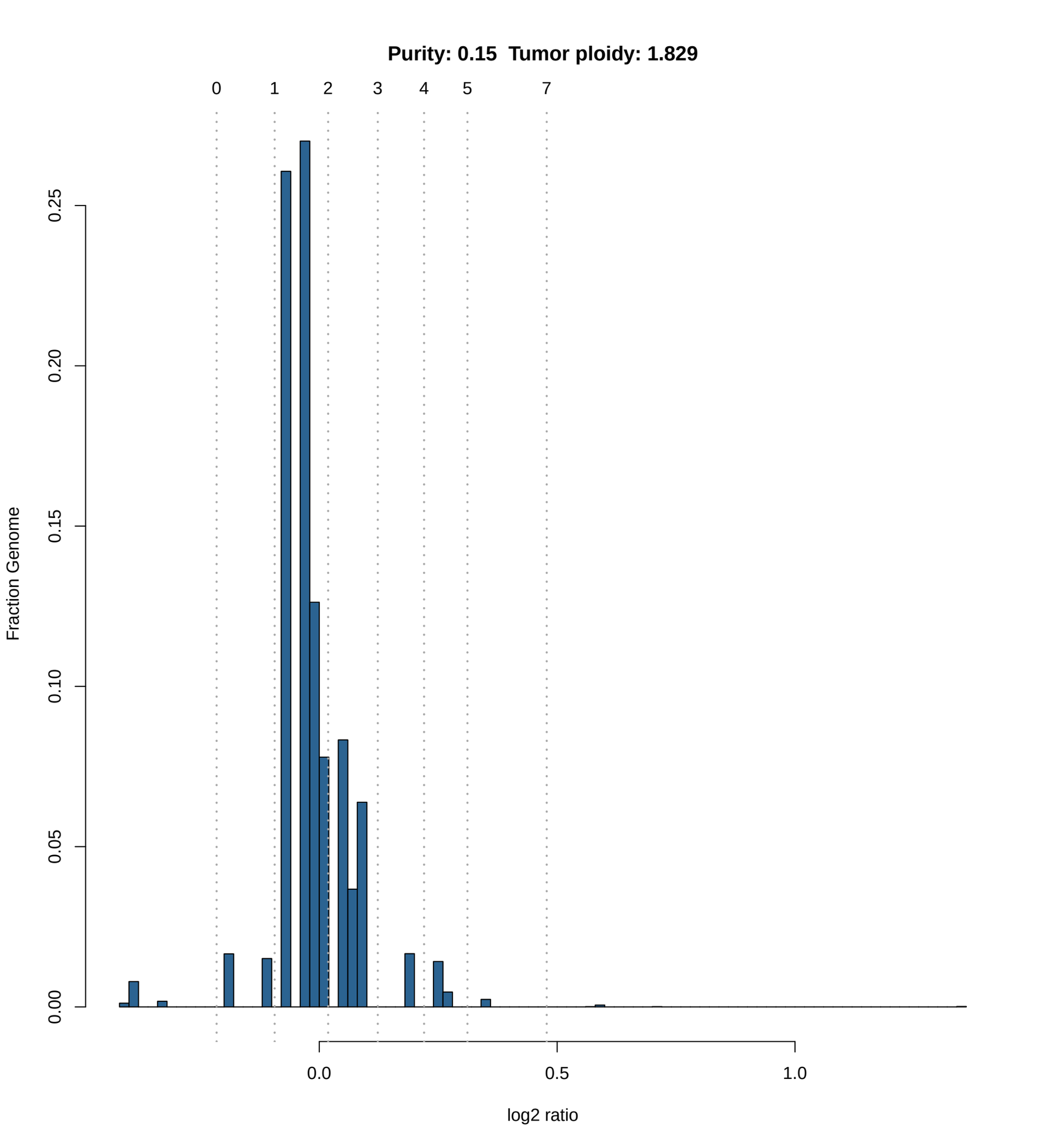
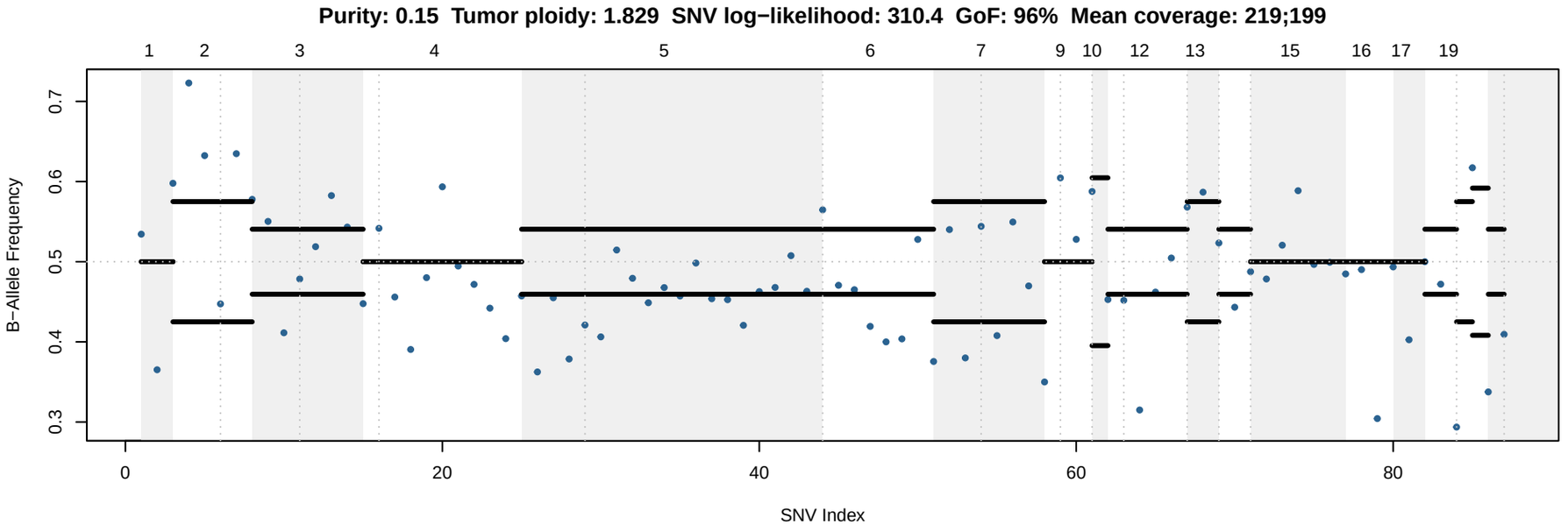
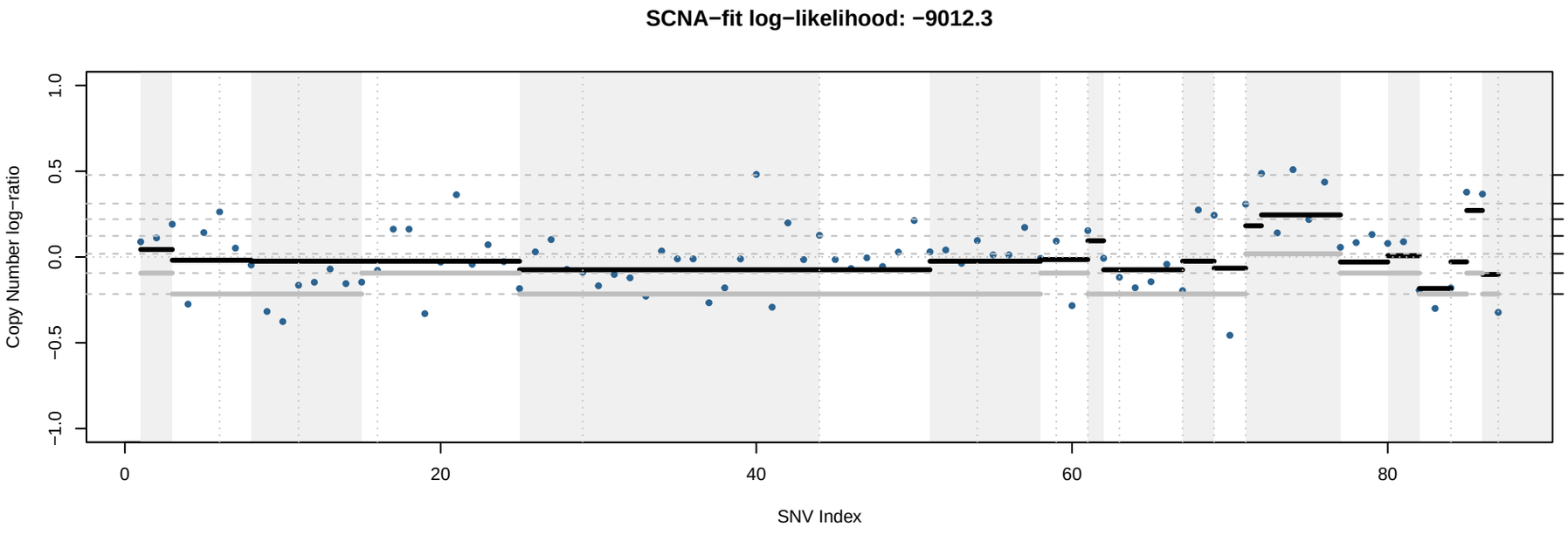
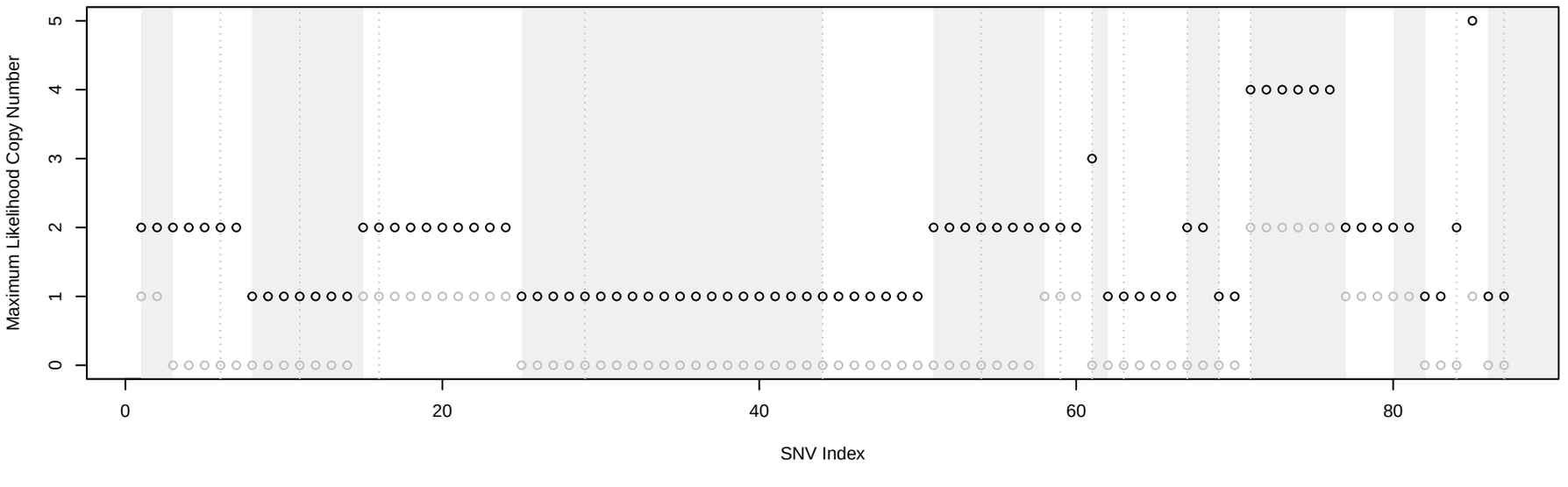
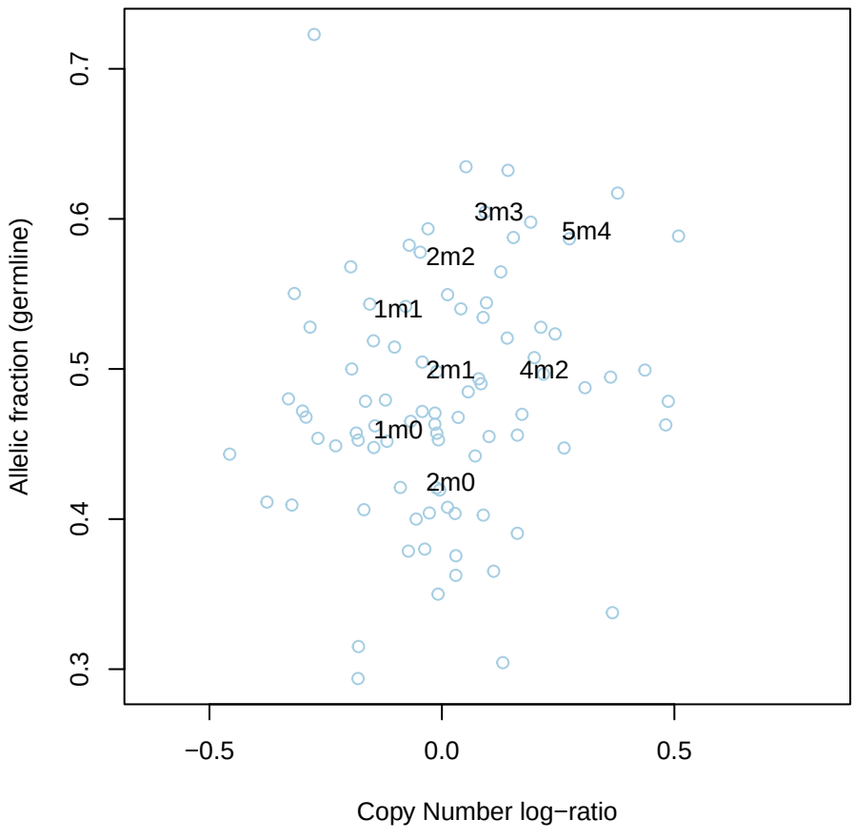
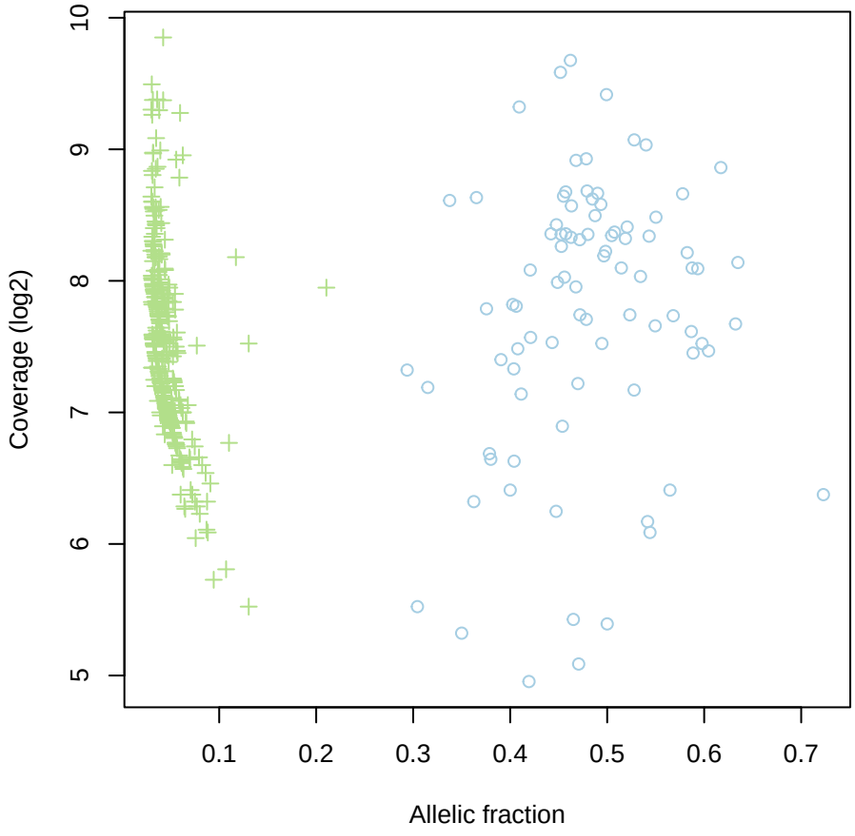

Purity: 0.15 Tumor ploidy: 1.829
0
1
2
3
4
5
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

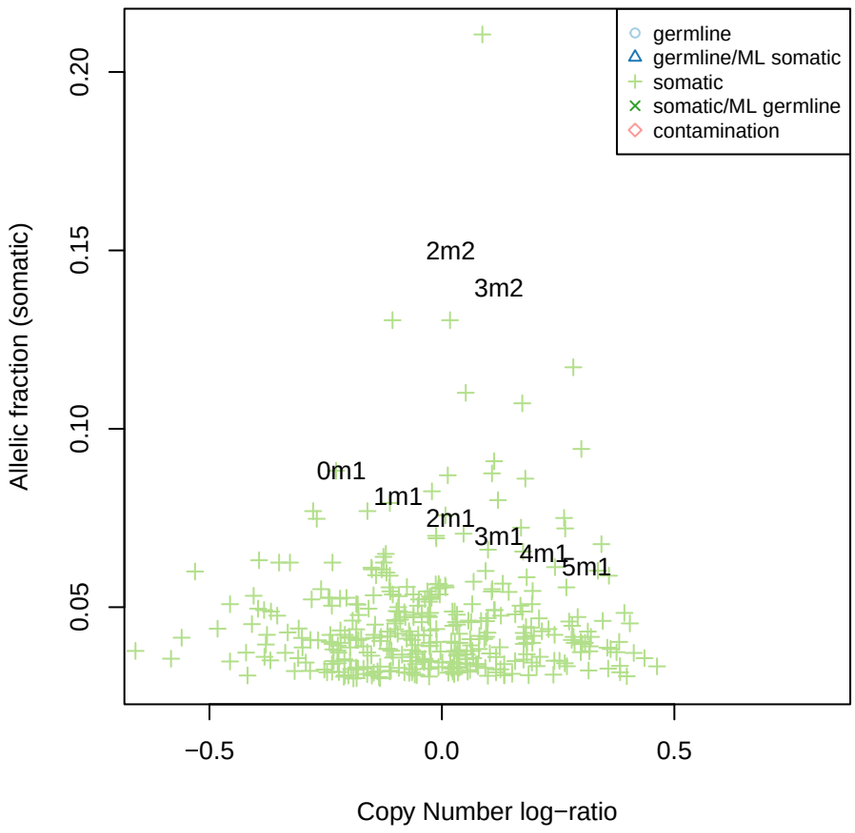

Purity: 0.15 Tumor ploidy: 1.829 SNV log−likelihood: 310.4 GoF: 96% Mean coverage: 219;199
1 2 3 4 5 6 7 9 10 12 13 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

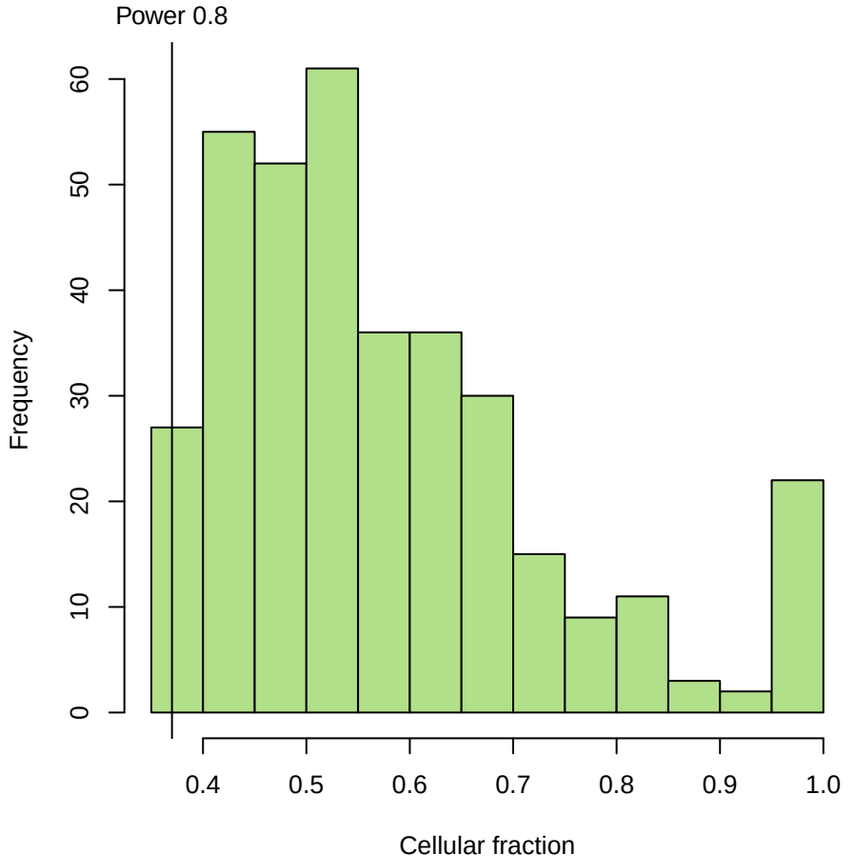

SCNA−fit log−likelihood: −9012.3
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4 7
0 20 40 60 80
SNV Index

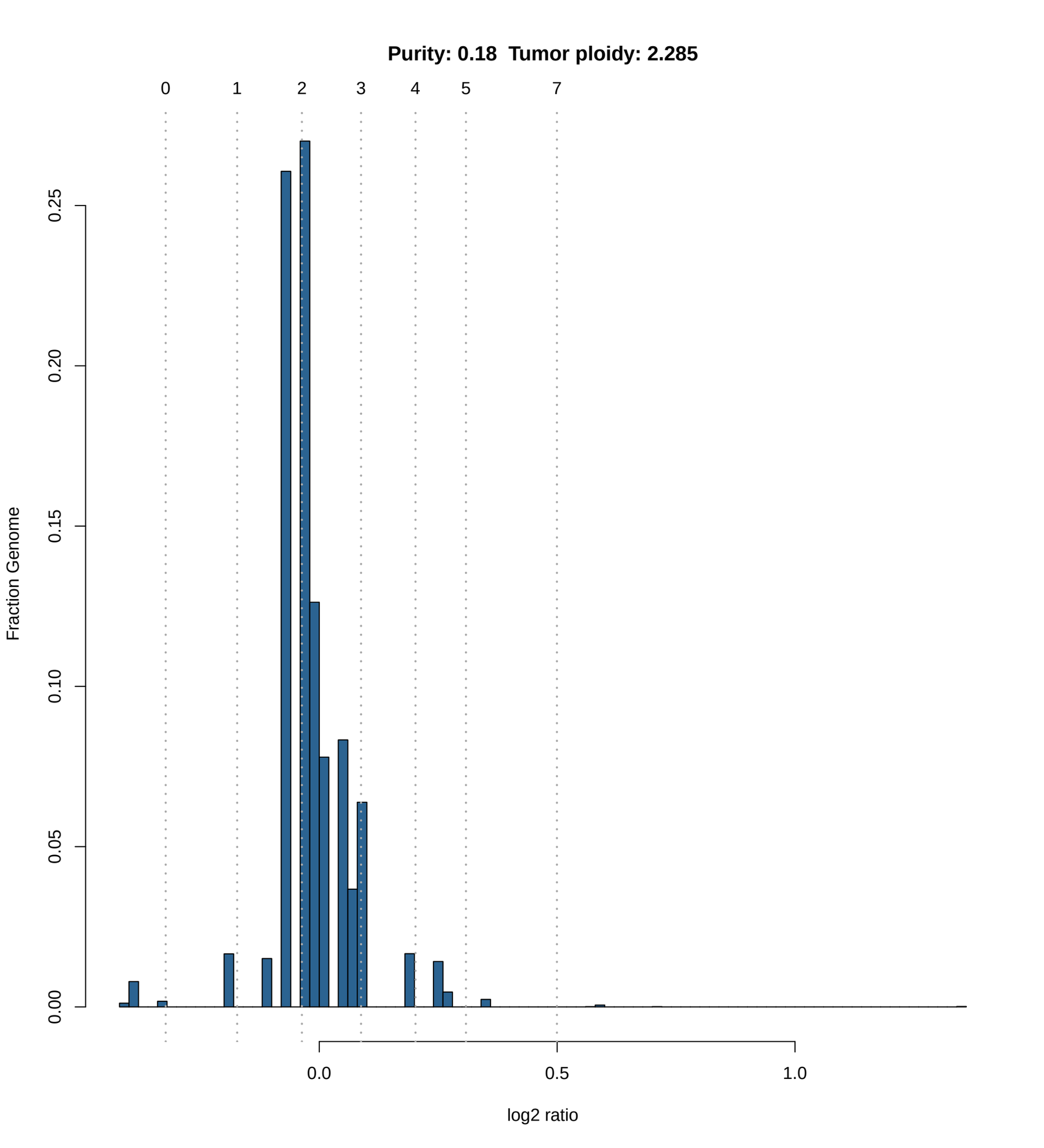

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80
SNV Index

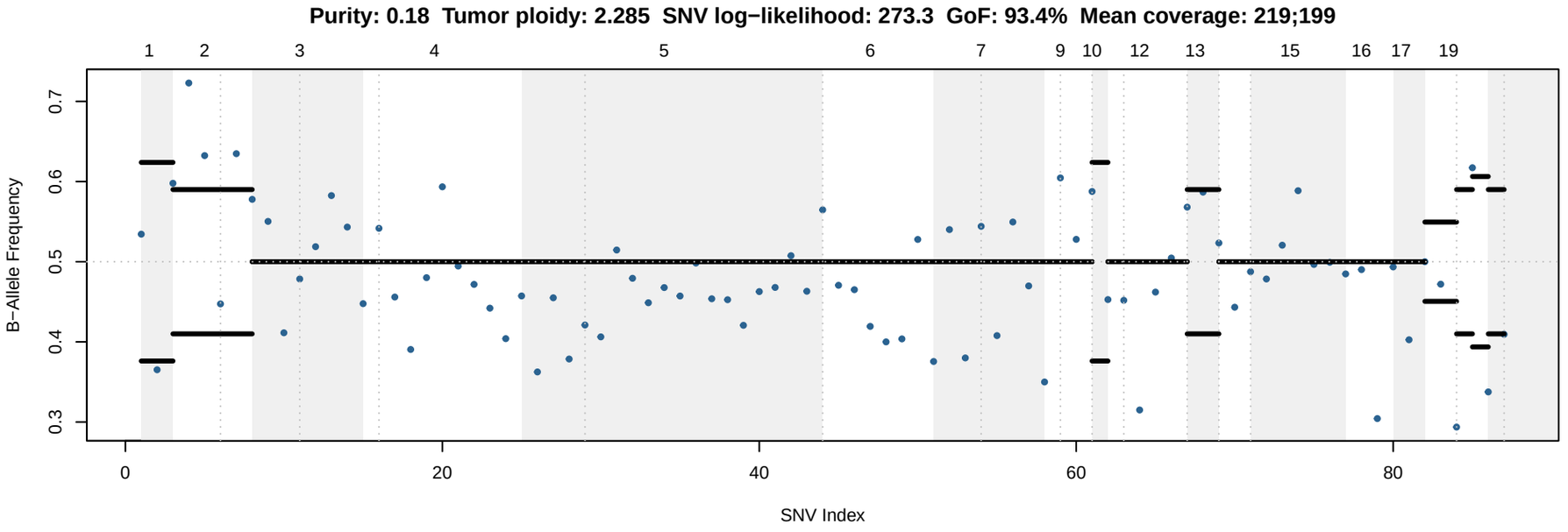

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
−0.5
0.0
0.5
Copy Number log−ratio
3m3
5m4
2m2
1m1
2m1
4m2
1m0
2m0

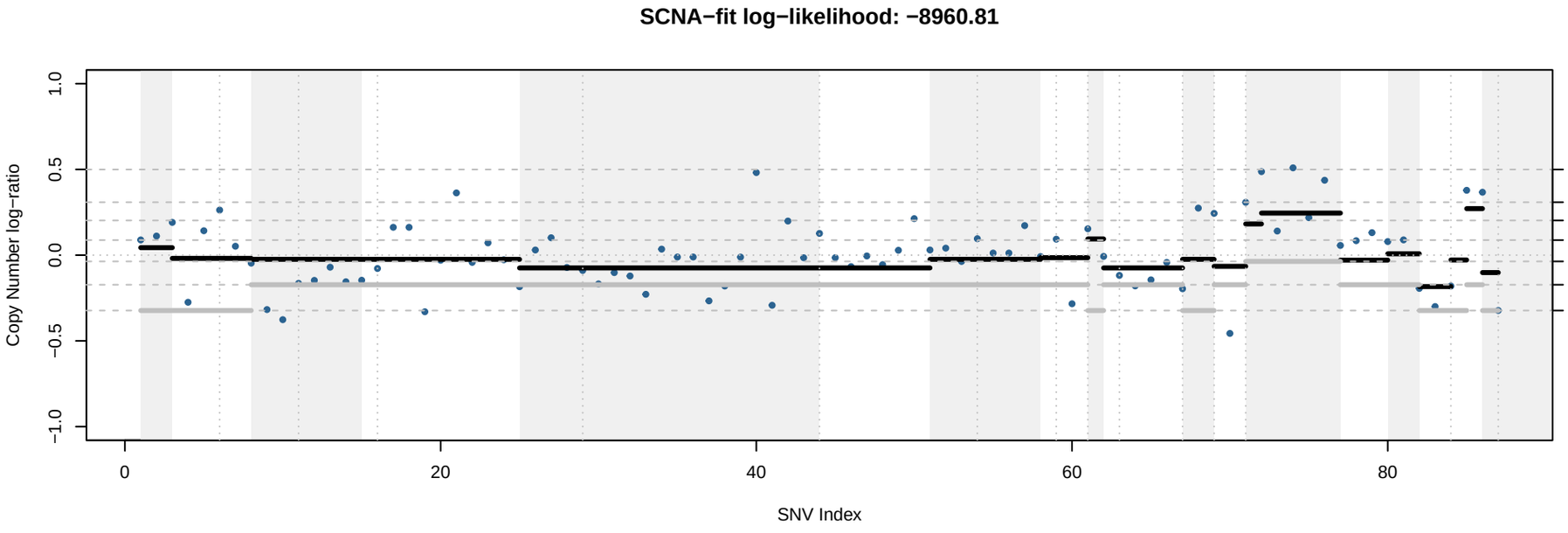

Coverage (log2)
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

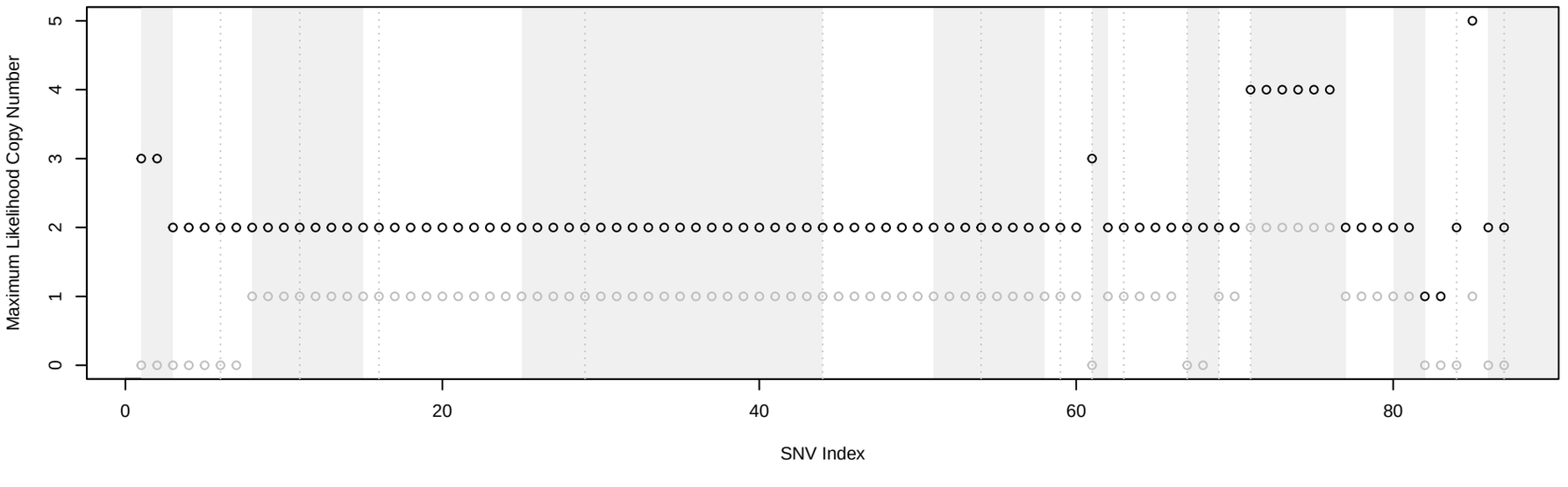

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
−0.5
0.0
0.5
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
3m2
0m1
1m1
2m1
3m1
4m1
5m1

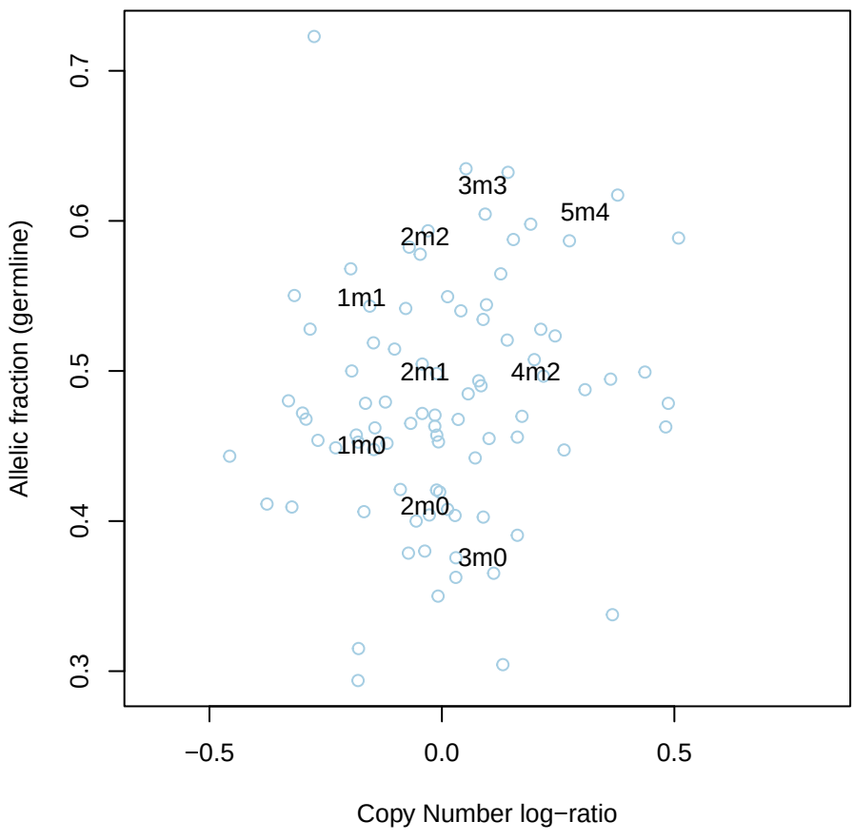

Power 0.8
Frequency
0
10
20
30
40
50
60
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

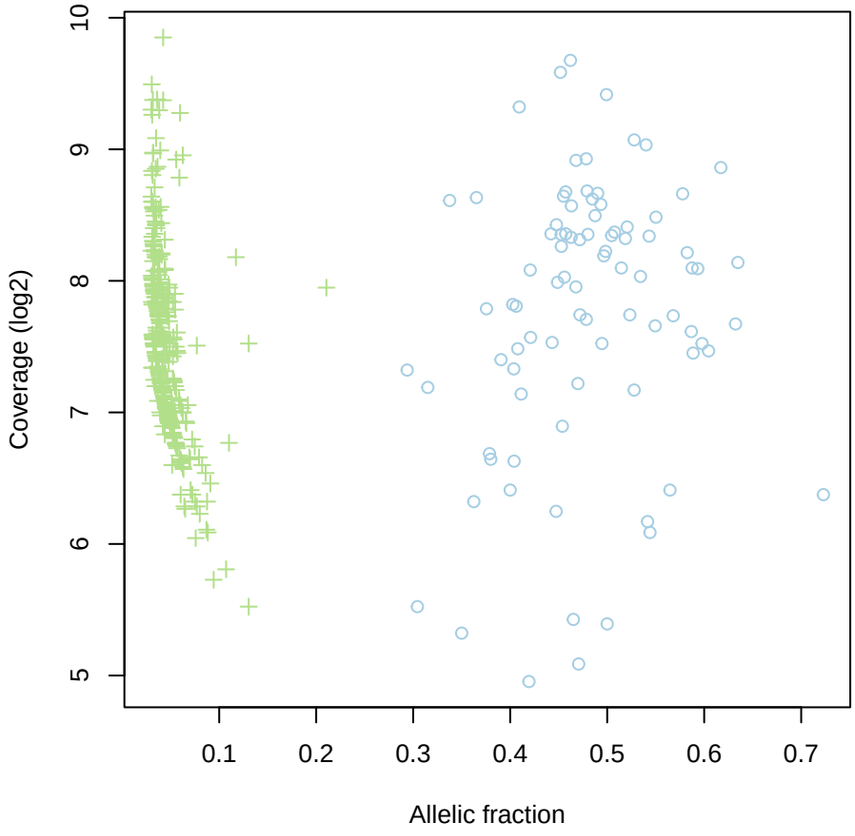

Purity: 0.18 Tumor ploidy: 2.285
0
1
2
3
4
5
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

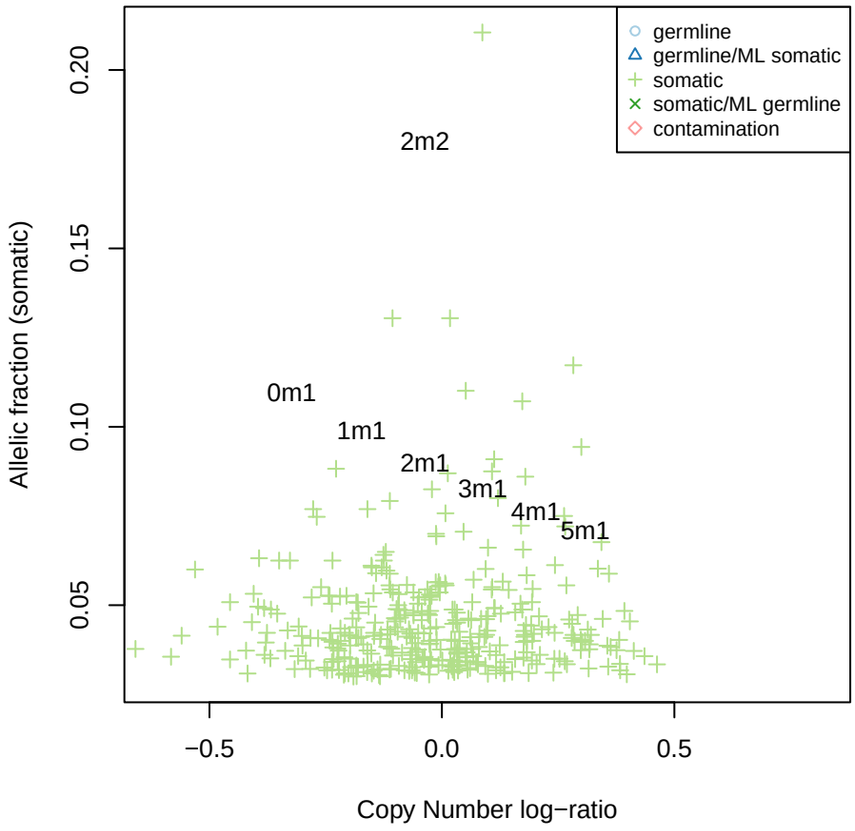

Purity: 0.18 Tumor ploidy: 2.285 SNV log−likelihood: 273.3 GoF: 93.4% Mean coverage: 219;199
1 2 3 4 5 6 7 9 10 12 13 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

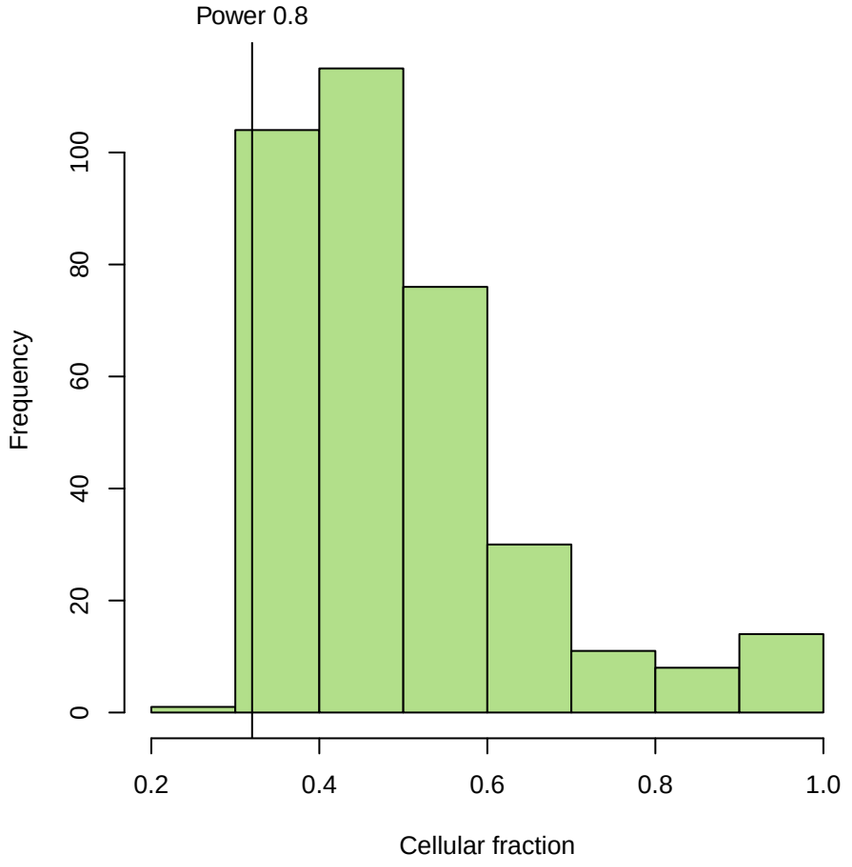

SCNA−fit log−likelihood: −8960.81
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 3 5 7
0 20 40 60 80
SNV Index

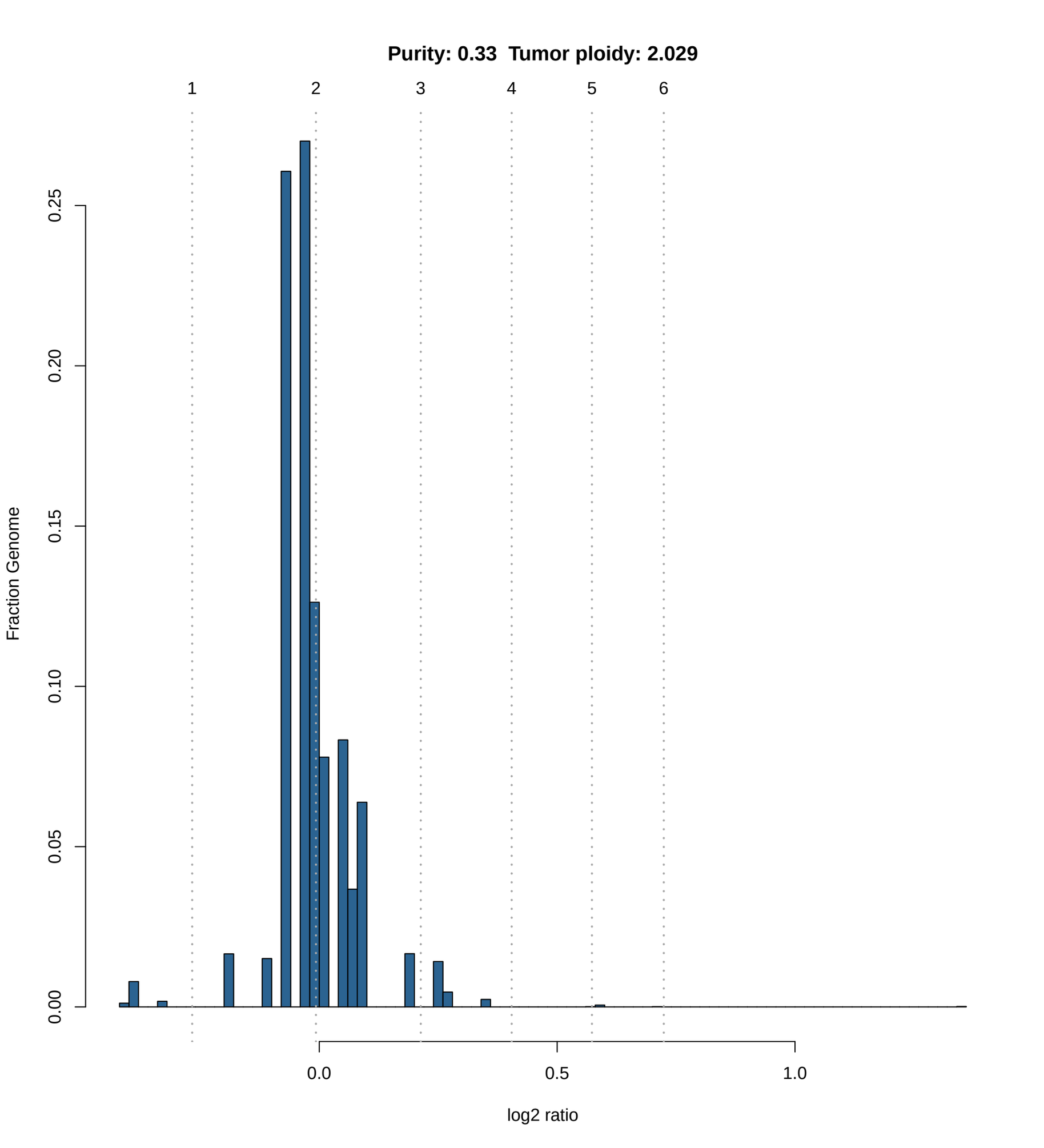

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80
SNV Index

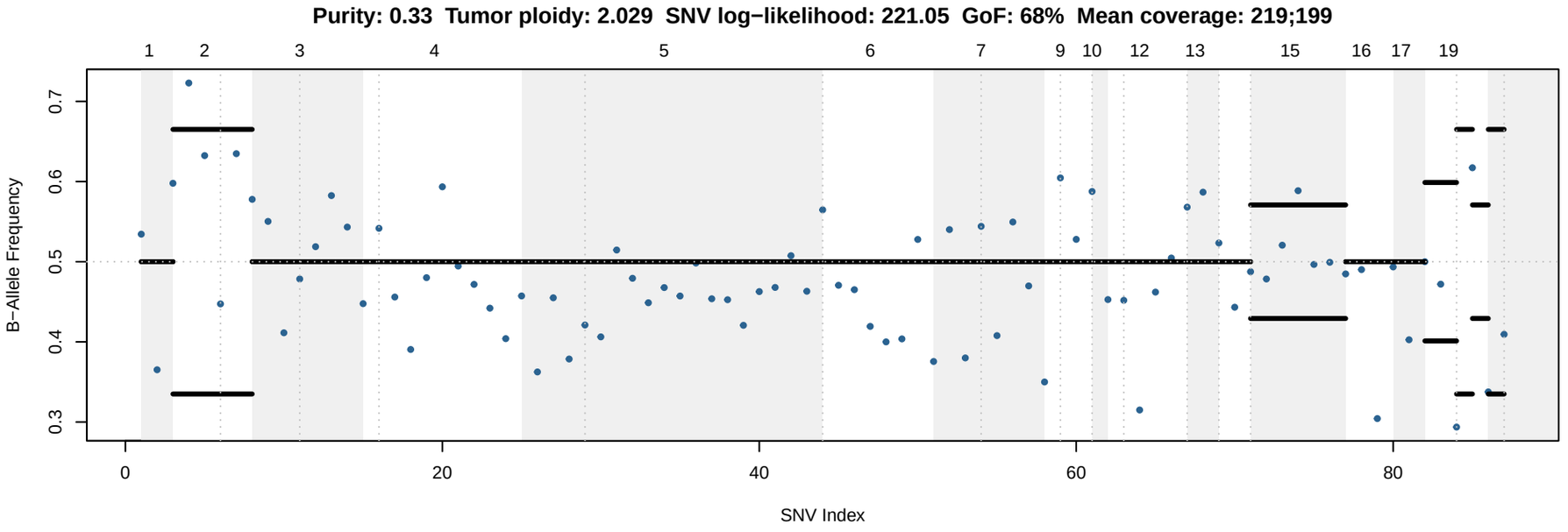

Allelic fraction (germline)
Copy Number log−ratio
3m3
5m4
2m2
1m1
2m1
4m2
1m0
2m0
3m0

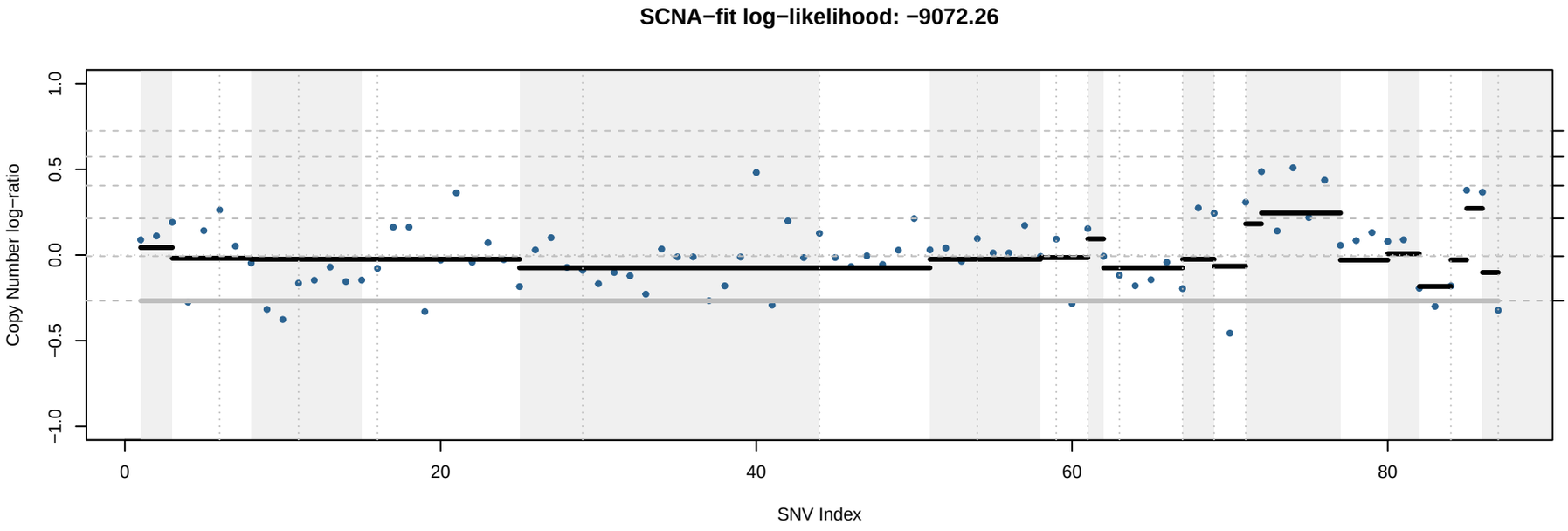

Coverage (log2)
Allelic fraction

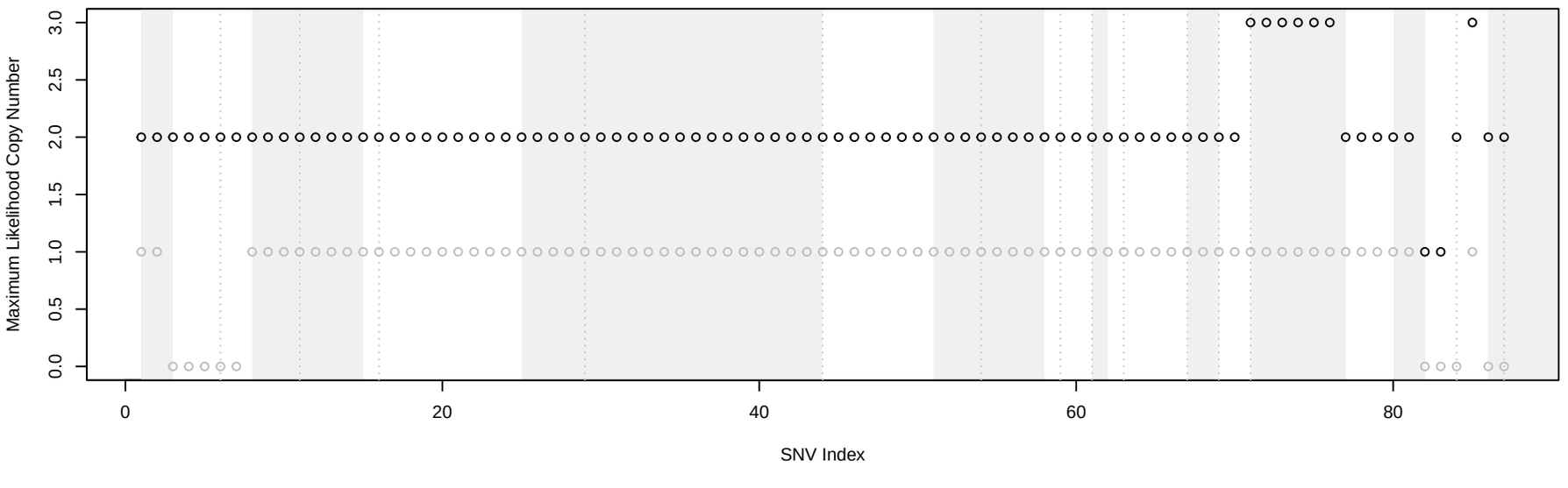

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
0m1
1m1
2m1
3m1
4m1
5m1

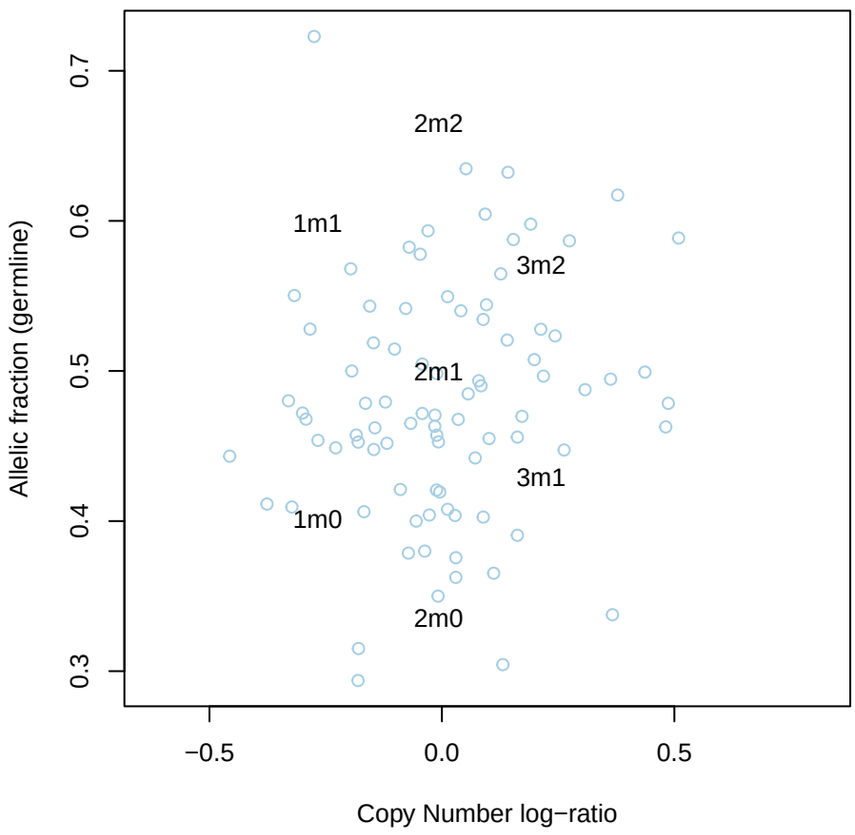

Power 0.8
Frequency
Cellular fraction

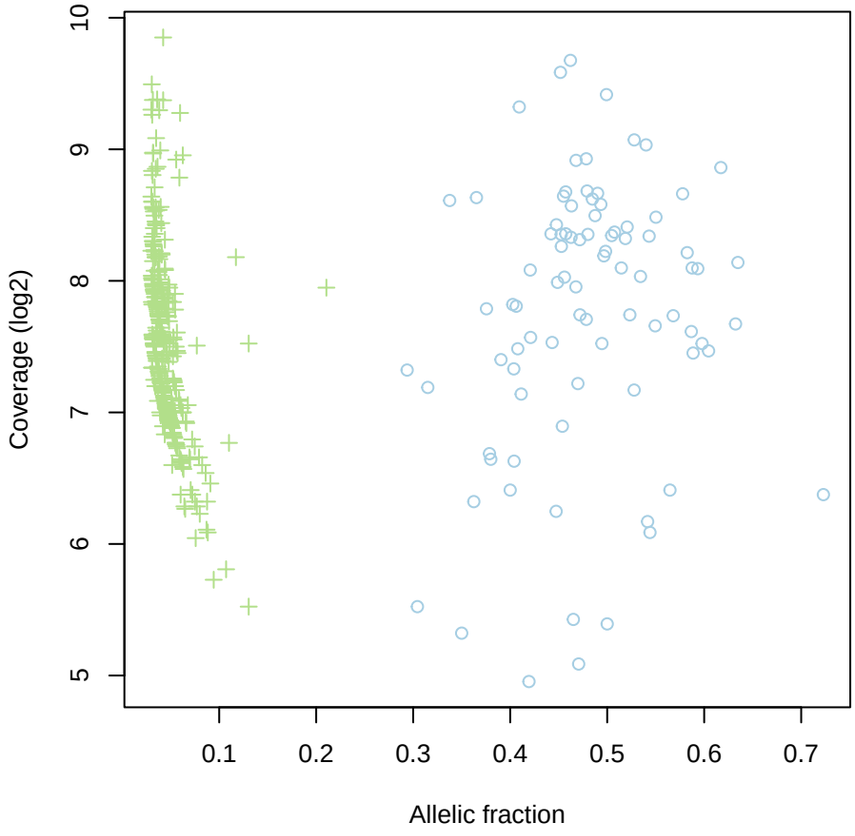

Purity: 0.33 Tumor ploidy: 2.029
1
2
3
4
5
6
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

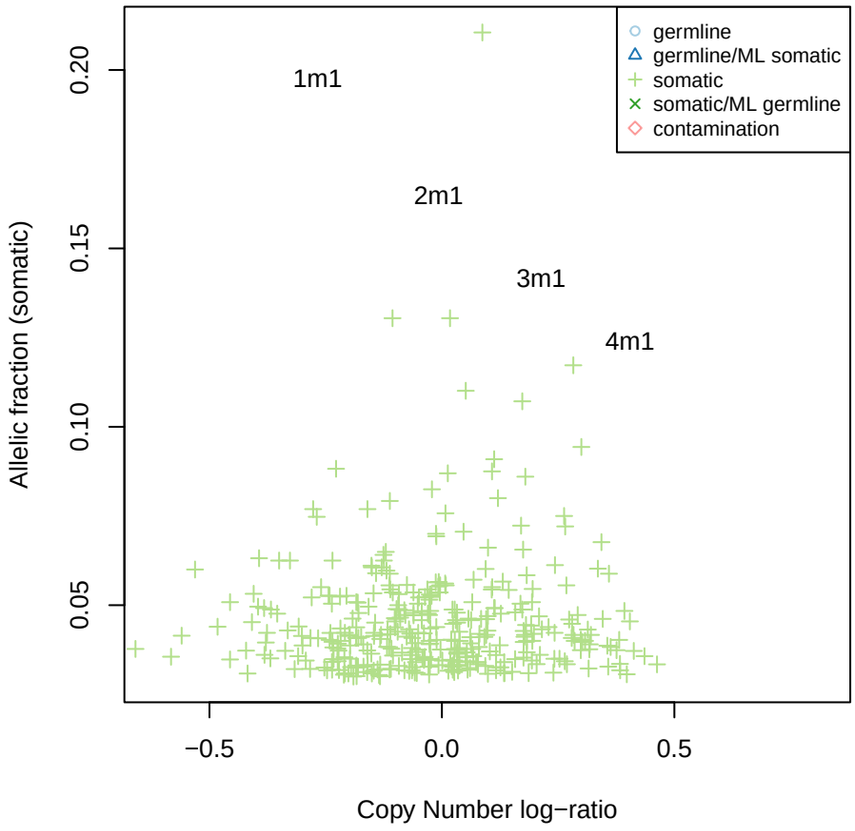

Purity: 0.33 Tumor ploidy: 2.029 SNV log−likelihood: 221.05 GoF: 68% Mean coverage: 219;199
1 2 3 4 5 6 7 9 10 12 13 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

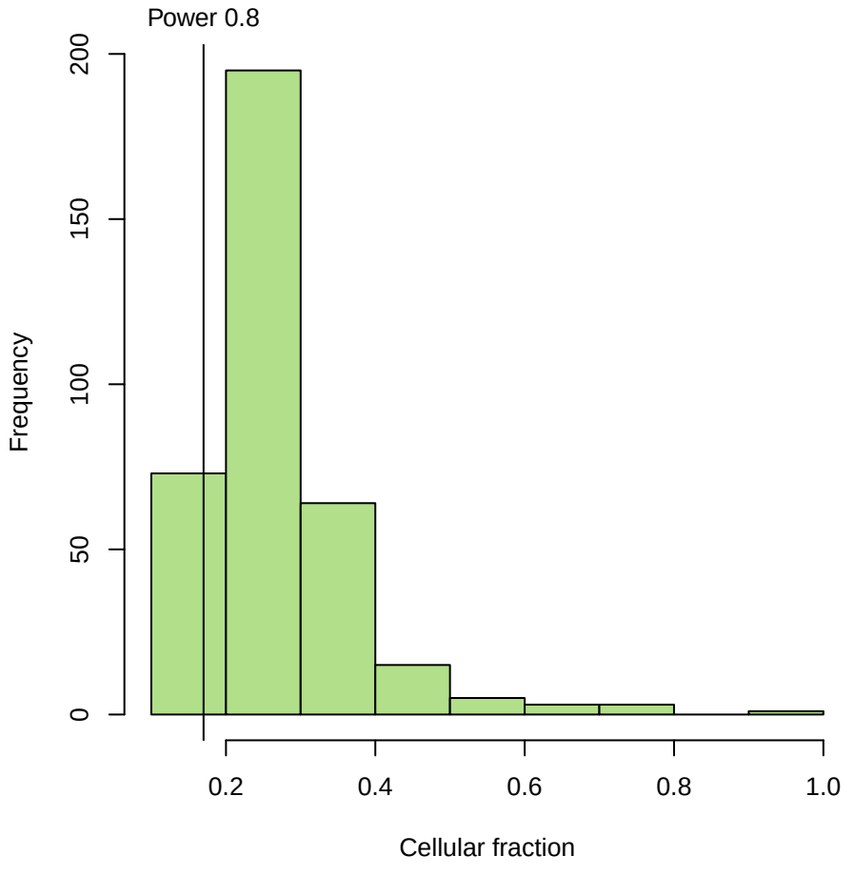

SCNA−fit log−likelihood: −9072.26
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6
0 20 40 60 80
SNV Index

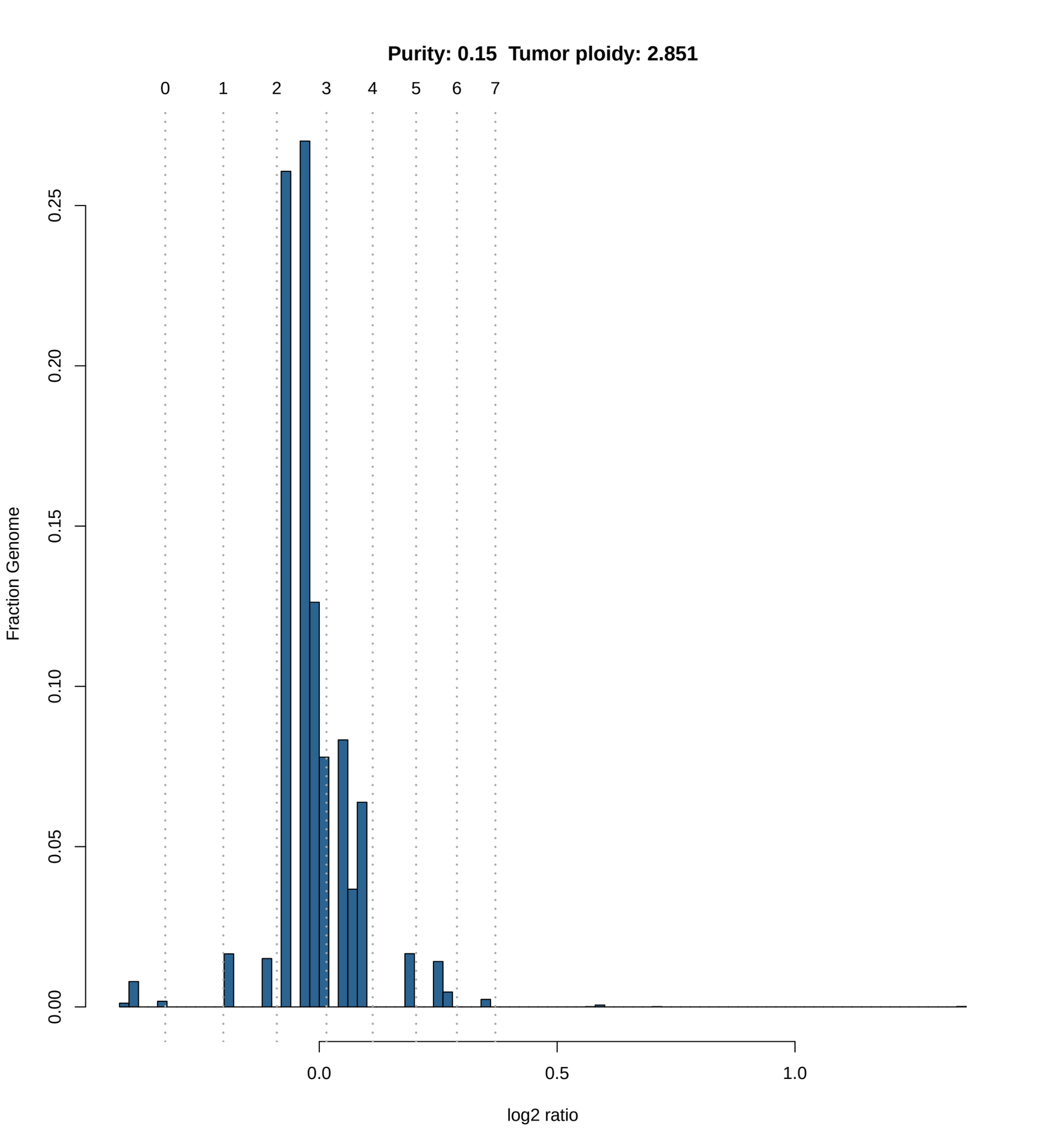

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80
SNV Index

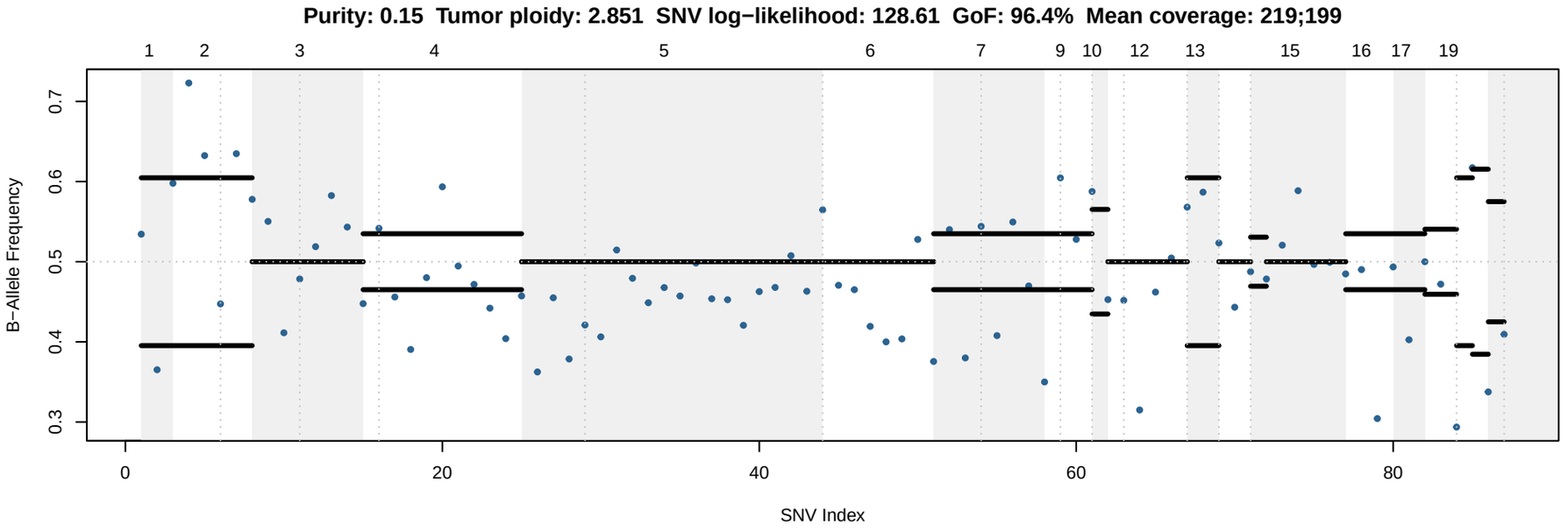

Allelic fraction (germline)
Copy Number log−ratio
2m2
1m1
3m2
2m1
3m1
1m0
2m0

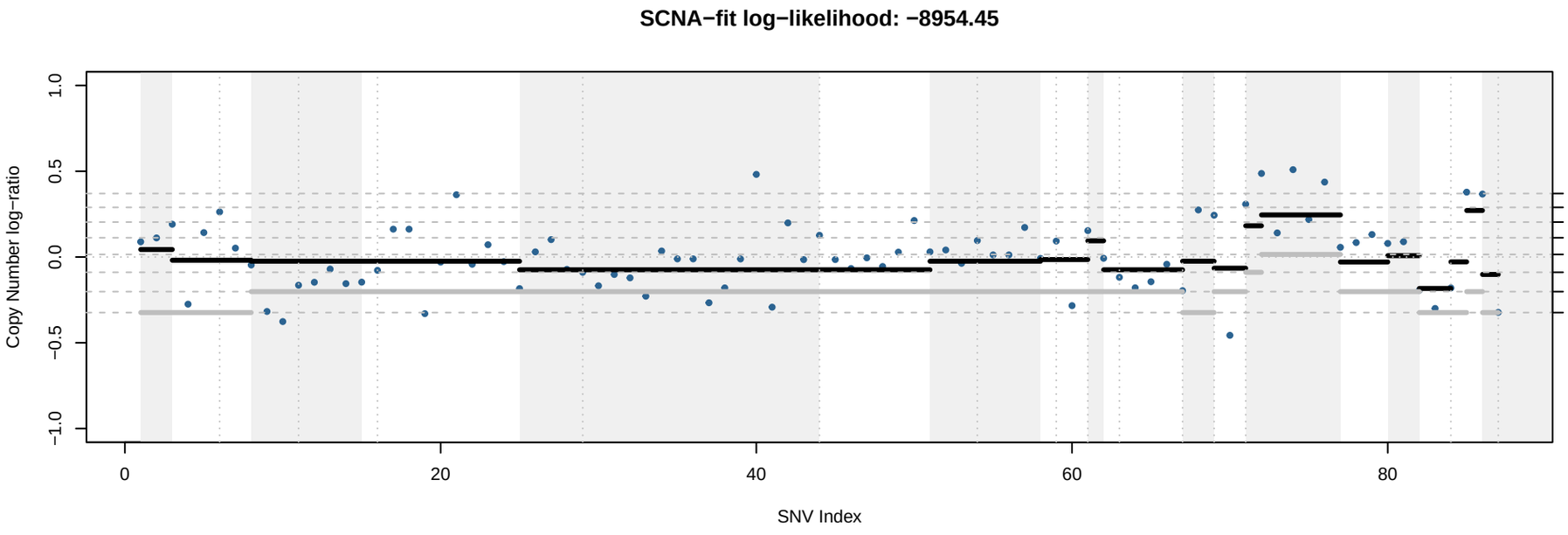

Coverage (log2)
Allelic fraction

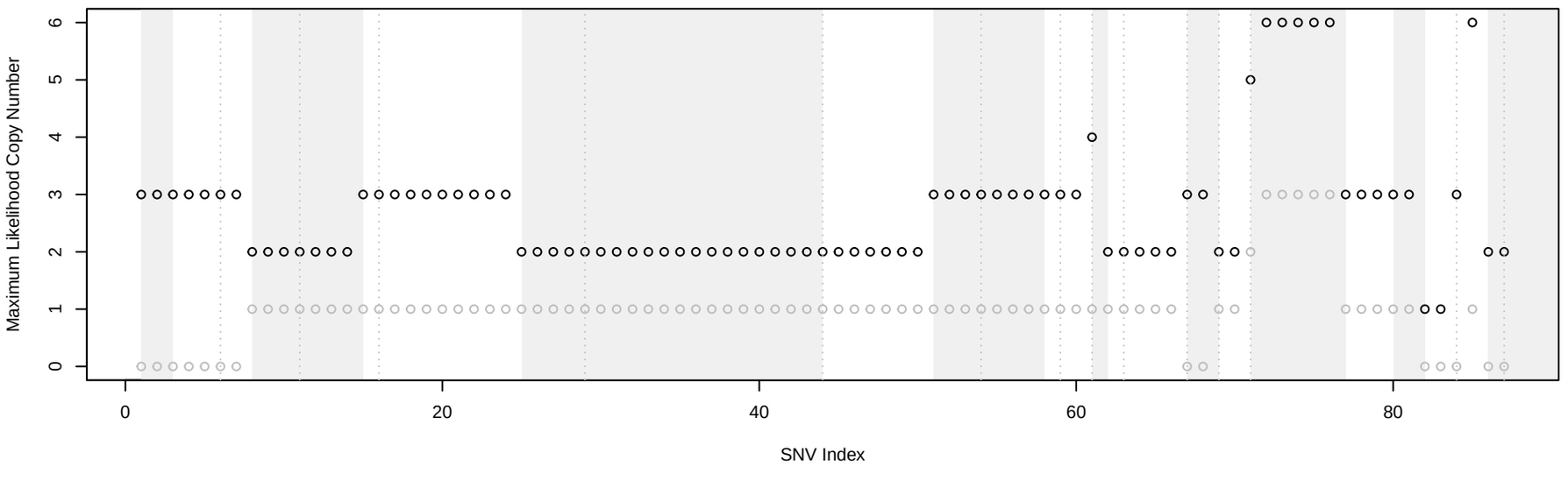

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
4m1

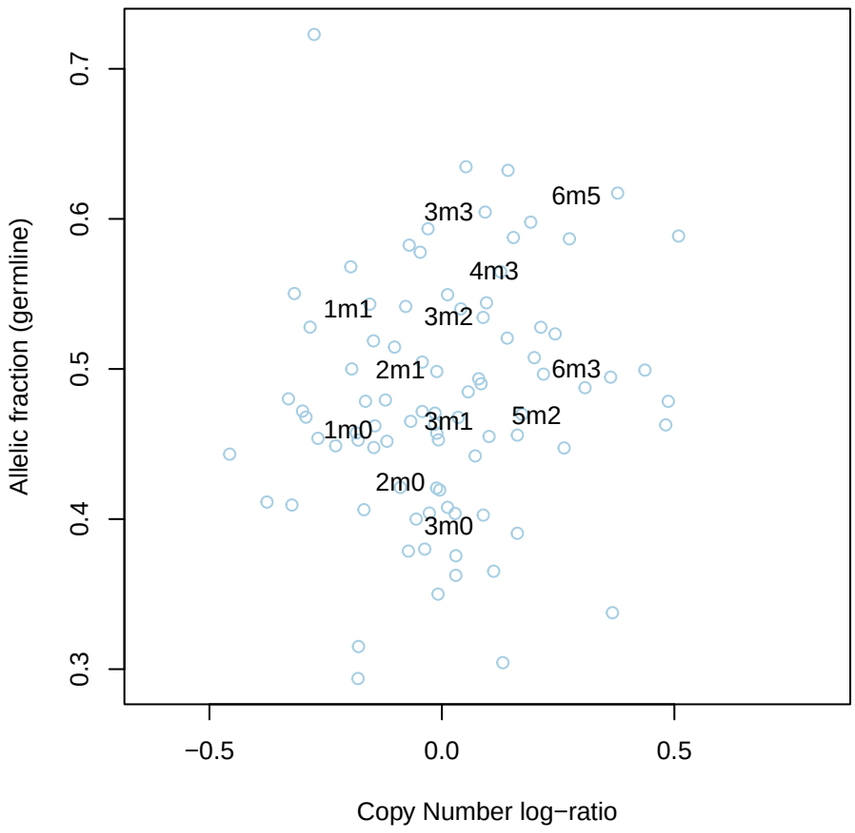

Power 0.8
Frequency
Cellular fraction

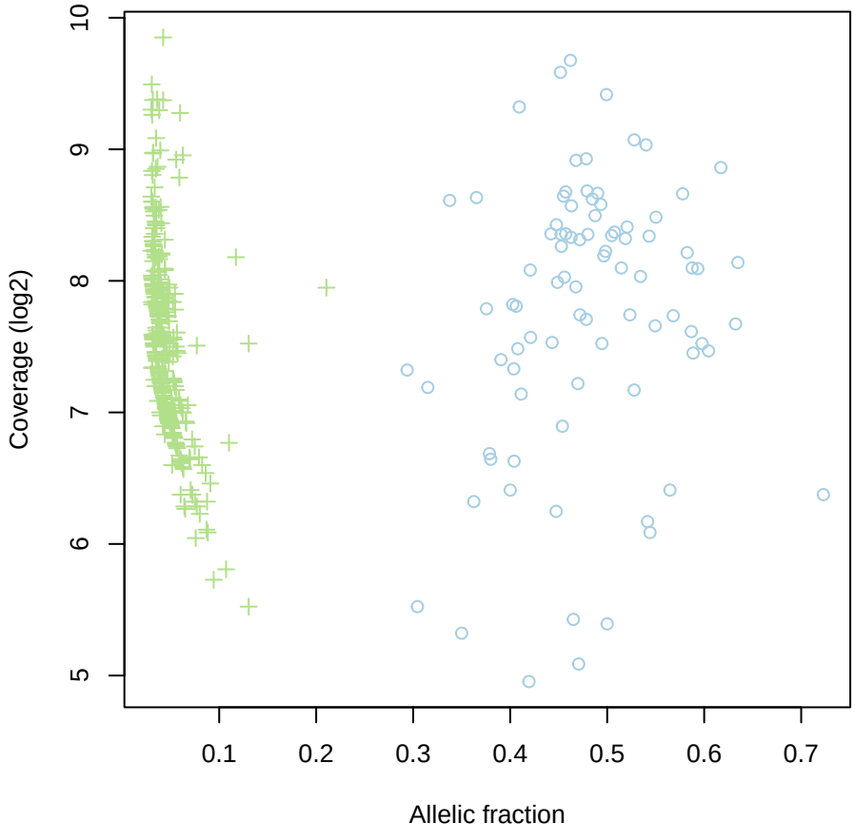

Purity: 0.15 Tumor ploidy: 2.851
0
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

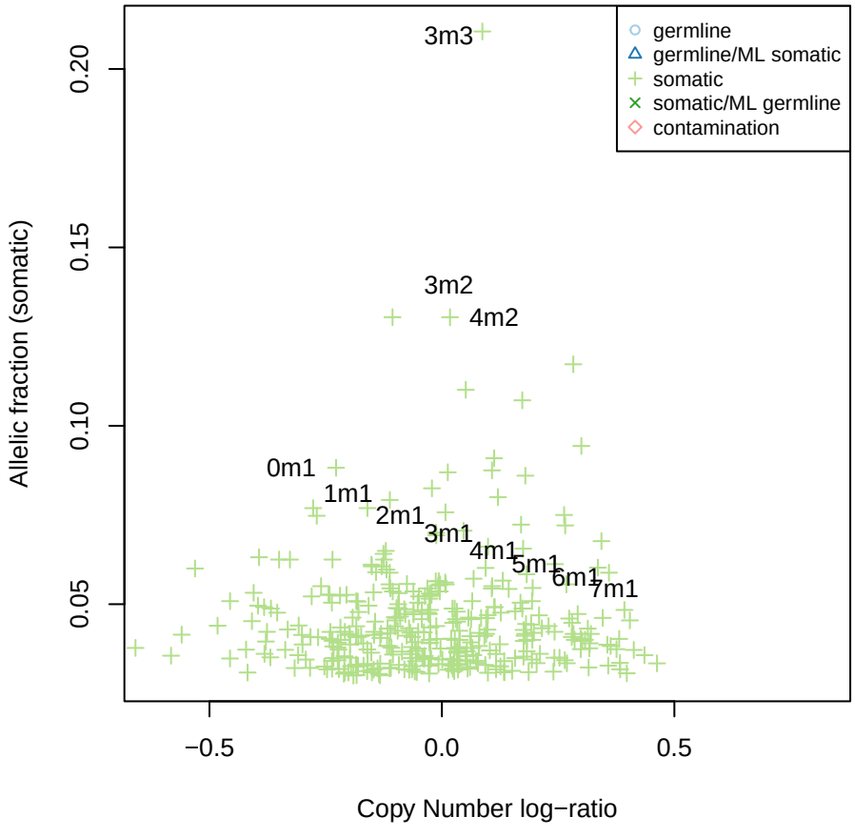

Purity: 0.15 Tumor ploidy: 2.851 SNV log−likelihood: 128.61 GoF: 96.4% Mean coverage: 219;199
1 2 3 4 5 6 7 9 10 12 13 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

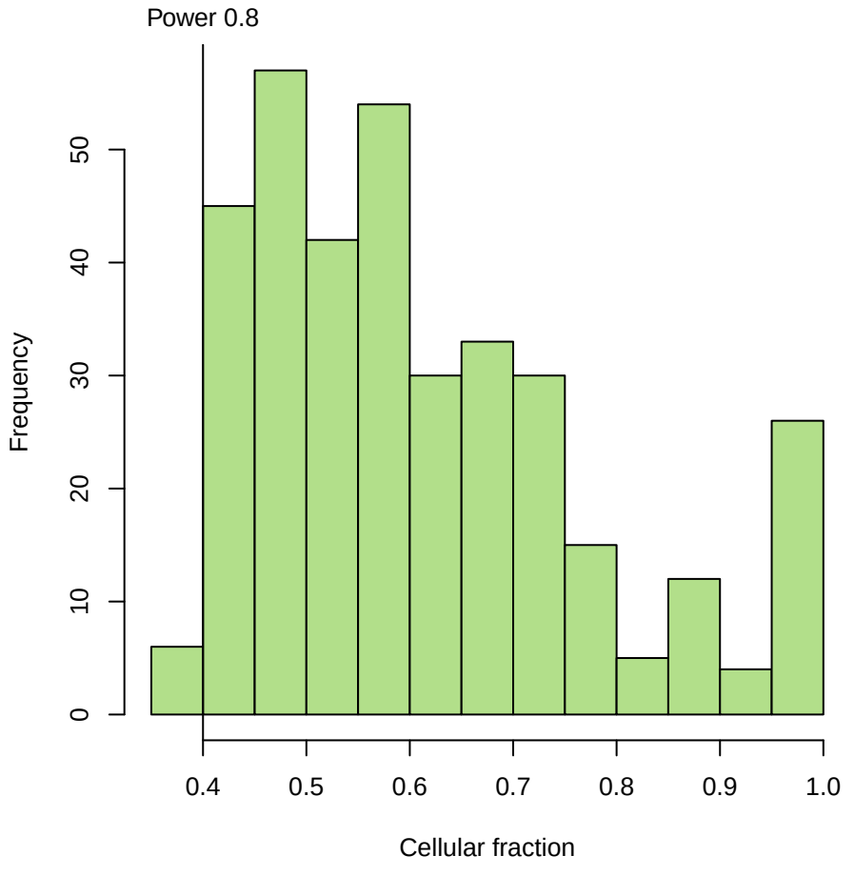

SCNA−fit log−likelihood: −8954.45
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4 6
0 20 40 60 80
SNV Index

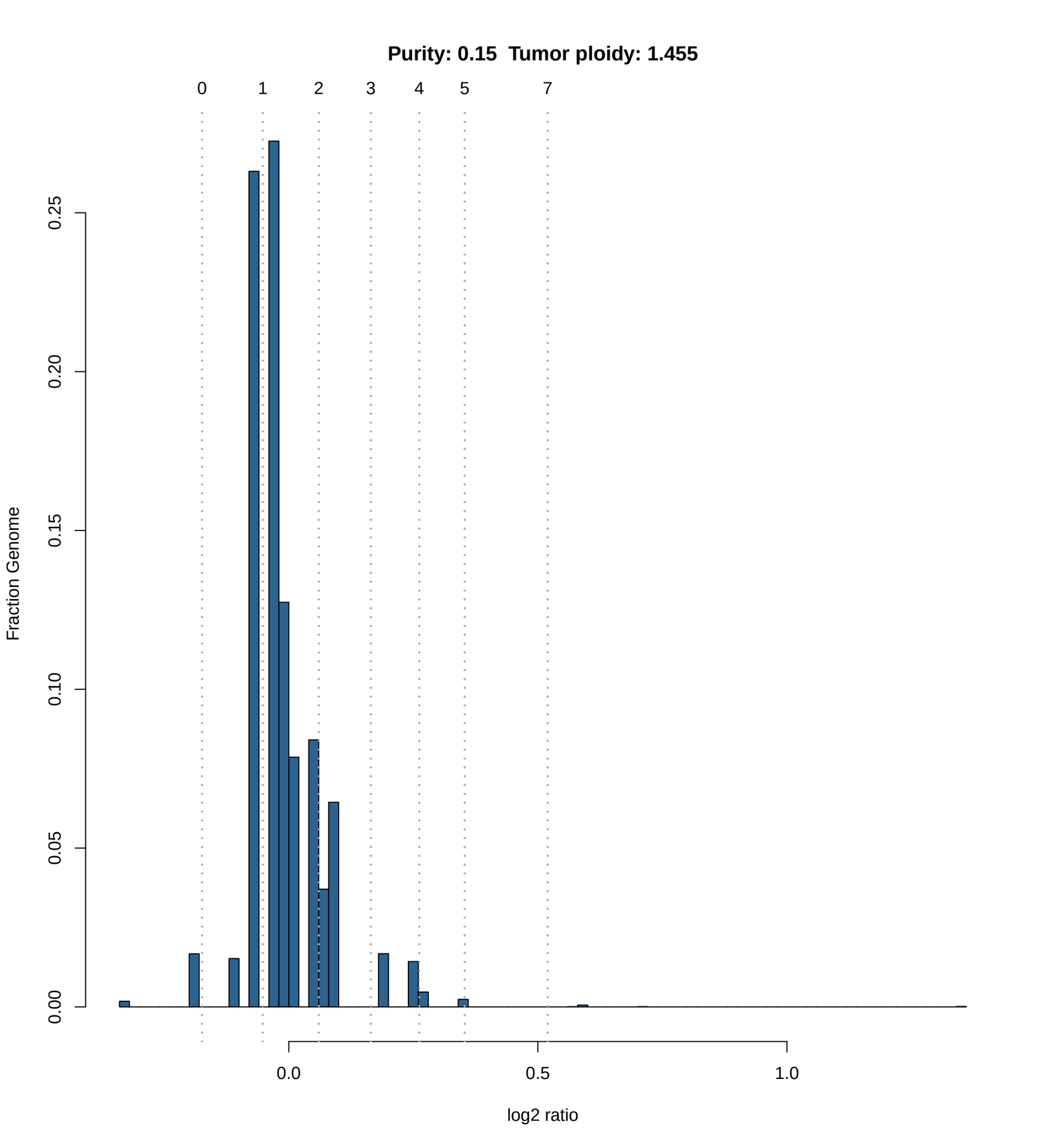

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80
SNV Index

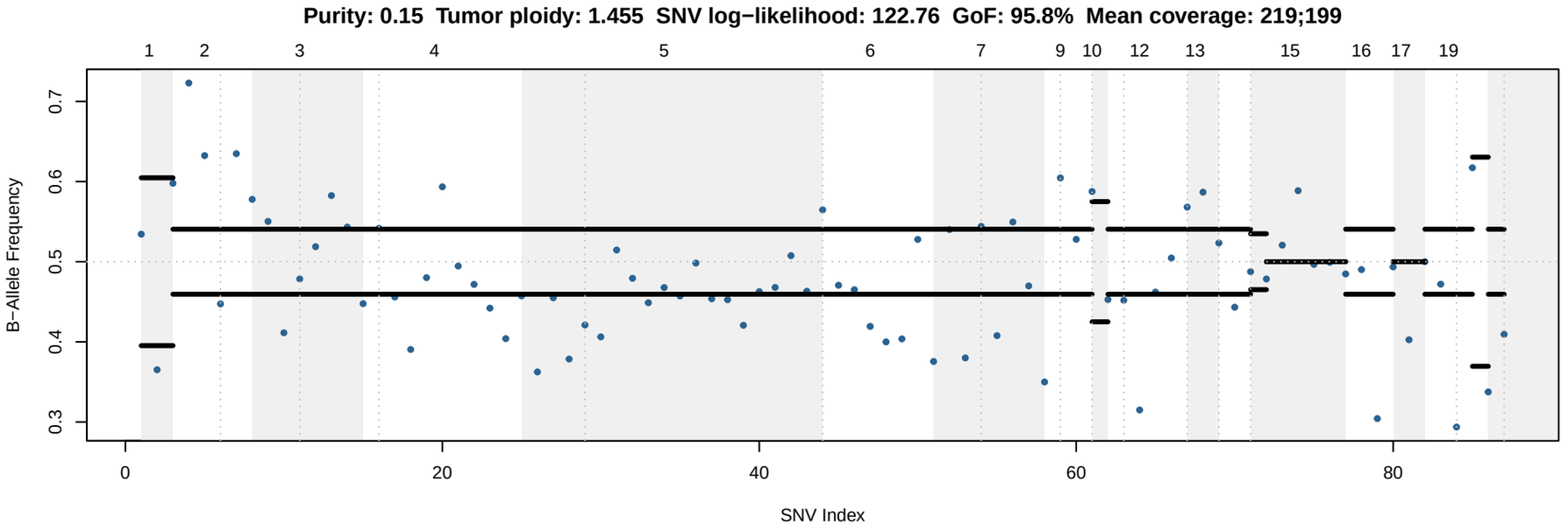

Allelic fraction (germline)
Copy Number log−ratio
6m5
3m3
4m3
1m1
3m2
2m1
6m3
3m1
5m2
1m0
2m0
3m0

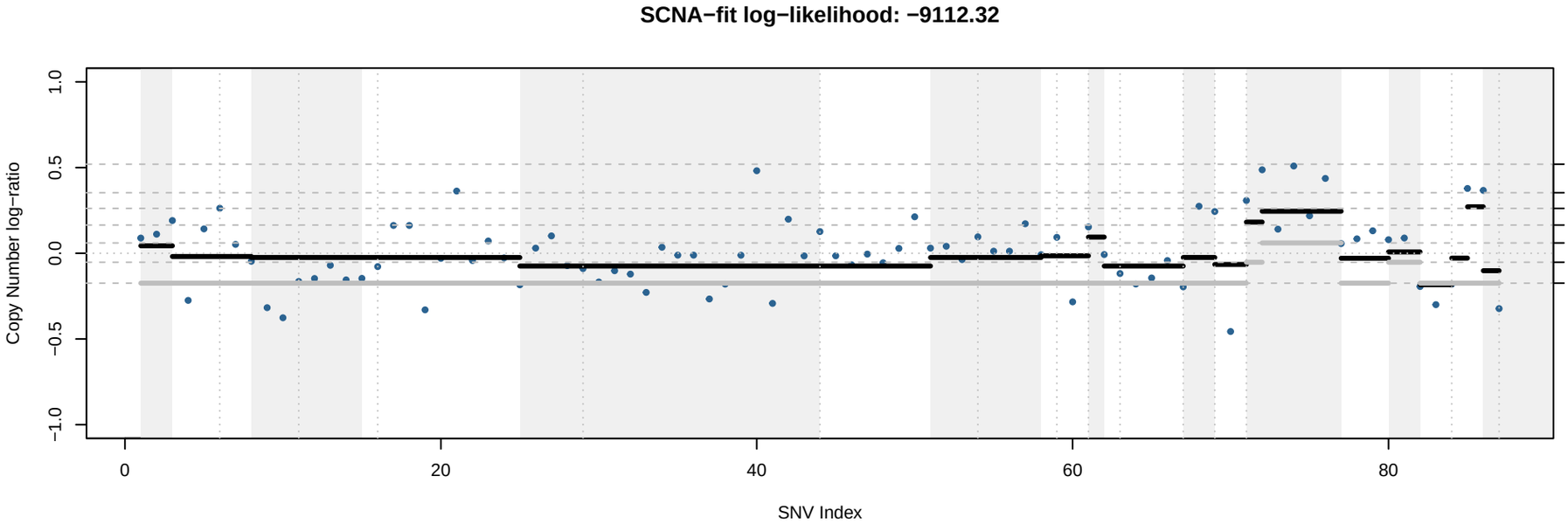

Coverage (log2)
Allelic fraction

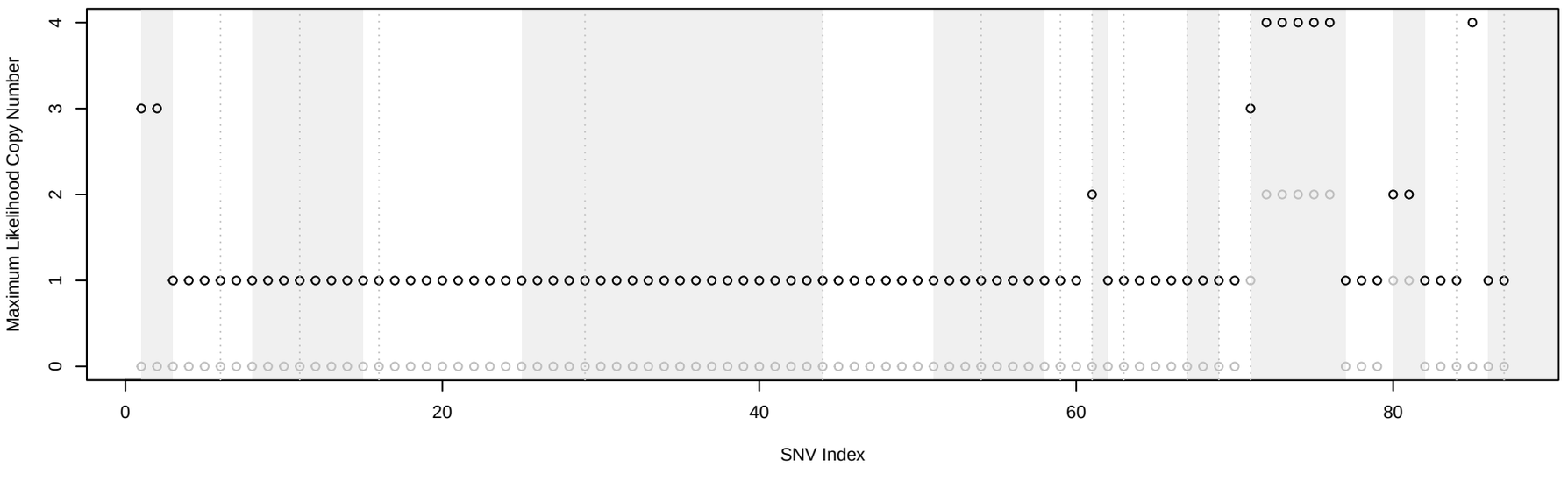

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m3
3m2
4m2
0m1
1m1
2m1
3m1
4m1
5m1
6m1
7m1

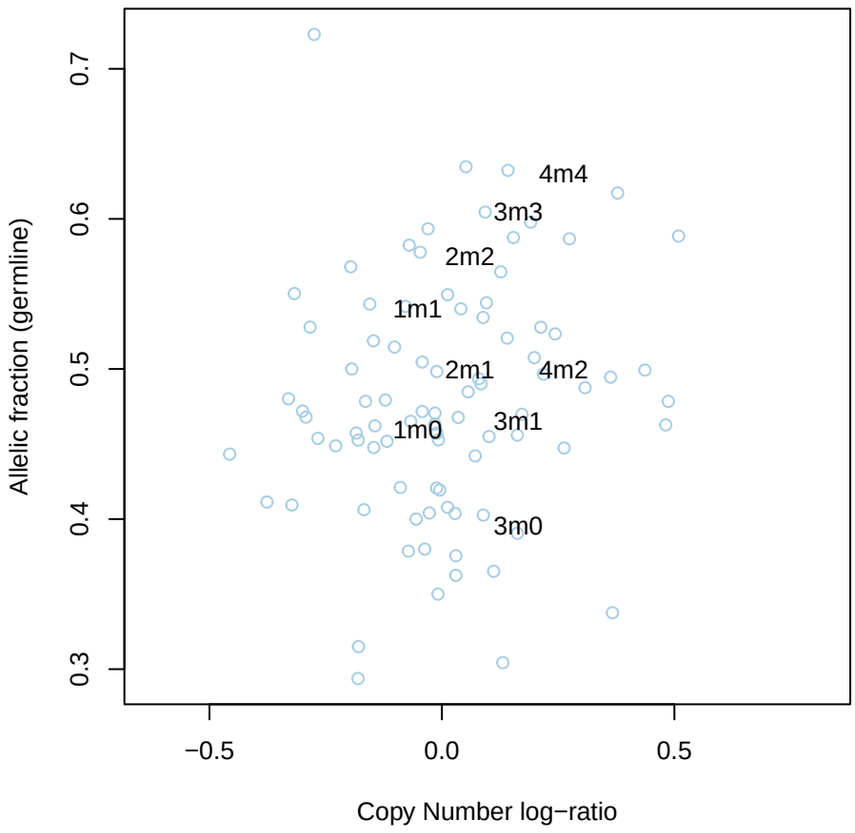

Power 0.8
Frequency
Cellular fraction

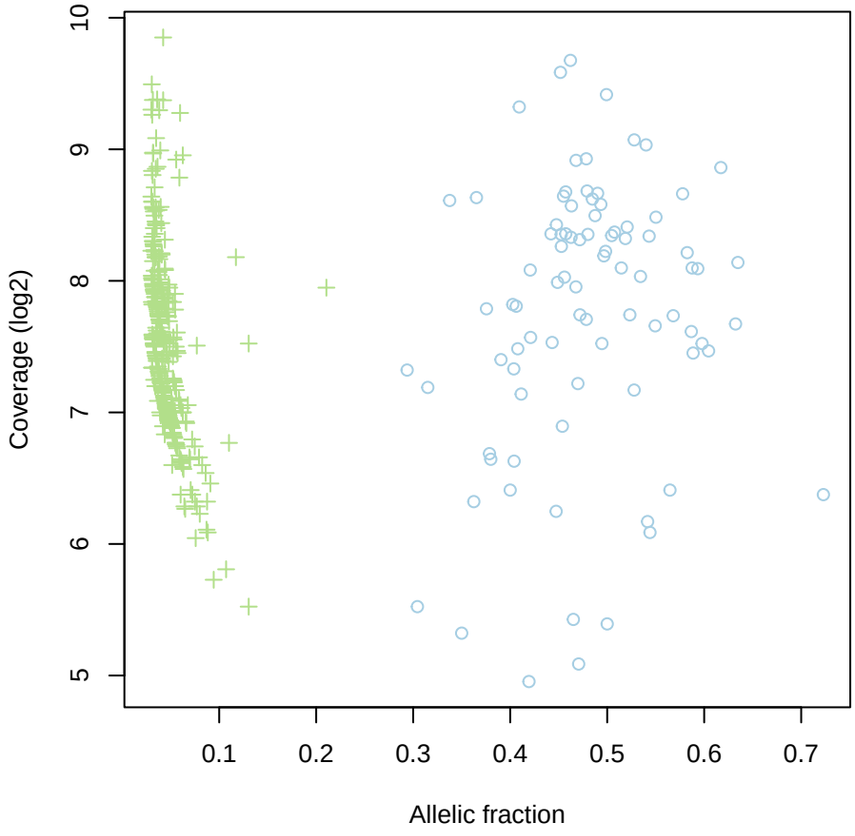

Purity: 0.15 Tumor ploidy: 1.455
0
1
2
3
4
5
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

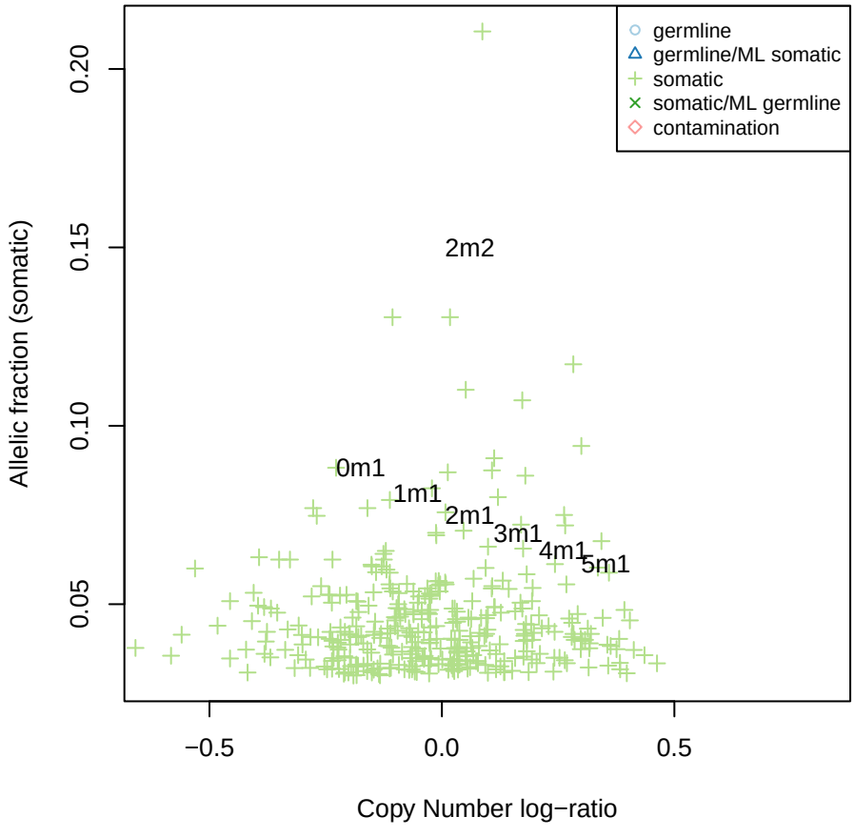

Purity: 0.15 Tumor ploidy: 1.455 SNV log−likelihood: 122.76 GoF: 95.8% Mean coverage: 219;199
1 2 3 4 5 6 7 9 10 12 13 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

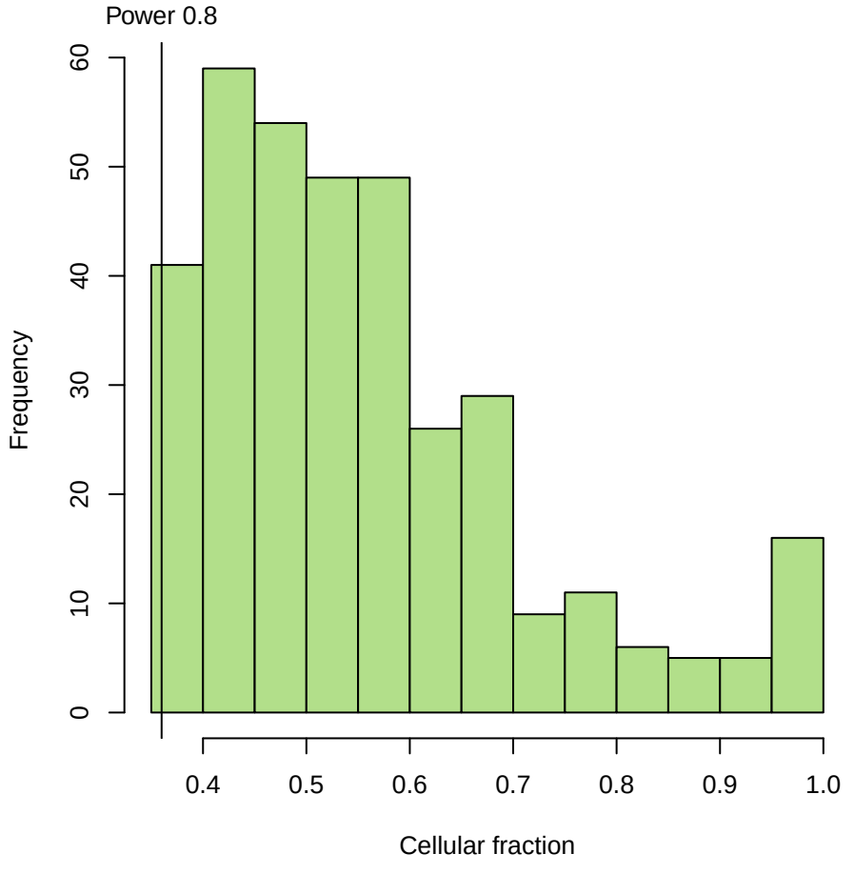

SCNA−fit log−likelihood: −9112.32
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4 7
0 20 40 60 80
SNV Index

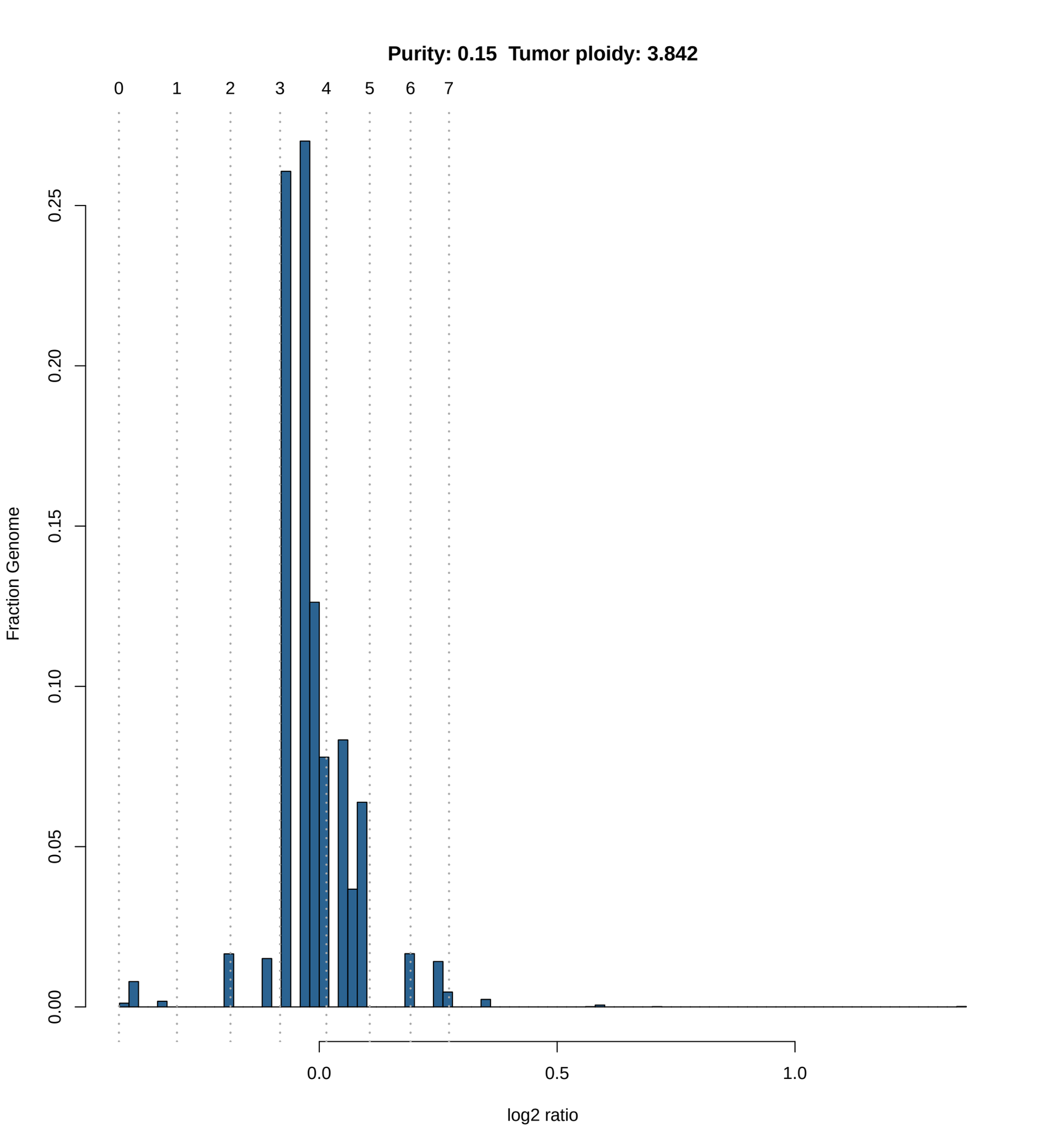

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80
SNV Index

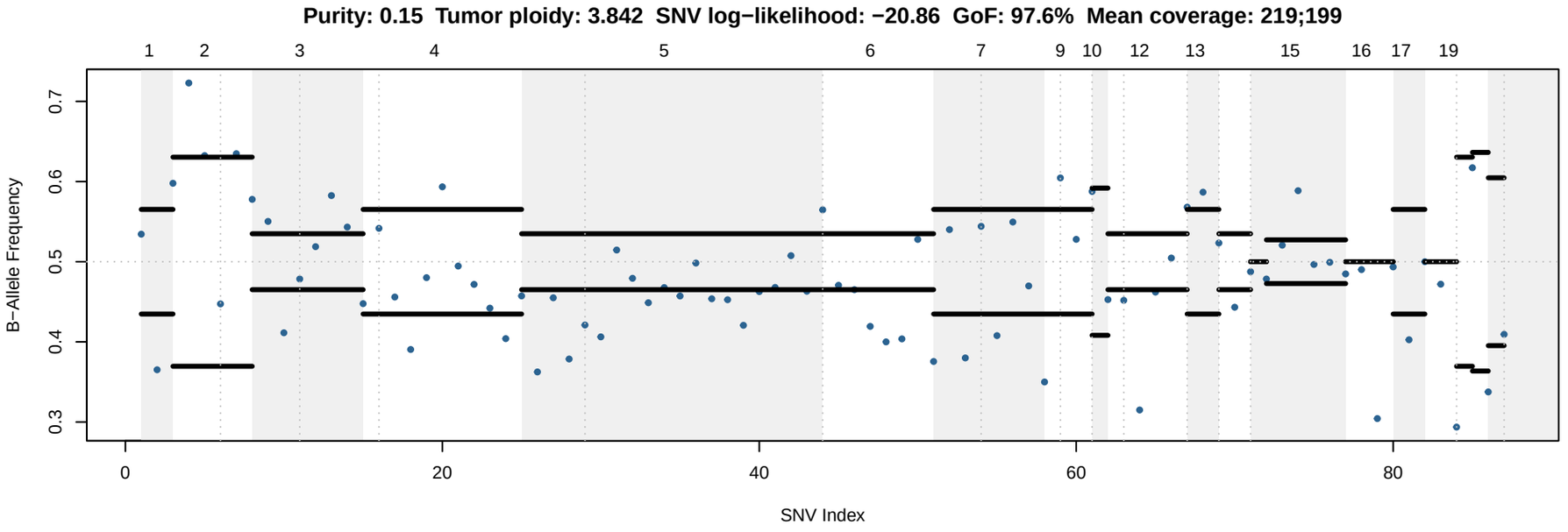

Allelic fraction (germline)
Copy Number log−ratio
4m4
3m3
2m2
1m1
2m1
4m2
3m1
1m0
3m0

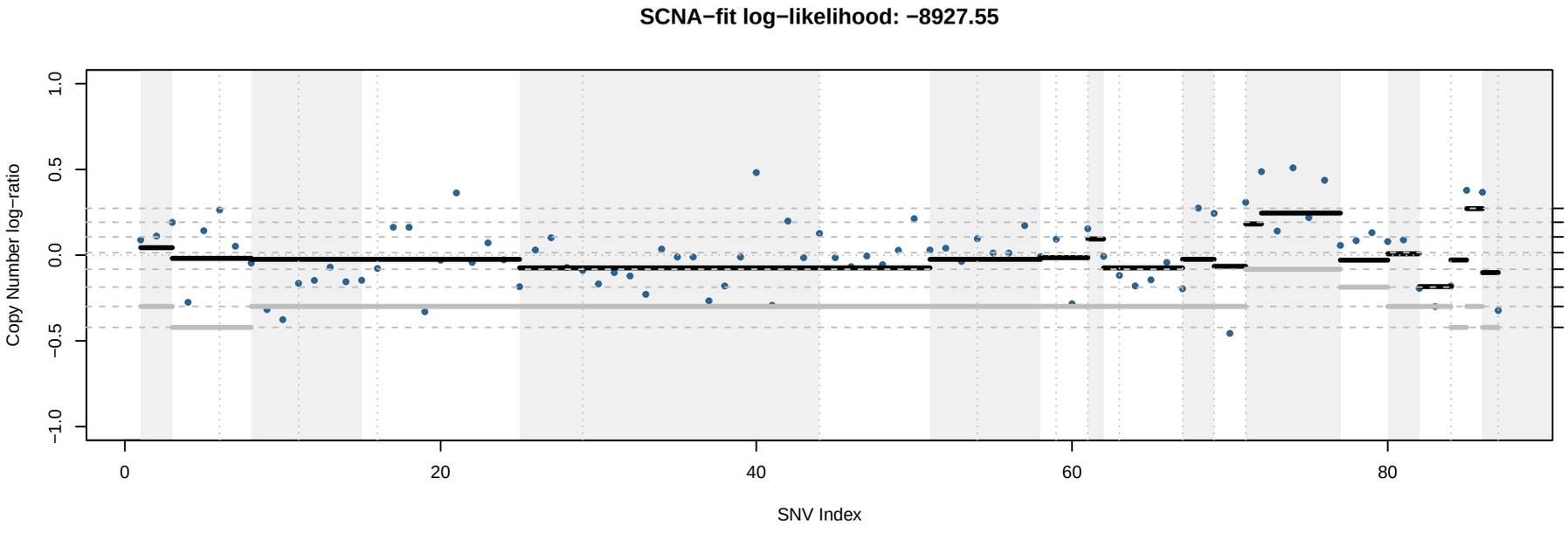

Coverage (log2)
Allelic fraction

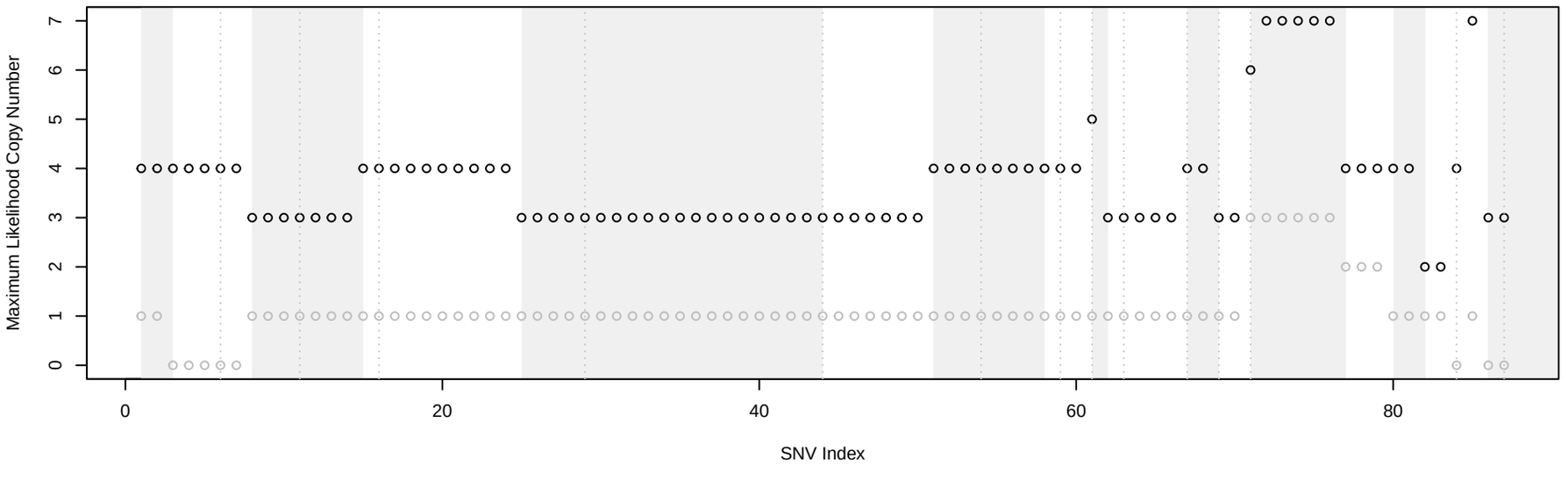

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
0m1
1m1
2m1
3m1
4m1
5m1

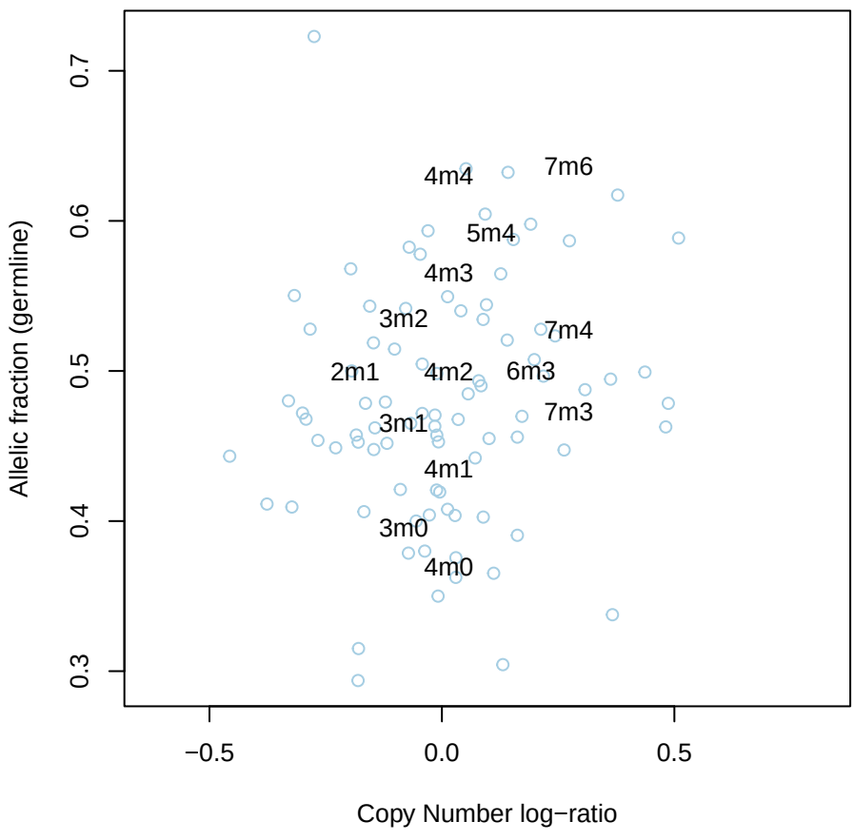

Power 0.8
Frequency
Cellular fraction

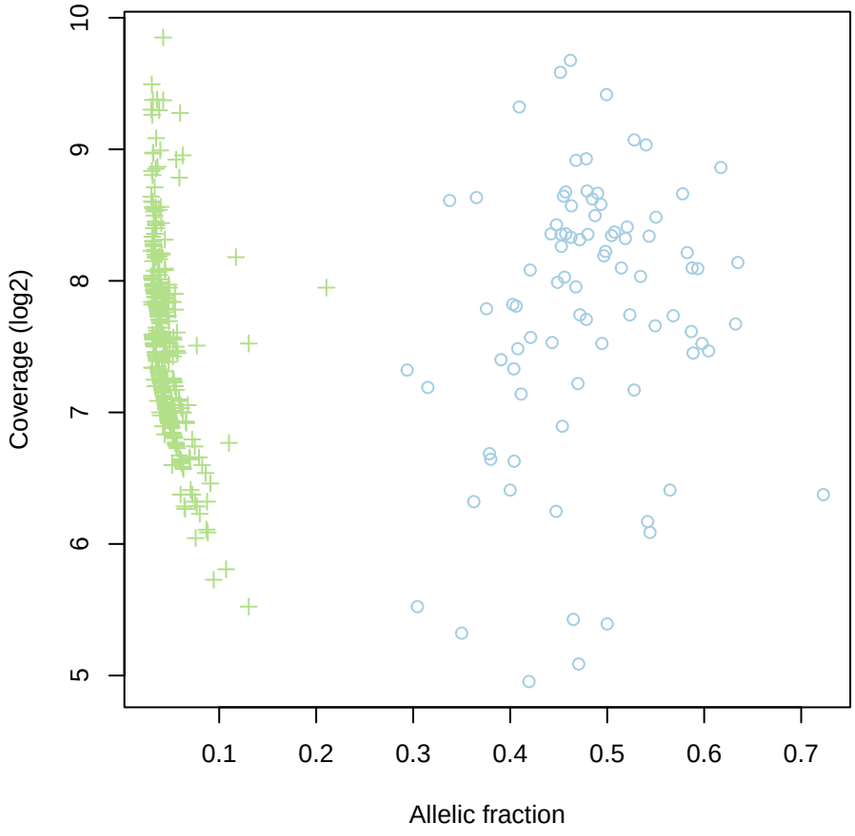

Purity: 0.15 Tumor ploidy: 3.842
0
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

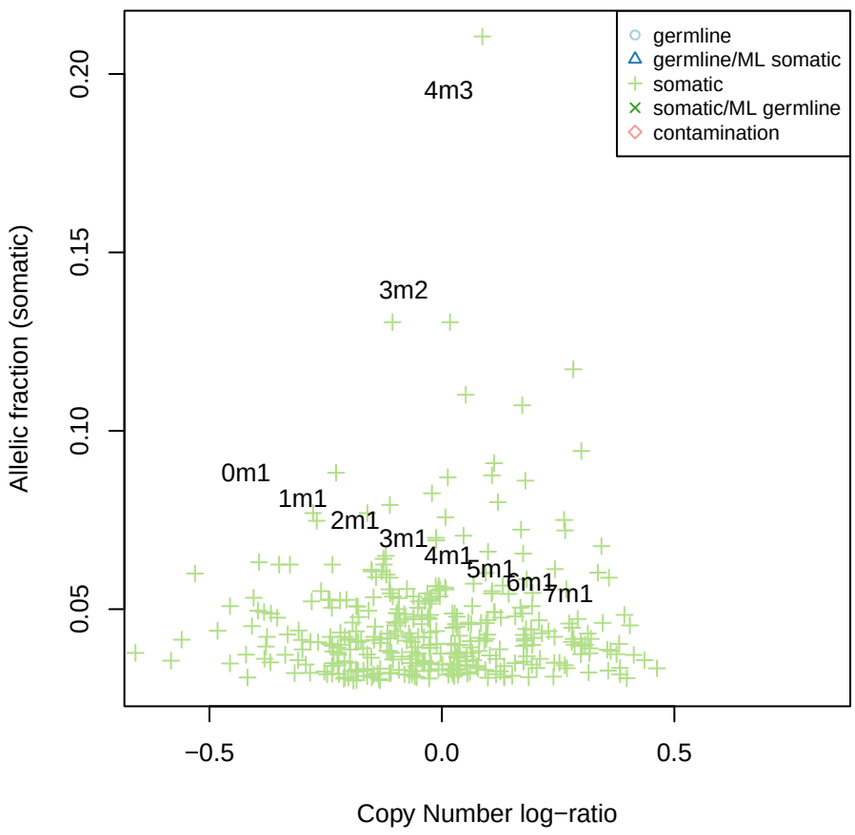

Purity: 0.15 Tumor ploidy: 3.842 SNV log−likelihood: −20.86 GoF: 97.6% Mean coverage: 219;199
1 2 3 4 5 6 7 9 10 12 13 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

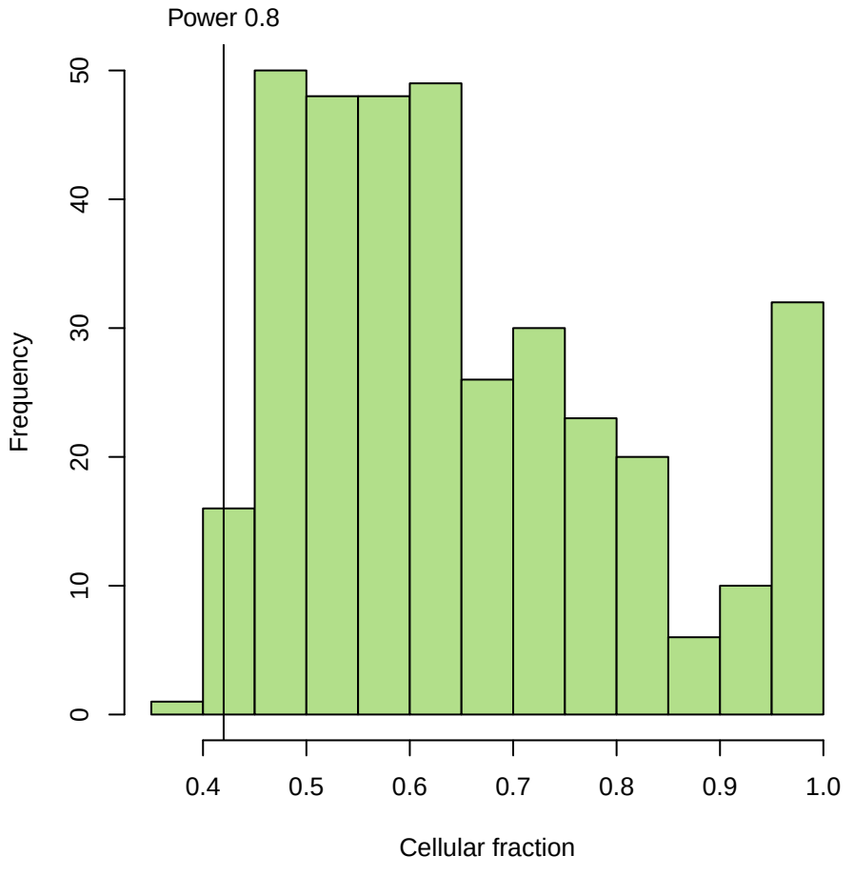

SCNA−fit log−likelihood: −8927.55
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4 6
0 20 40 60 80
SNV Index

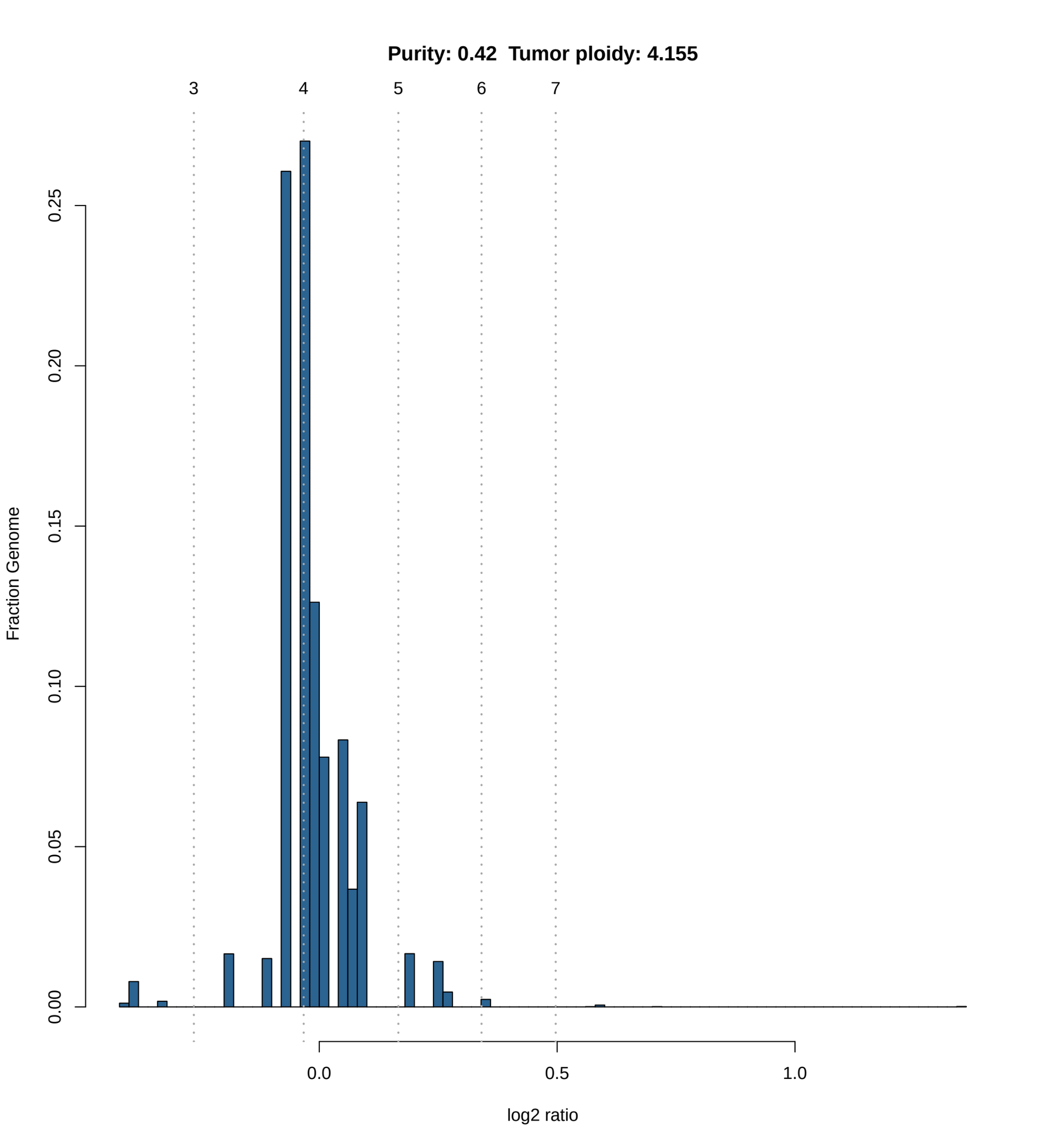

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

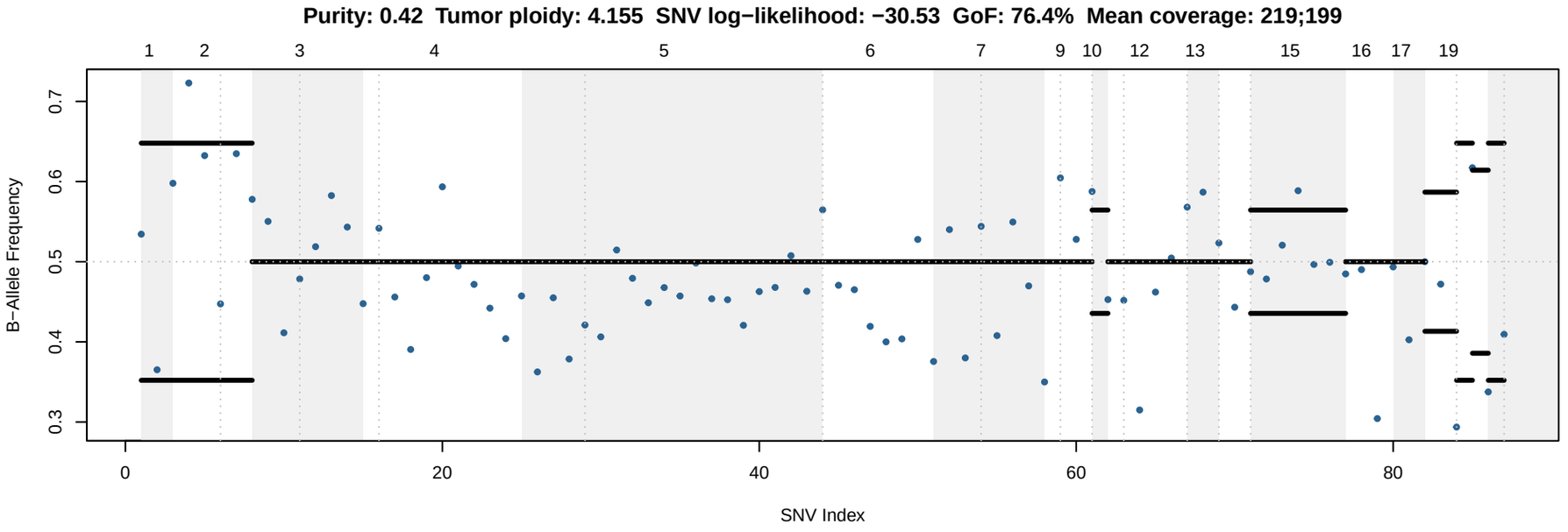

Allelic fraction (germline)
Copy Number log−ratio
7m6
4m4
5m4
4m3
3m2
7m4
2m1
4m2
6m3
7m3
3m1
4m1
3m0
4m0

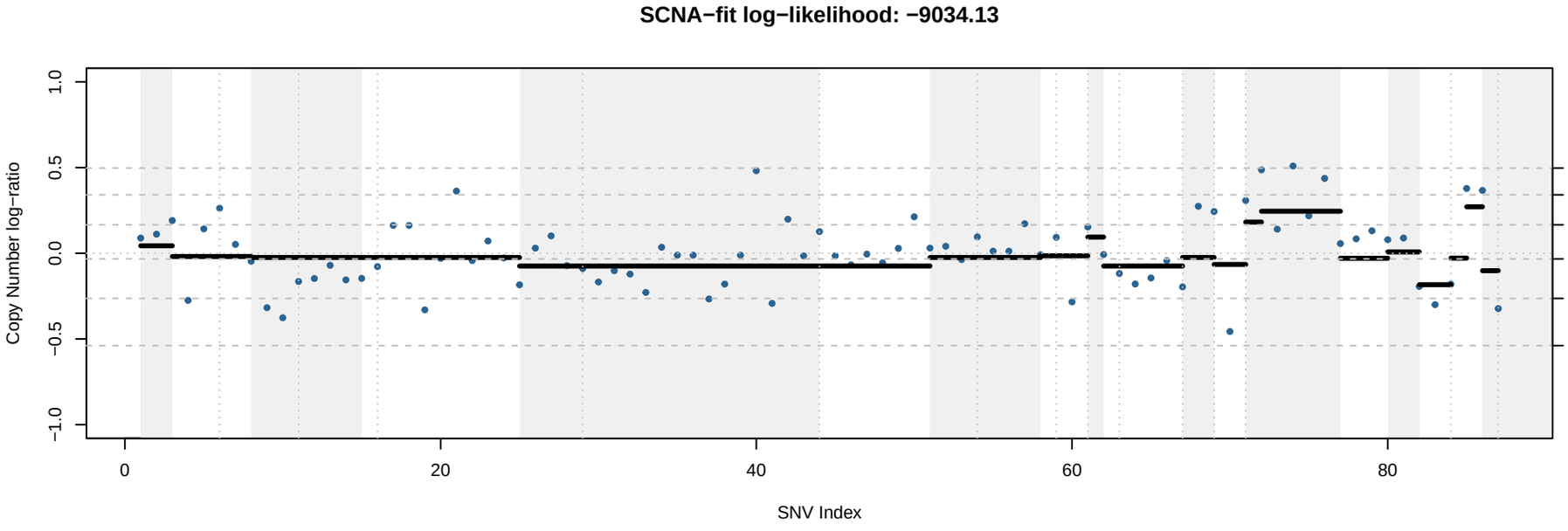

Coverage (log2)
Allelic fraction

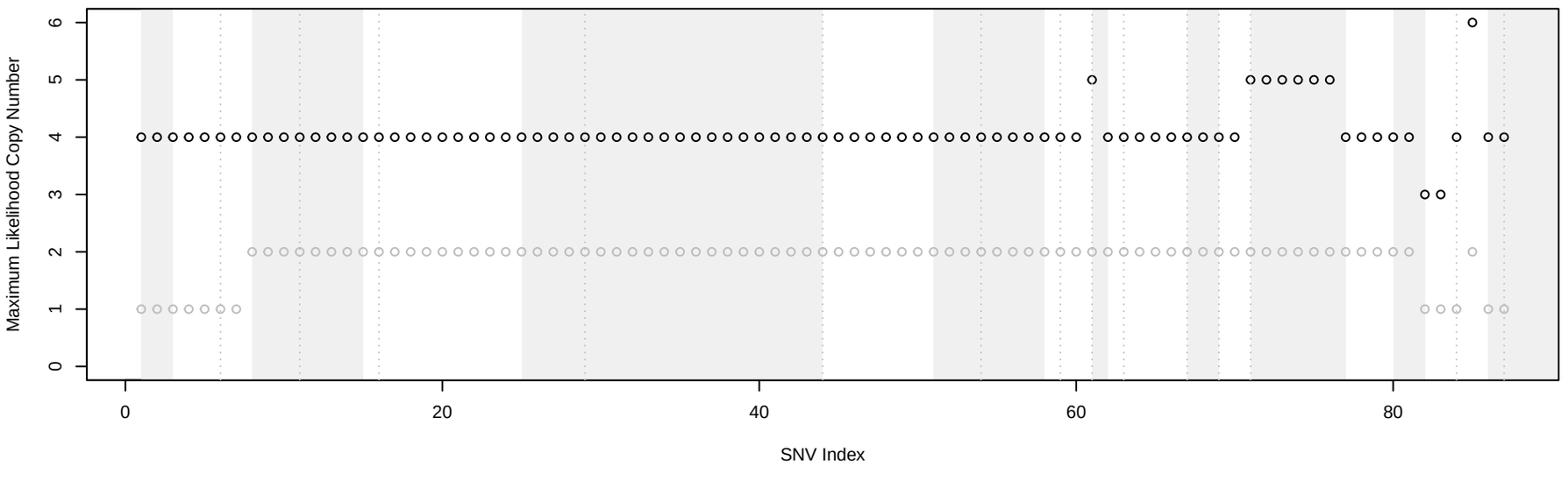

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m3
3m2
0m1
1m1
2m1
3m1
4m1
5m1
6m1
7m1

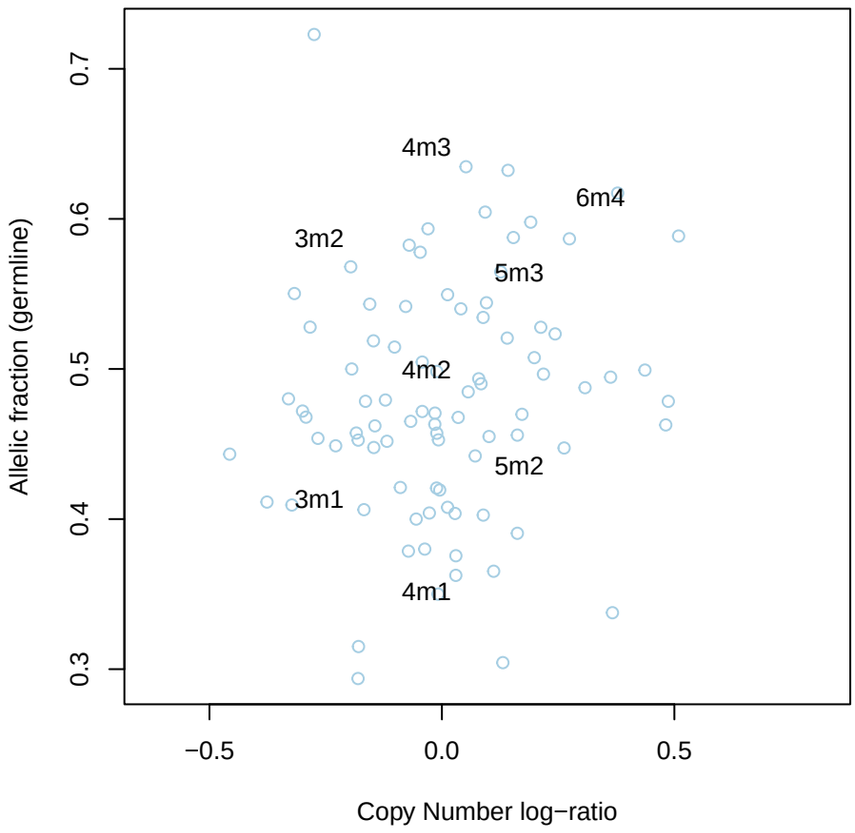

Power 0.8
Frequency
Cellular fraction

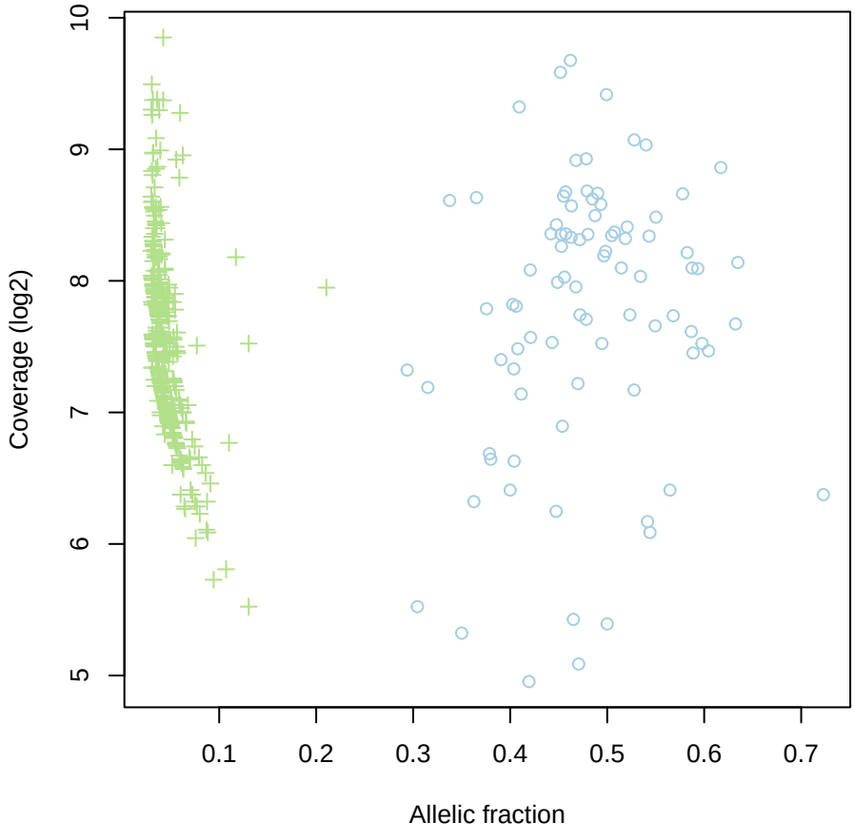

Purity: 0.42 Tumor ploidy: 4.155
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

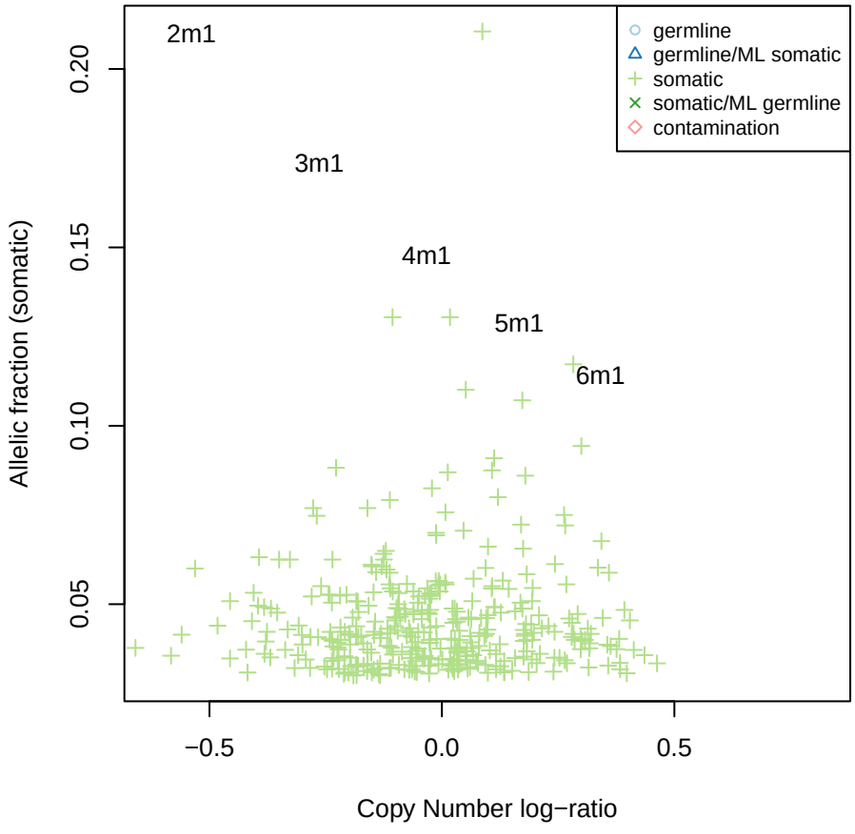

Purity: 0.42 Tumor ploidy: 4.155 SNV log−likelihood: −30.53 GoF: 76.4% Mean coverage: 219;199
1 2 3 4 5 6 7 9 10 12 13 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

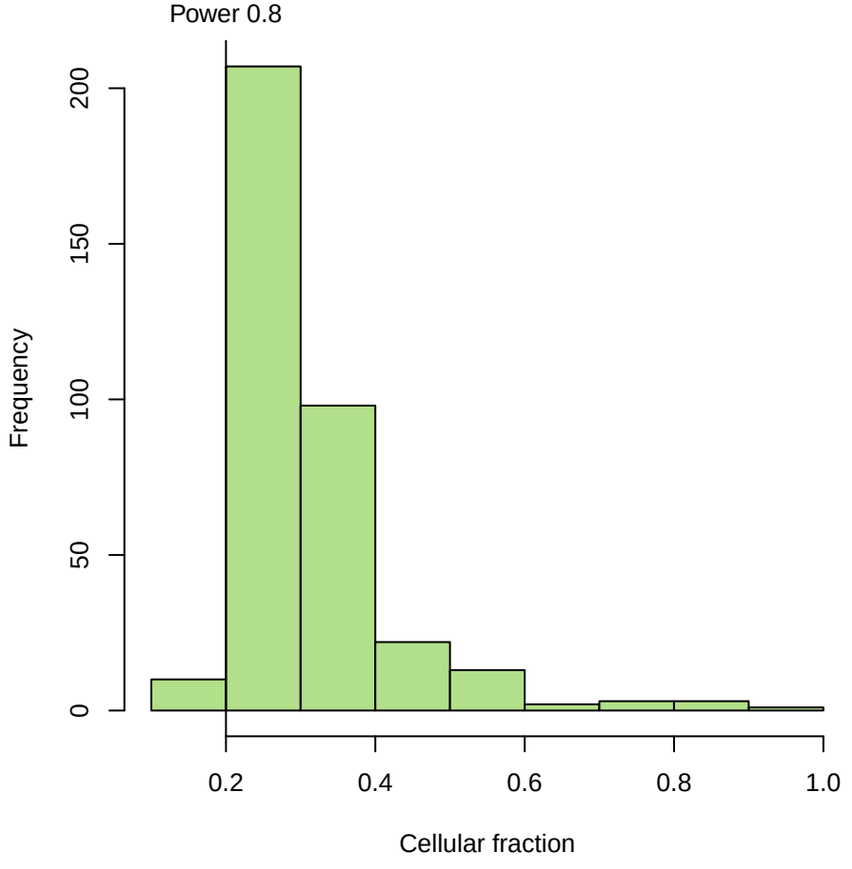

SCNA−fit log−likelihood: −9034.13
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 20 40 60 80
SNV Index

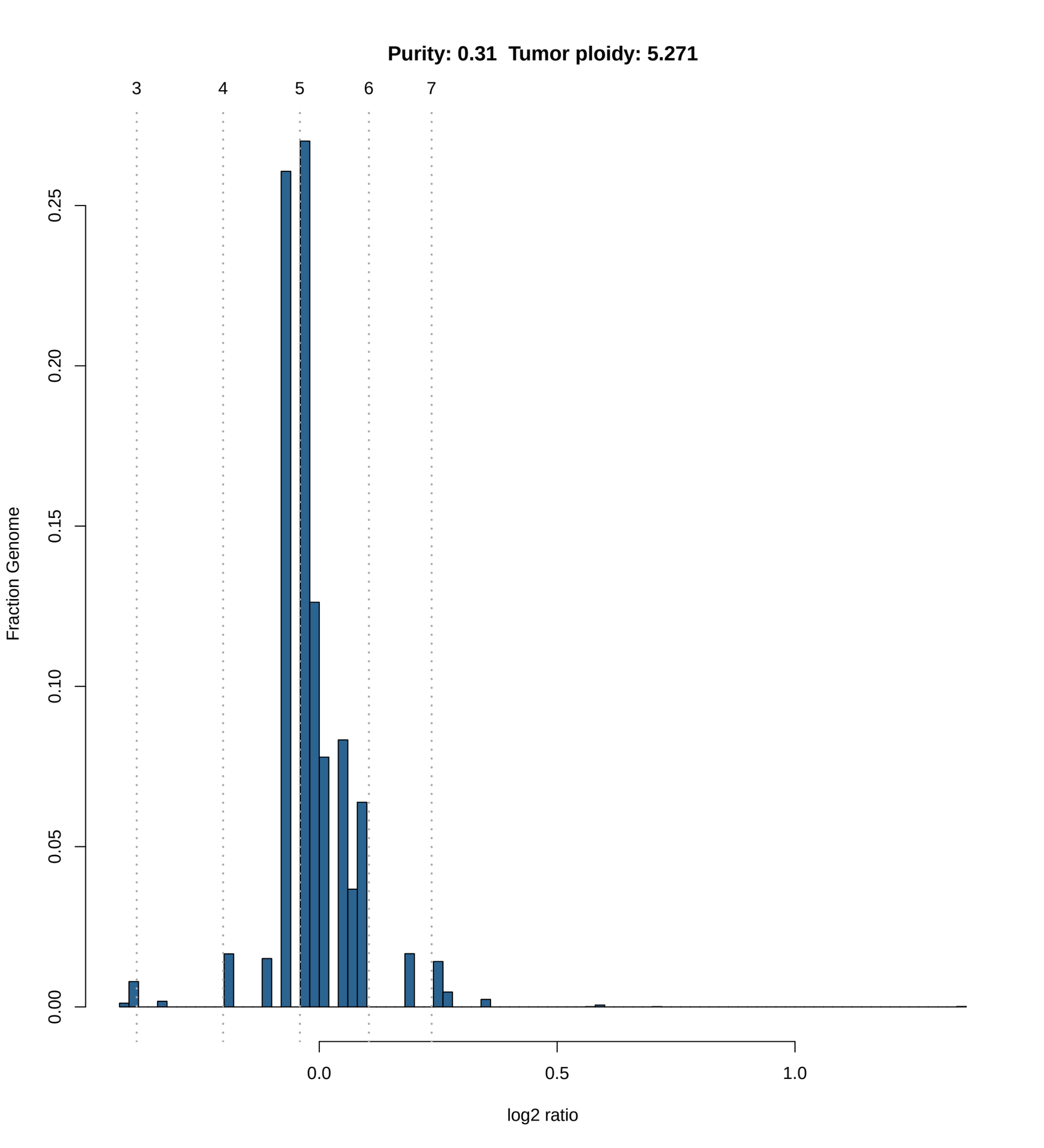

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80
SNV Index

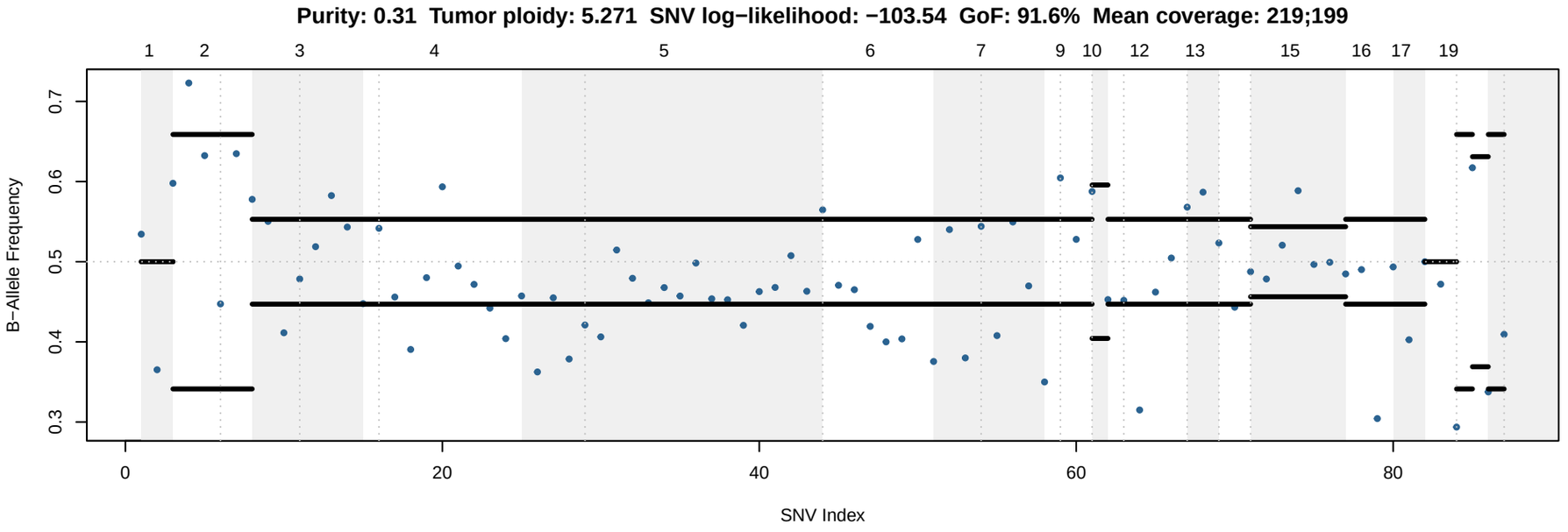

Allelic fraction (germline)
Copy Number log−ratio
4m3
6m4
3m2
5m3
4m2
5m2
3m1
4m1

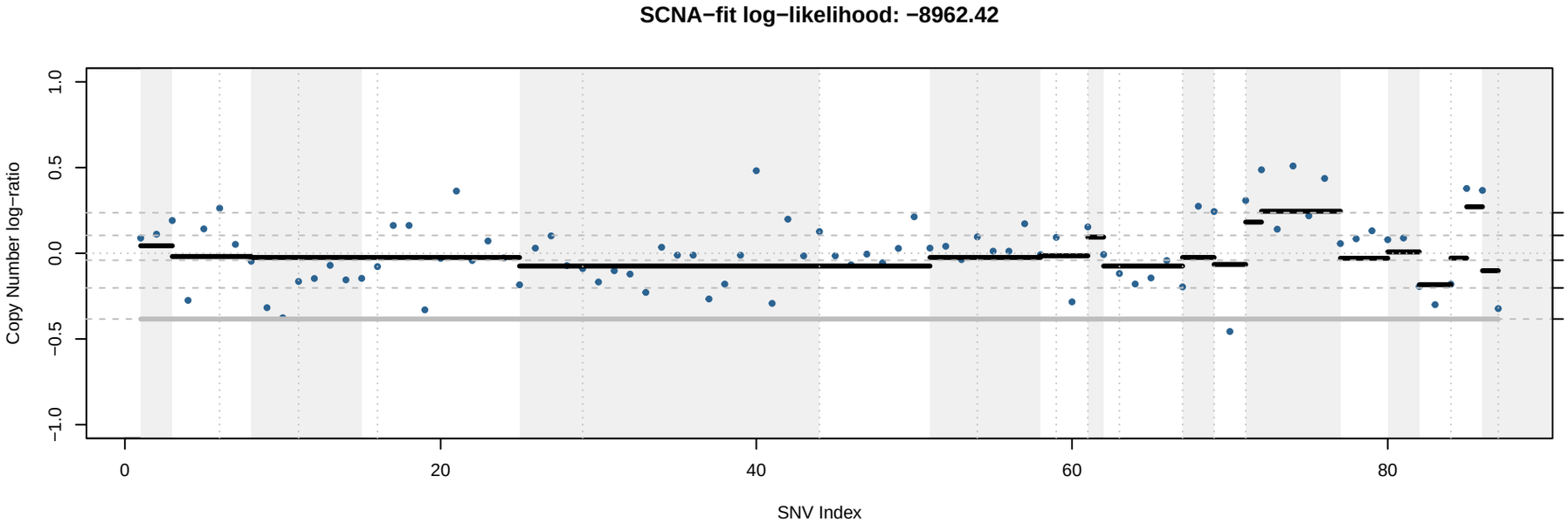

Coverage (log2)
Allelic fraction

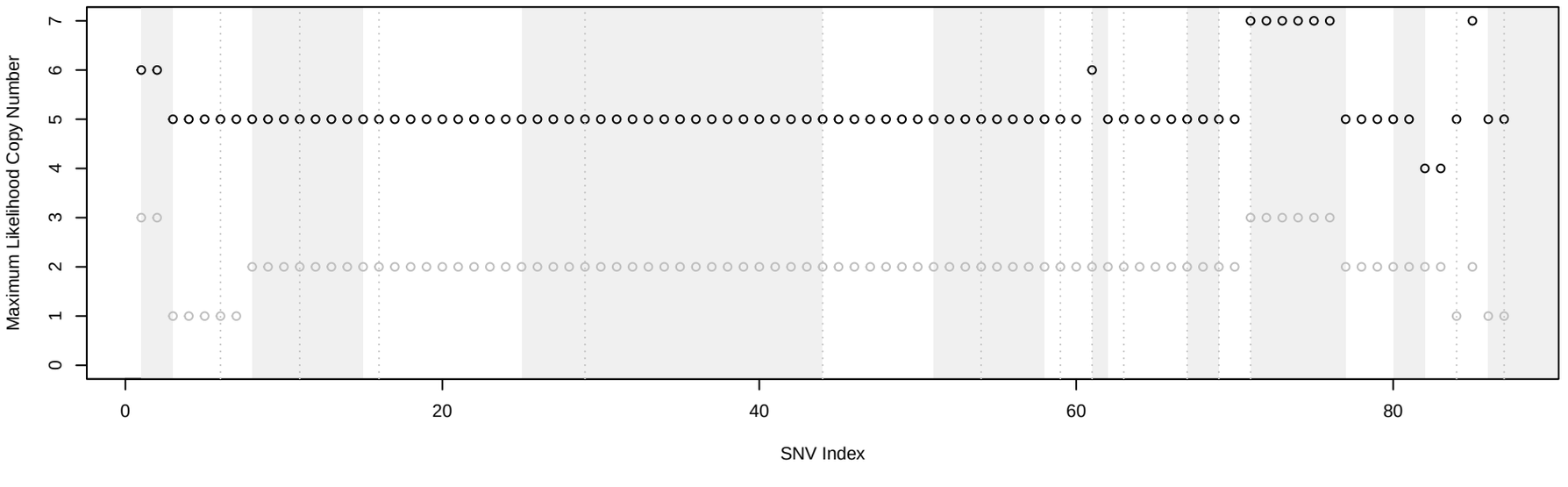

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1
5m1
6m1

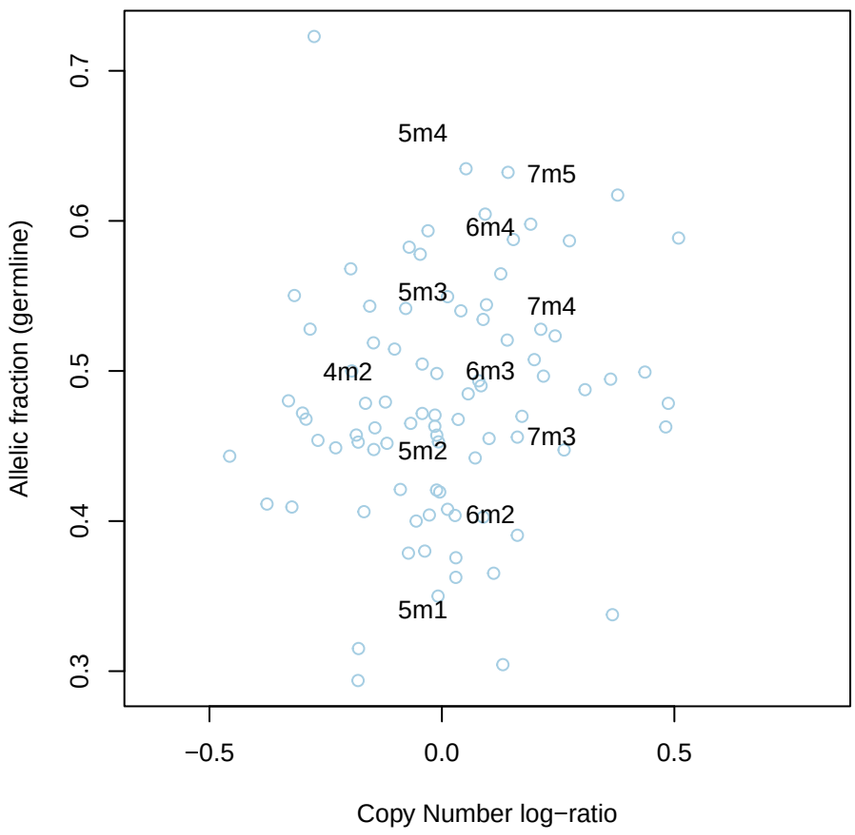

Power 0.8
Frequency
Cellular fraction

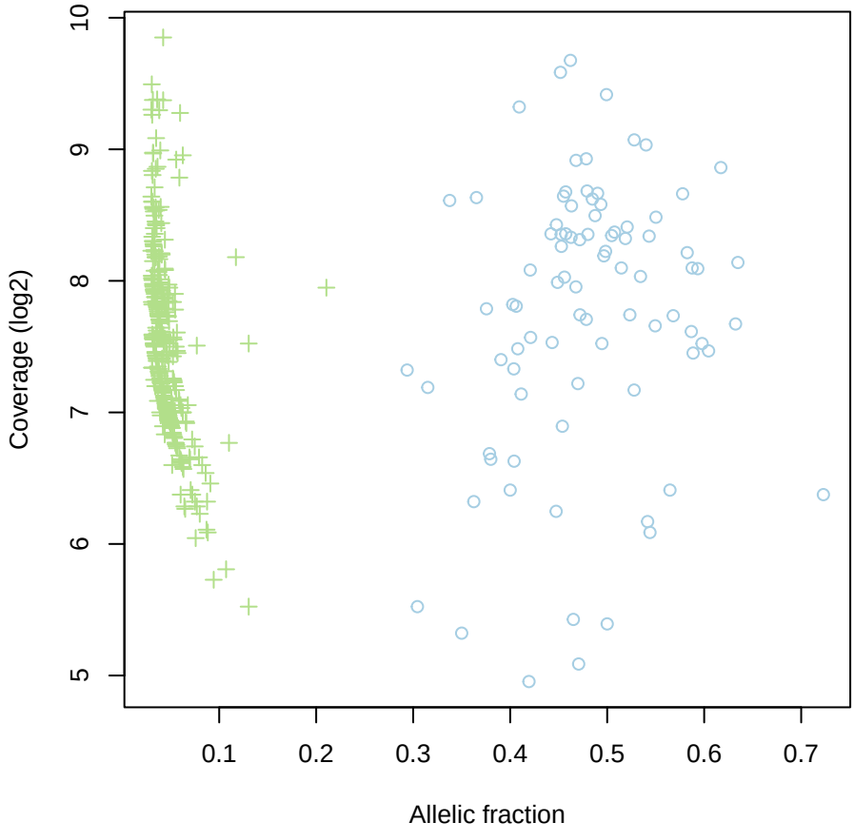

Purity: 0.31 Tumor ploidy: 5.271
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

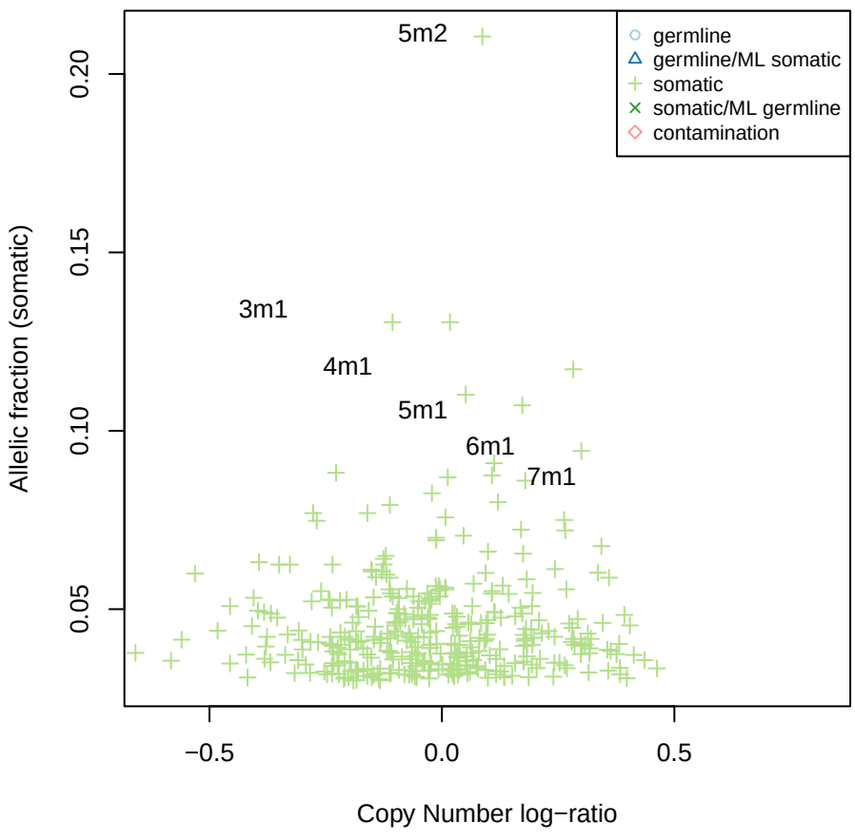

Purity: 0.31 Tumor ploidy: 5.271 SNV log−likelihood: −103.54 GoF: 91.6% Mean coverage: 219;199
1 2 3 4 5 6 7 9 10 12 13 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

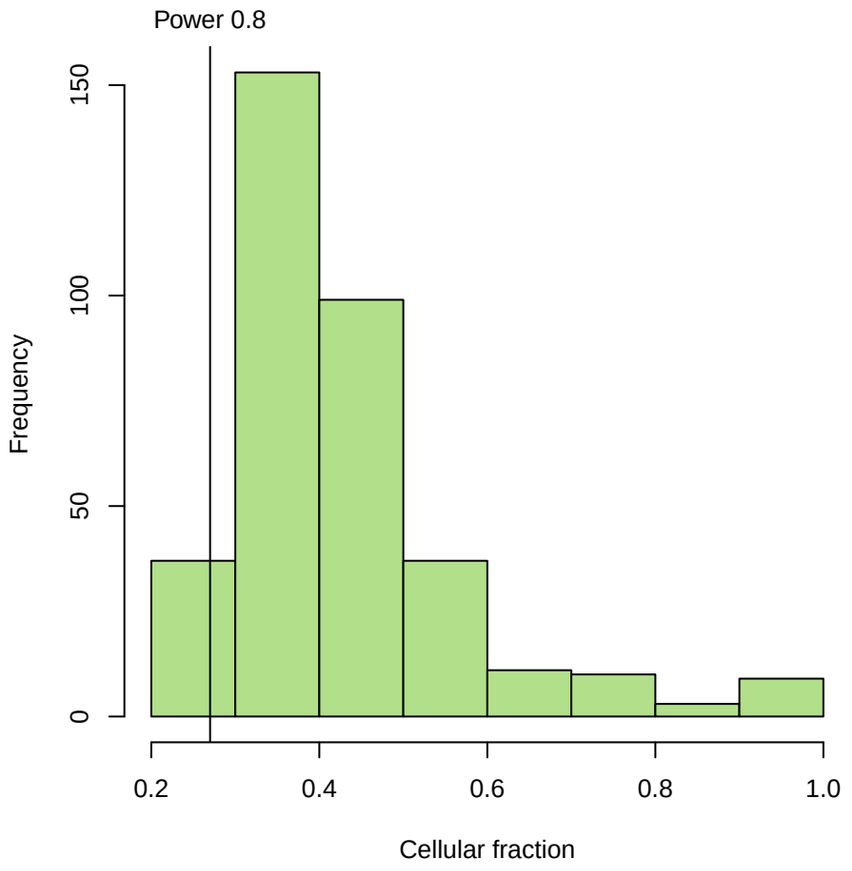

SCNA−fit log−likelihood: −8962.42
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6
0 20 40 60 80
SNV Index

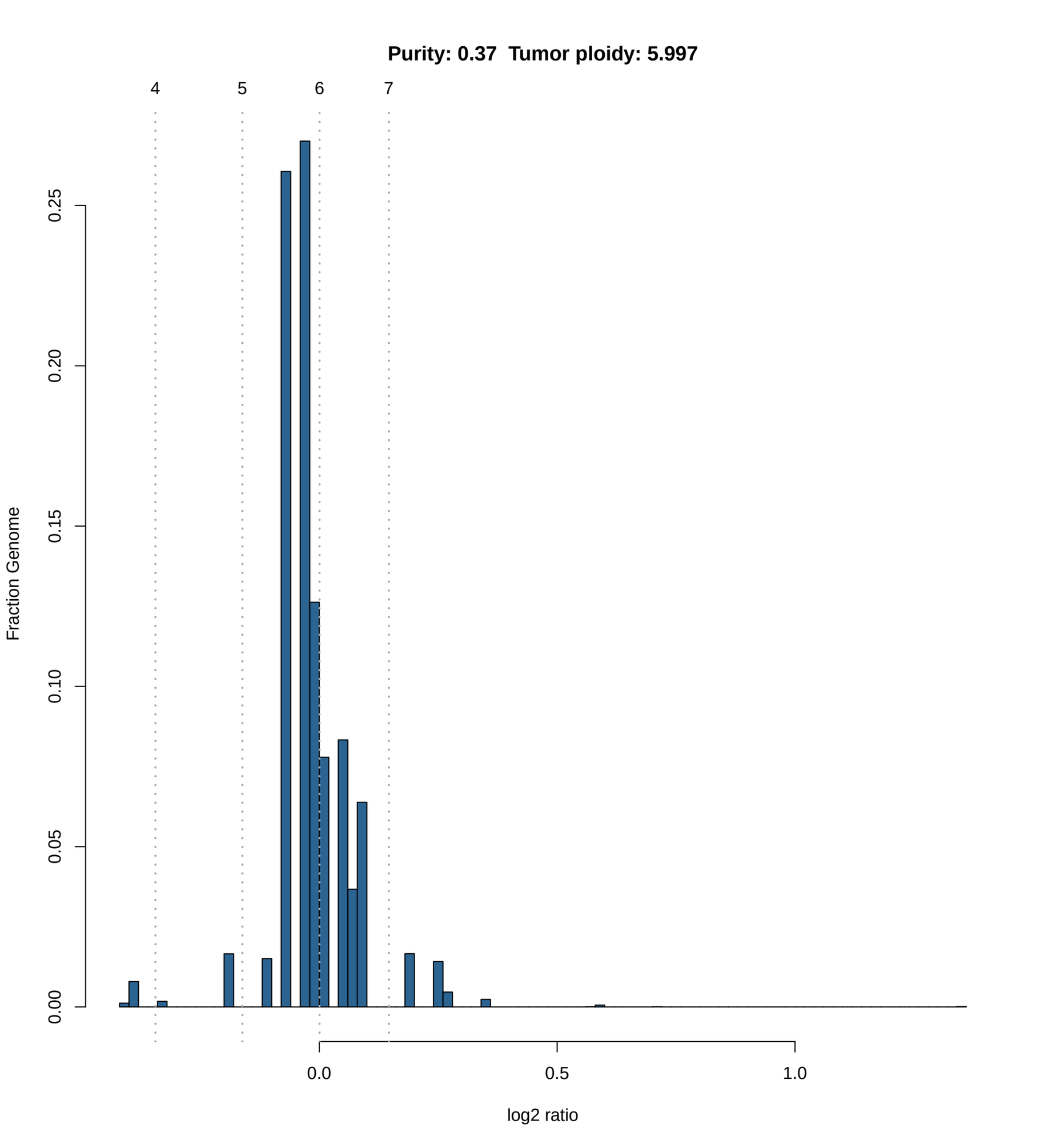

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

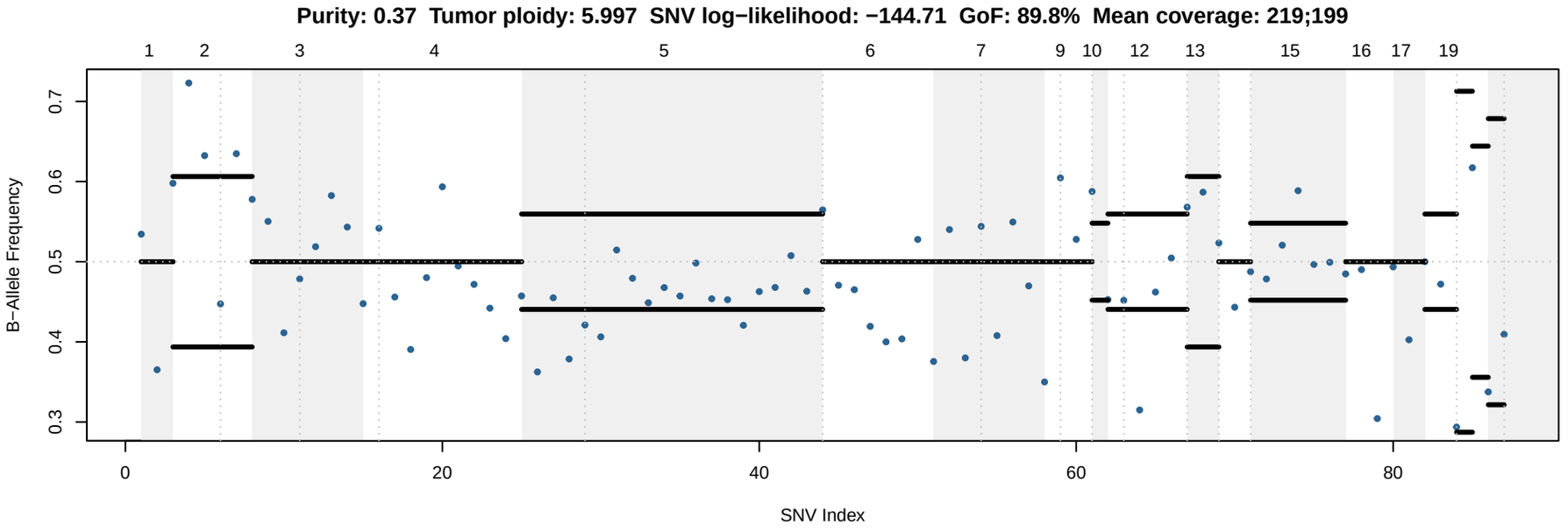

Allelic fraction (germline)
Copy Number log−ratio
5m4
7m5
6m4
5m3
7m4
4m2
6m3
7m3
5m2
6m2
5m1

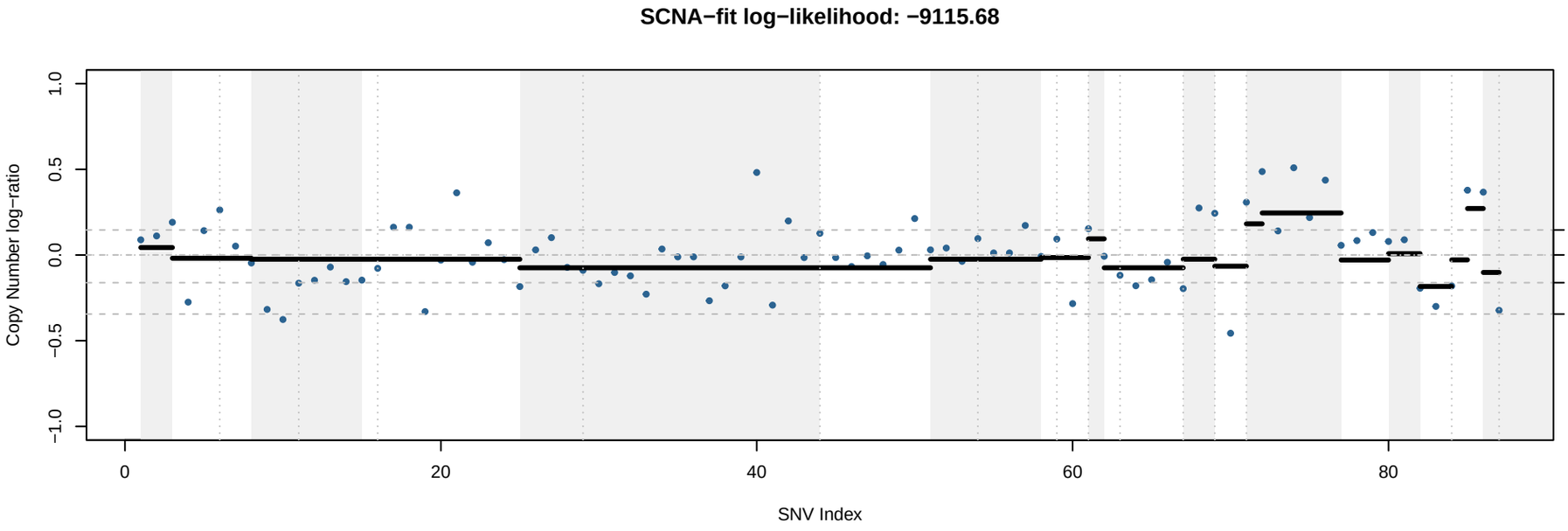

Coverage (log2)
Allelic fraction

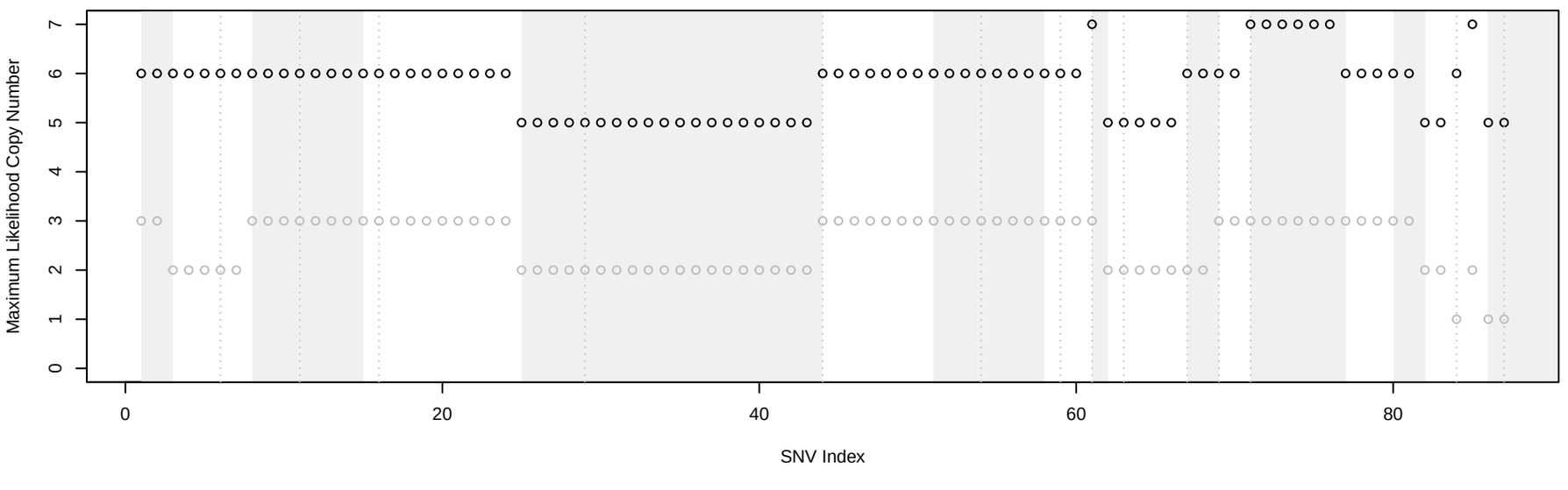

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m2
3m1
4m1
5m1
6m1
7m1

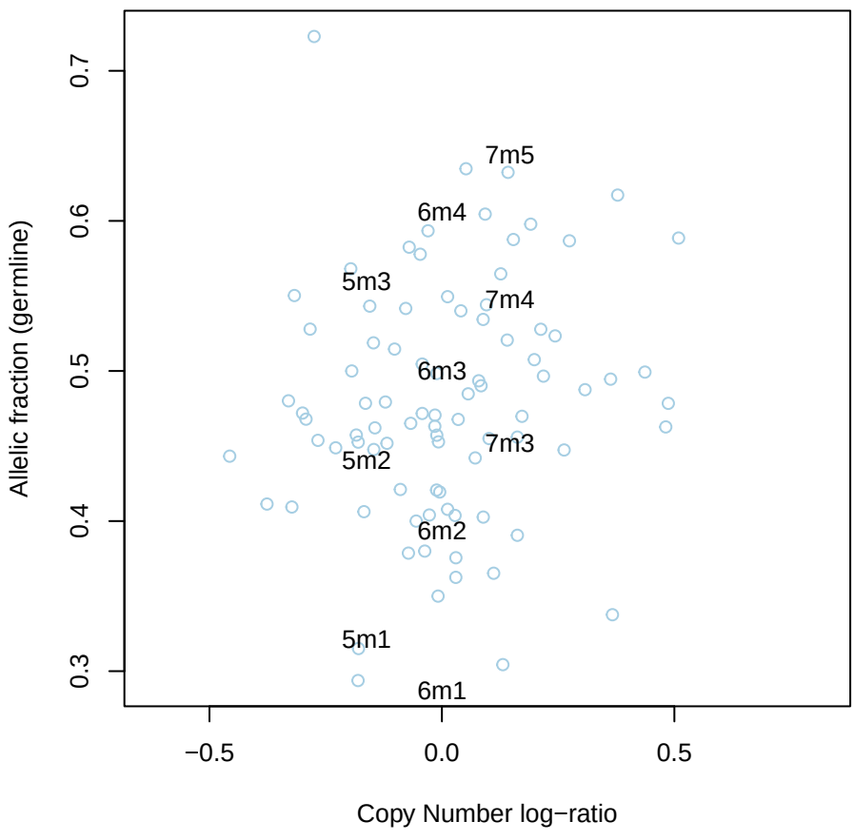

Power 0.8
Frequency
Cellular fraction

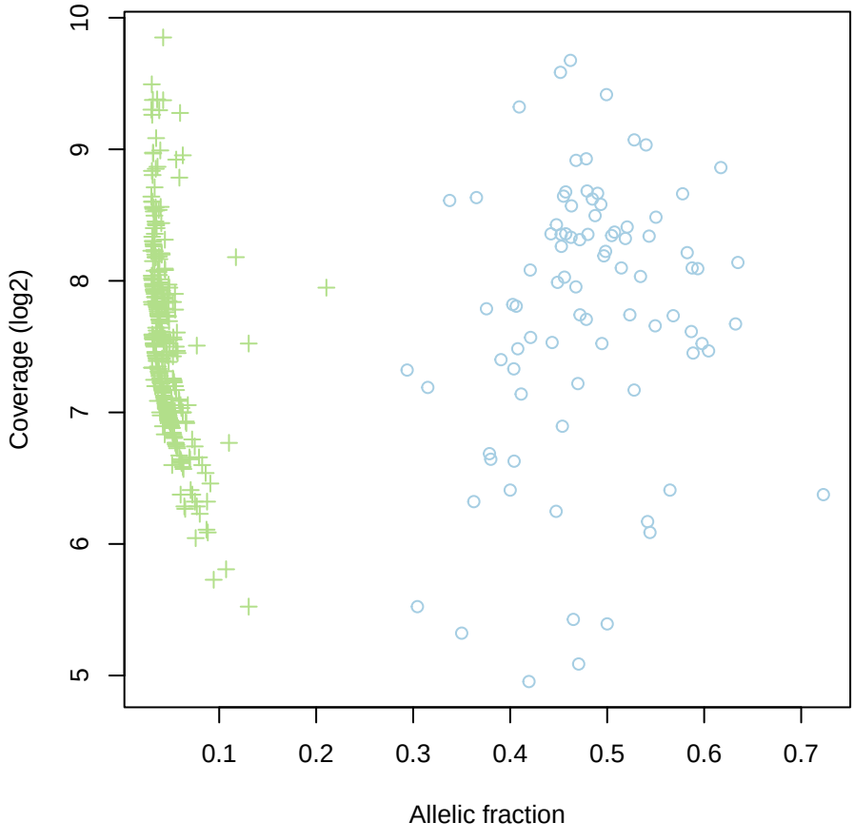

Purity: 0.37 Tumor ploidy: 5.997
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

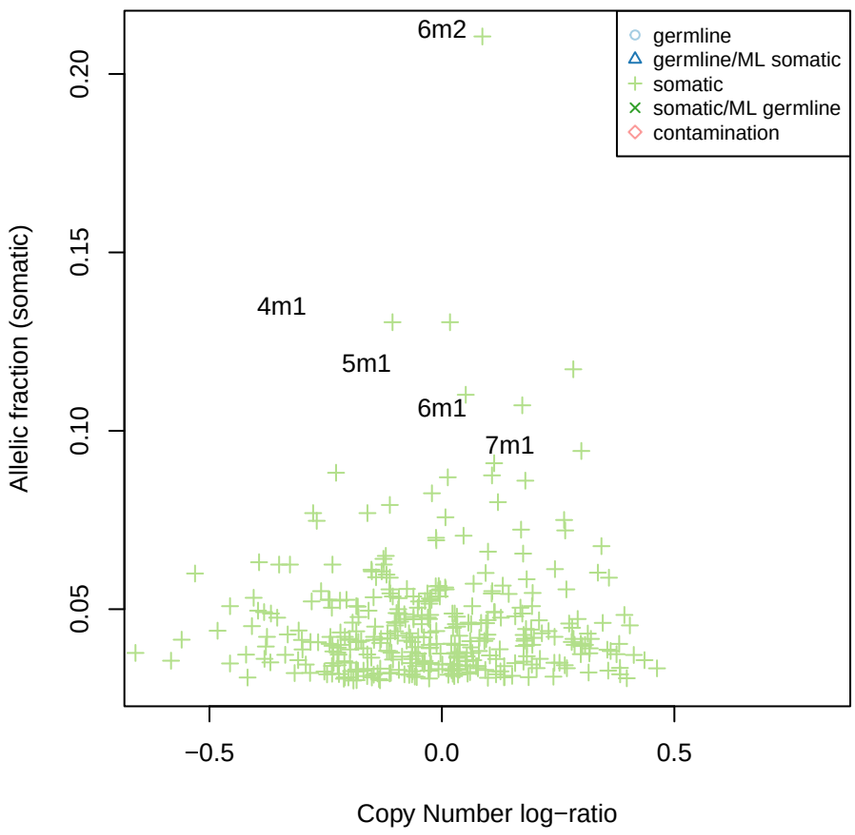

Purity: 0.37 Tumor ploidy: 5.997 SNV log−likelihood: −144.71 GoF: 89.8% Mean coverage: 219;199
1 2 3 4 5 6 7 9 10 12 13 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

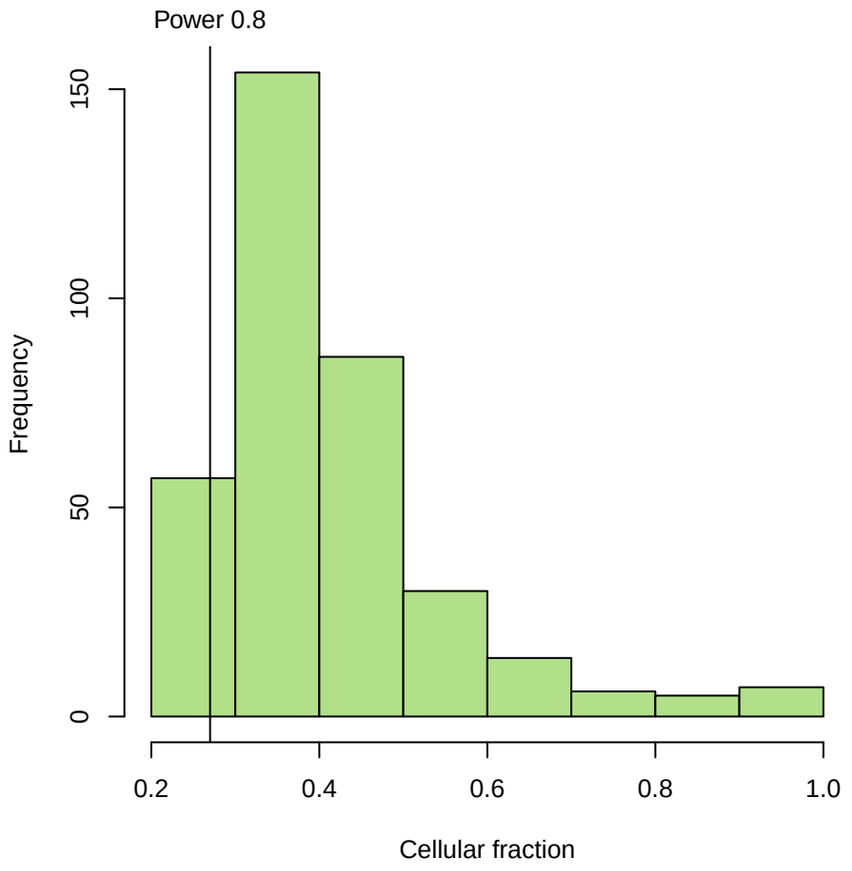

SCNA−fit log−likelihood: −9115.68
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5 6 7
0 20 40 60 80
SNV Index

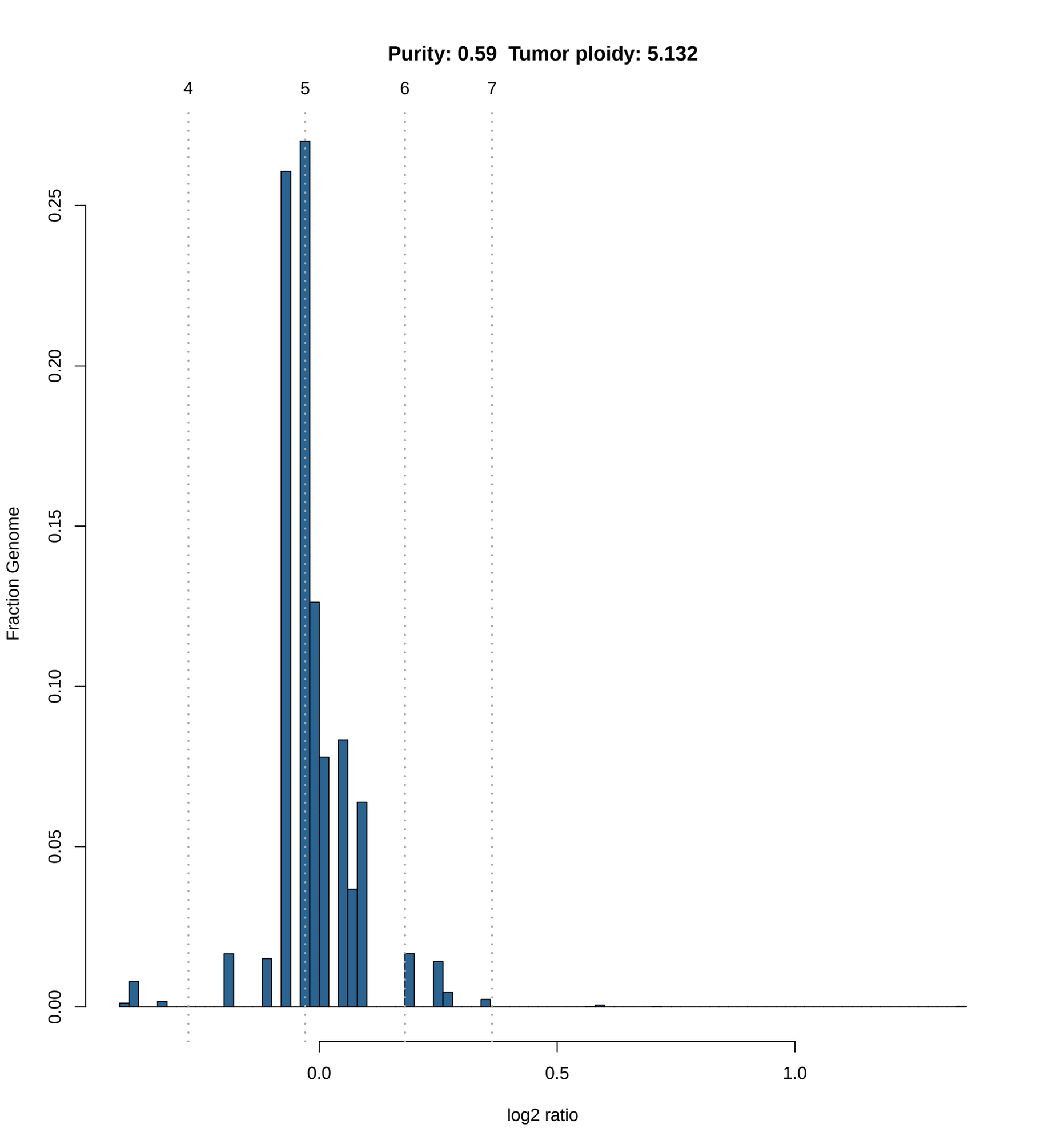

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

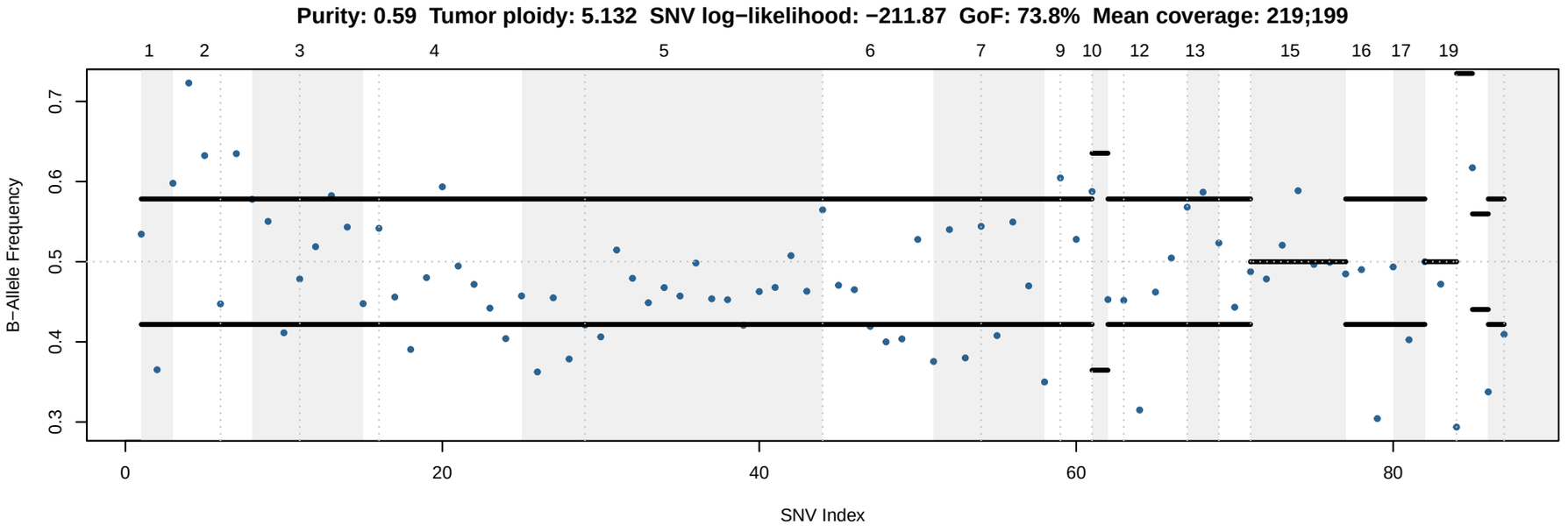

Allelic fraction (germline)
Copy Number log−ratio
7m5
6m4
5m3
7m4
6m3
7m3
5m2
6m2
5m1
6m1

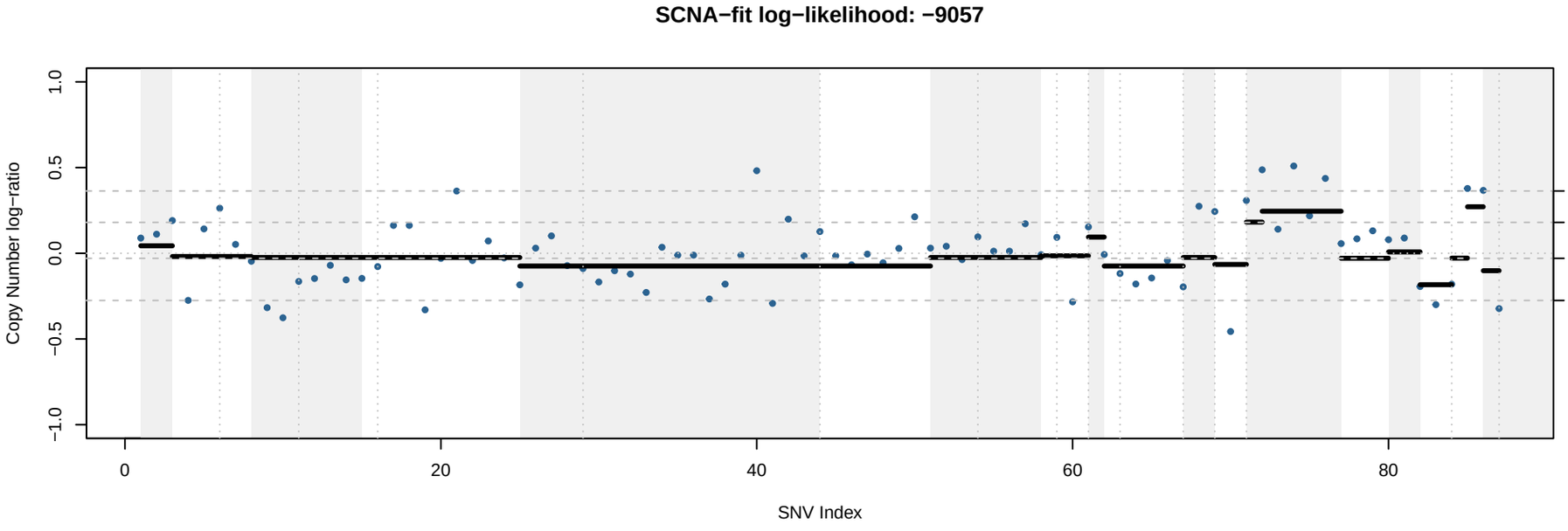

Coverage (log2)
Allelic fraction

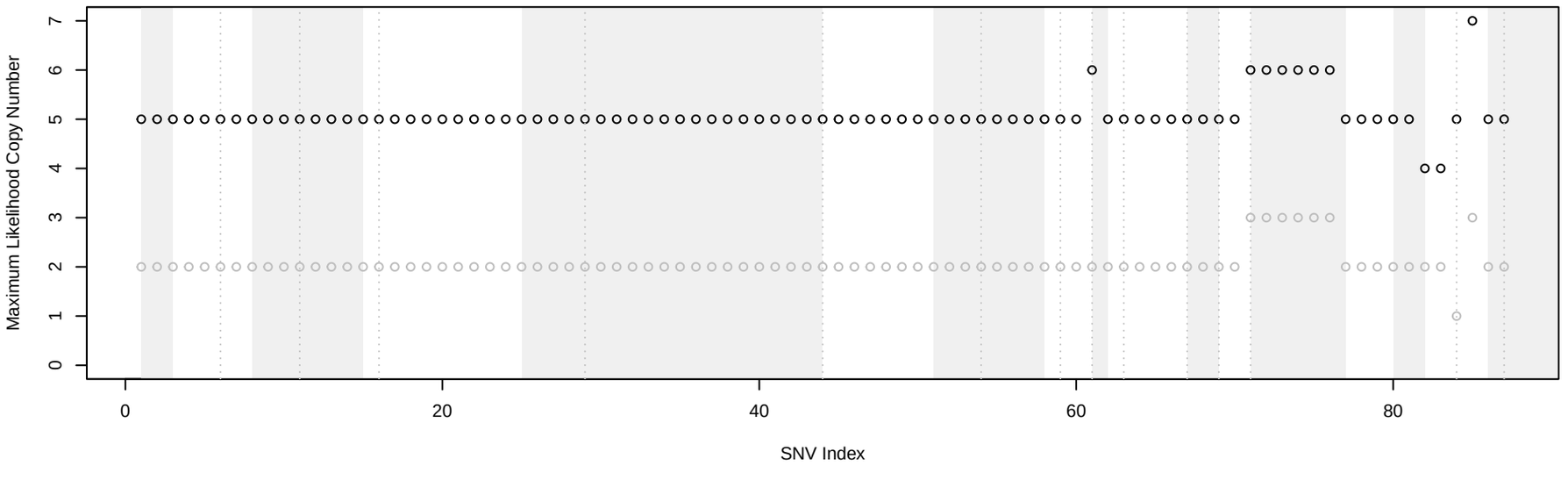

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m2
4m1
5m1
6m1
7m1

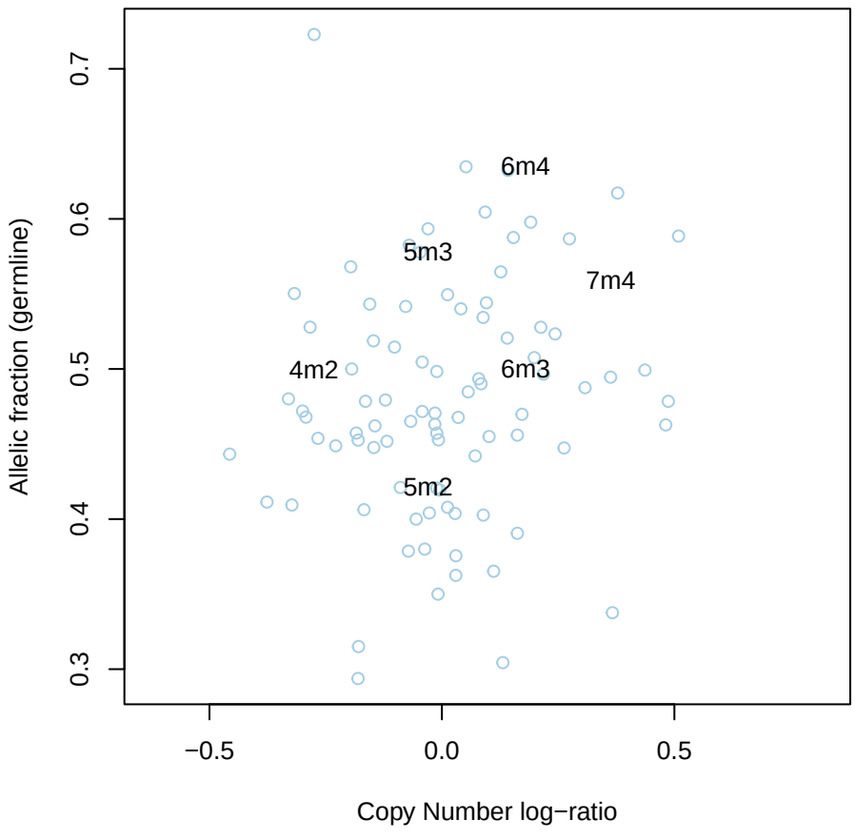

Power 0.8
Frequency
Cellular fraction

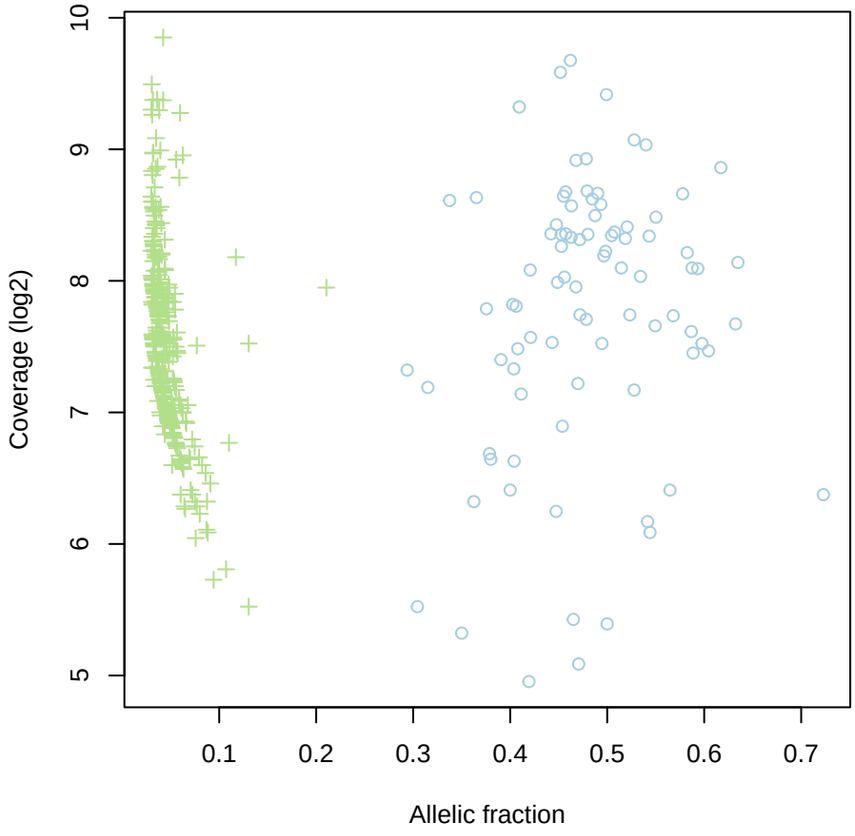

Purity: 0.59 Tumor ploidy: 5.132
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

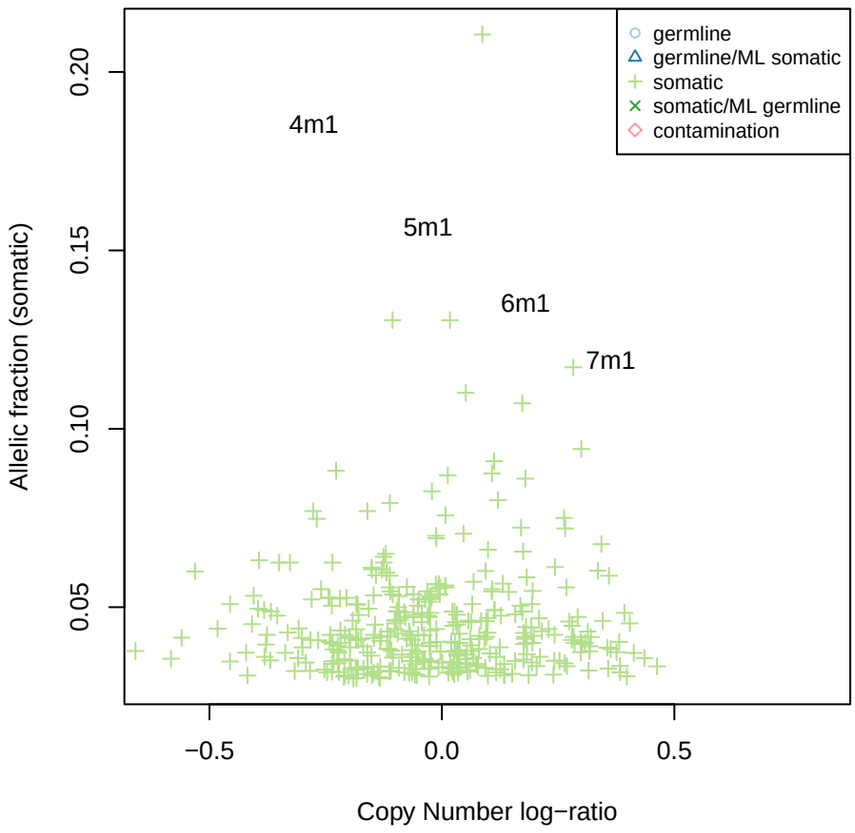

Purity: 0.59 Tumor ploidy: 5.132 SNV log−likelihood: −211.87 GoF: 73.8% Mean coverage: 219;199
1 2 3 4 5 6 7 9 10 12 13 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

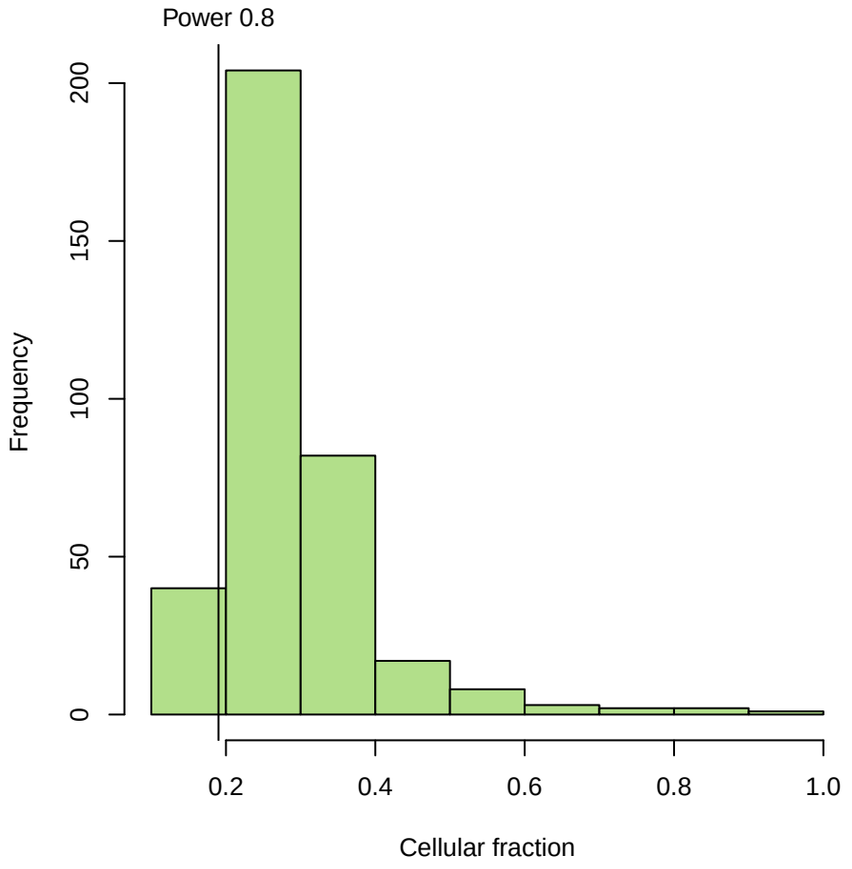

SCNA−fit log−likelihood: −9057
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5 6 7
0 20 40 60 80
SNV Index

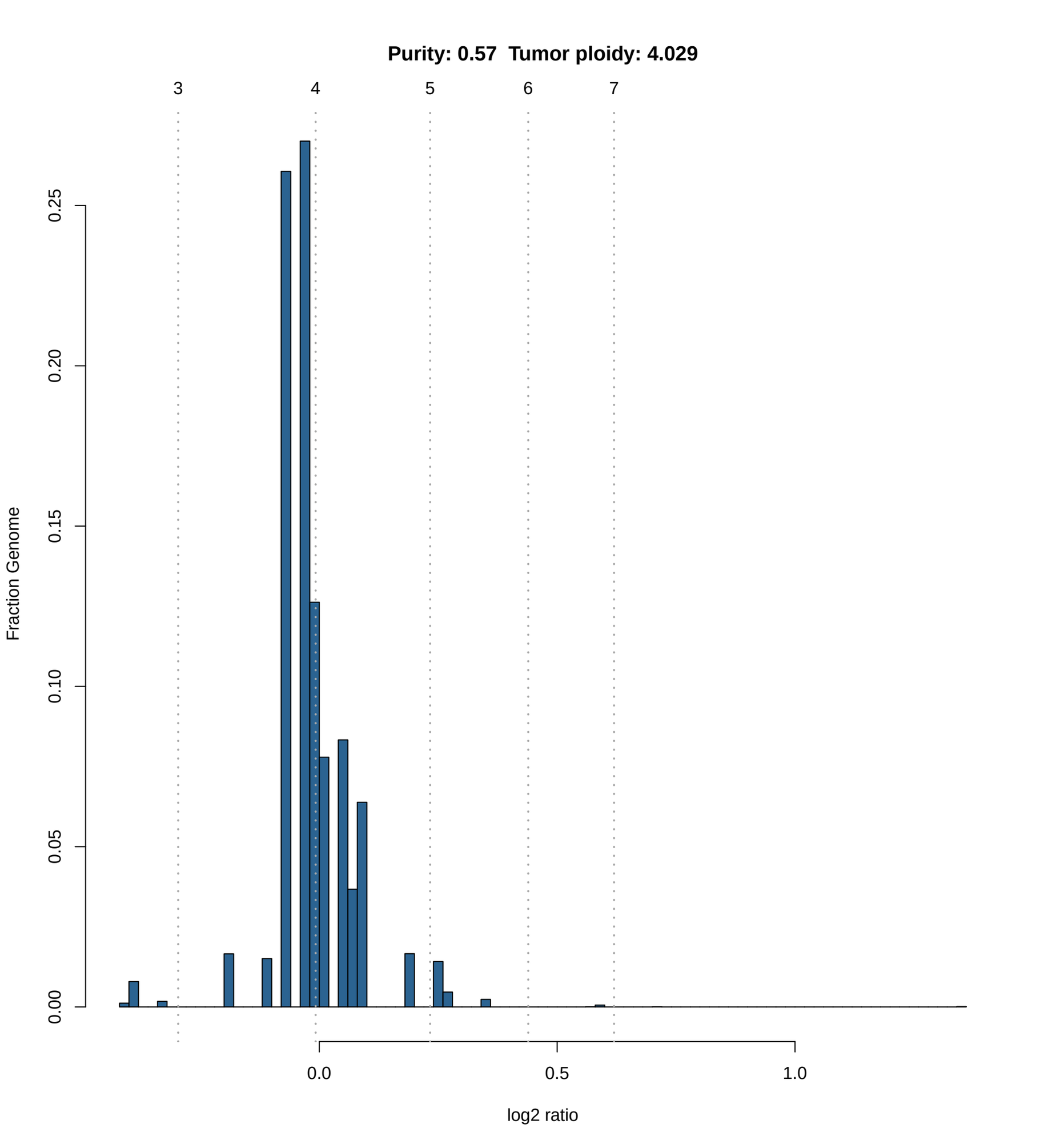

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

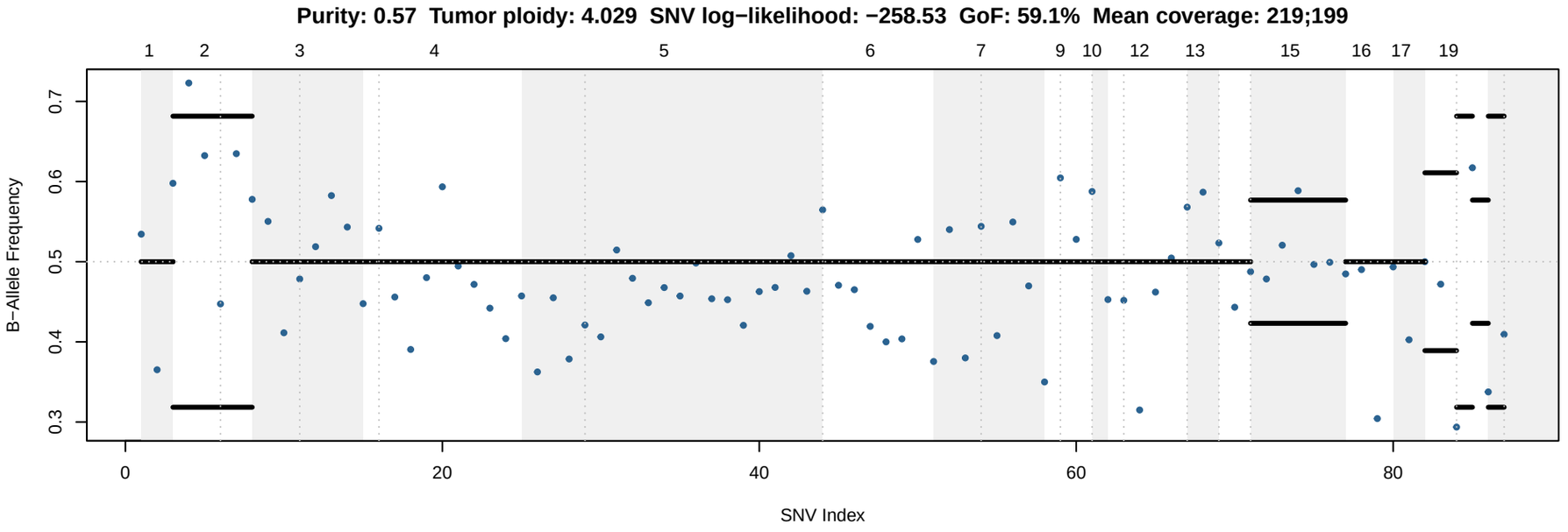

Allelic fraction (germline)
Copy Number log−ratio
6m4
5m3
7m4
4m2
6m3
5m2

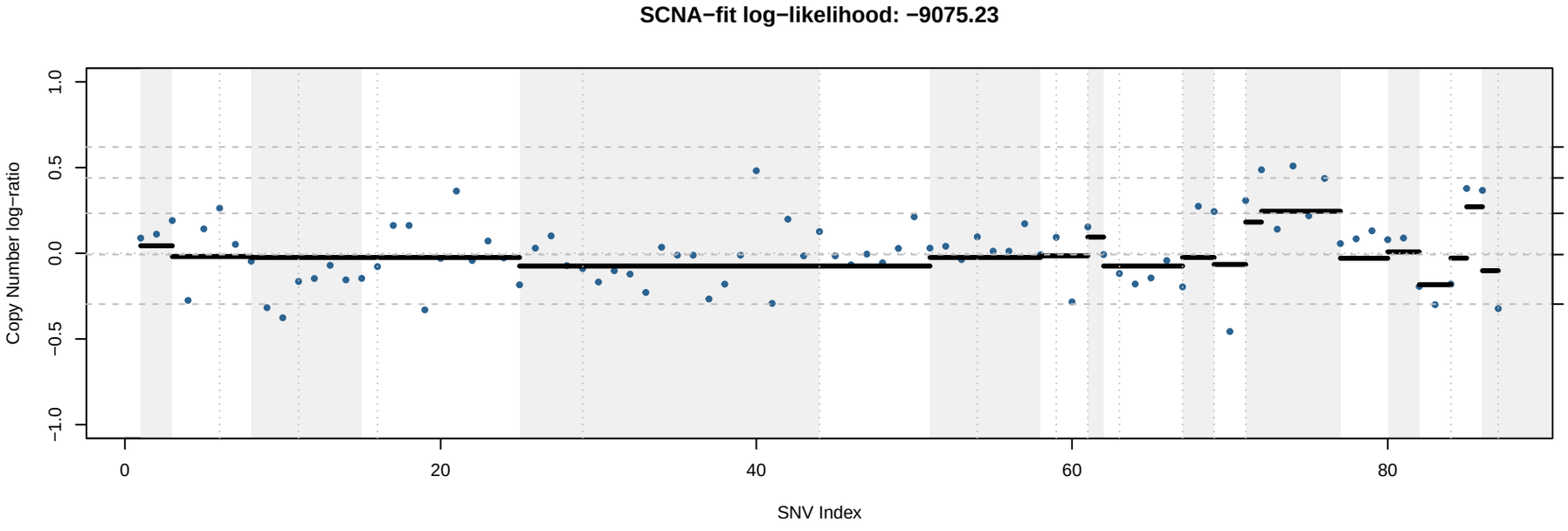

Coverage (log2)
Allelic fraction

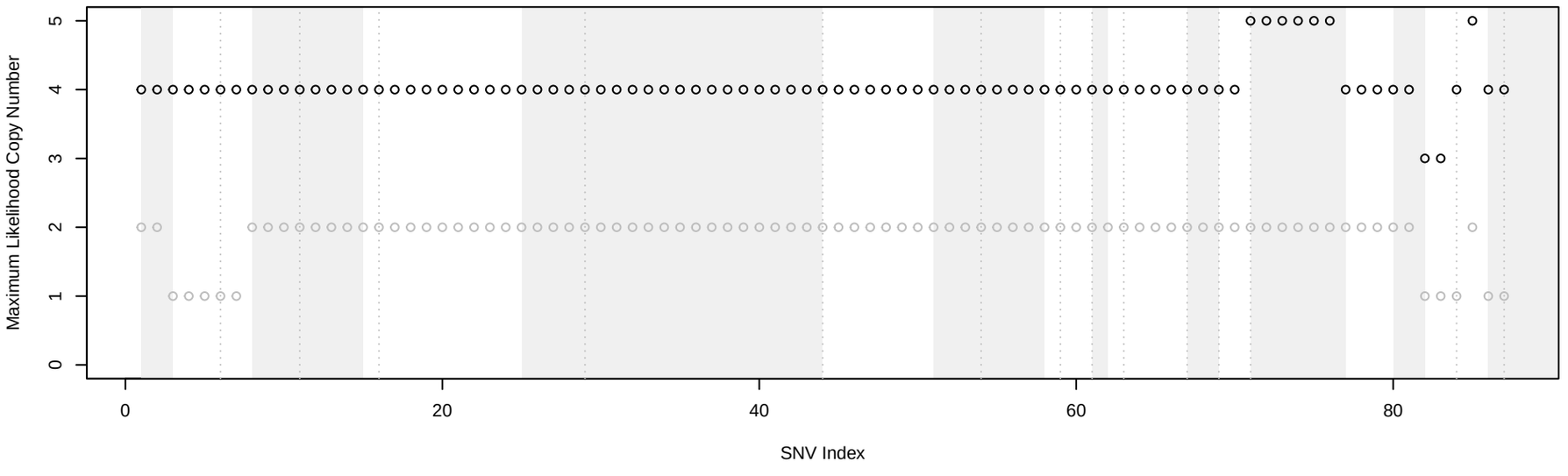

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
7m1

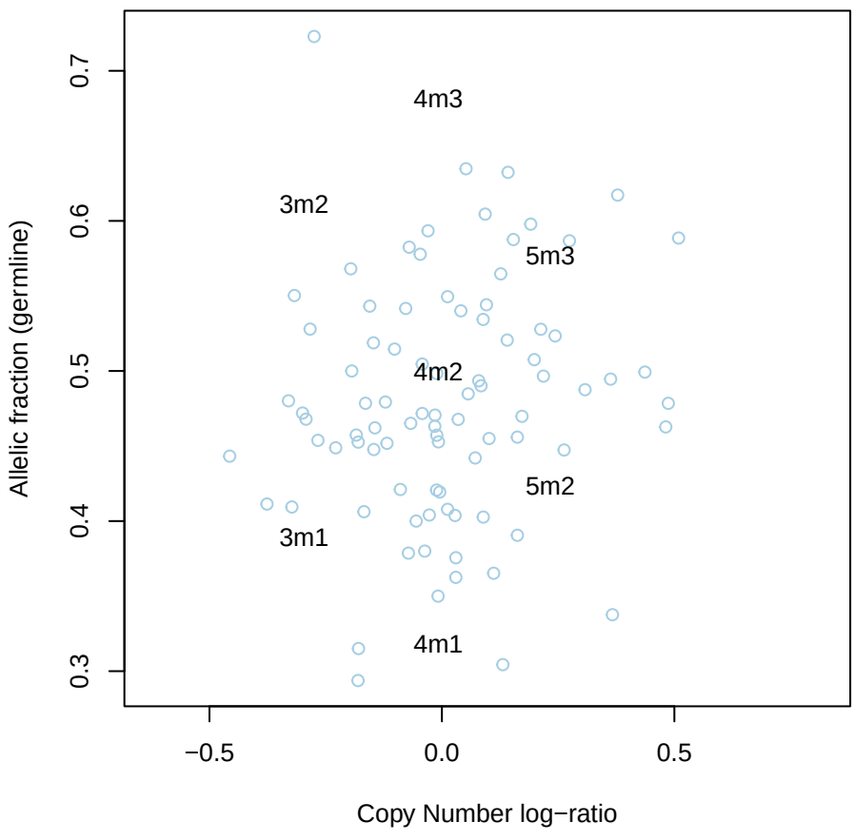

Power 0.8
Frequency
Cellular fraction

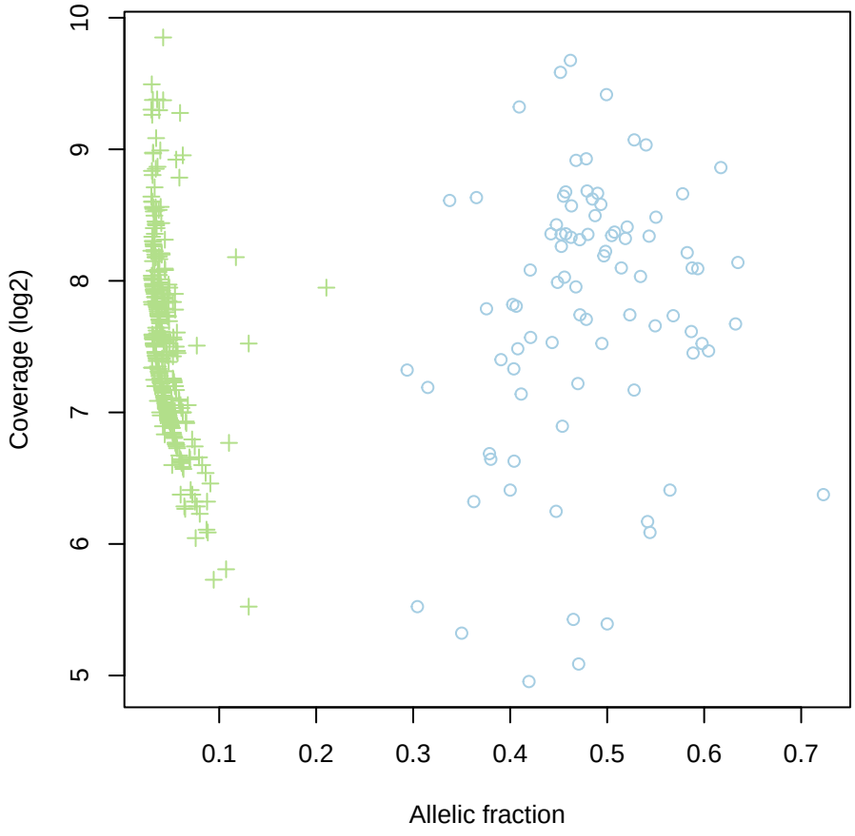

Purity: 0.57 Tumor ploidy: 4.029
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

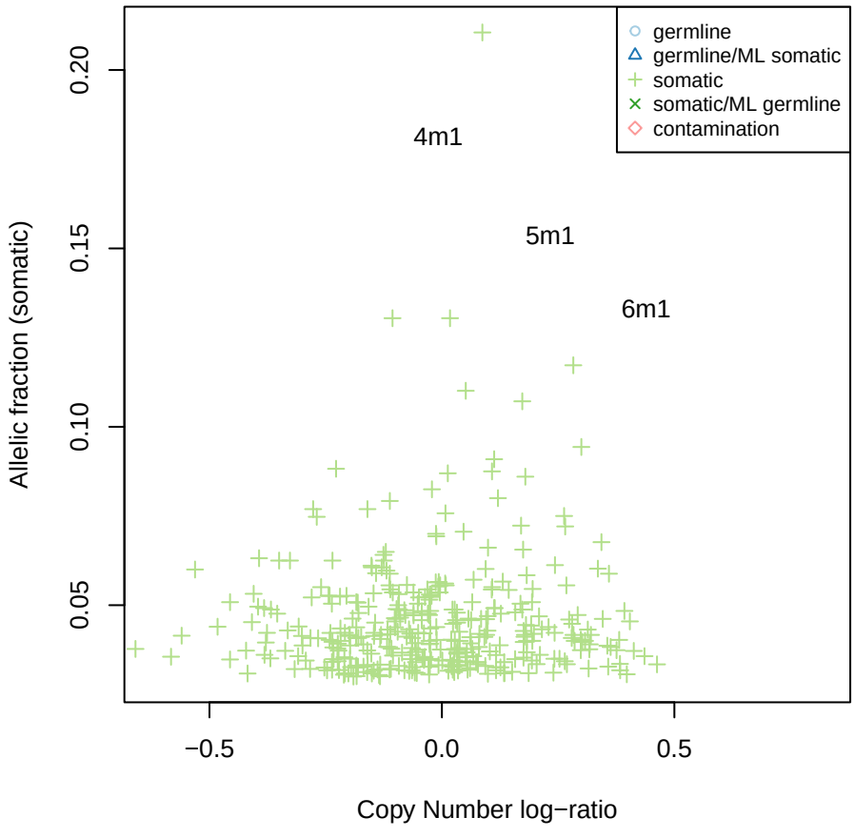

Purity: 0.57 Tumor ploidy: 4.029 SNV log−likelihood: −258.53 GoF: 59.1% Mean coverage: 219;199
1 2 3 4 5 6 7 9 10 12 13 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

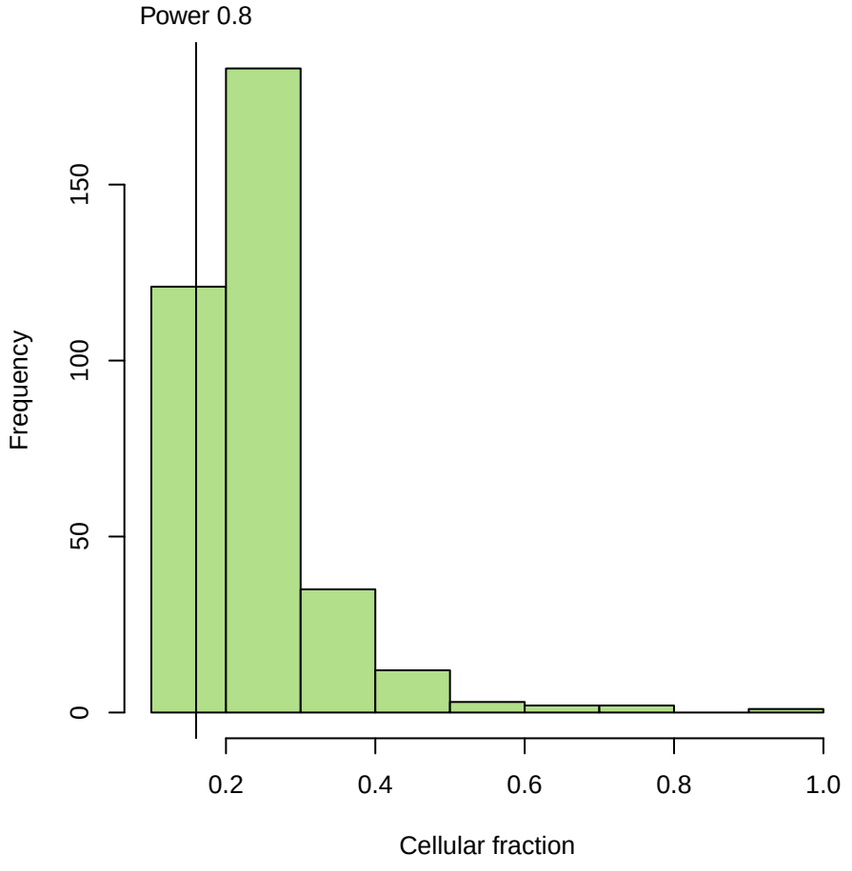

SCNA−fit log−likelihood: −9075.23
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 20 40 60 80
SNV Index

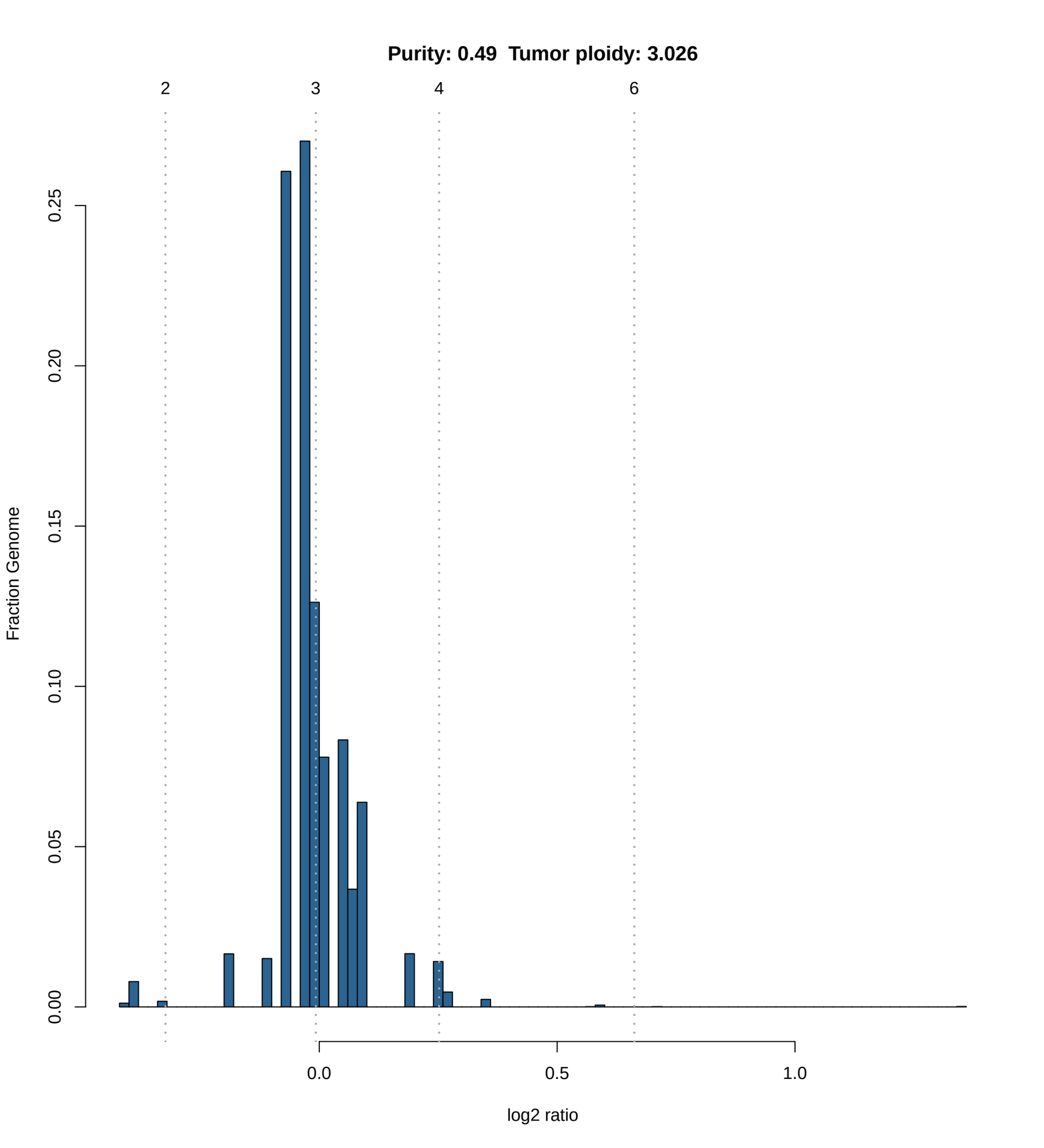

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80
SNV Index

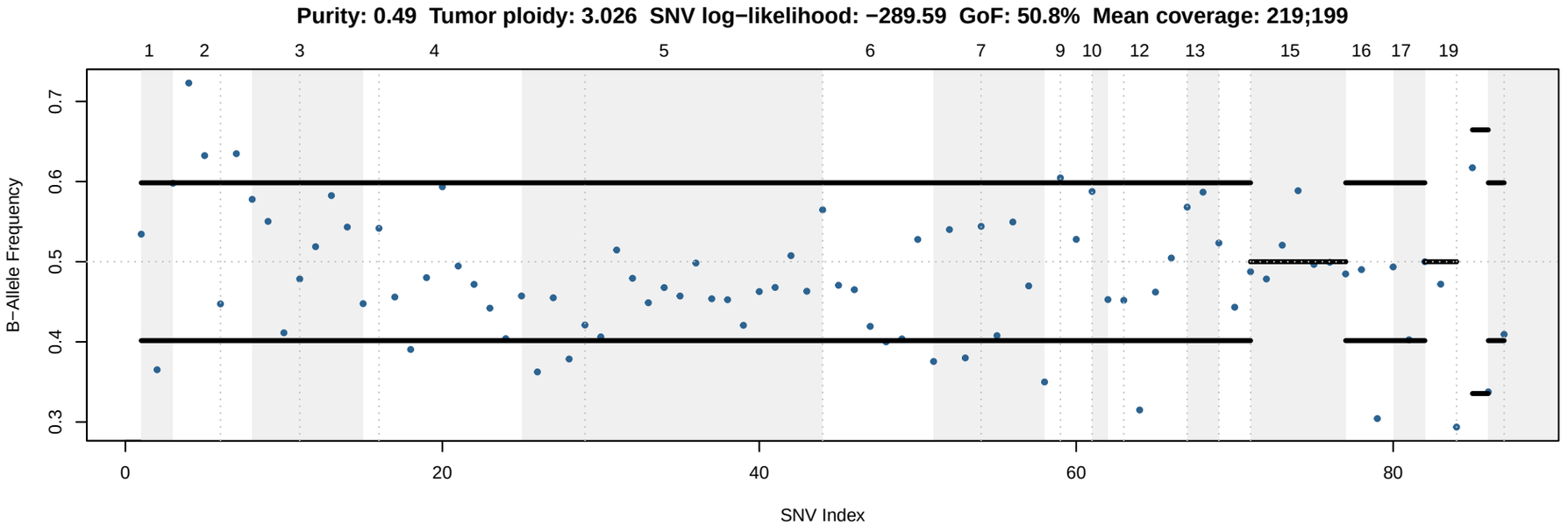

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
5m3
4m2
5m2
3m1
4m1

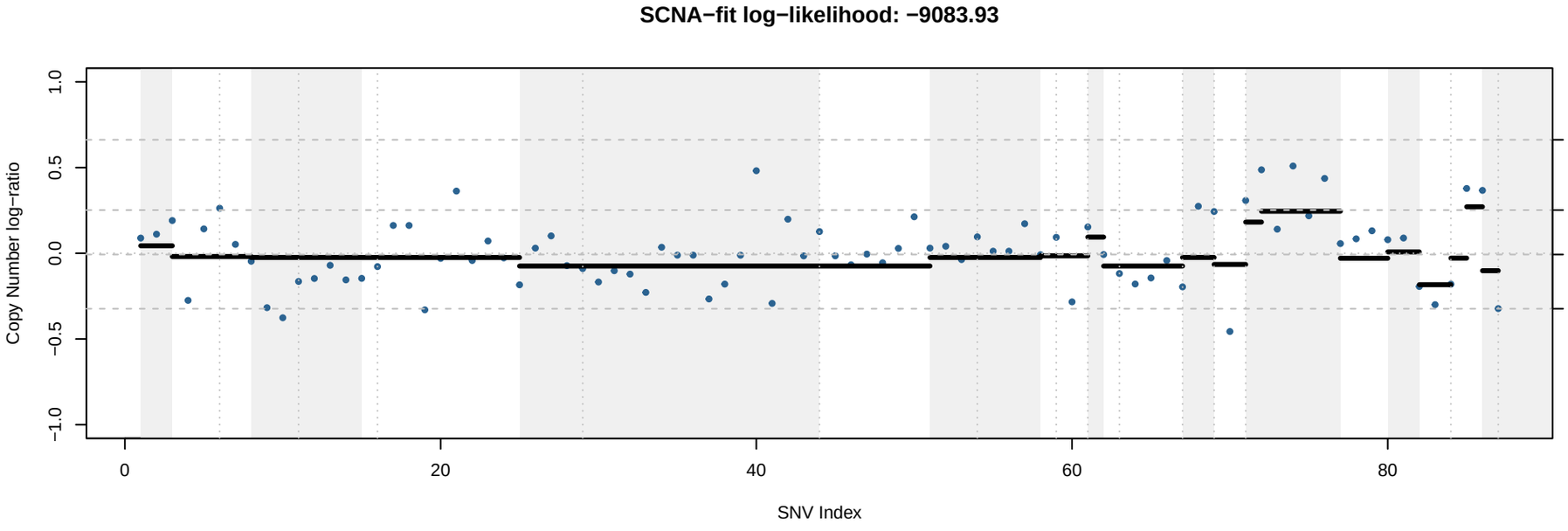

Coverage (log2)
Allelic fraction

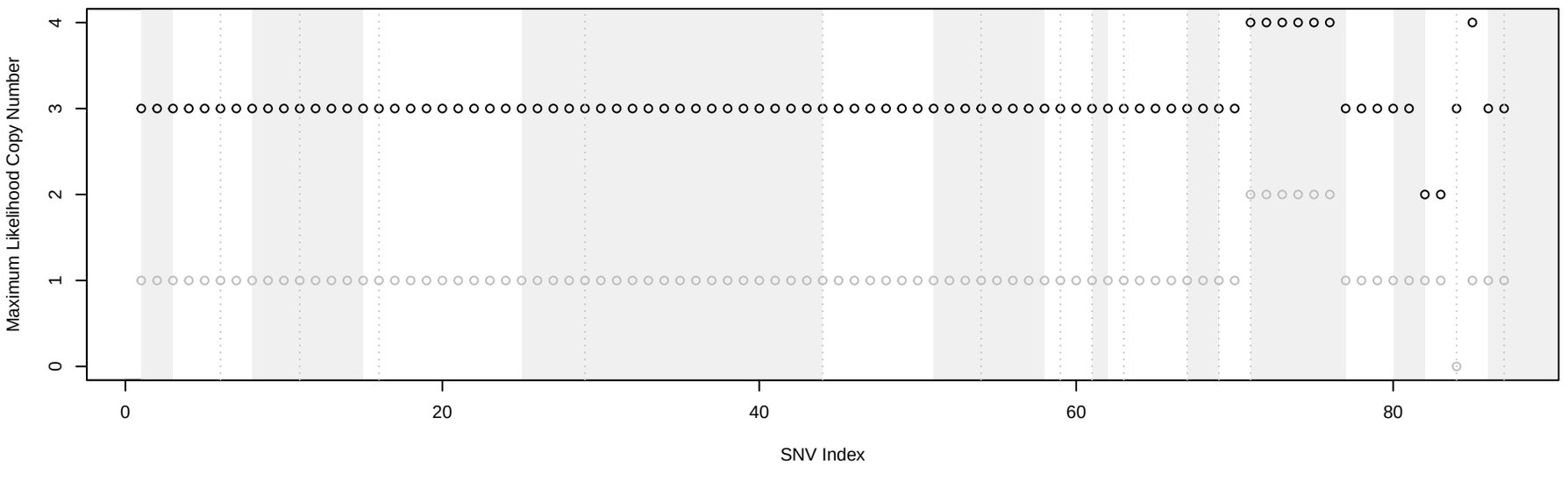

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
4m1
5m1
6m1

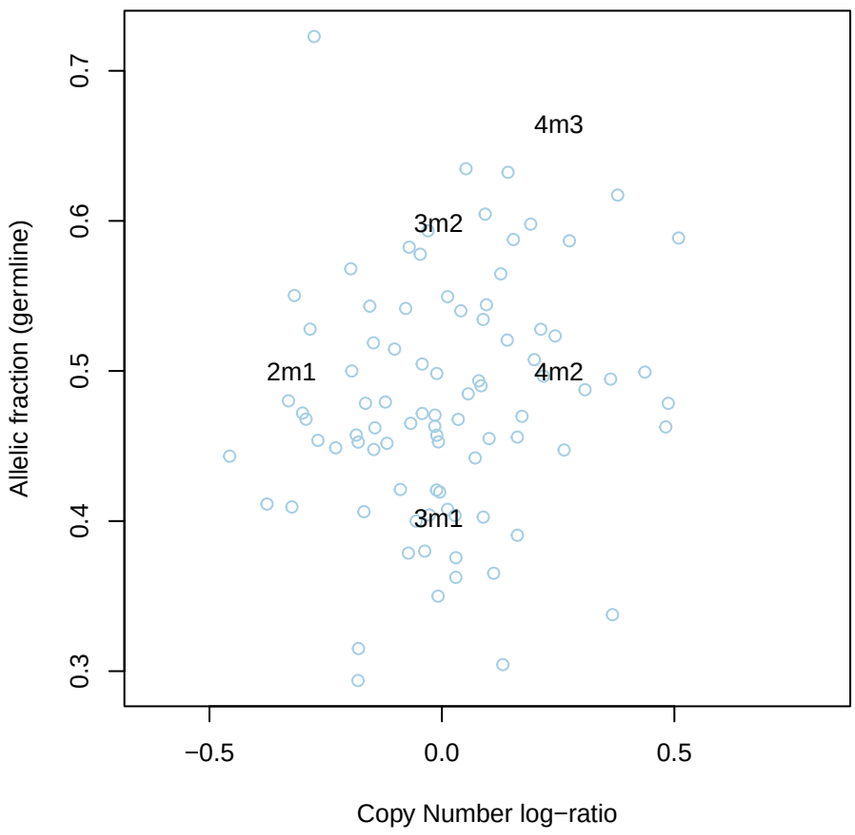

Power 0.8
Frequency
Cellular fraction

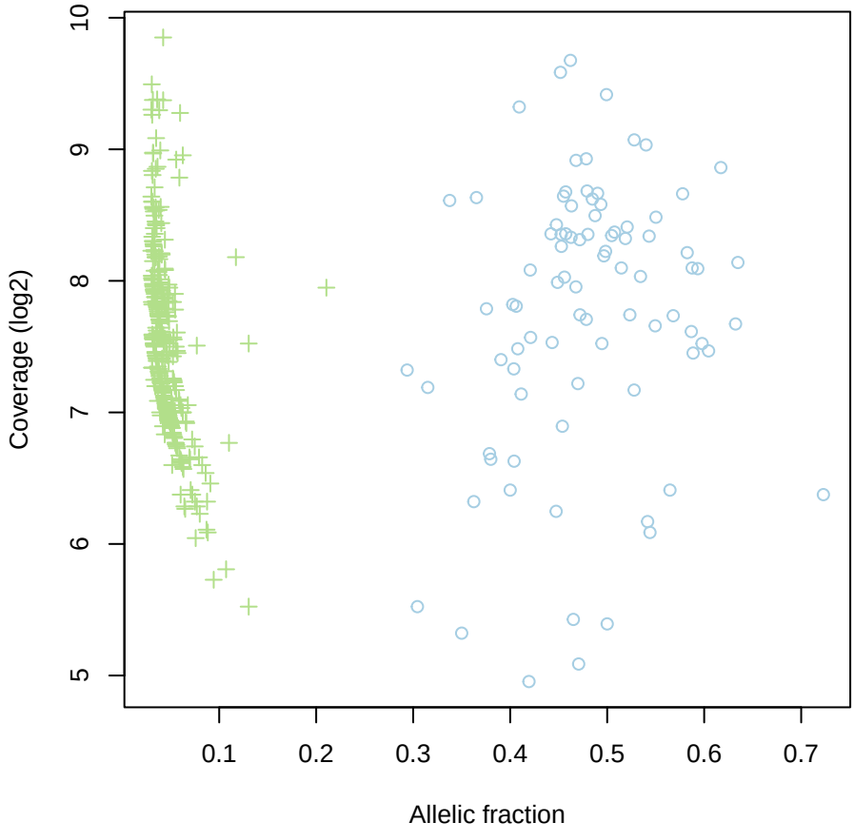

Purity: 0.49 Tumor ploidy: 3.026
2
3
4
6
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

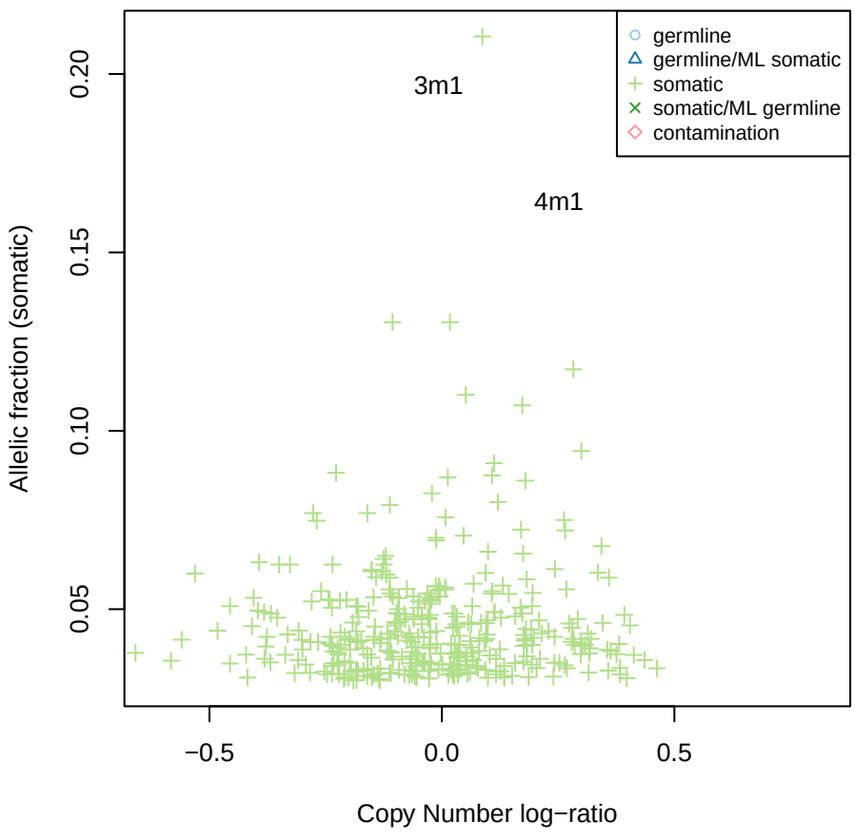

Purity: 0.49 Tumor ploidy: 3.026 SNV log−likelihood: −289.59 GoF: 50.8% Mean coverage: 219;199
1 2 3 4 5 6 7 9 10 12 13 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

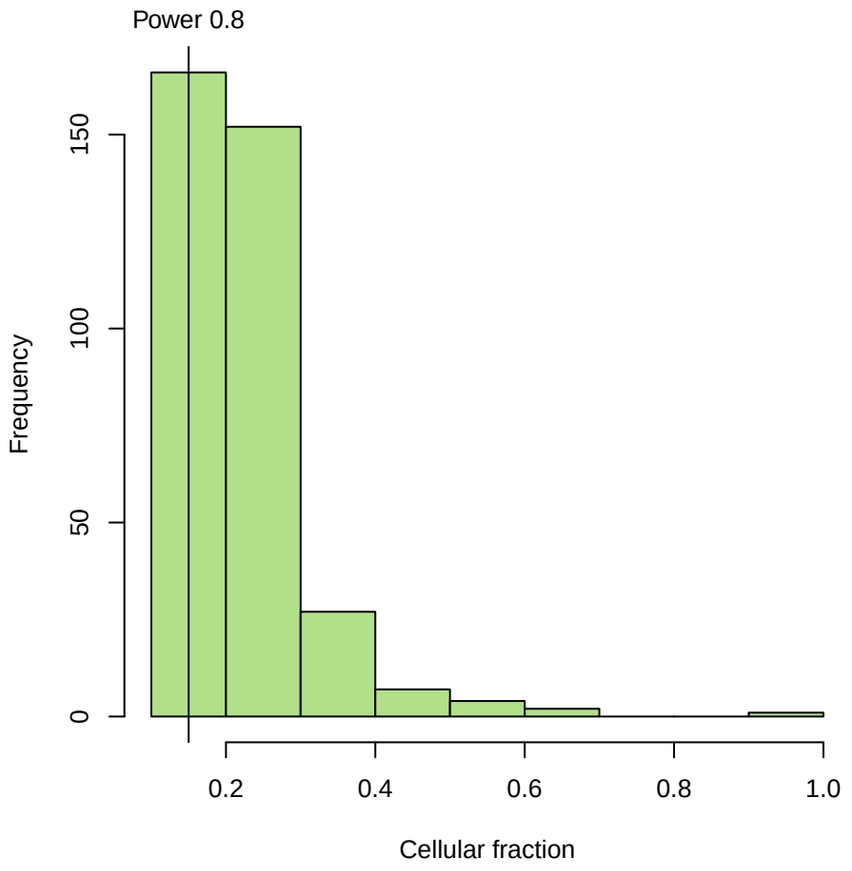

SCNA−fit log−likelihood: −9083.93
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 6
0 20 40 60 80
SNV Index

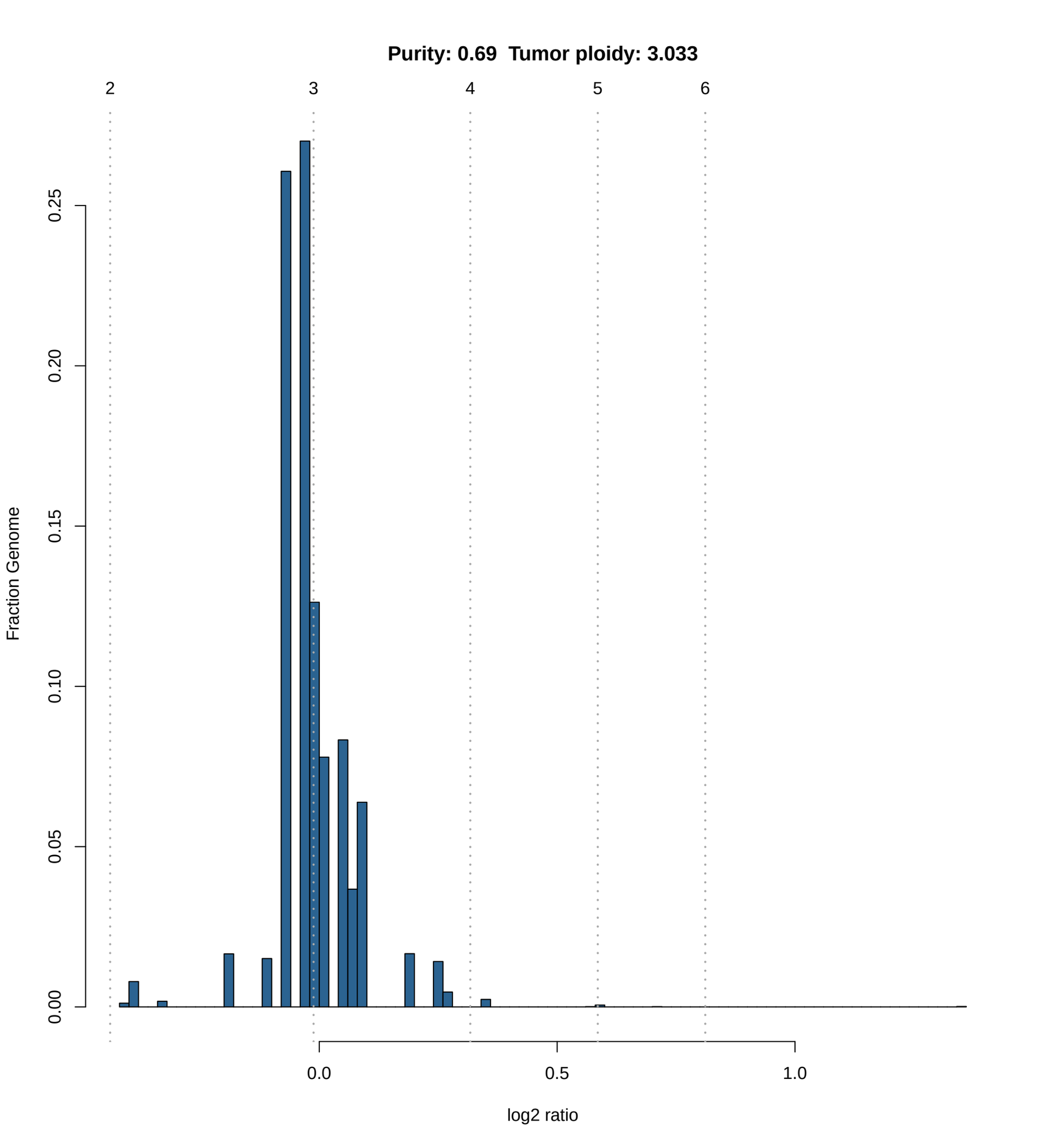

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80
SNV Index

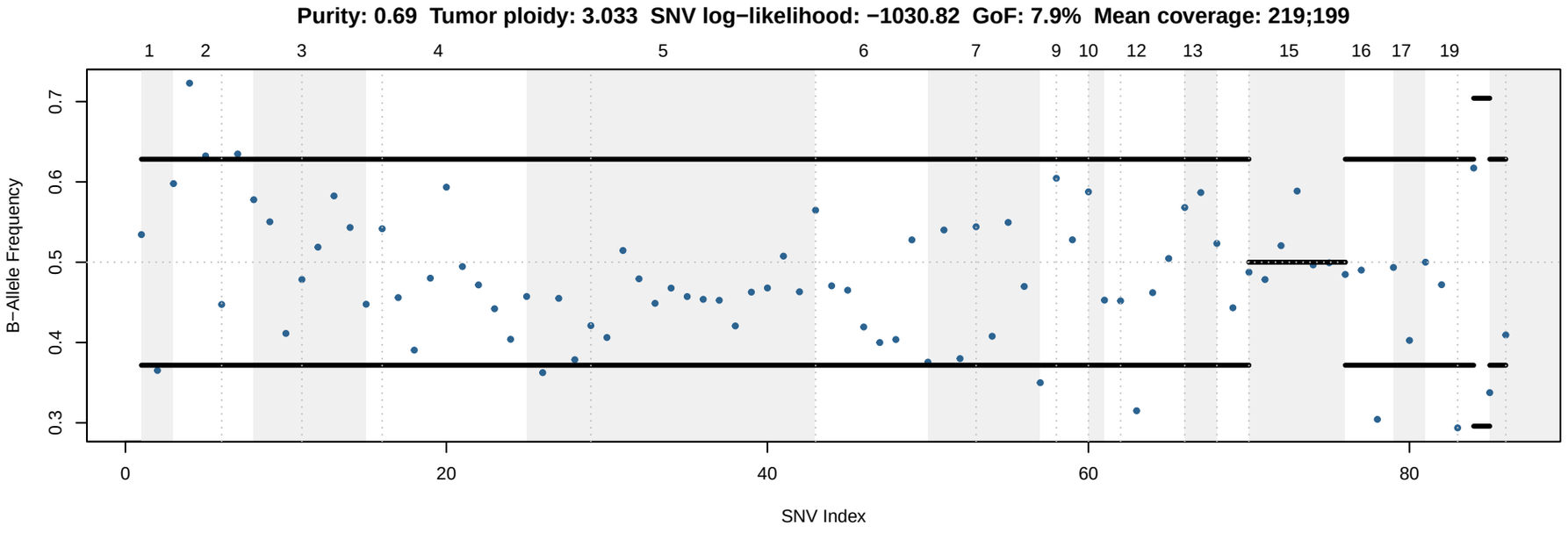

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
−0.5
0.0
0.5
Copy Number log−ratio
4m3
3m2
2m1
4m2
3m1

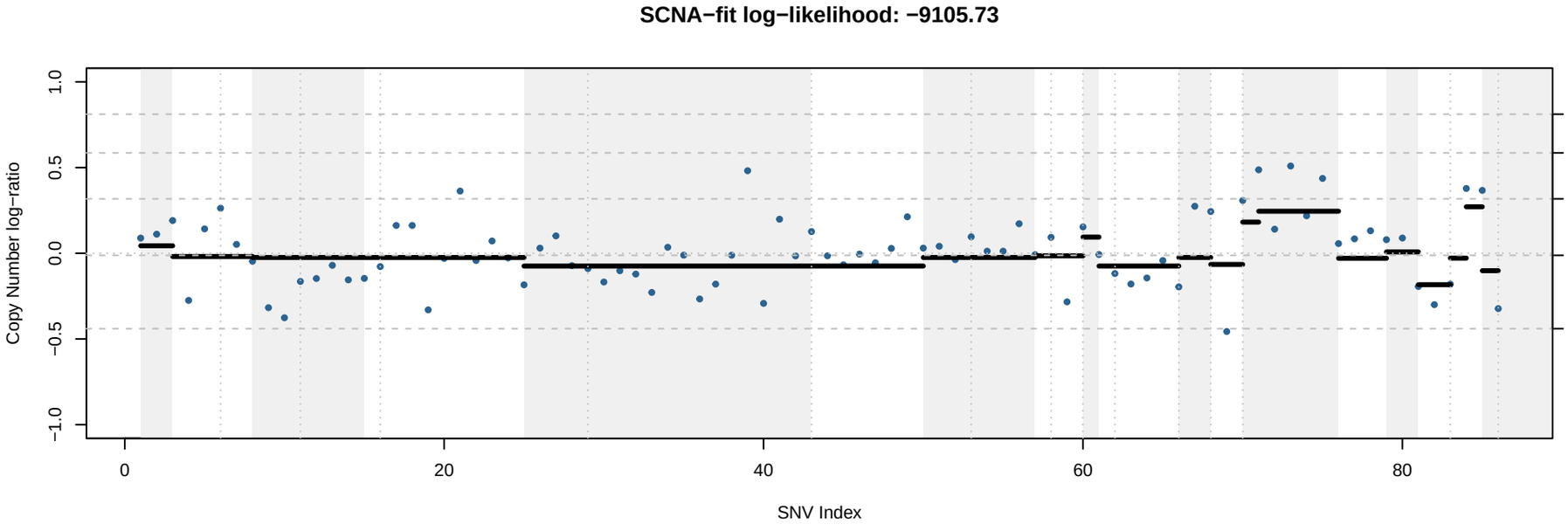

Coverage (log2)
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

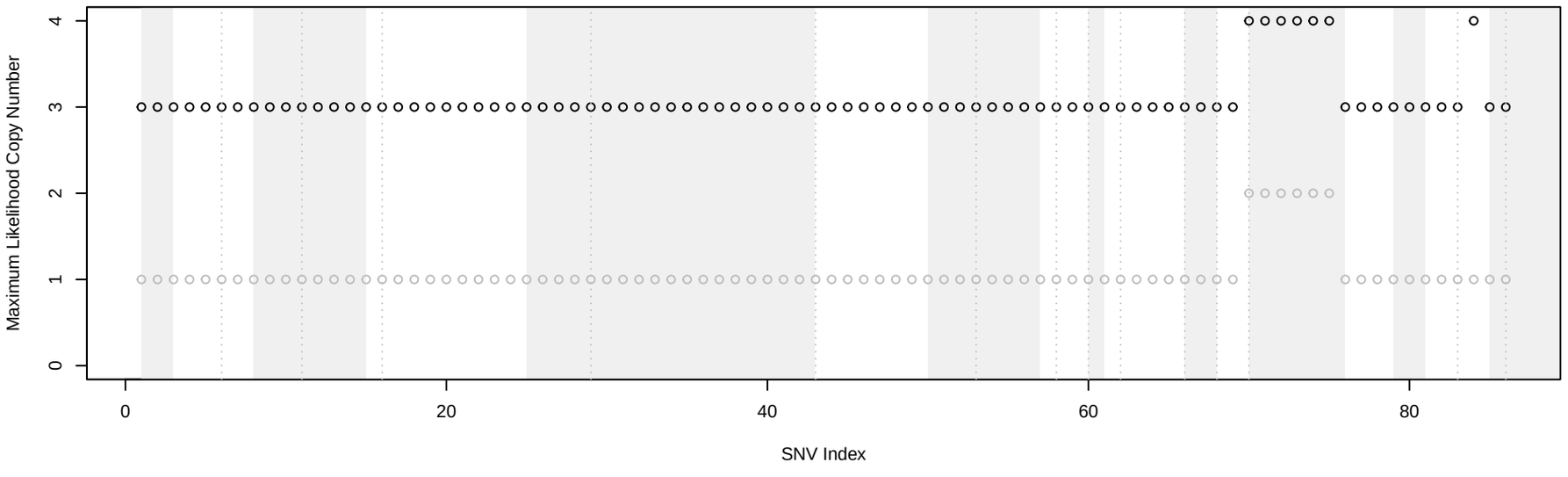

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
−0.5
0.0
0.5
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1

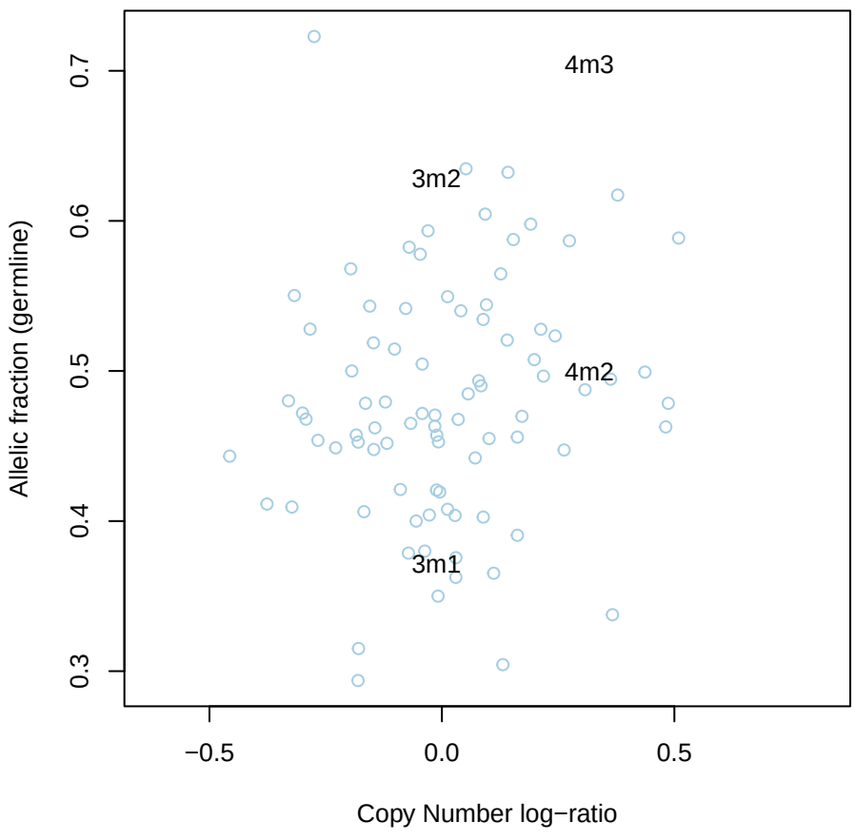

Power 0.8
Frequency
0
50
100
150
0.2
0.4
0.6
0.8
1.0
Cellular fraction

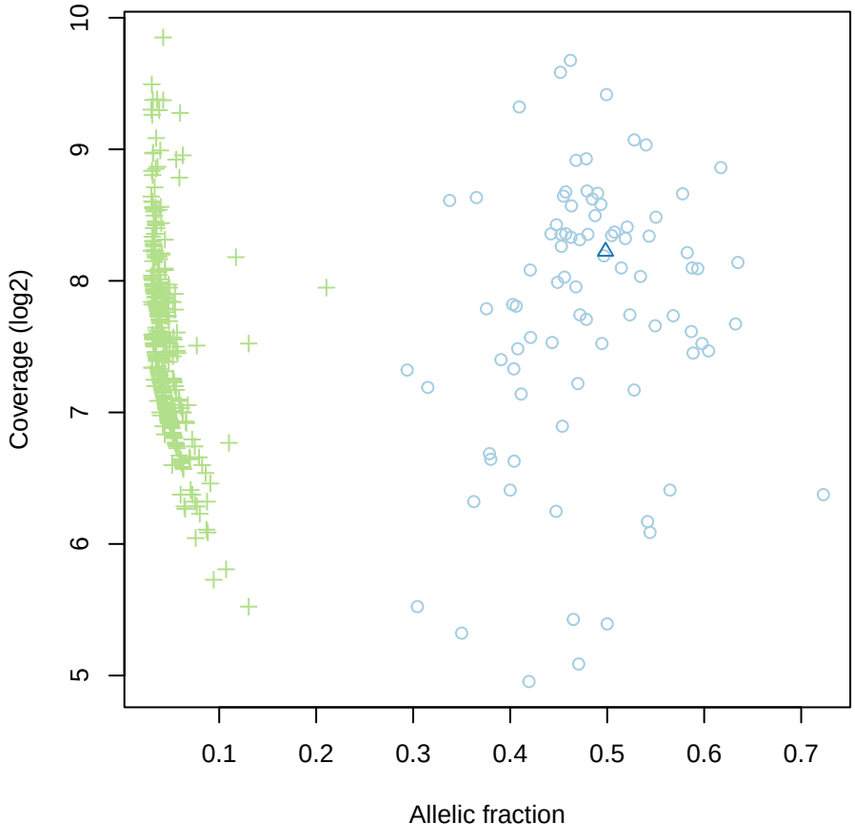

Purity: 0.69 Tumor ploidy: 3.033
2
3
4
5
6
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

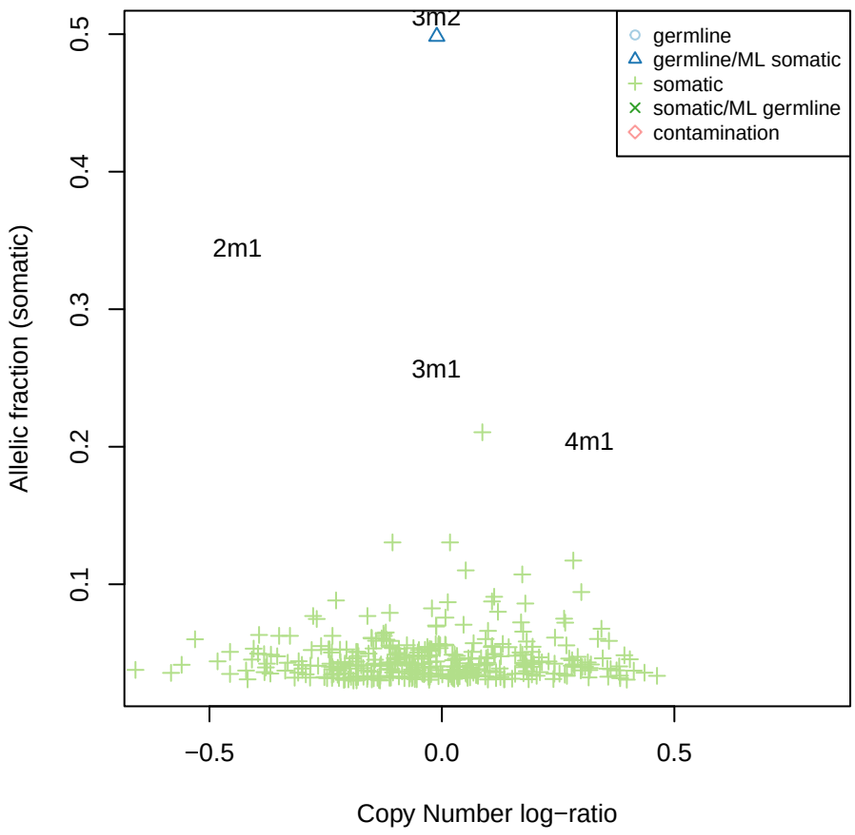

Purity: 0.69 Tumor ploidy: 3.033 SNV log−likelihood: −1030.82 GoF: 7.9% Mean coverage: 219;199
1 2 3 4 5 6 7 9 10 12 13 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

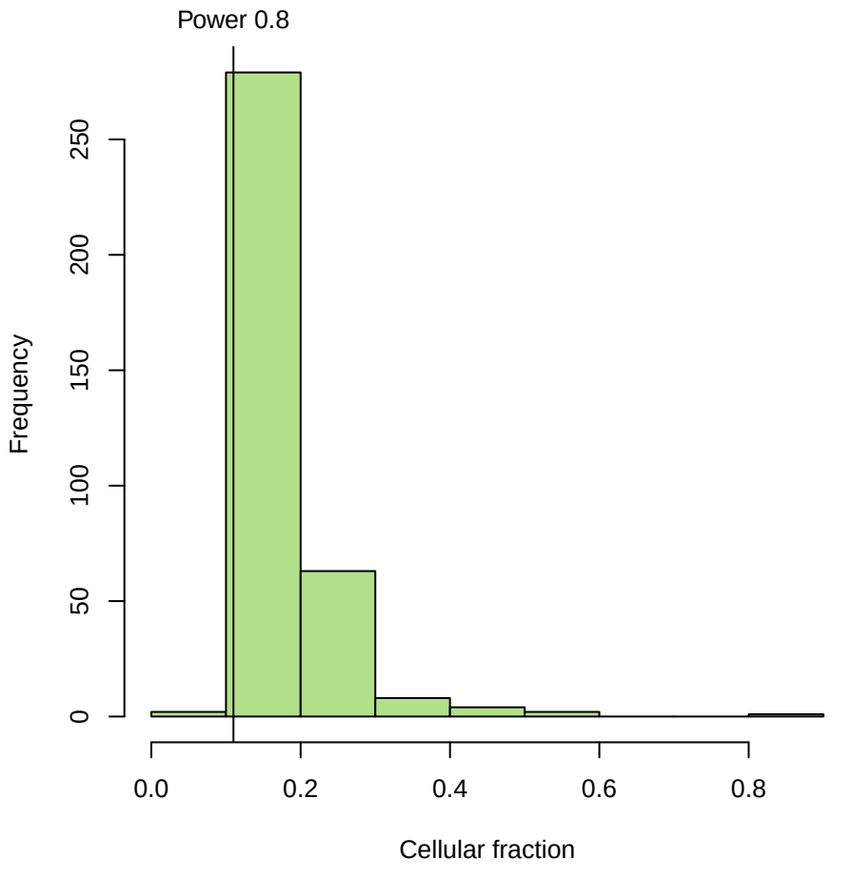

SCNA−fit log−likelihood: −9105.73
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6
0 20 40 60 80
SNV Index

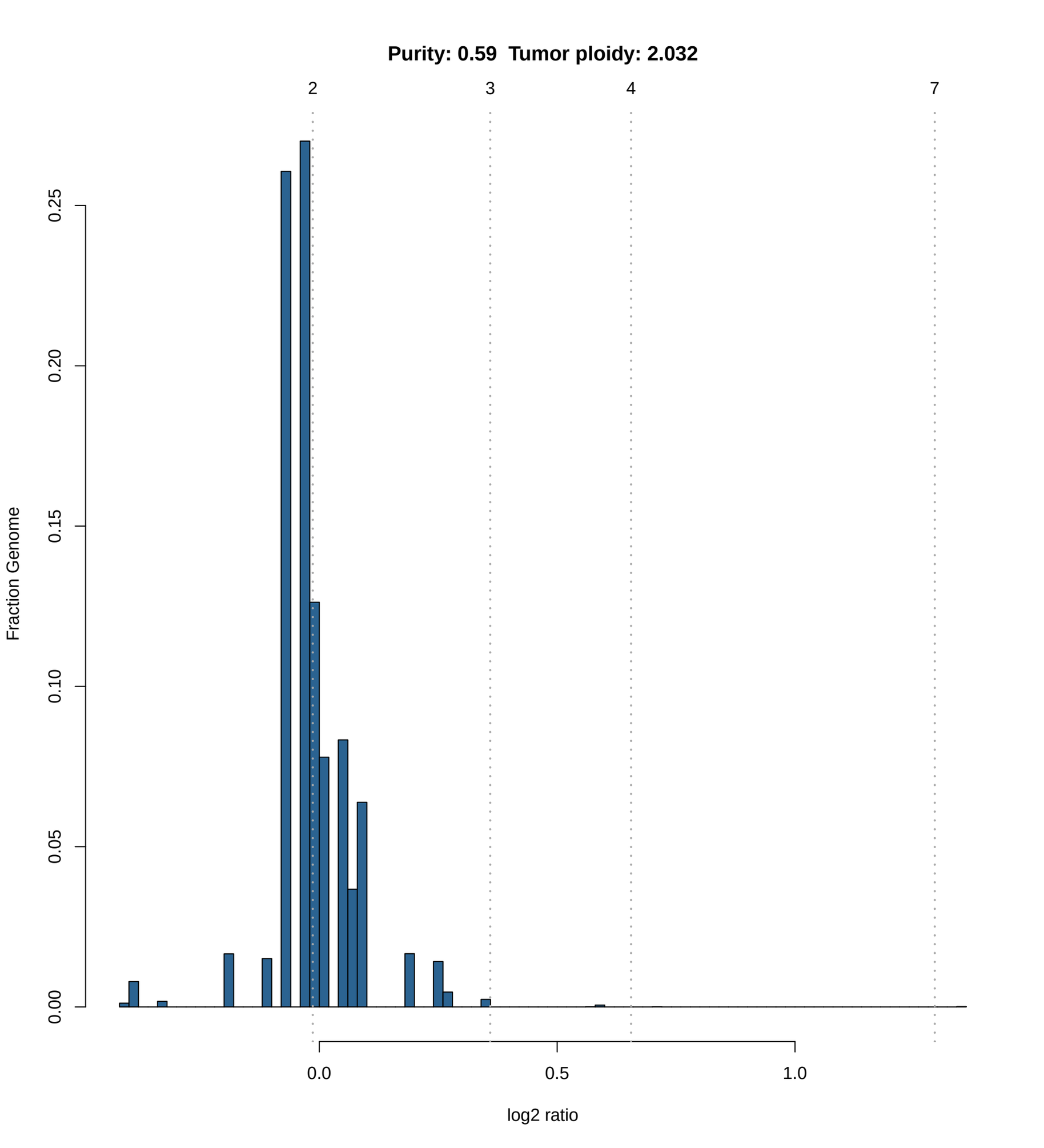

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80
SNV Index

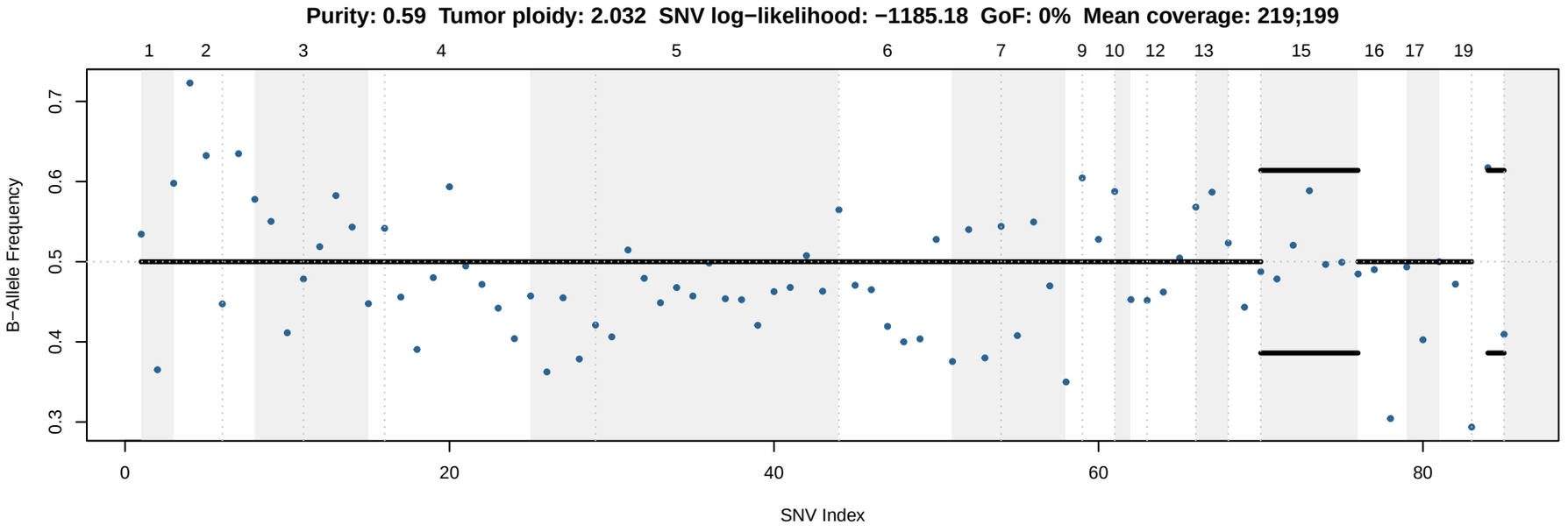

4m3
3m2
4m2
3m1
Allelic fraction (germline)
Copy Number log−ratio

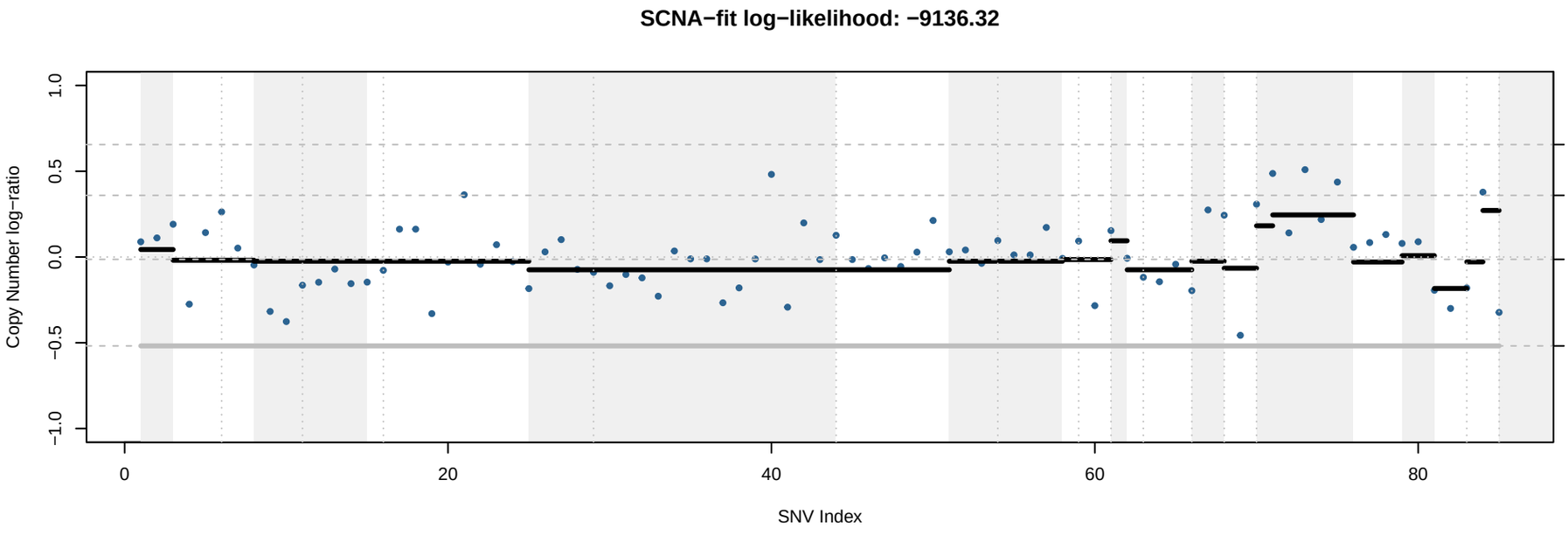

Coverage (log2)
Allelic fraction

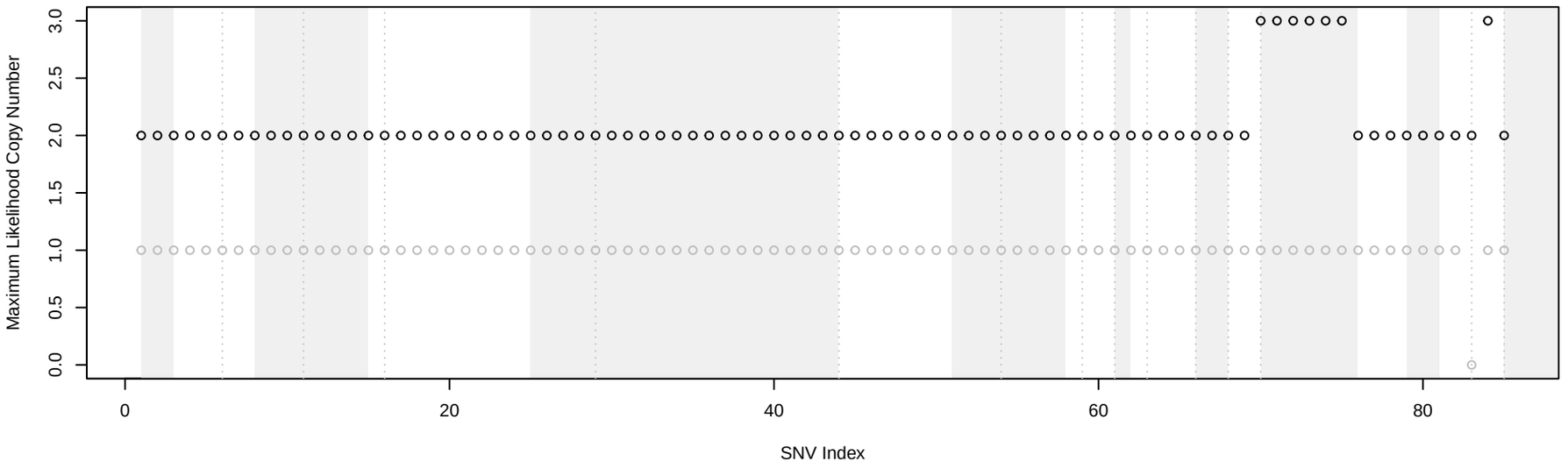

3m2
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1
Allelic fraction (somatic)
Copy Number log−ratio

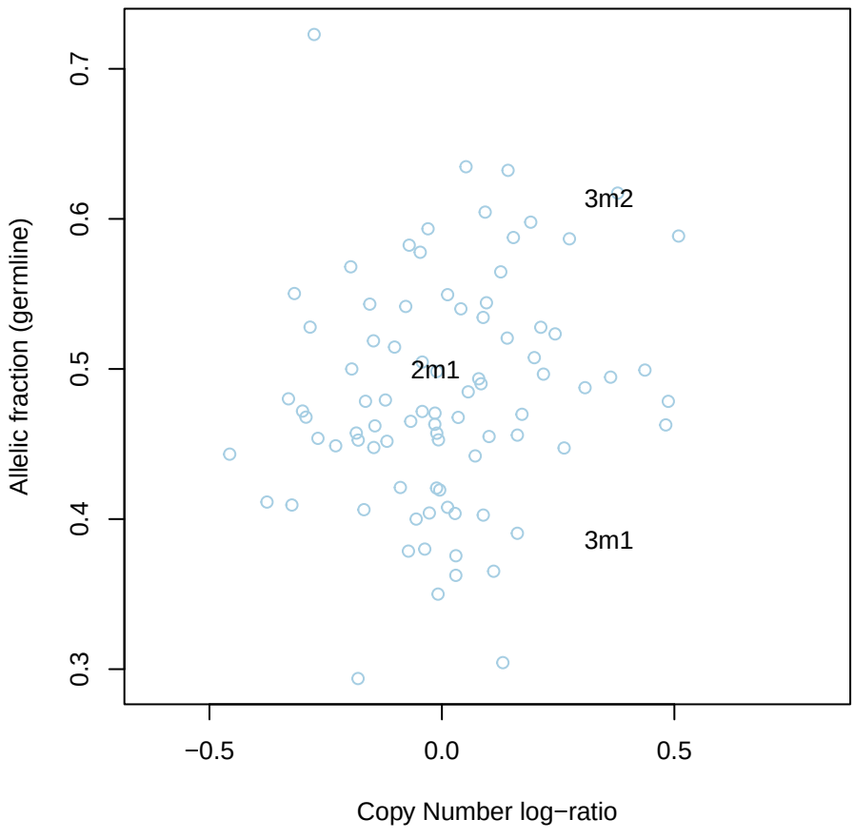

Power 0.8
Frequency
Cellular fraction

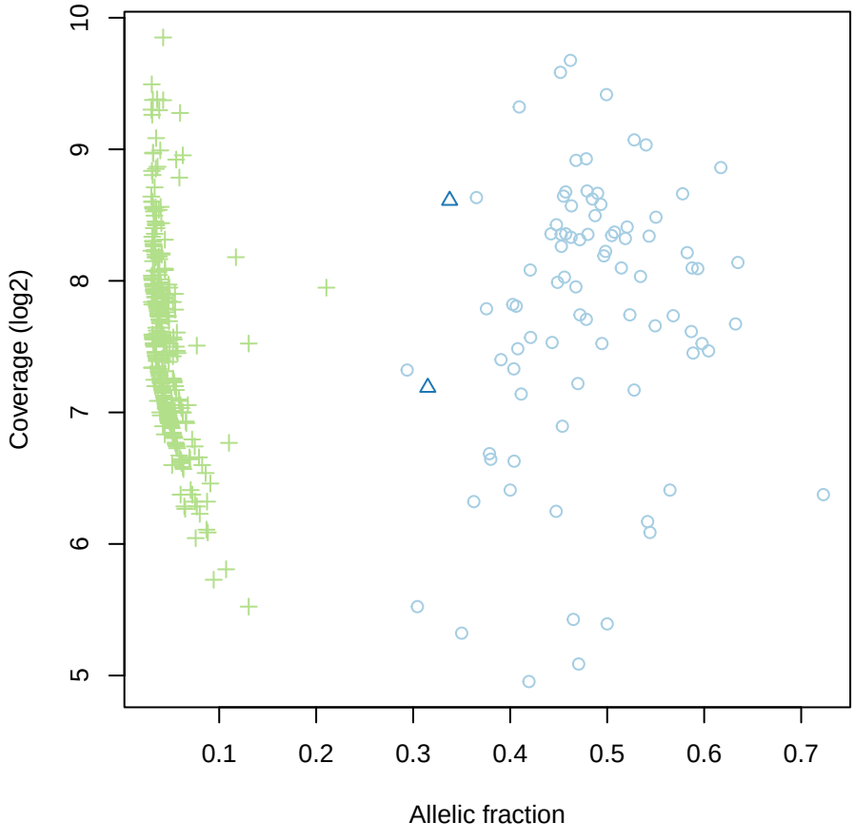

Purity: 0.59 Tumor ploidy: 2.032
2
3
4
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

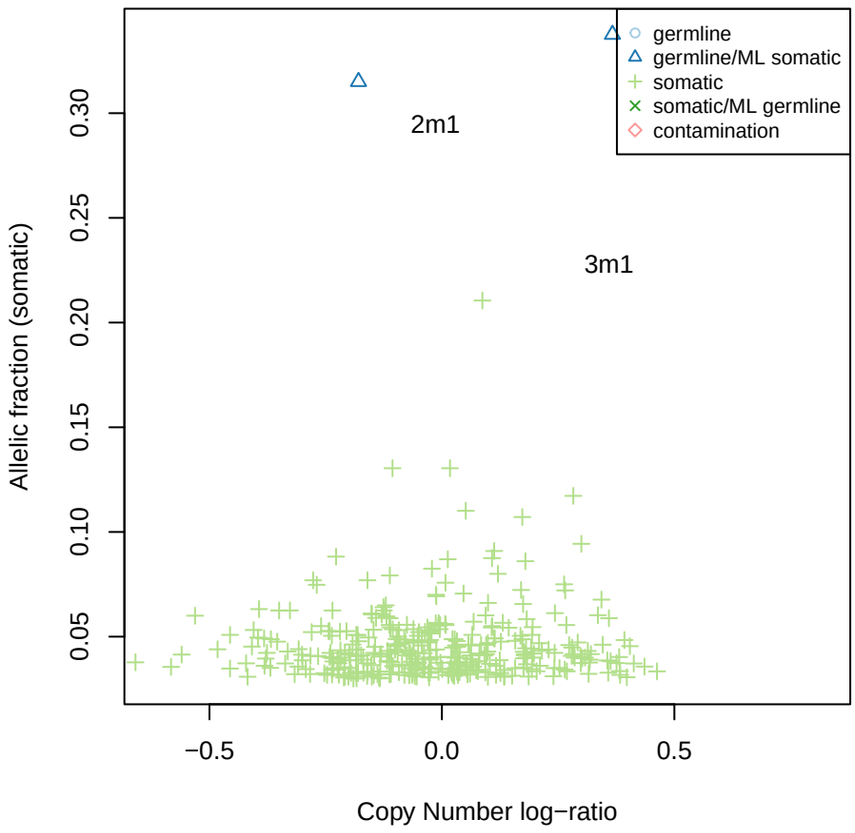

Purity: 0.59 Tumor ploidy: 2.032 SNV log−likelihood: −1185.18 GoF: 0% Mean coverage: 219;199
1 2 3 4 5 6 7 9 10 12 13 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

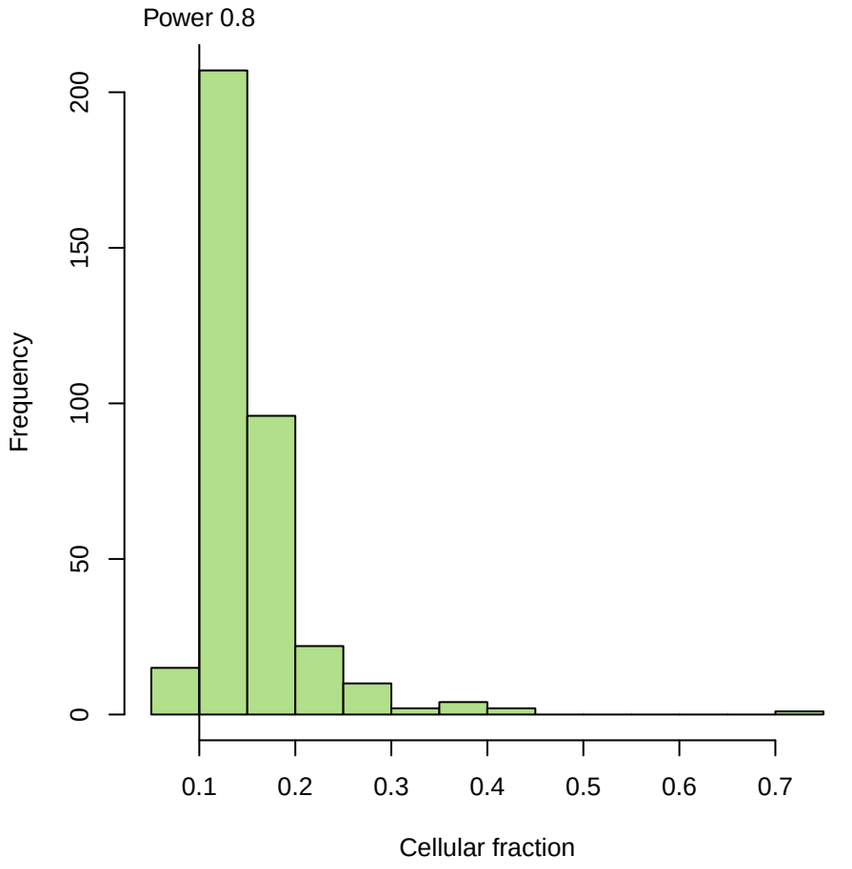

SCNA−fit log−likelihood: −9136.32
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4
0 20 40 60 80
SNV Index


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


Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
3m2
2m1
3m1
−0.5
0.0
0.5
Copy Number log−ratio


Coverage (log2)
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction


Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0.30
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
−0.5
0.0
0.5
Copy Number log−ratio


Power 0.8
Frequency
0
50
100
150
200
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Cellular fraction