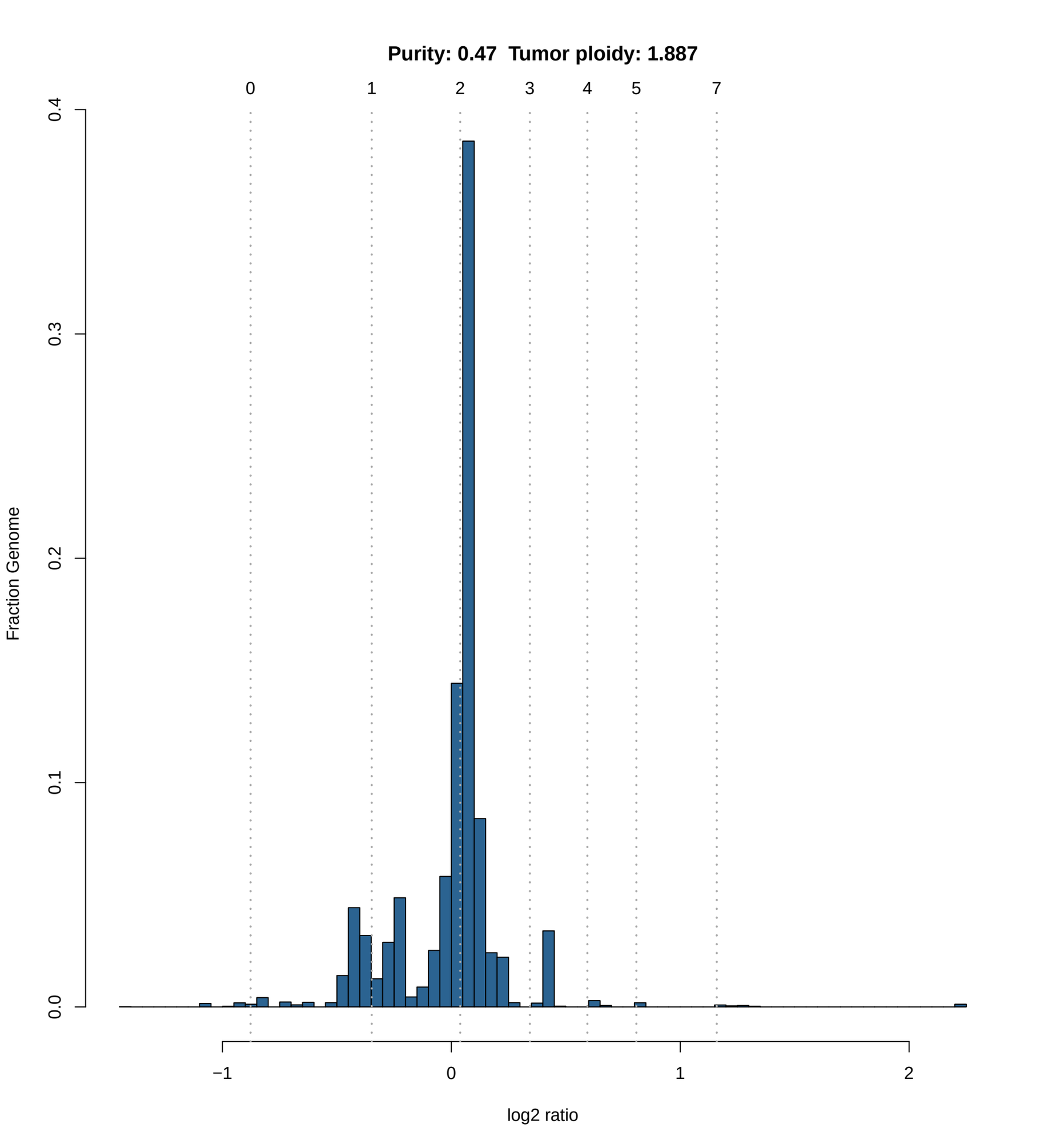
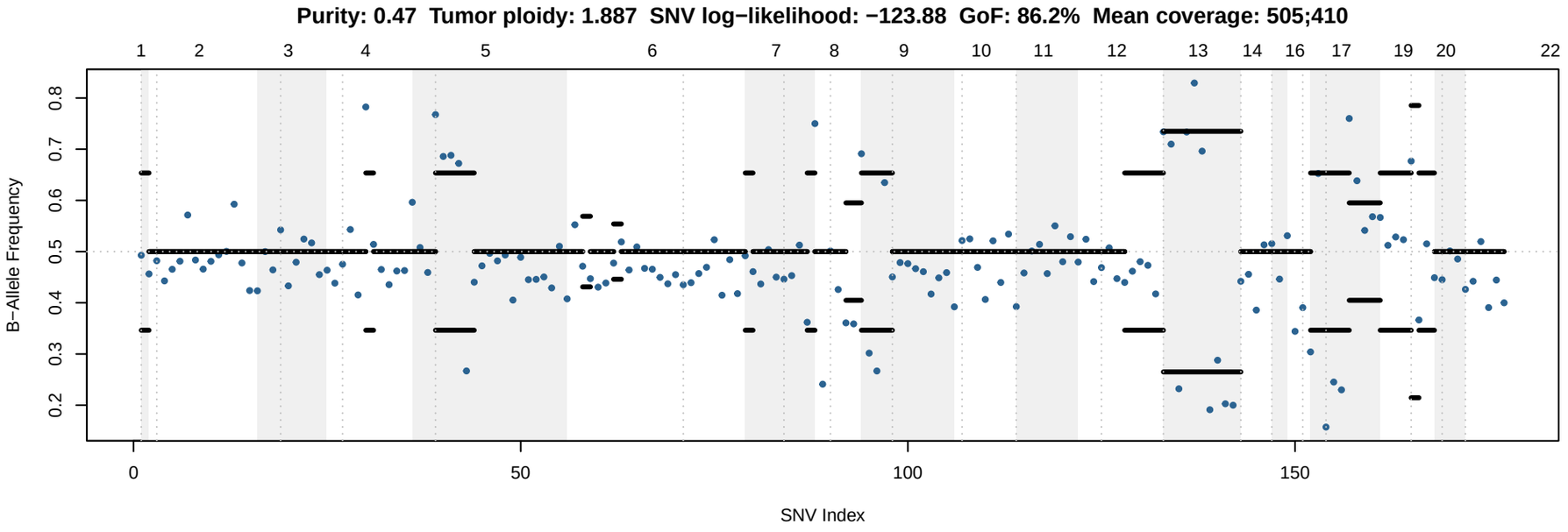
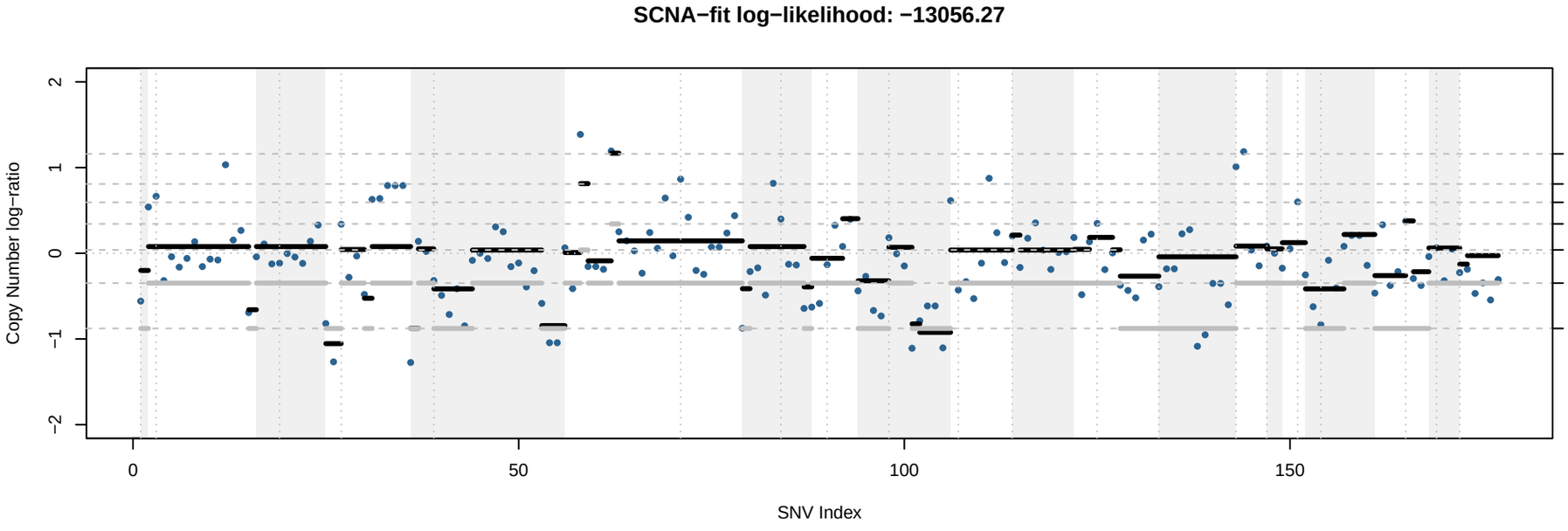
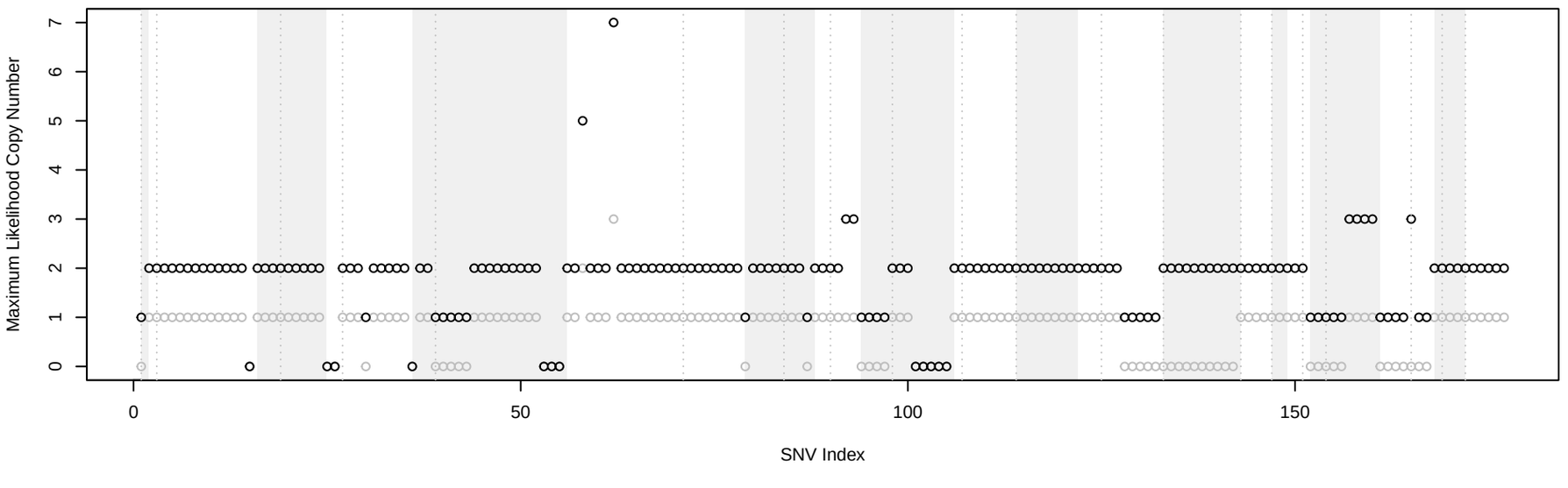
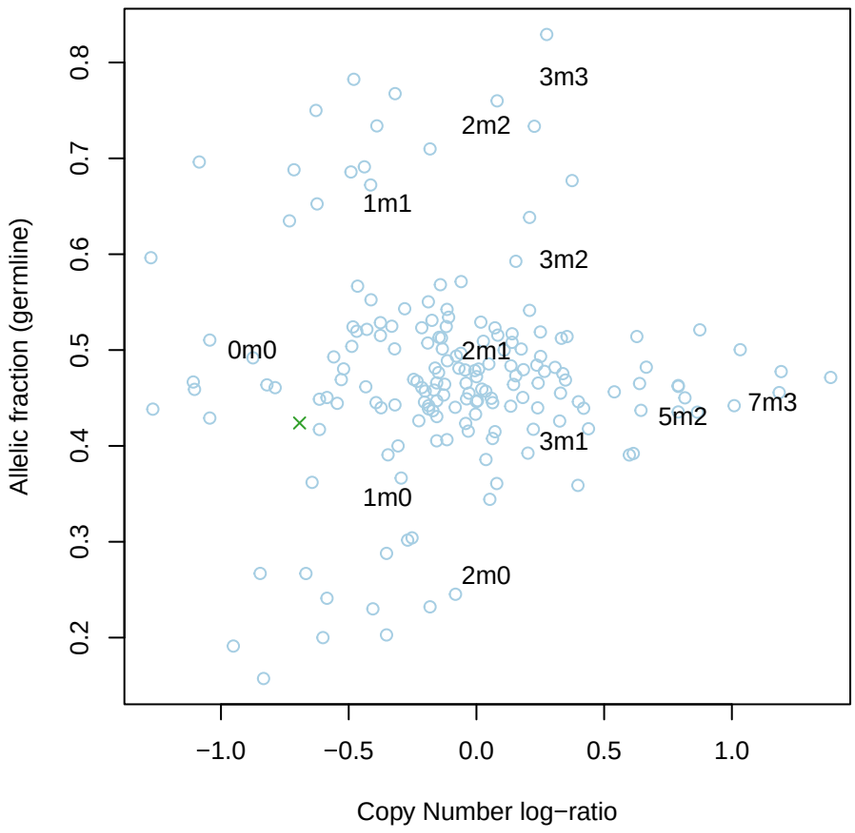
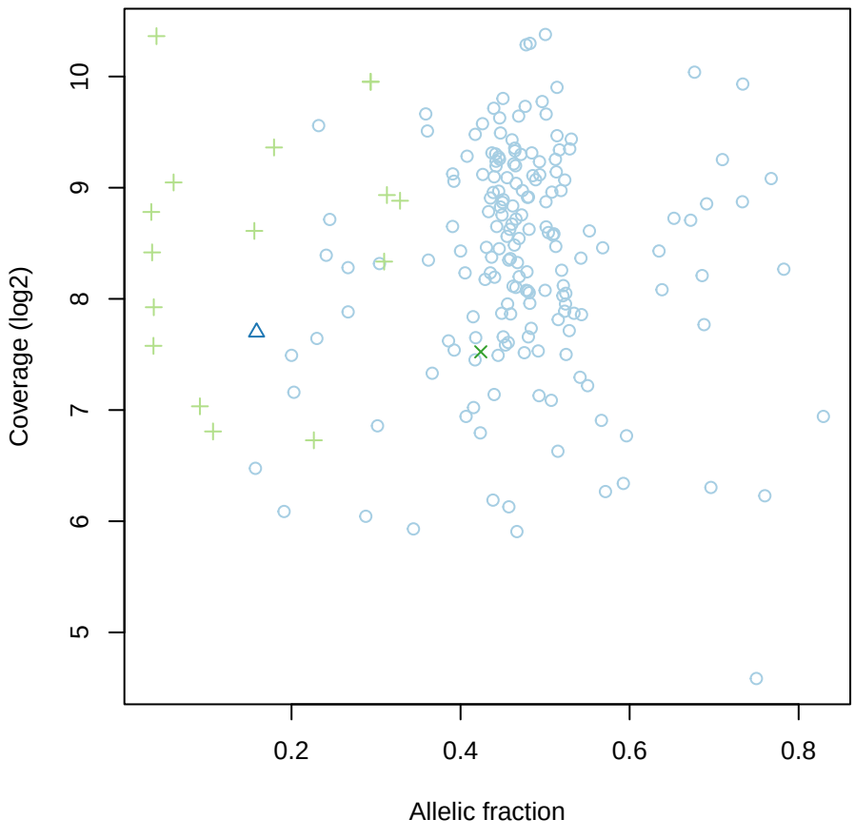

Purity: 0.47 Tumor ploidy: 1.887
0
1
2
3
4
5
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1
0
1
2
log2 ratio

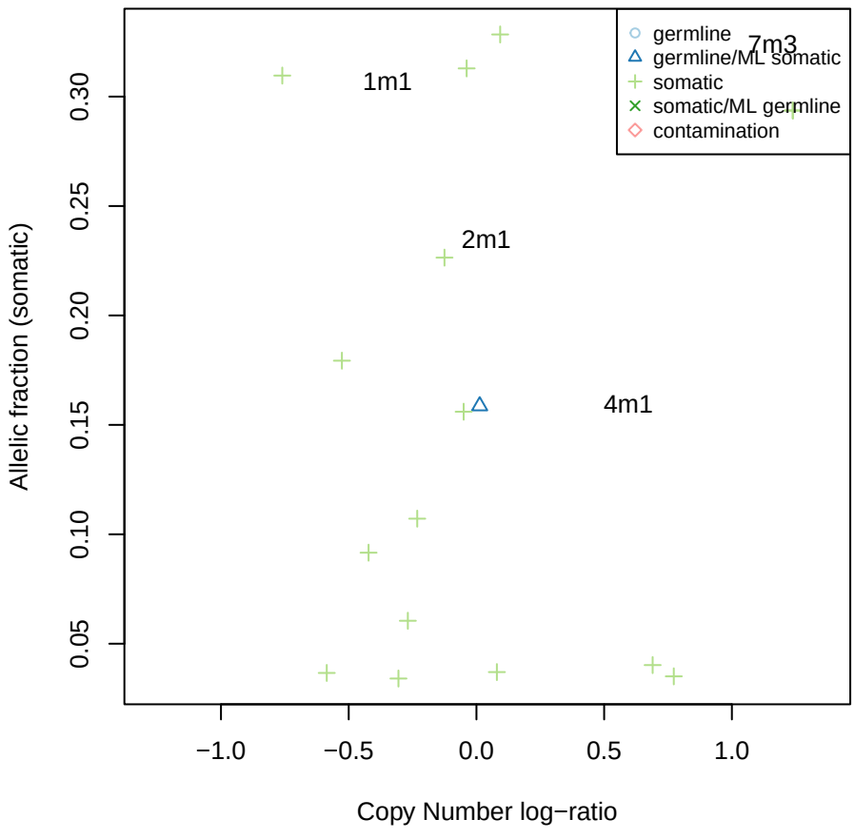

Purity: 0.47 Tumor ploidy: 1.887 SNV log−likelihood: −123.88 GoF: 86.2% Mean coverage: 505;410
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 19 20 22
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

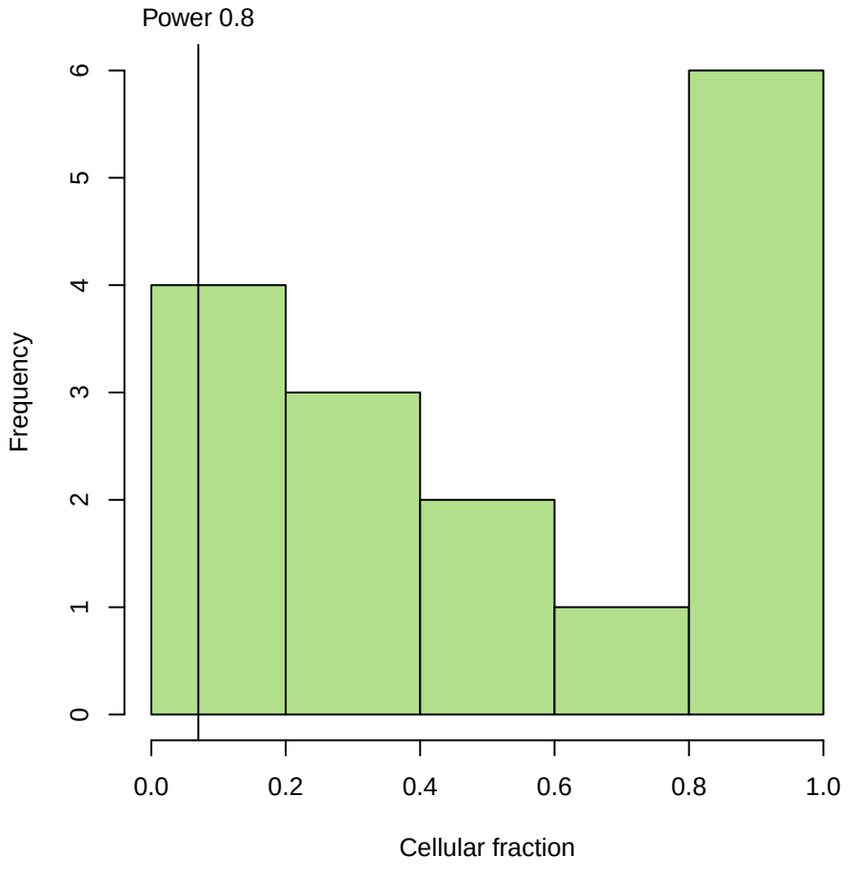

SCNA−fit log−likelihood: −13056.27
Copy Number log−ratio
−2 −1 0 1 2
0 1 2 3 5 7
0 50 100 150
SNV Index

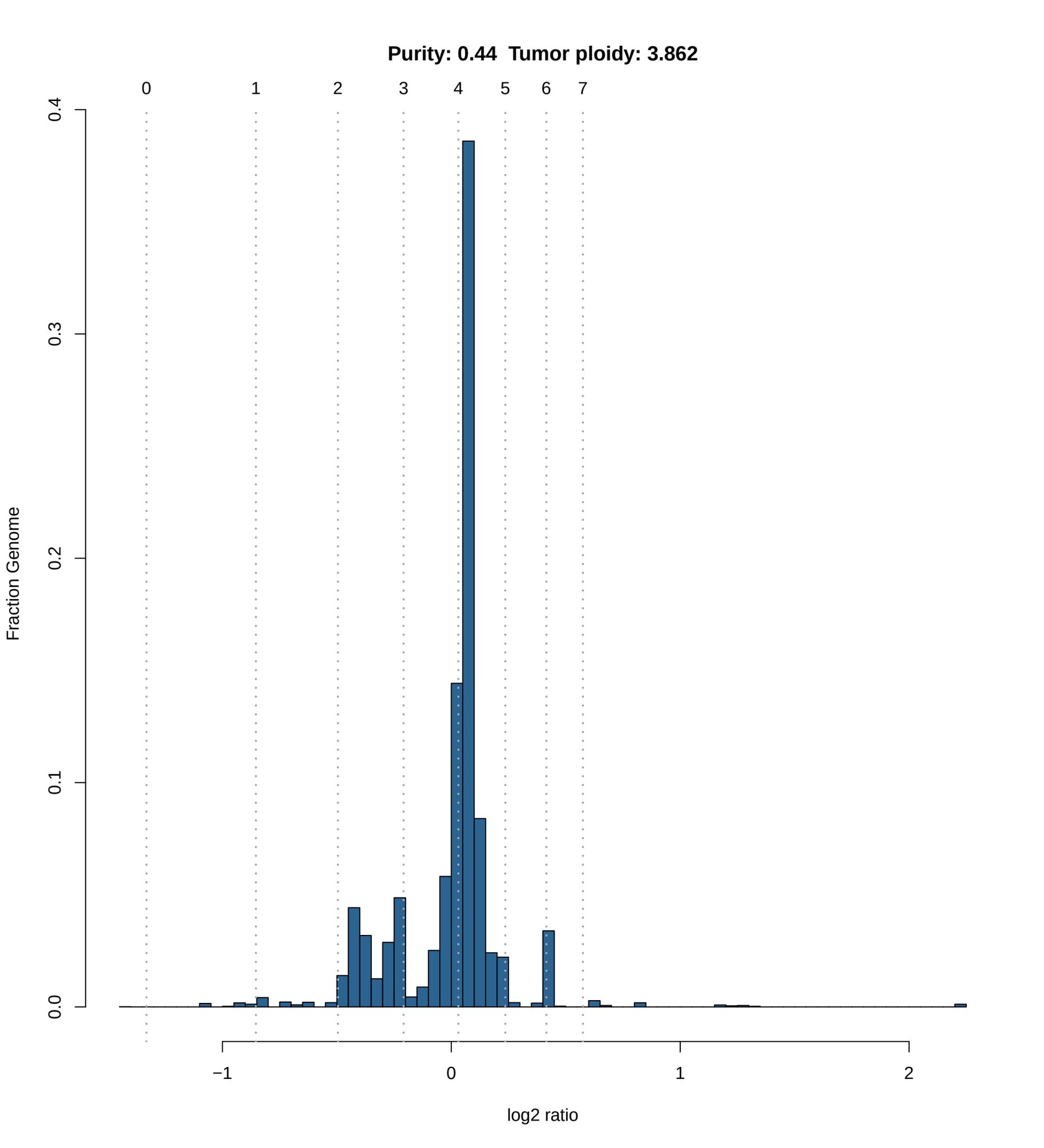

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

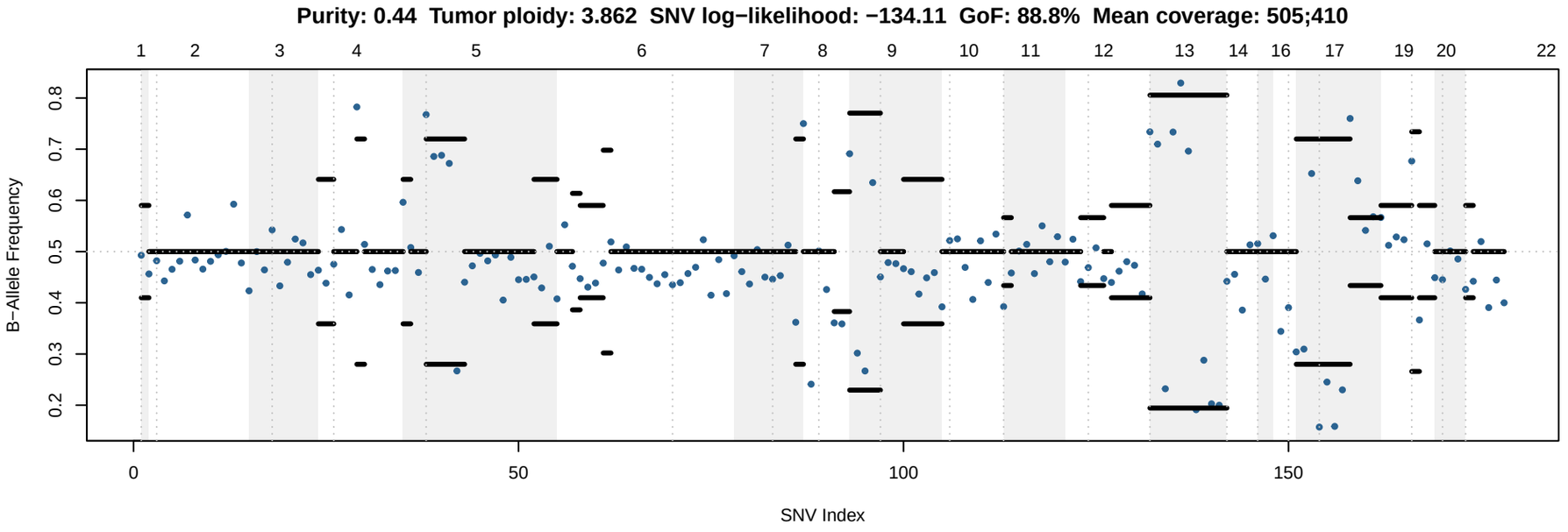

Allelic fraction (germline)
Copy Number log−ratio
0m0
1m0
1m1
2m0
2m1
2m2
3m1
3m2
3m3
5m2
7m3

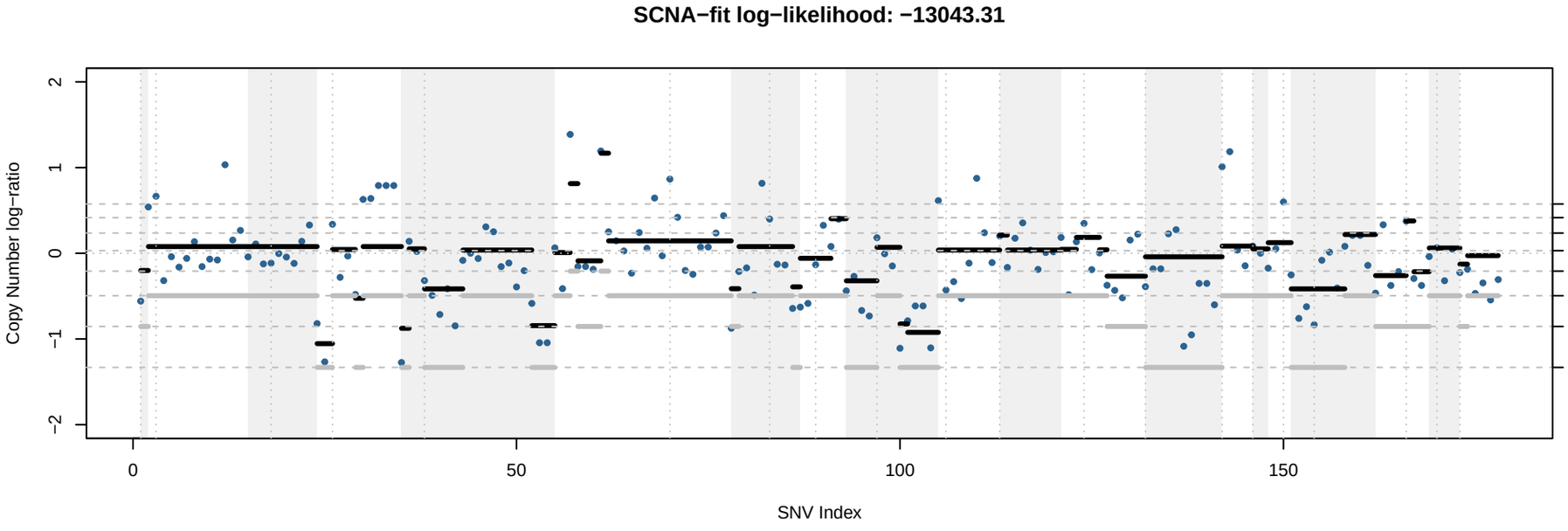

Coverage (log2)
Allelic fraction

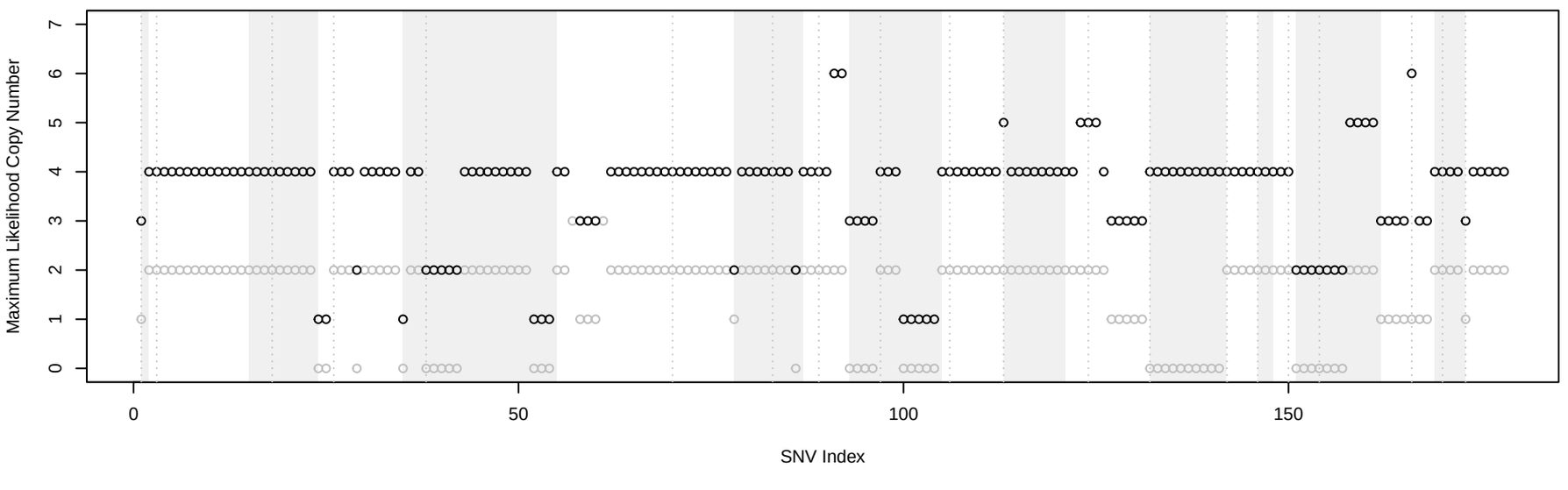

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
4m1
7m3

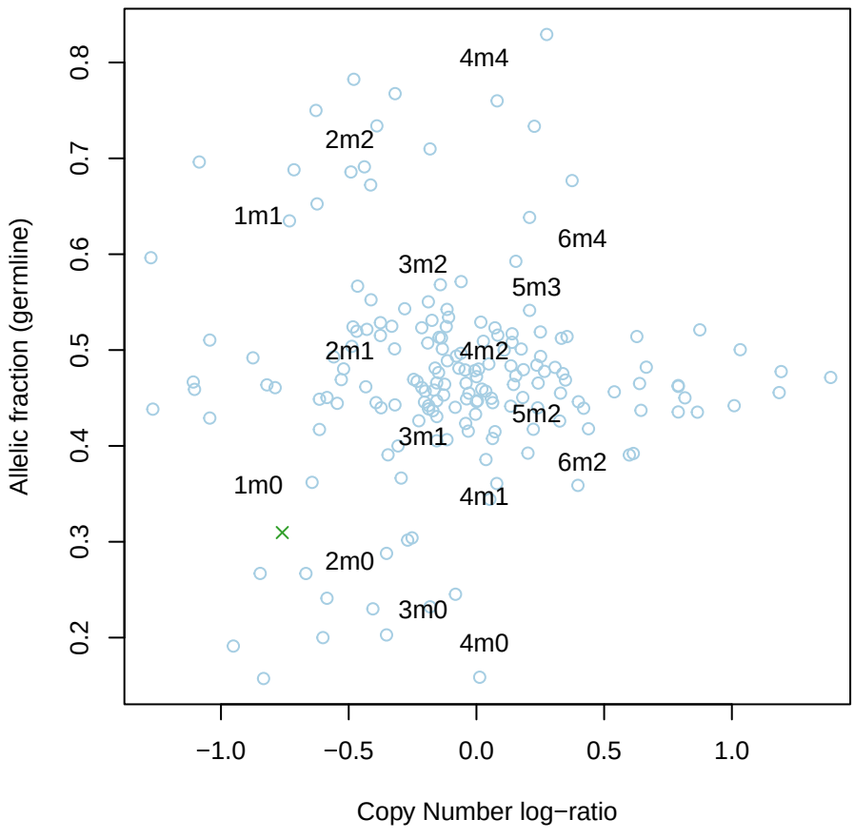

Power 0.8
Frequency
Cellular fraction

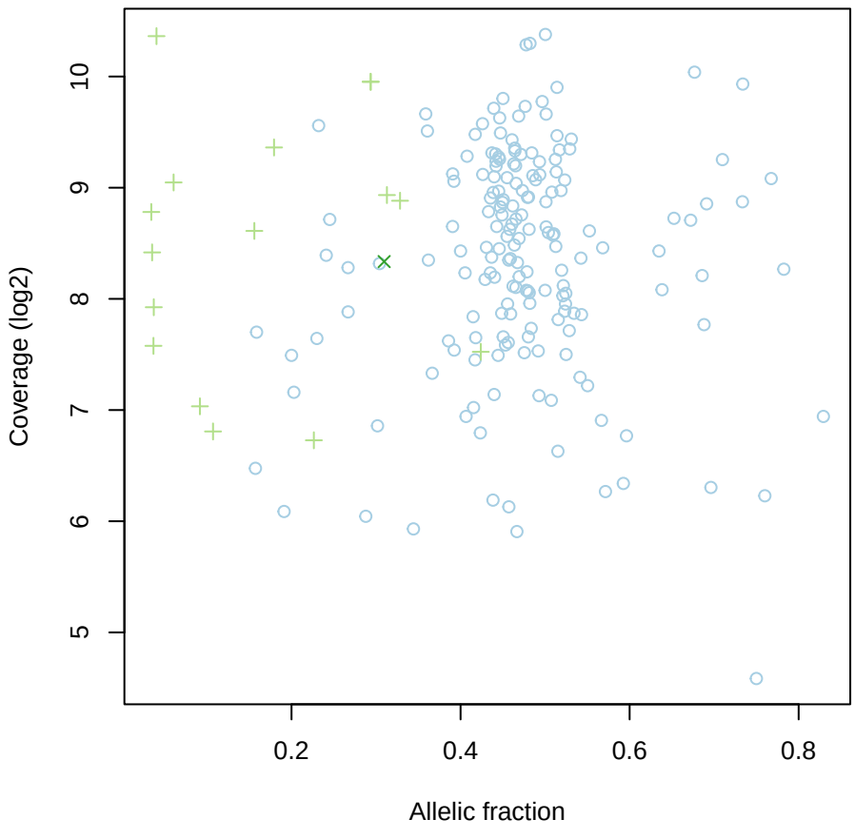

Purity: 0.44 Tumor ploidy: 3.862
0
1
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1
0
1
2
log2 ratio

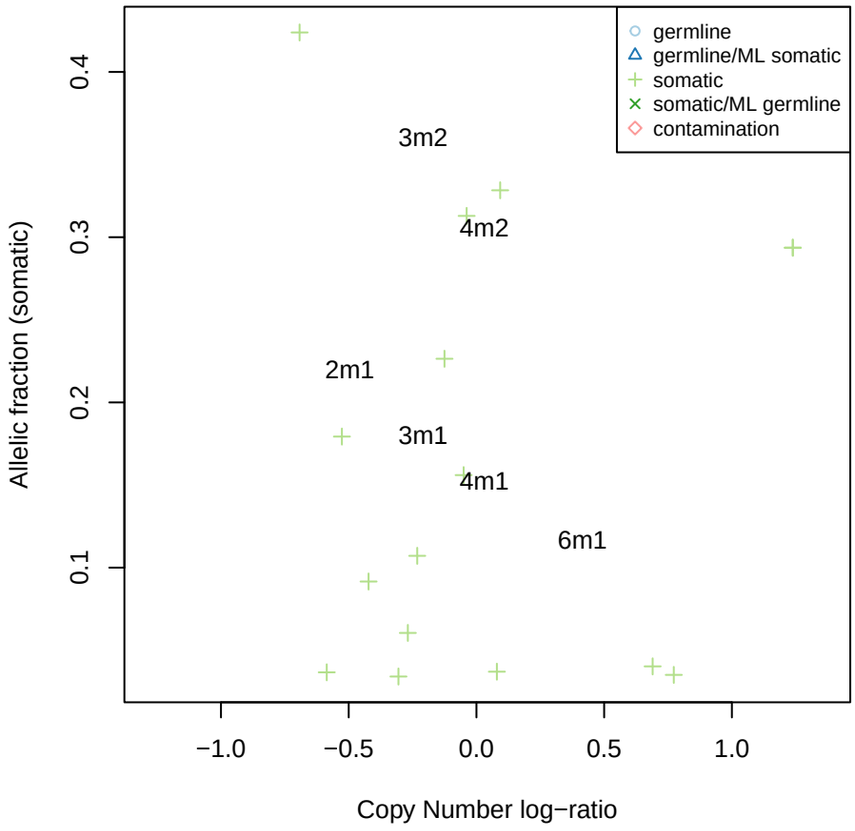

Purity: 0.44 Tumor ploidy: 3.862 SNV log−likelihood: −134.11 GoF: 88.8% Mean coverage: 505;410
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 19 20 22
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

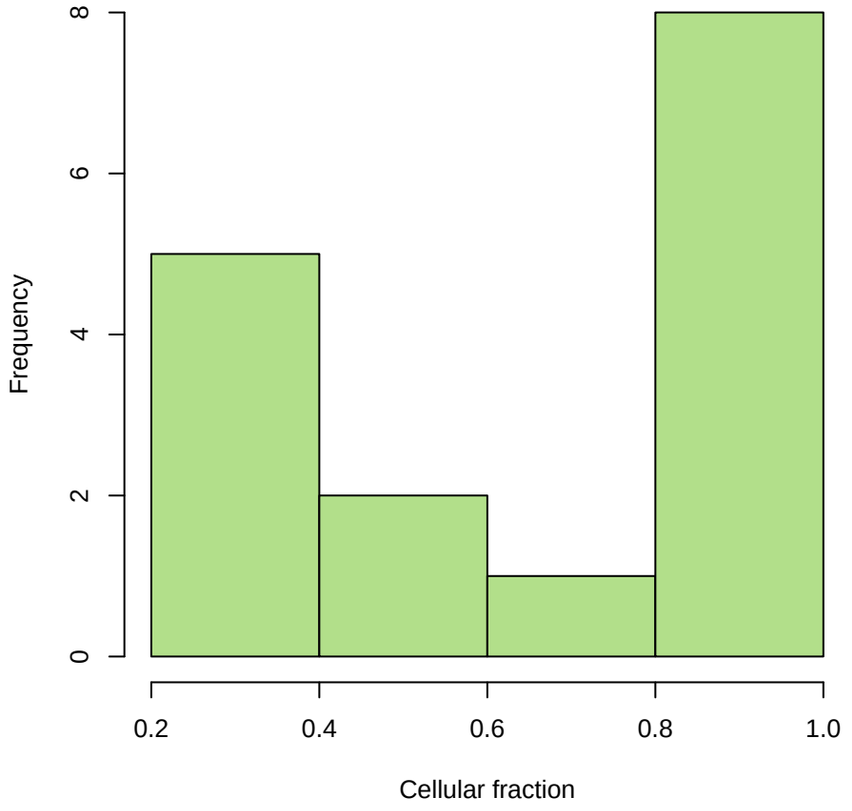

SCNA−fit log−likelihood: −13043.31
Copy Number log−ratio
−2 −1 0 1 2
0 1 2 4 6
0 50 100 150
SNV Index

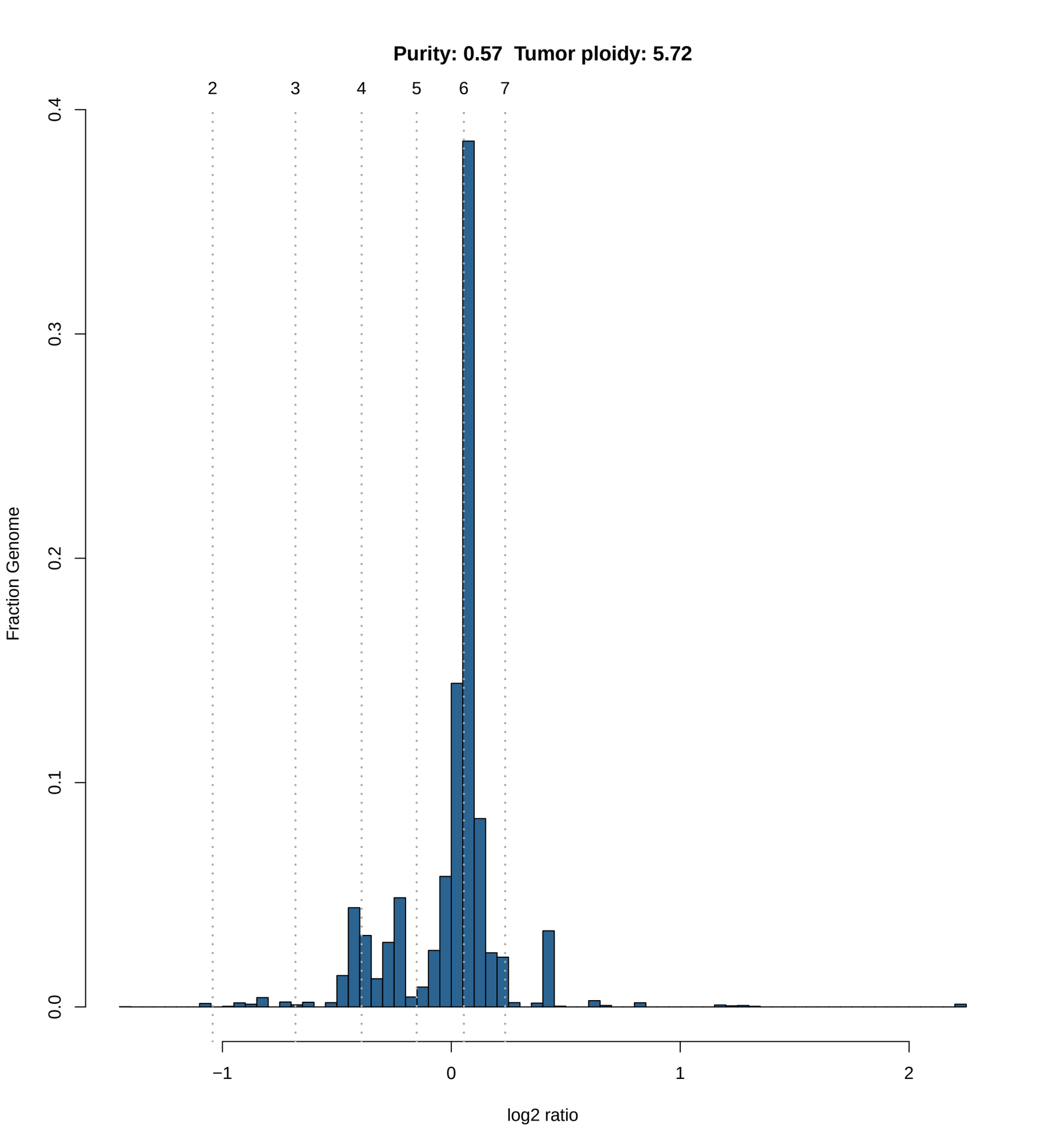

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

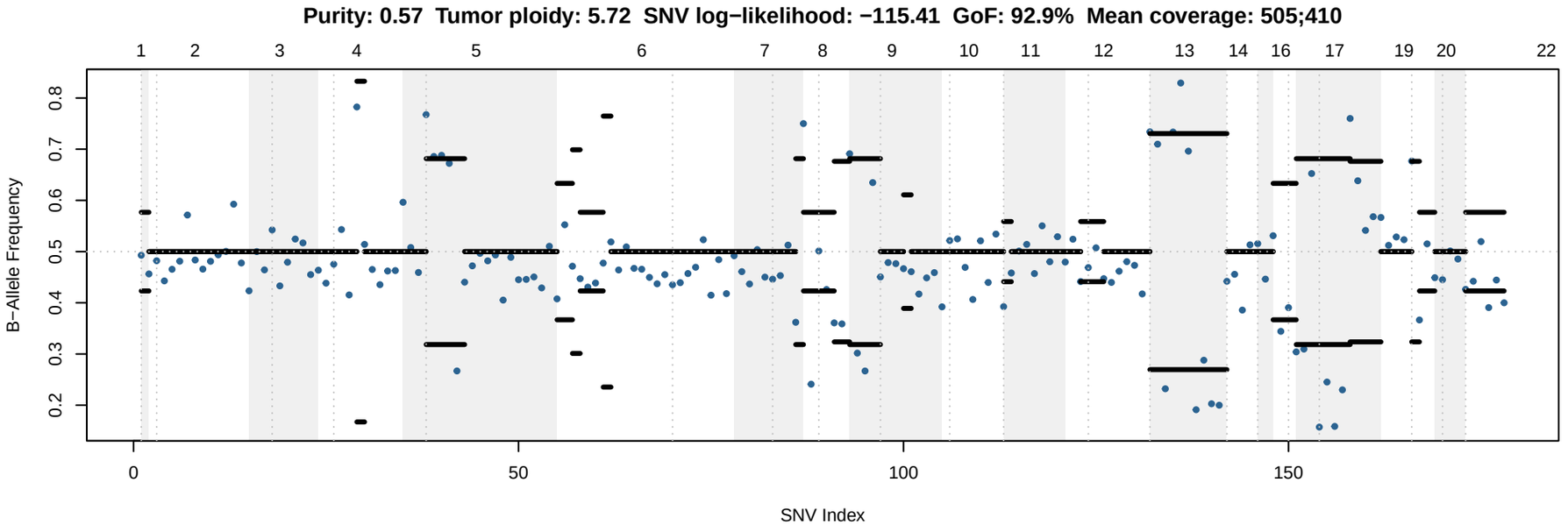

Allelic fraction (germline)
Copy Number log−ratio
4m4
2m2
1m1
6m4
3m2
5m3
2m1
4m2
5m2
3m1
6m2
1m0
4m1
2m0
3m0
4m0

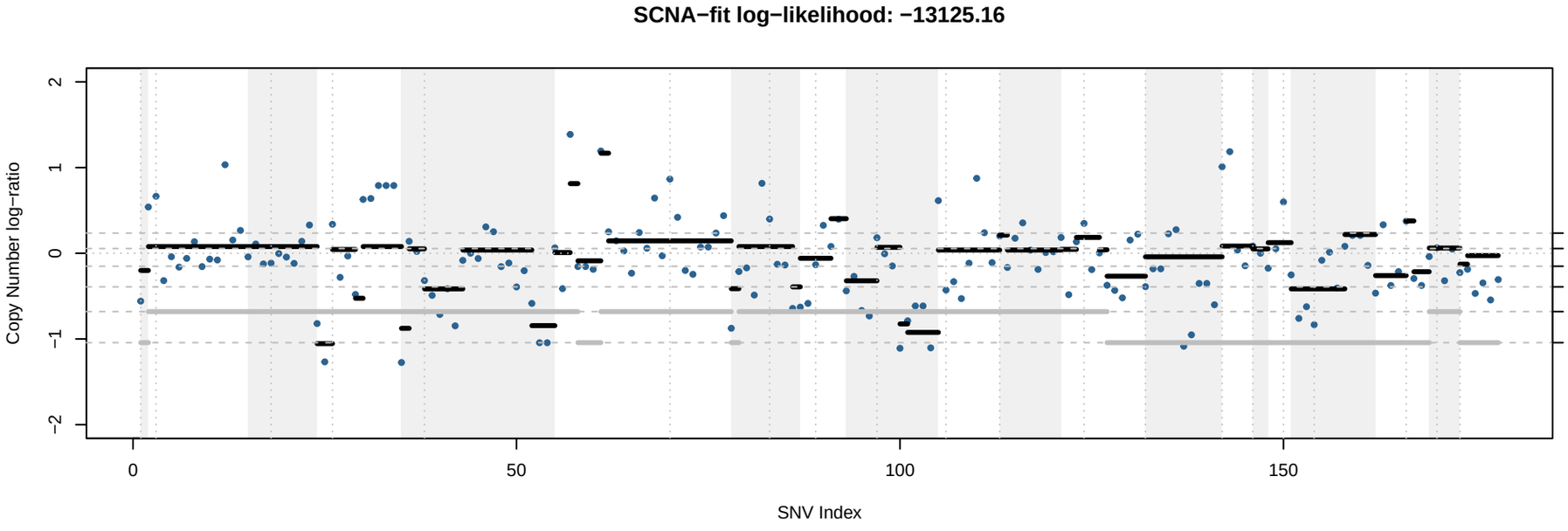

Coverage (log2)
Allelic fraction

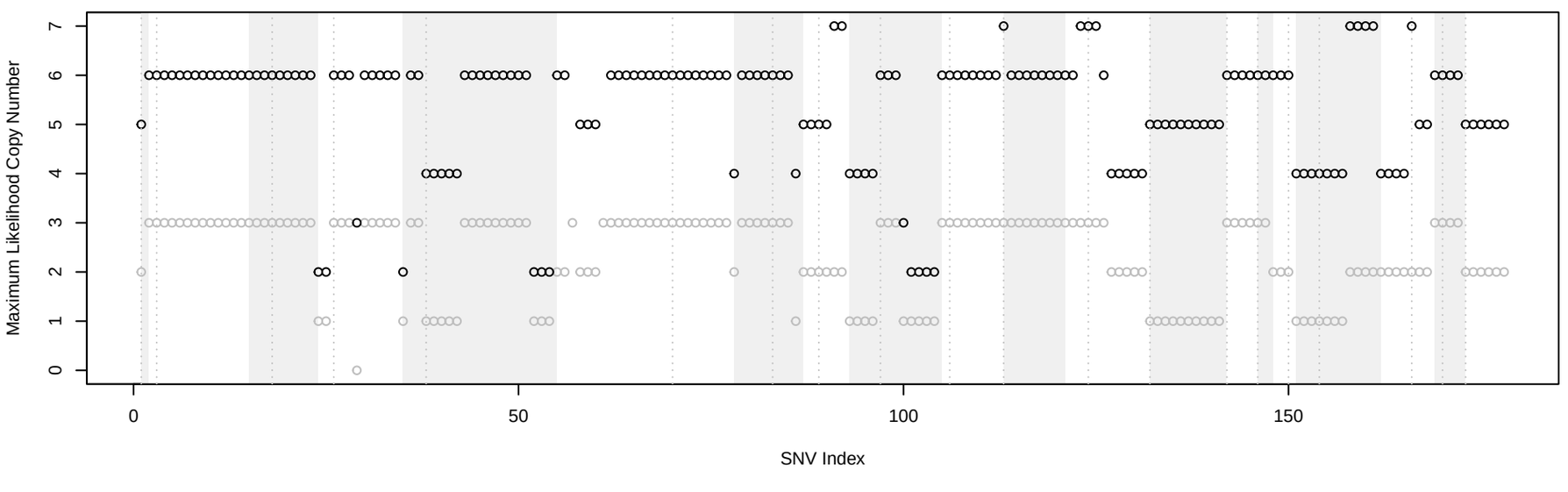

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m2
4m2
2m1
3m1
4m1
6m1

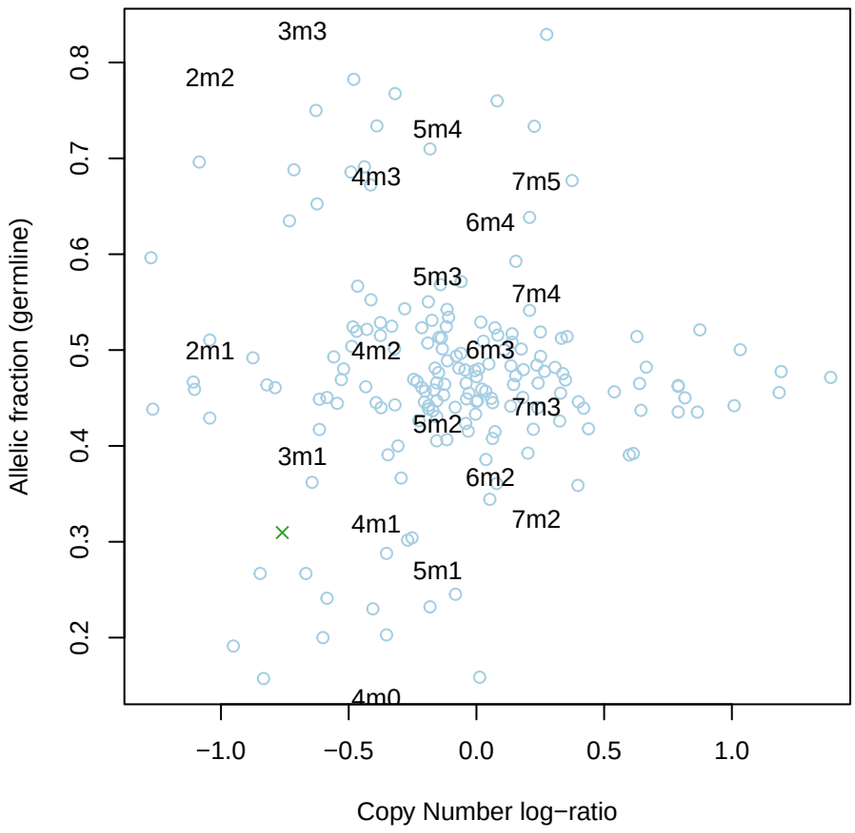

Frequency
Cellular fraction

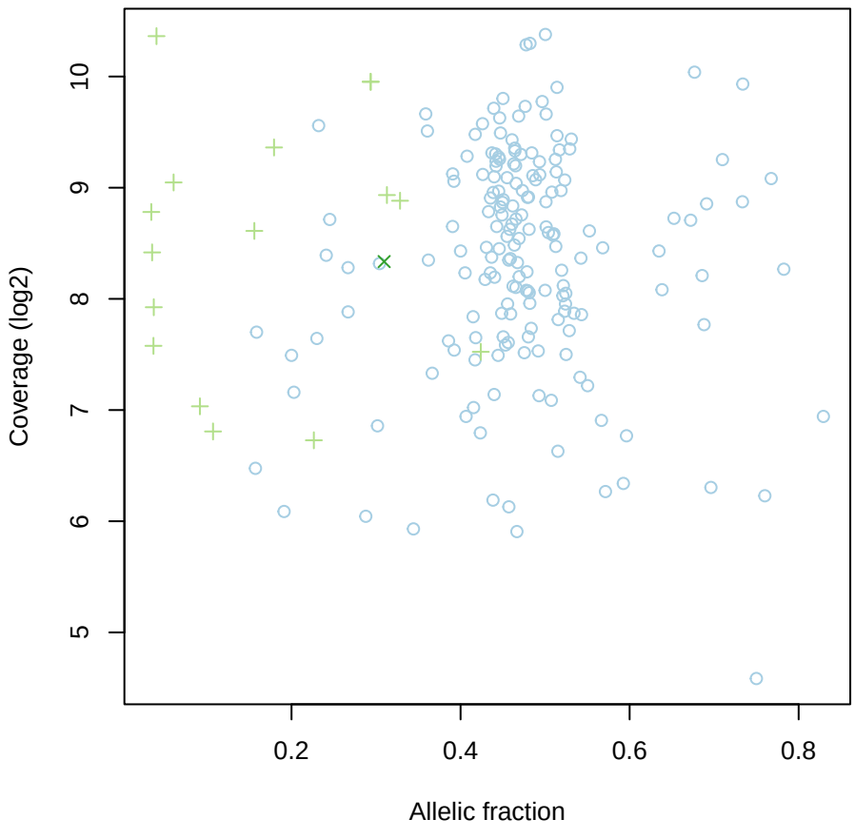

Purity: 0.57 Tumor ploidy: 5.72
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1
0
1
2
log2 ratio

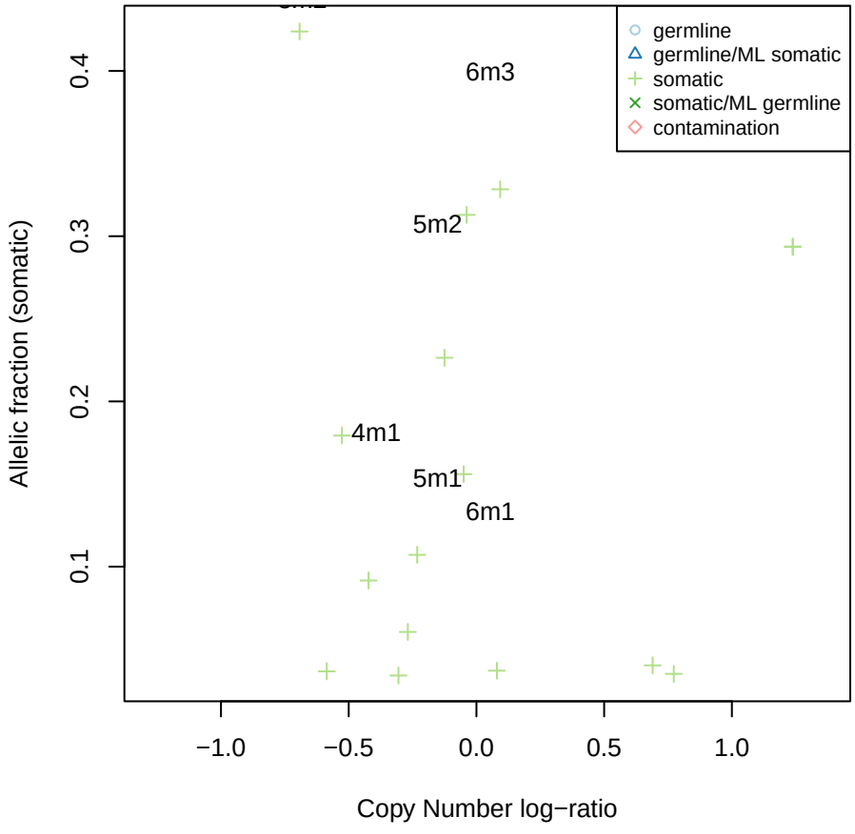

Purity: 0.57 Tumor ploidy: 5.72 SNV log−likelihood: −115.41 GoF: 92.9% Mean coverage: 505;410
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 19 20 22
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

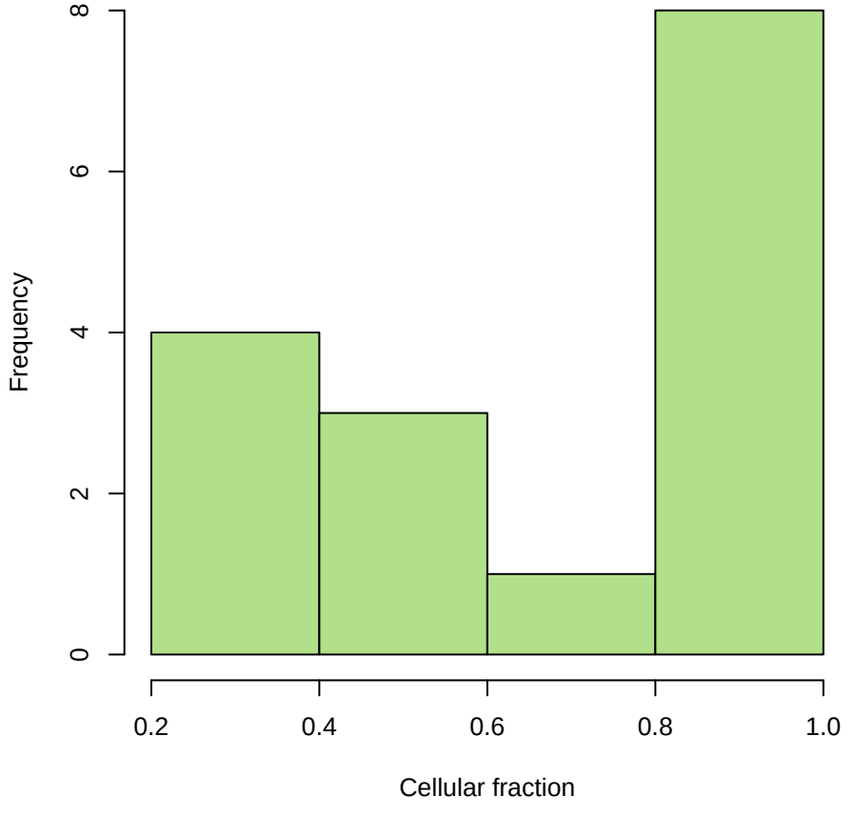

SCNA−fit log−likelihood: −13125.16
Copy Number log−ratio
2 1 0 −1 −2
2 3 4 6
0 50 100 150
SNV Index

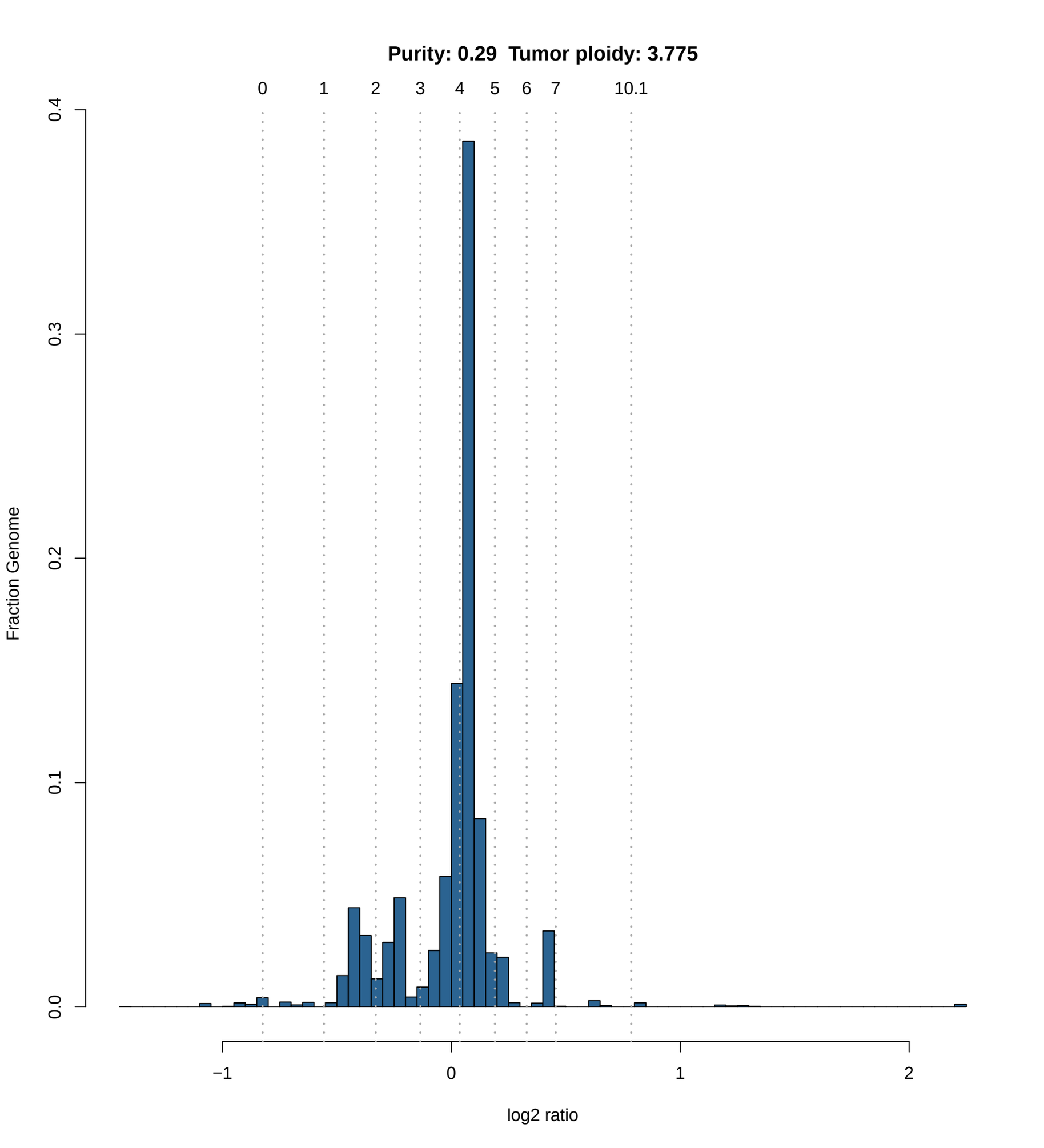

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

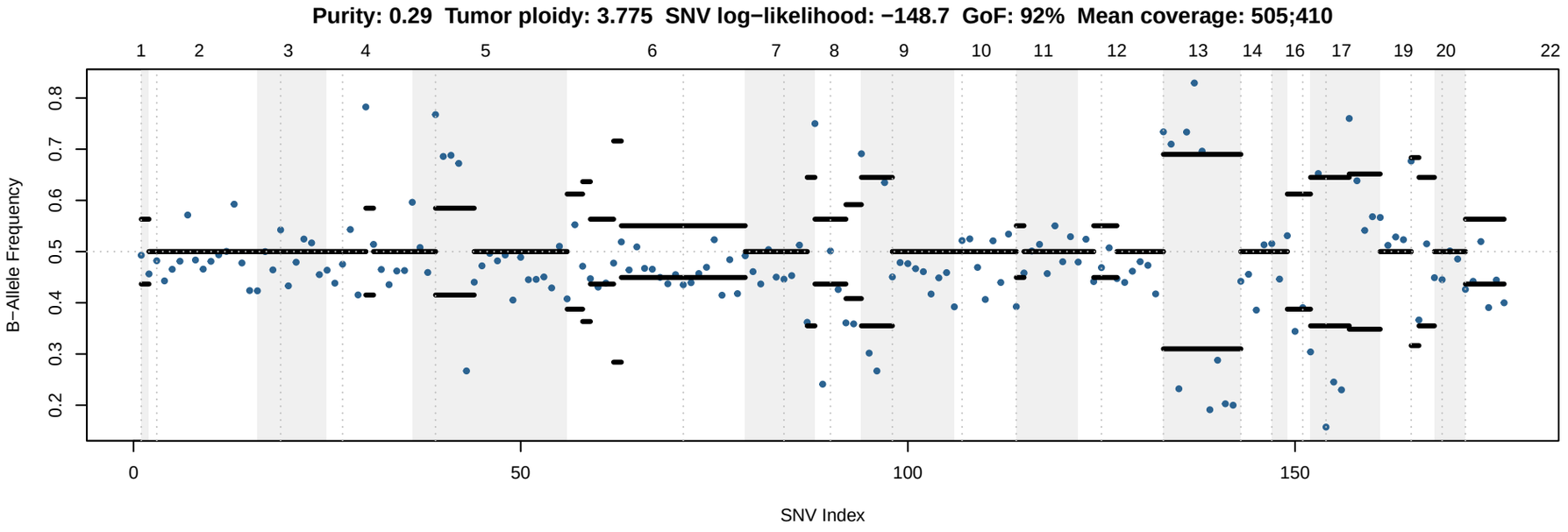

3m3
2m2
5m4
4m3
7m5
6m4
5m3
7m4
2m1
4m2
6m3
7m3
5m2
3m1
6m2
7m2
4m1
5m1
4m0
Allelic fraction (germline)
Copy Number log−ratio

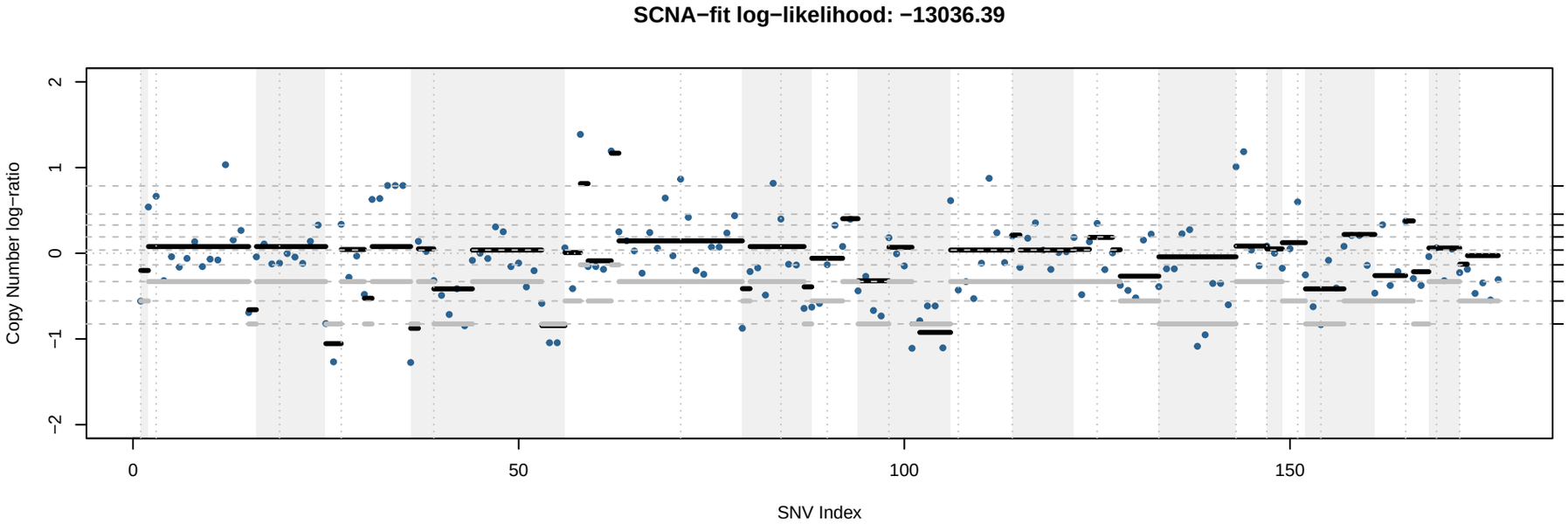

Coverage (log2)
Allelic fraction

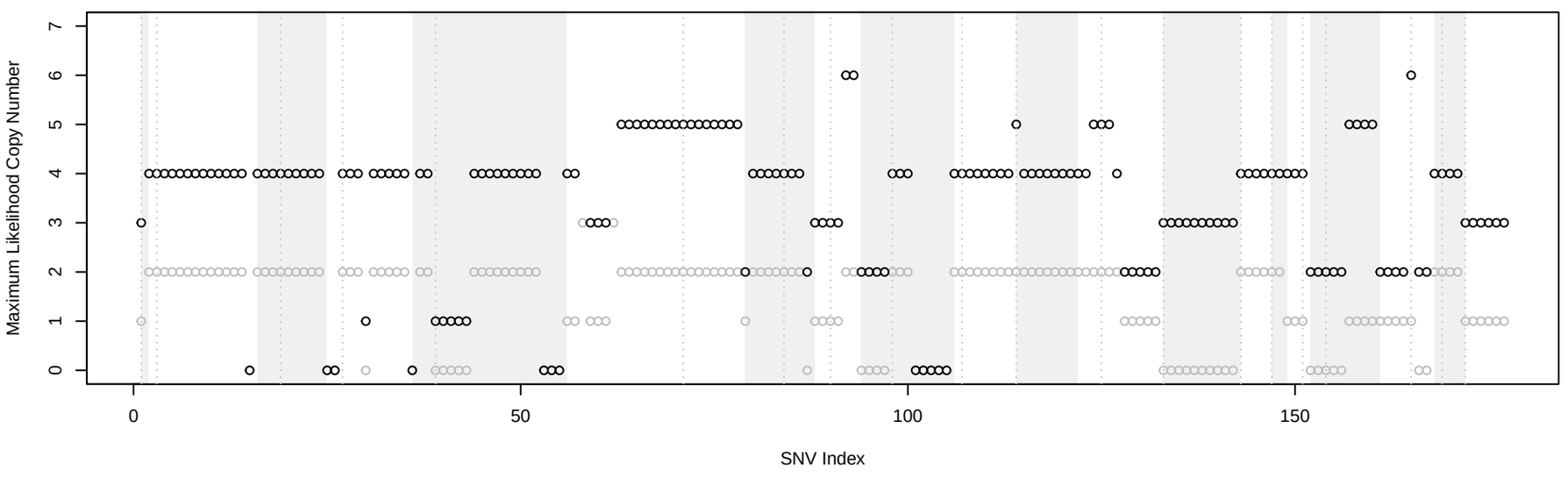

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m3
5m2
4m1
5m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio

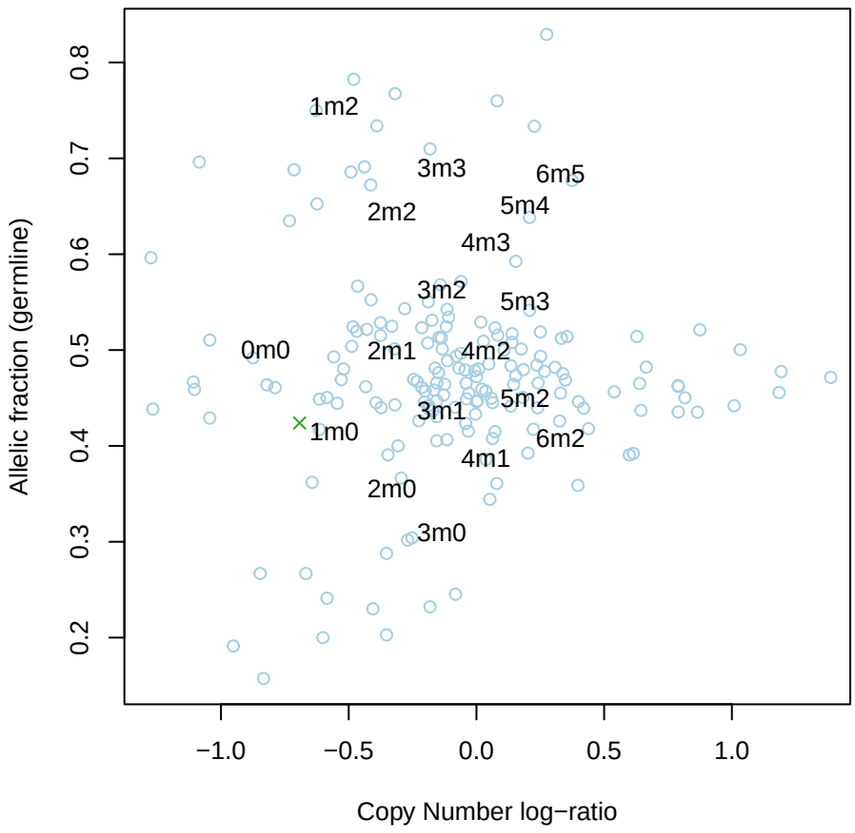

Frequency
Cellular fraction

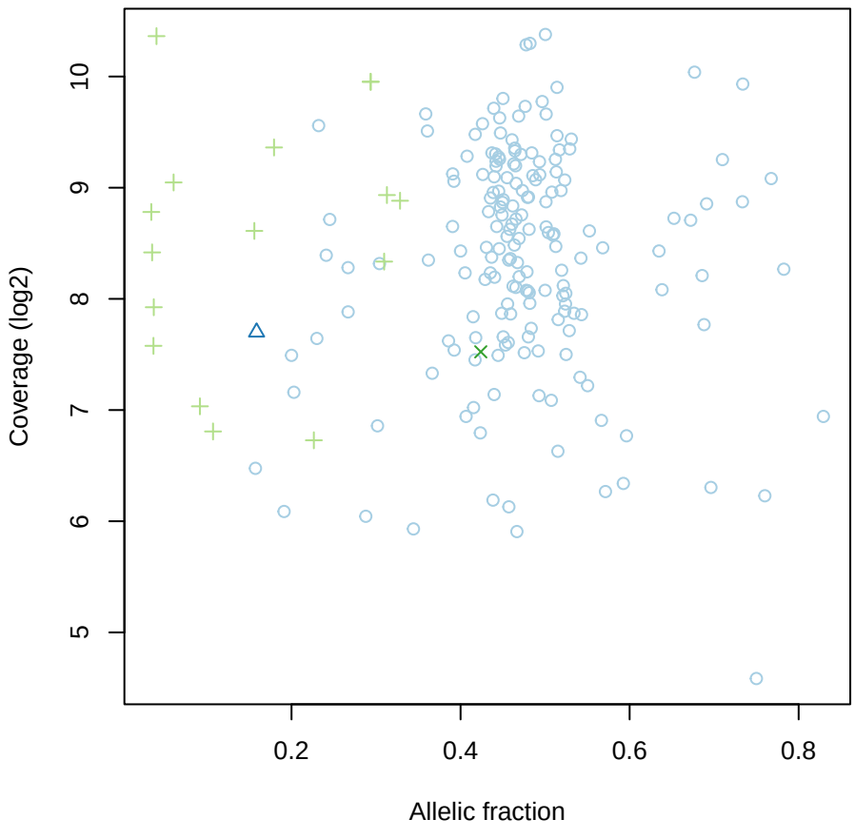

Purity: 0.29 Tumor ploidy: 3.775
0
1
2
3
4
5
6
7
10.1
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1
0
1
2
log2 ratio

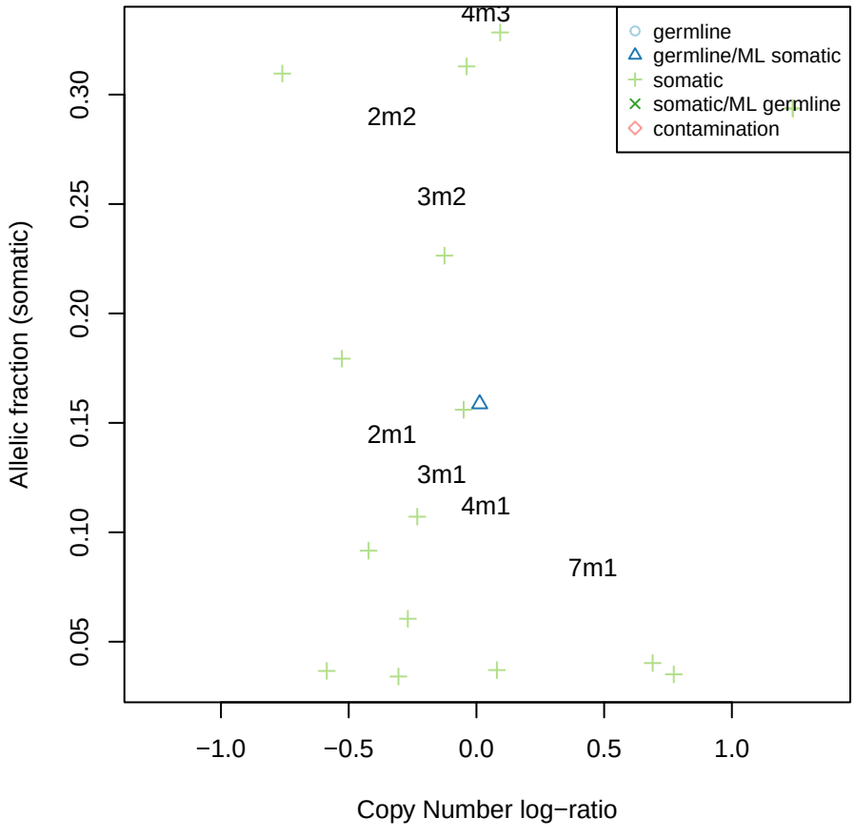

Purity: 0.29 Tumor ploidy: 3.775 SNV log−likelihood: −148.7 GoF: 92% Mean coverage: 505;410
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 19 20 22
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

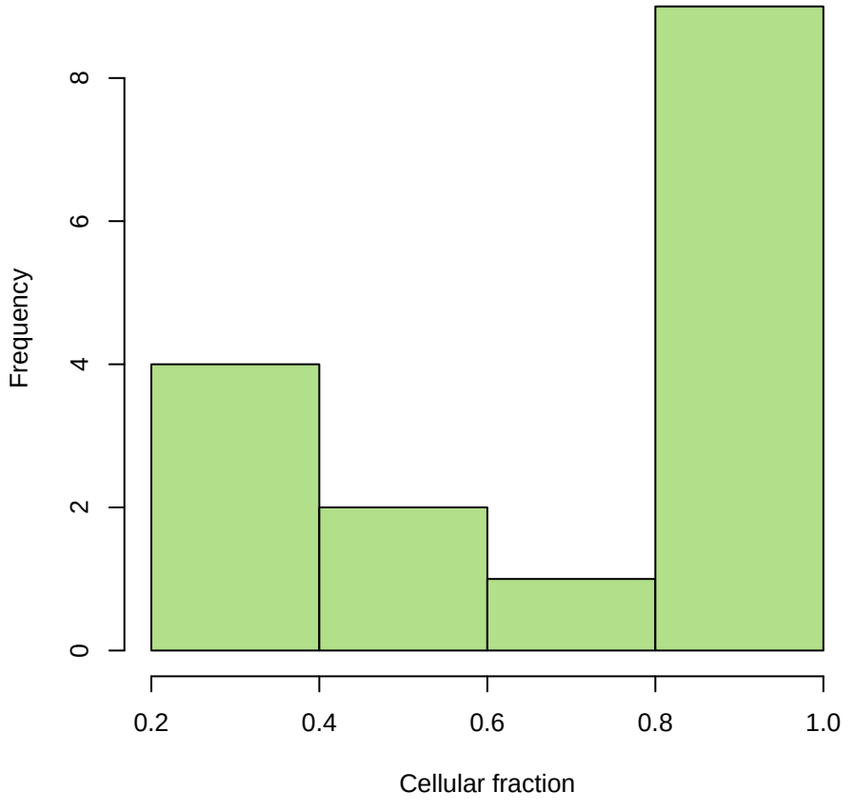

SCNA−fit log−likelihood: −13036.39
Copy Number log−ratio
−2 −1 0 1 2
0 2 4 6 10.1
0 50 100 150
SNV Index

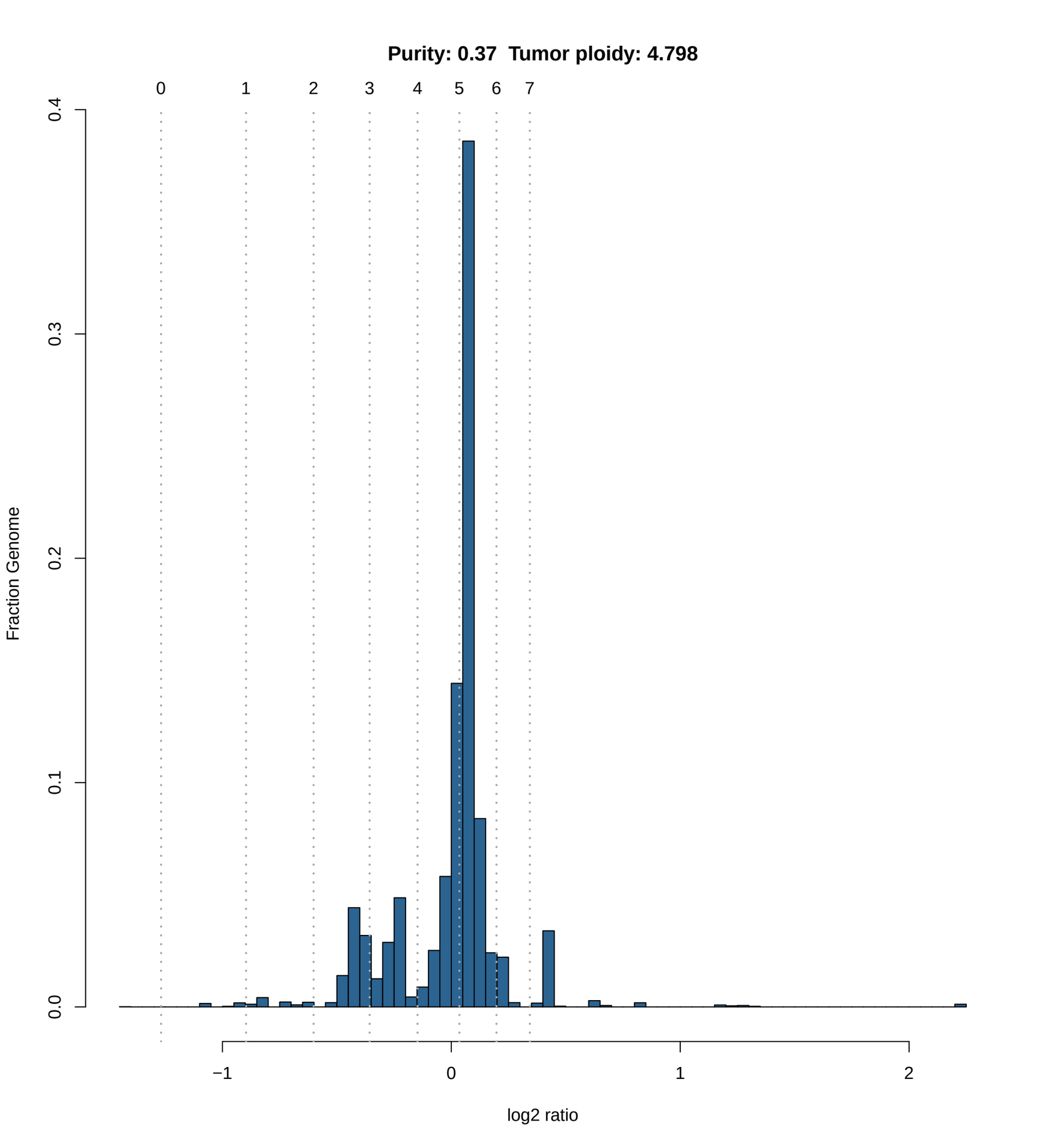

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

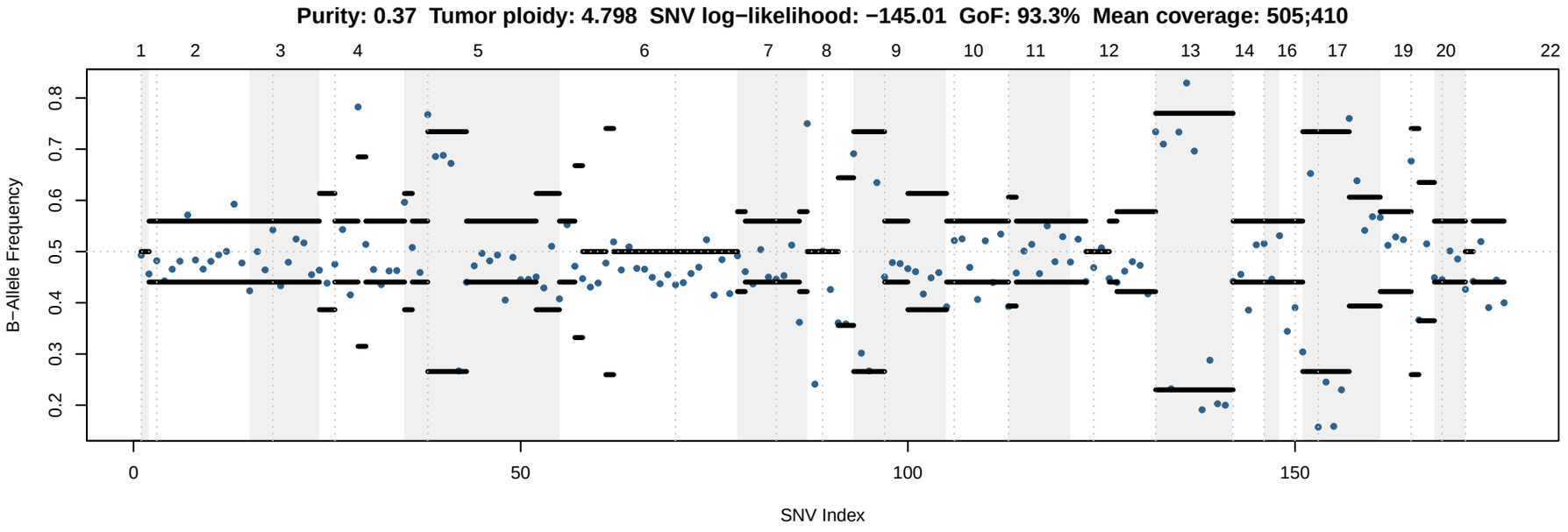

Allelic fraction (germline)
Copy Number log−ratio
1m2
3m3
6m5
2m2
5m4
4m3
3m2
5m3
0m0
2m1
4m2
5m2
3m1
1m0
6m2
4m1
2m0
3m0

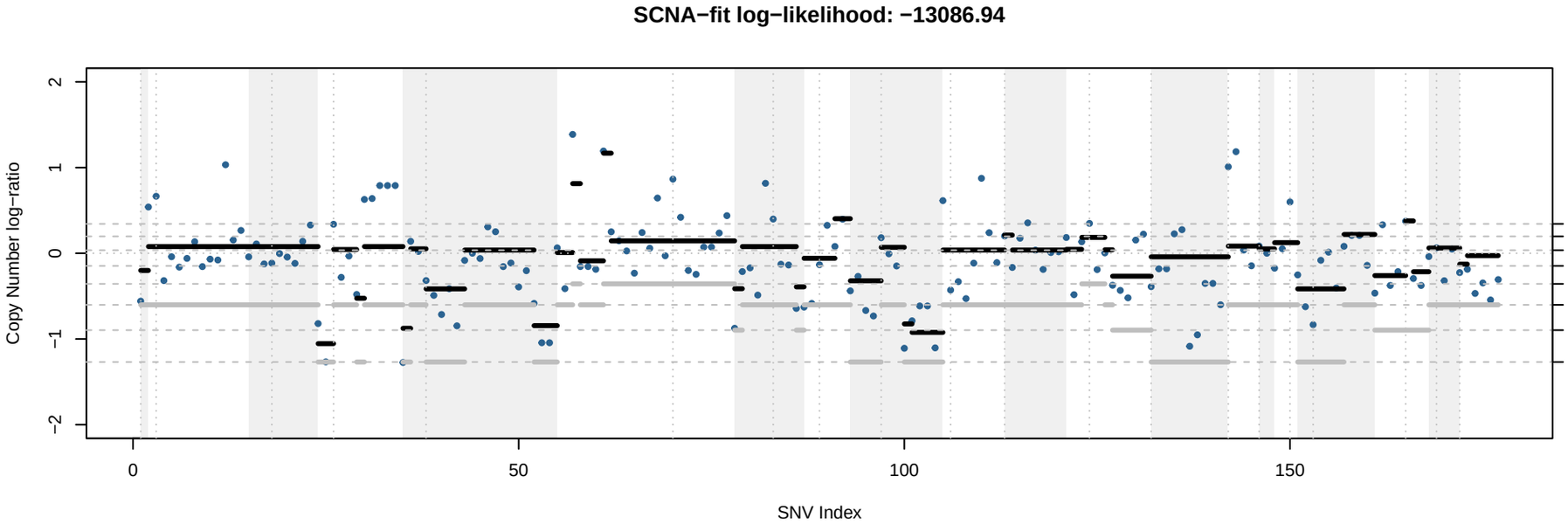

Coverage (log2)
Allelic fraction

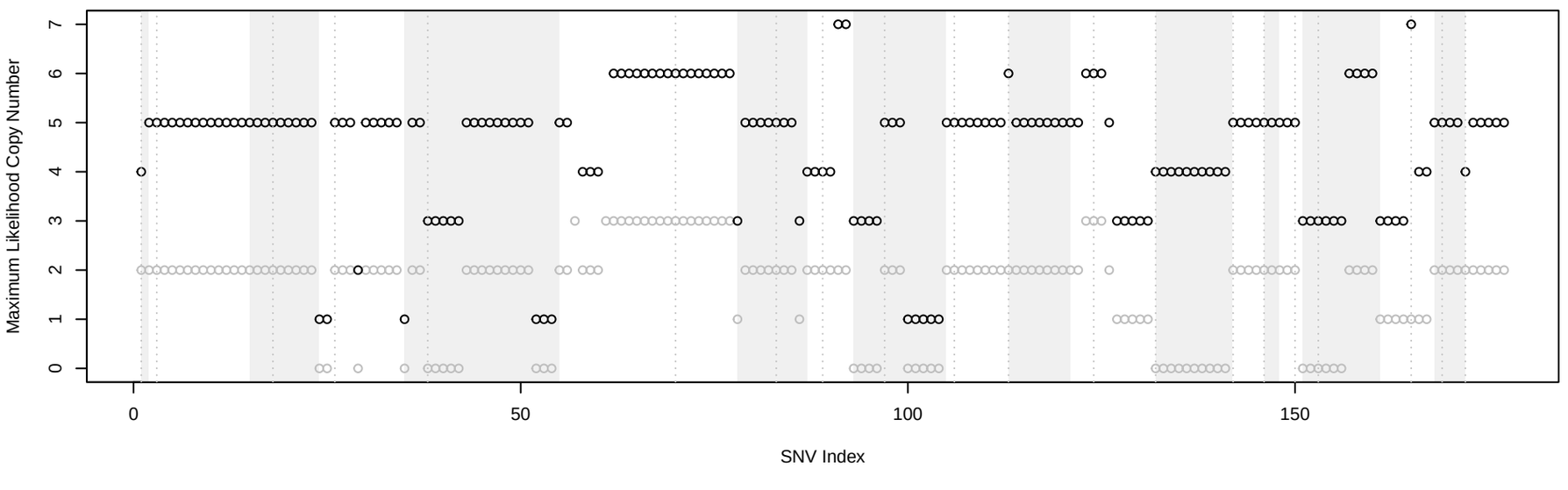

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m3
2m2
3m2
2m1
3m1
4m1
7m1

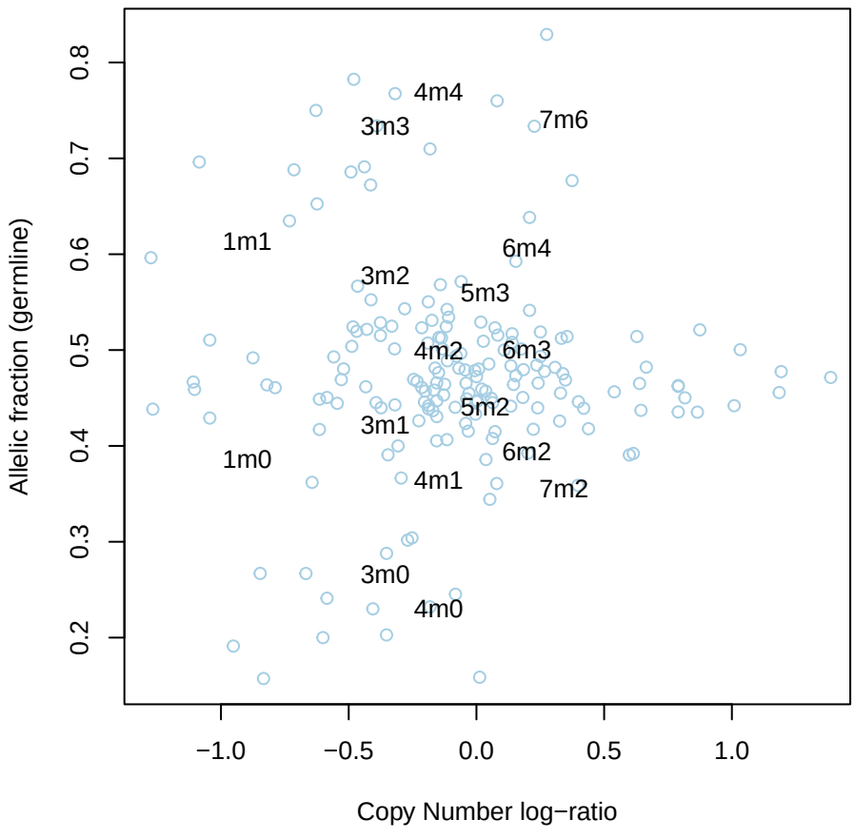

Frequency
Cellular fraction

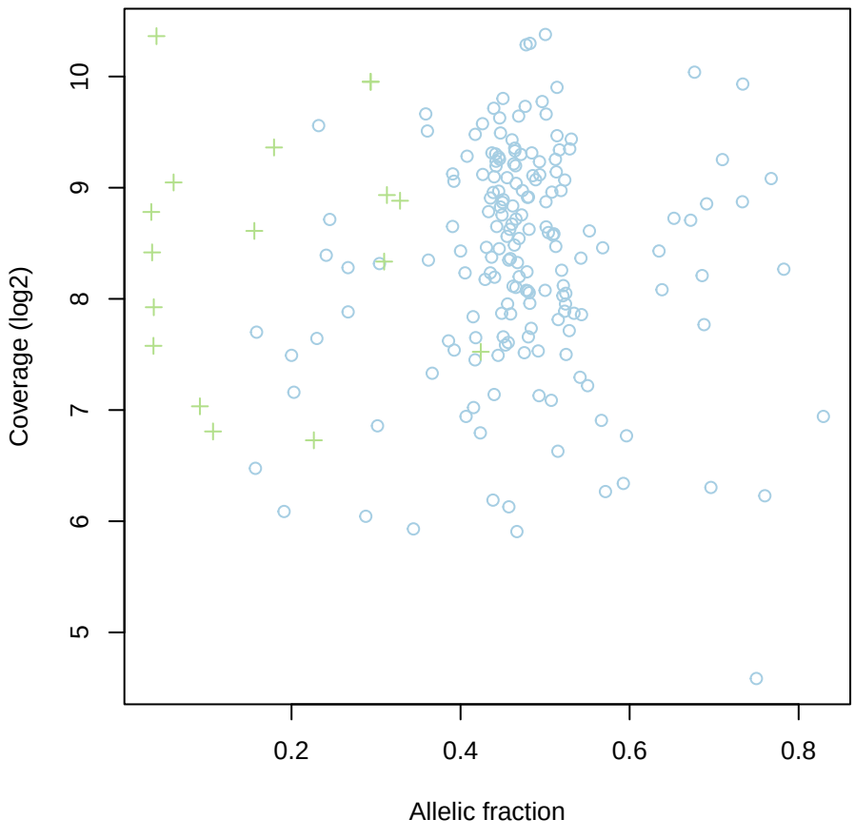

Purity: 0.37 Tumor ploidy: 4.798
0
1
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1
0
1
2
log2 ratio

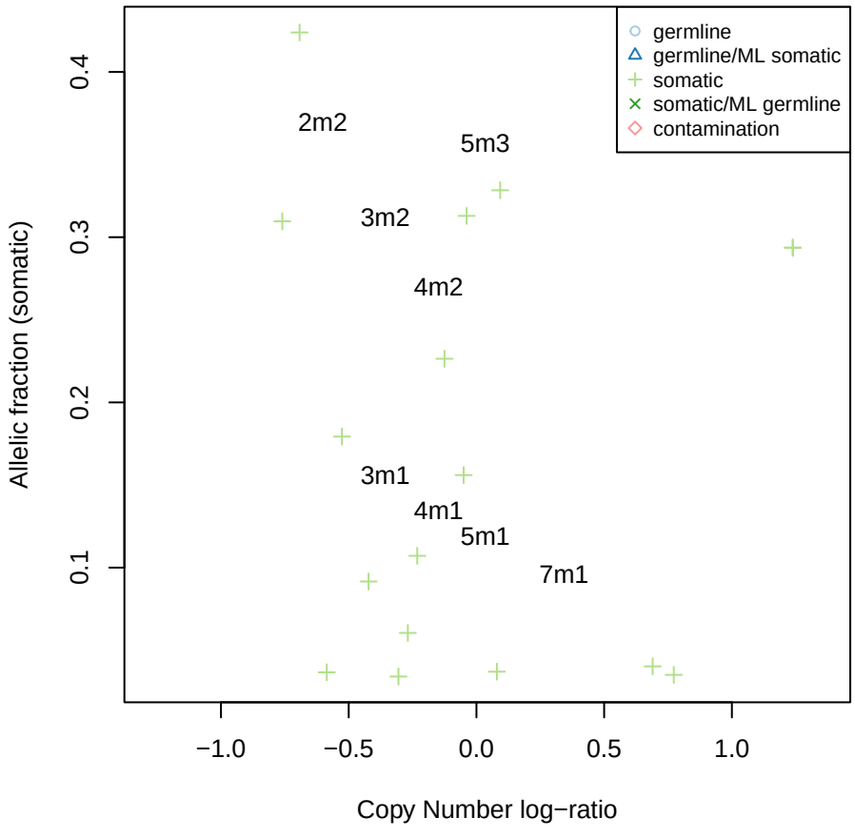

Purity: 0.37 Tumor ploidy: 4.798 SNV log−likelihood: −145.01 GoF: 93.3% Mean coverage: 505;410
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 19 20 22
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

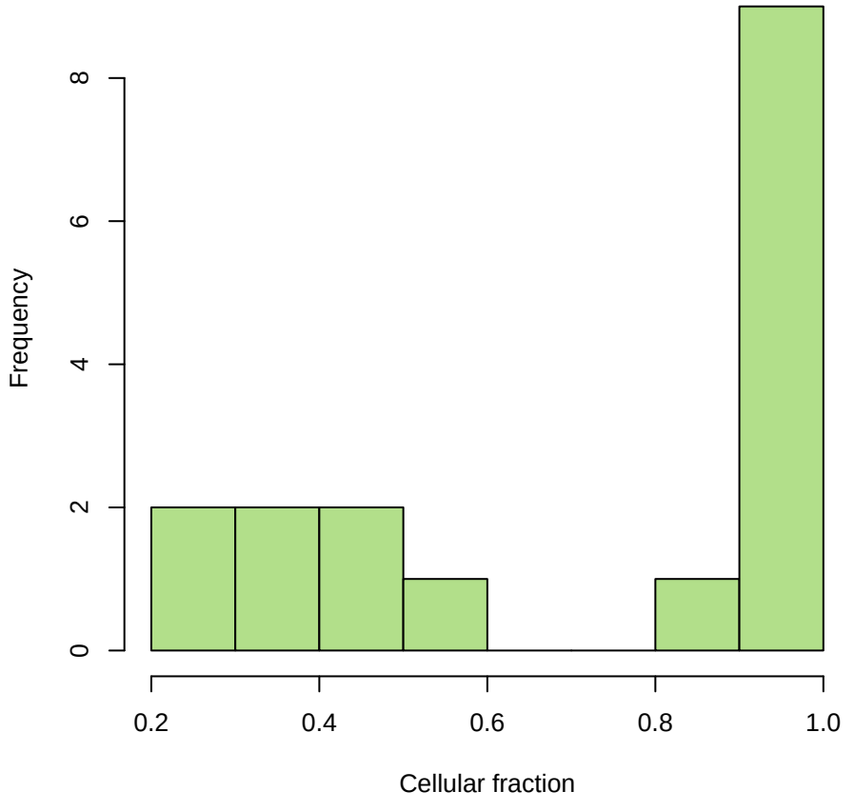

SCNA−fit log−likelihood: −13086.94
Copy Number log−ratio
−2 −1 0 1 2
0 1 2 4 6
0 50 100 150
SNV Index

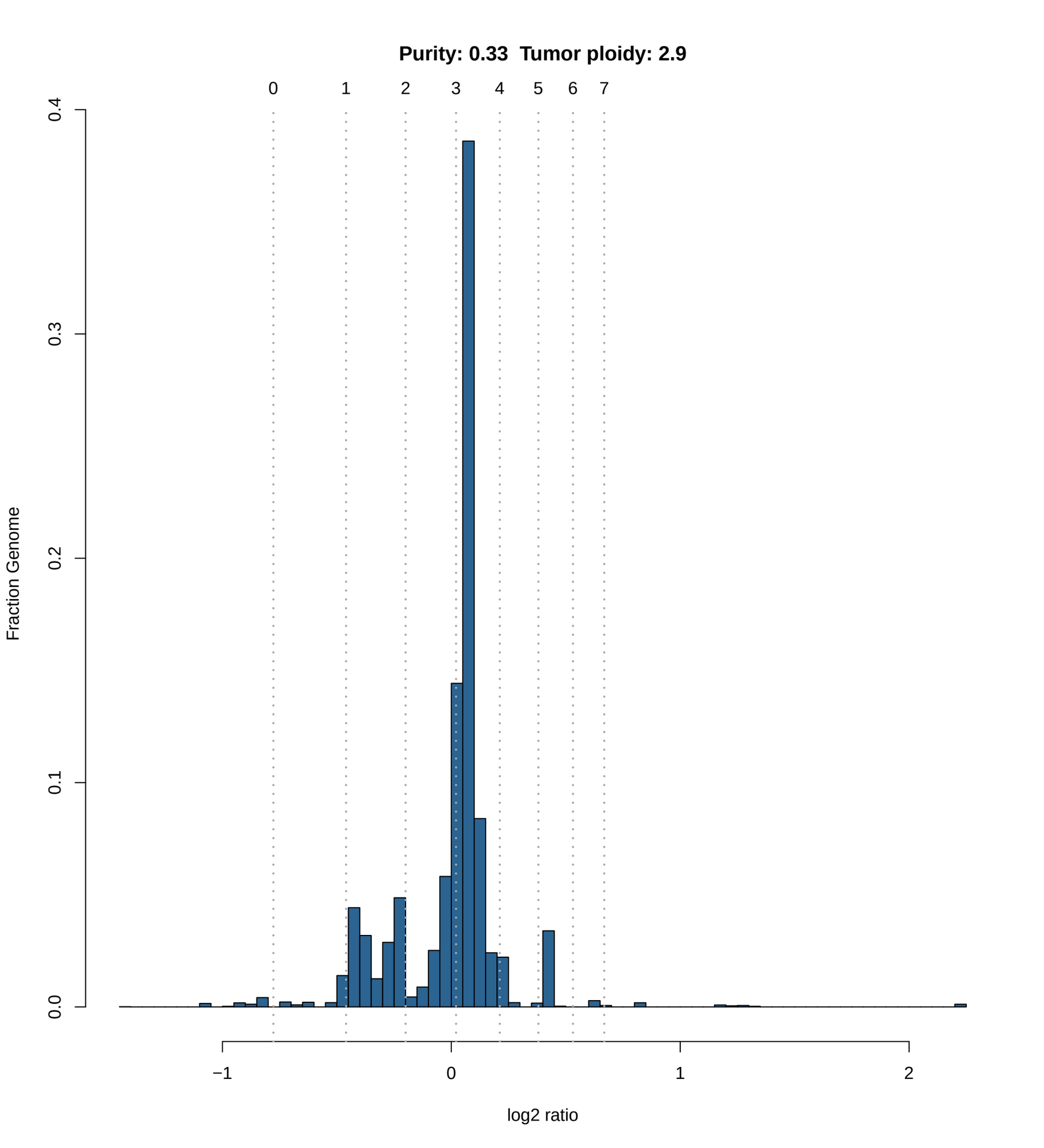

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

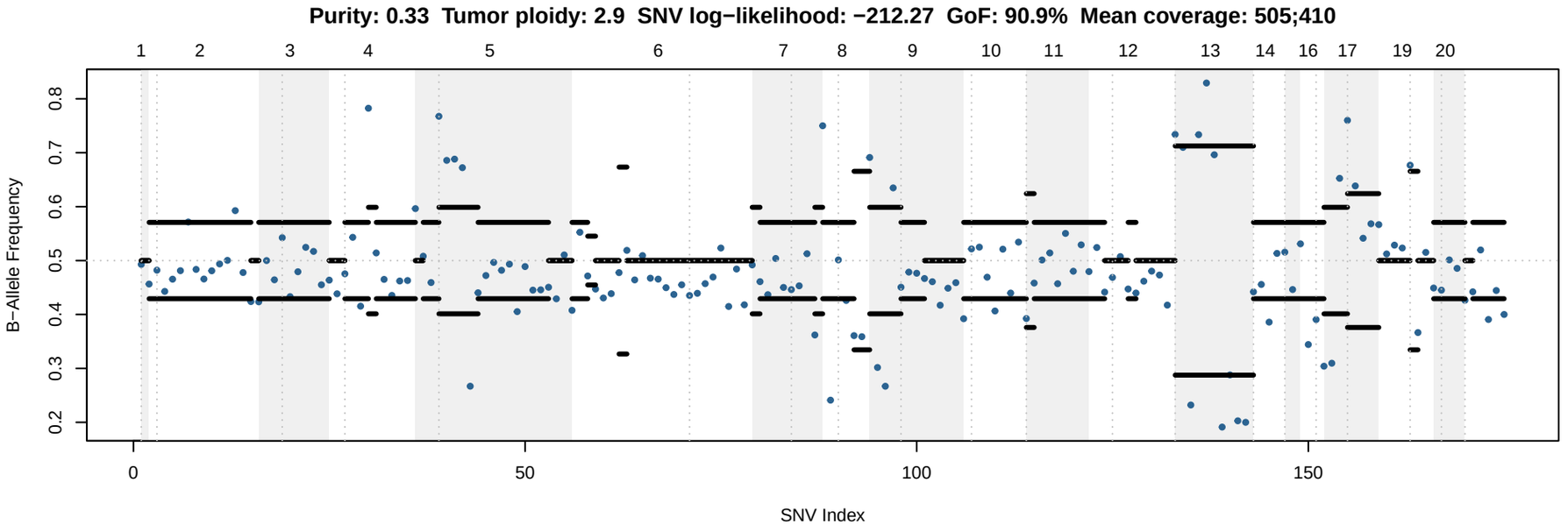

Allelic fraction (germline)
Copy Number log−ratio
4m4
3m3
7m6
1m1
6m4
3m2
5m3
4m2
6m3
5m2
3m1
6m2
1m0
4m1
7m2
3m0
4m0

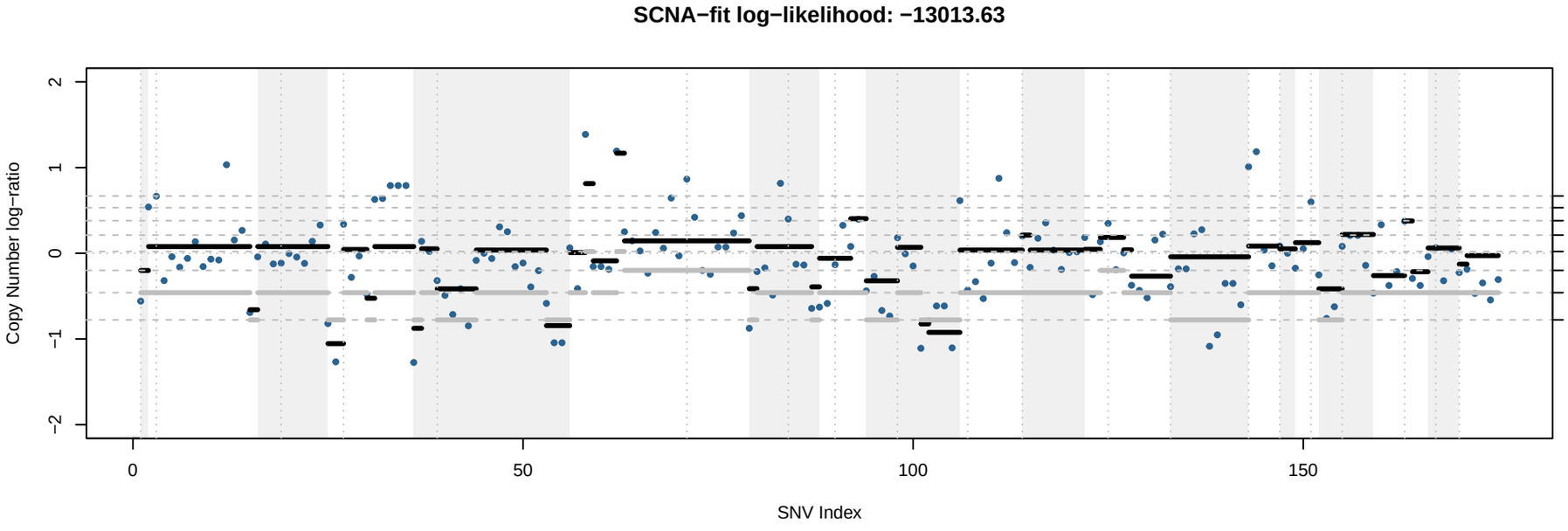

Coverage (log2)
Allelic fraction

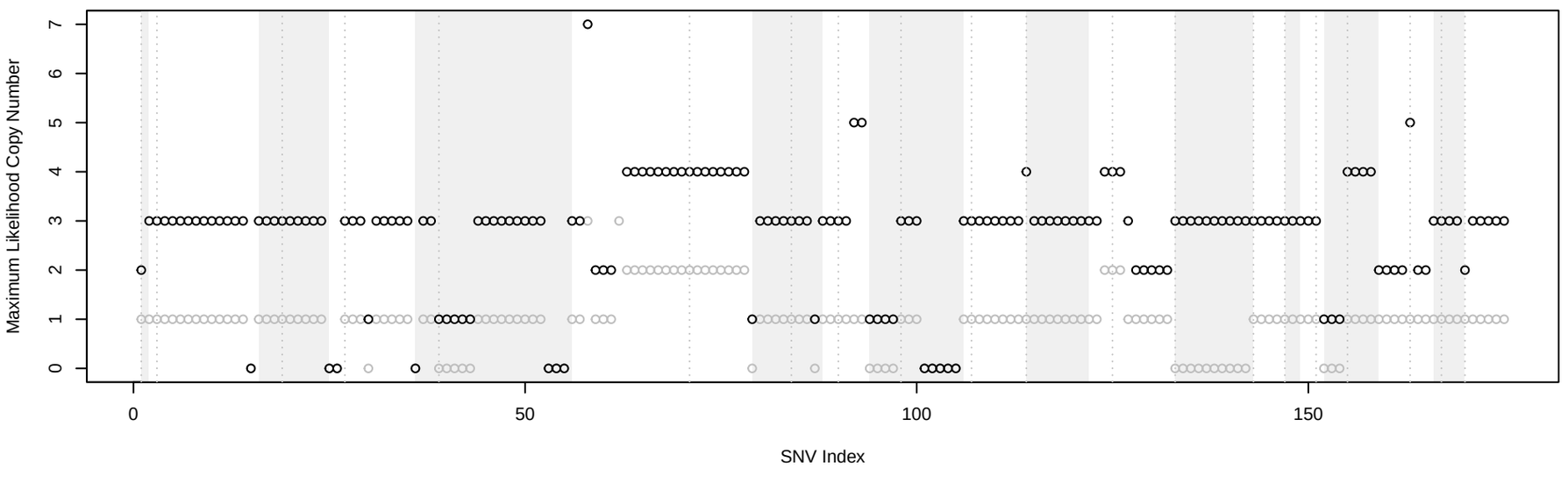

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m2
5m3
3m2
4m2
3m1
4m1
5m1
7m1


Frequency
Cellular fraction

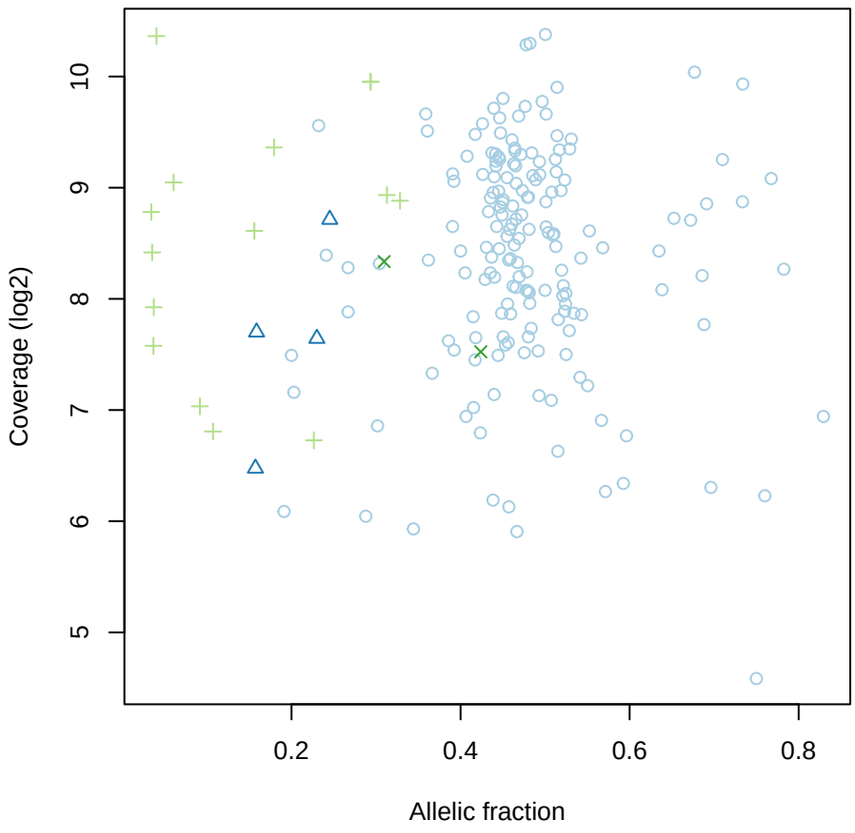

Purity: 0.33 Tumor ploidy: 2.9
0
1
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1
0
1
2
log2 ratio

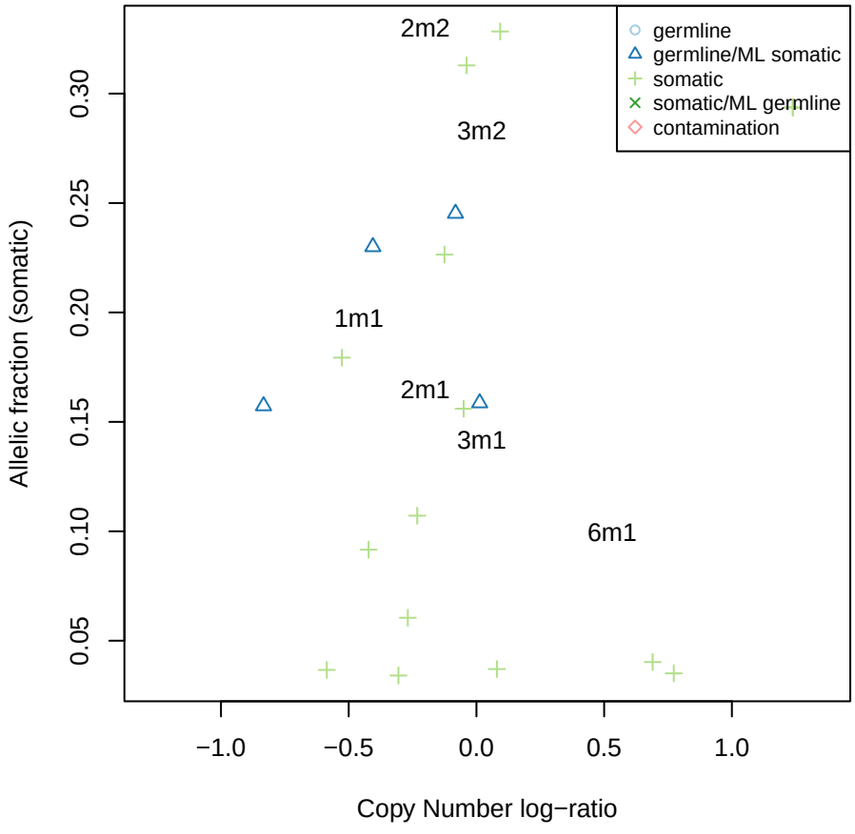

Purity: 0.33 Tumor ploidy: 2.9 SNV log−likelihood: −212.27 GoF: 90.9% Mean coverage: 505;410
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

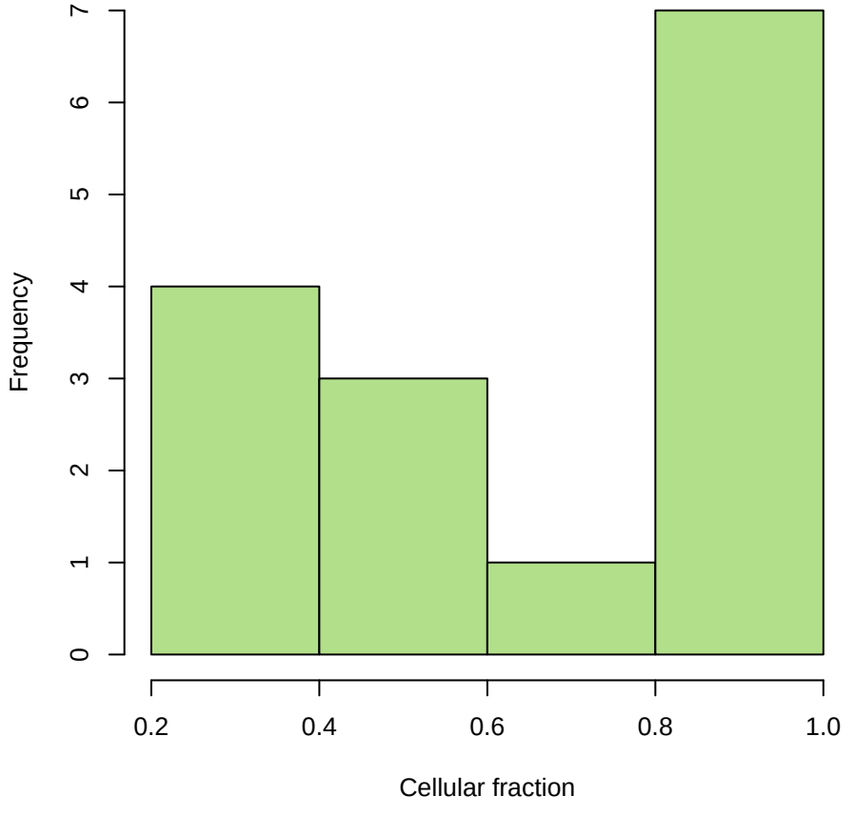

SCNA−fit log−likelihood: −13013.63
Copy Number log−ratio
−2 −1 0 1 2
0 1 3 5 7
0 50 100 150
SNV Index

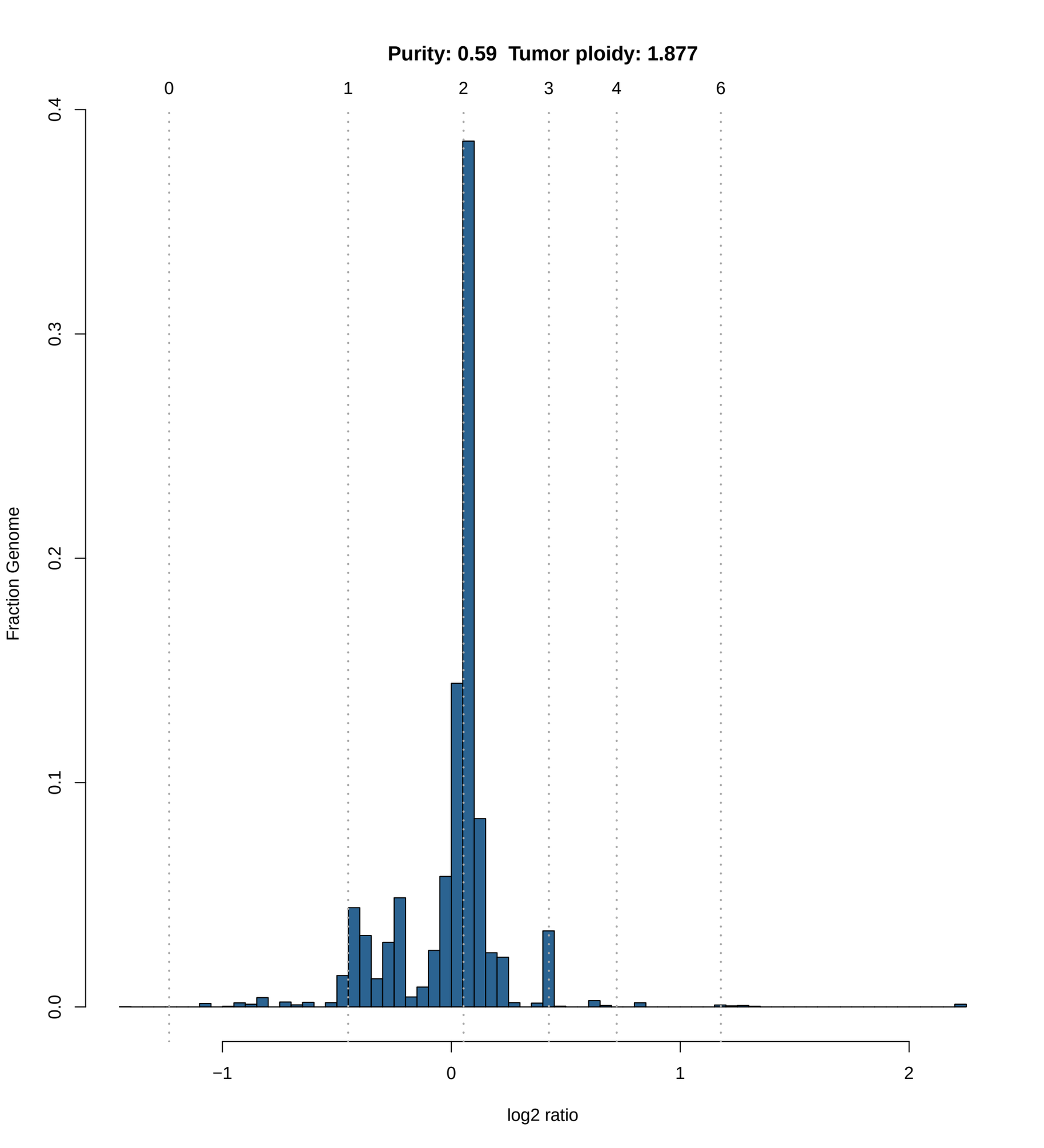

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

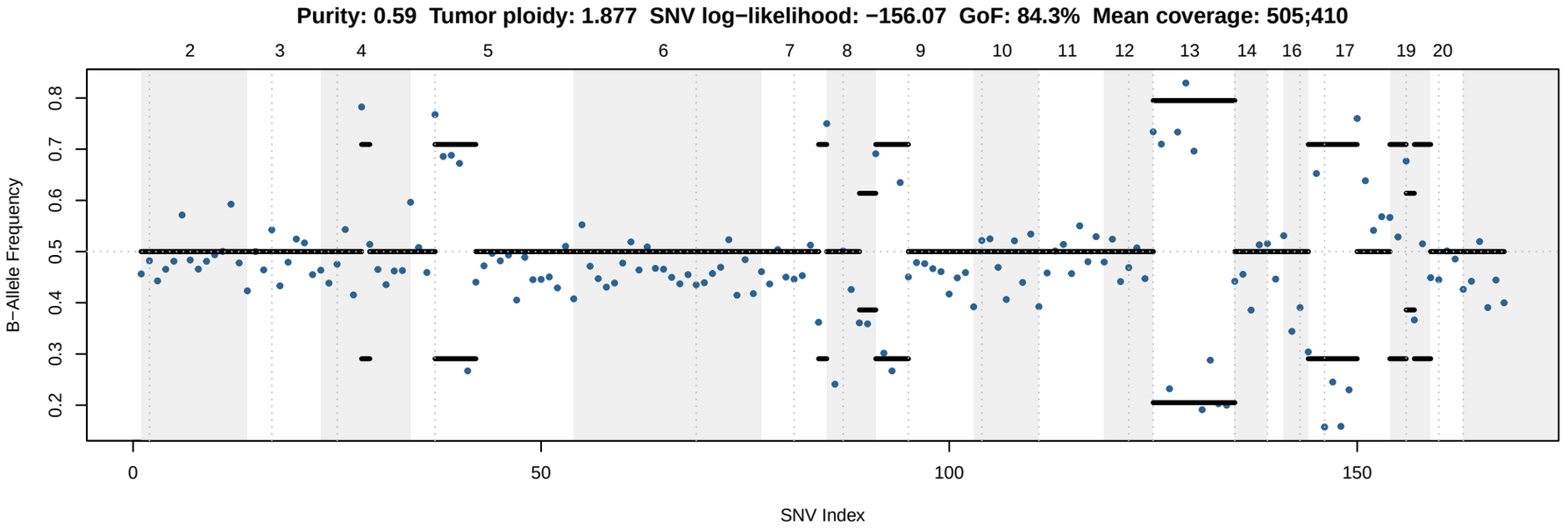
1m2
3m3
5m4
4m3
1m1
3m2
0m0
2m1
4m2
7m3
3m1
1m0
4m1
5m1
3m0
Allelic fraction (germline)
Copy Number log−ratio

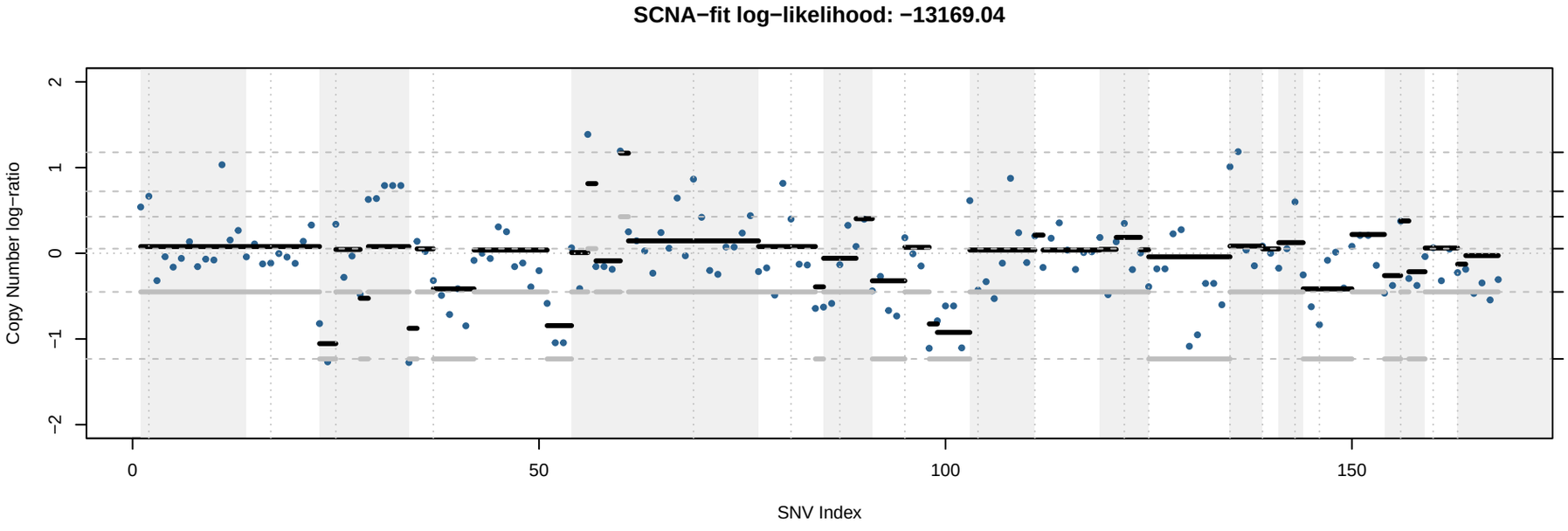

Coverage (log2)
Allelic fraction

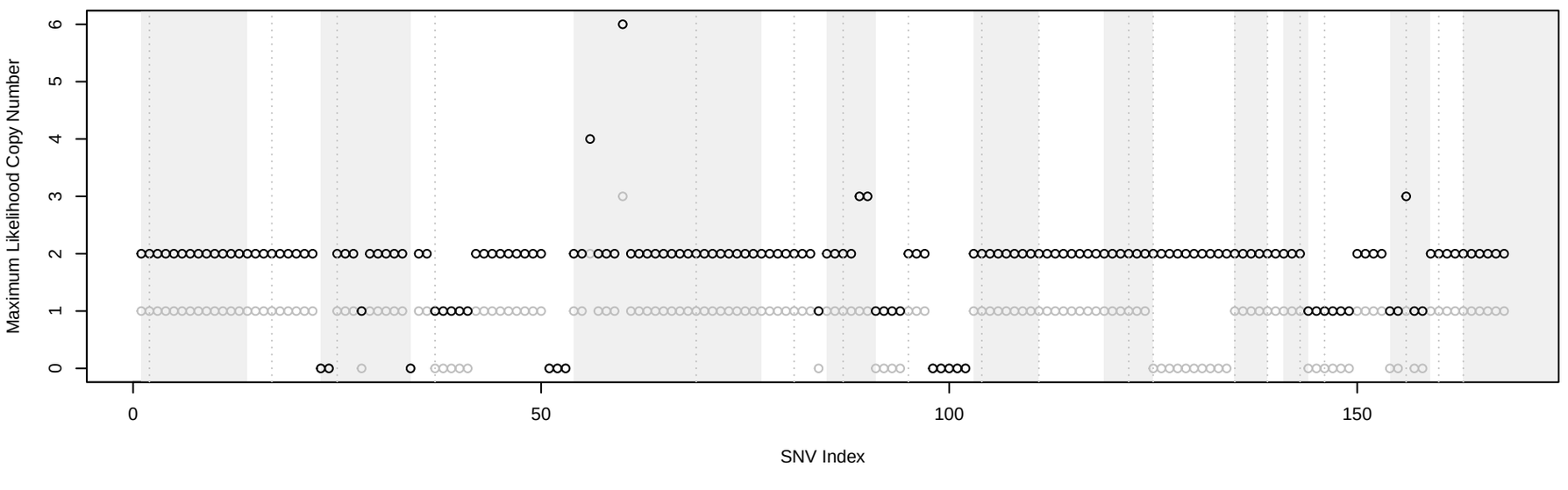

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
3m2
1m1
2m1
3m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio

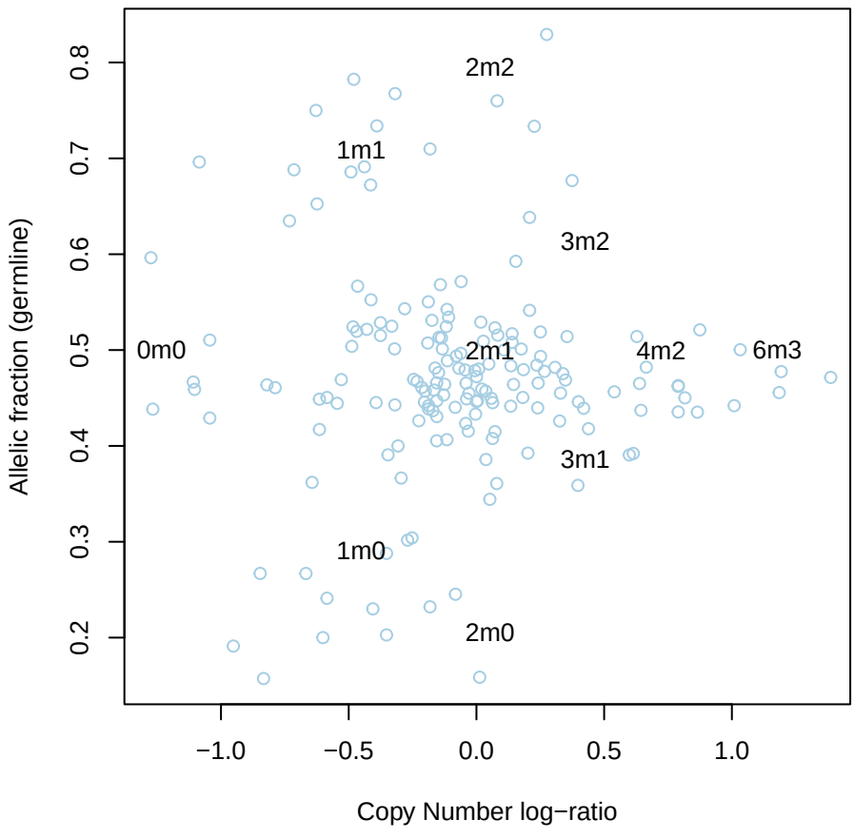

Frequency
Cellular fraction

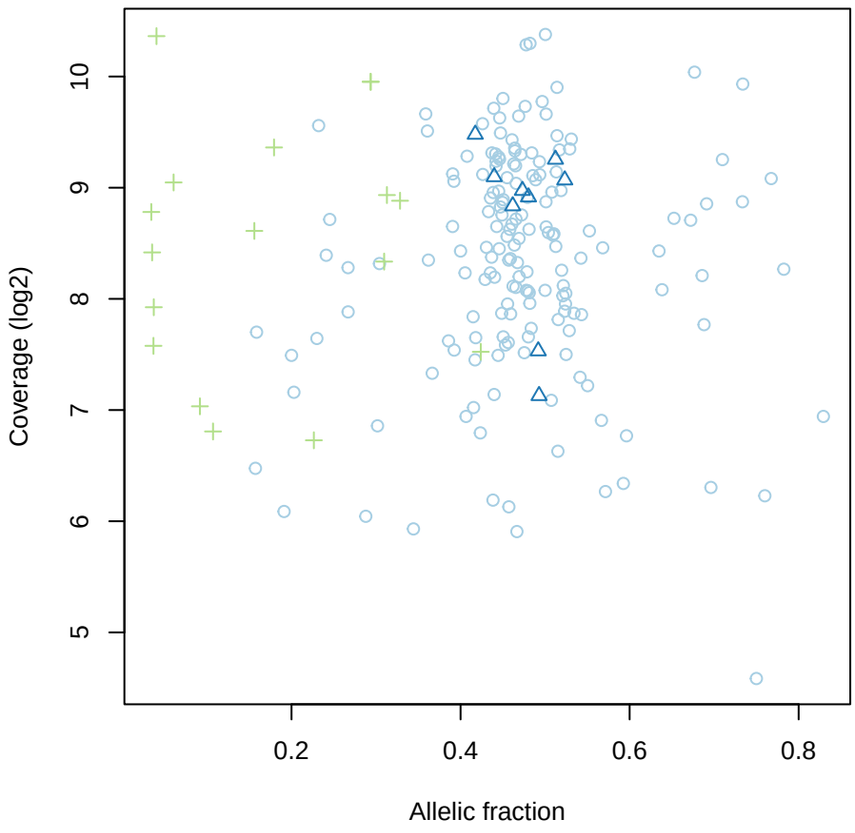

Purity: 0.59 Tumor ploidy: 1.877
0
1
2
3
4
6
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1
0
1
2
log2 ratio

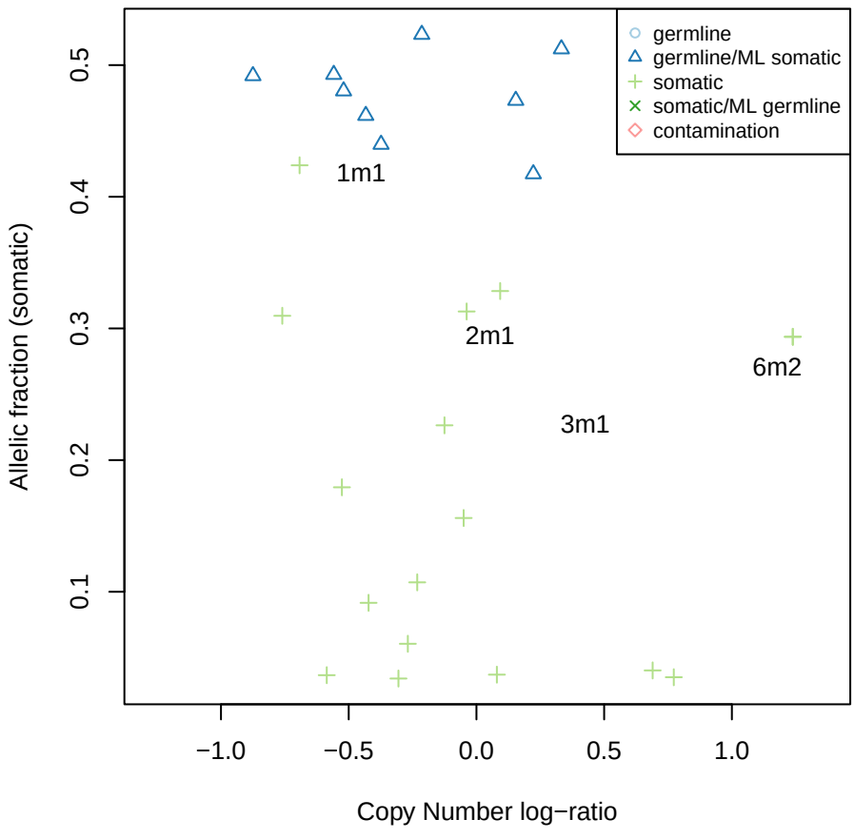

Purity: 0.59 Tumor ploidy: 1.877 SNV log−likelihood: −156.07 GoF: 84.3% Mean coverage: 505;410
2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

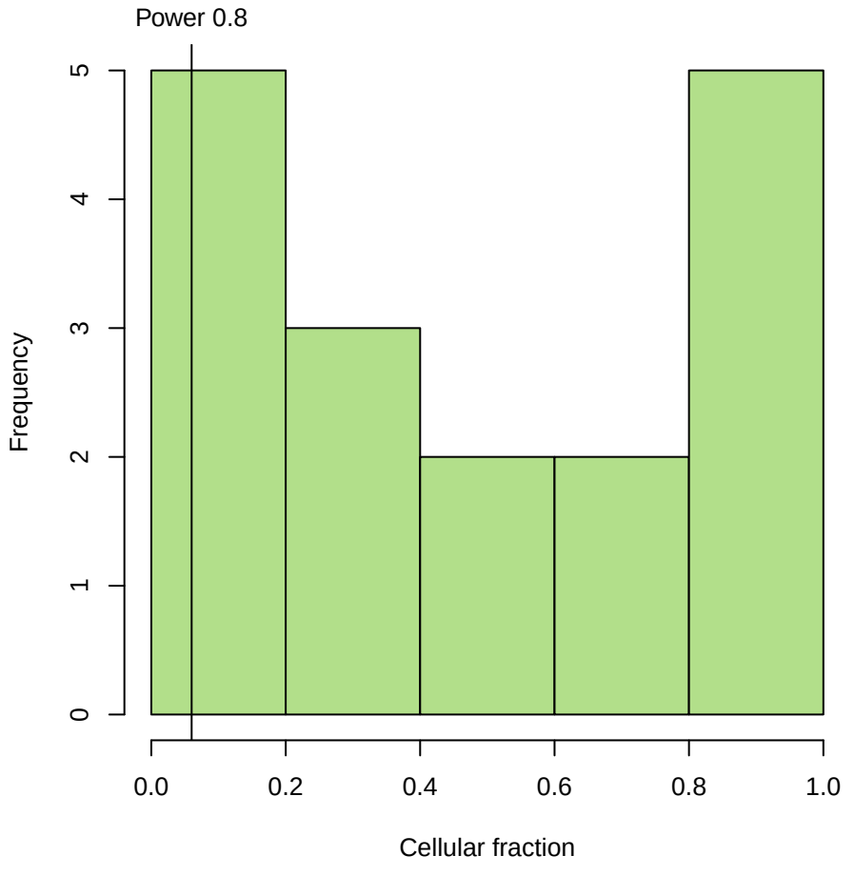

SCNA−fit log−likelihood: −13169.04
Copy Number log−ratio
−2 −1 0 1 2
0 1 2 3 4 6
0 50 100 150
SNV Index

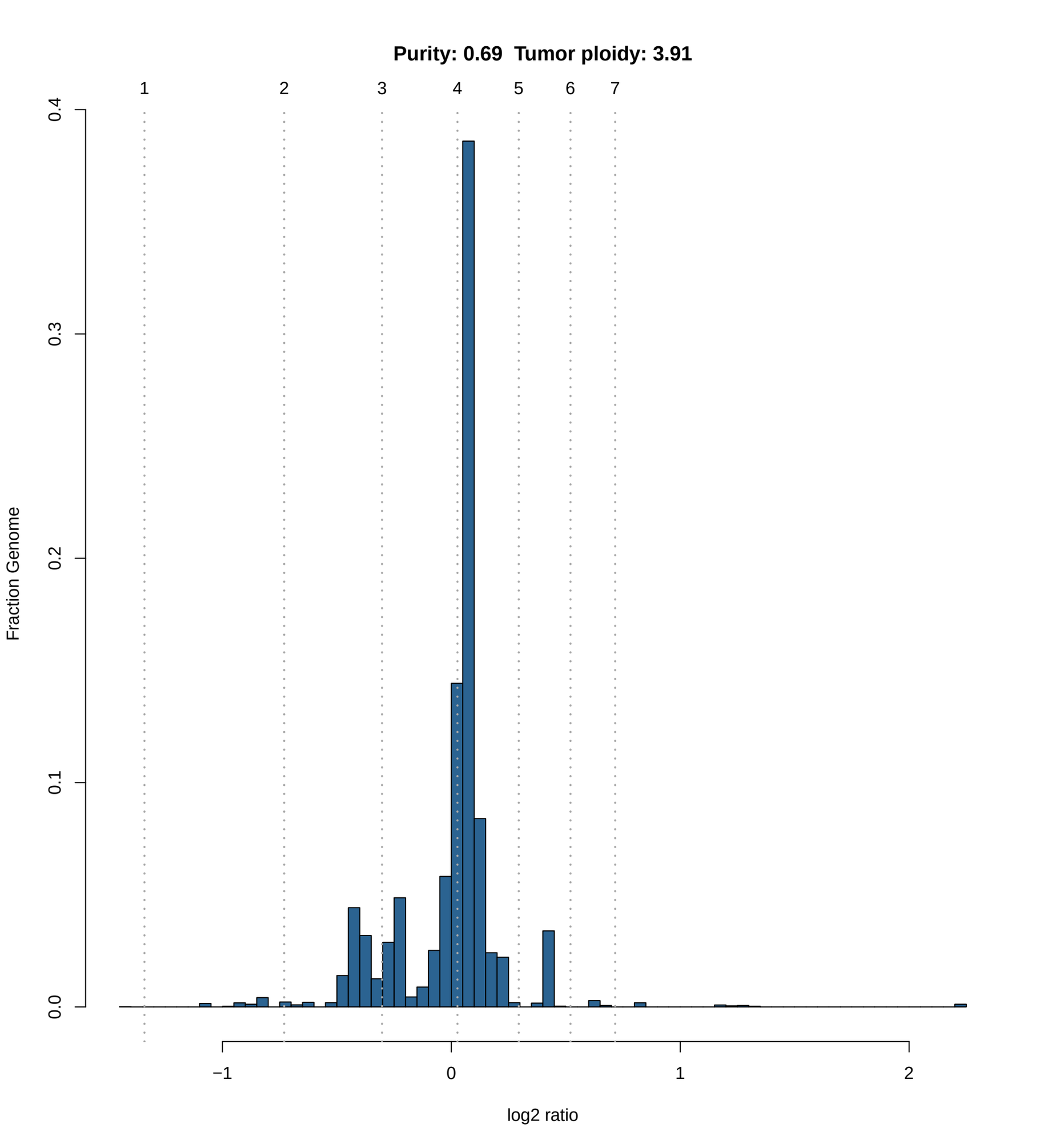

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

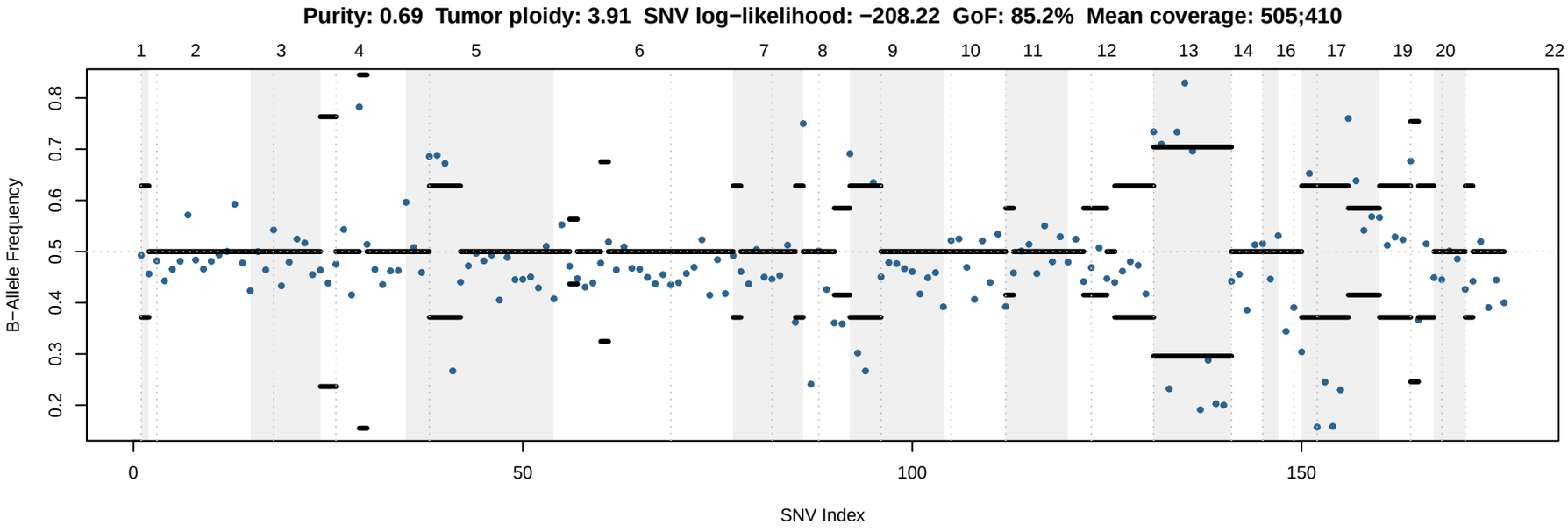

Allelic fraction (germline)
Copy Number log−ratio
0m0
1m0
1m1
2m0
2m1
2m2
3m1
3m2
4m2
6m3

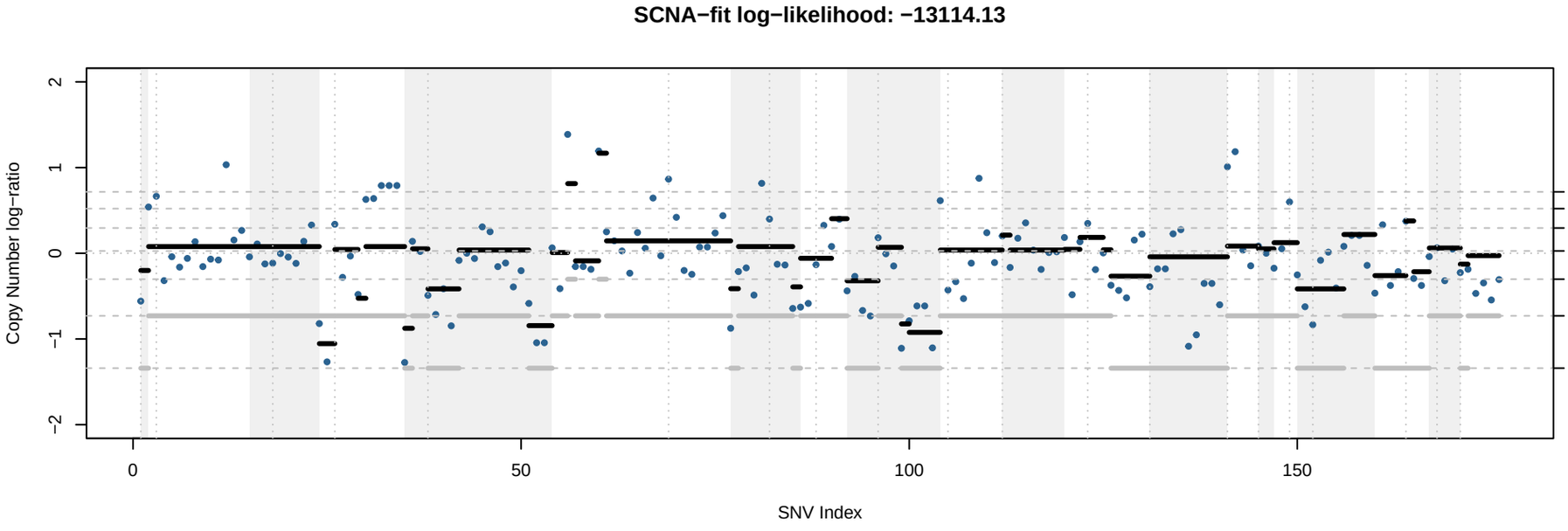

Coverage (log2)
Allelic fraction

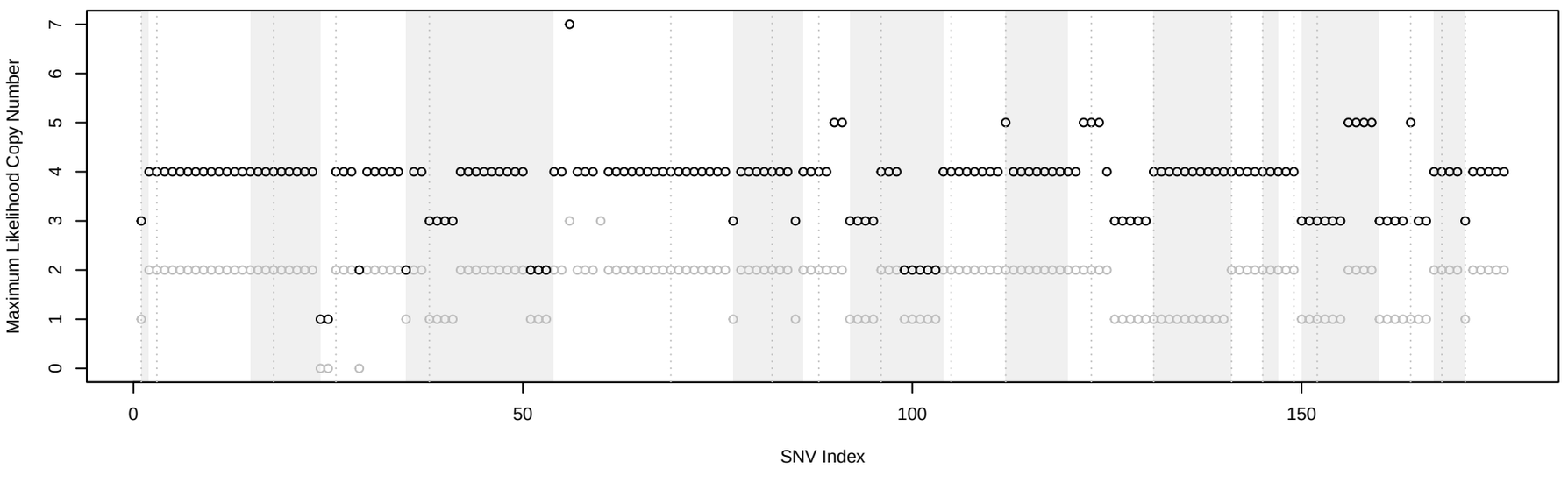

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
6m2

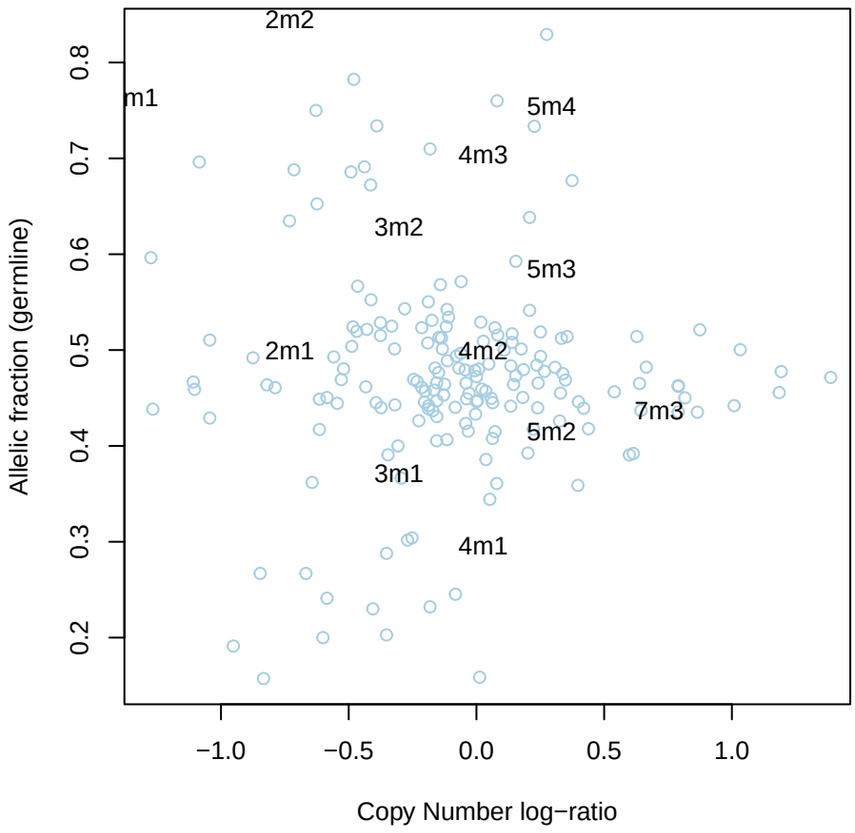

Power 0.8
Frequency
Cellular fraction

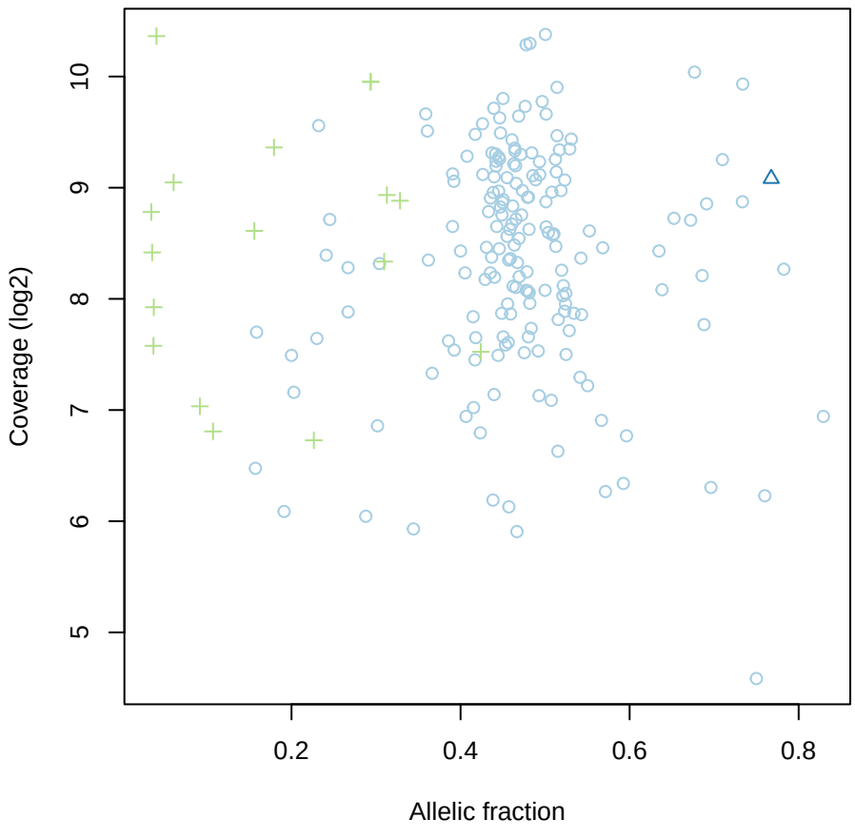

Purity: 0.69 Tumor ploidy: 3.91
1
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1
0
1
2
log2 ratio

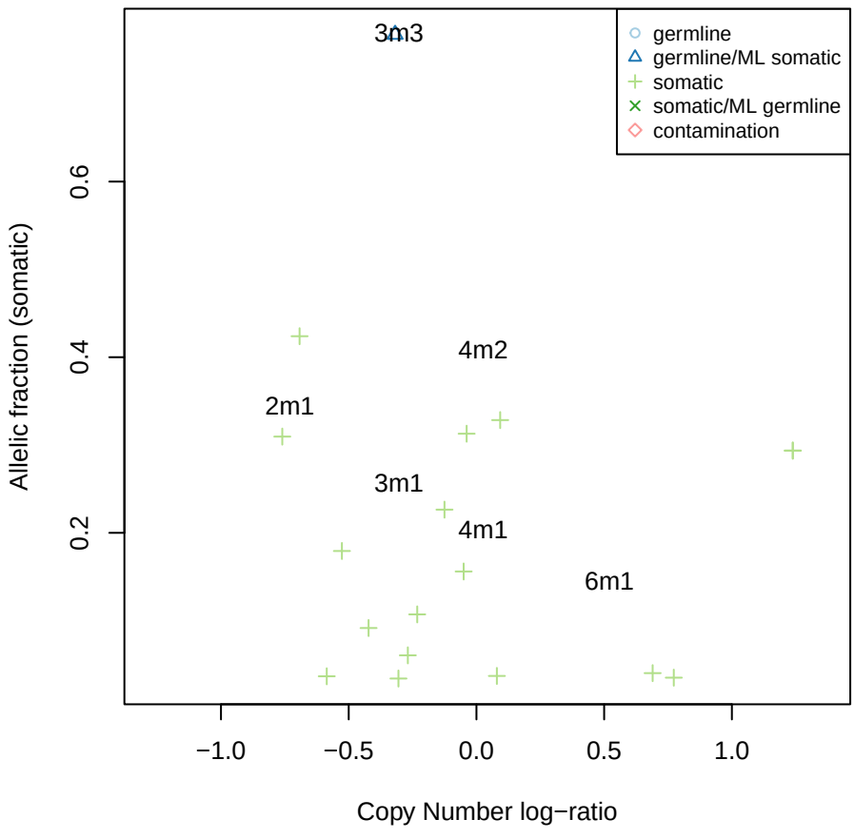

Purity: 0.69 Tumor ploidy: 3.91 SNV log−likelihood: −208.22 GoF: 85.2% Mean coverage: 505;410
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 19 20 22
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

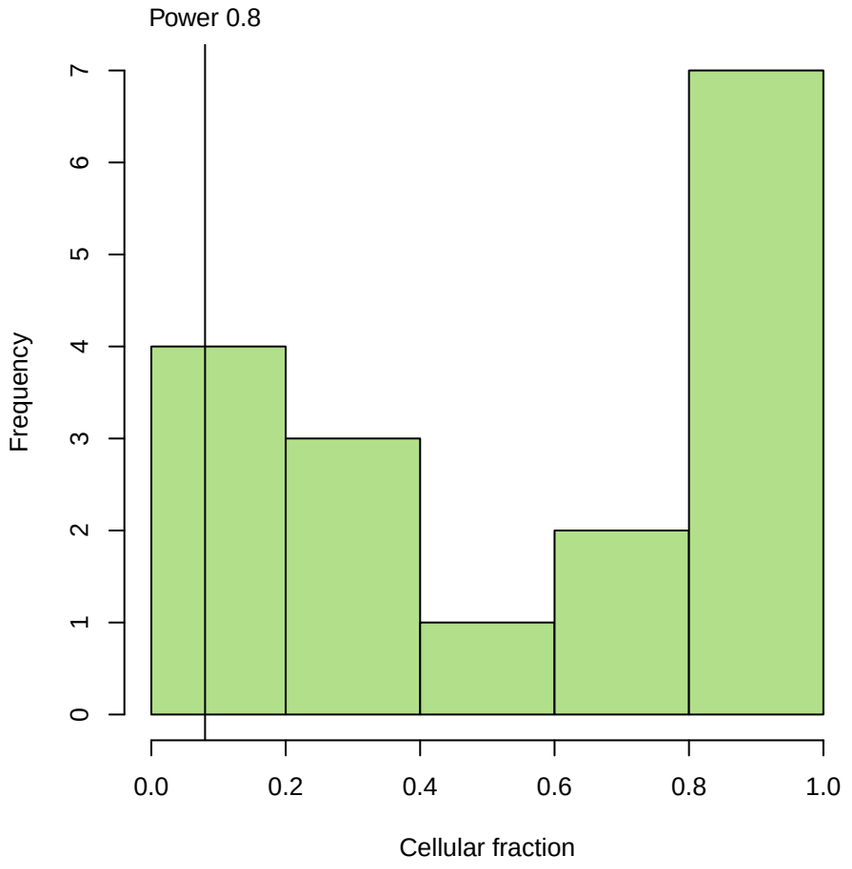

SCNA−fit log−likelihood: −13114.13
Copy Number log−ratio
−2 −1 0 1 2
1 2 3 4 5 6
0 50 100 150
SNV Index

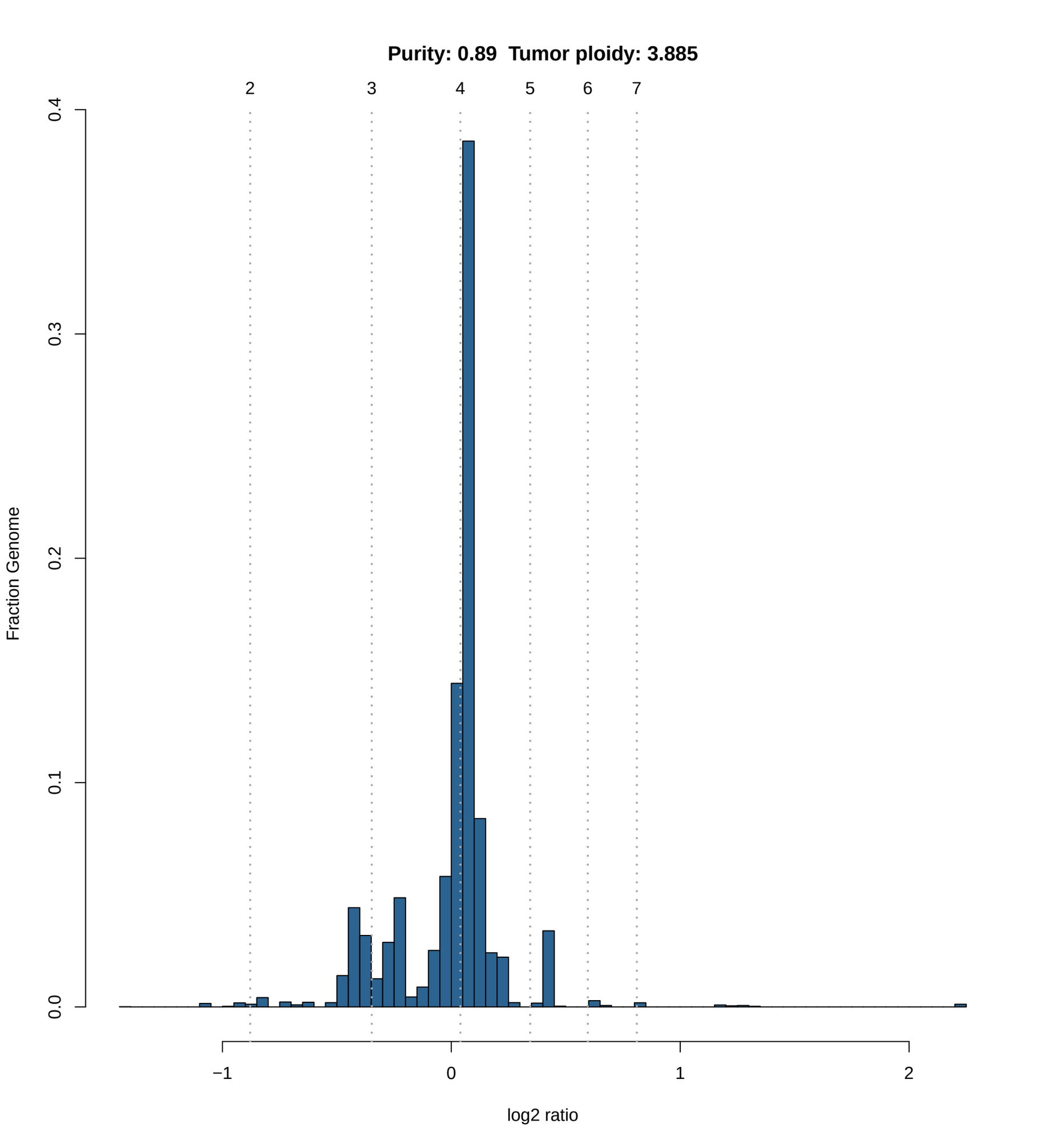

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

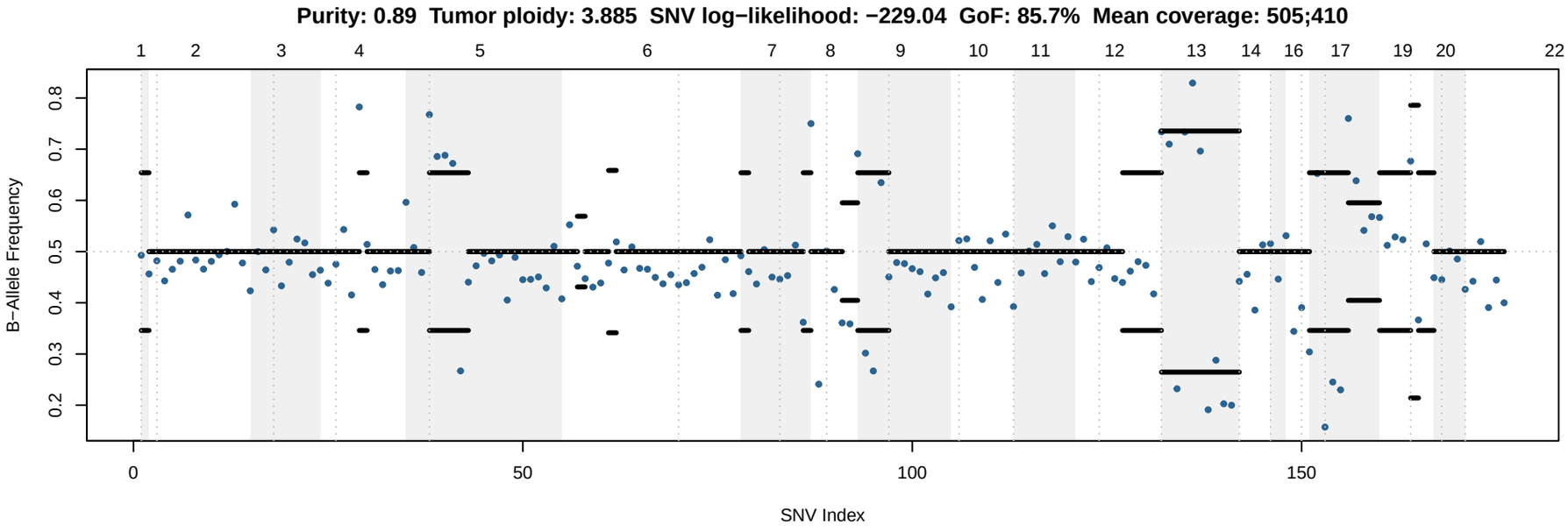

2m2
m1
5m4
4m3
3m2
5m3
2m1
4m2
7m3
5m2
3m1
4m1
Allelic fraction (germline)
Copy Number log−ratio

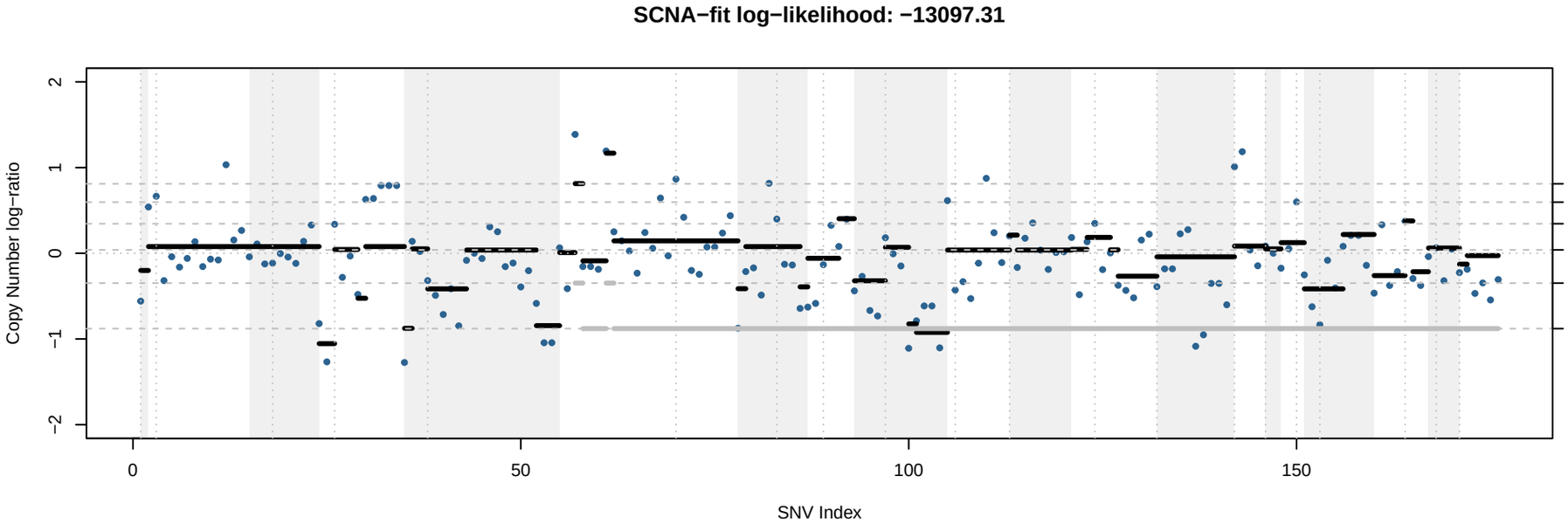

Coverage (log2)
Allelic fraction

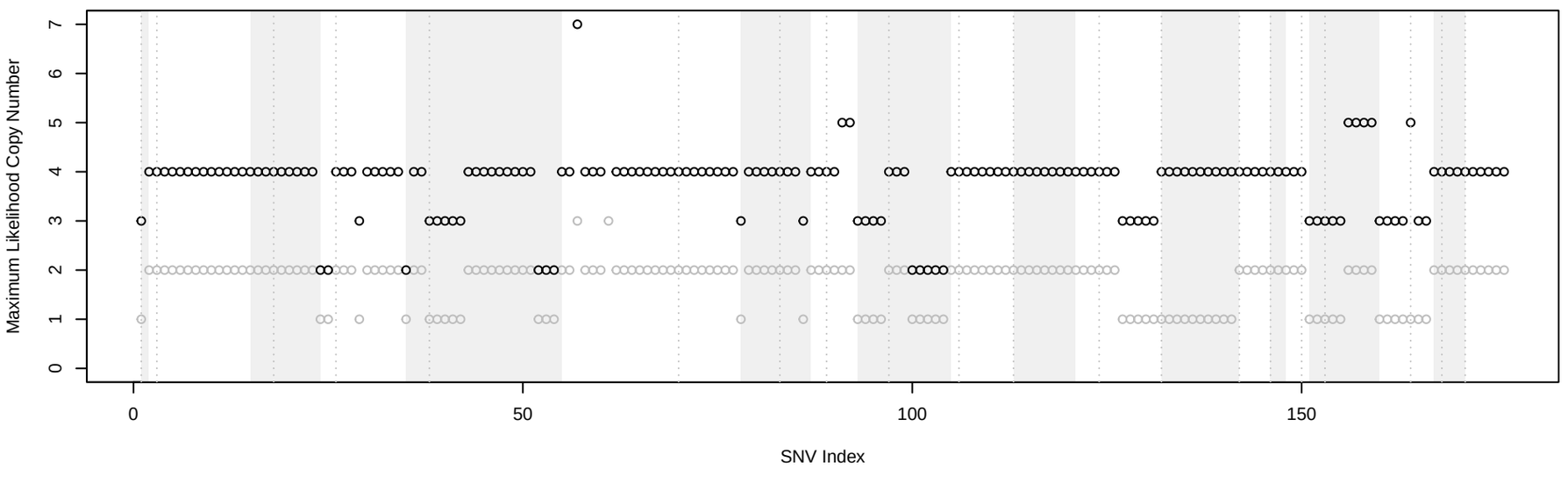

3m3
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m2
2m1
3m1
4m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio


Power 0.8
Frequency
Cellular fraction

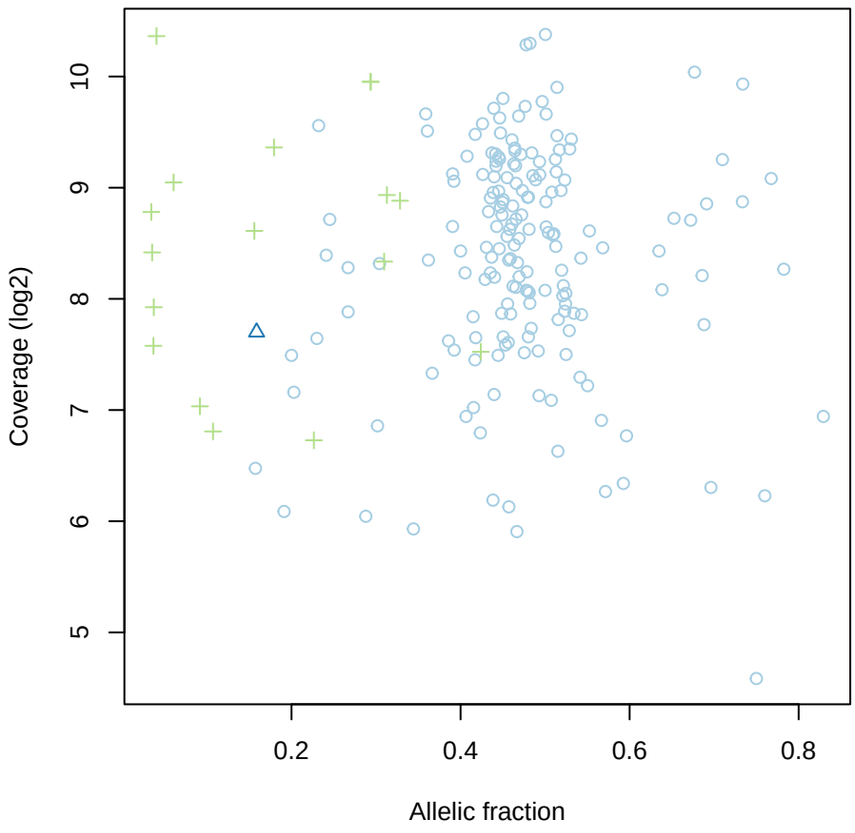

Purity: 0.89 Tumor ploidy: 3.885
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1
0
1
2
log2 ratio

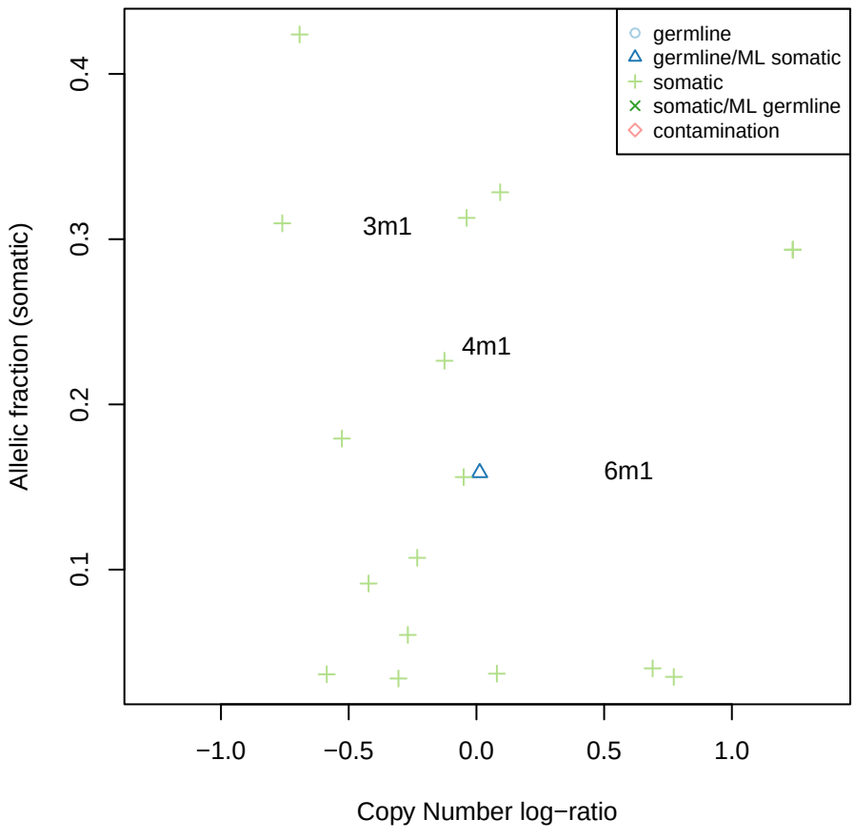

Purity: 0.89 Tumor ploidy: 3.885 SNV log−likelihood: −229.04 GoF: 85.7% Mean coverage: 505;410
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 19 20 22
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

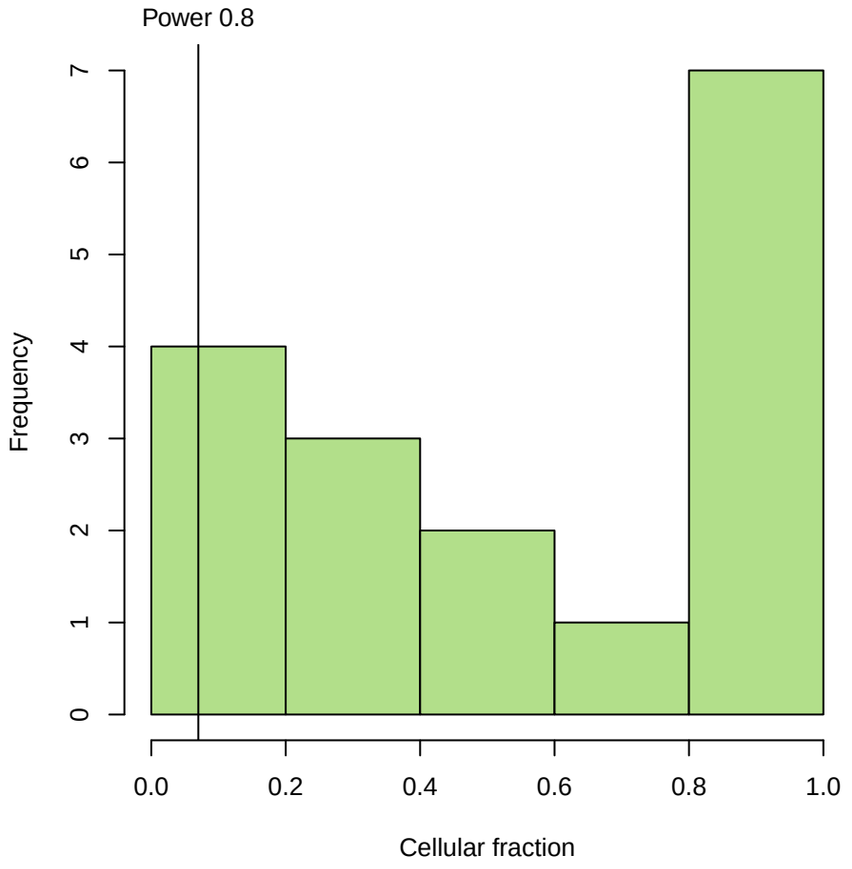

SCNA−fit log−likelihood: −13097.31
Copy Number log−ratio
−2 −1 0 1 2
2 3 4 5 7
0 50 100 150
SNV Index

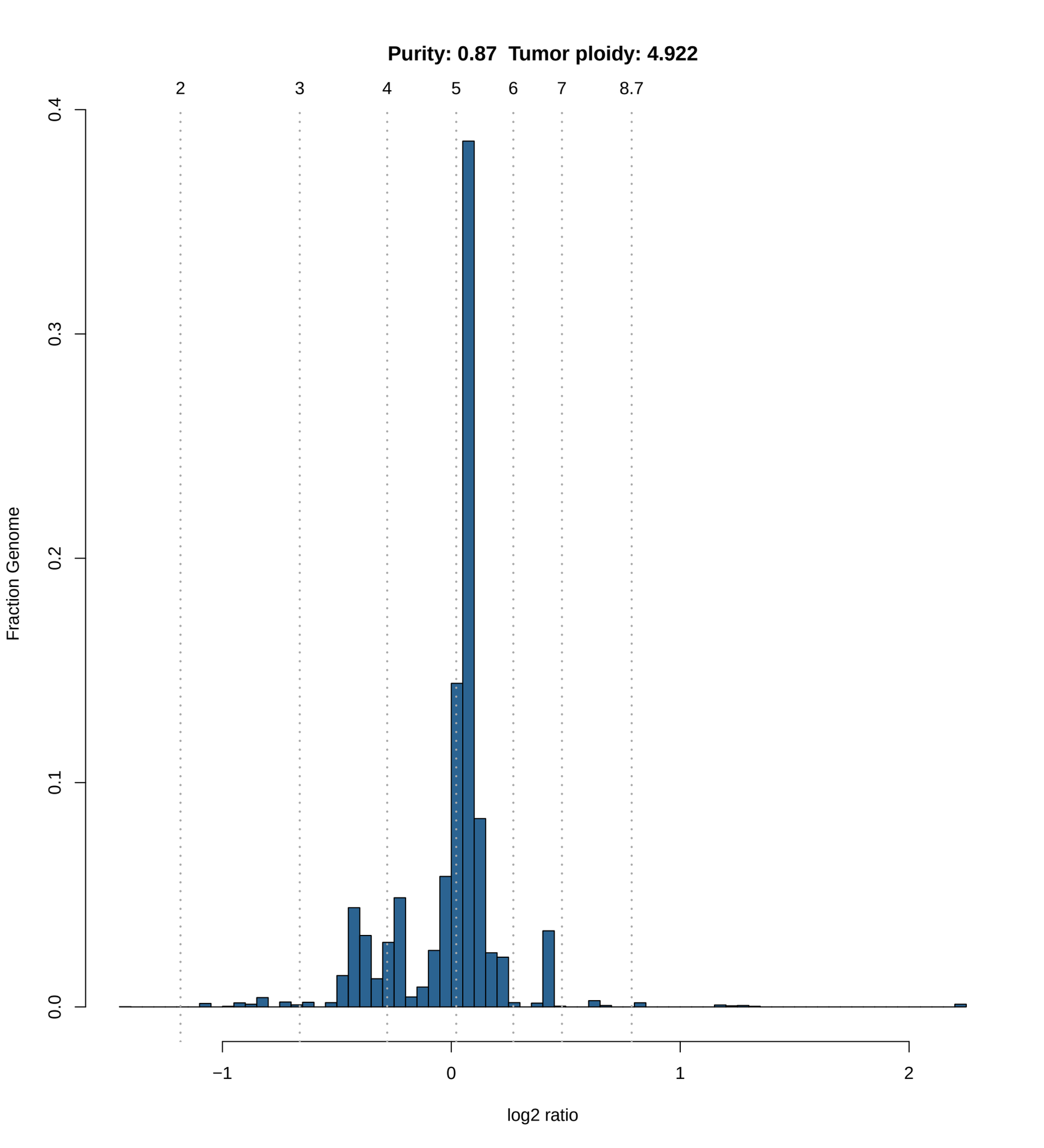

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

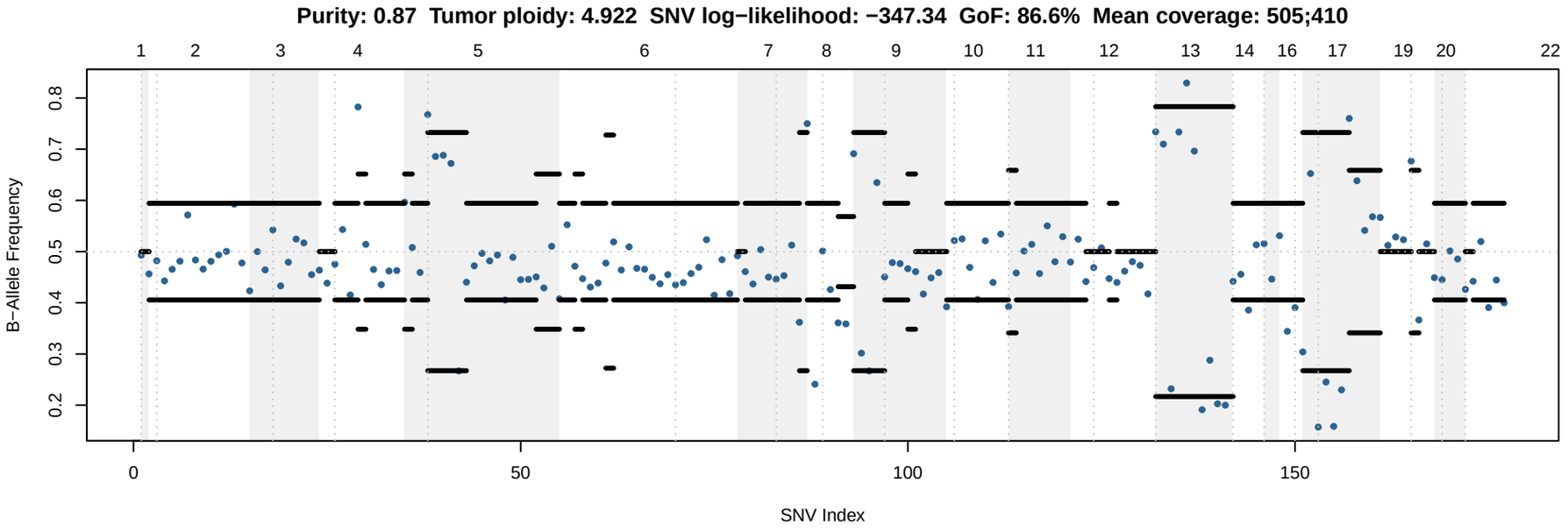
Allelic fraction (germline)
Copy Number log−ratio
5m4
4m3
3m2
5m3
2m1
4m2
7m3
5m2
3m1
4m1

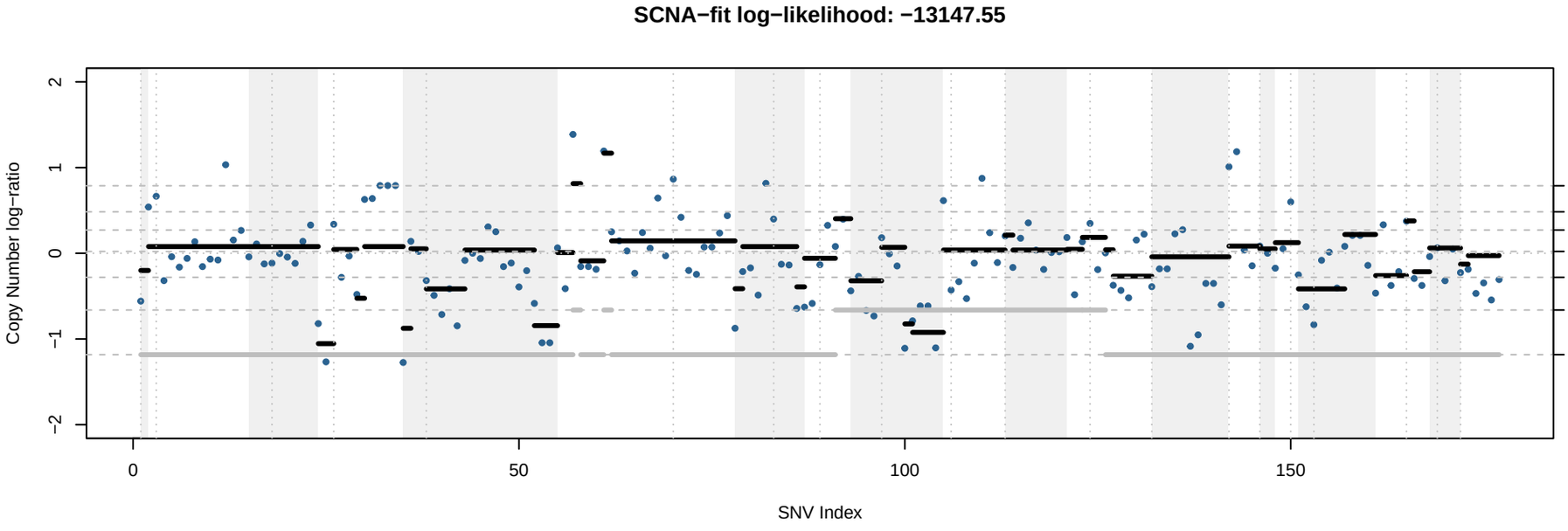

Coverage (log2)
Allelic fraction

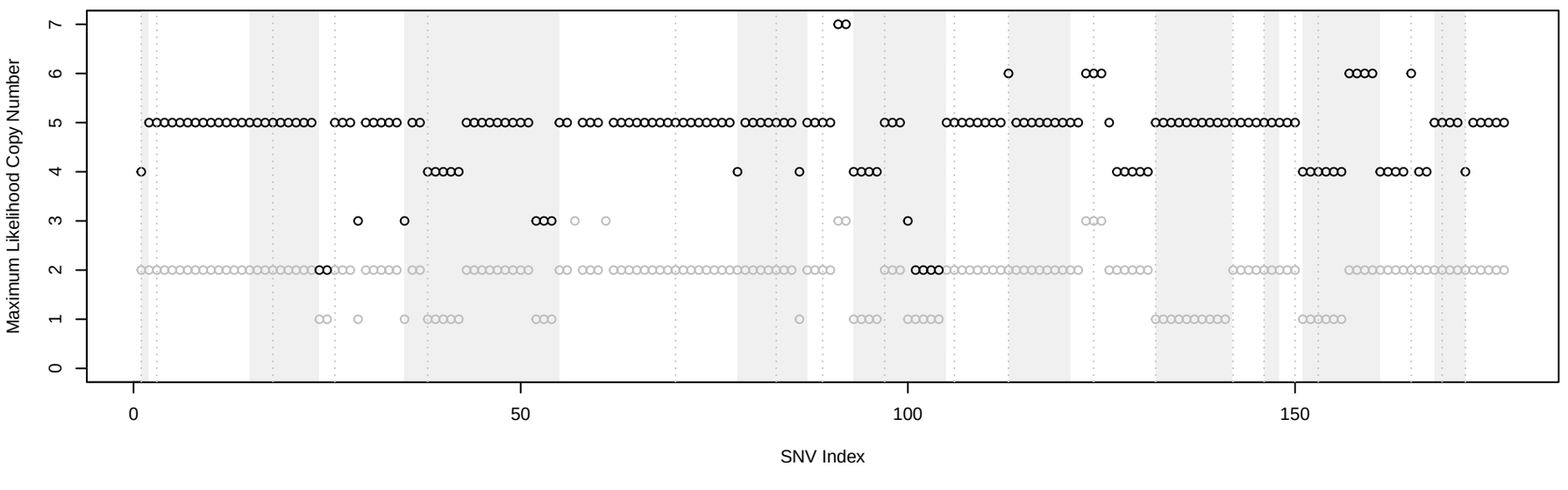

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m1
4m1
6m1

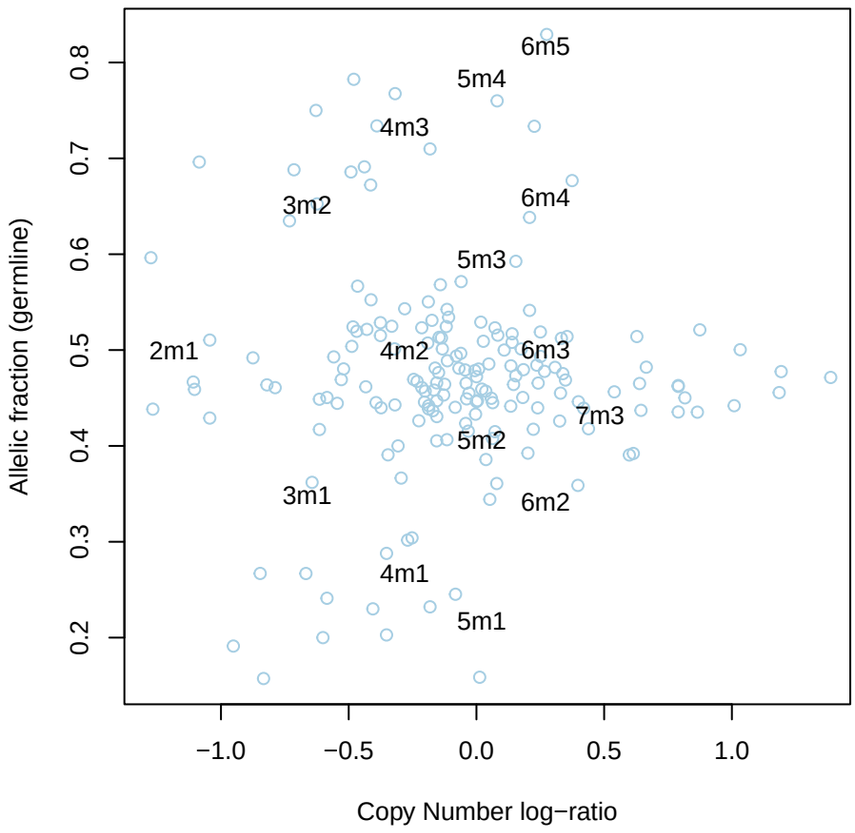

Power 0.8
Frequency
Cellular fraction

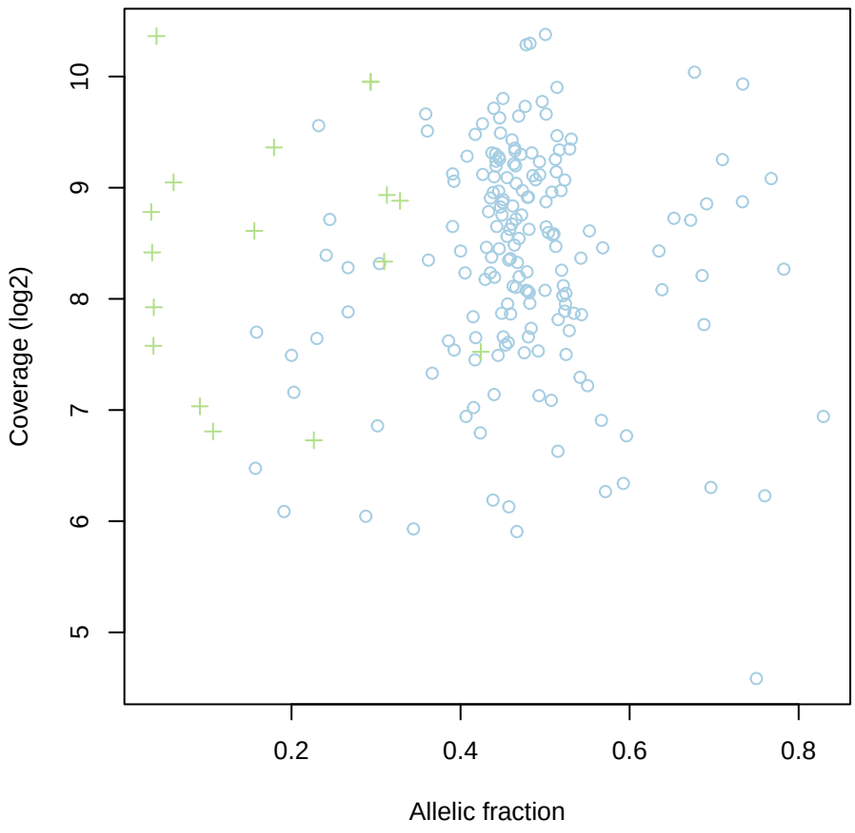

Purity: 0.87 Tumor ploidy: 4.922
2
3
4
5
6
7
8.7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1
0
1
2
log2 ratio

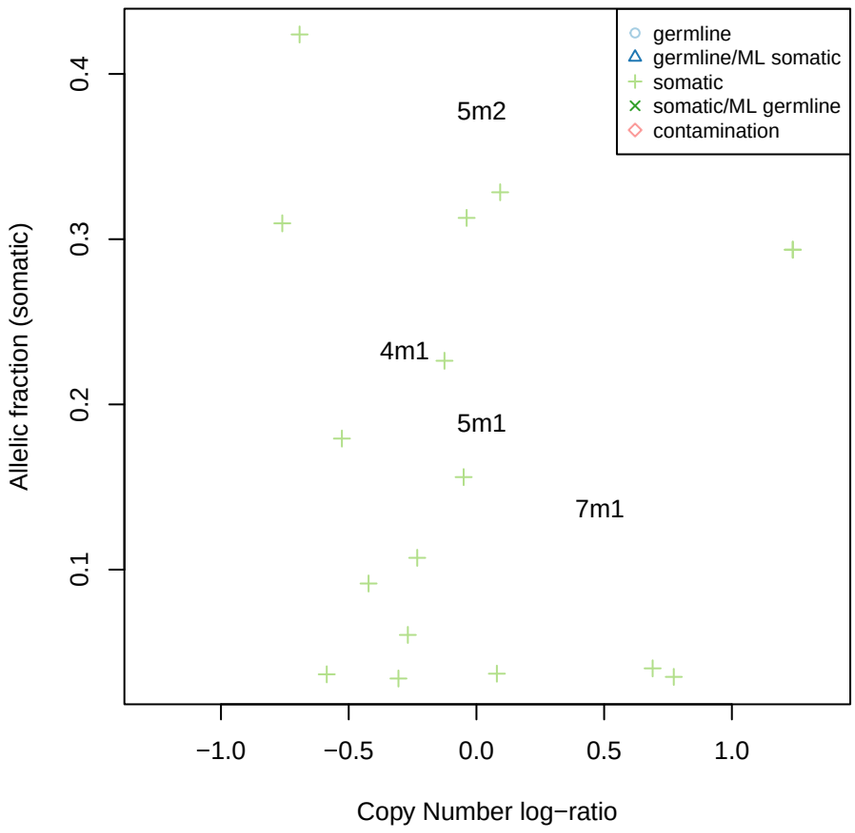

Purity: 0.87 Tumor ploidy: 4.922 SNV log−likelihood: −347.34 GoF: 86.6% Mean coverage: 505;410
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 19 20 22
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

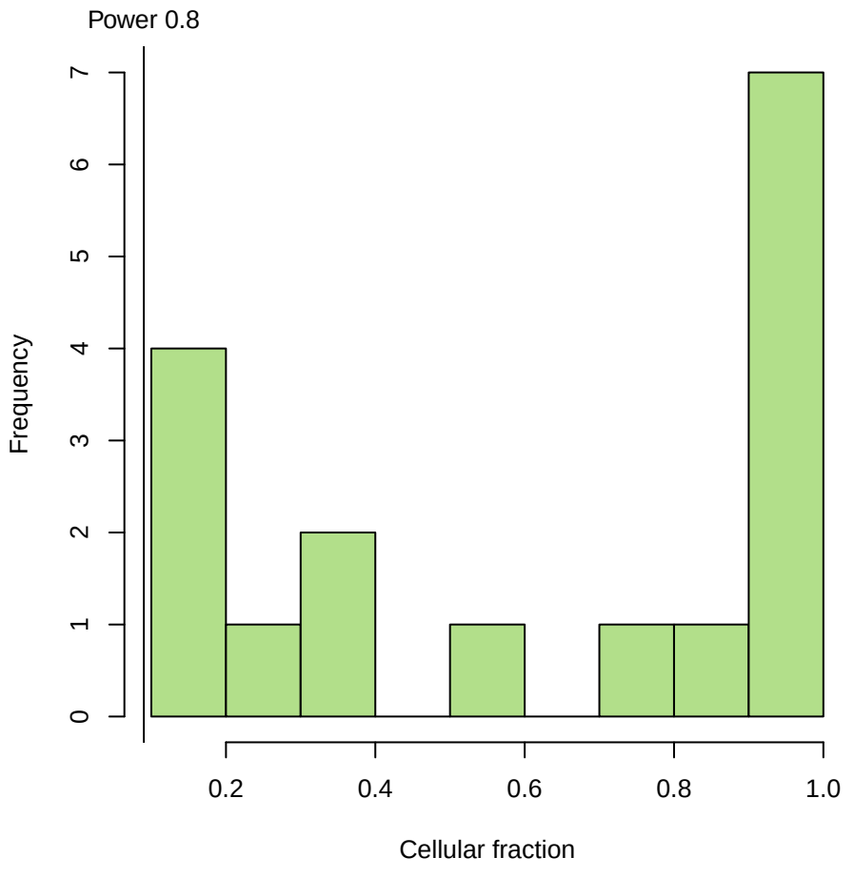

SCNA−fit log−likelihood: −13147.55
Copy Number log−ratio
−2 −1 0 1 2
2 3 4 5 6 7
0 50 100 150
SNV Index

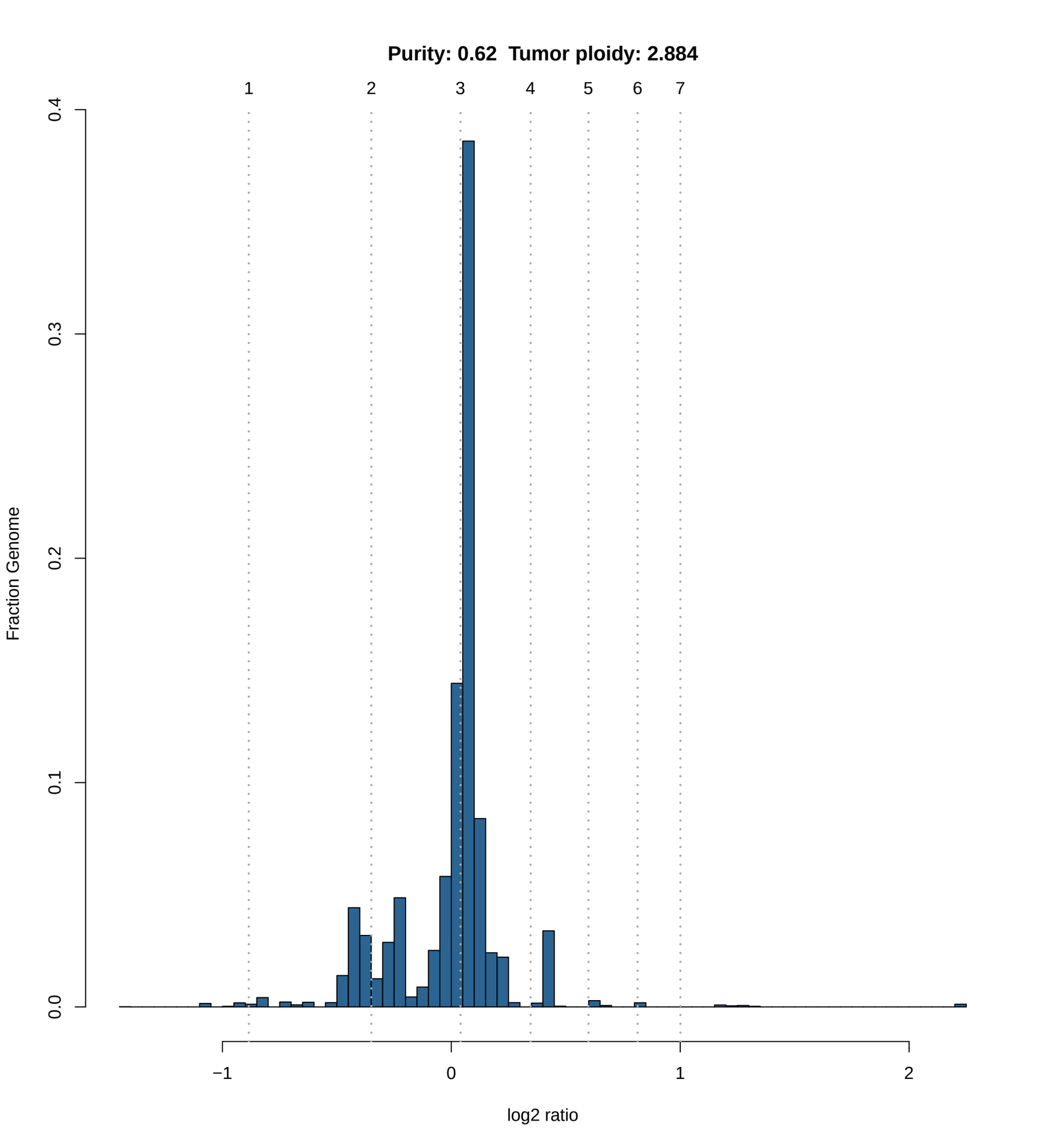

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

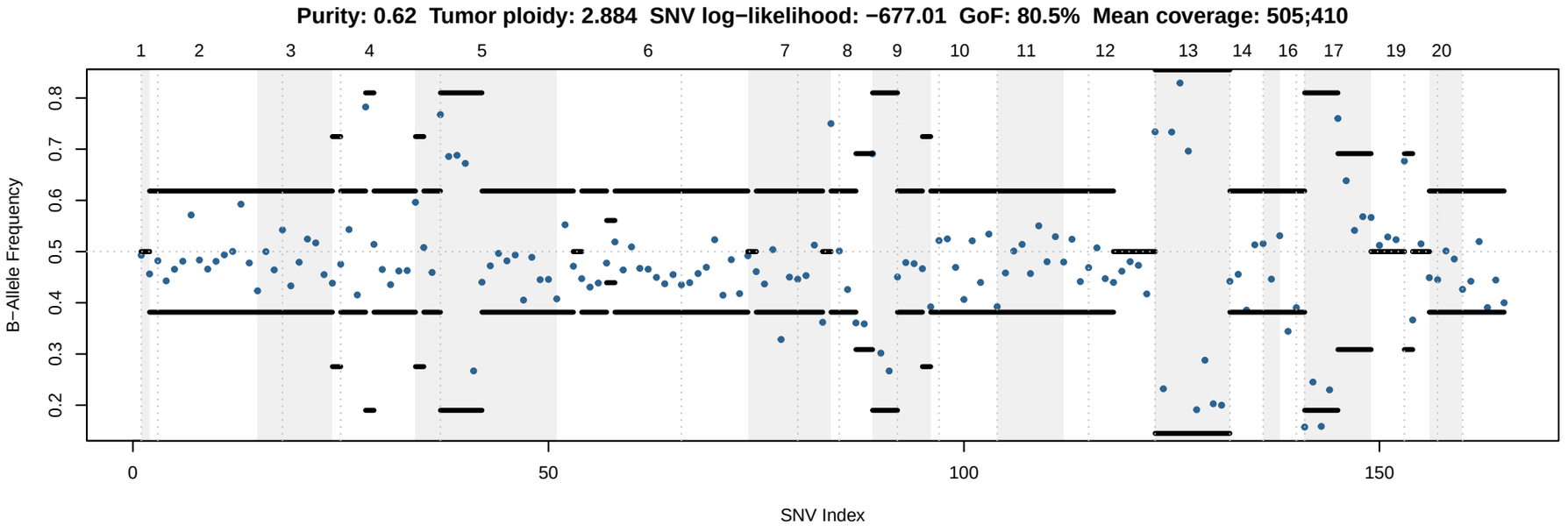

6m5
5m4
4m3
3m2
6m4
5m3
2m1
4m2
6m3
7m3
5m2
3m1
6m2
4m1
5m1
Allelic fraction (germline)
Copy Number log−ratio

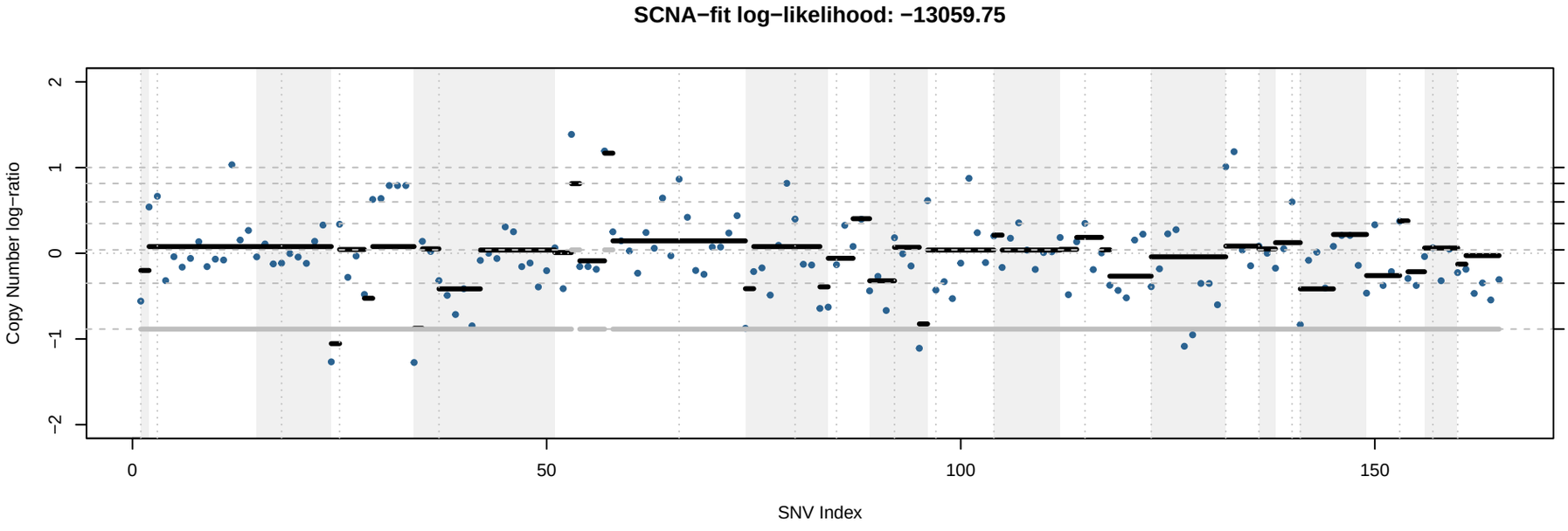

Coverage (log2)
Allelic fraction

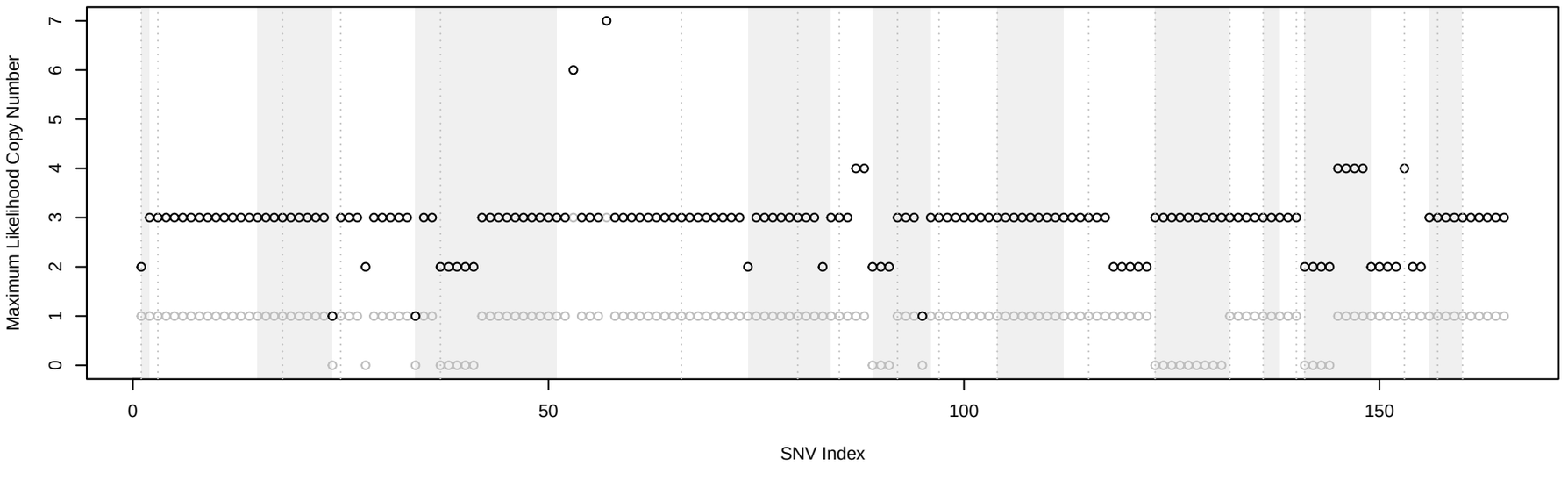

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m2
4m1
5m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

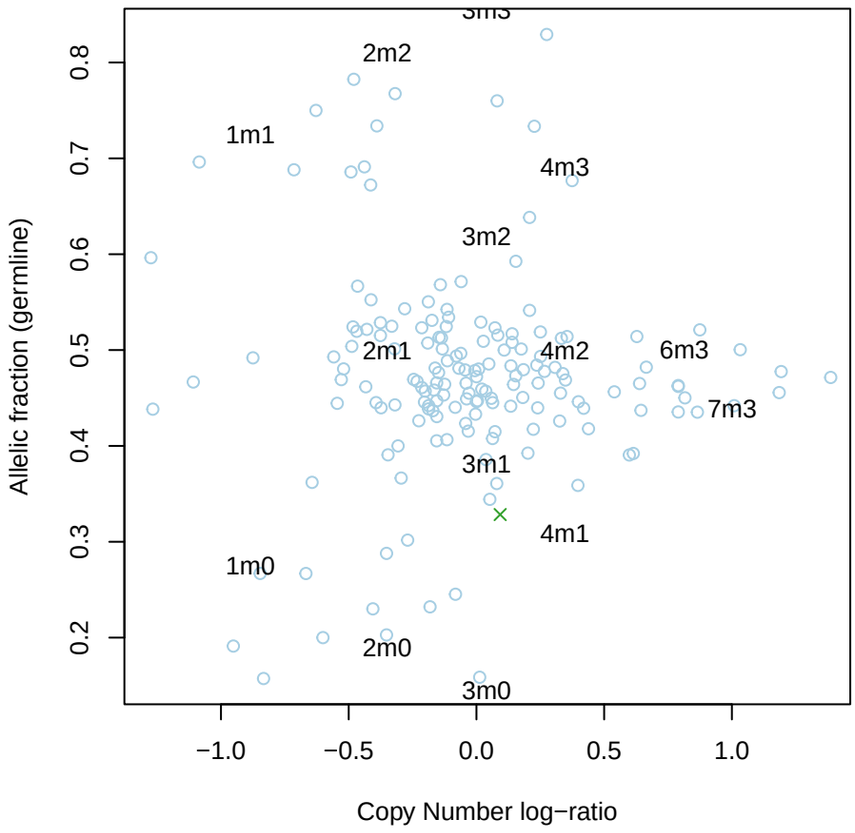

Power 0.8
Frequency
Cellular fraction

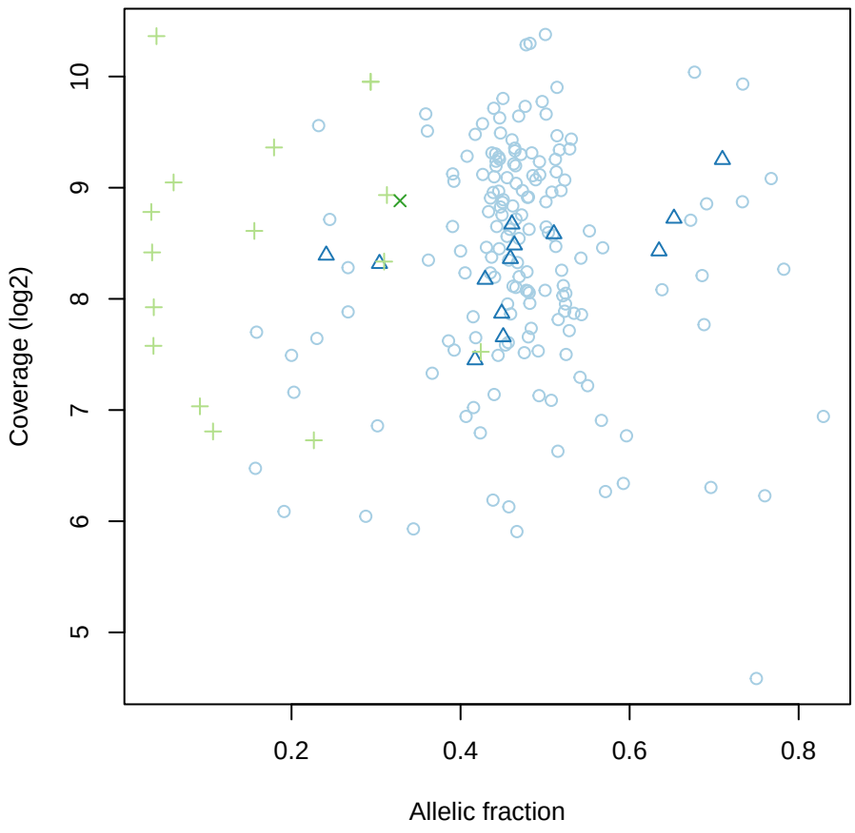

Purity: 0.62 Tumor ploidy: 2.884
1
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1
0
1
2
log2 ratio

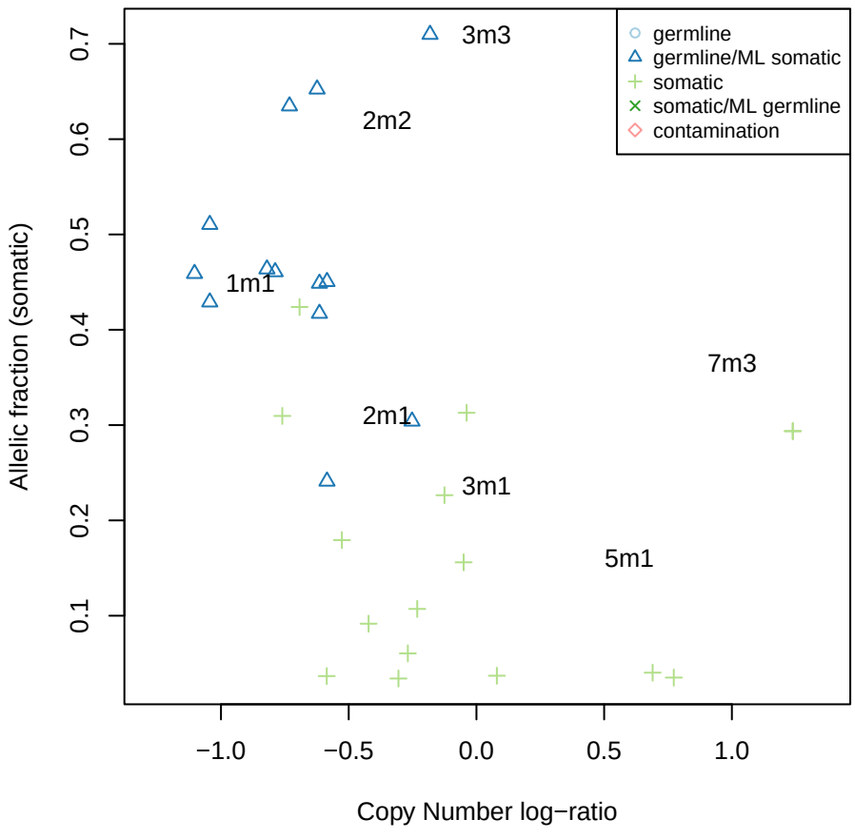

Purity: 0.62 Tumor ploidy: 2.884 SNV log−likelihood: −677.01 GoF: 80.5% Mean coverage: 505;410
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

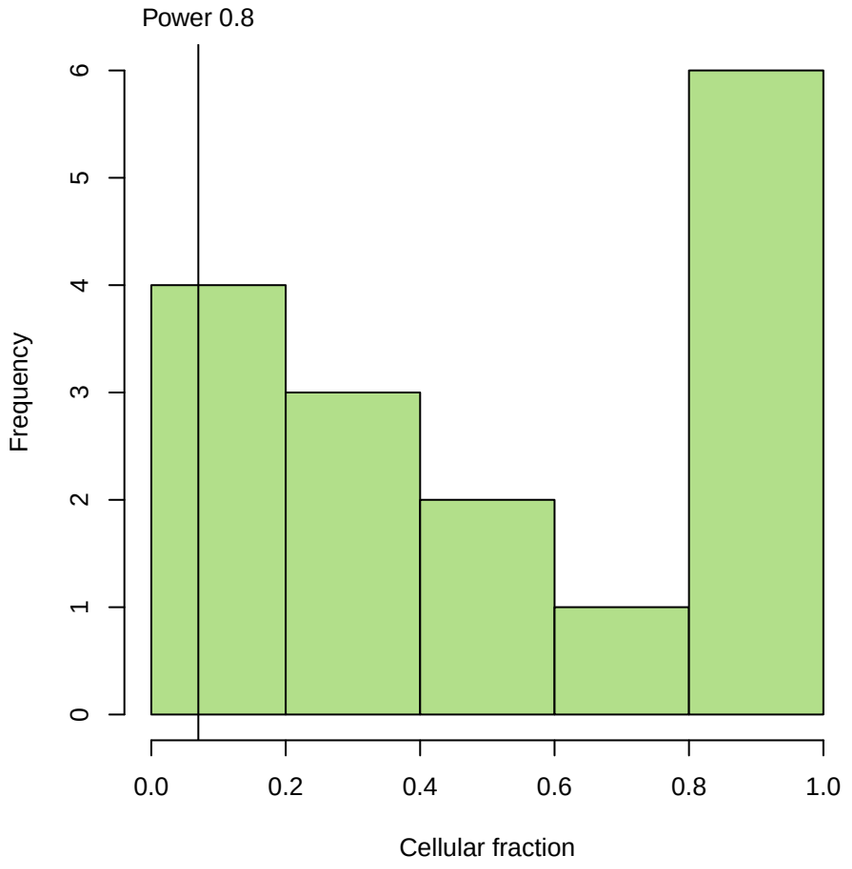

SCNA−fit log−likelihood: −13059.75
Copy Number log−ratio
−2 −1 0 1 2
1 2 3 4 6
0 50 100 150
SNV Index


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


3m3
2m2
1m1
4m3
3m2
2m1
4m2
6m3
7m3
3m1
4m1
1m0
2m0
3m0
Allelic fraction (germline)
Copy Number log−ratio


Coverage (log2)
Allelic fraction


germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m3
2m2
1m1
7m3
2m1
3m1
5m1
Allelic fraction (somatic)
Copy Number log−ratio


Power 0.8
Frequency
Cellular fraction