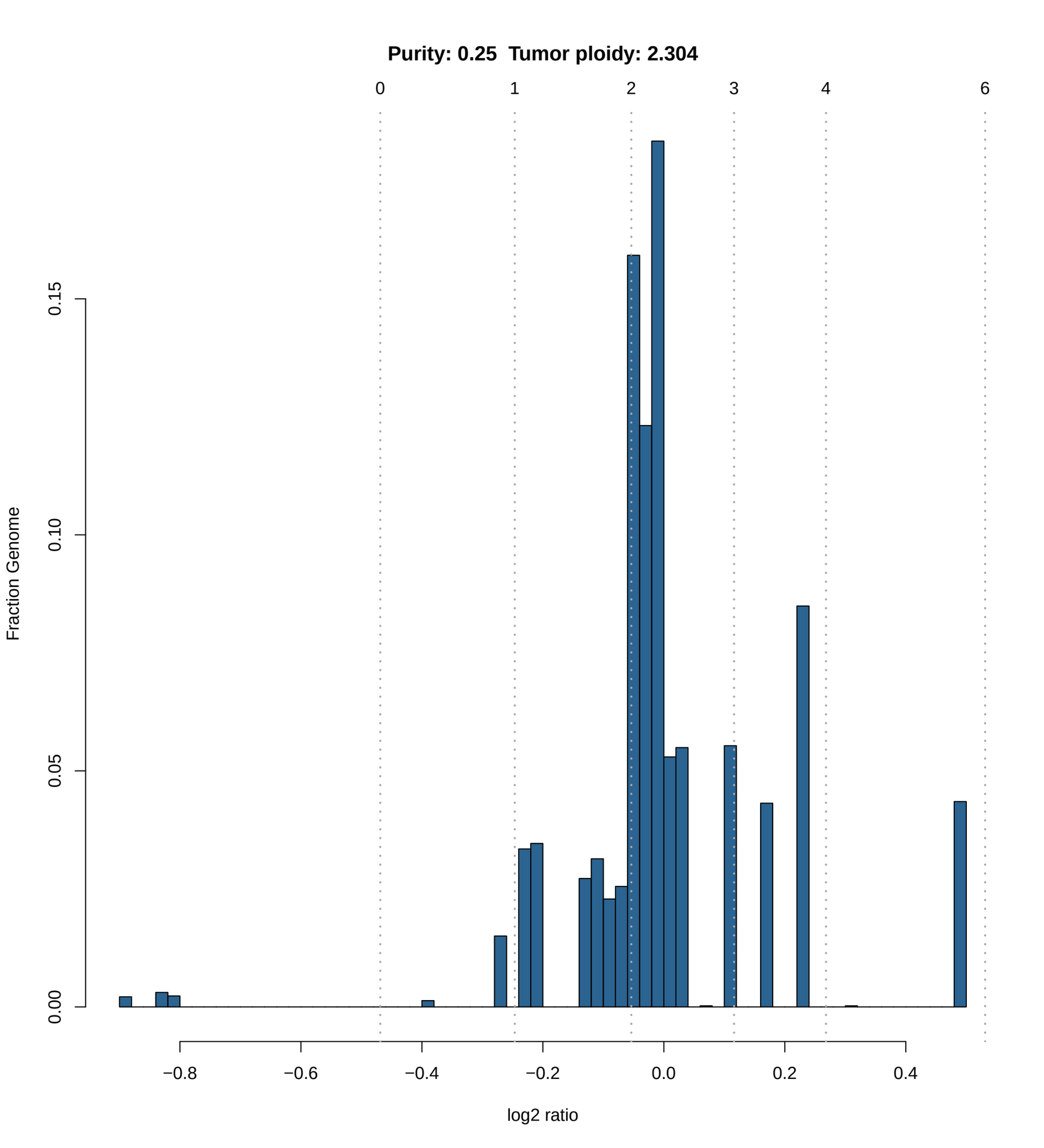
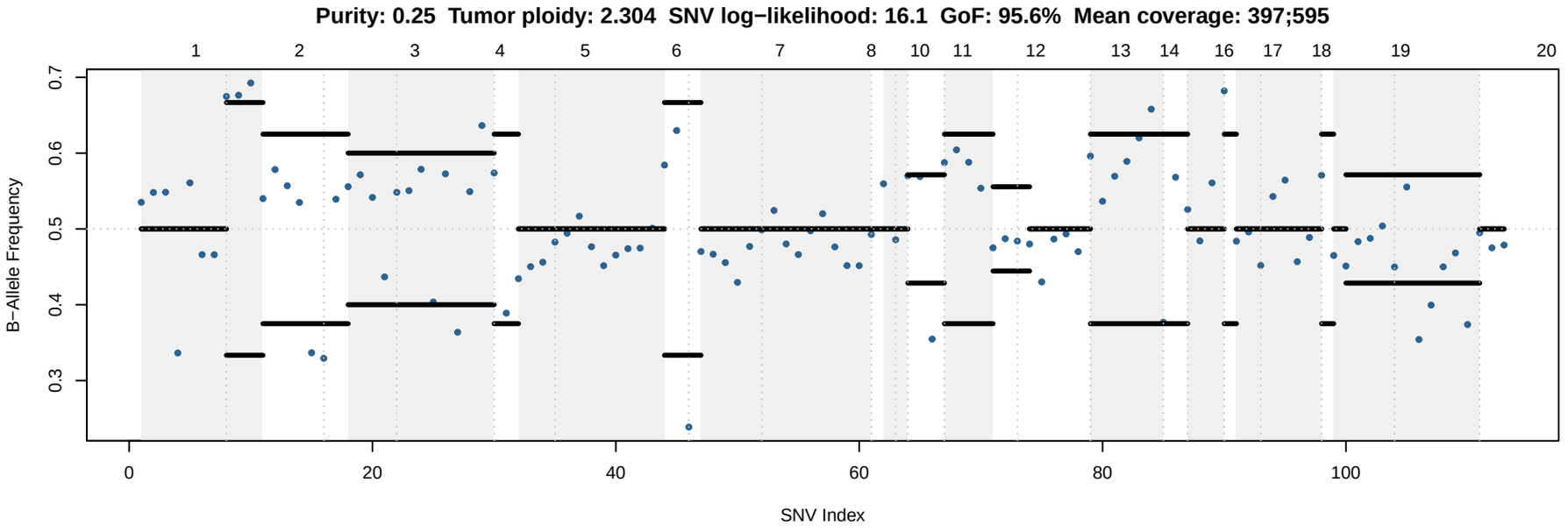
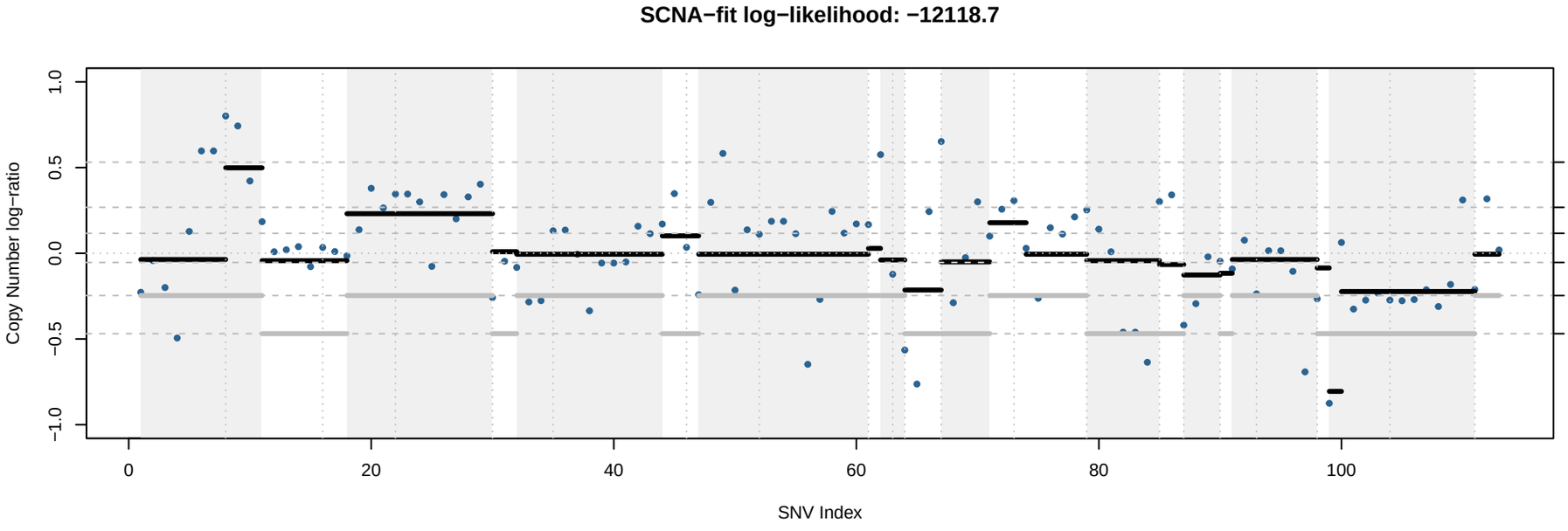
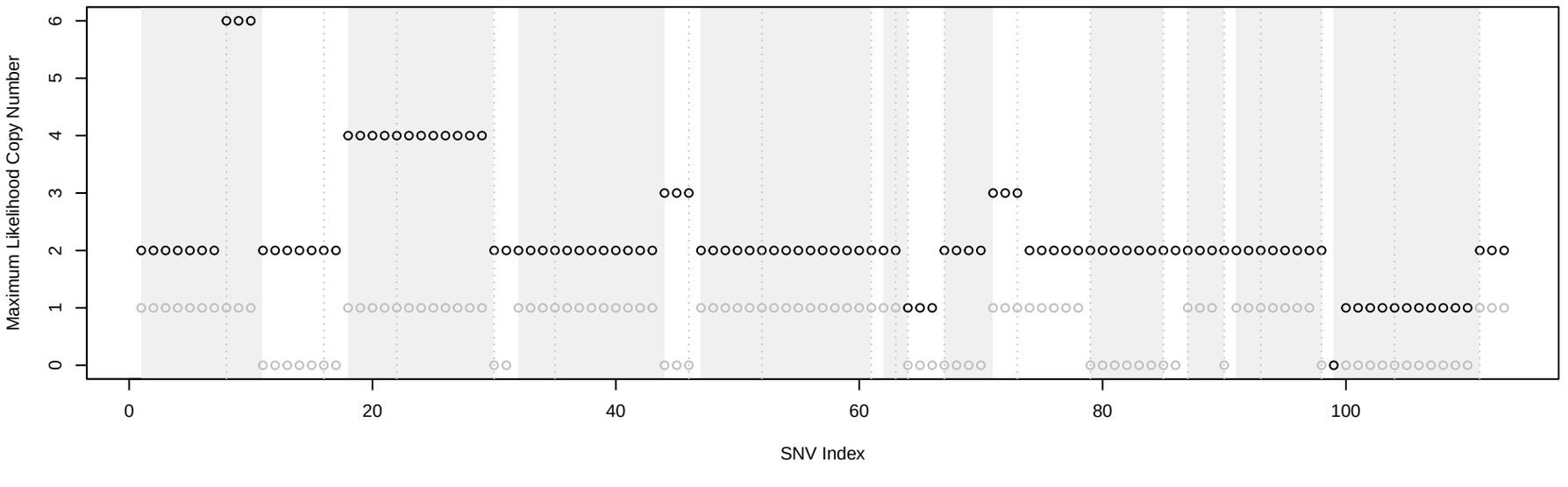
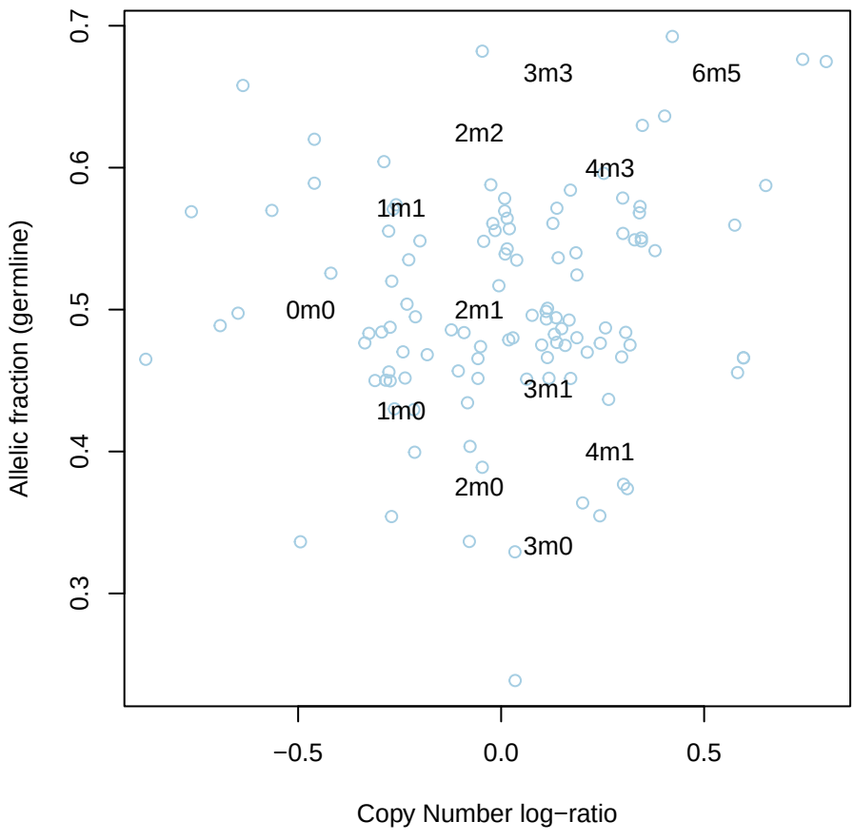
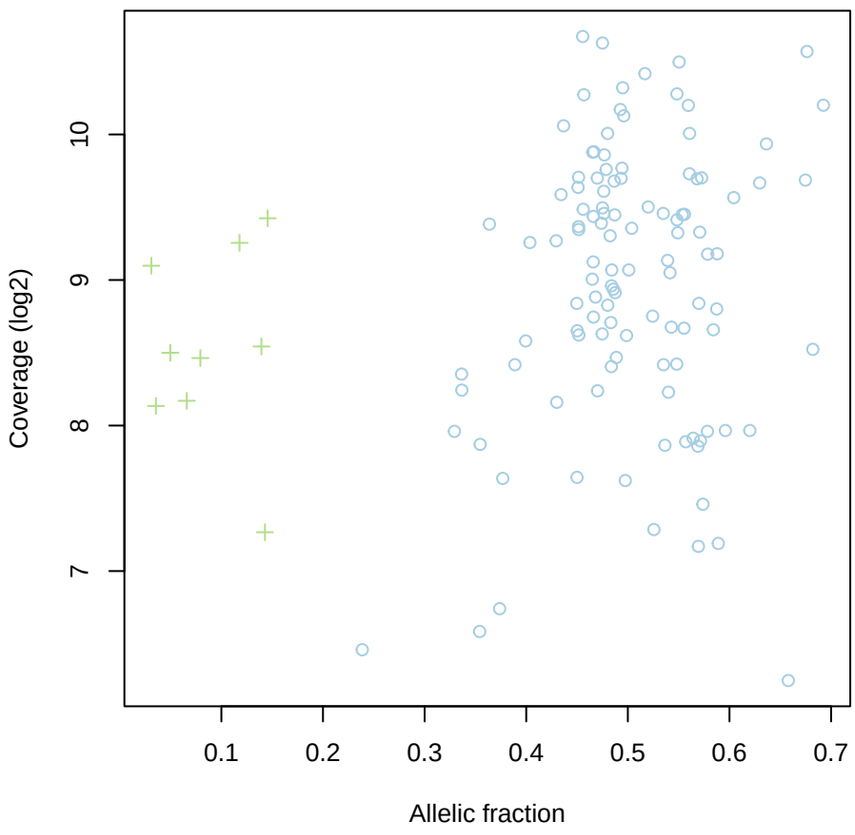

Purity: 0.25 Tumor ploidy: 2.304
0
1
2
3
4
6
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

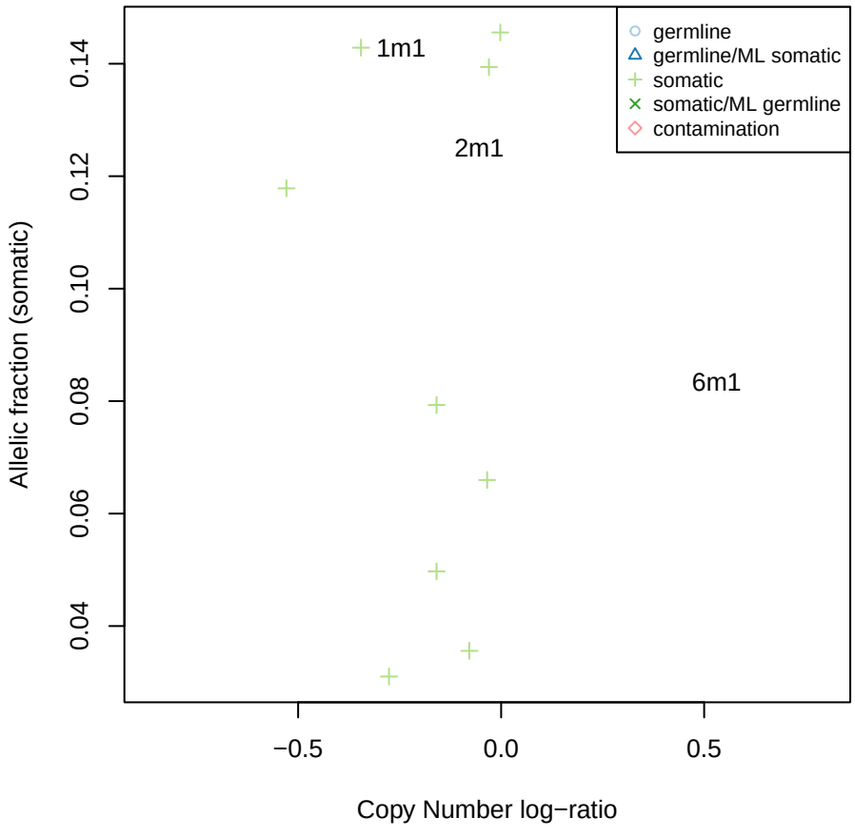

Purity: 0.25 Tumor ploidy: 2.304 SNV log−likelihood: 16.1 GoF: 95.6% Mean coverage: 397;595
B−Allele Frequency
SNV Index

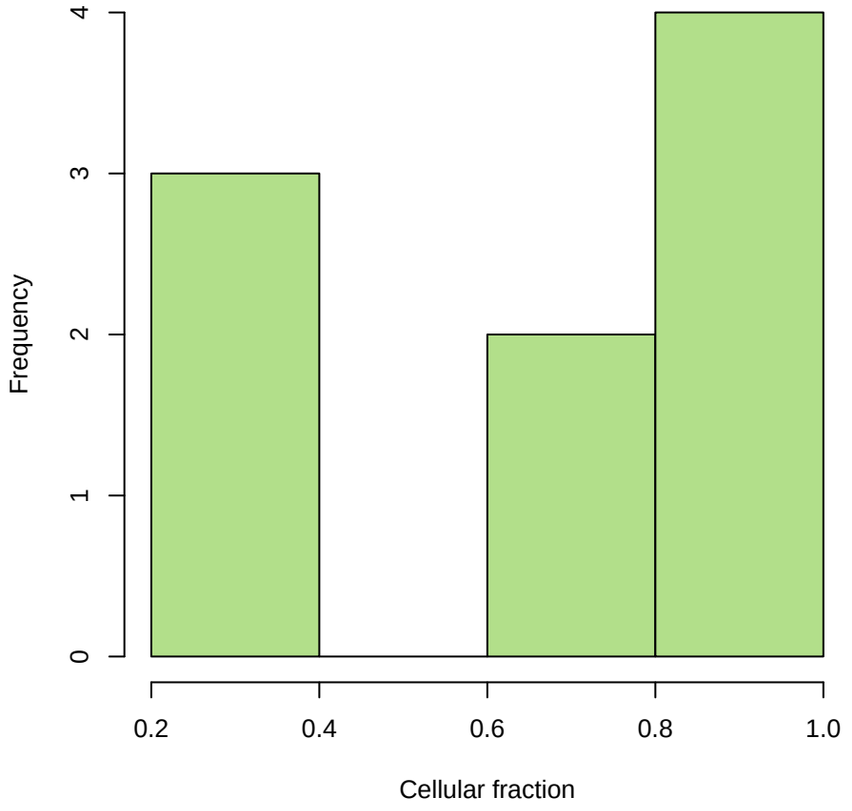

SCNA−fit log−likelihood: −12118.7
Copy Number log−ratio
SNV Index

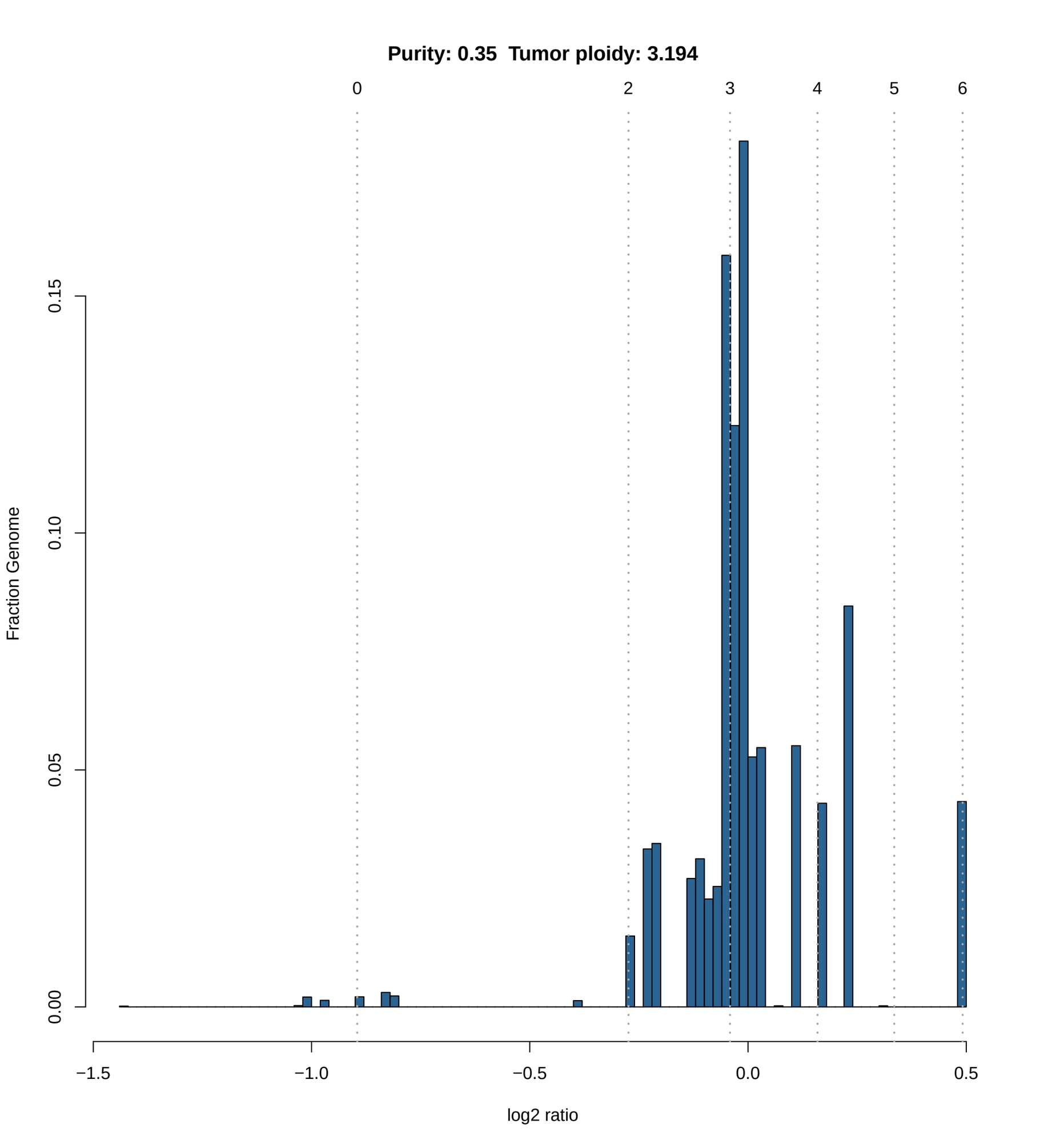

Maximum Likelihood Copy Number
SNV Index

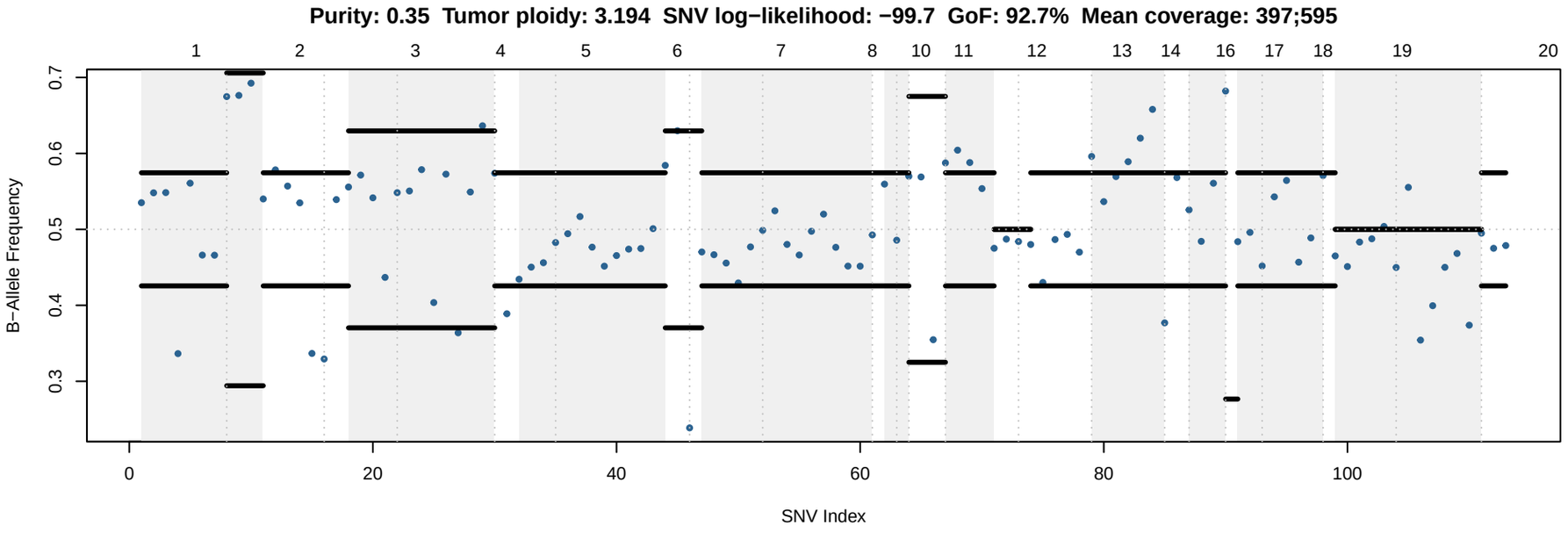

Allelic fraction (germline)
Copy Number log−ratio
0m0
1m1
2m2
3m3
4m3
6m5
2m1
3m1
1m0
4m1
2m0
3m0

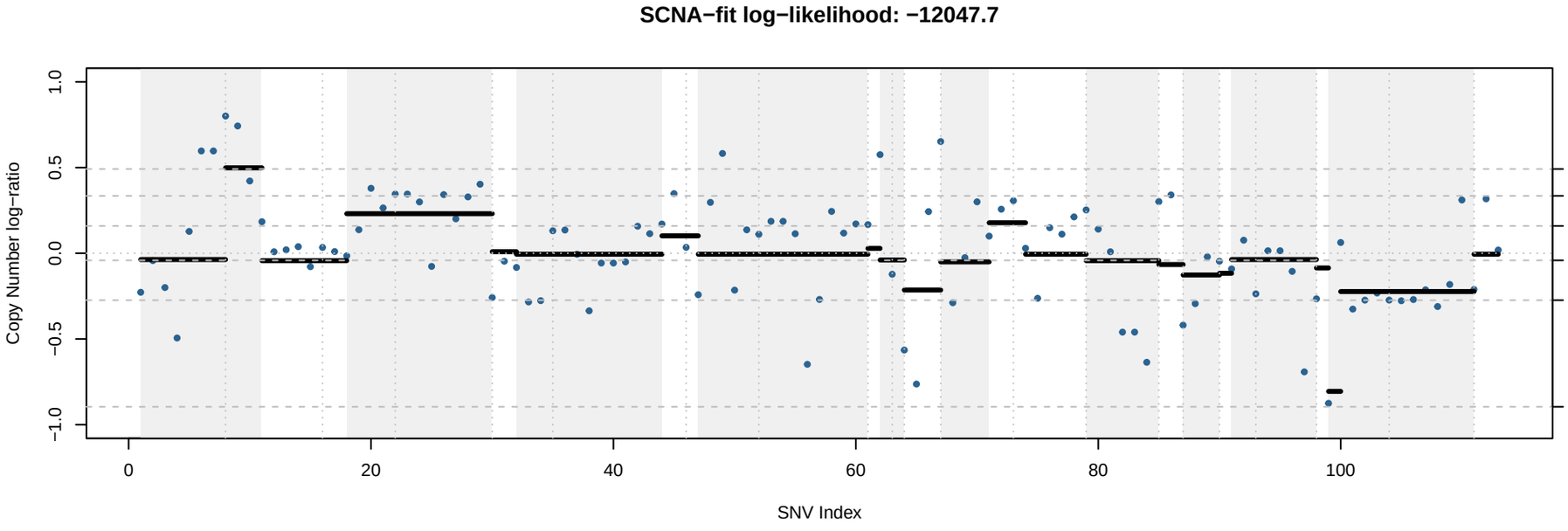

Coverage (log2)
Allelic fraction

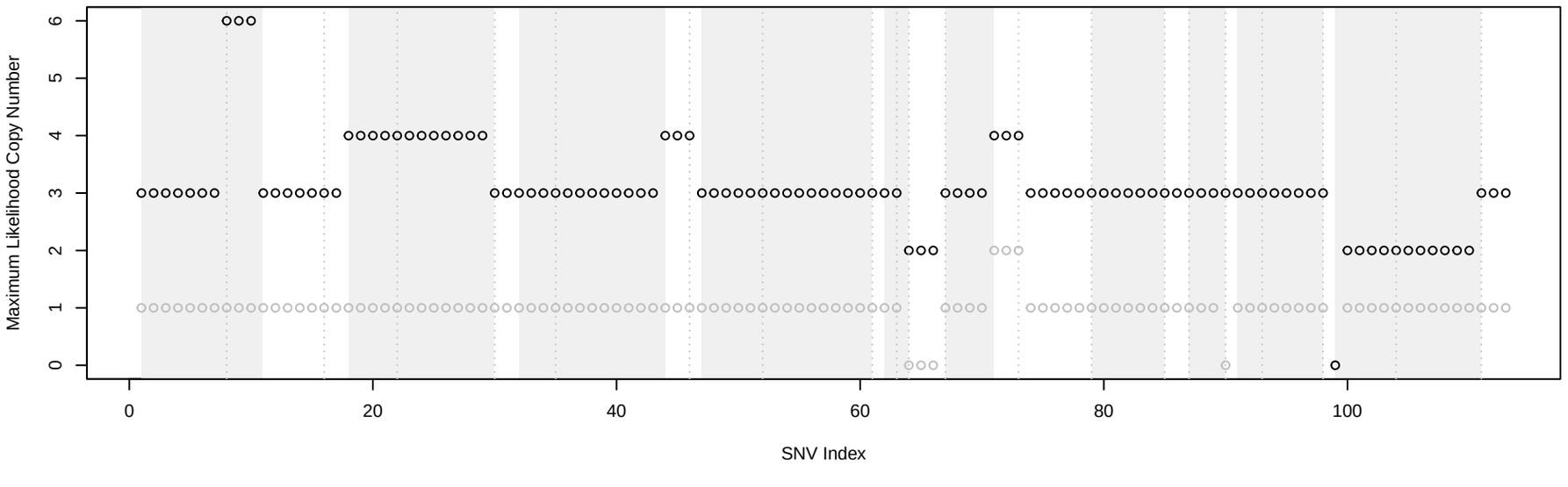

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
6m1

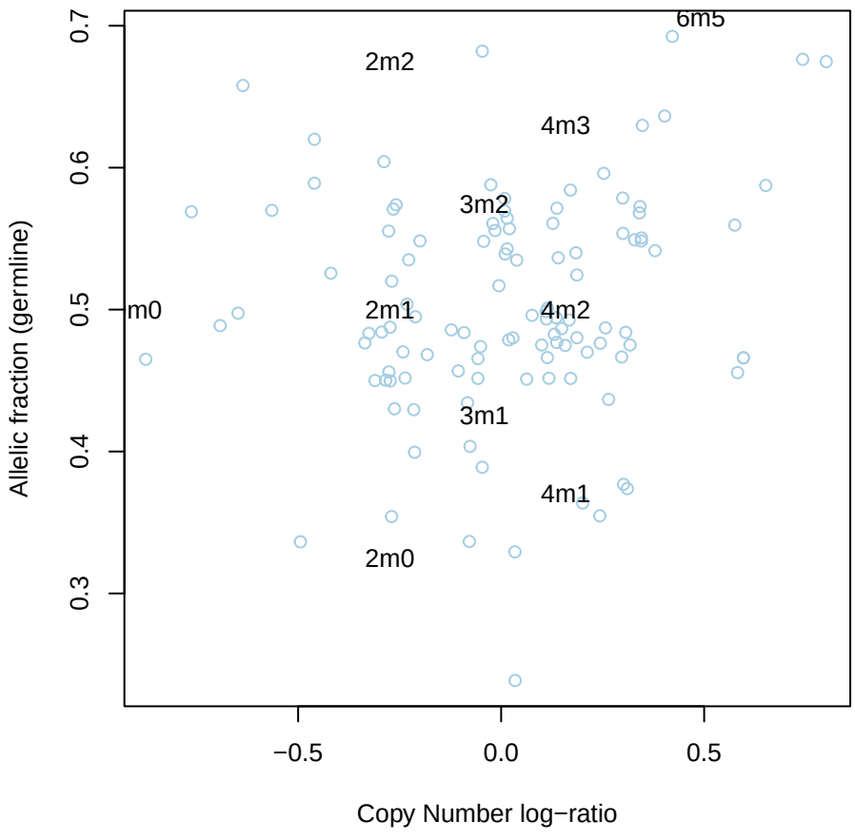

Frequency
Cellular fraction

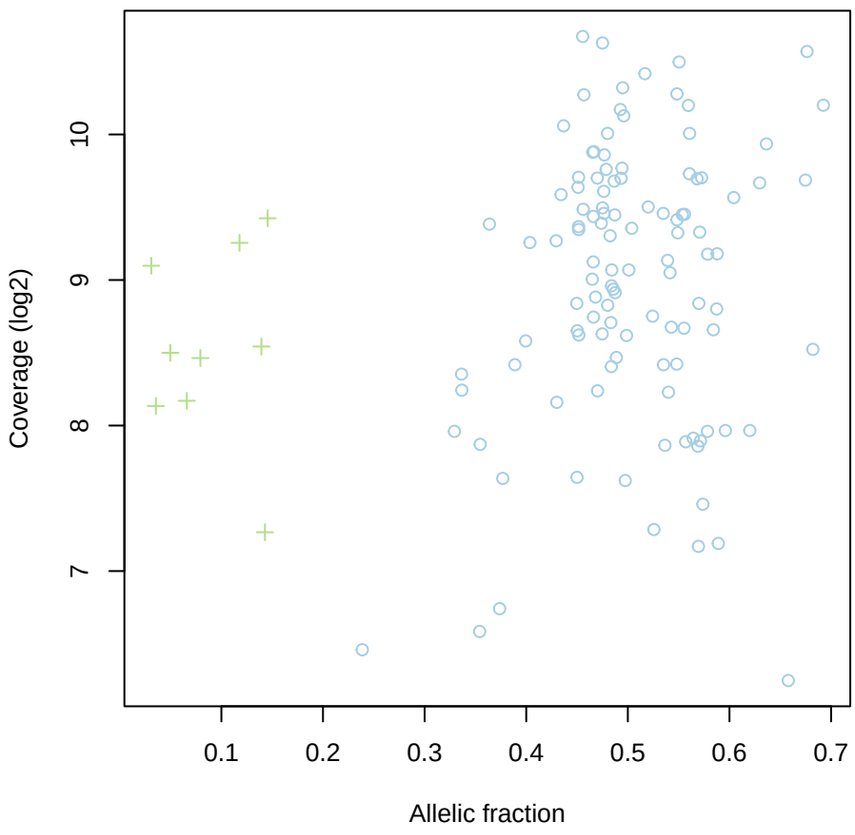

Purity: 0.35 Tumor ploidy: 3.194
0
2
3
4
5
6
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

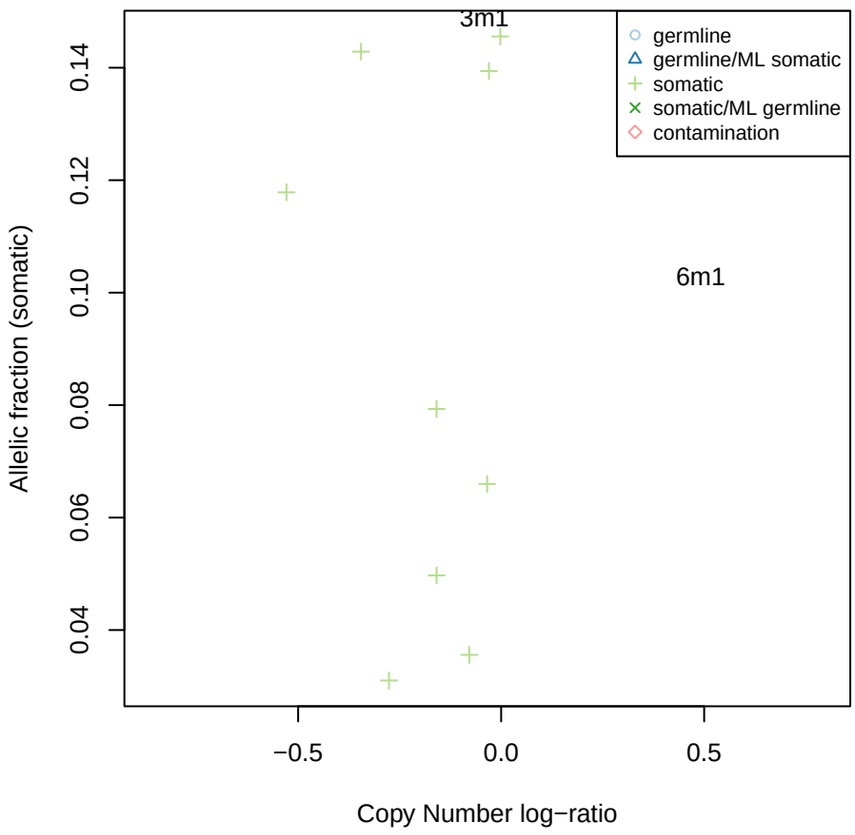

Purity: 0.35 Tumor ploidy: 3.194 SNV log−likelihood: −99.7 GoF: 92.7% Mean coverage: 397;595
B−Allele Frequency
SNV Index

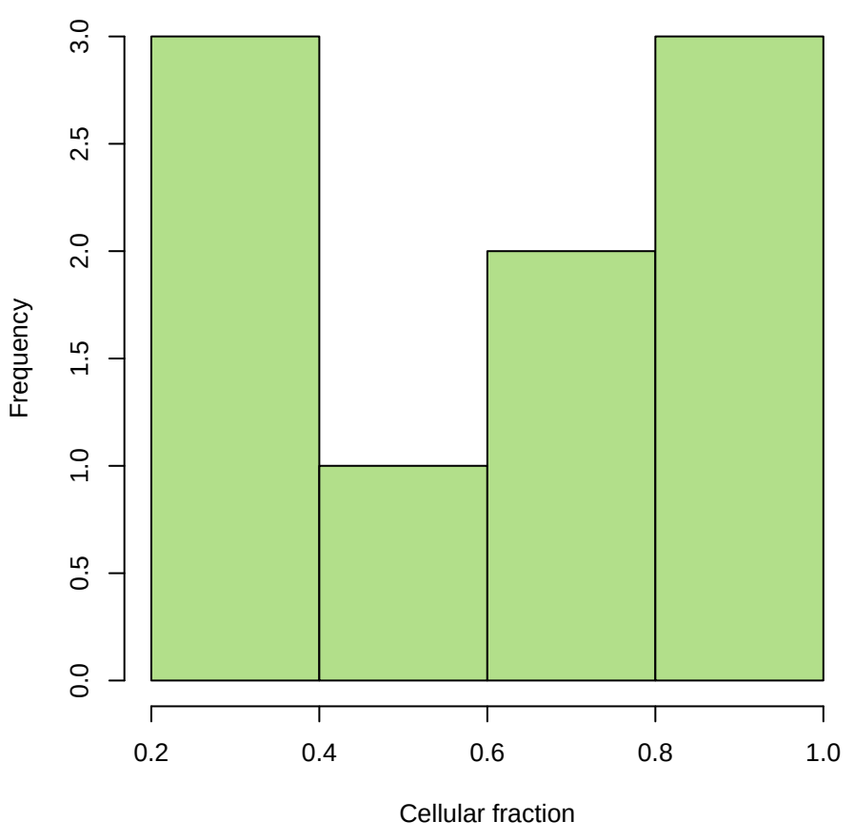

SCNA−fit log−likelihood: −12047.7
Copy Number log−ratio
SNV Index

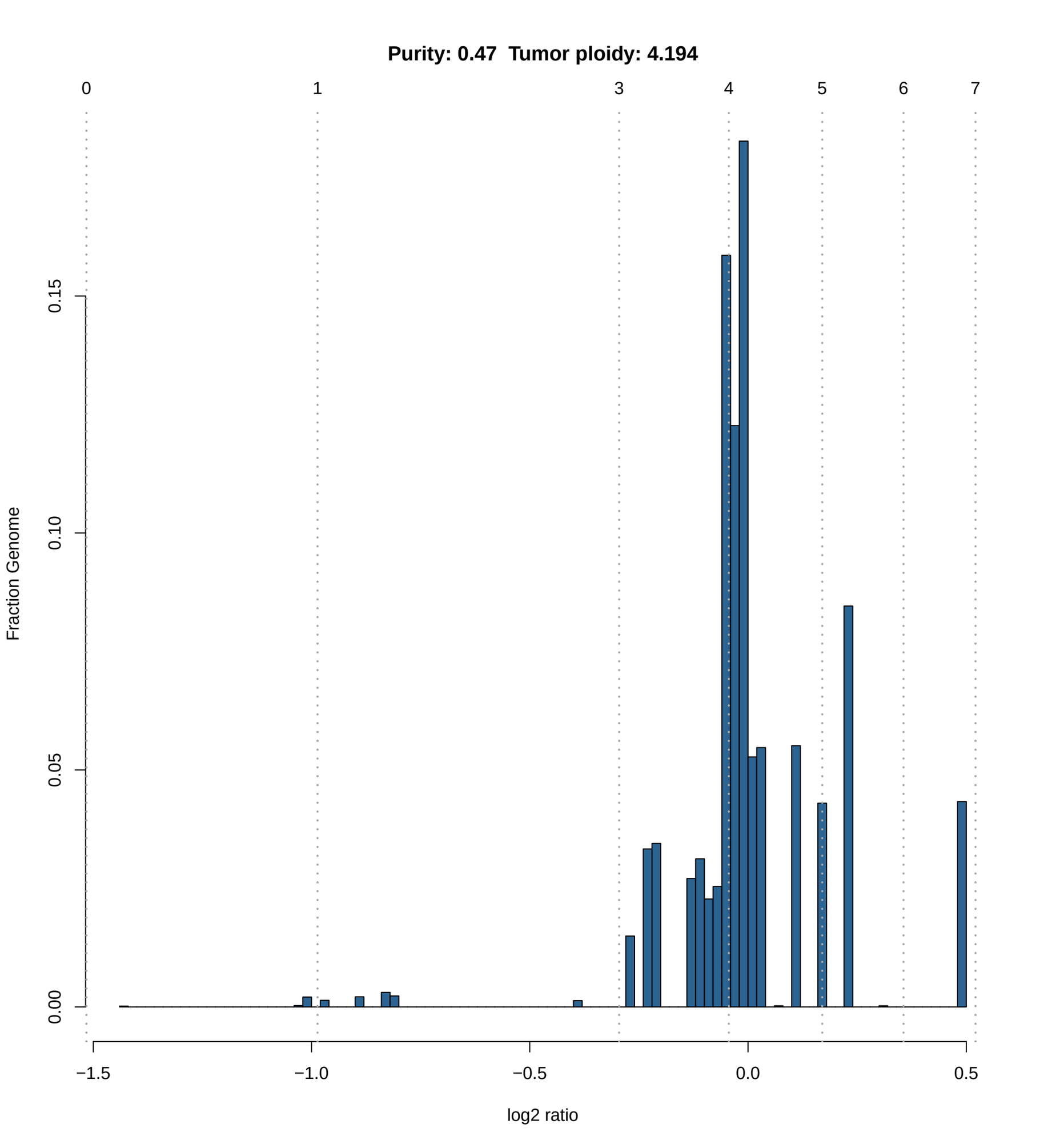

Maximum Likelihood Copy Number
SNV Index

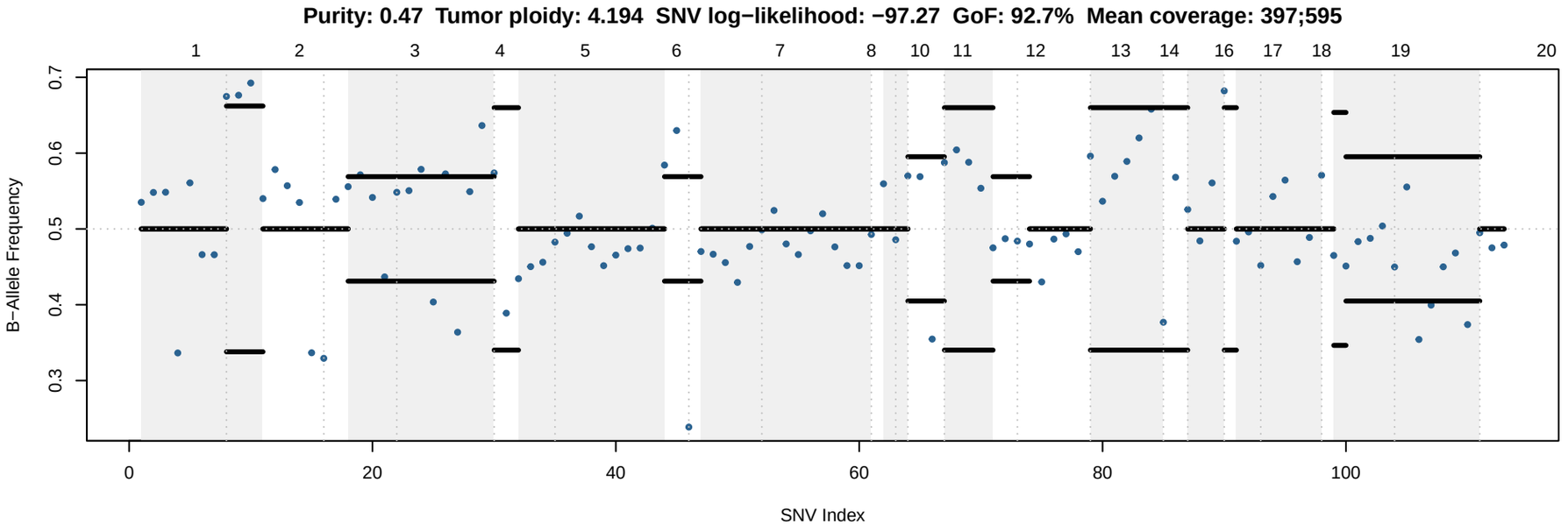

Allelic fraction (germline)
Copy Number log−ratio
6m5
2m2
4m3
3m2
m0
2m1
4m2
3m1
4m1
2m0

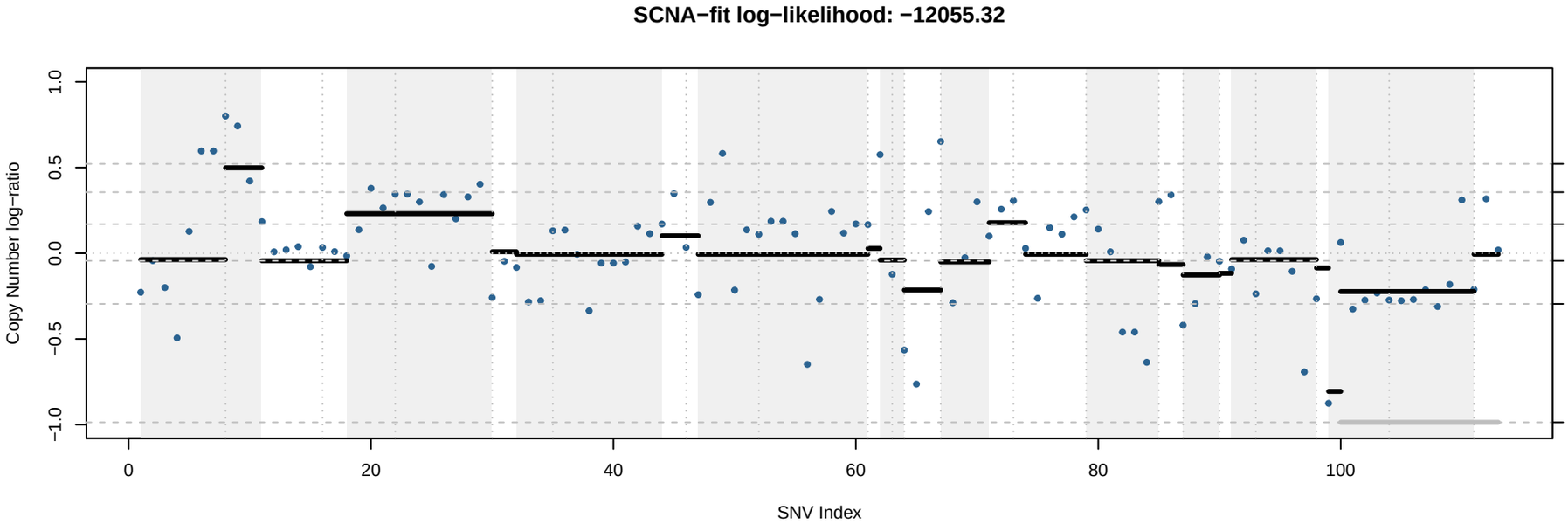

Coverage (log2)
Allelic fraction

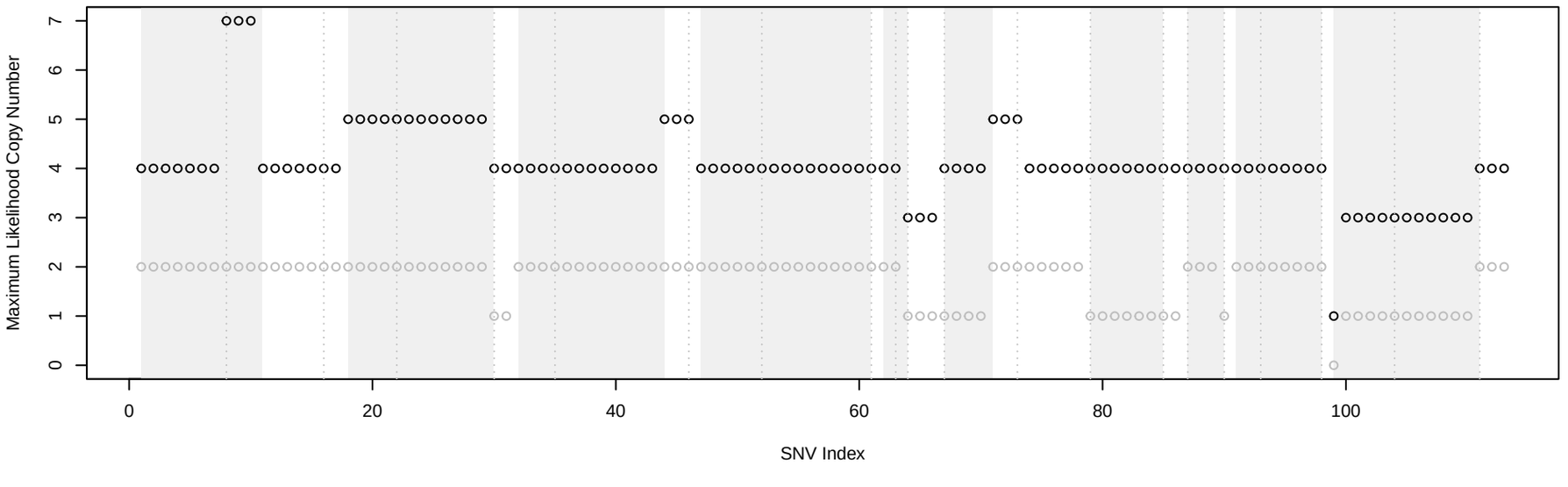

Allelic fraction (somatic)
Copy Number log−ratio
3m1
6m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

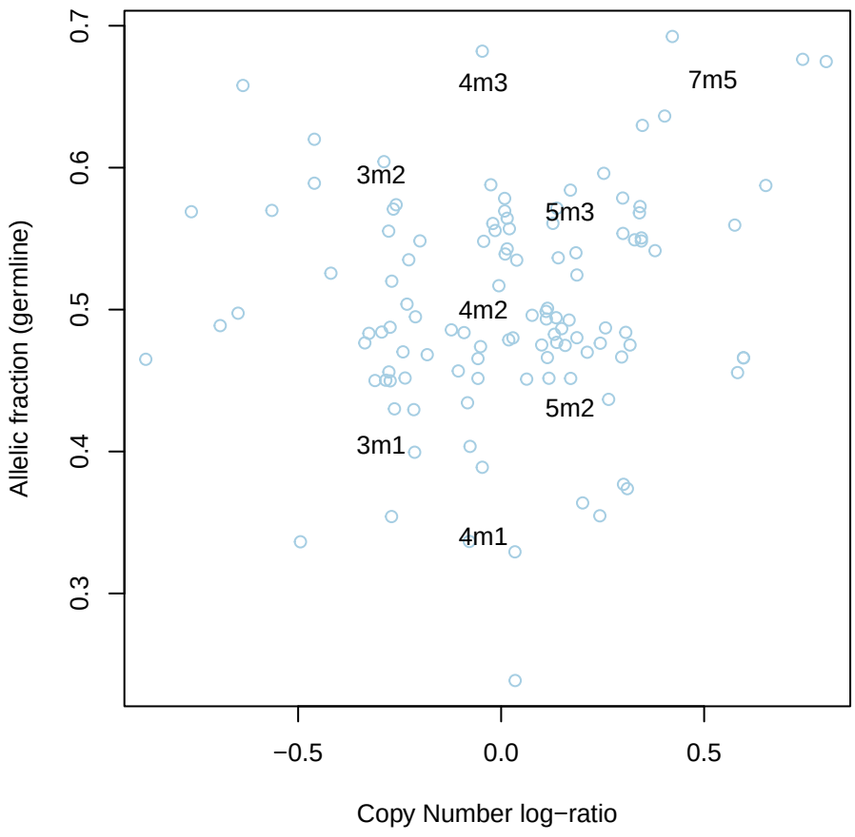

Frequency
Cellular fraction

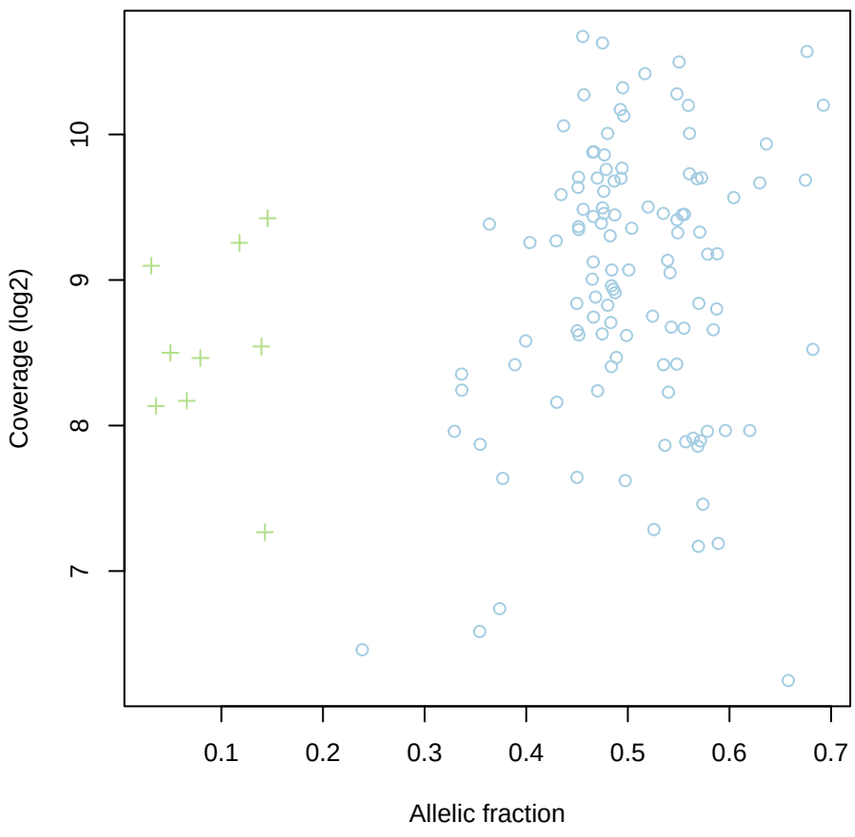

Purity: 0.47 Tumor ploidy: 4.194
0
1
3
4
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

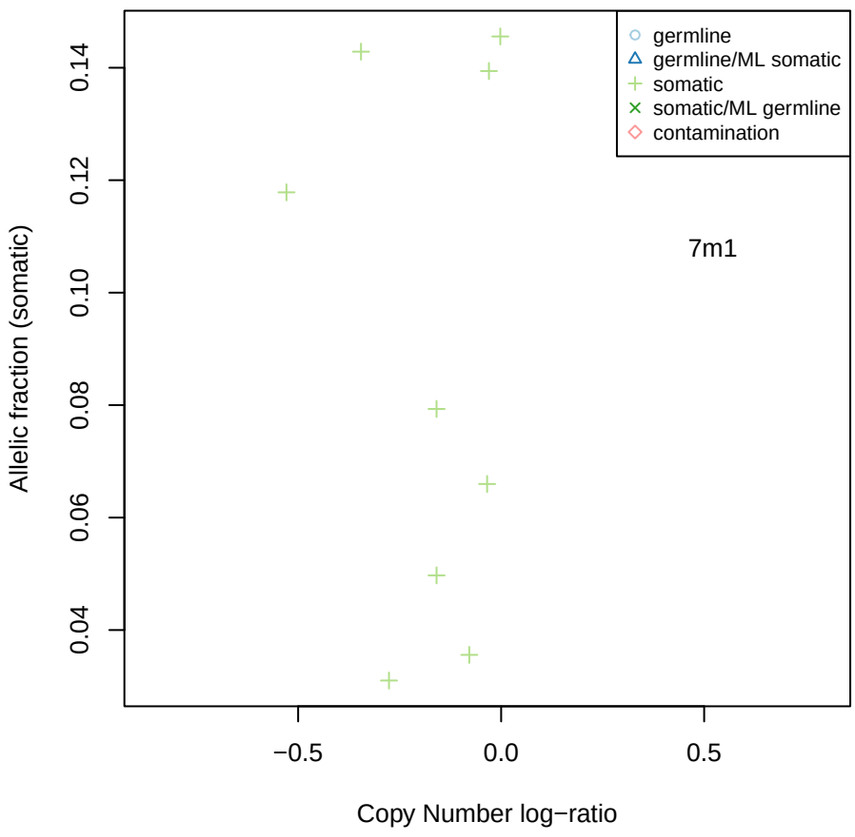

Purity: 0.47 Tumor ploidy: 4.194 SNV log−likelihood: −97.27 GoF: 92.7% Mean coverage: 397;595
B−Allele Frequency
SNV Index

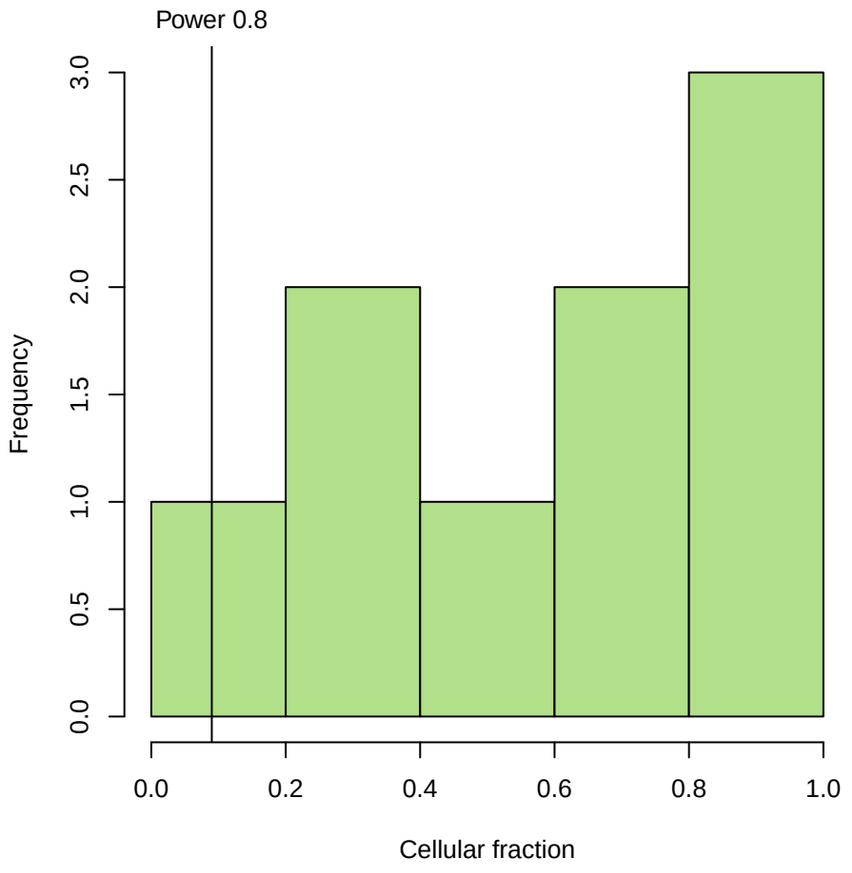

SCNA−fit log−likelihood: −12055.32
Copy Number log−ratio
SNV Index

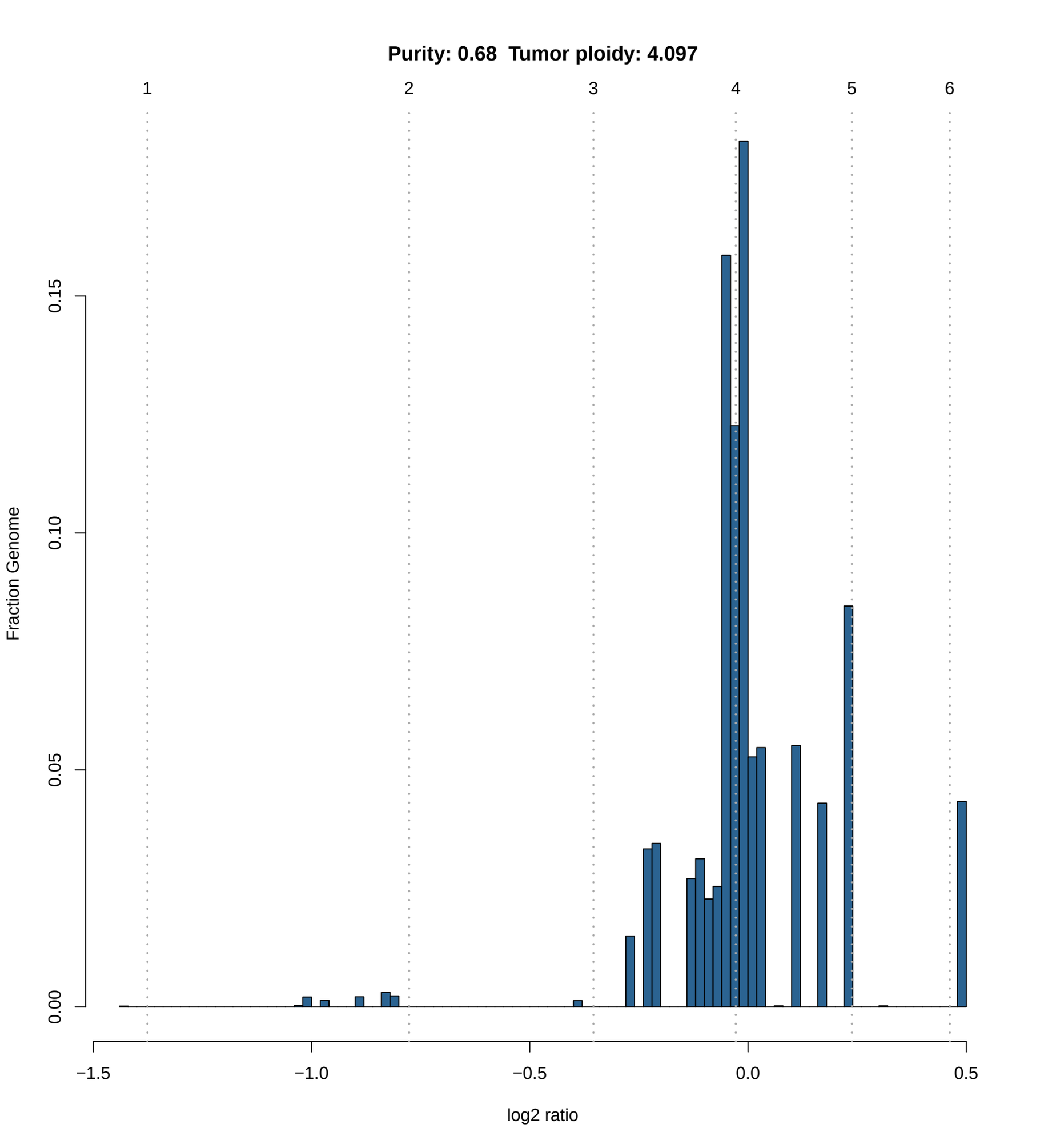

Maximum Likelihood Copy Number
SNV Index

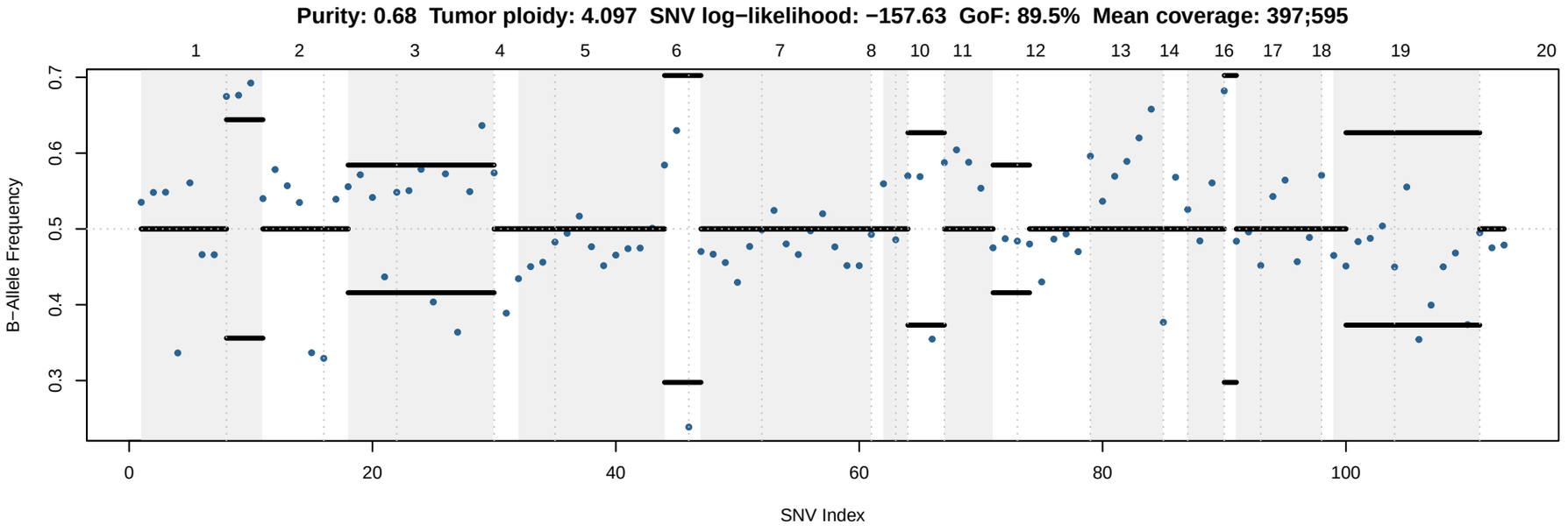

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
4m3
7m5
3m2
5m3
4m2
5m2
3m1
4m1
−0.5
0.0
0.5
Copy Number log−ratio

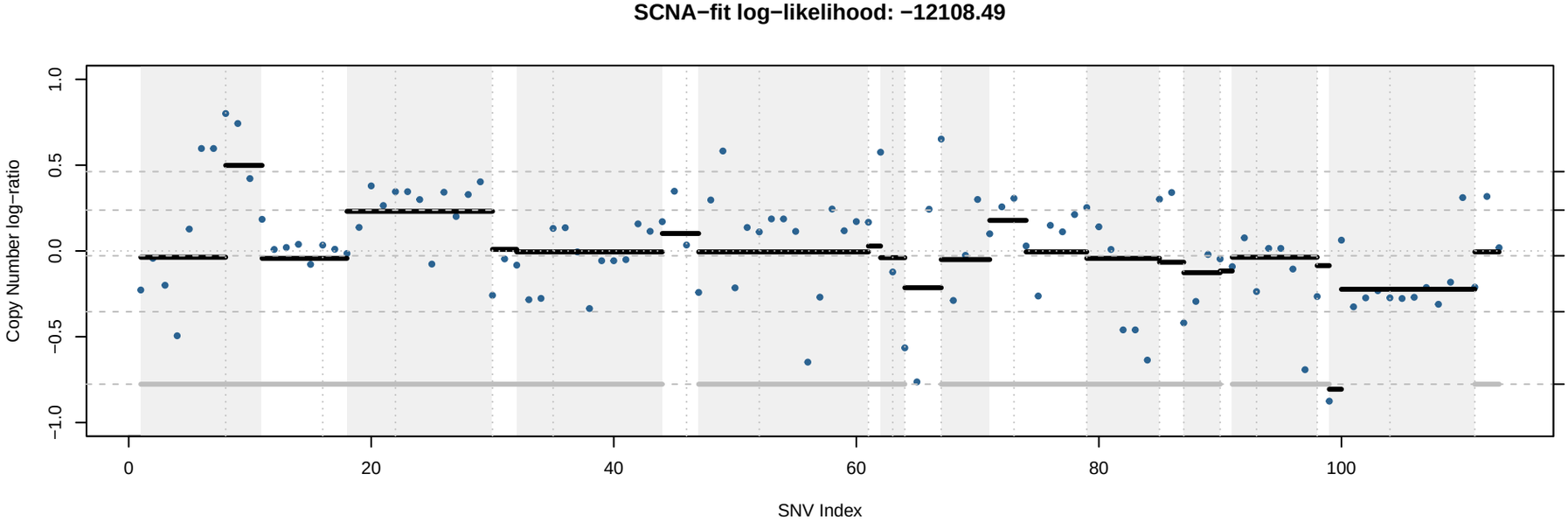

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

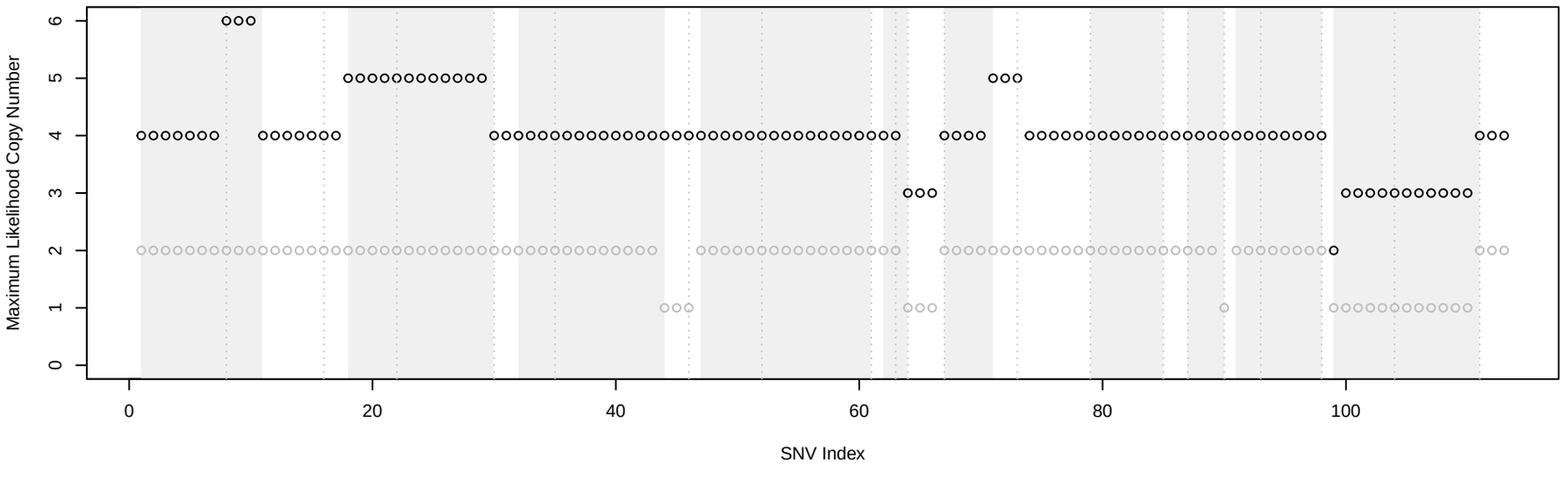

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
7m1
−0.5
0.0
0.5
Copy Number log−ratio

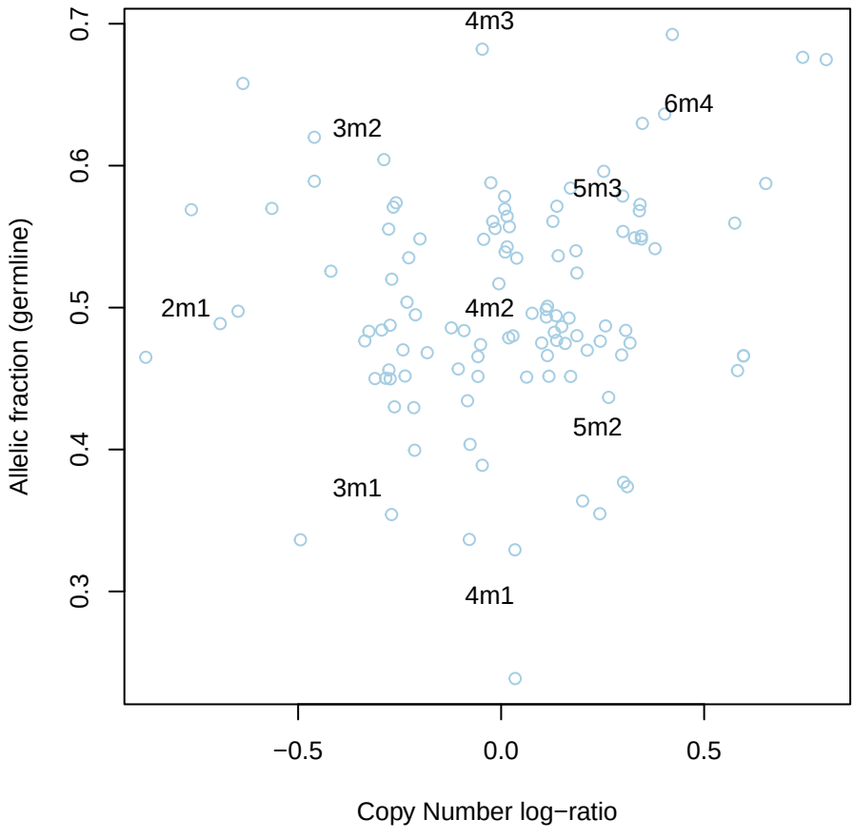

Power 0.8
Frequency
0.0
0.5
1.0
1.5
2.0
2.5
3.0
0.0
0.2
0.4
0.6
0.8
1.0
Cellular fraction

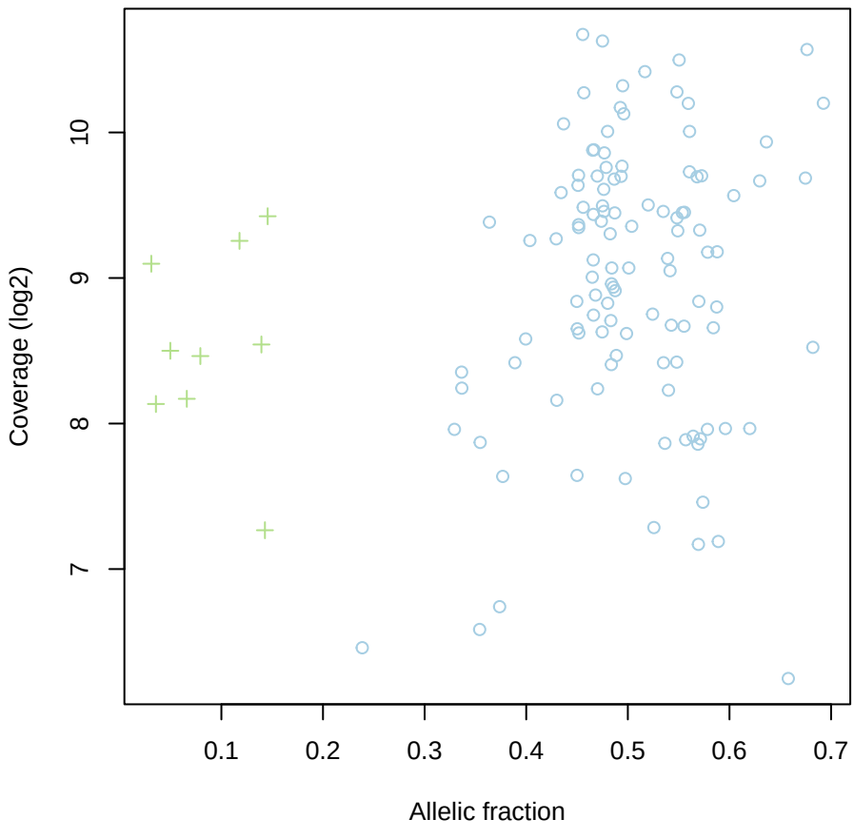

Purity: 0.68 Tumor ploidy: 4.097
1
2
3
4
5
6
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

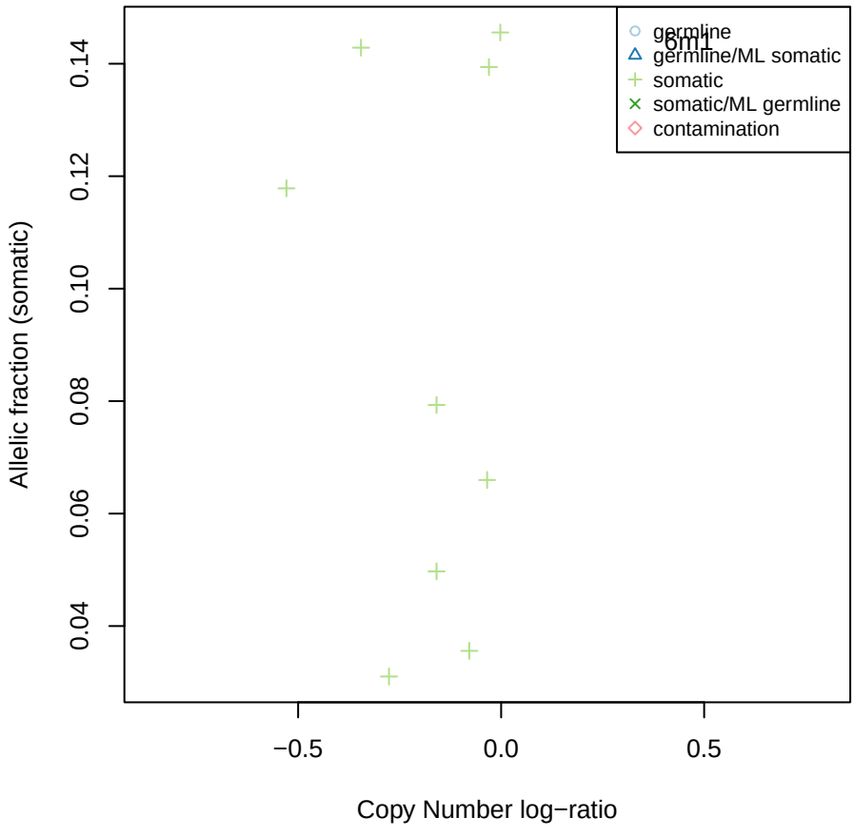

Purity: 0.68 Tumor ploidy: 4.097 SNV log−likelihood: −157.63 GoF: 89.5% Mean coverage: 397;595
B−Allele Frequency
SNV Index

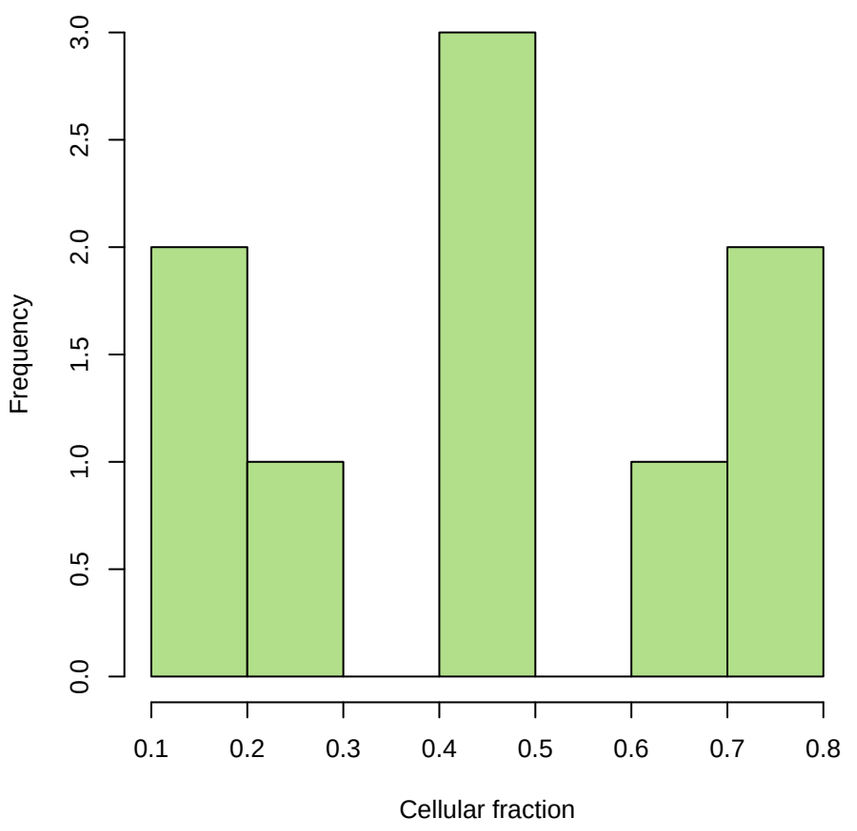

SCNA−fit log−likelihood: −12108.49
Copy Number log−ratio
SNV Index

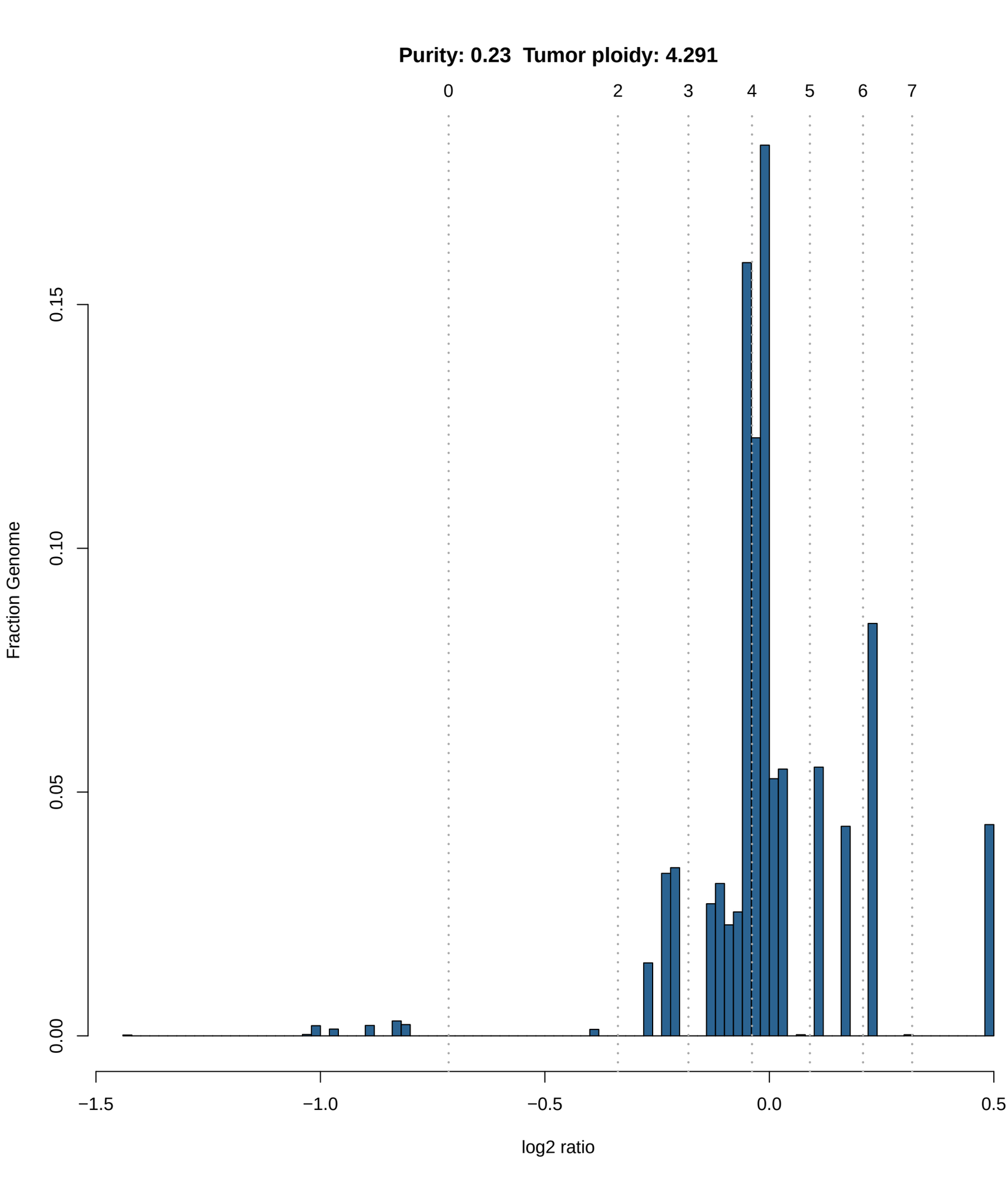

Maximum Likelihood Copy Number
SNV Index

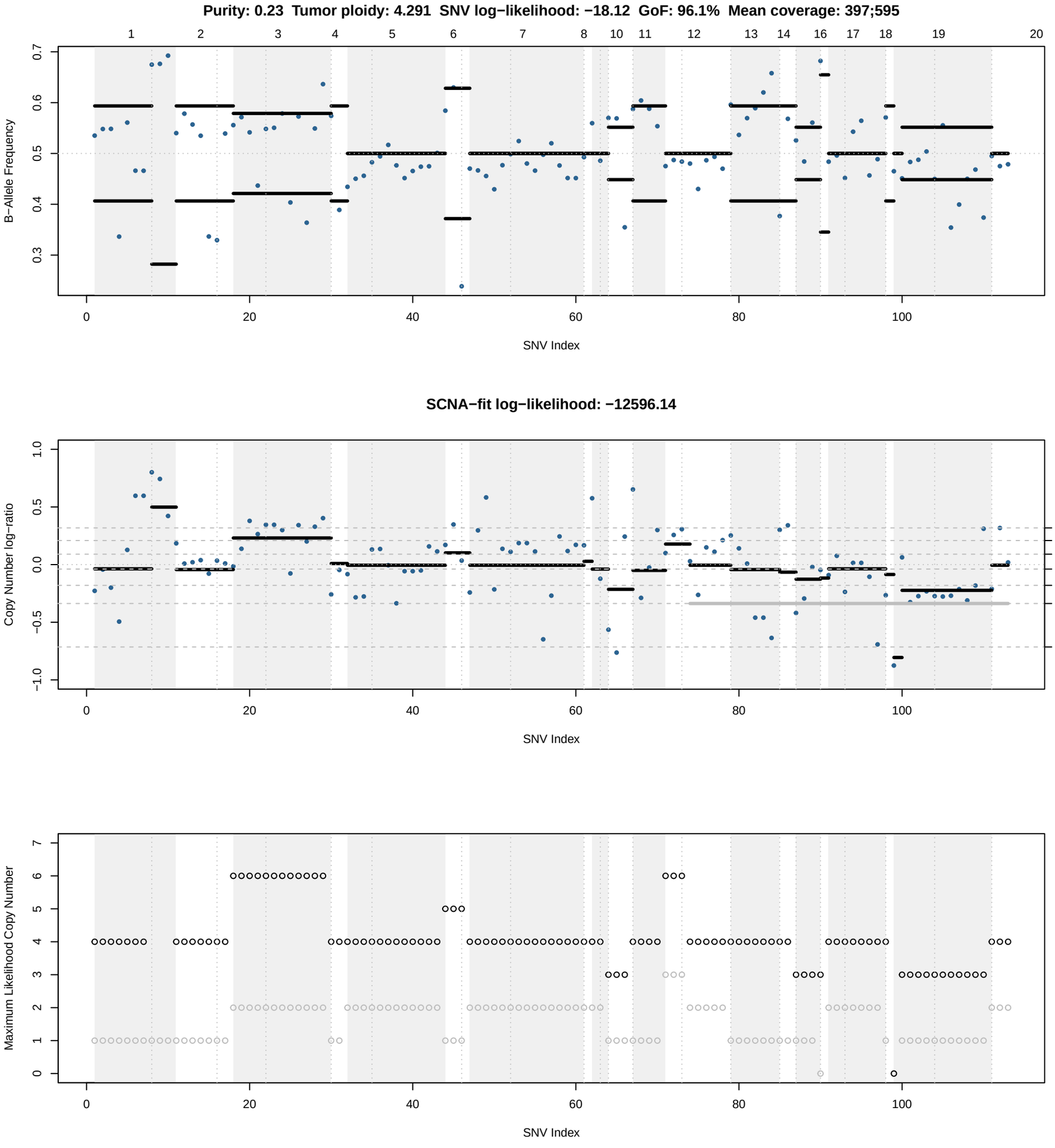

4m3
6m4
3m2
5m3
2m1
4m2
5m2
3m1
4m1
Allelic fraction (germline)
Copy Number log−ratio

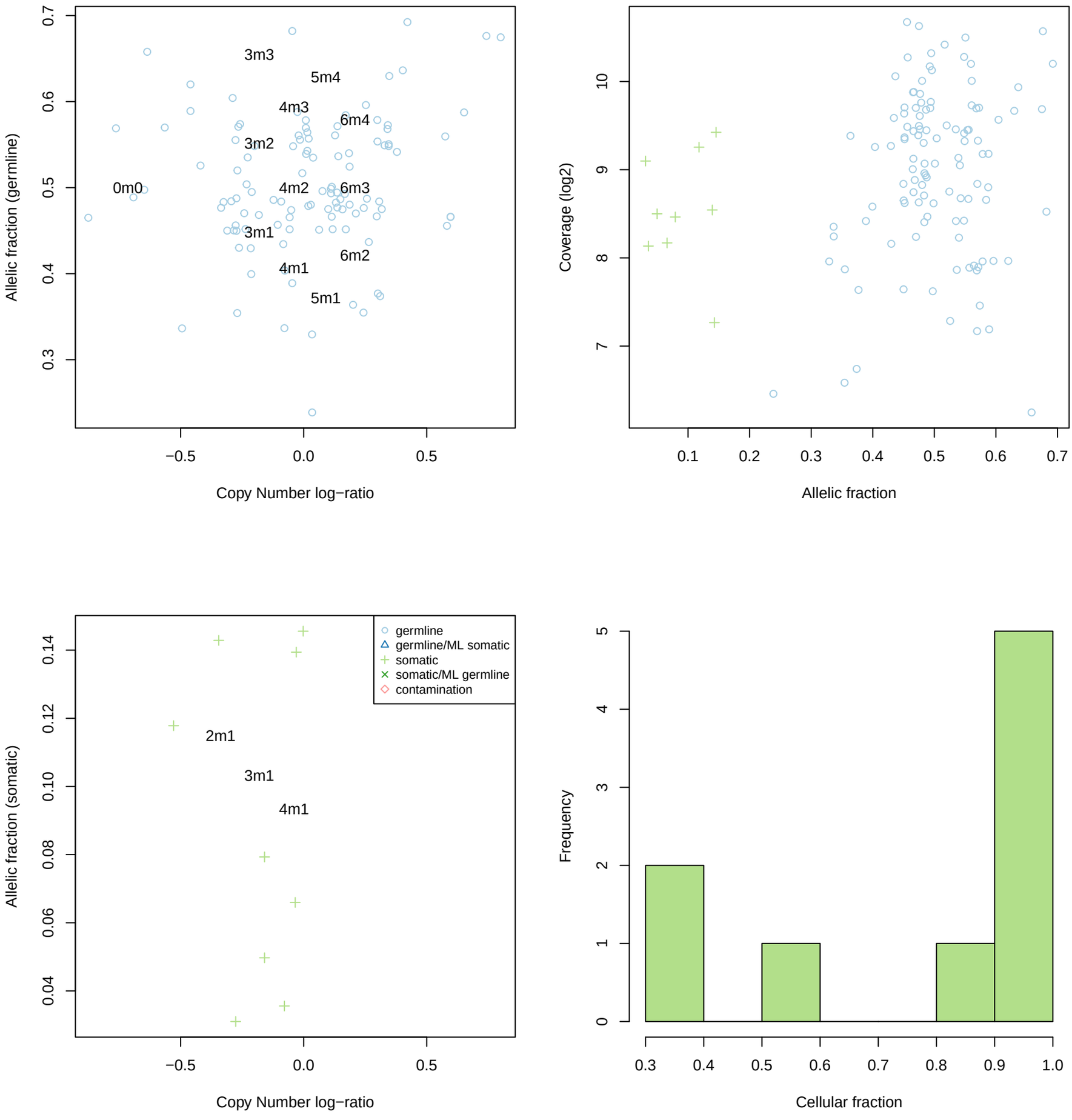

Coverage (log2)
Allelic fraction


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

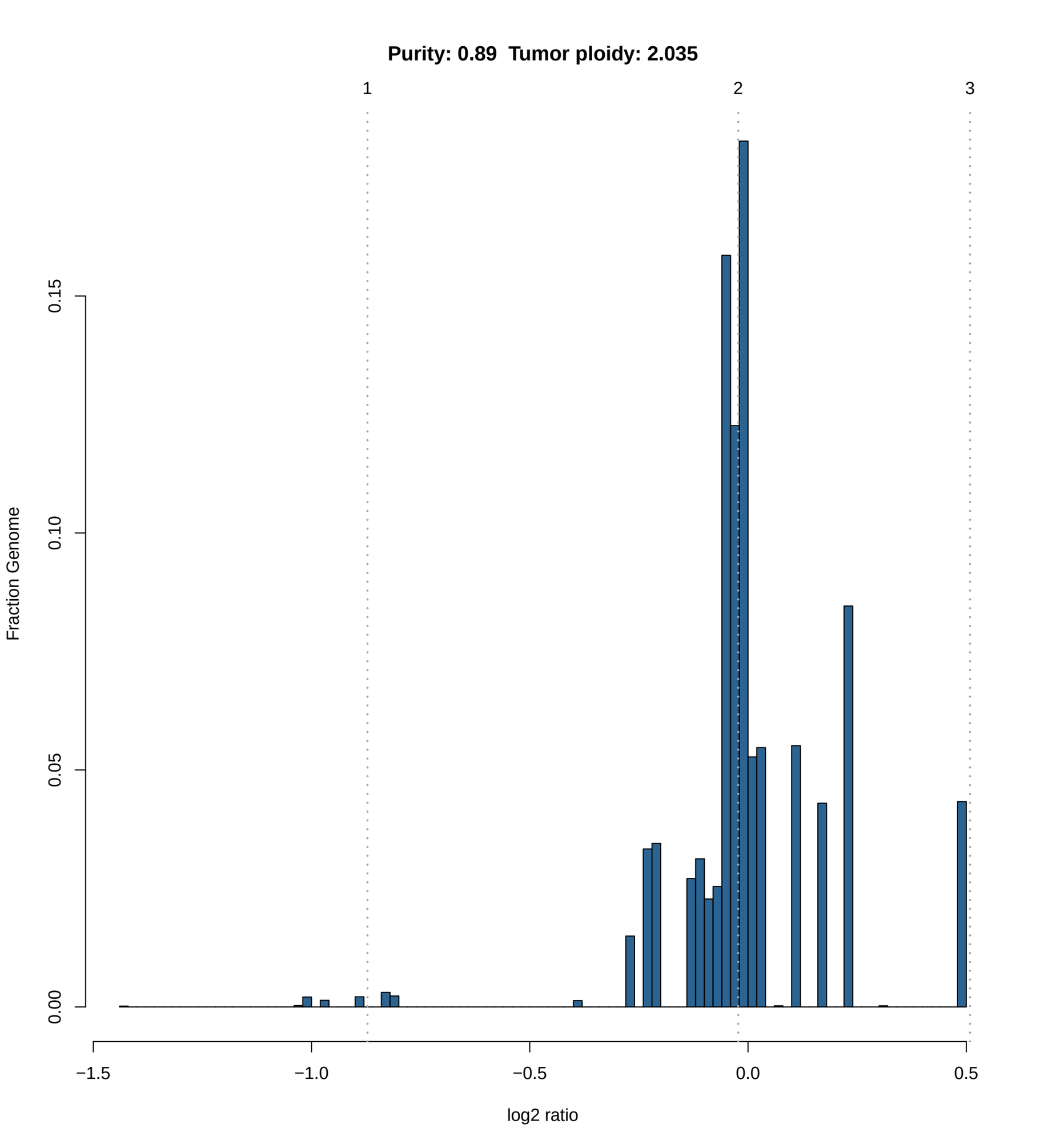

Frequency
Cellular fraction

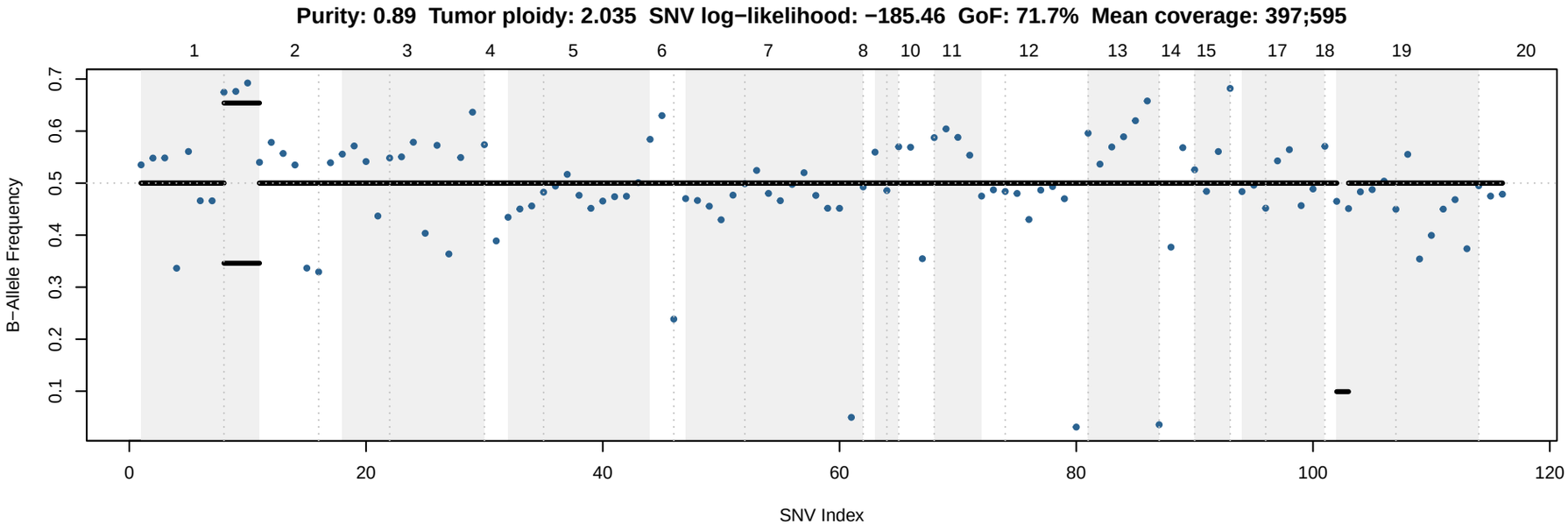

Purity: 0.23 Tumor ploidy: 4.291
0
2
3
4
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

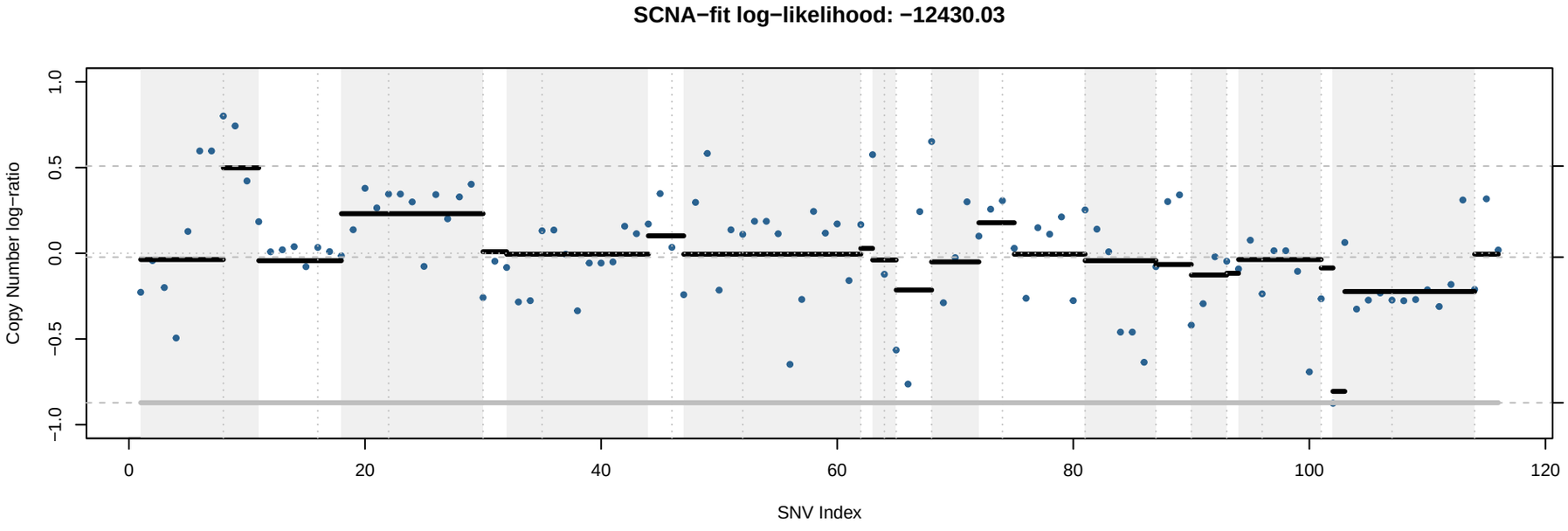

Purity: 0.23 Tumor ploidy: 4.291 SNV log−likelihood: −18.12 GoF: 96.1% Mean coverage: 397;595
B−Allele Frequency
SNV Index
SCNA−fit log−likelihood: −12596.14
Copy Number log−ratio
SNV Index
Maximum Likelihood Copy Number
SNV Index

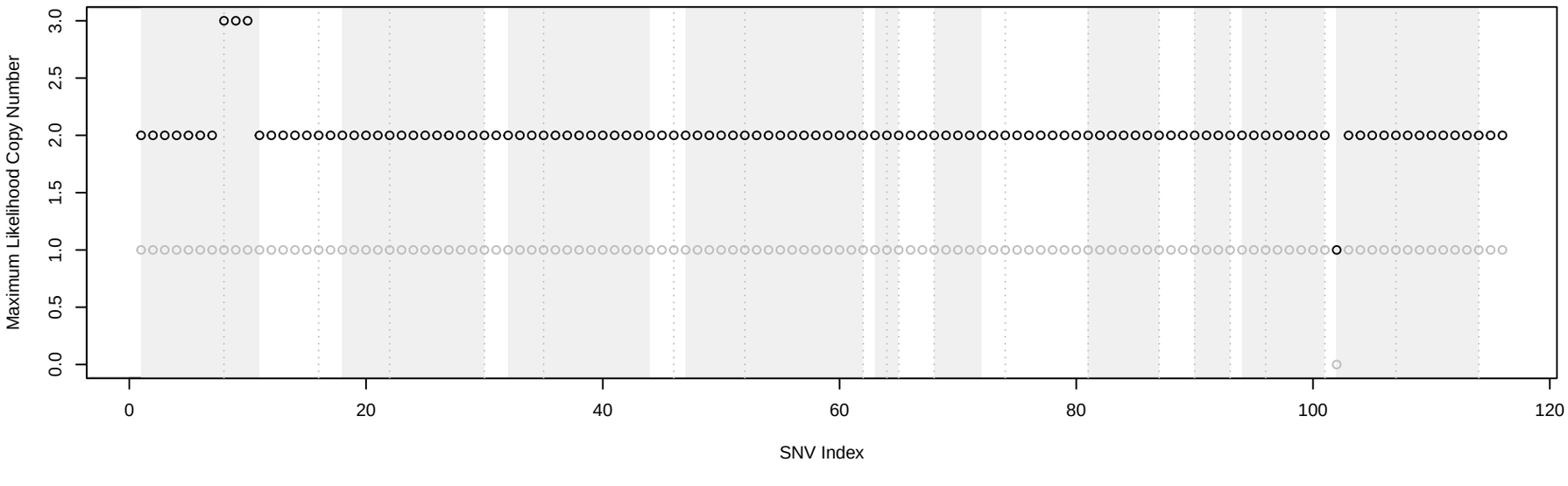


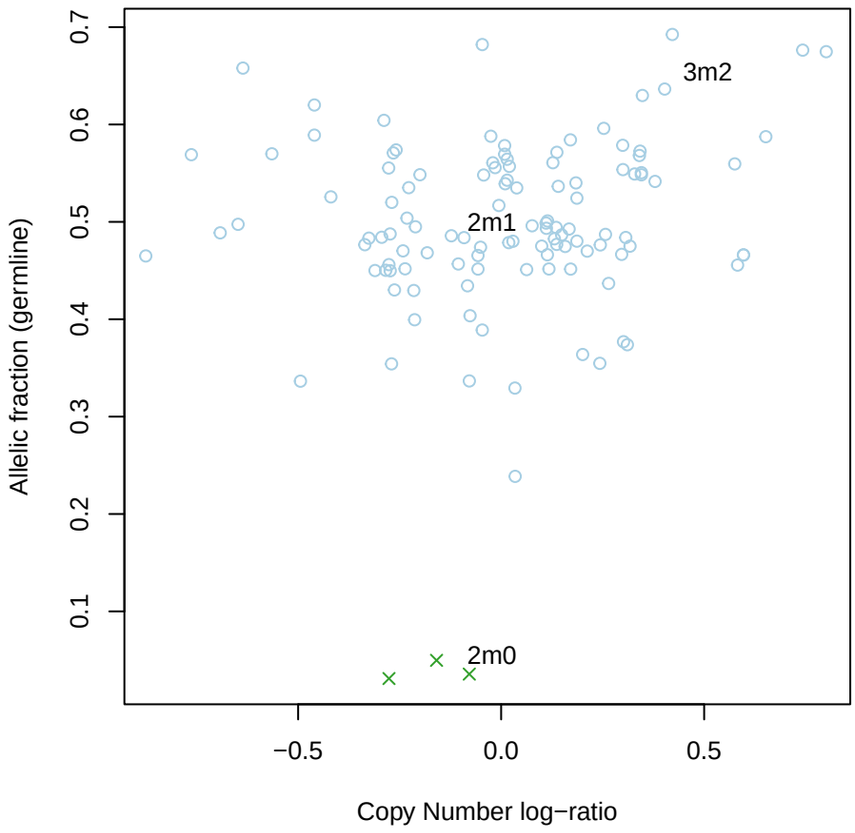
Allelic fraction (germline)
Copy Number log−ratio
3m3
5m4
4m3
6m4
3m2
0m0
4m2
6m3
3m1
6m2
4m1
5m1
Coverage (log2)
Allelic fraction
Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1
Frequency
Cellular fraction

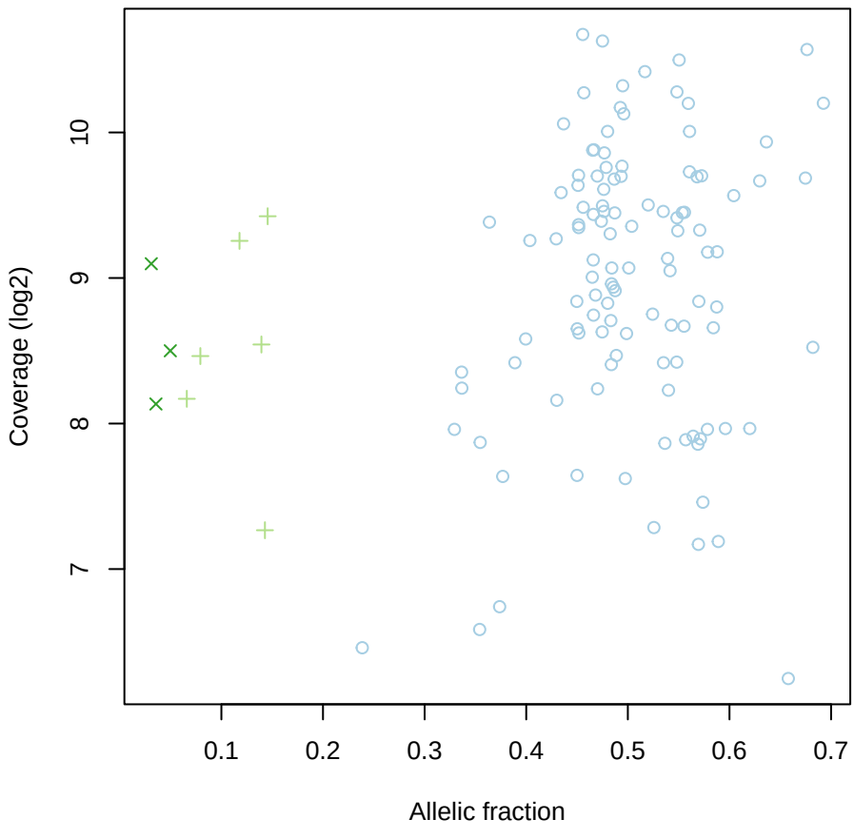

Purity: 0.89 Tumor ploidy: 2.035
1
2
3
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

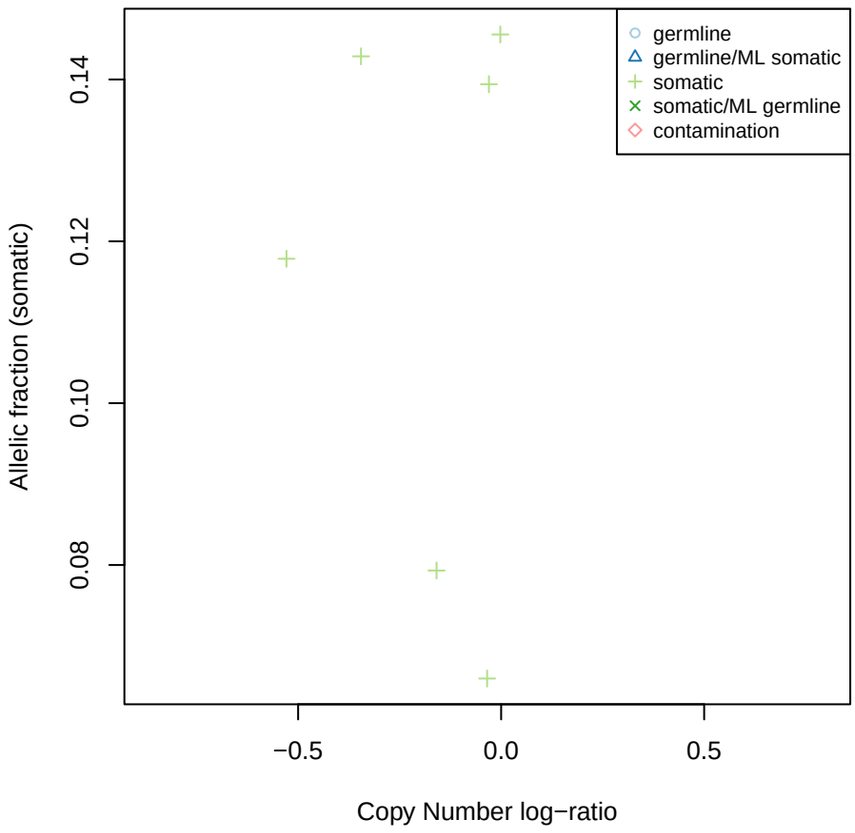

Purity: 0.89 Tumor ploidy: 2.035 SNV log−likelihood: −185.46 GoF: 71.7% Mean coverage: 397;595
1 2 3 4 5 6 7 8 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

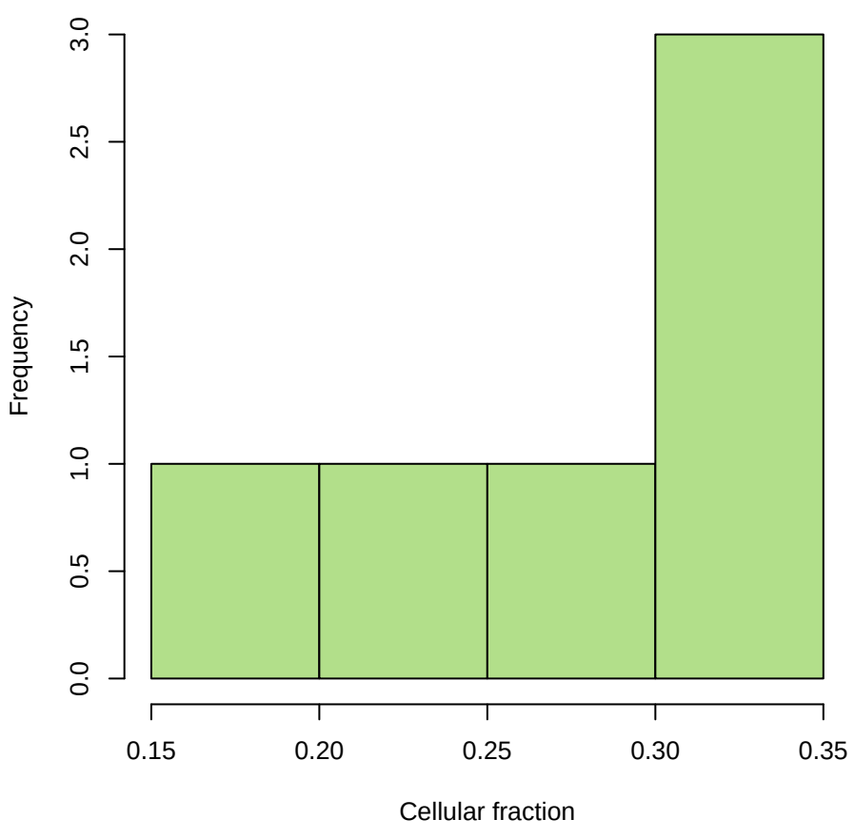

SCNA−fit log−likelihood: −12430.03
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3
0 20 40 60 80 100 120
SNV Index

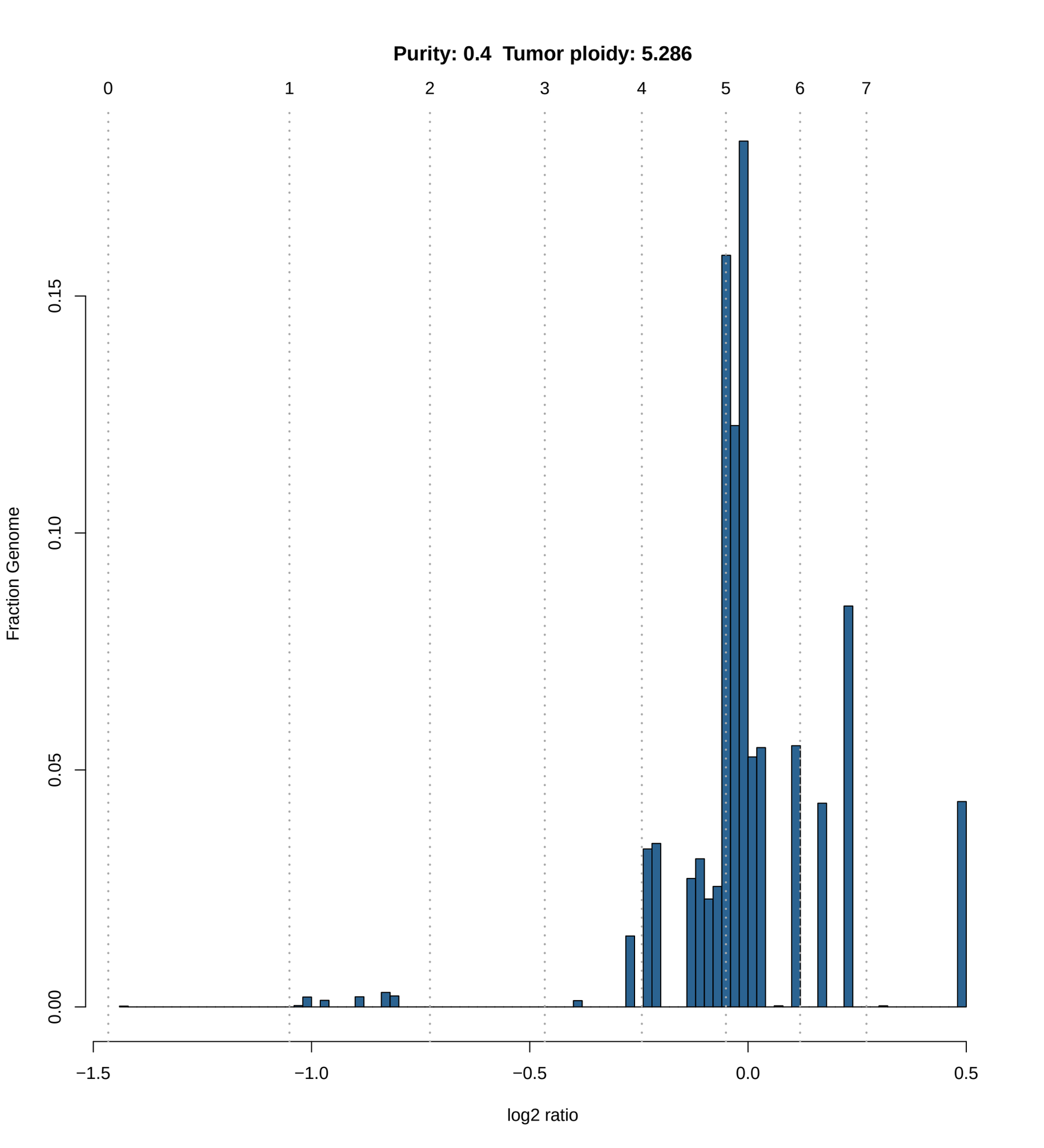

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120
SNV Index

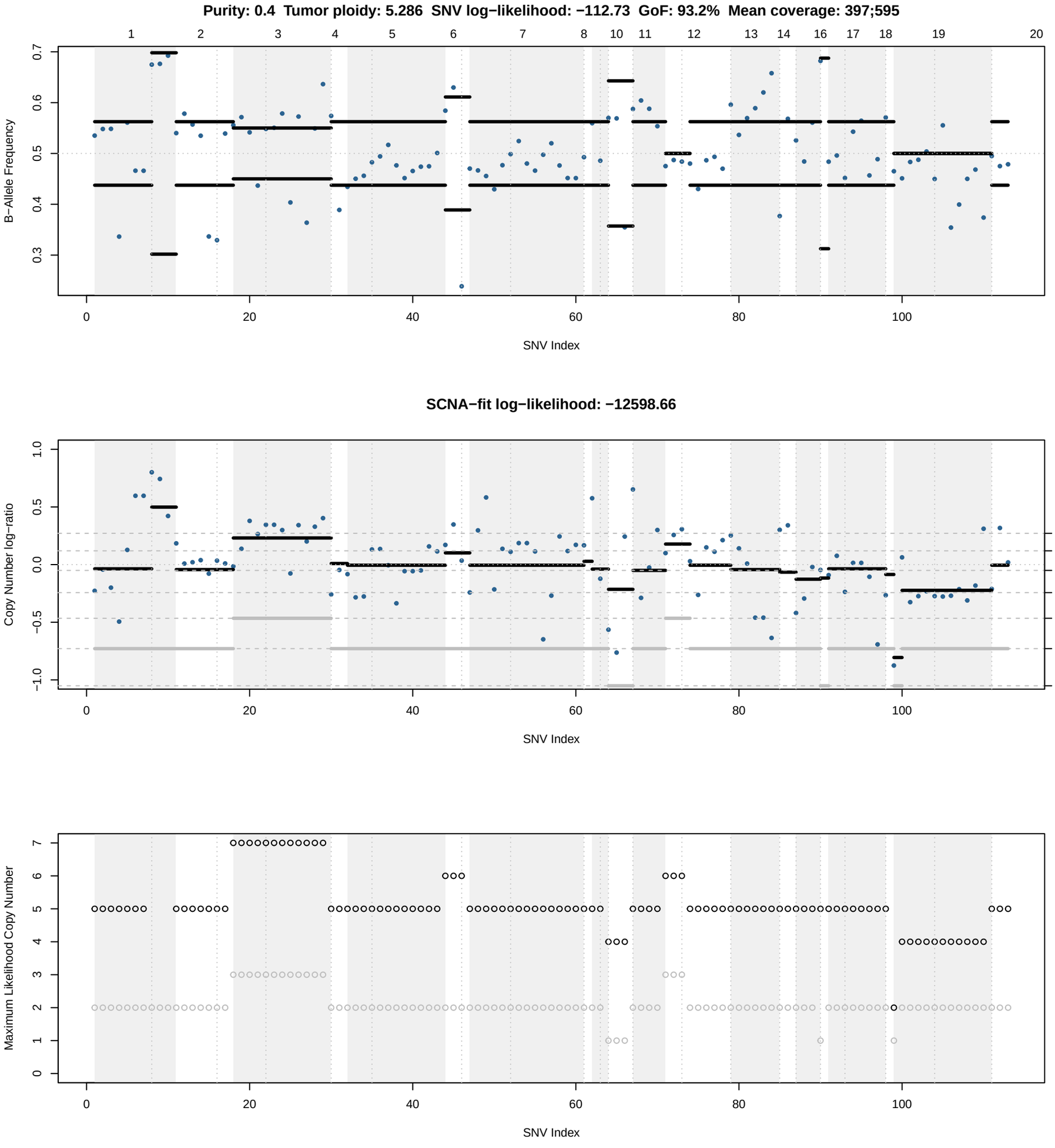

Allelic fraction (germline)
0.1
0.2
0.3
0.4
0.5
0.6
0.7
3m2
2m1
2m0
−0.5
0.0
0.5
Copy Number log−ratio

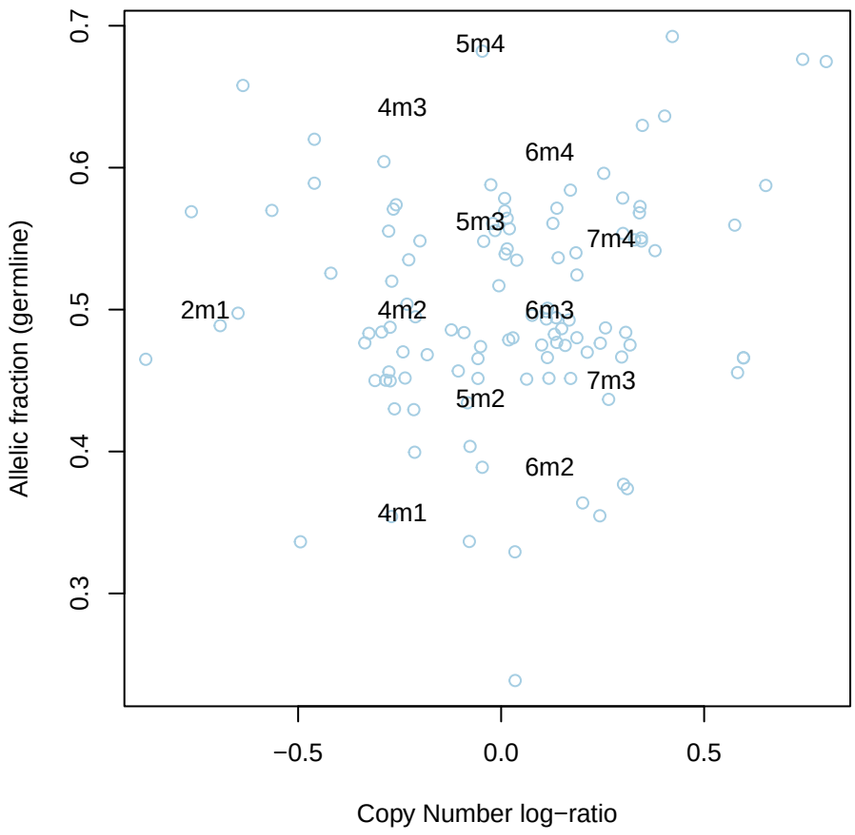

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

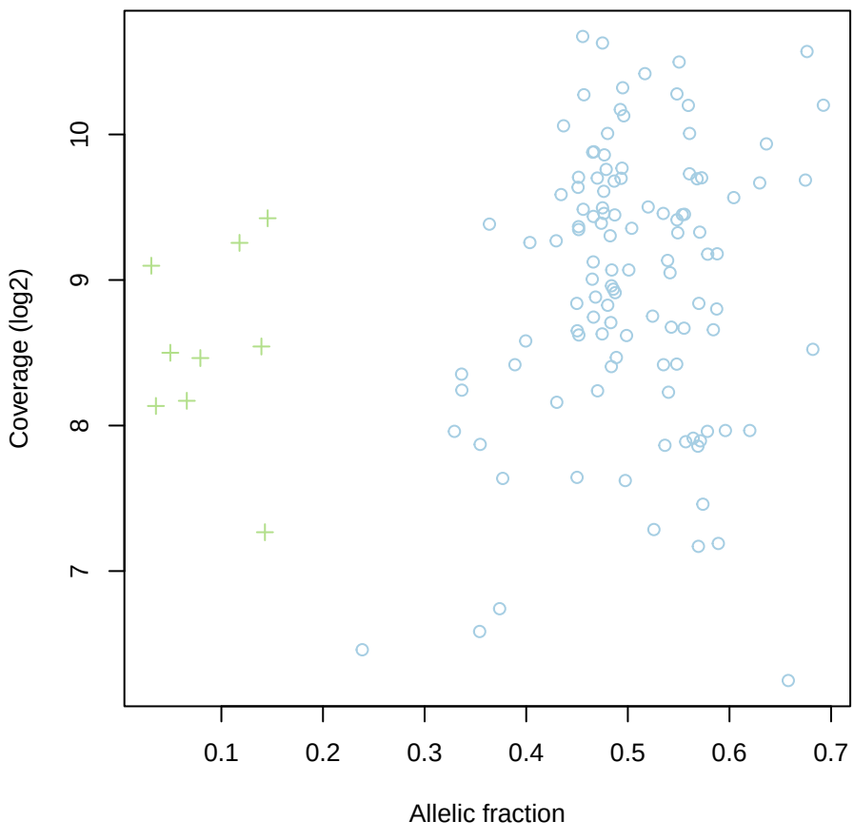

Allelic fraction (somatic)
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.5
0.0
0.5
Copy Number log−ratio

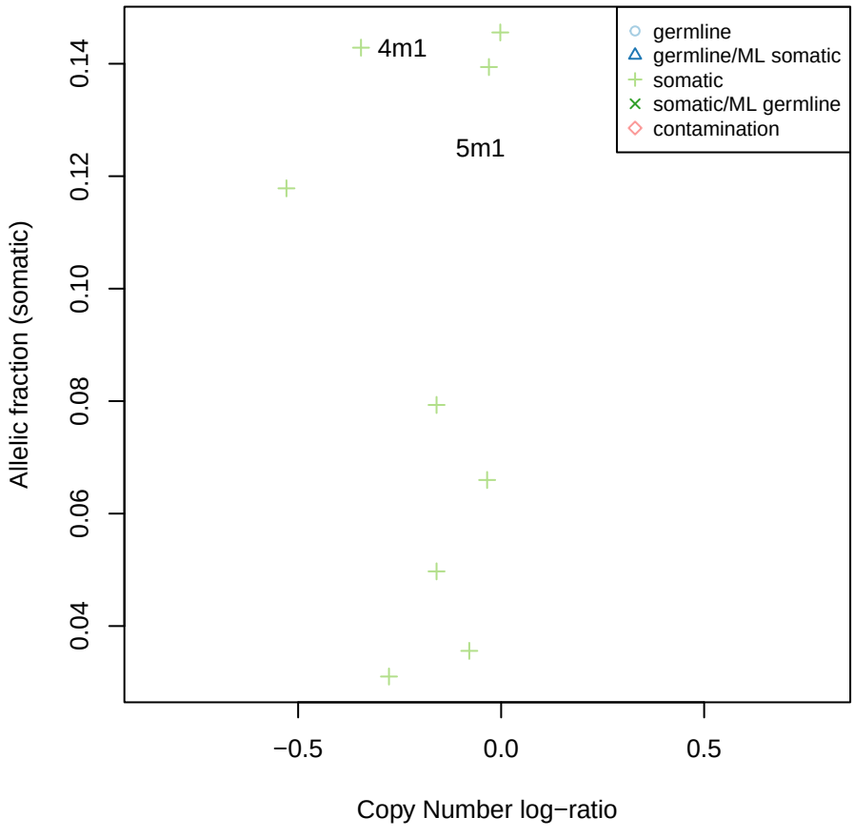

Frequency
0.0
0.5
1.0
1.5
2.0
2.5
3.0
0.15
0.20
0.25
0.30
0.35
Cellular fraction

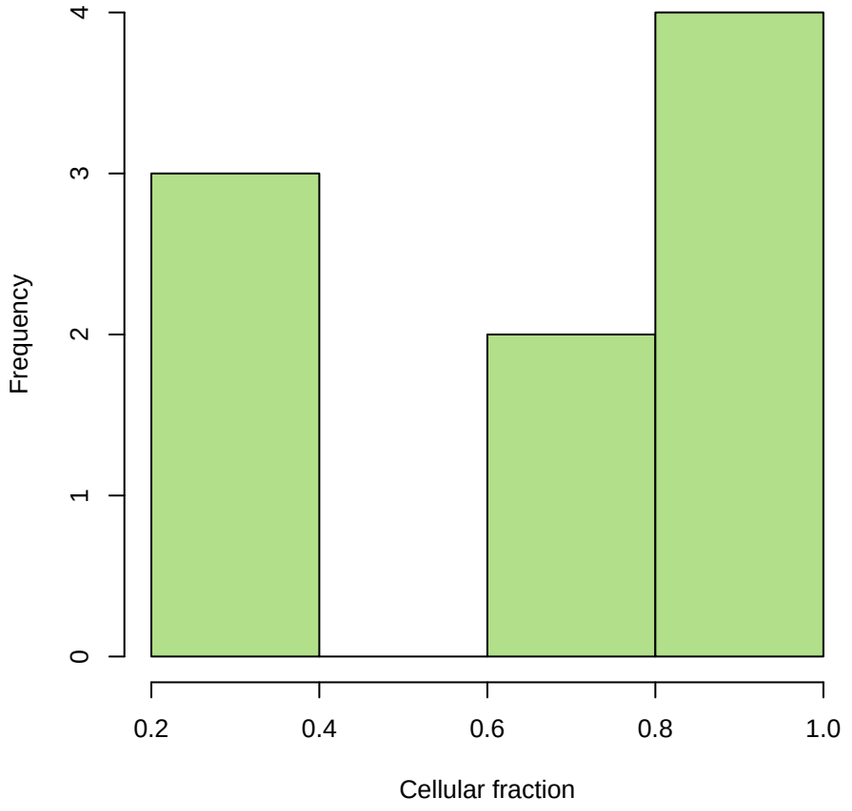

Purity: 0.4 Tumor ploidy: 5.286
0
1
2
3
4
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

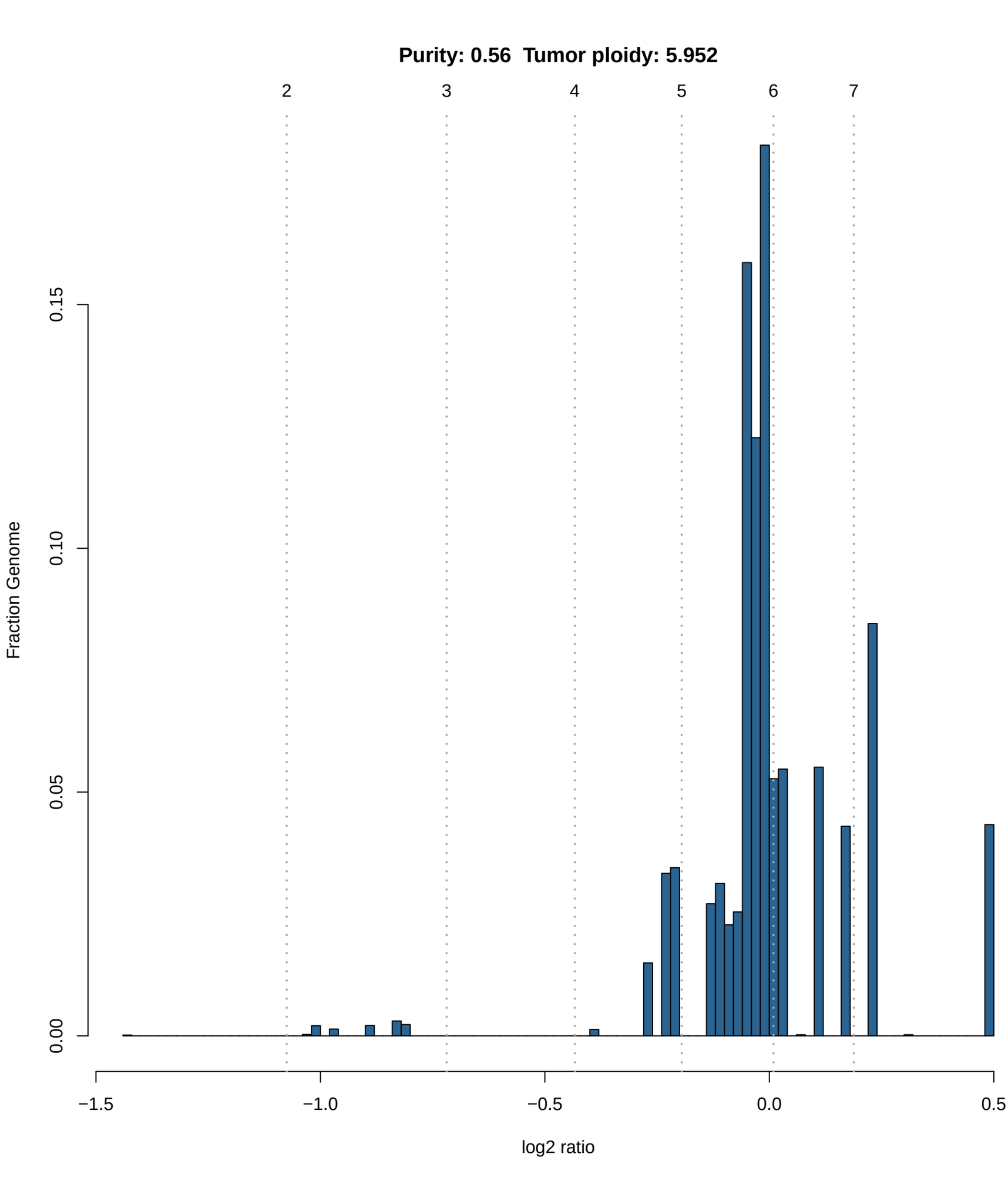

Purity: 0.4 Tumor ploidy: 5.286 SNV log−likelihood: −112.73 GoF: 93.2% Mean coverage: 397;595
B−Allele Frequency
SNV Index
SCNA−fit log−likelihood: −12598.66
Copy Number log−ratio
SNV Index
Maximum Likelihood Copy Number
SNV Index

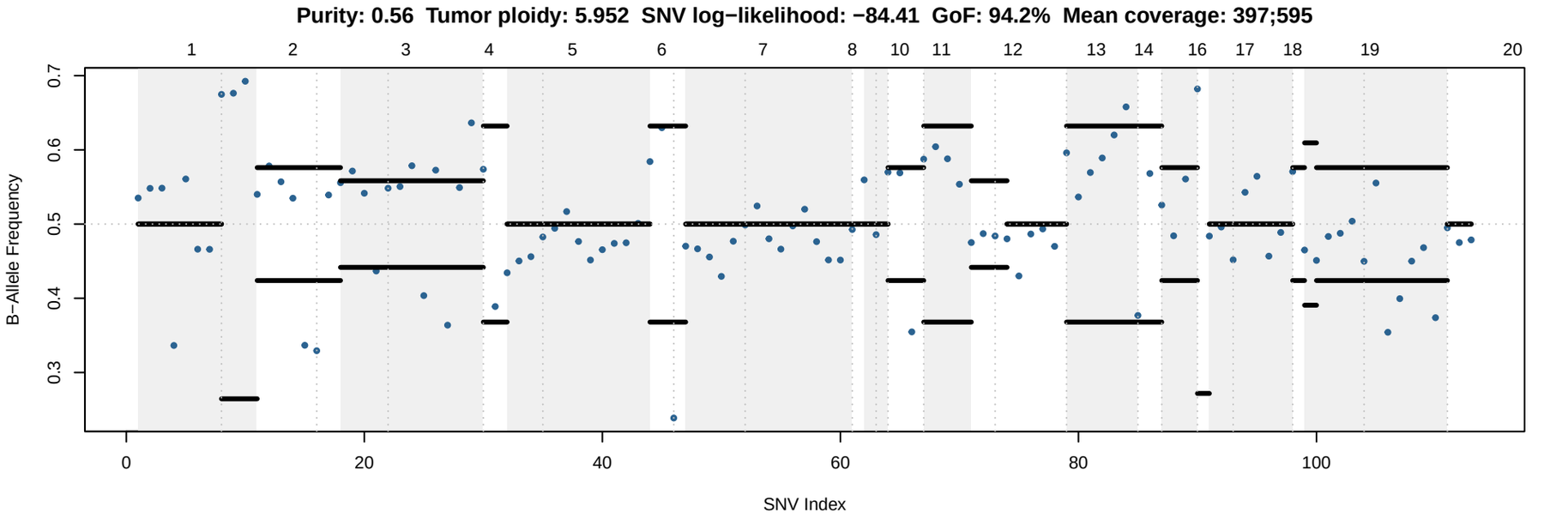

5m4
4m3
6m4
5m3
7m4
2m1
4m2
6m3
7m3
5m2
6m2
4m1
Allelic fraction (germline)
Copy Number log−ratio
0.3
0.4
0.5
0.6
0.7
−0.5
0.0
0.5

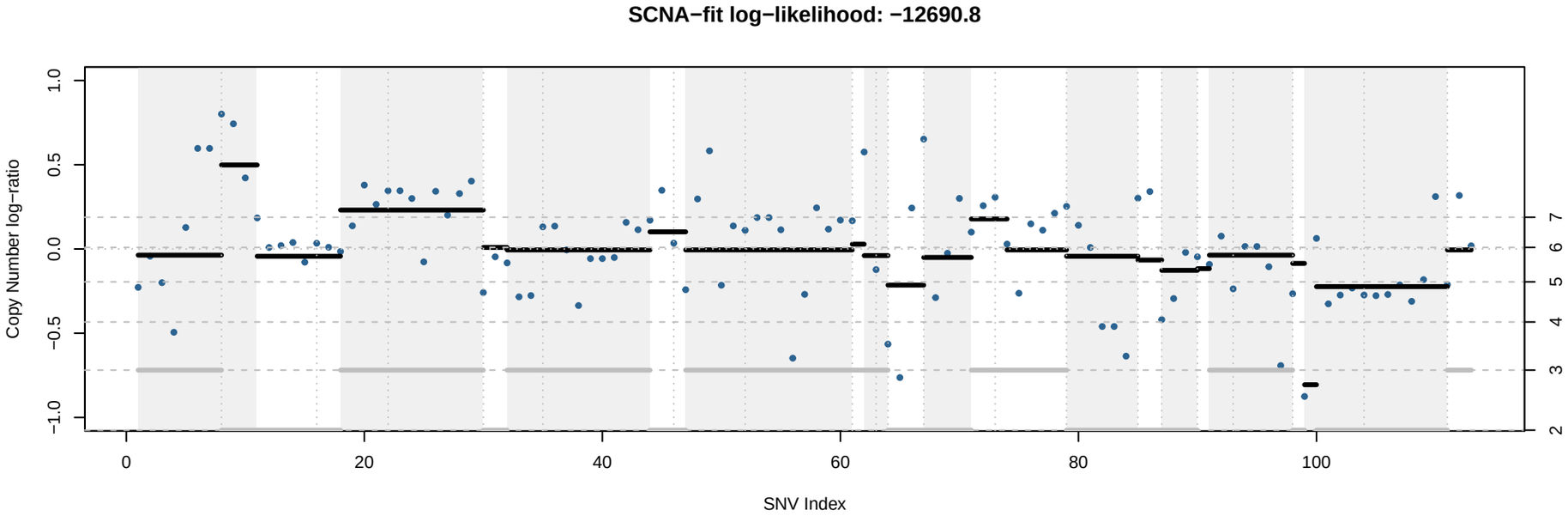

Coverage (log2)
Allelic fraction
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7

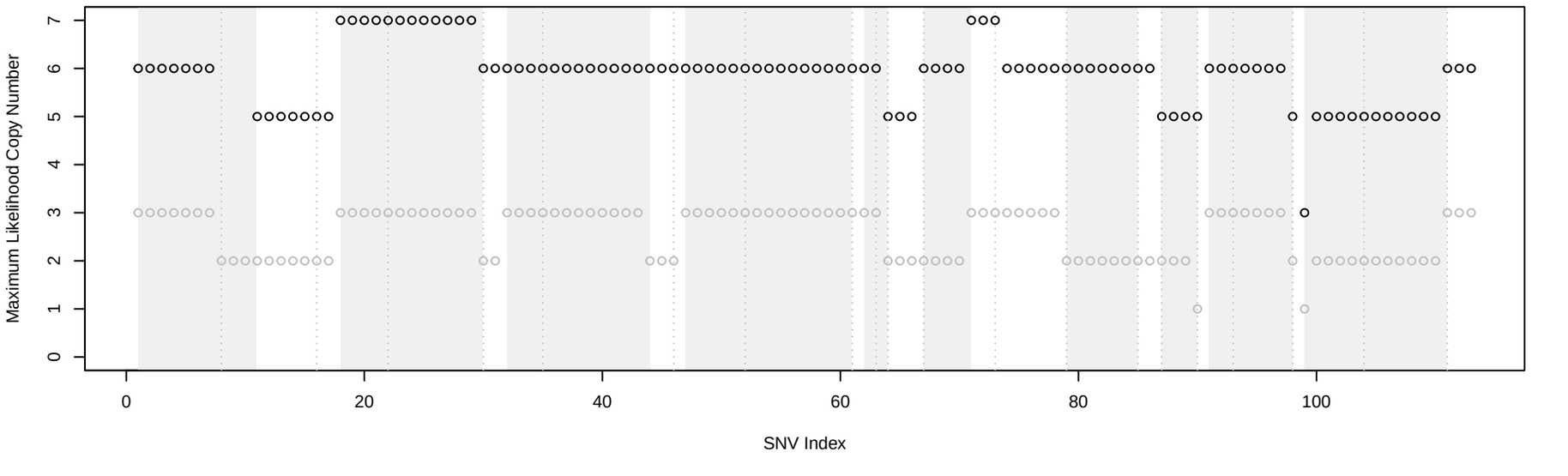

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
0.12
0.14
−0.5
0.0
0.5

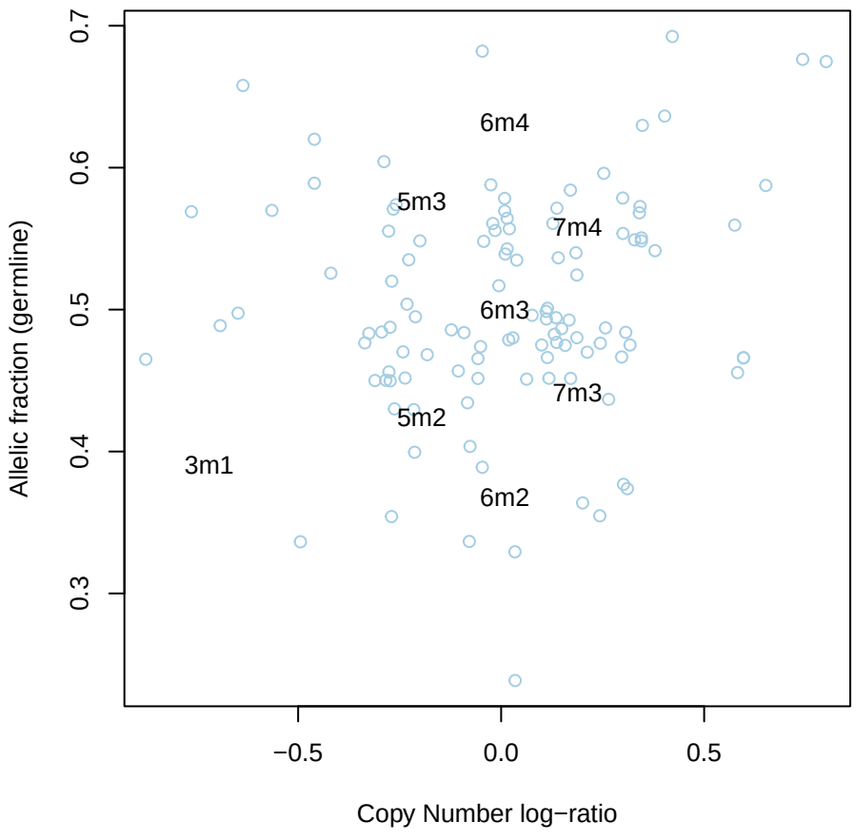

Frequency
Cellular fraction
0
1
2
3
4
0.2
0.4
0.6
0.8
1.0

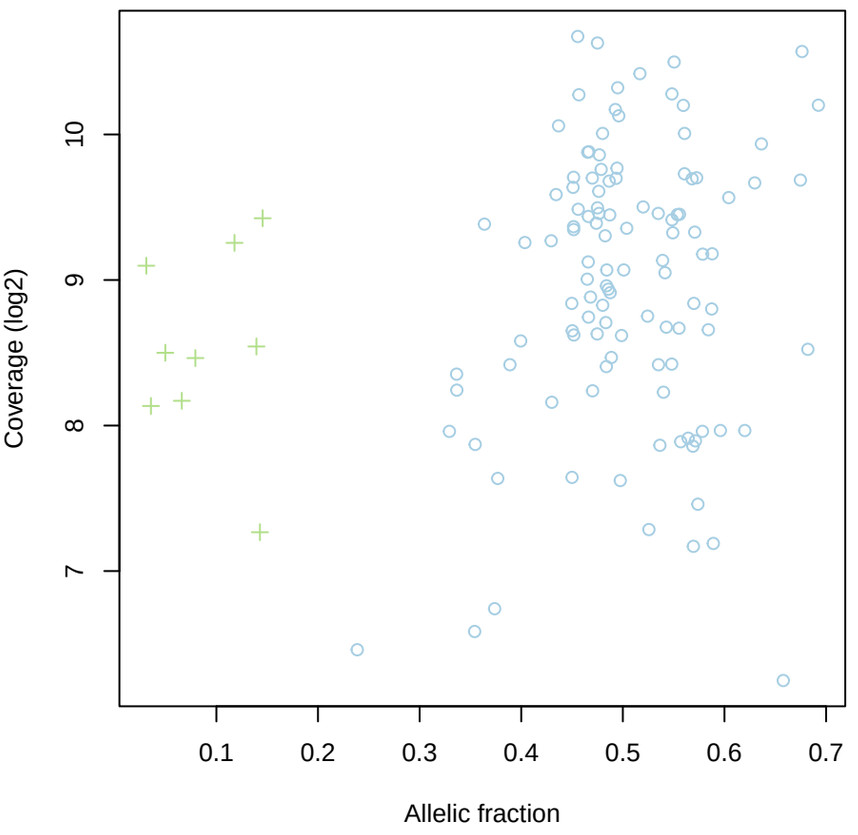

Purity: 0.56 Tumor ploidy: 5.952
2
3
4
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

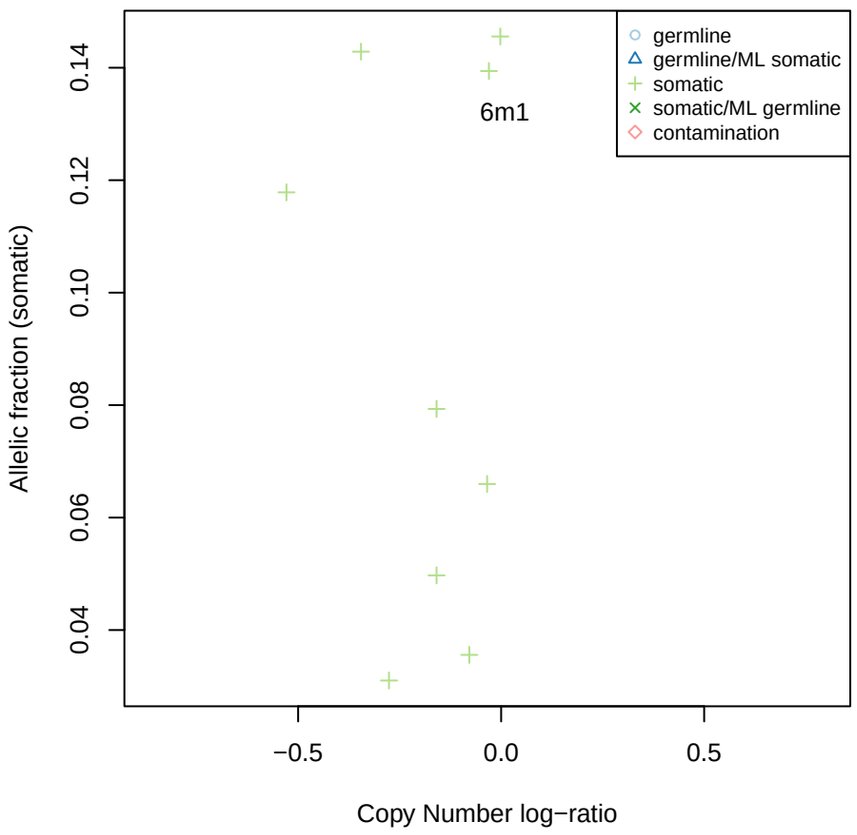

Purity: 0.56 Tumor ploidy: 5.952 SNV log−likelihood: −84.41 GoF: 94.2% Mean coverage: 397;595
B−Allele Frequency
SNV Index

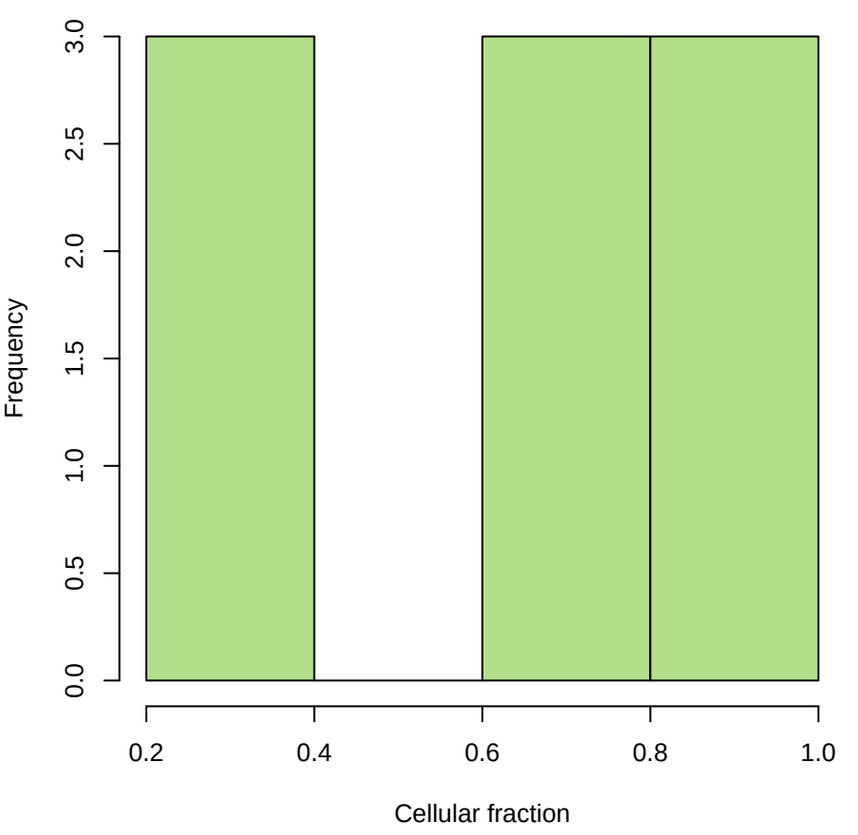

SCNA−fit log−likelihood: −12690.8
Copy Number log−ratio
SNV Index

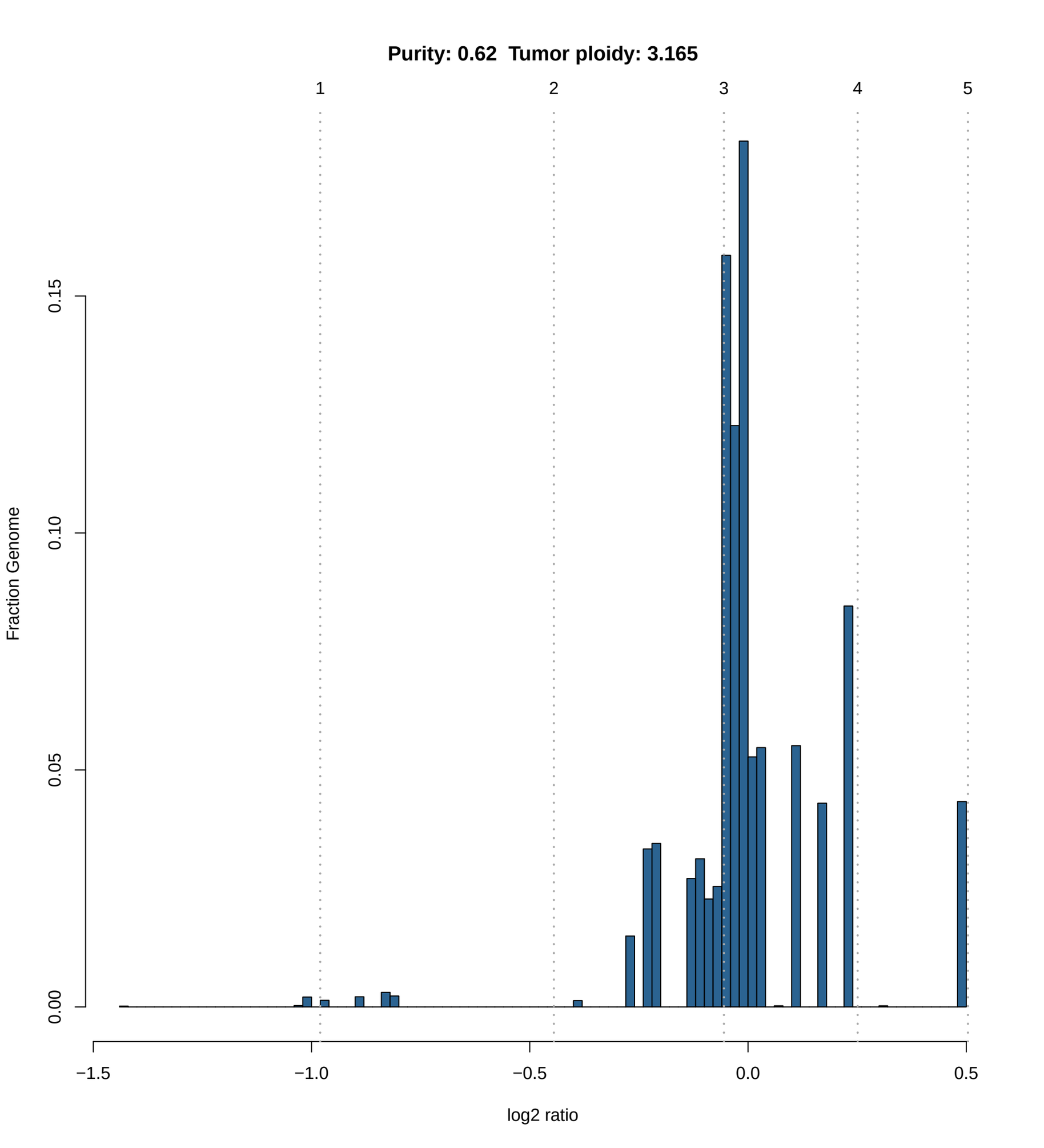

Maximum Likelihood Copy Number
SNV Index

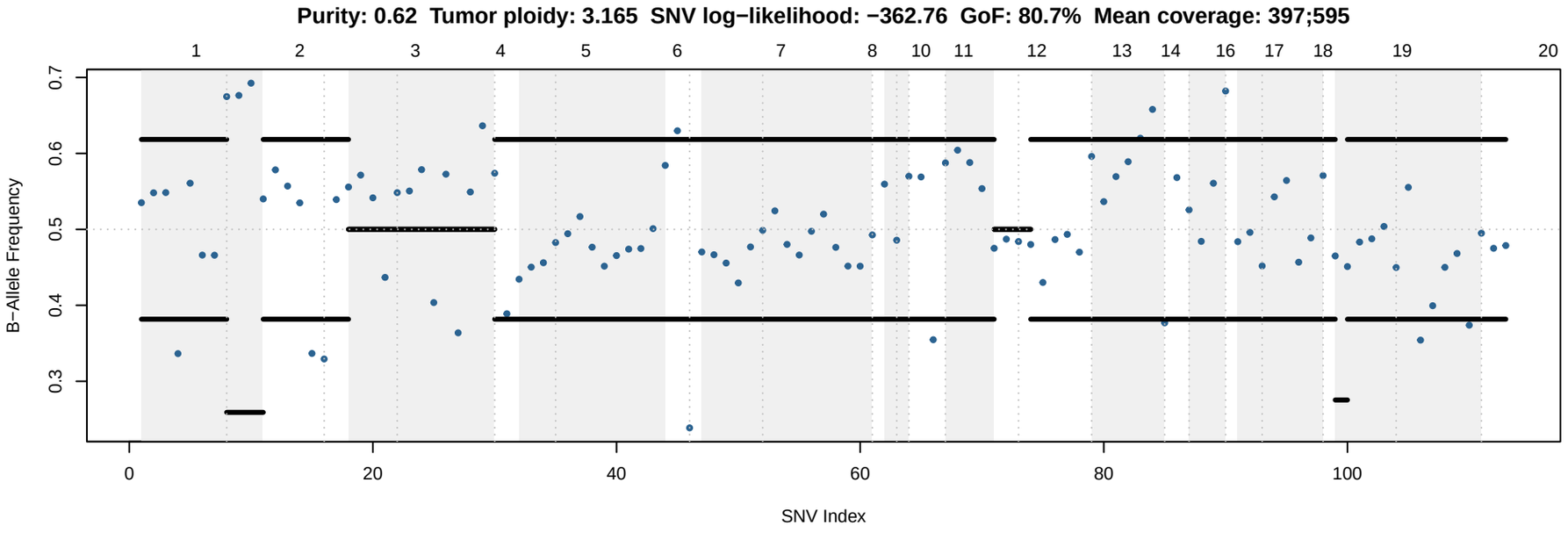

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
−0.5
0.0
0.5
Copy Number log−ratio
6m4
5m3
7m4
6m3
7m3
5m2
3m1
6m2

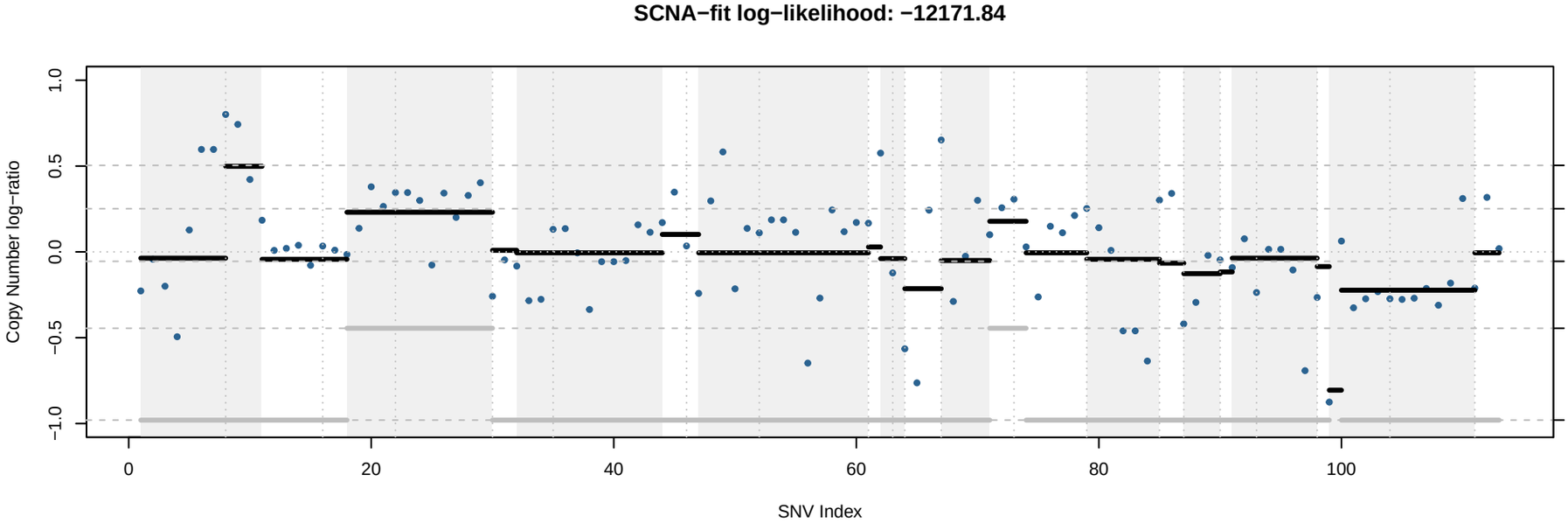

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

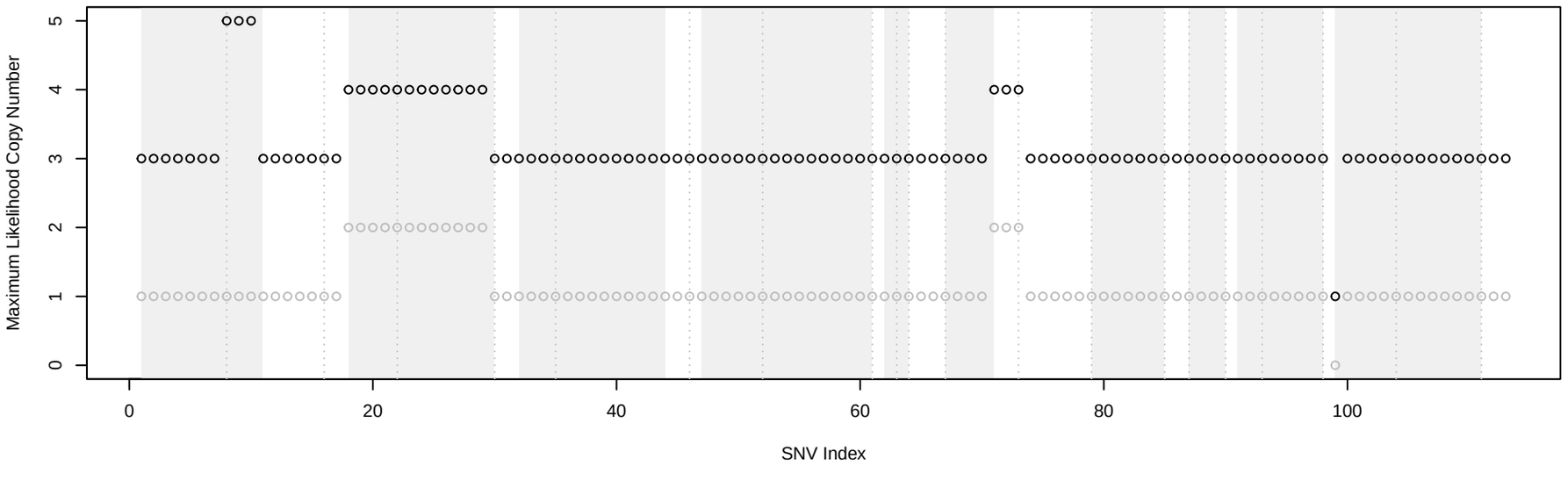

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
−0.5
0.0
0.5
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m1

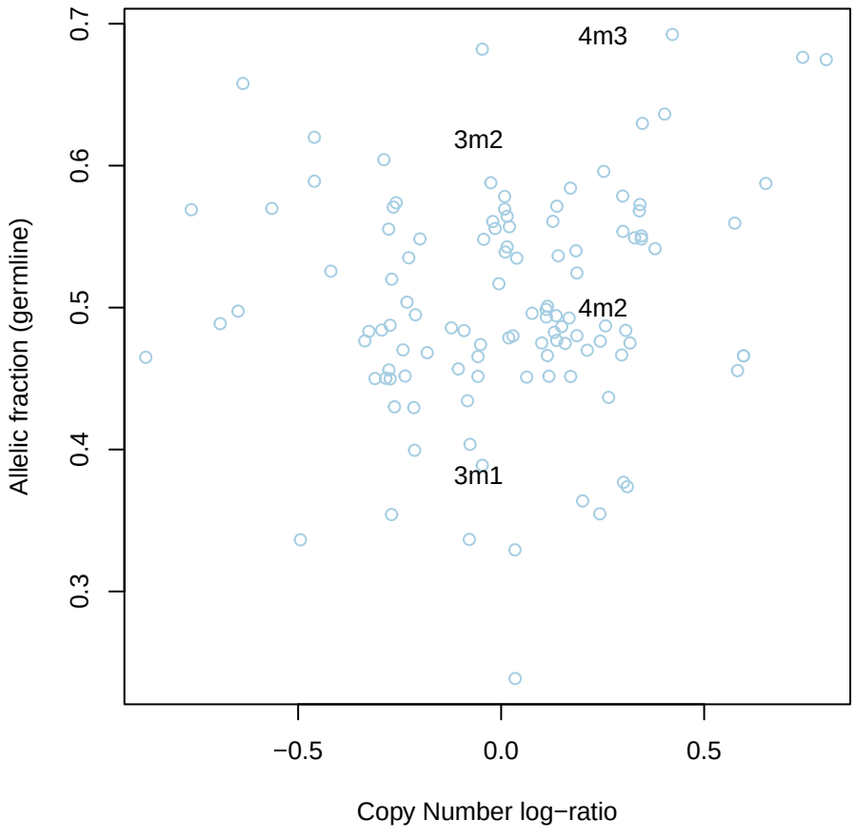

Frequency
0.0
0.5
1.0
1.5
2.0
2.5
3.0
0.2
0.4
0.6
0.8
1.0
Cellular fraction

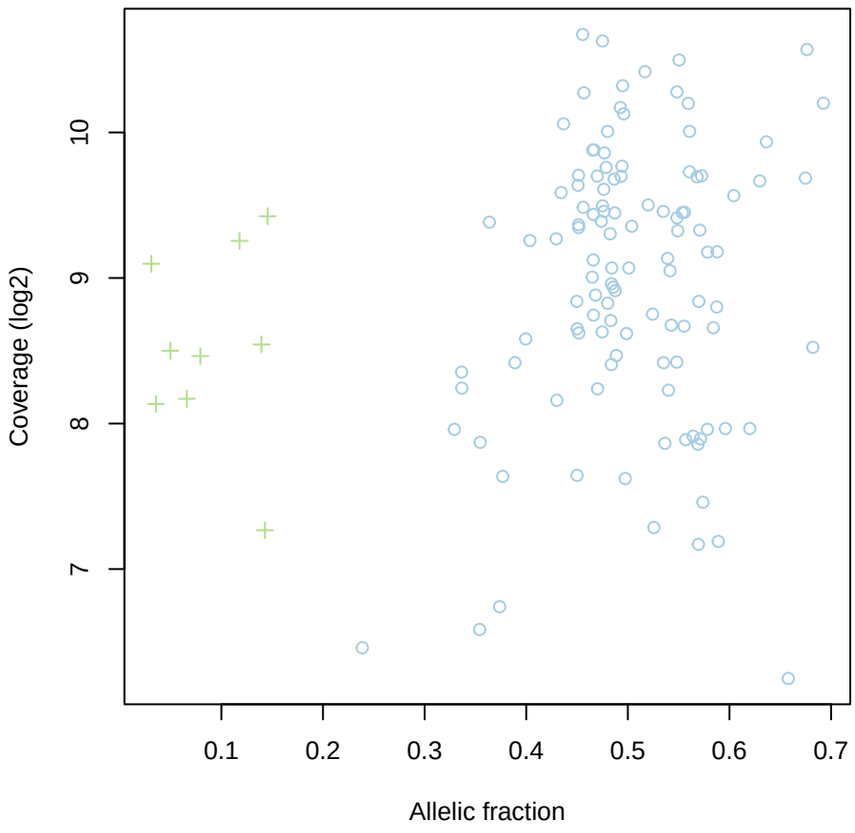

Purity: 0.62 Tumor ploidy: 3.165
1
2
3
4
5
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

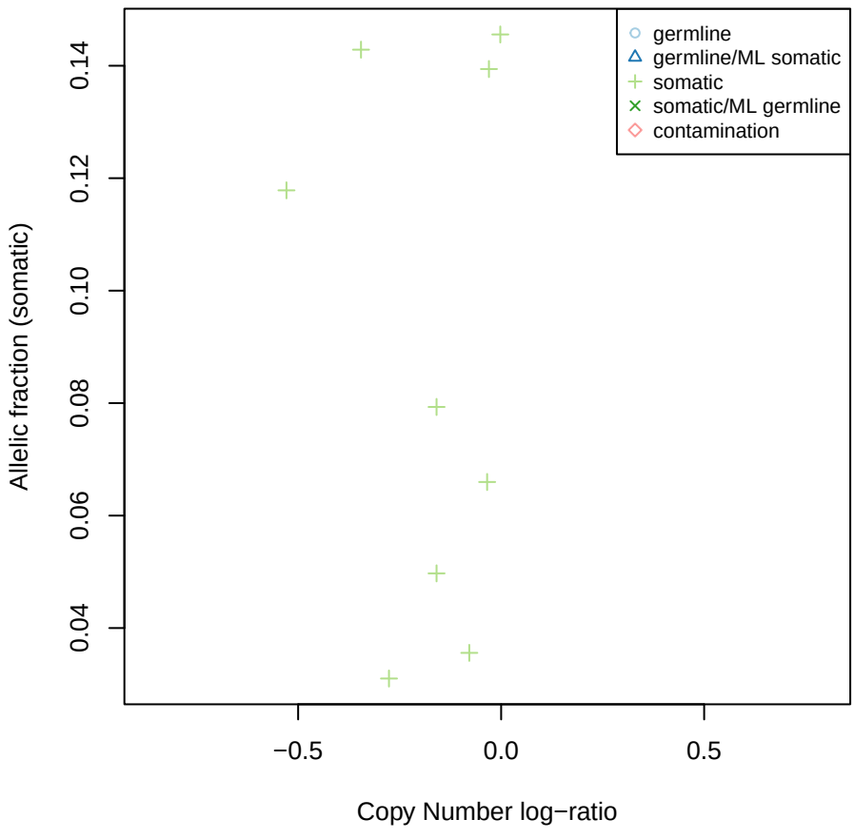

Purity: 0.62 Tumor ploidy: 3.165 SNV log−likelihood: −362.76 GoF: 80.7% Mean coverage: 397;595
B−Allele Frequency
SNV Index

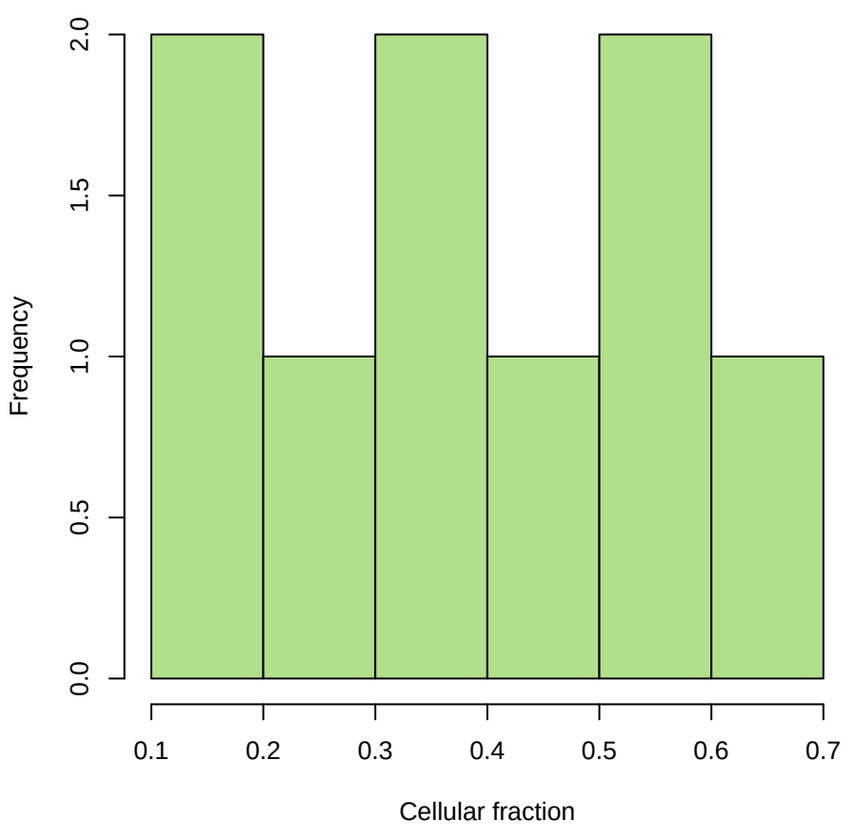

SCNA−fit log−likelihood: −12171.84
Copy Number log−ratio
SNV Index


Maximum Likelihood Copy Number
SNV Index


4m3
3m2
4m2
3m1
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