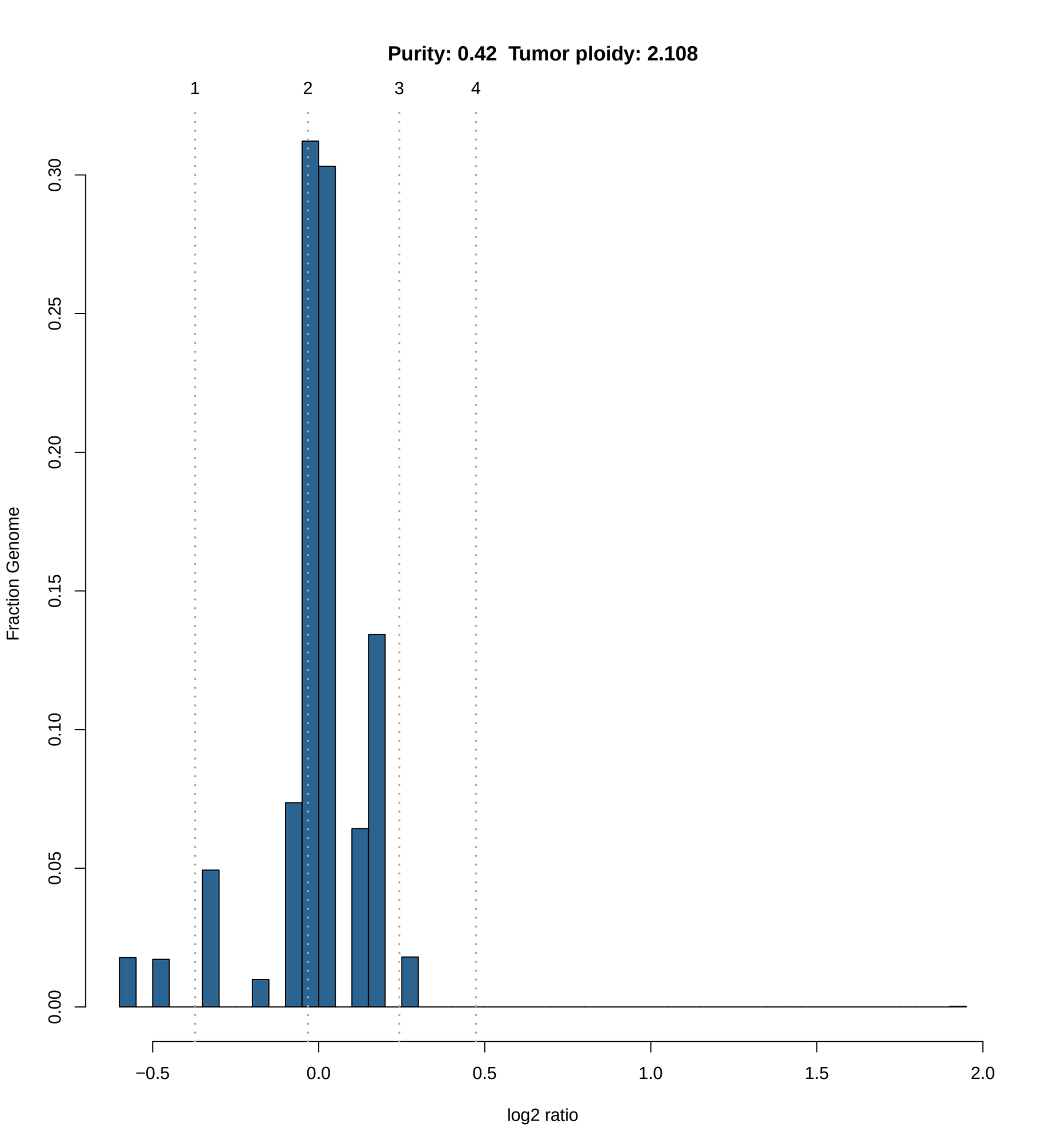
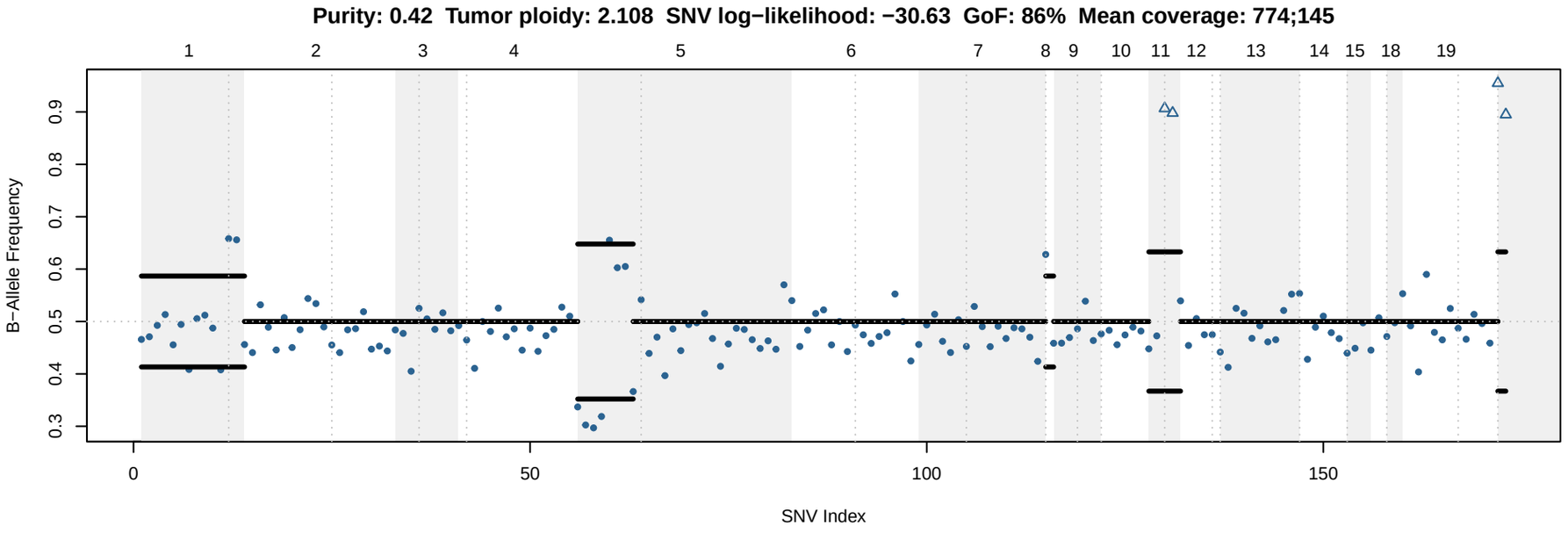
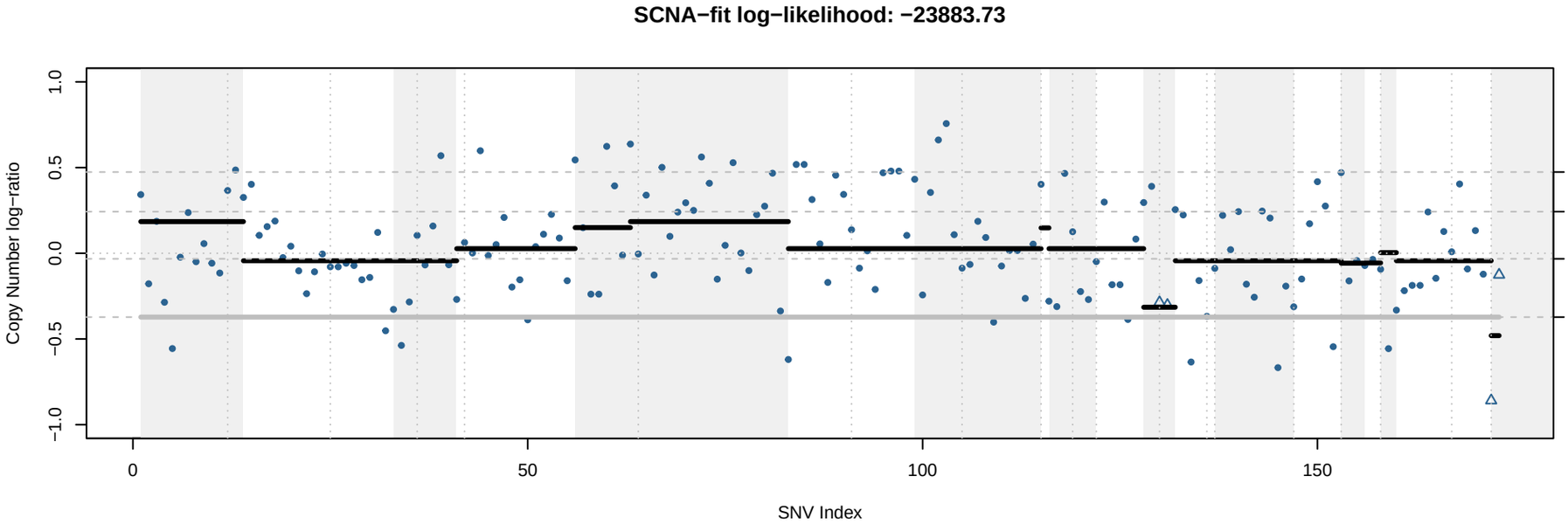
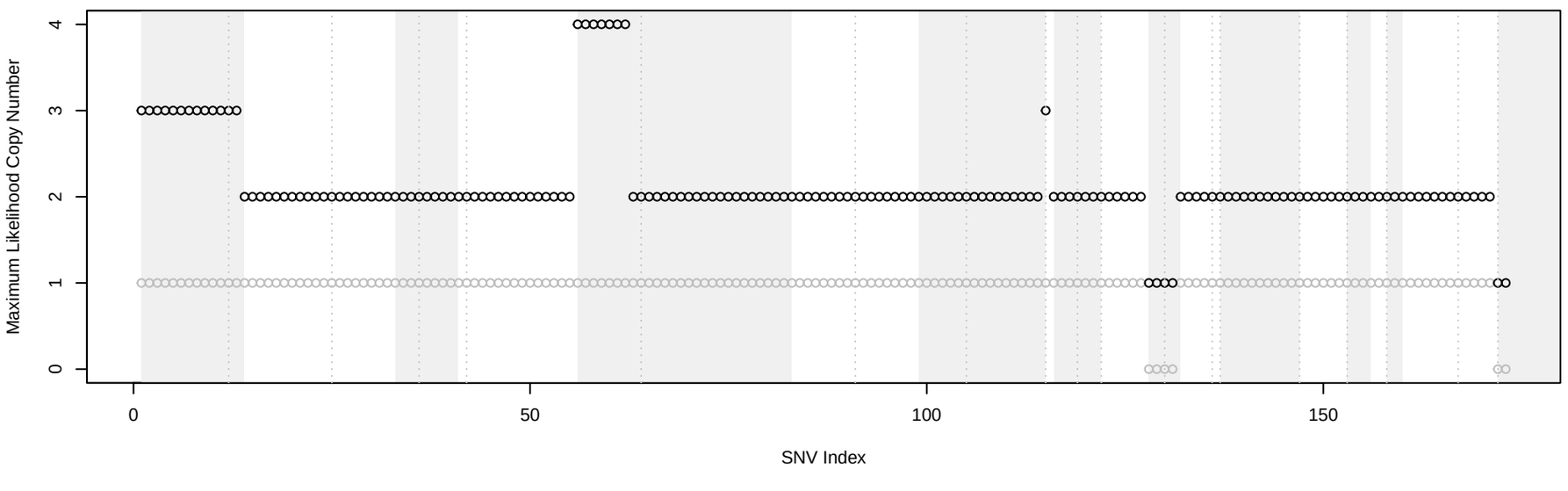
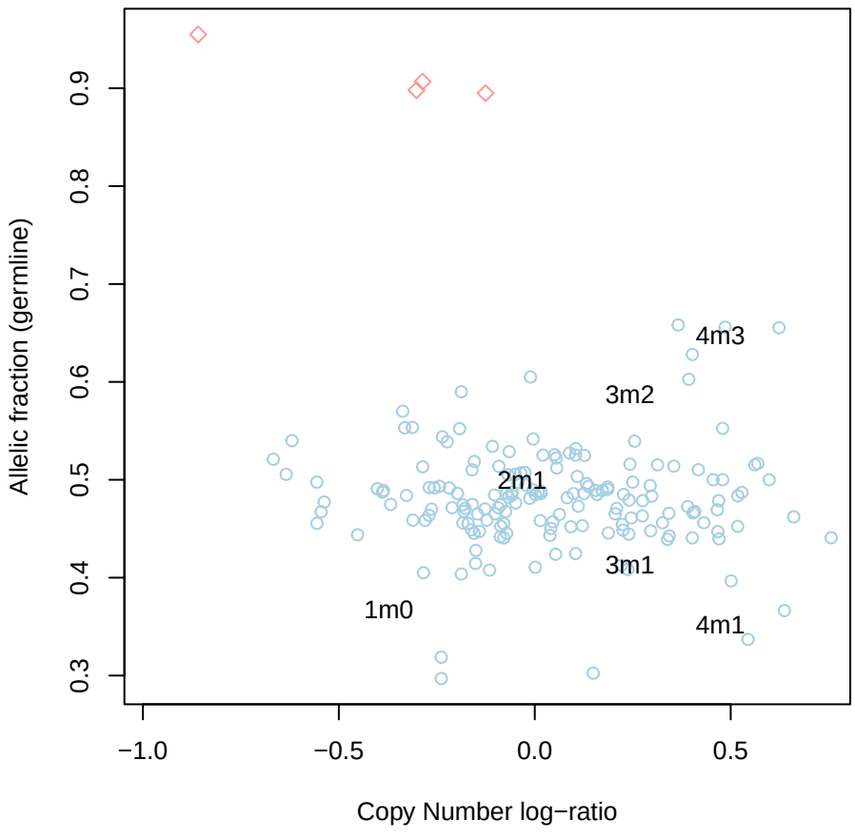
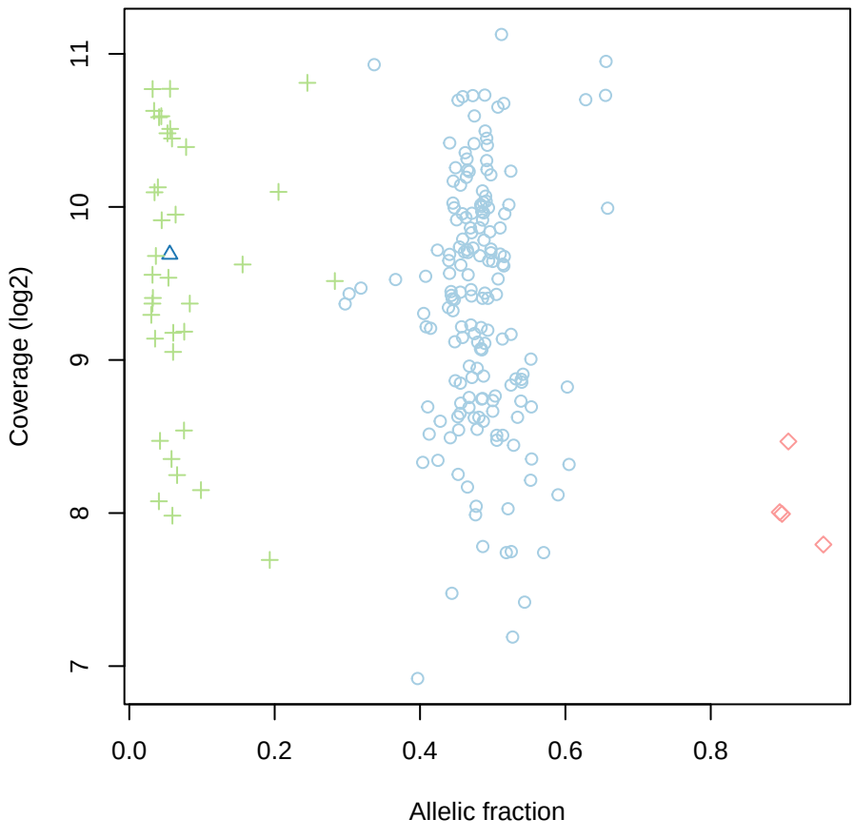

Purity: 0.42 Tumor ploidy: 2.108
1
2
3
4
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

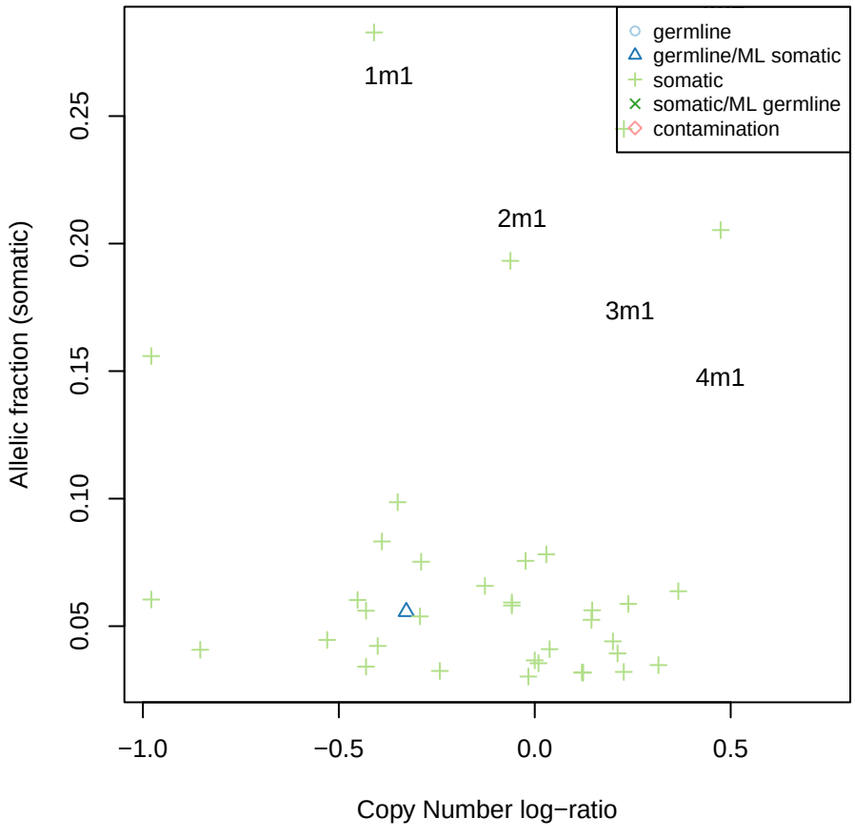

Purity: 0.42 Tumor ploidy: 2.108 SNV log−likelihood: −30.63 GoF: 86% Mean coverage: 774;145
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8 0.9
0 50 100 150
SNV Index

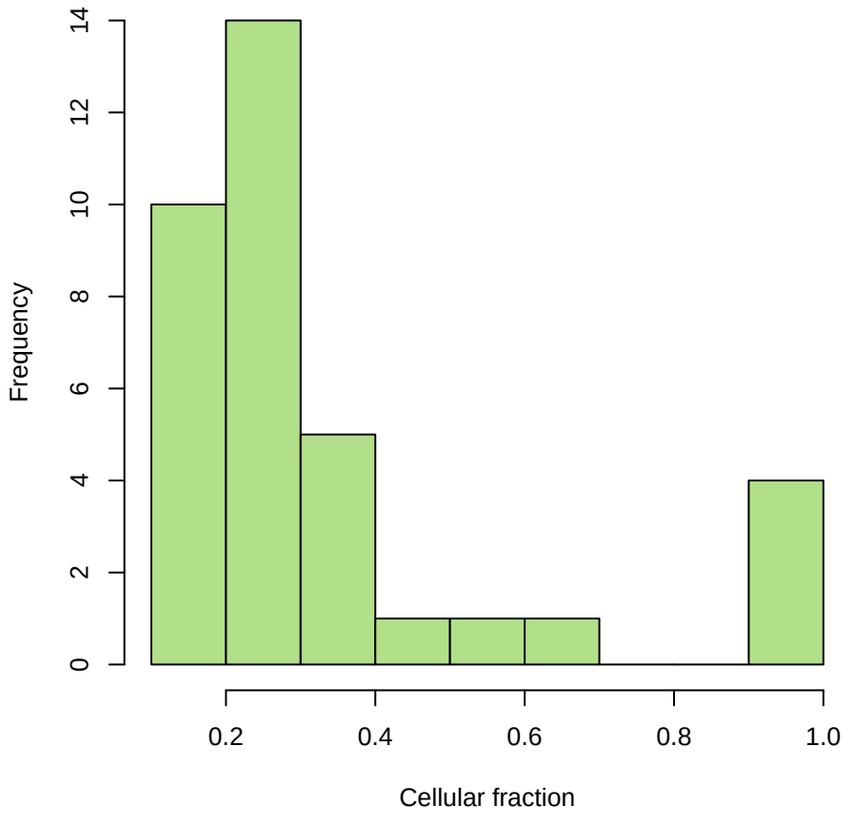

SCNA−fit log−likelihood: −23883.73
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4
0 50 100 150
SNV Index

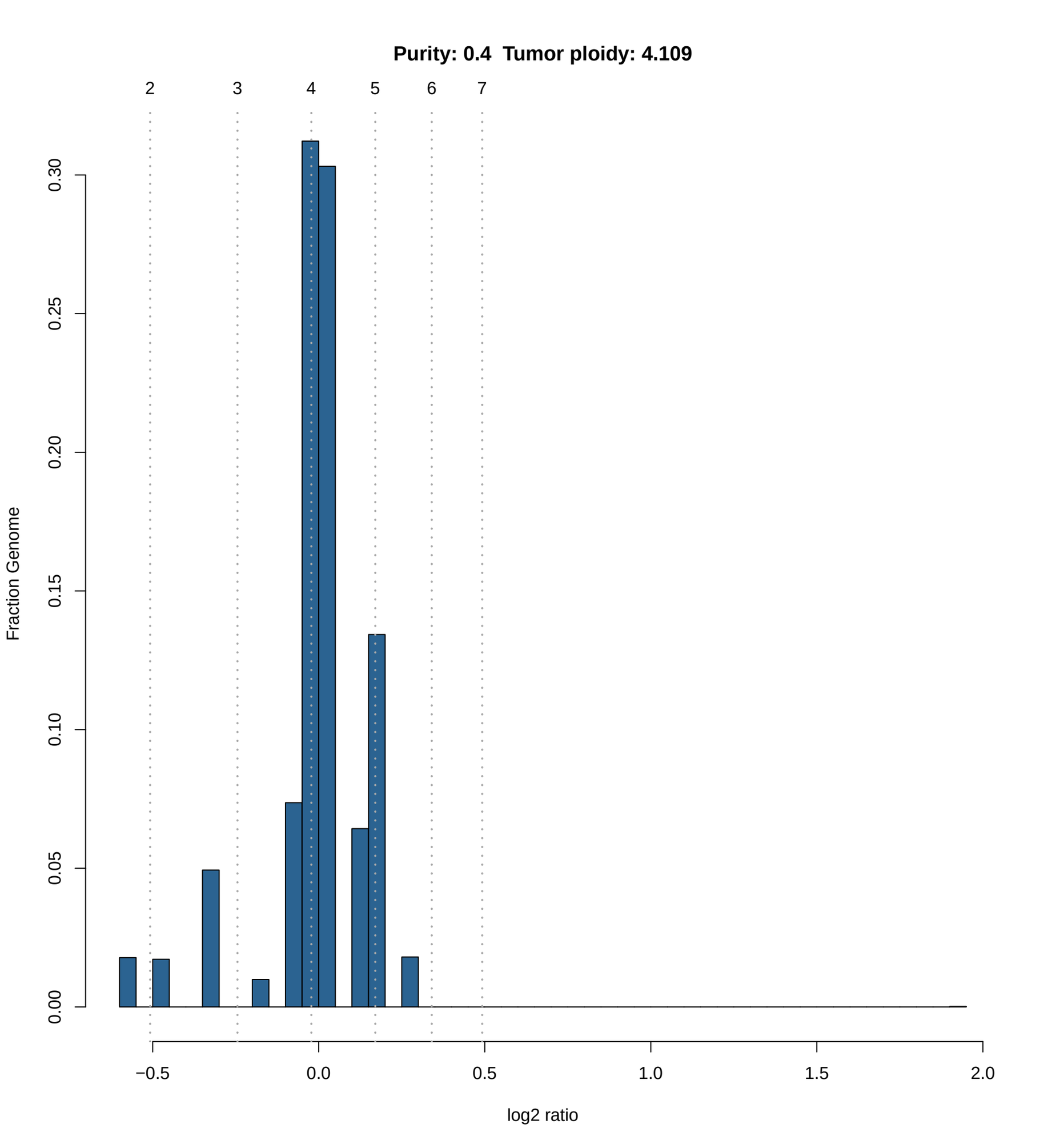

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

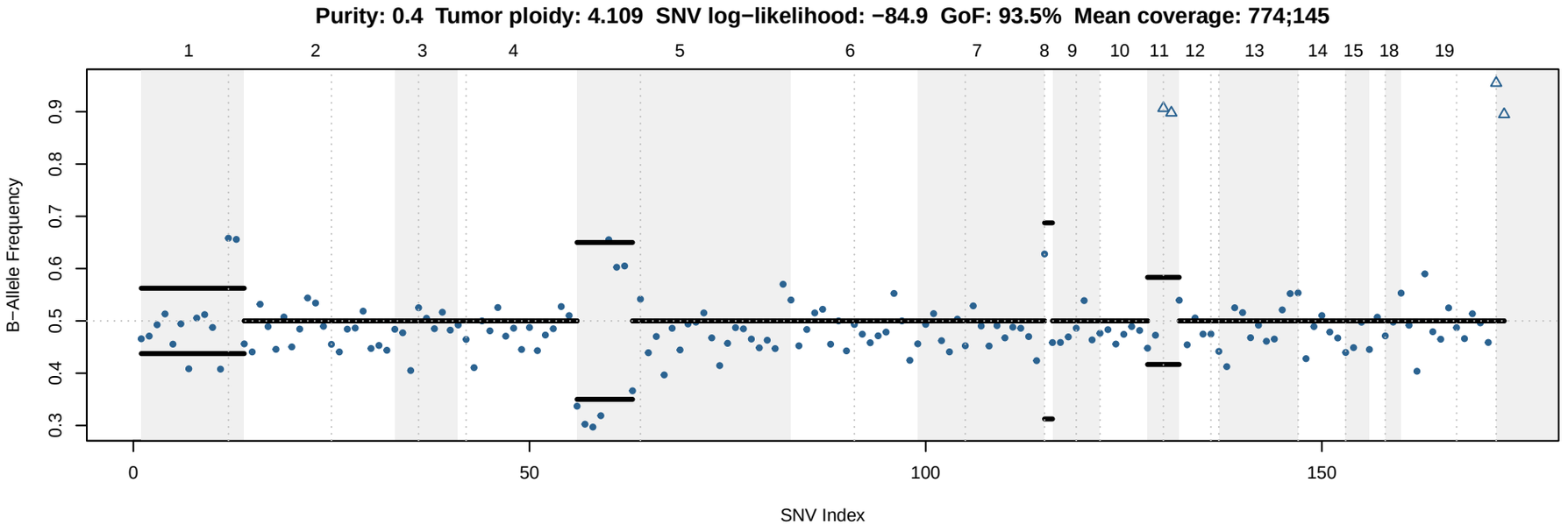

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
2m1
3m1
1m0
4m1

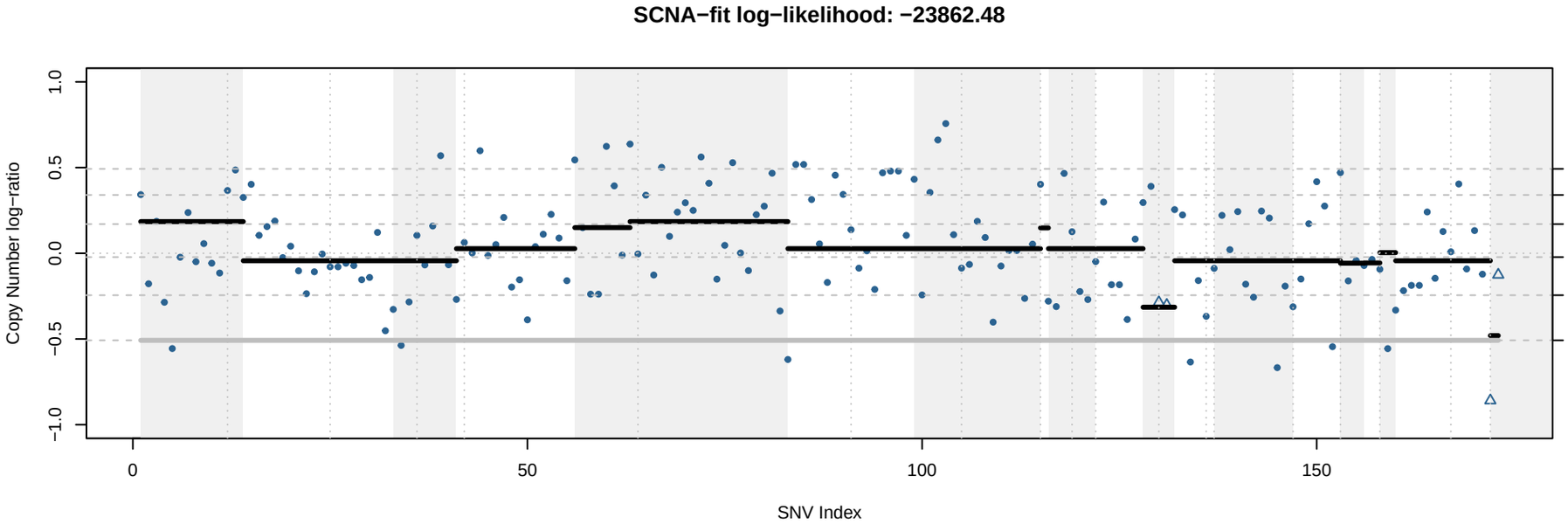

Coverage (log2)
Allelic fraction

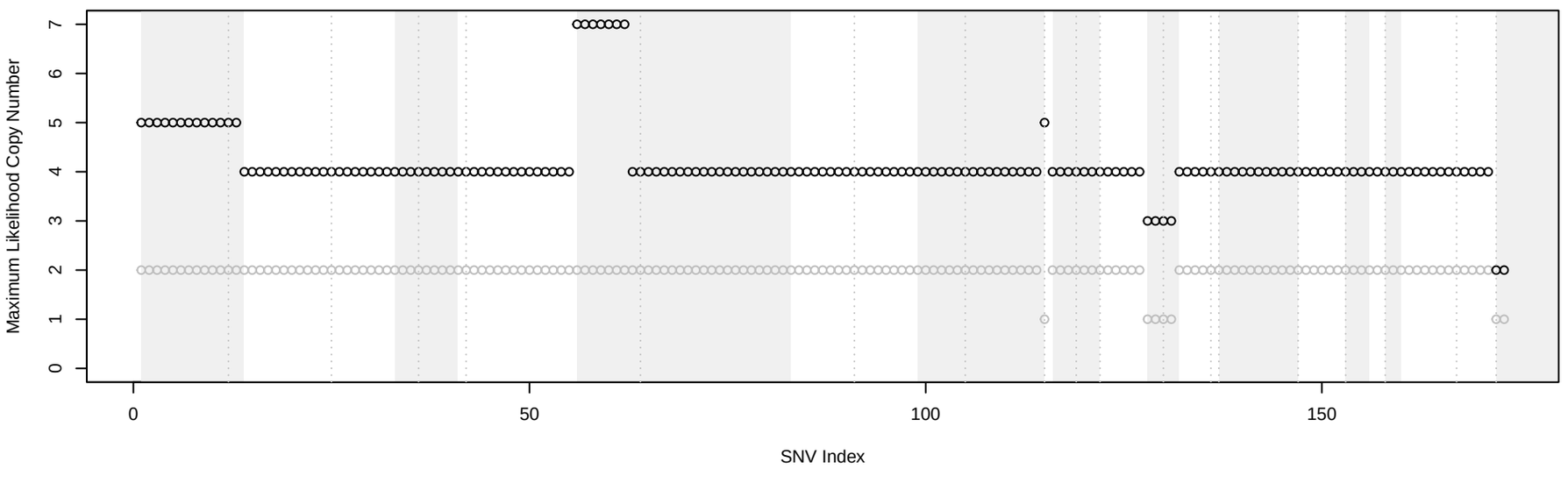

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1
3m1
4m1

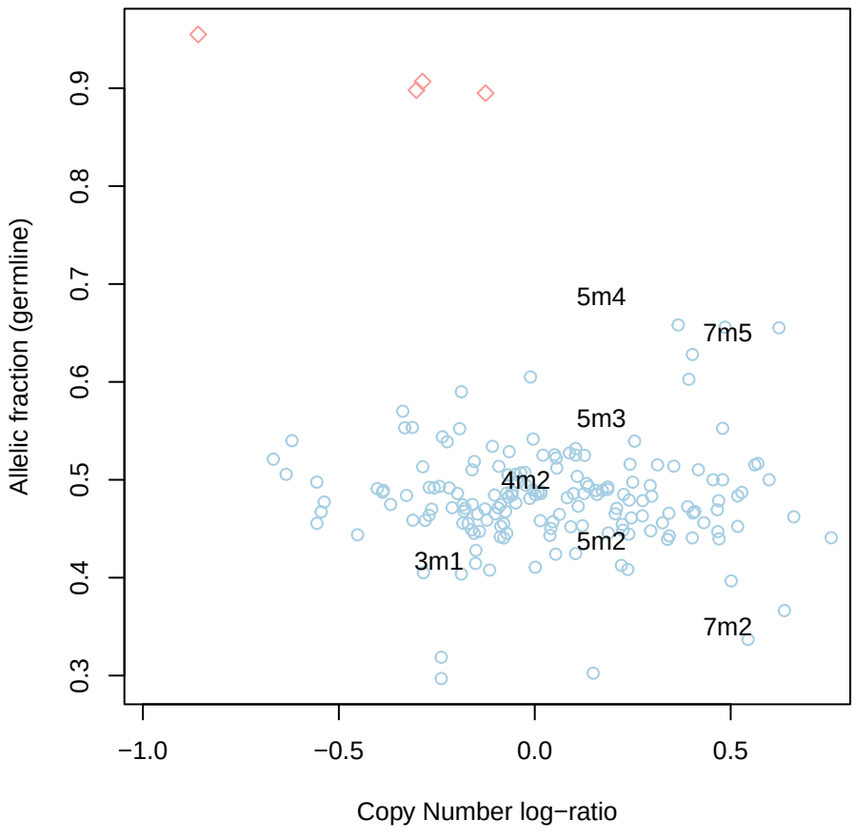

Frequency
Cellular fraction

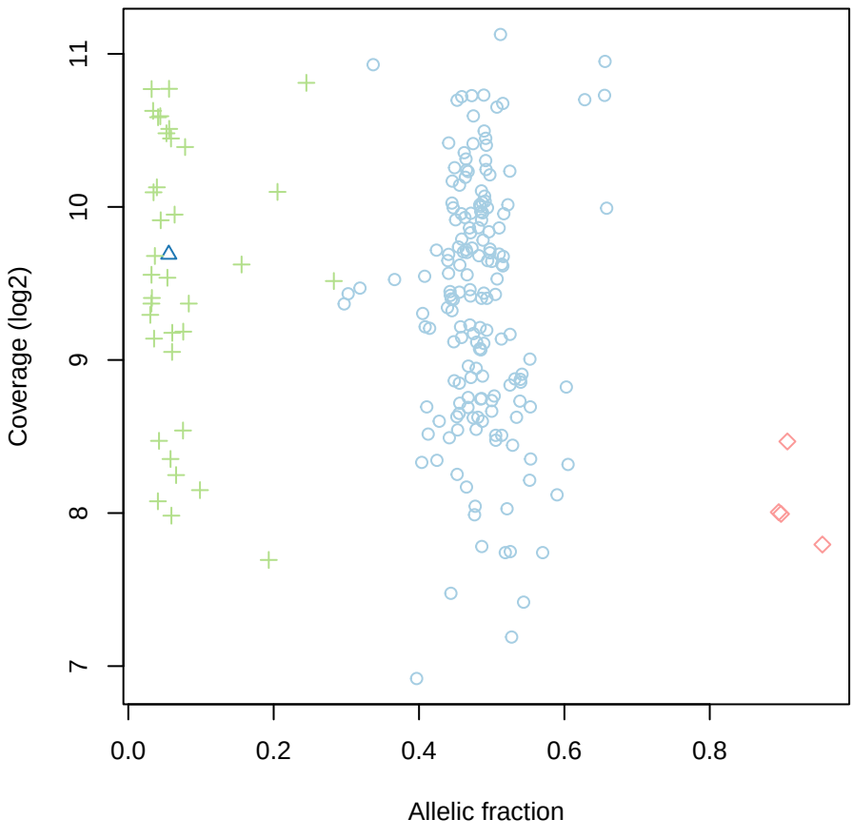

Purity: 0.4 Tumor ploidy: 4.109
2
3
4
5
6
7
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

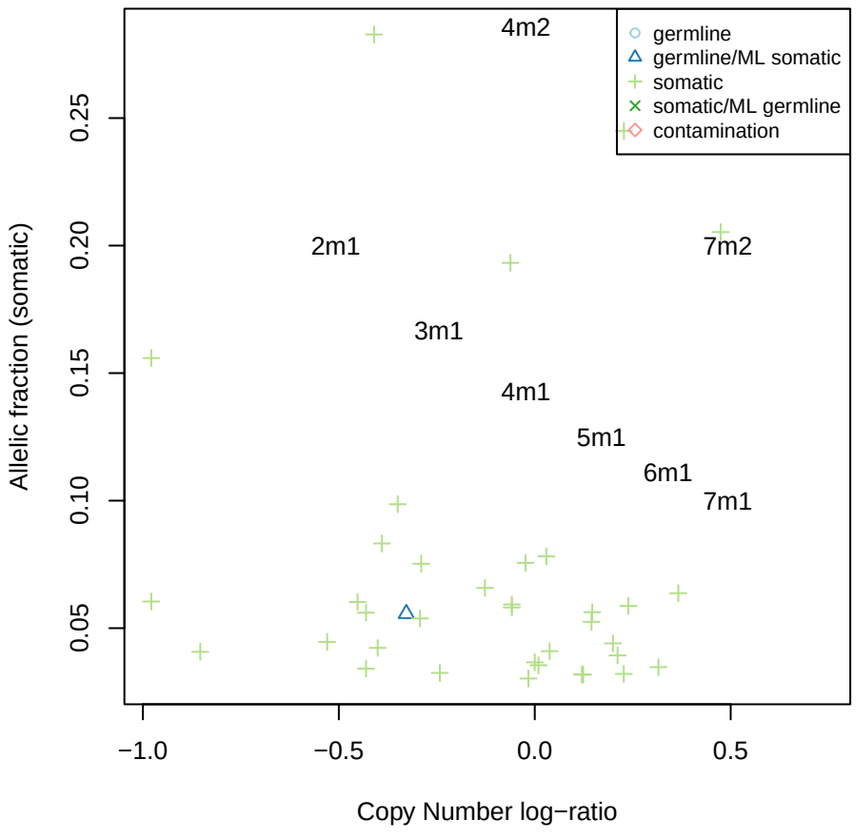

Purity: 0.4 Tumor ploidy: 4.109 SNV log−likelihood: −84.9 GoF: 93.5% Mean coverage: 774;145
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8 0.9
0 50 100 150
SNV Index

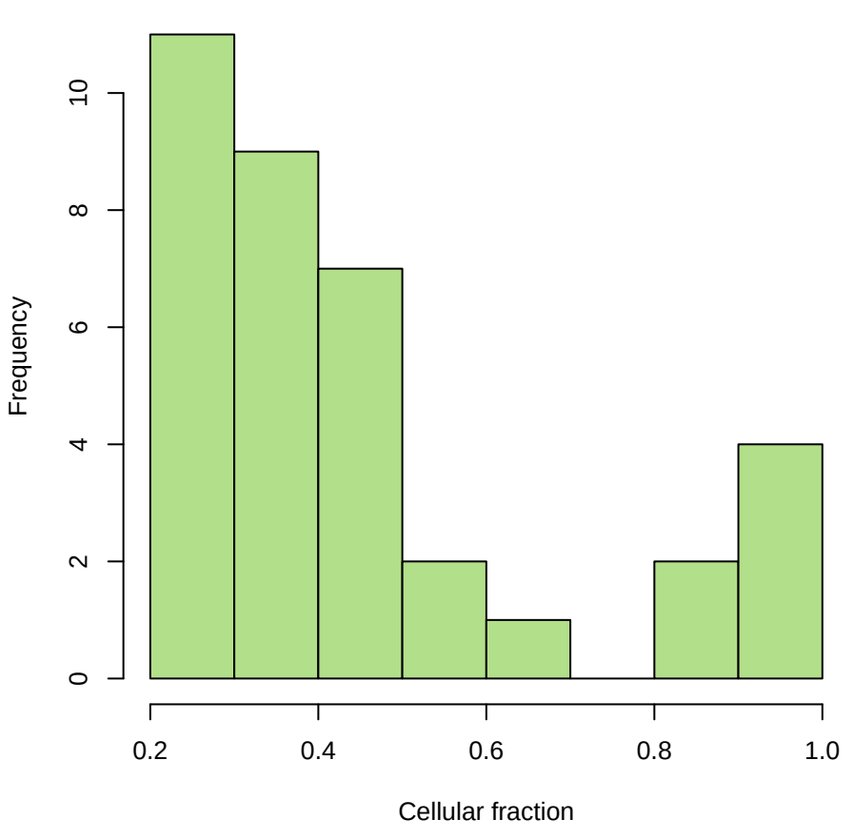

SCNA−fit log−likelihood: −23862.48
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 50 100 150
SNV Index

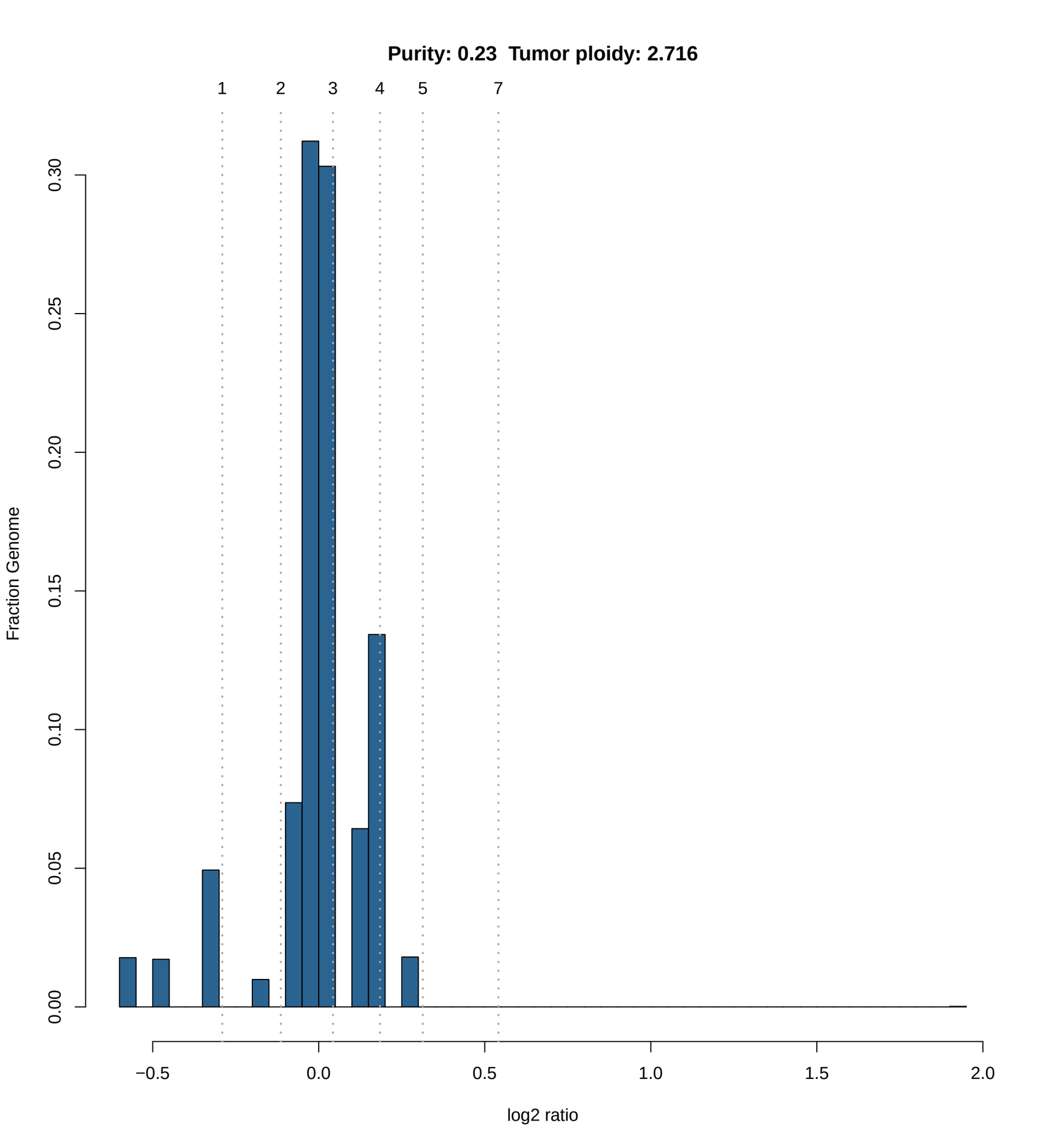

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

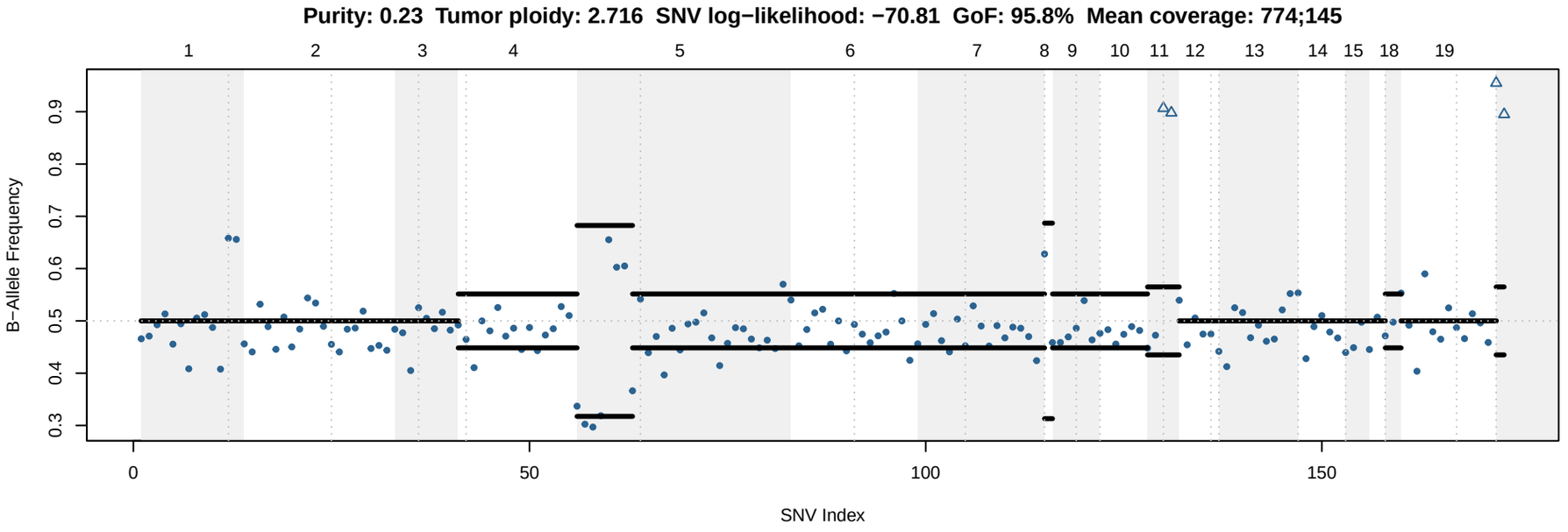

Allelic fraction (germline)
Copy Number log−ratio
5m4
7m5
5m3
4m2
5m2
3m1
7m2

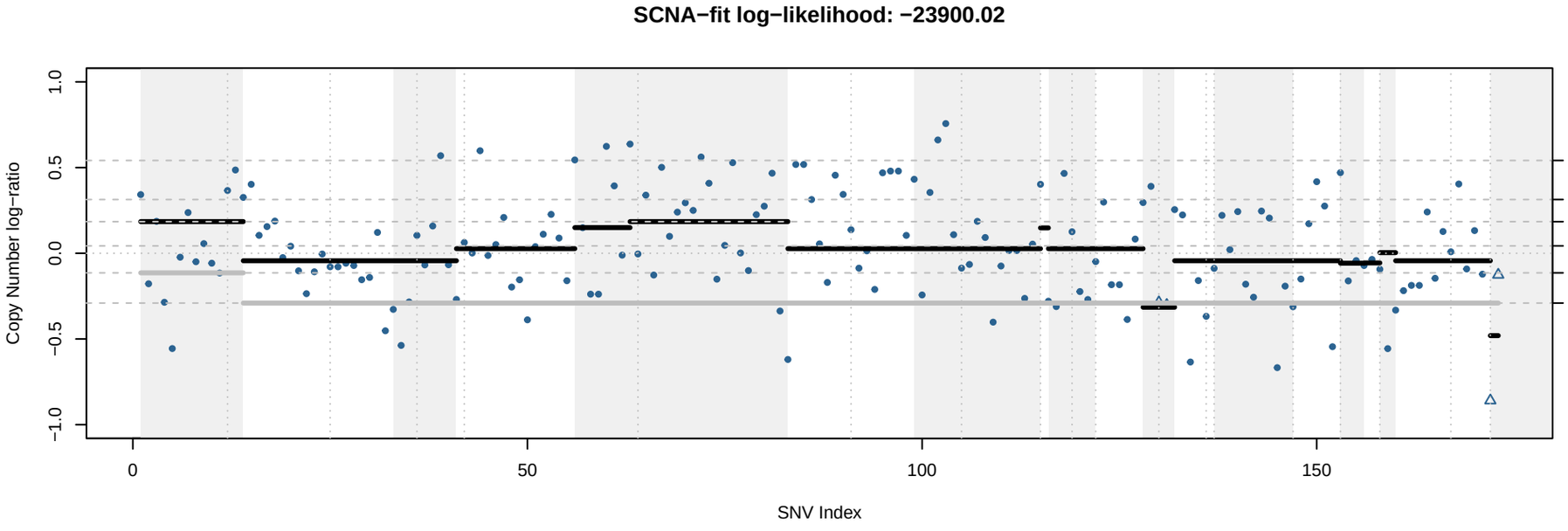

Coverage (log2)
Allelic fraction

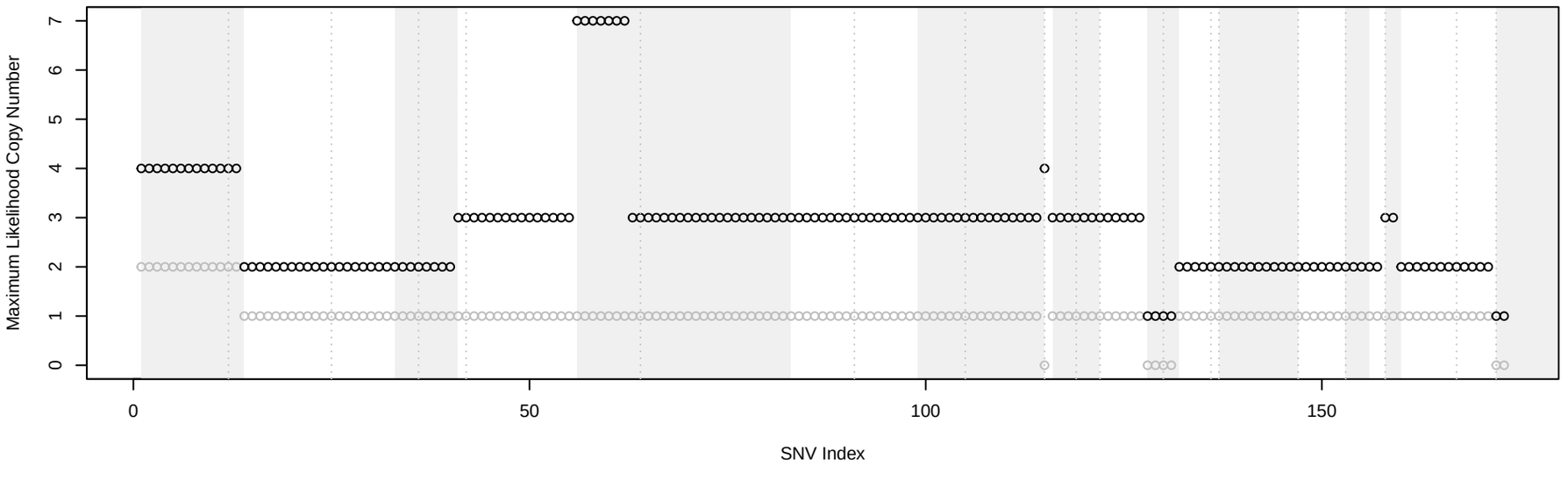

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m2
2m1
7m2
3m1
4m1
5m1
6m1
7m1

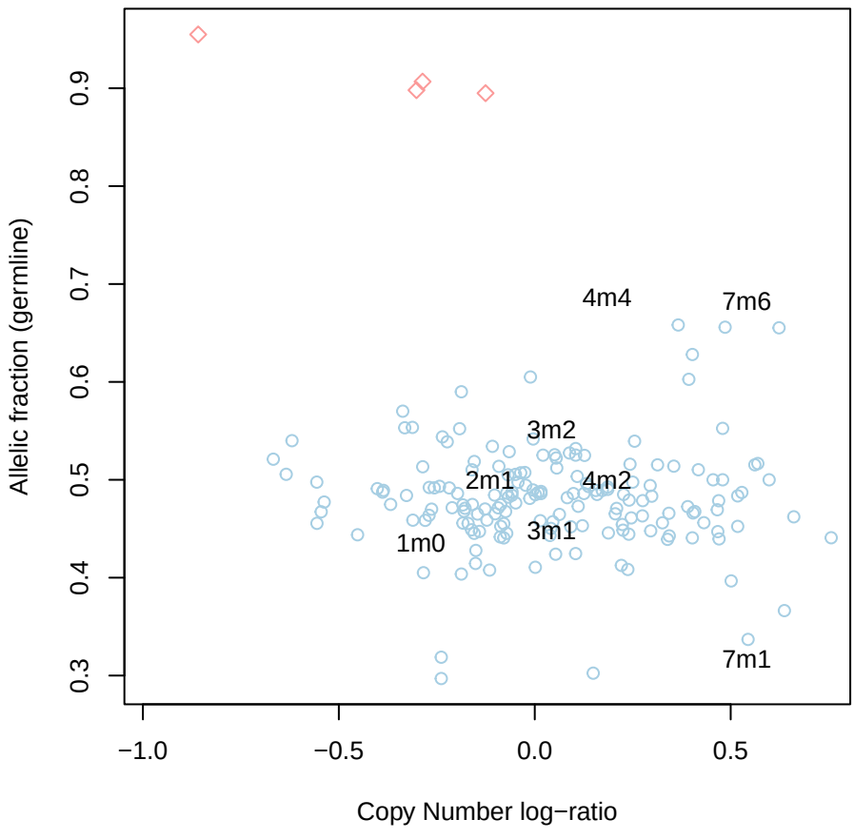

Frequency
Cellular fraction

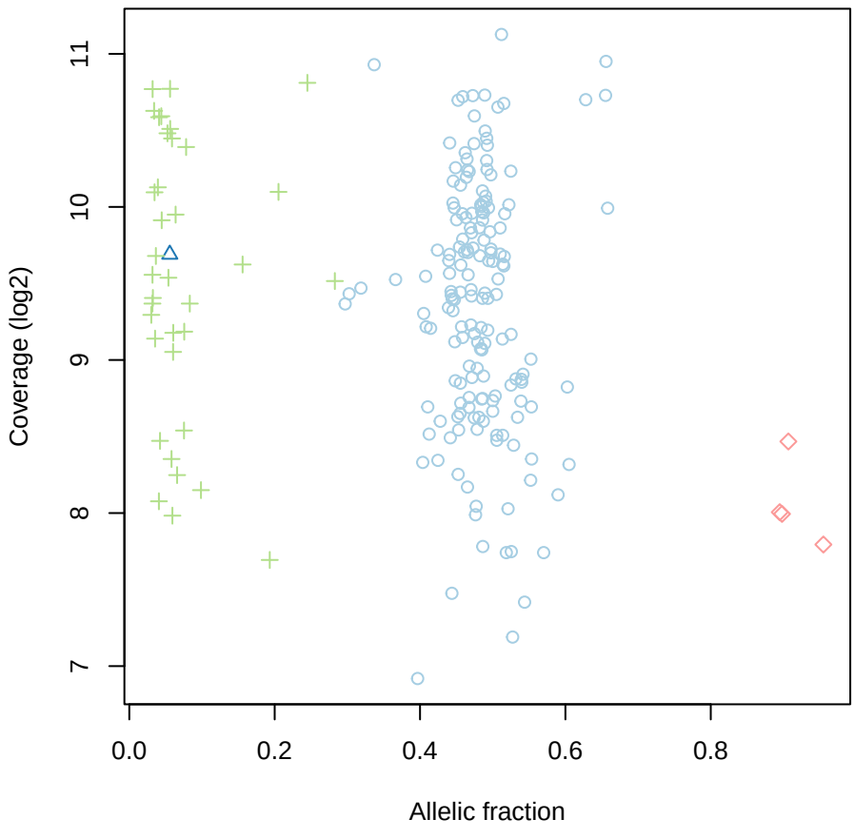

Purity: 0.23 Tumor ploidy: 2.716
1
2
3
4
5
7
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

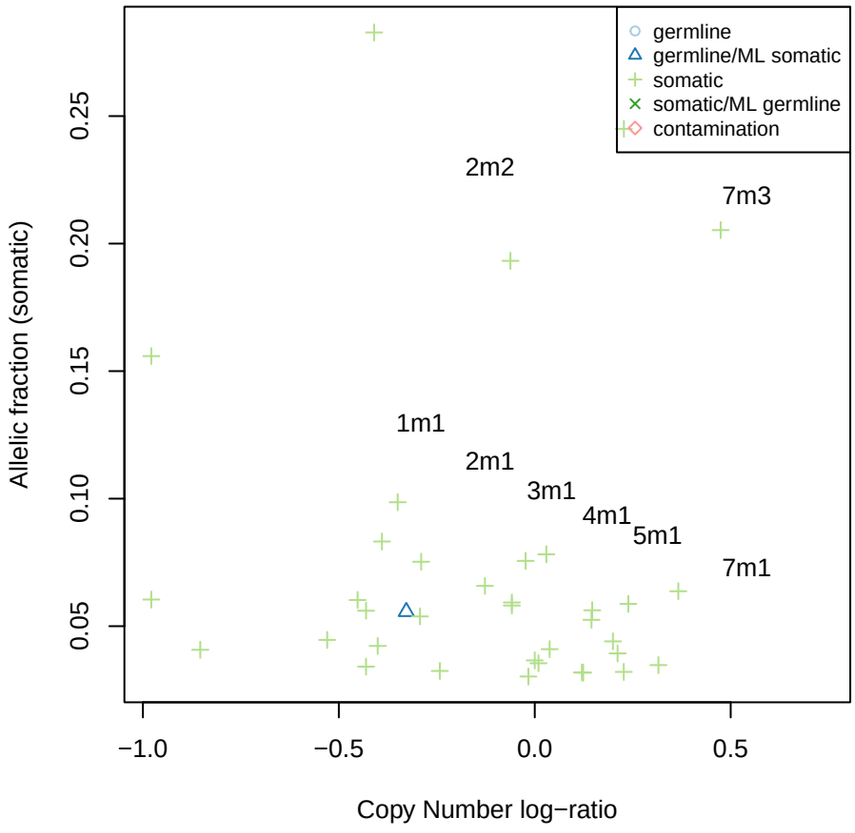

Purity: 0.23 Tumor ploidy: 2.716 SNV log−likelihood: −70.81 GoF: 95.8% Mean coverage: 774;145
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8 0.9
0 50 100 150
SNV Index

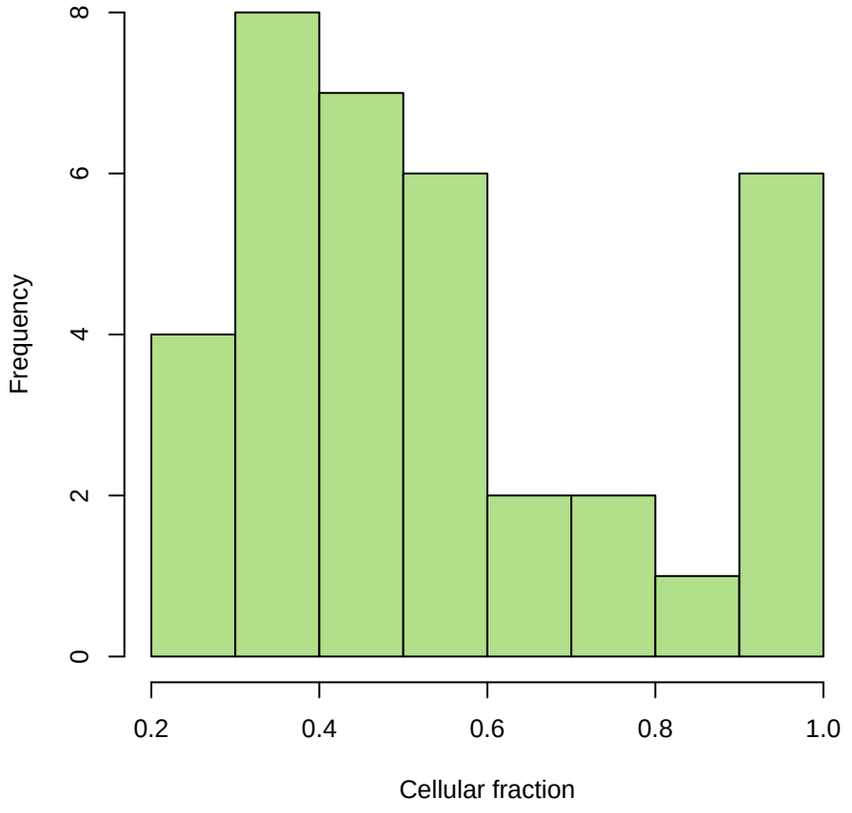

SCNA−fit log−likelihood: −23900.02
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 5 7
0 50 100 150
SNV Index

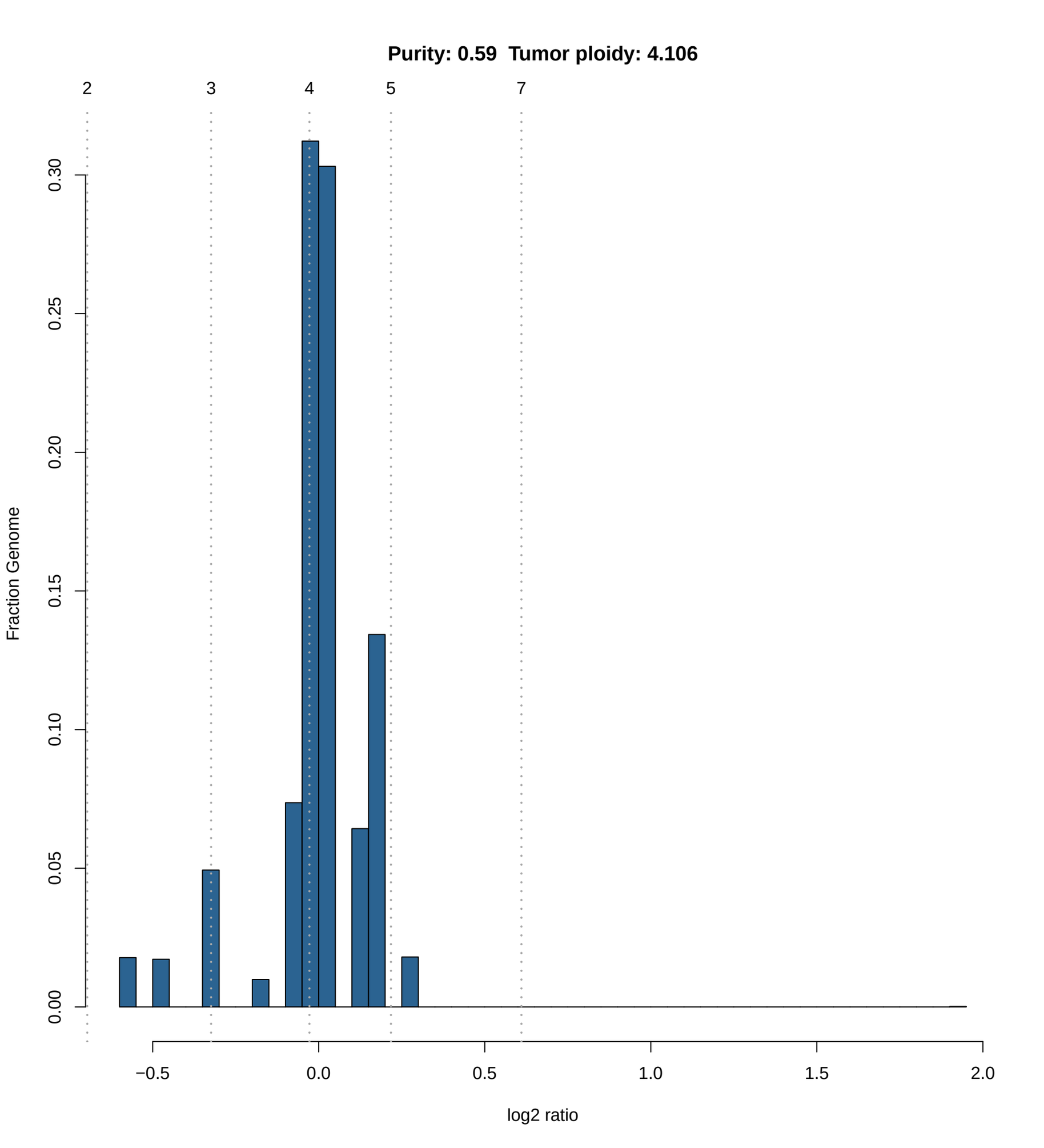

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

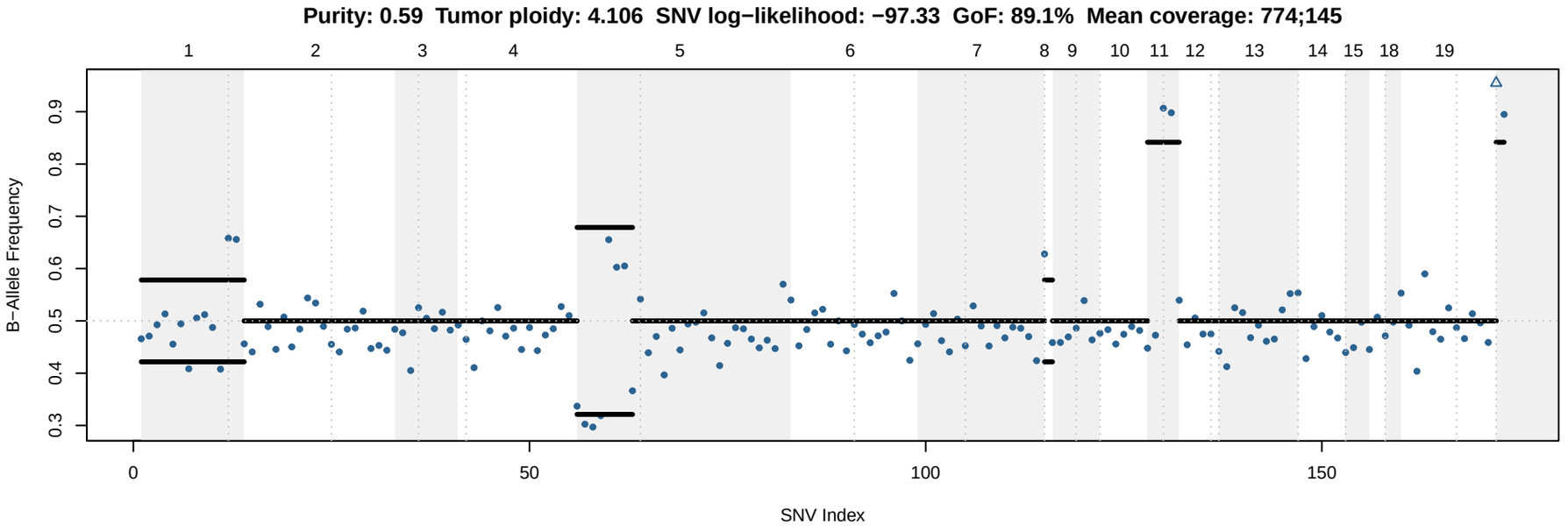

Allelic fraction (germline)
Copy Number log−ratio
4m4
7m6
3m2
2m1
4m2
3m1
1m0
7m1

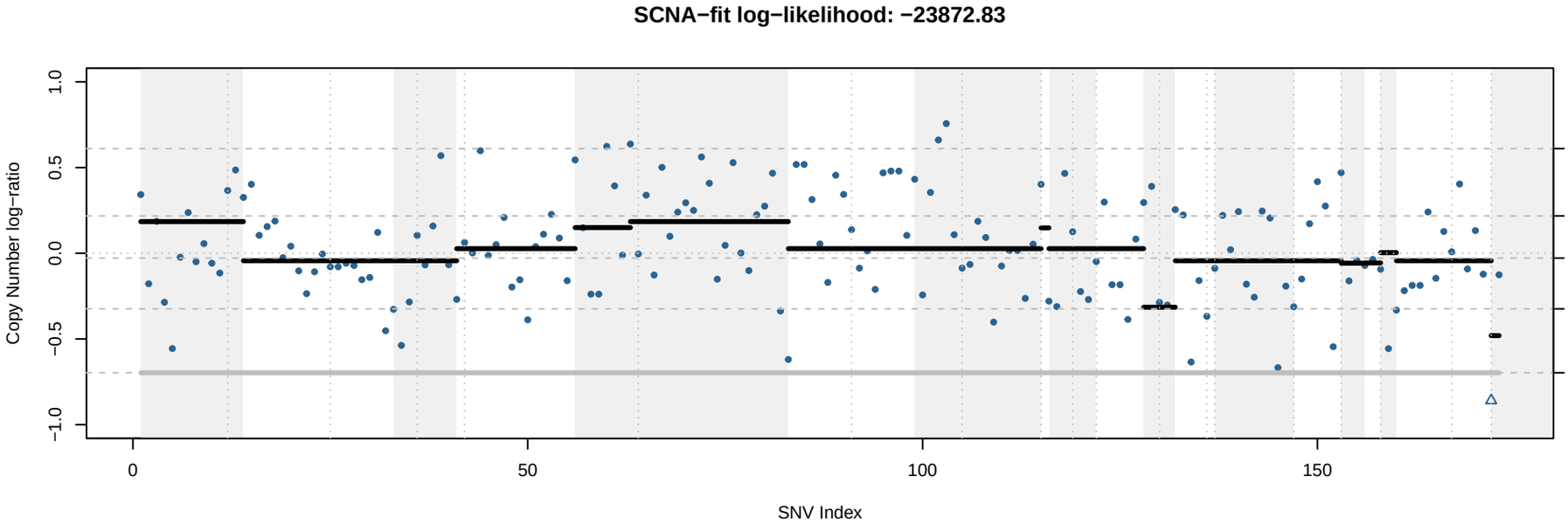

Coverage (log2)
Allelic fraction

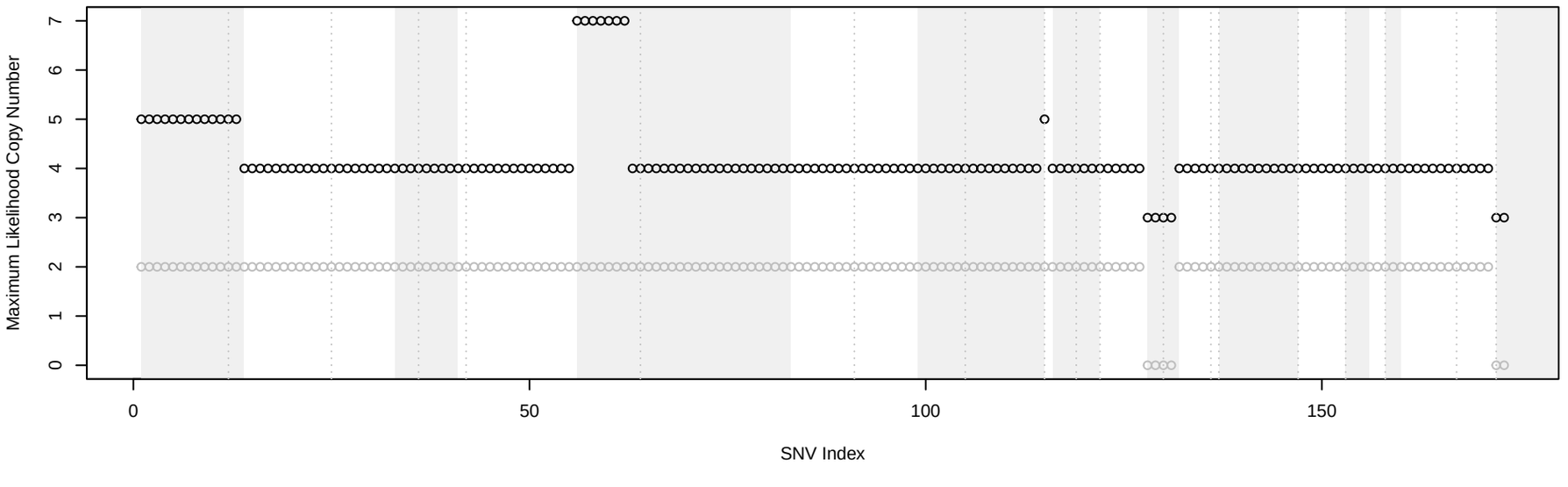

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m2
7m3
1m1
2m1
3m1
4m1
5m1
7m1

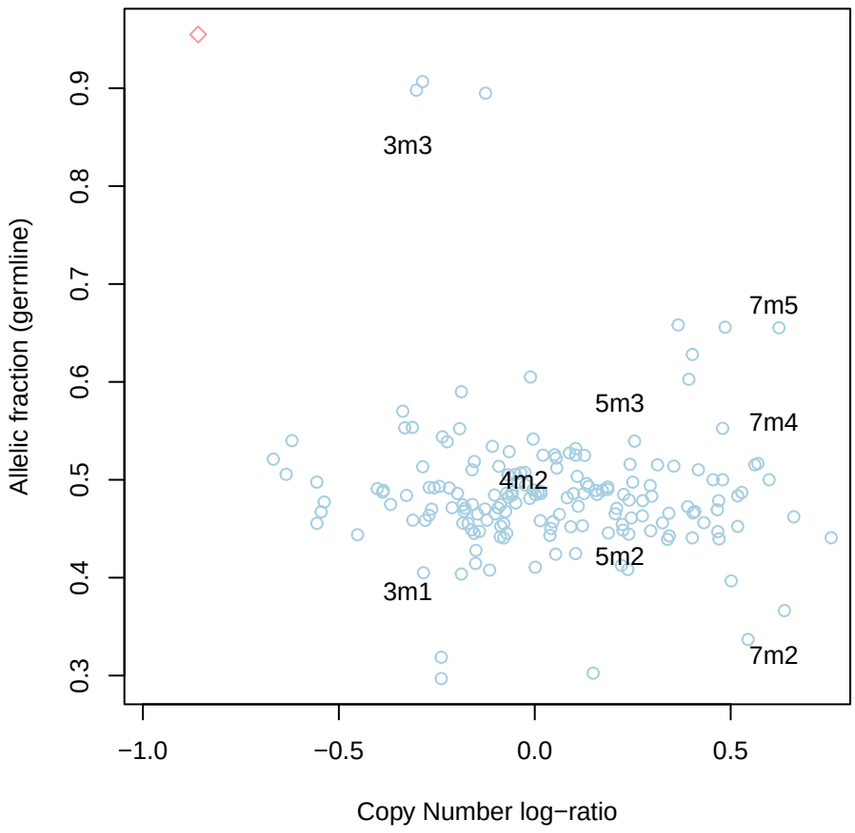

Frequency
Cellular fraction

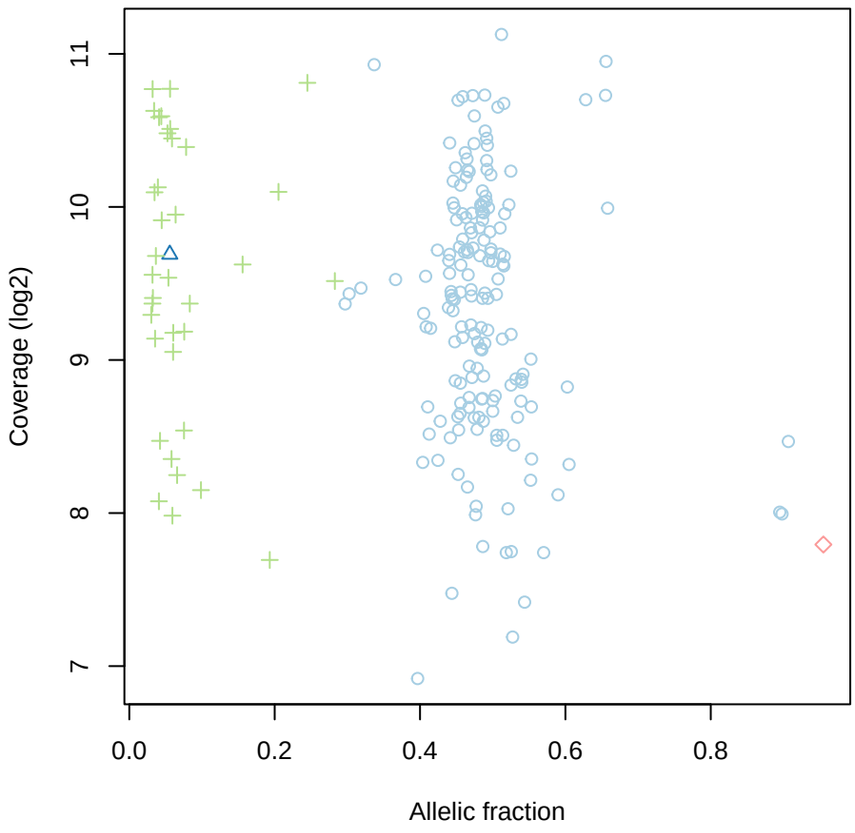

Purity: 0.59 Tumor ploidy: 4.106
2
3
4
5
7
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

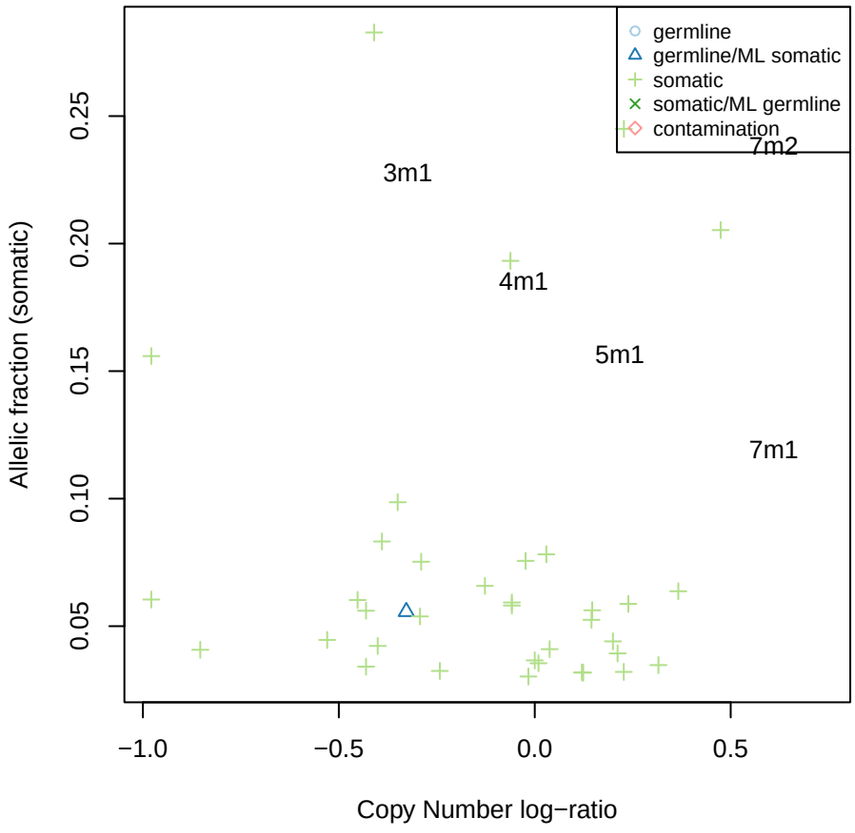

Purity: 0.59 Tumor ploidy: 4.106 SNV log−likelihood: −97.33 GoF: 89.1% Mean coverage: 774;145
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8 0.9
0 50 100 150
SNV Index

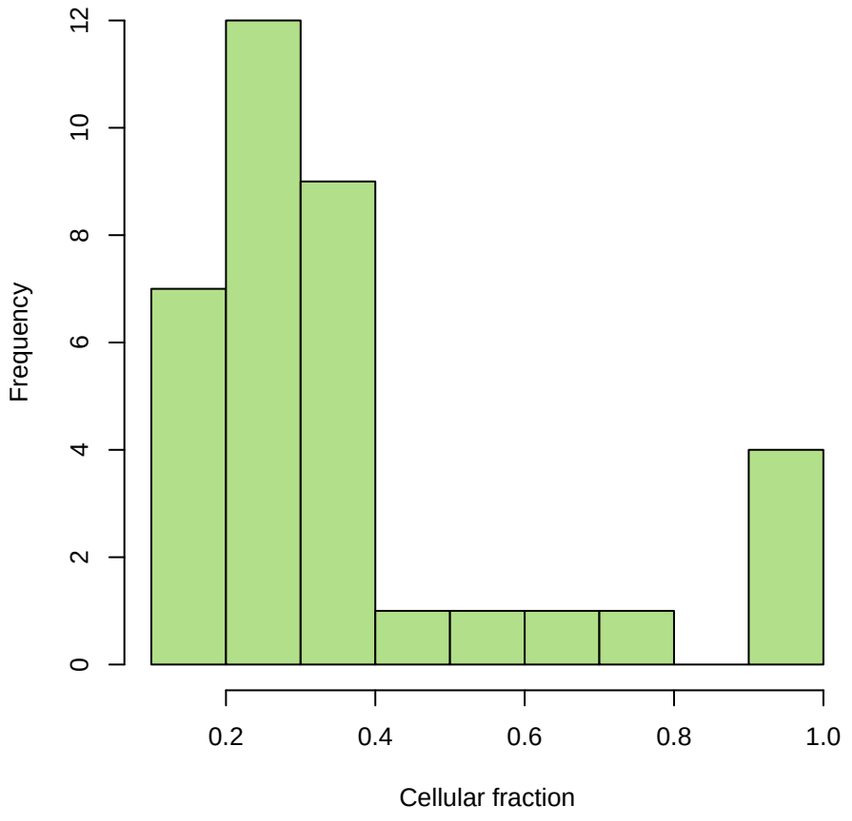

SCNA−fit log−likelihood: −23872.83
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 7
0 50 100 150
SNV Index

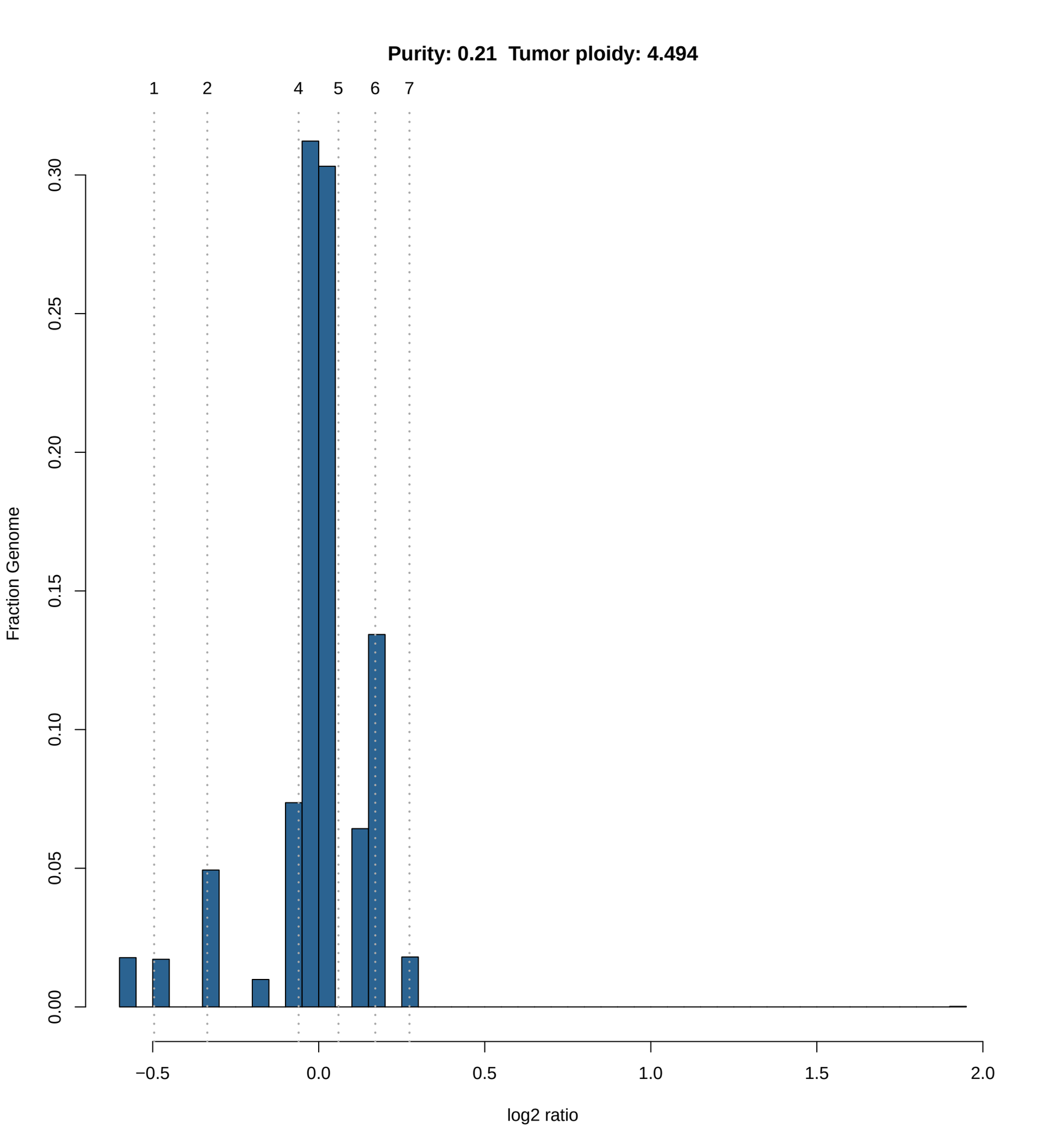

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

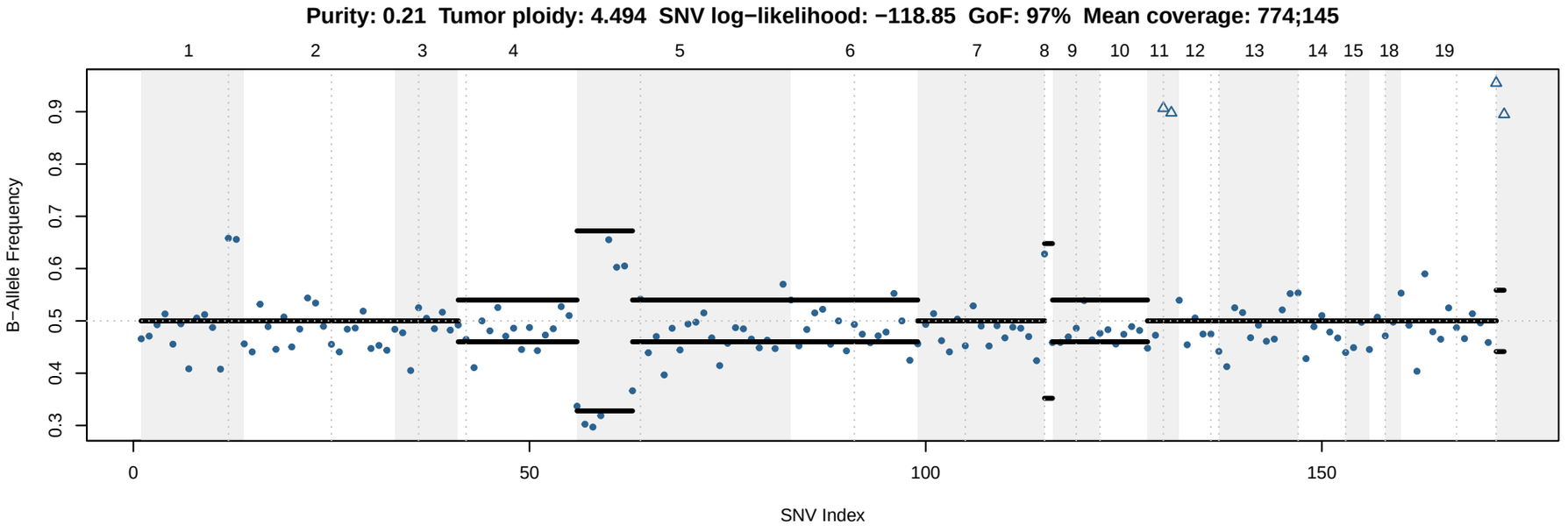

Allelic fraction (germline)
Copy Number log−ratio
3m3
7m5
5m3
7m4
4m2
5m2
3m1
7m2

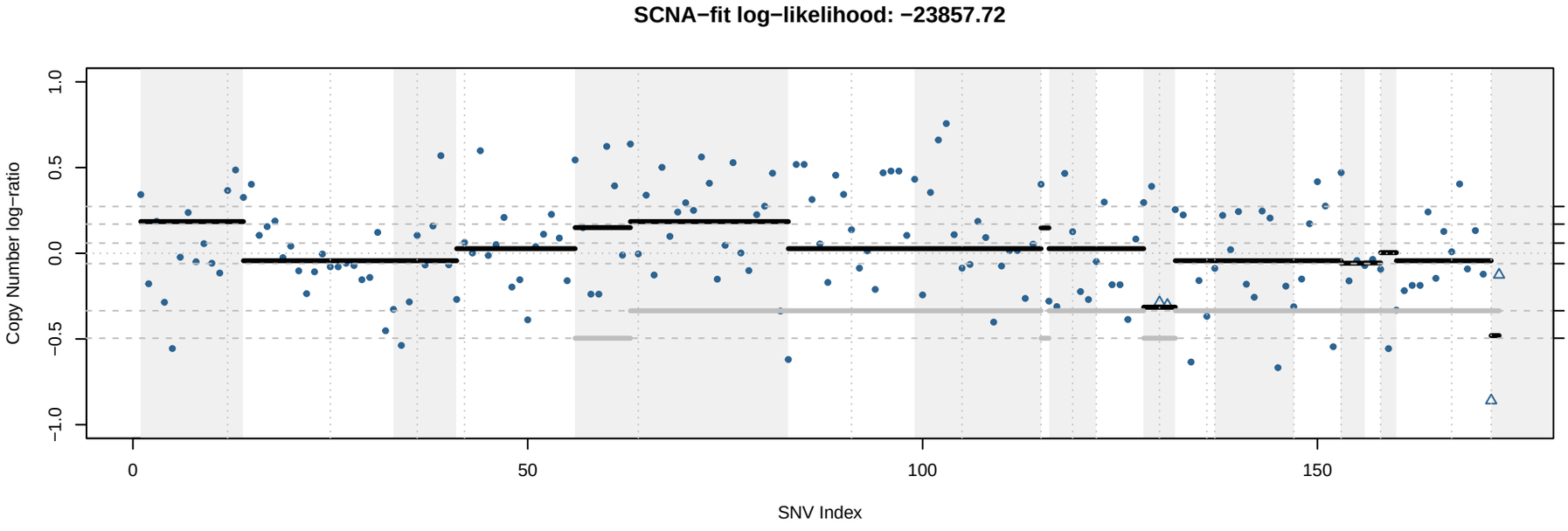

Coverage (log2)
Allelic fraction

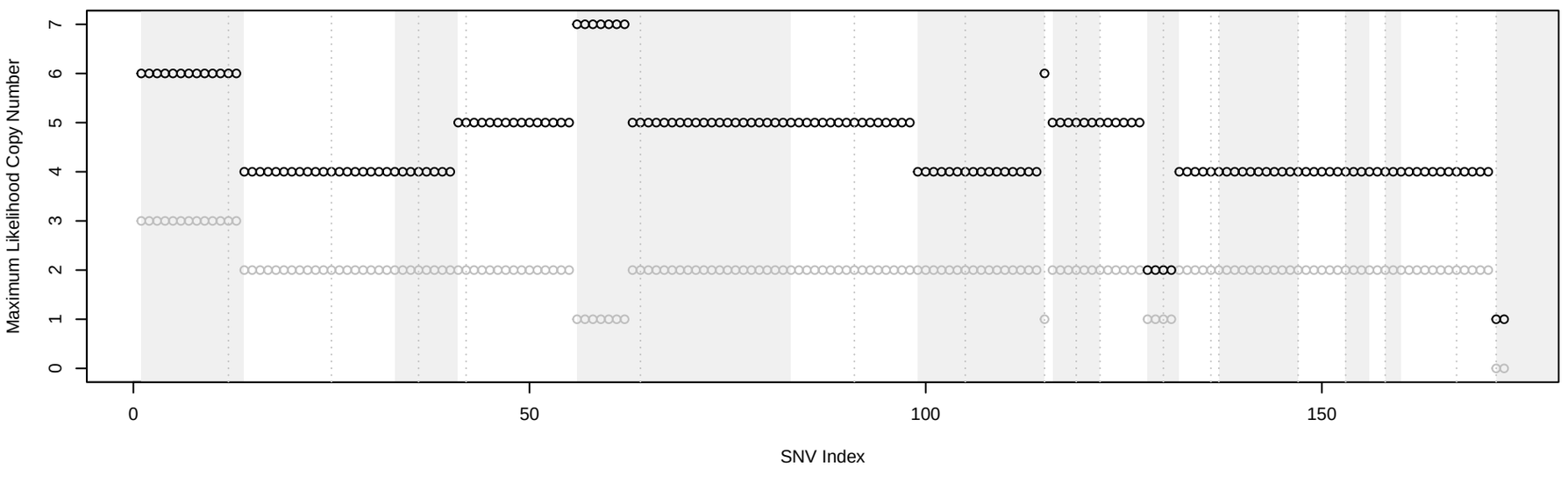

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
7m2
3m1
4m1
5m1
7m1

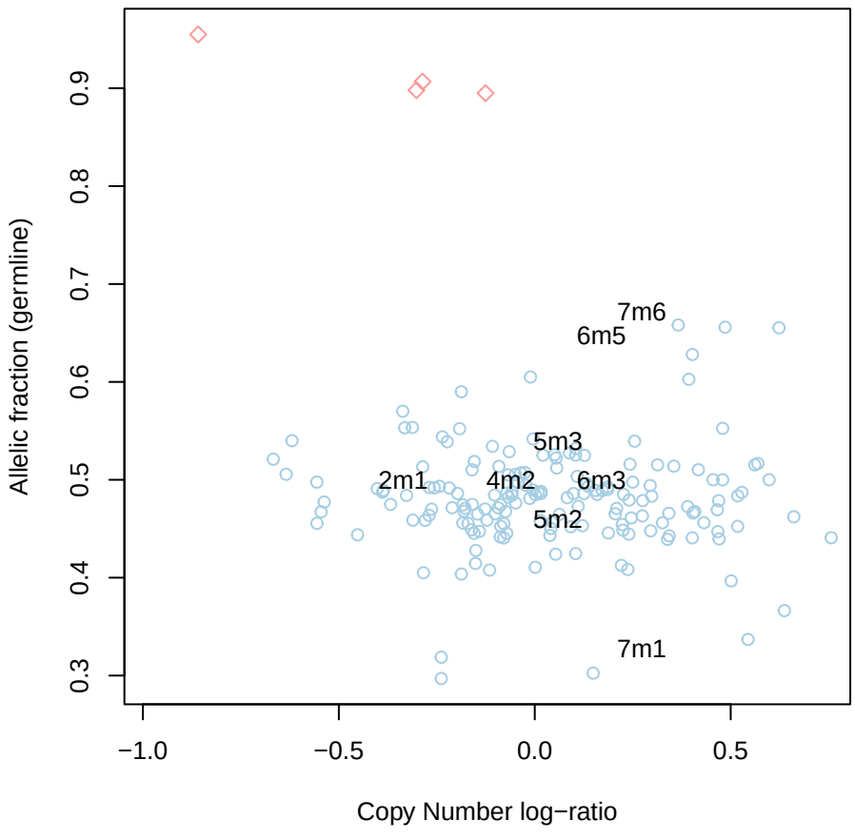

Frequency
Cellular fraction

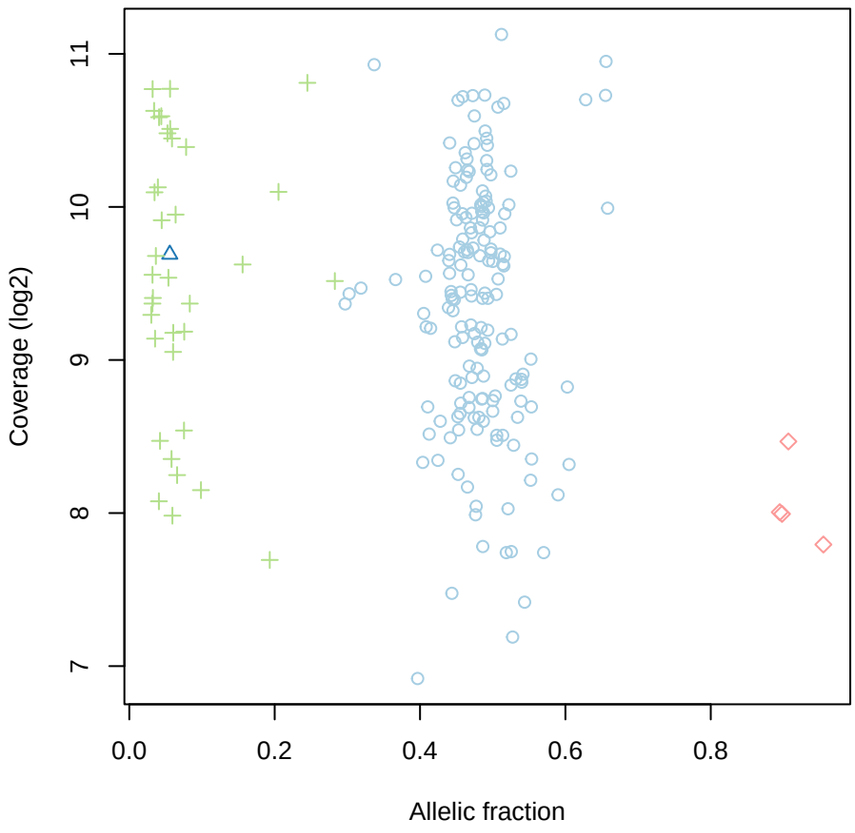

Purity: 0.21 Tumor ploidy: 4.494
1
2
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

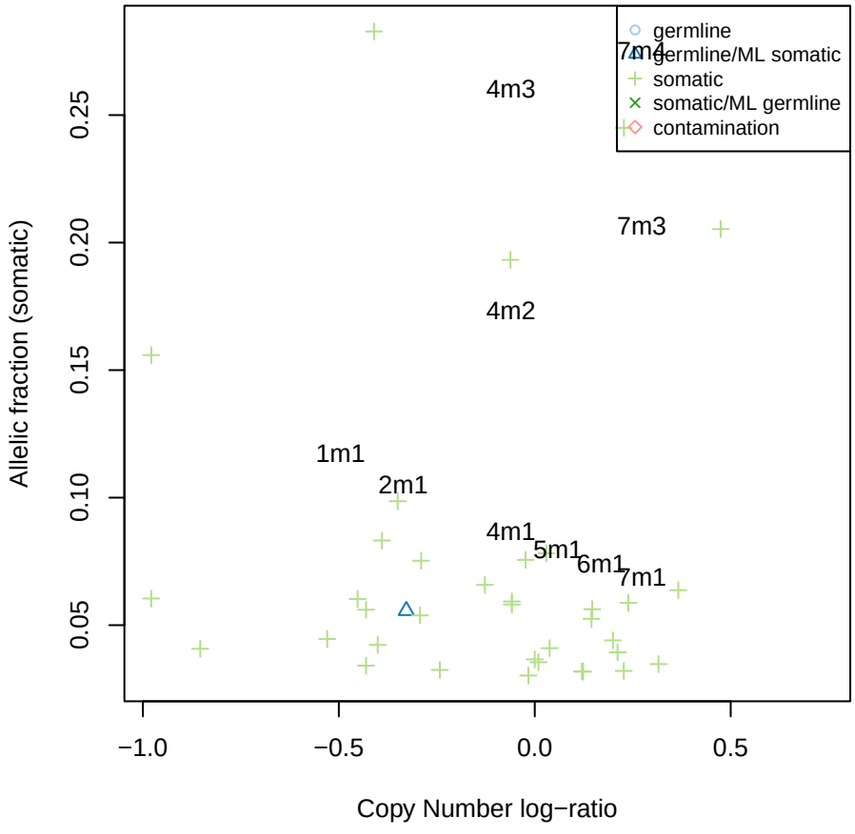

Purity: 0.21 Tumor ploidy: 4.494 SNV log−likelihood: −118.85 GoF: 97% Mean coverage: 774;145
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8 0.9
0 50 100 150
SNV Index

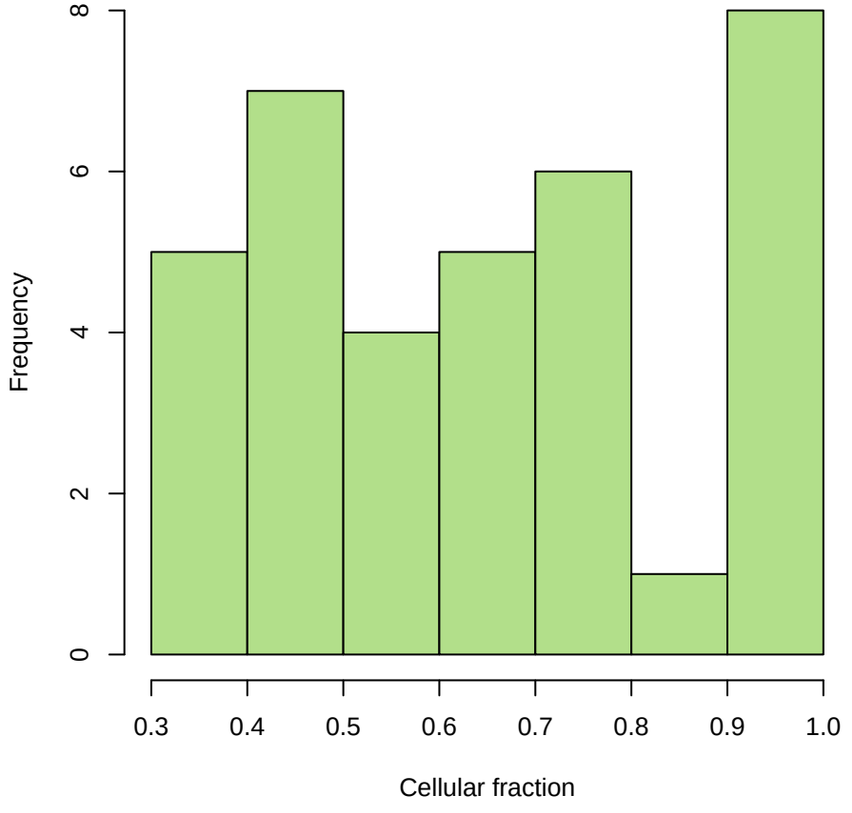

SCNA−fit log−likelihood: −23857.72
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 4 6
0 50 100 150
SNV Index

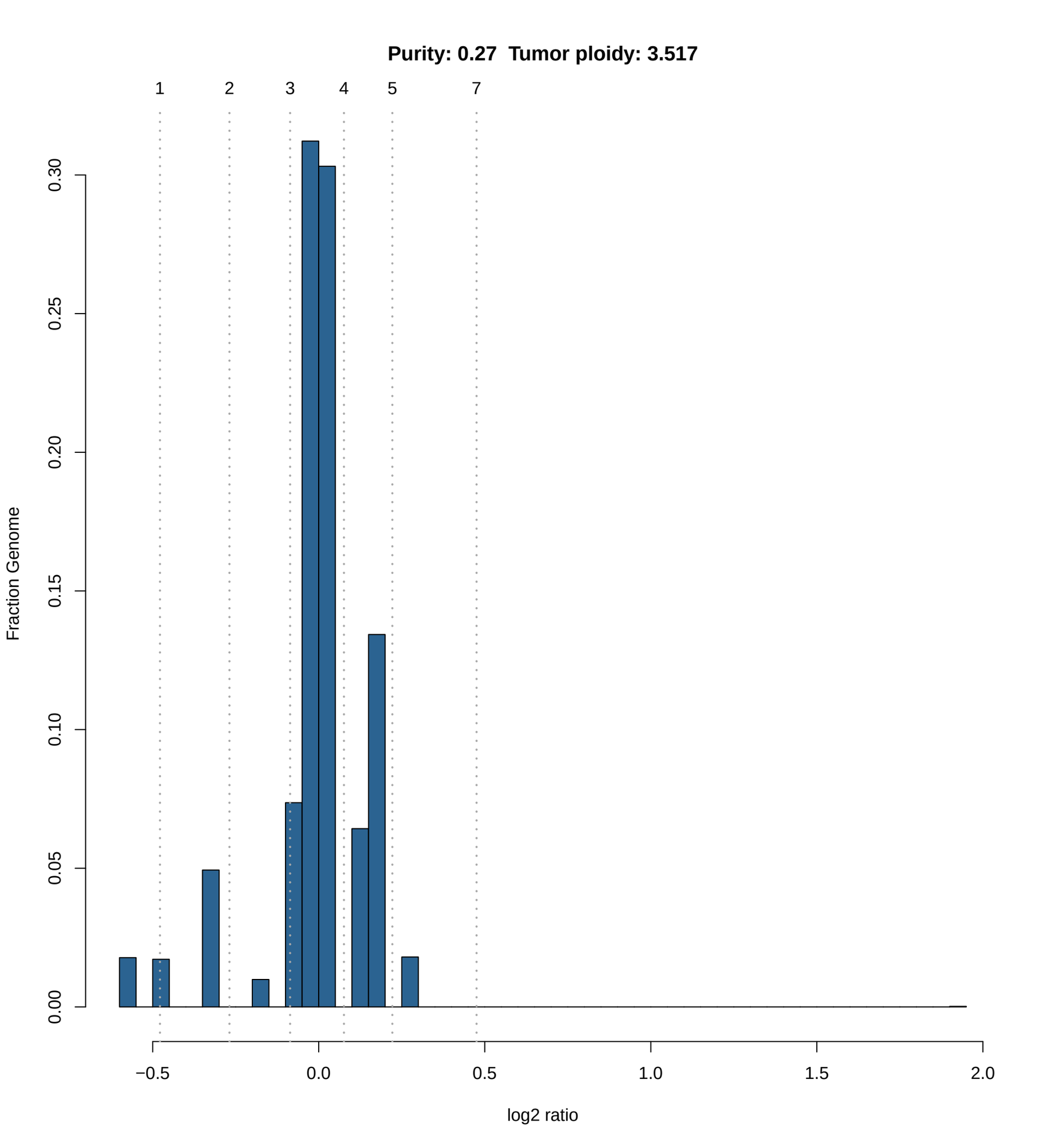

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

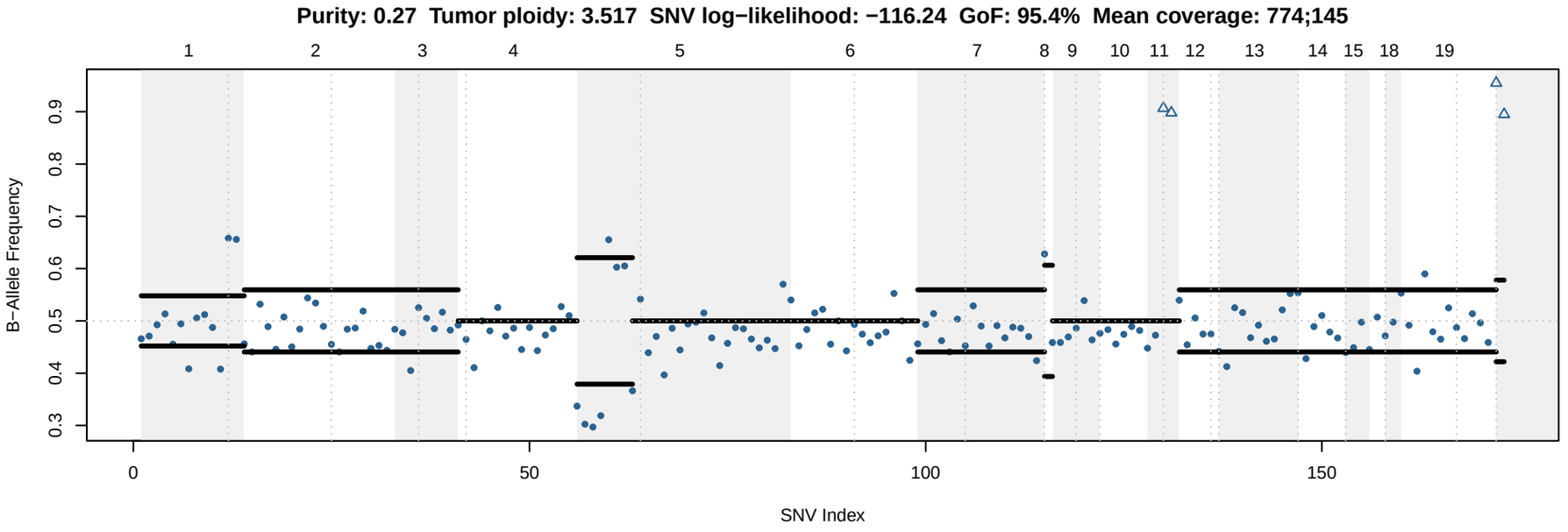

Allelic fraction (germline)
Copy Number log−ratio
7m6
6m5
5m3
2m1
4m2
6m3
5m2
7m1

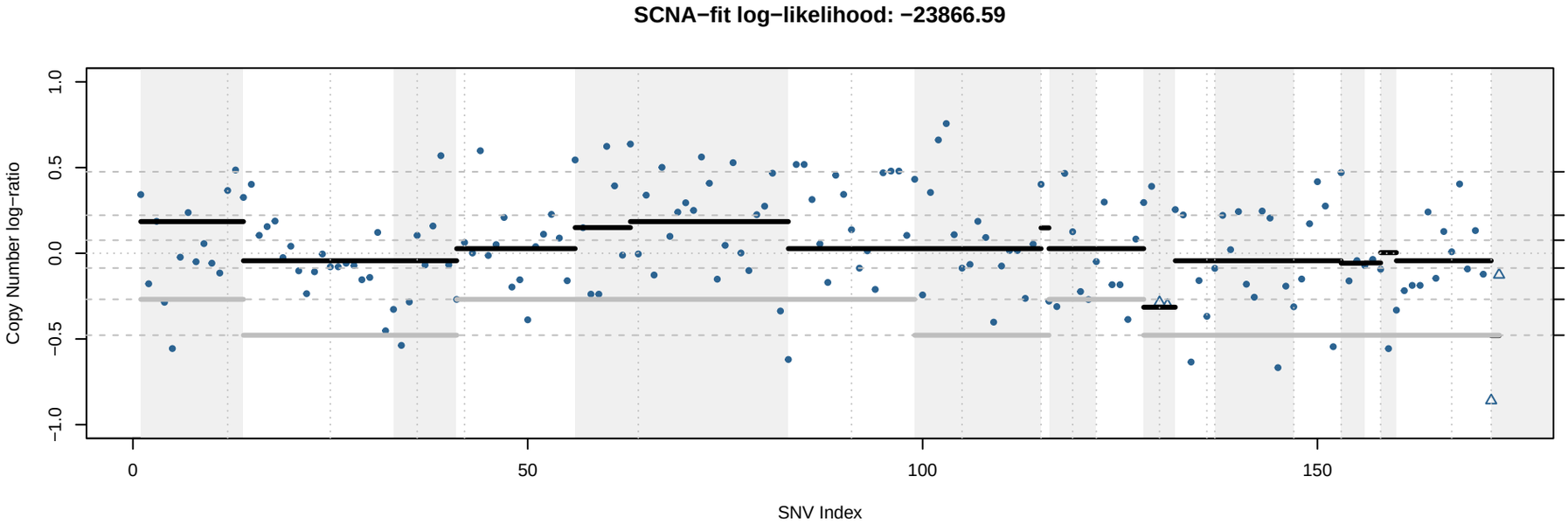

Coverage (log2)
Allelic fraction

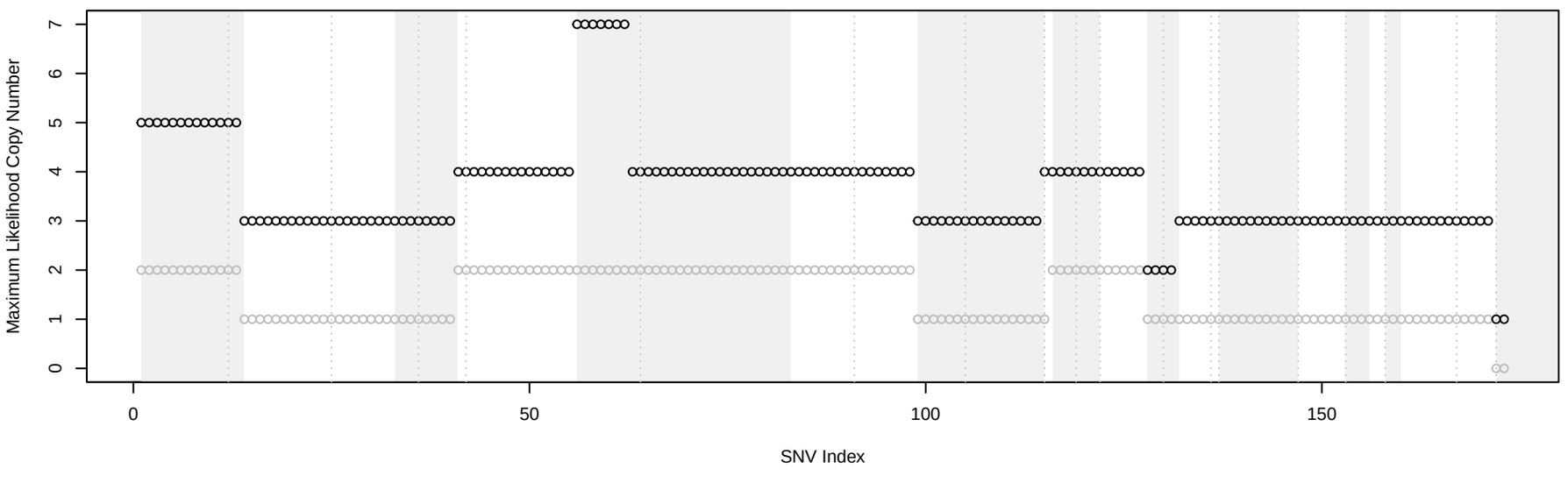

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
7m4
4m3
7m3
4m2
1m1
2m1
4m1
5m1
6m1
7m1

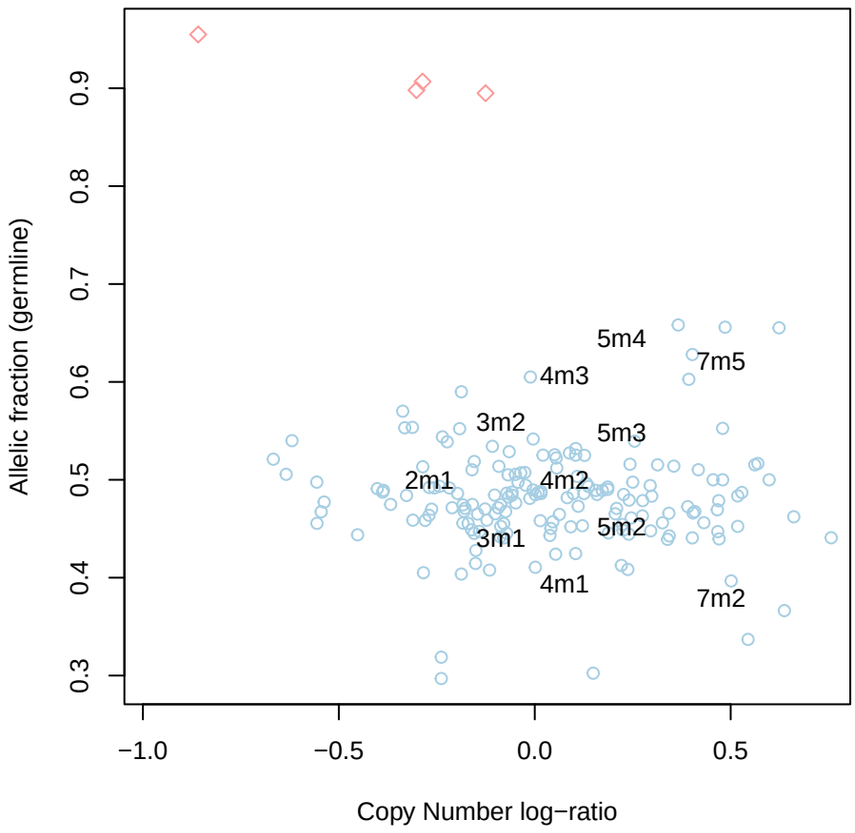

Frequency
Cellular fraction

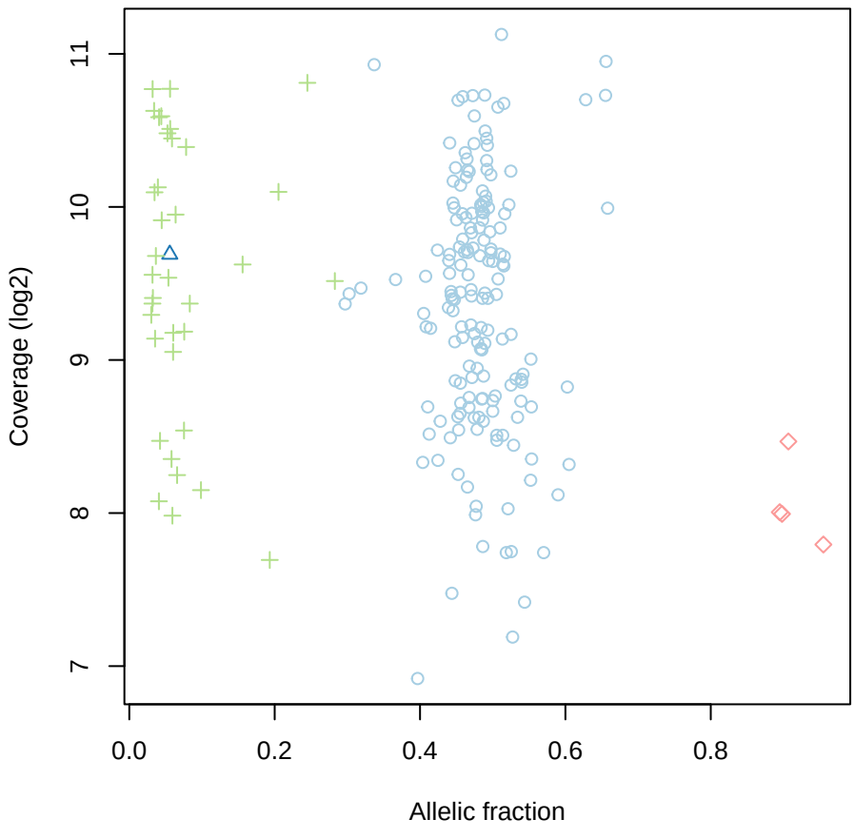

Purity: 0.27 Tumor ploidy: 3.517
1
2
3
4
5
7
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

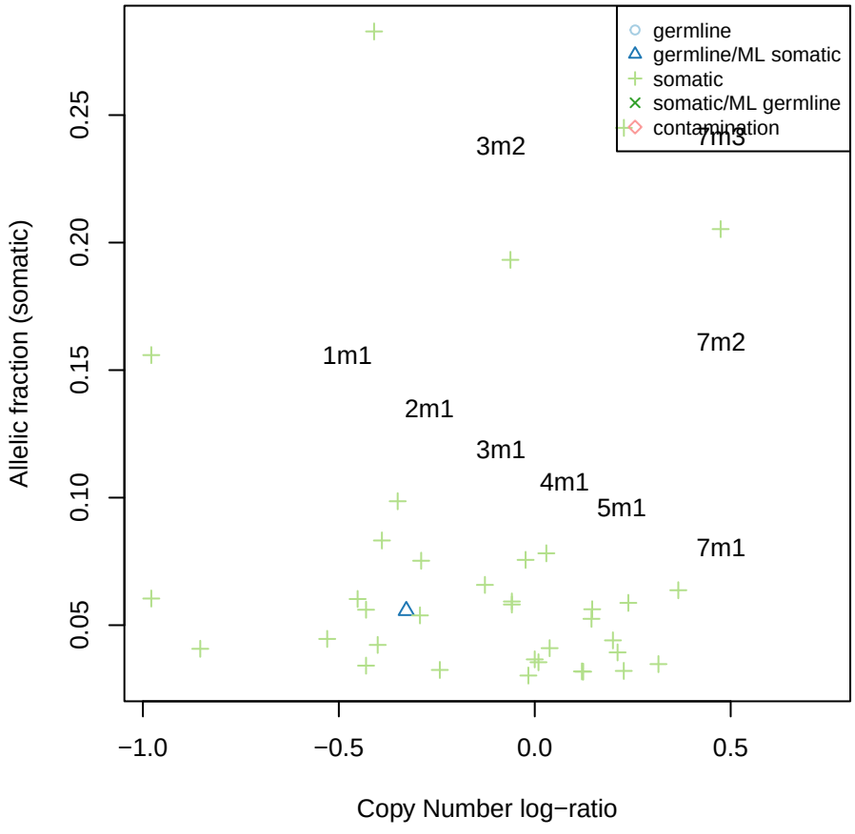

Purity: 0.27 Tumor ploidy: 3.517 SNV log−likelihood: −116.24 GoF: 95.4% Mean coverage: 774;145
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8 0.9
0 50 100 150
SNV Index

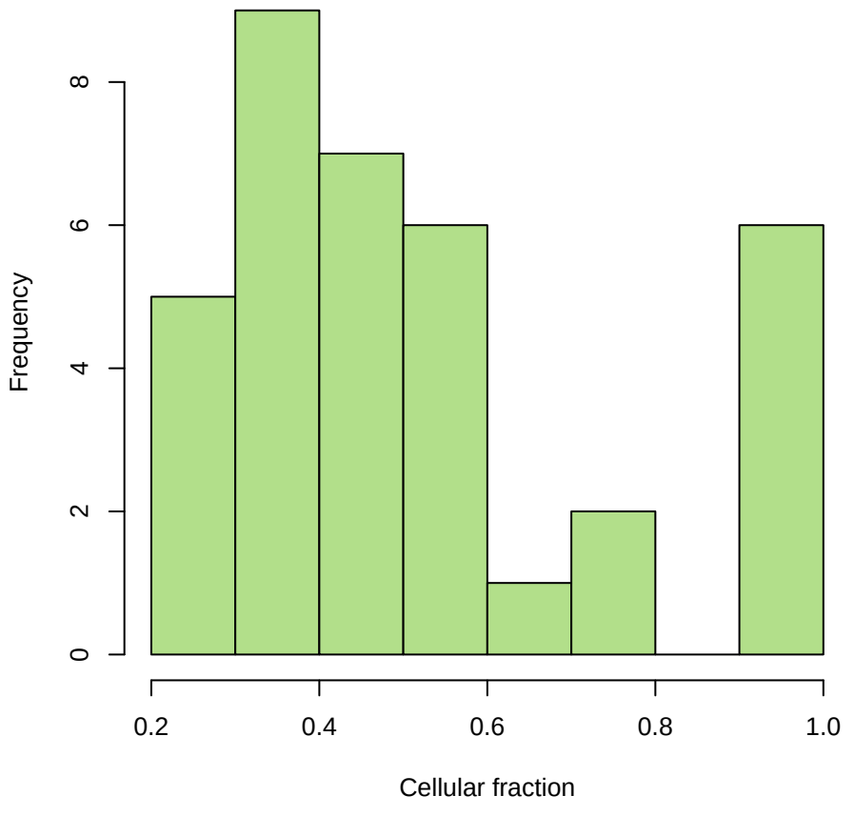

SCNA−fit log−likelihood: −23866.59
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 7
0 50 100 150
SNV Index

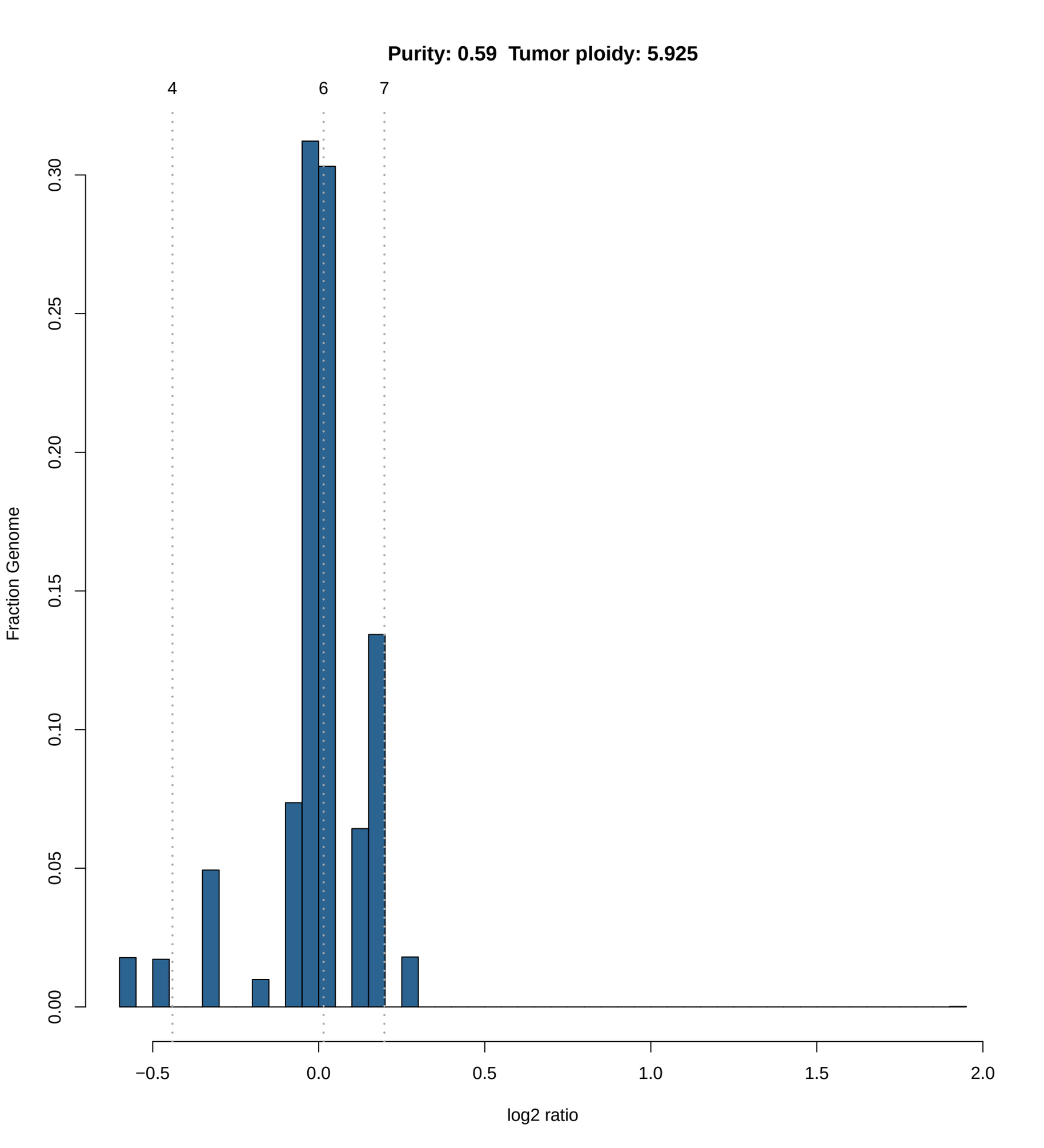

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

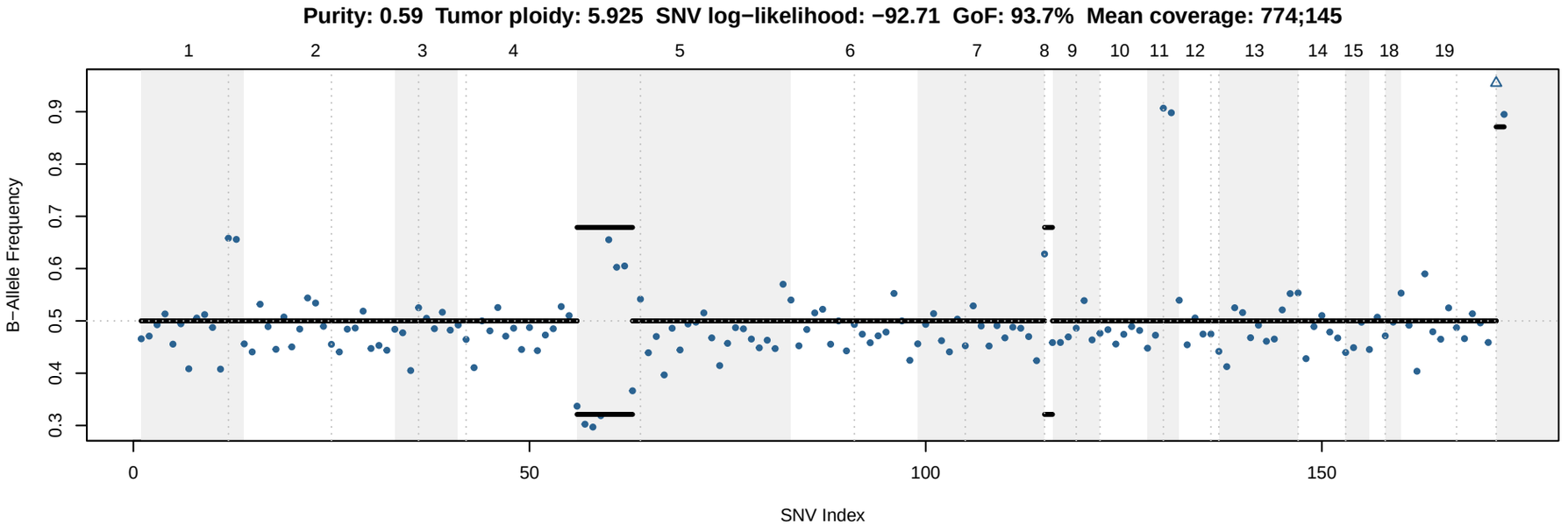

Allelic fraction (germline)
Copy Number log−ratio
5m4
7m5
4m3
3m2
5m3
2m1
4m2
5m2
3m1
4m1
7m2

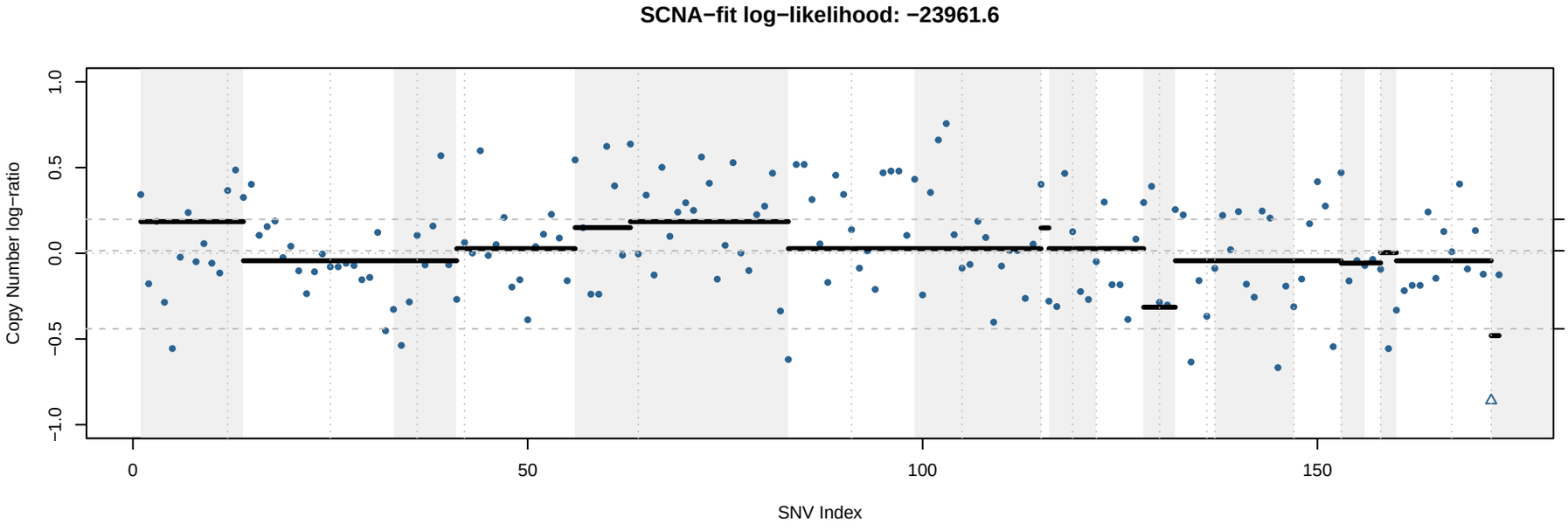

Coverage (log2)
Allelic fraction

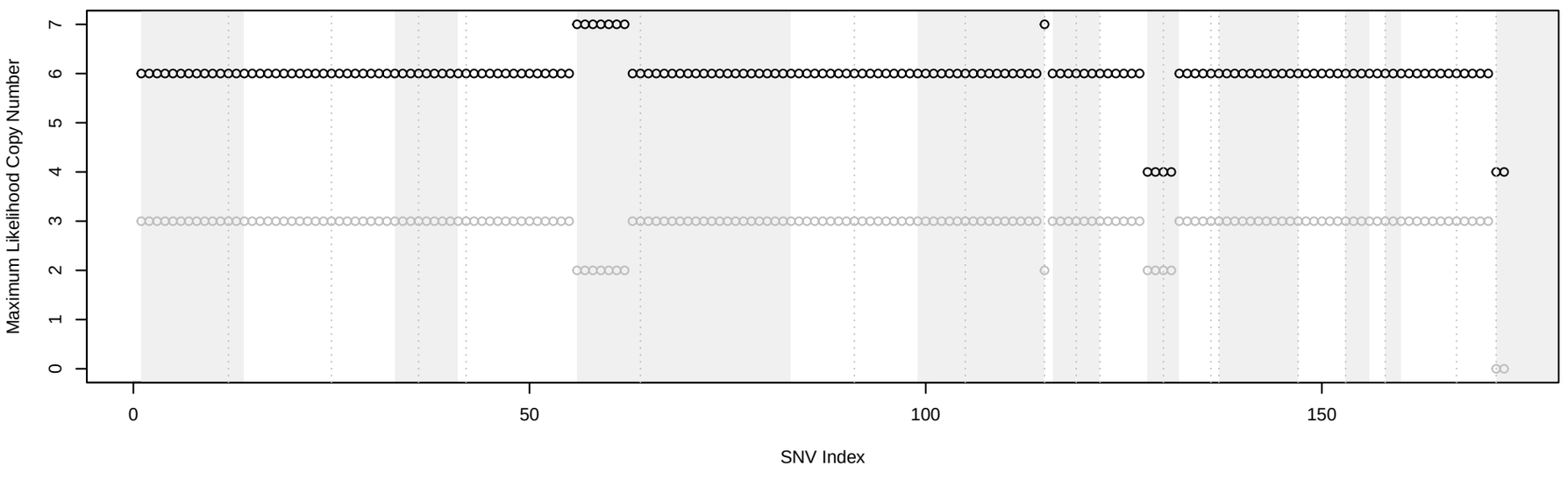

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m2
7m3
7m2
1m1
2m1
3m1
4m1
5m1
7m1


Frequency
Cellular fraction

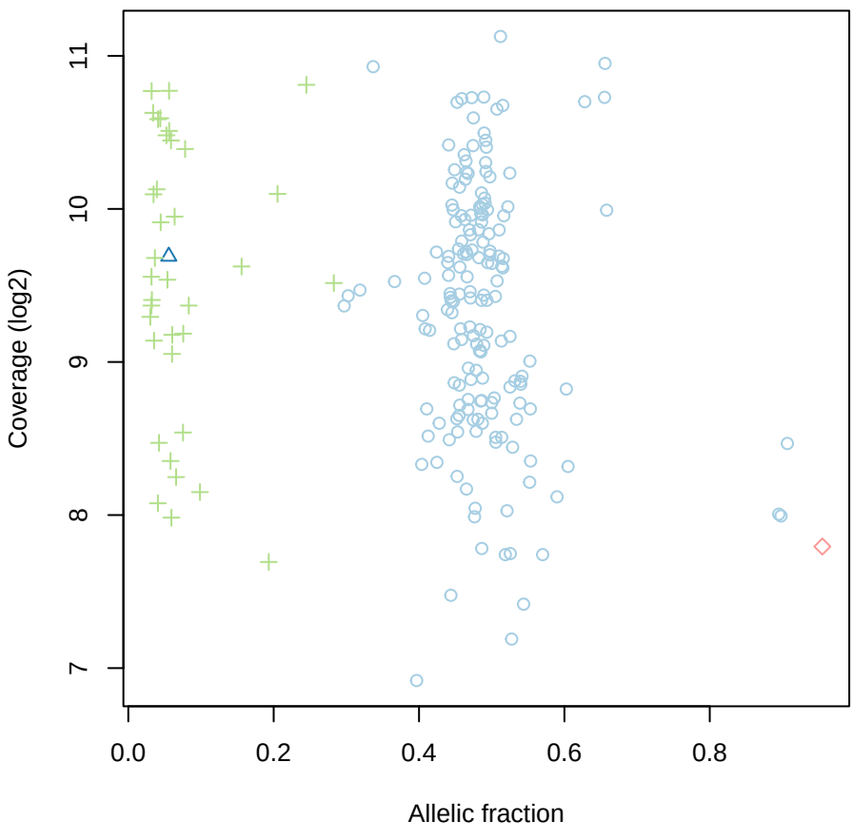

Purity: 0.59 Tumor ploidy: 5.925
4
6
7
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

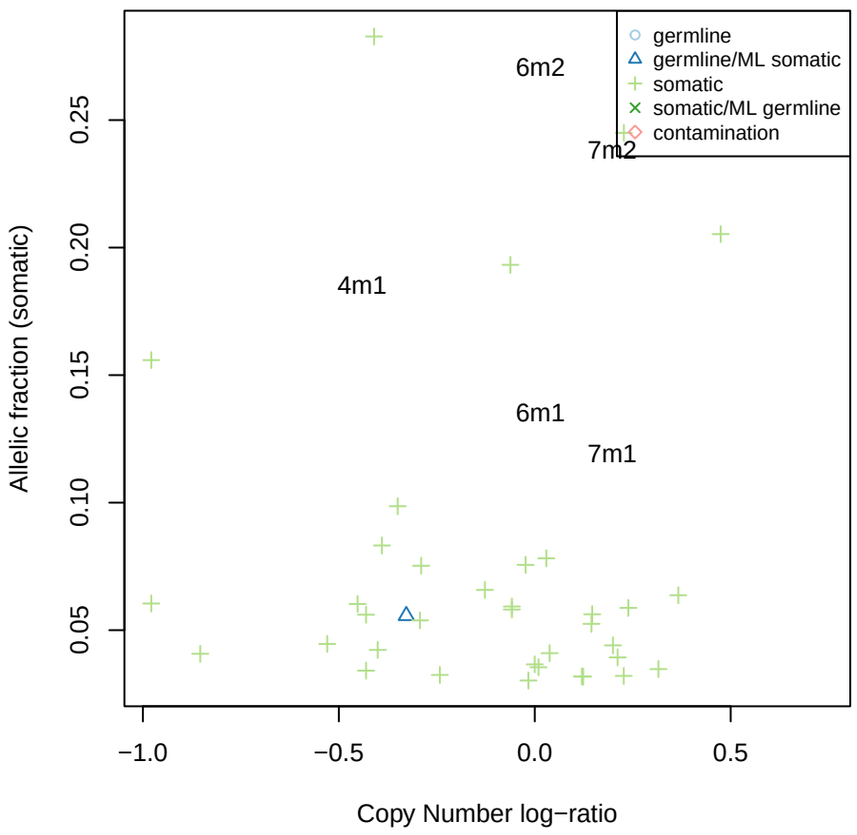

Purity: 0.59 Tumor ploidy: 5.925 SNV log−likelihood: −92.71 GoF: 93.7% Mean coverage: 774;145
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8 0.9
0 50 100 150
SNV Index

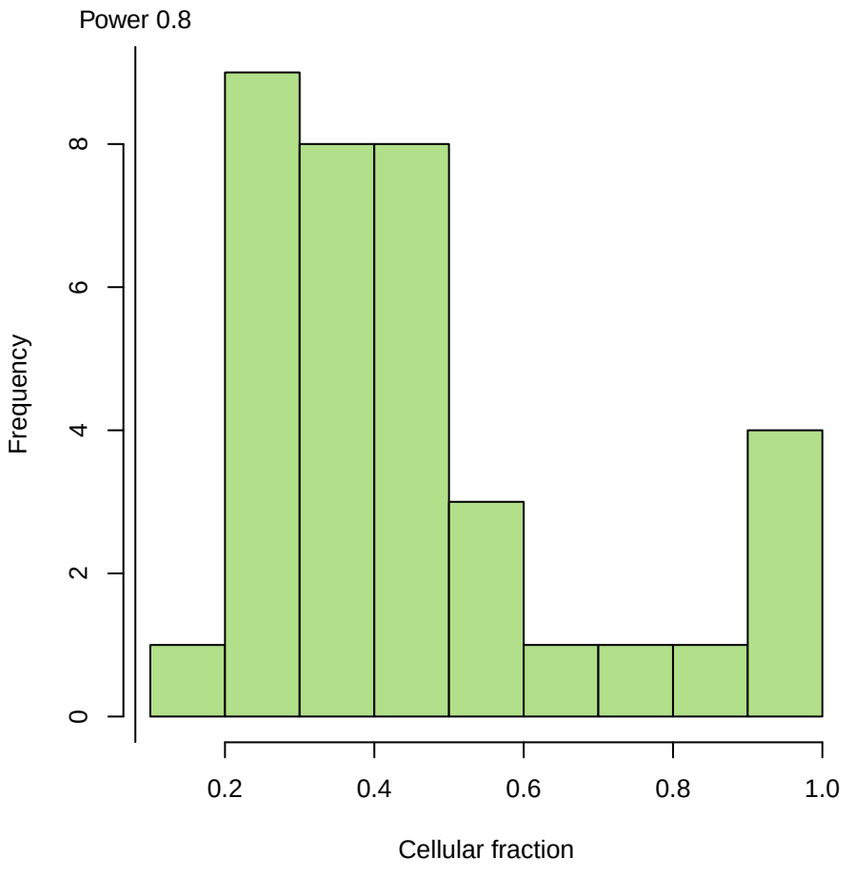

SCNA−fit log−likelihood: −23961.6
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 6 7
0 50 100 150
SNV Index

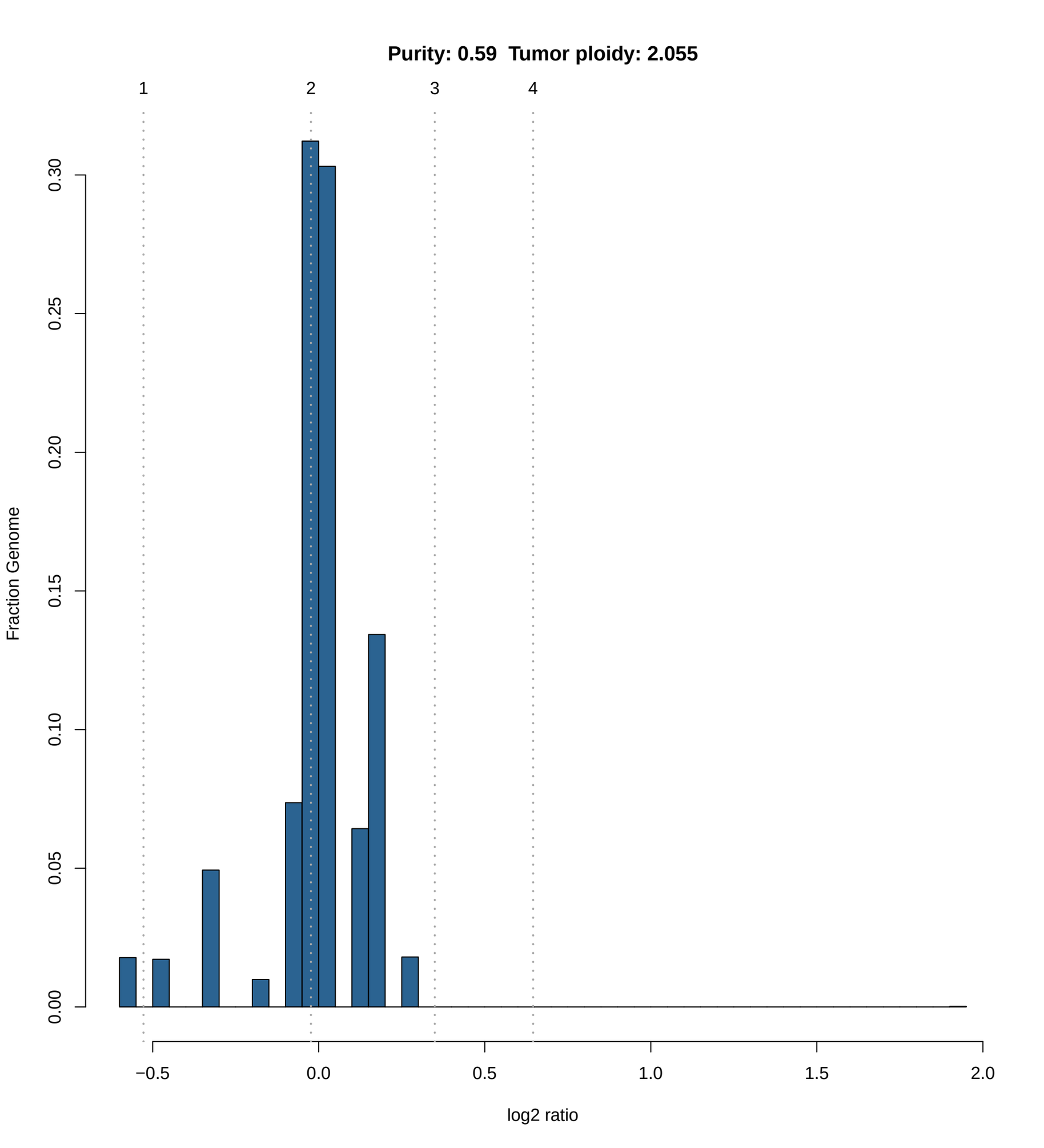

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

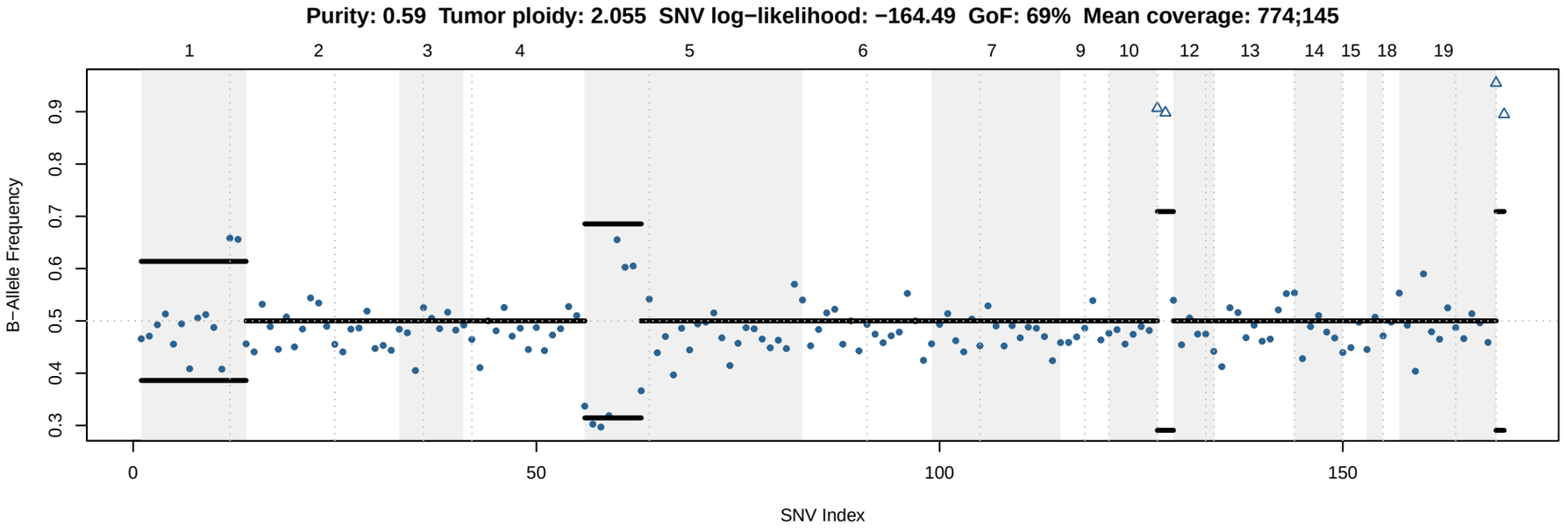
Allelic fraction (germline)
Copy Number log−ratio
4m4
7m5
6m4
4m2
6m3
7m2

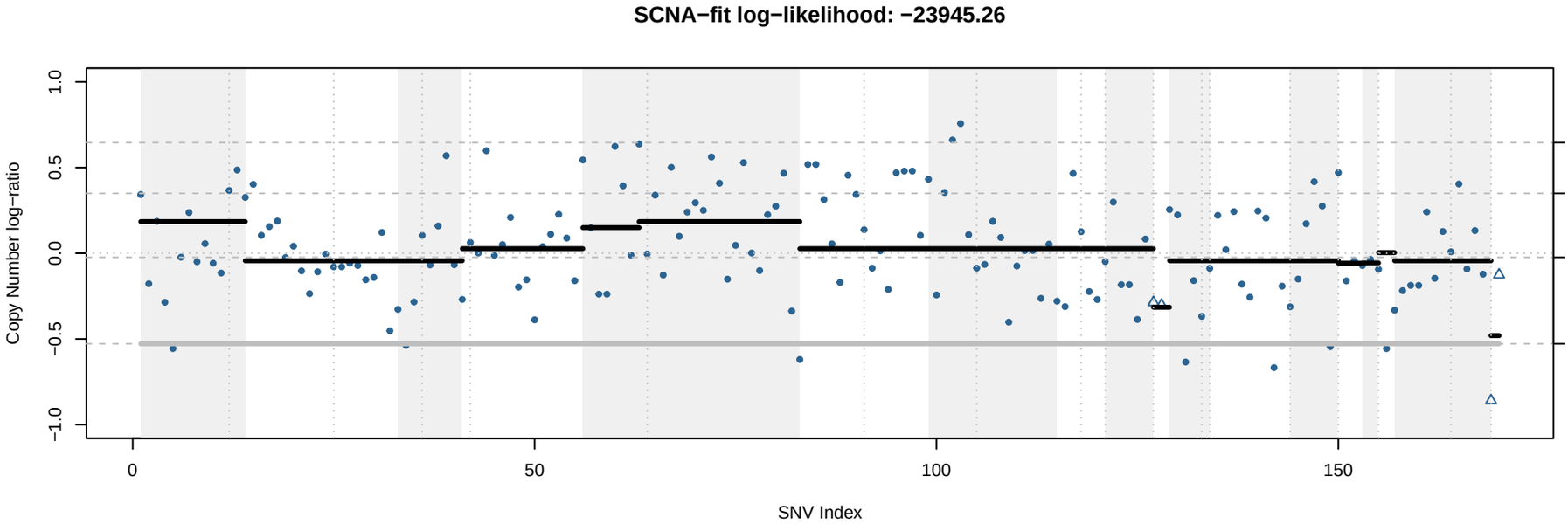

Coverage (log2)
Allelic fraction

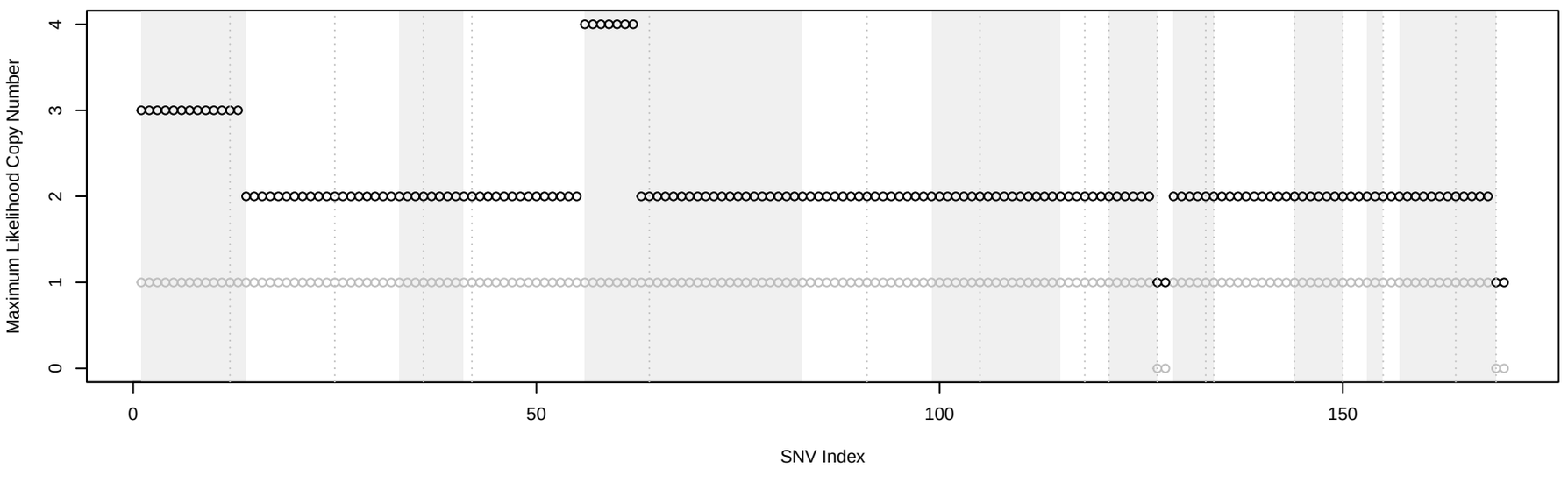

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m2
7m2
4m1
6m1
7m1

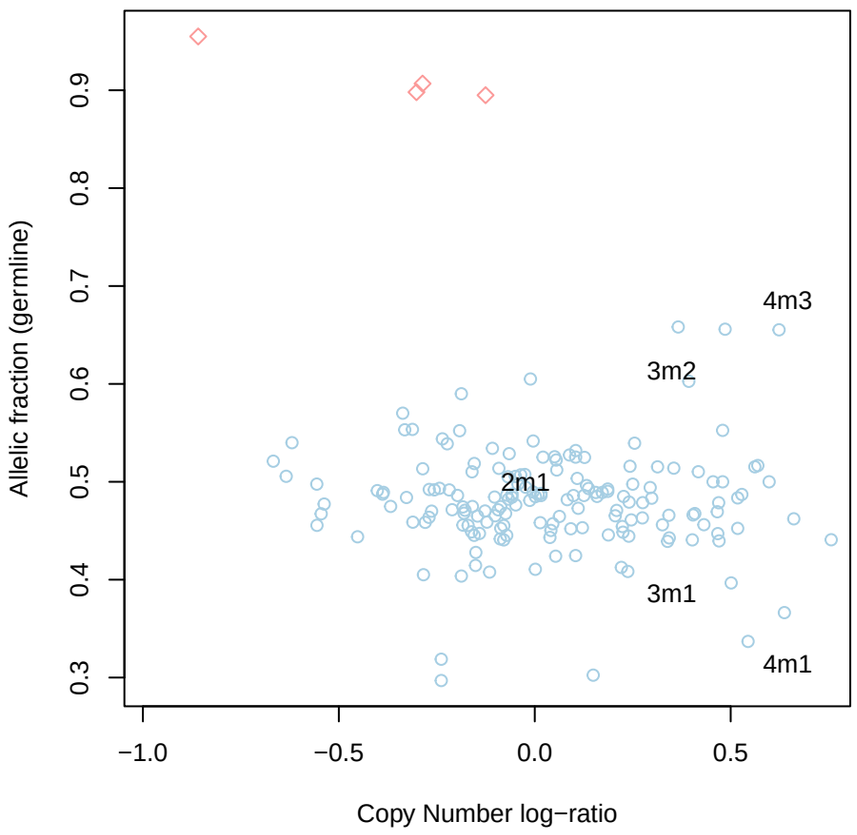

Power 0.8
Frequency
Cellular fraction

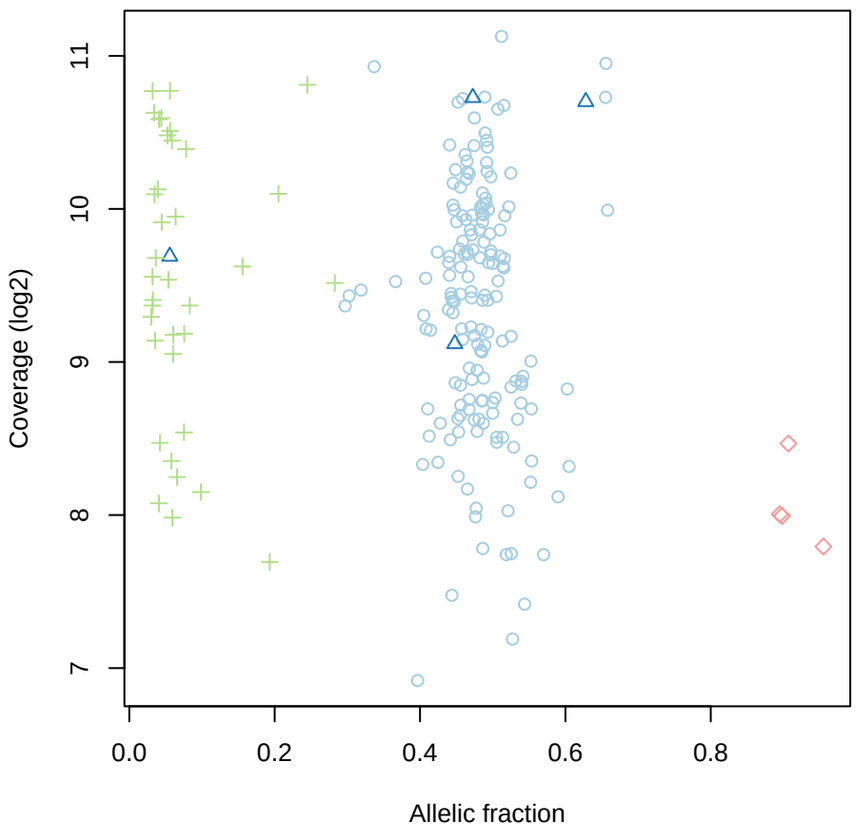

Purity: 0.59 Tumor ploidy: 2.055
1
2
3
4
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

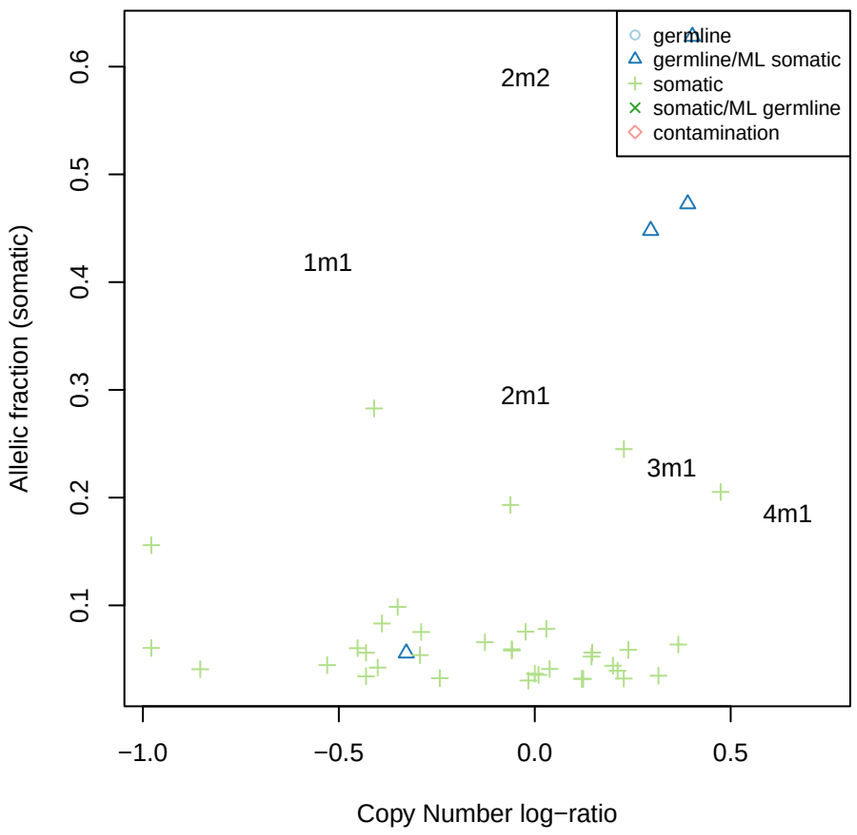

Purity: 0.59 Tumor ploidy: 2.055 SNV log−likelihood: −164.49 GoF: 69% Mean coverage: 774;145
1 2 3 4 5 6 7 9 10 12 13 14 15 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8 0.9
0 50 100 150
SNV Index

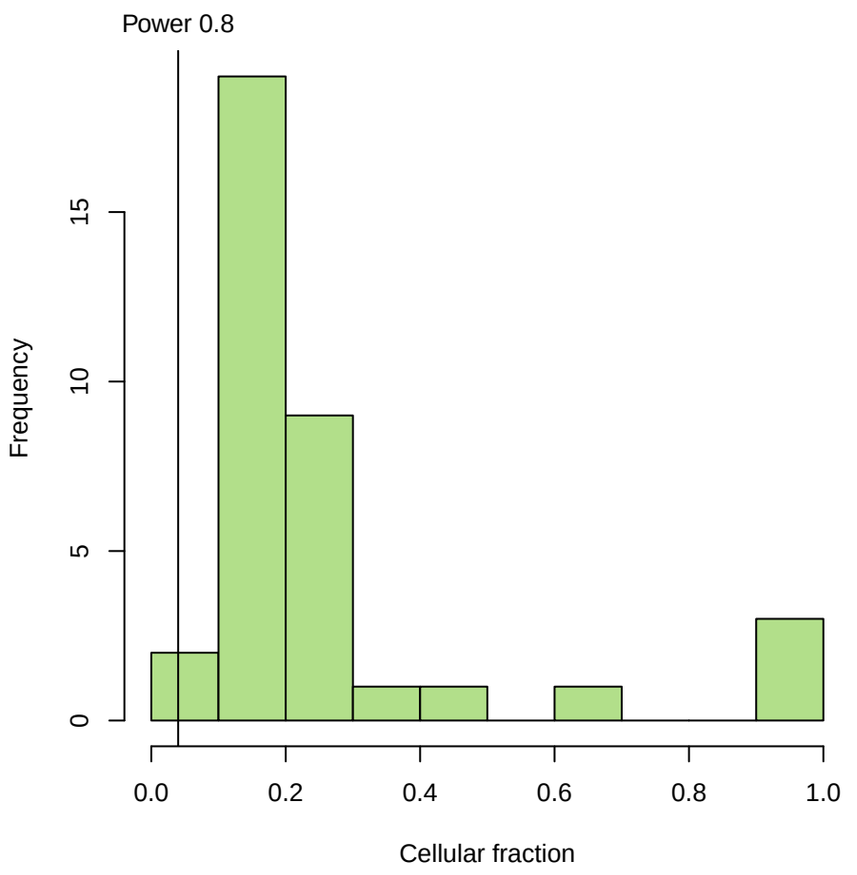

SCNA−fit log−likelihood: −23945.26
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4
0 50 100 150
SNV Index

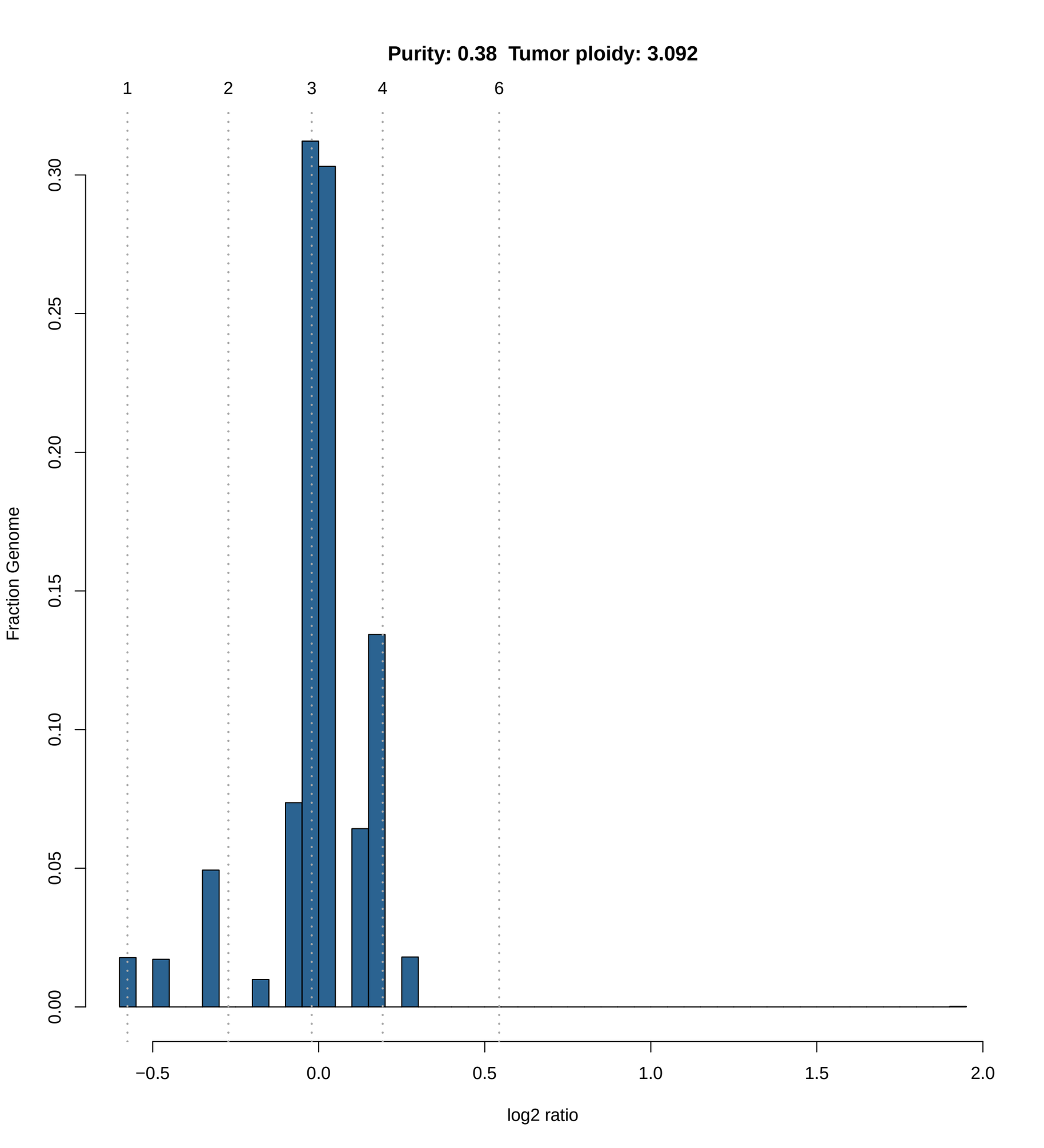

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

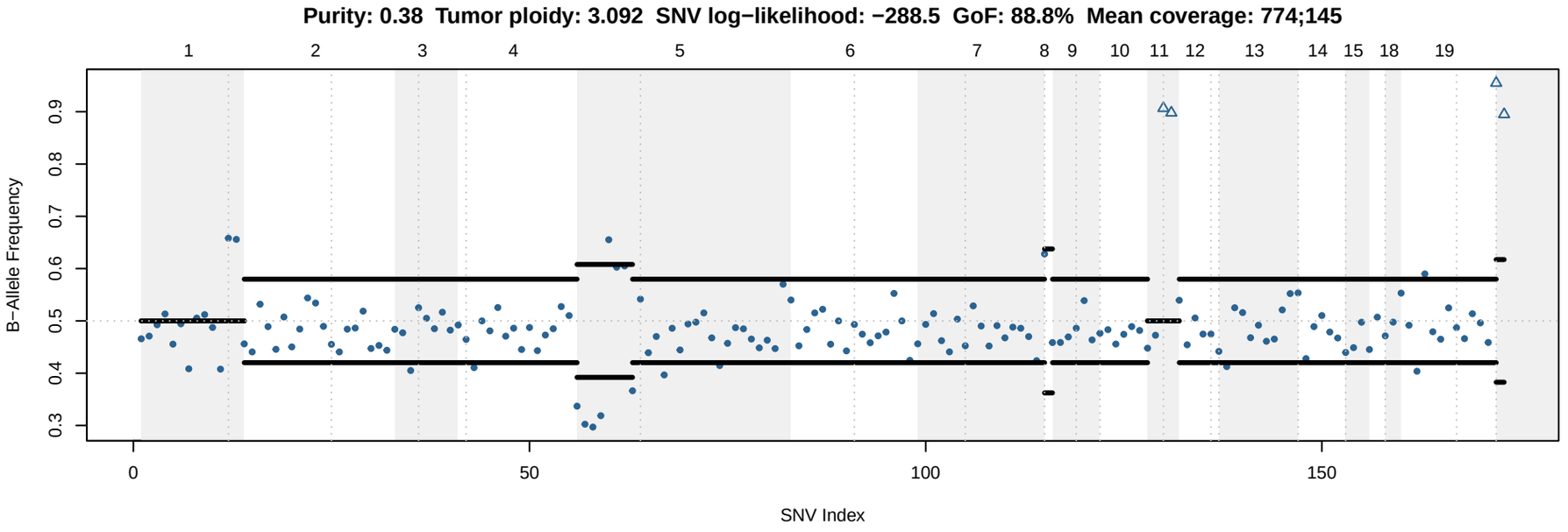

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
2m1
3m1
4m1

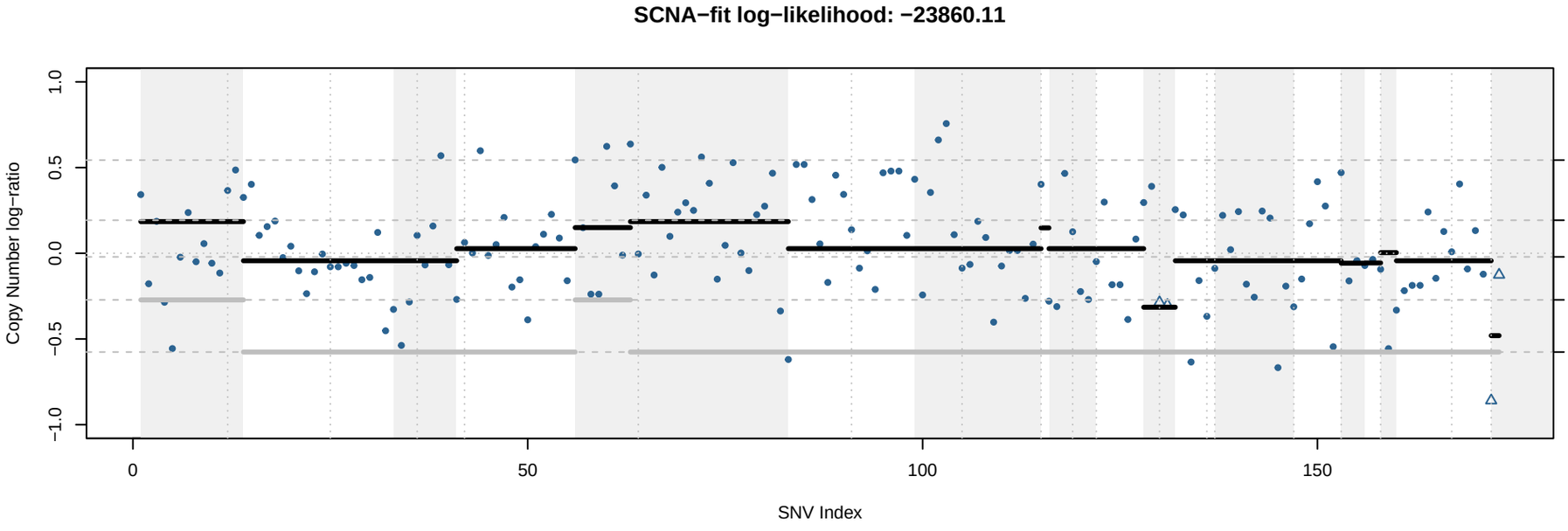

Coverage (log2)
Allelic fraction

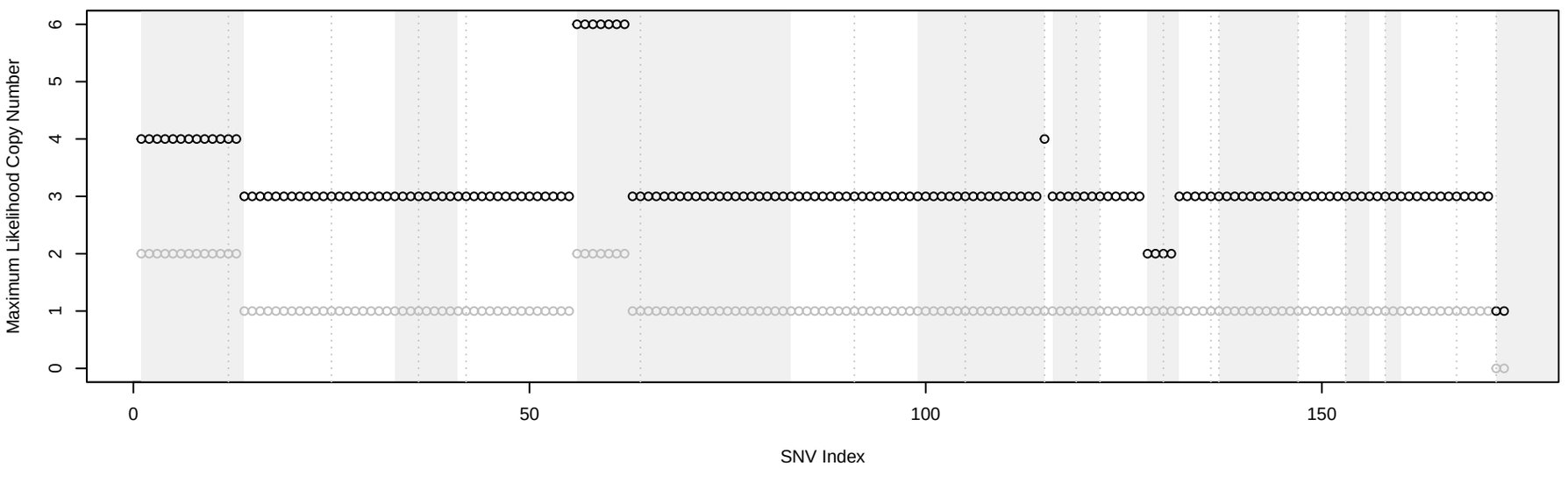

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
1m1
2m1
3m1
4m1

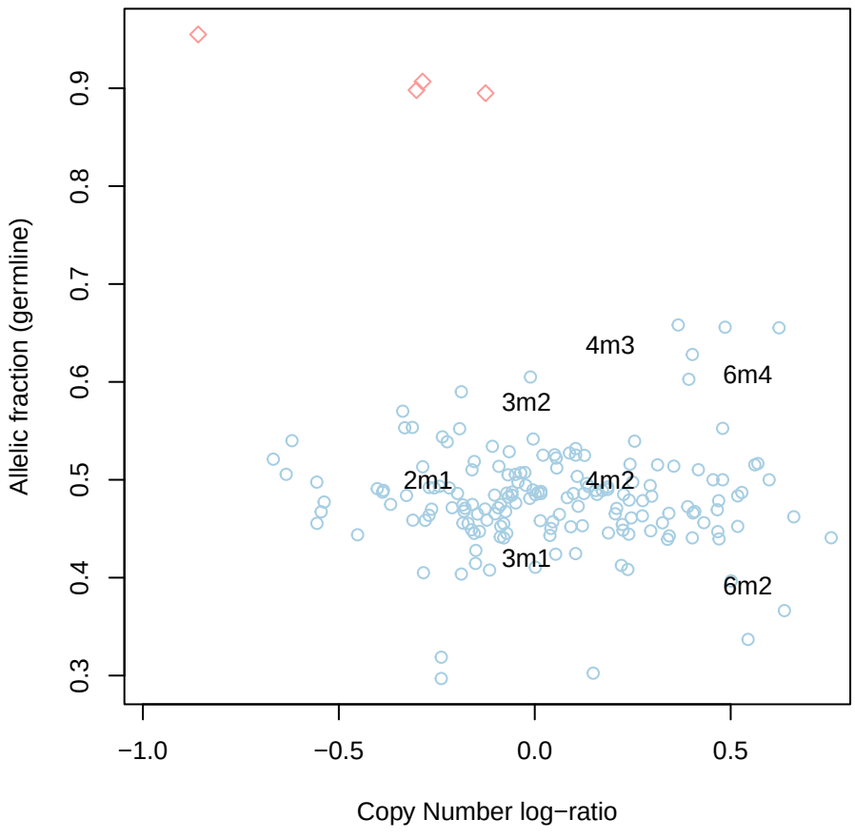

Power 0.8
Frequency
Cellular fraction

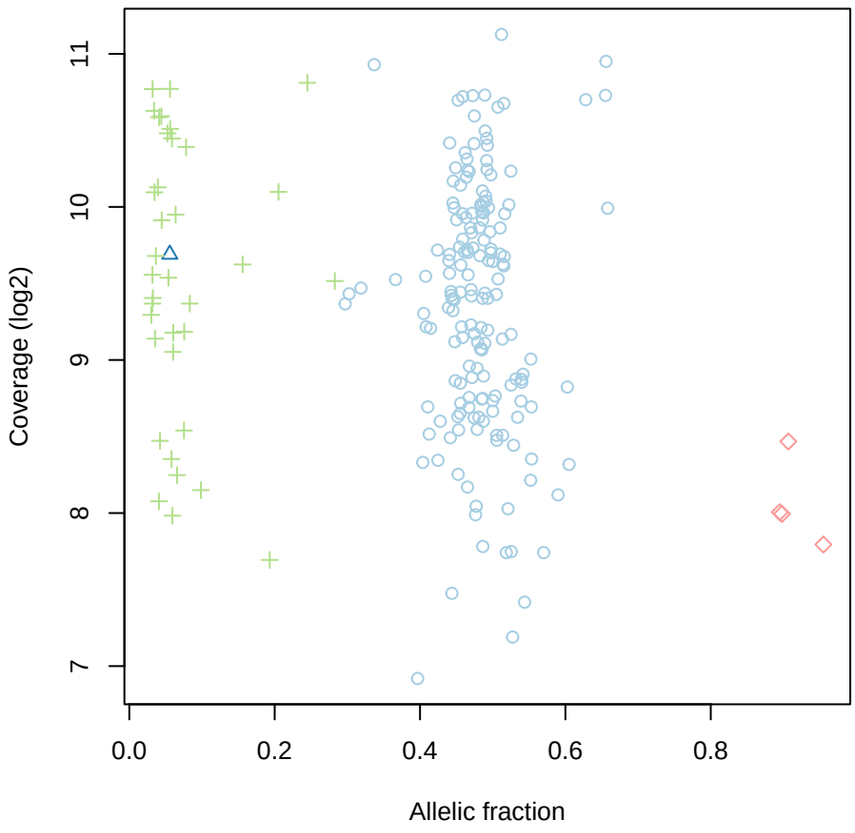

Purity: 0.38 Tumor ploidy: 3.092
1
2
3
4
6
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

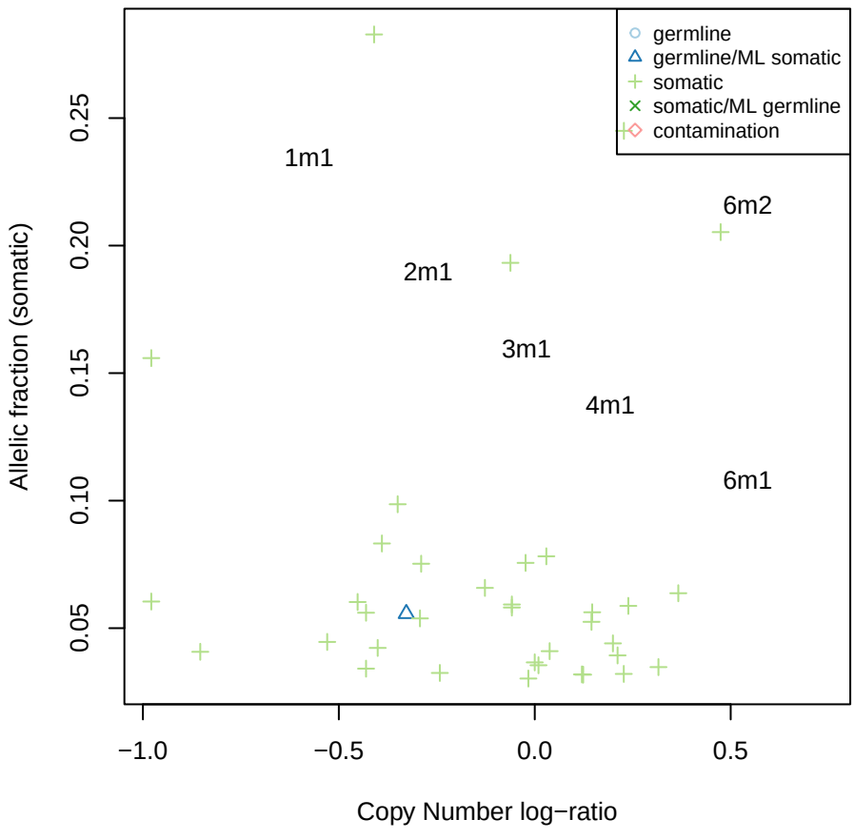

Purity: 0.38 Tumor ploidy: 3.092 SNV log−likelihood: −288.5 GoF: 88.8% Mean coverage: 774;145
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8 0.9
0 50 100 150
SNV Index

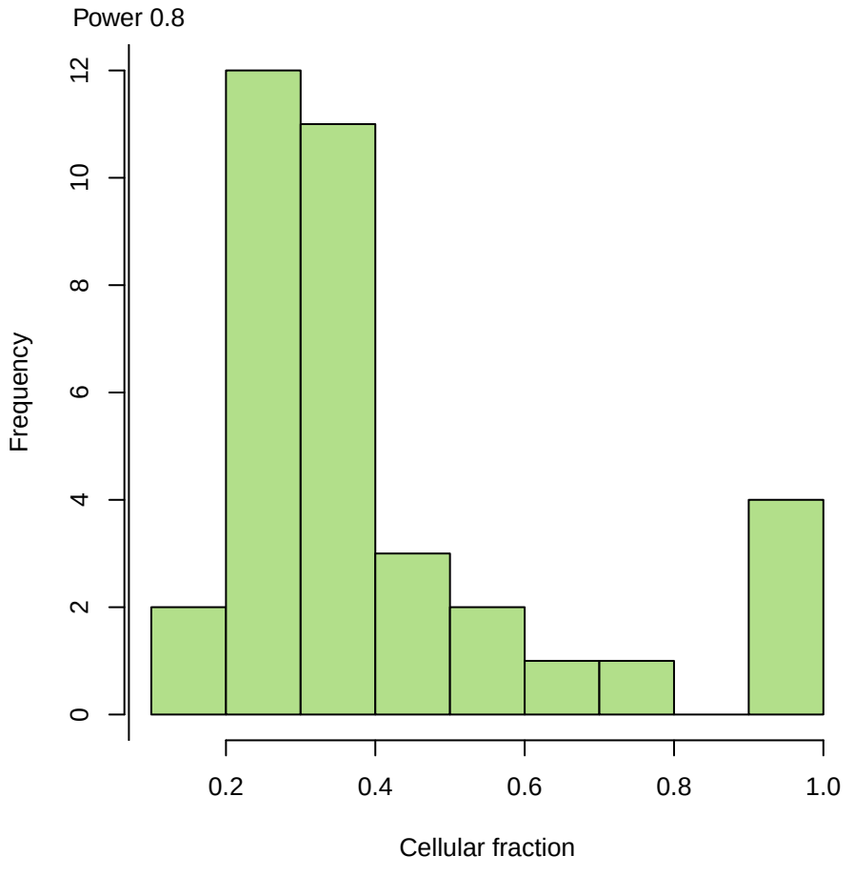

SCNA−fit log−likelihood: −23860.11
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 6
0 50 100 150
SNV Index

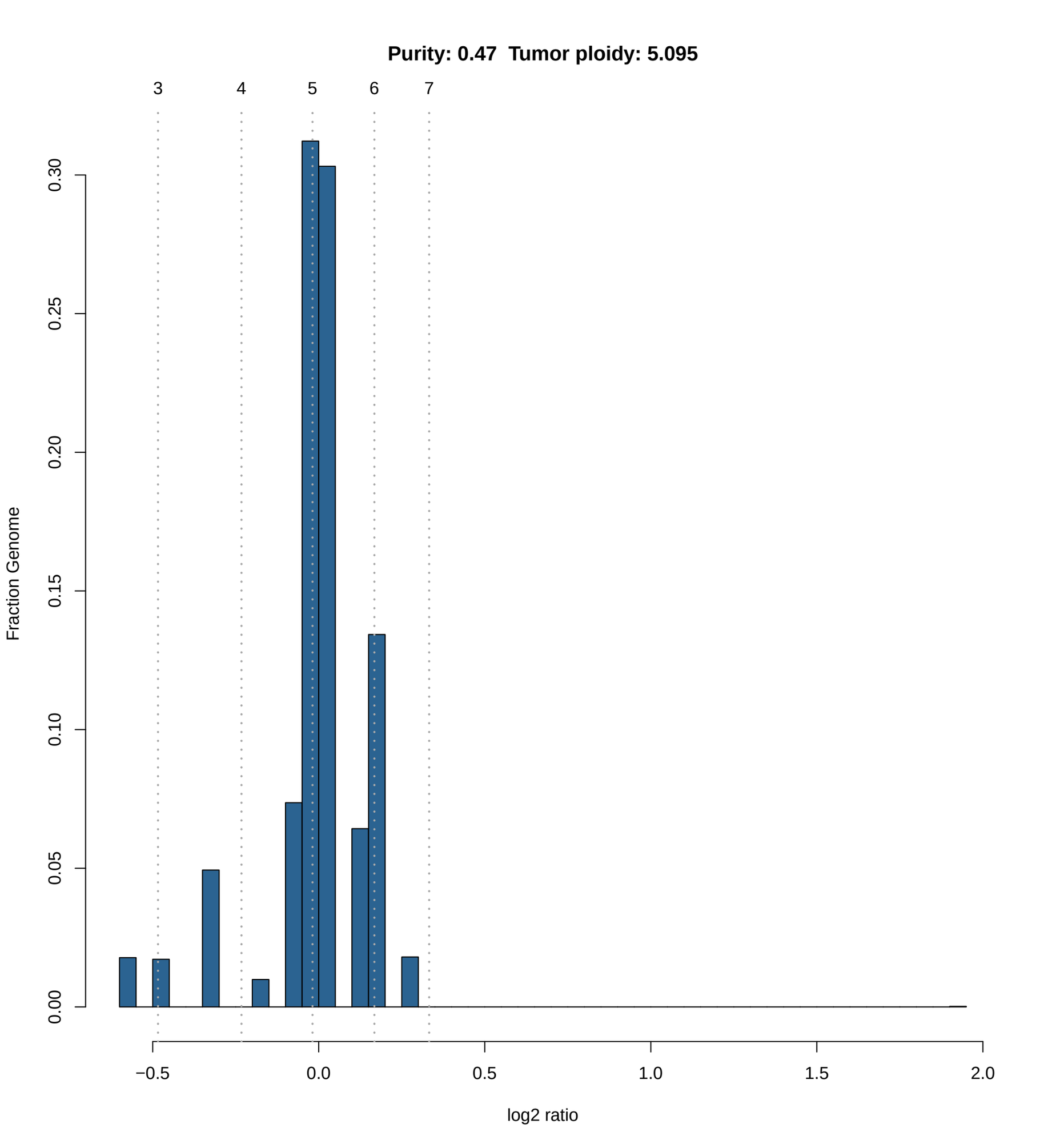

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

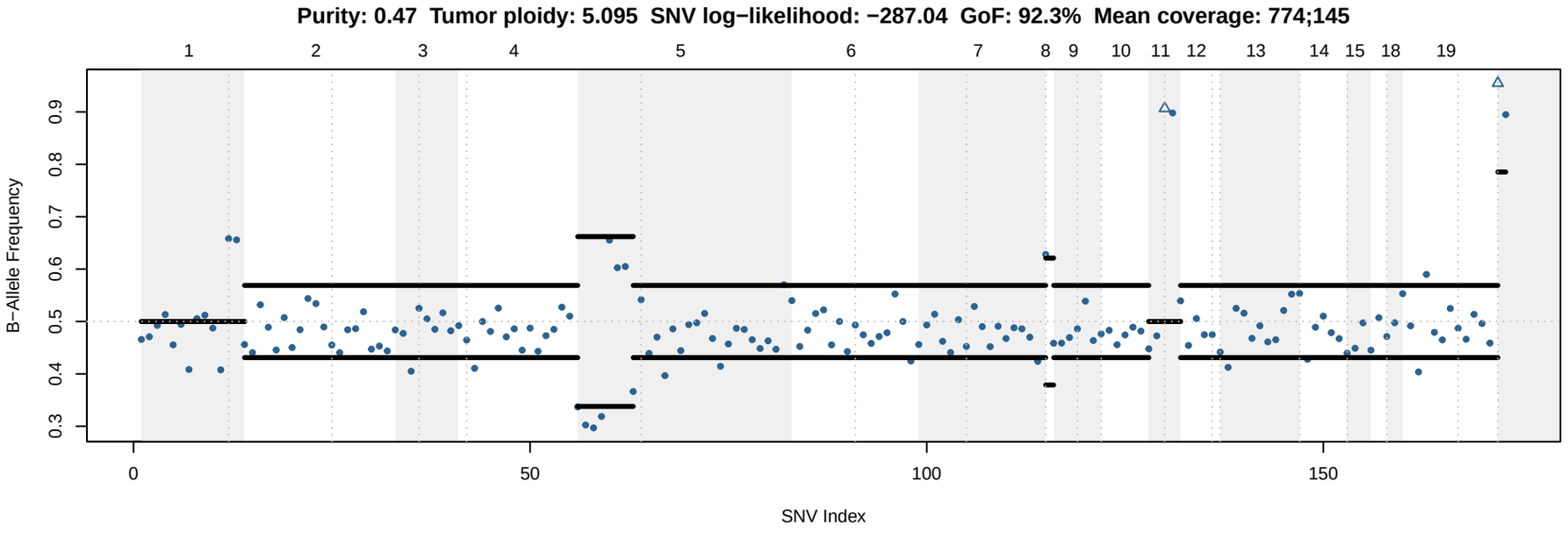

Allelic fraction (germline)
Copy Number log−ratio
4m3
6m4
3m2
2m1
4m2
3m1
6m2

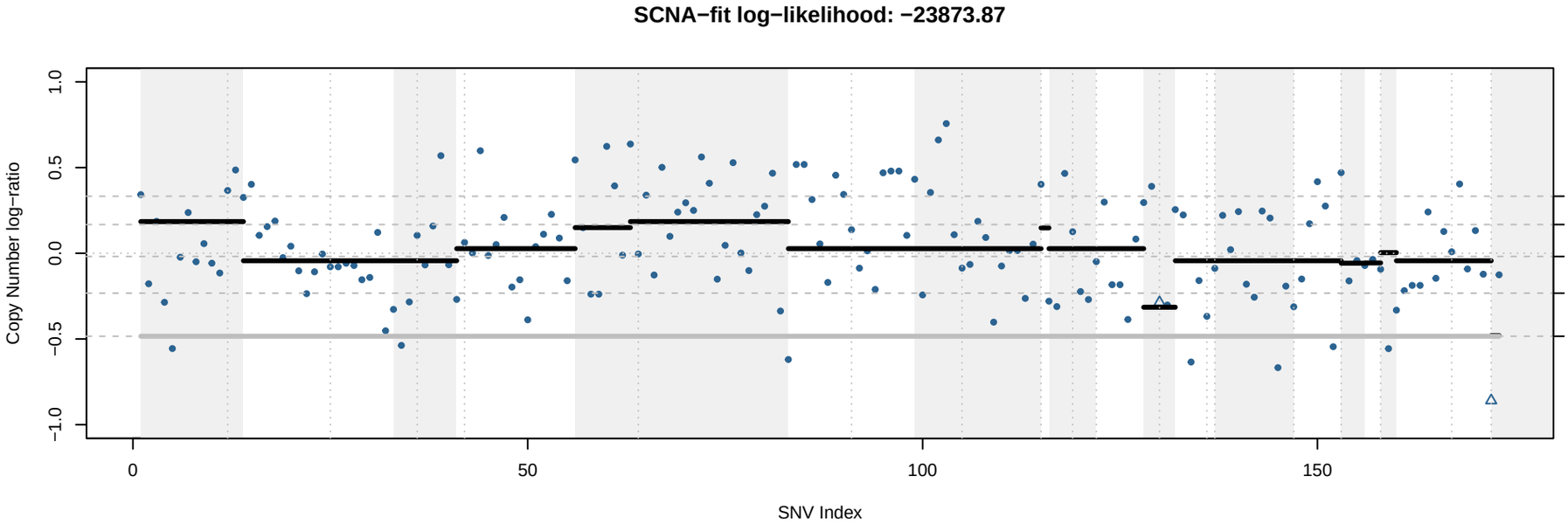

Coverage (log2)
Allelic fraction

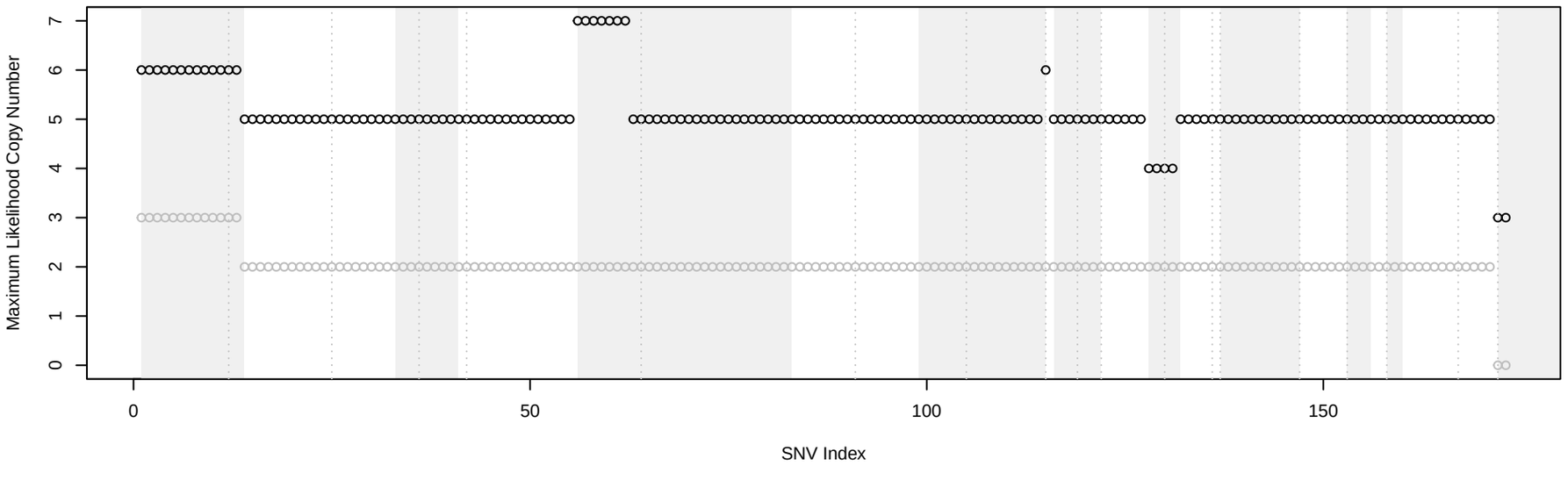

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
6m2
2m1
3m1
4m1
6m1

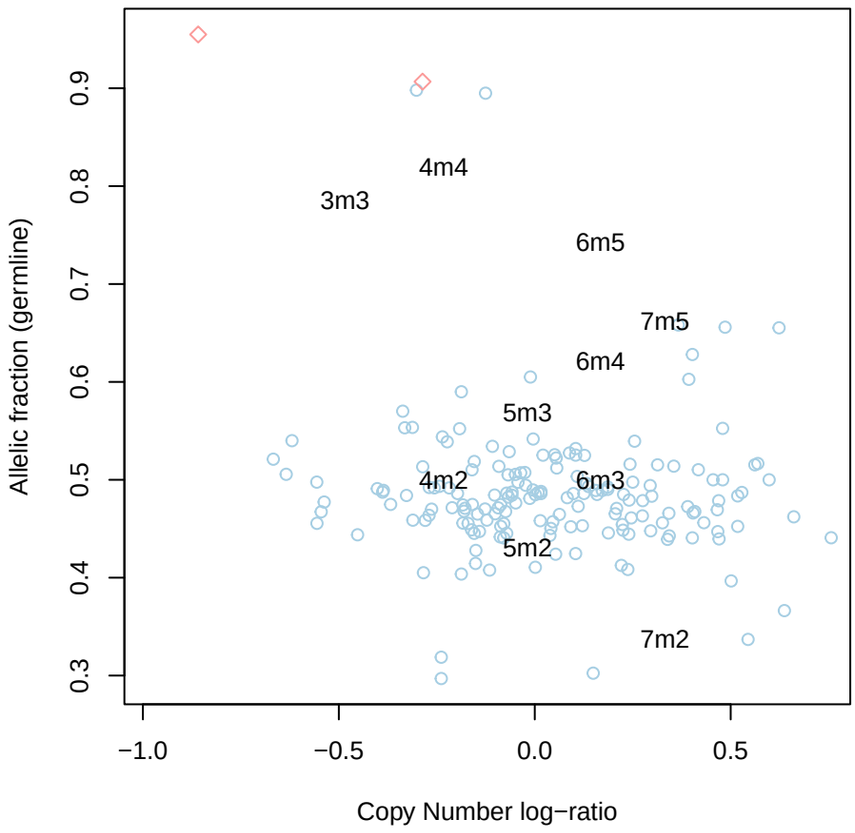

Power 0.8
Frequency
Cellular fraction

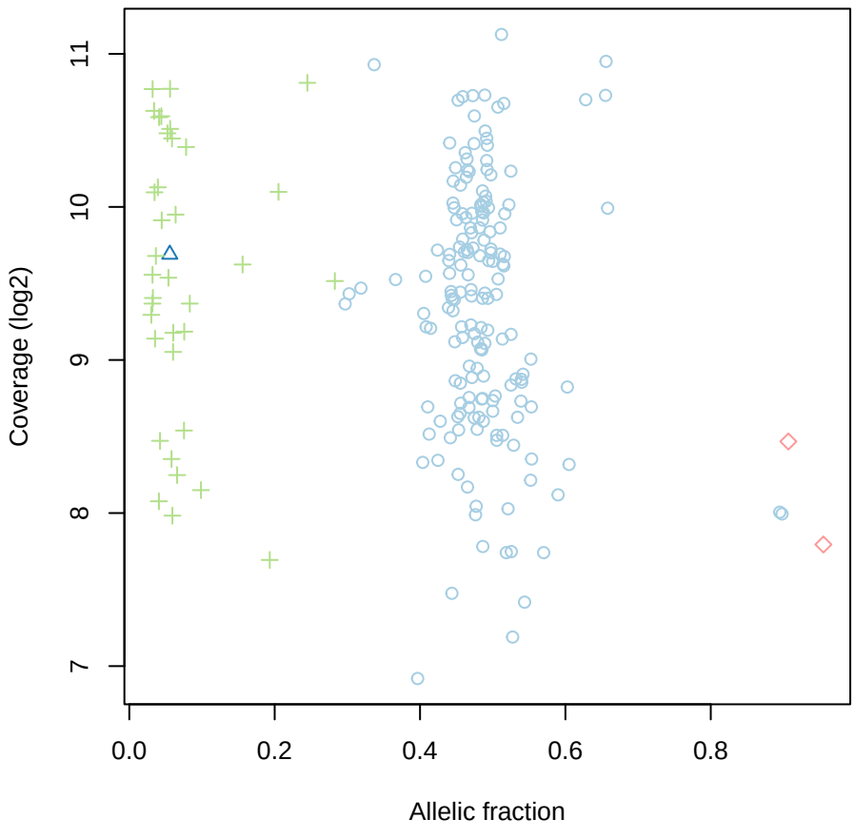

Purity: 0.47 Tumor ploidy: 5.095
3
4
5
6
7
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

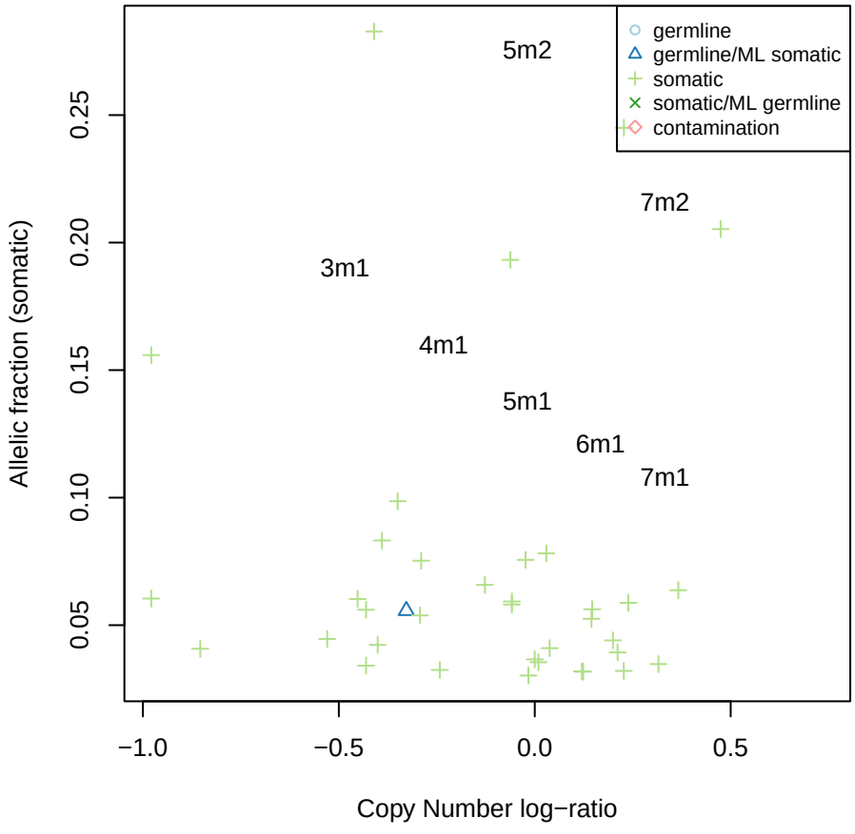

Purity: 0.47 Tumor ploidy: 5.095 SNV log−likelihood: −287.04 GoF: 92.3% Mean coverage: 774;145
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8 0.9
0 50 100 150
SNV Index

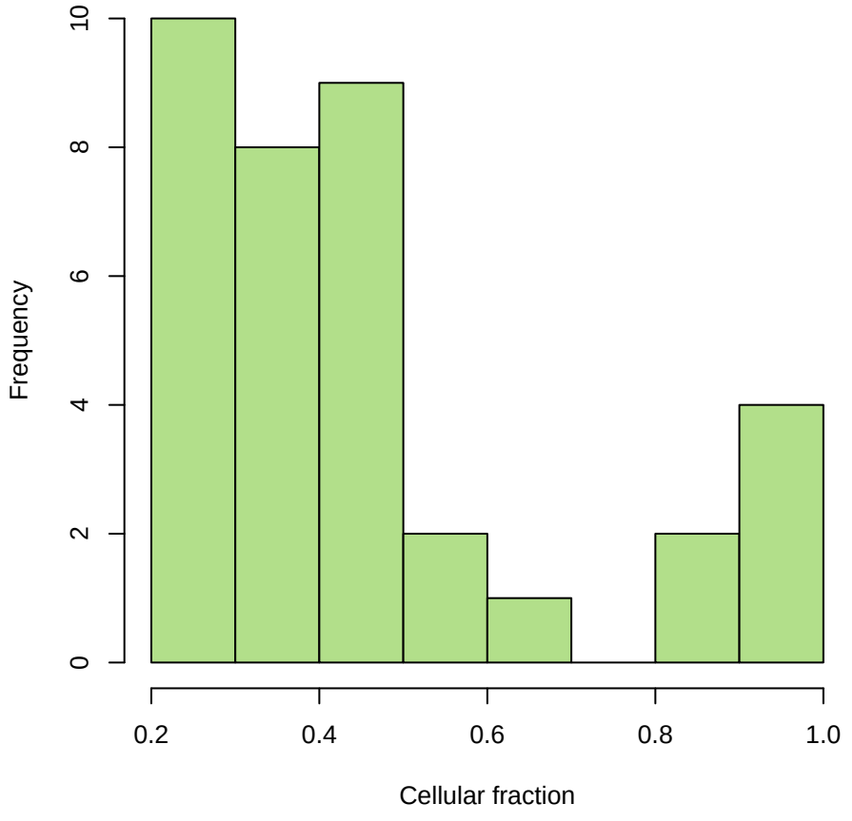

SCNA−fit log−likelihood: −23873.87
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 50 100 150
SNV Index

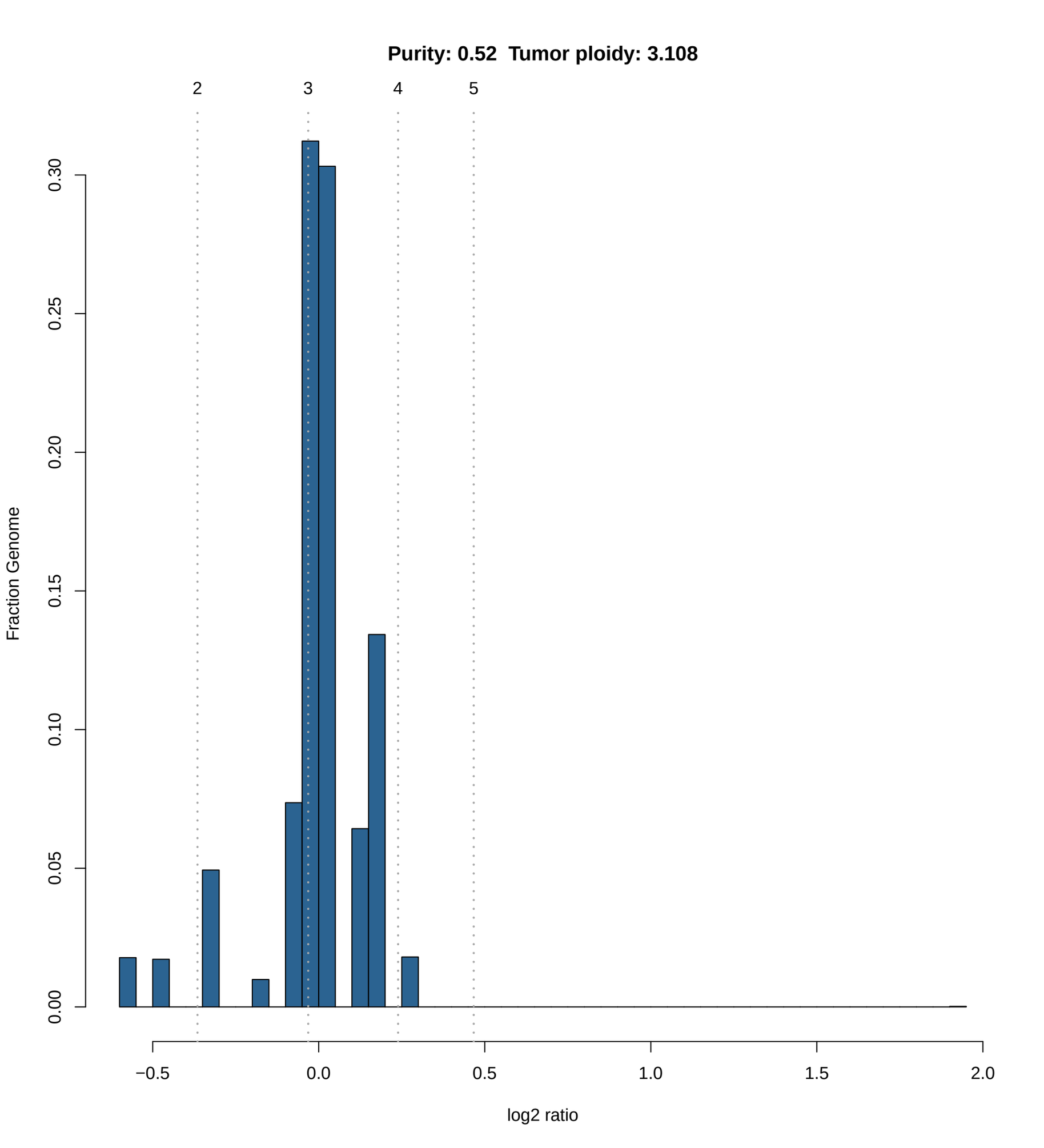

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

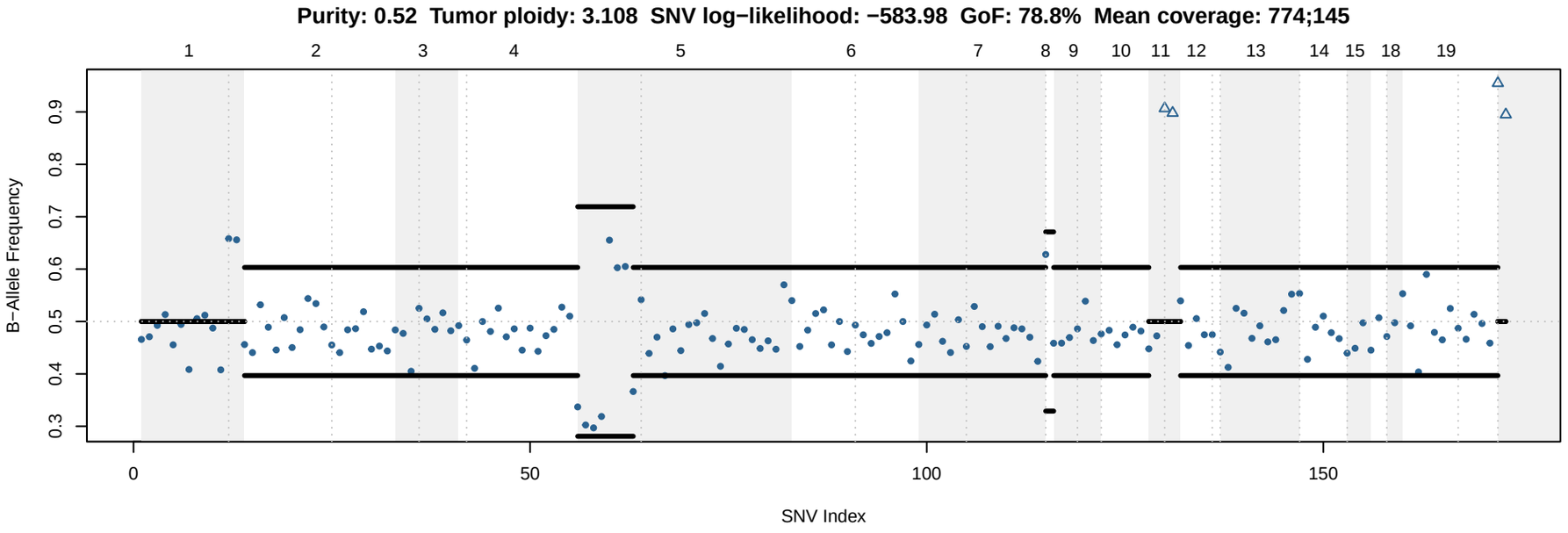

Allelic fraction (germline)
Copy Number log−ratio
4m4
3m3
6m5
7m5
6m4
5m3
4m2
6m3
5m2
7m2

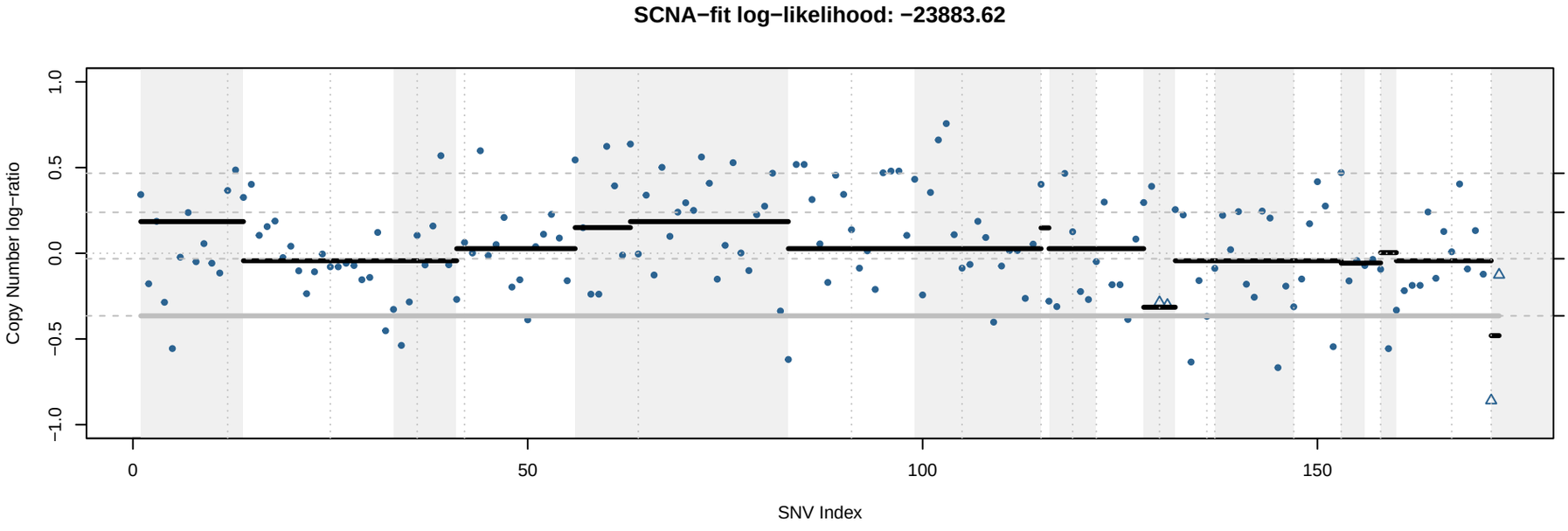

Coverage (log2)
Allelic fraction

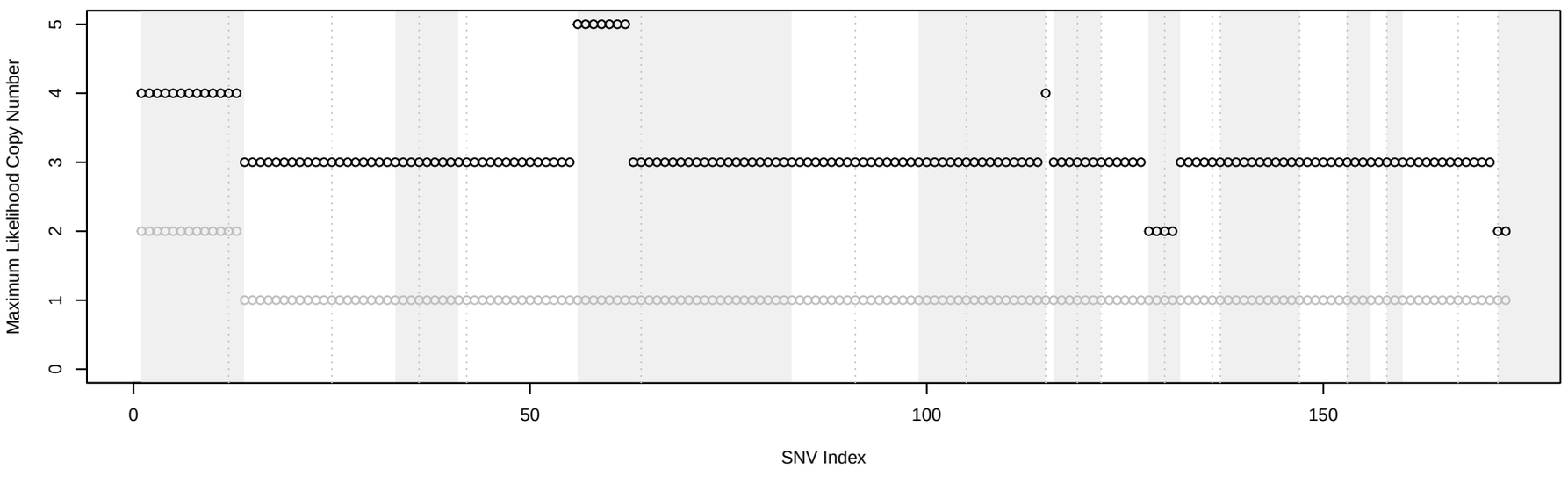

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
5m2
7m2
3m1
4m1
5m1
6m1
7m1


Frequency
Cellular fraction

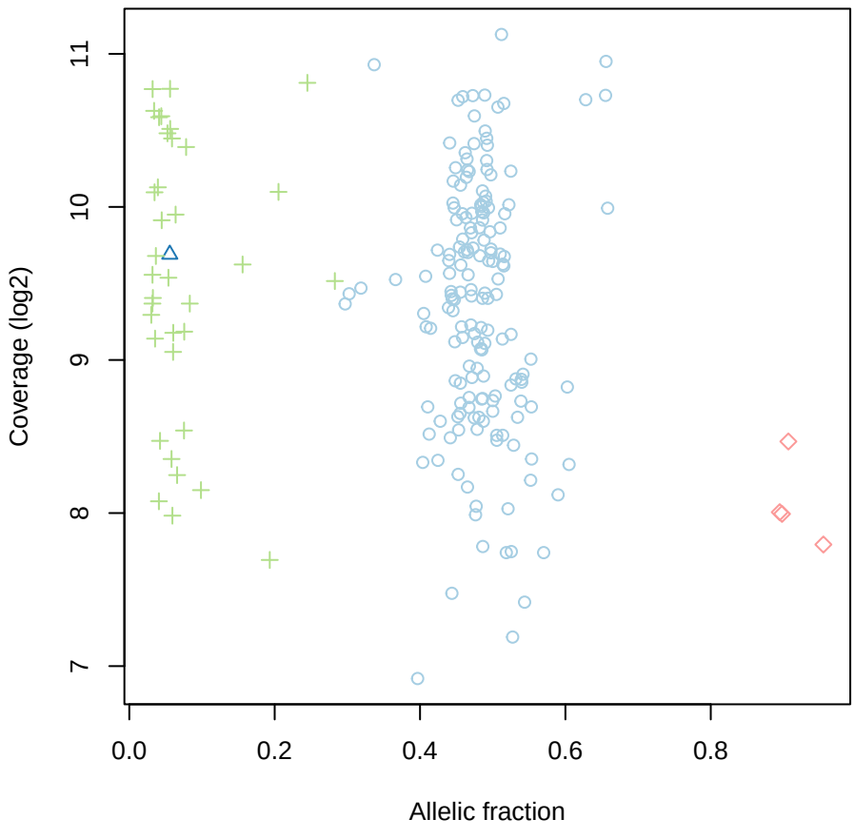

Purity: 0.52 Tumor ploidy: 3.108
2
3
4
5
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

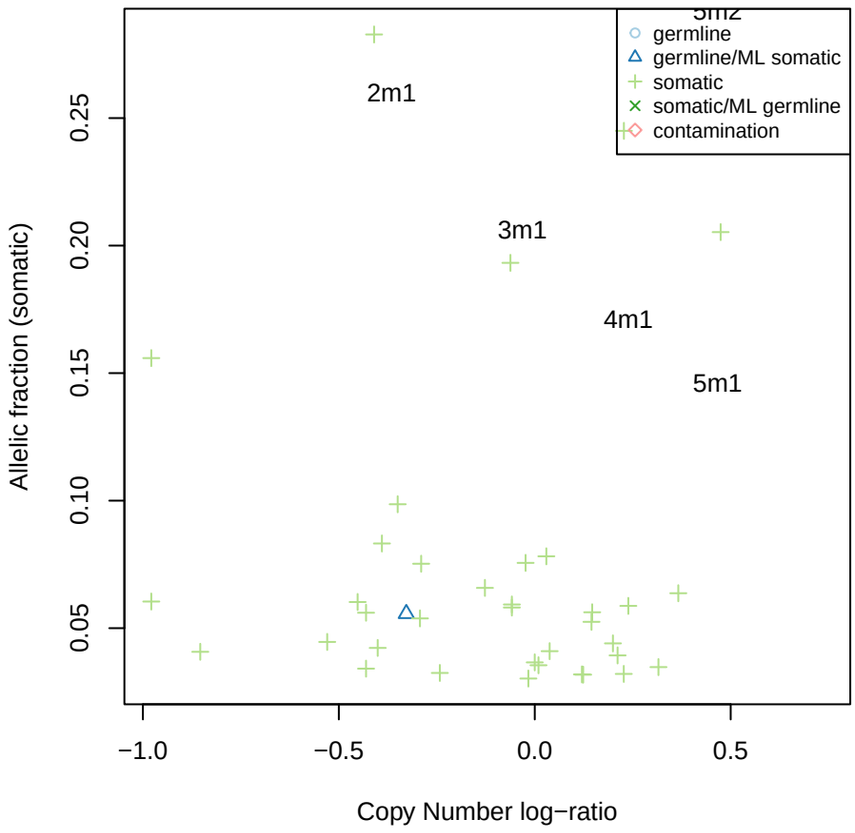

Purity: 0.52 Tumor ploidy: 3.108 SNV log−likelihood: −583.98 GoF: 78.8% Mean coverage: 774;145
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8 0.9
0 50 100 150
SNV Index

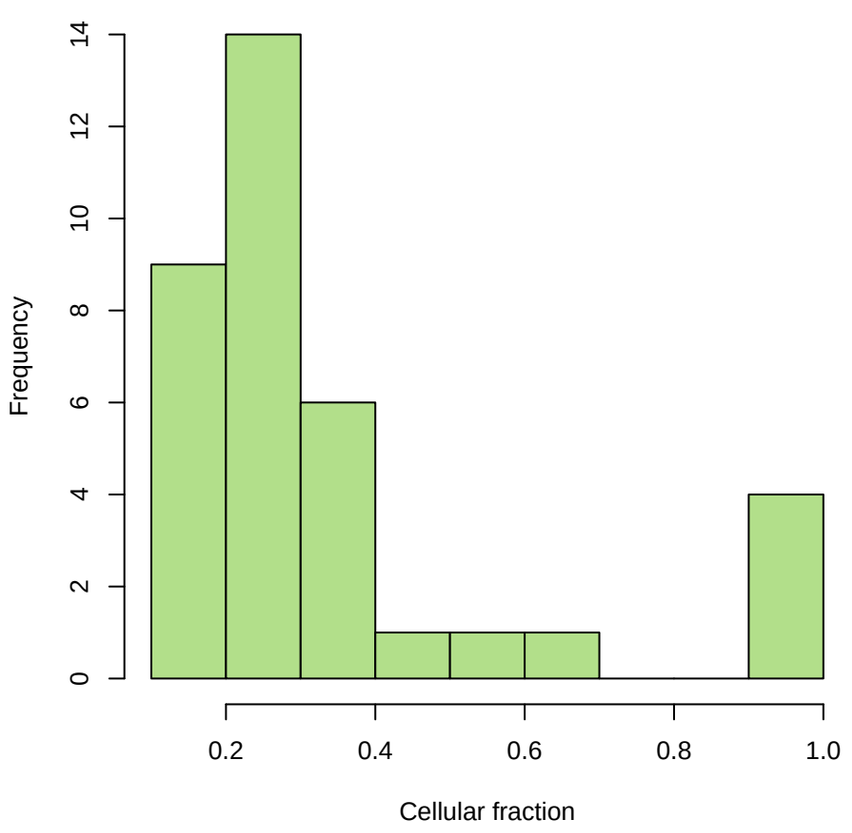

SCNA−fit log−likelihood: −23883.62
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5
0 50 100 150
SNV Index


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

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


Coverage (log2)
Allelic fraction


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


Frequency
Cellular fraction