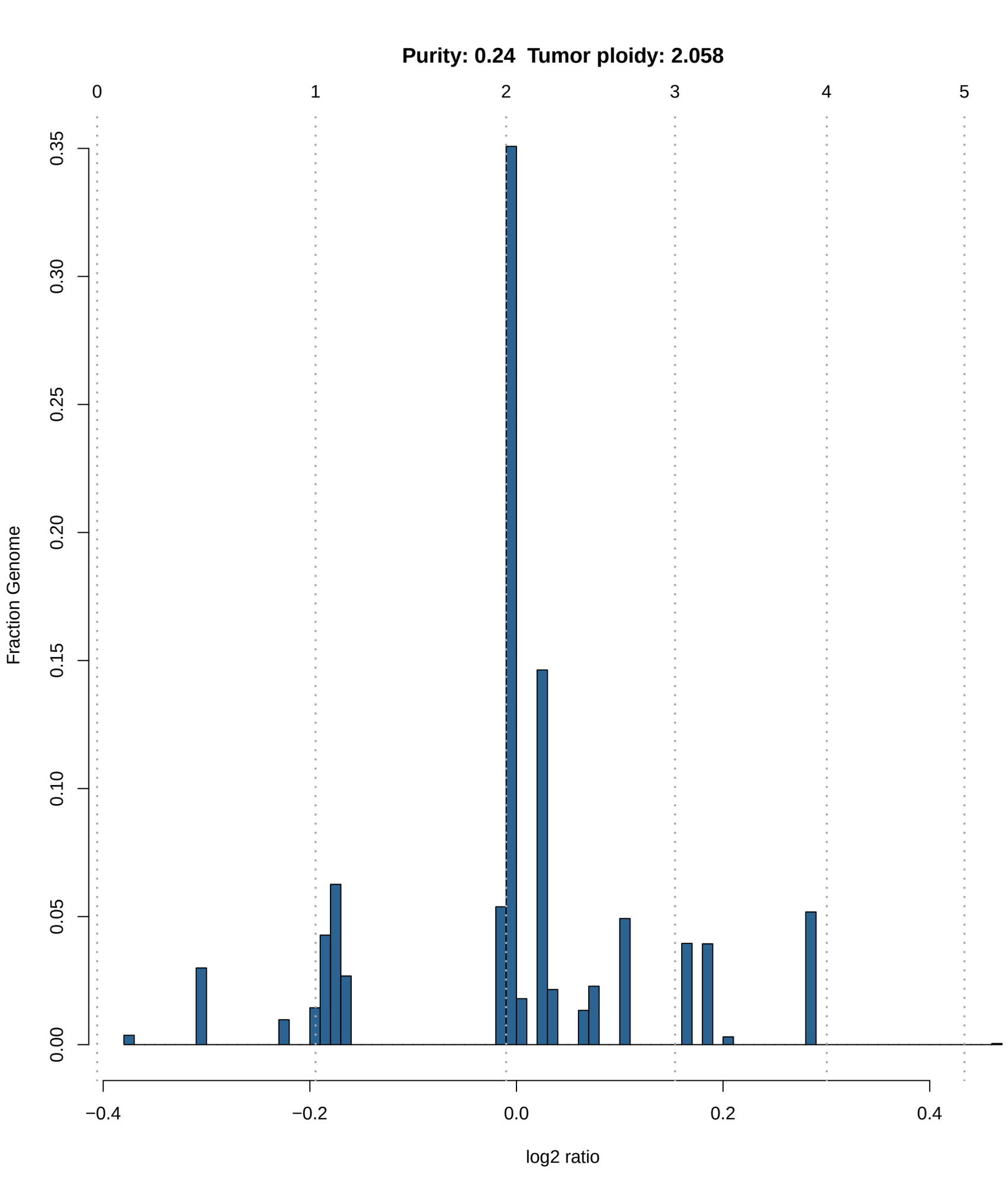
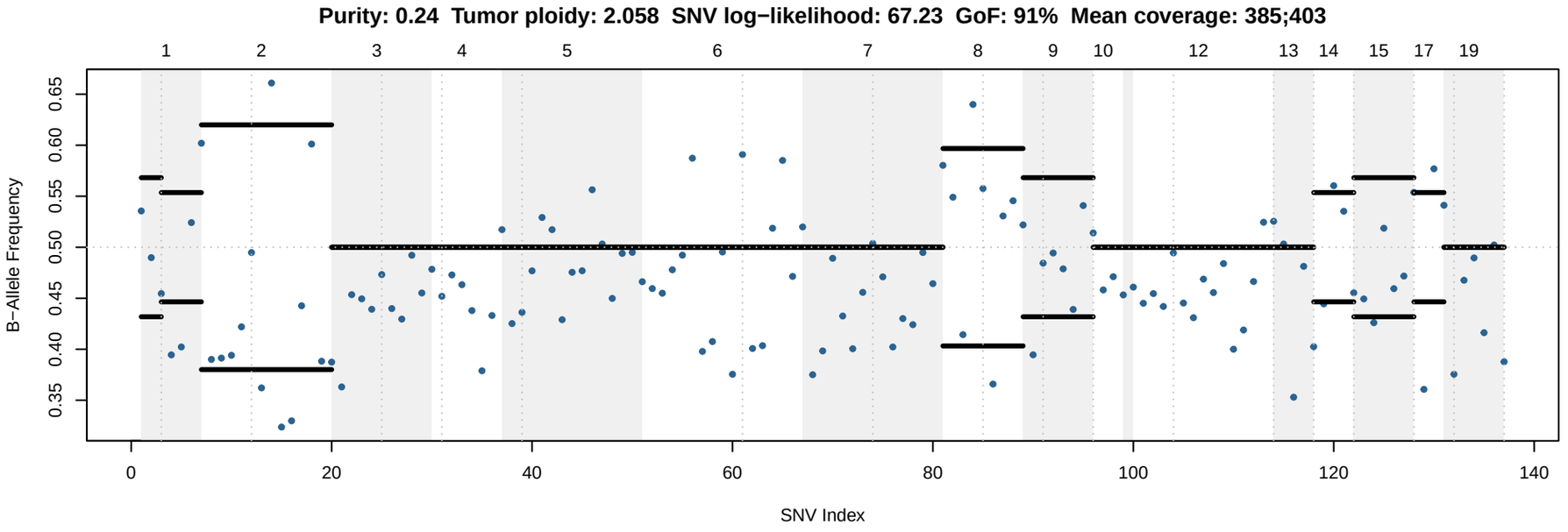
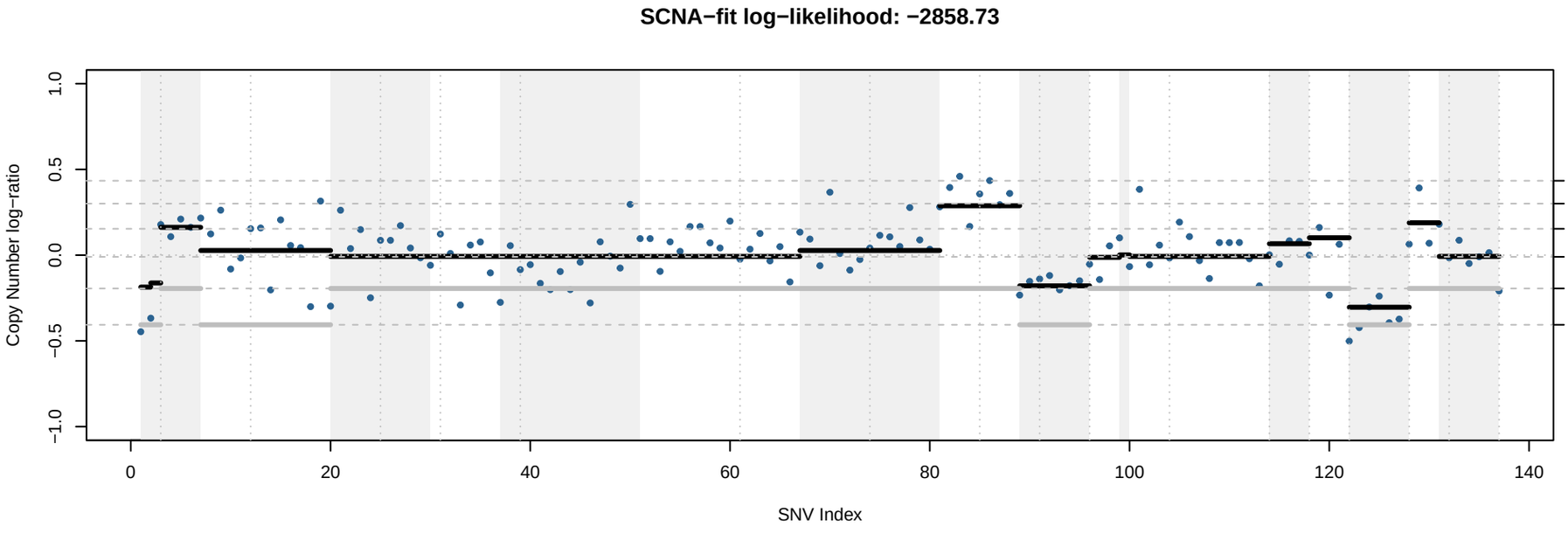
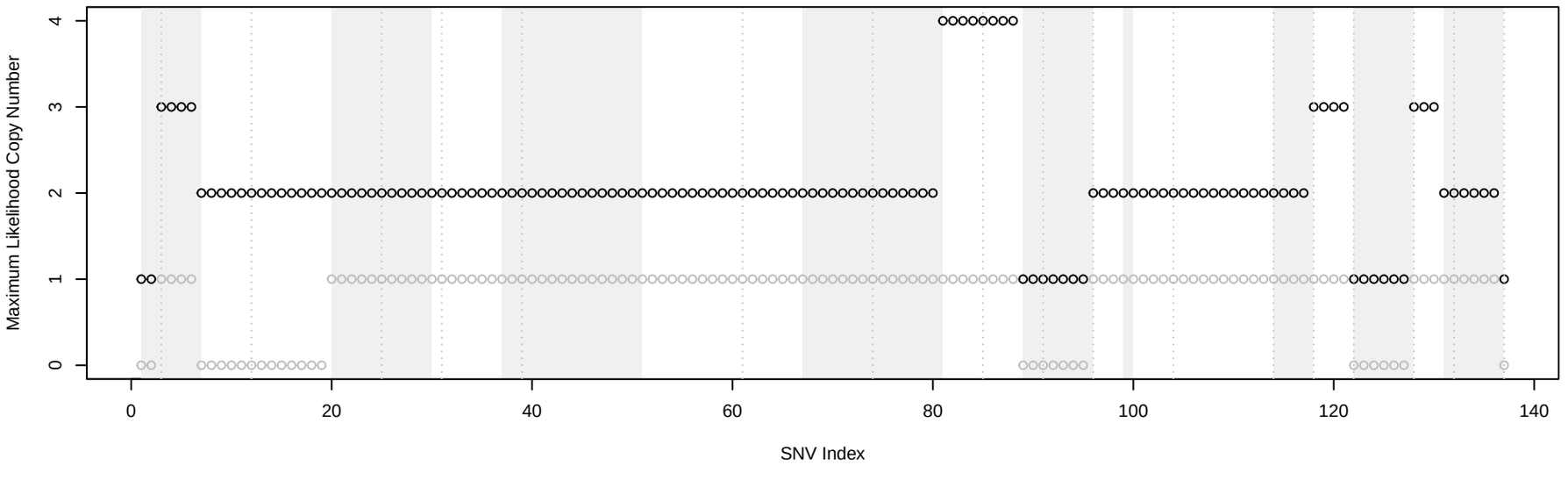
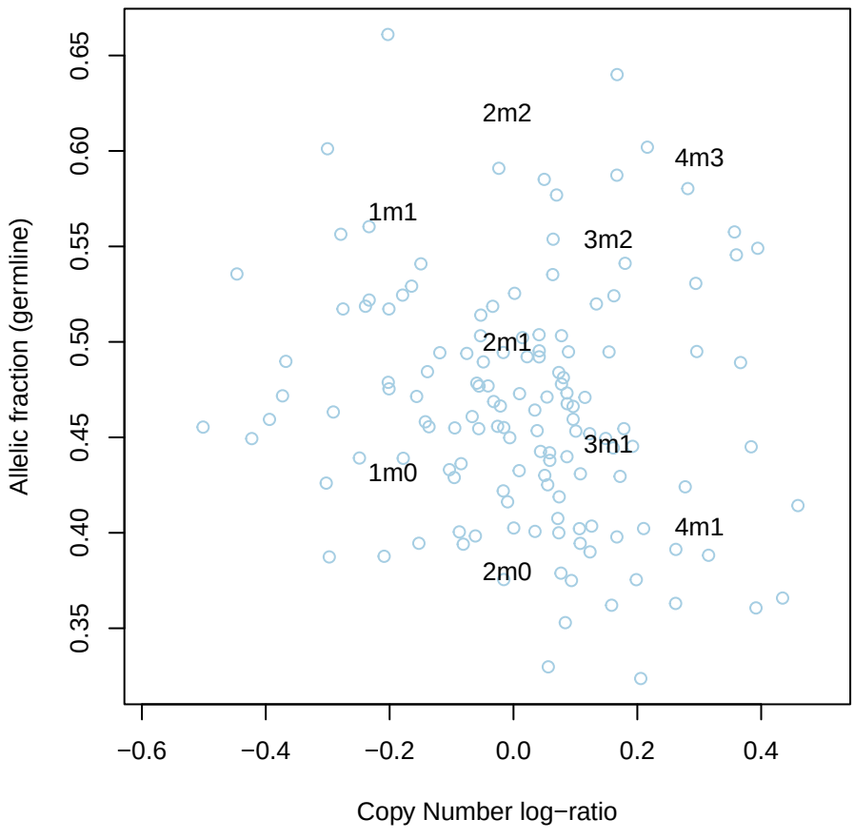
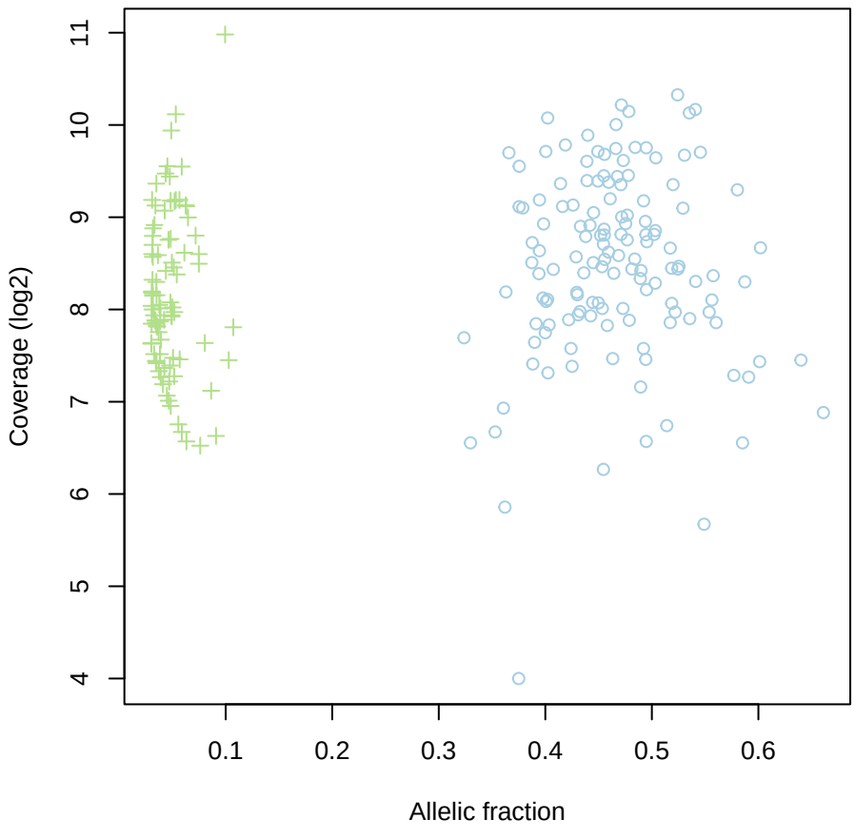

Purity: 0.24 Tumor ploidy: 2.058
0
1
2
3
4
5
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

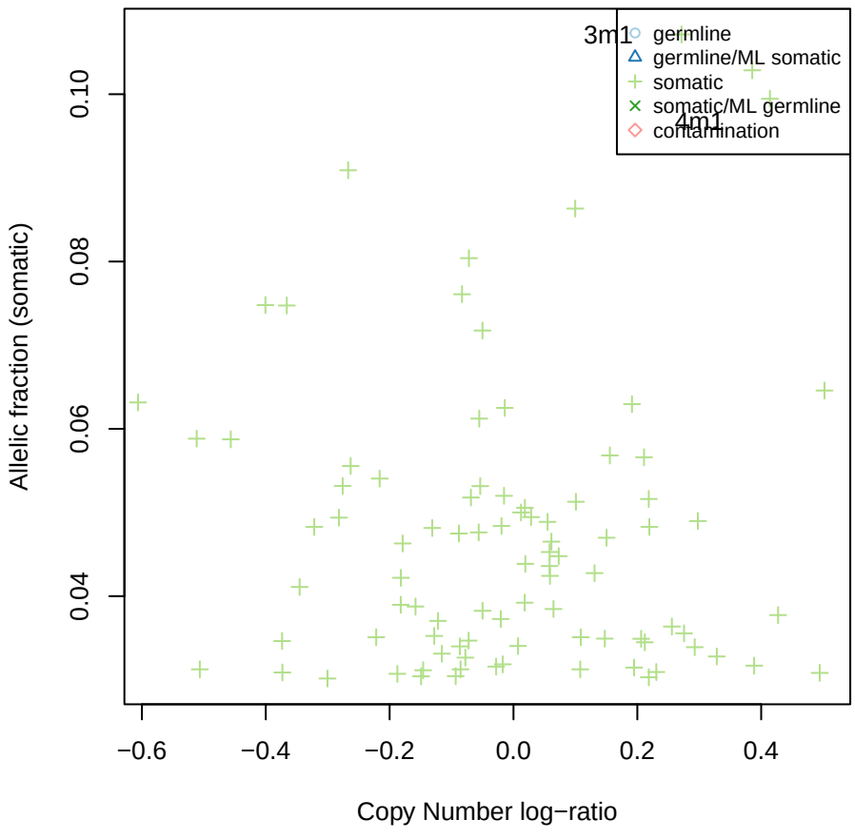

Purity: 0.24 Tumor ploidy: 2.058 SNV log−likelihood: 67.23 GoF: 91% Mean coverage: 385;403
1 2 3 4 5 6 7 8 9 10 12 13 14 15 17 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

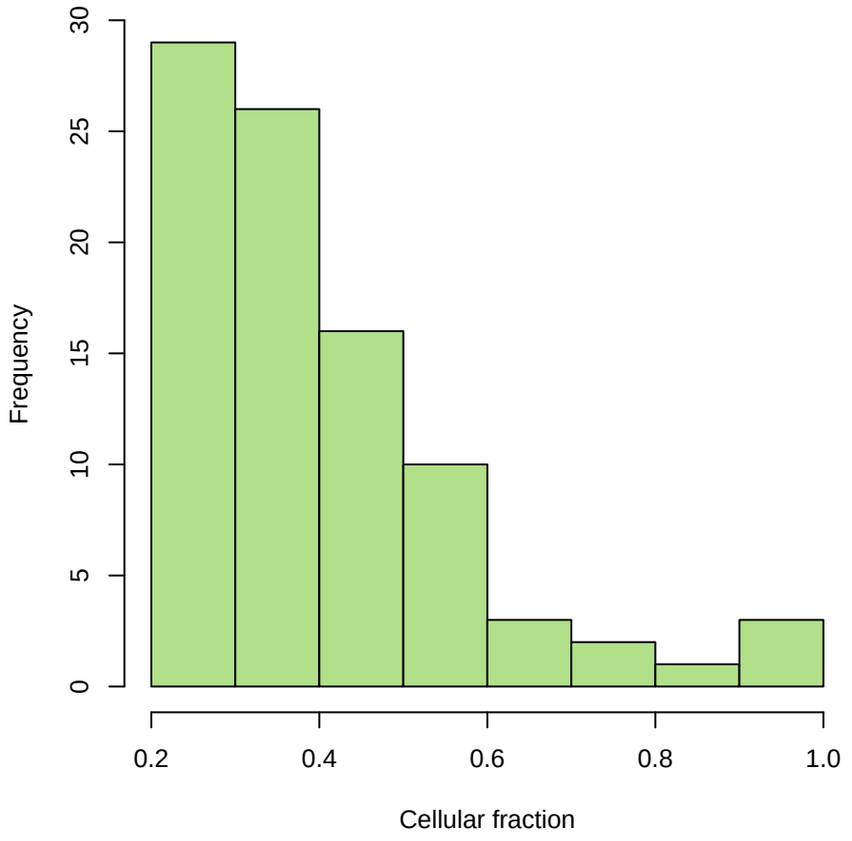

SCNA−fit log−likelihood: −2858.73
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
0 1 2 3 4
0 20 40 60 80 100 120 140
SNV Index

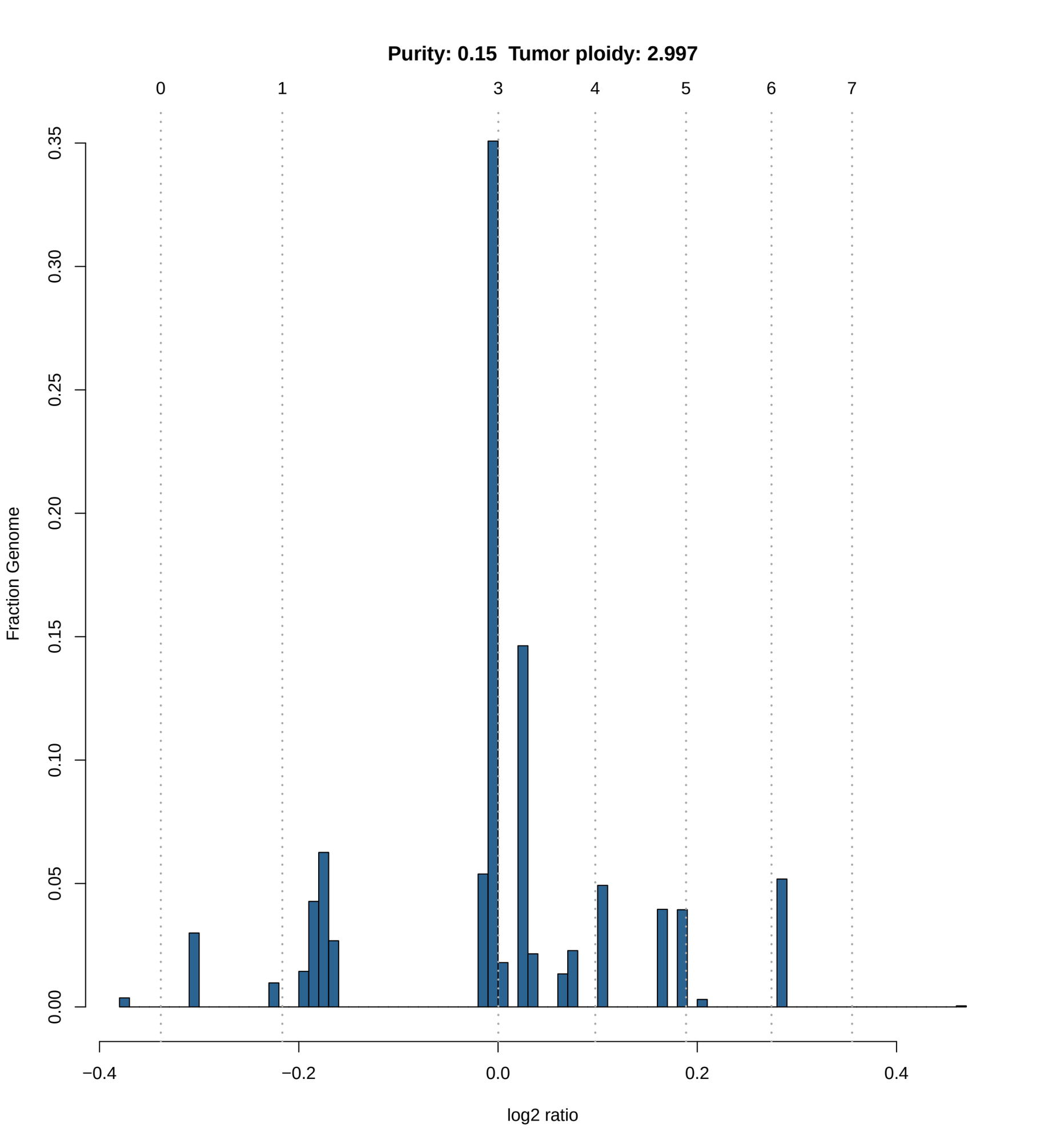

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120 140
SNV Index

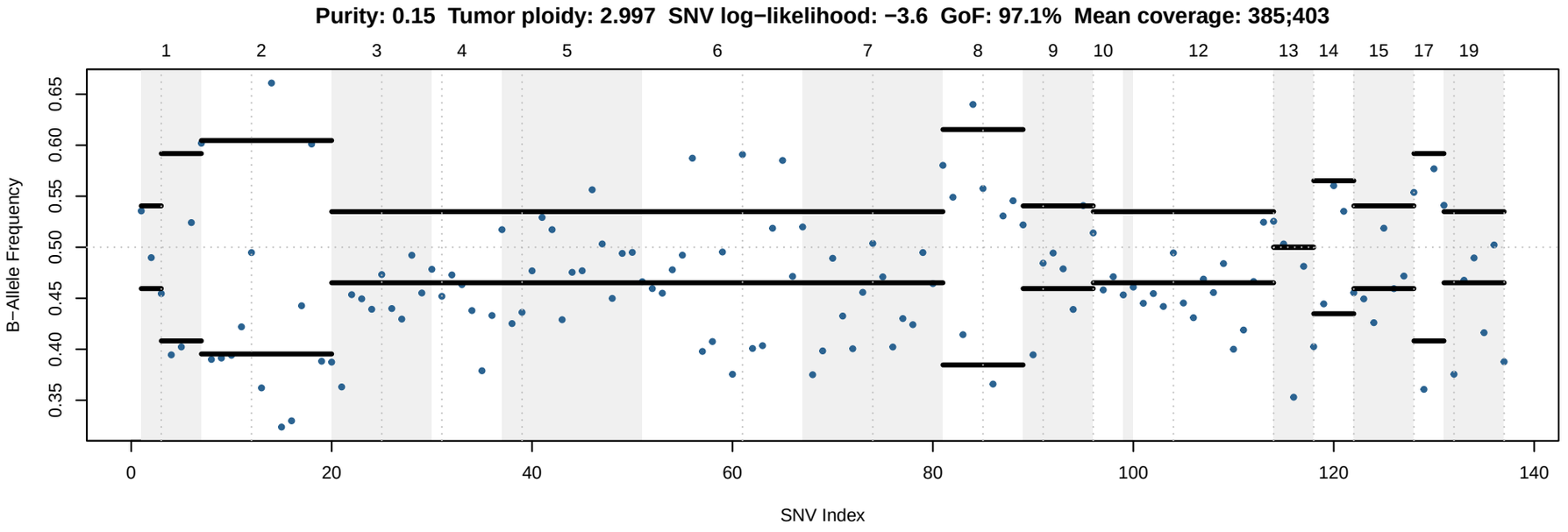

Allelic fraction (germline)
Copy Number log−ratio
2m2
4m3
1m1
3m2
2m1
3m1
1m0
4m1
2m0

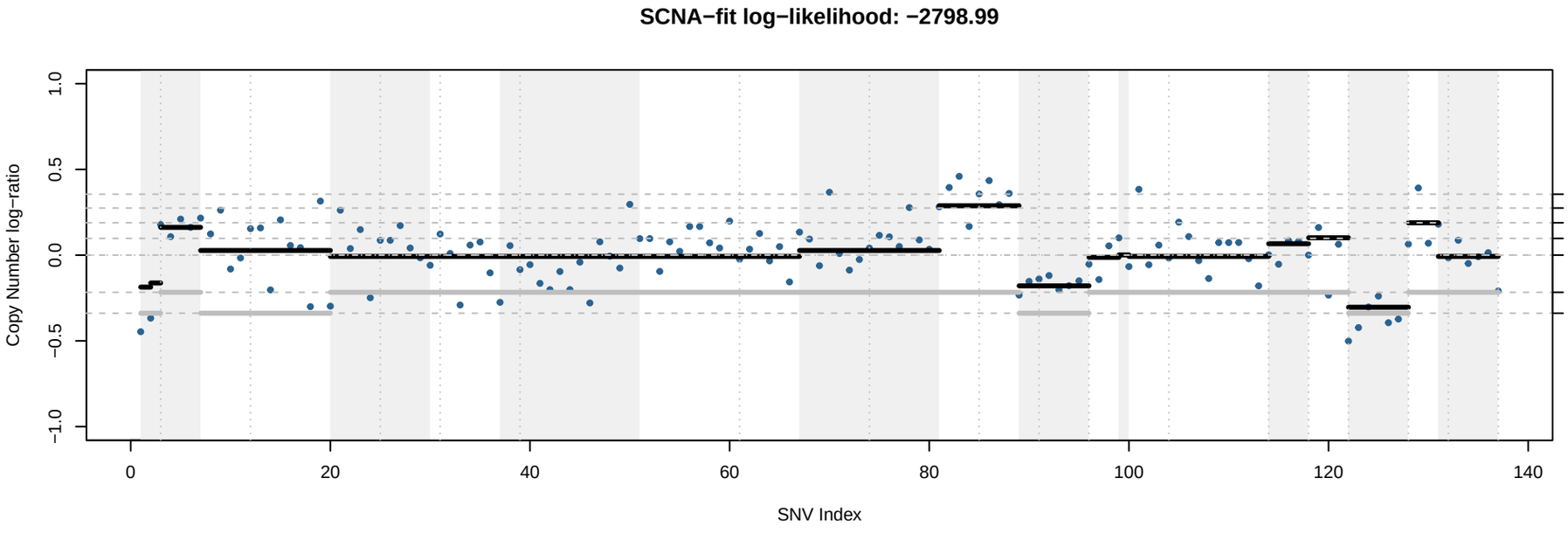

Coverage (log2)
Allelic fraction

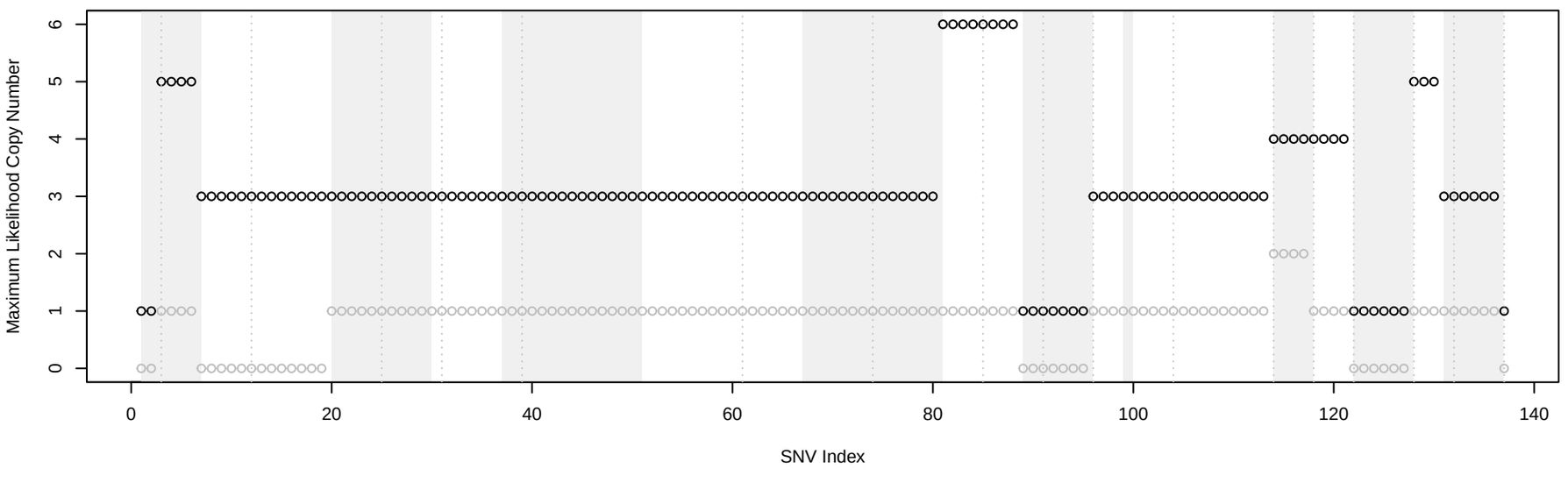

Allelic fraction (somatic)
Copy Number log−ratio
3m1
4m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

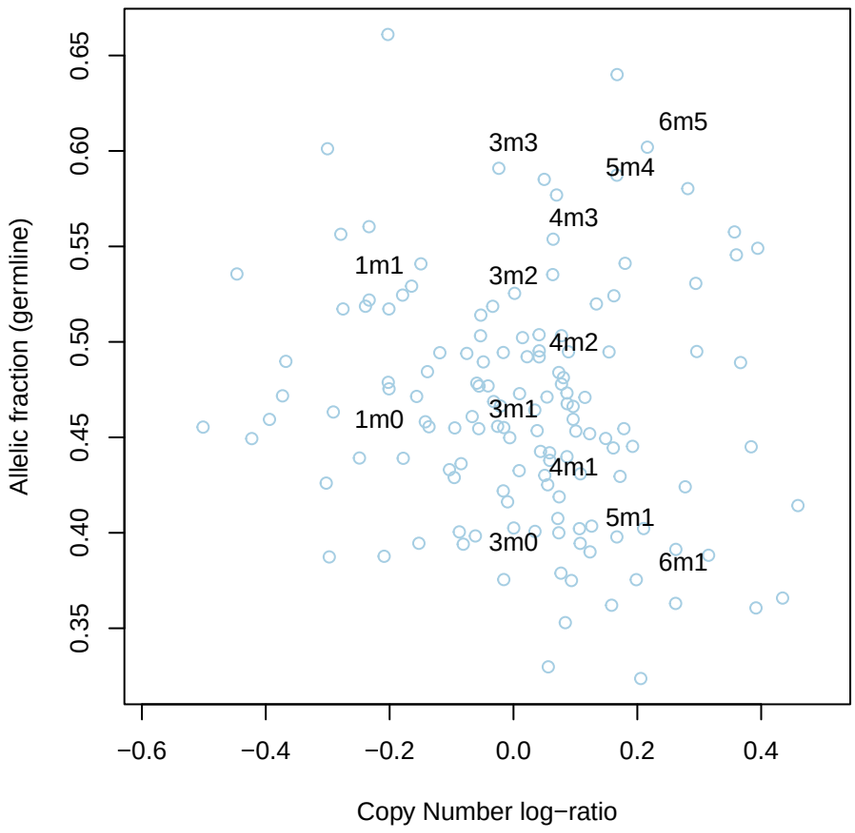

Frequency
Cellular fraction

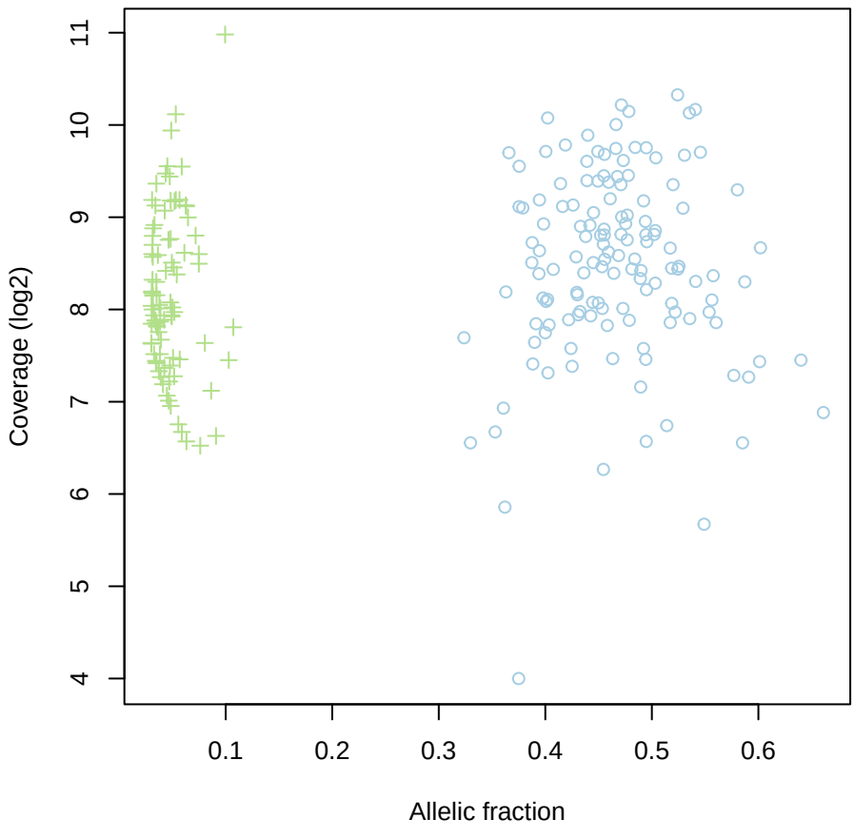

Purity: 0.15 Tumor ploidy: 2.997
0
1
3
4
5
6
7
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

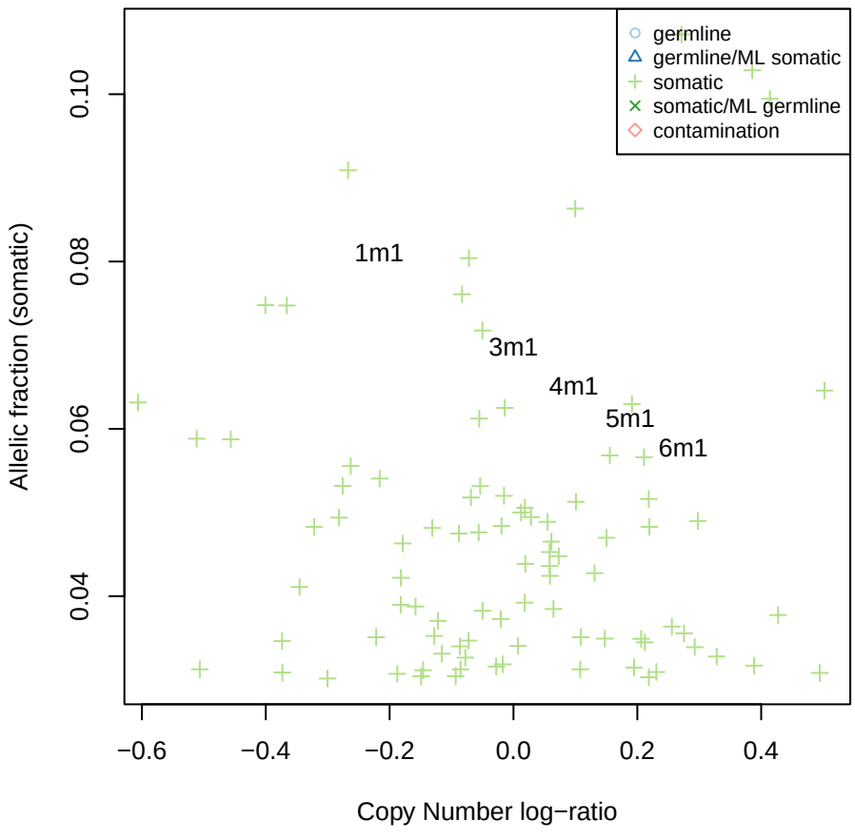

Purity: 0.15 Tumor ploidy: 2.997 SNV log−likelihood: −3.6 GoF: 97.1% Mean coverage: 385;403
1 2 3 4 5 6 7 8 9 10 12 13 14 15 17 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

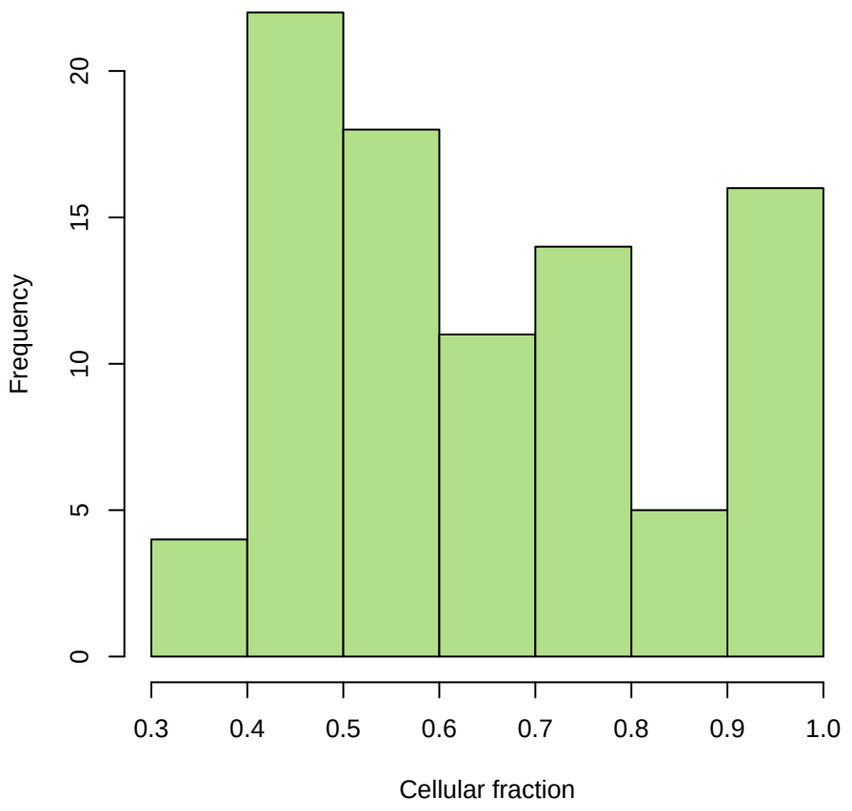

SCNA−fit log−likelihood: −2798.99
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
0 3 5 7
0 20 40 60 80 100 120 140
SNV Index

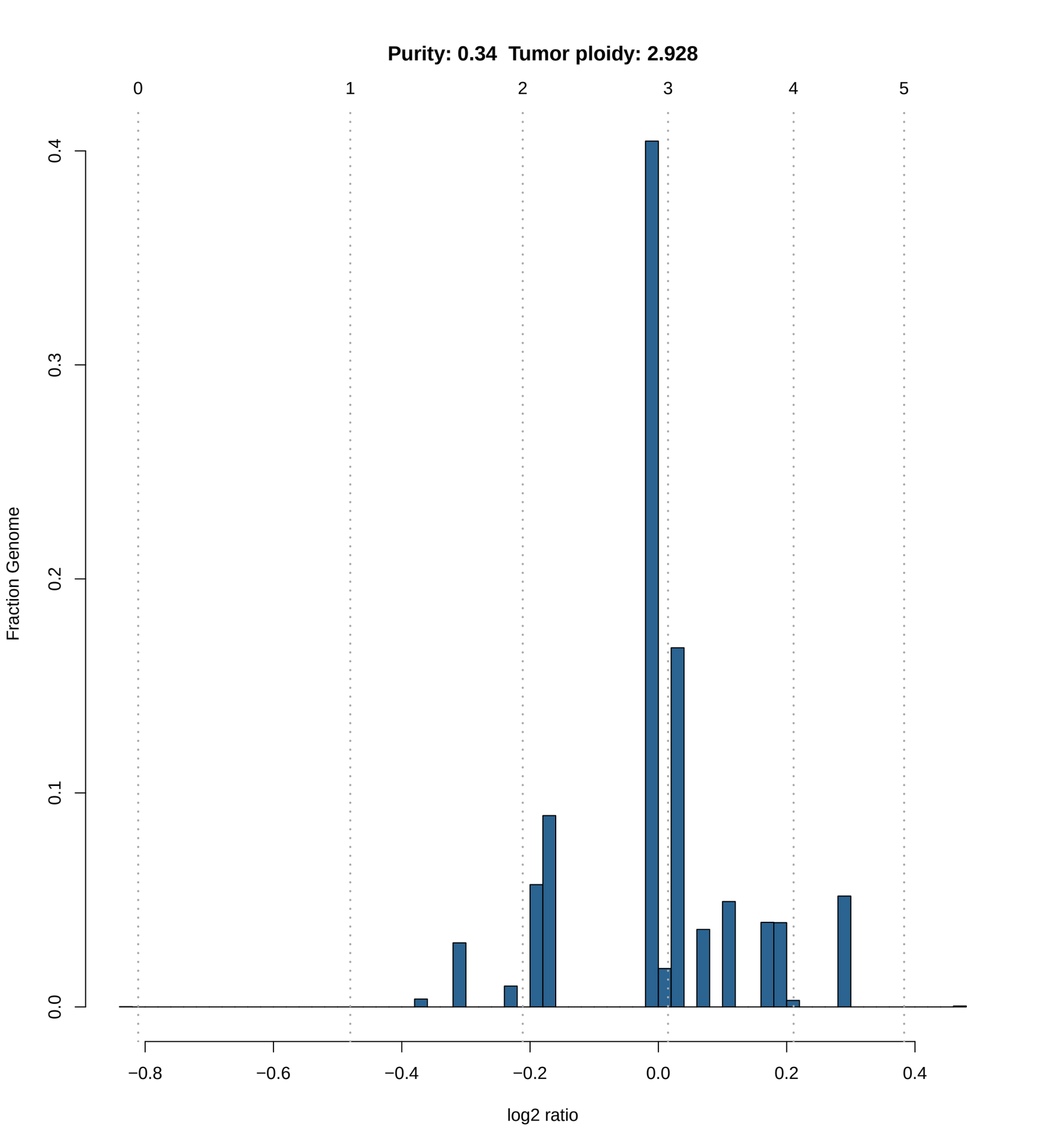

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

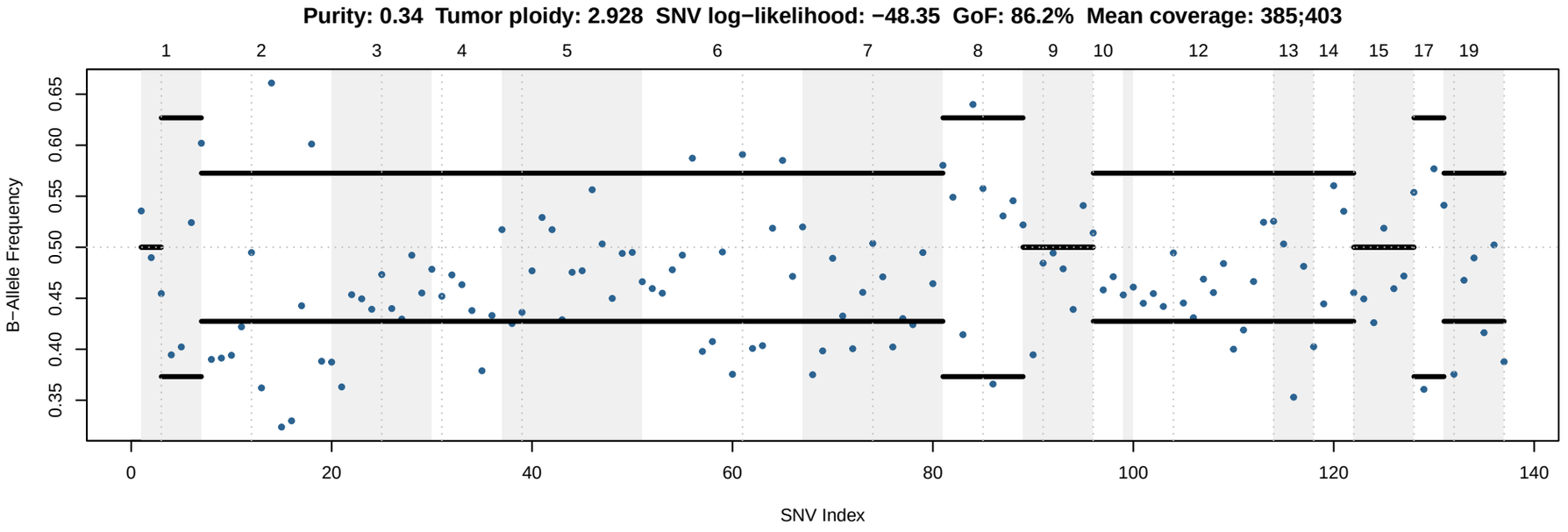

Allelic fraction (germline)
Copy Number log−ratio
0.35
0.40
0.45
0.50
0.55
0.60
0.65
−0.6
−0.4
−0.2
0.0
0.2
0.4
1m1
1m0
3m3
3m2
3m1
3m0
4m3
4m2
4m1
5m4
5m1
6m5
6m1

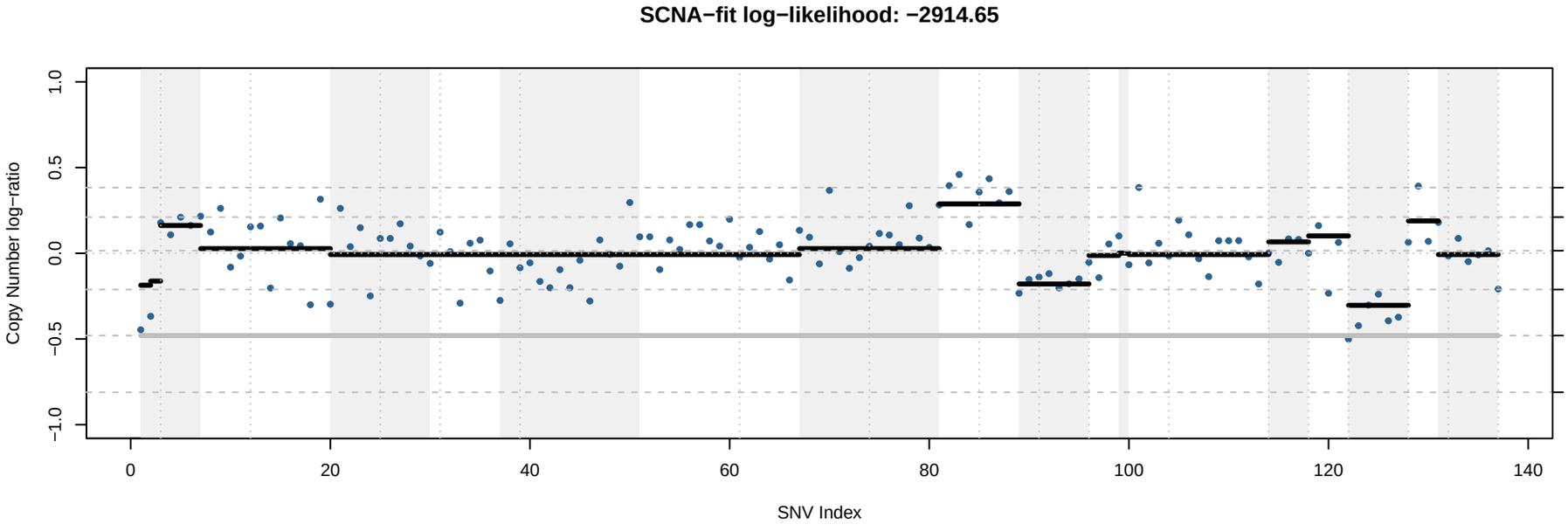

Coverage (log2)
Allelic fraction
4
5
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6

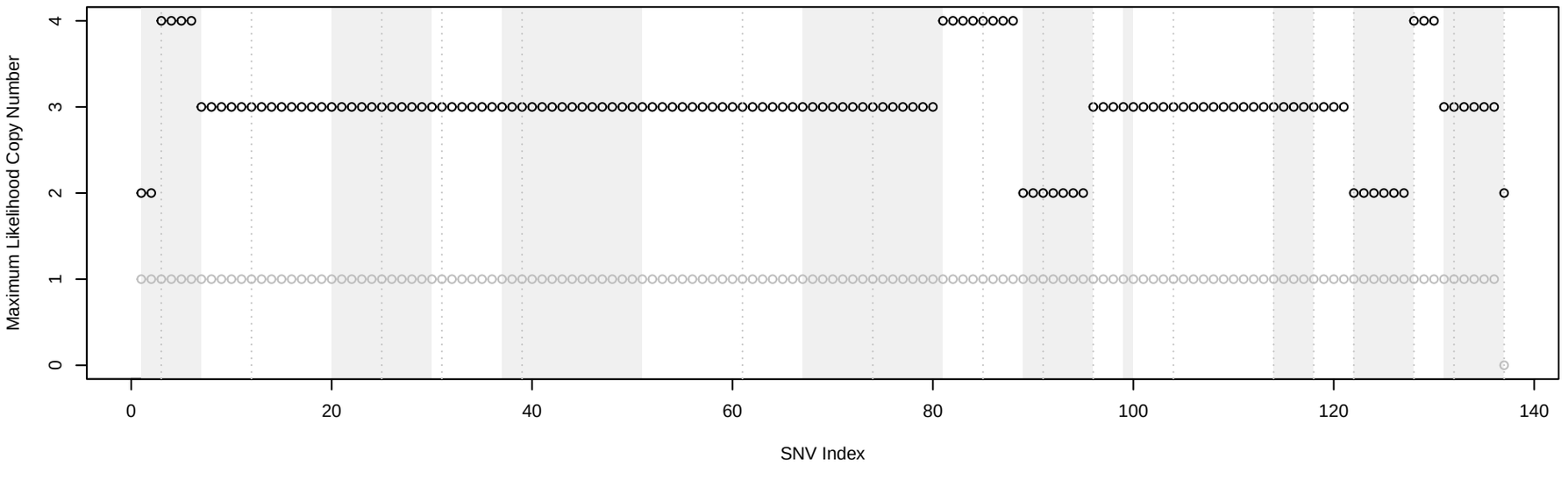

Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
−0.6
−0.4
−0.2
0.0
0.2
0.4
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
3m1
4m1
5m1
6m1

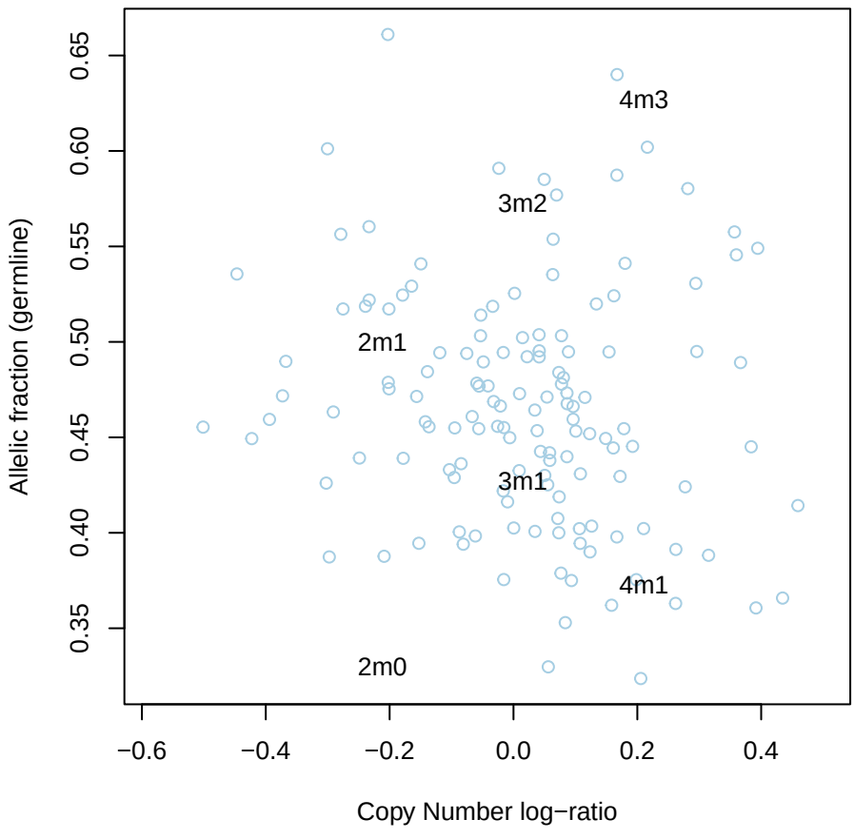

Frequency
Cellular fraction
0
5
10
15
20
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0

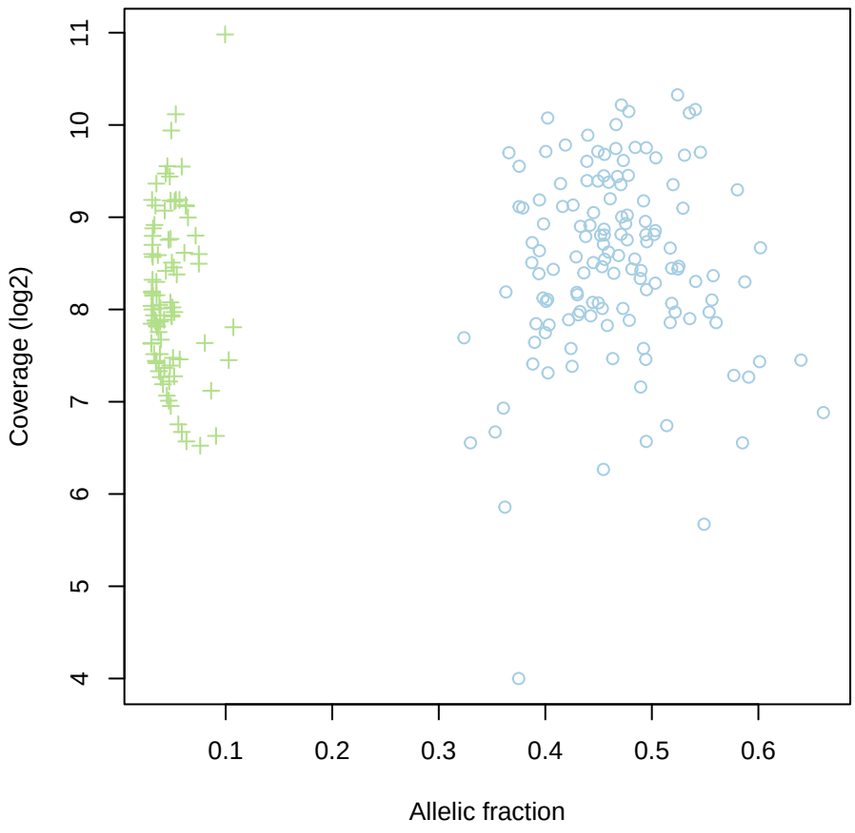

Purity: 0.34 Tumor ploidy: 2.928
0
1
2
3
4
5
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

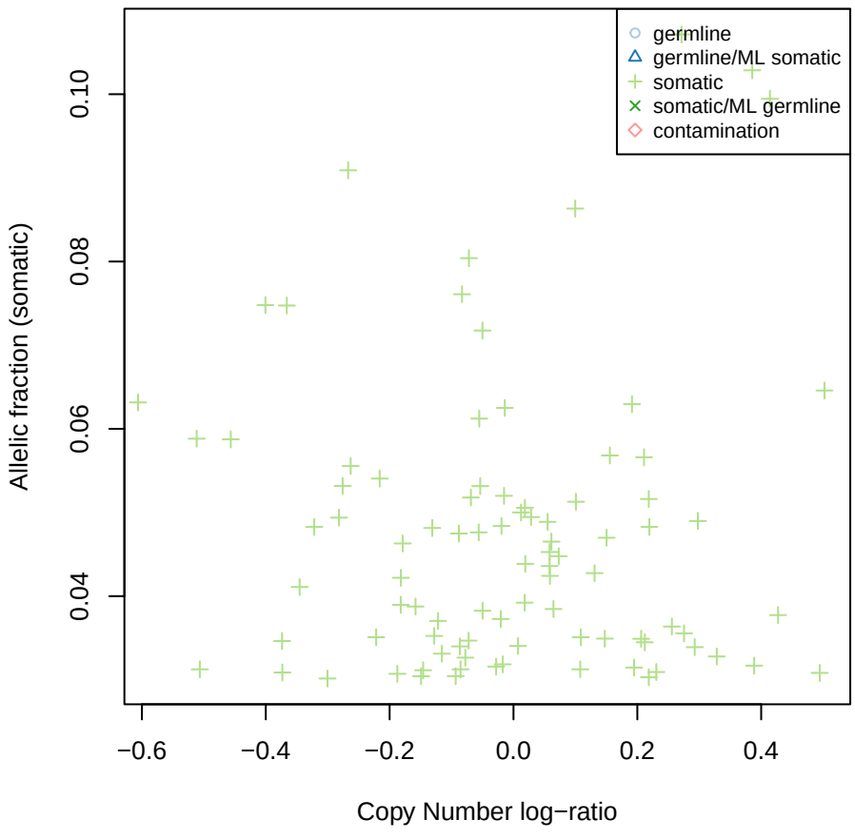

Purity: 0.34 Tumor ploidy: 2.928 SNV log−likelihood: −48.35 GoF: 86.2% Mean coverage: 385;403
1 2 3 4 5 6 7 8 9 10 12 13 14 15 17 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

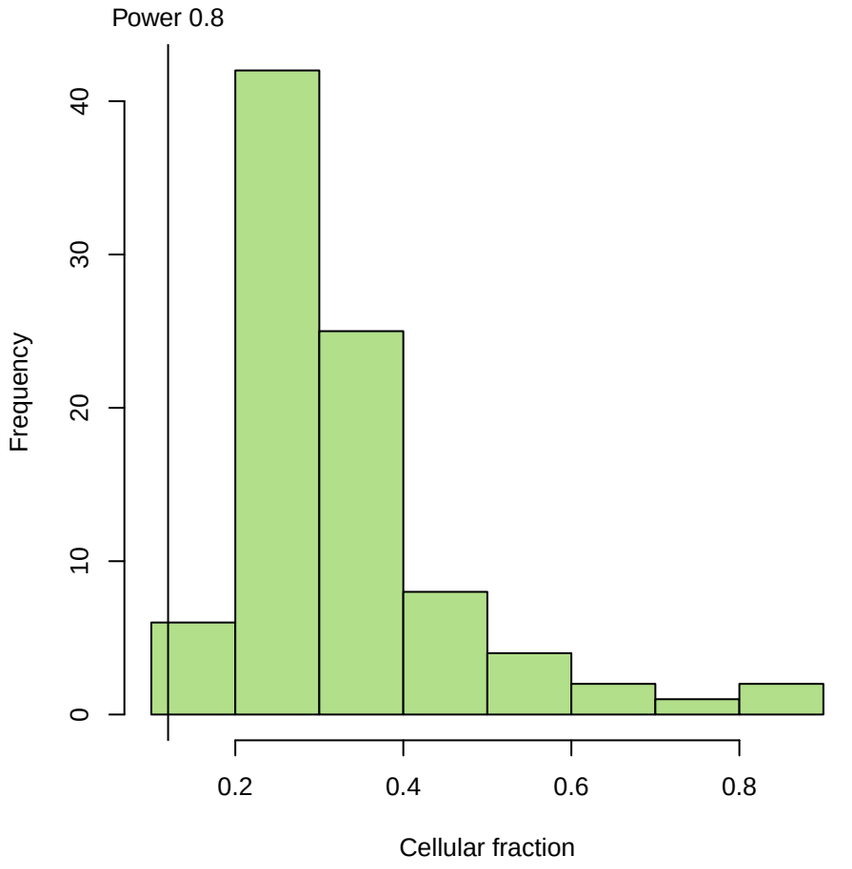

SCNA−fit log−likelihood: −2914.65
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
0 1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

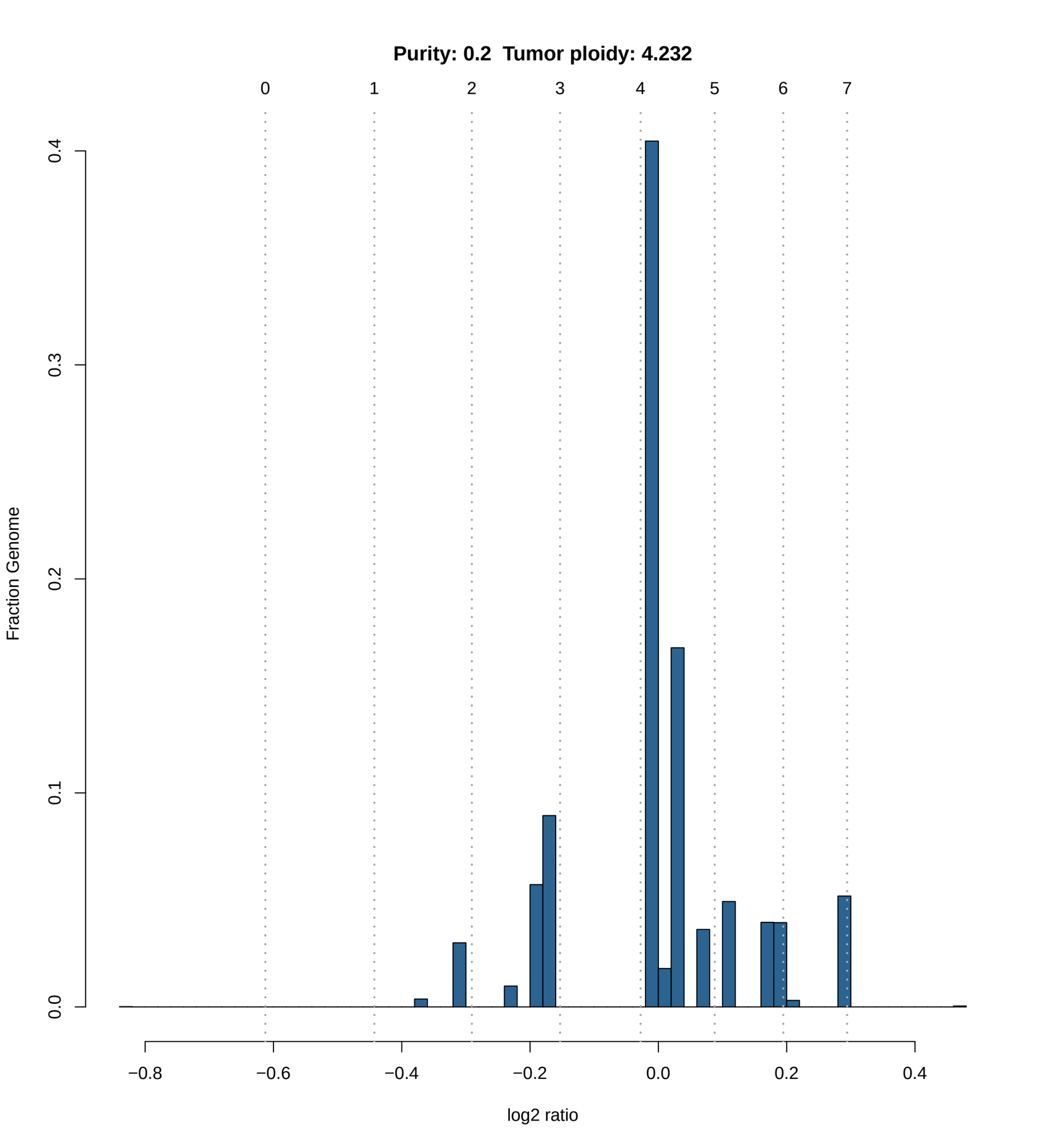

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120 140
SNV Index

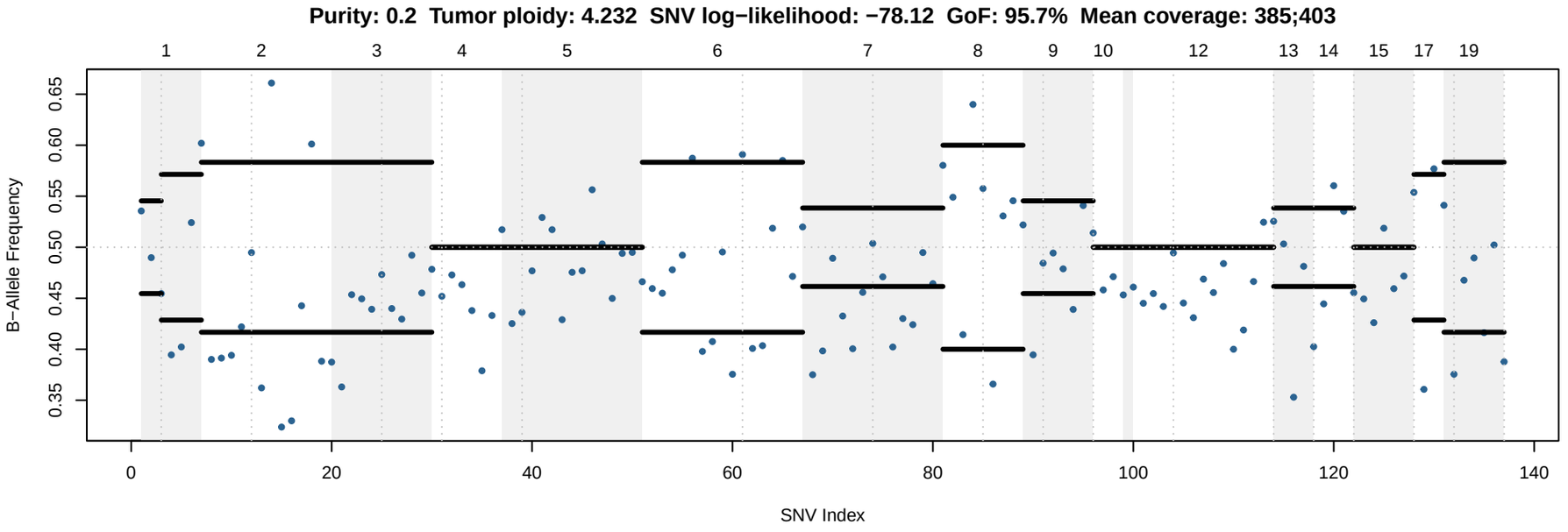

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
2m1
3m1
4m1
2m0

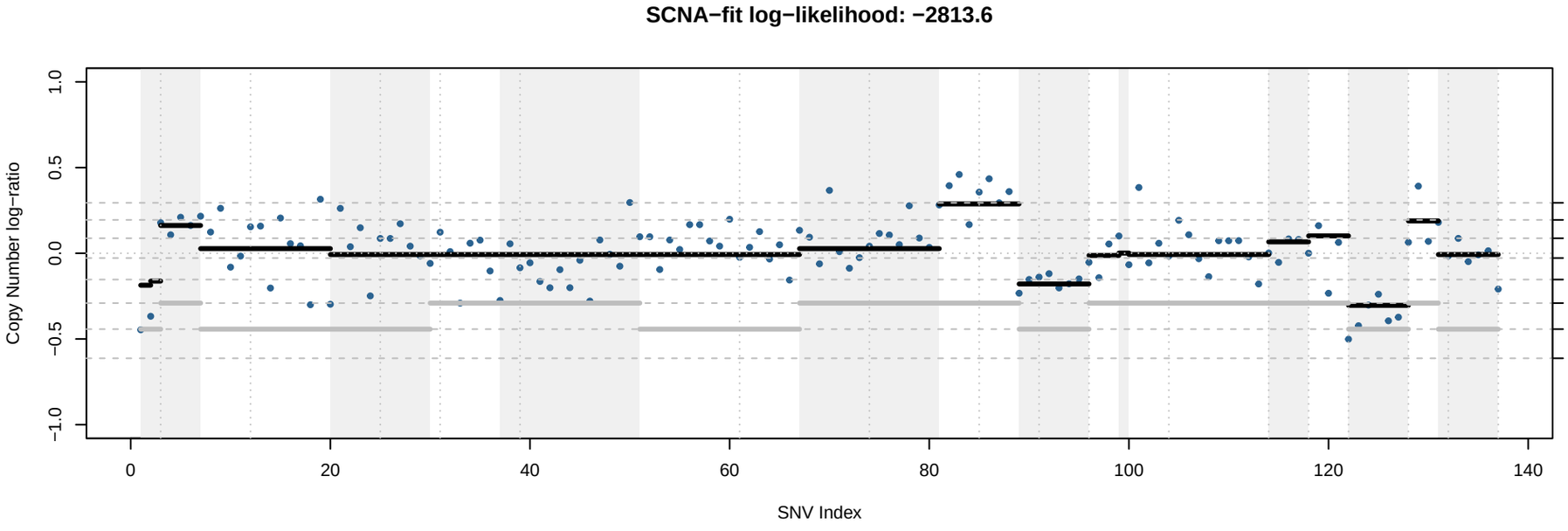

Coverage (log2)
Allelic fraction

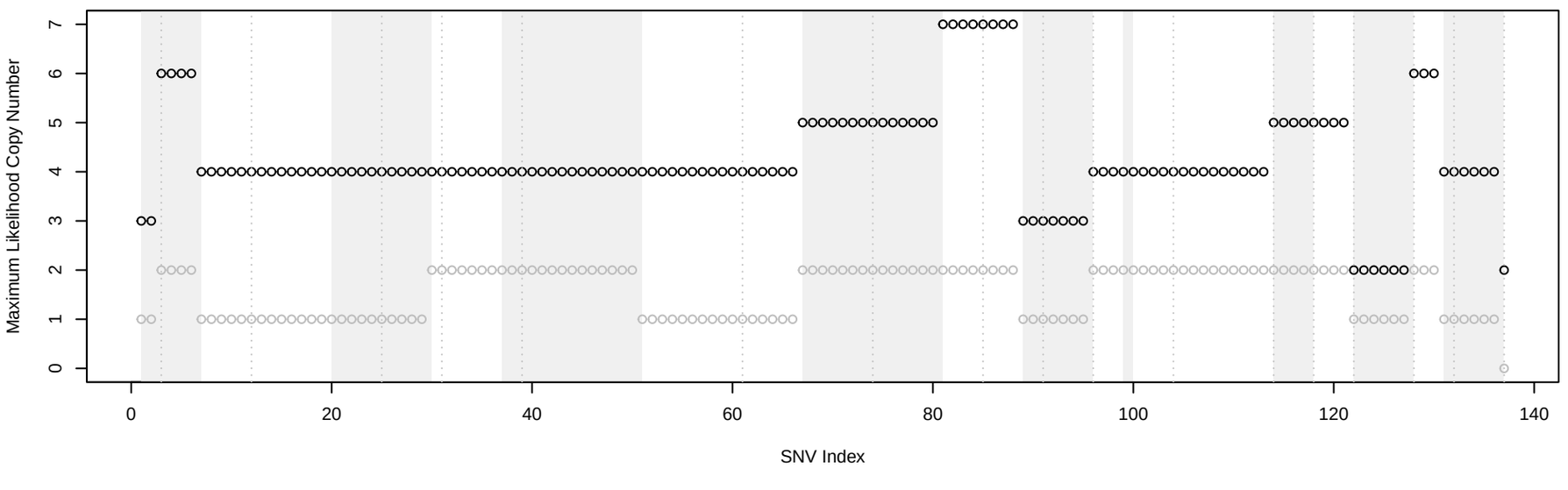

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

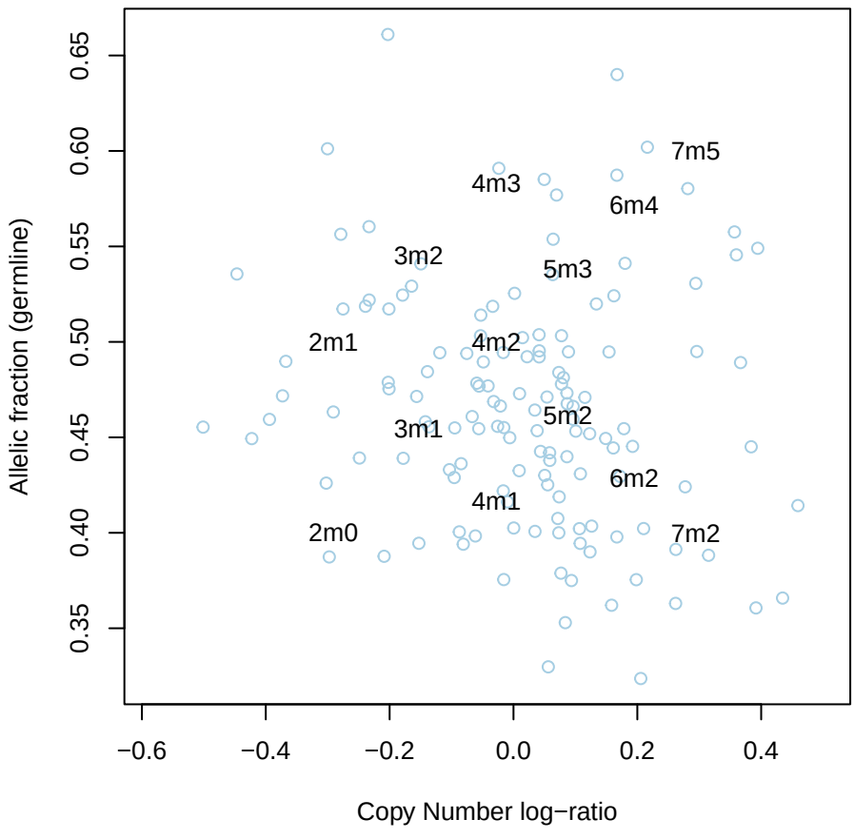

Power 0.8
Frequency
Cellular fraction

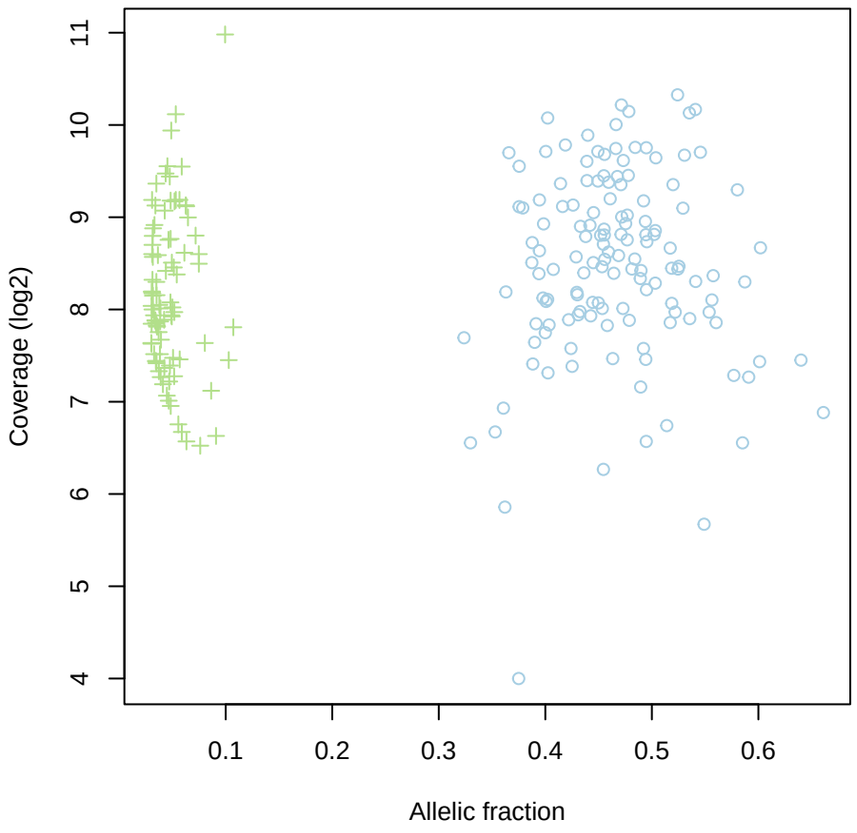

Purity: 0.2 Tumor ploidy: 4.232
0
1
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

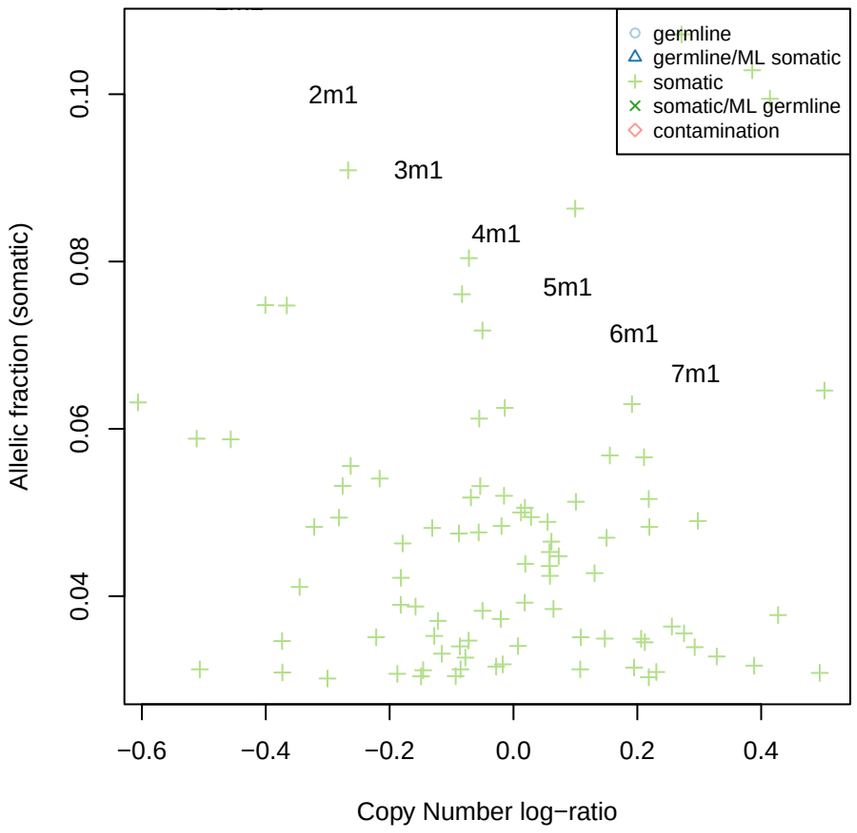

Purity: 0.2 Tumor ploidy: 4.232 SNV log−likelihood: −78.12 GoF: 95.7% Mean coverage: 385;403
1 2 3 4 5 6 7 8 9 10 12 13 14 15 17 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

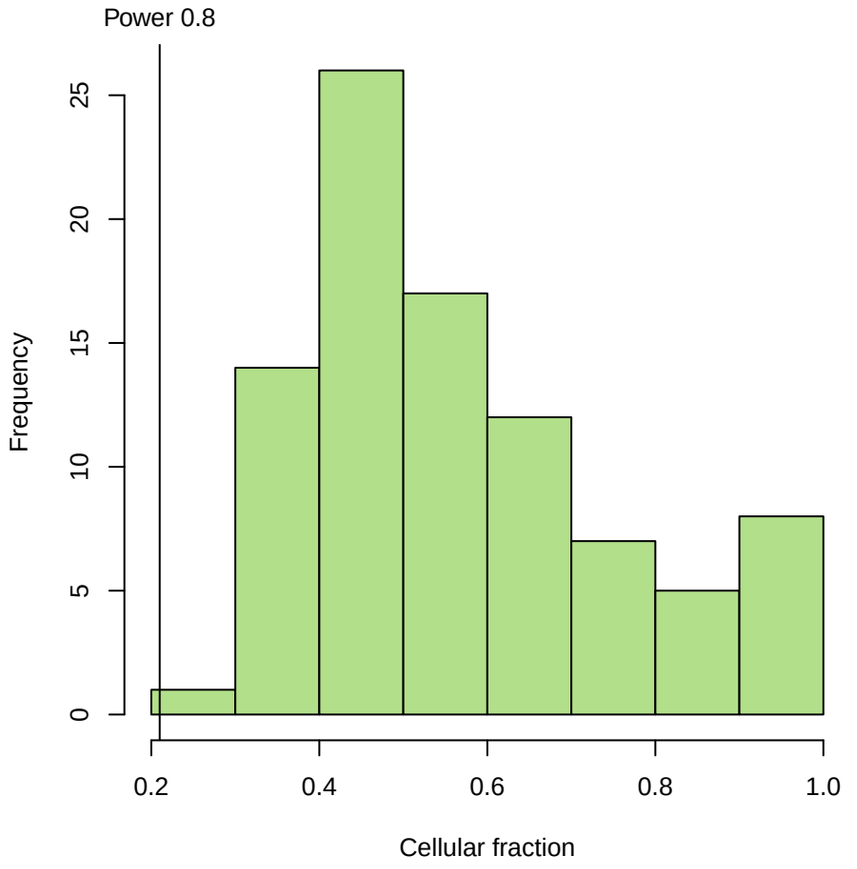

SCNA−fit log−likelihood: −2813.6
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 4 6
0 20 40 60 80 100 120 140
SNV Index

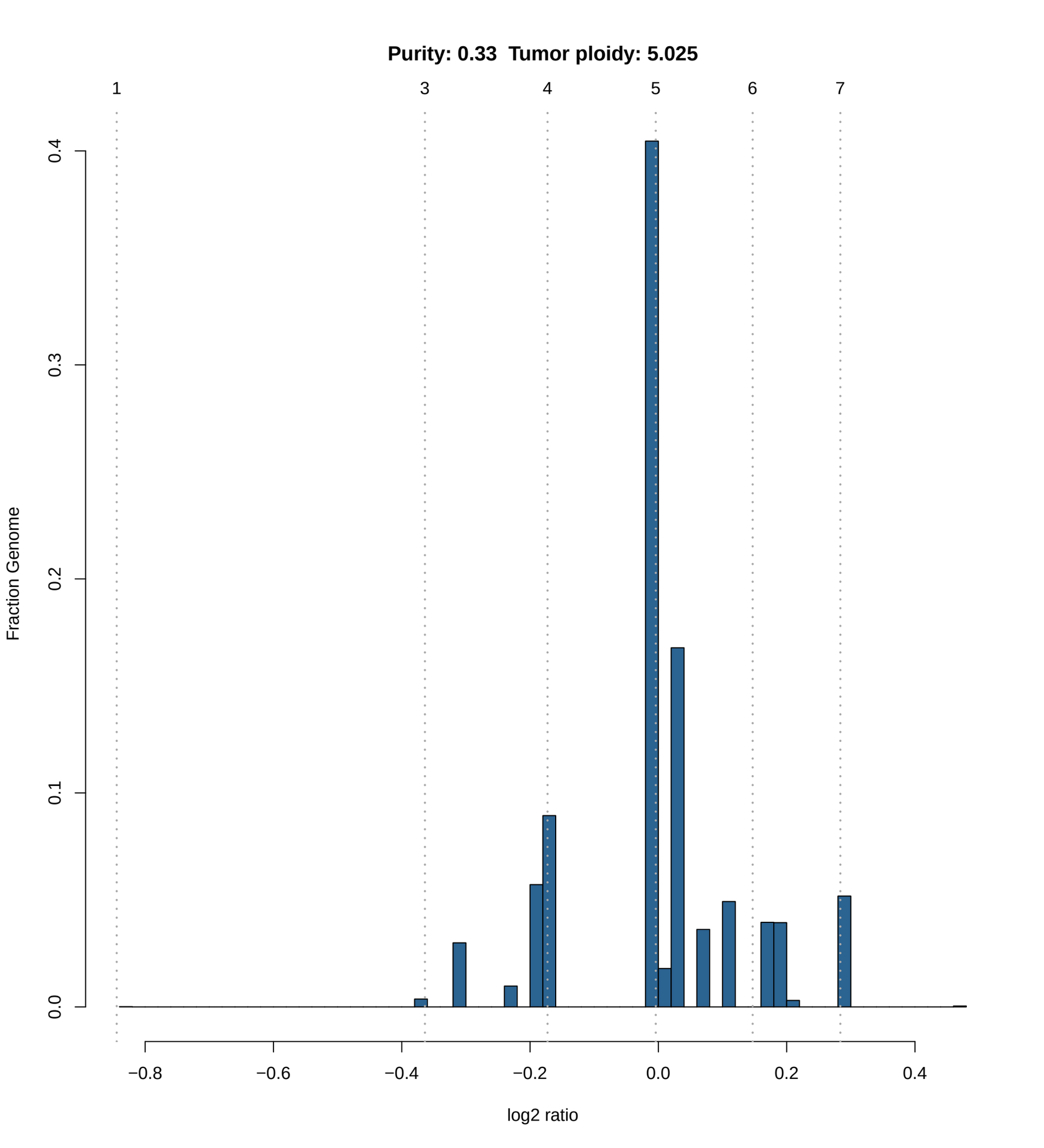

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

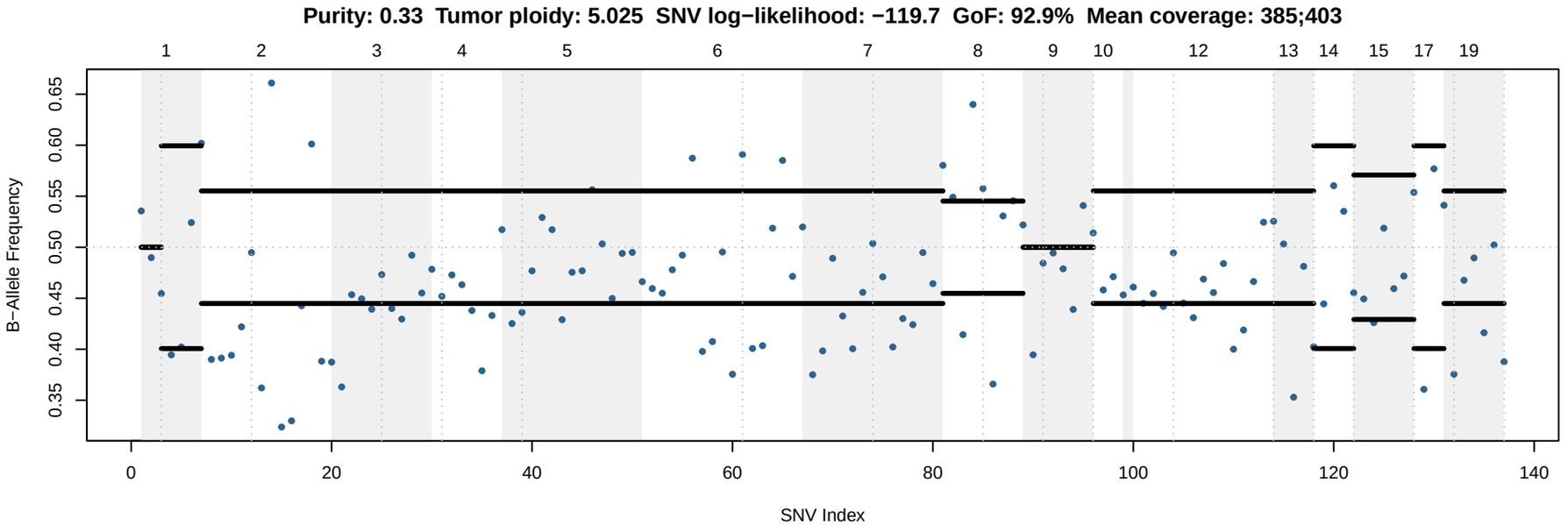

Allelic fraction (germline)
Copy Number log−ratio
7m5
4m3
6m4
3m2
5m3
2m1
4m2
5m2
3m1
6m2
4m1
2m0
7m2

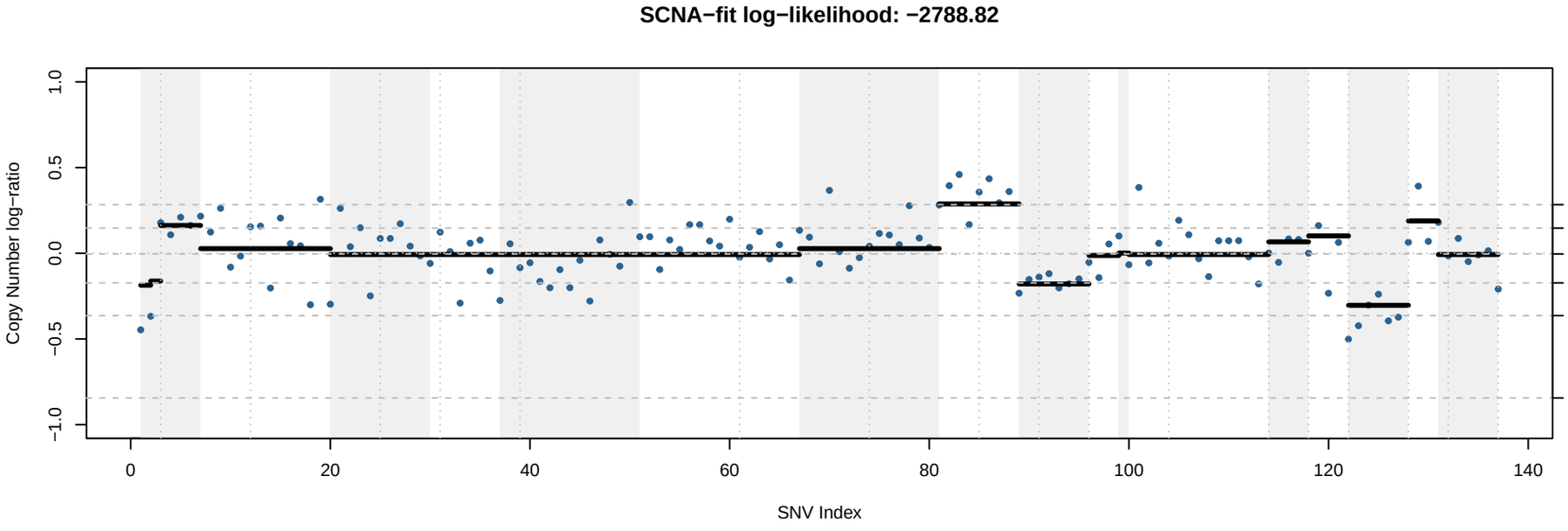

Coverage (log2)
Allelic fraction

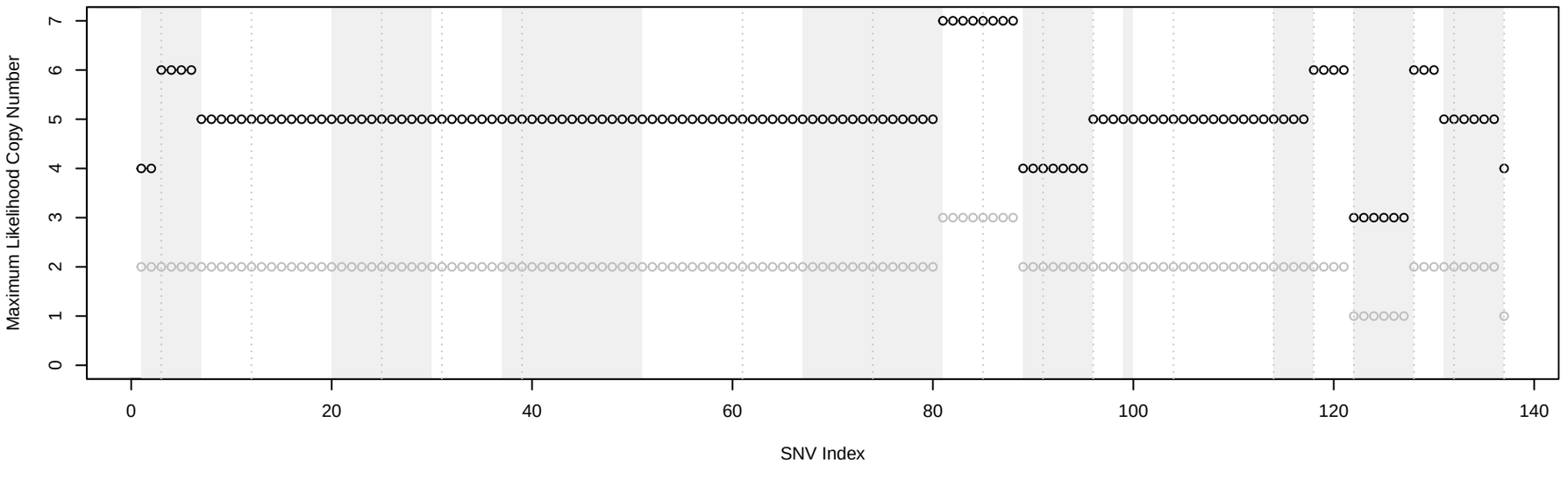

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m1
3m1
4m1
5m1
6m1
7m1

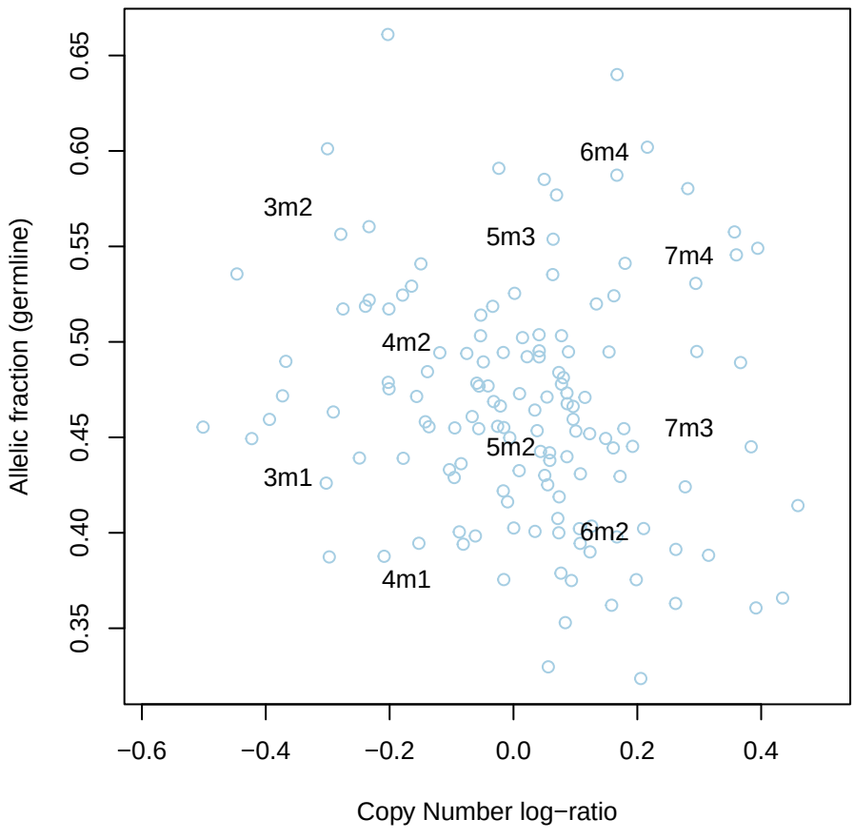

Power 0.8
Frequency
Cellular fraction

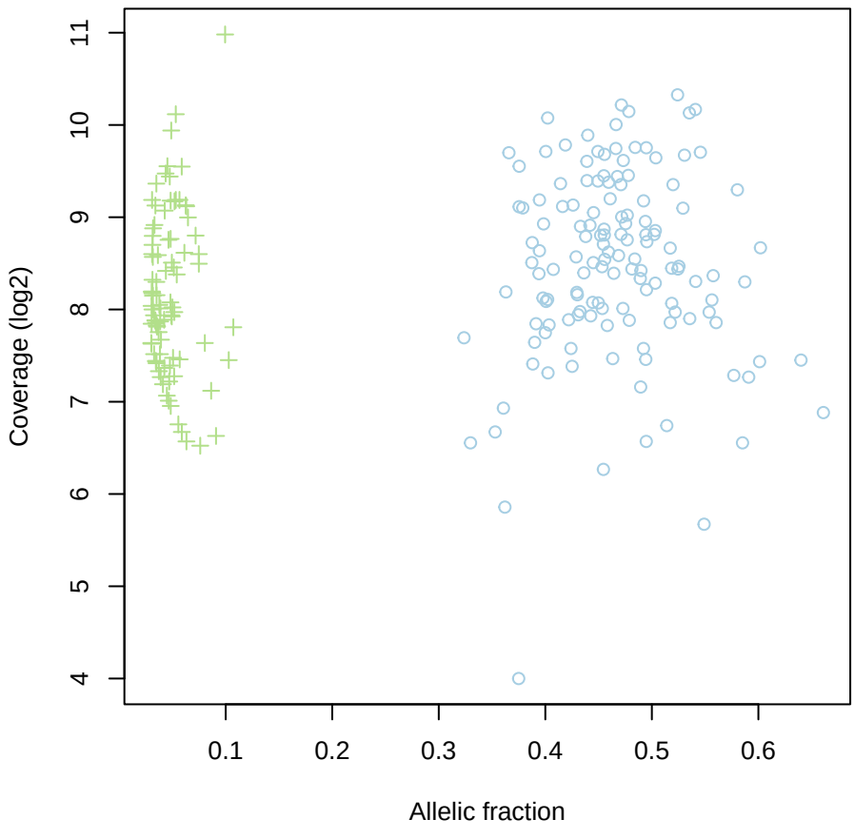

Purity: 0.33 Tumor ploidy: 5.025
1
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

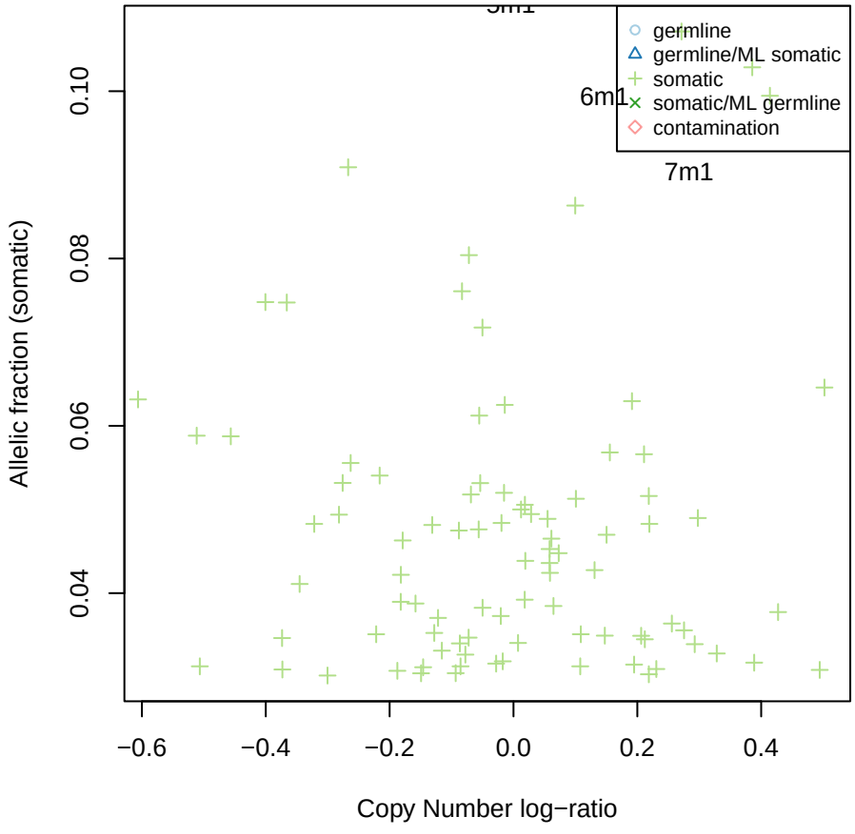

Purity: 0.33 Tumor ploidy: 5.025 SNV log−likelihood: −119.7 GoF: 92.9% Mean coverage: 385;403
1 2 3 4 5 6 7 8 9 10 12 13 14 15 17 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

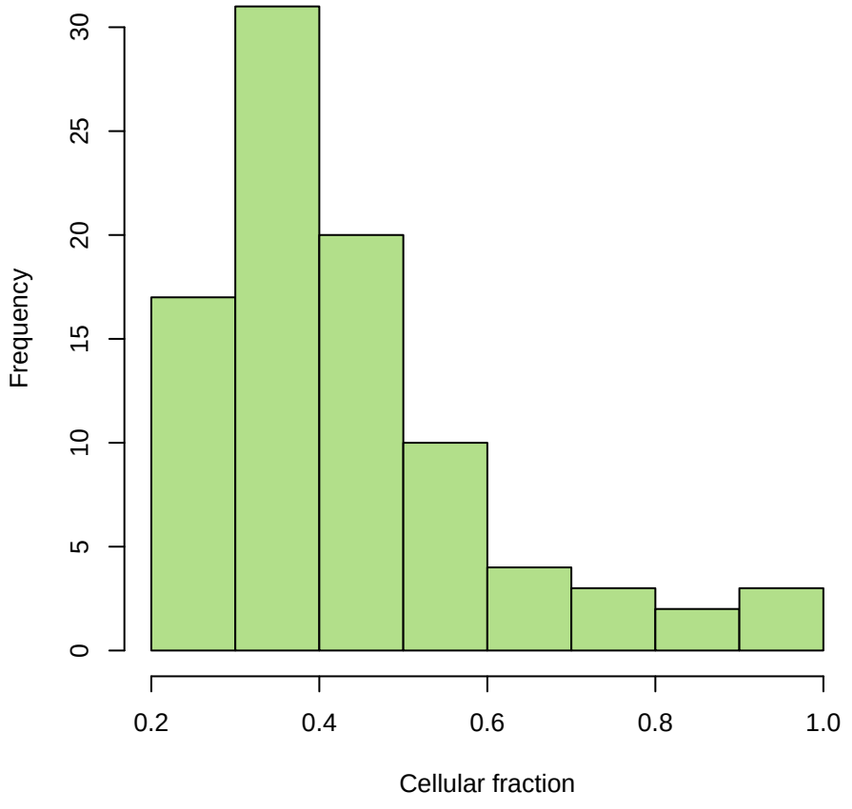

SCNA−fit log−likelihood: −2788.82
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
1 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

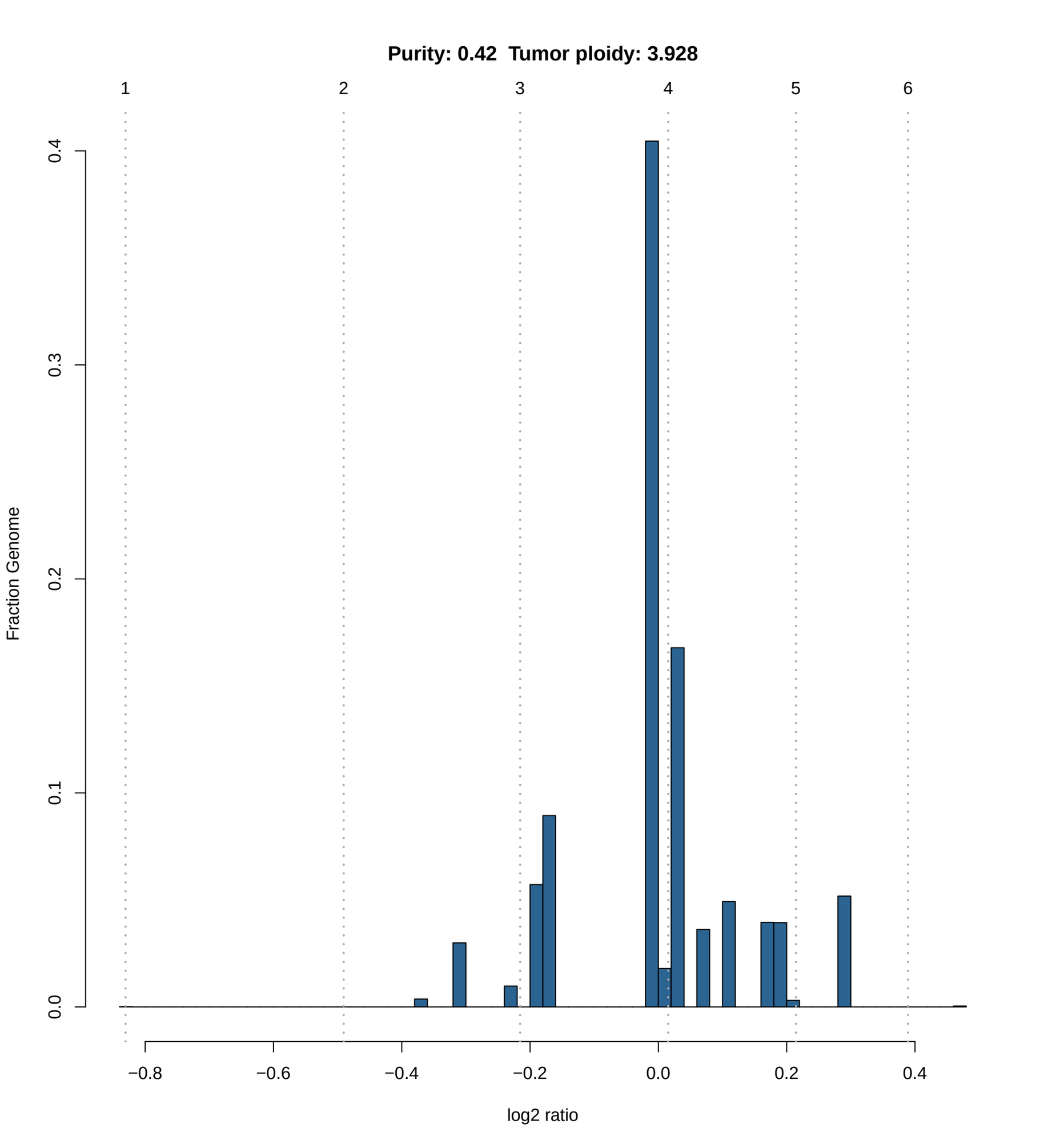

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

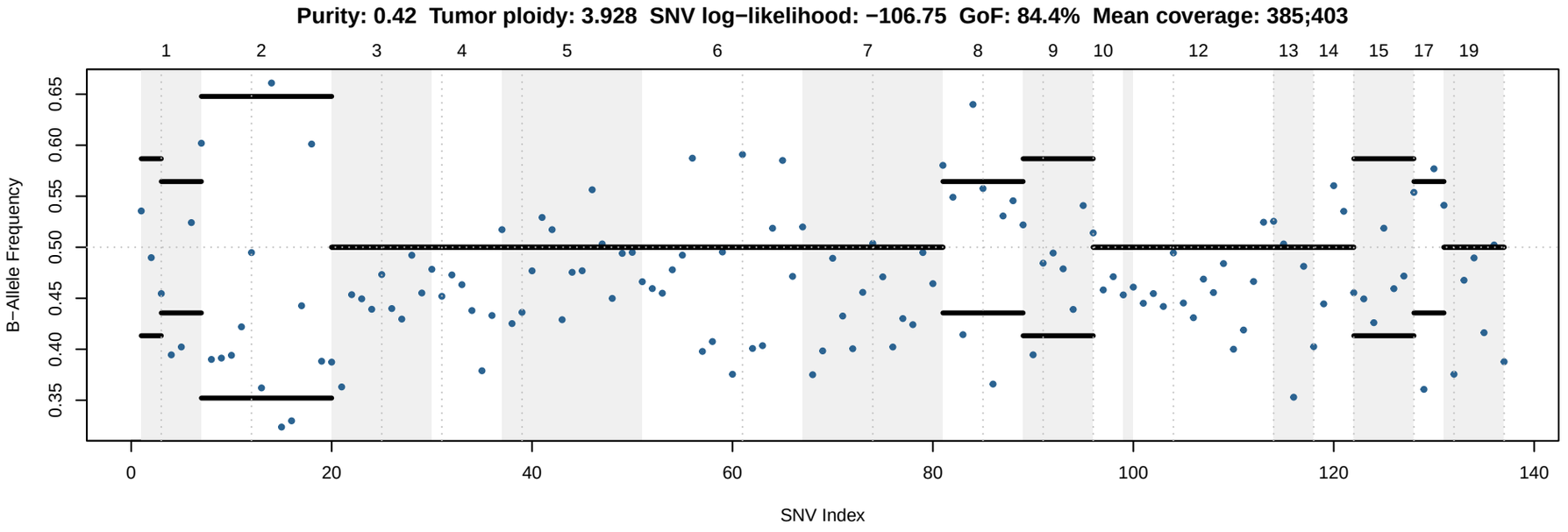

Allelic fraction (germline)
Copy Number log−ratio
3m2
6m4
5m3
7m4
4m2
7m3
5m2
3m1
6m2
4m1

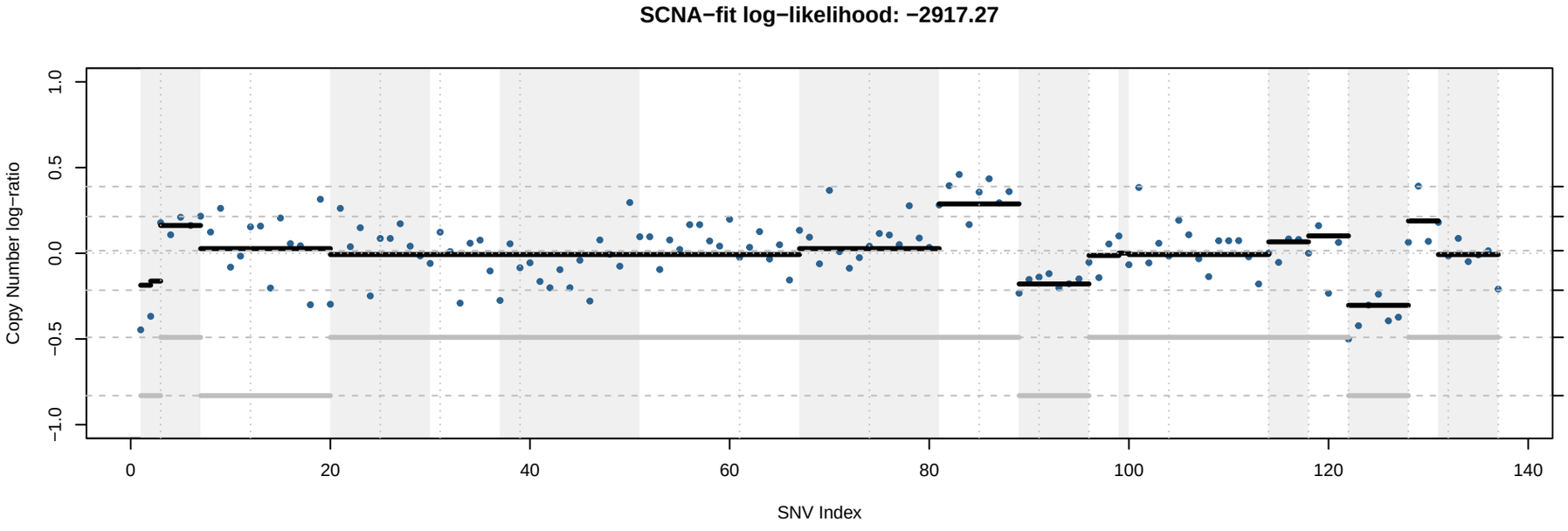

Coverage (log2)
Allelic fraction

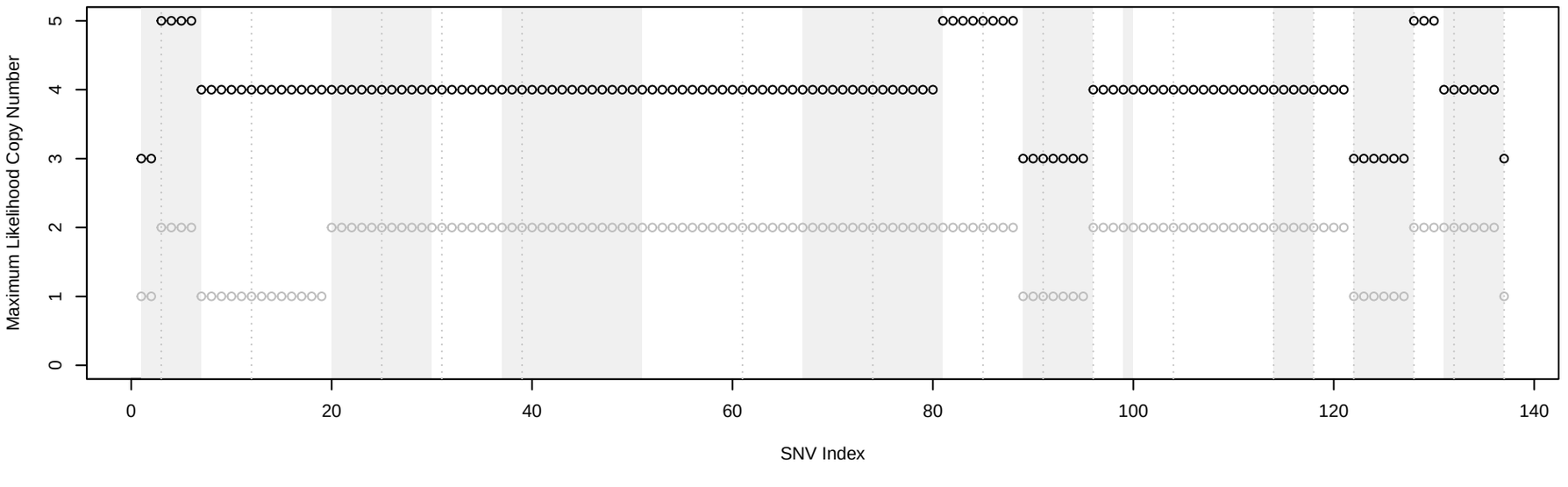

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m1
7m1

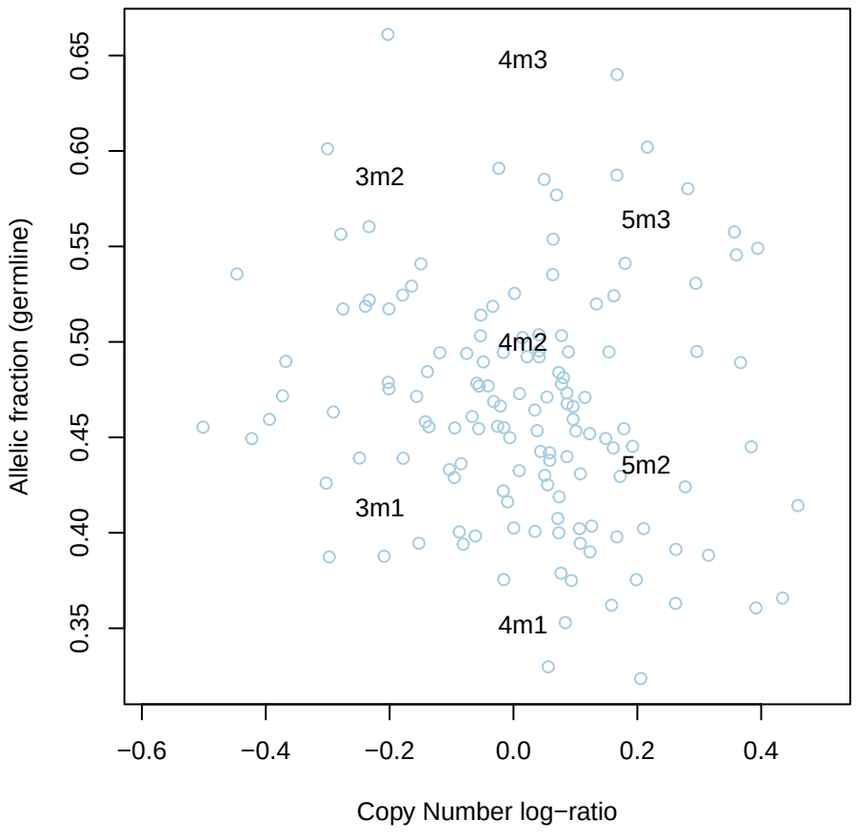

Frequency
Cellular fraction

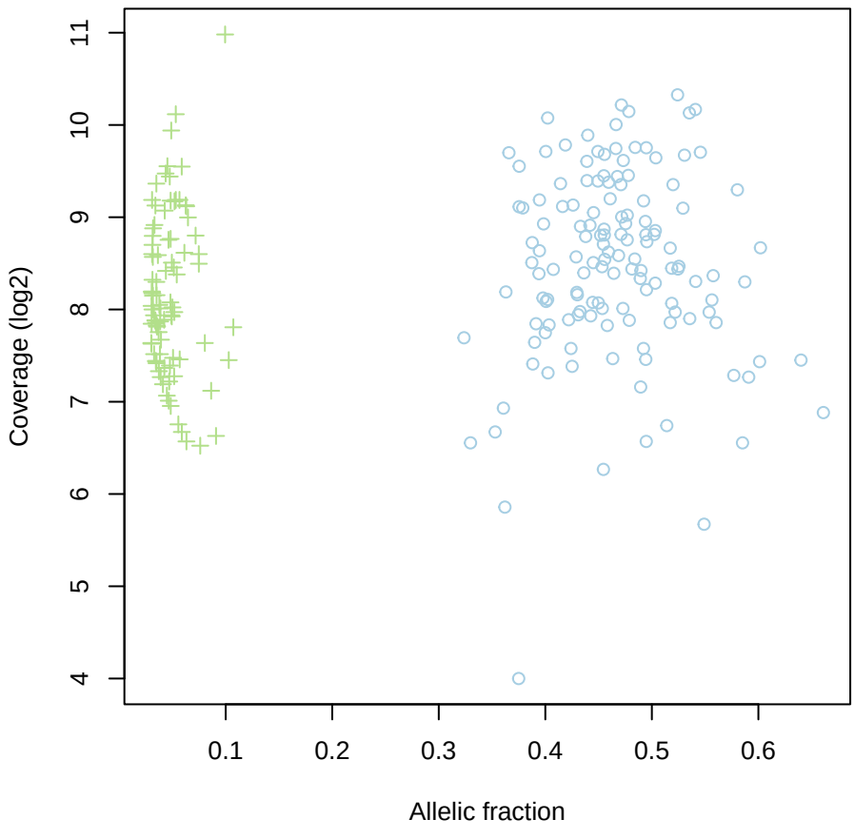

Purity: 0.42 Tumor ploidy: 3.928
1
2
3
4
5
6
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

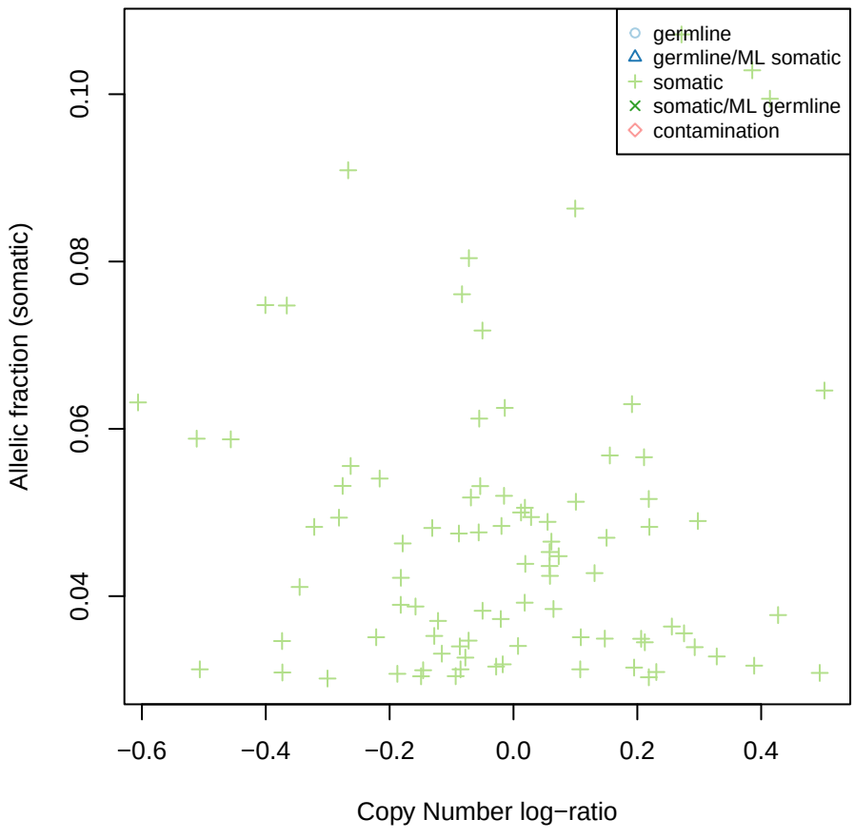

Purity: 0.42 Tumor ploidy: 3.928 SNV log−likelihood: −106.75 GoF: 84.4% Mean coverage: 385;403
1 2 3 4 5 6 7 8 9 10 12 13 14 15 17 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

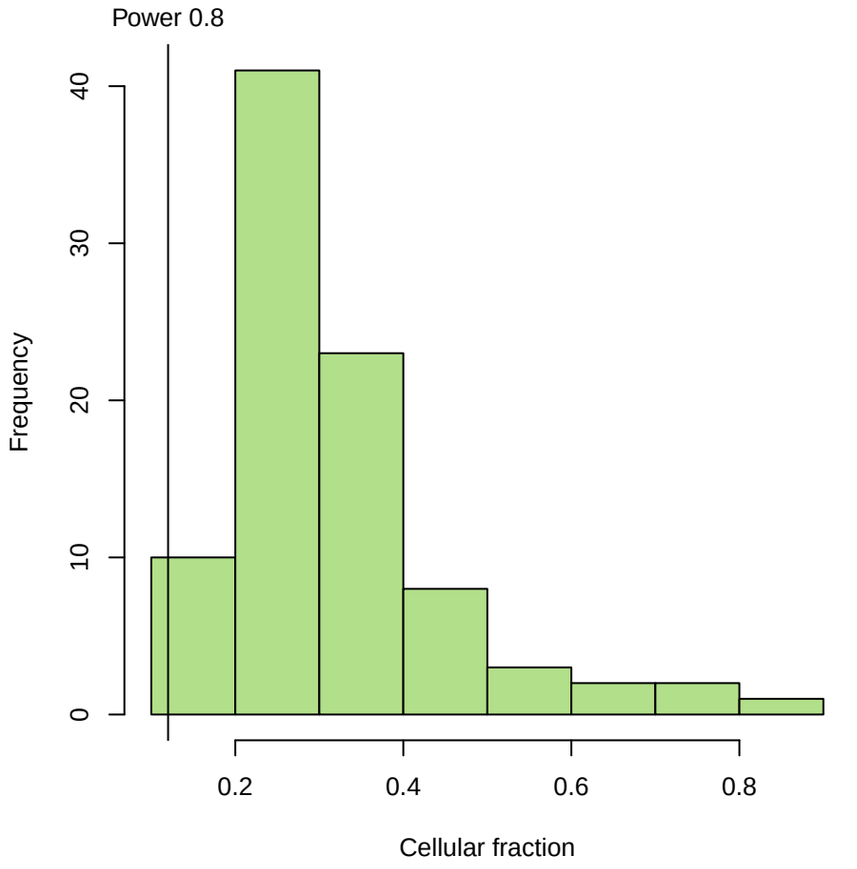

SCNA−fit log−likelihood: −2917.27
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

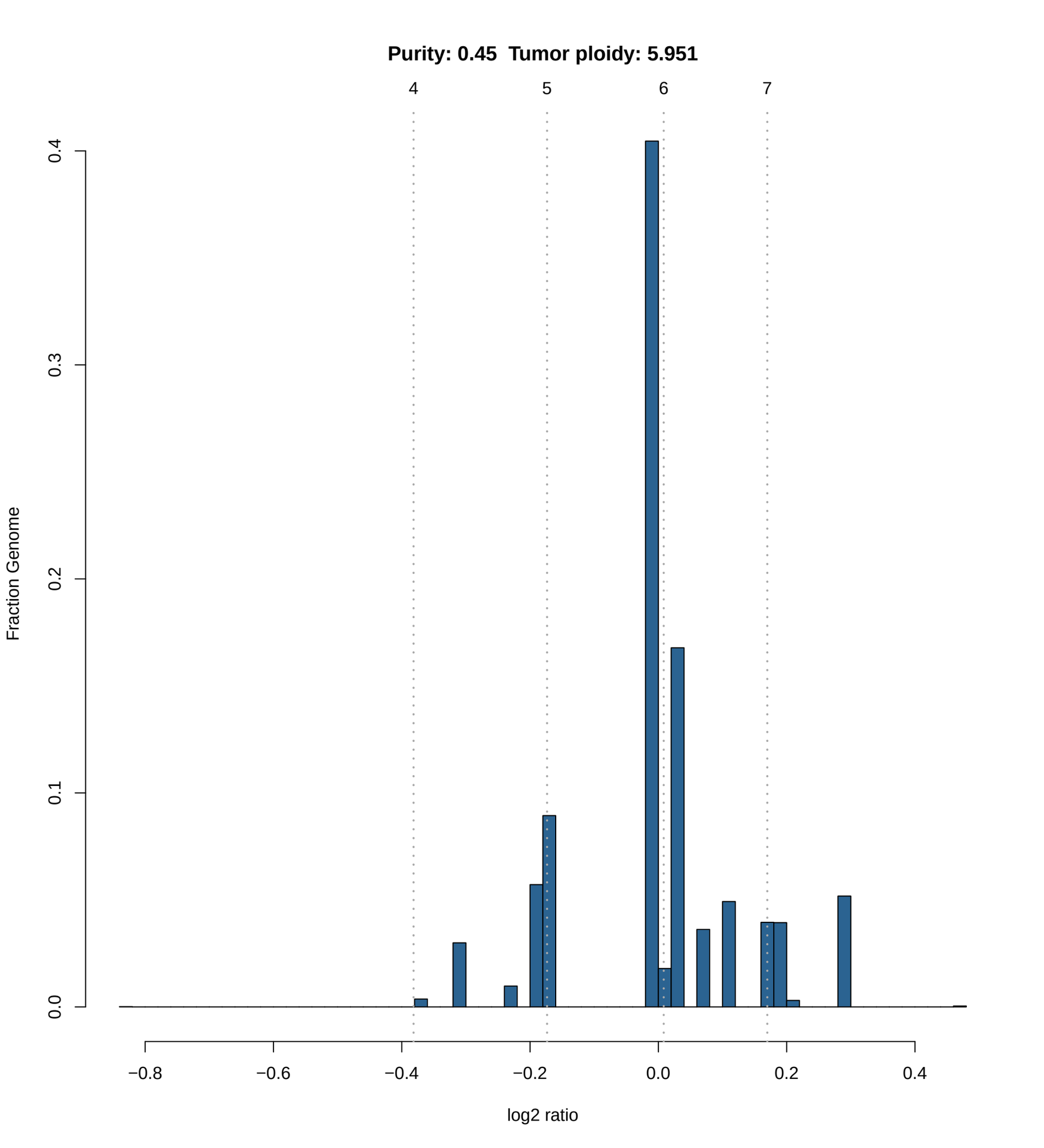

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

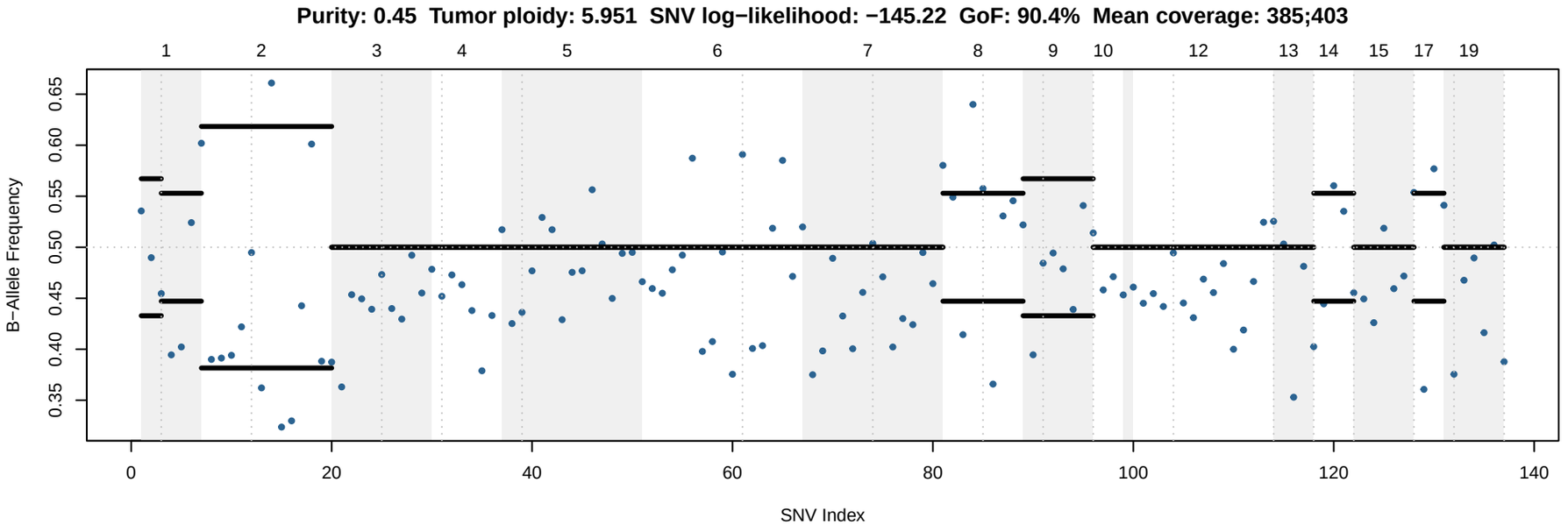

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
5m3
4m2
5m2
3m1
4m1

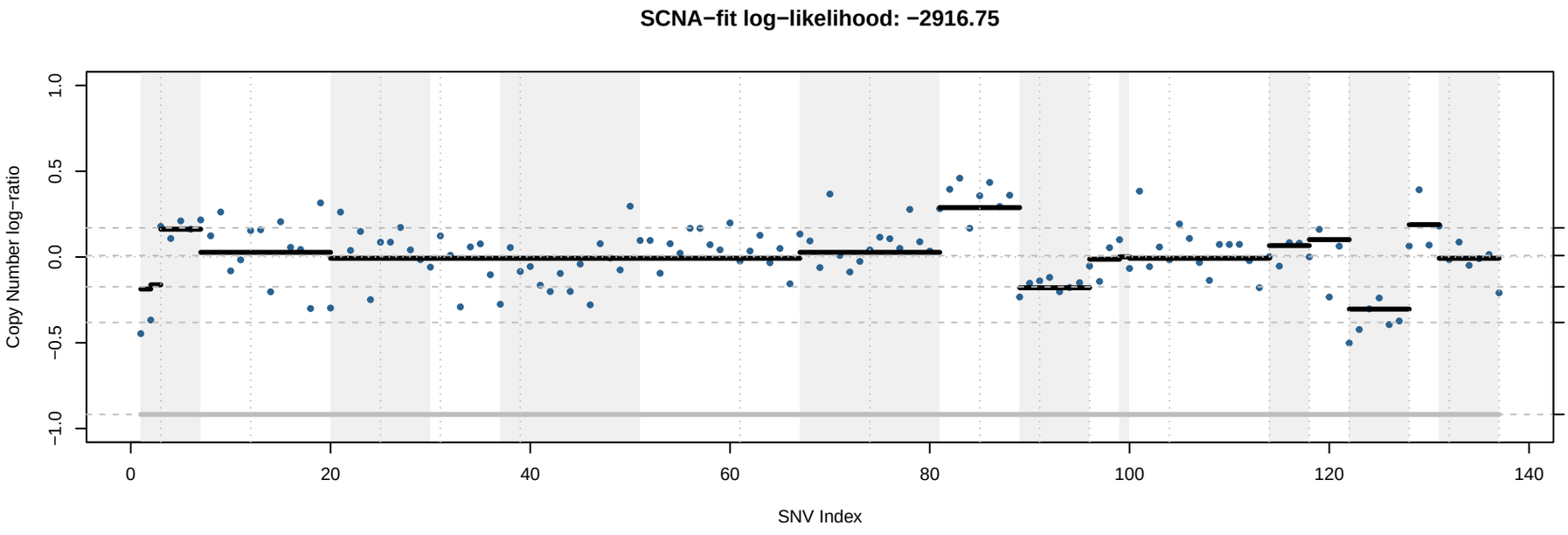

Coverage (log2)
Allelic fraction

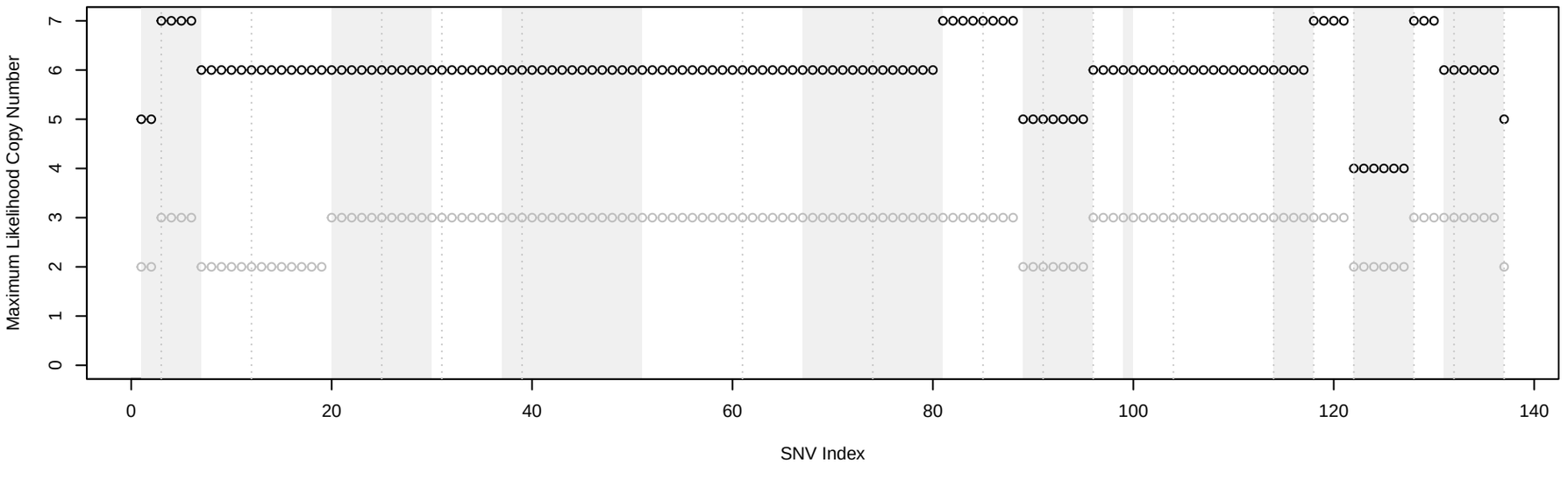

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

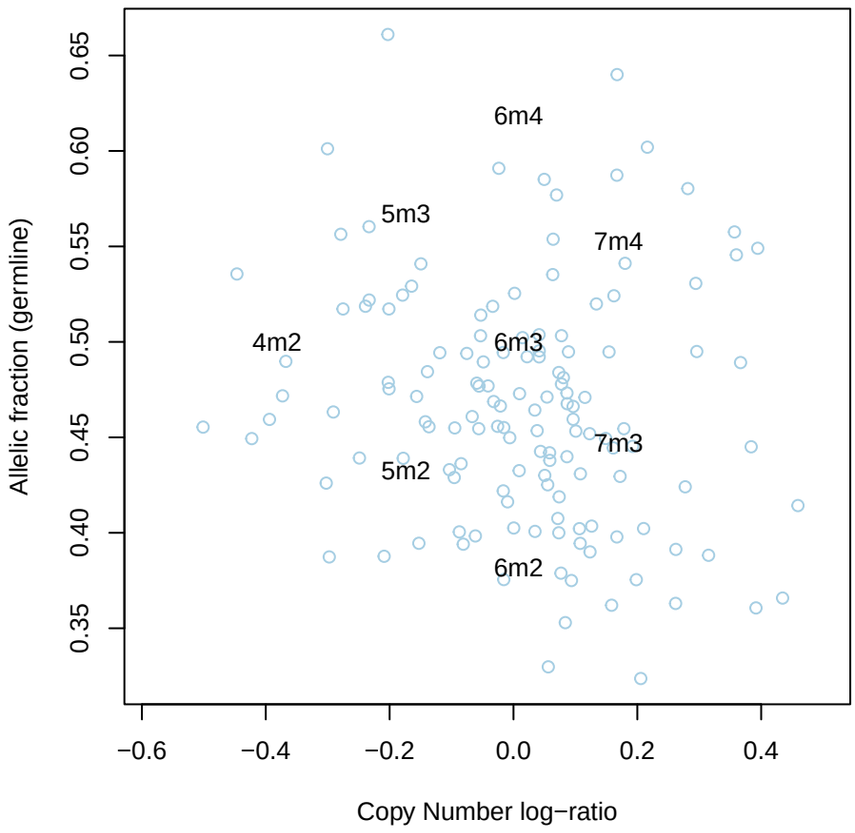

Power 0.8
Frequency
Cellular fraction

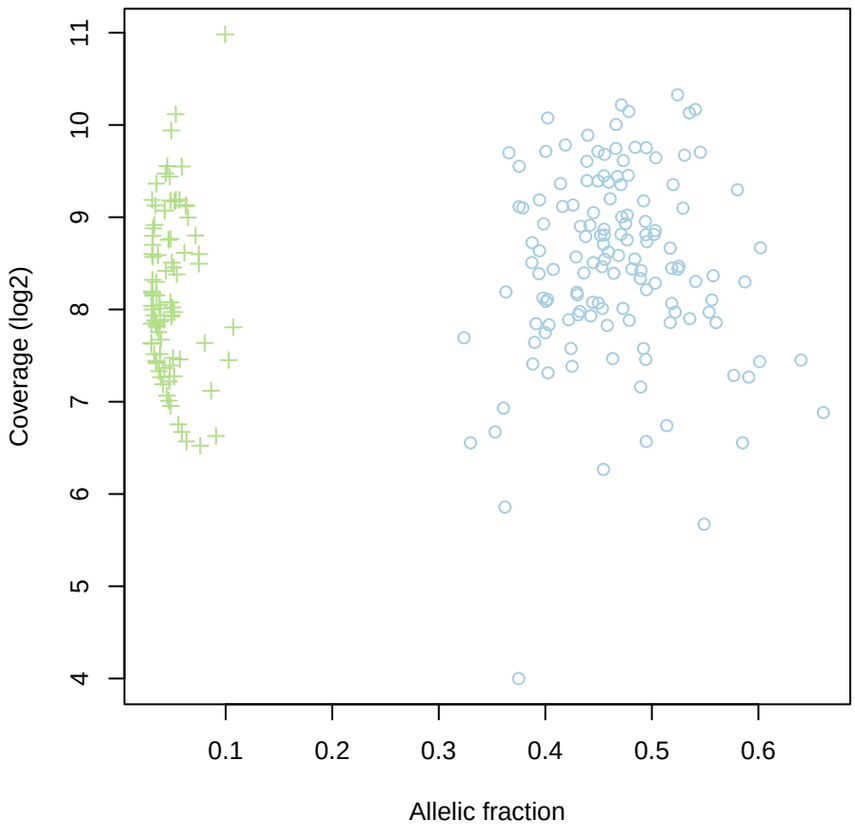

Purity: 0.45 Tumor ploidy: 5.951
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

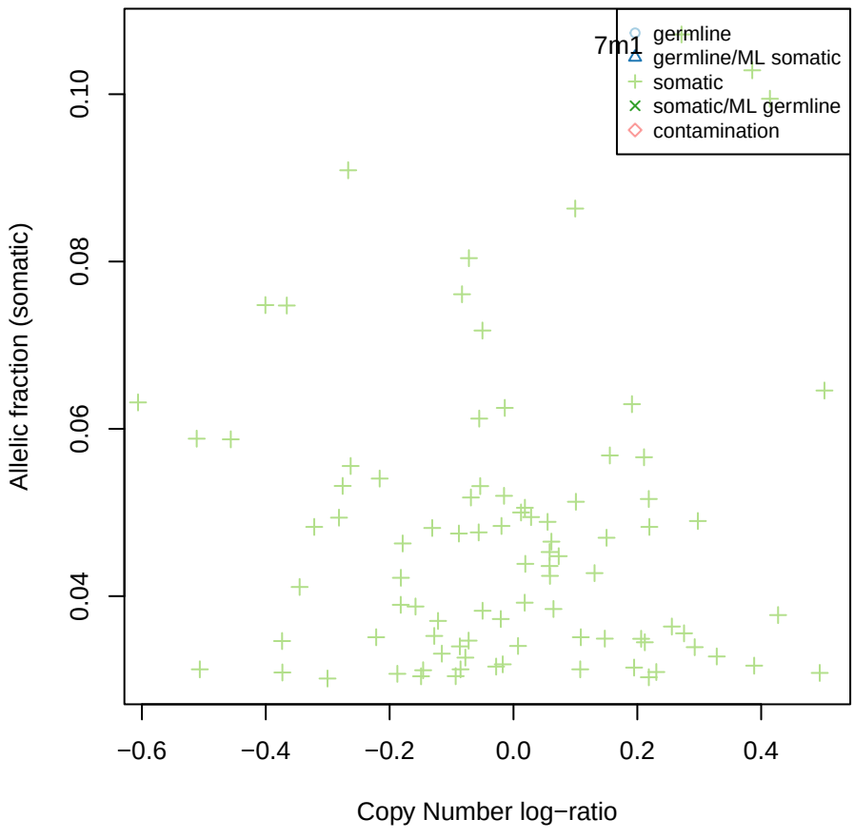

Purity: 0.45 Tumor ploidy: 5.951 SNV log−likelihood: −145.22 GoF: 90.4% Mean coverage: 385;403
1 2 3 4 5 6 7 8 9 10 12 13 14 15 17 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

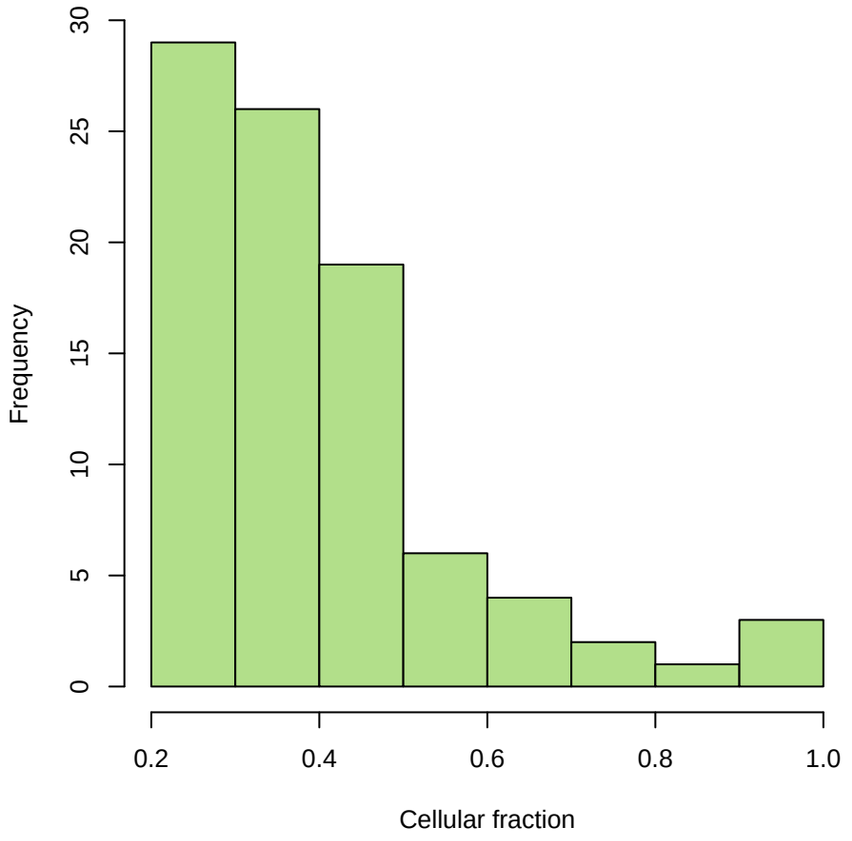

SCNA−fit log−likelihood: −2916.75
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
7 6 5 4 2
0 20 40 60 80 100 120 140
SNV Index

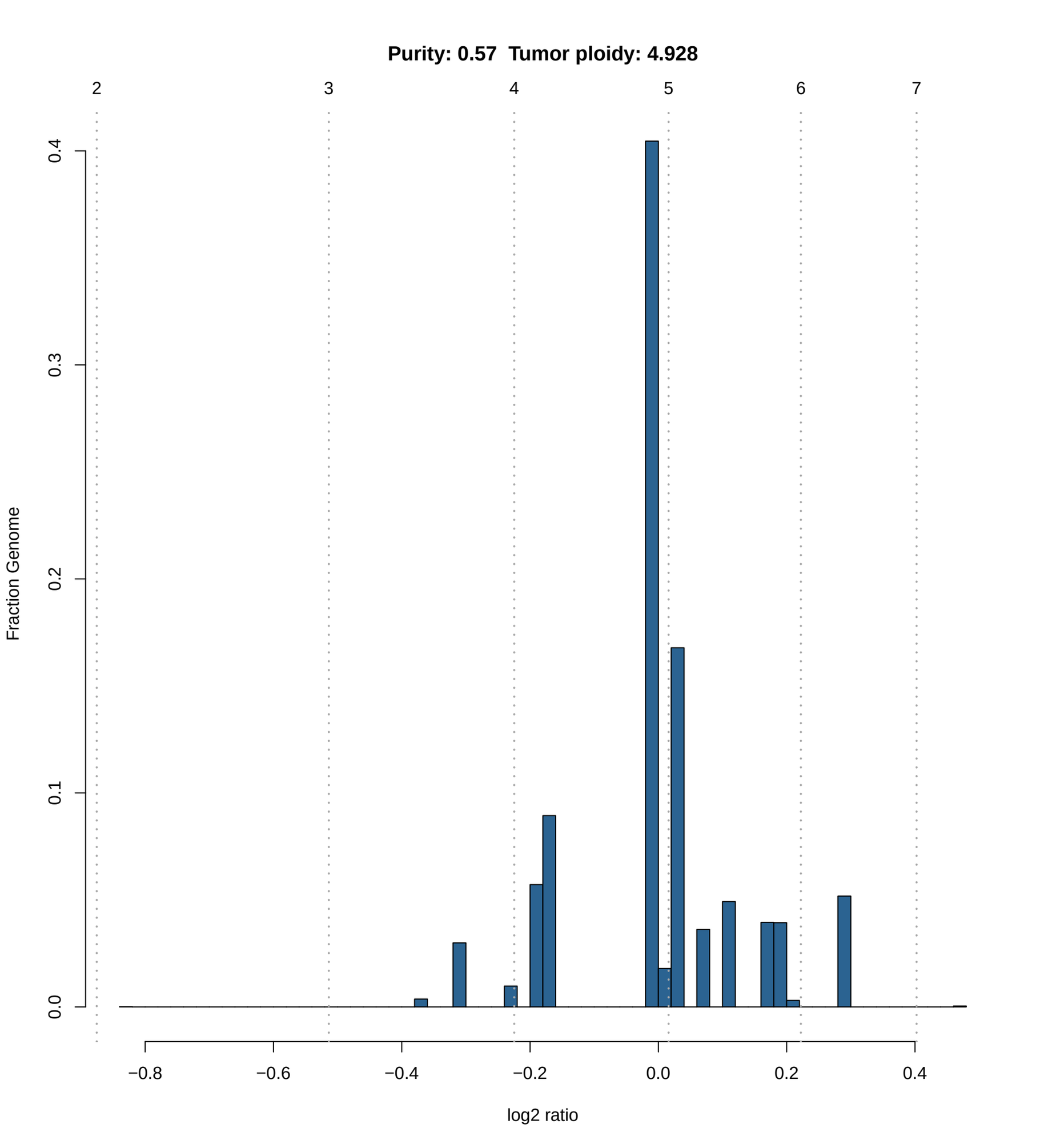

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

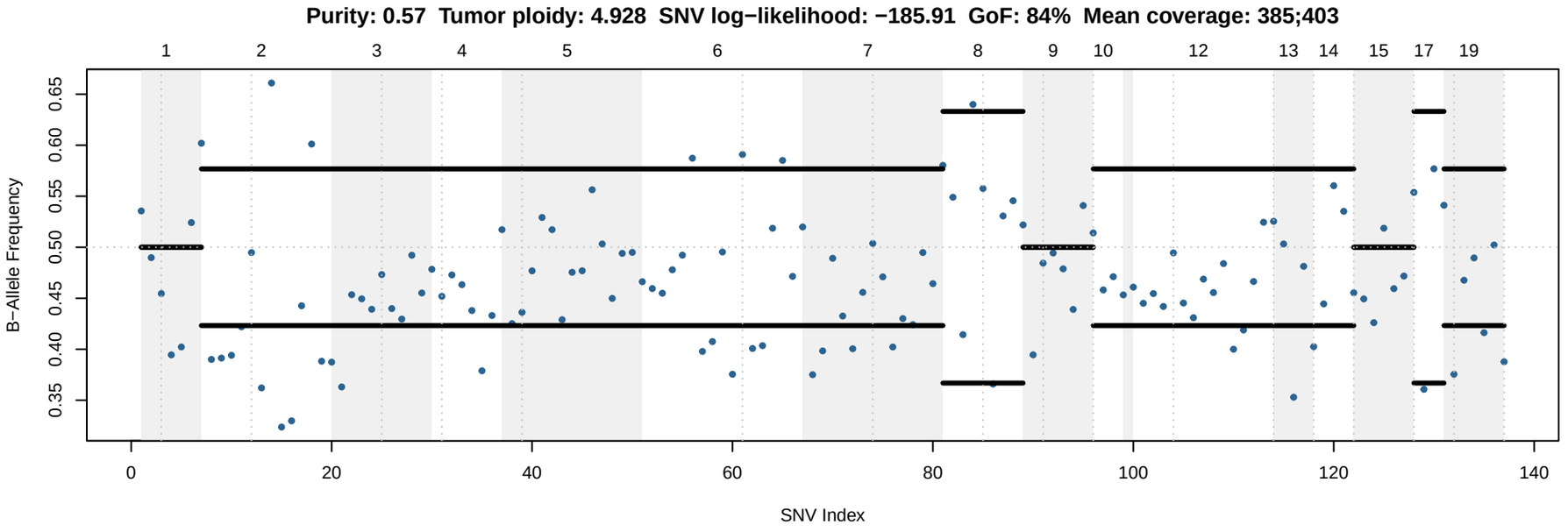

Allelic fraction (germline)
Copy Number log−ratio
6m4
5m3
7m4
4m2
6m3
7m3
5m2
6m2

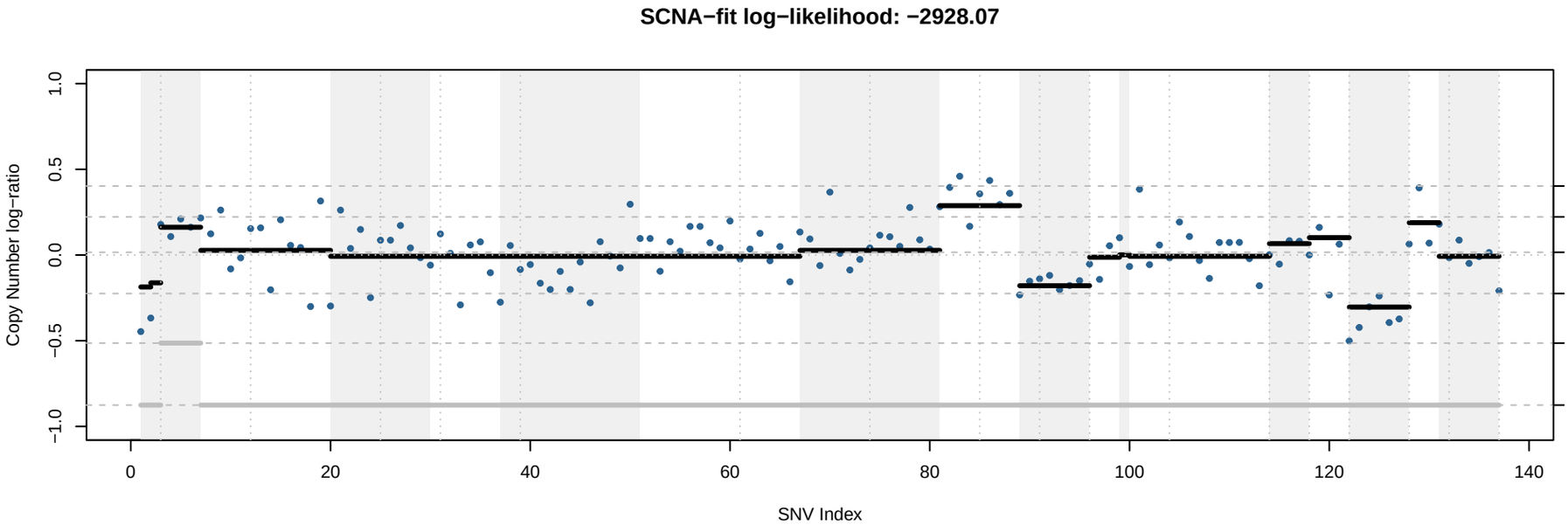

Coverage (log2)
Allelic fraction

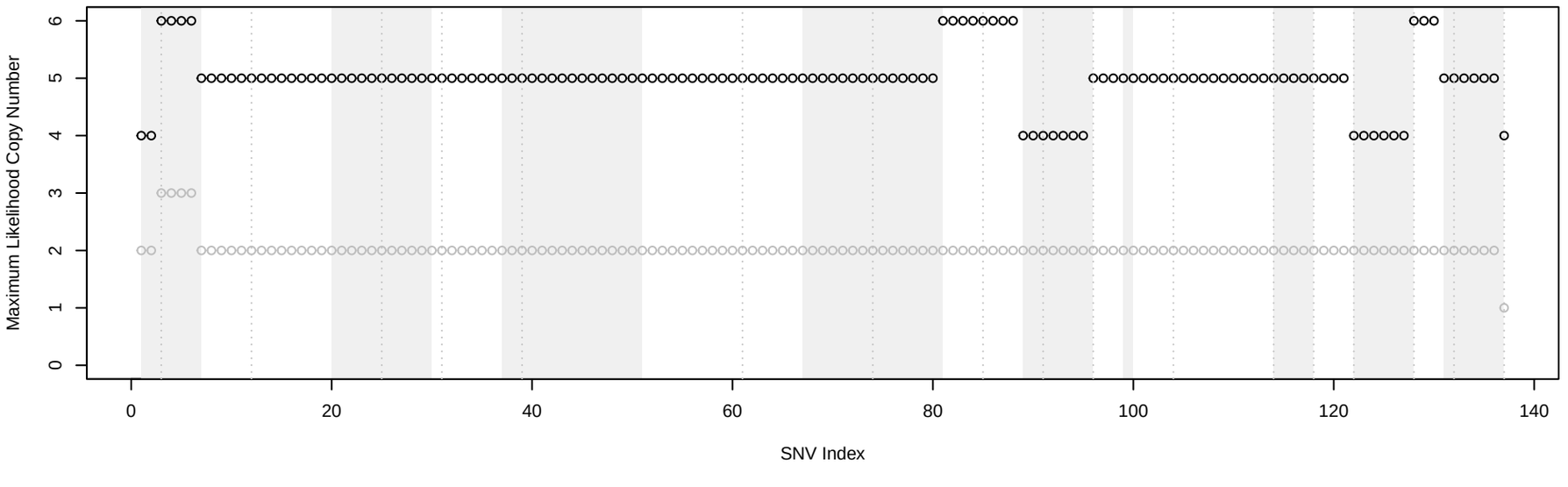

Allelic fraction (somatic)
Copy Number log−ratio
7m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

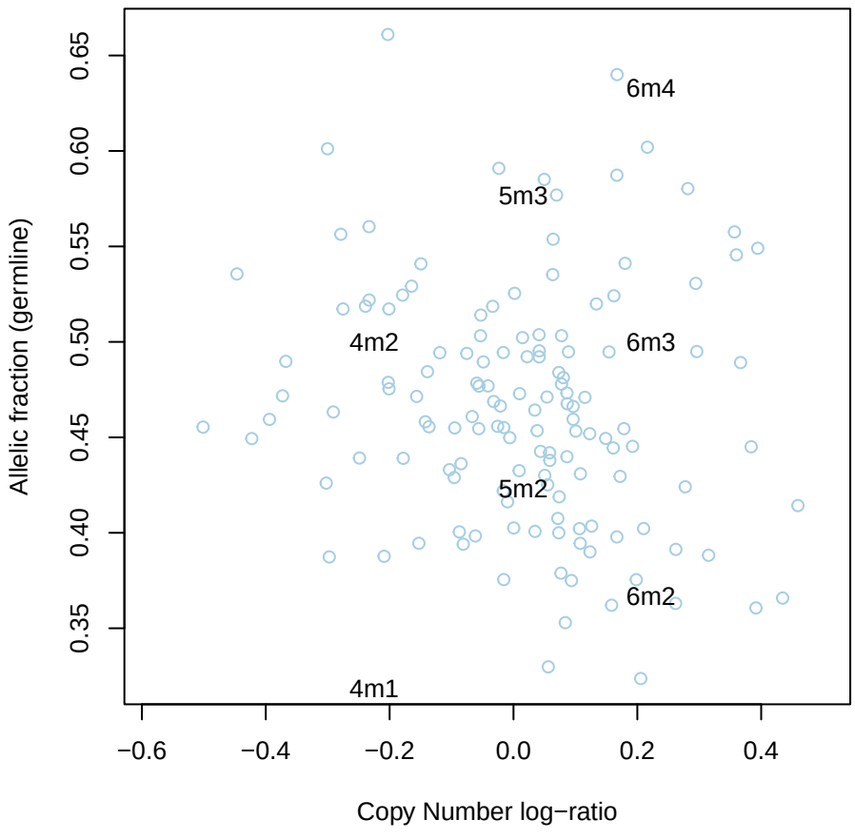

Frequency
Cellular fraction

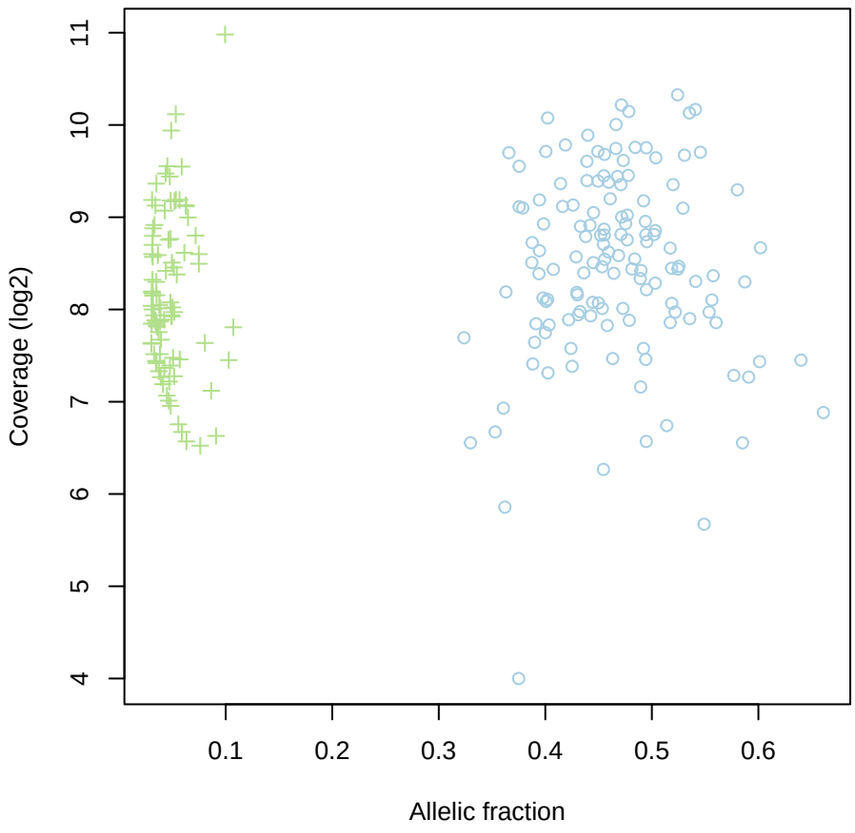

Purity: 0.57 Tumor ploidy: 4.928
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

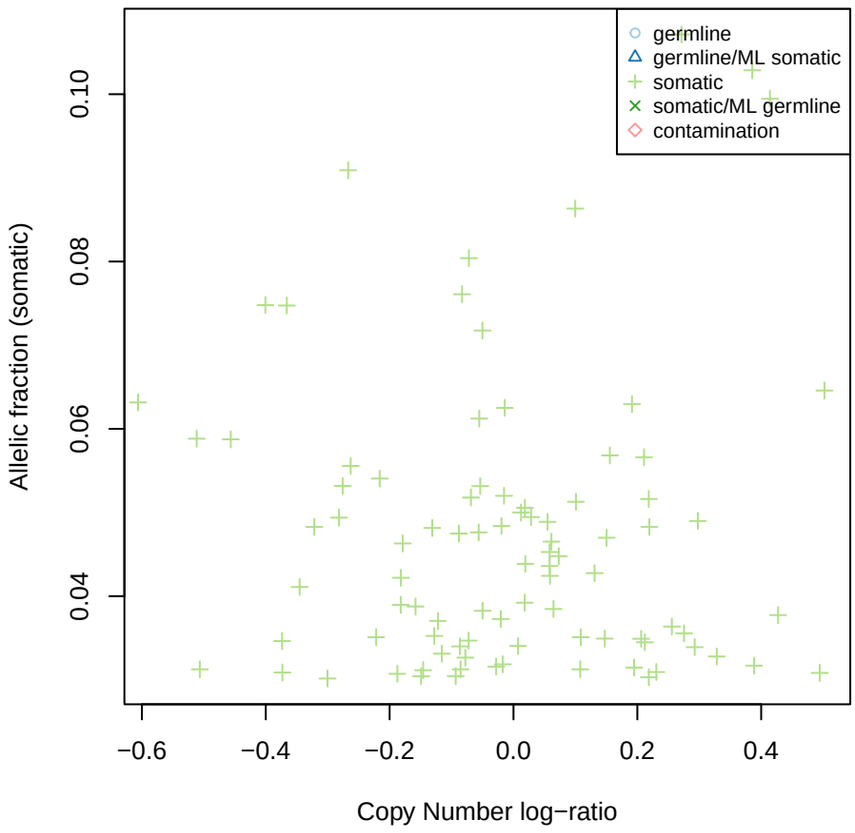

Purity: 0.57 Tumor ploidy: 4.928 SNV log−likelihood: −185.91 GoF: 84% Mean coverage: 385;403
1 2 3 4 5 6 7 8 9 10 12 13 14 15 17 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

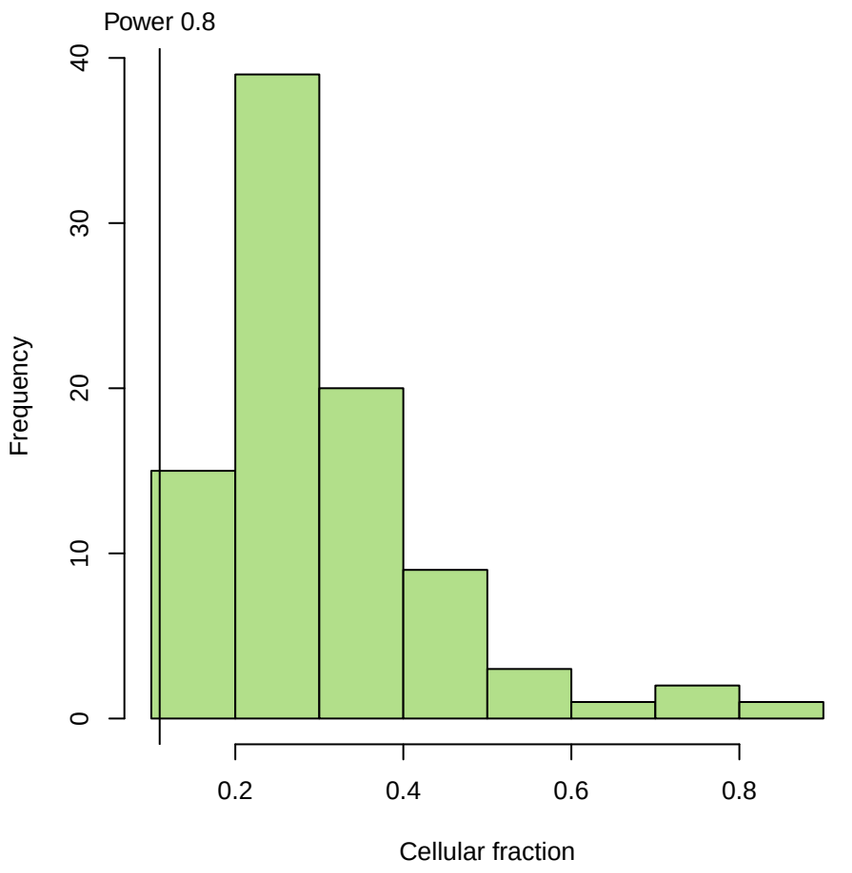

SCNA−fit log−likelihood: −2928.07
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

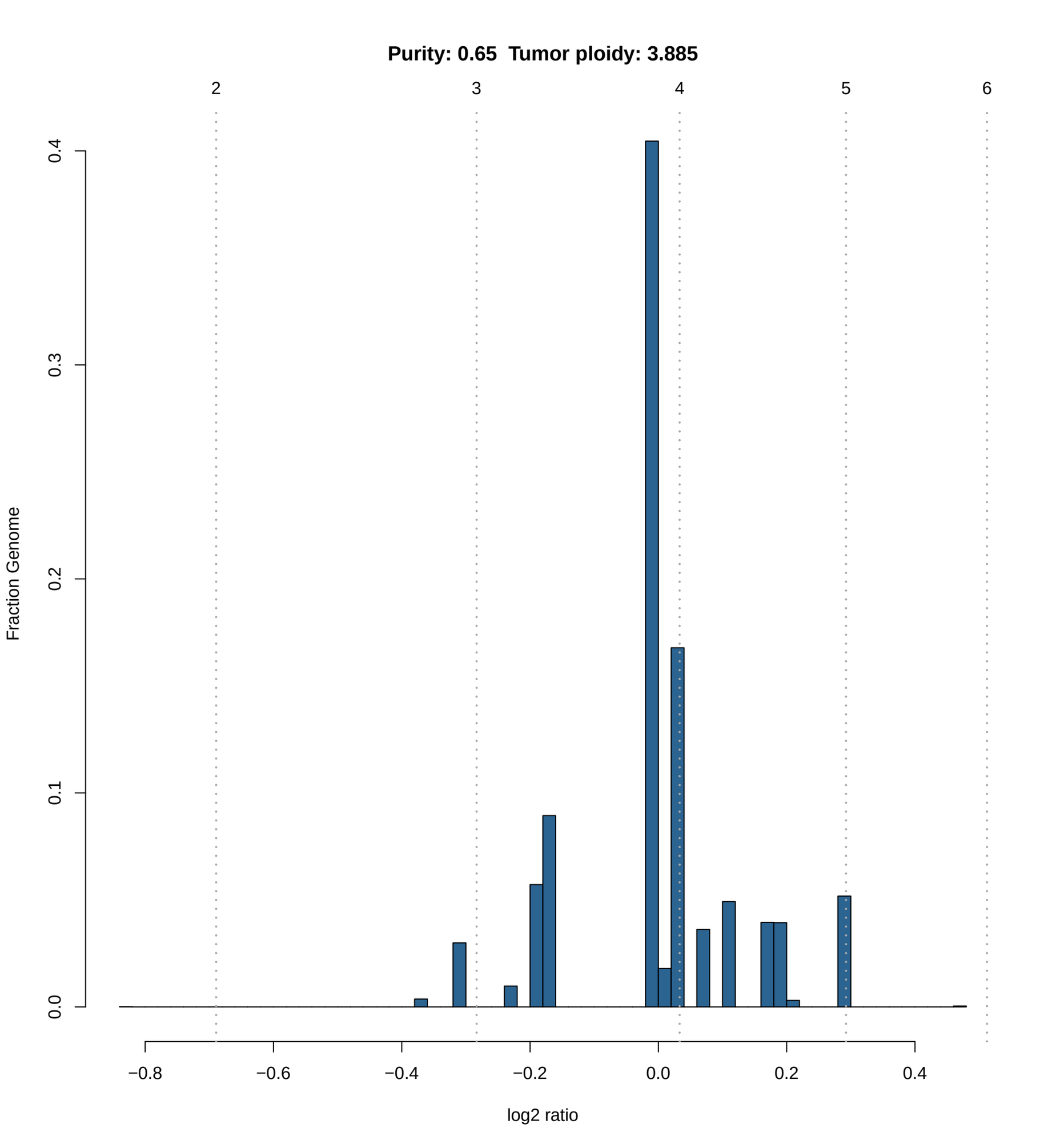

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

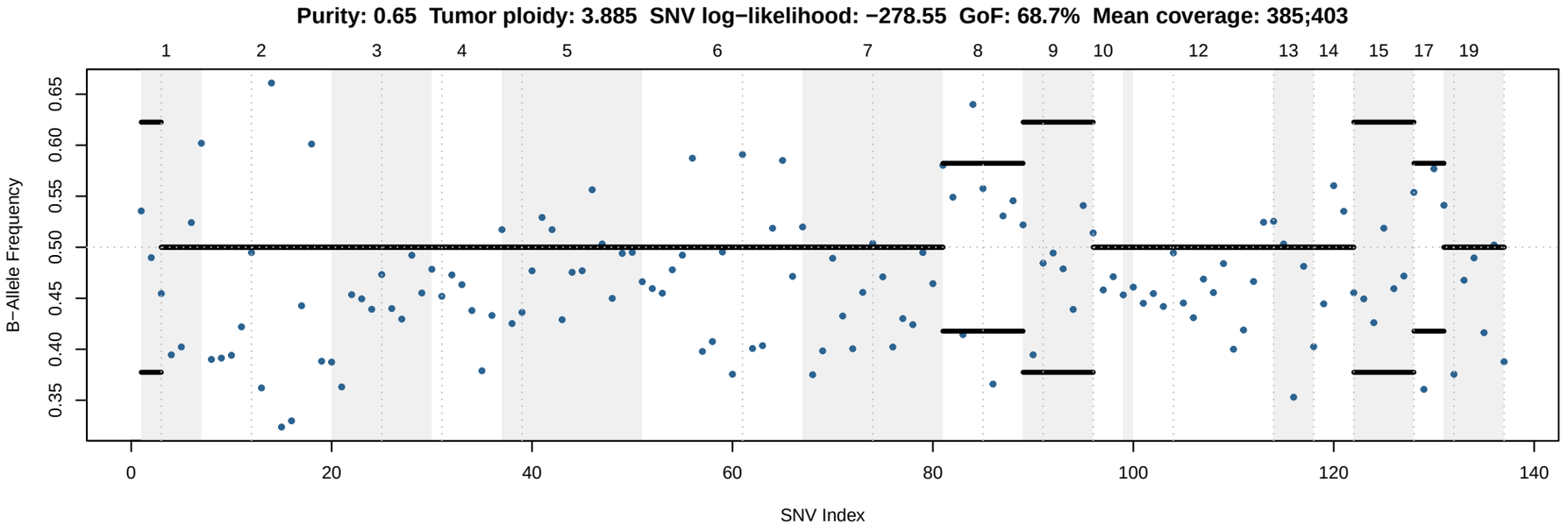

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
6m4
5m3
4m2
6m3
5m2
6m2
4m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

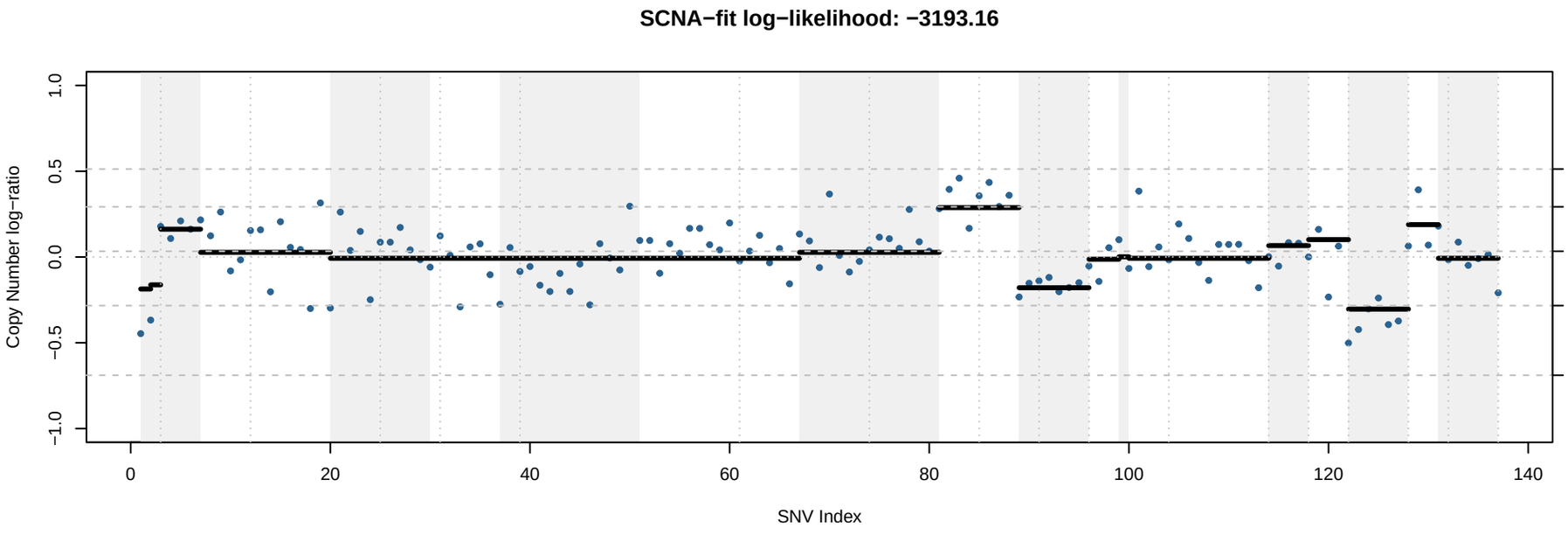

Coverage (log2)
4
5
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

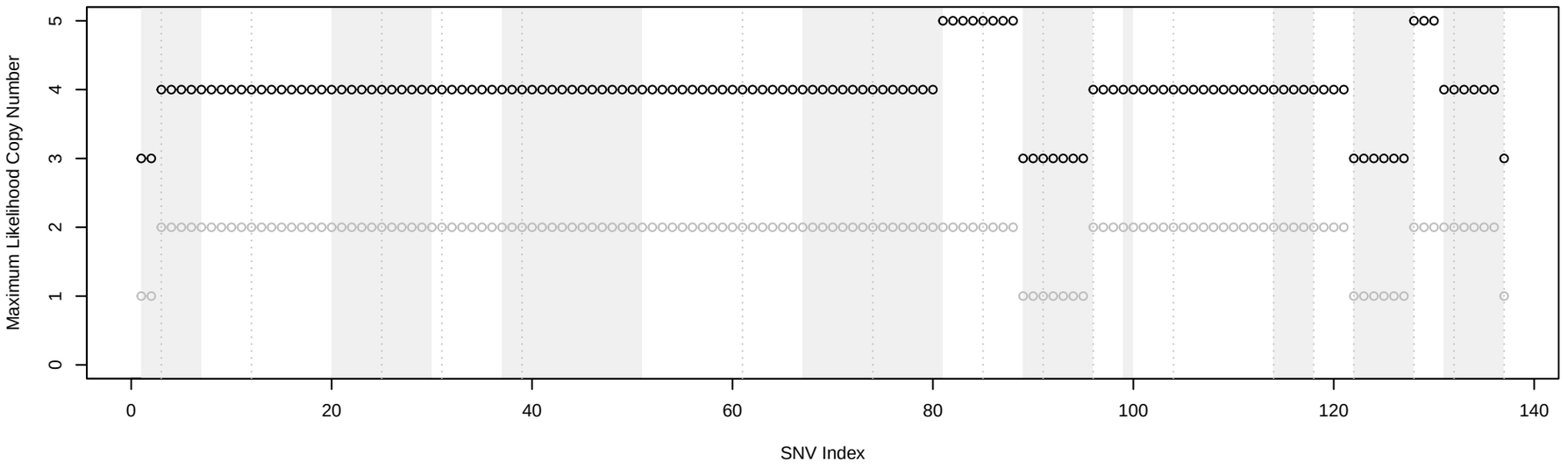

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

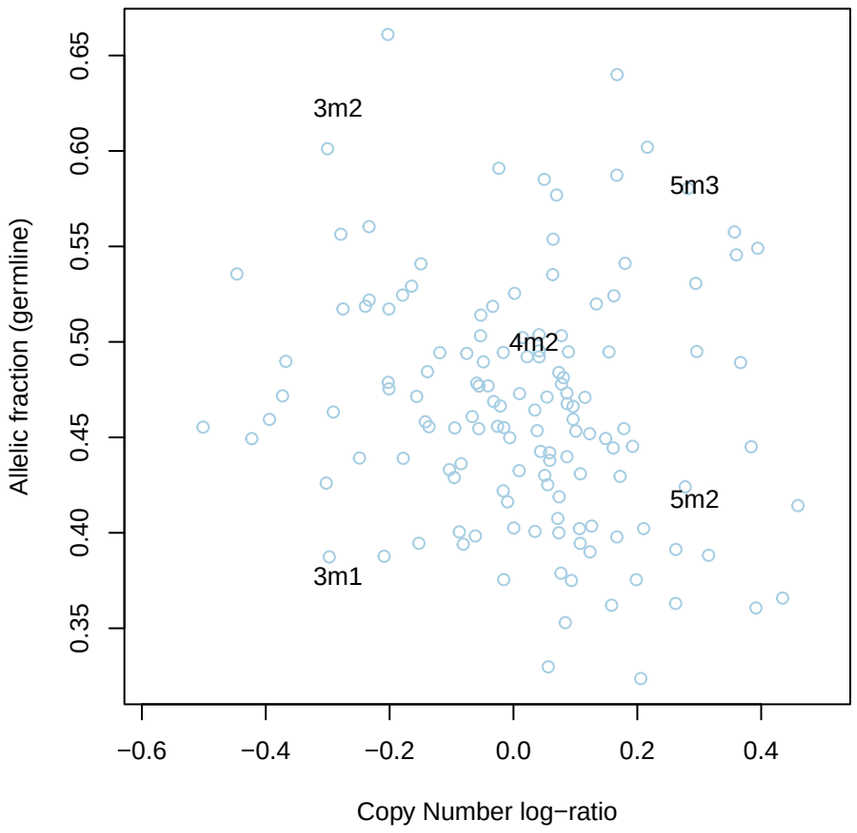

Power 0.8
Frequency
0
10
20
30
40
0.2
0.4
0.6
0.8
Cellular fraction

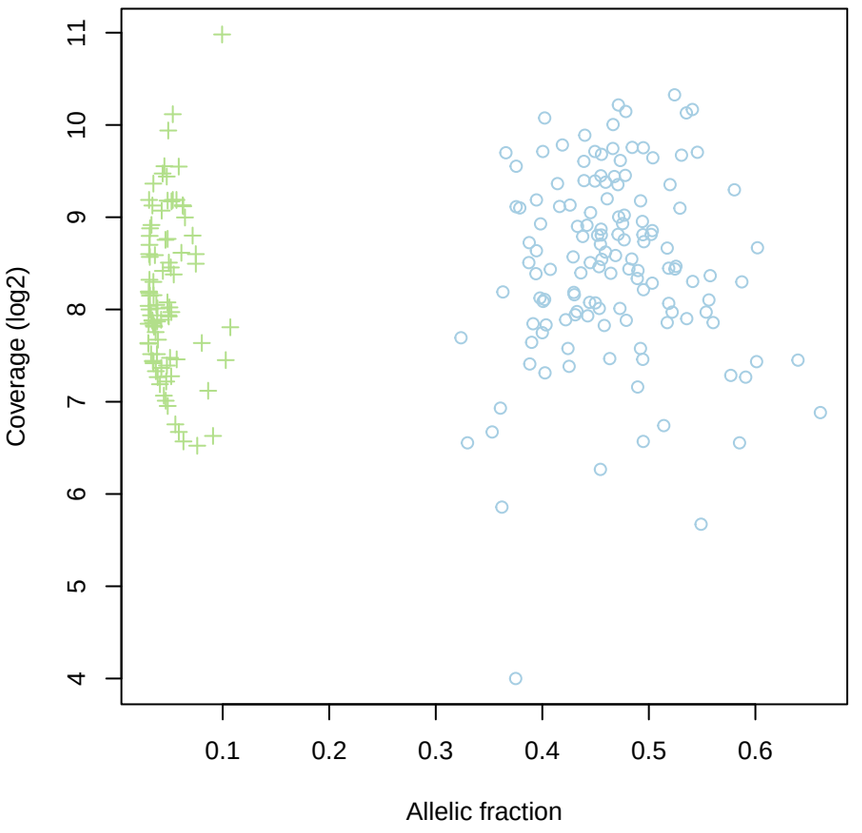

Purity: 0.65 Tumor ploidy: 3.885
2
3
4
5
6
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

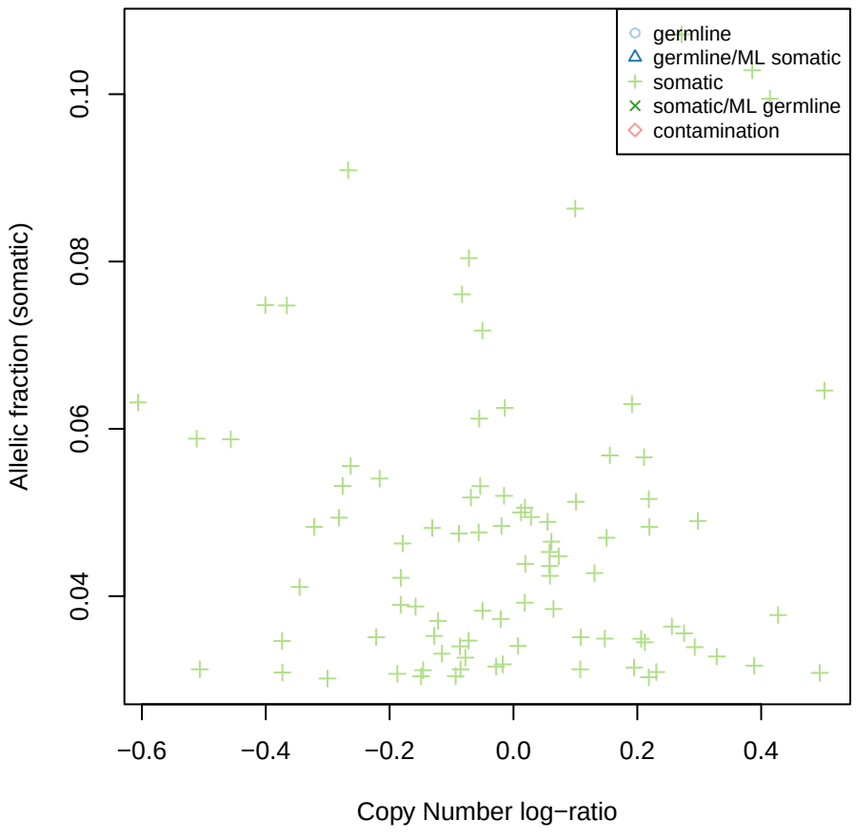

Purity: 0.65 Tumor ploidy: 3.885 SNV log−likelihood: −278.55 GoF: 68.7% Mean coverage: 385;403
1 2 3 4 5 6 7 8 9 10 12 13 14 15 17 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

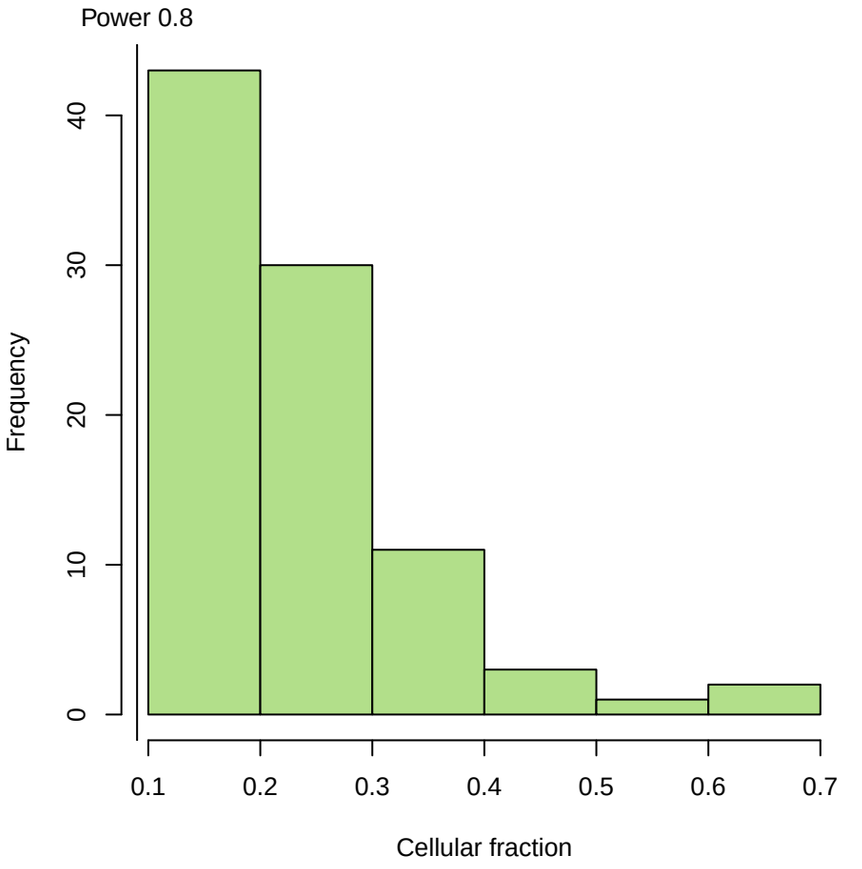

SCNA−fit log−likelihood: −3193.16
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

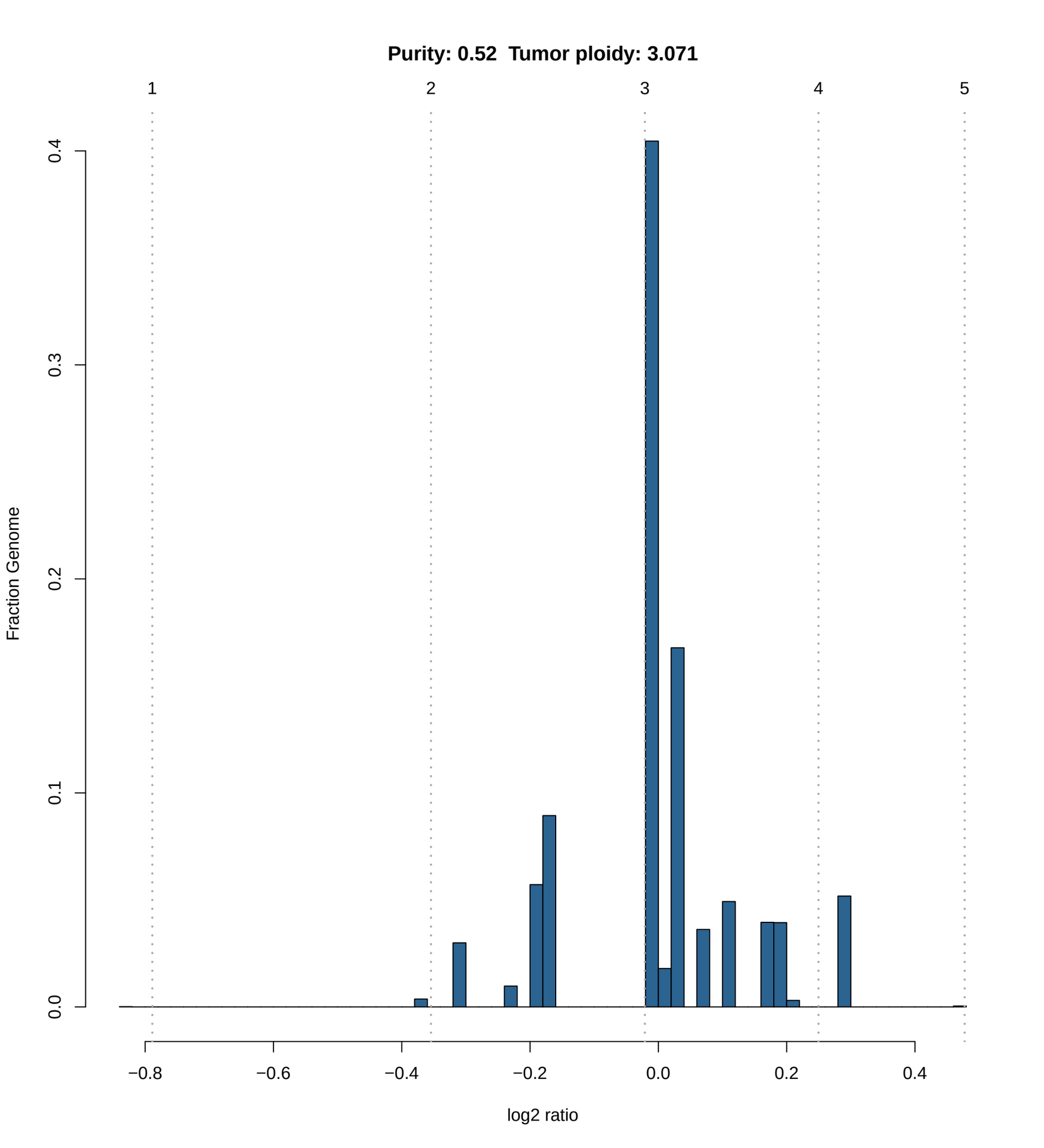

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

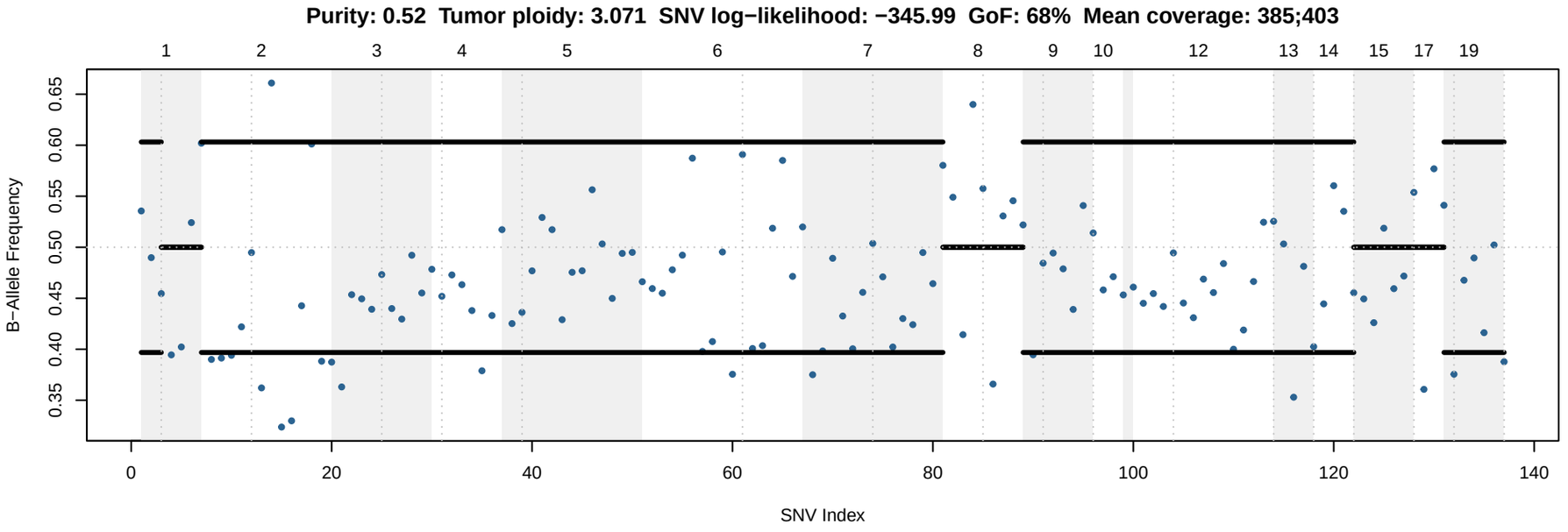

3m2
5m3
4m2
5m2
3m1
Allelic fraction (germline)
Copy Number log−ratio
0.35
0.40
0.45
0.50
0.55
0.60
0.65
−0.6
−0.4
−0.2
0.0
0.2
0.4

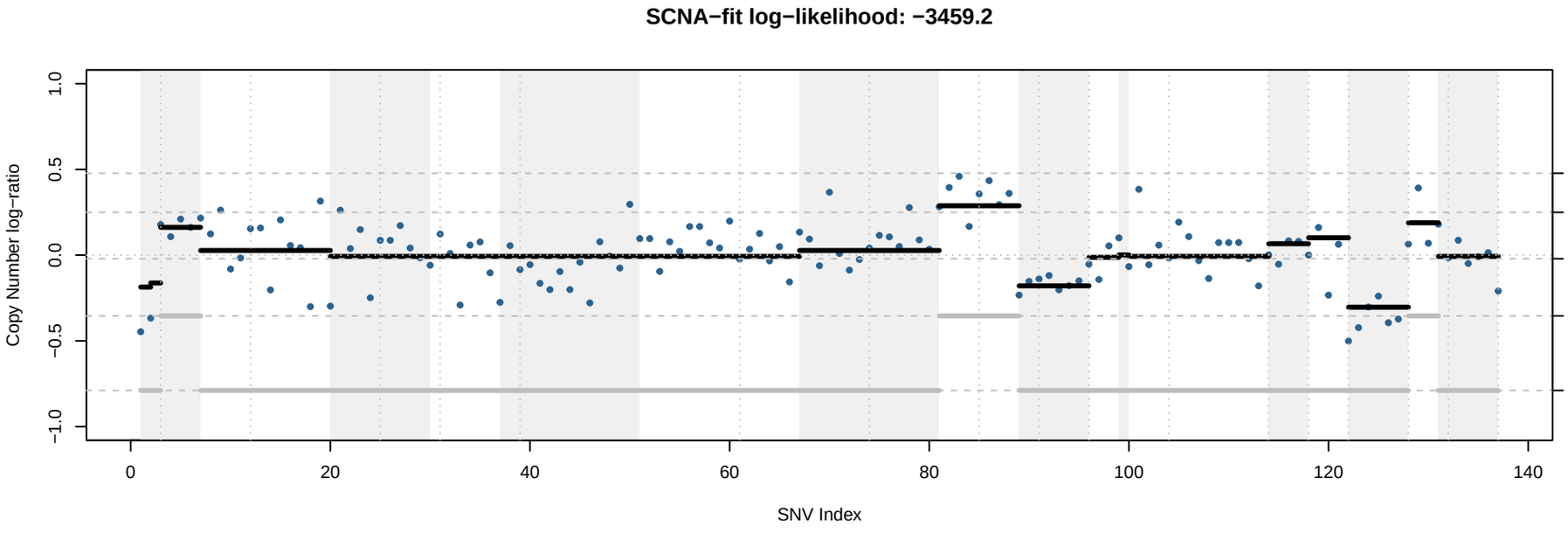

Coverage (log2)
Allelic fraction
4
5
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6

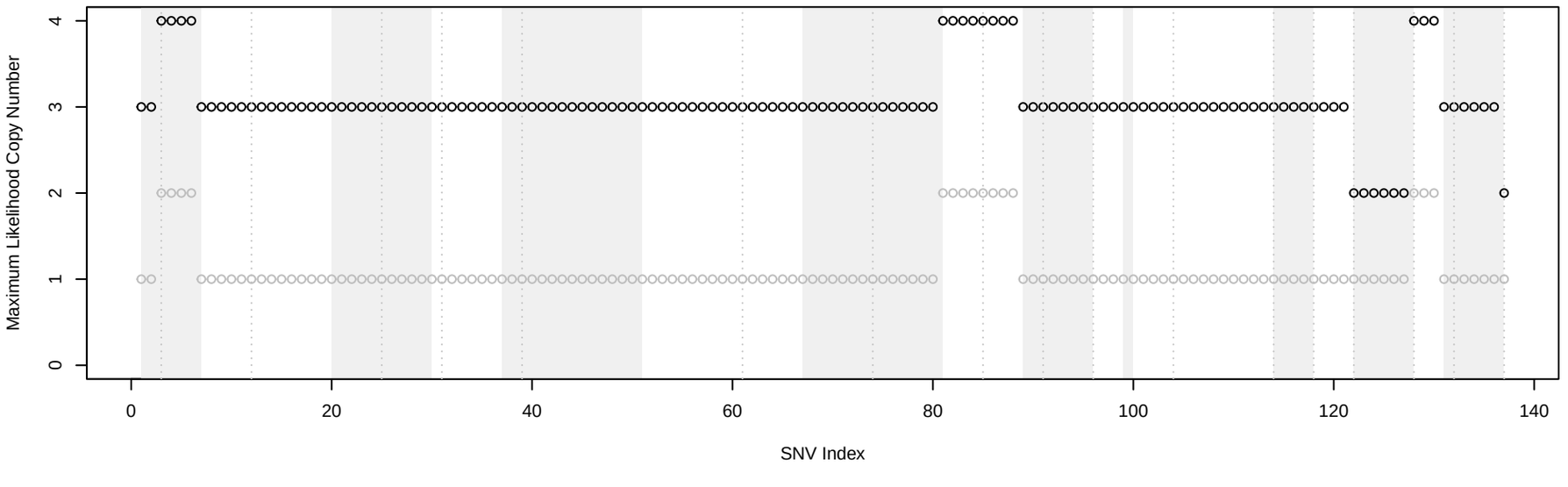

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
−0.6
−0.4
−0.2
0.0
0.2
0.4

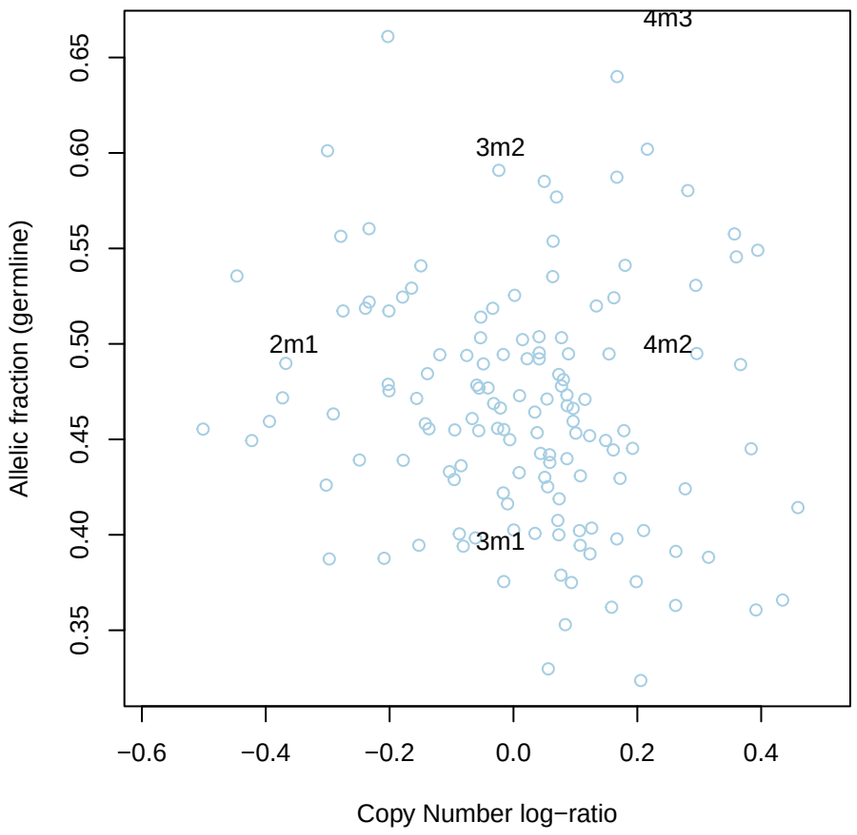

Power 0.8
Frequency
Cellular fraction
0
10
20
30
40
0.1
0.2
0.3
0.4
0.5
0.6
0.7

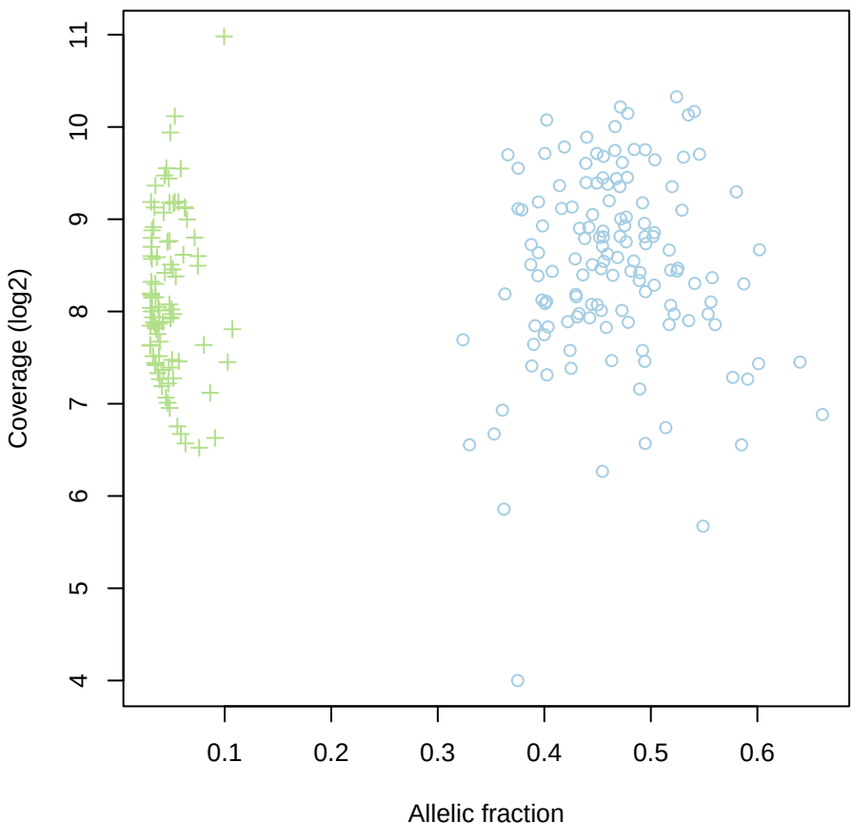

Purity: 0.52 Tumor ploidy: 3.071
1
2
3
4
5
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

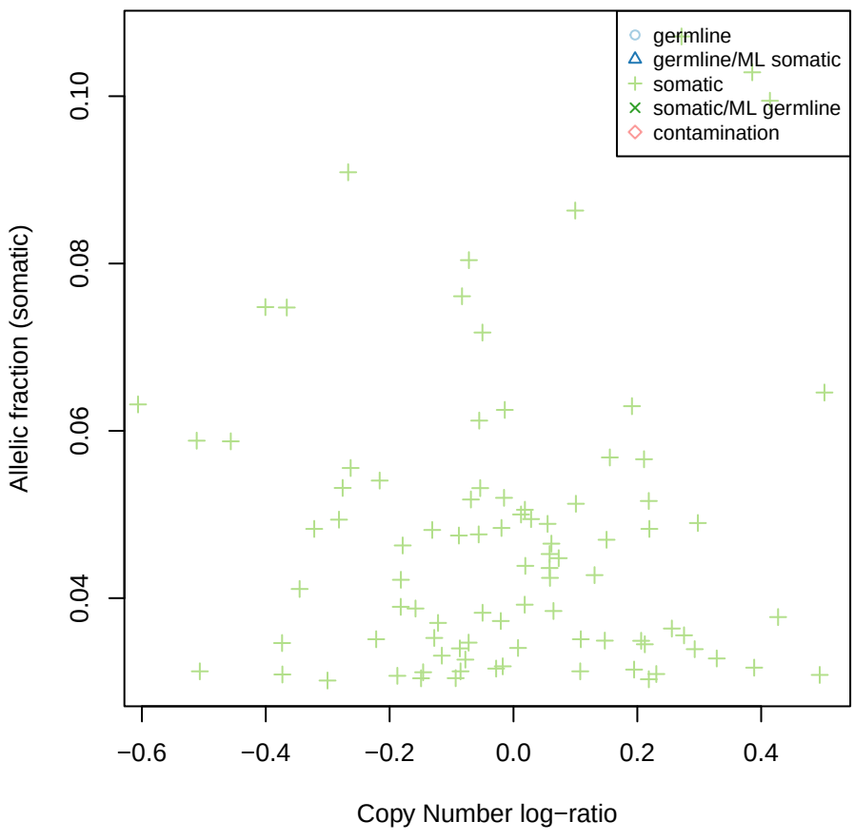

Purity: 0.52 Tumor ploidy: 3.071 SNV log−likelihood: −345.99 GoF: 68% Mean coverage: 385;403
1 2 3 4 5 6 7 8 9 10 12 13 14 15 17 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

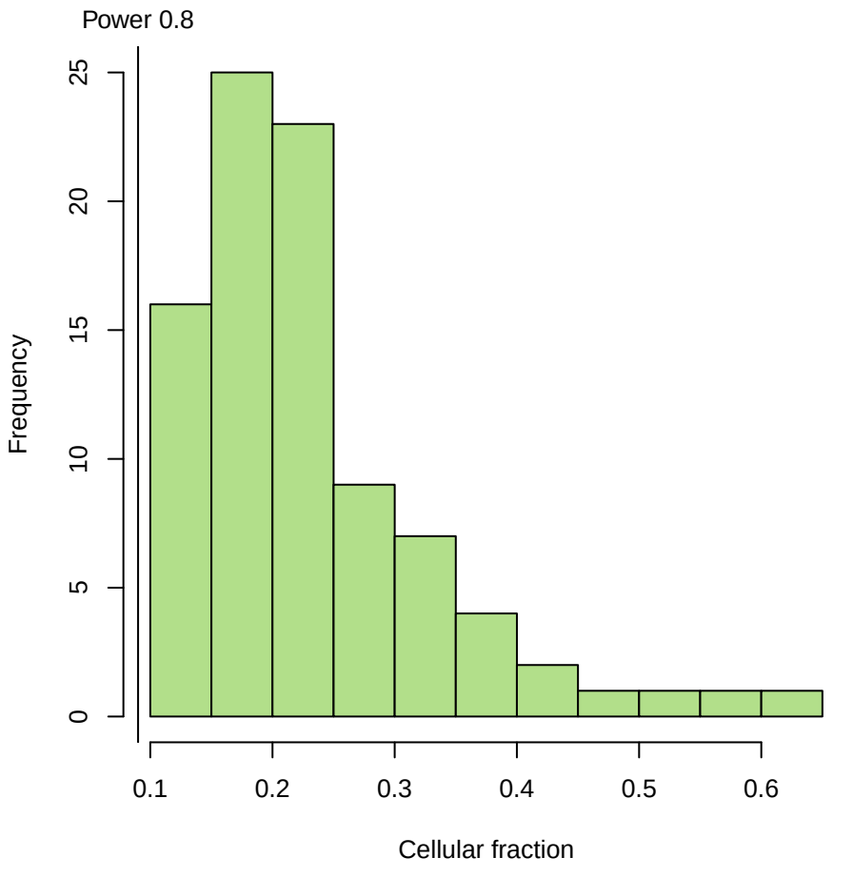

SCNA−fit log−likelihood: −3459.2
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

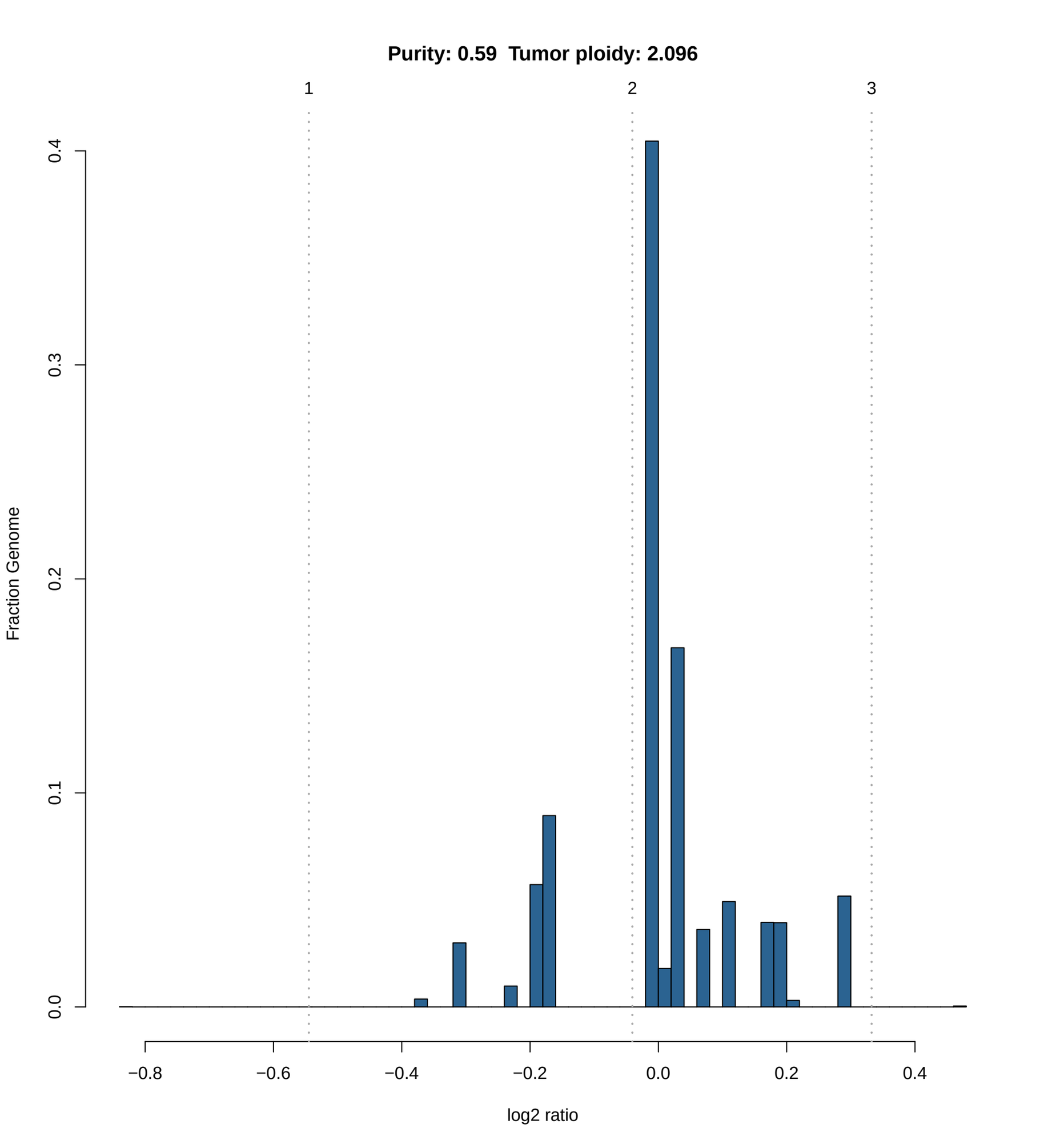

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120 140
SNV Index

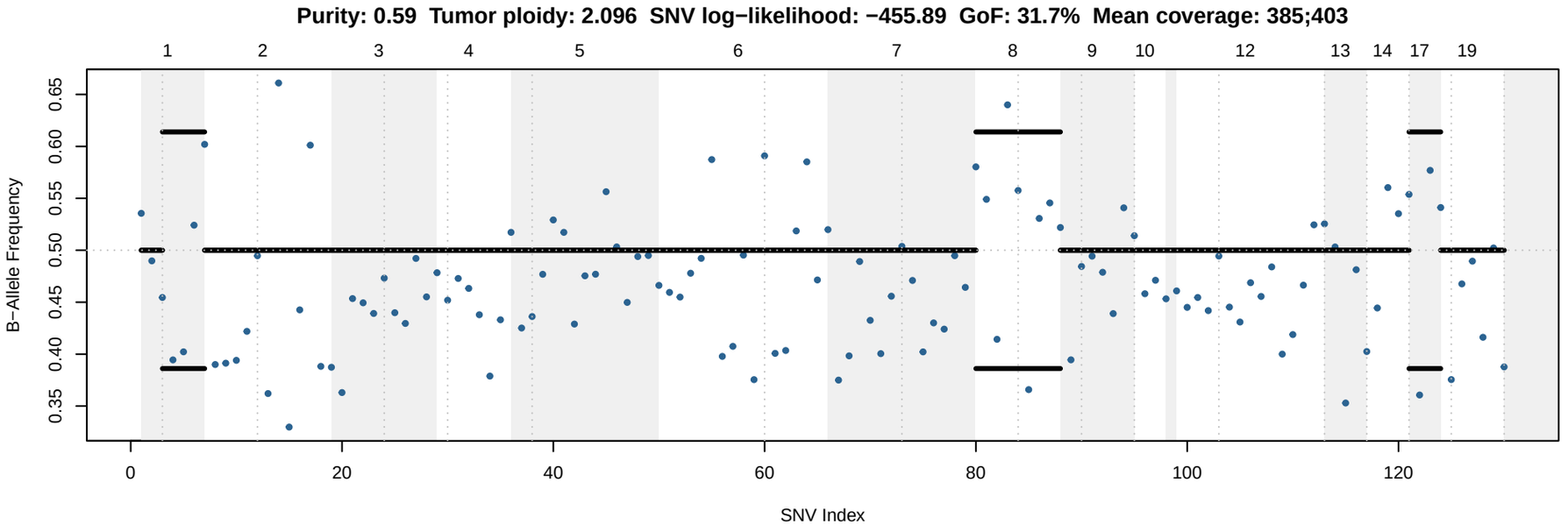

4m3
3m2
2m1
4m2
3m1
Allelic fraction (germline)
Copy Number log−ratio

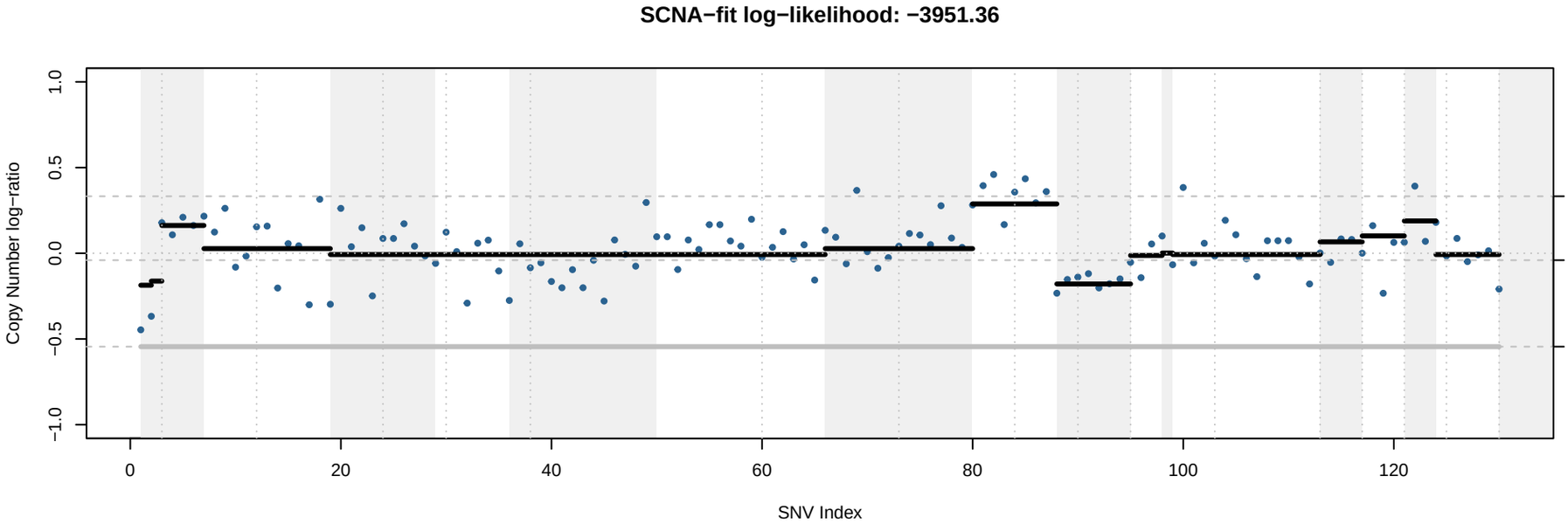

Coverage (log2)
Allelic fraction

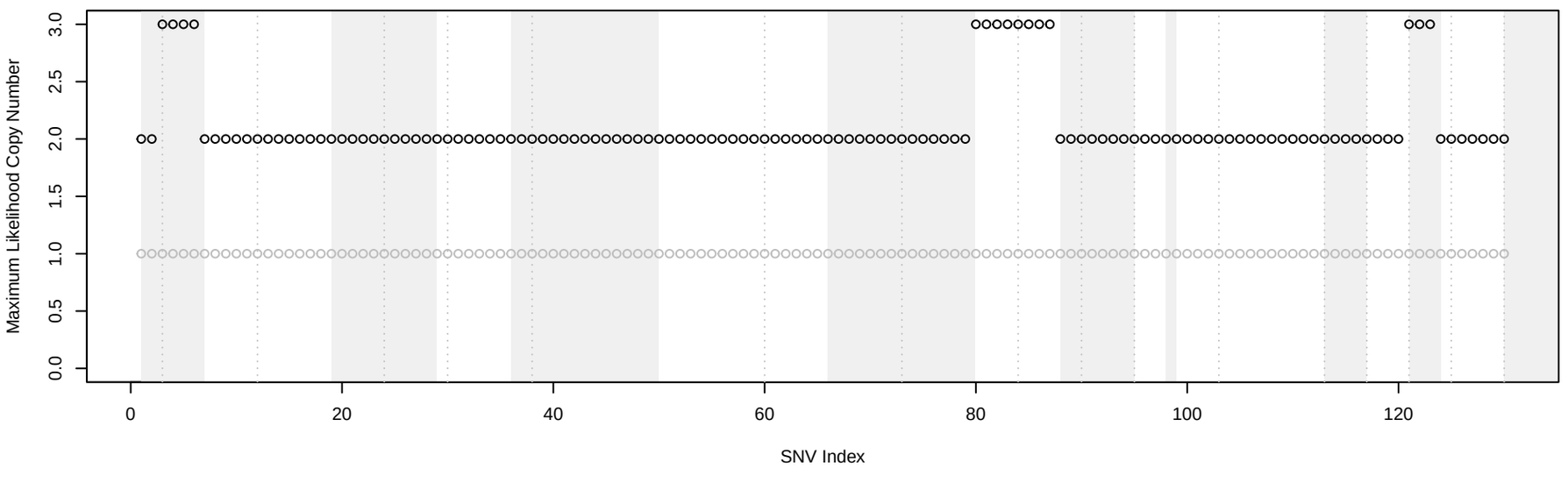

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

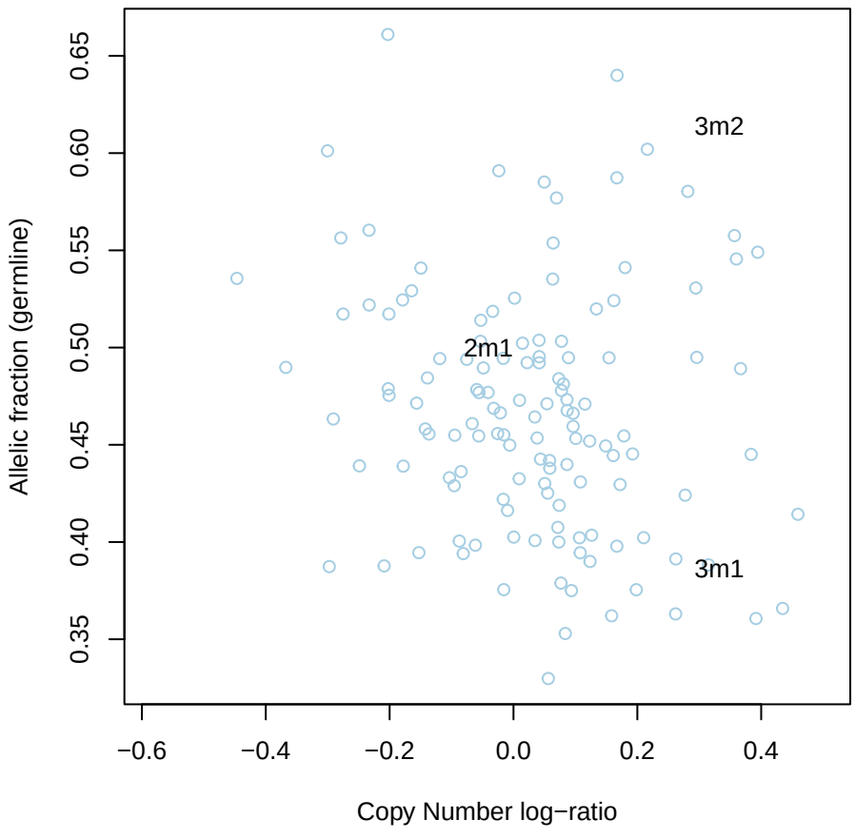

Power 0.8
Frequency
Cellular fraction

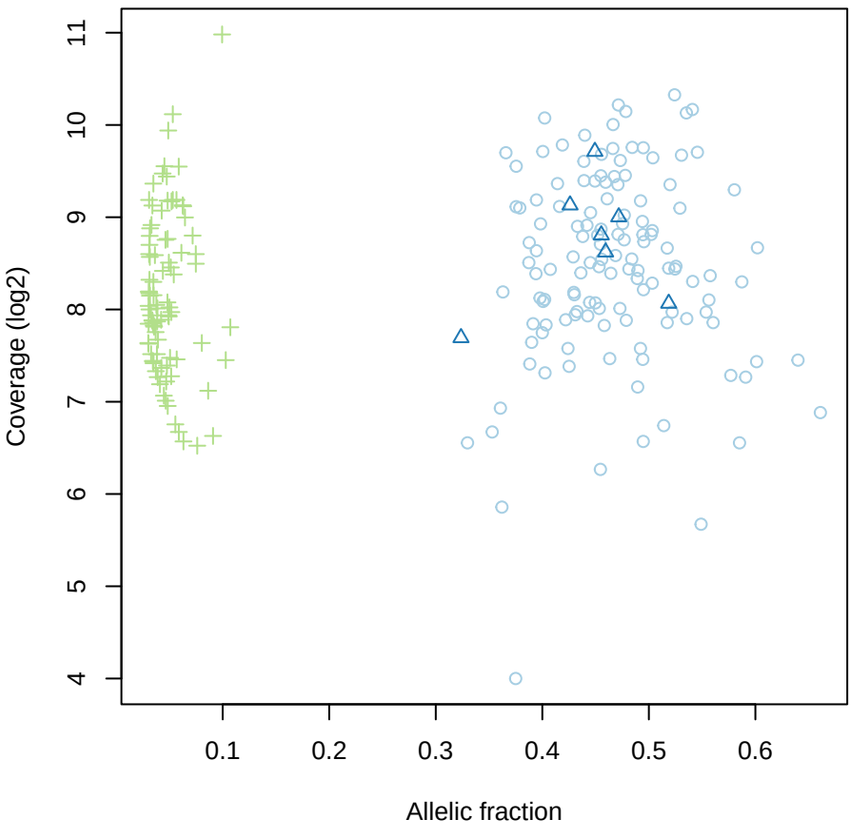

Purity: 0.59 Tumor ploidy: 2.096
1
2
3
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

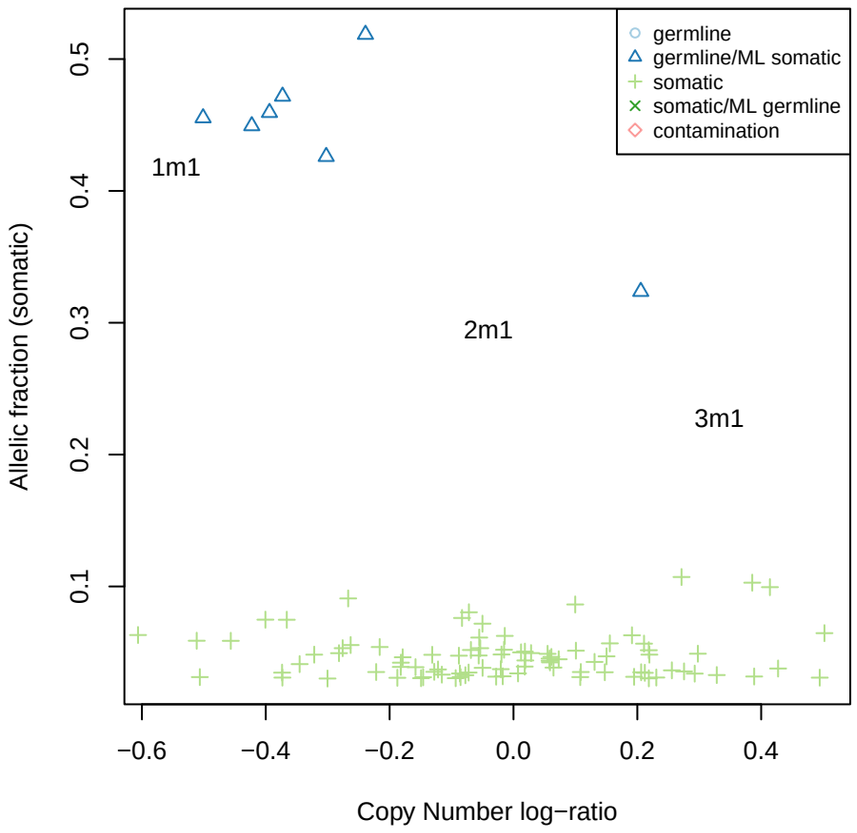

Purity: 0.59 Tumor ploidy: 2.096 SNV log−likelihood: −455.89 GoF: 31.7% Mean coverage: 385;403
1 2 3 4 5 6 7 8 9 10 12 13 14 17 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120
SNV Index

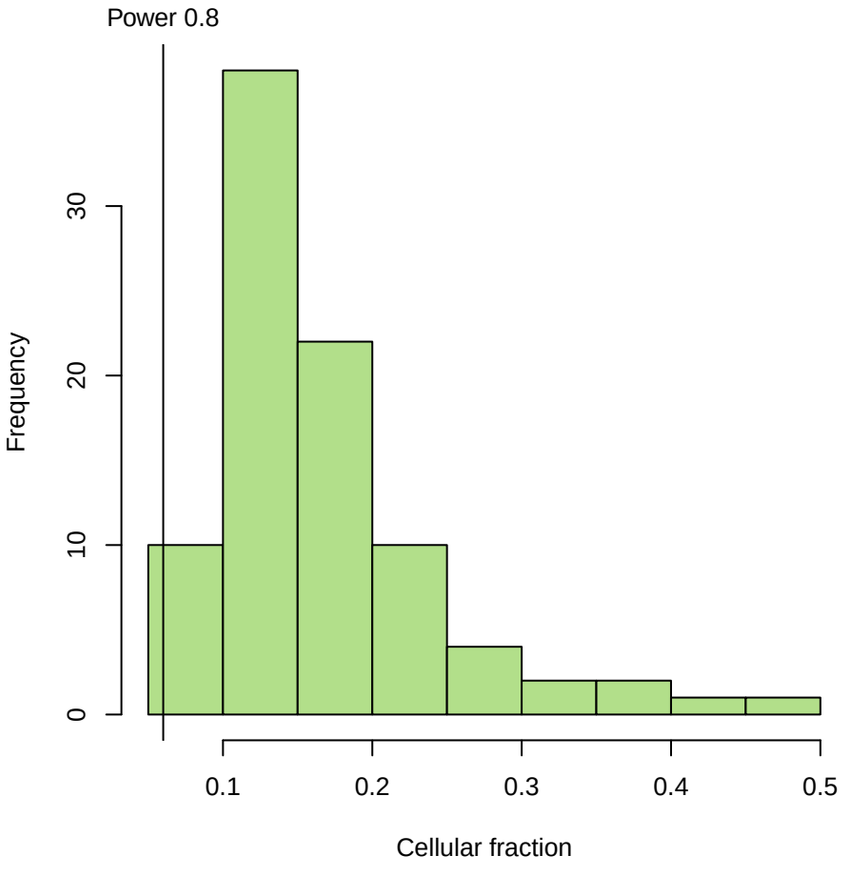

SCNA−fit log−likelihood: −3951.36
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3
0 20 40 60 80 100 120
SNV Index

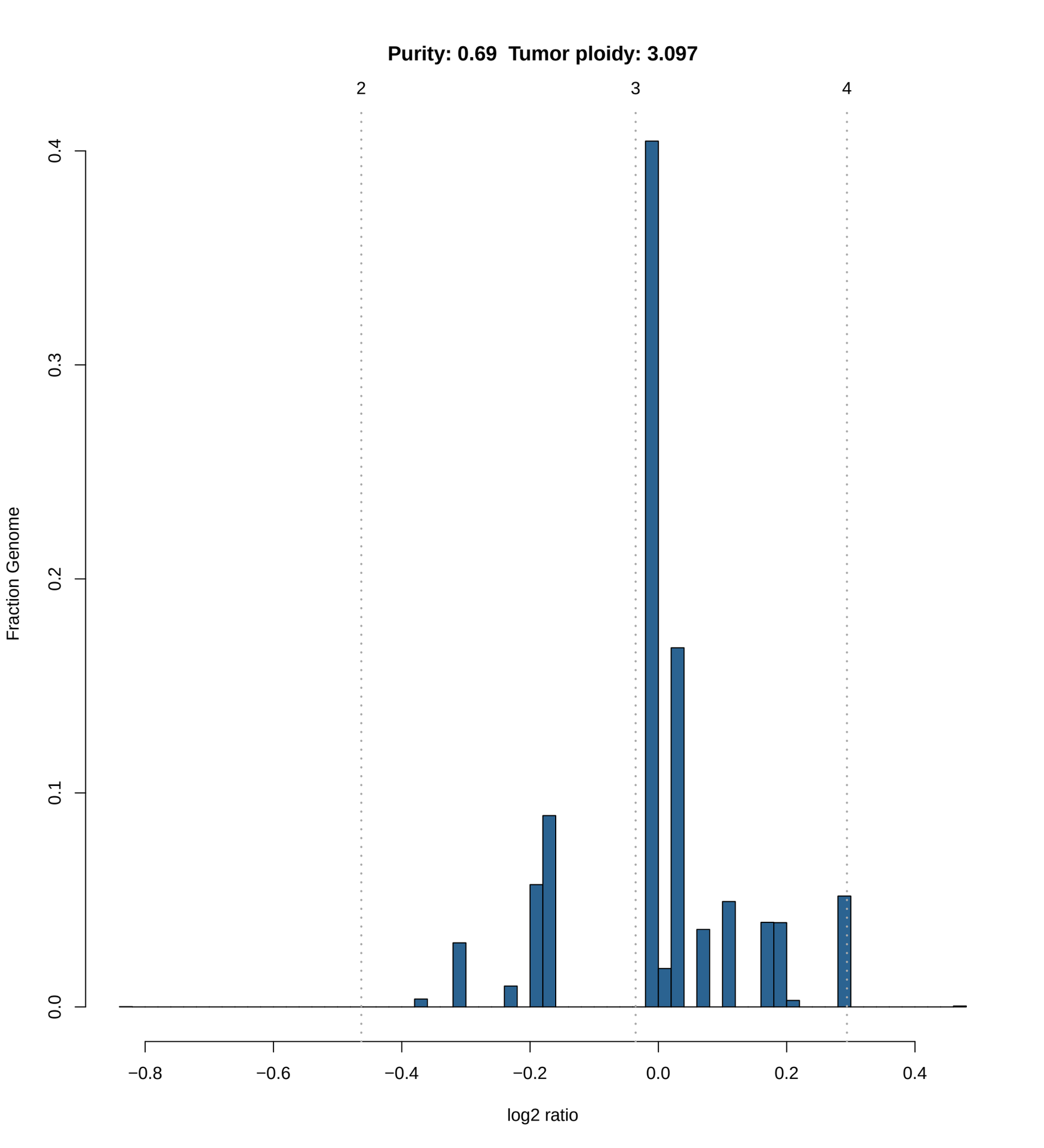

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120
SNV Index

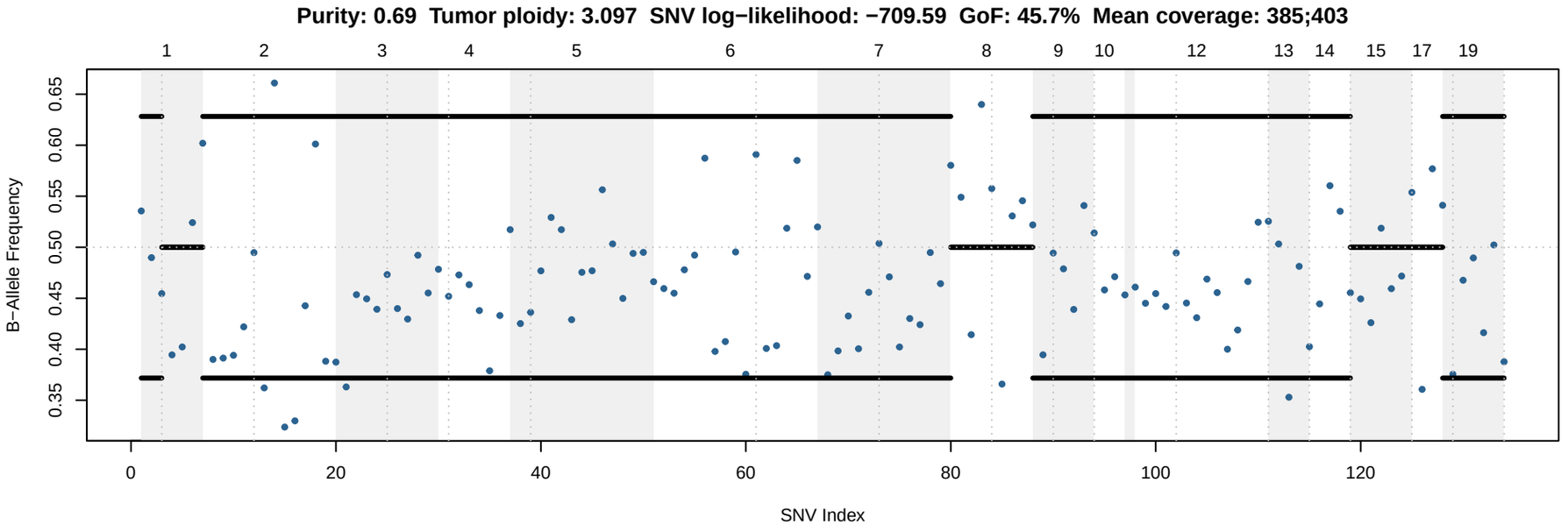

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
3m2
2m1
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

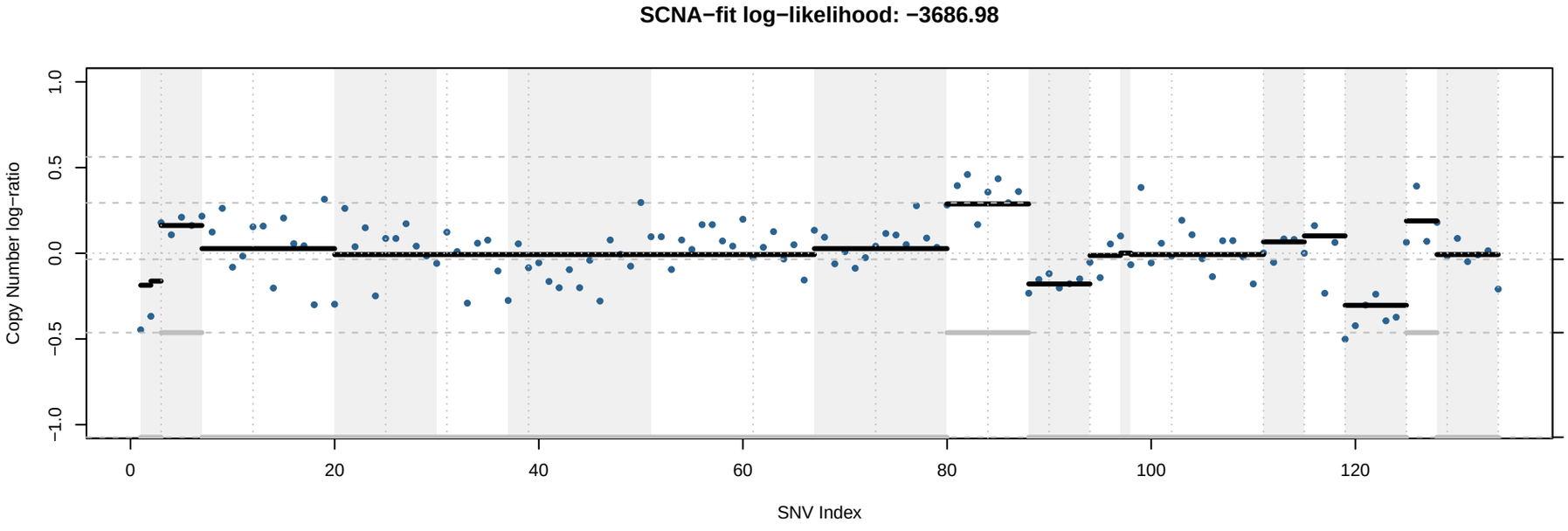

Coverage (log2)
4
5
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

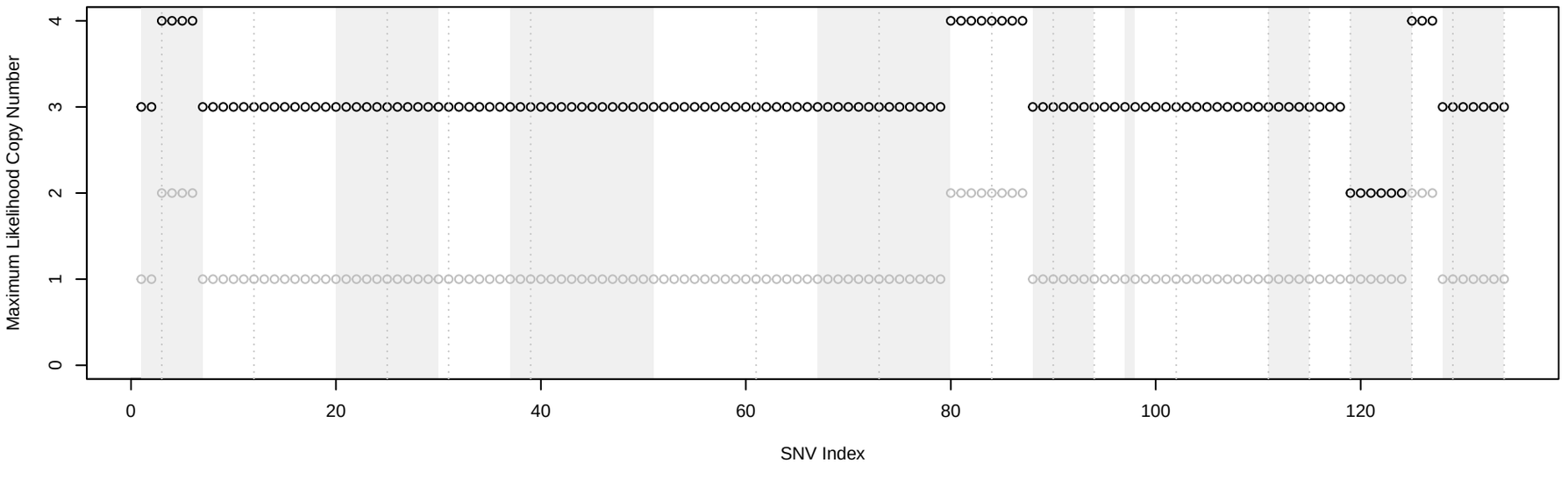

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.1
0.2
0.3
0.4
0.5
1m1
2m1
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

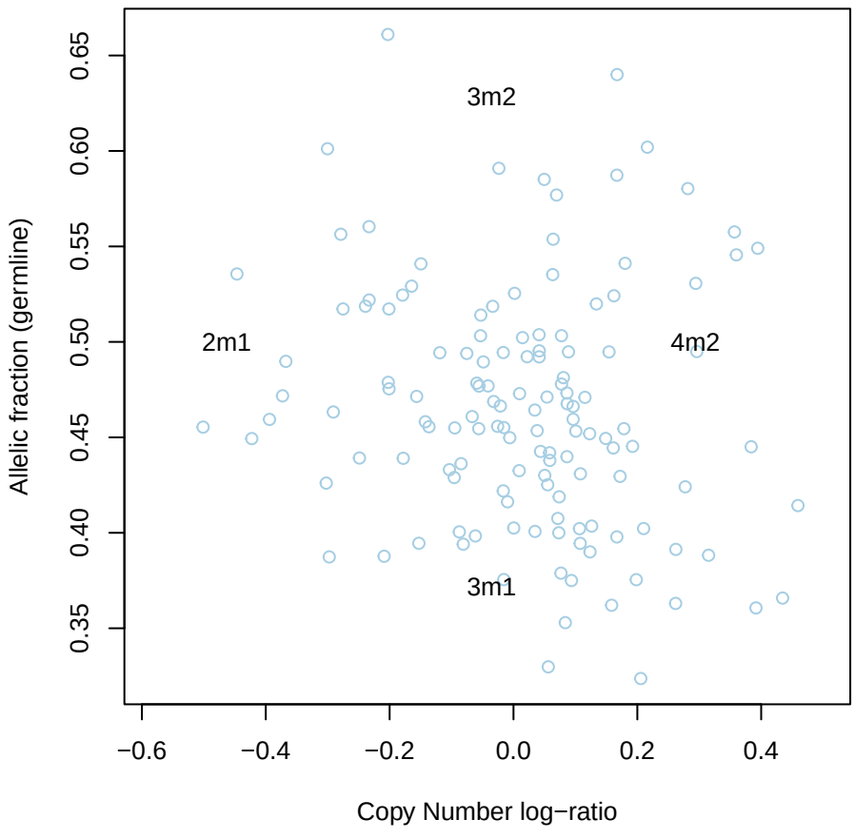

Power 0.8
Frequency
0
10
20
30
0.1
0.2
0.3
0.4
0.5
Cellular fraction

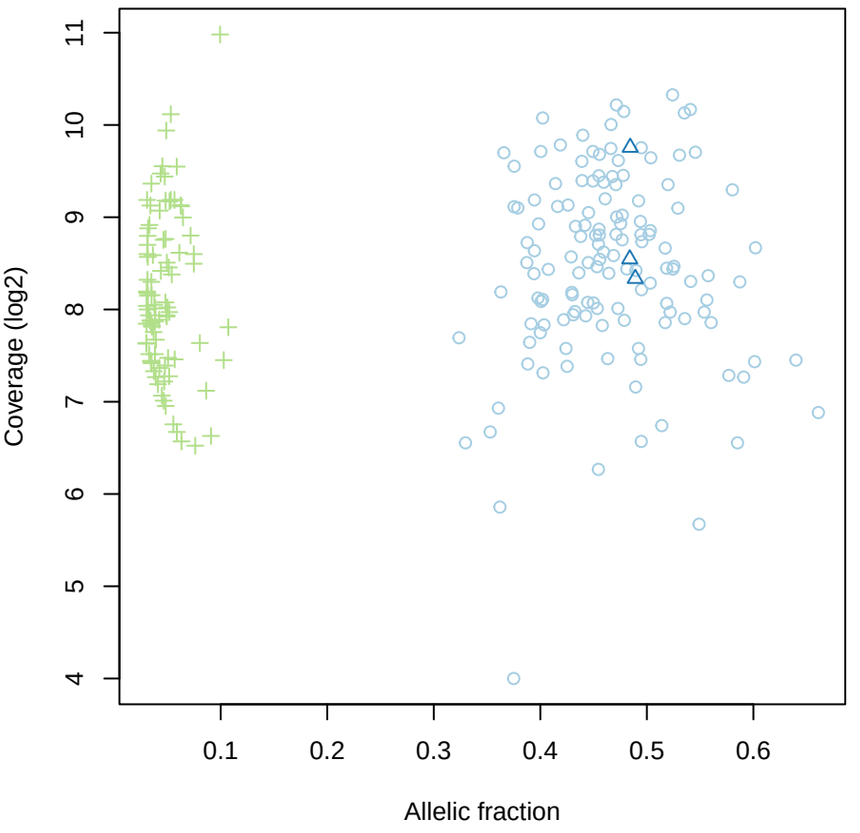

Purity: 0.69 Tumor ploidy: 3.097
2
3
4
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

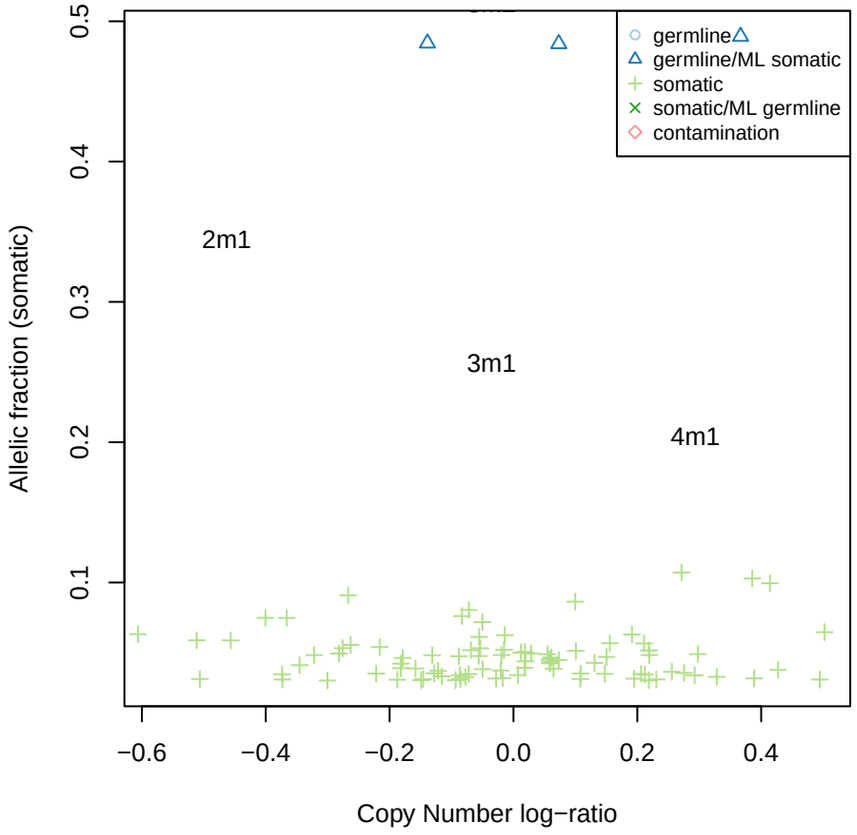

Purity: 0.69 Tumor ploidy: 3.097 SNV log−likelihood: −709.59 GoF: 45.7% Mean coverage: 385;403
1 2 3 4 5 6 7 8 9 10 12 13 14 15 17 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120
SNV Index

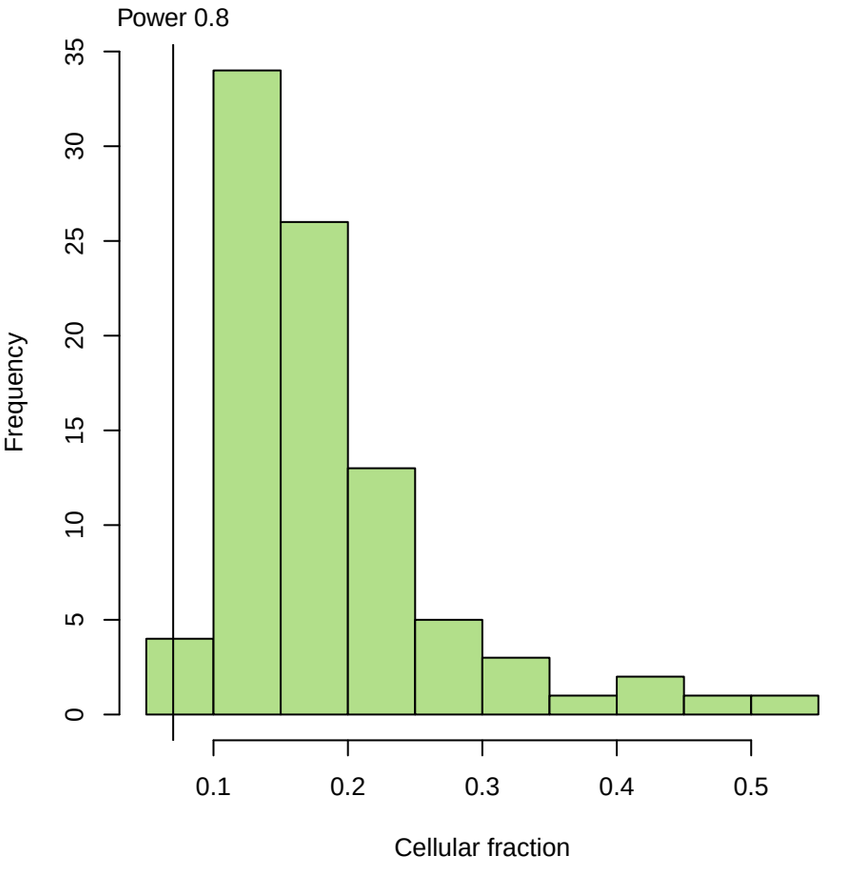

SCNA−fit log−likelihood: −3686.98
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5
0 20 40 60 80 100 120
SNV Index


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


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


Coverage (log2)
Allelic fraction


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


Power 0.8
Frequency
Cellular fraction