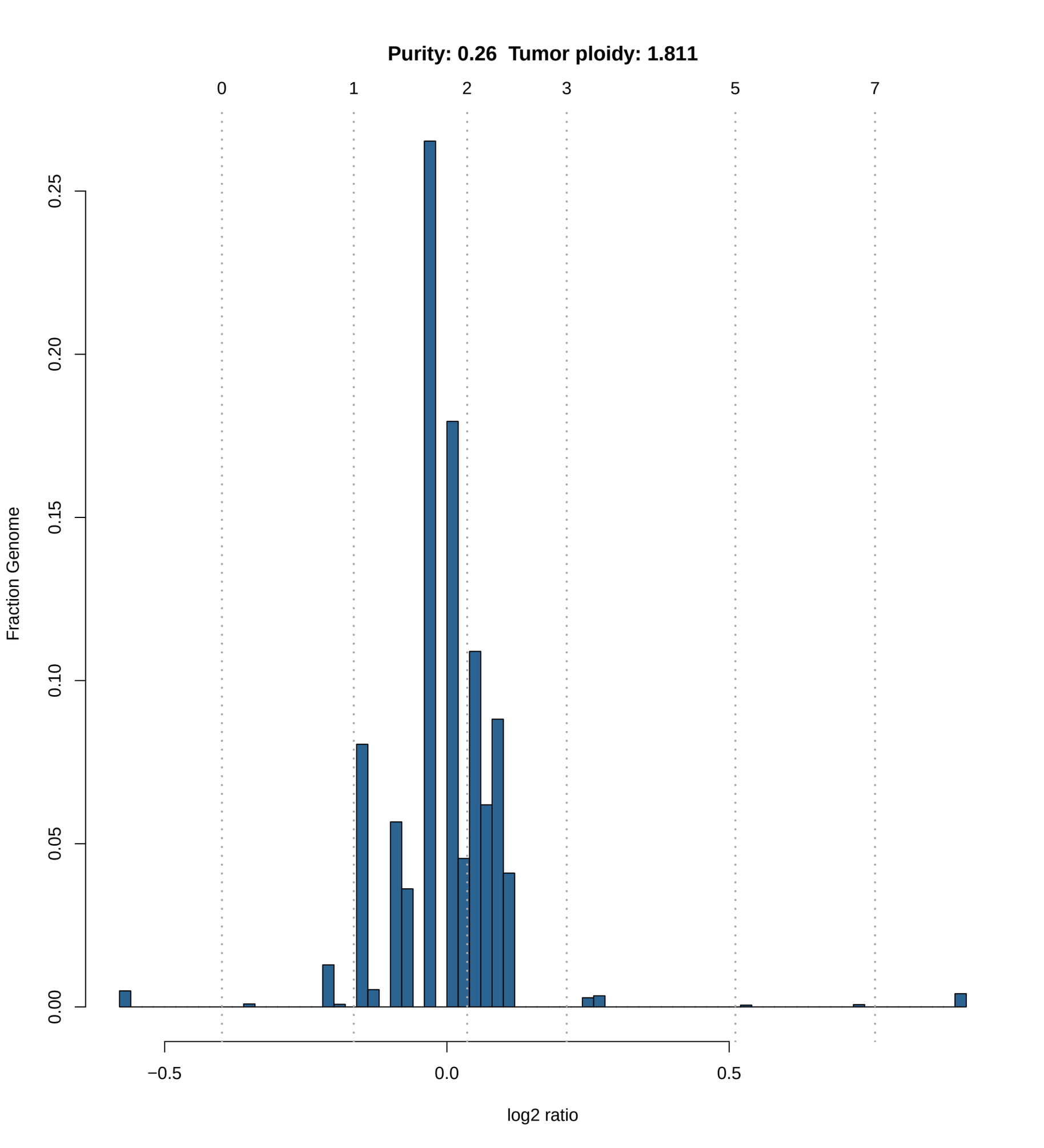
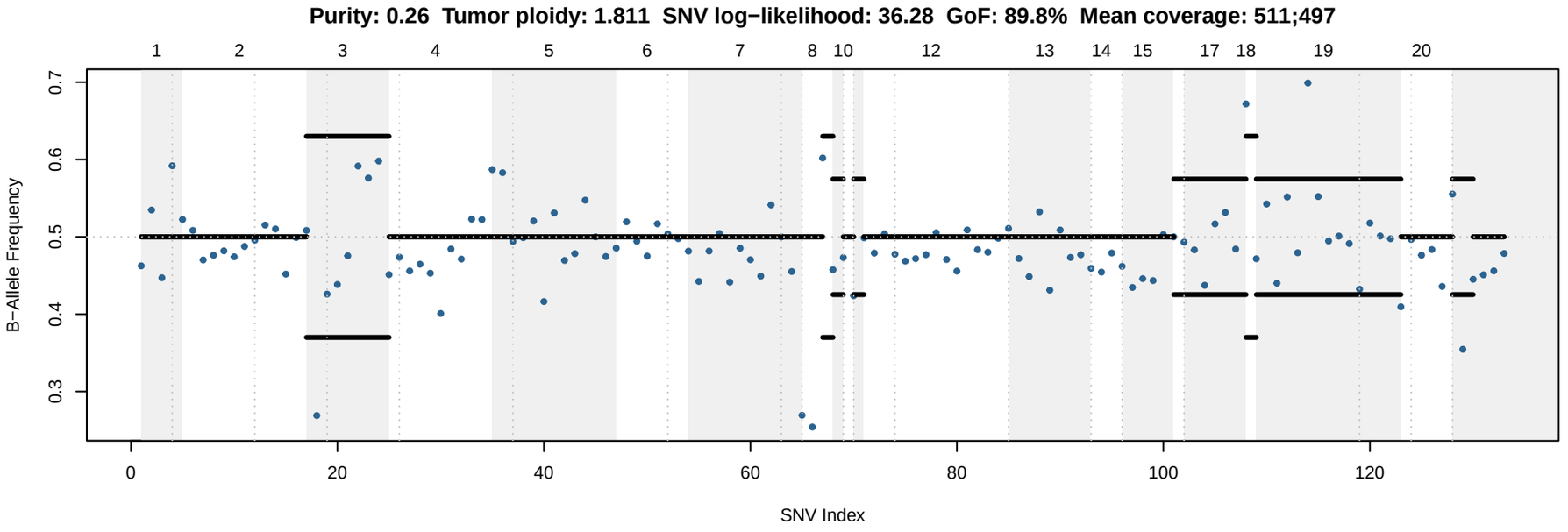
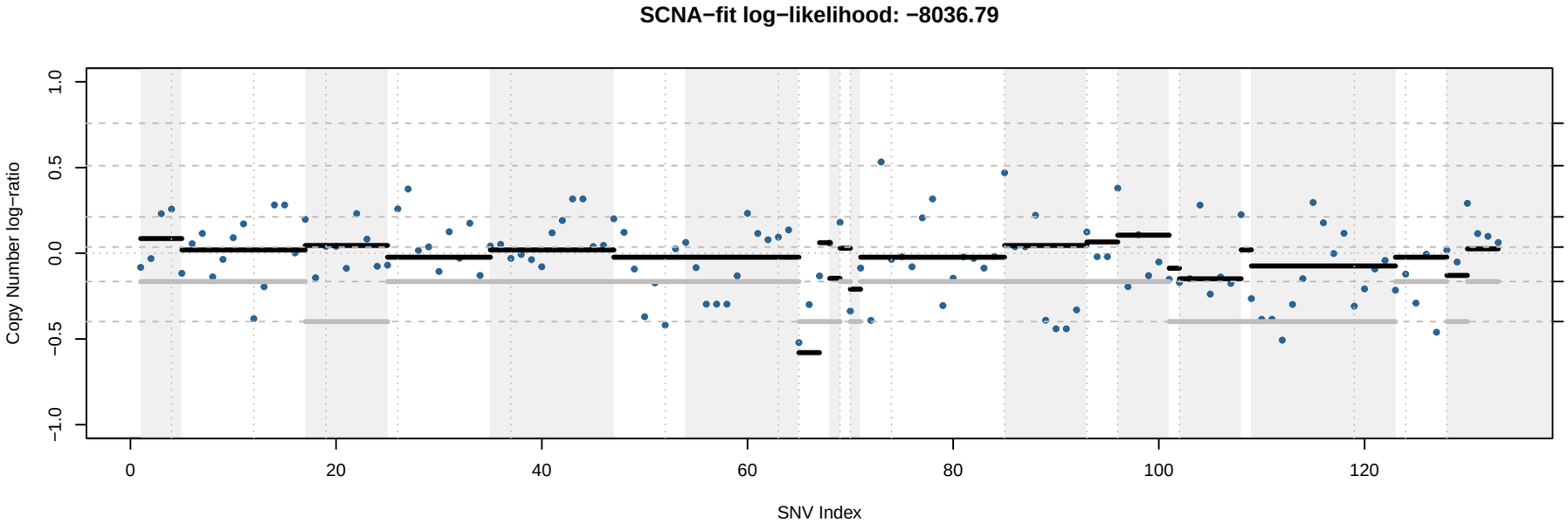
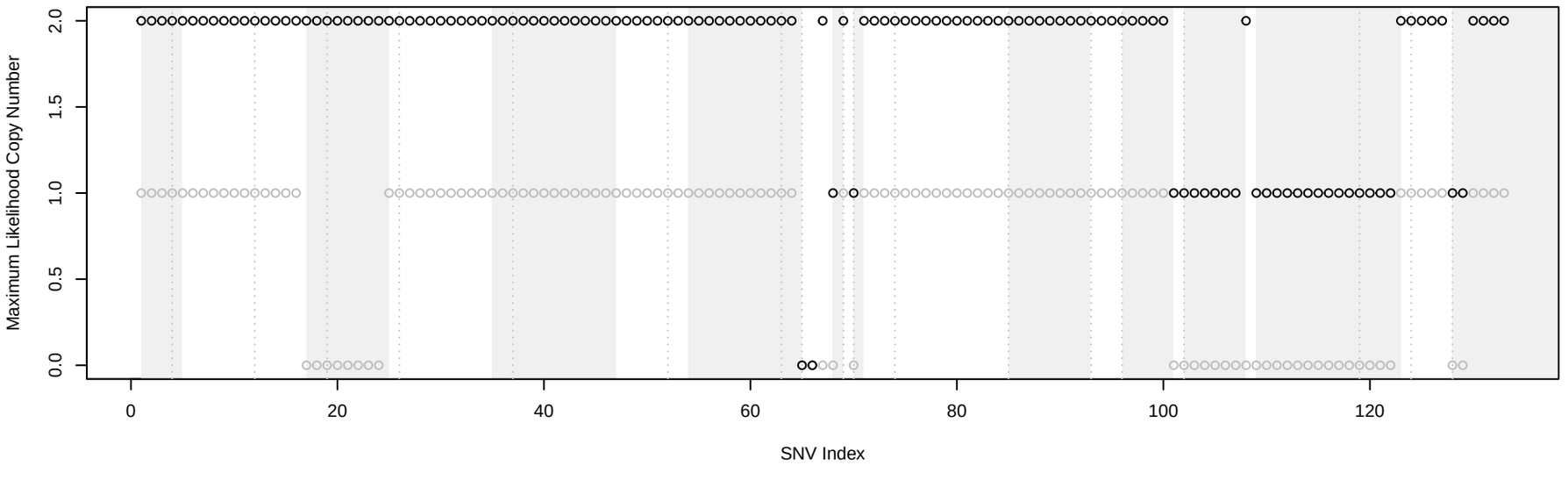
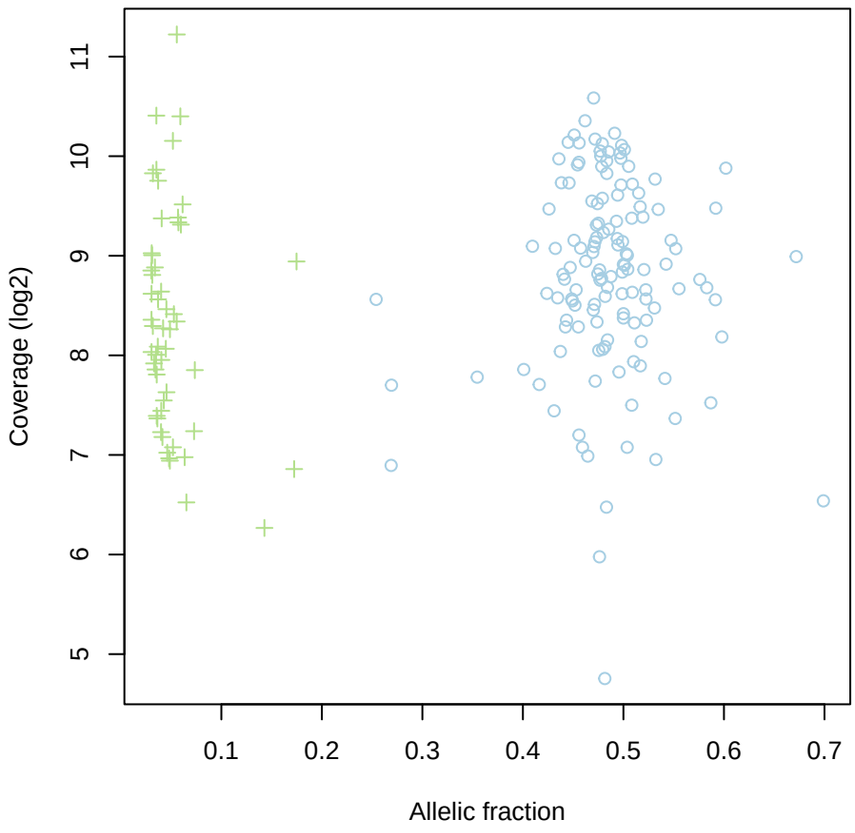

Purity: 0.26 Tumor ploidy: 1.811
0
1
2
3
5
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

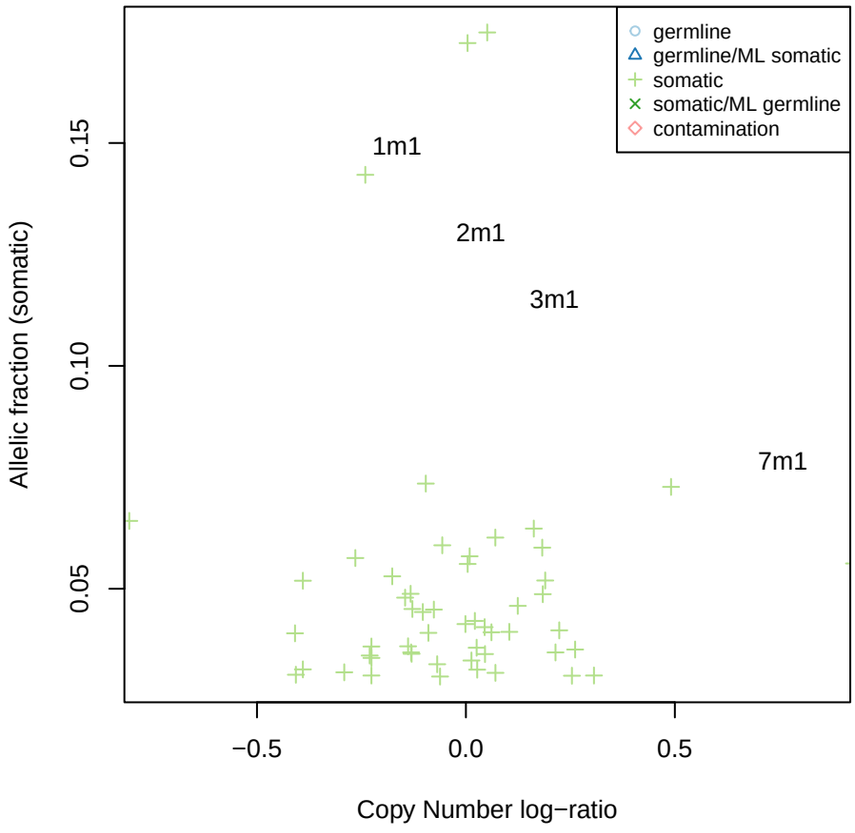

Purity: 0.26 Tumor ploidy: 1.811 SNV log−likelihood: 36.28 GoF: 89.8% Mean coverage: 511;497
1 2 3 4 5 6 7 8 10 12 13 14 15 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

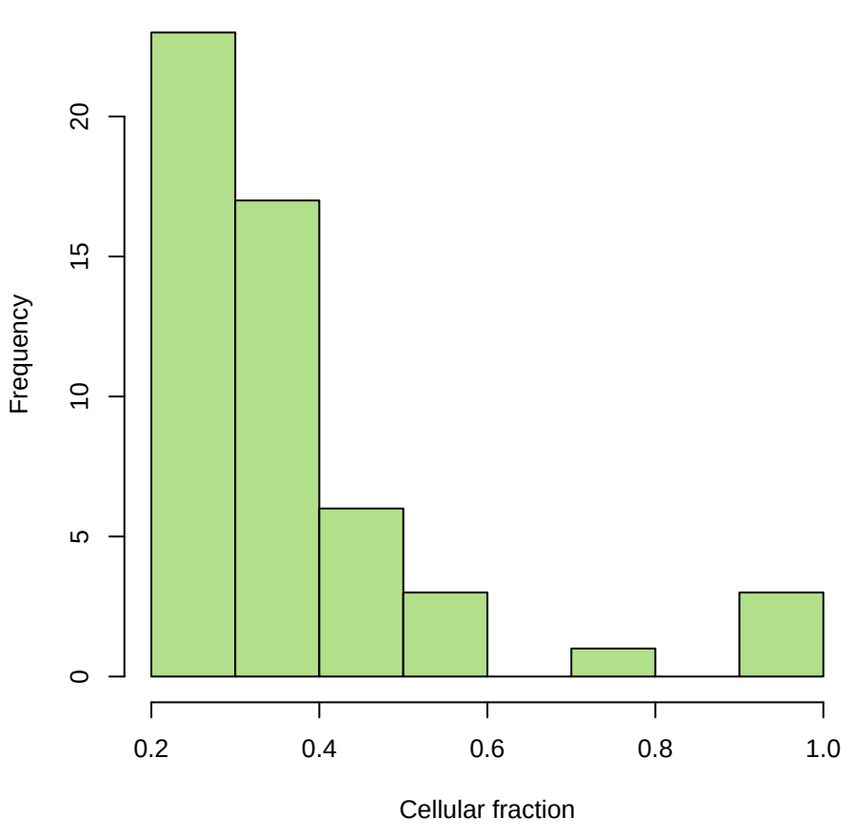

SCNA−fit log−likelihood: −8036.79
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 5 7
0 20 40 60 80 100 120
SNV Index

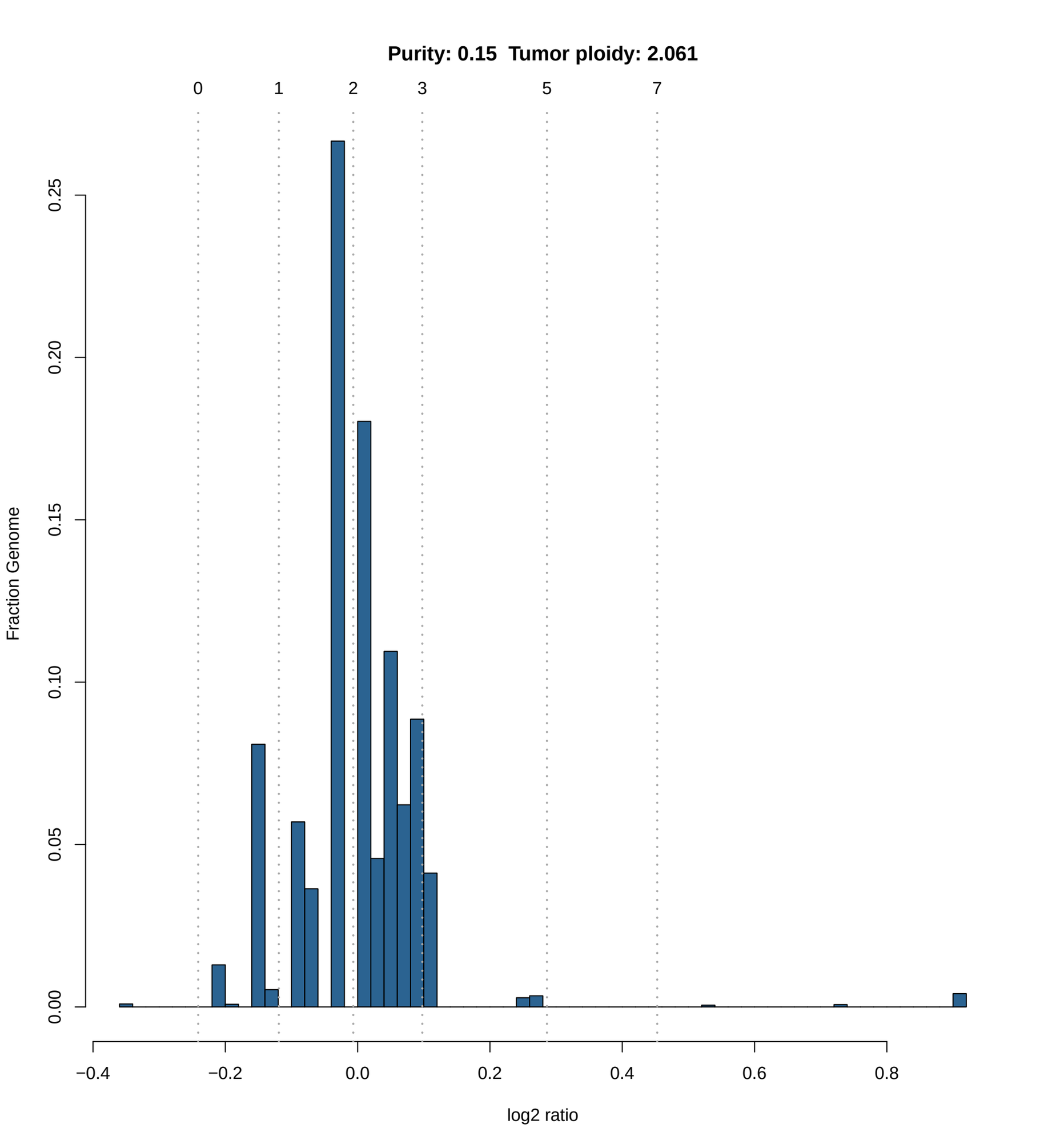

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 20 40 60 80 100 120
SNV Index

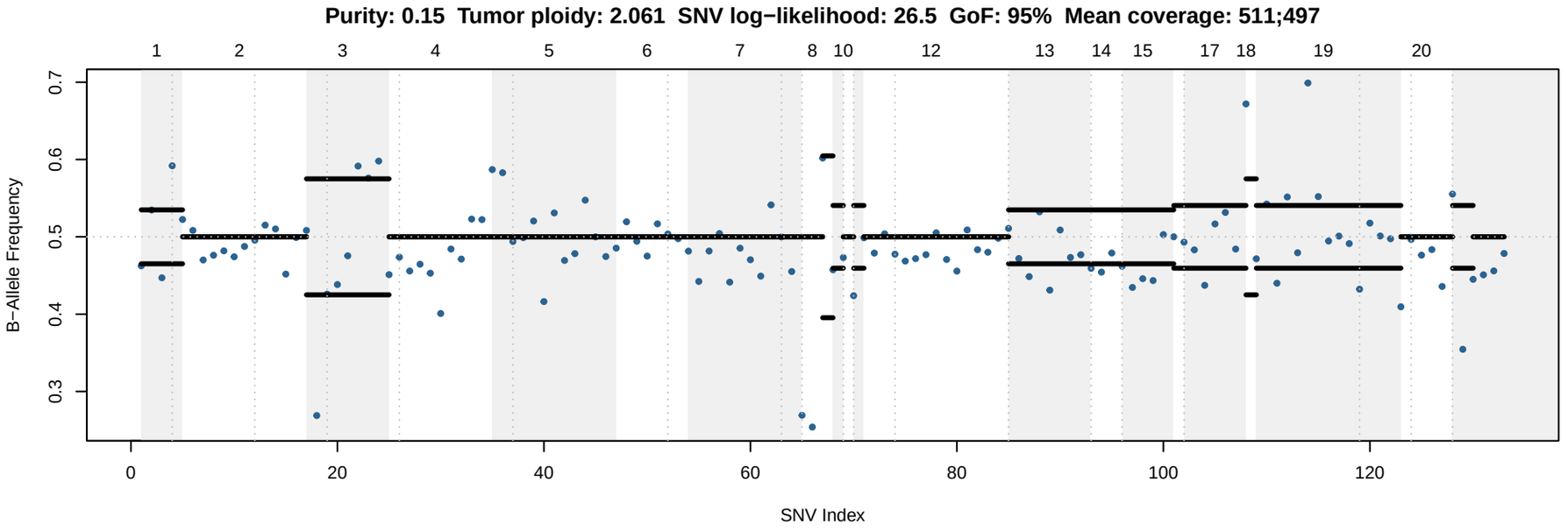
Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
−0.5
0.0
0.5
Copy Number log−ratio
2m2
1m1
0m0
2m1
1m0
2m0

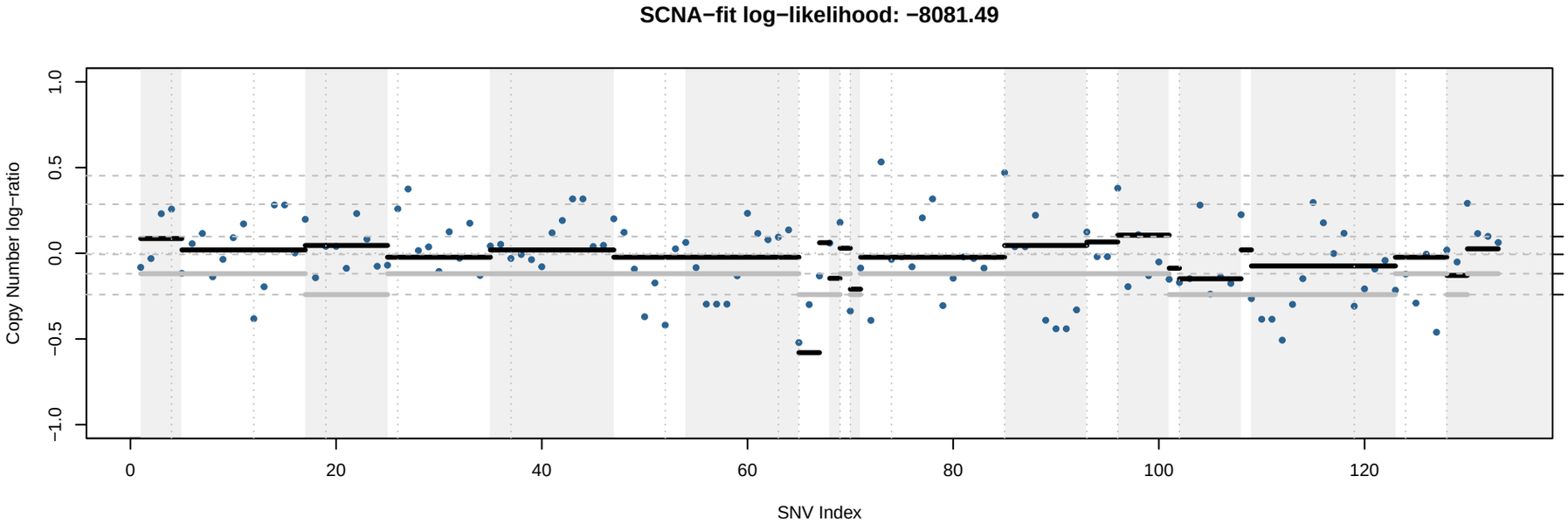

Coverage (log2)
5
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

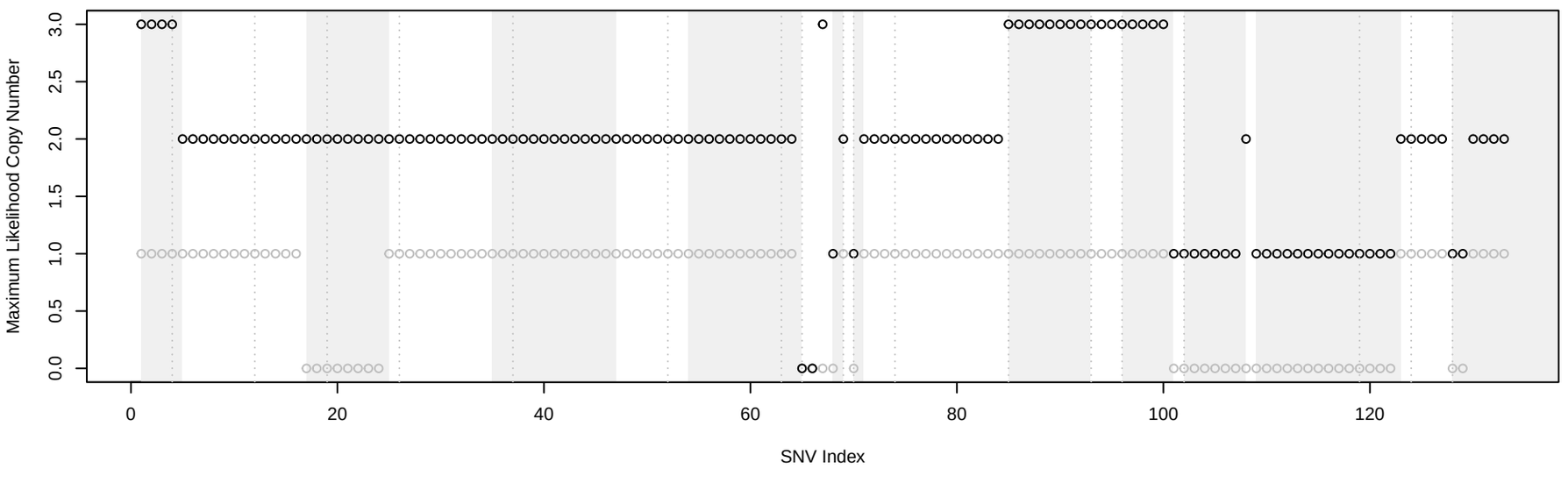

Allelic fraction (somatic)
0.05
0.10
0.15
−0.5
0.0
0.5
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
7m1

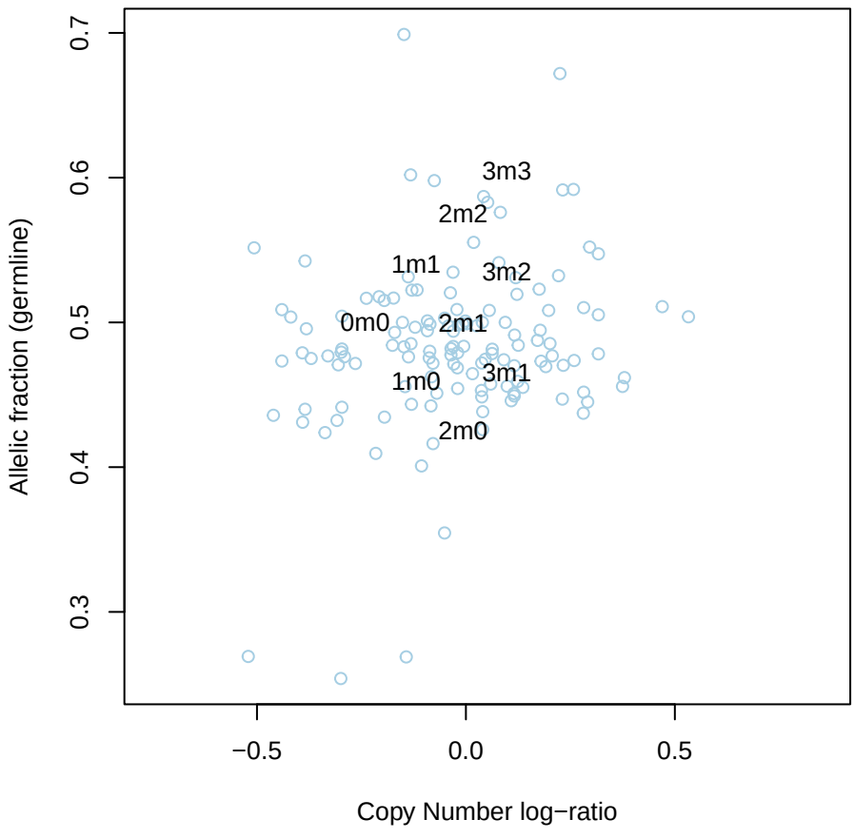

Frequency
0
5
10
15
20
0.2
0.4
0.6
0.8
1.0
Cellular fraction

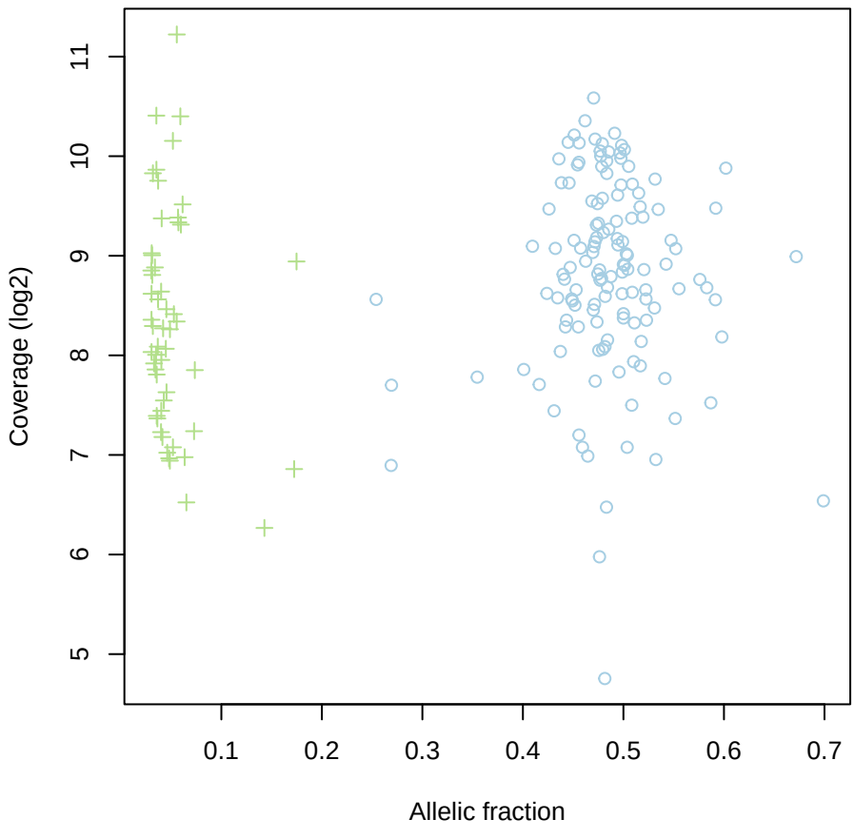

Purity: 0.15 Tumor ploidy: 2.061
0
1
2
3
5
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
log2 ratio

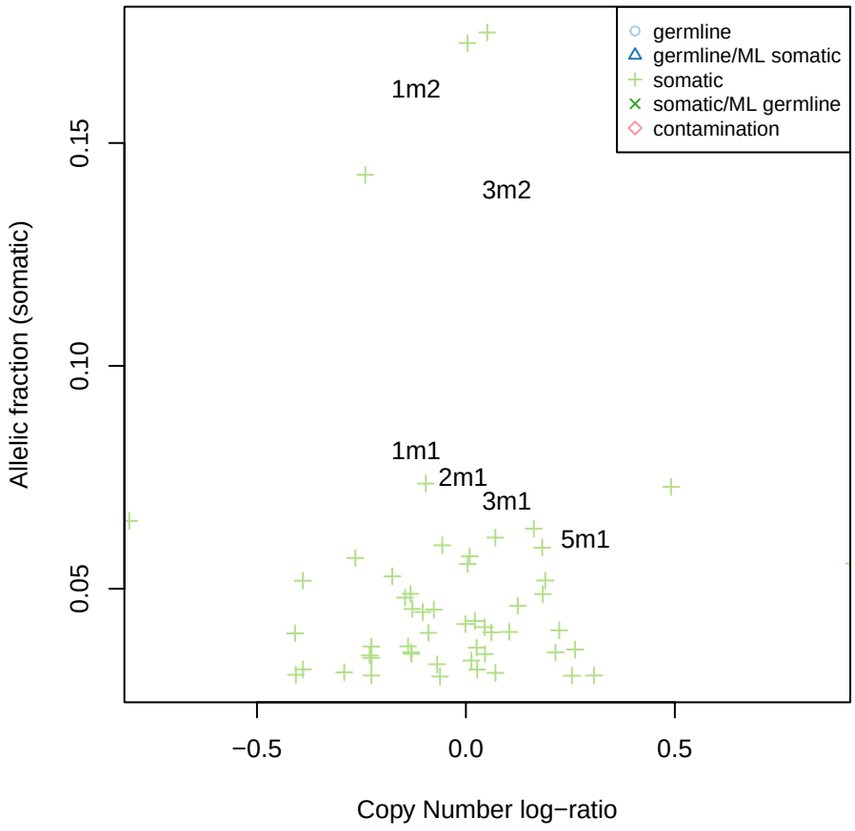

Purity: 0.15 Tumor ploidy: 2.061 SNV log−likelihood: 26.5 GoF: 95% Mean coverage: 511;497
1 2 3 4 5 6 7 8 10 12 13 14 15 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

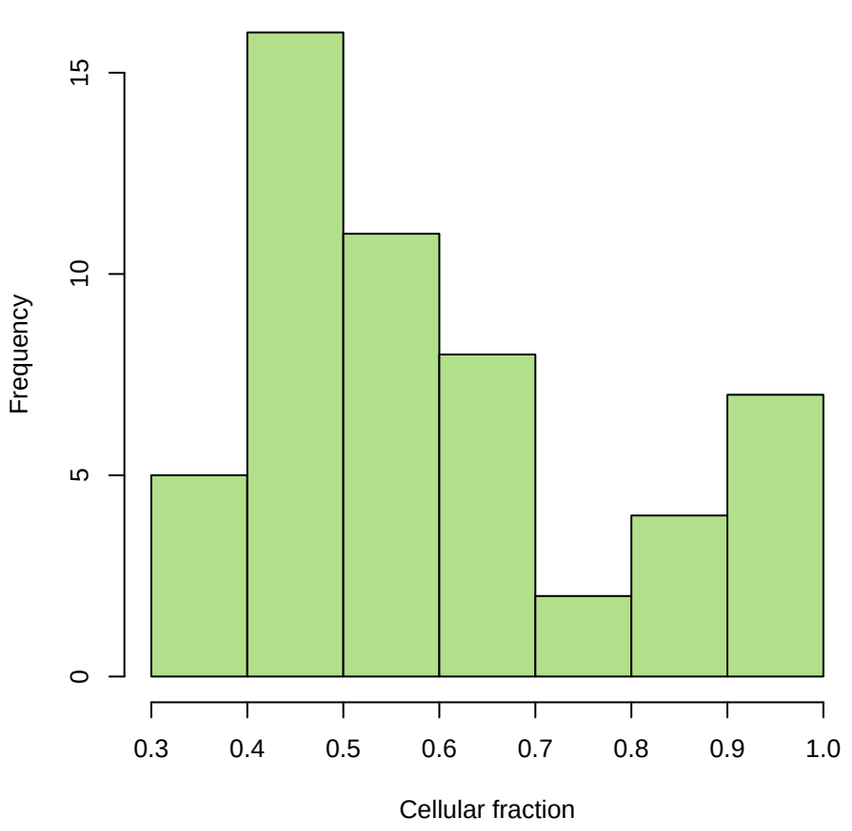

SCNA−fit log−likelihood: −8081.49
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 5 7
0 20 40 60 80 100 120
SNV Index

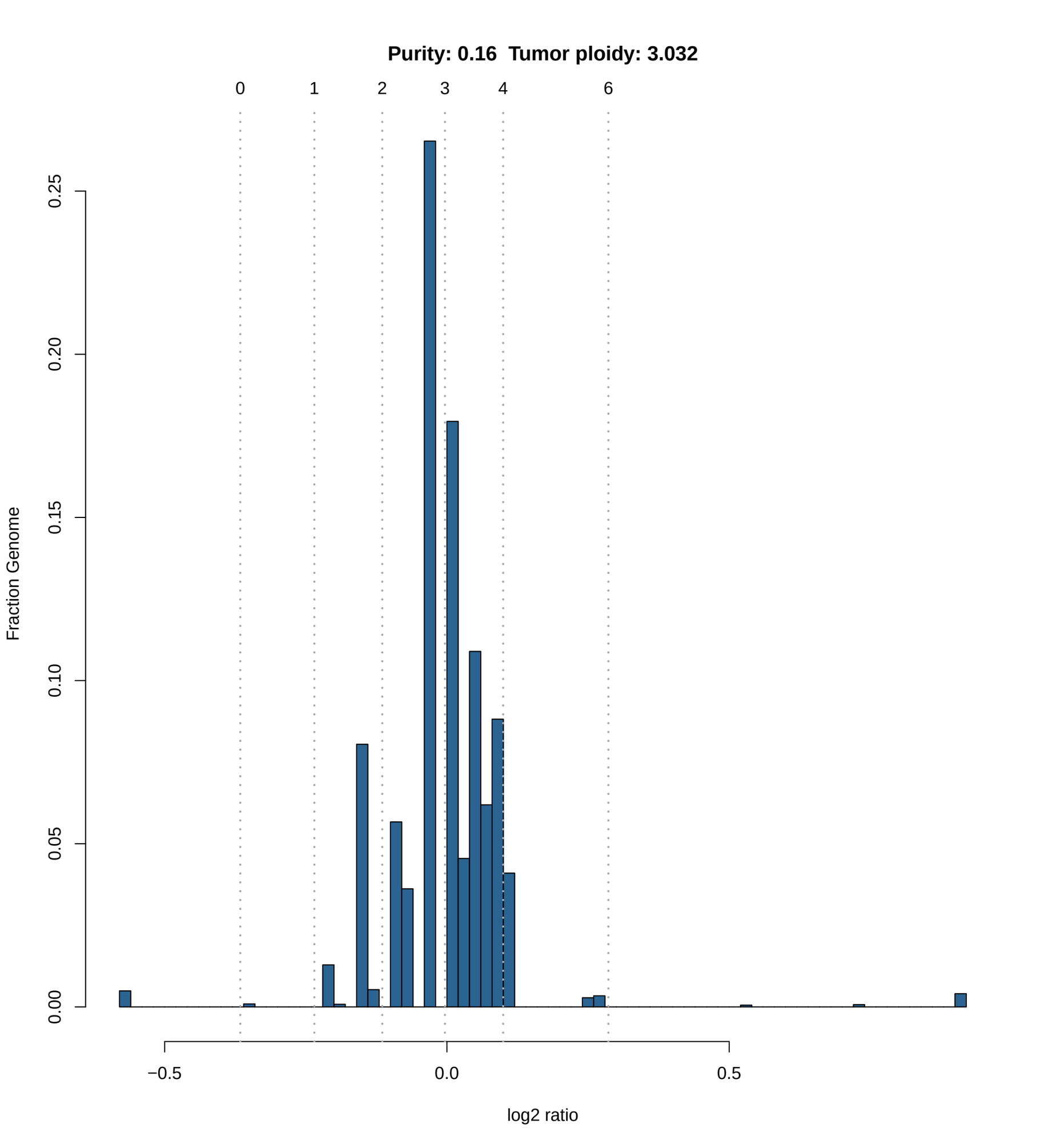

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120
SNV Index

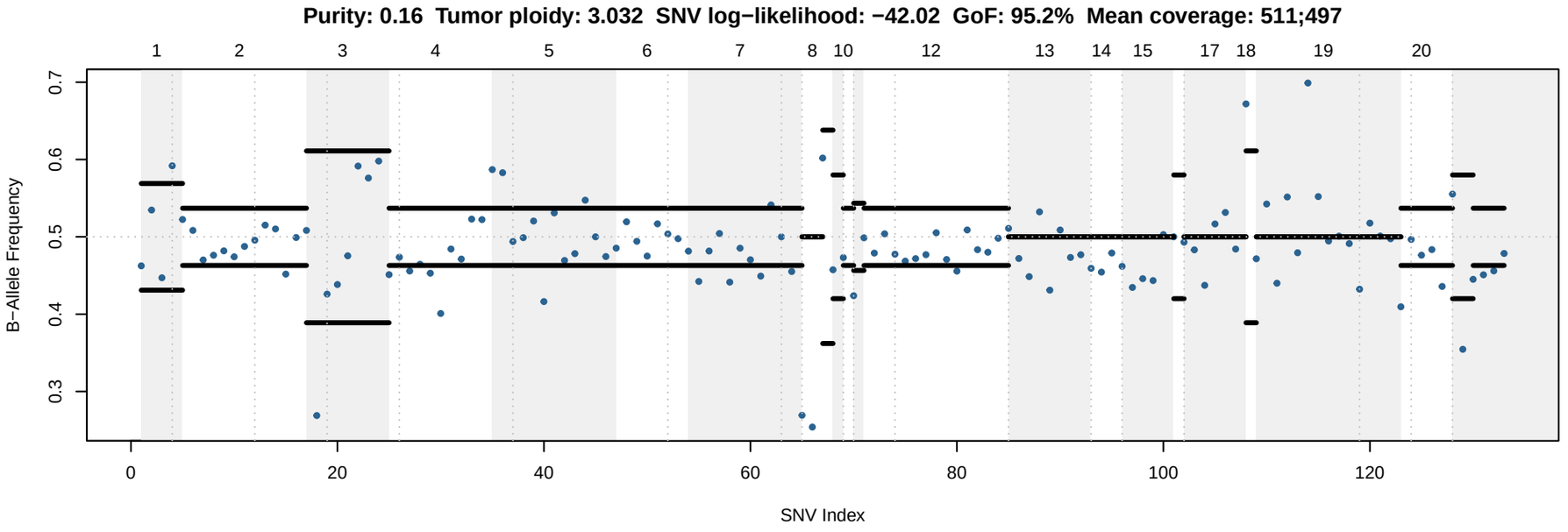

Allelic fraction (germline)
Copy Number log−ratio
3m3
2m2
1m1
3m2
0m0
2m1
3m1
1m0
2m0

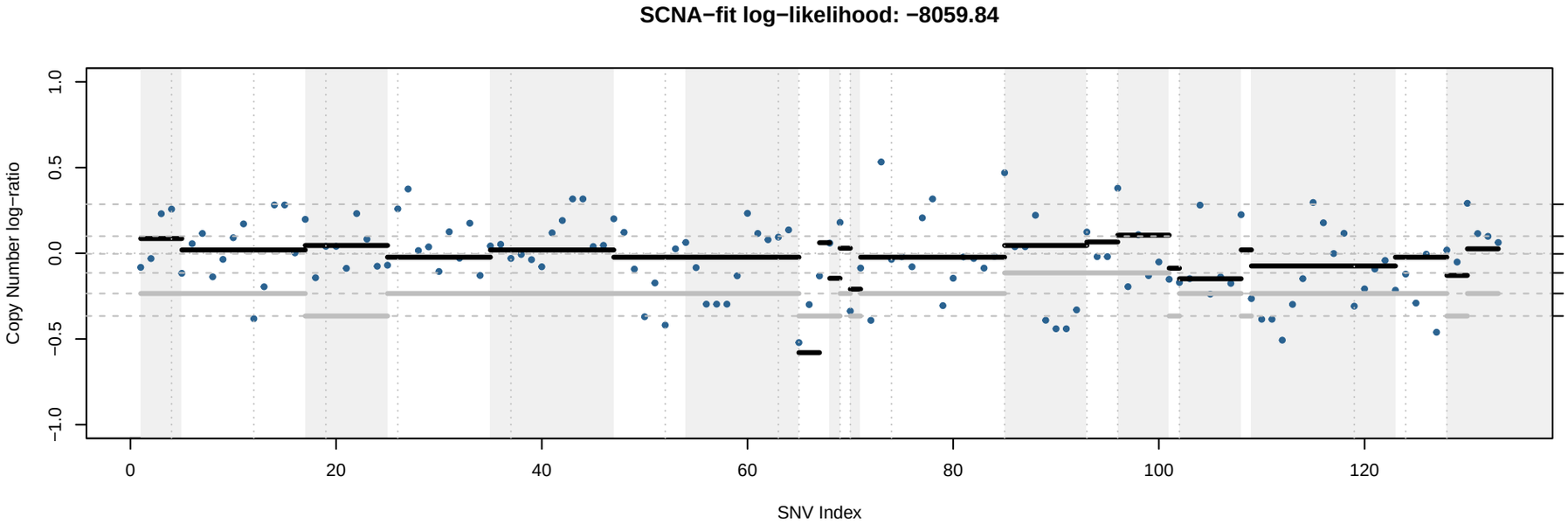

Coverage (log2)
Allelic fraction

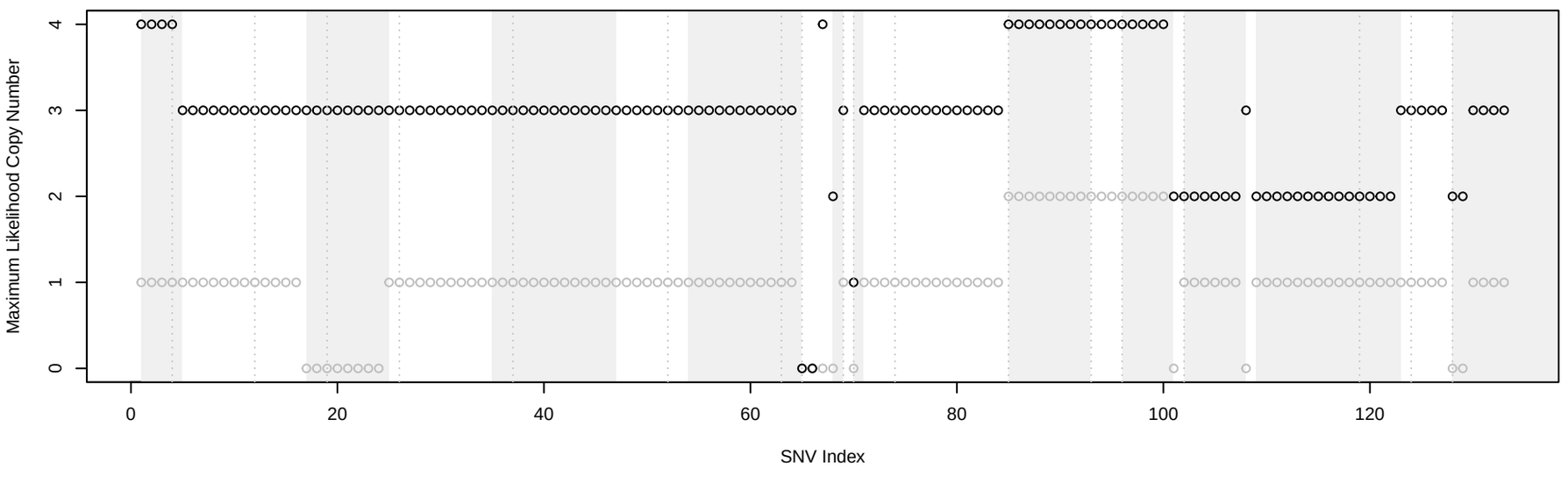

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m2
3m2
1m1
2m1
3m1
5m1


Frequency
Cellular fraction

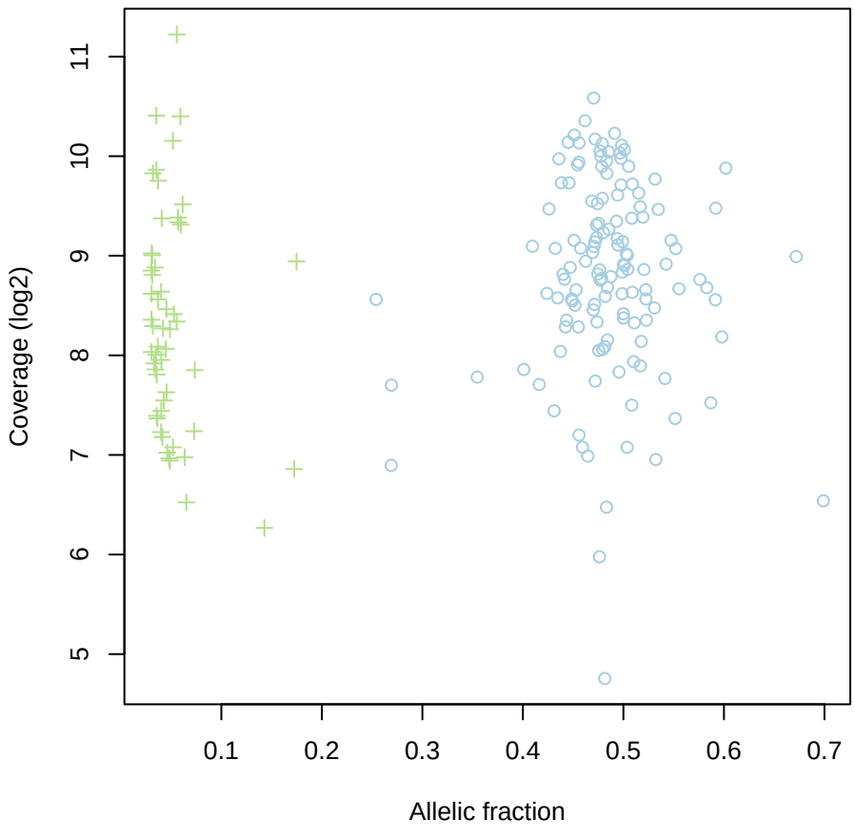

Purity: 0.16 Tumor ploidy: 3.032
0
1
2
3
4
6
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

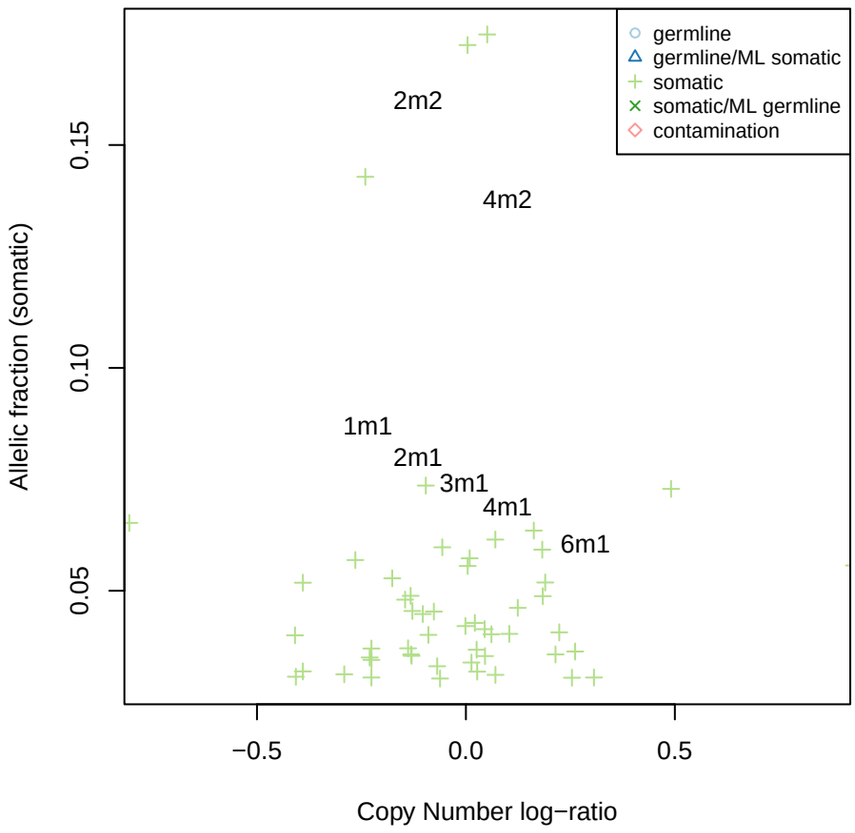

Purity: 0.16 Tumor ploidy: 3.032 SNV log−likelihood: −42.02 GoF: 95.2% Mean coverage: 511;497
1 2 3 4 5 6 7 8 10 12 13 14 15 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

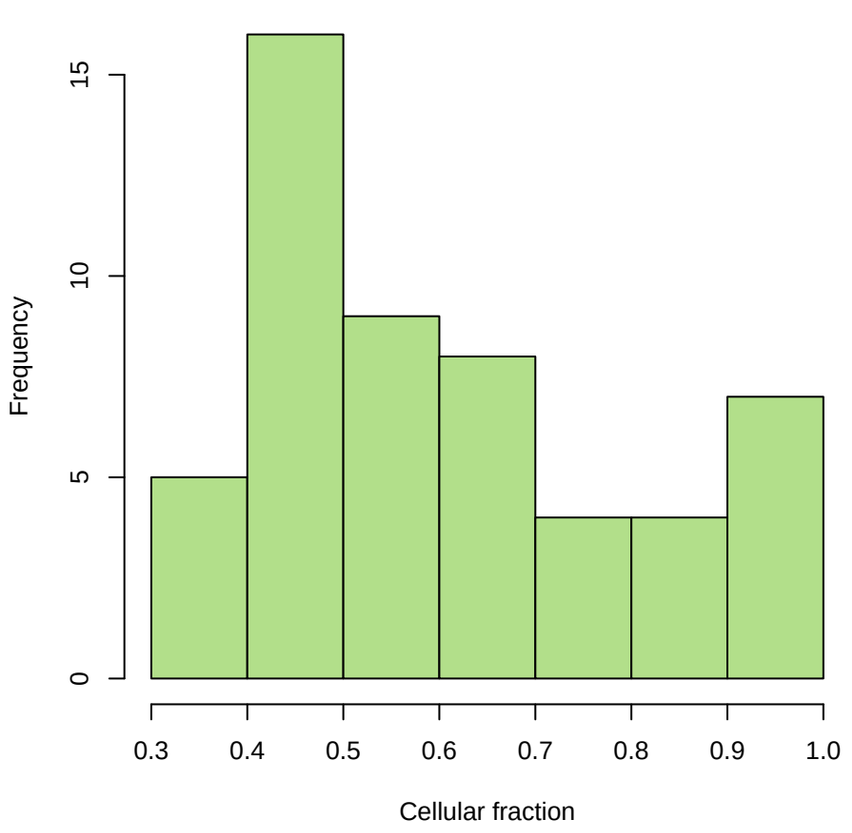

SCNA−fit log−likelihood: −8059.84
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4 6
0 20 40 60 80 100 120
SNV Index

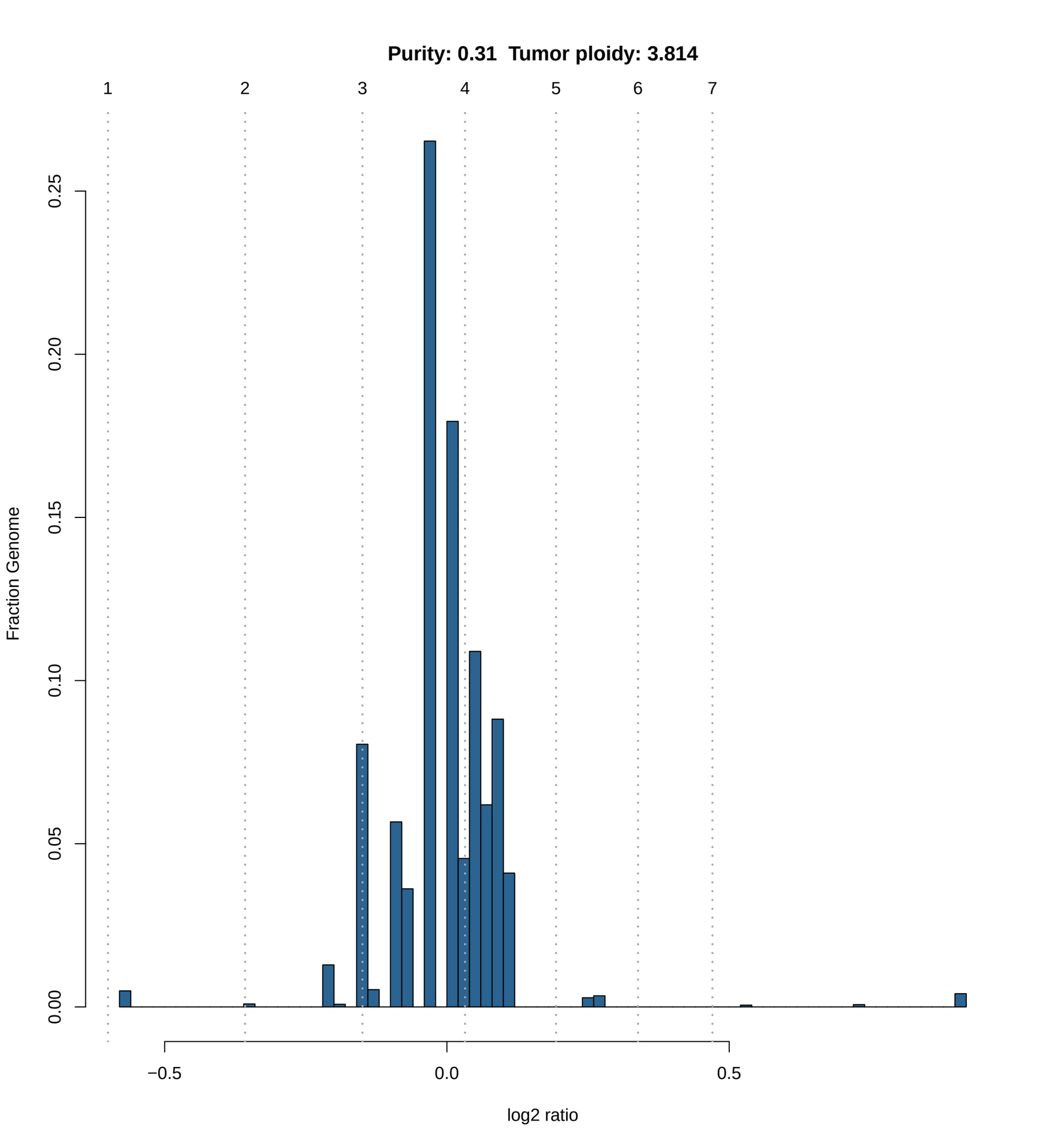

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120
SNV Index

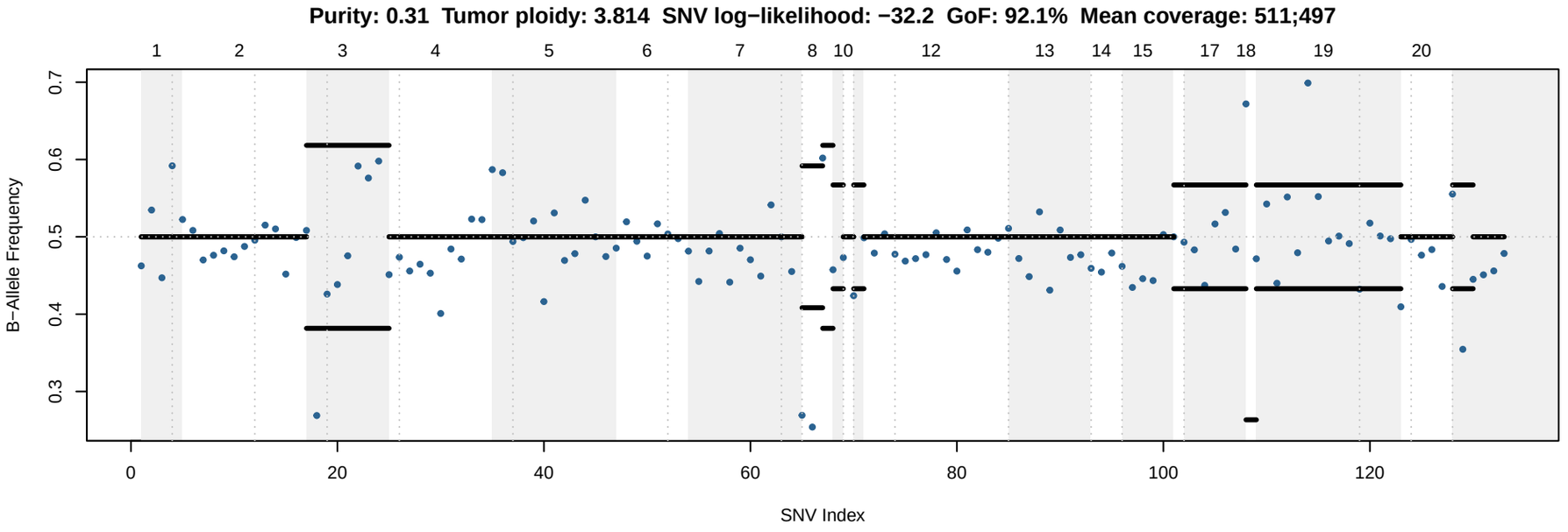
Allelic fraction (germline)
Copy Number log−ratio
4m4
3m3
2m2
4m3
3m2
0m0
2m1
4m2
1m0
3m1
4m1
2m0
3m0

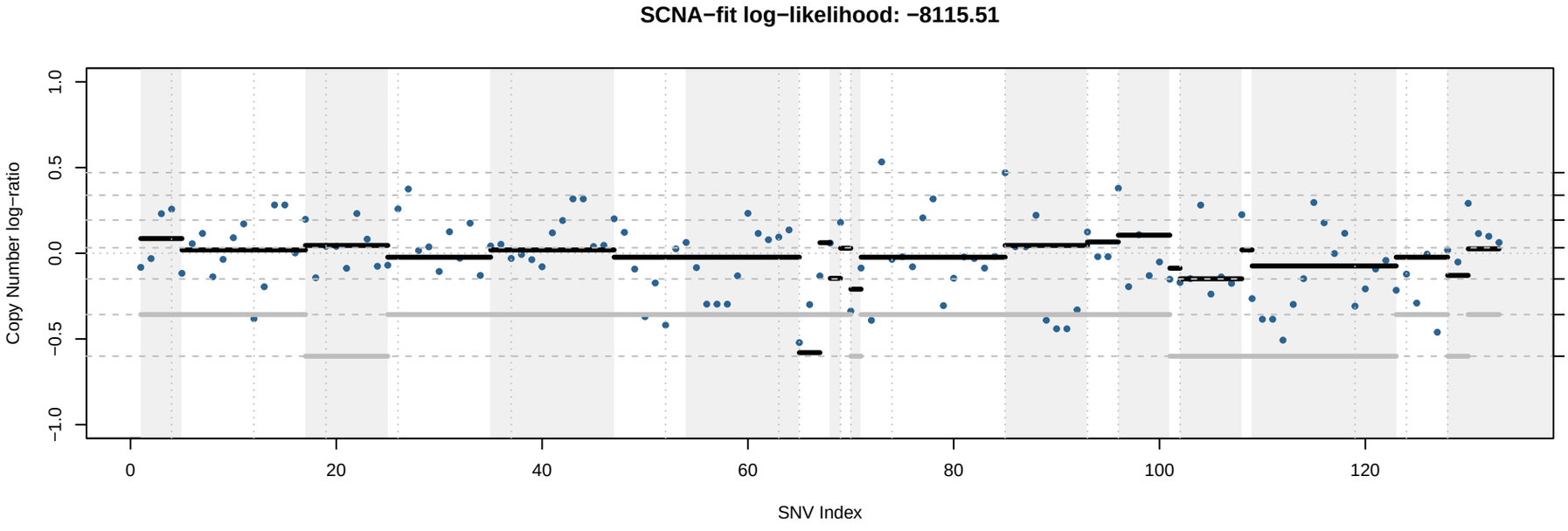

Coverage (log2)
Allelic fraction

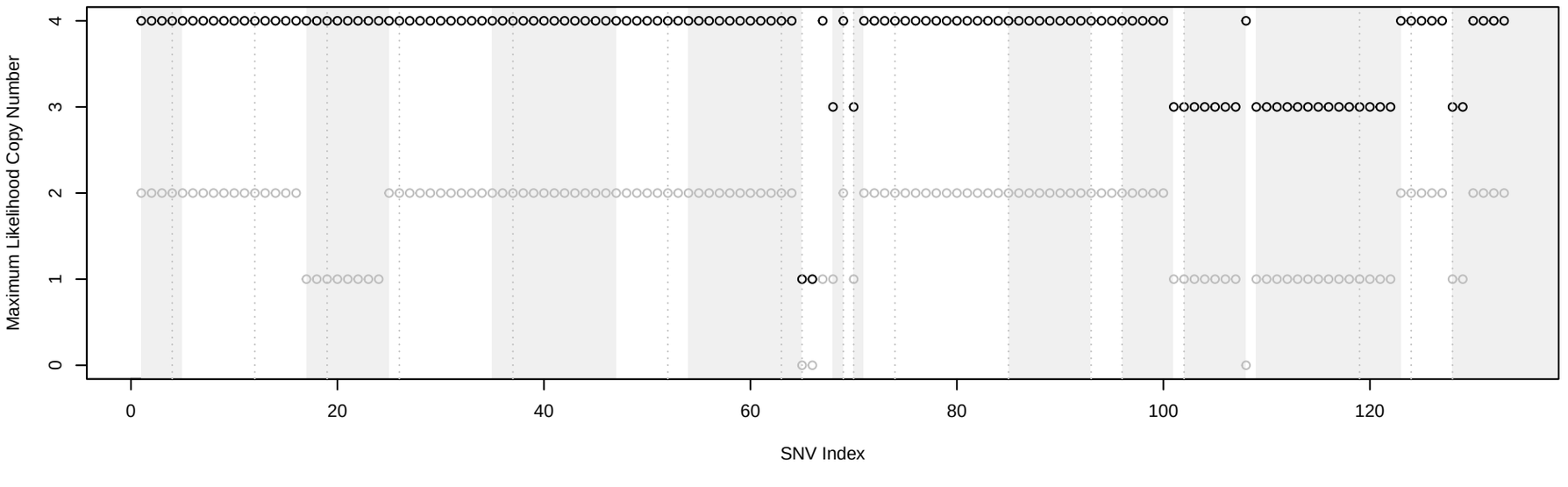

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m2
4m2
1m1
2m1
3m1
4m1
6m1

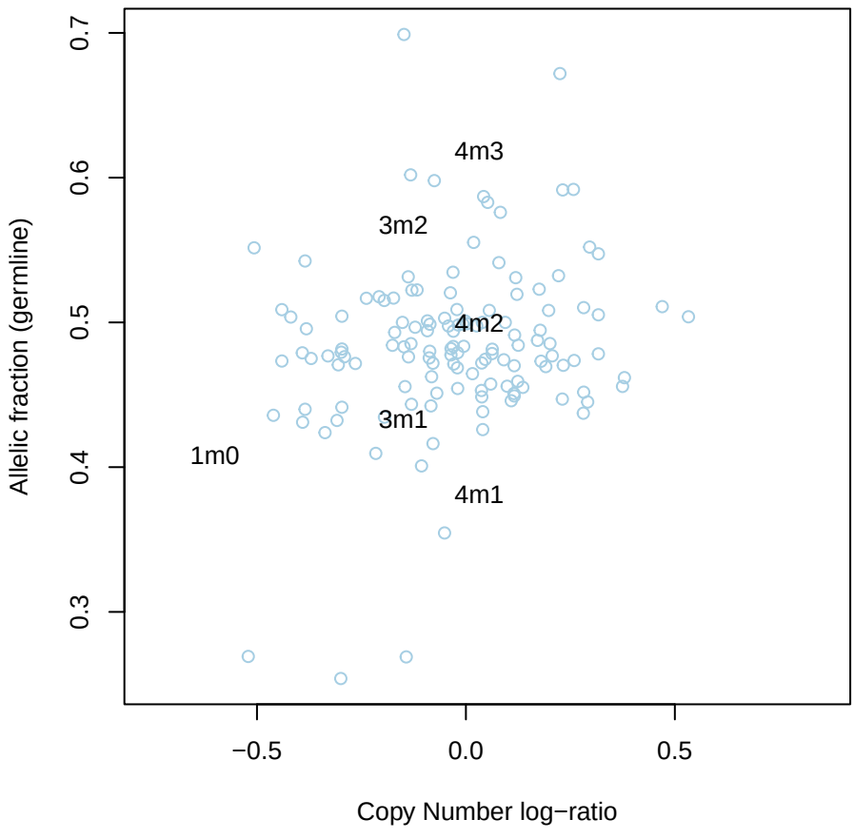

Frequency
Cellular fraction

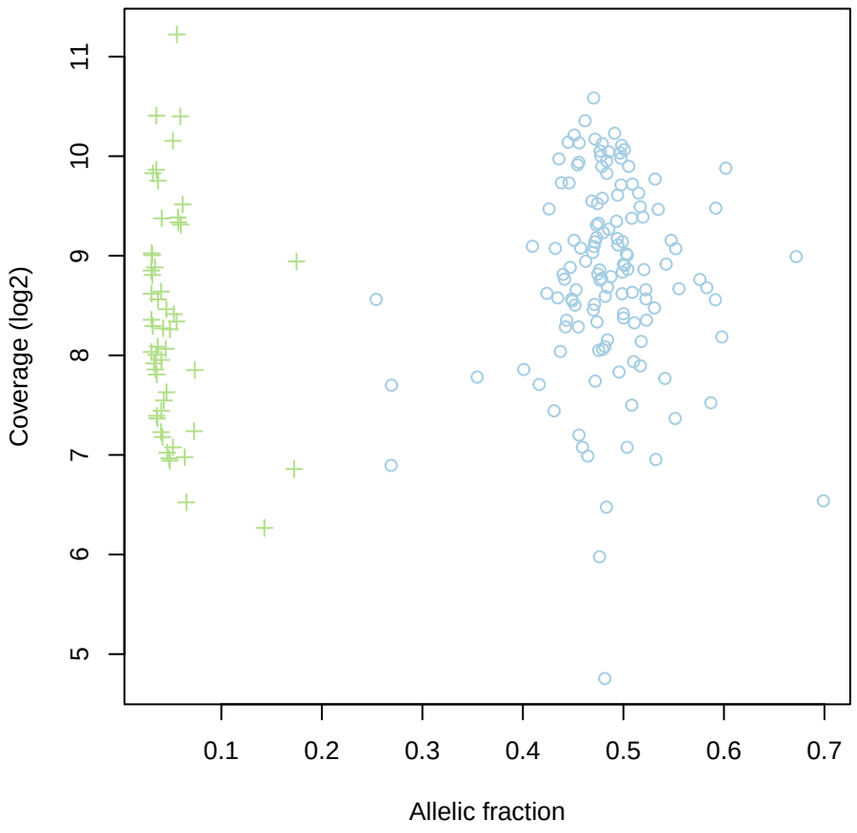

Purity: 0.31 Tumor ploidy: 3.814
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

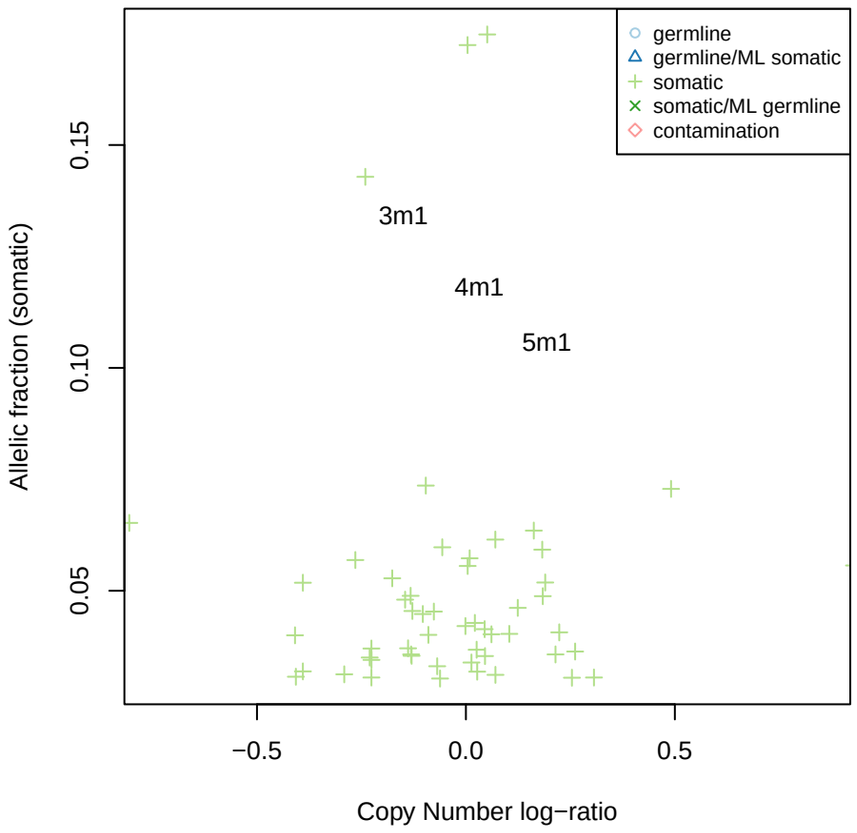

Purity: 0.31 Tumor ploidy: 3.814 SNV log−likelihood: −32.2 GoF: 92.1% Mean coverage: 511;497
1 2 3 4 5 6 7 8 10 12 13 14 15 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

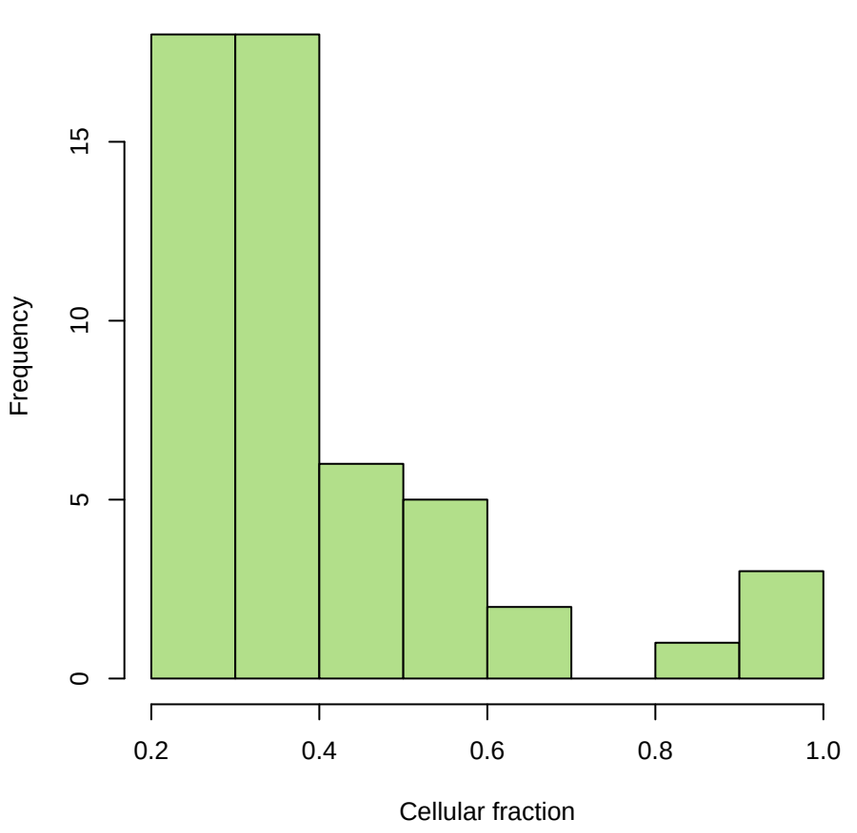

SCNA−fit log−likelihood: −8115.51
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6
0 20 40 60 80 100 120
SNV Index

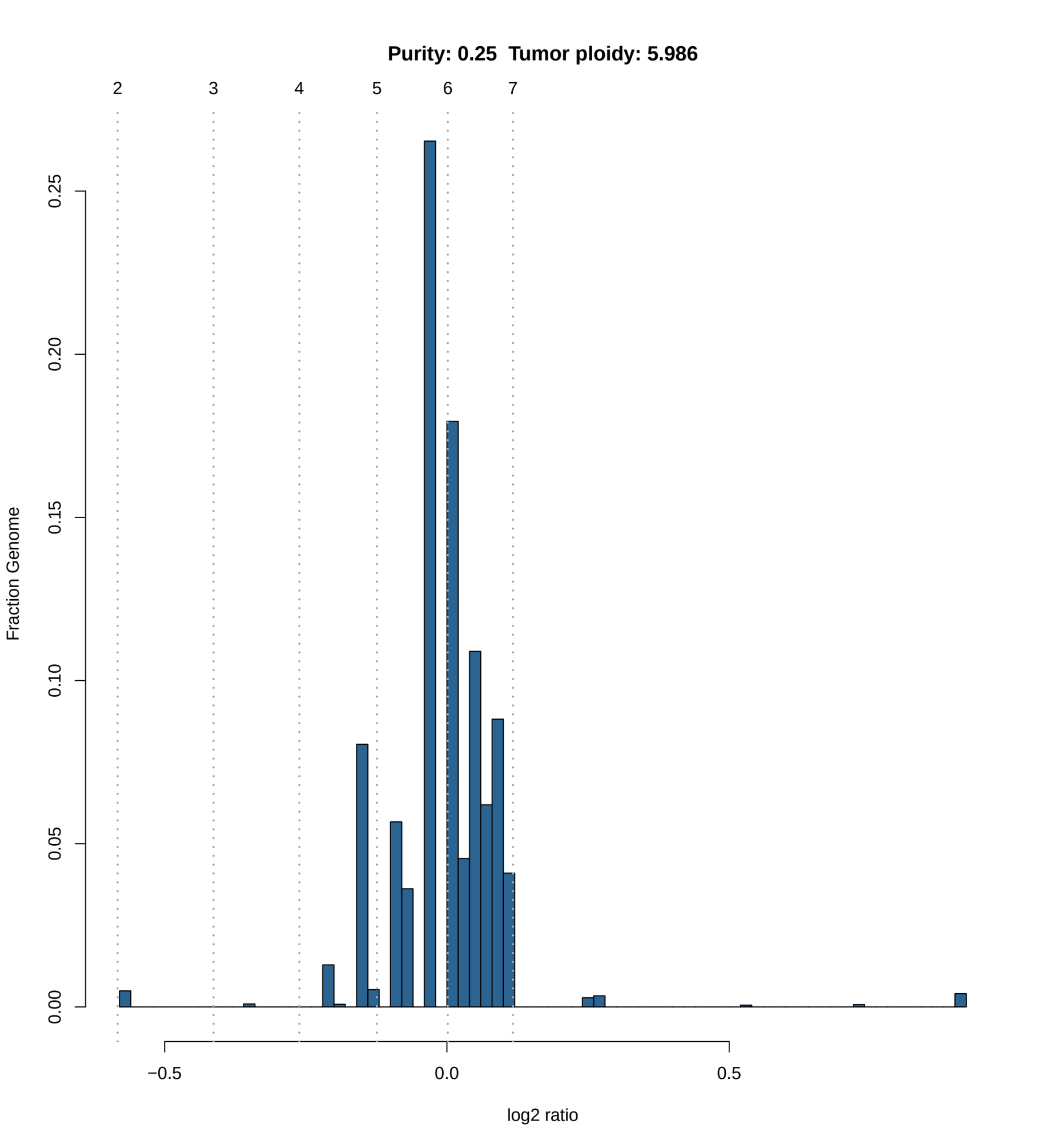

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120
SNV Index

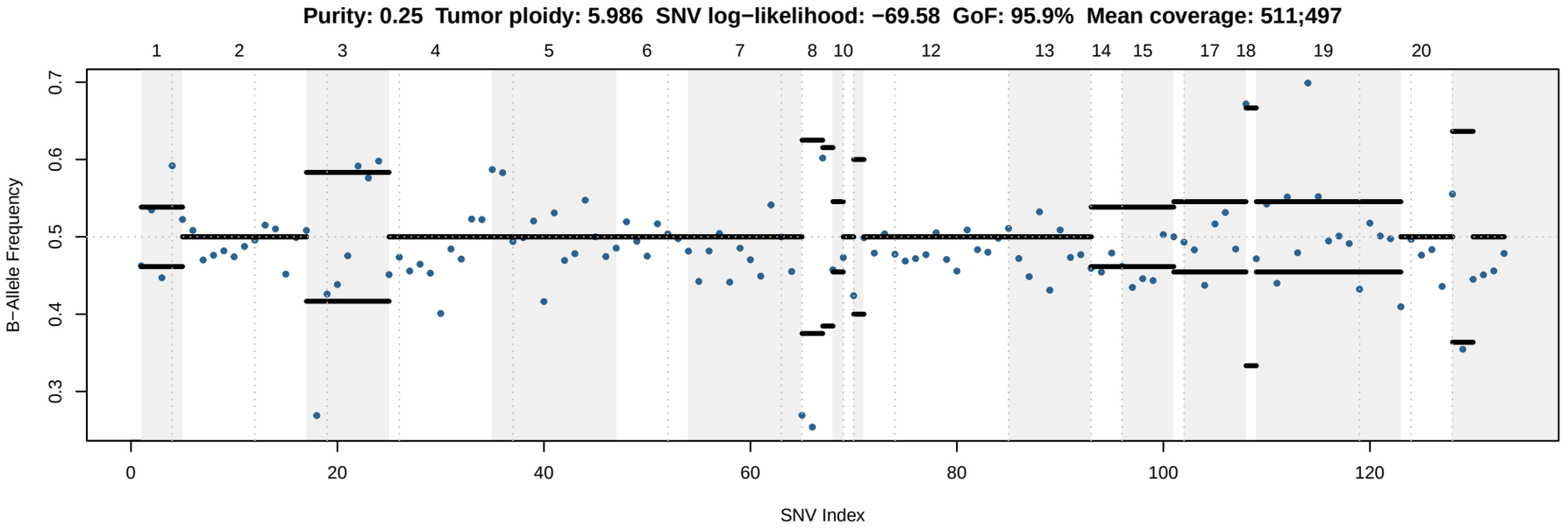

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
4m3
3m2
4m2
3m1
1m0
4m1
−0.5
0.0
0.5
Copy Number log−ratio

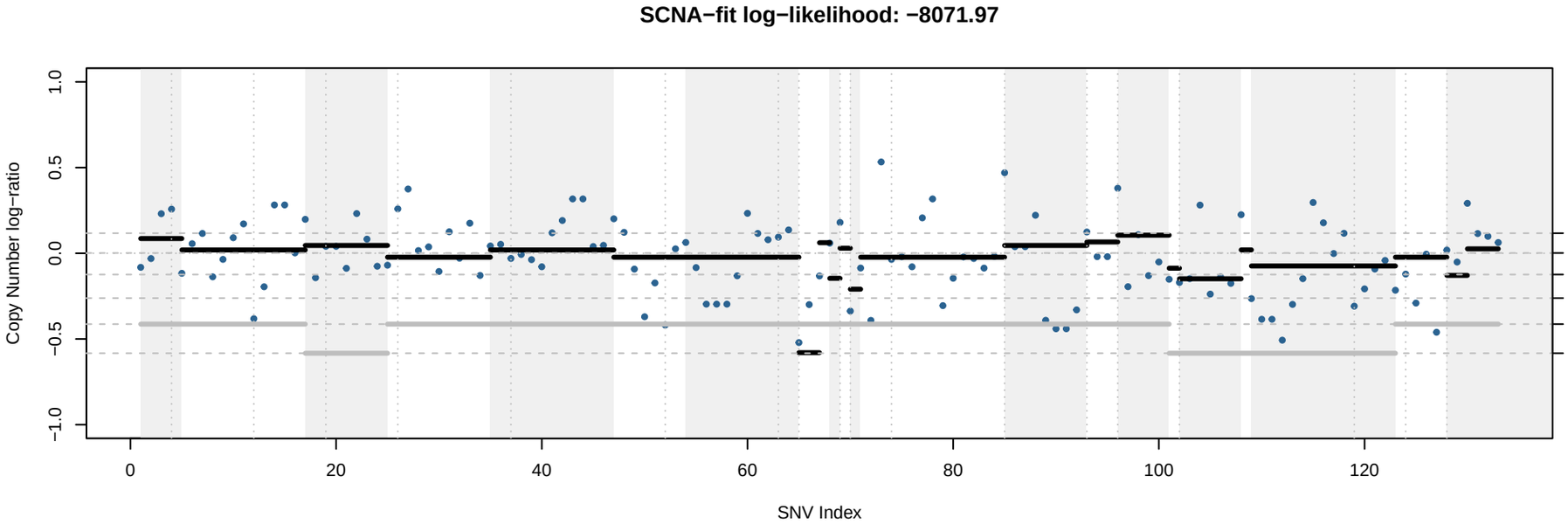

Coverage (log2)
5
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

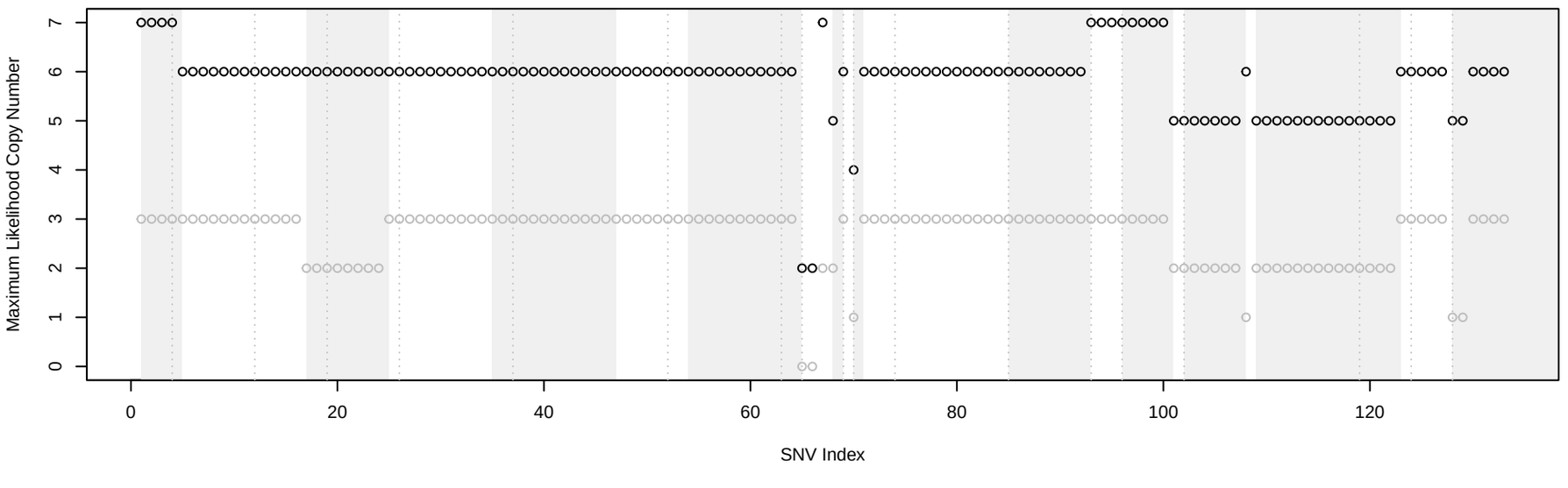

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
3m1
4m1
5m1
−0.5
0.0
0.5
Copy Number log−ratio

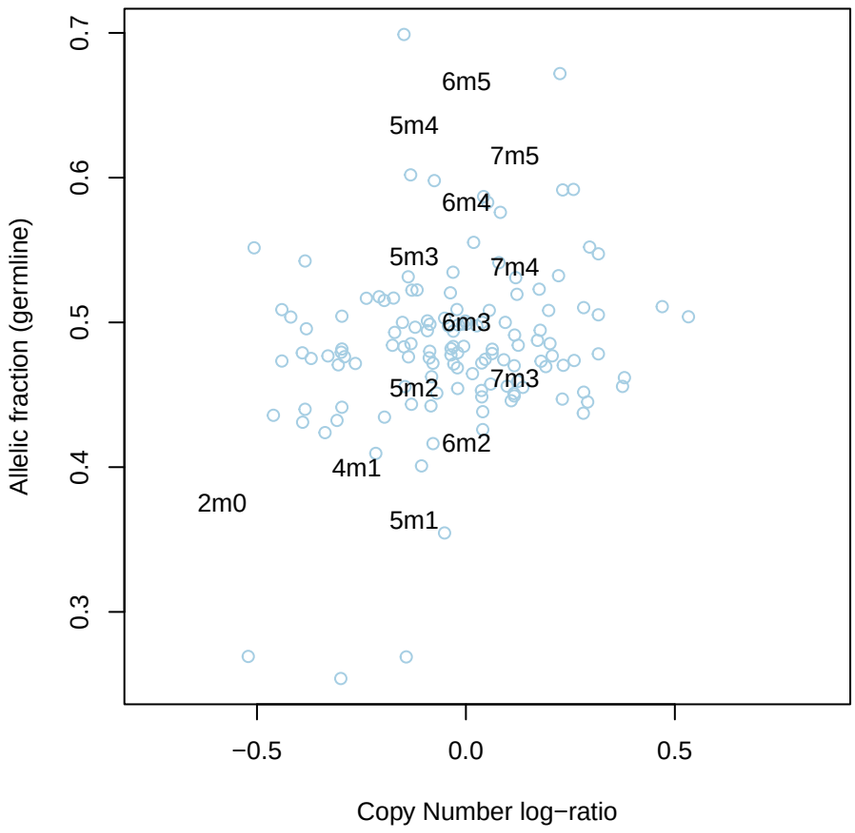

Frequency
0
5
10
15
0.2
0.4
0.6
0.8
1.0
Cellular fraction

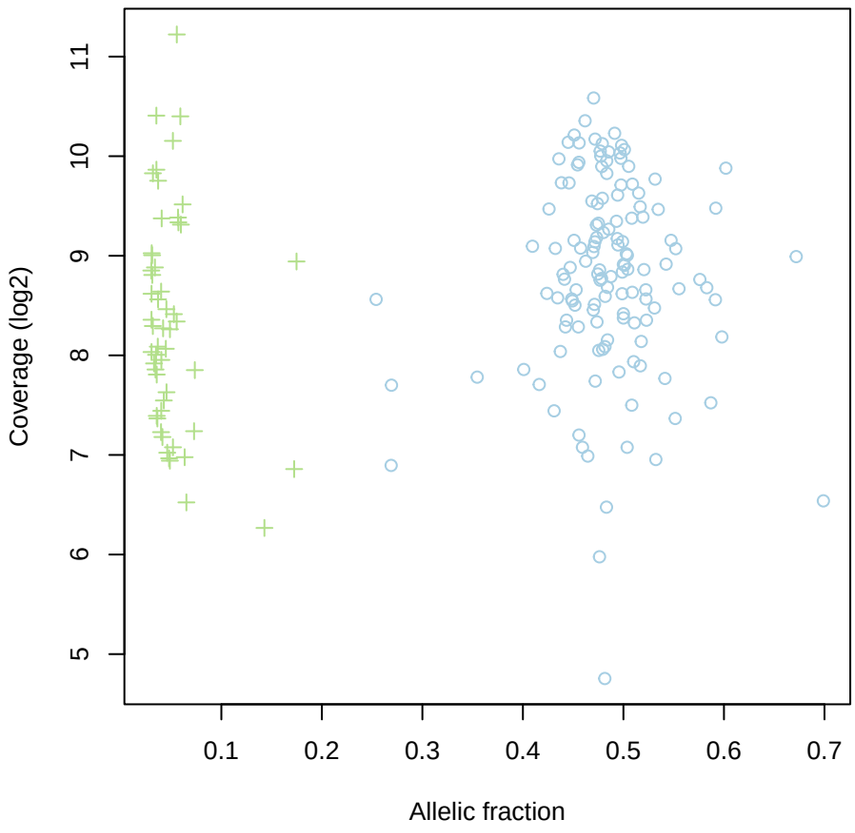

Purity: 0.25 Tumor ploidy: 5.986
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

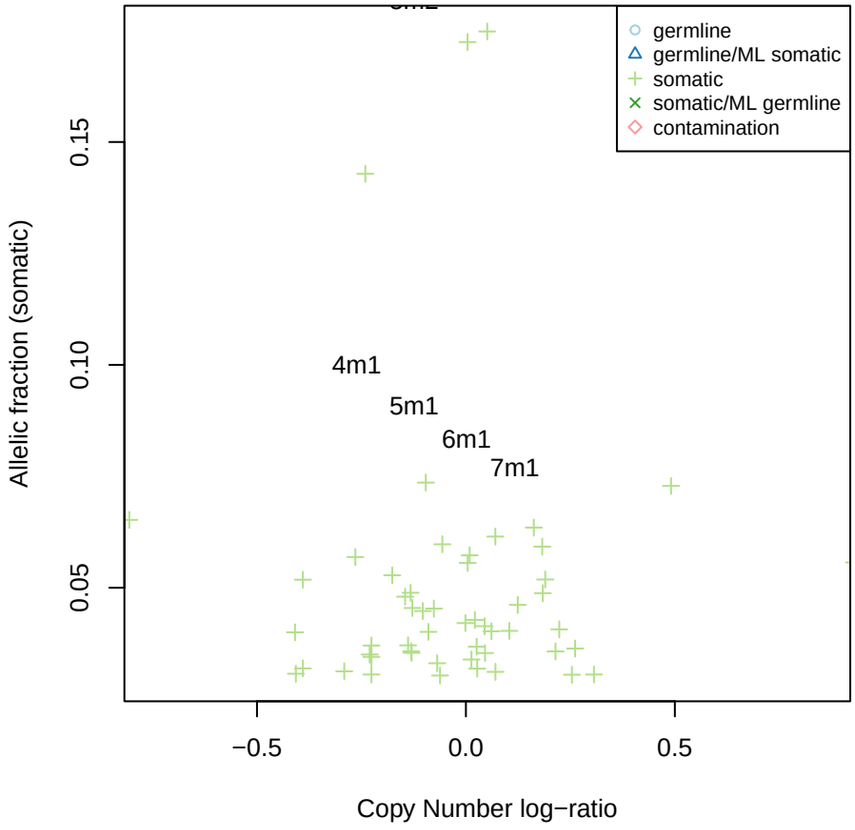

Purity: 0.25 Tumor ploidy: 5.986 SNV log−likelihood: −69.58 GoF: 95.9% Mean coverage: 511;497
1 2 3 4 5 6 7 8 10 12 13 14 15 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

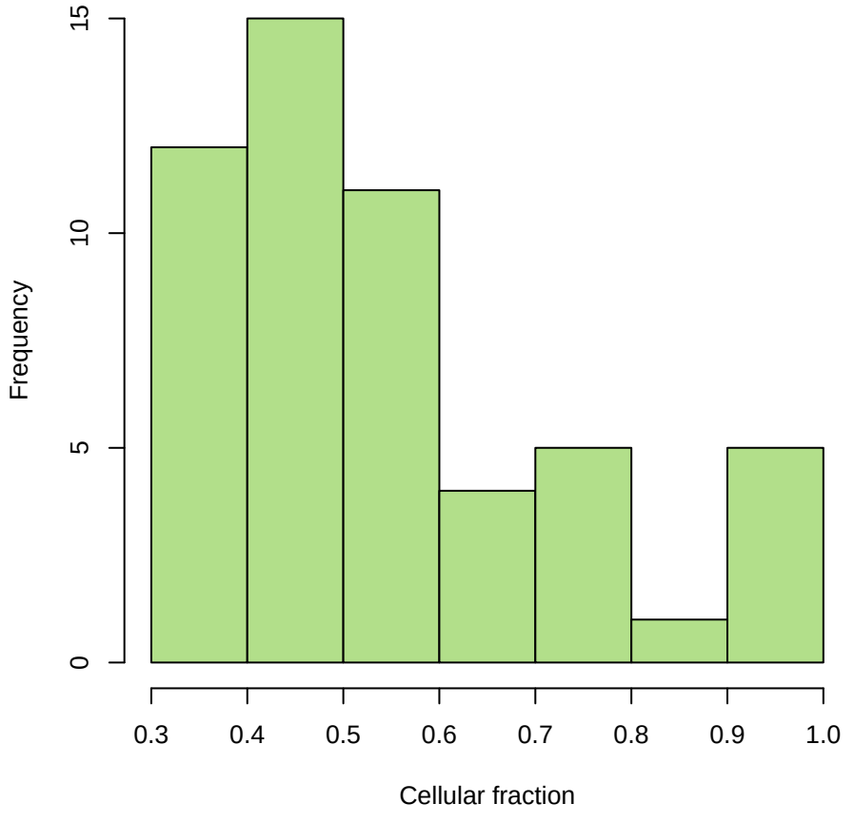

SCNA−fit log−likelihood: −8071.97
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 6
0 20 40 60 80 100 120
SNV Index

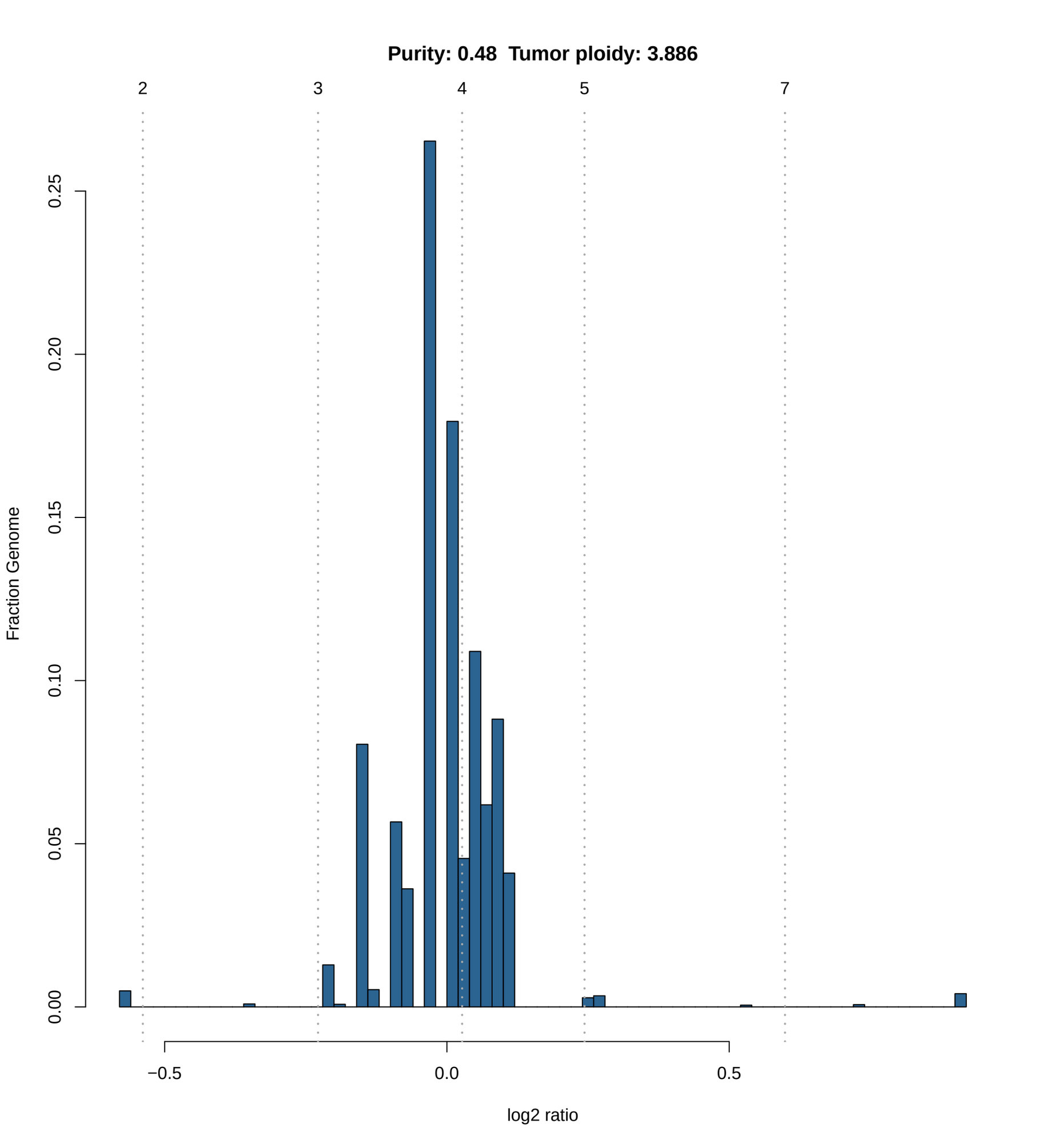

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

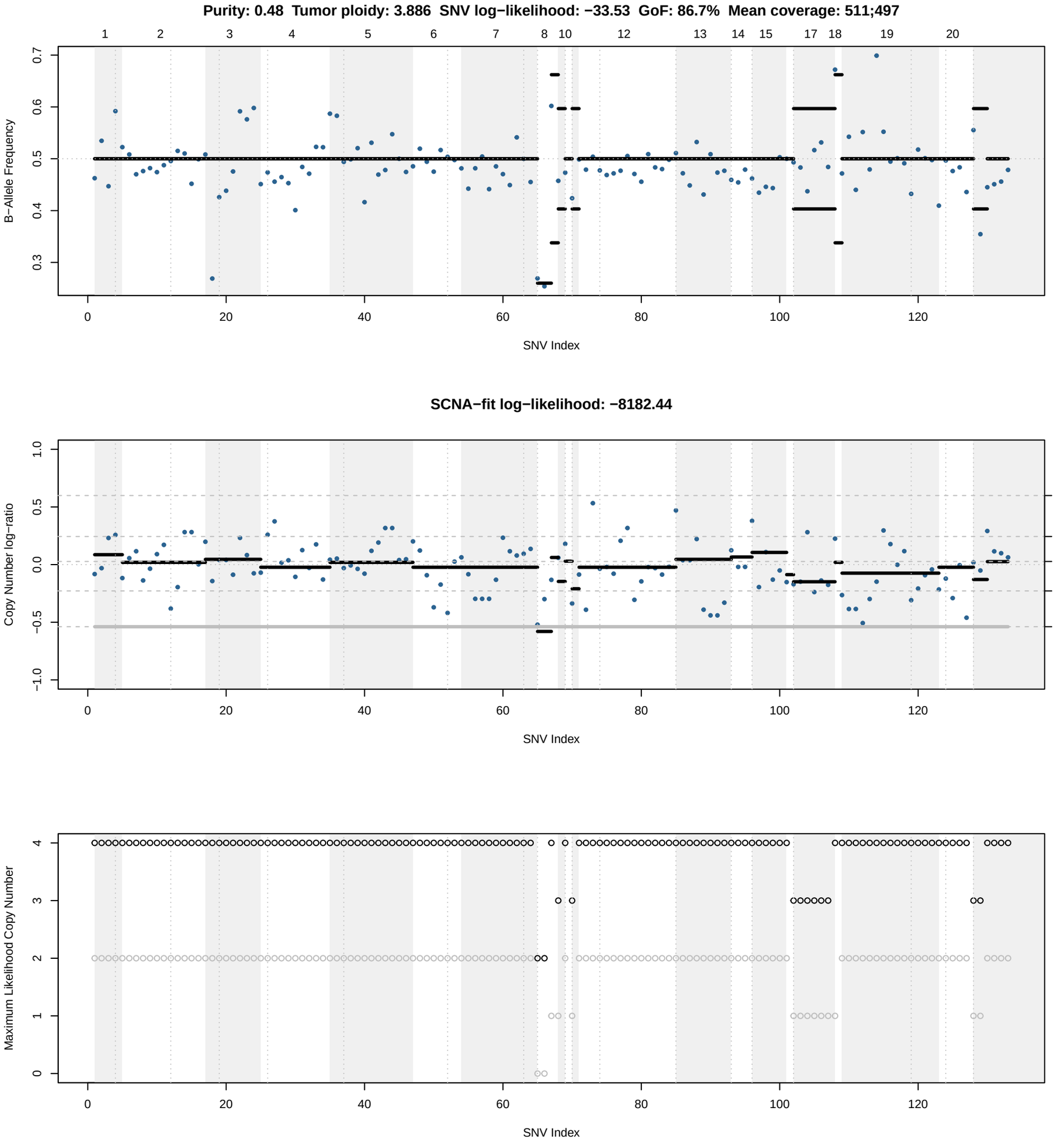

Allelic fraction (germline)
Copy Number log−ratio
6m5
5m4
7m5
6m4
5m3
7m4
6m3
7m3
5m2
6m2
4m1
2m0
5m1

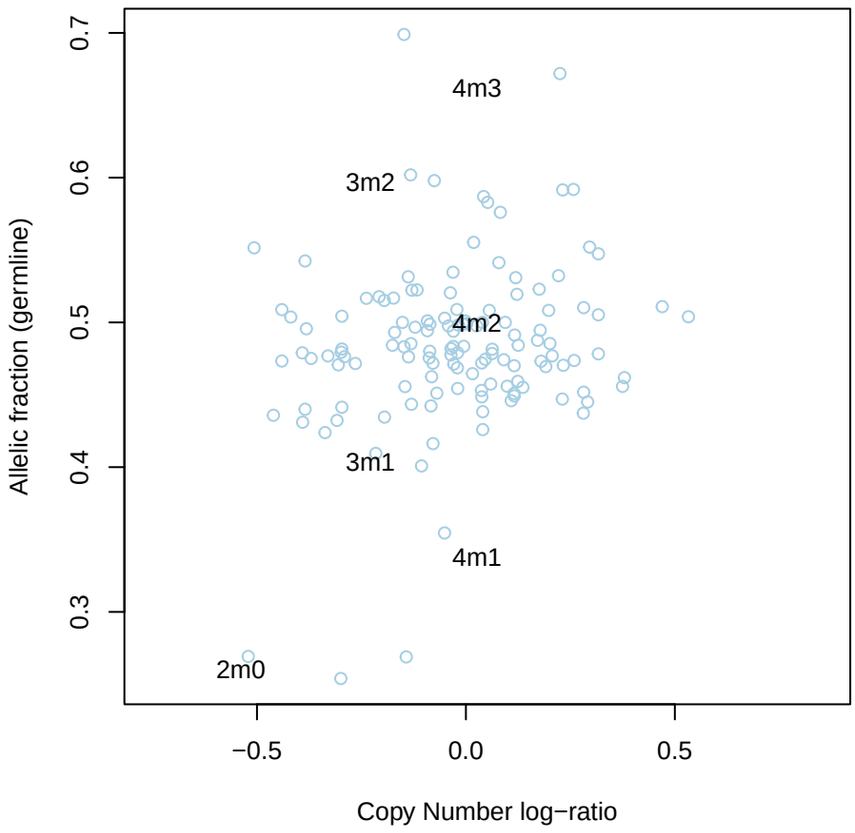

Coverage (log2)
Allelic fraction

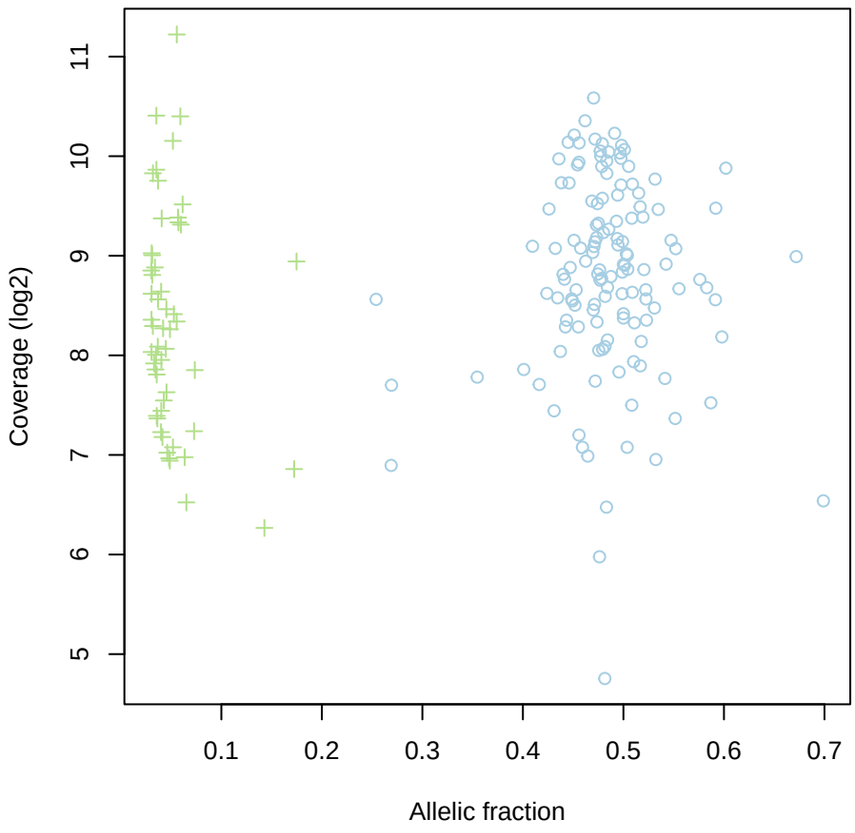

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
4m1
5m1
6m1
7m1

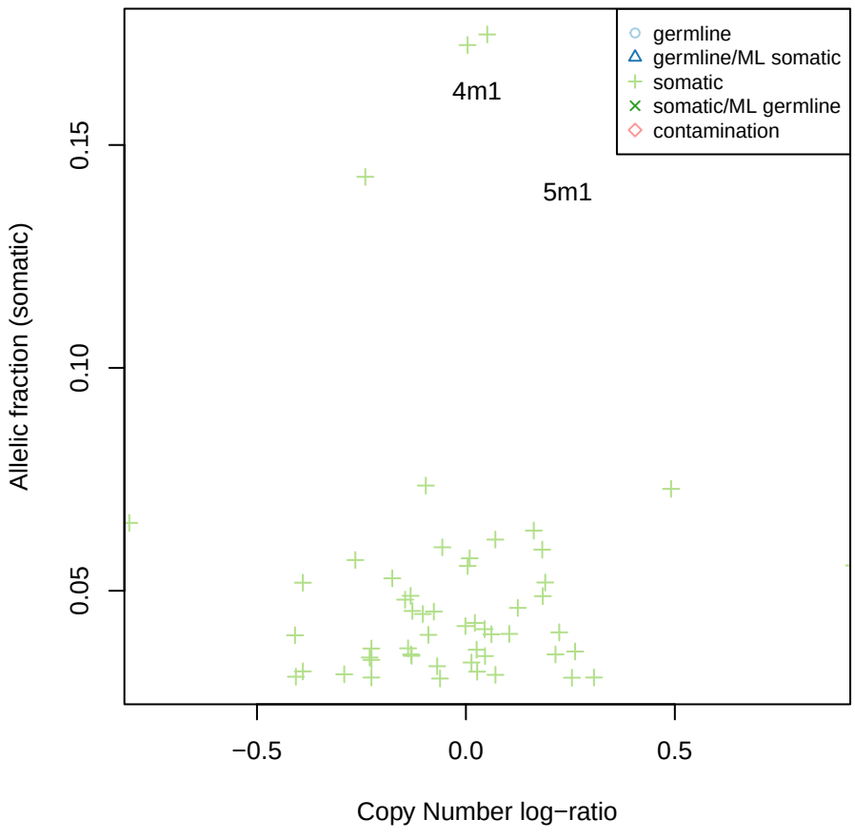

Frequency
Cellular fraction

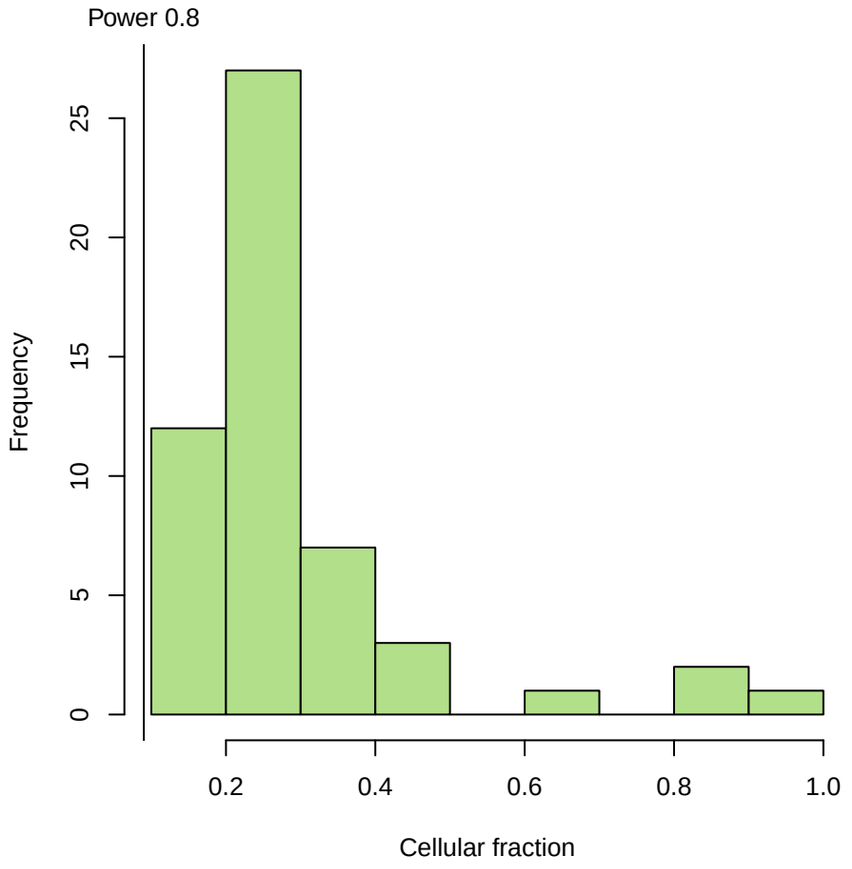

Purity: 0.48 Tumor ploidy: 3.886
2
3
4
5
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

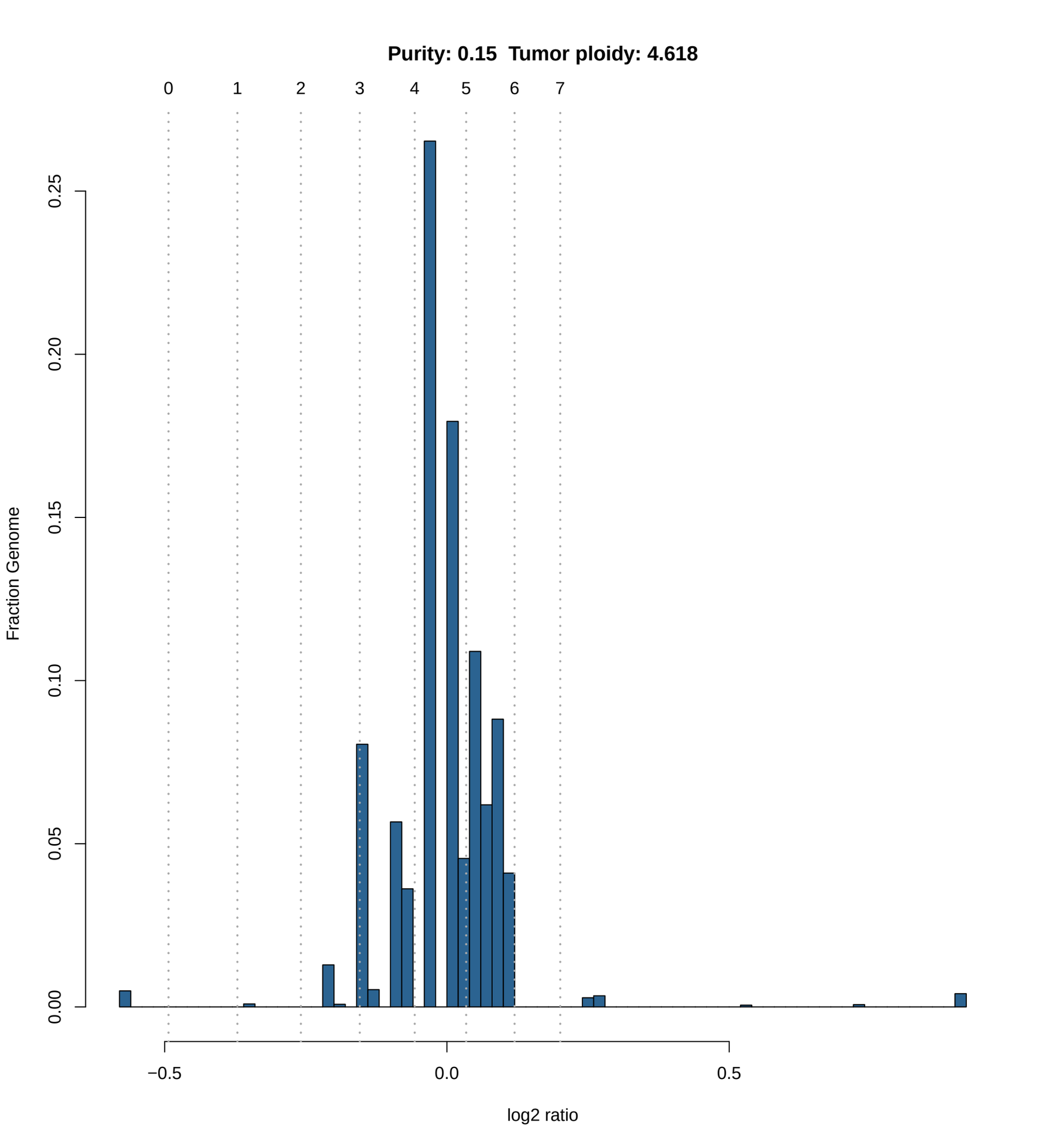

Purity: 0.48 Tumor ploidy: 3.886 SNV log−likelihood: −33.53 GoF: 86.7% Mean coverage: 511;497
1 2 3 4 5 6 7 8 10 12 13 14 15 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index
SCNA−fit log−likelihood: −8182.44
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 7
0 20 40 60 80 100 120
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120
SNV Index

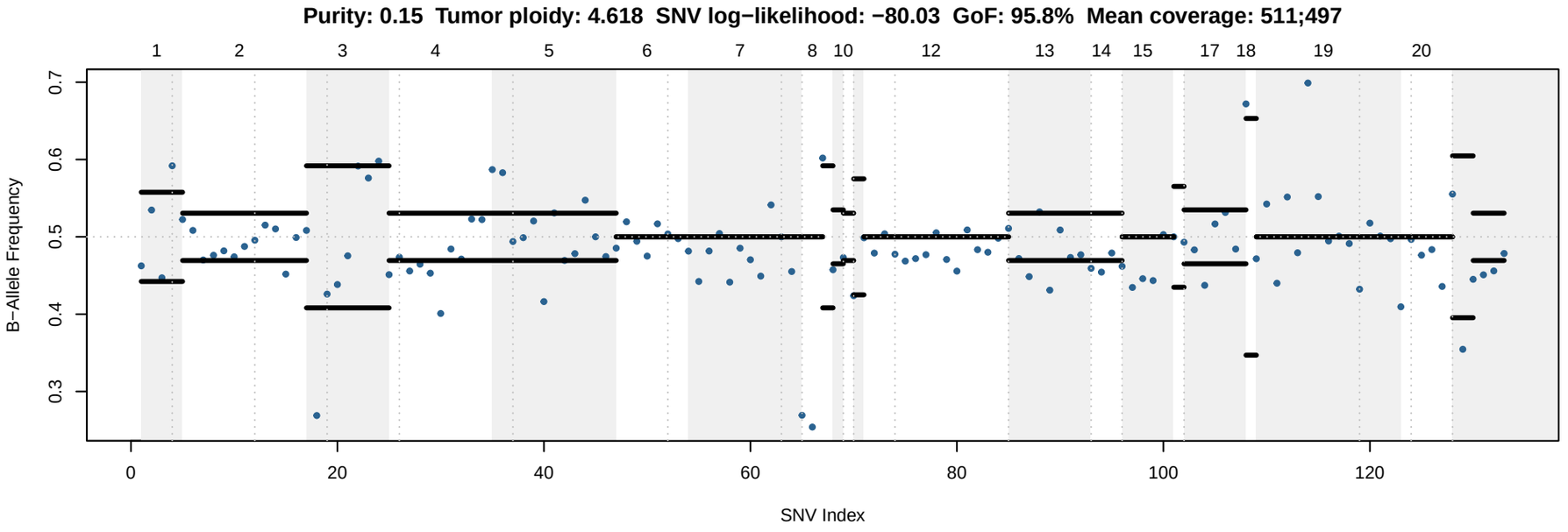

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
4m2
3m1
4m1
2m0

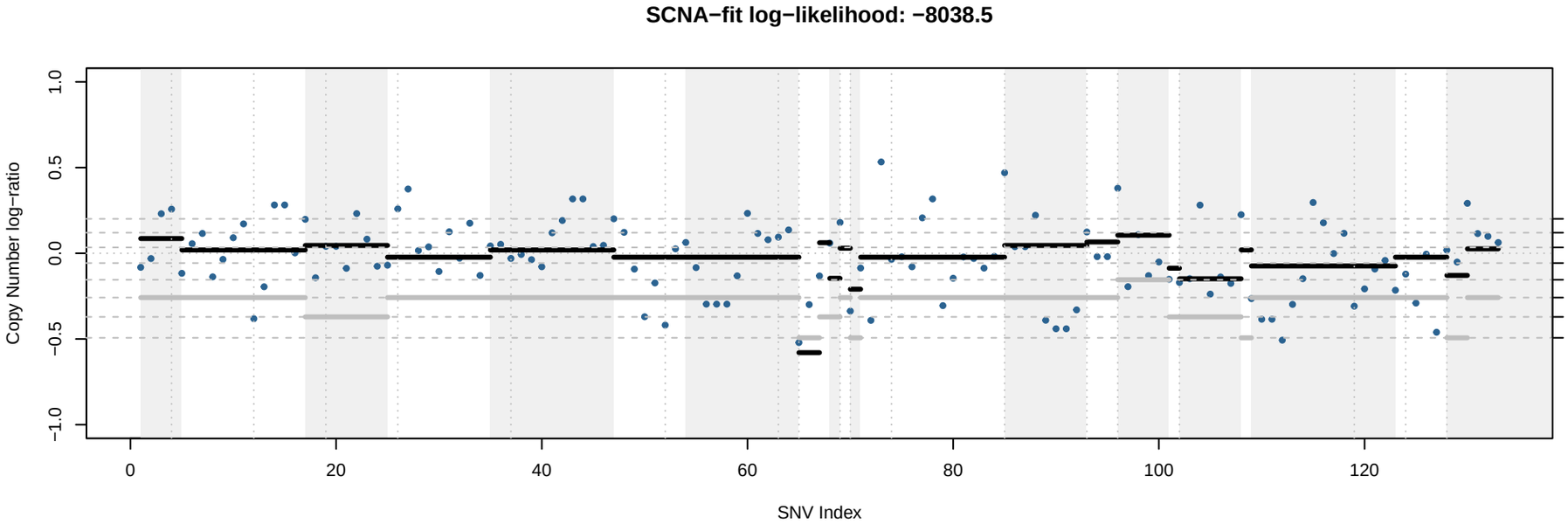

Coverage (log2)
Allelic fraction

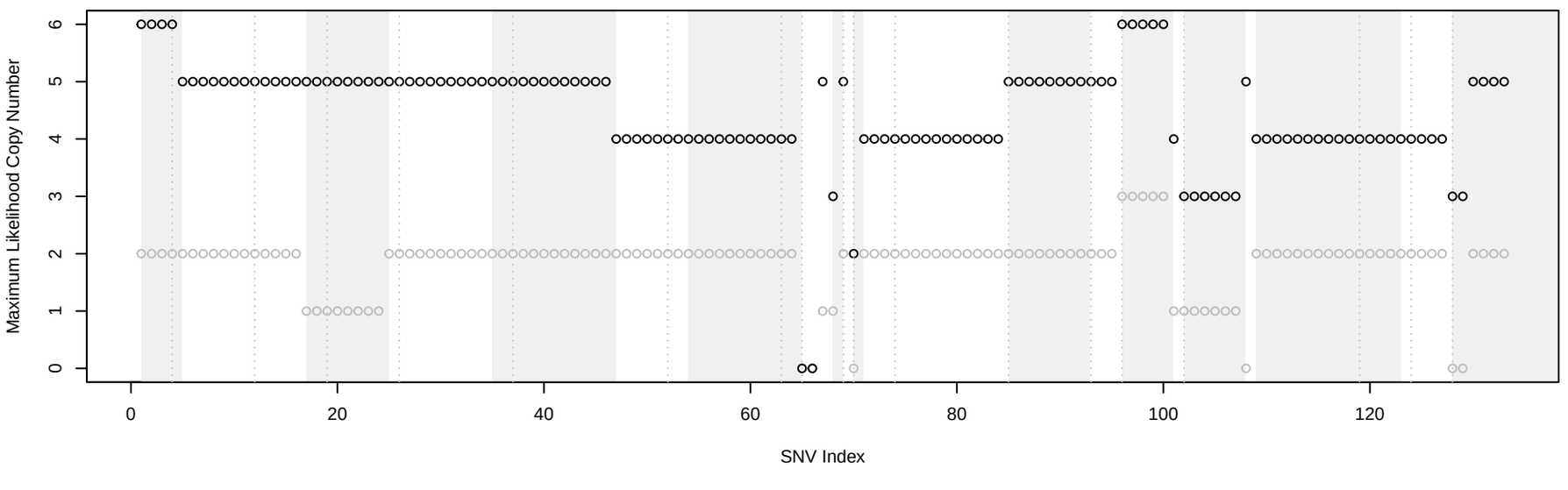

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1

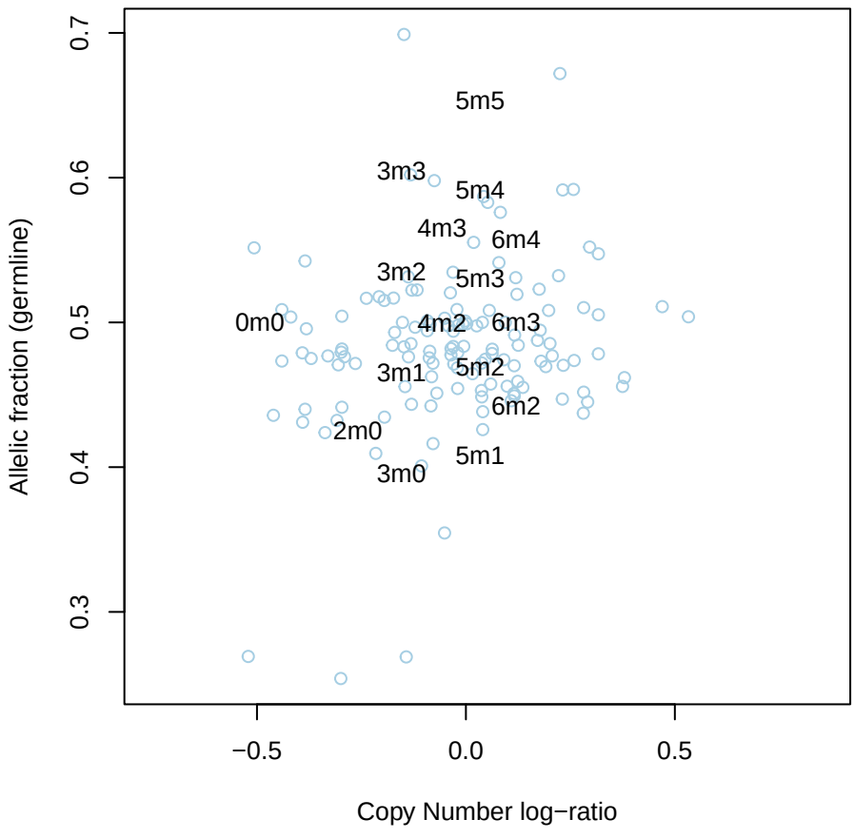

Power 0.8
Frequency
Cellular fraction

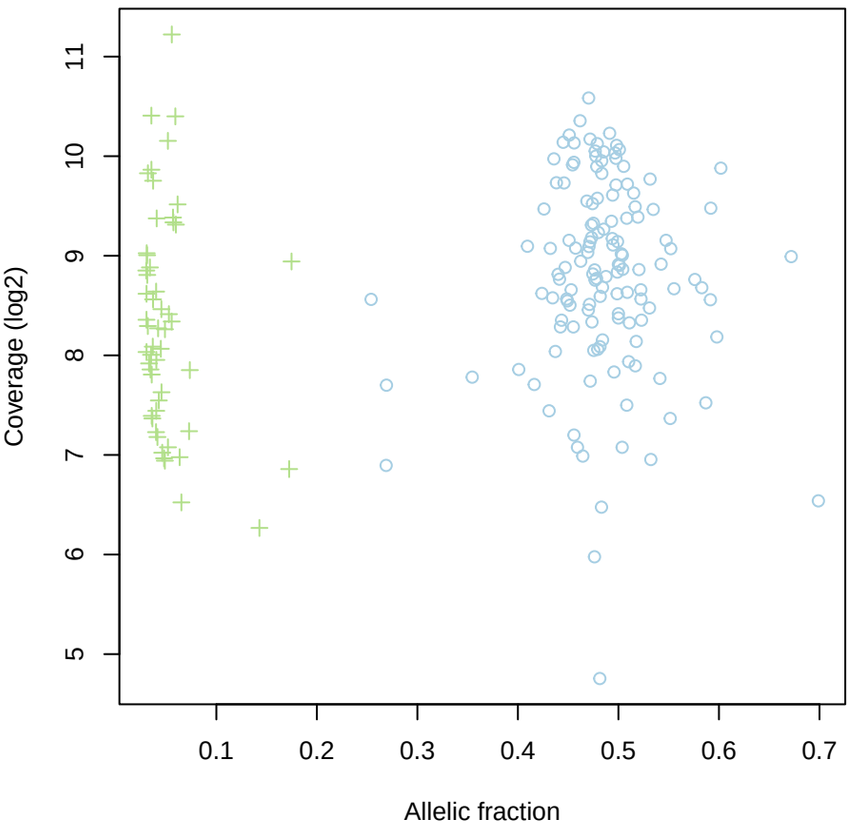

Purity: 0.15 Tumor ploidy: 4.618
0
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

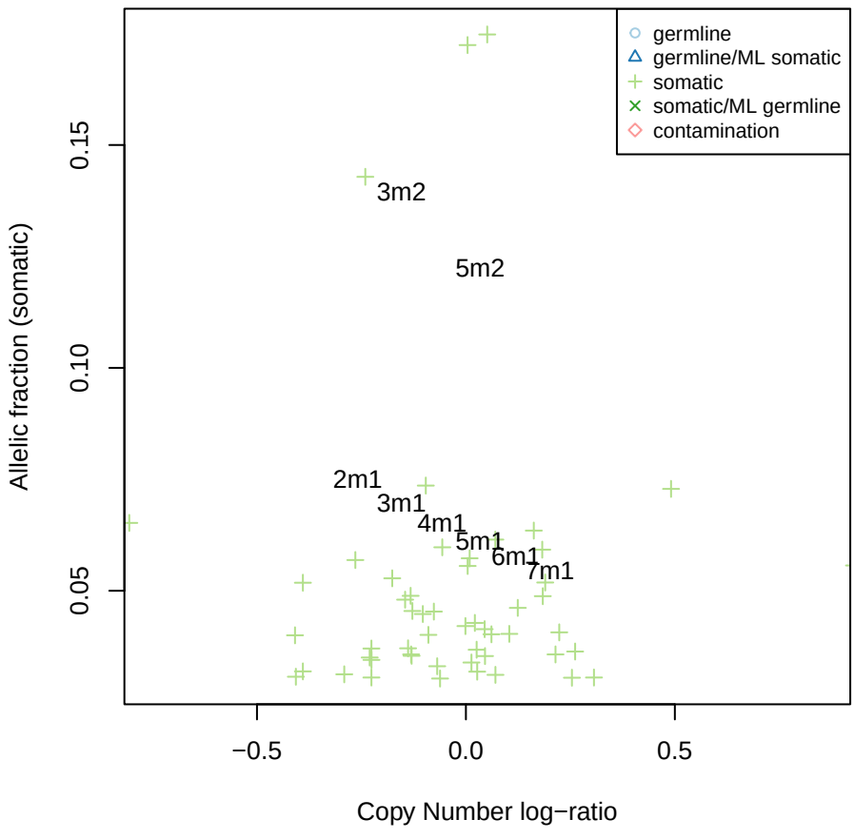

Purity: 0.15 Tumor ploidy: 4.618 SNV log−likelihood: −80.03 GoF: 95.8% Mean coverage: 511;497
1 2 3 4 5 6 7 8 10 12 13 14 15 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

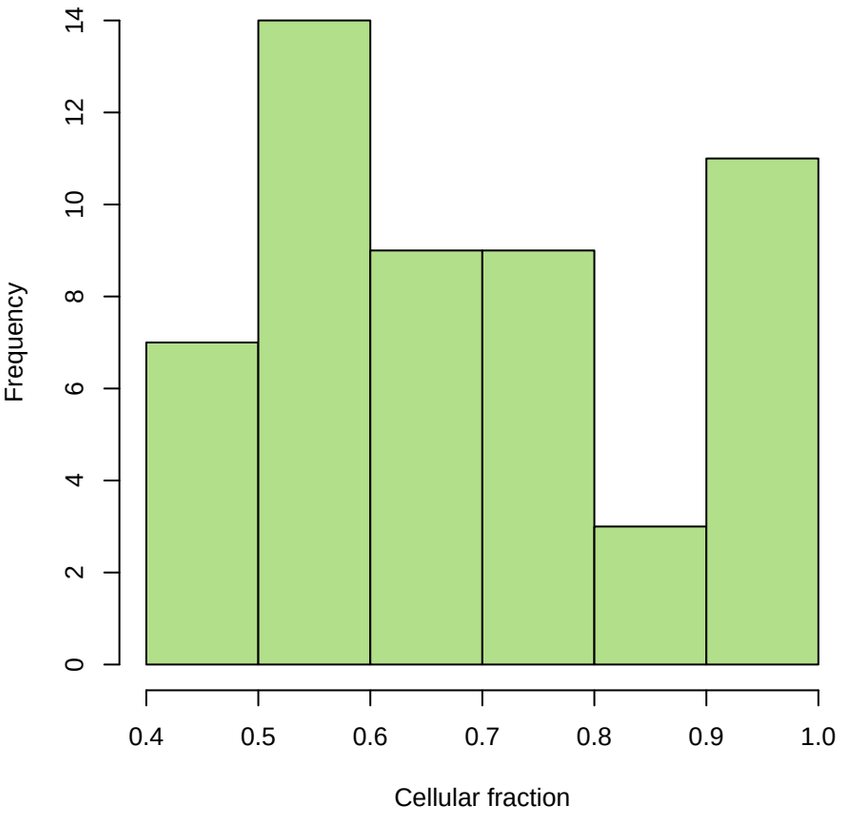

SCNA−fit log−likelihood: −8038.5
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4 6
0 20 40 60 80 100 120
SNV Index

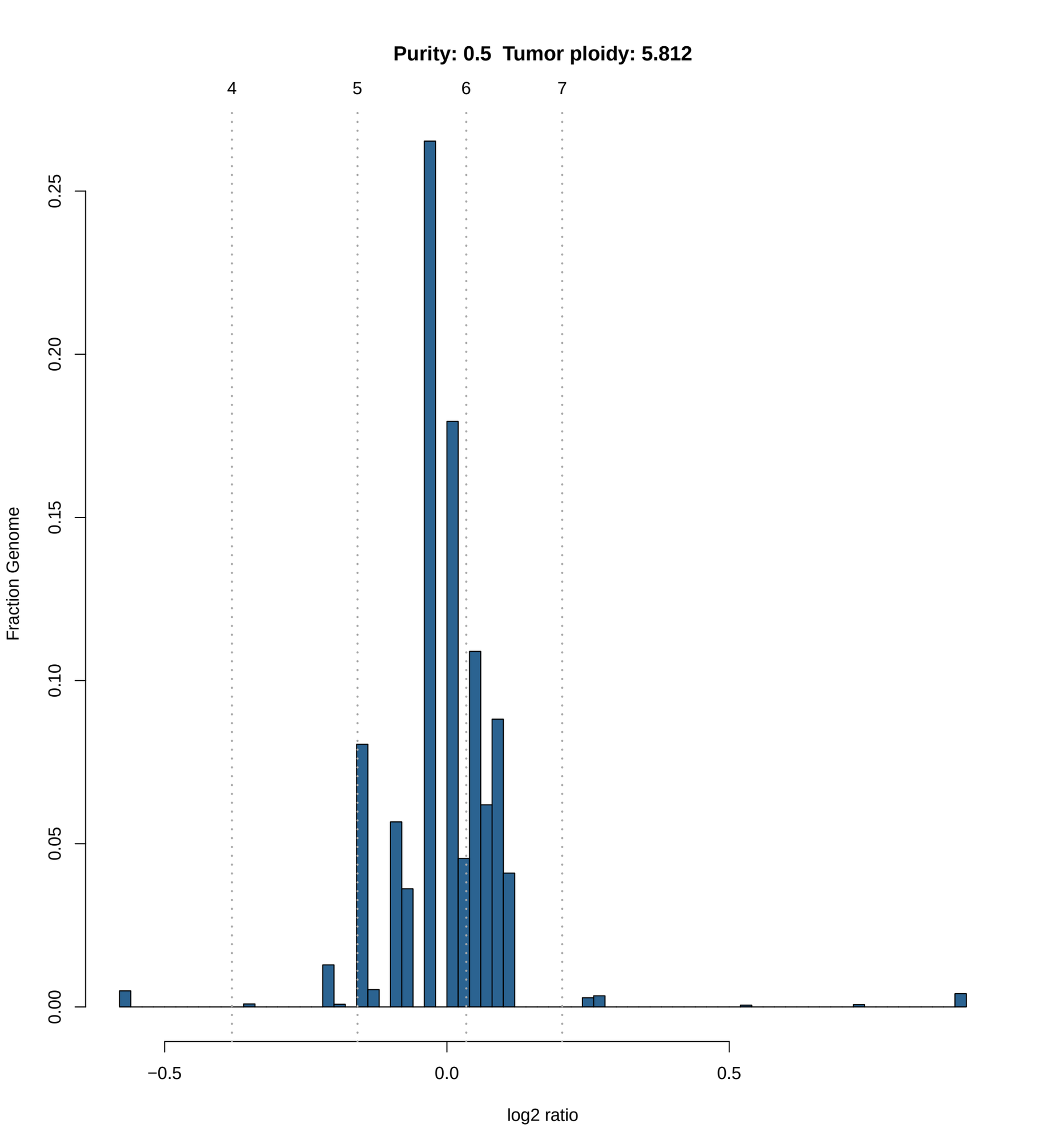

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120
SNV Index

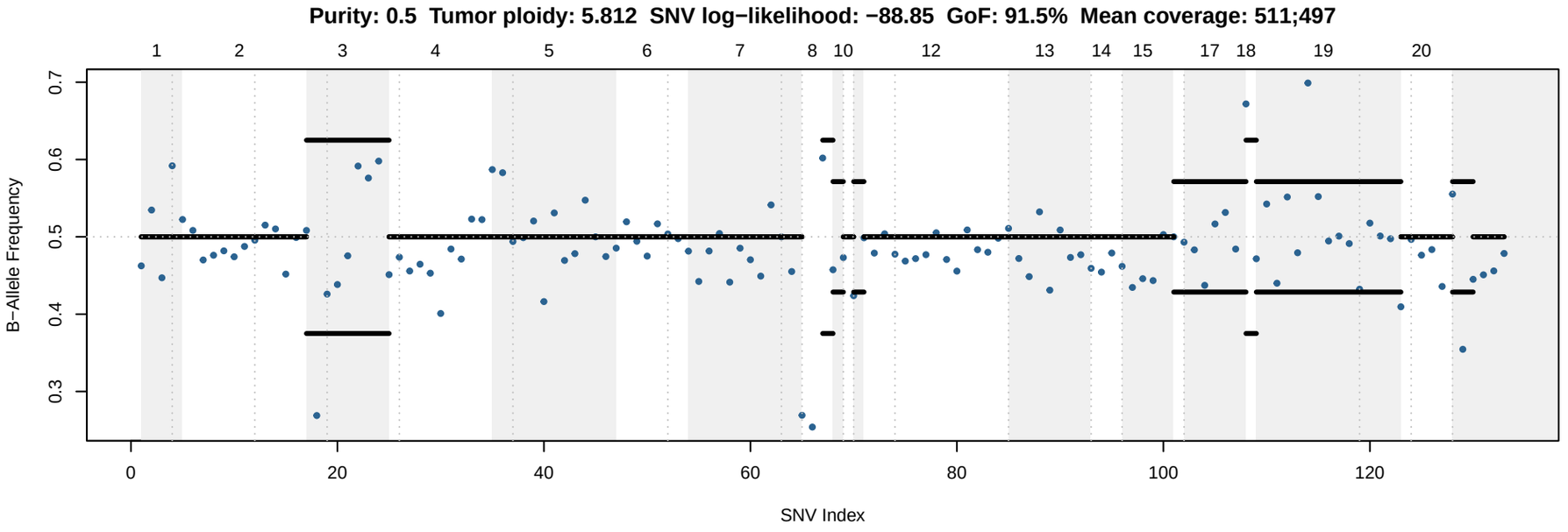

Allelic fraction (germline)
Copy Number log−ratio
0m0
2m0
3m0
3m1
3m2
3m3
4m2
4m3
5m1
5m2
5m3
5m4
5m5
6m2
6m3
6m4

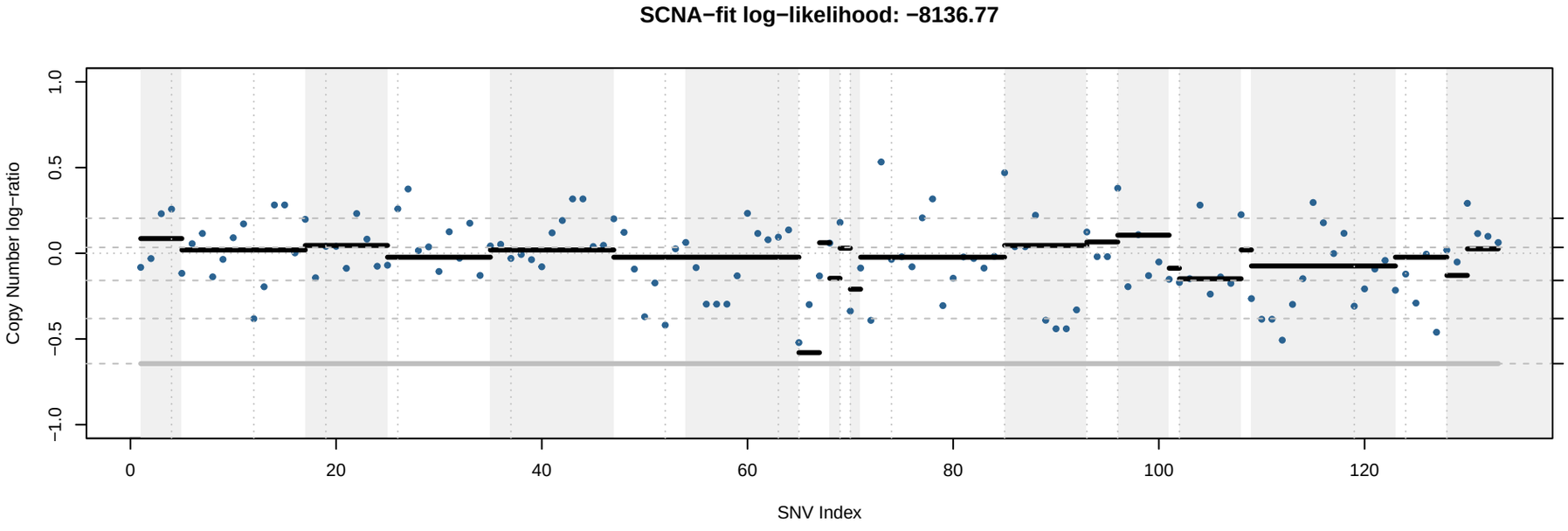

Coverage (log2)
Allelic fraction

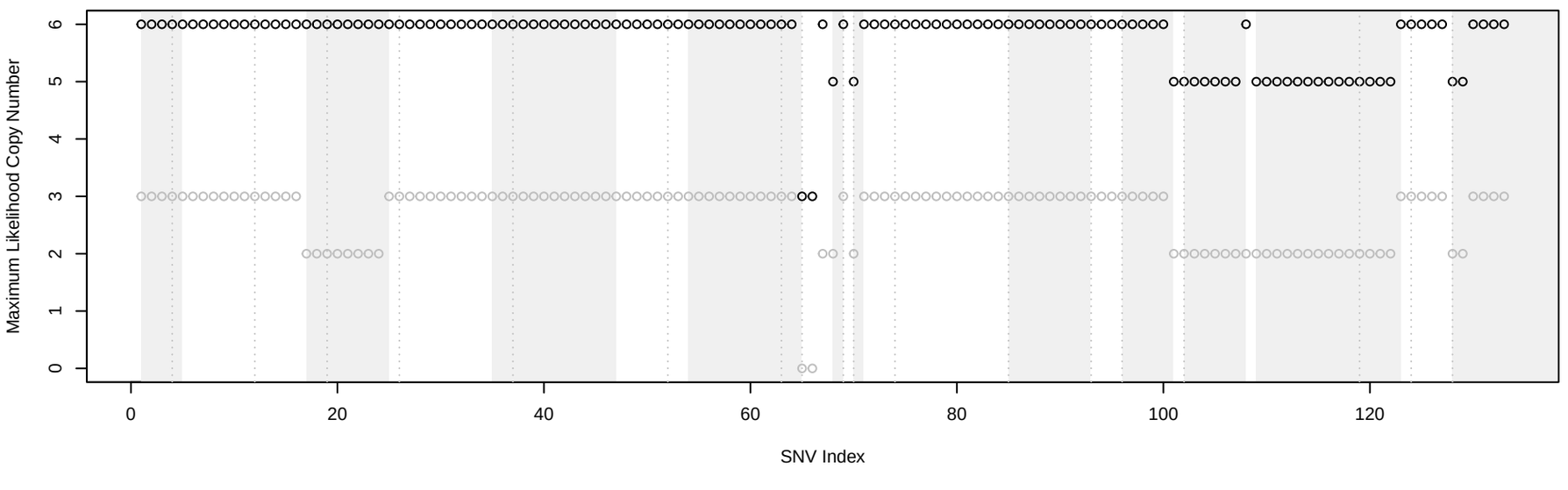

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m1
3m1
3m2
4m1
5m1
5m2
6m1
7m1

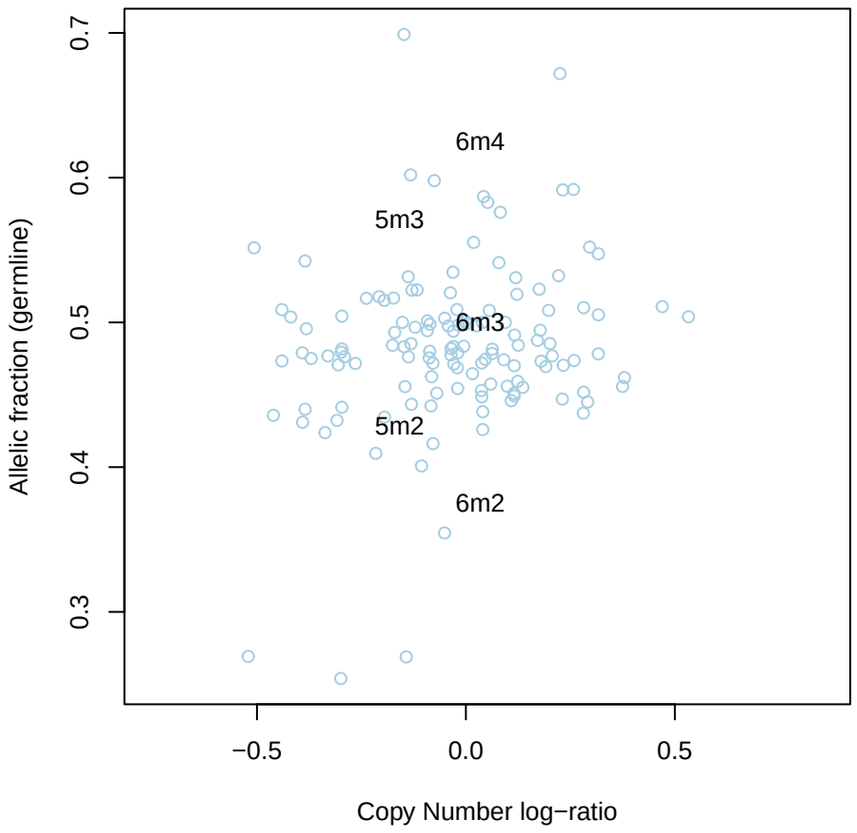

Frequency
Cellular fraction

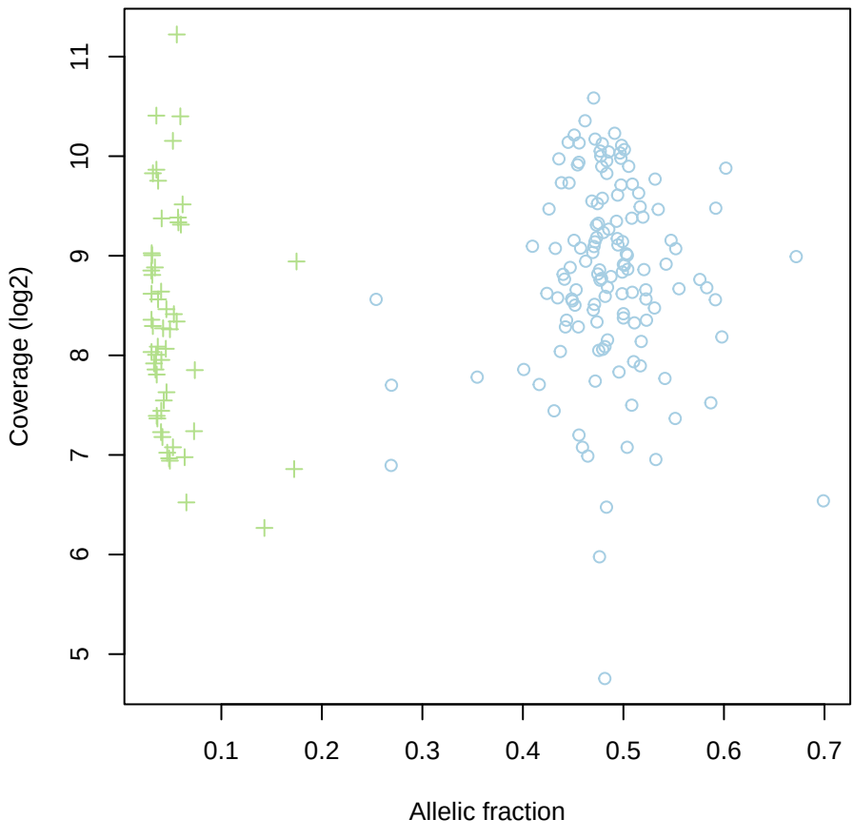

Purity: 0.5 Tumor ploidy: 5.812
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

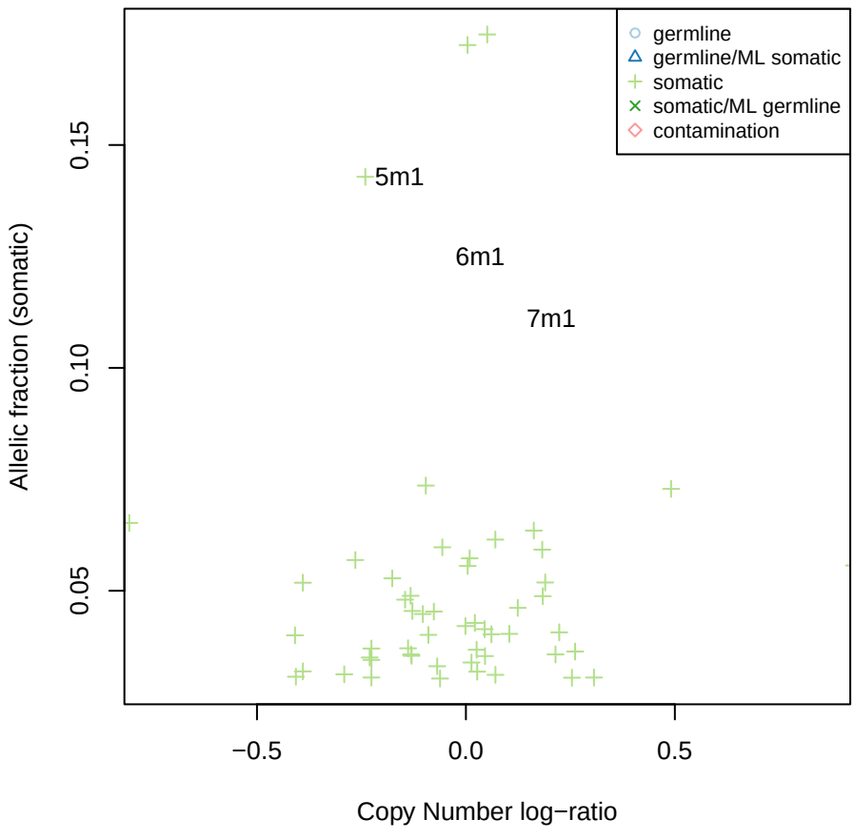

Purity: 0.5 Tumor ploidy: 5.812 SNV log−likelihood: −88.85 GoF: 91.5% Mean coverage: 511;497
1 2 3 4 5 6 7 8 10 12 13 14 15 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

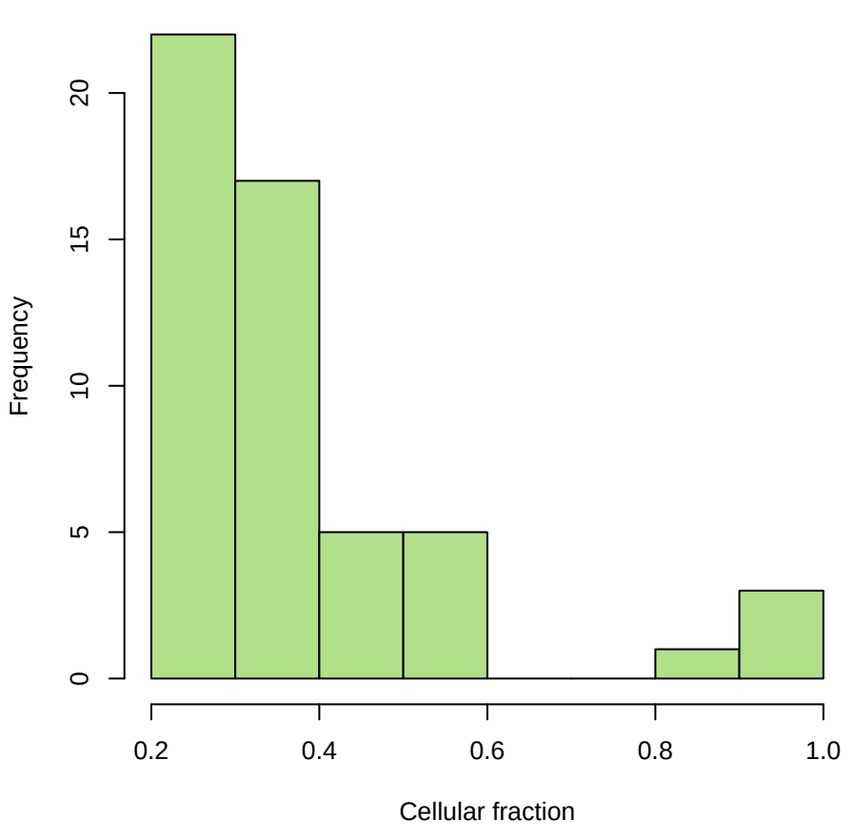

SCNA−fit log−likelihood: −8136.77
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

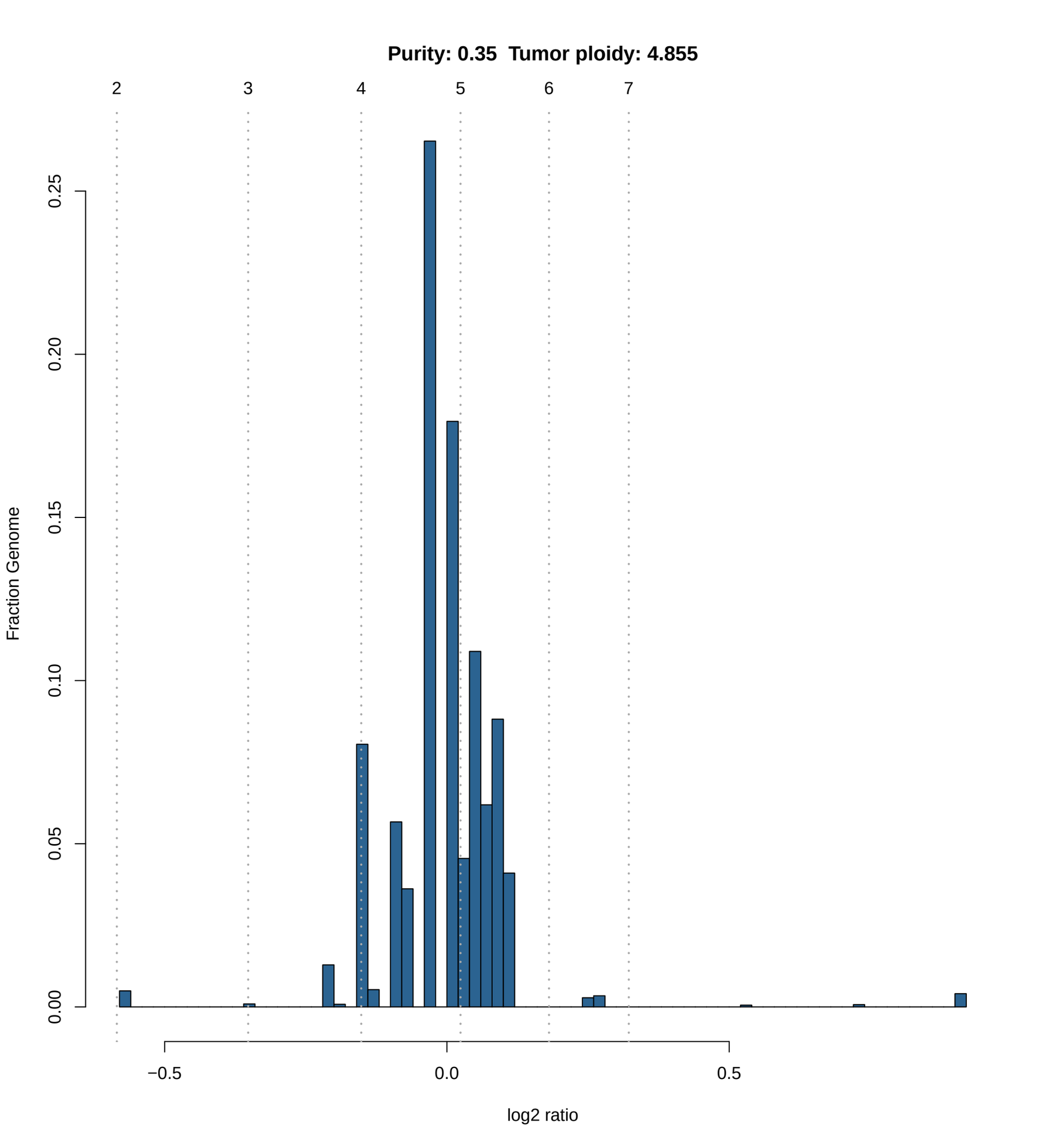

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120
SNV Index

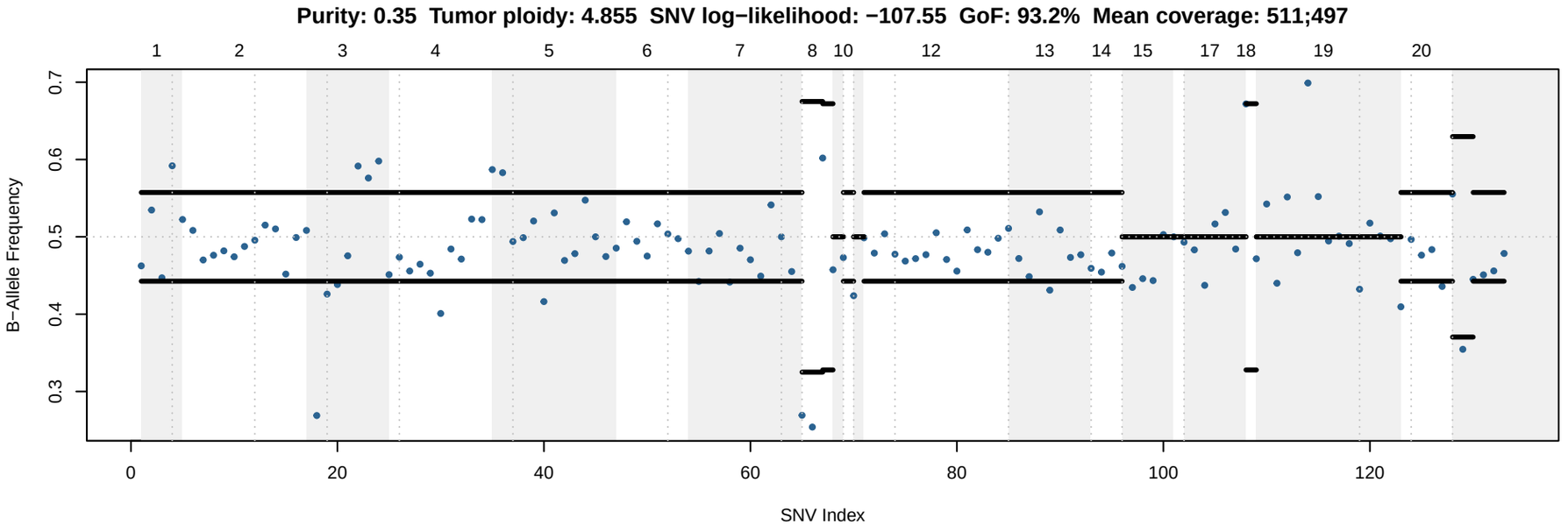

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
6m4
5m3
6m3
5m2
6m2
−0.5
0.0
0.5
Copy Number log−ratio

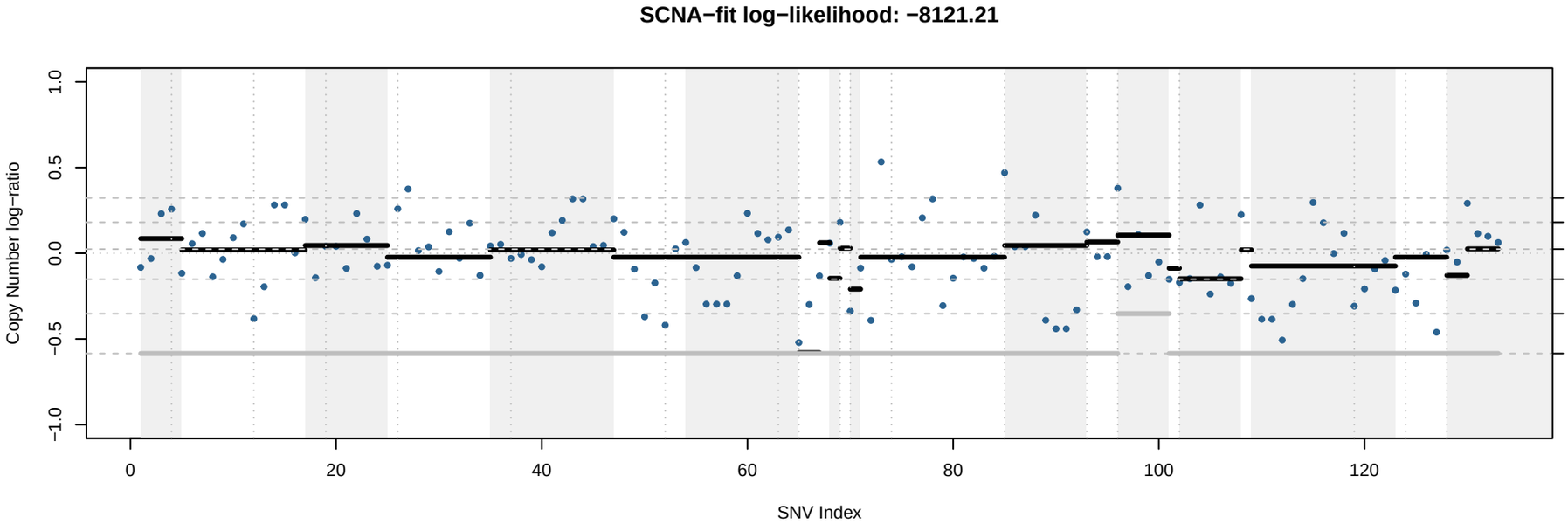

Coverage (log2)
5
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

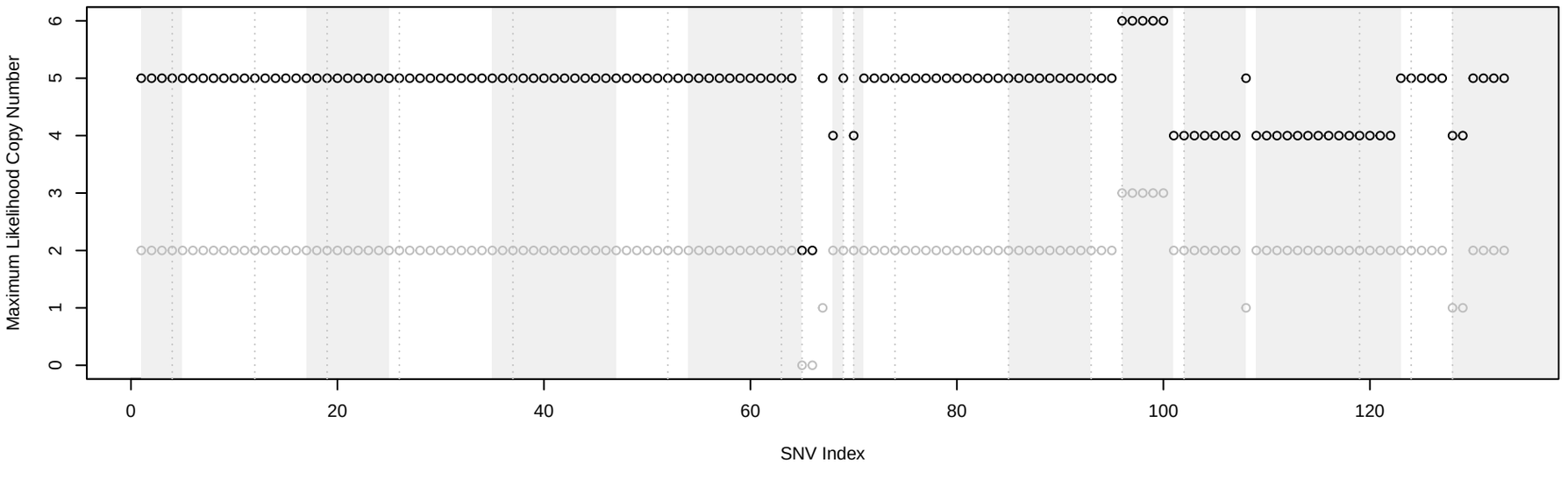

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
5m1
6m1
7m1
−0.5
0.0
0.5
Copy Number log−ratio

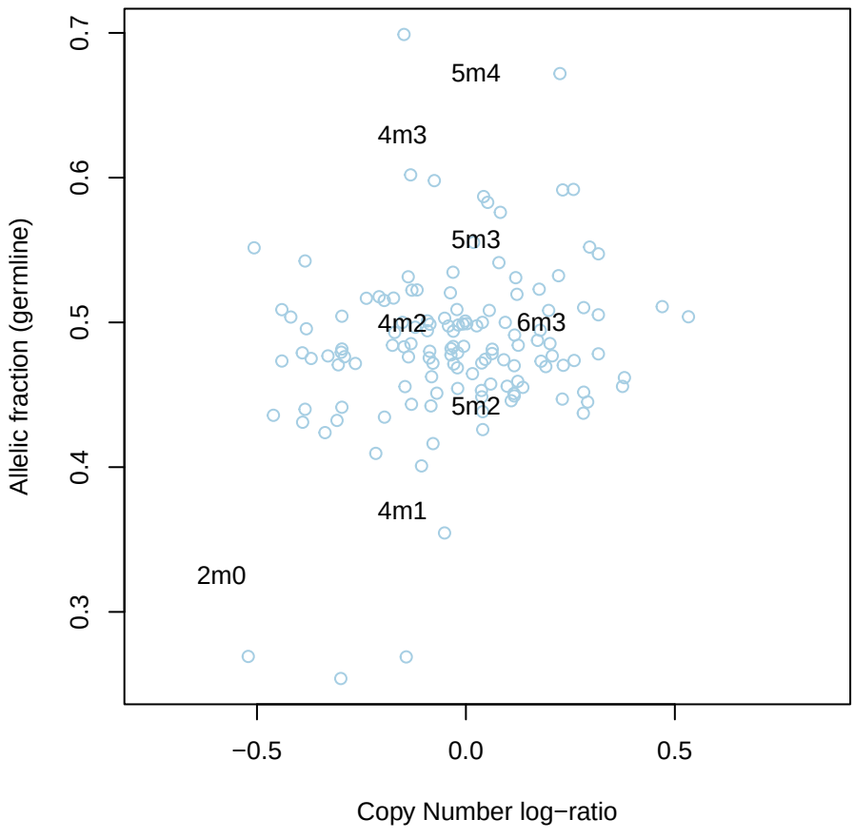

Frequency
0
5
10
15
20
0.2
0.4
0.6
0.8
1.0
Cellular fraction

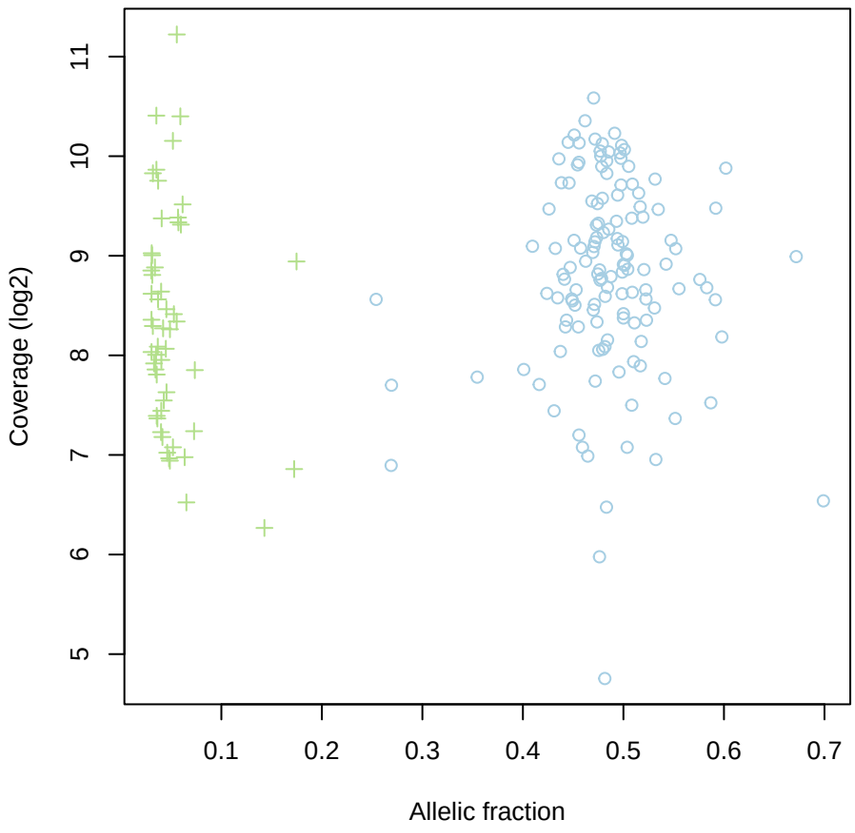

Purity: 0.35 Tumor ploidy: 4.855
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

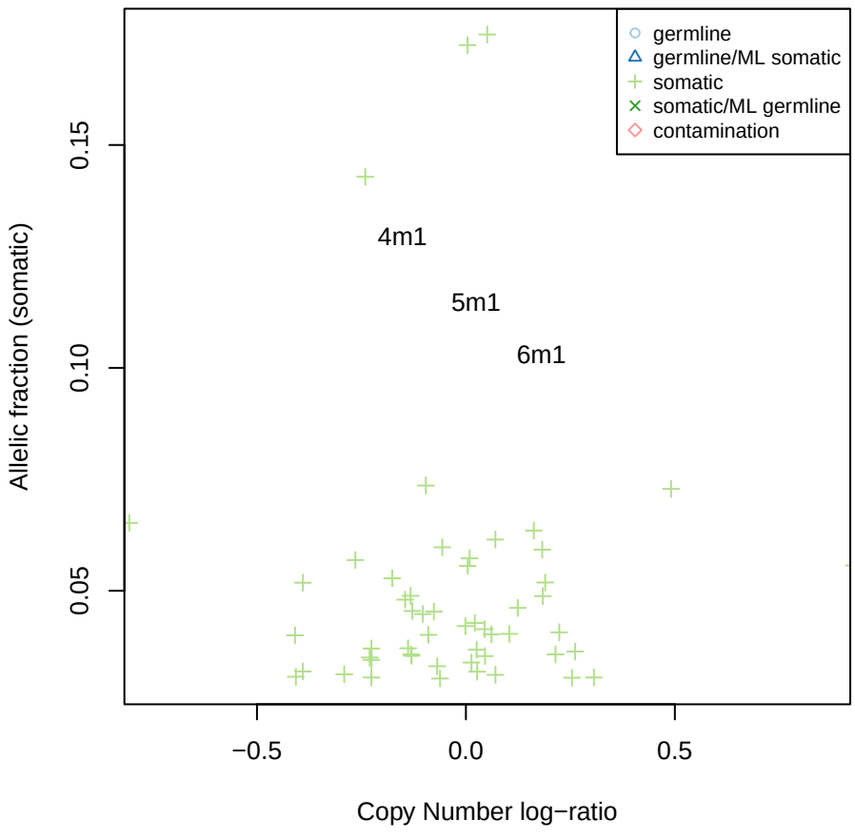

Purity: 0.35 Tumor ploidy: 4.855 SNV log−likelihood: −107.55 GoF: 93.2% Mean coverage: 511;497
1 2 3 4 5 6 7 8 10 12 13 14 15 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

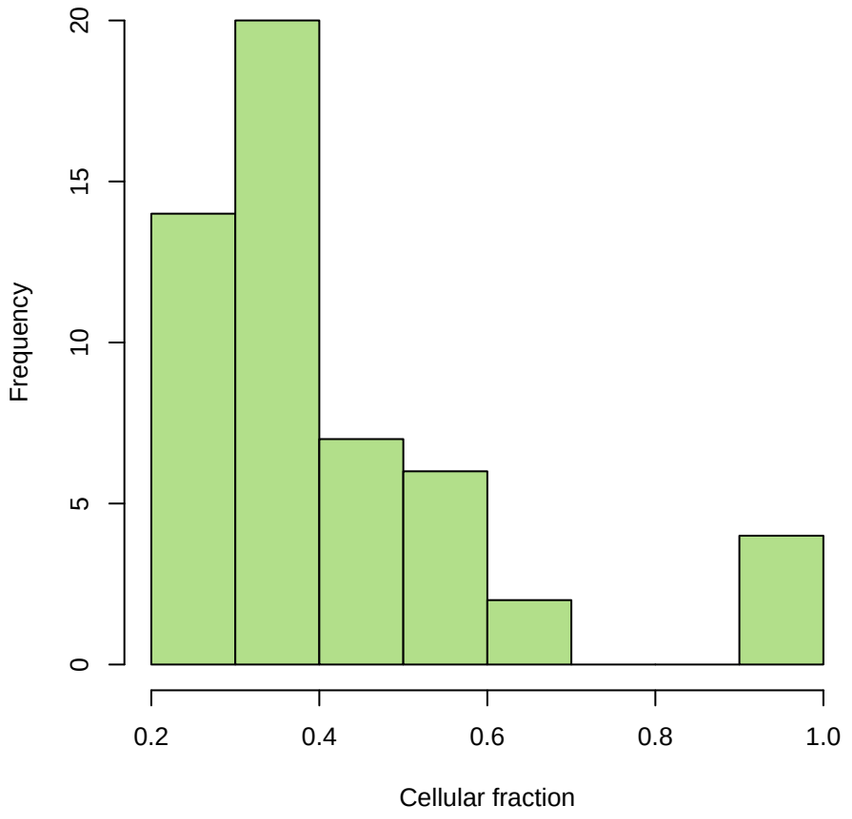

SCNA−fit log−likelihood: −8121.21
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6
0 20 40 60 80 100 120
SNV Index

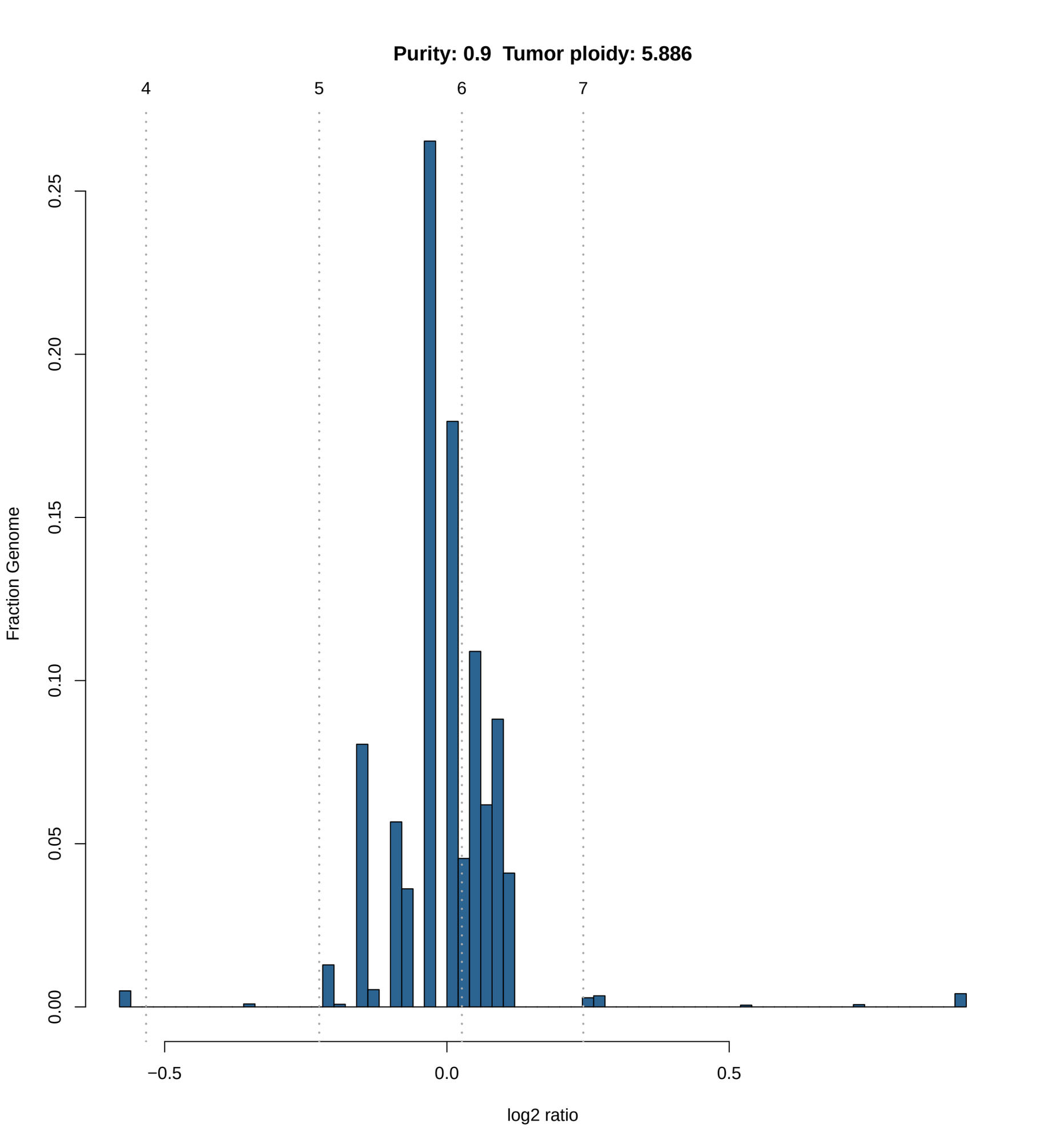

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120
SNV Index

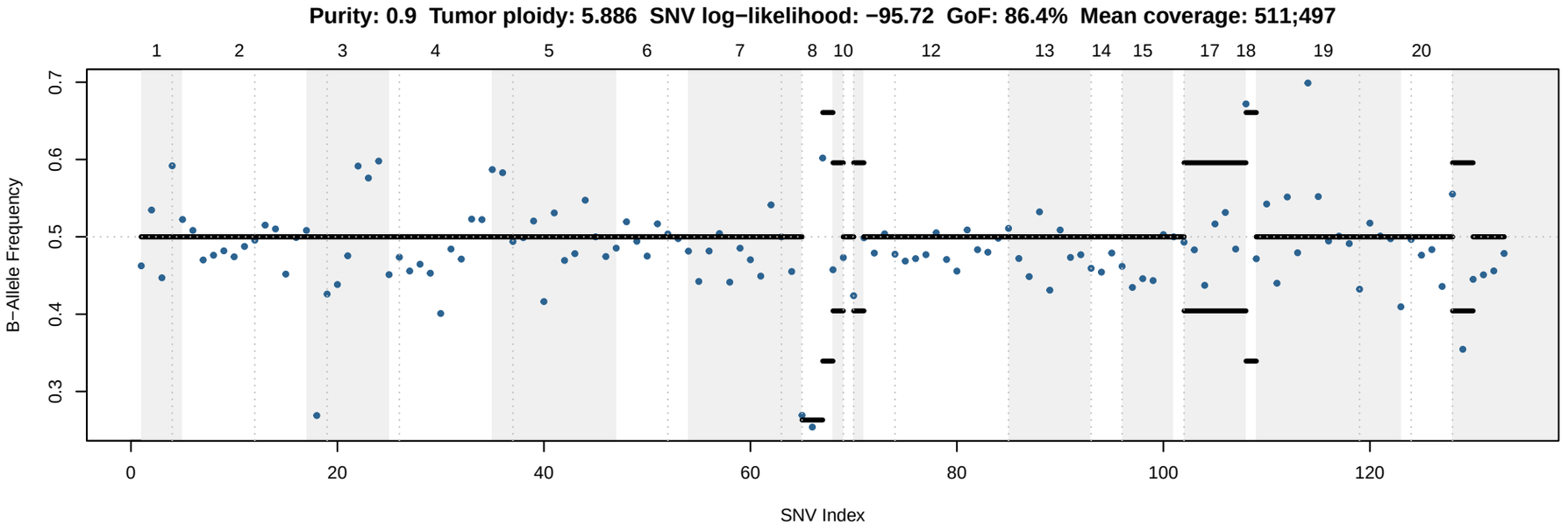

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
5m4
4m3
5m3
4m2
6m3
5m2
4m1
2m0
−0.5
0.0
0.5
Copy Number log−ratio

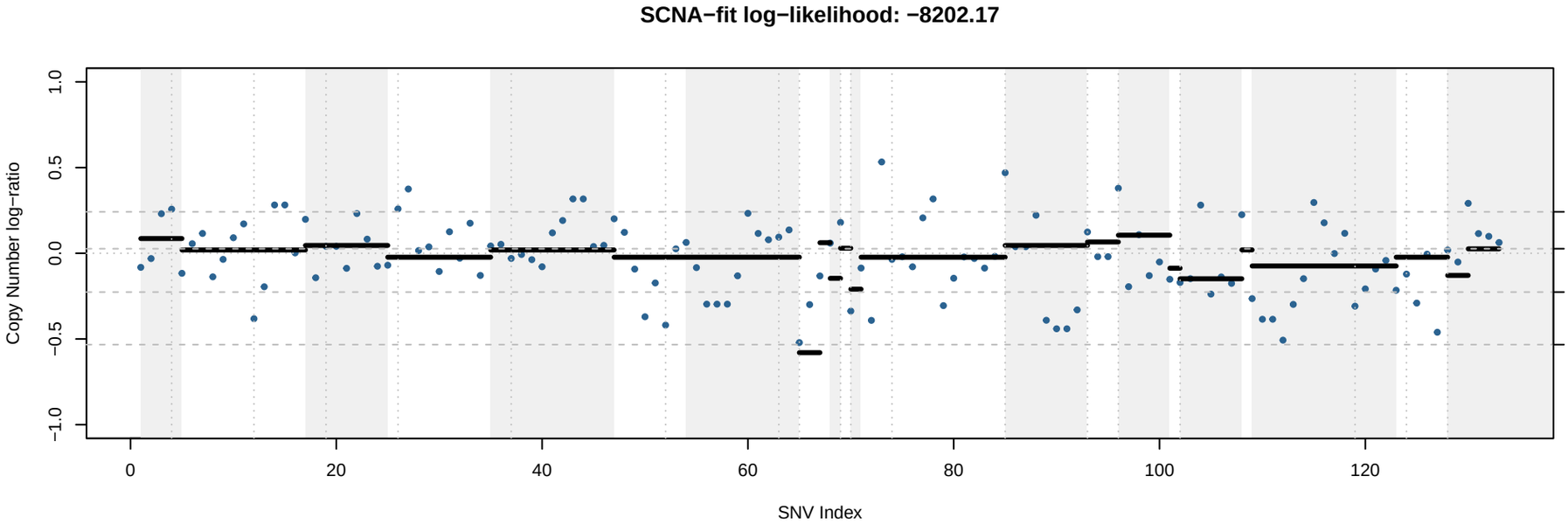

Coverage (log2)
5
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

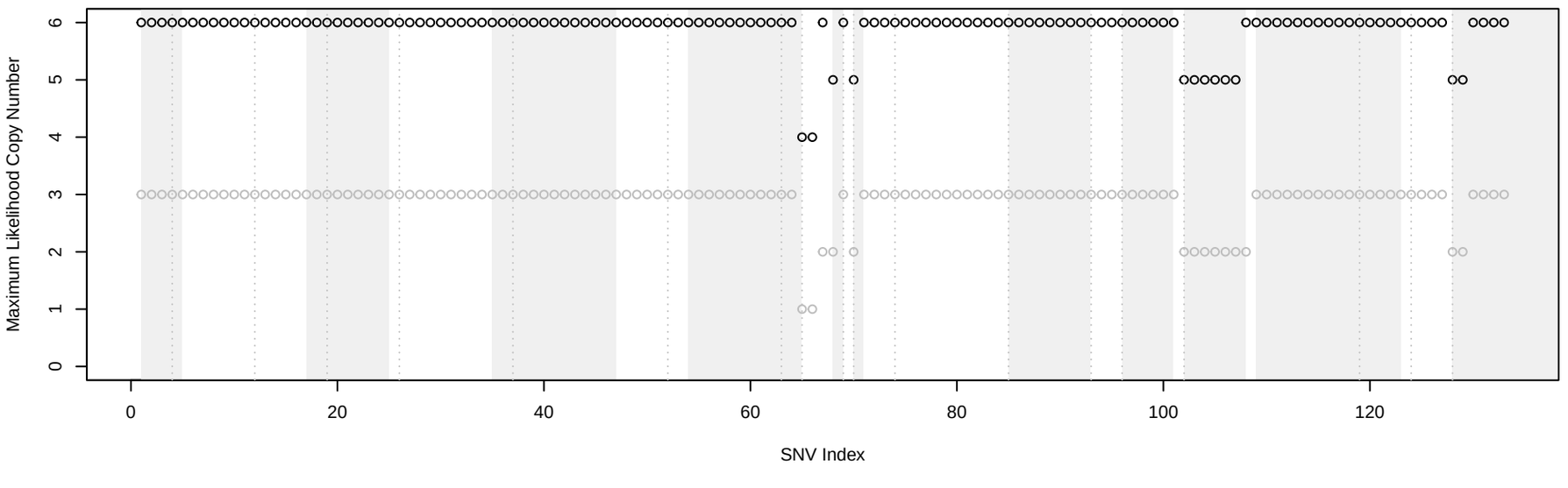

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
4m1
5m1
6m1
−0.5
0.0
0.5
Copy Number log−ratio

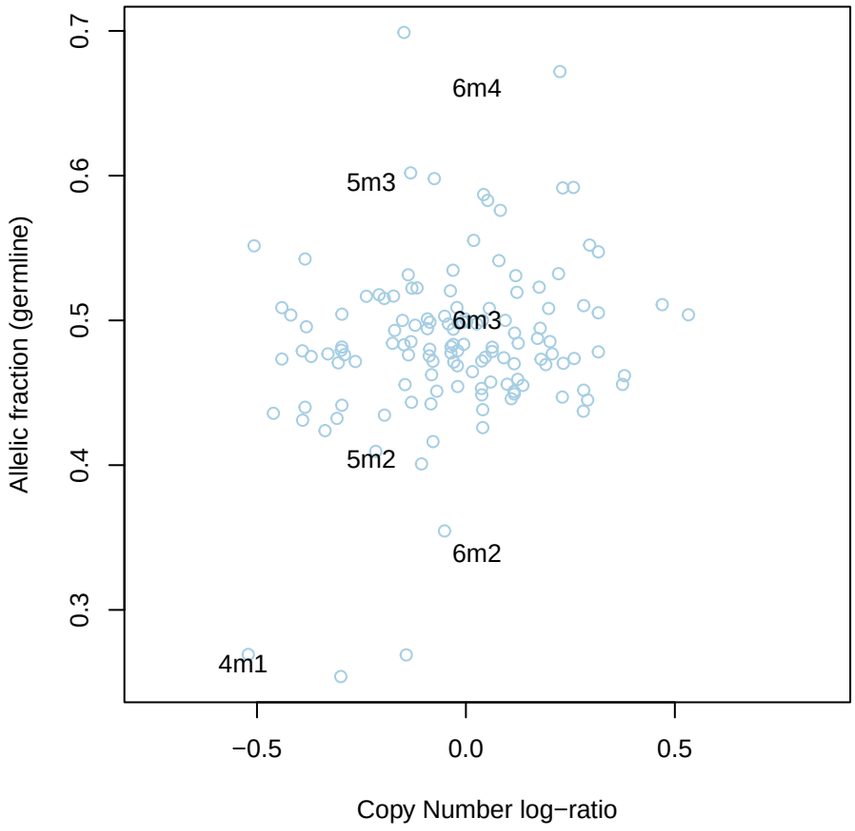

Frequency
0
5
10
15
20
0.2
0.4
0.6
0.8
1.0
Cellular fraction

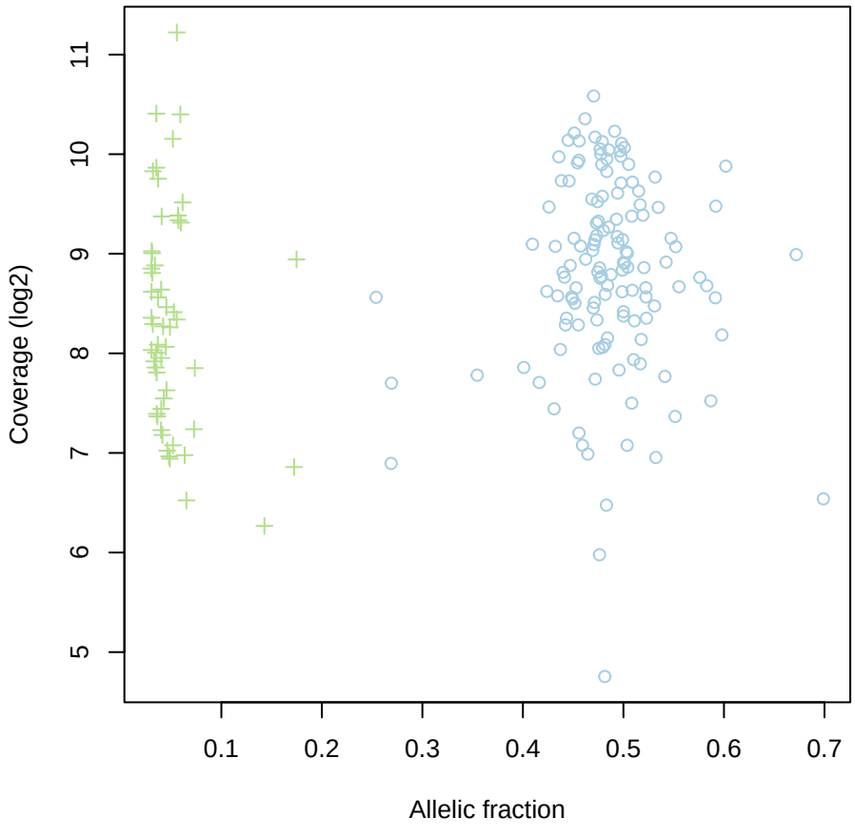

Purity: 0.9 Tumor ploidy: 5.886
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

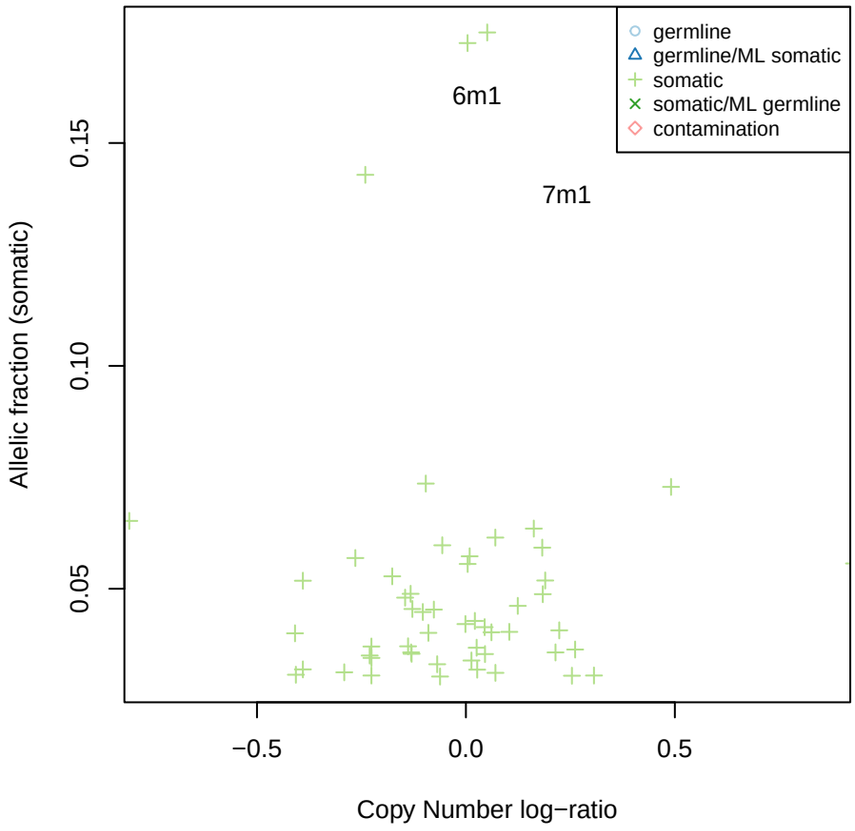

Purity: 0.9 Tumor ploidy: 5.886 SNV log−likelihood: −95.72 GoF: 86.4% Mean coverage: 511;497
1 2 3 4 5 6 7 8 10 12 13 14 15 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

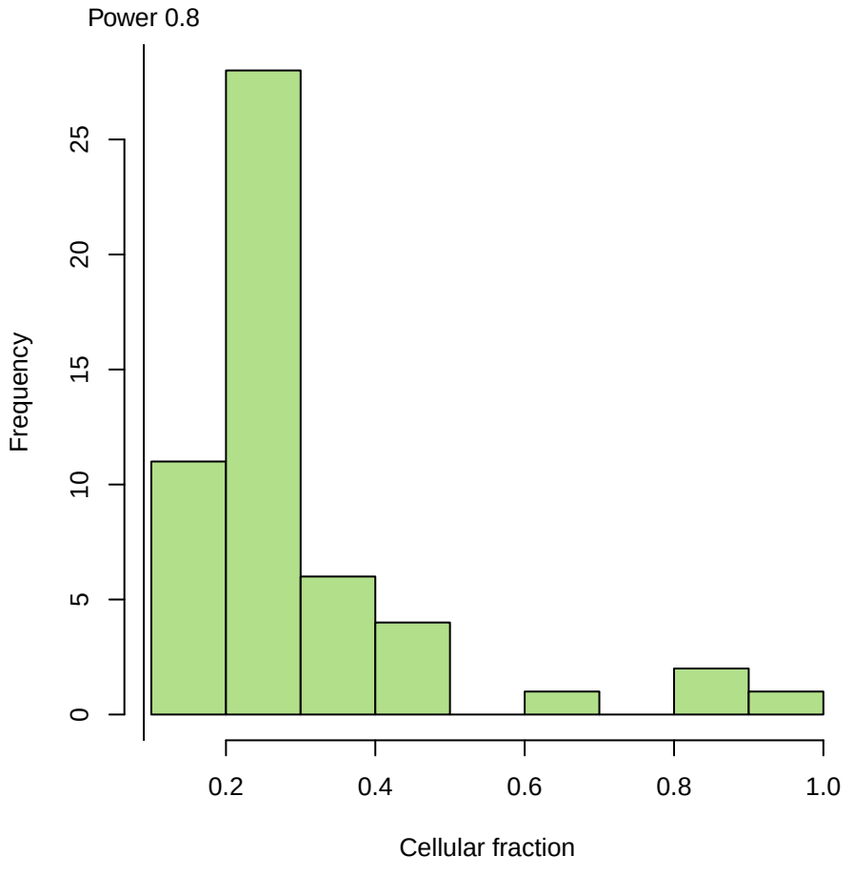

SCNA−fit log−likelihood: −8202.17
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5 6 7
0 20 40 60 80 100 120
SNV Index

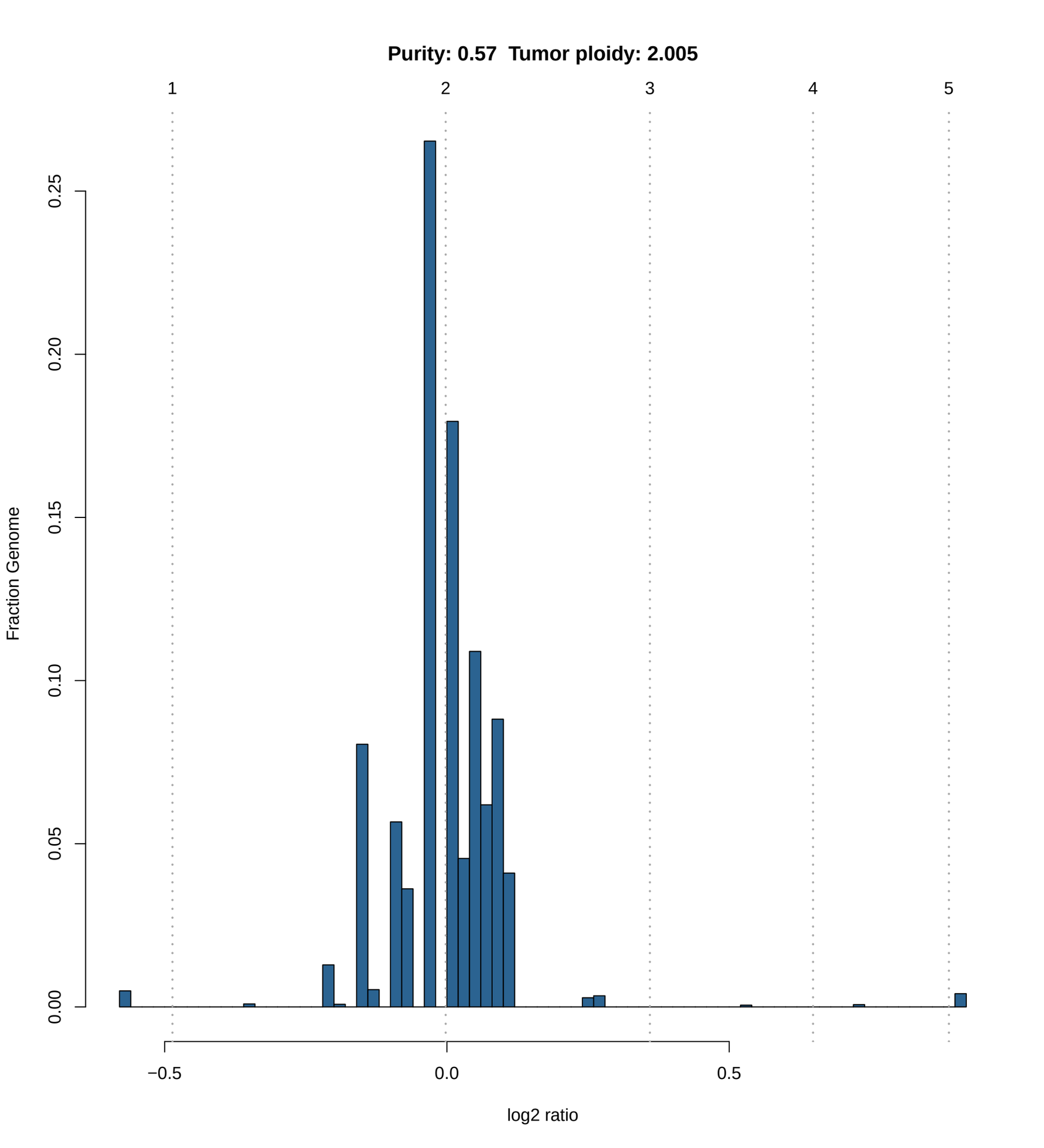

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120
SNV Index

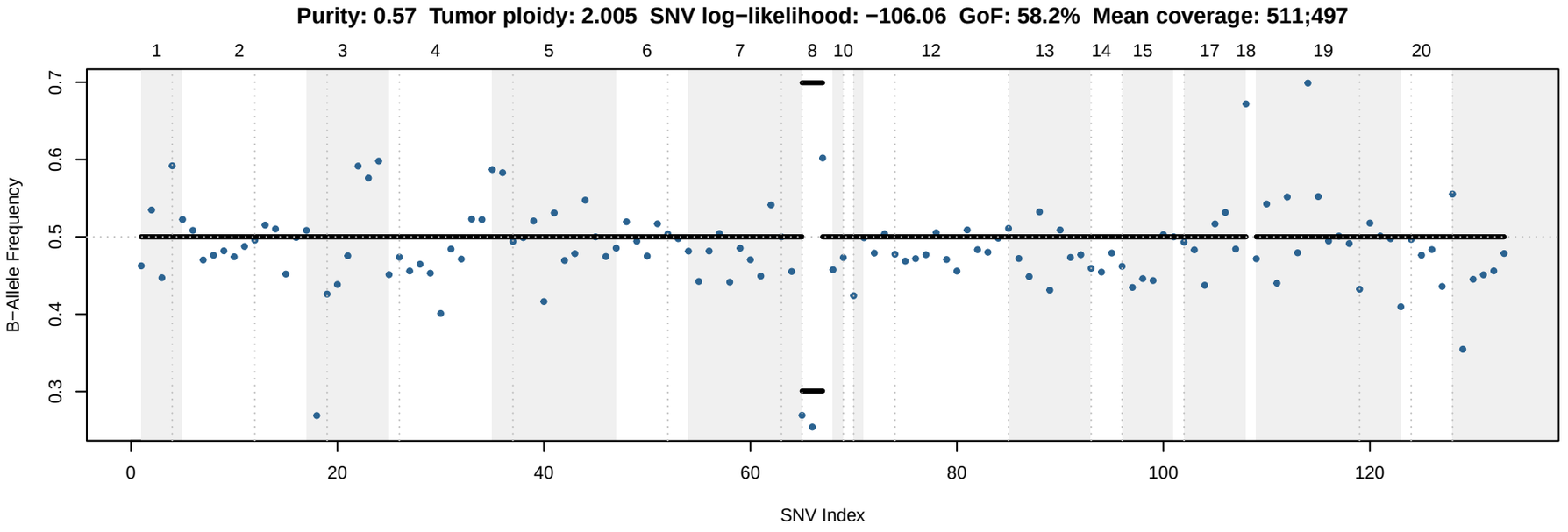

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
6m4
5m3
6m3
5m2
6m2
4m1
−0.5
0.0
0.5
Copy Number log−ratio

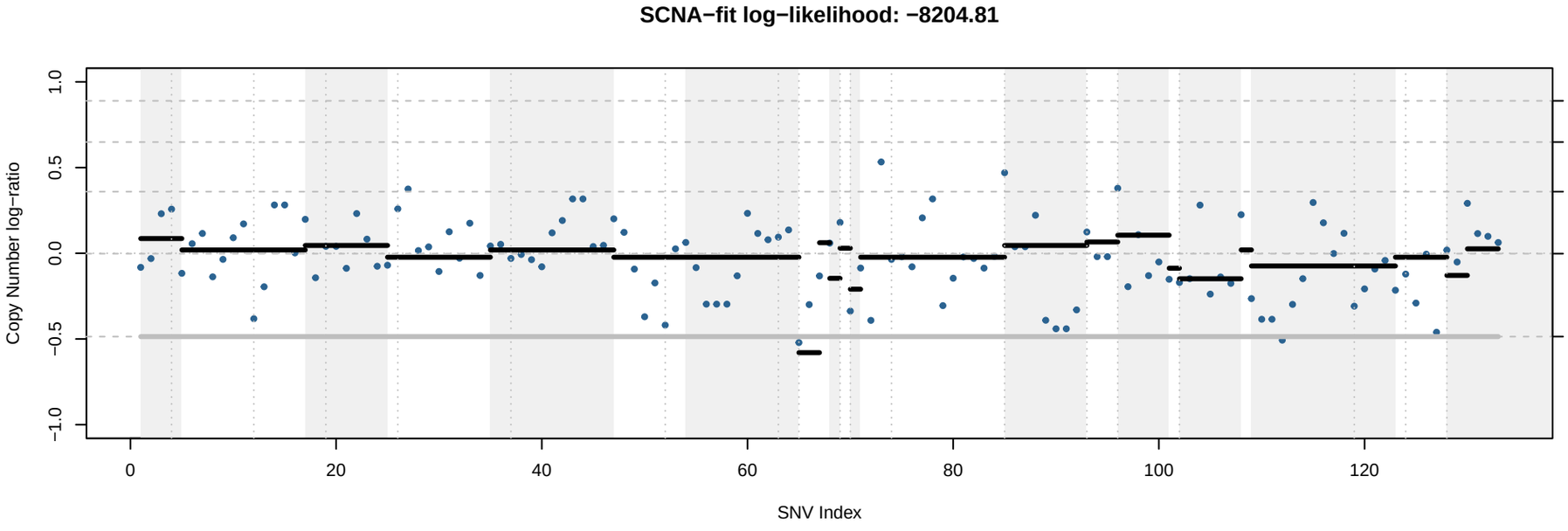

Coverage (log2)
5
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

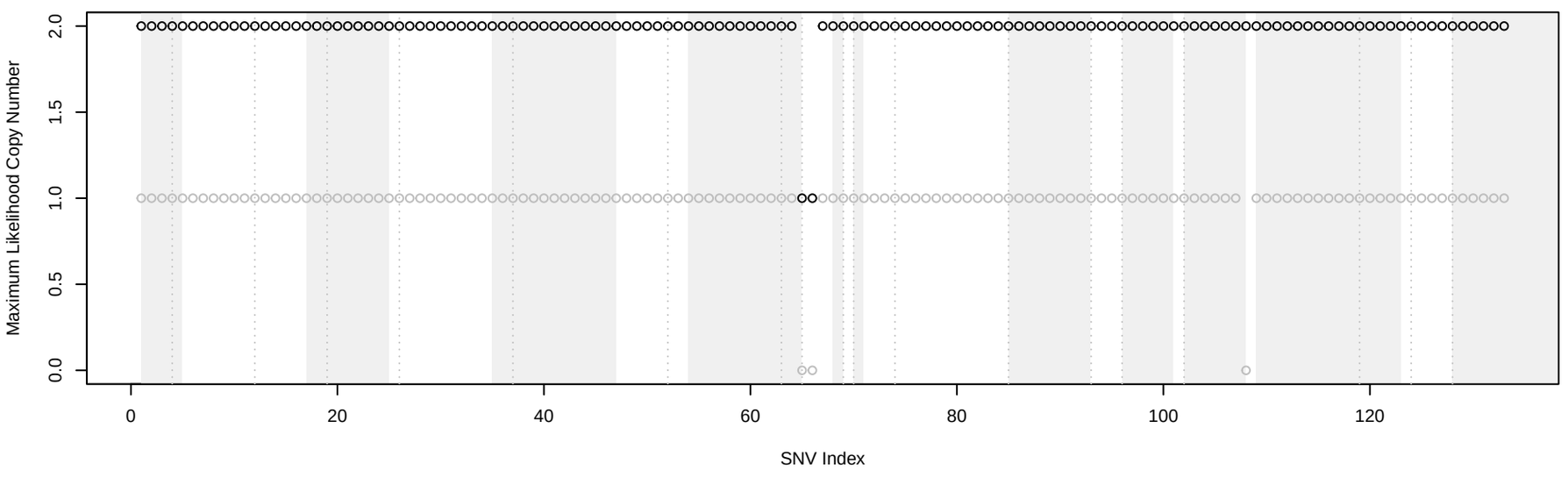

Allelic fraction (somatic)
0.05
0.10
0.15
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m1
7m1
−0.5
0.0
0.5
Copy Number log−ratio

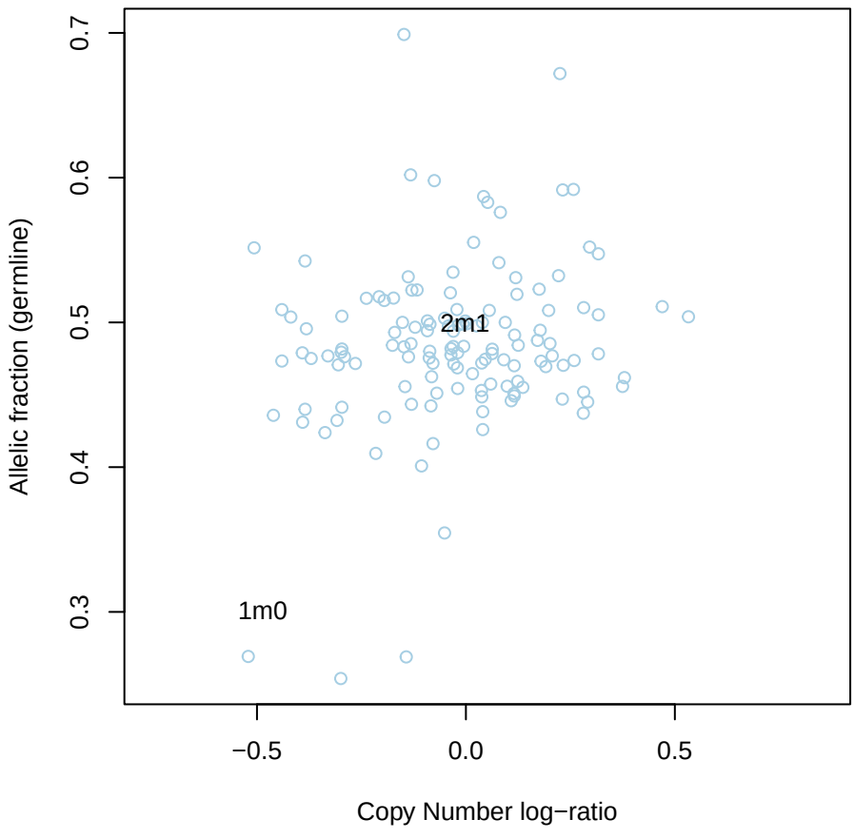

Power 0.8
Frequency
0
5
10
15
20
25
0.2
0.4
0.6
0.8
1.0
Cellular fraction

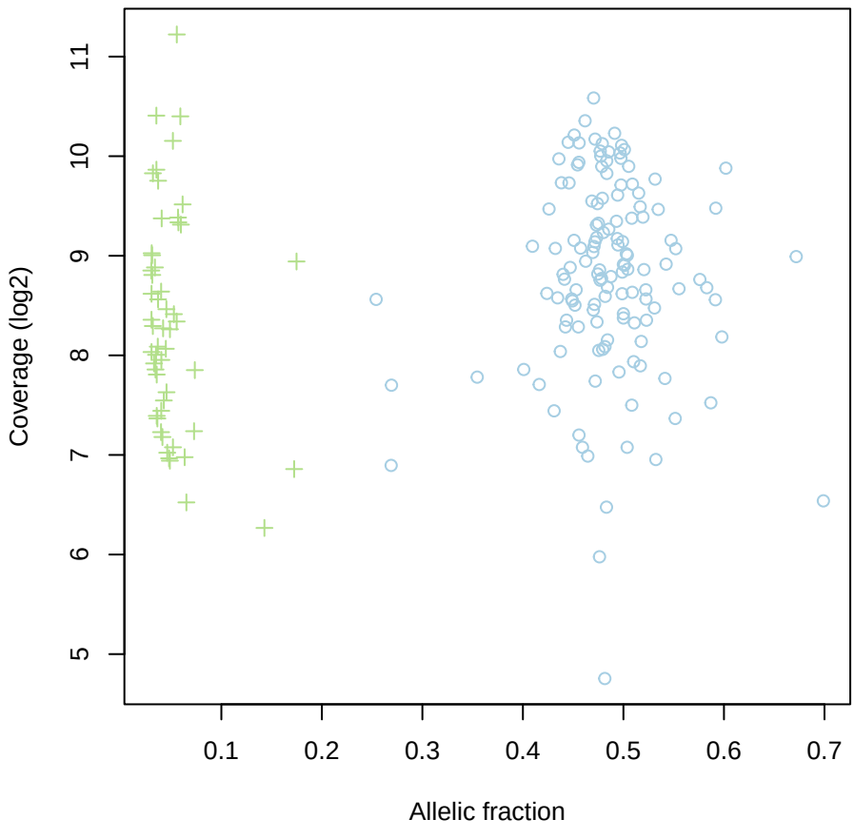

Purity: 0.57 Tumor ploidy: 2.005
1
2
3
4
5
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

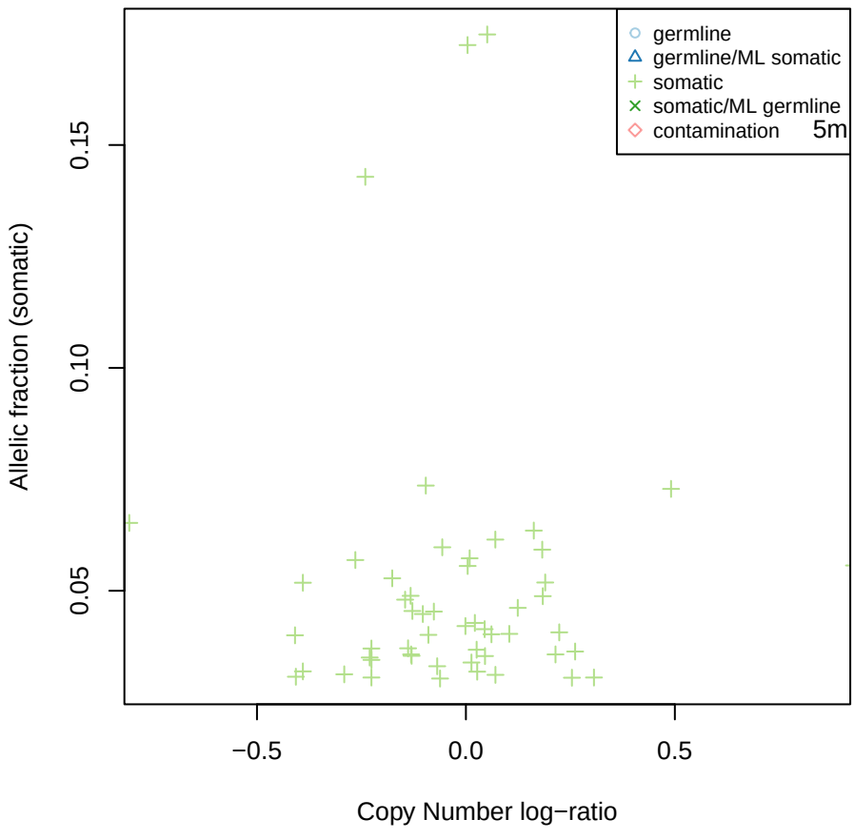

Purity: 0.57 Tumor ploidy: 2.005 SNV log−likelihood: −106.06 GoF: 58.2% Mean coverage: 511;497
1 2 3 4 5 6 7 8 10 12 13 14 15 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

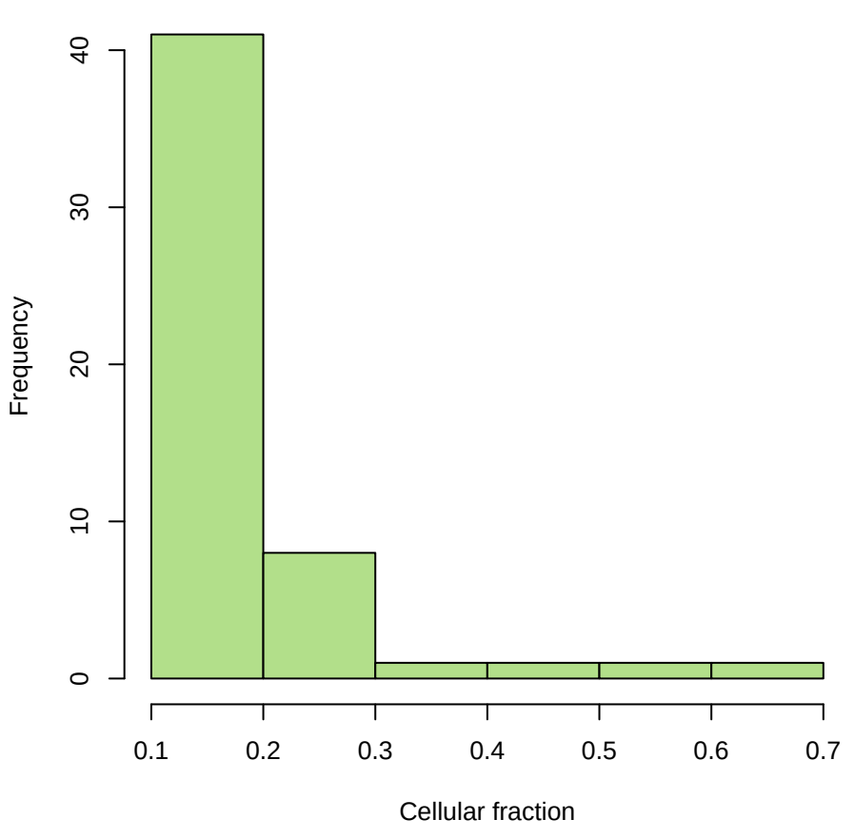

SCNA−fit log−likelihood: −8204.81
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5
0 20 40 60 80 100 120
SNV Index

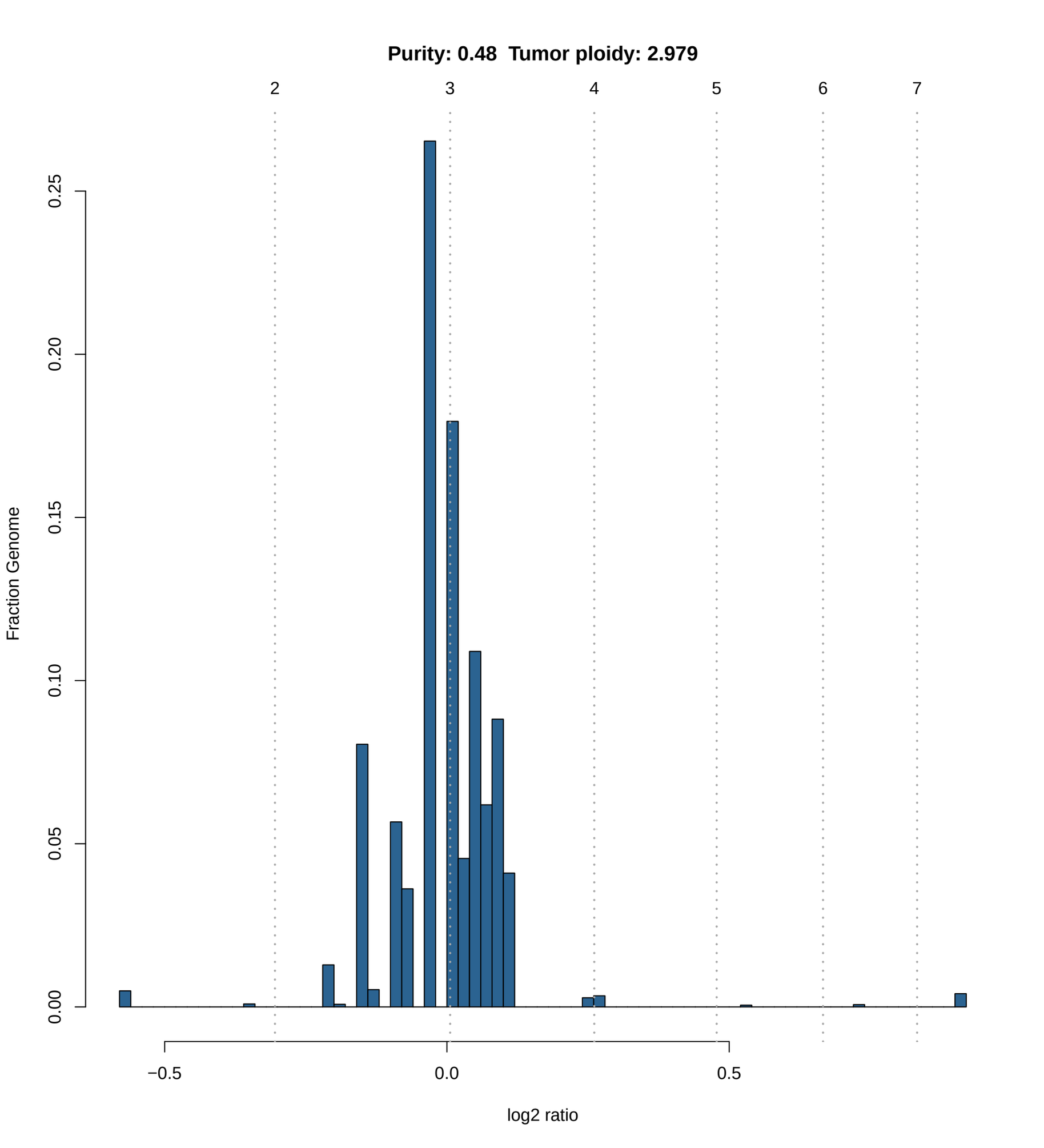

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 20 40 60 80 100 120
SNV Index

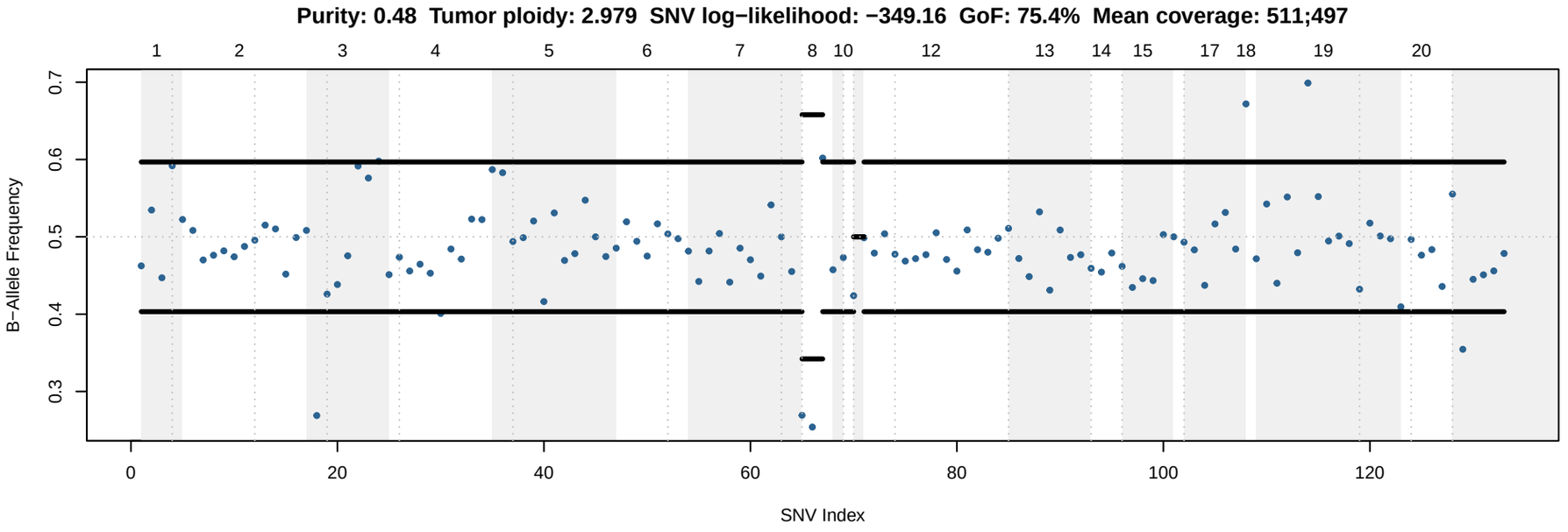

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
2m1
1m0
−0.5
0.0
0.5
Copy Number log−ratio

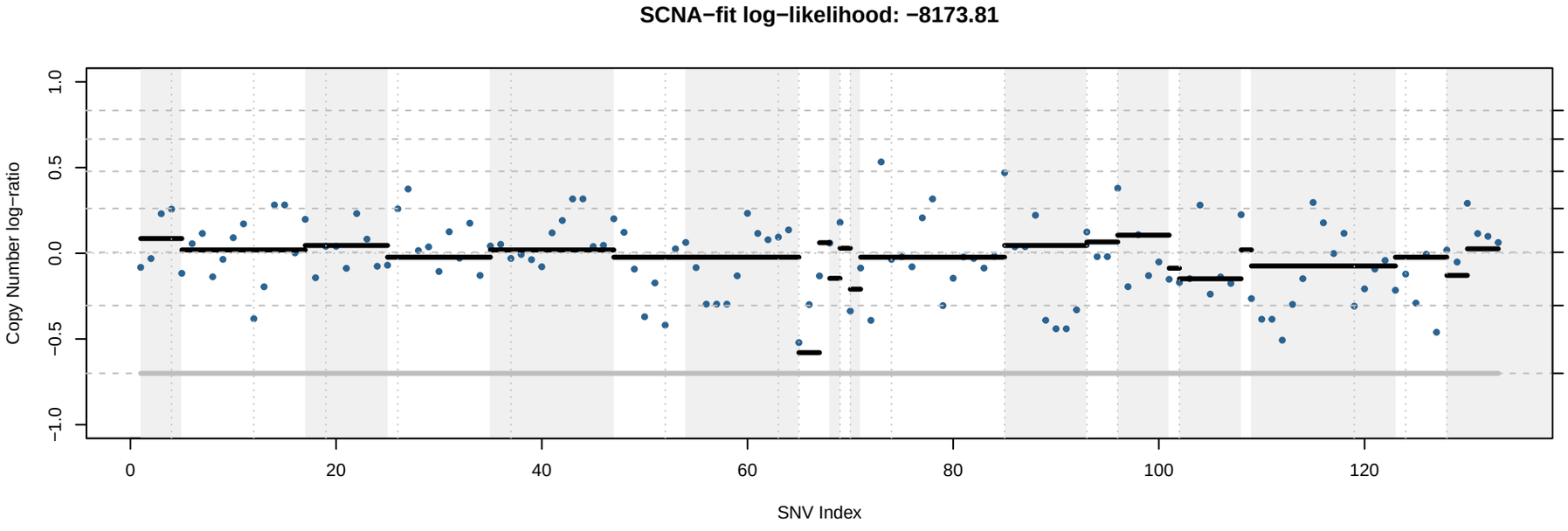

Coverage (log2)
5
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

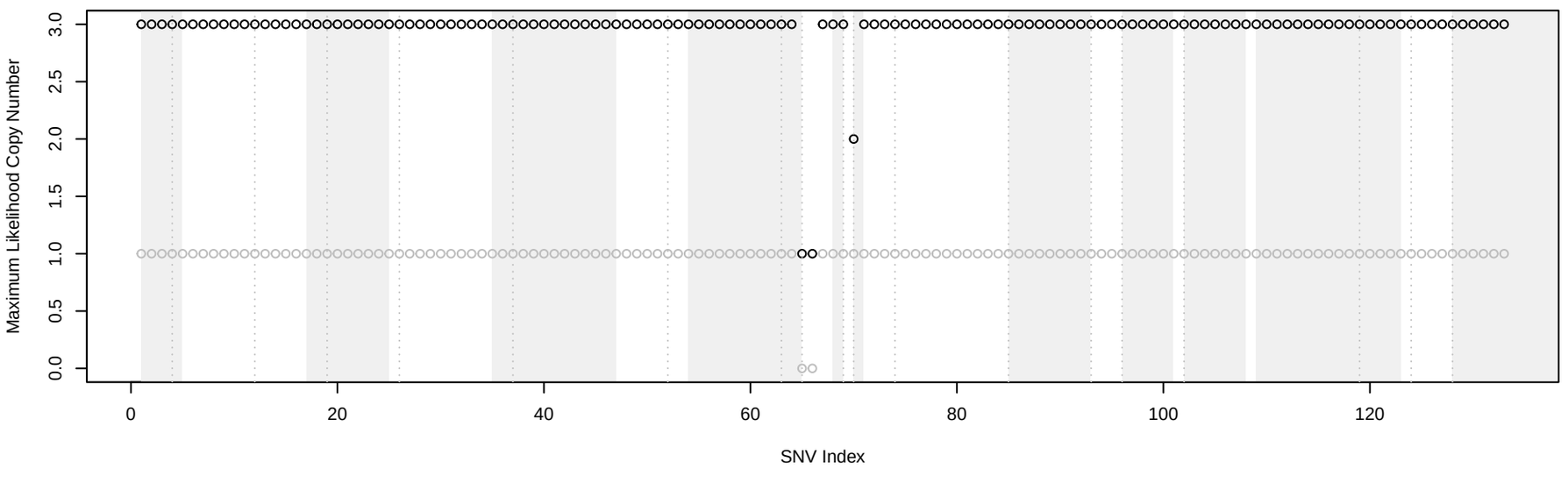

Allelic fraction (somatic)
0.05
0.10
0.15
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m
−0.5
0.0
0.5
Copy Number log−ratio

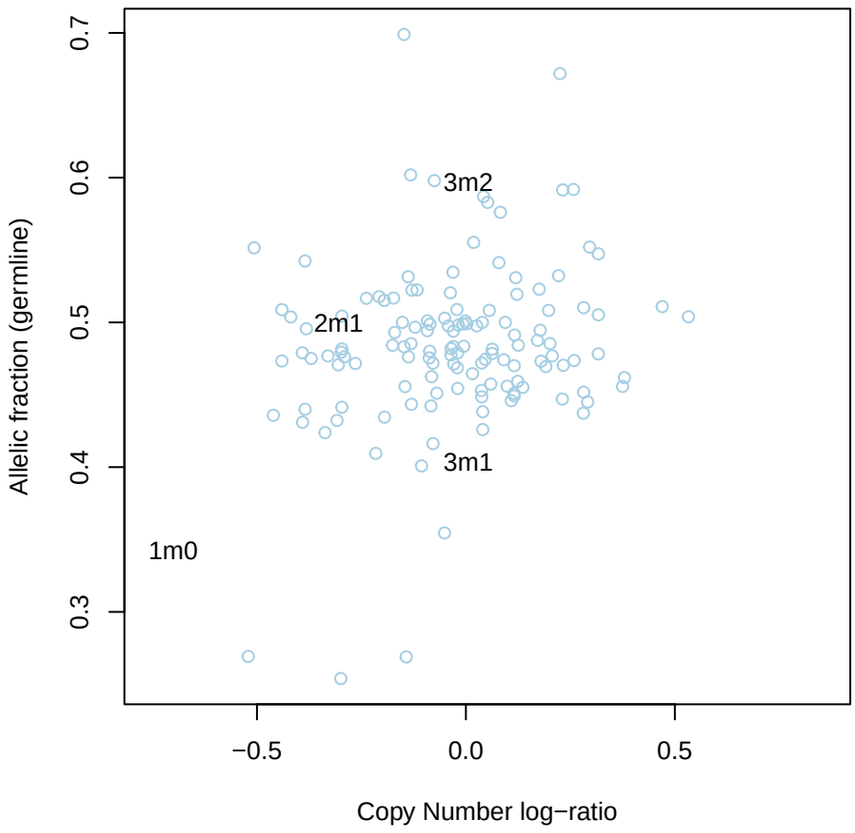

Frequency
0
10
20
30
40
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Cellular fraction

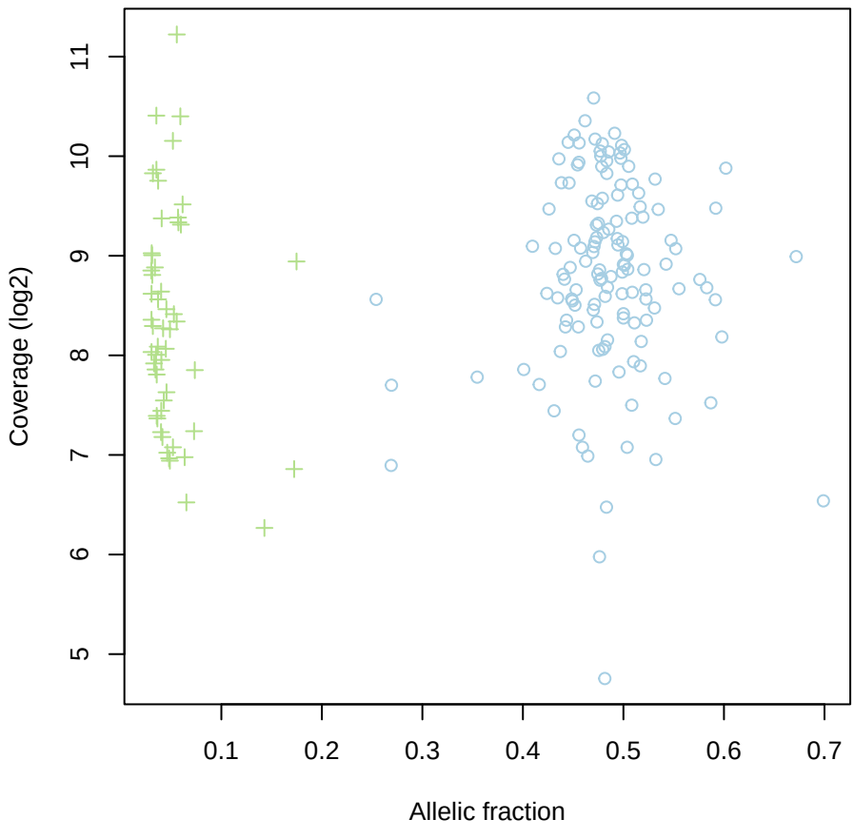

Purity: 0.48 Tumor ploidy: 2.979
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

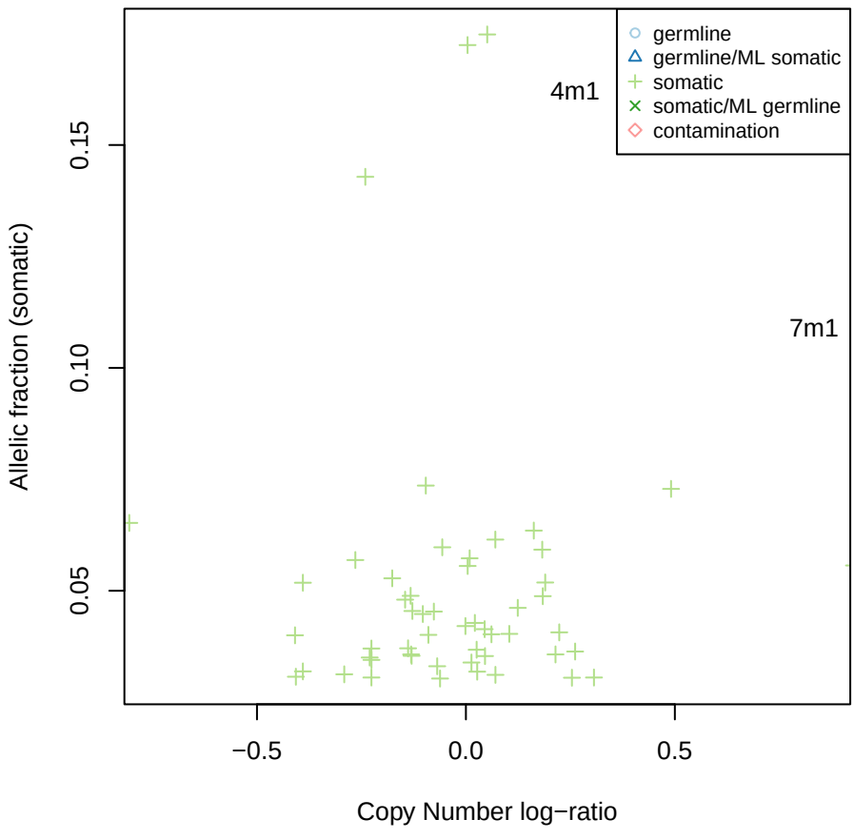

Purity: 0.48 Tumor ploidy: 2.979 SNV log−likelihood: −349.16 GoF: 75.4% Mean coverage: 511;497
1 2 3 4 5 6 7 8 10 12 13 14 15 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

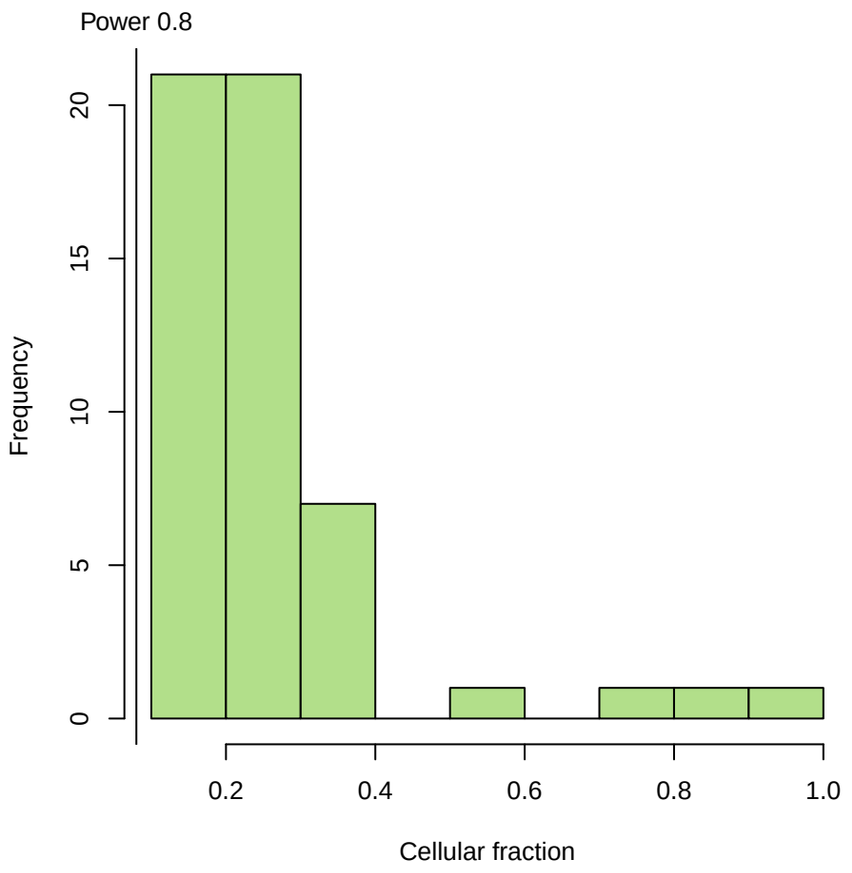

SCNA−fit log−likelihood: −8173.81
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

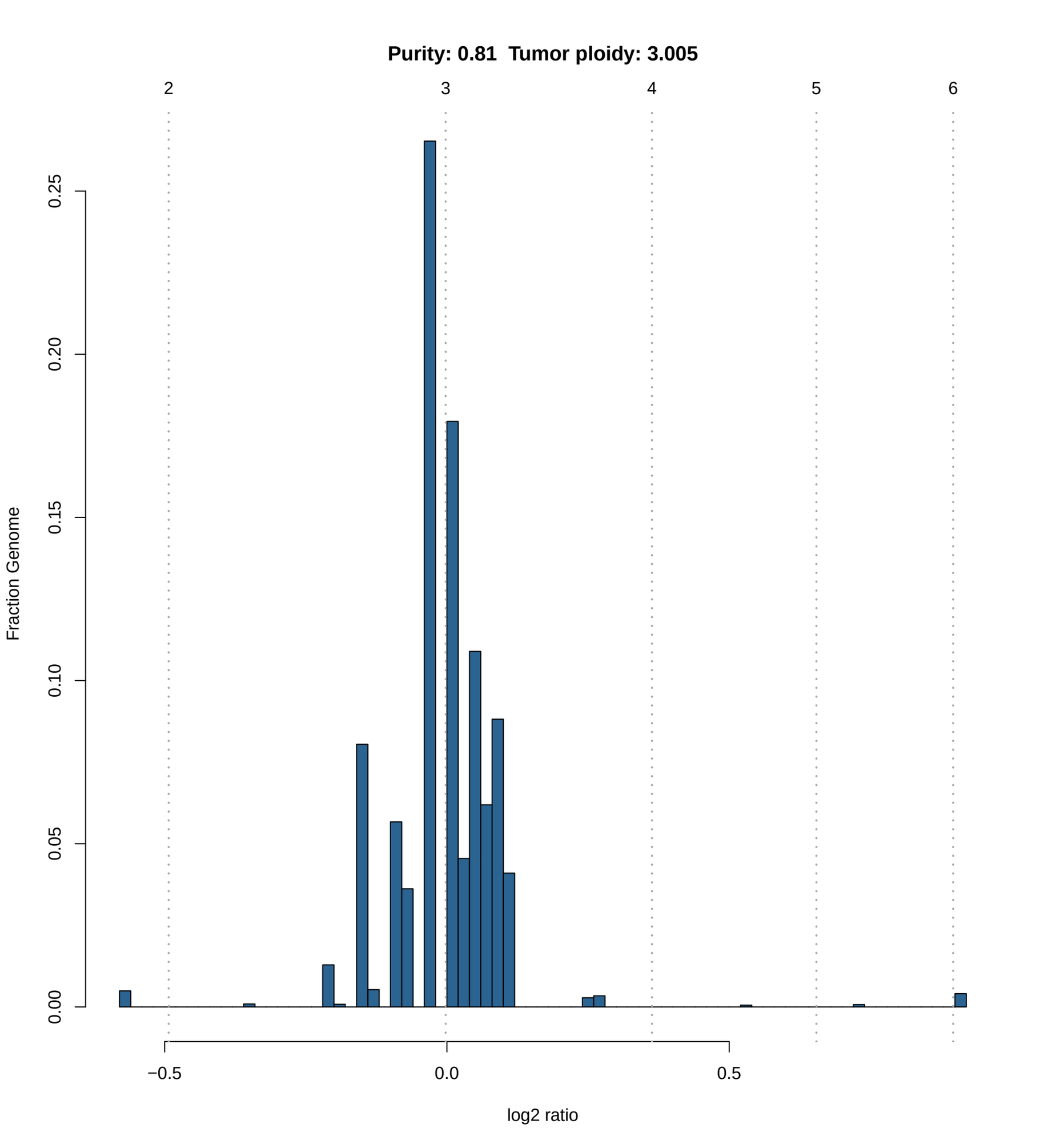

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120
SNV Index

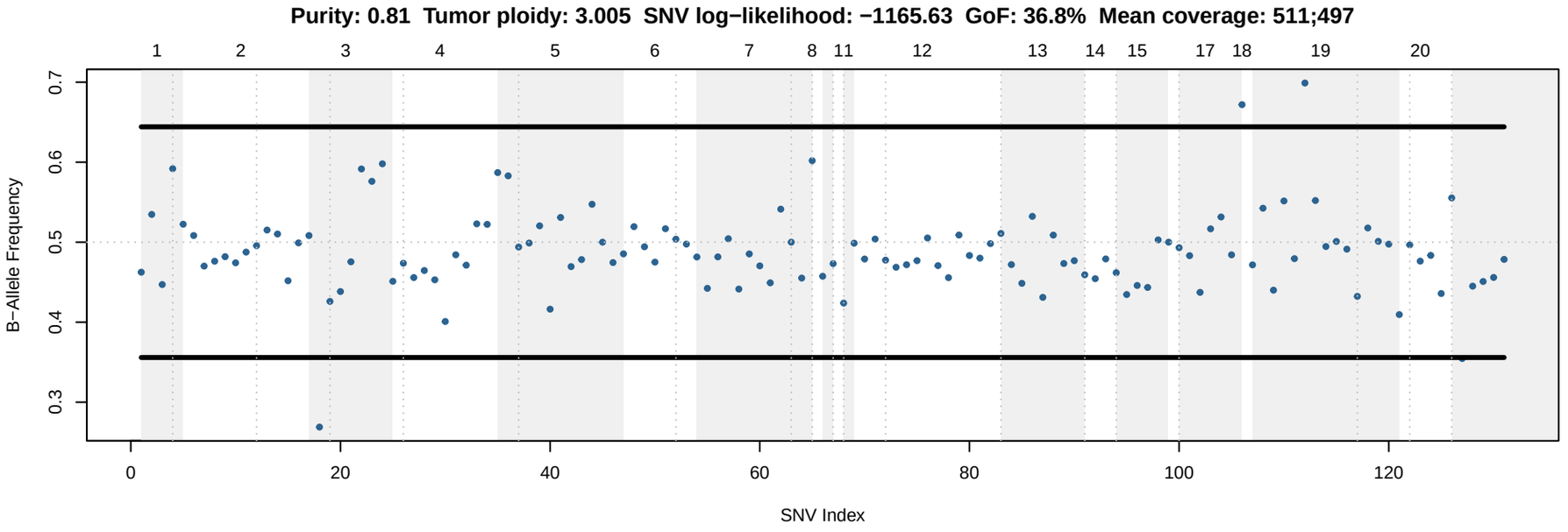

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
3m2
2m1
3m1
1m0
−0.5
0.0
0.5
Copy Number log−ratio

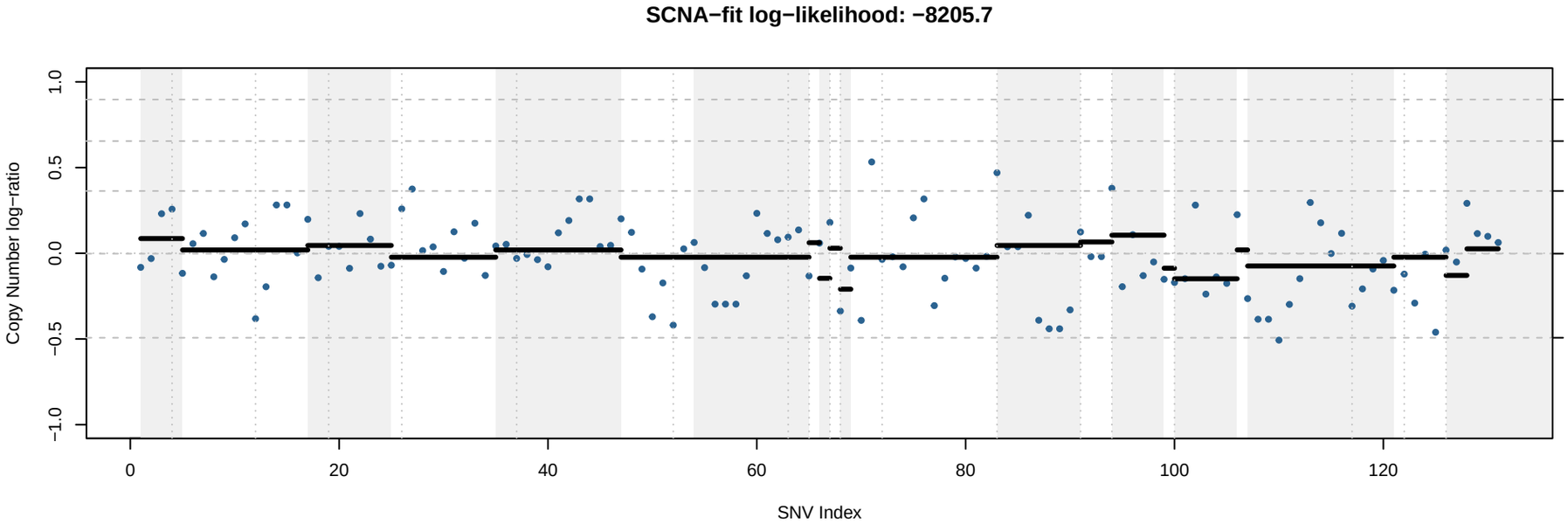

Coverage (log2)
5
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

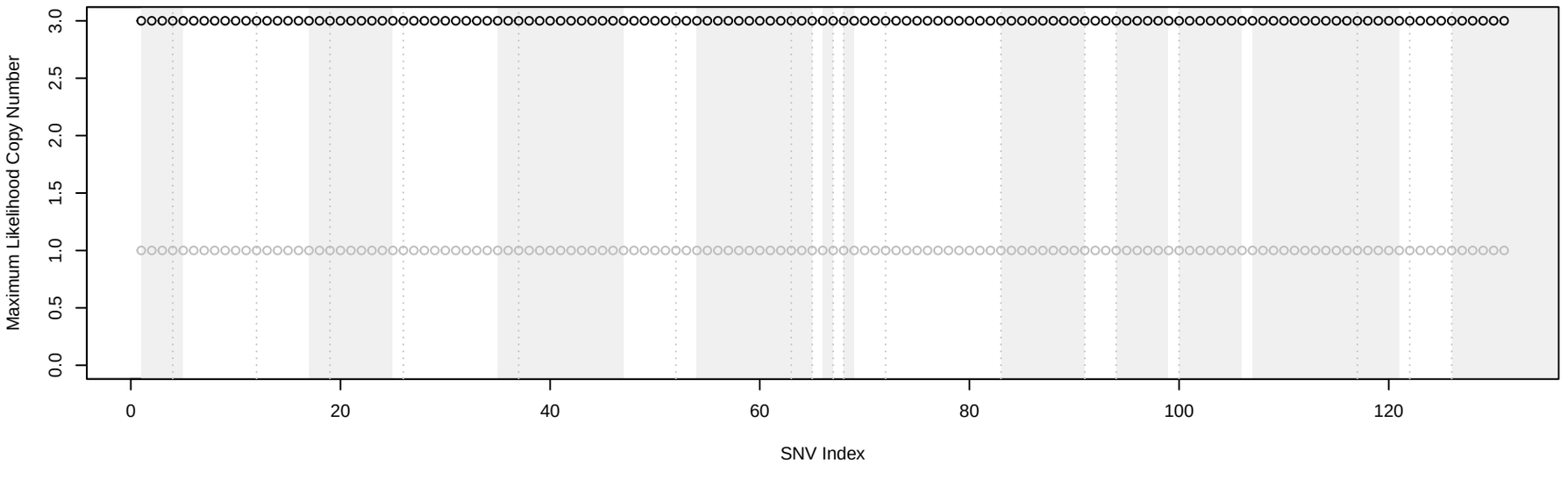

Allelic fraction (somatic)
0.05
0.10
0.15
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
7m1
−0.5
0.0
0.5
Copy Number log−ratio

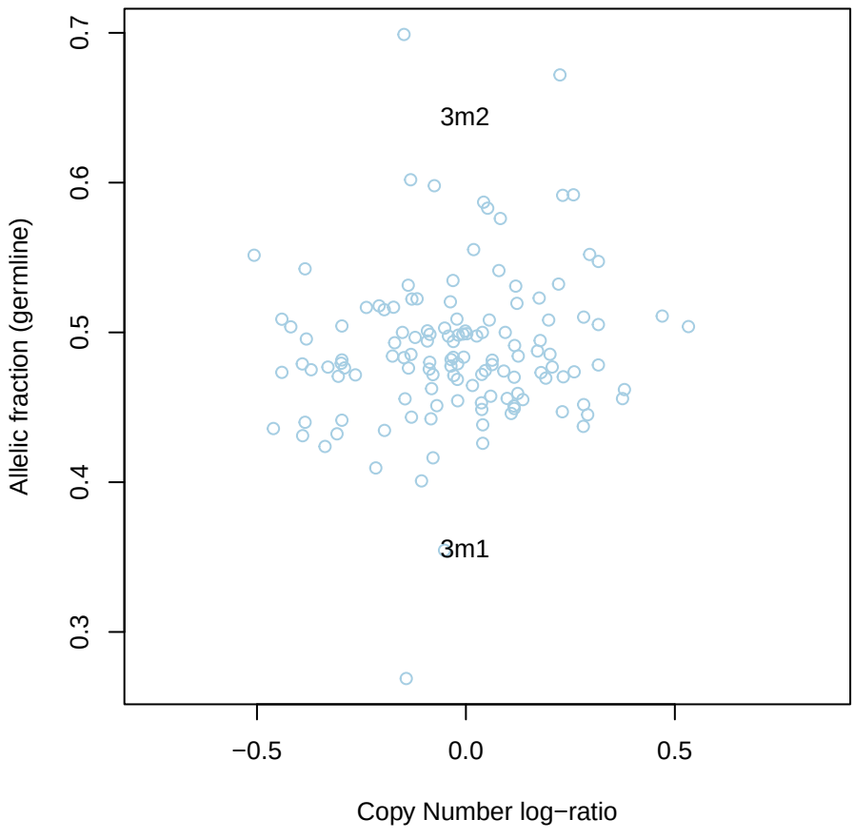

Power 0.8
Frequency
0
5
10
15
20
0.2
0.4
0.6
0.8
1.0
Cellular fraction

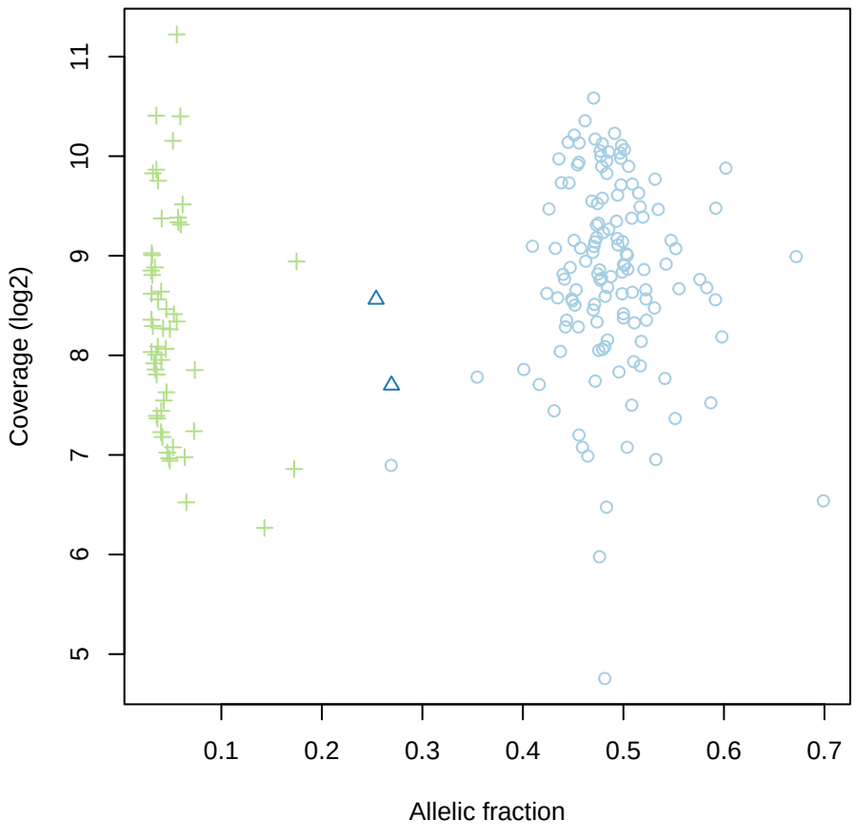

Purity: 0.81 Tumor ploidy: 3.005
2
3
4
5
6
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

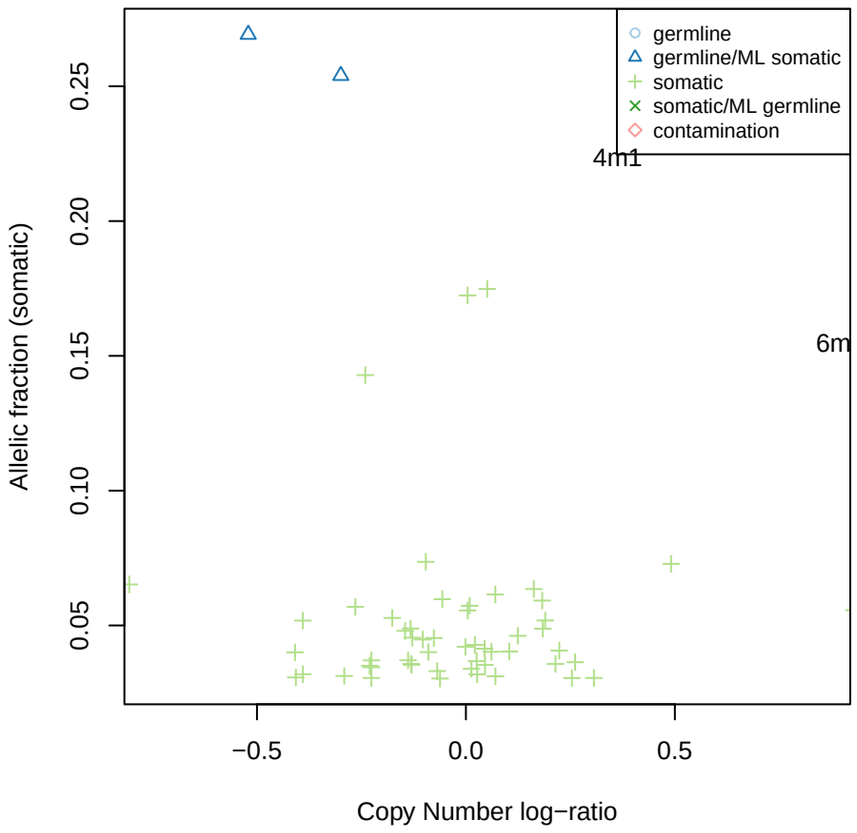

Purity: 0.81 Tumor ploidy: 3.005 SNV log−likelihood: −1165.63 GoF: 36.8% Mean coverage: 511;497
1 2 3 4 5 6 7 8 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

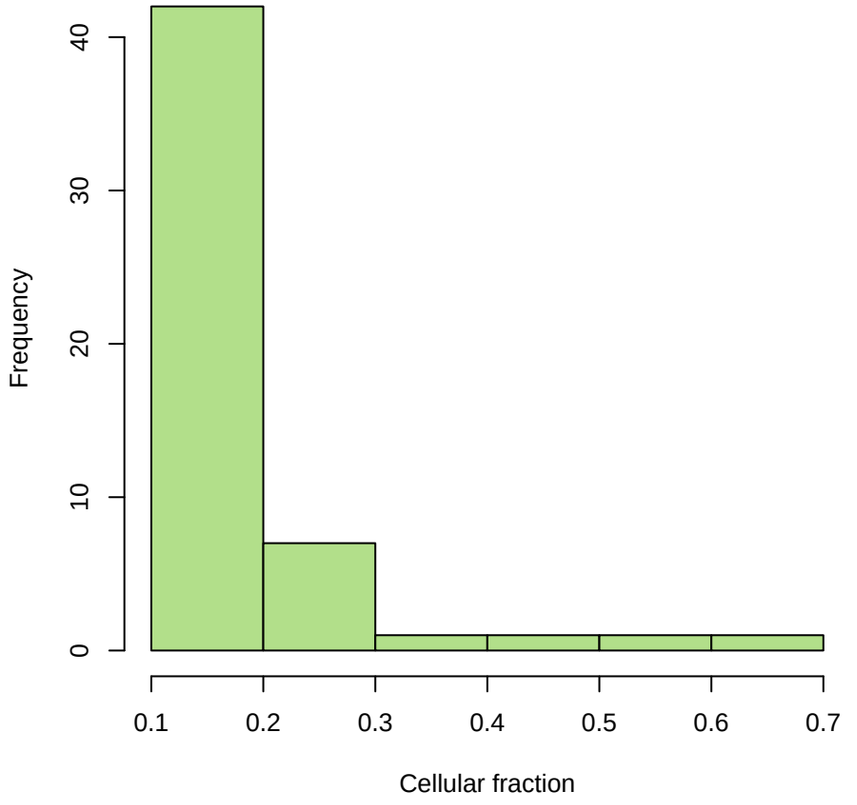

SCNA−fit log−likelihood: −8205.7
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6
0 20 40 60 80 100 120
SNV Index


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)
0.3
0.4
0.5
0.6
0.7
3m2
3m1
−0.5
0.0
0.5
Copy Number log−ratio


Coverage (log2)
5
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction


Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
6m
−0.5
0.0
0.5
Copy Number log−ratio


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