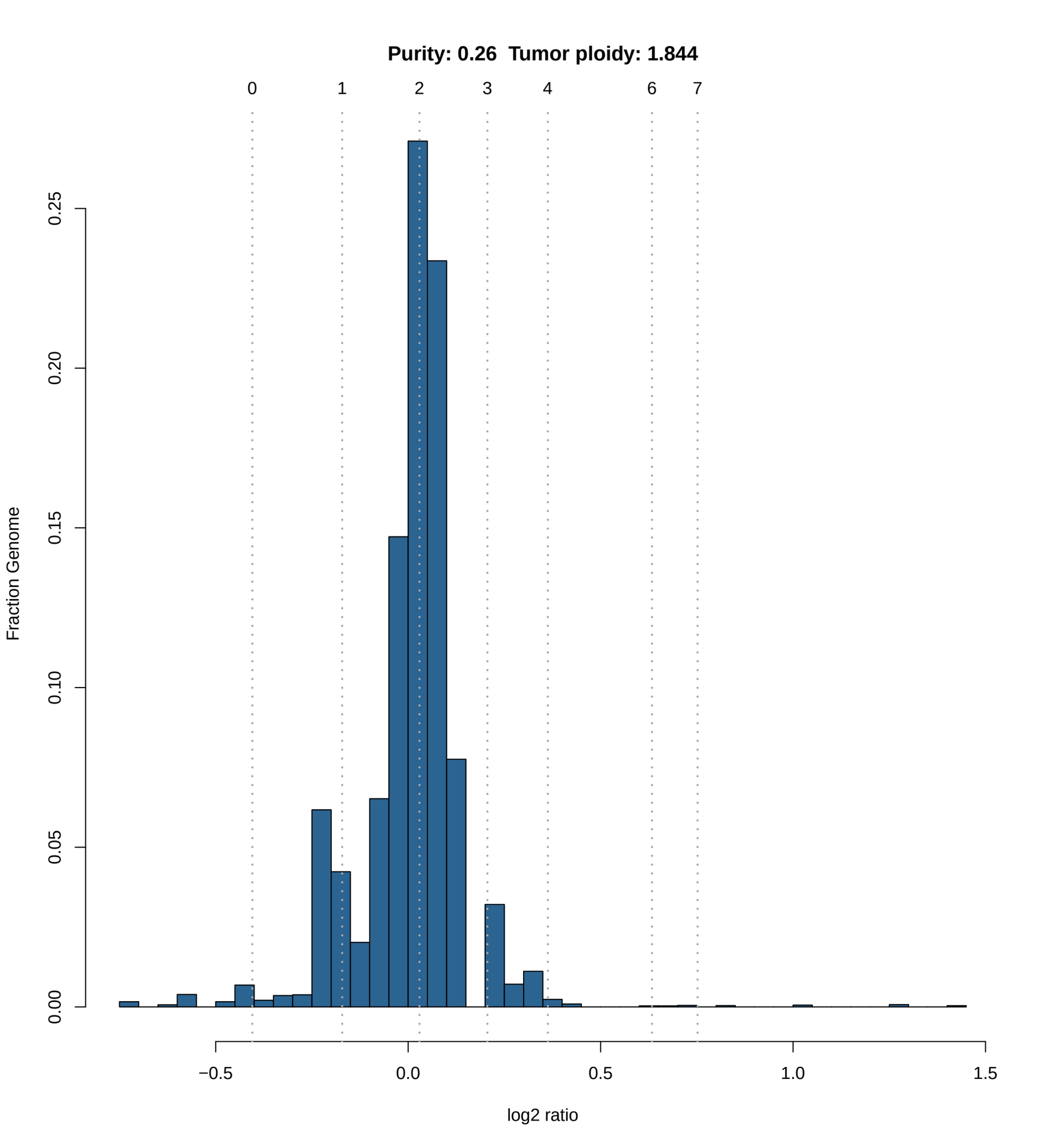
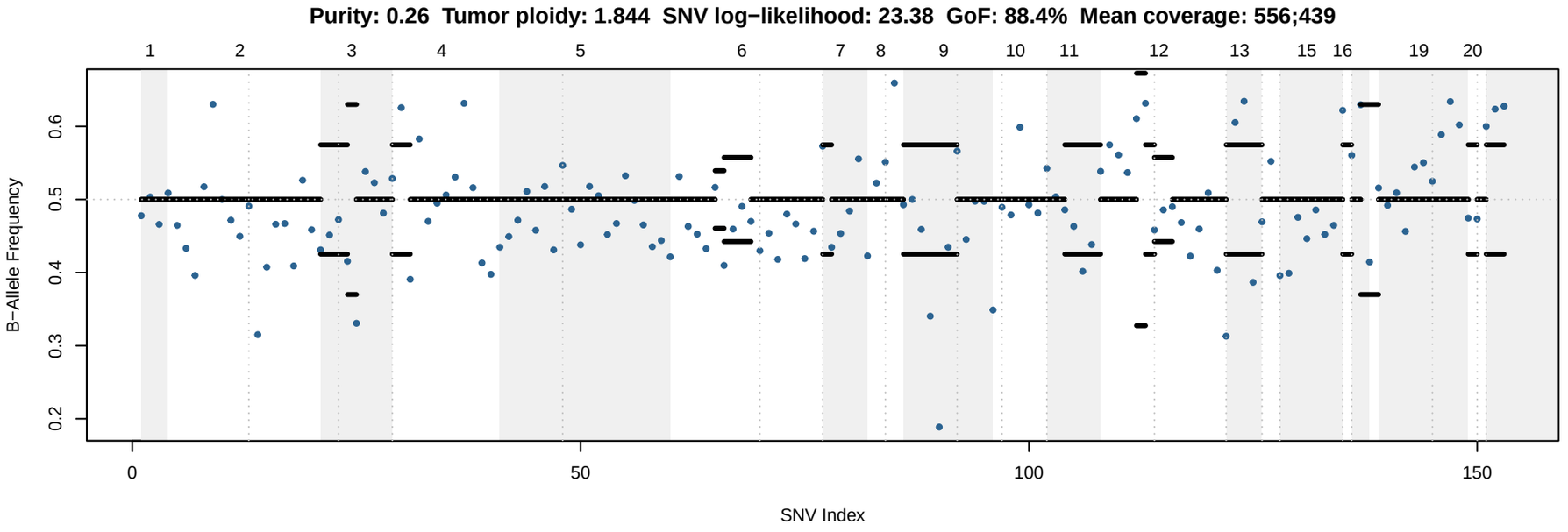
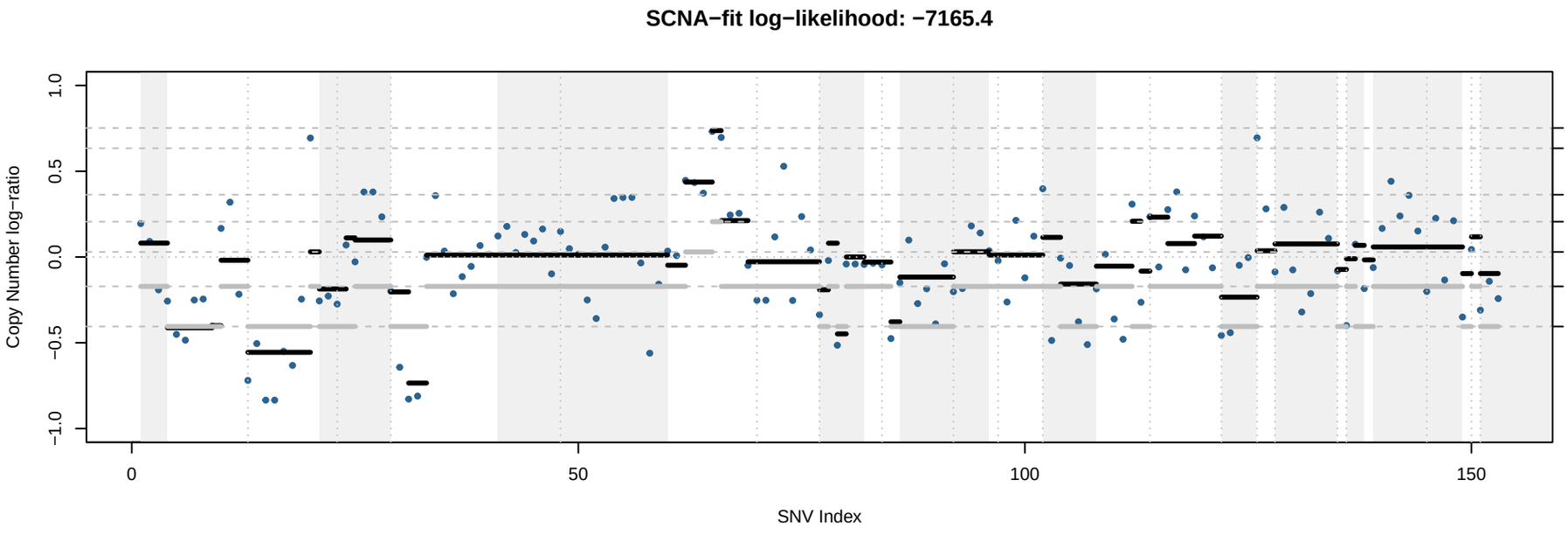
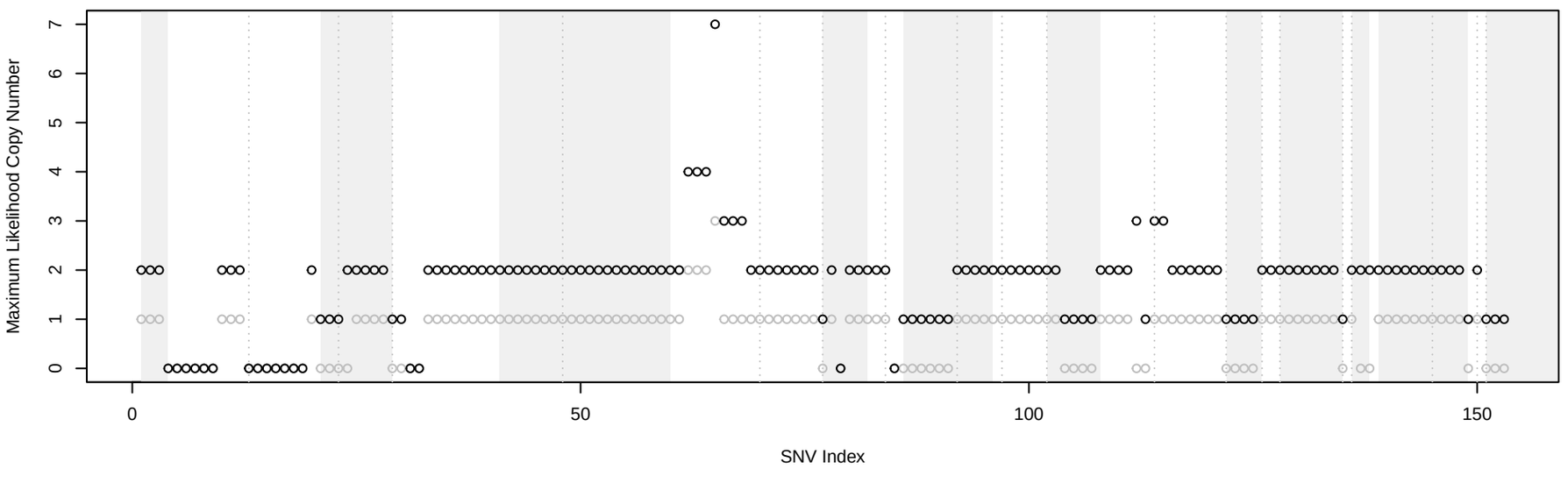
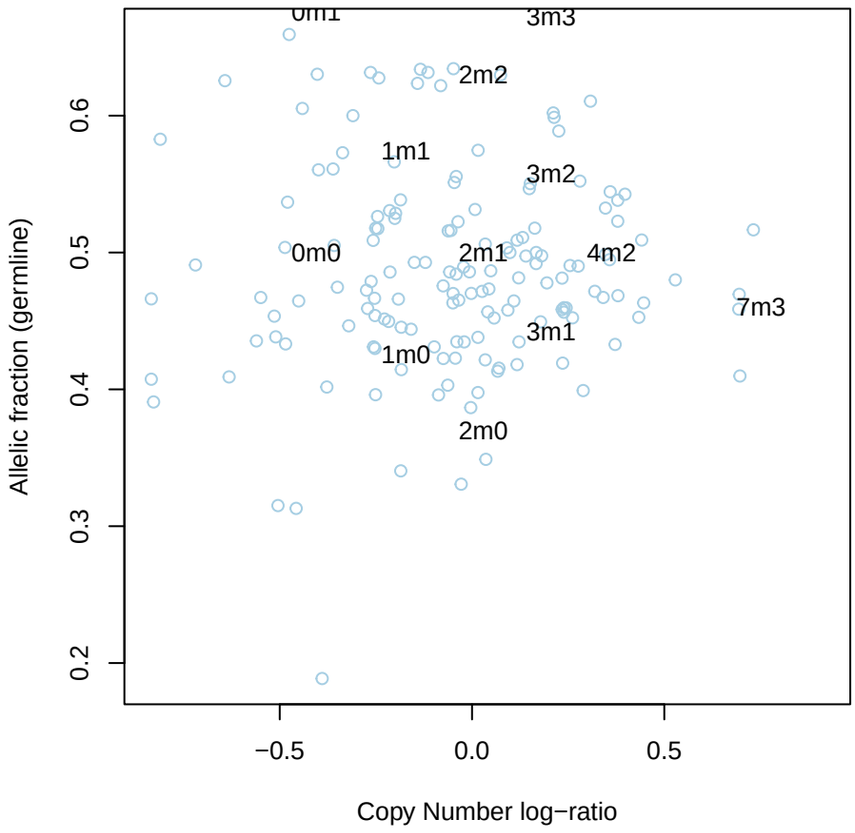
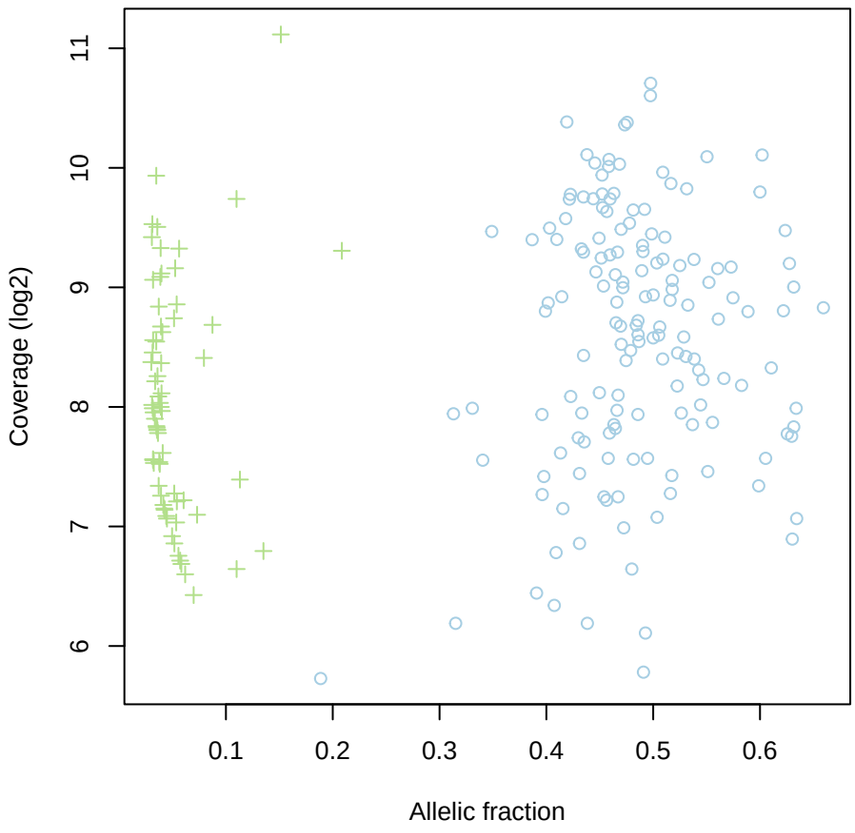

Purity: 0.26 Tumor ploidy: 1.844
0
1
2
3
4
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

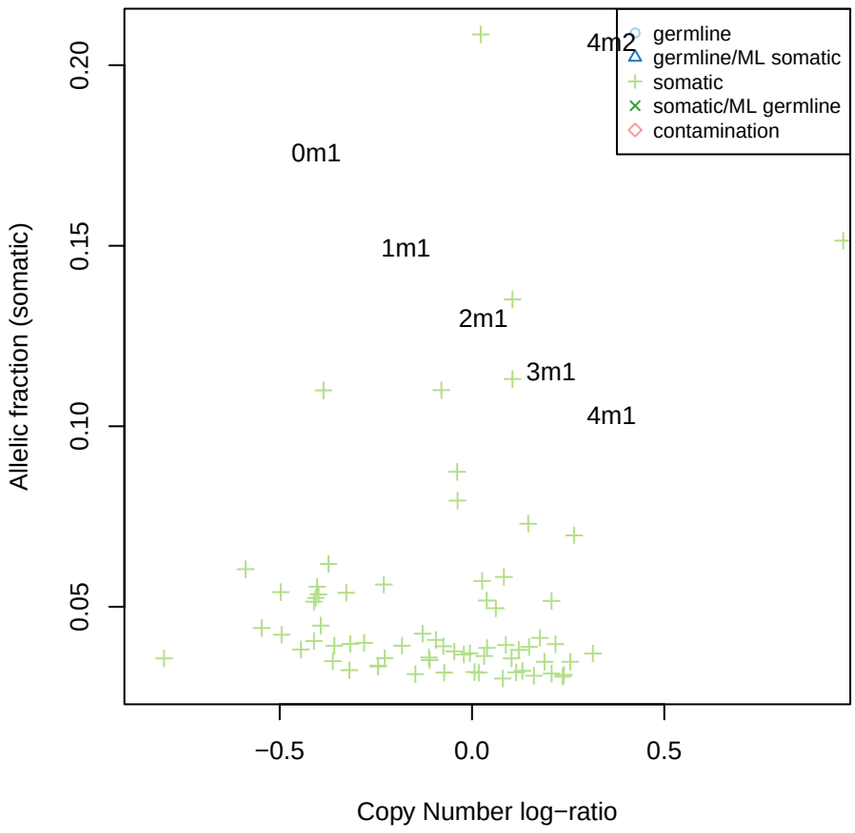

Purity: 0.26 Tumor ploidy: 1.844 SNV log−likelihood: 23.38 GoF: 88.4% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

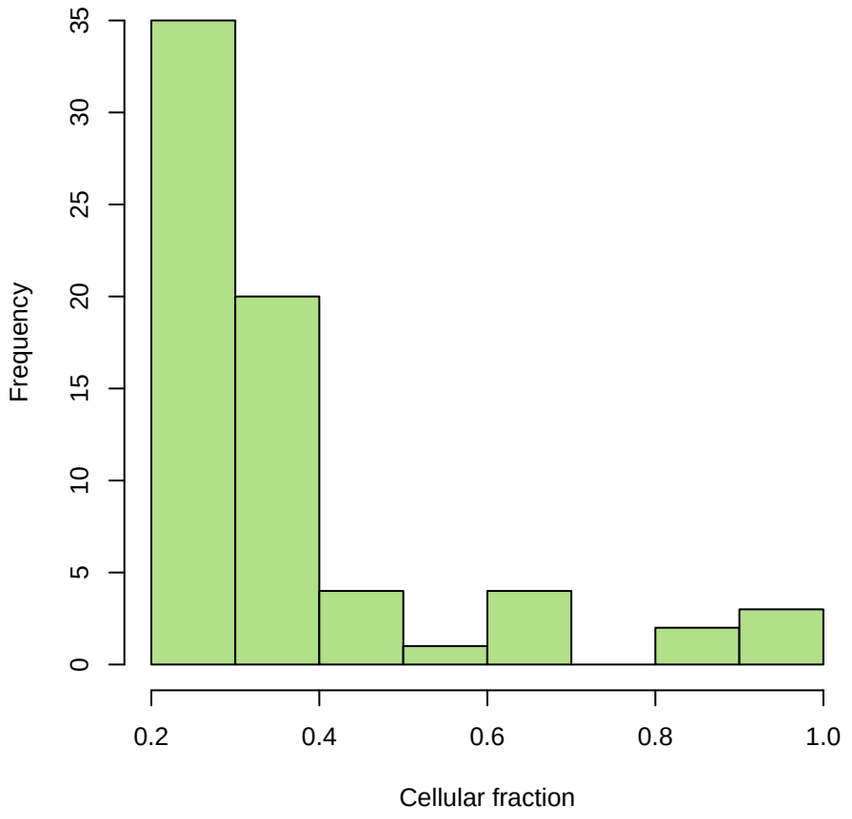

SCNA−fit log−likelihood: −7165.4
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 6
0 50 100 150
SNV Index

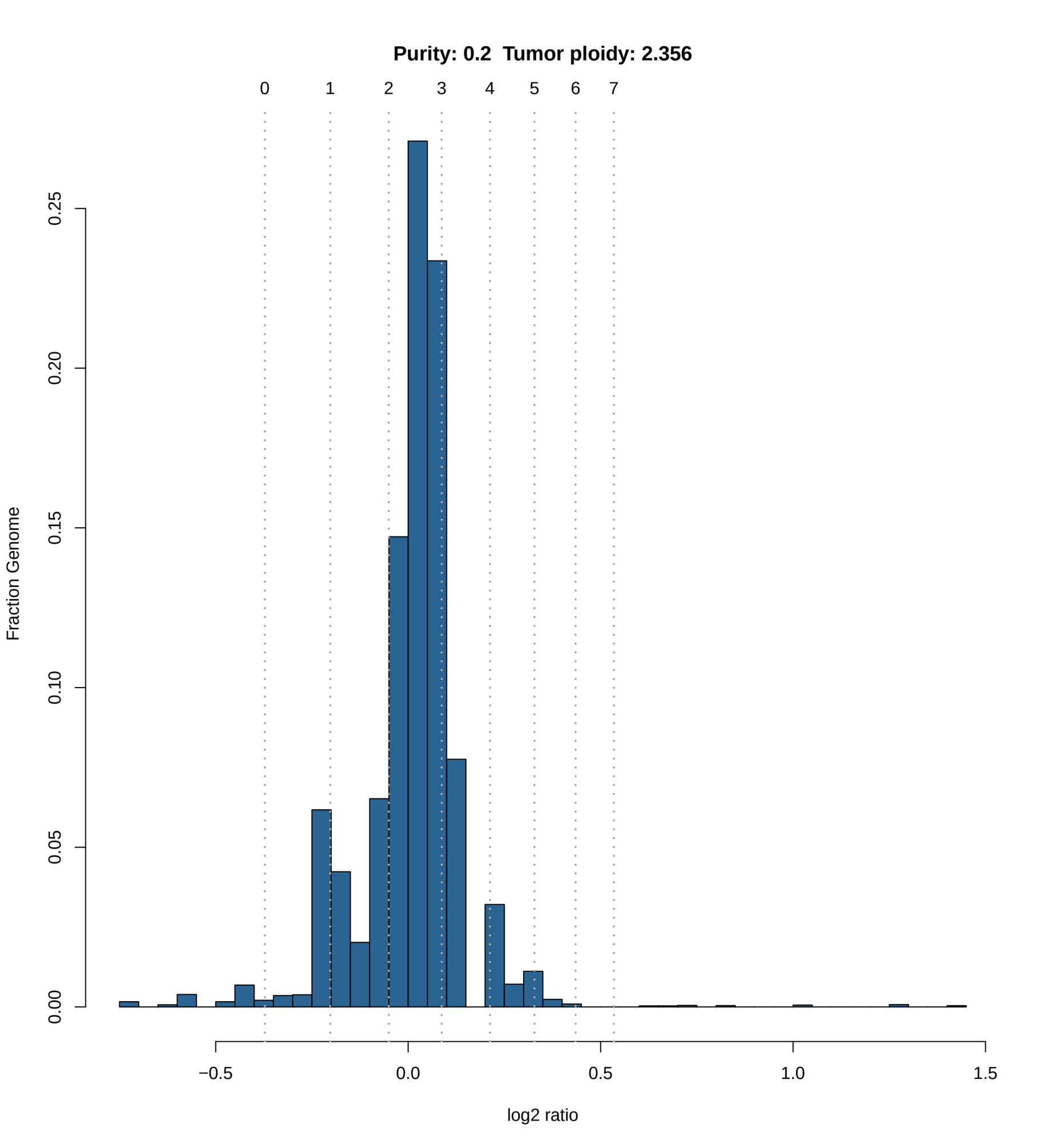

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

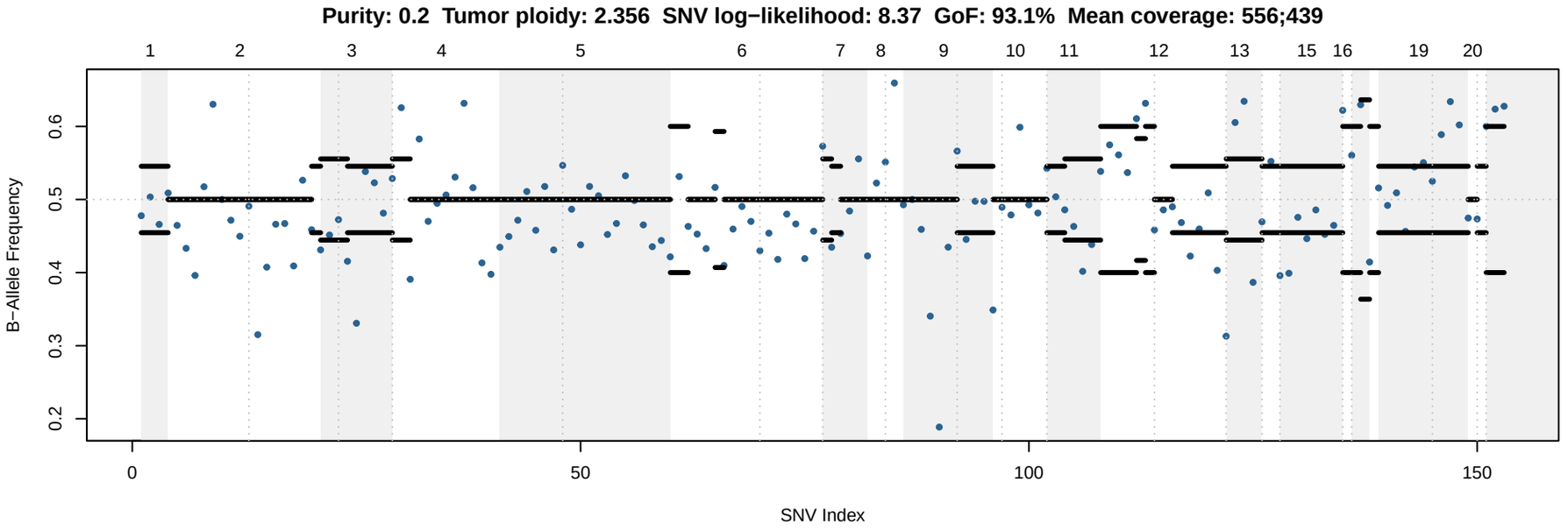

0m1
3m3
2m2
1m1
3m2
0m0
2m1
4m2
7m3
3m1
1m0
2m0
Allelic fraction (germline)
Copy Number log−ratio

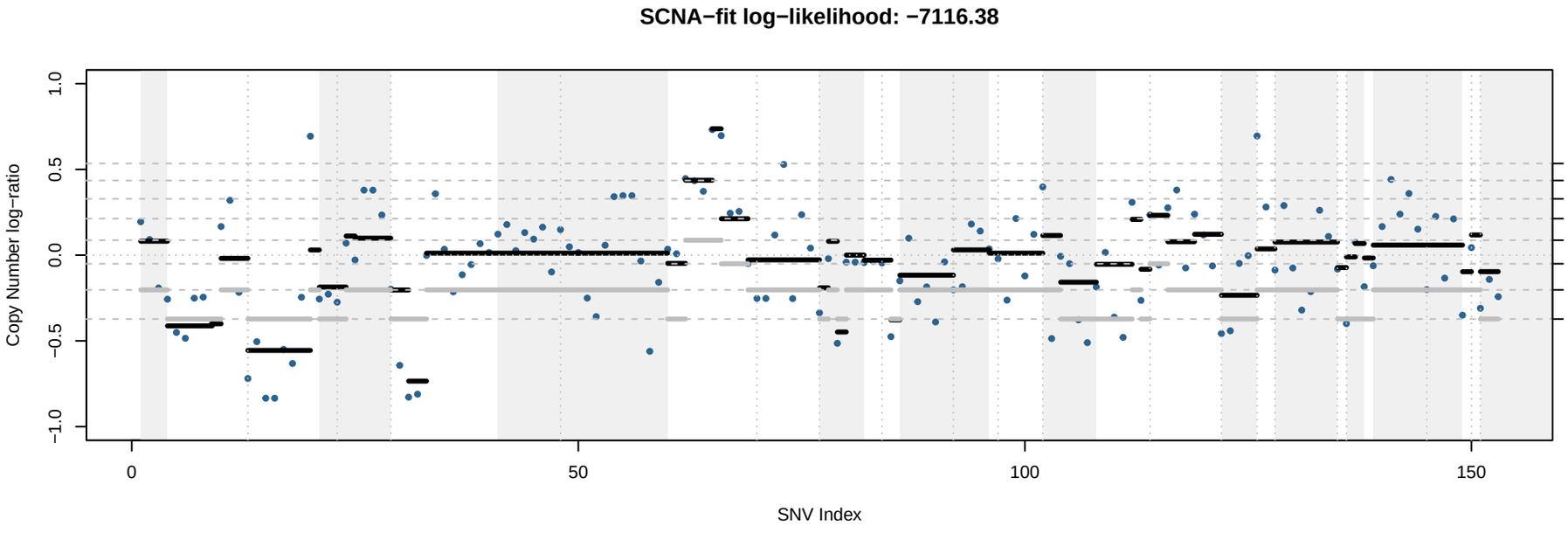

Coverage (log2)
Allelic fraction

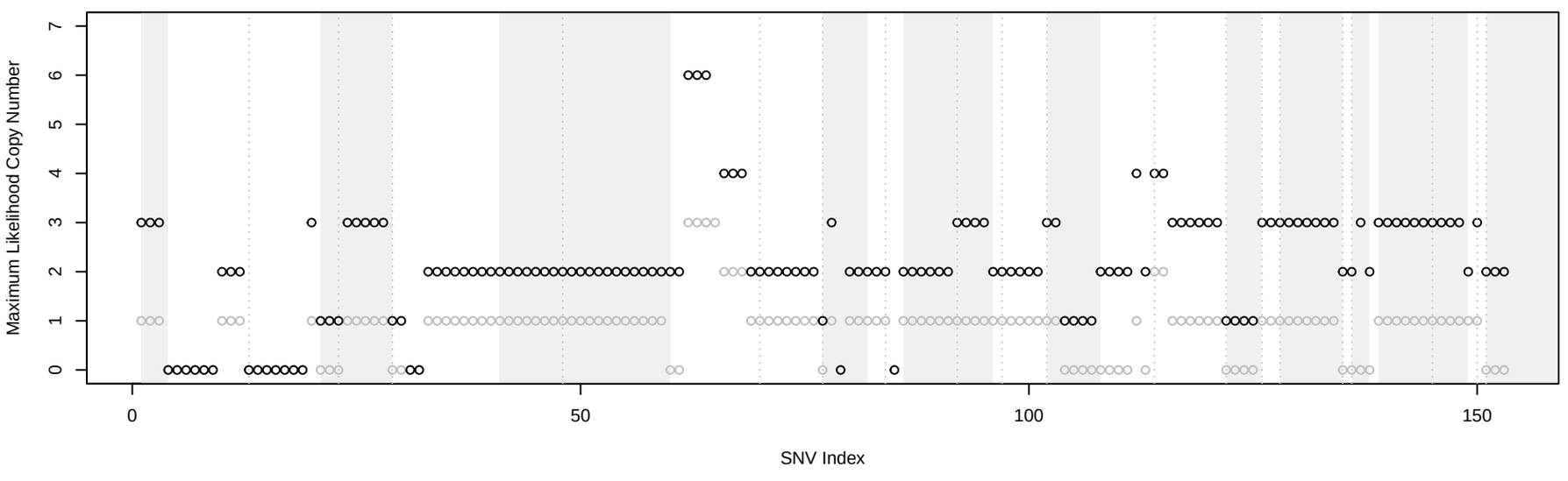

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m2
0m1
1m1
2m1
3m1
4m1
Allelic fraction (somatic)
Copy Number log−ratio

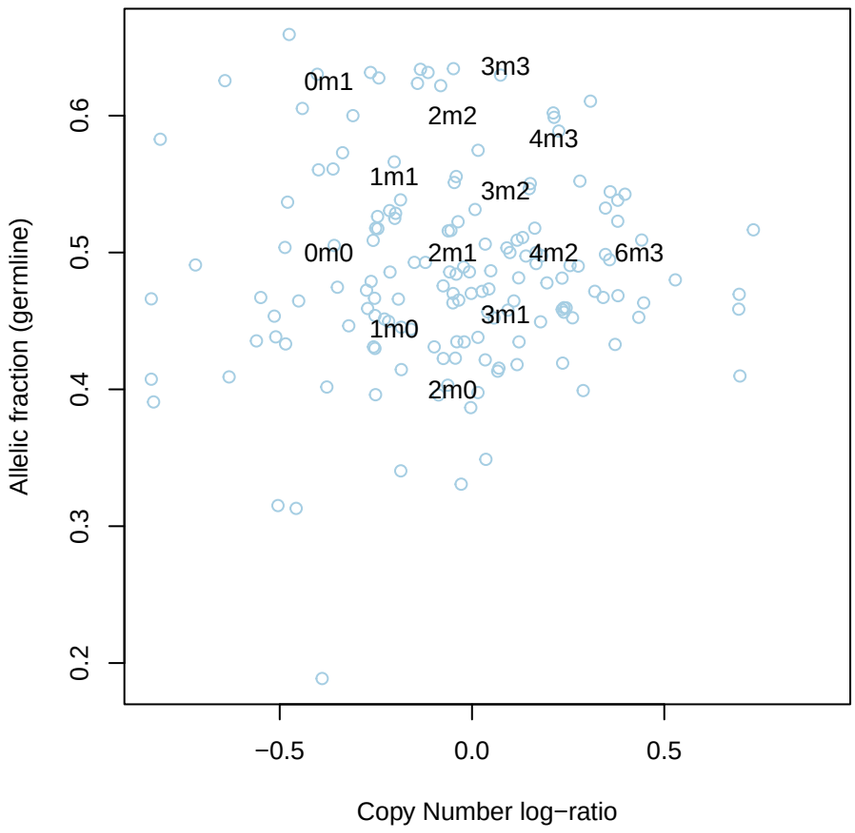

Frequency
Cellular fraction

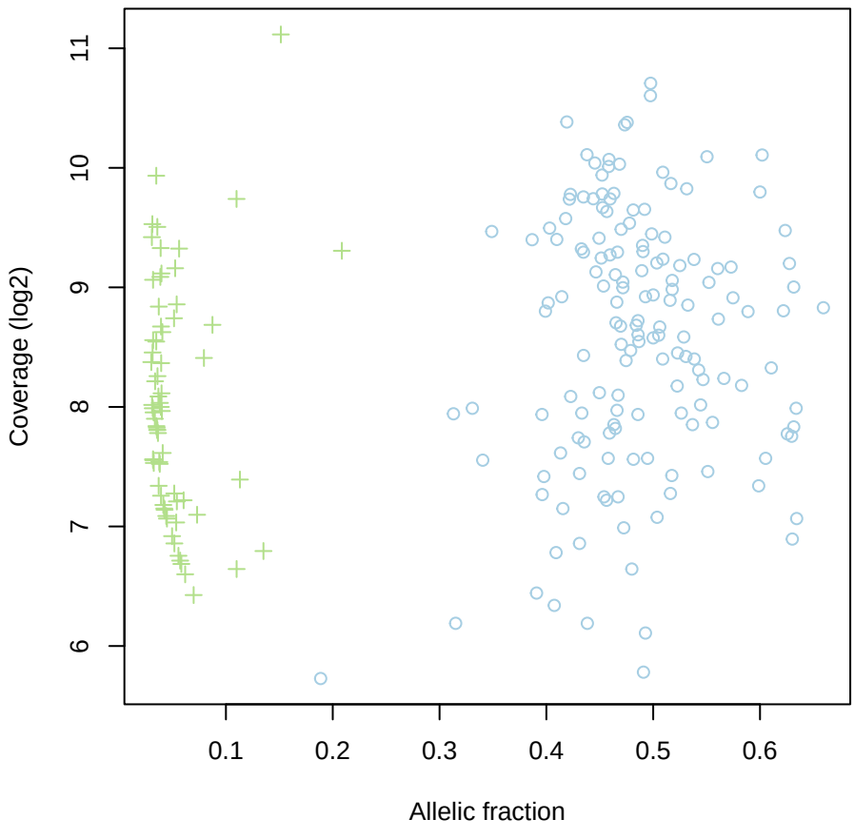

Purity: 0.2 Tumor ploidy: 2.356
0
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

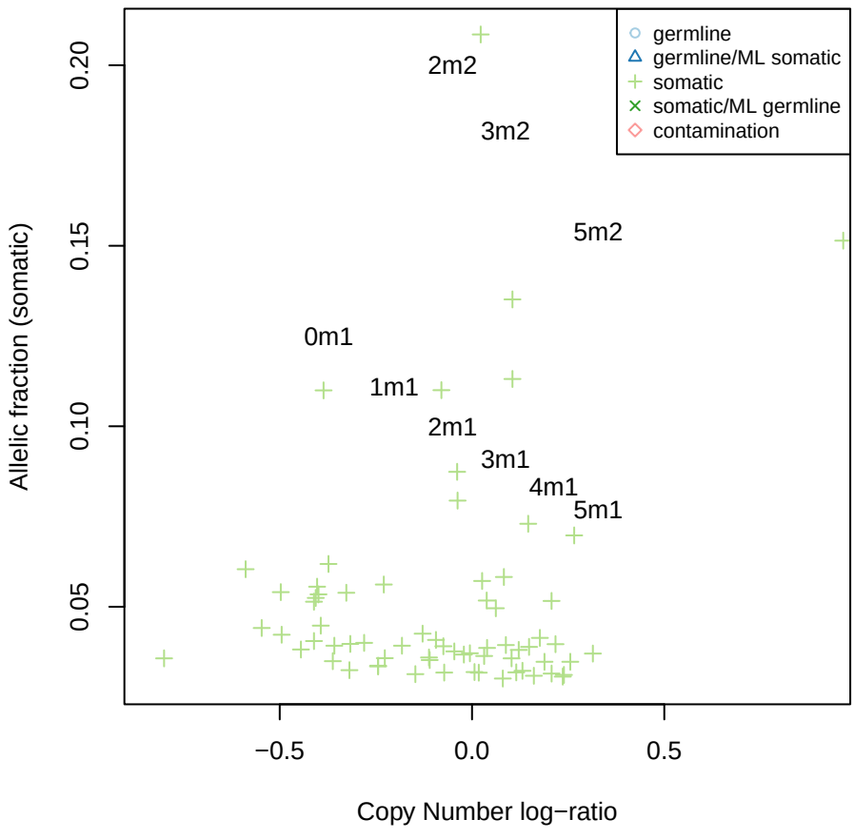

Purity: 0.2 Tumor ploidy: 2.356 SNV log−likelihood: 8.37 GoF: 93.1% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

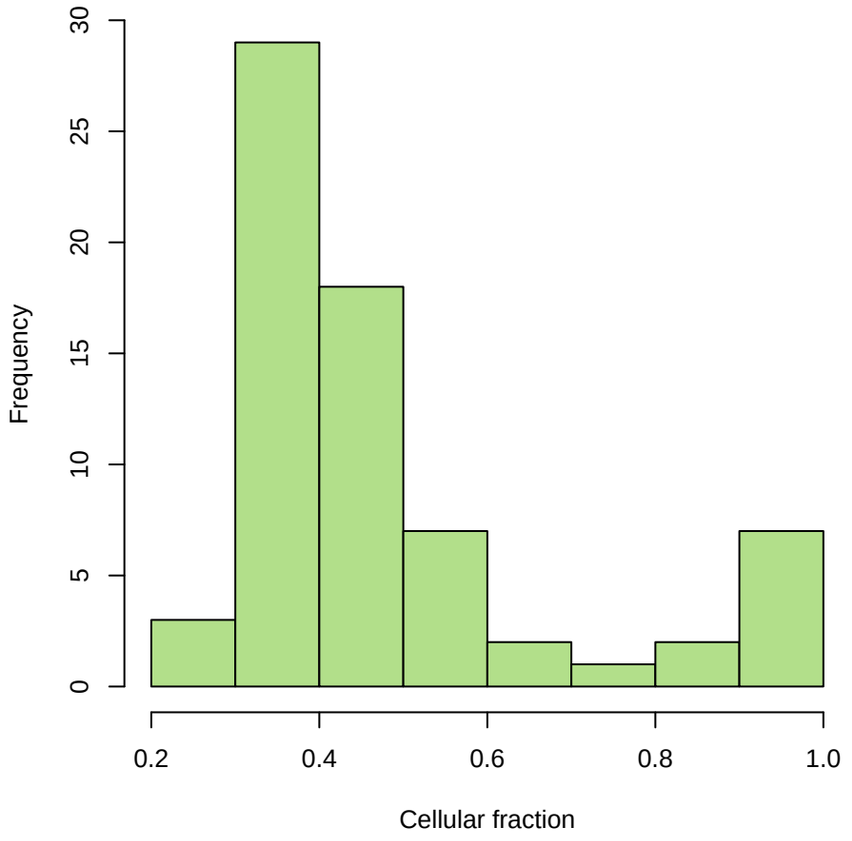

SCNA−fit log−likelihood: −7116.38
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 4 6
0 50 100 150
SNV Index

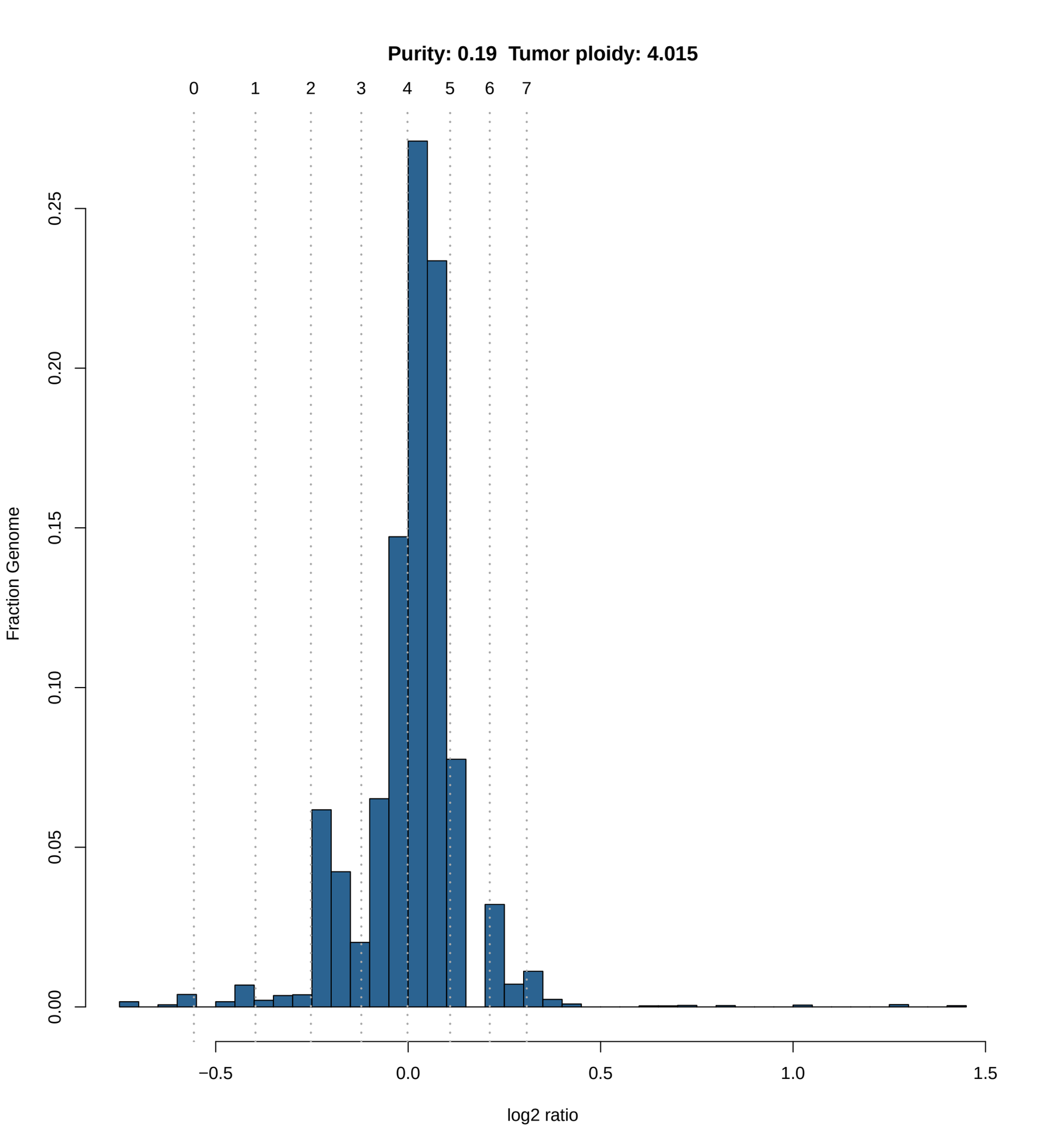

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

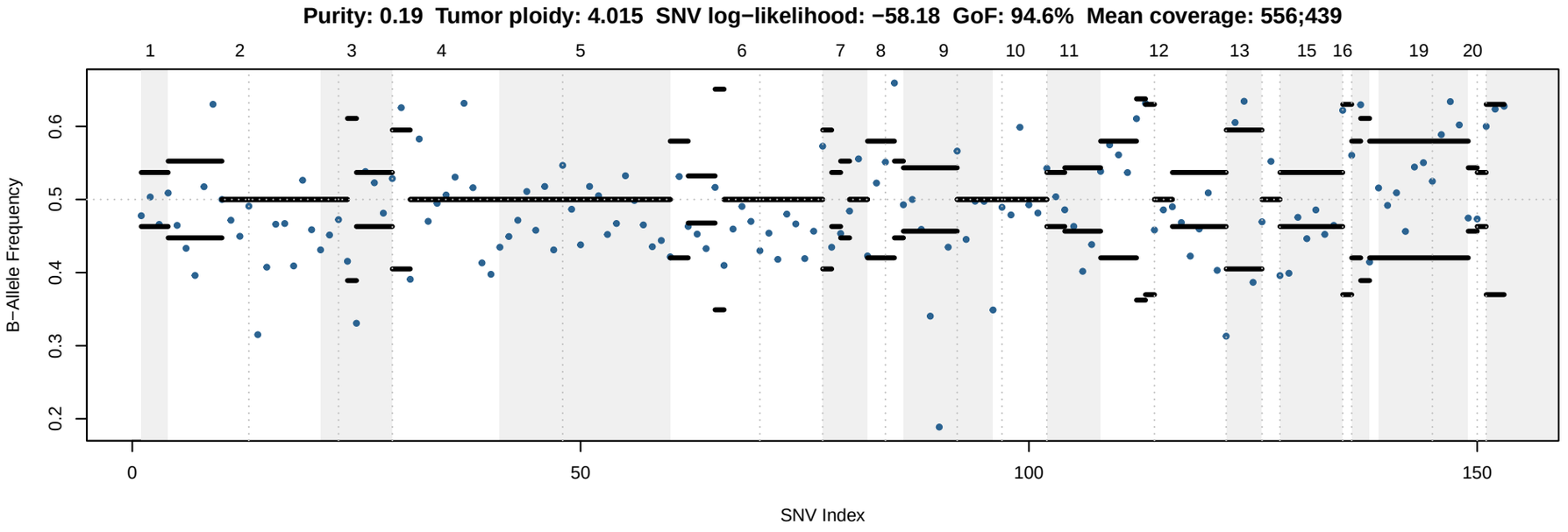

Allelic fraction (germline)
Copy Number log−ratio
0m1
3m3
2m2
4m3
1m1
3m2
0m0
2m1
4m2
6m3
3m1
1m0
2m0

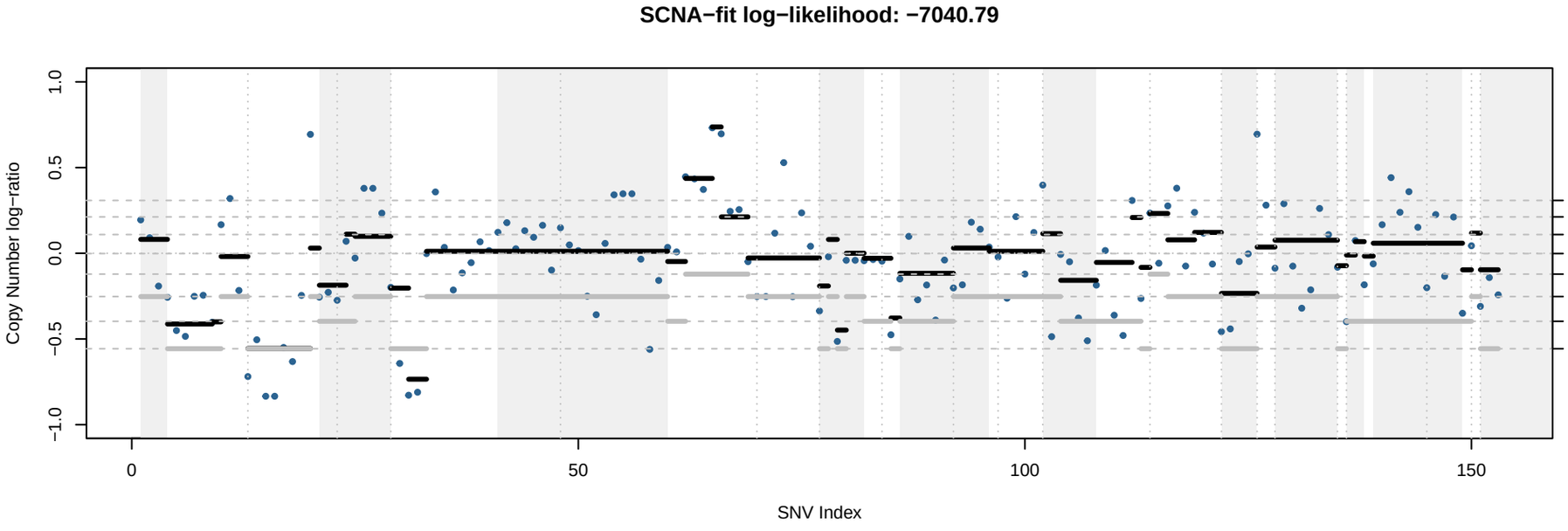

Coverage (log2)
Allelic fraction

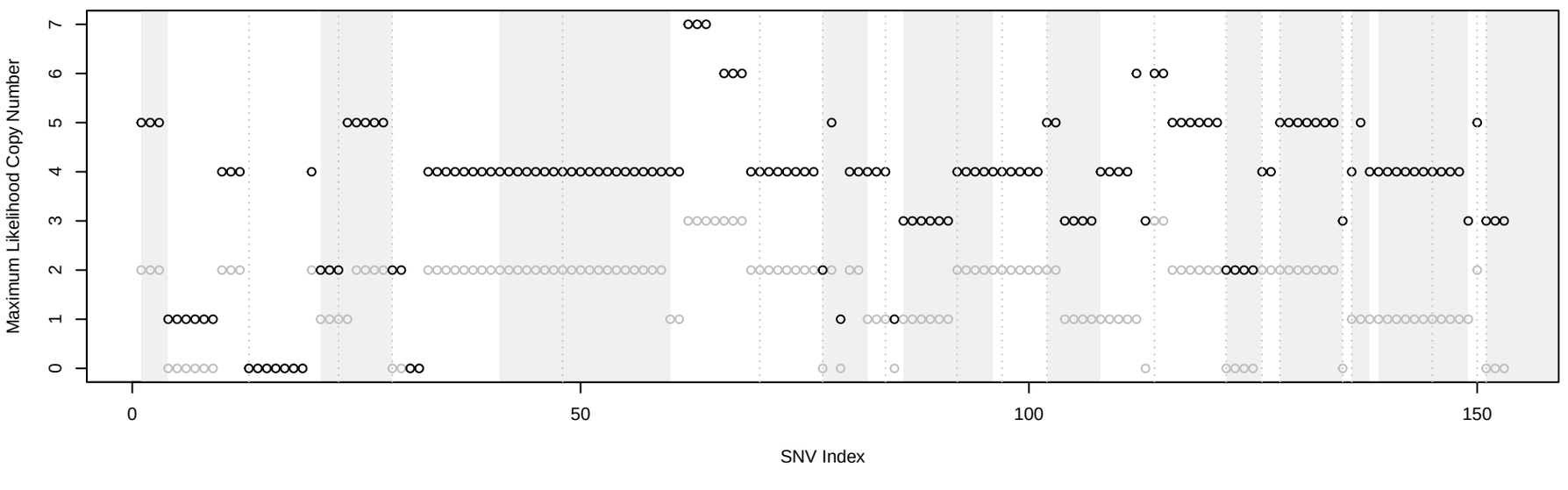

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
3m2
5m2
0m1
1m1
2m1
3m1
4m1
5m1

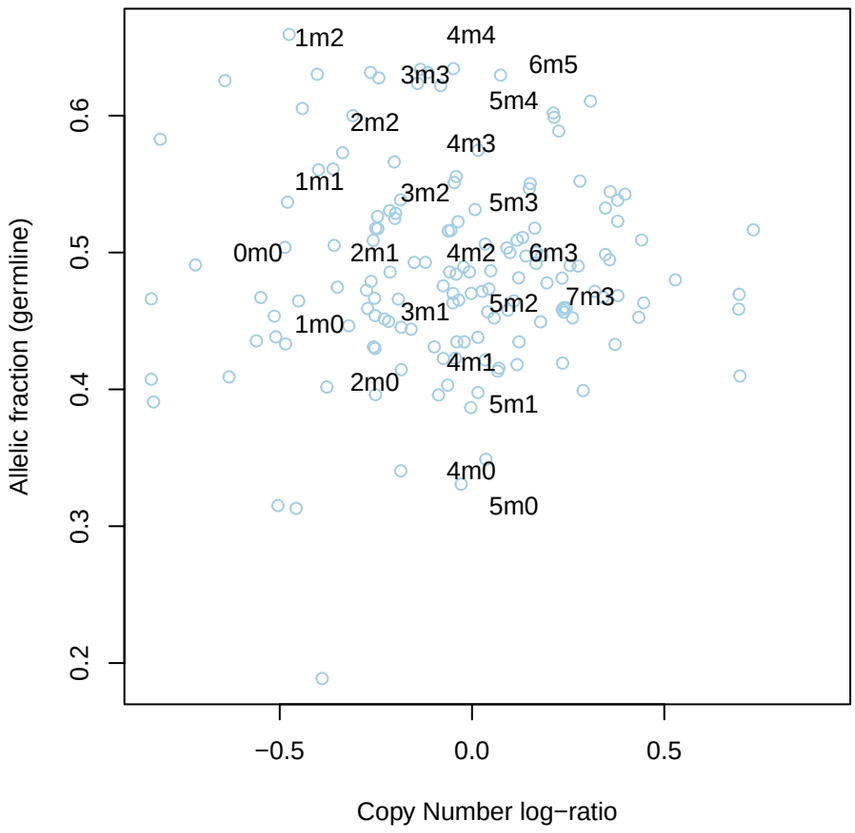

Frequency
Cellular fraction

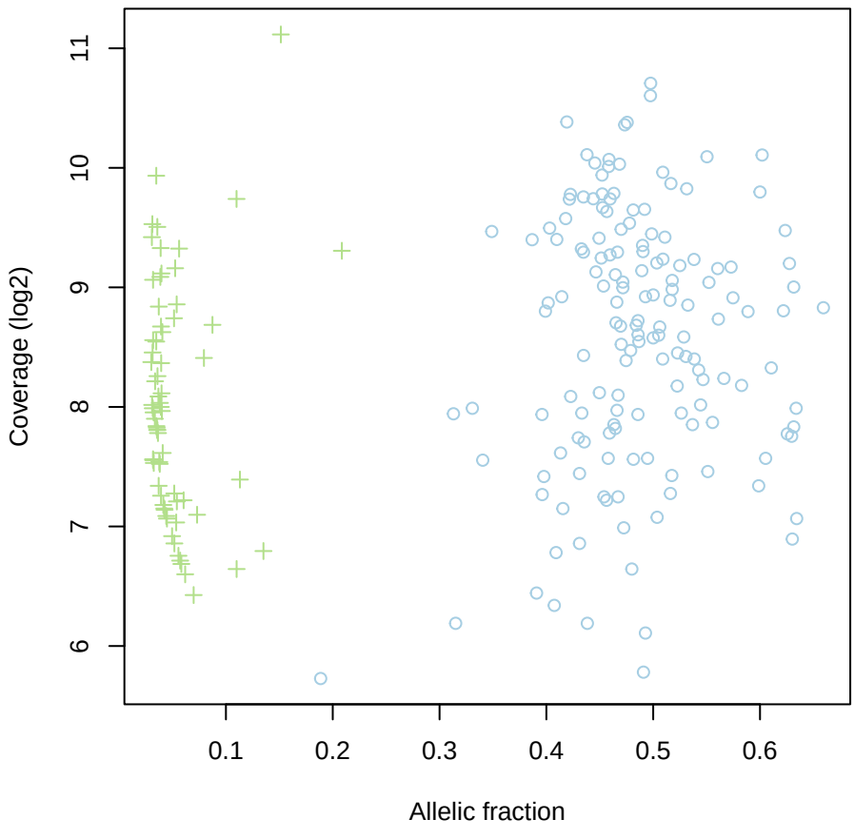

Purity: 0.19 Tumor ploidy: 4.015
0
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

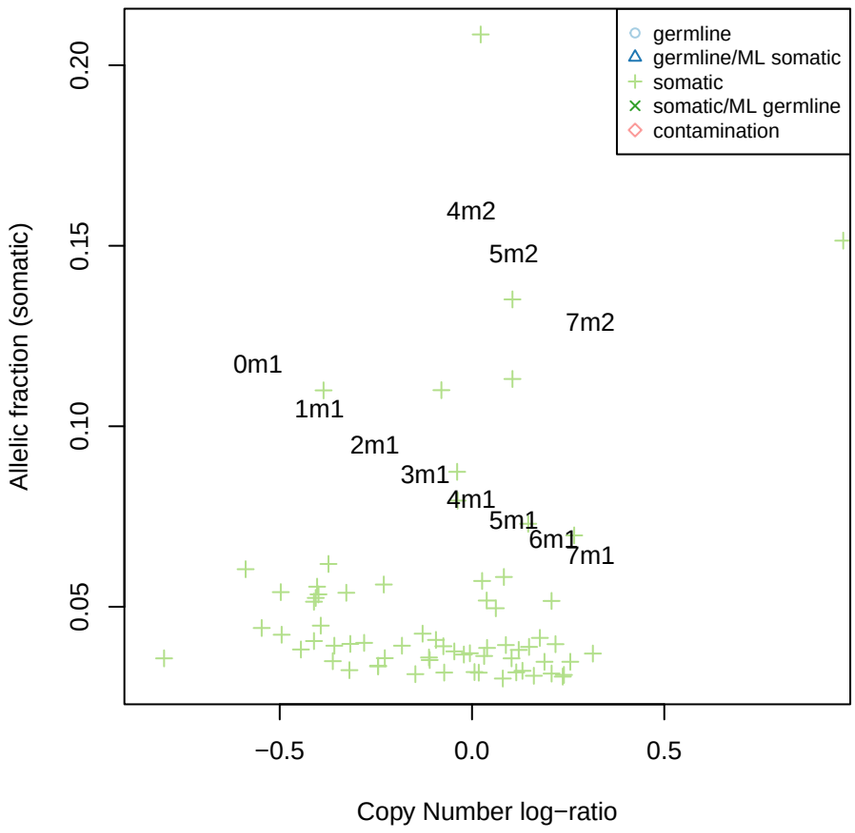

Purity: 0.19 Tumor ploidy: 4.015 SNV log−likelihood: −58.18 GoF: 94.6% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

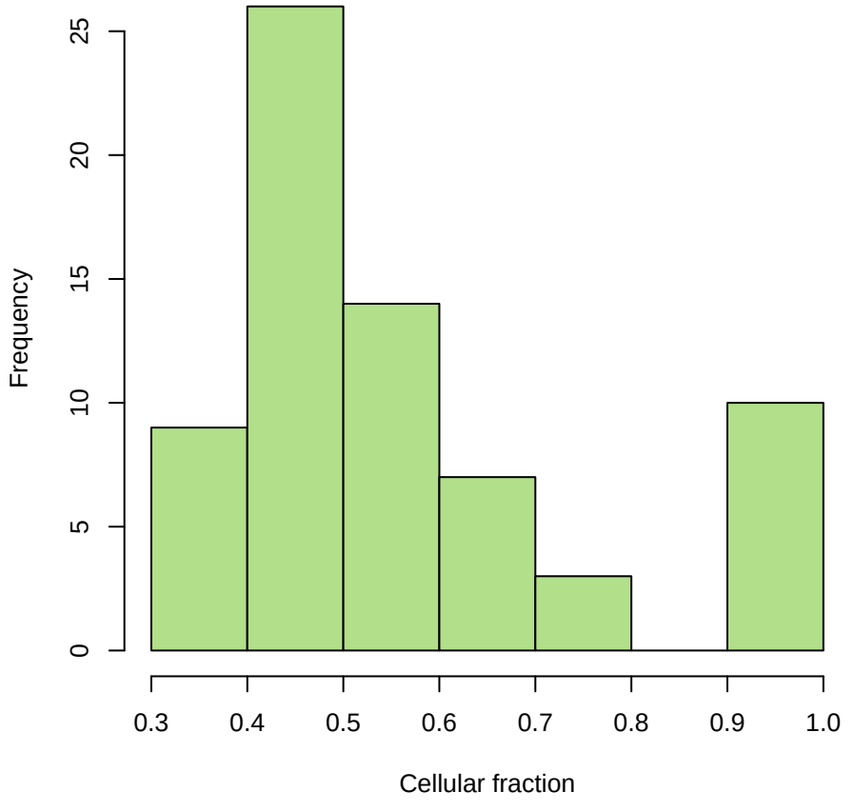

SCNA−fit log−likelihood: −7040.79
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 4 6
0 50 100 150
SNV Index

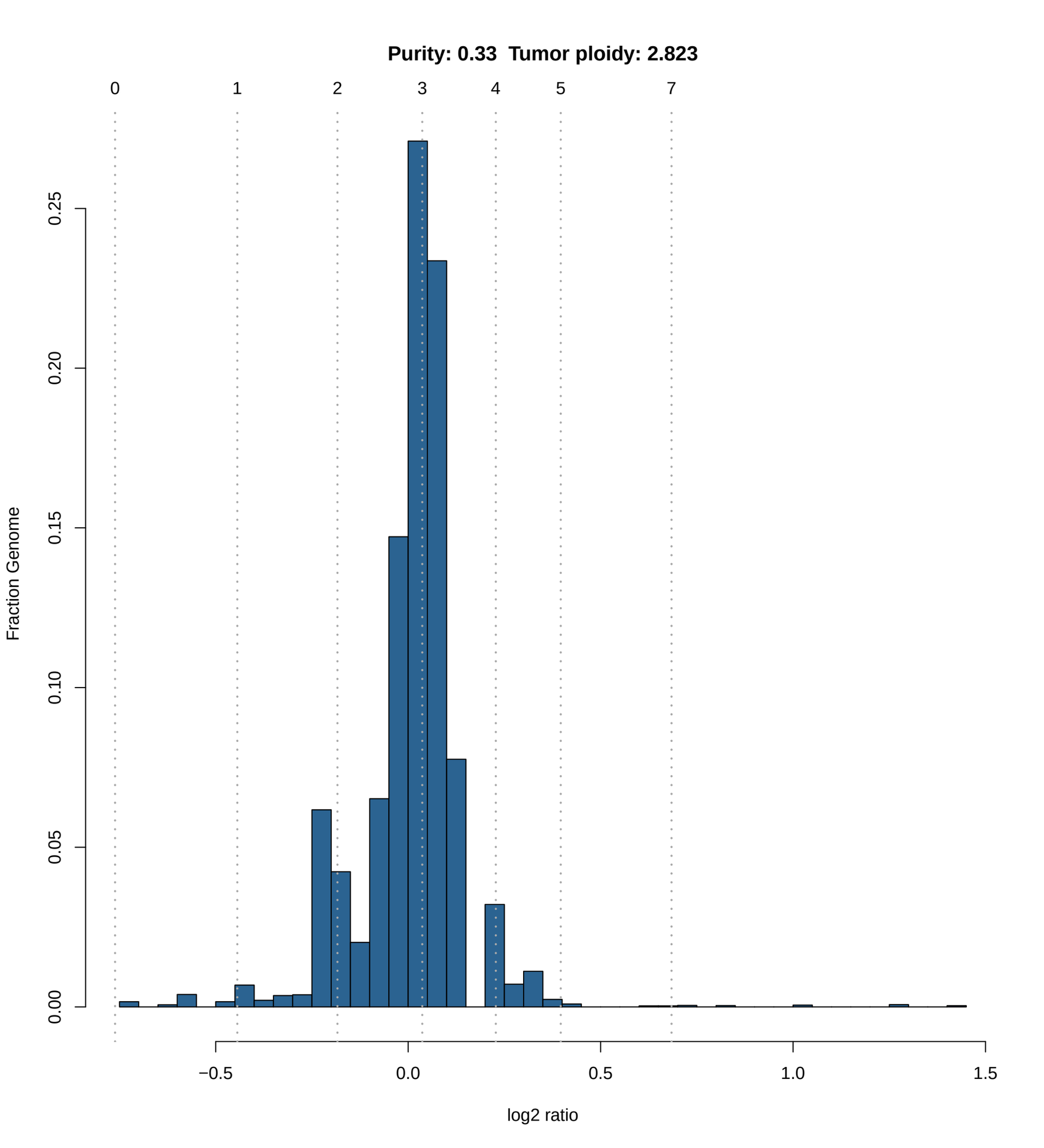

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

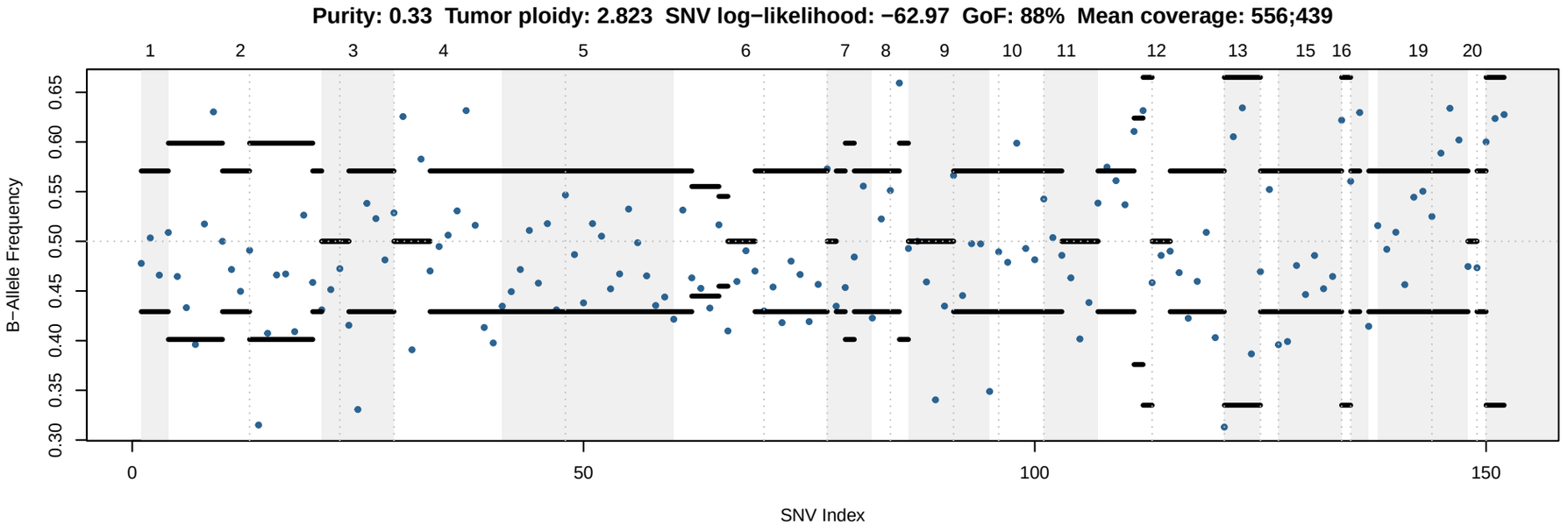

1m2
4m4
3m3
6m5
5m4
2m2
4m3
1m1
3m2
5m3
0m0
2m1
4m2
6m3
5m2
7m3
3m1
1m0
4m1
2m0
5m1
4m0
5m0
Allelic fraction (germline)
Copy Number log−ratio

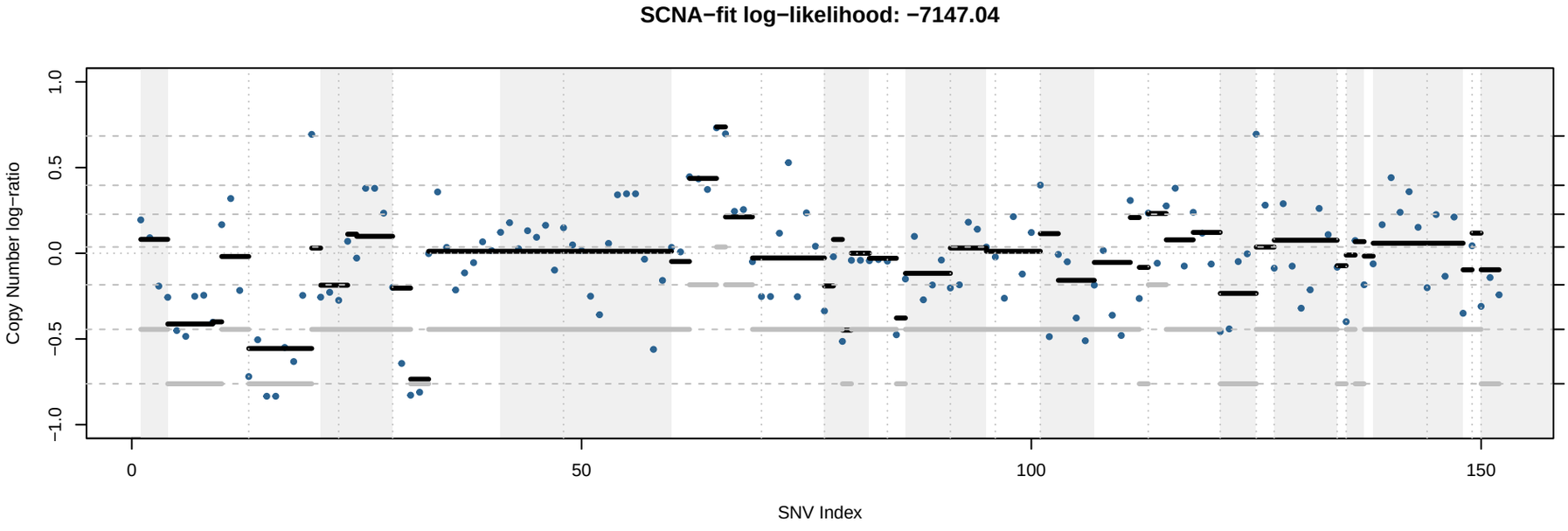

Coverage (log2)
Allelic fraction

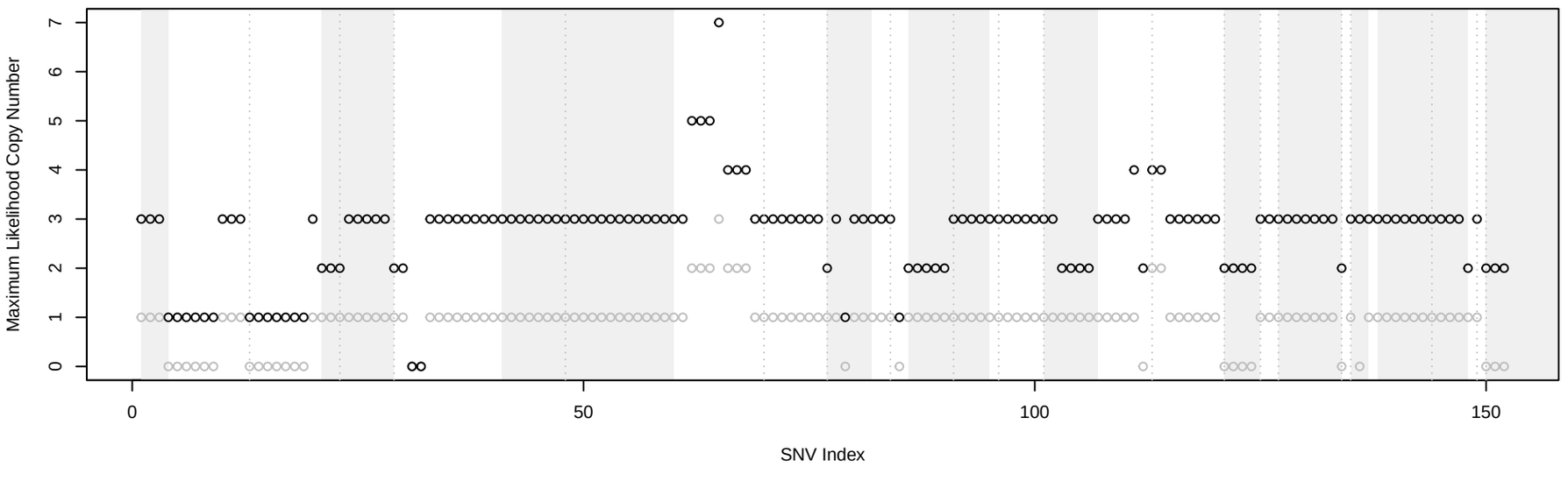

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m2
5m2
7m2
0m1
1m1
2m1
3m1
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

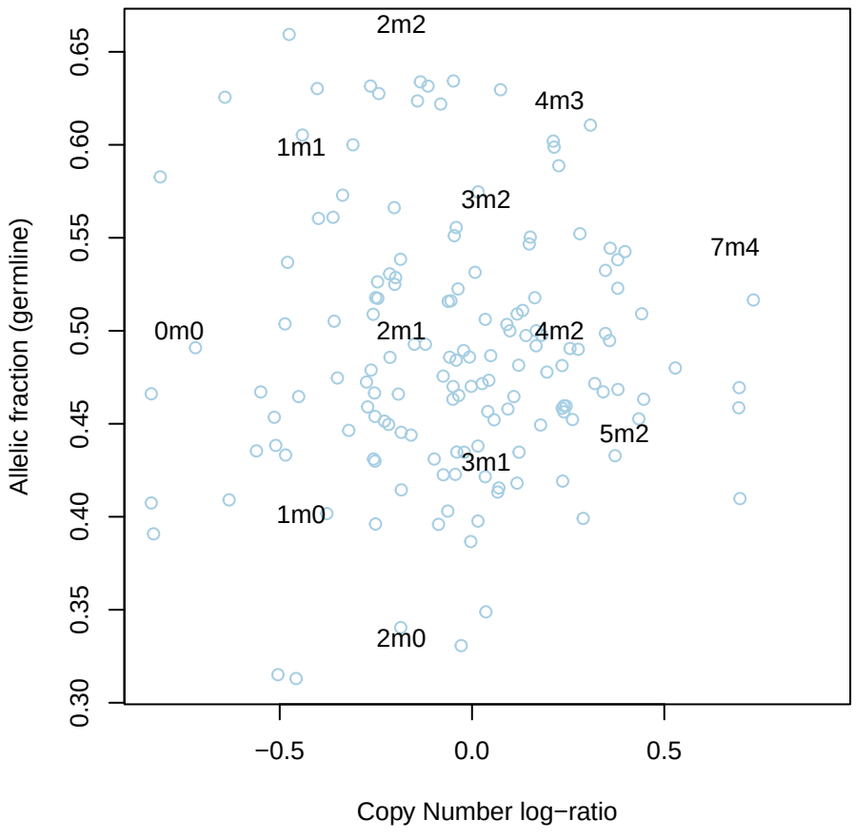

Frequency
Cellular fraction

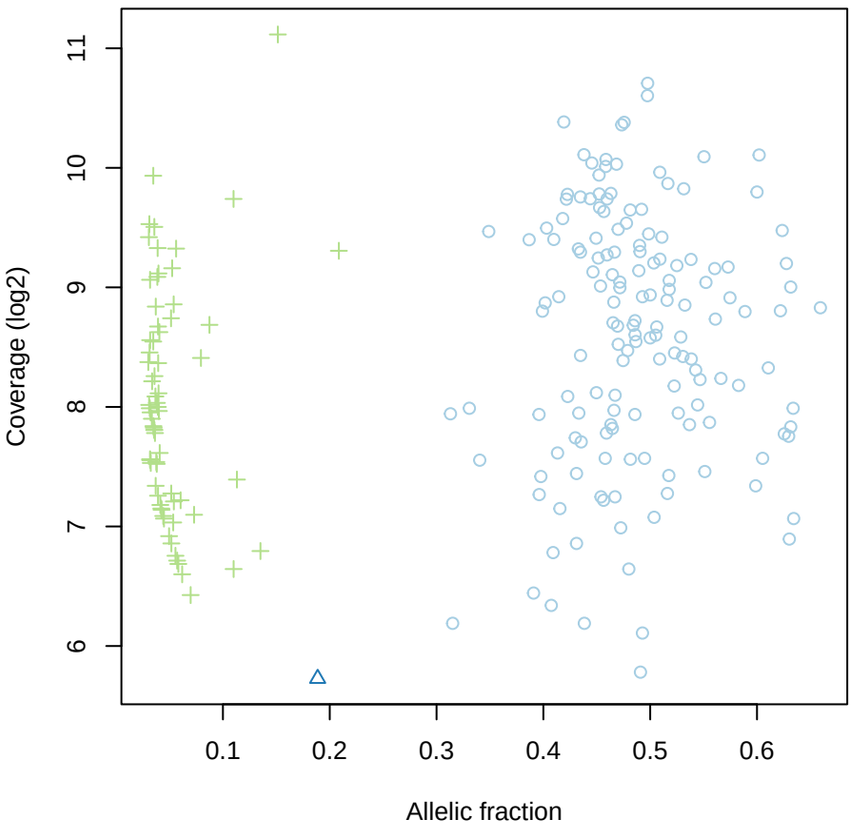

Purity: 0.33 Tumor ploidy: 2.823
0
1
2
3
4
5
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

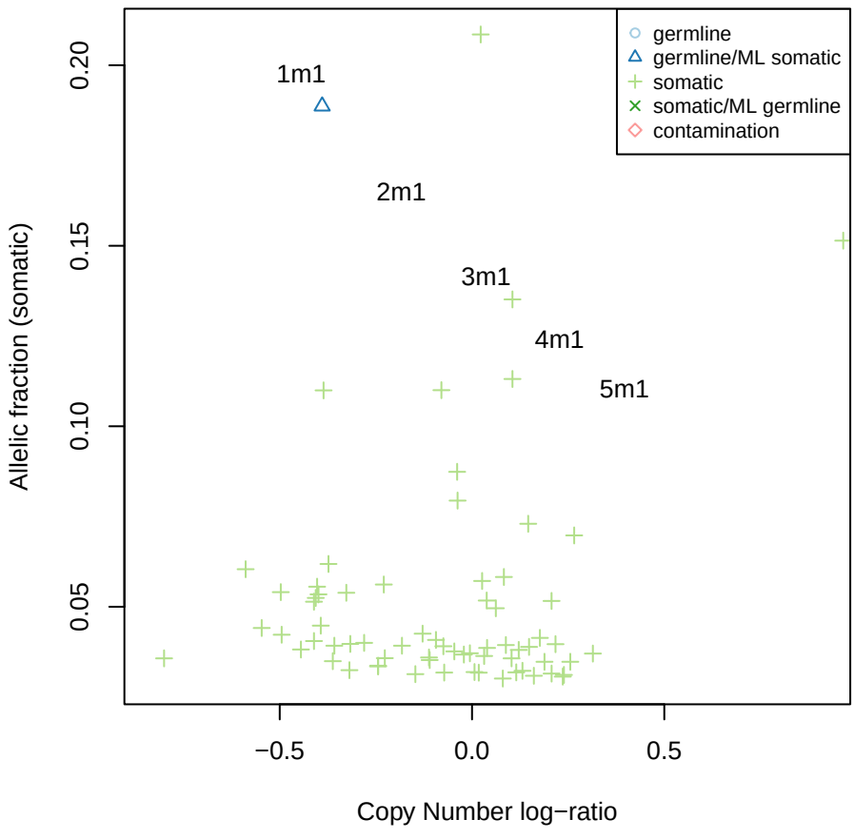

Purity: 0.33 Tumor ploidy: 2.823 SNV log−likelihood: −62.97 GoF: 88% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 50 100 150
SNV Index

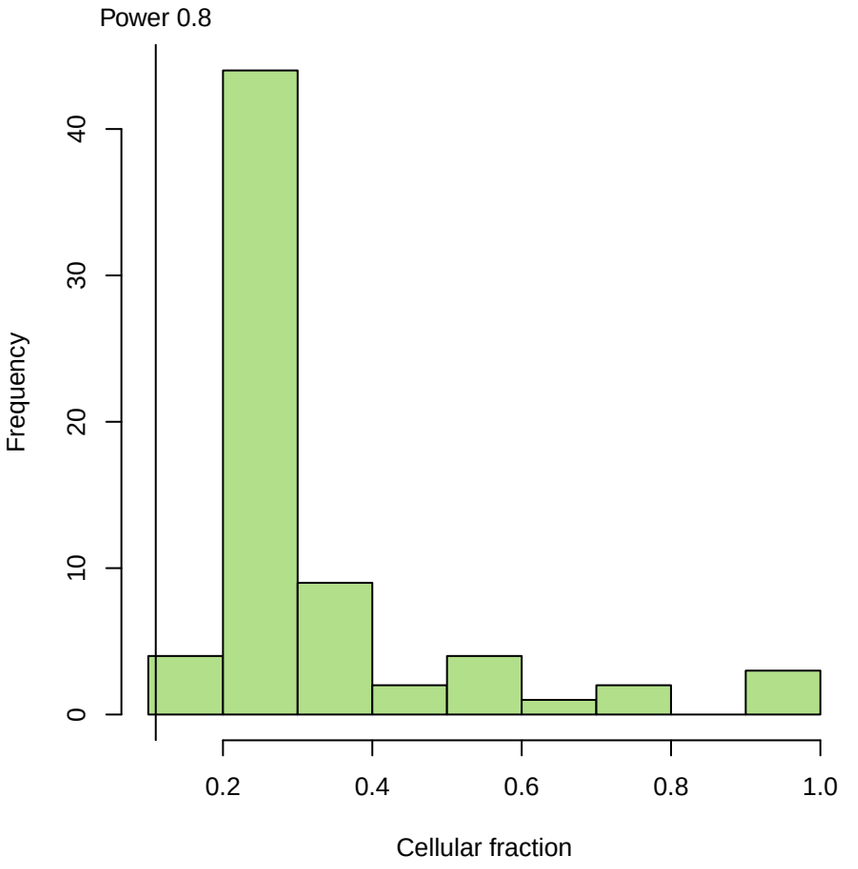

SCNA−fit log−likelihood: −7147.04
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 7
0 50 100 150
SNV Index

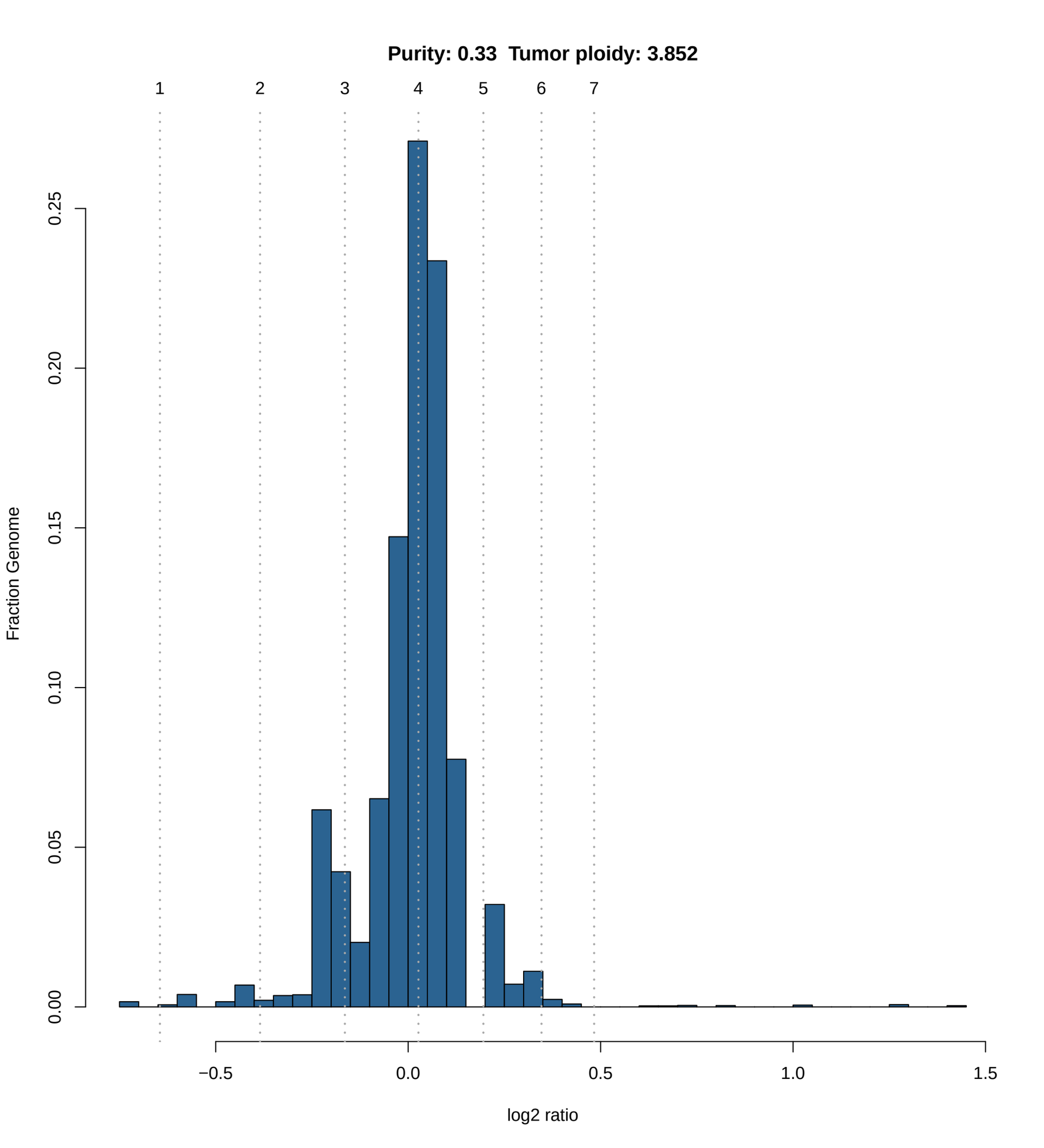

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

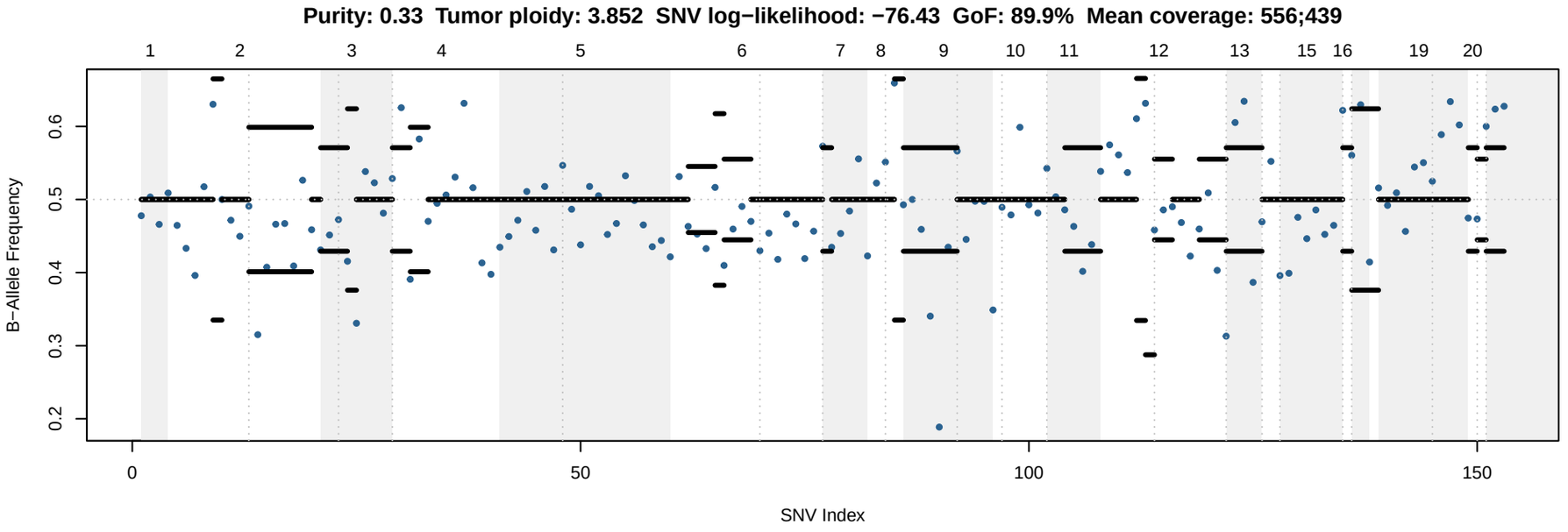

2m2
4m3
1m1
3m2
7m4
0m0
2m1
4m2
5m2
3m1
1m0
2m0
Allelic fraction (germline)
Copy Number log−ratio
0.30
0.35
0.40
0.45
0.50
0.55
0.60
0.65
−0.5
0.0
0.5

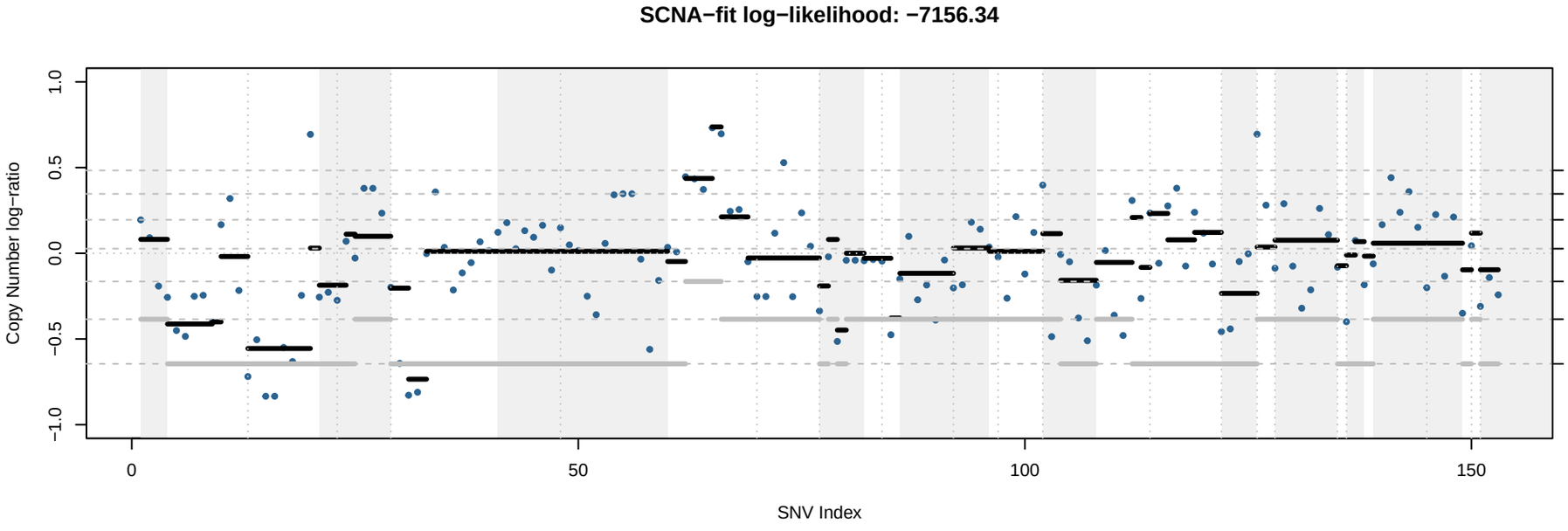

Coverage (log2)
Allelic fraction
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6

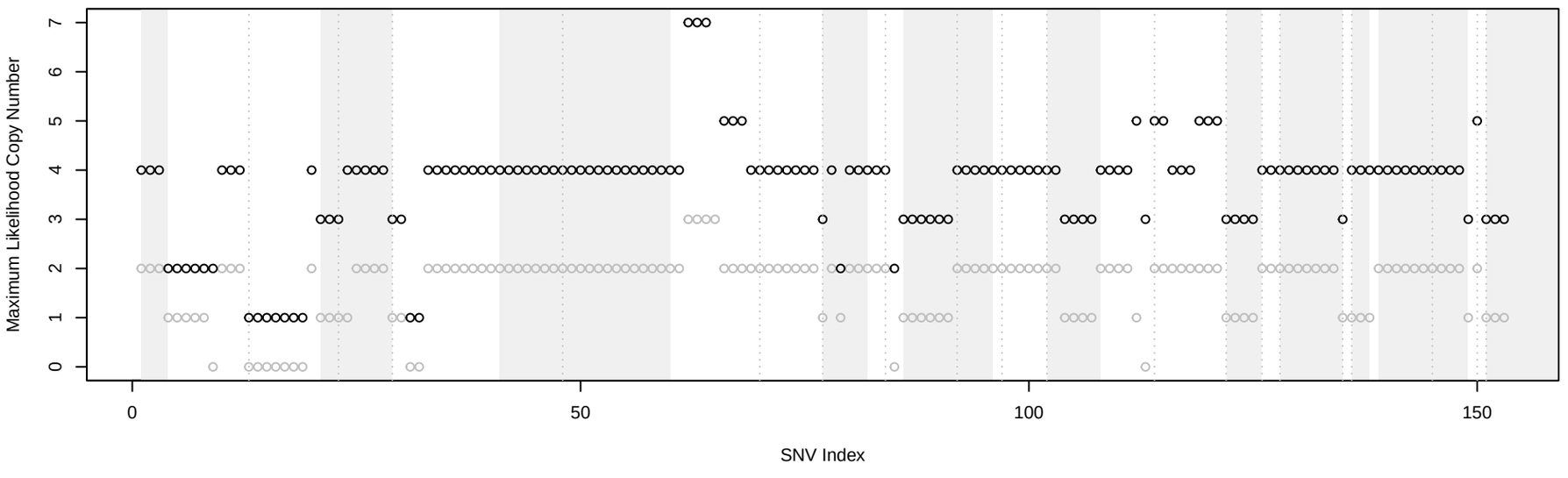

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
4m1
5m1
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
−0.5
0.0
0.5

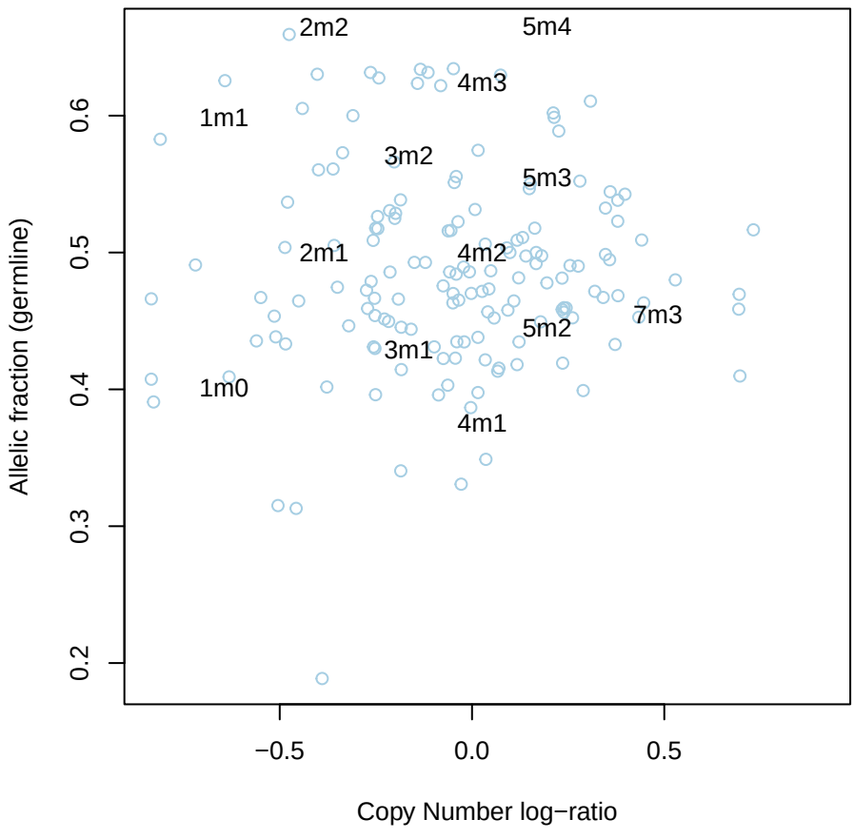

Power 0.8
Frequency
Cellular fraction
0
10
20
30
40
0.2
0.4
0.6
0.8
1.0

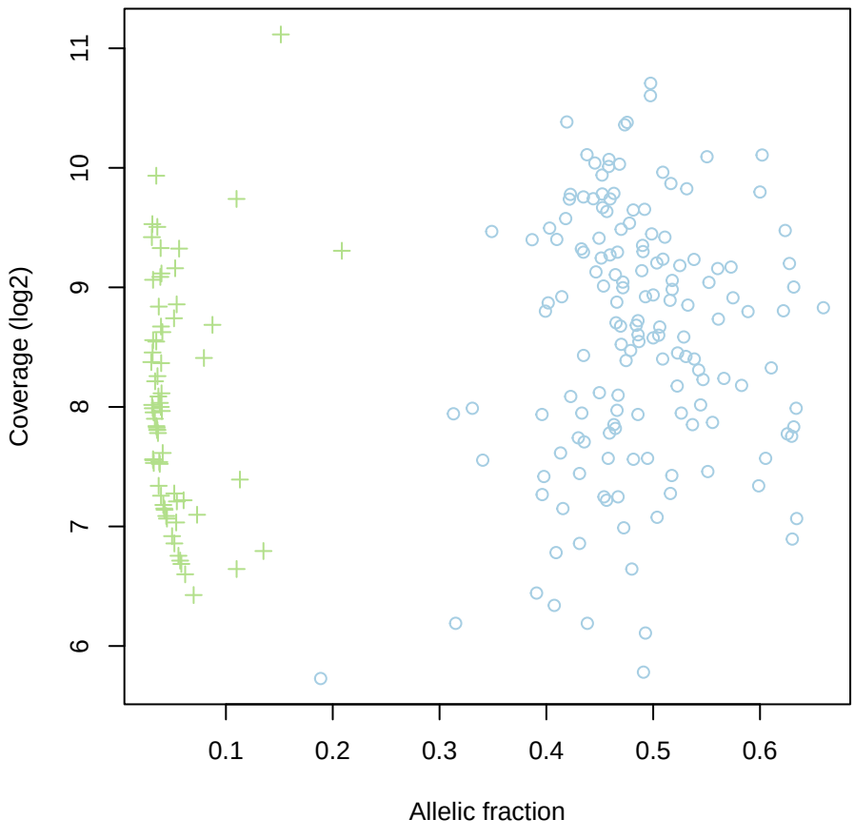

Purity: 0.33 Tumor ploidy: 3.852
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

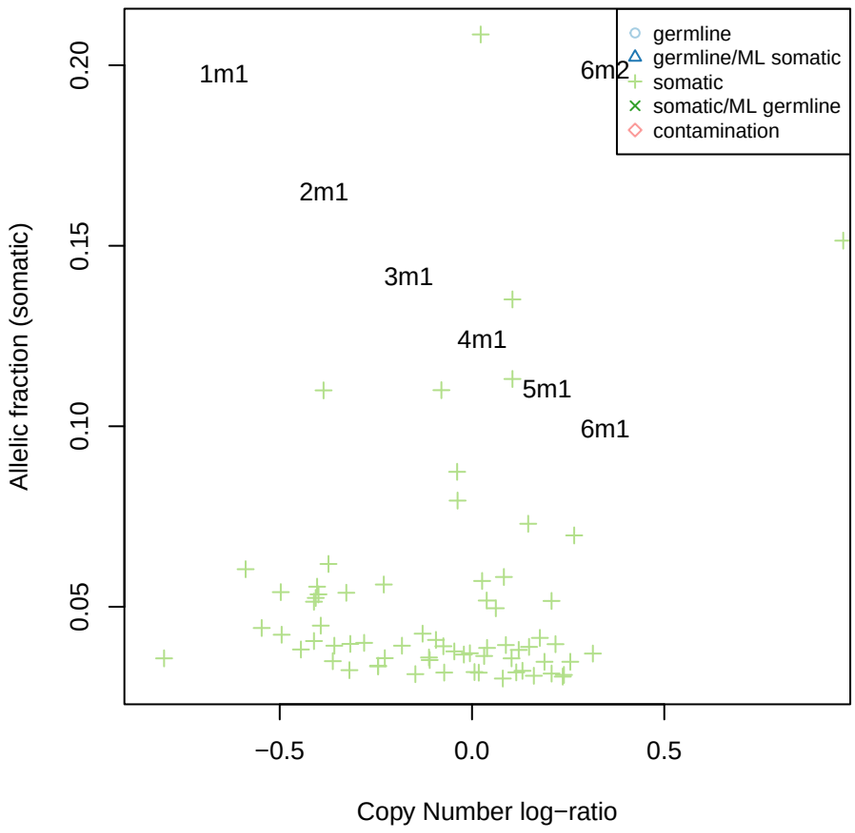

Purity: 0.33 Tumor ploidy: 3.852 SNV log−likelihood: −76.43 GoF: 89.9% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

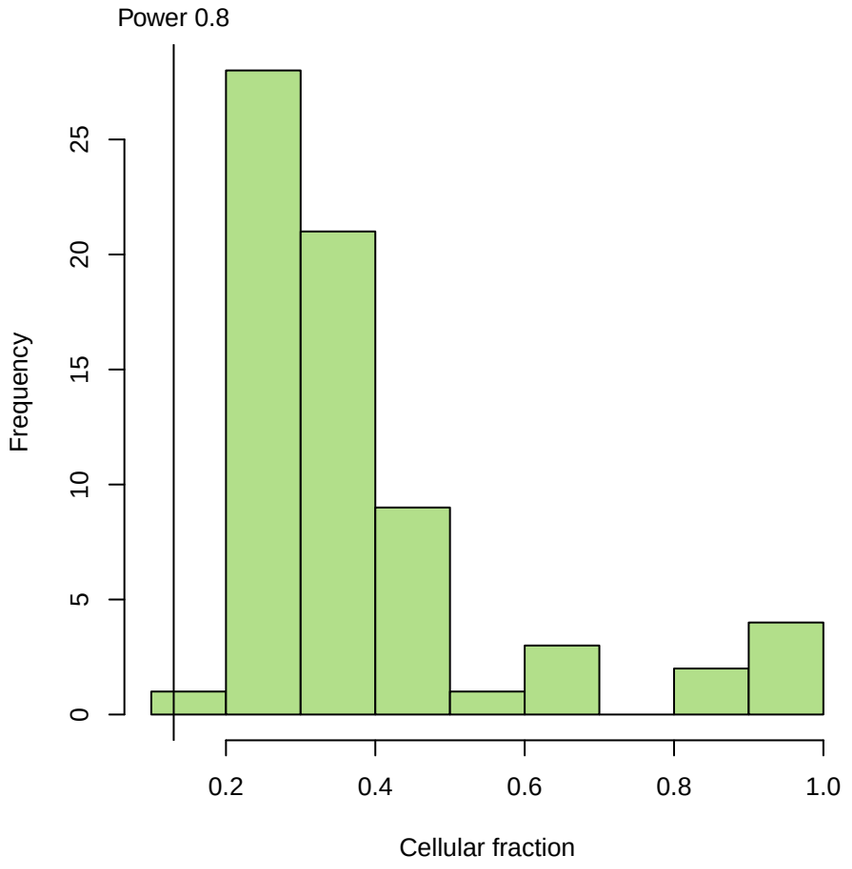

SCNA−fit log−likelihood: −7156.34
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6
0 50 100 150
SNV Index

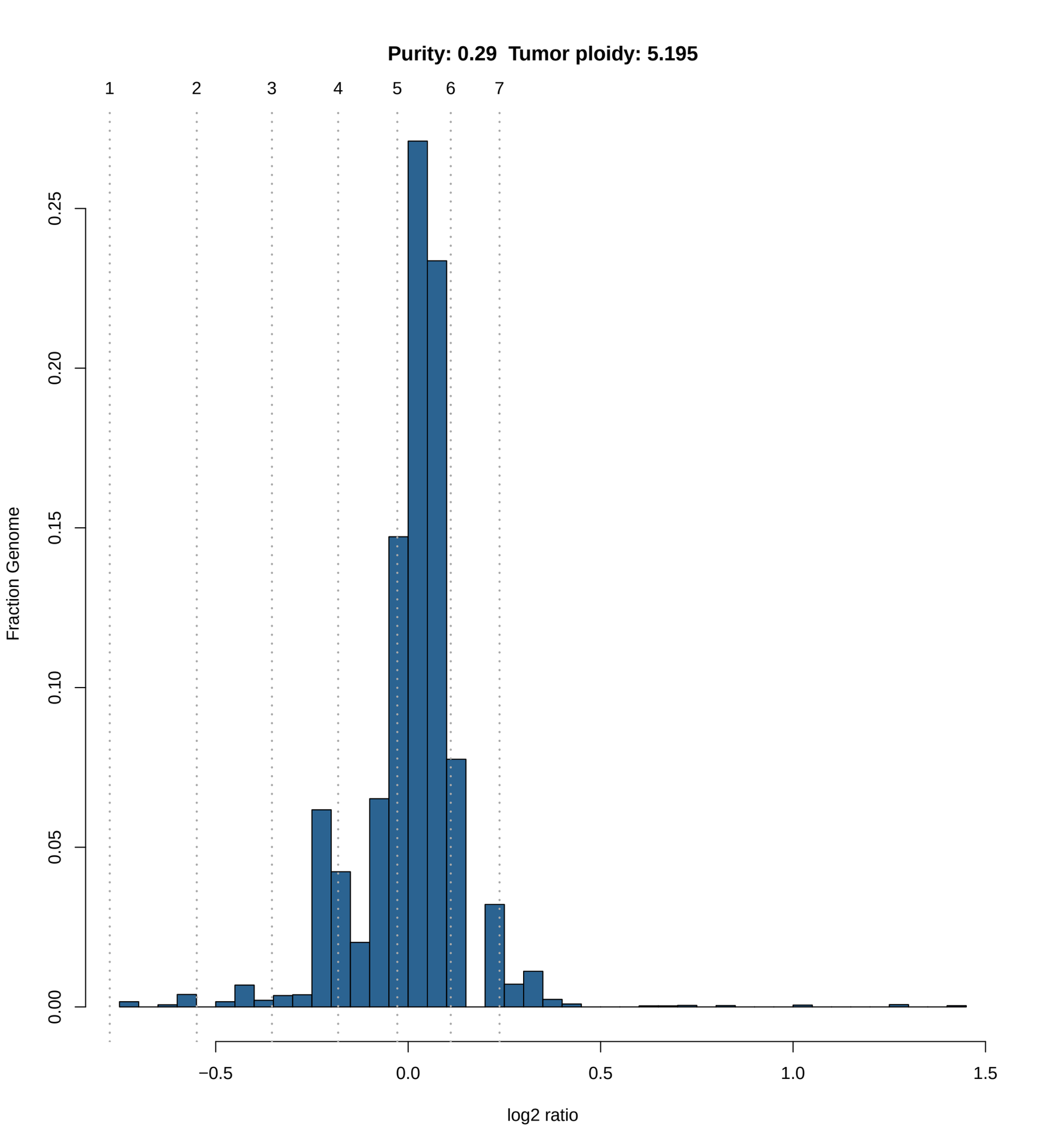

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

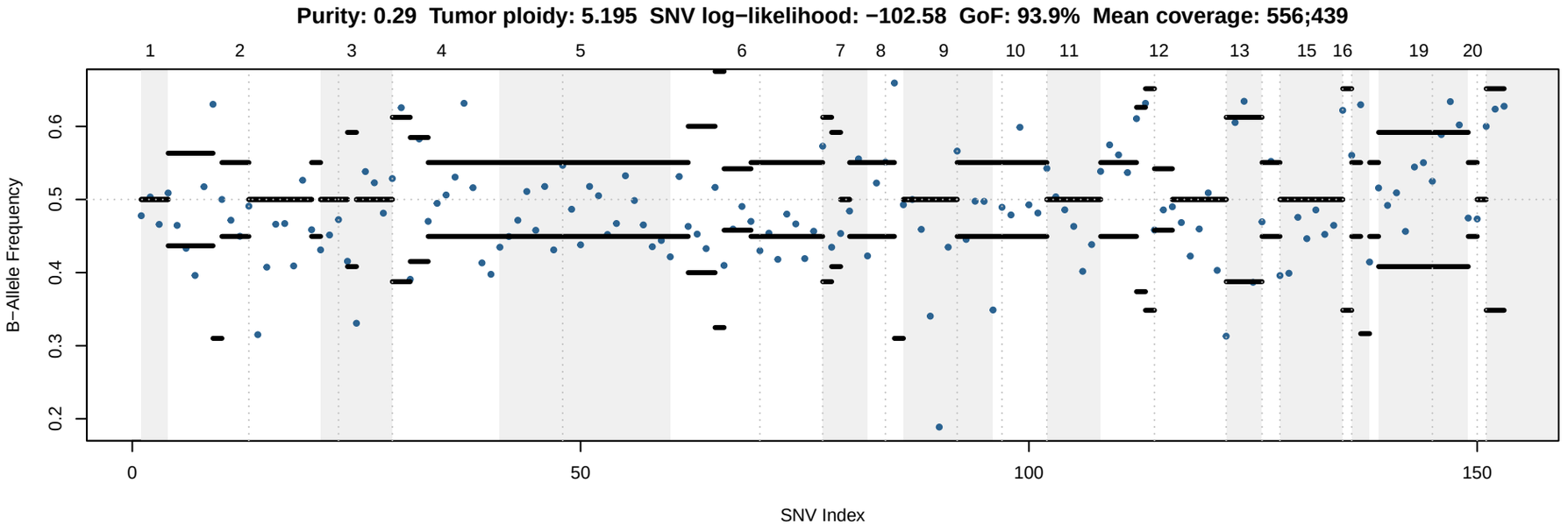

2m2
5m4
4m3
1m1
3m2
5m3
2m1
4m2
7m3
5m2
3m1
1m0
4m1
Allelic fraction (germline)
Copy Number log−ratio

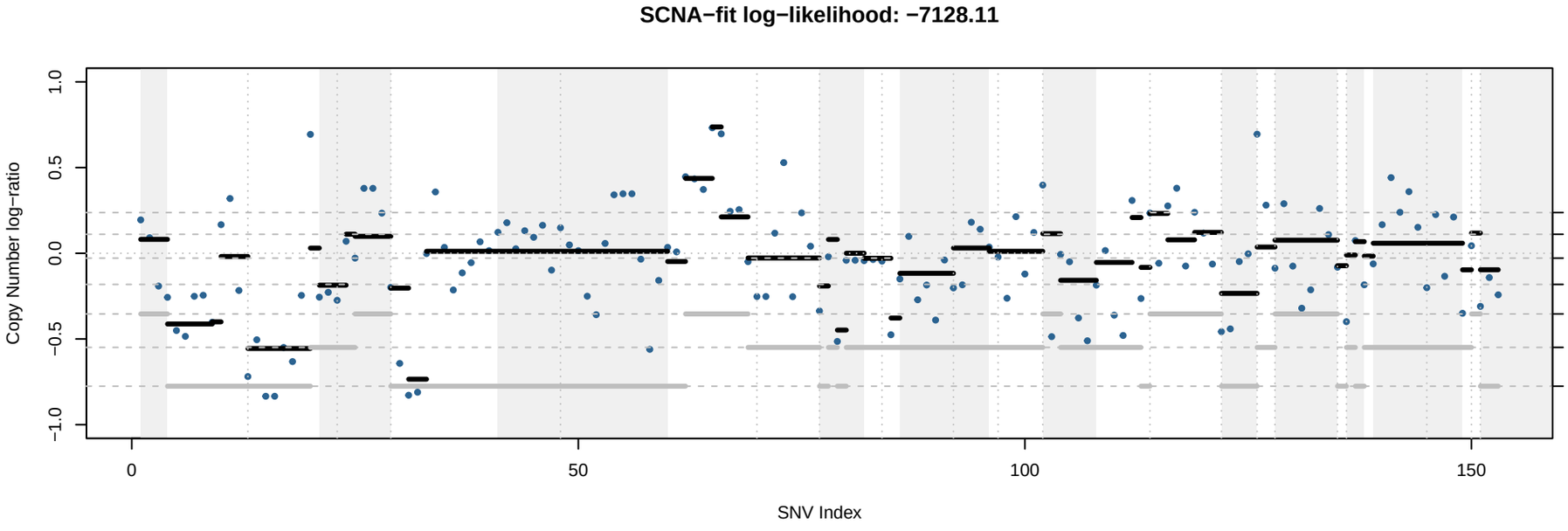

Coverage (log2)
Allelic fraction

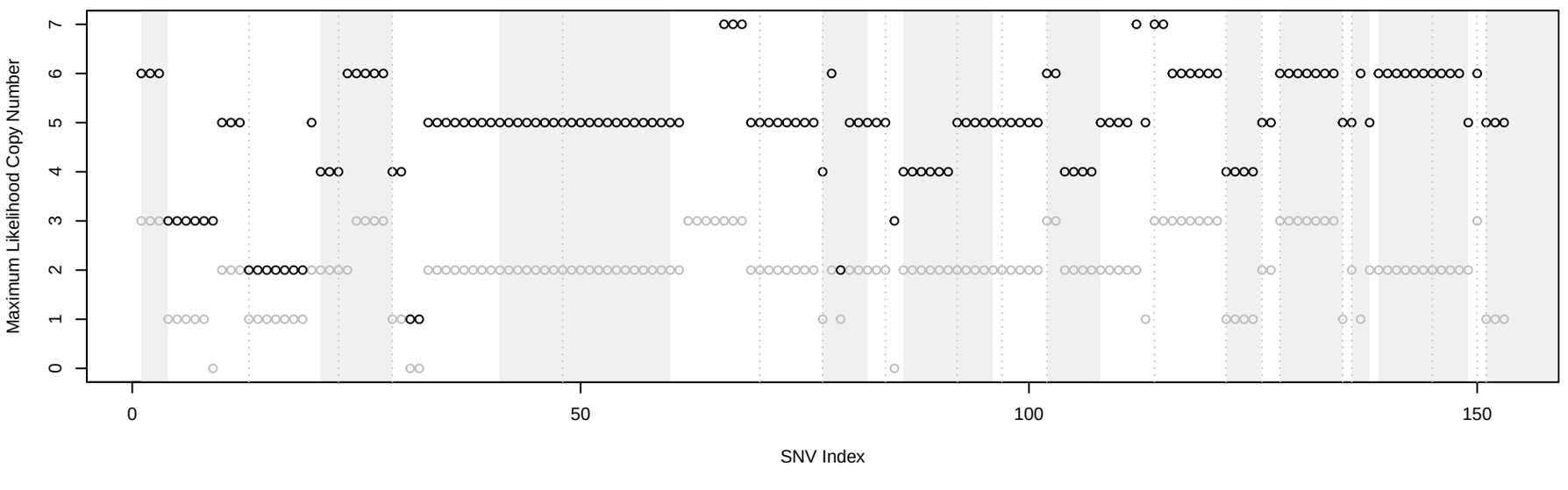

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
6m2
2m1
3m1
4m1
5m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio

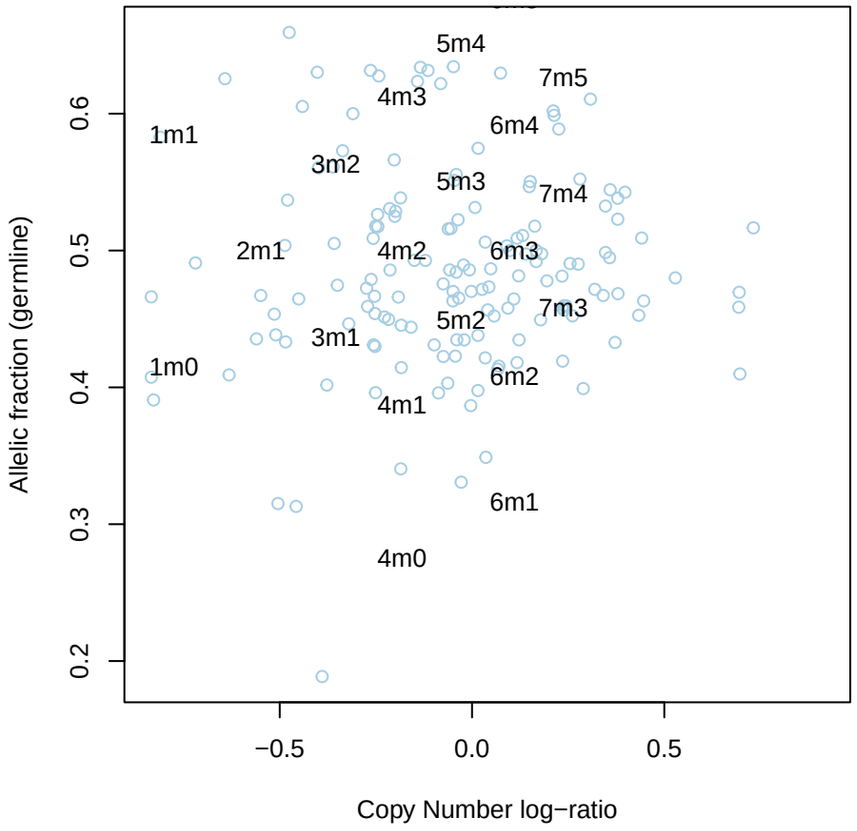

Power 0.8
Frequency
Cellular fraction

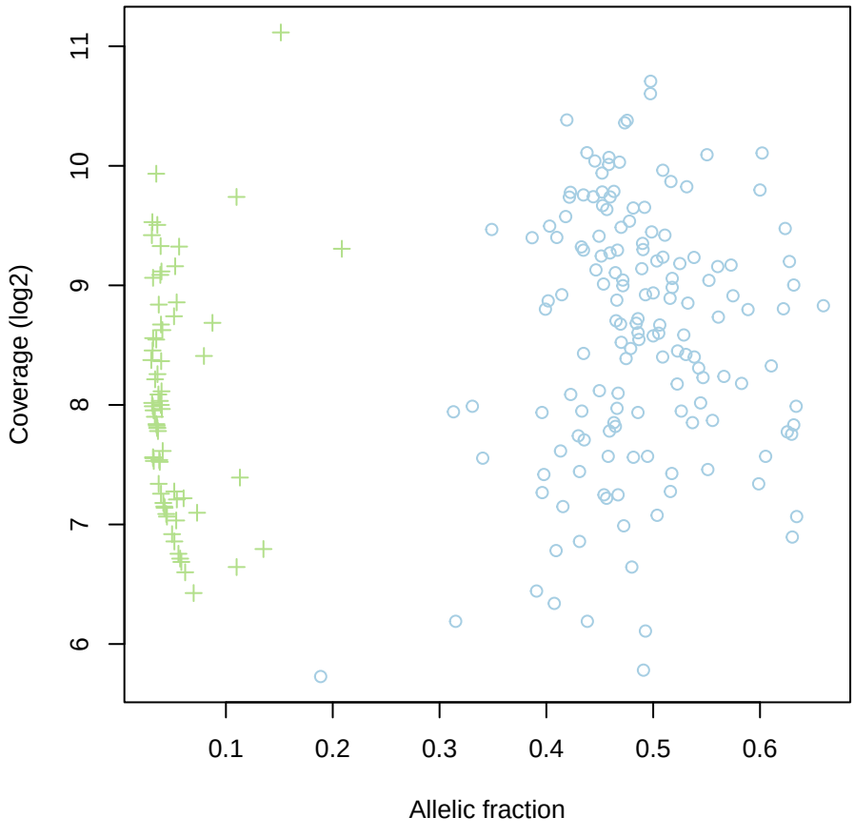

Purity: 0.29 Tumor ploidy: 5.195
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

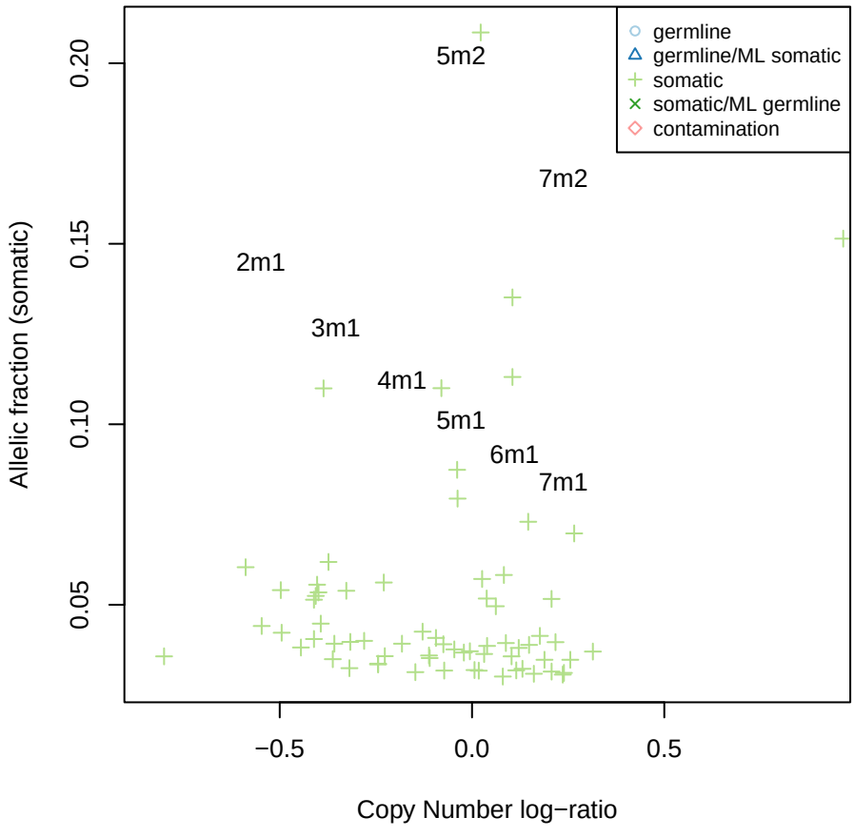

Purity: 0.29 Tumor ploidy: 5.195 SNV log−likelihood: −102.58 GoF: 93.9% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

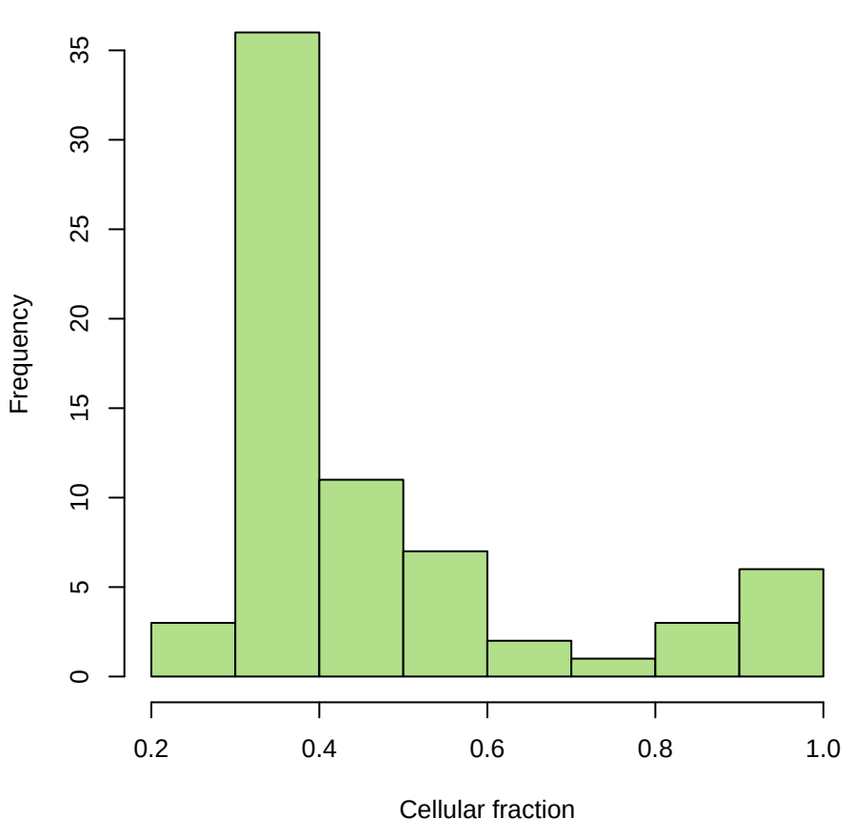

SCNA−fit log−likelihood: −7128.11
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 7
0 50 100 150
SNV Index

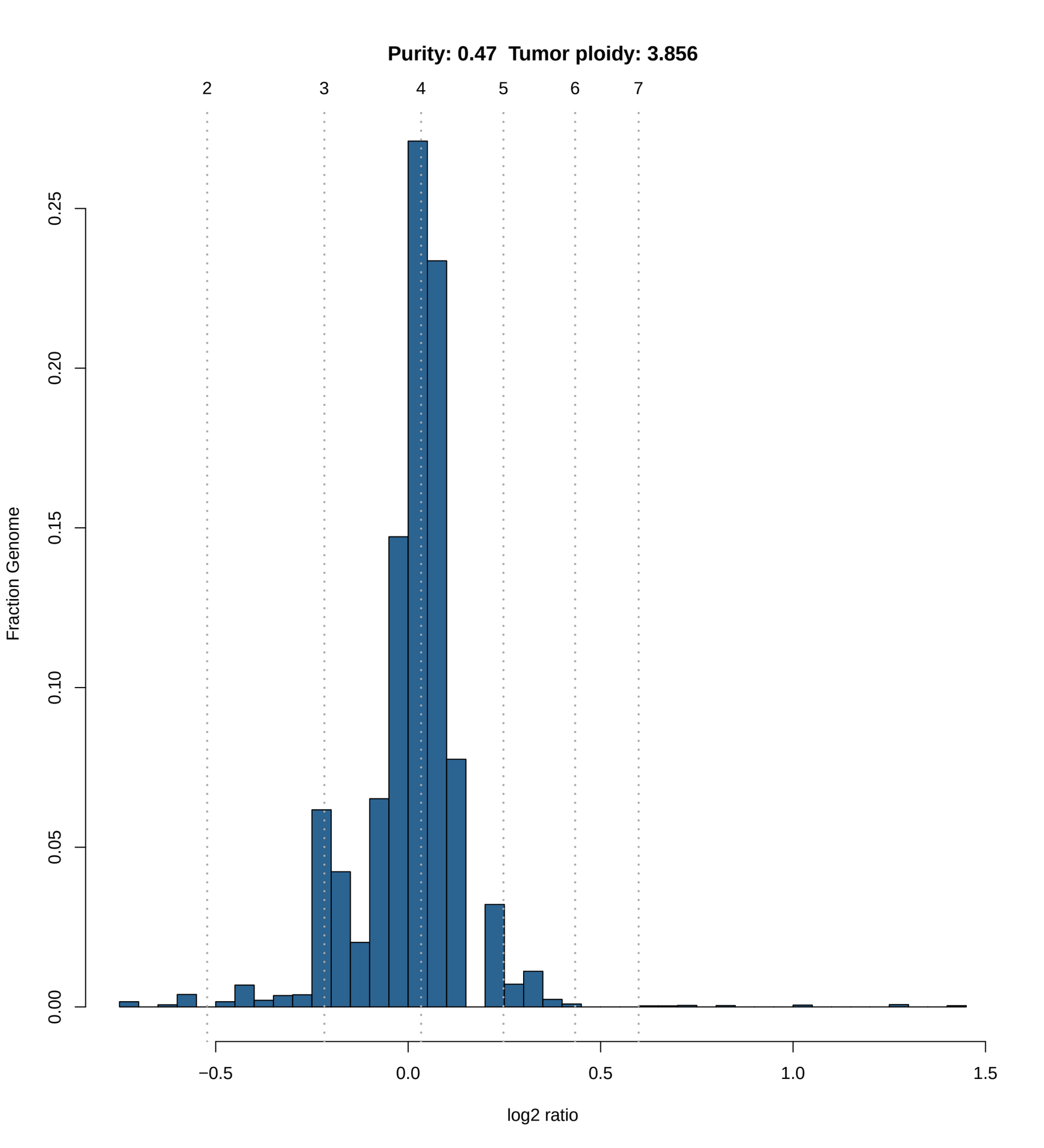

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

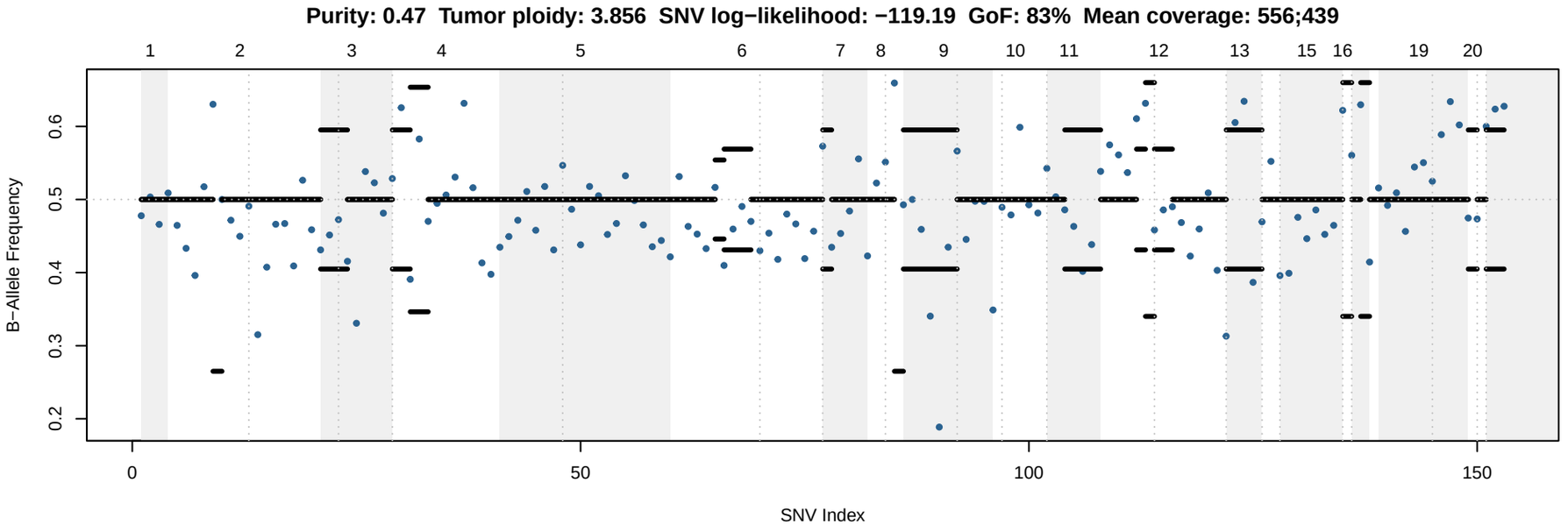

Allelic fraction (germline)
Copy Number log−ratio
1m1
2m1
1m0
3m2
3m1
4m3
4m2
4m1
4m0
5m4
5m3
5m2
5m1
6m4
6m3
6m2
6m1
7m5
7m4
7m3
7m2
7m1
6m5

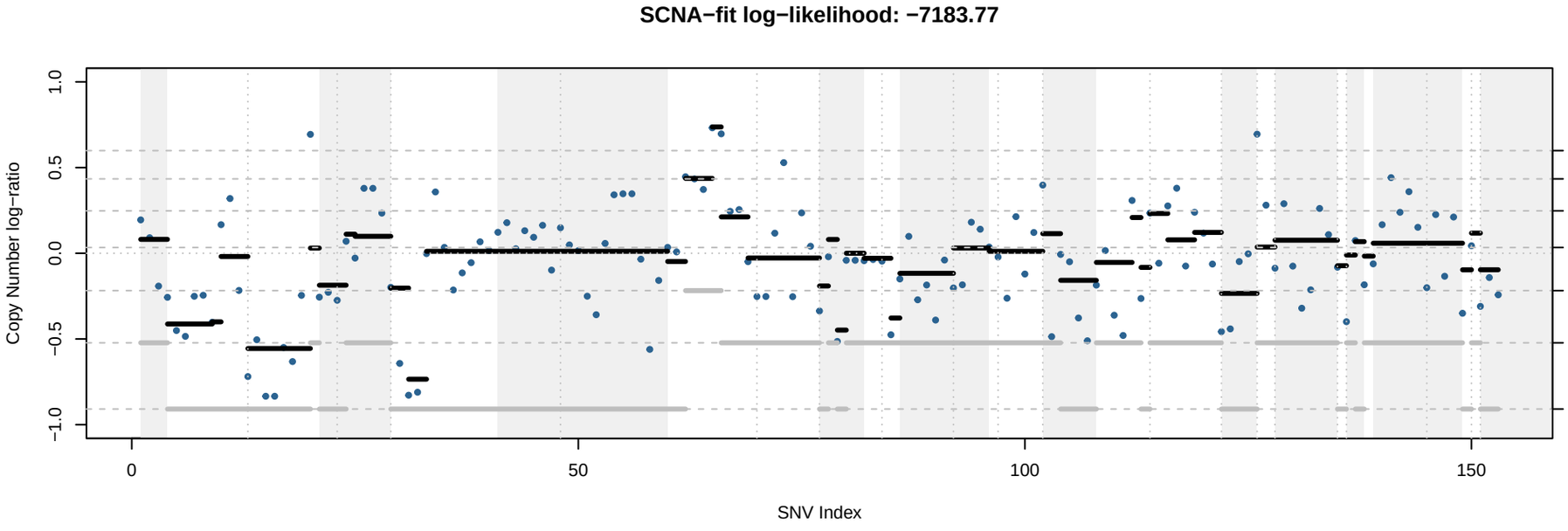

Coverage (log2)
Allelic fraction

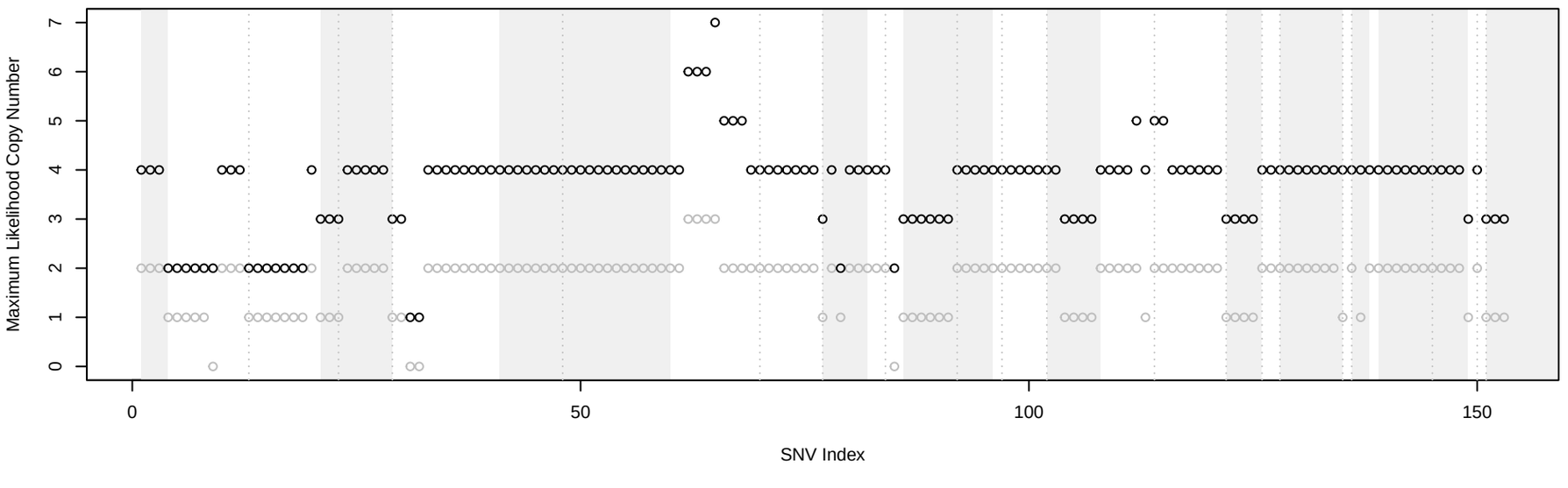

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m2
7m2
2m1
3m1
4m1
5m1
6m1
7m1

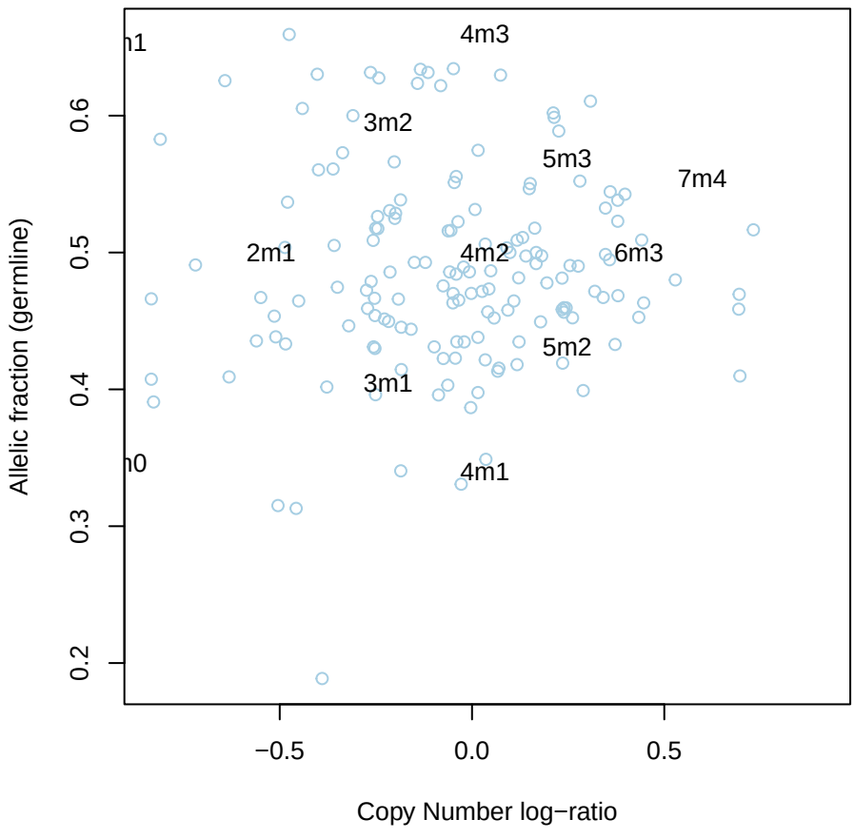

Frequency
Cellular fraction

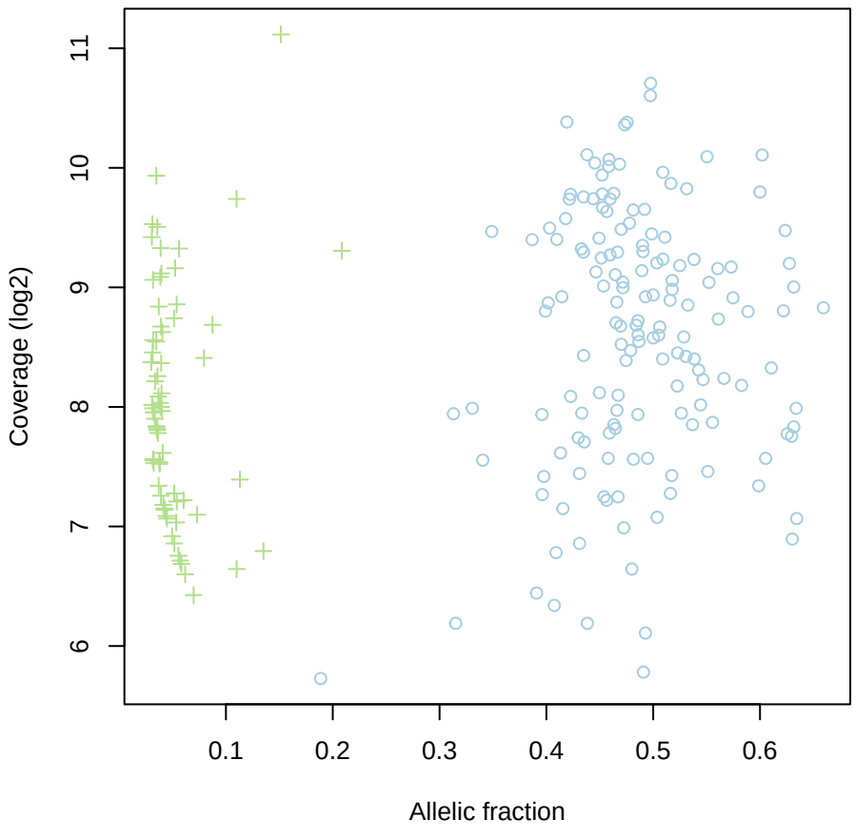

Purity: 0.47 Tumor ploidy: 3.856
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

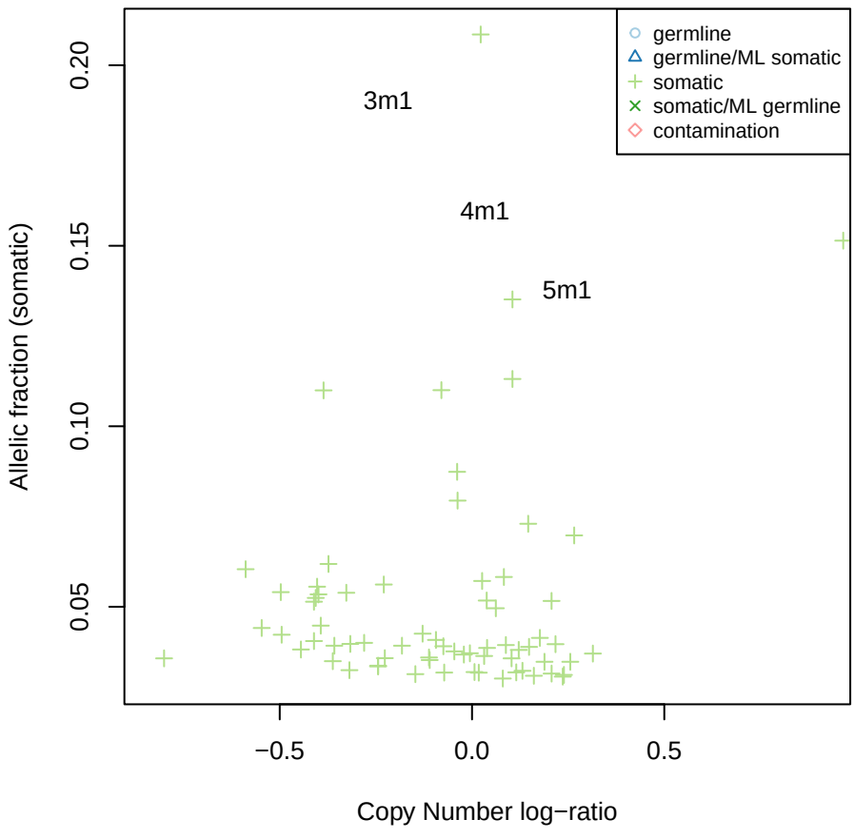

Purity: 0.47 Tumor ploidy: 3.856 SNV log−likelihood: −119.19 GoF: 83% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

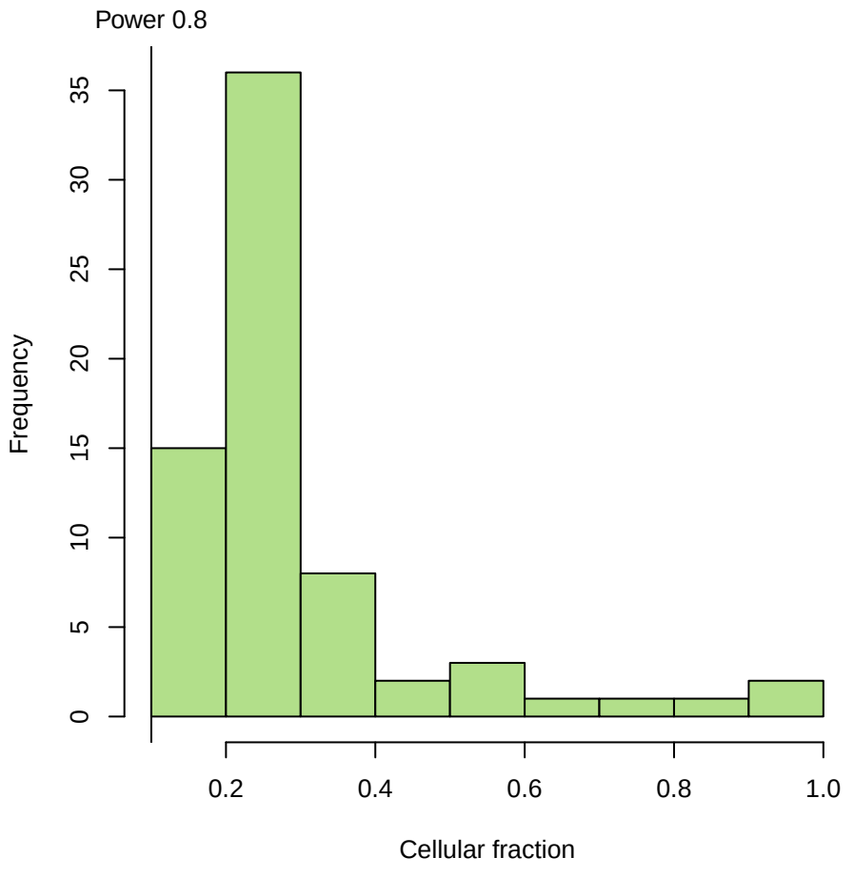

SCNA−fit log−likelihood: −7183.77
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6 7
0 50 100 150
SNV Index

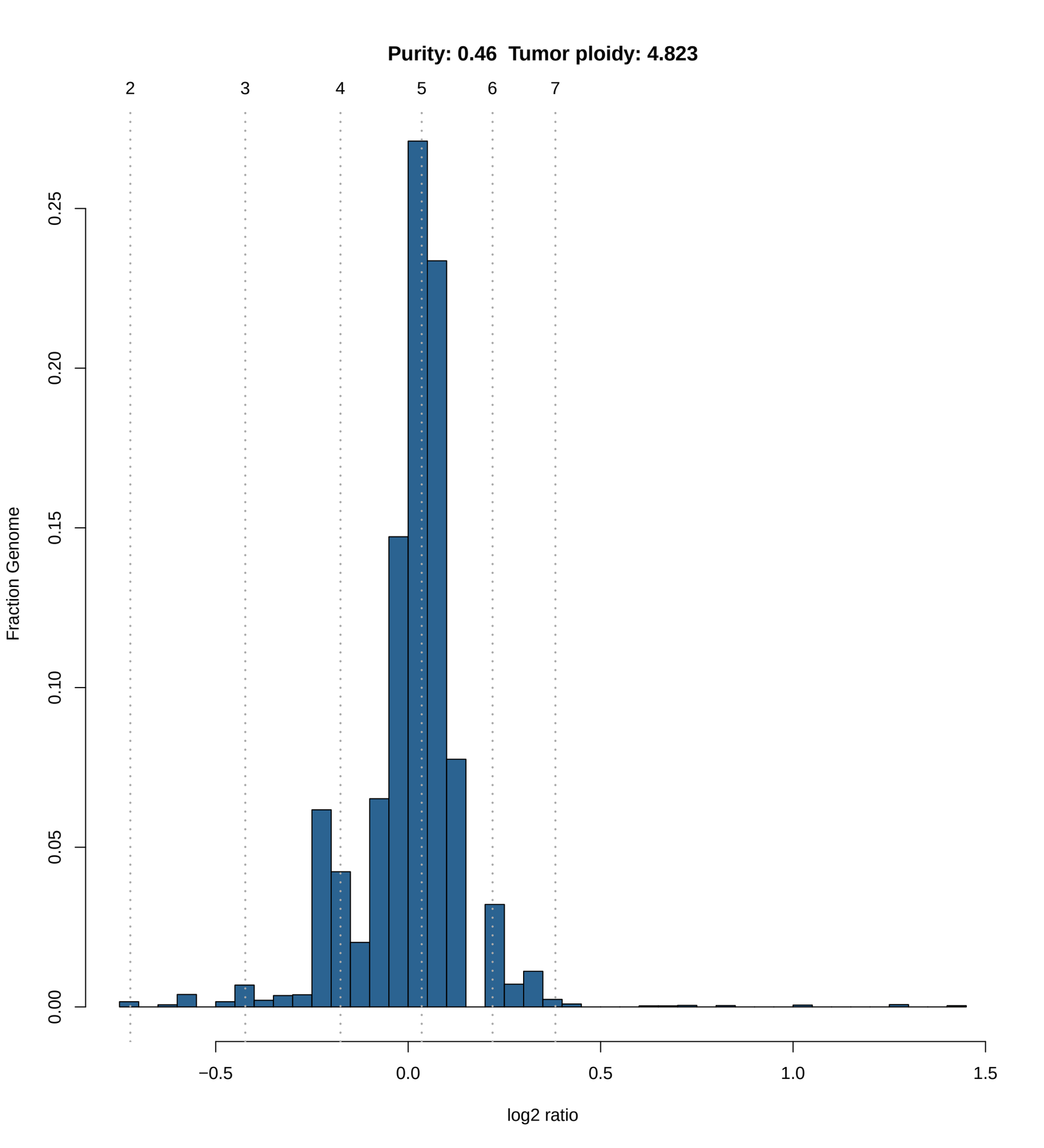

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

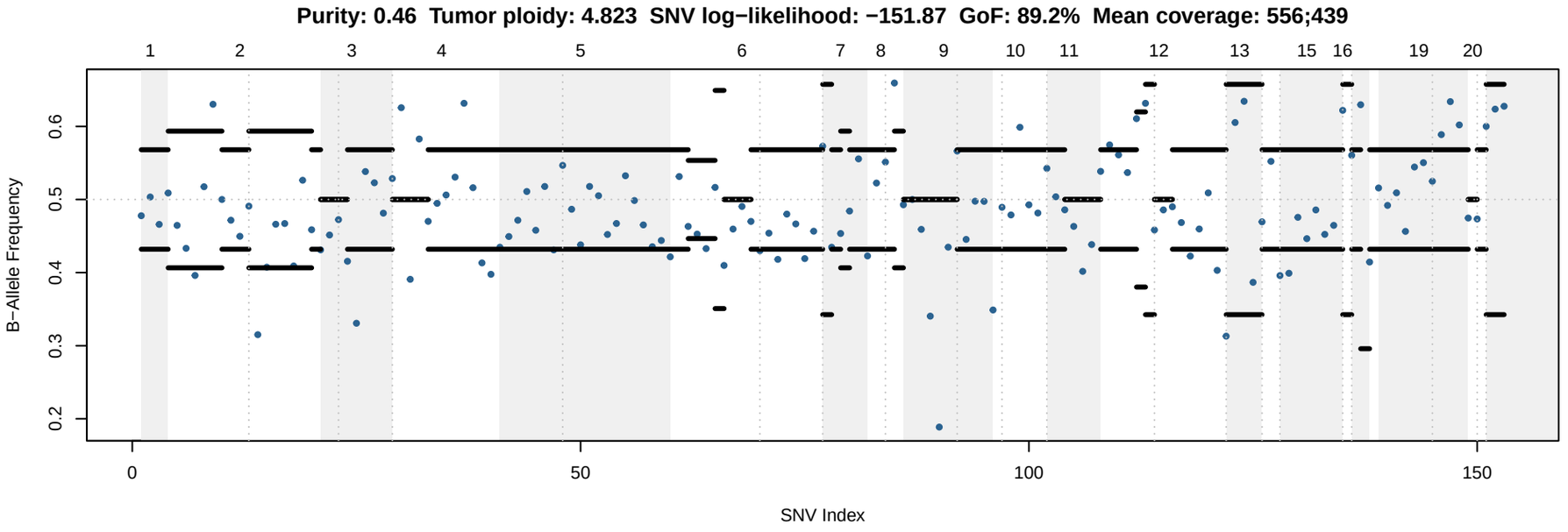

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
5m3
7m4
2m1
4m2
6m3
5m2
3m1
4m1

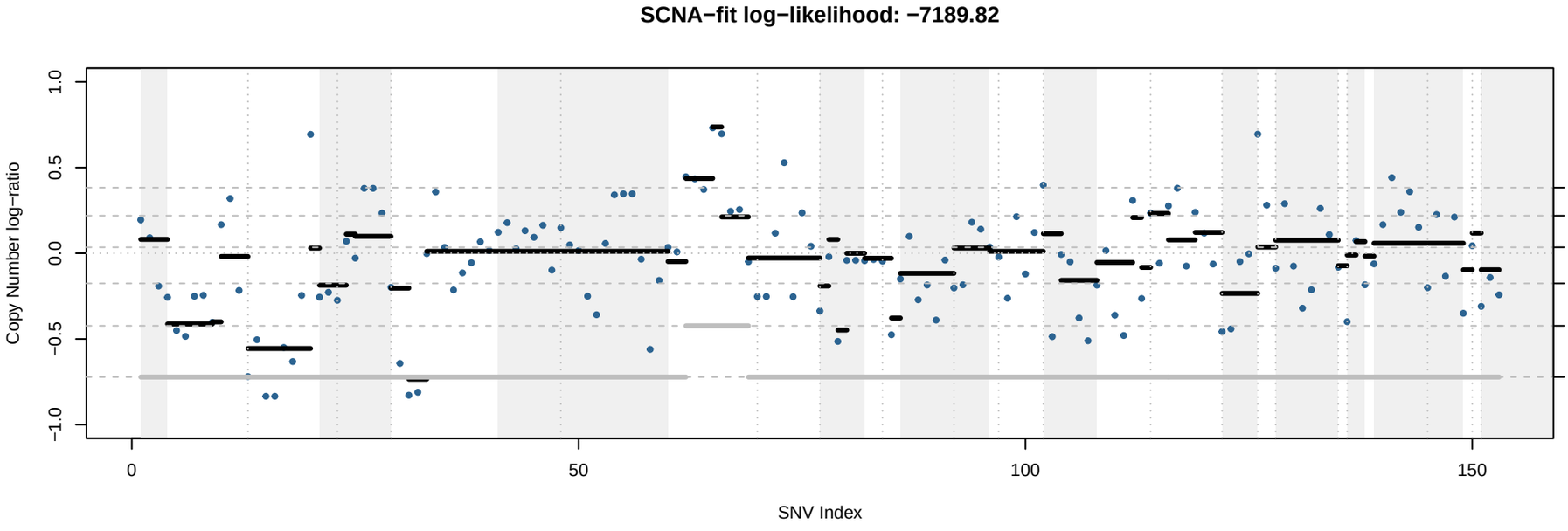

Coverage (log2)
Allelic fraction

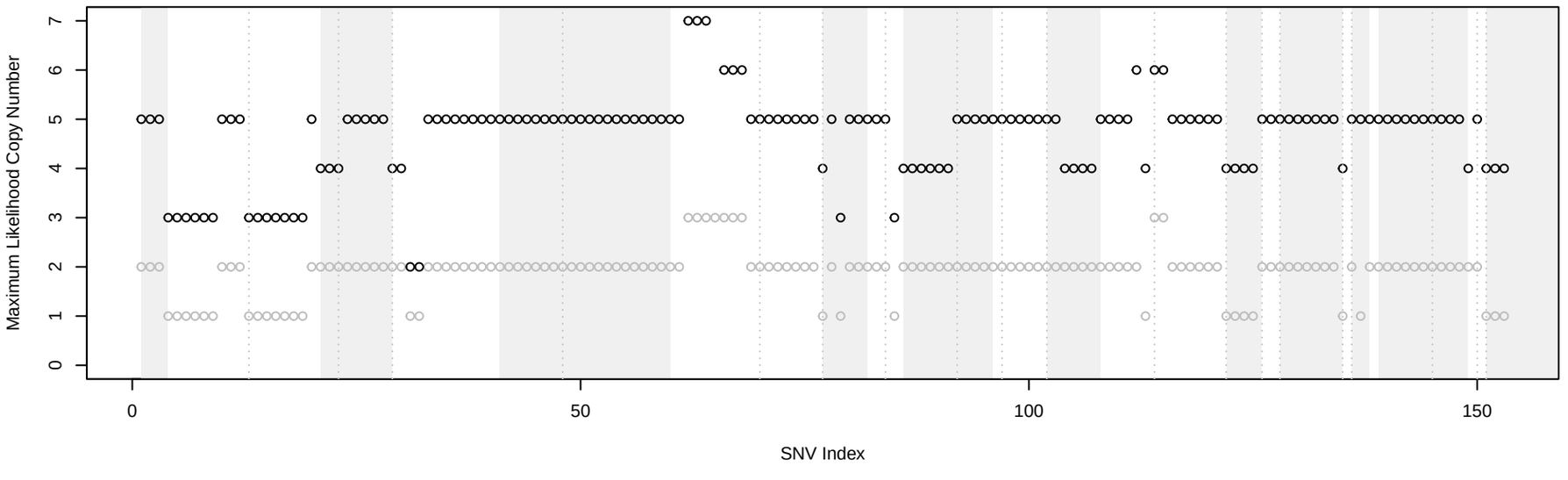

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m1
4m1
5m1

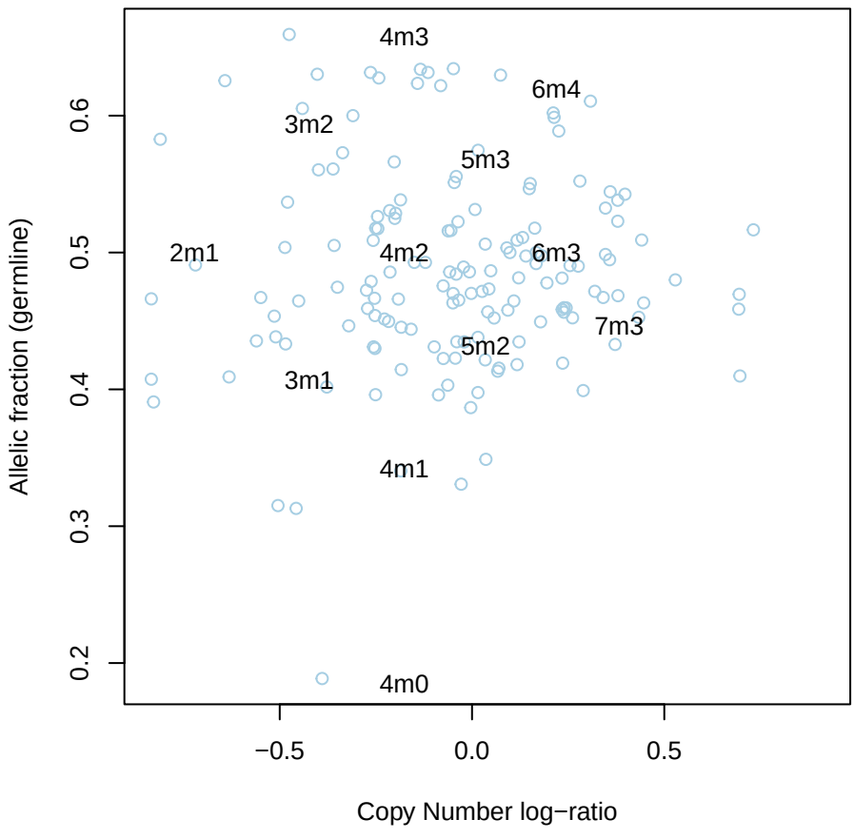

Power 0.8
Frequency
Cellular fraction

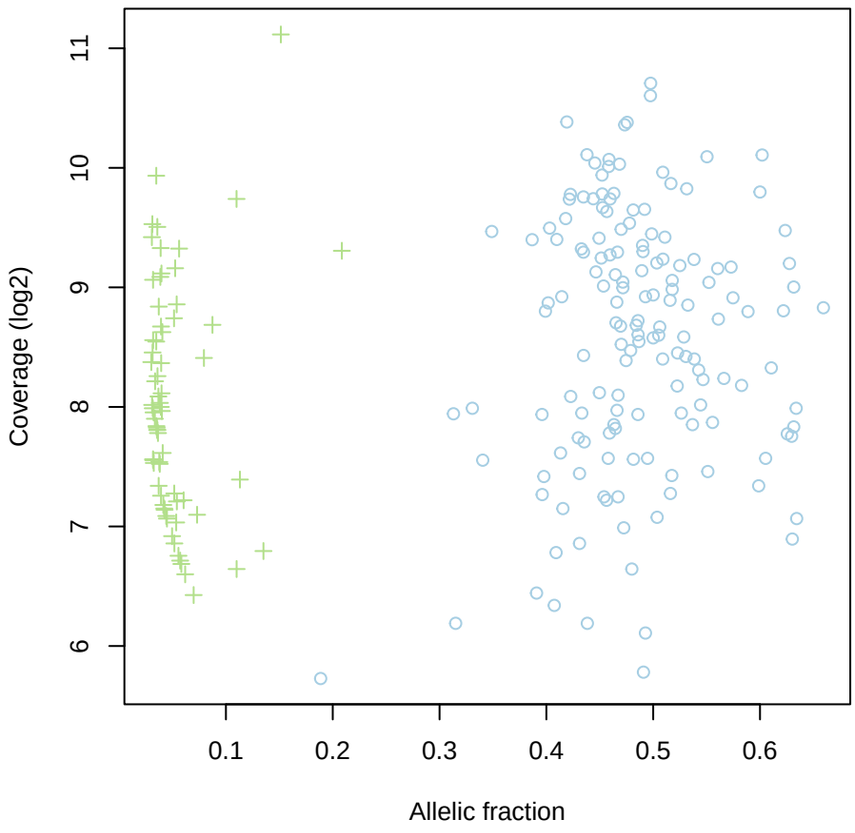

Purity: 0.46 Tumor ploidy: 4.823
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

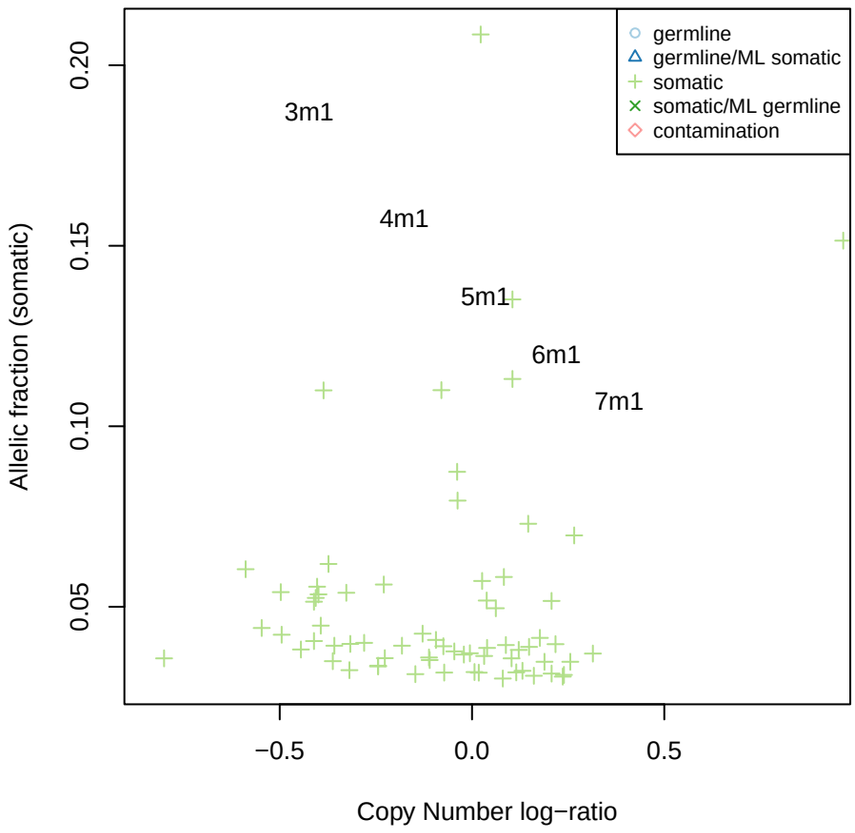

Purity: 0.46 Tumor ploidy: 4.823 SNV log−likelihood: −151.87 GoF: 89.2% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

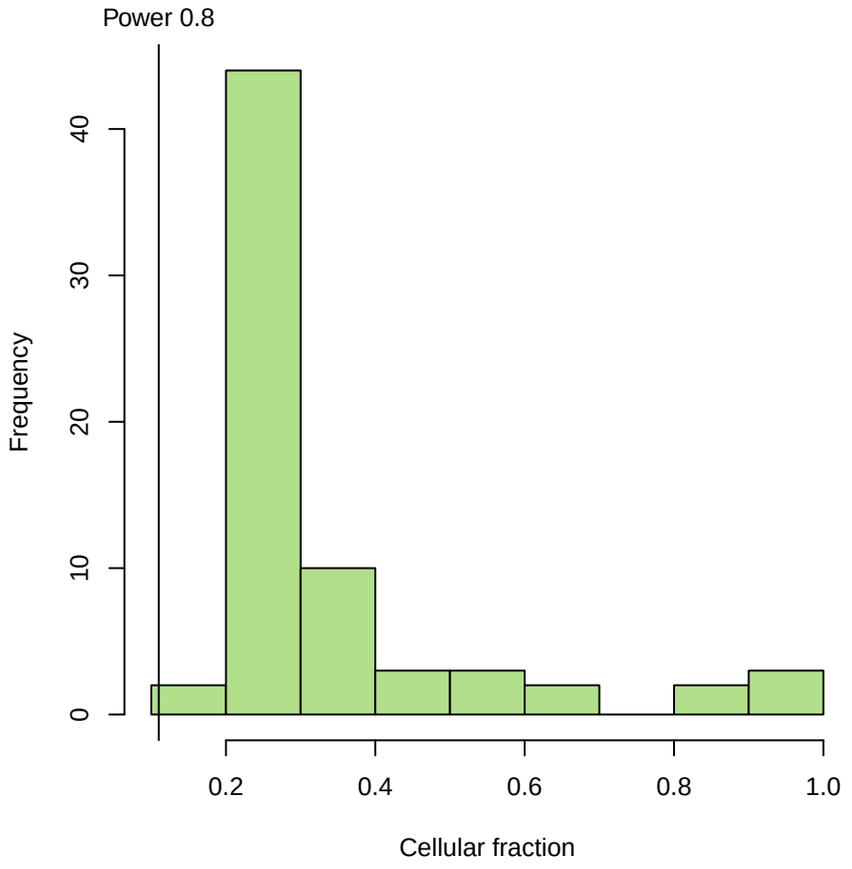

SCNA−fit log−likelihood: −7189.82
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 50 100 150
SNV Index

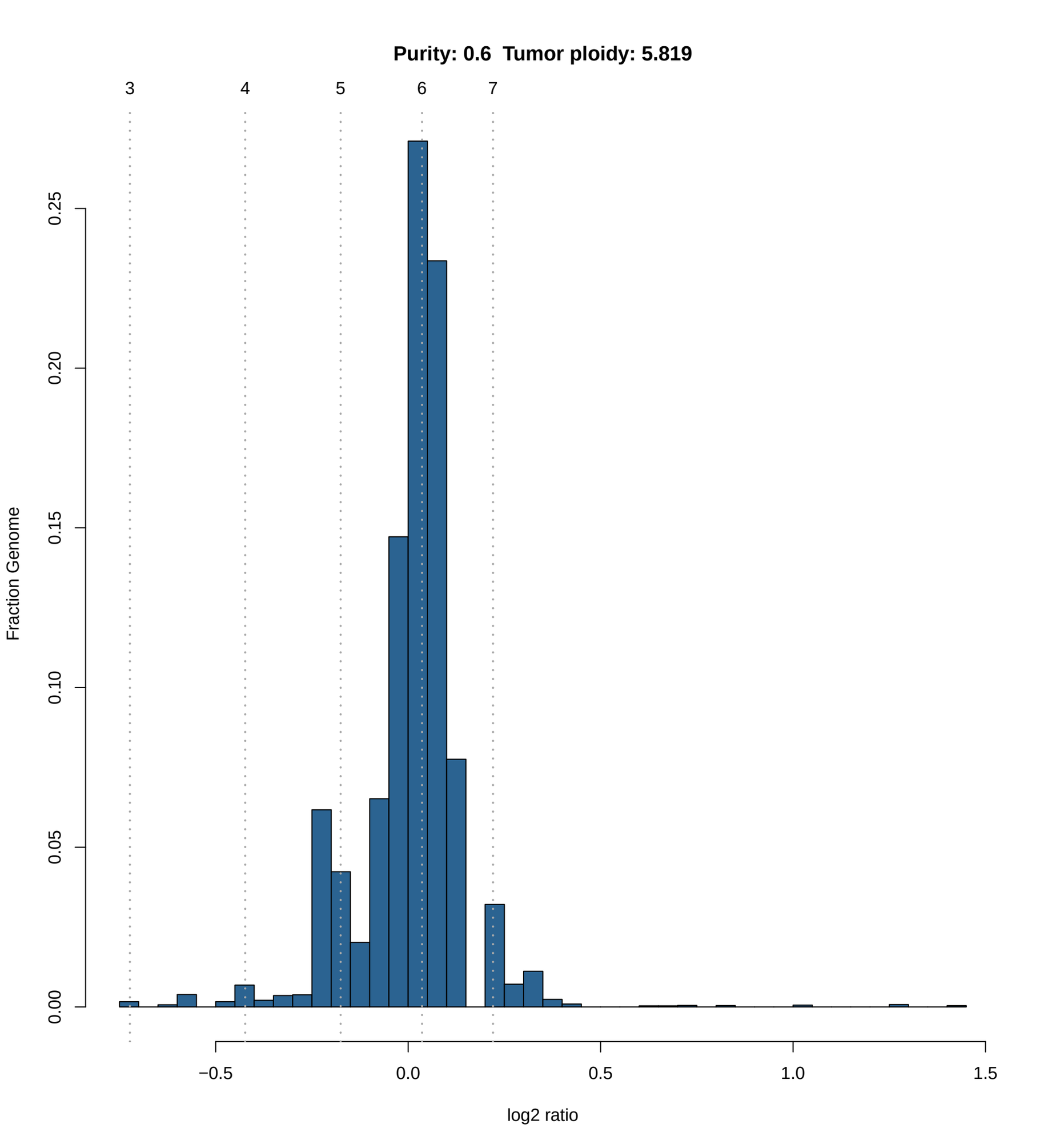

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

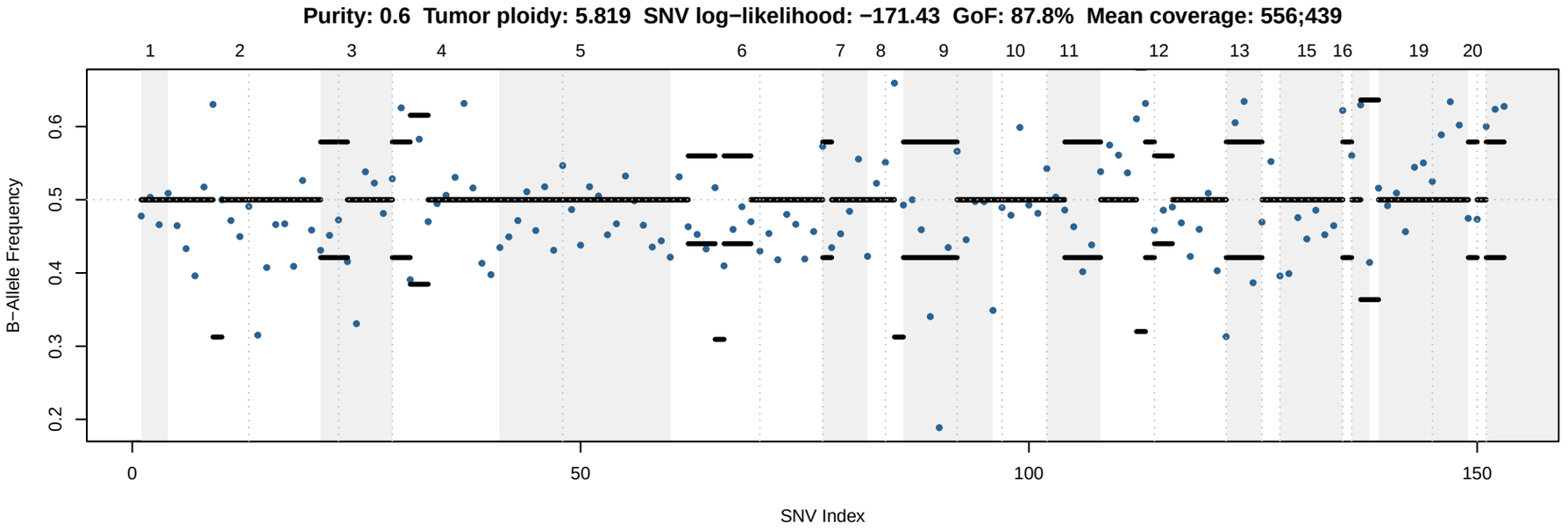

4m3
6m4
3m2
5m3
2m1
4m2
6m3
7m3
5m2
3m1
4m1
4m0
Allelic fraction (germline)
Copy Number log−ratio
0.2
0.3
0.4
0.5
0.6
−0.5
0.0
0.5

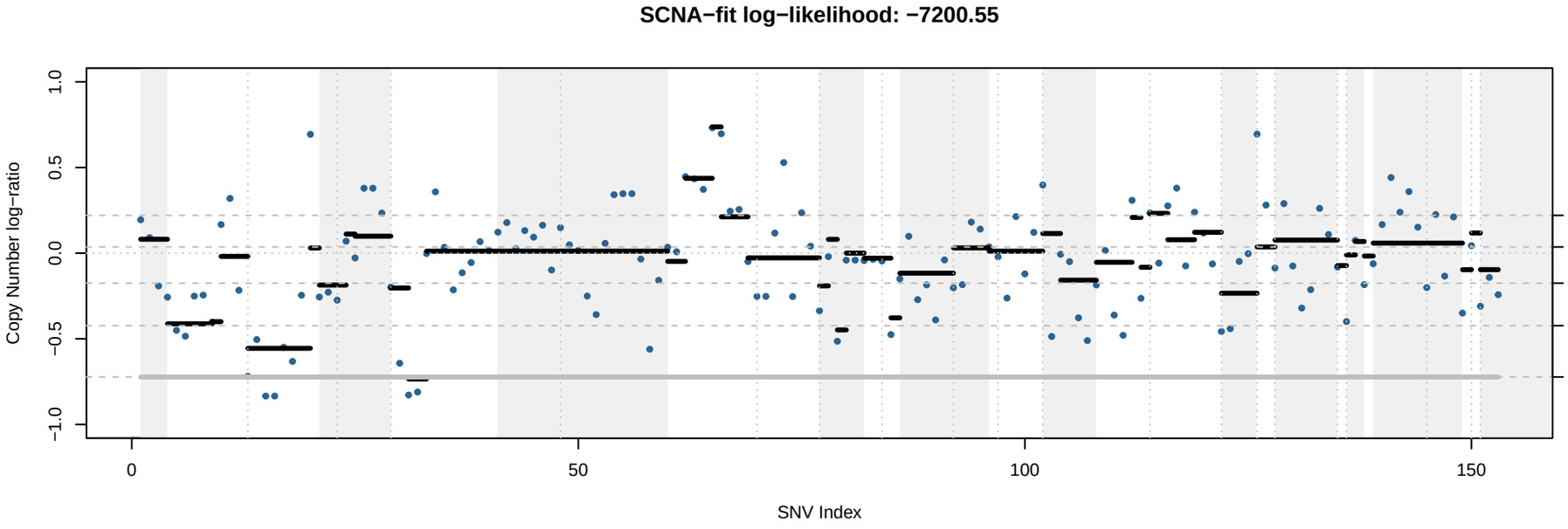

Coverage (log2)
Allelic fraction
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6

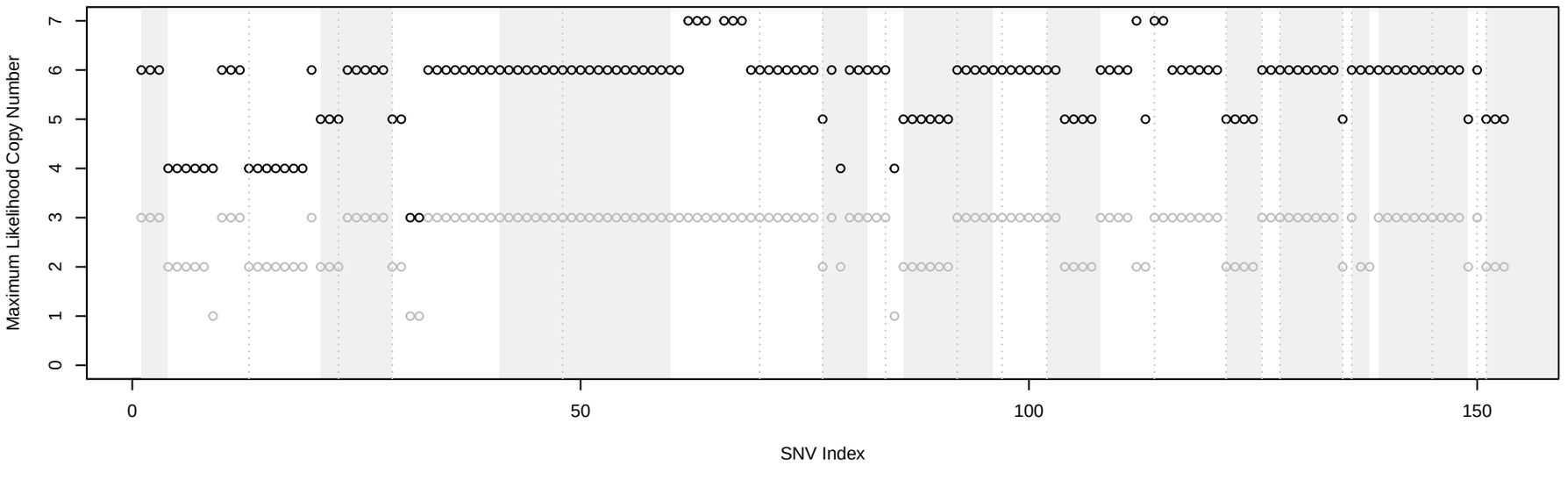

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
−0.5
0.0
0.5

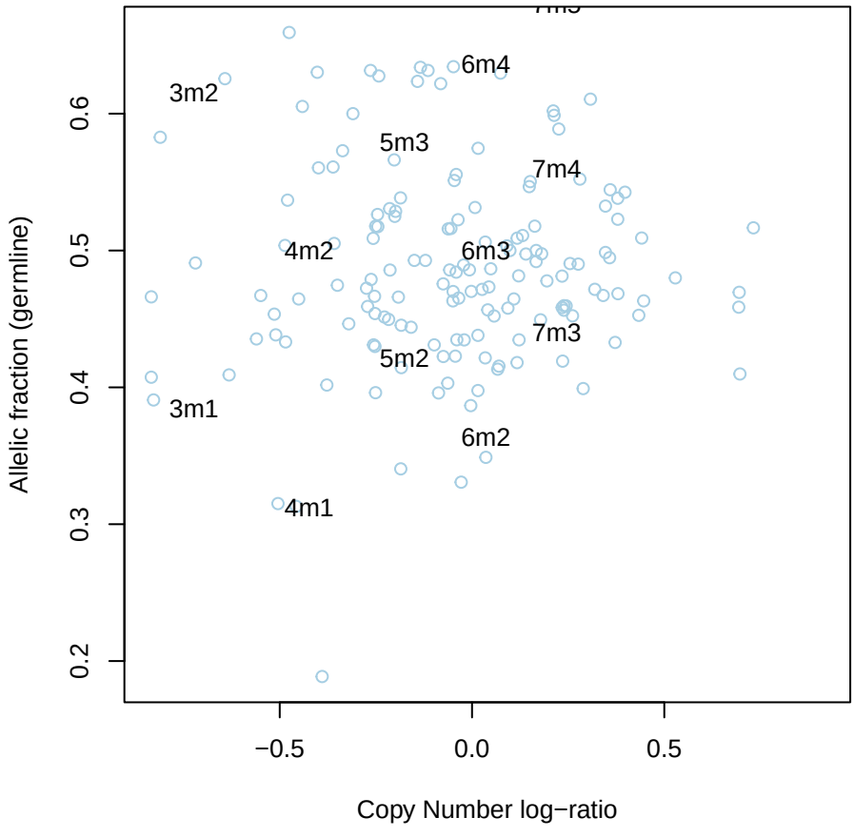

Power 0.8
Frequency
Cellular fraction
0
10
20
30
40
0.2
0.4
0.6
0.8
1.0

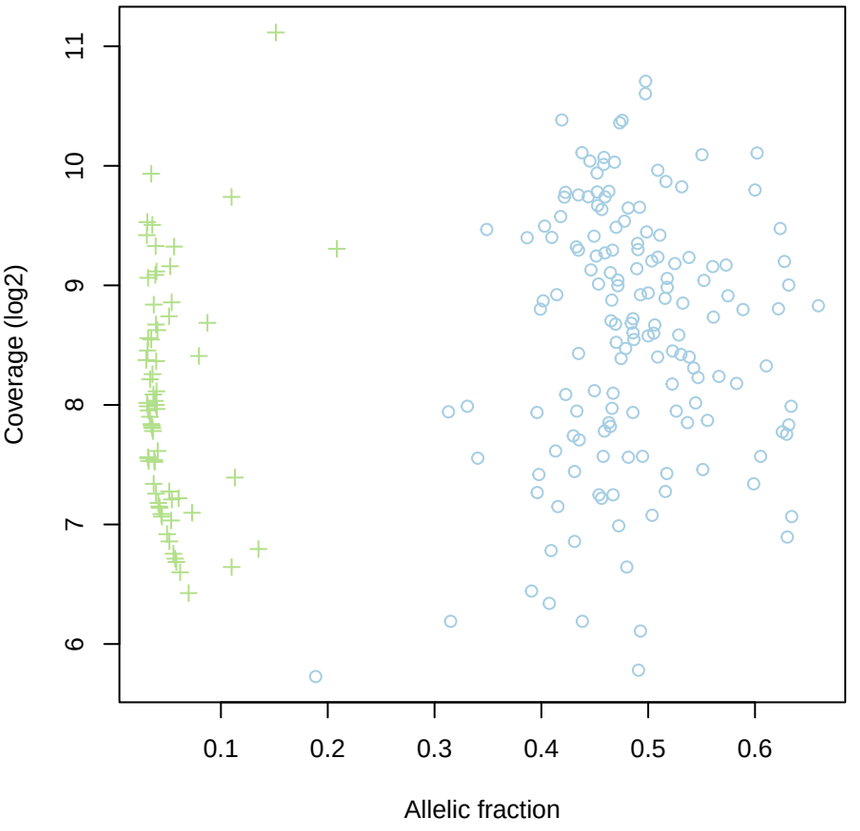

Purity: 0.6 Tumor ploidy: 5.819
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

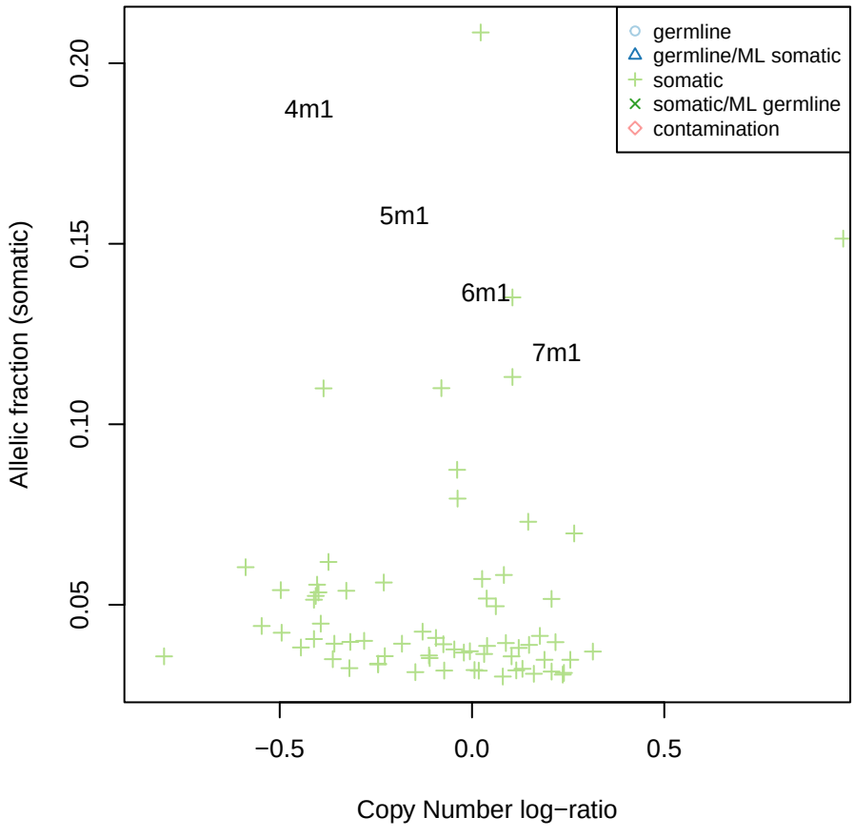

Purity: 0.6 Tumor ploidy: 5.819 SNV log−likelihood: −171.43 GoF: 87.8% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

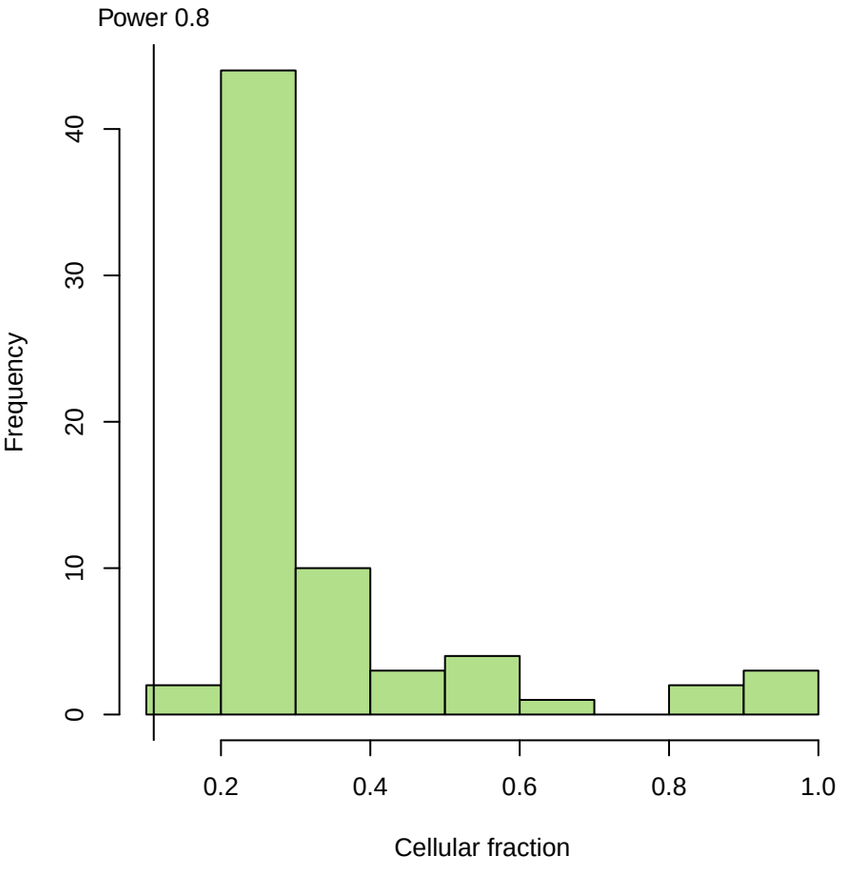

SCNA−fit log−likelihood: −7200.55
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 50 100 150
SNV Index

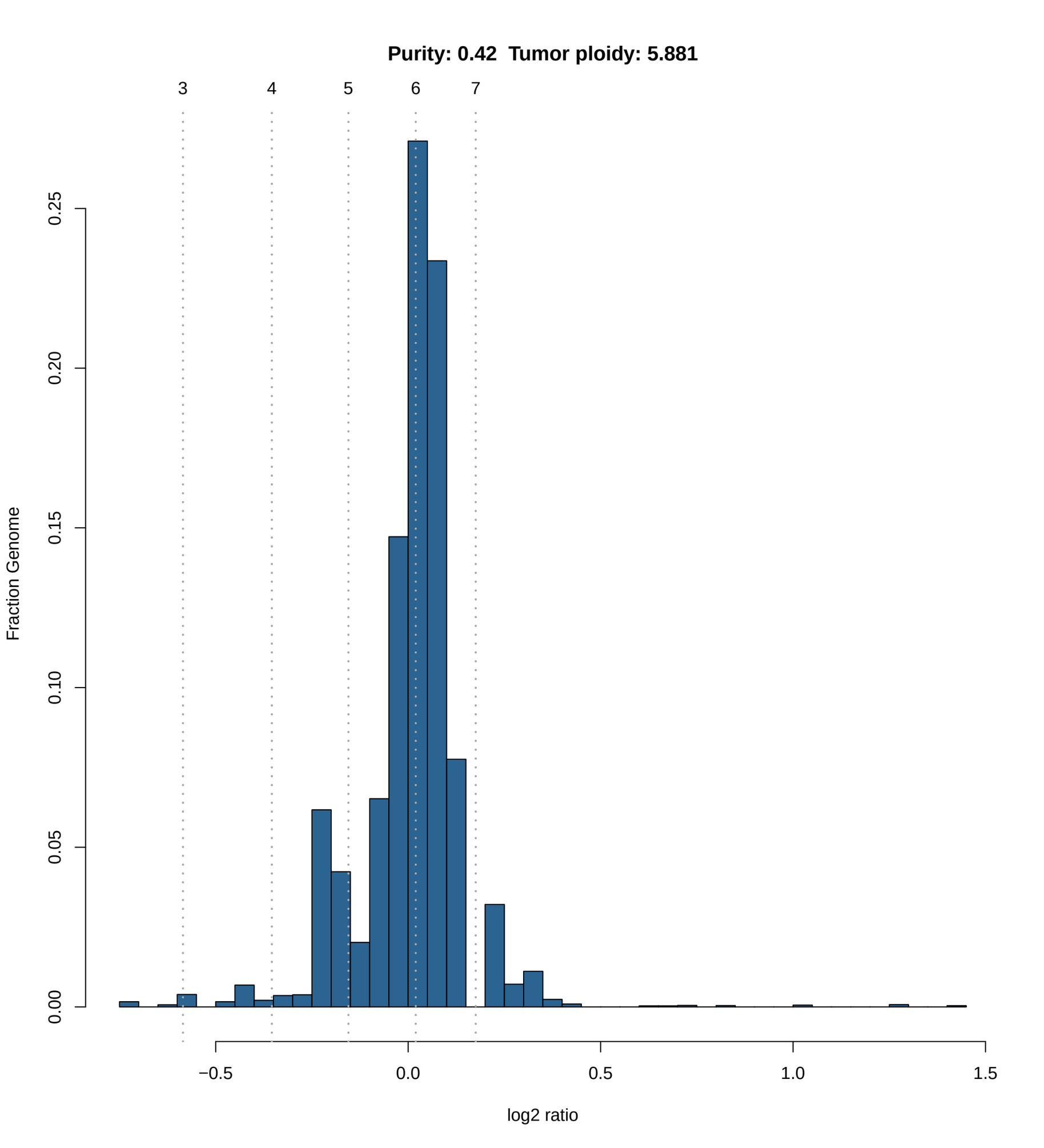

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

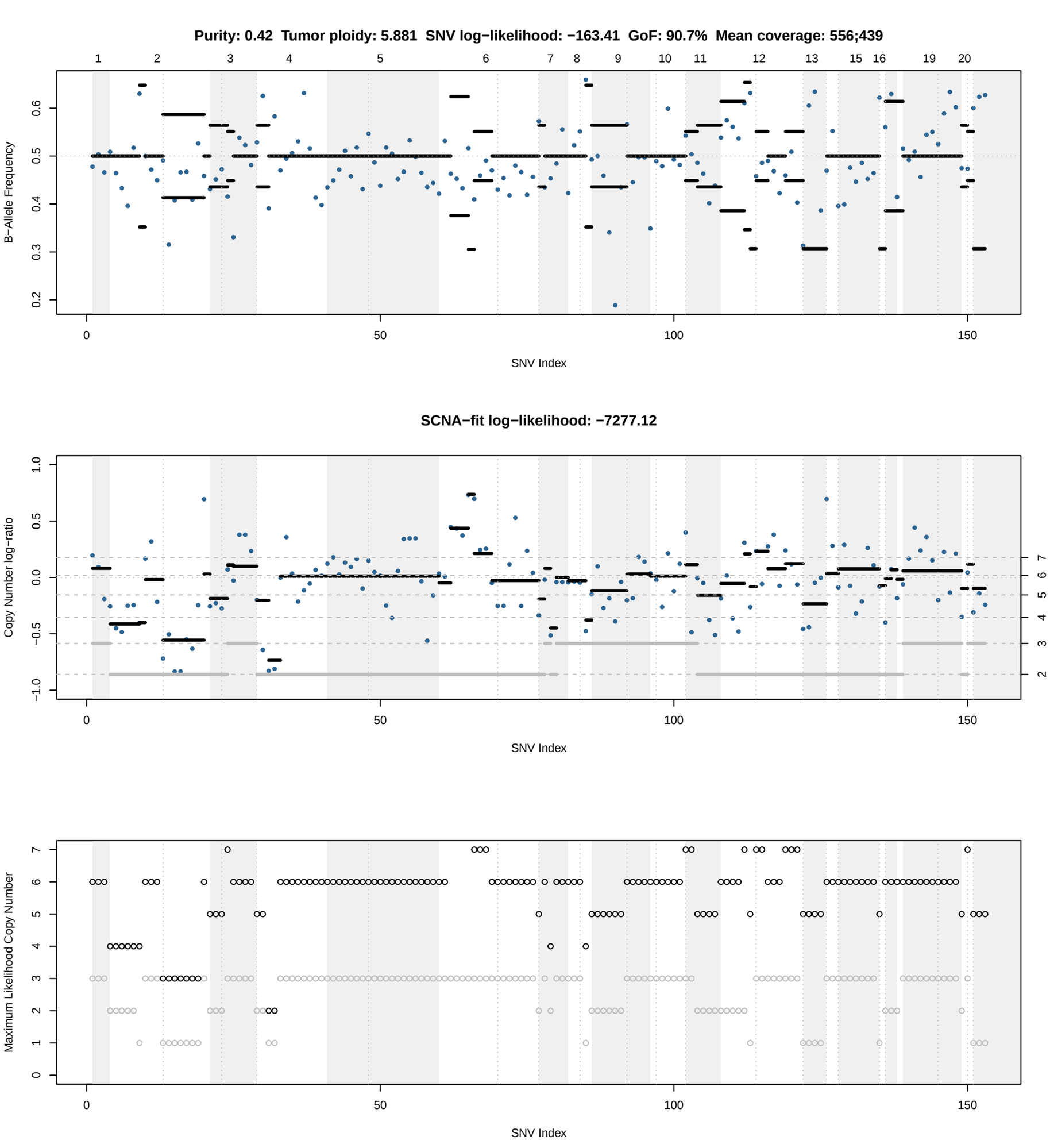

Allelic fraction (germline)
Copy Number log−ratio
3m2
6m4
5m3
7m4
4m2
6m3
7m3
5m2
3m1
6m2
4m1

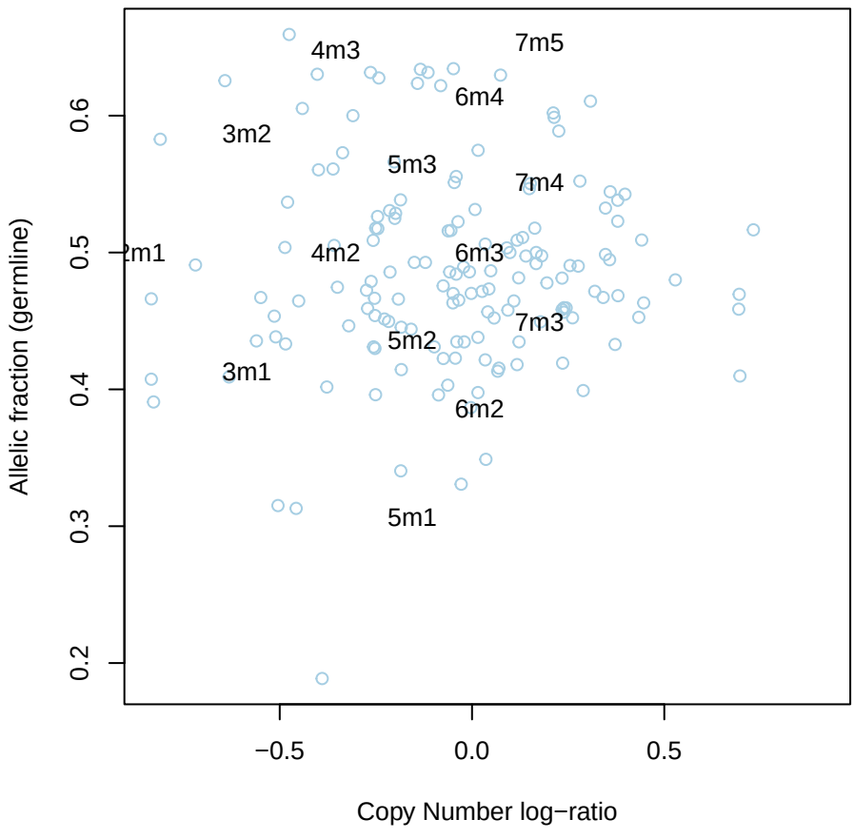

Coverage (log2)
Allelic fraction

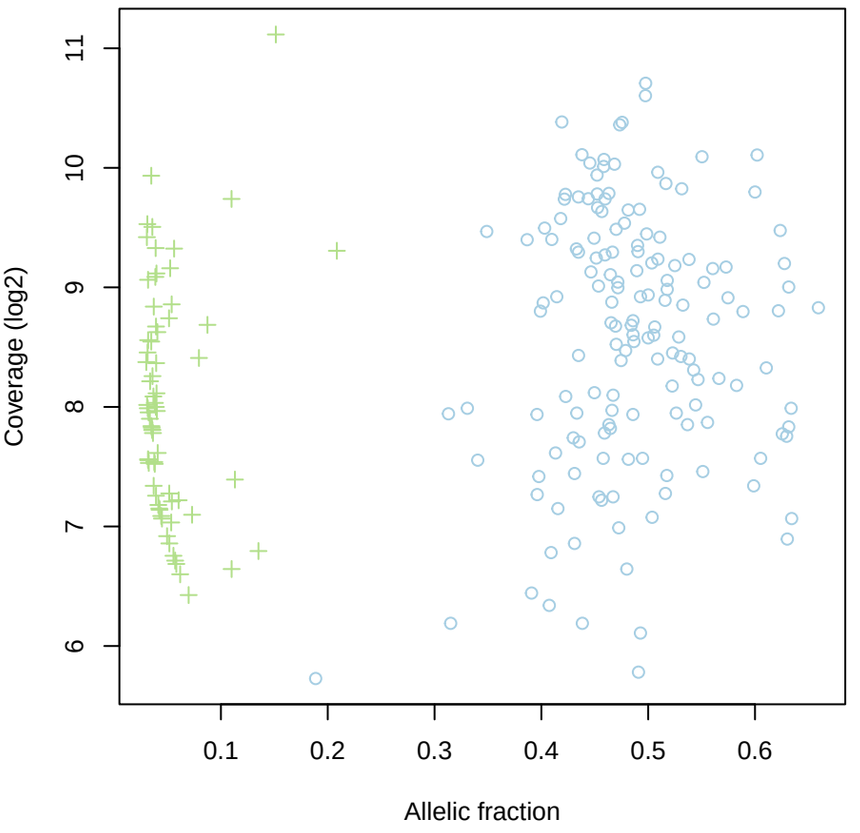

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
7m1

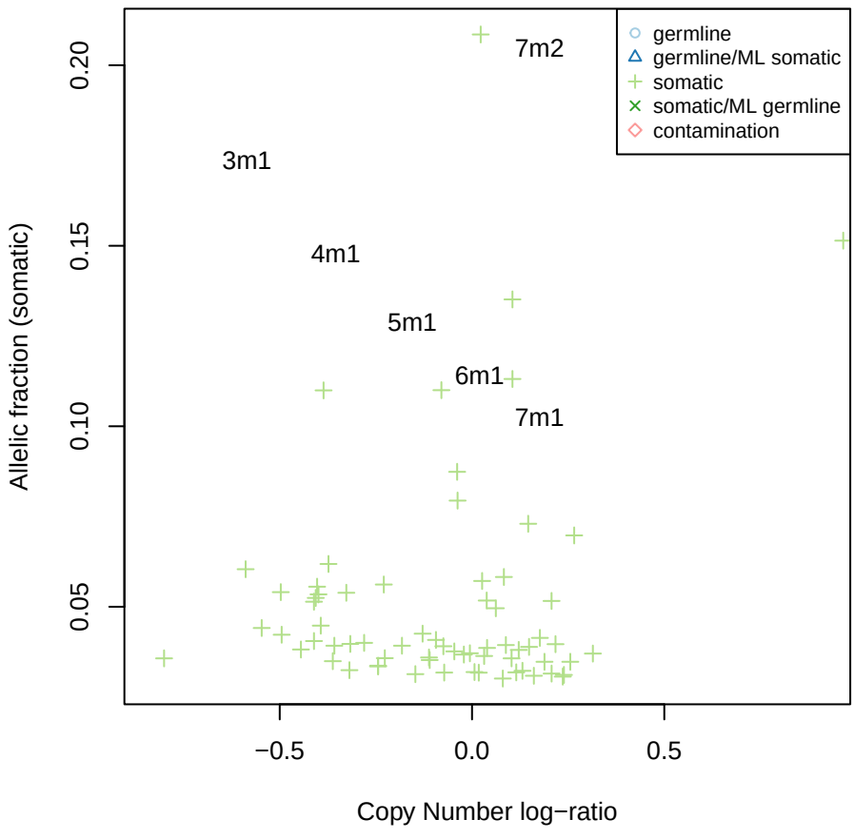

Power 0.8
Frequency
Cellular fraction

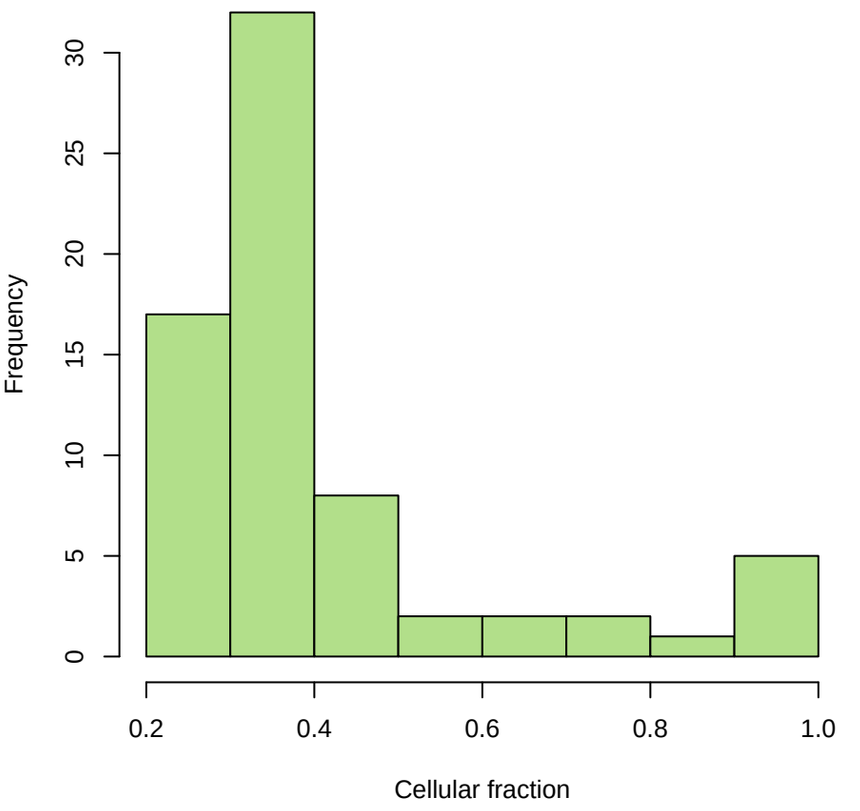

Purity: 0.42 Tumor ploidy: 5.881
3
4
5
6
7
Fraction Genome
0.00
0.05
0.10
0.15
0.20
0.25
−0.5
0.0
0.5
1.0
1.5
log2 ratio

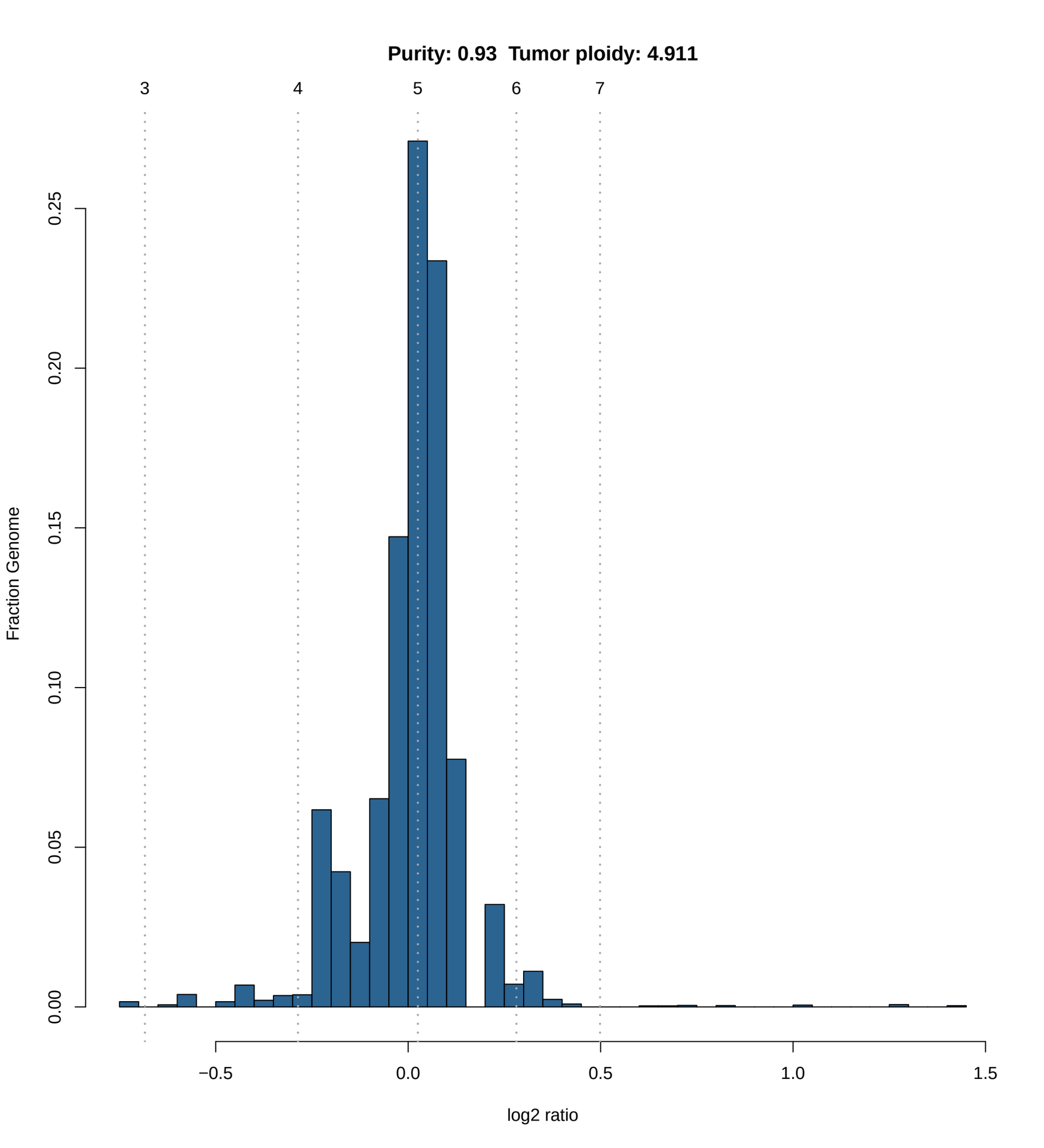

Purity: 0.42 Tumor ploidy: 5.881 SNV log−likelihood: −163.41 GoF: 90.7% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index
SCNA−fit log−likelihood: −7277.12
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 50 100 150
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

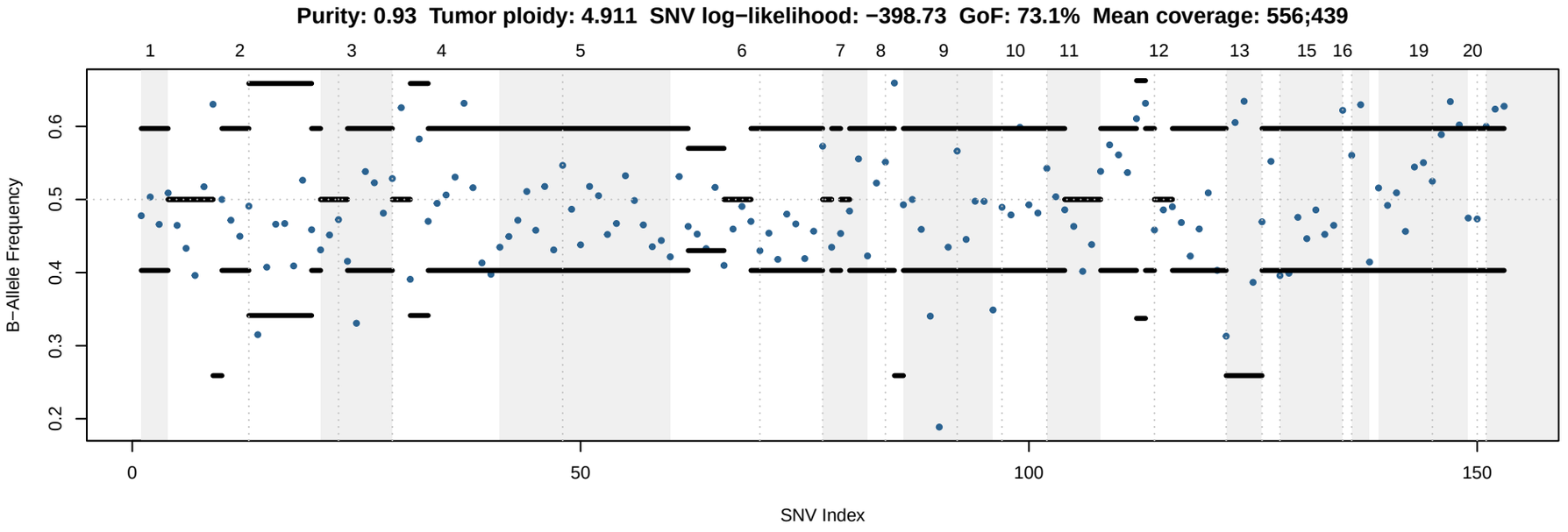

4m3
7m5
6m4
3m2
5m3
7m4
4m2
6m3
7m3
5m2
3m1
6m2
5m1
Allelic fraction (germline)
Copy Number log−ratio

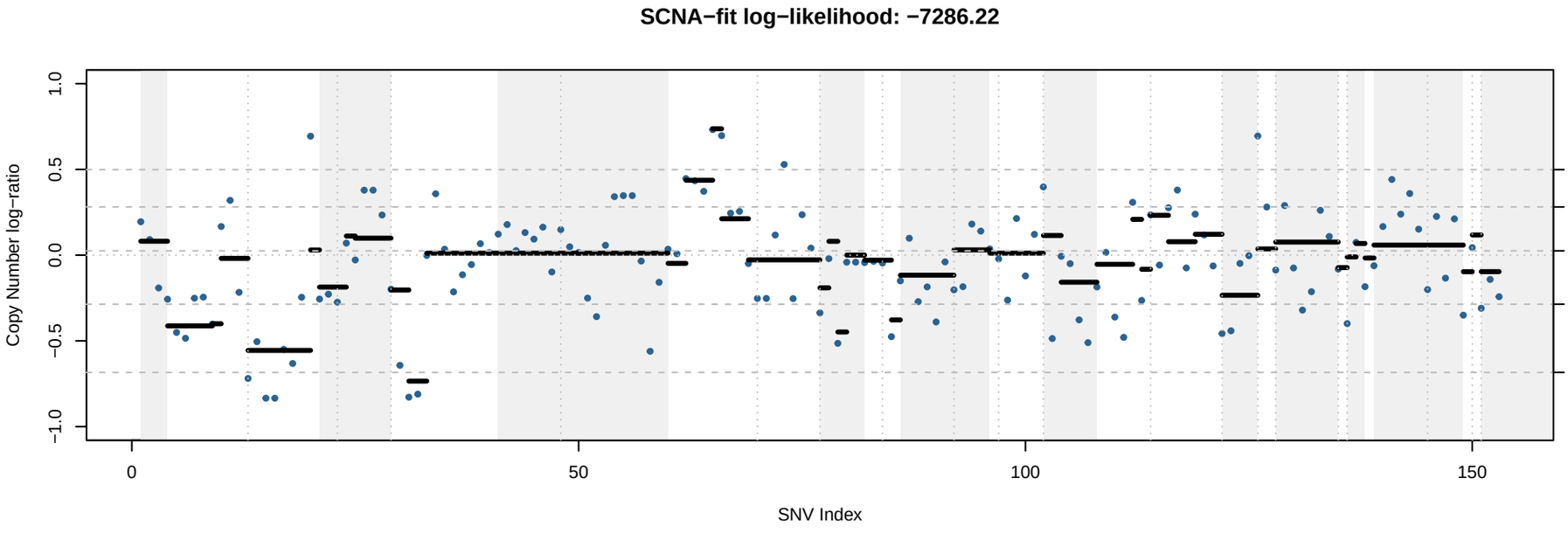

Coverage (log2)
Allelic fraction

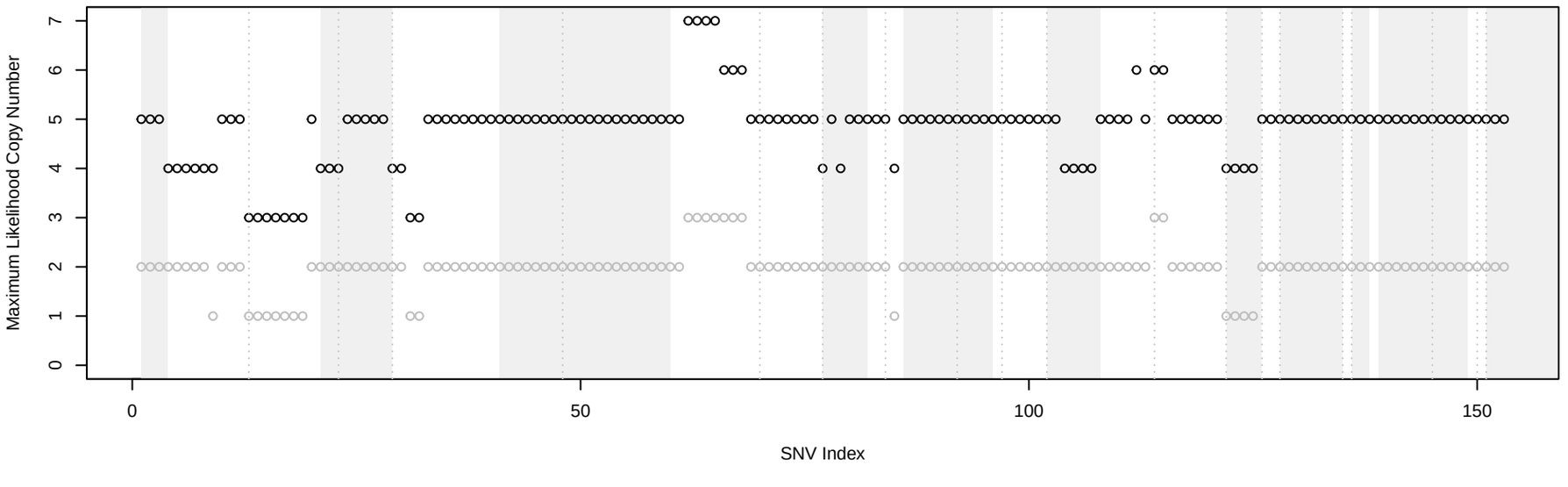

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
7m2
3m1
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

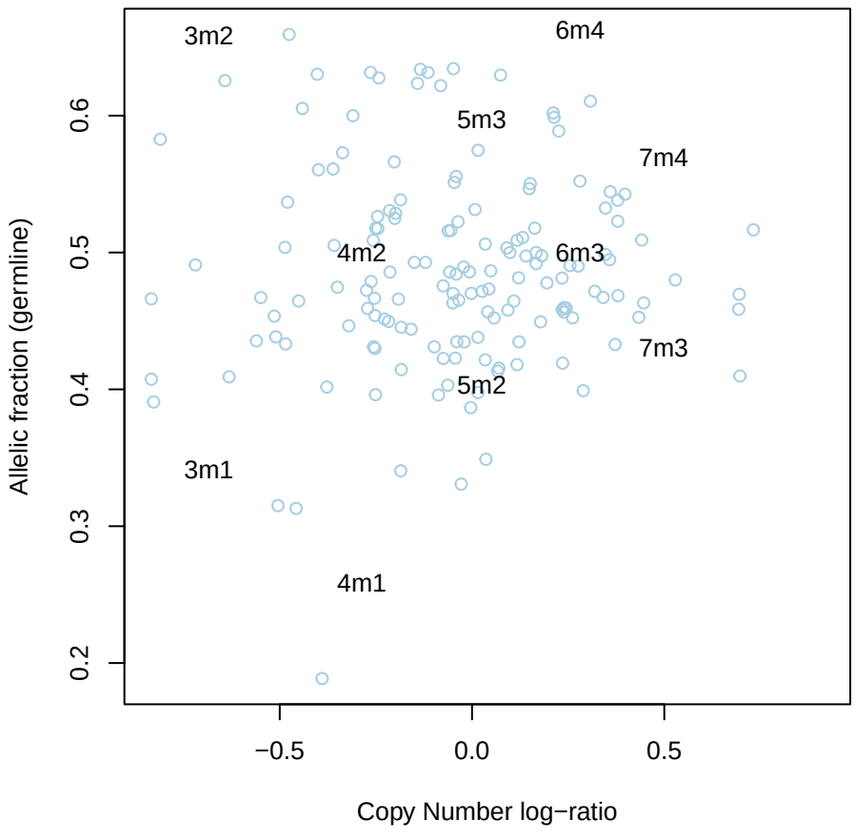

Frequency
Cellular fraction

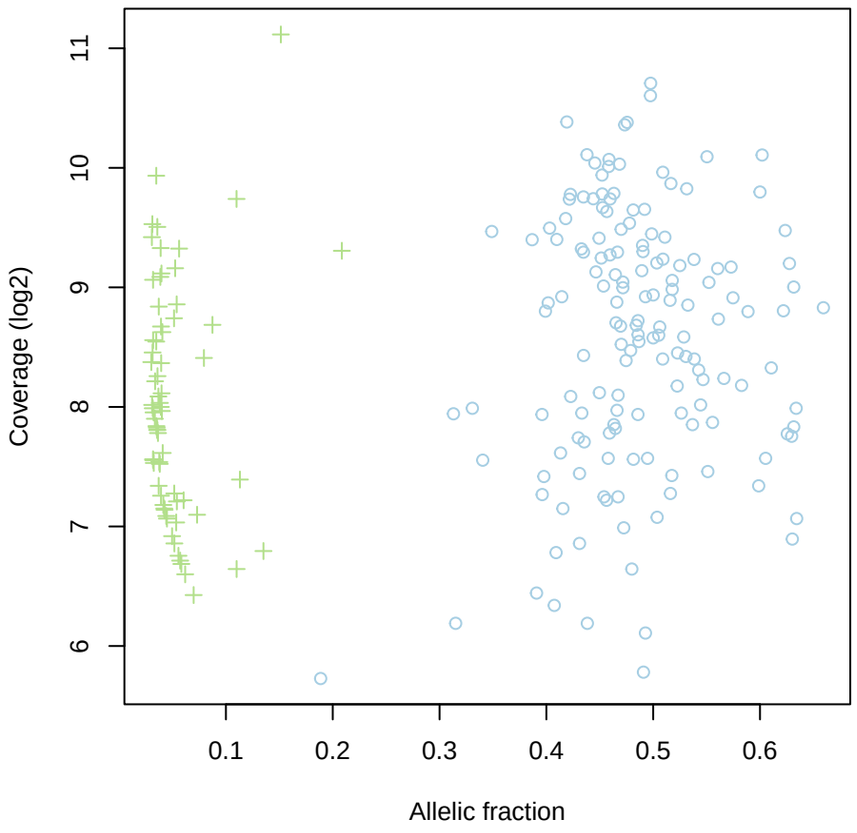

Purity: 0.93 Tumor ploidy: 4.911
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

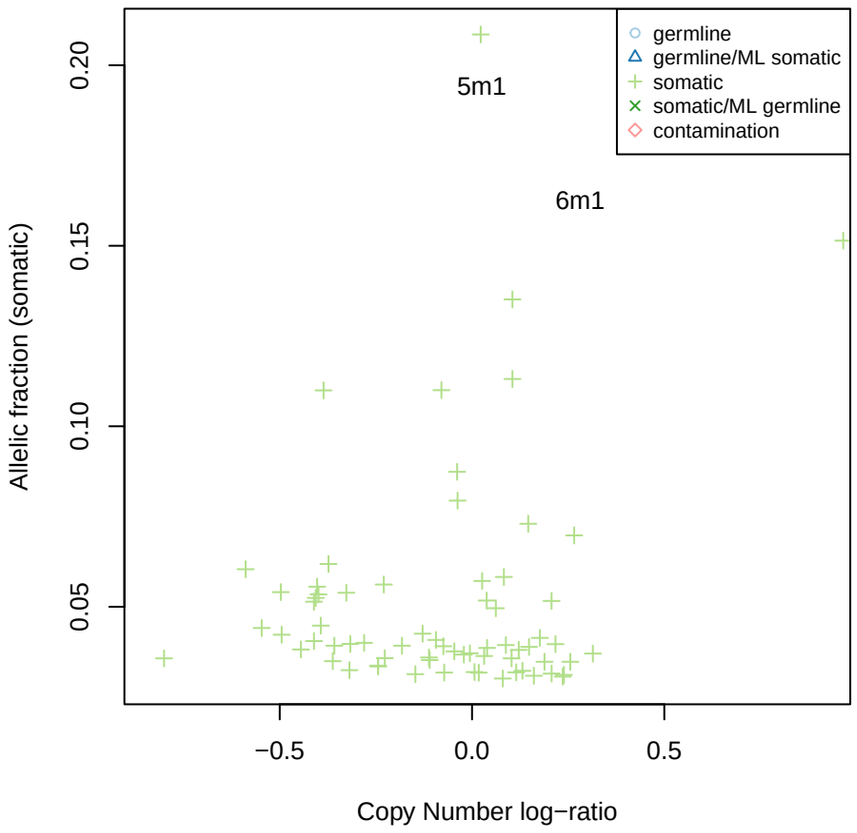

Purity: 0.93 Tumor ploidy: 4.911 SNV log−likelihood: −398.73 GoF: 73.1% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

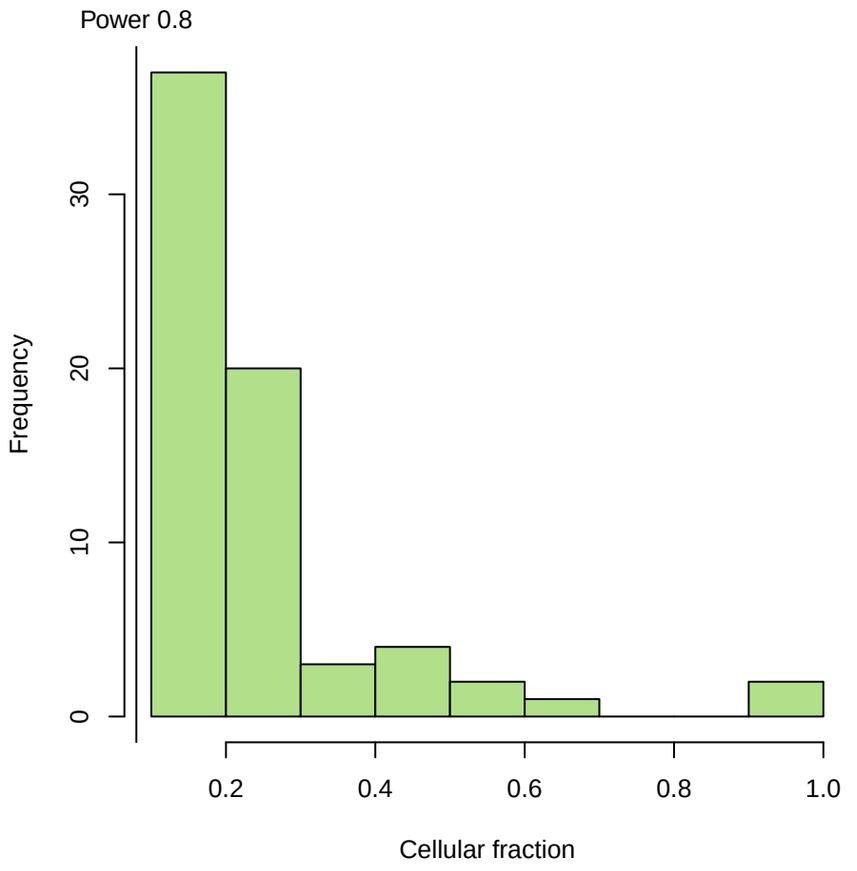

SCNA−fit log−likelihood: −7286.22
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 50 100 150
SNV Index

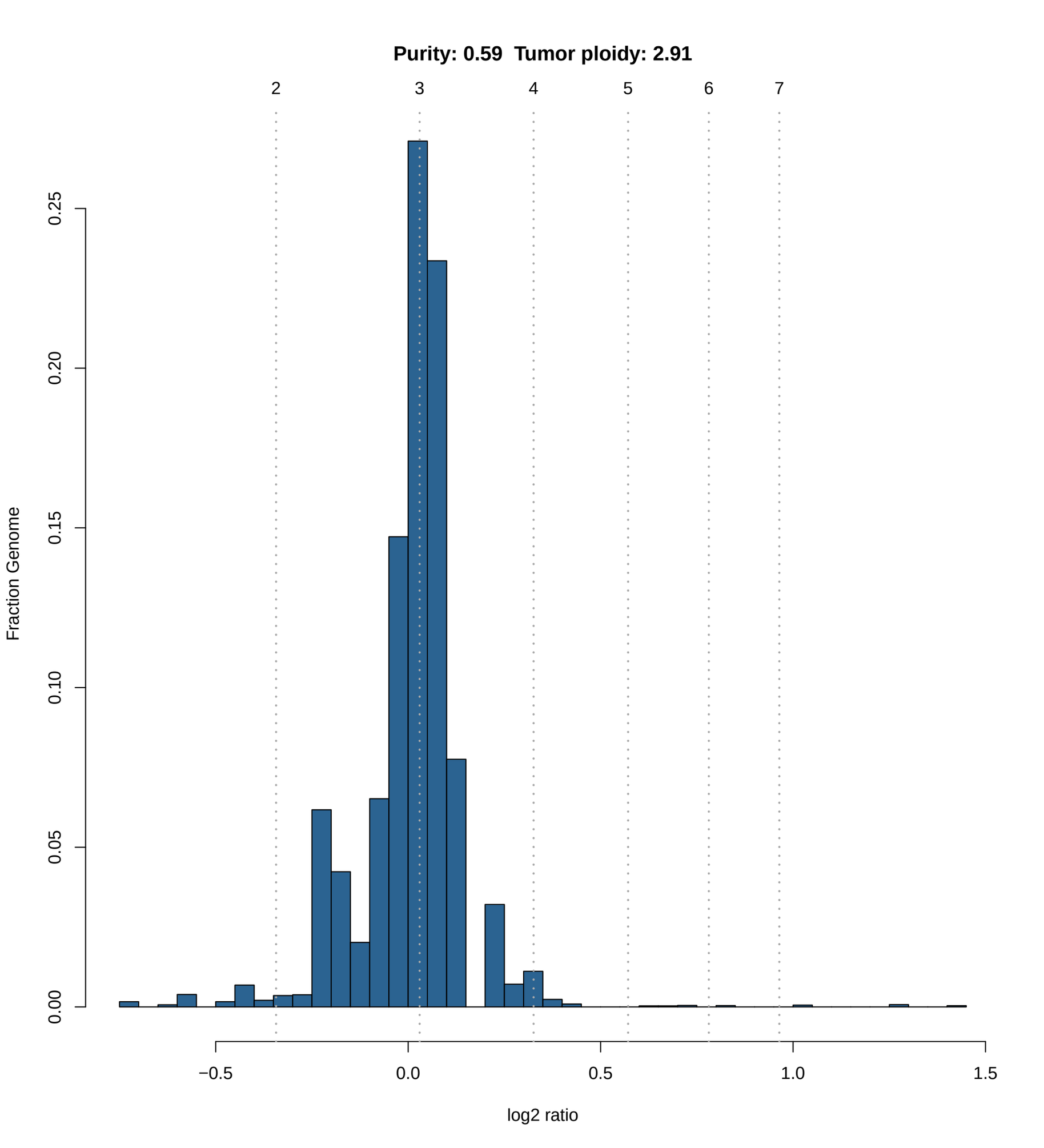

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

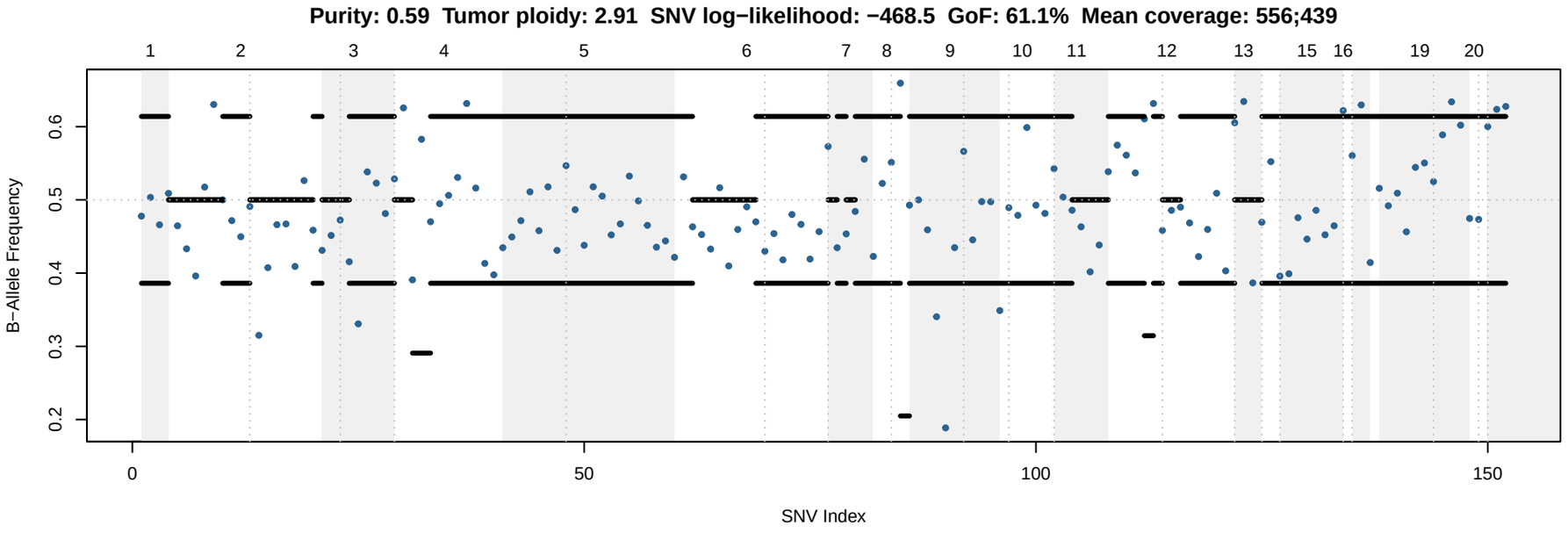

3m2
6m4
5m3
7m4
4m2
6m3
7m3
5m2
3m1
4m1
Allelic fraction (germline)
Copy Number log−ratio

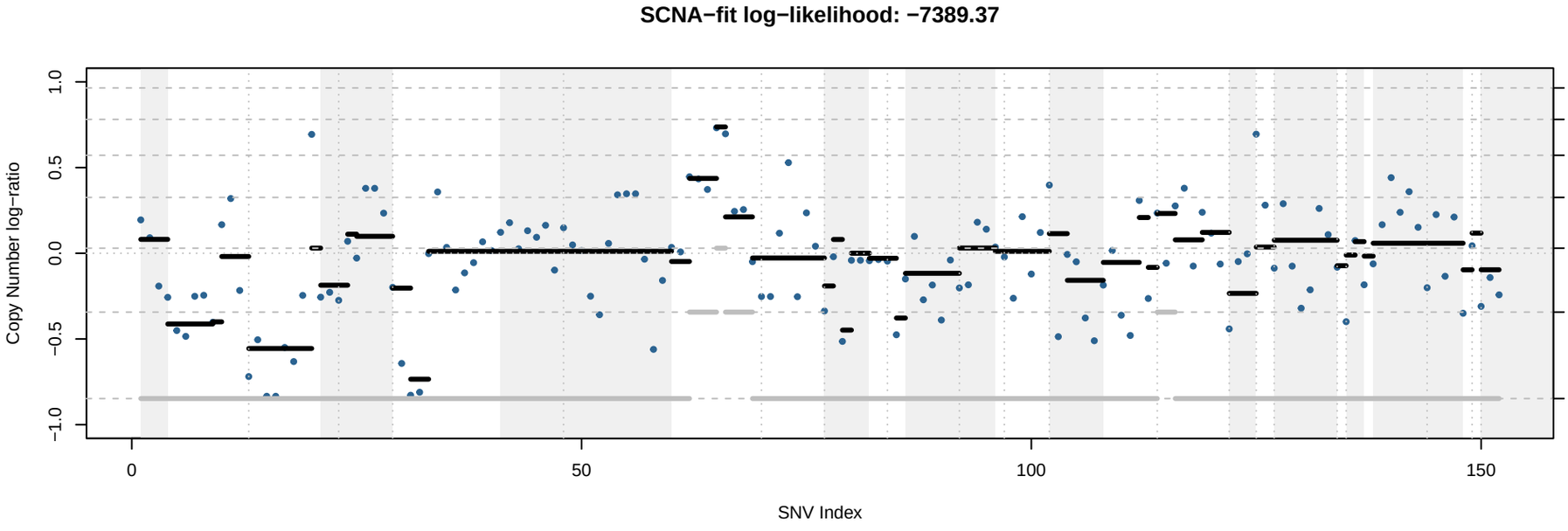

Coverage (log2)
Allelic fraction

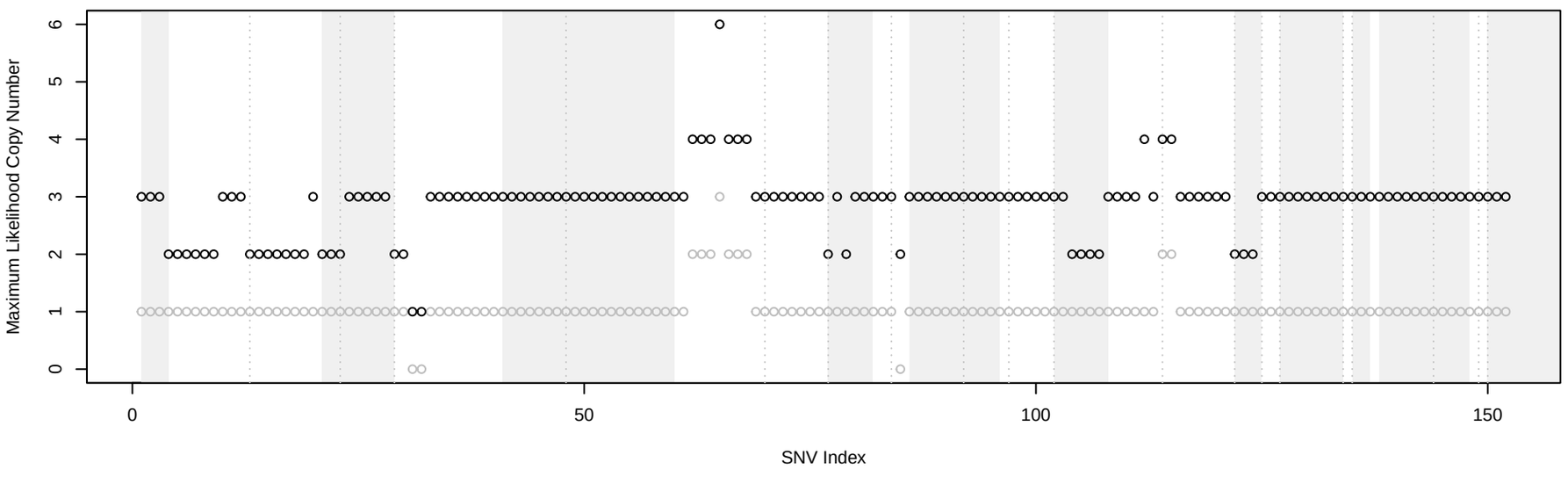

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio

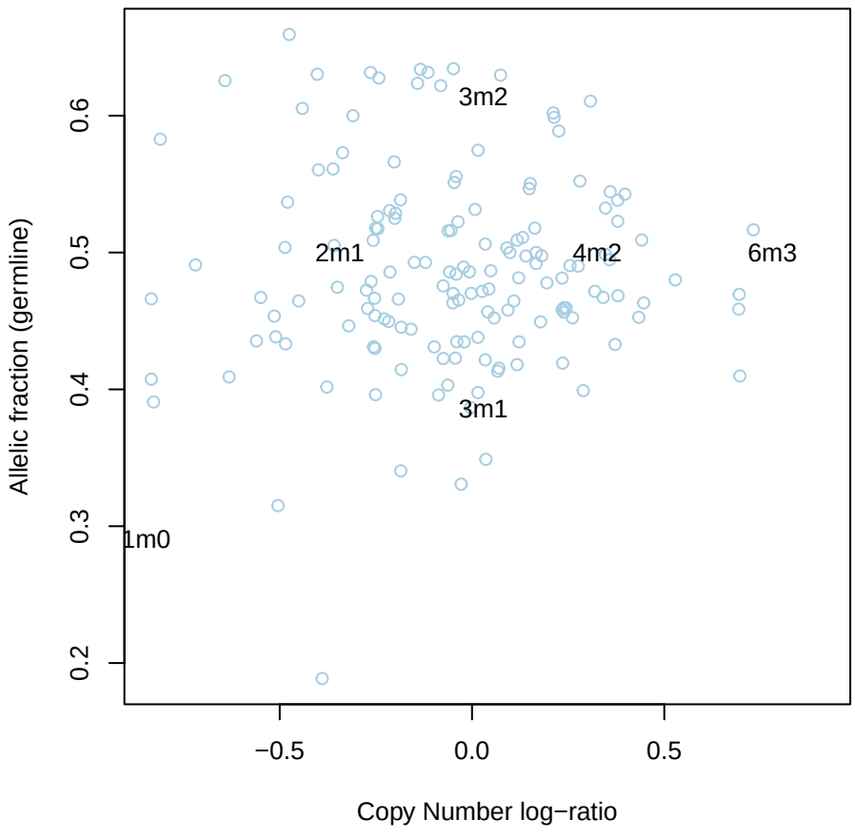

Power 0.8
Frequency
Cellular fraction

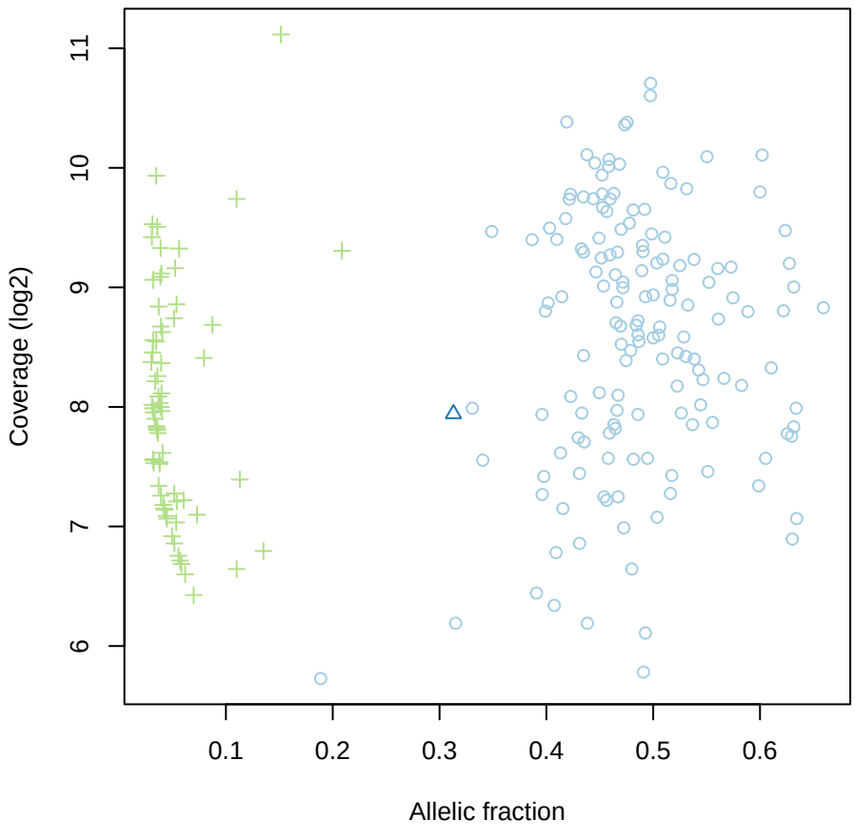

Purity: 0.59 Tumor ploidy: 2.91
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

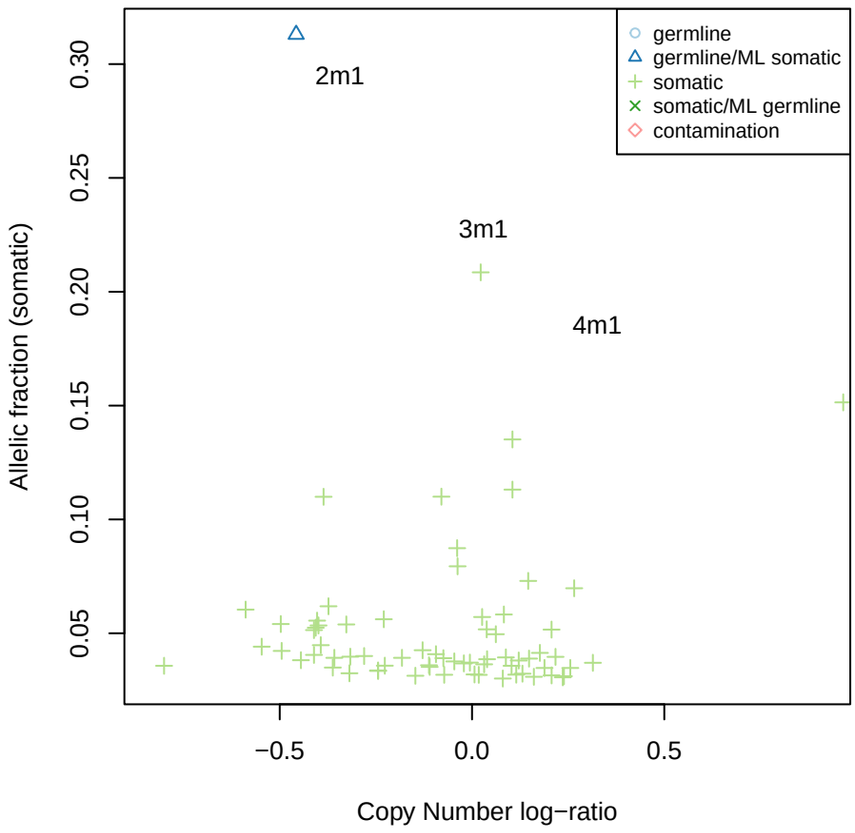

Purity: 0.59 Tumor ploidy: 2.91 SNV log−likelihood: −468.5 GoF: 61.1% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

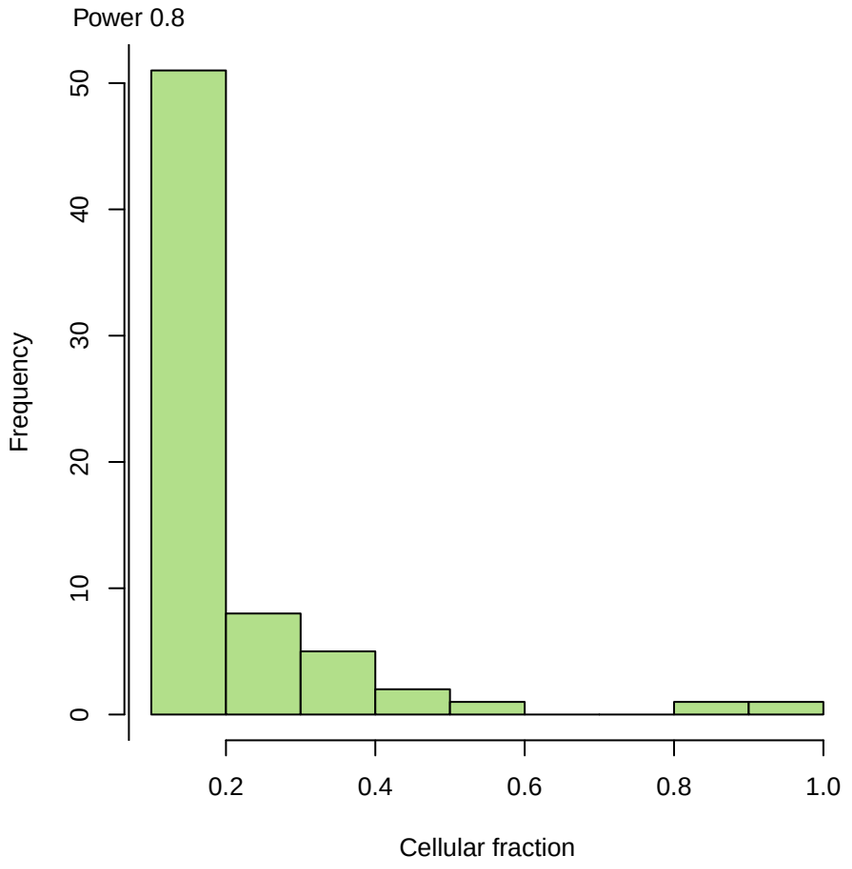

SCNA−fit log−likelihood: −7389.37
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6 7
0 50 100 150
SNV Index

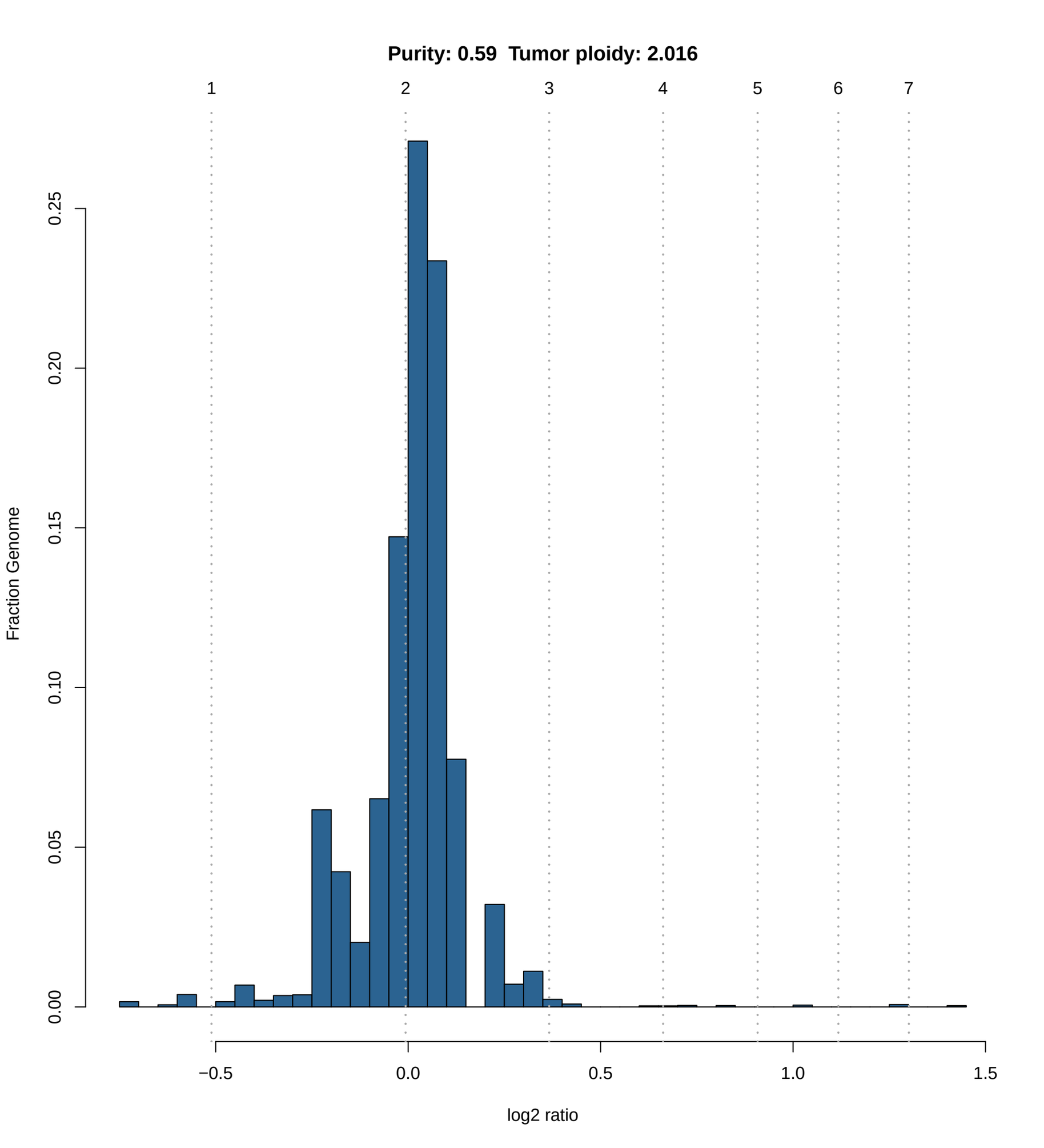

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

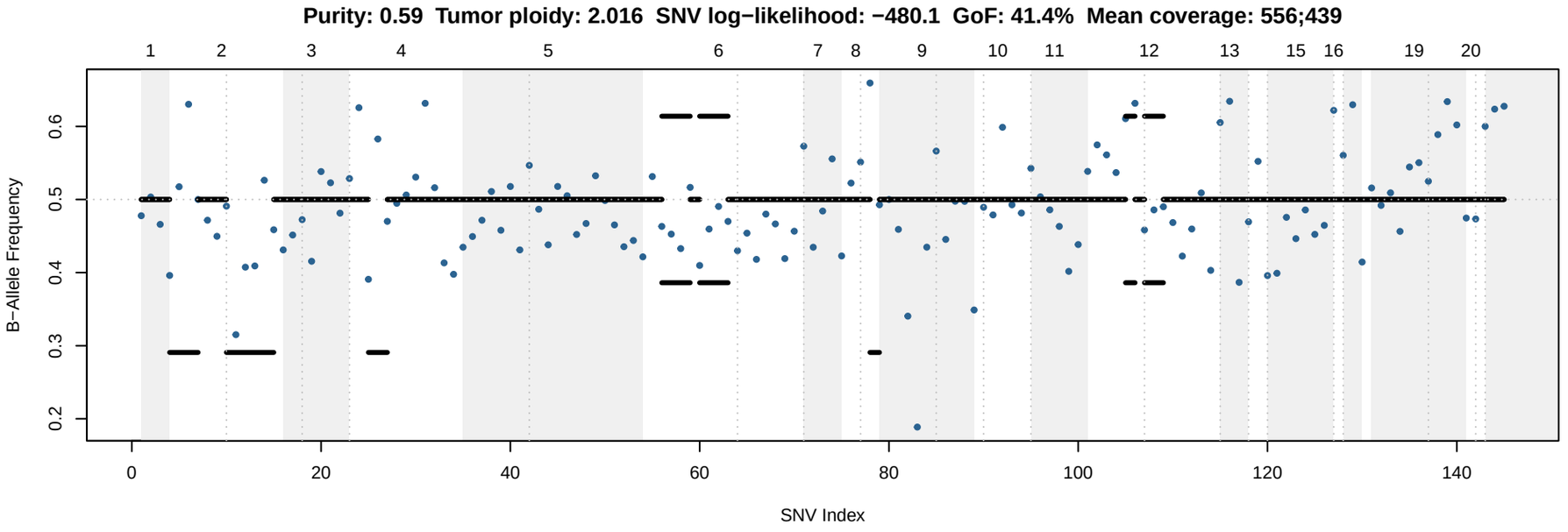

Allelic fraction (germline)
Copy Number log−ratio
3m2
2m1
4m2
6m3
3m1
1m0

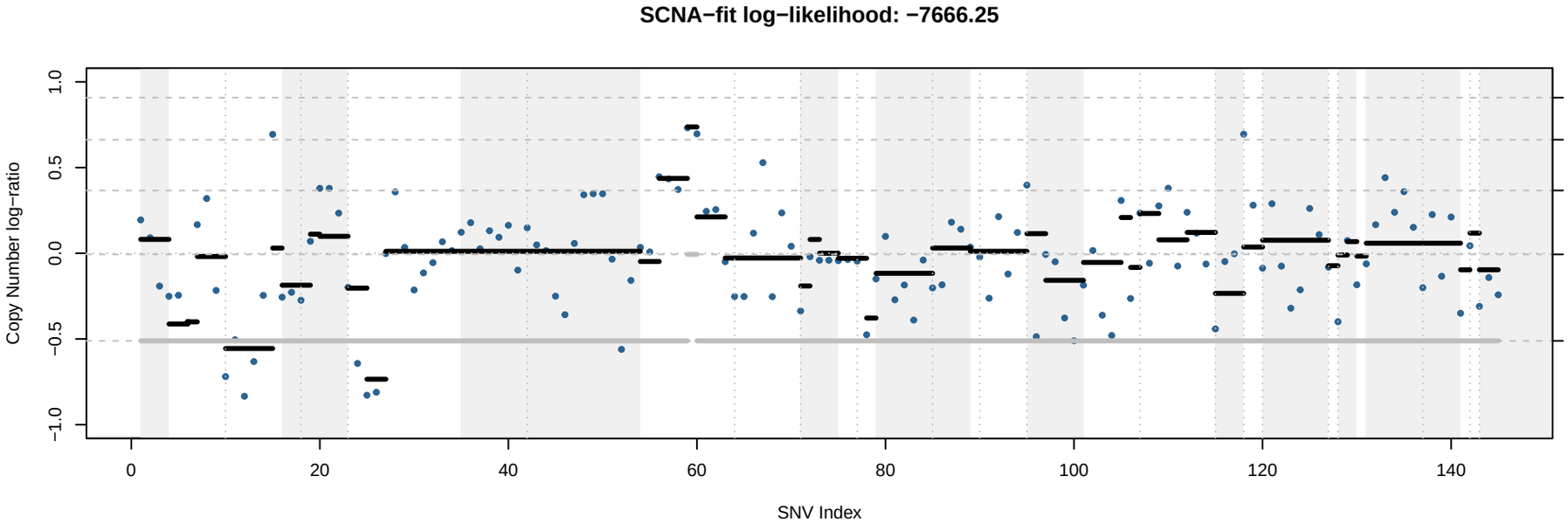

Coverage (log2)
Allelic fraction

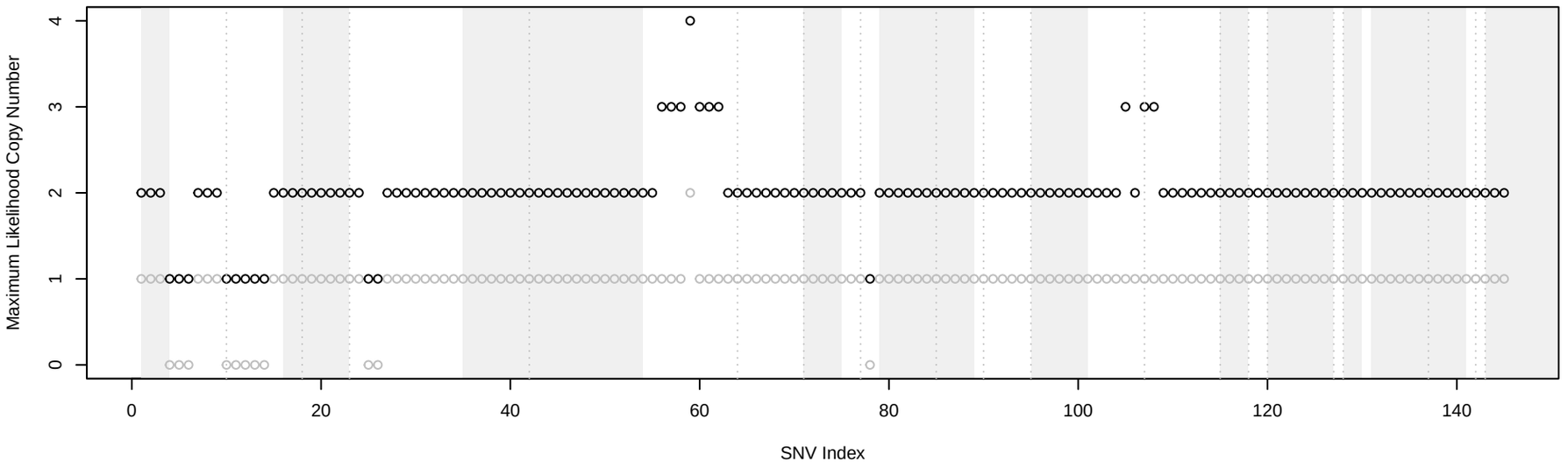

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1

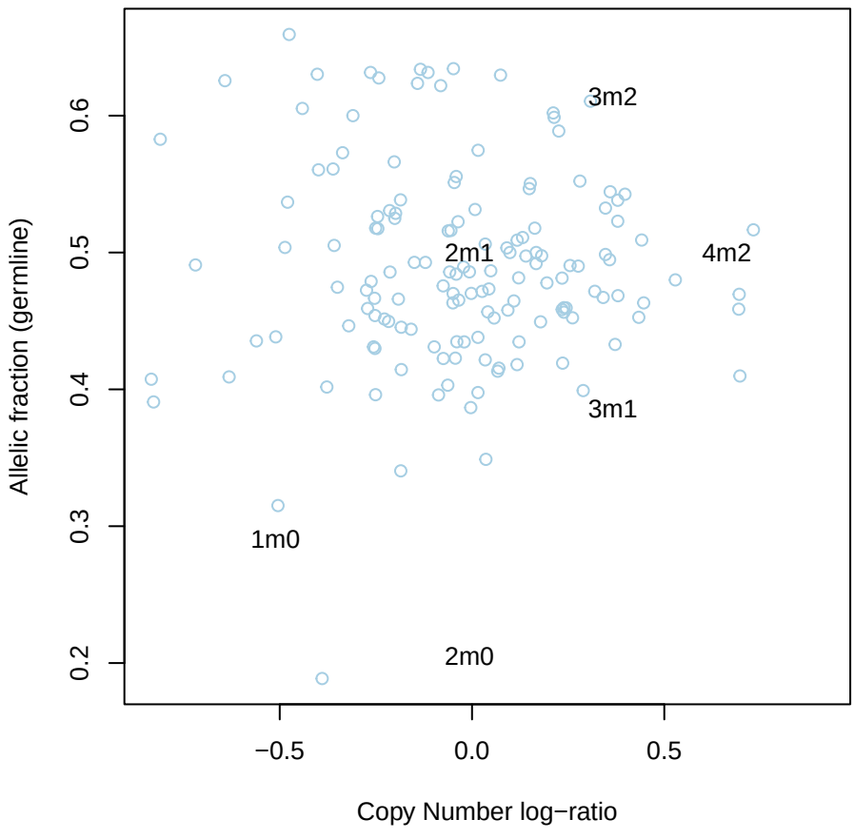

Power 0.8
Frequency
Cellular fraction

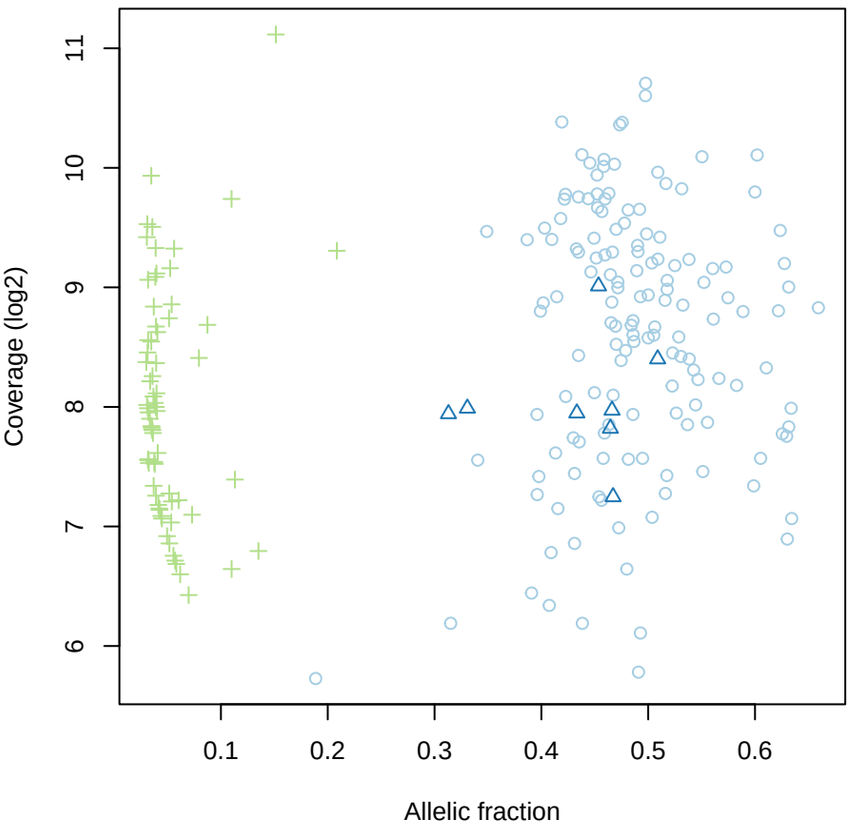

Purity: 0.59 Tumor ploidy: 2.016
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

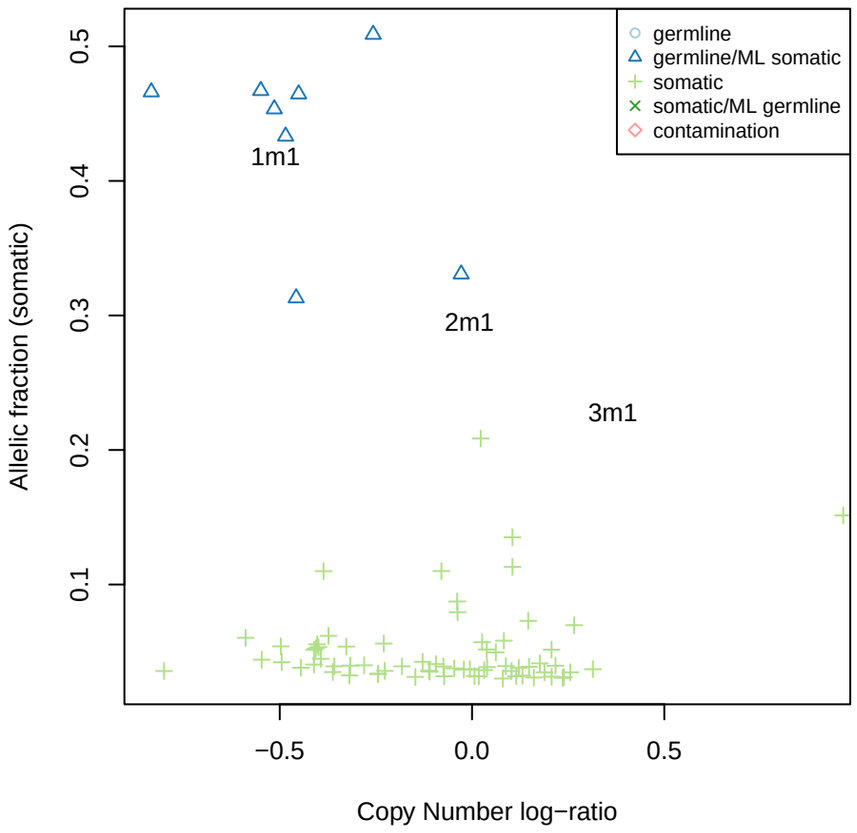

Purity: 0.59 Tumor ploidy: 2.016 SNV log−likelihood: −480.1 GoF: 41.4% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 20 40 60 80 100 120 140
SNV Index

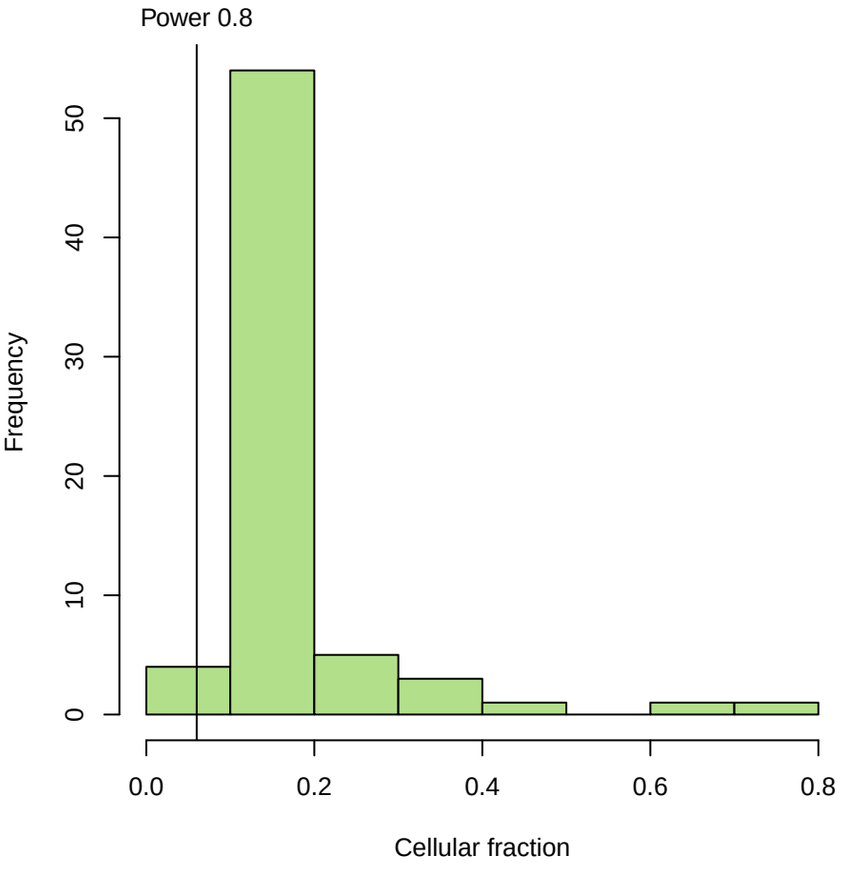

SCNA−fit log−likelihood: −7666.25
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

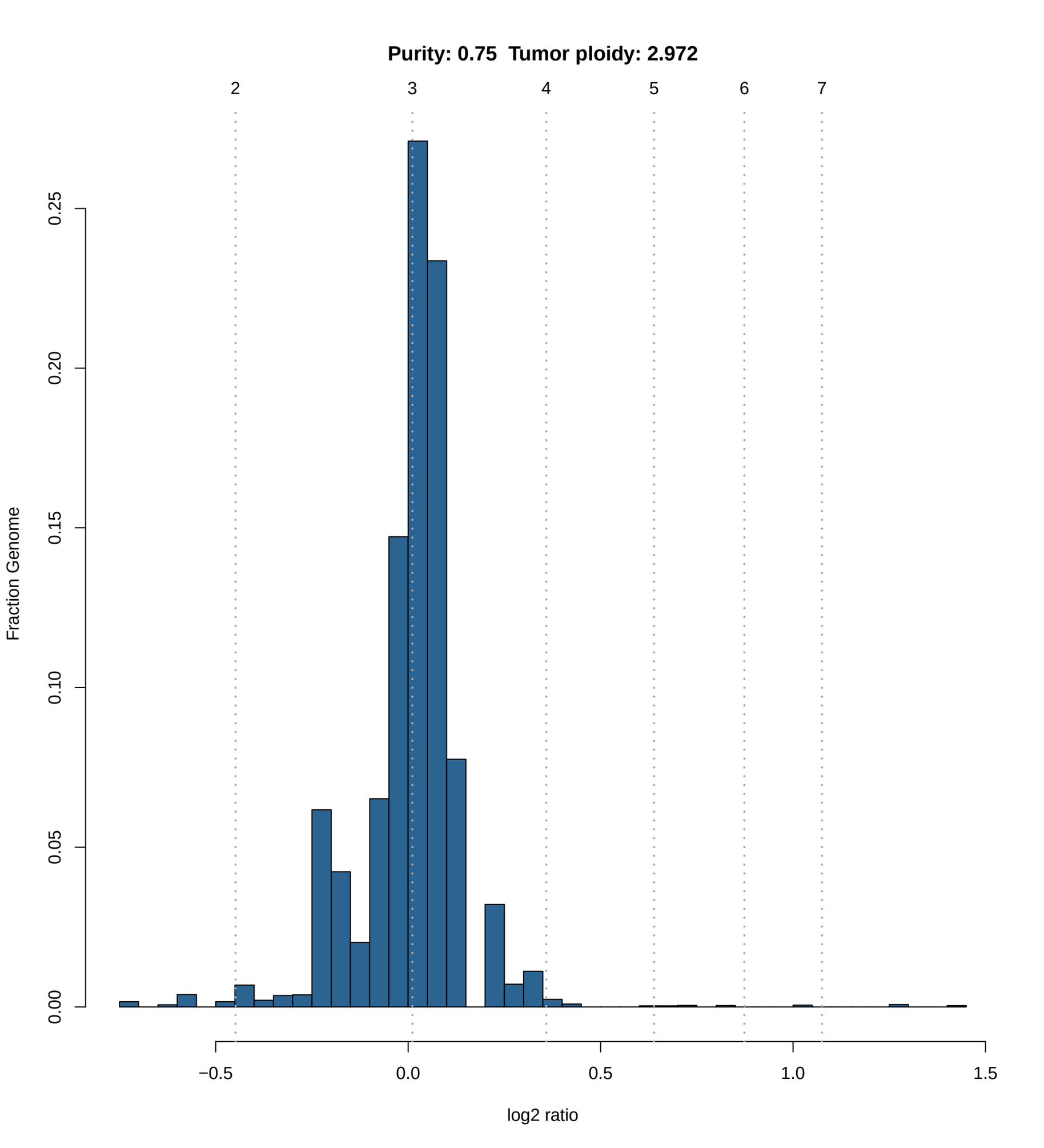

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120 140
SNV Index

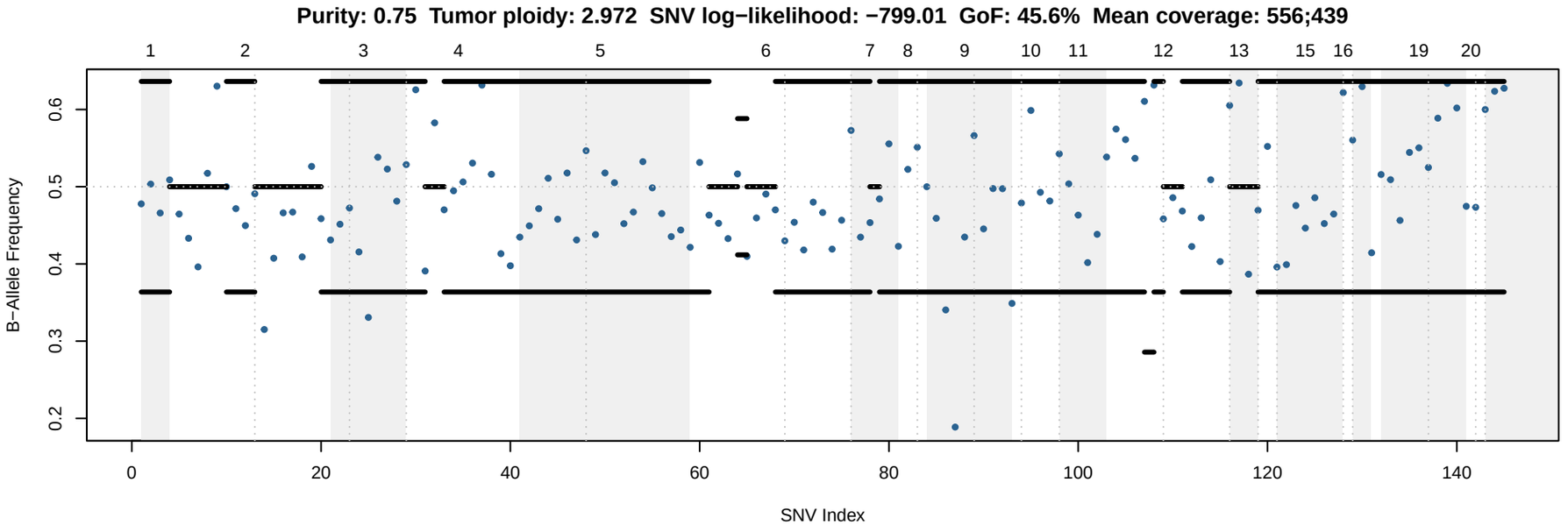

Allelic fraction (germline)
Copy Number log−ratio
3m2
2m1
4m2
3m1
1m0
2m0

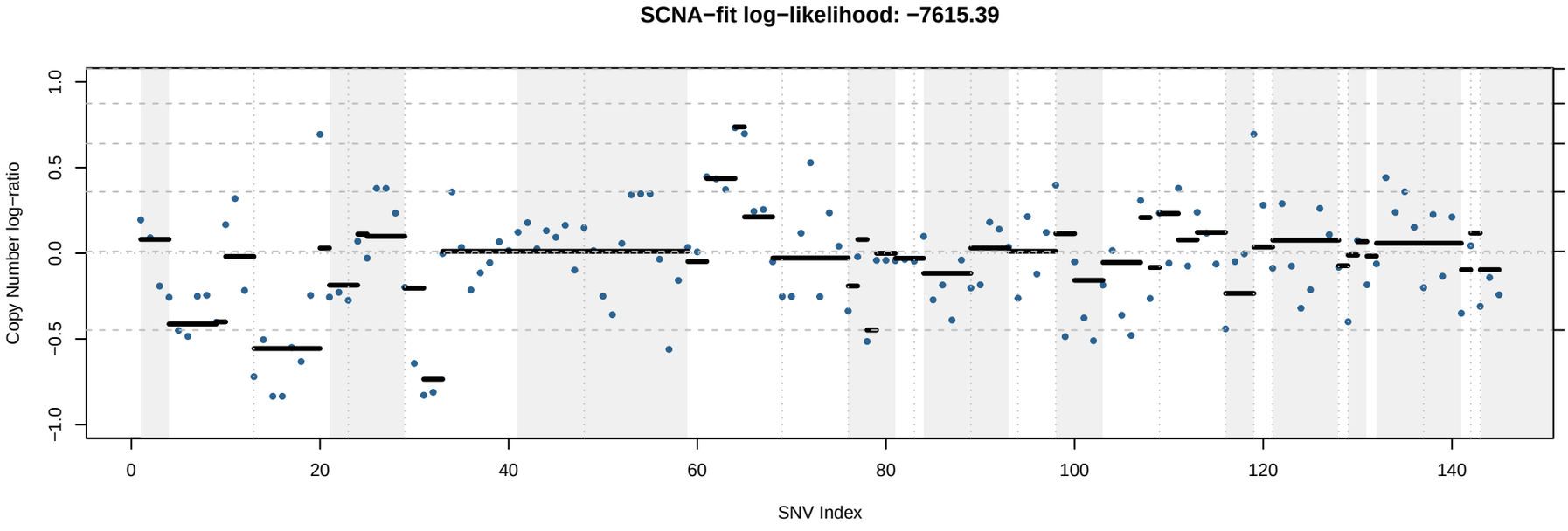

Coverage (log2)
Allelic fraction

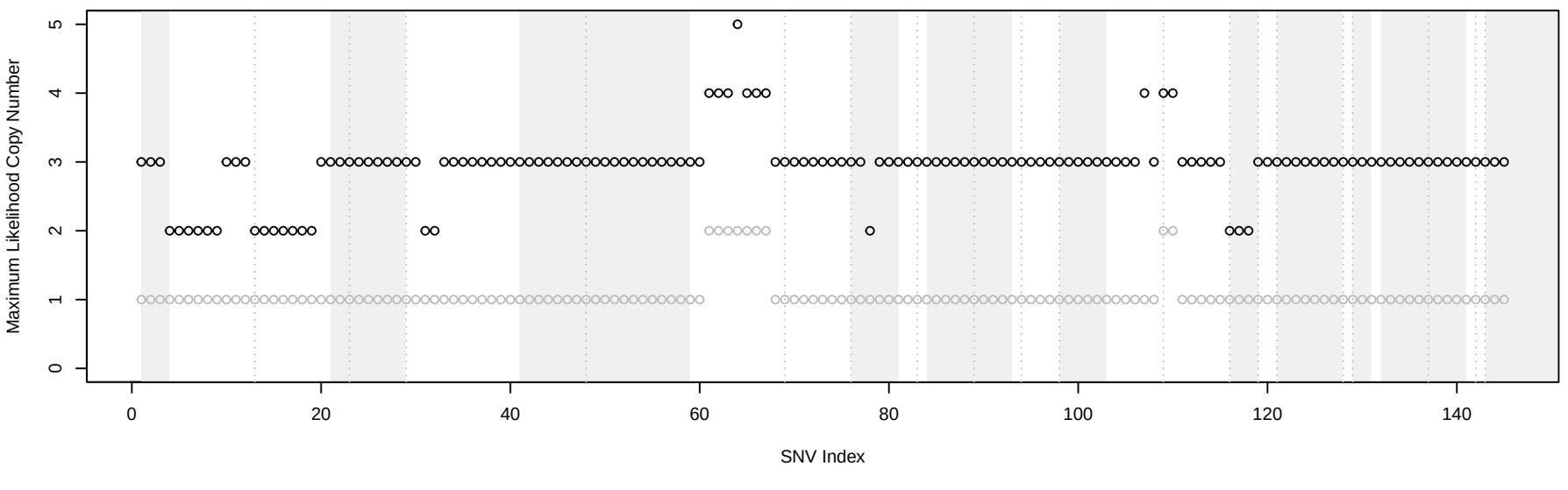

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1

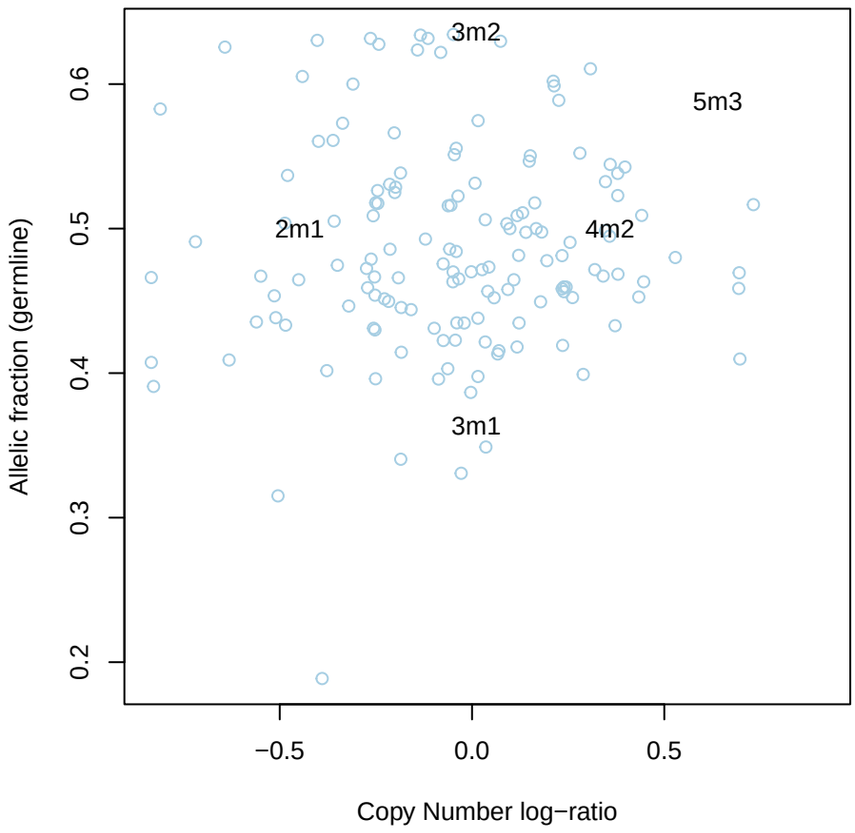

Power 0.8
Frequency
Cellular fraction

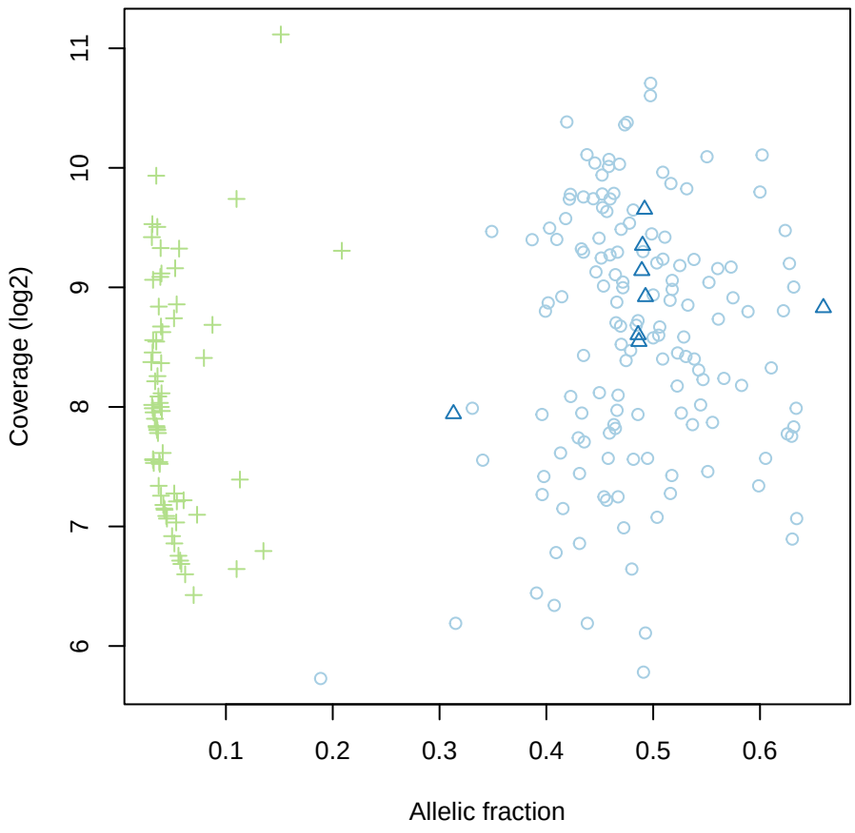

Purity: 0.75 Tumor ploidy: 2.972
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

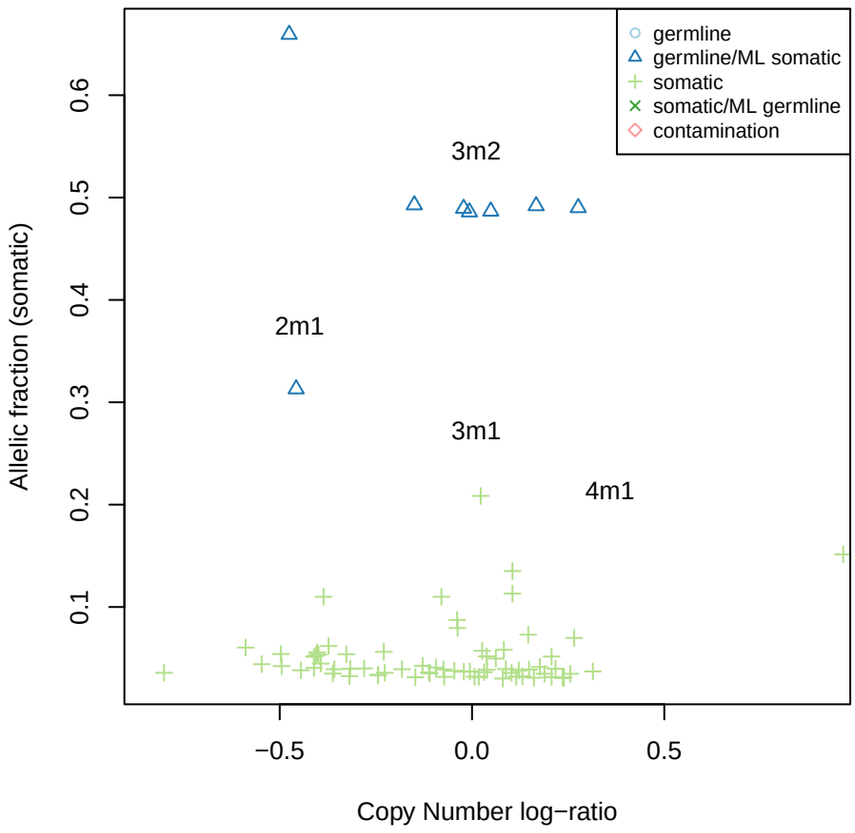

Purity: 0.75 Tumor ploidy: 2.972 SNV log−likelihood: −799.01 GoF: 45.6% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 20 40 60 80 100 120 140
SNV Index

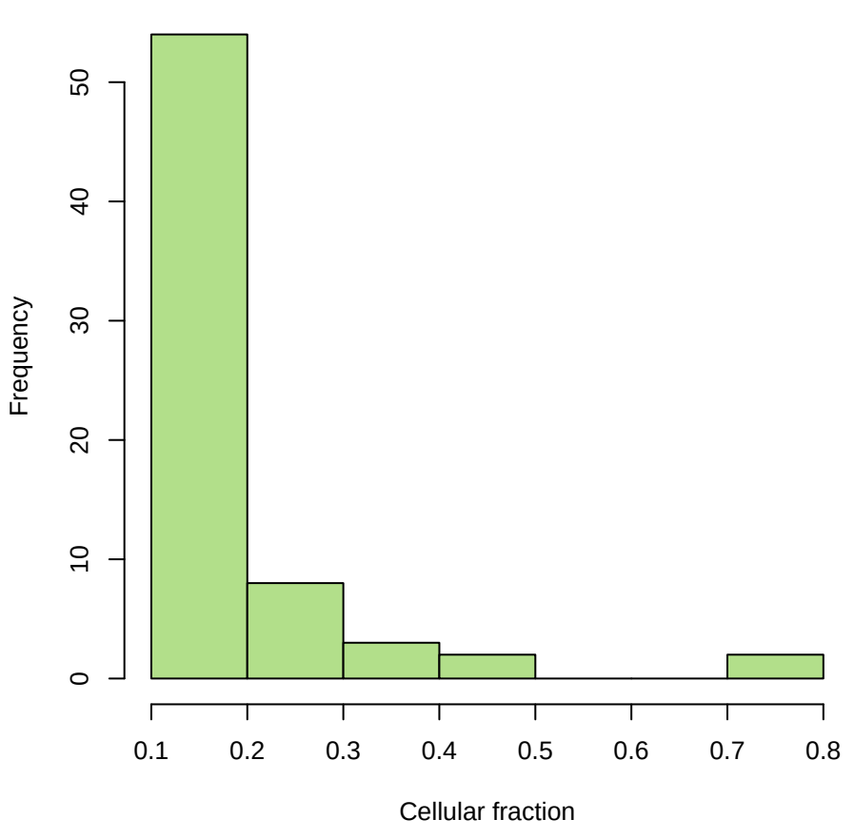

SCNA−fit log−likelihood: −7615.39
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index


Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index


3m2
5m3
2m1
4m2
3m1
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
11
0.1
0.2
0.3
0.4
0.5
0.6


germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m2
2m1
3m1
4m1
Allelic fraction (somatic)
Copy Number log−ratio
0.1
0.2
0.3
0.4
0.5
0.6
−0.5
0.0
0.5


Frequency
Cellular fraction
0
10
20
30
40
50
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8