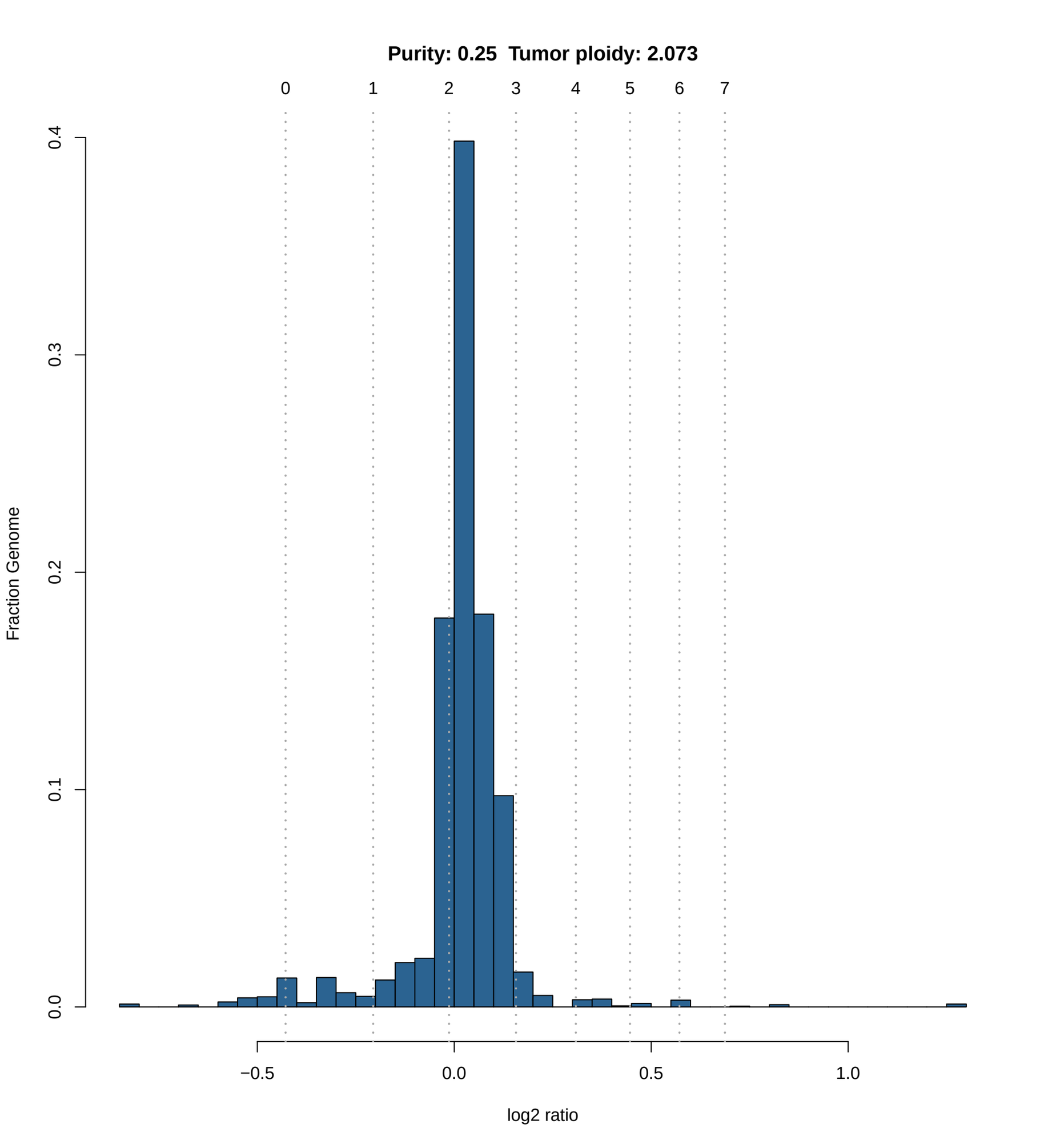
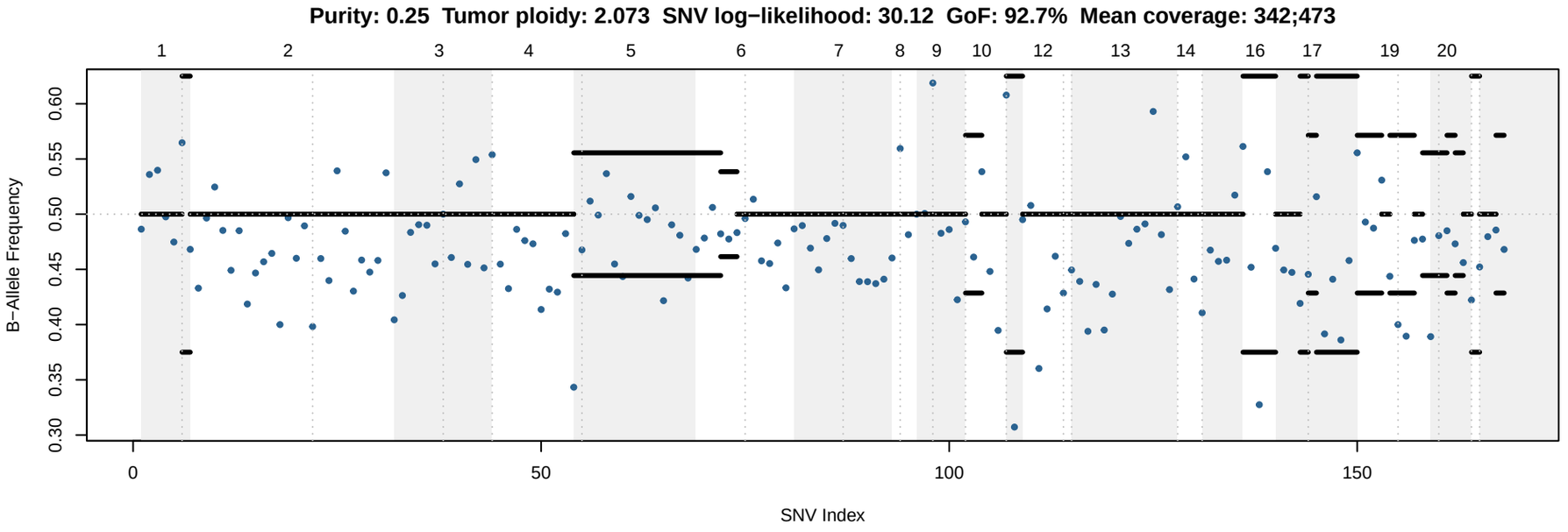
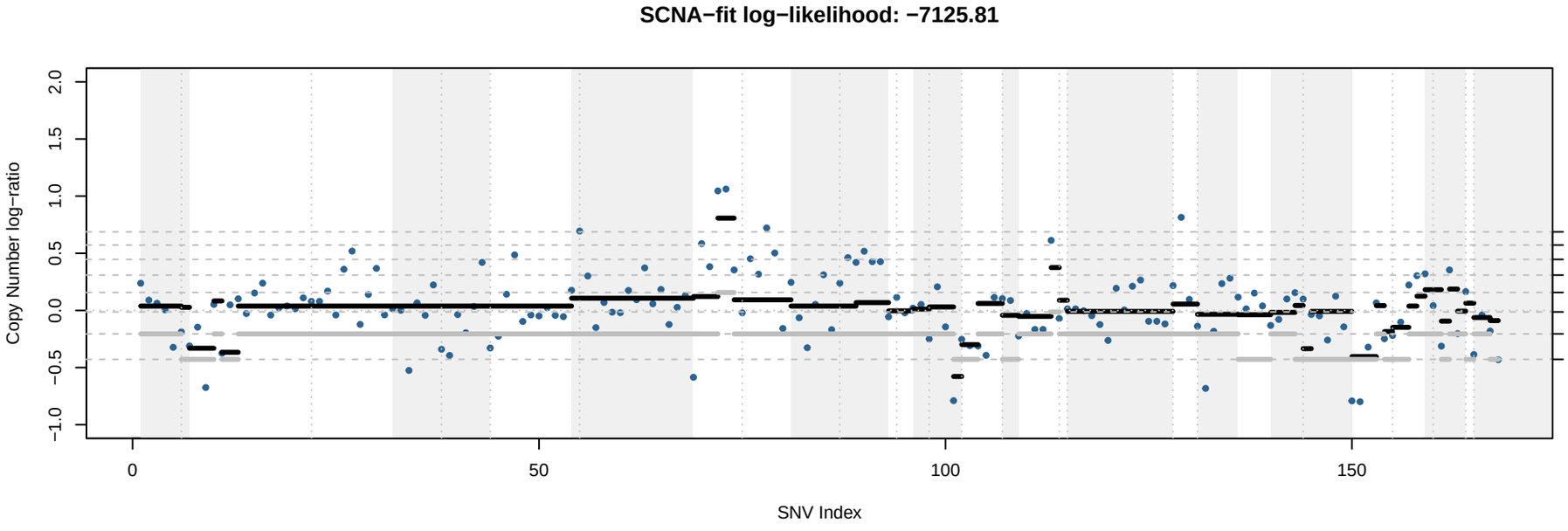
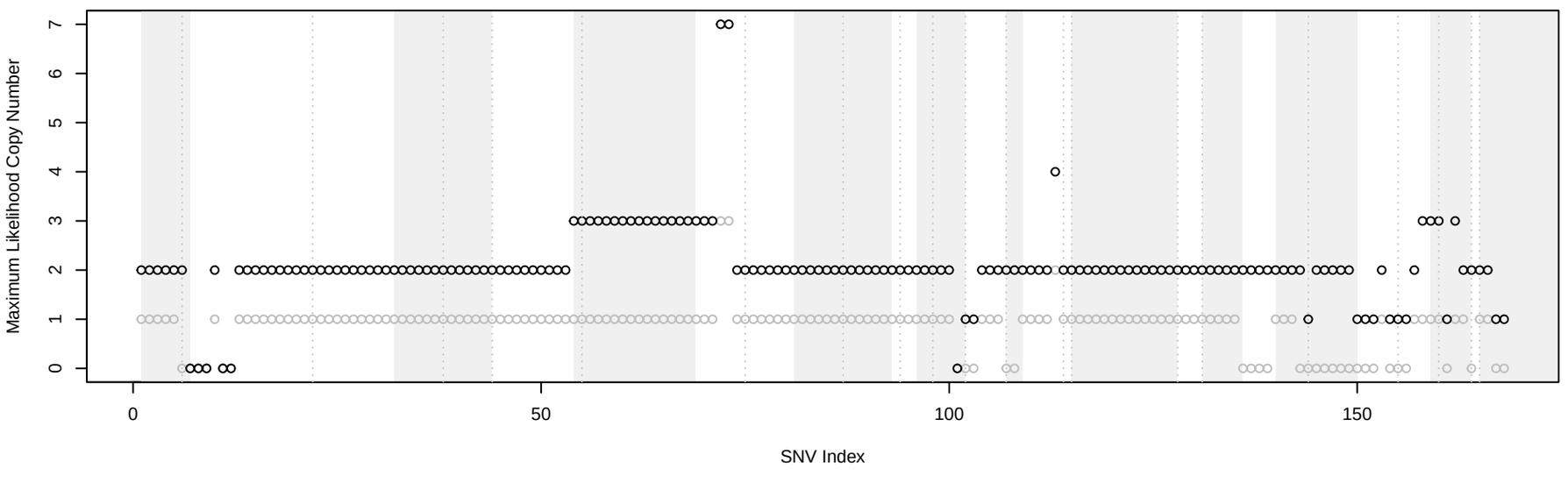
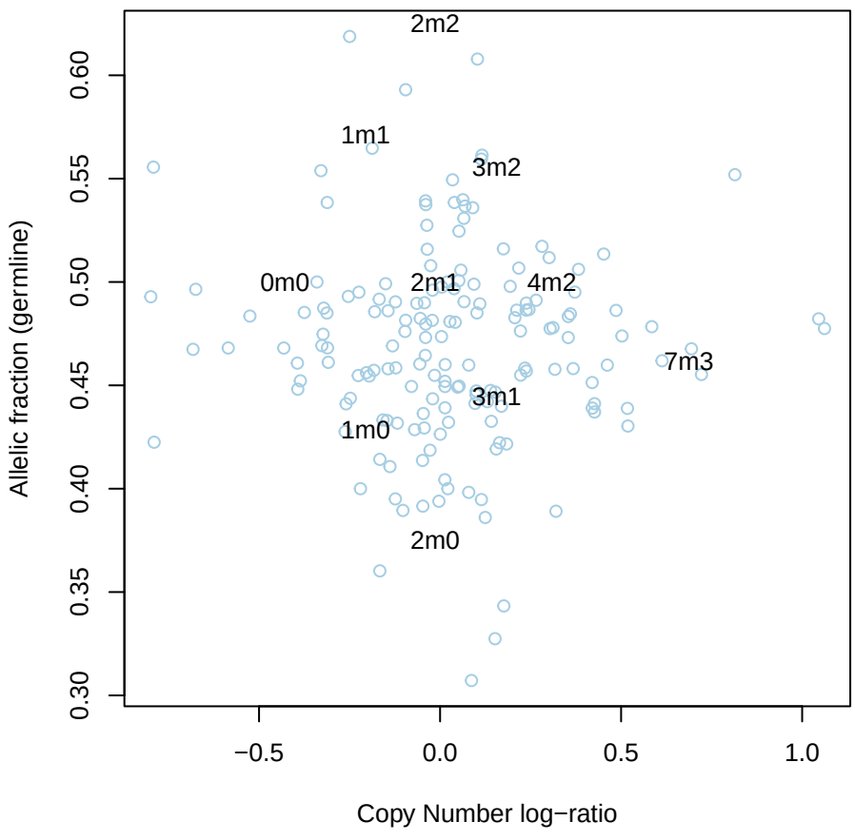
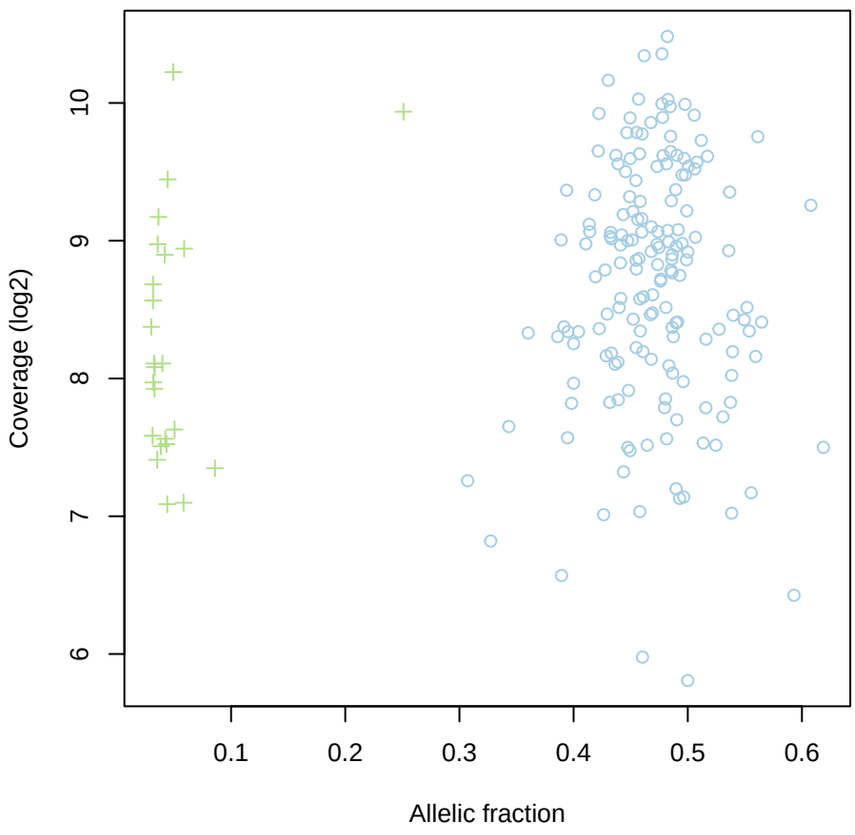

Purity: 0.25 Tumor ploidy: 2.073
0
1
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

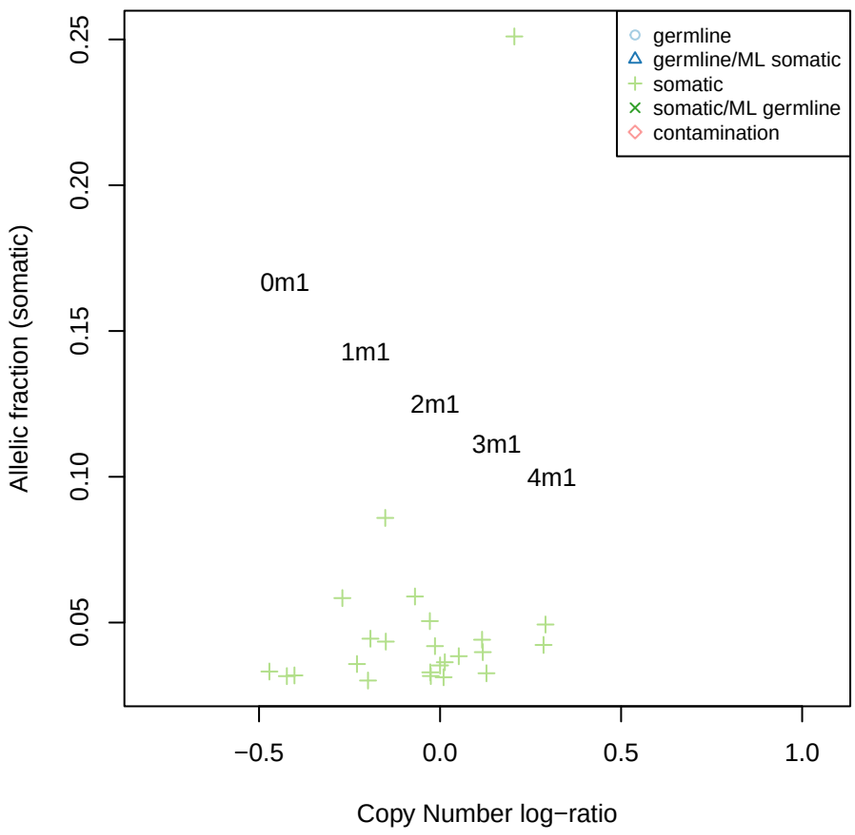

Purity: 0.25 Tumor ploidy: 2.073 SNV log−likelihood: 30.12 GoF: 92.7% Mean coverage: 342;473
1 2 3 4 5 6 7 8 9 10 12 13 14 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

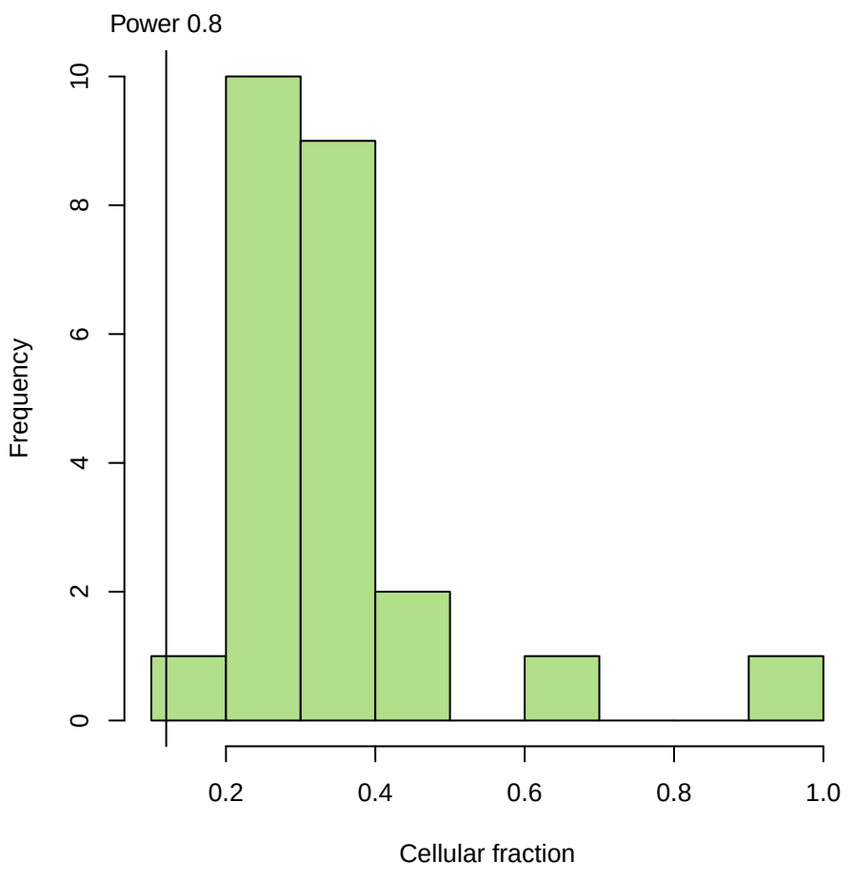

SCNA−fit log−likelihood: −7125.81
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
0 1 3 5 7
0 50 100 150
SNV Index

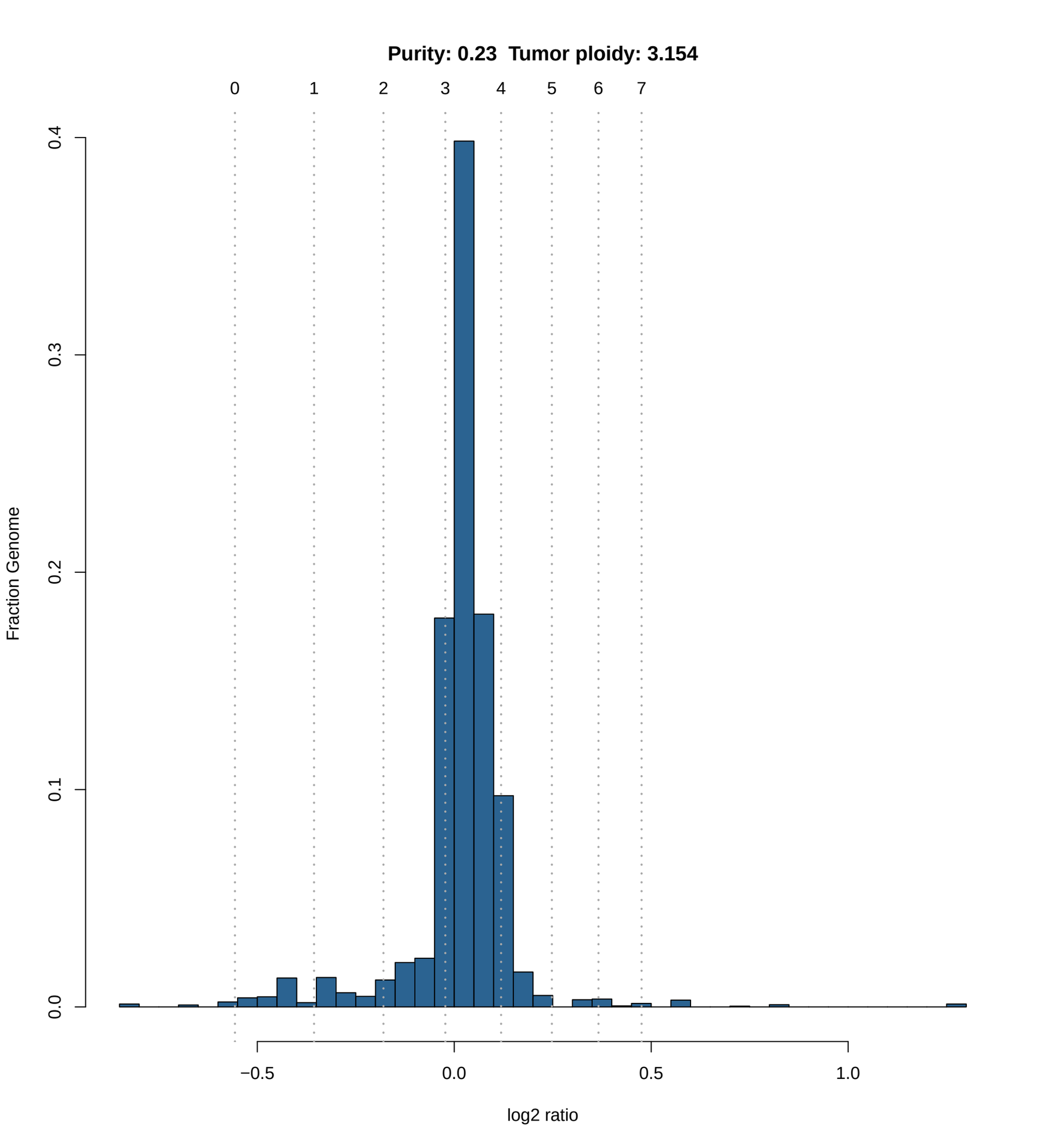

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

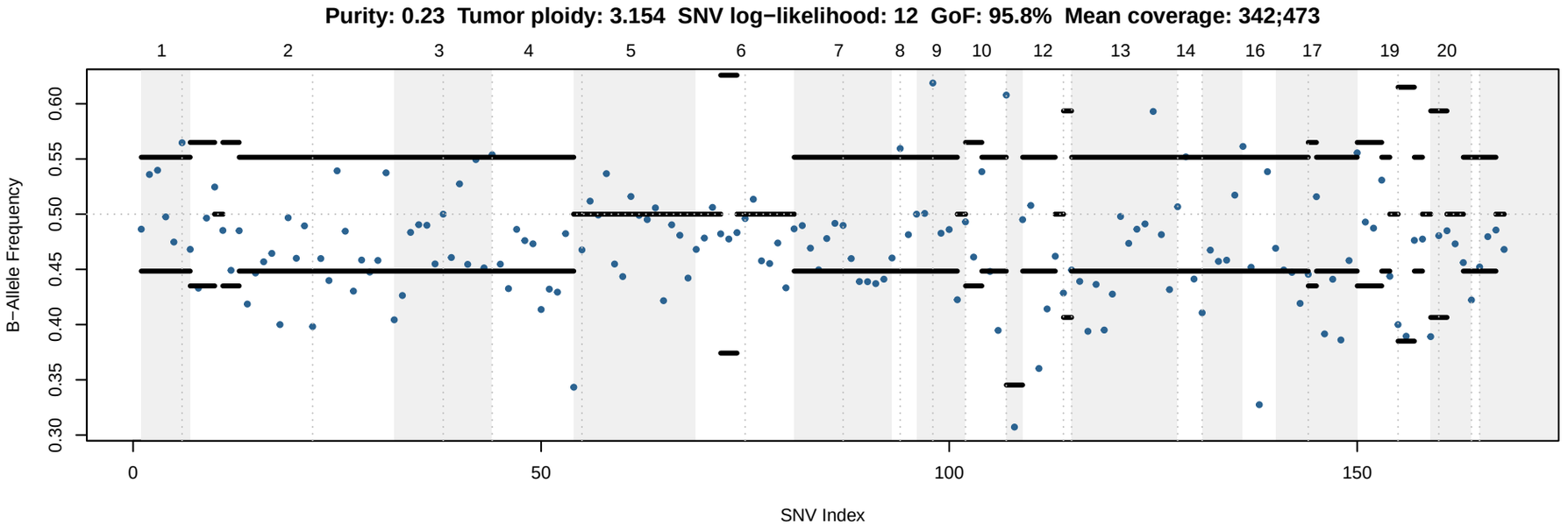

2m2
1m1
3m2
0m0
2m1
4m2
7m3
3m1
1m0
2m0
Allelic fraction (germline)
Copy Number log−ratio
0.30
0.35
0.40
0.45
0.50
0.55
0.60
−0.5
0.0
0.5
1.0

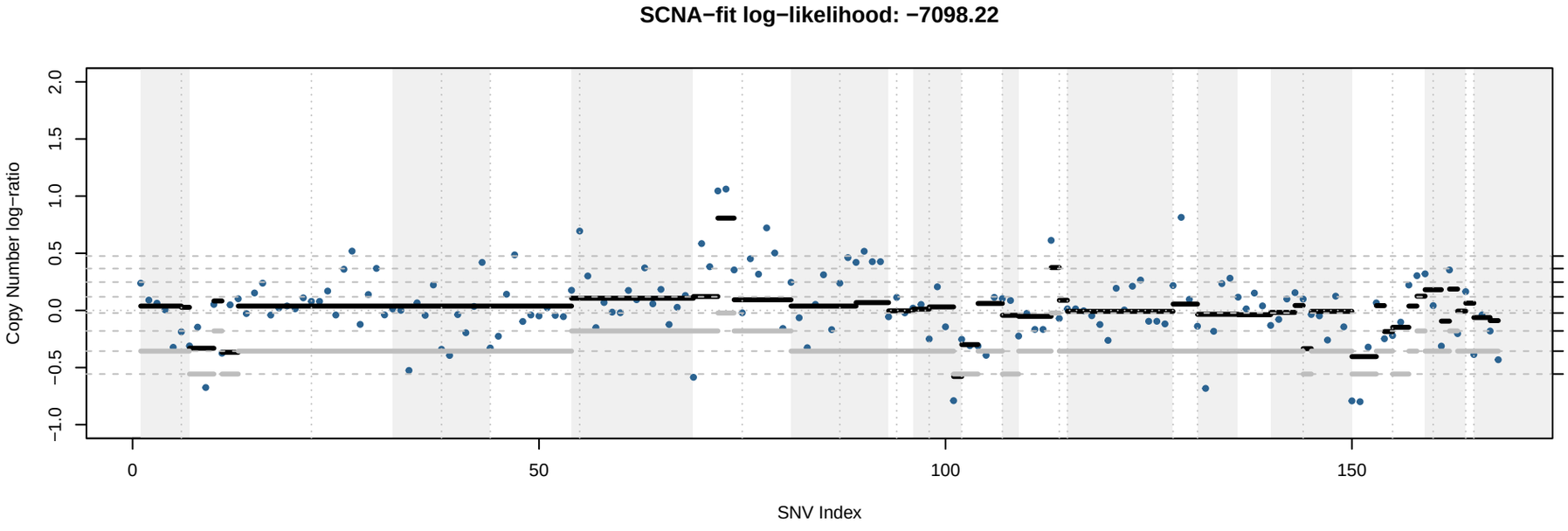

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

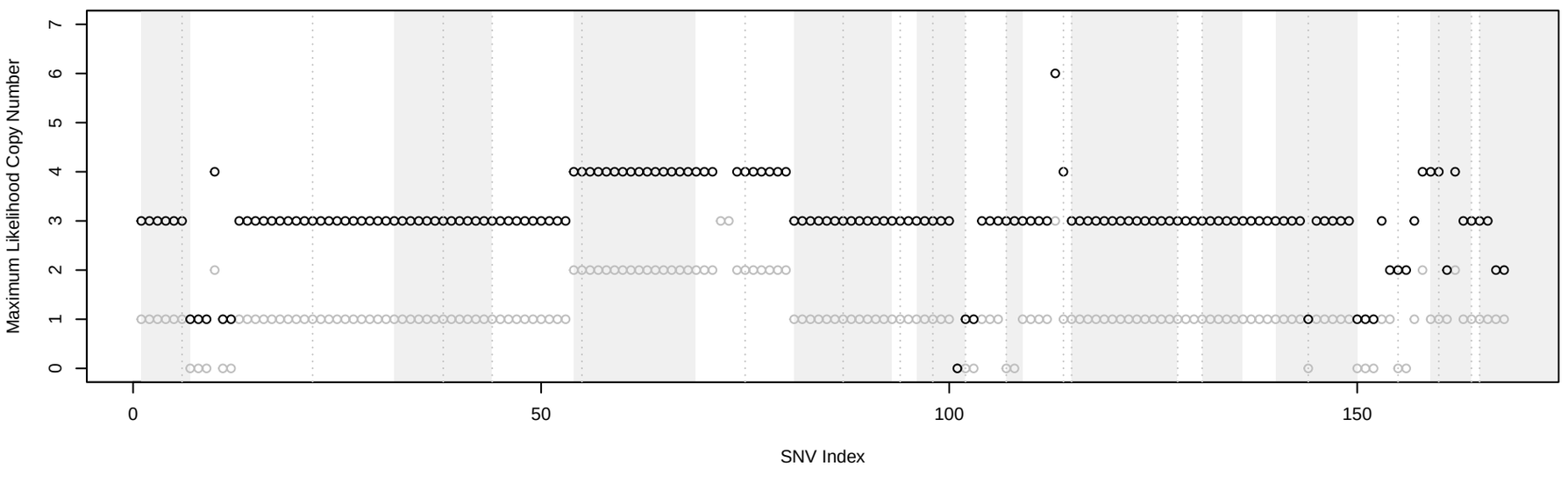

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
0m1
1m1
2m1
3m1
4m1
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
0.25
−0.5
0.0
0.5
1.0

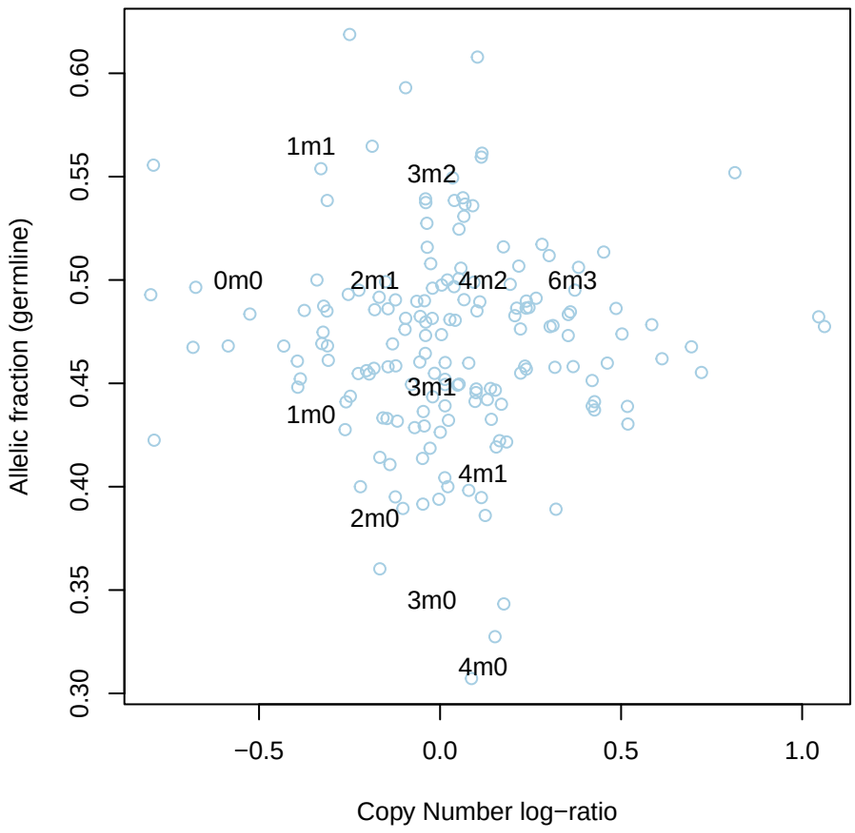

Power 0.8
Frequency
Cellular fraction
0
2
4
6
8
10
0.2
0.4
0.6
0.8
1.0

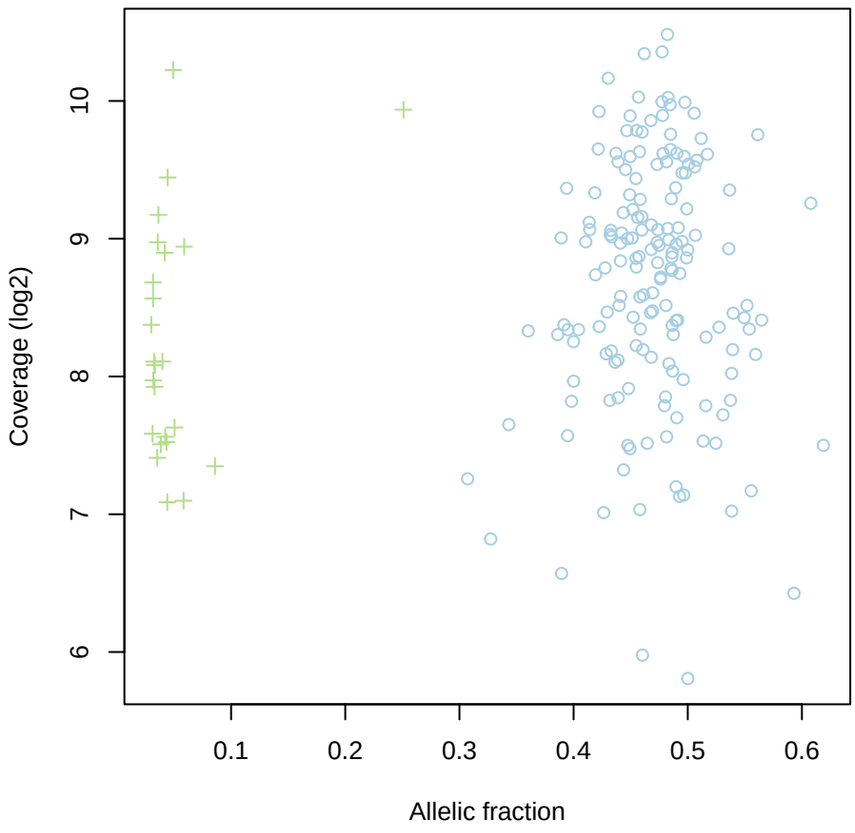

Purity: 0.23 Tumor ploidy: 3.154
0
1
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

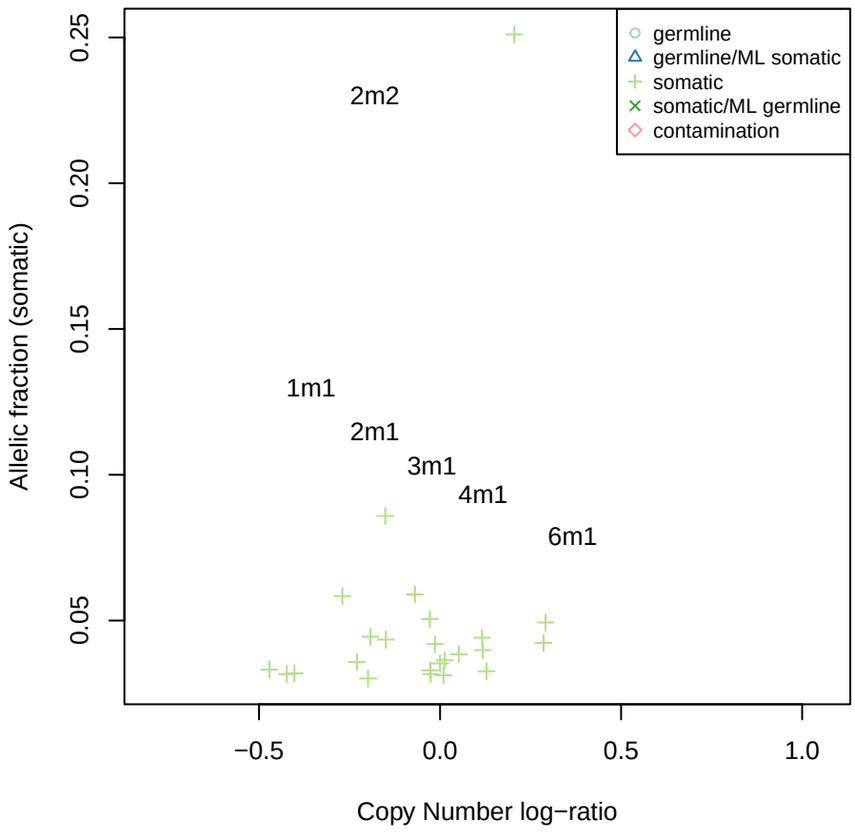

Purity: 0.23 Tumor ploidy: 3.154 SNV log−likelihood: 12 GoF: 95.8% Mean coverage: 342;473
1 2 3 4 5 6 7 8 9 10 12 13 14 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

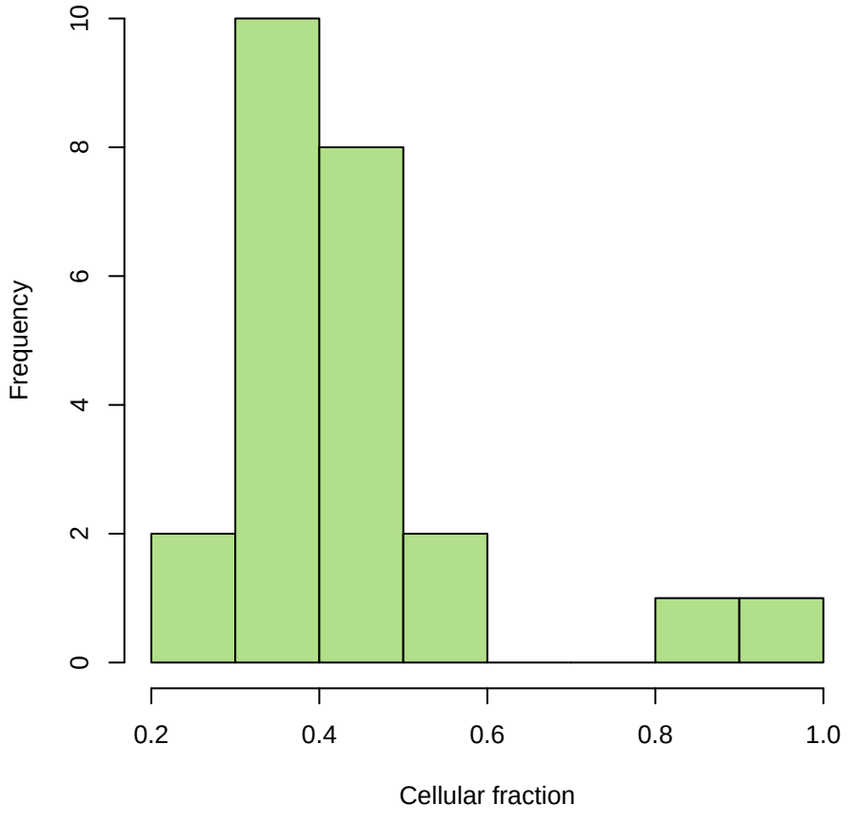

SCNA−fit log−likelihood: −7098.22
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
0 2 4 6
0 50 100 150
SNV Index

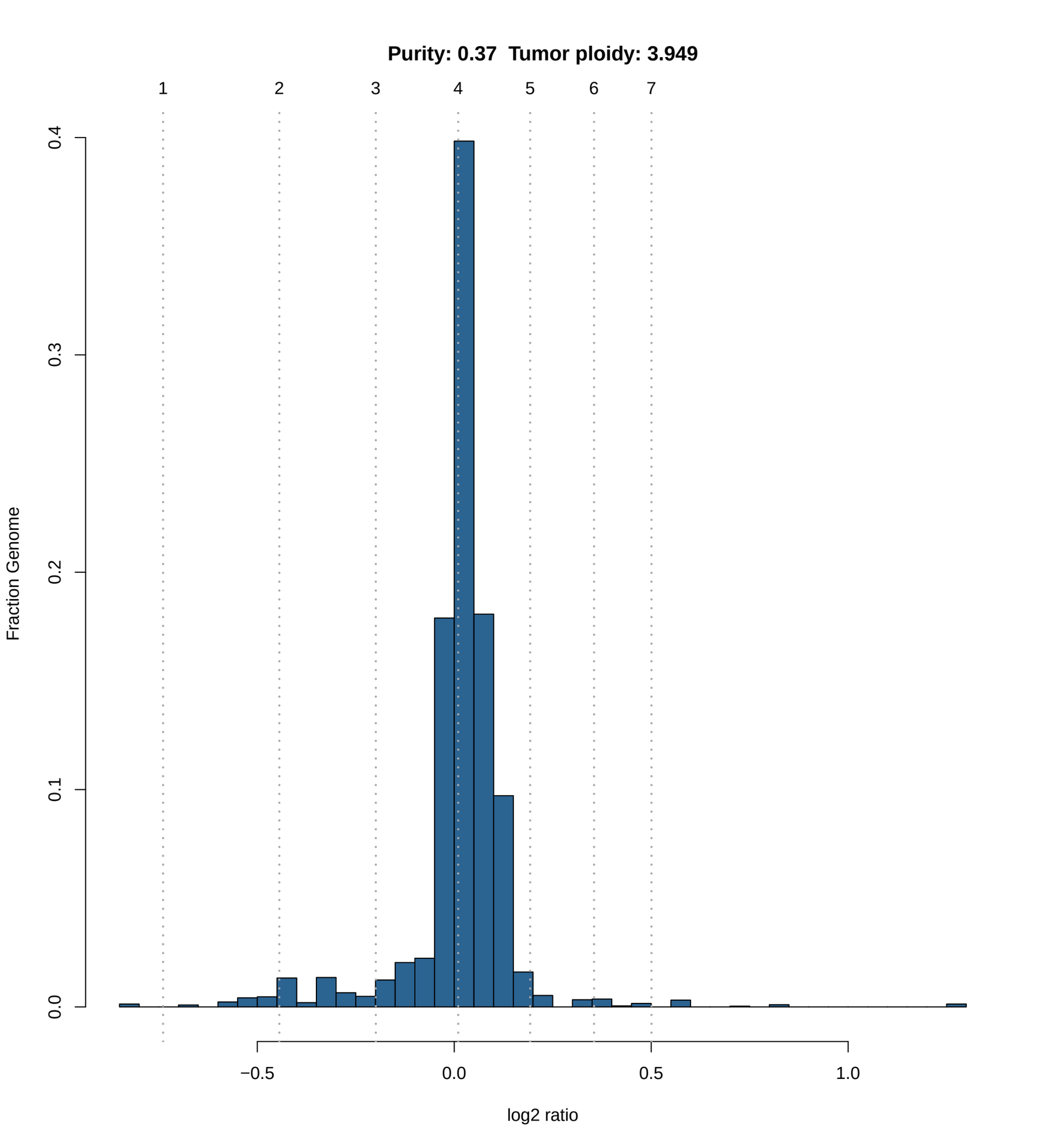

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

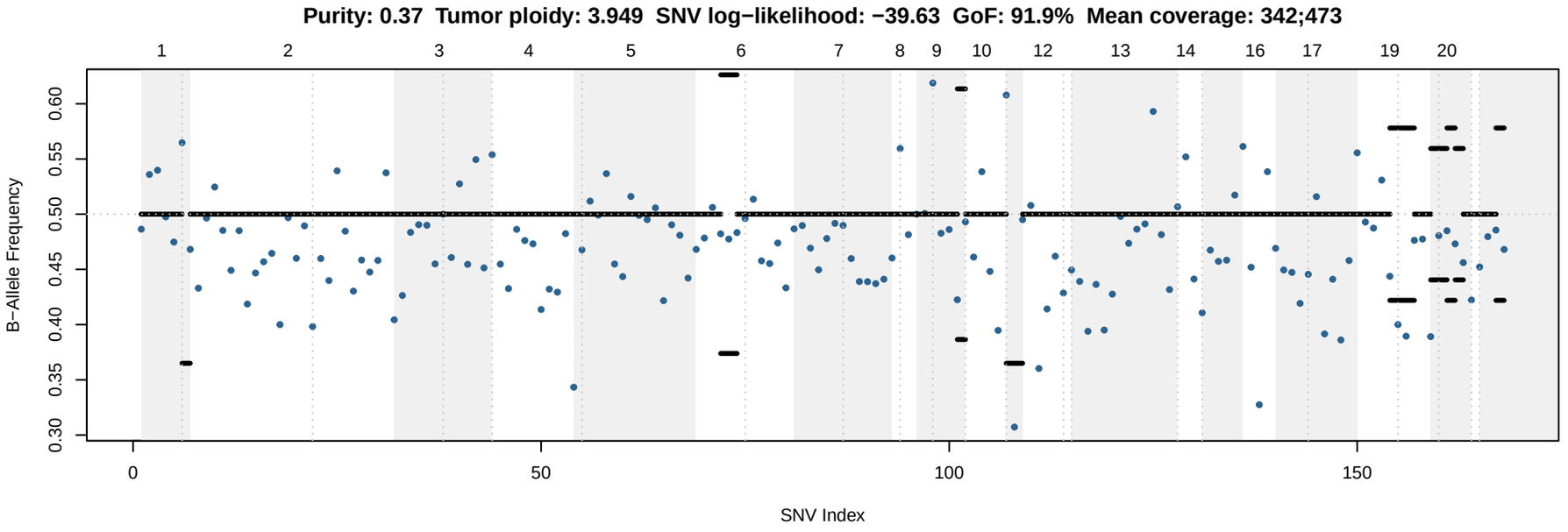

Allelic fraction (germline)
Copy Number log−ratio
0.30
0.35
0.40
0.45
0.50
0.55
0.60
−0.5
0.0
0.5
1.0
1m1
3m2
0m0
2m1
4m2
6m3
3m1
1m0
4m1
2m0
3m0
4m0

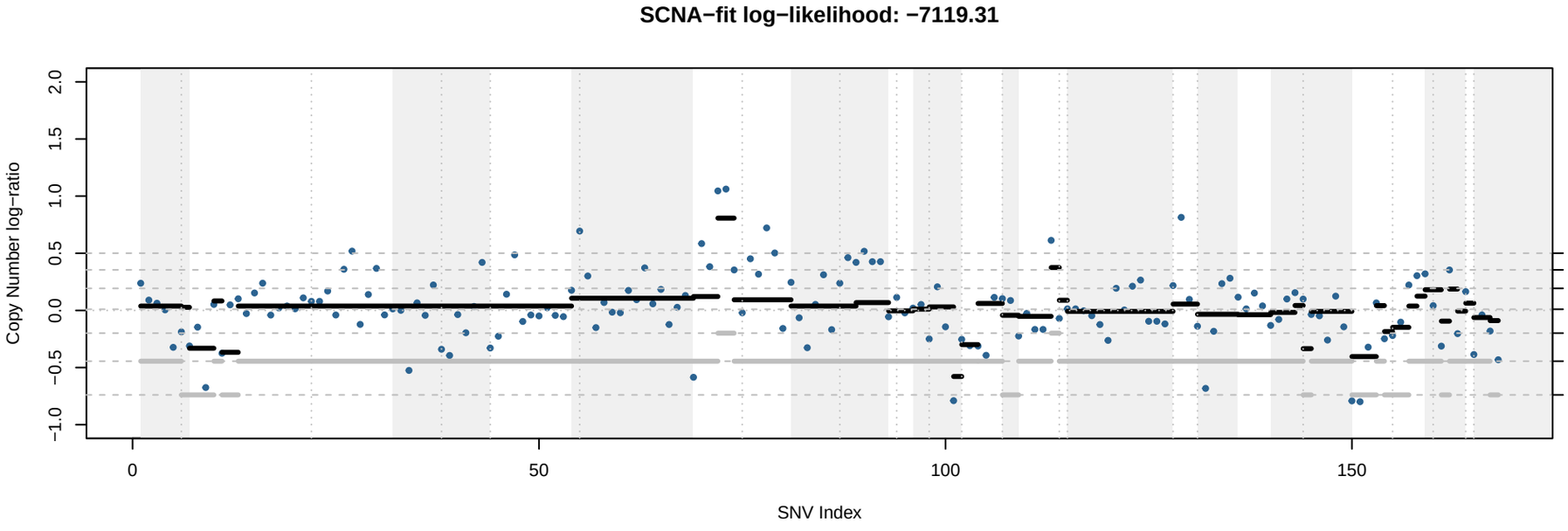

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

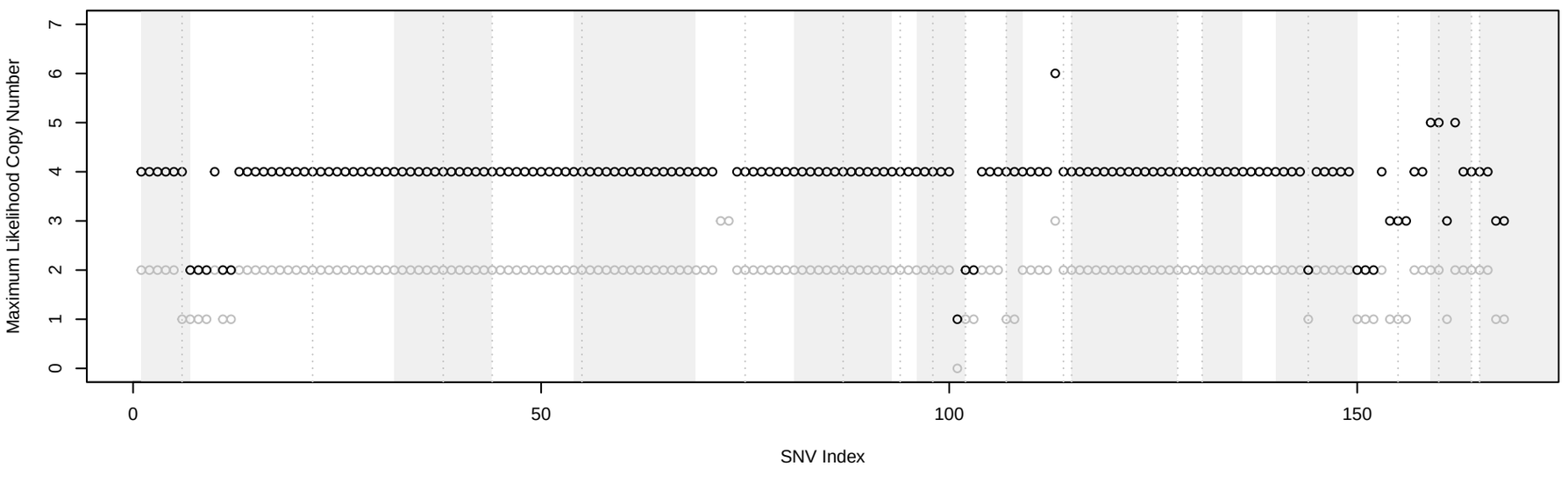

Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
0.25
−0.5
0.0
0.5
1.0
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
1m1
2m1
3m1
4m1
6m1

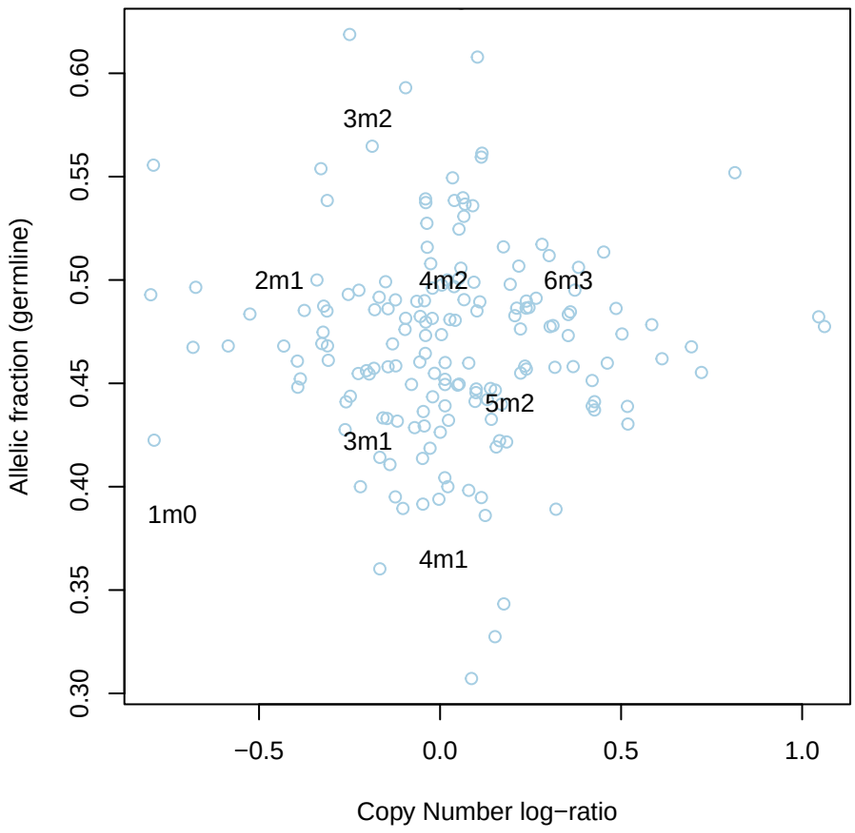

Frequency
Cellular fraction
0
2
4
6
8
10
0.2
0.4
0.6
0.8
1.0

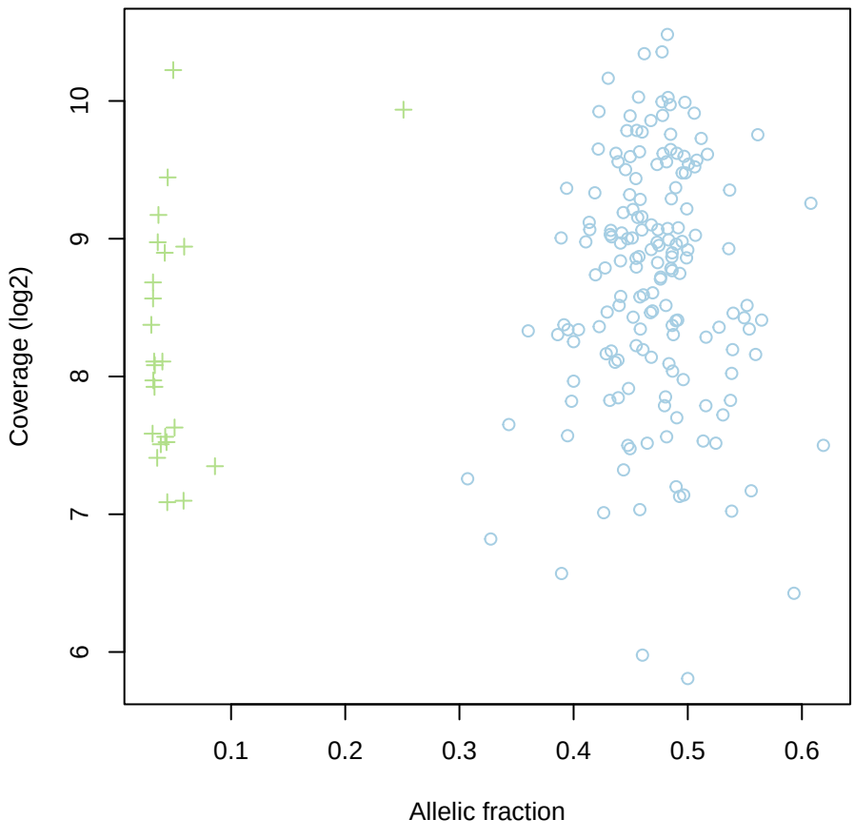

Purity: 0.37 Tumor ploidy: 3.949
1
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

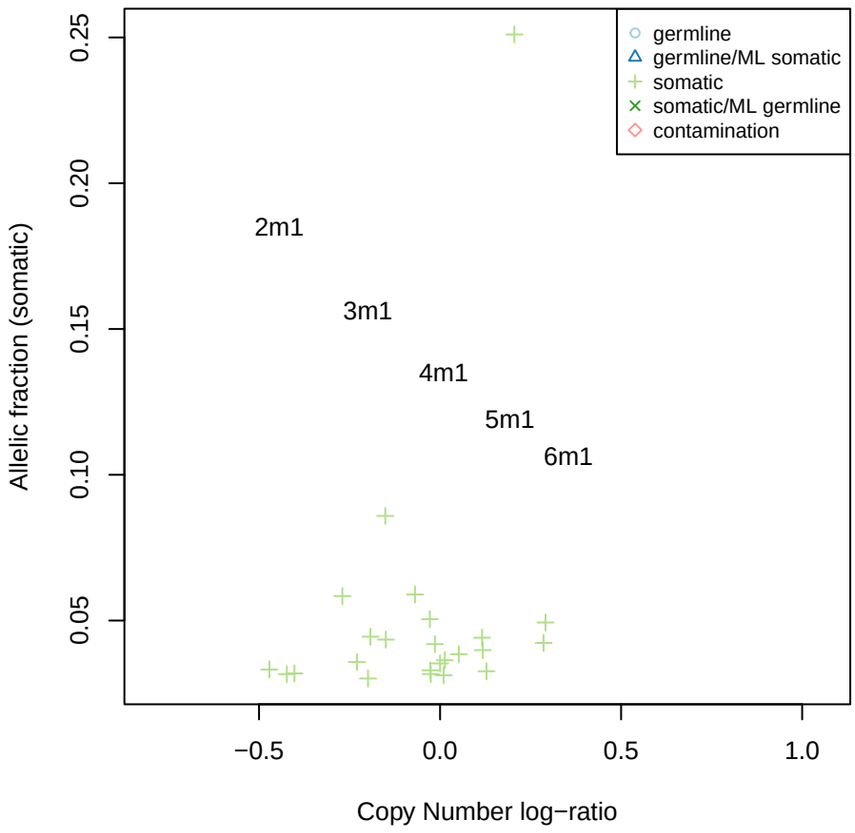

Purity: 0.37 Tumor ploidy: 3.949 SNV log−likelihood: −39.63 GoF: 91.9% Mean coverage: 342;473
1 2 3 4 5 6 7 8 9 10 12 13 14 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

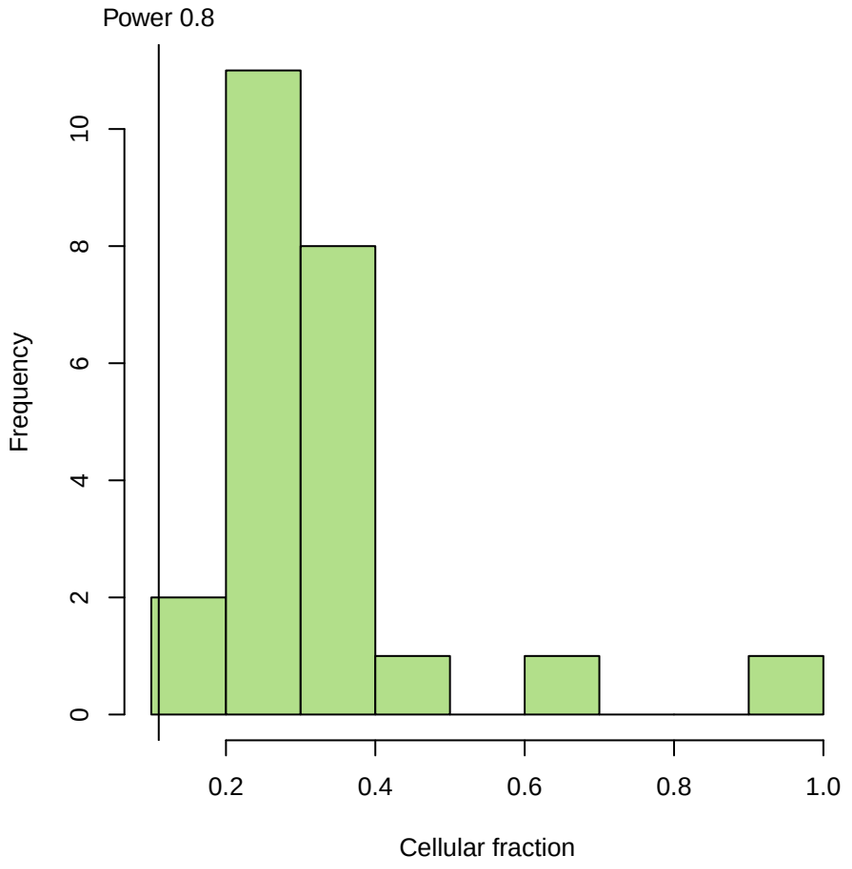

SCNA−fit log−likelihood: −7119.31
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
1 2 3 5 7
0 50 100 150
SNV Index

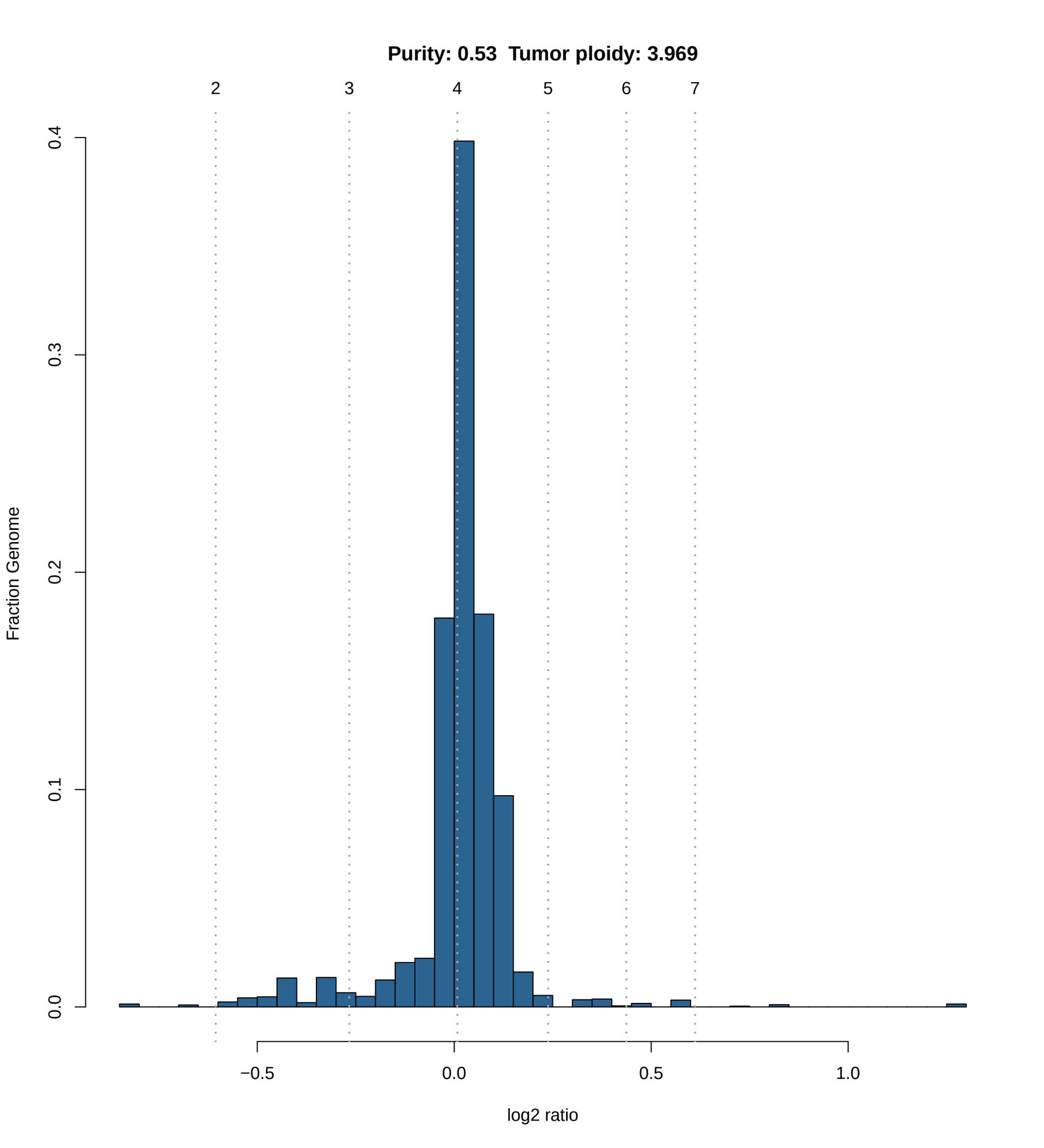

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

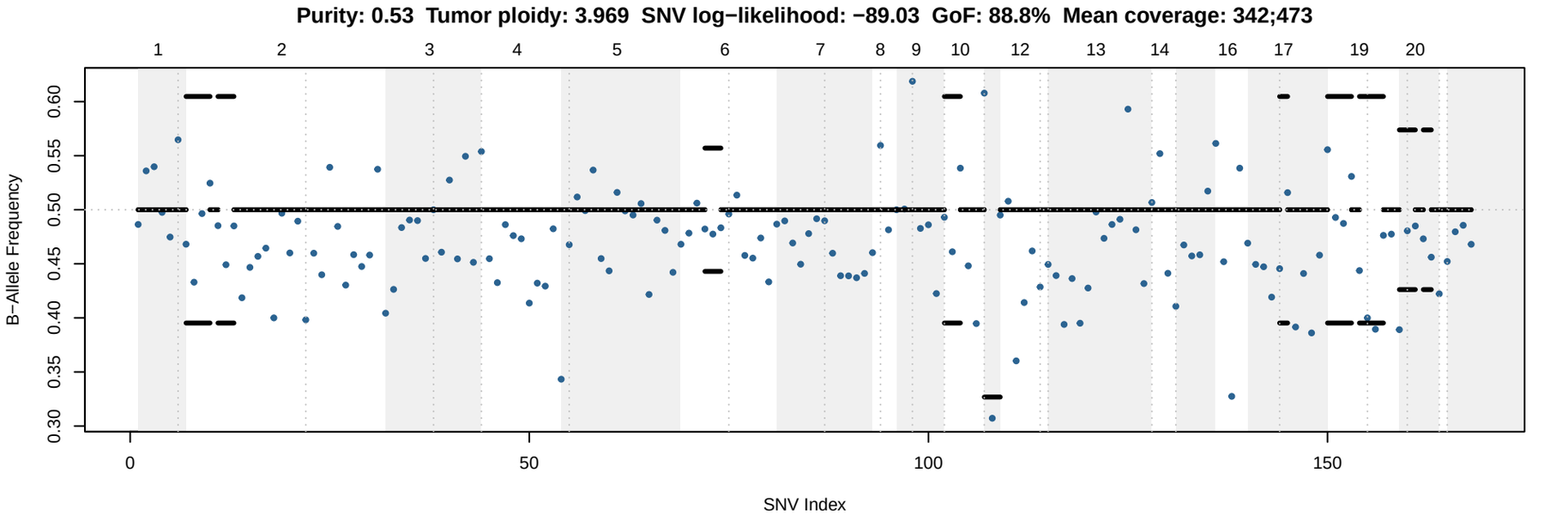

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
3m2
2m1
4m2
6m3
5m2
3m1
1m0
4m1
−0.5
0.0
0.5
1.0
Copy Number log−ratio

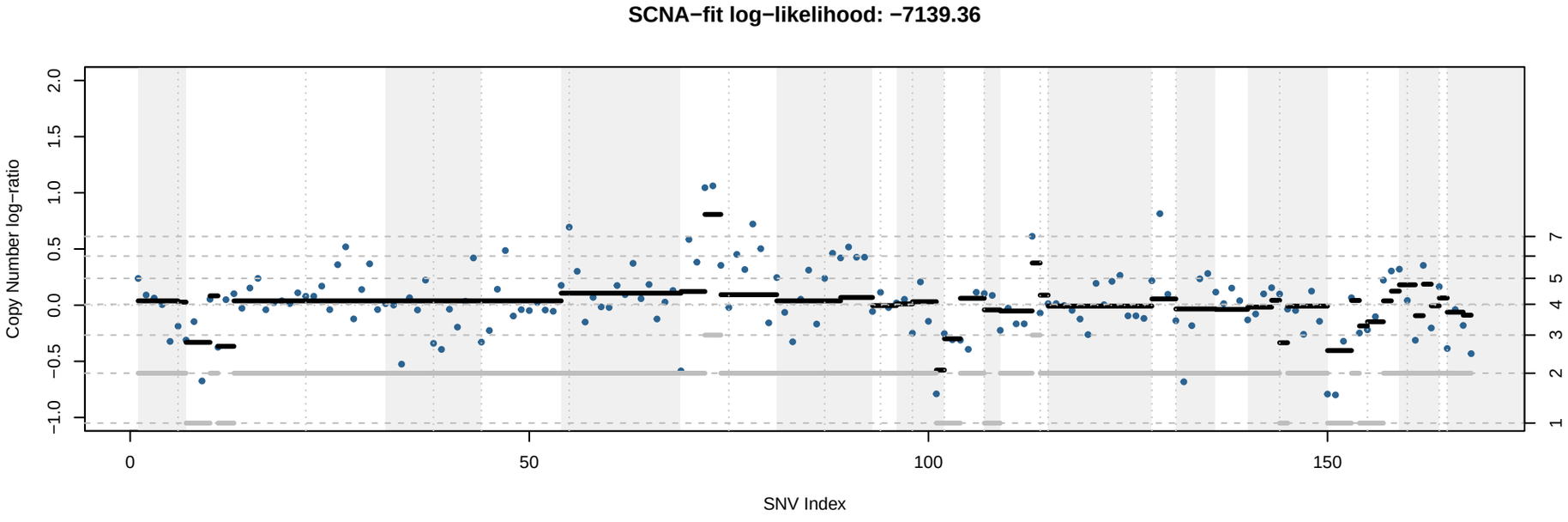

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

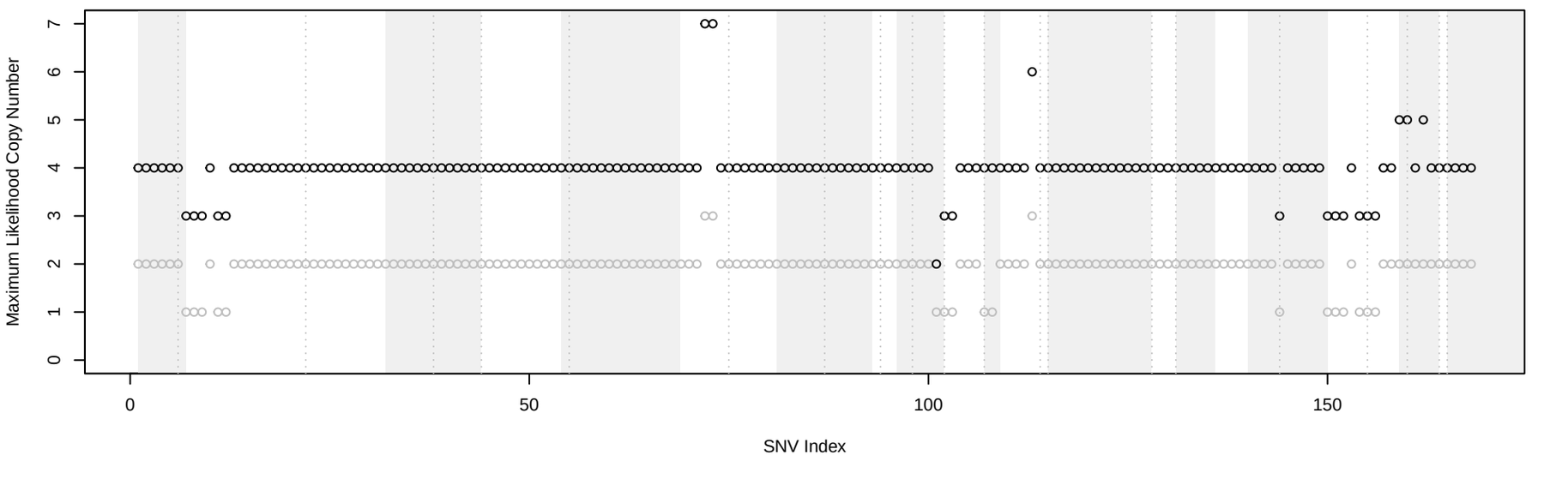

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
2m1
3m1
4m1
5m1
6m1
−0.5
0.0
0.5
1.0
Copy Number log−ratio

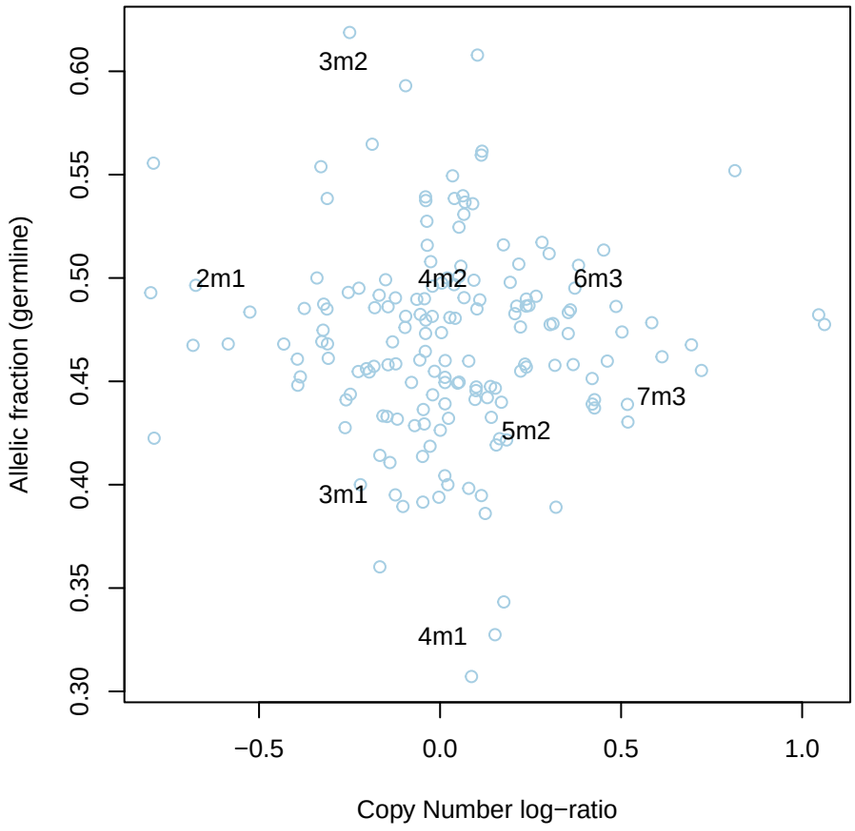

Power 0.8
Frequency
0
2
4
6
8
10
0.2
0.4
0.6
0.8
1.0
Cellular fraction

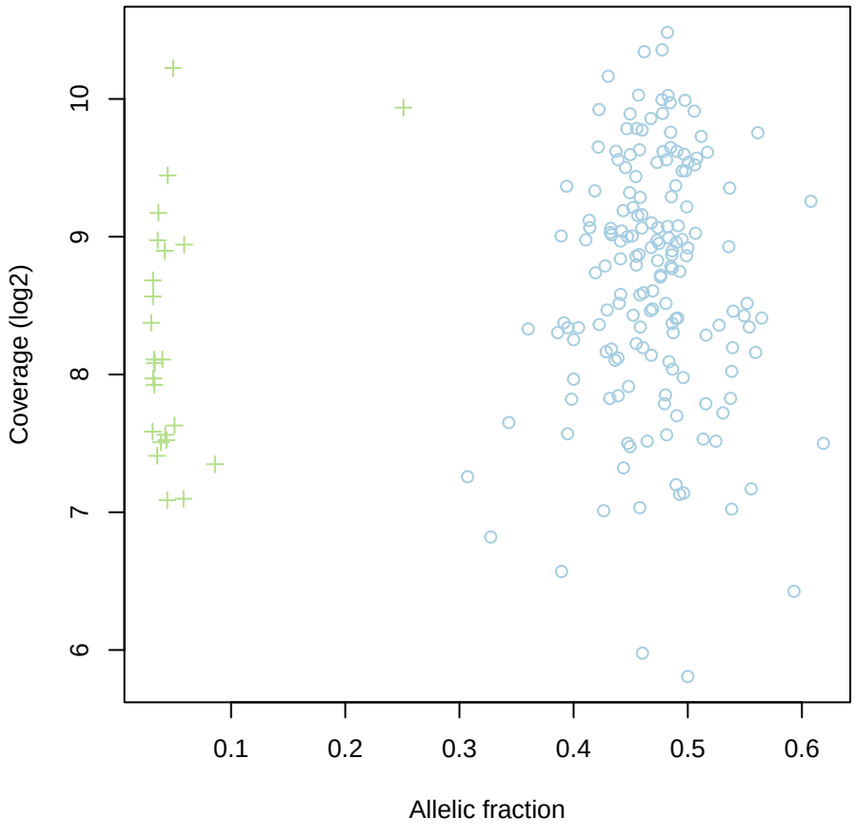

Purity: 0.53 Tumor ploidy: 3.969
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

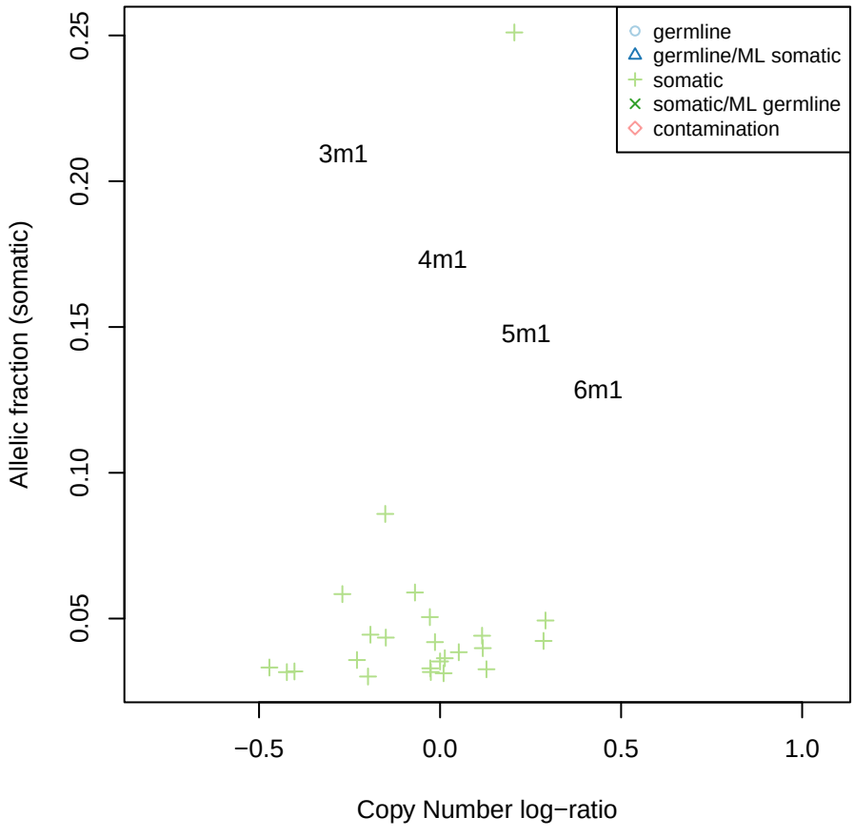

Purity: 0.53 Tumor ploidy: 3.969 SNV log−likelihood: −89.03 GoF: 88.8% Mean coverage: 342;473
1 2 3 4 5 6 7 8 9 10 12 13 14 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

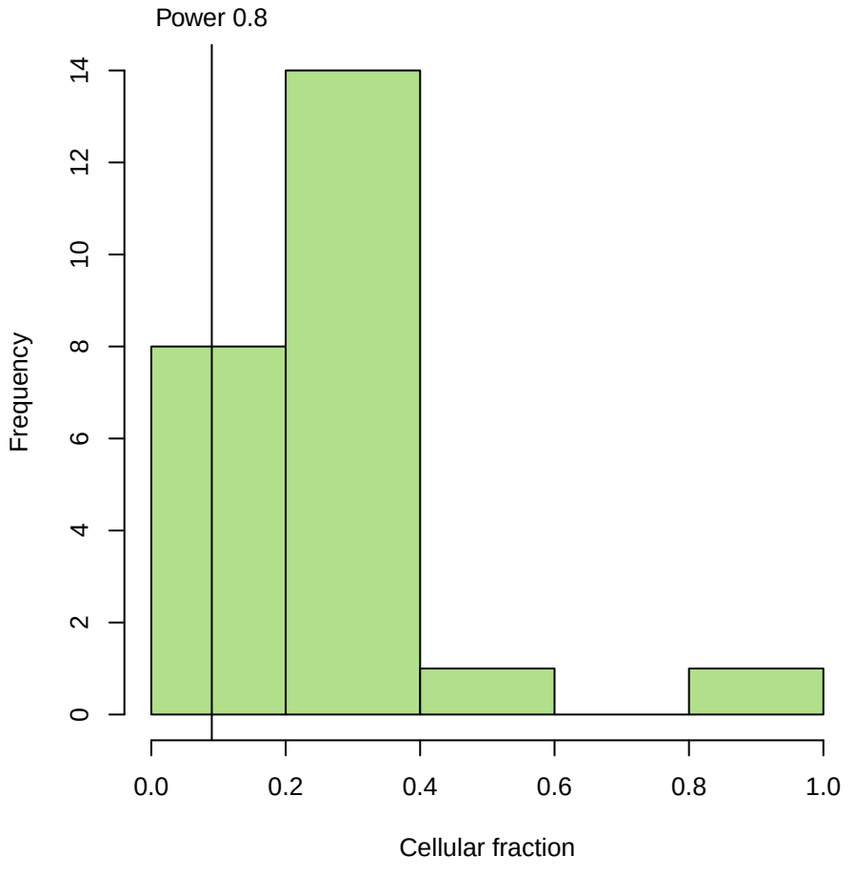

SCNA−fit log−likelihood: −7139.36
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
1 2 3 4 5 7
0 50 100 150
SNV Index

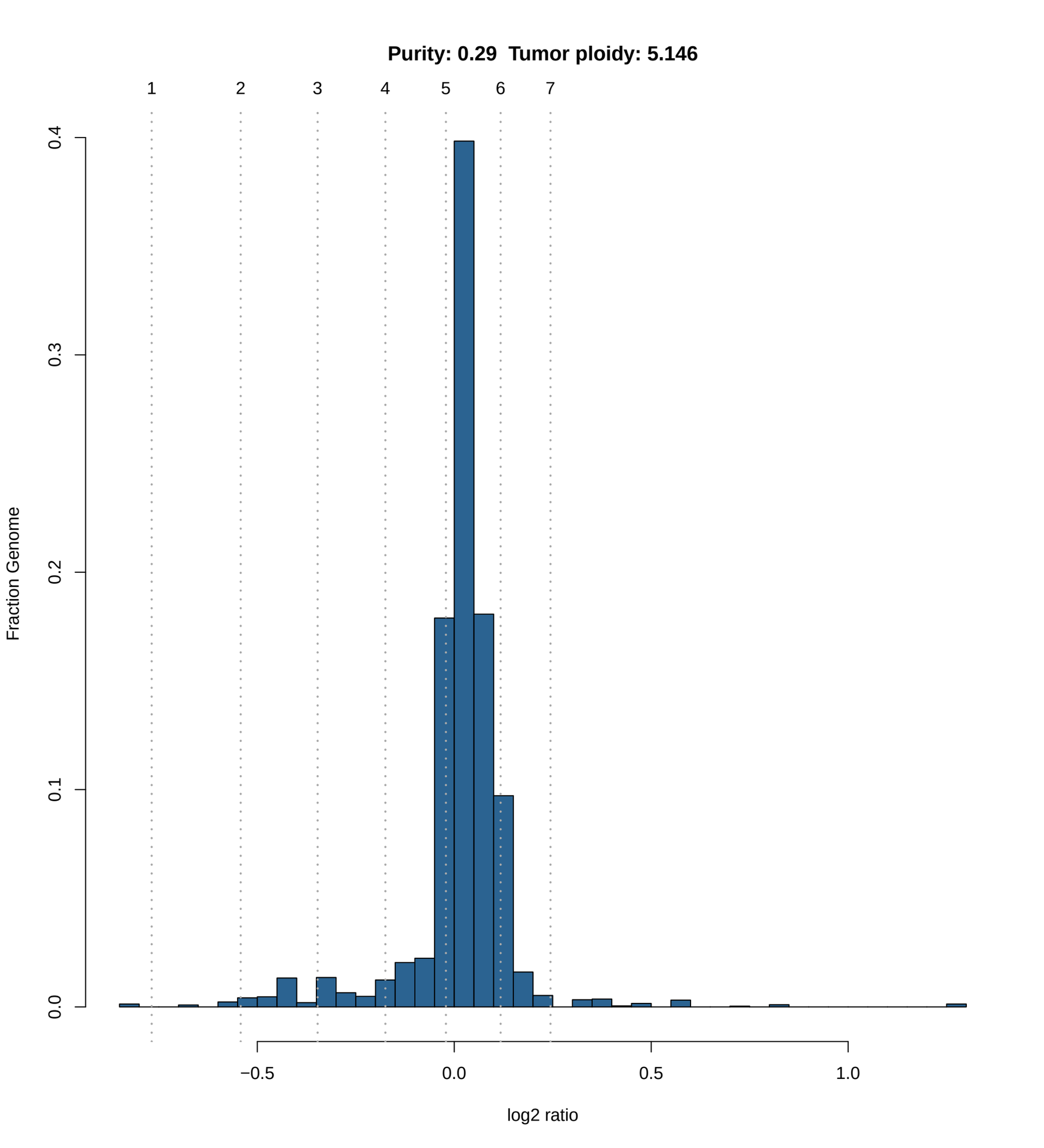

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

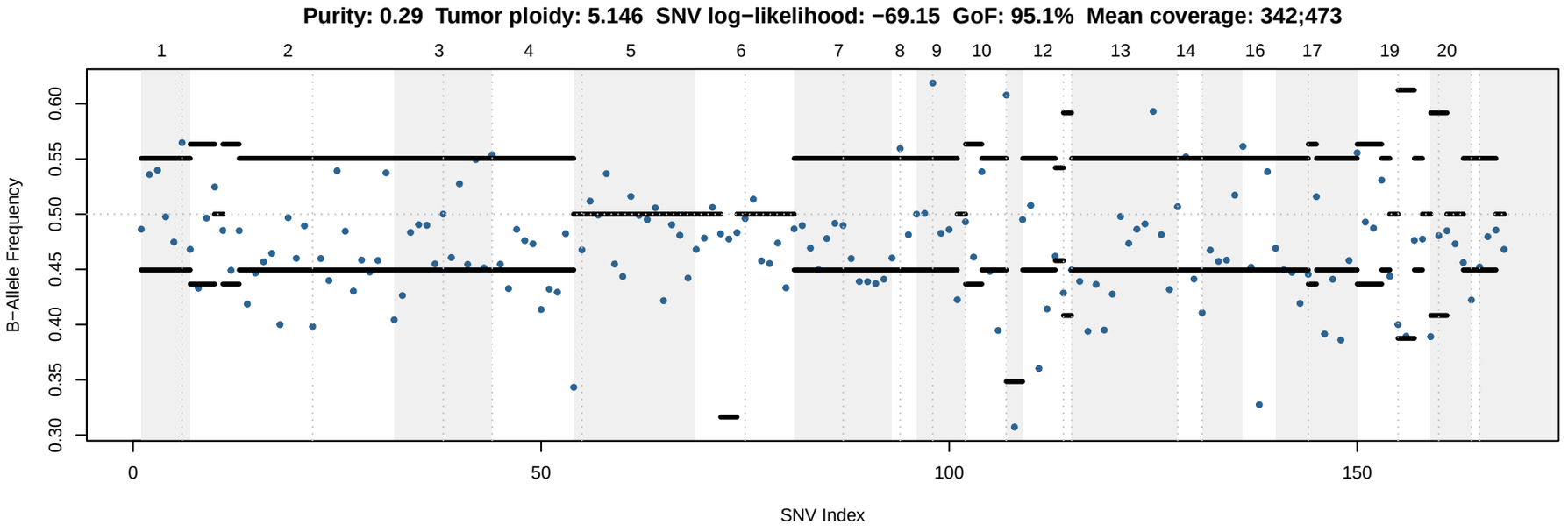

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
3m2
2m1
4m2
6m3
7m3
5m2
3m1
4m1
−0.5
0.0
0.5
1.0
Copy Number log−ratio

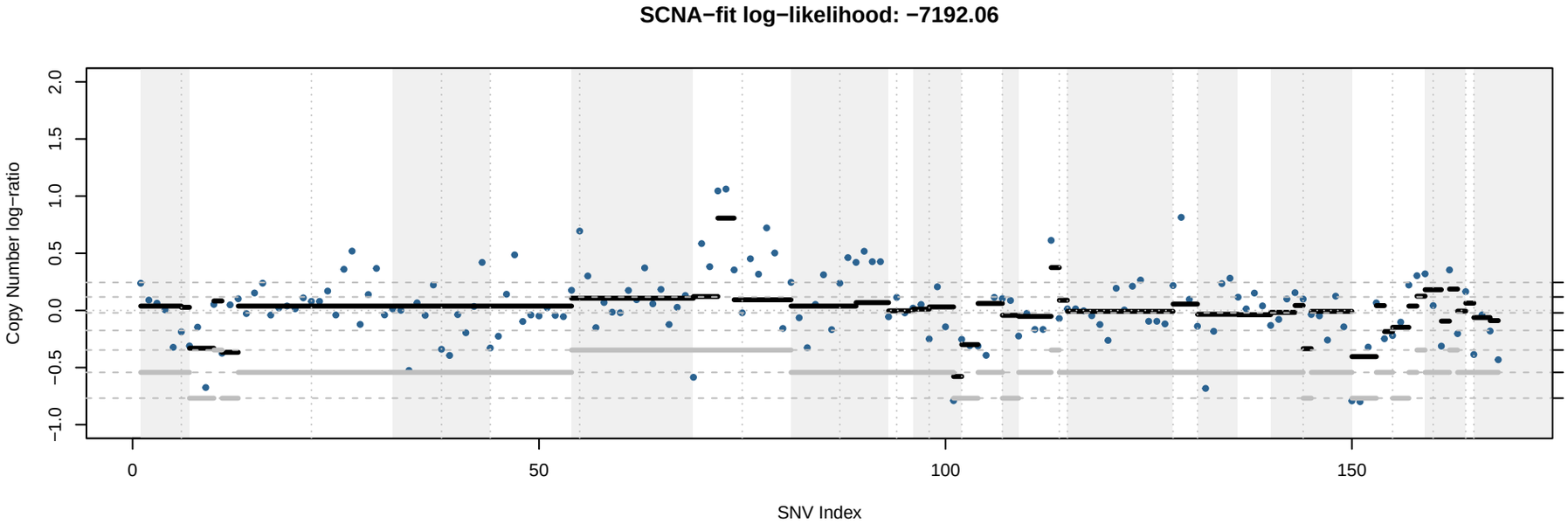

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

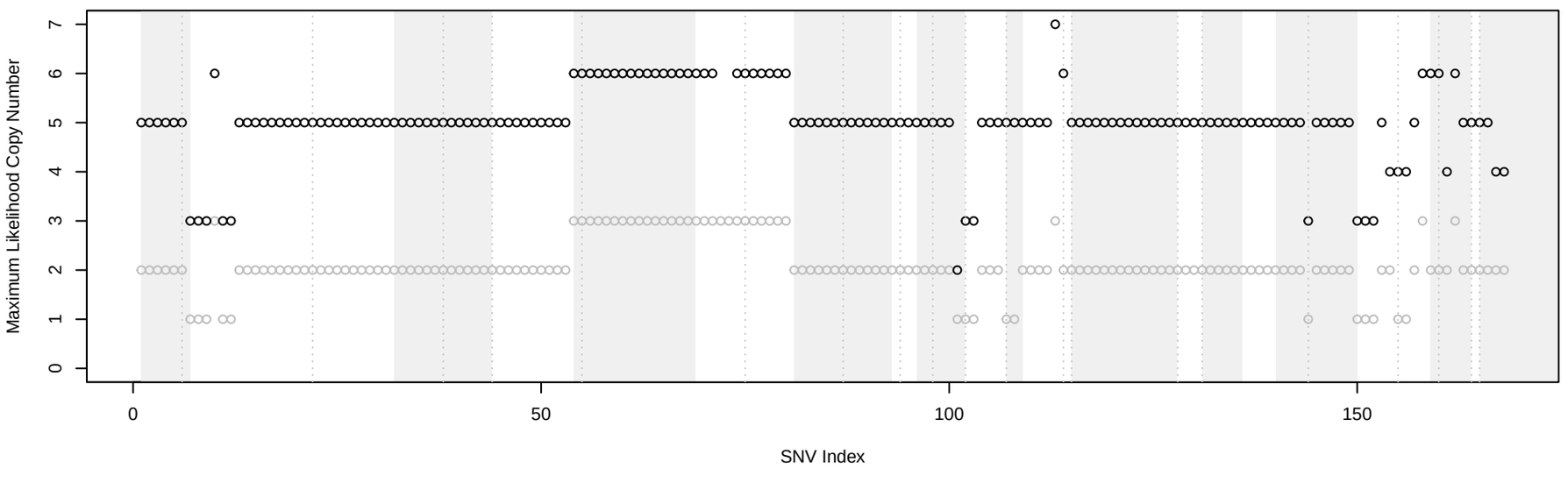

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
3m1
4m1
5m1
6m1
−0.5
0.0
0.5
1.0
Copy Number log−ratio

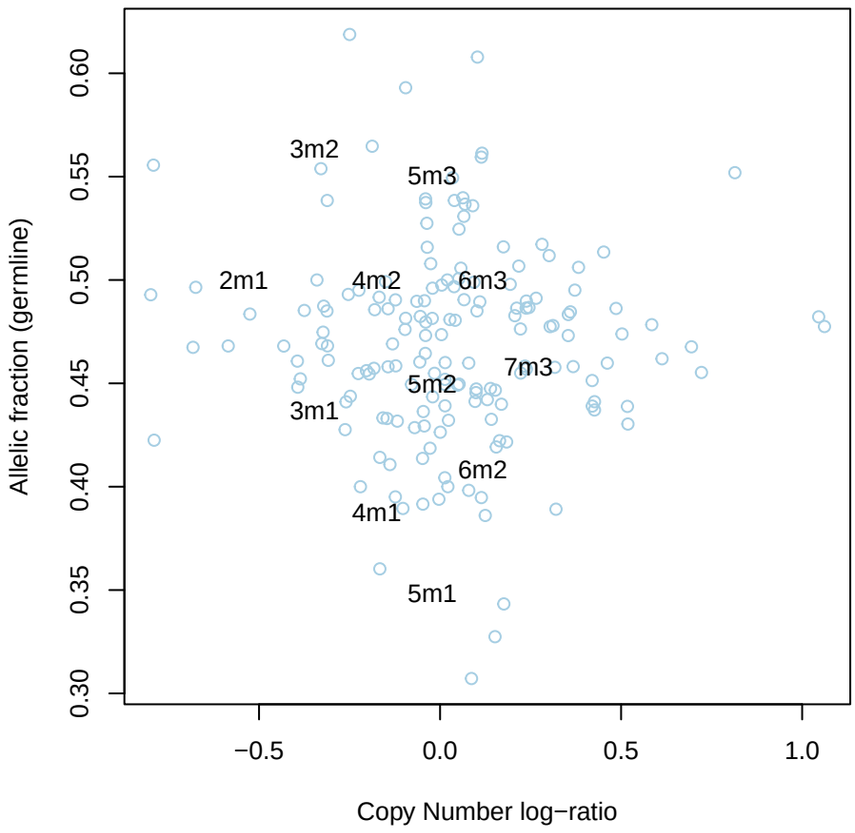

Power 0.8
Frequency
0
2
4
6
8
10
12
14
0.0
0.2
0.4
0.6
0.8
1.0
Cellular fraction

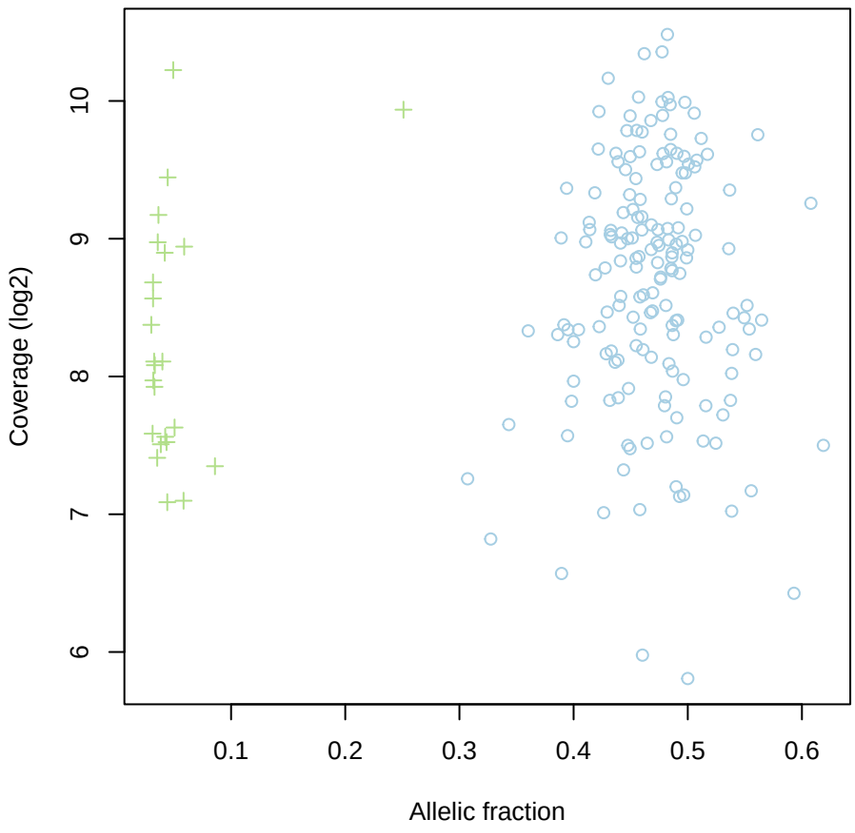

Purity: 0.29 Tumor ploidy: 5.146
1
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

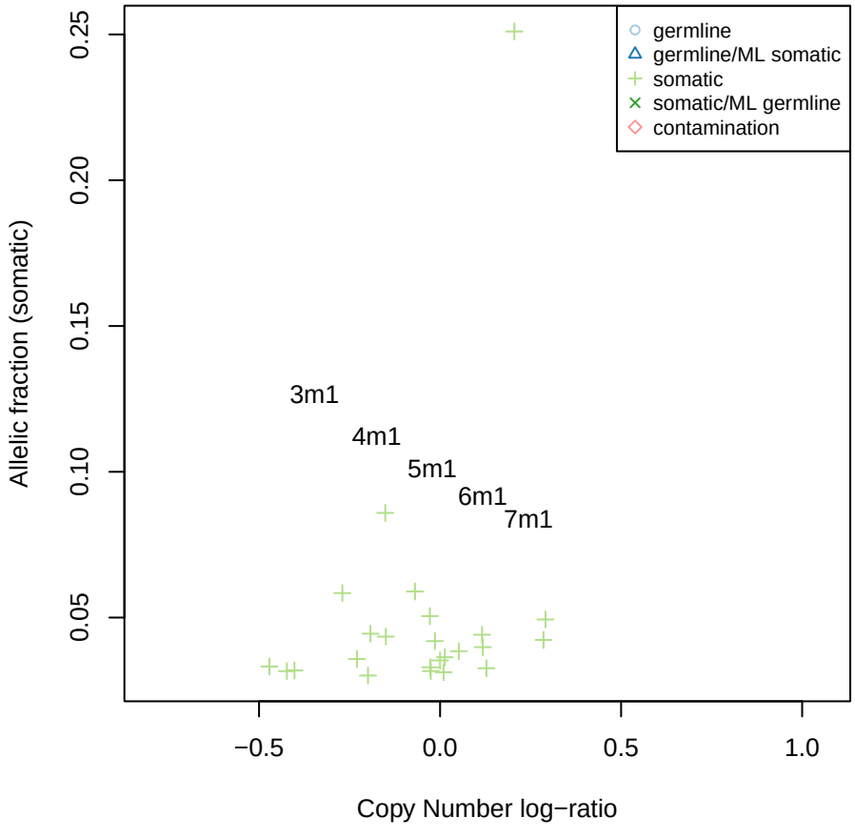

Purity: 0.29 Tumor ploidy: 5.146 SNV log−likelihood: −69.15 GoF: 95.1% Mean coverage: 342;473
1 2 3 4 5 6 7 8 9 10 12 13 14 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

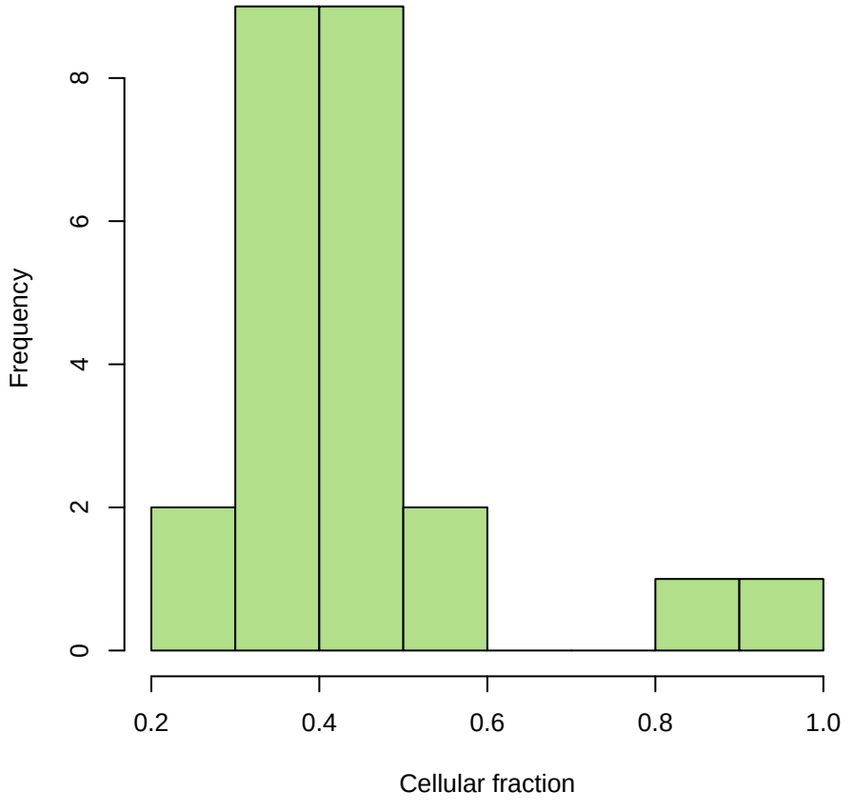

SCNA−fit log−likelihood: −7192.06
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
1 2 4 6
0 50 100 150
SNV Index

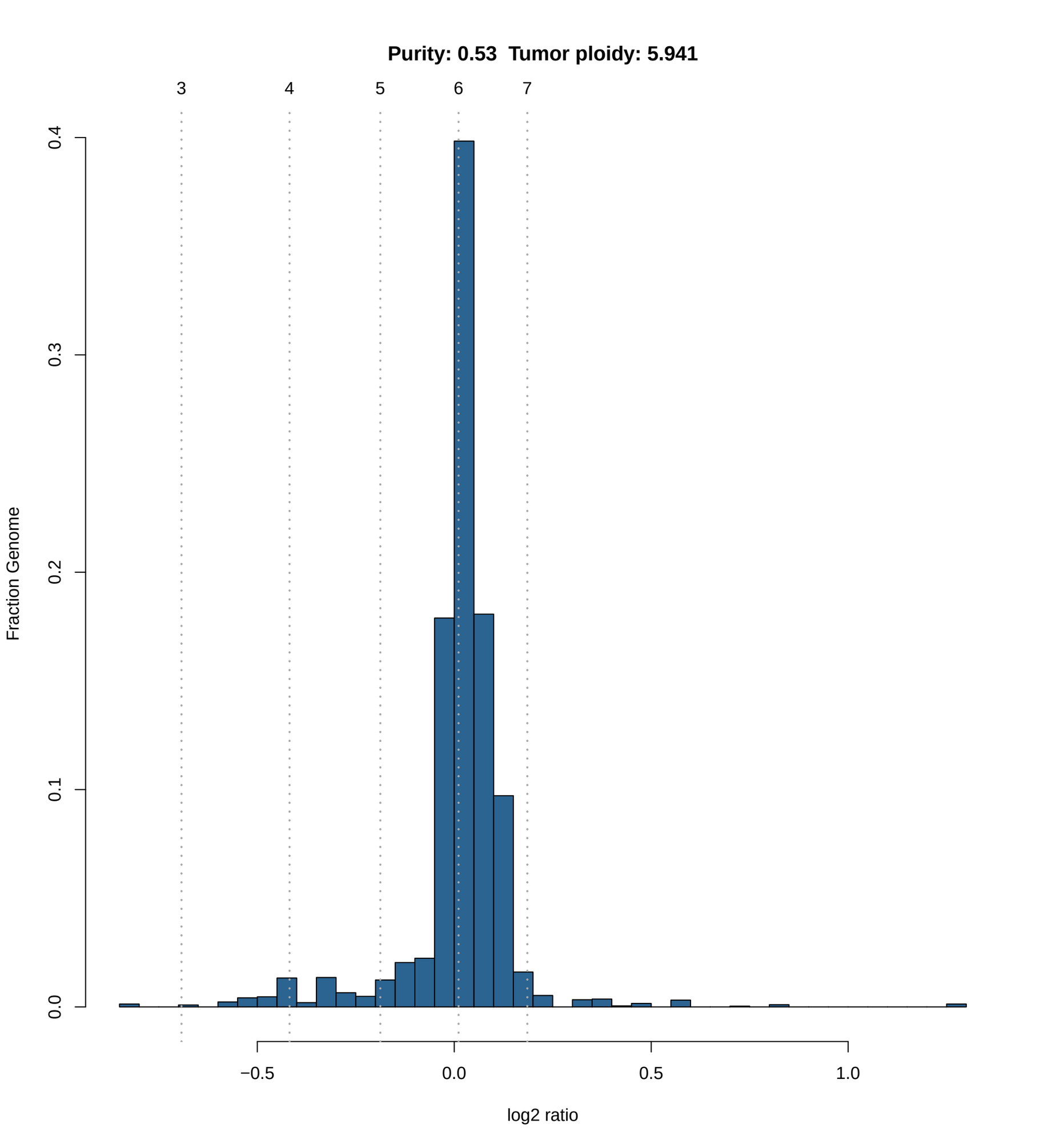

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

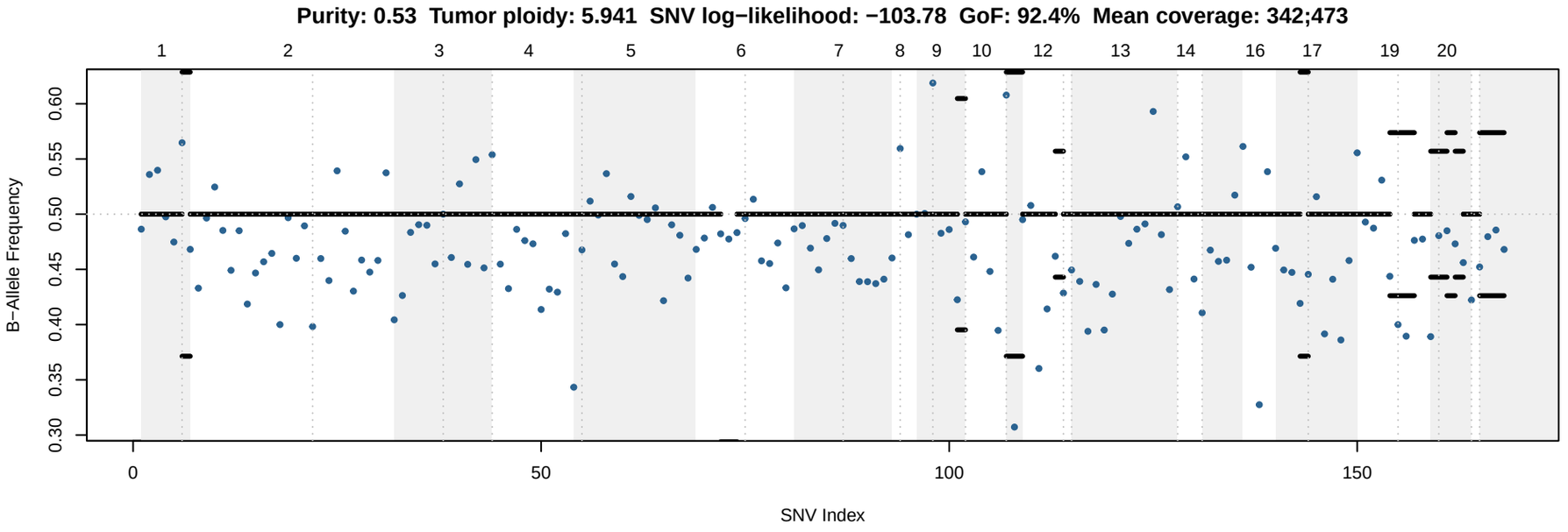

Allelic fraction (germline)
Copy Number log−ratio
3m2
5m3
2m1
4m2
6m3
7m3
5m2
3m1
6m2
4m1
5m1

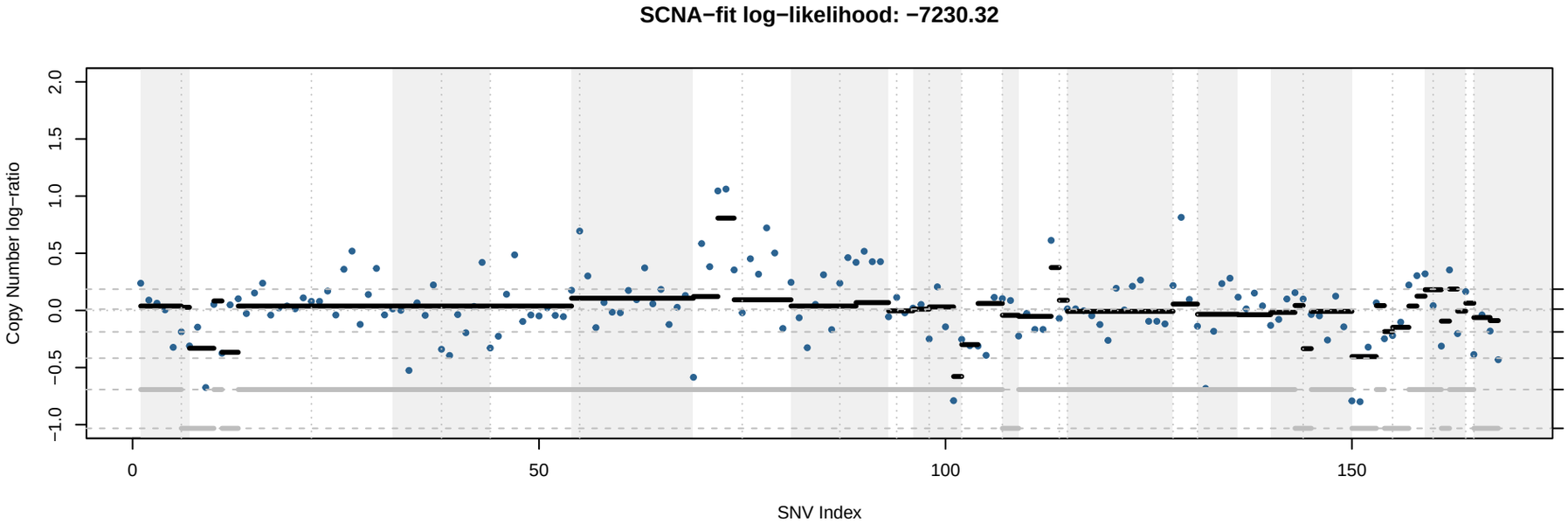

Coverage (log2)
Allelic fraction

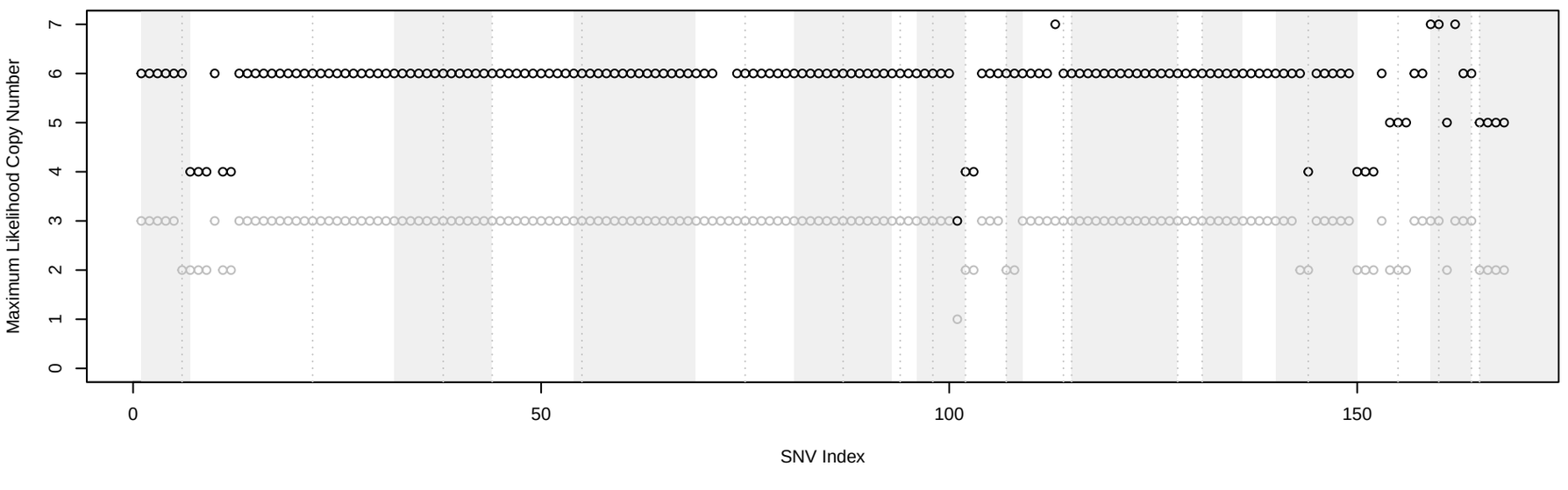

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m1
4m1
5m1
6m1
7m1

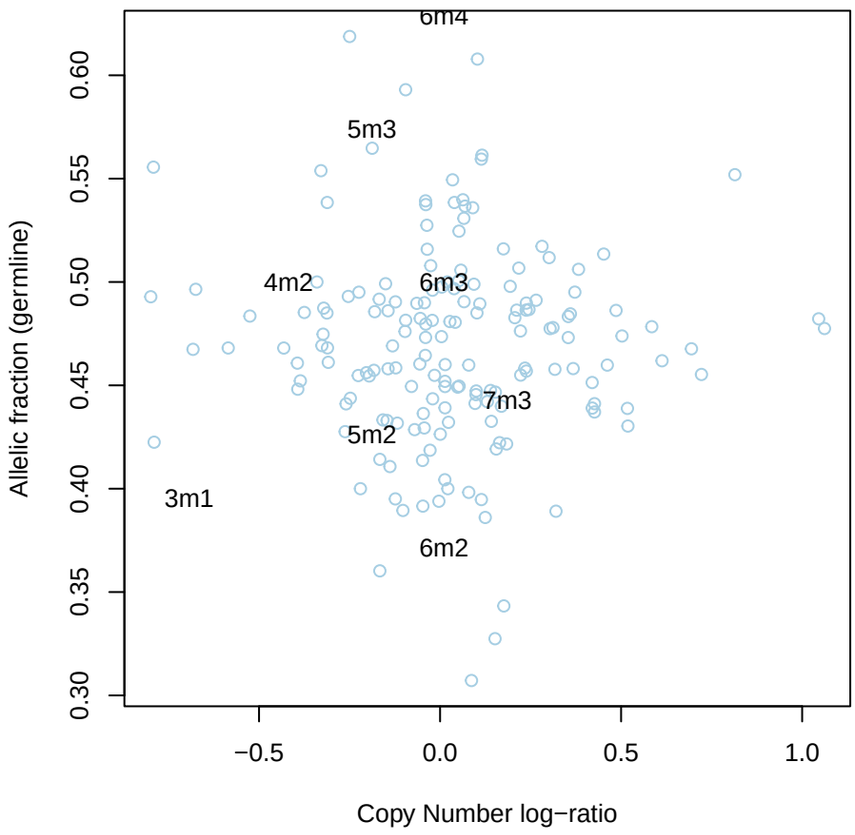

Frequency
Cellular fraction

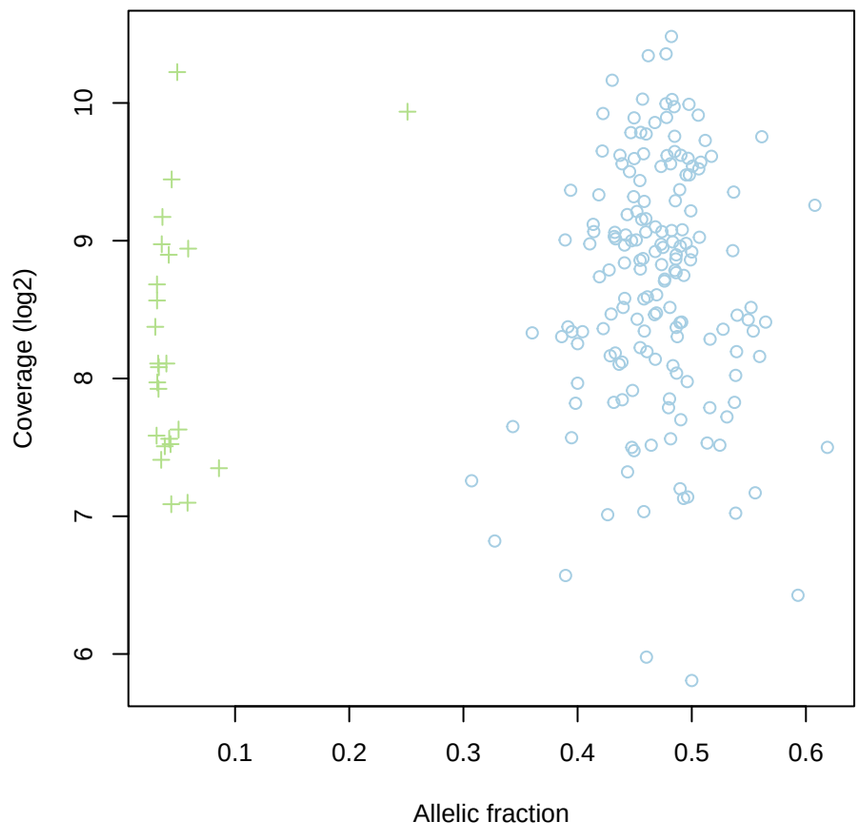

Purity: 0.53 Tumor ploidy: 5.941
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

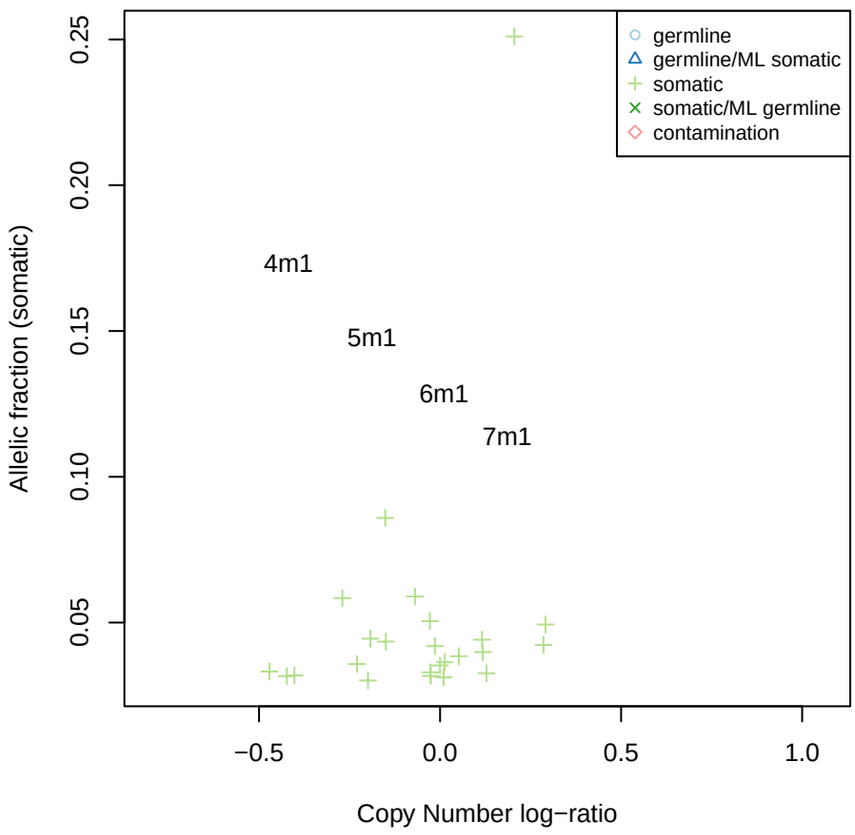

Purity: 0.53 Tumor ploidy: 5.941 SNV log−likelihood: −103.78 GoF: 92.4% Mean coverage: 342;473
1 2 3 4 5 6 7 8 9 10 12 13 14 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

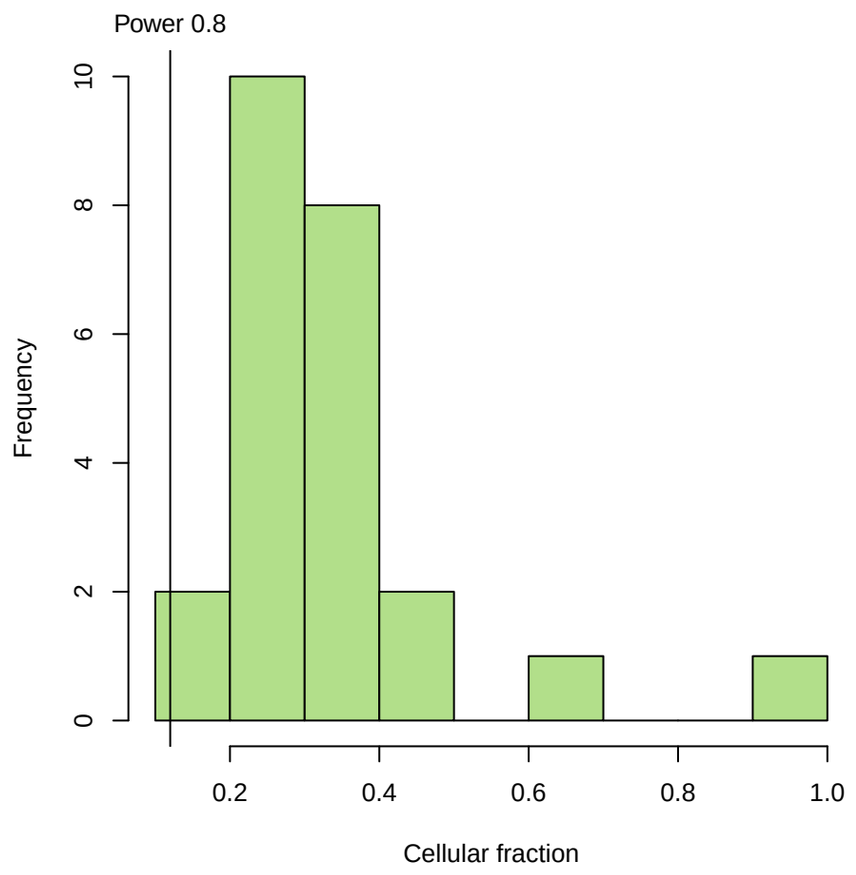

SCNA−fit log−likelihood: −7230.32
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
2 3 4 5 7
0 50 100 150
SNV Index

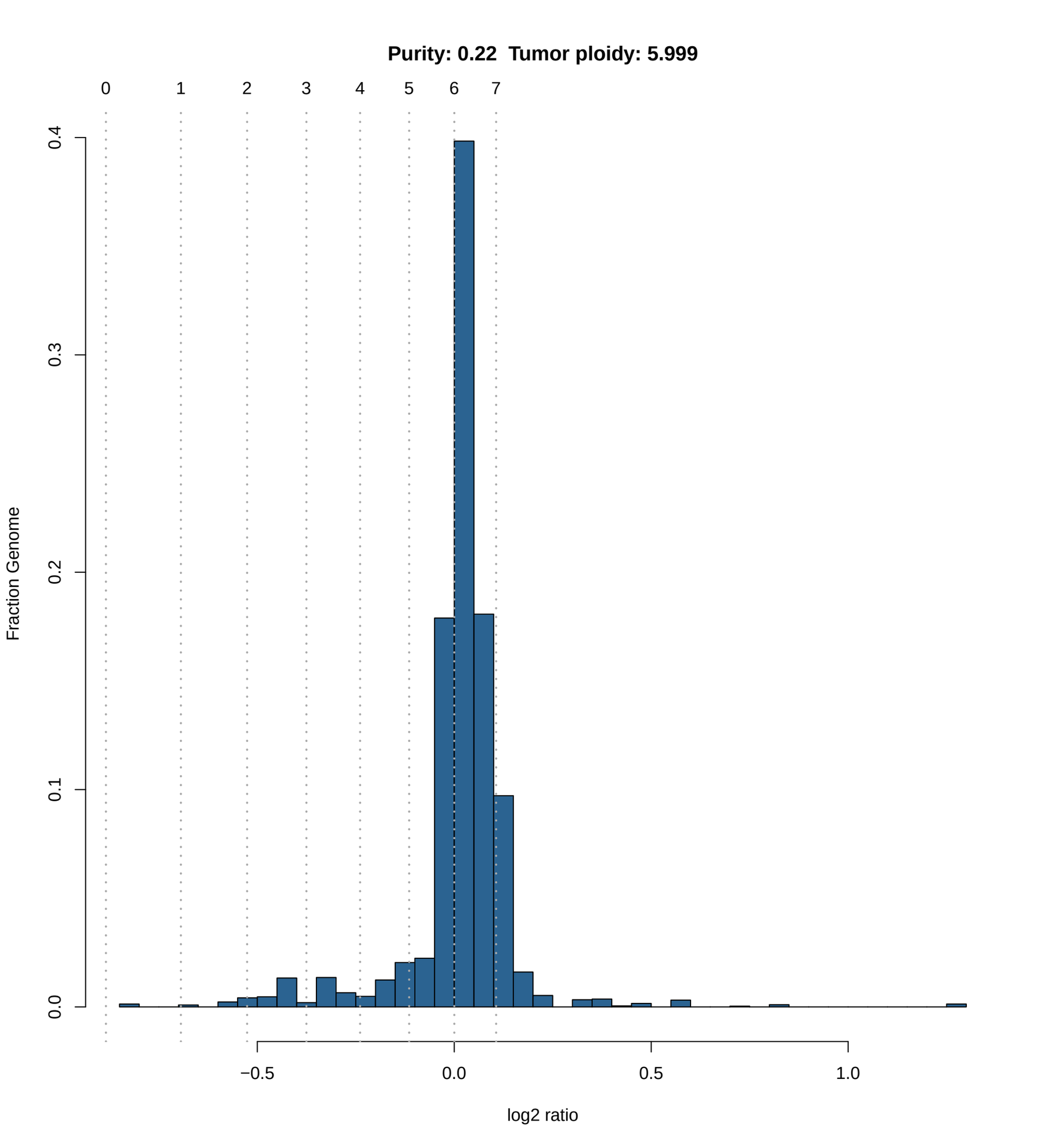

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

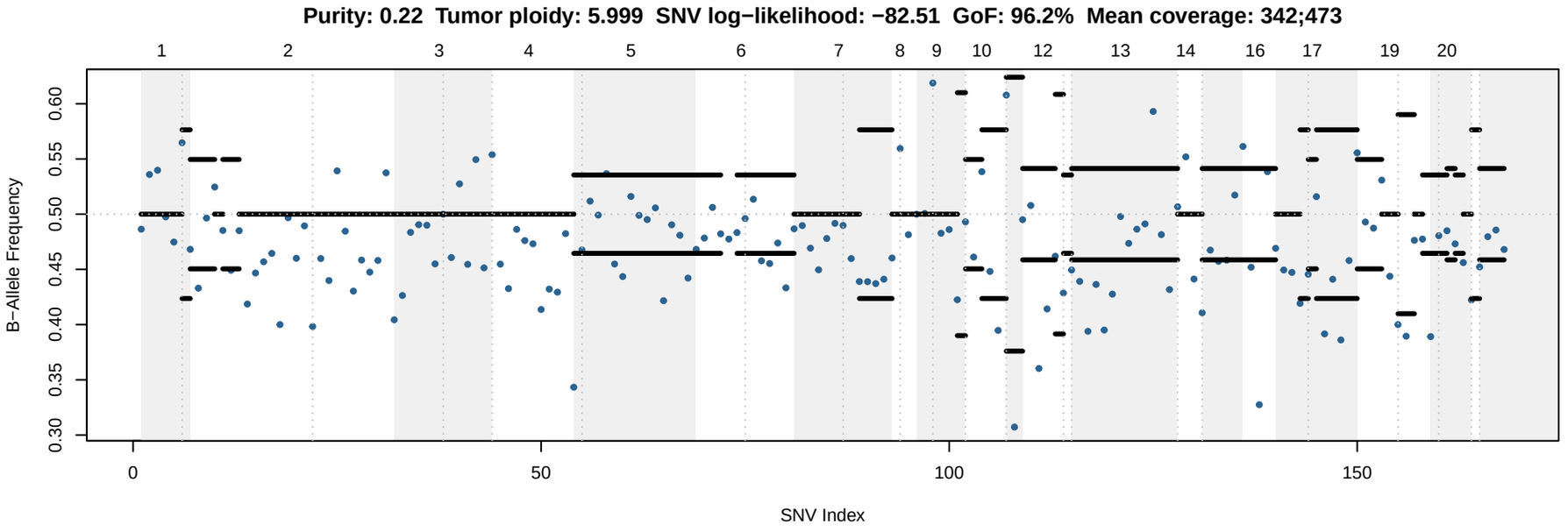

6m4
5m3
4m2
6m3
7m3
5m2
3m1
6m2
Allelic fraction (germline)
Copy Number log−ratio

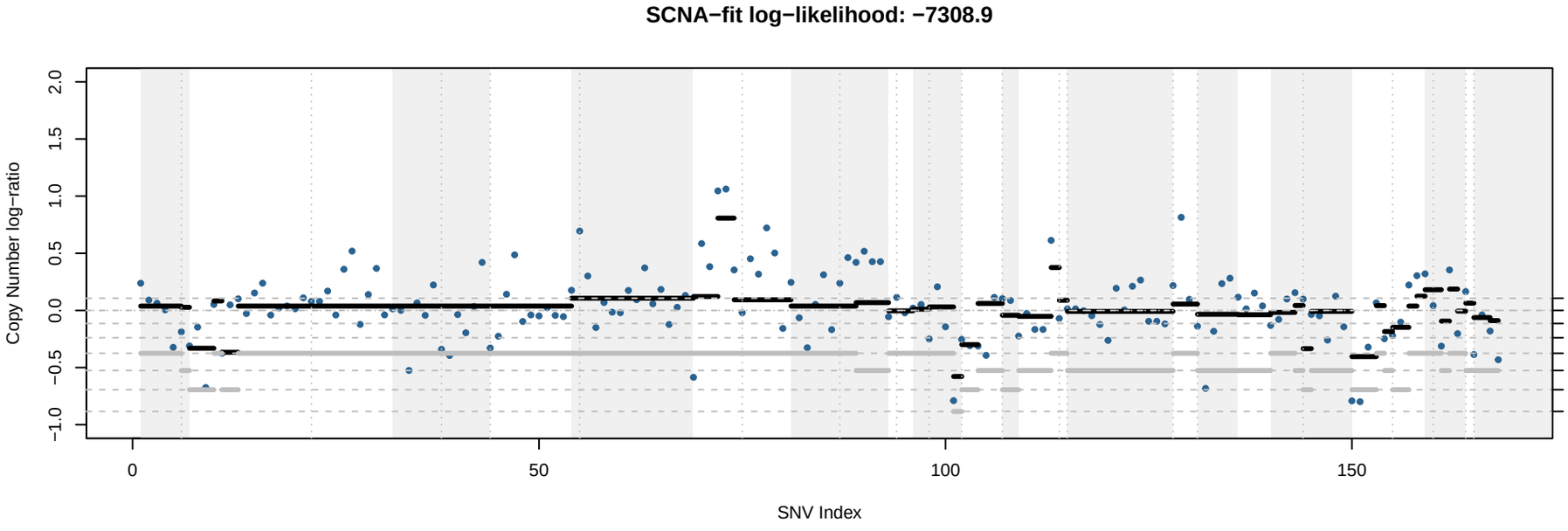

Coverage (log2)
Allelic fraction

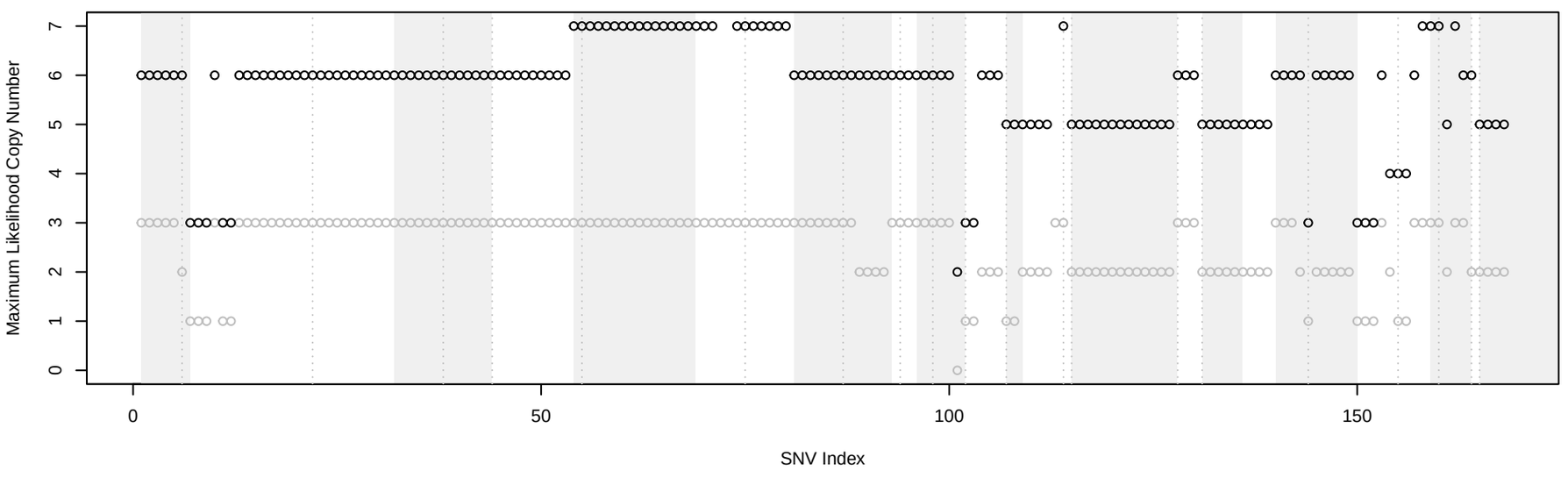

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

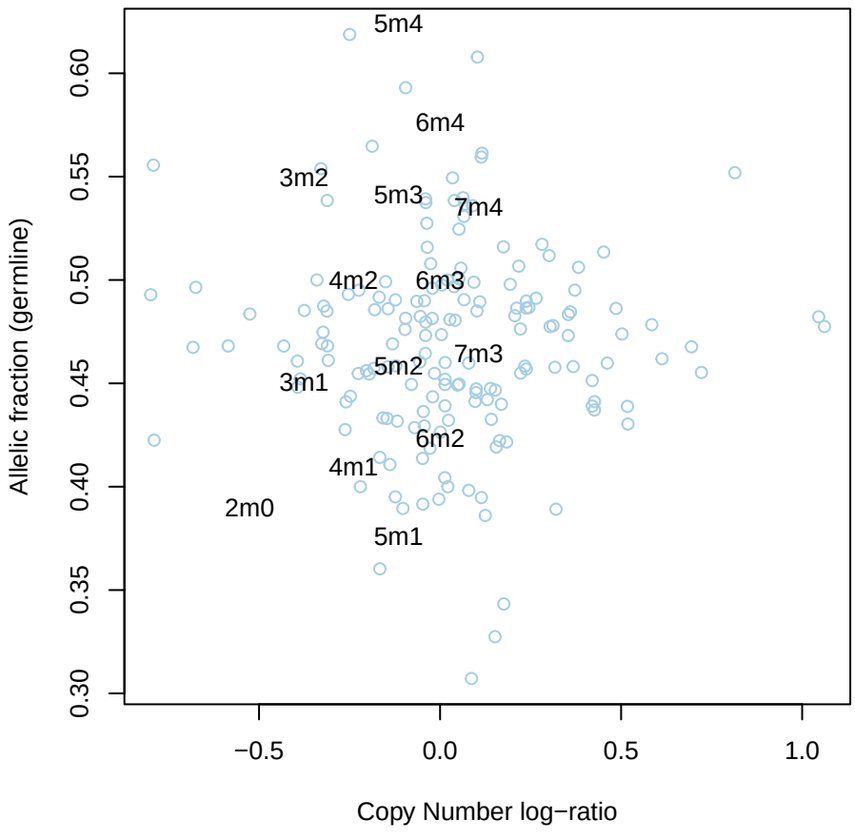

Power 0.8
Frequency
Cellular fraction

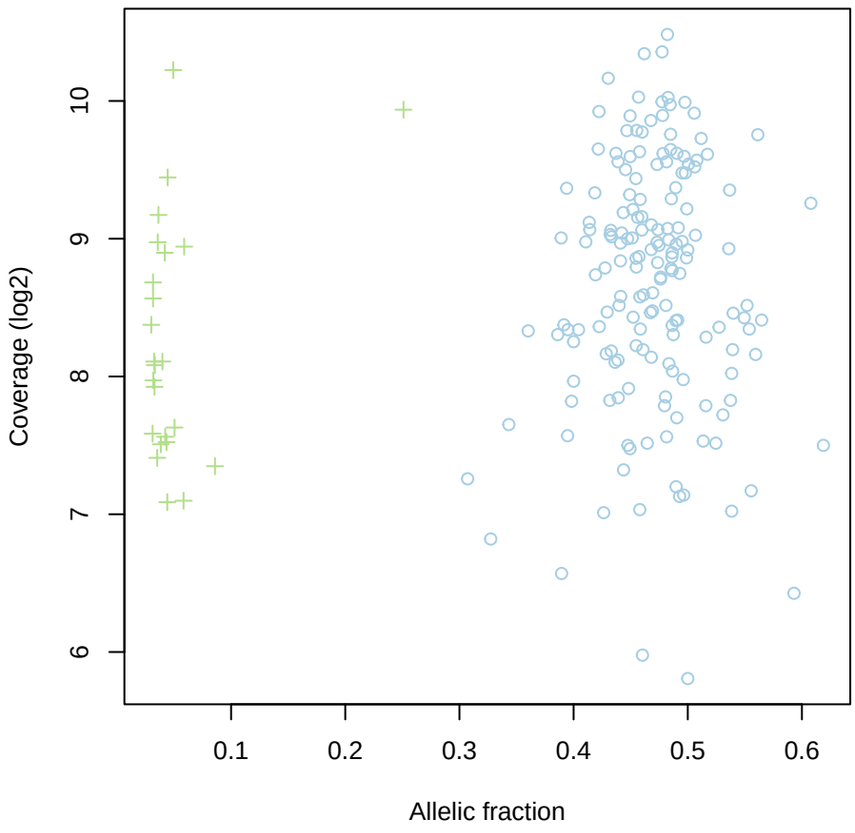

Purity: 0.22 Tumor ploidy: 5.999
0
1
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

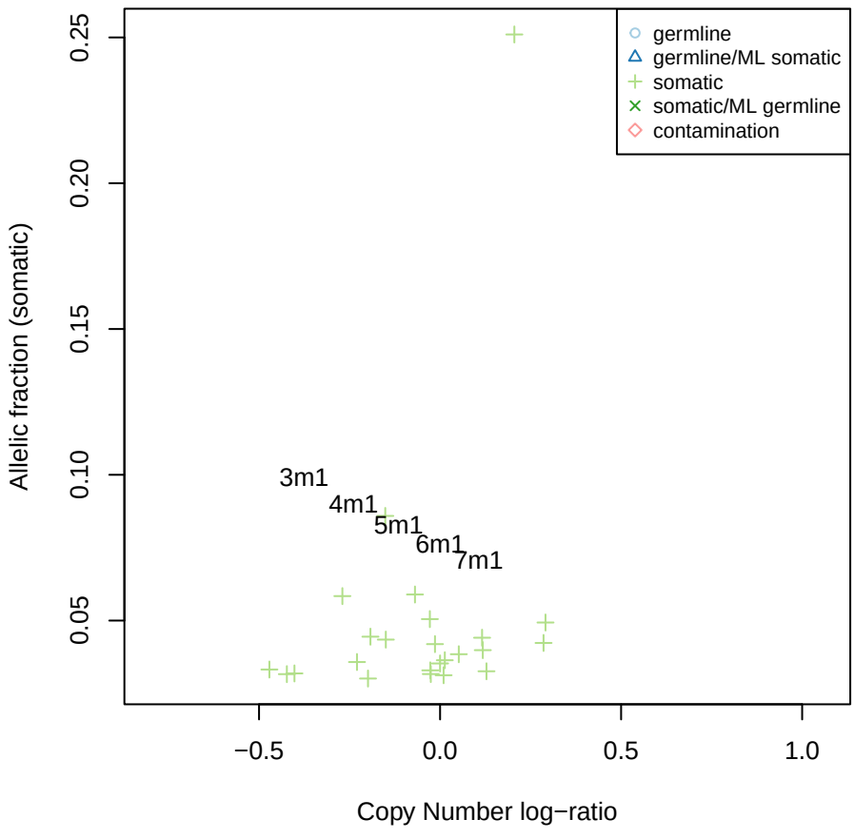

Purity: 0.22 Tumor ploidy: 5.999 SNV log−likelihood: −82.51 GoF: 96.2% Mean coverage: 342;473
1 2 3 4 5 6 7 8 9 10 12 13 14 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

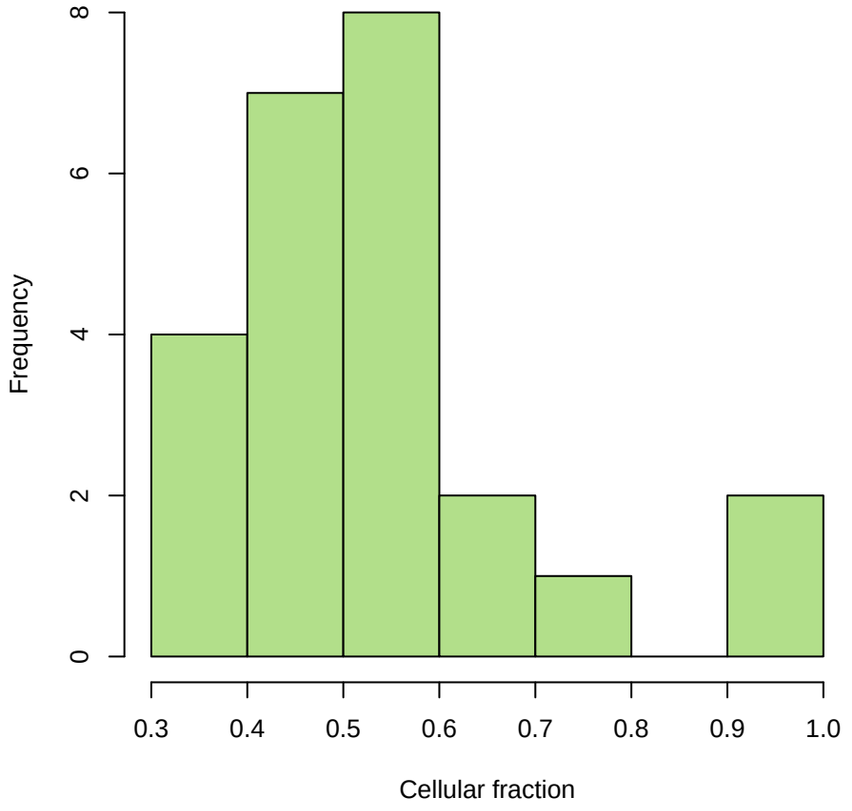

SCNA−fit log−likelihood: −7308.9
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
0 2 4 6
0 50 100 150
SNV Index

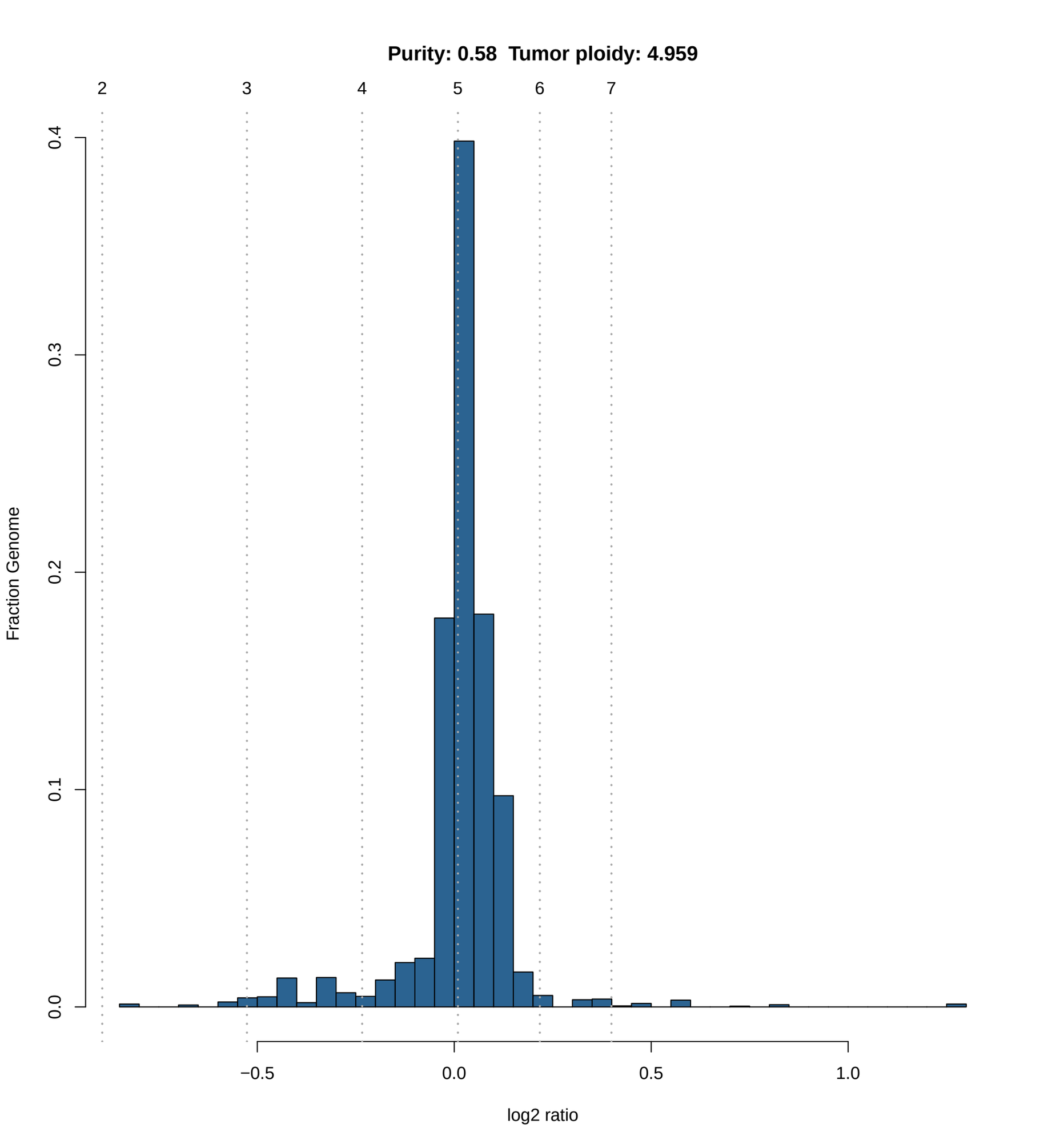

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

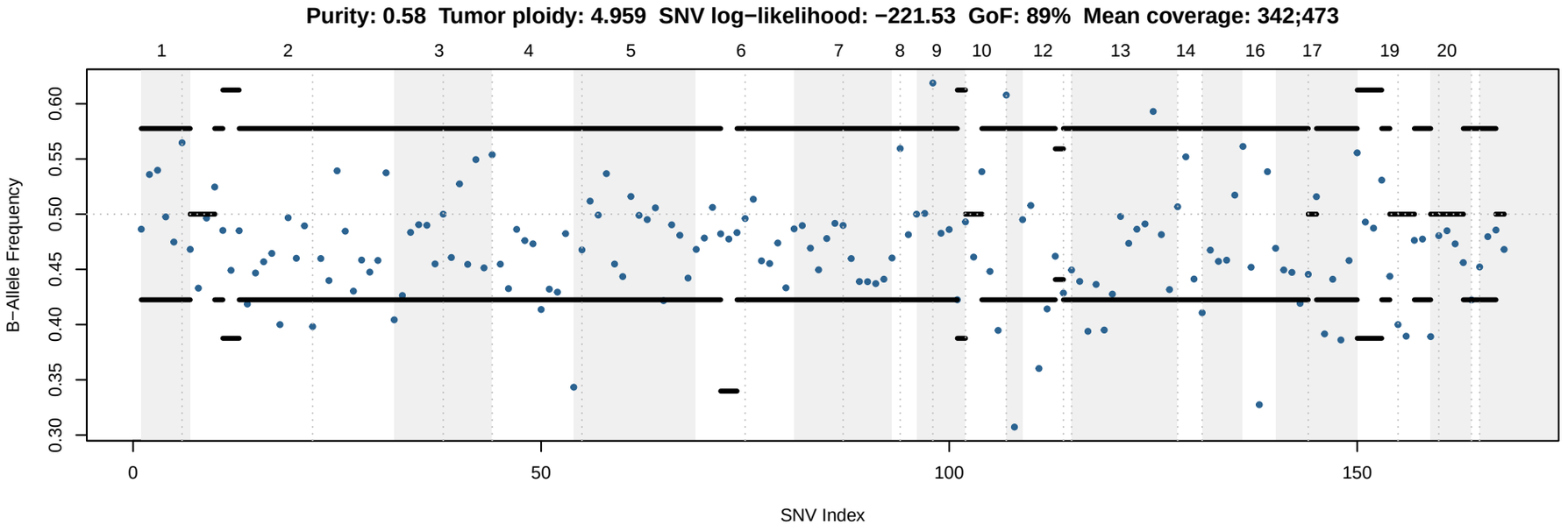

5m4
6m4
3m2
5m3
7m4
4m2
6m3
7m3
5m2
3m1
6m2
4m1
2m0
5m1
Allelic fraction (germline)
Copy Number log−ratio
0.30
0.35
0.40
0.45
0.50
0.55
0.60
−0.5
0.0
0.5
1.0

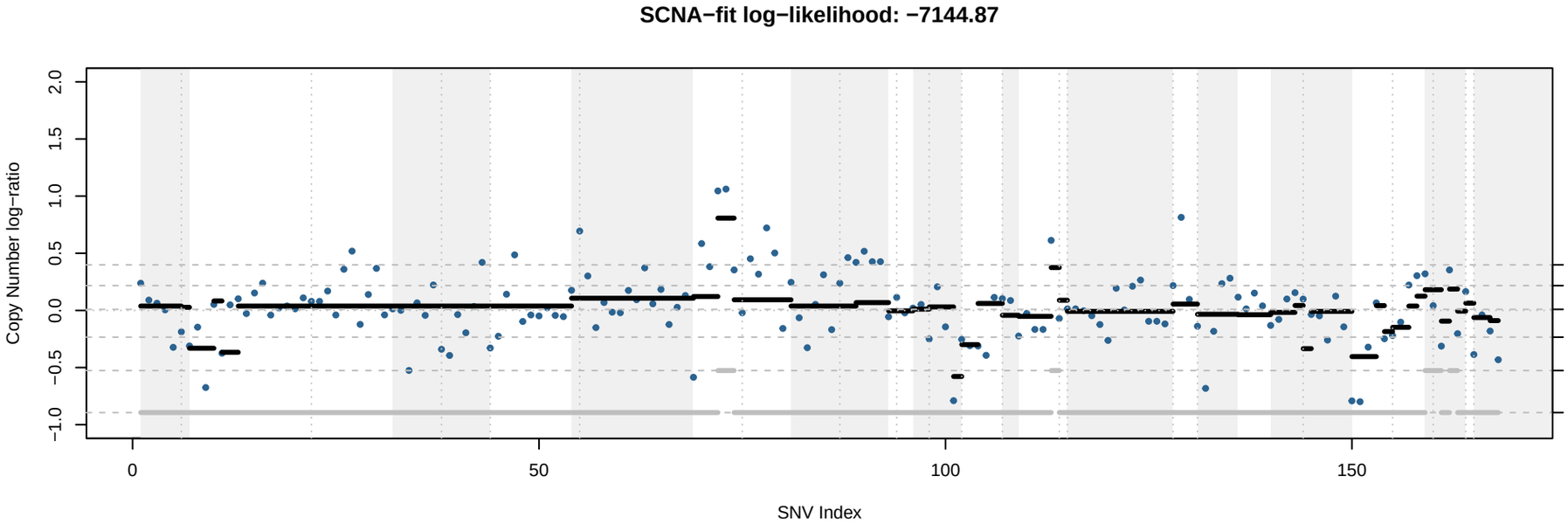

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

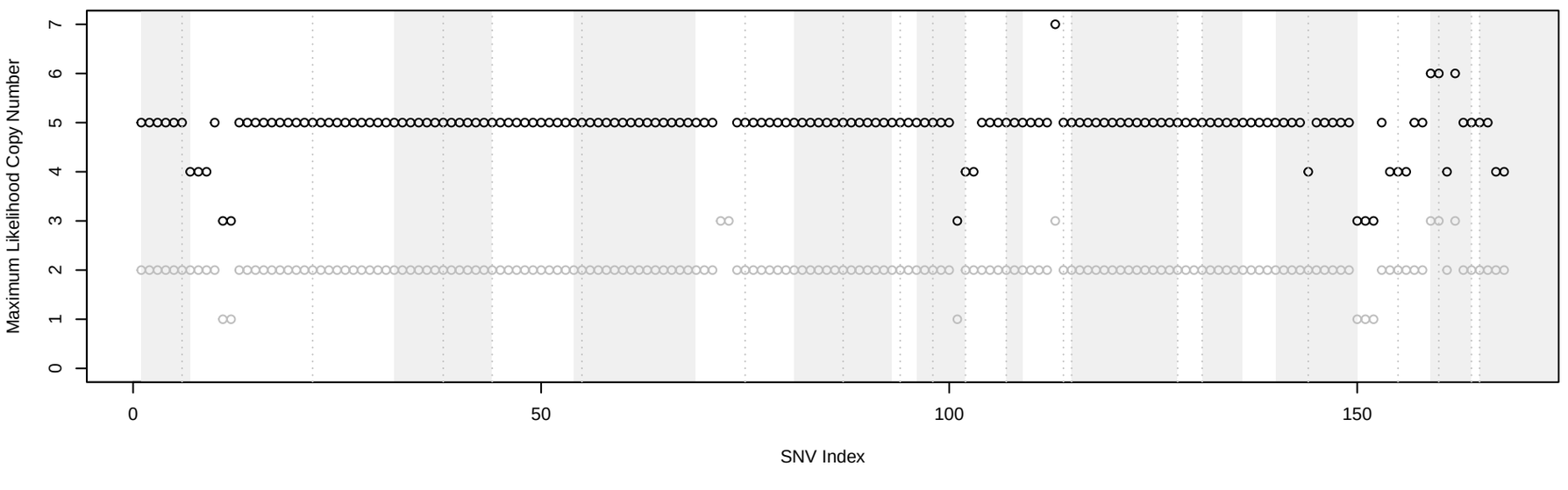

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
0.25
−0.5
0.0
0.5
1.0

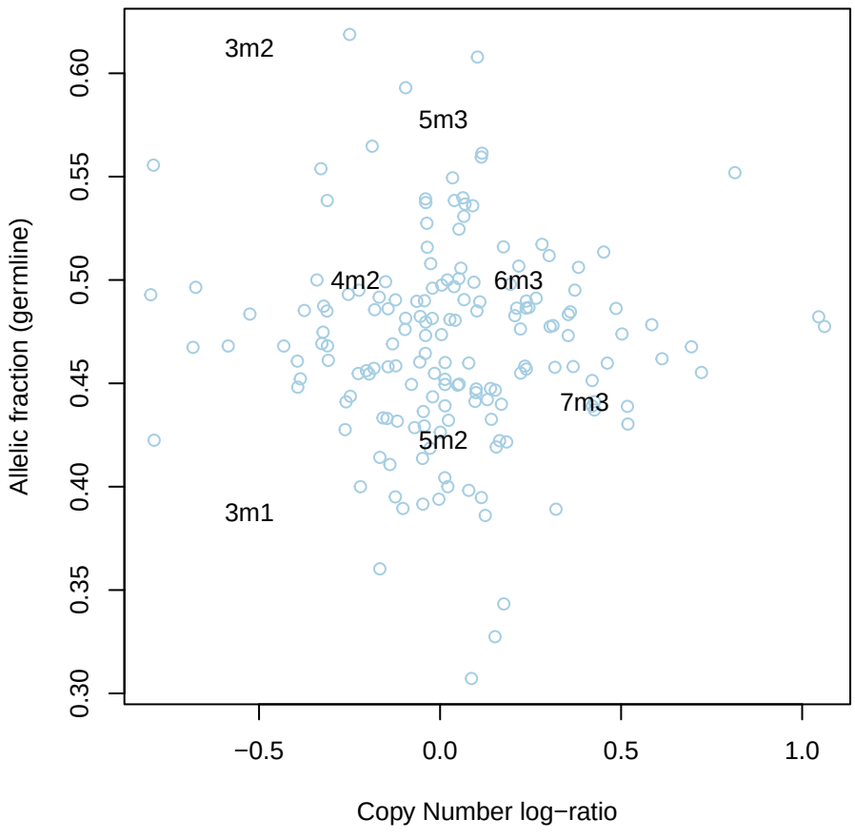

Frequency
Cellular fraction
0
2
4
6
8
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0

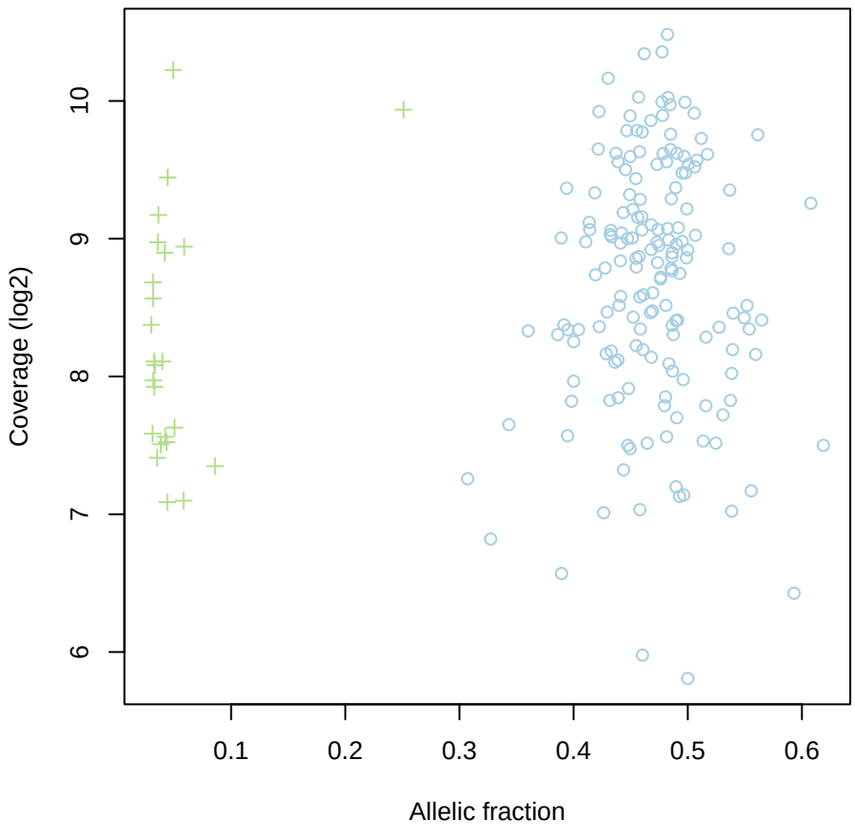

Purity: 0.58 Tumor ploidy: 4.959
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

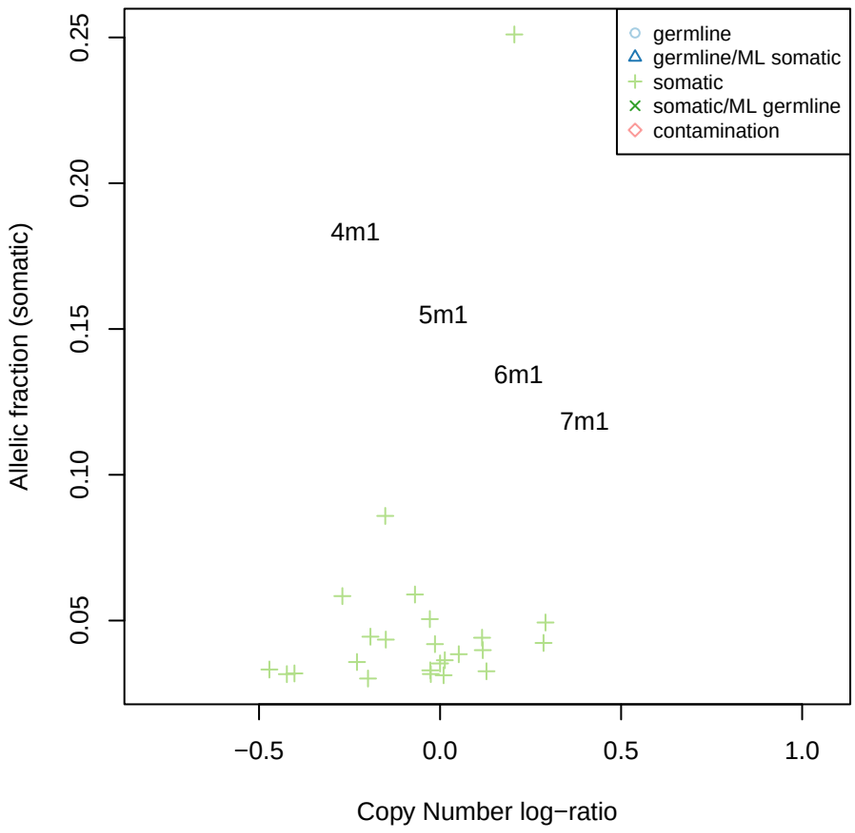

Purity: 0.58 Tumor ploidy: 4.959 SNV log−likelihood: −221.53 GoF: 89% Mean coverage: 342;473
1 2 3 4 5 6 7 8 9 10 12 13 14 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

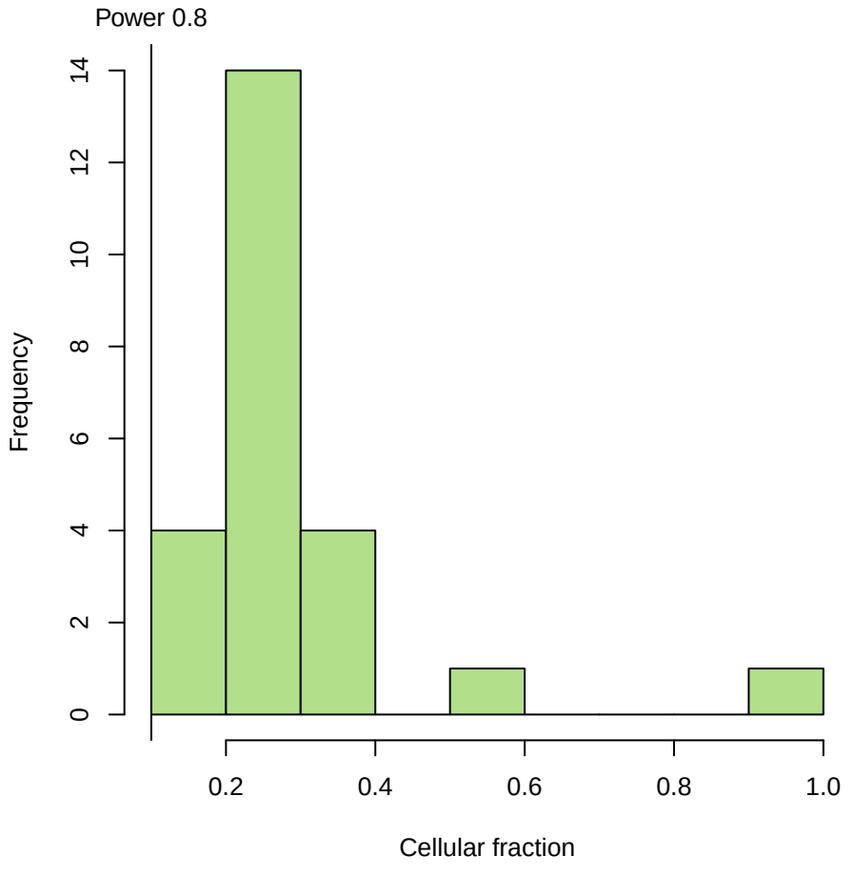

SCNA−fit log−likelihood: −7144.87
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
2 3 4 5 7
0 50 100 150
SNV Index

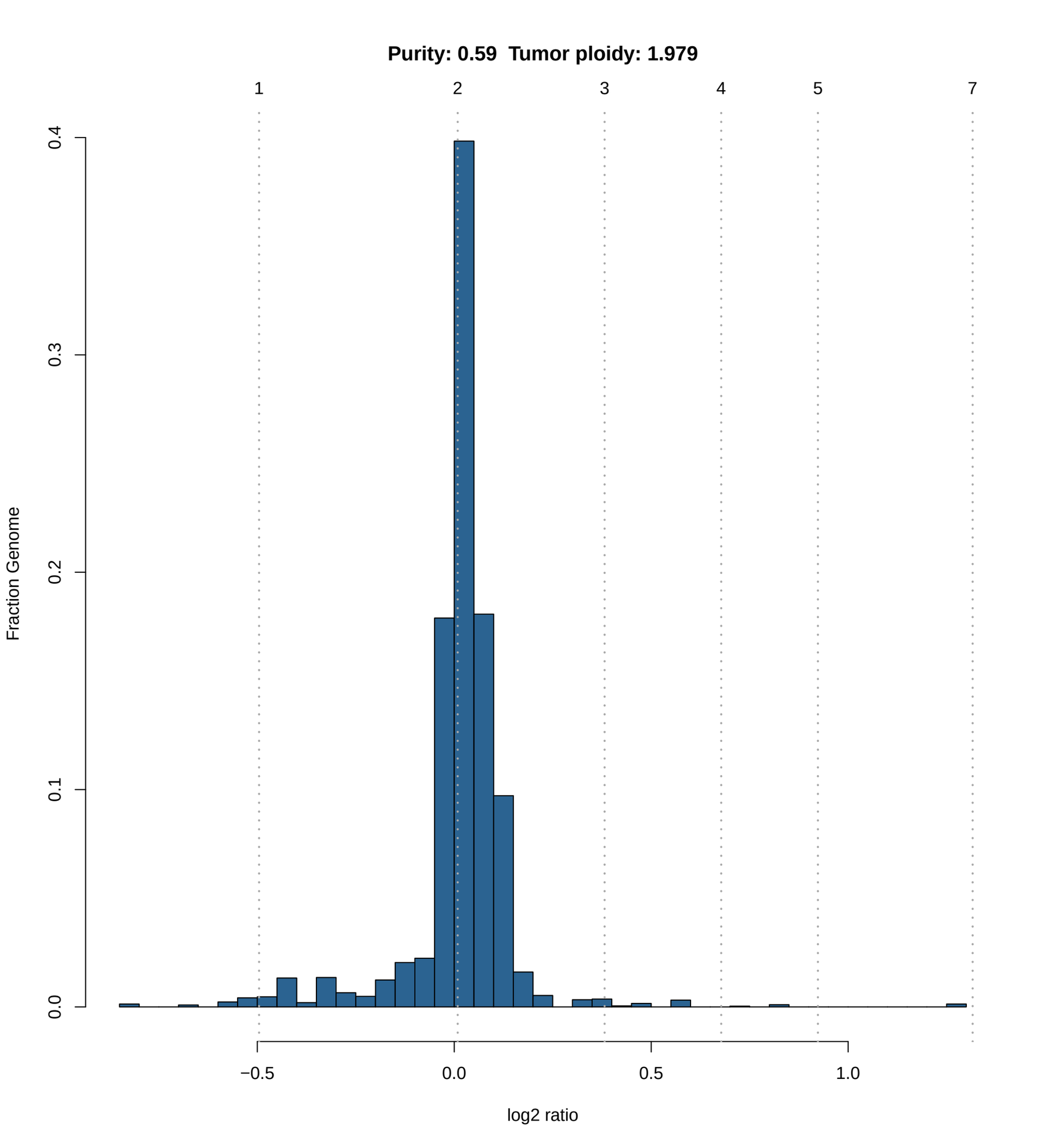

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

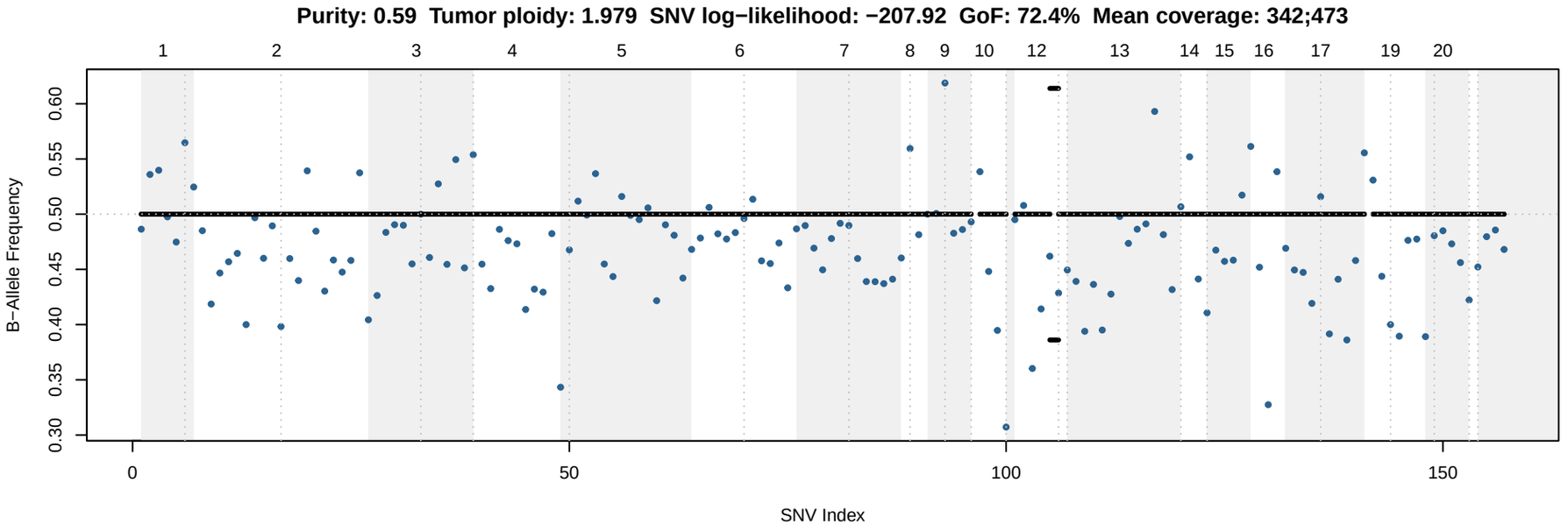

3m2
5m3
4m2
6m3
7m3
5m2
3m1
Allelic fraction (germline)
Copy Number log−ratio
0.30
0.35
0.40
0.45
0.50
0.55
0.60
−0.5
0.0
0.5
1.0

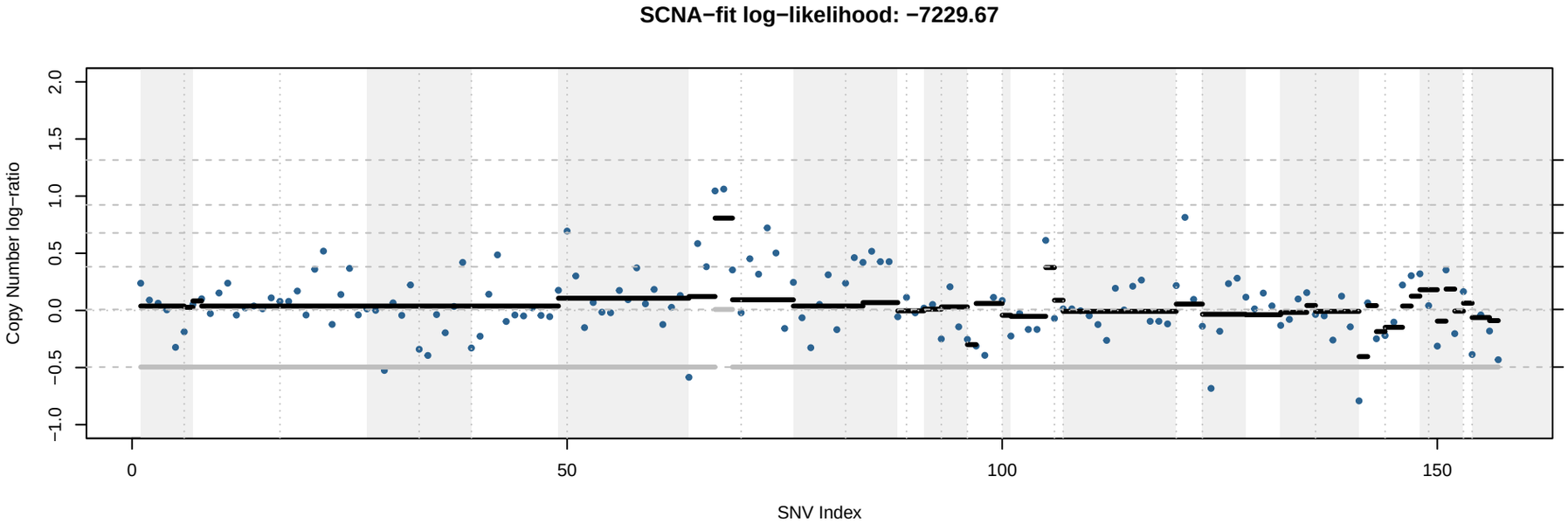

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

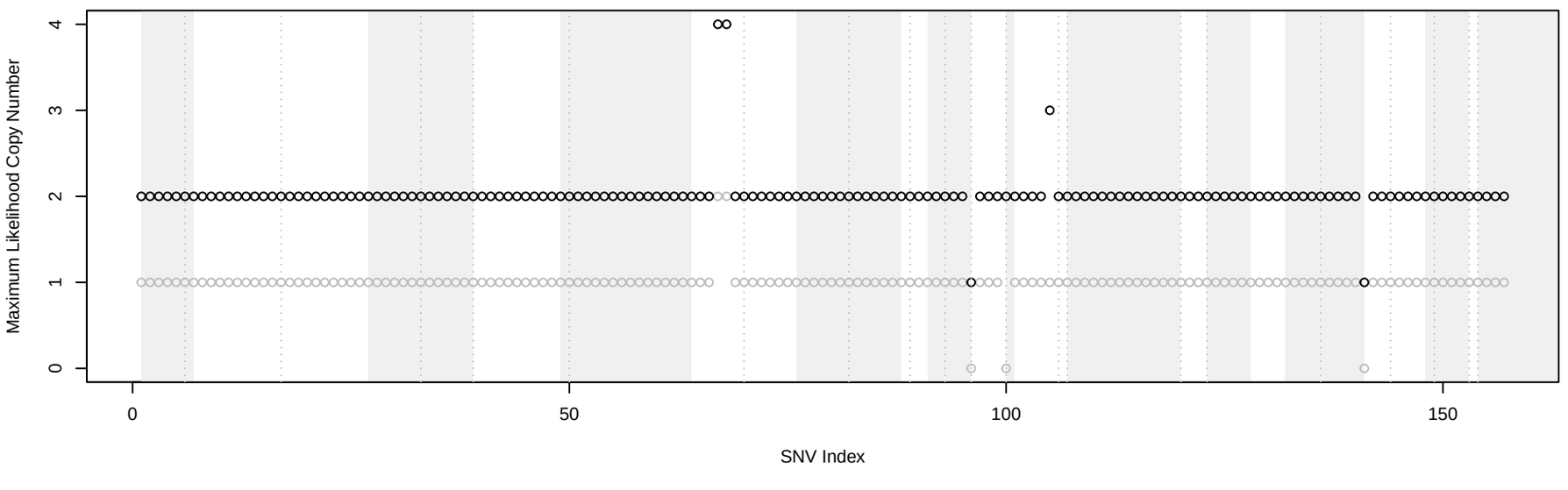

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
0.25
−0.5
0.0
0.5
1.0

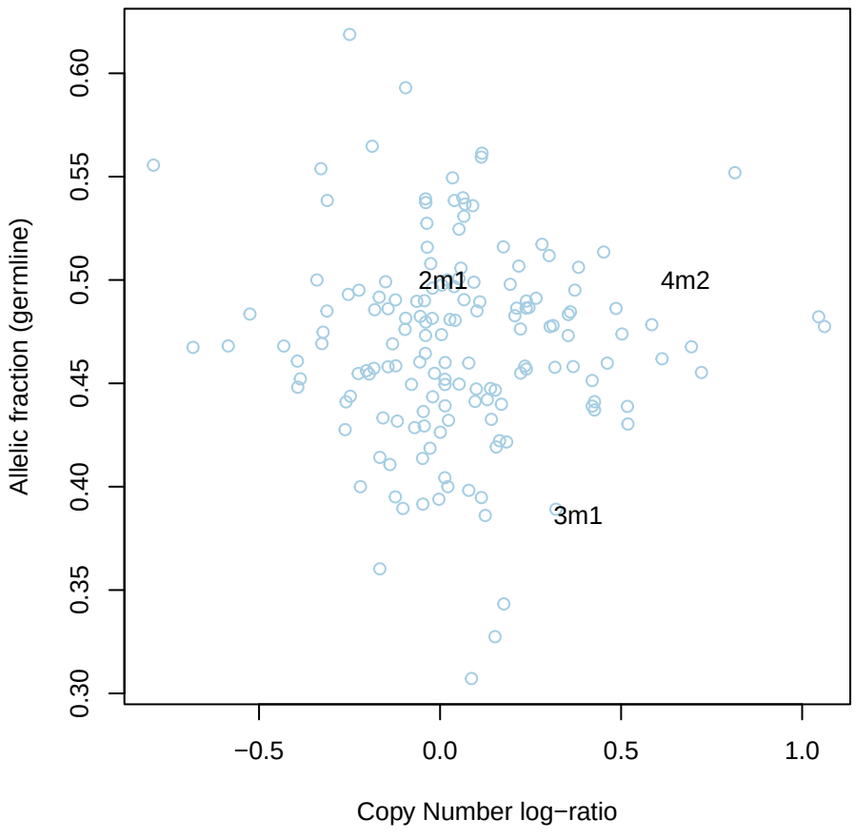

Power 0.8
Frequency
Cellular fraction
0
2
4
6
8
10
12
14
0.2
0.4
0.6
0.8
1.0

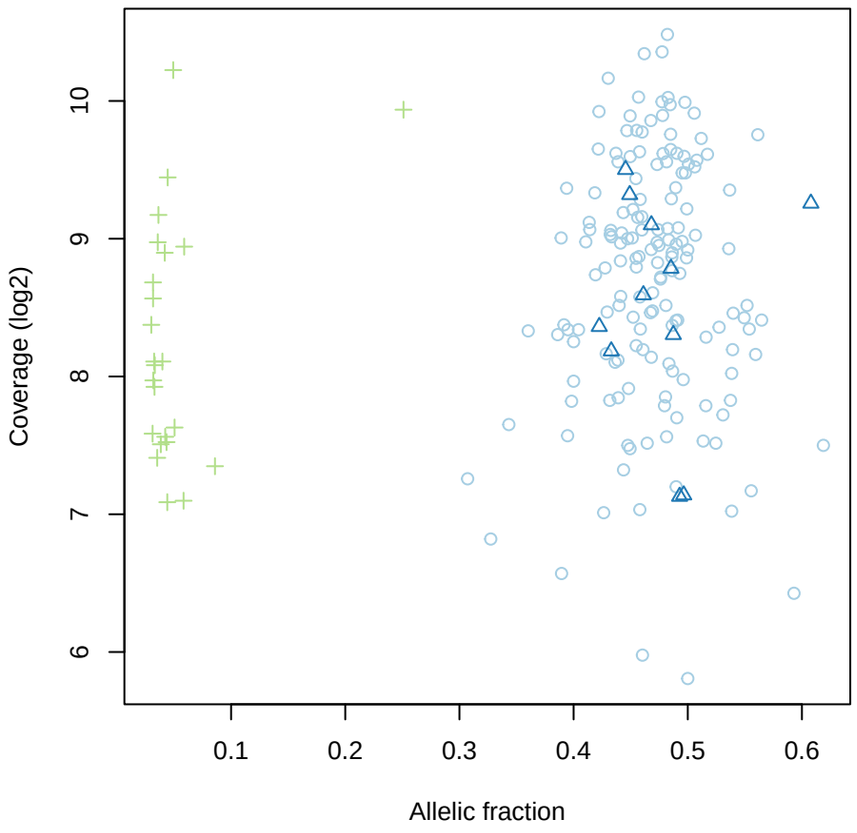

Purity: 0.59 Tumor ploidy: 1.979
1
2
3
4
5
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

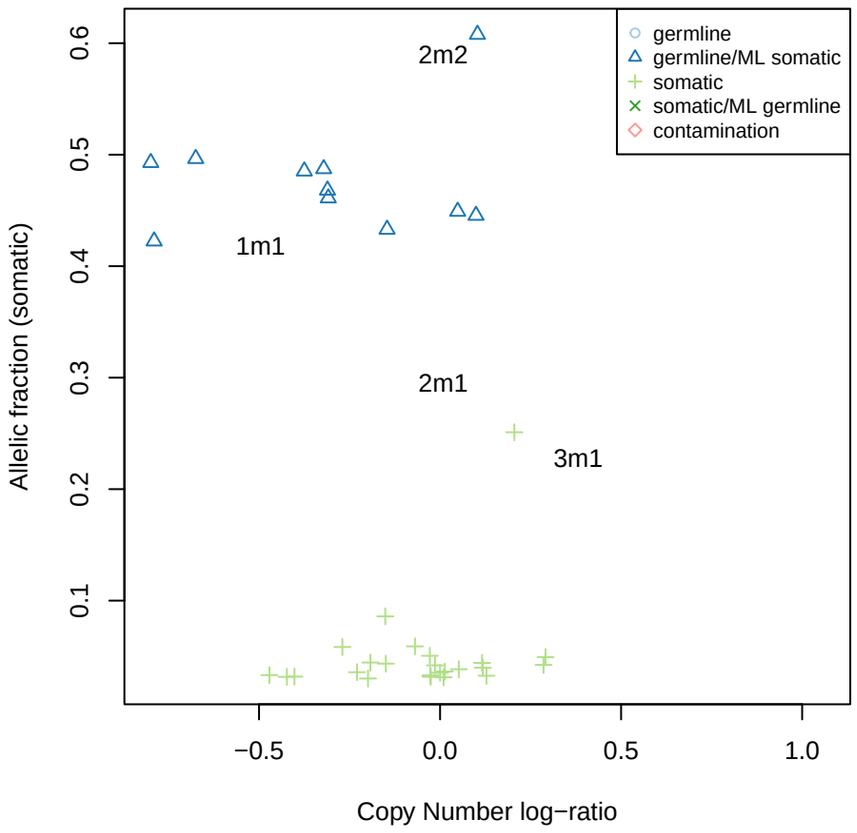

Purity: 0.59 Tumor ploidy: 1.979 SNV log−likelihood: −207.92 GoF: 72.4% Mean coverage: 342;473
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

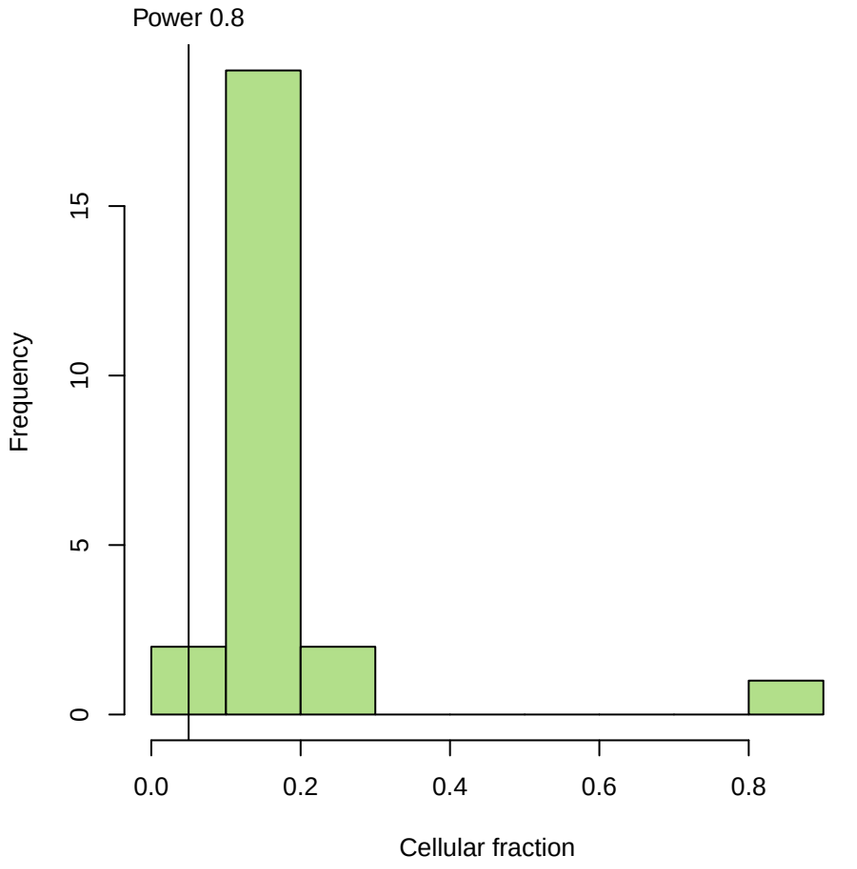

SCNA−fit log−likelihood: −7229.67
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
1 2 3 4 5 7
0 50 100 150
SNV Index

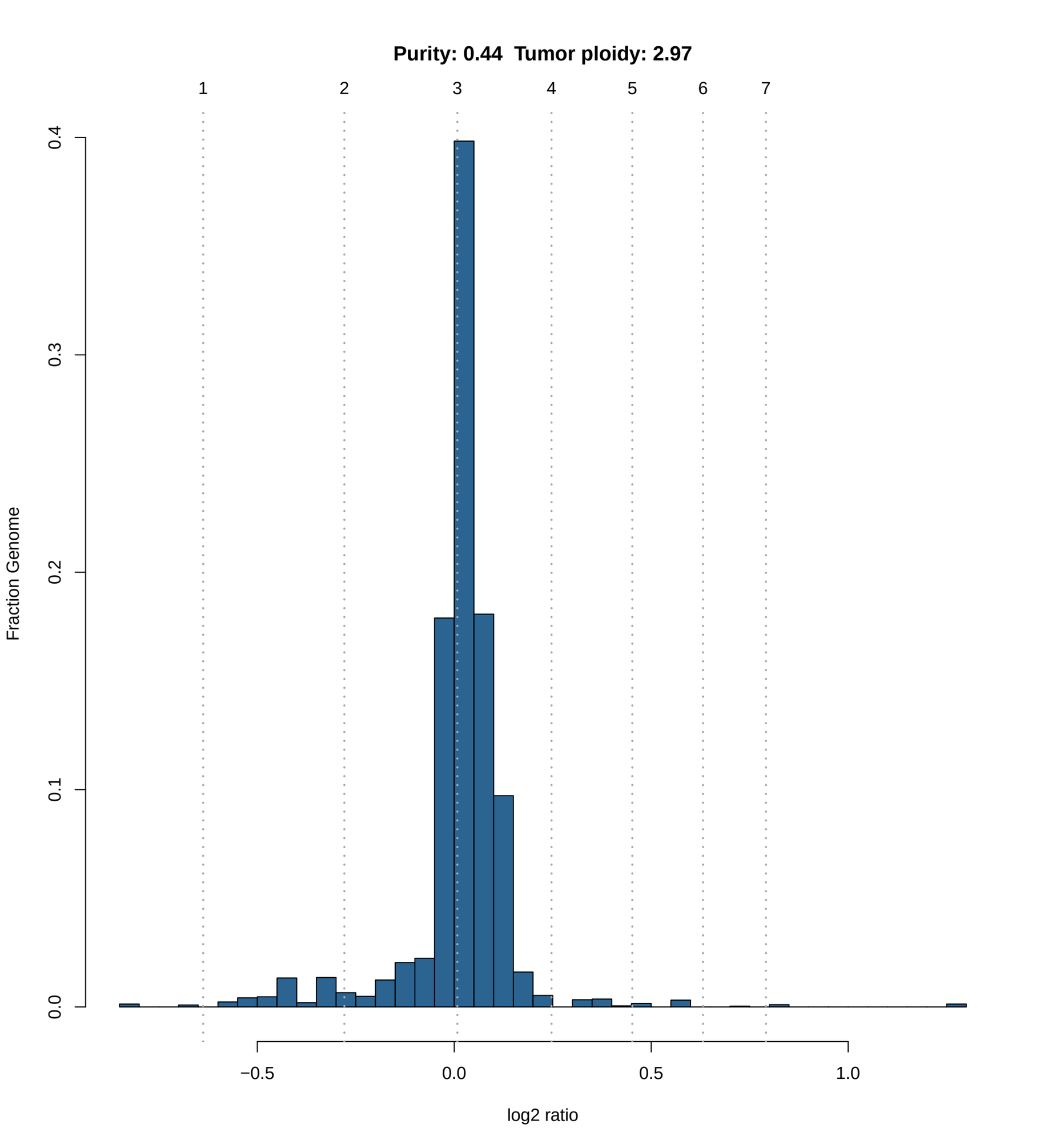

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

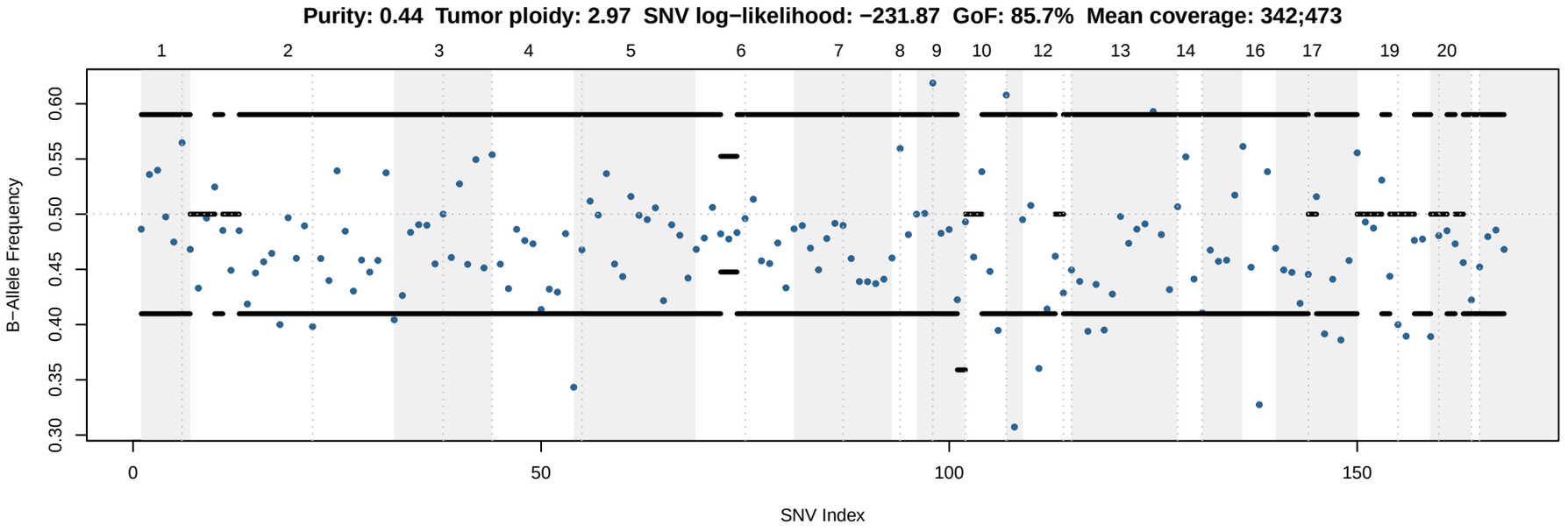

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
−0.5
0.0
0.5
1.0
Copy Number log−ratio
2m1
4m2
3m1

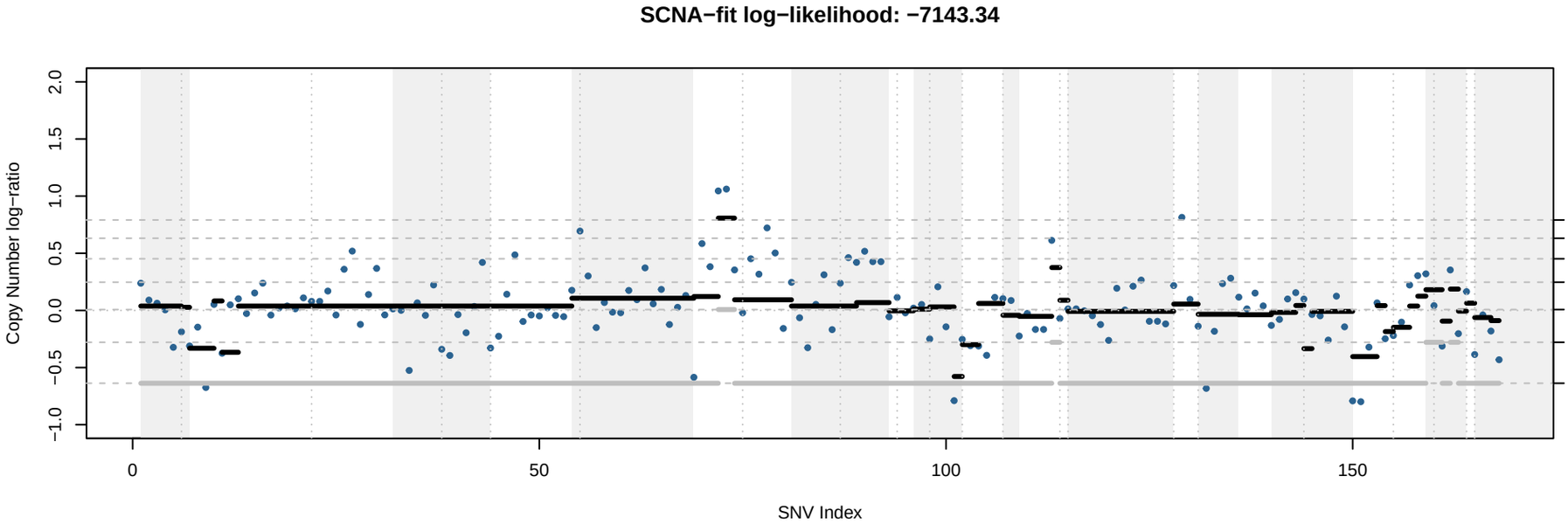

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

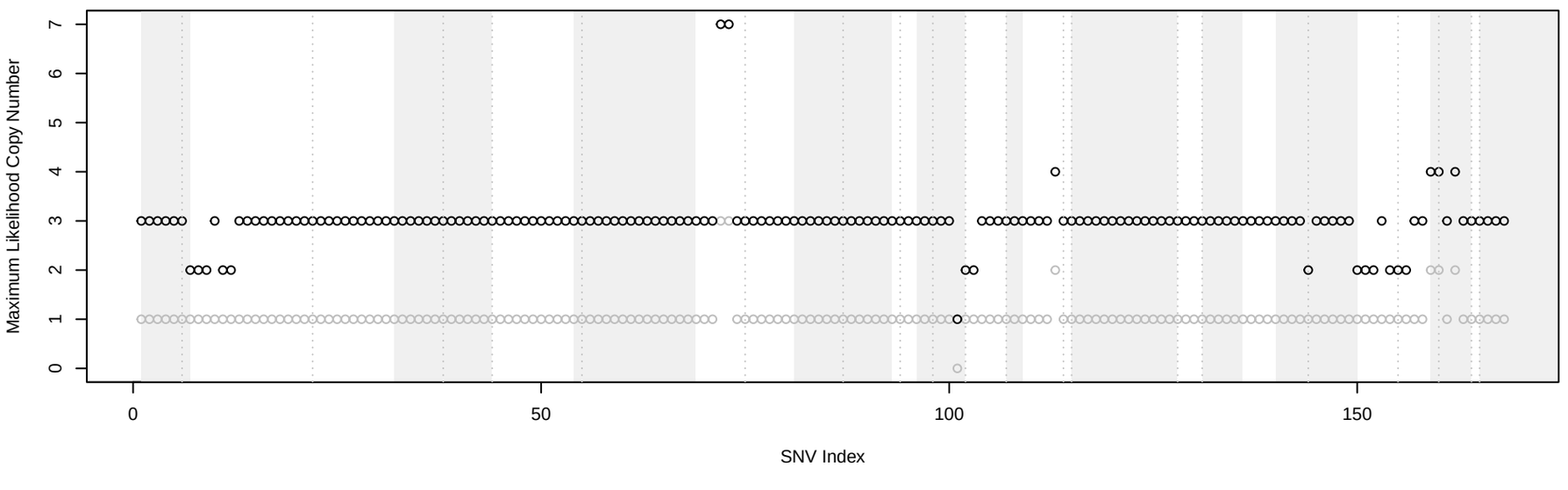

Allelic fraction (somatic)
0.1
0.2
0.3
0.4
0.5
0.6
−0.5
0.0
0.5
1.0
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
1m1
2m1
3m1

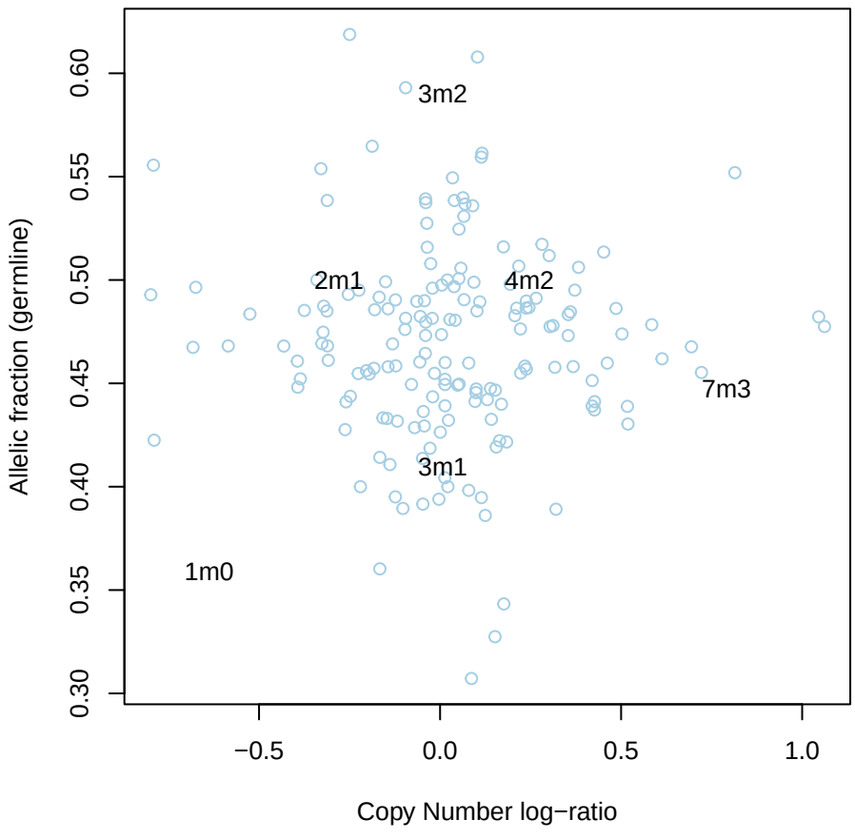

Power 0.8
Frequency
0
5
10
15
0.0
0.2
0.4
0.6
0.8
Cellular fraction

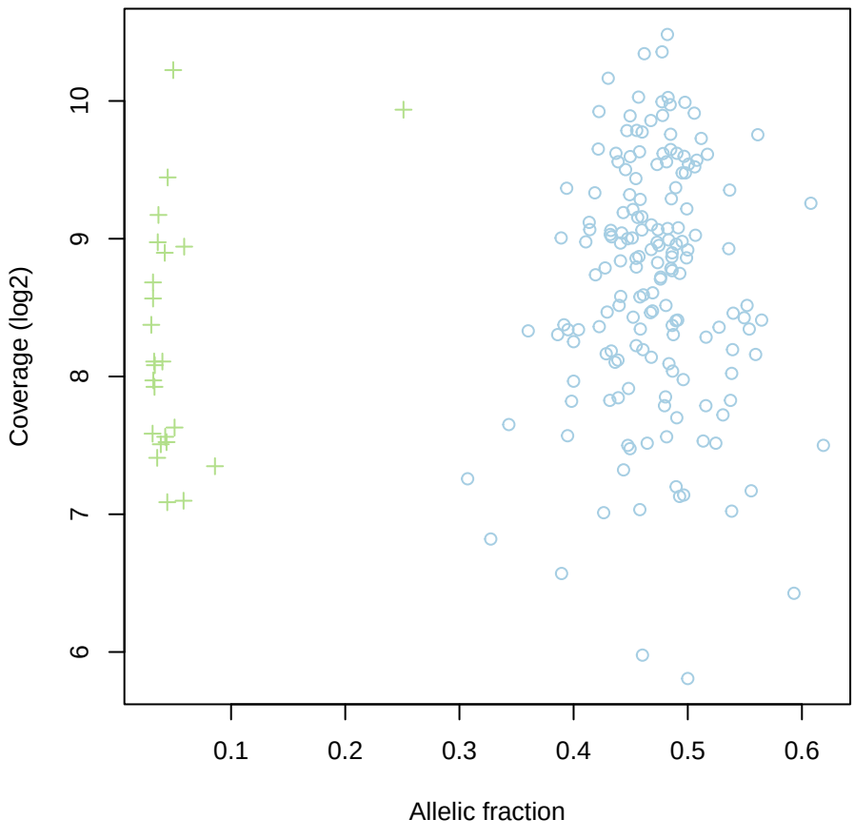

Purity: 0.44 Tumor ploidy: 2.97
1
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

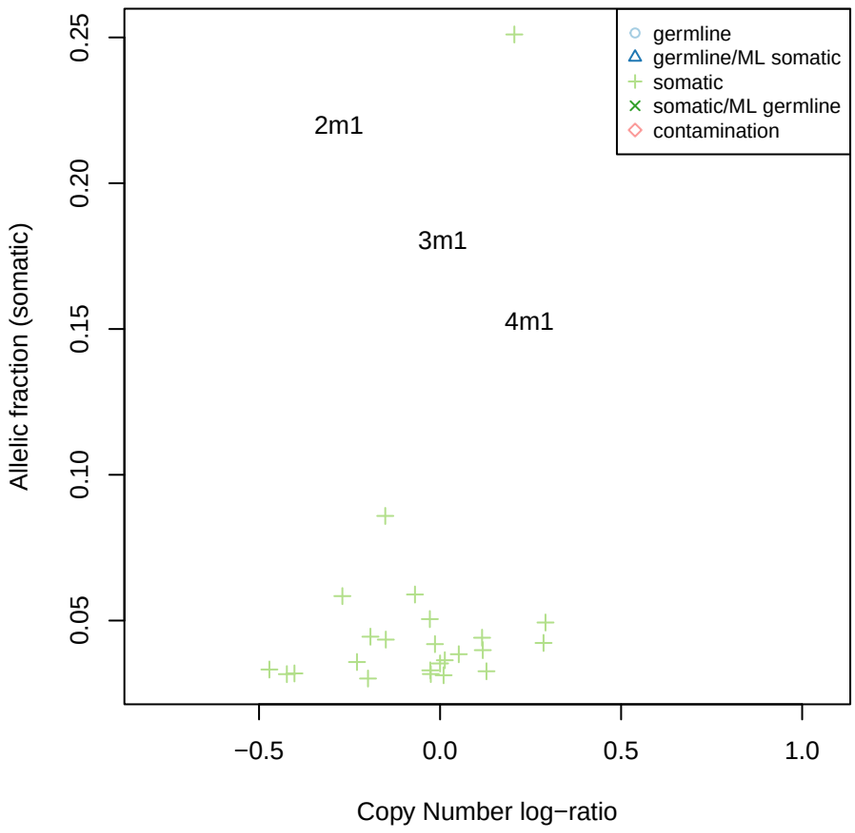

Purity: 0.44 Tumor ploidy: 2.97 SNV log−likelihood: −231.87 GoF: 85.7% Mean coverage: 342;473
1 2 3 4 5 6 7 8 9 10 12 13 14 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

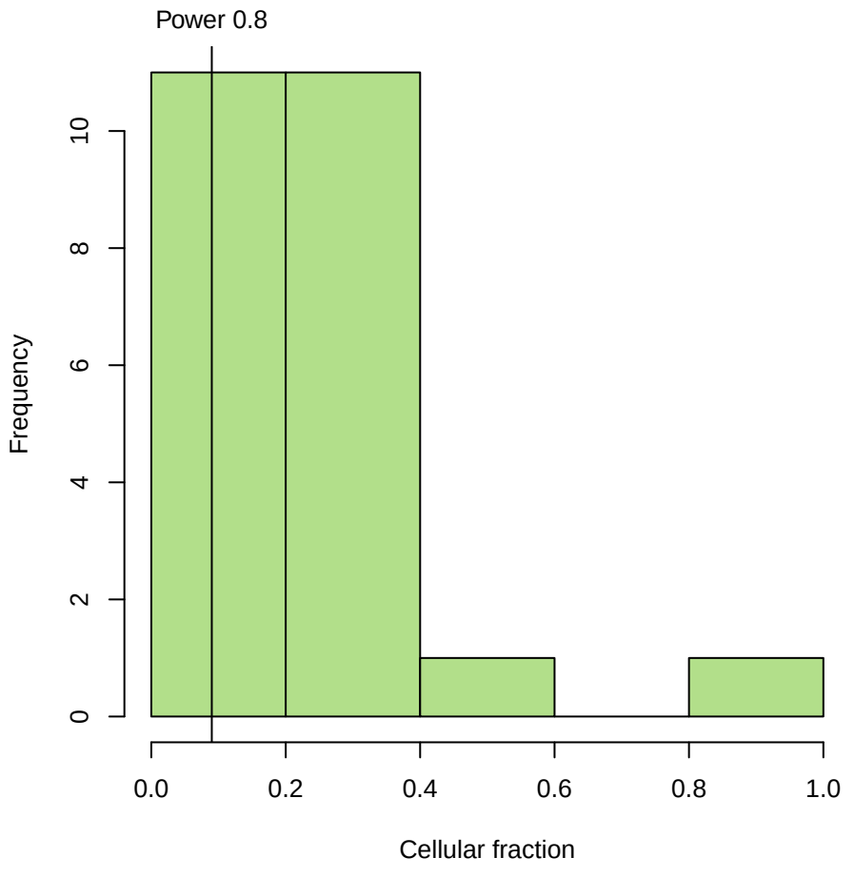

SCNA−fit log−likelihood: −7143.34
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
1 2 3 4 6
0 50 100 150
SNV Index

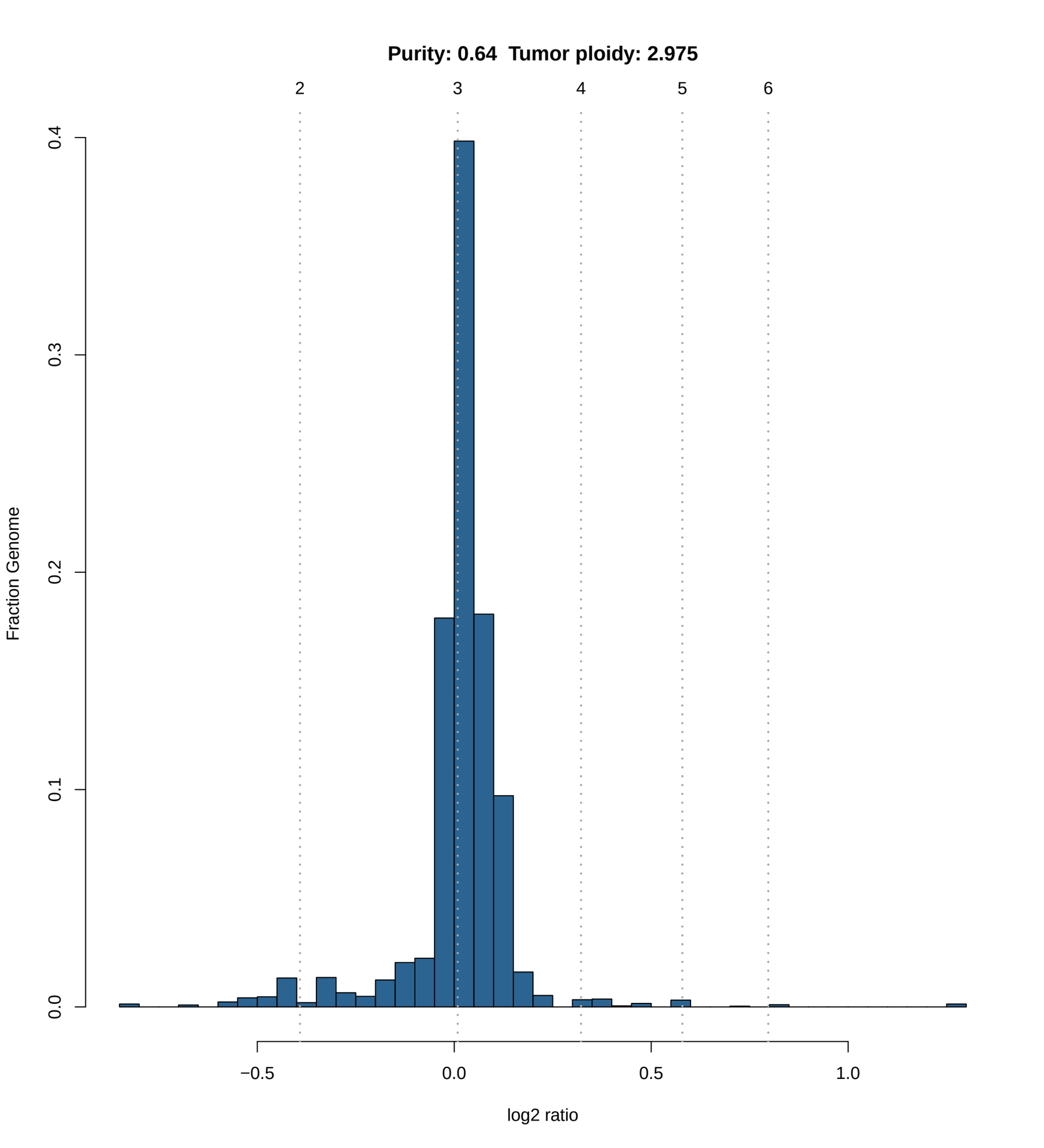

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

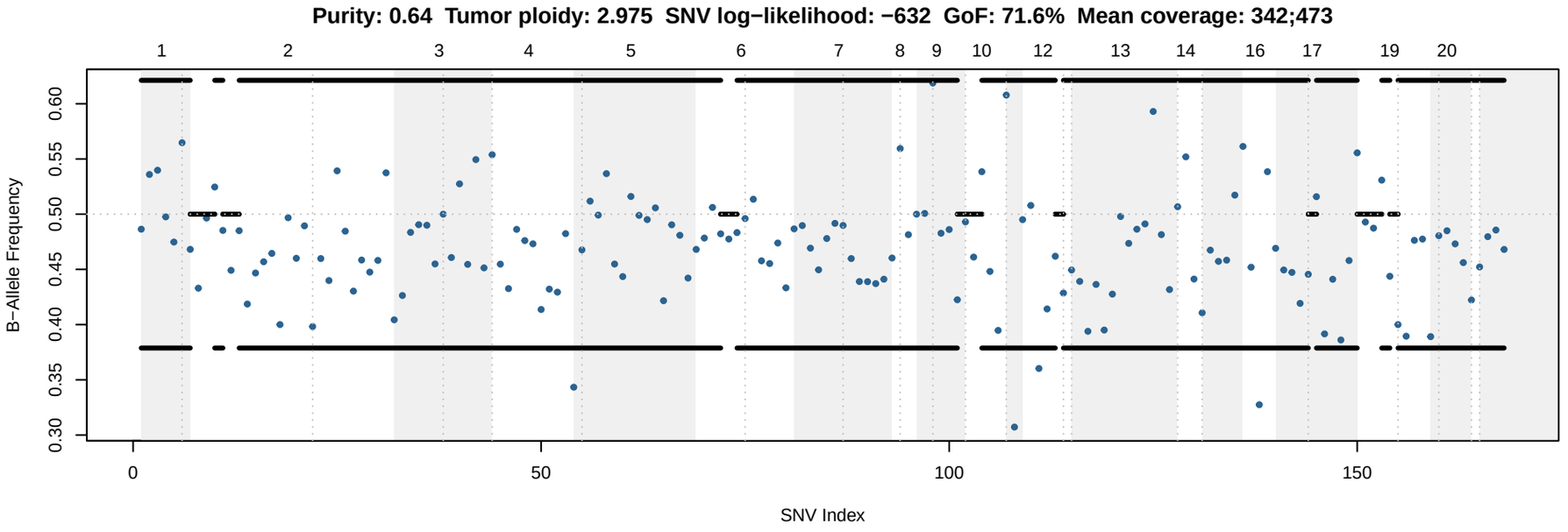

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
3m2
2m1
4m2
7m3
3m1
1m0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

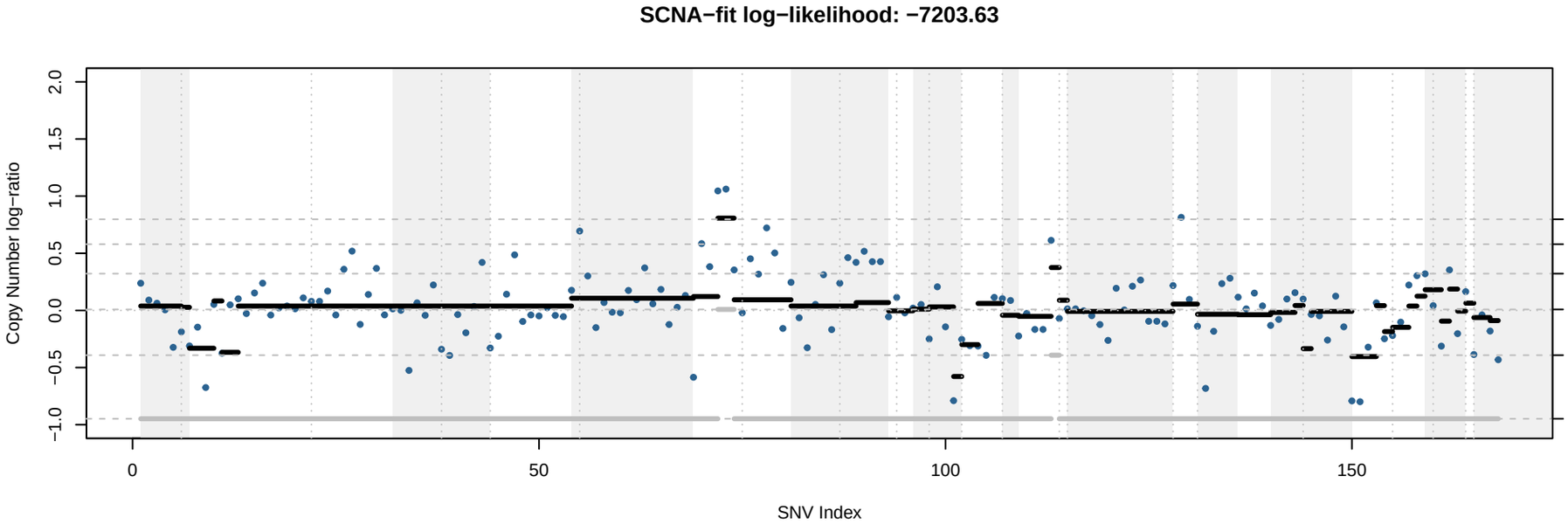

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

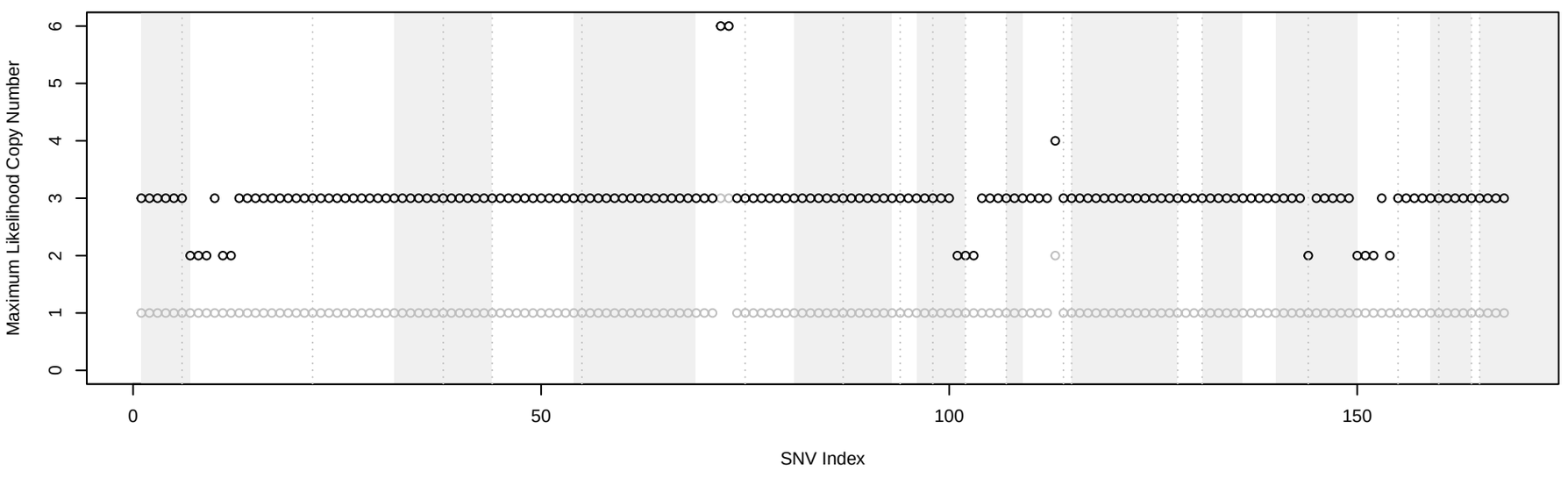

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1
−0.5
0.0
0.5
1.0
Copy Number log−ratio

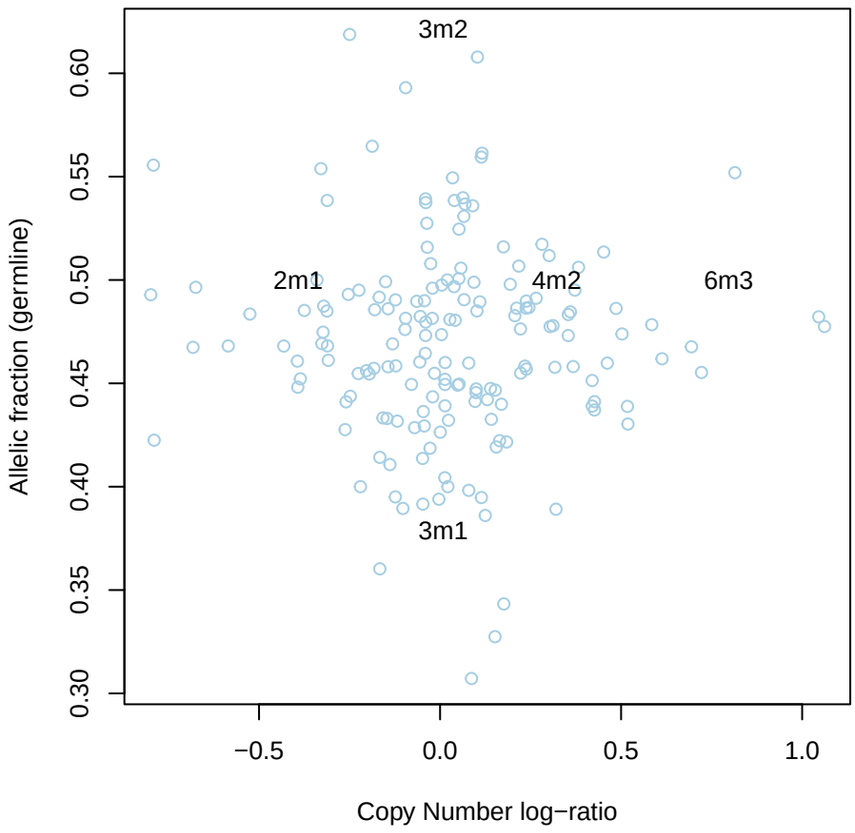

Power 0.8
Frequency
0
2
4
6
8
10
0.0
0.2
0.4
0.6
0.8
1.0
Cellular fraction

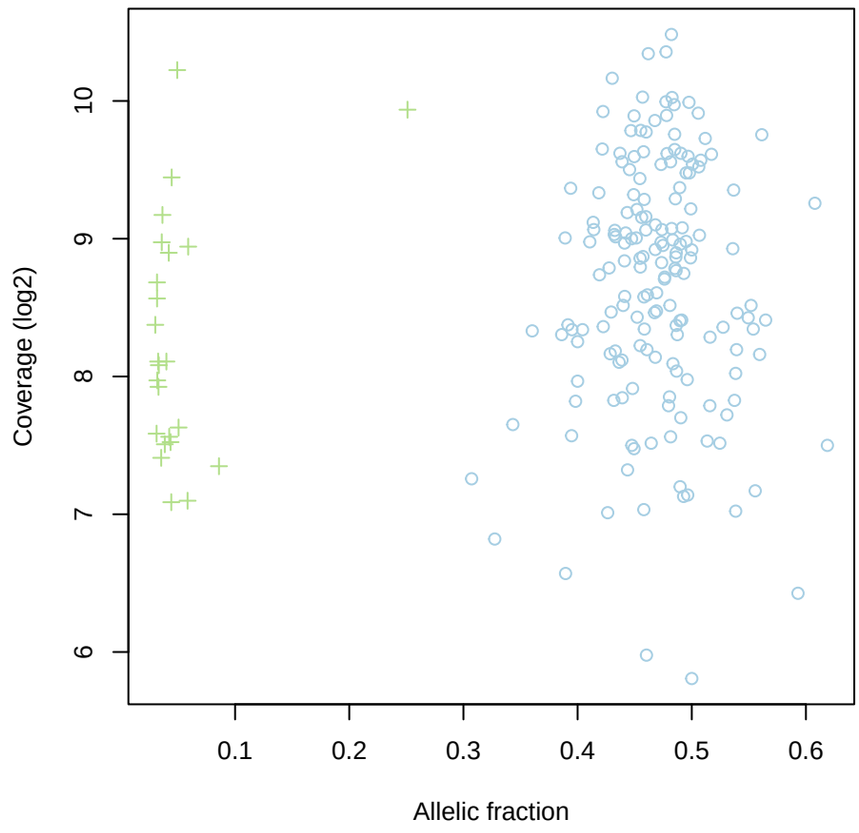

Purity: 0.64 Tumor ploidy: 2.975
2
3
4
5
6
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

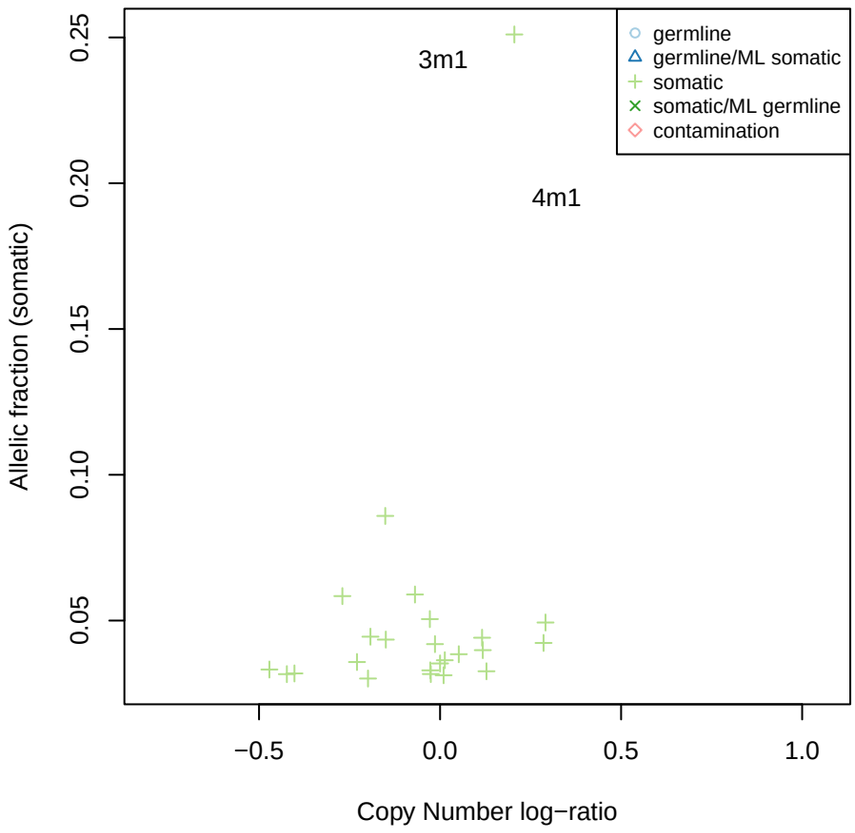

Purity: 0.64 Tumor ploidy: 2.975 SNV log−likelihood: −632 GoF: 71.6% Mean coverage: 342;473
1 2 3 4 5 6 7 8 9 10 12 13 14 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

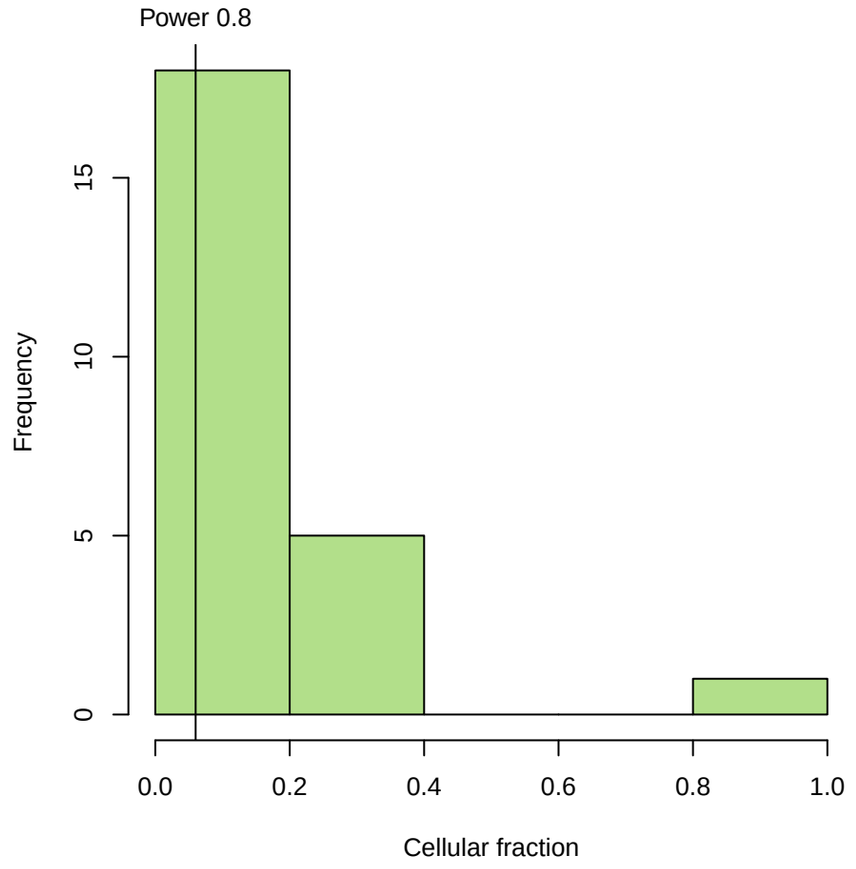

SCNA−fit log−likelihood: −7203.63
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
1 2 3 4 5 6
0 50 100 150
SNV Index

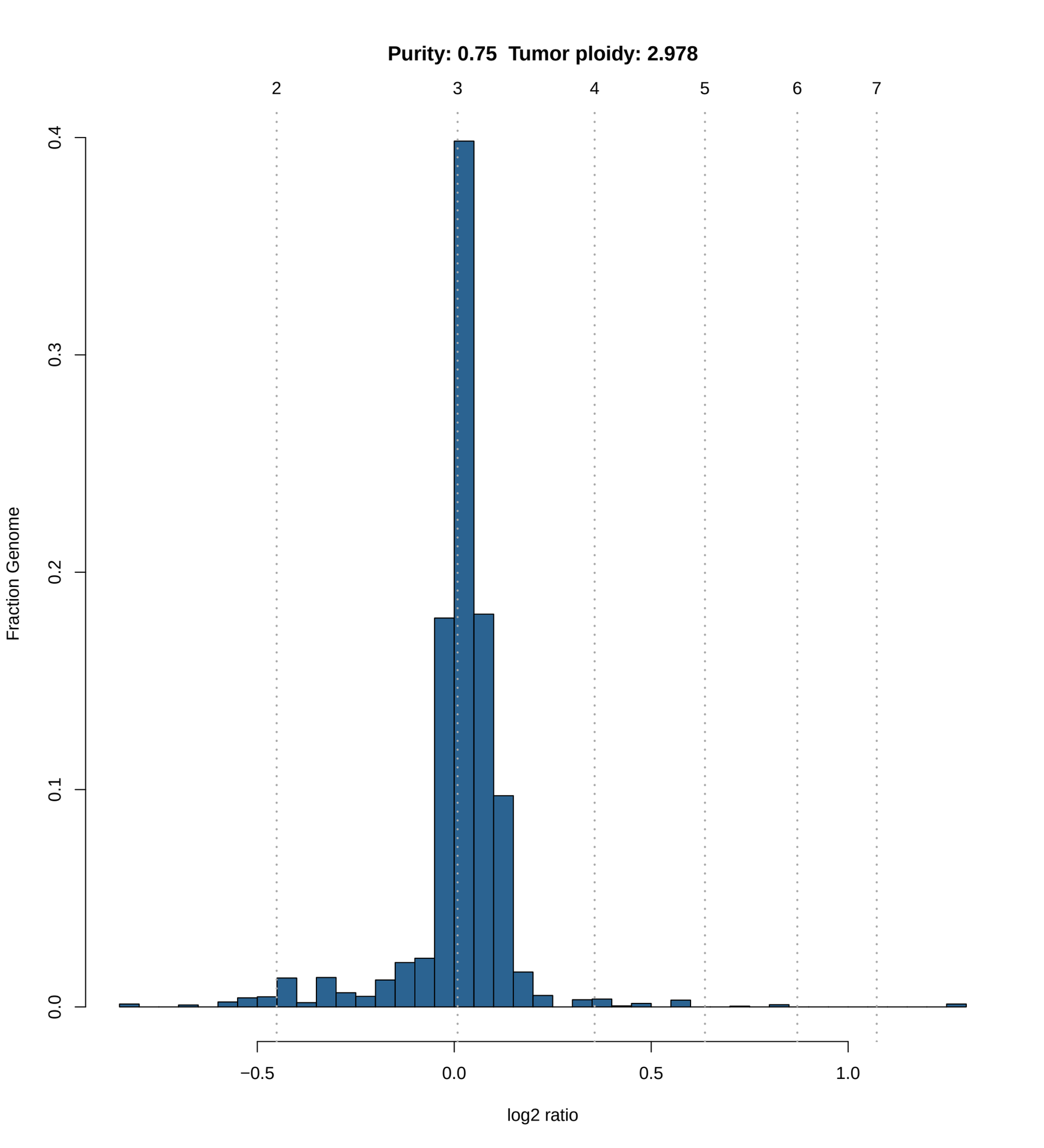

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

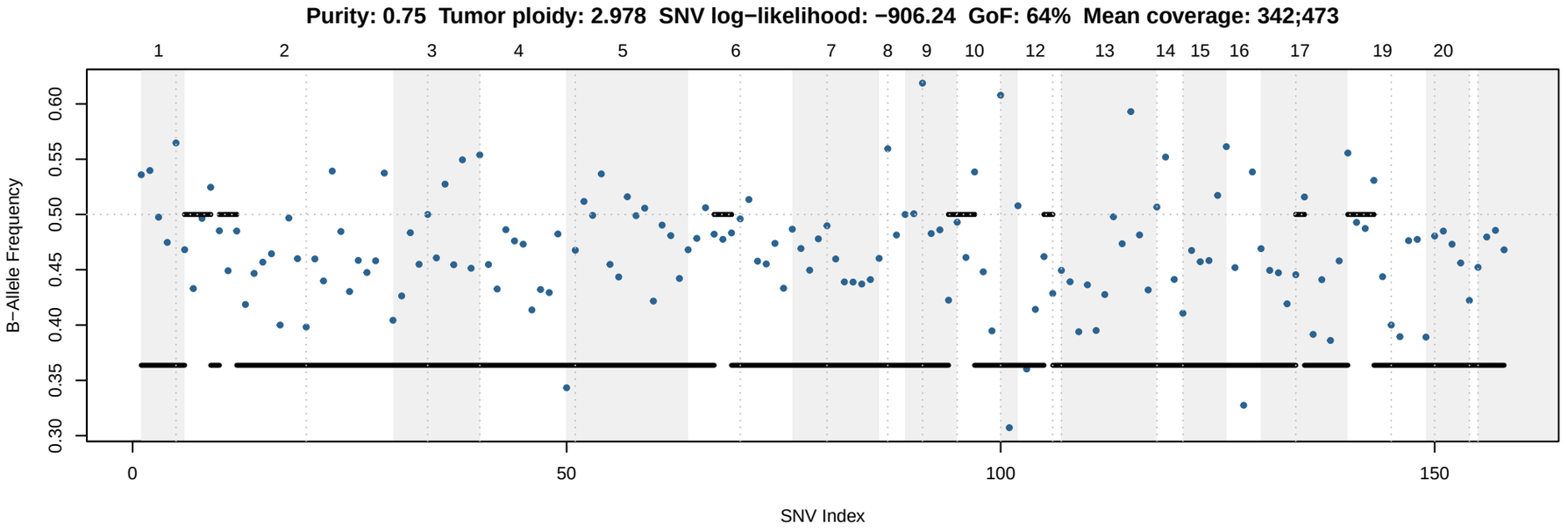

3m2
2m1
4m2
6m3
3m1
Allelic fraction (germline)
Copy Number log−ratio
0.30
0.35
0.40
0.45
0.50
0.55
0.60
−0.5
0.0
0.5
1.0

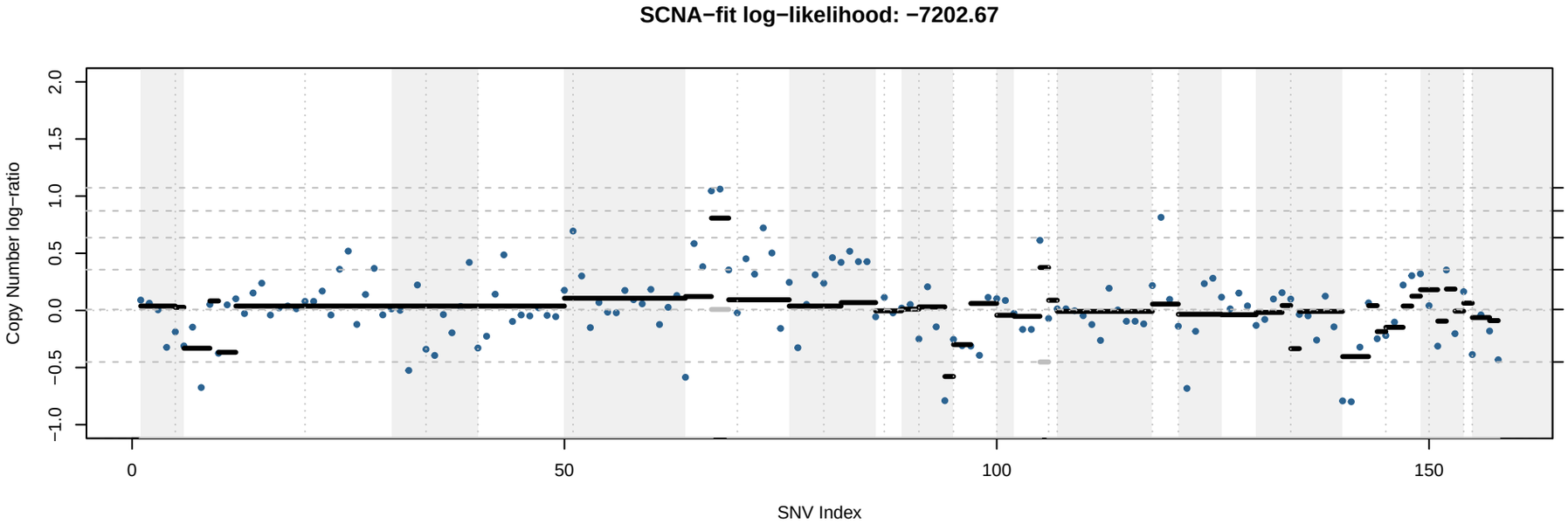

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

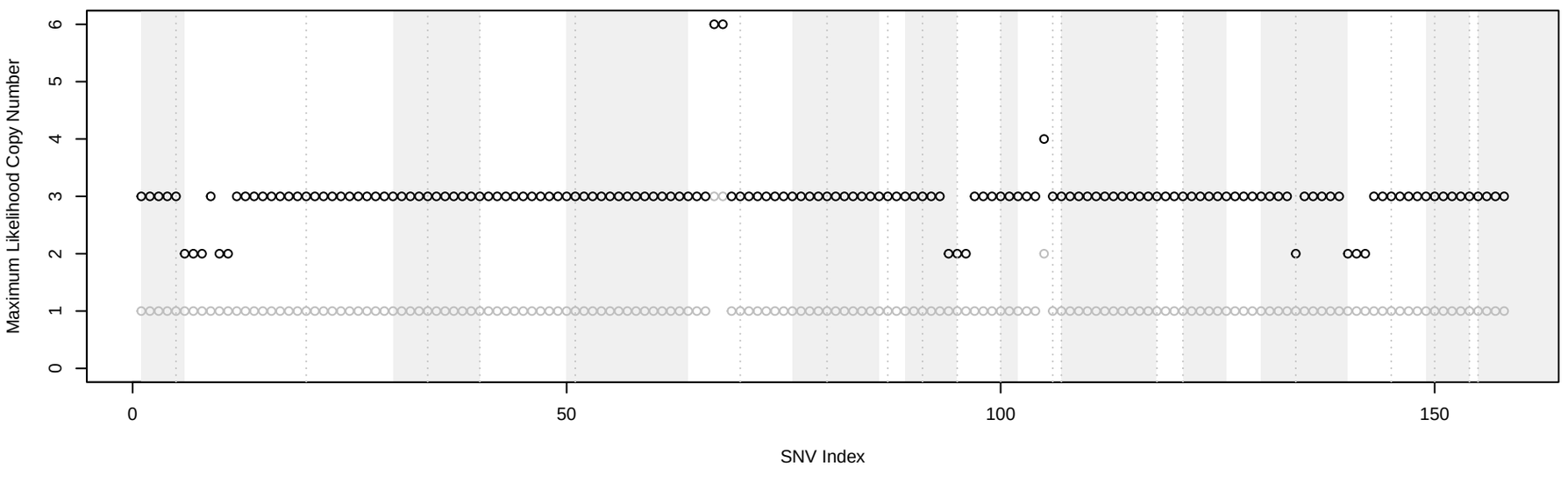

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
0.25
−0.5
0.0
0.5
1.0

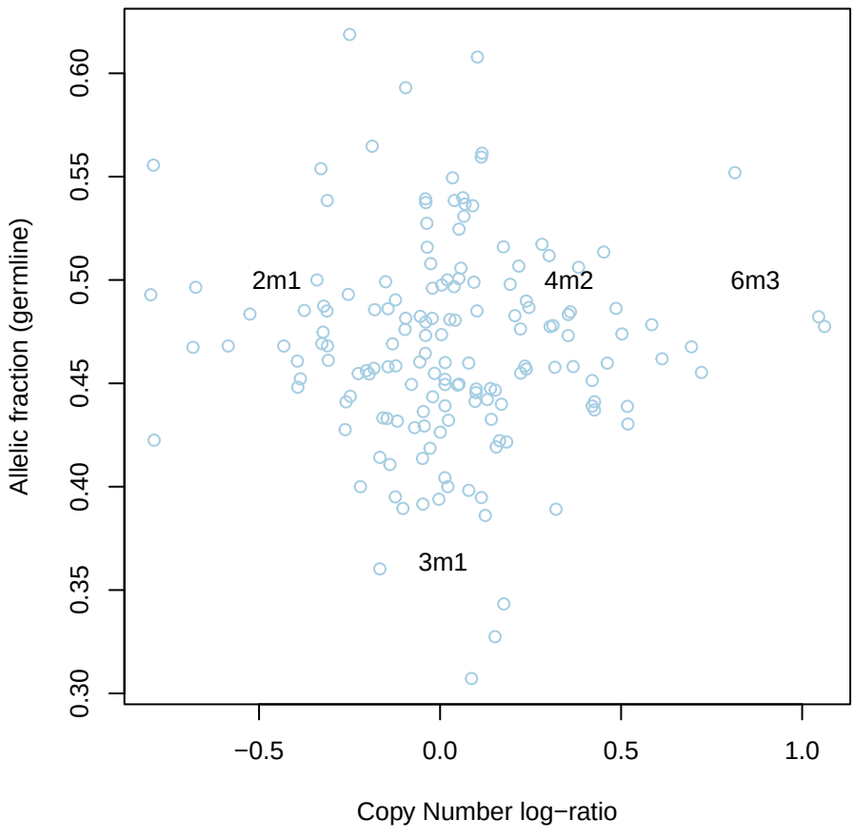

Power 0.8
Frequency
Cellular fraction
0
5
10
15
0.0
0.2
0.4
0.6
0.8
1.0

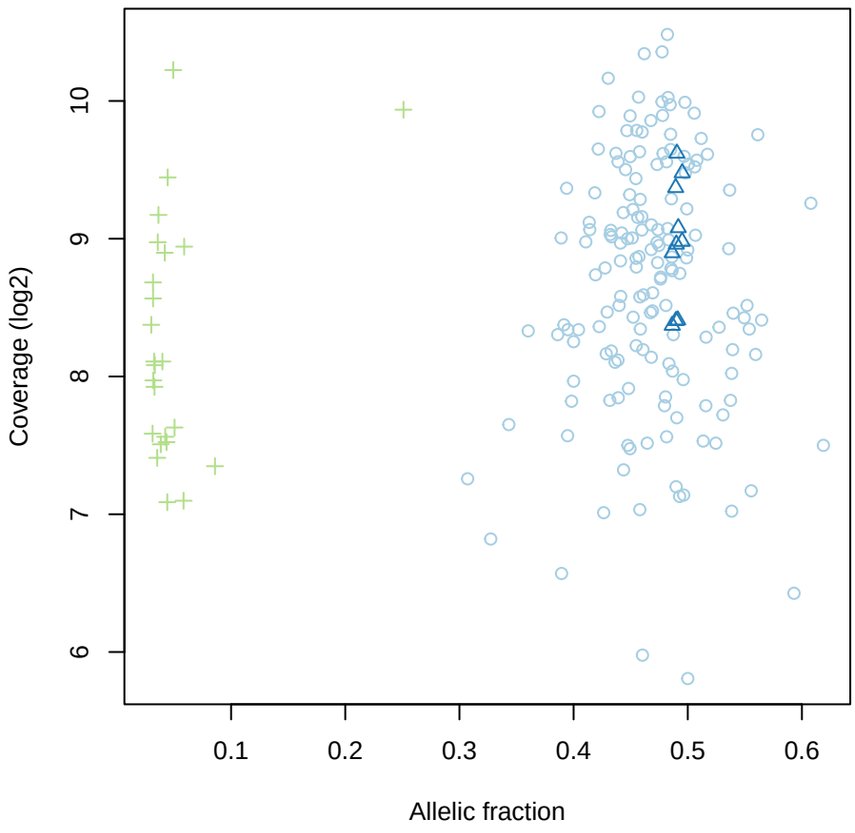

Purity: 0.75 Tumor ploidy: 2.978
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

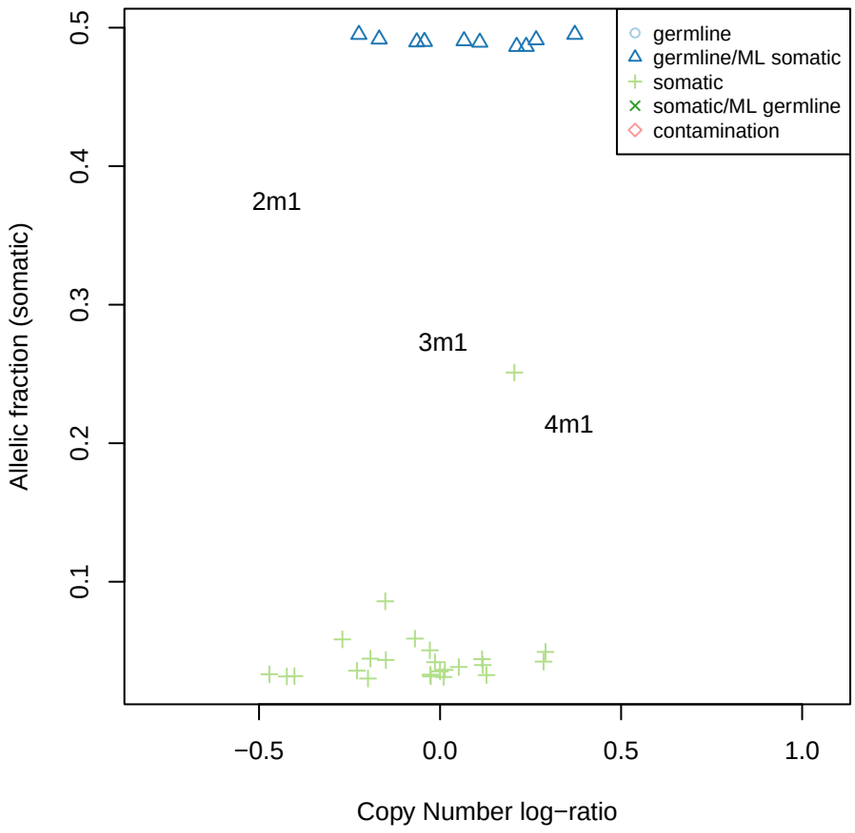

Purity: 0.75 Tumor ploidy: 2.978 SNV log−likelihood: −906.24 GoF: 64% Mean coverage: 342;473
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

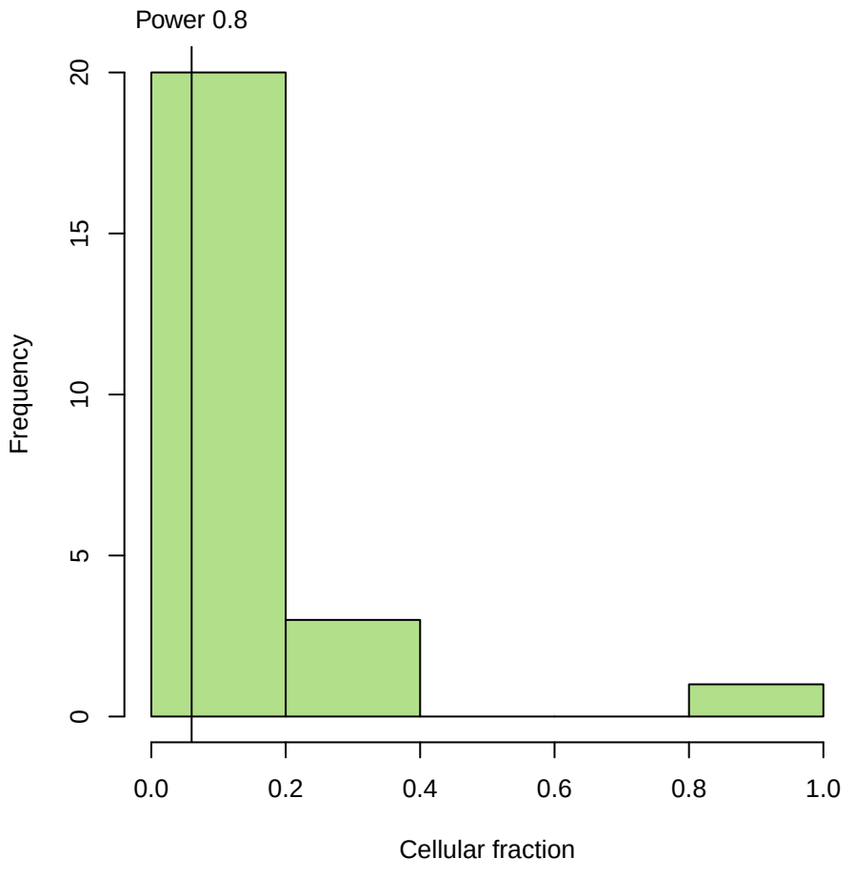

SCNA−fit log−likelihood: −7202.67
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
2 3 4 5 6
0 50 100 150
SNV Index


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


Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
2m1
4m2
6m3
3m1
−0.5
0.0
0.5
1.0
Copy Number log−ratio


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


Allelic fraction (somatic)
0.1
0.2
0.3
0.4
0.5
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1
−0.5
0.0
0.5
1.0
Copy Number log−ratio


Power 0.8
Frequency
0
5
10
15
20
0.0
0.2
0.4
0.6
0.8
1.0
Cellular fraction