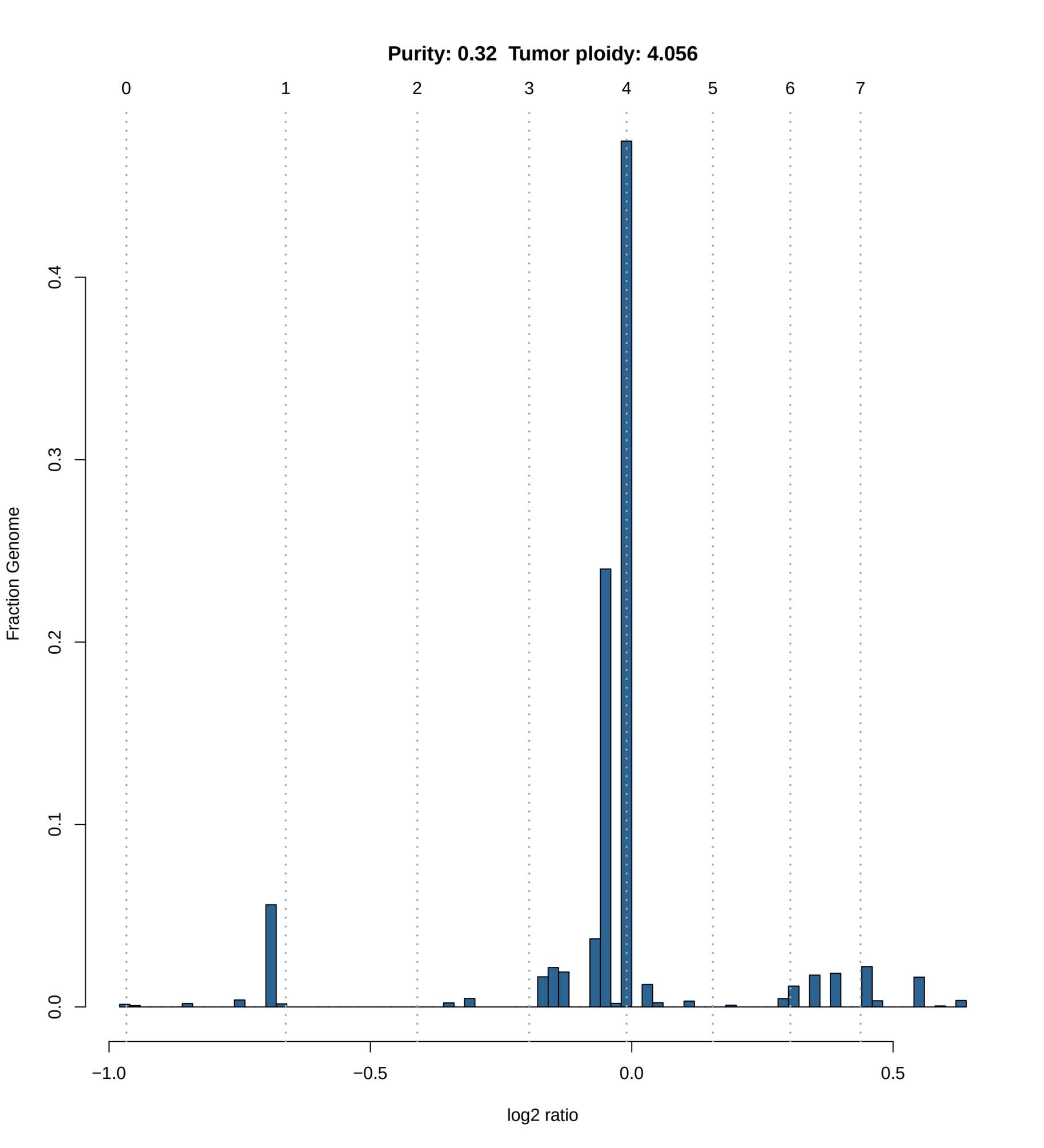
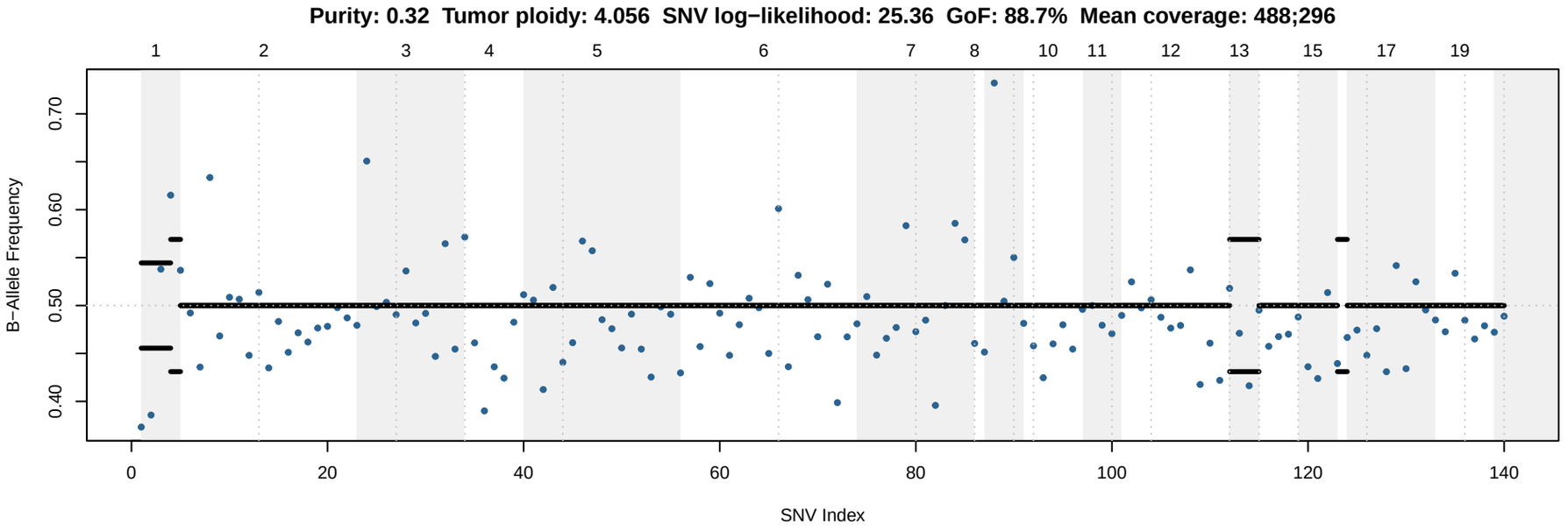
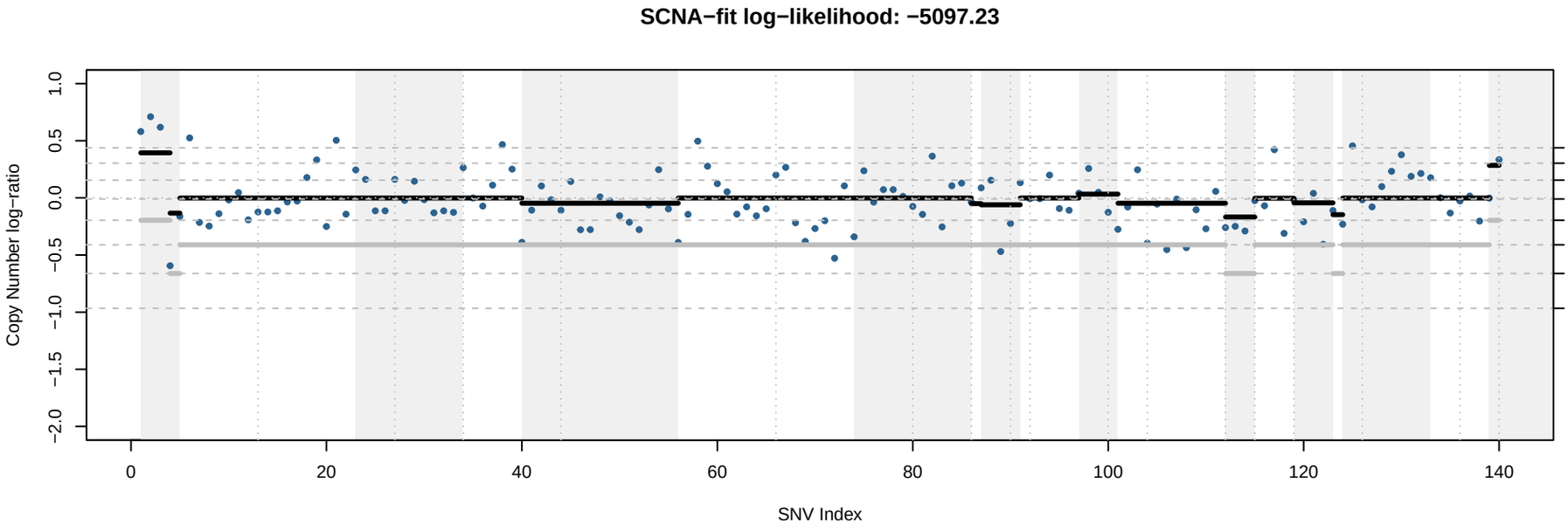
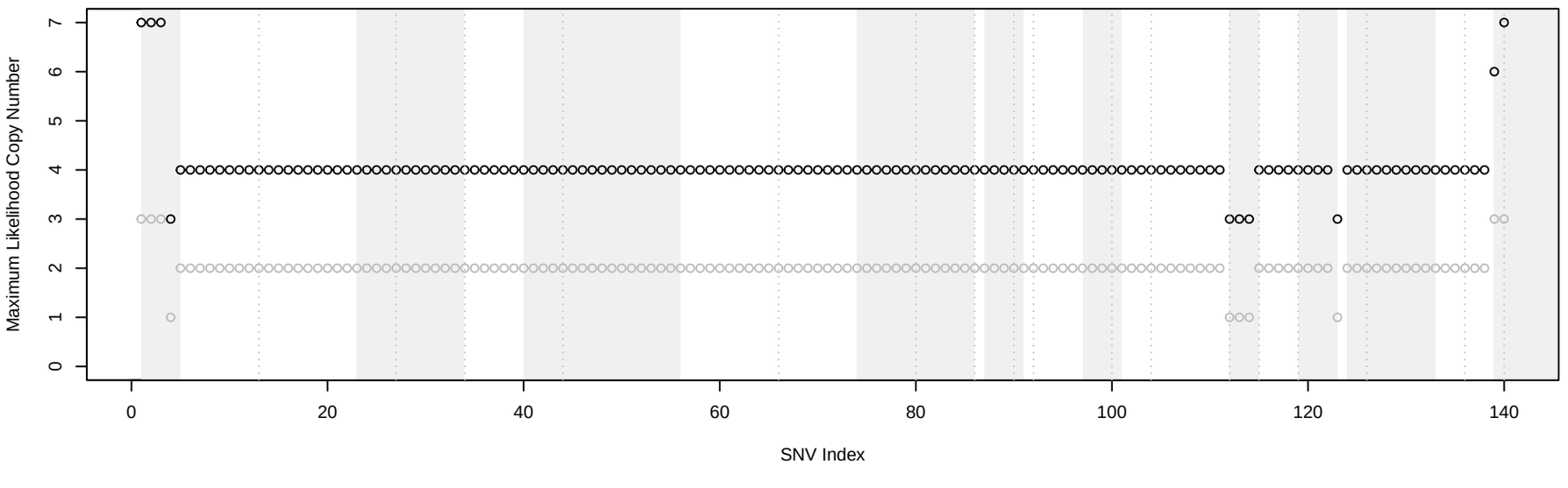
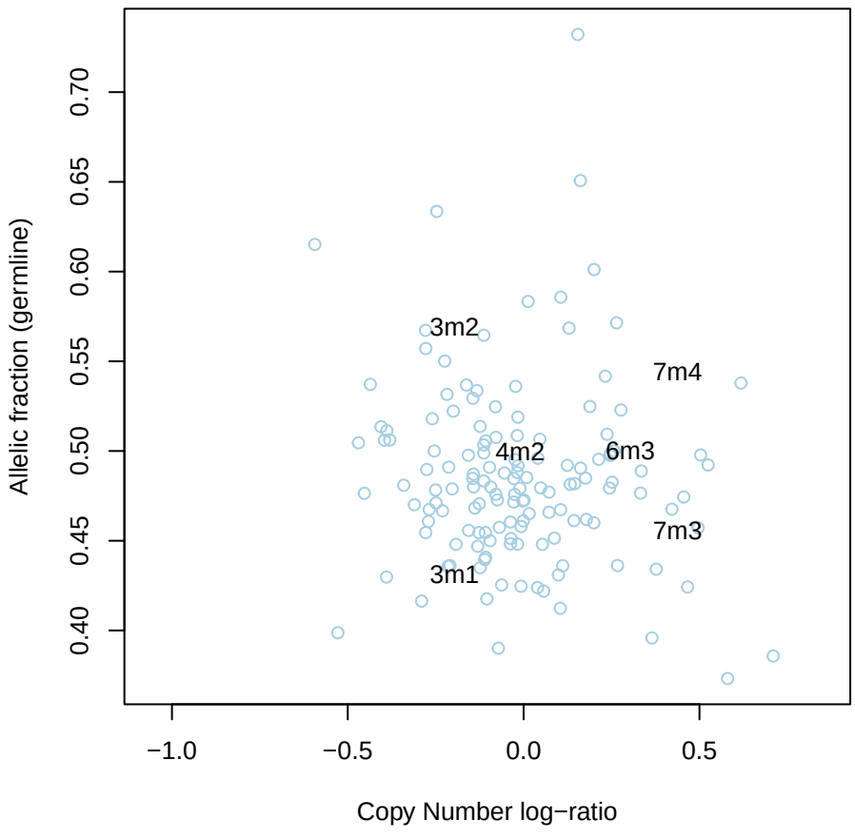
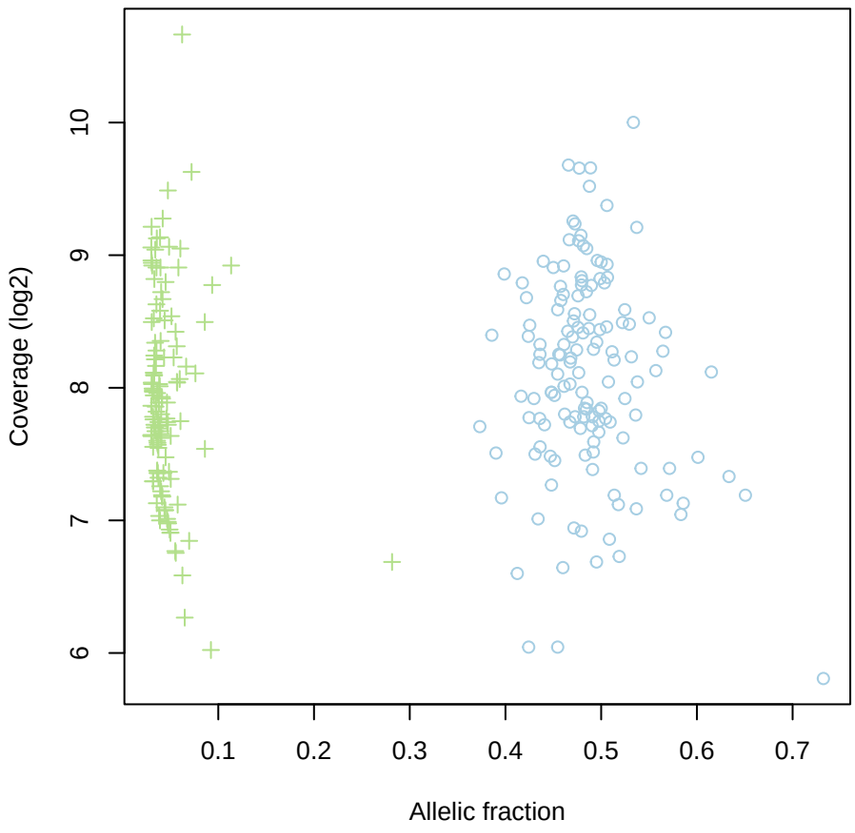

Purity: 0.32 Tumor ploidy: 4.056
0
1
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

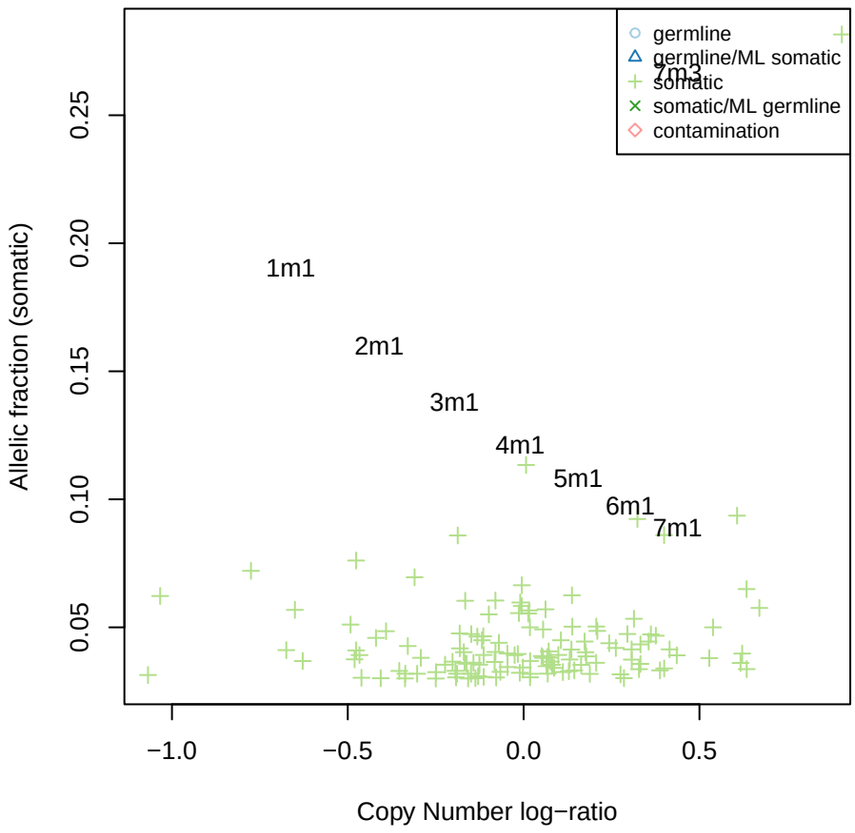

Purity: 0.32 Tumor ploidy: 4.056 SNV log−likelihood: 25.36 GoF: 88.7% Mean coverage: 488;296
1 2 3 4 5 6 7 8 10 11 12 13 15 17 19
B−Allele Frequency
0.40 0.50 0.60 0.70
0 20 40 60 80 100 120 140
SNV Index

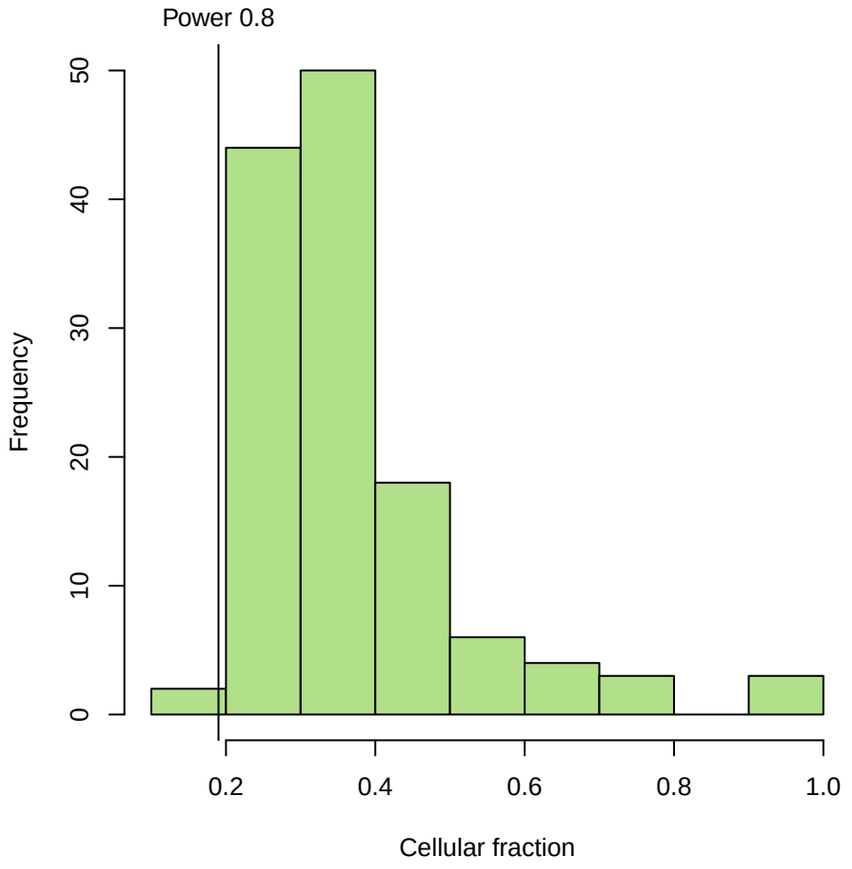

SCNA−fit log−likelihood: −5097.23
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 4 6
0 20 40 60 80 100 120 140
SNV Index

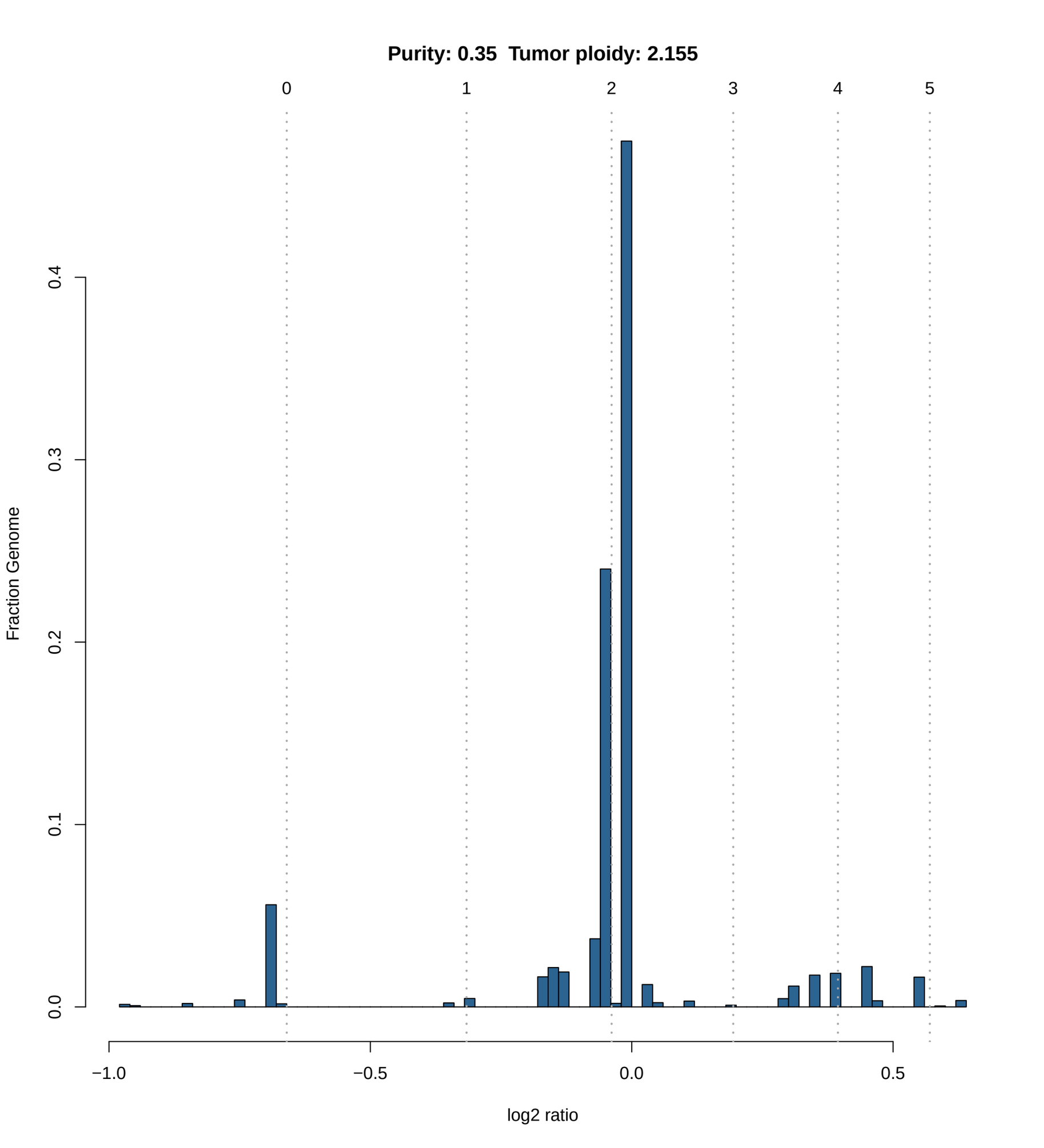

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

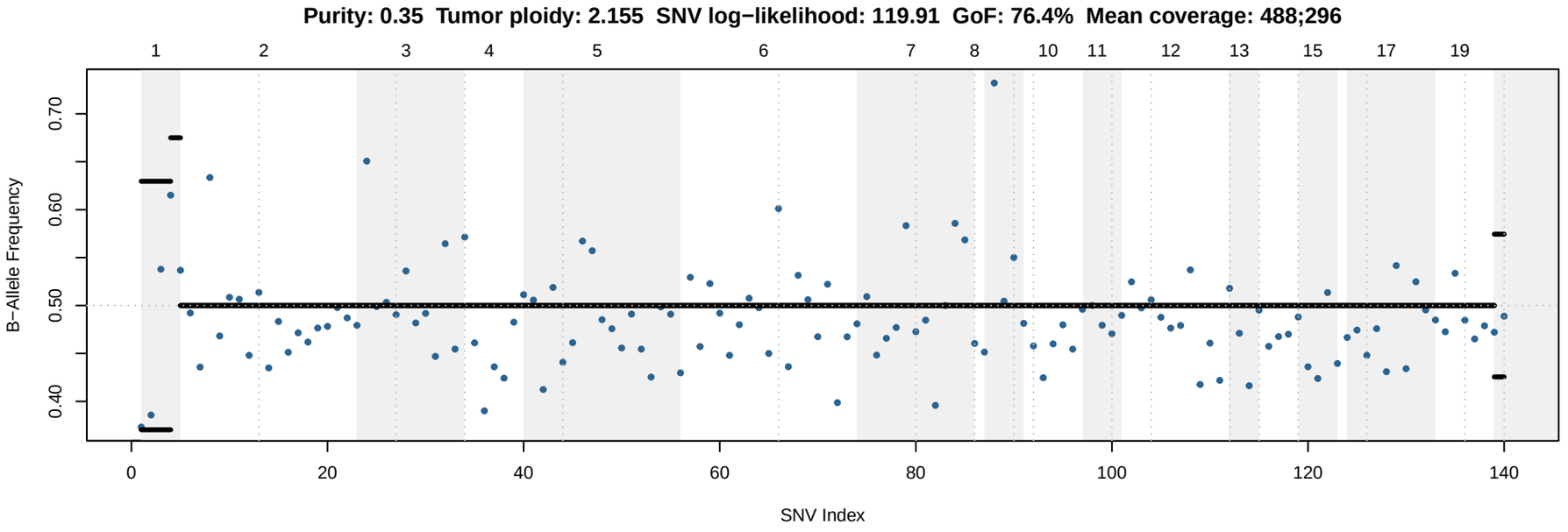

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
0.70
3m2
7m4
4m2
6m3
7m3
3m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

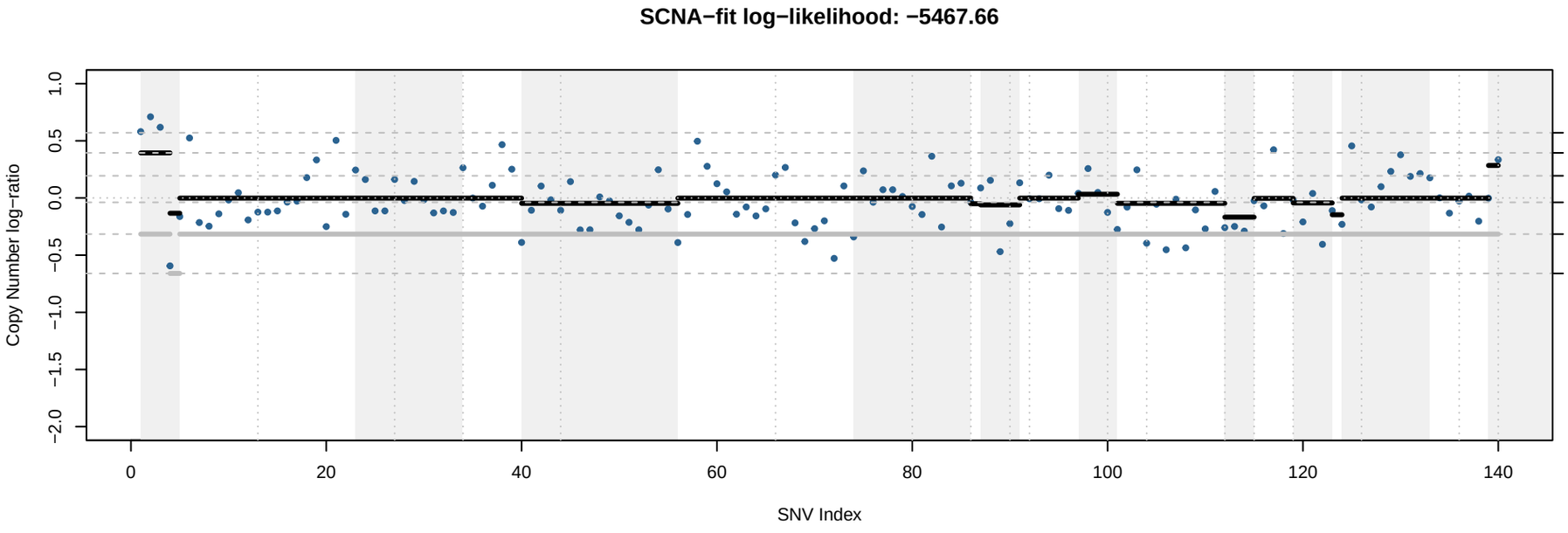

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

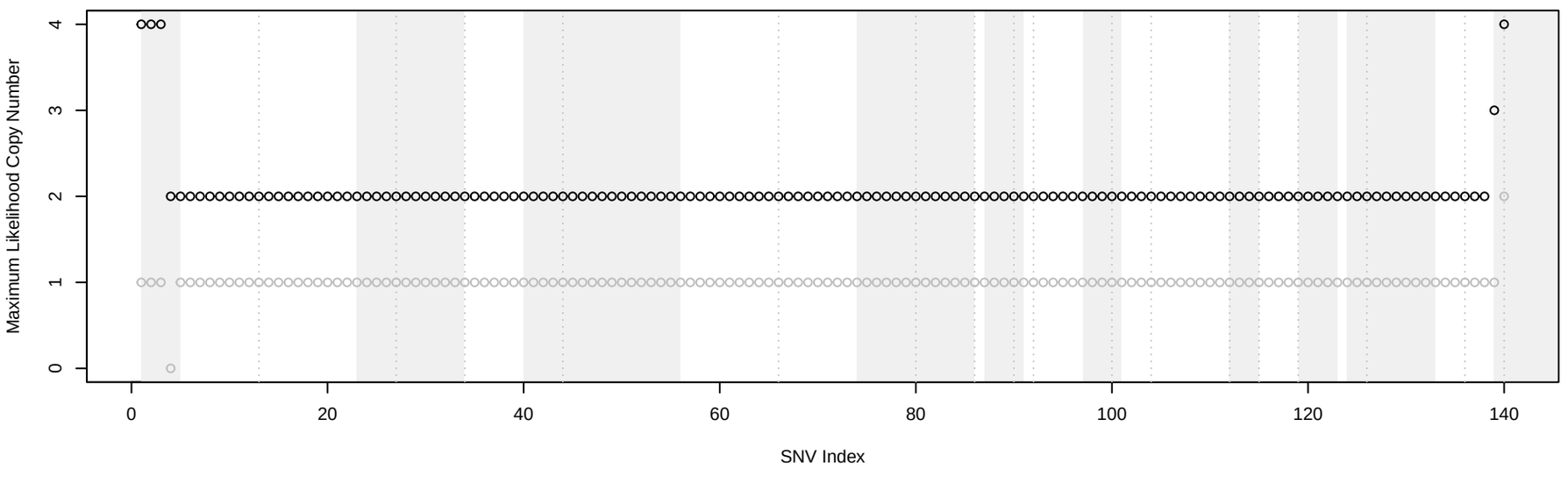

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
1m1
2m1
3m1
4m1
5m1
6m1
7m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

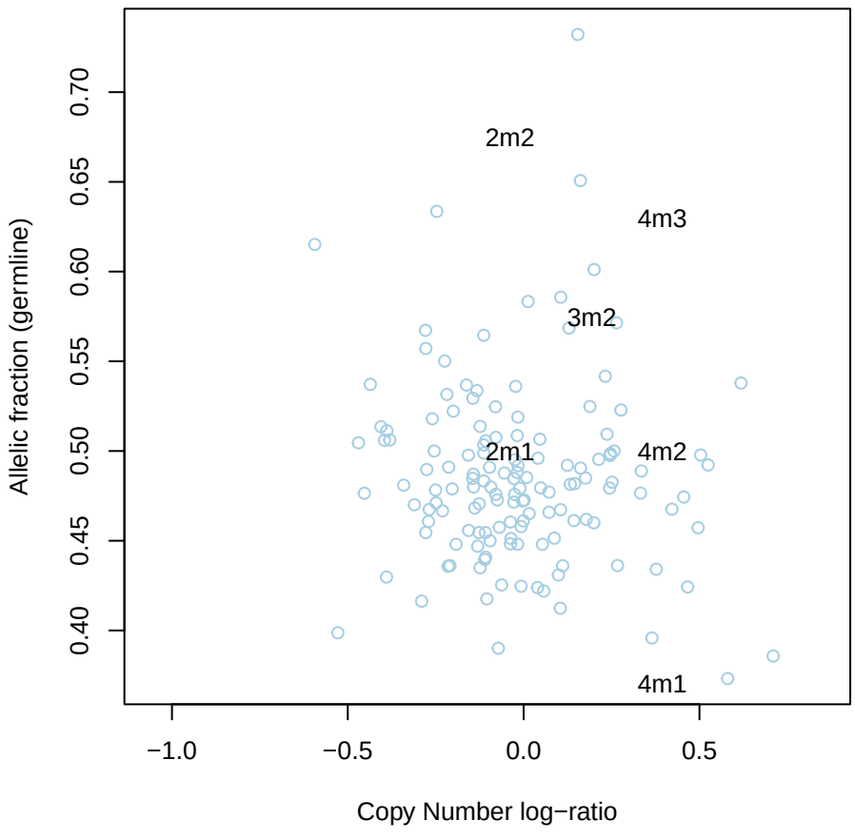

Power 0.8
Frequency
0
10
20
30
40
50
0.2
0.4
0.6
0.8
1.0
Cellular fraction

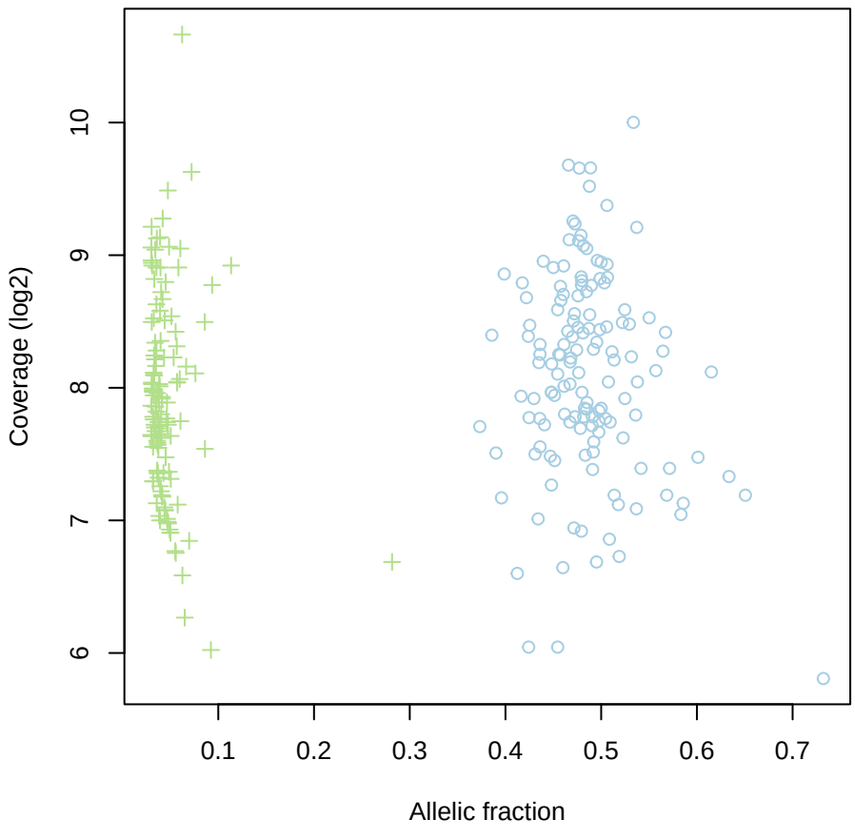

Purity: 0.35 Tumor ploidy: 2.155
0
1
2
3
4
5
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

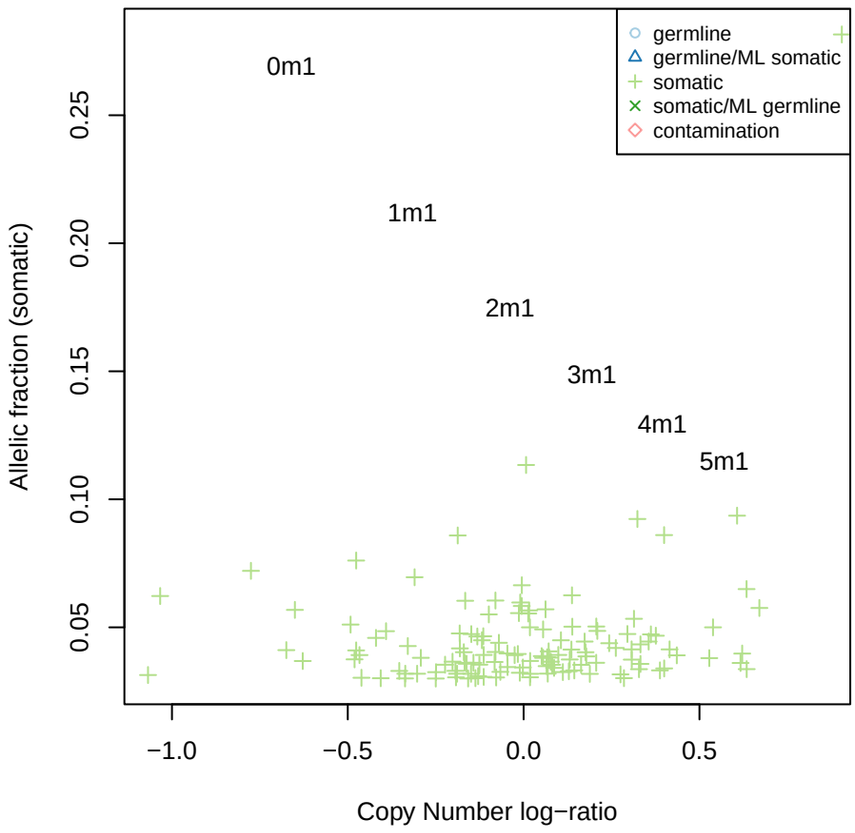

Purity: 0.35 Tumor ploidy: 2.155 SNV log−likelihood: 119.91 GoF: 76.4% Mean coverage: 488;296
1 2 3 4 5 6 7 8 10 11 12 13 15 17 19
B−Allele Frequency
0.40 0.50 0.60 0.70
0 20 40 60 80 100 120 140
SNV Index

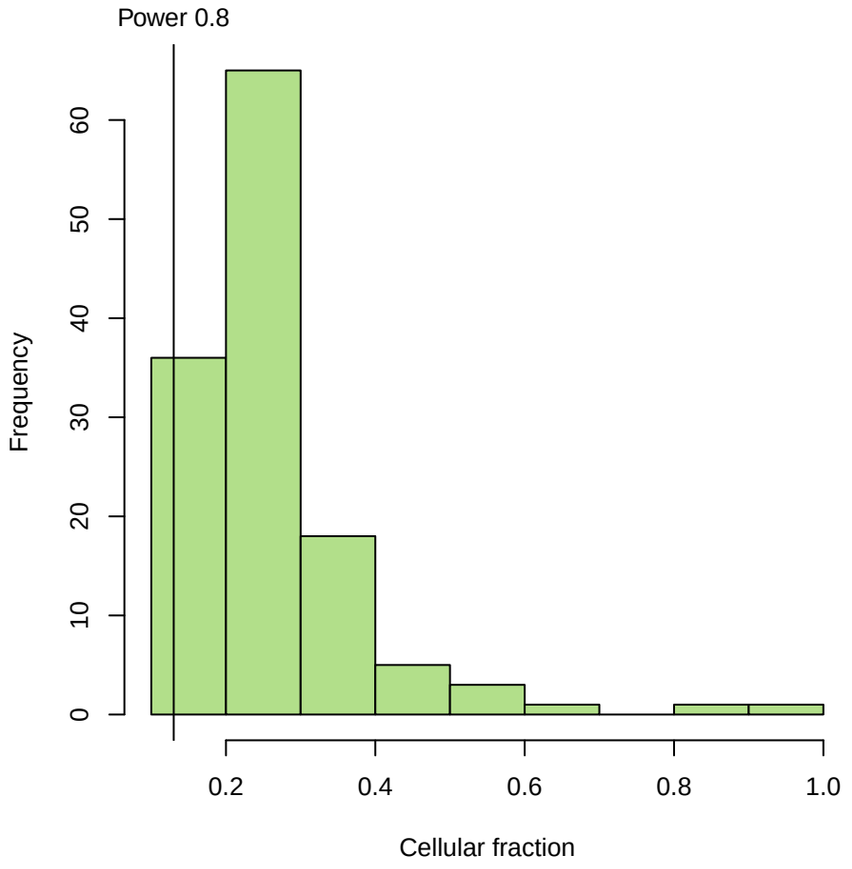

SCNA−fit log−likelihood: −5467.66
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

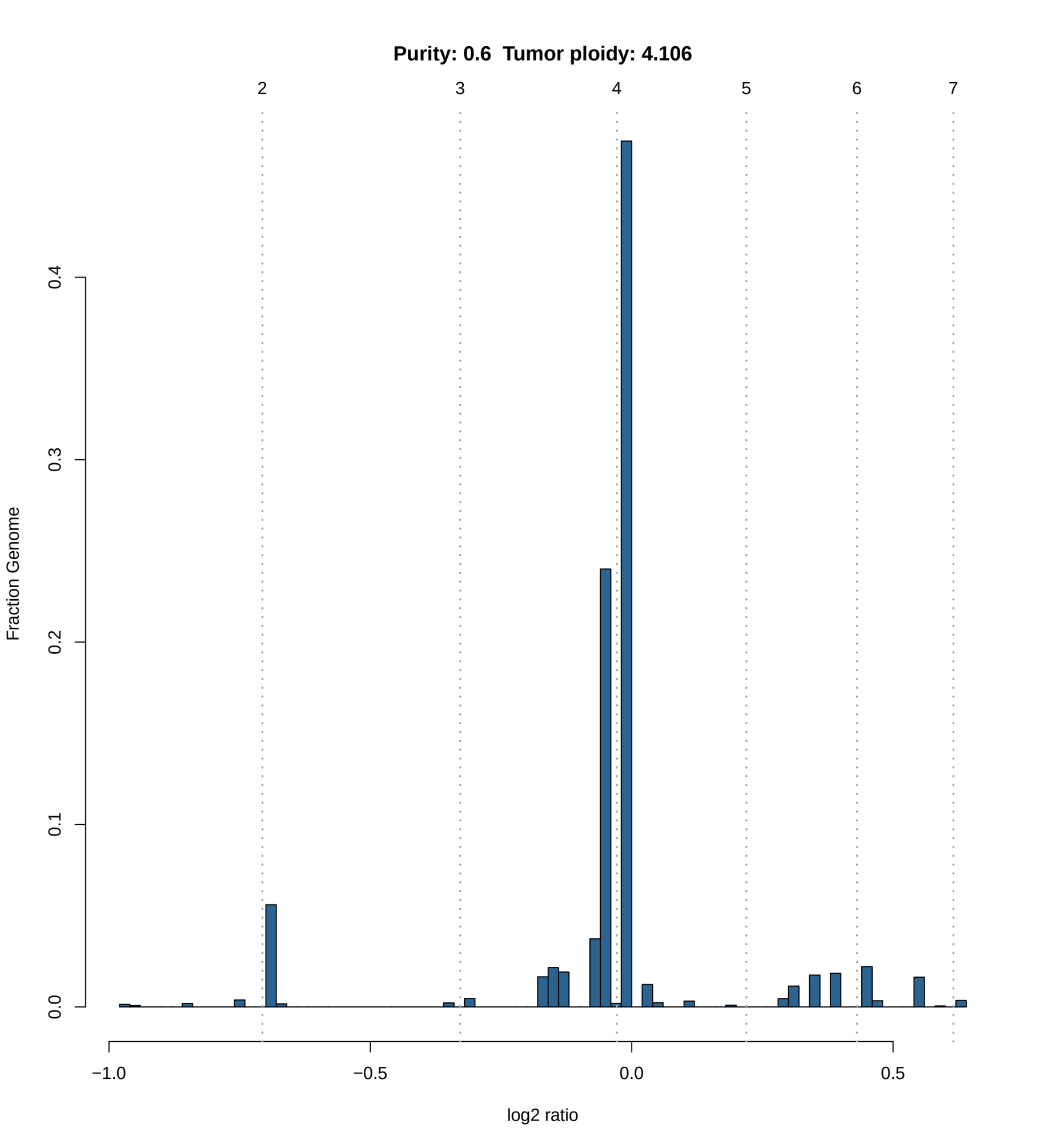

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120 140
SNV Index

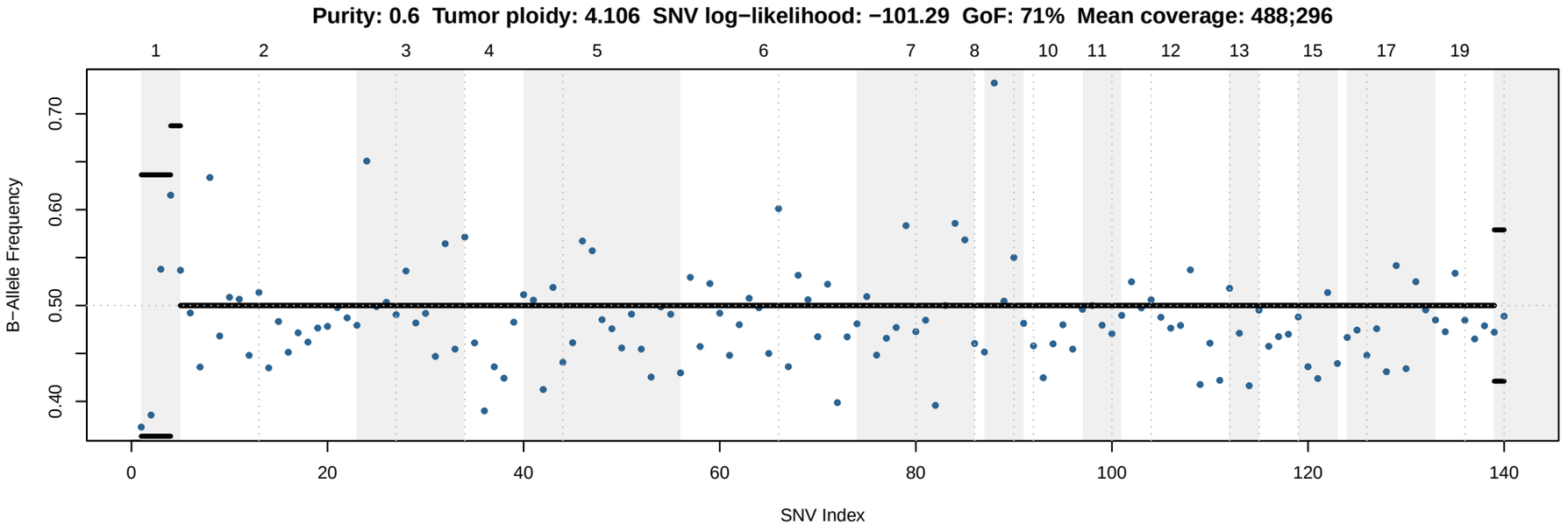

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
0.70
2m2
4m3
3m2
2m1
4m2
4m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

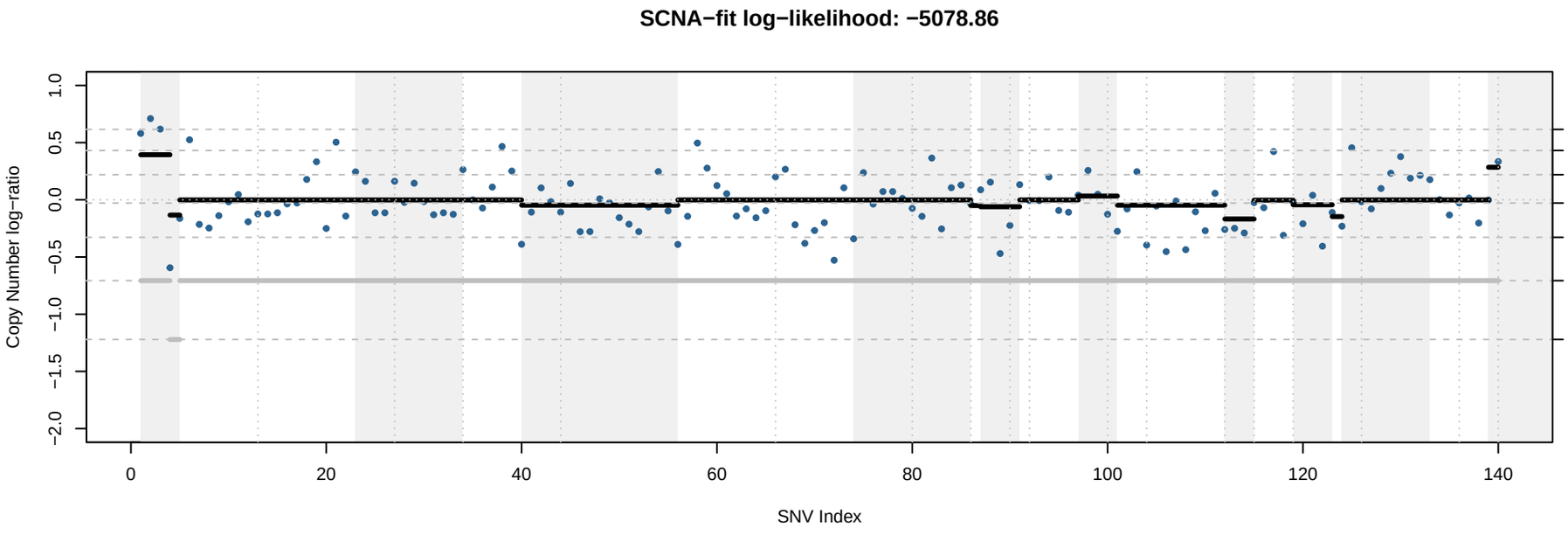

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

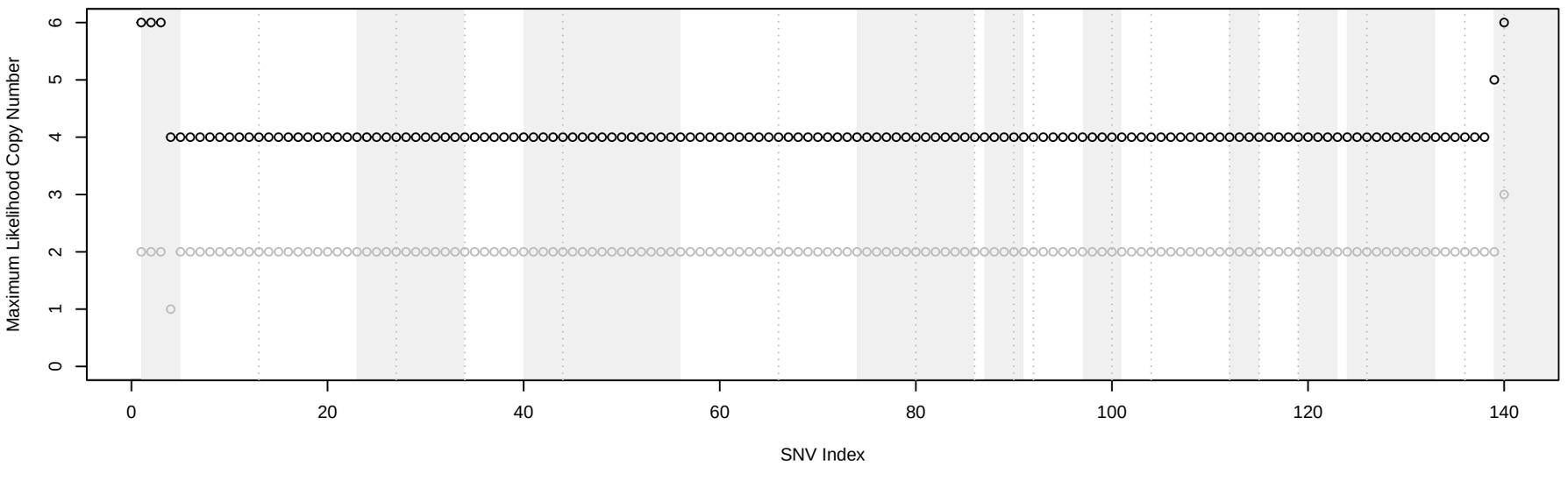

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0m1
1m1
2m1
3m1
4m1
5m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

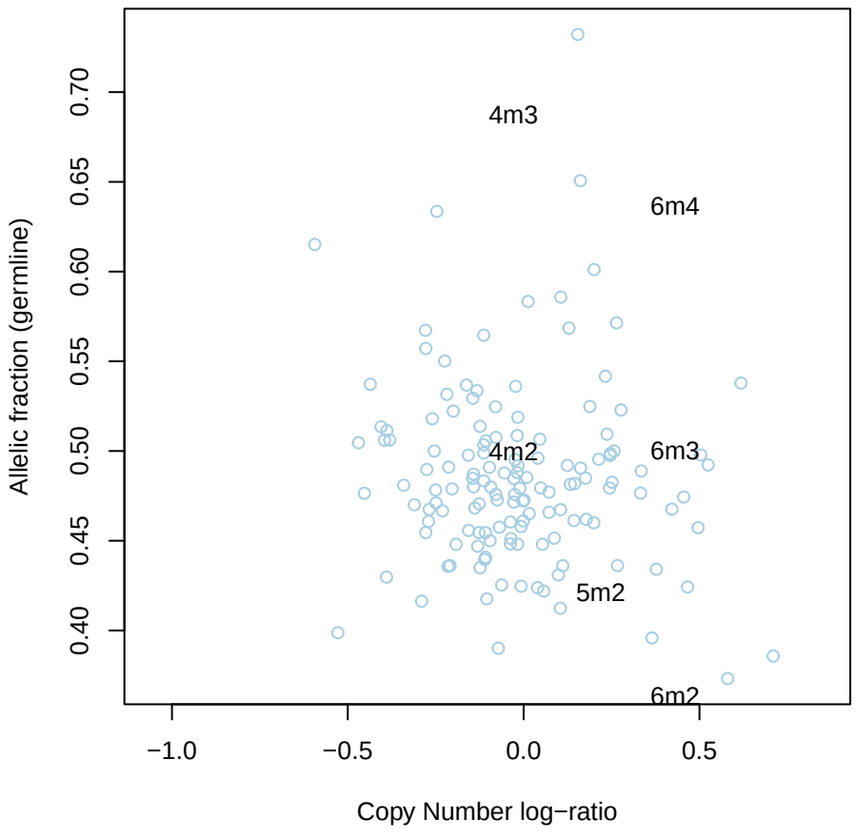

Power 0.8
Frequency
0
10
20
30
40
50
60
0.2
0.4
0.6
0.8
1.0
Cellular fraction

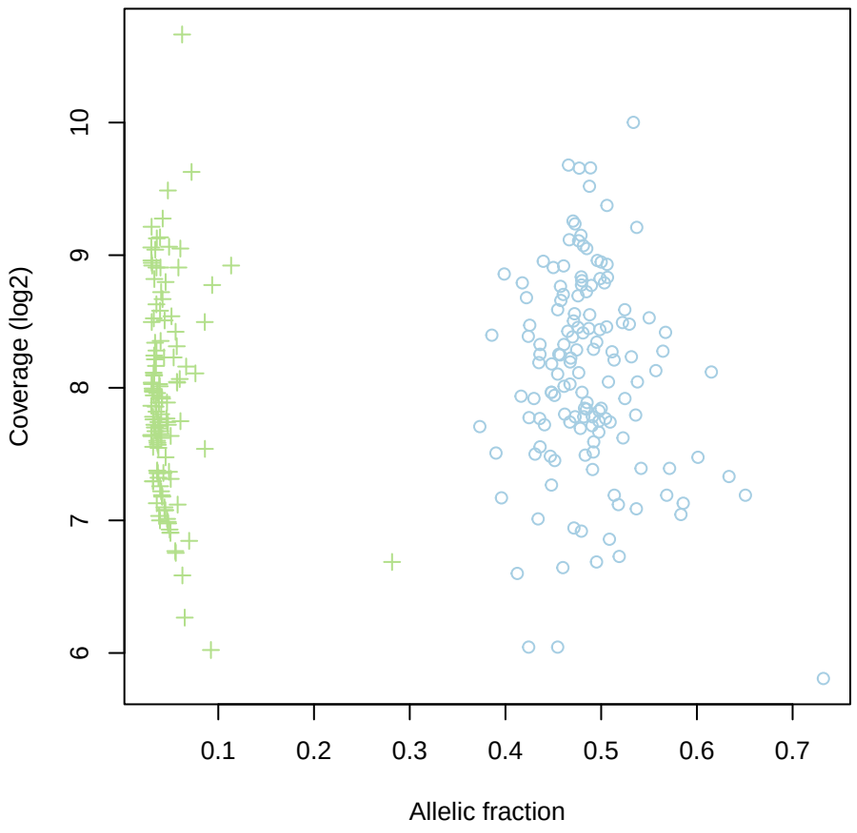

Purity: 0.6 Tumor ploidy: 4.106
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

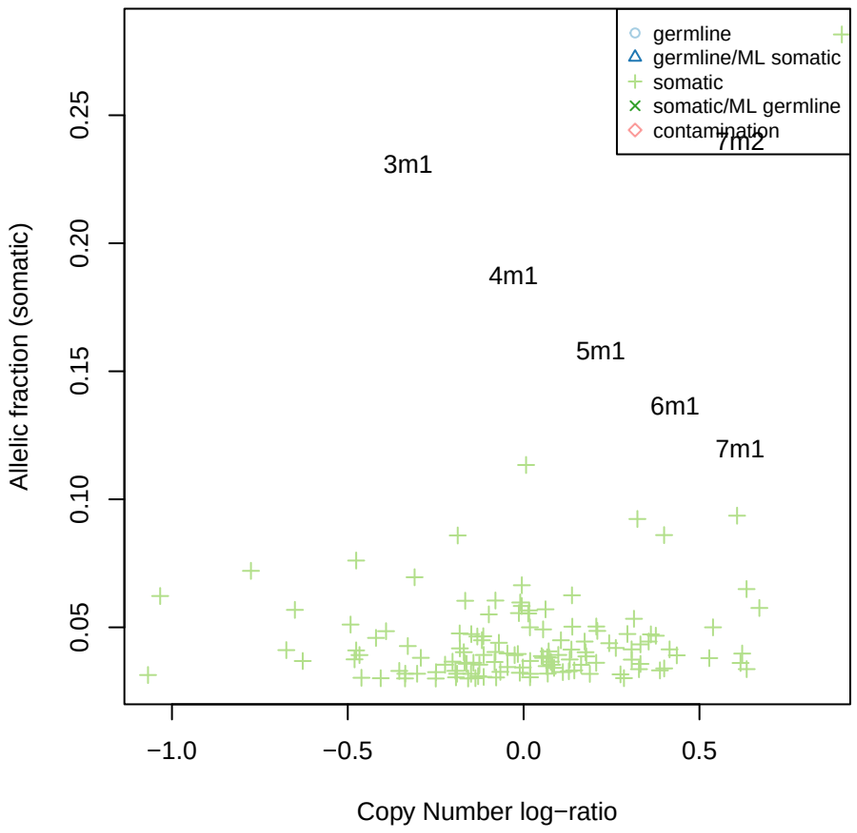

Purity: 0.6 Tumor ploidy: 4.106 SNV log−likelihood: −101.29 GoF: 71% Mean coverage: 488;296
1 2 3 4 5 6 7 8 10 11 12 13 15 17 19
B−Allele Frequency
0.40 0.50 0.60 0.70
0 20 40 60 80 100 120 140
SNV Index

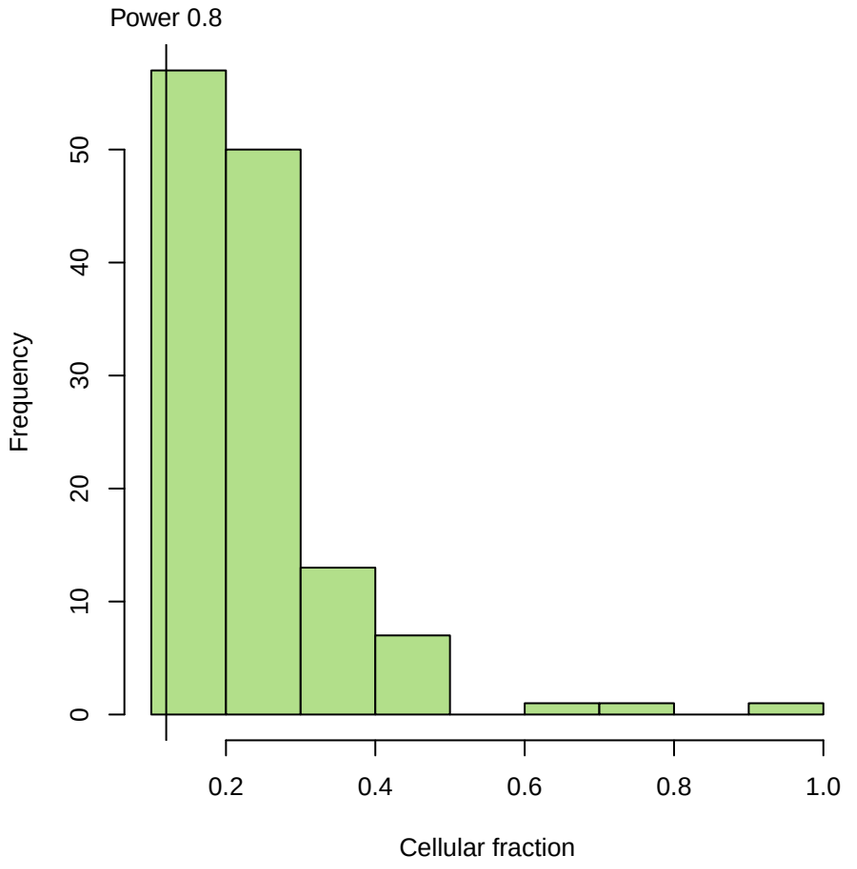

SCNA−fit log−likelihood: −5078.86
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 7
0 20 40 60 80 100 120 140
SNV Index

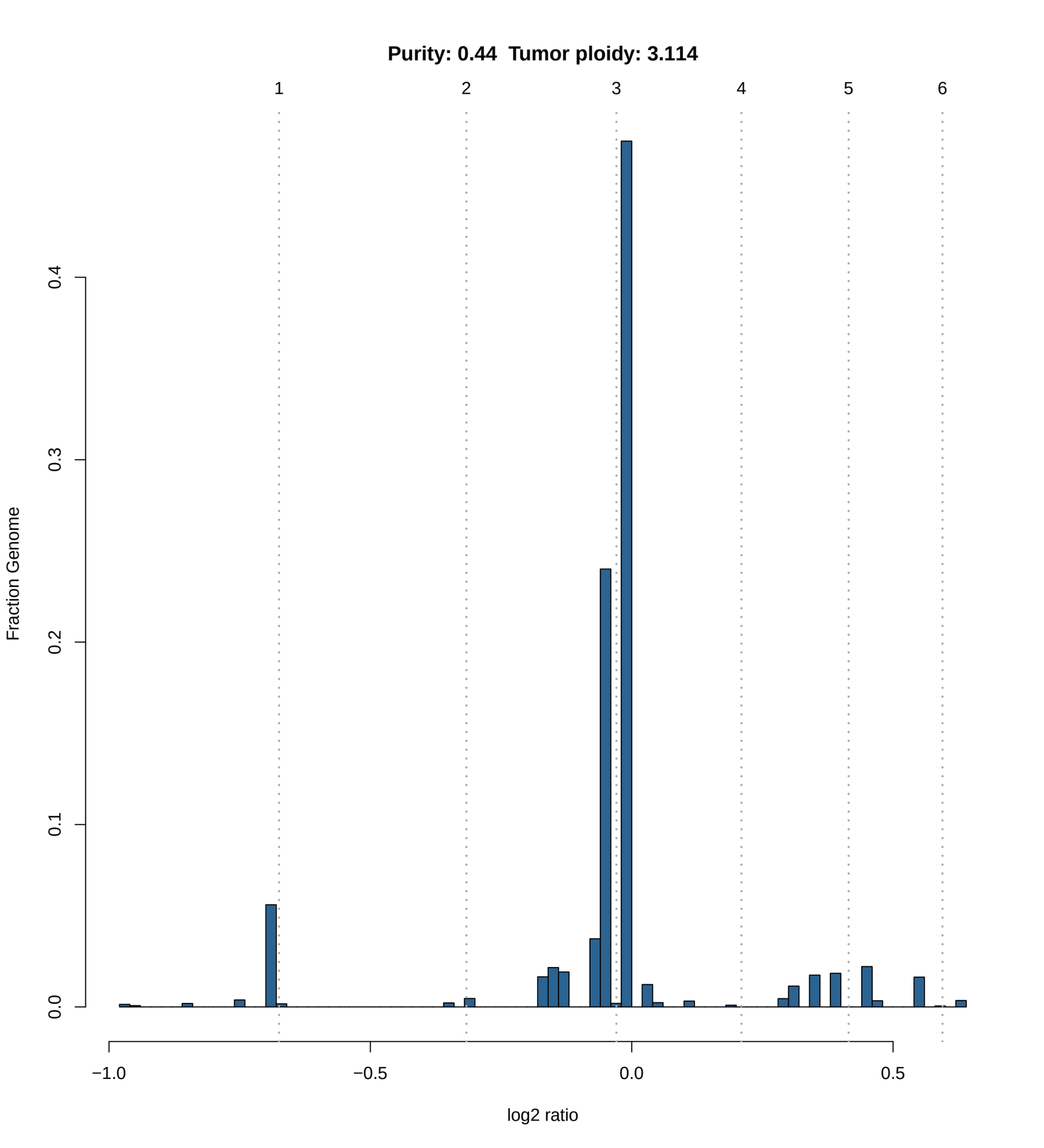

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

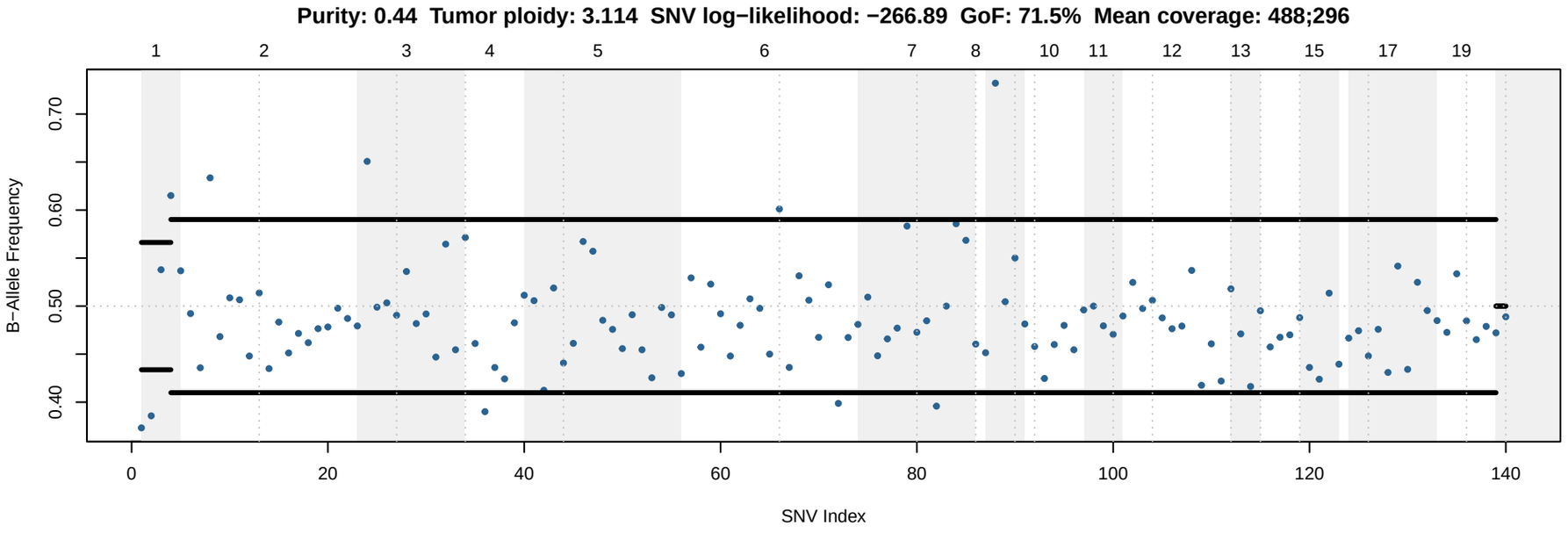

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
0.70
4m3
6m4
4m2
6m3
5m2
6m2
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

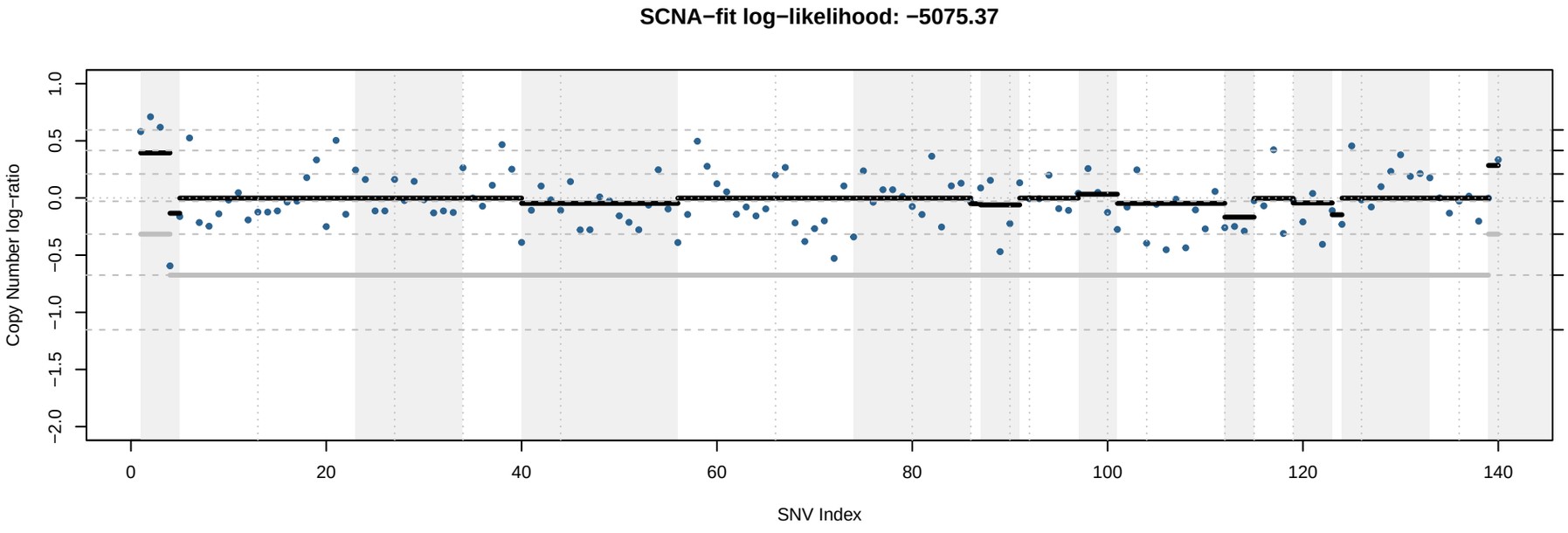

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

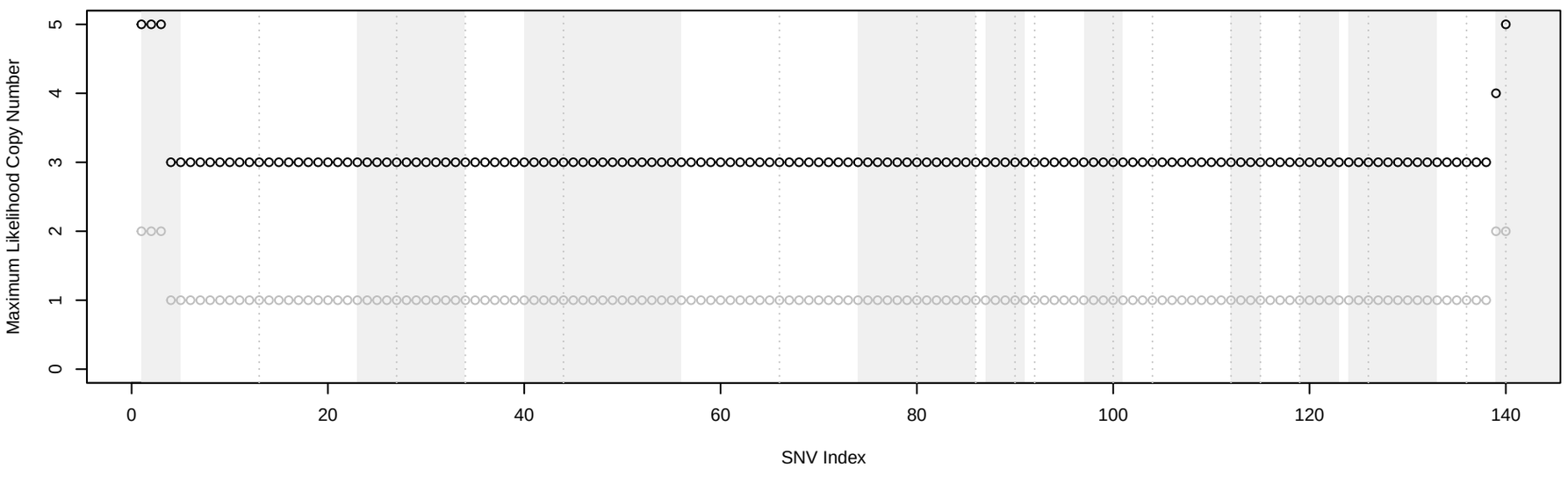

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
7m2
3m1
4m1
5m1
6m1
7m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

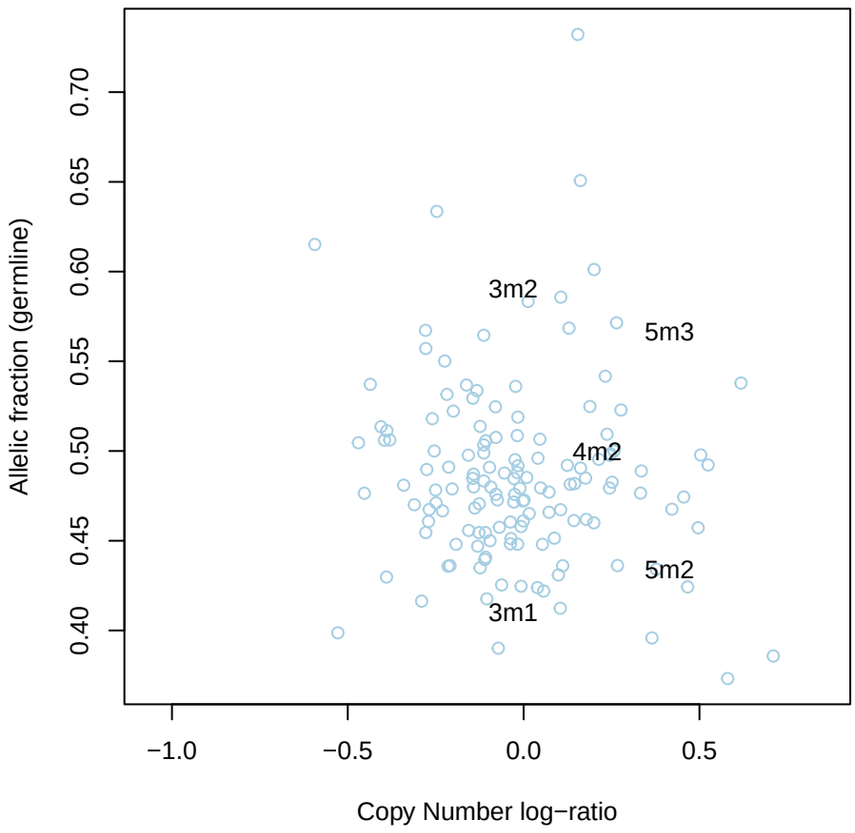

Power 0.8
Frequency
0
10
20
30
40
50
0.2
0.4
0.6
0.8
1.0
Cellular fraction

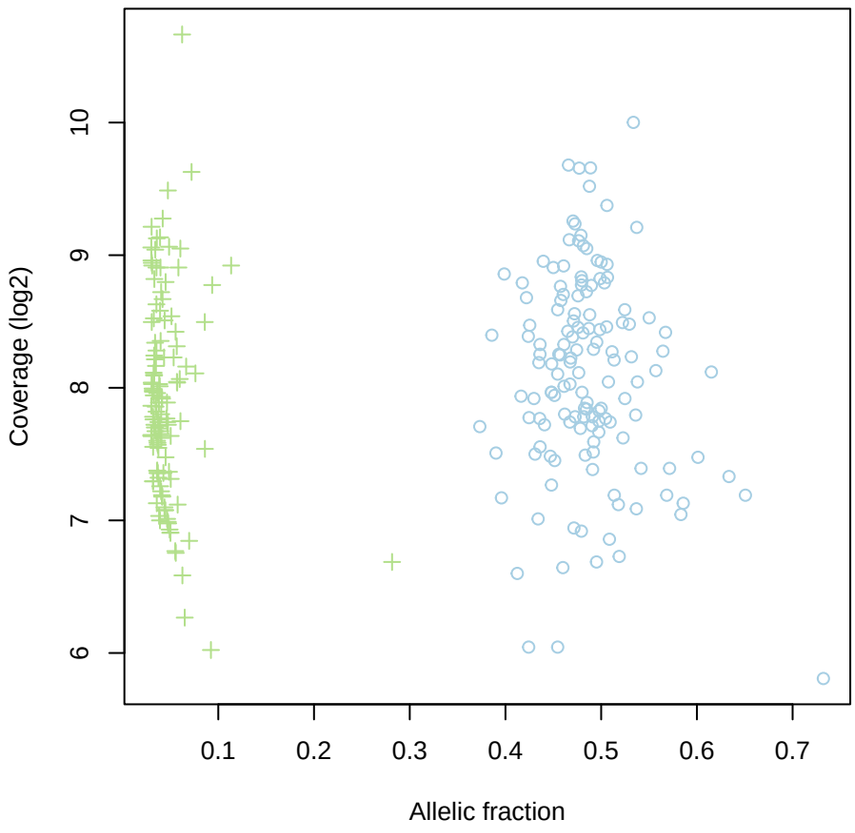

Purity: 0.44 Tumor ploidy: 3.114
1
2
3
4
5
6
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

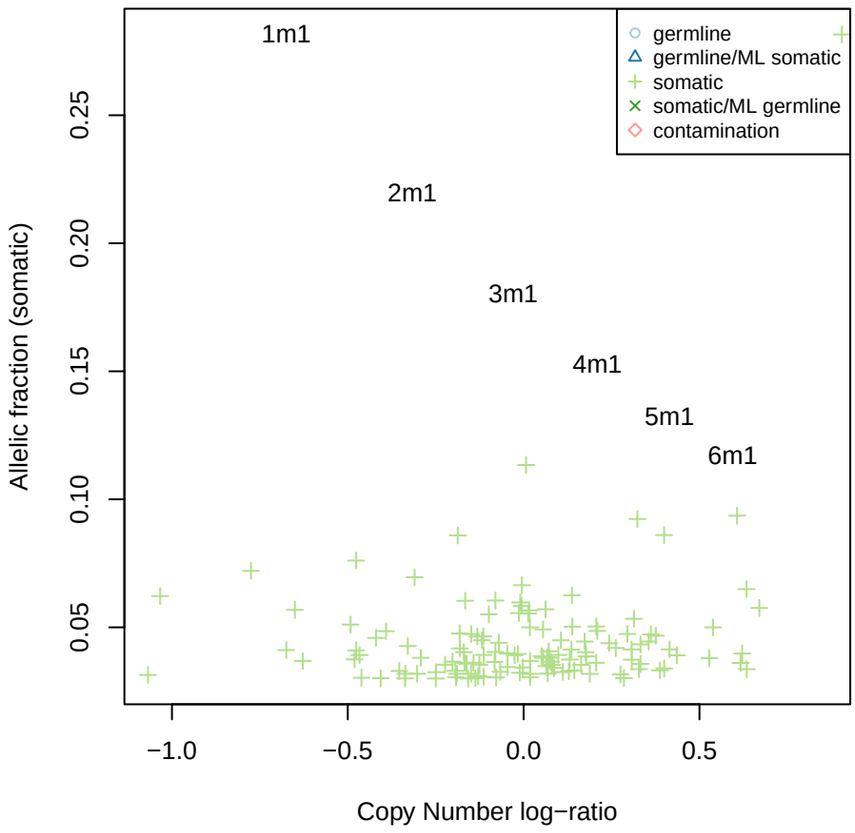

Purity: 0.44 Tumor ploidy: 3.114 SNV log−likelihood: −266.89 GoF: 71.5% Mean coverage: 488;296
1 2 3 4 5 6 7 8 10 11 12 13 15 17 19
B−Allele Frequency
0.40 0.50 0.60 0.70
0 20 40 60 80 100 120 140
SNV Index

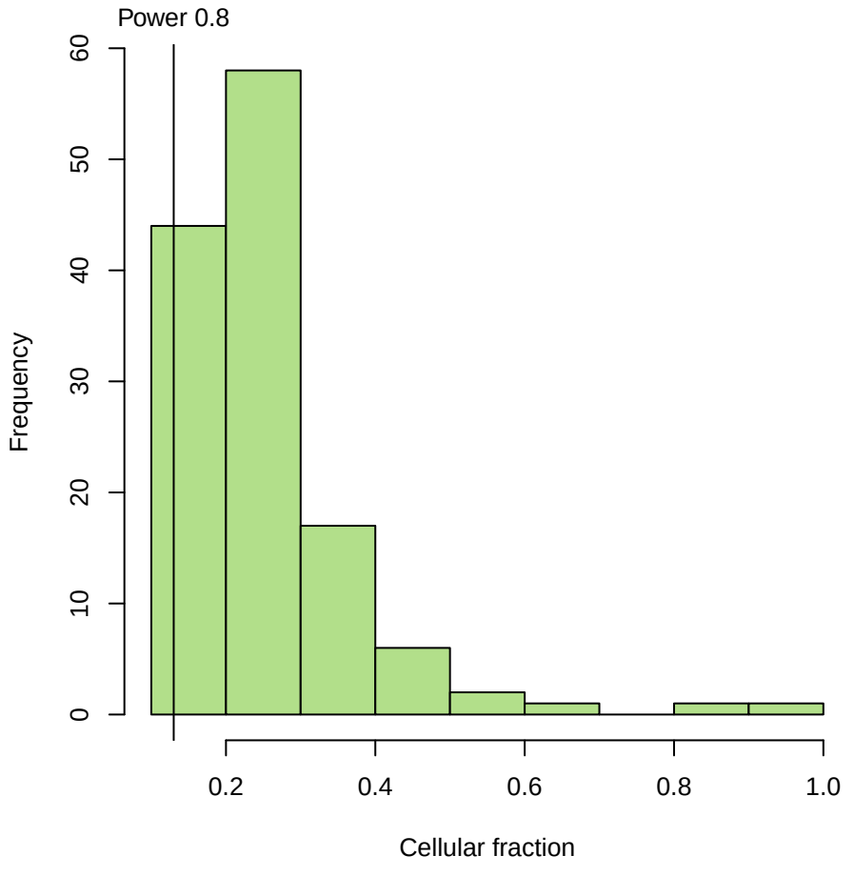

SCNA−fit log−likelihood: −5075.37
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

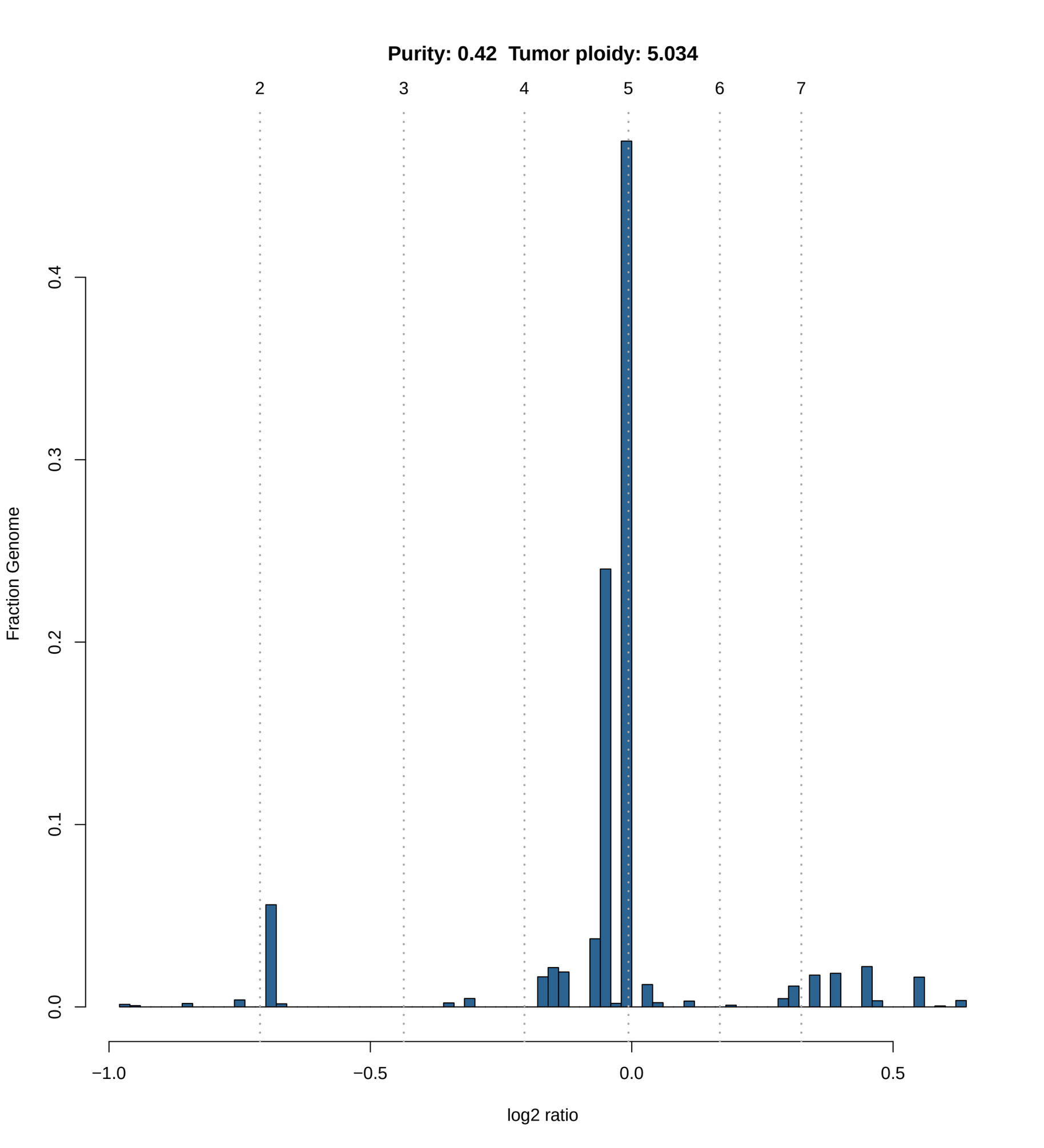

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

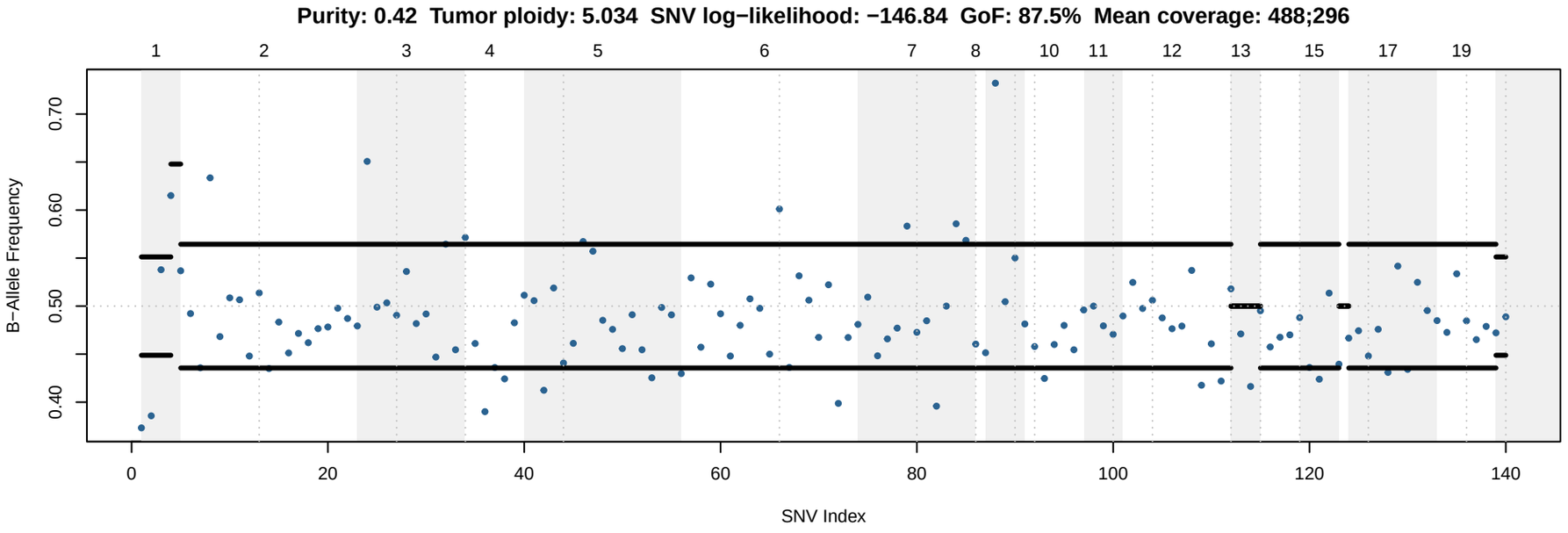

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
0.70
3m2
5m3
4m2
5m2
3m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

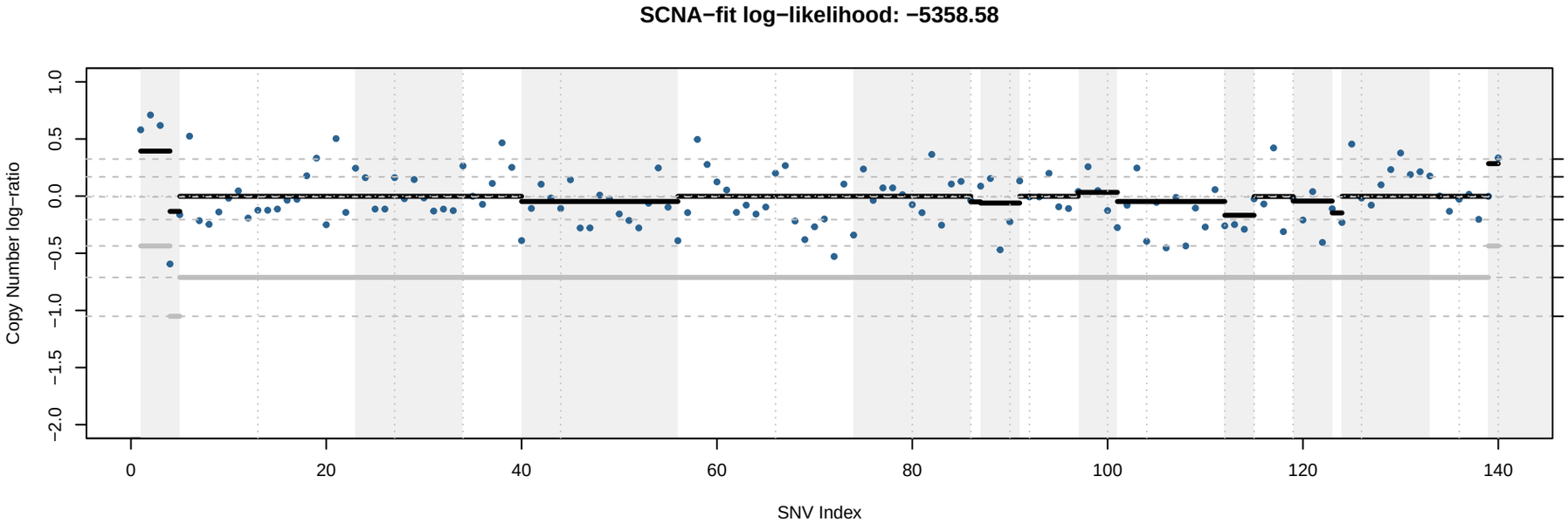

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

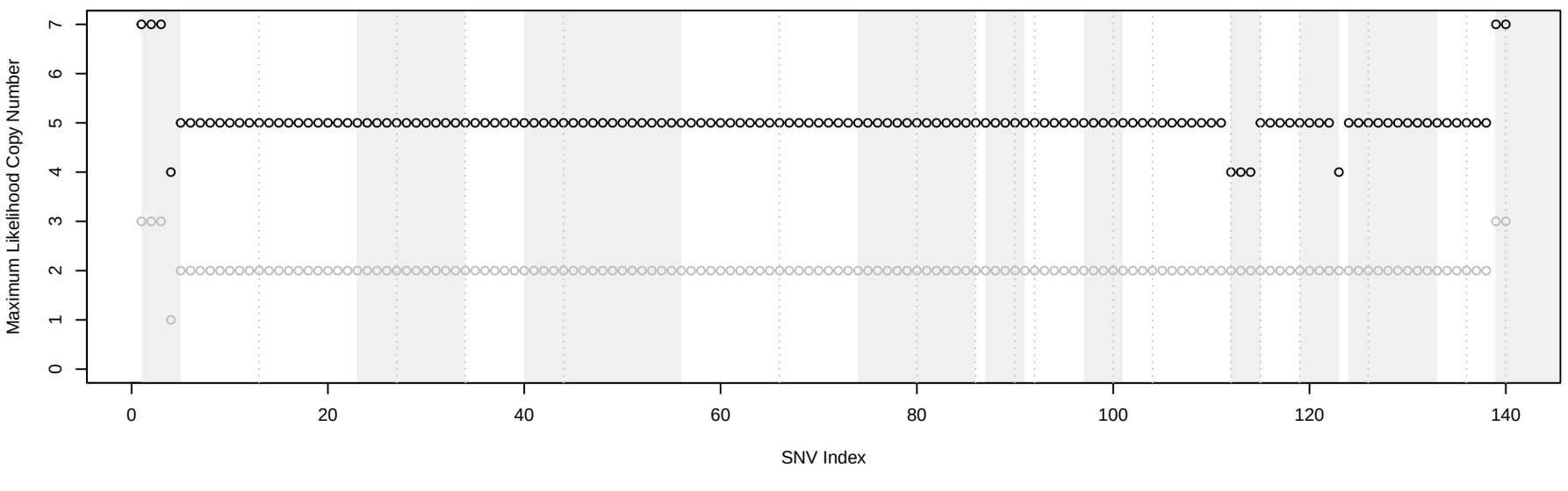

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
1m1
2m1
3m1
4m1
5m1
6m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

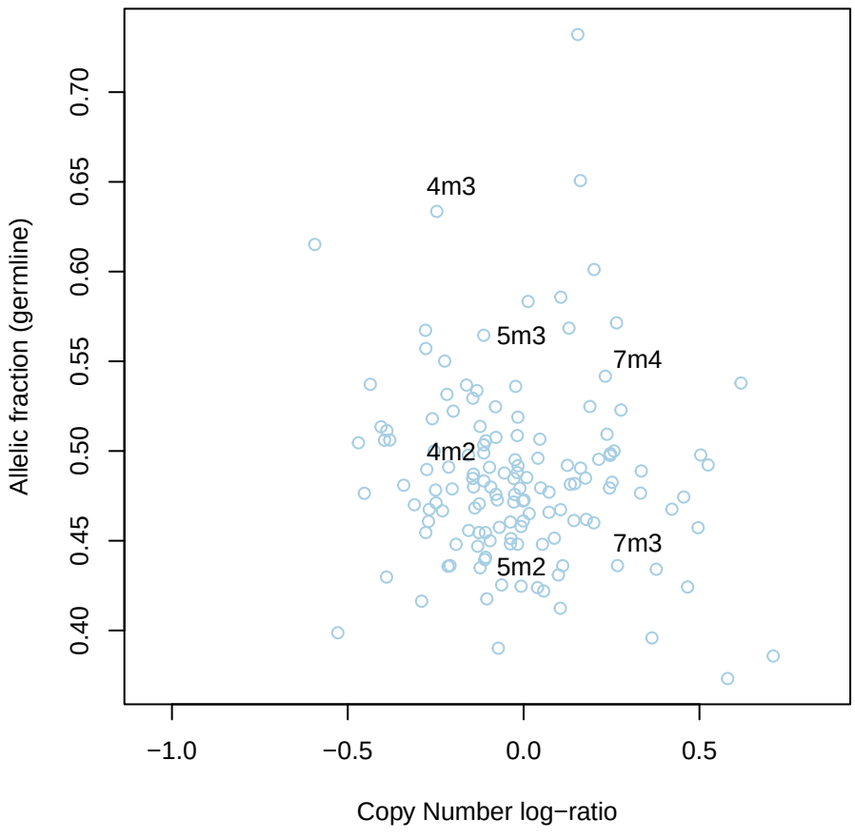

Power 0.8
Frequency
0
10
20
30
40
50
60
0.2
0.4
0.6
0.8
1.0
Cellular fraction

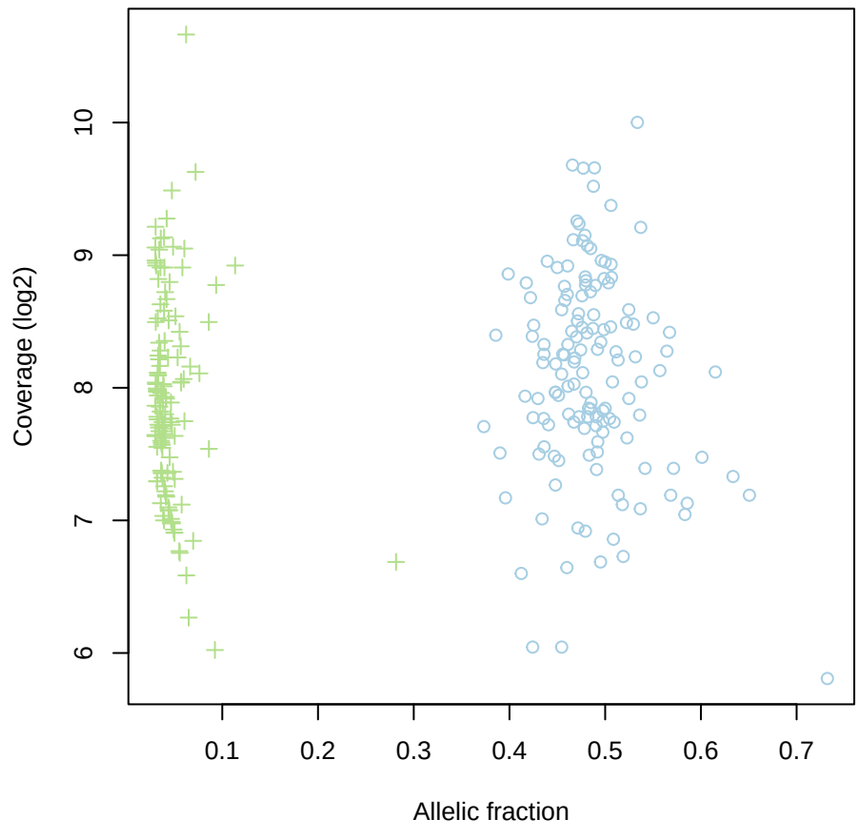

Purity: 0.42 Tumor ploidy: 5.034
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

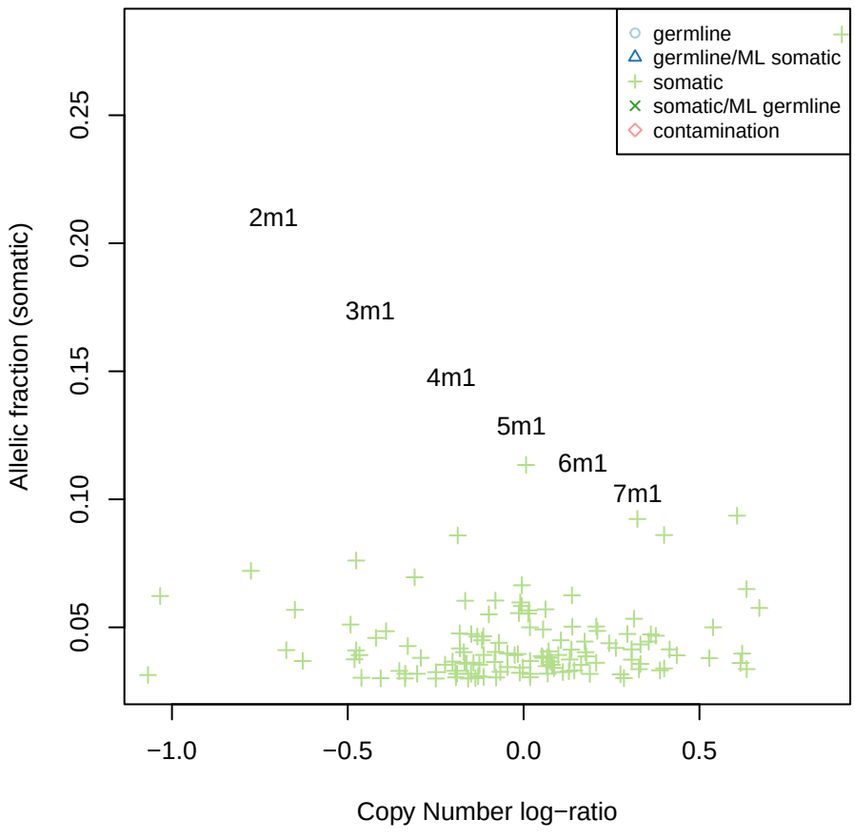

Purity: 0.42 Tumor ploidy: 5.034 SNV log−likelihood: −146.84 GoF: 87.5% Mean coverage: 488;296
1 2 3 4 5 6 7 8 10 11 12 13 15 17 19
B−Allele Frequency
0.40 0.50 0.60 0.70
0 20 40 60 80 100 120 140
SNV Index

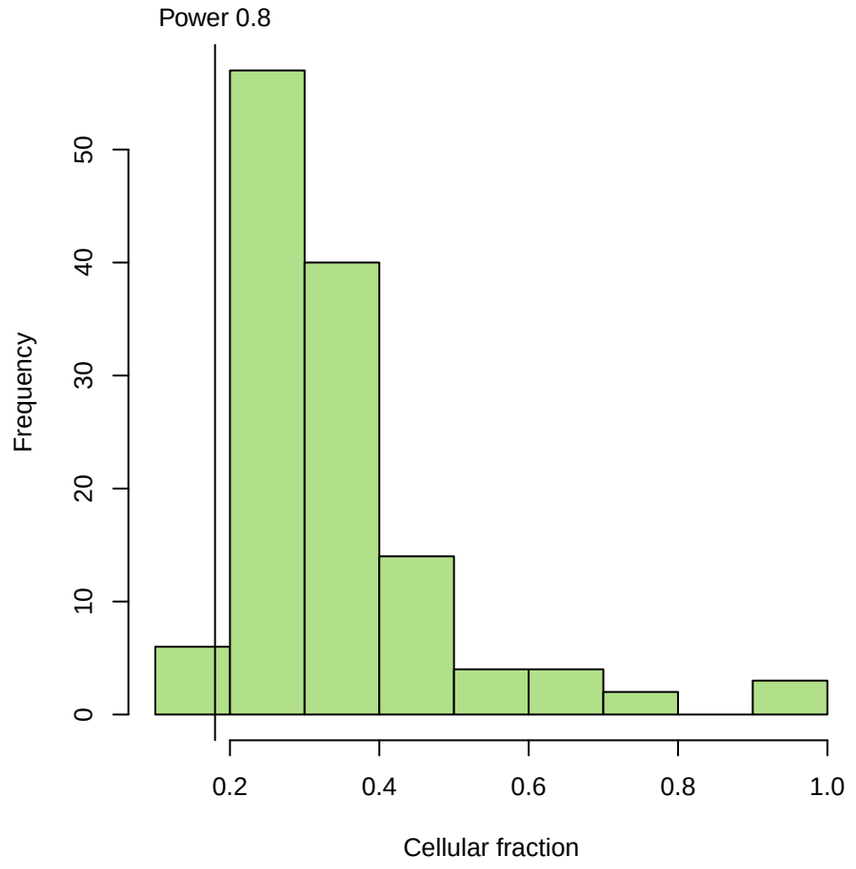

SCNA−fit log−likelihood: −5358.58
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
1 2 3 4 6
0 20 40 60 80 100 120 140
SNV Index

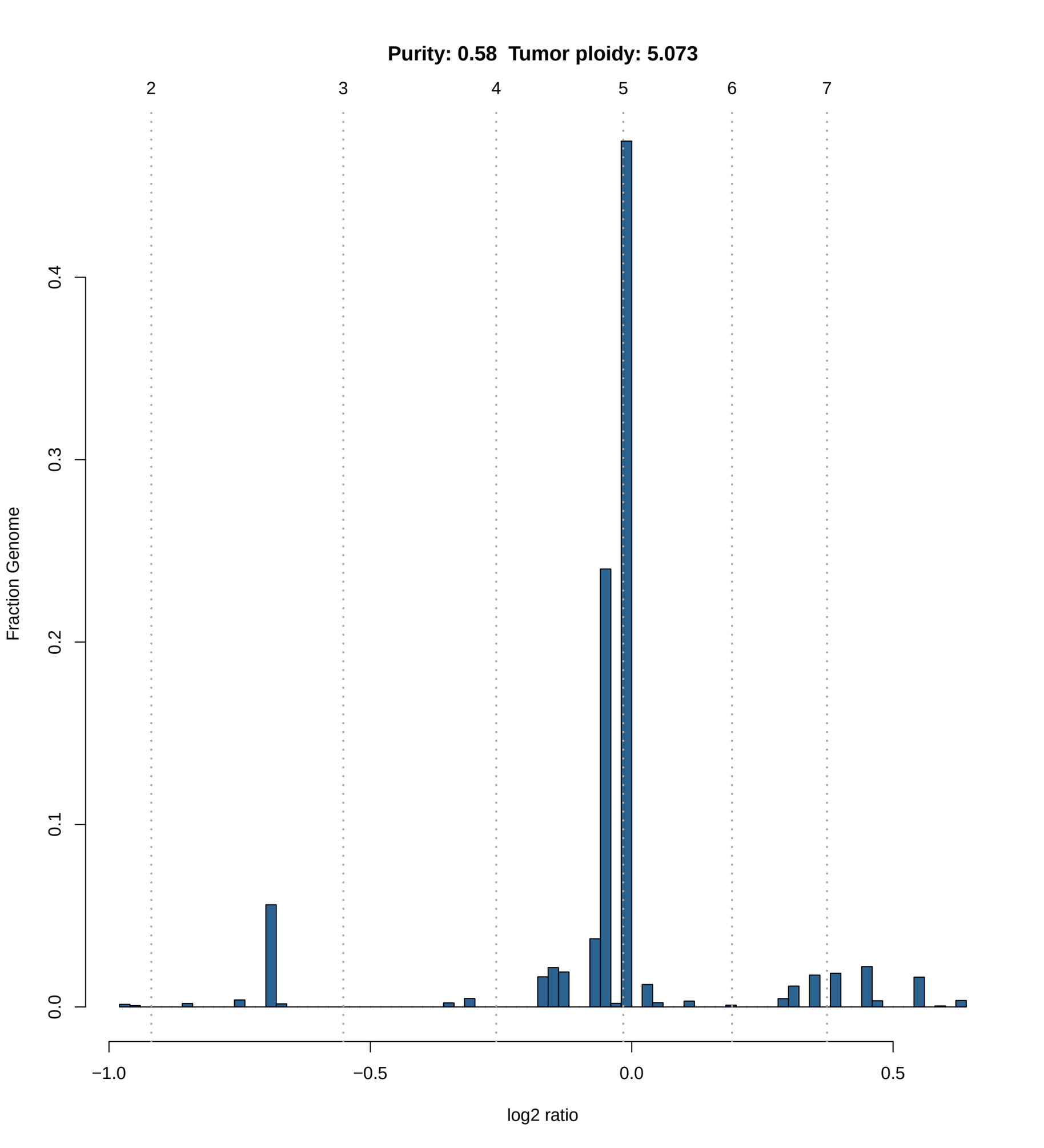

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

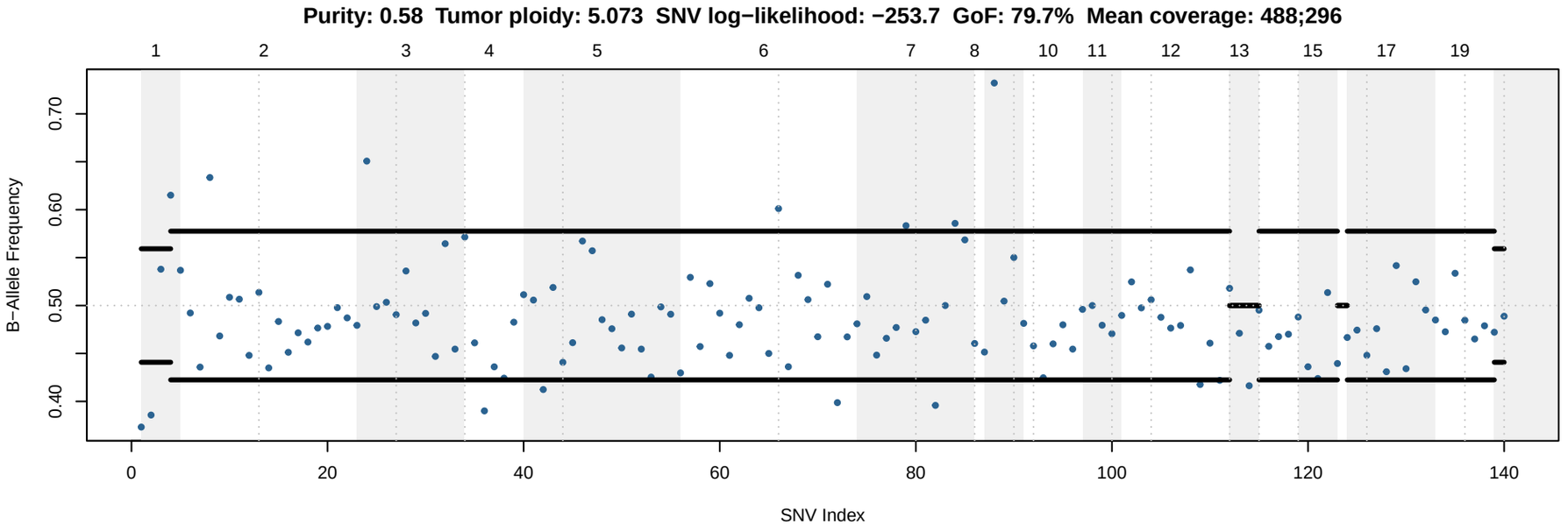

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
0.70
4m3
5m3
7m4
4m2
7m3
5m2
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

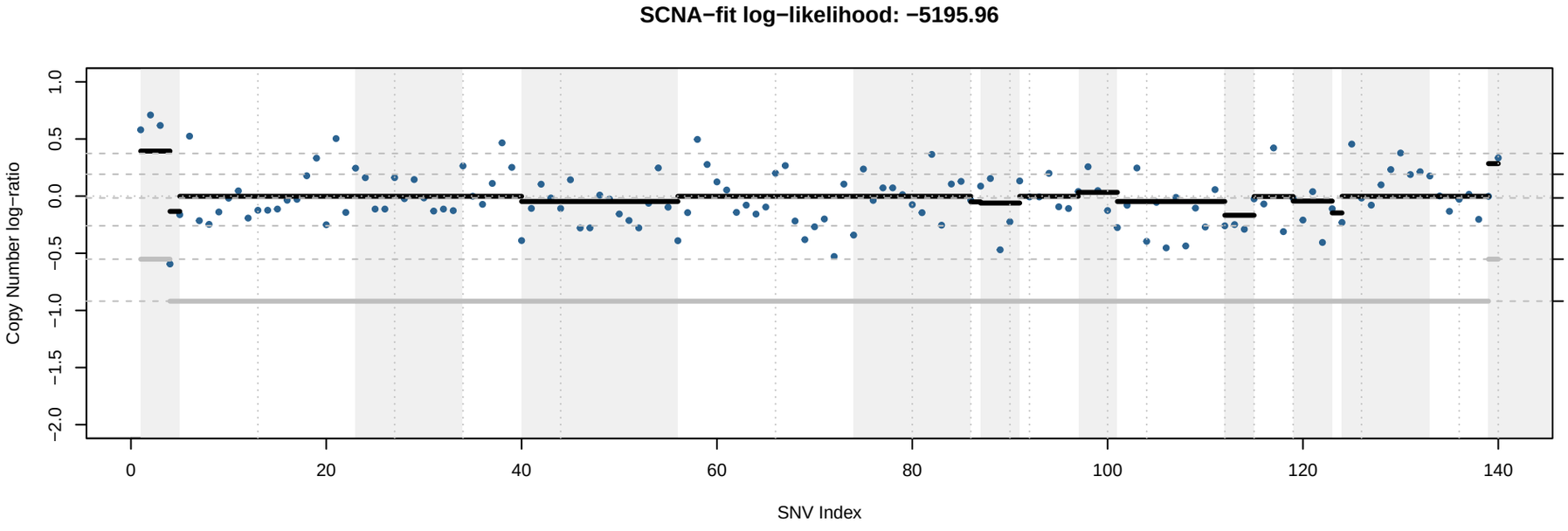

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

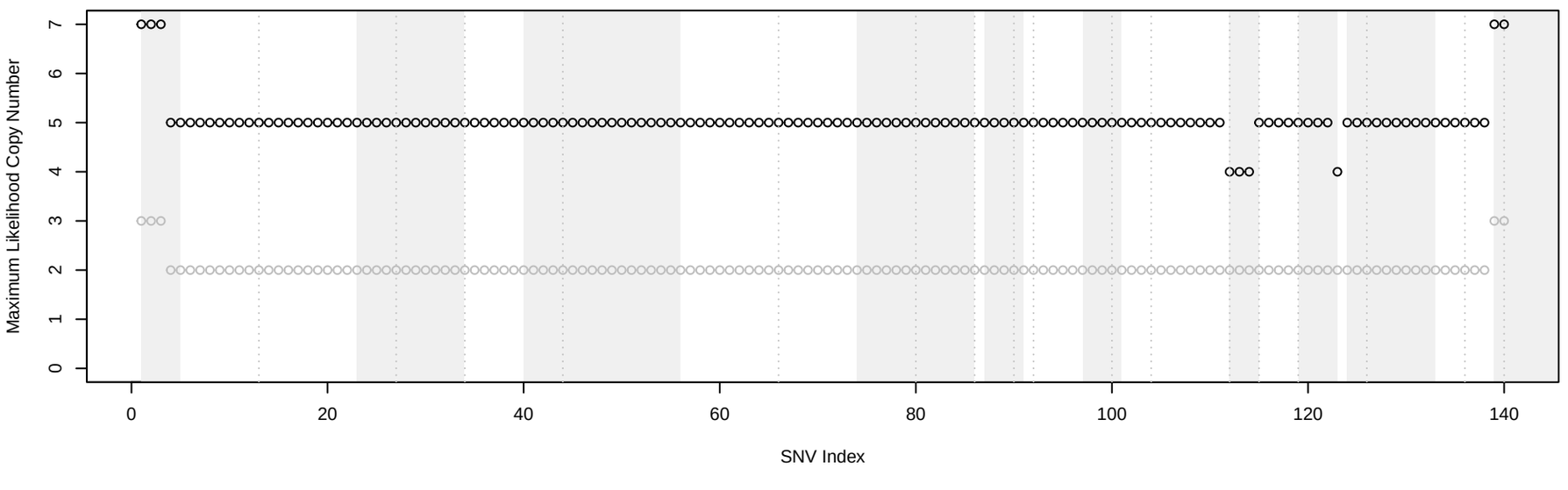

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
2m1
3m1
4m1
5m1
6m1
7m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

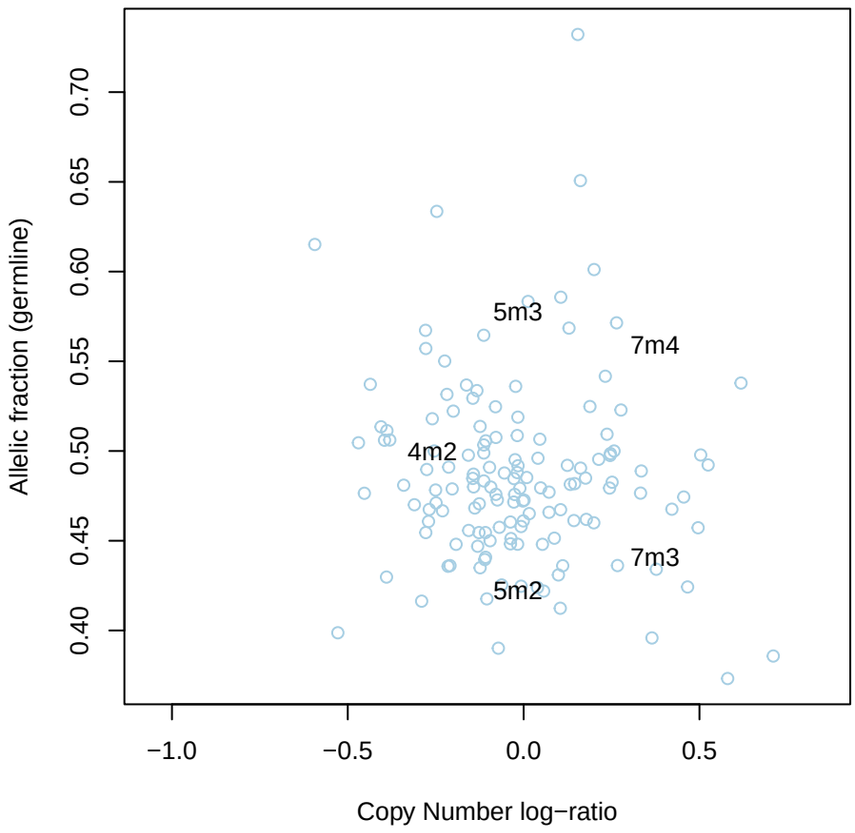

Power 0.8
Frequency
0
10
20
30
40
50
0.2
0.4
0.6
0.8
1.0
Cellular fraction

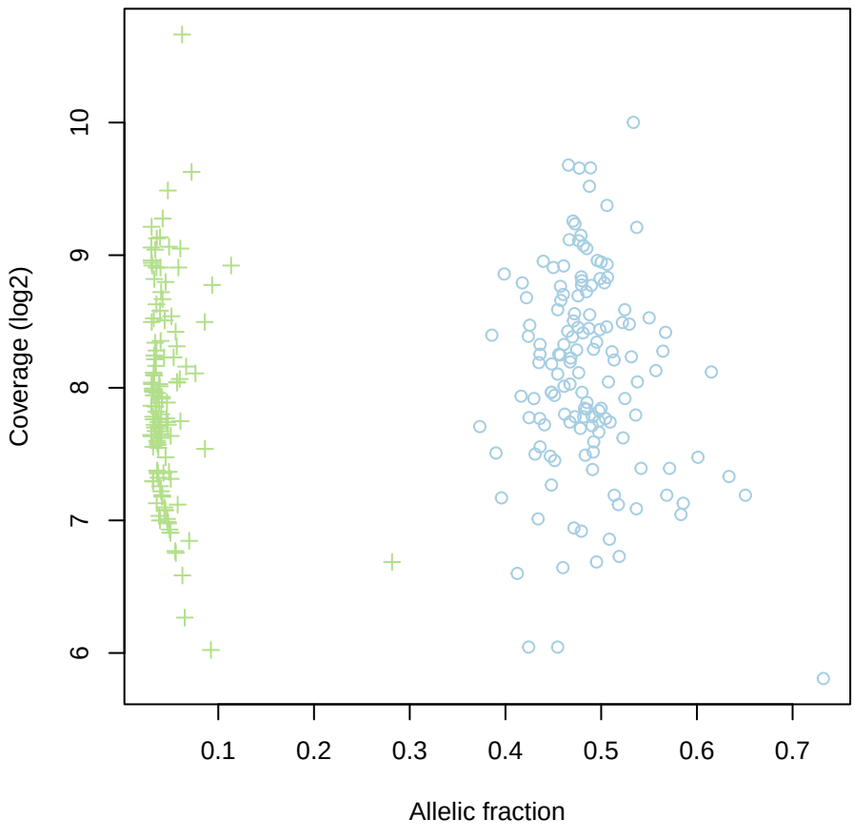

Purity: 0.58 Tumor ploidy: 5.073
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

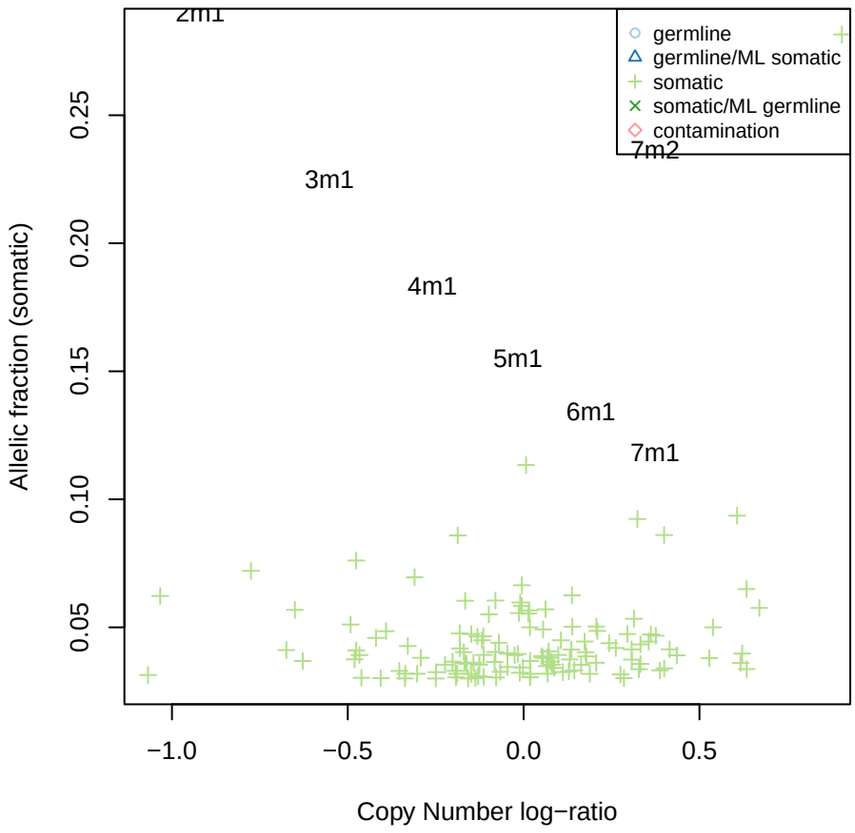

Purity: 0.58 Tumor ploidy: 5.073 SNV log−likelihood: −253.7 GoF: 79.7% Mean coverage: 488;296
1 2 3 4 5 6 7 8 10 11 12 13 15 17 19
B−Allele Frequency
0.40 0.50 0.60 0.70
0 20 40 60 80 100 120 140
SNV Index

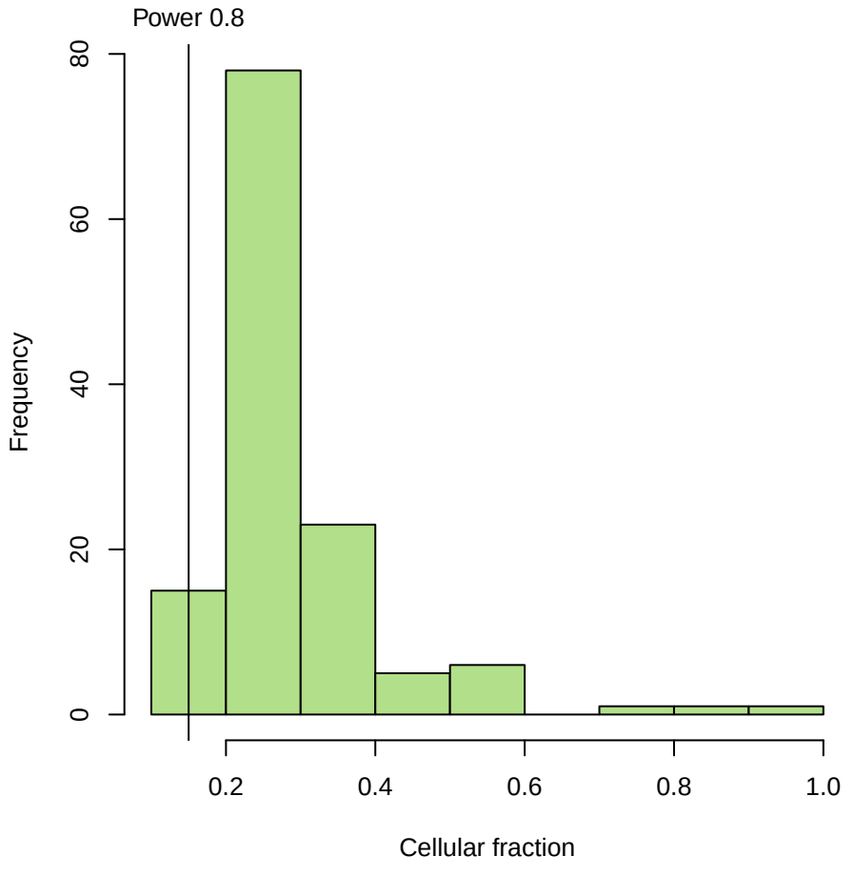

SCNA−fit log−likelihood: −5195.96
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
2 3 4 5 7
0 20 40 60 80 100 120 140
SNV Index

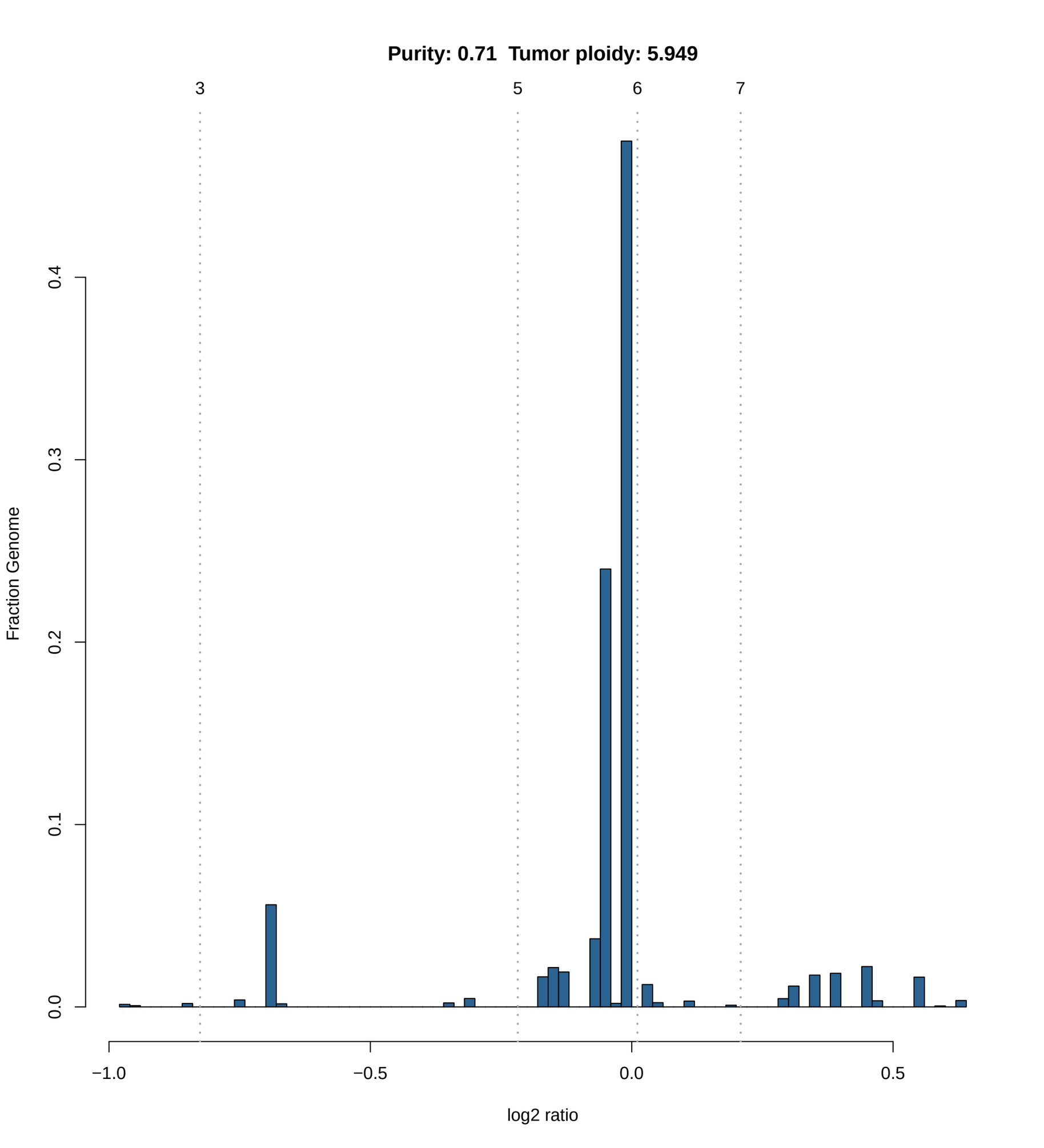

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

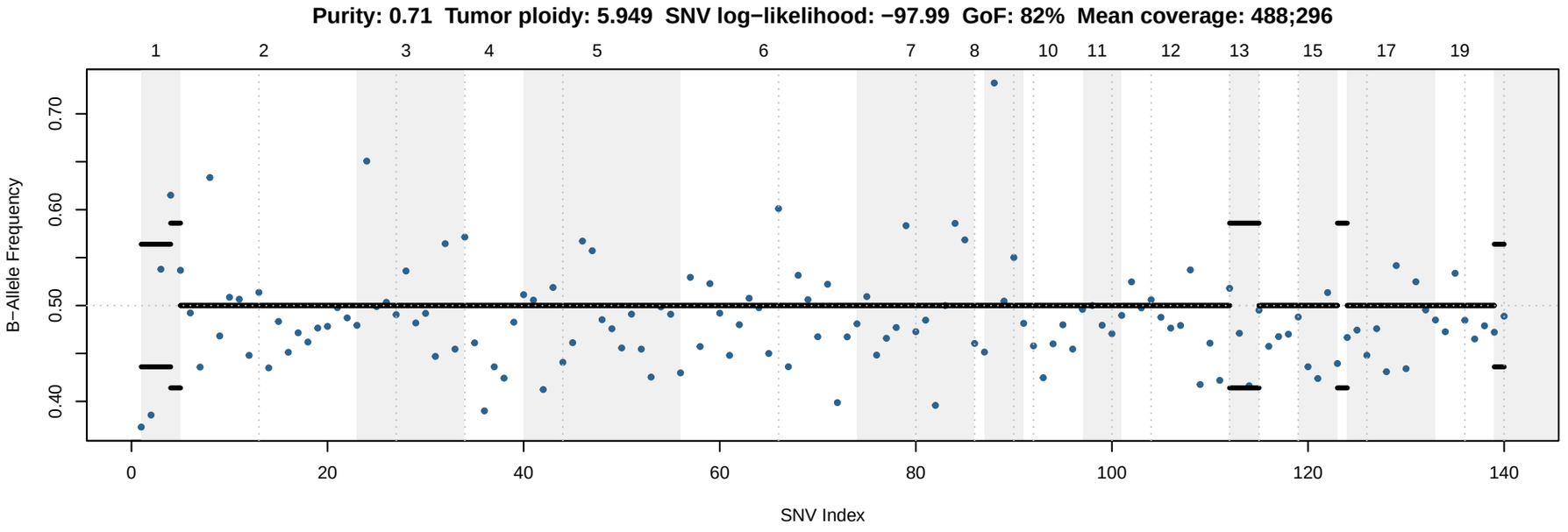

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
0.70
5m3
7m4
4m2
7m3
5m2
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

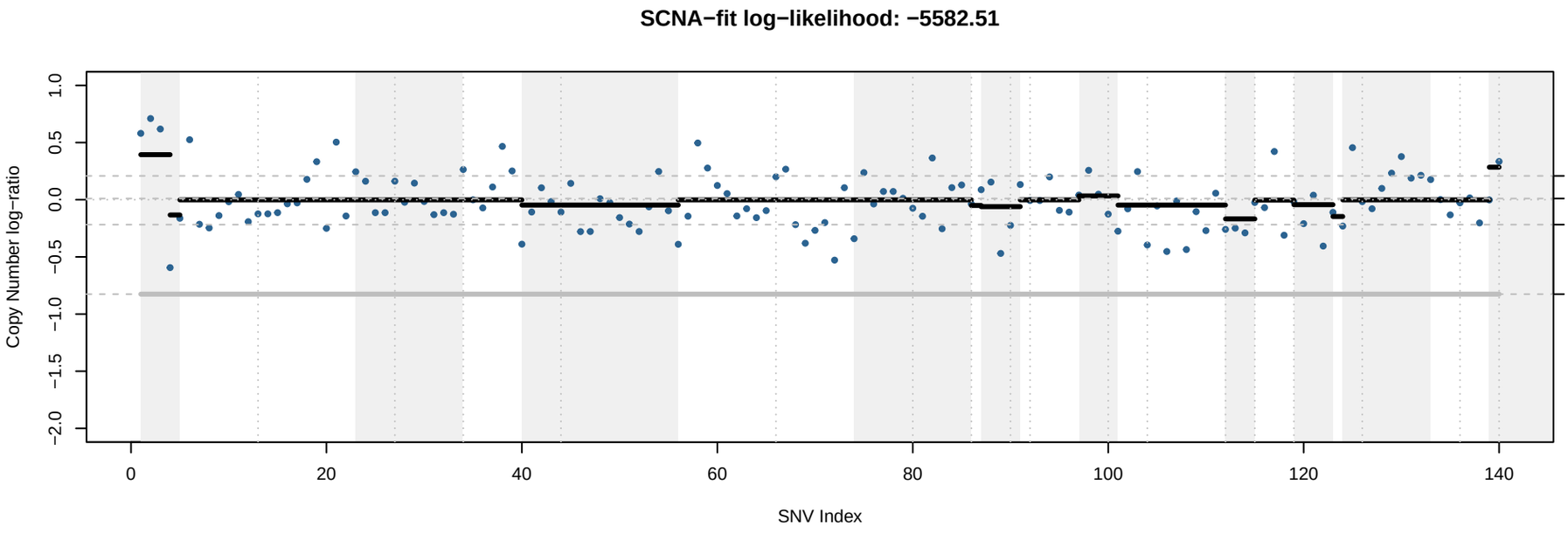

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

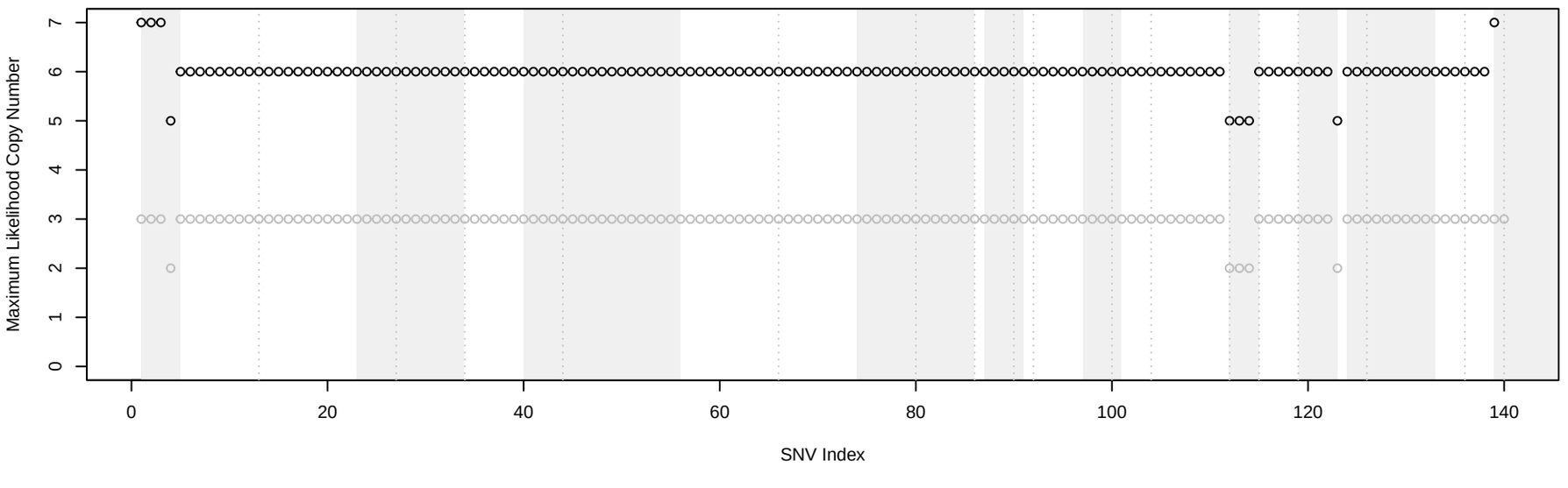

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
2m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
7m2
3m1
4m1
5m1
6m1
7m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio


Power 0.8
Frequency
0
20
40
60
80
0.2
0.4
0.6
0.8
1.0
Cellular fraction

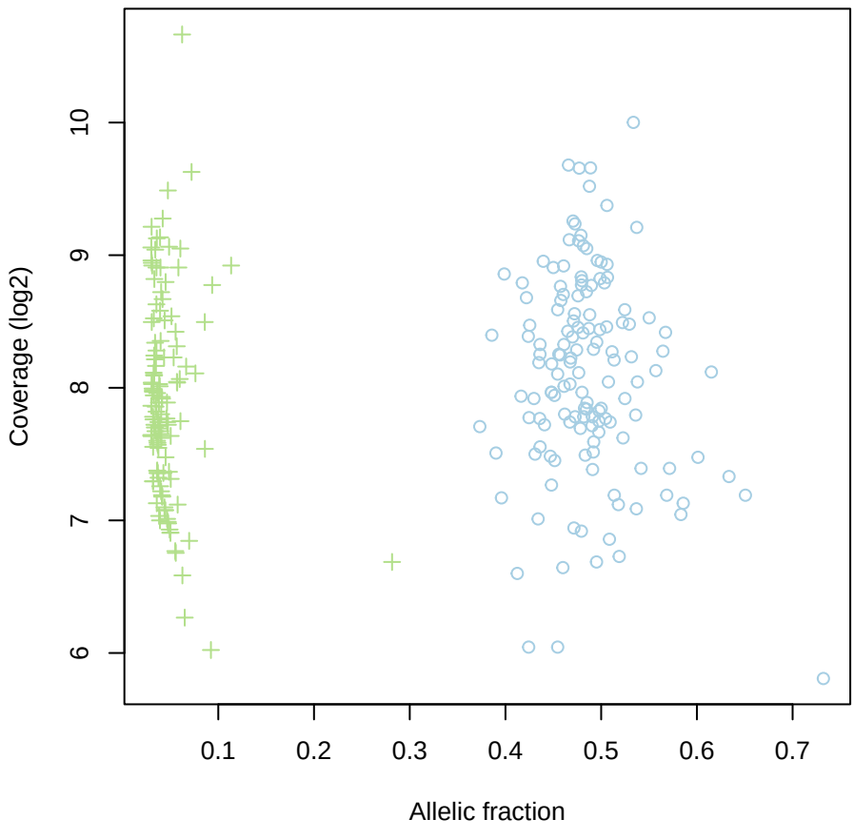

Purity: 0.71 Tumor ploidy: 5.949
3
5
6
7
Fraction Genome
0.0
0.1
0.2
0.3
0.4
−1.0
−0.5
0.0
0.5
log2 ratio

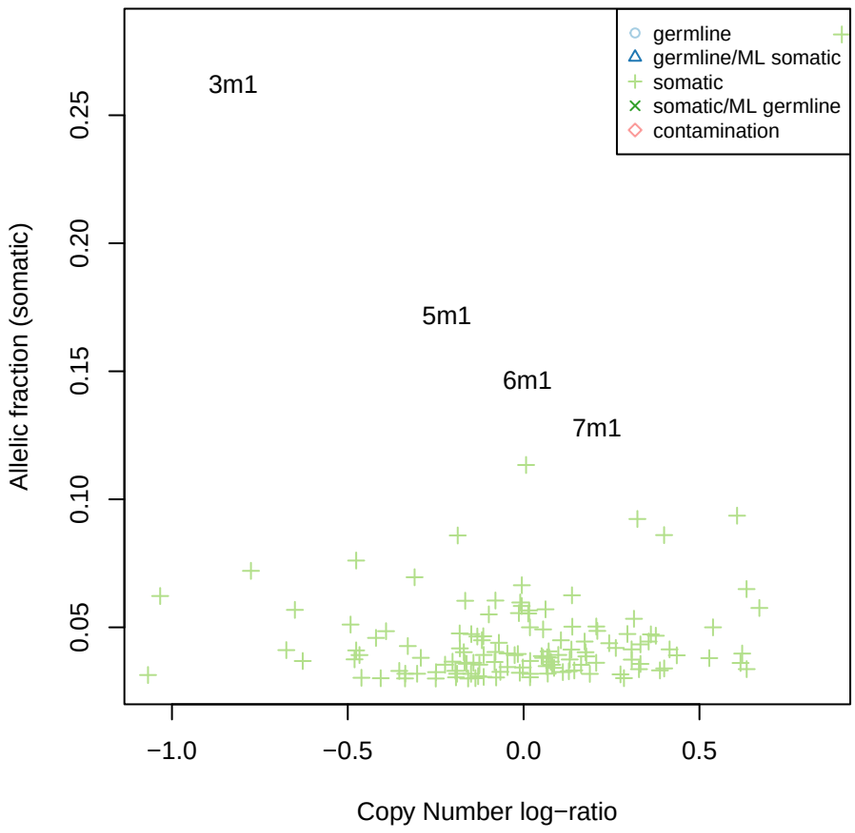

Purity: 0.71 Tumor ploidy: 5.949 SNV log−likelihood: −97.99 GoF: 82% Mean coverage: 488;296
1 2 3 4 5 6 7 8 10 11 12 13 15 17 19
B−Allele Frequency
0.40 0.50 0.60 0.70
0 20 40 60 80 100 120 140
SNV Index

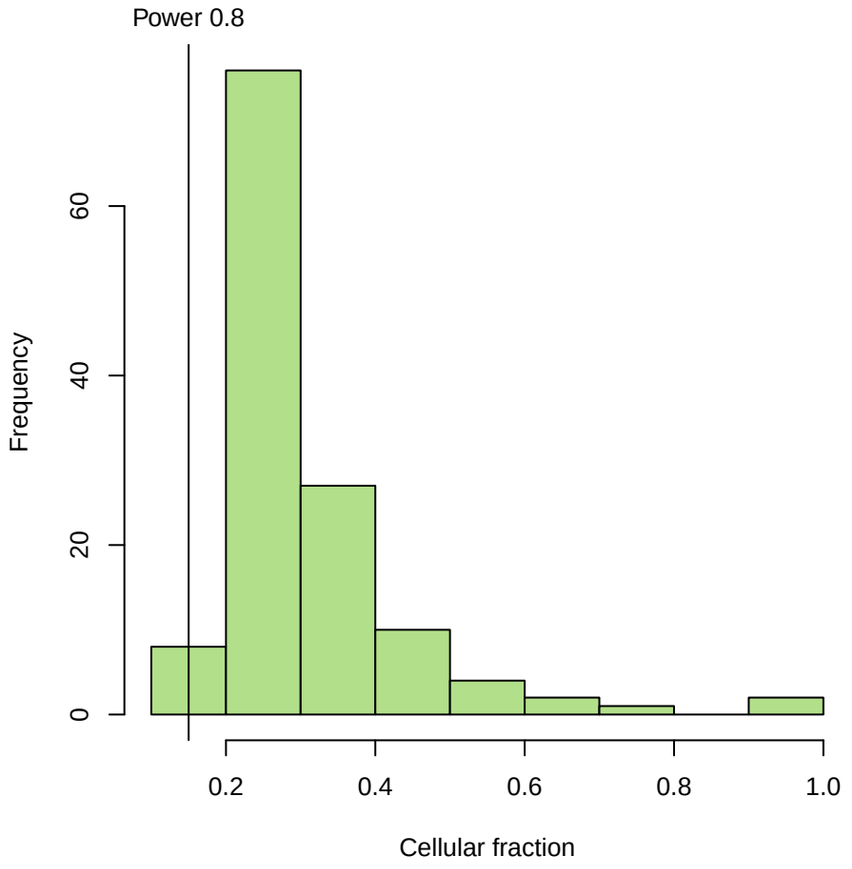

SCNA−fit log−likelihood: −5582.51
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
3 5 6
0 20 40 60 80 100 120 140
SNV Index

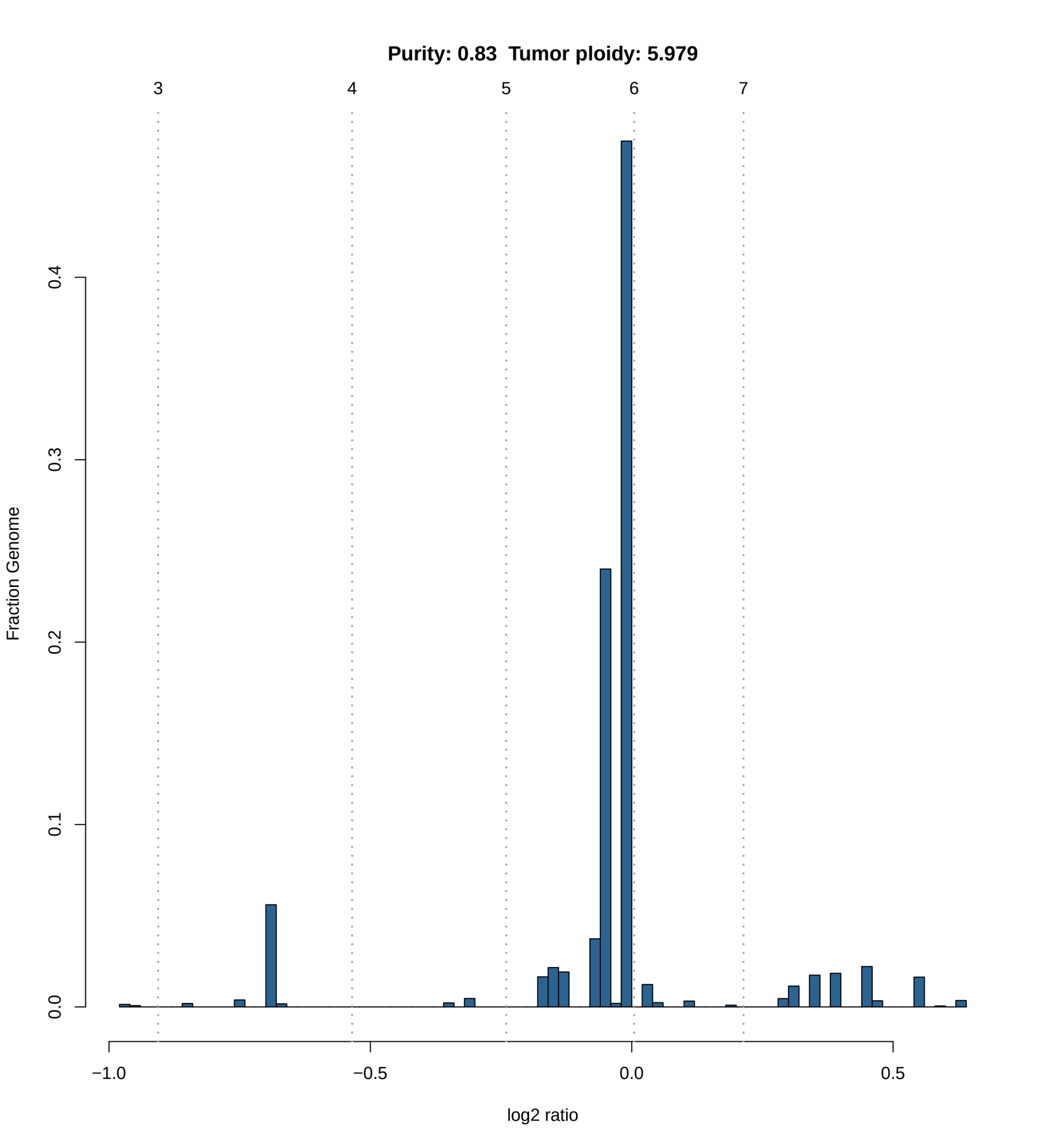

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

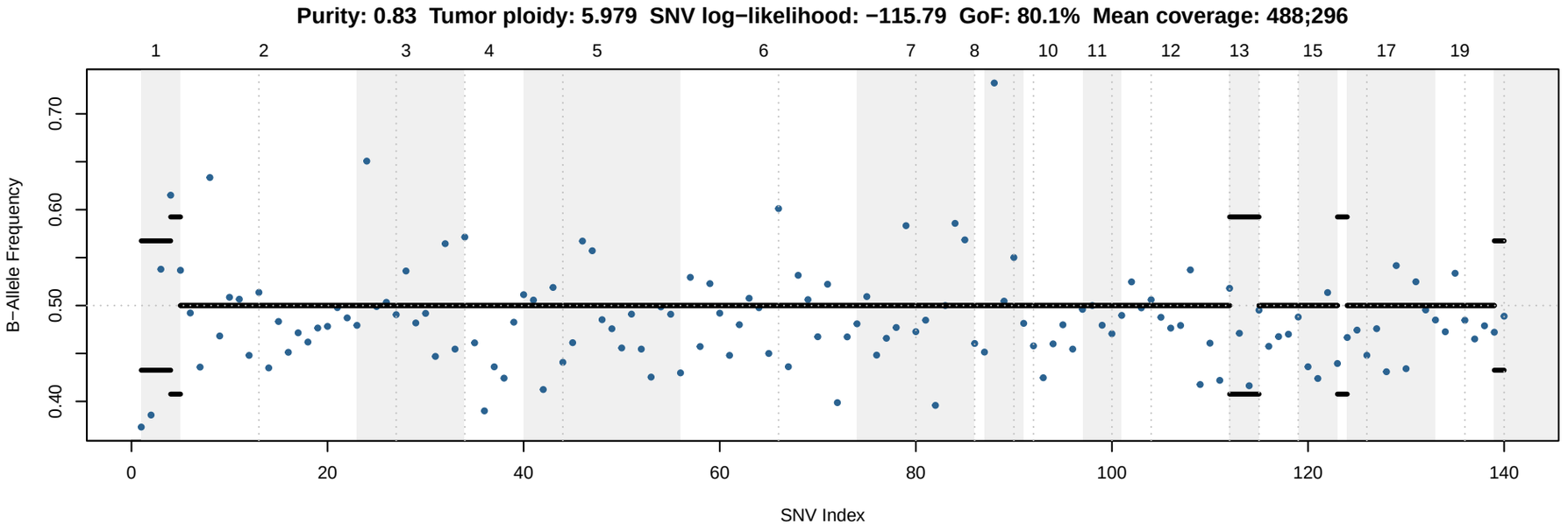
Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
0.70
6m4
5m3
7m4
6m3
7m3
5m2
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

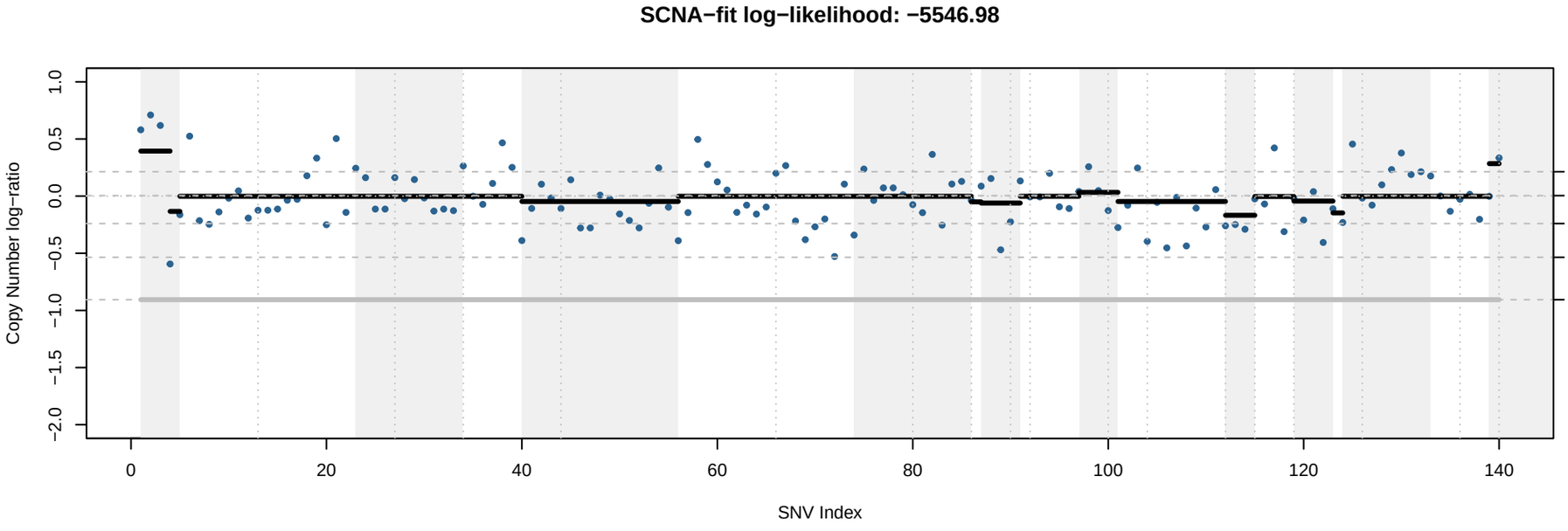

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

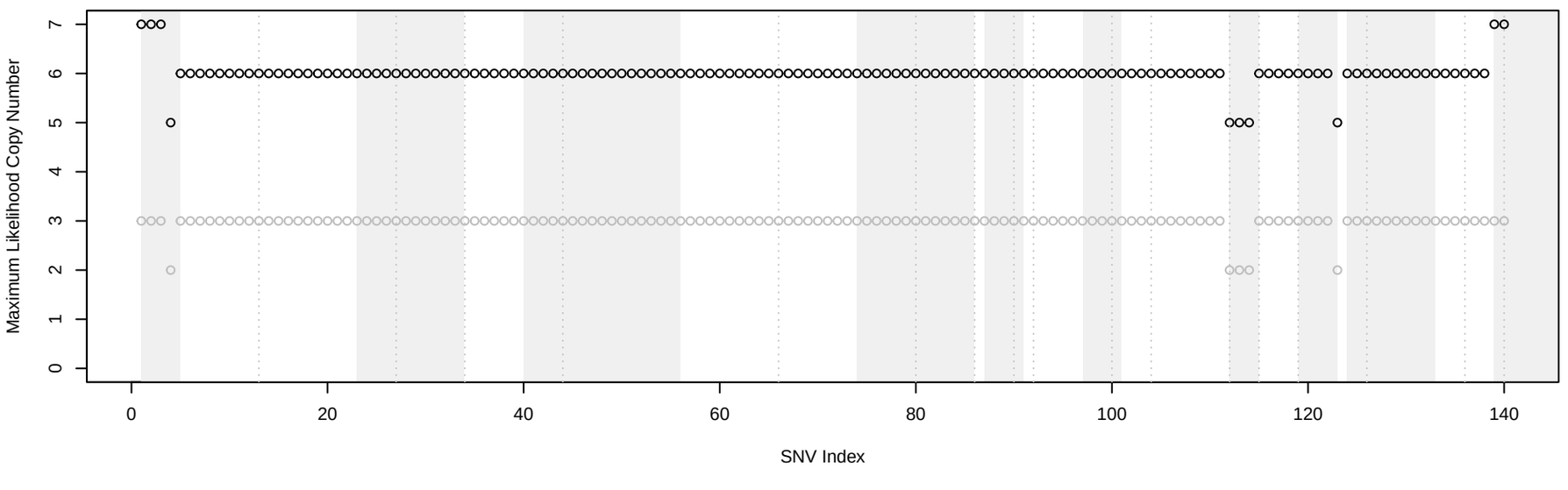

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
5m1
6m1
7m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

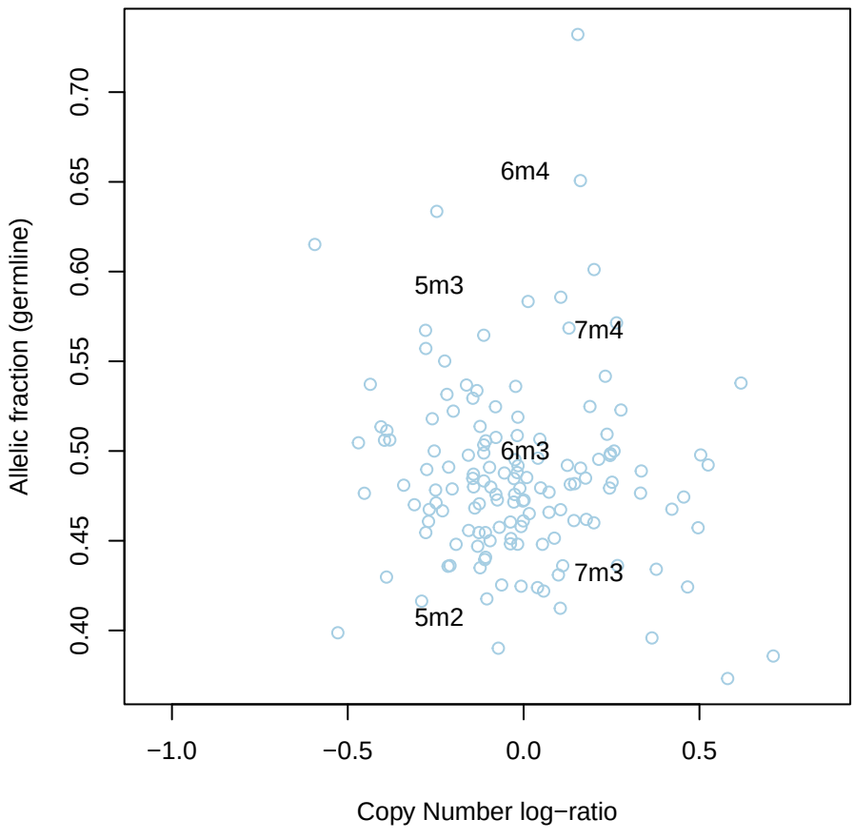

Power 0.8
Frequency
0
20
40
60
0.2
0.4
0.6
0.8
1.0
Cellular fraction

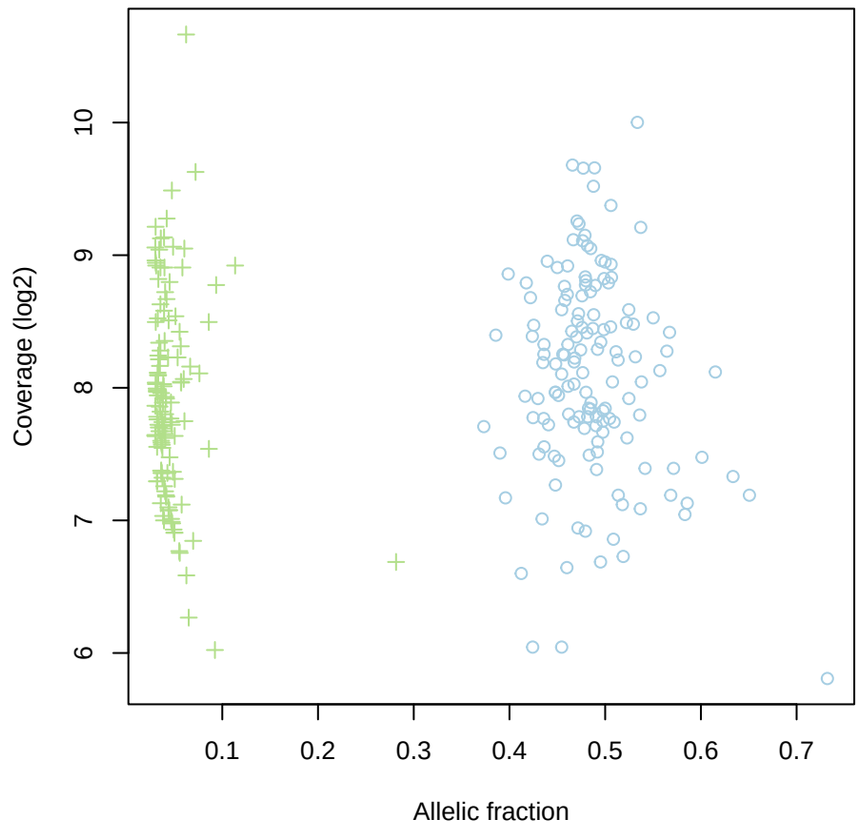

Purity: 0.83 Tumor ploidy: 5.979
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

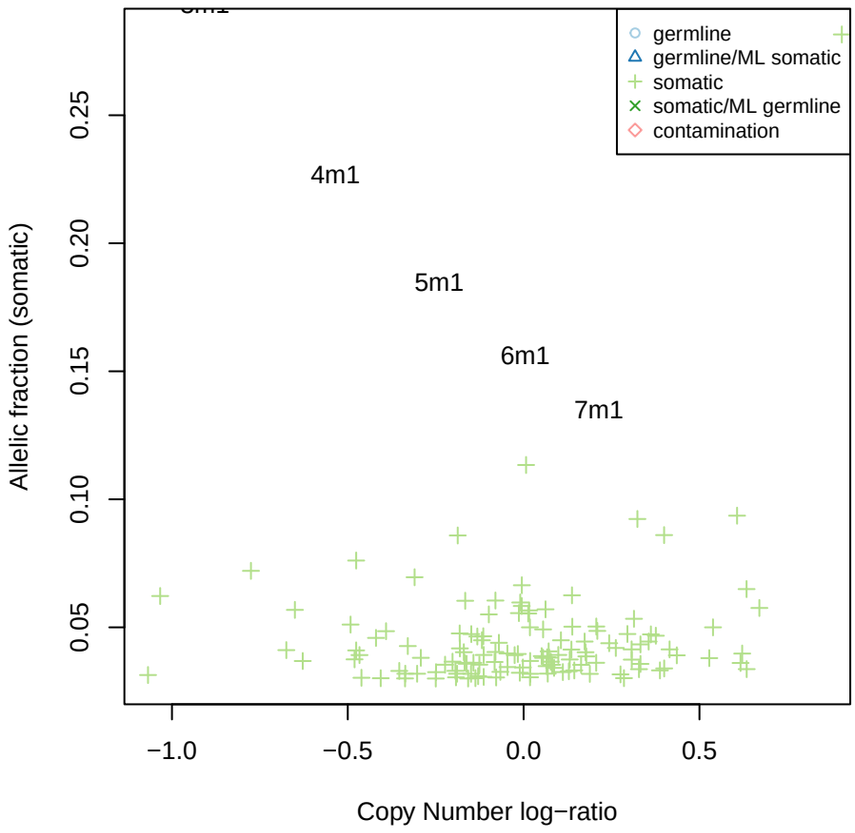

Purity: 0.83 Tumor ploidy: 5.979 SNV log−likelihood: −115.79 GoF: 80.1% Mean coverage: 488;296
1 2 3 4 5 6 7 8 10 11 12 13 15 17 19
B−Allele Frequency
0.40 0.50 0.60 0.70
0 20 40 60 80 100 120 140
SNV Index

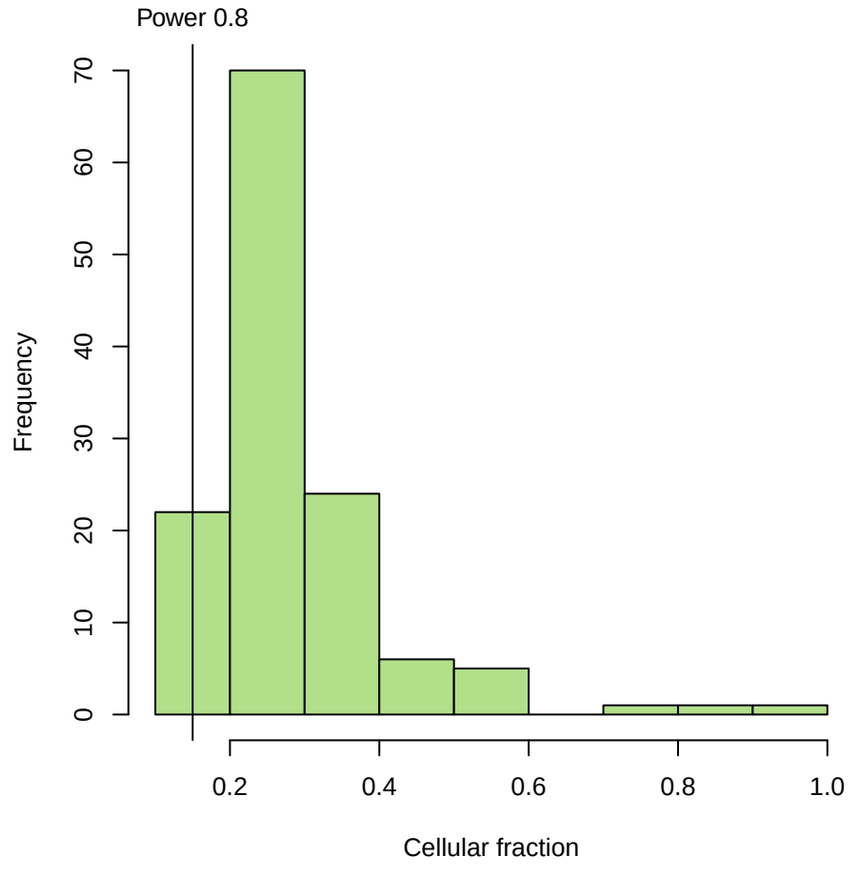

SCNA−fit log−likelihood: −5546.98
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

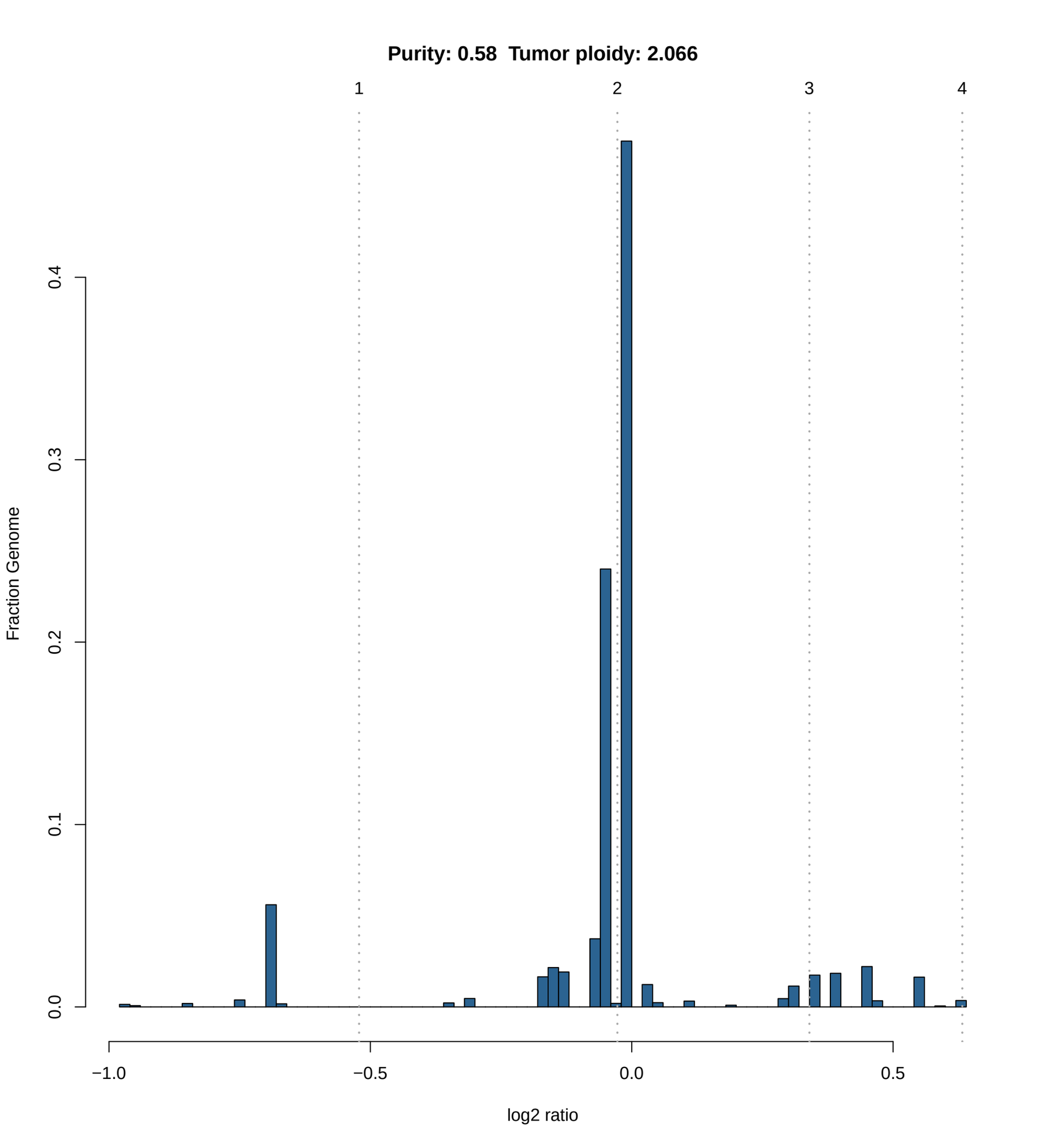

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

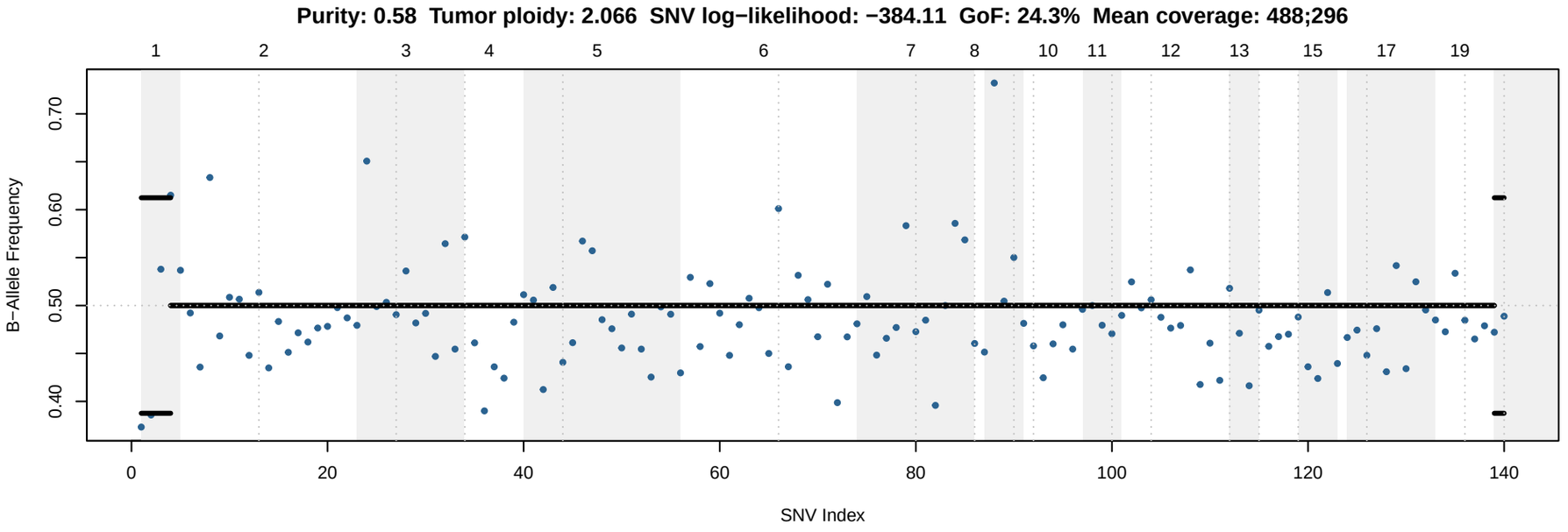

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
0.70
6m4
5m3
7m4
6m3
7m3
5m2
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

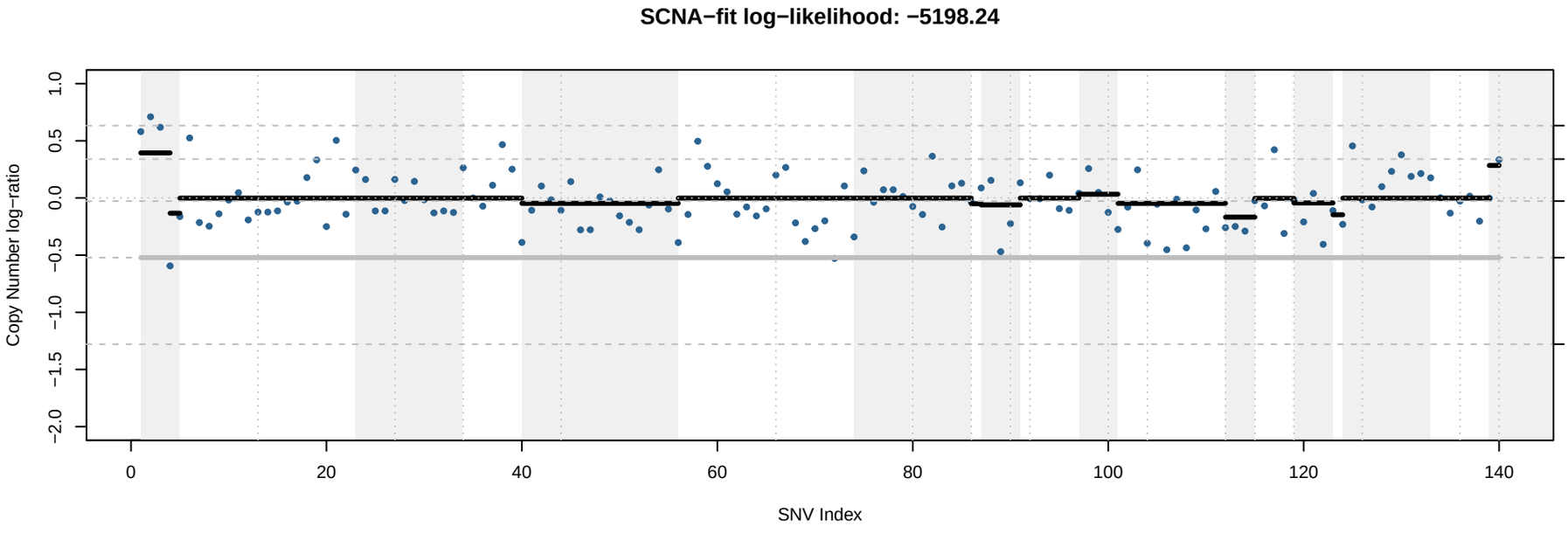

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

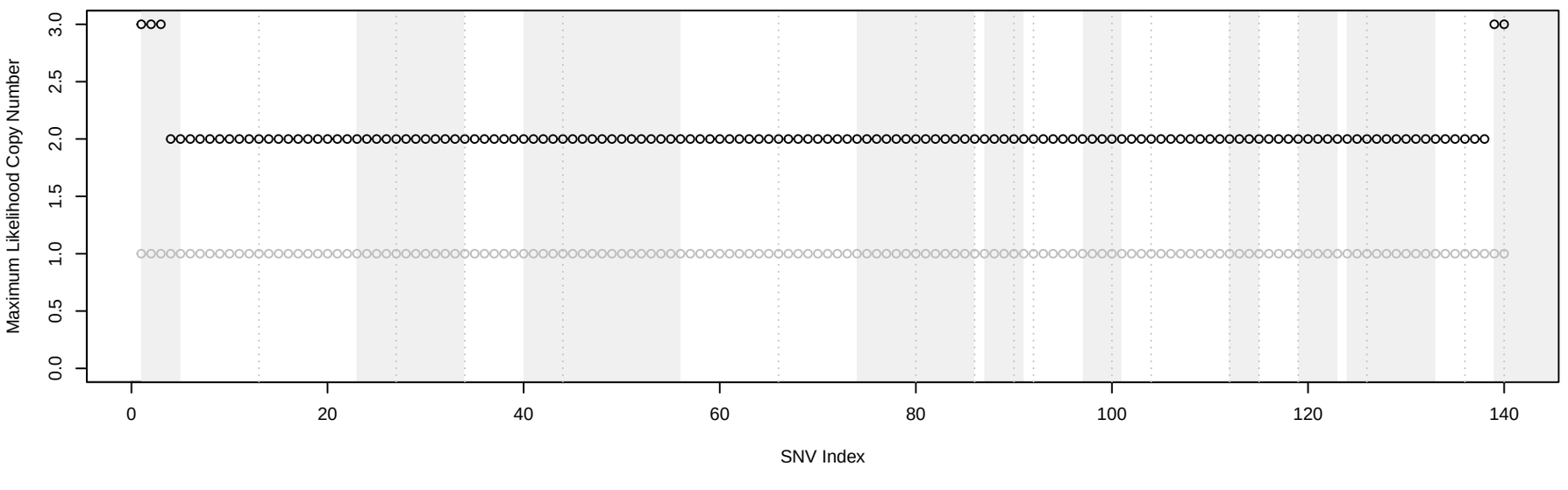

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
4m1
5m1
6m1
7m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

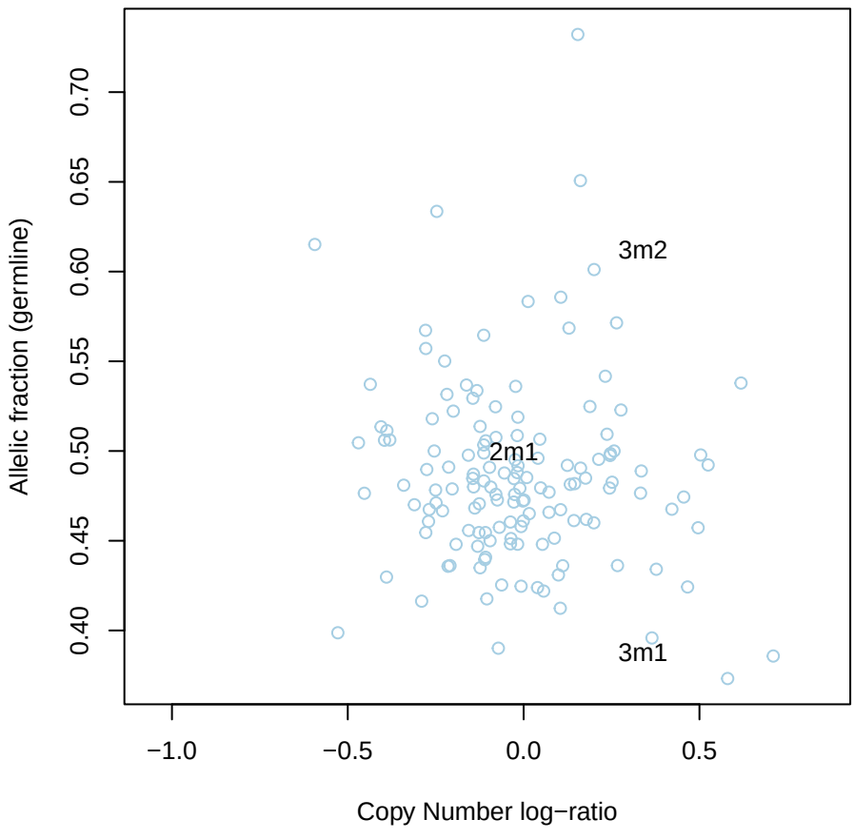

Power 0.8
Frequency
0
10
20
30
40
50
60
70
0.2
0.4
0.6
0.8
1.0
Cellular fraction

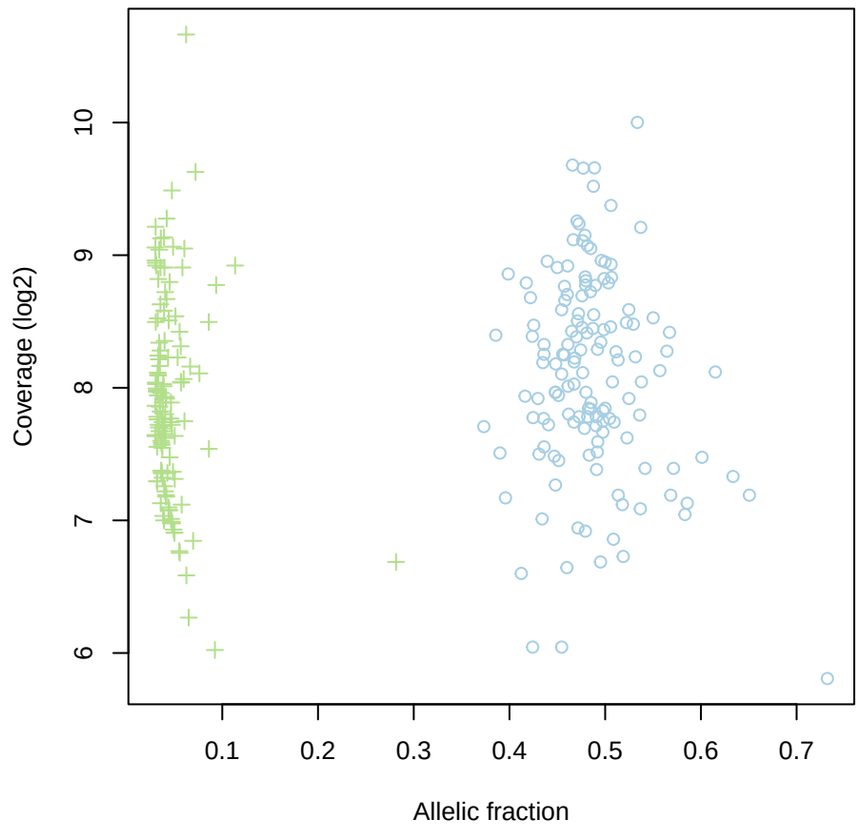

Purity: 0.58 Tumor ploidy: 2.066
1
2
3
4
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

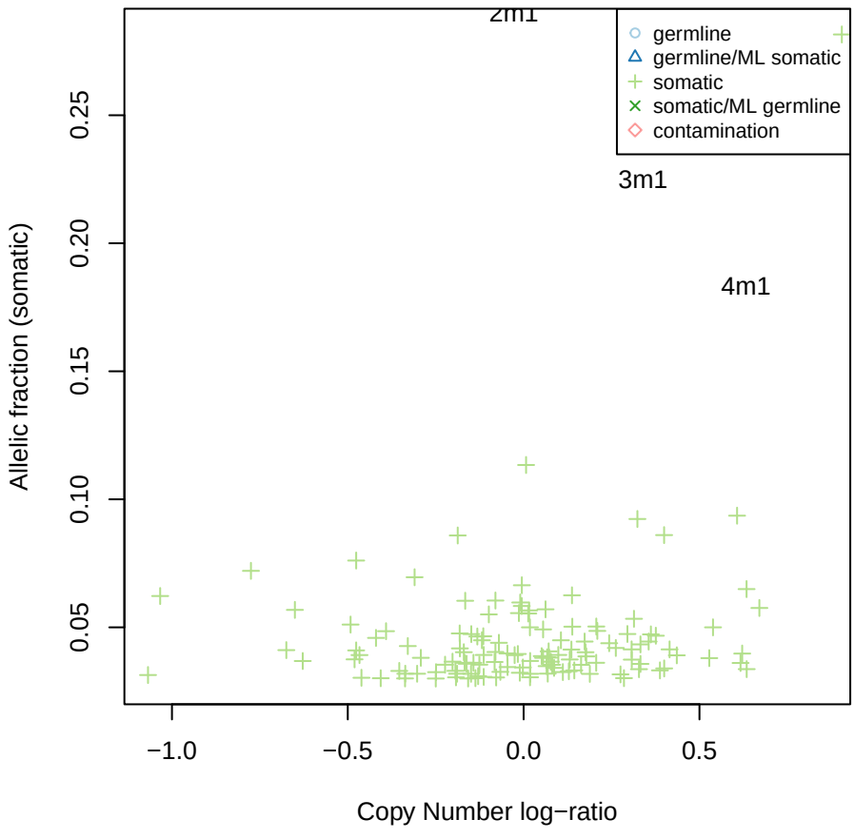

Purity: 0.58 Tumor ploidy: 2.066 SNV log−likelihood: −384.11 GoF: 24.3% Mean coverage: 488;296
1 2 3 4 5 6 7 8 10 11 12 13 15 17 19
B−Allele Frequency
0.40 0.50 0.60 0.70
0 20 40 60 80 100 120 140
SNV Index

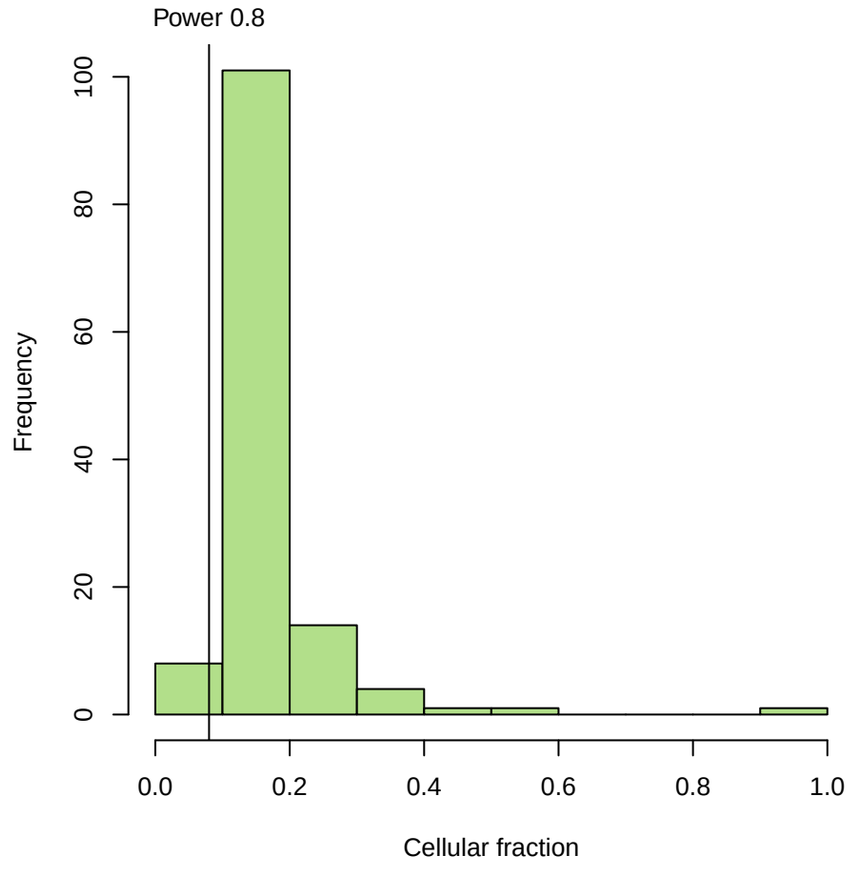

SCNA−fit log−likelihood: −5198.24
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4
0 20 40 60 80 100 120 140
SNV Index

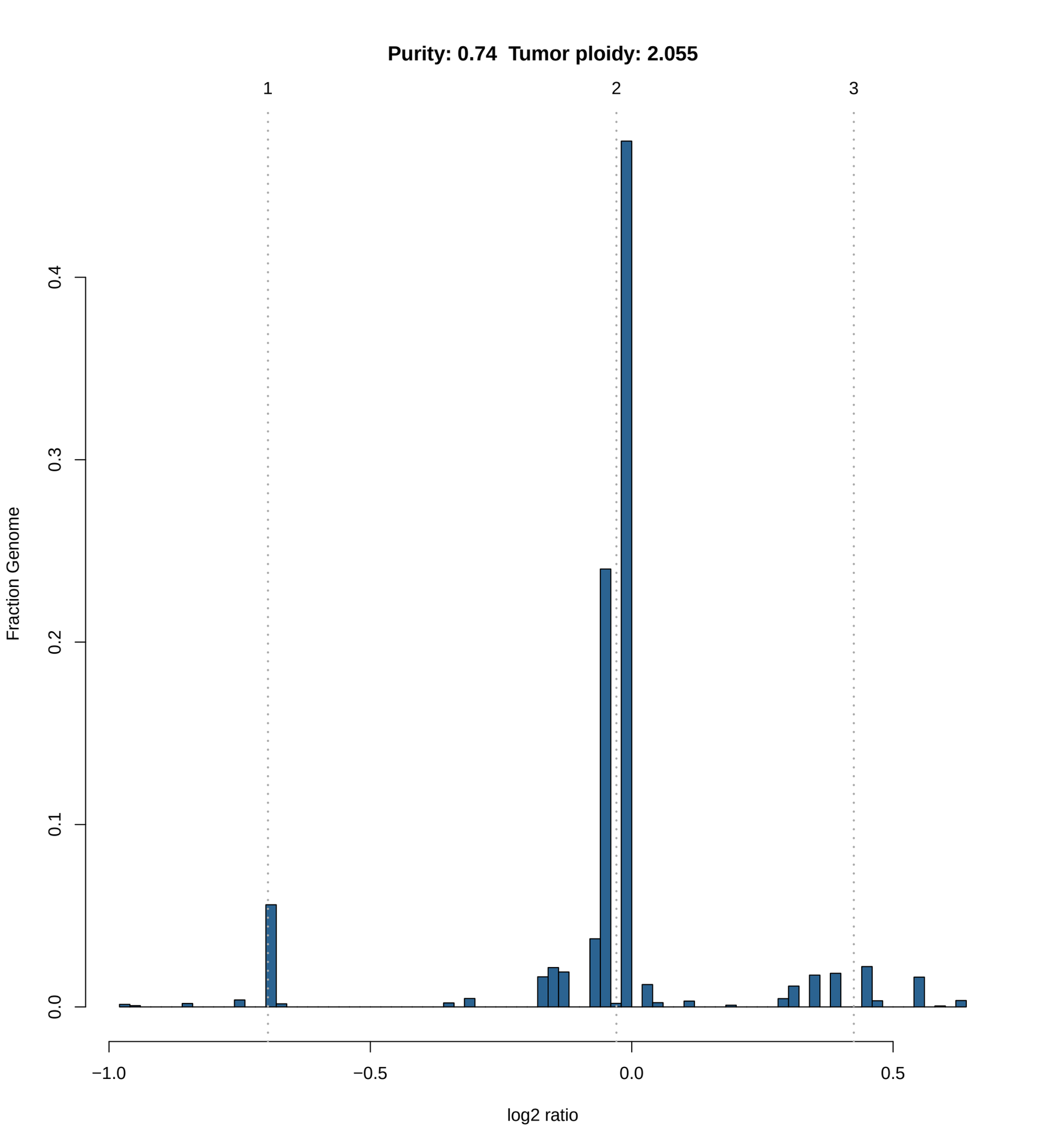

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120 140
SNV Index

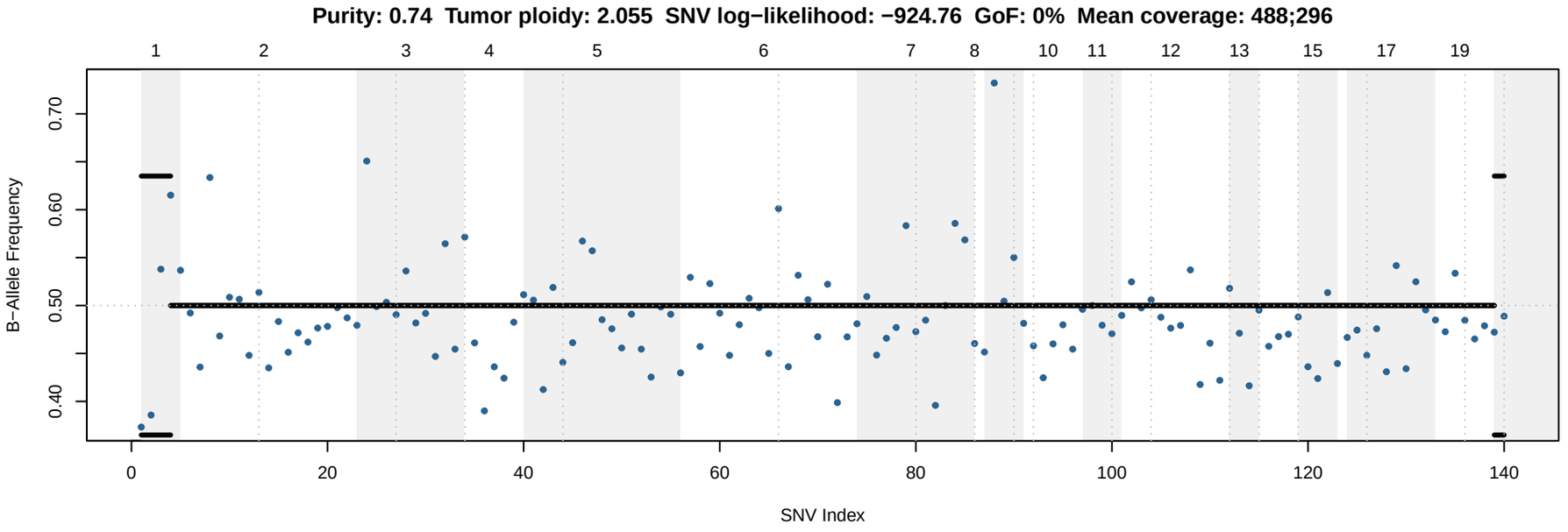

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
0.70
3m2
2m1
3m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

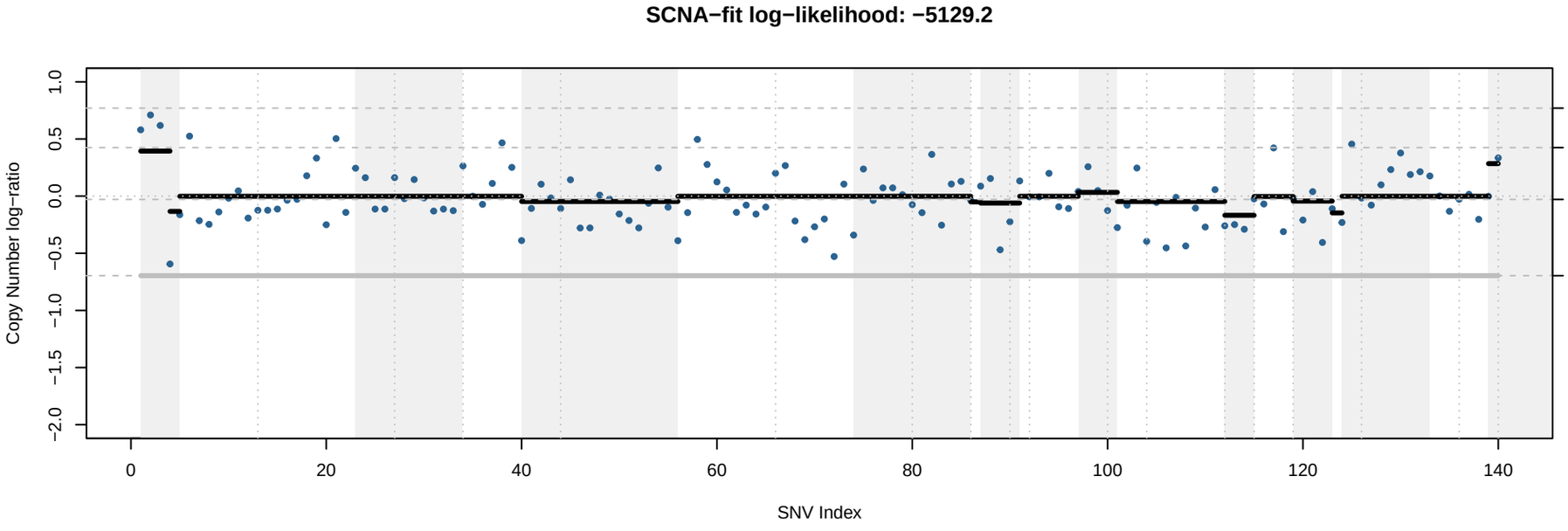

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

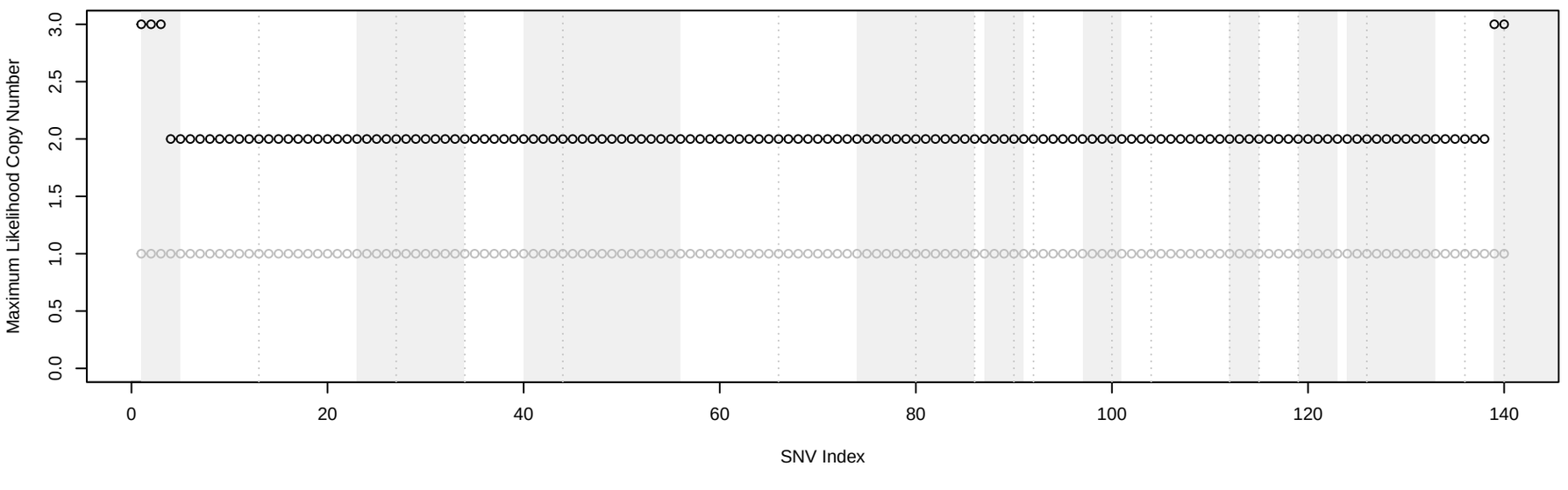

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
2m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

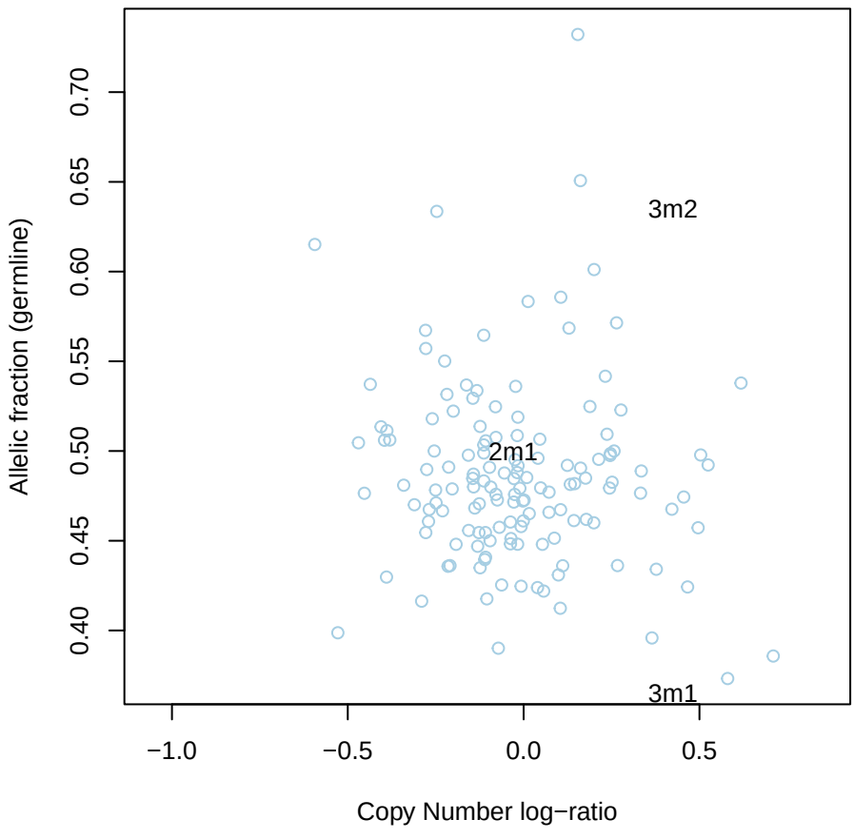

Power 0.8
Frequency
0
20
40
60
80
100
0.0
0.2
0.4
0.6
0.8
1.0
Cellular fraction

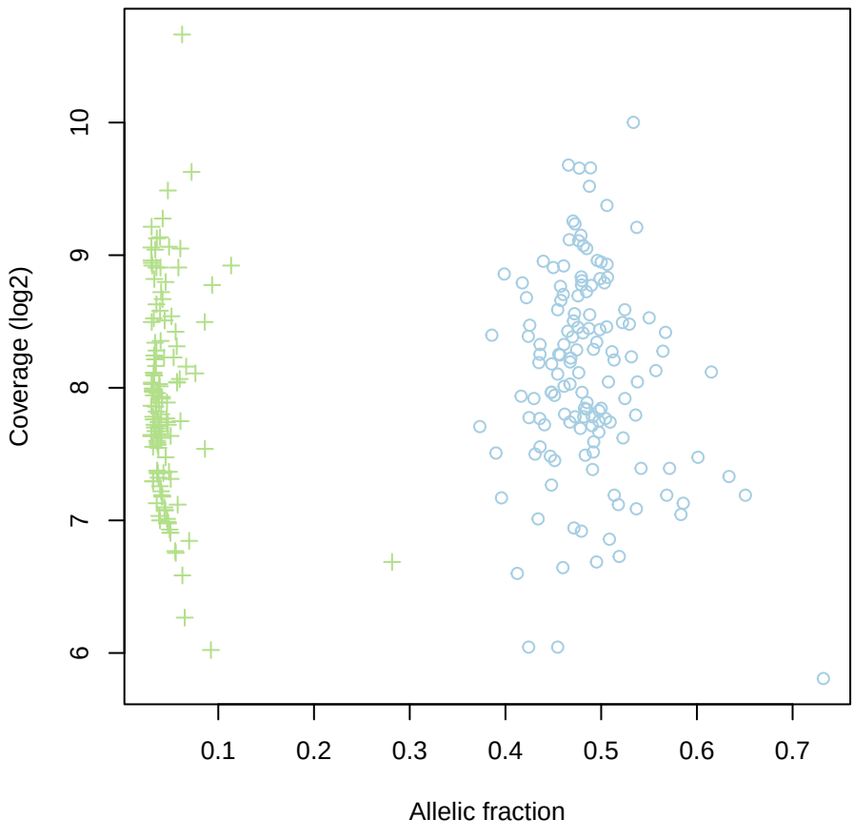

Purity: 0.74 Tumor ploidy: 2.055
1
2
3
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

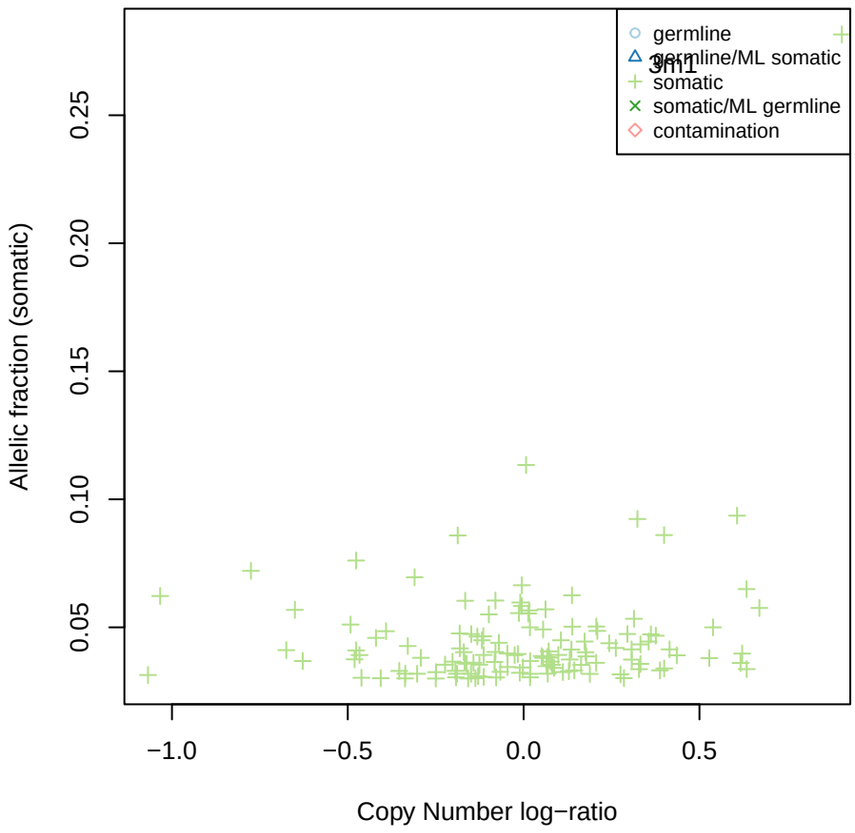

Purity: 0.74 Tumor ploidy: 2.055 SNV log−likelihood: −924.76 GoF: 0% Mean coverage: 488;296
1 2 3 4 5 6 7 8 10 11 12 13 15 17 19
B−Allele Frequency
0.40 0.50 0.60 0.70
0 20 40 60 80 100 120 140
SNV Index

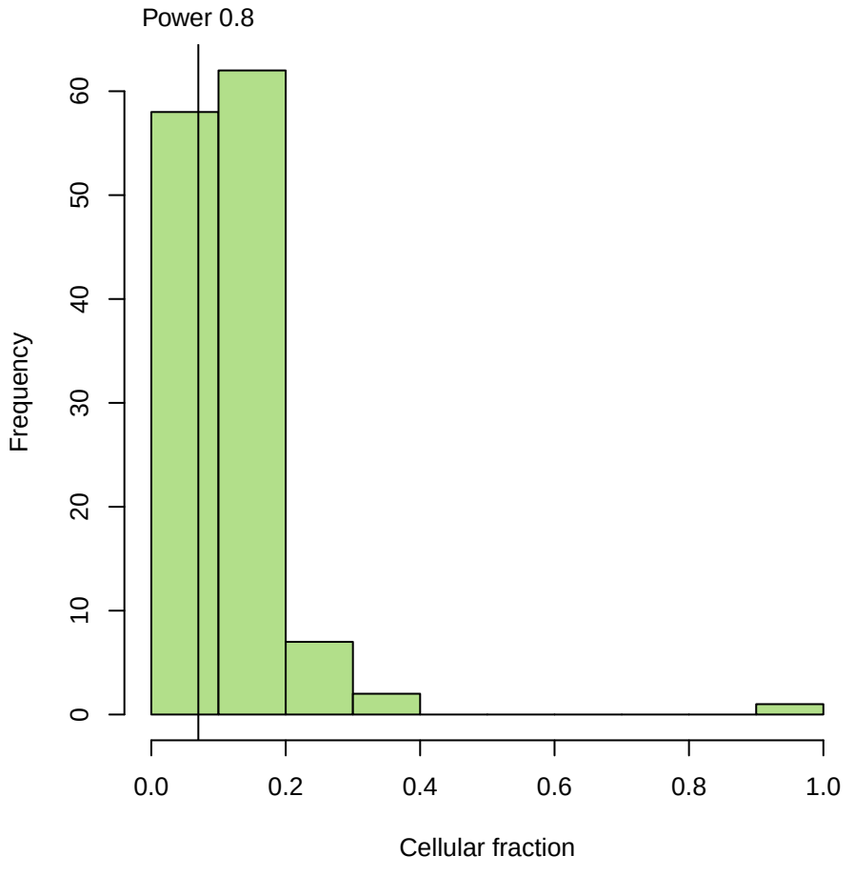

SCNA−fit log−likelihood: −5129.2
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
1 2 3 4
0 20 40 60 80 100 120 140
SNV Index

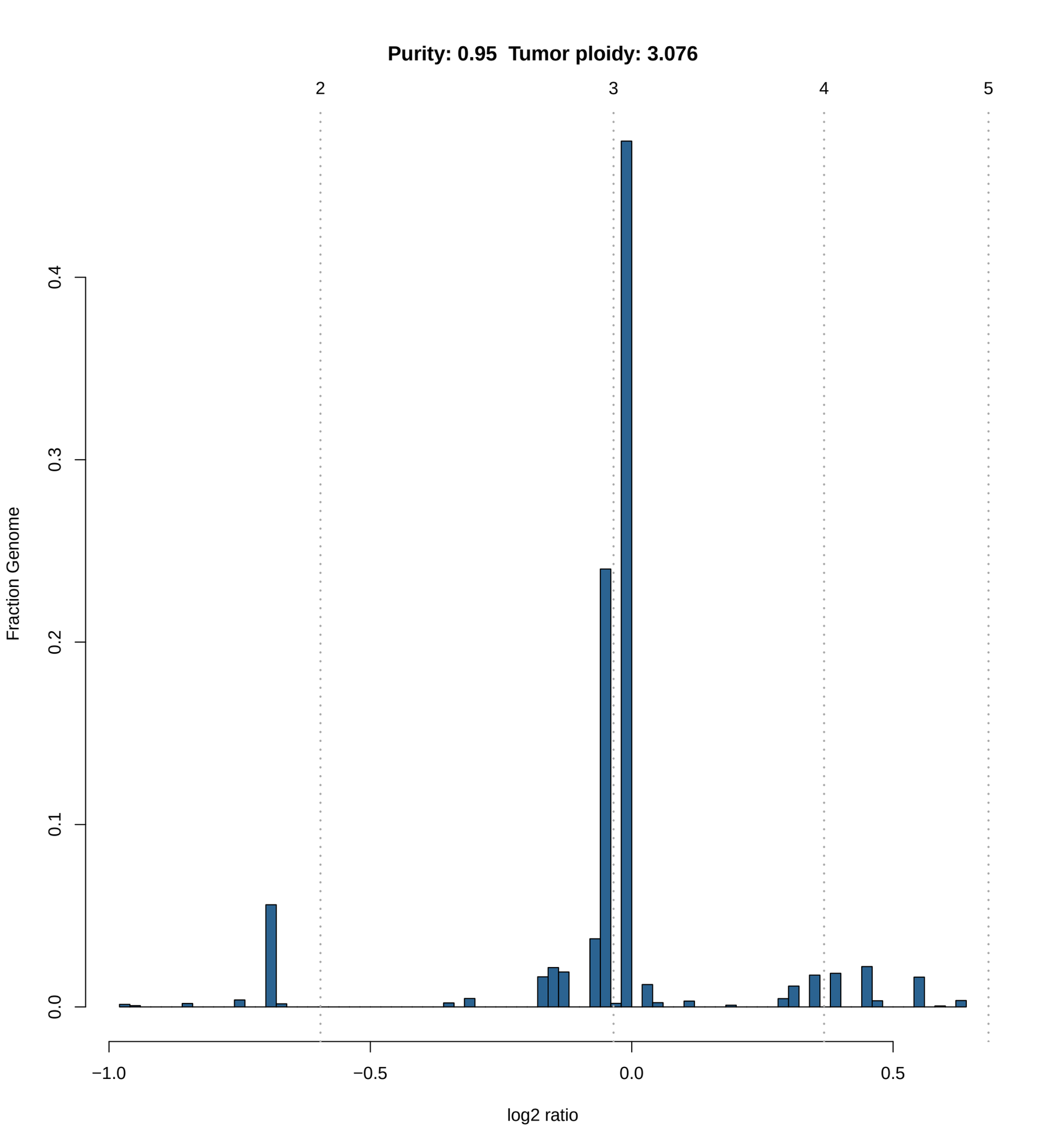

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120 140
SNV Index

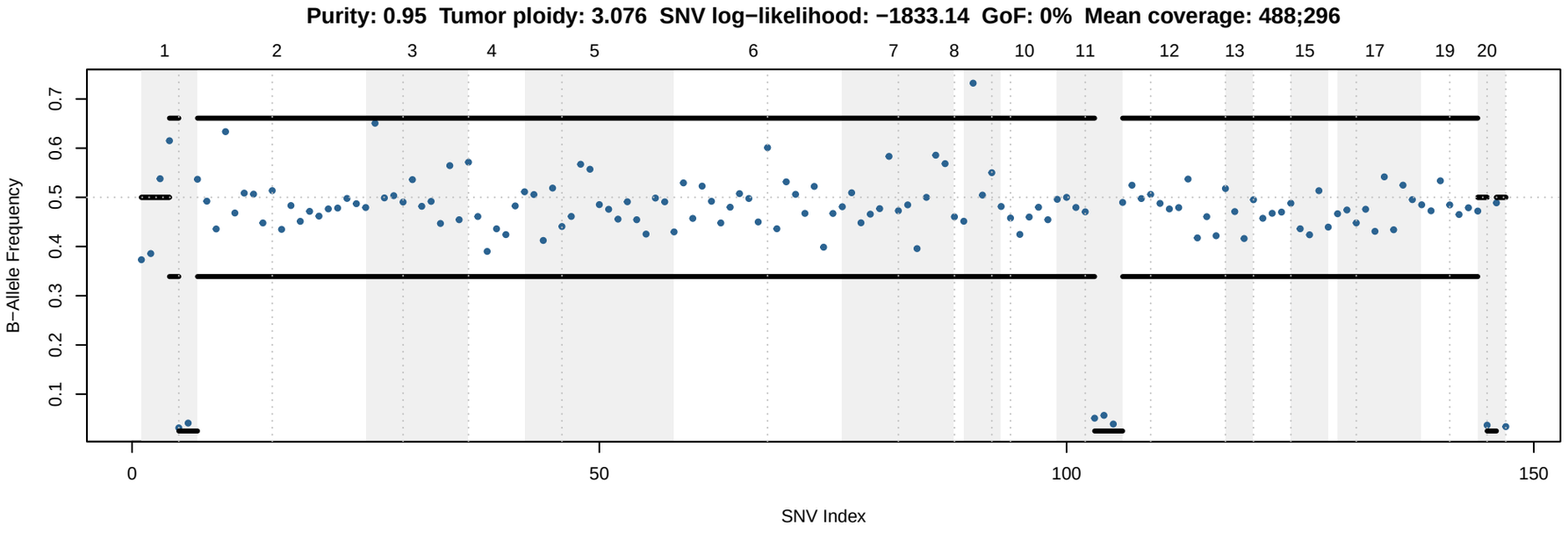

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
0.70
3m2
2m1
3m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

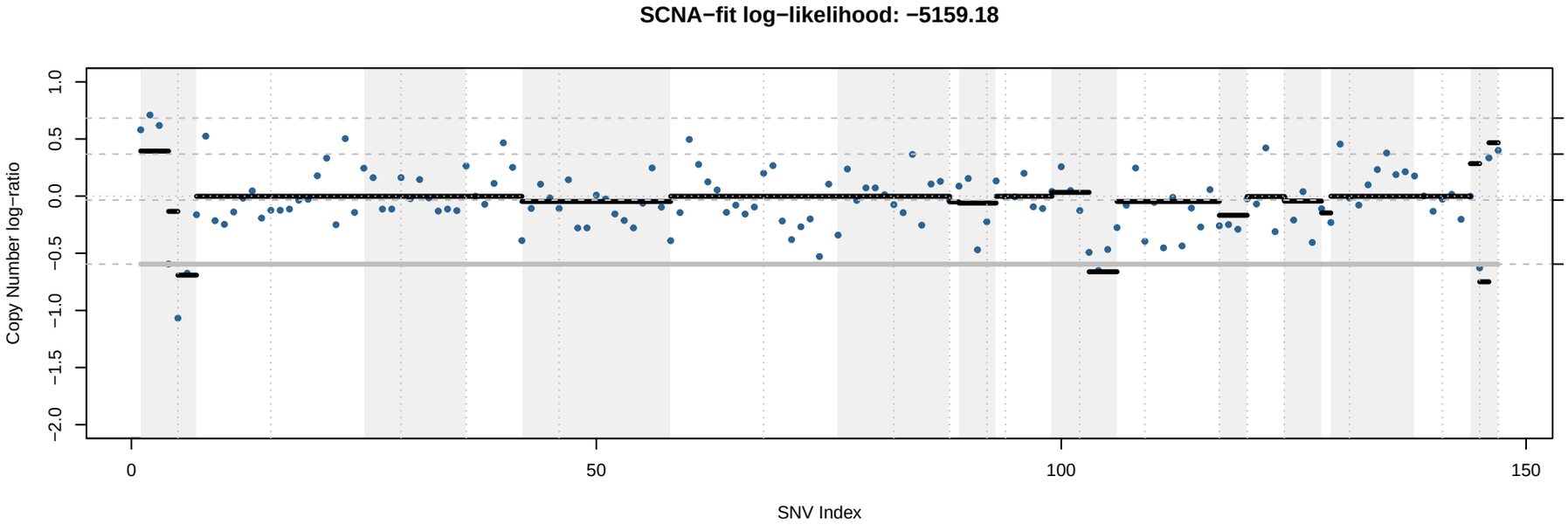

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

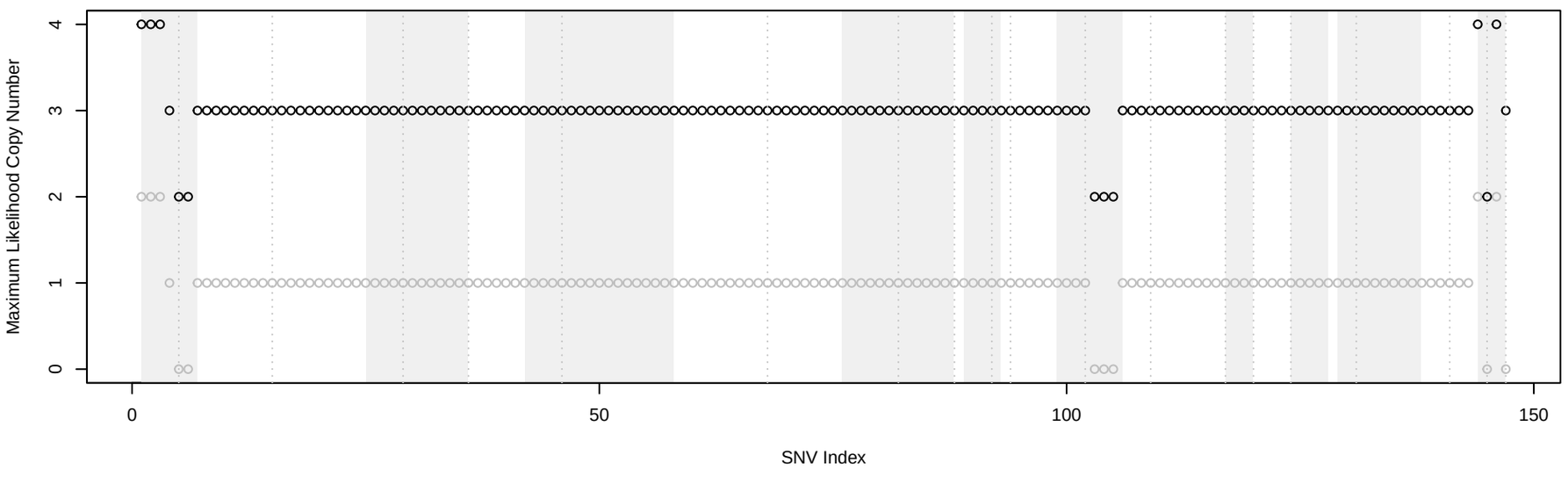

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

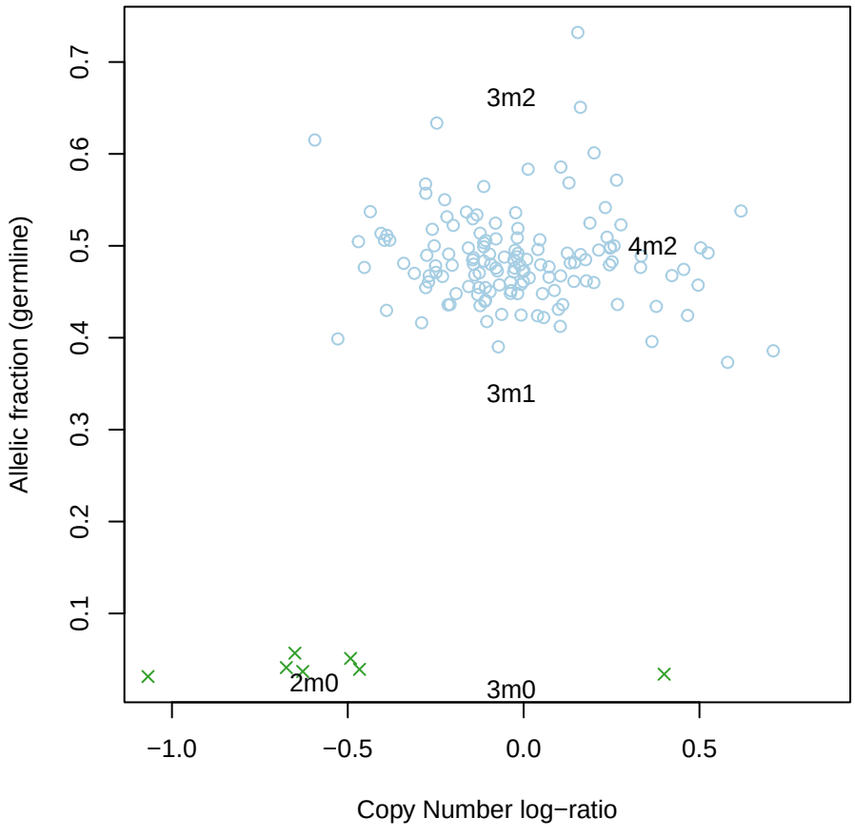

Power 0.8
Frequency
0
10
20
30
40
50
60
0.0
0.2
0.4
0.6
0.8
1.0
Cellular fraction

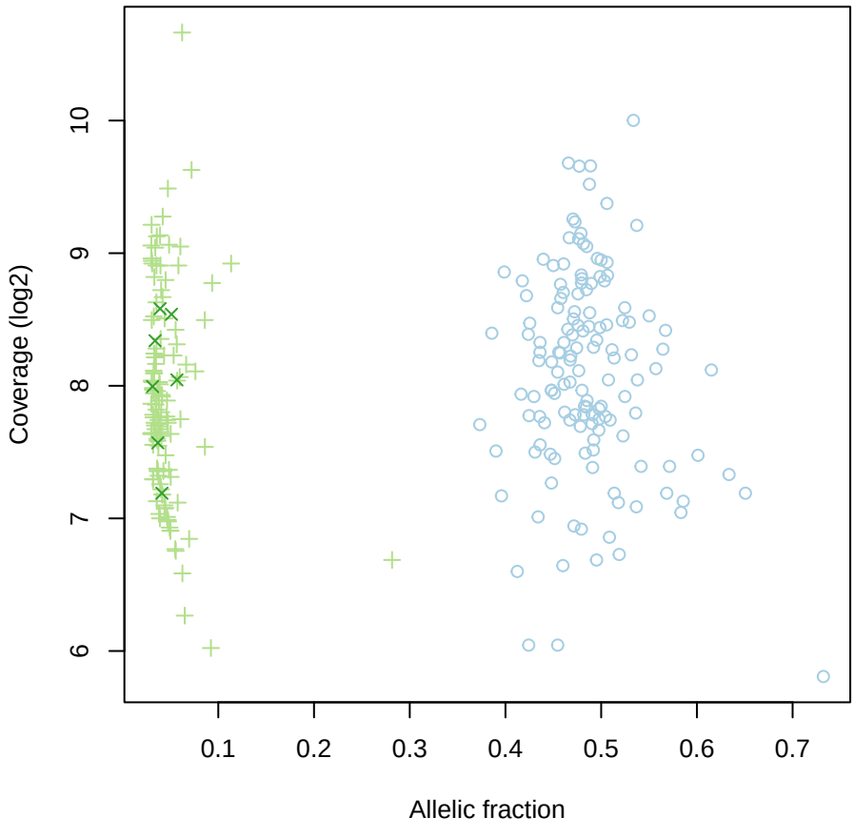

Purity: 0.95 Tumor ploidy: 3.076
2
3
4
5
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

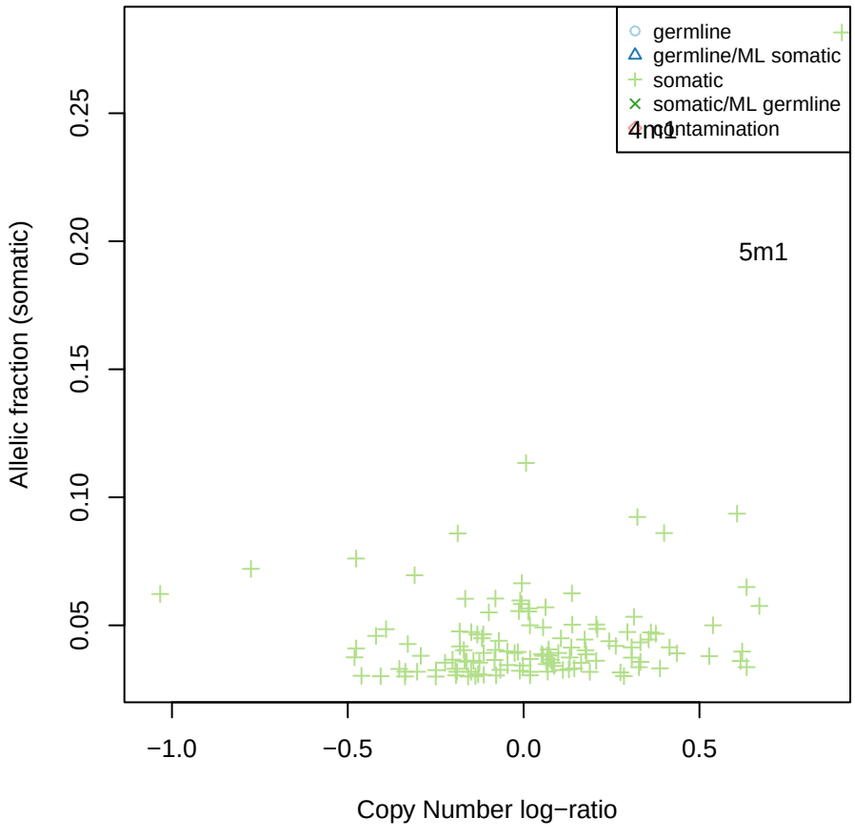

Purity: 0.95 Tumor ploidy: 3.076 SNV log−likelihood: −1833.14 GoF: 0% Mean coverage: 488;296
1 2 3 4 5 6 7 8 10 11 12 13 15 17 19 20
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

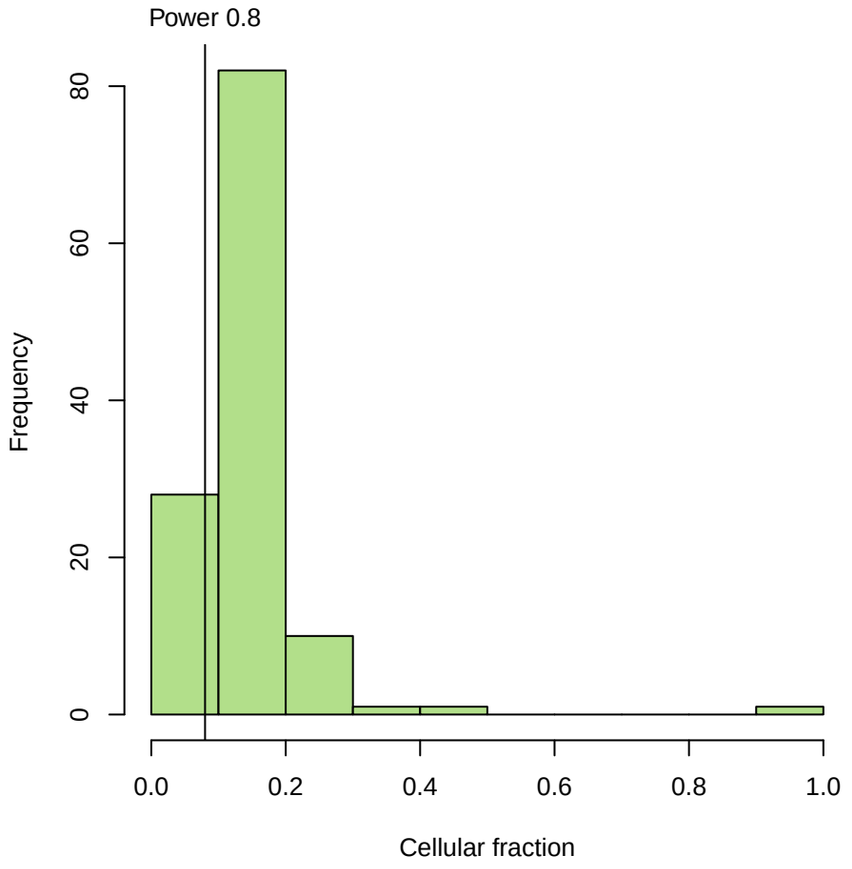

SCNA−fit log−likelihood: −5159.18
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
5 4 3 2
0 50 100 150
SNV Index


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


Allelic fraction (germline)
0.1
0.2
0.3
0.4
0.5
0.6
0.7
3m2
4m2
3m1
2m0
3m0
−1.0
−0.5
0.0
0.5
Copy Number log−ratio


Coverage (log2)
6
7
8
9
10
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
5m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio


Power 0.8
Frequency
0
20
40
60
80
0.0
0.2
0.4
0.6
0.8
1.0
Cellular fraction