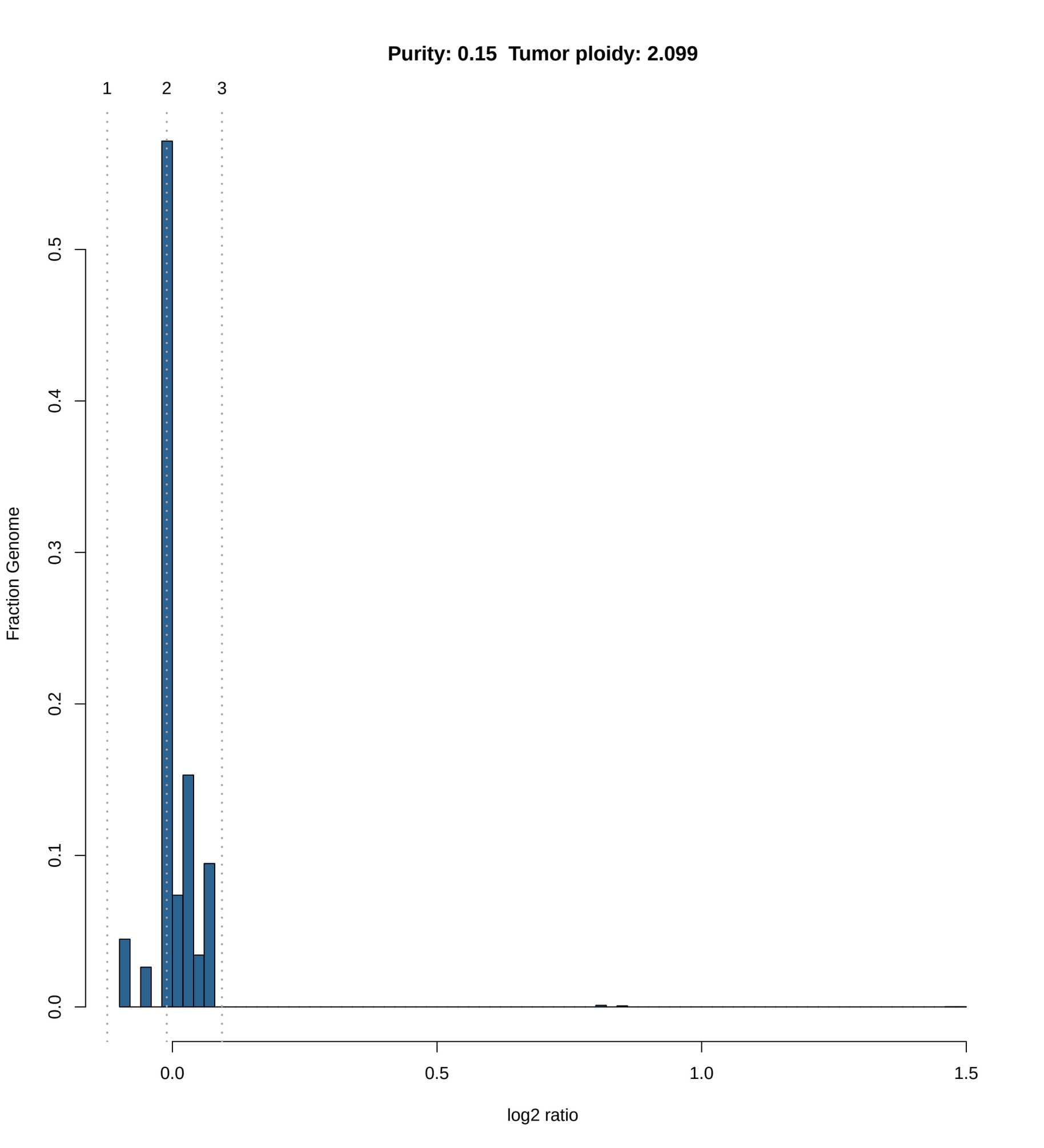
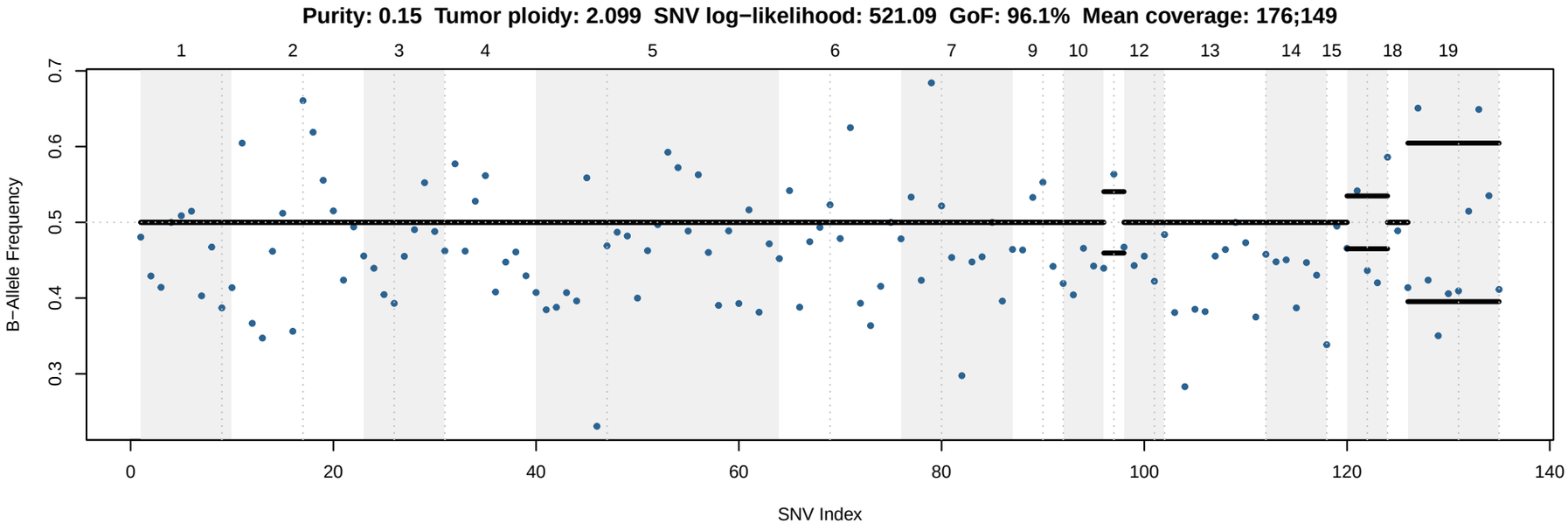
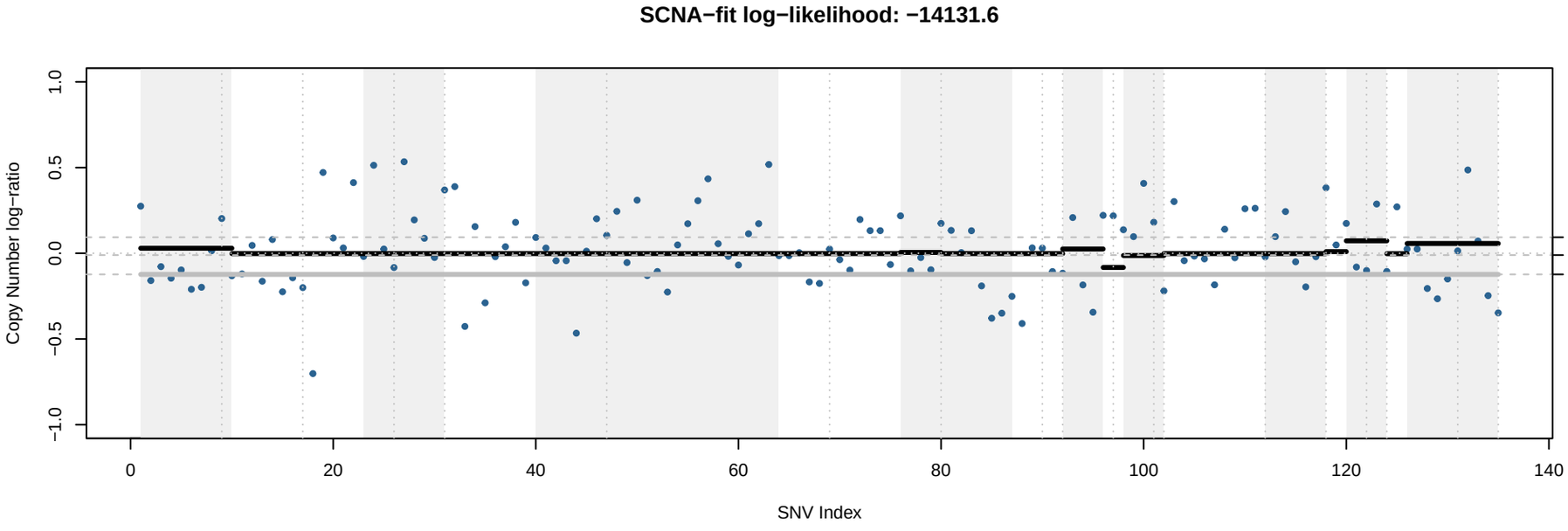
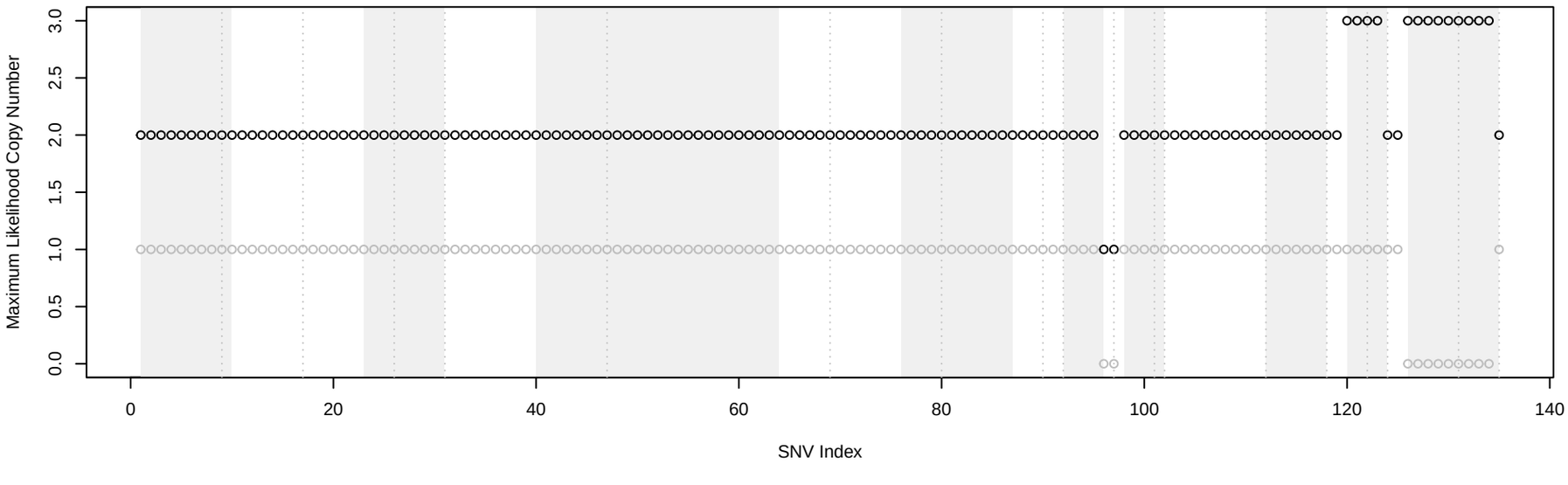
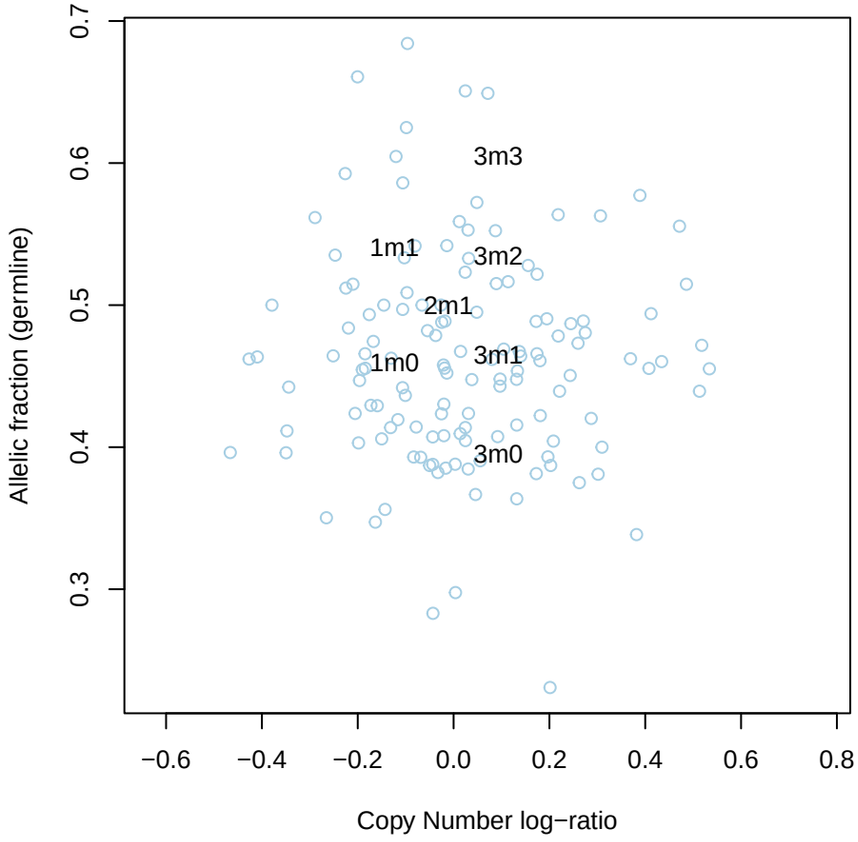
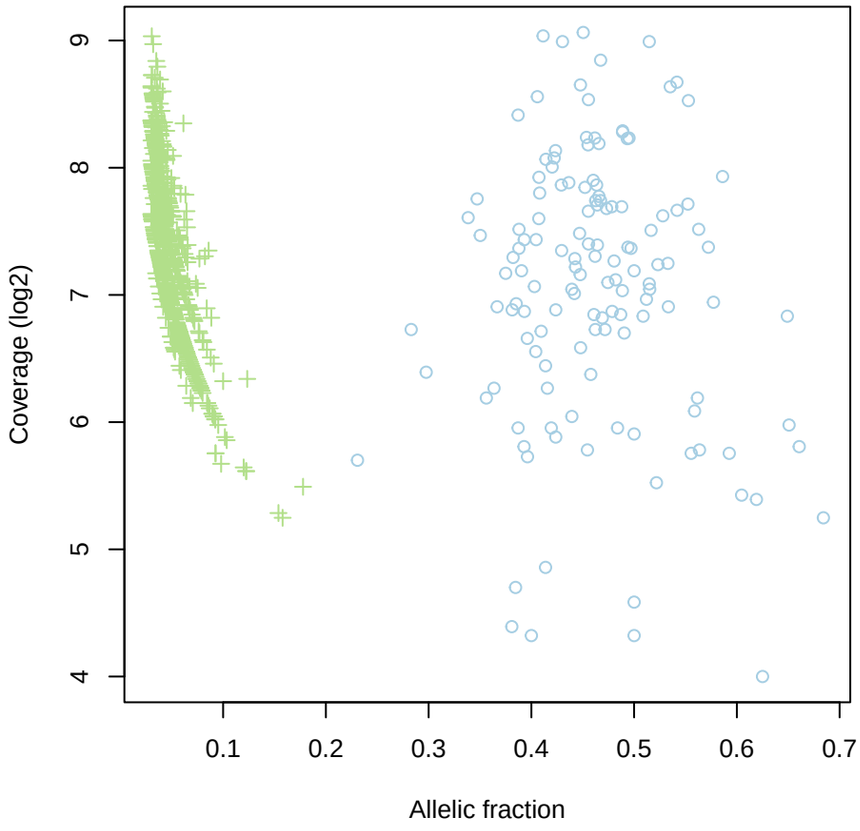

Purity: 0.15 Tumor ploidy: 2.099
1
2
3
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.0
0.5
1.0
1.5
log2 ratio

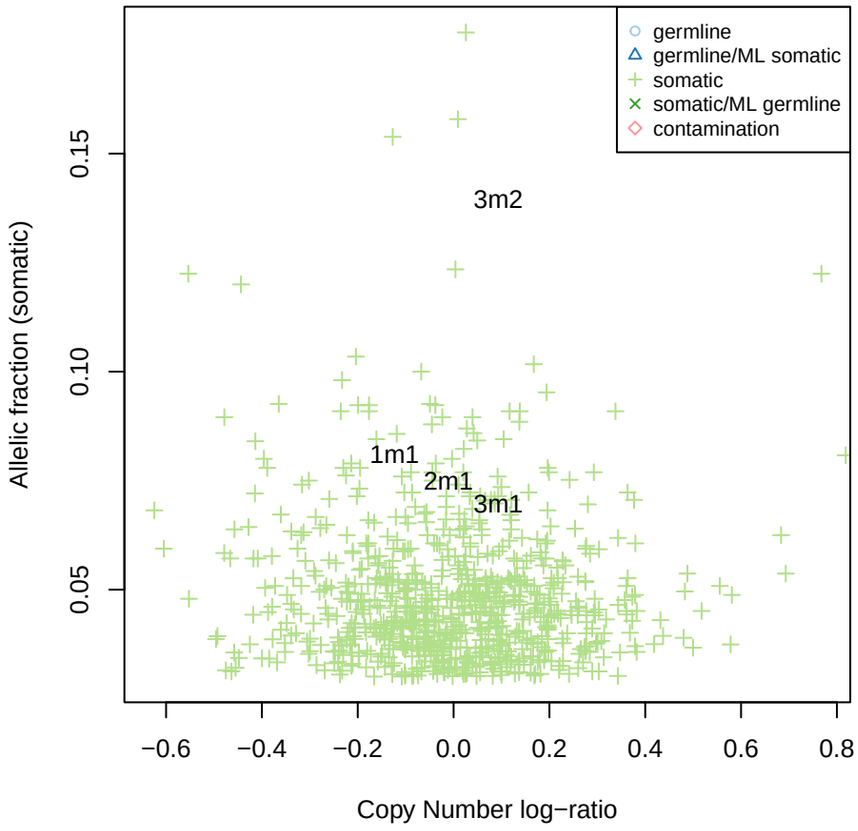

Purity: 0.15 Tumor ploidy: 2.099 SNV log−likelihood: 521.09 GoF: 96.1% Mean coverage: 176;149
1 2 3 4 5 6 7 9 10 12 13 14 15 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120 140
SNV Index

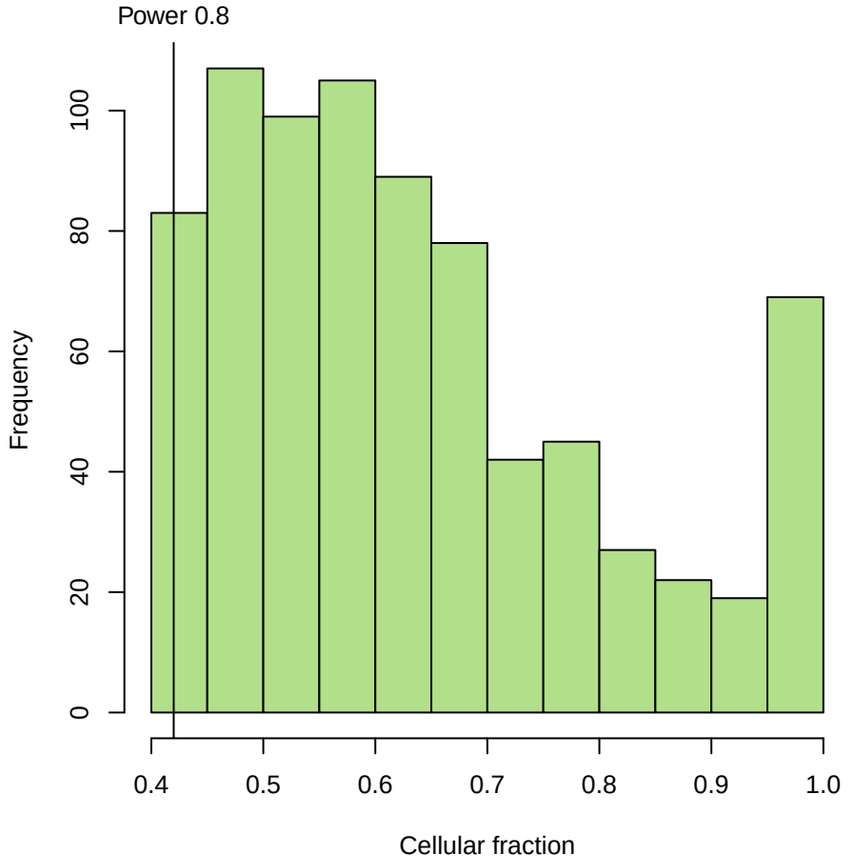

SCNA−fit log−likelihood: −14131.6
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 3
0 20 40 60 80 100 120 140
SNV Index

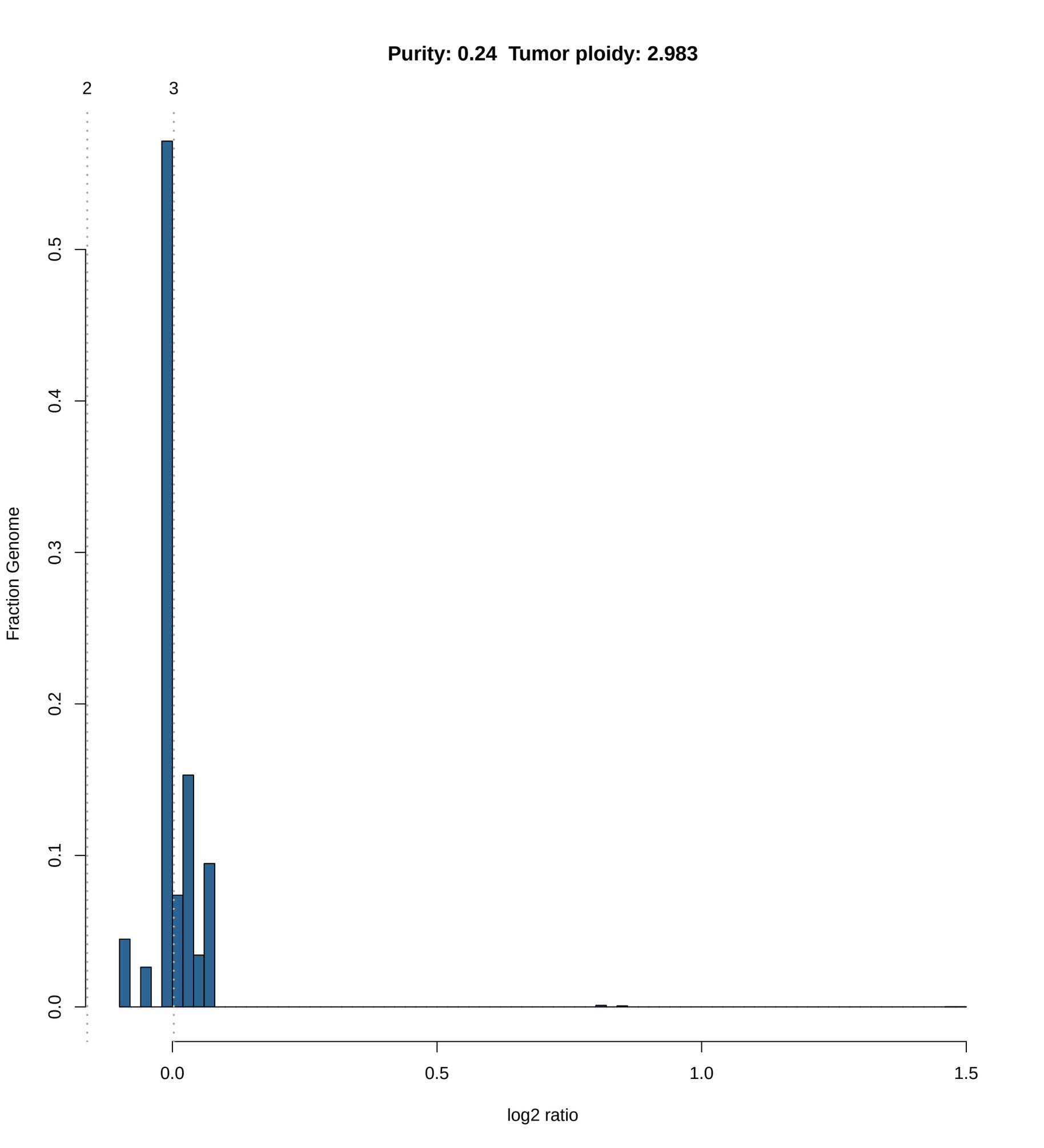

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120 140
SNV Index

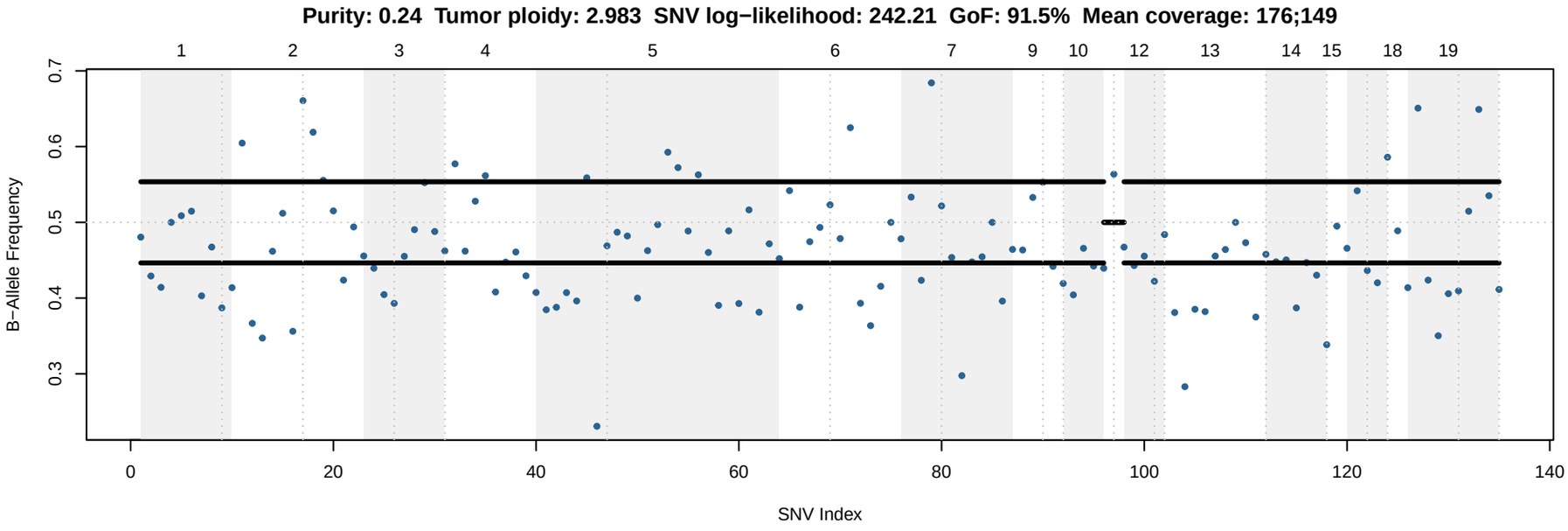

Allelic fraction (germline)
Copy Number log−ratio
3m3
1m1
3m2
2m1
1m0
3m1
3m0

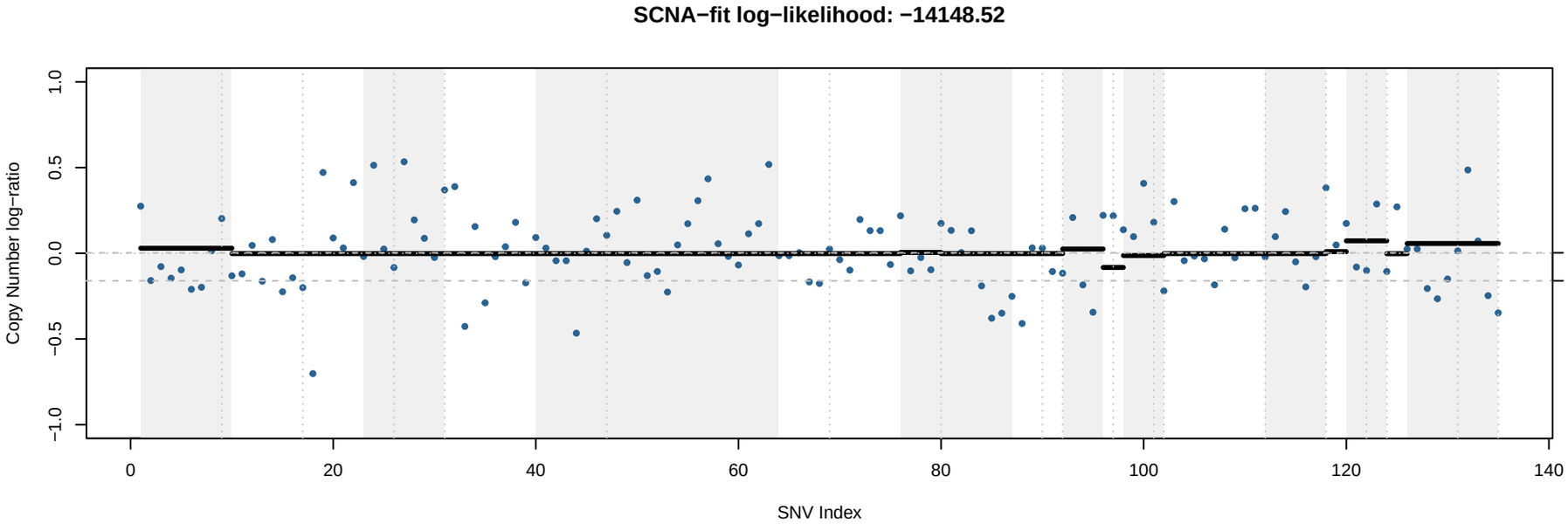

Coverage (log2)
Allelic fraction

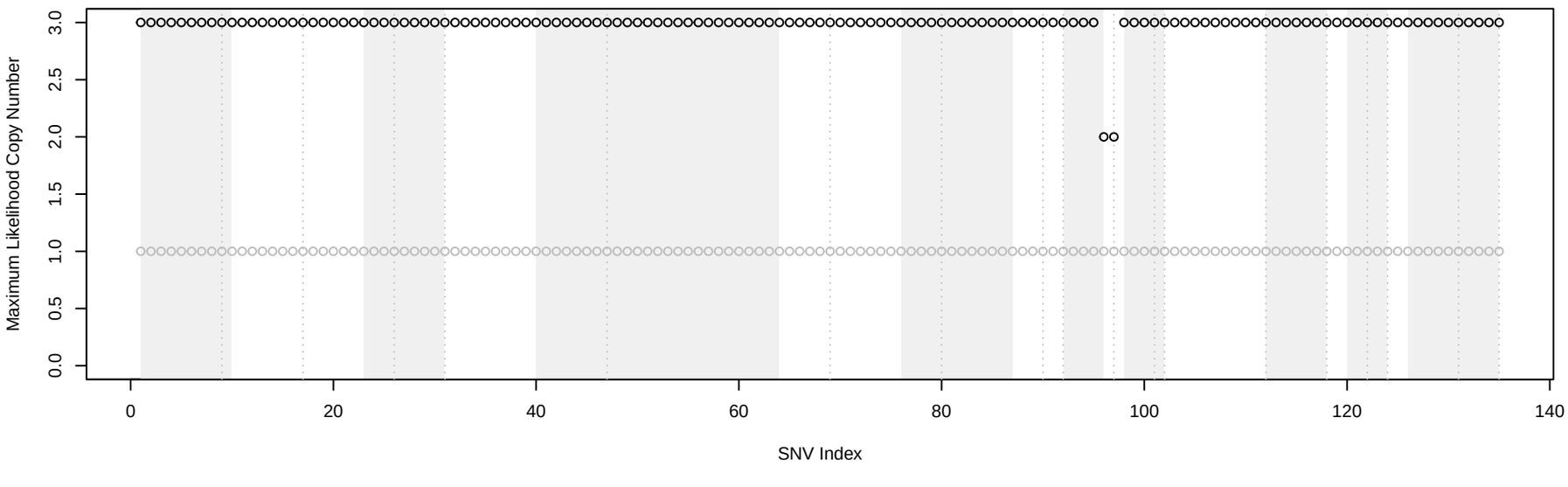

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m2
1m1
2m1
3m1

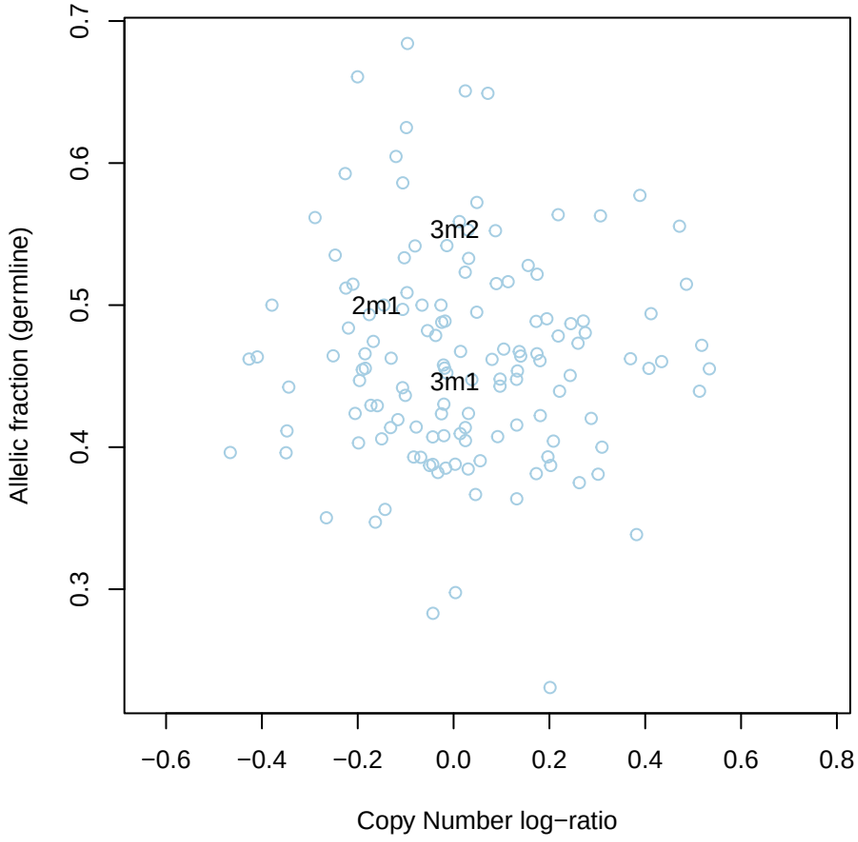

Power 0.8
Frequency
Cellular fraction

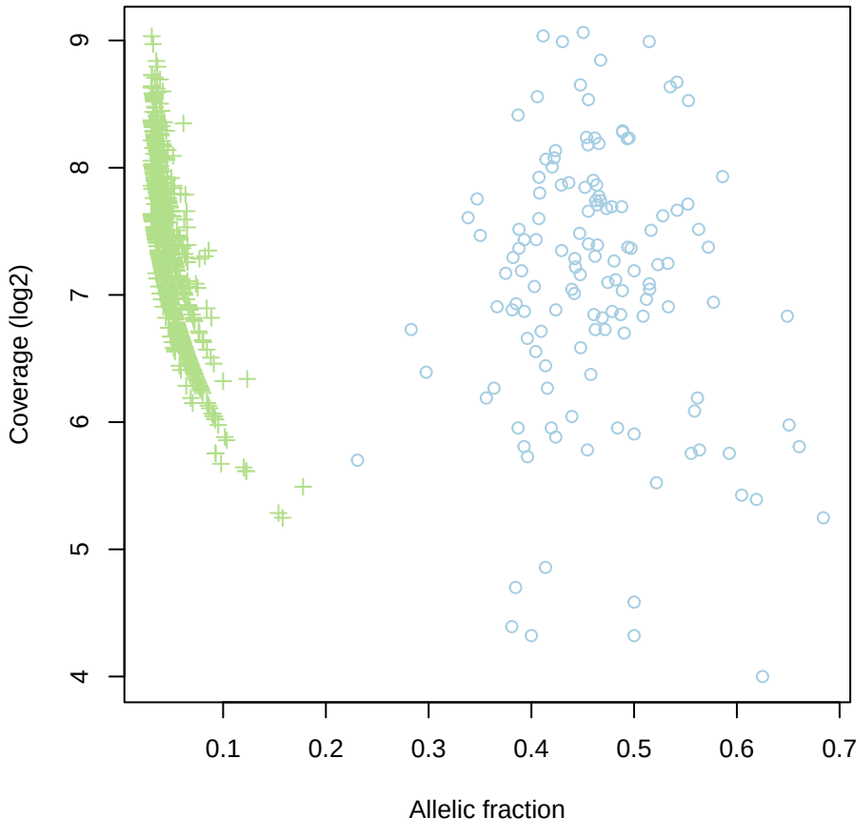

Purity: 0.24 Tumor ploidy: 2.983
2
3
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
0.0
0.5
1.0
1.5
log2 ratio

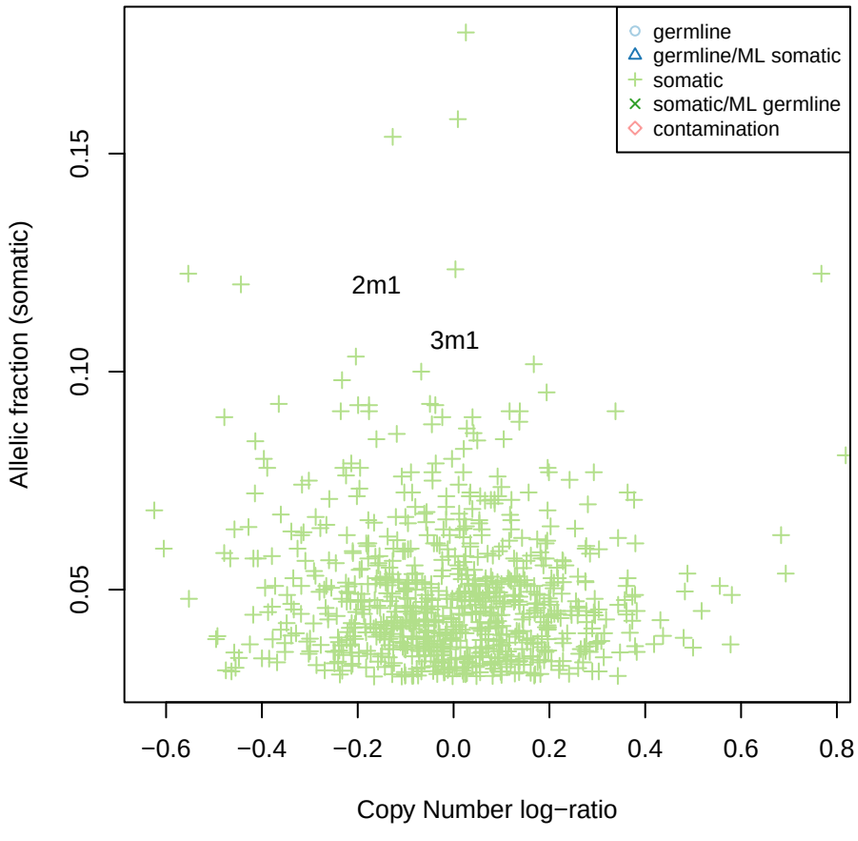

Purity: 0.24 Tumor ploidy: 2.983 SNV log−likelihood: 242.21 GoF: 91.5% Mean coverage: 176;149
1 2 3 4 5 6 7 9 10 12 13 14 15 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120 140
SNV Index

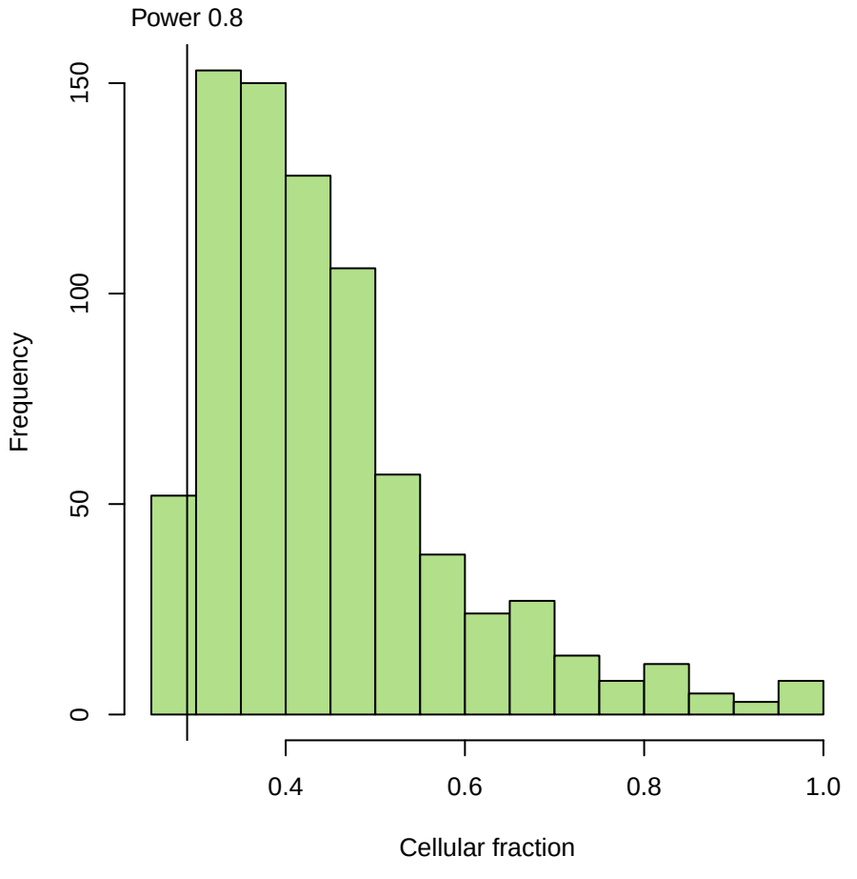

SCNA−fit log−likelihood: −14148.52
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3
0 20 40 60 80 100 120 140
SNV Index

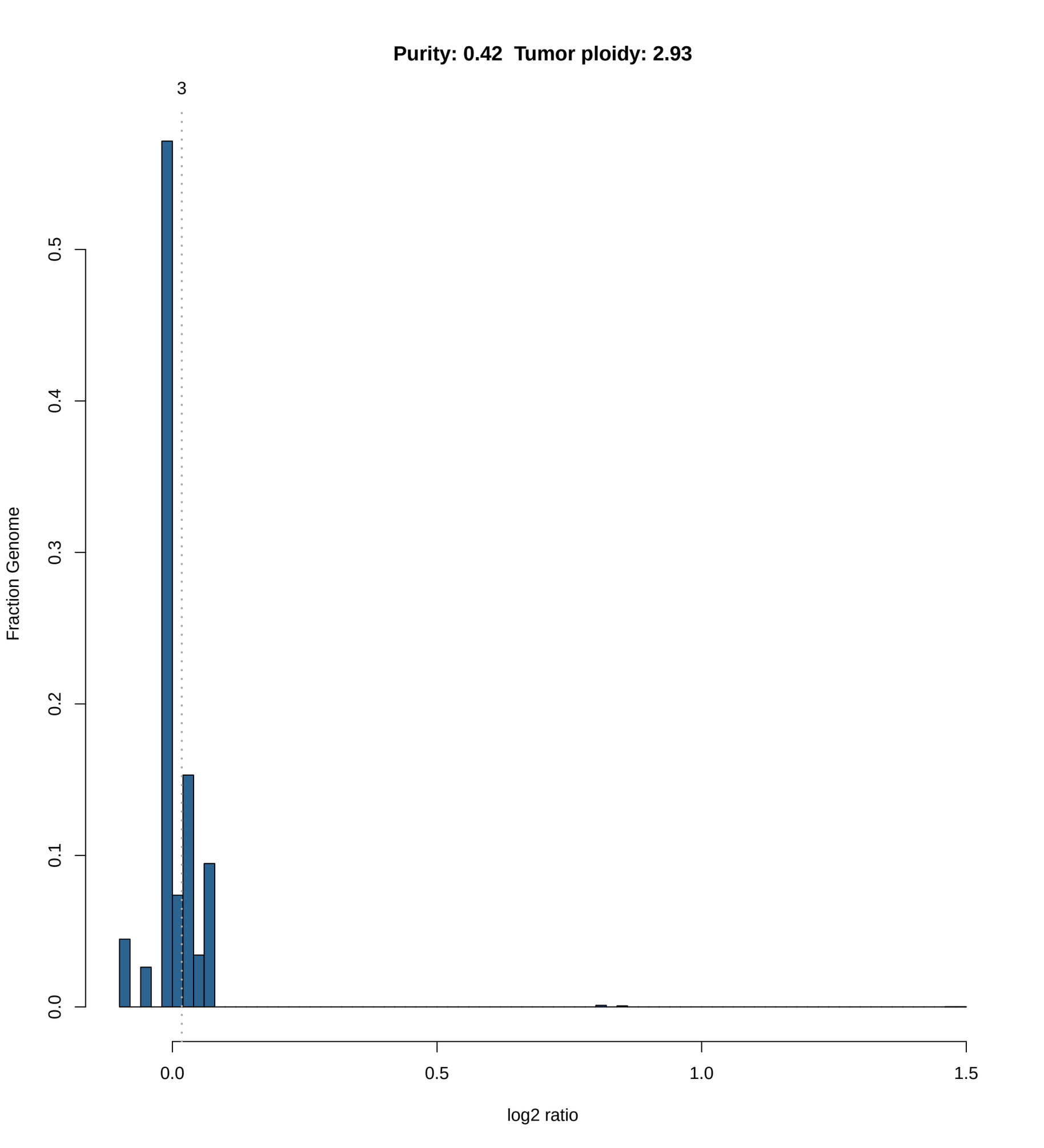

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120 140
SNV Index

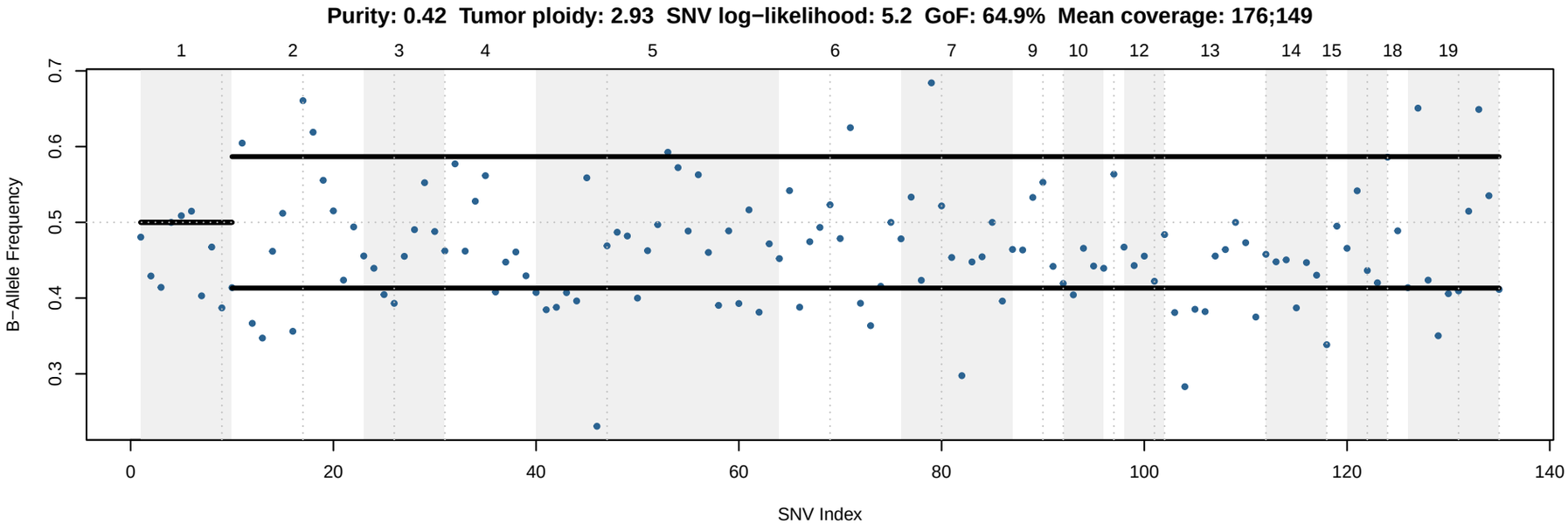

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
3m2
2m1
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

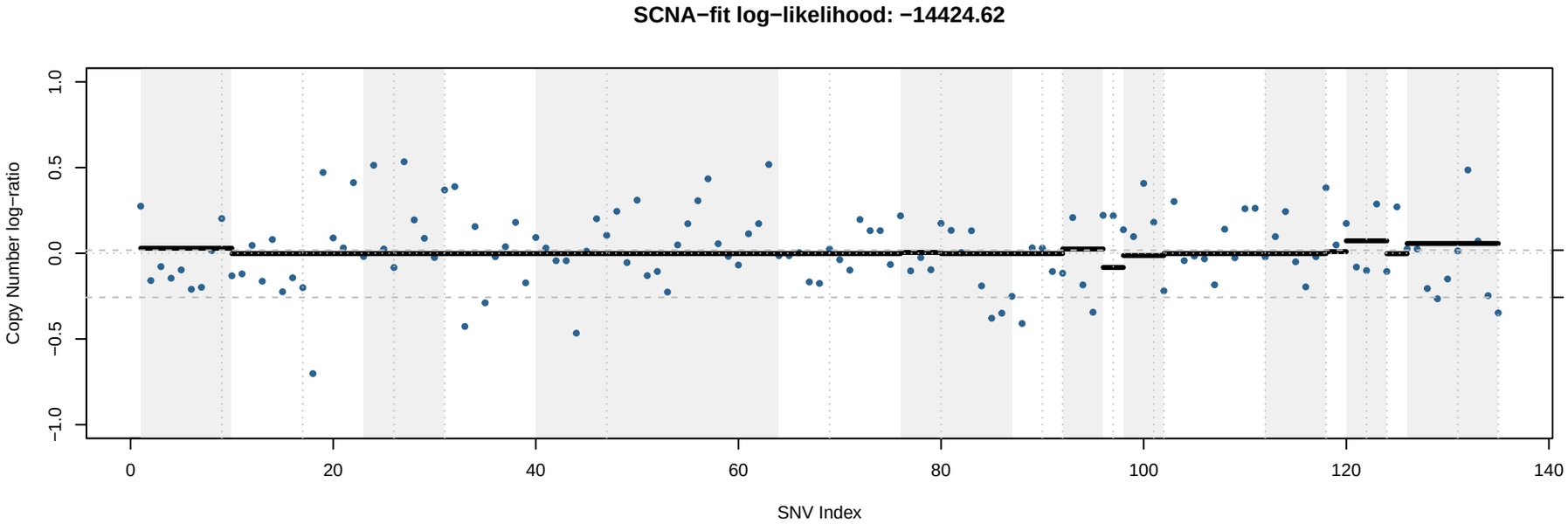

Coverage (log2)
4
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

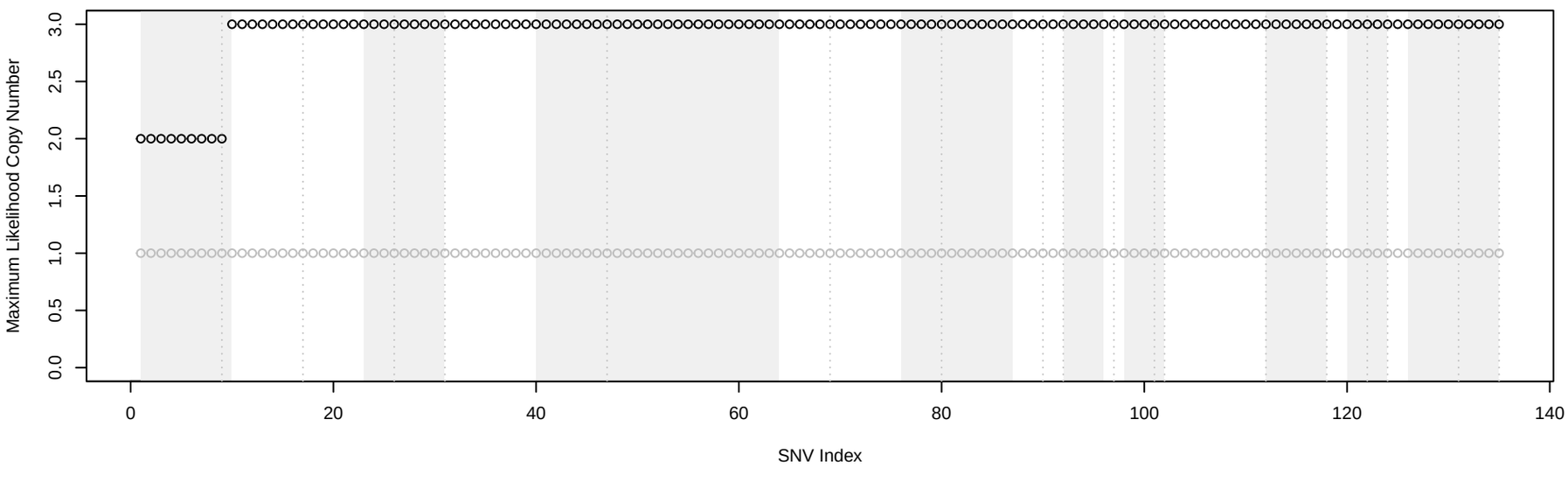

Allelic fraction (somatic)
0.05
0.10
0.15
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

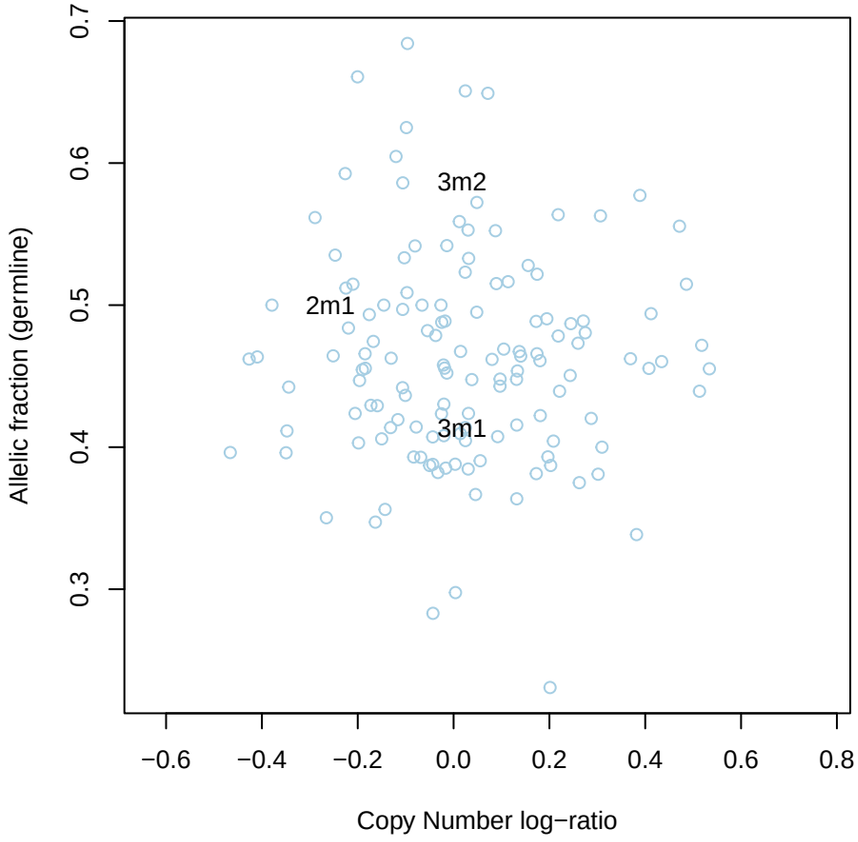

Power 0.8
Frequency
0
50
100
150
0.4
0.6
0.8
1.0
Cellular fraction

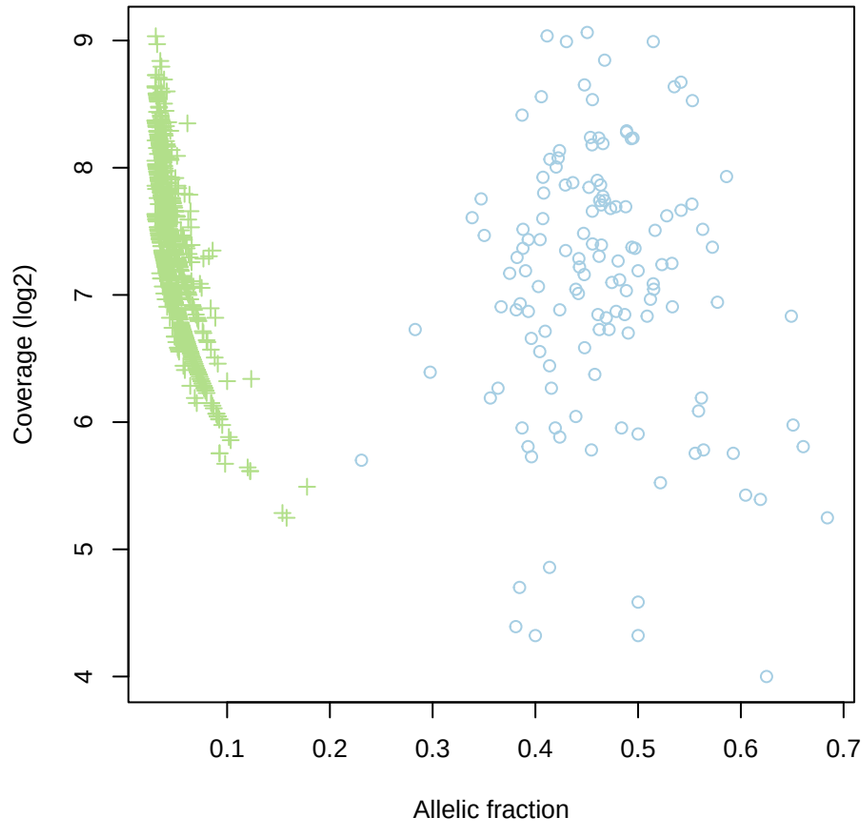

Purity: 0.42 Tumor ploidy: 2.93
3
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.0
0.5
1.0
1.5
log2 ratio

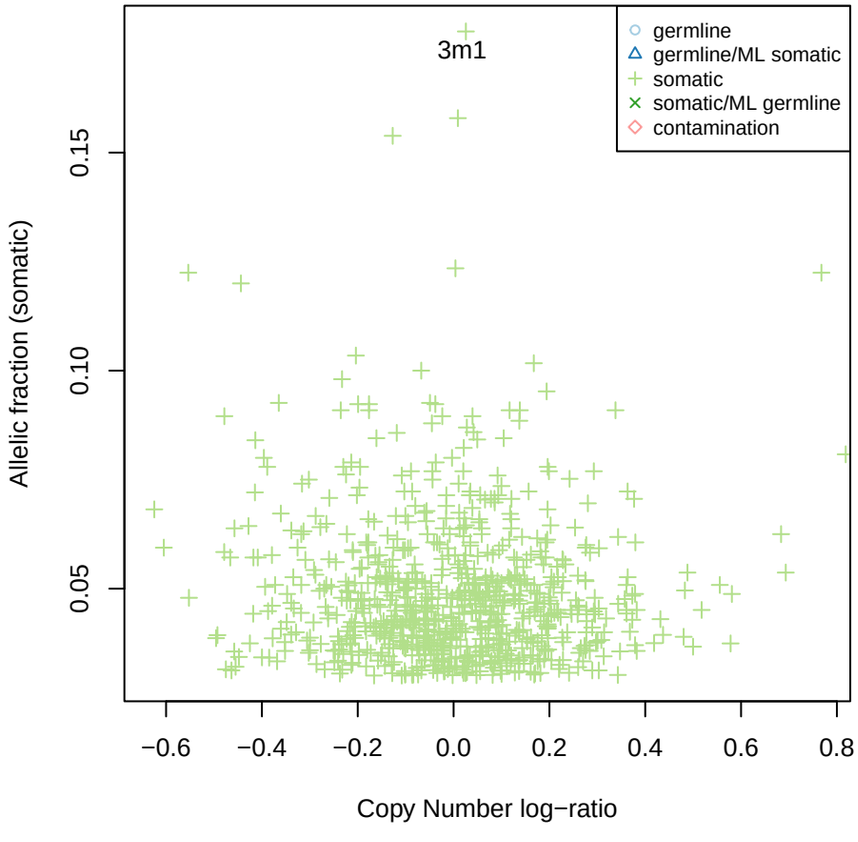

Purity: 0.42 Tumor ploidy: 2.93 SNV log−likelihood: 5.2 GoF: 64.9% Mean coverage: 176;149
1 2 3 4 5 6 7 9 10 12 13 14 15 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120 140
SNV Index

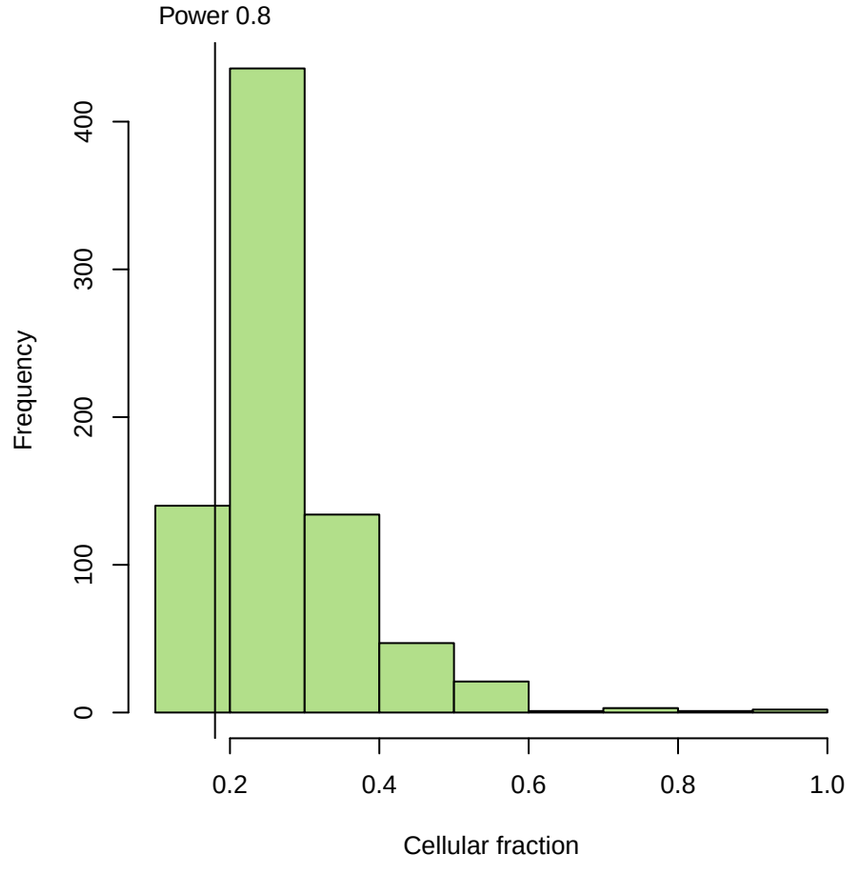

SCNA−fit log−likelihood: −14424.62
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3
0 20 40 60 80 100 120 140
SNV Index

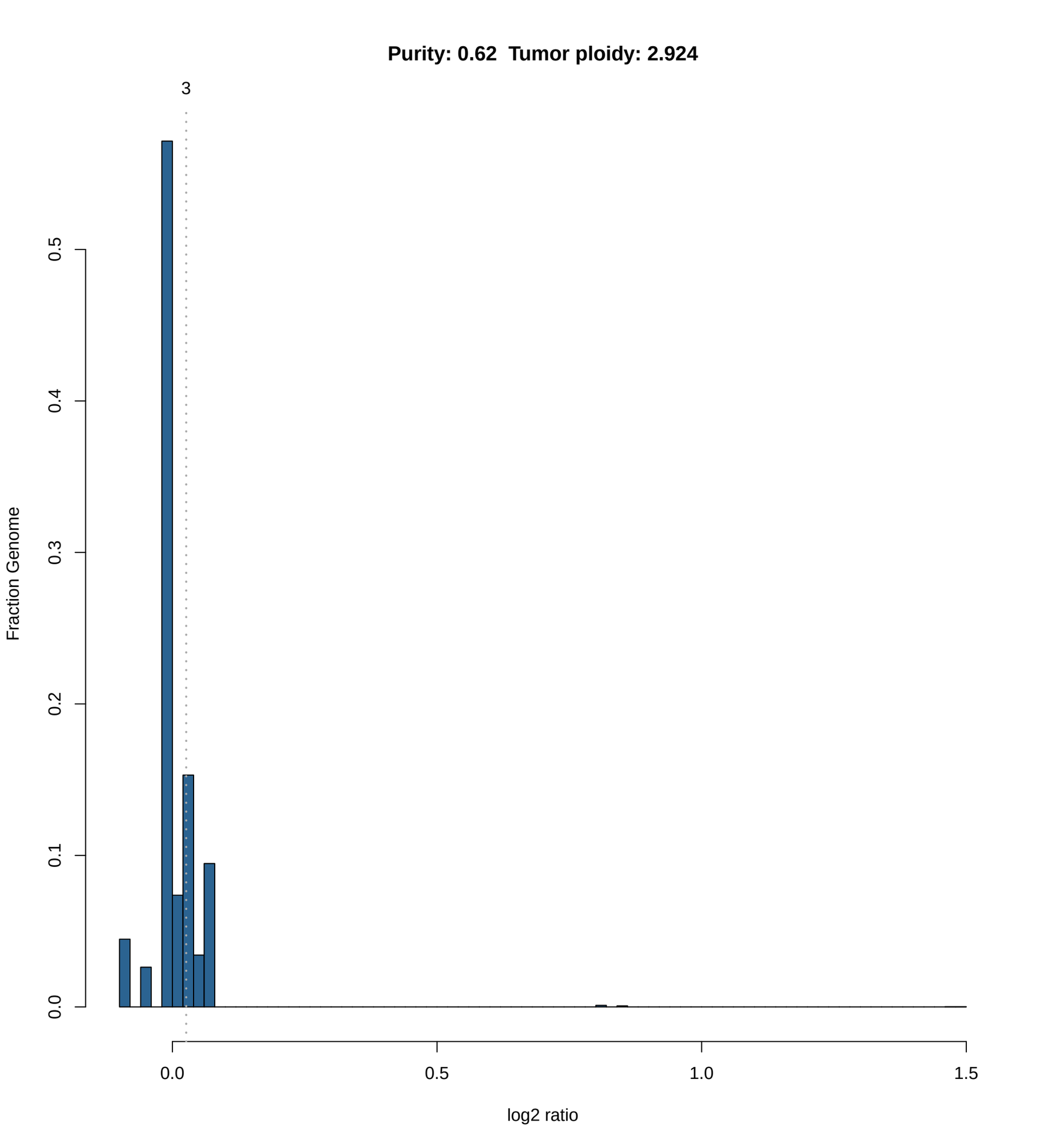

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120 140
SNV Index

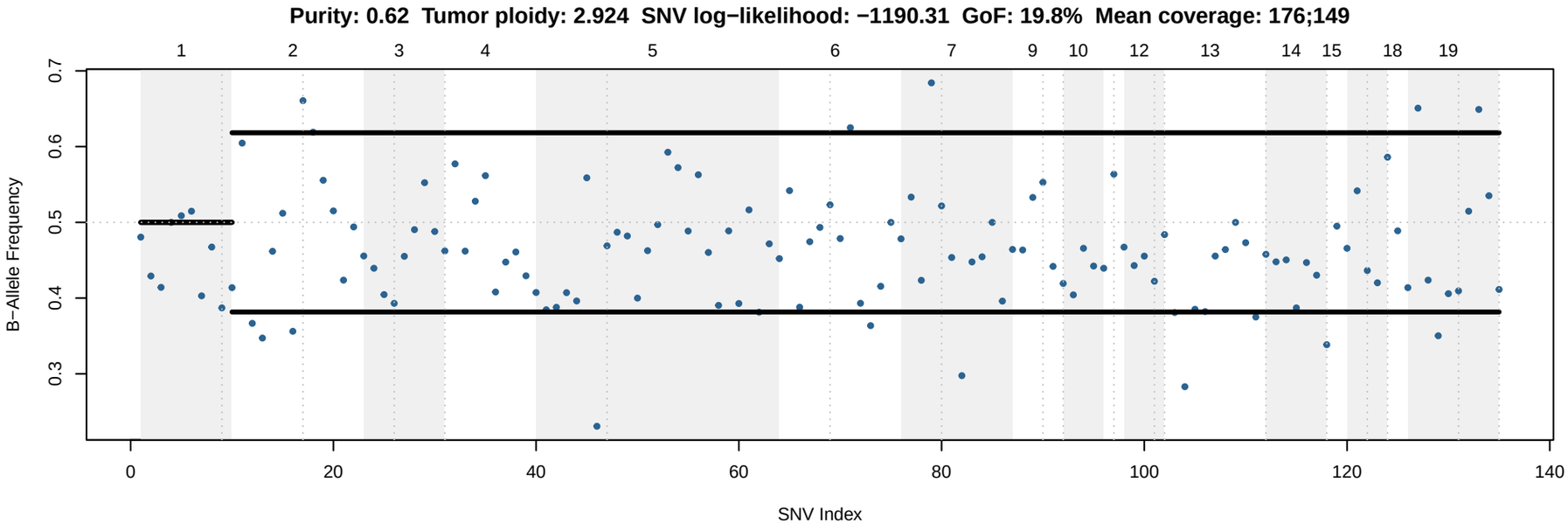

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
3m2
2m1
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

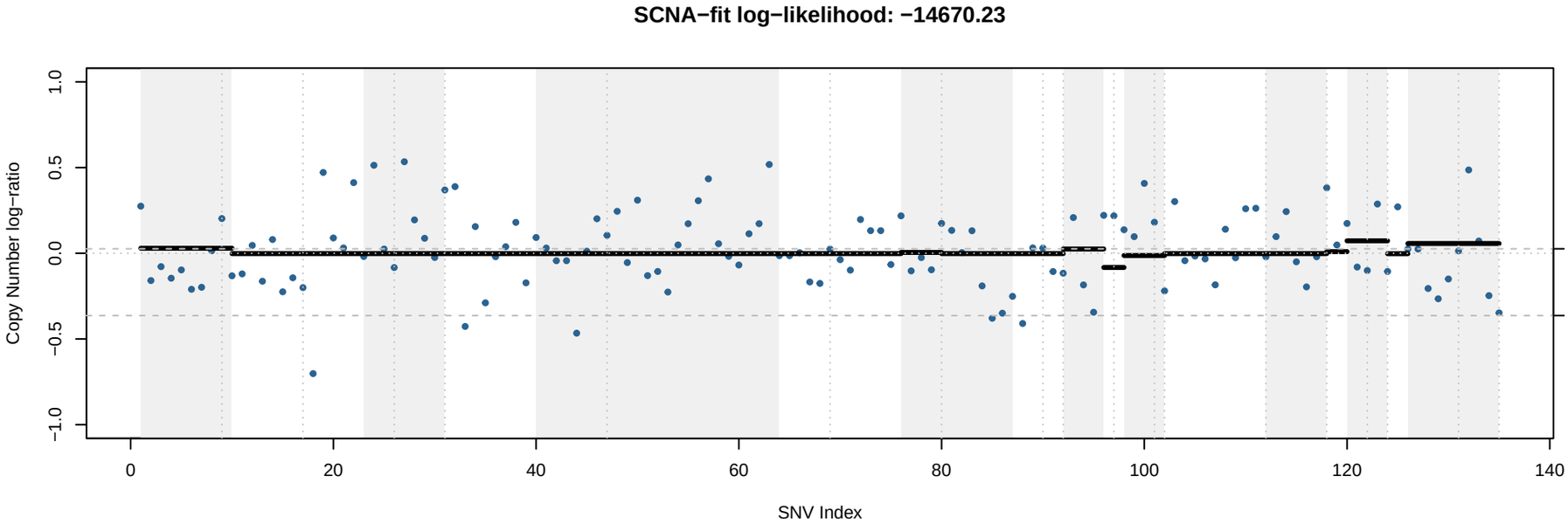

Coverage (log2)
4
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

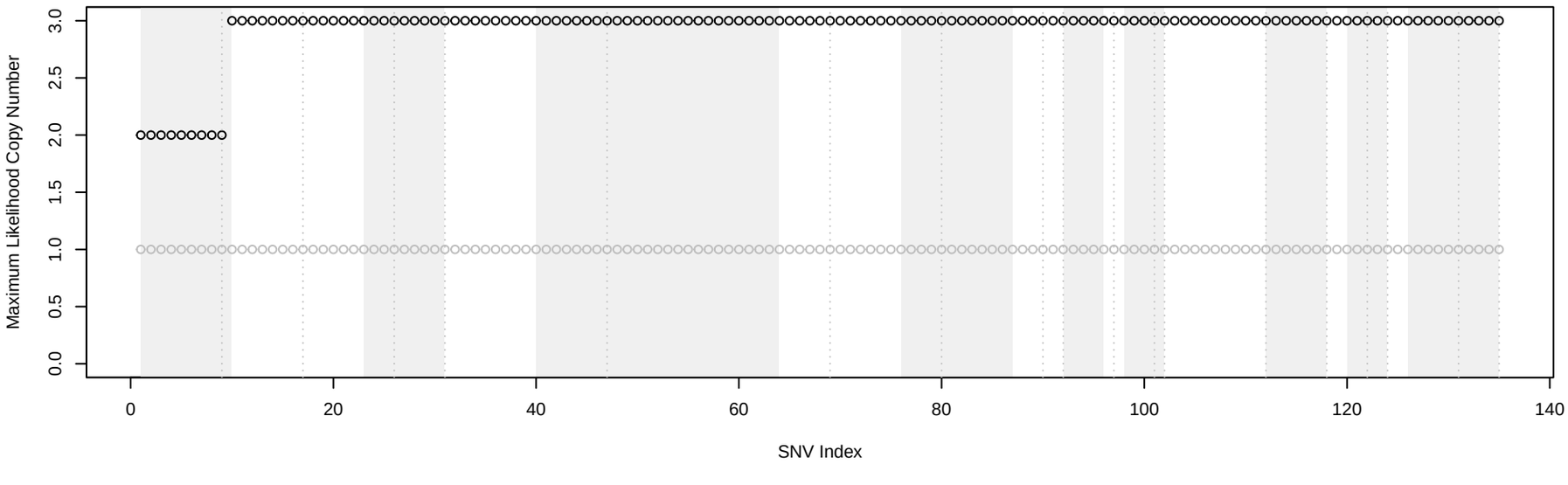

Allelic fraction (somatic)
0.05
0.10
0.15
3m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

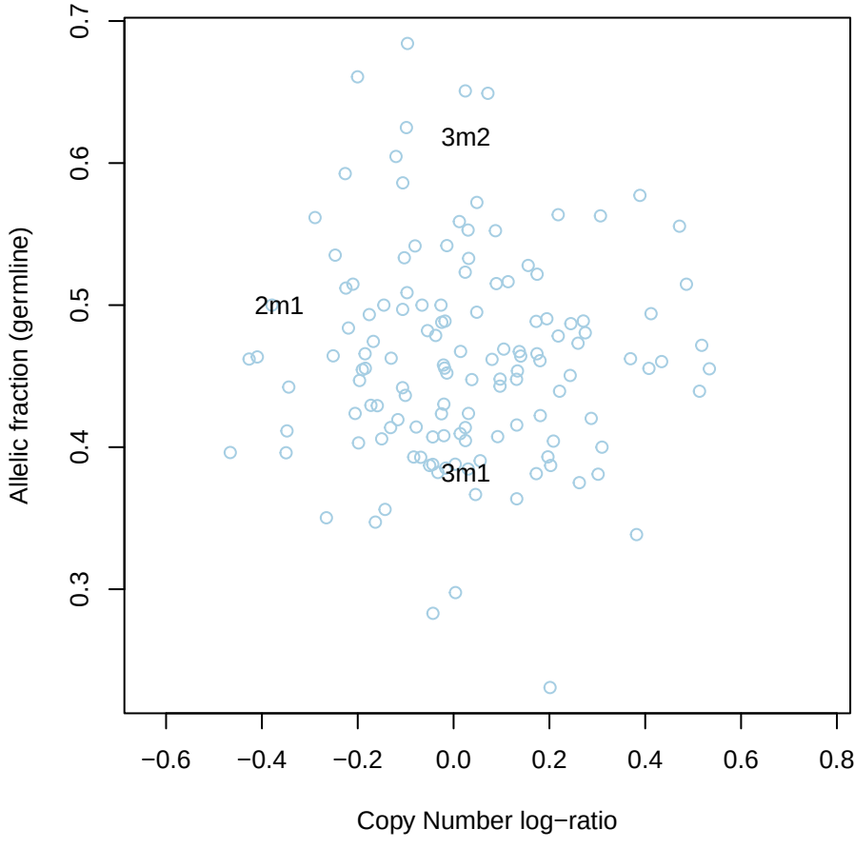

Power 0.8
Frequency
0
100
200
300
400
0.2
0.4
0.6
0.8
1.0
Cellular fraction

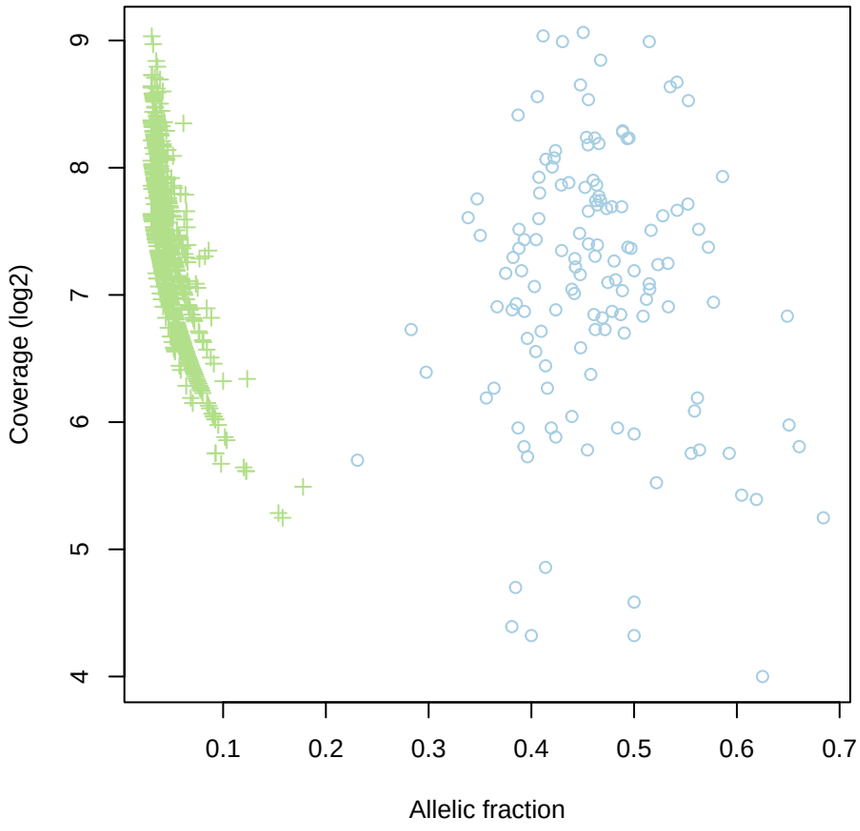

Purity: 0.62 Tumor ploidy: 2.924
3
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.0
0.5
1.0
1.5
log2 ratio

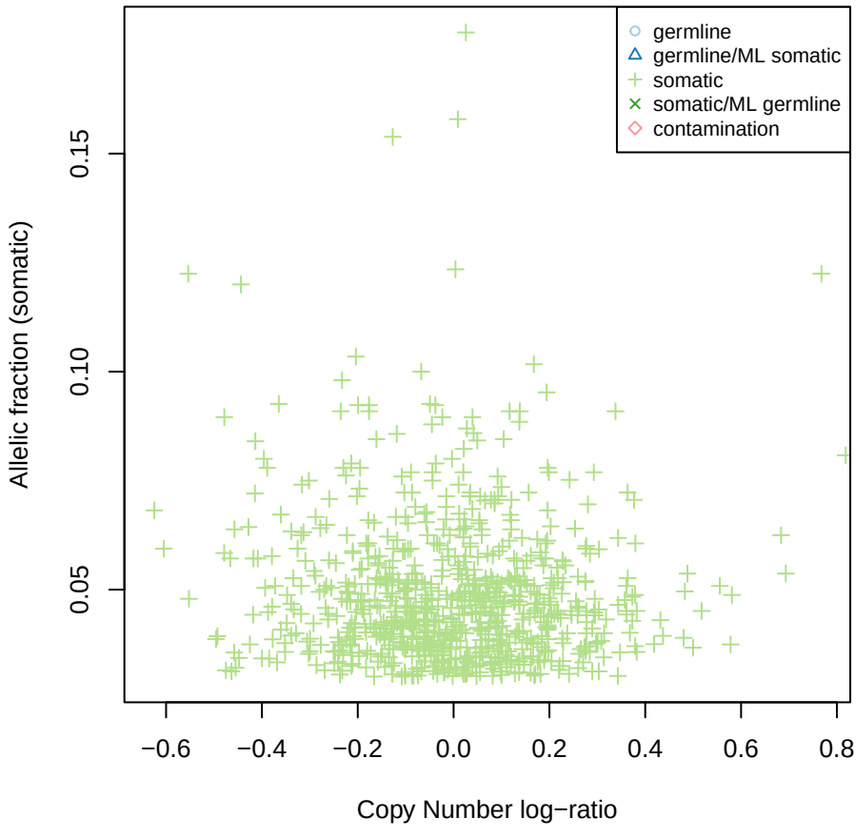

Purity: 0.62 Tumor ploidy: 2.924 SNV log−likelihood: −1190.31 GoF: 19.8% Mean coverage: 176;149
1 2 3 4 5 6 7 9 10 12 13 14 15 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120 140
SNV Index

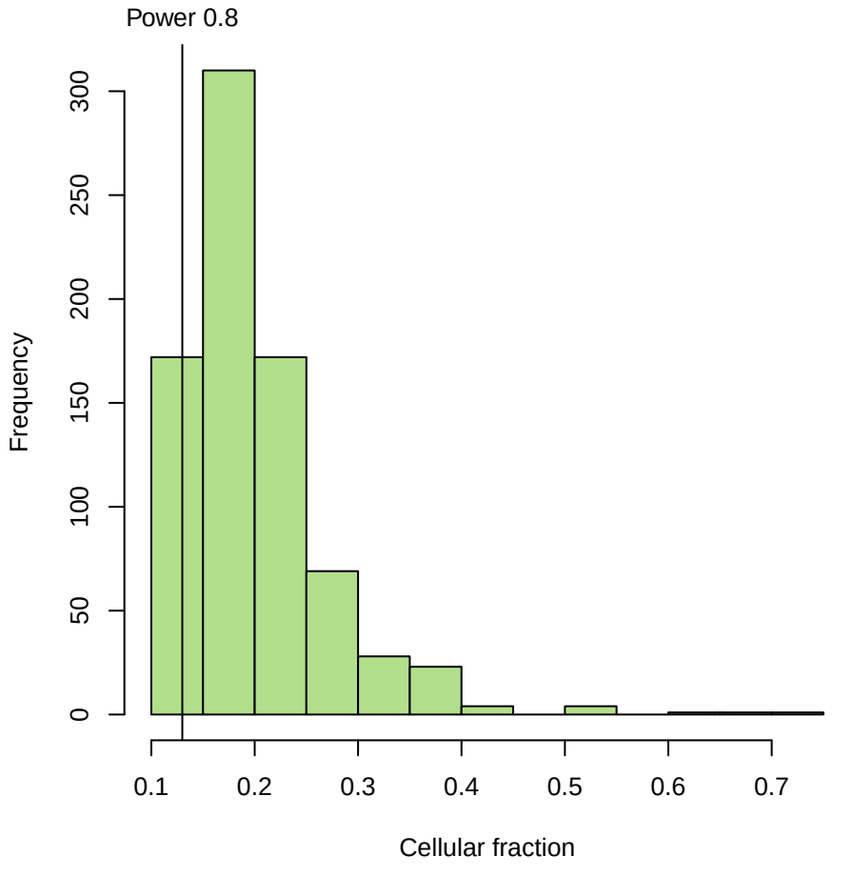

SCNA−fit log−likelihood: −14670.23
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3
0 20 40 60 80 100 120 140
SNV Index

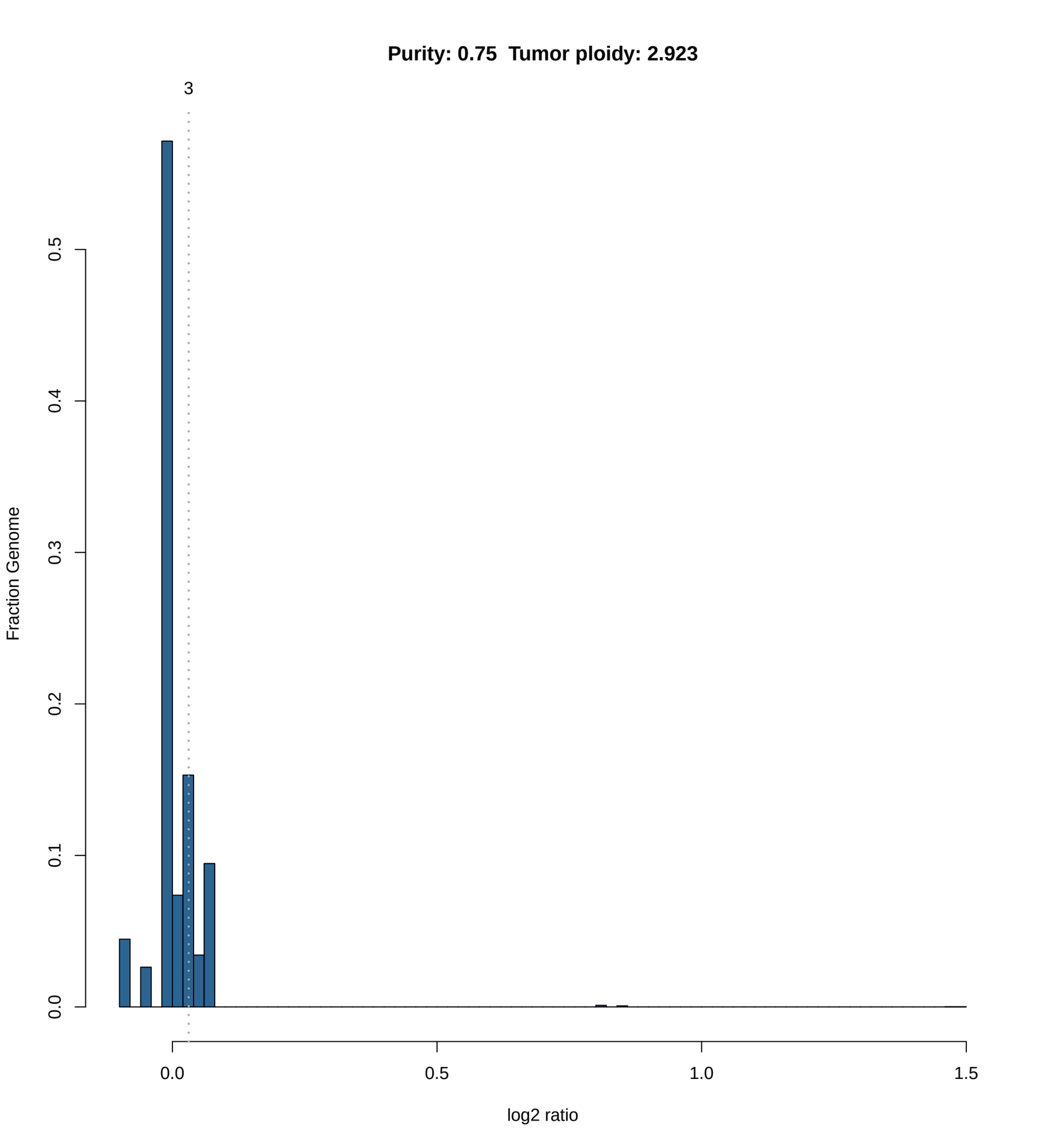

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120 140
SNV Index

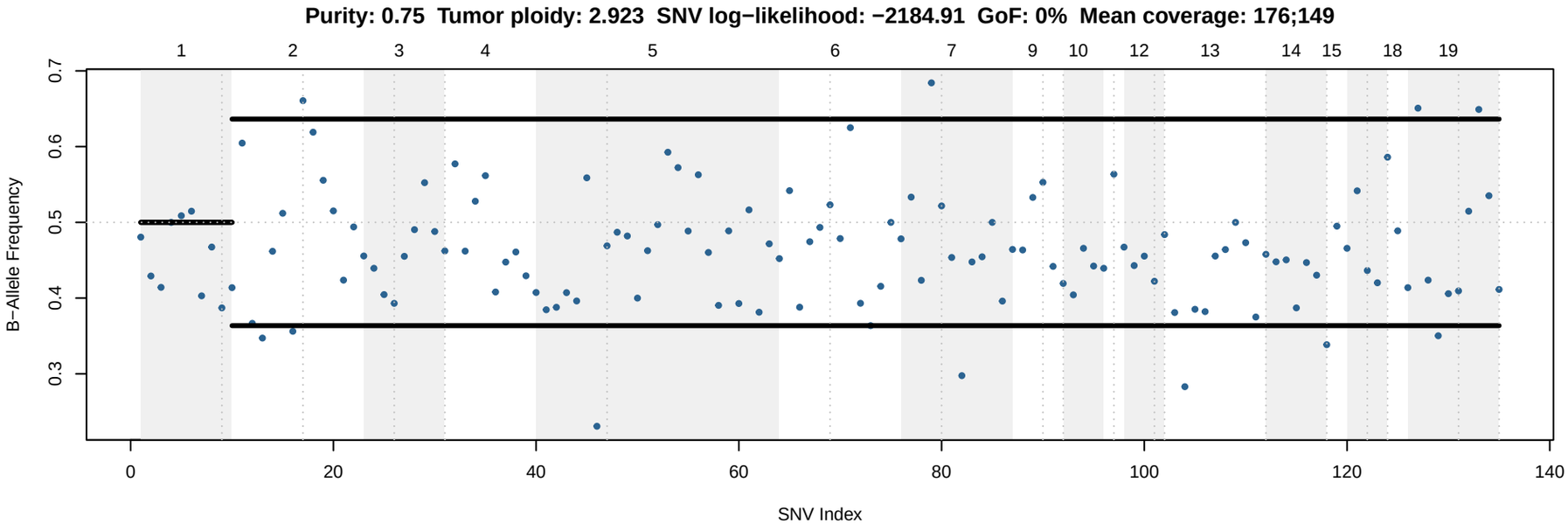

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
3m2
2m1
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

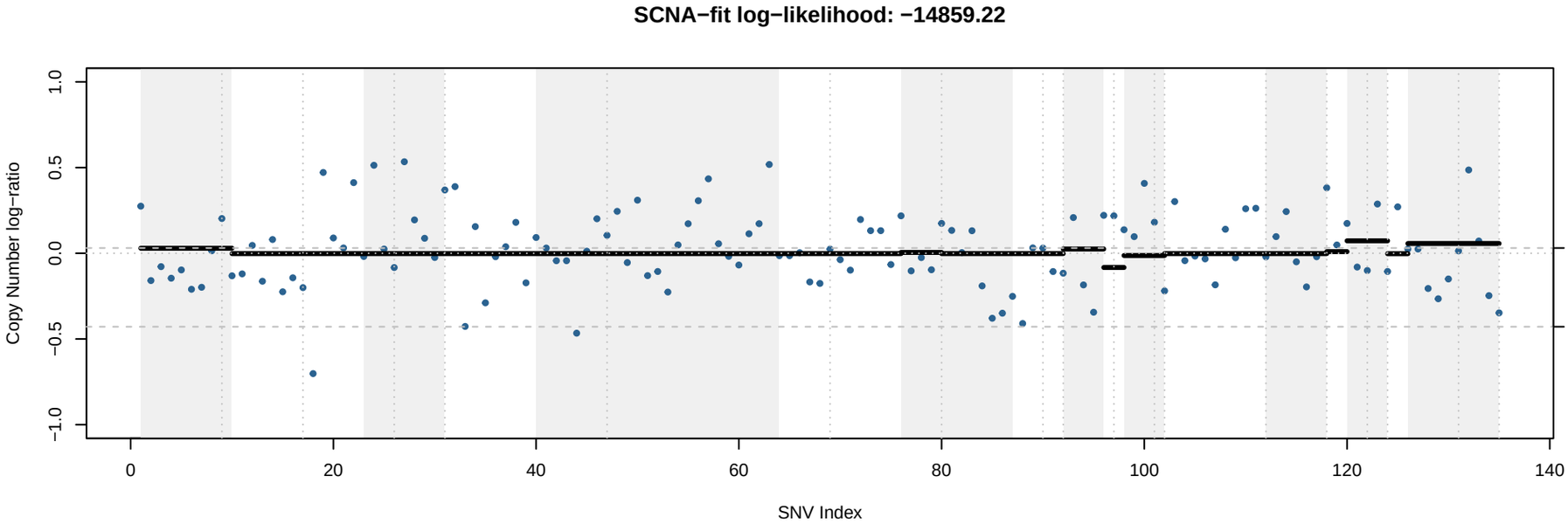

Coverage (log2)
4
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

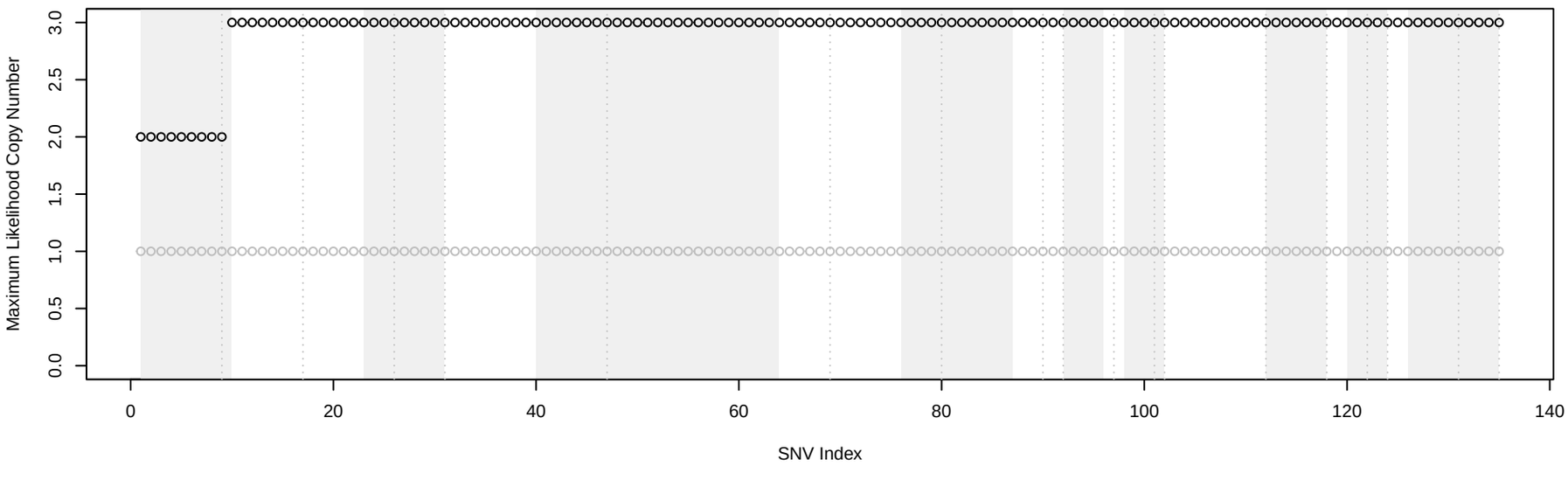

Allelic fraction (somatic)
0.05
0.10
0.15
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

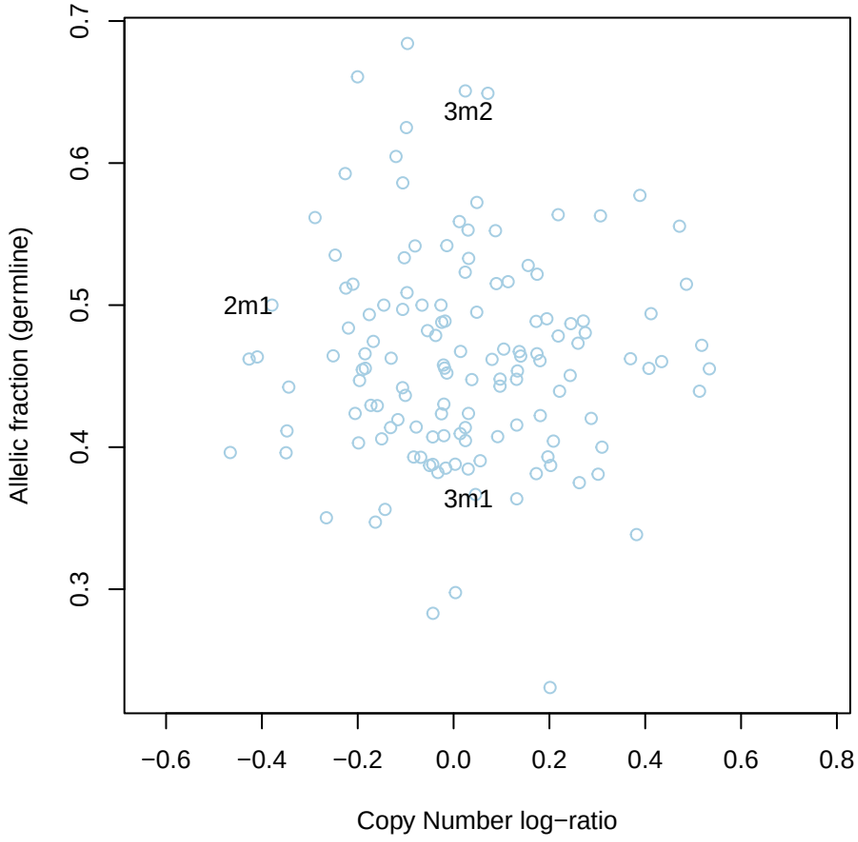

Power 0.8
Frequency
0
50
100
150
200
250
300
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Cellular fraction

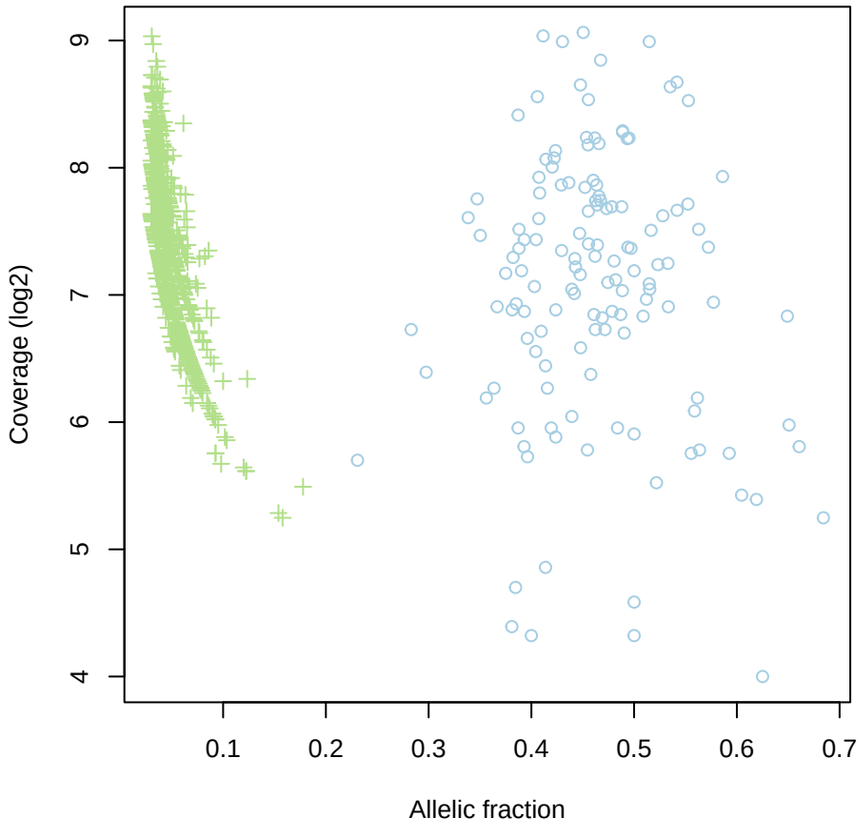

Purity: 0.75 Tumor ploidy: 2.923
3
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.0
0.5
1.0
1.5
log2 ratio

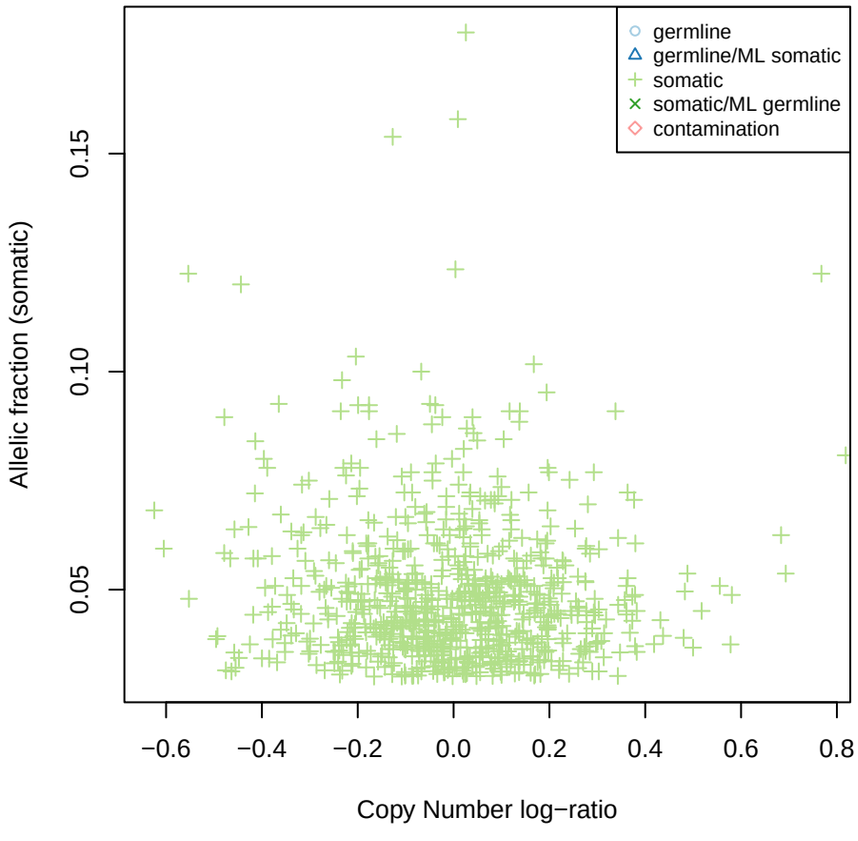

Purity: 0.75 Tumor ploidy: 2.923 SNV log−likelihood: −2184.91 GoF: 0% Mean coverage: 176;149
1 2 3 4 5 6 7 9 10 12 13 14 15 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120 140
SNV Index

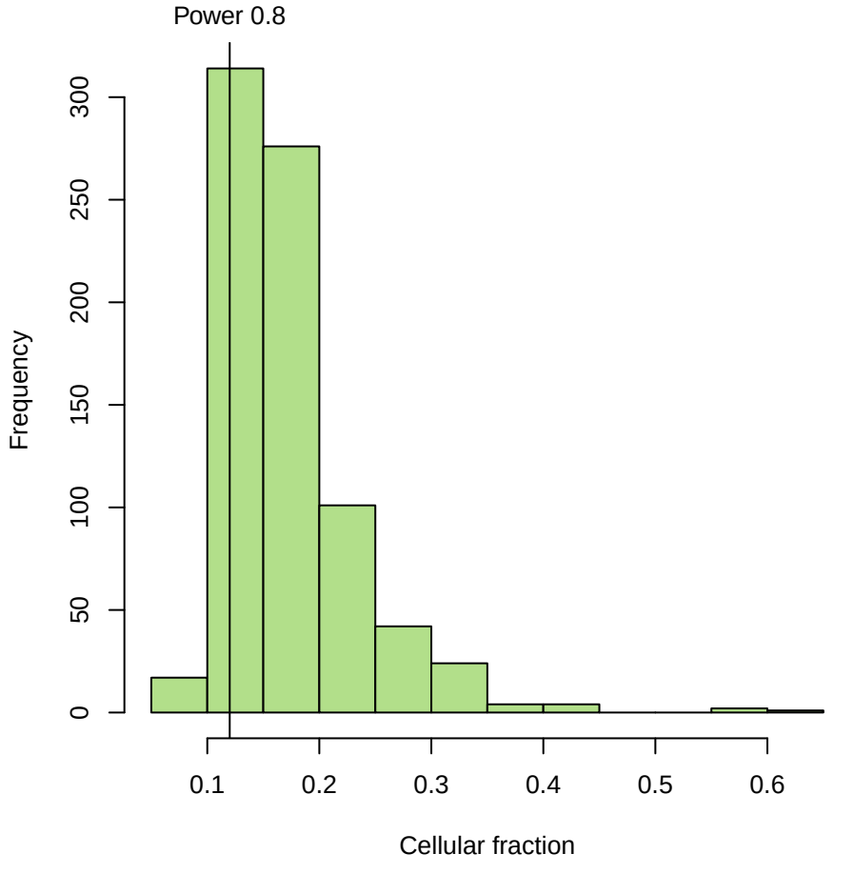

SCNA−fit log−likelihood: −14859.22
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3
0 20 40 60 80 100 120 140
SNV Index

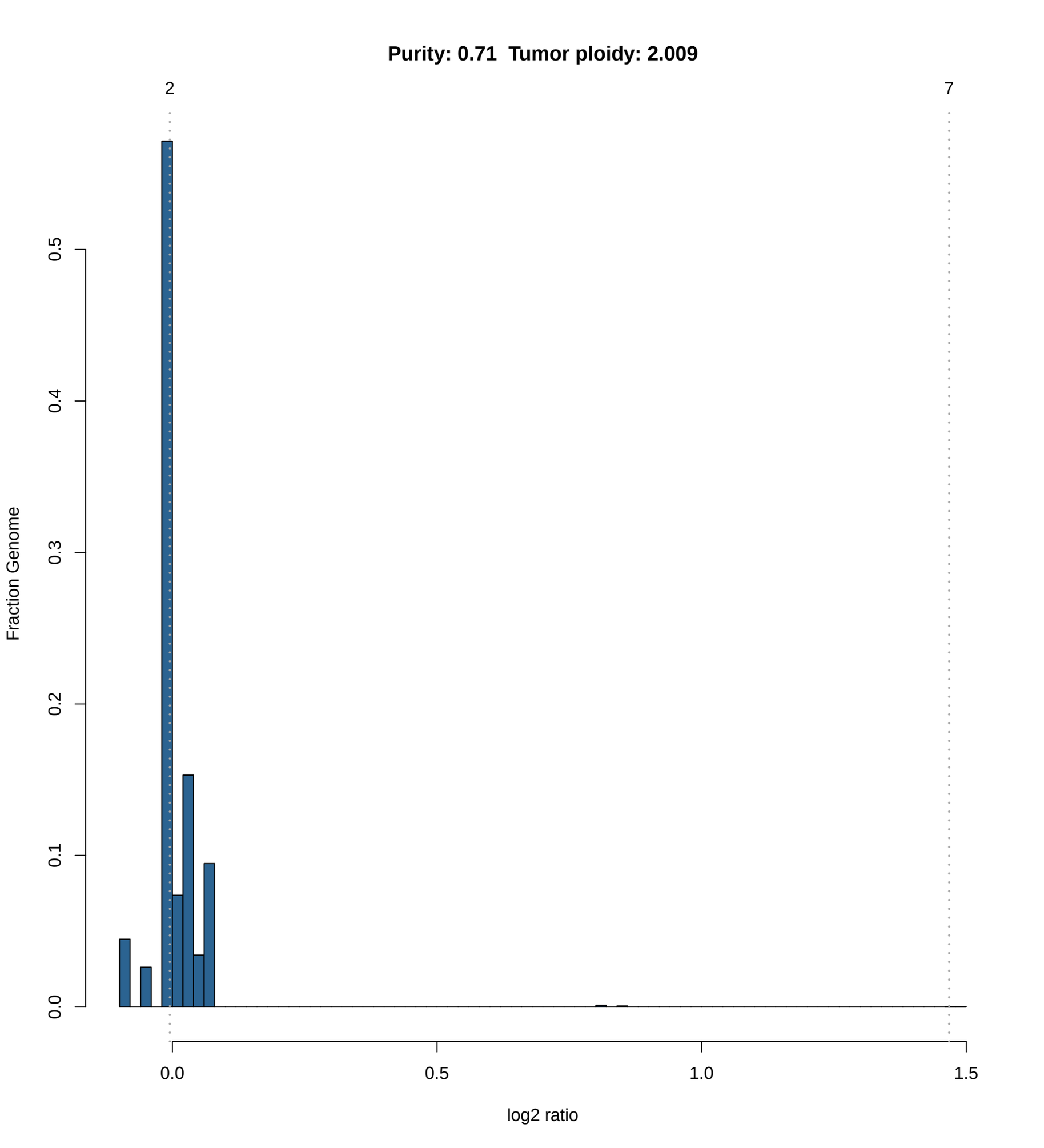

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120 140
SNV Index

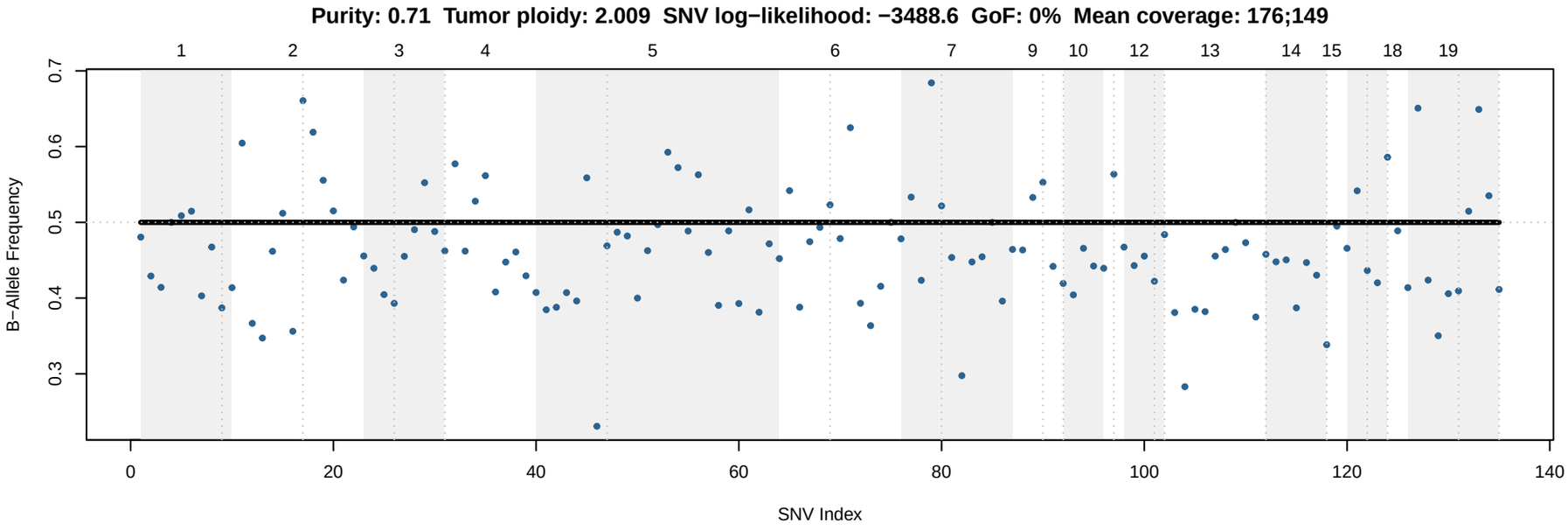

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
2m1
3m2
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

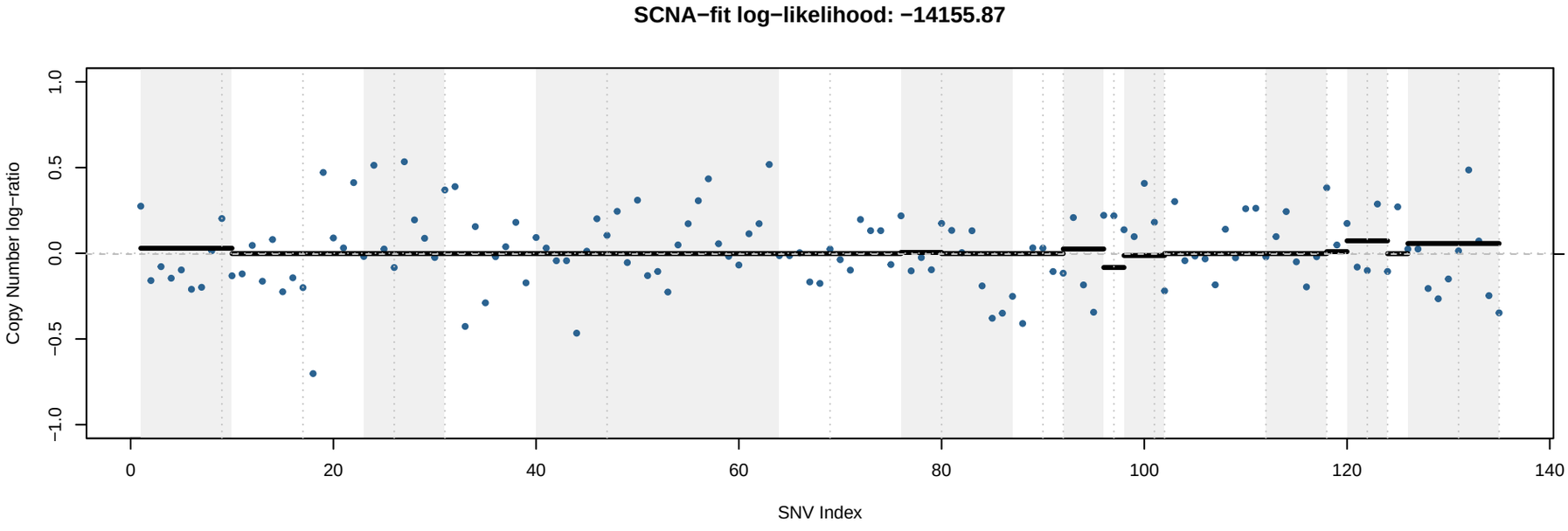

Coverage (log2)
4
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

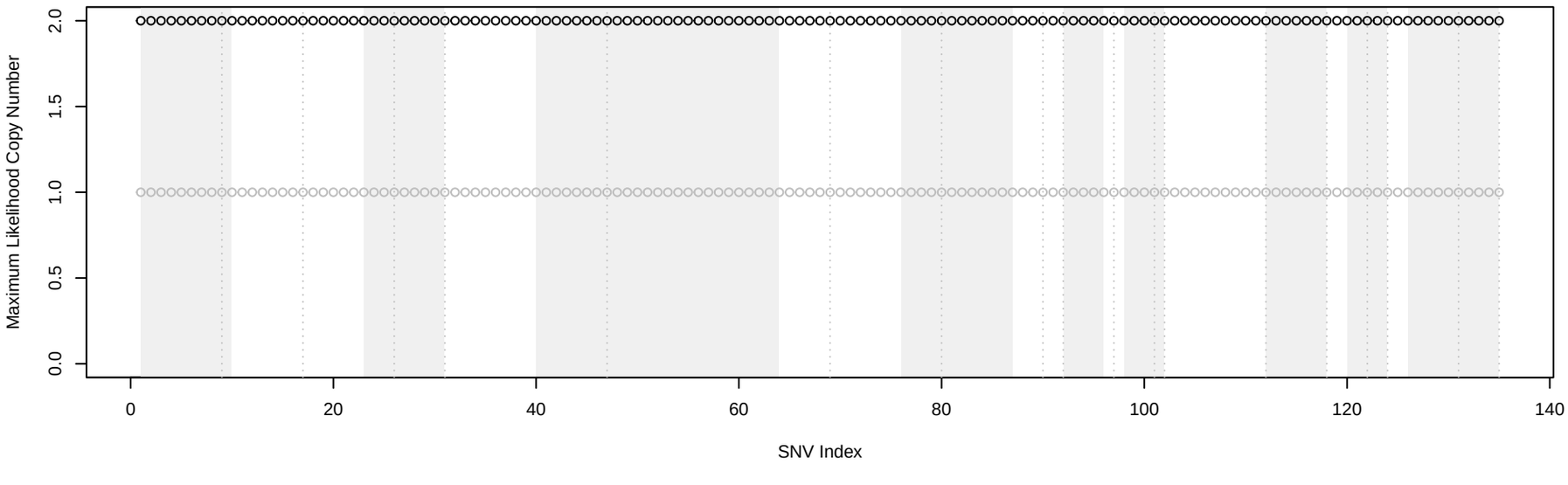

Allelic fraction (somatic)
0.05
0.10
0.15
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

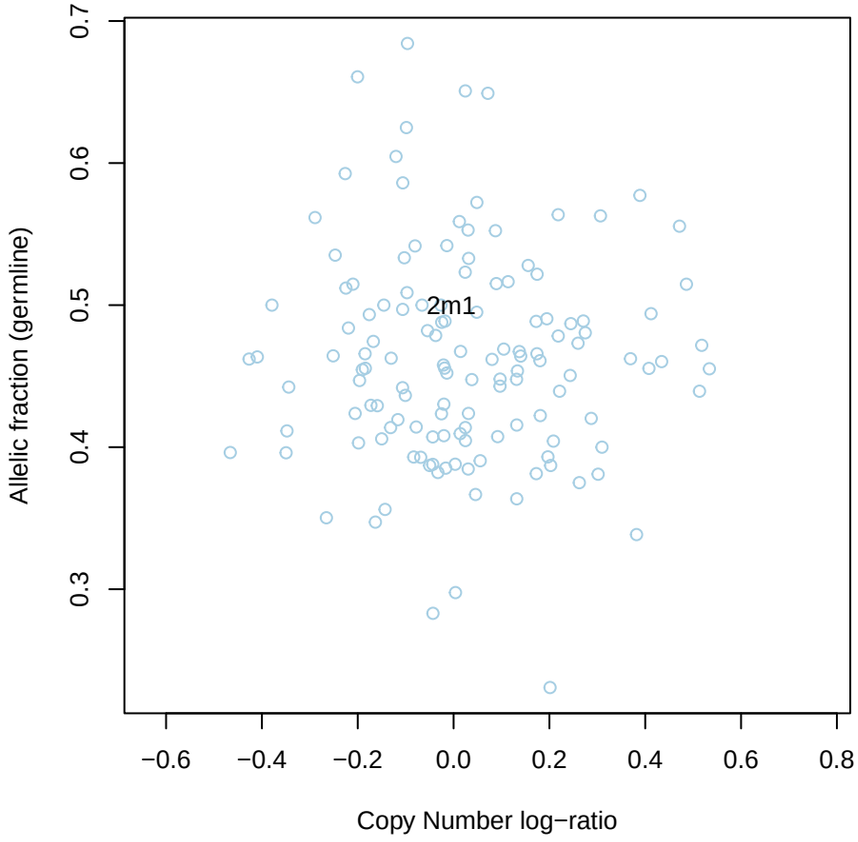

Power 0.8
Frequency
0
50
100
150
200
250
300
0.1
0.2
0.3
0.4
0.5
0.6
Cellular fraction

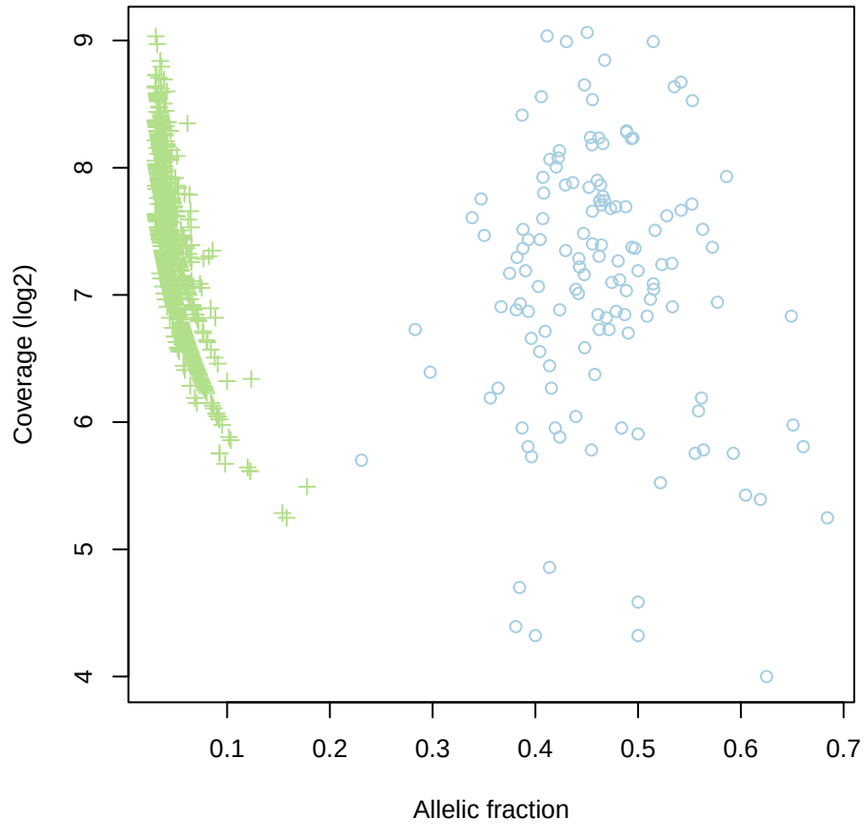

Purity: 0.71 Tumor ploidy: 2.009
2
7
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.0
0.5
1.0
1.5
log2 ratio

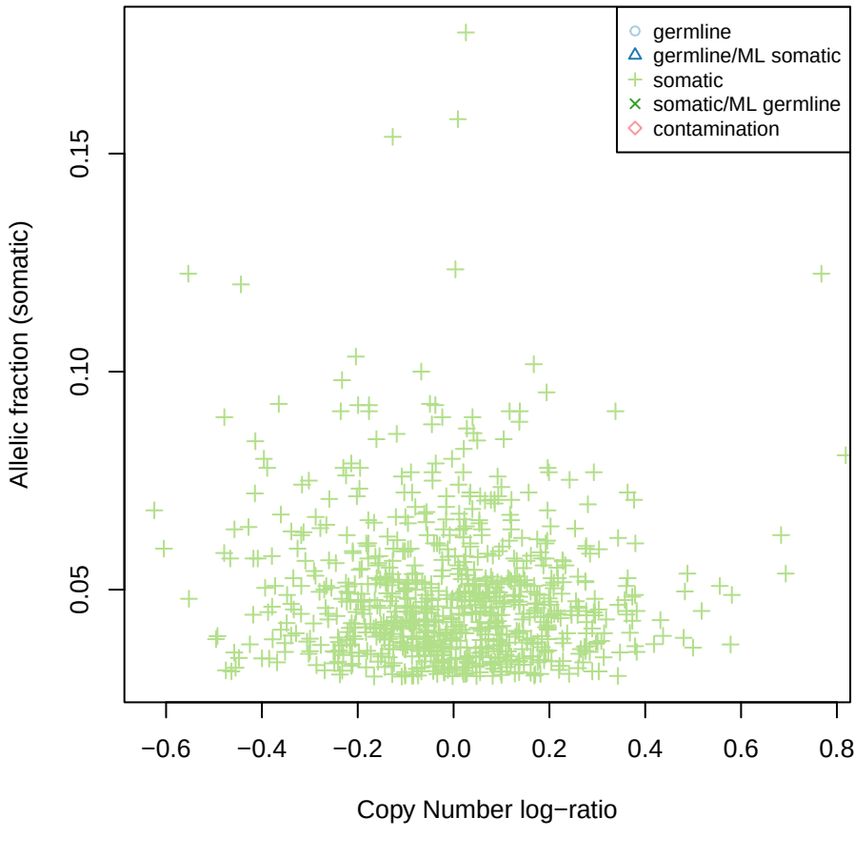

Purity: 0.71 Tumor ploidy: 2.009 SNV log−likelihood: −3488.6 GoF: 0% Mean coverage: 176;149
1 2 3 4 5 6 7 9 10 12 13 14 15 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120 140
SNV Index

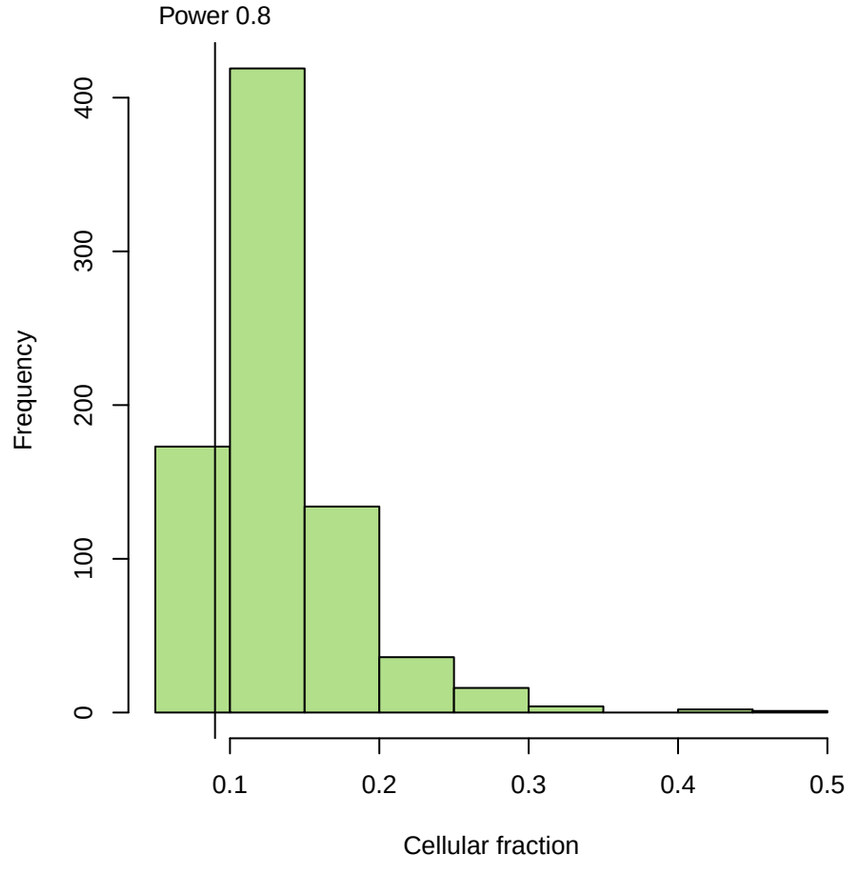

SCNA−fit log−likelihood: −14155.87
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2
0 20 40 60 80 100 120 140
SNV Index

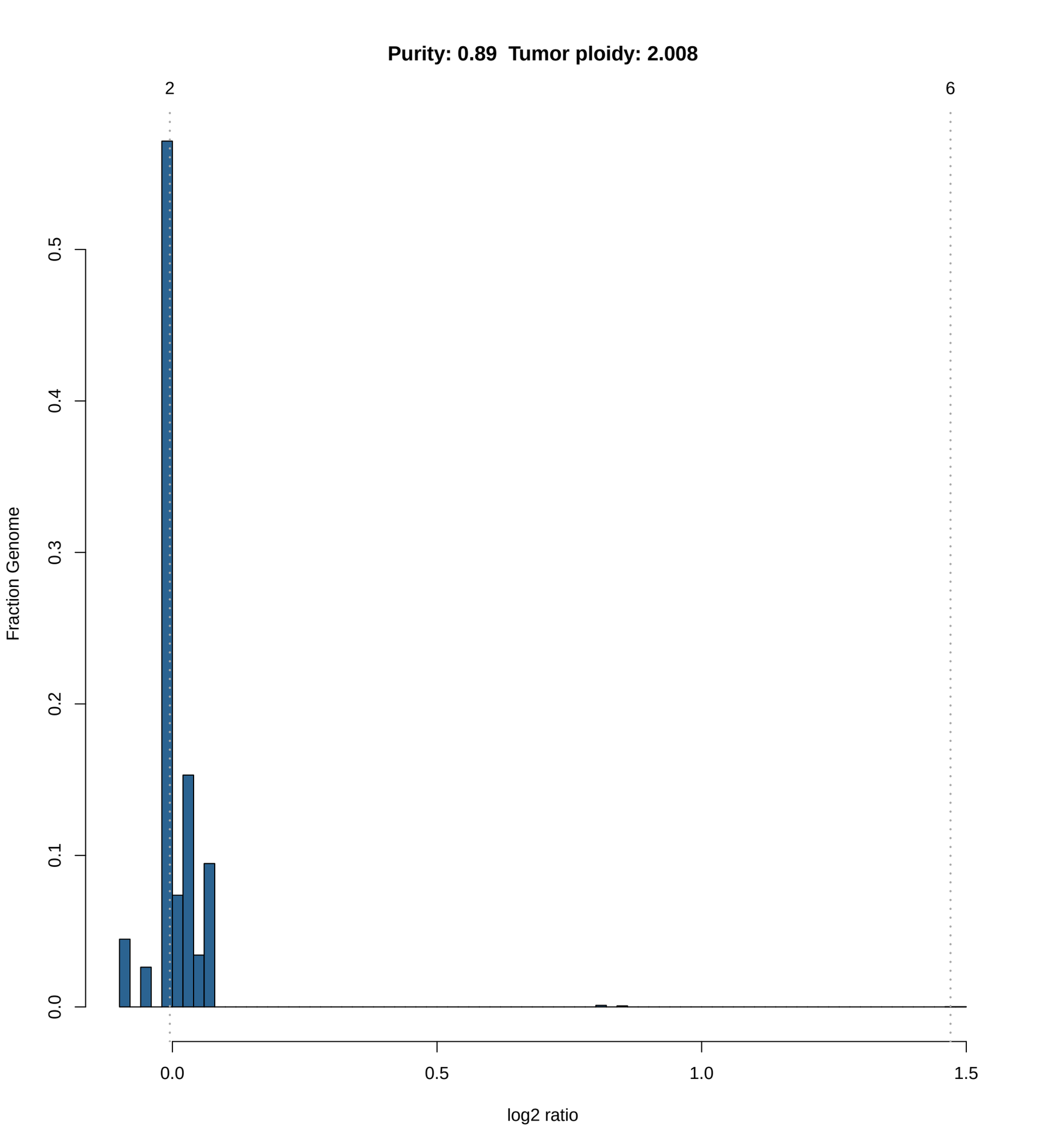

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 20 40 60 80 100 120 140
SNV Index

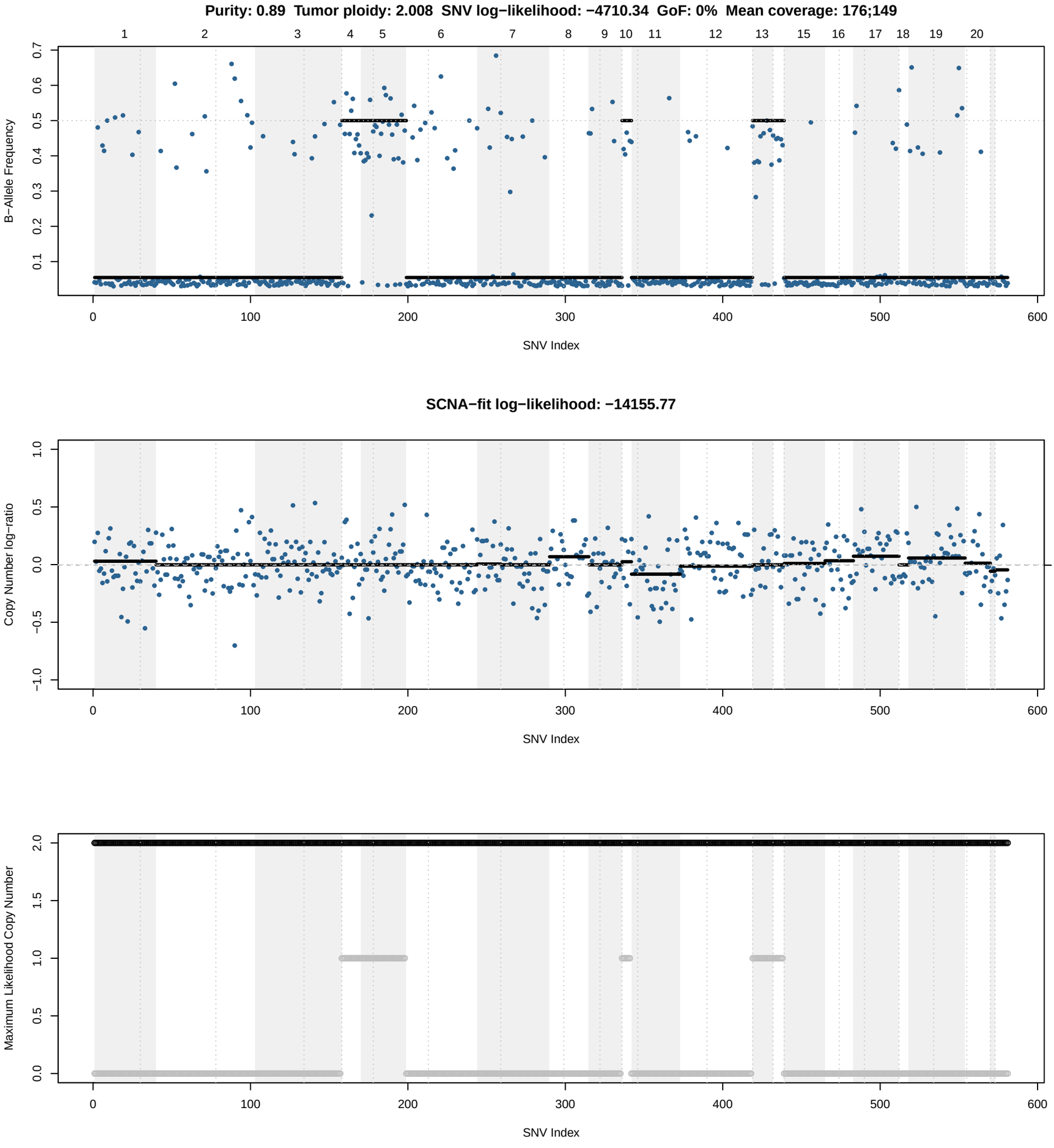

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
2m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

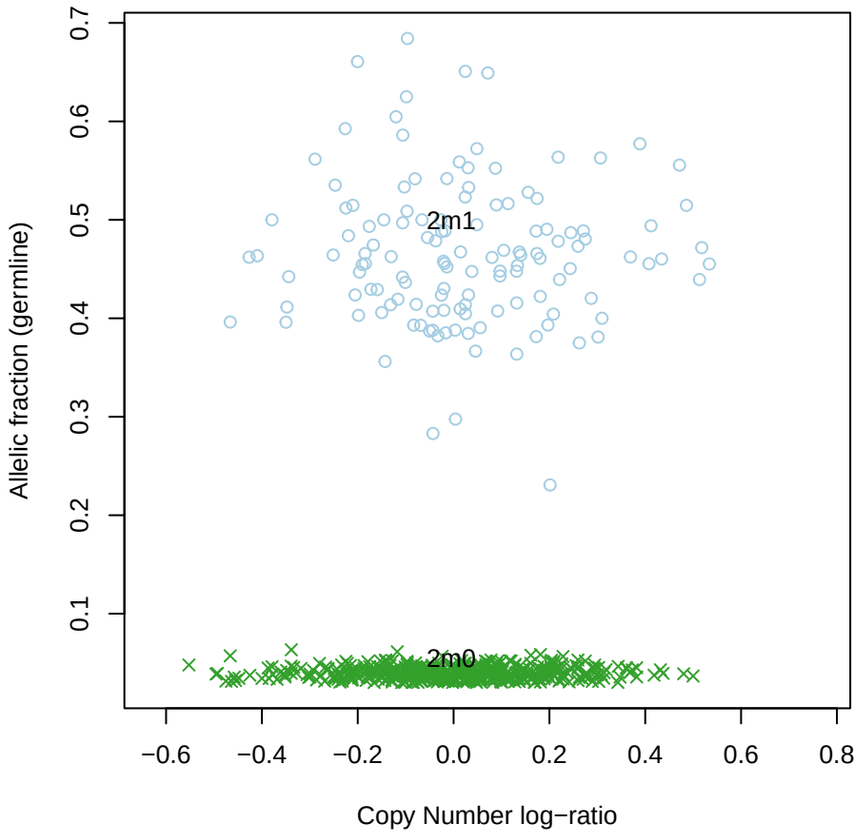

Coverage (log2)
4
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

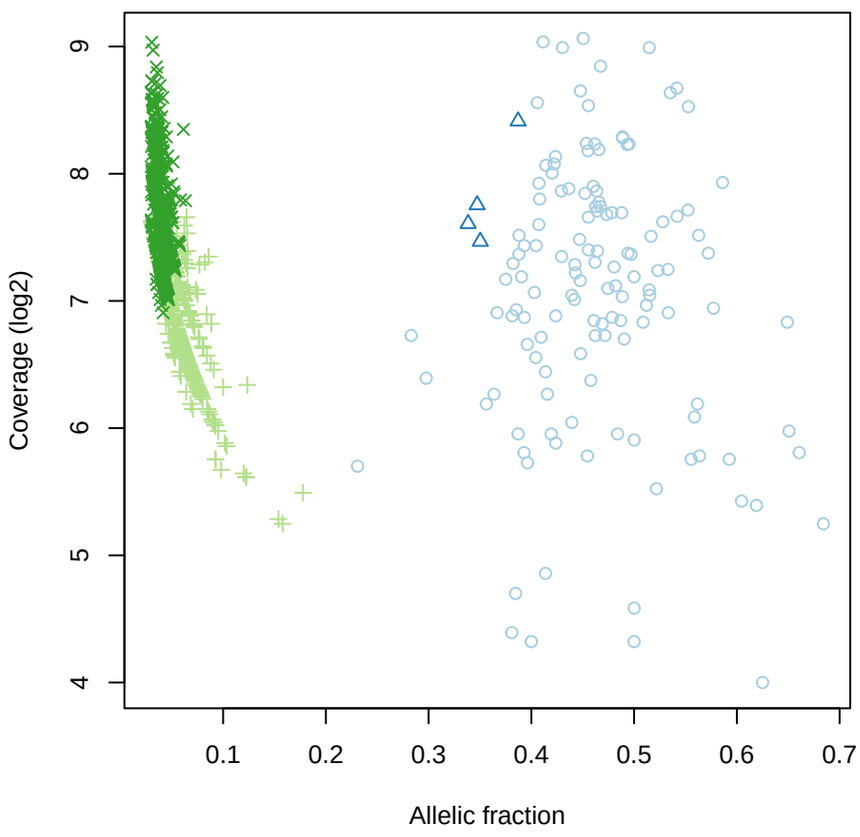

Allelic fraction (somatic)
0.05
0.10
0.15
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

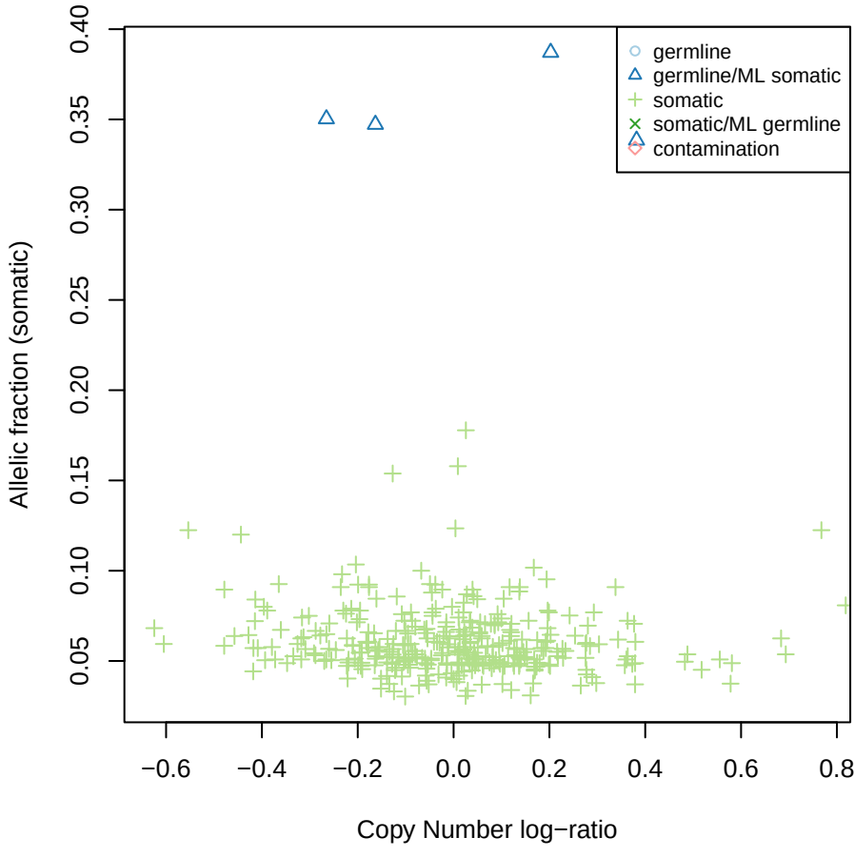

Power 0.8
Frequency
0
100
200
300
400
0.1
0.2
0.3
0.4
0.5
Cellular fraction

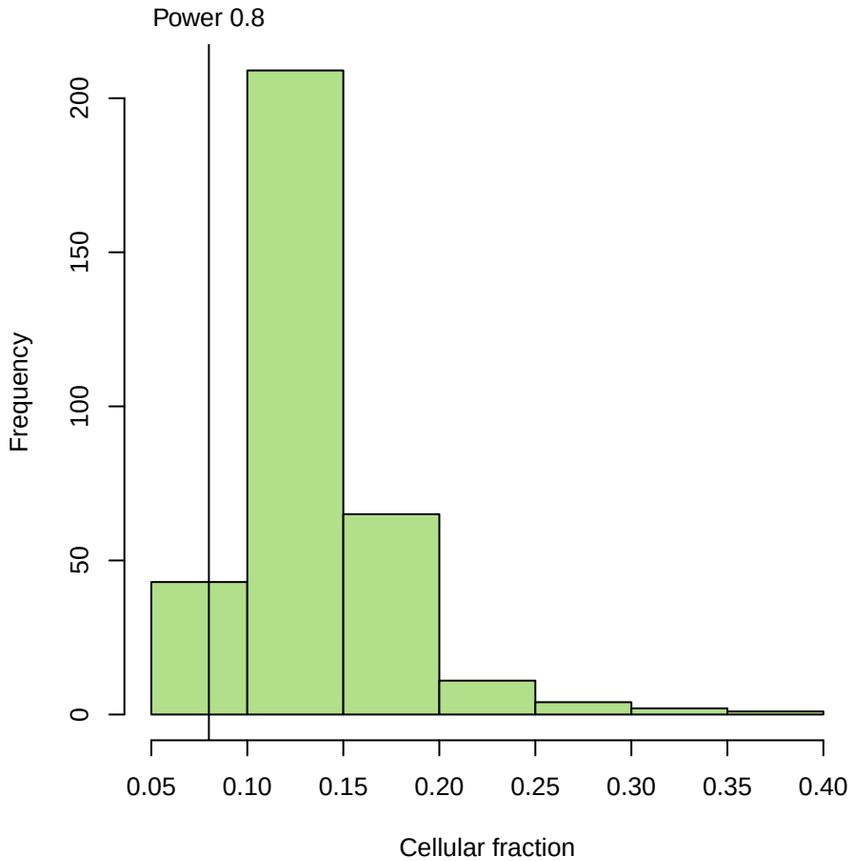

Purity: 0.89 Tumor ploidy: 2.008
2
6
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
0.0
0.5
1.0
1.5
log2 ratio


Purity: 0.89 Tumor ploidy: 2.008 SNV log−likelihood: −4710.34 GoF: 0% Mean coverage: 176;149
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 18 19 20
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6 0.7
0 100 200 300 400 500 600
SNV Index
SCNA−fit log−likelihood: −14155.77
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2
0 100 200 300 400 500 600
SNV Index
Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 100 200 300 400 500 600
SNV Index


Allelic fraction (germline)
Copy Number log−ratio
2m1
2m0


Coverage (log2)
Allelic fraction


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


Power 0.8
Frequency
Cellular fraction