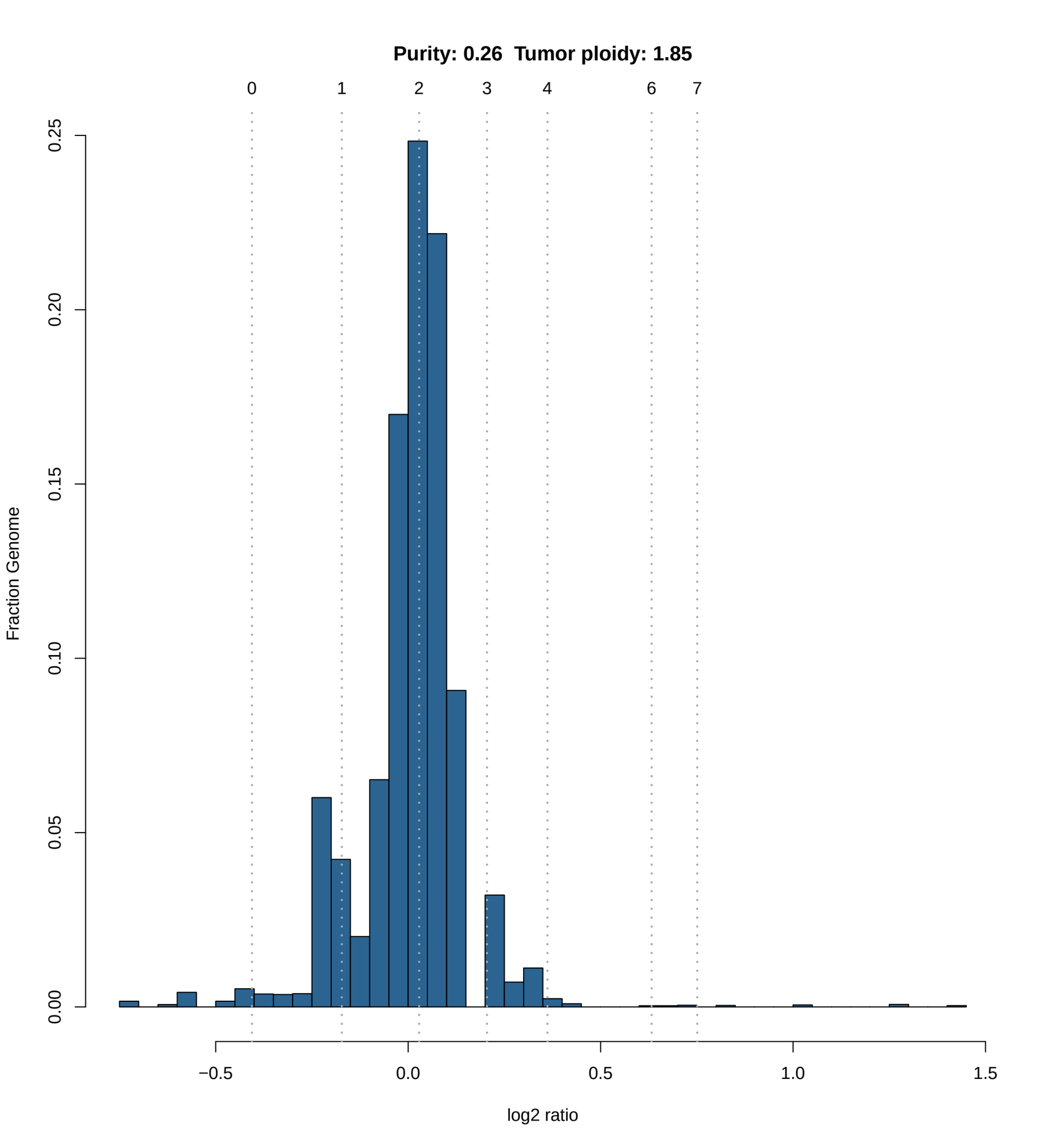
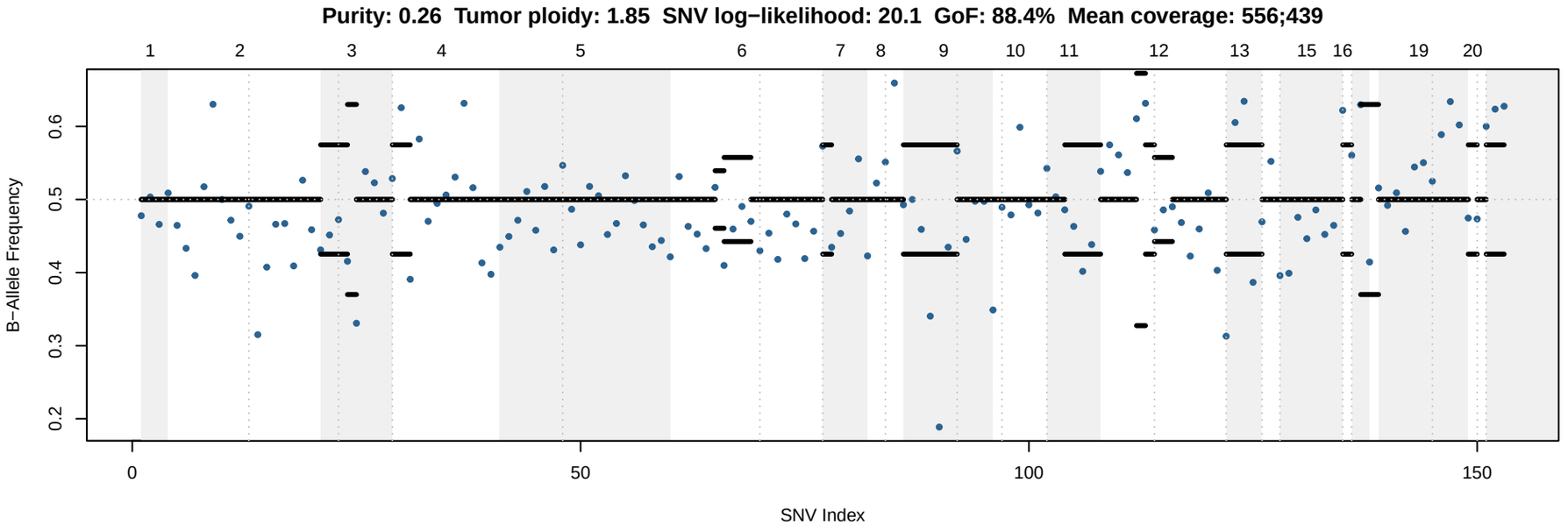
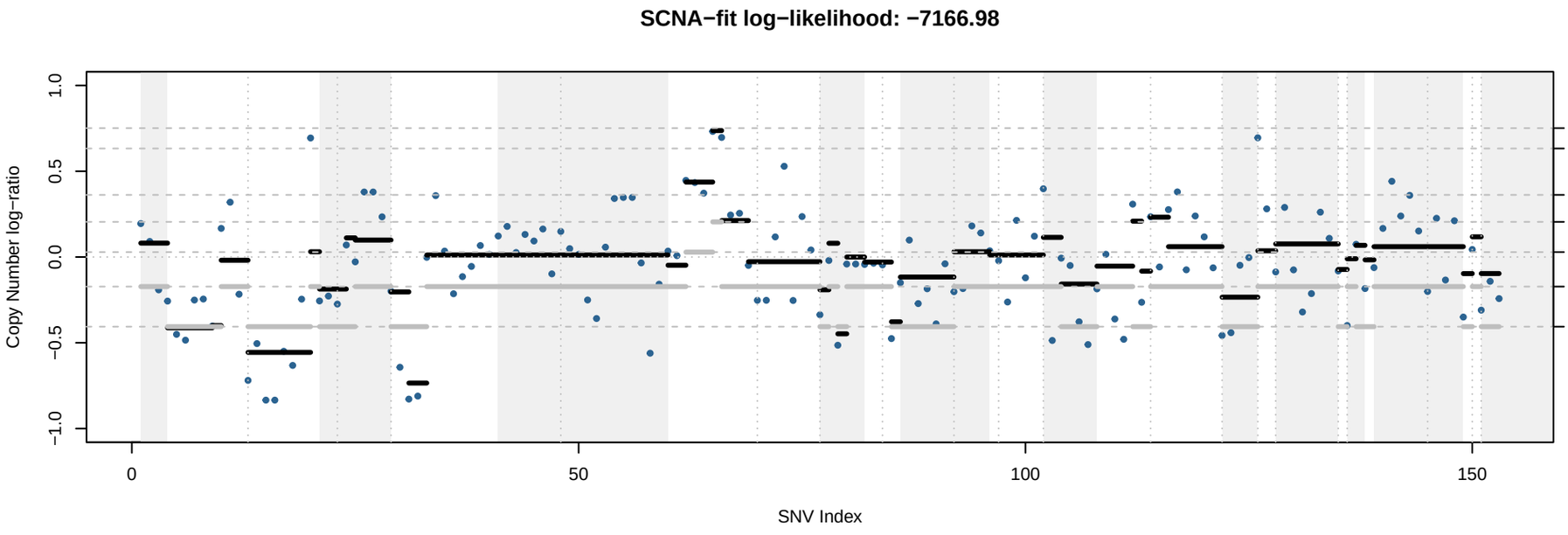
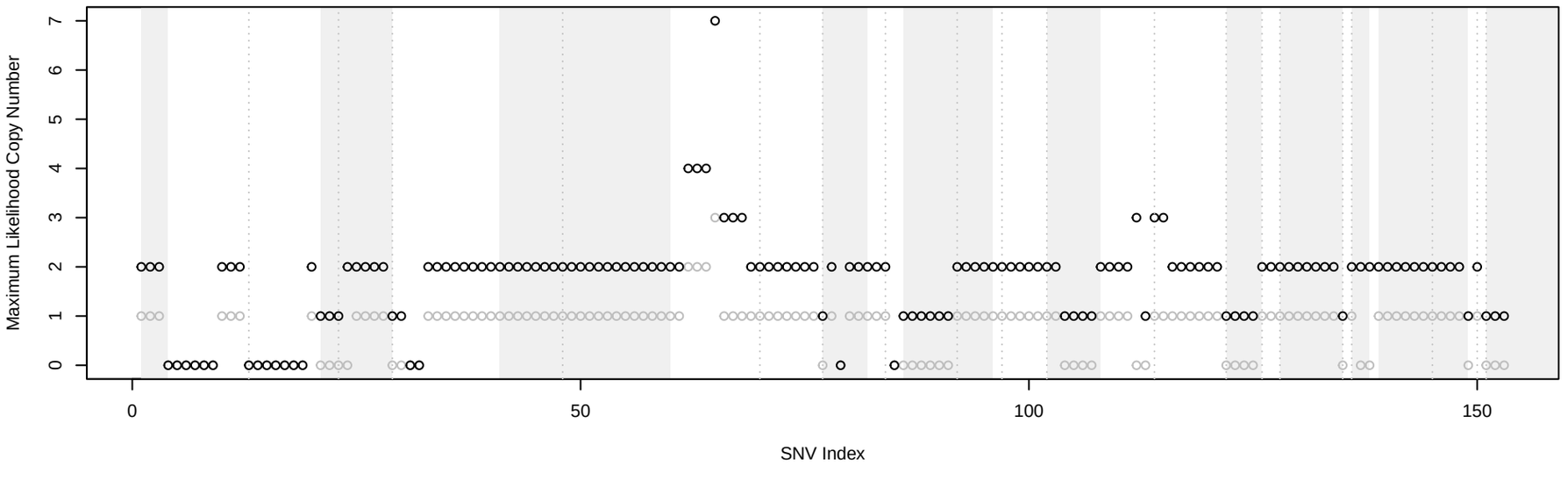
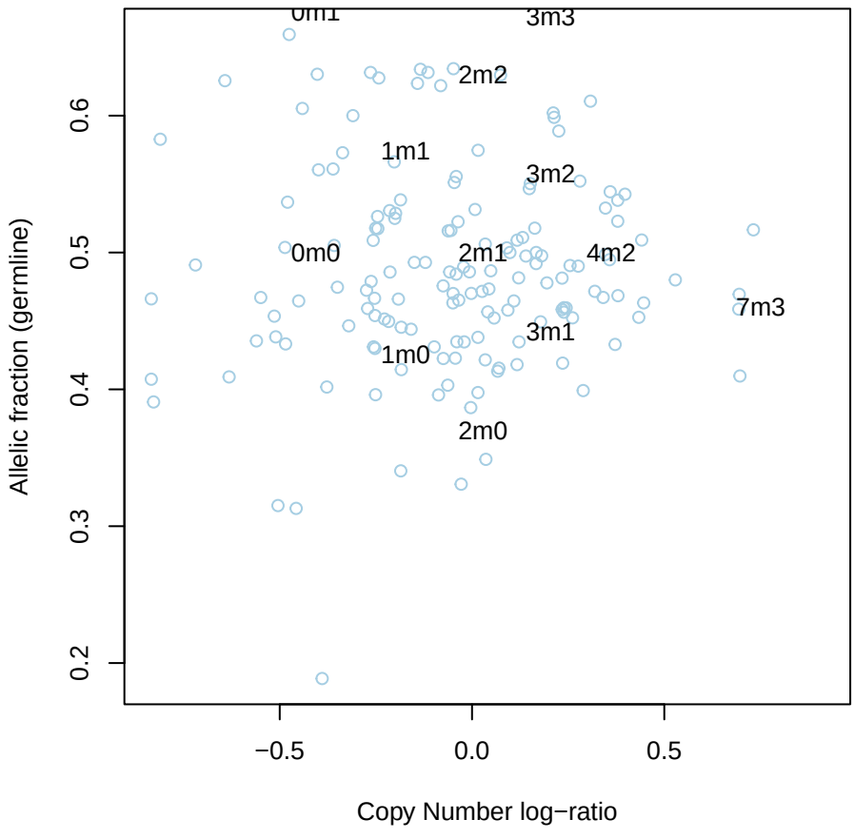
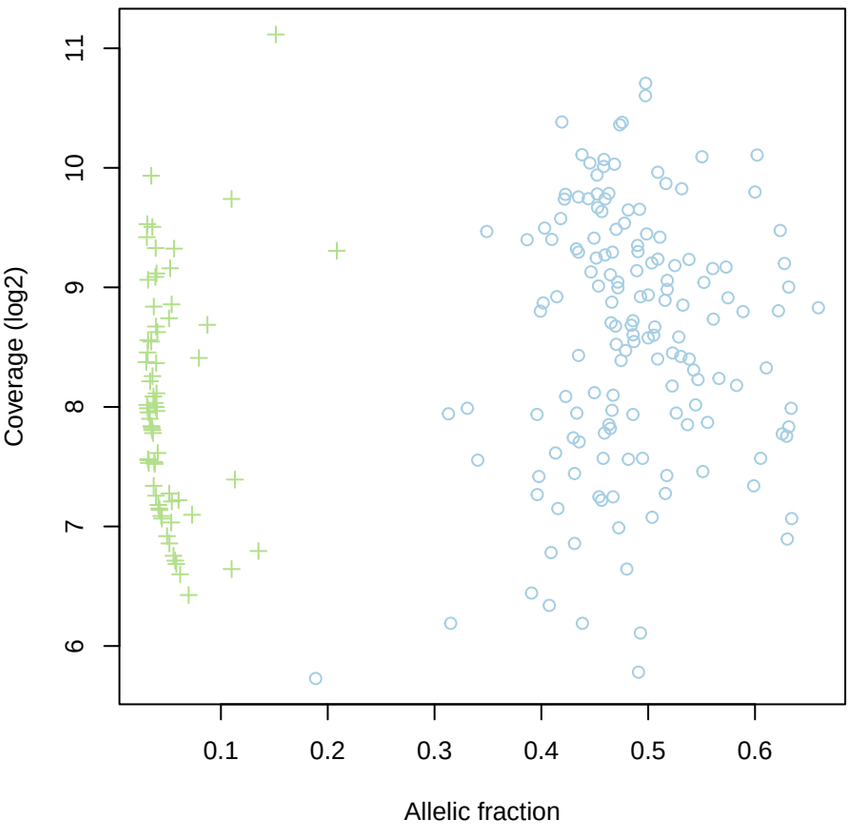

Purity: 0.26 Tumor ploidy: 1.85
0
1
2
3
4
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

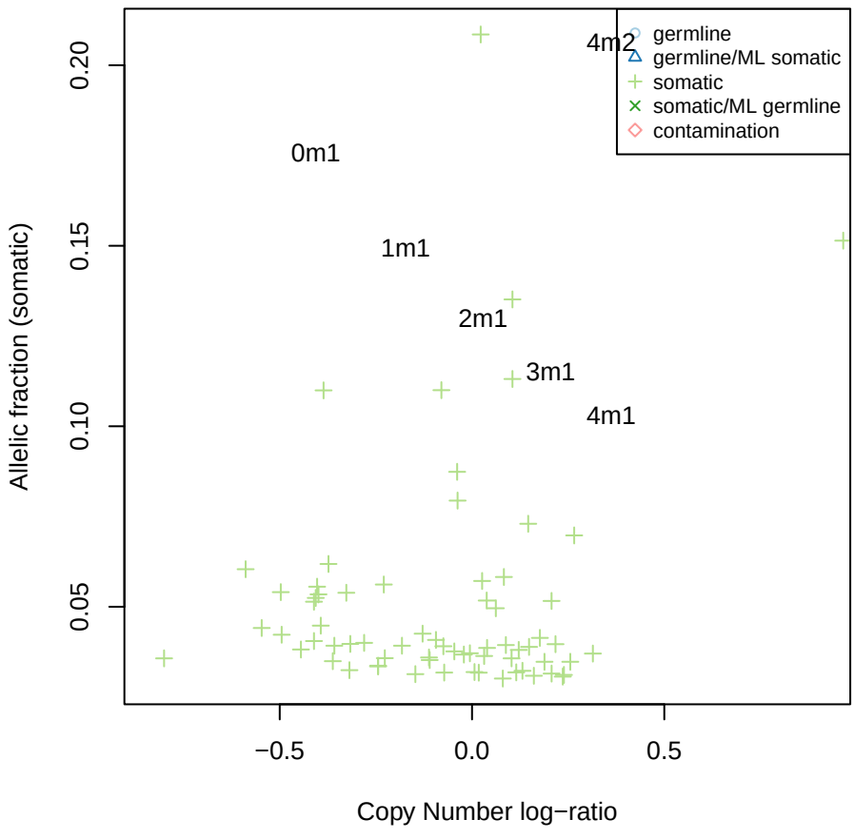

Purity: 0.26 Tumor ploidy: 1.85 SNV log−likelihood: 20.1 GoF: 88.4% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

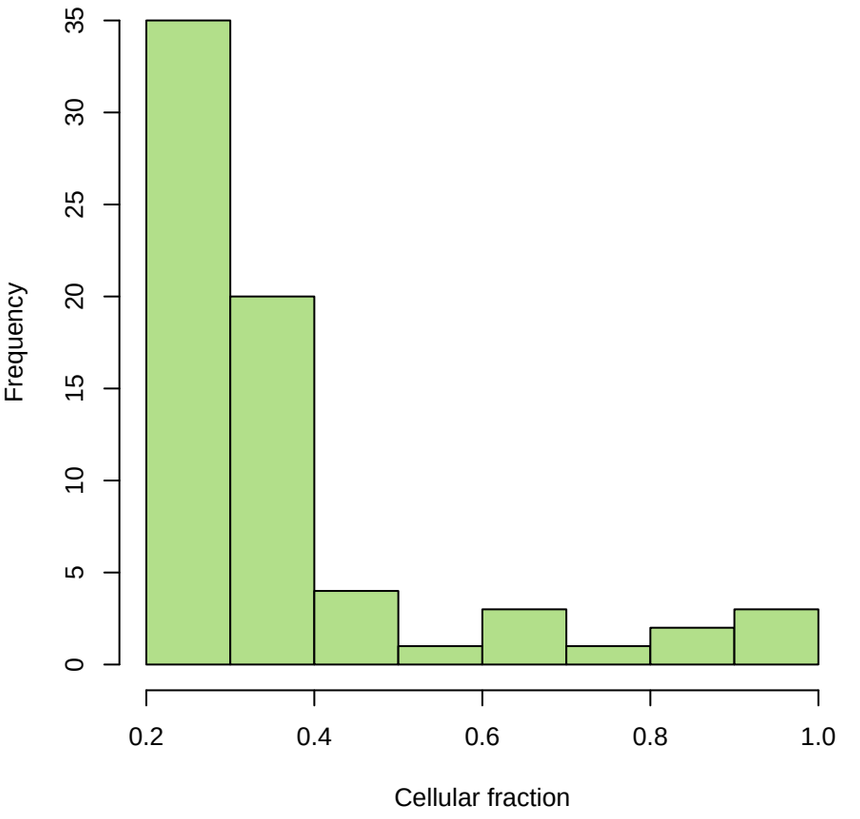

SCNA−fit log−likelihood: −7166.98
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 6
0 50 100 150
SNV Index

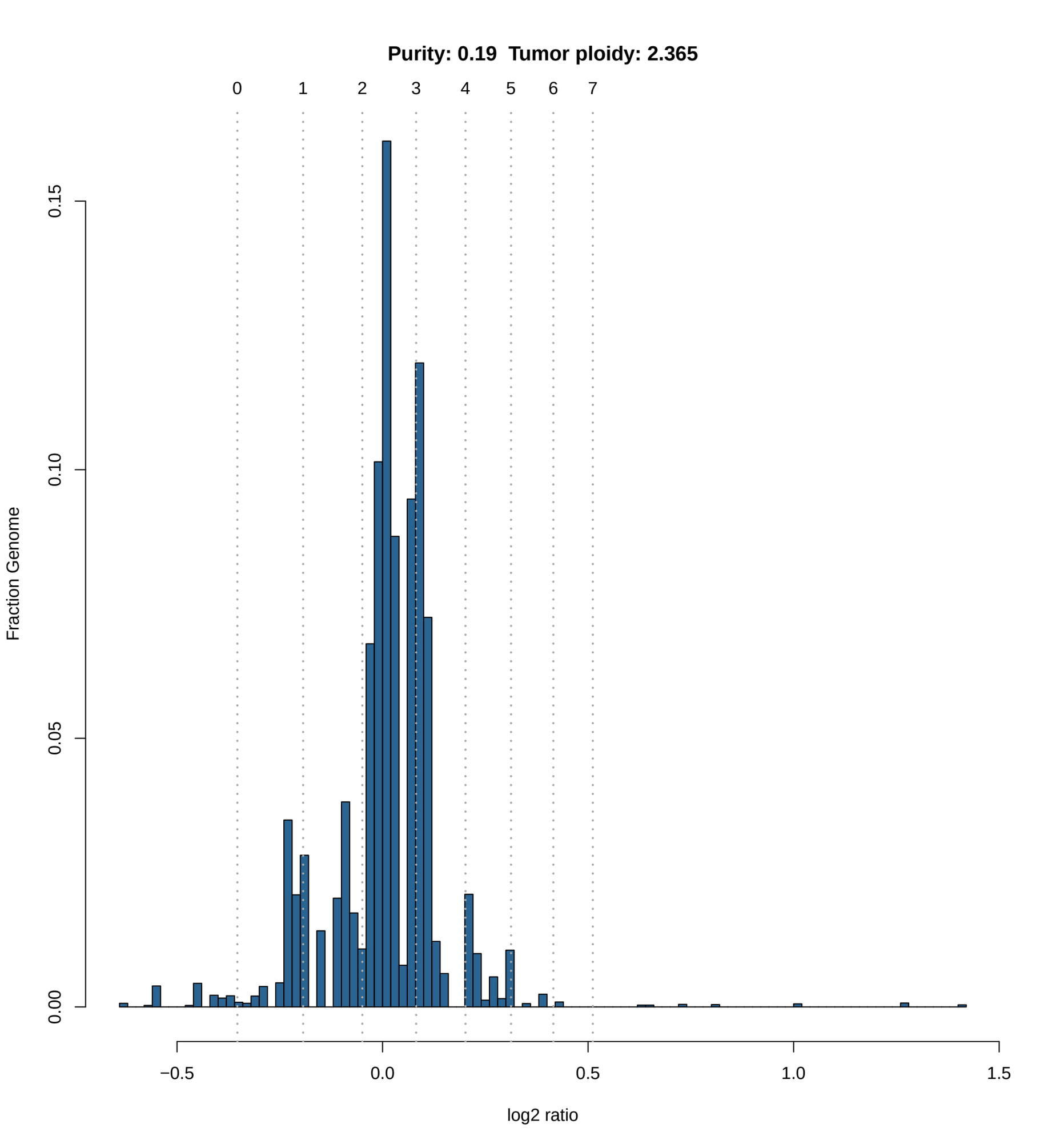

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

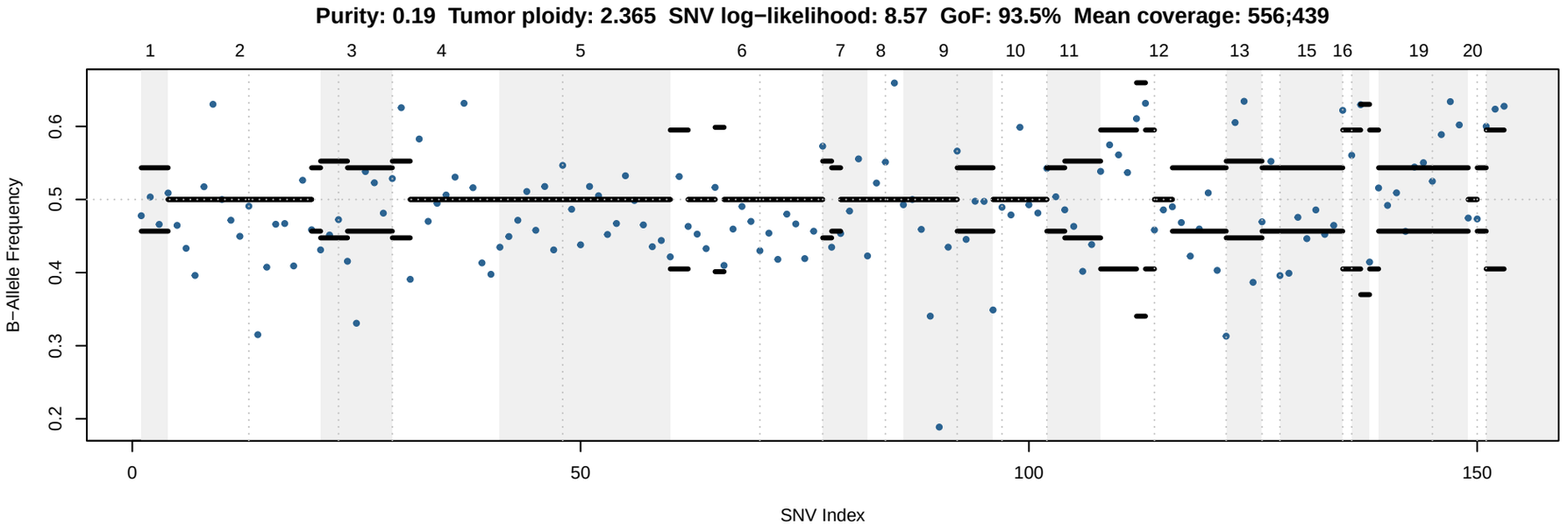

0m1
3m3
2m2
1m1
3m2
0m0
2m1
4m2
7m3
3m1
1m0
2m0
Allelic fraction (germline)
Copy Number log−ratio

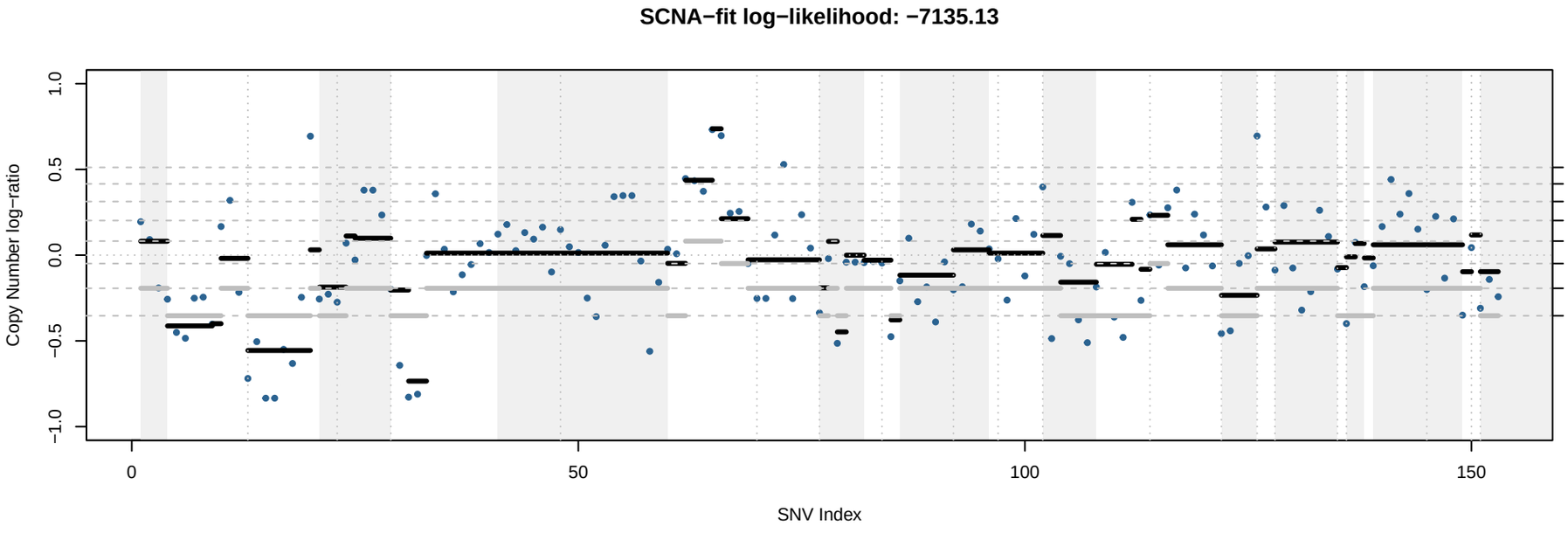

Coverage (log2)
Allelic fraction

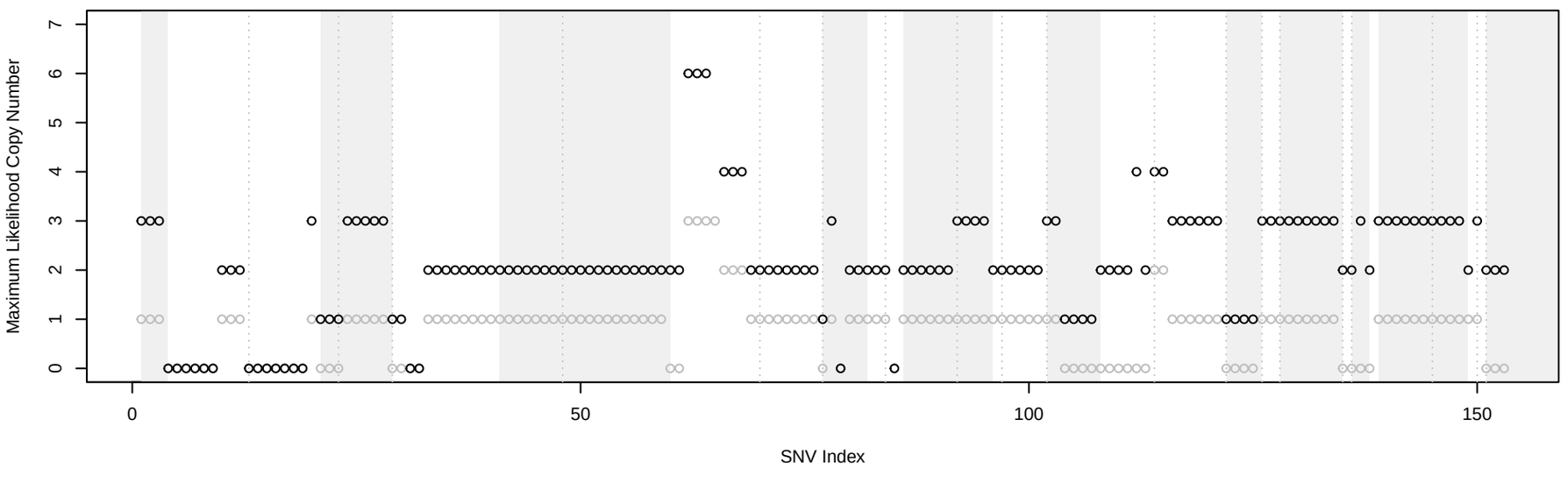

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m2
0m1
1m1
2m1
3m1
4m1
Allelic fraction (somatic)
Copy Number log−ratio

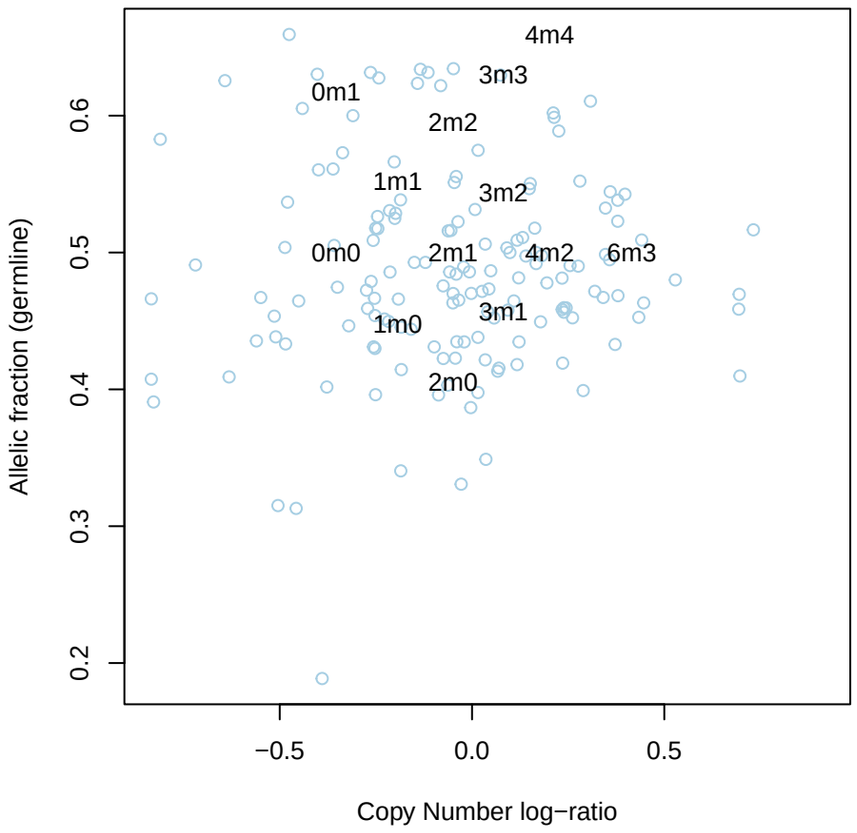

Frequency
Cellular fraction

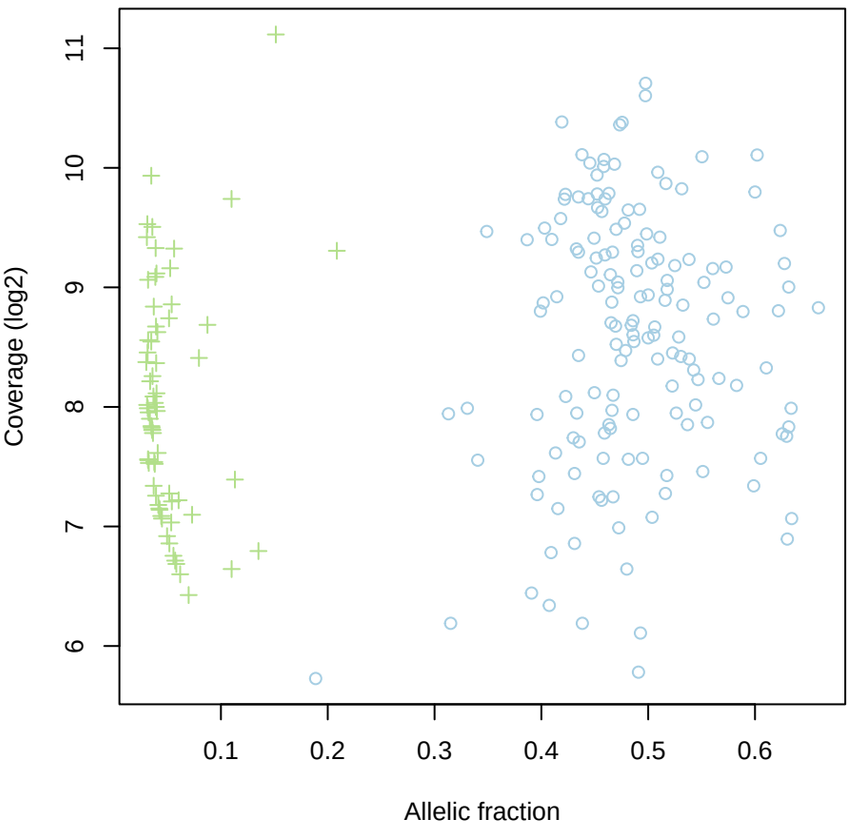

Purity: 0.19 Tumor ploidy: 2.365
0
1
2
3
4
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

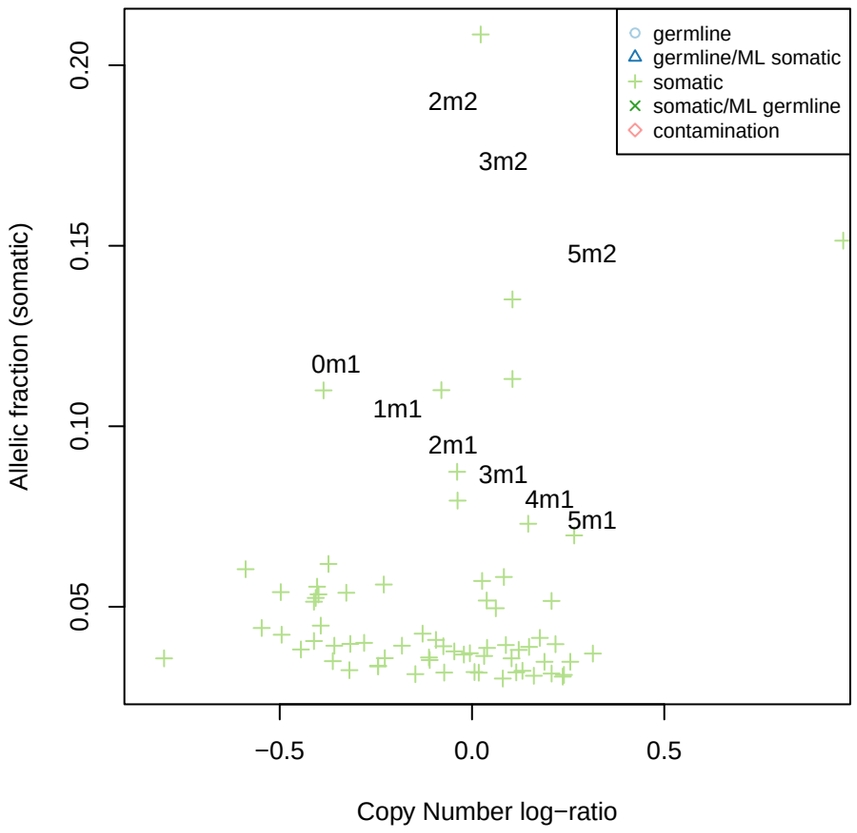

Purity: 0.19 Tumor ploidy: 2.365 SNV log−likelihood: 8.57 GoF: 93.5% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

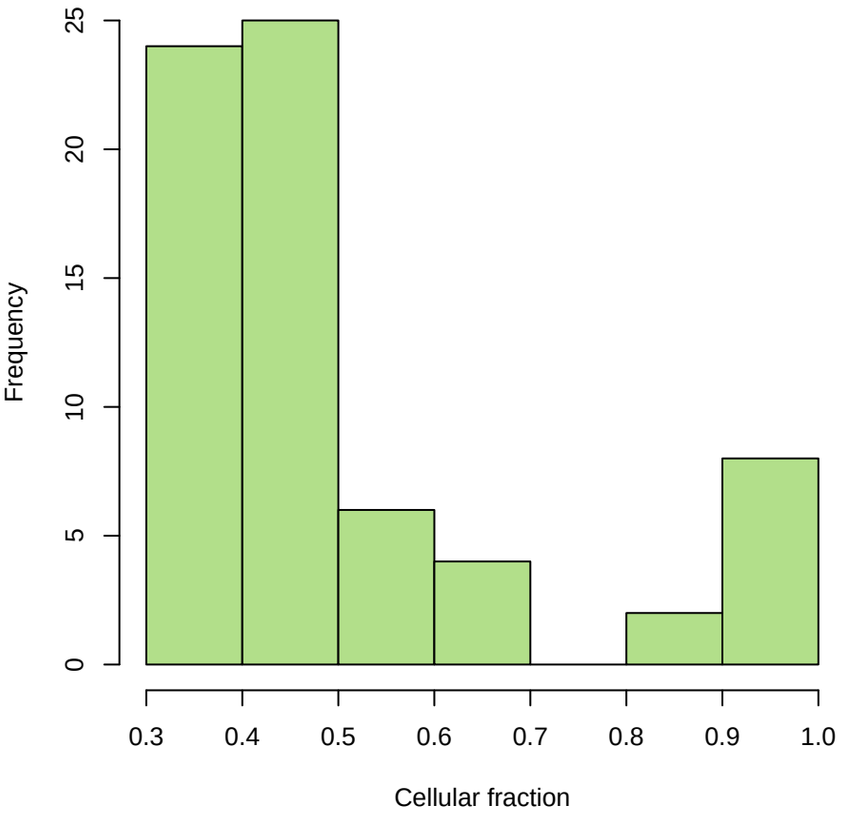

SCNA−fit log−likelihood: −7135.13
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 4 6
0 50 100 150
SNV Index

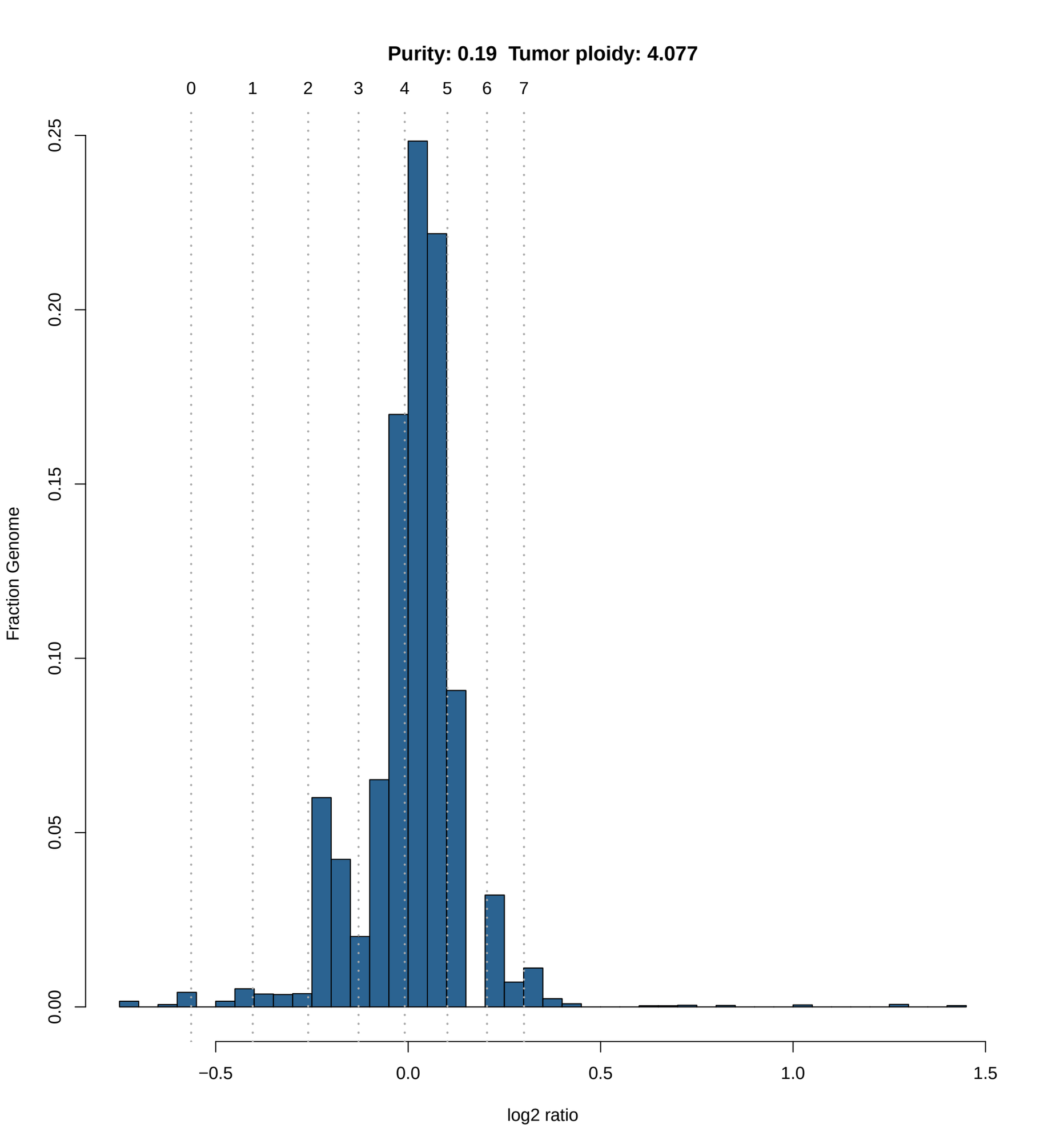

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

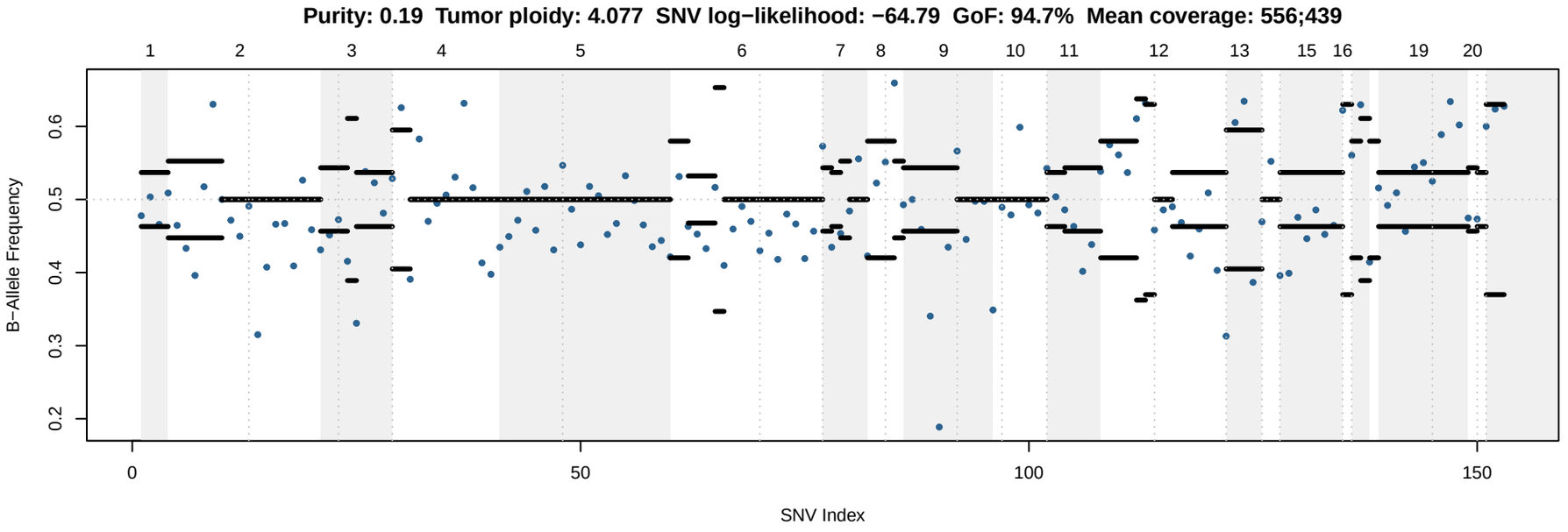

4m4
3m3
0m1
2m2
1m1
3m2
0m0
2m1
4m2
6m3
1m0
3m1
2m0
Allelic fraction (germline)
Copy Number log−ratio

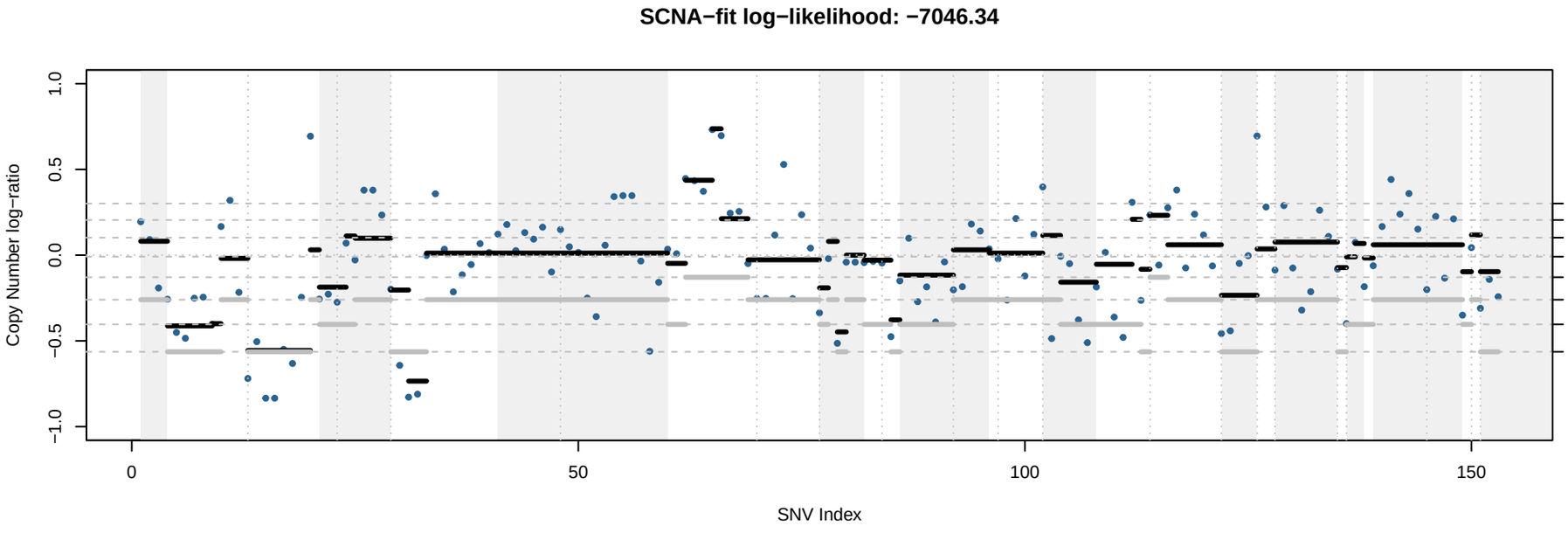

Coverage (log2)
Allelic fraction

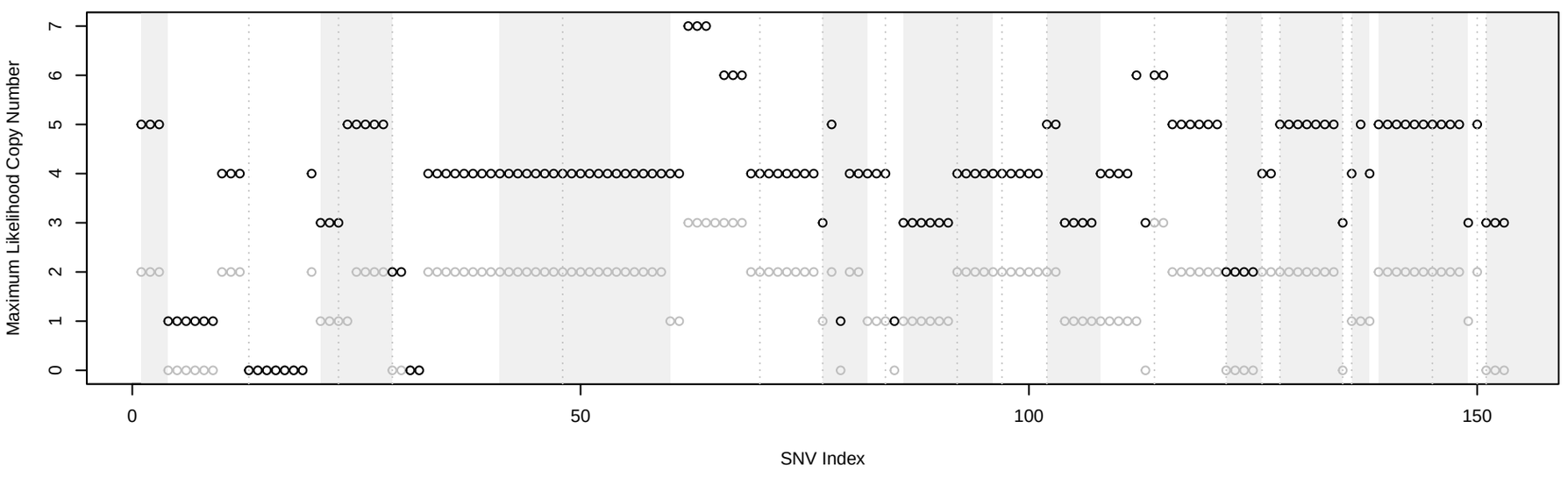

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
3m2
5m2
0m1
1m1
2m1
3m1
4m1
5m1
Allelic fraction (somatic)
Copy Number log−ratio

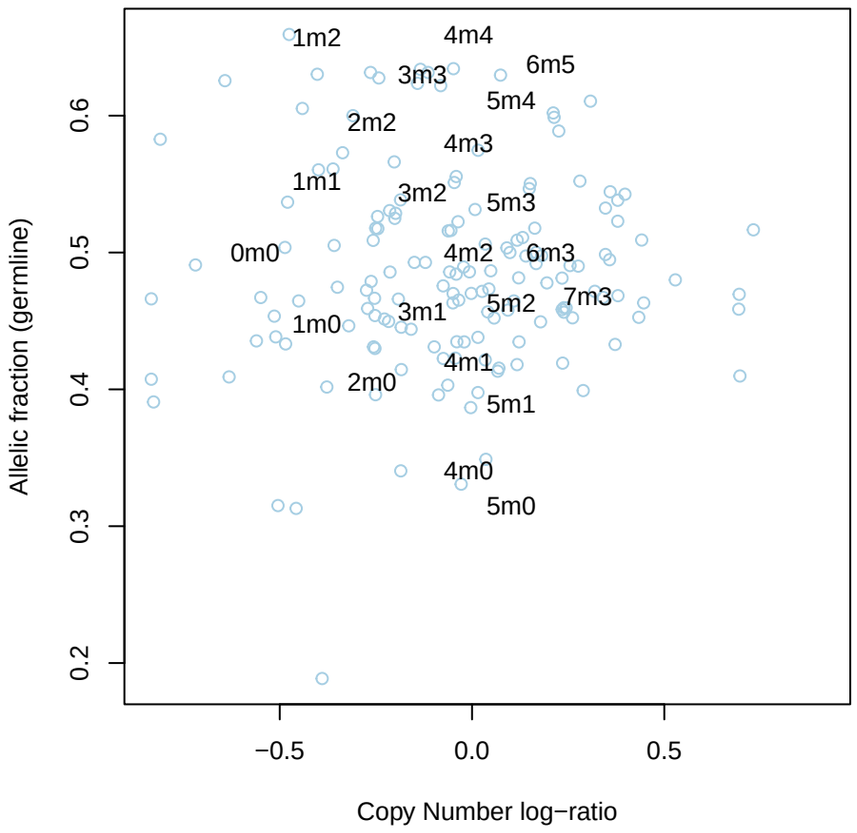

Frequency
Cellular fraction

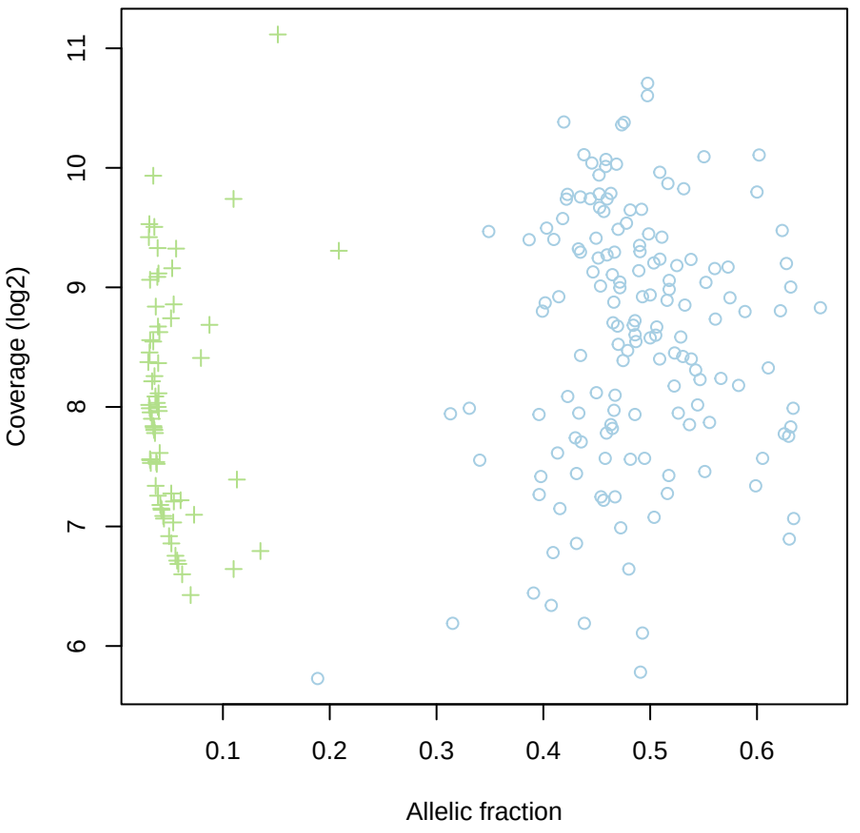

Purity: 0.19 Tumor ploidy: 4.077
0
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

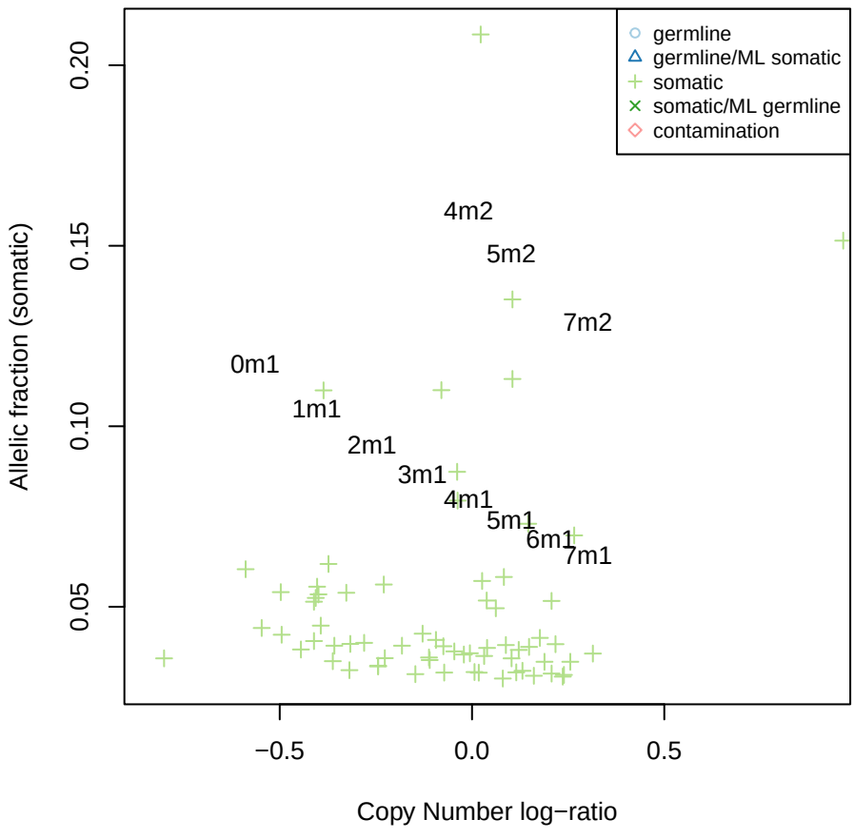

Purity: 0.19 Tumor ploidy: 4.077 SNV log−likelihood: −64.79 GoF: 94.7% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

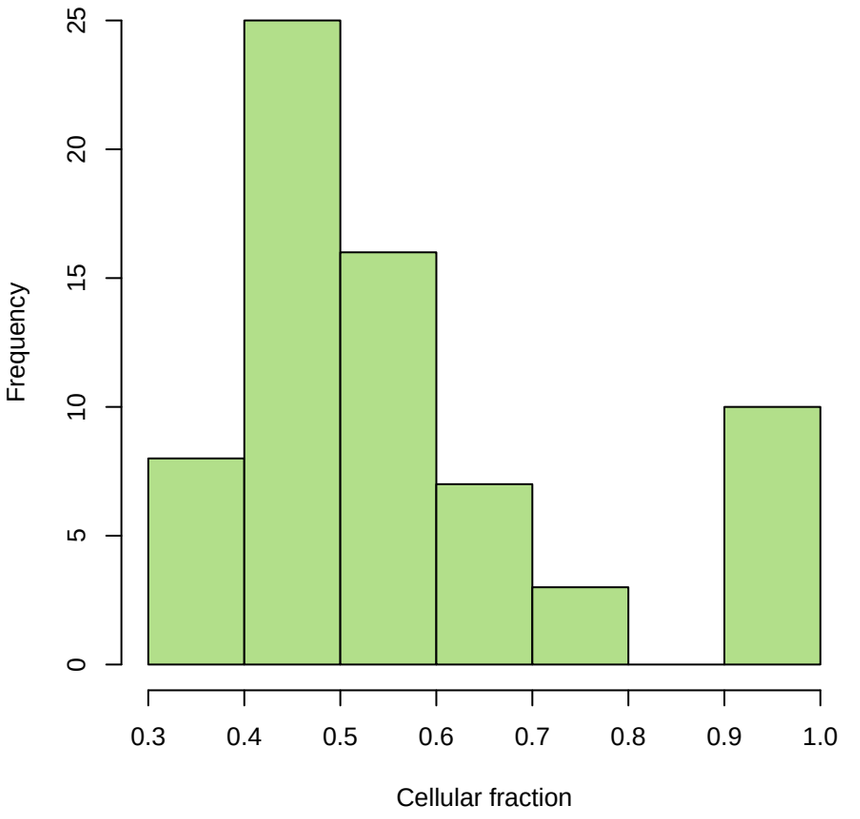

SCNA−fit log−likelihood: −7046.34
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 4 6
0 50 100 150
SNV Index

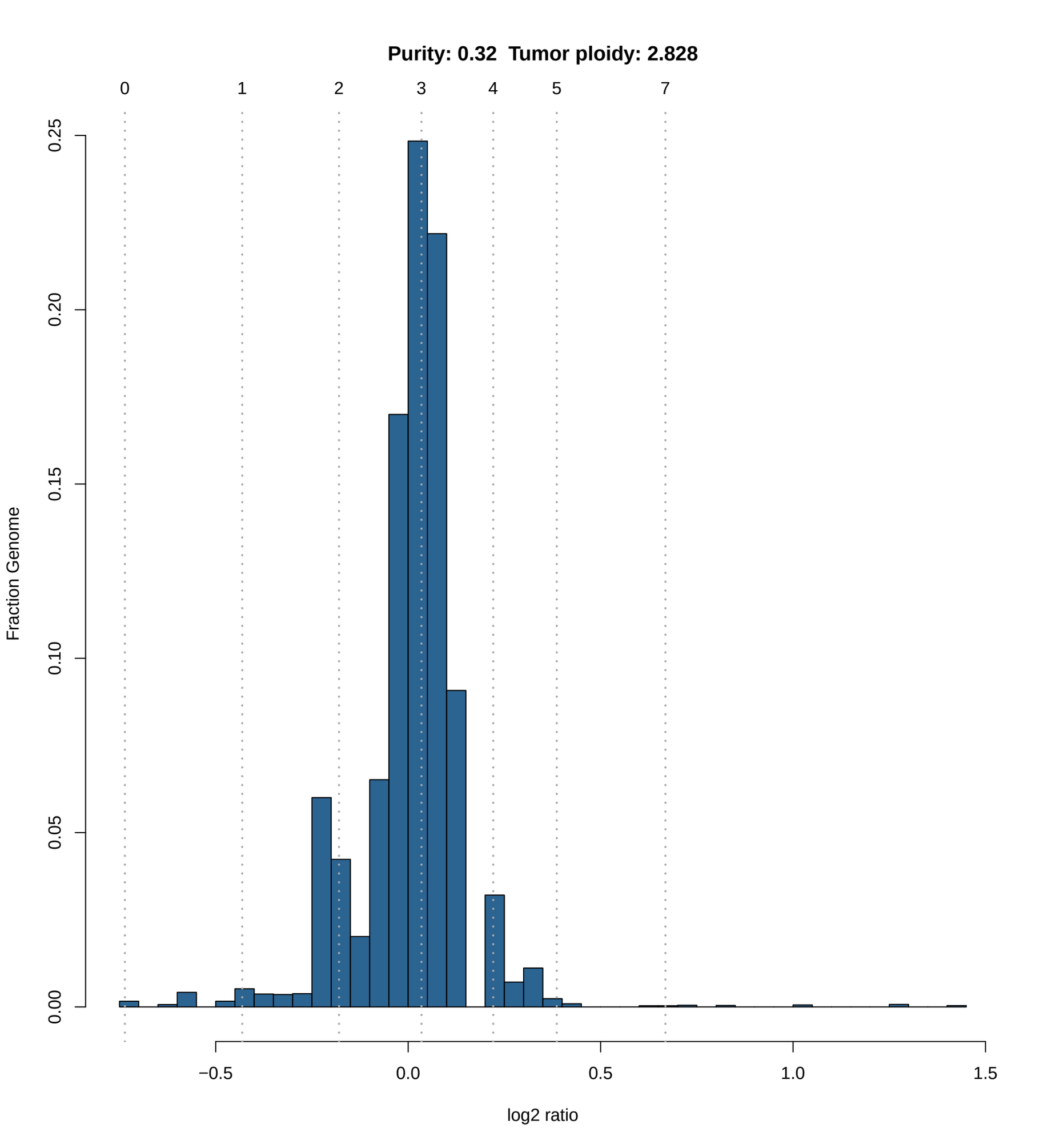

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

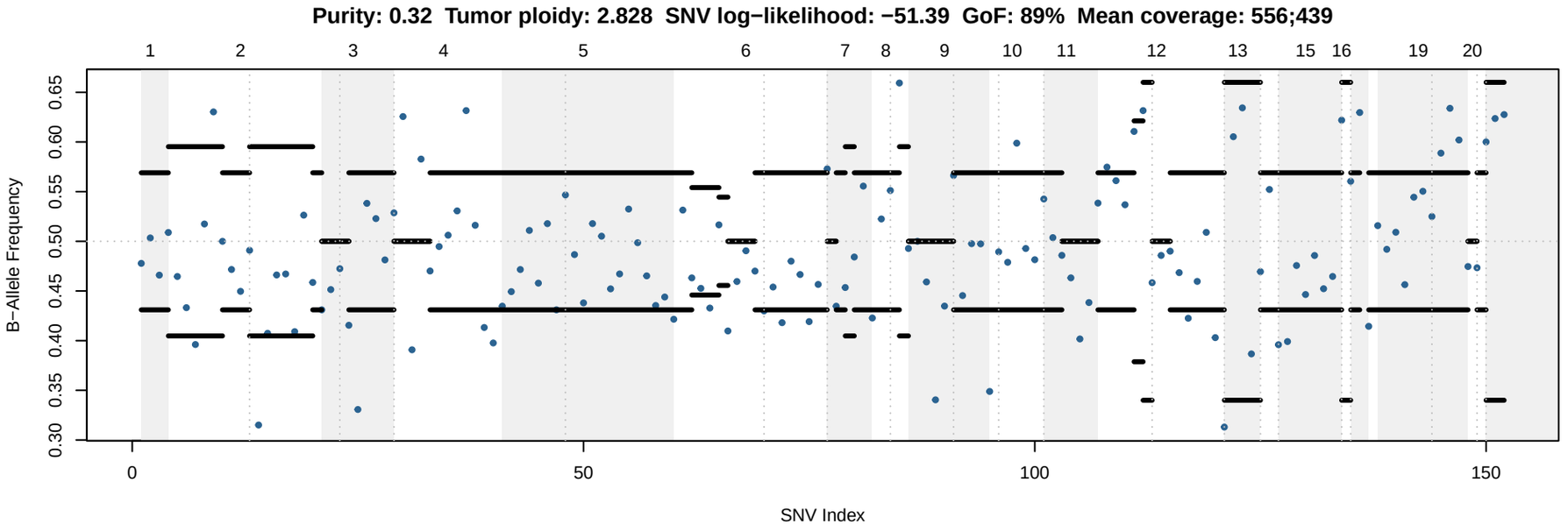

1m2
4m4
3m3
6m5
5m4
2m2
4m3
1m1
3m2
5m3
0m0
4m2
6m3
7m3
5m2
3m1
1m0
4m1
2m0
5m1
4m0
5m0
Allelic fraction (germline)
Copy Number log−ratio

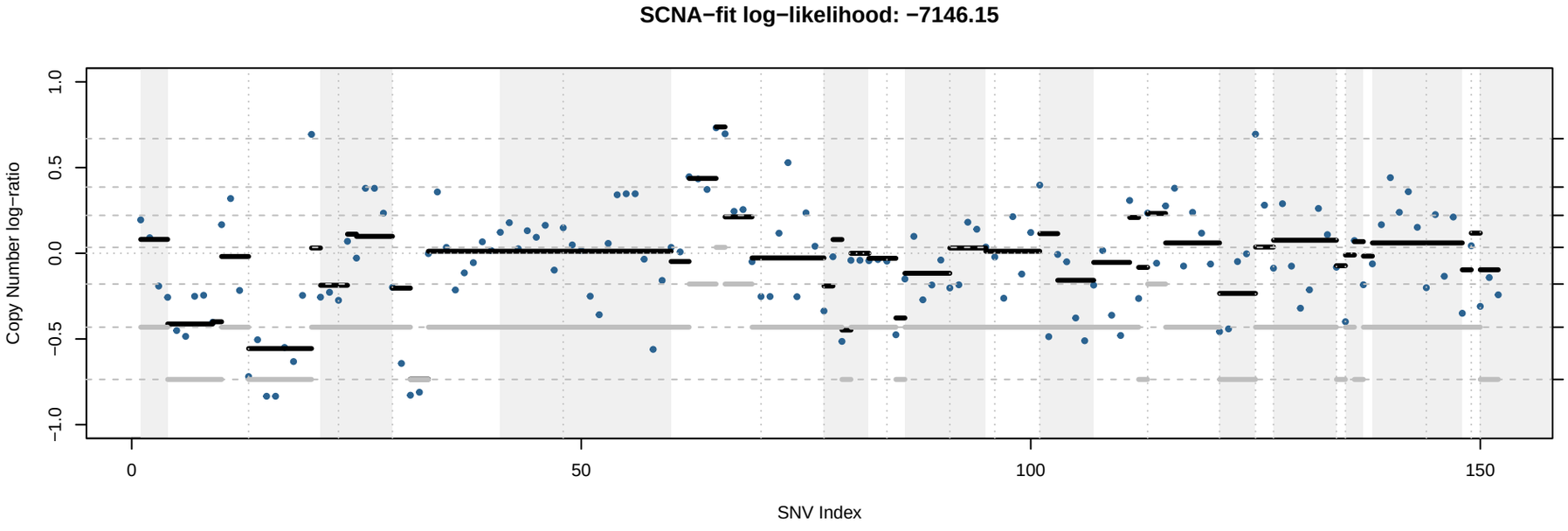

Coverage (log2)
Allelic fraction

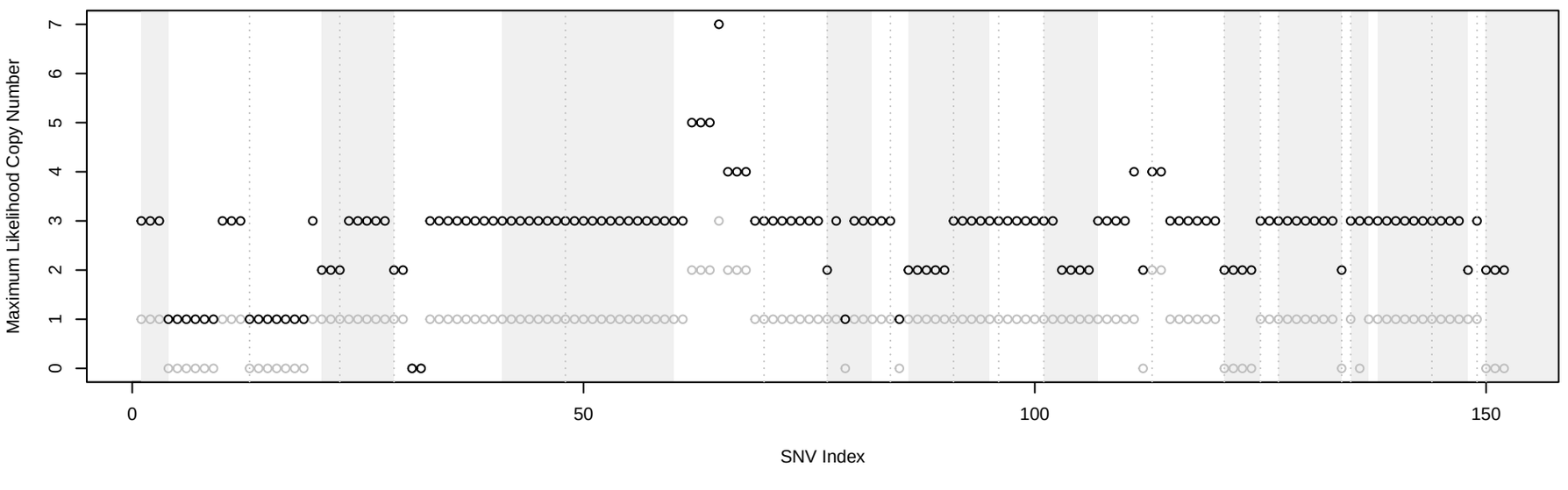

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m2
5m2
7m2
0m1
1m1
2m1
3m1
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

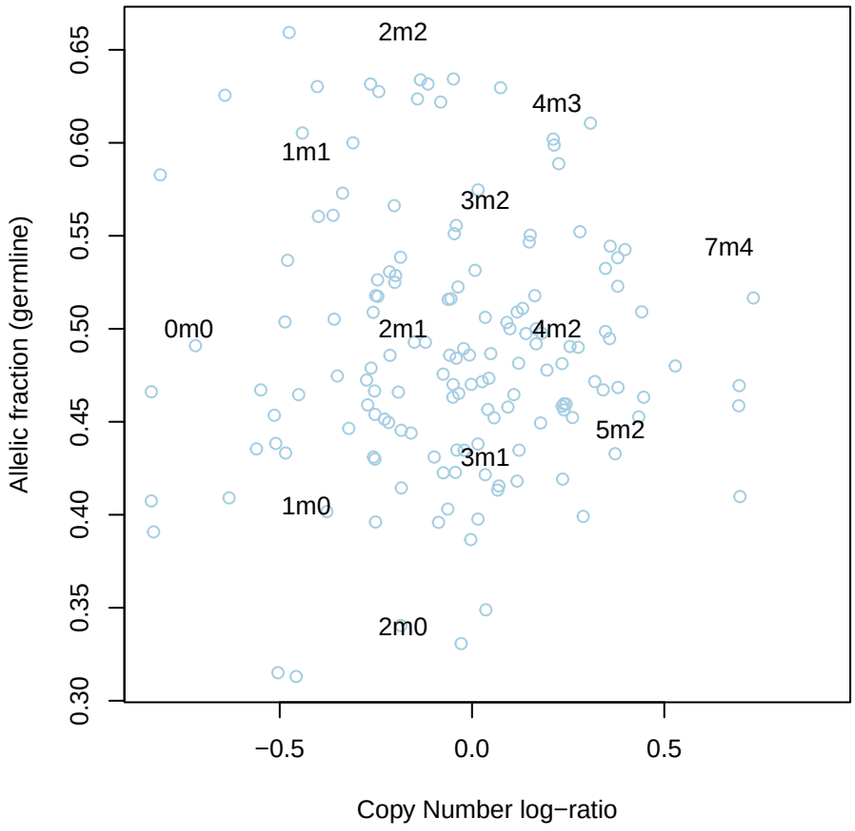

Frequency
Cellular fraction

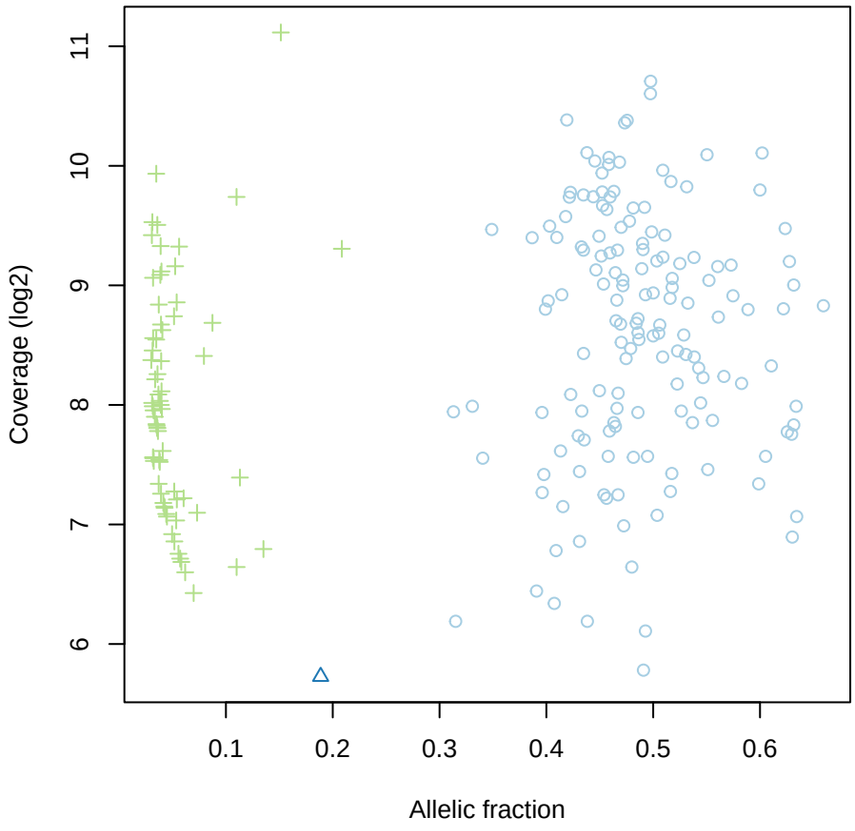

Purity: 0.32 Tumor ploidy: 2.828
0
1
2
3
4
5
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

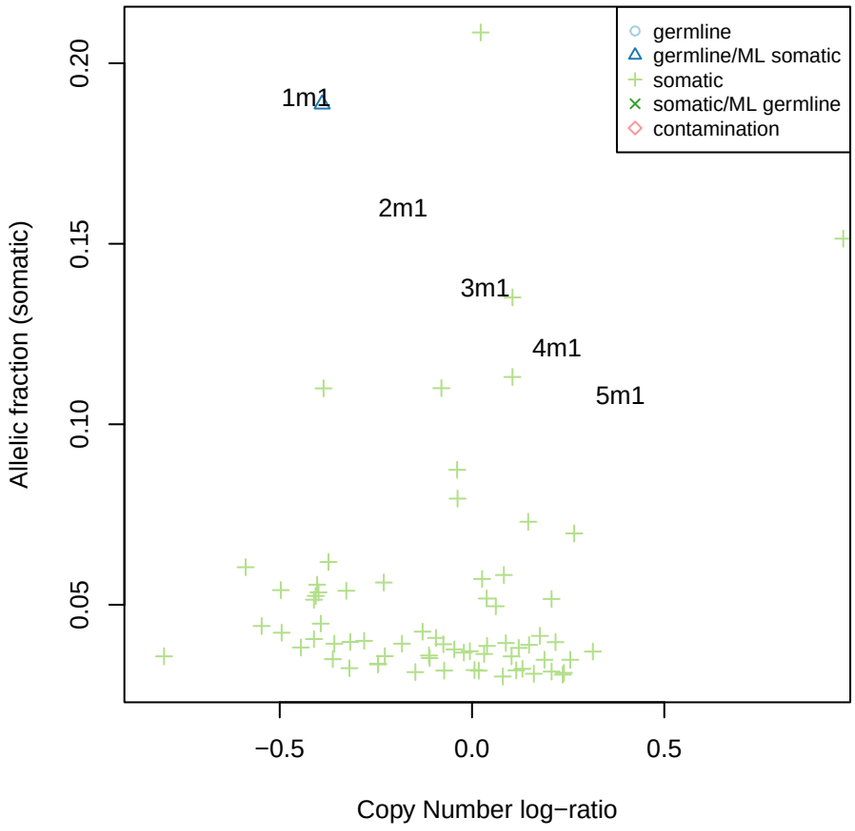

Purity: 0.32 Tumor ploidy: 2.828 SNV log−likelihood: −51.39 GoF: 89% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 50 100 150
SNV Index

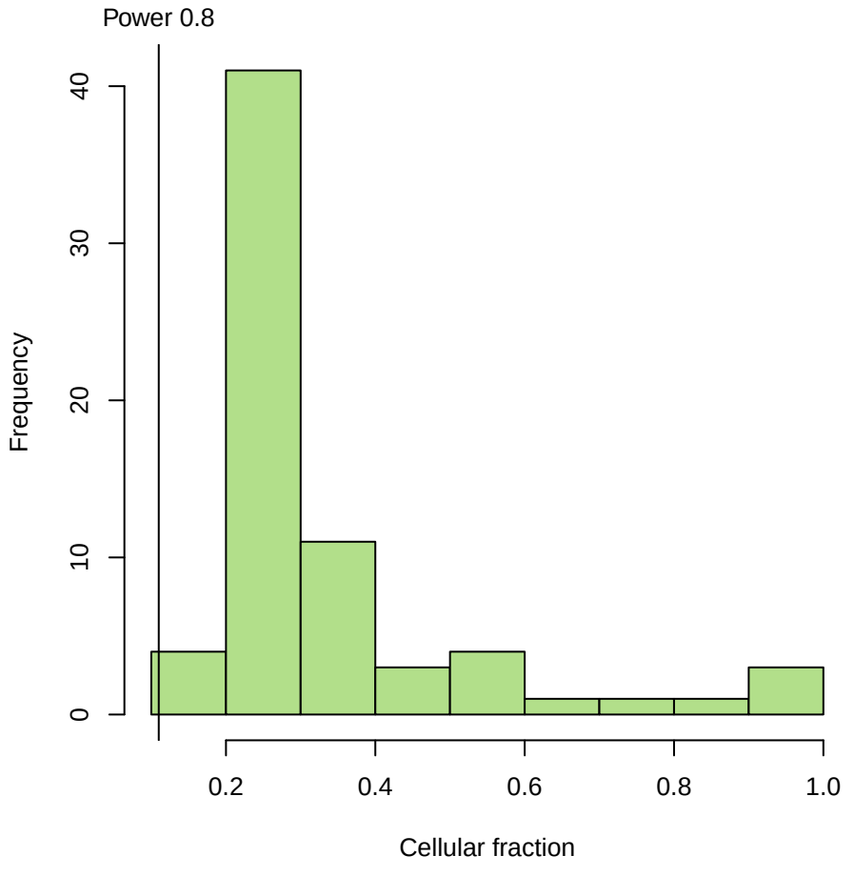

SCNA−fit log−likelihood: −7146.15
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 7
0 50 100 150
SNV Index

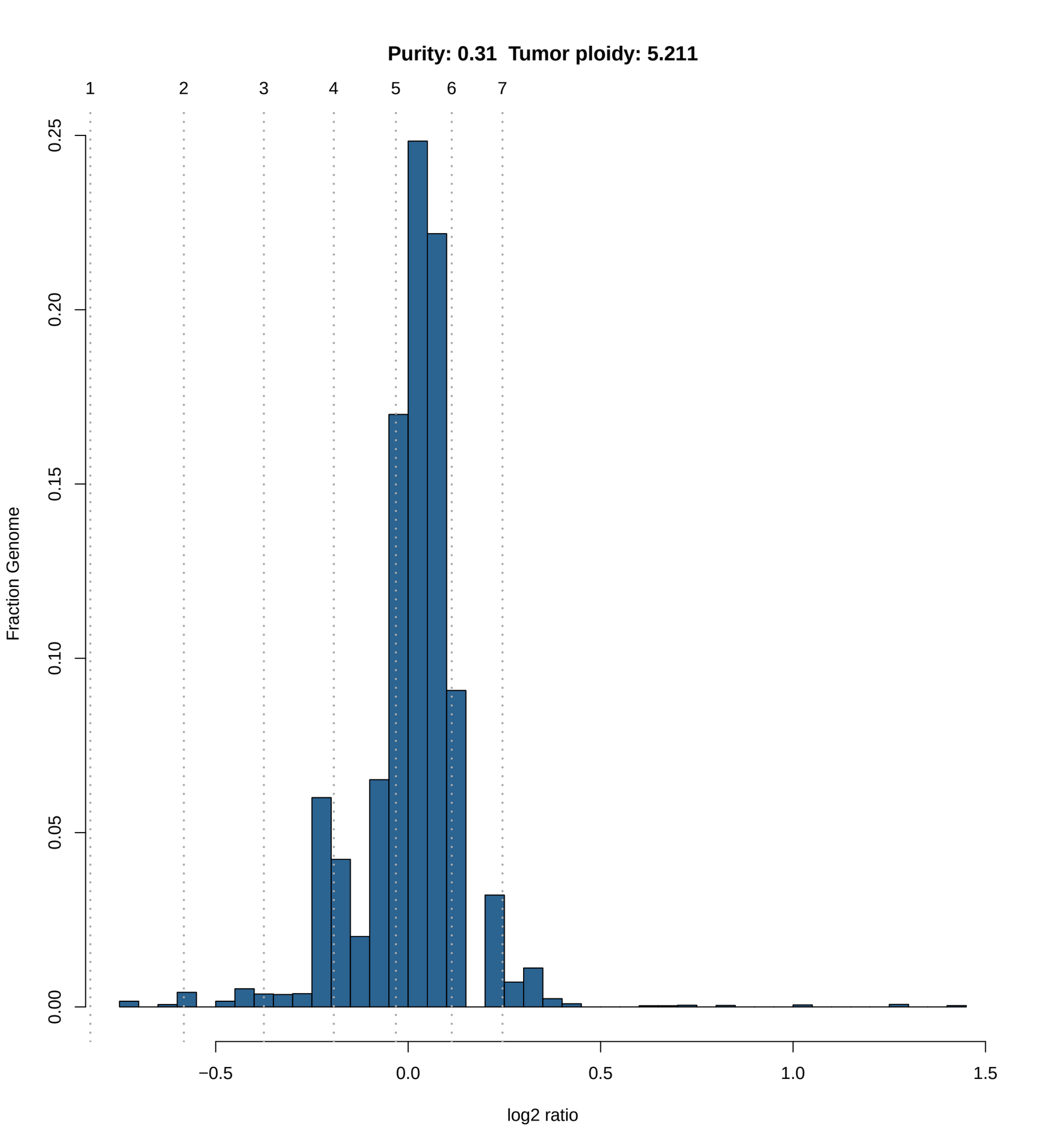

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

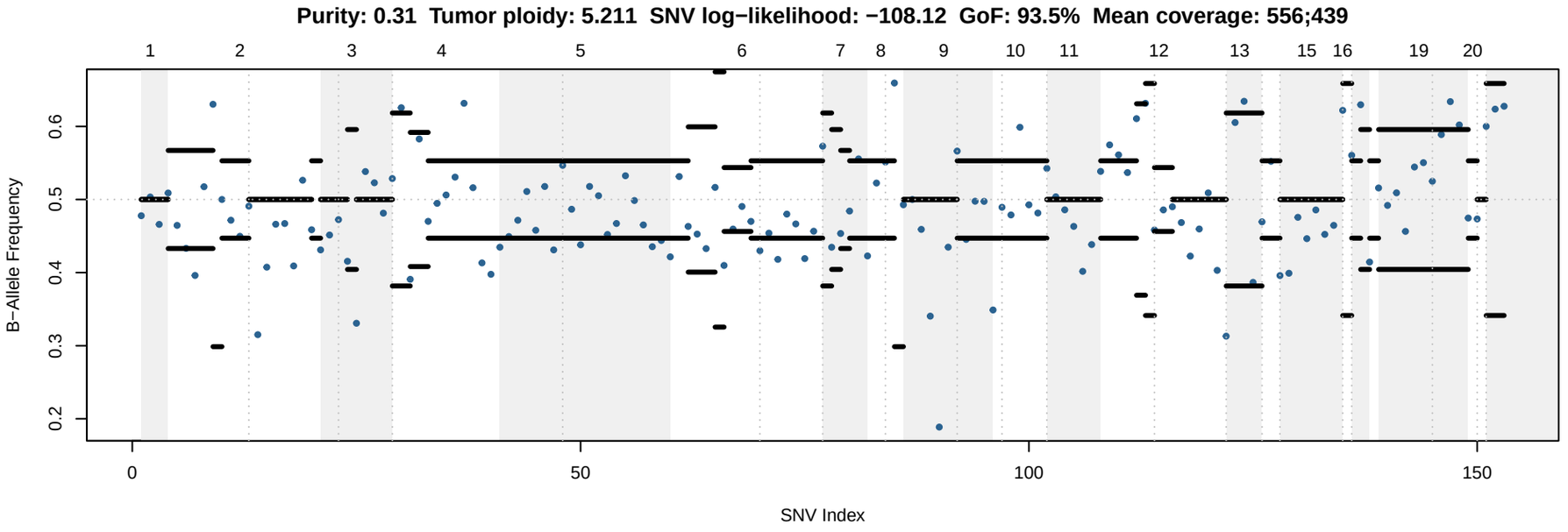

2m2
4m3
1m1
3m2
7m4
0m0
2m1
4m2
5m2
3m1
1m0
2m0
Allelic fraction (germline)
Copy Number log−ratio

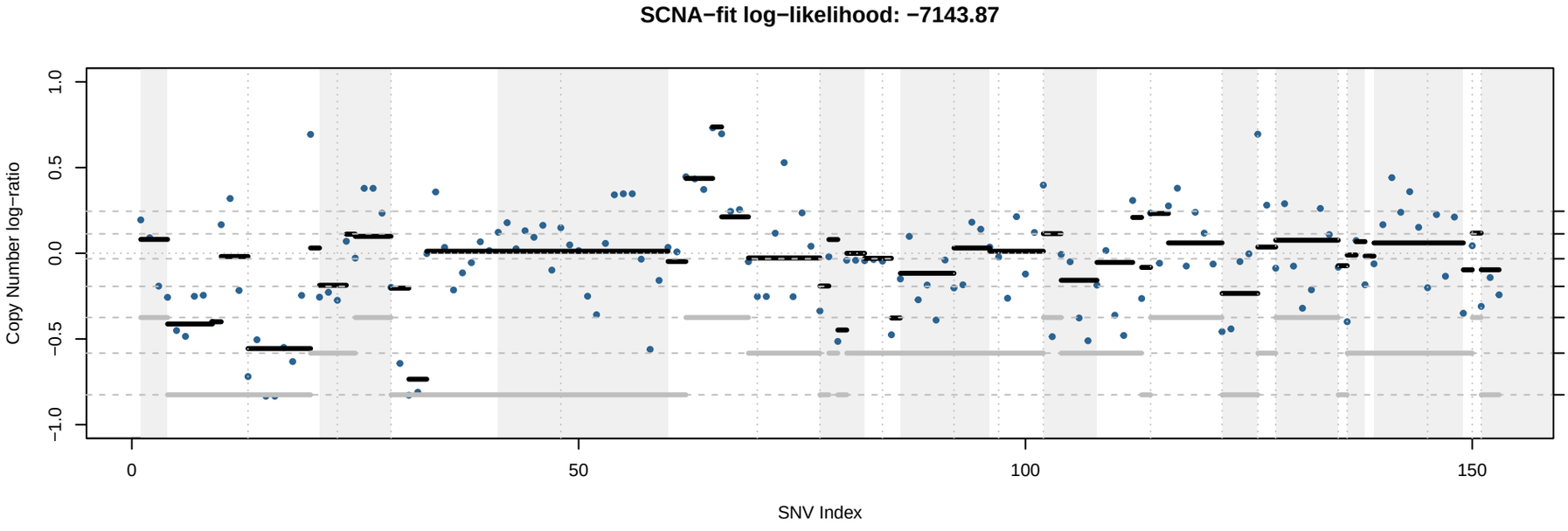

Coverage (log2)
Allelic fraction

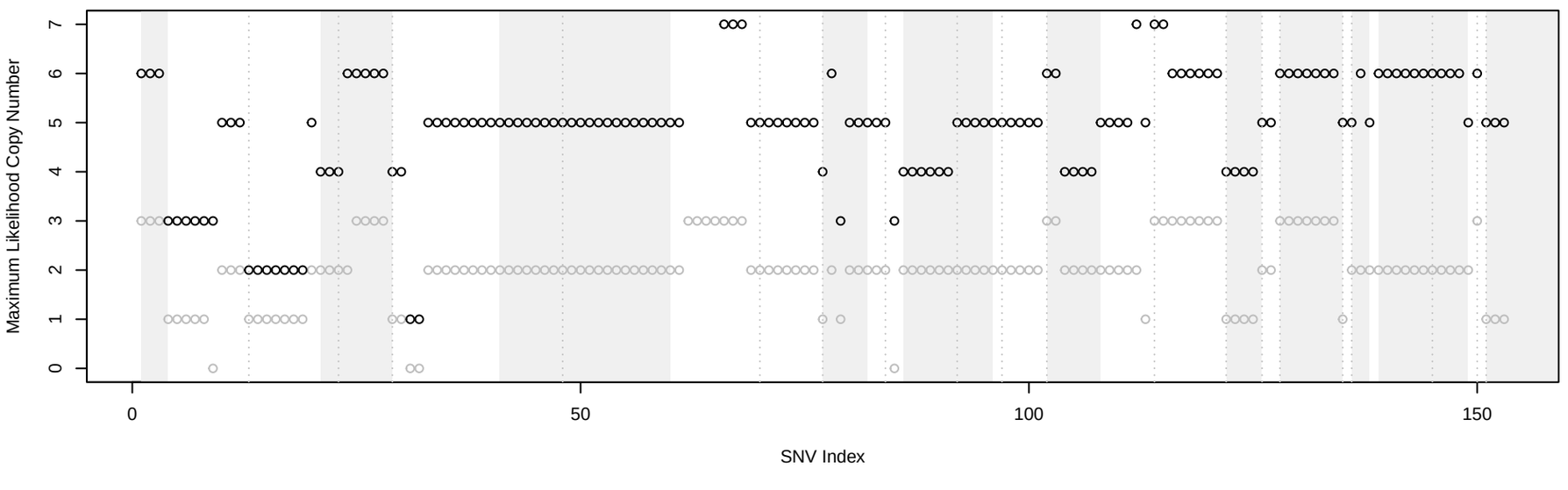

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
4m1
5m1
Allelic fraction (somatic)
Copy Number log−ratio

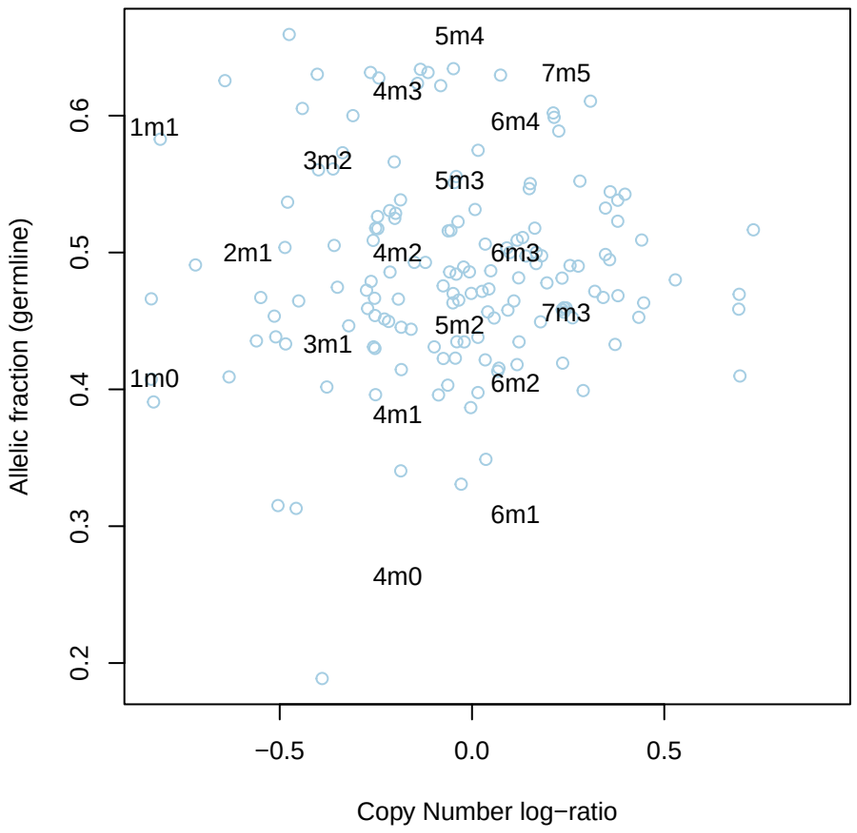

Power 0.8
Frequency
Cellular fraction

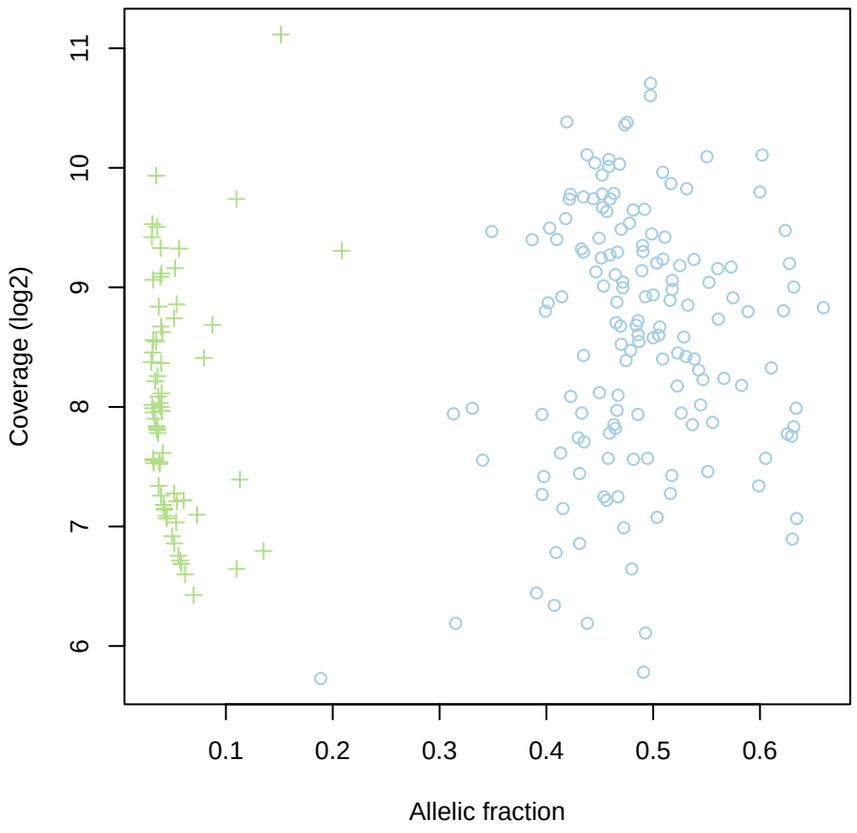

Purity: 0.31 Tumor ploidy: 5.211
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

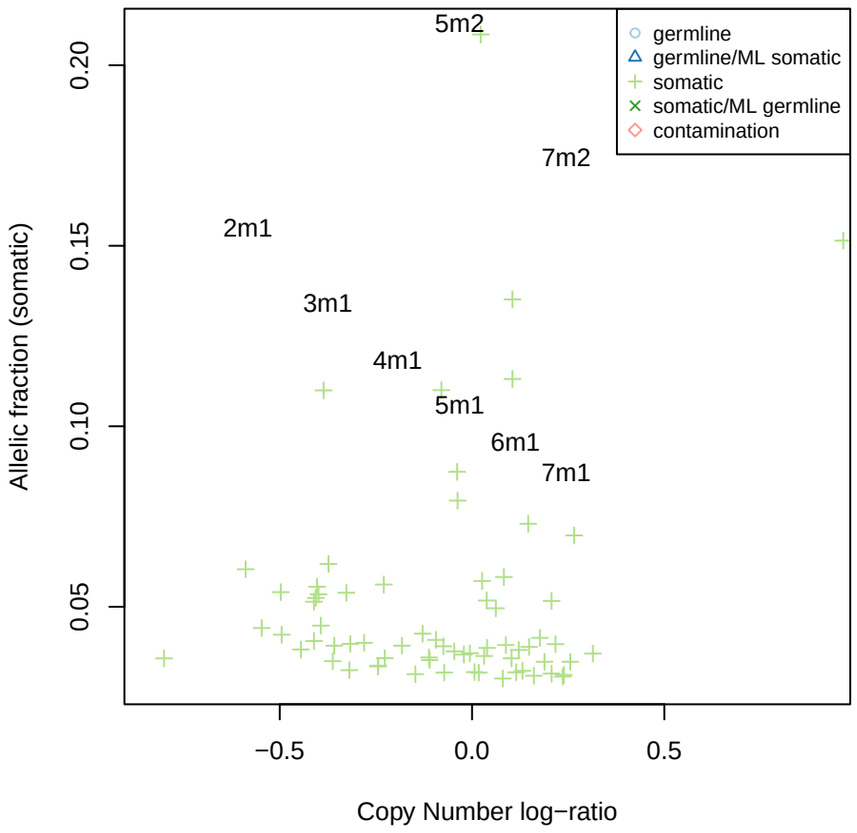

Purity: 0.31 Tumor ploidy: 5.211 SNV log−likelihood: −108.12 GoF: 93.5% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

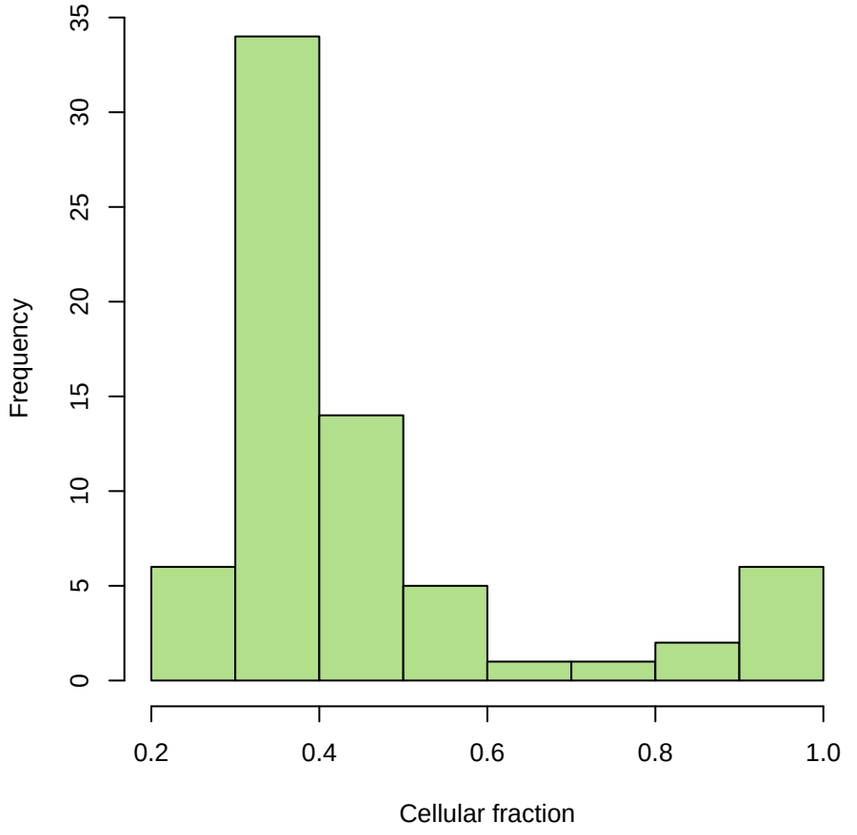

SCNA−fit log−likelihood: −7143.87
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6
0 50 100 150
SNV Index

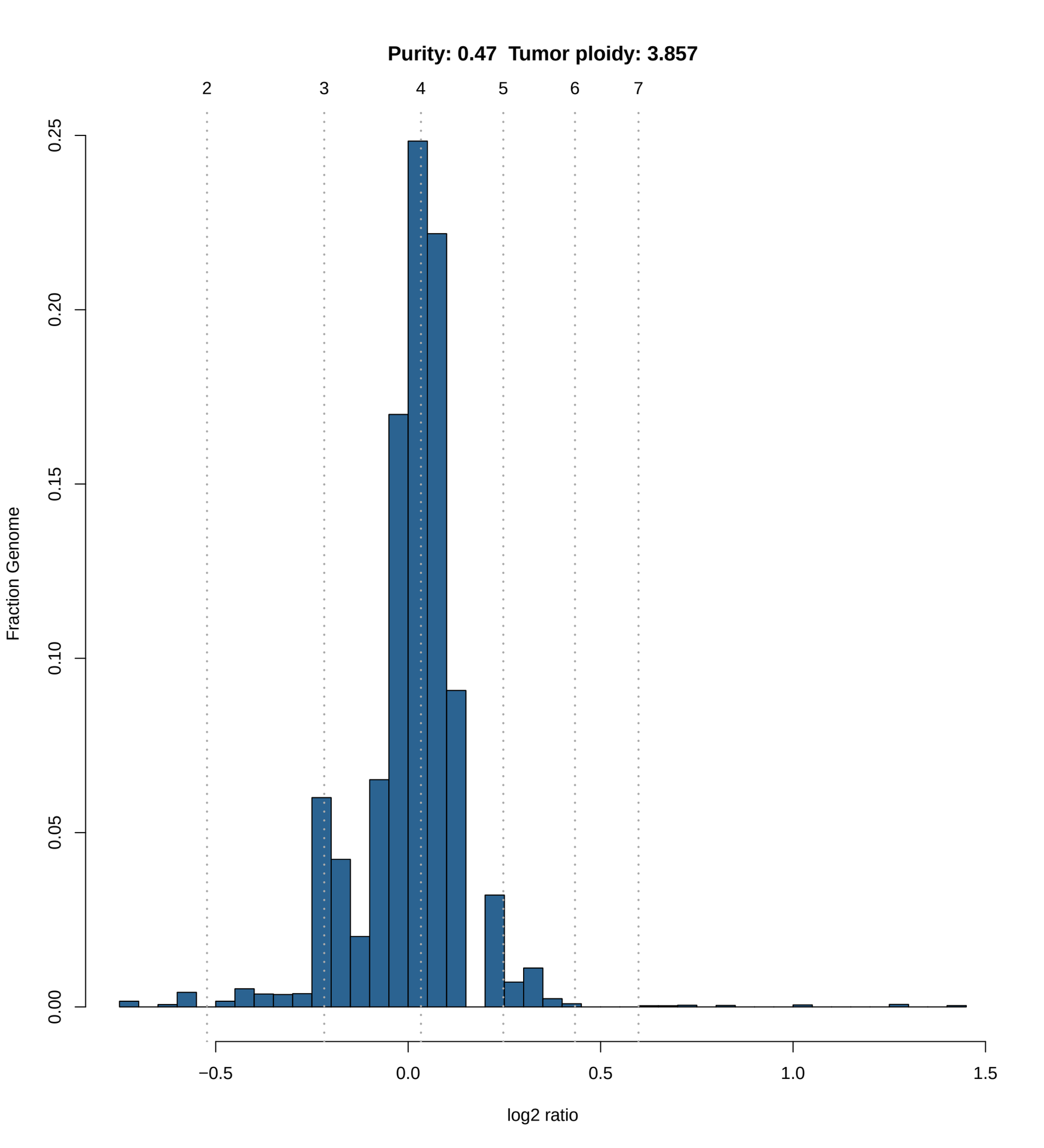

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

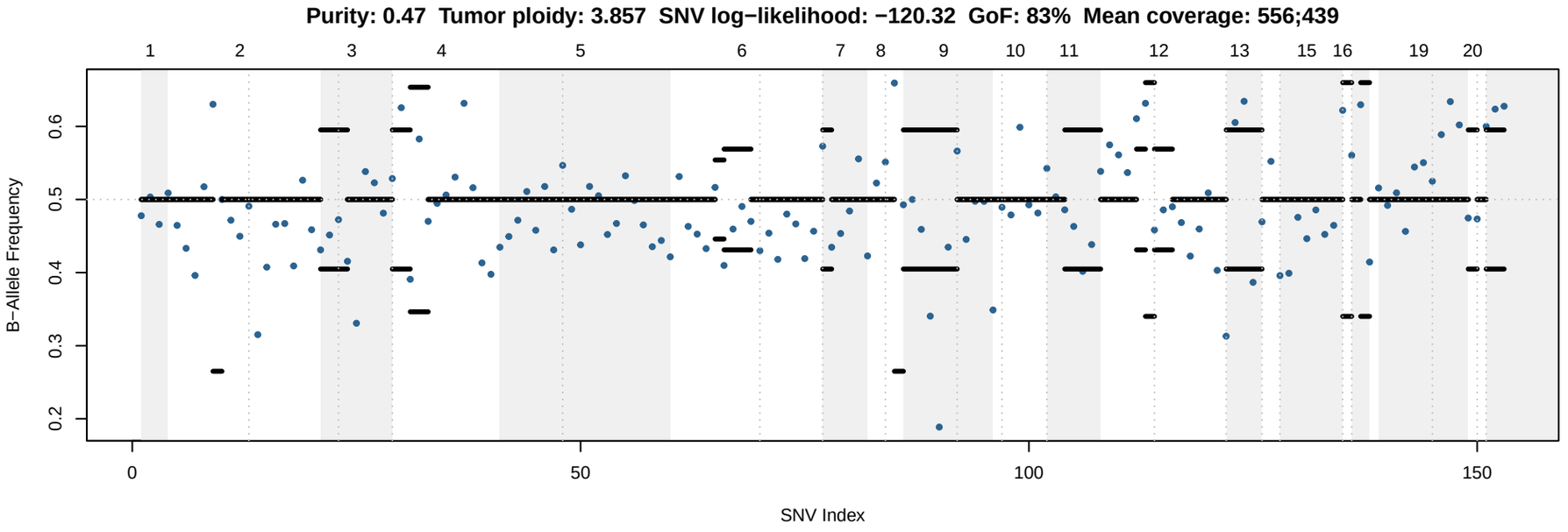

5m4
7m5
4m3
1m1
6m4
3m2
5m3
2m1
4m2
6m3
7m3
5m2
3m1
1m0
6m2
4m1
6m1
4m0
Allelic fraction (germline)
Copy Number log−ratio

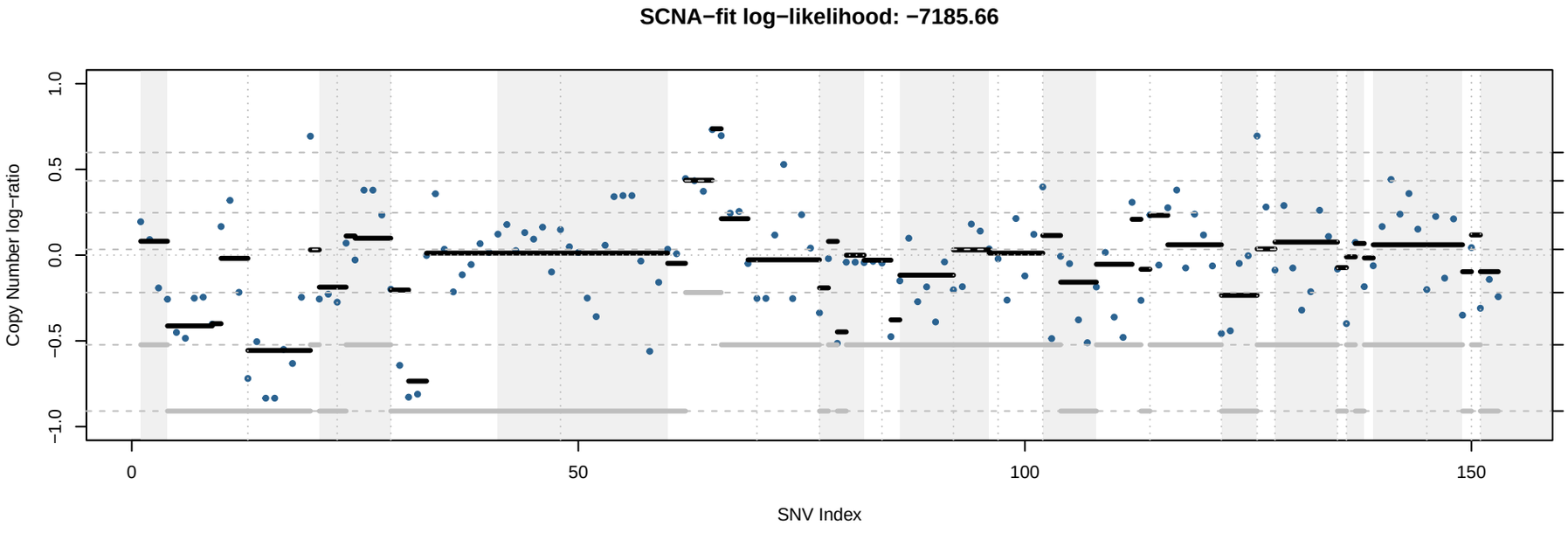

Coverage (log2)
Allelic fraction

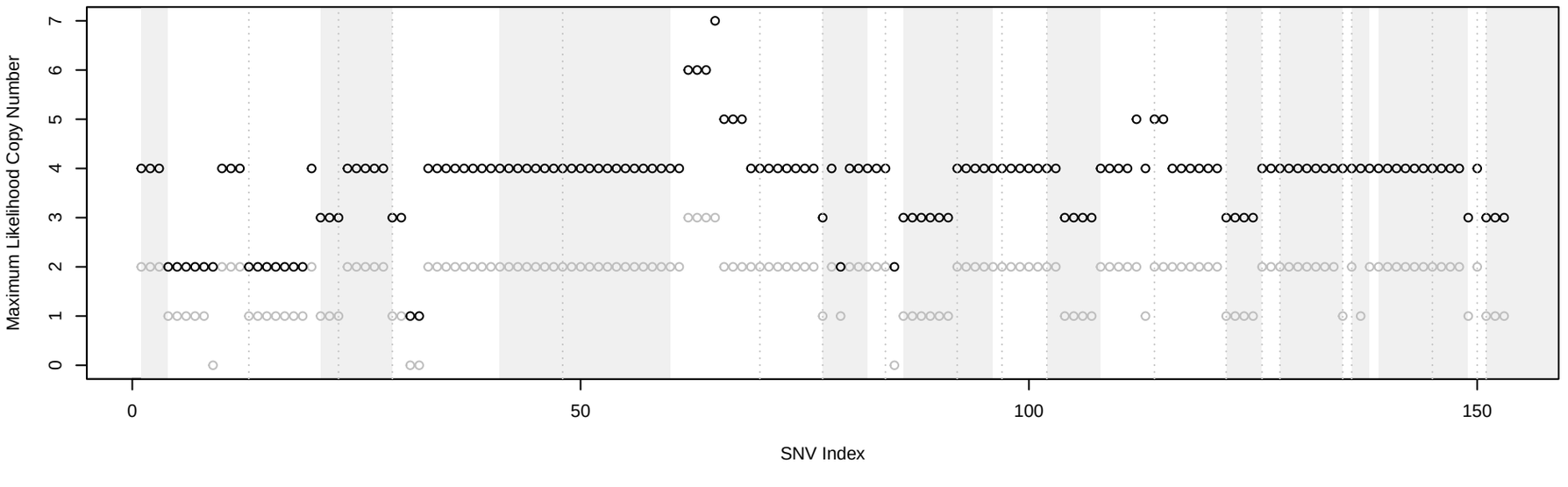

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m2
7m2
2m1
3m1
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

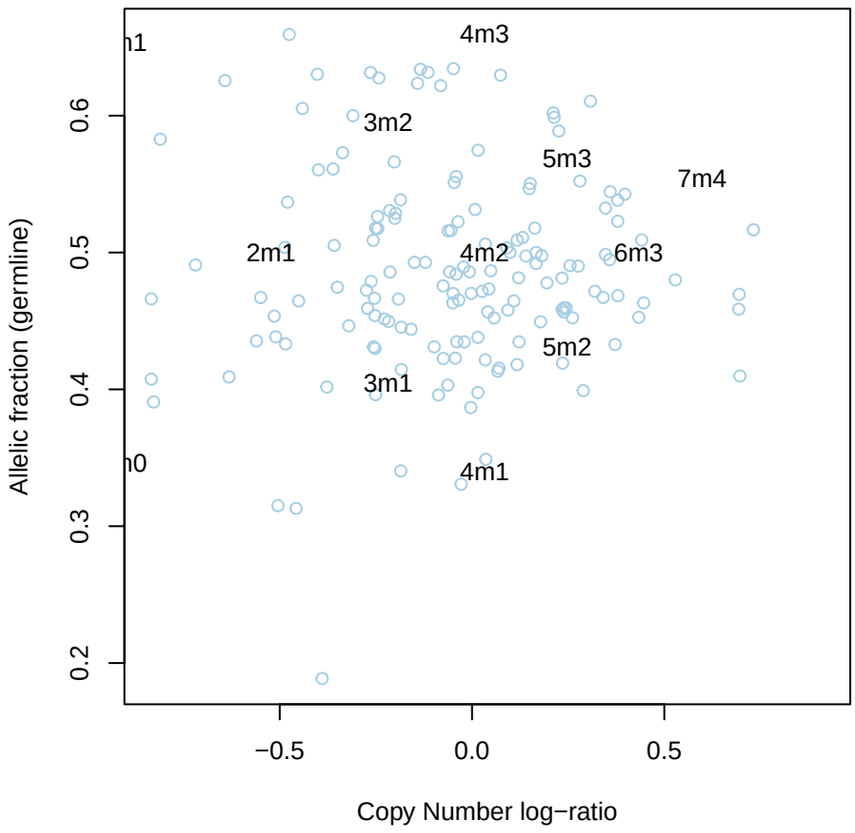

Frequency
Cellular fraction

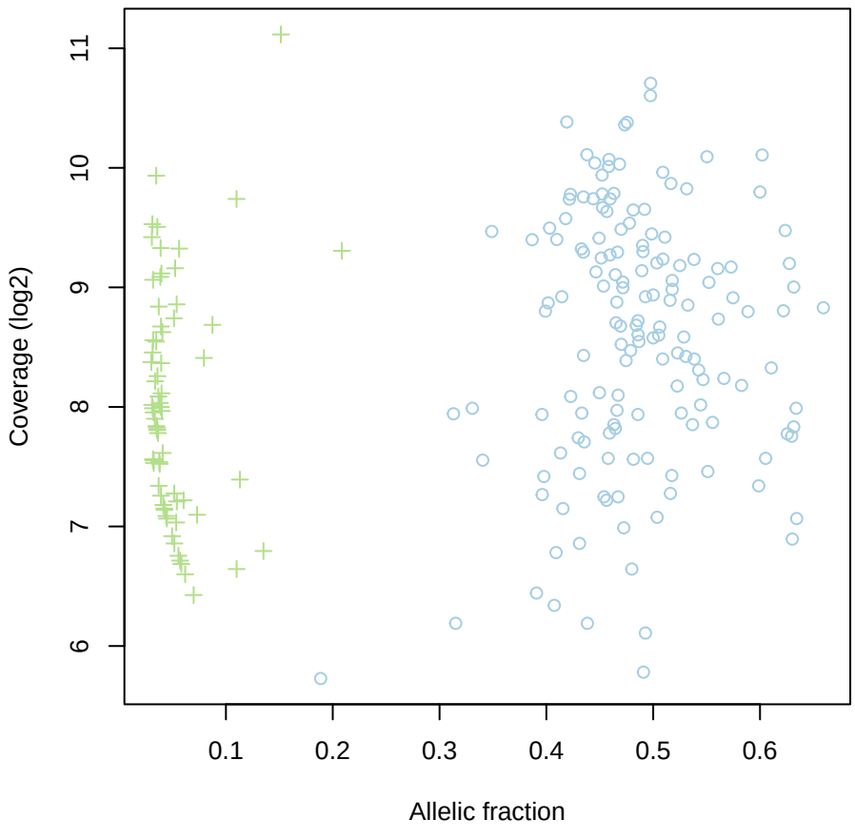

Purity: 0.47 Tumor ploidy: 3.857
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

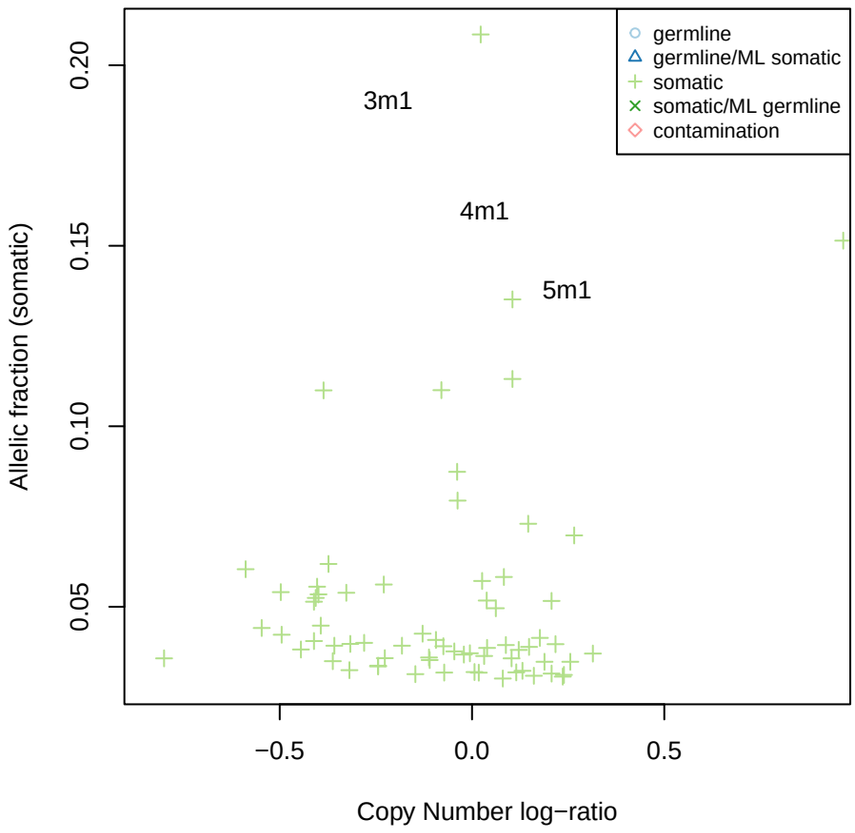

Purity: 0.47 Tumor ploidy: 3.857 SNV log−likelihood: −120.32 GoF: 83% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

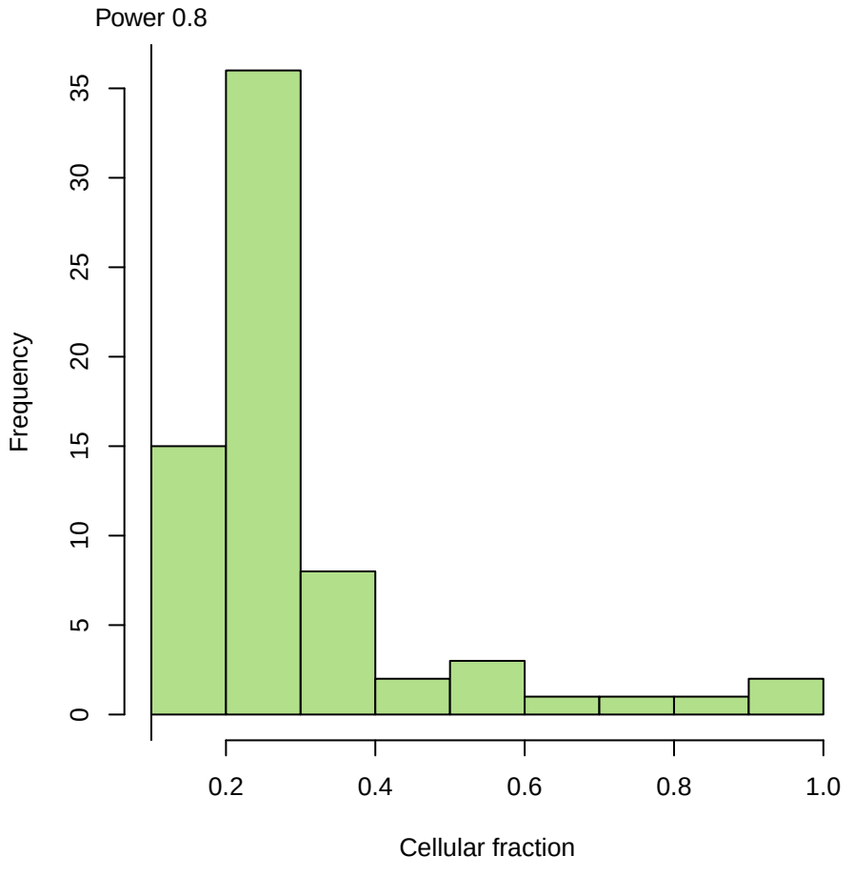

SCNA−fit log−likelihood: −7185.66
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6 7
0 50 100 150
SNV Index

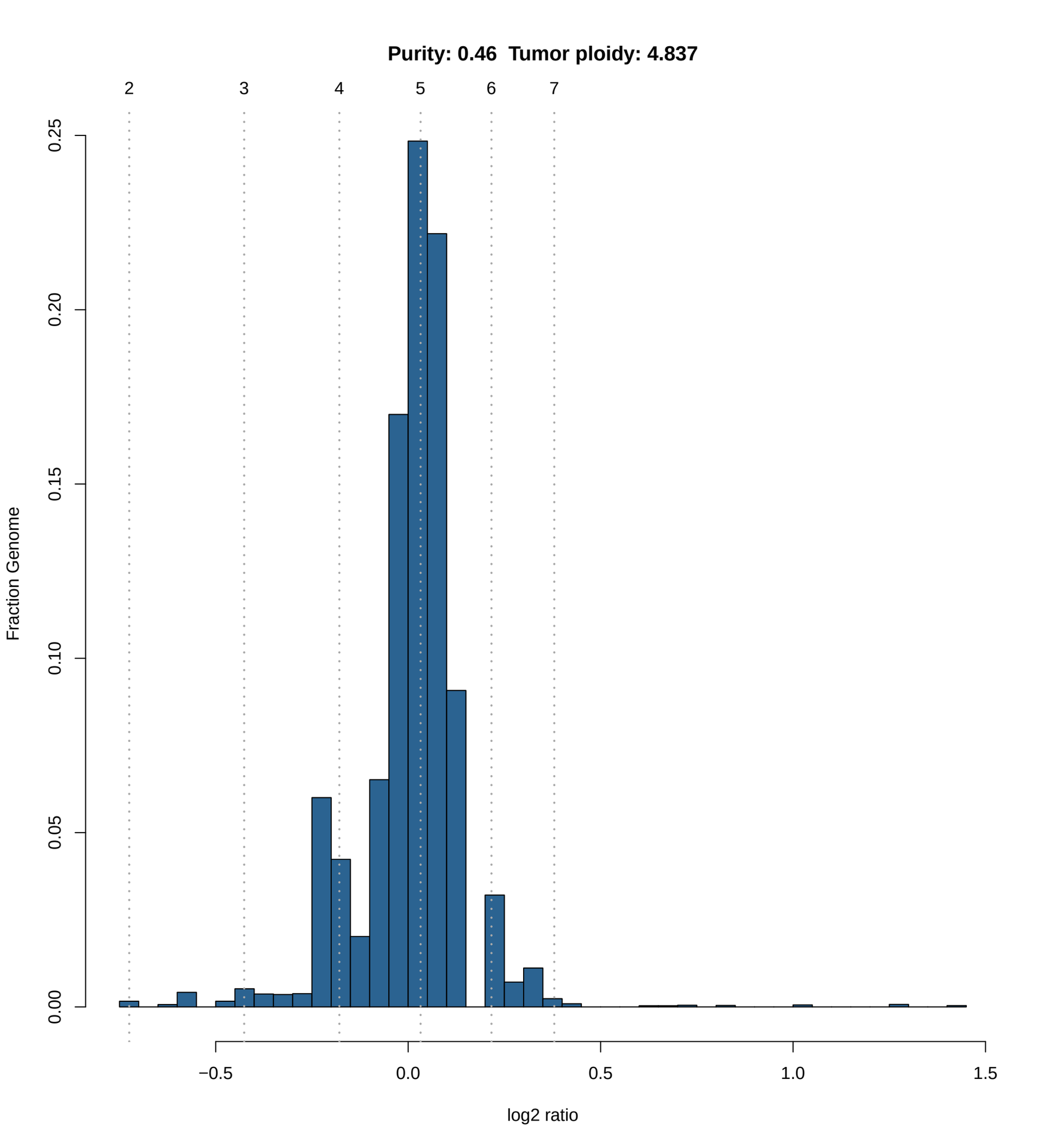

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

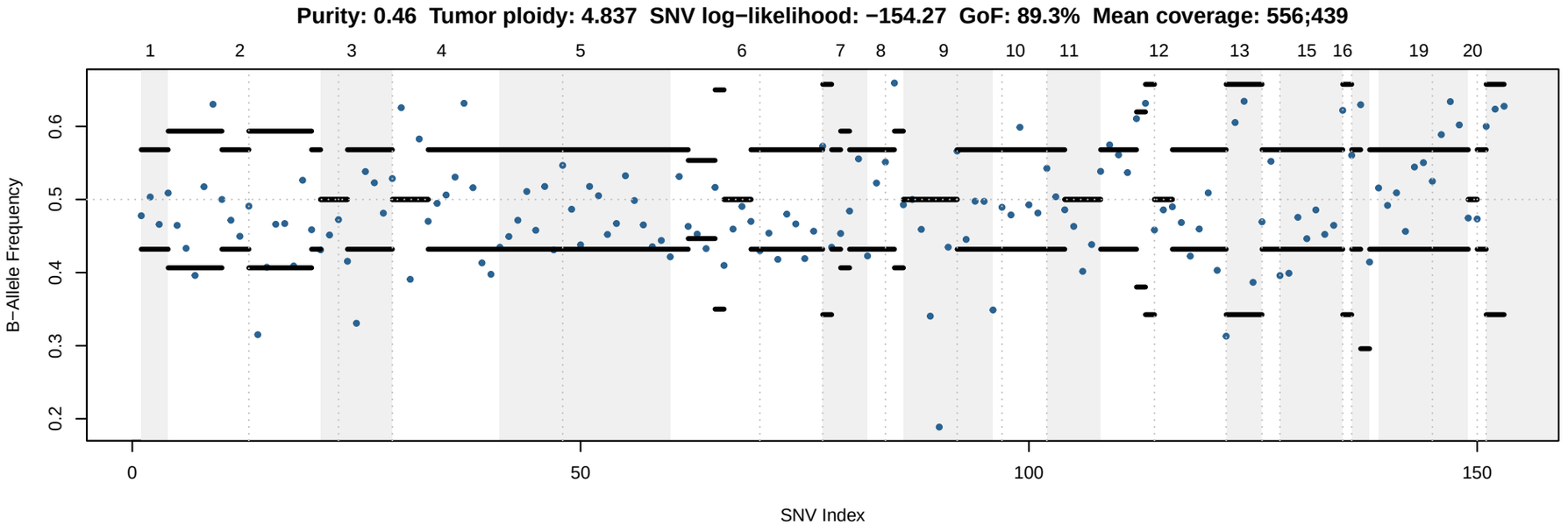

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
5m3
7m4
2m1
4m2
6m3
5m2
3m1
4m1

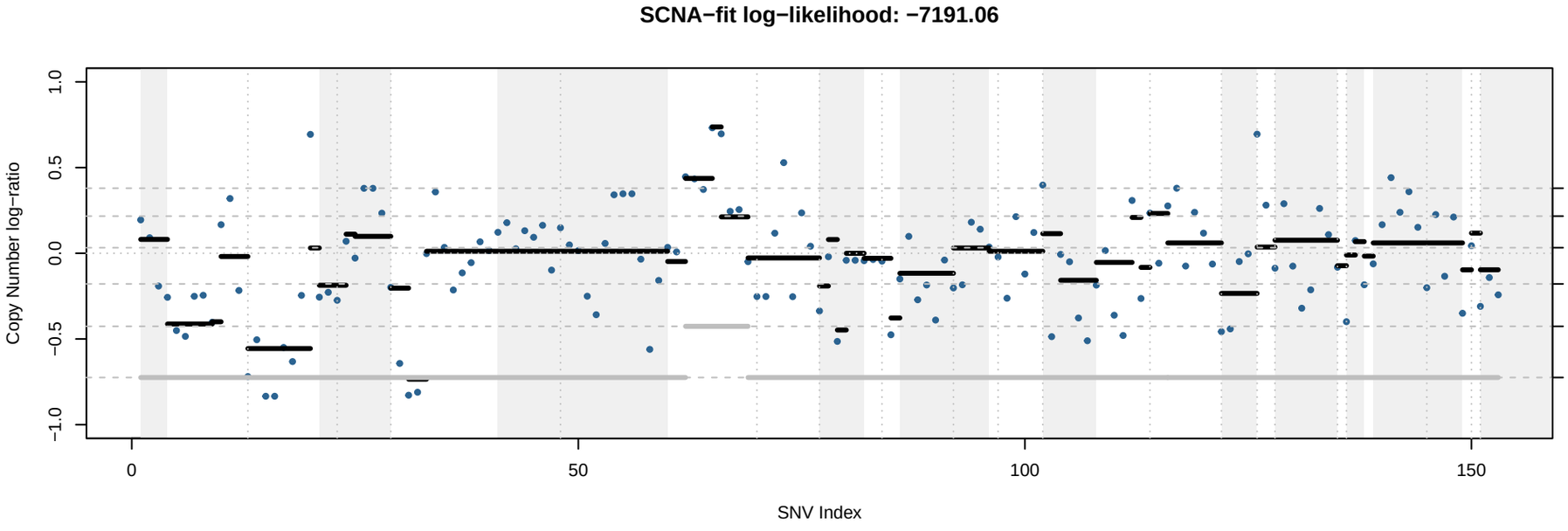

Coverage (log2)
Allelic fraction

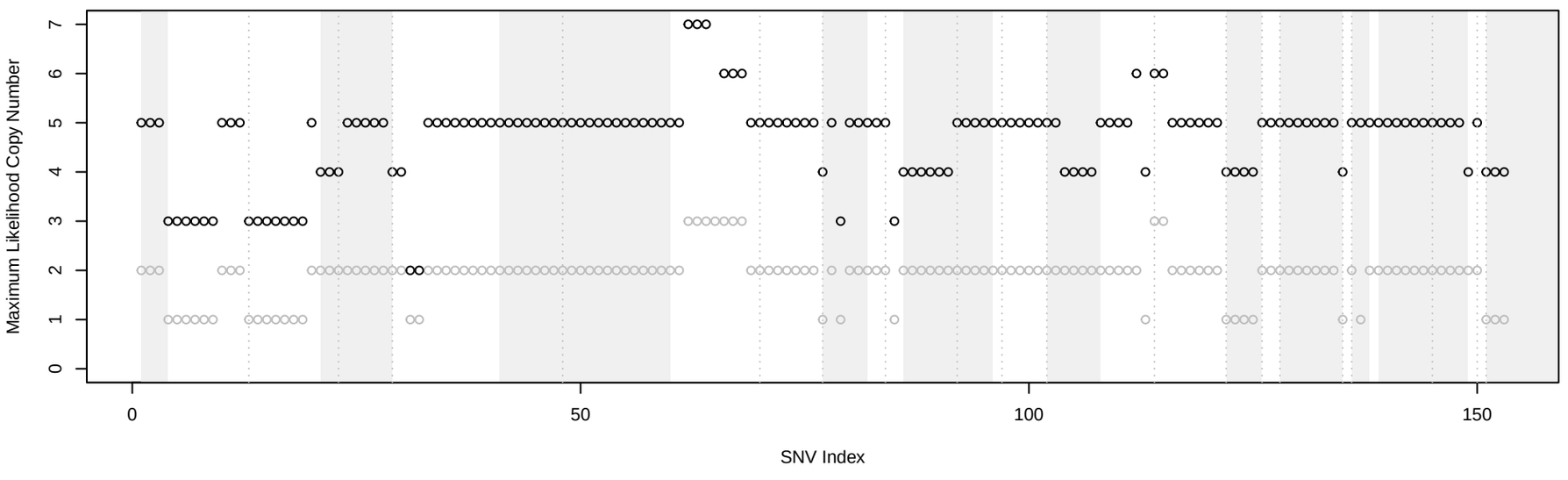

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m1
4m1
5m1

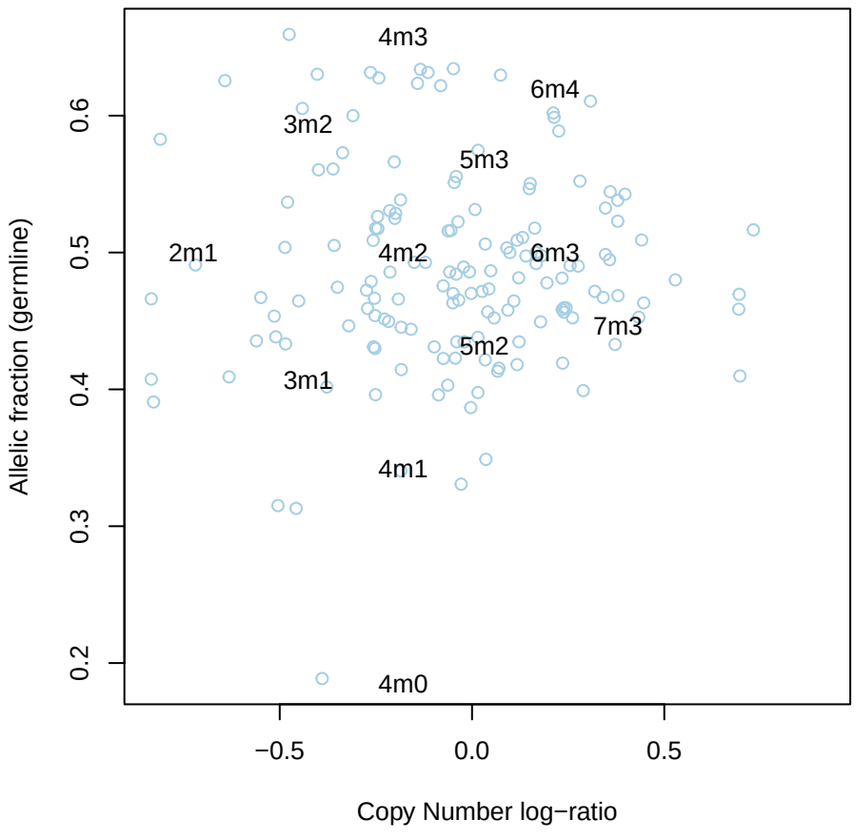

Power 0.8
Frequency
Cellular fraction

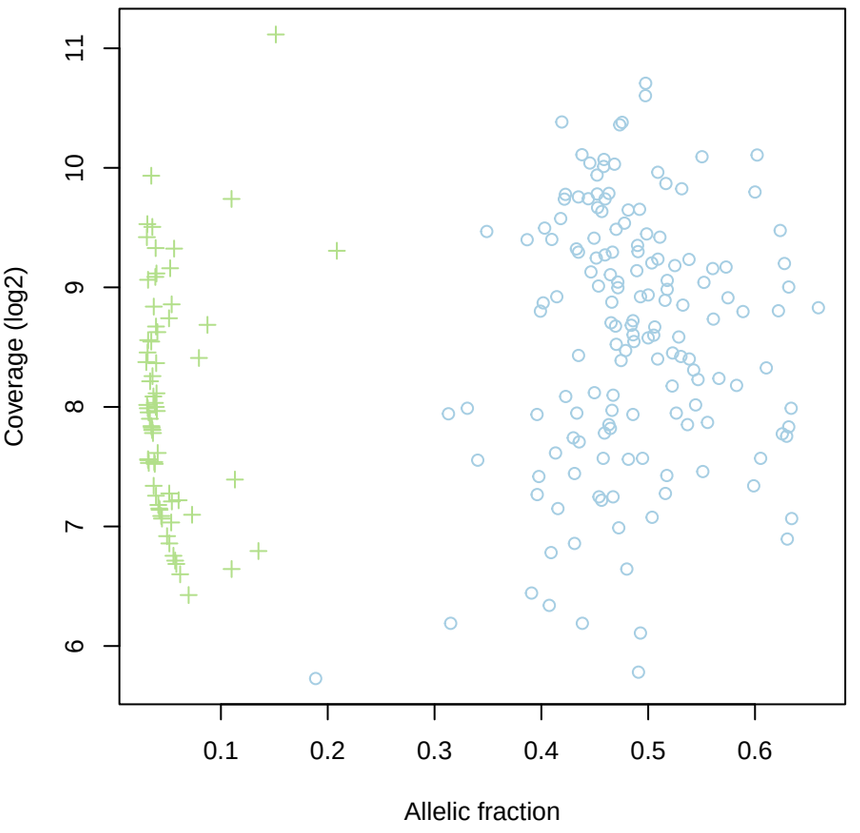

Purity: 0.46 Tumor ploidy: 4.837
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

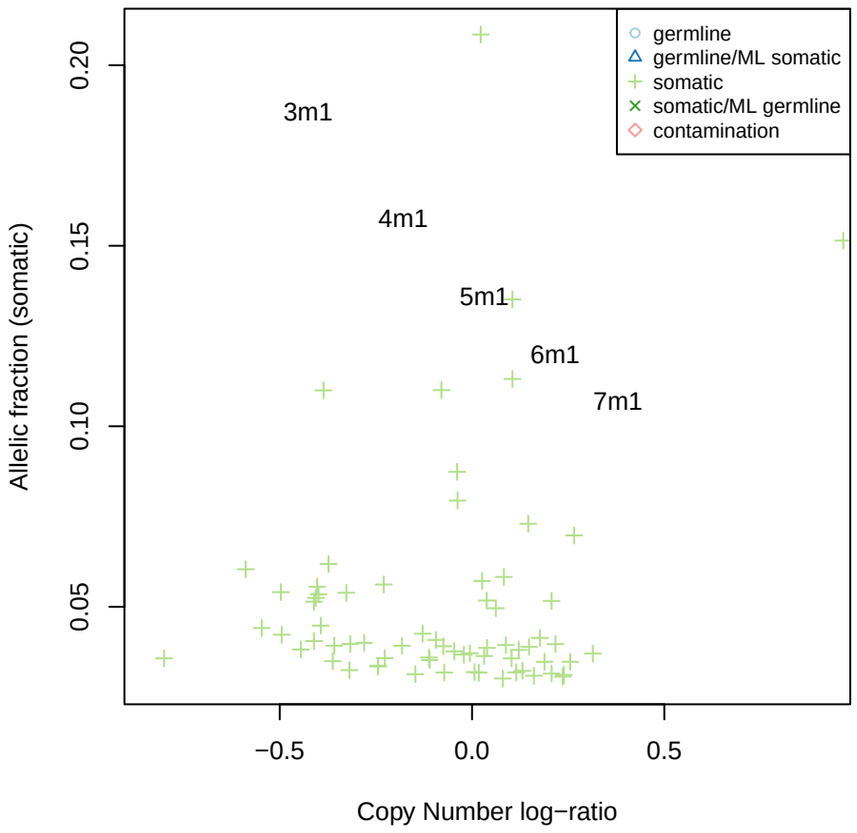

Purity: 0.46 Tumor ploidy: 4.837 SNV log−likelihood: −154.27 GoF: 89.3% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

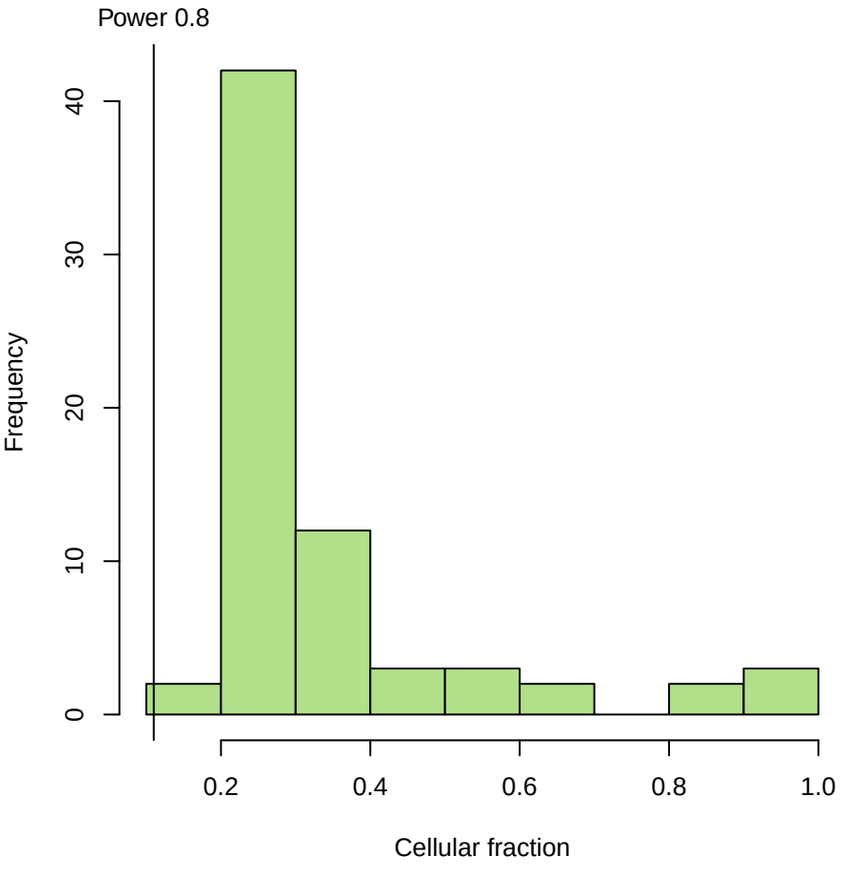

SCNA−fit log−likelihood: −7191.06
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 50 100 150
SNV Index

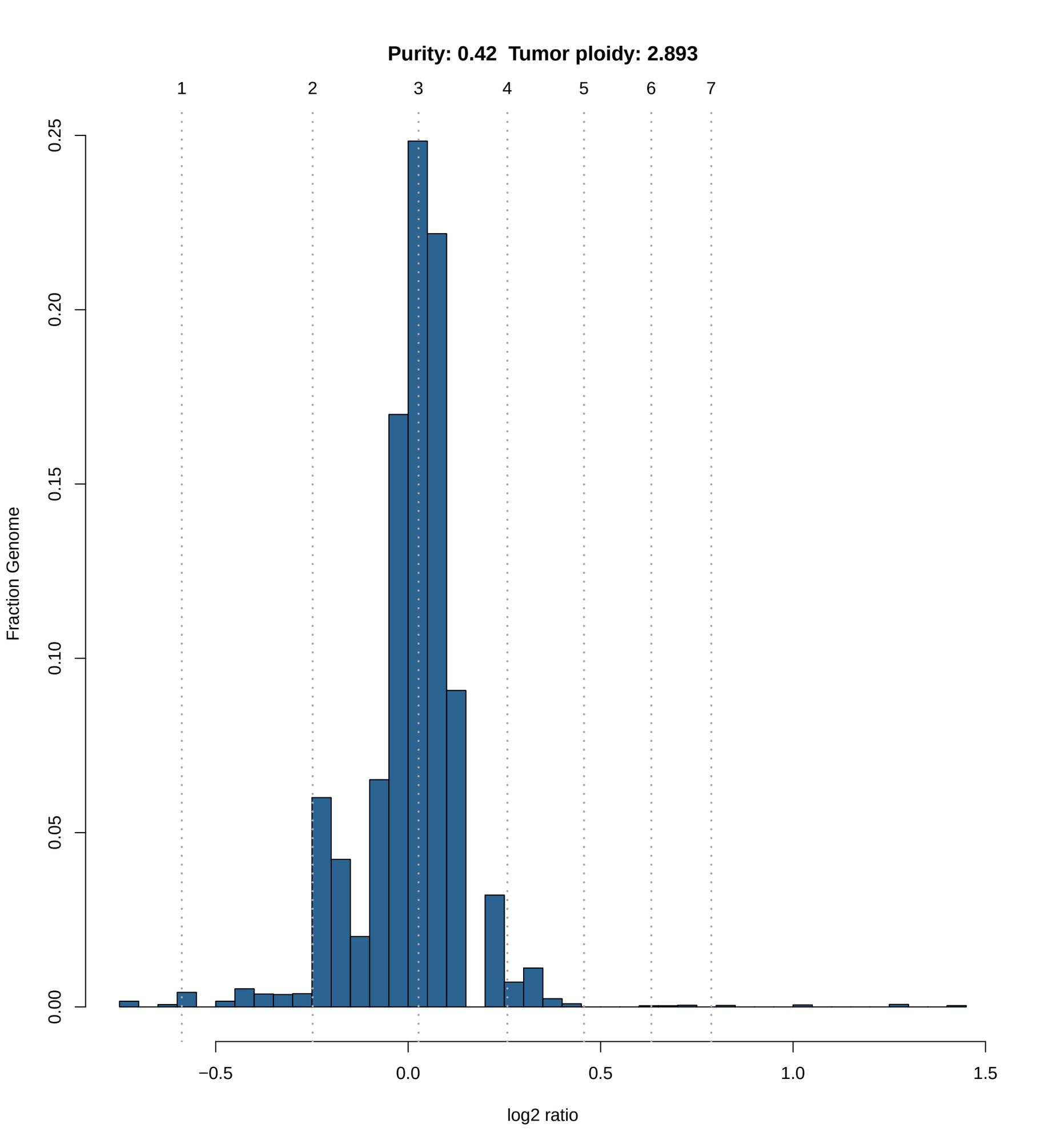

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

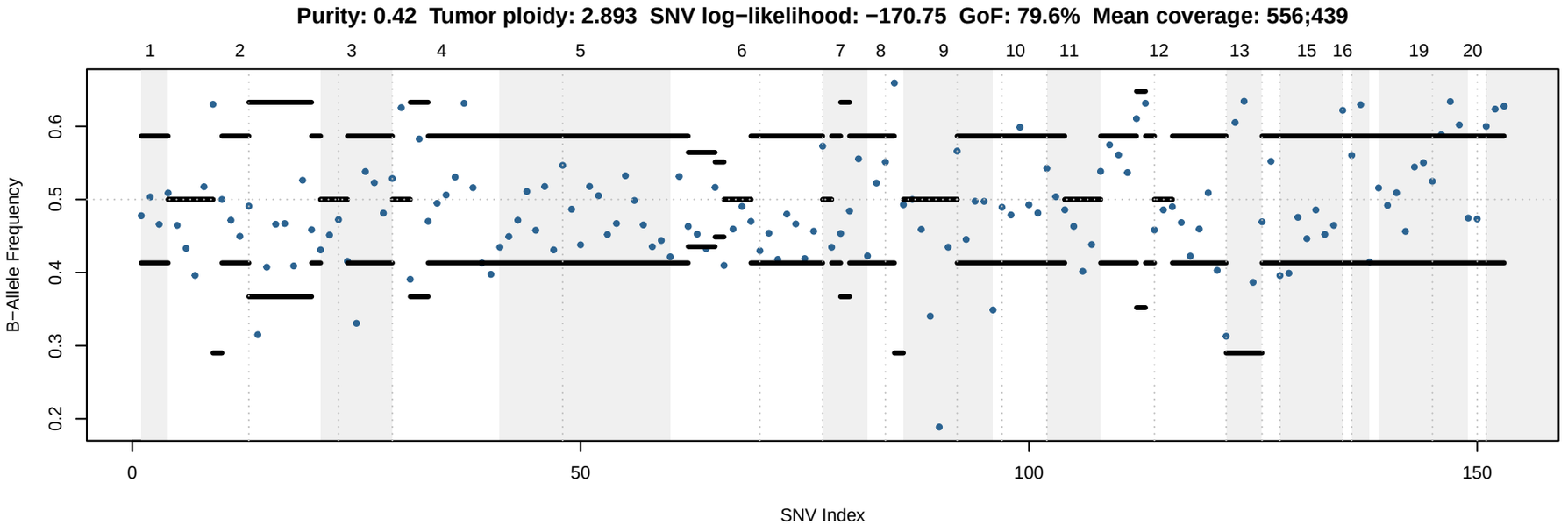

4m3
6m4
3m2
5m3
2m1
4m2
6m3
7m3
5m2
3m1
4m1
4m0
Allelic fraction (germline)
Copy Number log−ratio

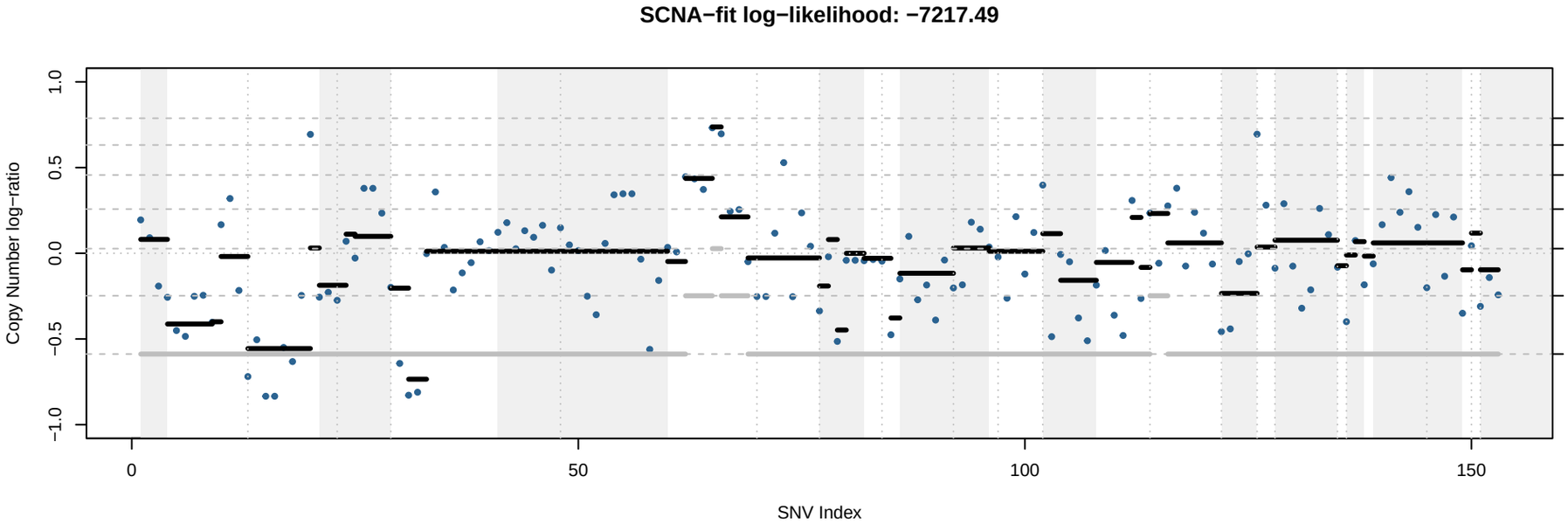

Coverage (log2)
Allelic fraction

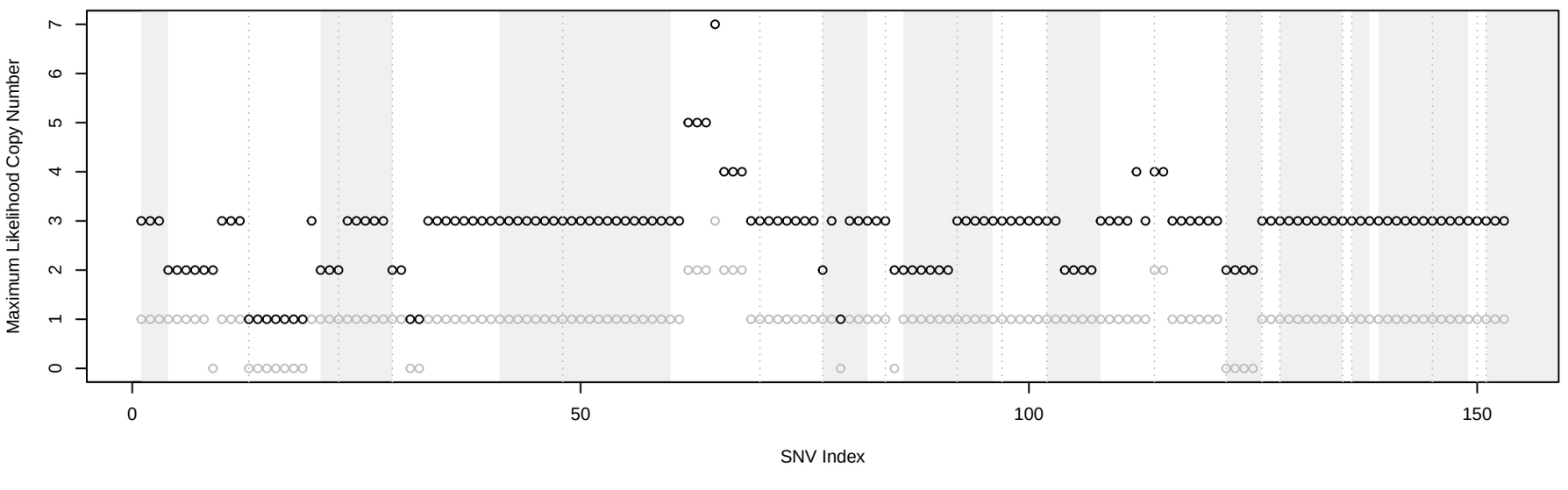

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

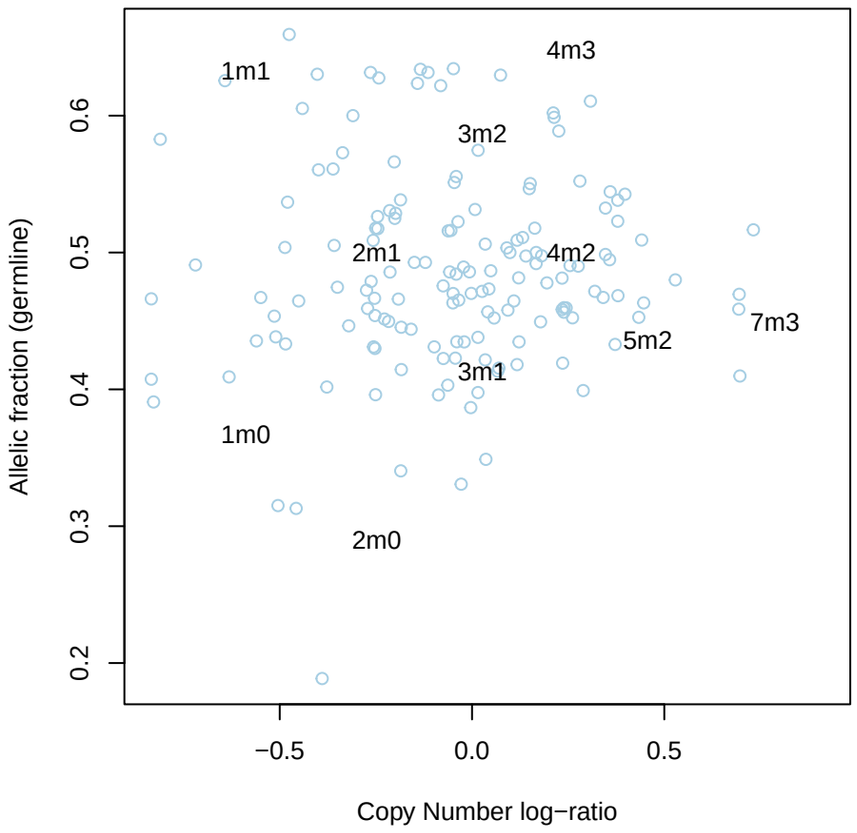

Power 0.8
Frequency
Cellular fraction

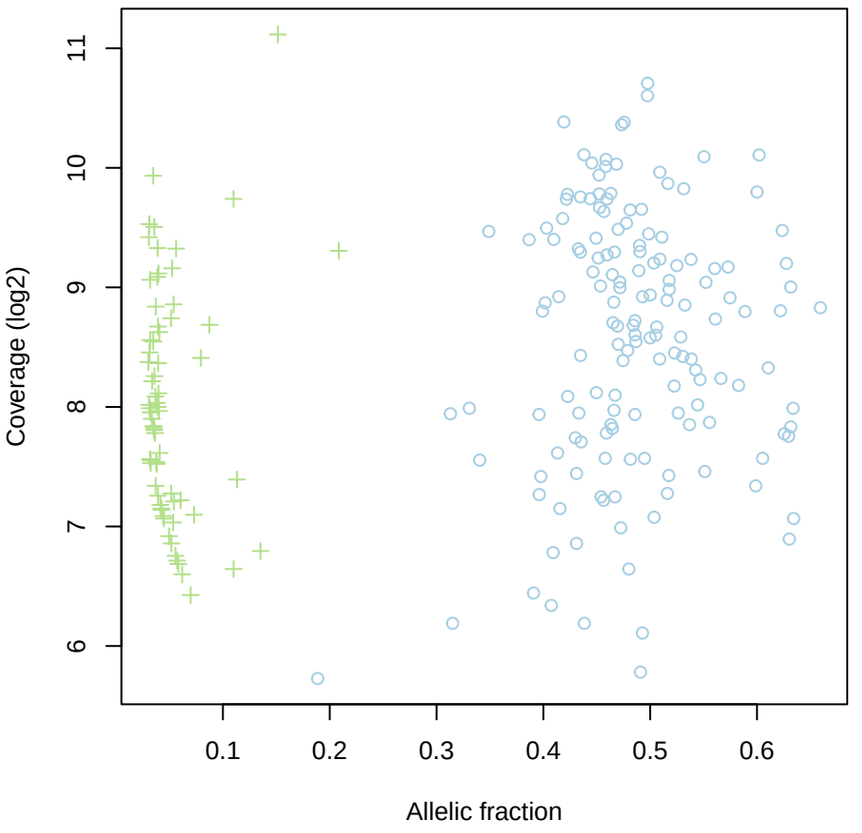

Purity: 0.42 Tumor ploidy: 2.893
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

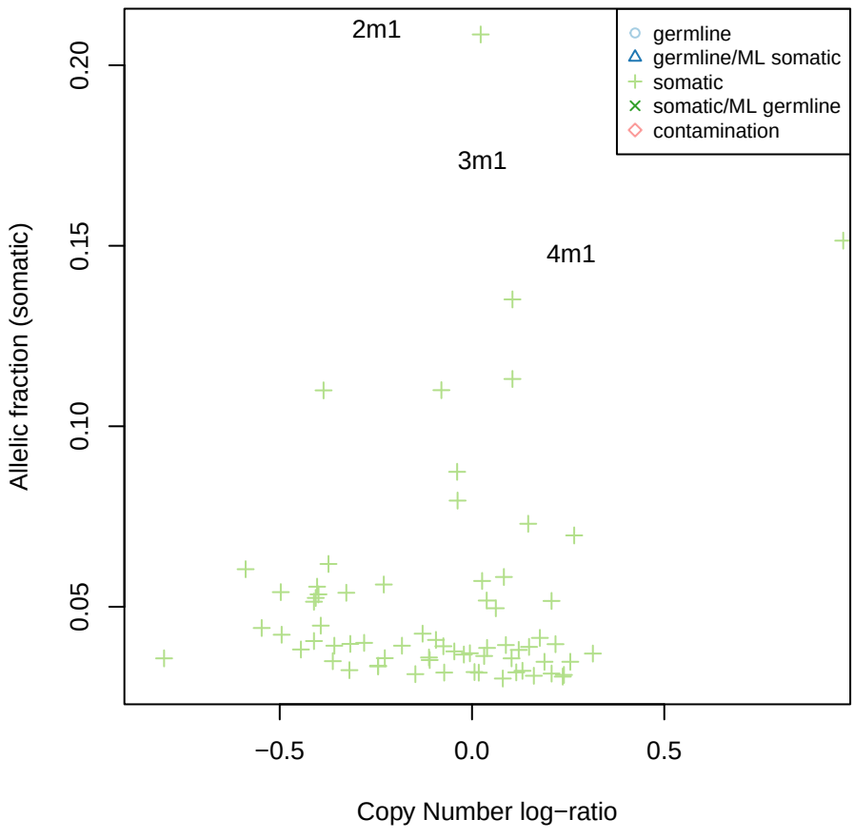

Purity: 0.42 Tumor ploidy: 2.893 SNV log−likelihood: −170.75 GoF: 79.6% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

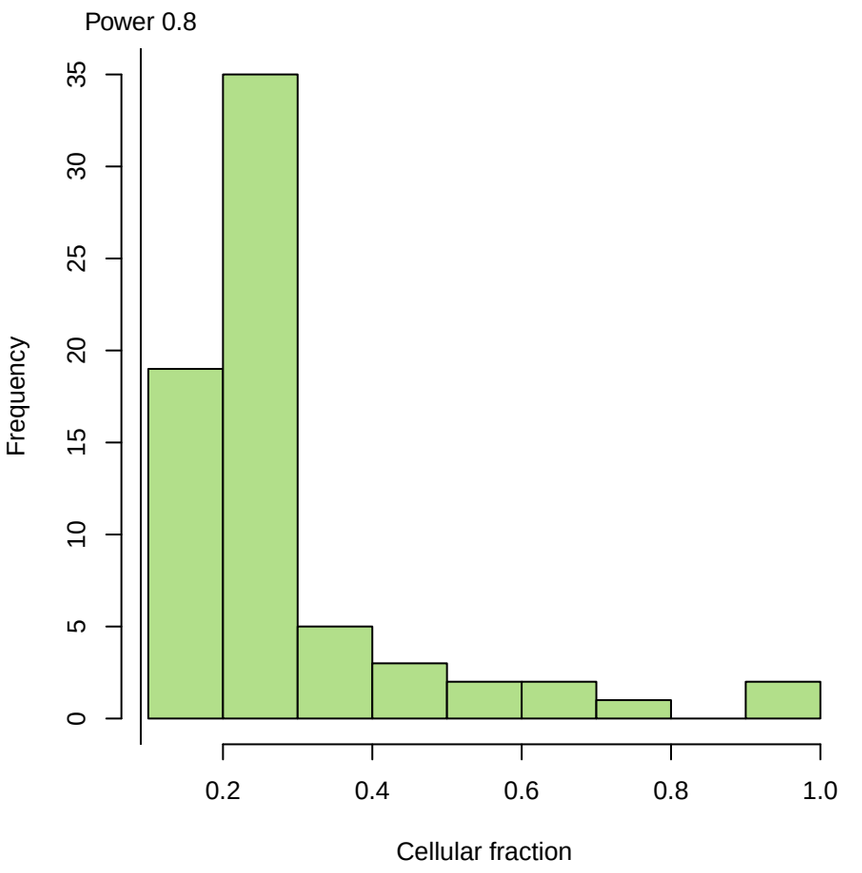

SCNA−fit log−likelihood: −7217.49
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6 7
0 50 100 150
SNV Index

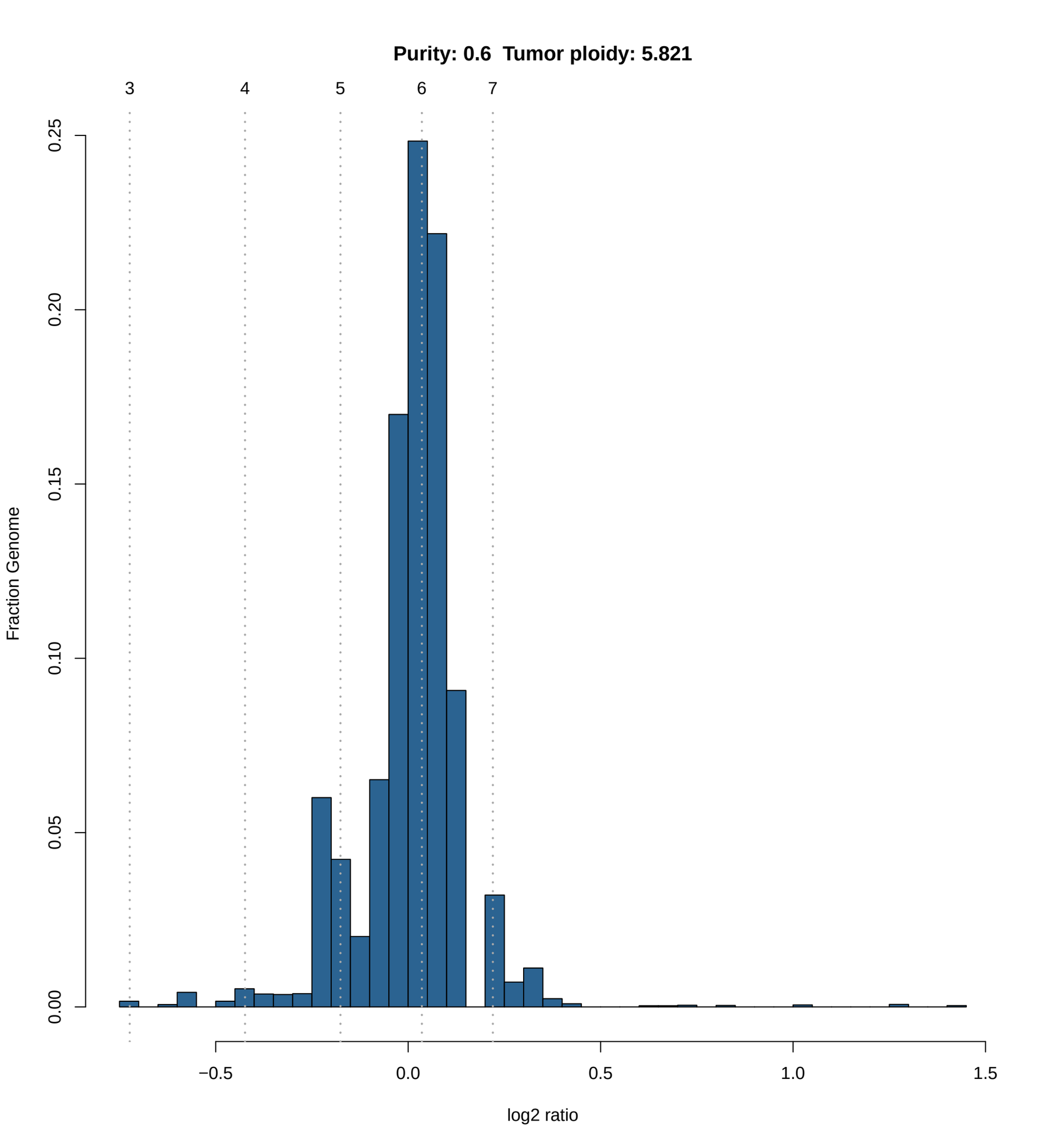

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

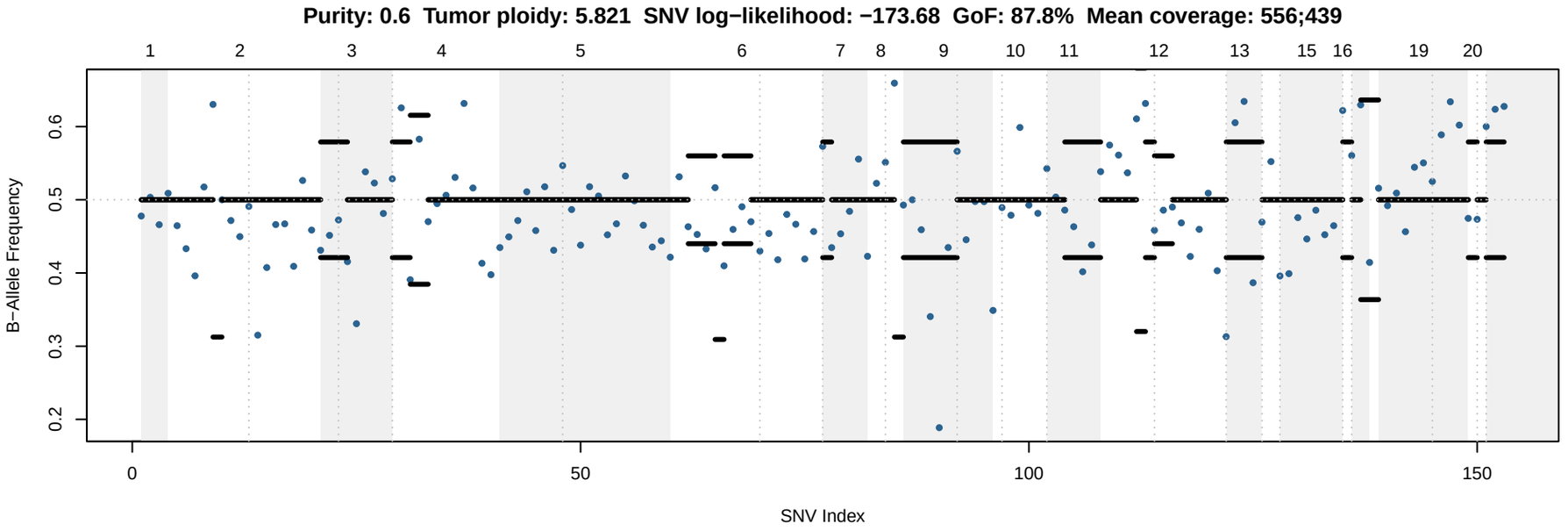

1m1
4m3
3m2
2m1
4m2
7m3
5m2
3m1
1m0
2m0
Allelic fraction (germline)
Copy Number log−ratio
0.2
0.3
0.4
0.5
0.6
−0.5
0.0
0.5

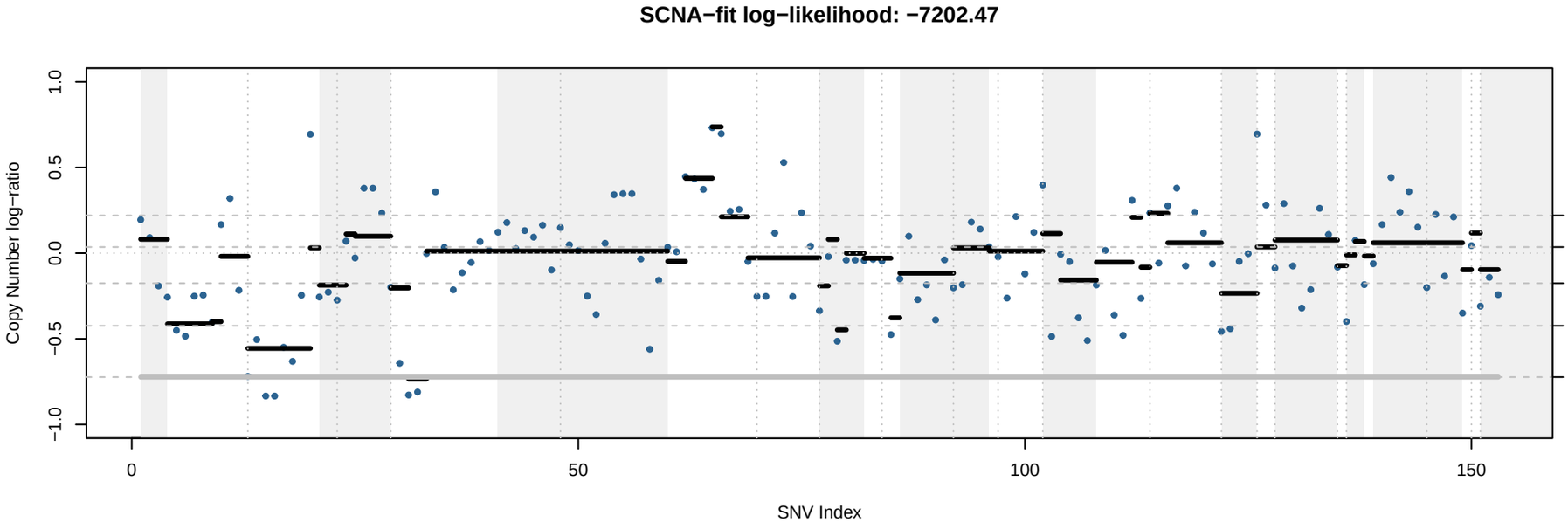

Coverage (log2)
Allelic fraction
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6

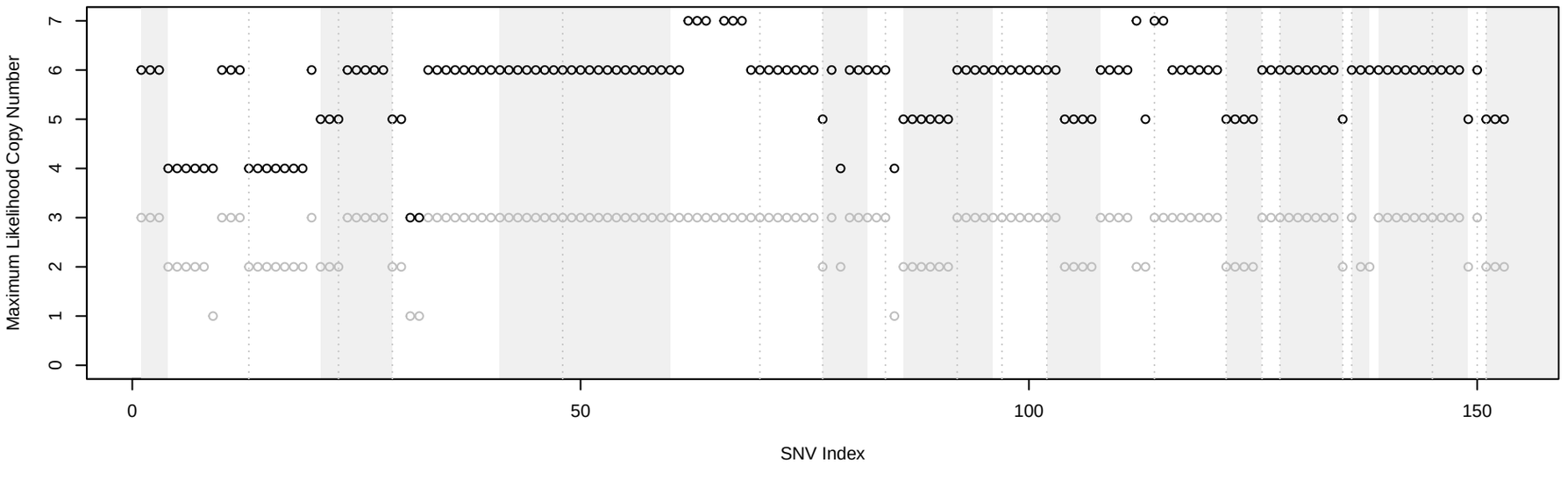

2m1
3m1
4m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
−0.5
0.0
0.5

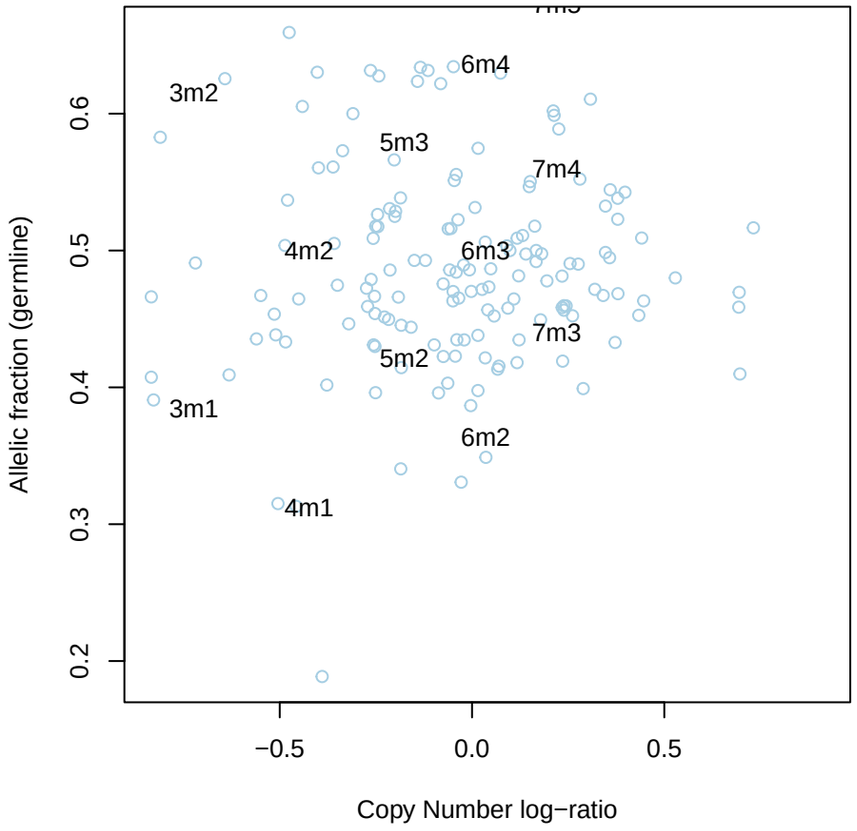

Power 0.8
Frequency
Cellular fraction
0
5
10
15
20
25
30
35
0.2
0.4
0.6
0.8
1.0

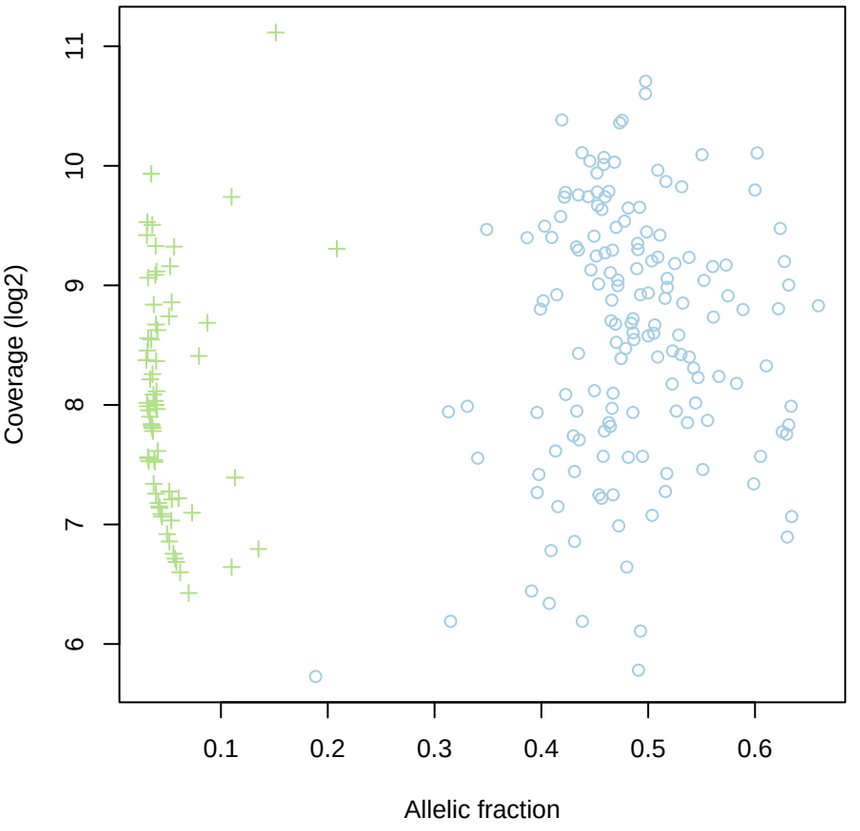

Purity: 0.6 Tumor ploidy: 5.821
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

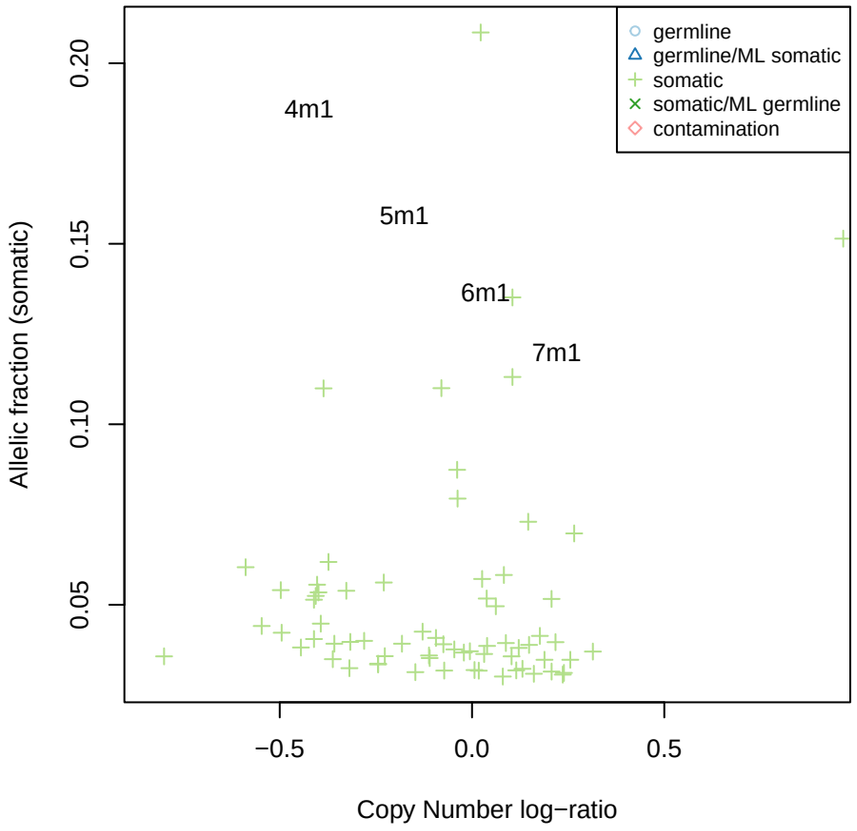

Purity: 0.6 Tumor ploidy: 5.821 SNV log−likelihood: −173.68 GoF: 87.8% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

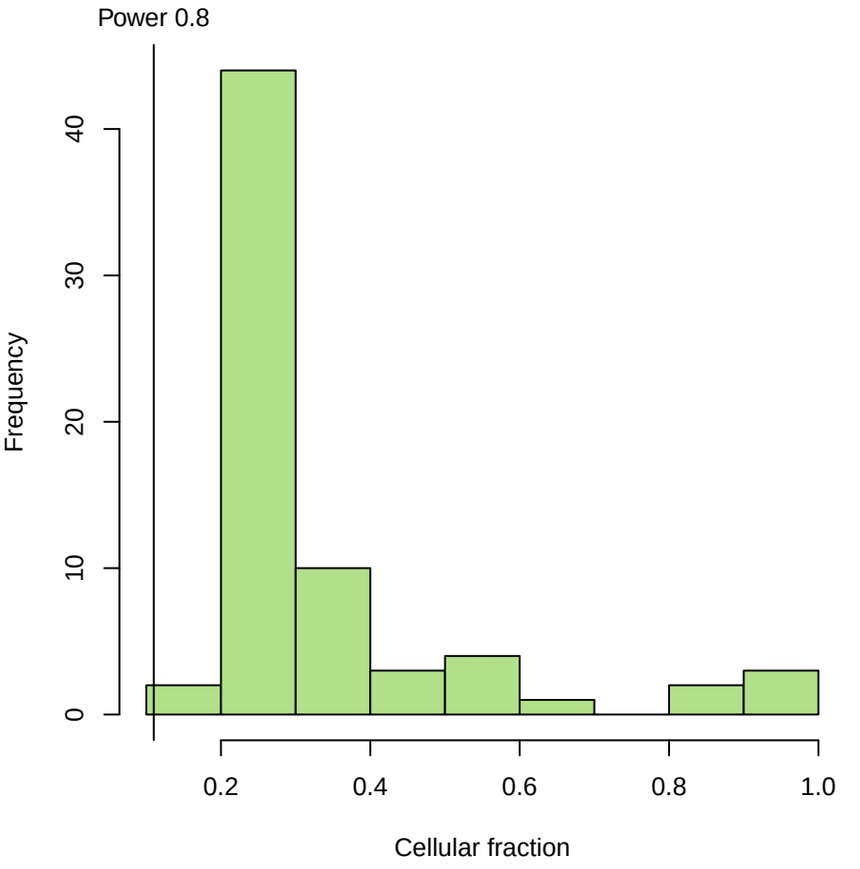

SCNA−fit log−likelihood: −7202.47
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 50 100 150
SNV Index

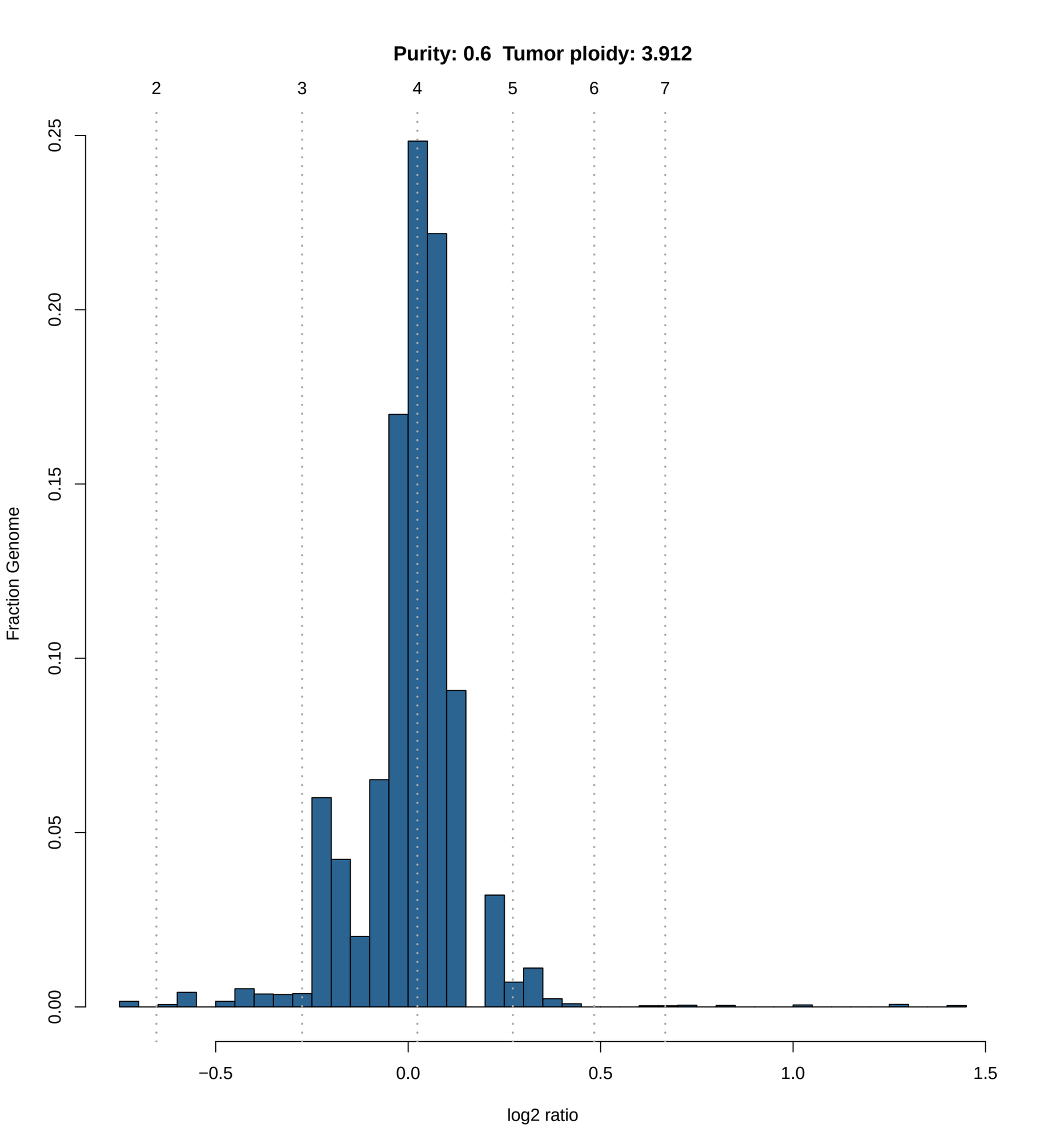

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

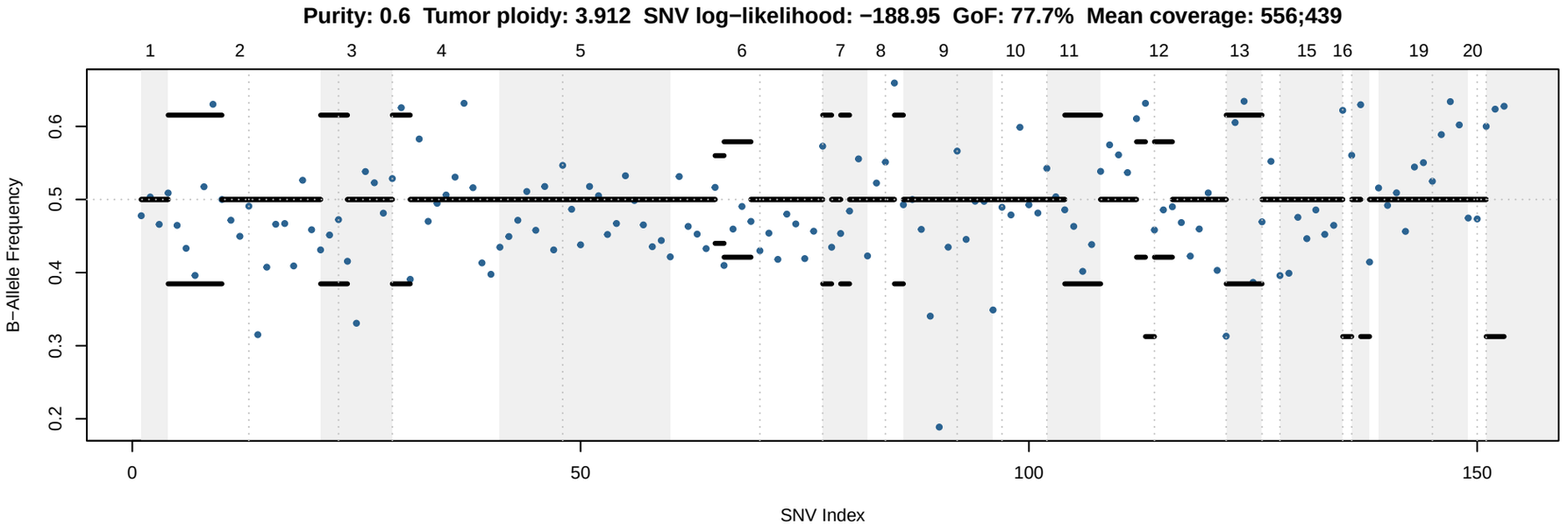

Allelic fraction (germline)
Copy Number log−ratio
3m2
6m4
5m3
7m4
4m2
6m3
7m3
5m2
3m1
6m2
4m1

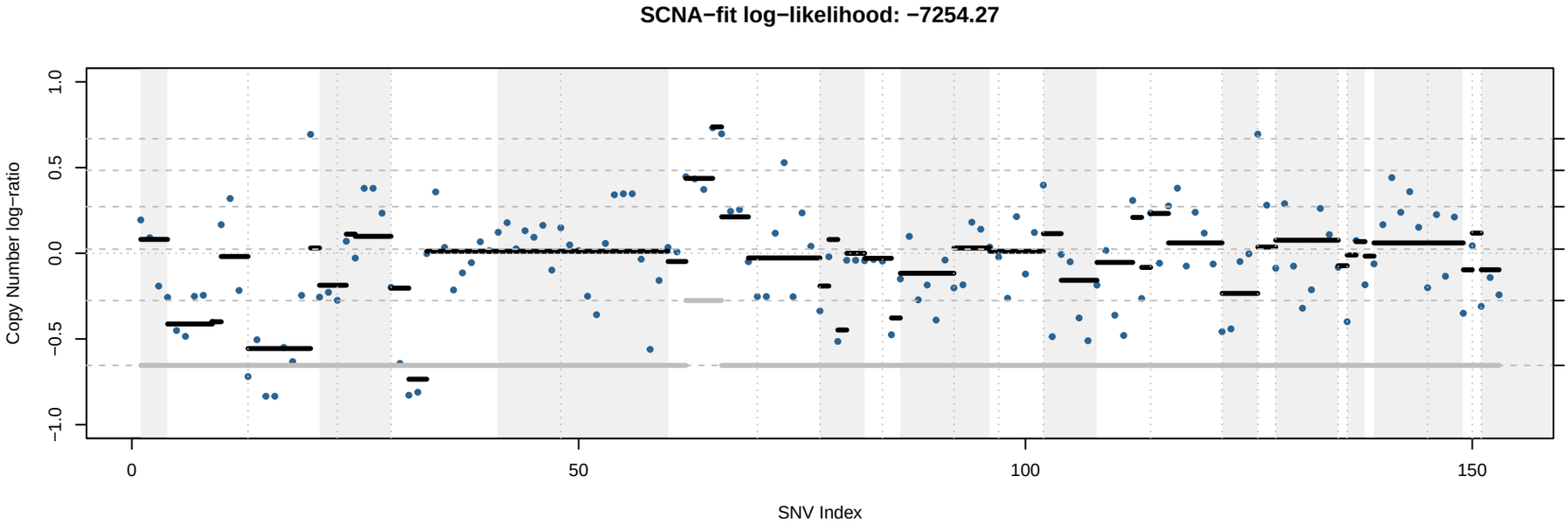

Coverage (log2)
Allelic fraction

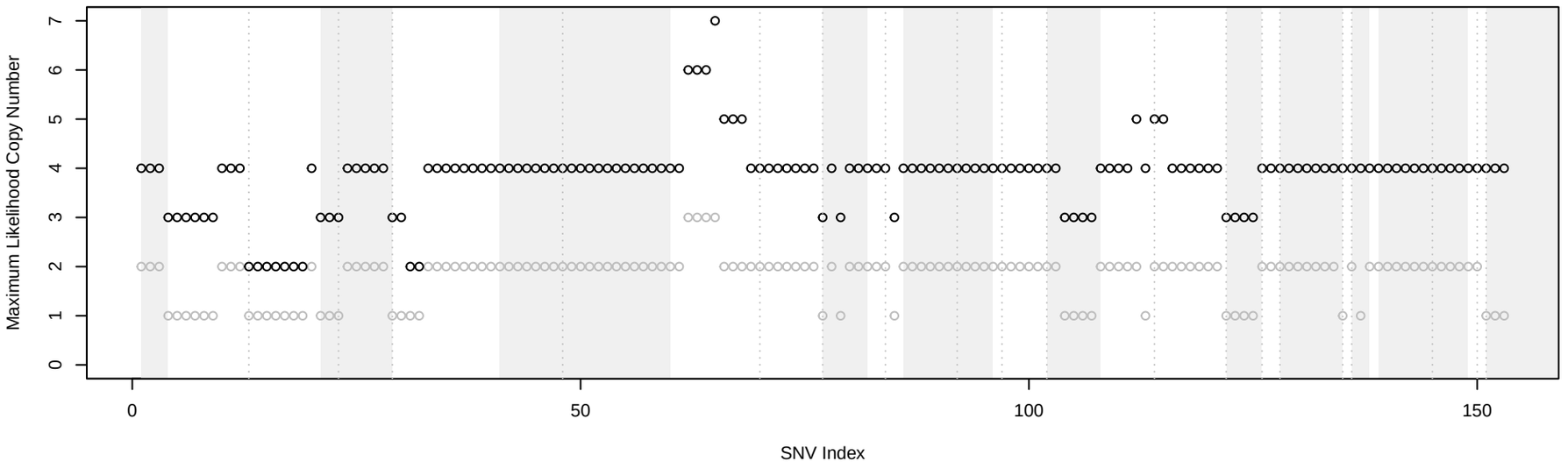

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
7m1

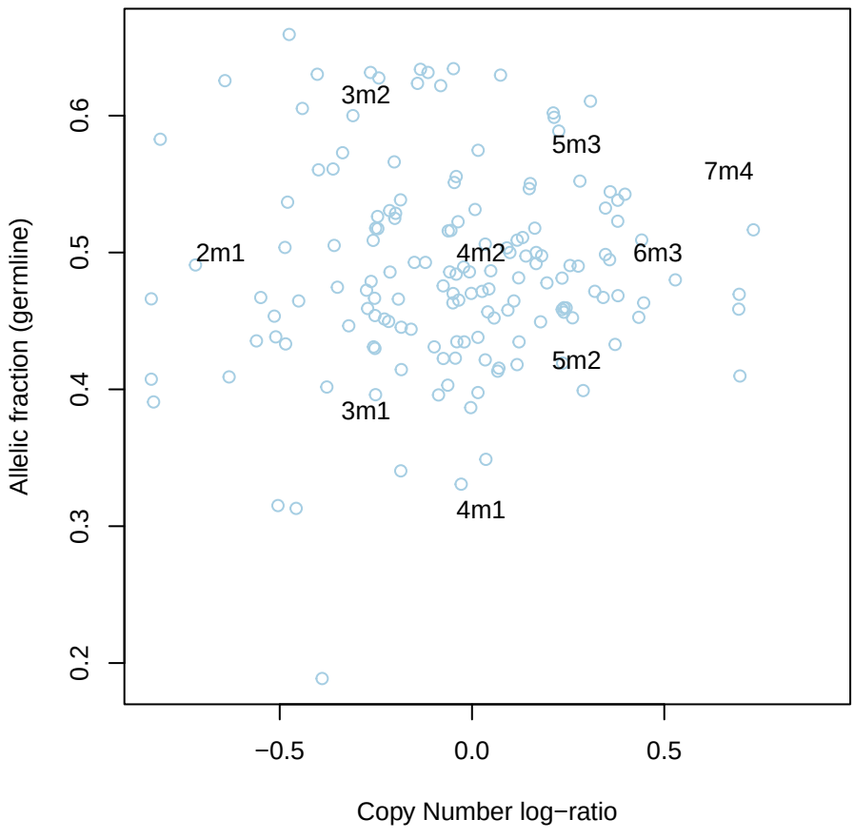

Power 0.8
Frequency
Cellular fraction

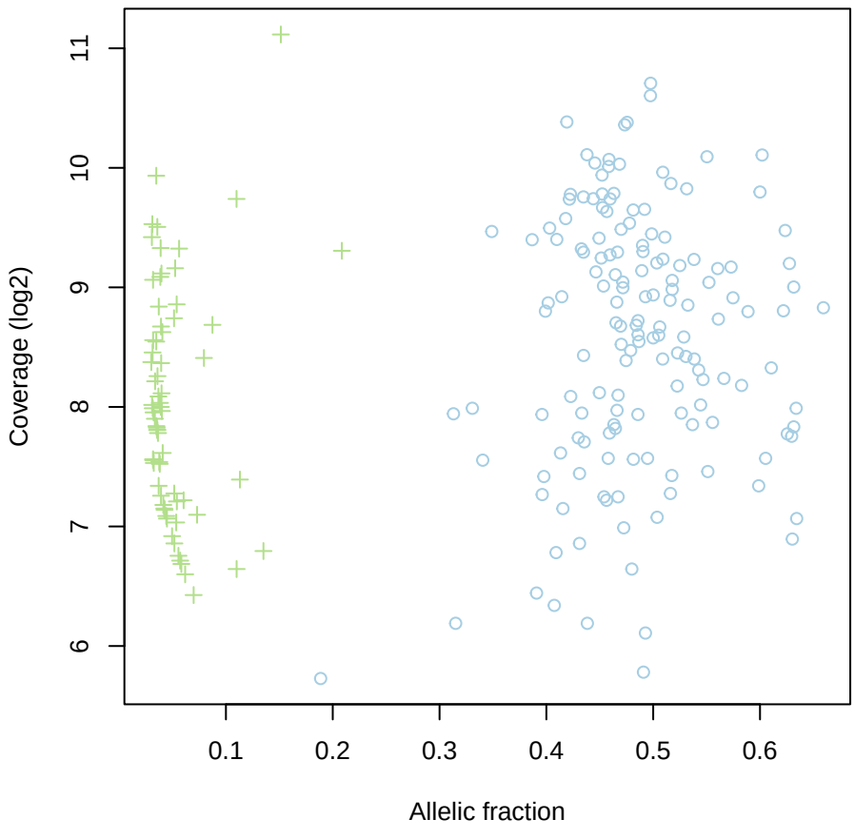

Purity: 0.6 Tumor ploidy: 3.912
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

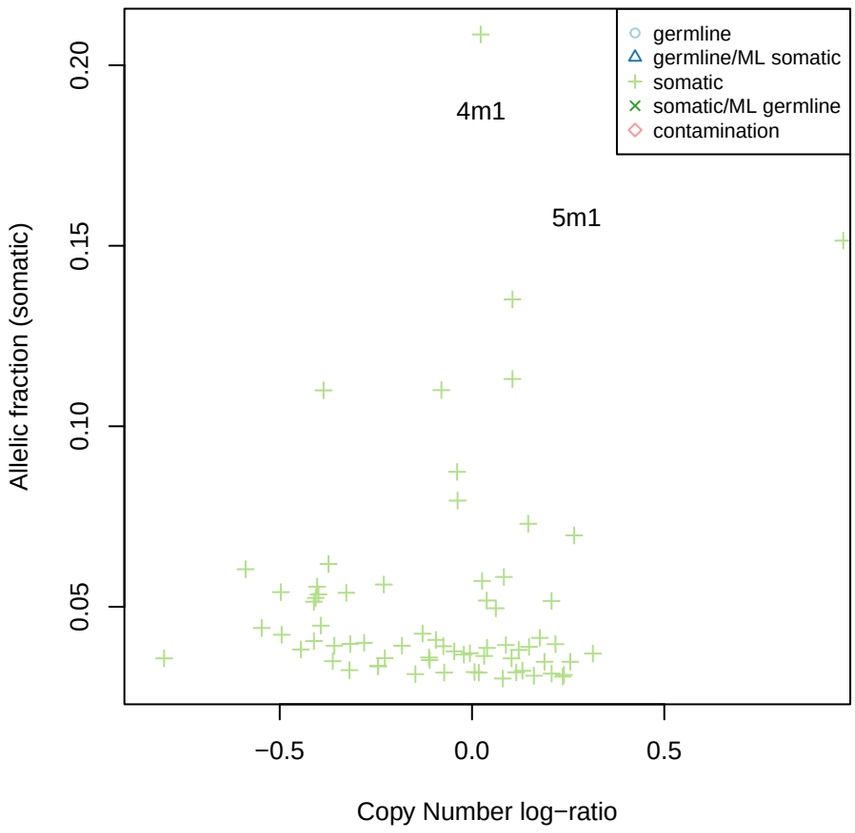

Purity: 0.6 Tumor ploidy: 3.912 SNV log−likelihood: −188.95 GoF: 77.7% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

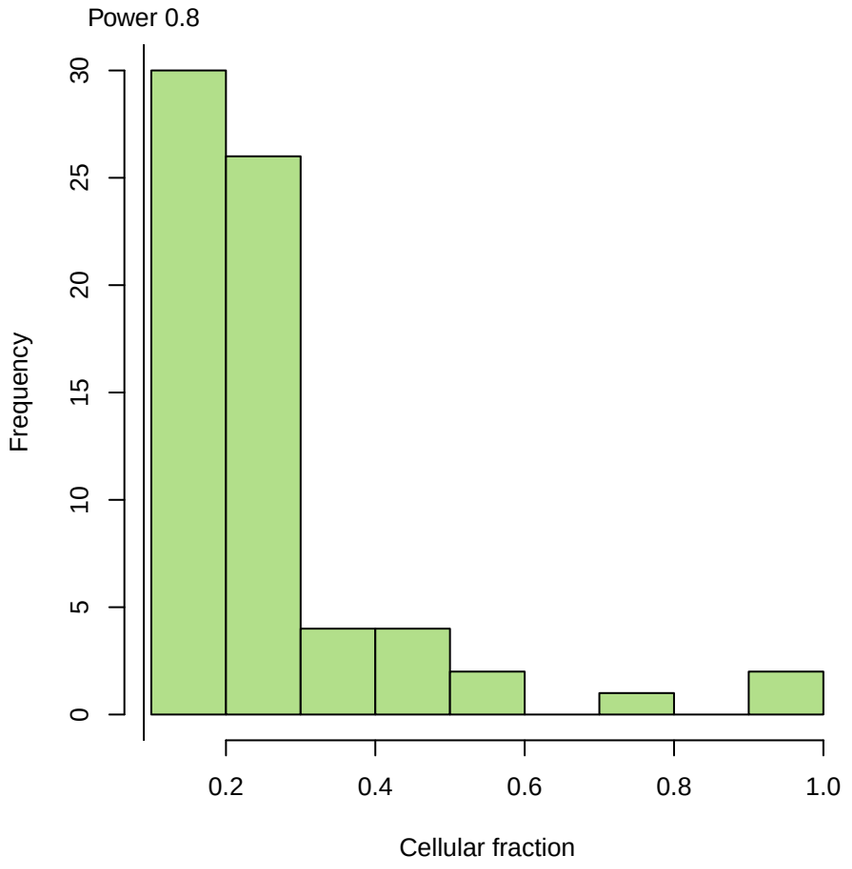

SCNA−fit log−likelihood: −7254.27
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 50 100 150
SNV Index

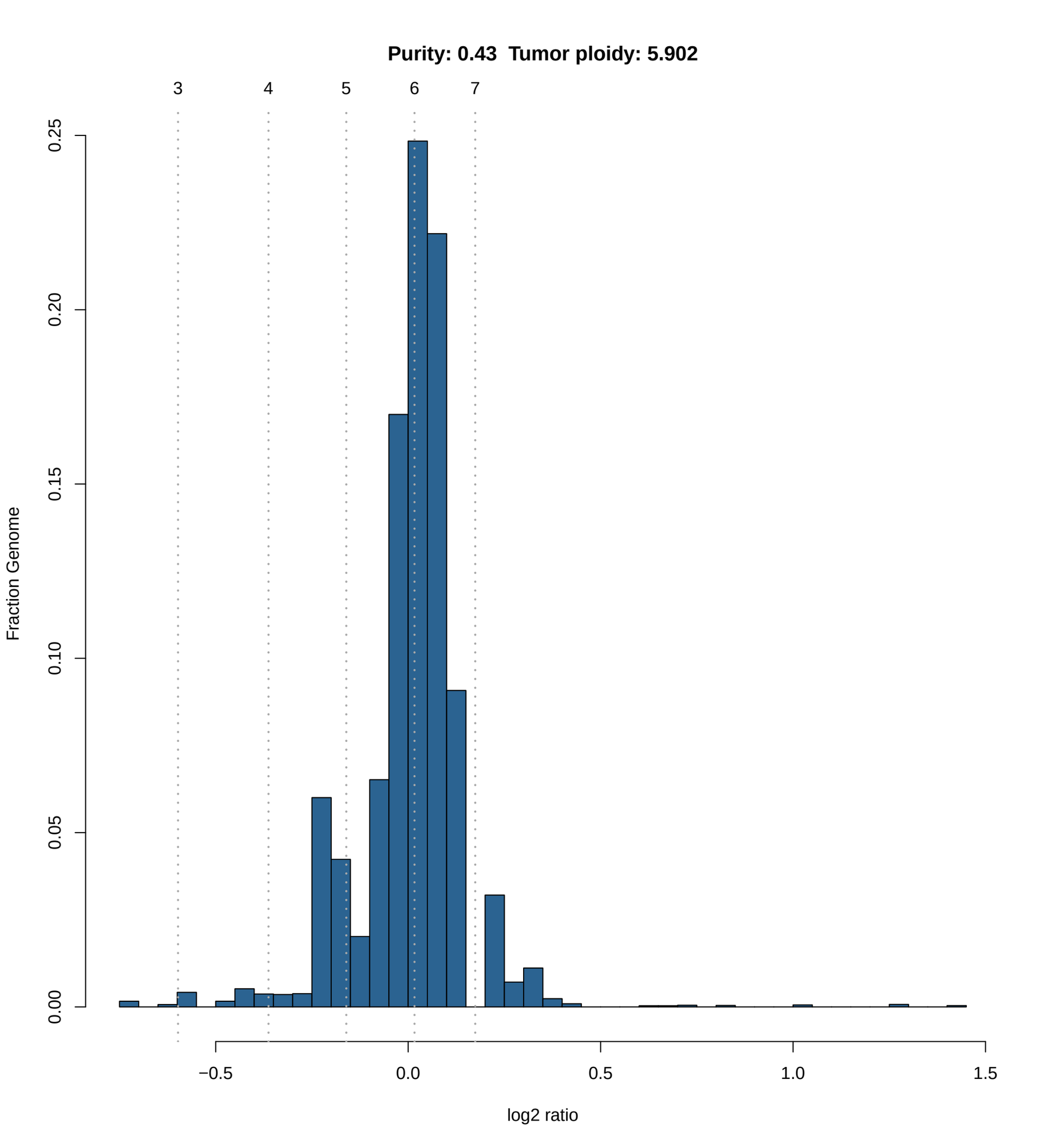

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

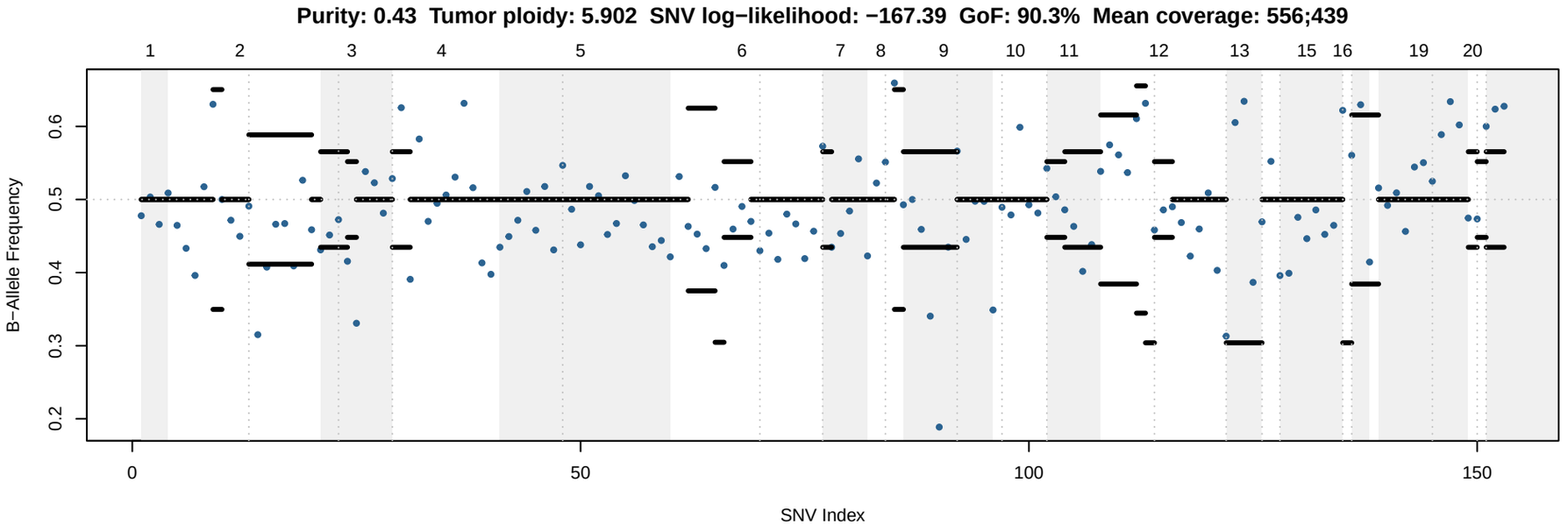

Allelic fraction (germline)
Copy Number log−ratio
3m2
5m3
7m4
2m1
4m2
6m3
5m2
3m1
4m1

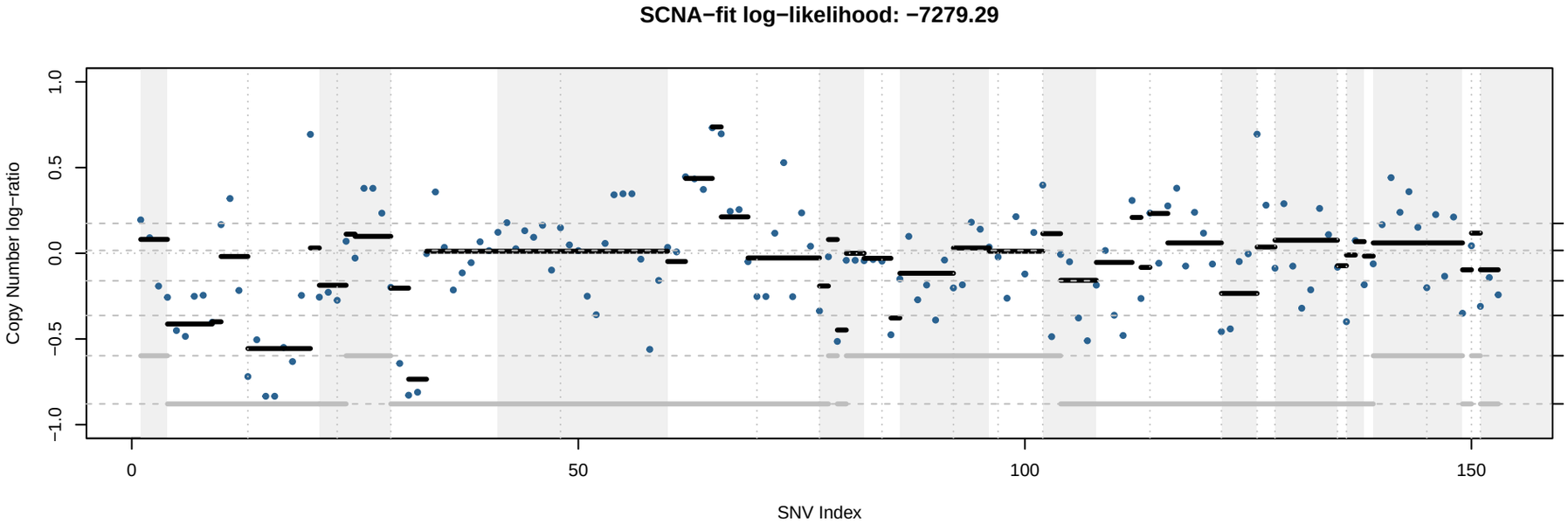

Coverage (log2)
Allelic fraction

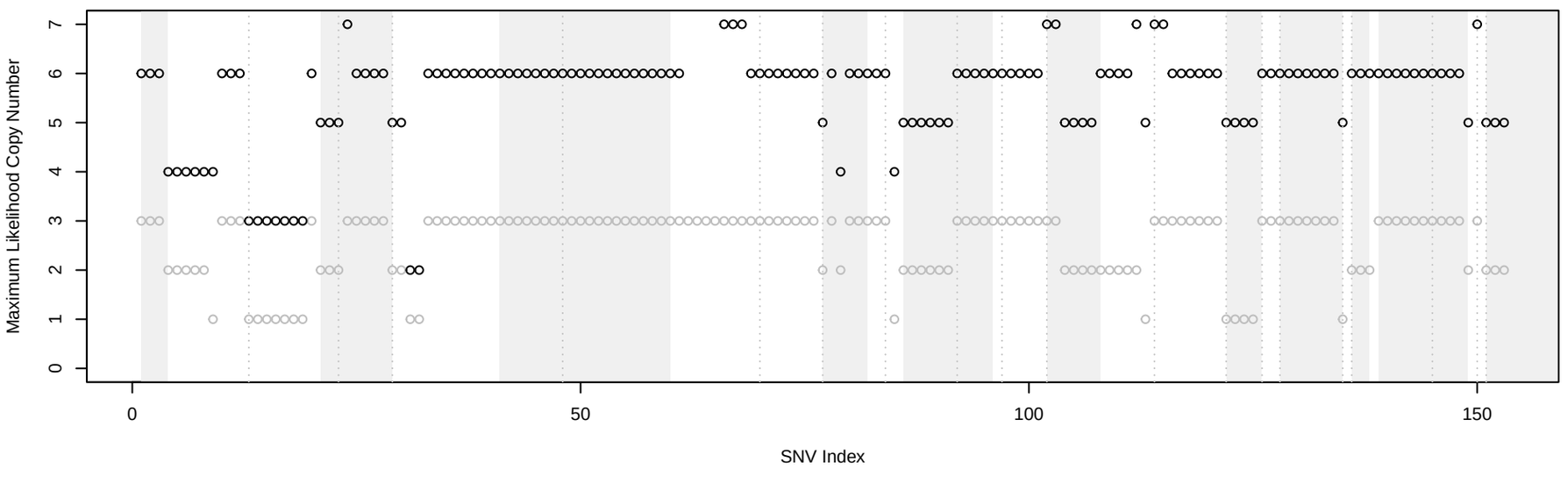

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1

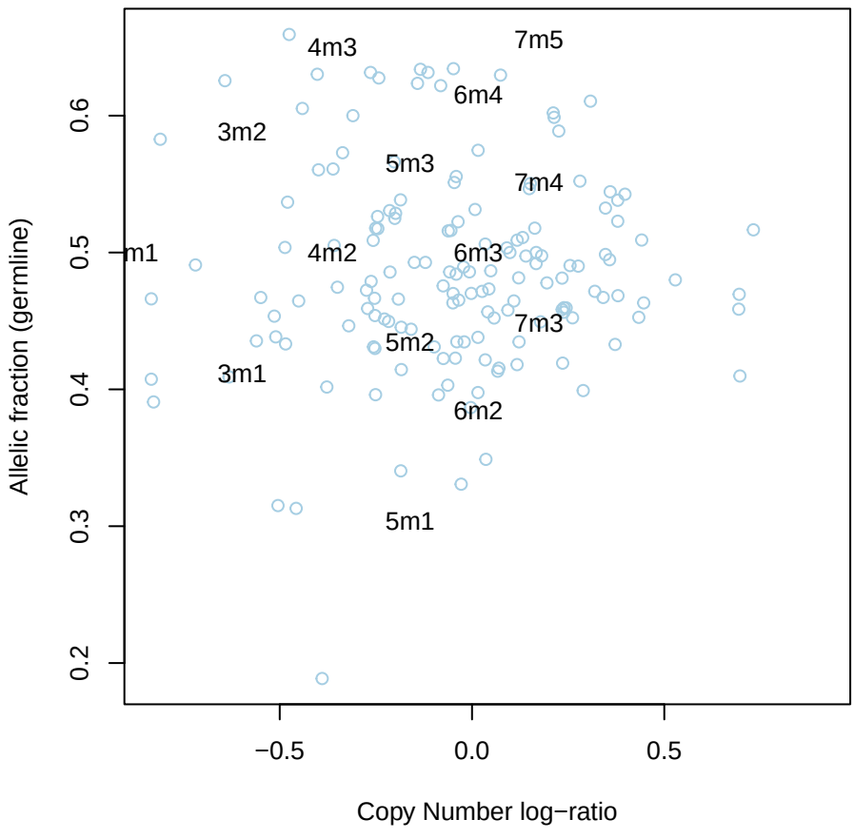

Power 0.8
Frequency
Cellular fraction

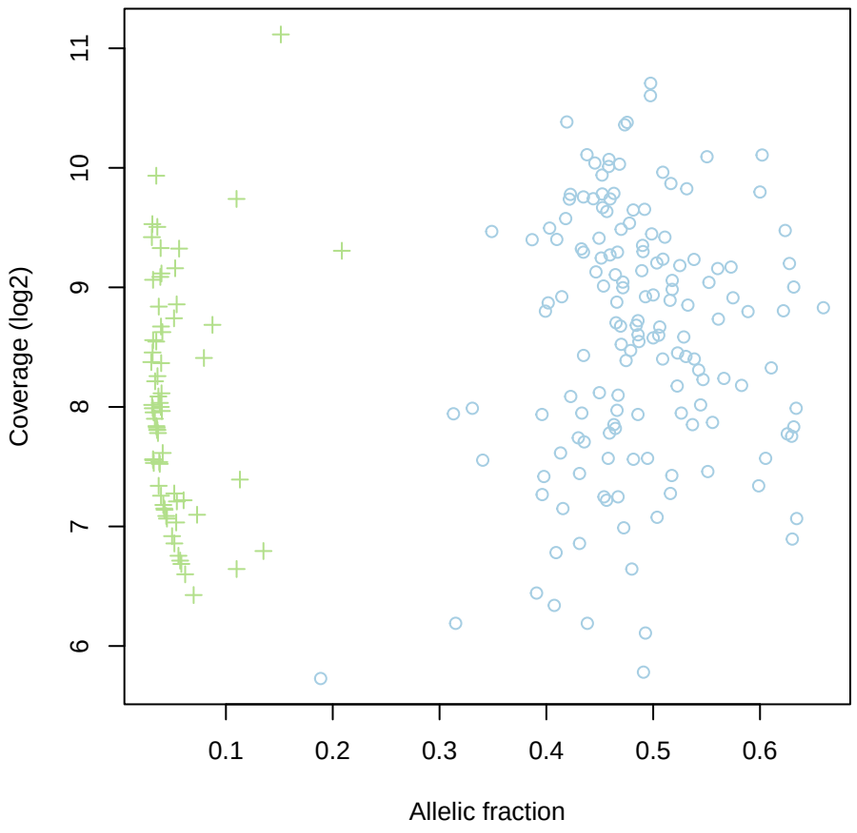

Purity: 0.43 Tumor ploidy: 5.902
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

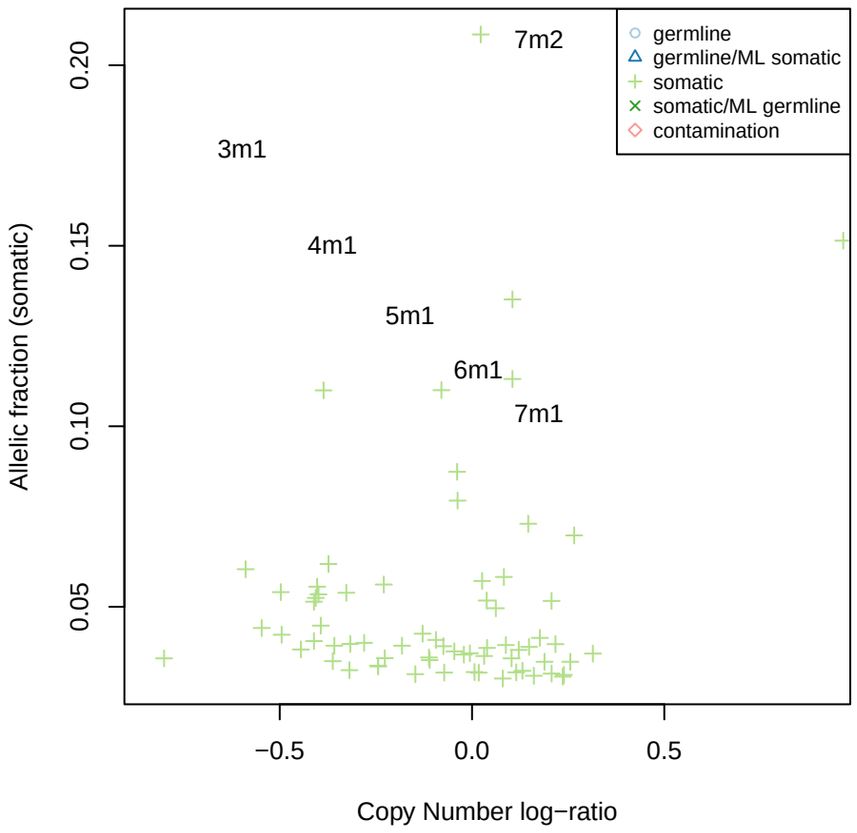

Purity: 0.43 Tumor ploidy: 5.902 SNV log−likelihood: −167.39 GoF: 90.3% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

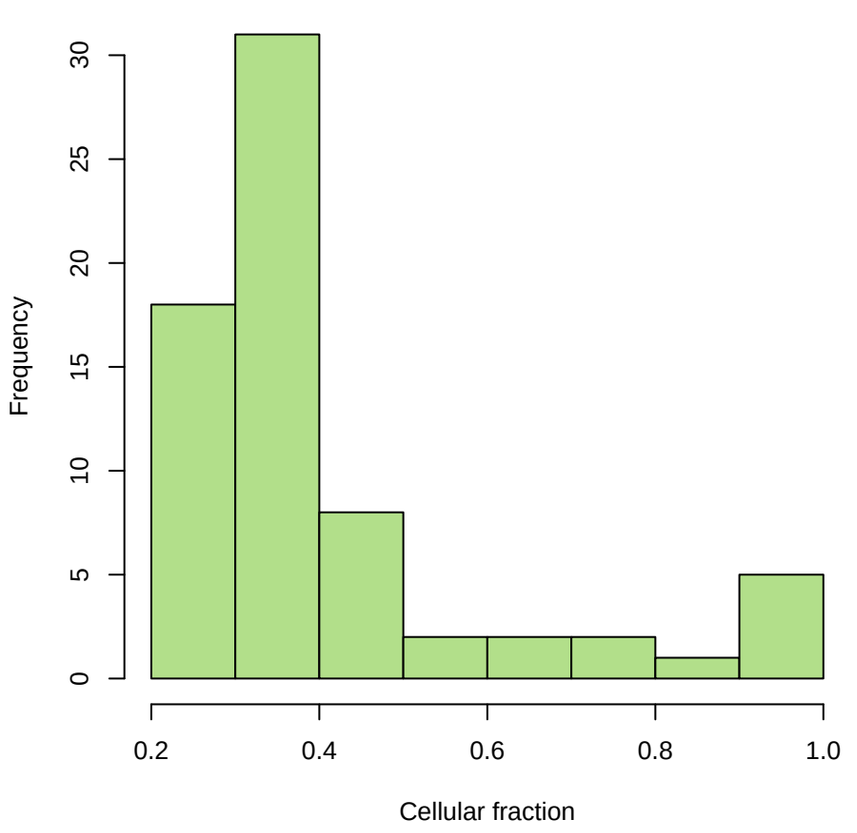

SCNA−fit log−likelihood: −7279.29
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 50 100 150
SNV Index

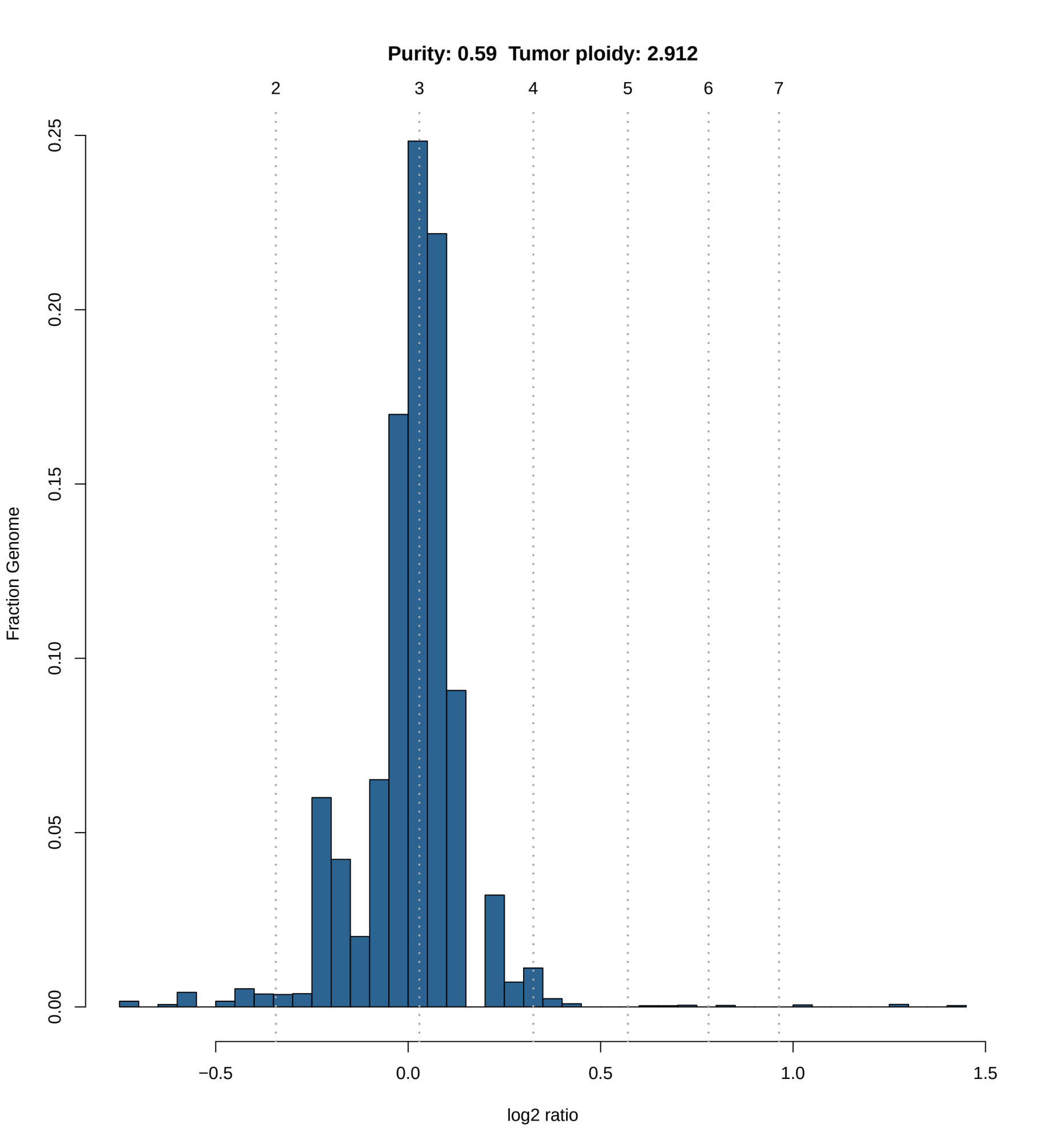

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

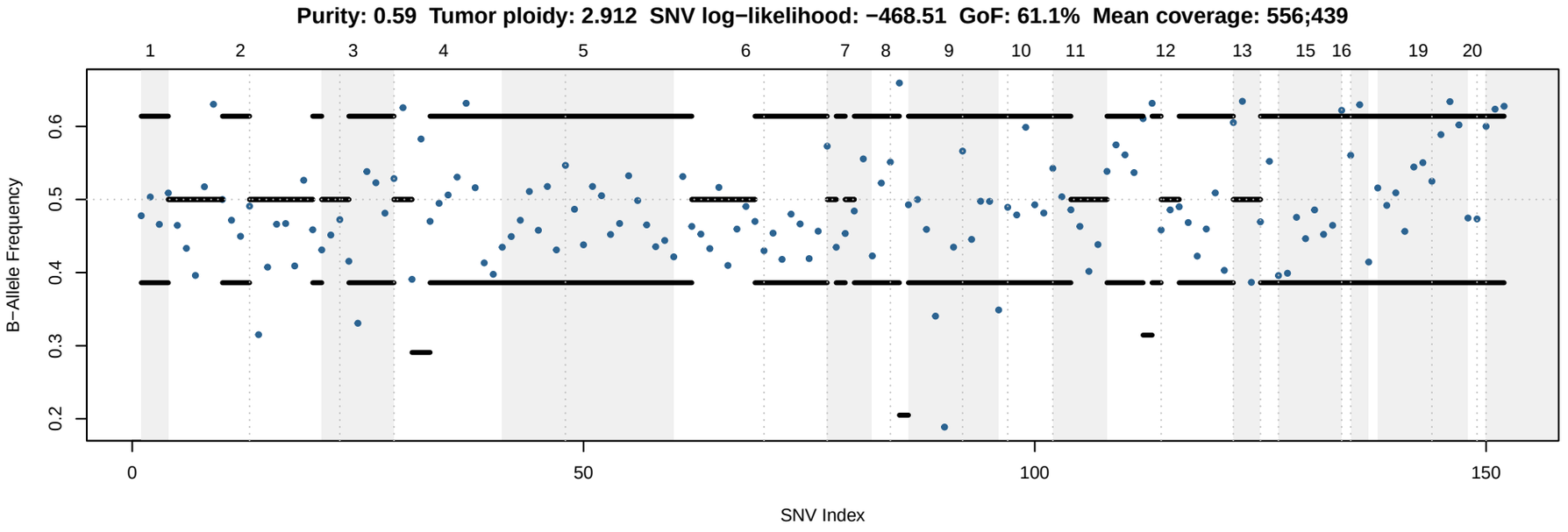

4m3
7m5
6m4
3m2
5m3
7m4
m1
4m2
6m3
7m3
5m2
3m1
6m2
5m1
Allelic fraction (germline)
Copy Number log−ratio

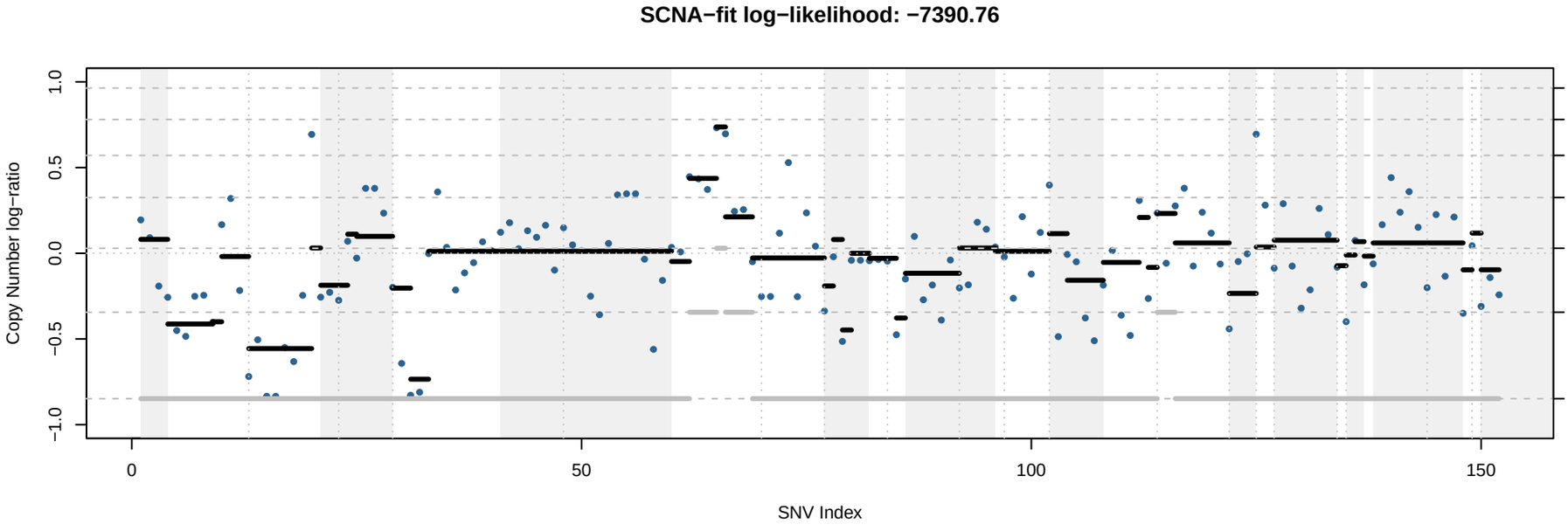

Coverage (log2)
Allelic fraction

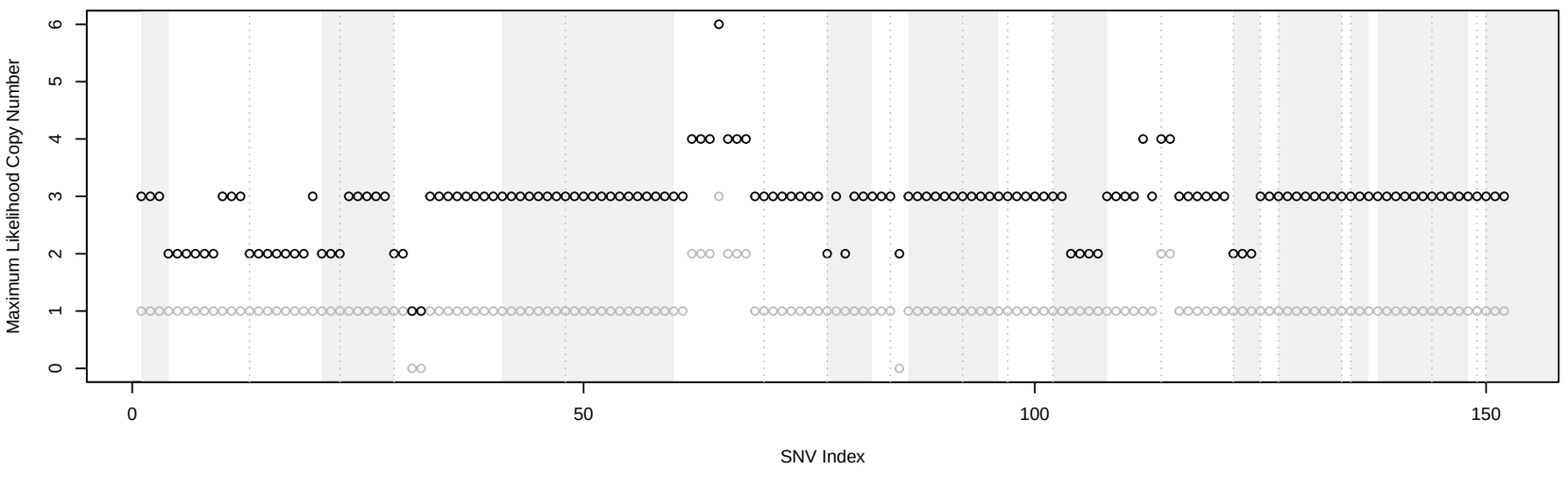

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
7m2
3m1
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

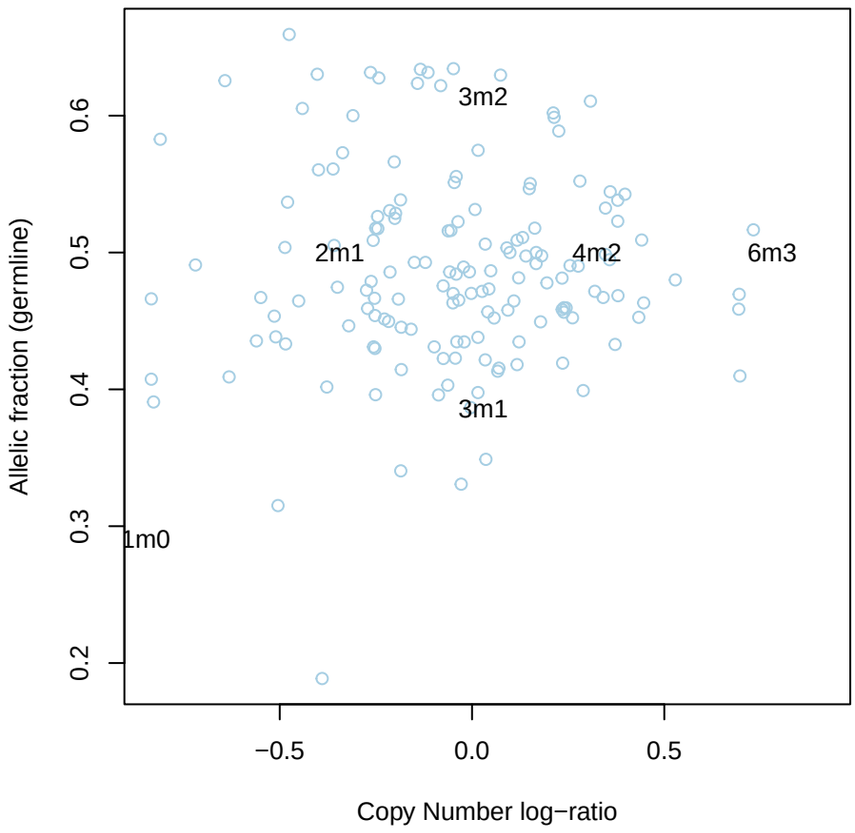

Frequency
Cellular fraction

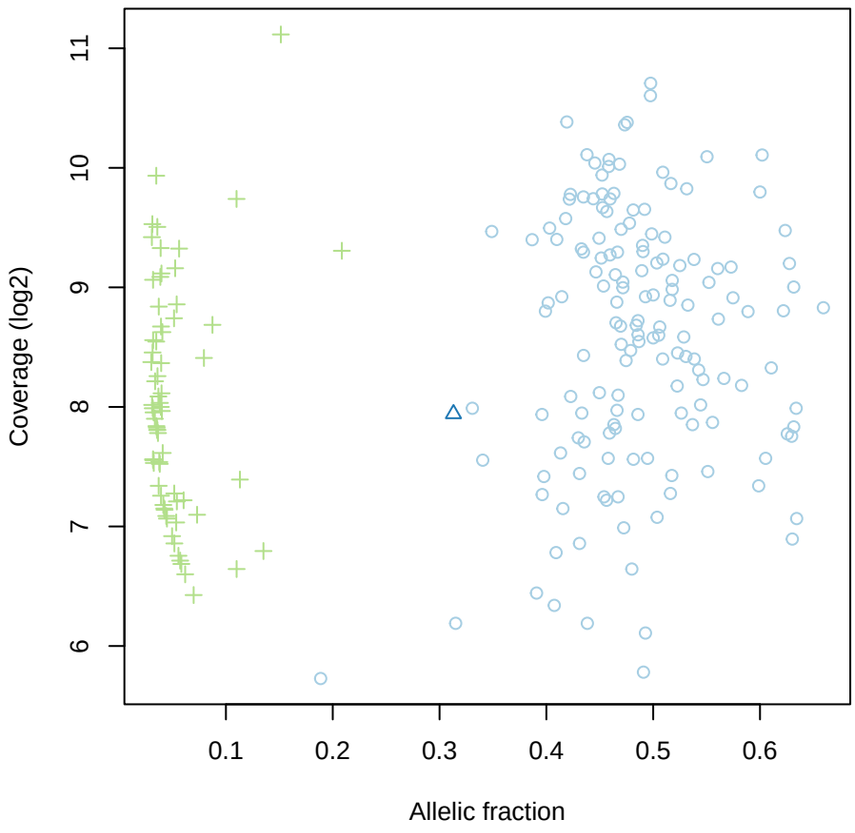

Purity: 0.59 Tumor ploidy: 2.912
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

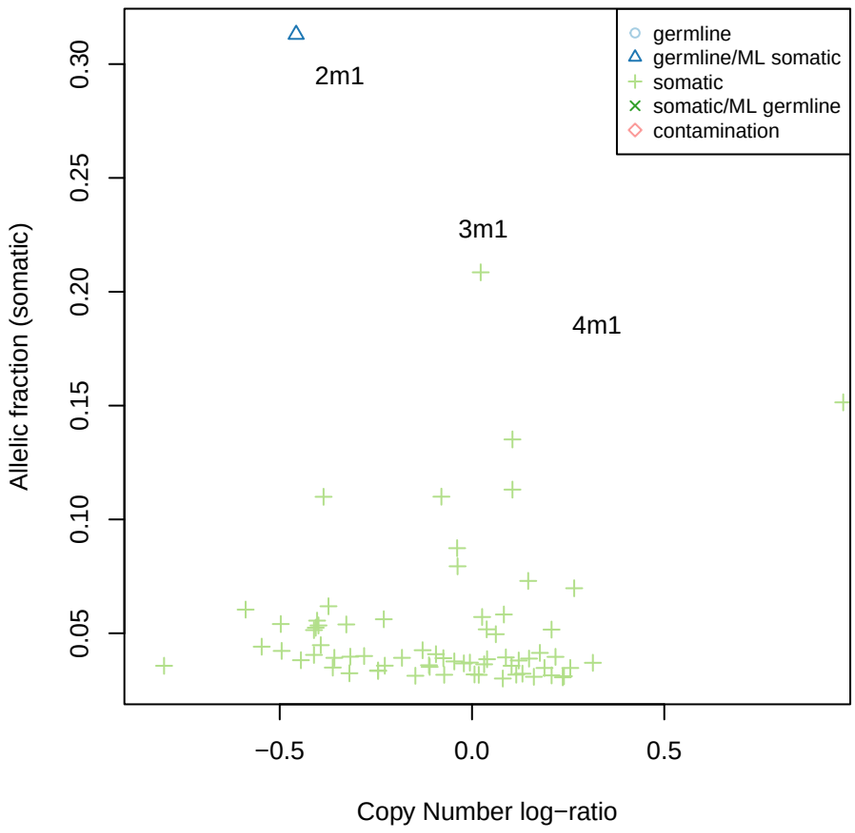

Purity: 0.59 Tumor ploidy: 2.912 SNV log−likelihood: −468.51 GoF: 61.1% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

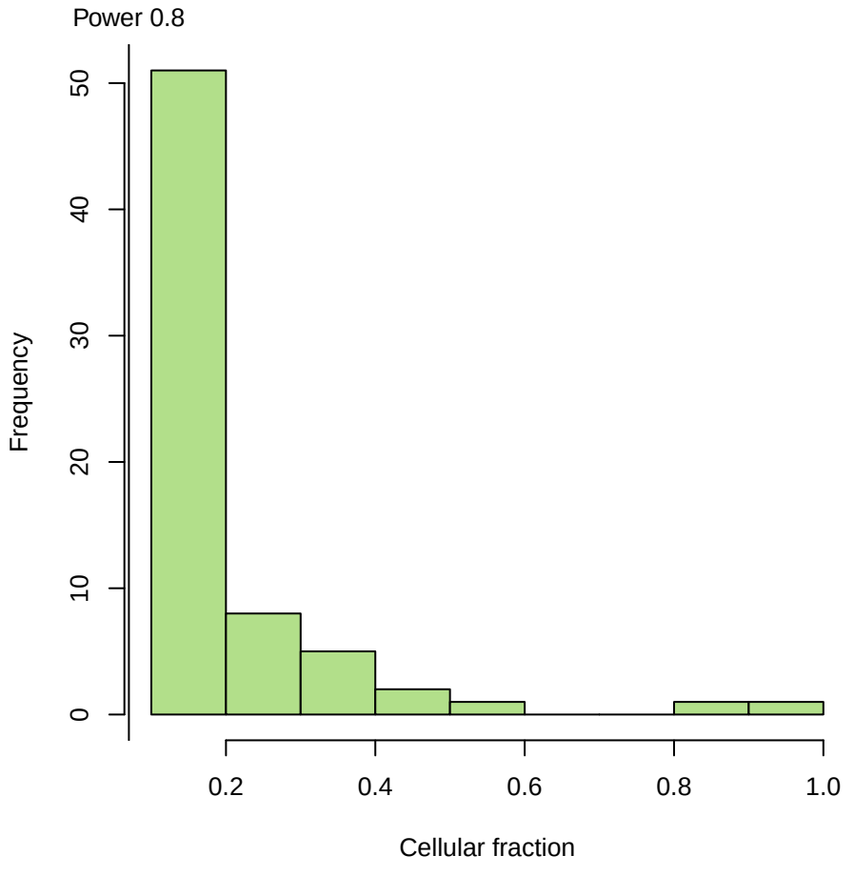

SCNA−fit log−likelihood: −7390.76
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6 7
0 50 100 150
SNV Index

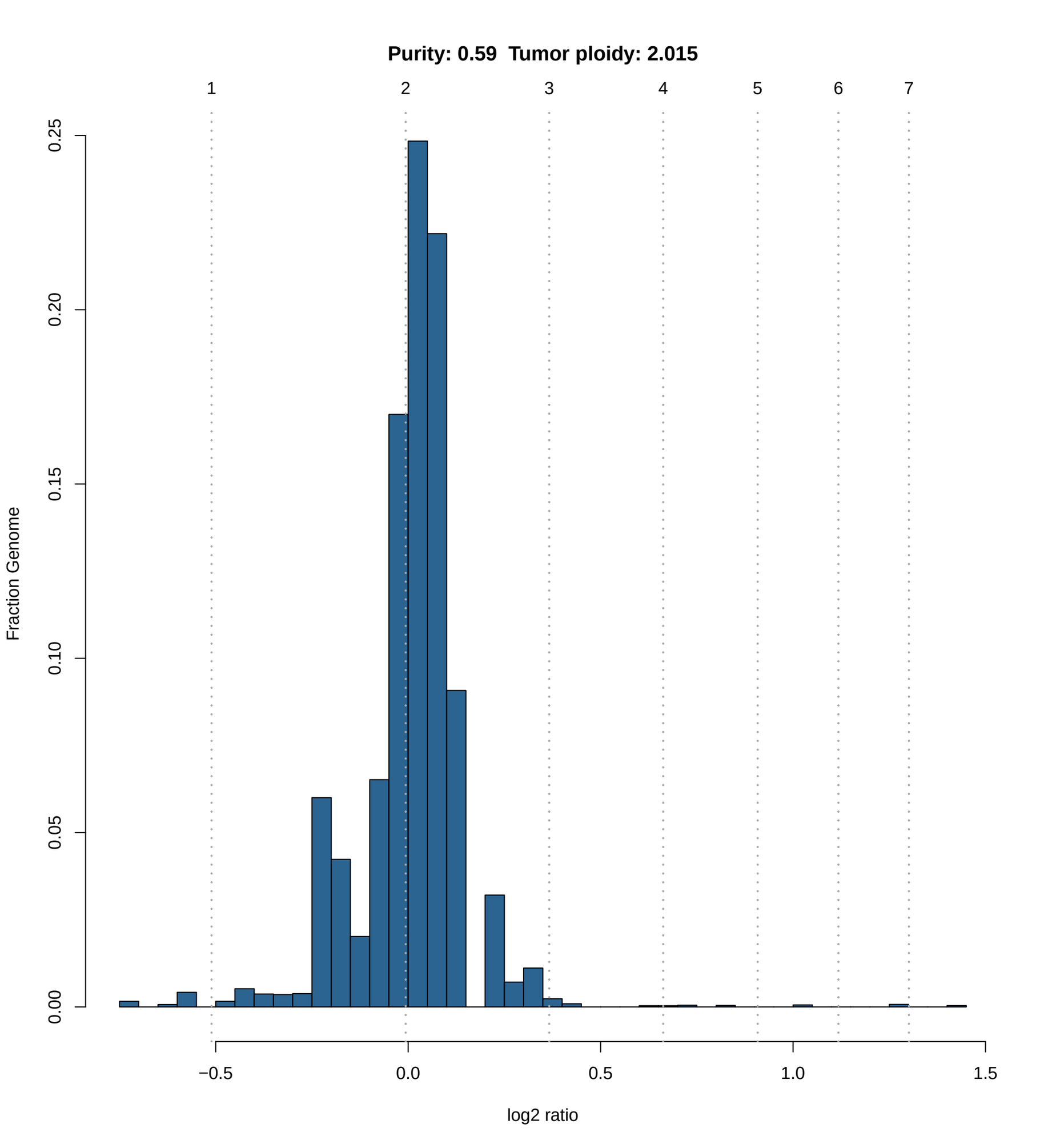

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

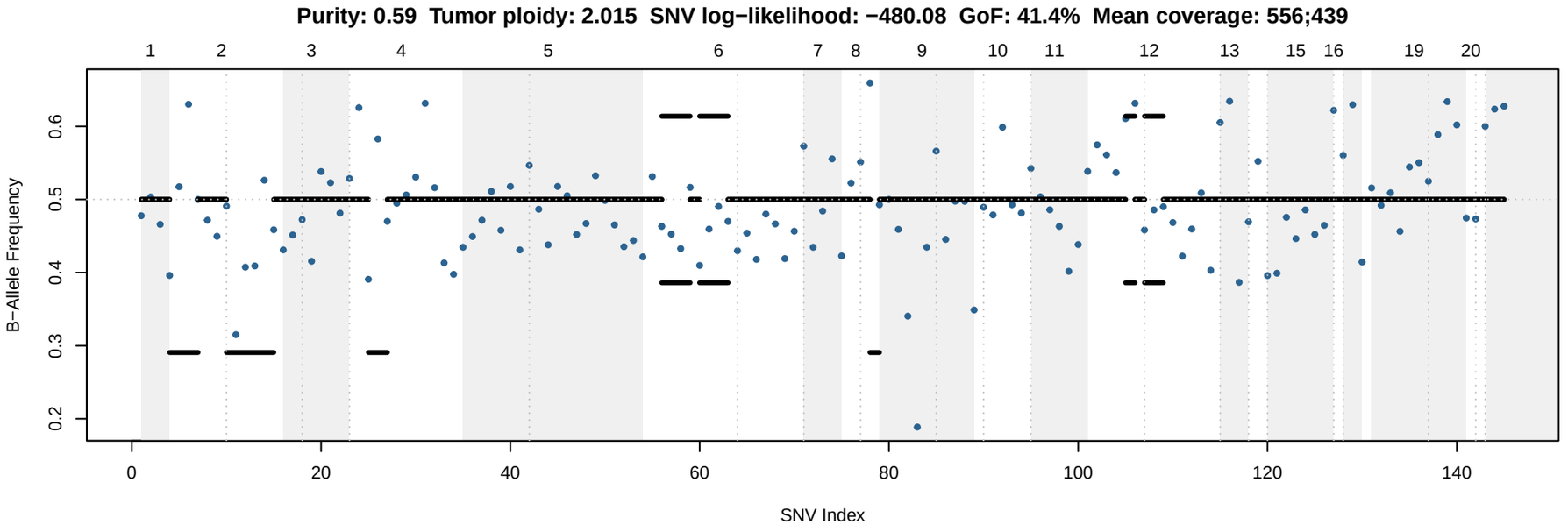

Allelic fraction (germline)
Copy Number log−ratio
3m2
2m1
4m2
6m3
3m1
1m0

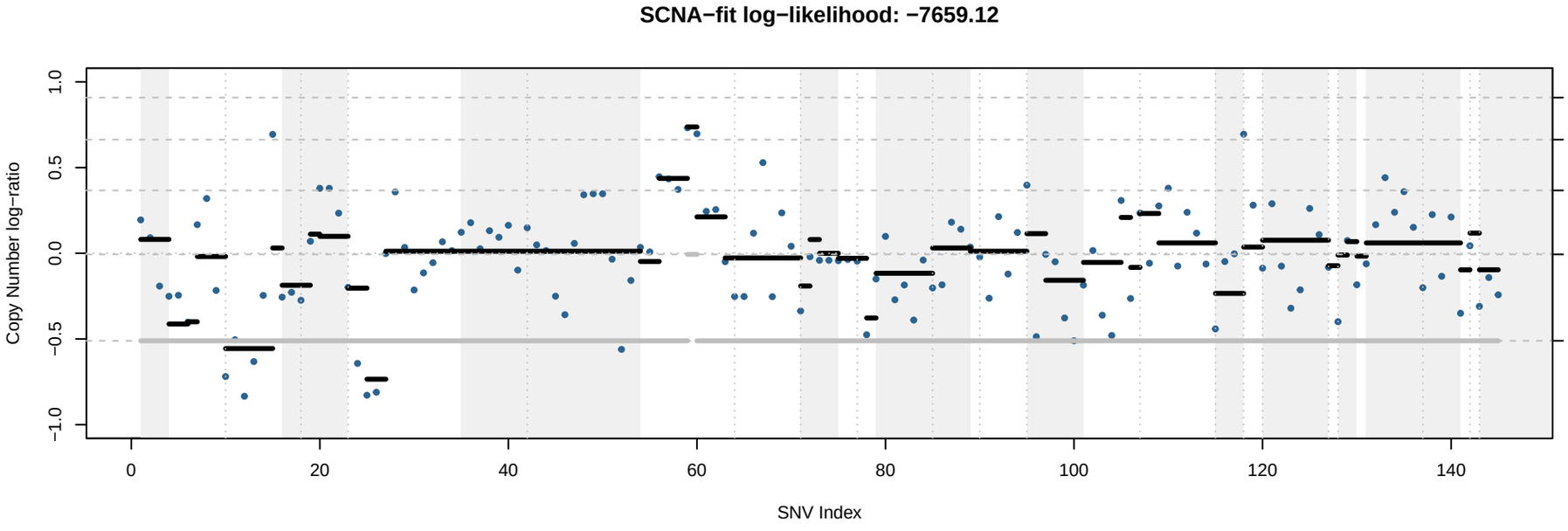

Coverage (log2)
Allelic fraction

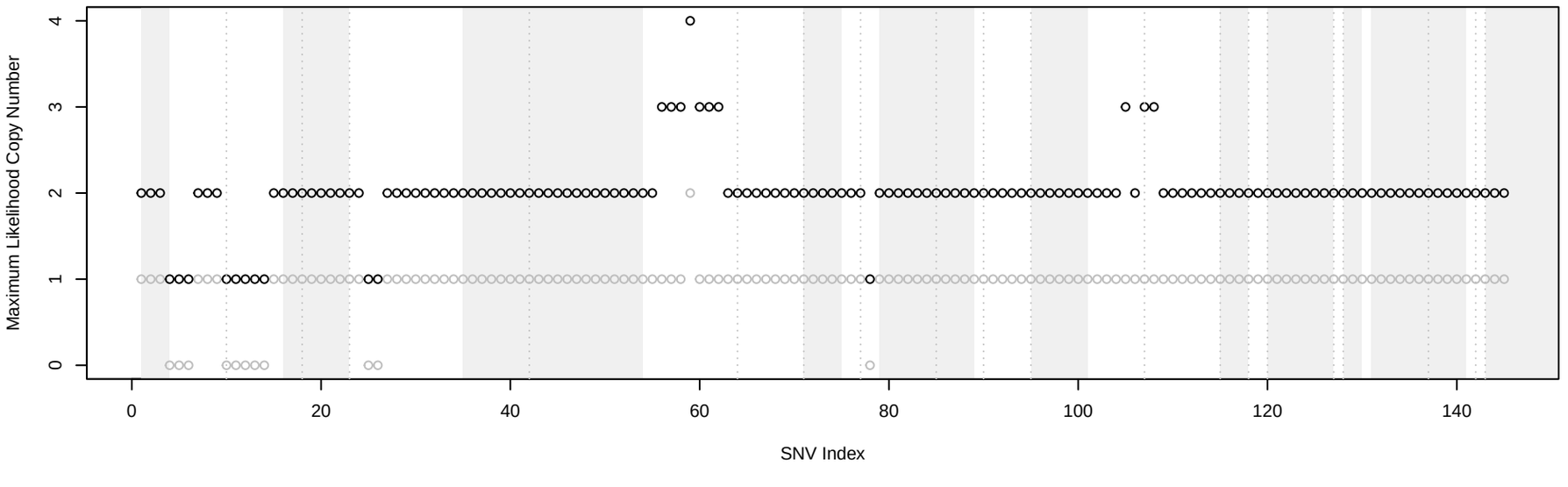

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1

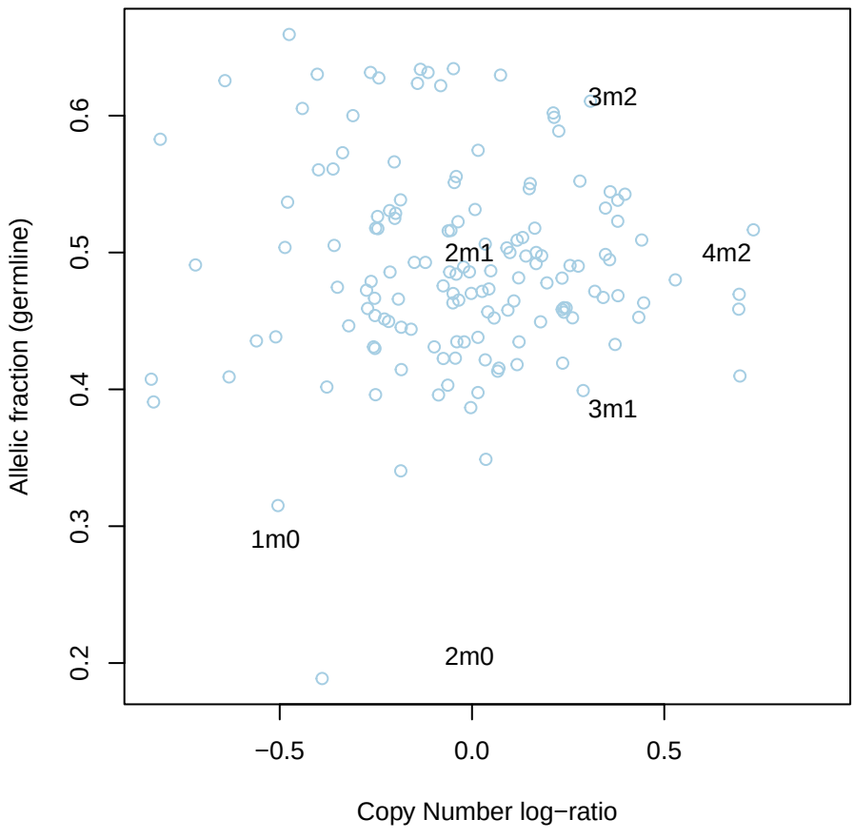

Power 0.8
Frequency
Cellular fraction

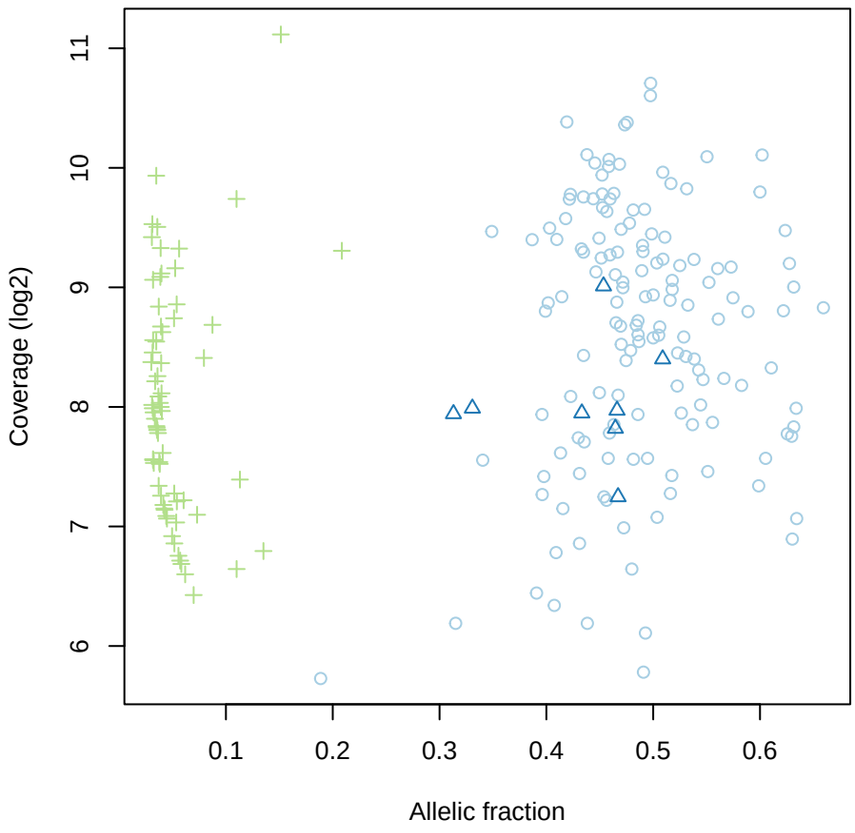

Purity: 0.59 Tumor ploidy: 2.015
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

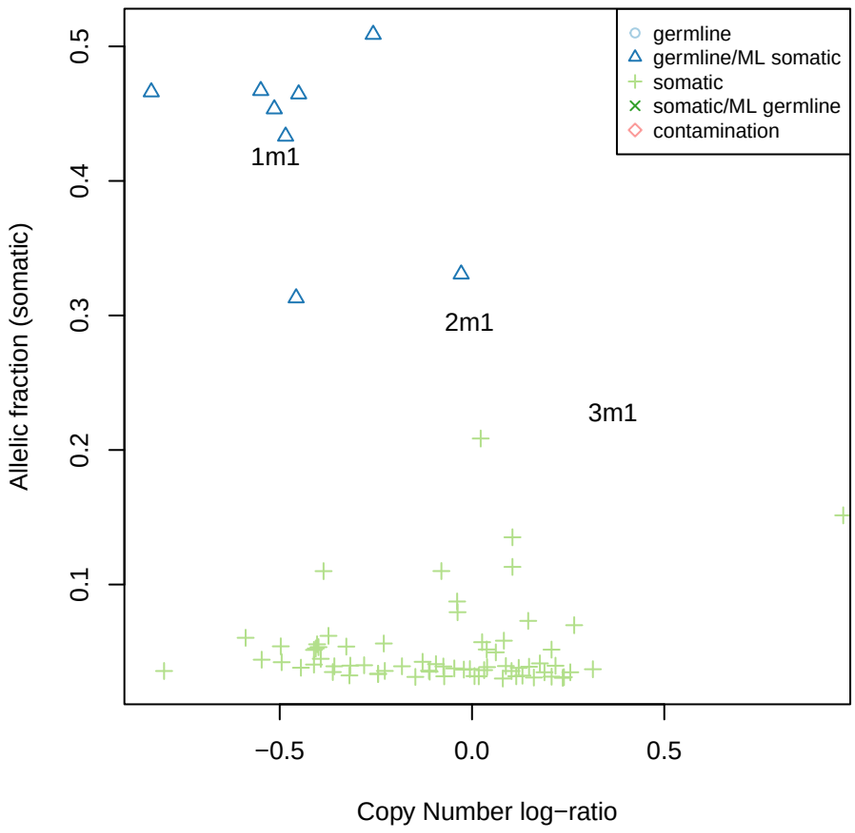

Purity: 0.59 Tumor ploidy: 2.015 SNV log−likelihood: −480.08 GoF: 41.4% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 20 40 60 80 100 120 140
SNV Index

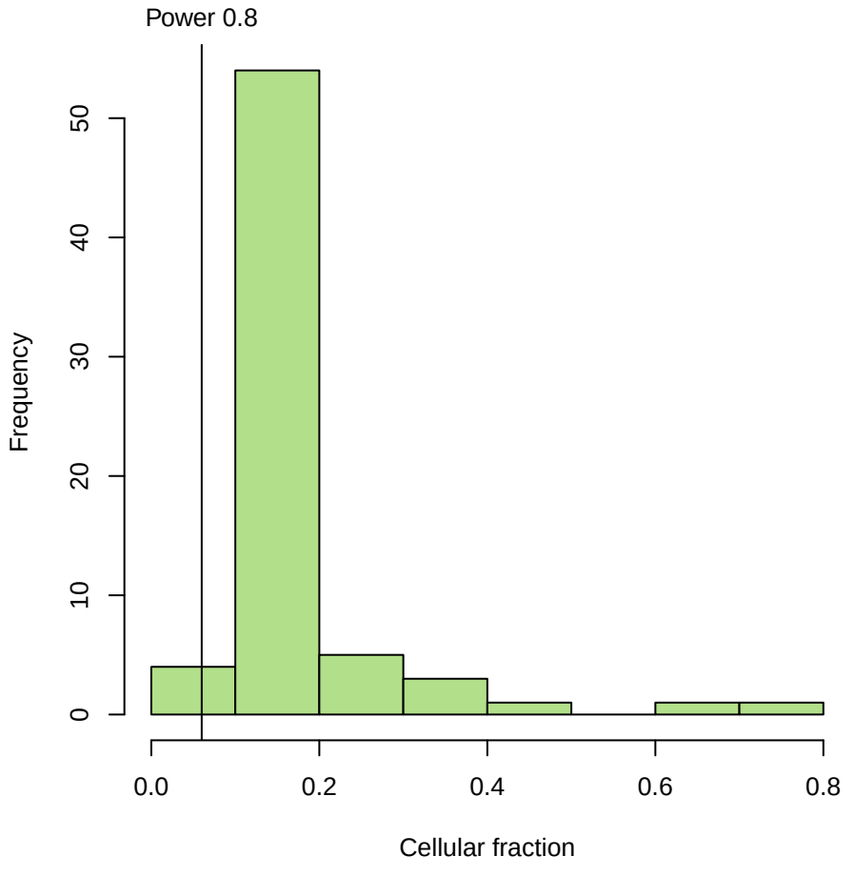

SCNA−fit log−likelihood: −7659.12
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

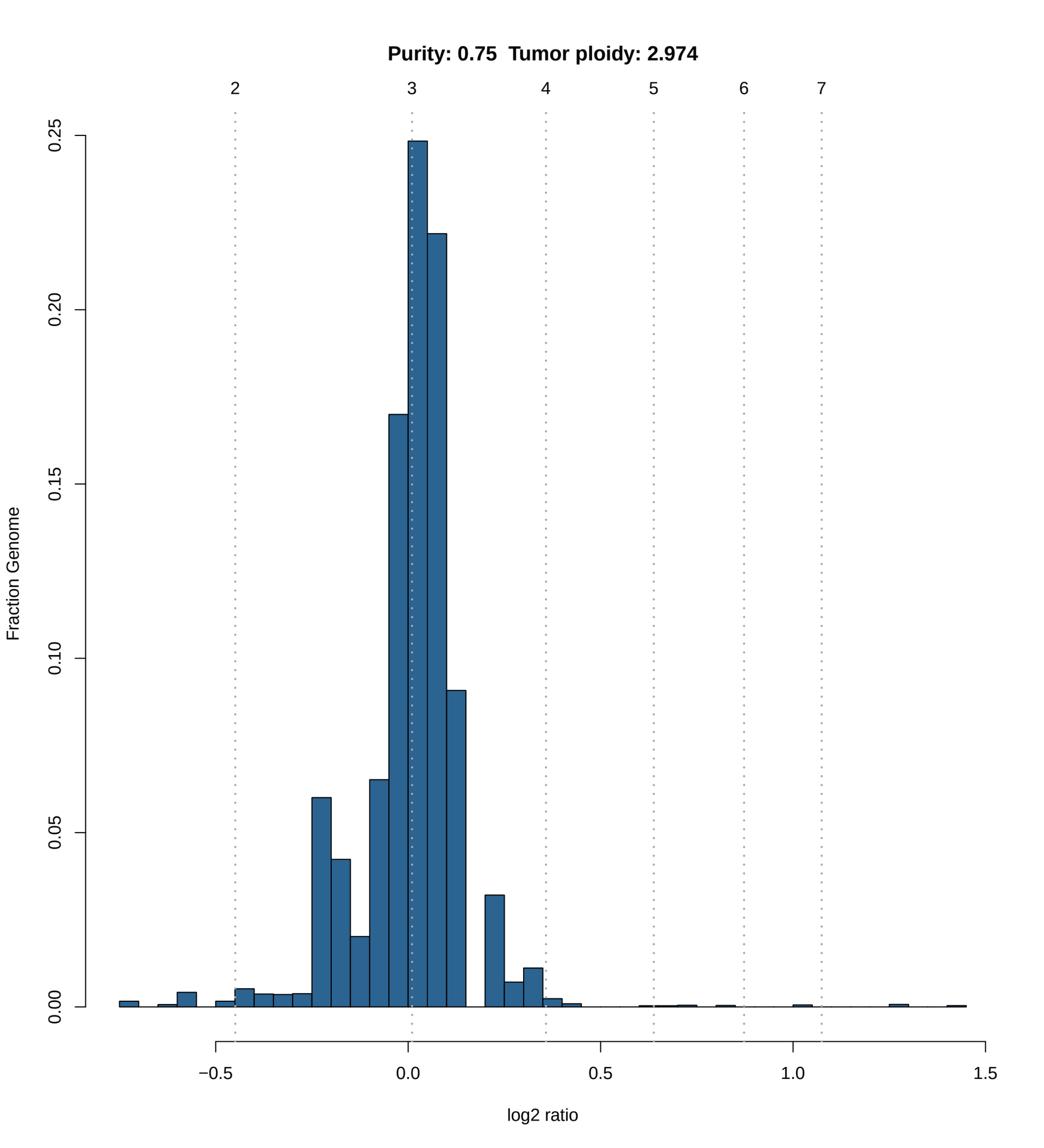

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120 140
SNV Index

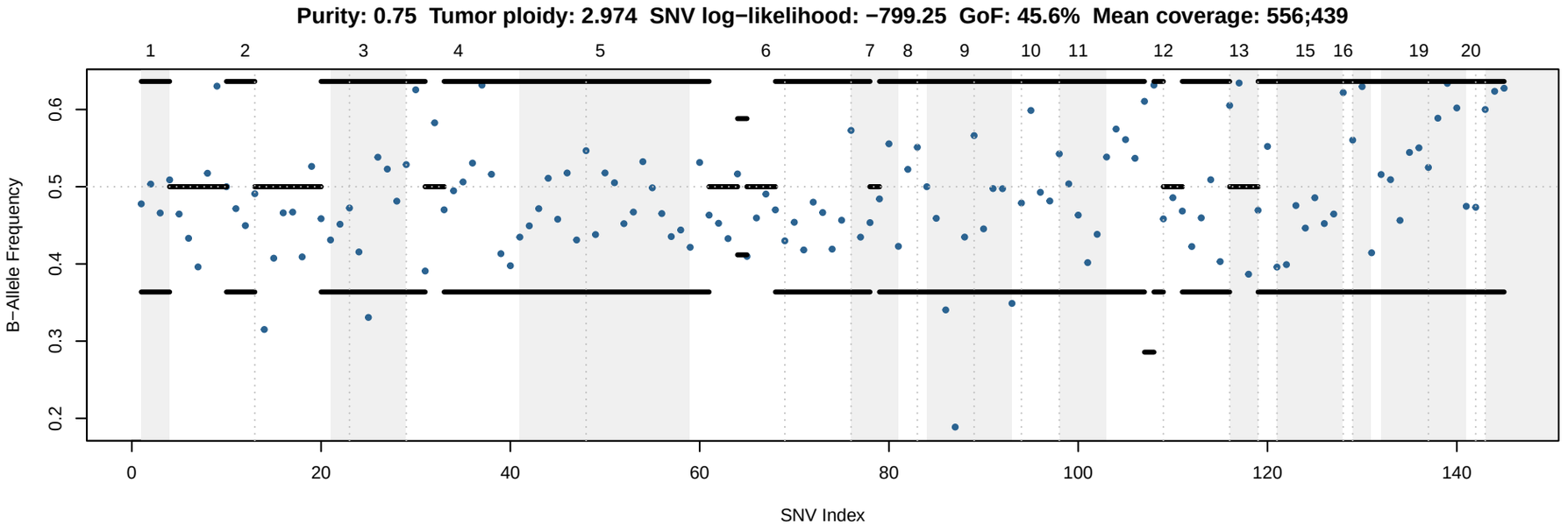

Allelic fraction (germline)
Copy Number log−ratio
3m2
2m1
4m2
3m1
1m0
2m0

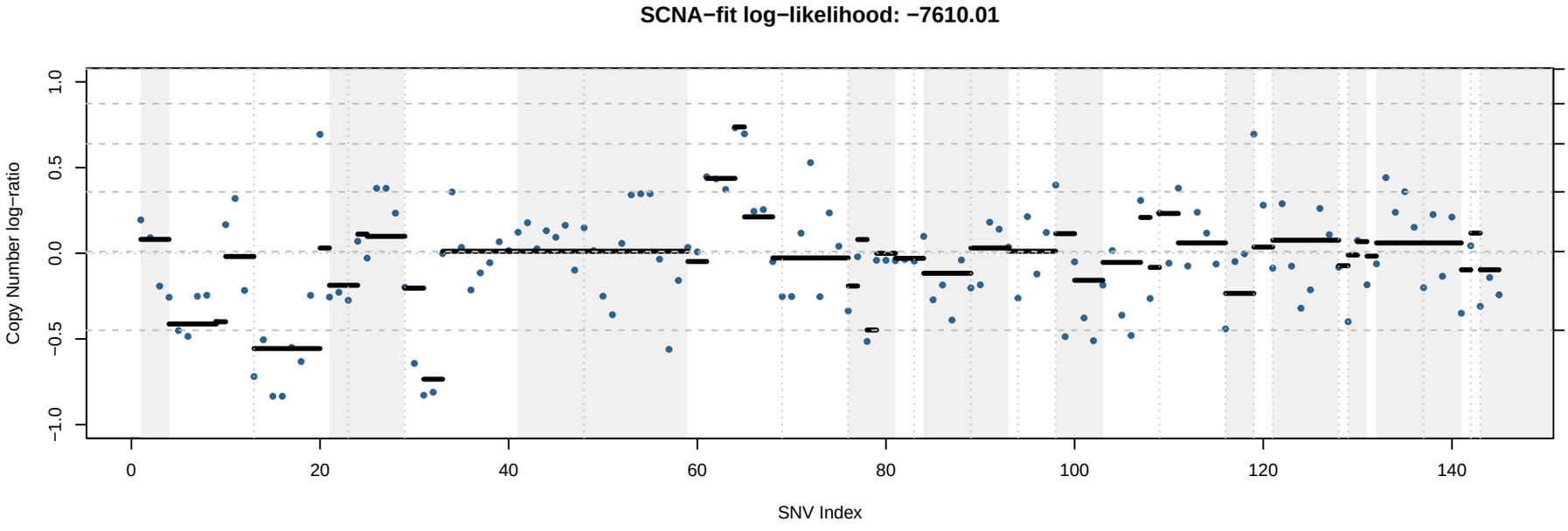

Coverage (log2)
Allelic fraction

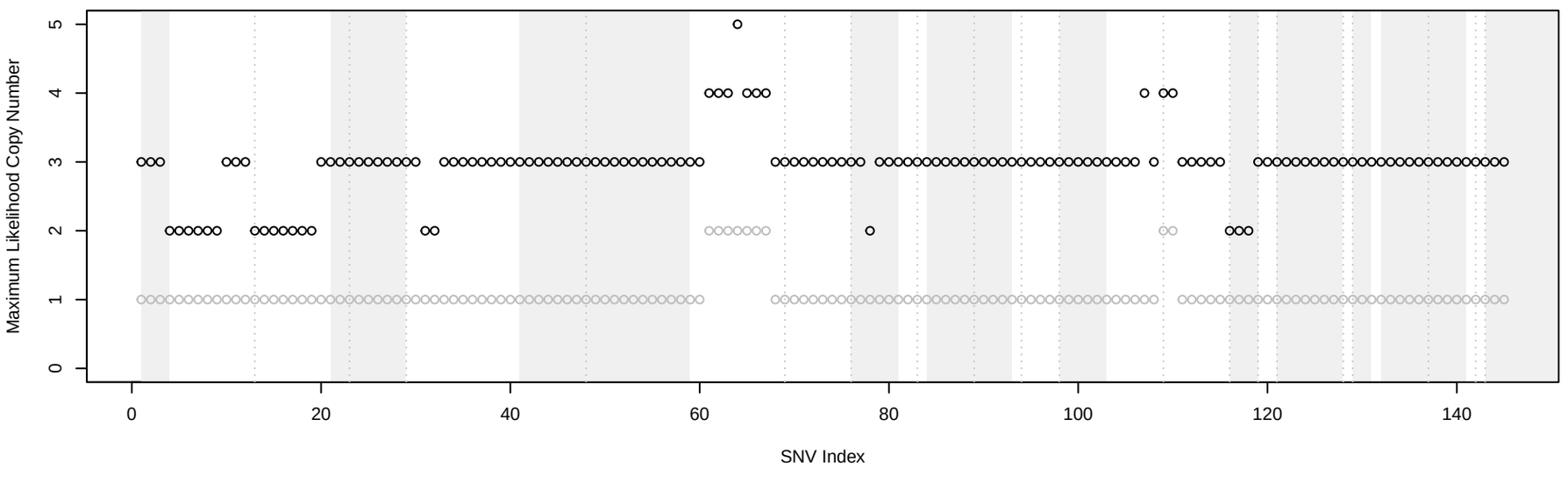

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1

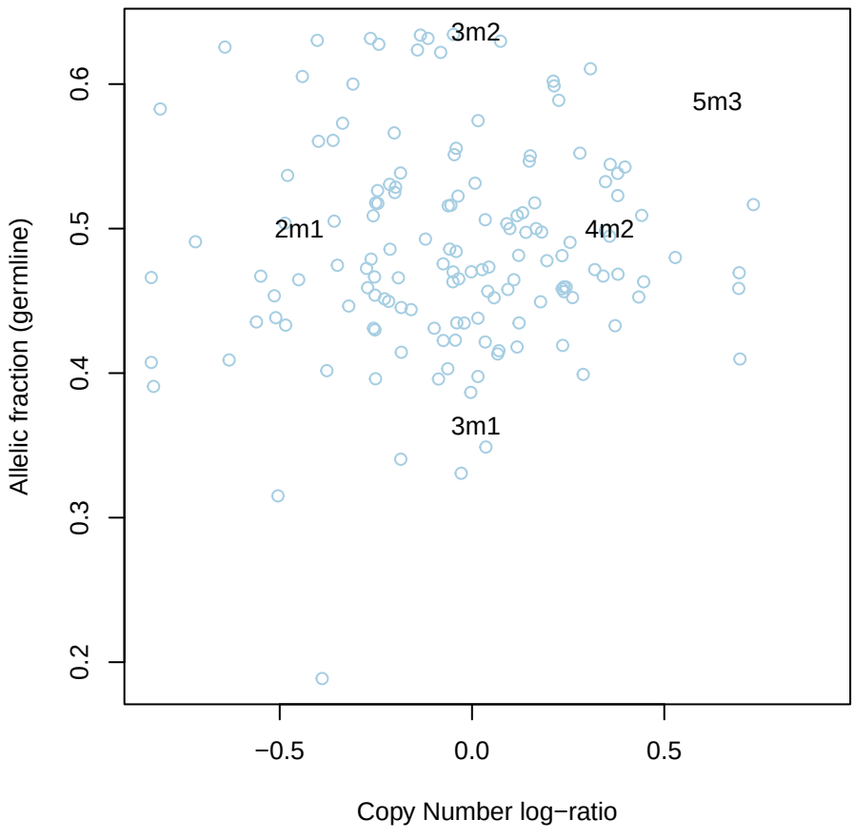

Power 0.8
Frequency
Cellular fraction

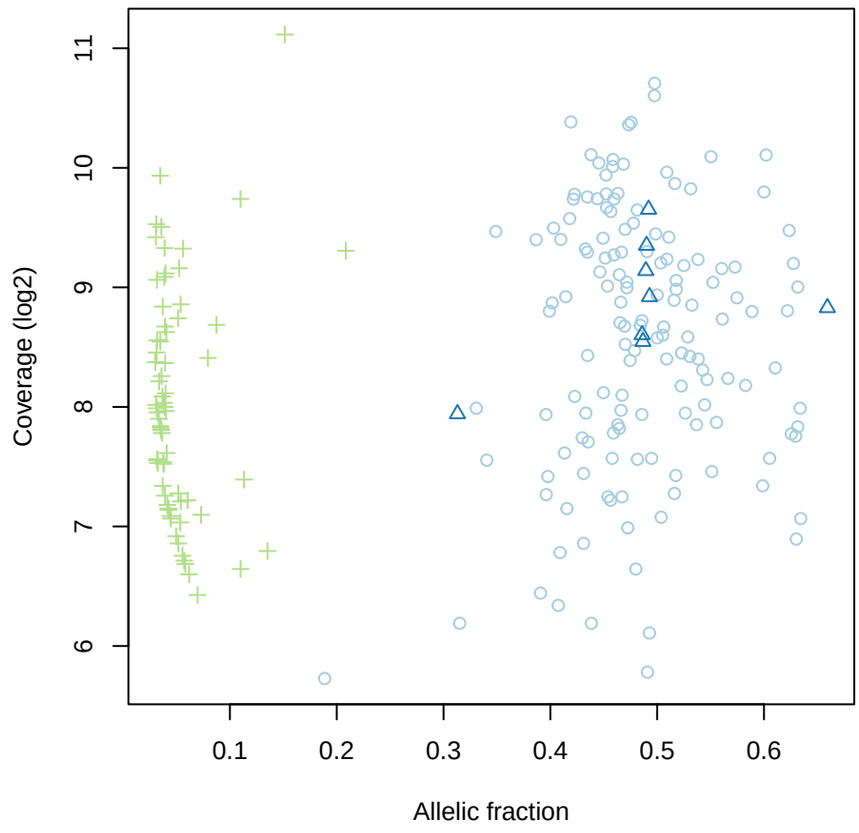

Purity: 0.75 Tumor ploidy: 2.974
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

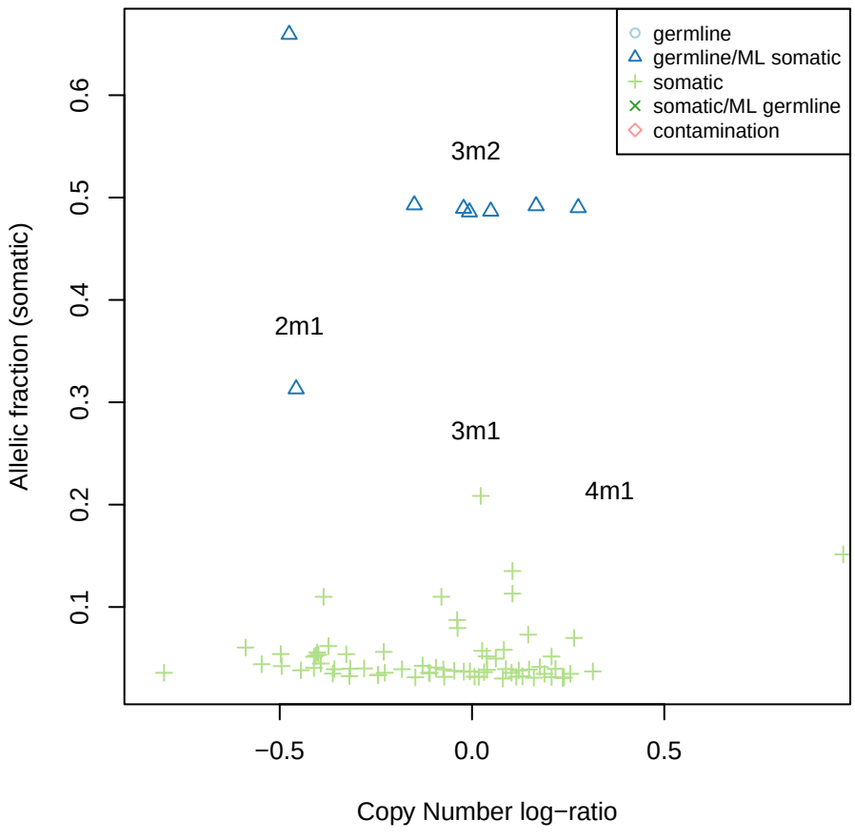

Purity: 0.75 Tumor ploidy: 2.974 SNV log−likelihood: −799.25 GoF: 45.6% Mean coverage: 556;439
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 20 40 60 80 100 120 140
SNV Index

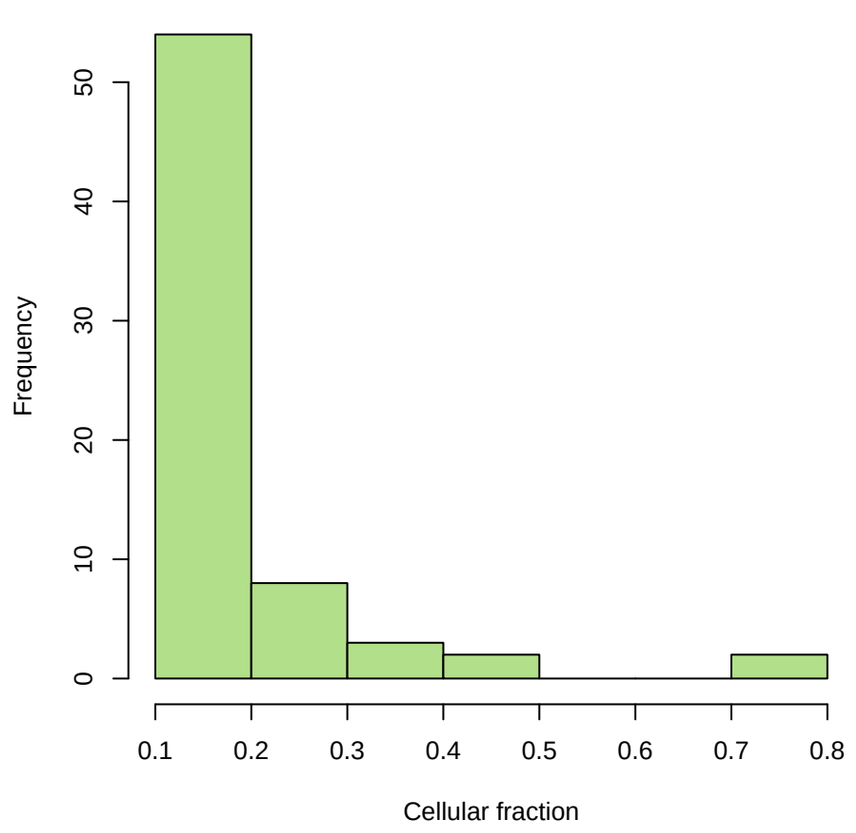

SCNA−fit log−likelihood: −7610.01
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index


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