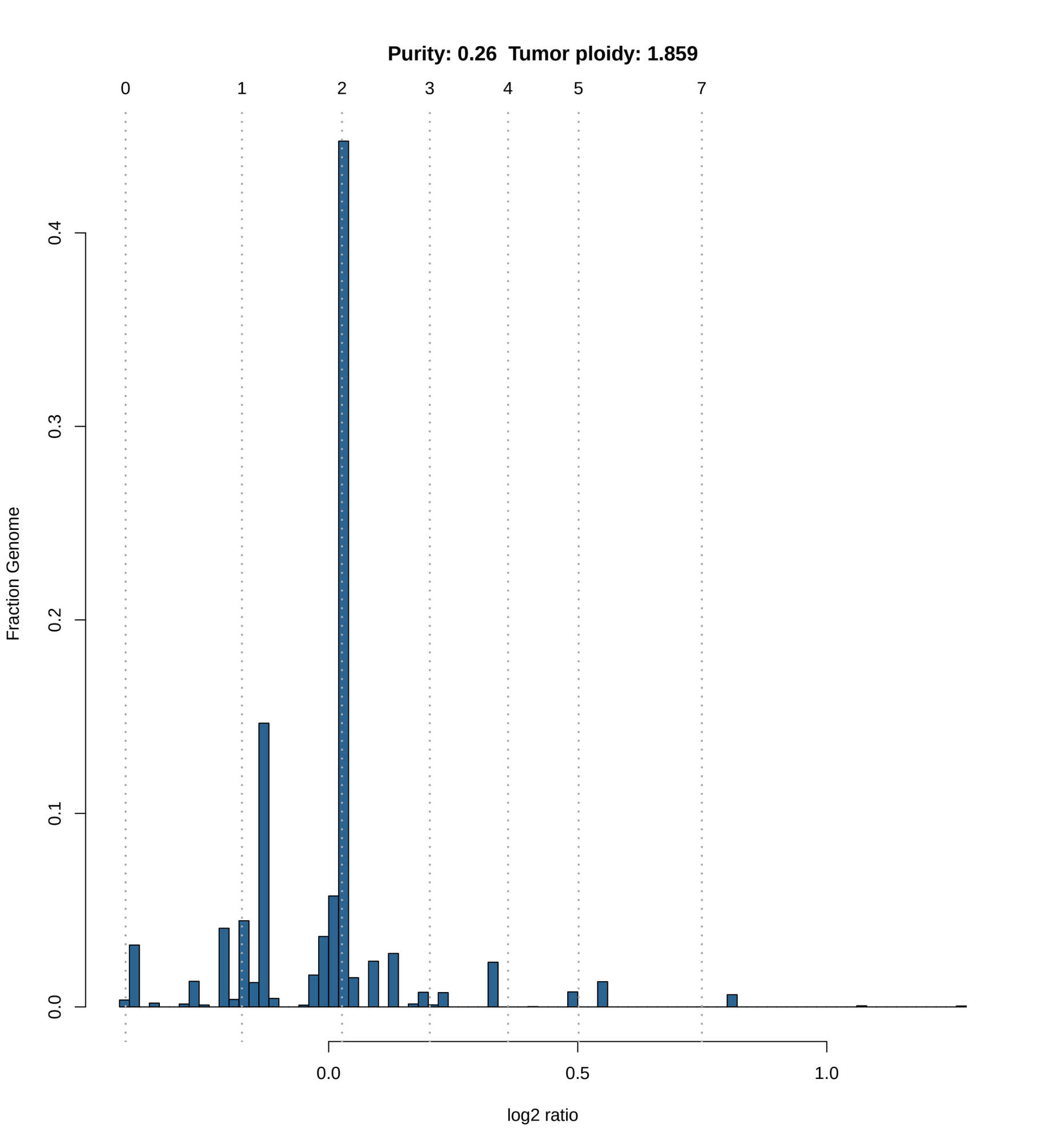
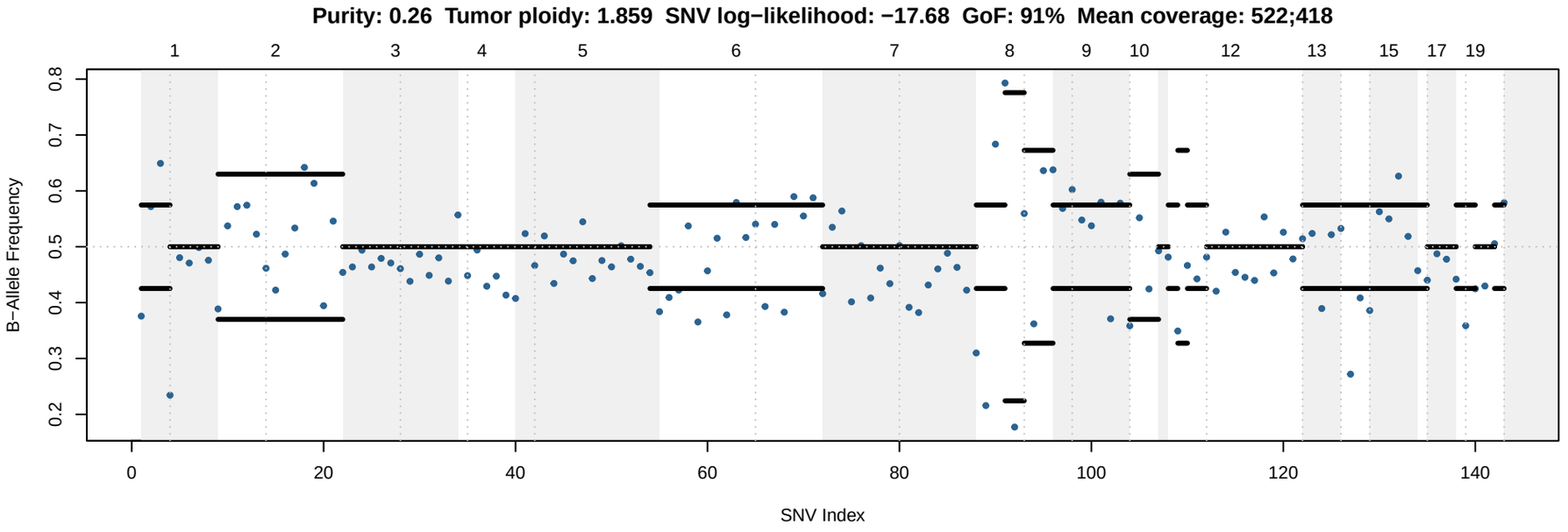
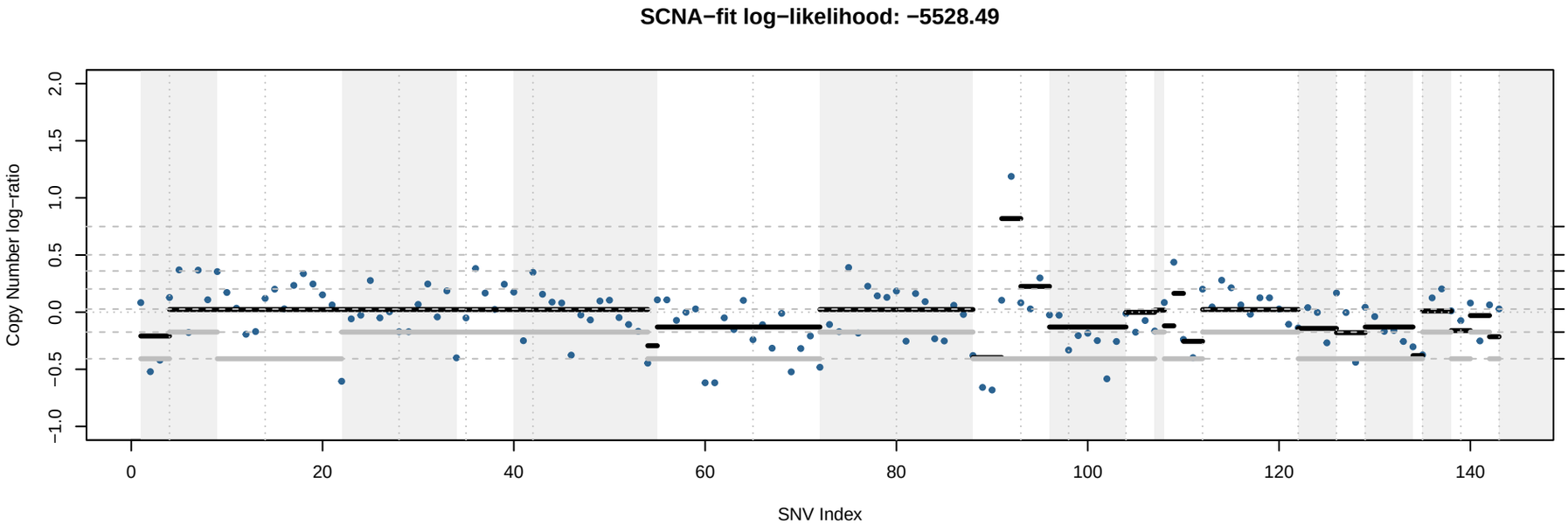
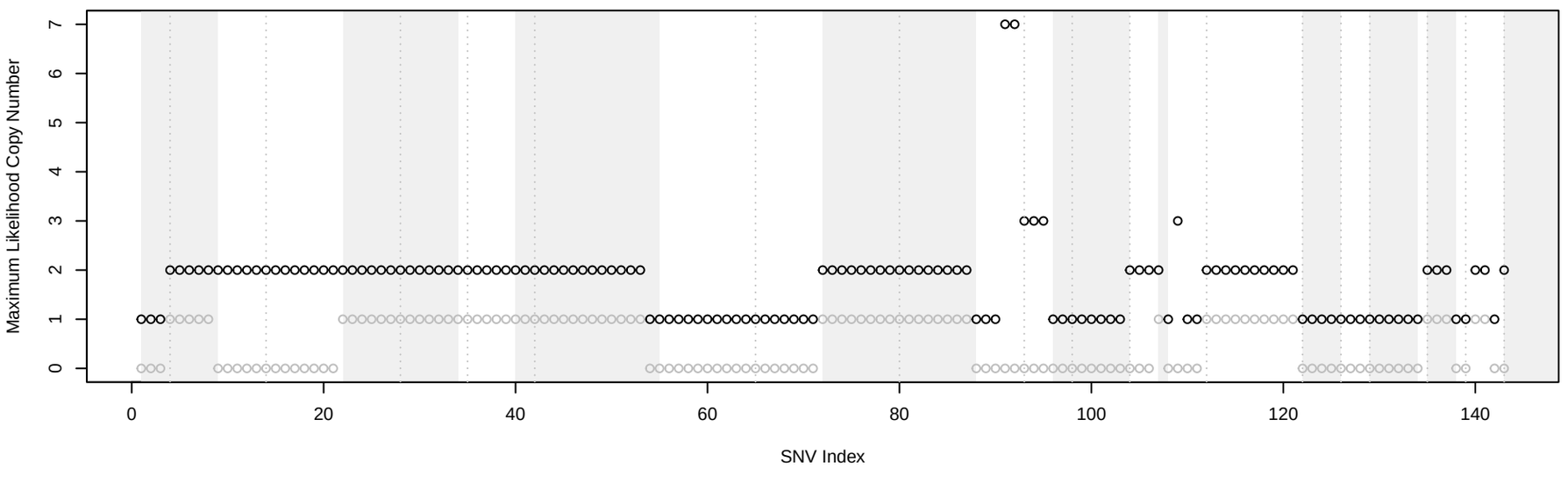
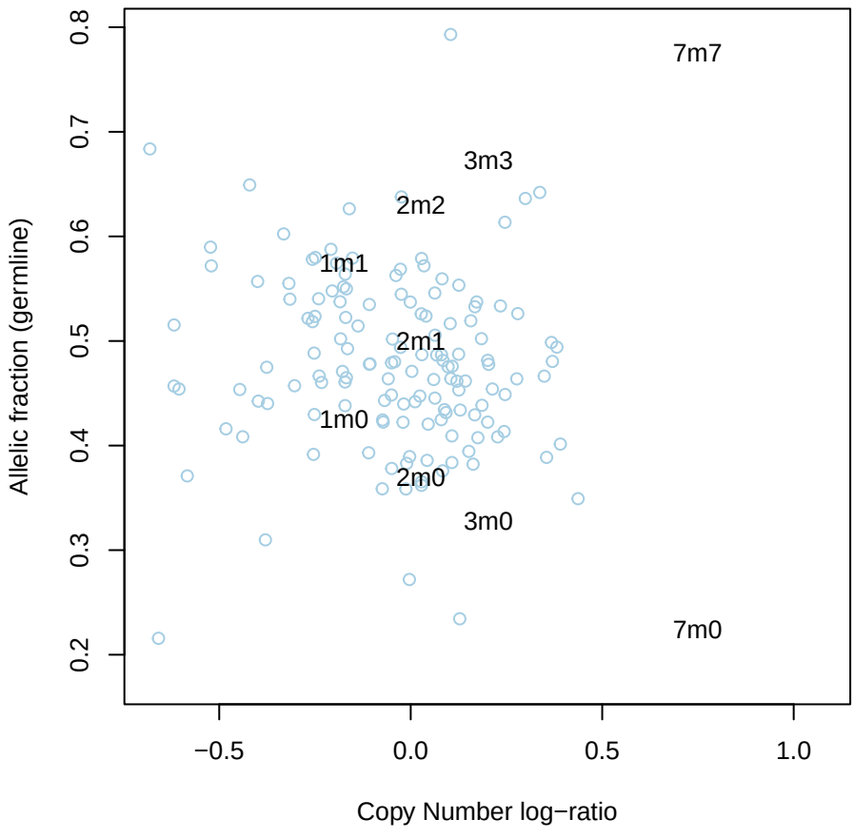
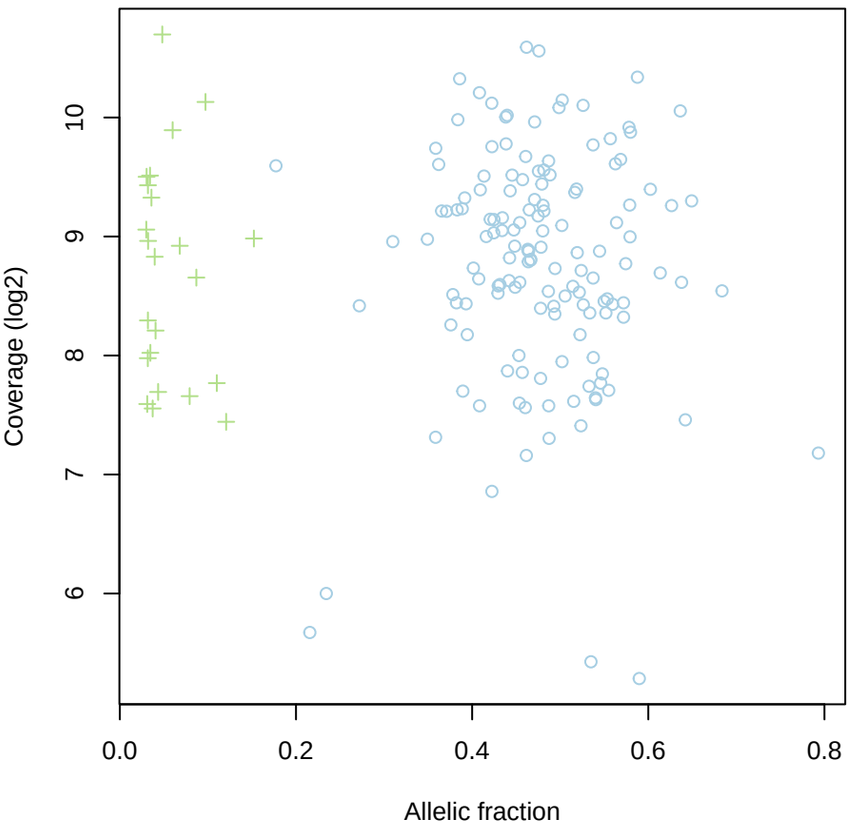

Purity: 0.26 Tumor ploidy: 1.859
0
1
2
3
4
5
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
0.0
0.5
1.0
log2 ratio

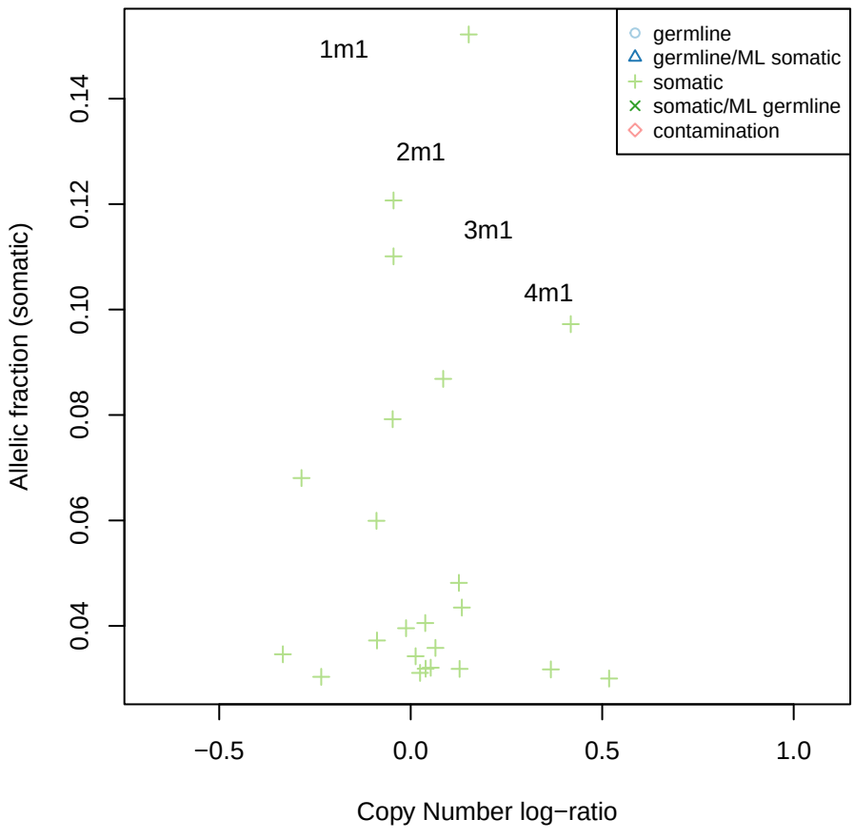

Purity: 0.26 Tumor ploidy: 1.859 SNV log−likelihood: −17.68 GoF: 91% Mean coverage: 522;418
1 2 3 4 5 6 7 8 9 10 12 13 15 17 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index

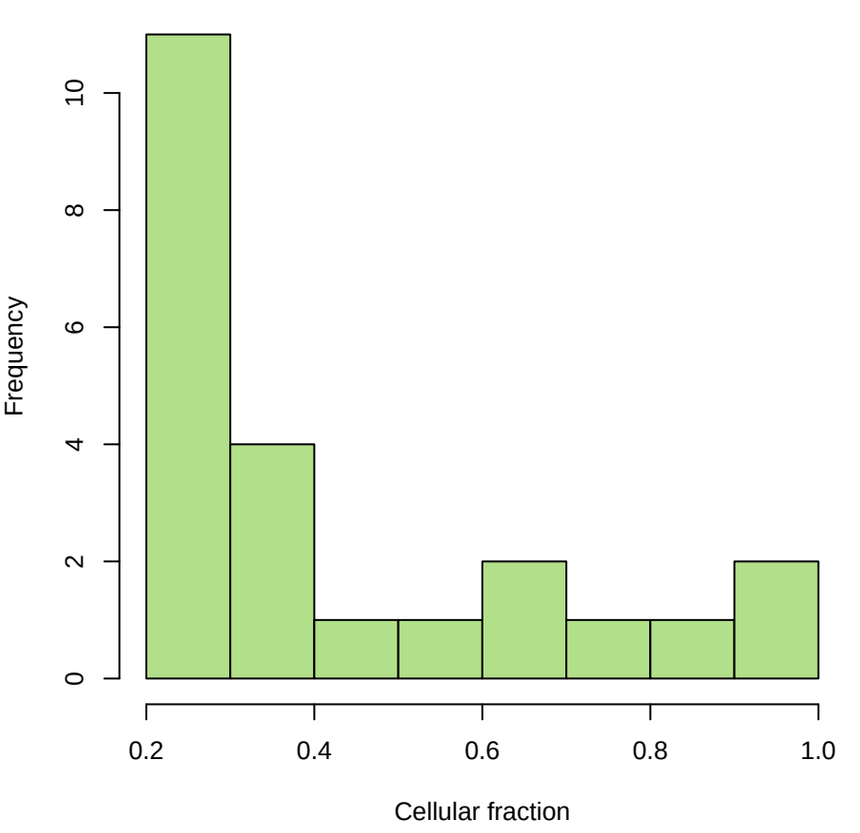

SCNA−fit log−likelihood: −5528.49
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
0 1 3 5 7
0 20 40 60 80 100 120 140
SNV Index

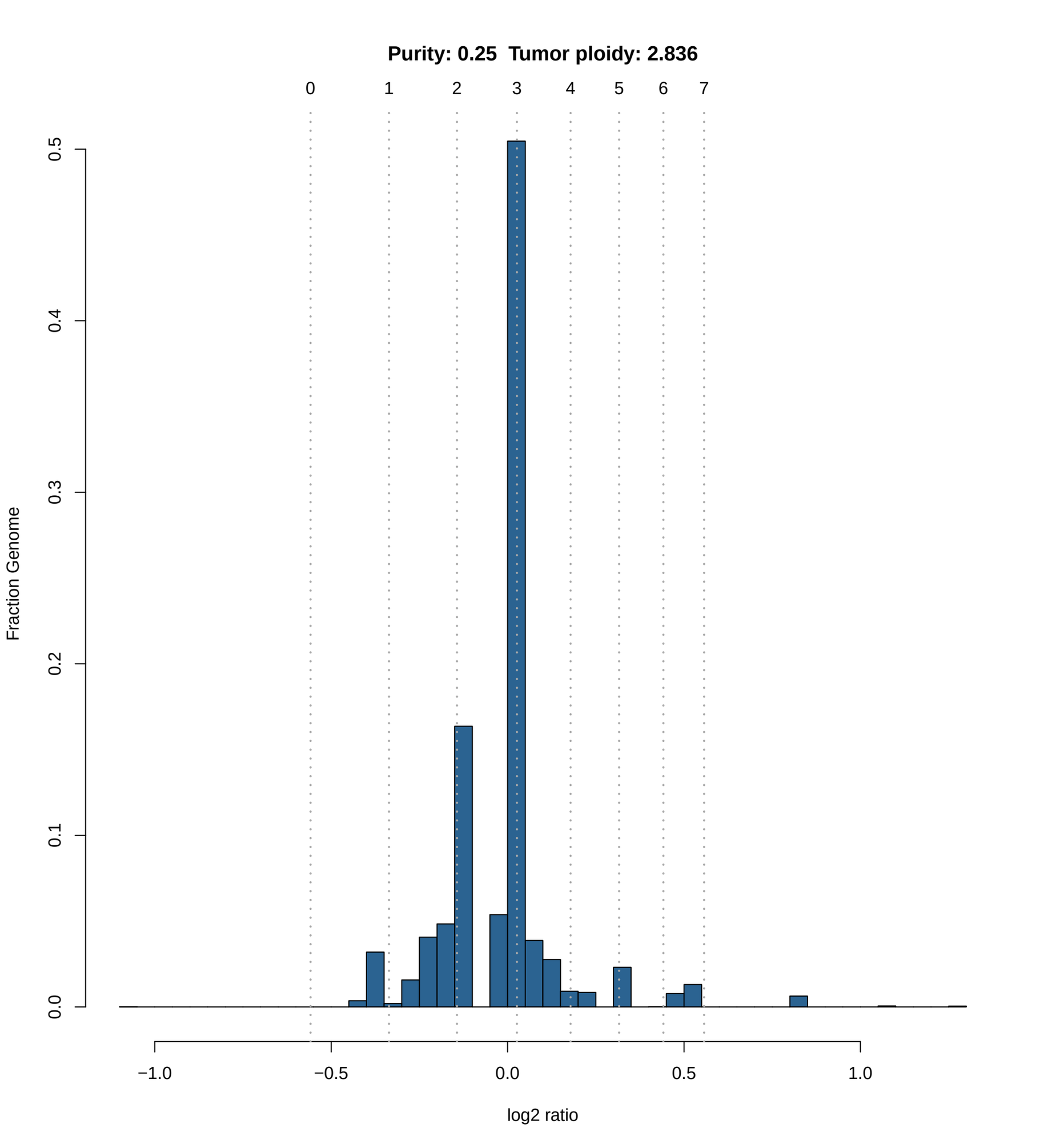

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

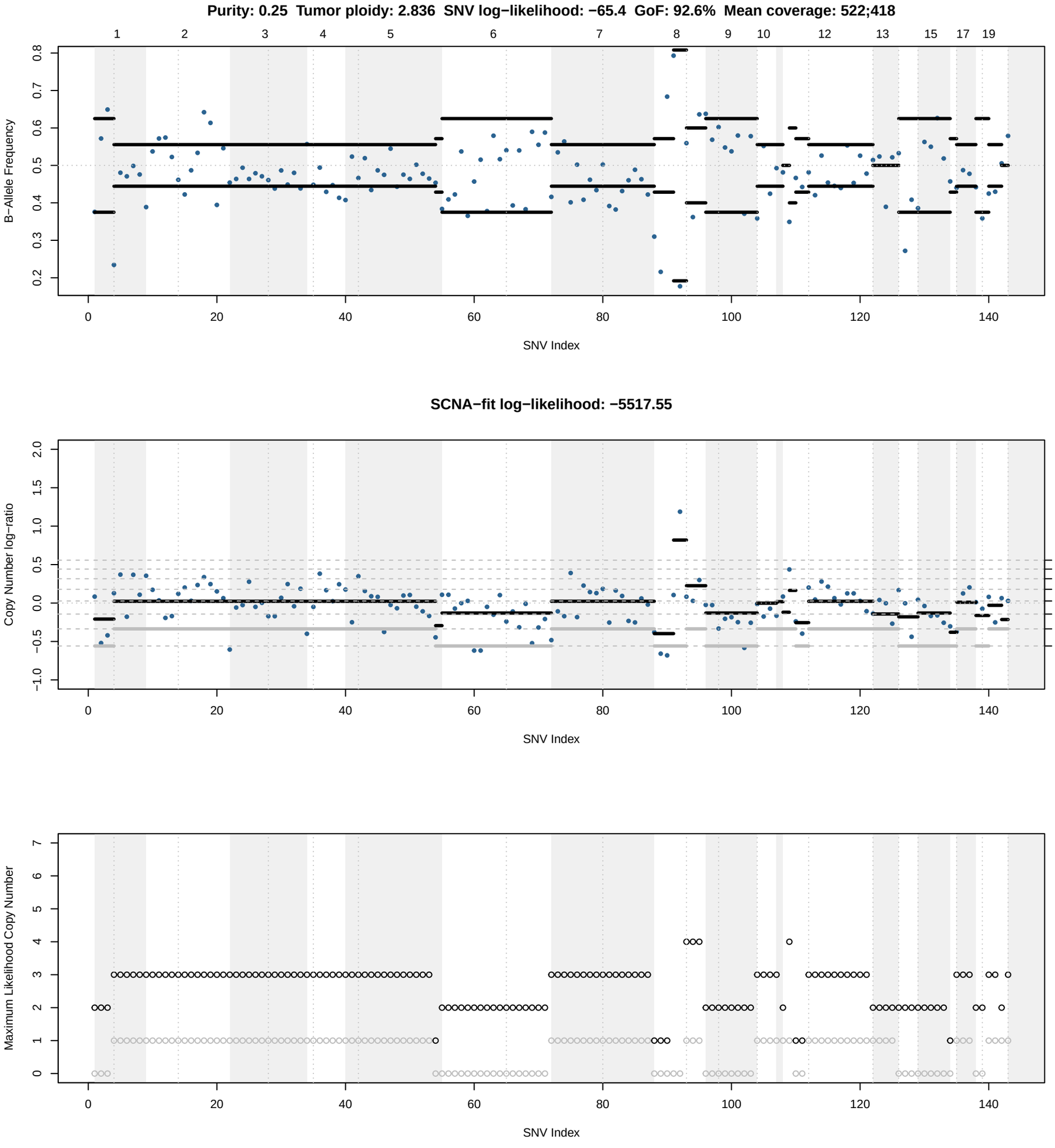

7m7
3m3
2m2
1m1
2m1
1m0
2m0
3m0
7m0
Allelic fraction (germline)
Copy Number log−ratio
0.2
0.3
0.4
0.5
0.6
0.7
0.8
−0.5
0.0
0.5
1.0

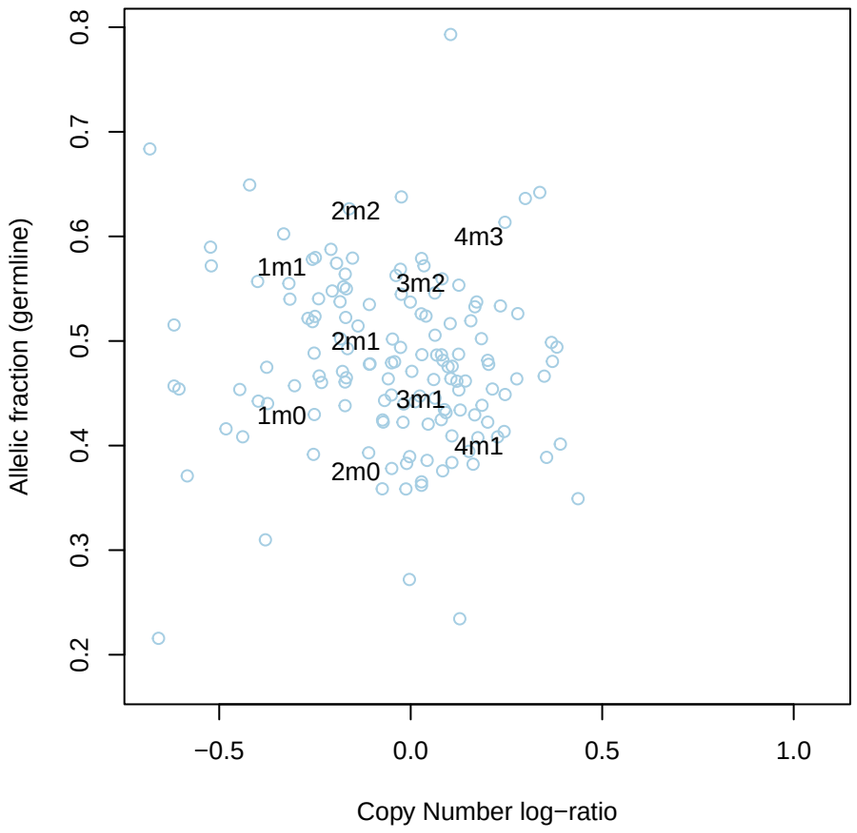

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.0
0.2
0.4
0.6
0.8

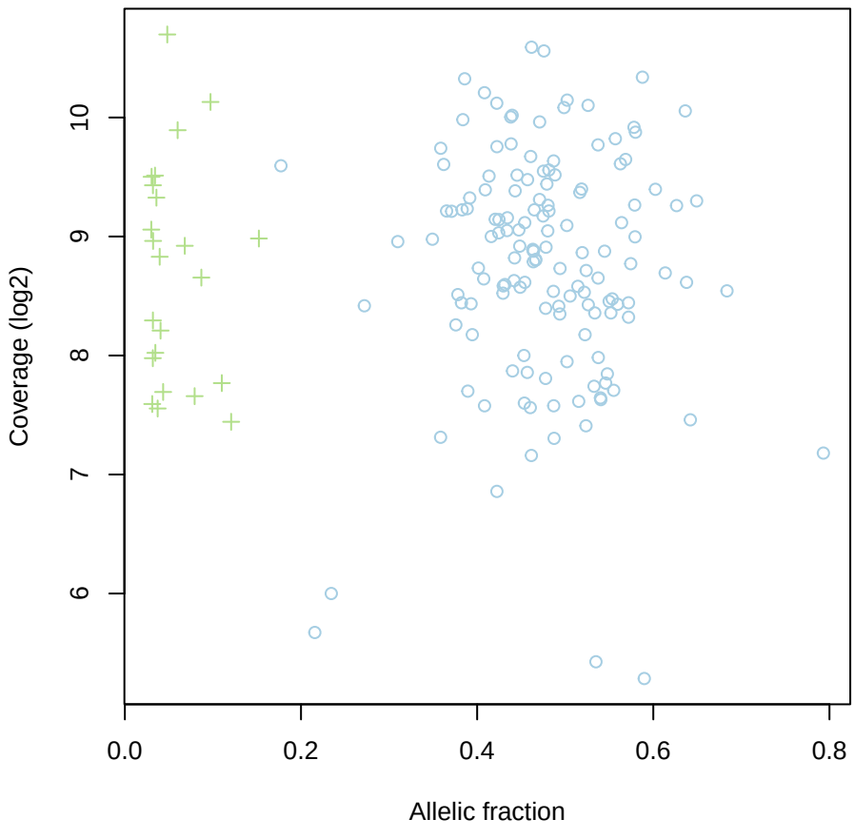

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
4m1
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
0.12
0.14
−0.5
0.0
0.5
1.0

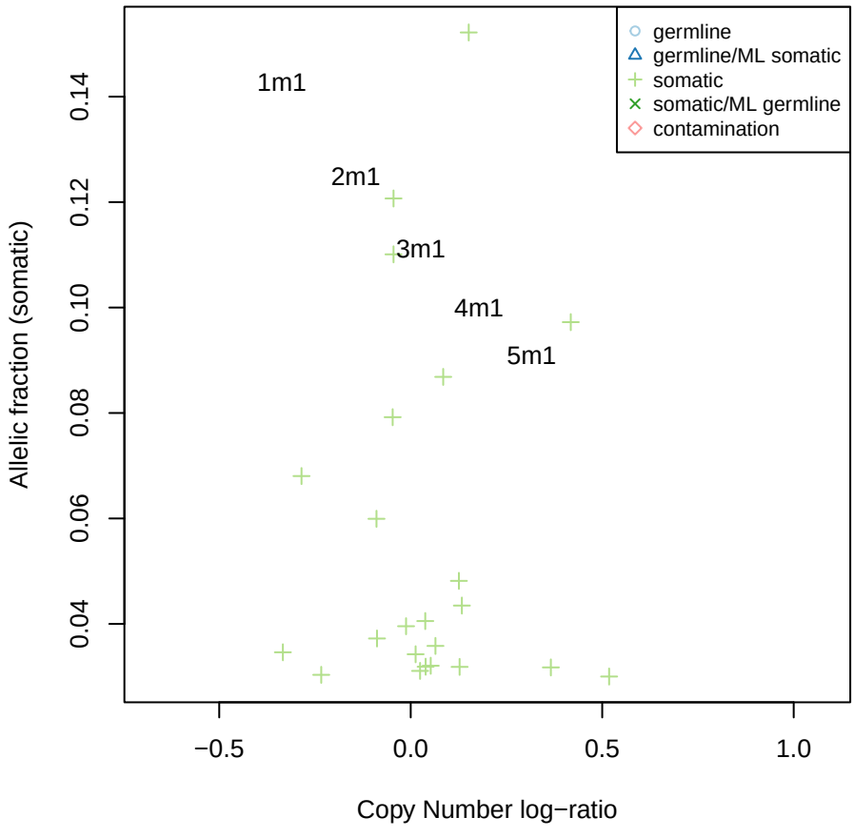

Frequency
Cellular fraction
0
2
4
6
8
10
0.2
0.4
0.6
0.8
1.0

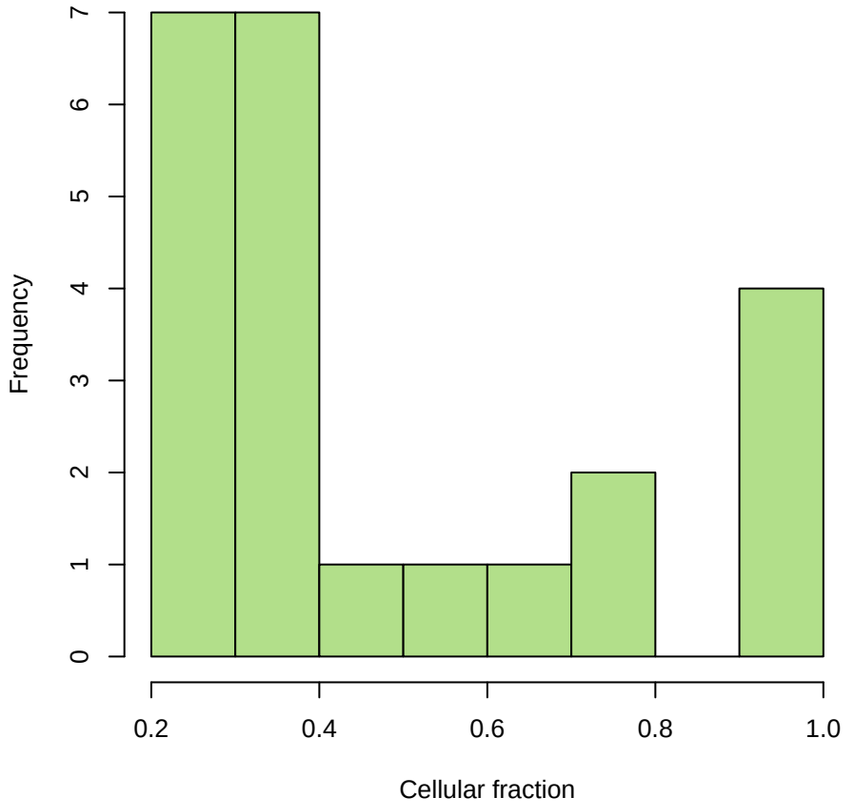

Purity: 0.25 Tumor ploidy: 2.836
0
1
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

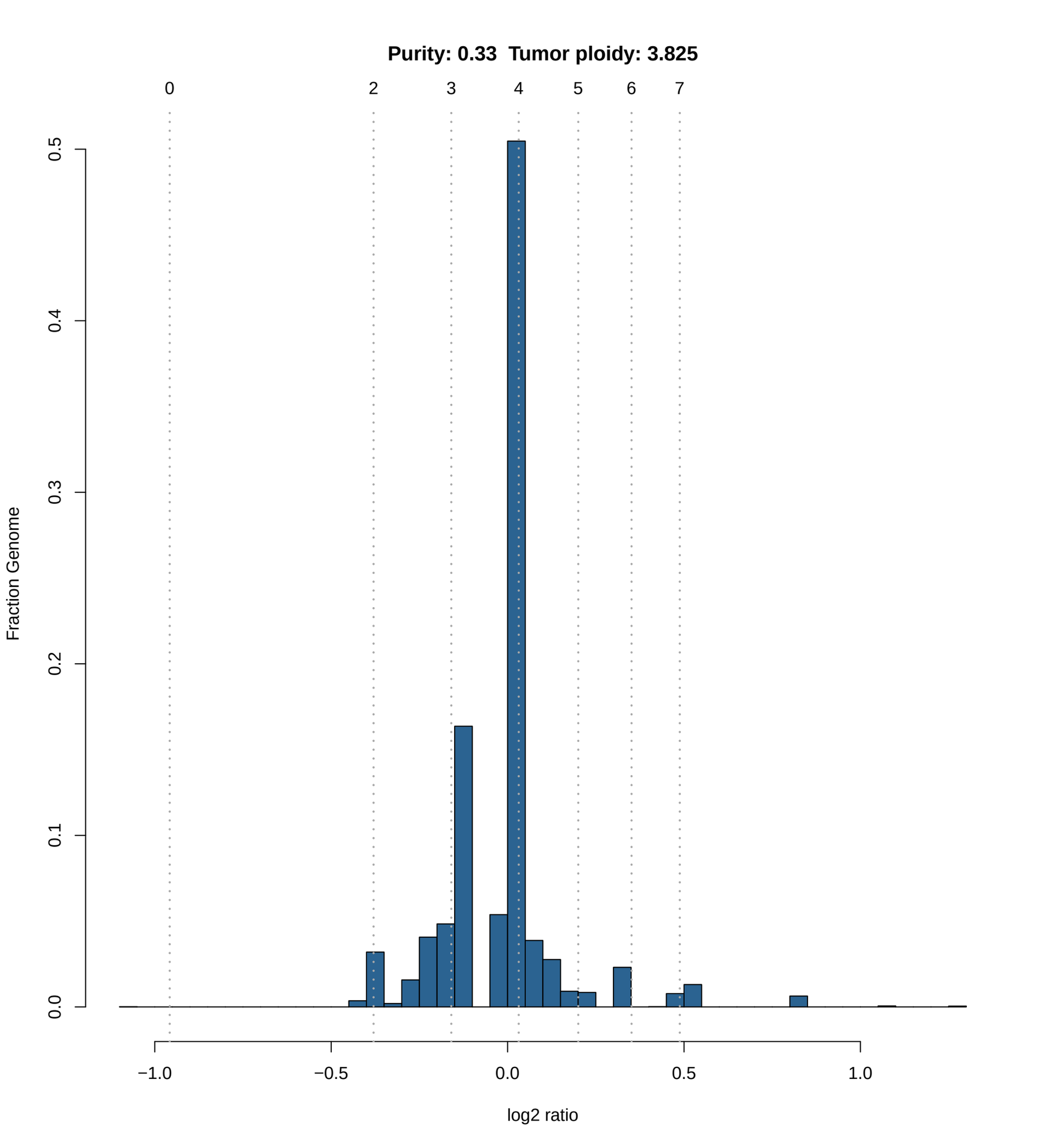

Purity: 0.25 Tumor ploidy: 2.836 SNV log−likelihood: −65.4 GoF: 92.6% Mean coverage: 522;418
1 2 3 4 5 6 7 8 9 10 12 13 15 17 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index
SCNA−fit log−likelihood: −5517.55
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
0 1 3 5 7
0 20 40 60 80 100 120 140
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

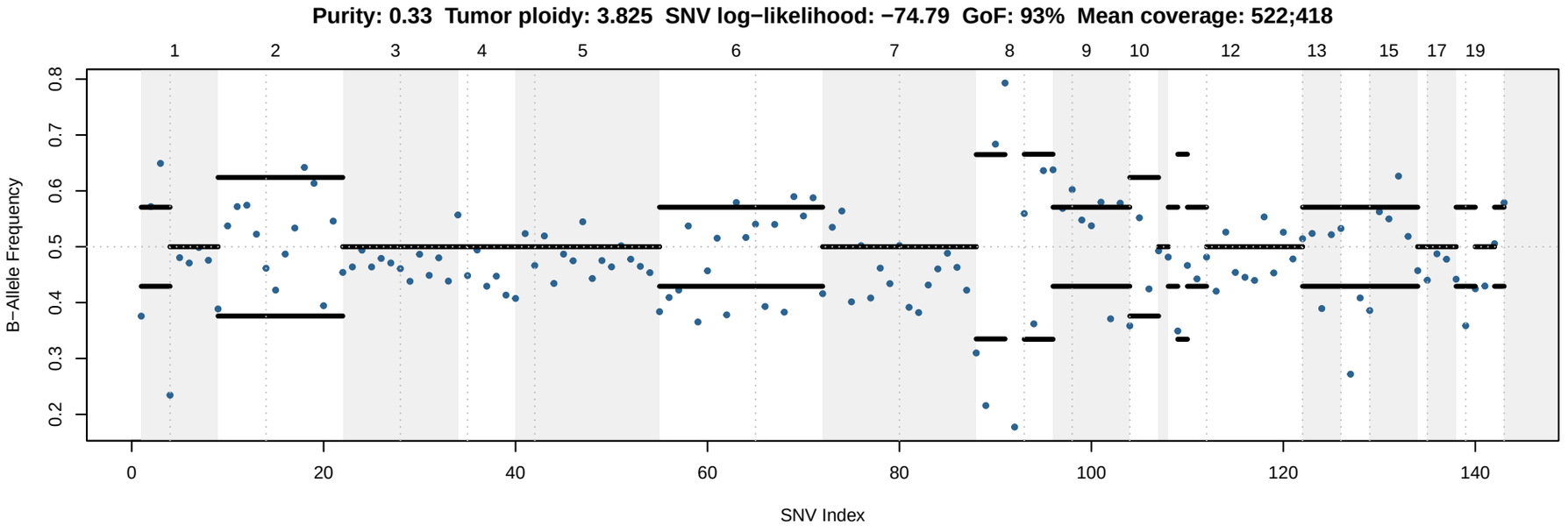

Allelic fraction (germline)
Copy Number log−ratio
2m2
4m3
1m1
3m2
2m1
3m1
1m0
4m1
2m0

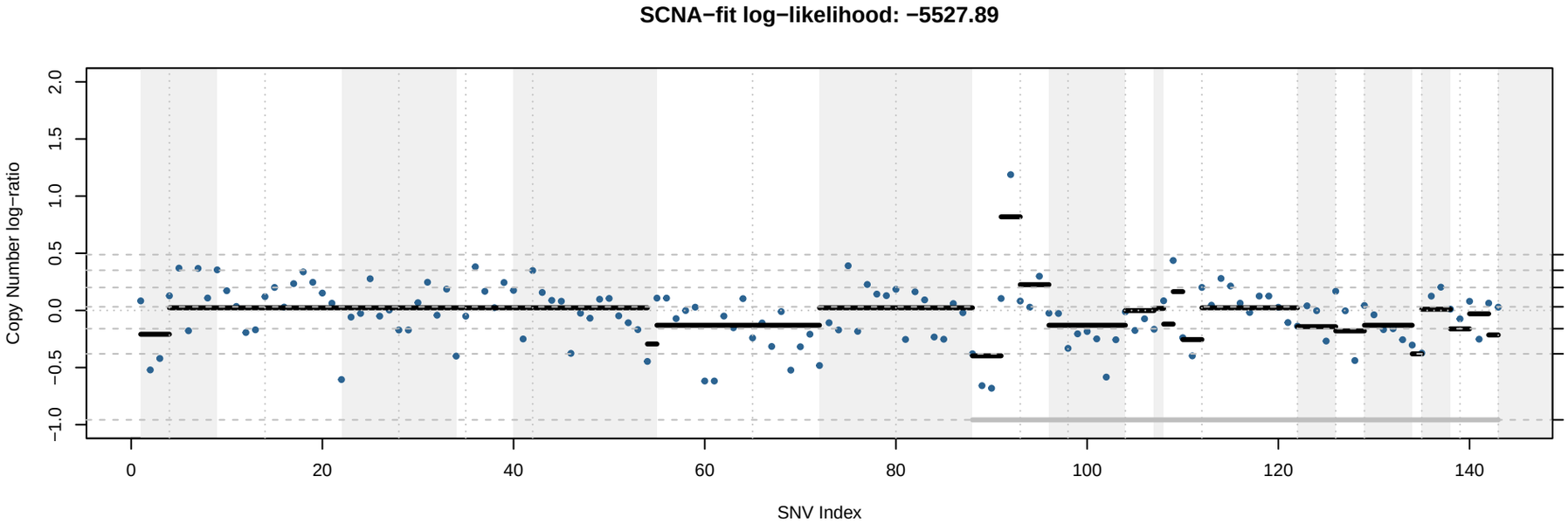

Coverage (log2)
Allelic fraction

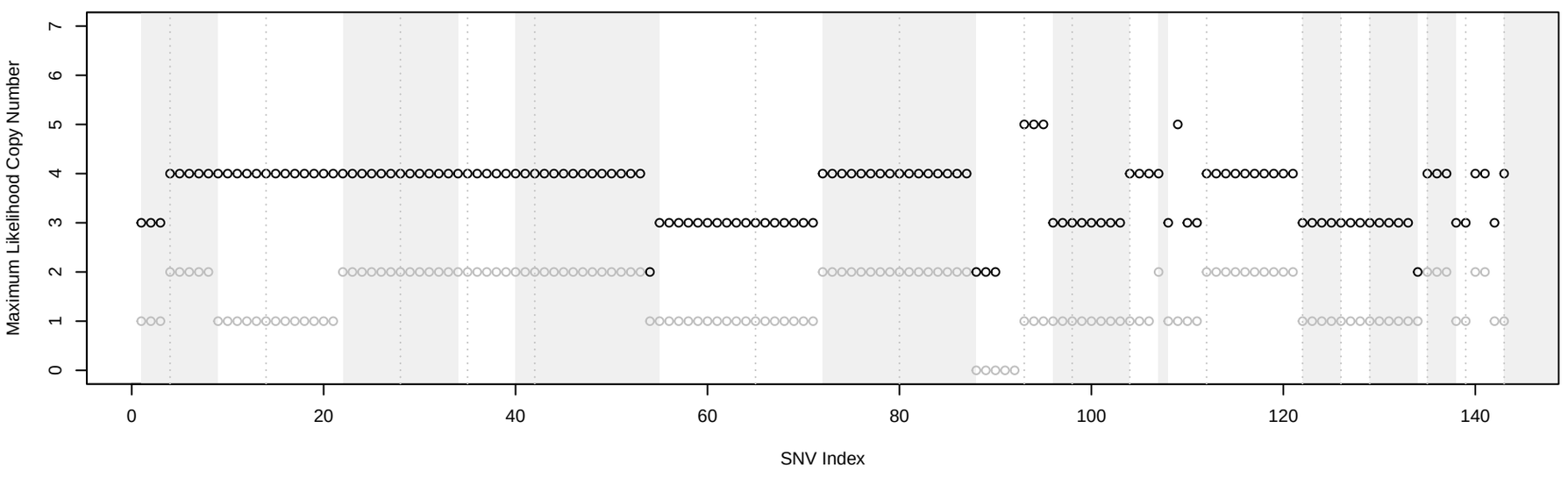

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1
3m1
4m1
5m1

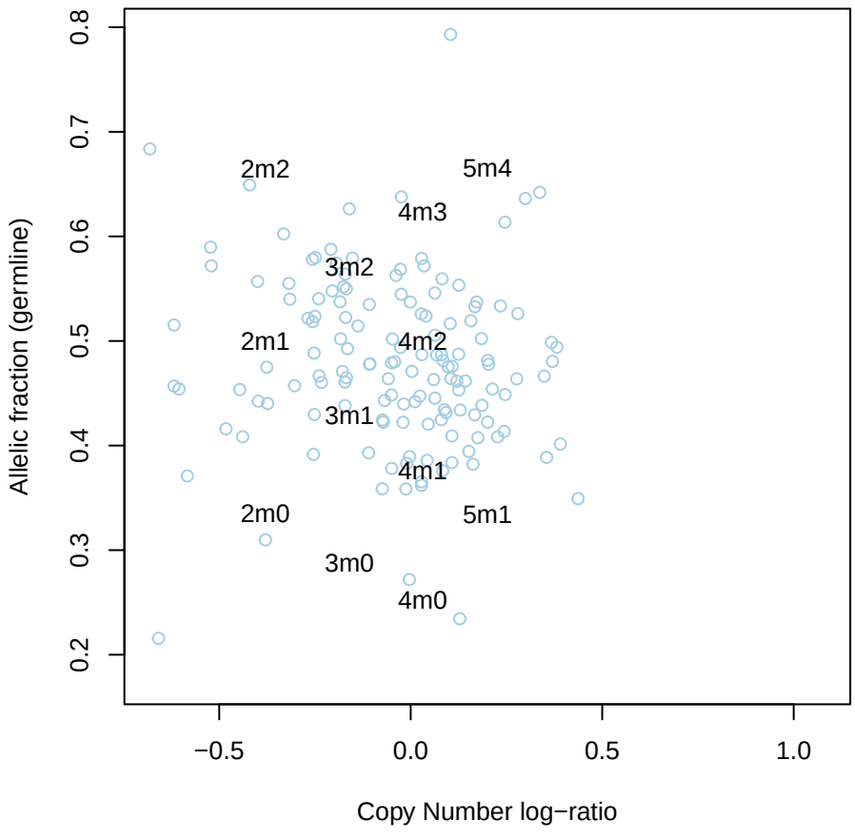

Frequency
Cellular fraction

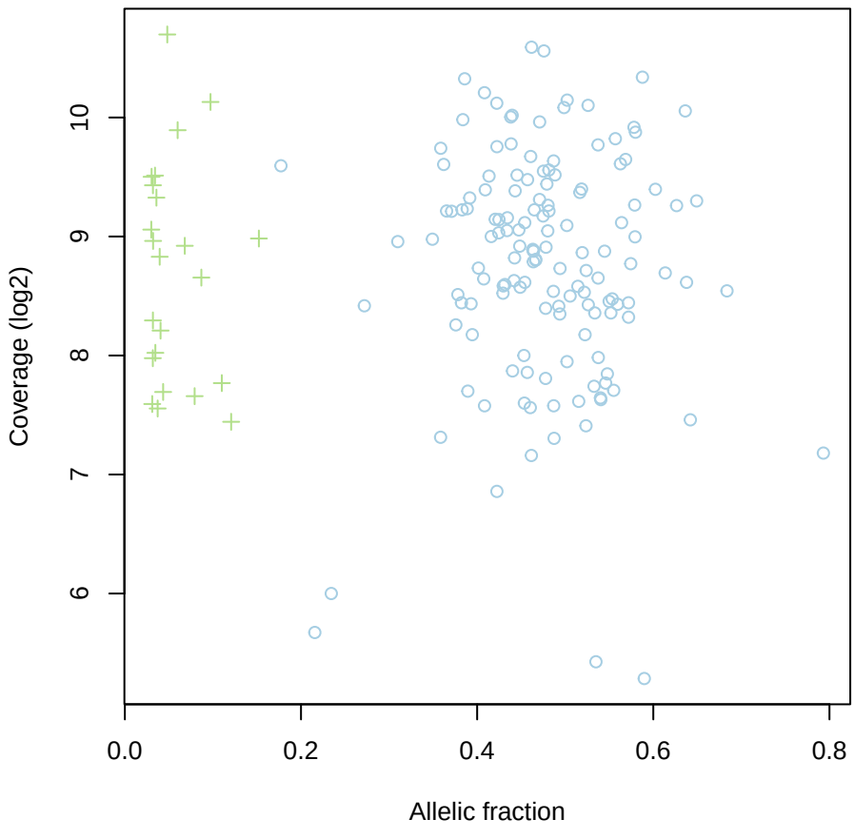

Purity: 0.33 Tumor ploidy: 3.825
0
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

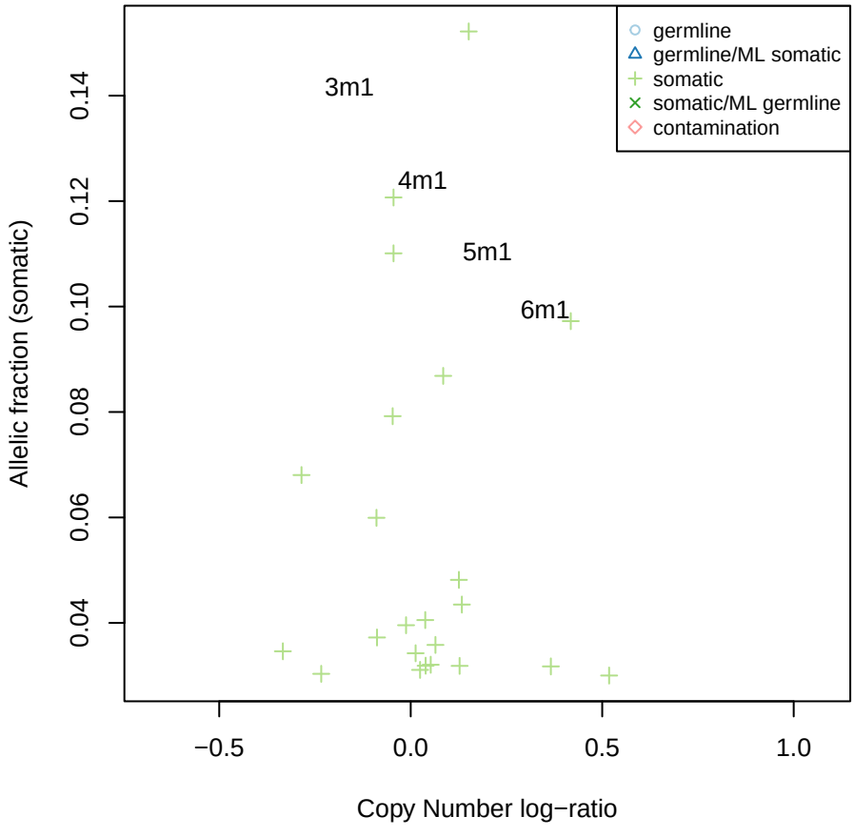

Purity: 0.33 Tumor ploidy: 3.825 SNV log−likelihood: −74.79 GoF: 93% Mean coverage: 522;418
1 2 3 4 5 6 7 8 9 10 12 13 15 17 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index

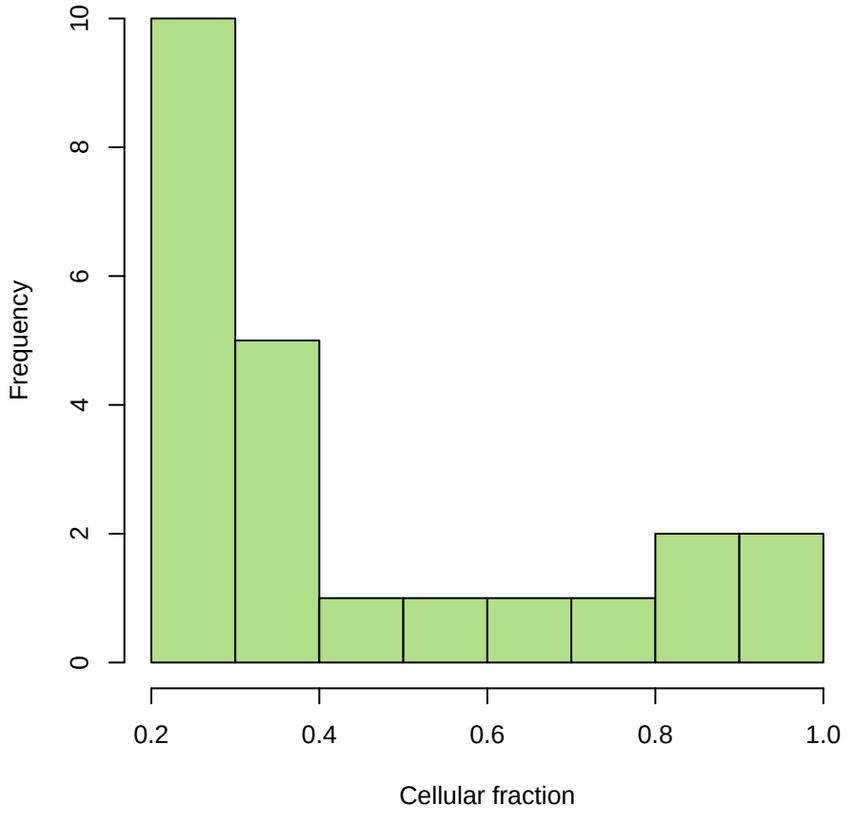

SCNA−fit log−likelihood: −5527.89
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
0 2 3 5 7
0 20 40 60 80 100 120 140
SNV Index

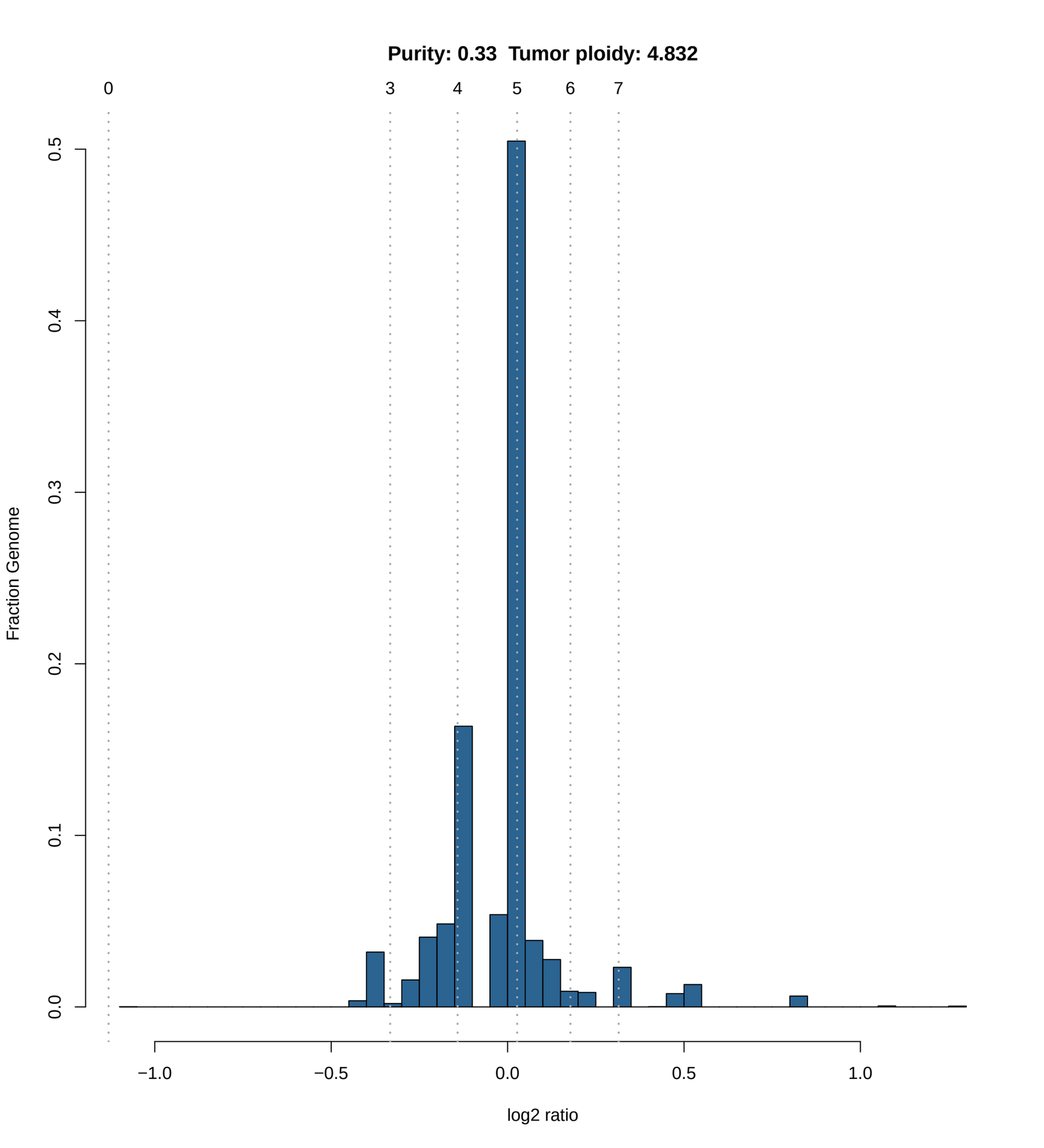

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

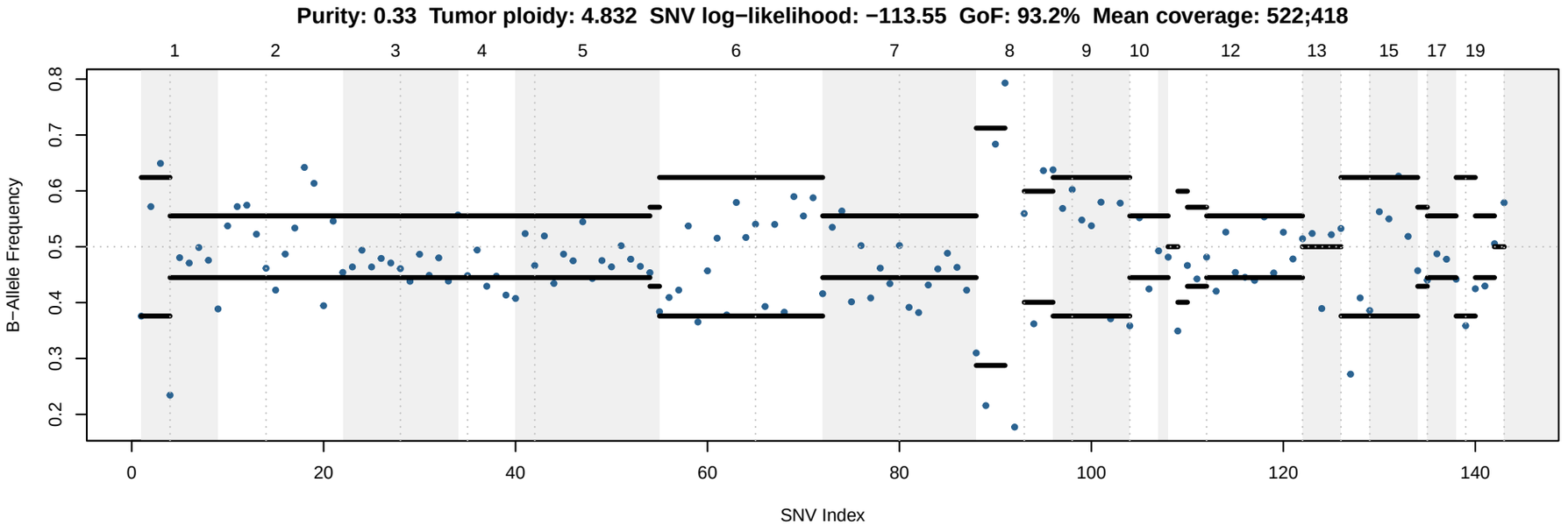

Allelic fraction (germline)
Copy Number log−ratio
2m2
5m4
4m3
3m2
2m1
4m2
3m1
4m1
2m0
5m1
3m0
4m0

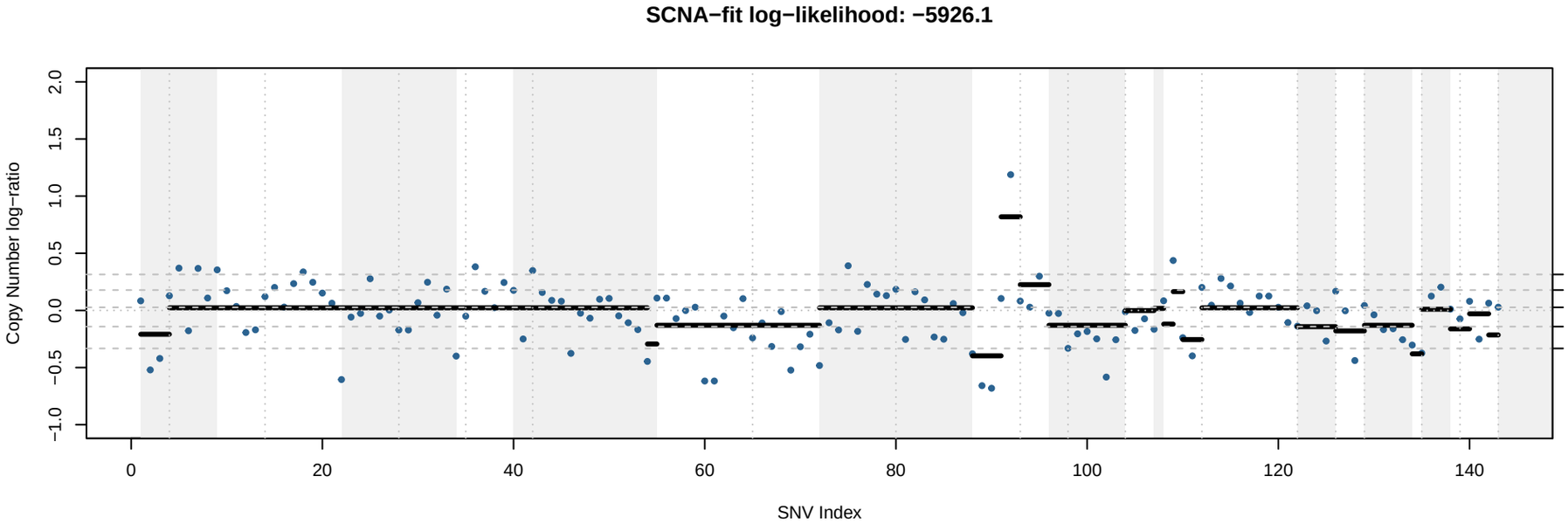

Coverage (log2)
Allelic fraction

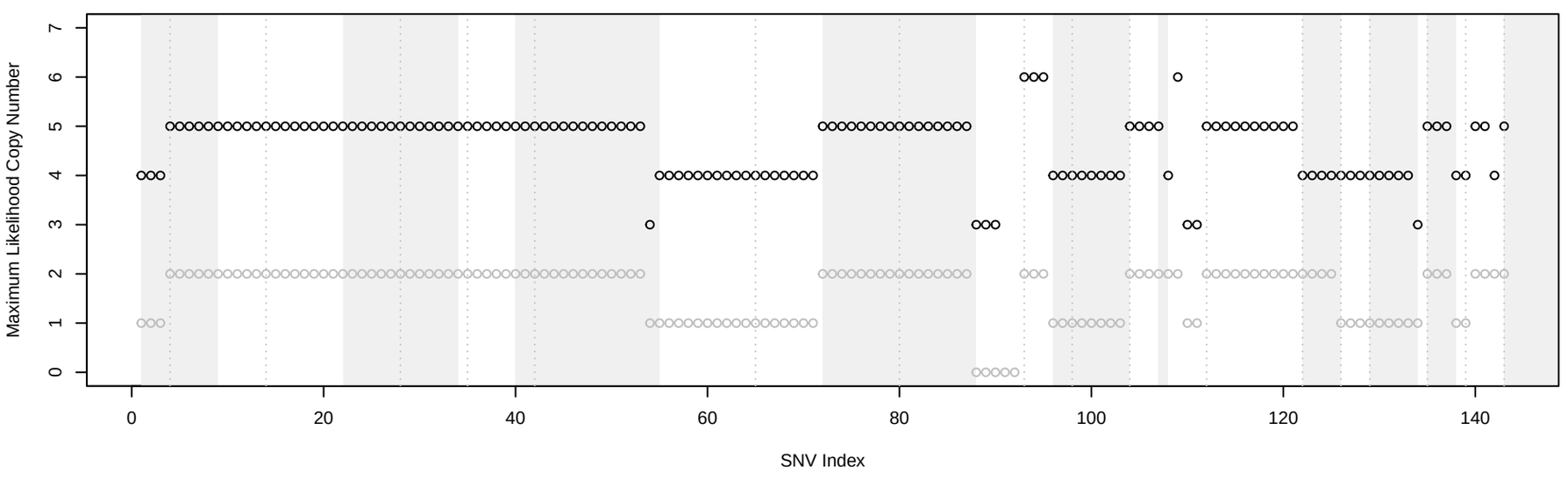

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
6m1

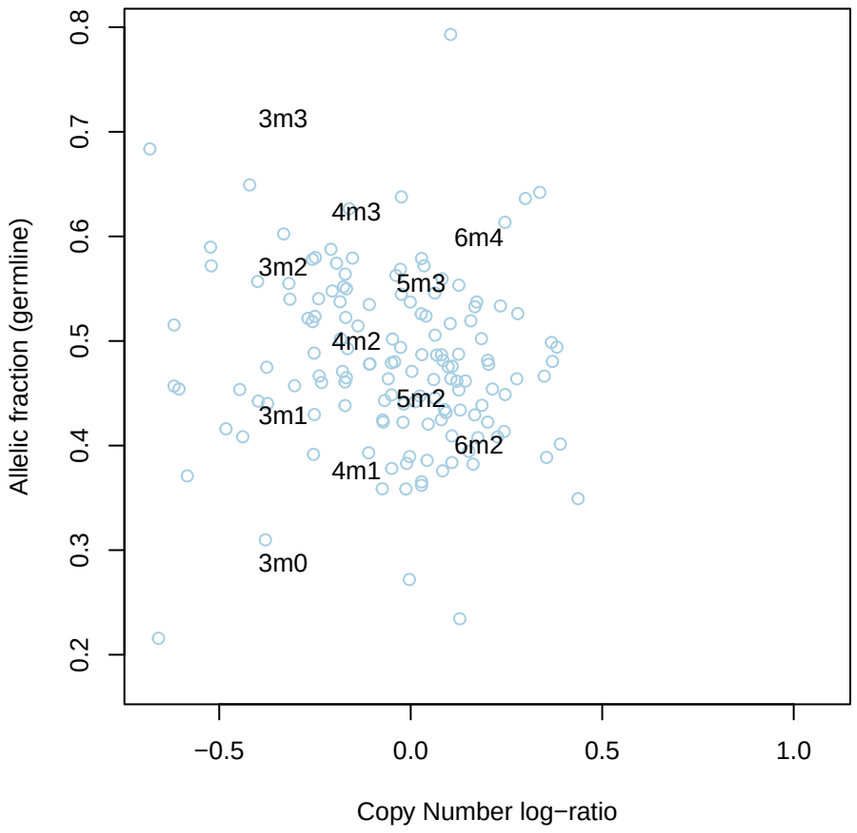

Frequency
Cellular fraction

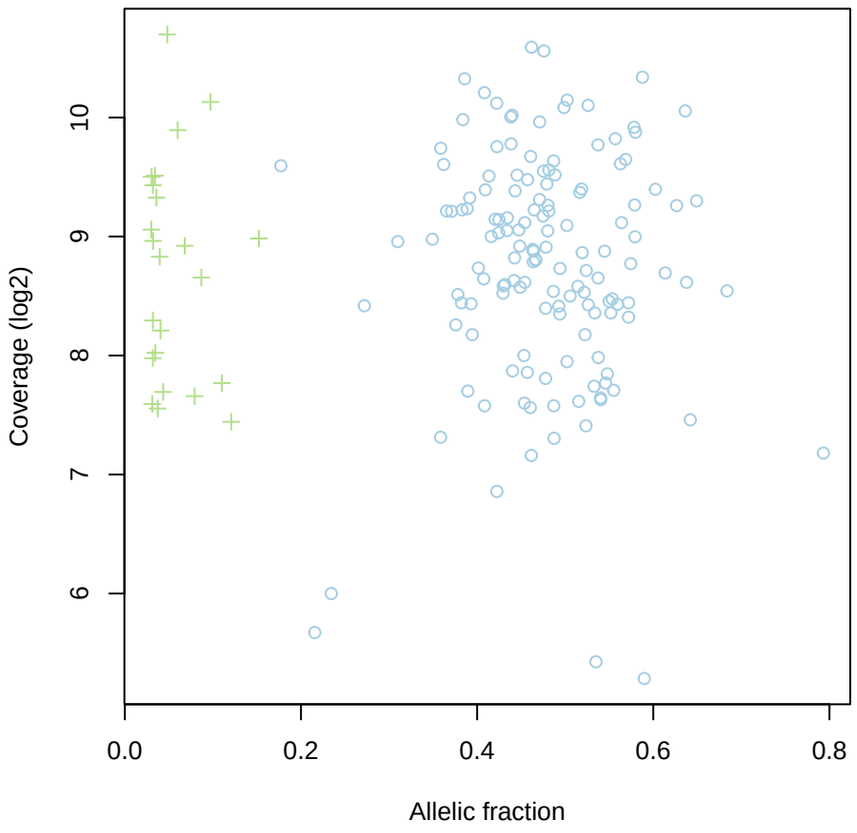

Purity: 0.33 Tumor ploidy: 4.832
0
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

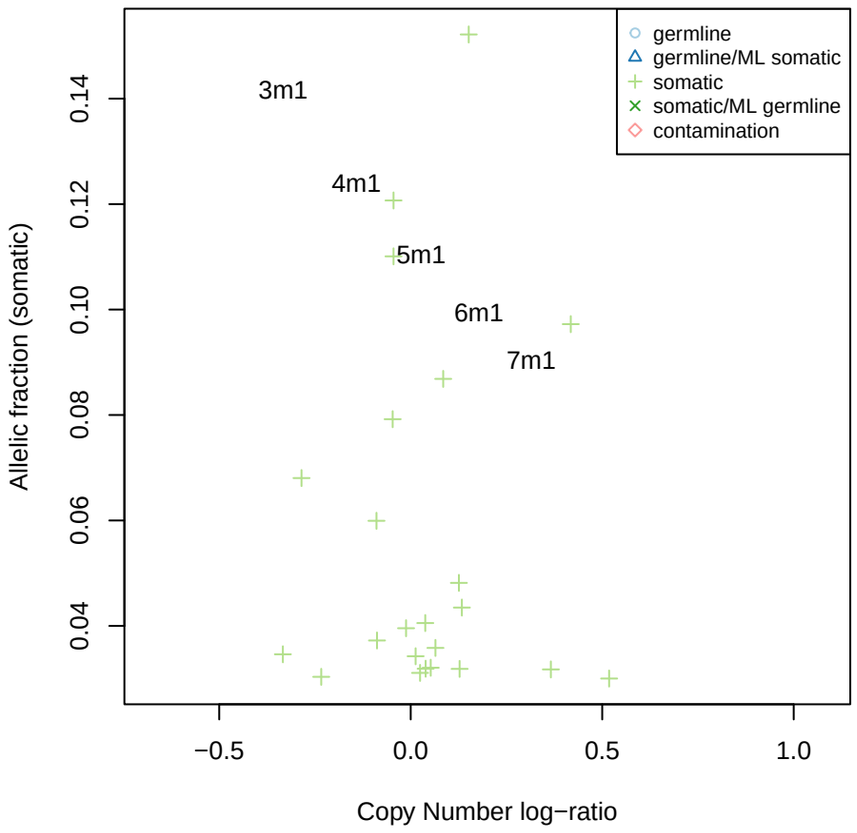

Purity: 0.33 Tumor ploidy: 4.832 SNV log−likelihood: −113.55 GoF: 93.2% Mean coverage: 522;418
1 2 3 4 5 6 7 8 9 10 12 13 15 17 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index

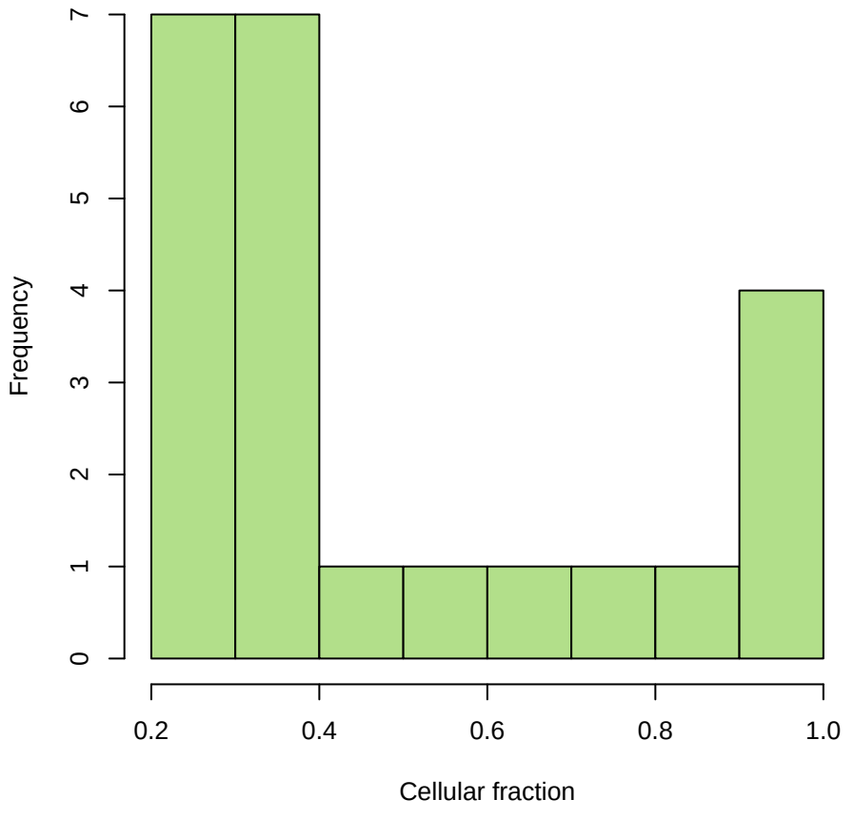

SCNA−fit log−likelihood: −5926.1
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
3 5 7
0 20 40 60 80 100 120 140
SNV Index

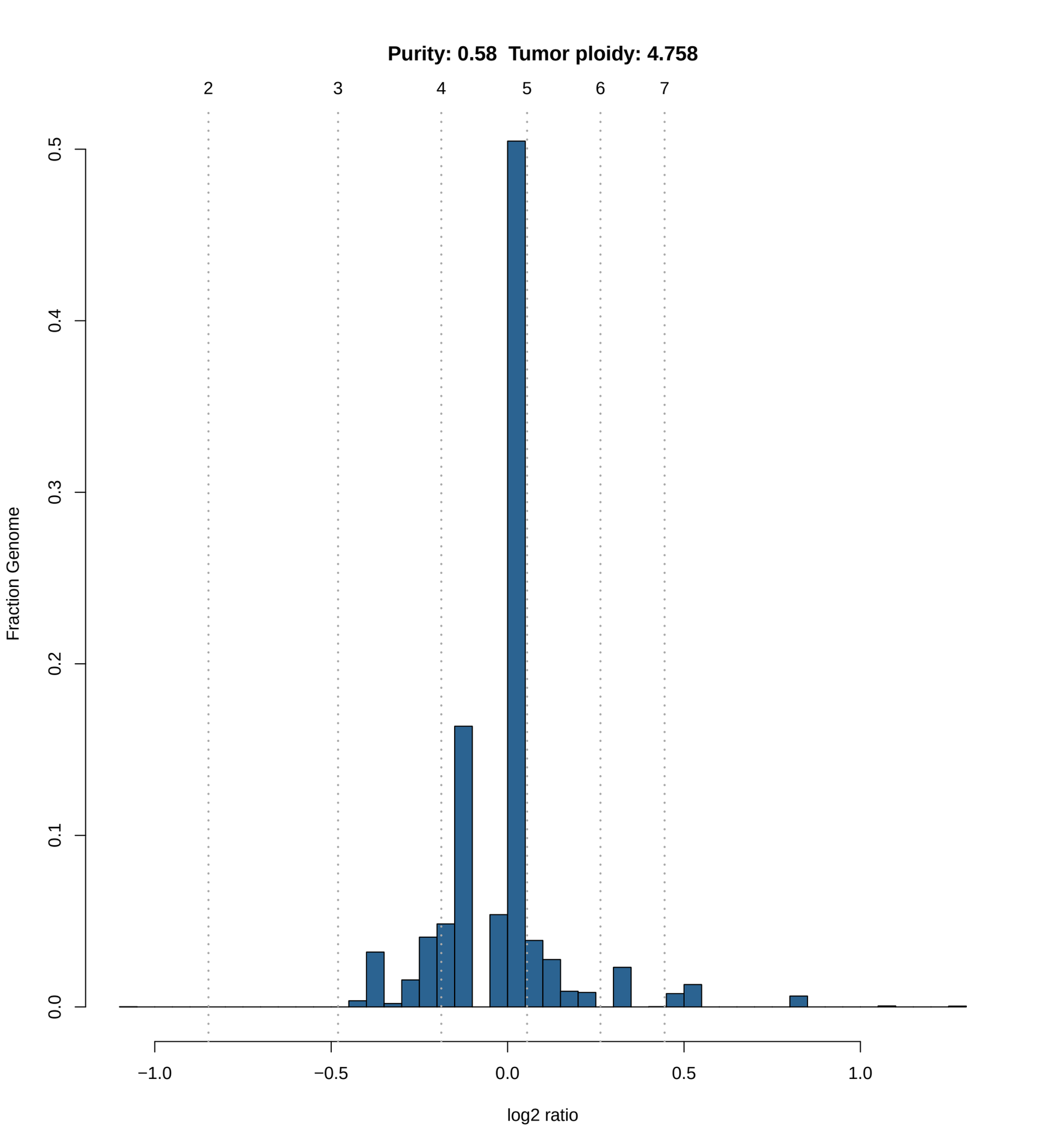

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

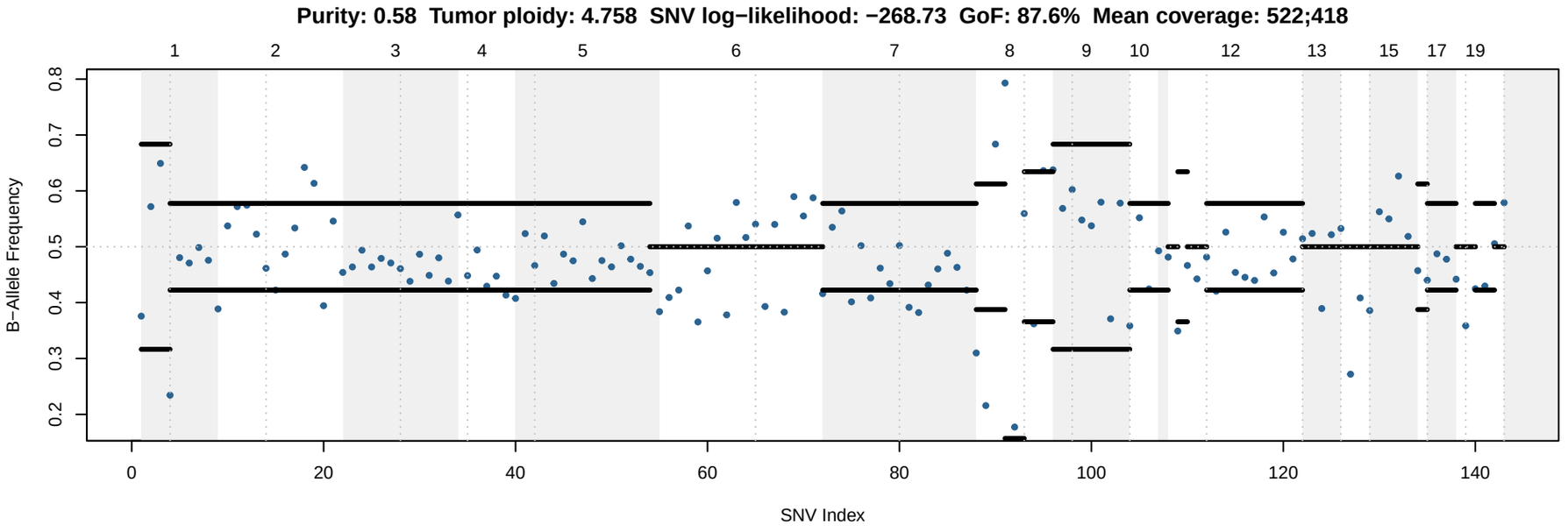

Allelic fraction (germline)
Copy Number log−ratio
3m3
4m3
6m4
3m2
5m3
4m2
5m2
3m1
6m2
4m1
3m0

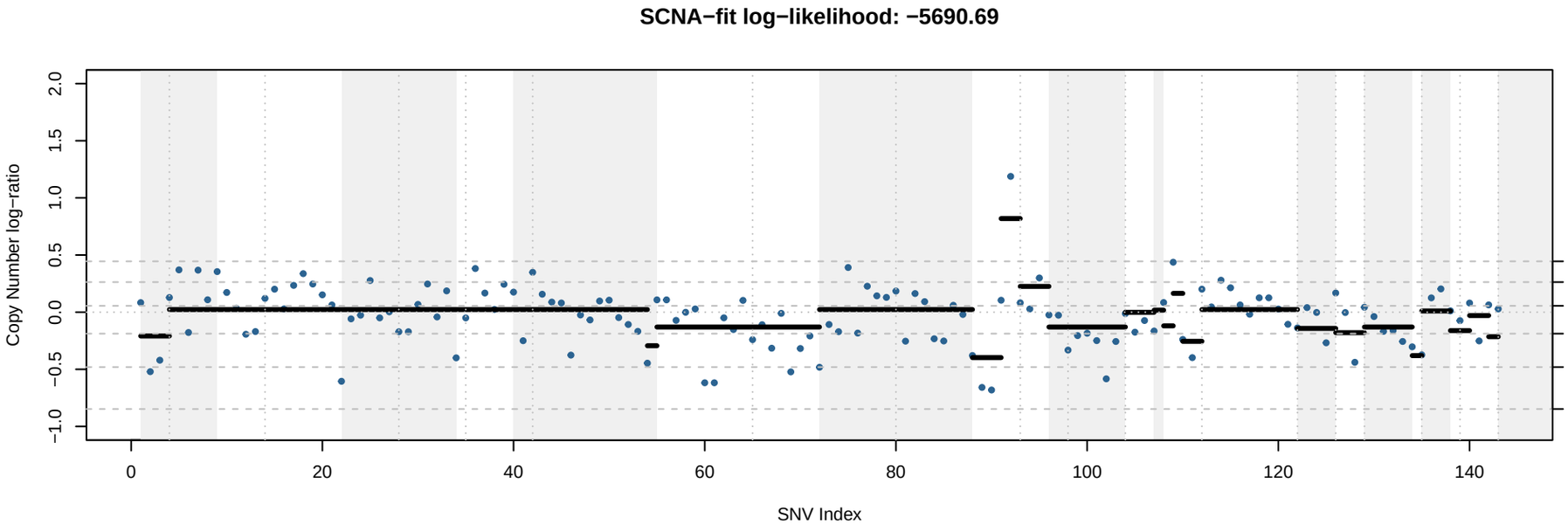

Coverage (log2)
Allelic fraction

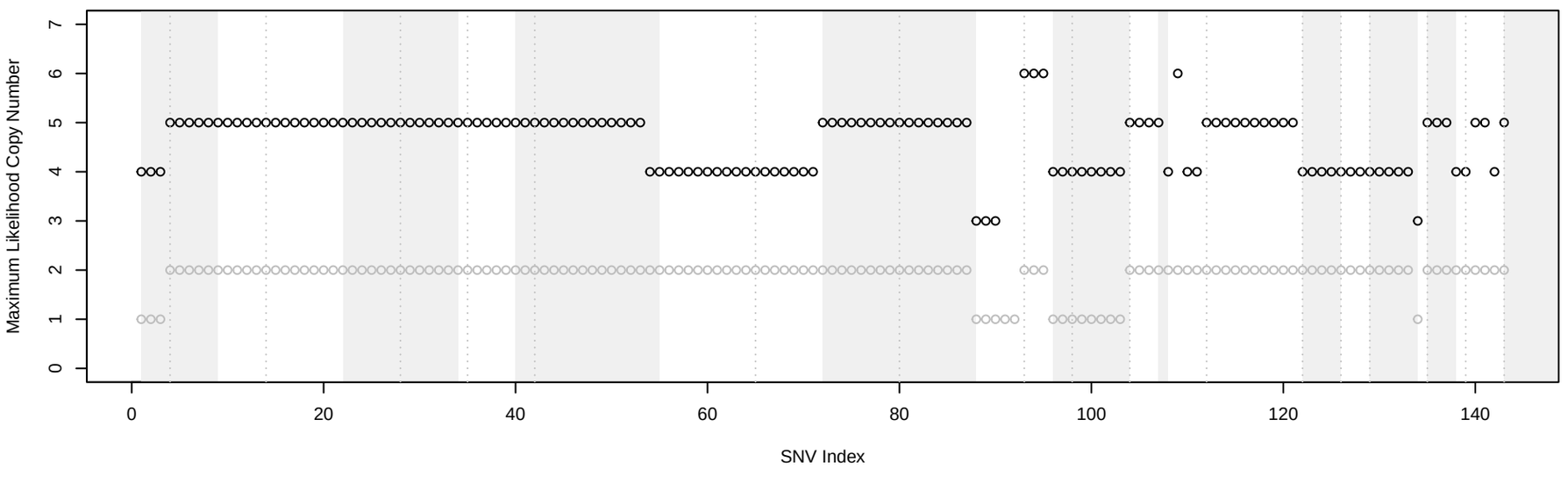

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m1
4m1
5m1
6m1
7m1

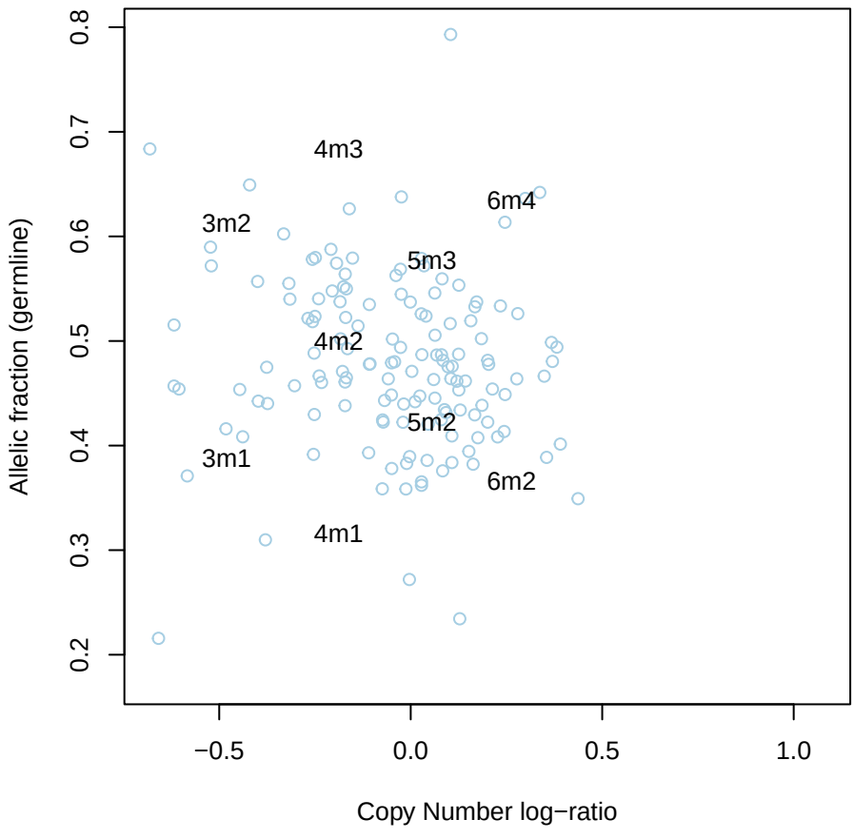

Frequency
Cellular fraction

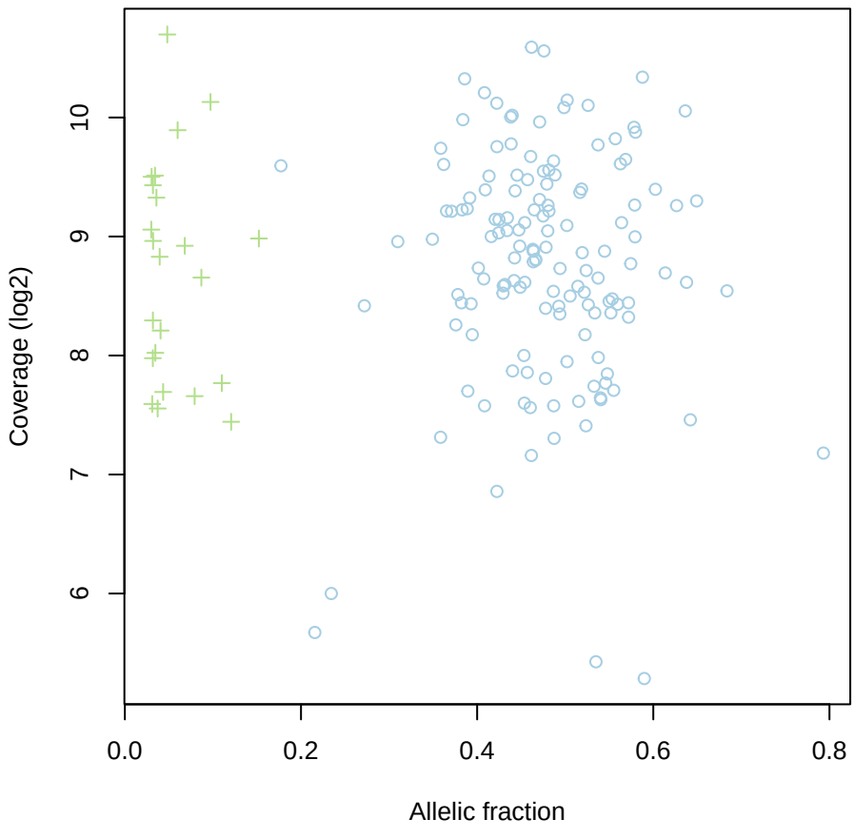

Purity: 0.58 Tumor ploidy: 4.758
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

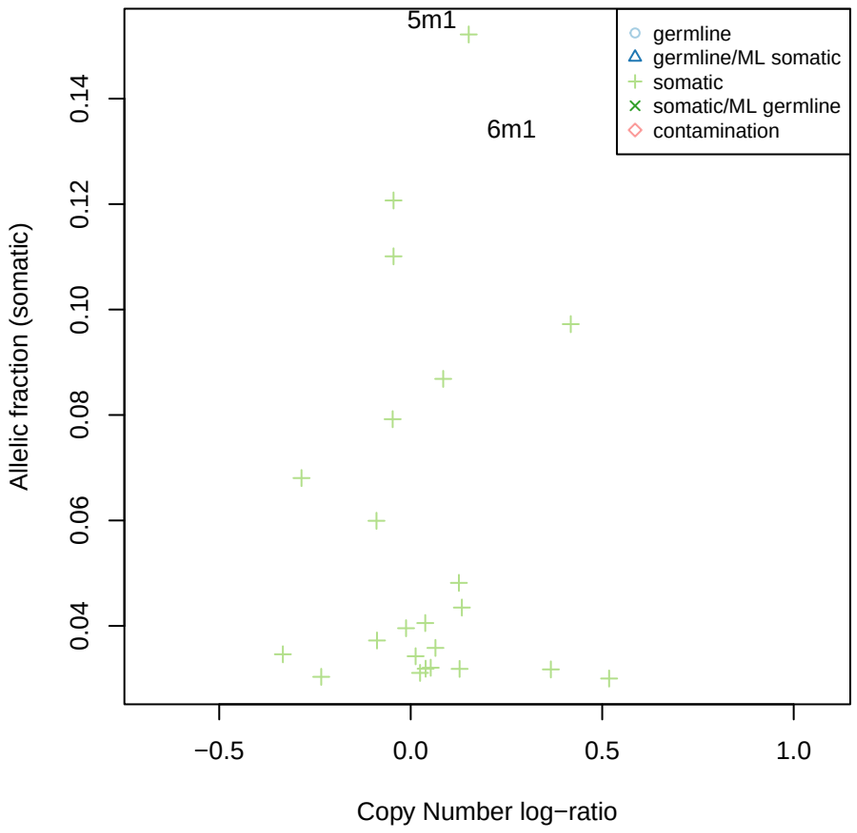

Purity: 0.58 Tumor ploidy: 4.758 SNV log−likelihood: −268.73 GoF: 87.6% Mean coverage: 522;418
1 2 3 4 5 6 7 8 9 10 12 13 15 17 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index

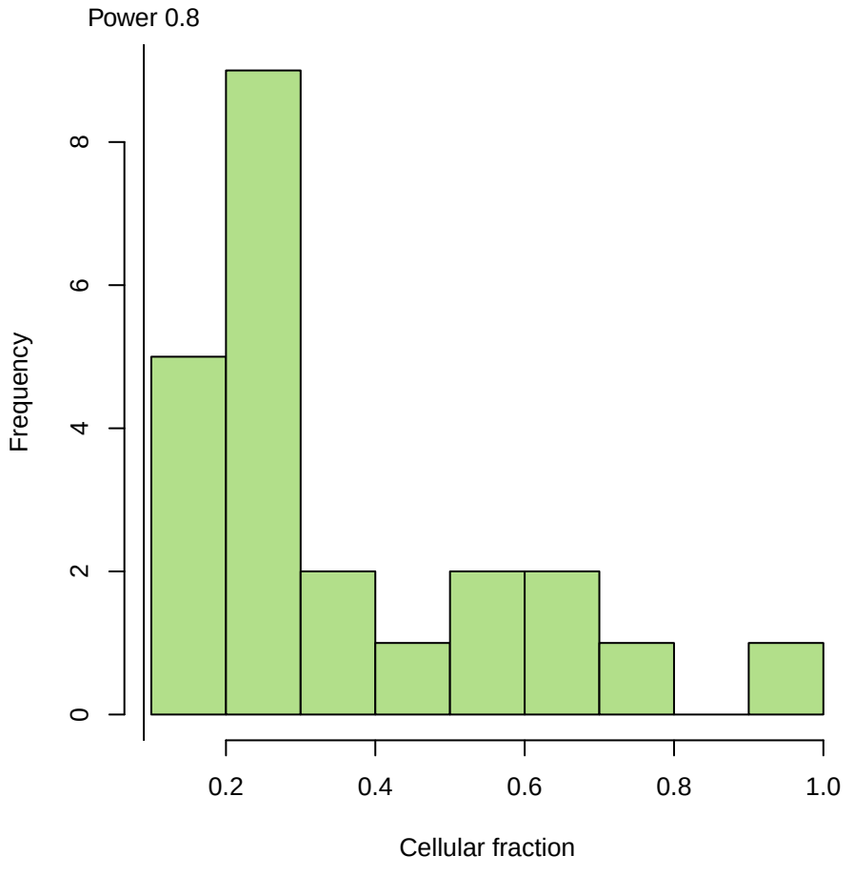

SCNA−fit log−likelihood: −5690.69
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

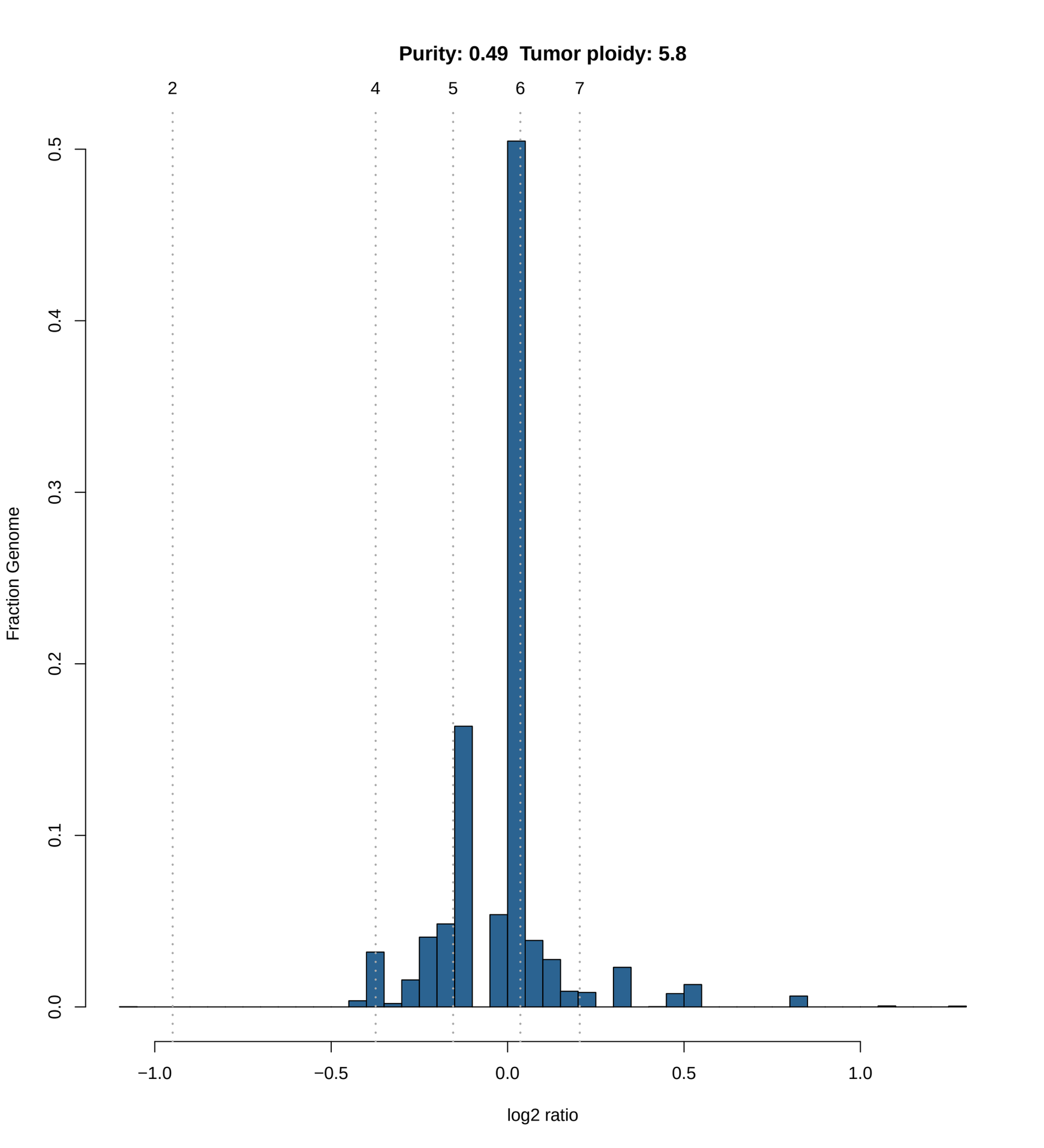

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

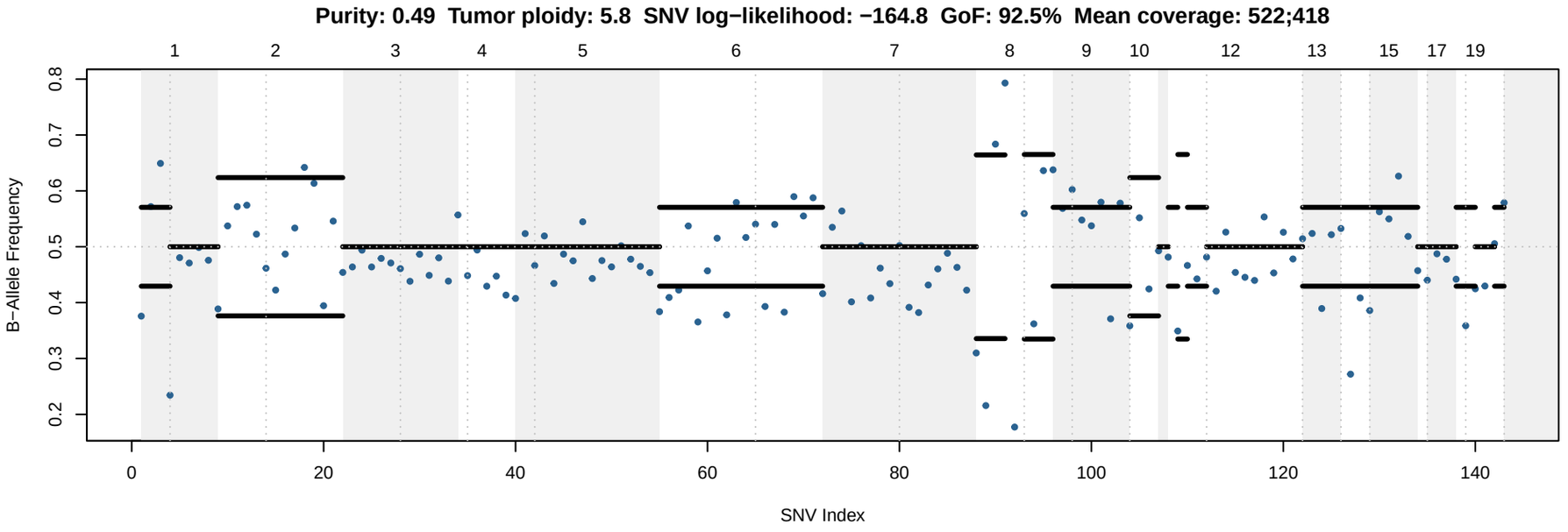

Allelic fraction (germline)
Copy Number log−ratio
4m3
6m4
3m2
5m3
4m2
5m2
3m1
6m2
4m1

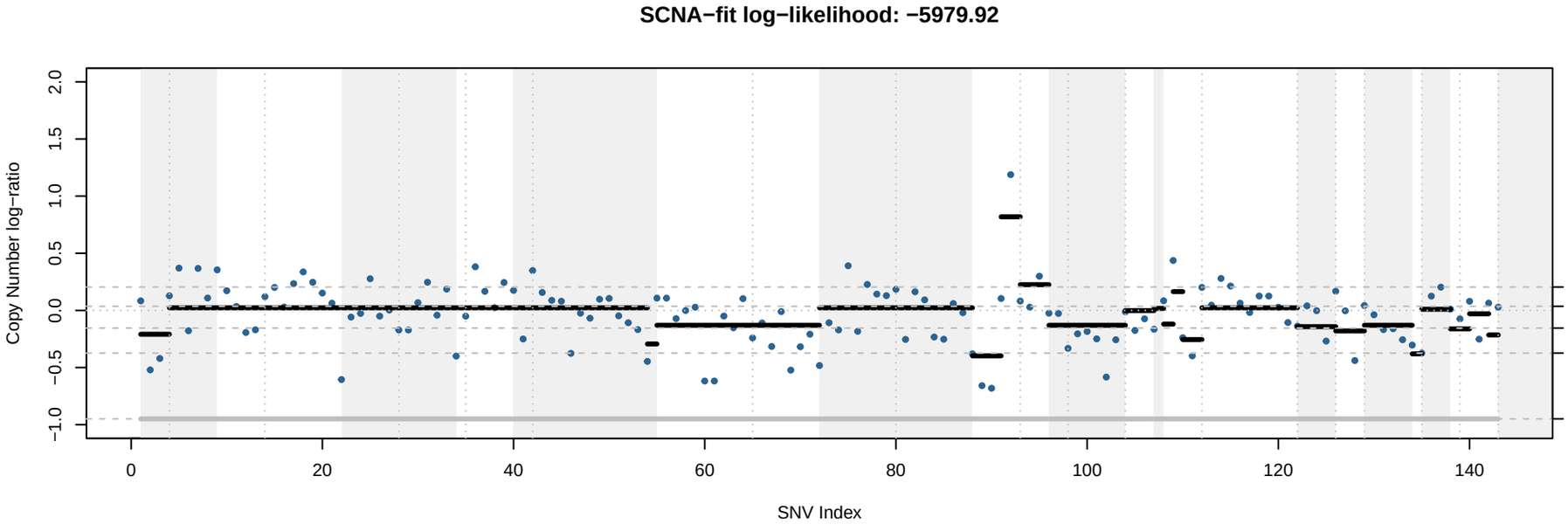

Coverage (log2)
Allelic fraction

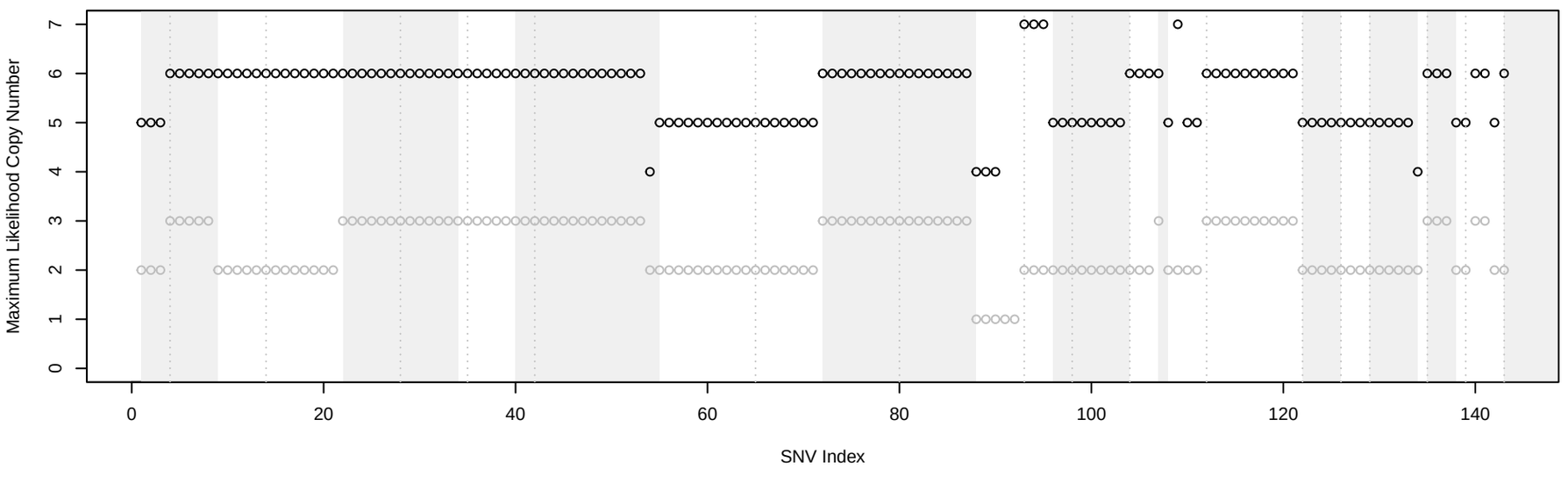

Allelic fraction (somatic)
Copy Number log−ratio
5m1
6m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

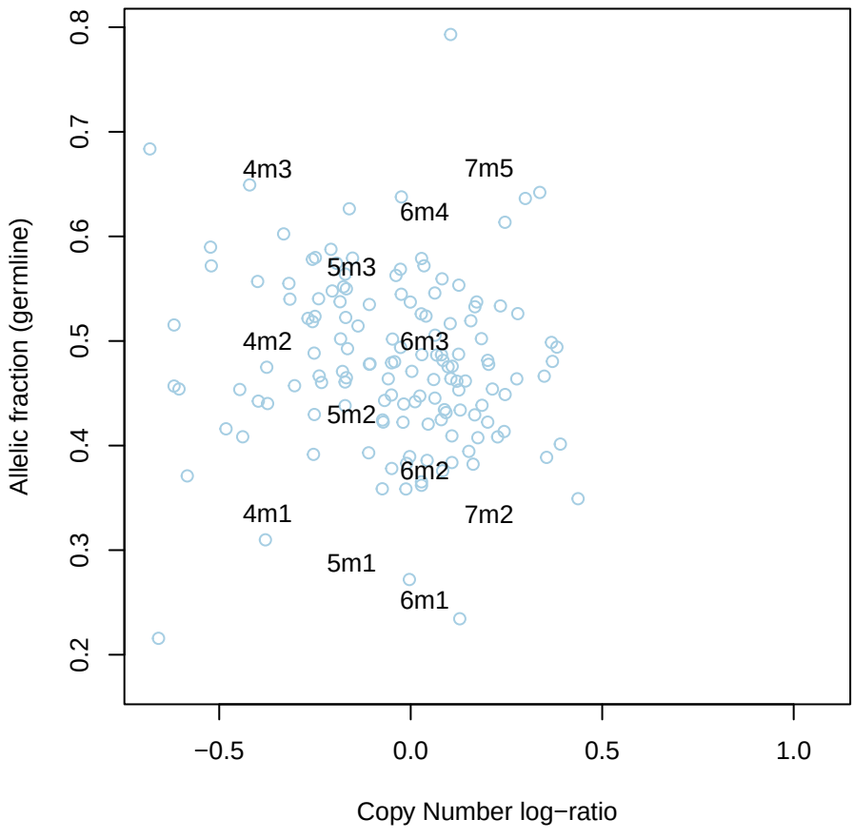

Power 0.8
Frequency
Cellular fraction

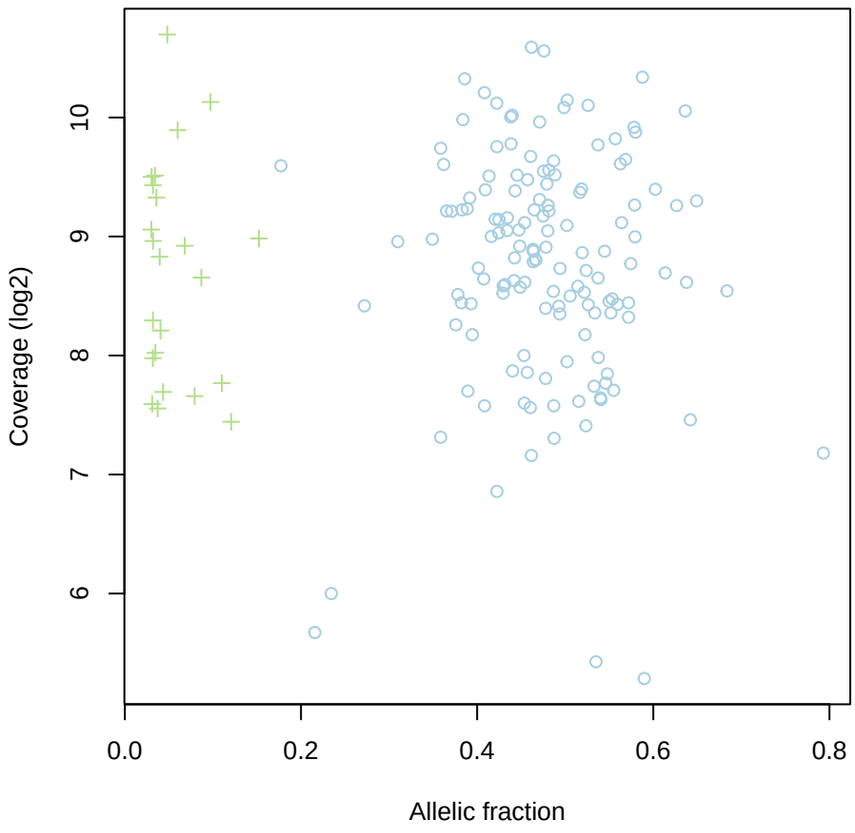

Purity: 0.49 Tumor ploidy: 5.8
2
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

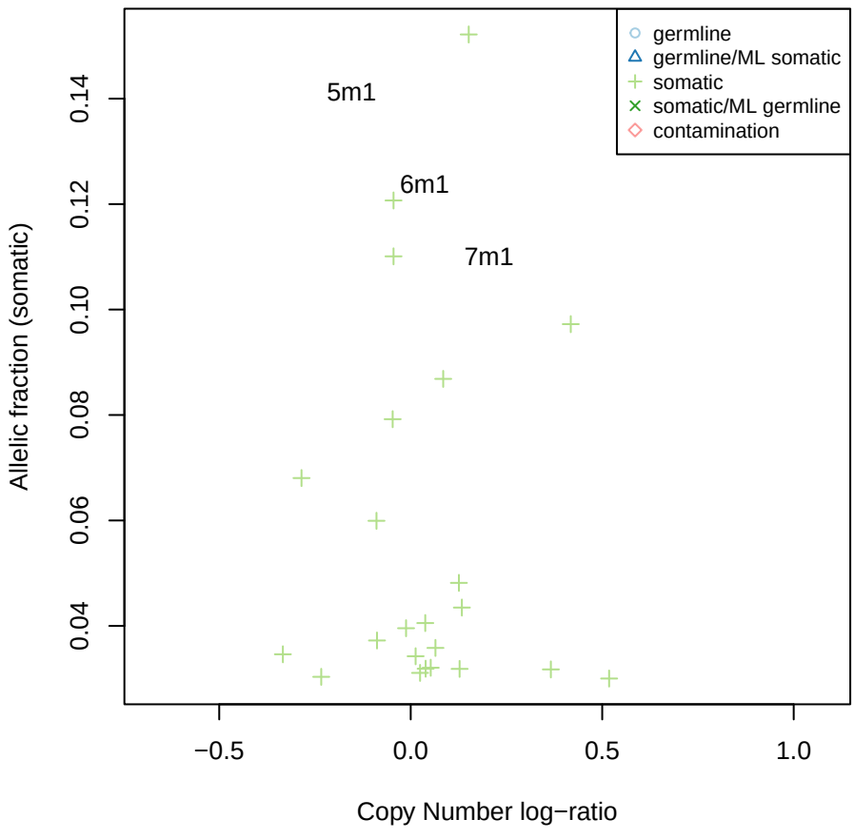

Purity: 0.49 Tumor ploidy: 5.8 SNV log−likelihood: −164.8 GoF: 92.5% Mean coverage: 522;418
1 2 3 4 5 6 7 8 9 10 12 13 15 17 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index

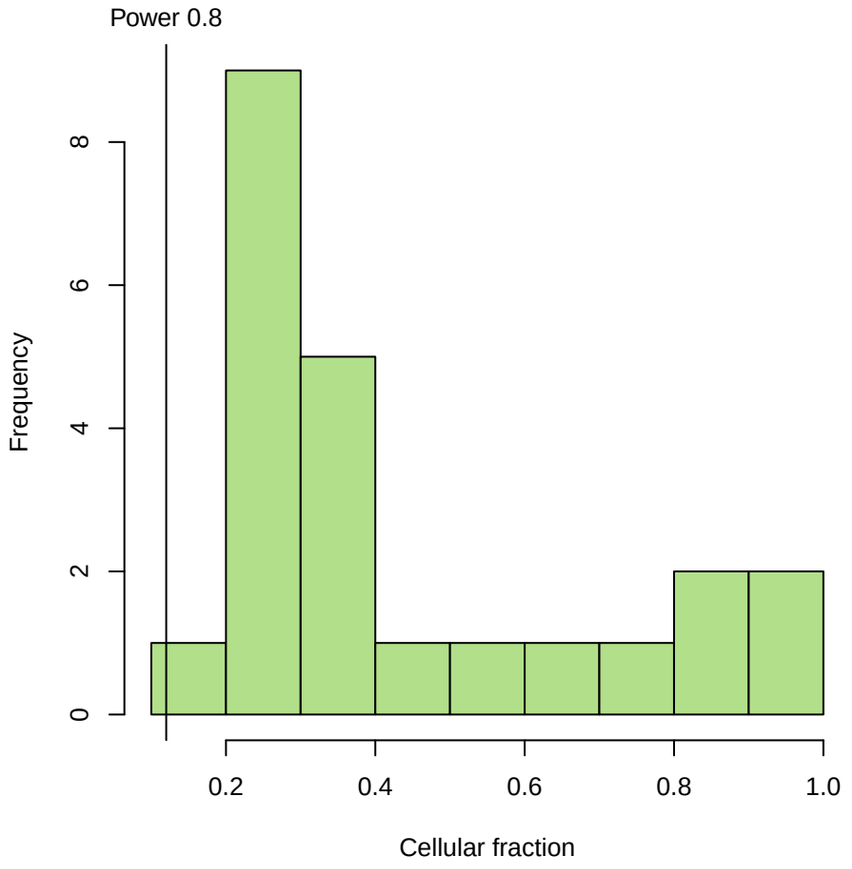

SCNA−fit log−likelihood: −5979.92
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
2 4 5 7
0 20 40 60 80 100 120 140
SNV Index

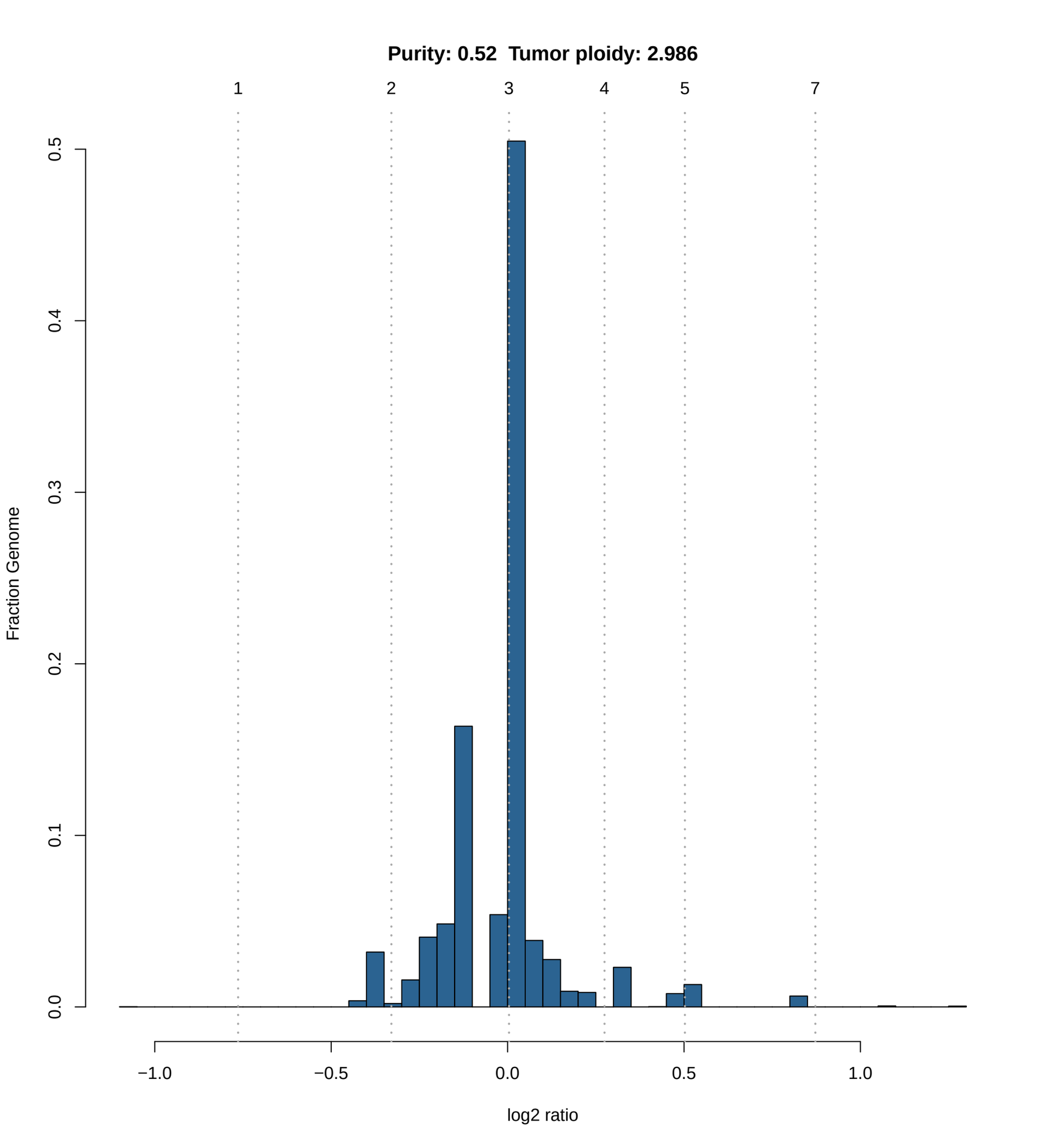

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

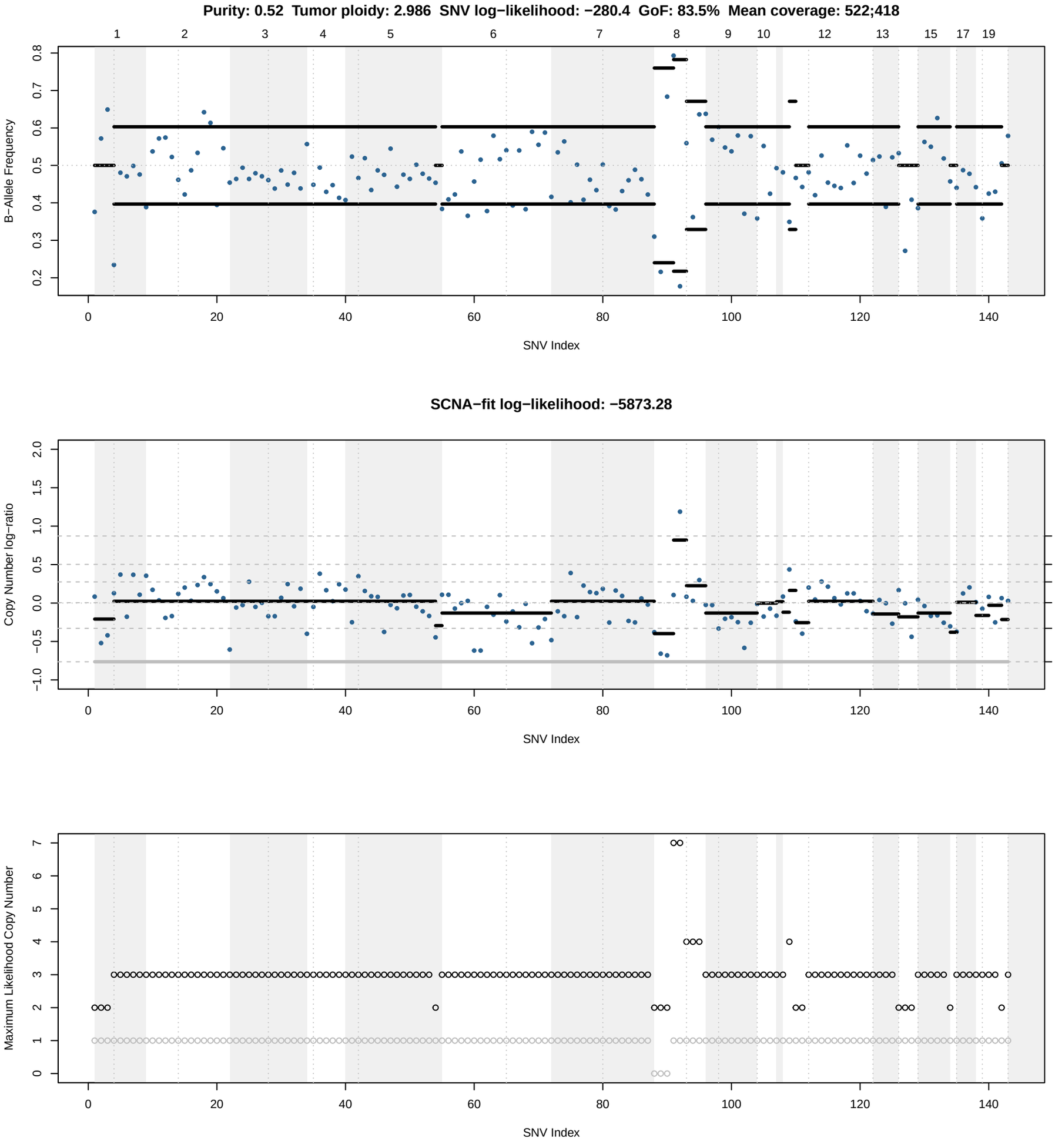

Allelic fraction (germline)
Copy Number log−ratio
4m3
7m5
6m4
5m3
4m2
6m3
5m2
6m2
4m1
7m2
5m1
6m1

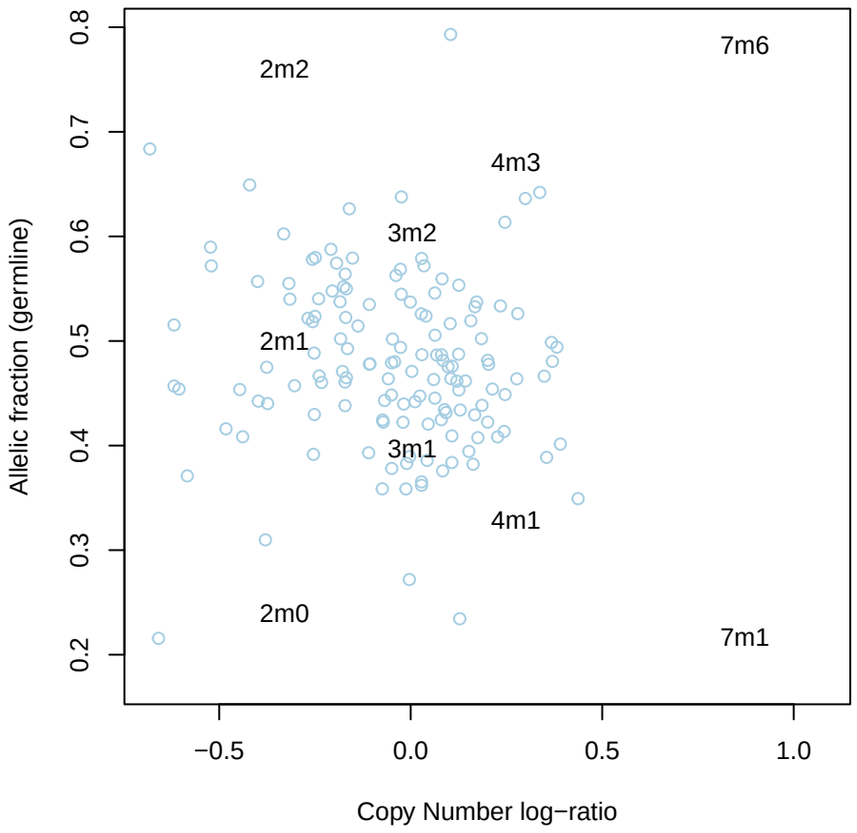

Coverage (log2)
Allelic fraction

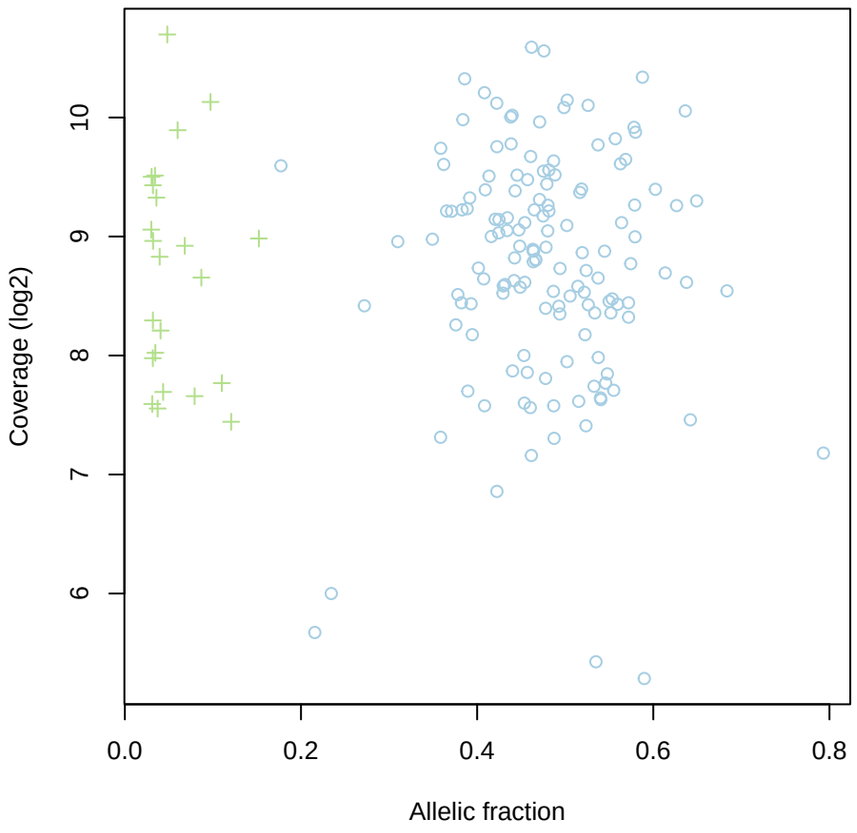

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
6m1
7m1

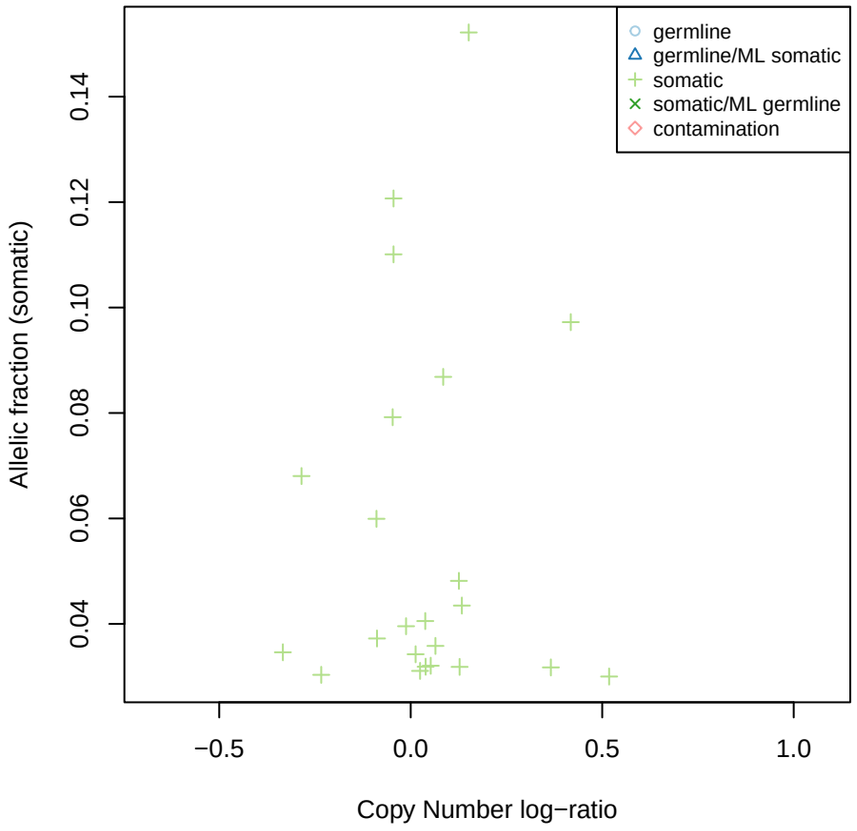

Power 0.8
Frequency
Cellular fraction

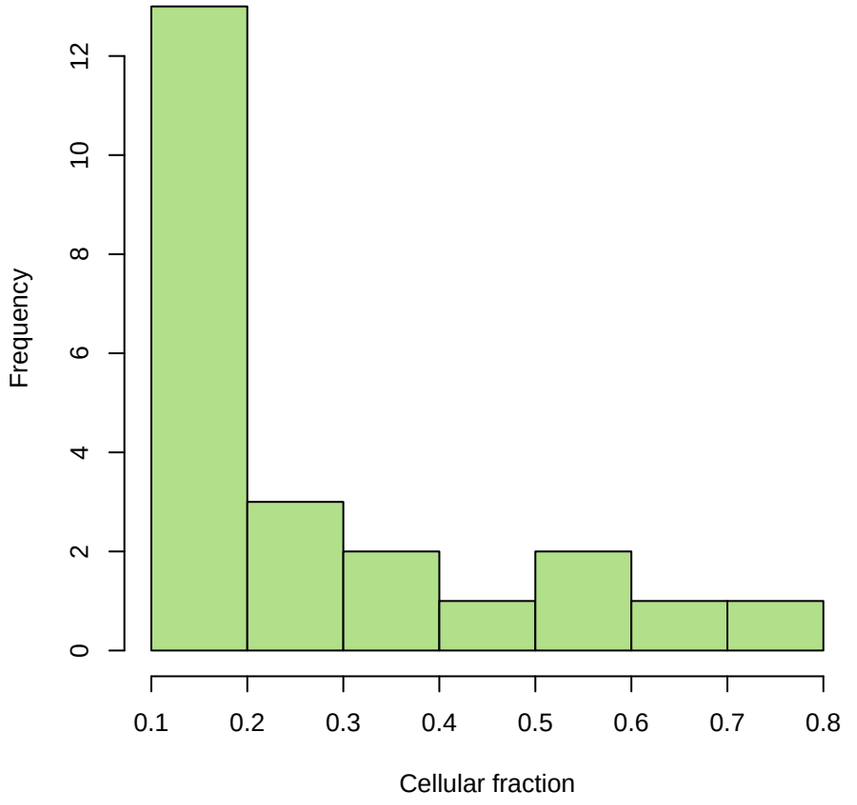

Purity: 0.52 Tumor ploidy: 2.986
1
2
3
4
5
7
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

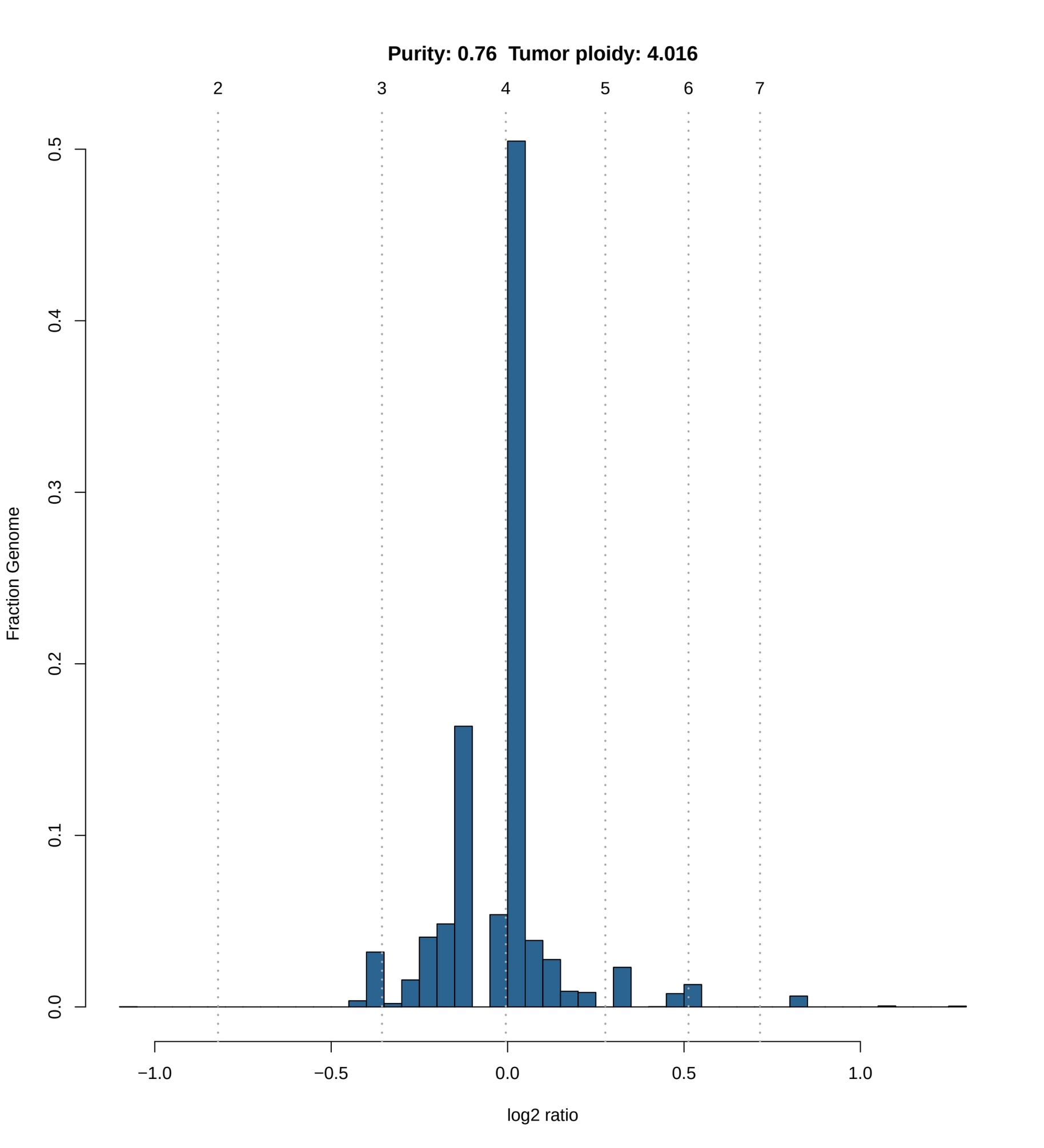

Purity: 0.52 Tumor ploidy: 2.986 SNV log−likelihood: −280.4 GoF: 83.5% Mean coverage: 522;418
1 2 3 4 5 6 7 8 9 10 12 13 15 17 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index
SCNA−fit log−likelihood: −5873.28
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
1 2 3 4 5 7
0 20 40 60 80 100 120 140
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

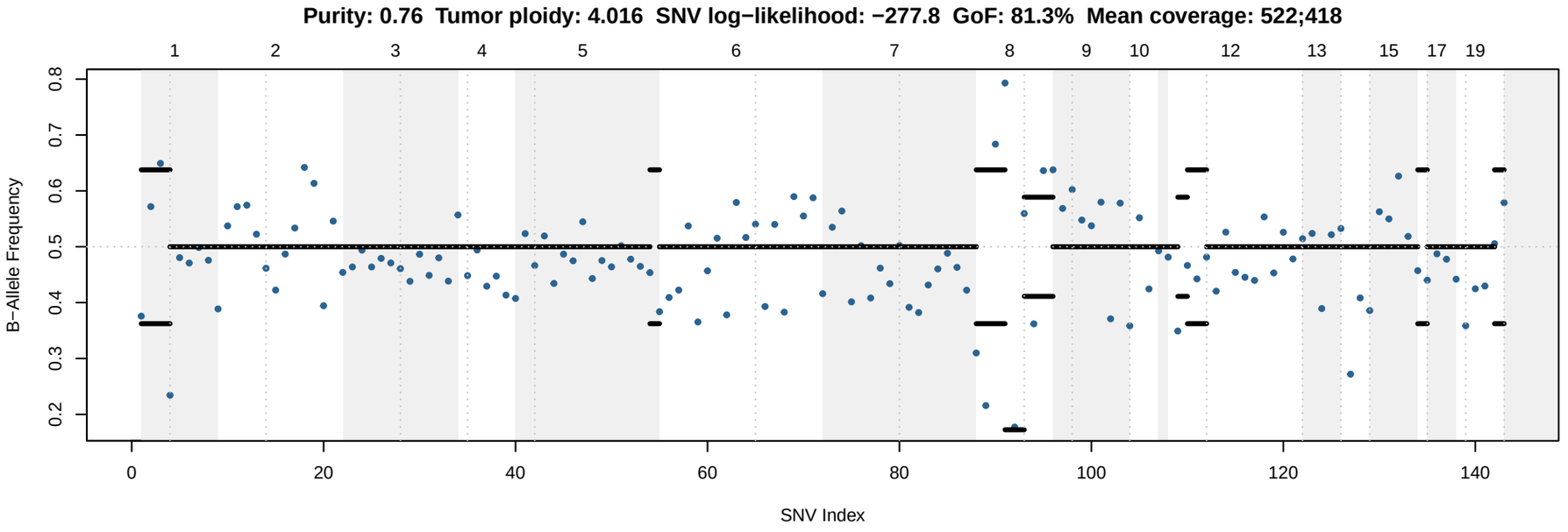

Allelic fraction (germline)
Copy Number log−ratio
2m2
7m6
4m3
3m2
2m1
3m1
4m1
2m0
7m1

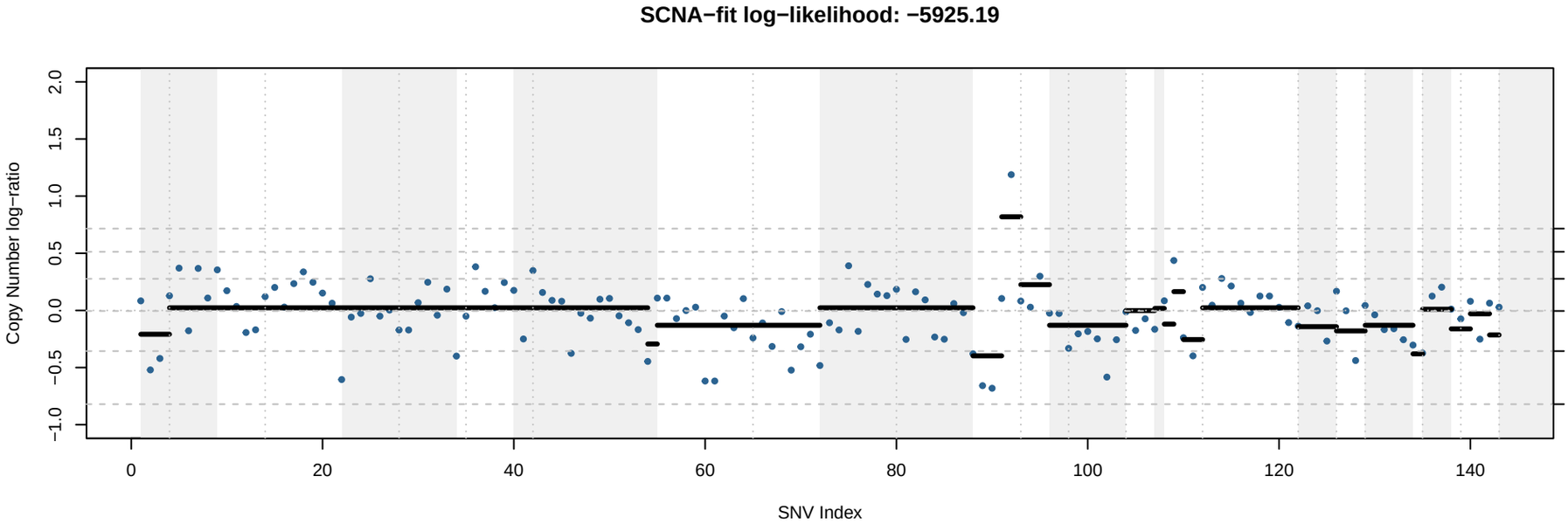

Coverage (log2)
Allelic fraction

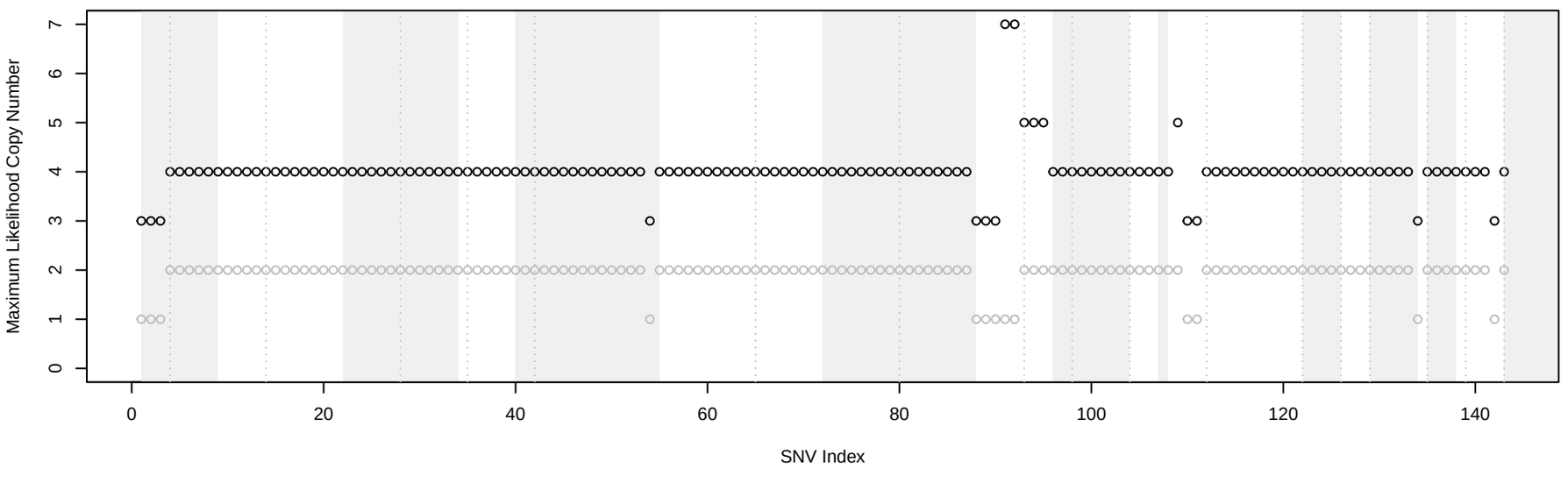

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

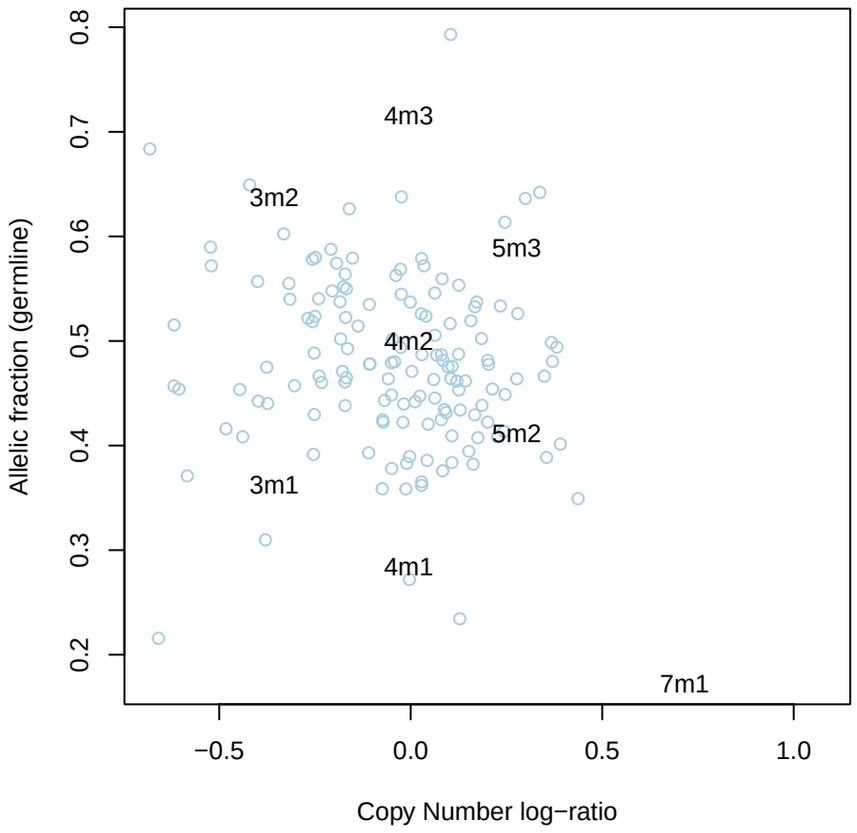

Frequency
Cellular fraction

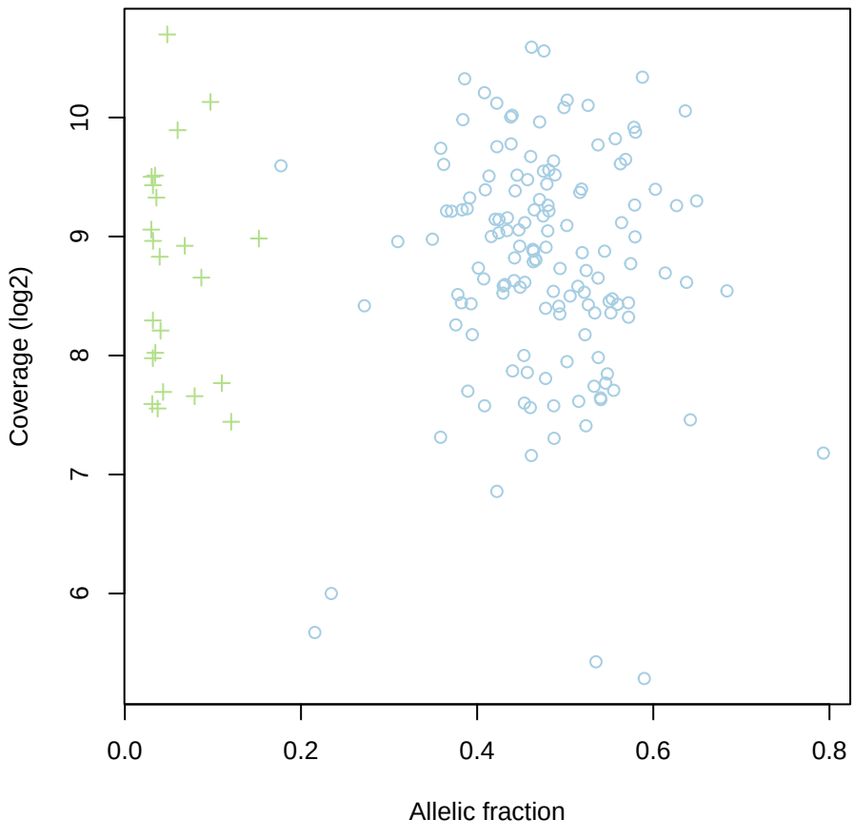

Purity: 0.76 Tumor ploidy: 4.016
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

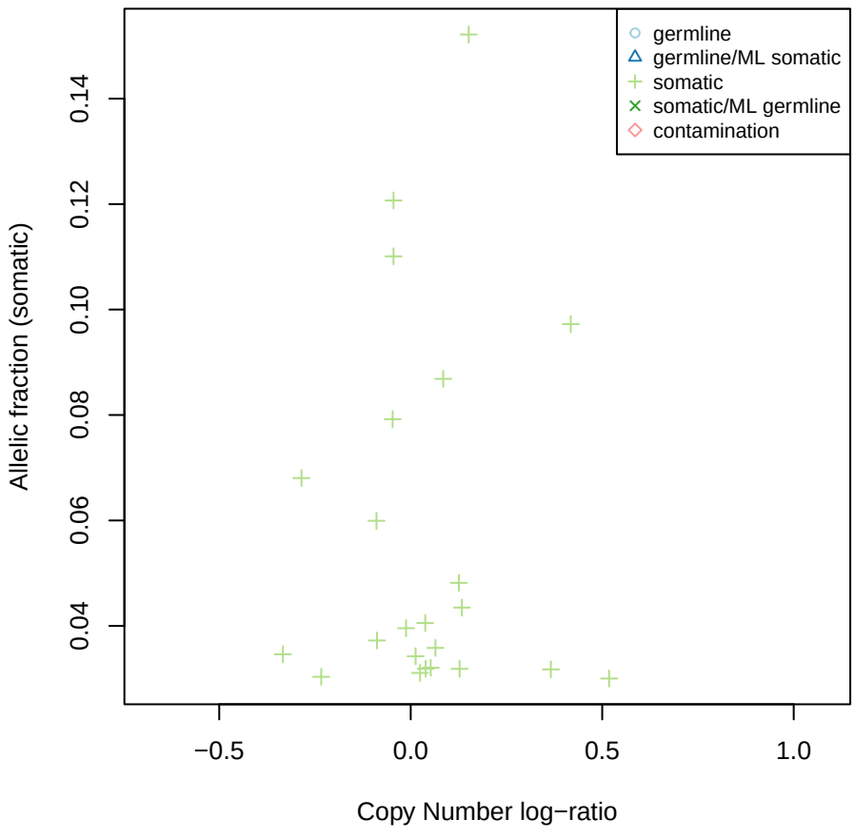

Purity: 0.76 Tumor ploidy: 4.016 SNV log−likelihood: −277.8 GoF: 81.3% Mean coverage: 522;418
1 2 3 4 5 6 7 8 9 10 12 13 15 17 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index

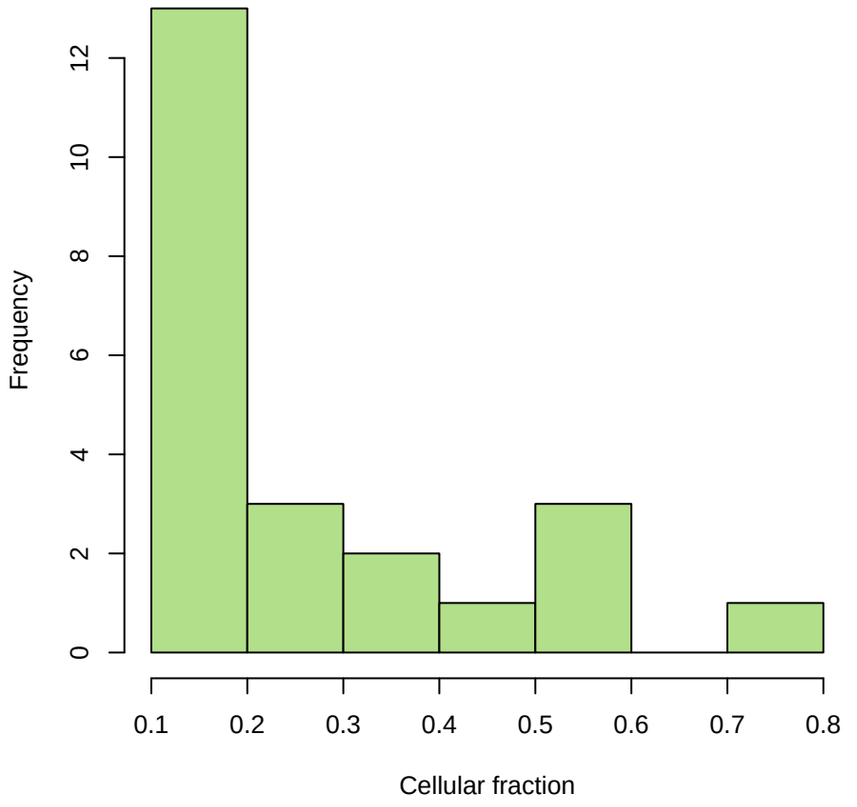

SCNA−fit log−likelihood: −5925.19
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

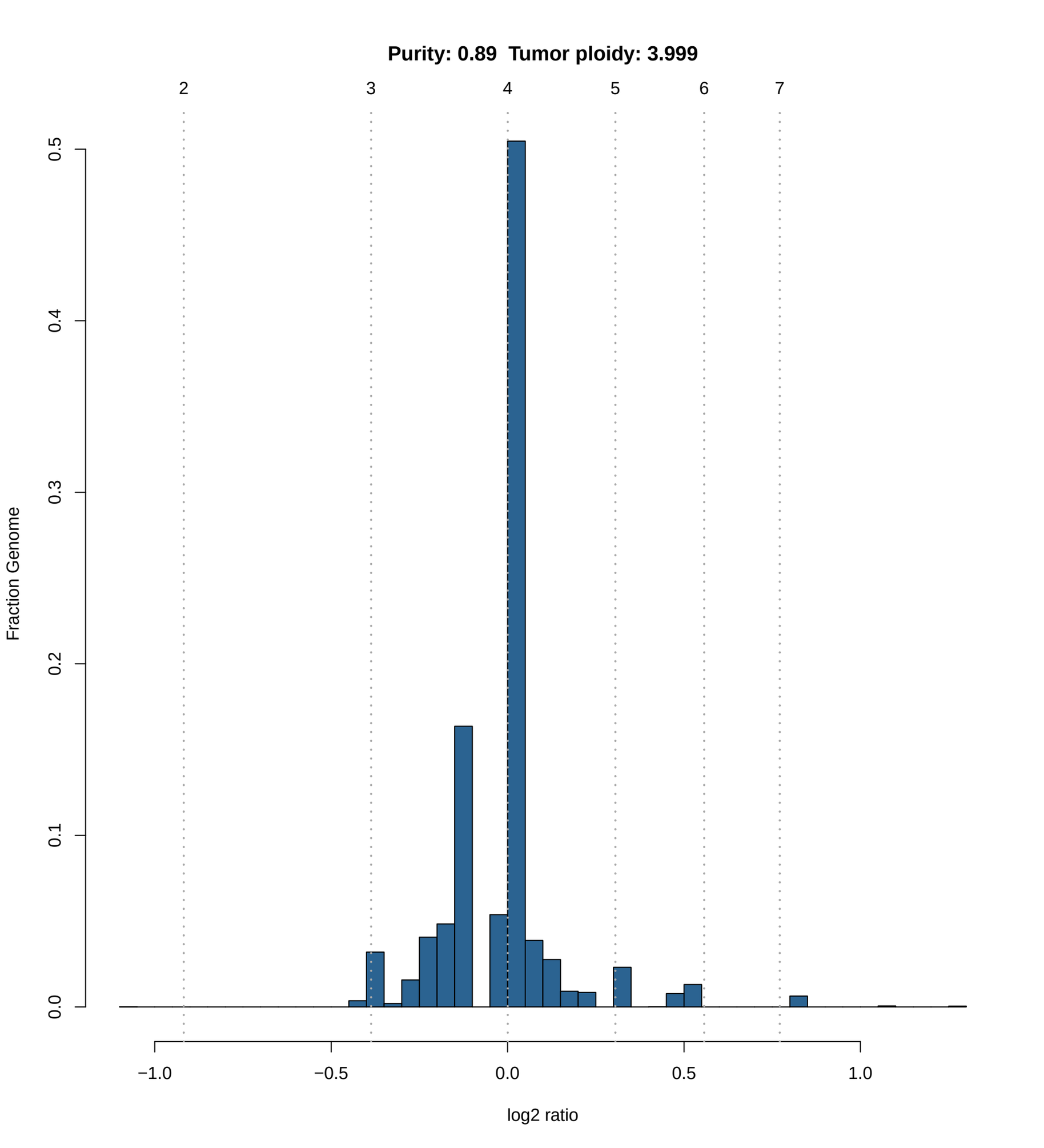

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

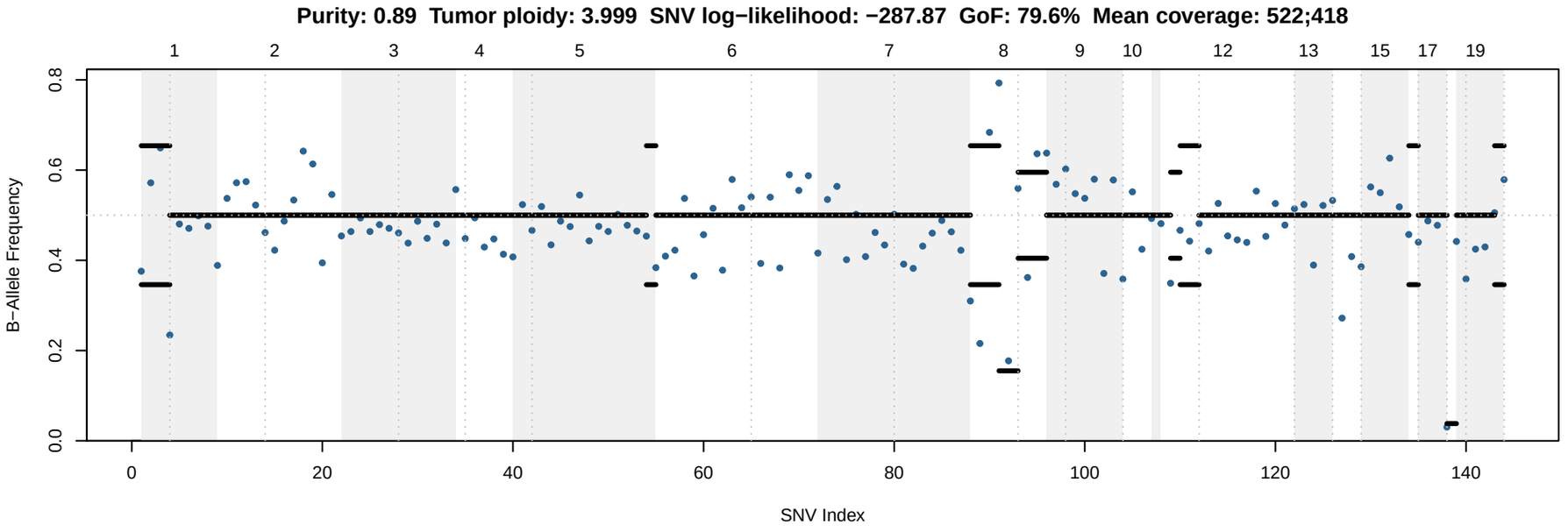

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
5m3
4m2
5m2
3m1
4m1
7m1

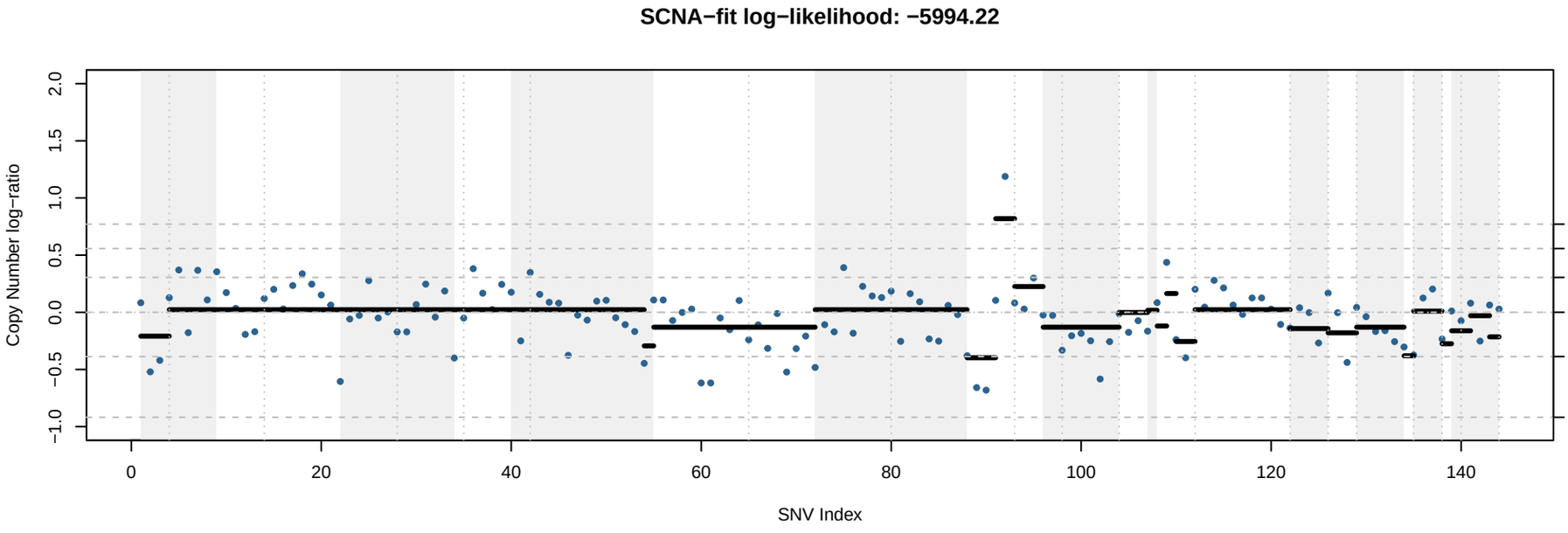

Coverage (log2)
Allelic fraction

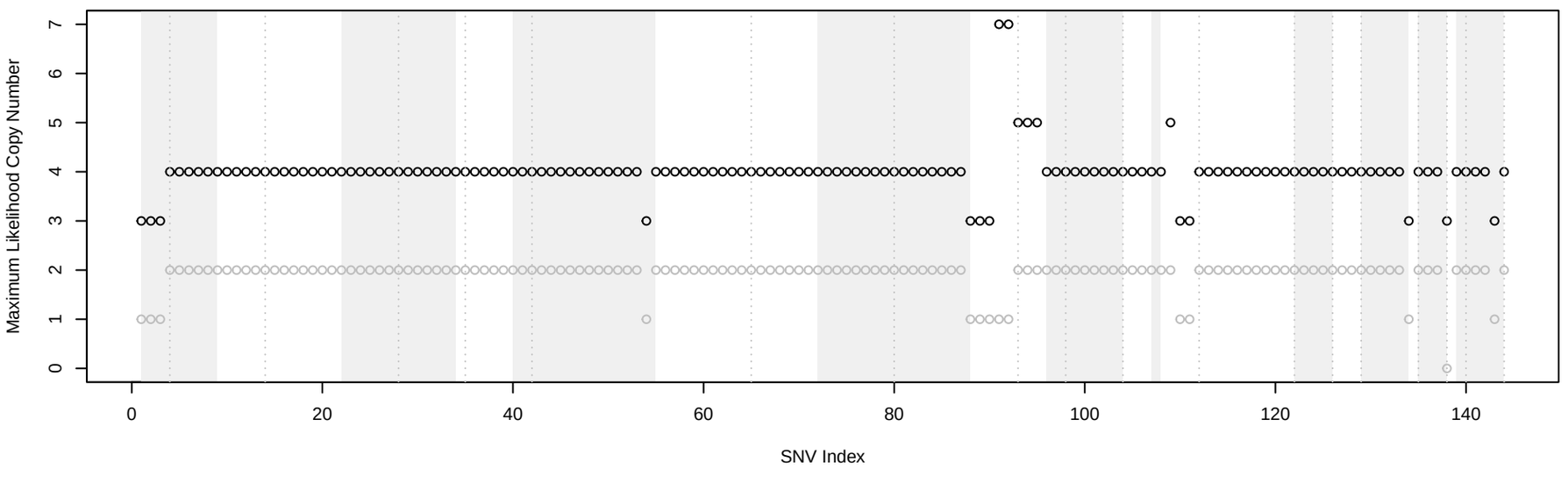

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

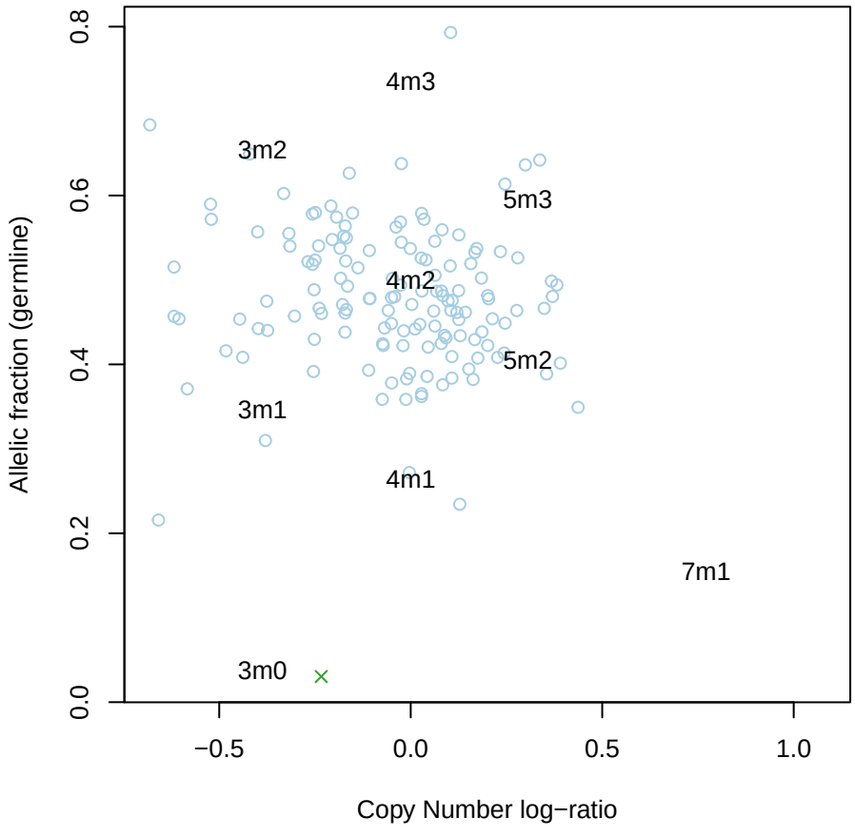

Frequency
Cellular fraction

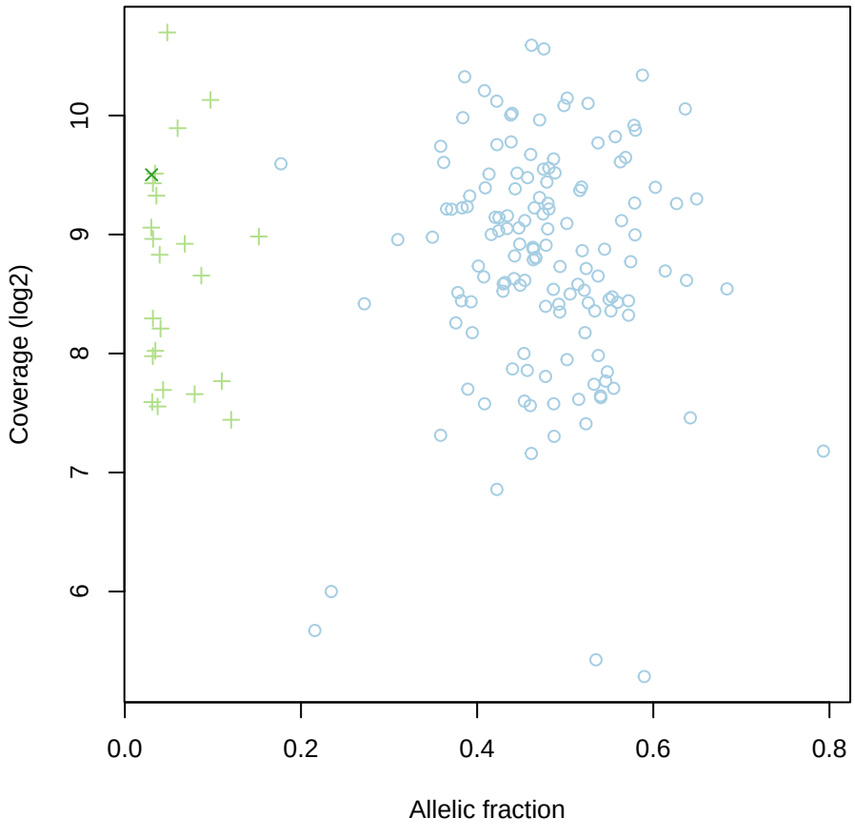

Purity: 0.89 Tumor ploidy: 3.999
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

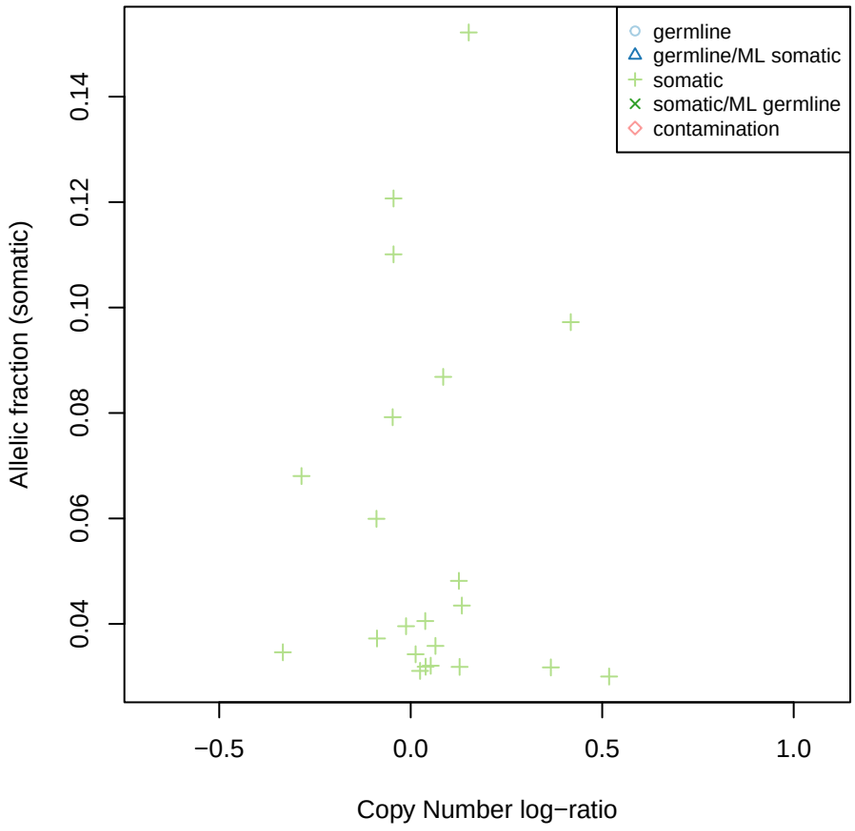

Purity: 0.89 Tumor ploidy: 3.999 SNV log−likelihood: −287.87 GoF: 79.6% Mean coverage: 522;418
1 2 3 4 5 6 7 8 9 10 12 13 15 17 19
B−Allele Frequency
0.0 0.2 0.4 0.6 0.8
0 20 40 60 80 100 120 140
SNV Index

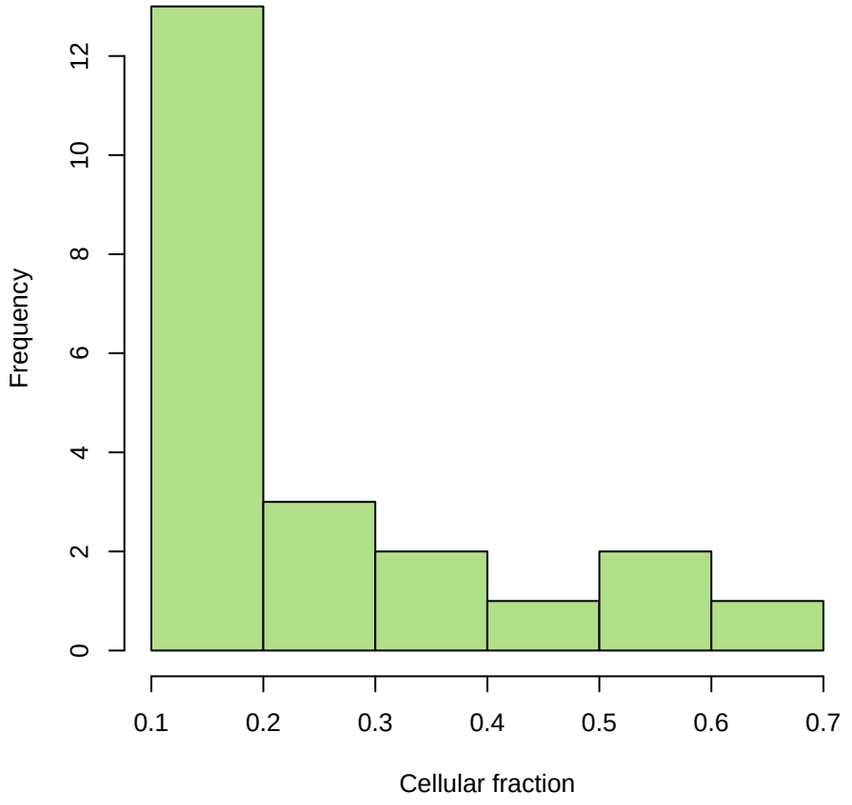

SCNA−fit log−likelihood: −5994.22
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

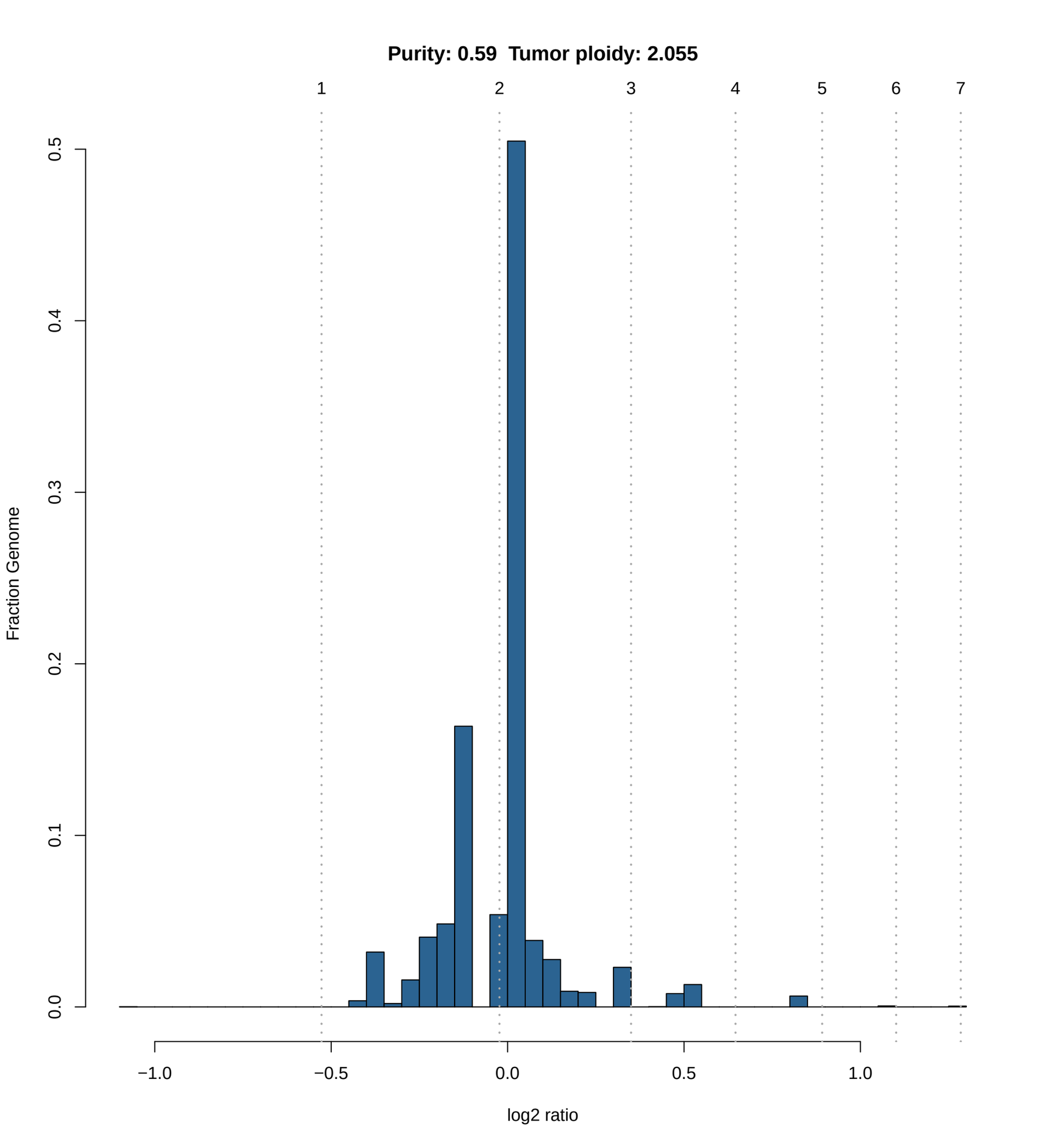

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

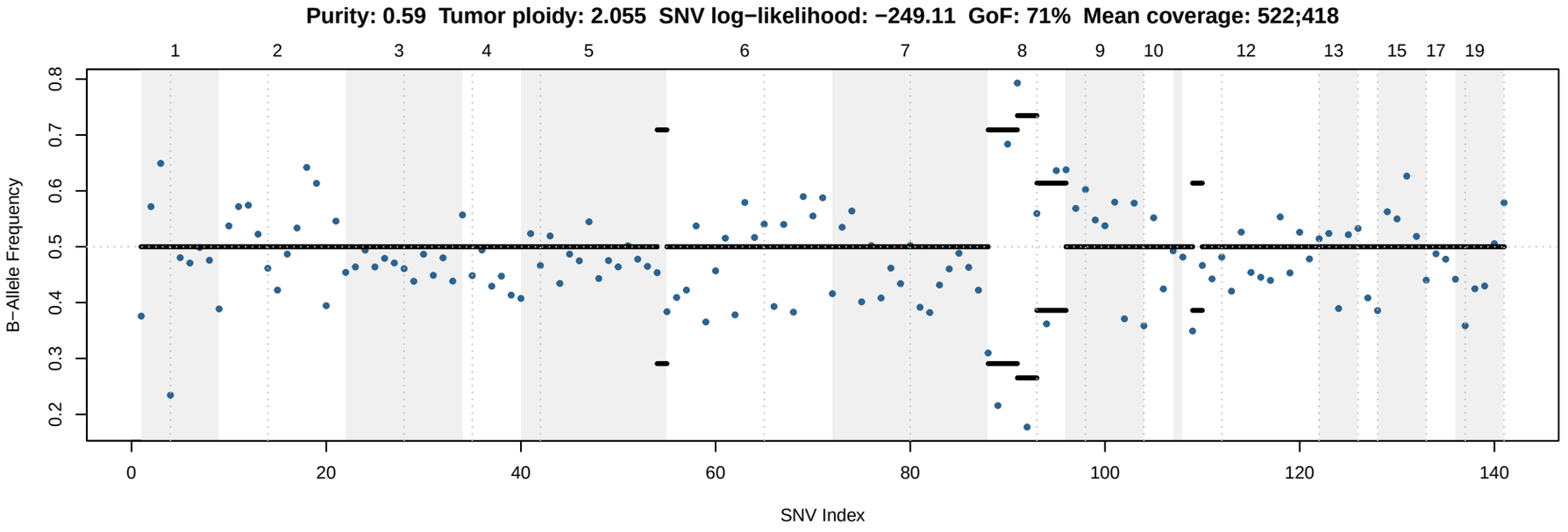

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
5m3
4m2
5m2
3m1
4m1
7m1
3m0

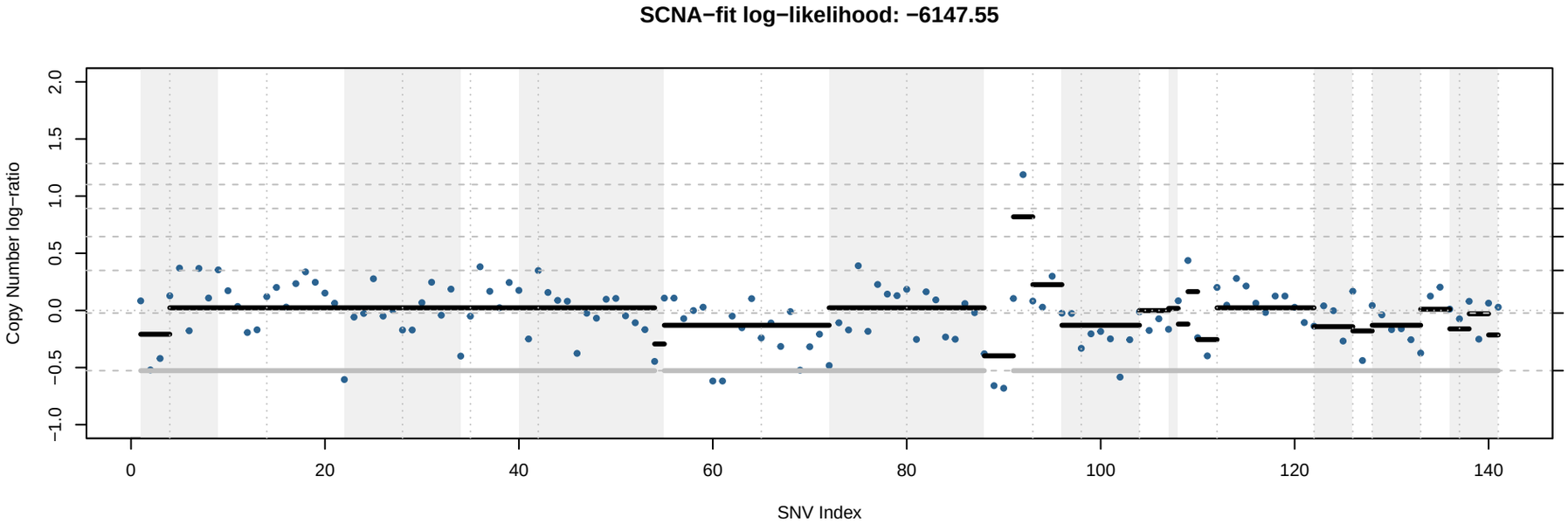

Coverage (log2)
Allelic fraction

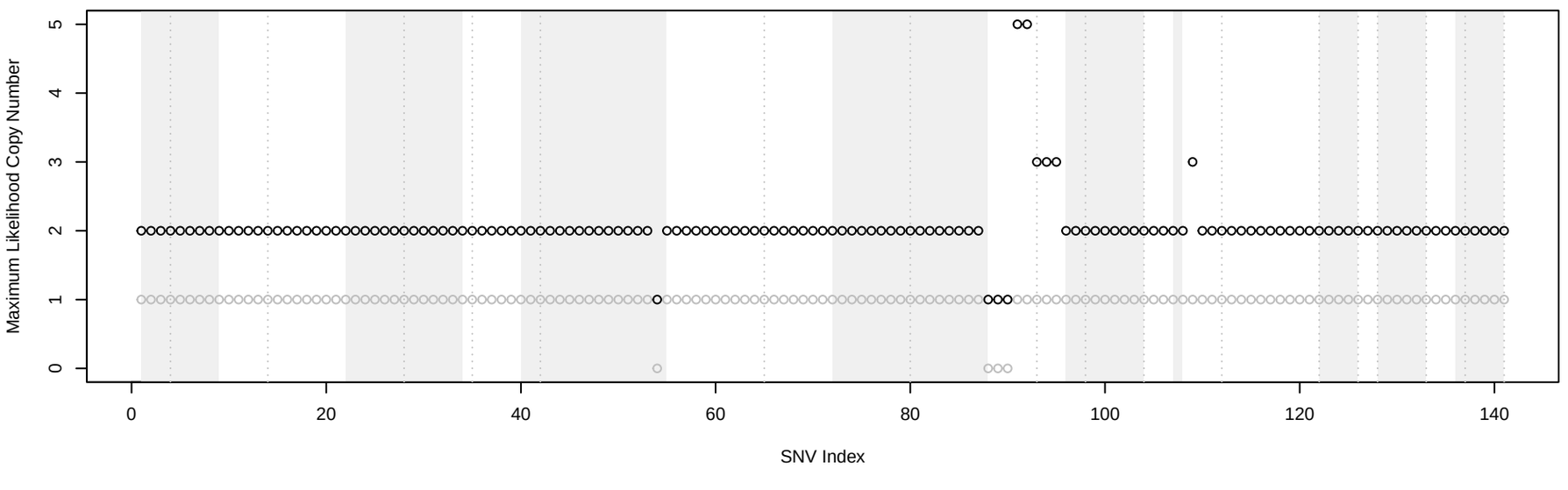

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

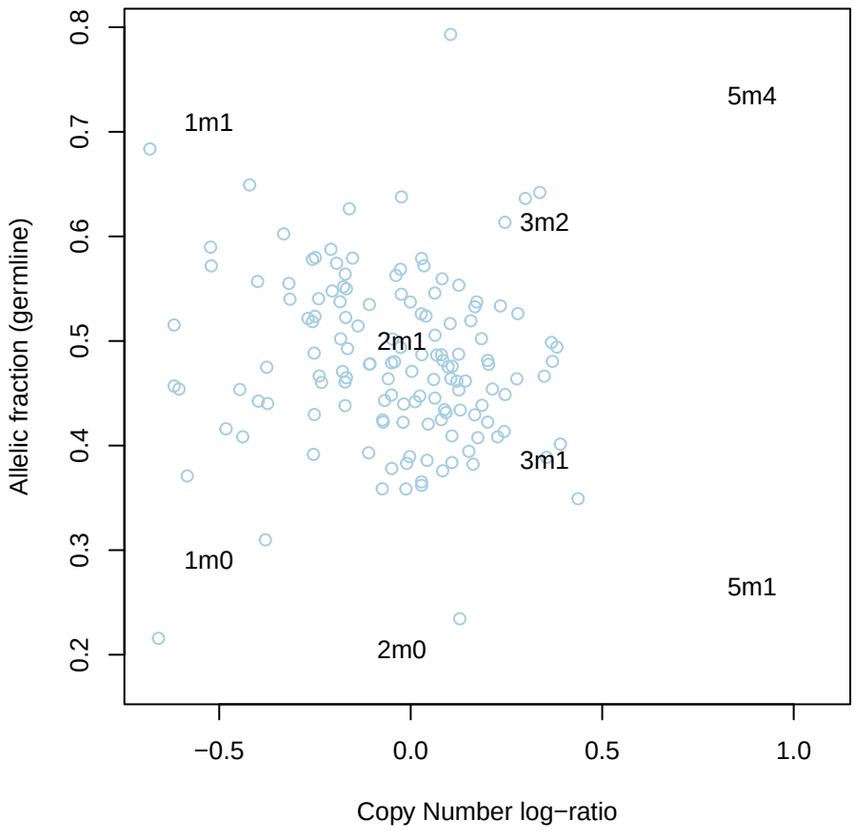

Frequency
Cellular fraction

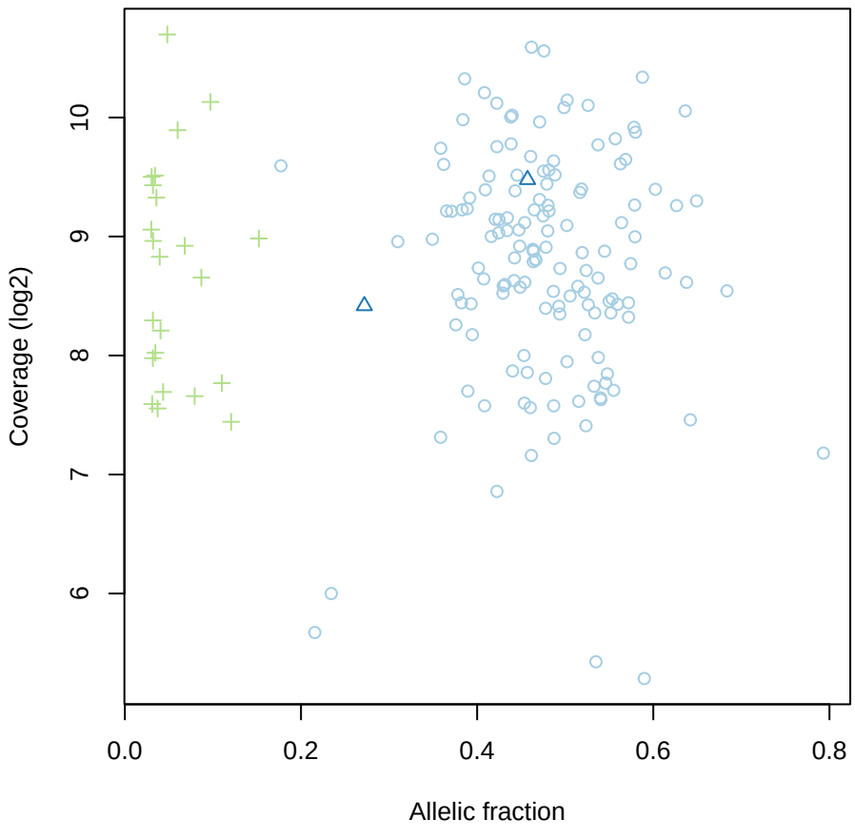

Purity: 0.59 Tumor ploidy: 2.055
1
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

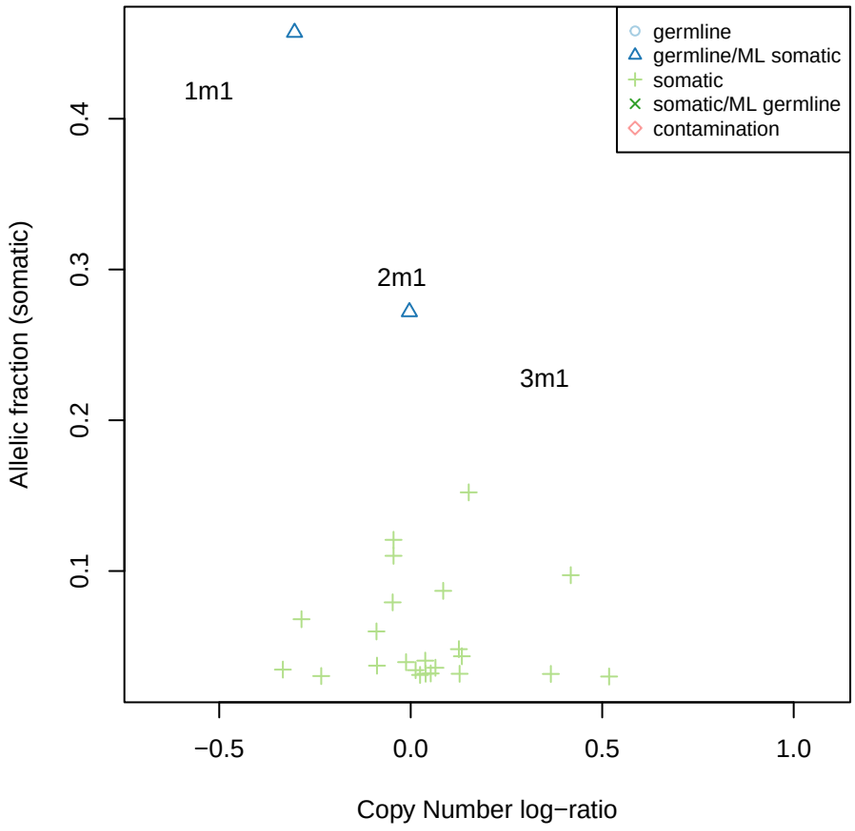

Purity: 0.59 Tumor ploidy: 2.055 SNV log−likelihood: −249.11 GoF: 71% Mean coverage: 522;418
1 2 3 4 5 6 7 8 9 10 12 13 15 17 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index

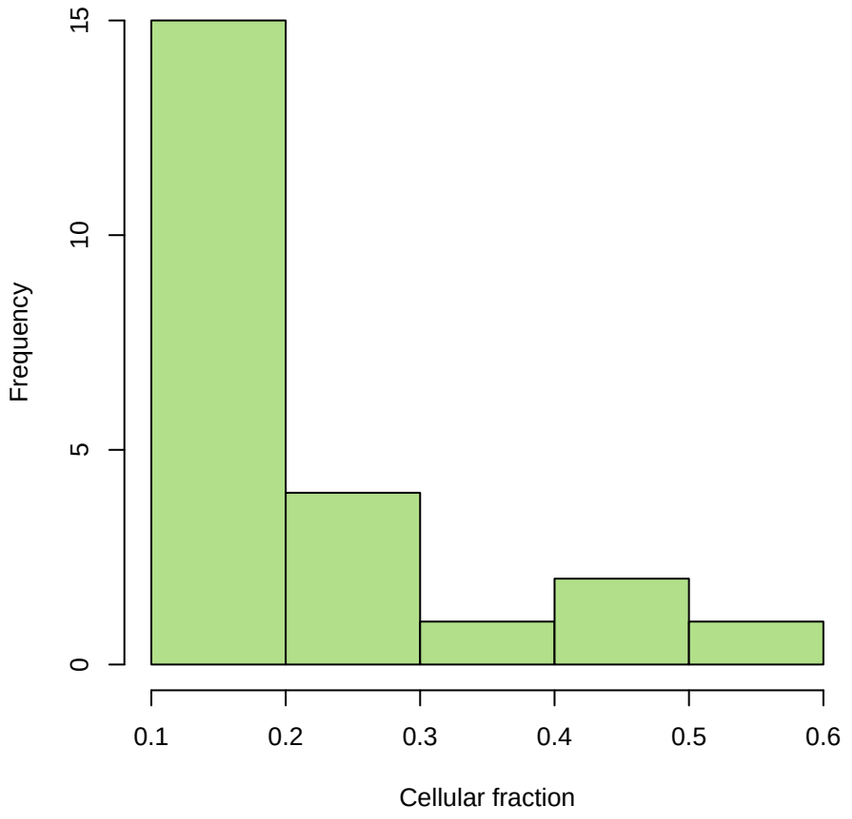

SCNA−fit log−likelihood: −6147.55
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
1 2 3 4 5 7
0 20 40 60 80 100 120 140
SNV Index

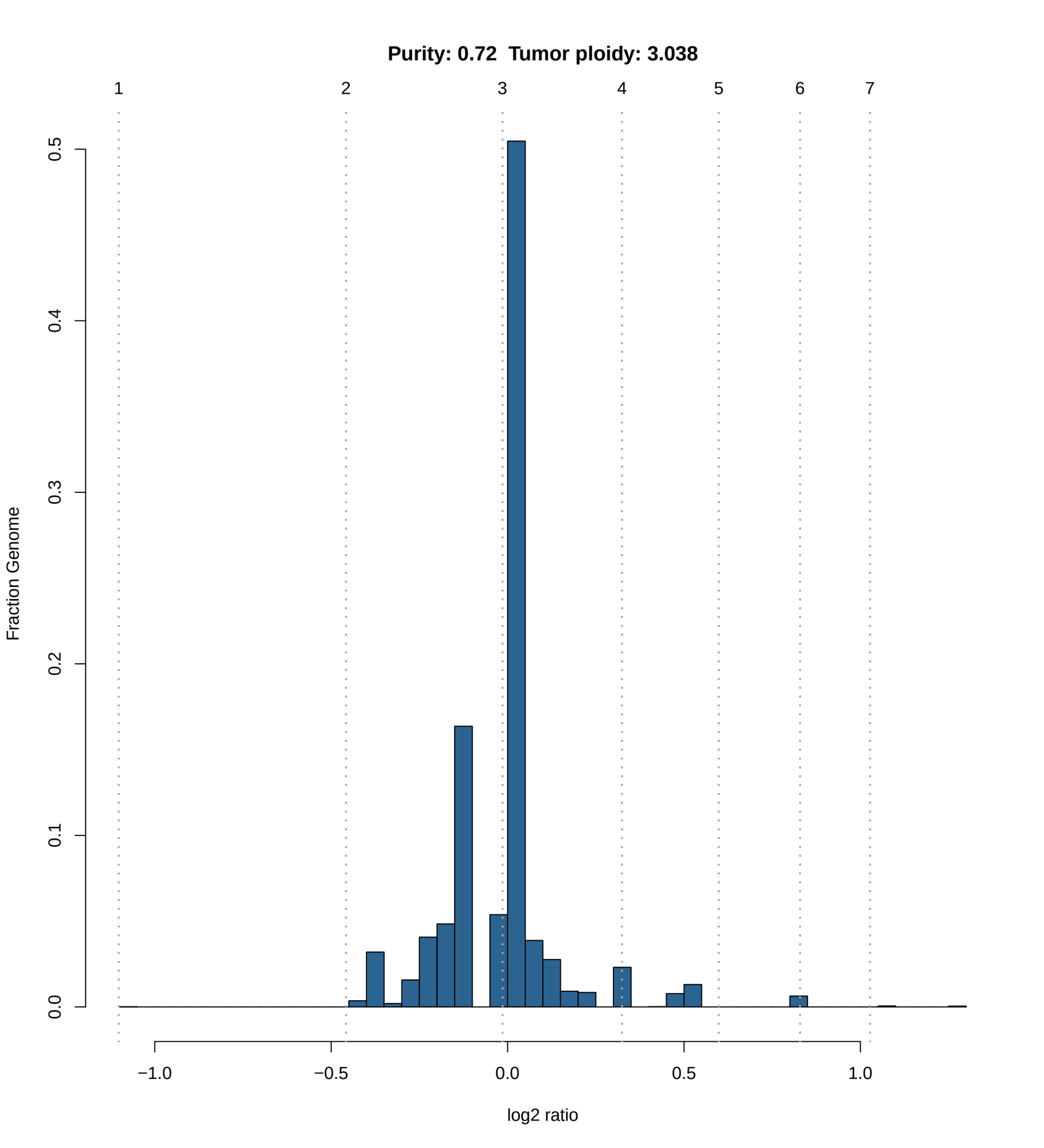

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

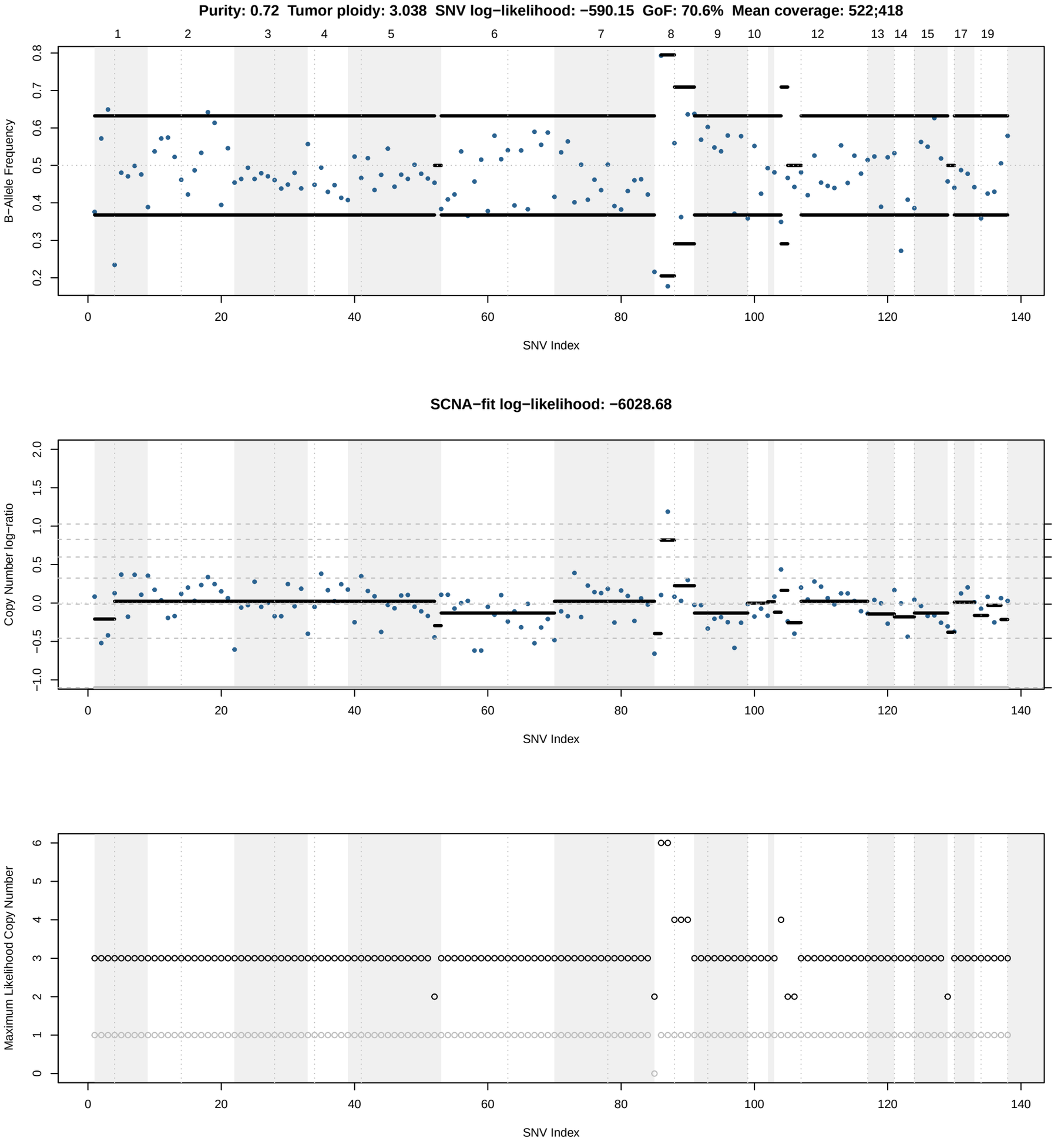

Allelic fraction (germline)
Copy Number log−ratio
1m1
5m4
3m2
2m1
3m1
1m0
5m1
2m0

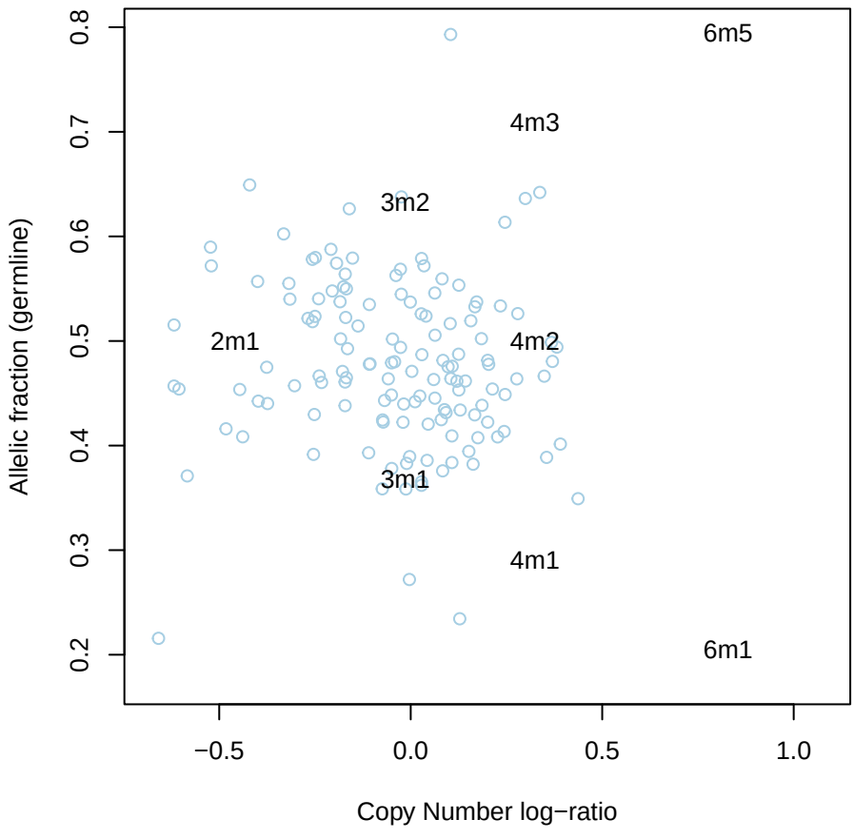

Coverage (log2)
Allelic fraction

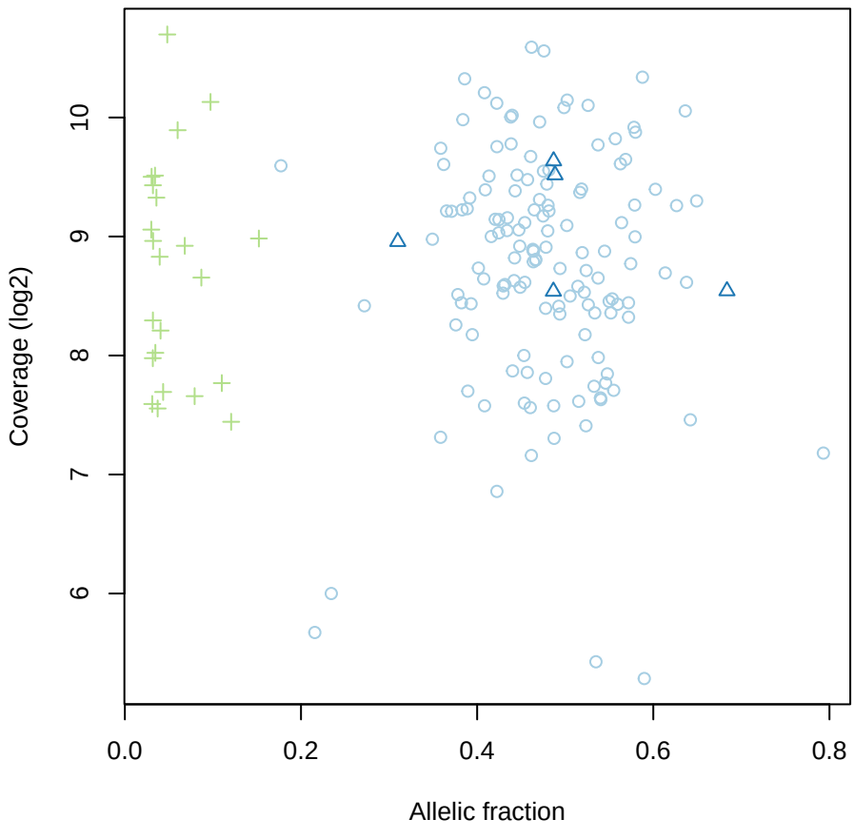

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1
3m1

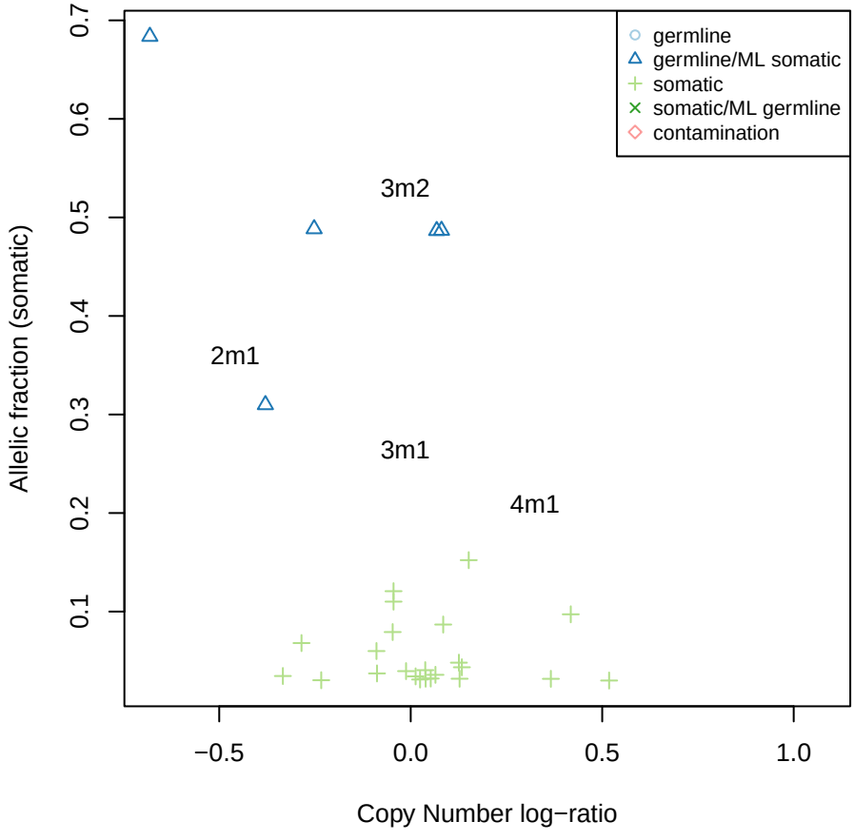

Frequency
Cellular fraction

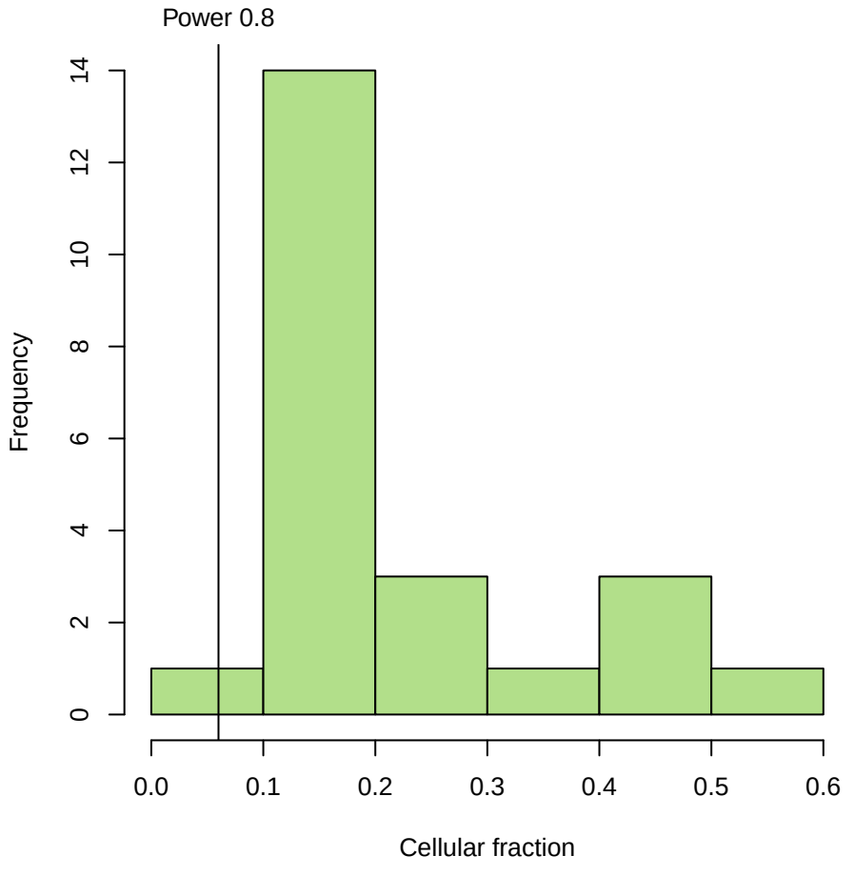

Purity: 0.72 Tumor ploidy: 3.038
1
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio


Purity: 0.72 Tumor ploidy: 3.038 SNV log−likelihood: −590.15 GoF: 70.6% Mean coverage: 522;418
1 2 3 4 5 6 7 8 9 10 12 13 14 15 17 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index
SCNA−fit log−likelihood: −6028.68
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index


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


Coverage (log2)
Allelic fraction


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


Power 0.8
Frequency
Cellular fraction