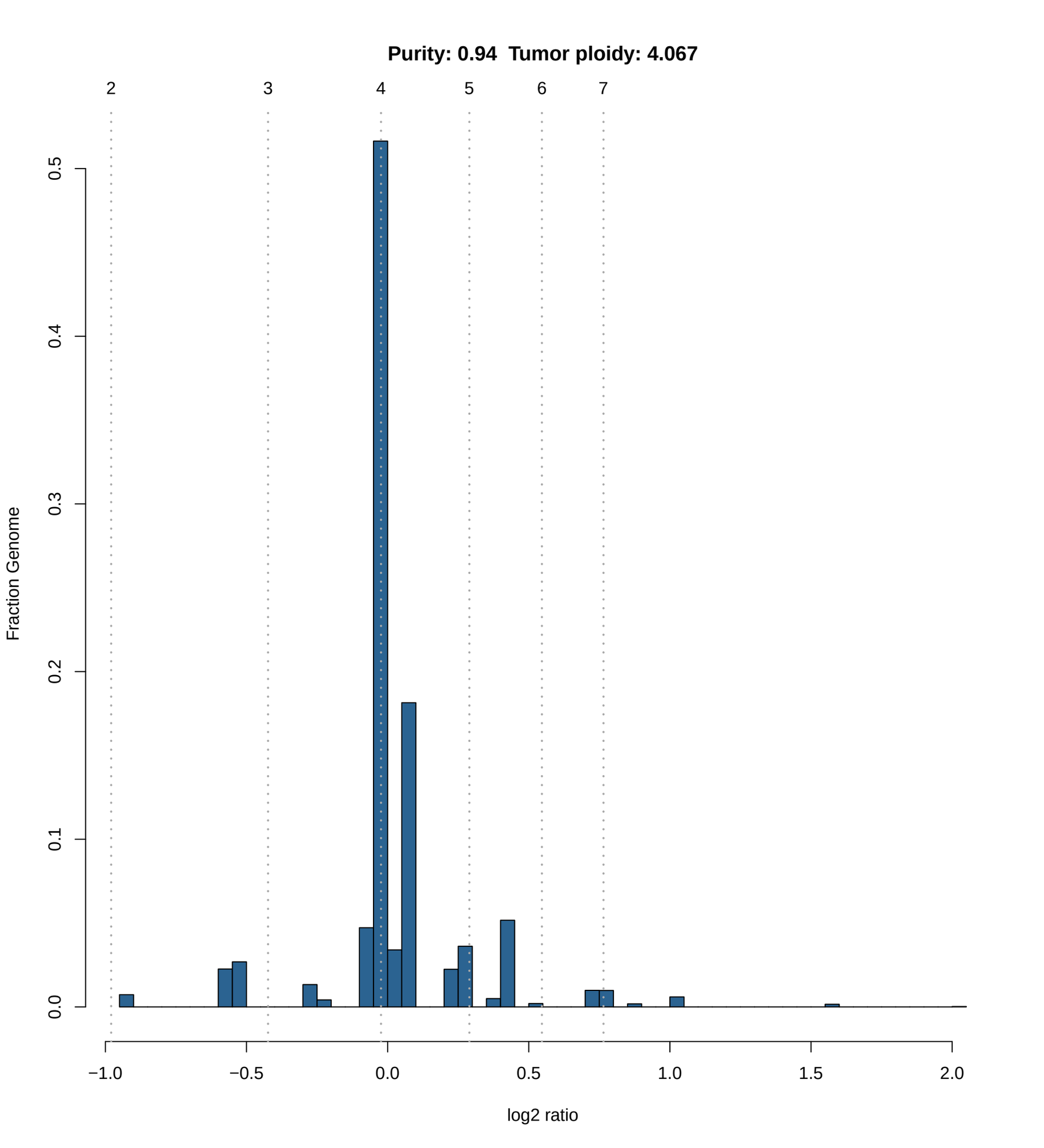

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

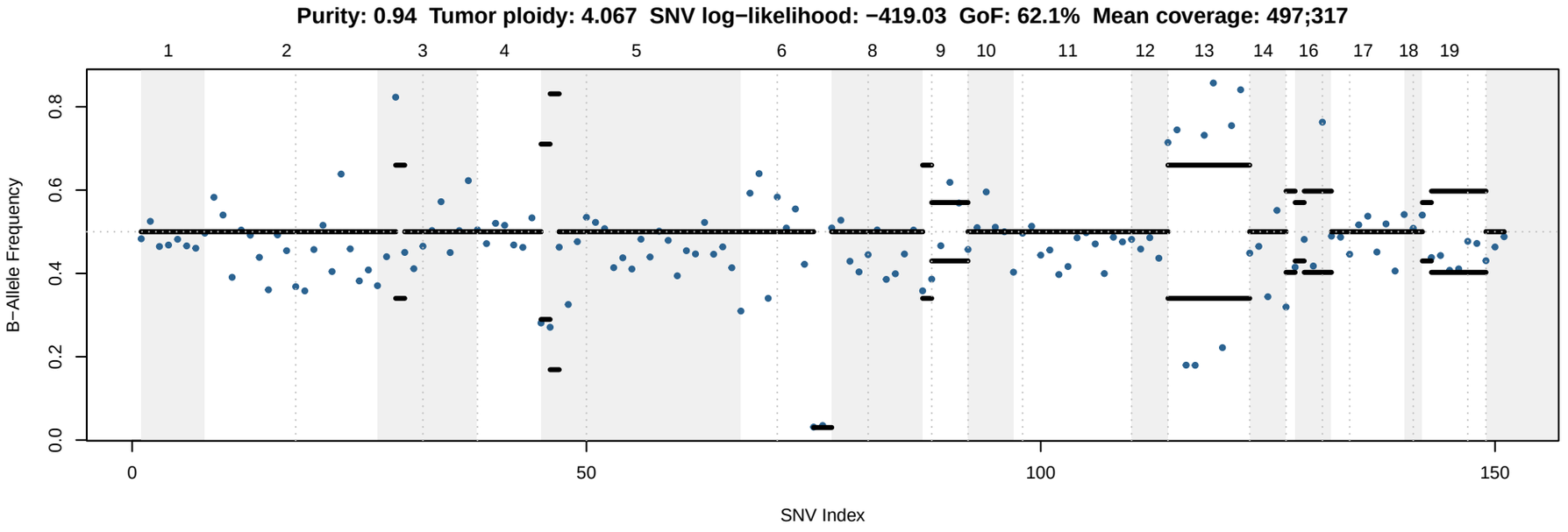

3m3
5m4
1m1
5m3
2m1
4m2
5m2
3m1
4m1
1m0
Allelic fraction (germline)
Copy Number log−ratio

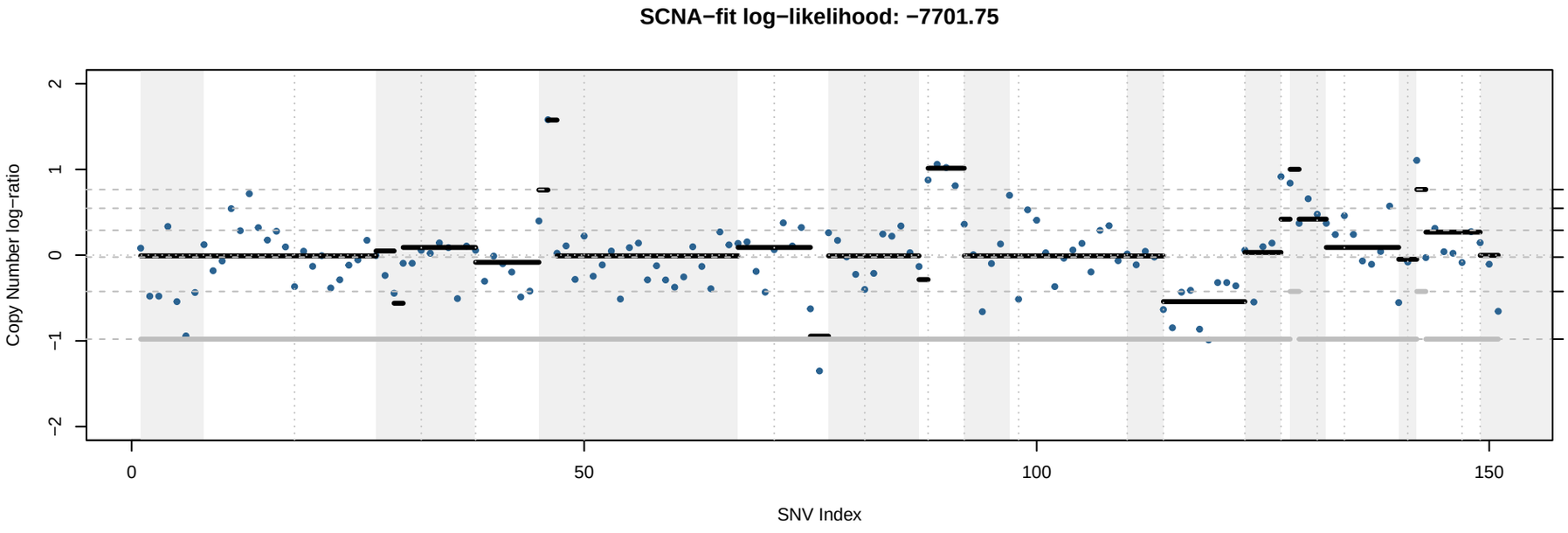

Coverage (log2)
Allelic fraction

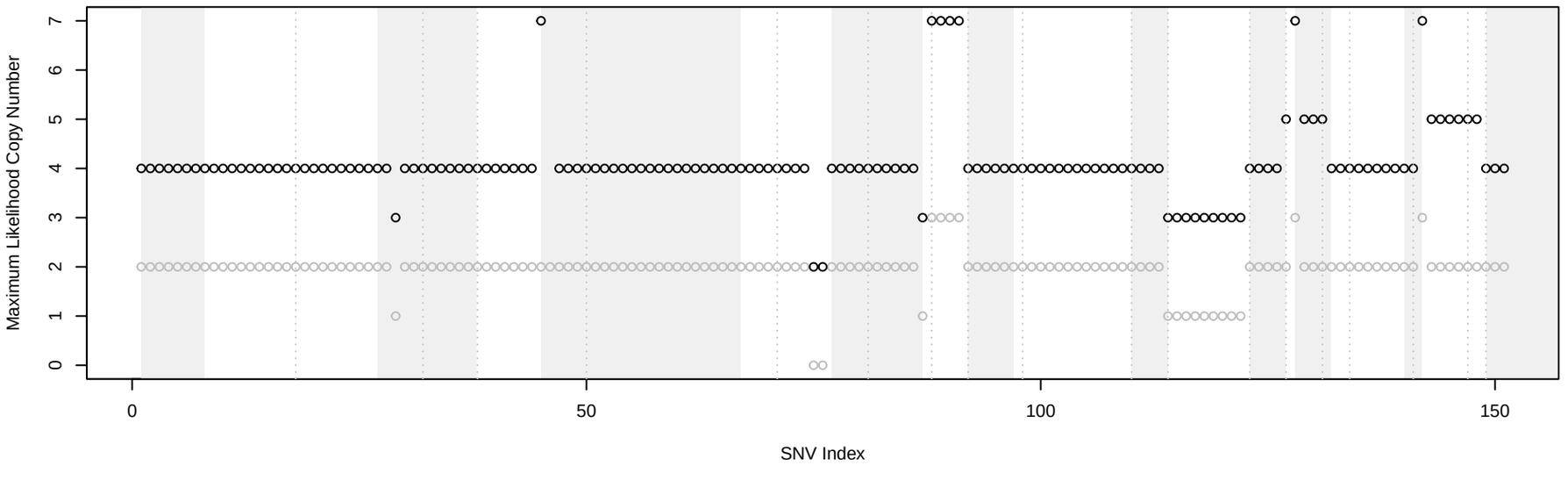

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1
Allelic fraction (somatic)
Copy Number log−ratio

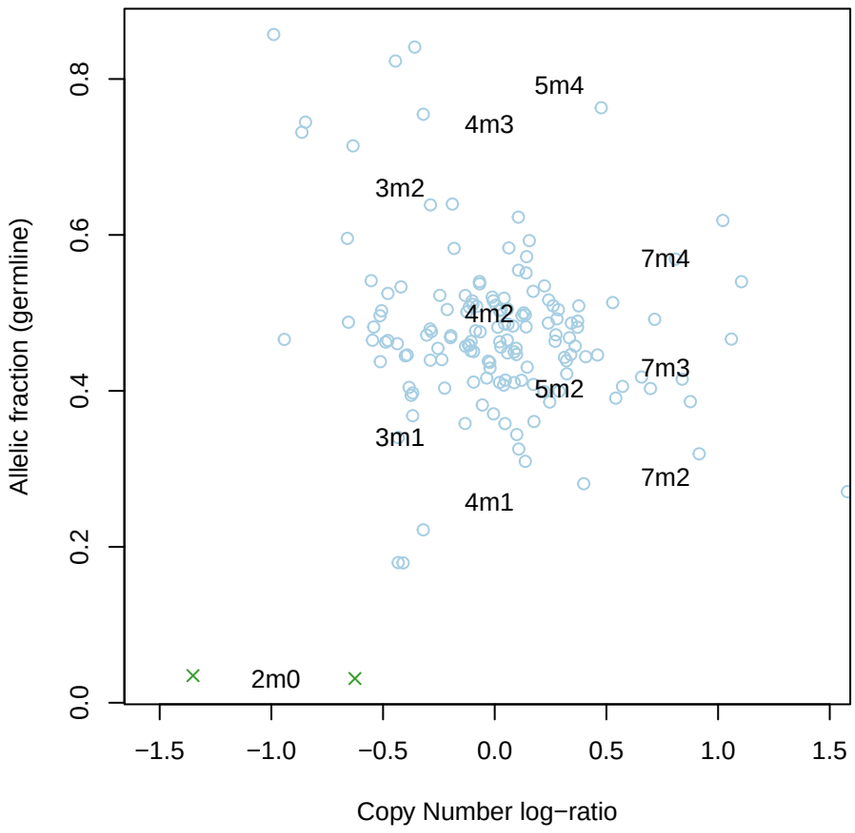

Power 0.8
Frequency
Cellular fraction

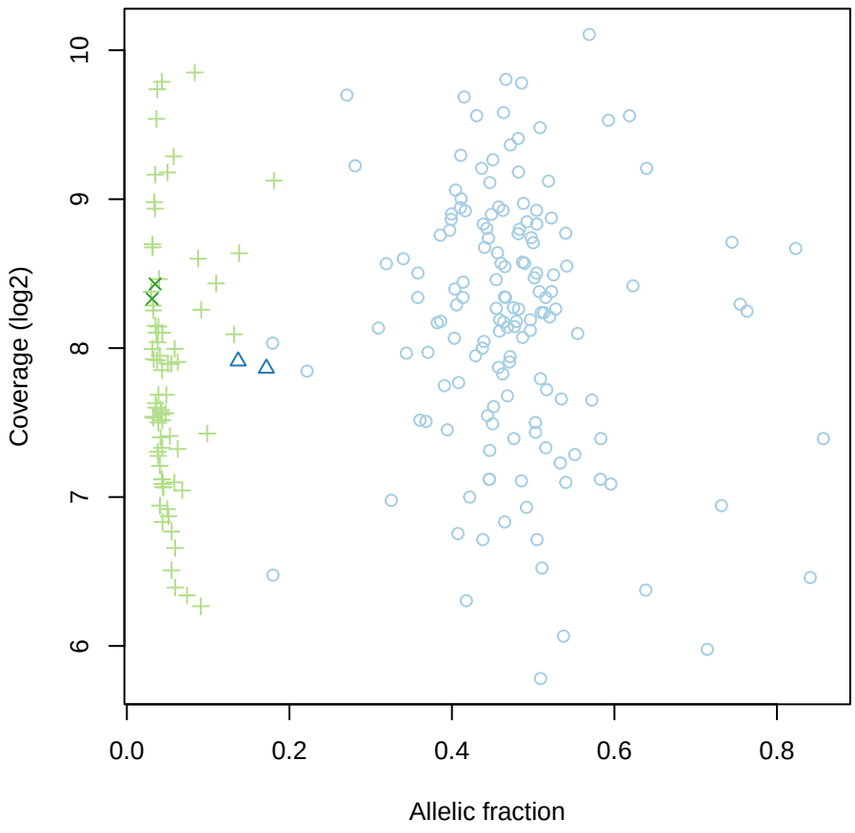

Purity: 0.94 Tumor ploidy: 4.067
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

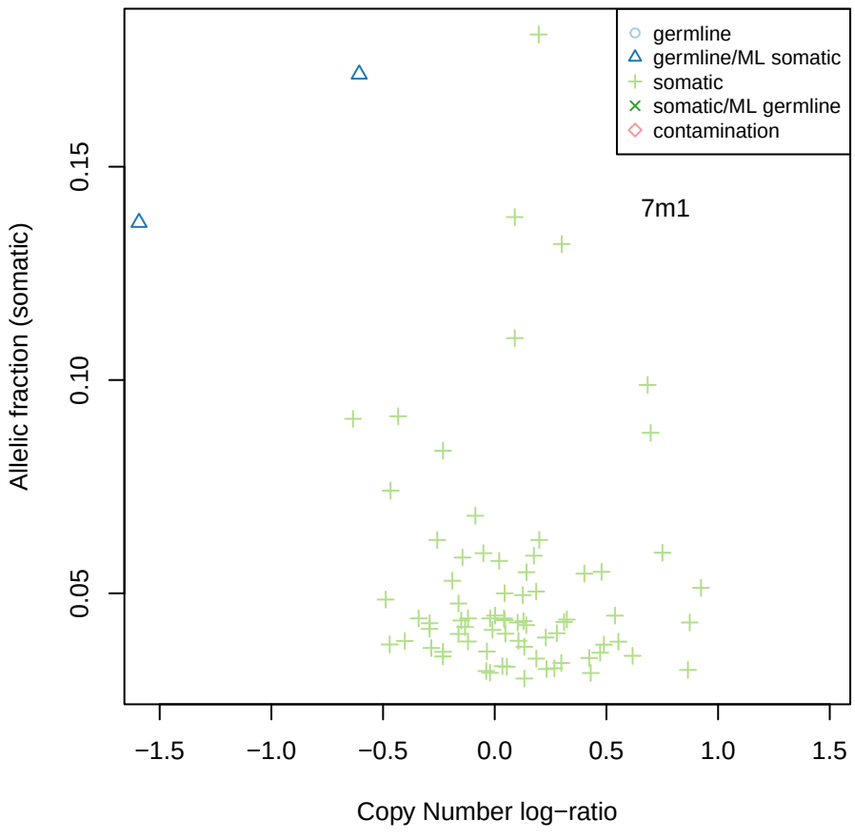

Purity: 0.94 Tumor ploidy: 4.067 SNV log−likelihood: −419.03 GoF: 62.1% Mean coverage: 497;317
1 2 3 4 5 6 8 9 10 11 12 13 14 16 17 18 19
B−Allele Frequency
0.0 0.2 0.4 0.6 0.8
0 50 100 150
SNV Index

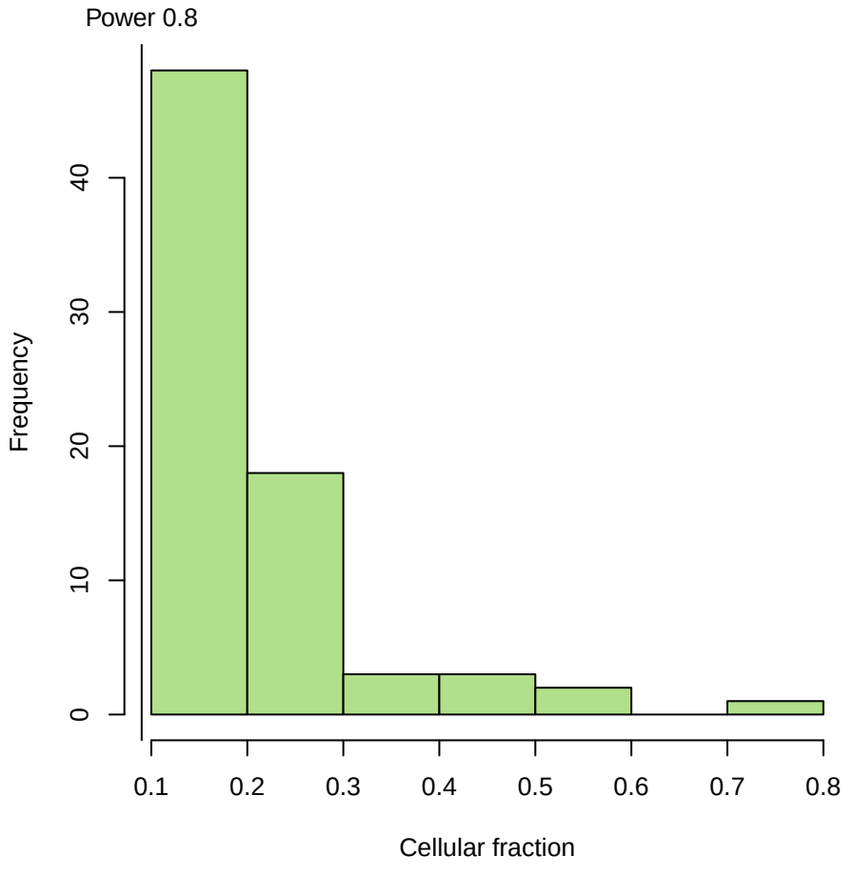

SCNA−fit log−likelihood: −7701.75
Copy Number log−ratio
−2 −1 0 1 2
2 3 4 5 7
0 50 100 150
SNV Index

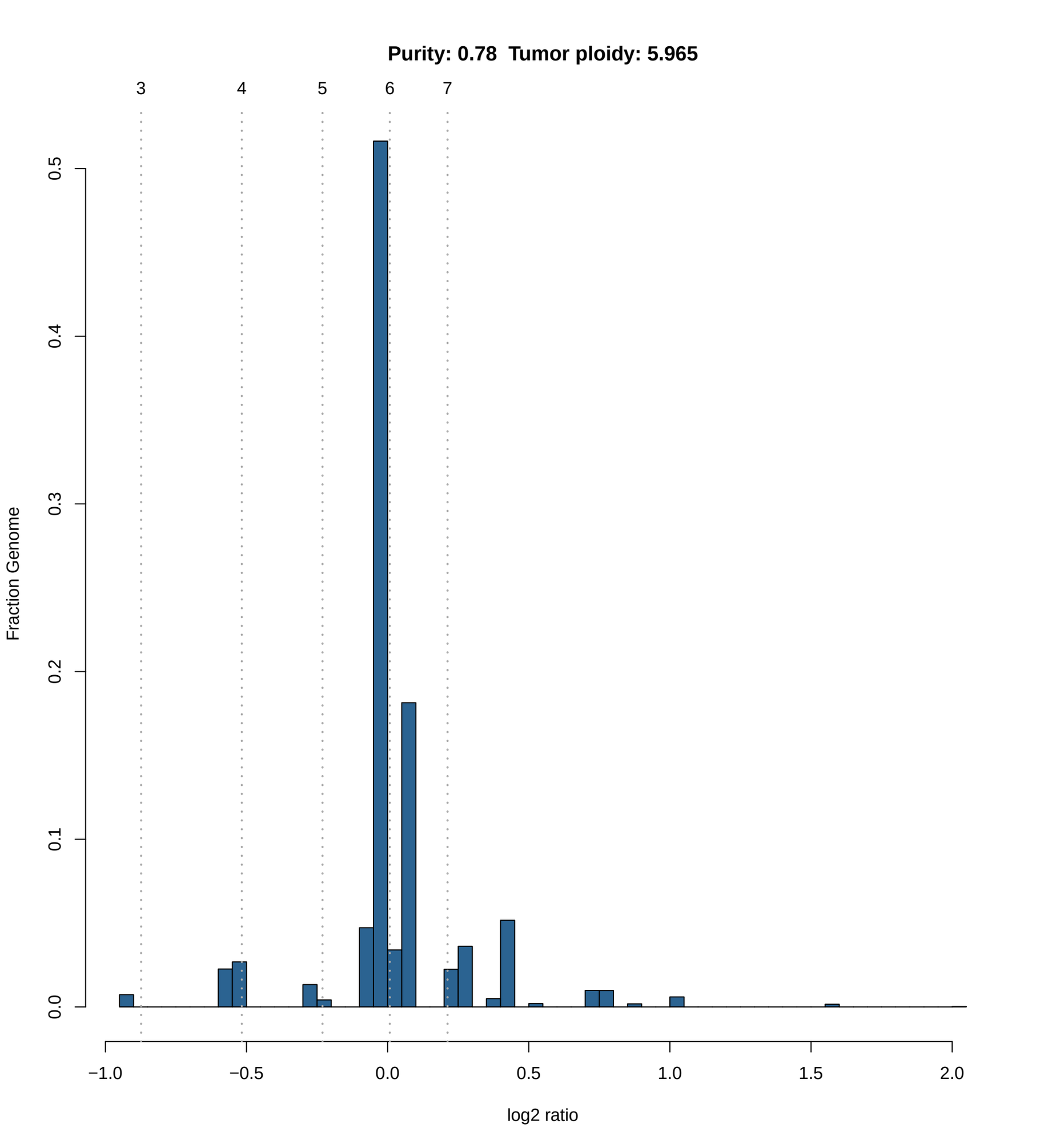

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

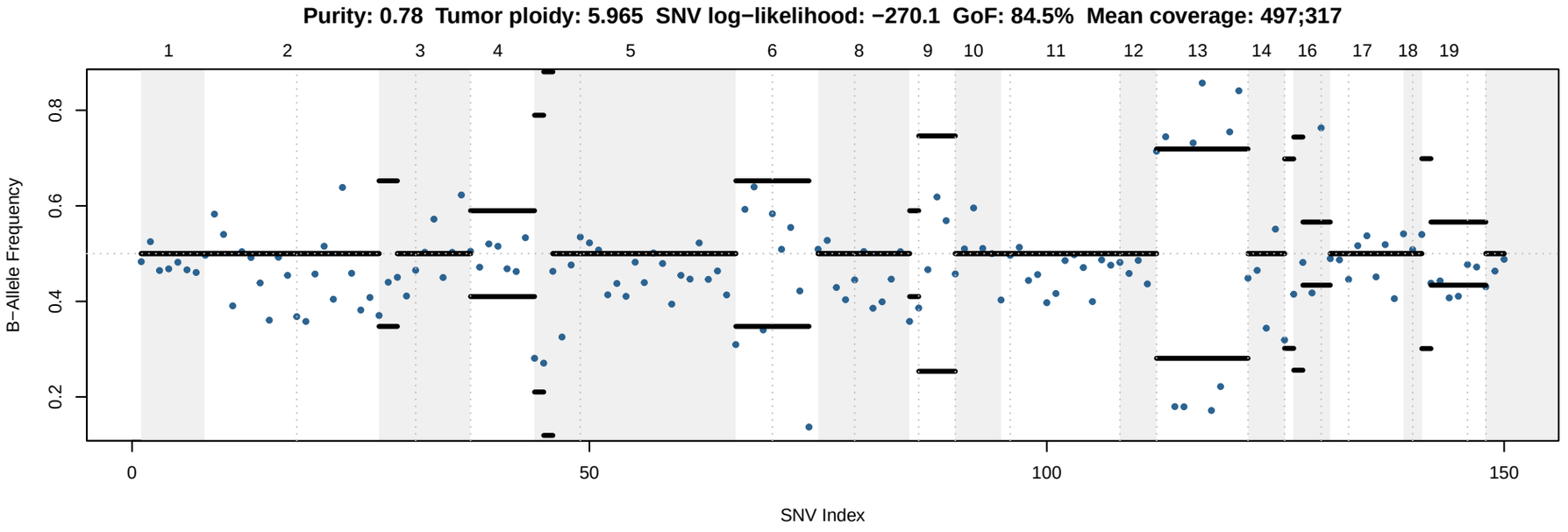

Allelic fraction (germline)
Copy Number log−ratio
5m4
4m3
3m2
7m4
4m2
7m3
5m2
3m1
7m2
4m1
2m0

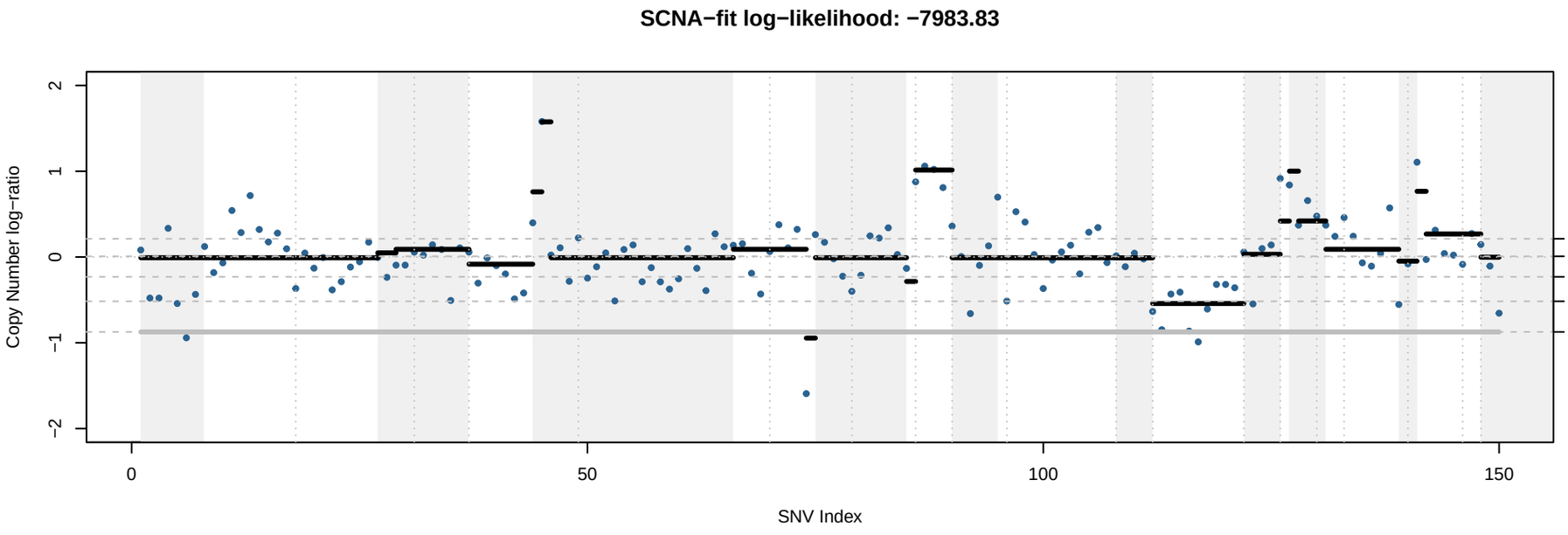

Coverage (log2)
Allelic fraction

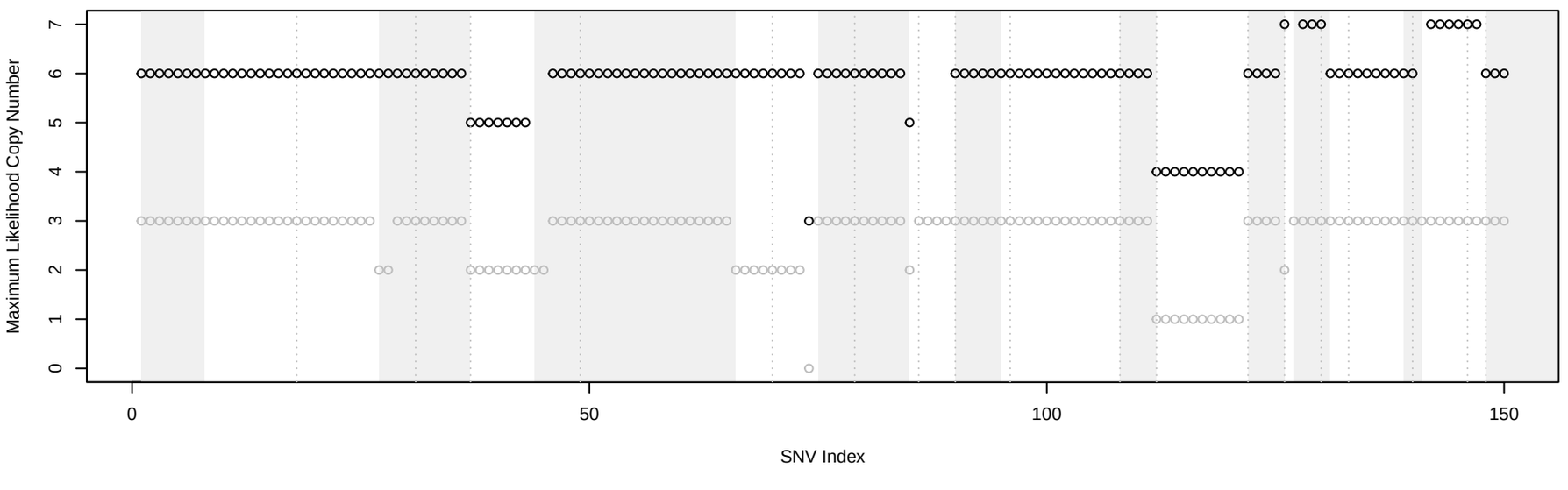

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
7m1

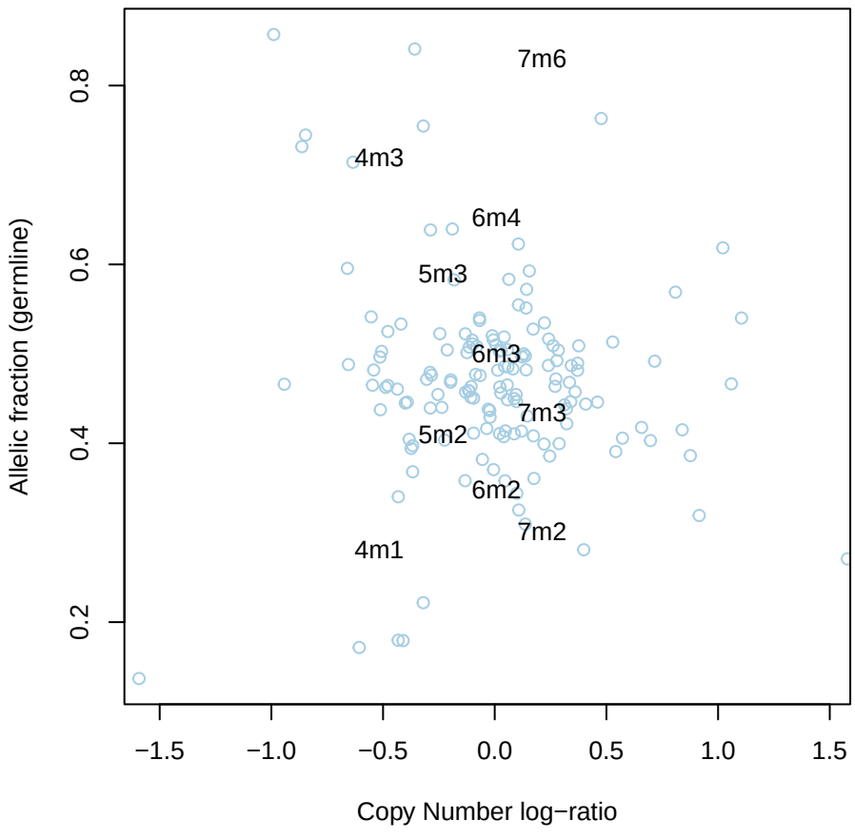

Power 0.8
Frequency
Cellular fraction

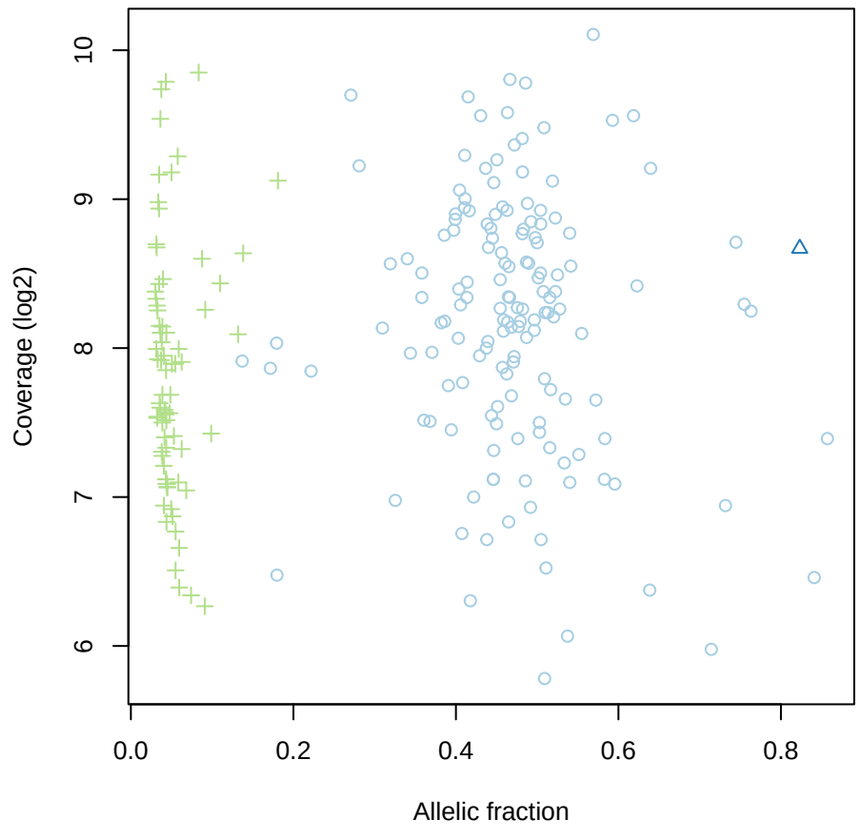

Purity: 0.78 Tumor ploidy: 5.965
3
4
5
6
7
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

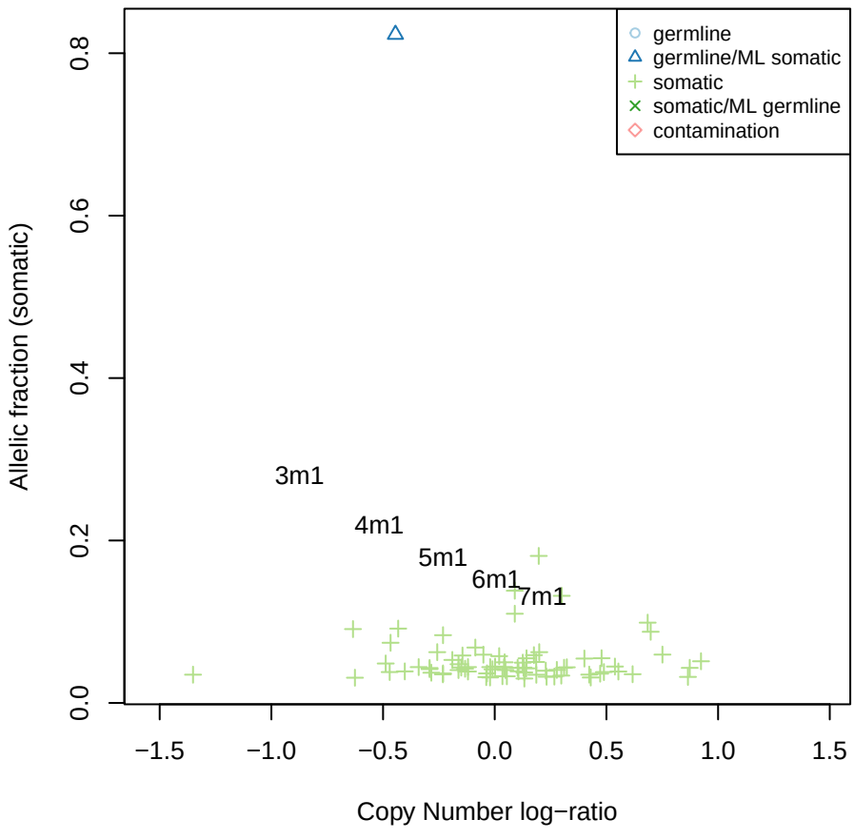

Purity: 0.78 Tumor ploidy: 5.965 SNV log−likelihood: −270.1 GoF: 84.5% Mean coverage: 497;317
1 2 3 4 5 6 8 9 10 11 12 13 14 16 17 18 19
B−Allele Frequency
0.2 0.4 0.6 0.8
0 50 100 150
SNV Index

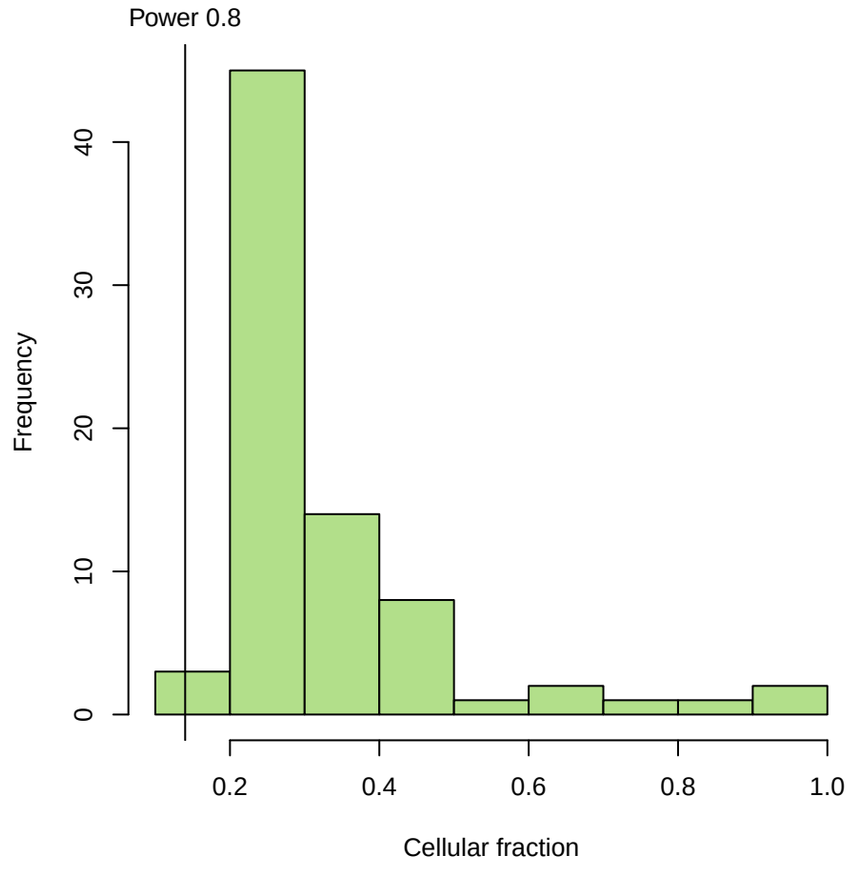

SCNA−fit log−likelihood: −7983.83
Copy Number log−ratio
−2 −1 0 1 2
3 4 6
0 50 100 150
SNV Index

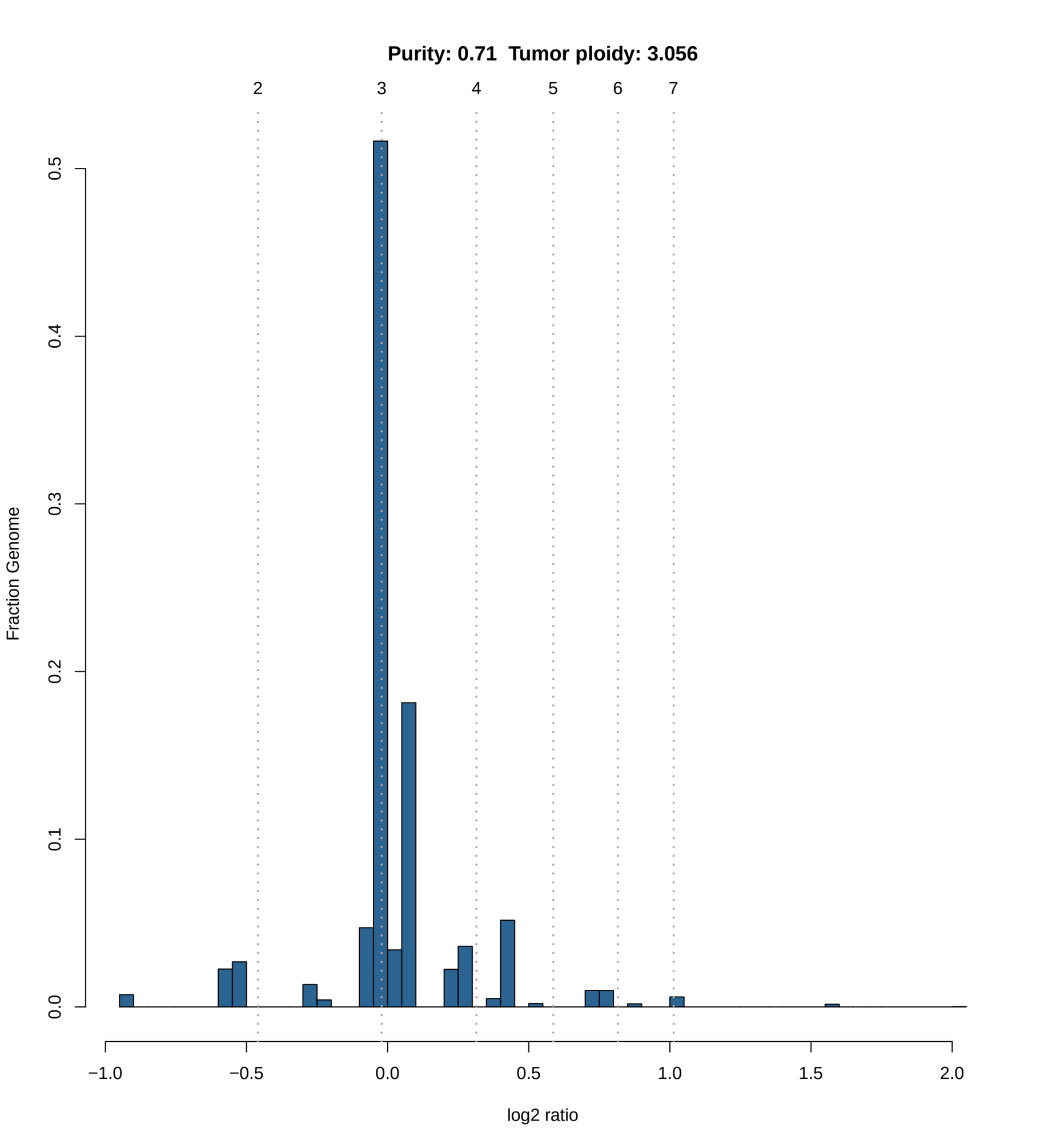

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

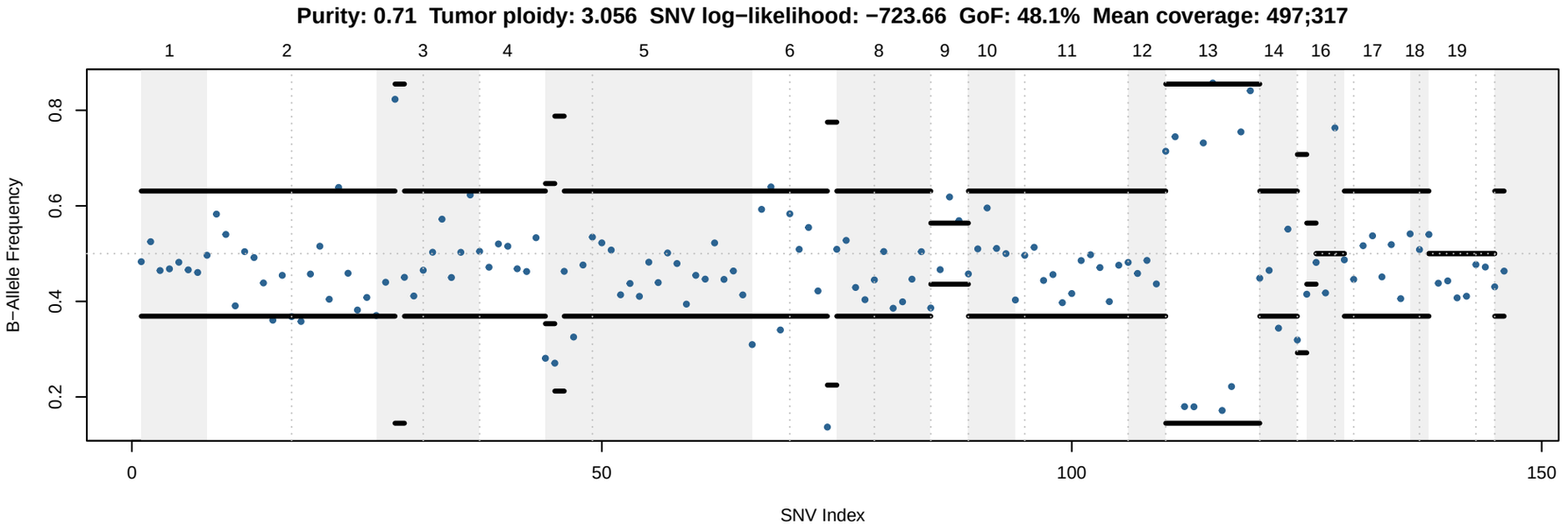

7m6
4m3
6m4
5m3
6m3
7m3
5m2
6m2
7m2
4m1
Allelic fraction (germline)
Copy Number log−ratio

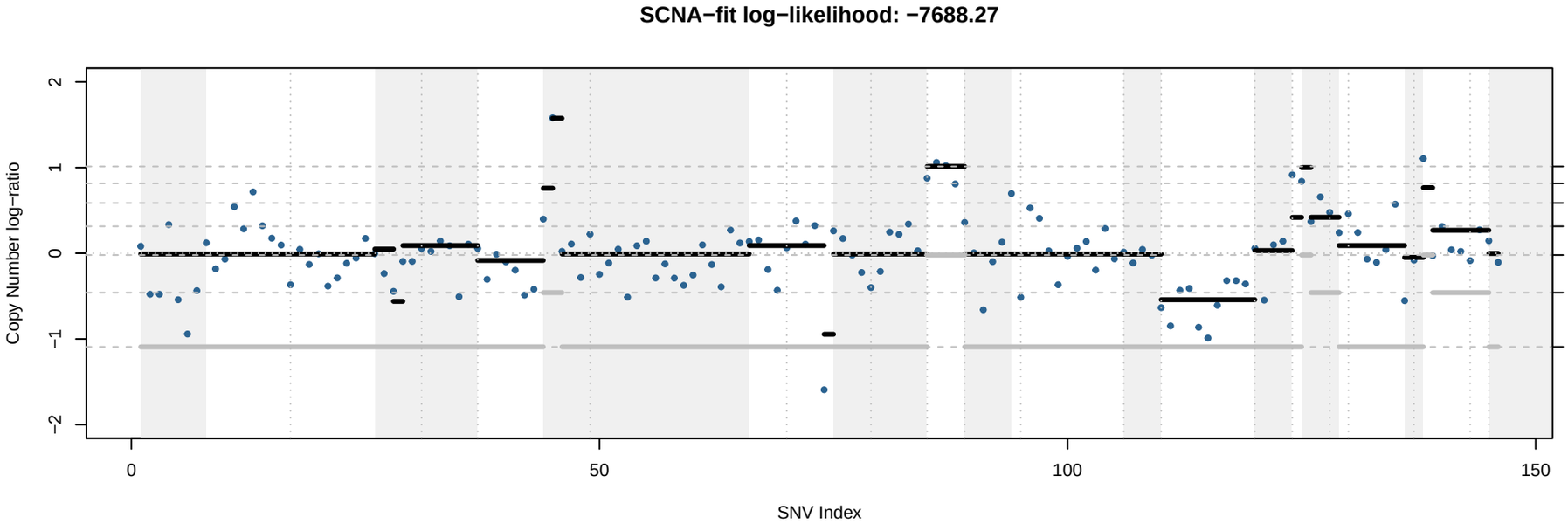

Coverage (log2)
Allelic fraction

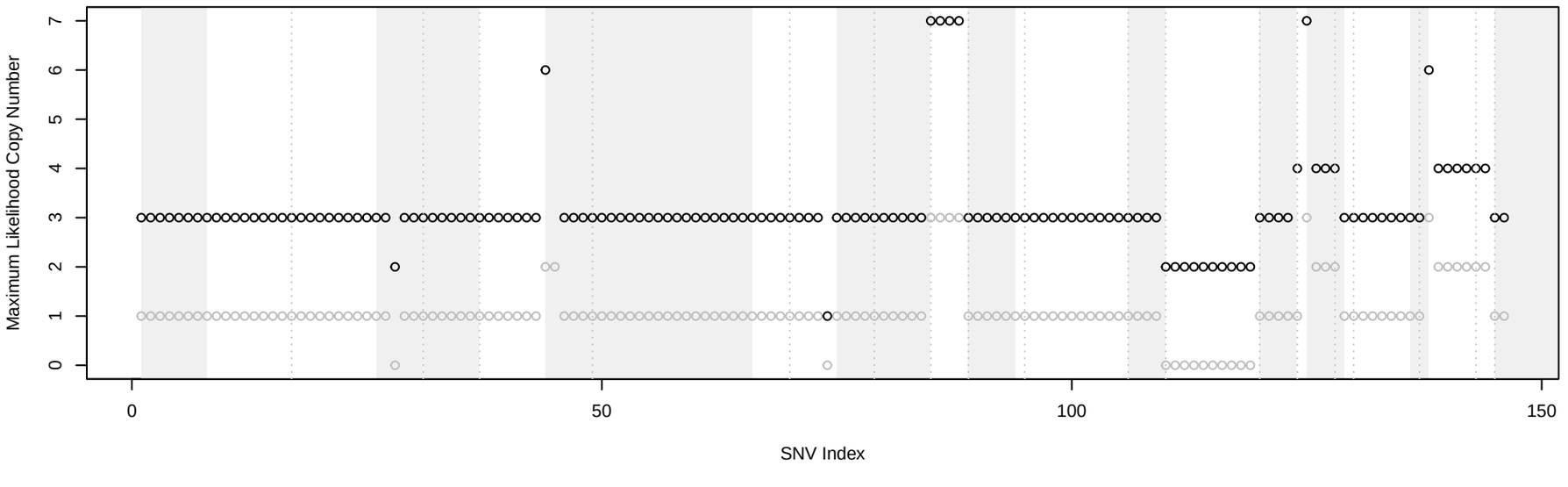

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

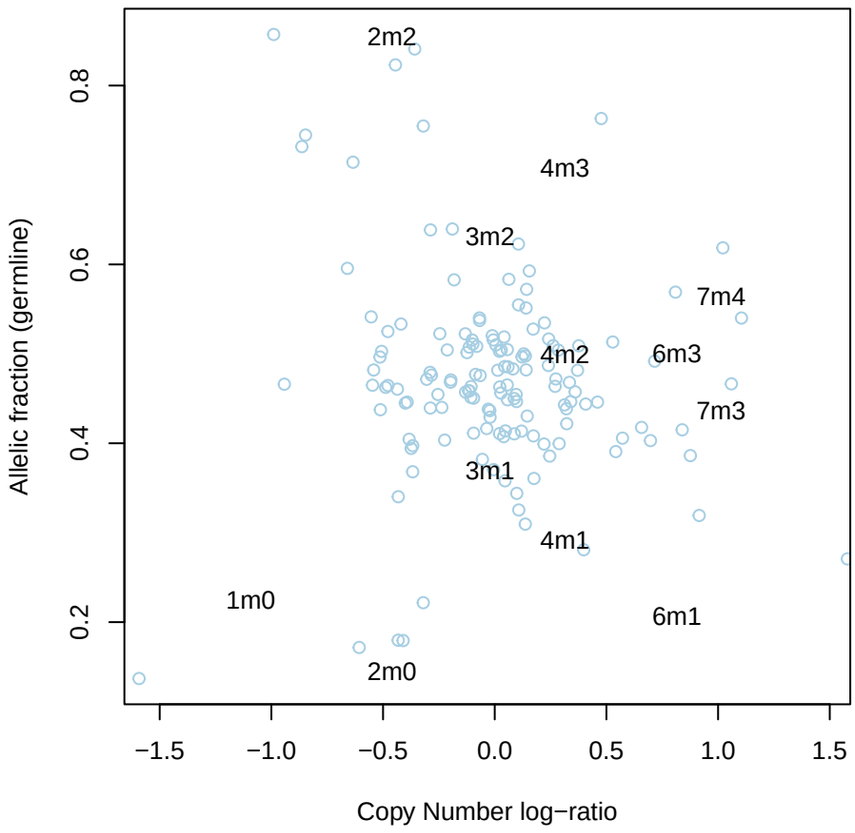

Power 0.8
Frequency
Cellular fraction

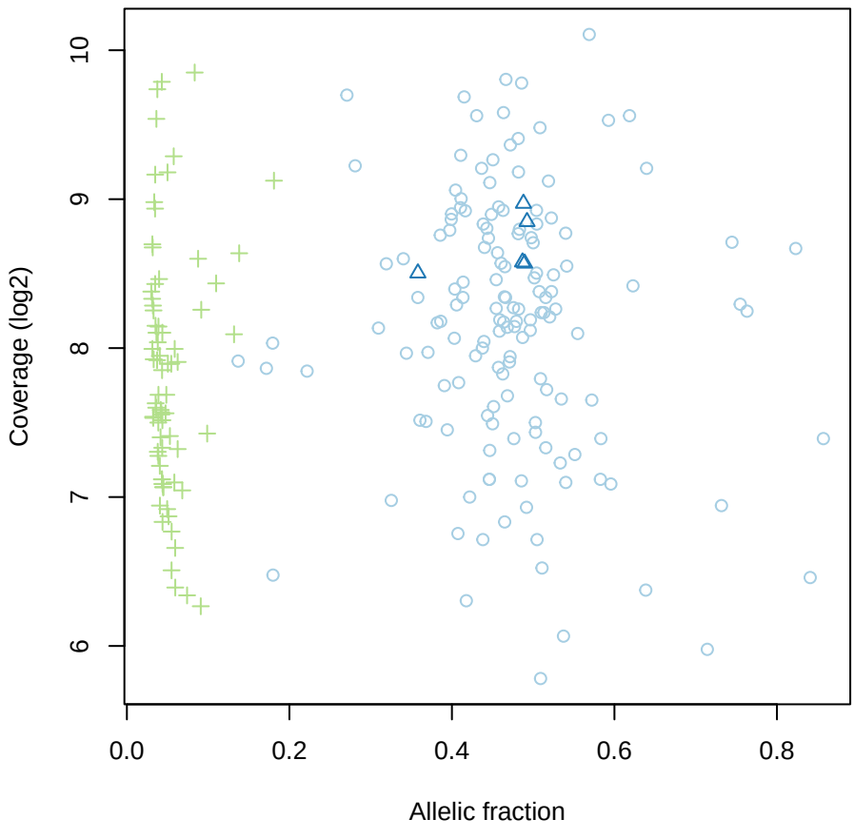

Purity: 0.71 Tumor ploidy: 3.056
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

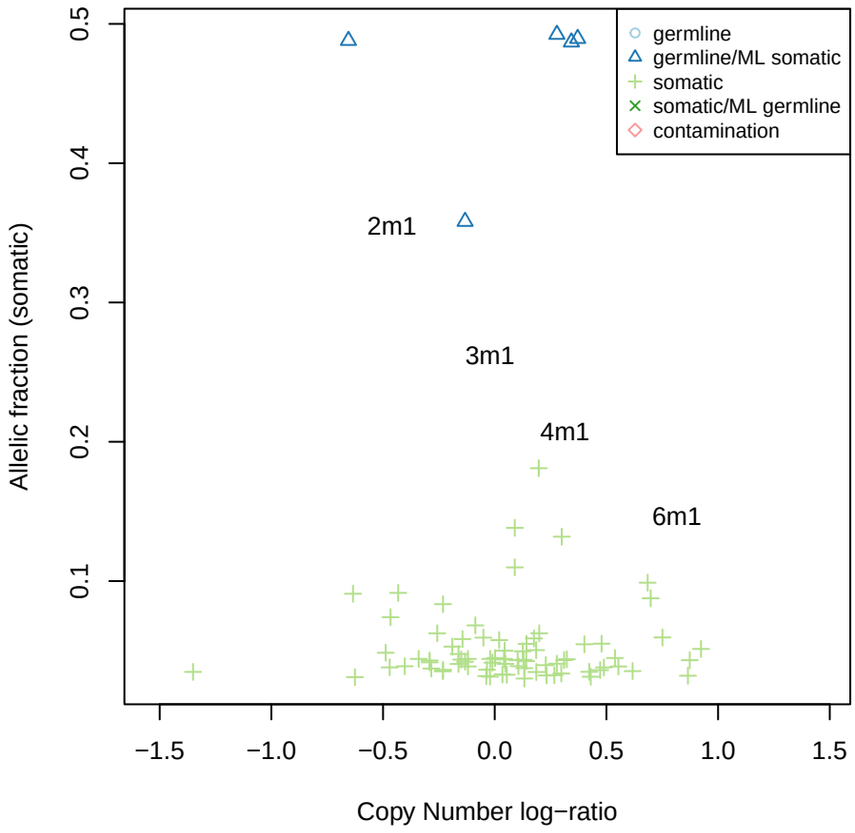

Purity: 0.71 Tumor ploidy: 3.056 SNV log−likelihood: −723.66 GoF: 48.1% Mean coverage: 497;317
1 2 3 4 5 6 8 9 10 11 12 13 14 16 17 18 19
B−Allele Frequency
0.2 0.4 0.6 0.8
0 50 100 150
SNV Index

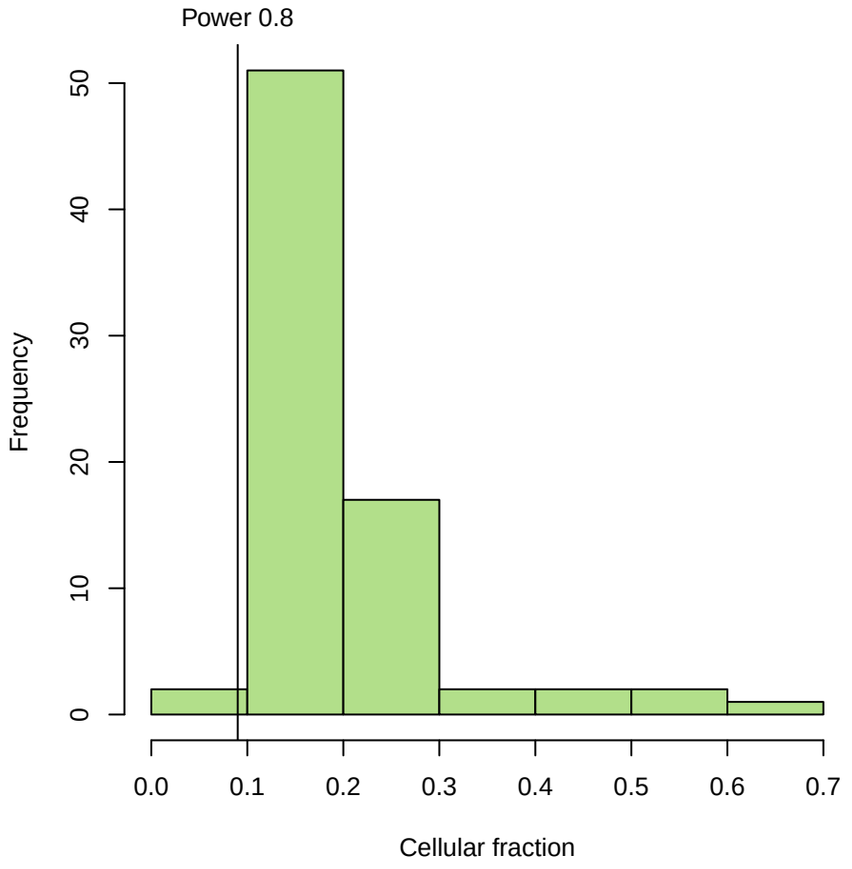

SCNA−fit log−likelihood: −7688.27
Copy Number log−ratio
−2 −1 0 1 2
1 2 3 4 6
0 50 100 150
SNV Index


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


2m2
4m3
3m2
7m4
4m2
6m3
7m3
3m1
4m1
1m0
6m1
2m0
Allelic fraction (germline)
Copy Number log−ratio


Coverage (log2)
Allelic fraction


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


Power 0.8
Frequency
Cellular fraction