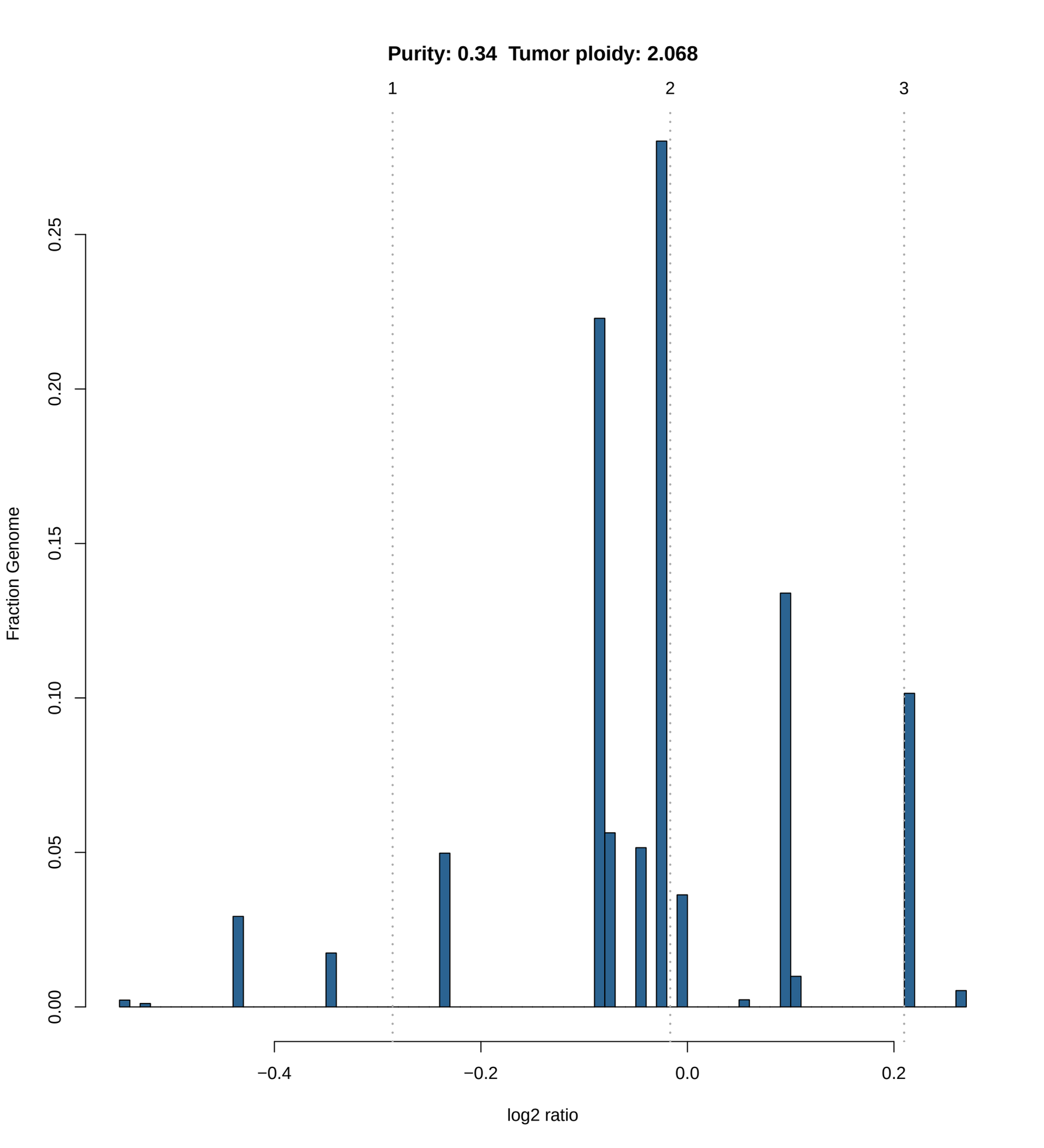
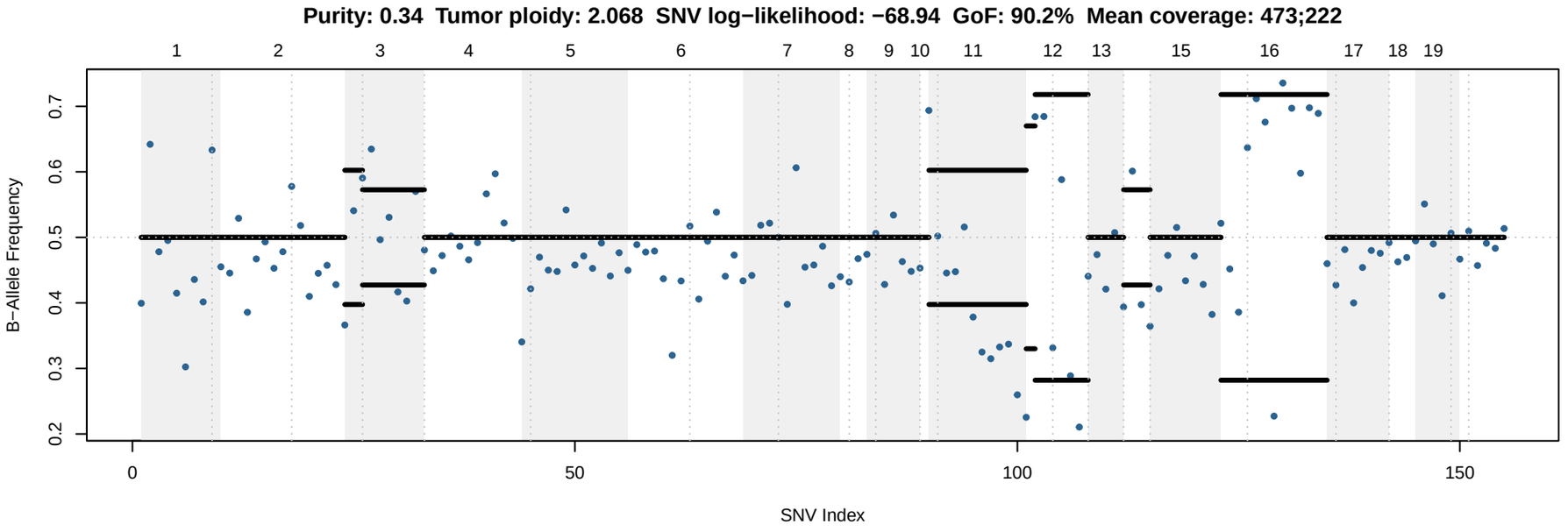
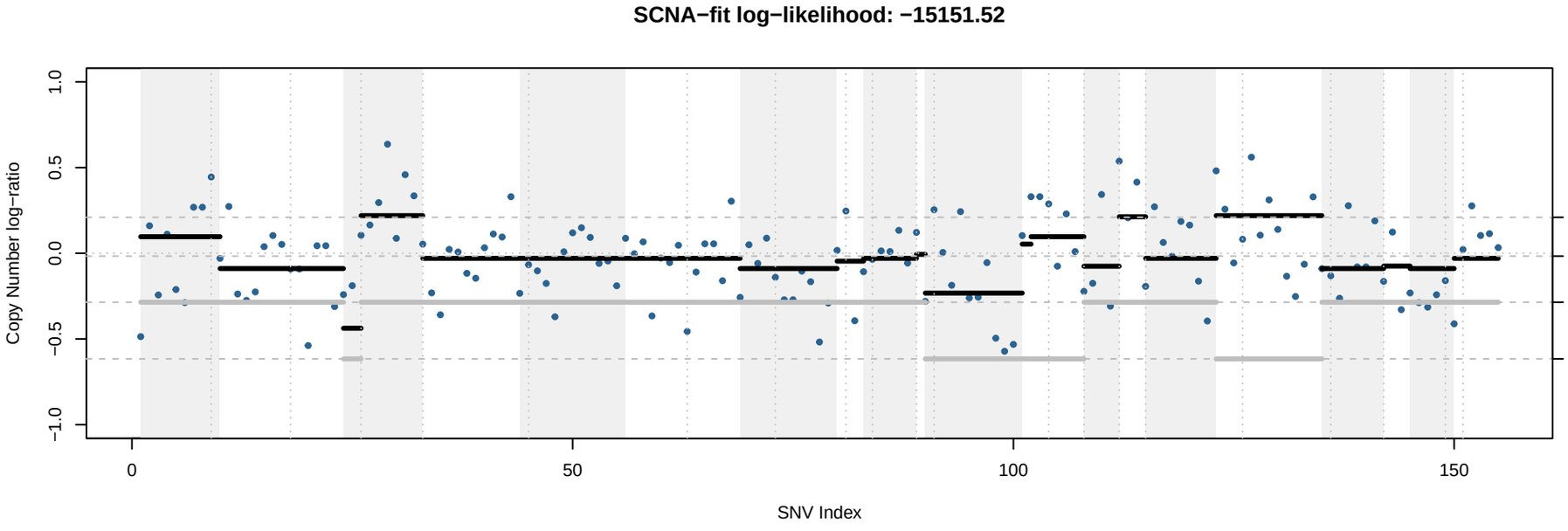
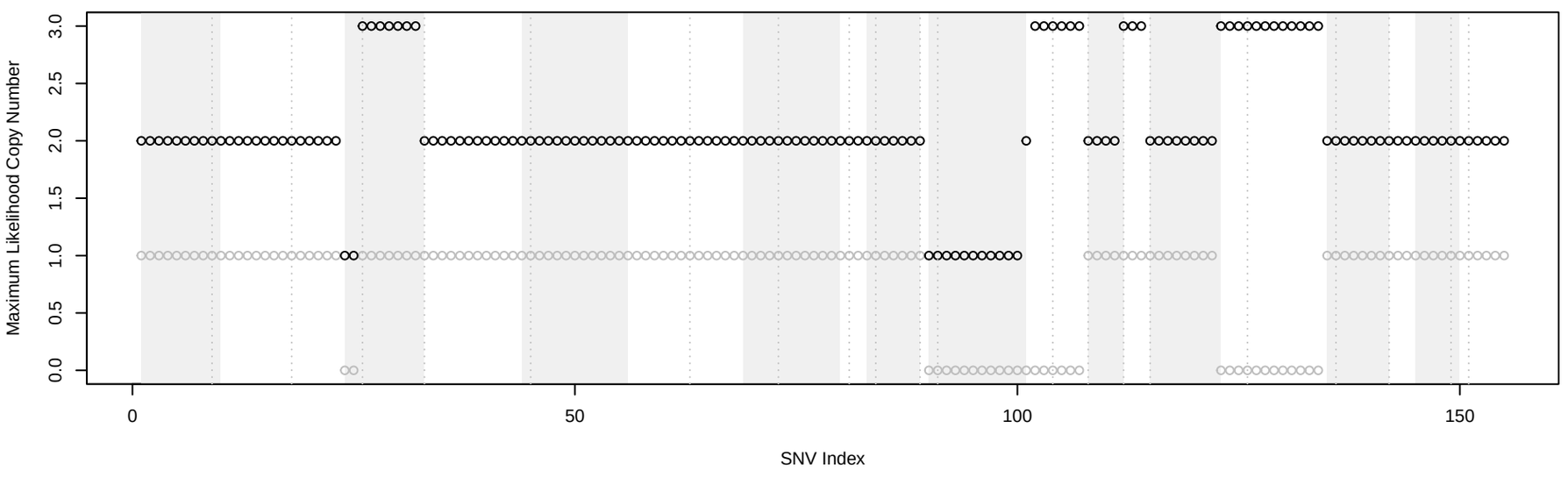
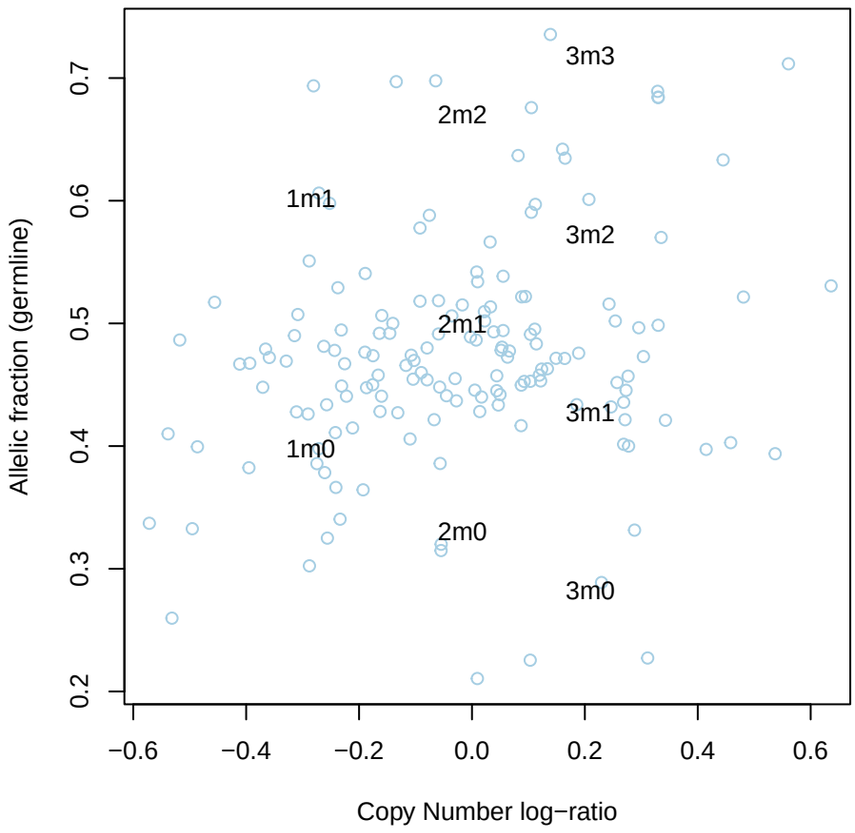
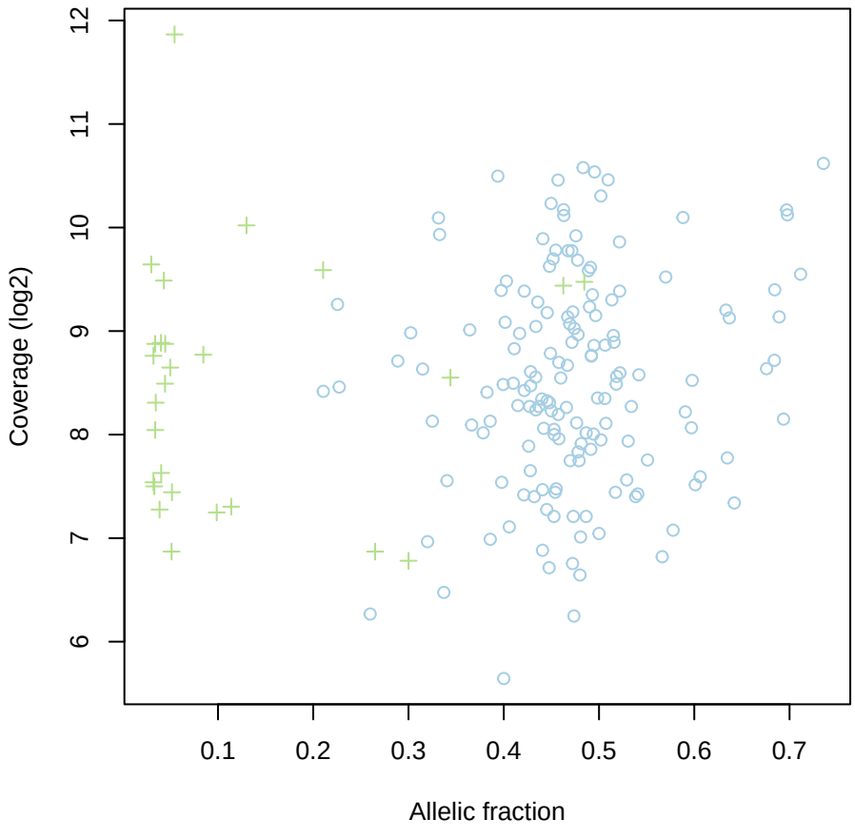

Purity: 0.34 Tumor ploidy: 2.068
1
2
3
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
log2 ratio

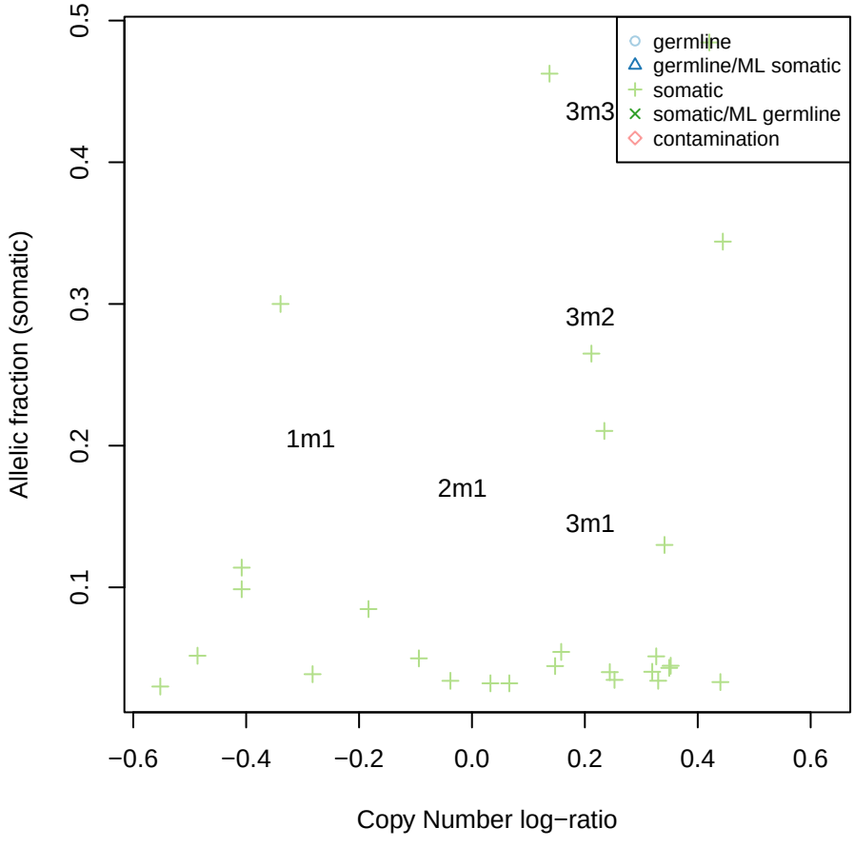

Purity: 0.34 Tumor ploidy: 2.068 SNV log−likelihood: −68.94 GoF: 90.2% Mean coverage: 473;222
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

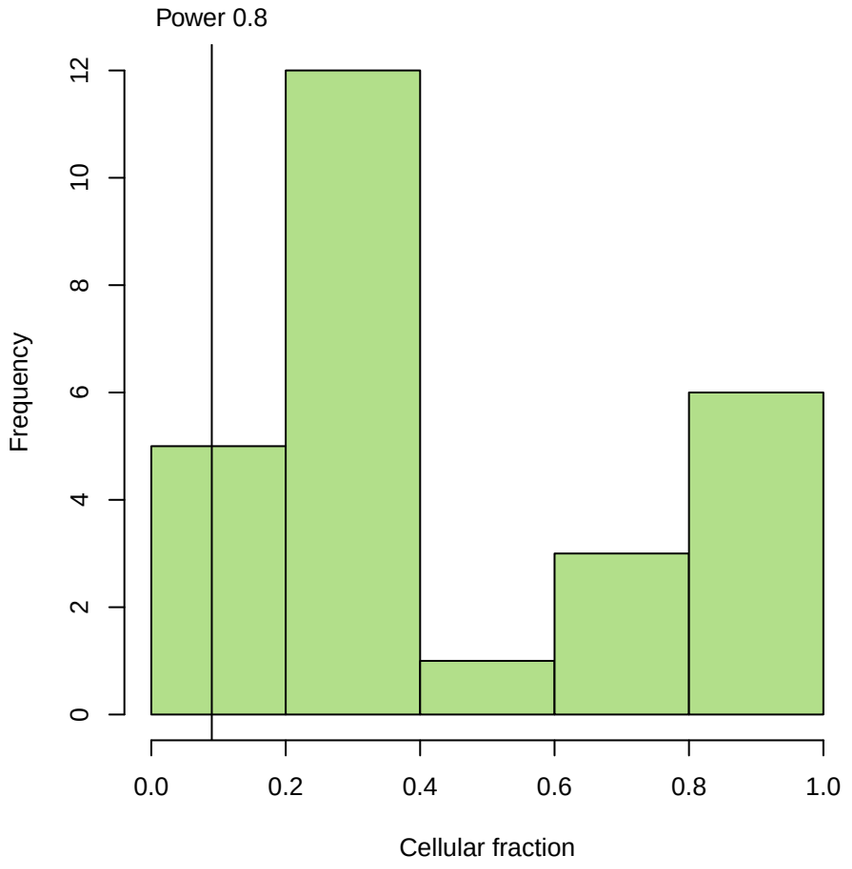

SCNA−fit log−likelihood: −15151.52
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3
0 50 100 150
SNV Index

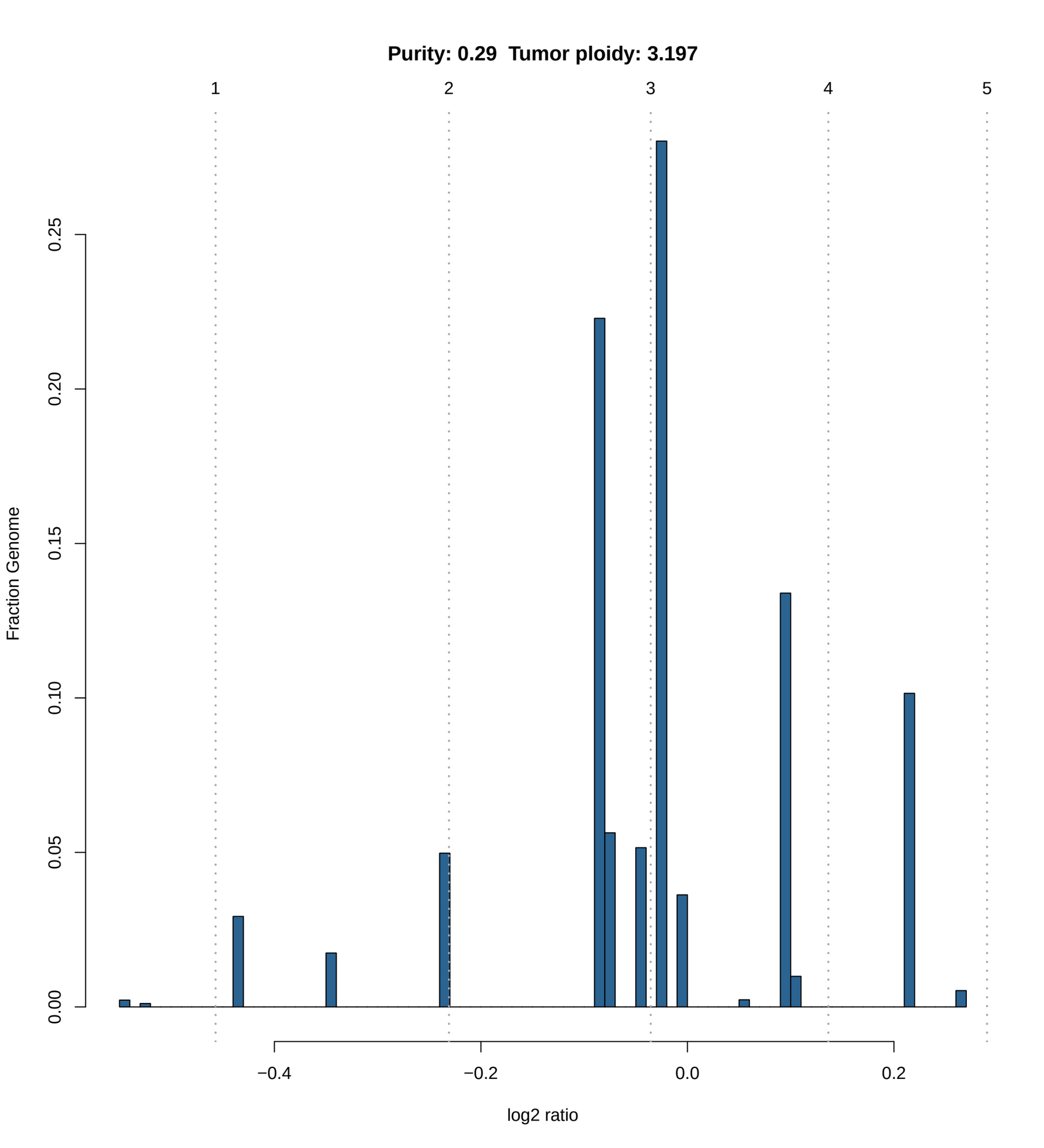

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

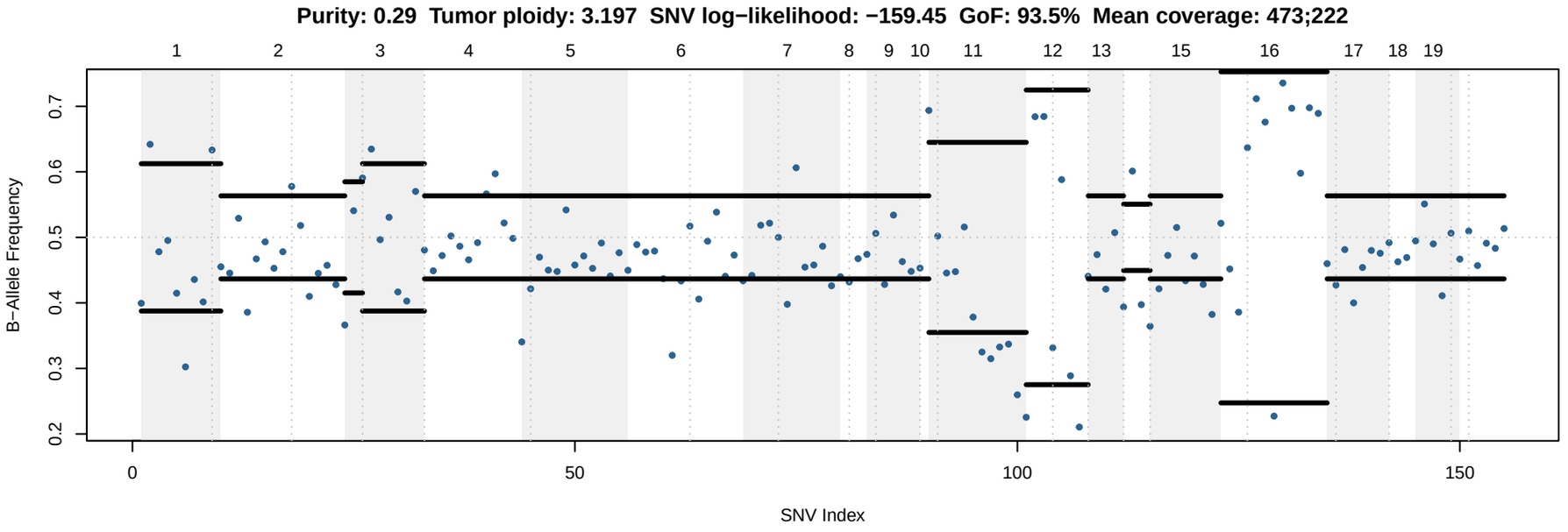

Allelic fraction (germline)
Copy Number log−ratio
3m3
2m2
1m1
3m2
2m1
3m1
1m0
2m0
3m0

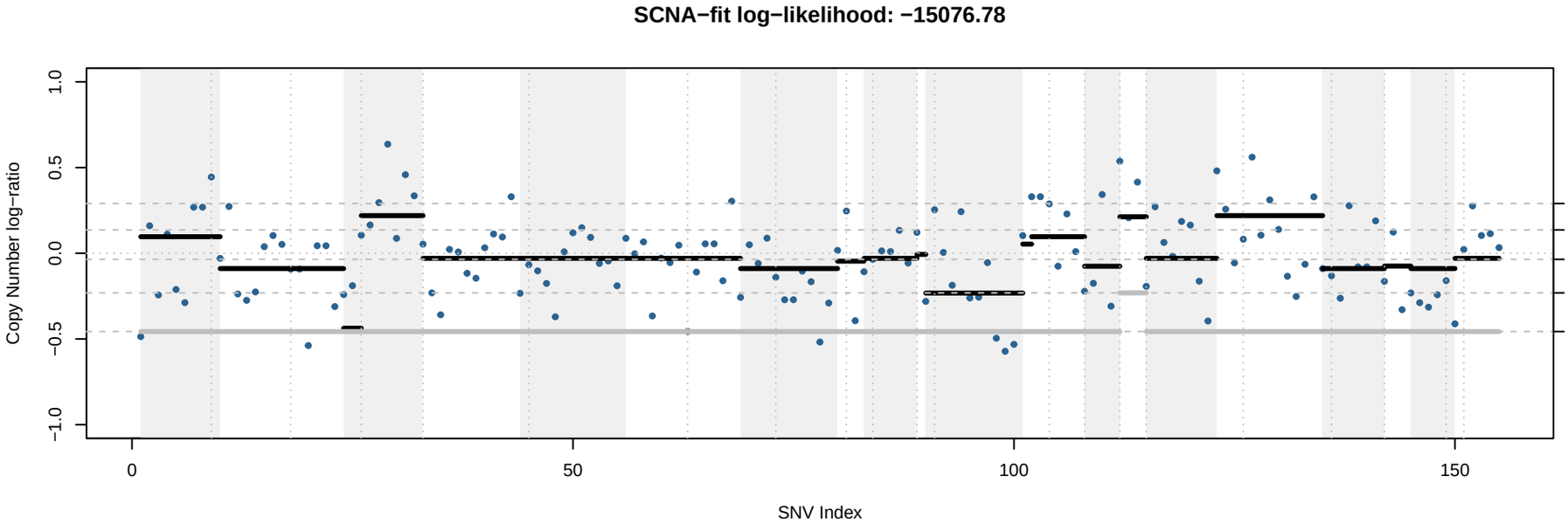

Coverage (log2)
Allelic fraction

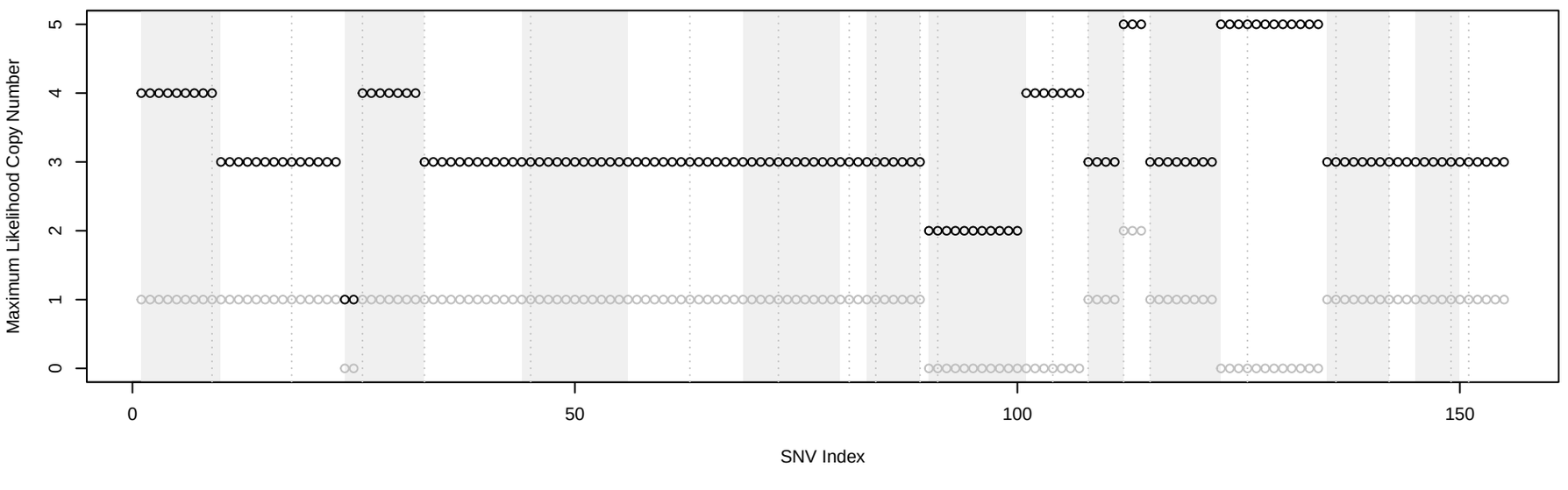

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m3
3m2
1m1
2m1
3m1

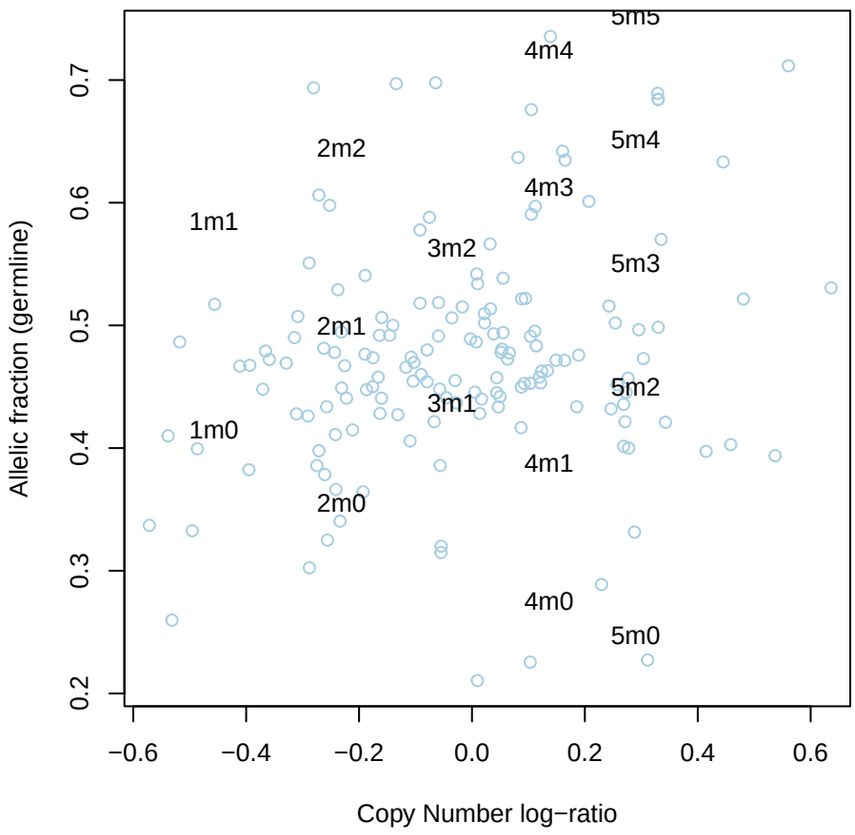

Power 0.8
Frequency
Cellular fraction

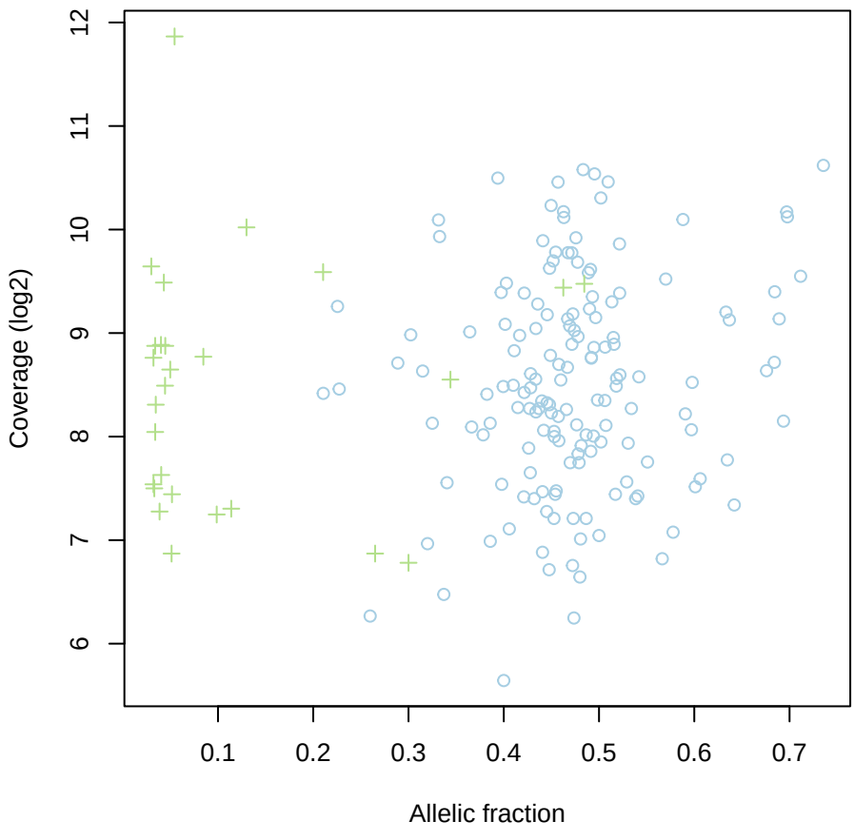

Purity: 0.29 Tumor ploidy: 3.197
1
2
3
4
5
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
log2 ratio

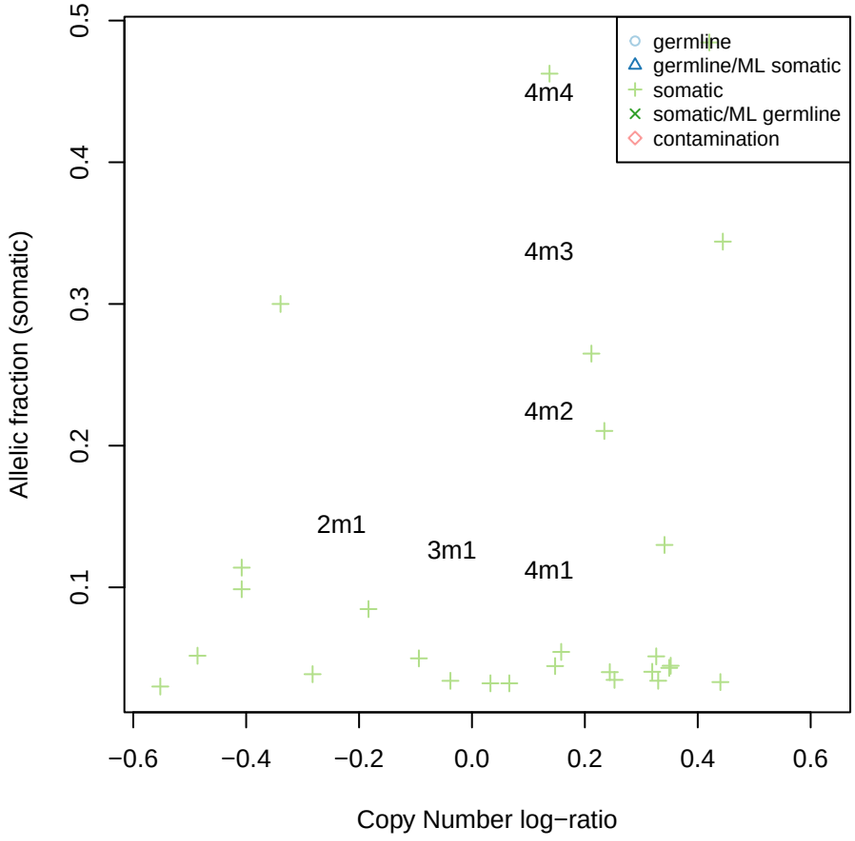

Purity: 0.29 Tumor ploidy: 3.197 SNV log−likelihood: −159.45 GoF: 93.5% Mean coverage: 473;222
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

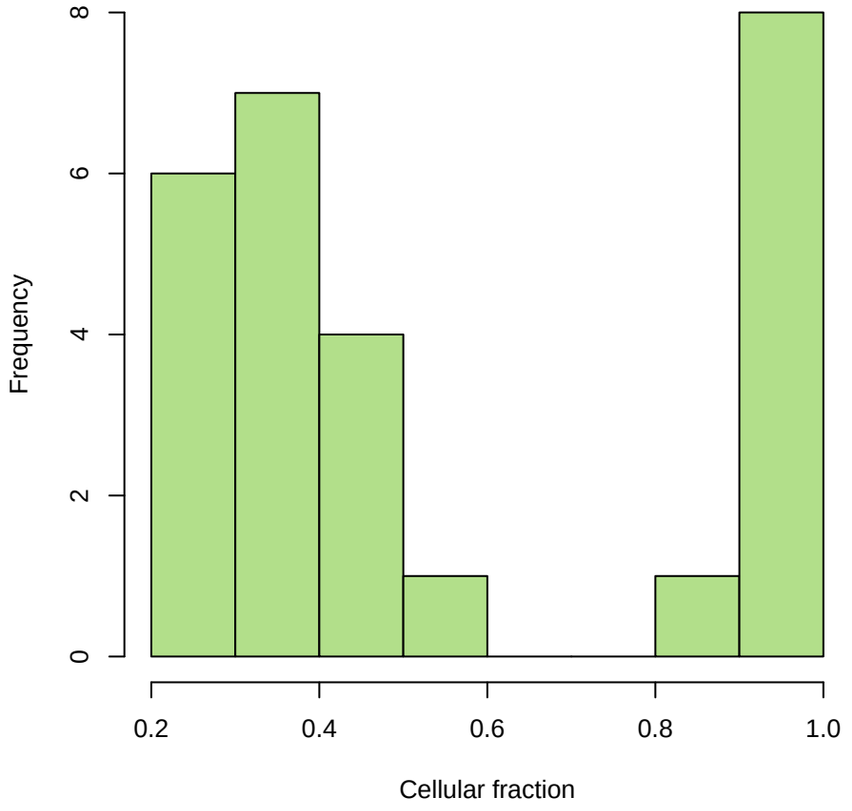

SCNA−fit log−likelihood: −15076.78
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5
0 50 100 150
SNV Index

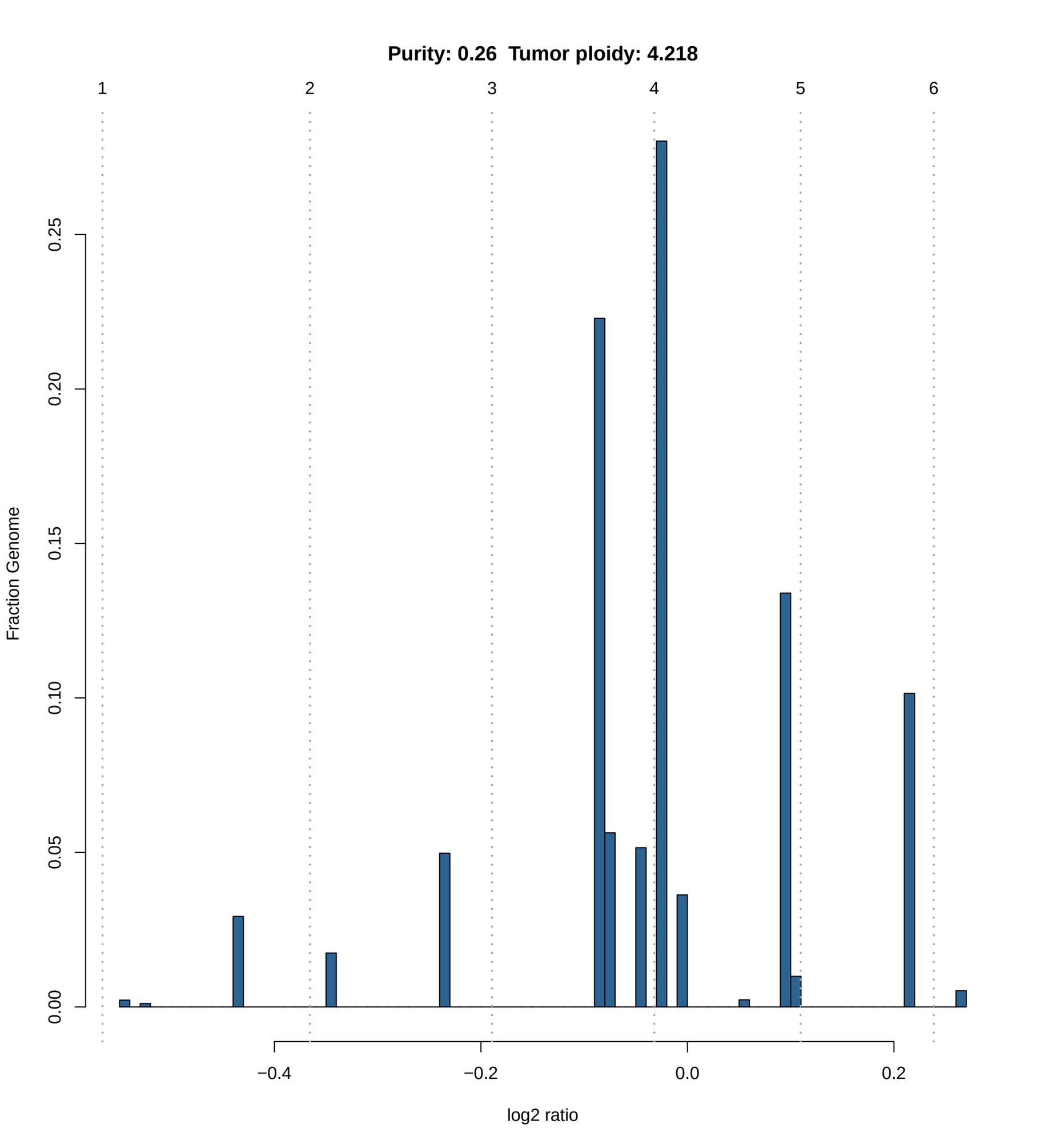

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

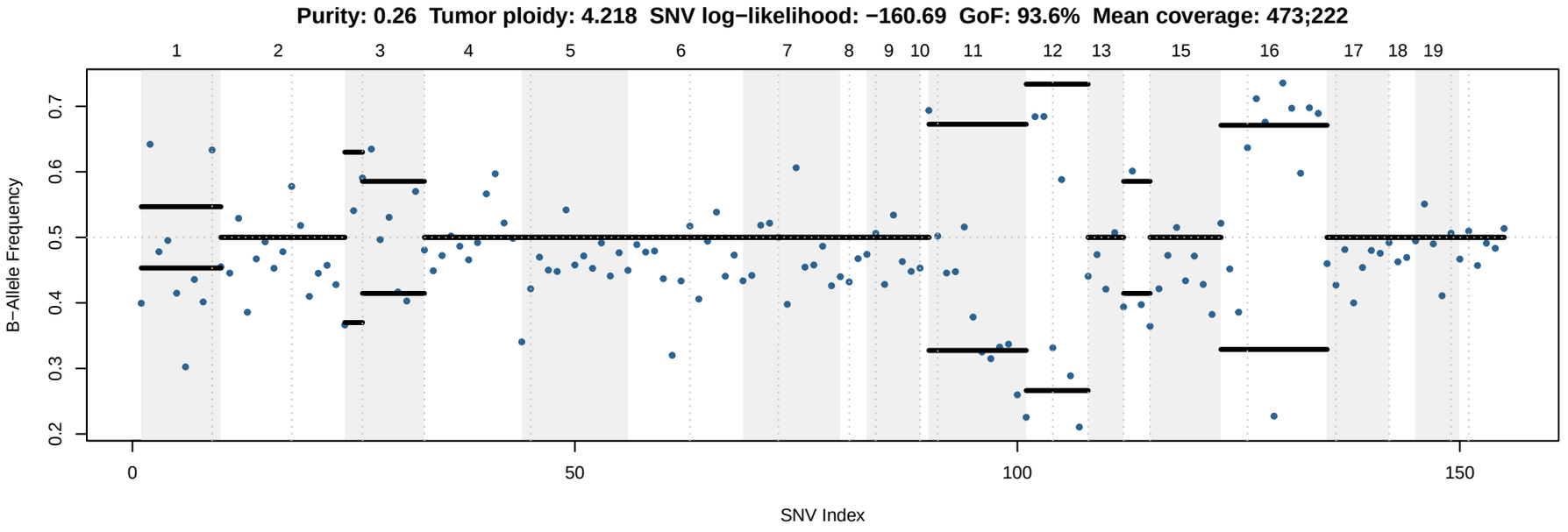

Allelic fraction (germline)
Copy Number log−ratio
5m5
4m4
5m4
2m2
4m3
1m1
3m2
5m3
2m1
5m2
3m1
1m0
4m1
2m0
4m0
5m0

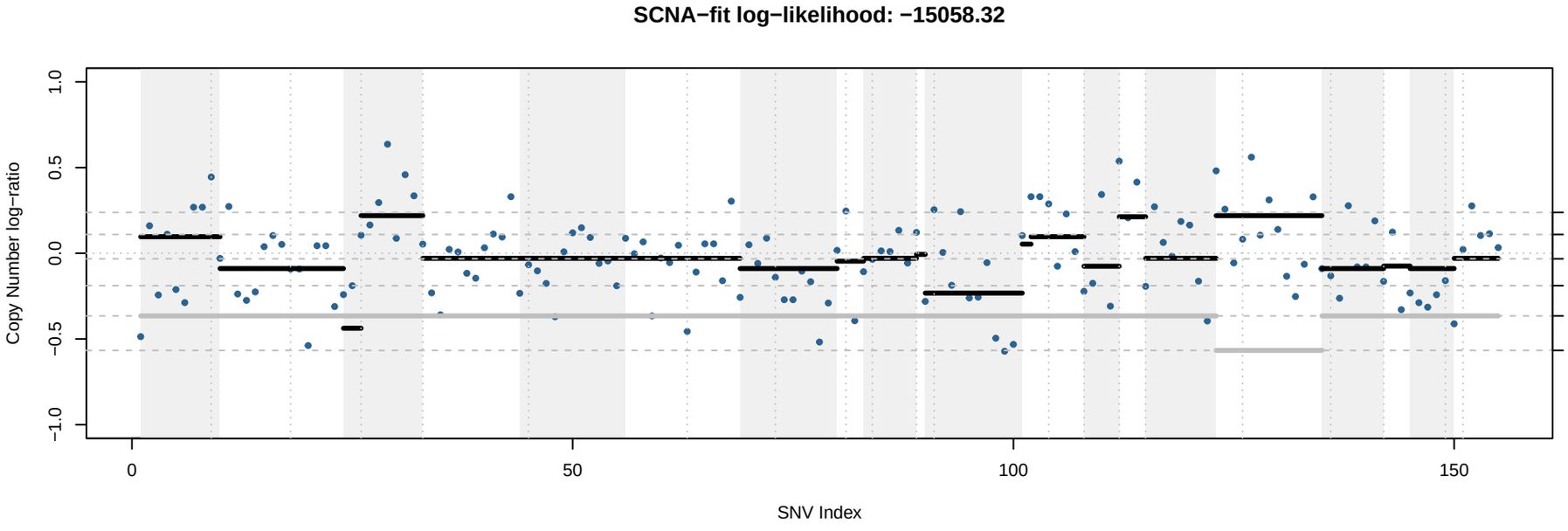

Coverage (log2)
Allelic fraction

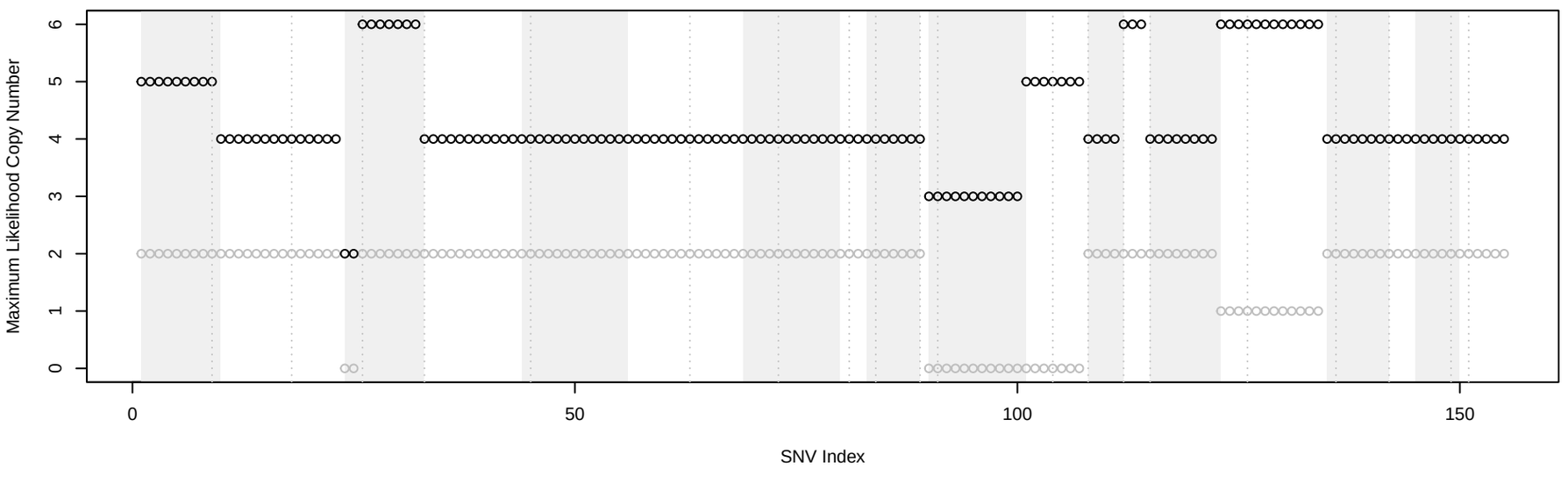

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m4
4m3
4m2
2m1
3m1
4m1

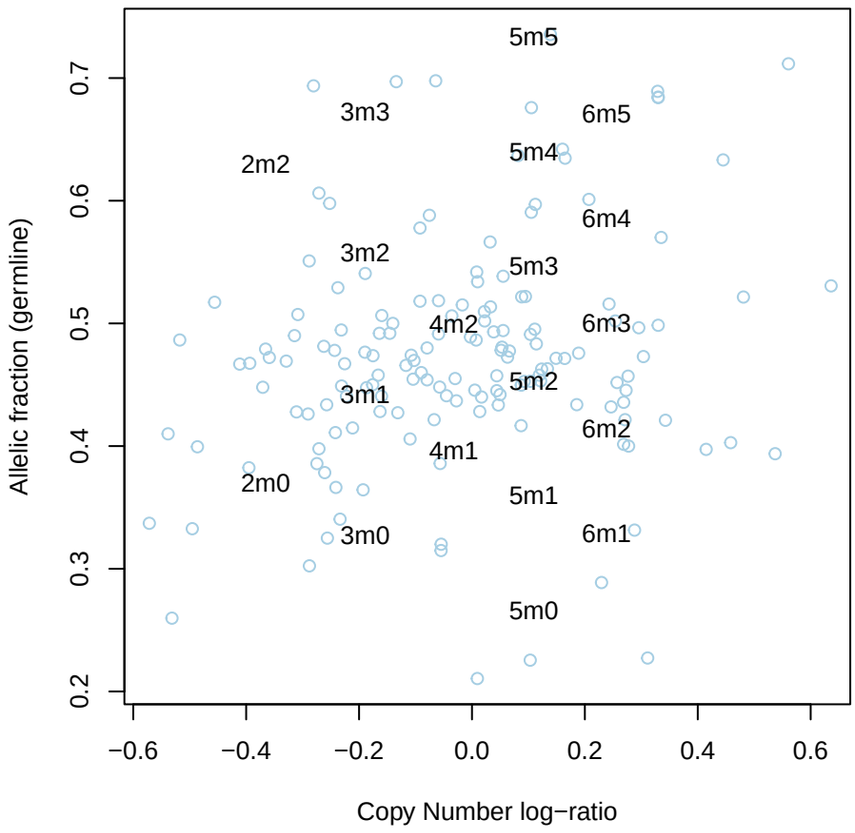

Frequency
Cellular fraction

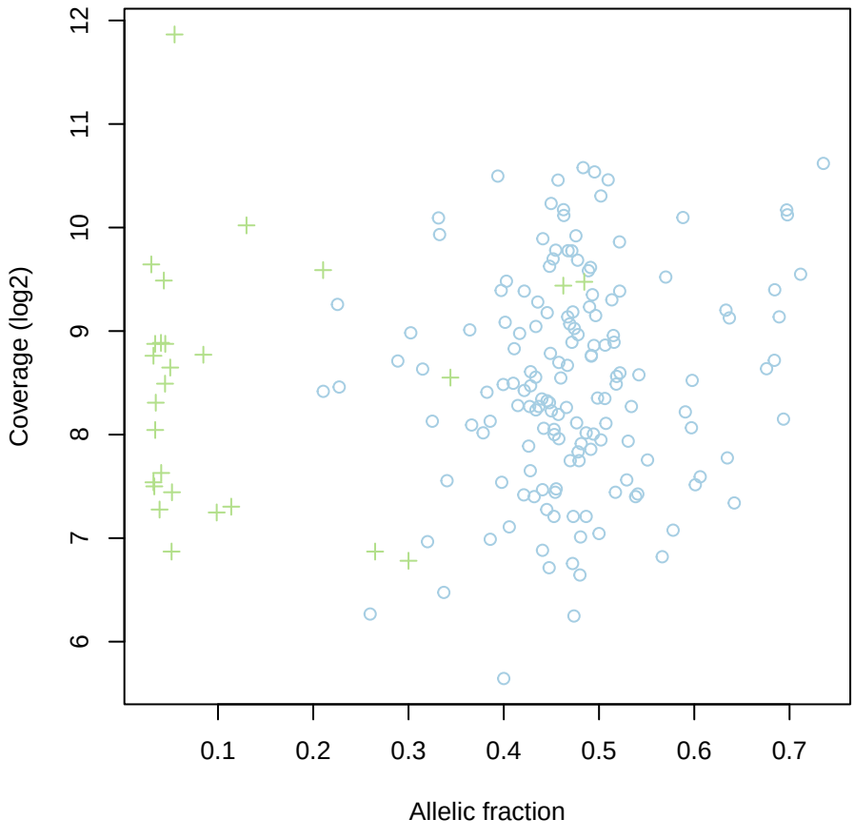

Purity: 0.26 Tumor ploidy: 4.218
1
2
3
4
5
6
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
log2 ratio

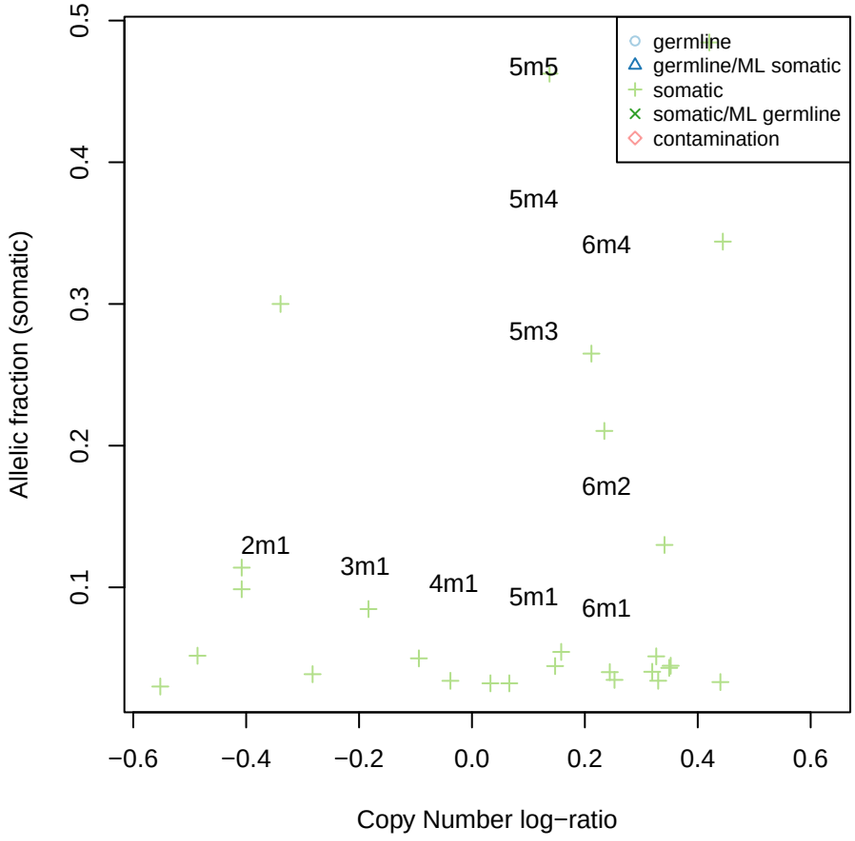

Purity: 0.26 Tumor ploidy: 4.218 SNV log−likelihood: −160.69 GoF: 93.6% Mean coverage: 473;222
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

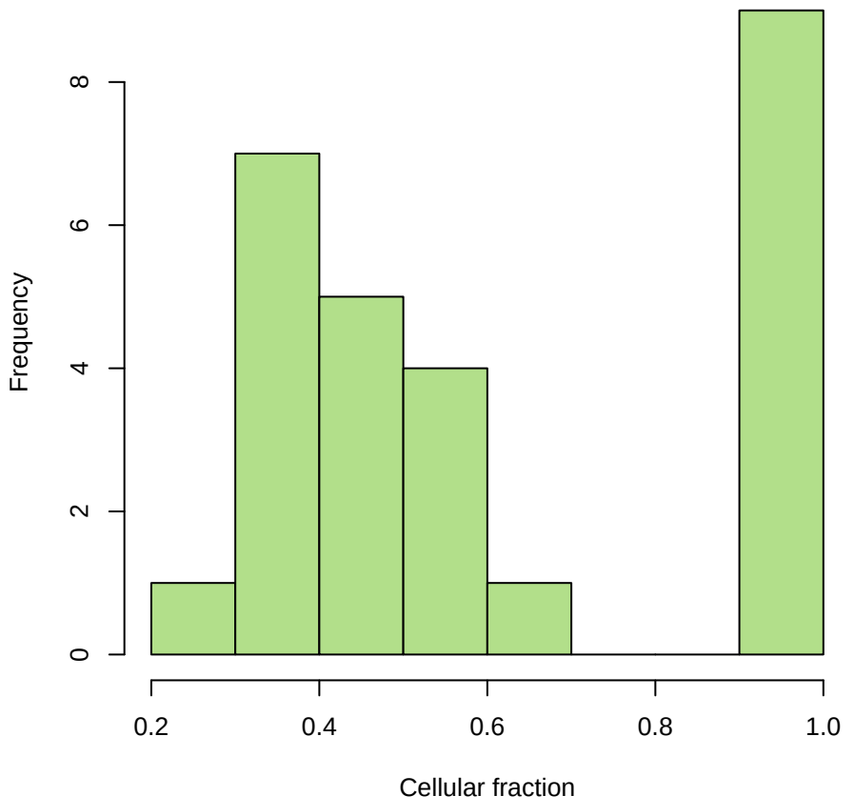

SCNA−fit log−likelihood: −15058.32
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 6
0 50 100 150
SNV Index

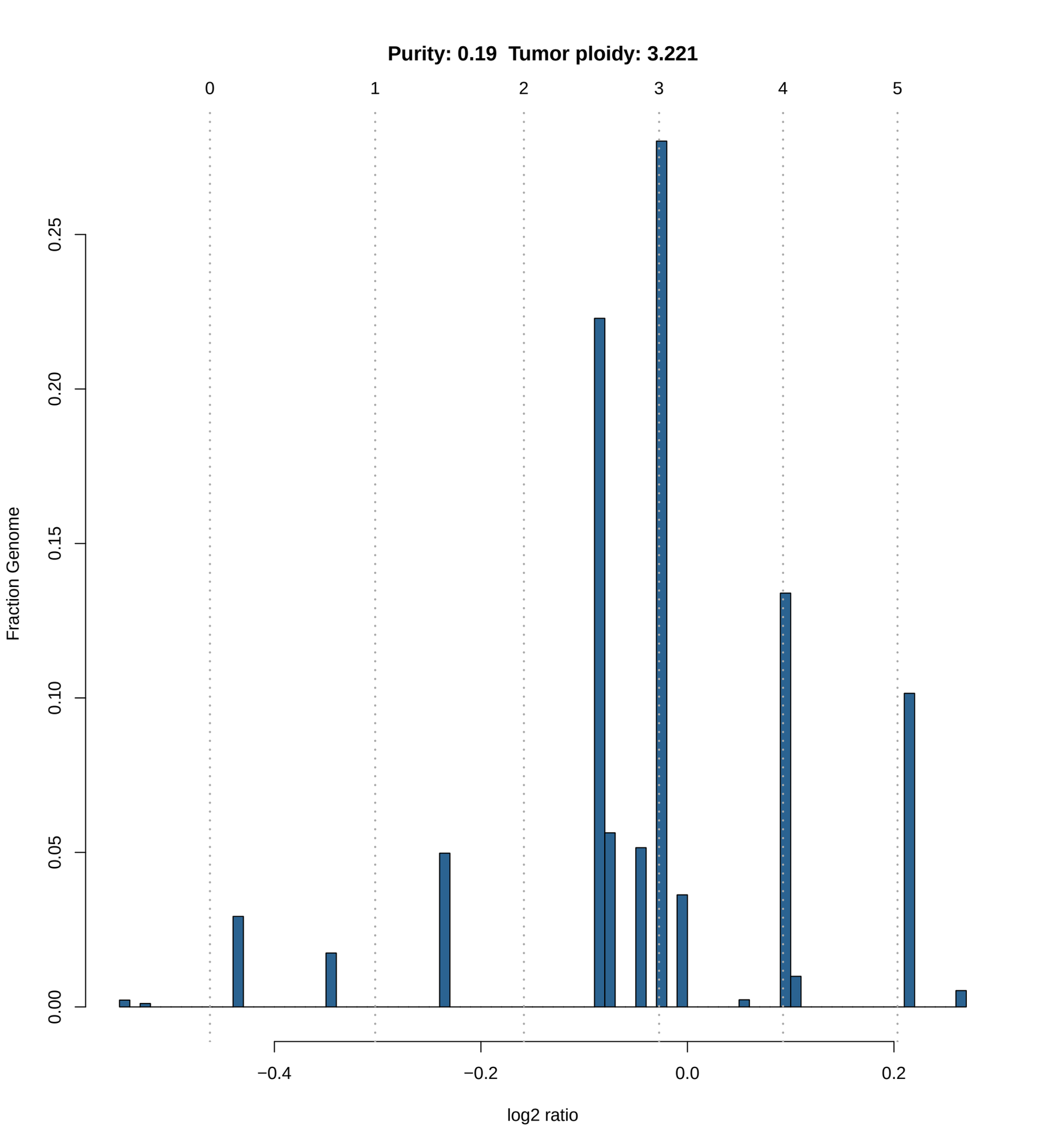

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

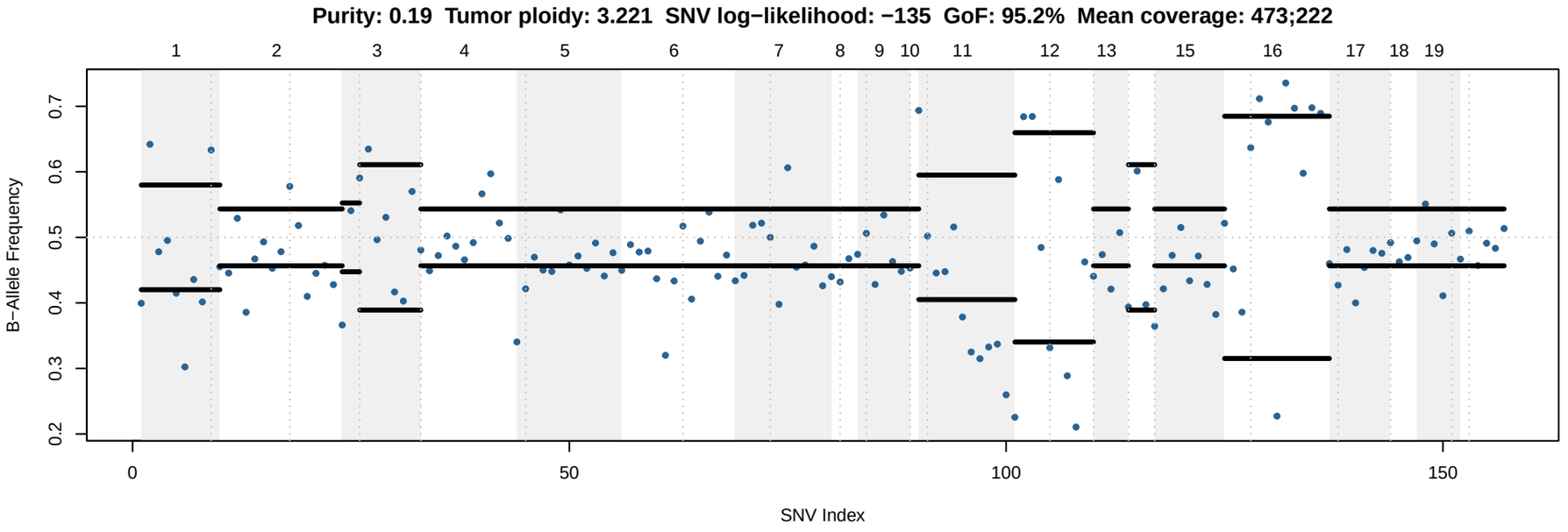

Allelic fraction (germline)
Copy Number log−ratio
5m5
3m3
6m5
2m2
5m4
6m4
3m2
5m3
4m2
6m3
5m2
3m1
6m2
4m1
2m0
5m1
3m0
6m1
5m0

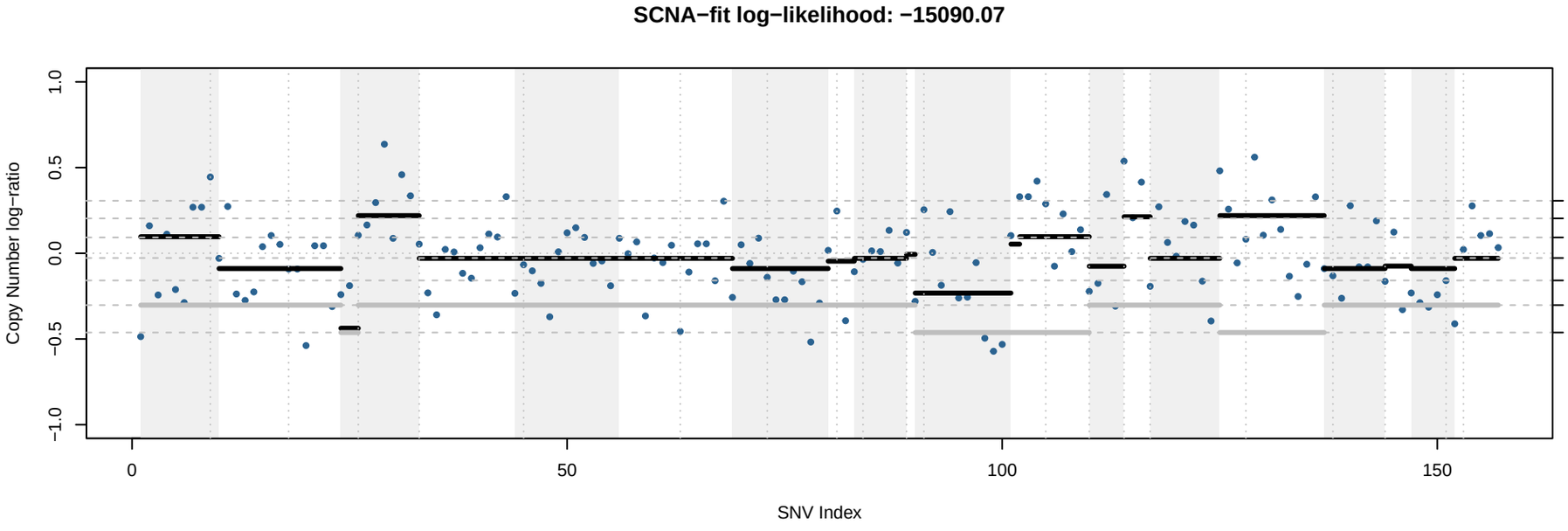

Coverage (log2)
Allelic fraction

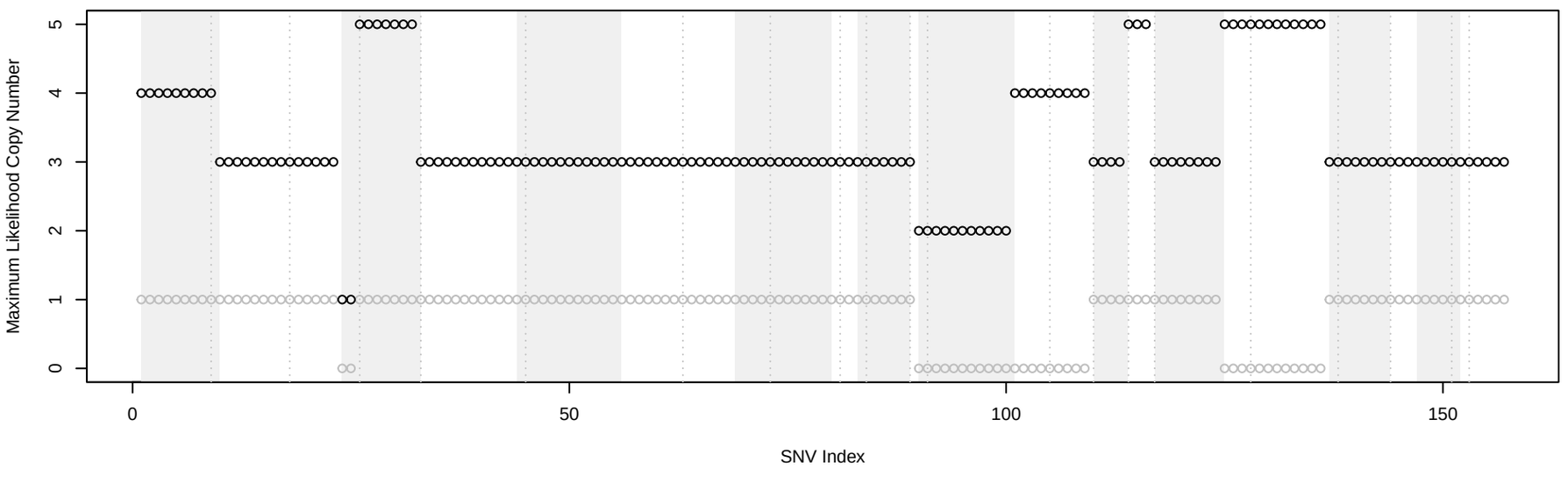

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
5m5
5m4
6m4
5m3
6m2
2m1
3m1
4m1
5m1
6m1

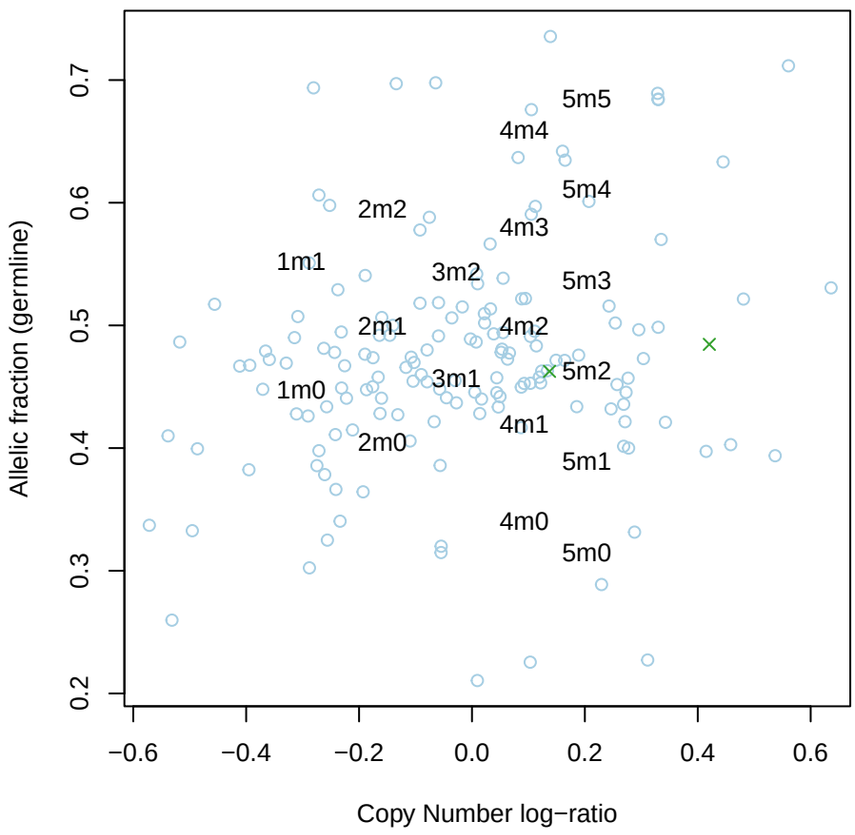

Frequency
Cellular fraction

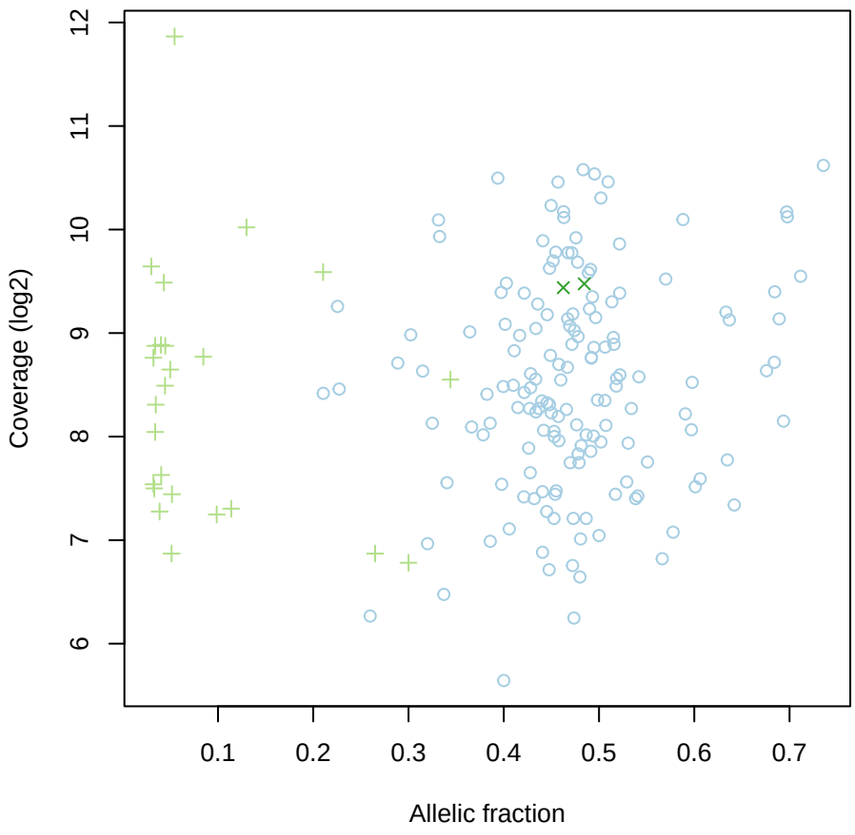

Purity: 0.19 Tumor ploidy: 3.221
0
1
2
3
4
5
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
log2 ratio

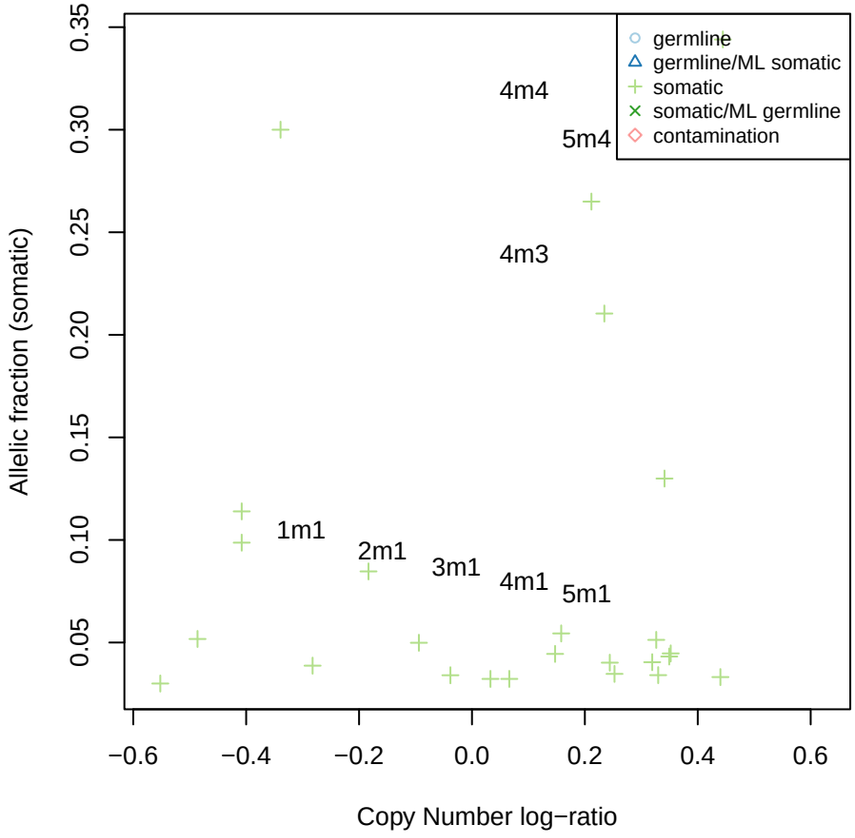

Purity: 0.19 Tumor ploidy: 3.221 SNV log−likelihood: −135 GoF: 95.2% Mean coverage: 473;222
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

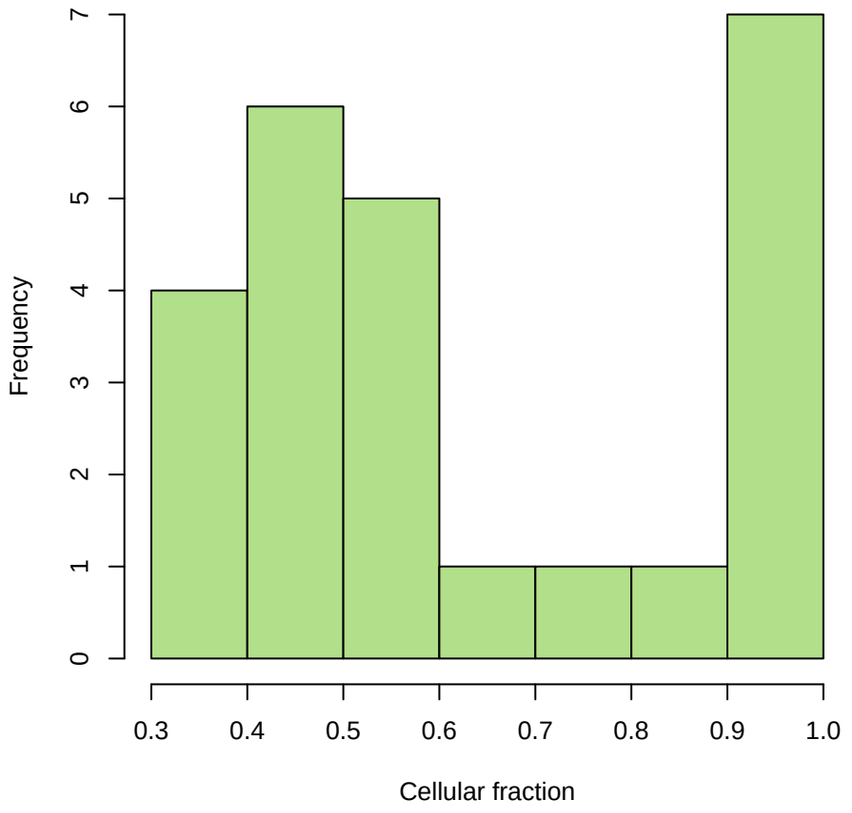

SCNA−fit log−likelihood: −15090.07
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 4 6
0 50 100 150
SNV Index

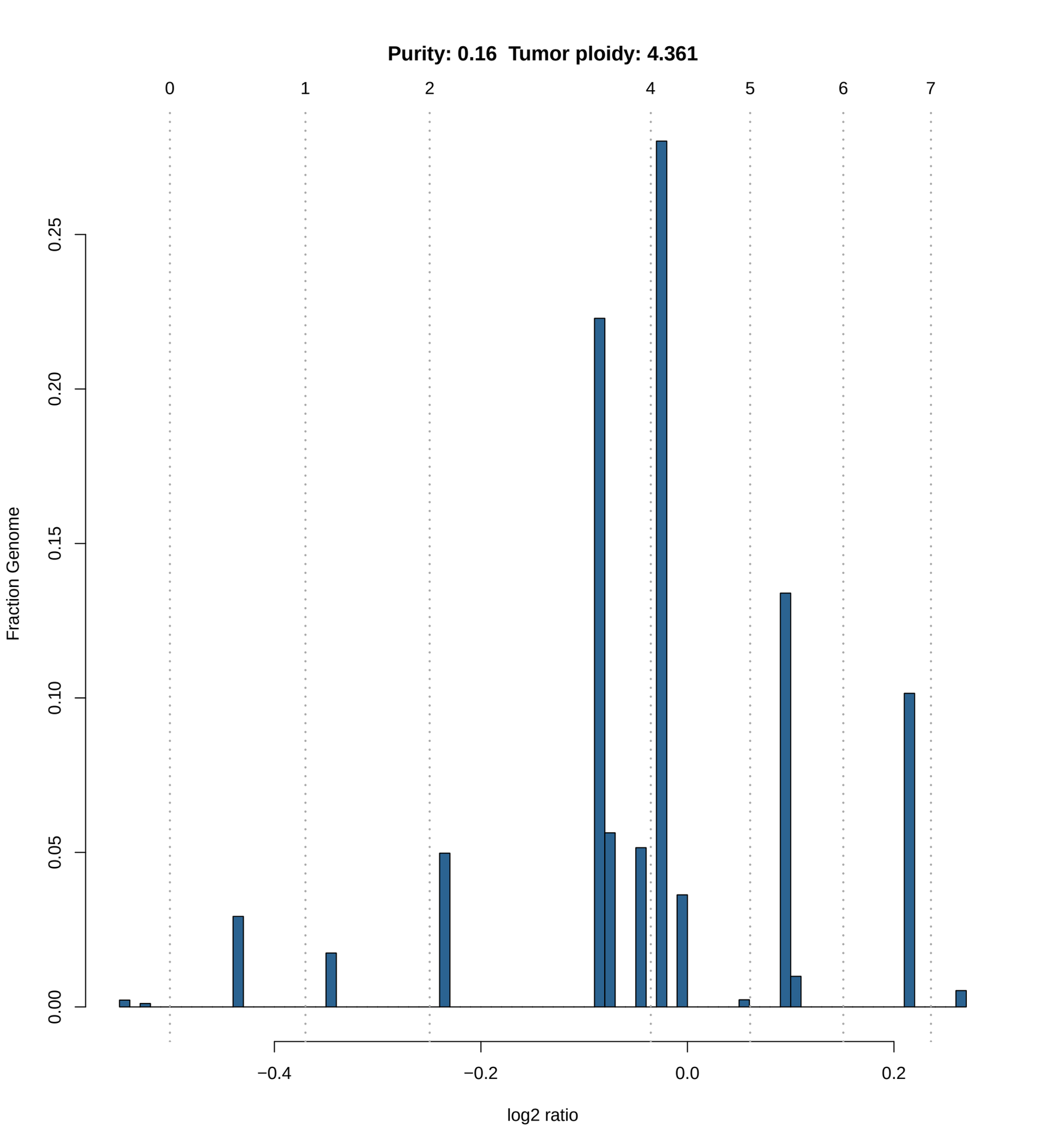

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

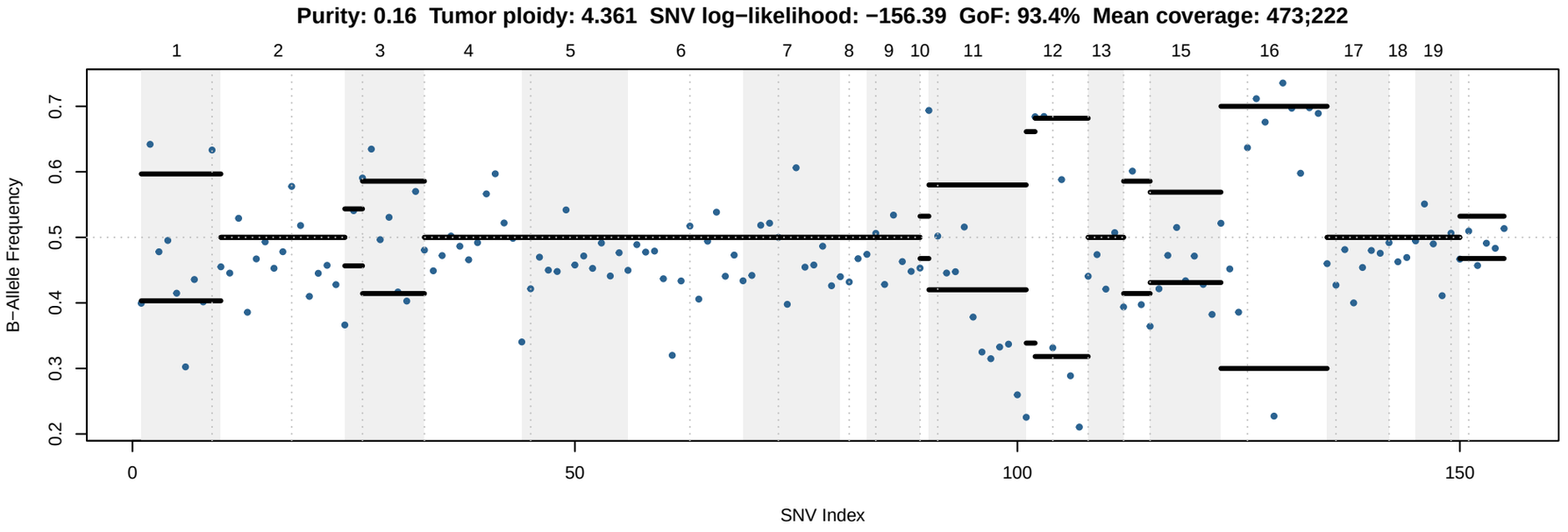

Allelic fraction (germline)
Copy Number log−ratio
5m5
4m4
5m4
2m2
4m3
1m1
3m2
5m3
2m1
4m2
5m2
3m1
1m0
4m1
2m0
5m1
4m0
5m0

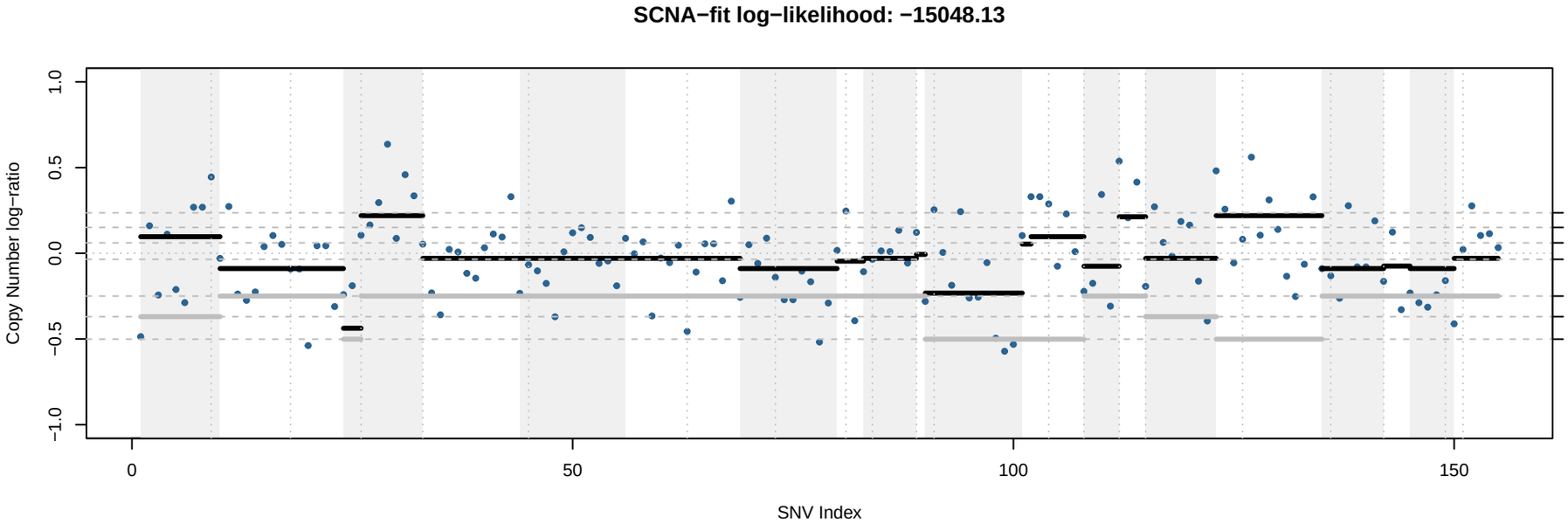

Coverage (log2)
Allelic fraction

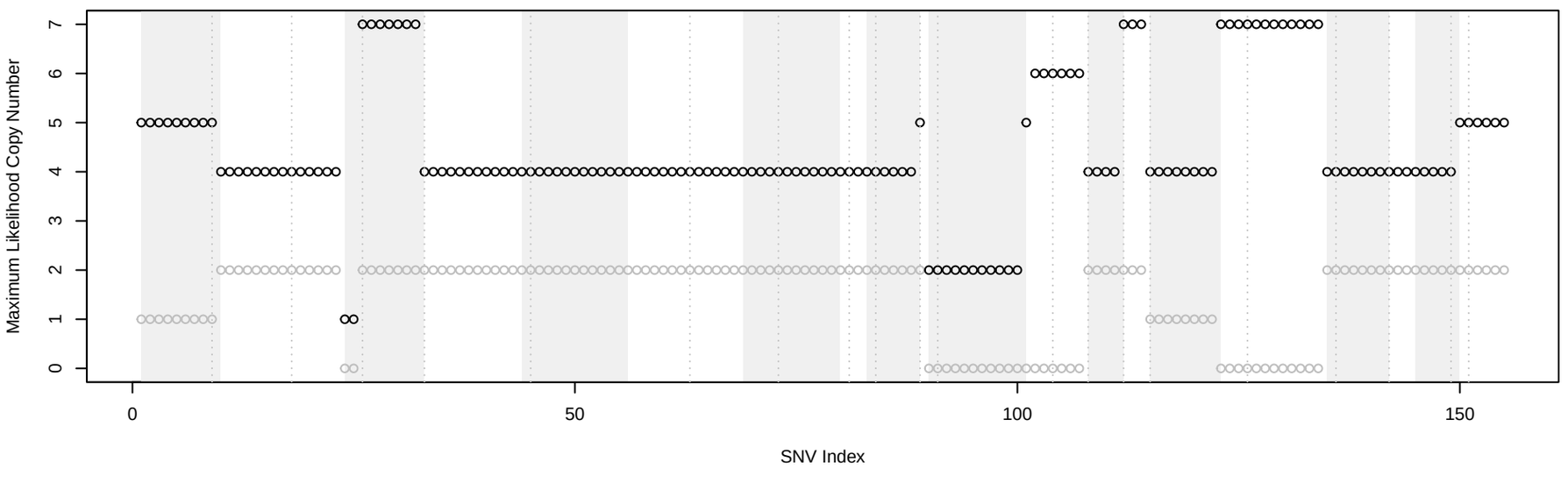

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m4
5m4
4m3
1m1
2m1
3m1
4m1
5m1

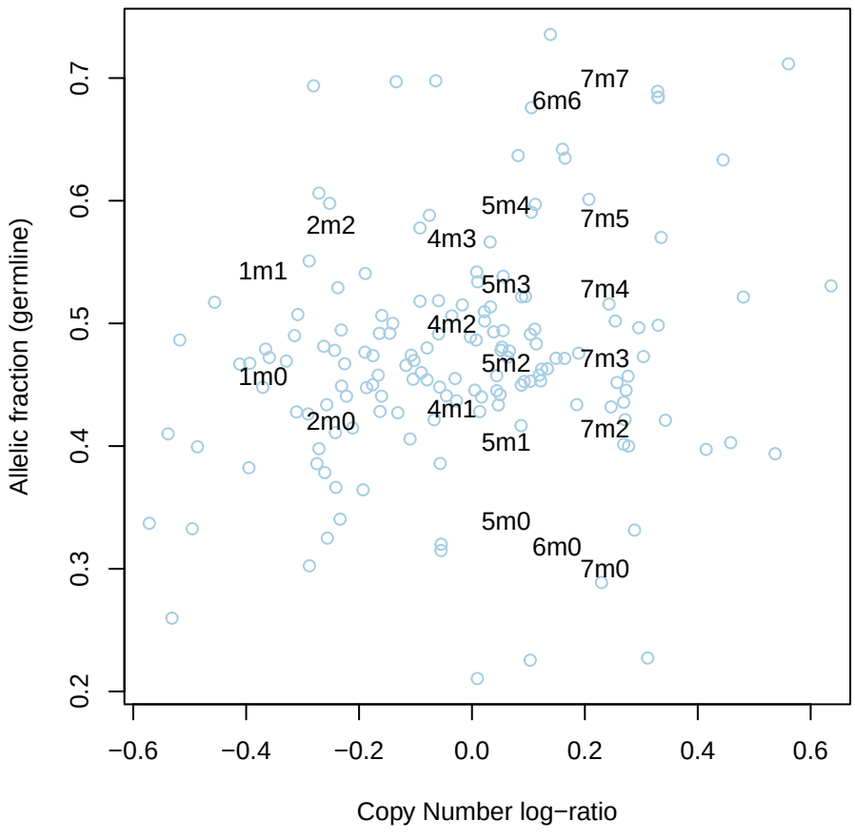

Frequency
Cellular fraction

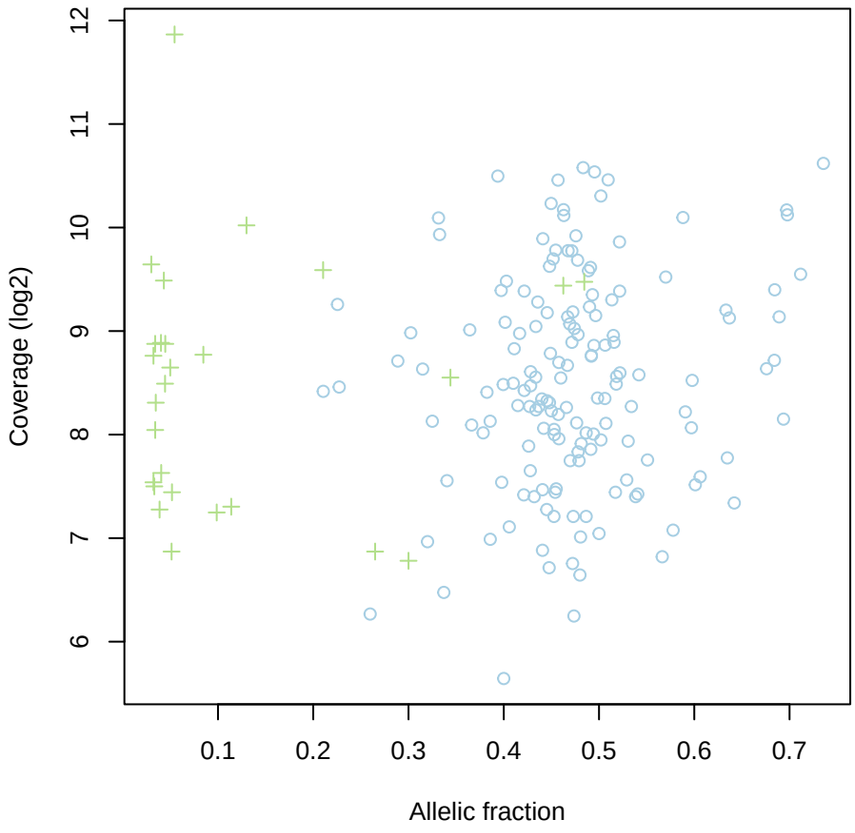

Purity: 0.16 Tumor ploidy: 4.361
0
1
2
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
log2 ratio

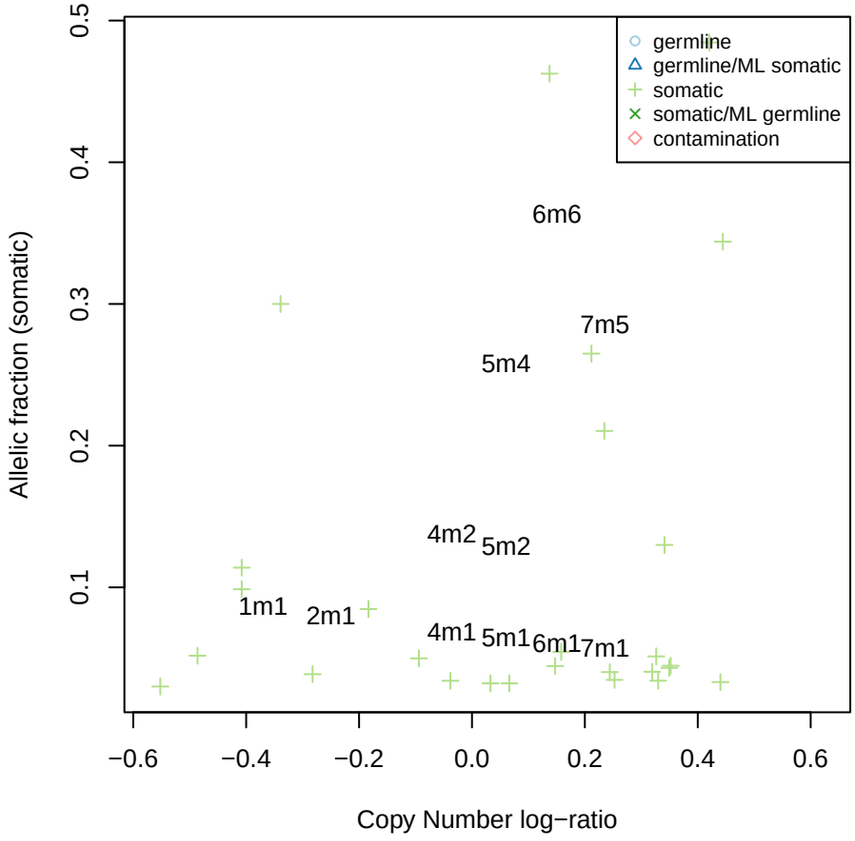

Purity: 0.16 Tumor ploidy: 4.361 SNV log−likelihood: −156.39 GoF: 93.4% Mean coverage: 473;222
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

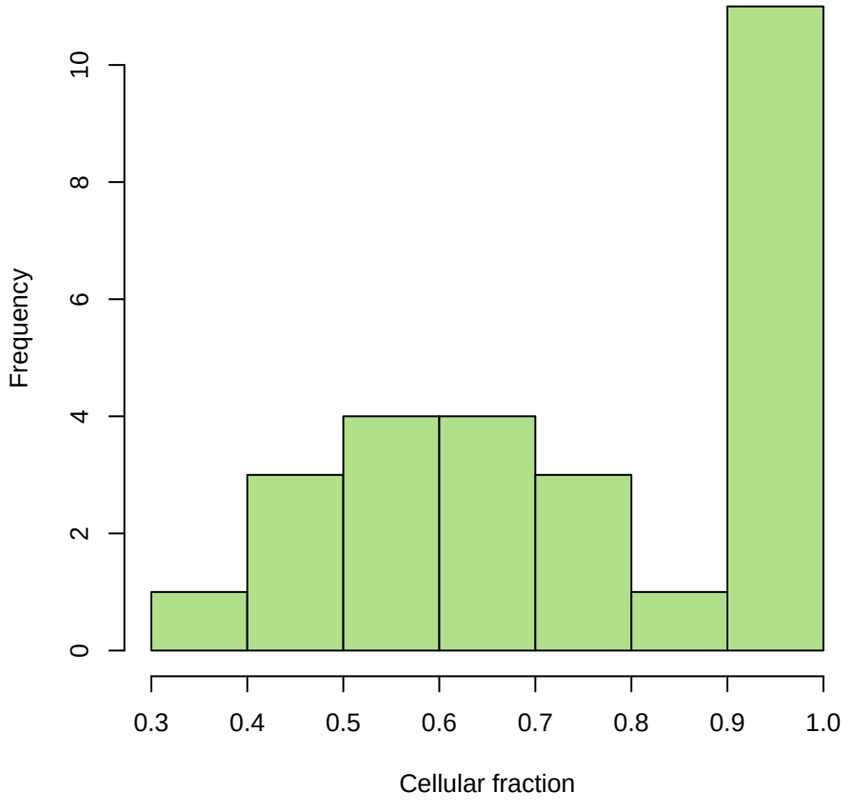

SCNA−fit log−likelihood: −15048.13
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4 6
0 50 100 150
SNV Index

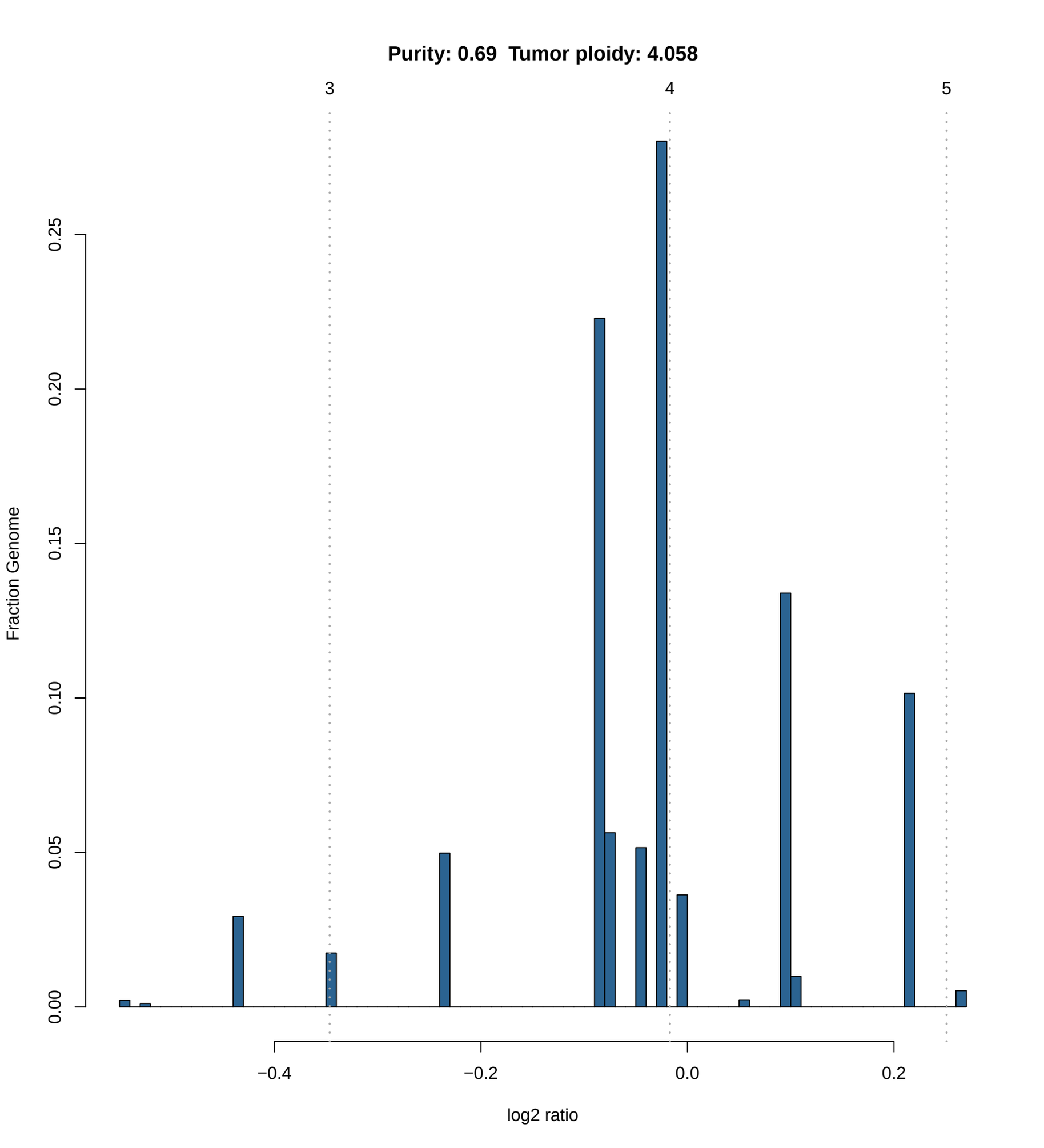

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

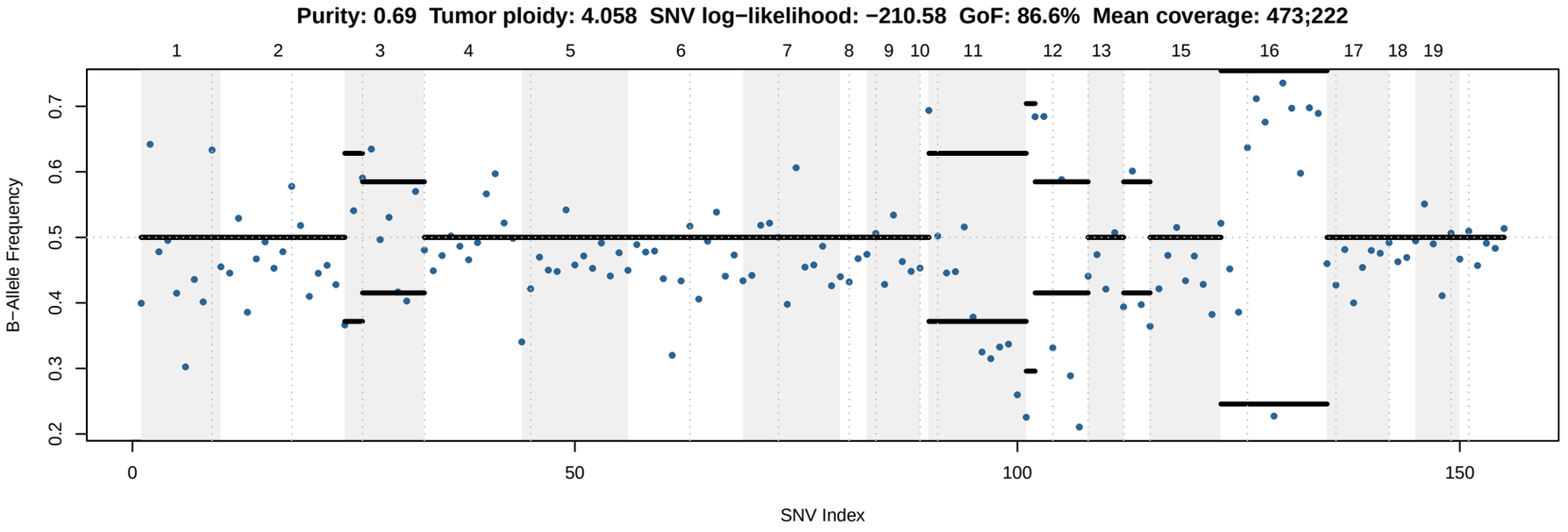

Allelic fraction (germline)
Copy Number log−ratio
7m7
6m6
5m4
7m5
2m2
4m3
1m1
5m3
7m4
4m2
1m0
5m2
7m3
4m1
2m0
7m2
5m1
5m0
6m0
7m0

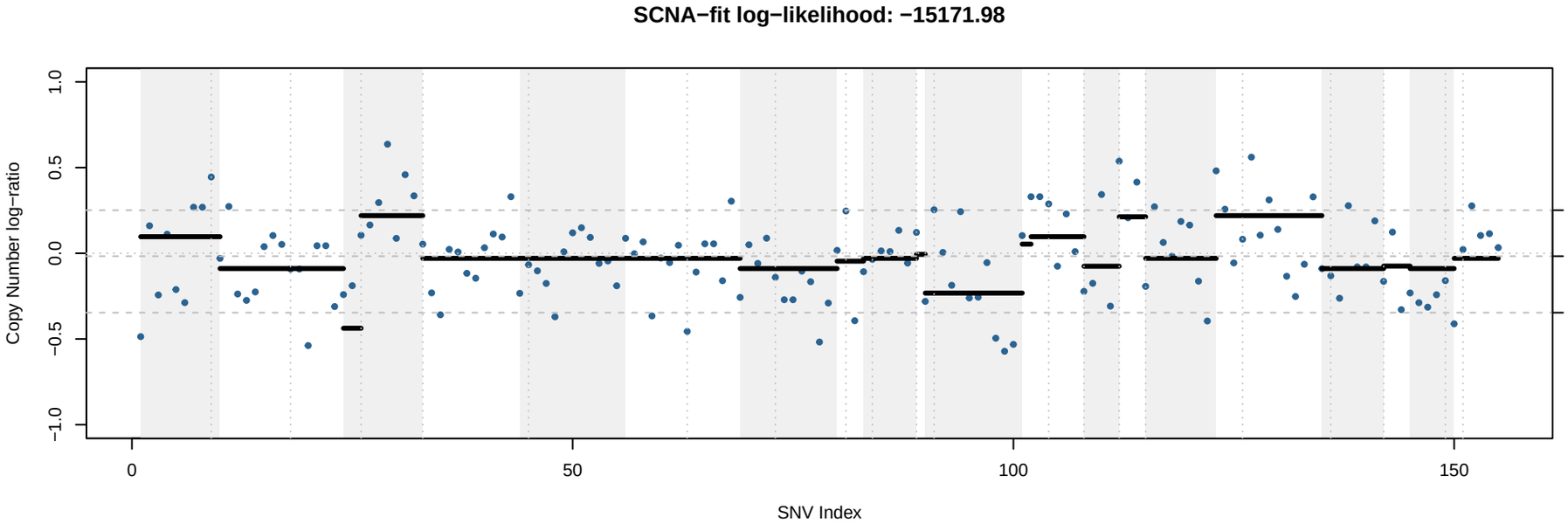

Coverage (log2)
Allelic fraction

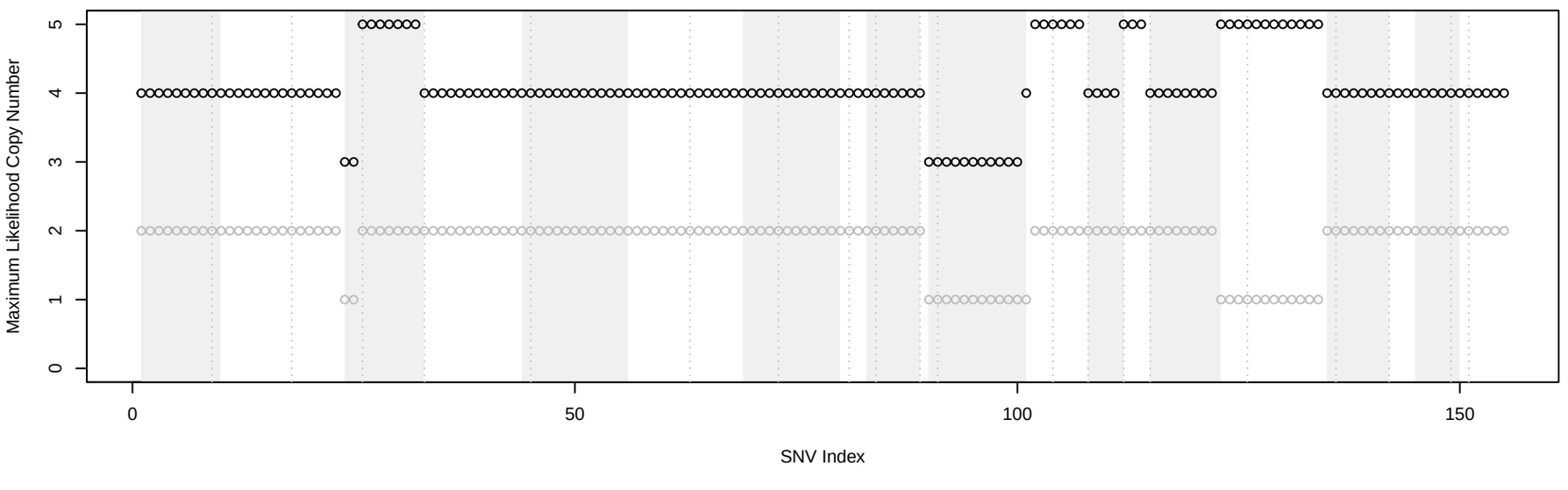

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
6m6
7m5
5m4
4m2
5m2
1m1
2m1
4m1
5m1
6m1
7m1

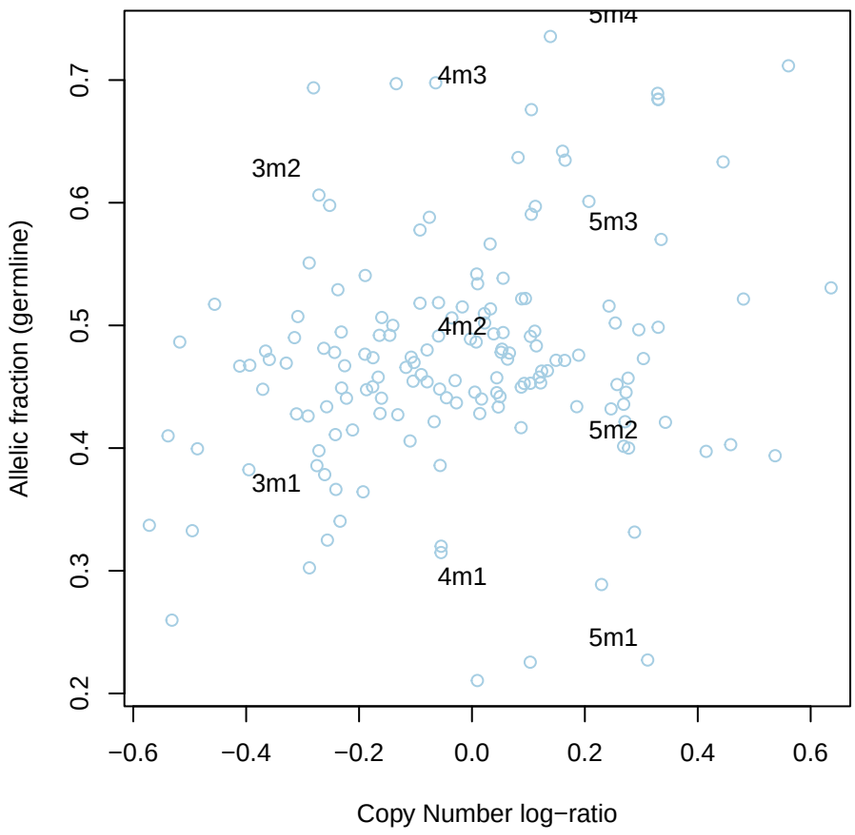

Frequency
Cellular fraction

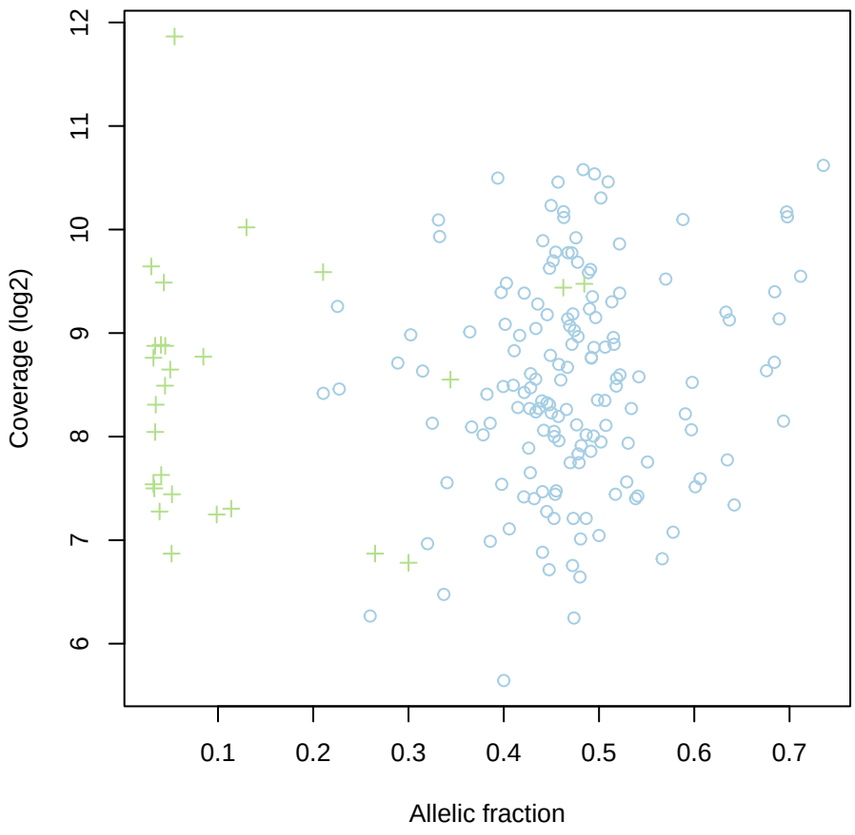

Purity: 0.69 Tumor ploidy: 4.058
3
4
5
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
log2 ratio

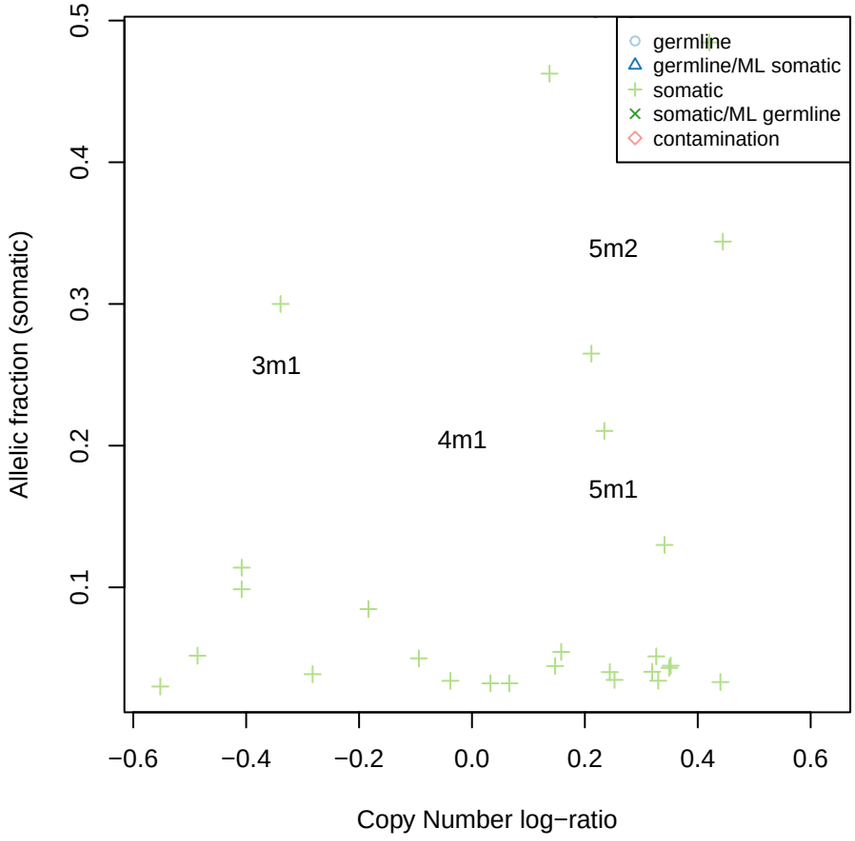

Purity: 0.69 Tumor ploidy: 4.058 SNV log−likelihood: −210.58 GoF: 86.6% Mean coverage: 473;222
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

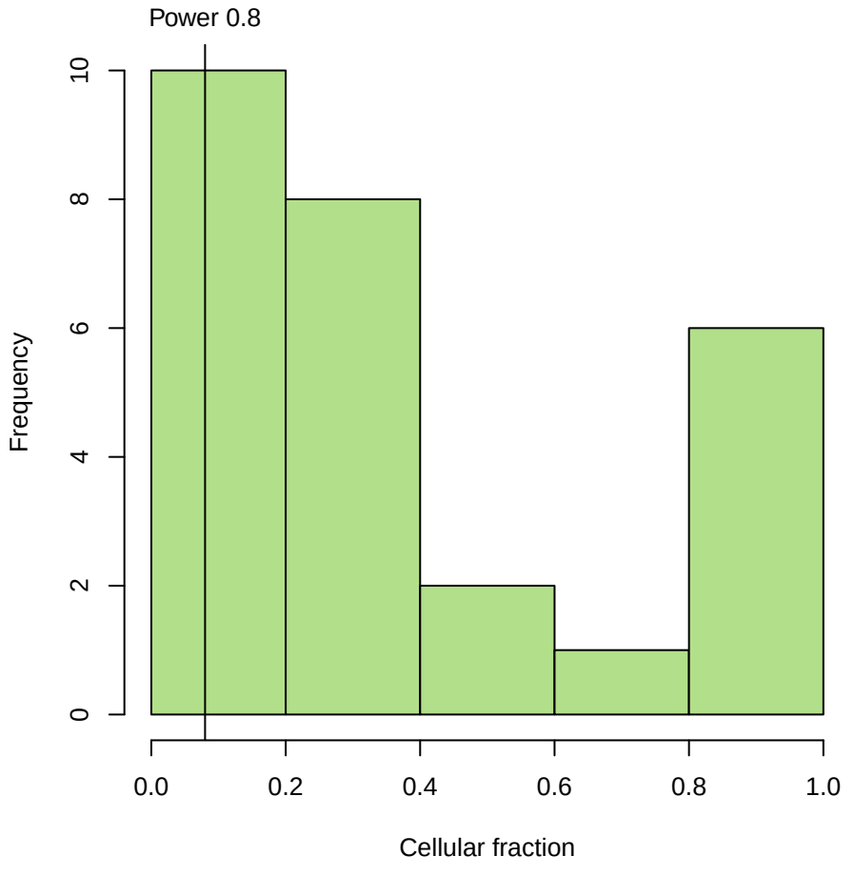

SCNA−fit log−likelihood: −15171.98
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5
0 50 100 150
SNV Index

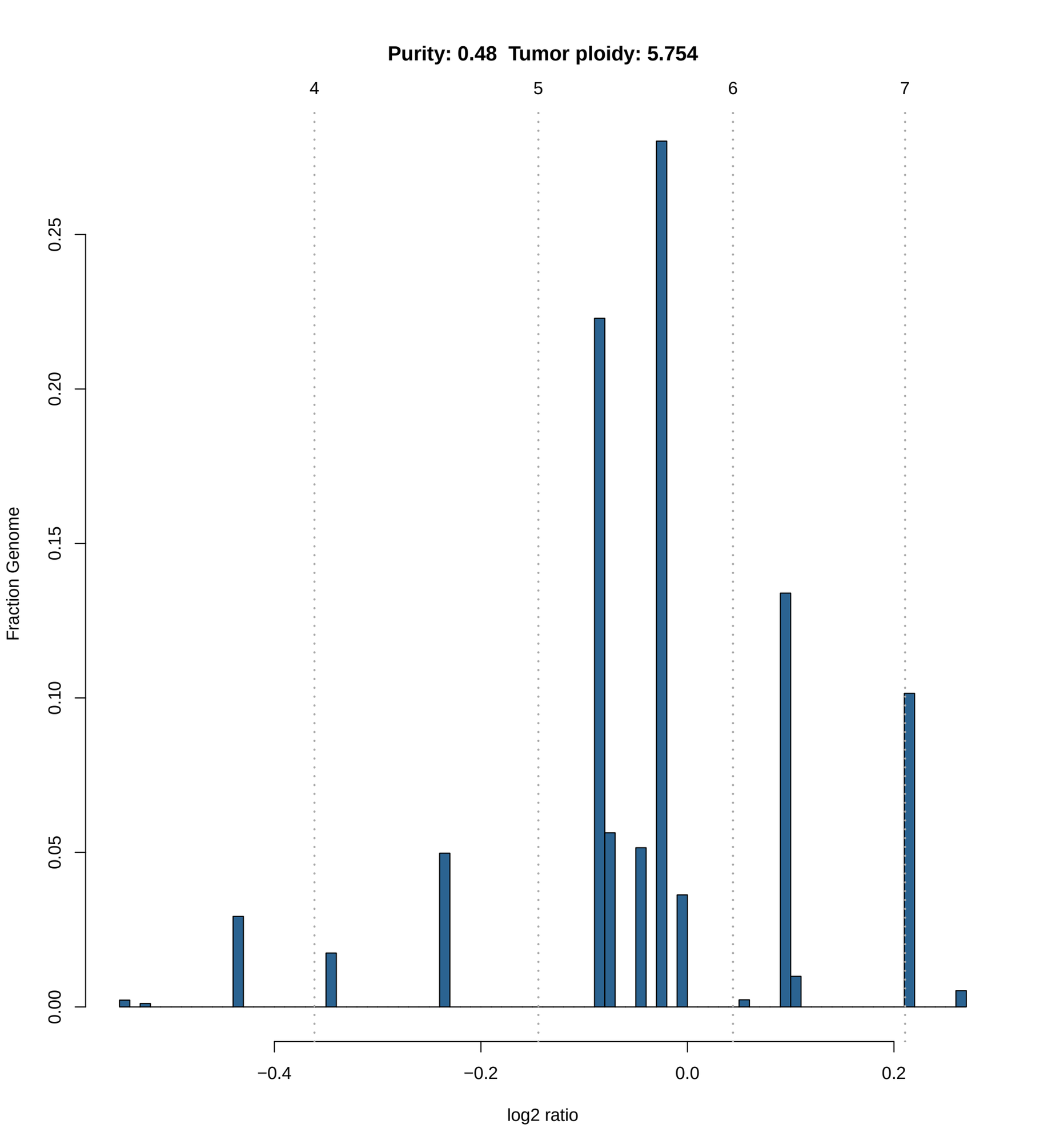

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

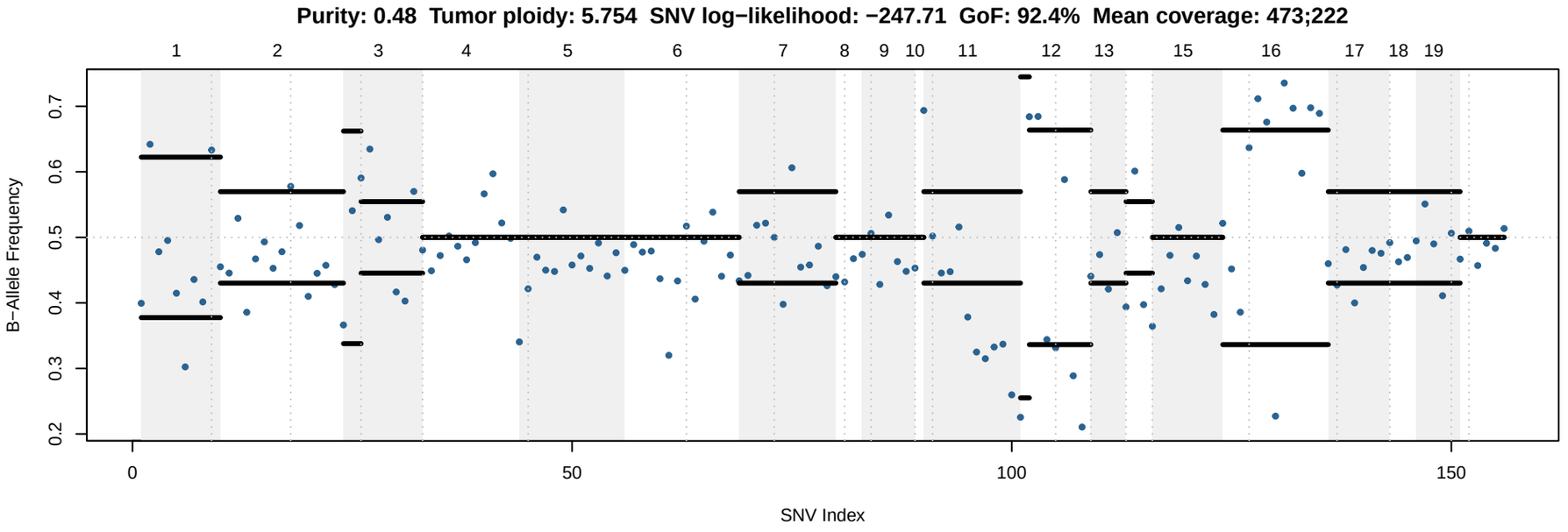

Allelic fraction (germline)
Copy Number log−ratio
5m4
4m3
3m2
5m3
4m2
5m2
3m1
4m1
5m1

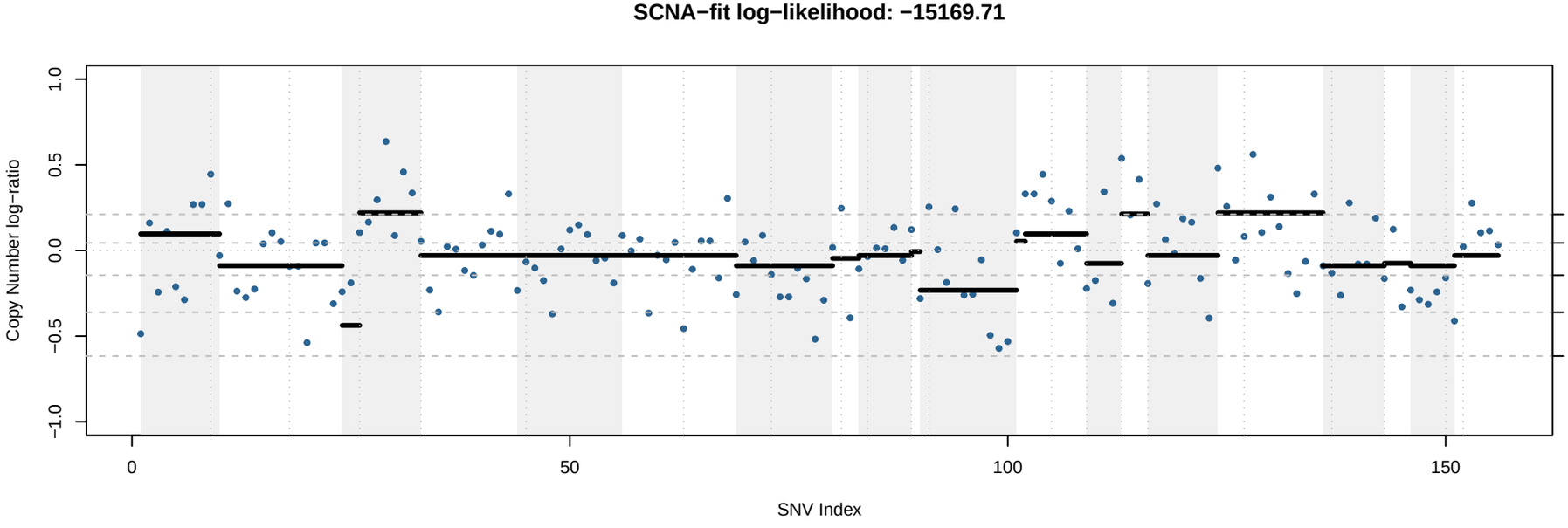

Coverage (log2)
Allelic fraction

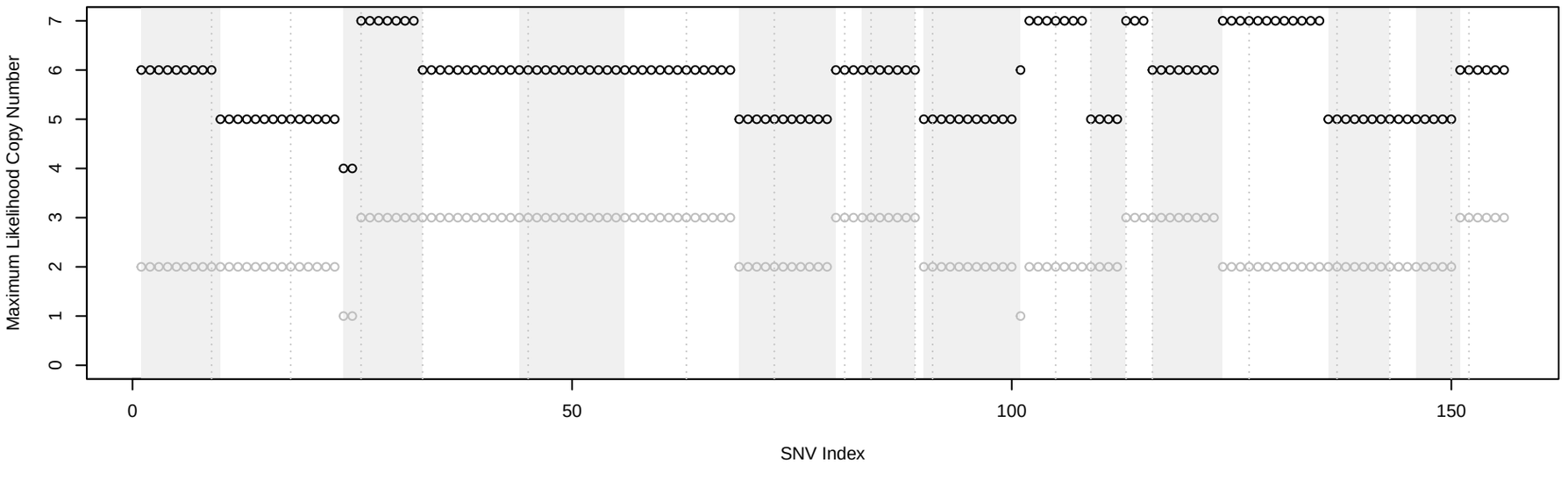

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m2
3m1
4m1
5m1

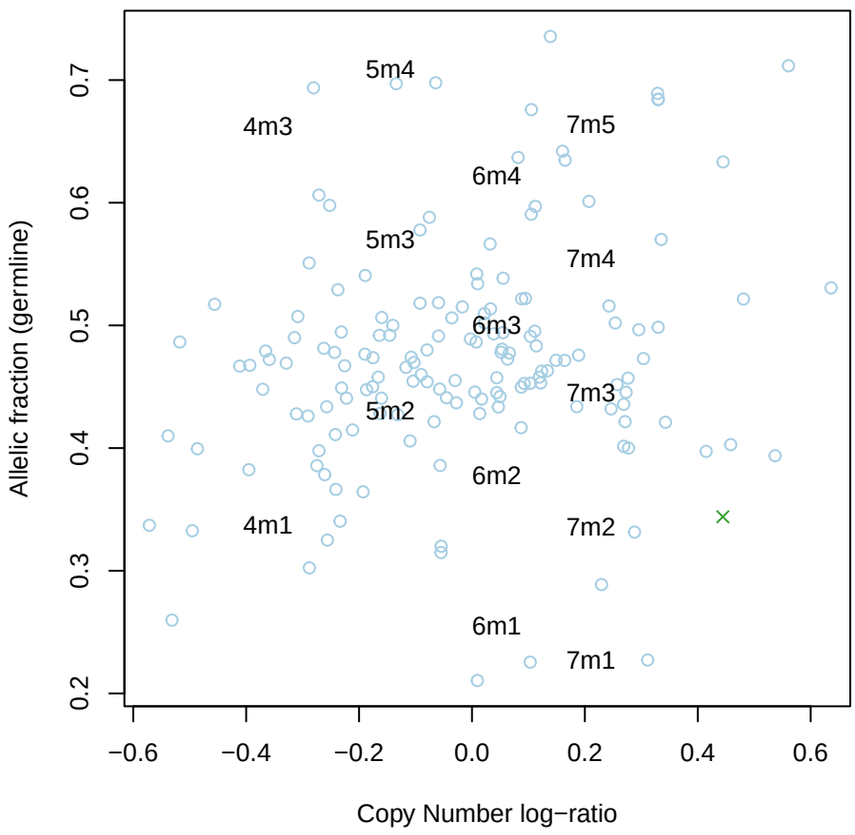

Power 0.8
Frequency
Cellular fraction

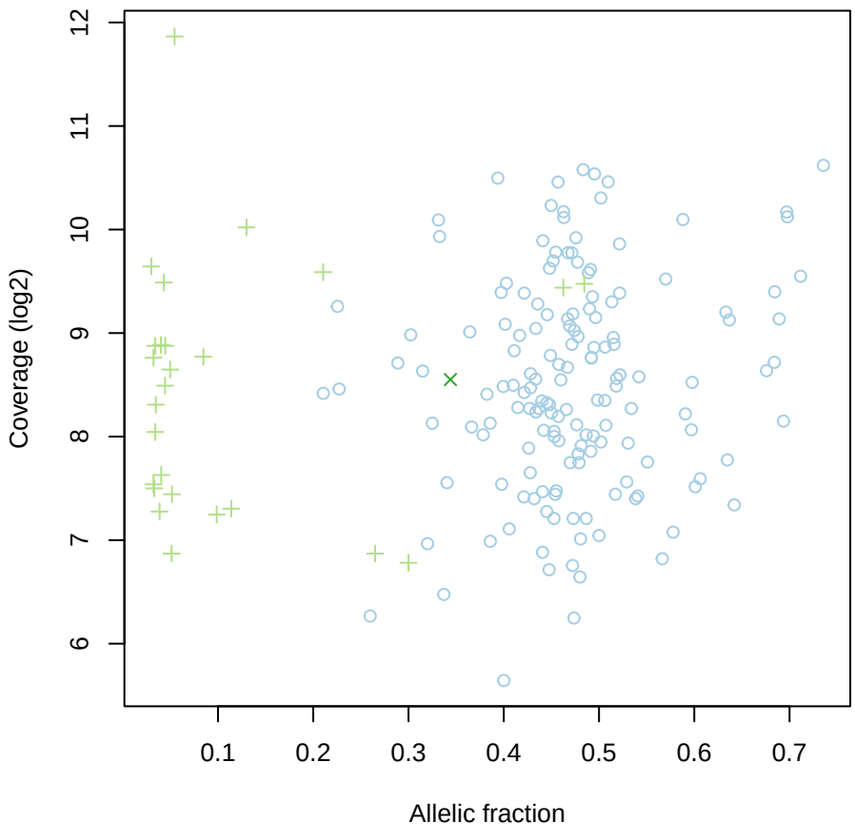

Purity: 0.48 Tumor ploidy: 5.754
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
log2 ratio

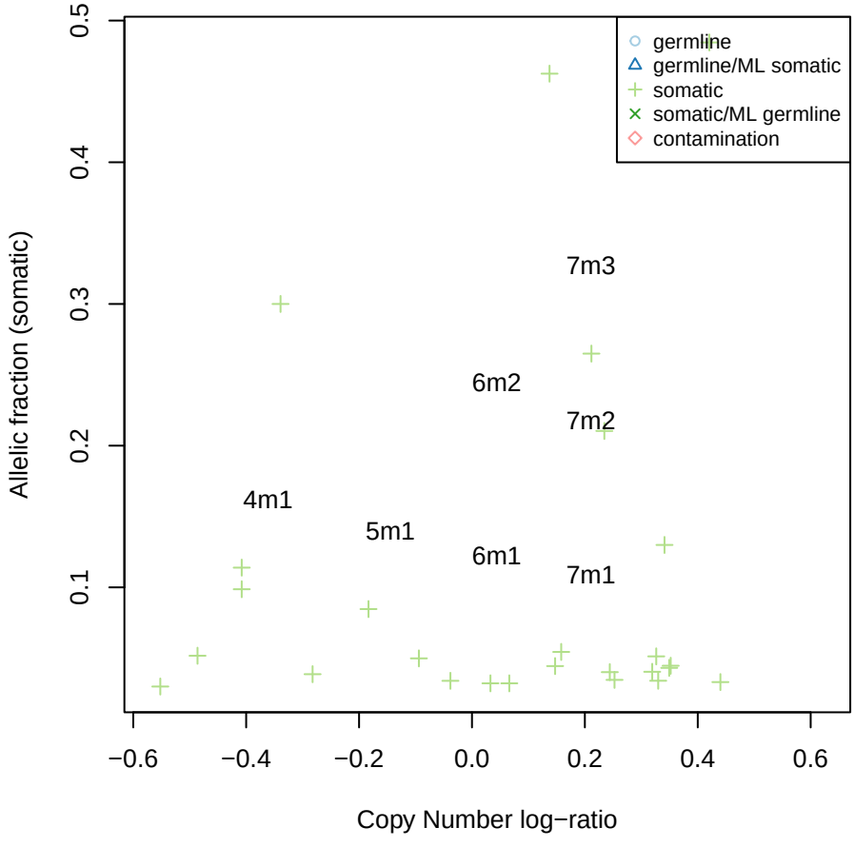

Purity: 0.48 Tumor ploidy: 5.754 SNV log−likelihood: −247.71 GoF: 92.4% Mean coverage: 473;222
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

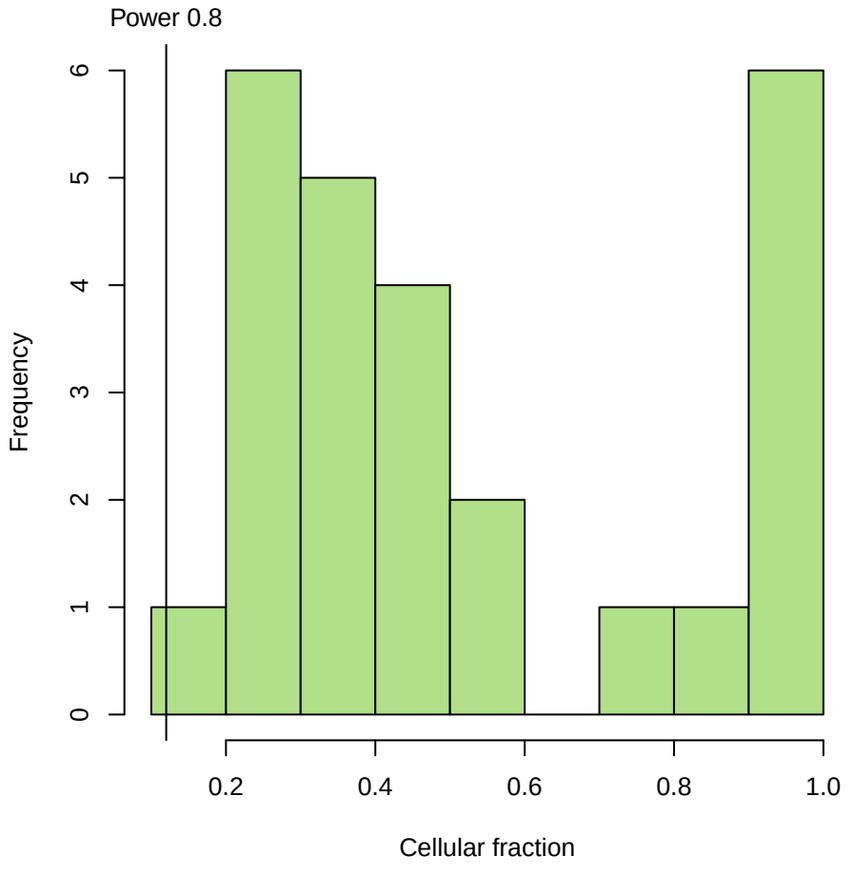

SCNA−fit log−likelihood: −15169.71
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 50 100 150
SNV Index

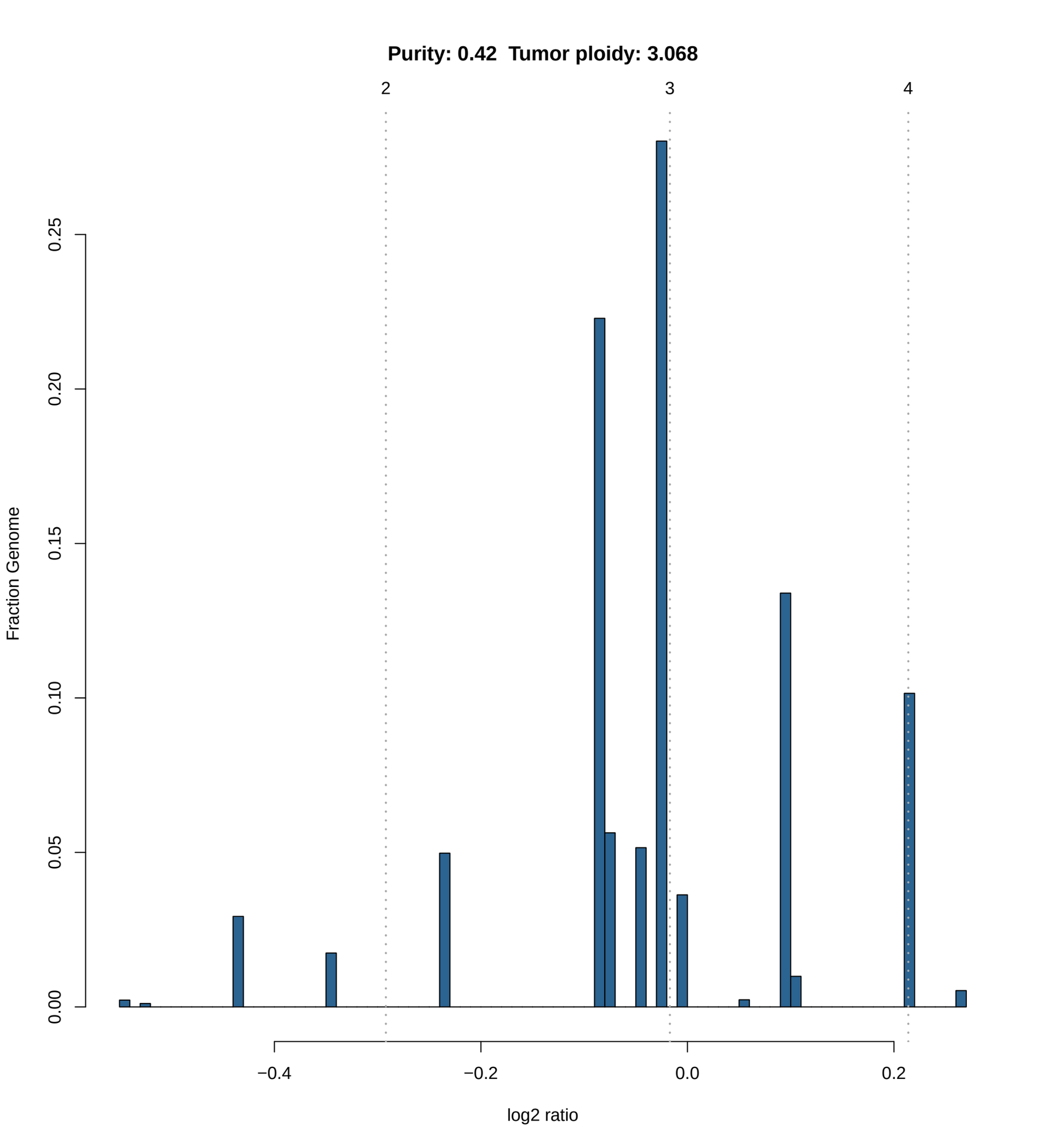

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

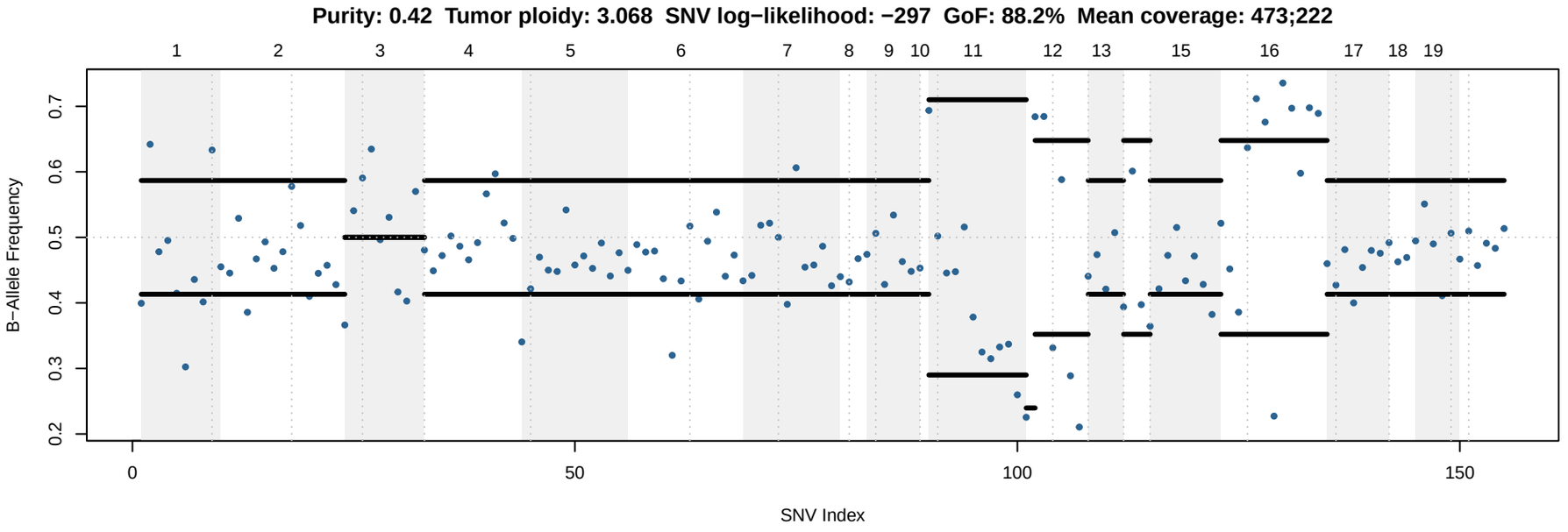

Allelic fraction (germline)
Copy Number log−ratio
5m4
4m3
7m5
6m4
5m3
7m4
6m3
7m3
5m2
6m2
4m1
7m2
6m1
7m1

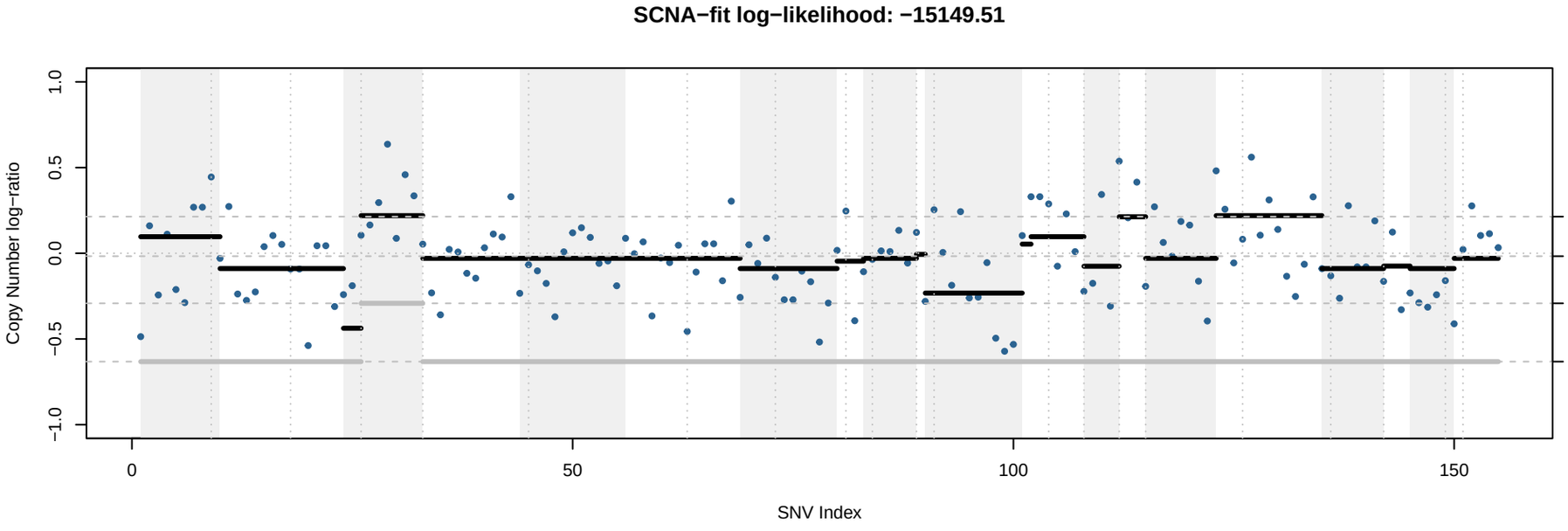

Coverage (log2)
Allelic fraction

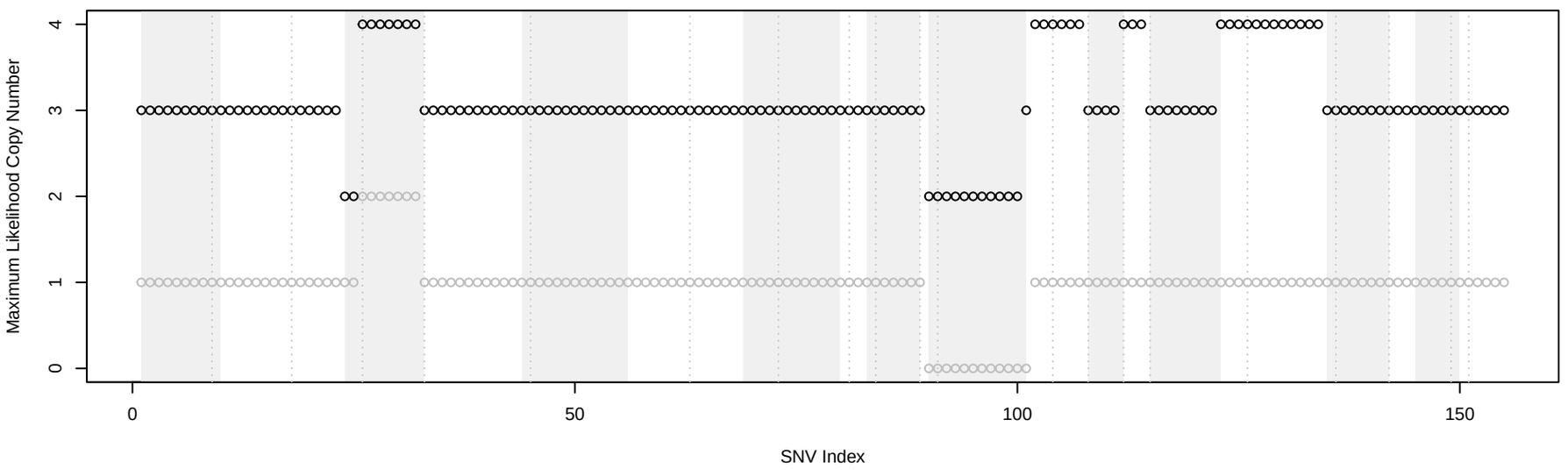

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
7m3
6m2
7m2
4m1
5m1
6m1
7m1

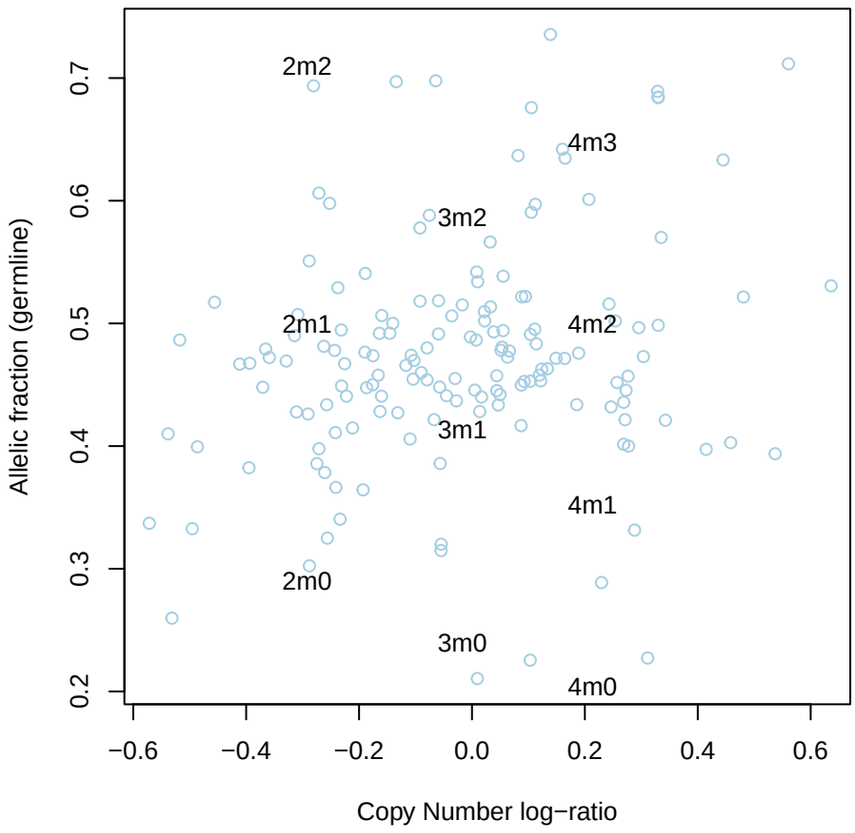

Power 0.8
Frequency
Cellular fraction

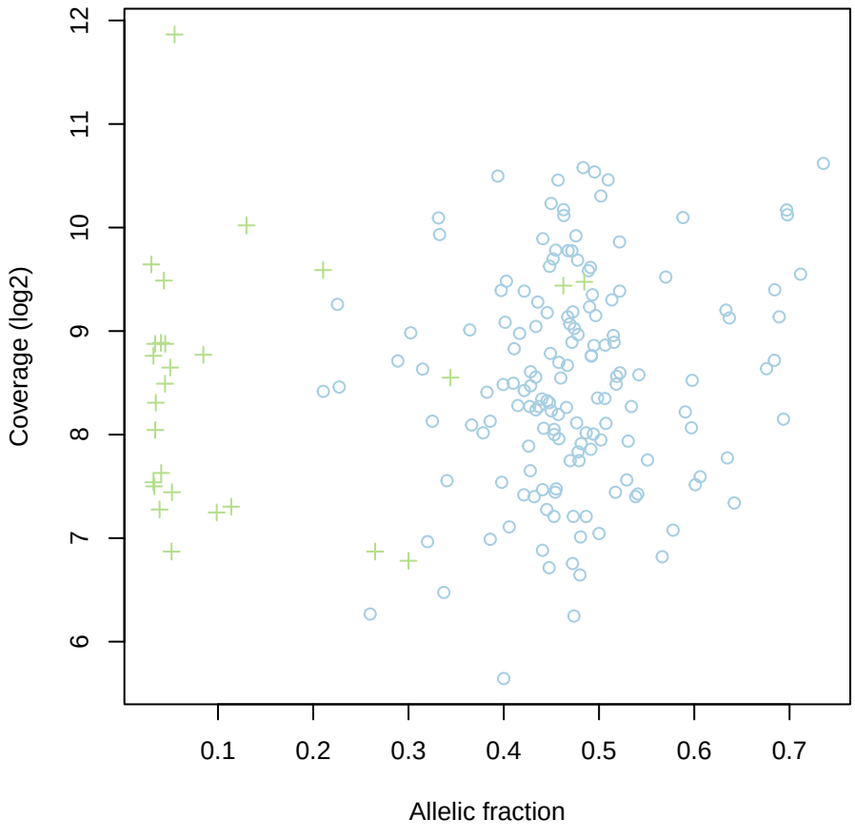

Purity: 0.42 Tumor ploidy: 3.068
2
3
4
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
log2 ratio

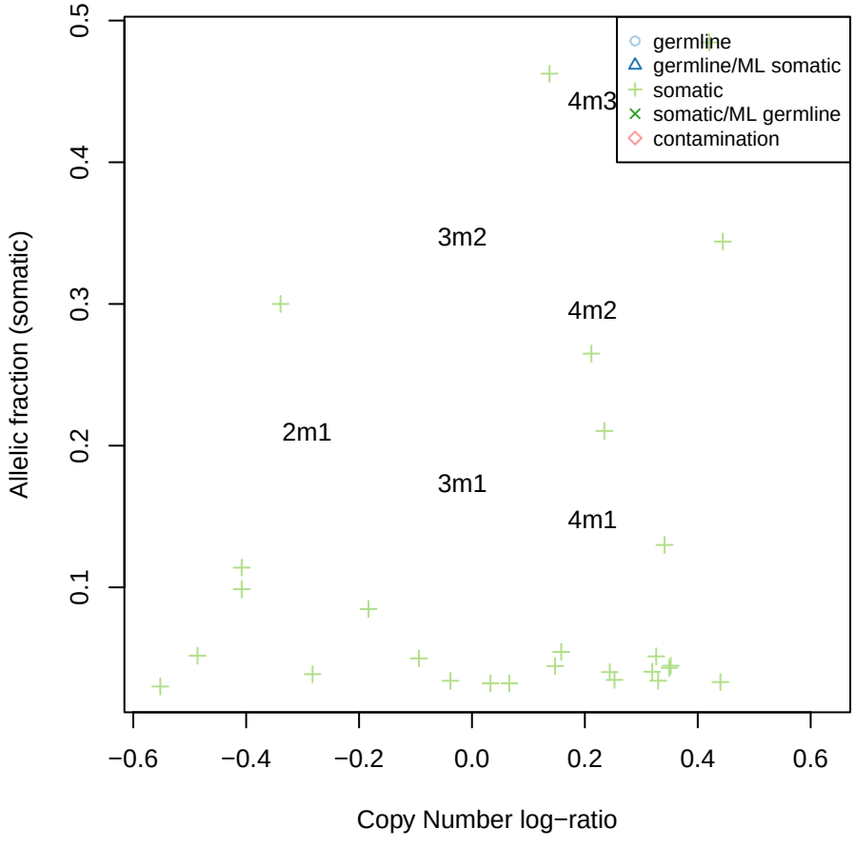

Purity: 0.42 Tumor ploidy: 3.068 SNV log−likelihood: −297 GoF: 88.2% Mean coverage: 473;222
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

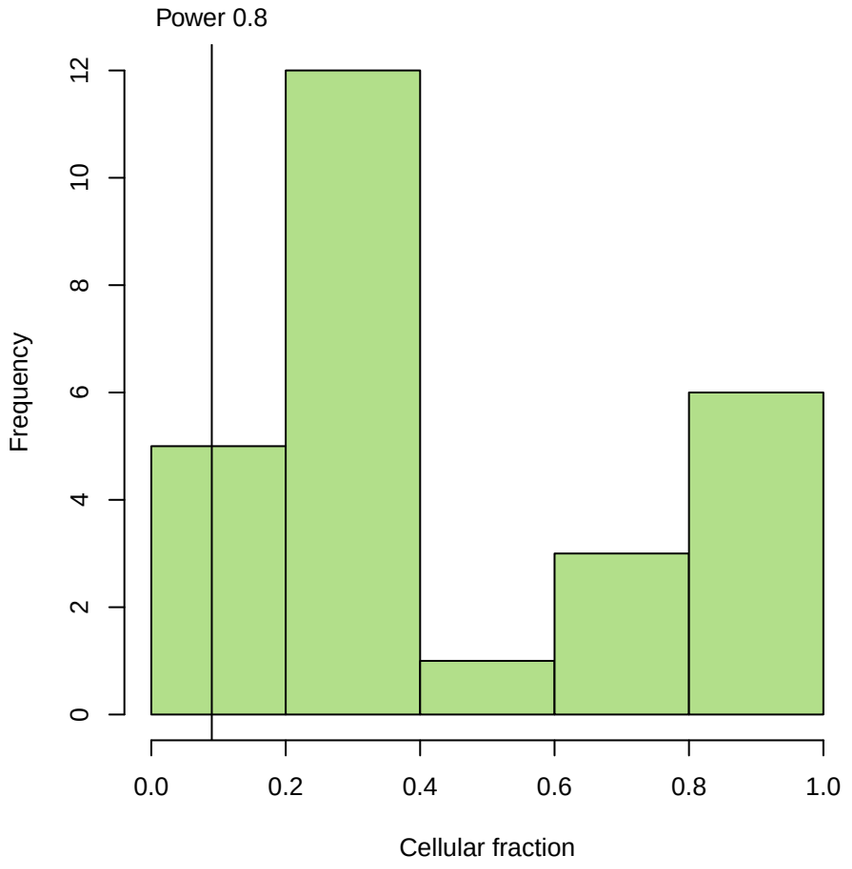

SCNA−fit log−likelihood: −15149.51
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4
0 50 100 150
SNV Index

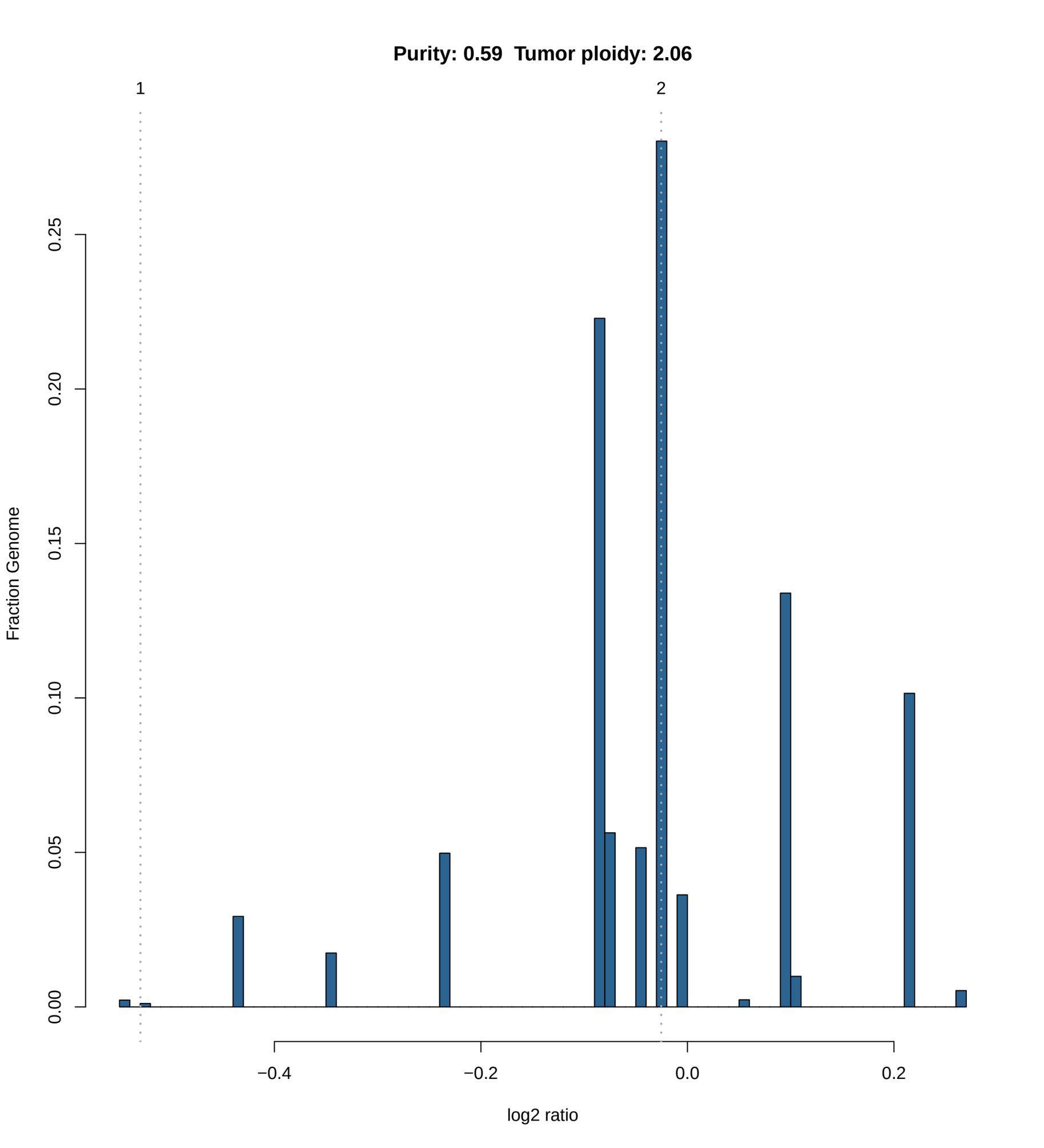

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

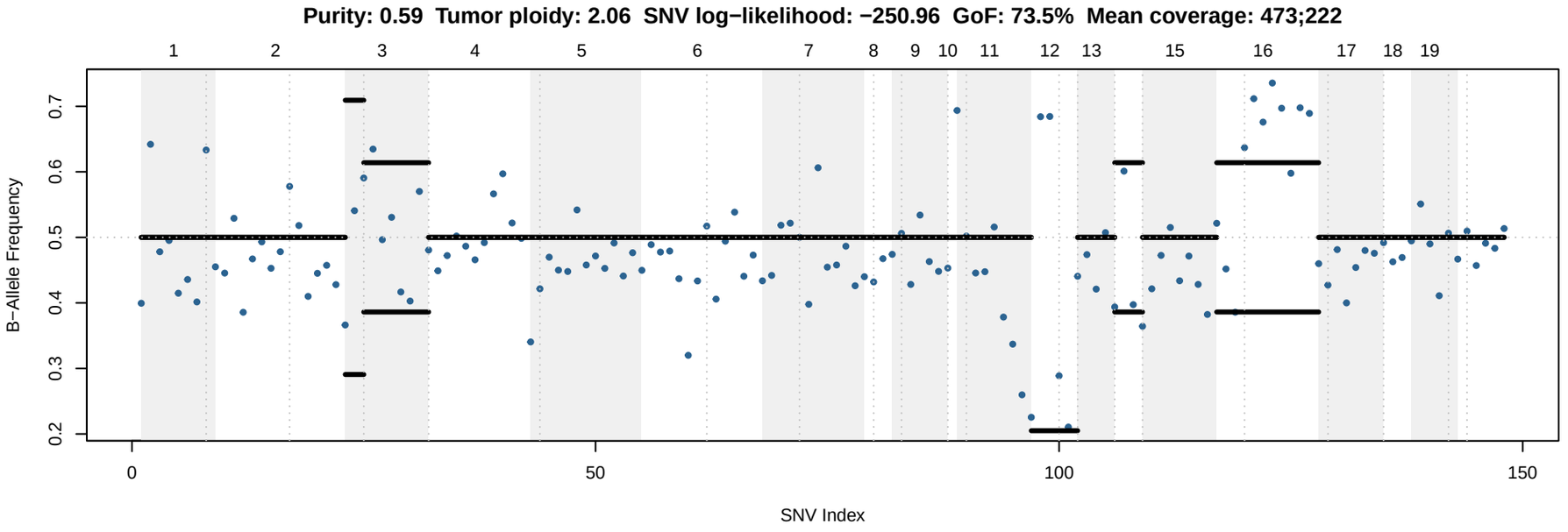

Allelic fraction (germline)
Copy Number log−ratio
2m2
4m3
3m2
2m1
4m2
3m1
4m1
2m0
3m0
4m0

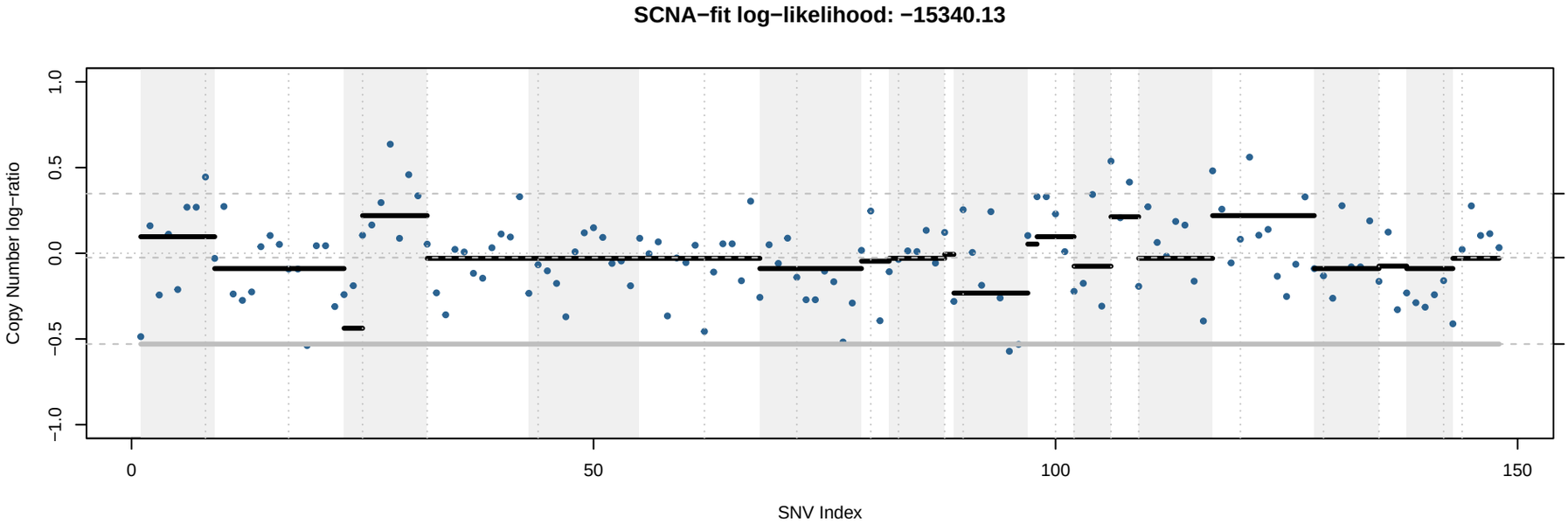

Coverage (log2)
Allelic fraction

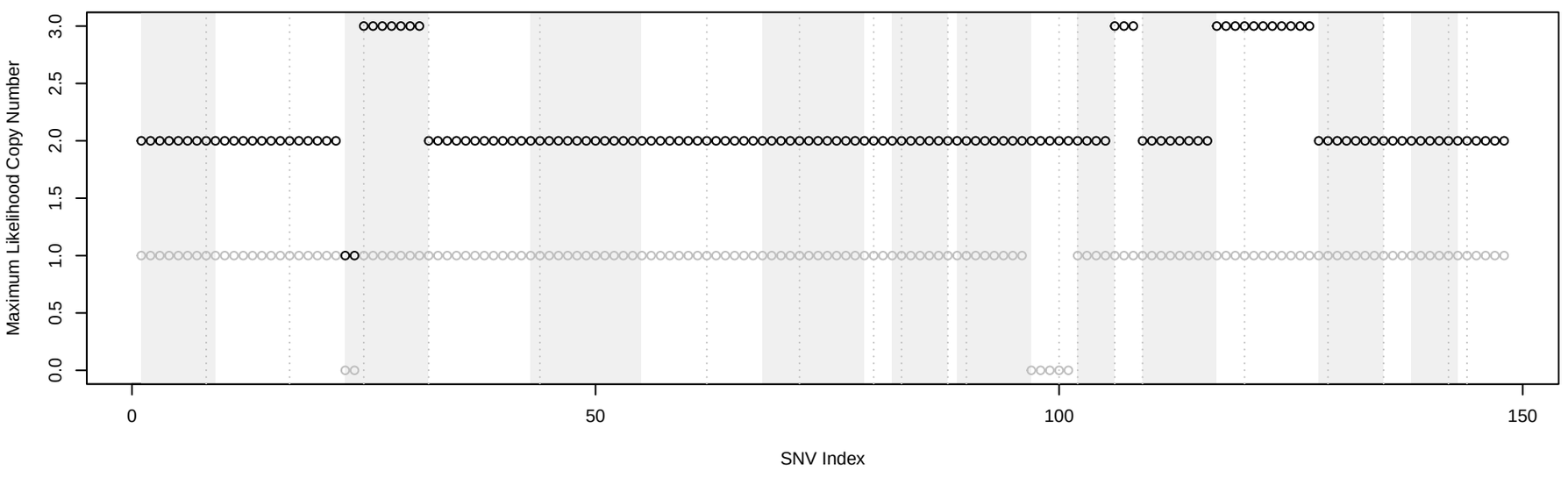

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m3
3m2
4m2
2m1
3m1
4m1

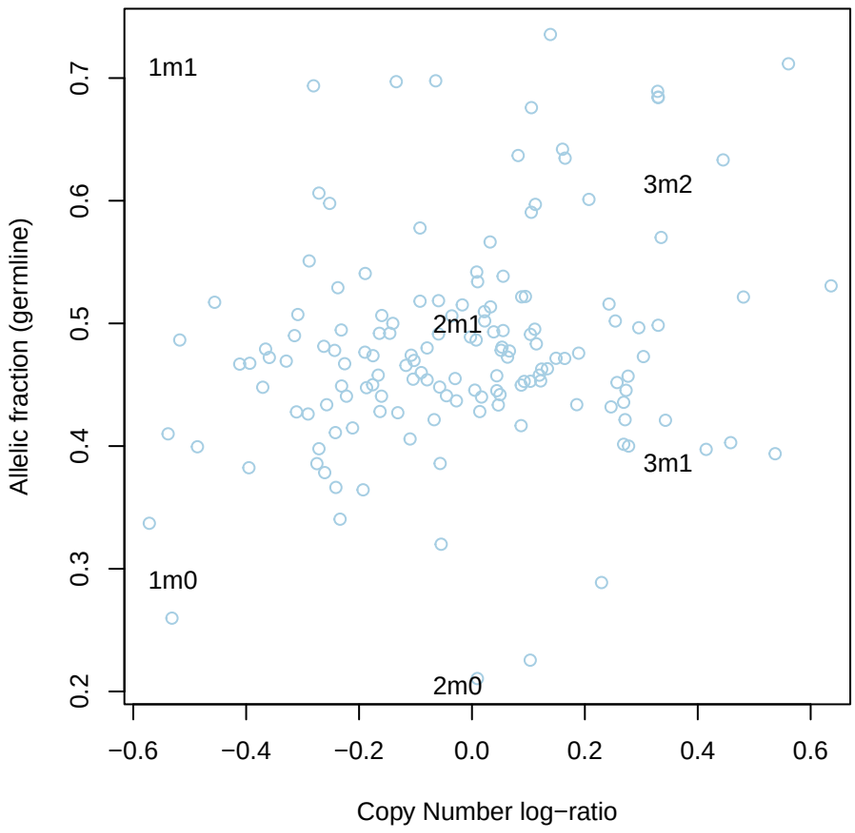

Power 0.8
Frequency
Cellular fraction

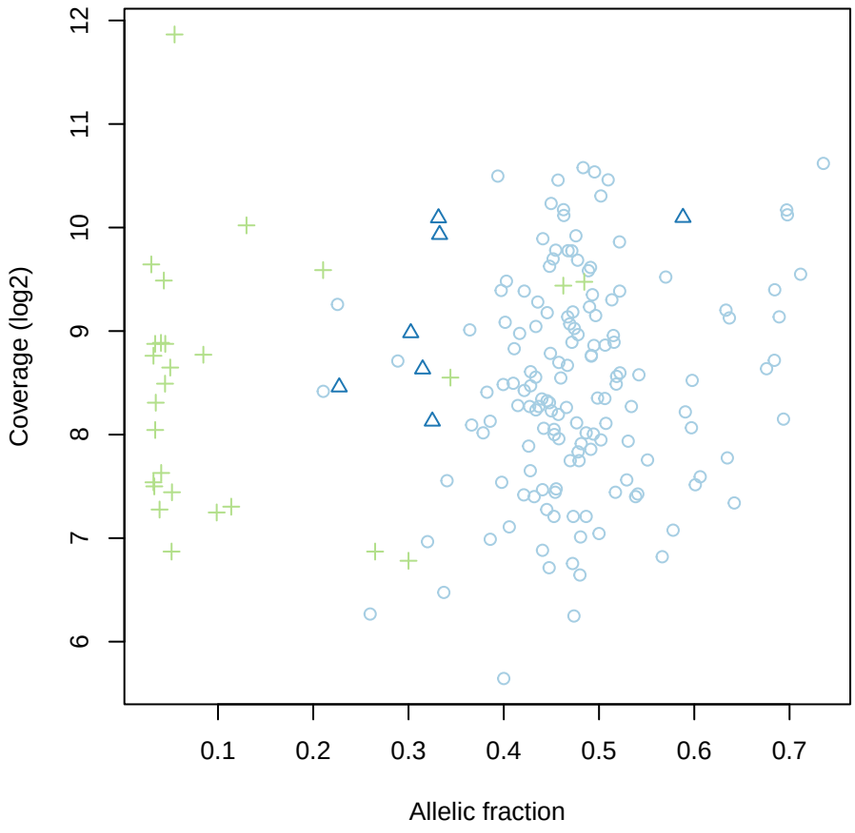

Purity: 0.59 Tumor ploidy: 2.06
1
2
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
log2 ratio

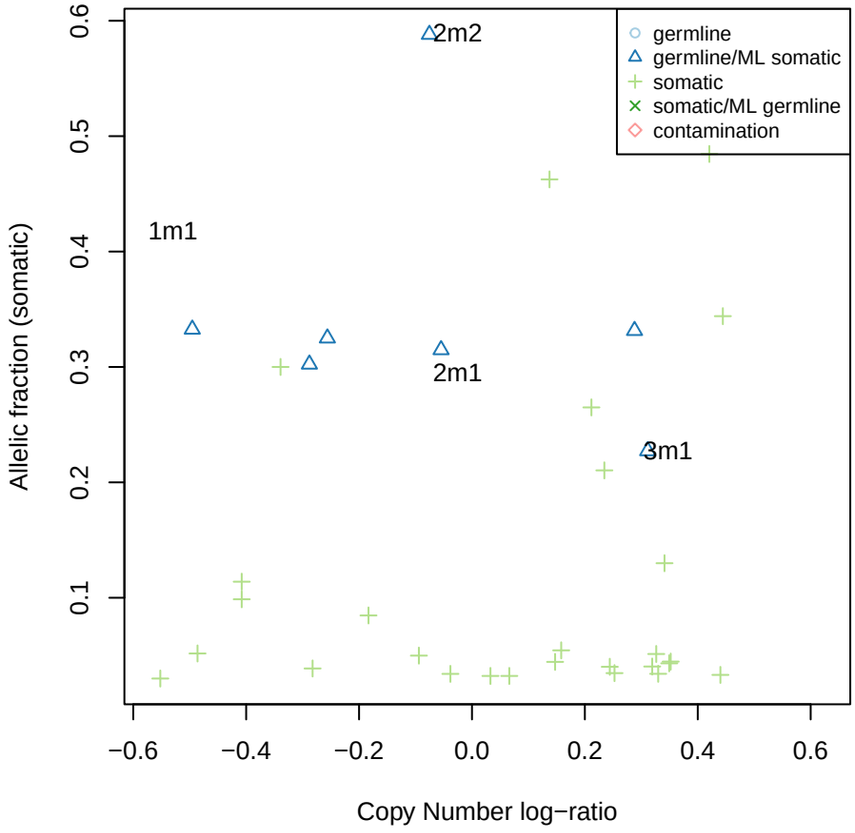

Purity: 0.59 Tumor ploidy: 2.06 SNV log−likelihood: −250.96 GoF: 73.5% Mean coverage: 473;222
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

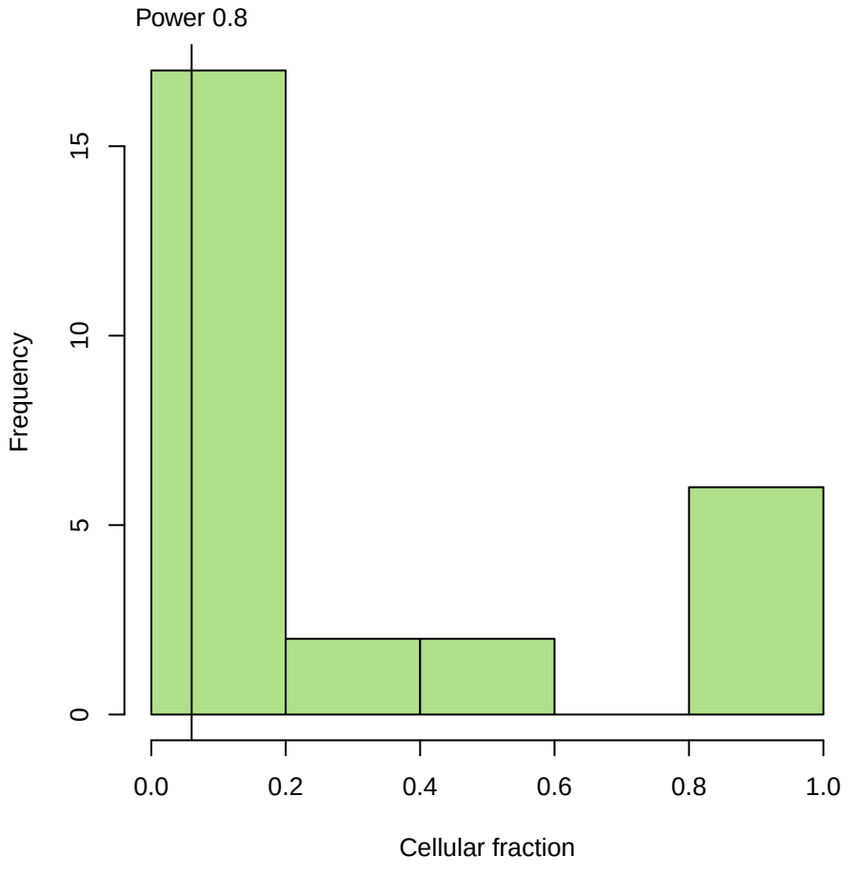

SCNA−fit log−likelihood: −15340.13
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3
0 50 100 150
SNV Index

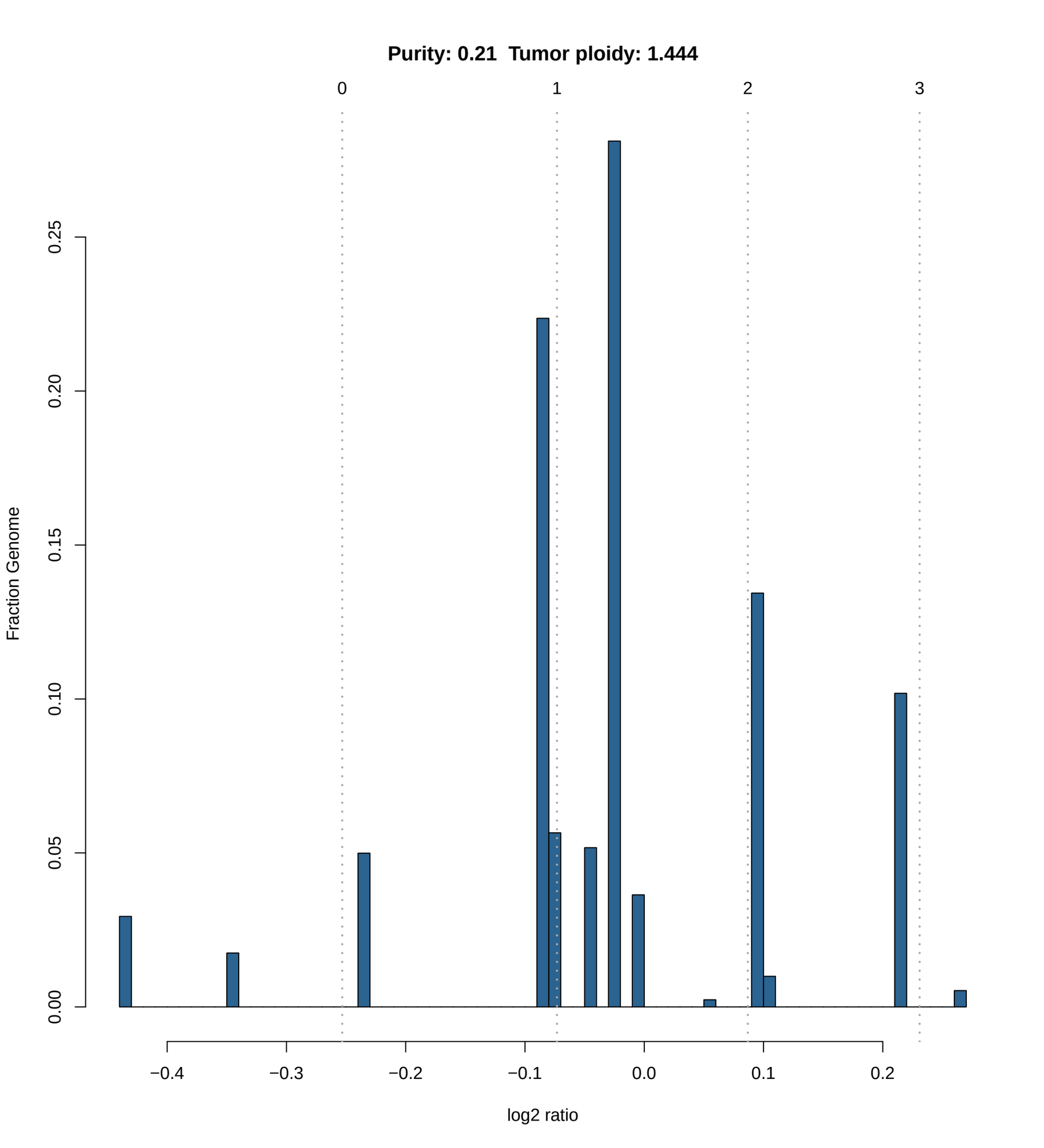

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

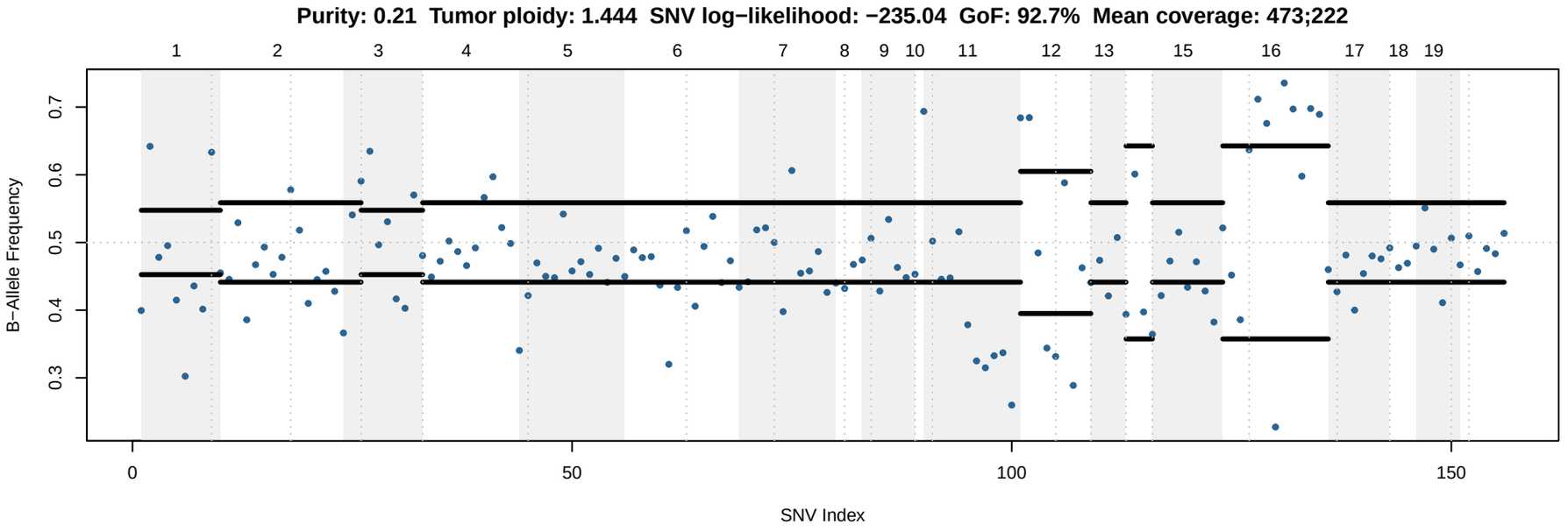

1m1
3m2
2m1
3m1
1m0
2m0
Allelic fraction (germline)
Copy Number log−ratio

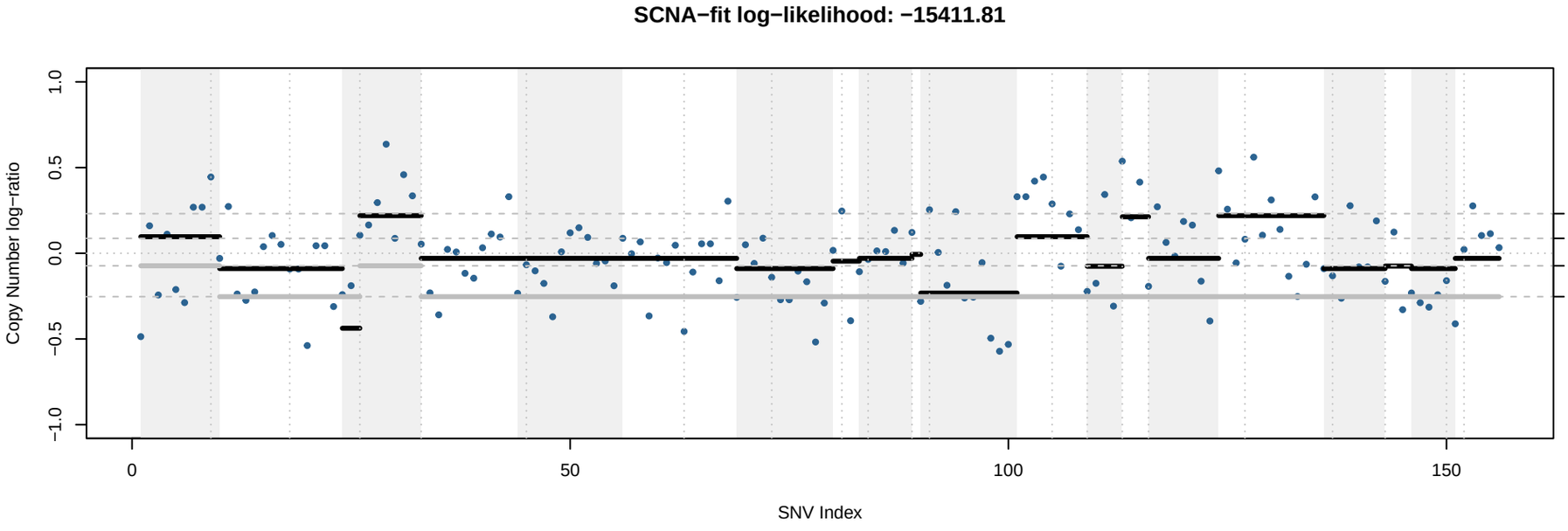

Coverage (log2)
Allelic fraction

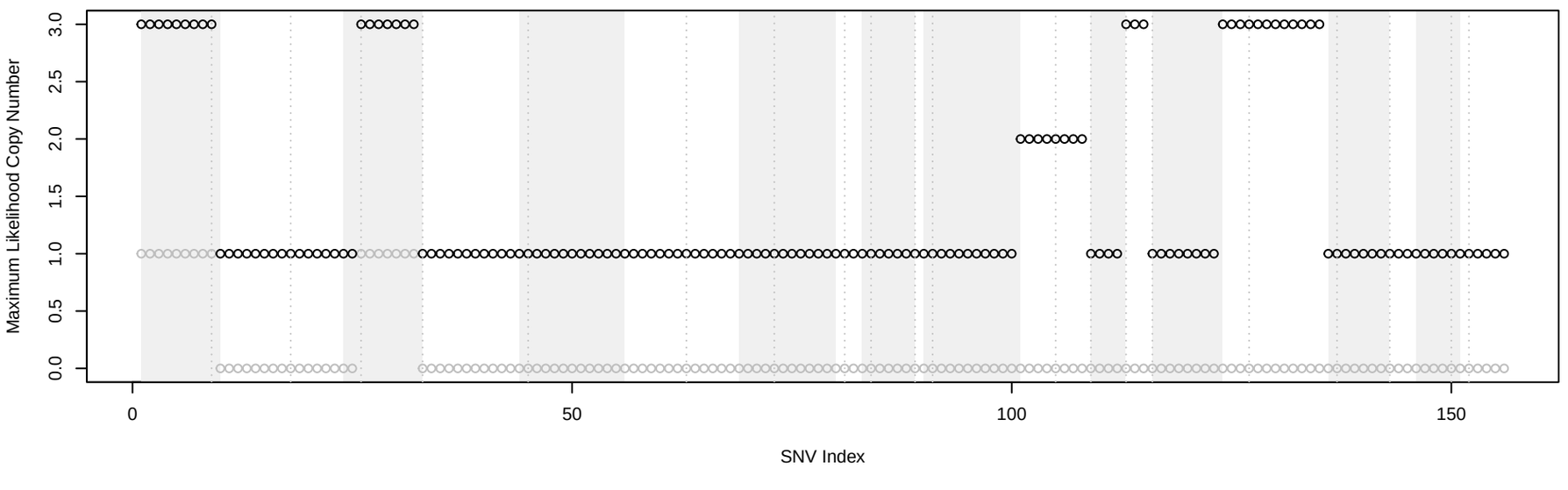

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
1m1
2m1
3m1
Allelic fraction (somatic)
Copy Number log−ratio

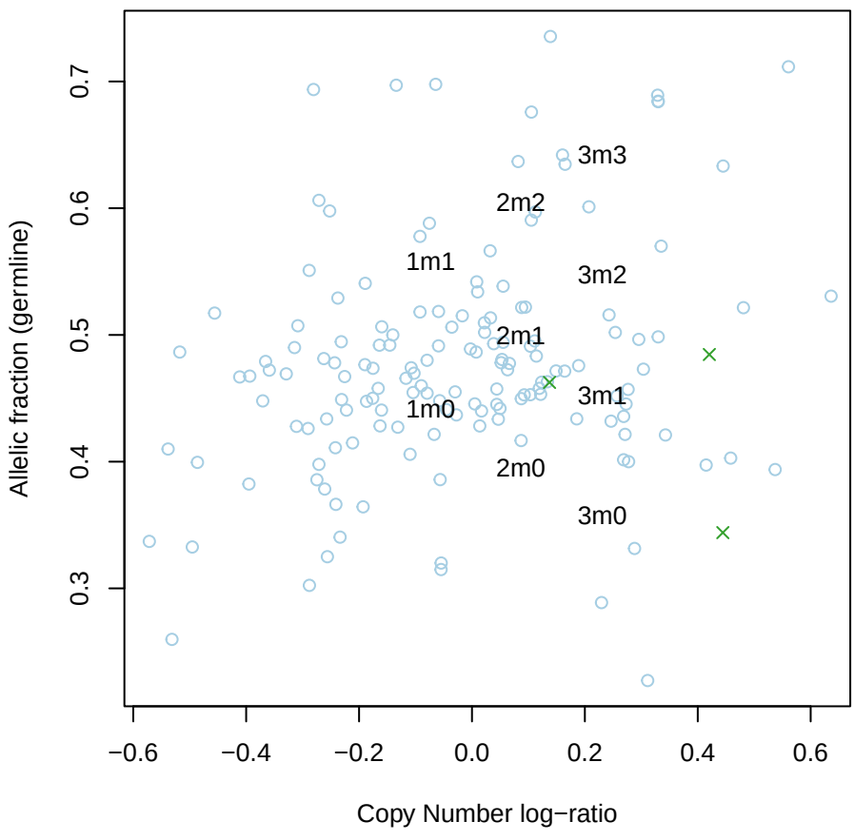

Power 0.8
Frequency
Cellular fraction

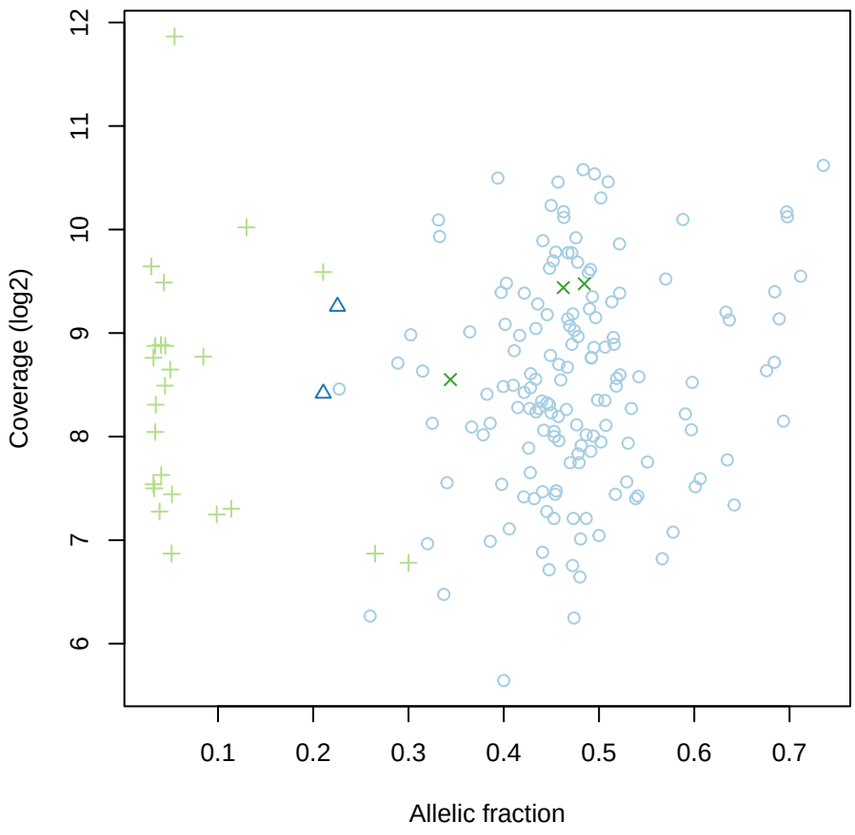

Purity: 0.21 Tumor ploidy: 1.444
0
1
2
3
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.3
−0.2
−0.1
0.0
0.1
0.2
log2 ratio

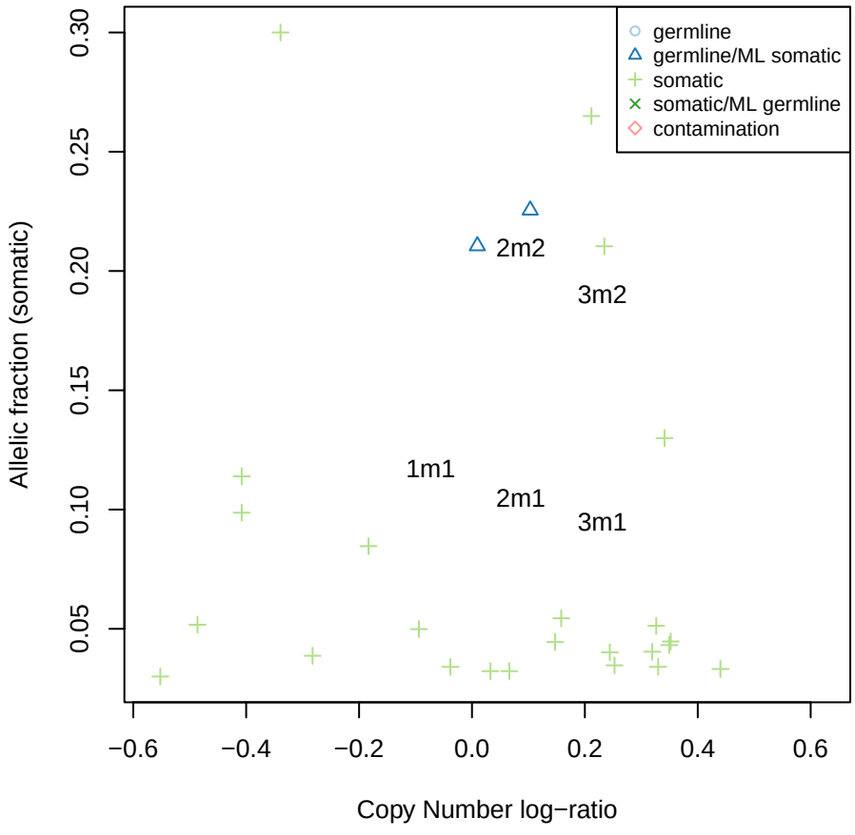

Purity: 0.21 Tumor ploidy: 1.444 SNV log−likelihood: −235.04 GoF: 92.7% Mean coverage: 473;222
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

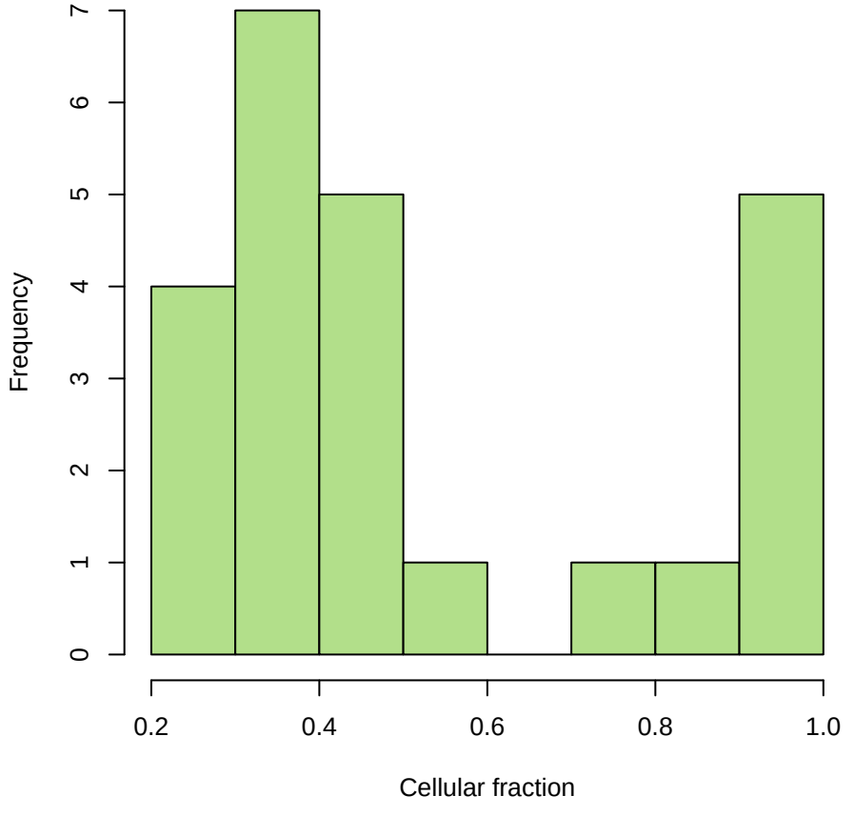

SCNA−fit log−likelihood: −15411.81
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3
0 50 100 150
SNV Index

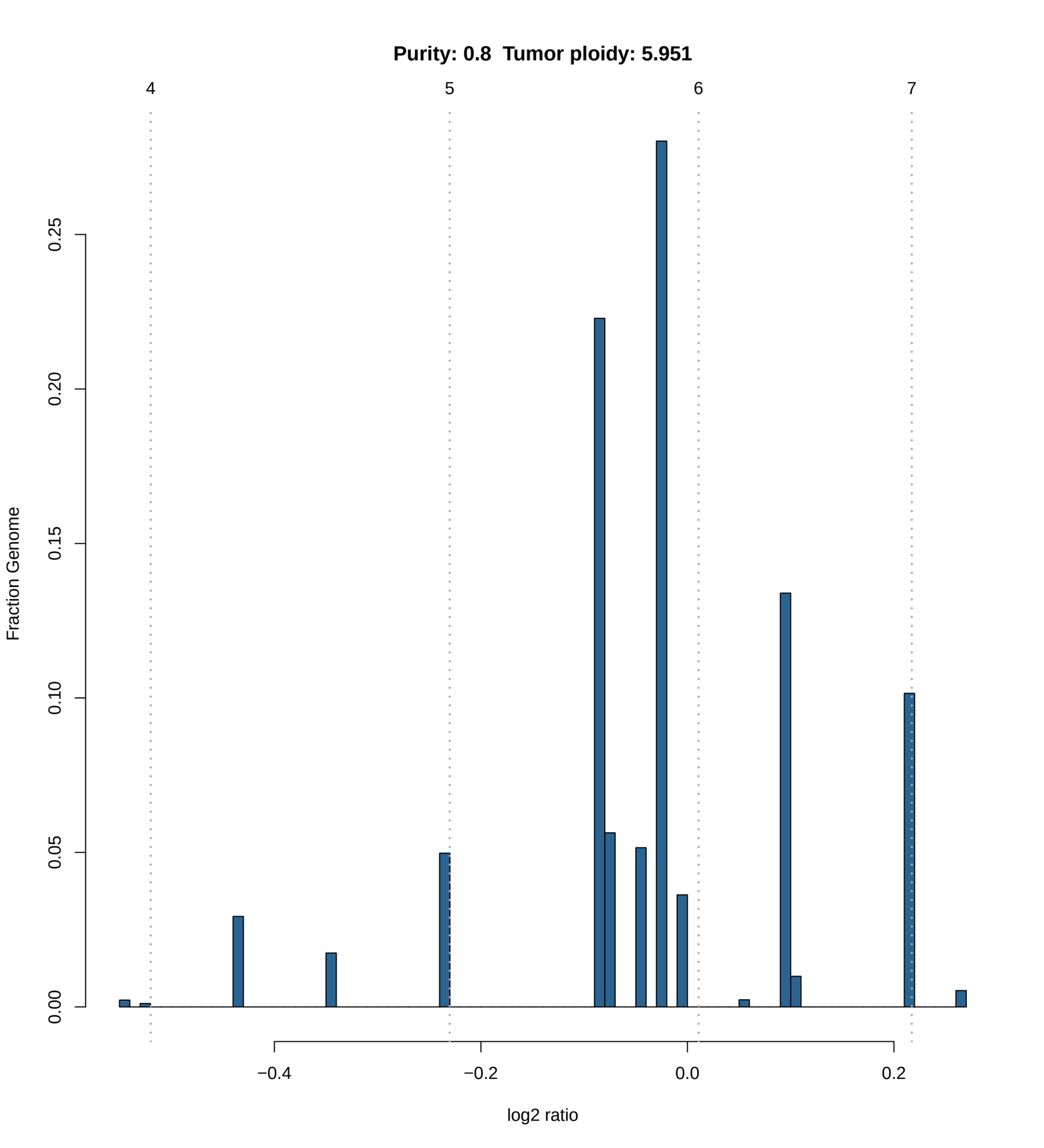

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

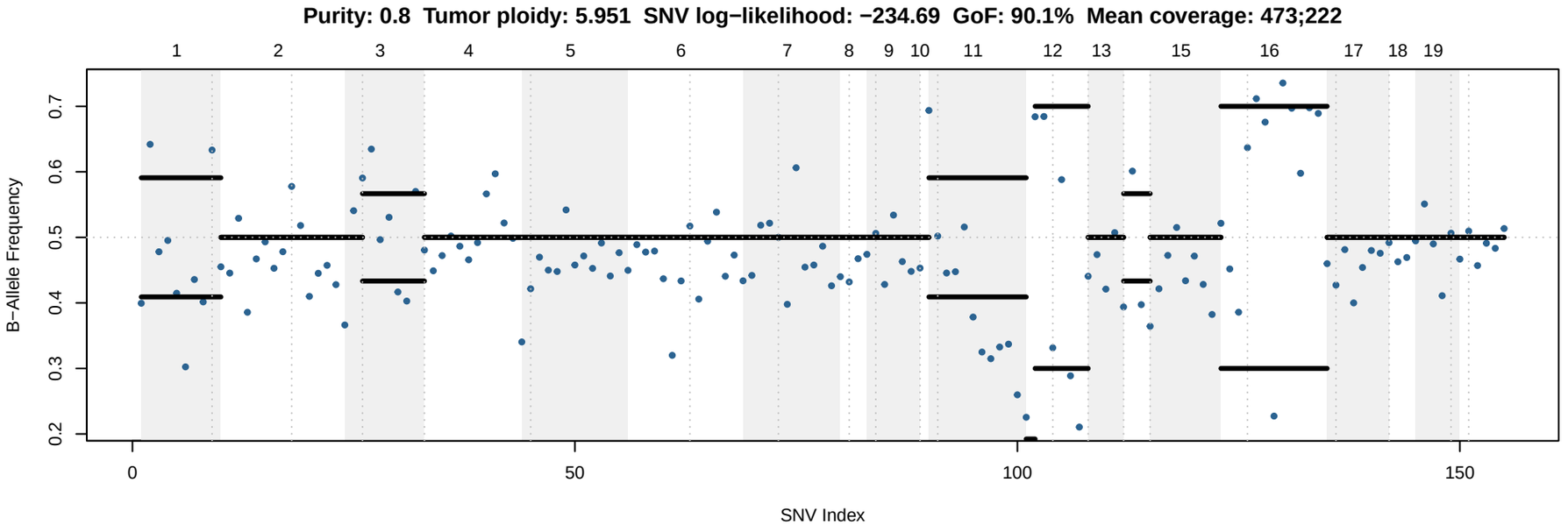

Allelic fraction (germline)
Copy Number log−ratio
3m3
2m2
1m1
3m2
2m1
3m1
1m0
2m0
3m0

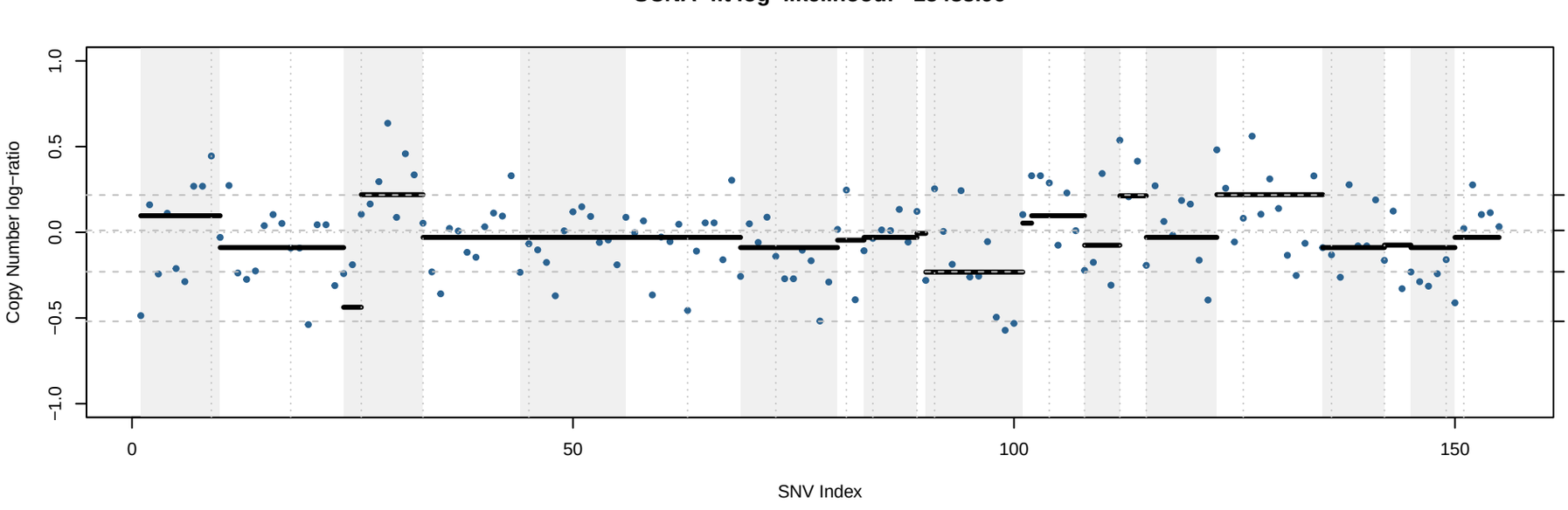

Coverage (log2)
Allelic fraction

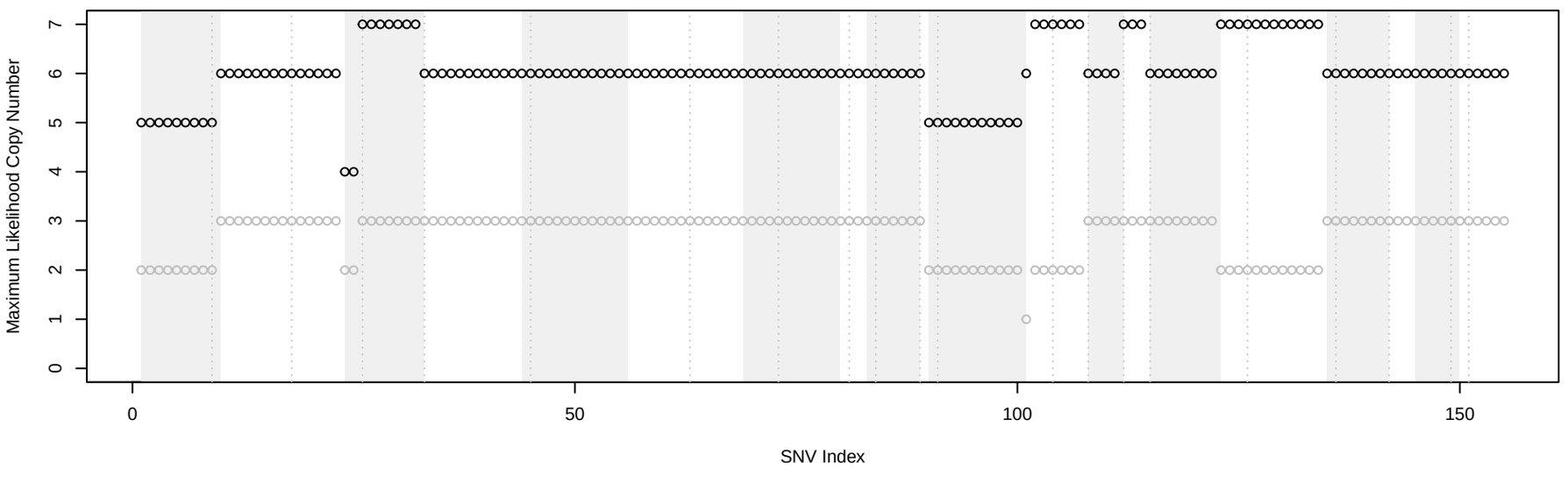

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
3m2
1m1
2m1
3m1

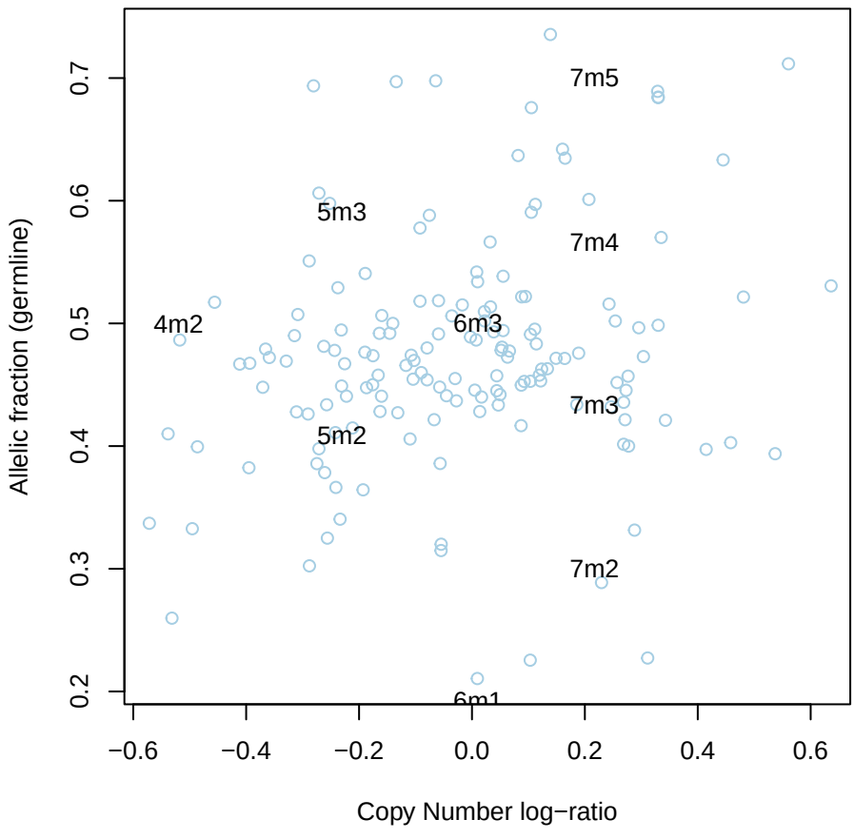

Frequency
Cellular fraction

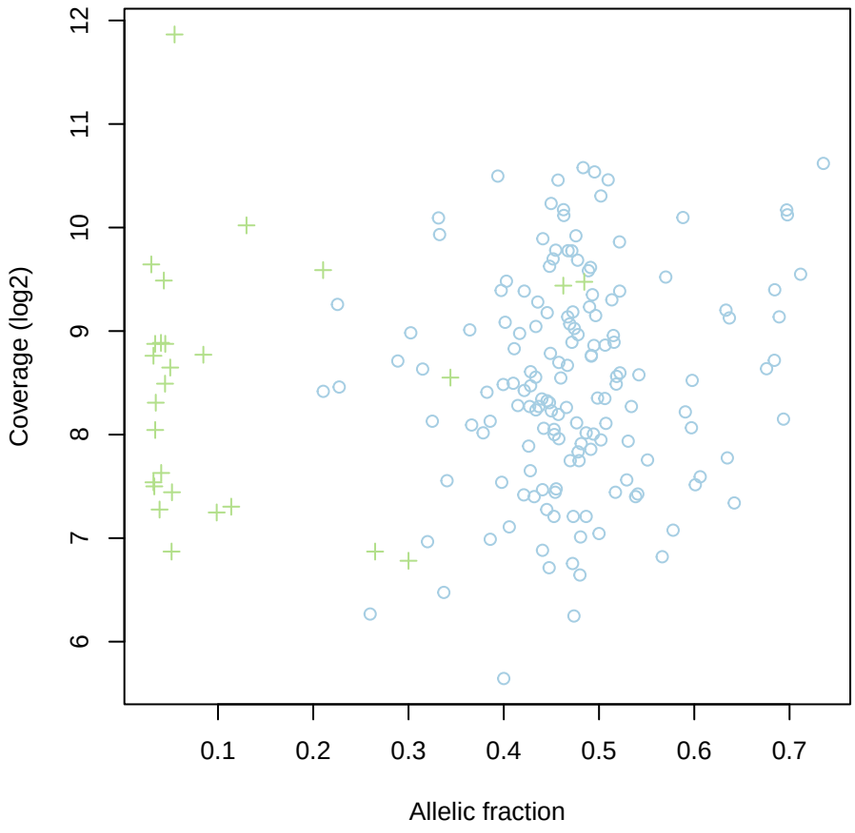

Purity: 0.8 Tumor ploidy: 5.951
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
log2 ratio

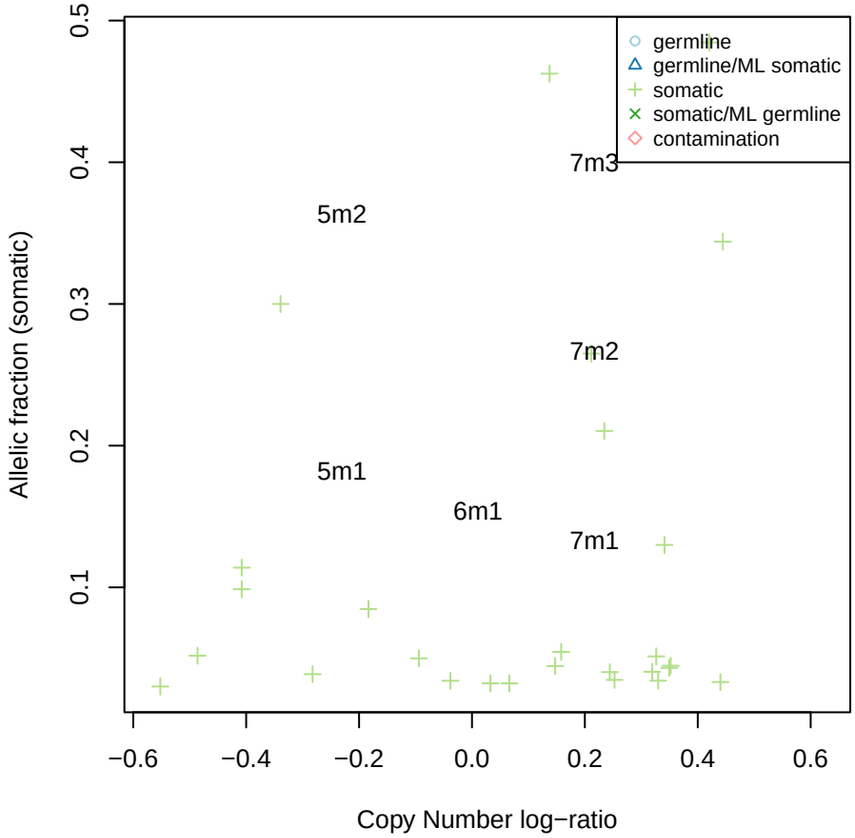

Purity: 0.8 Tumor ploidy: 5.951 SNV log−likelihood: −234.69 GoF: 90.1% Mean coverage: 473;222
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

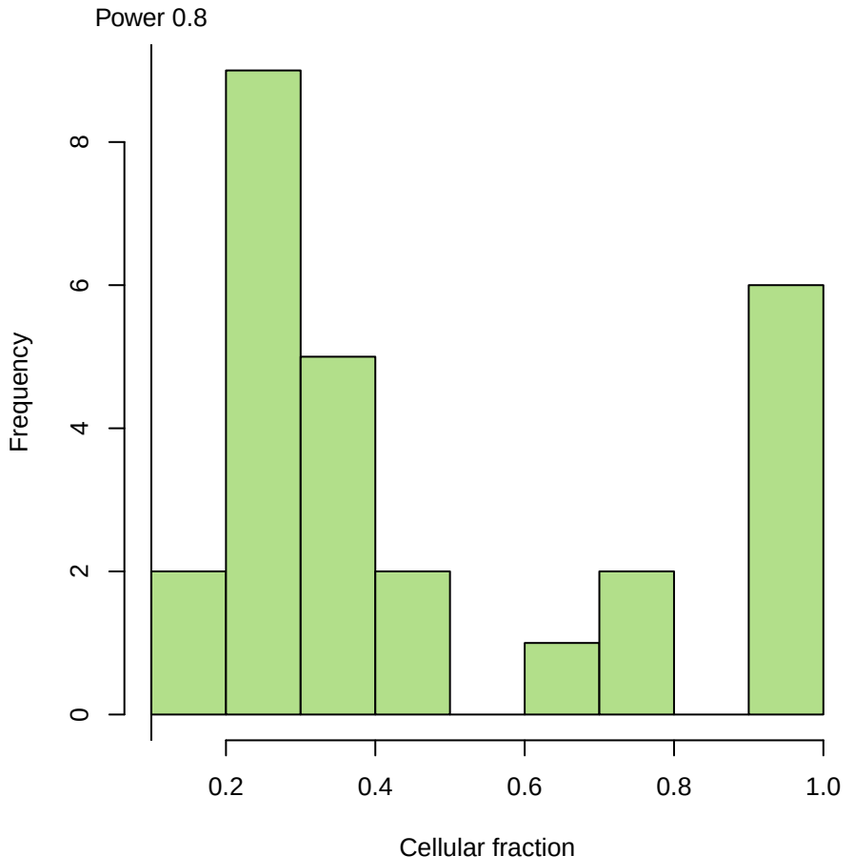

SCNA−fit log−likelihood: −15488.96
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5 6 7
0 50 100 150
SNV Index

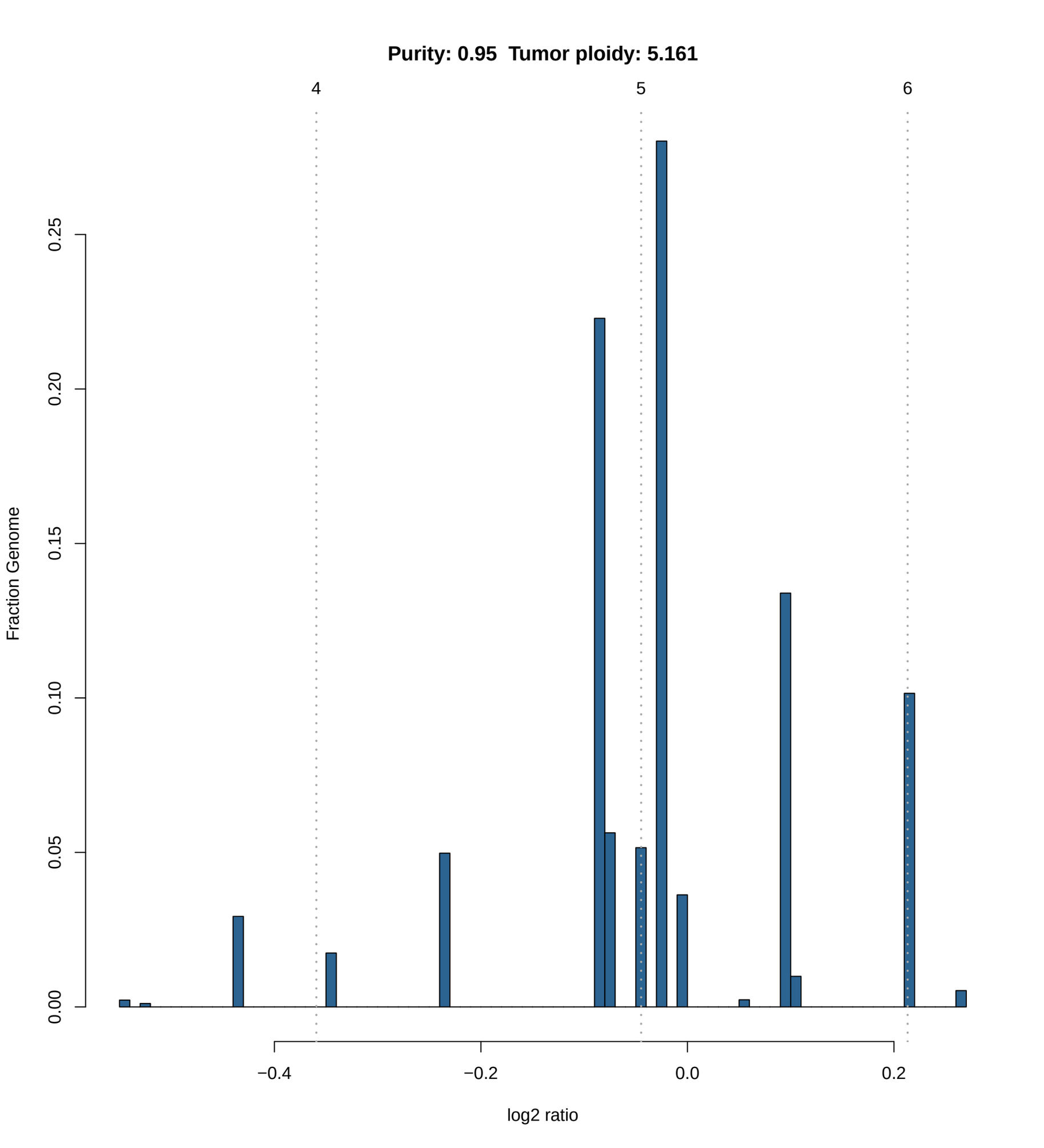

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

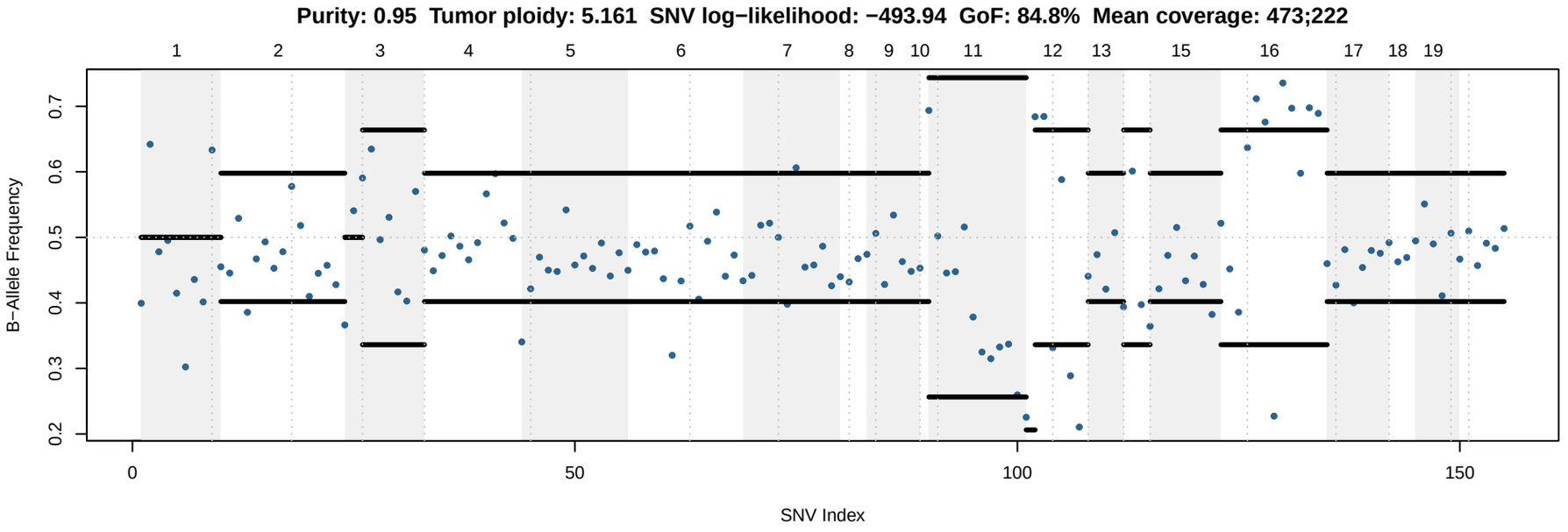

Allelic fraction (germline)
Copy Number log−ratio
7m5
5m3
7m4
4m2
6m3
7m3
5m2
7m2
6m1

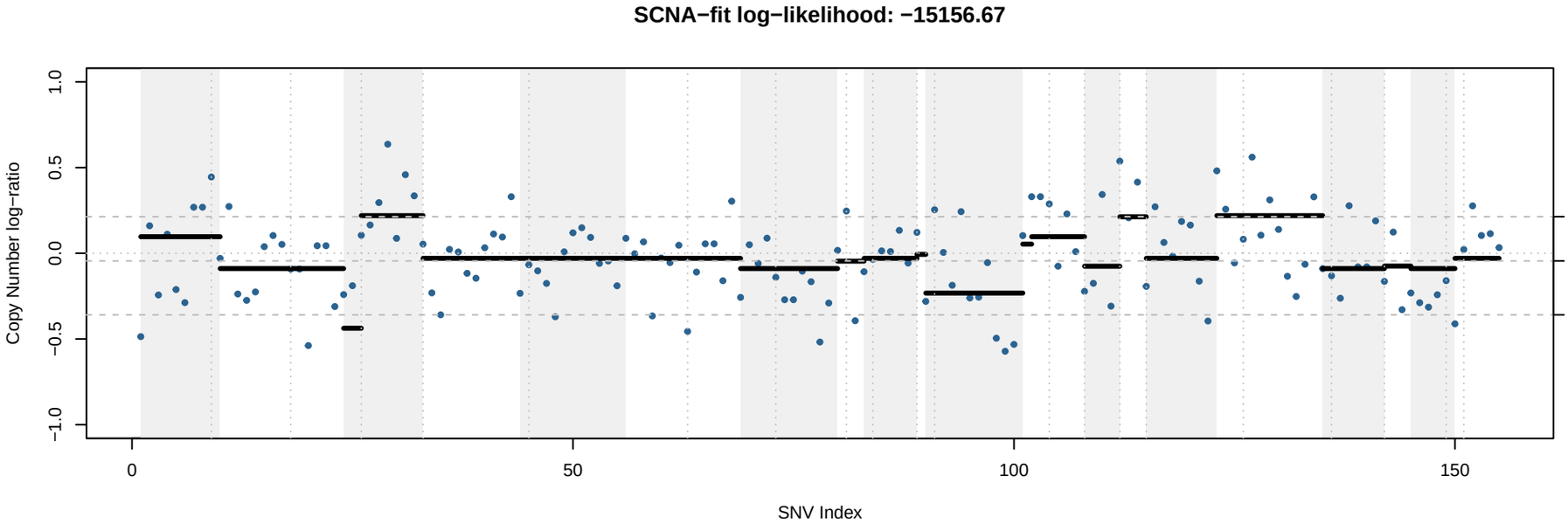

Coverage (log2)
Allelic fraction

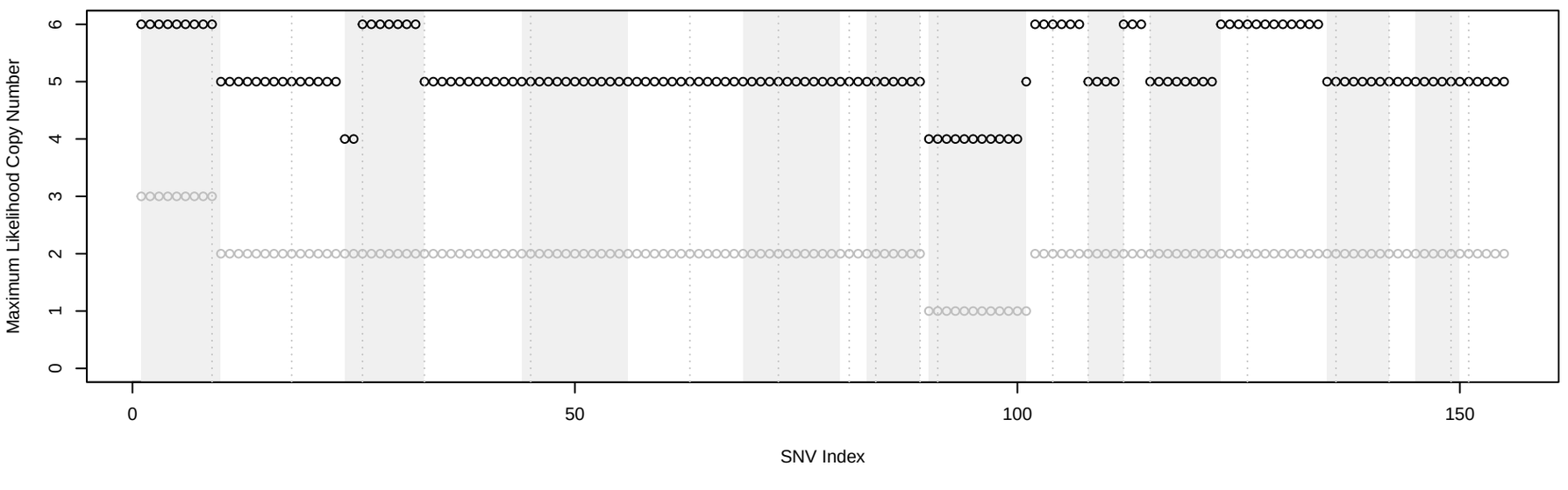

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
7m3
5m2
7m2
5m1
6m1
7m1


Power 0.8
Frequency
Cellular fraction

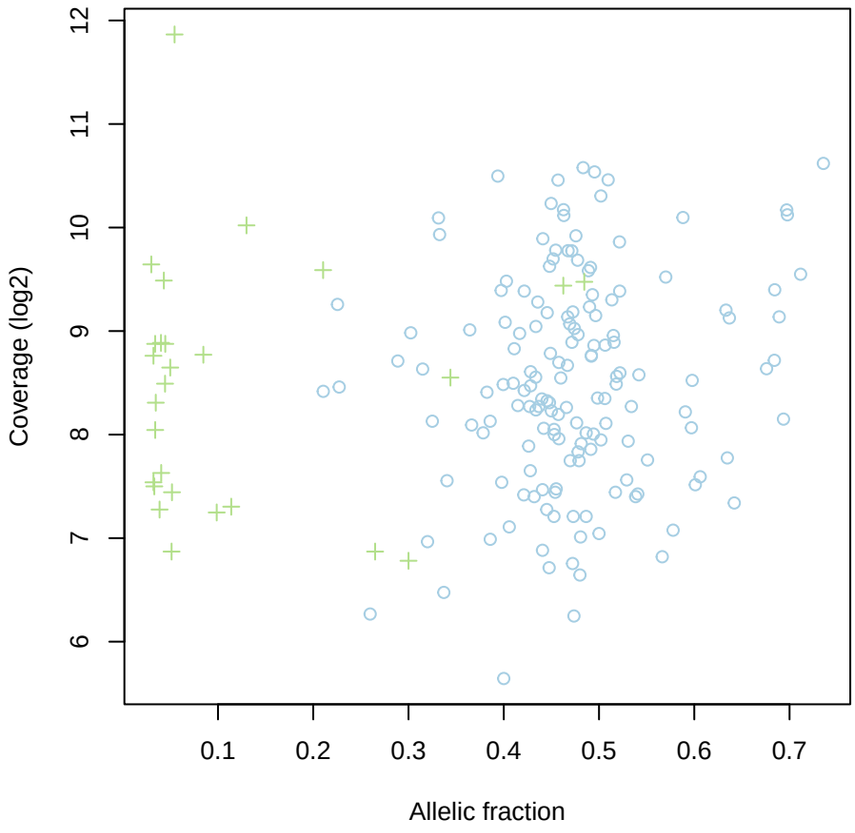

Purity: 0.95 Tumor ploidy: 5.161
4
5
6
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
log2 ratio

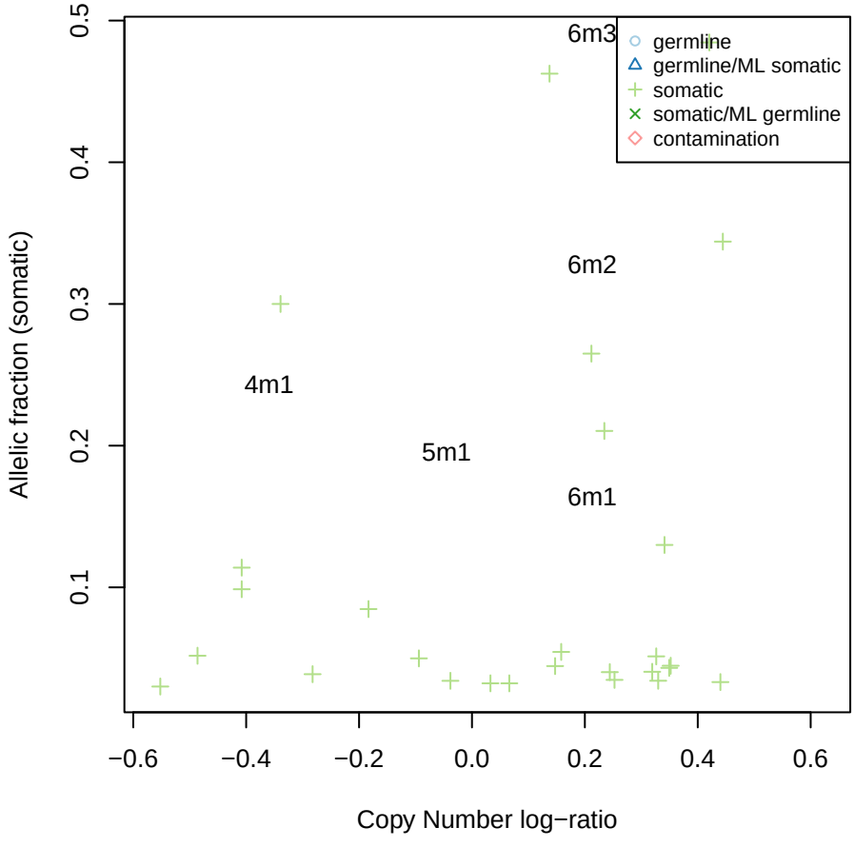

Purity: 0.95 Tumor ploidy: 5.161 SNV log−likelihood: −493.94 GoF: 84.8% Mean coverage: 473;222
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

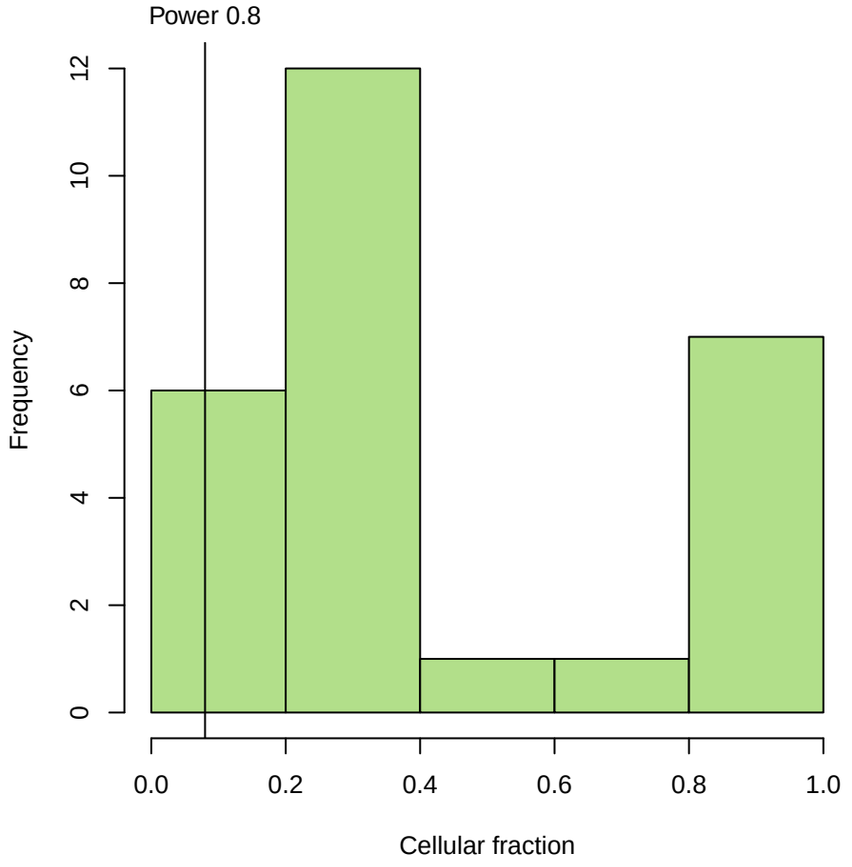

SCNA−fit log−likelihood: −15156.67
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5 6
0 50 100 150
SNV Index

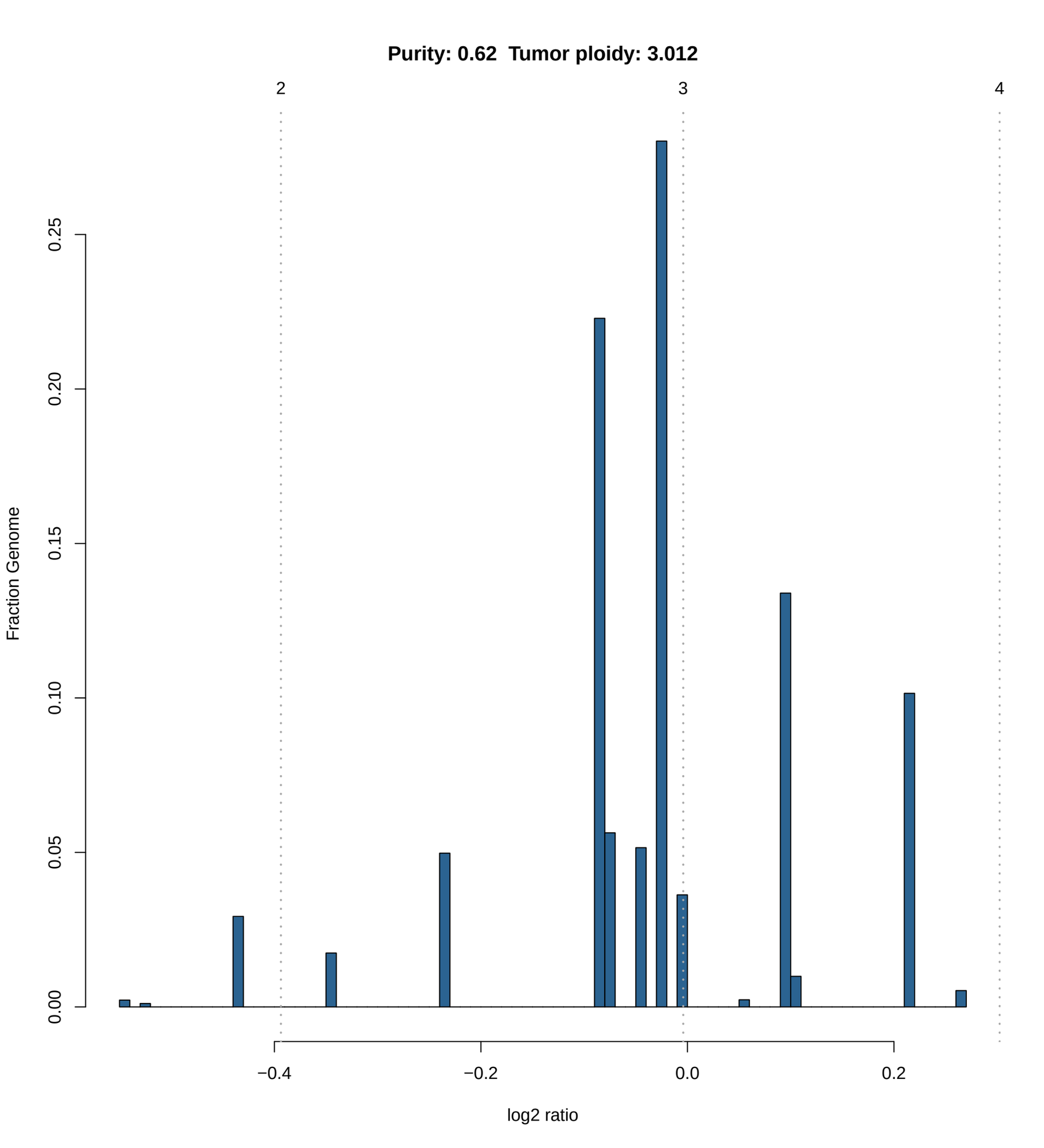

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

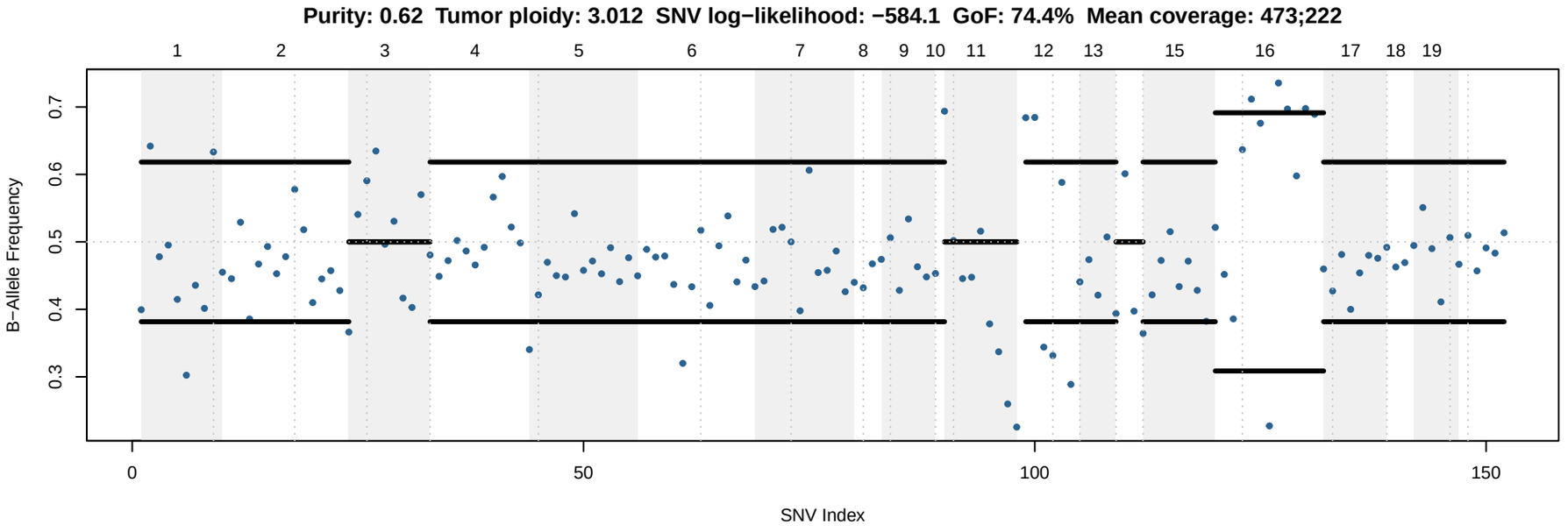
4m3
6m4
5m3
4m2
6m3
5m2
6m2
4m1
5m1
Allelic fraction (germline)
Copy Number log−ratio

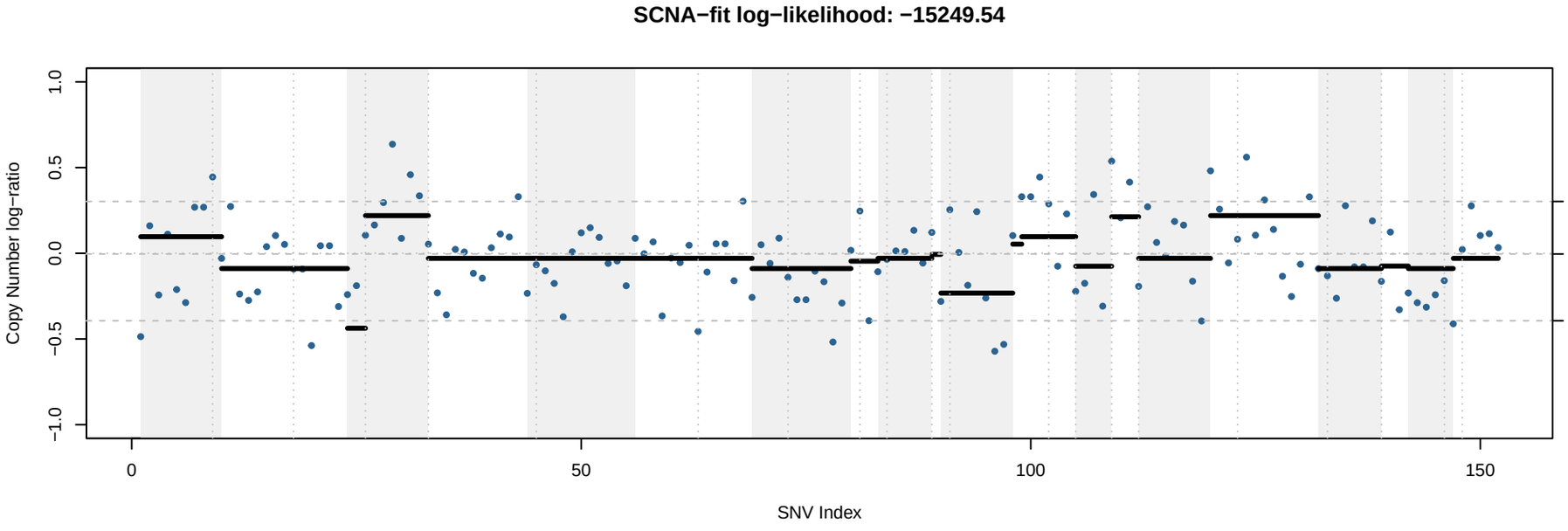

Coverage (log2)
Allelic fraction

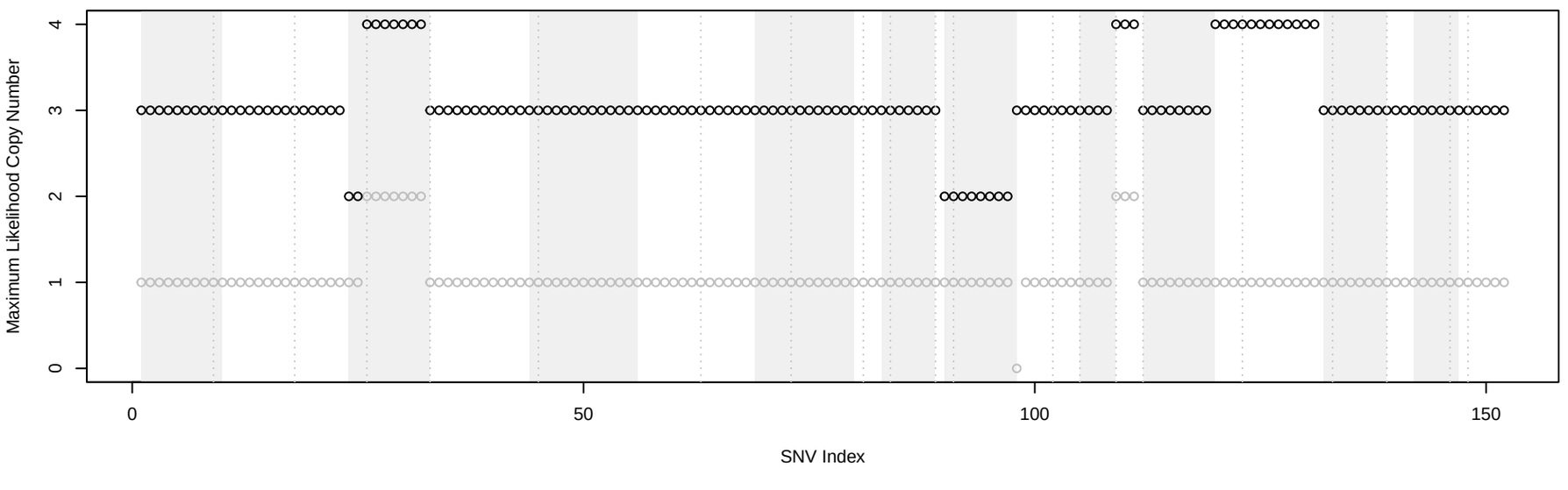

6m3
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m2
4m1
5m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio

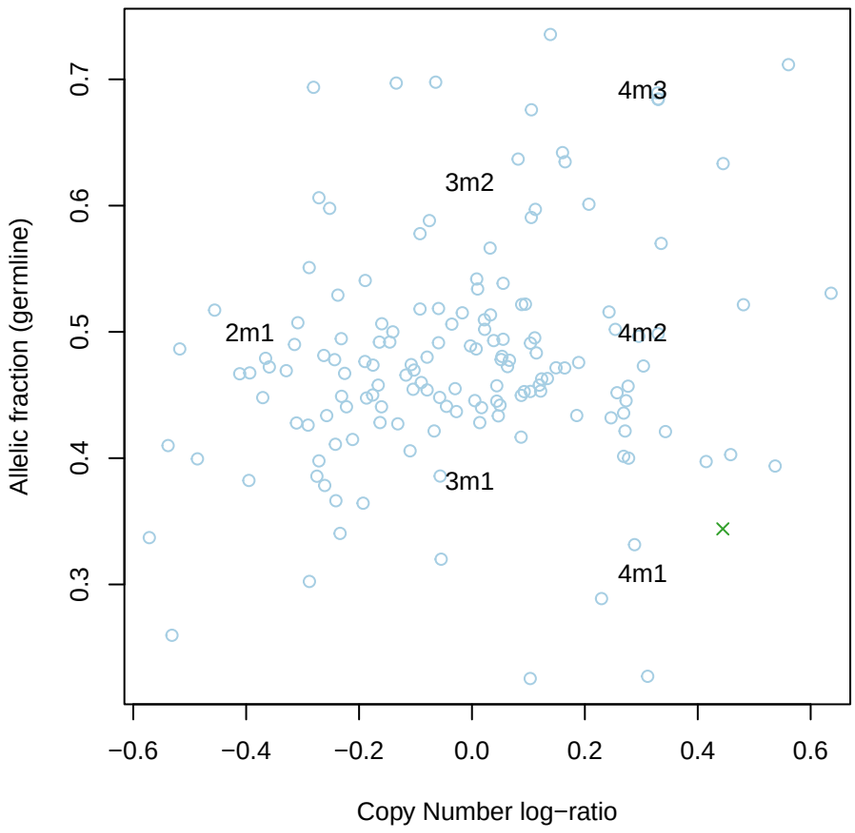

Power 0.8
Frequency
Cellular fraction

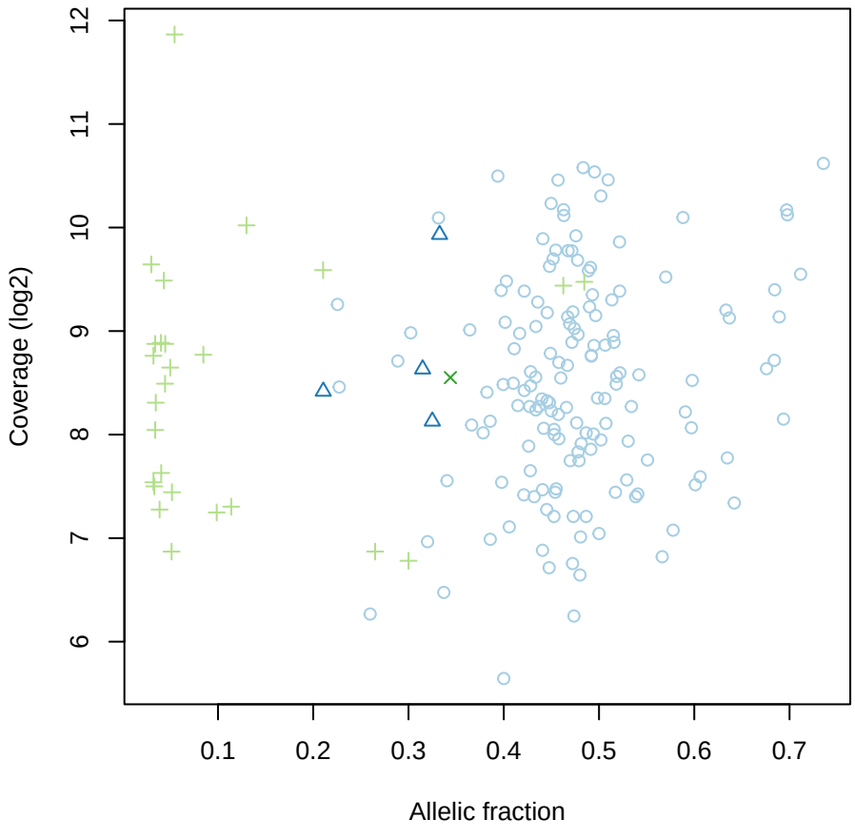

Purity: 0.62 Tumor ploidy: 3.012
2
3
4
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
log2 ratio

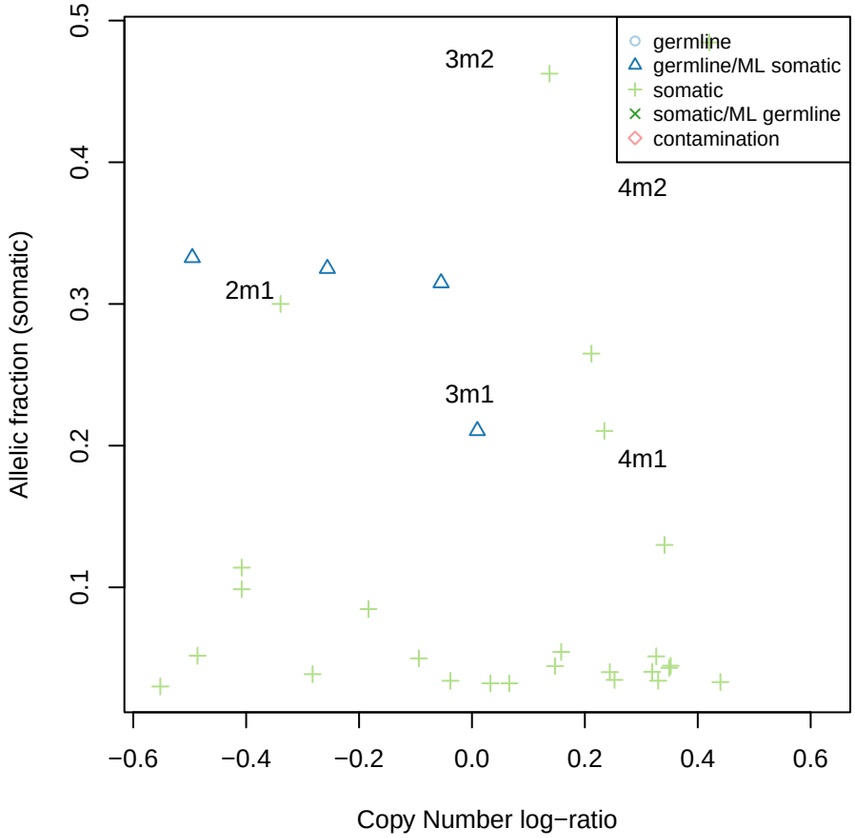

Purity: 0.62 Tumor ploidy: 3.012 SNV log−likelihood: −584.1 GoF: 74.4% Mean coverage: 473;222
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

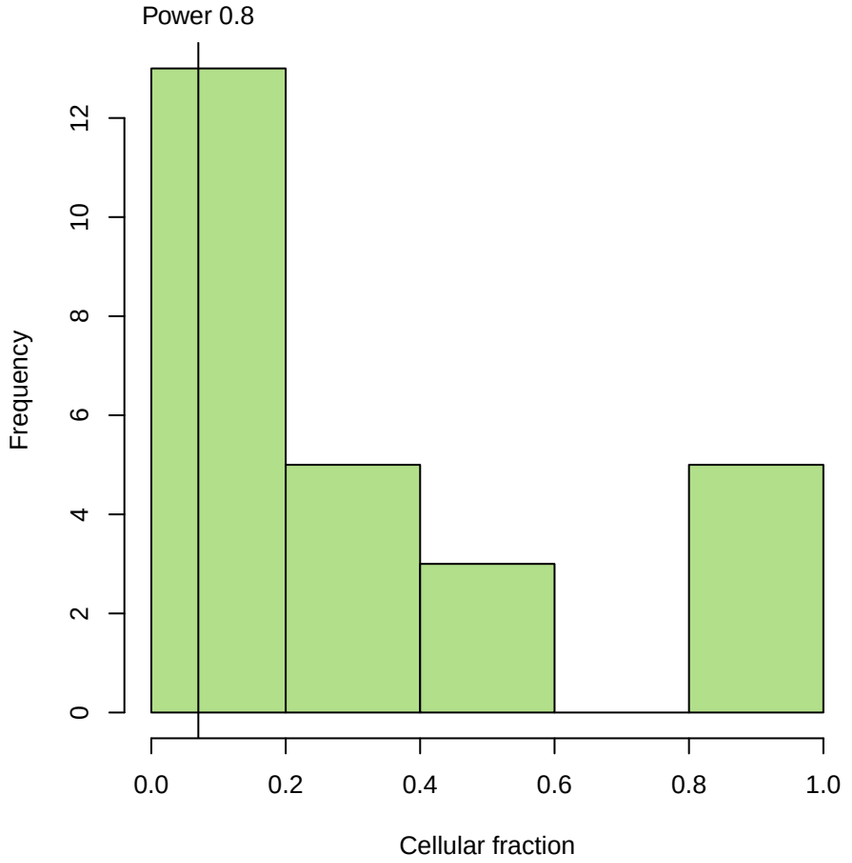

SCNA−fit log−likelihood: −15249.54
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4
0 50 100 150
SNV Index


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


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


Coverage (log2)
Allelic fraction


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


Power 0.8
Frequency
Cellular fraction