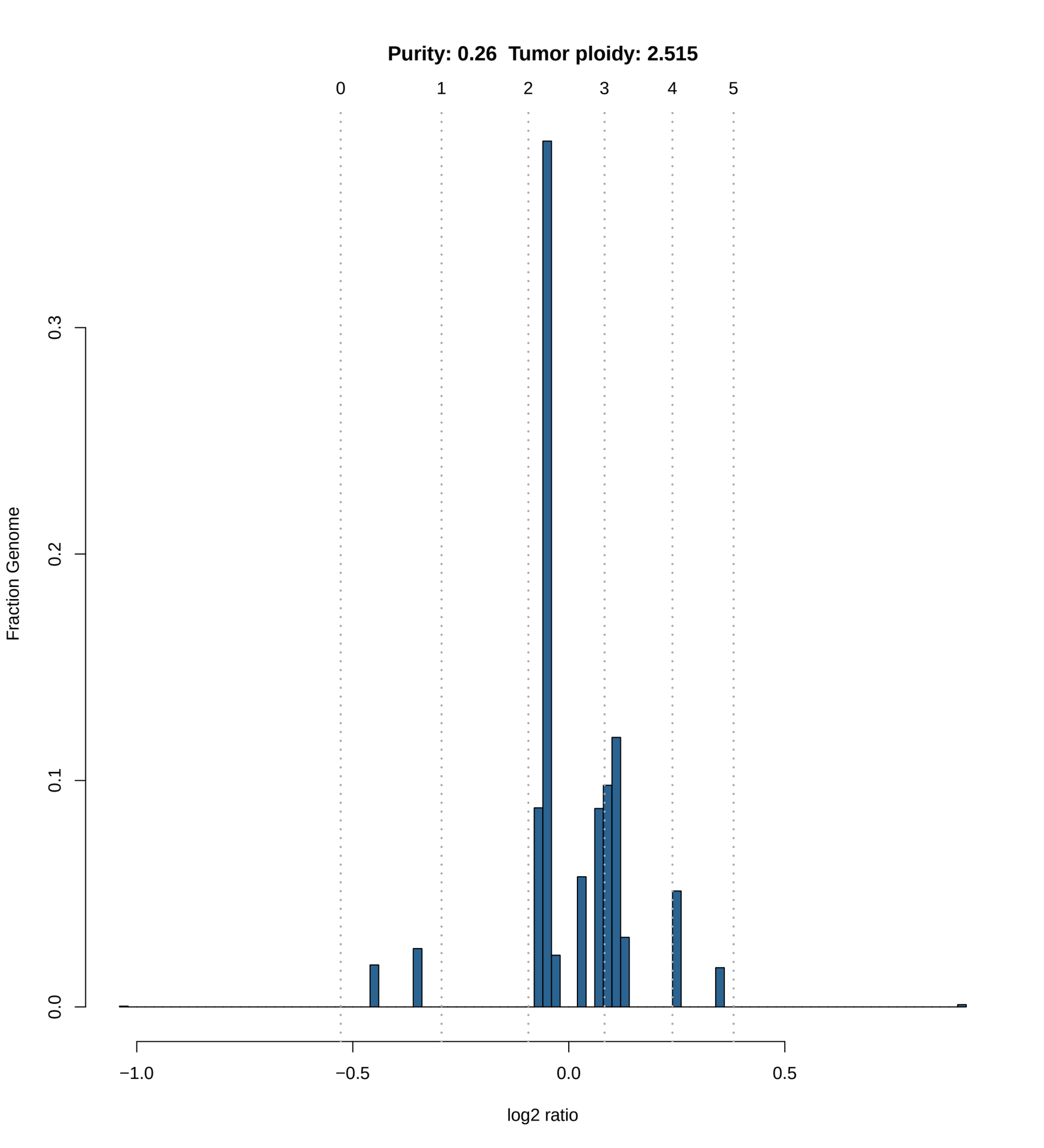
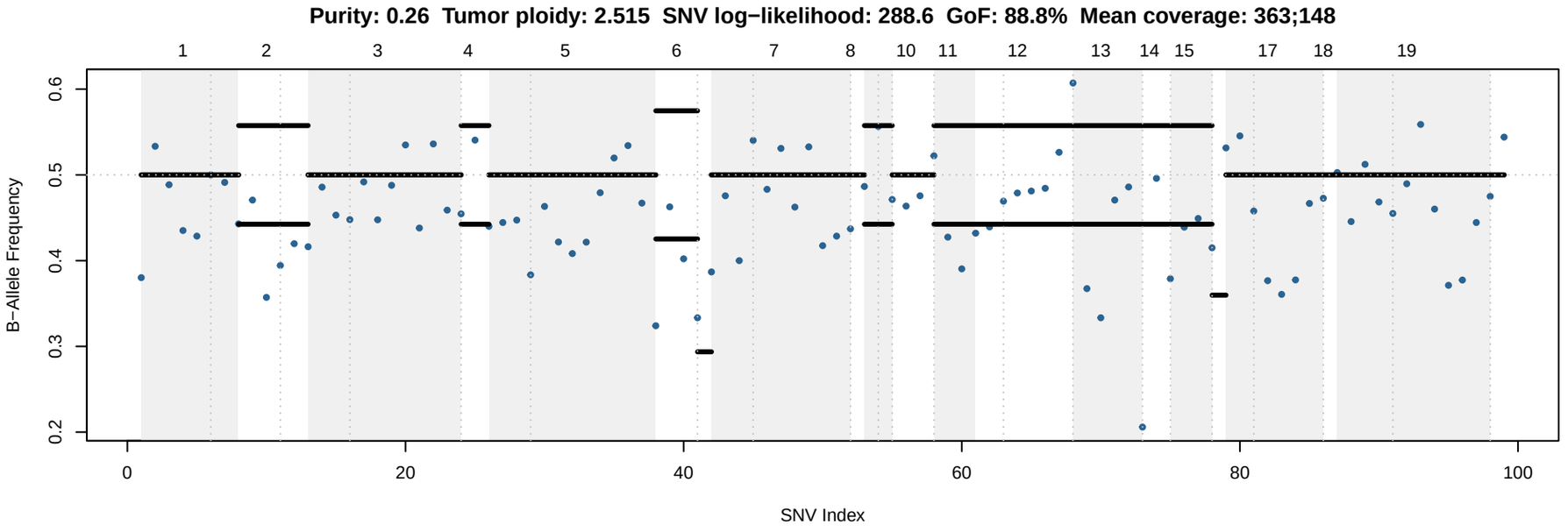
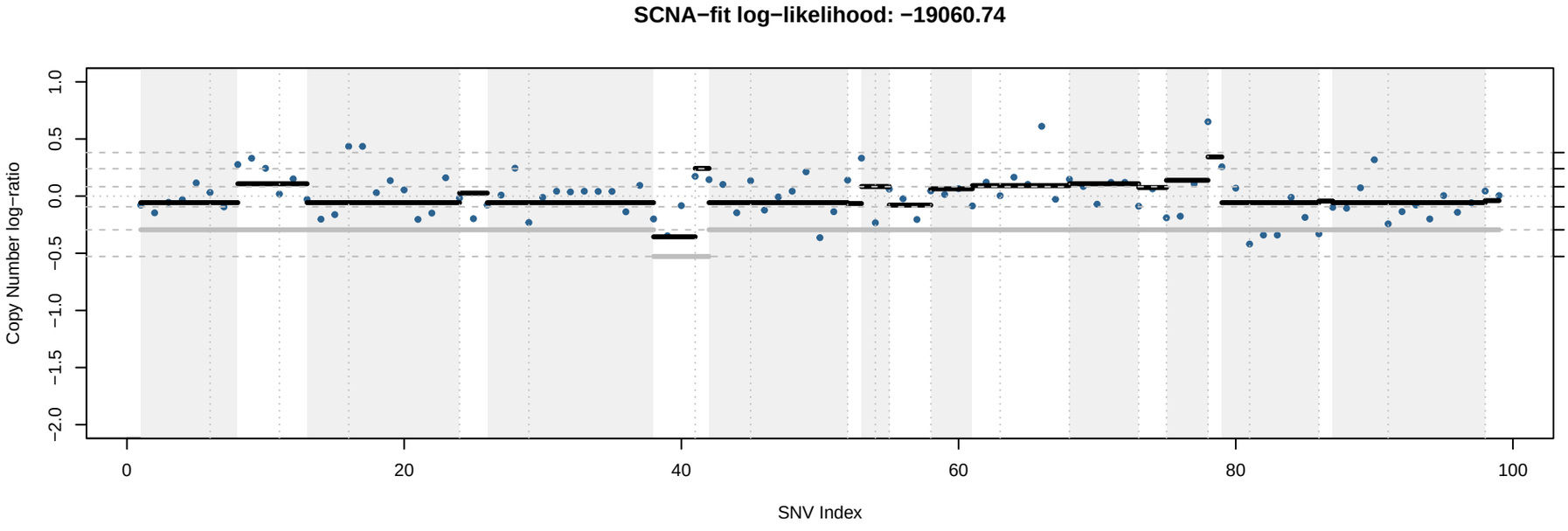
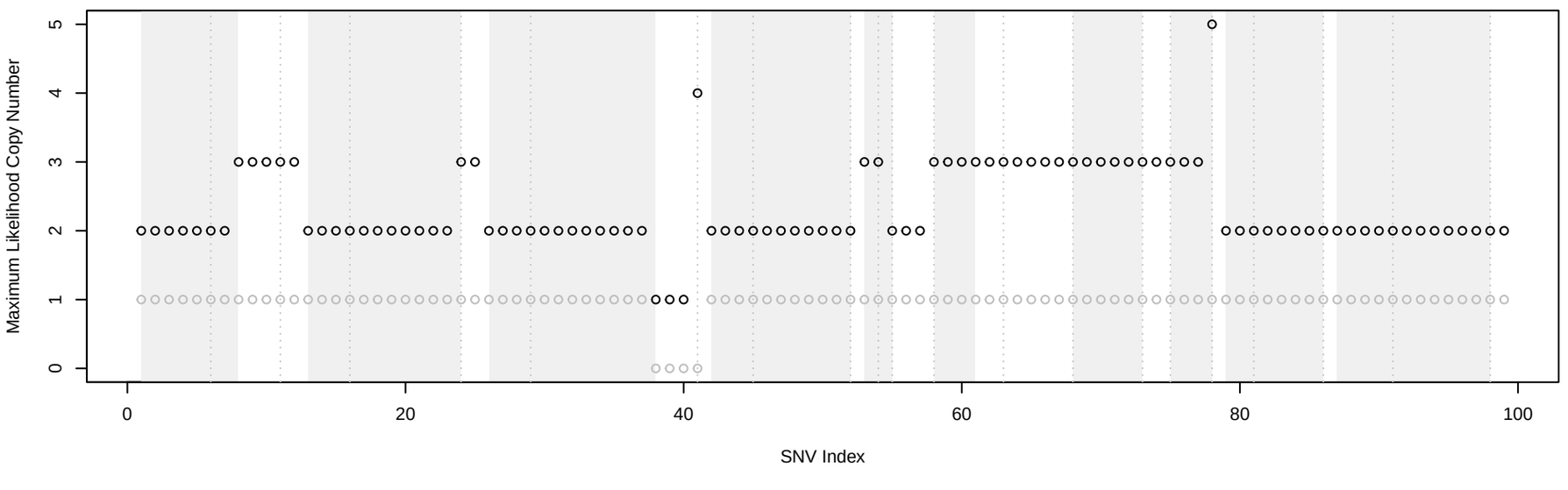
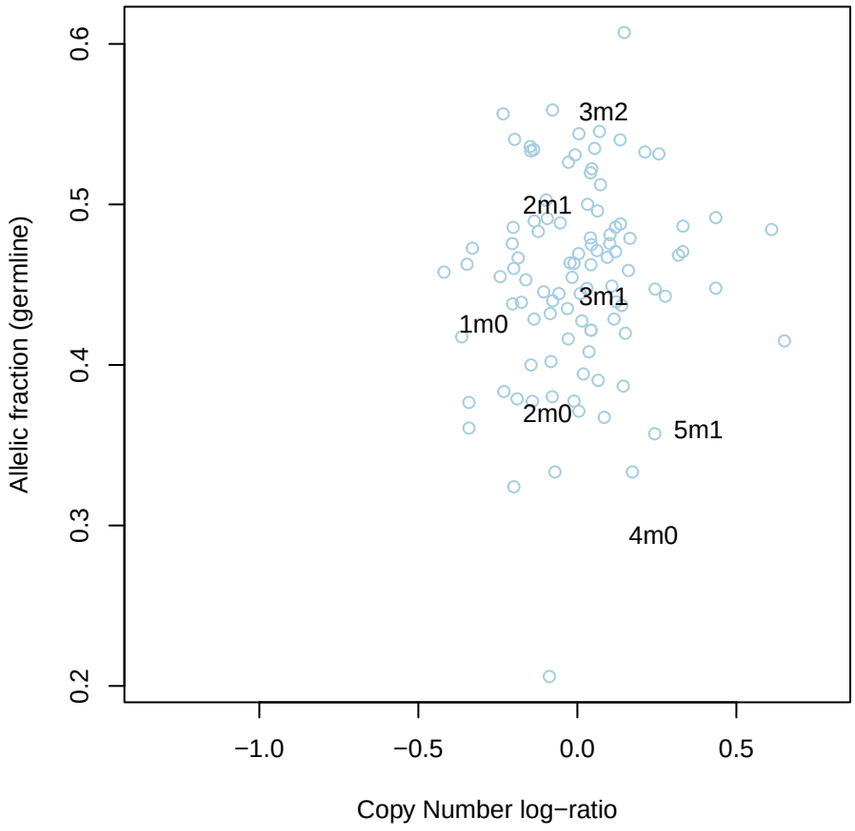
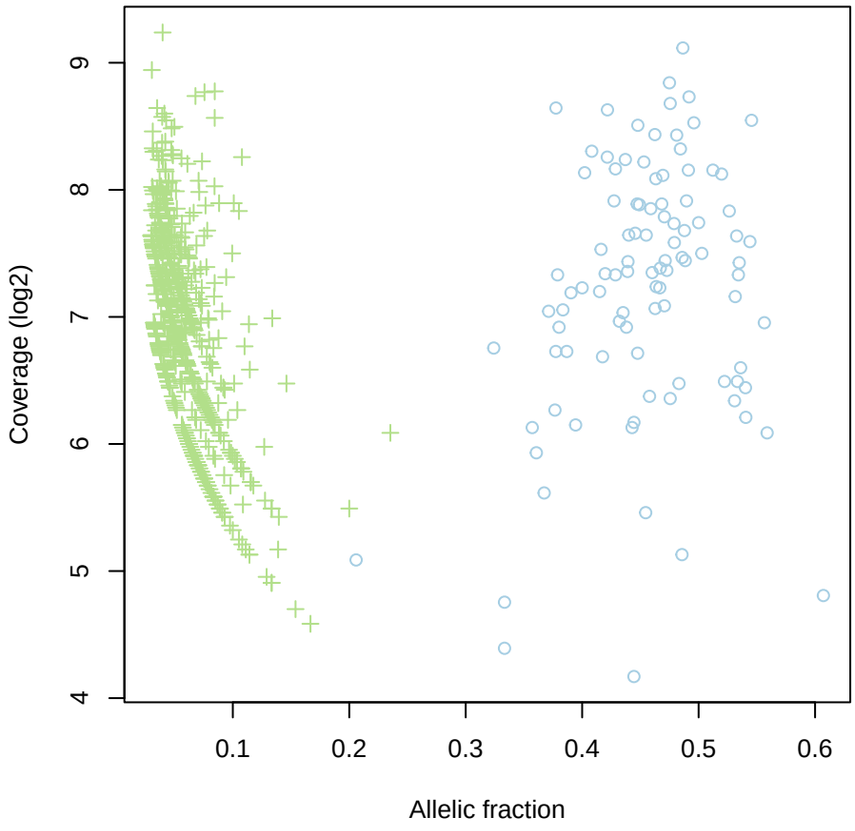

Purity: 0.26 Tumor ploidy: 2.515
0
1
2
3
4
5
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

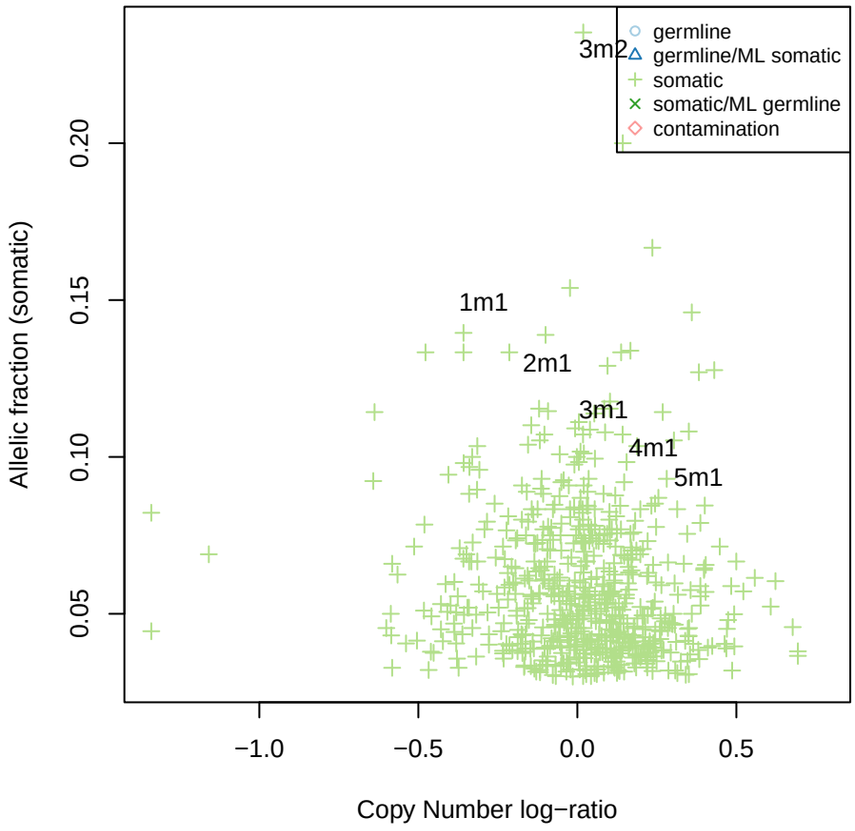

Purity: 0.26 Tumor ploidy: 2.515 SNV log−likelihood: 288.6 GoF: 88.8% Mean coverage: 363;148
1 2 3 4 5 6 7 8 10 11 12 13 14 15 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 20 40 60 80 100
SNV Index

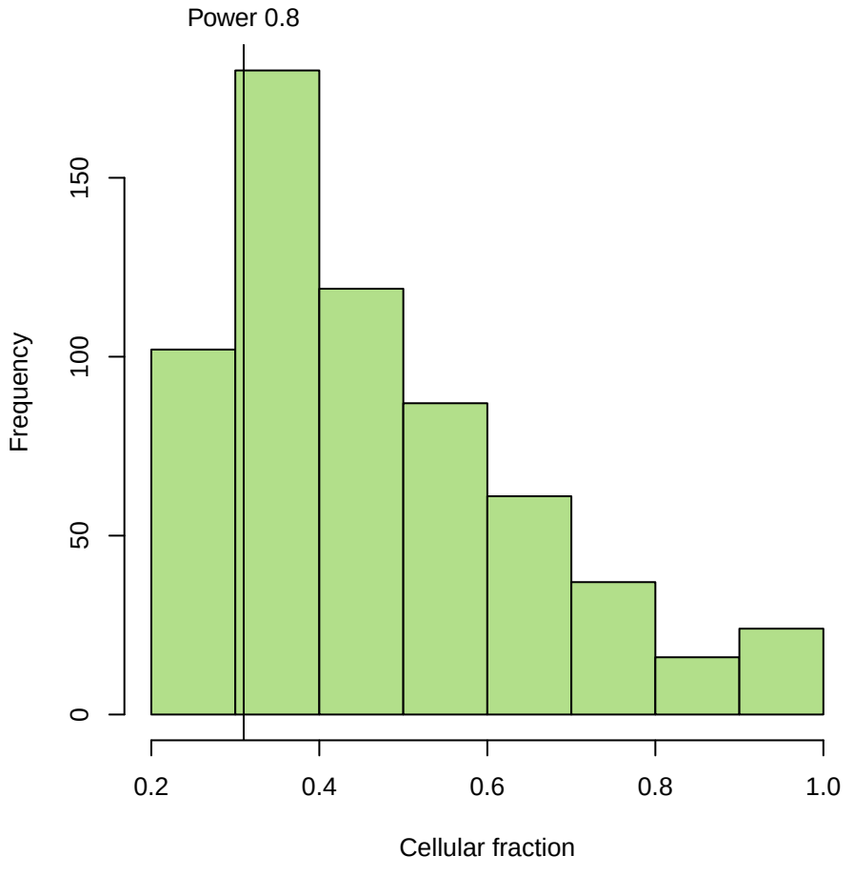

SCNA−fit log−likelihood: −19060.74
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 3 5
0 20 40 60 80 100
SNV Index

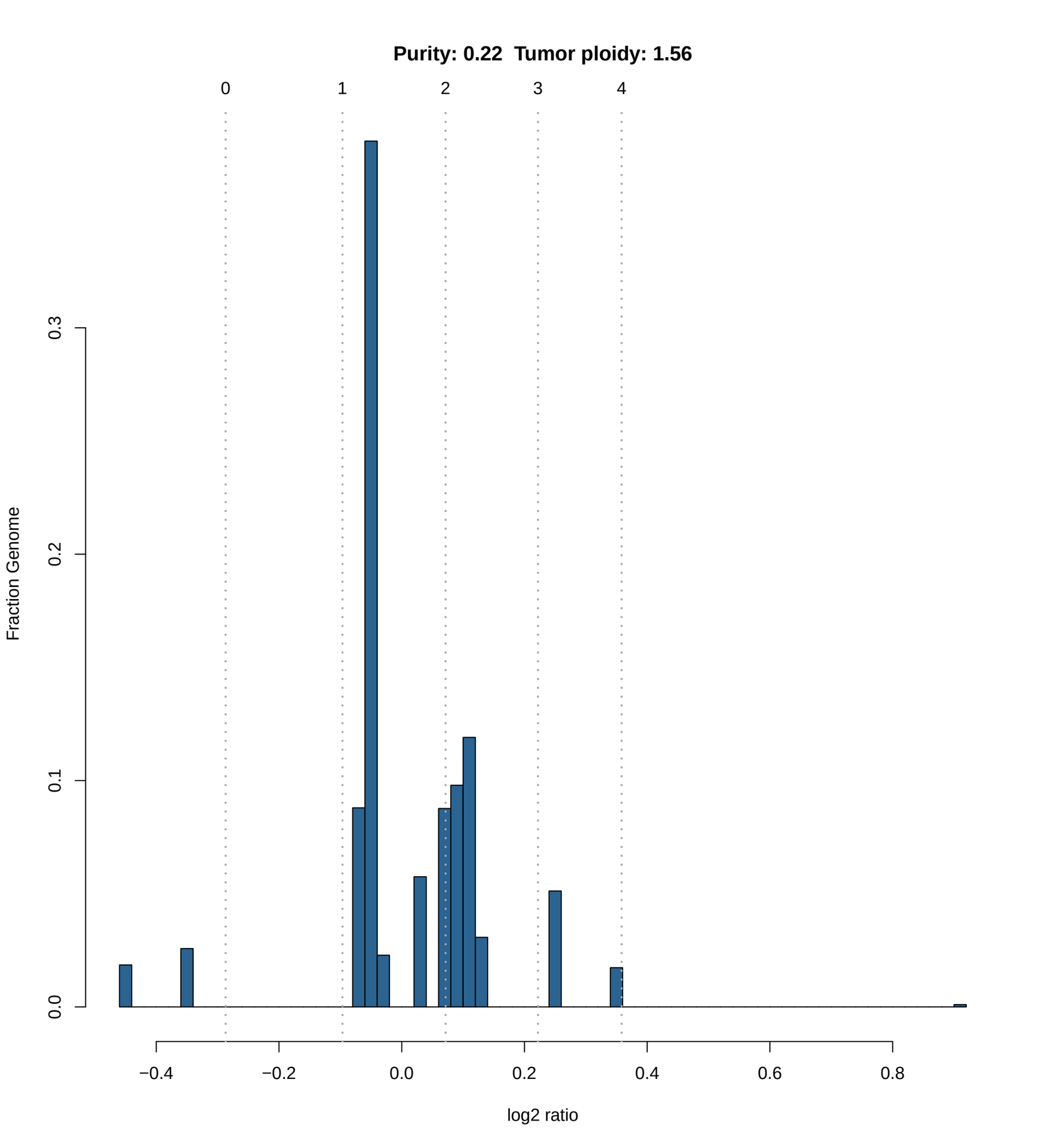

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100
SNV Index

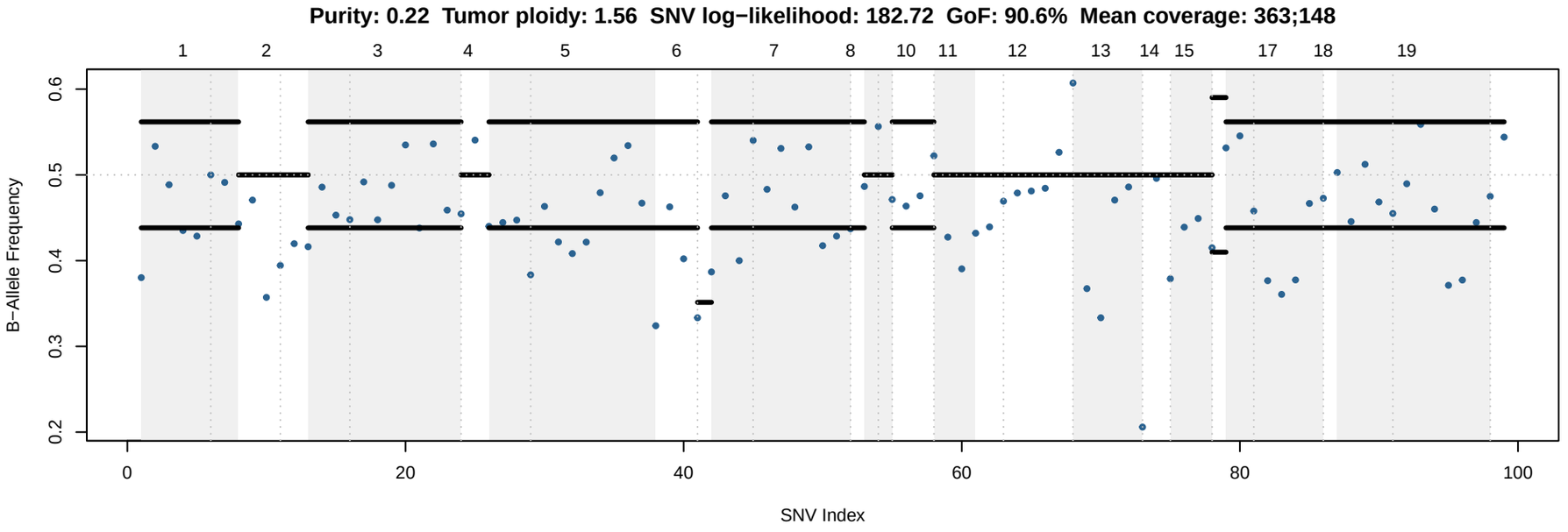

Allelic fraction (germline)
Copy Number log−ratio
3m2
2m1
3m1
1m0
2m0
5m1
4m0

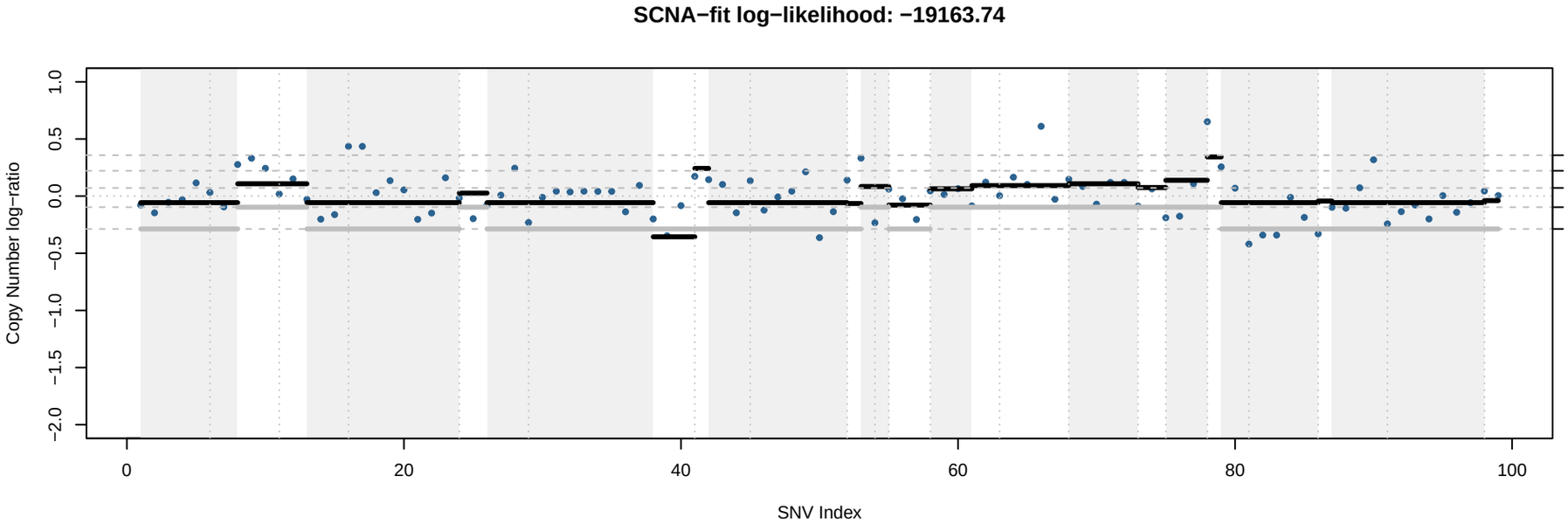

Coverage (log2)
Allelic fraction

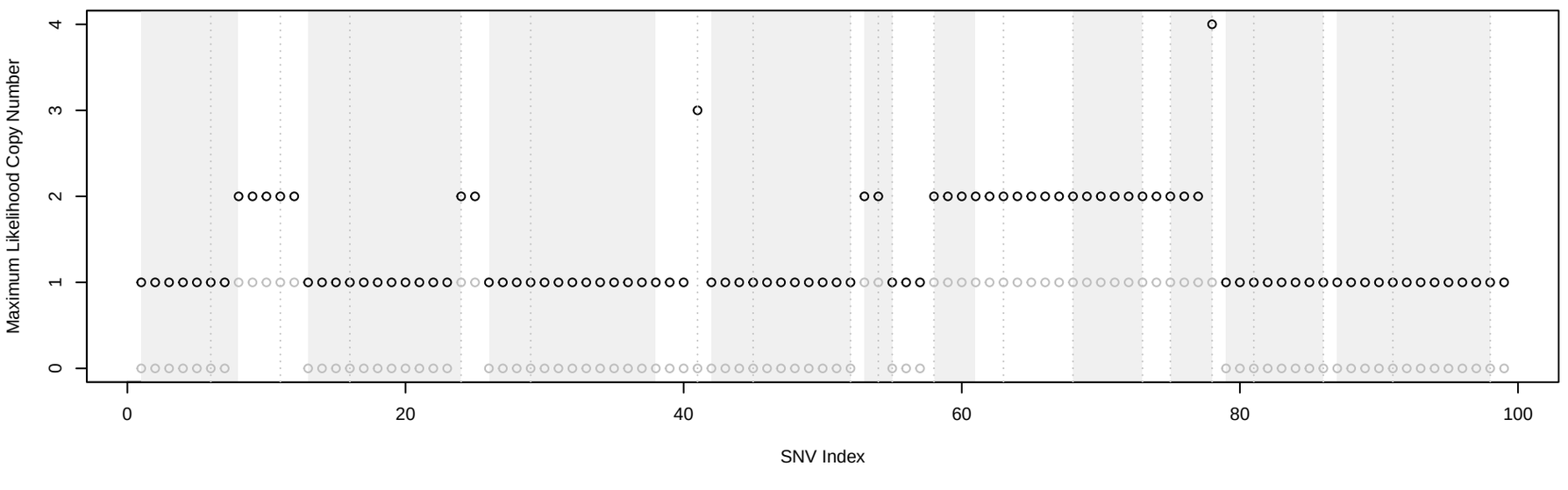

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m2
1m1
2m1
3m1
4m1
5m1

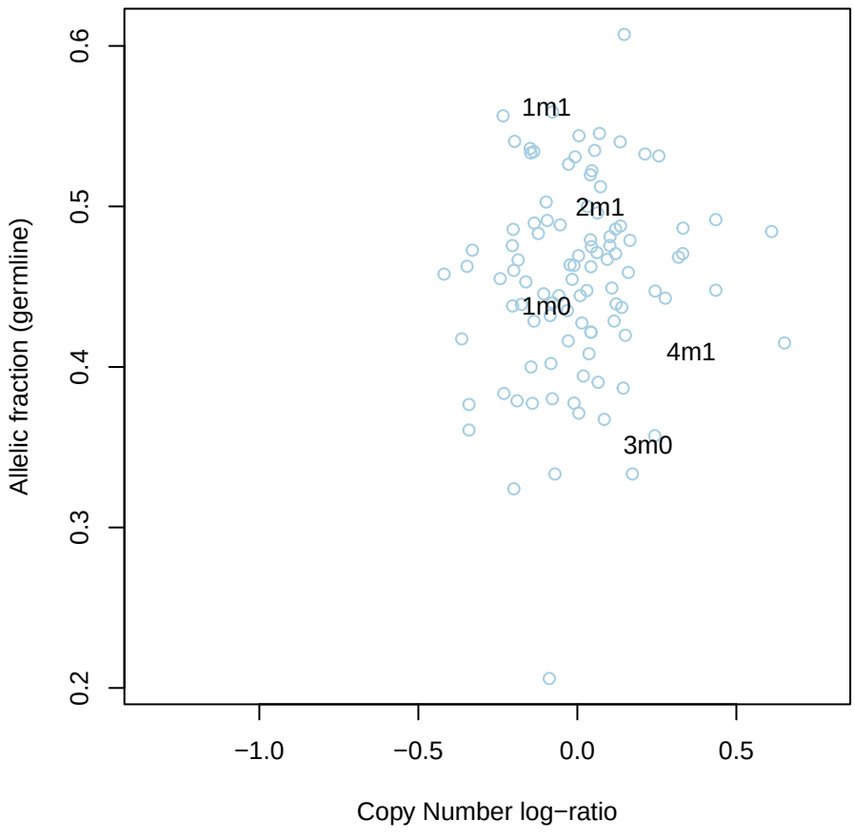

Power 0.8
Frequency
Cellular fraction

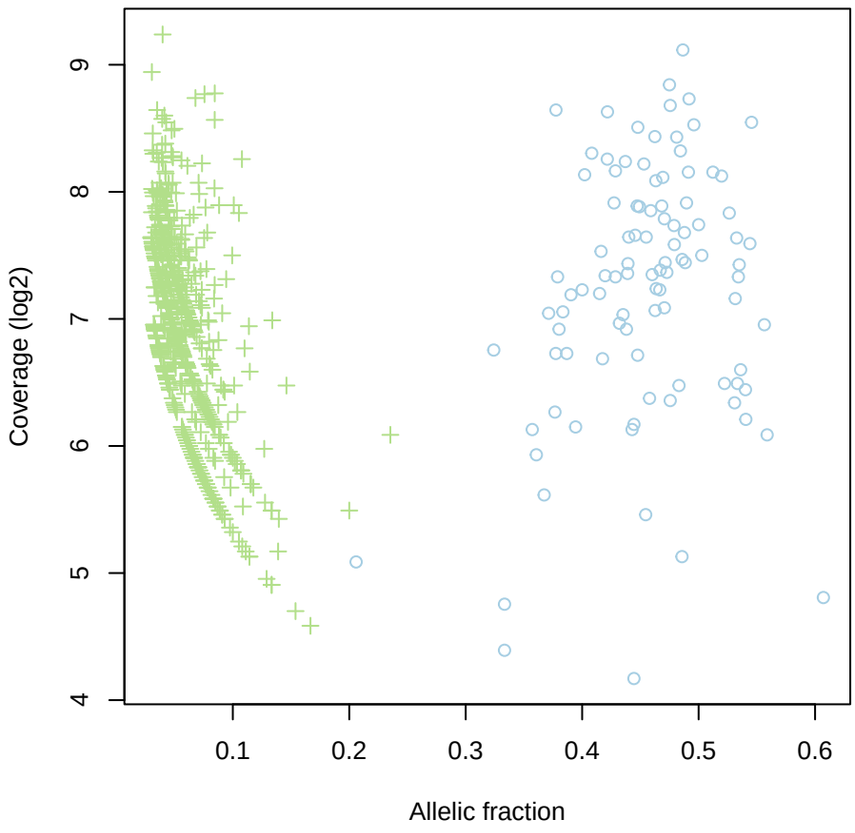

Purity: 0.22 Tumor ploidy: 1.56
0
1
2
3
4
Fraction Genome
0.0
0.1
0.2
0.3
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
log2 ratio

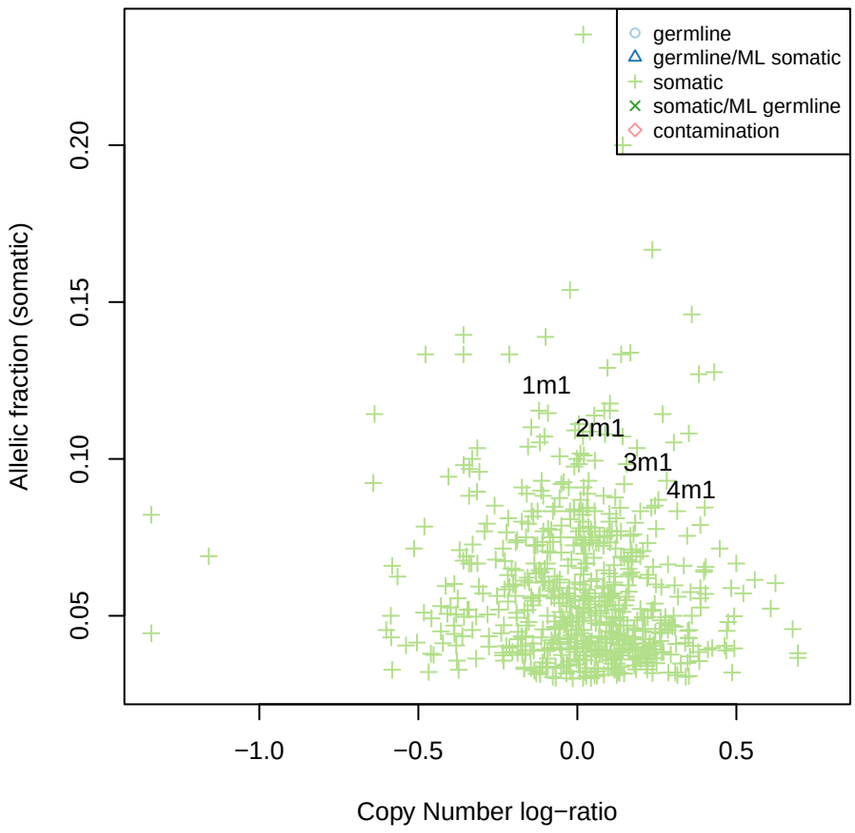

Purity: 0.22 Tumor ploidy: 1.56 SNV log−likelihood: 182.72 GoF: 90.6% Mean coverage: 363;148
1 2 3 4 5 6 7 8 10 11 12 13 14 15 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 20 40 60 80 100
SNV Index

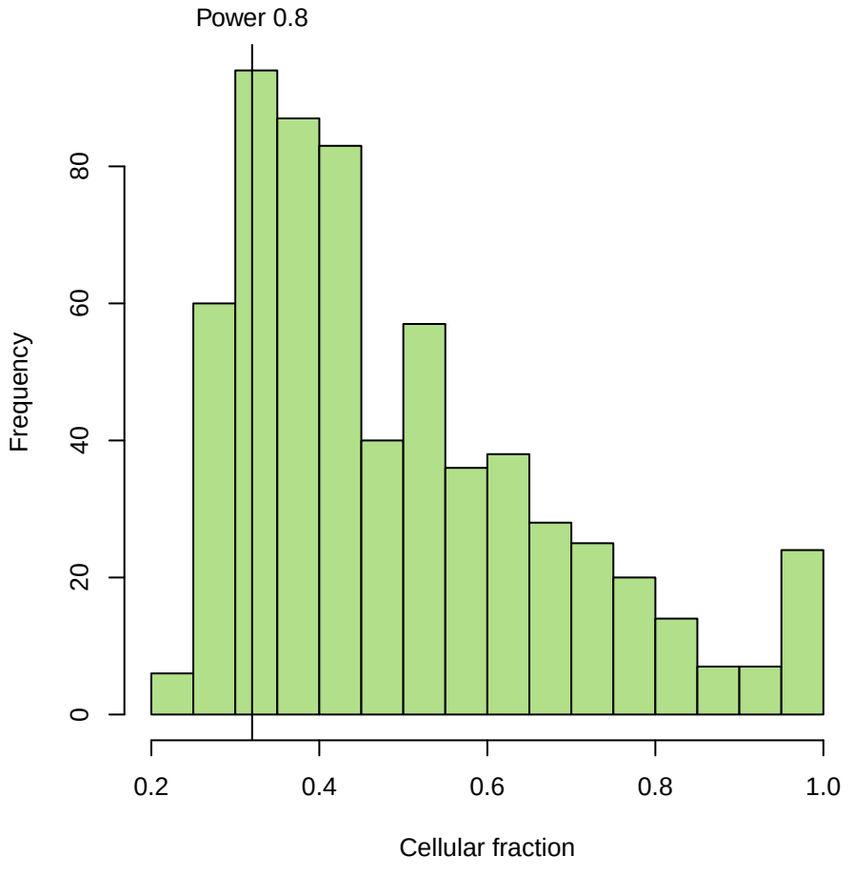

SCNA−fit log−likelihood: −19163.74
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
0 2 4
0 20 40 60 80 100
SNV Index

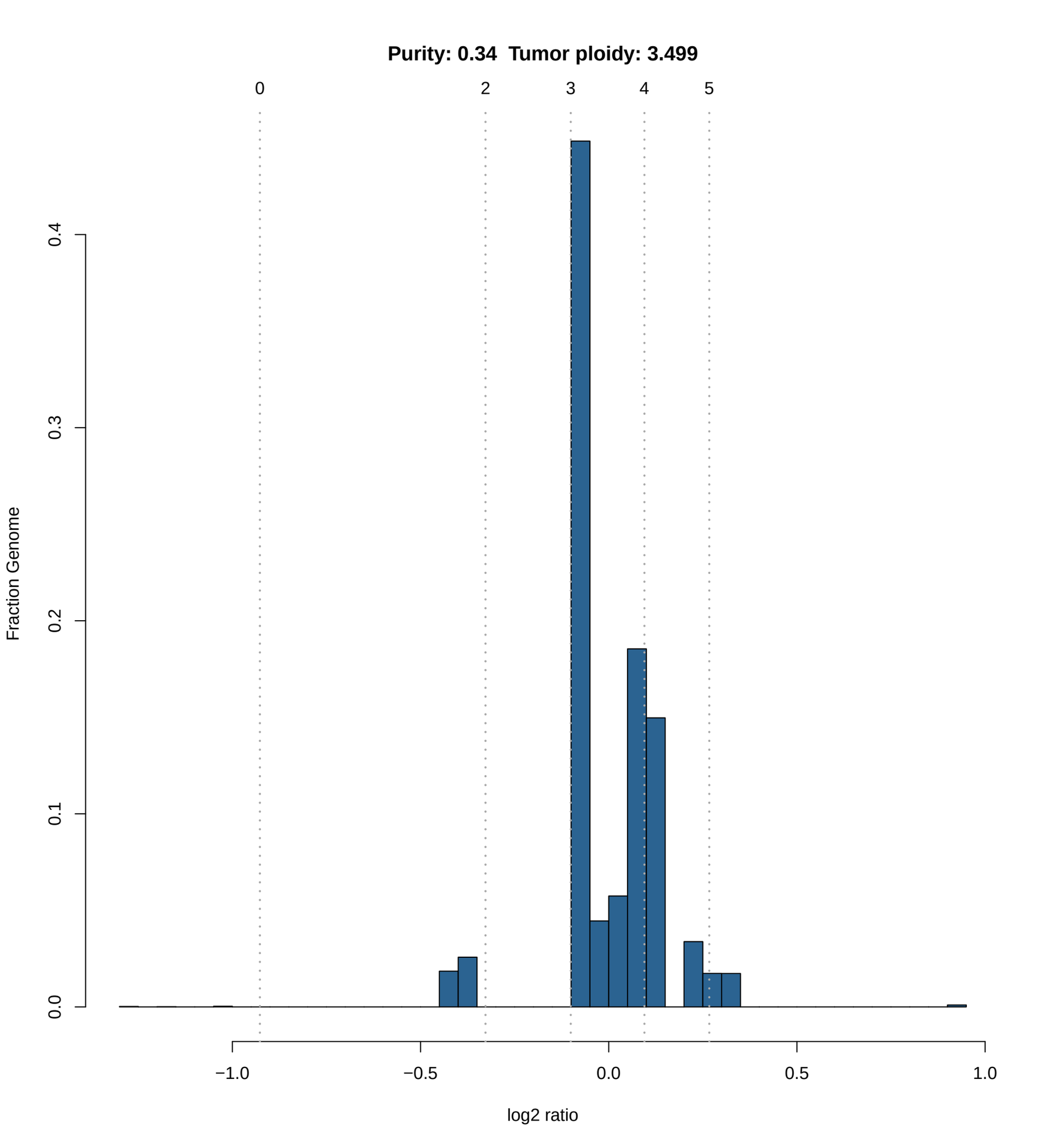

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100
SNV Index

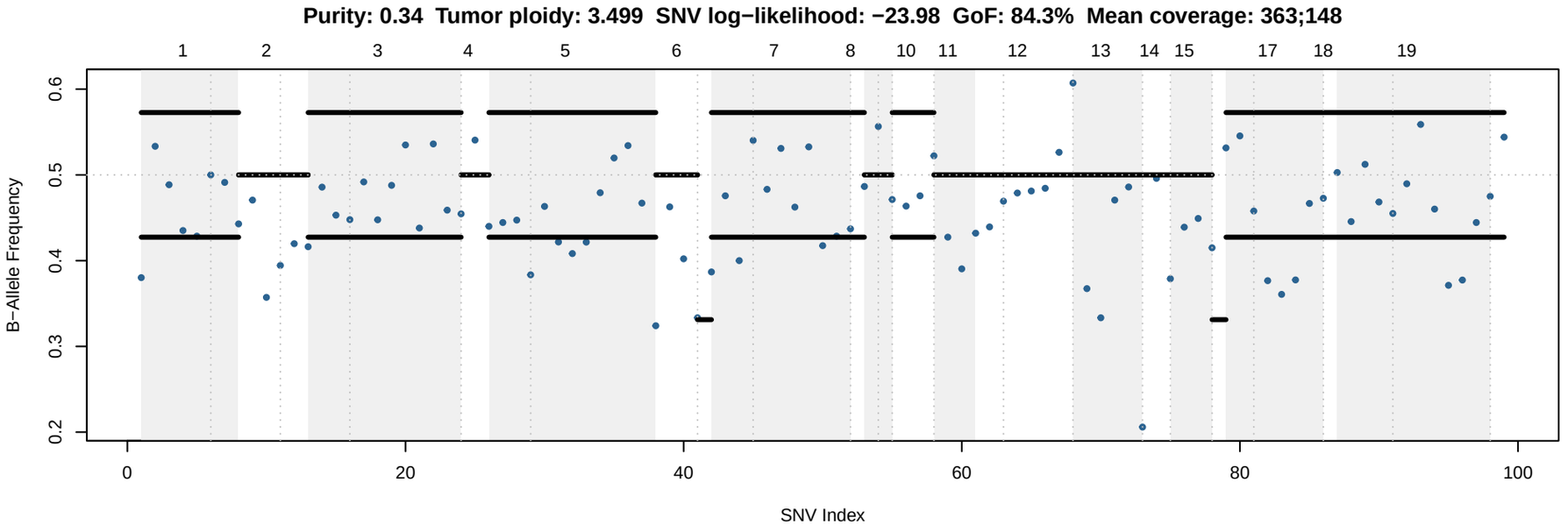

Allelic fraction (germline)
0.2
0.3
0.4
0.5
0.6
1m1
2m1
1m0
4m1
3m0
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

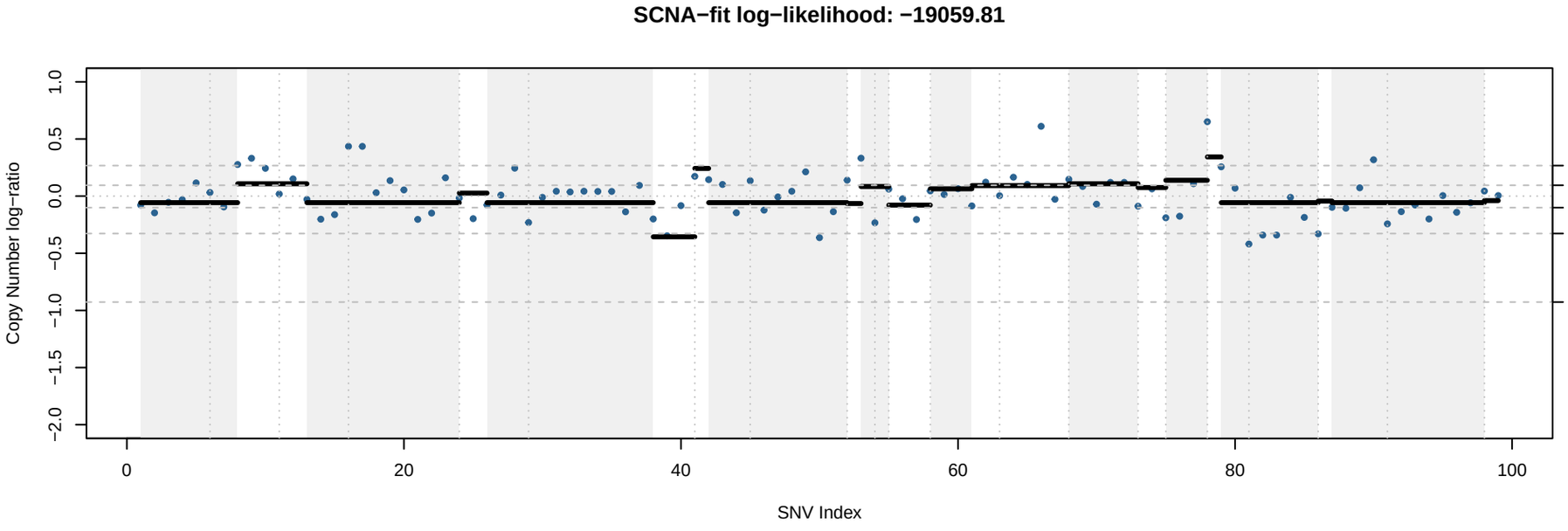

Coverage (log2)
4
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

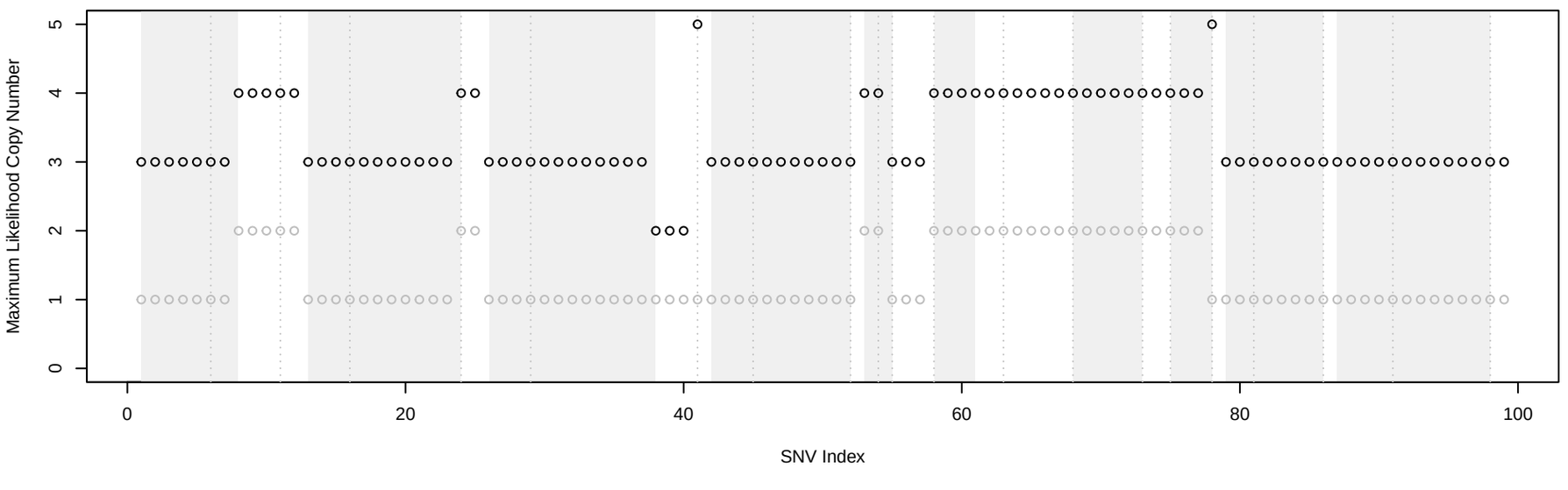

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
1m1
2m1
3m1
4m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

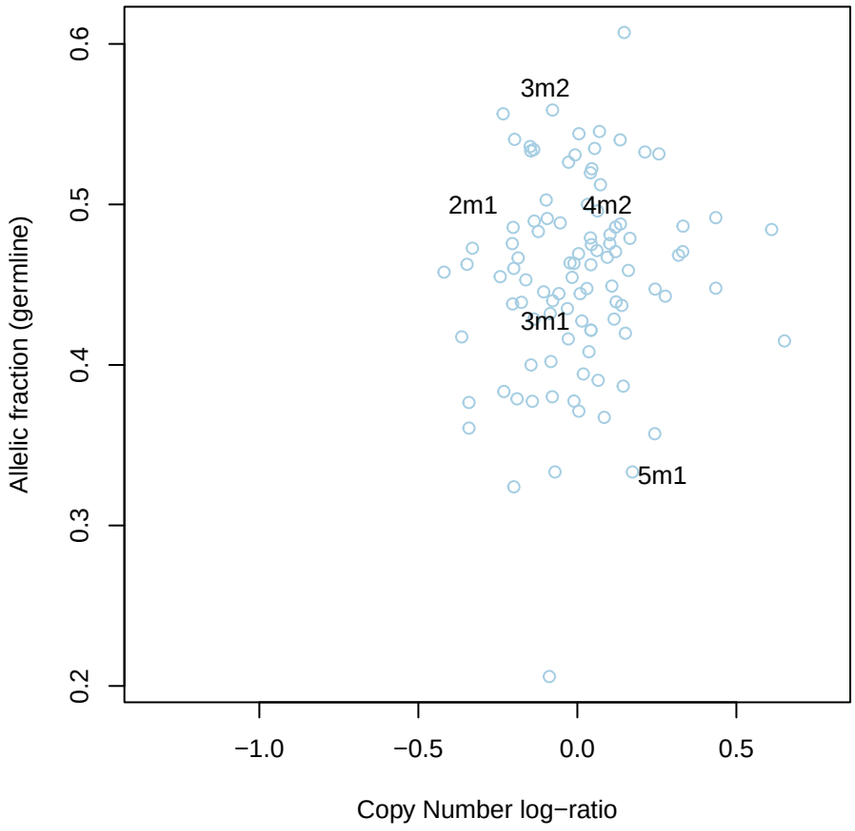

Power 0.8
Frequency
0
20
40
60
80
0.2
0.4
0.6
0.8
1.0
Cellular fraction

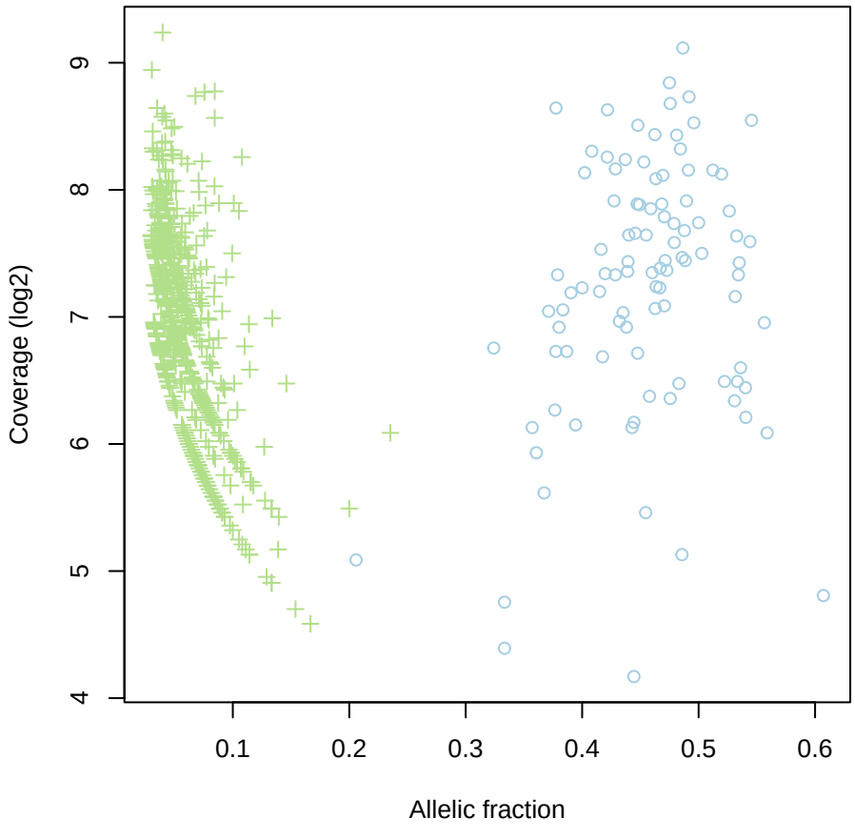

Purity: 0.34 Tumor ploidy: 3.499
0
2
3
4
5
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

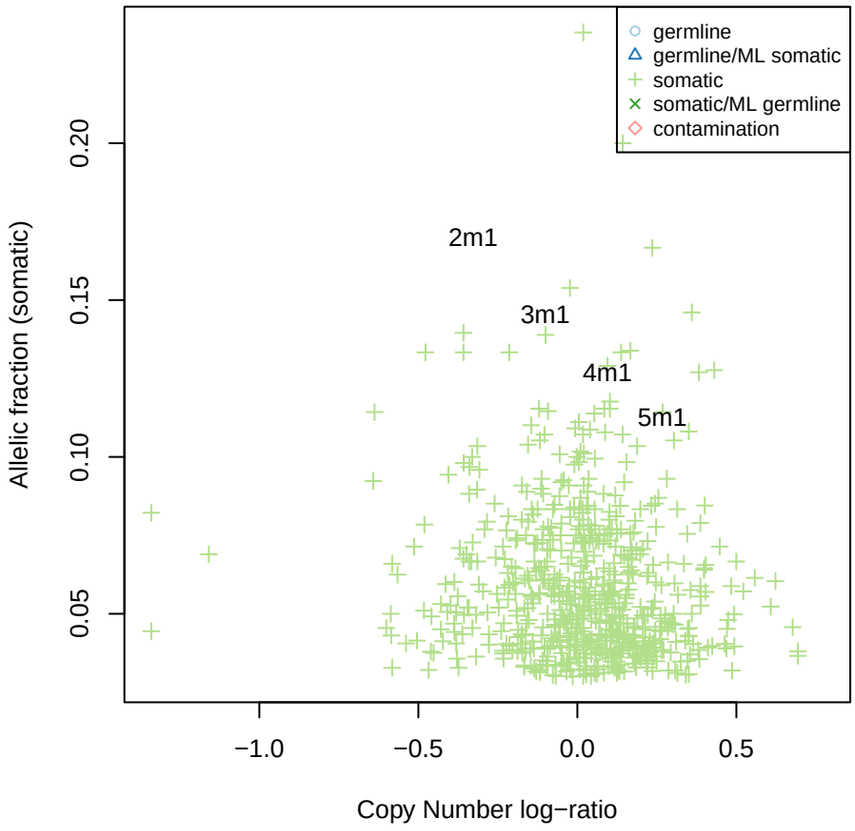

Purity: 0.34 Tumor ploidy: 3.499 SNV log−likelihood: −23.98 GoF: 84.3% Mean coverage: 363;148
1 2 3 4 5 6 7 8 10 11 12 13 14 15 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 20 40 60 80 100
SNV Index

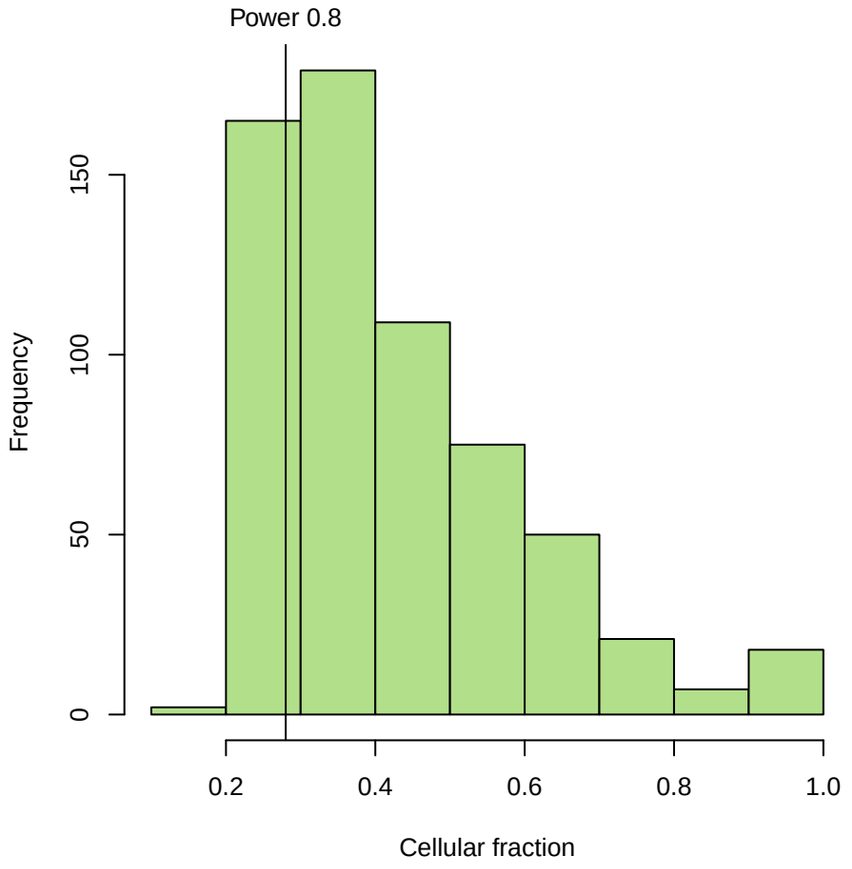

SCNA−fit log−likelihood: −19059.81
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 2 3 5
0 20 40 60 80 100
SNV Index

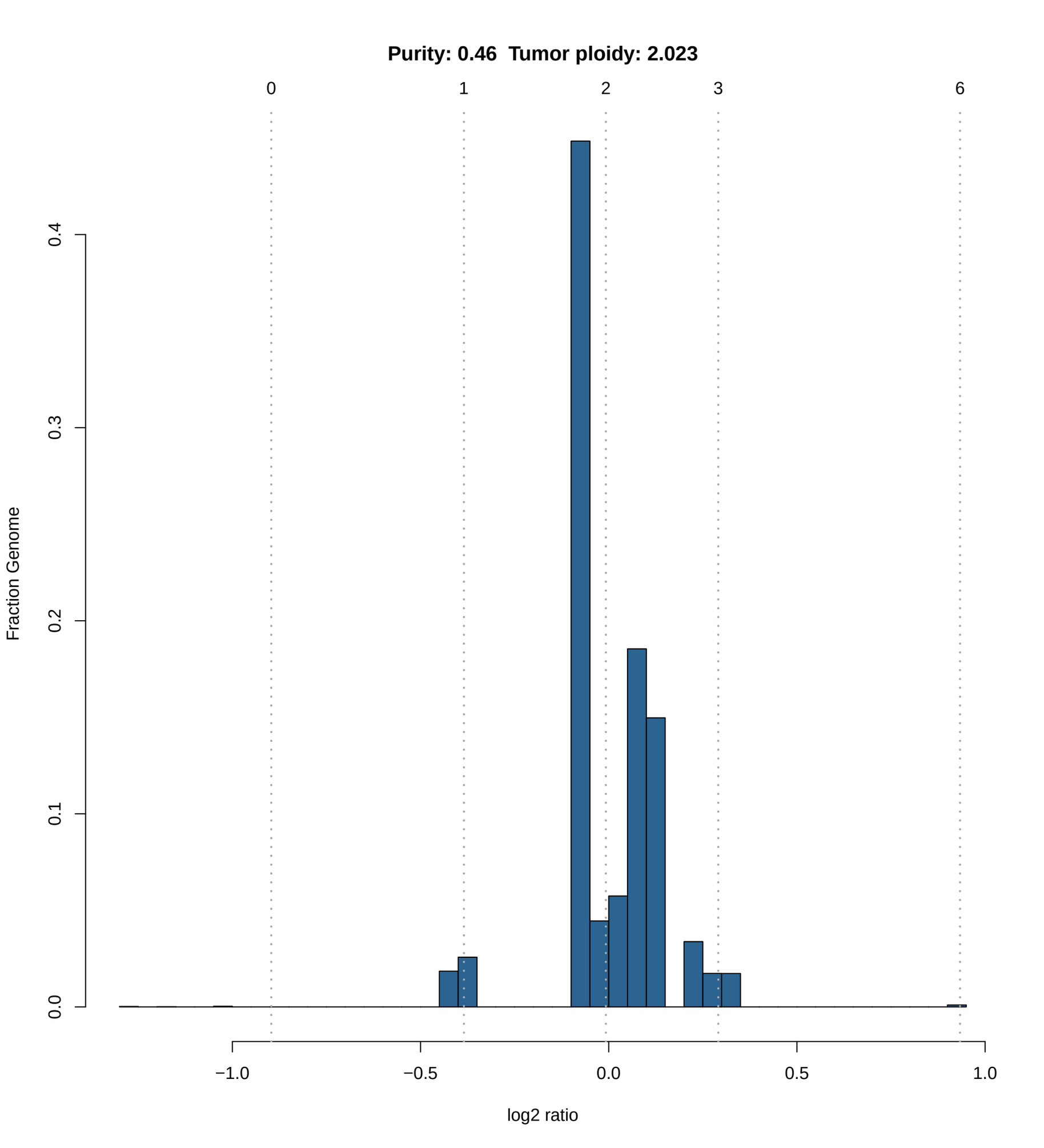

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100
SNV Index

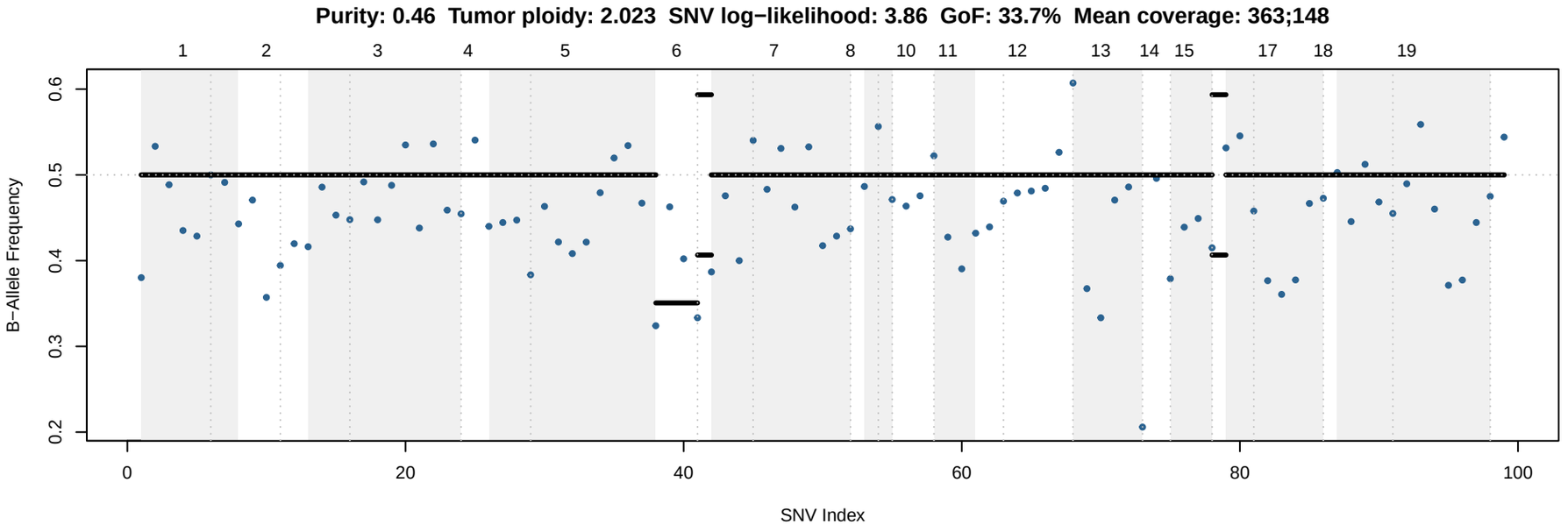

Allelic fraction (germline)
0.2
0.3
0.4
0.5
0.6
3m2
2m1
4m2
3m1
5m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

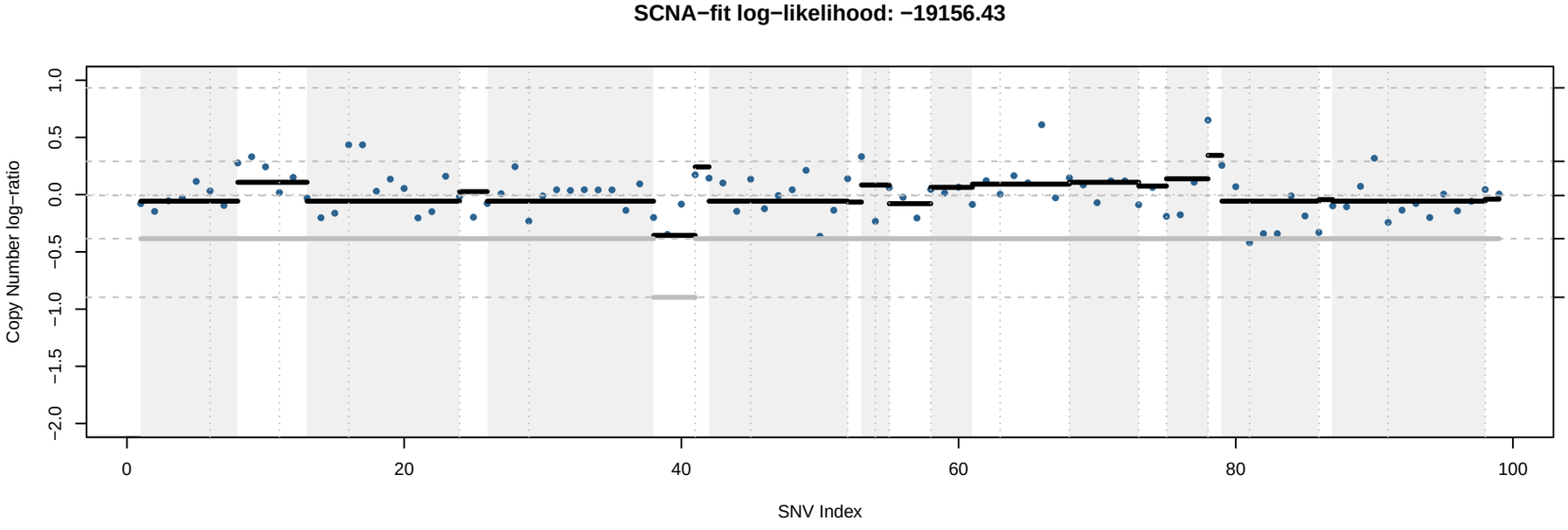

Coverage (log2)
4
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

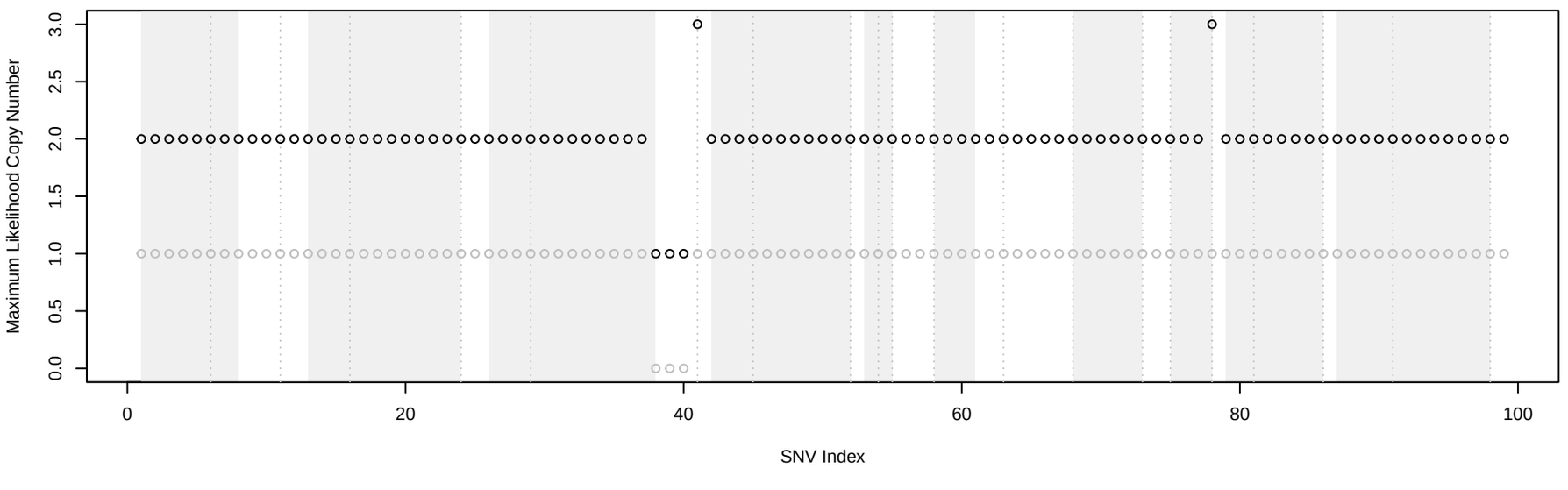

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
2m1
3m1
4m1
5m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

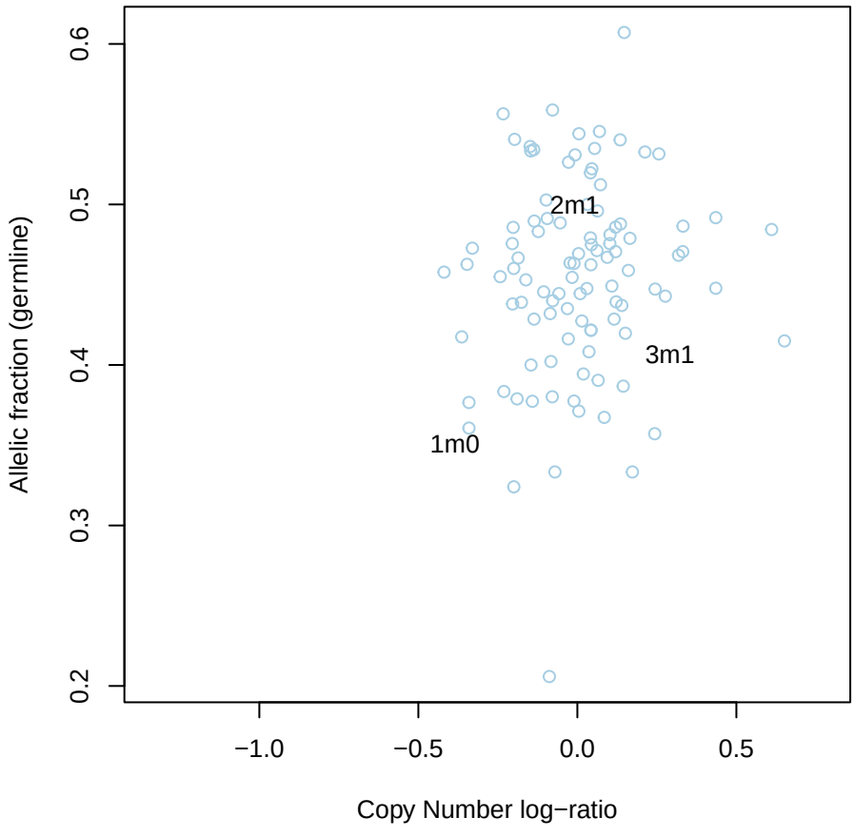

Power 0.8
Frequency
0
50
100
150
0.2
0.4
0.6
0.8
1.0
Cellular fraction

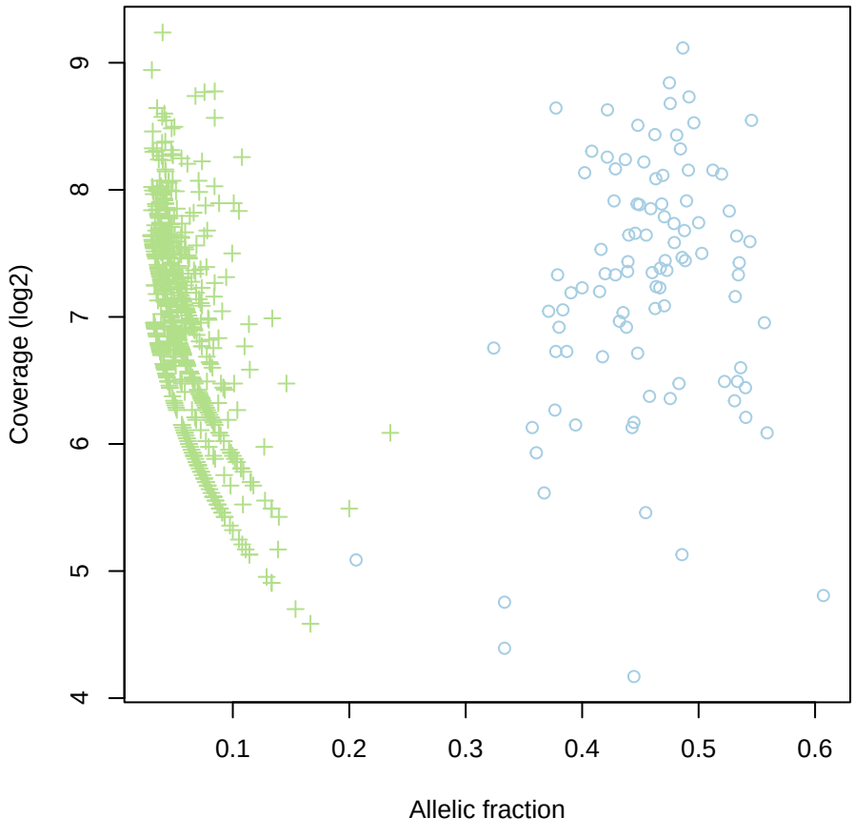

Purity: 0.46 Tumor ploidy: 2.023
0
1
2
3
6
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

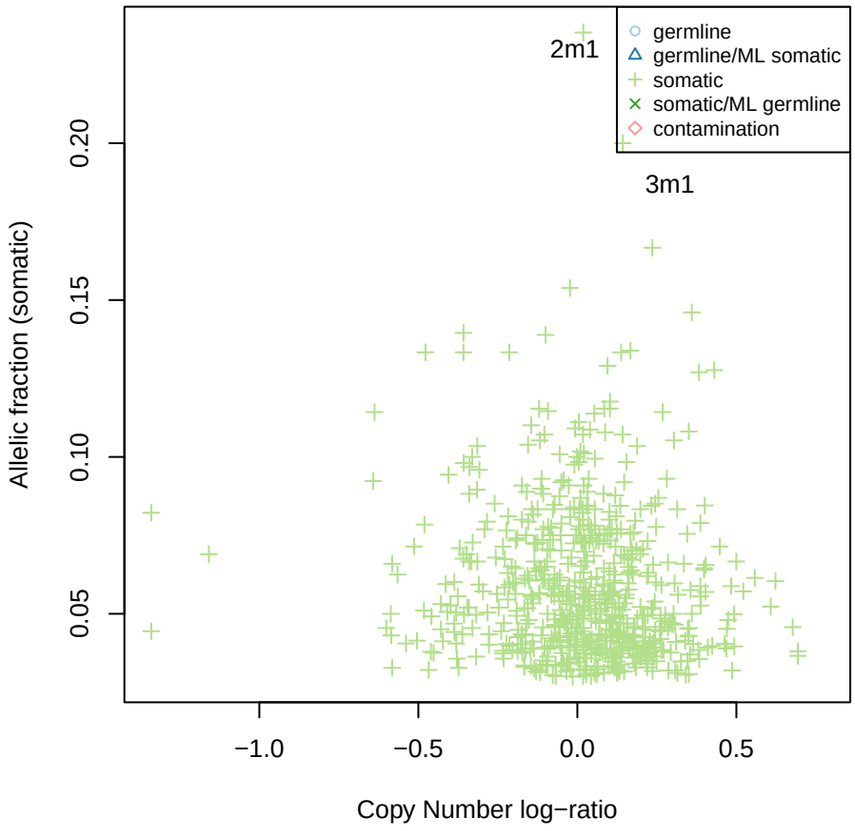

Purity: 0.46 Tumor ploidy: 2.023 SNV log−likelihood: 3.86 GoF: 33.7% Mean coverage: 363;148
1 2 3 4 5 6 7 8 10 11 12 13 14 15 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 20 40 60 80 100
SNV Index

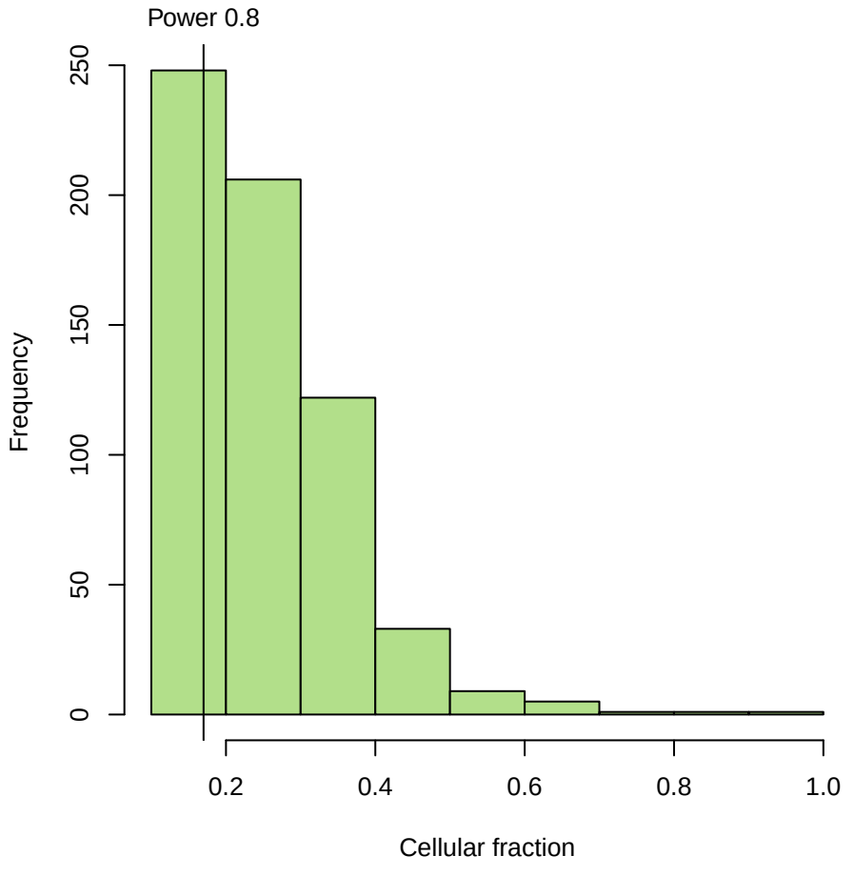

SCNA−fit log−likelihood: −19156.43
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 6
0 20 40 60 80 100
SNV Index

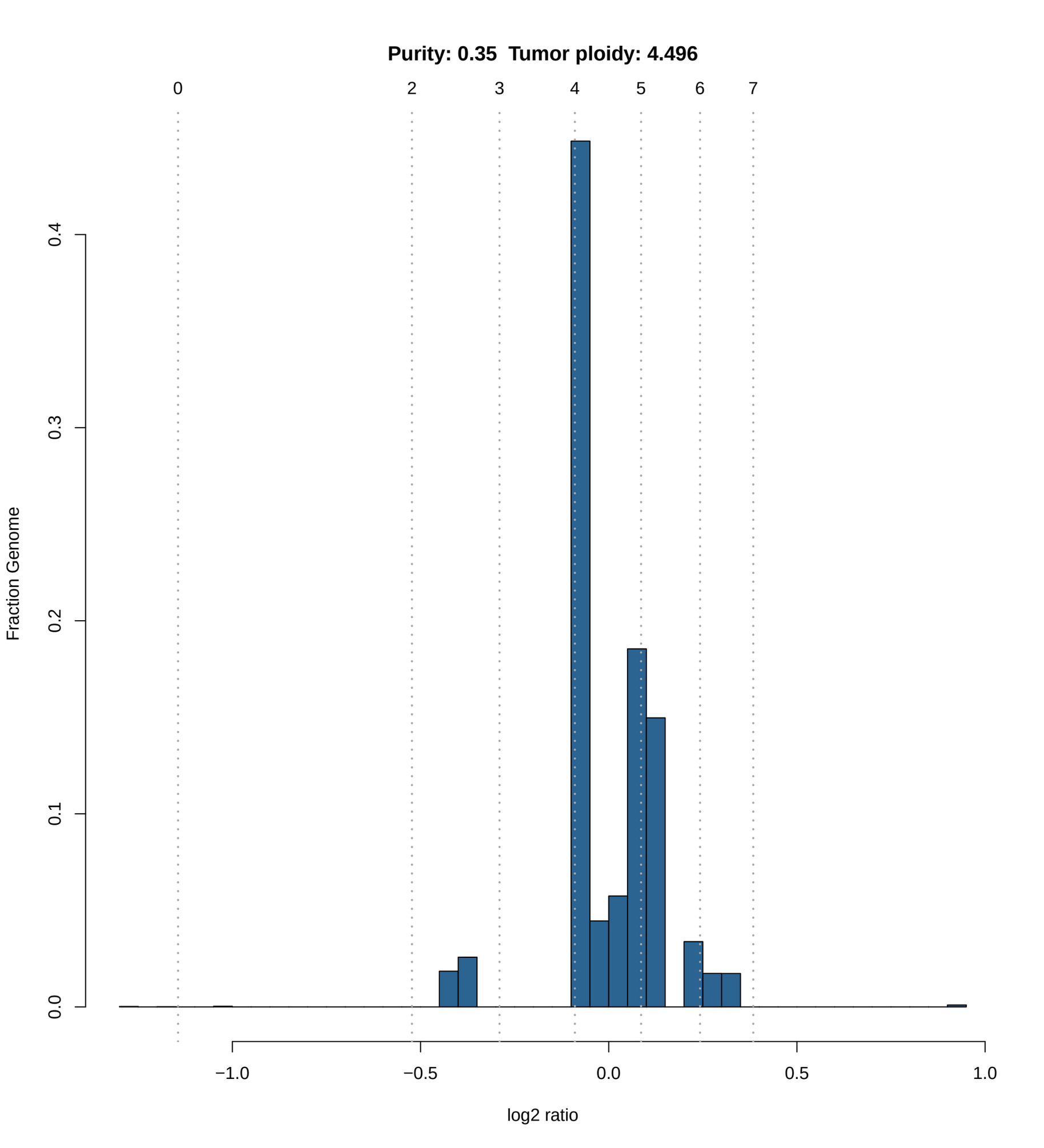

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100
SNV Index

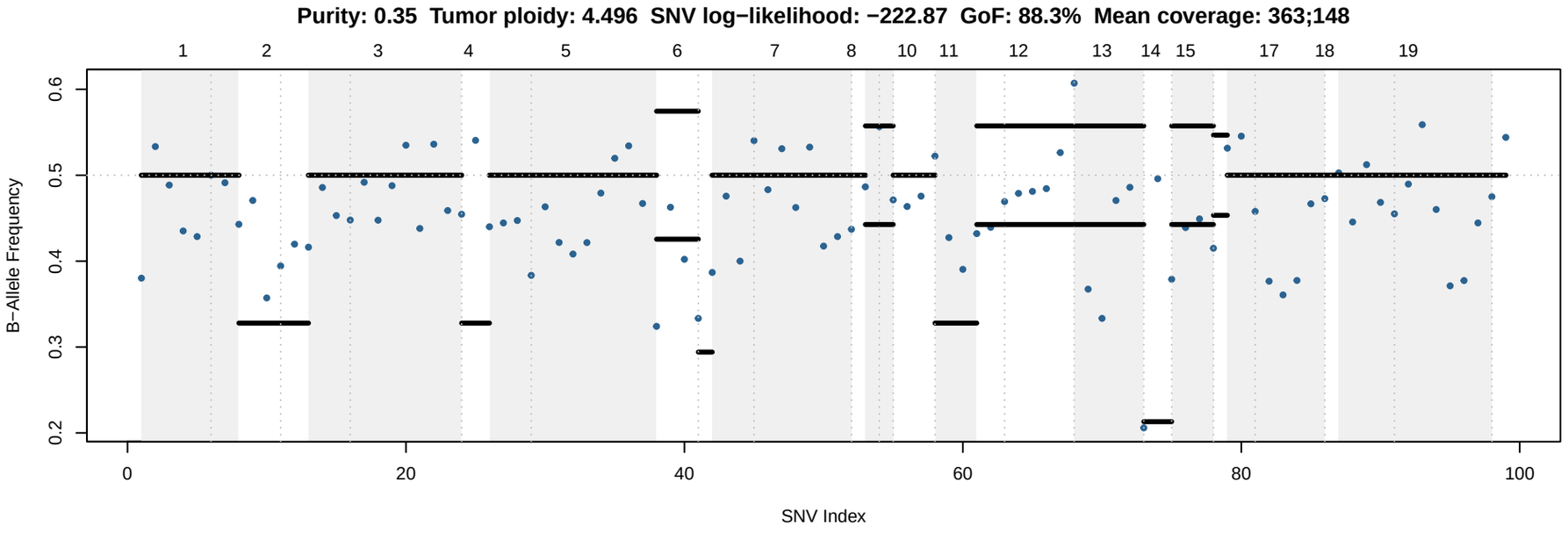

Allelic fraction (germline)
0.2
0.3
0.4
0.5
0.6
2m1
3m1
1m0
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

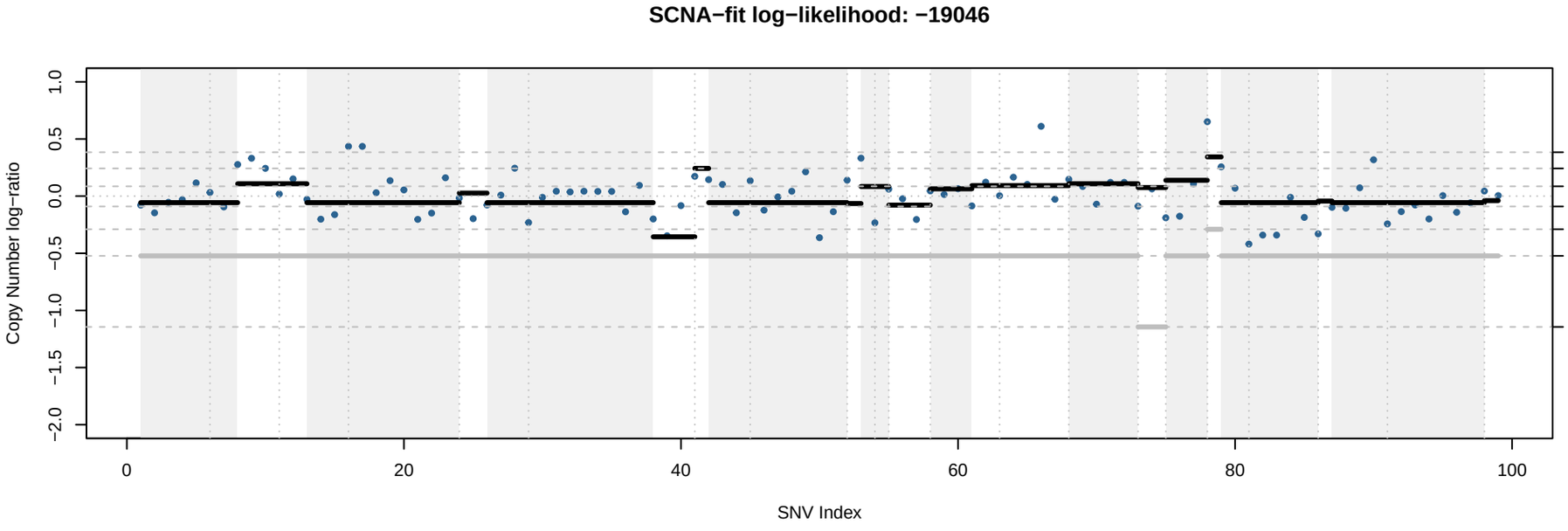

Coverage (log2)
4
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

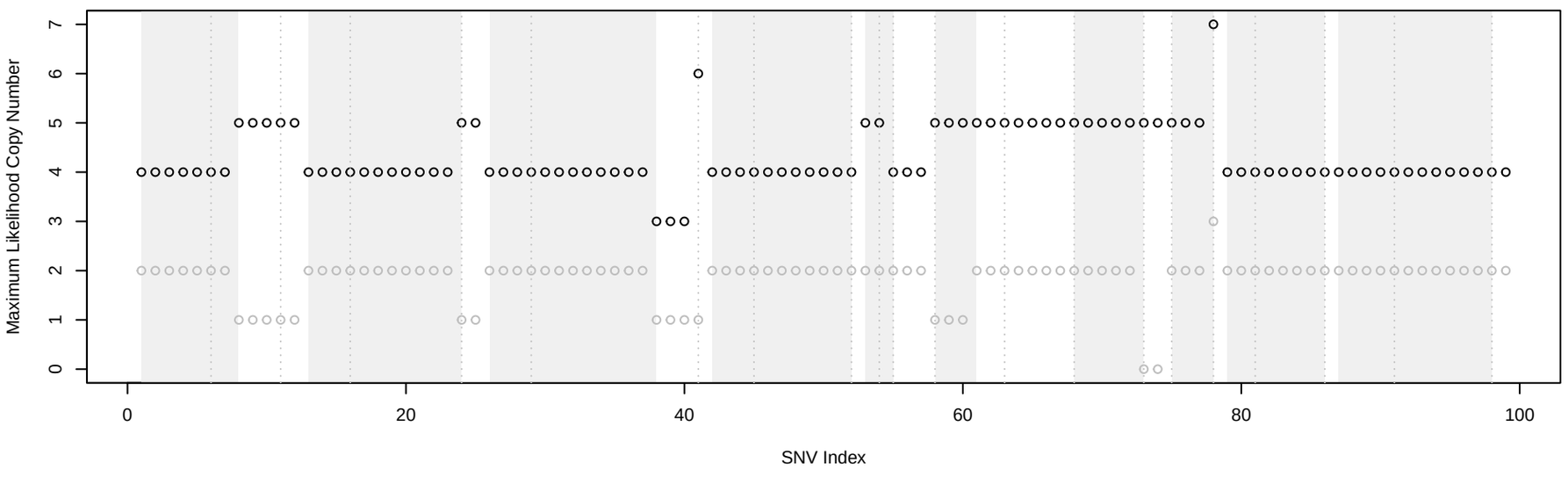

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

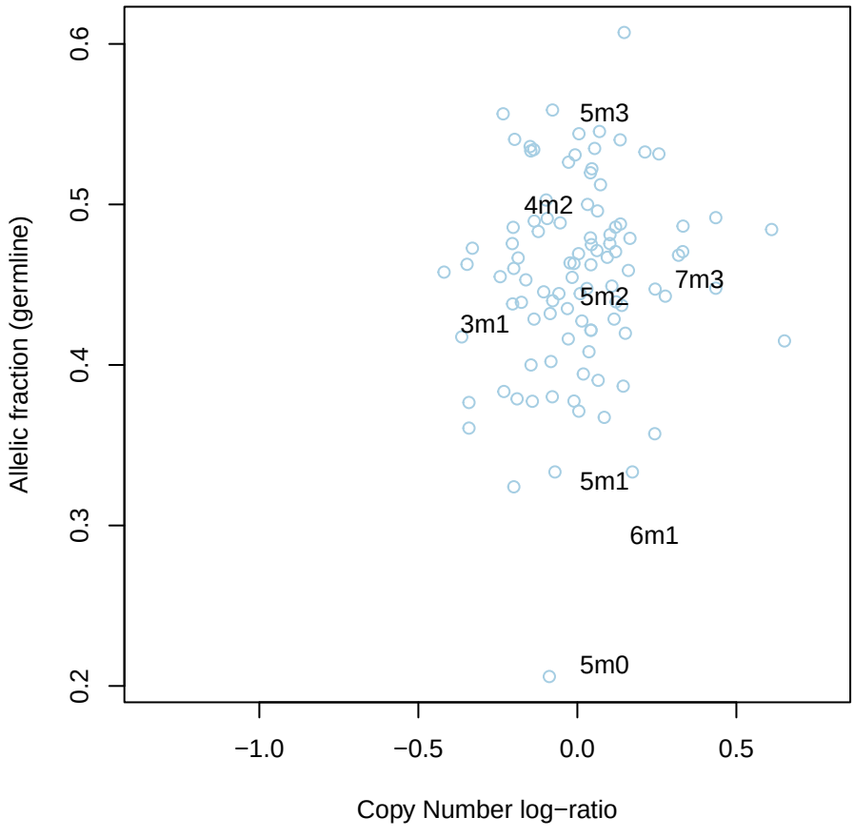

Power 0.8
Frequency
0
50
100
150
200
250
0.2
0.4
0.6
0.8
1.0
Cellular fraction

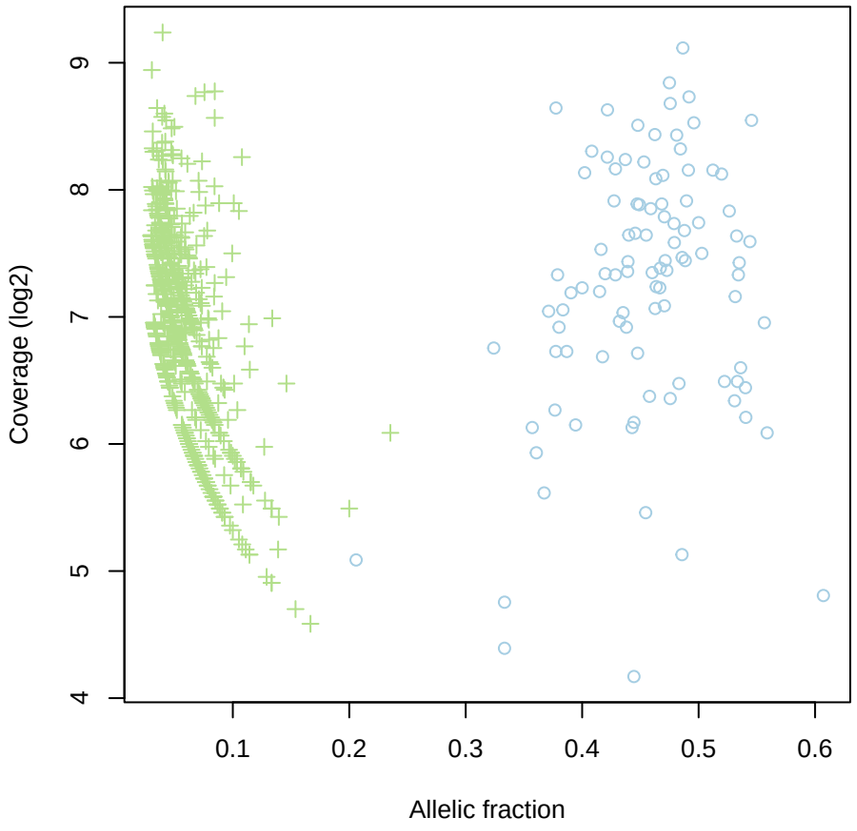

Purity: 0.35 Tumor ploidy: 4.496
0
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

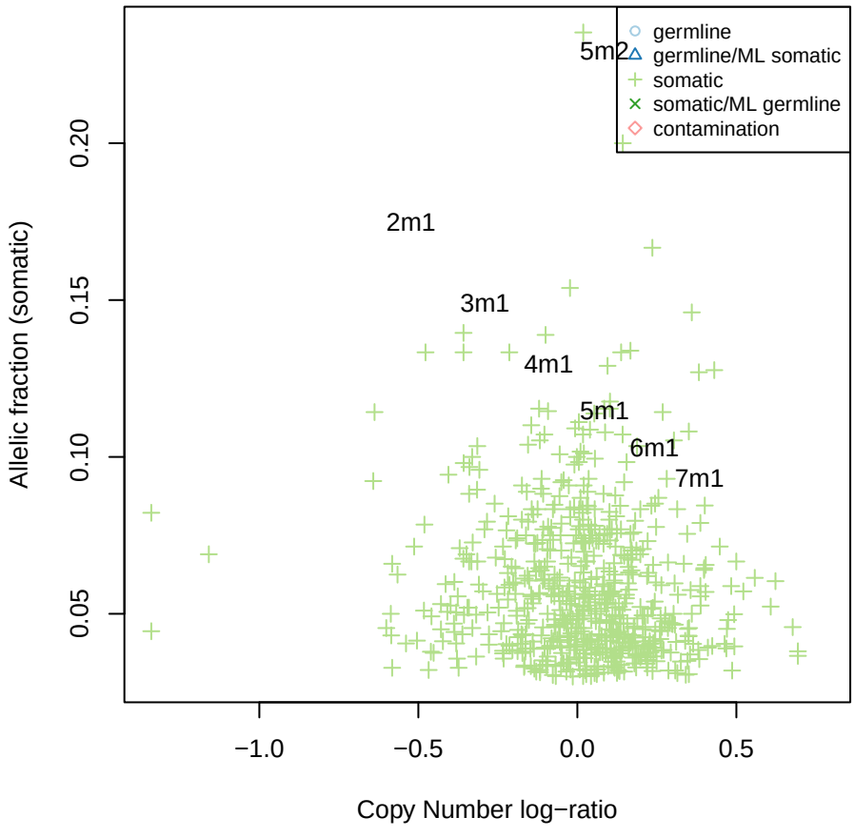

Purity: 0.35 Tumor ploidy: 4.496 SNV log−likelihood: −222.87 GoF: 88.3% Mean coverage: 363;148
1 2 3 4 5 6 7 8 10 11 12 13 14 15 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 20 40 60 80 100
SNV Index

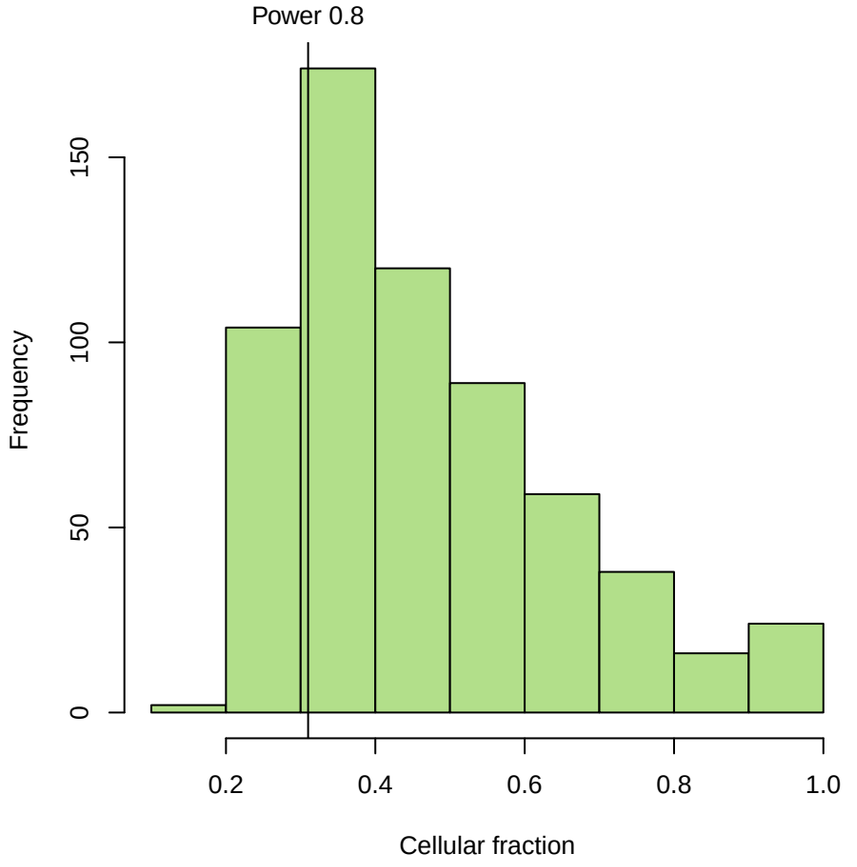

SCNA−fit log−likelihood: −19046
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 2 3 5 7
0 20 40 60 80 100
SNV Index

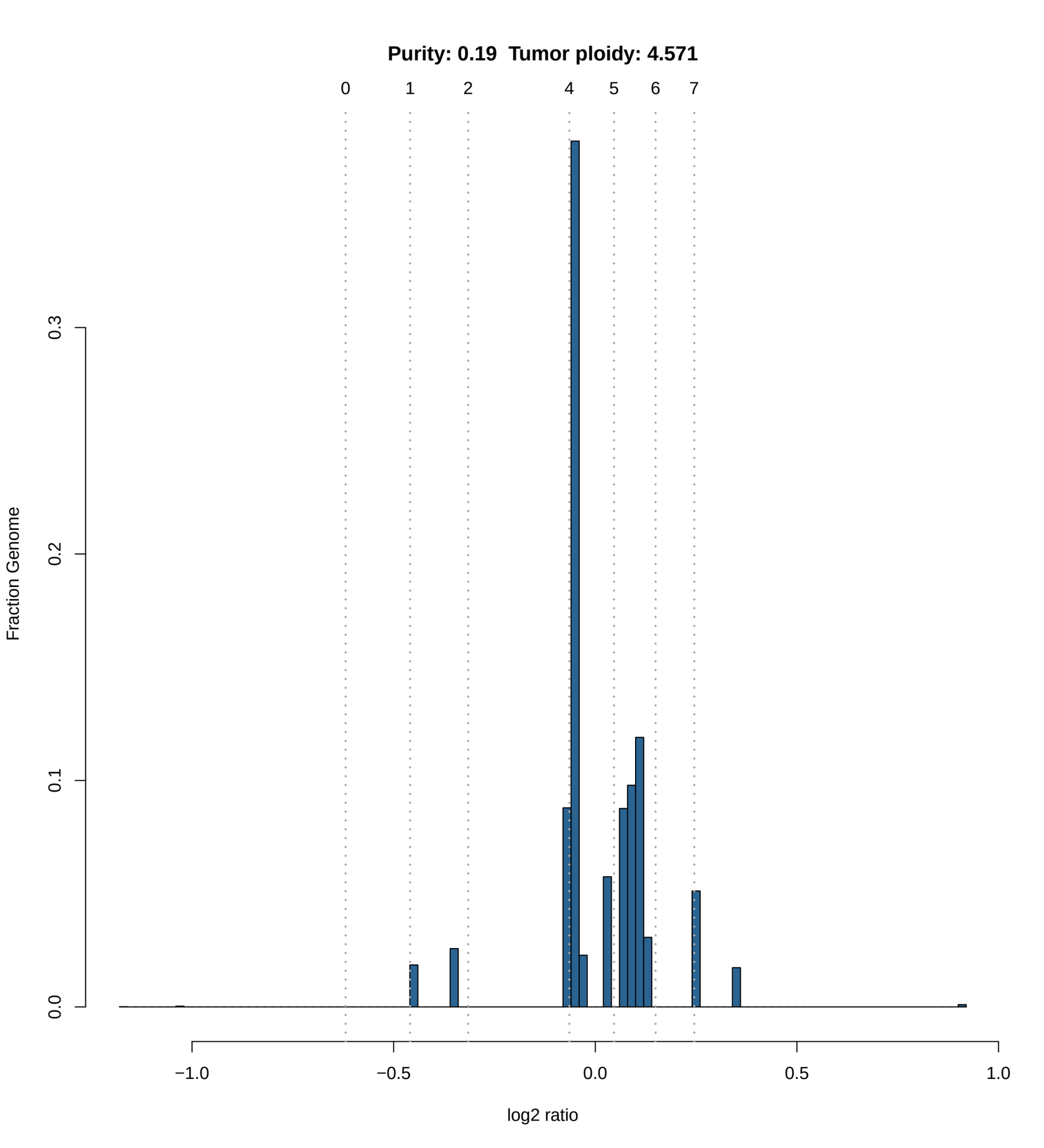

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

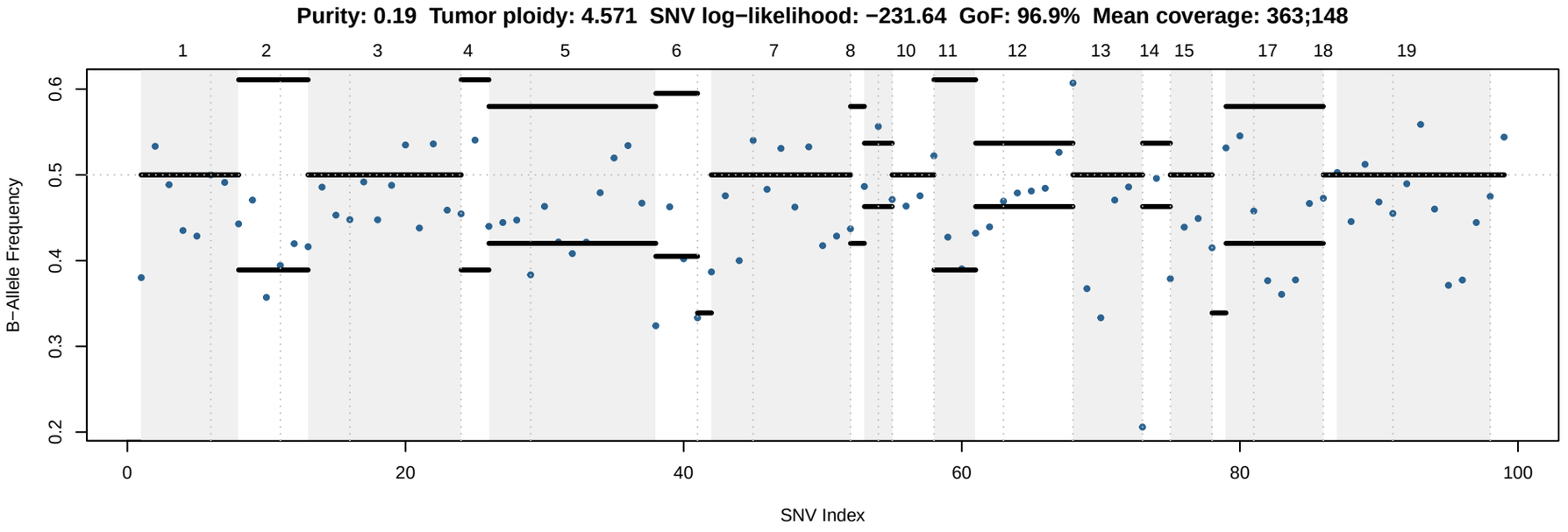

Allelic fraction (germline)
Copy Number log−ratio
5m3
4m2
7m3
5m2
3m1
5m1
6m1
5m0

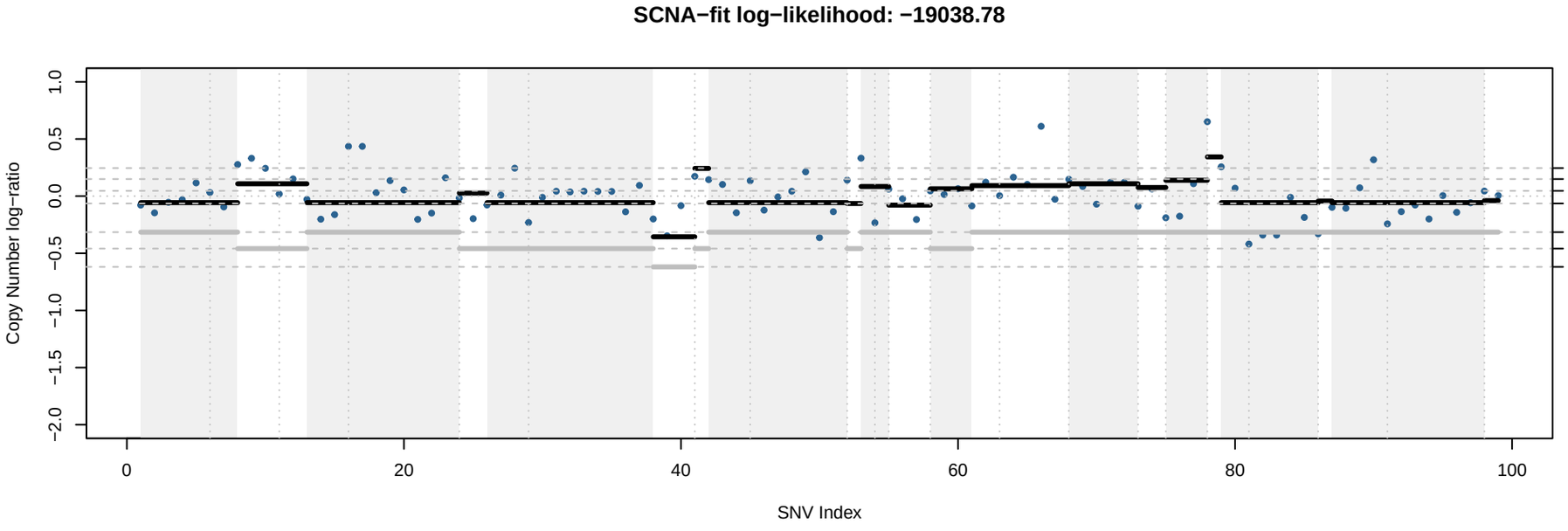

Coverage (log2)
Allelic fraction

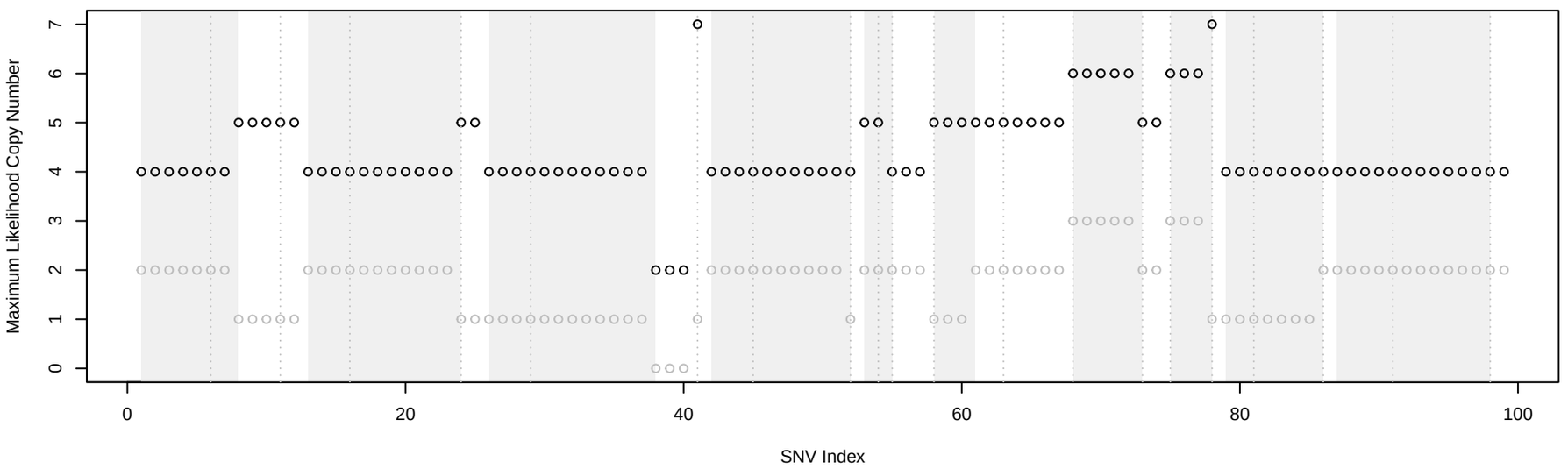

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
5m2
2m1
3m1
4m1
5m1
6m1
7m1

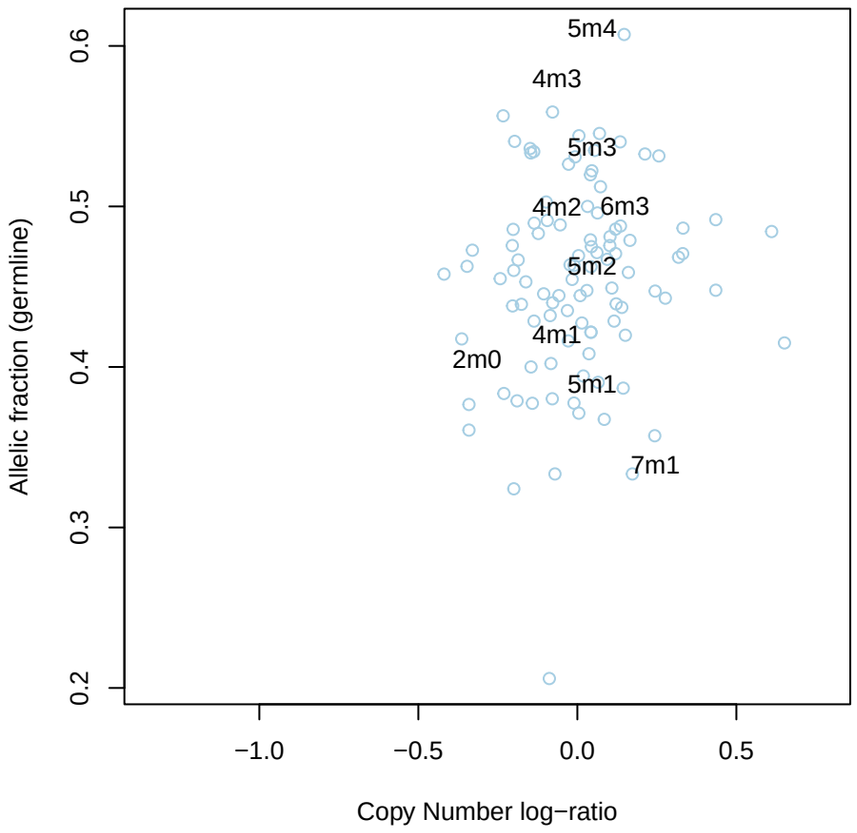

Power 0.8
Frequency
Cellular fraction

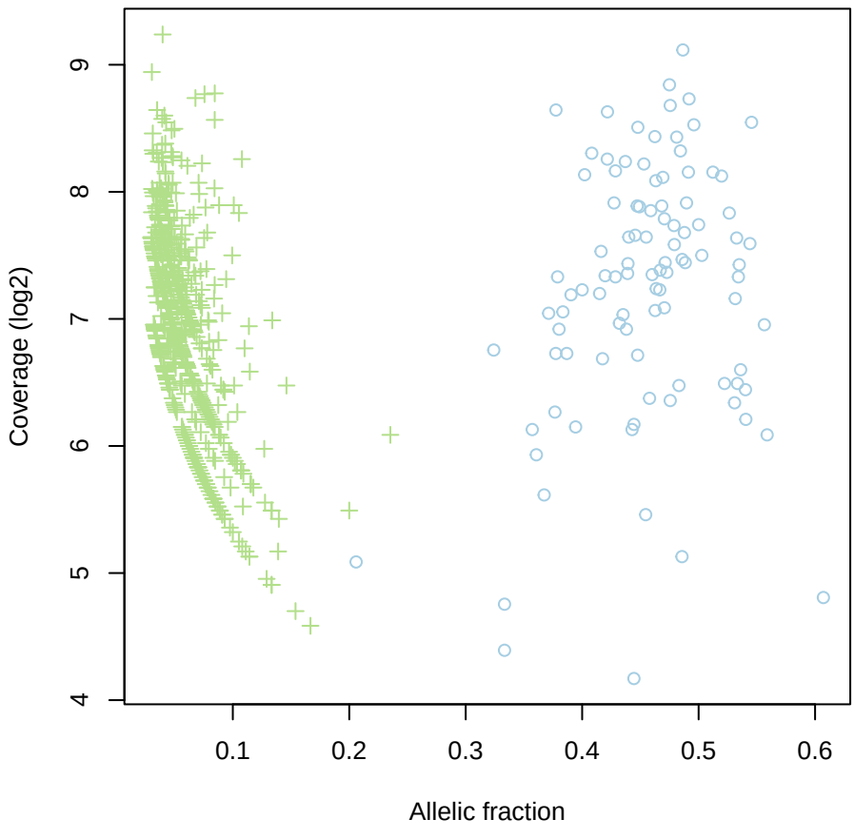

Purity: 0.19 Tumor ploidy: 4.571
0
1
2
4
5
6
7
0.0
0.1
0.2
0.3
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

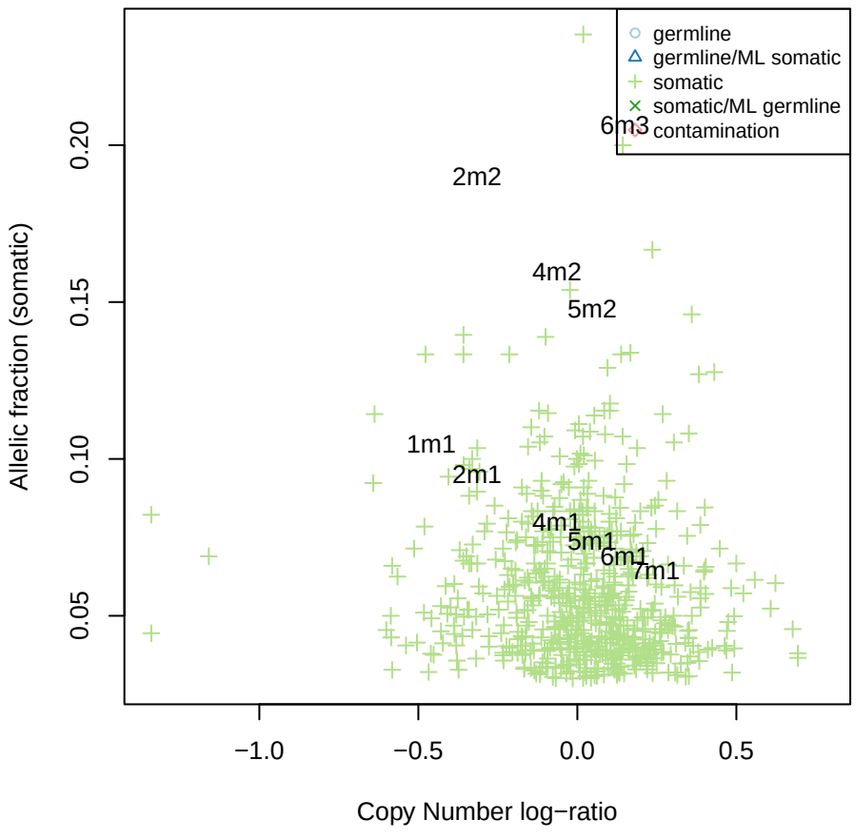

Purity: 0.19 Tumor ploidy: 4.571 SNV log−likelihood: −231.64 GoF: 96.9% Mean coverage: 363;148
1 2 3 4 5 6 7 8 10 11 12 13 14 15 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 20 40 60 80 100
SNV Index

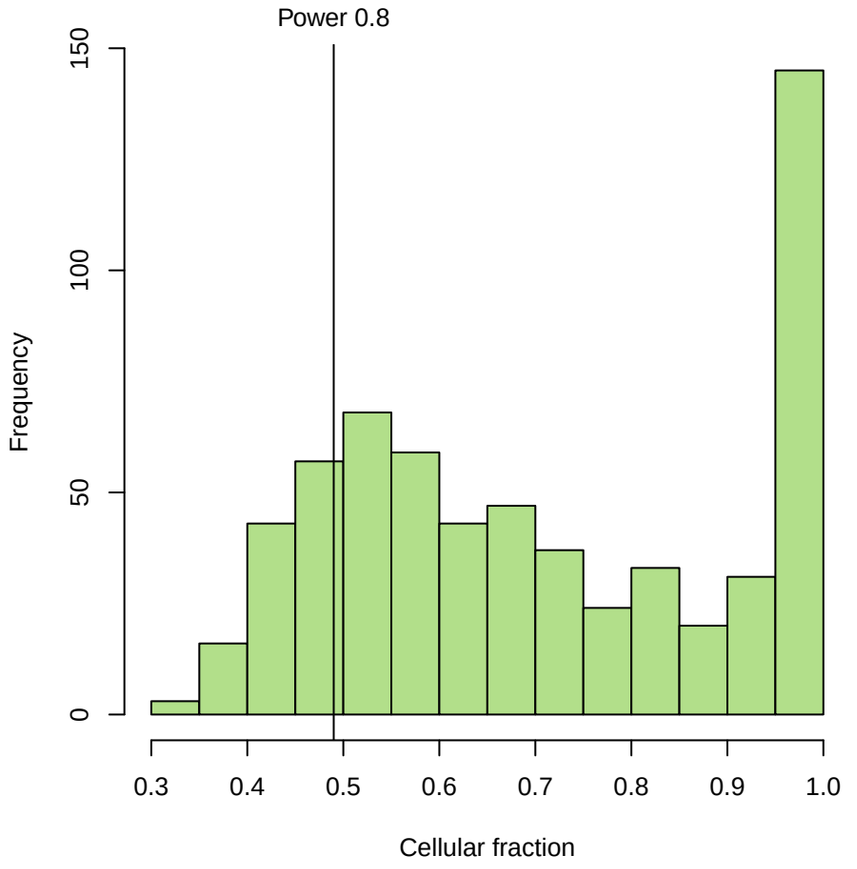

SCNA−fit log−likelihood: −19038.78
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 2 4 7
0 20 40 60 80 100
SNV Index

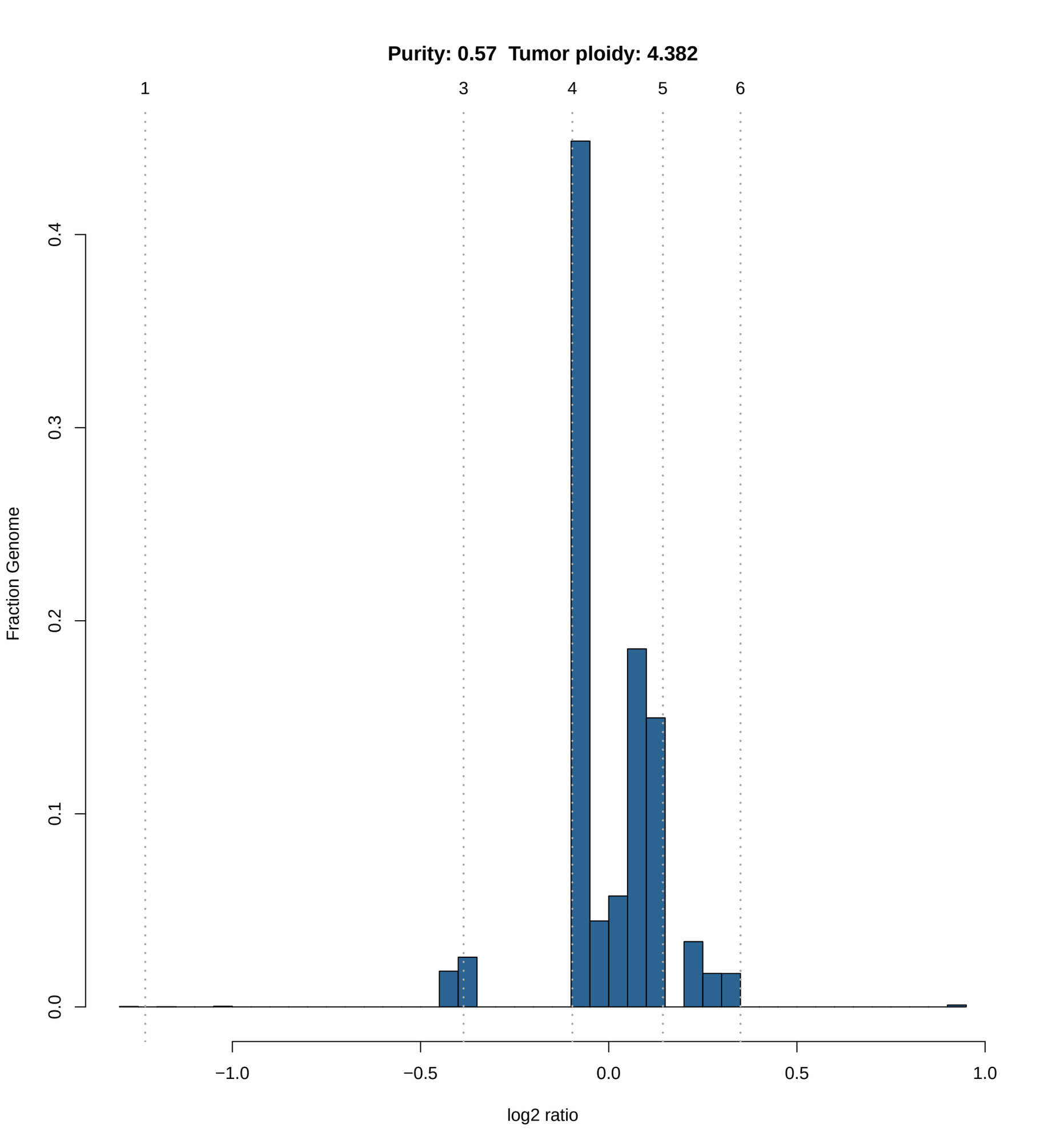

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

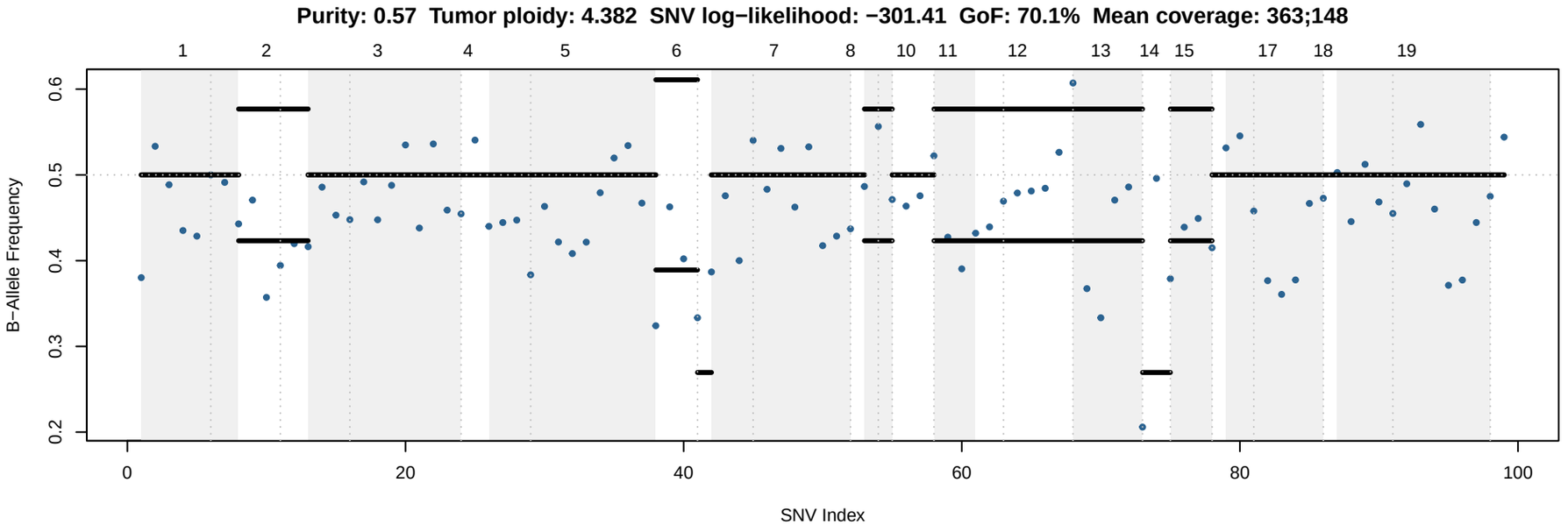

5m4
4m3
5m3
4m2
6m3
5m2
4m1
2m0
5m1
7m1
Allelic fraction (germline)
Copy Number log−ratio

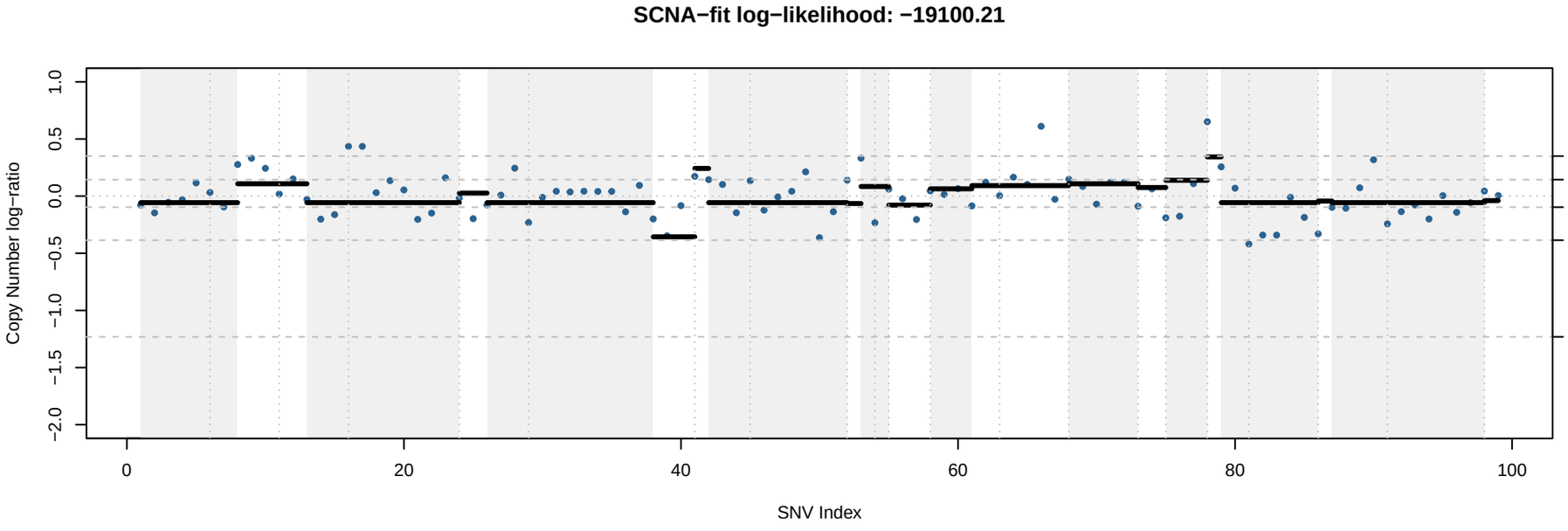

Coverage (log2)
Allelic fraction

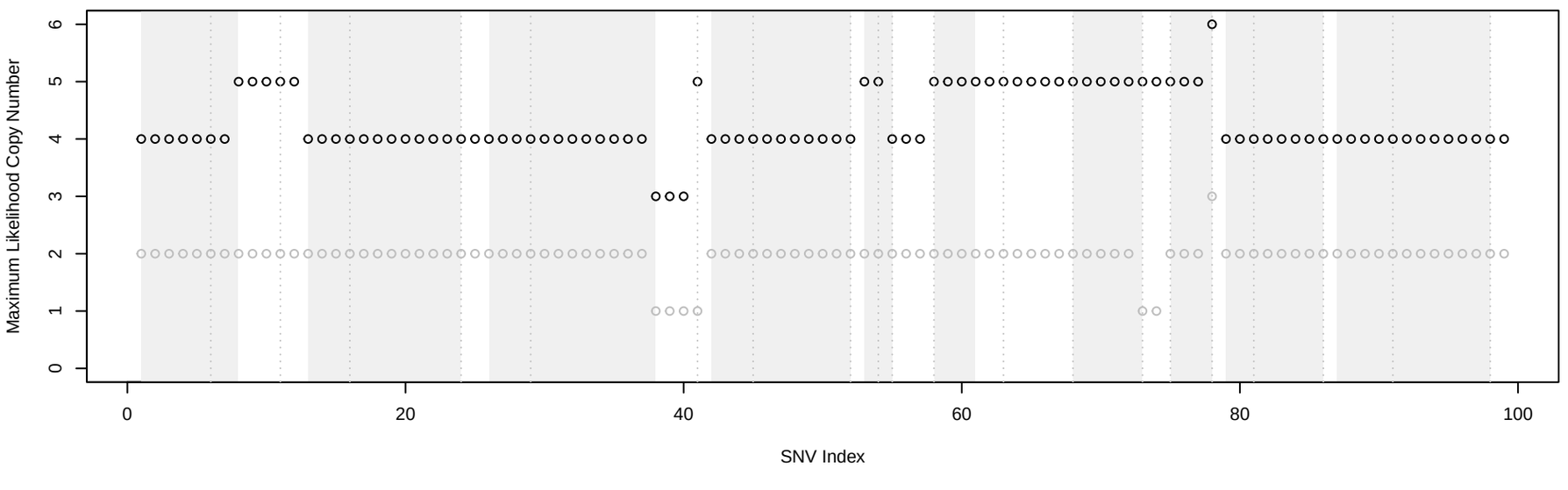

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m3
2m2
4m2
5m2
1m1
2m1
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

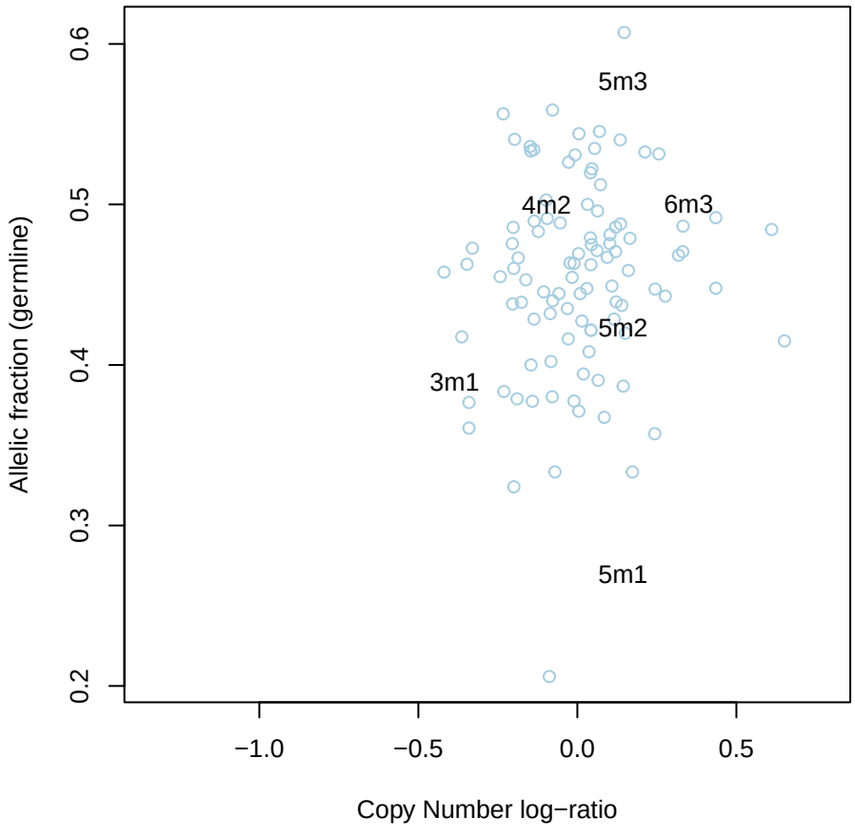

Power 0.8
Frequency
Cellular fraction

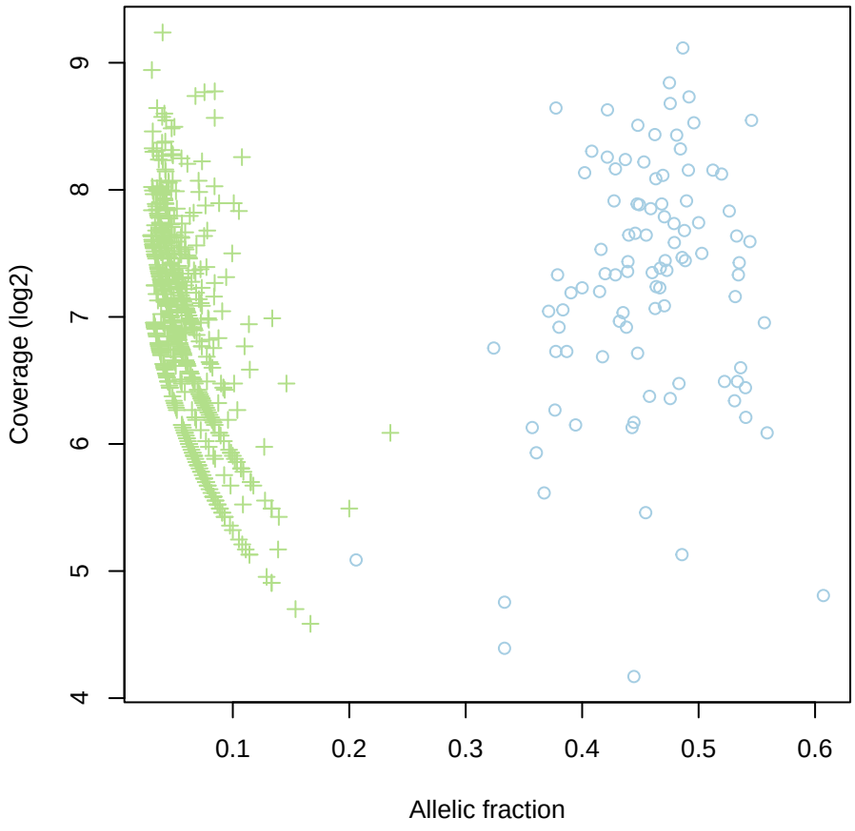

Purity: 0.57 Tumor ploidy: 4.382
1
3
4
5
6
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

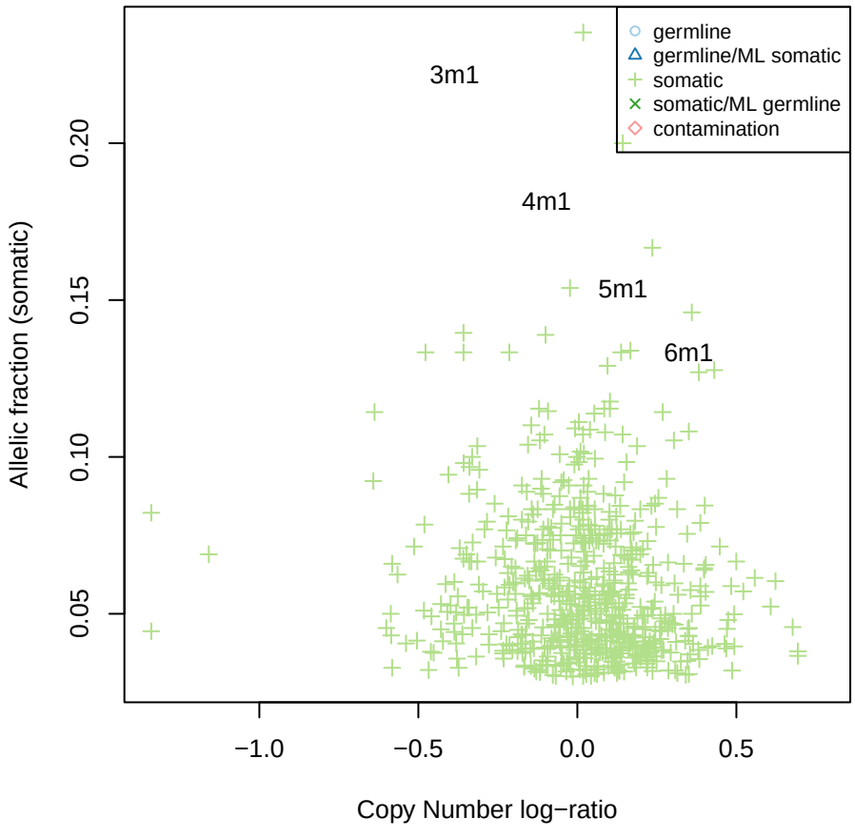

Purity: 0.57 Tumor ploidy: 4.382 SNV log−likelihood: −301.41 GoF: 70.1% Mean coverage: 363;148
1 2 3 4 5 6 7 8 10 11 12 13 14 15 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 20 40 60 80 100
SNV Index

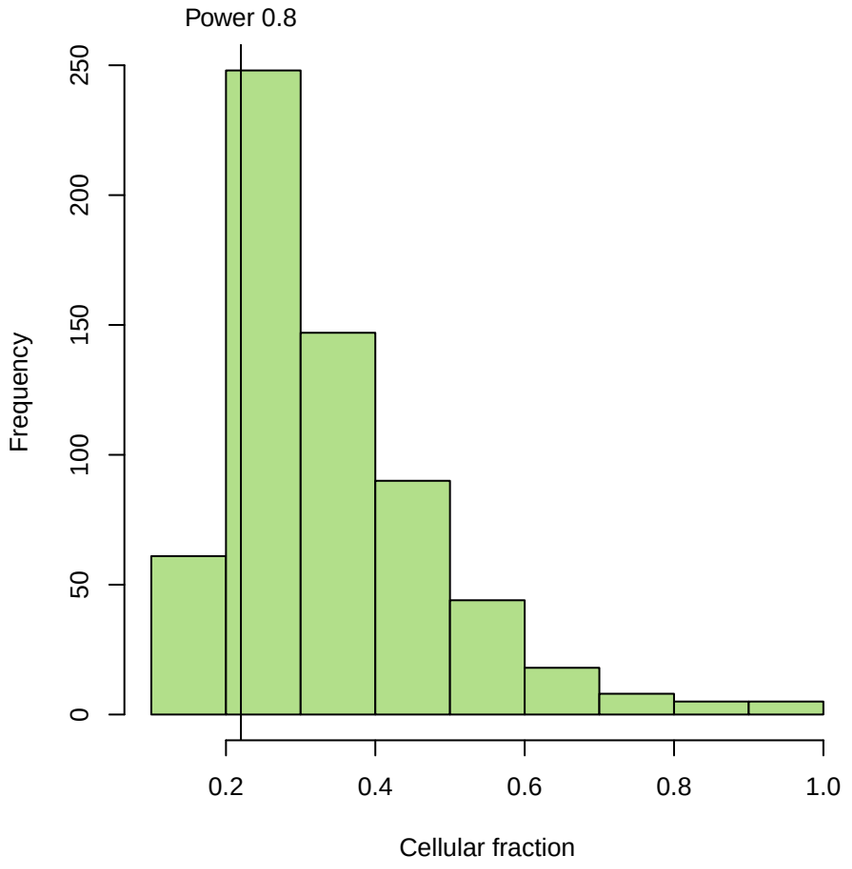

SCNA−fit log−likelihood: −19100.21
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
1 3 4 5
0 20 40 60 80 100
SNV Index

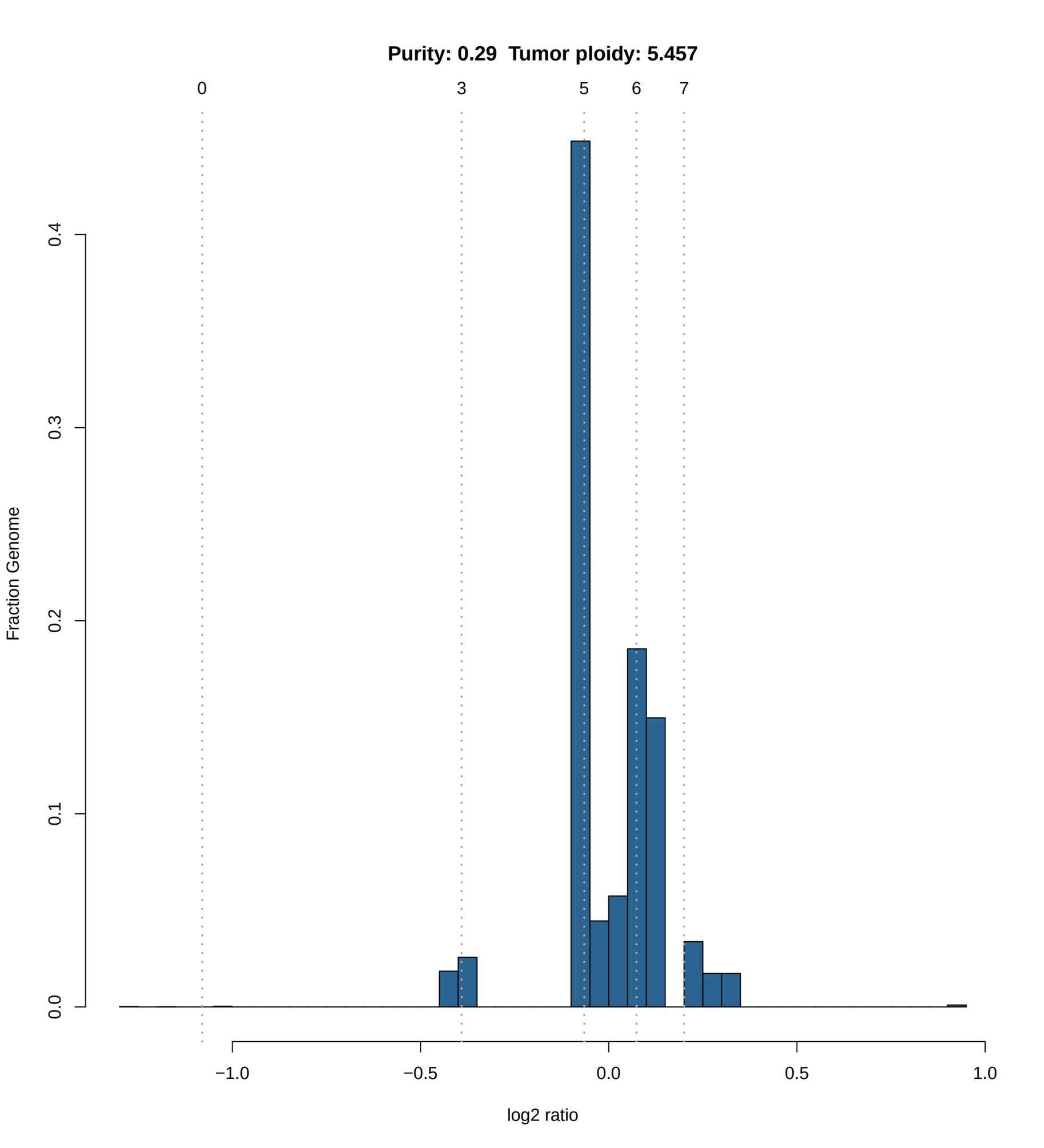

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100
SNV Index

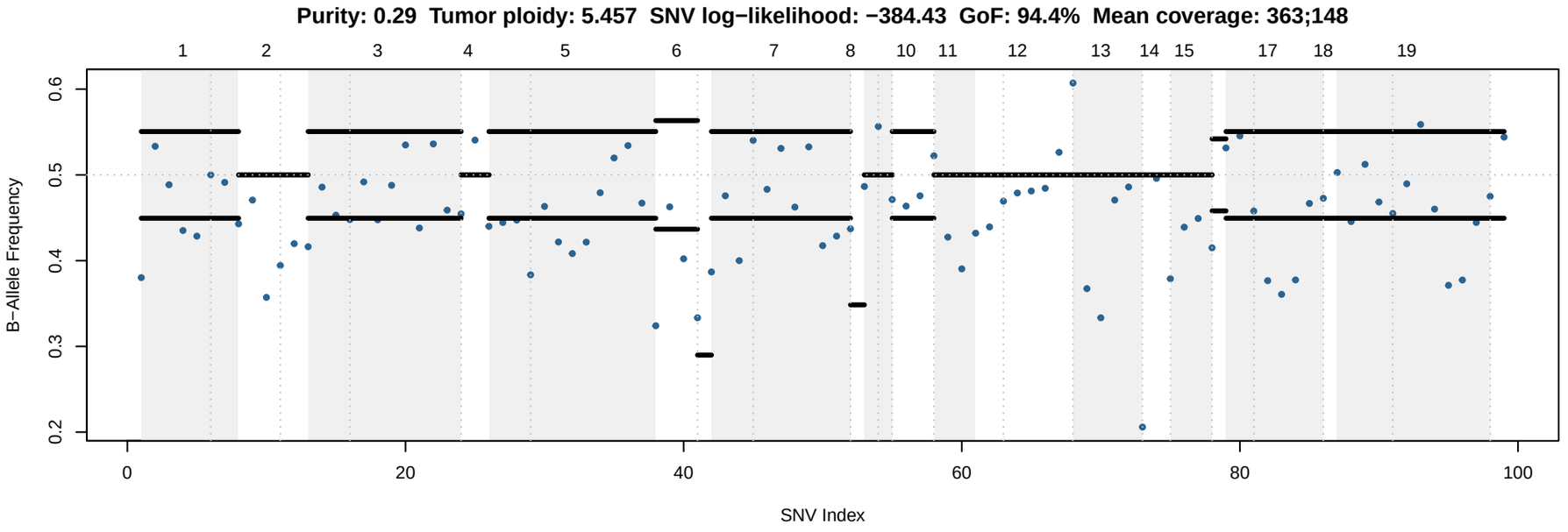

Allelic fraction (germline)
Copy Number log−ratio
5m3
4m2
6m3
5m2
3m1
5m1

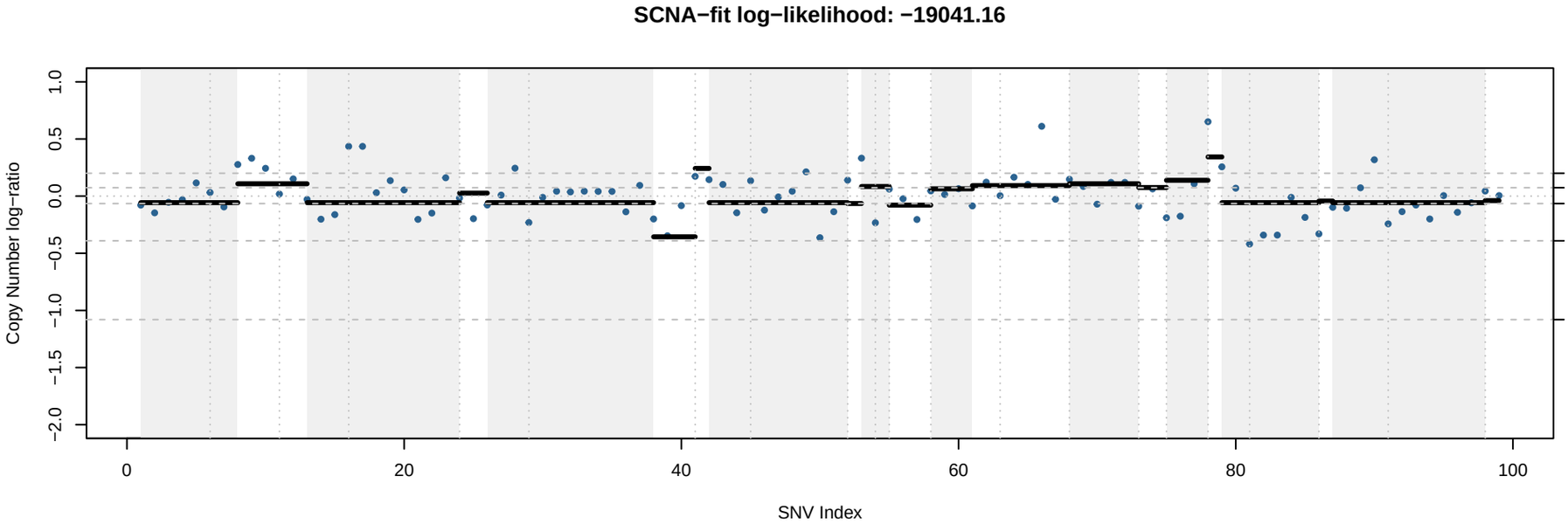

Coverage (log2)
Allelic fraction

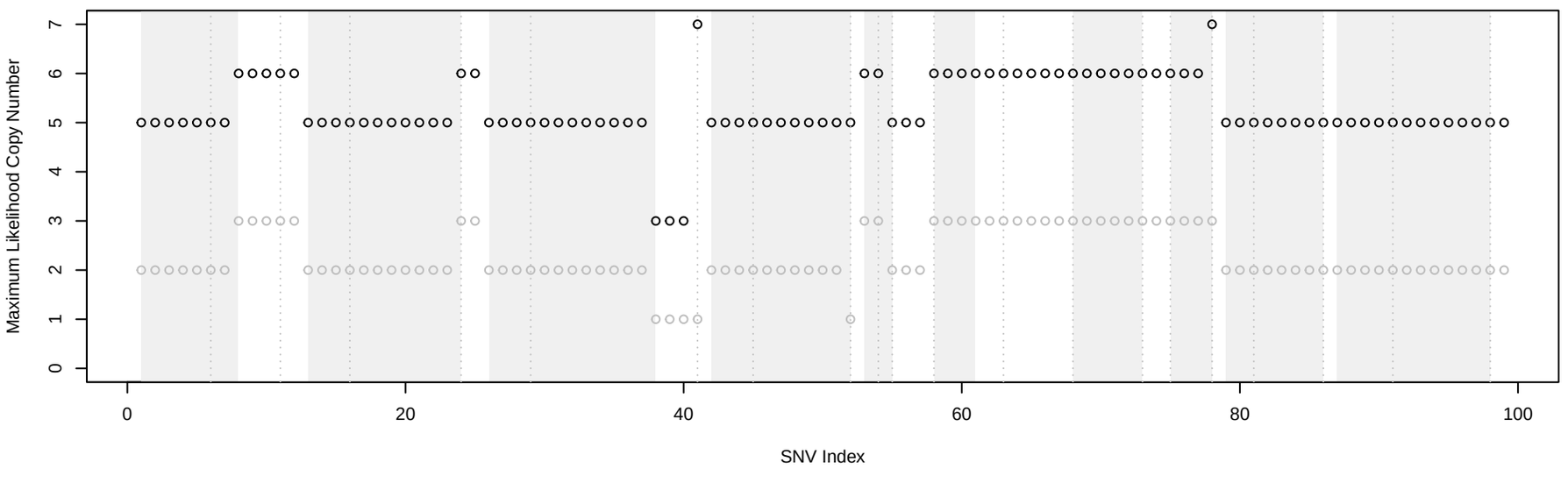

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
6m1

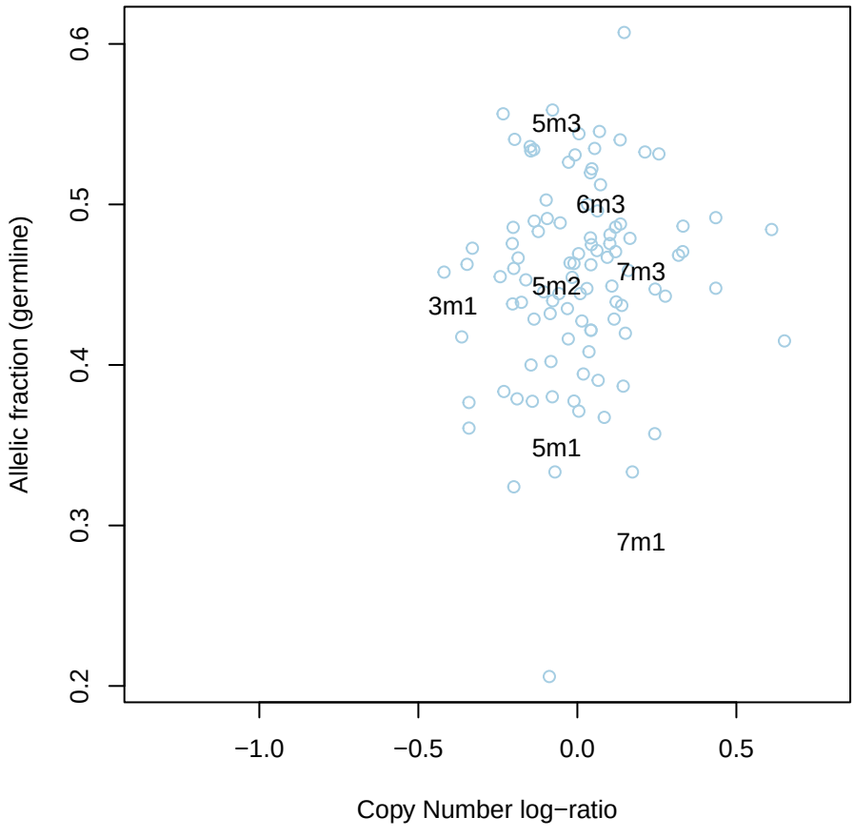

Power 0.8
Frequency
Cellular fraction

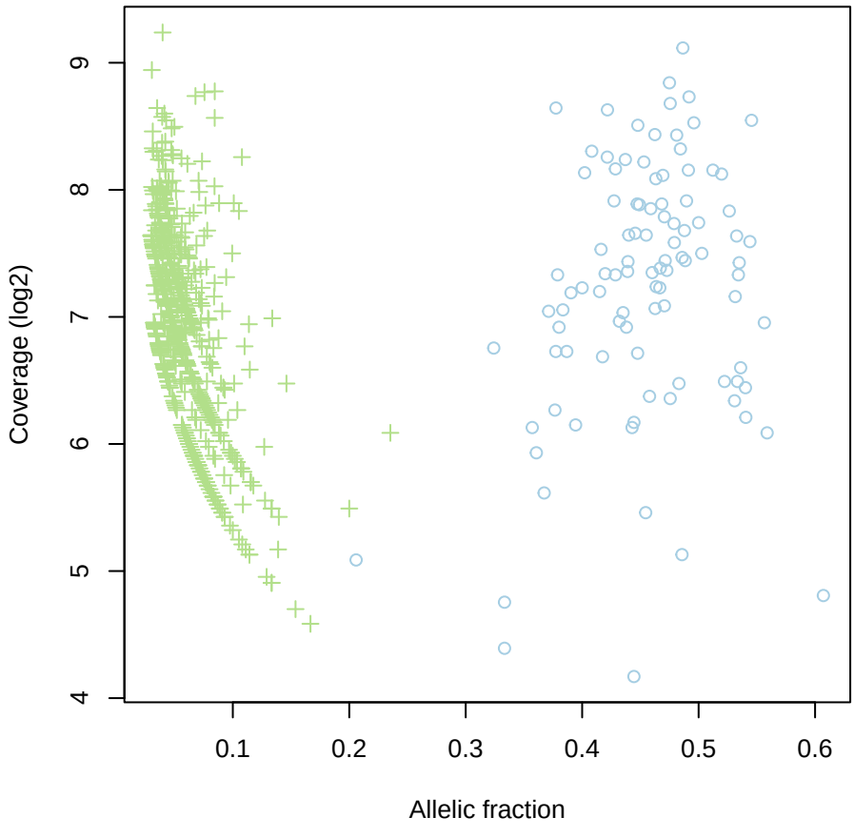

Purity: 0.29 Tumor ploidy: 5.457
0
3
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

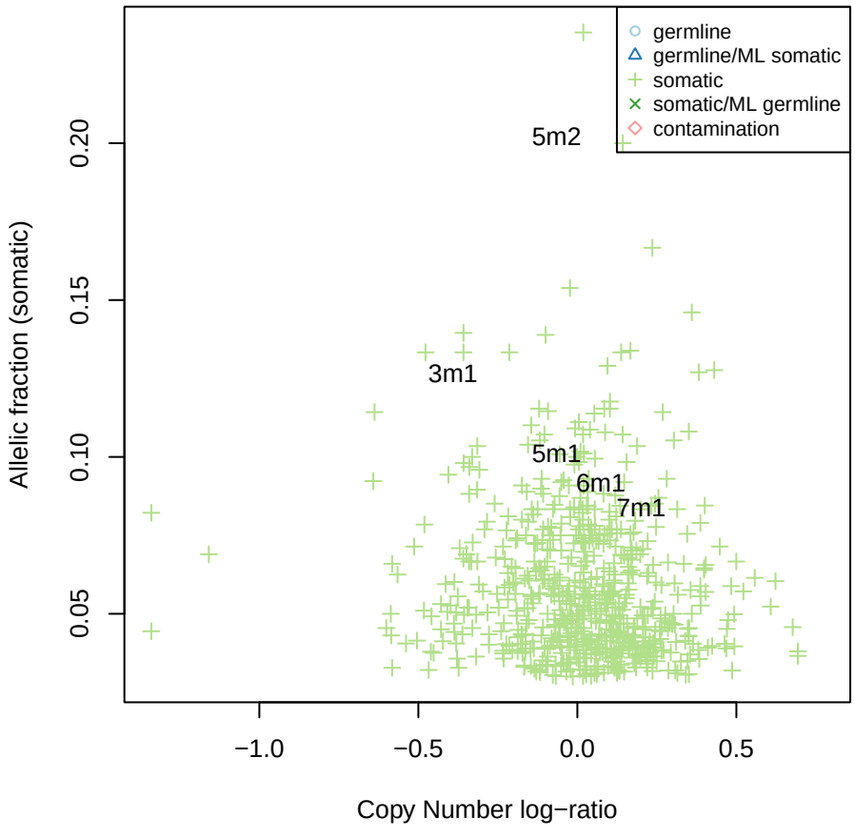

Purity: 0.29 Tumor ploidy: 5.457 SNV log−likelihood: −384.43 GoF: 94.4% Mean coverage: 363;148
1 2 3 4 5 6 7 8 10 11 12 13 14 15 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 20 40 60 80 100
SNV Index

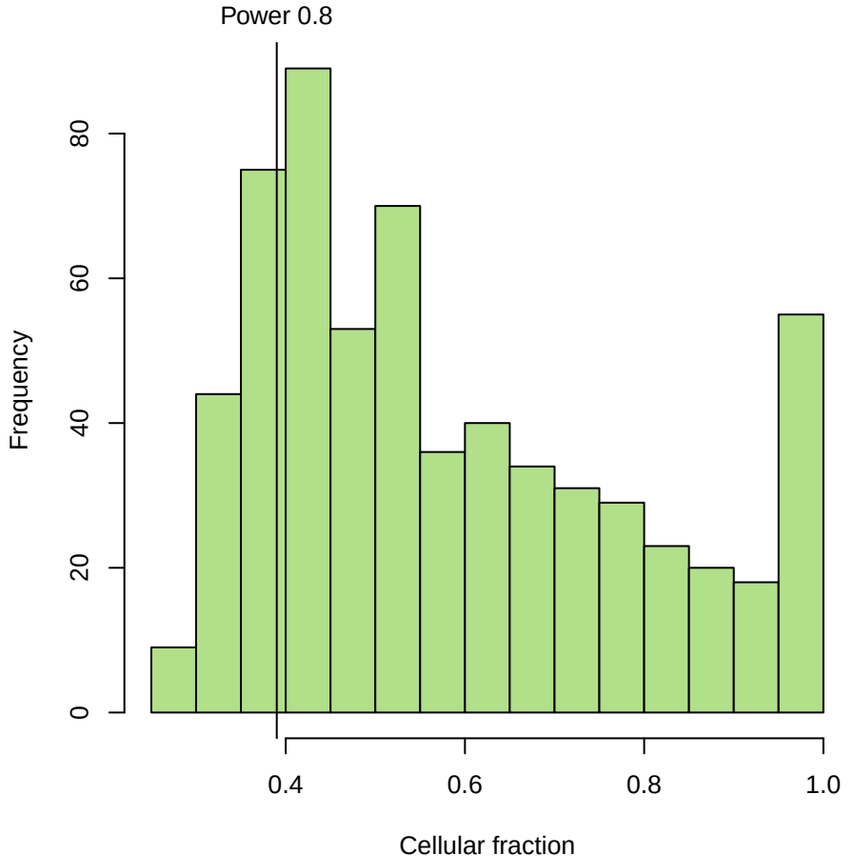

SCNA−fit log−likelihood: −19041.16
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 3 5 7
0 20 40 60 80 100
SNV Index

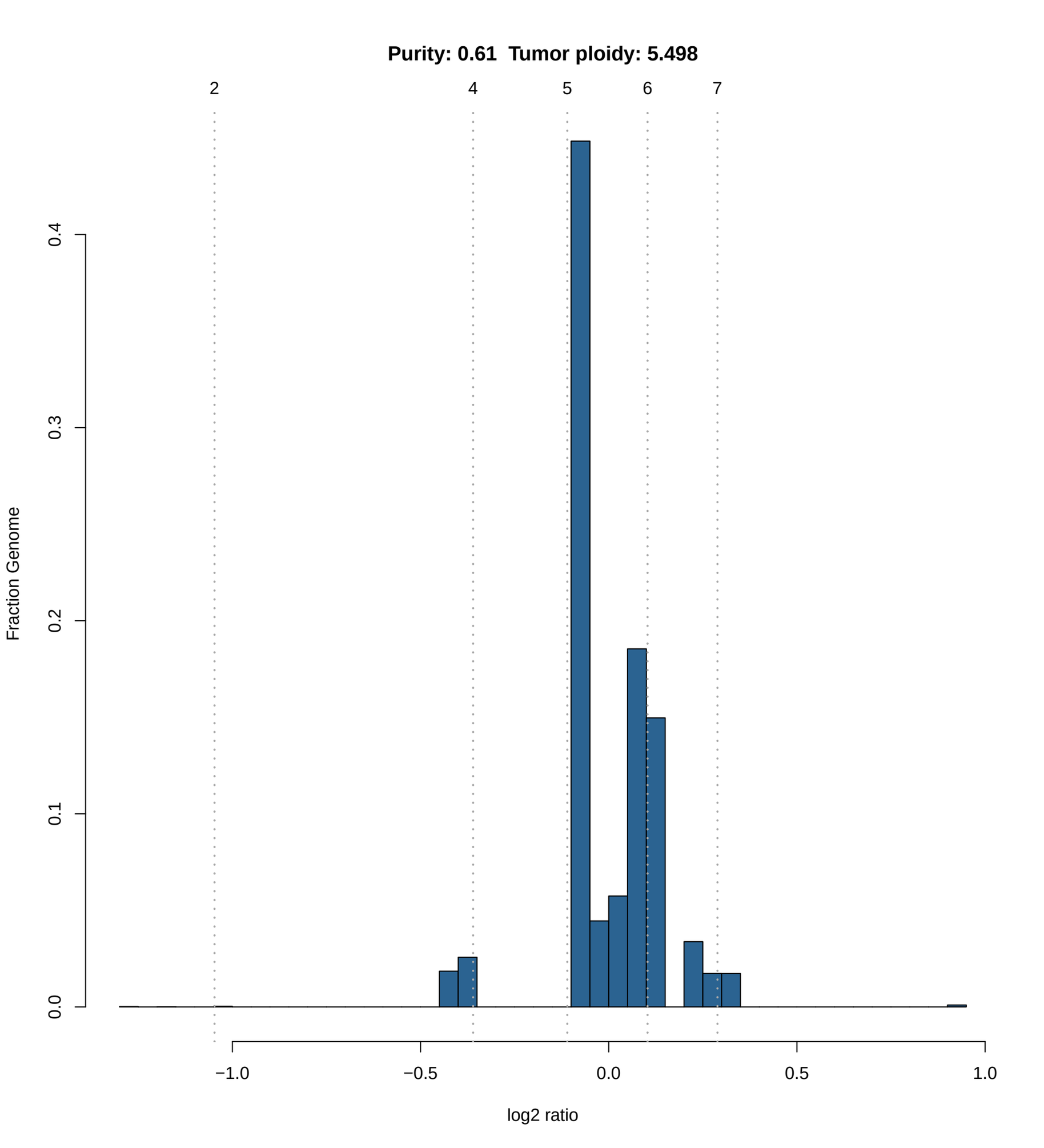

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

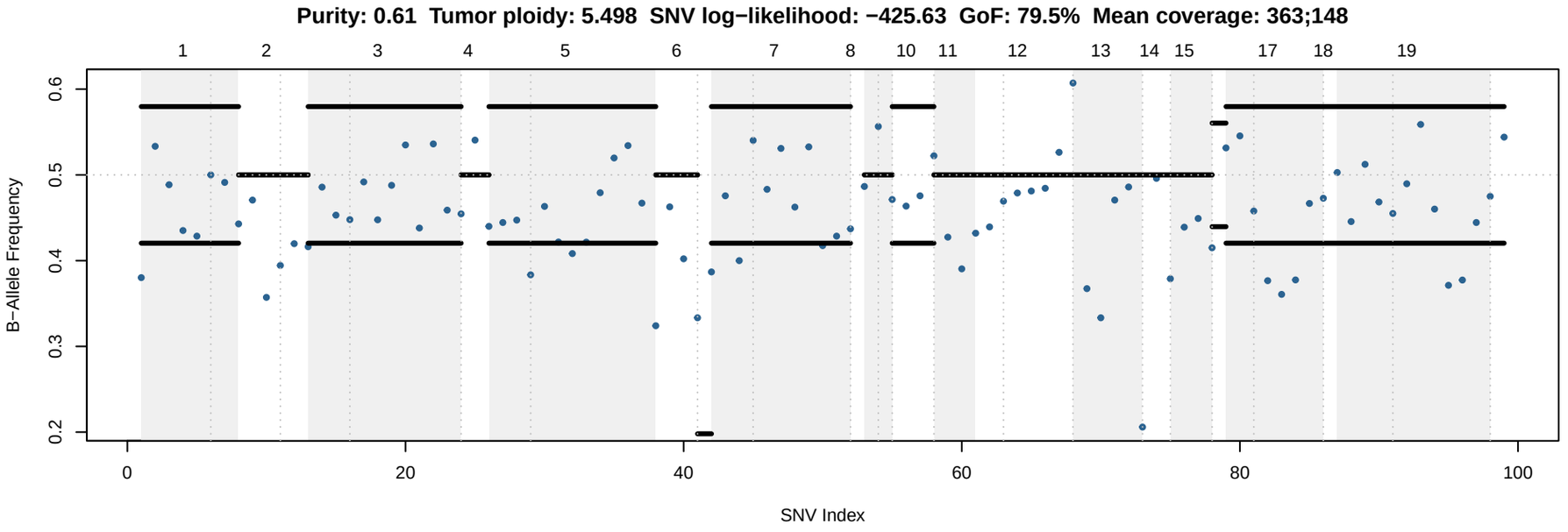

Allelic fraction (germline)
0.2
0.3
0.4
0.5
0.6
5m3
6m3
7m3
5m2
3m1
5m1
7m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

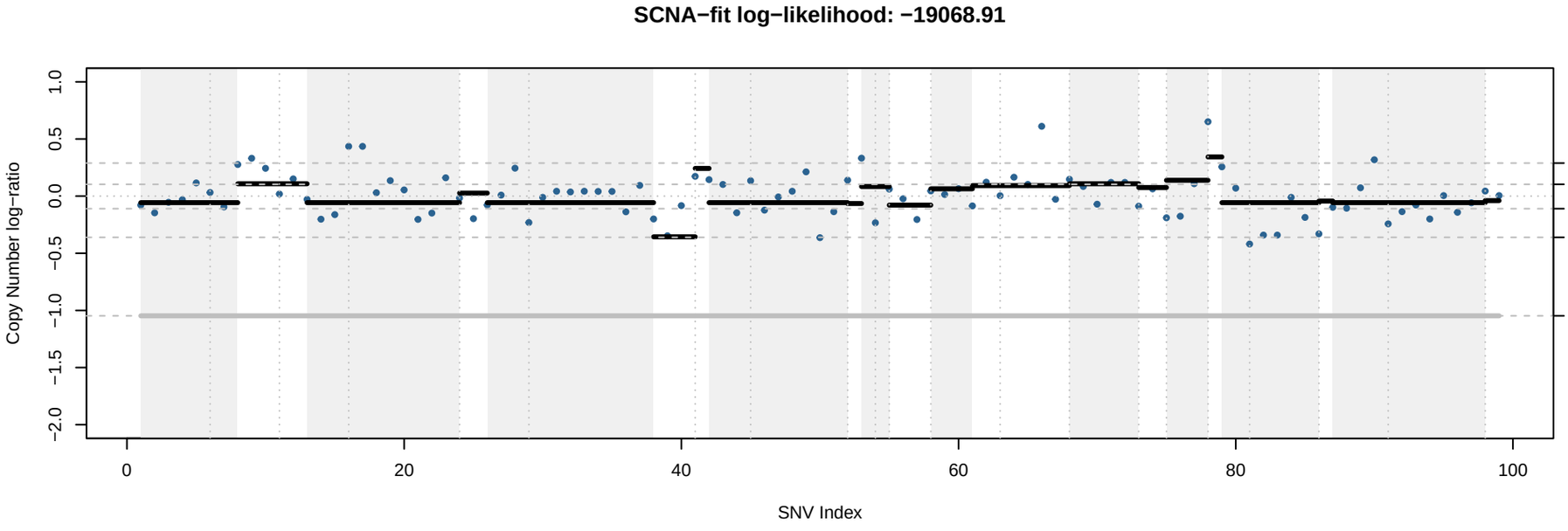

Coverage (log2)
4
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

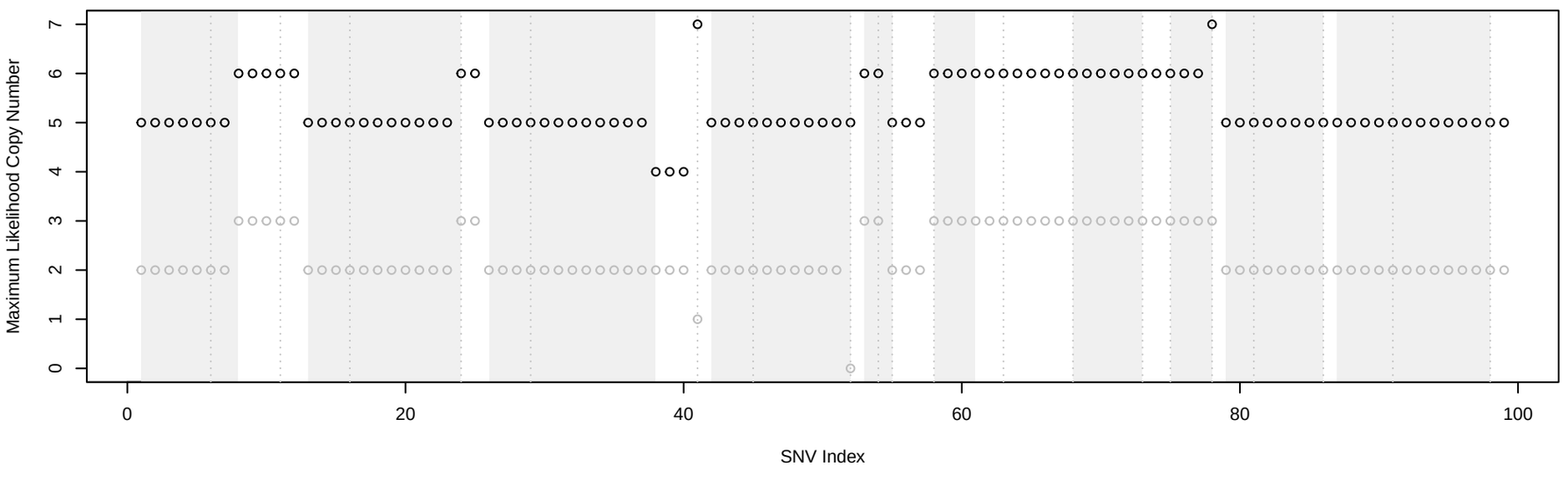

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m2
3m1
5m1
6m1
7m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

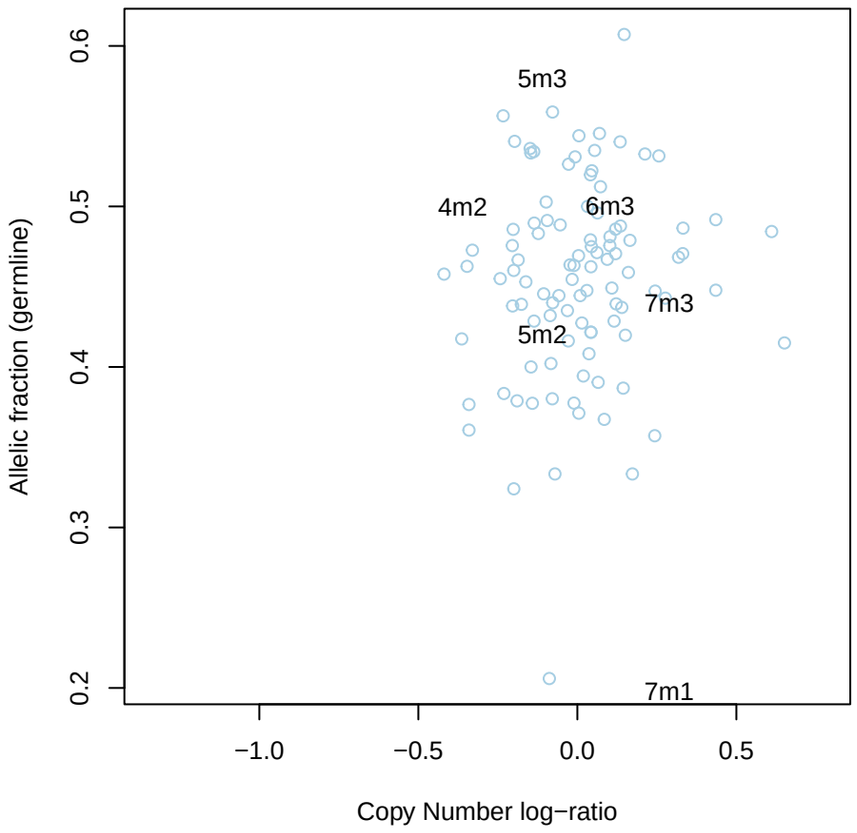

Power 0.8
Frequency
0
20
40
60
80
0.4
0.6
0.8
1.0
Cellular fraction

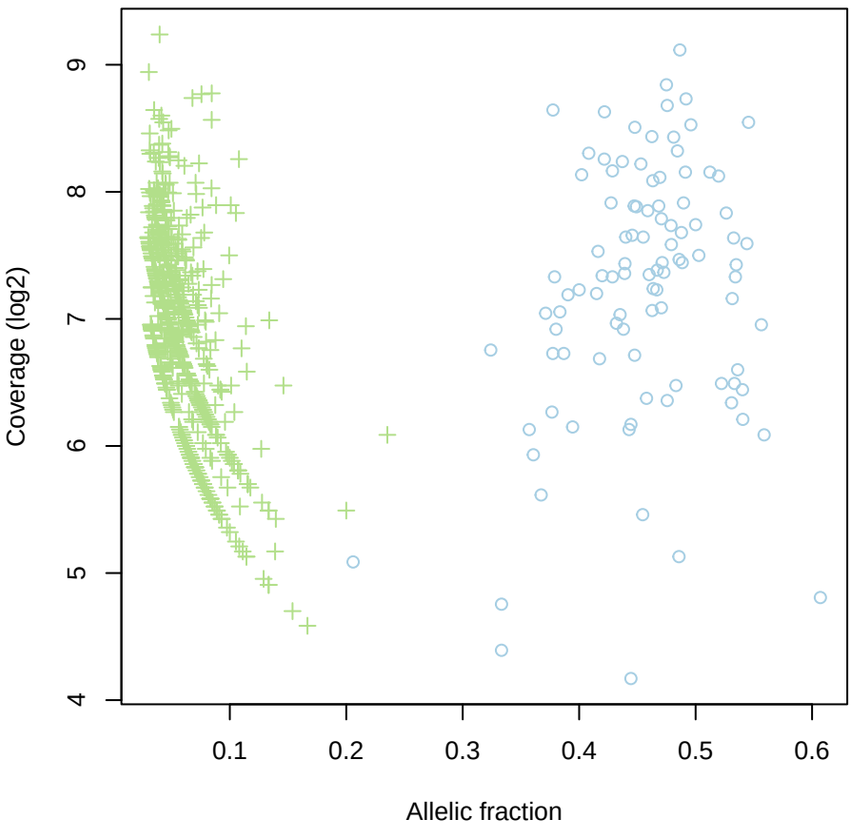

Purity: 0.61 Tumor ploidy: 5.498
2
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

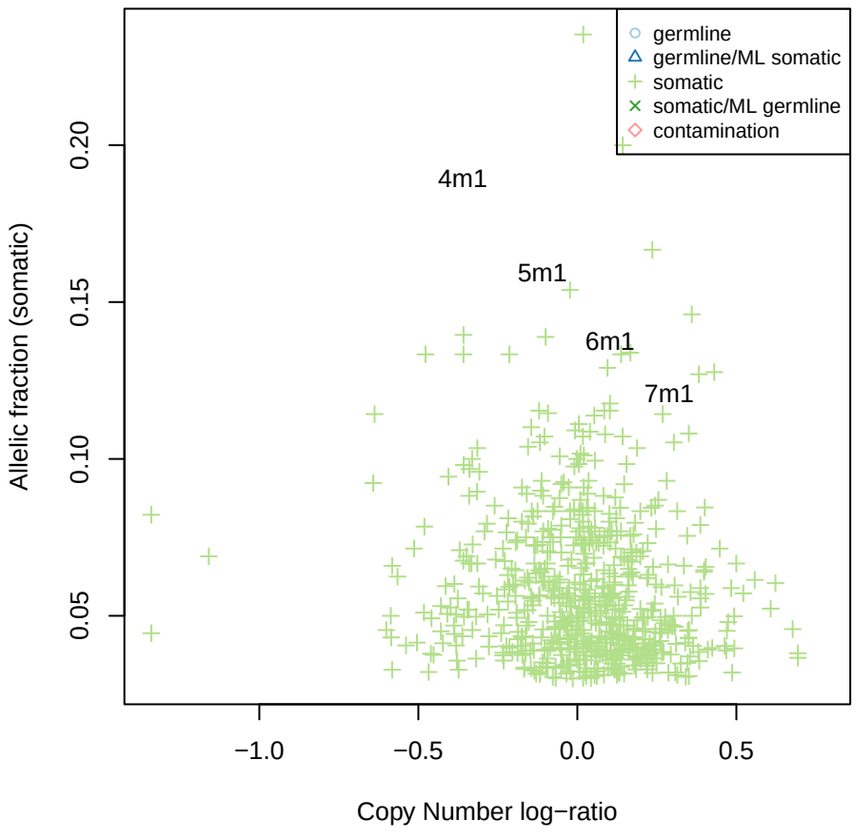

Purity: 0.61 Tumor ploidy: 5.498 SNV log−likelihood: −425.63 GoF: 79.5% Mean coverage: 363;148
1 2 3 4 5 6 7 8 10 11 12 13 14 15 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 20 40 60 80 100
SNV Index

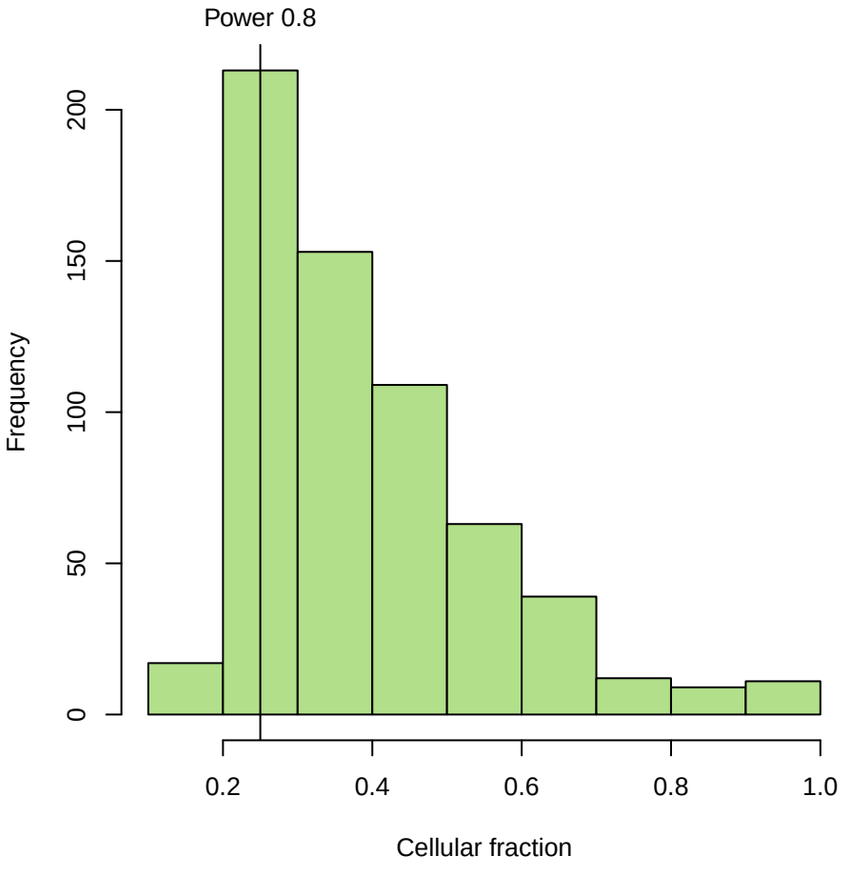

SCNA−fit log−likelihood: −19068.91
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
7 5 4 2
0 20 40 60 80 100
SNV Index

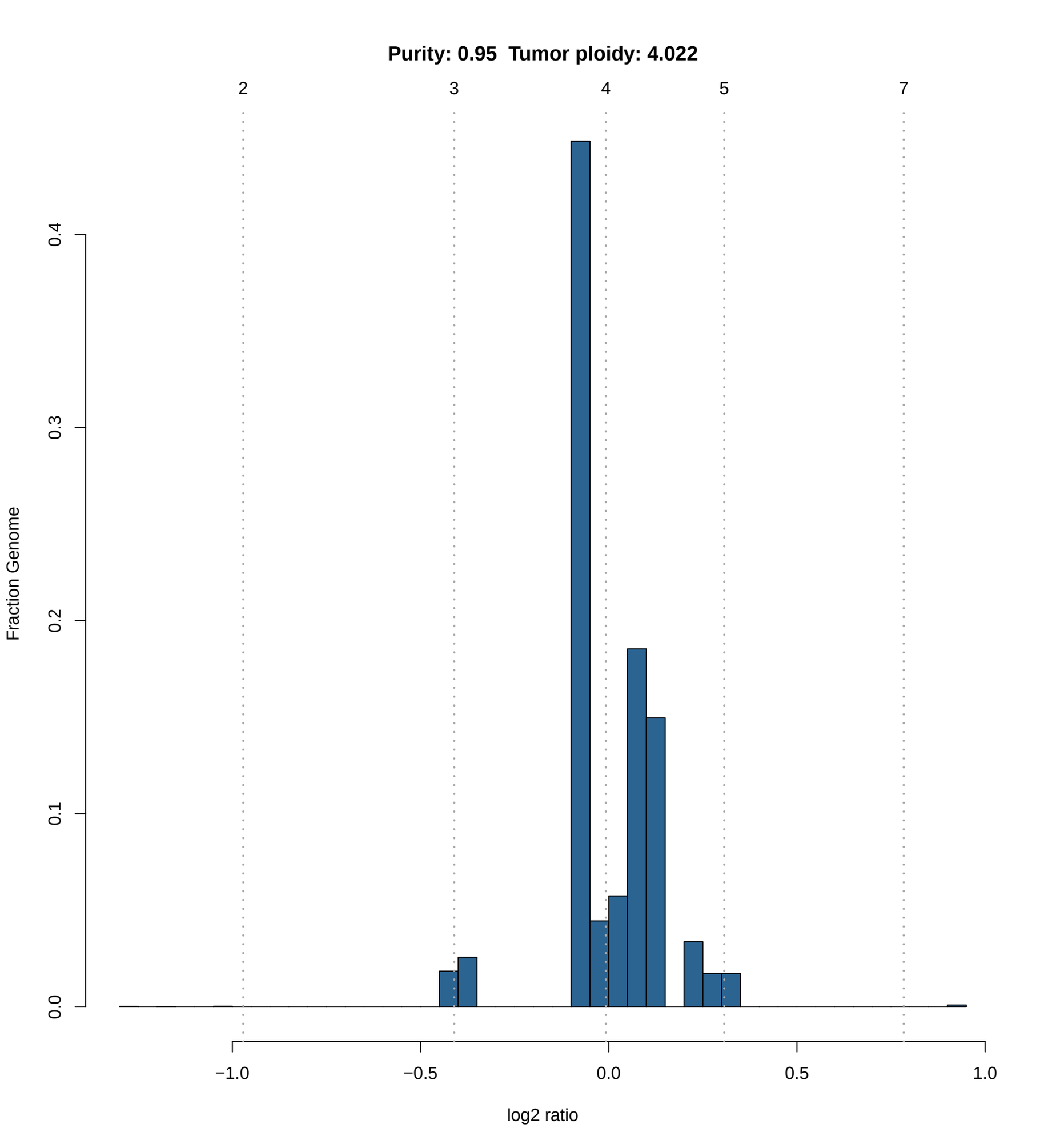

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

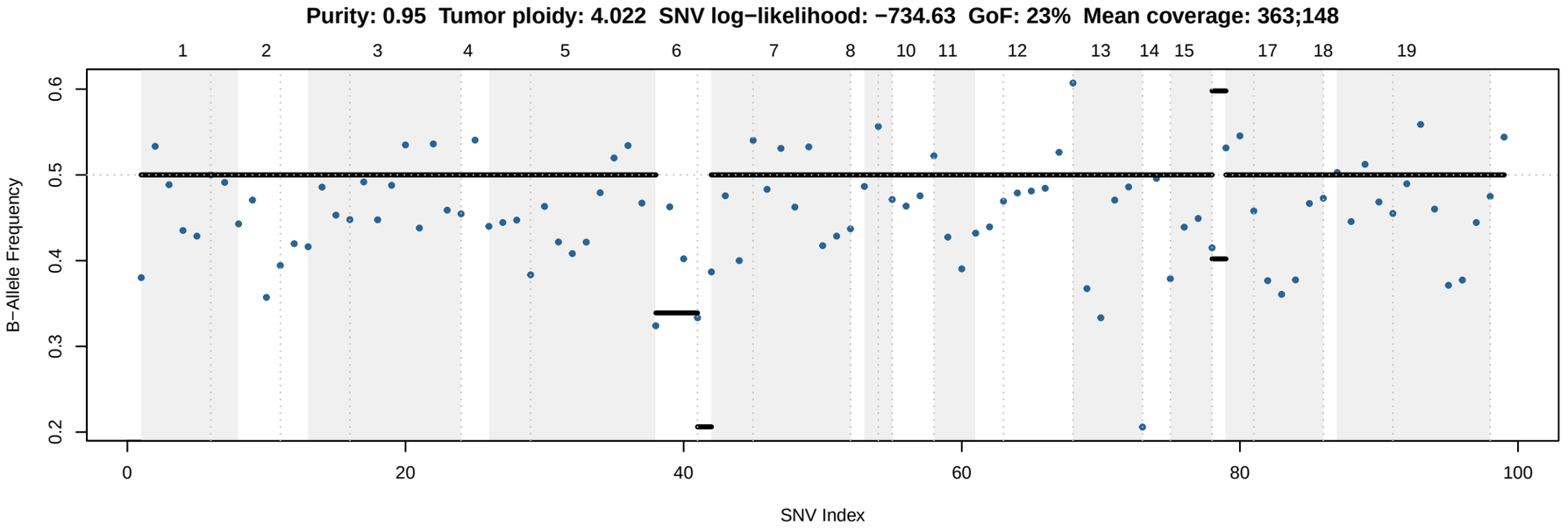

Allelic fraction (germline)
0.2
0.3
0.4
0.5
0.6
5m3
4m2
6m3
7m3
5m2
7m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

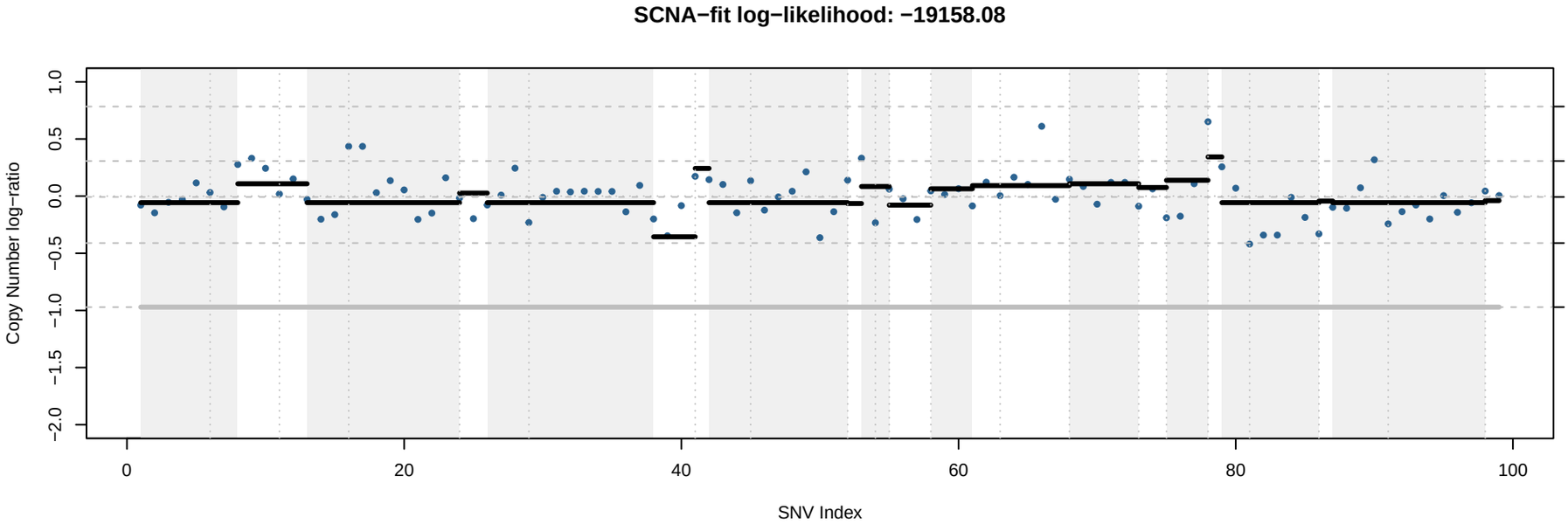

Coverage (log2)
4
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

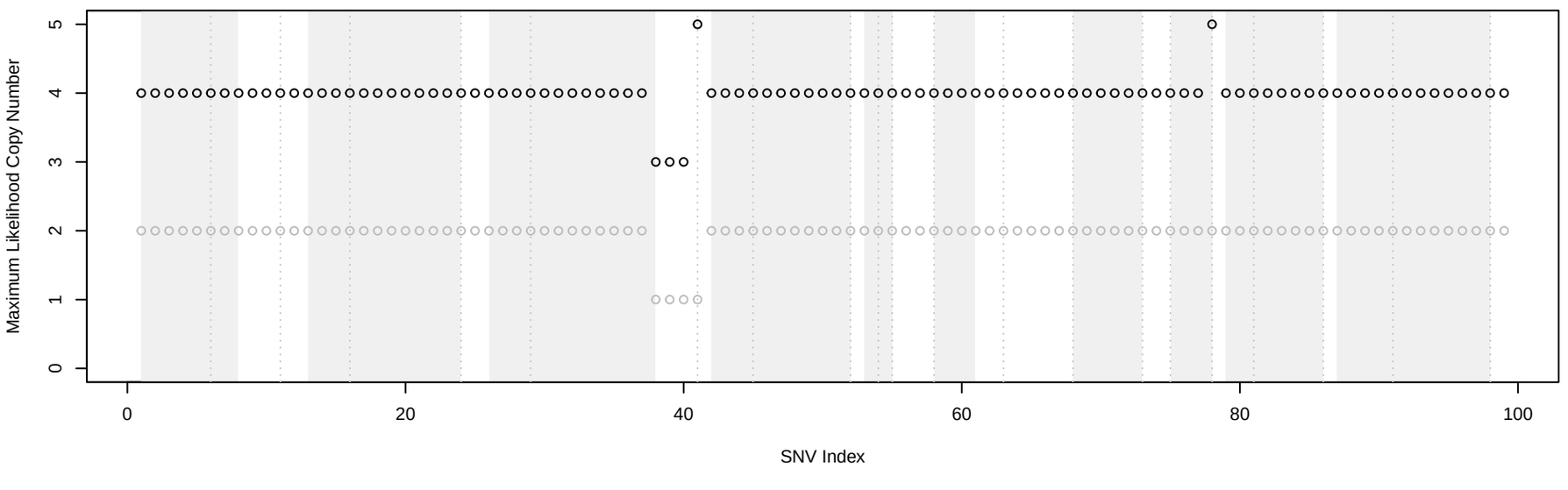

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
4m1
5m1
6m1
7m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

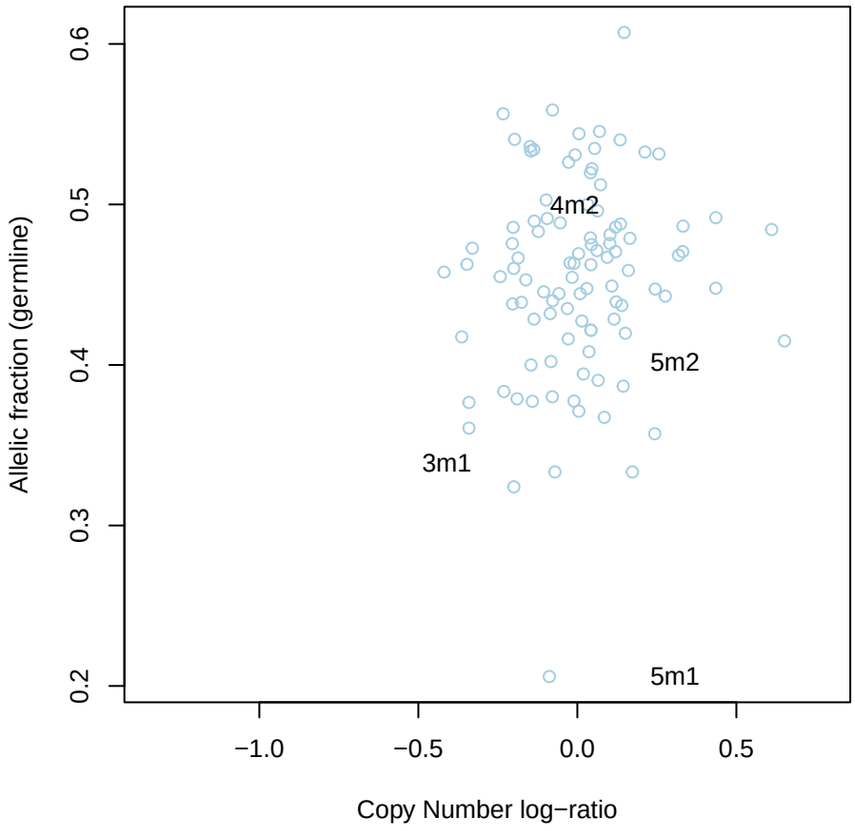

Power 0.8
Frequency
0
50
100
150
200
0.2
0.4
0.6
0.8
1.0
Cellular fraction

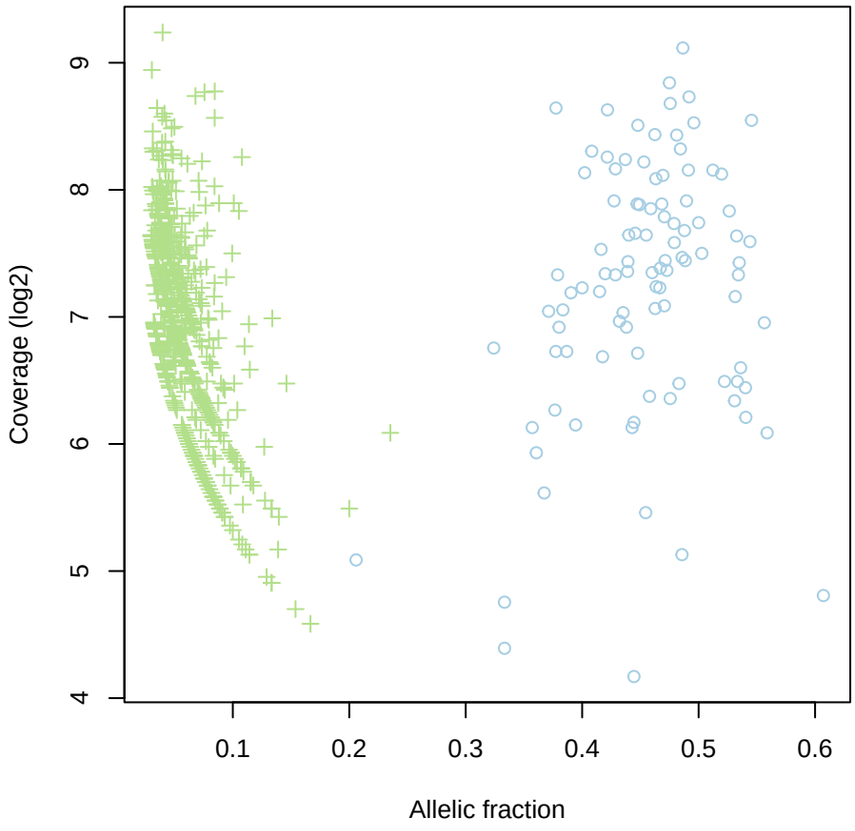

Purity: 0.95 Tumor ploidy: 4.022
2
3
4
5
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

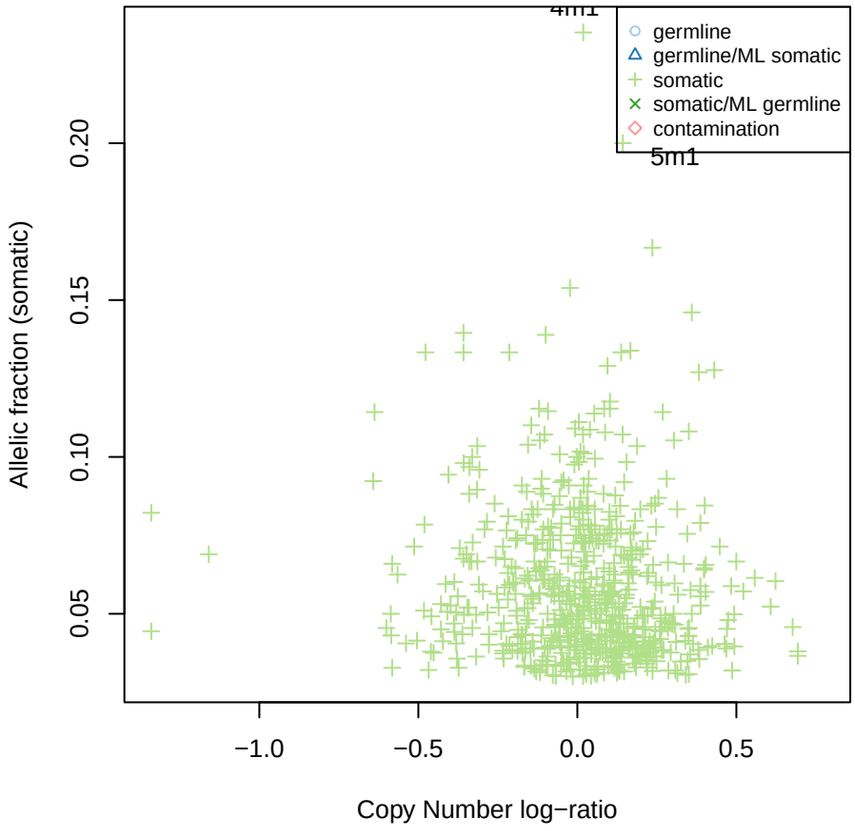

Purity: 0.95 Tumor ploidy: 4.022 SNV log−likelihood: −734.63 GoF: 23% Mean coverage: 363;148
1 2 3 4 5 6 7 8 10 11 12 13 14 15 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 20 40 60 80 100
SNV Index

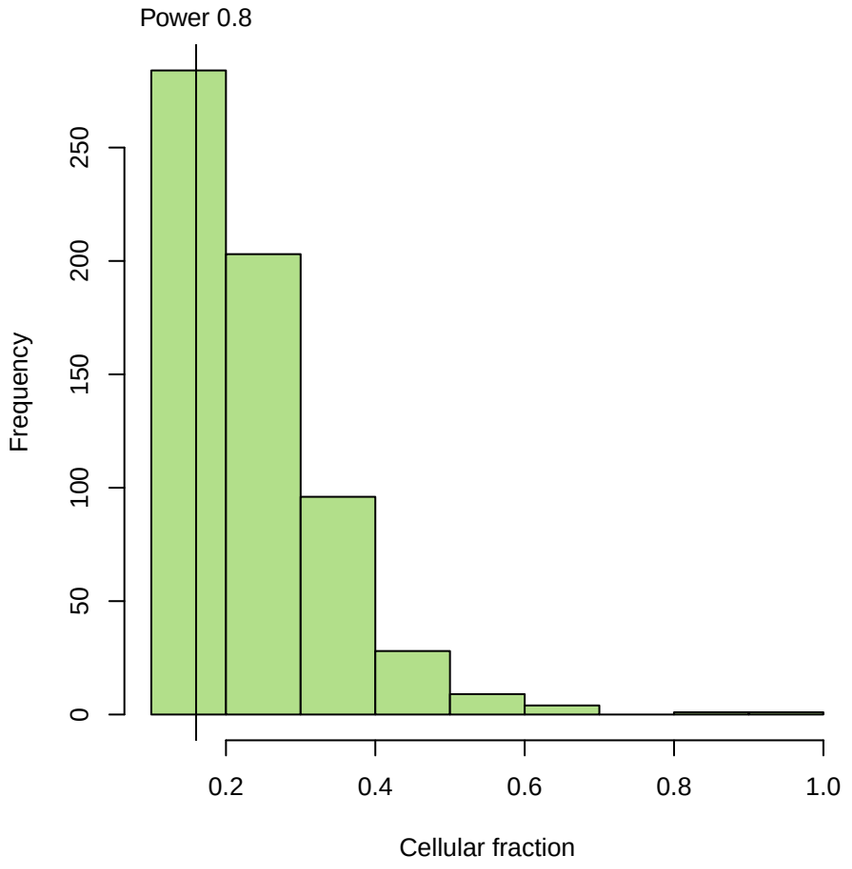

SCNA−fit log−likelihood: −19158.08
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
2 3 4 5 7
0 20 40 60 80 100
SNV Index

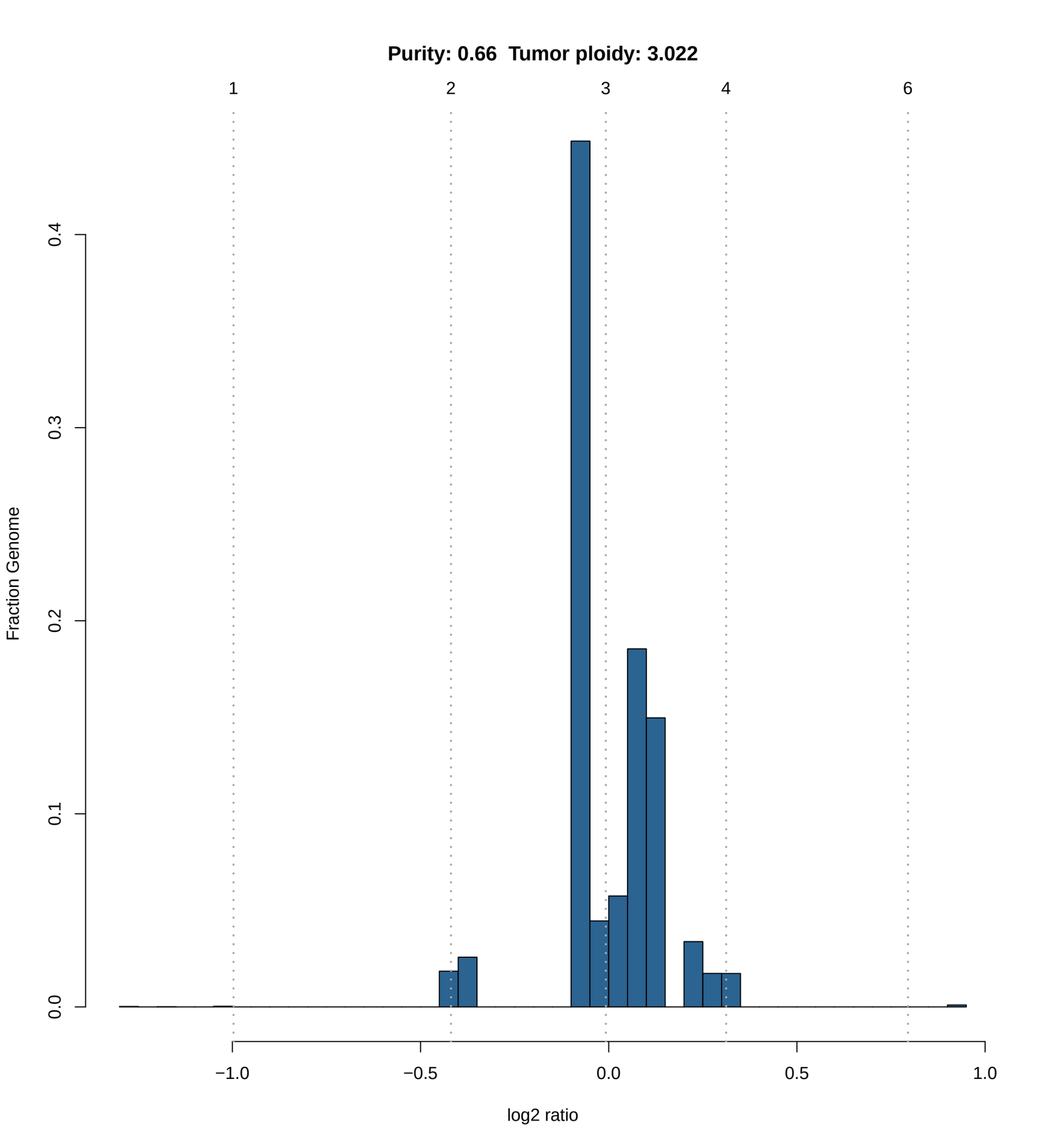

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100
SNV Index

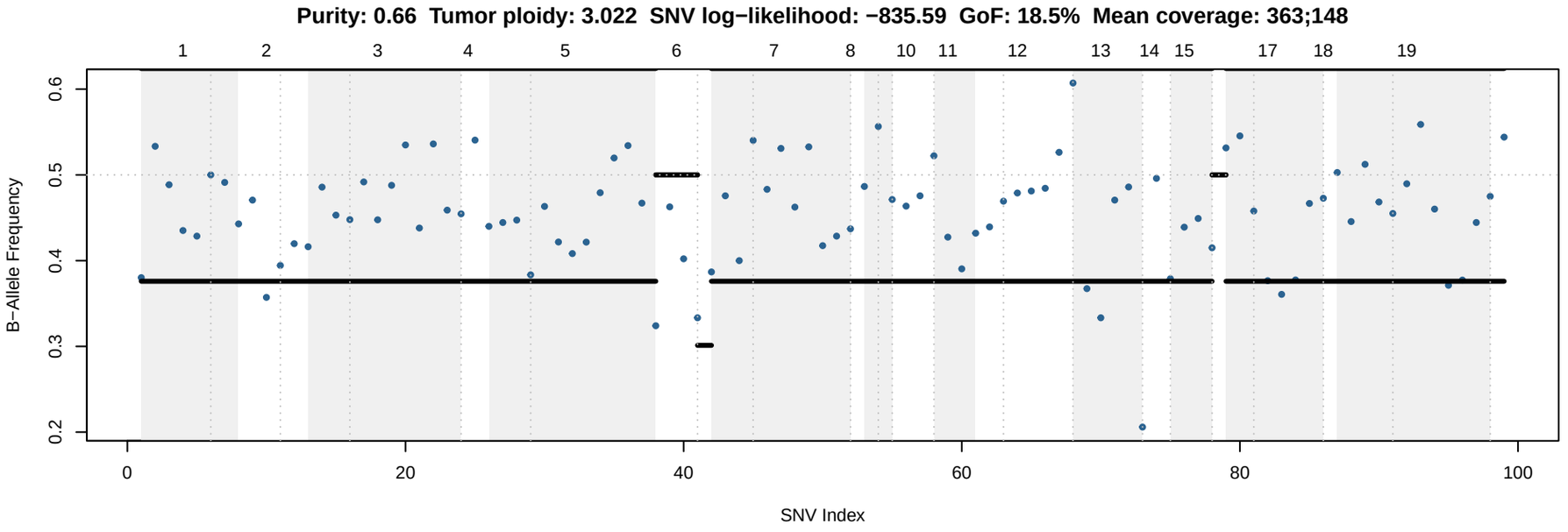

Allelic fraction (germline)
0.2
0.3
0.4
0.5
0.6
4m2
5m2
3m1
5m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

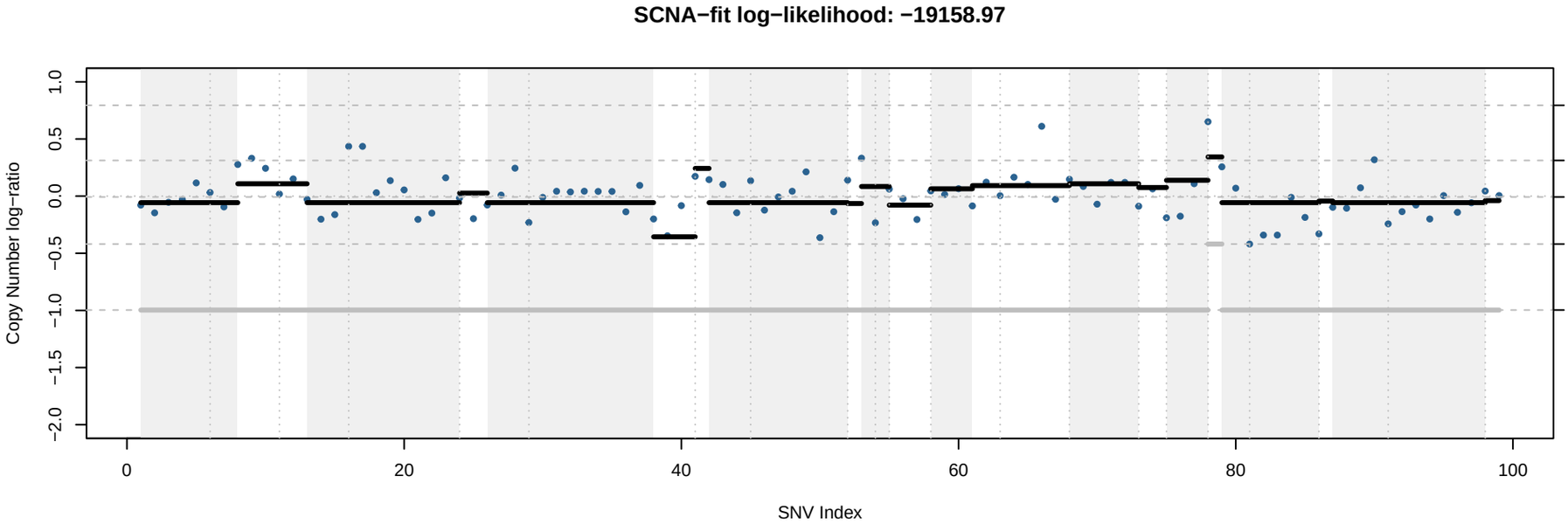

Coverage (log2)
4
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

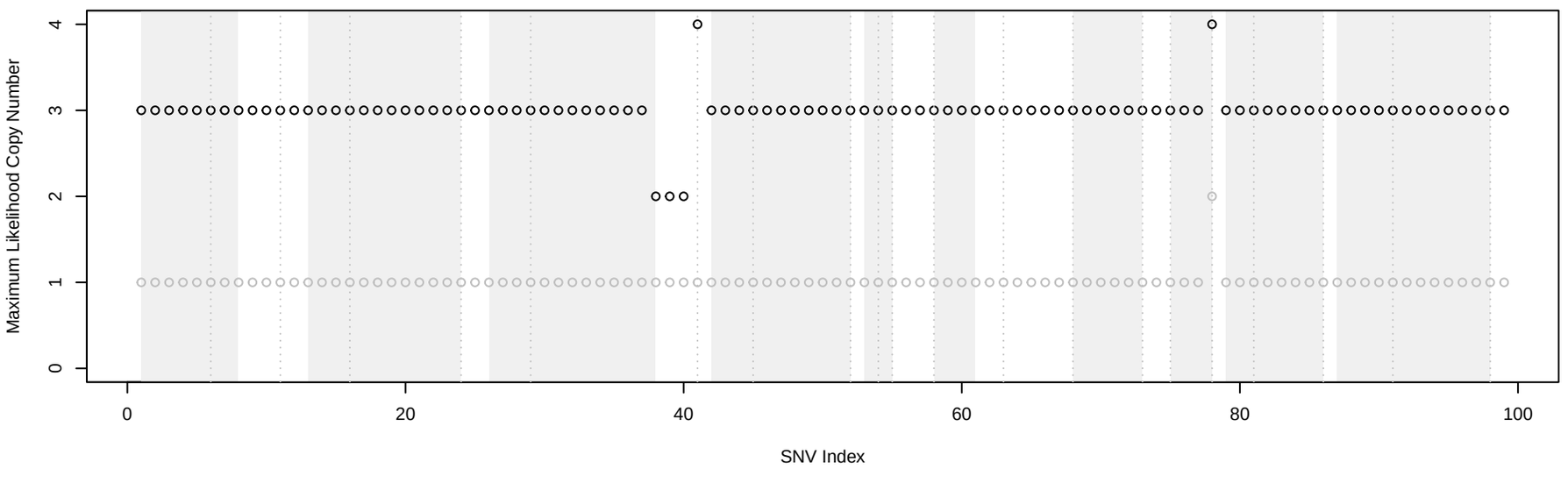

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

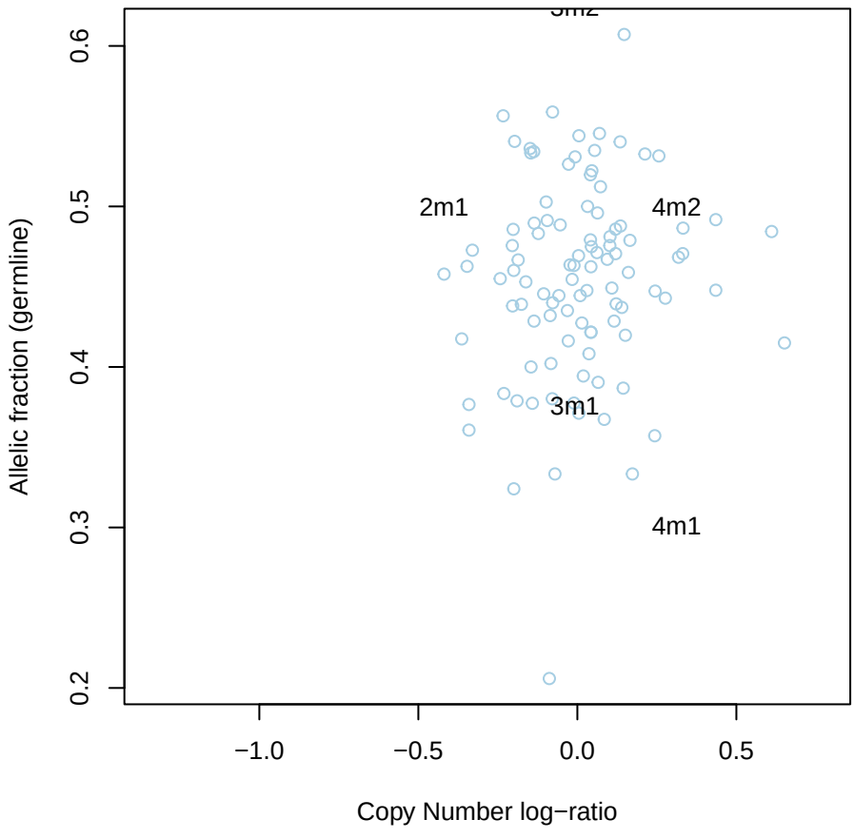

Power 0.8
Frequency
0
50
100
150
200
250
0.2
0.4
0.6
0.8
1.0
Cellular fraction

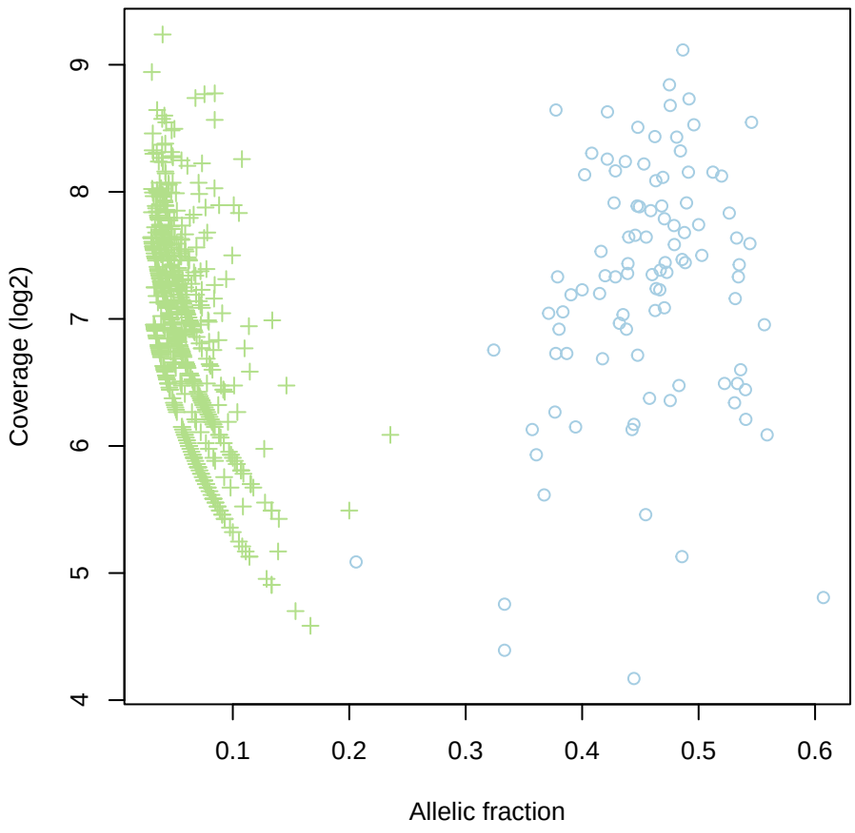

Purity: 0.66 Tumor ploidy: 3.022
1
2
3
4
6
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

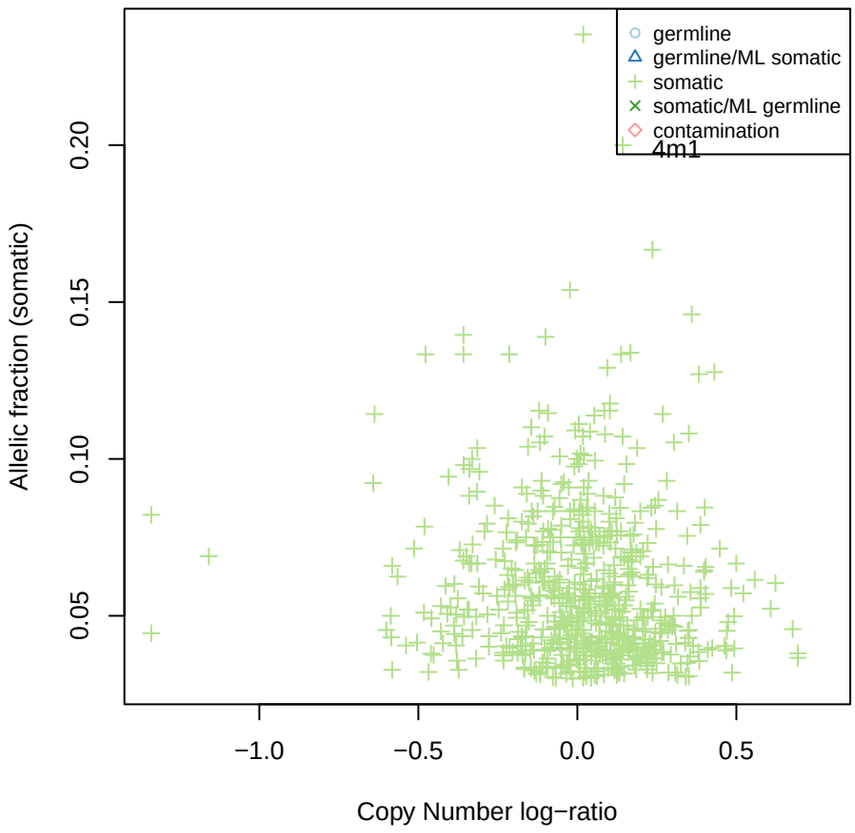

Purity: 0.66 Tumor ploidy: 3.022 SNV log−likelihood: −835.59 GoF: 18.5% Mean coverage: 363;148
1 2 3 4 5 6 7 8 10 11 12 13 14 15 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 20 40 60 80 100
SNV Index

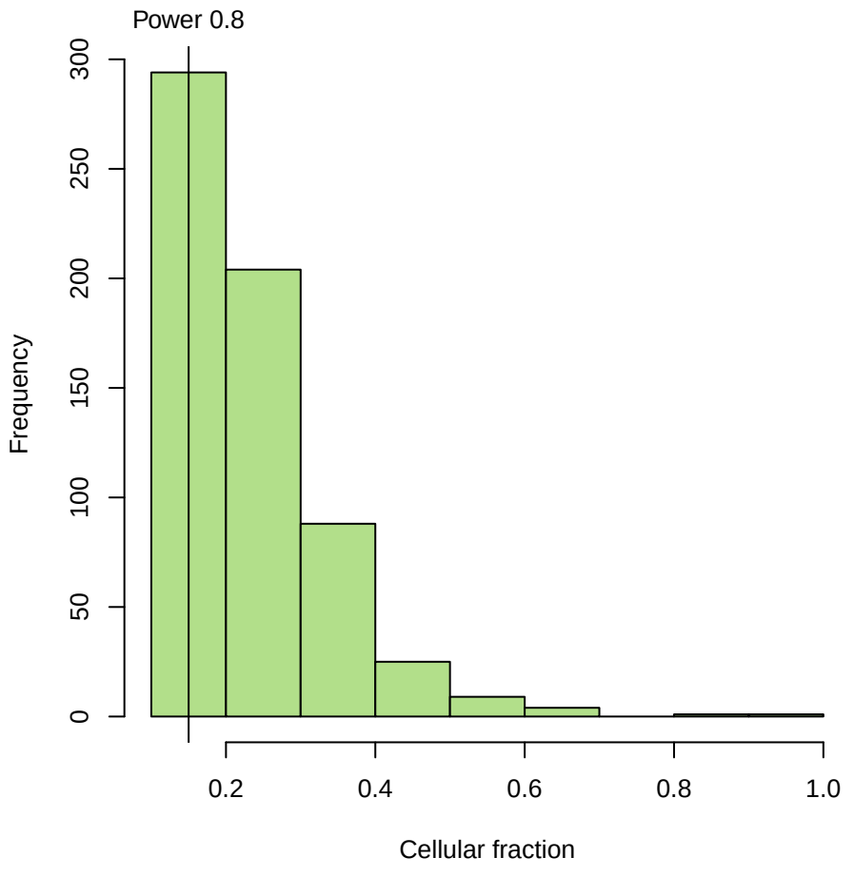

SCNA−fit log−likelihood: −19158.97
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
1 2 3 4 6
0 20 40 60 80 100
SNV Index

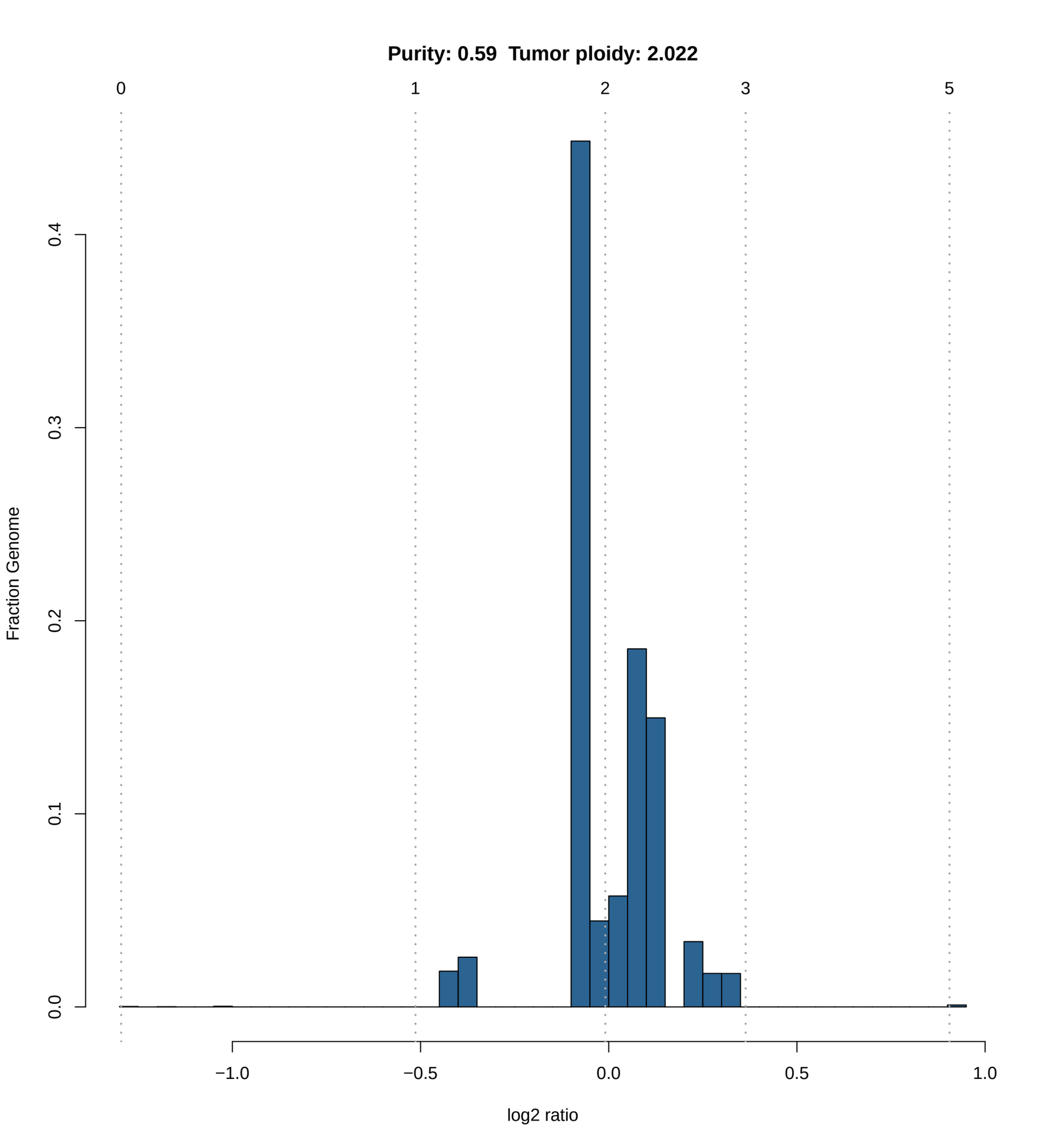

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100
SNV Index

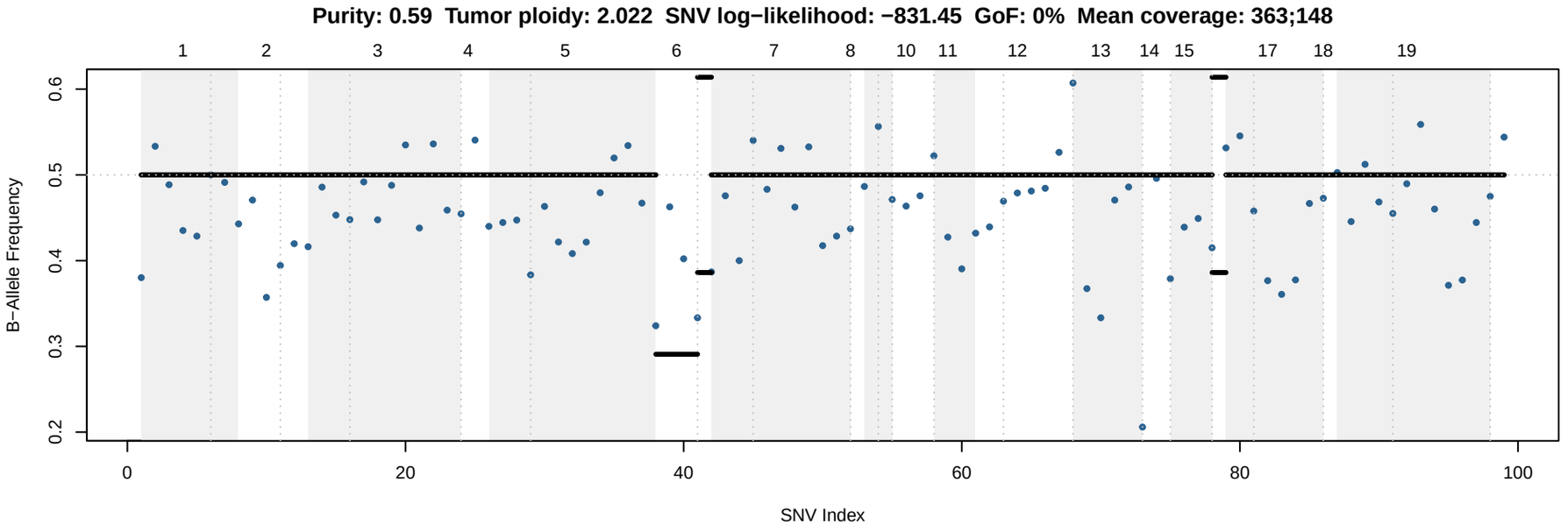

2m1
4m2
3m1
4m1
Allelic fraction (germline)
Copy Number log−ratio

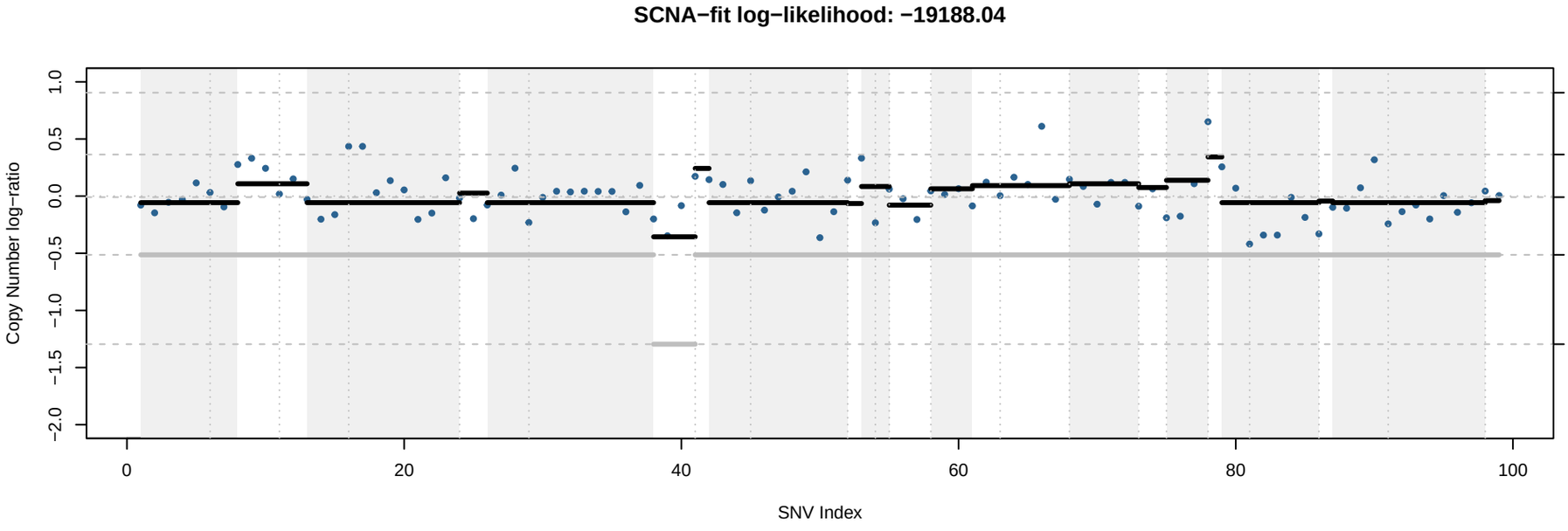

Coverage (log2)
Allelic fraction

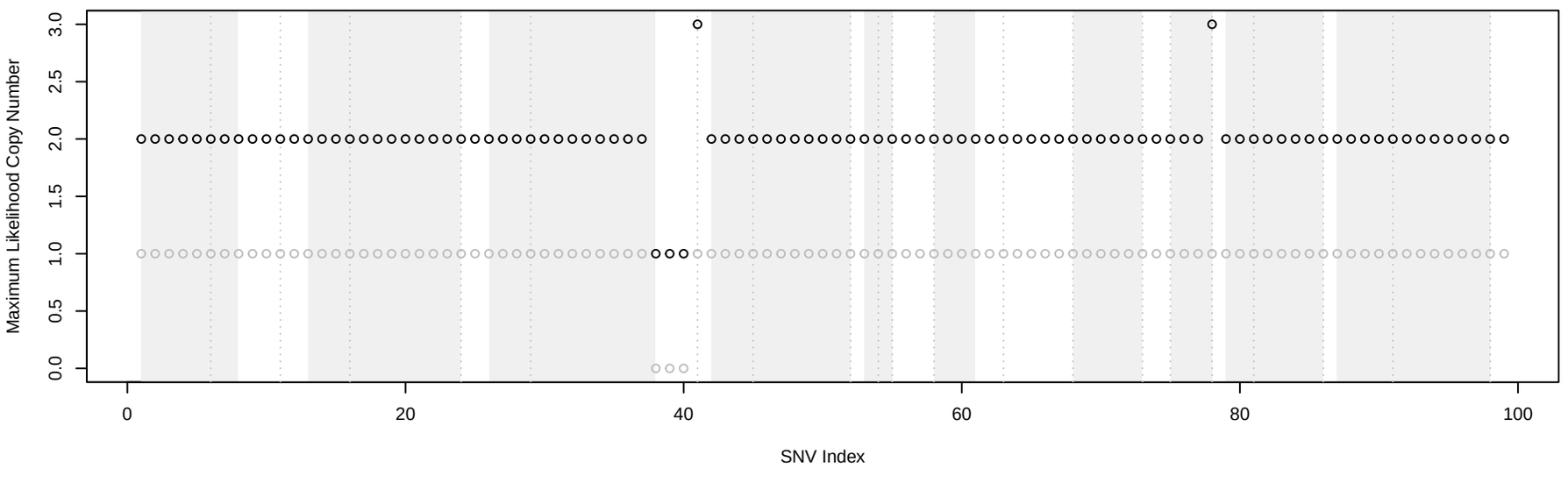

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
Allelic fraction (somatic)
Copy Number log−ratio

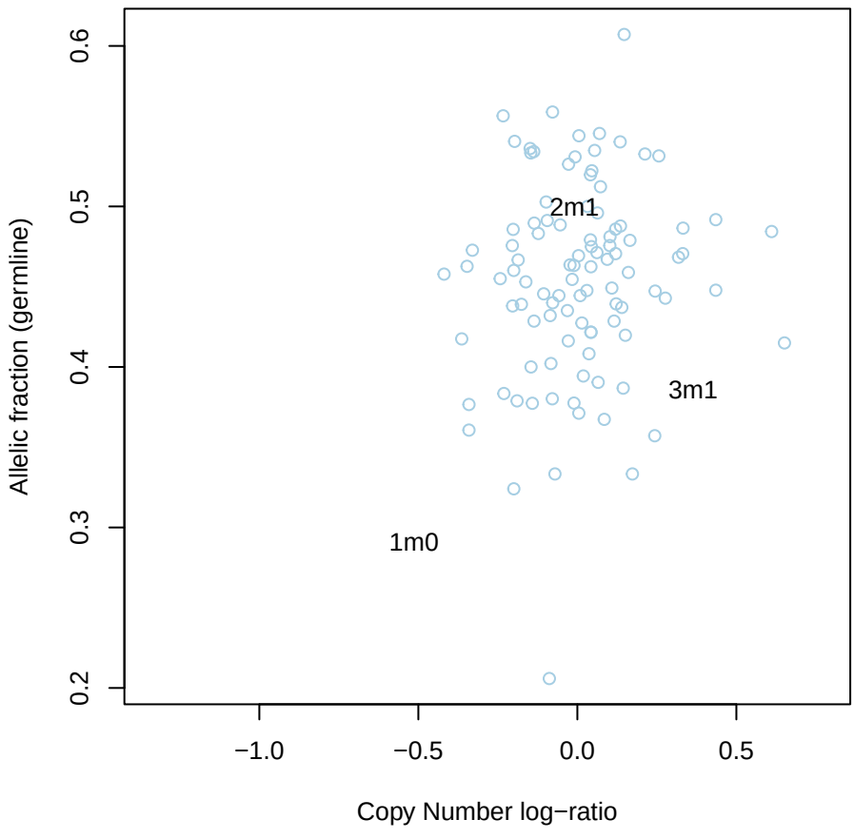

Power 0.8
Frequency
Cellular fraction

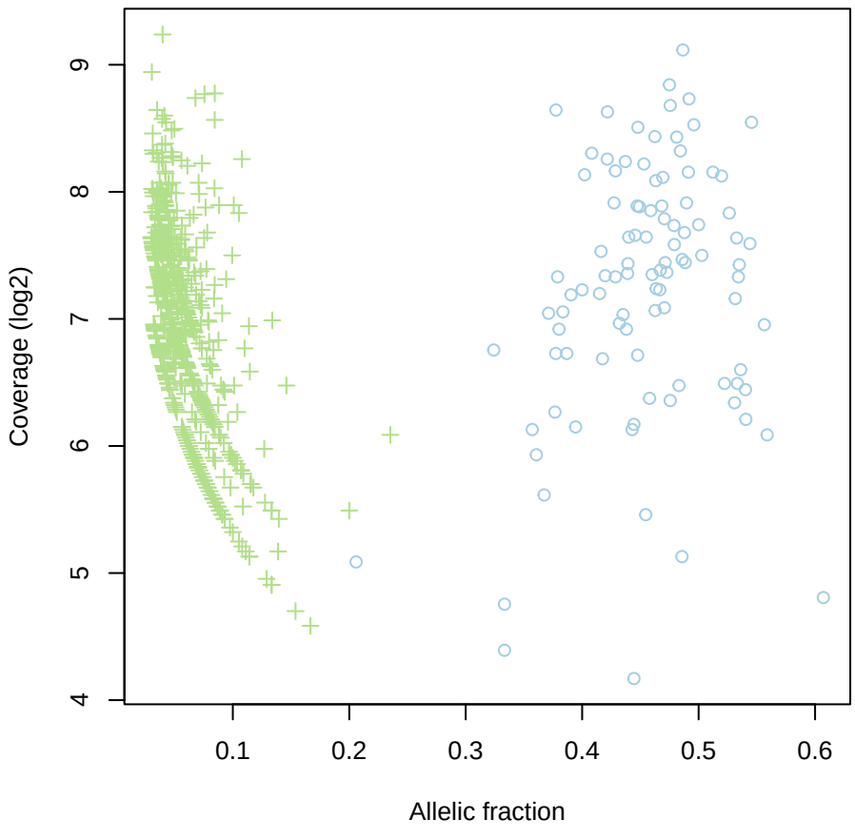

Purity: 0.59 Tumor ploidy: 2.022
0
1
2
3
5
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

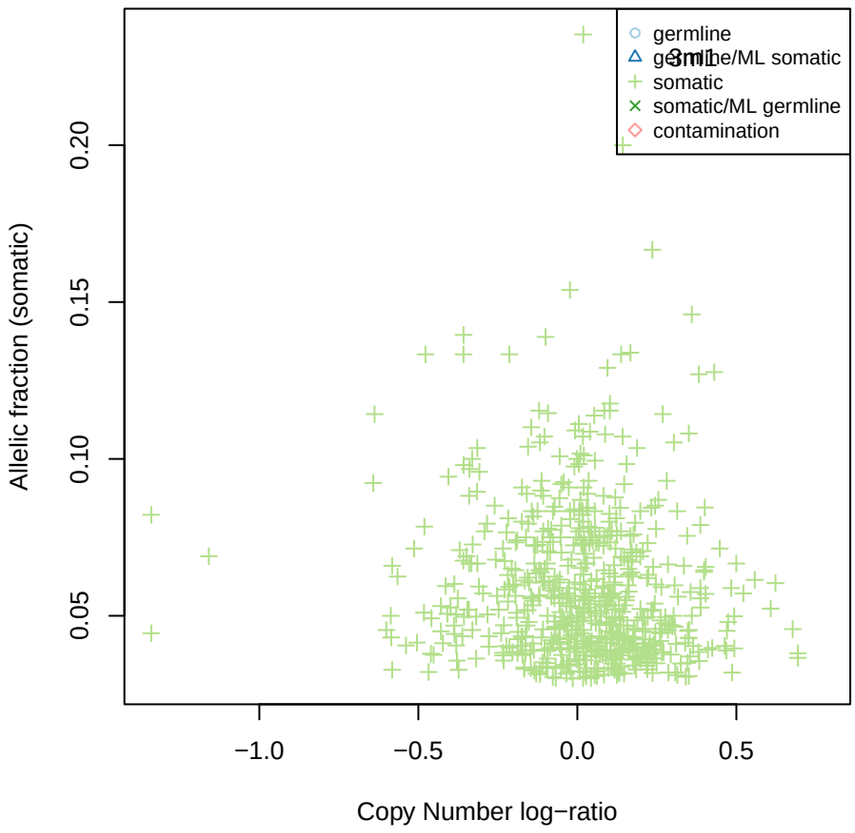

Purity: 0.59 Tumor ploidy: 2.022 SNV log−likelihood: −831.45 GoF: 0% Mean coverage: 363;148
1 2 3 4 5 6 7 8 10 11 12 13 14 15 17 18 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 20 40 60 80 100
SNV Index

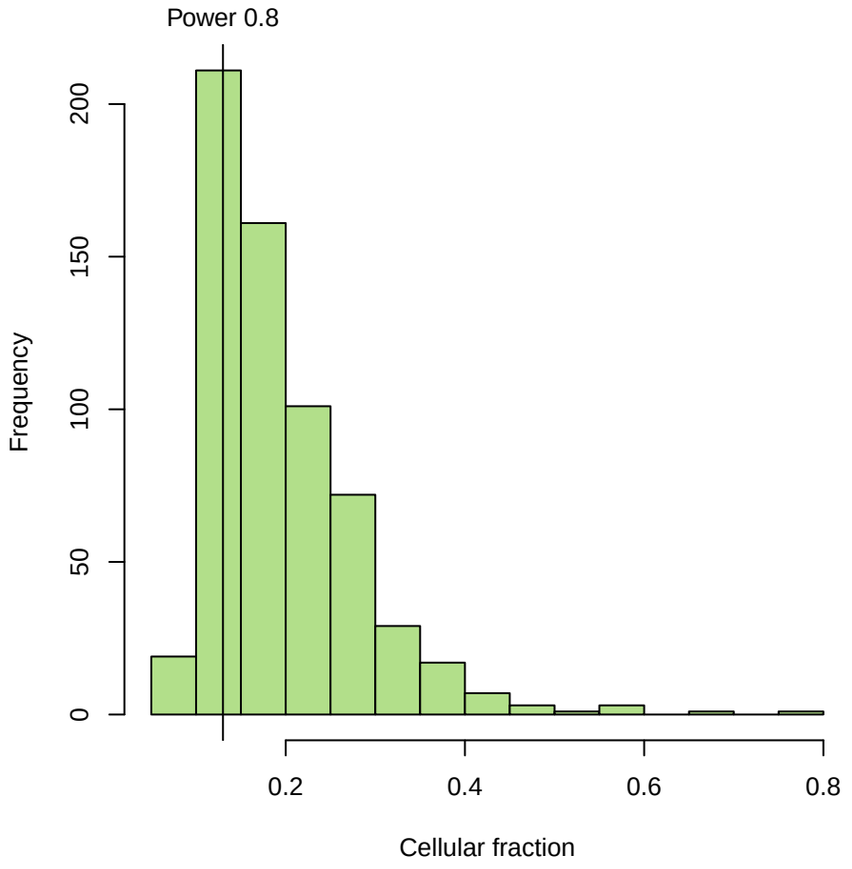

SCNA−fit log−likelihood: −19188.04
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 5
0 20 40 60 80 100
SNV Index


Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100
SNV Index


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


Coverage (log2)
Allelic fraction


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


Power 0.8
Frequency
Cellular fraction