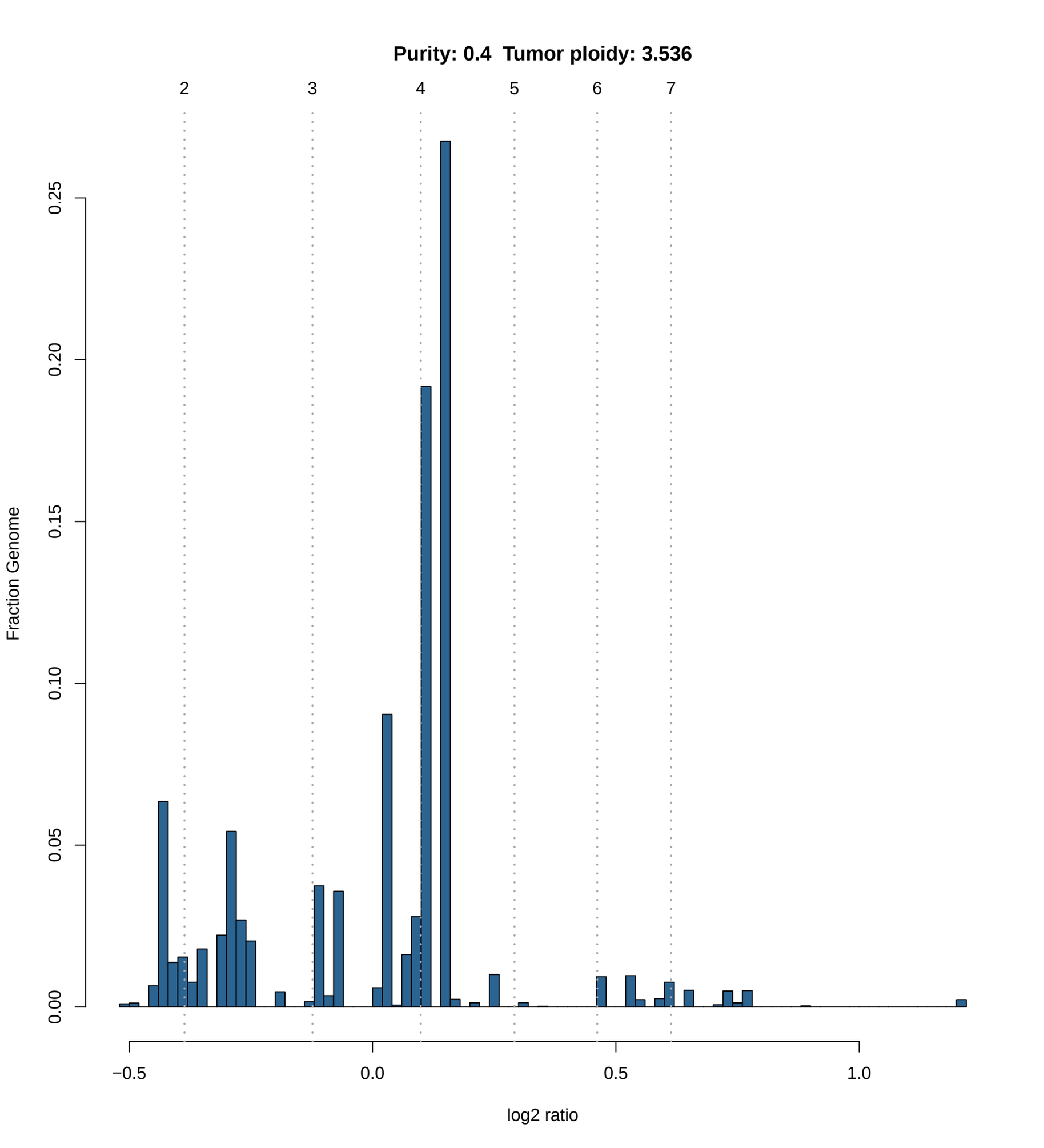
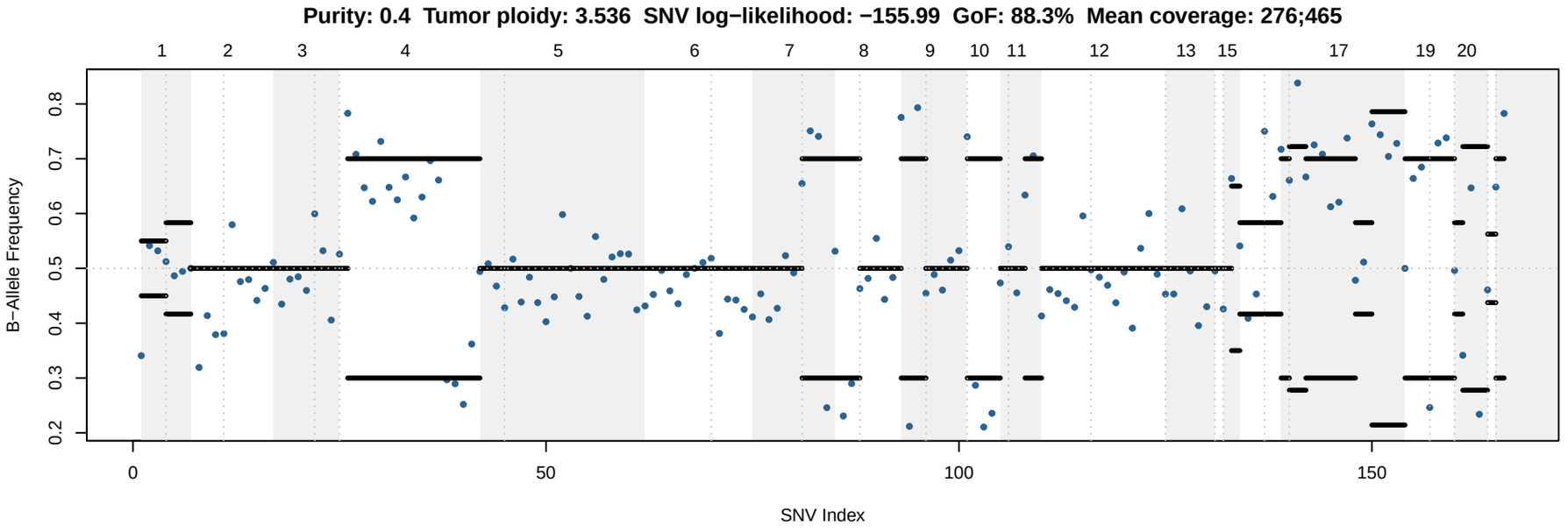
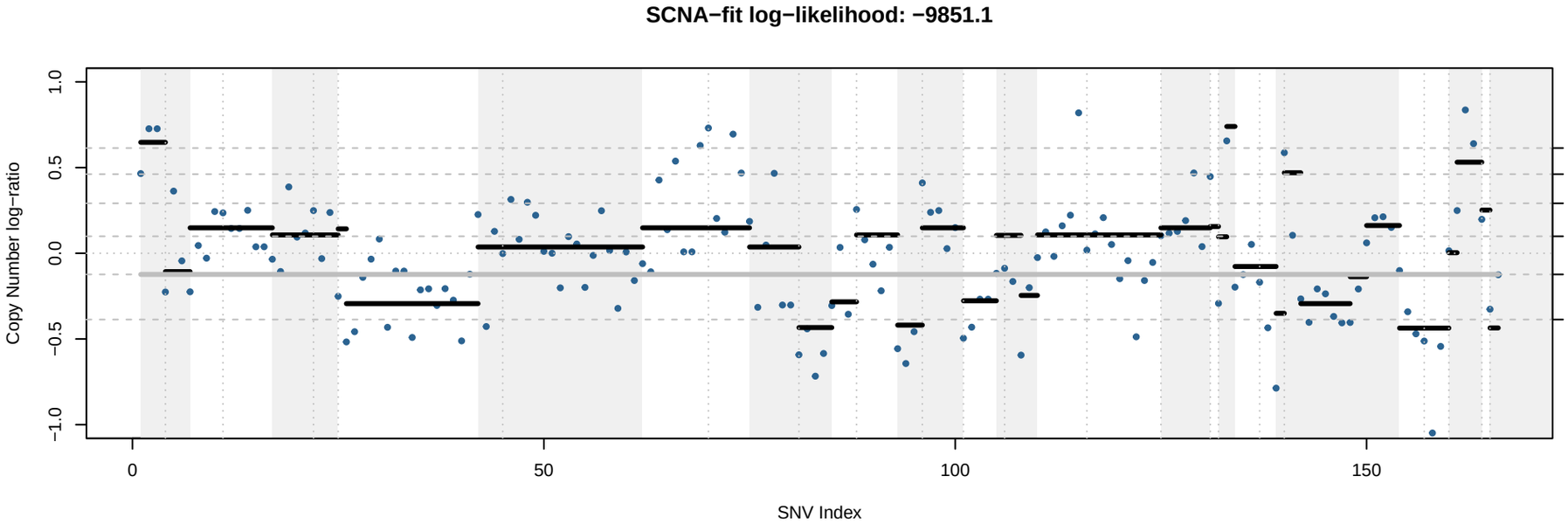
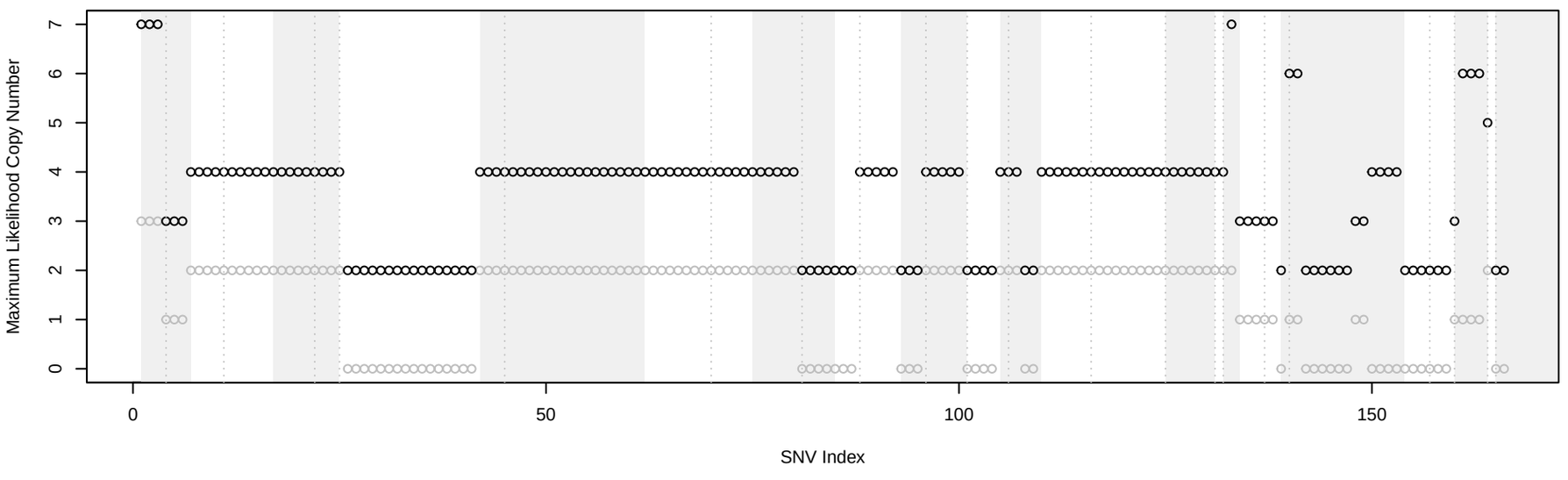
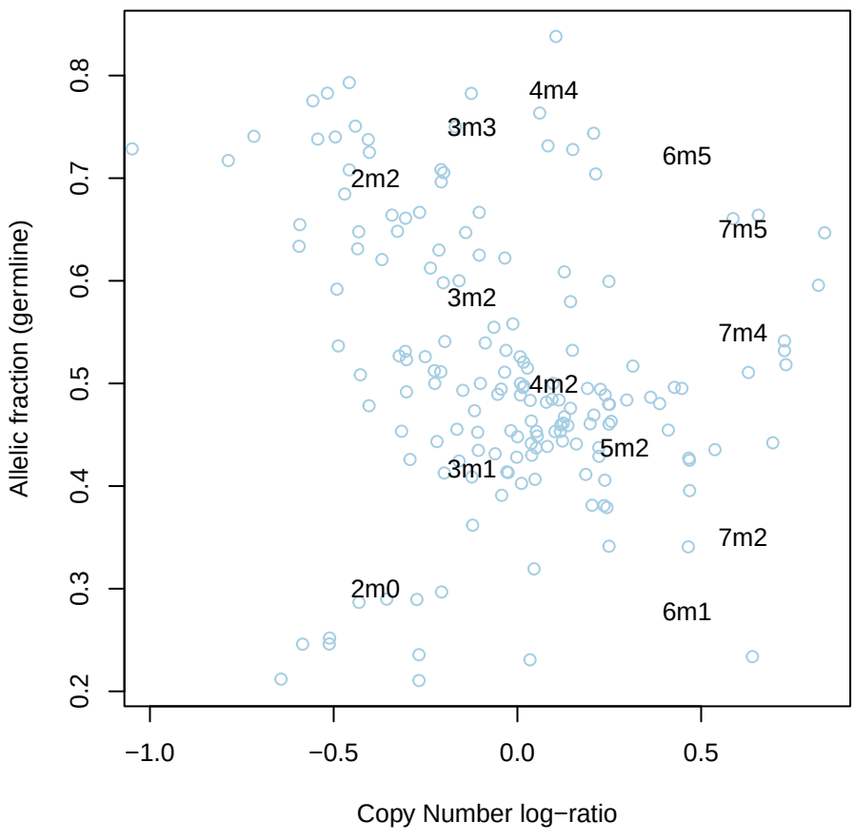
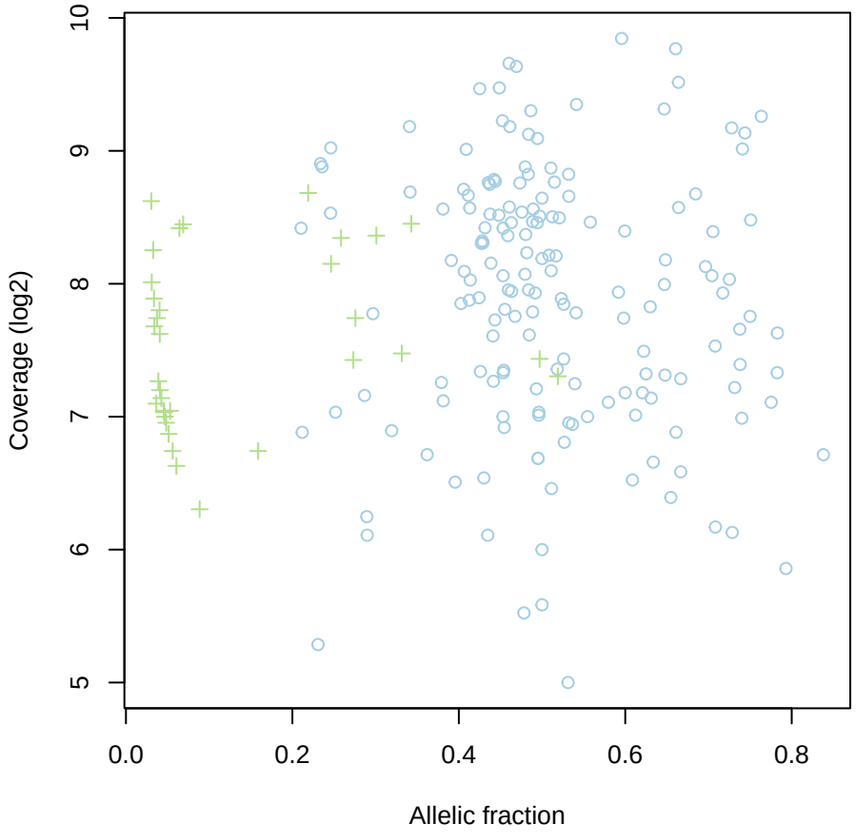

Purity: 0.4 Tumor ploidy: 3.536
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

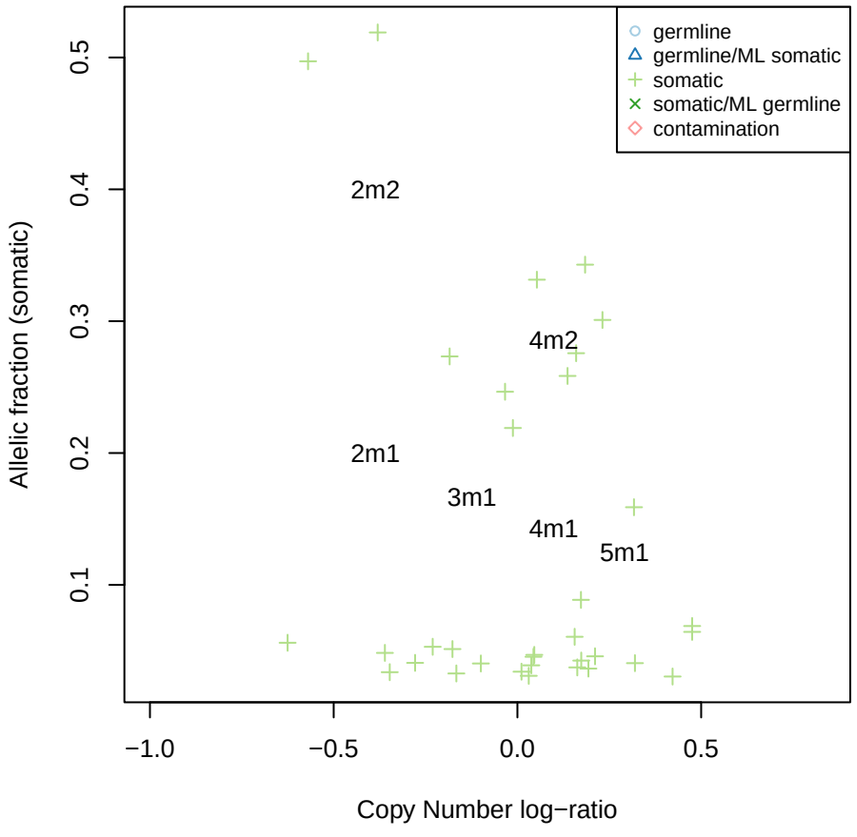

Purity: 0.4 Tumor ploidy: 3.536 SNV log−likelihood: −155.99 GoF: 88.3% Mean coverage: 276;465
1 2 3 4 5 6 7 8 9 10 11 12 13 15 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

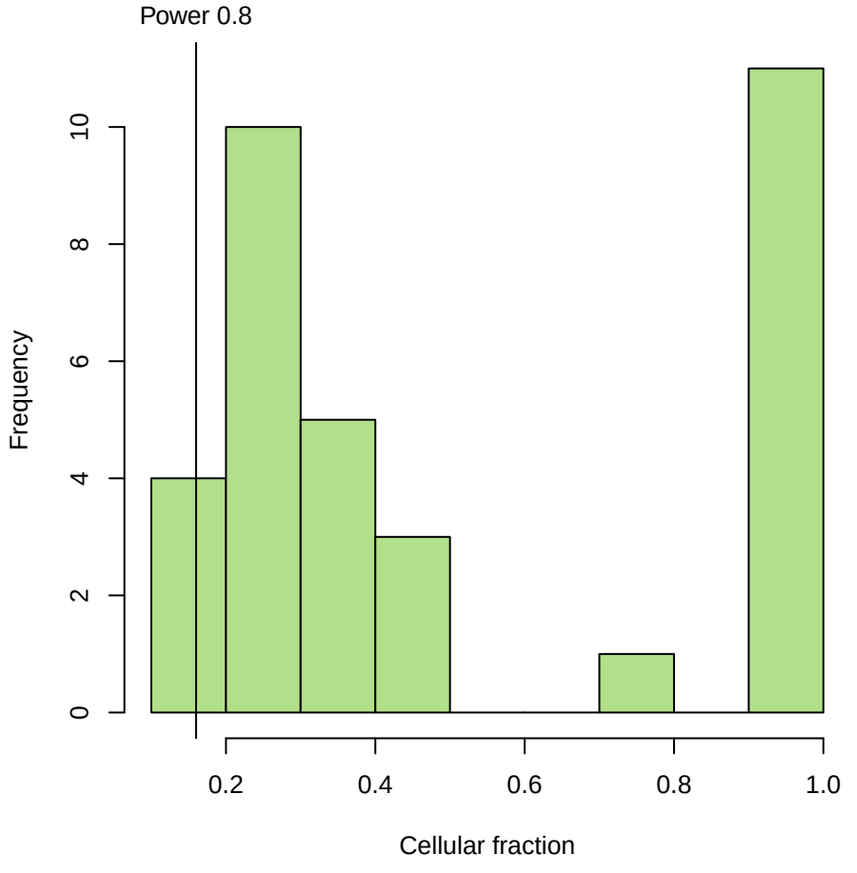

SCNA−fit log−likelihood: −9851.1
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 50 100 150
SNV Index

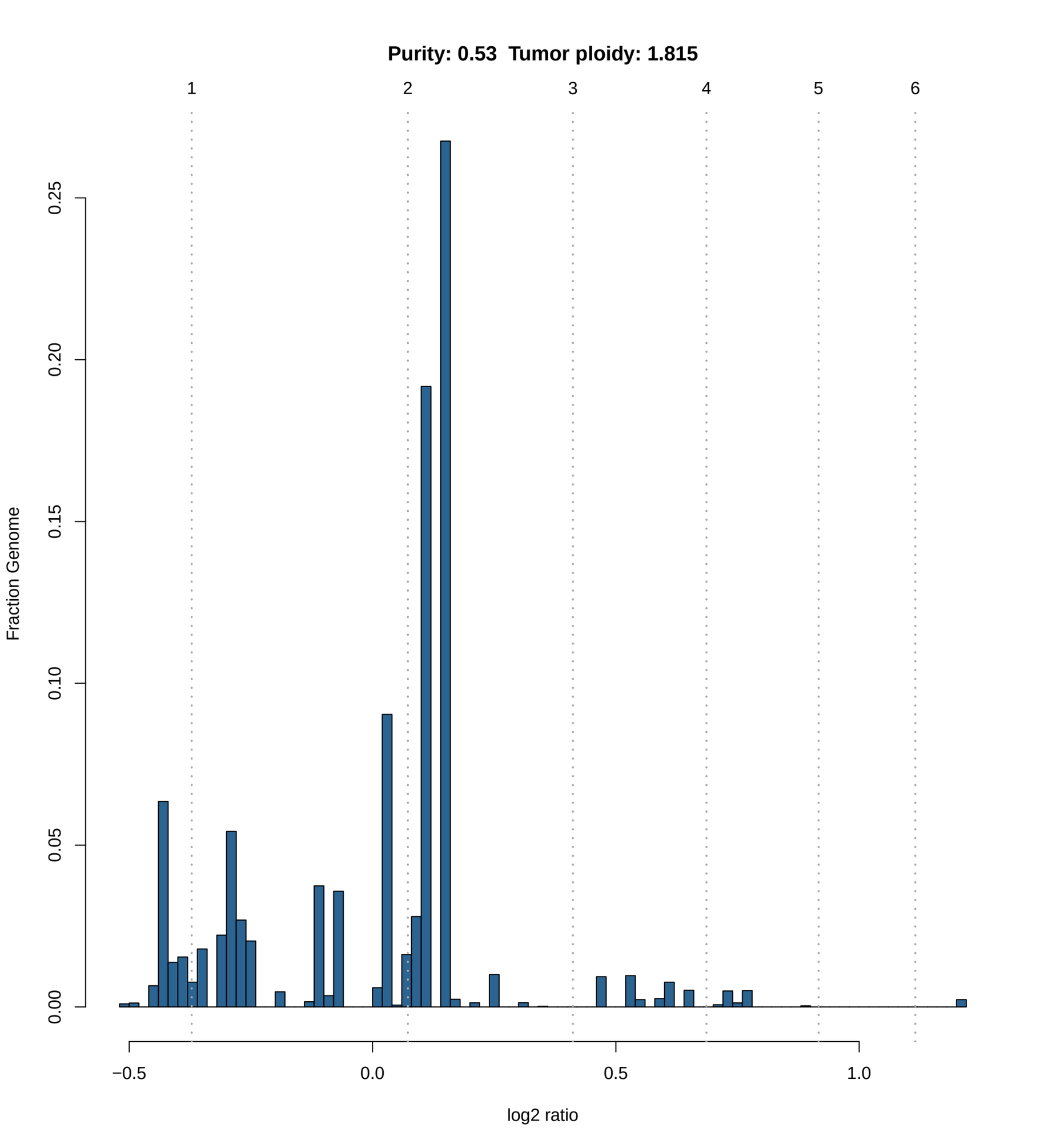

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

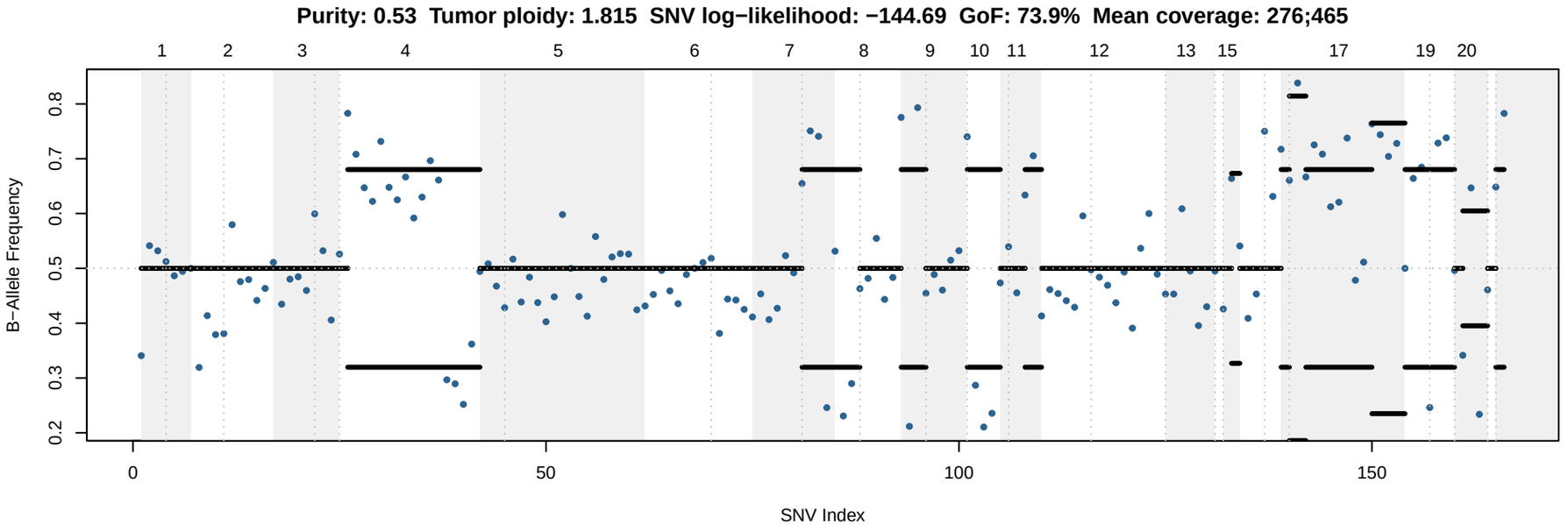

Allelic fraction (germline)
Copy Number log−ratio
4m4
3m3
6m5
2m2
7m5
3m2
7m4
4m2
5m2
3m1
7m2
2m0
6m1

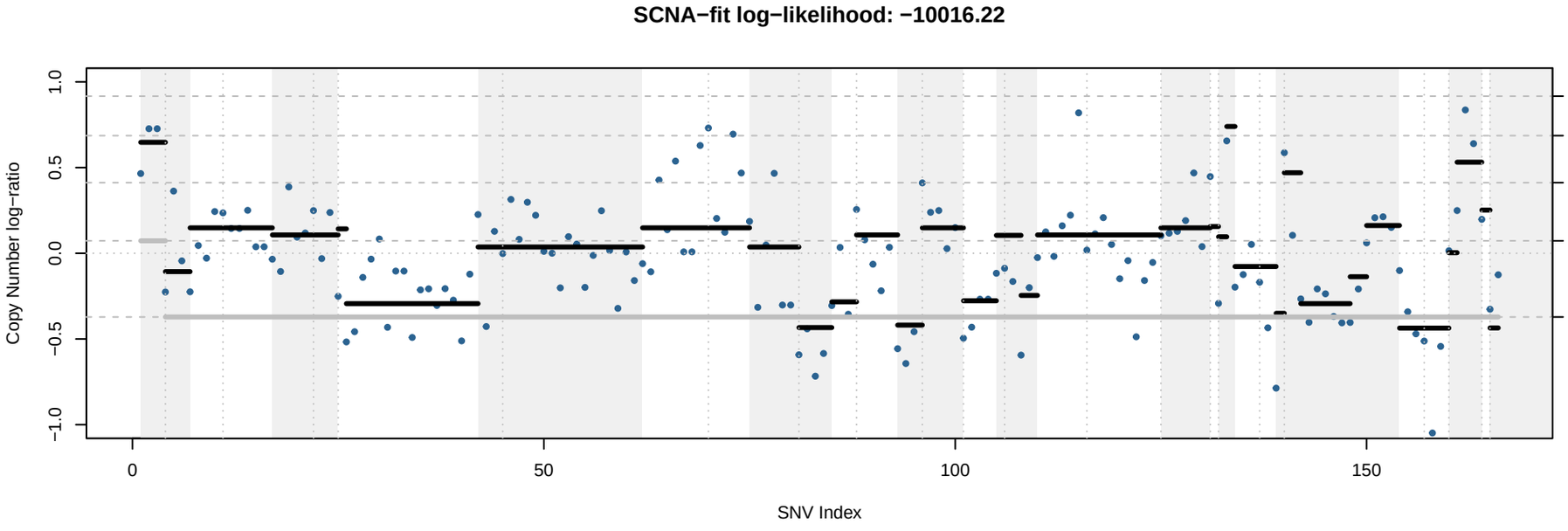

Coverage (log2)
Allelic fraction

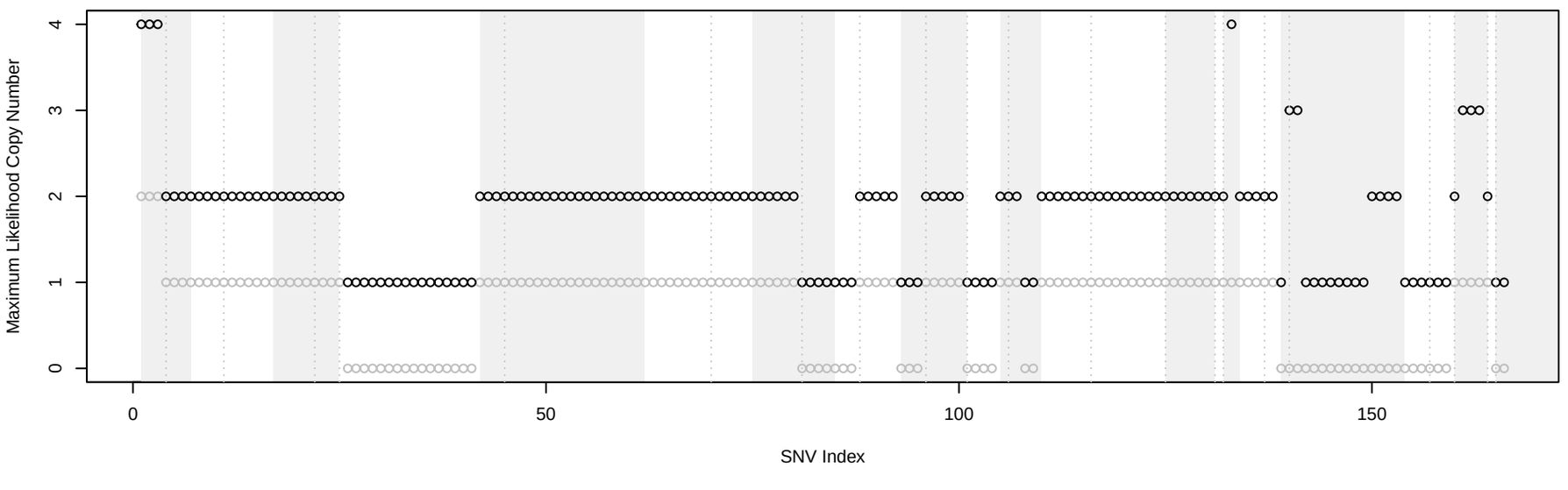

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m2
4m2
2m1
3m1
4m1
5m1

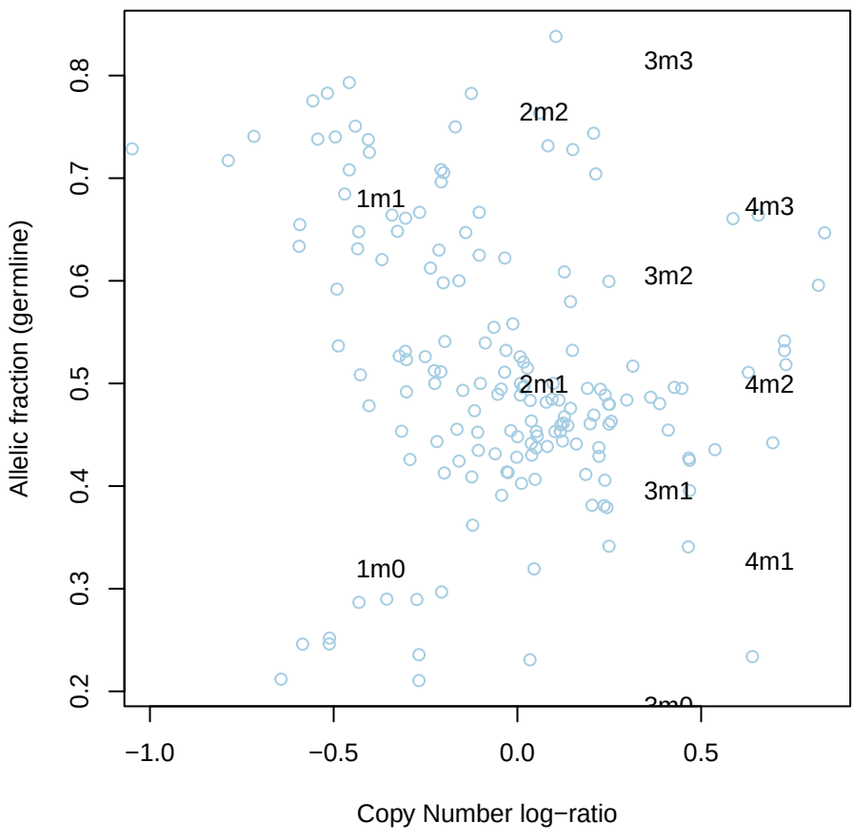

Power 0.8
Frequency
Cellular fraction

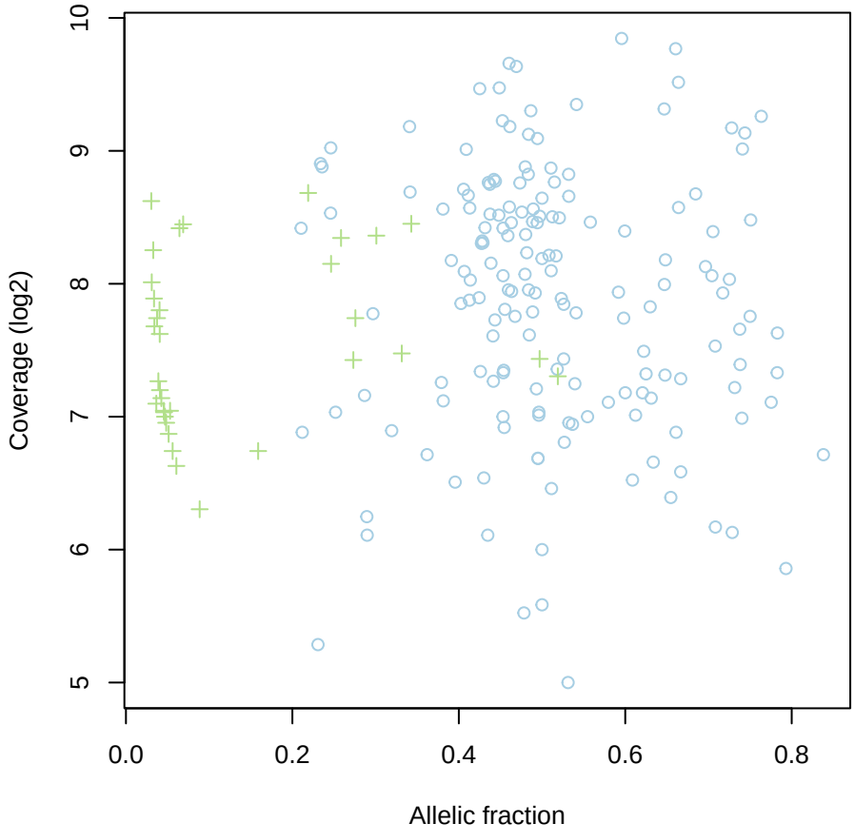

Purity: 0.53 Tumor ploidy: 1.815
1
2
3
4
5
6
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

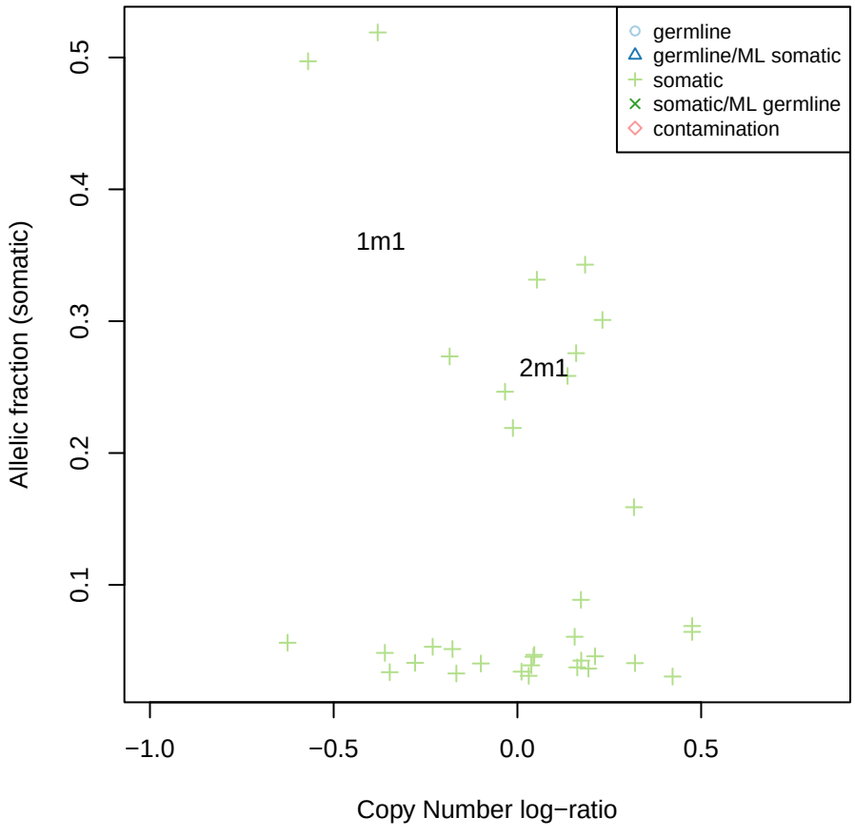

Purity: 0.53 Tumor ploidy: 1.815 SNV log−likelihood: −144.69 GoF: 73.9% Mean coverage: 276;465
1 2 3 4 5 6 7 8 9 10 11 12 13 15 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

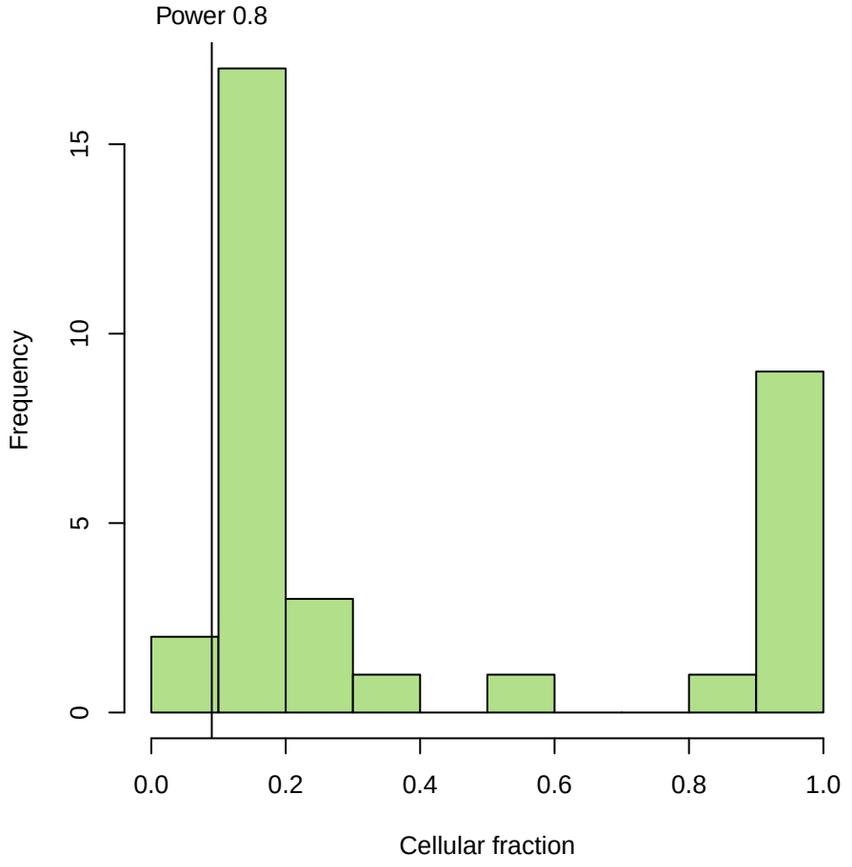

SCNA−fit log−likelihood: −10016.22
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5
0 50 100 150
SNV Index

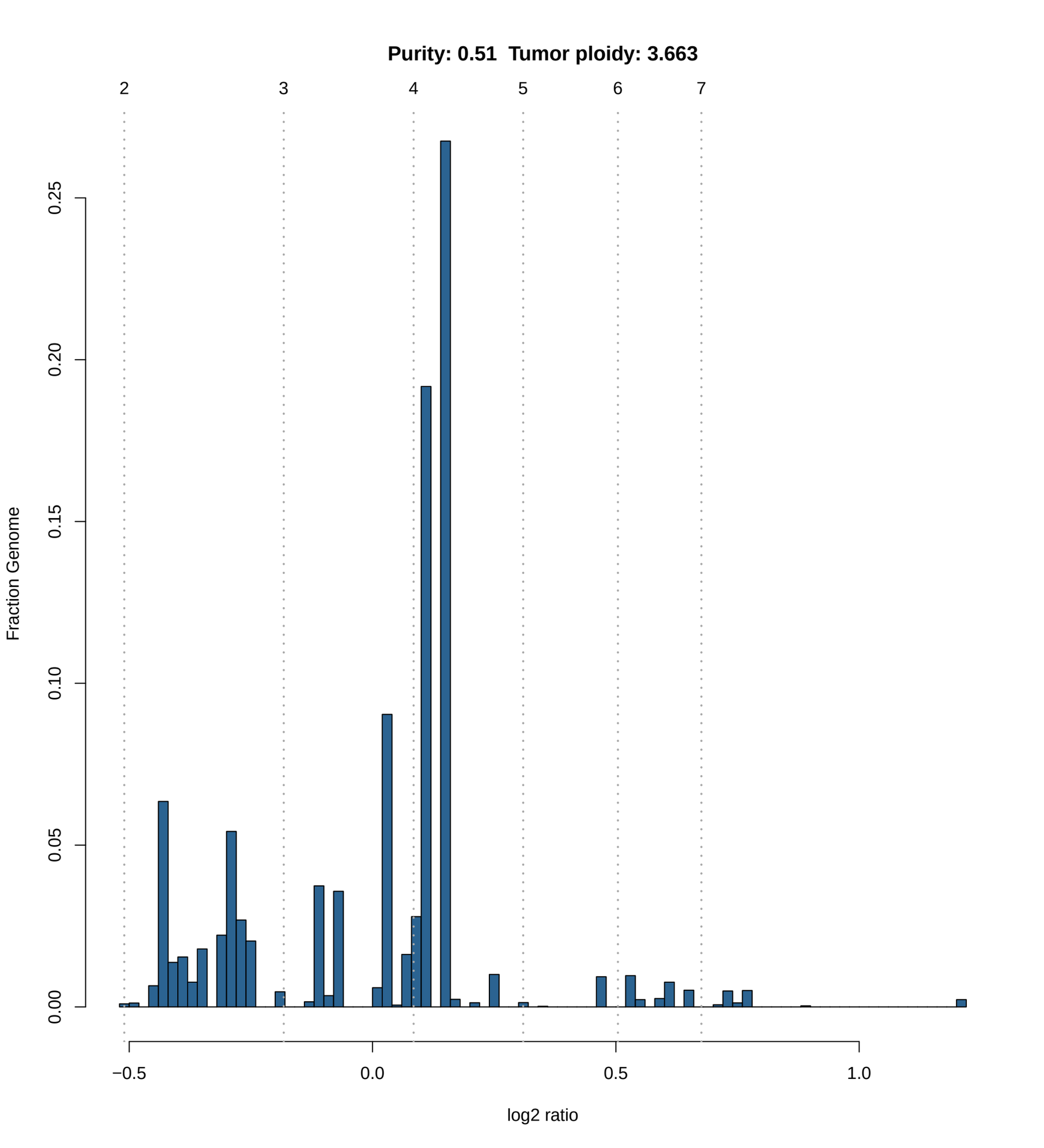

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

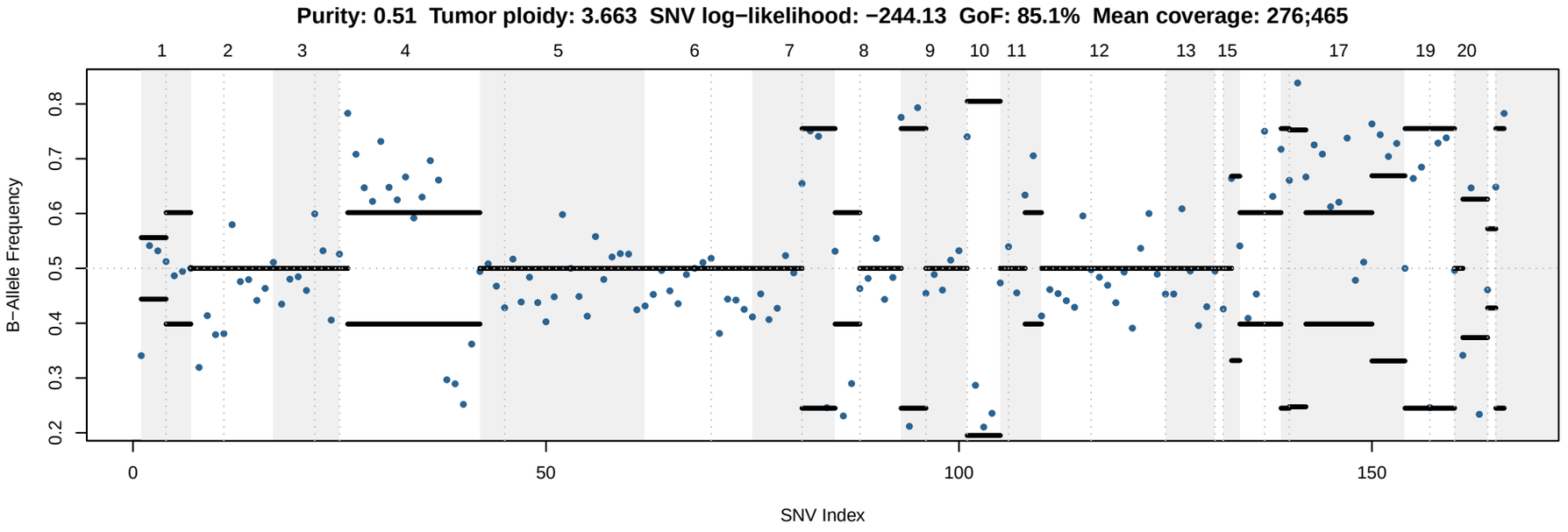

Allelic fraction (germline)
Copy Number log−ratio
1m1
2m2
3m3
4m3
3m2
2m1
4m2
3m1
1m0
4m1

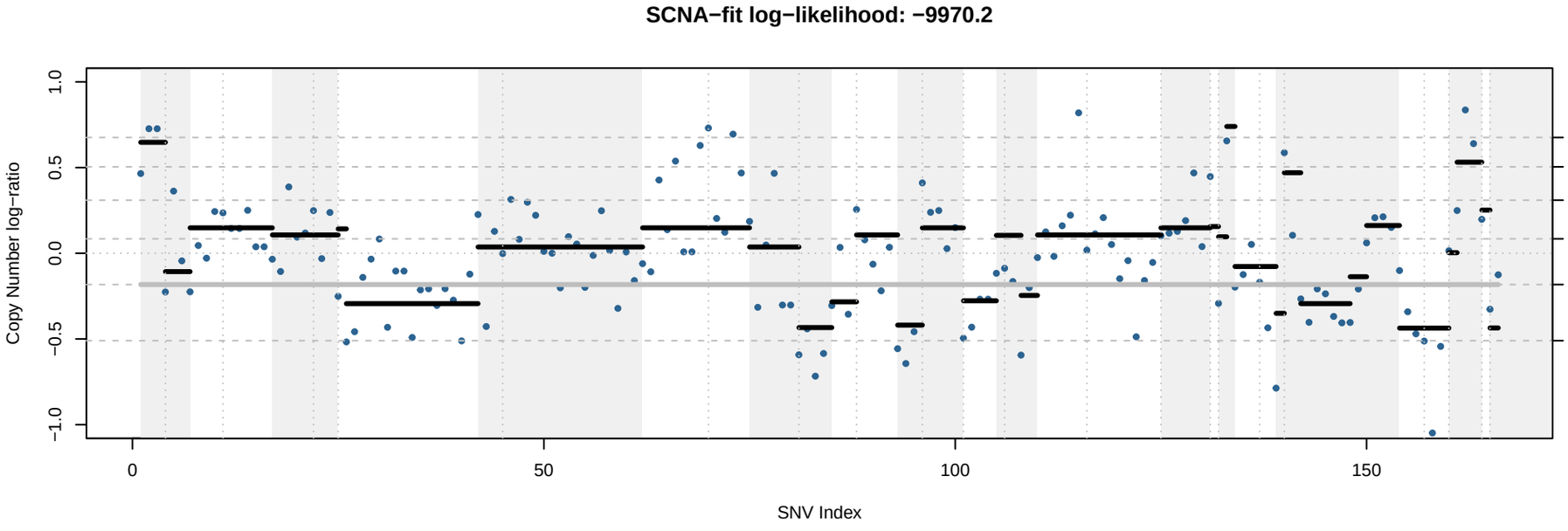

Coverage (log2)
Allelic fraction

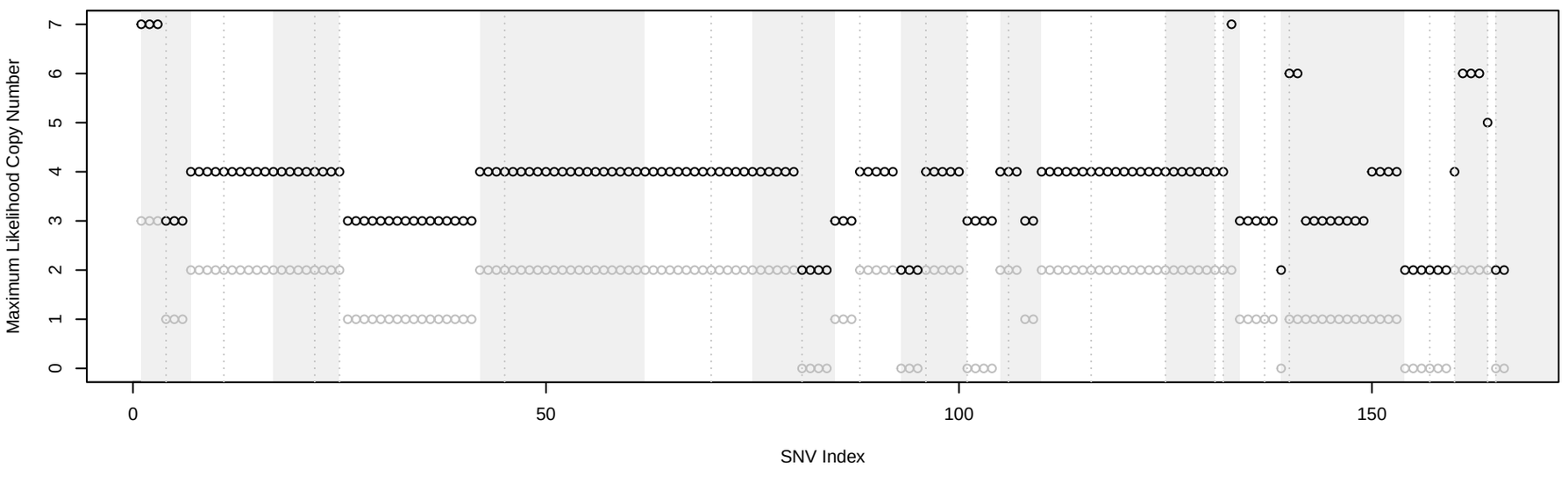

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1

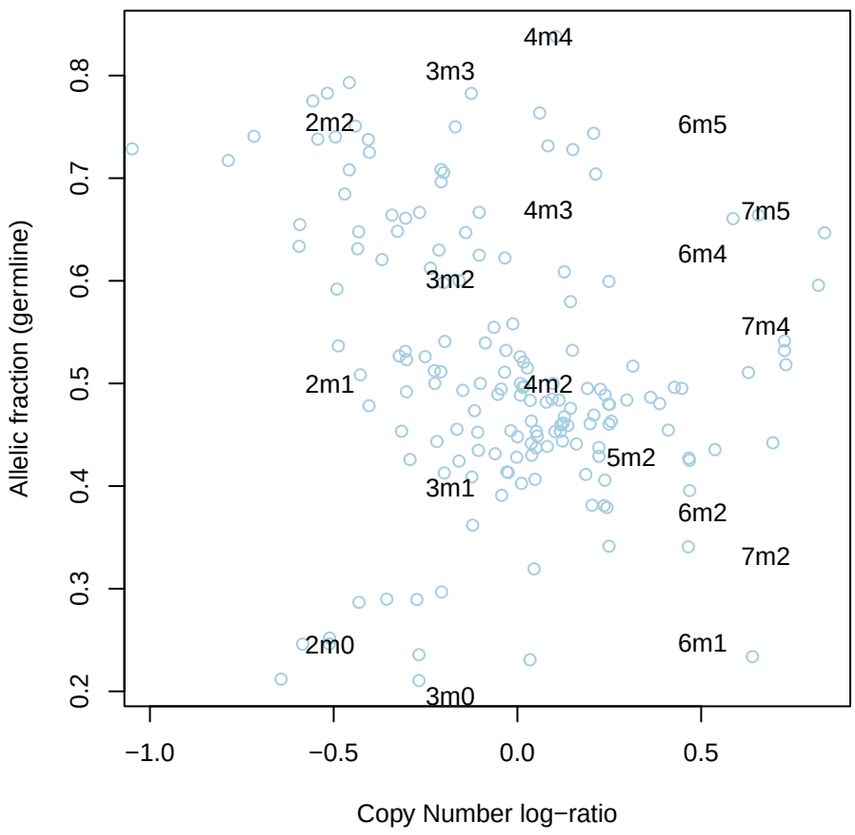

Power 0.8
Frequency
Cellular fraction

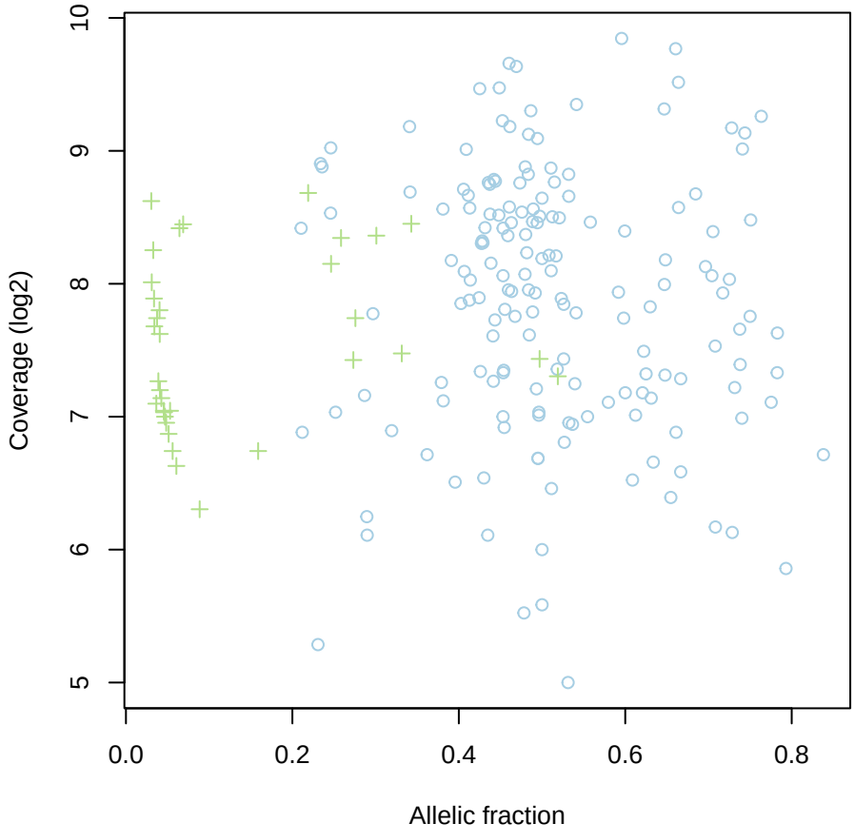

Purity: 0.51 Tumor ploidy: 3.663
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

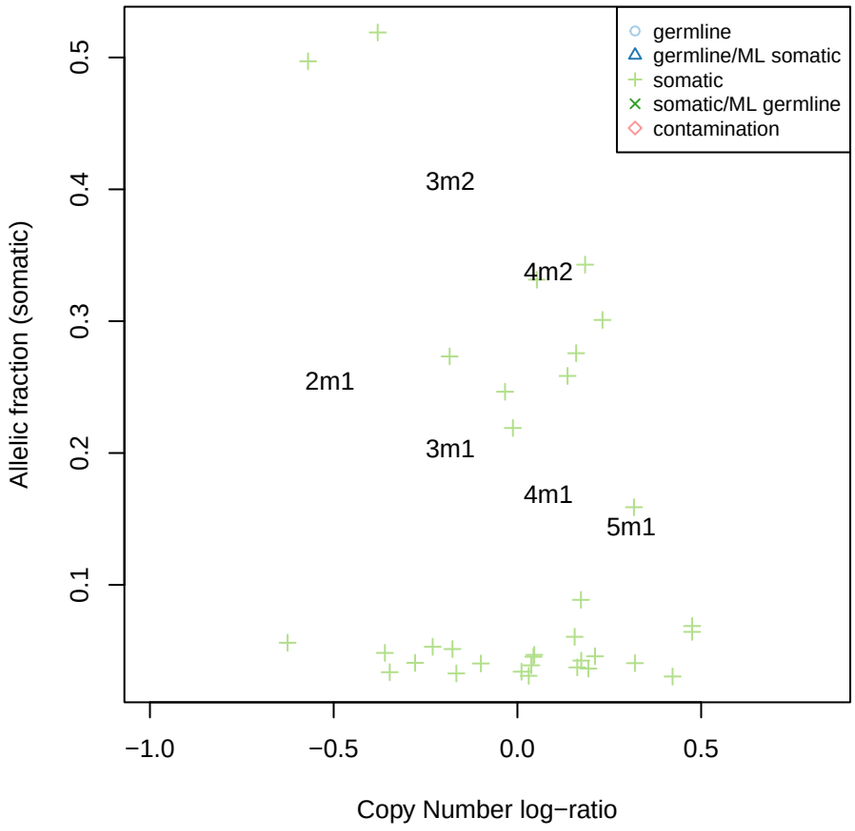

Purity: 0.51 Tumor ploidy: 3.663 SNV log−likelihood: −244.13 GoF: 85.1% Mean coverage: 276;465
1 2 3 4 5 6 7 8 9 10 11 12 13 15 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

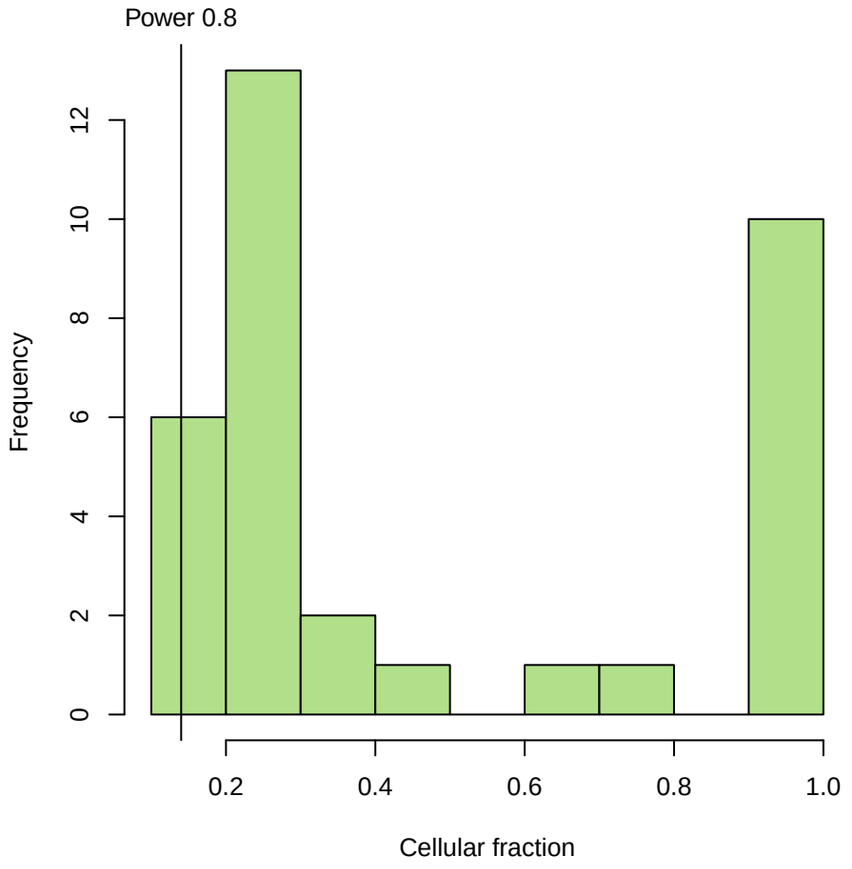

SCNA−fit log−likelihood: −9970.2
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
2 3 4 5 6 7
0 50 100 150
SNV Index

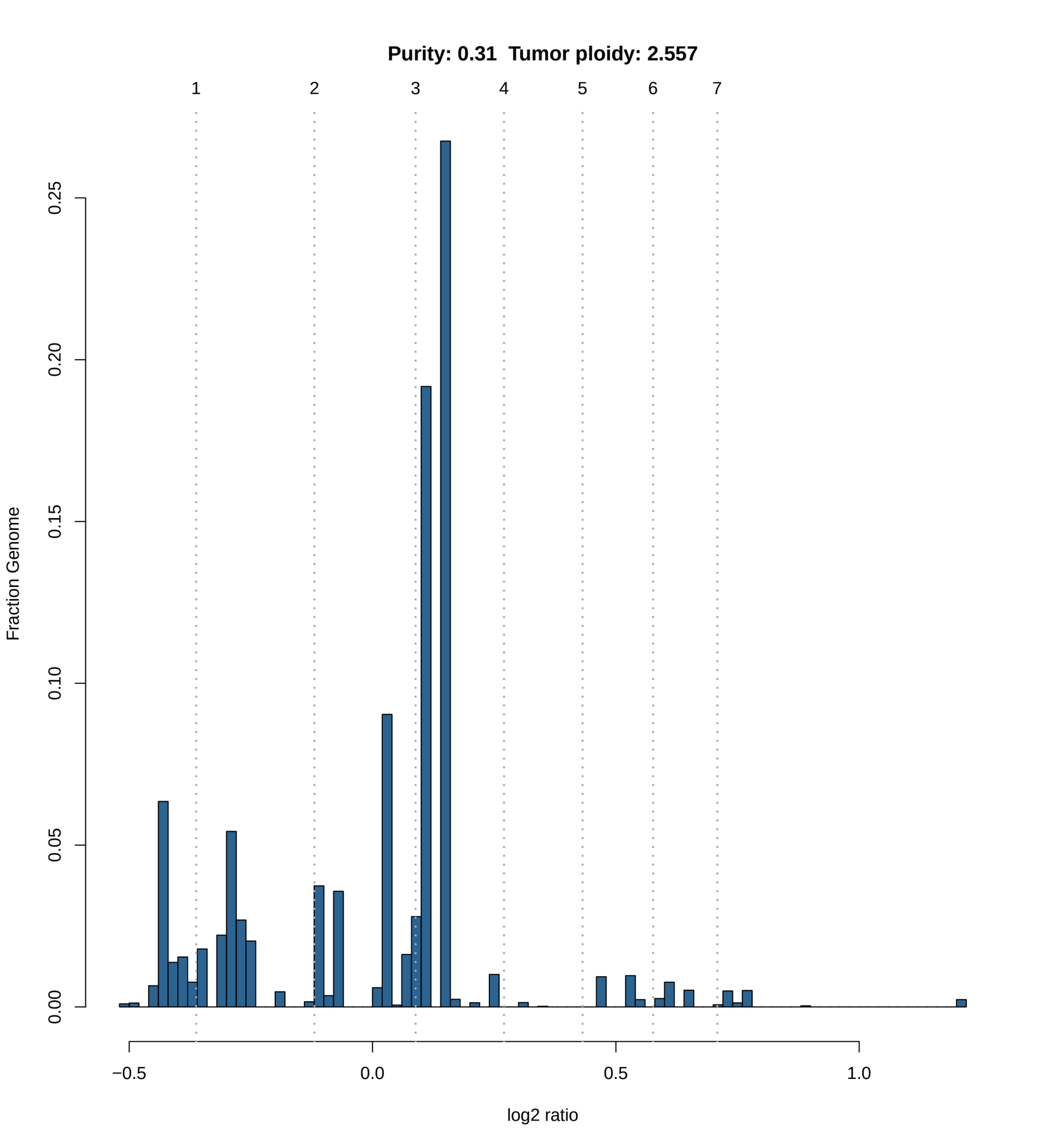

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

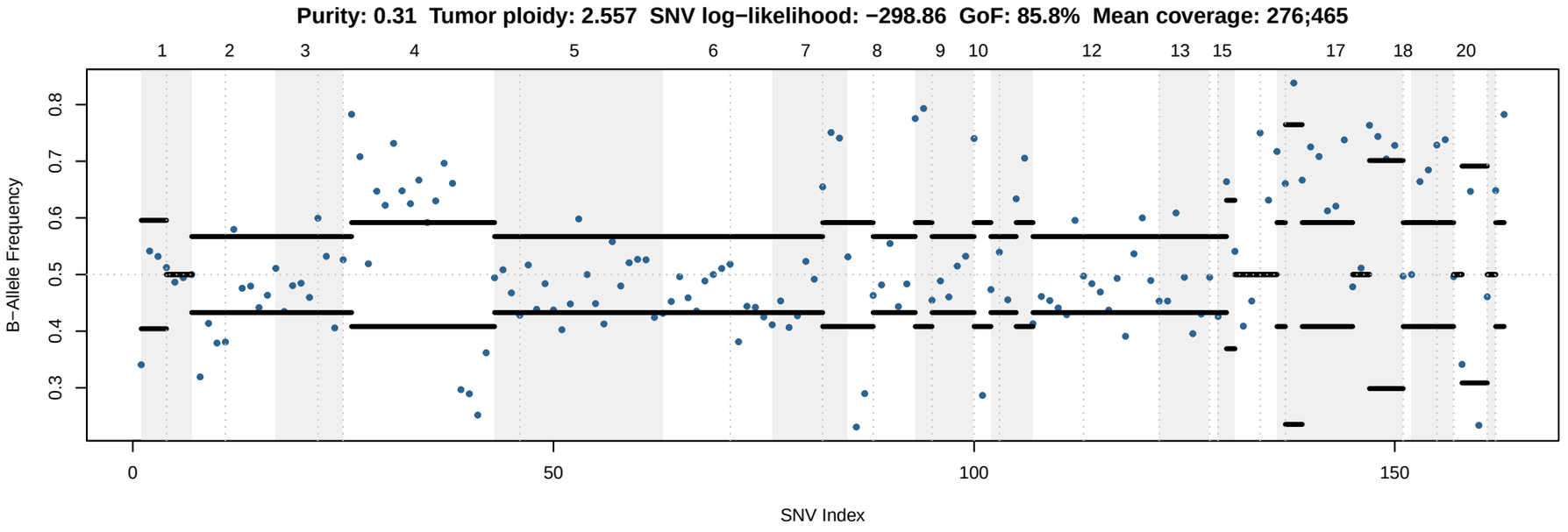

4m4
3m3
2m2
6m5
4m3
7m5
6m4
3m2
7m4
2m1
4m2
5m2
3m1
6m2
7m2
2m0
6m1
3m0
Allelic fraction (germline)
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
0.2
0.3
0.4
0.5
0.6
0.7
0.8

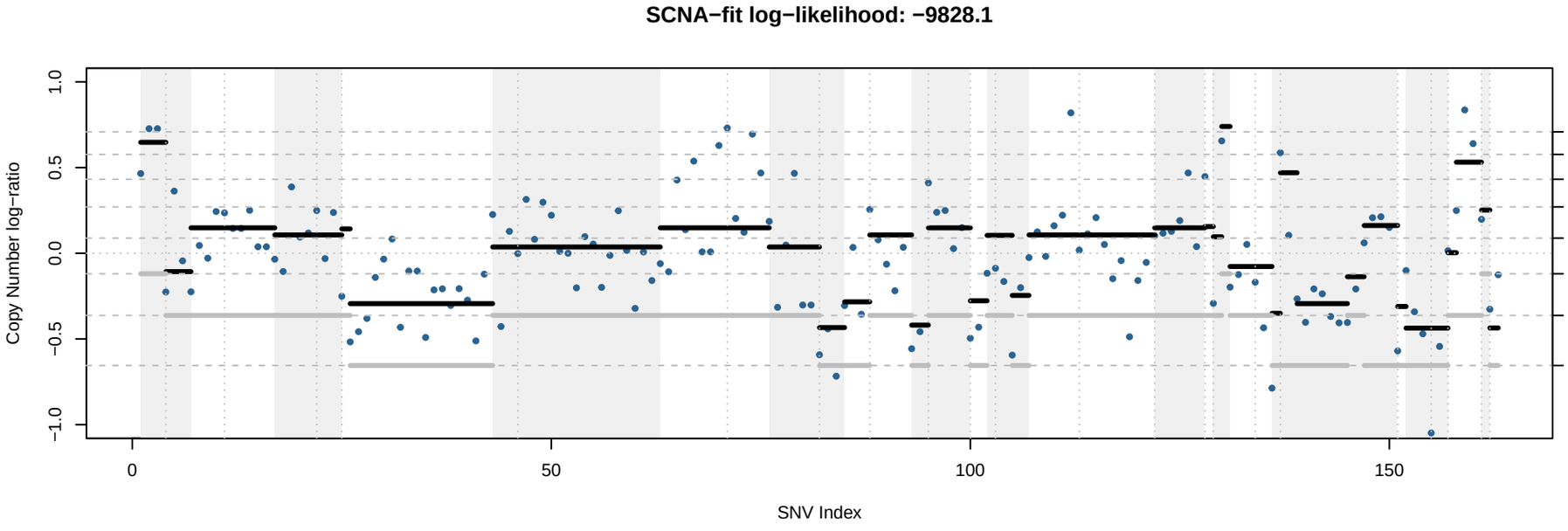

Coverage (log2)
Allelic fraction
0.0
0.2
0.4
0.6
0.8
5
6
7
8
9
10

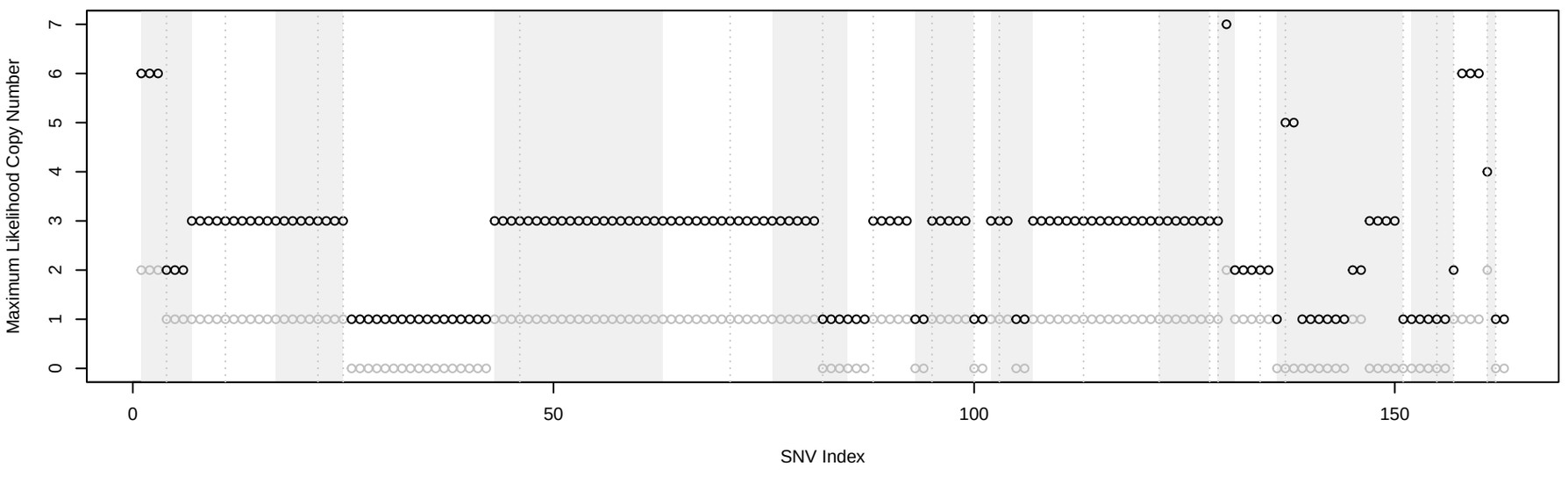

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m2
4m2
2m1
3m1
4m1
5m1
Allelic fraction (somatic)
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
0.1
0.2
0.3
0.4
0.5

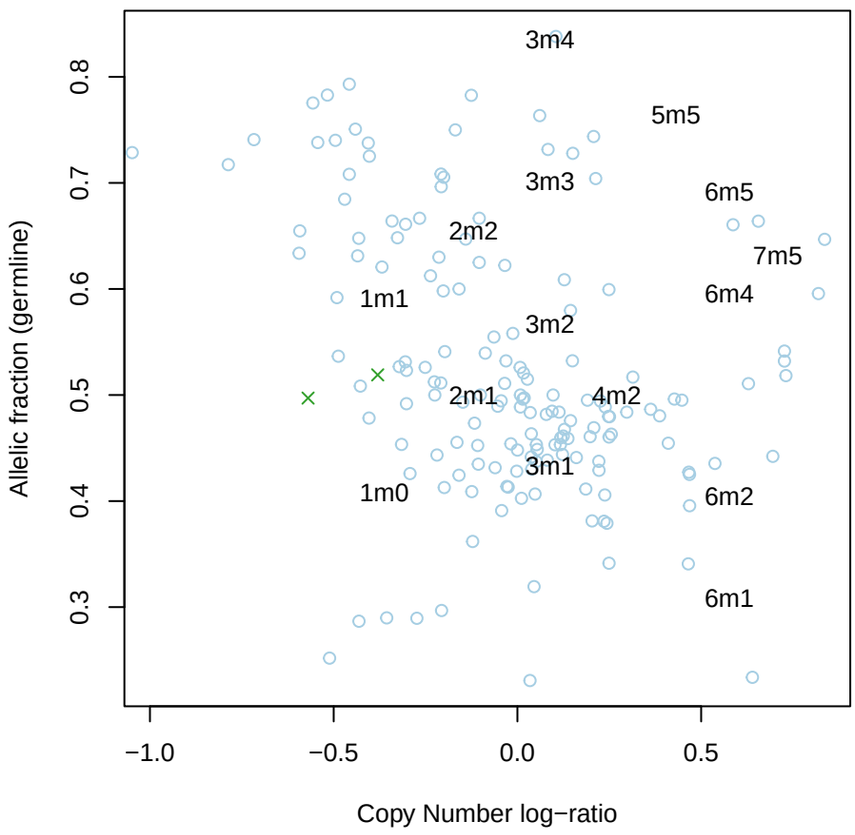

Power 0.8
Frequency
Cellular fraction
0.2
0.4
0.6
0.8
1.0
0
2
4
6
8
10
12

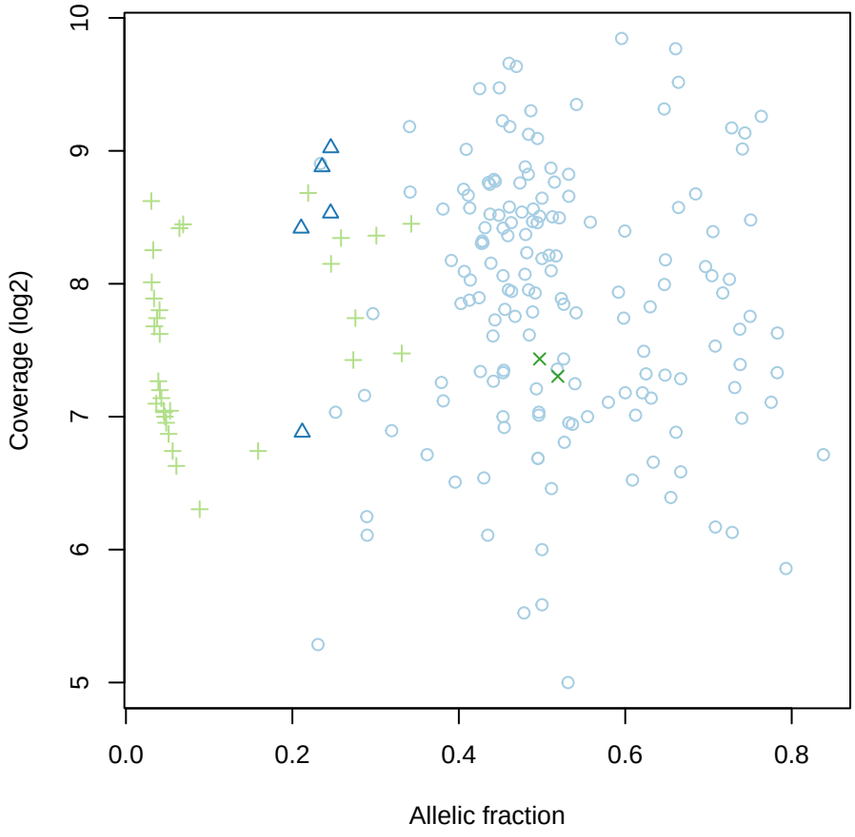

Purity: 0.31 Tumor ploidy: 2.557
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

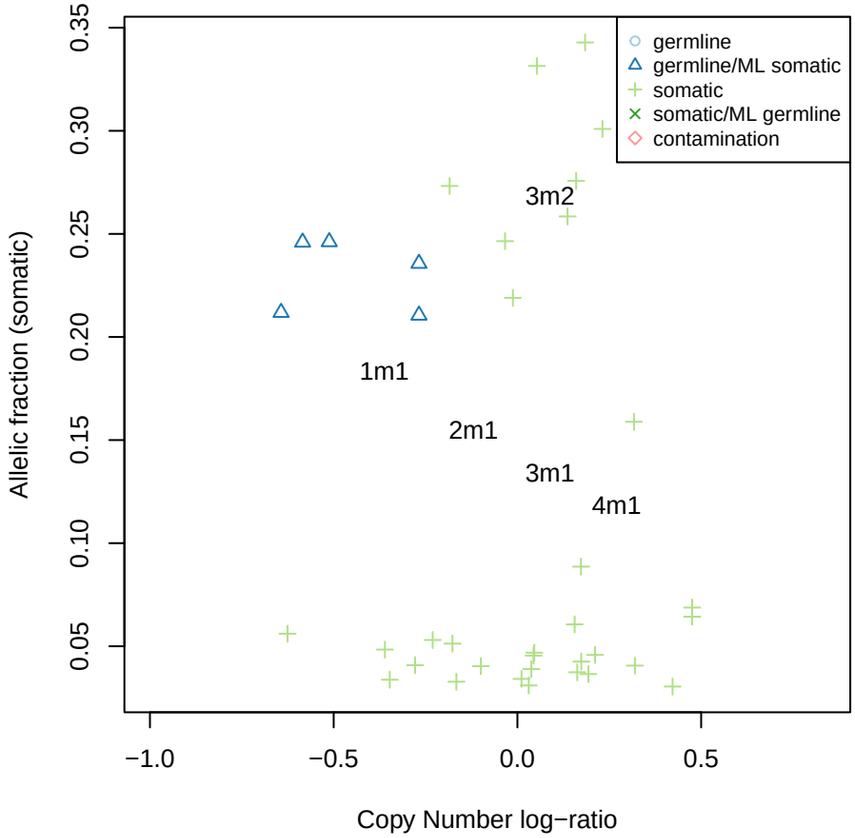

Purity: 0.31 Tumor ploidy: 2.557 SNV log−likelihood: −298.86 GoF: 85.8% Mean coverage: 276;465
1 2 3 4 5 6 7 8 9 10 12 13 15 17 18 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

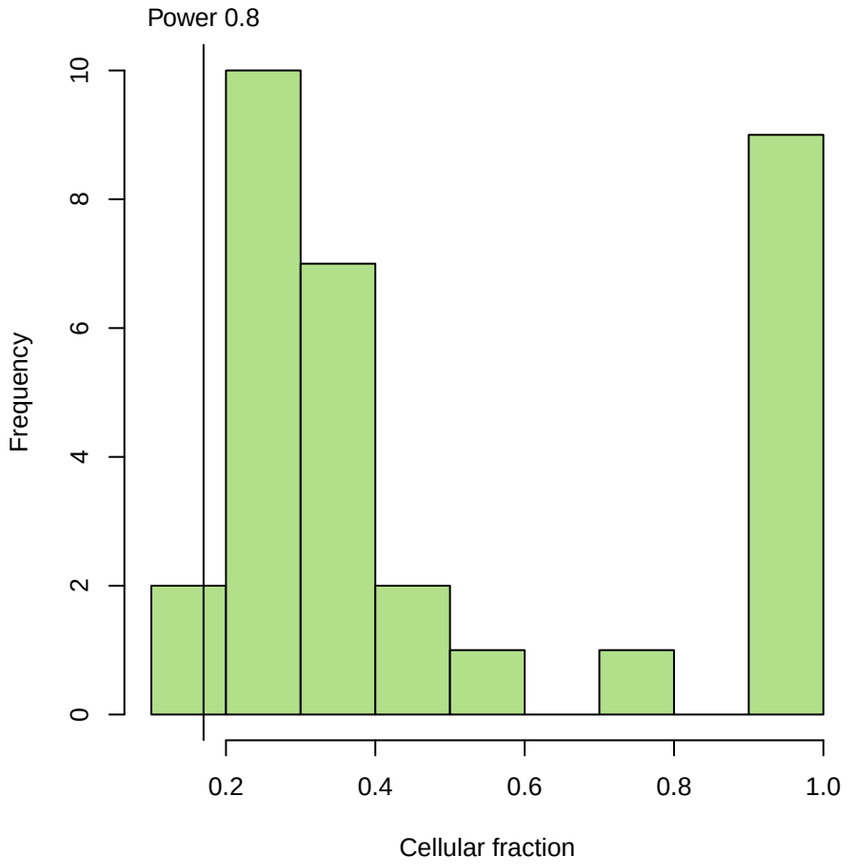

SCNA−fit log−likelihood: −9828.1
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 6
0 50 100 150
SNV Index

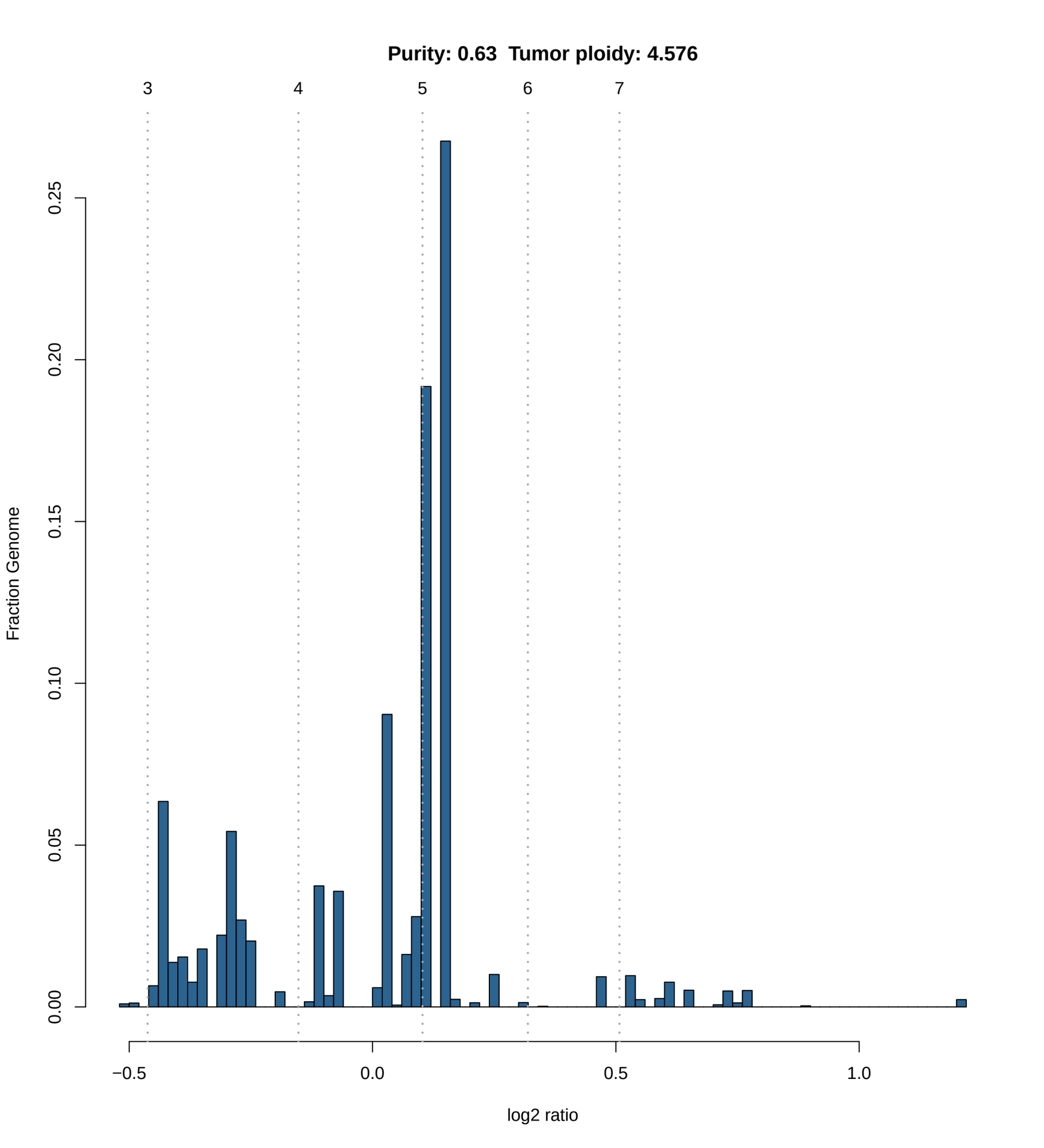

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

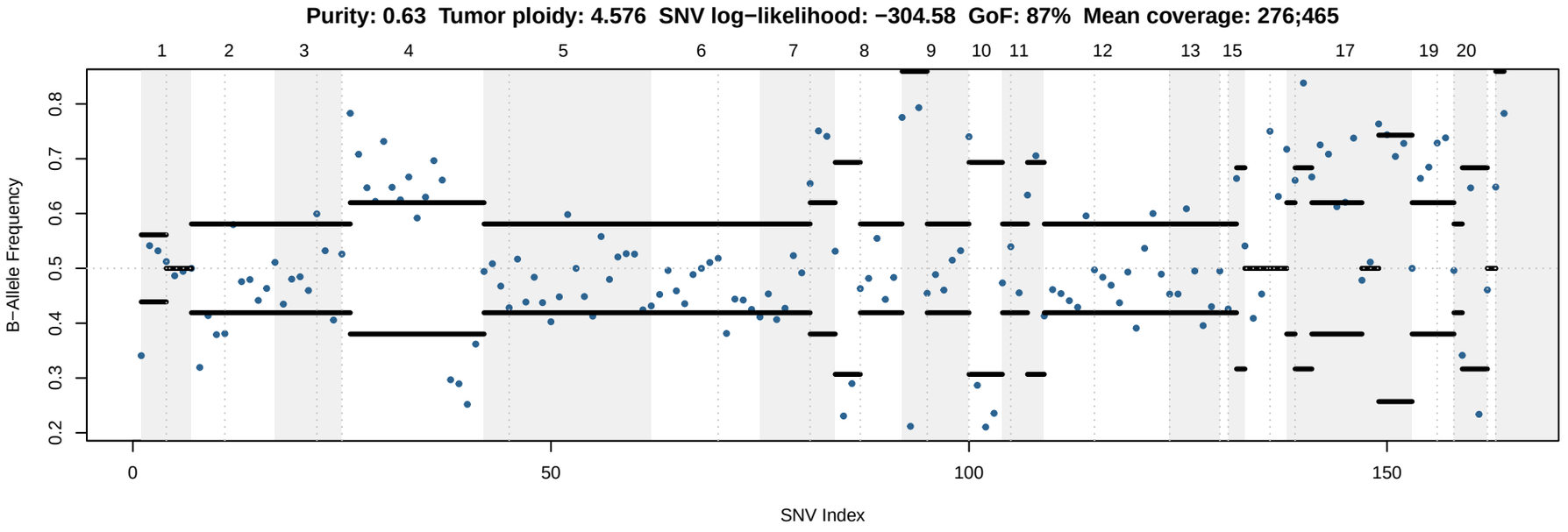

3m4
5m5
3m3
6m5
2m2
7m5
1m1
6m4
3m2
2m1
4m2
3m1
1m0
6m2
6m1
Allelic fraction (germline)
Copy Number log−ratio

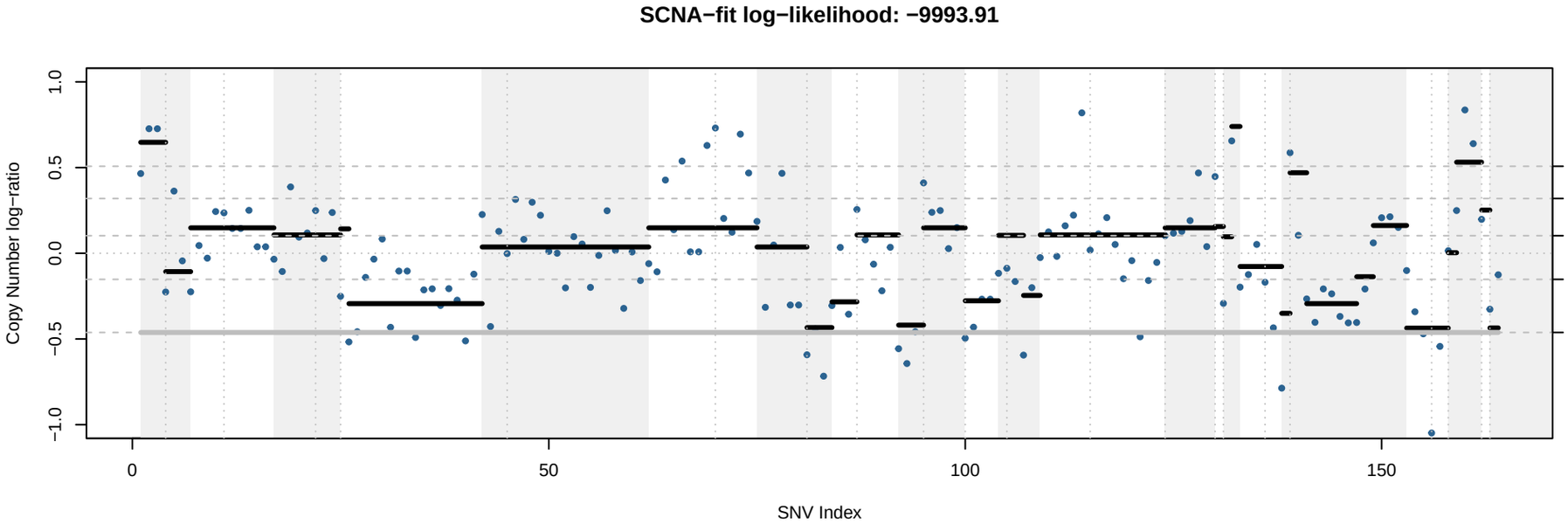

Coverage (log2)
Allelic fraction

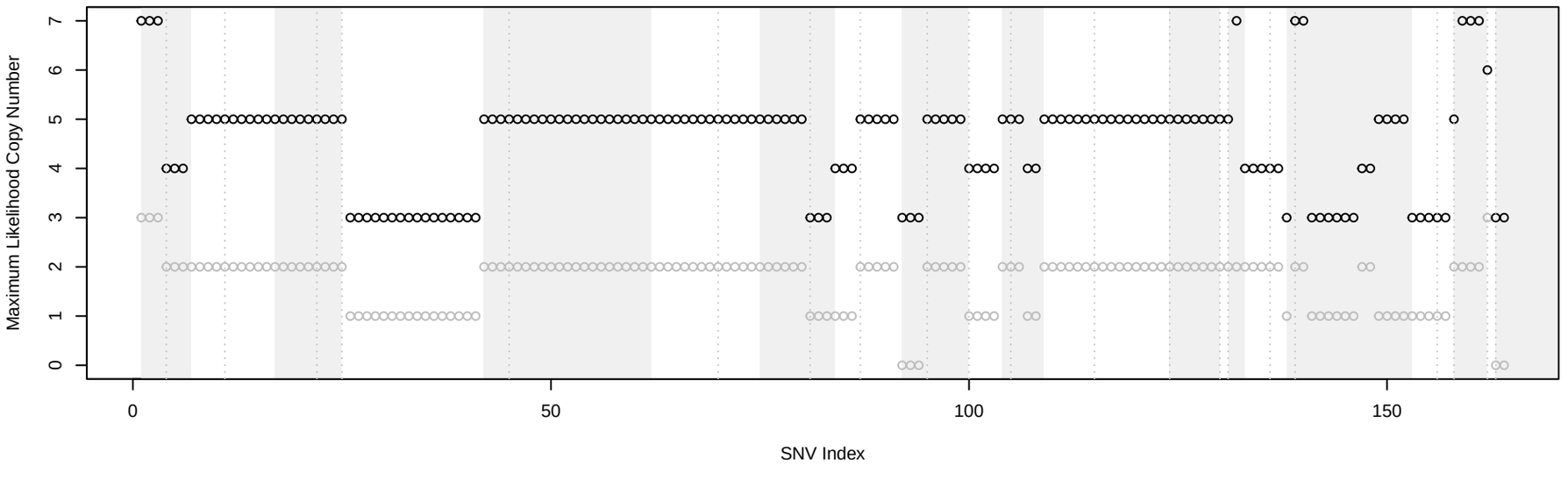

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m2
1m1
2m1
3m1
4m1
Allelic fraction (somatic)
Copy Number log−ratio

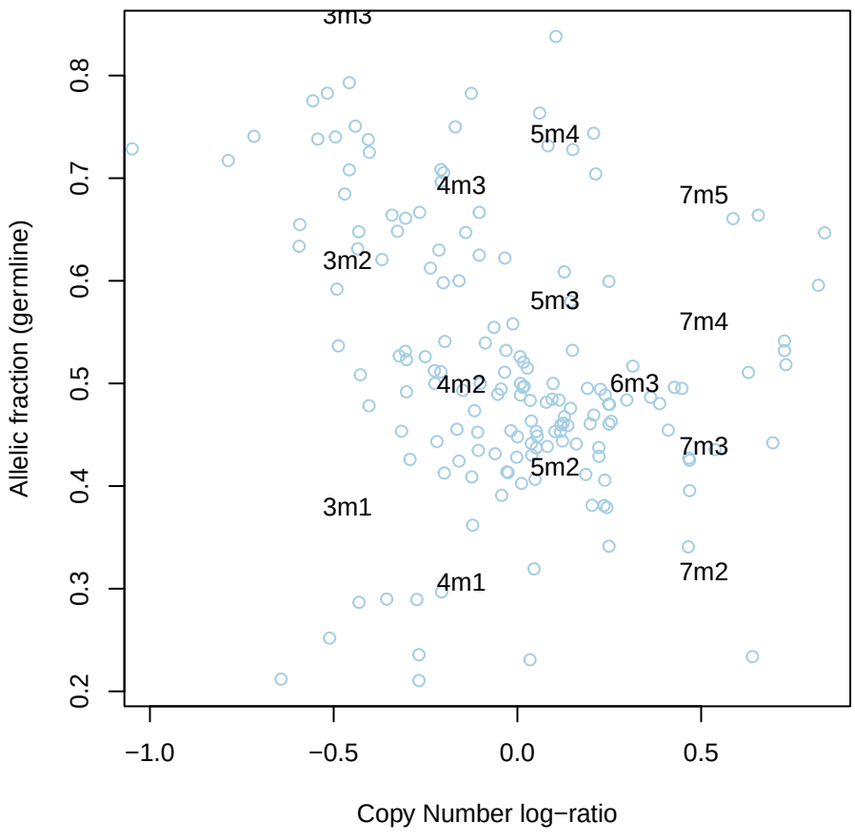

Power 0.8
Frequency
Cellular fraction

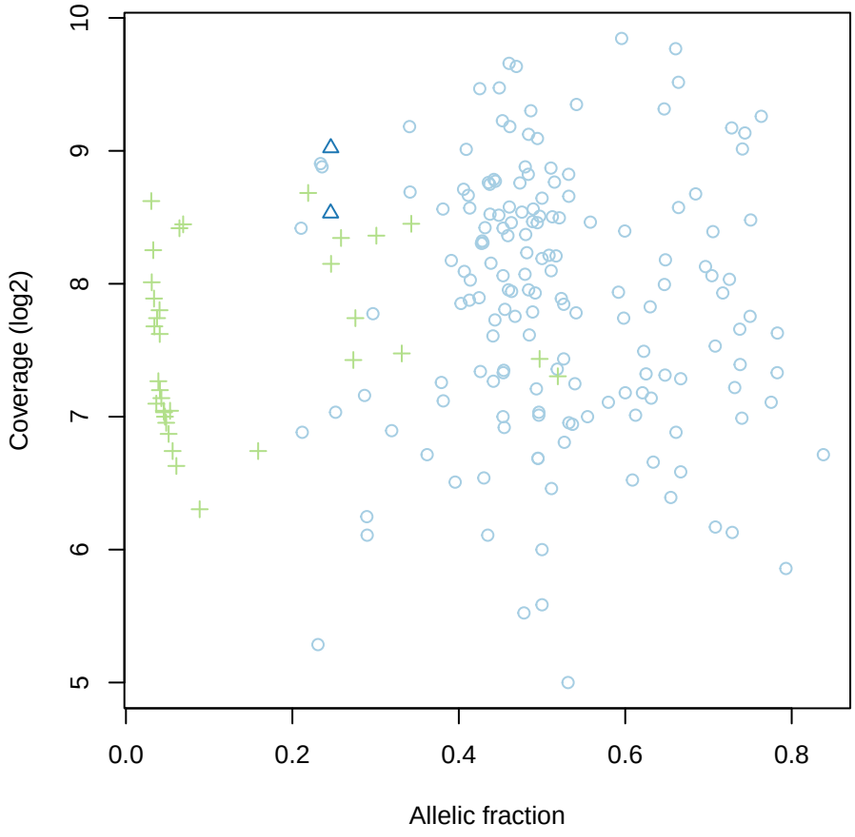

Purity: 0.63 Tumor ploidy: 4.576
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

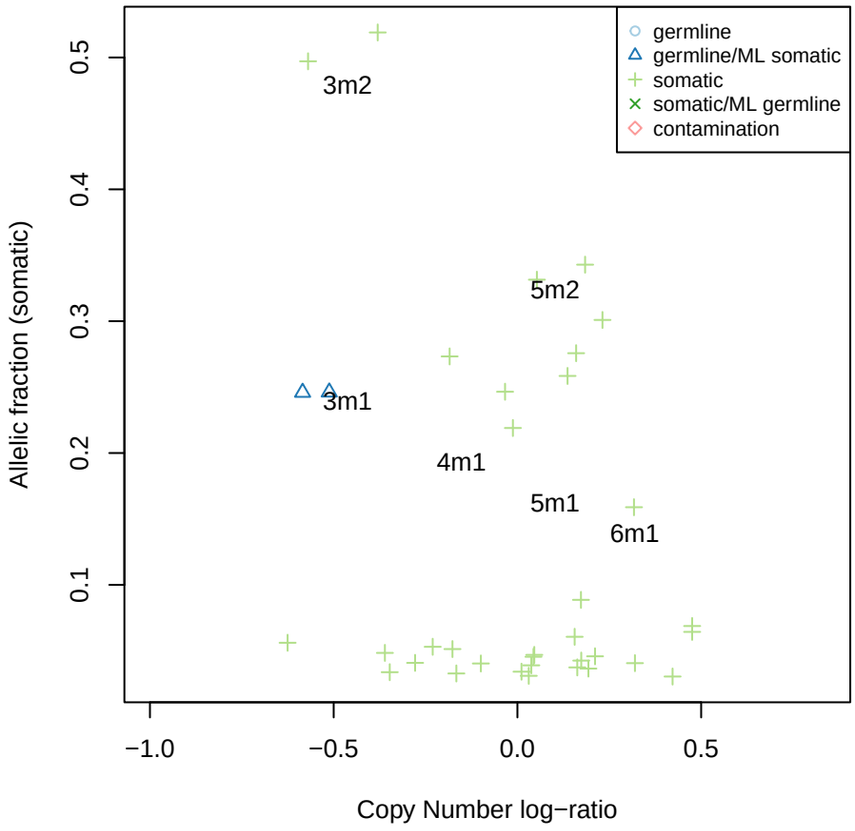

Purity: 0.63 Tumor ploidy: 4.576 SNV log−likelihood: −304.58 GoF: 87% Mean coverage: 276;465
1 2 3 4 5 6 7 8 9 10 11 12 13 15 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

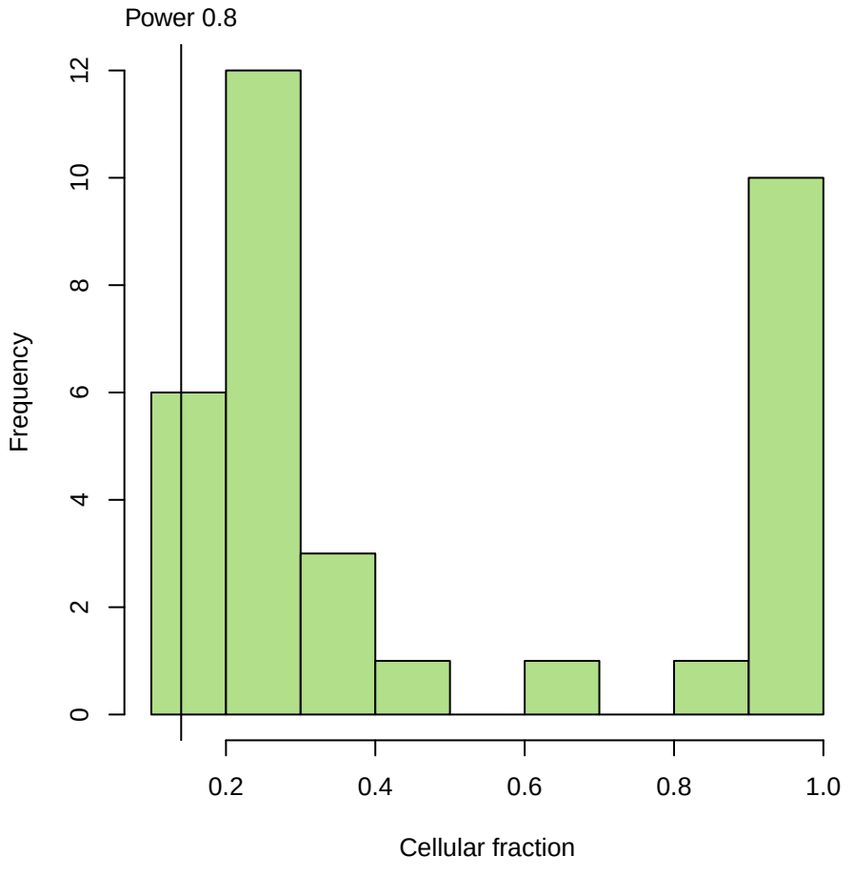

SCNA−fit log−likelihood: −9993.91
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 50 100 150
SNV Index

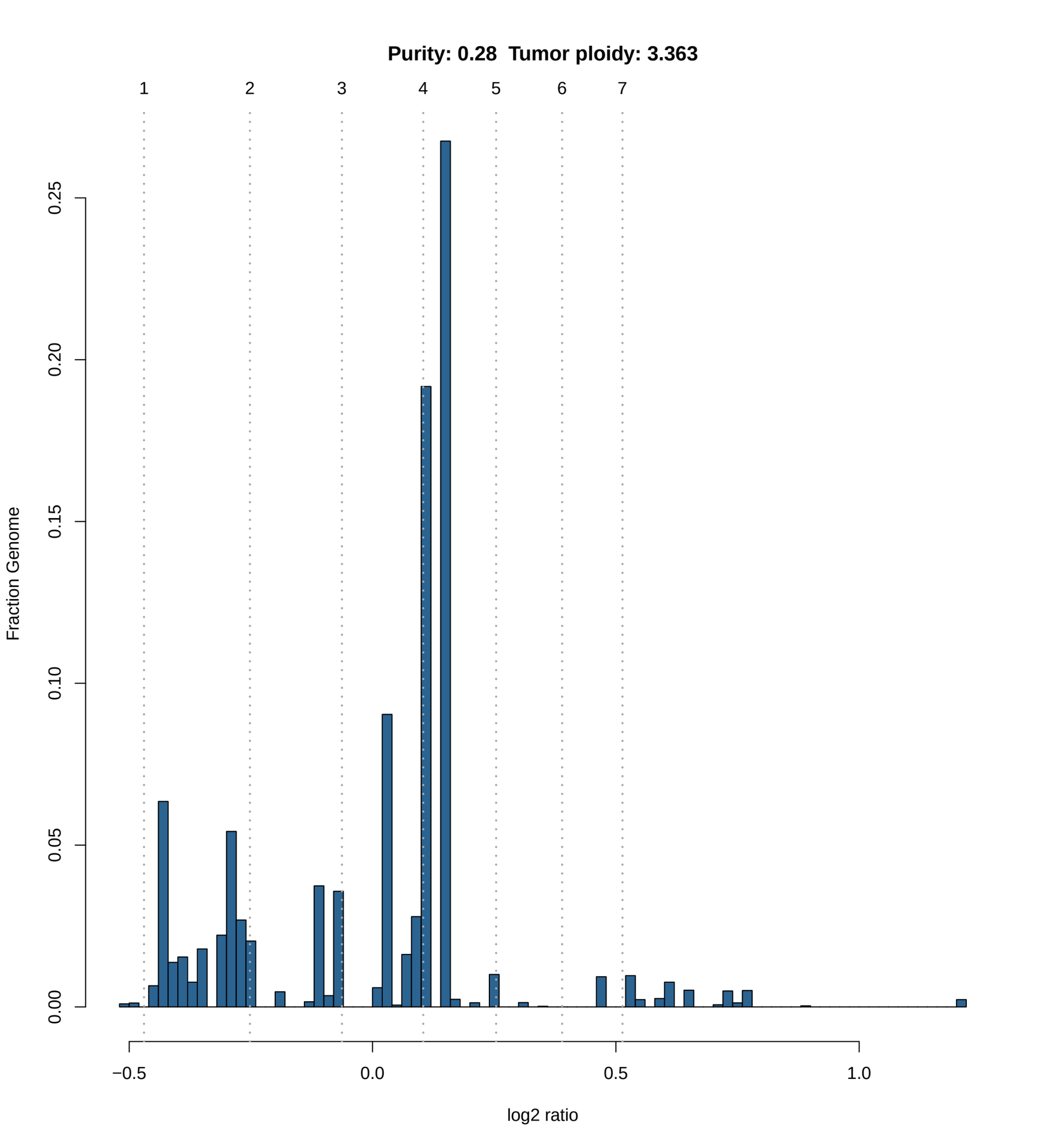

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

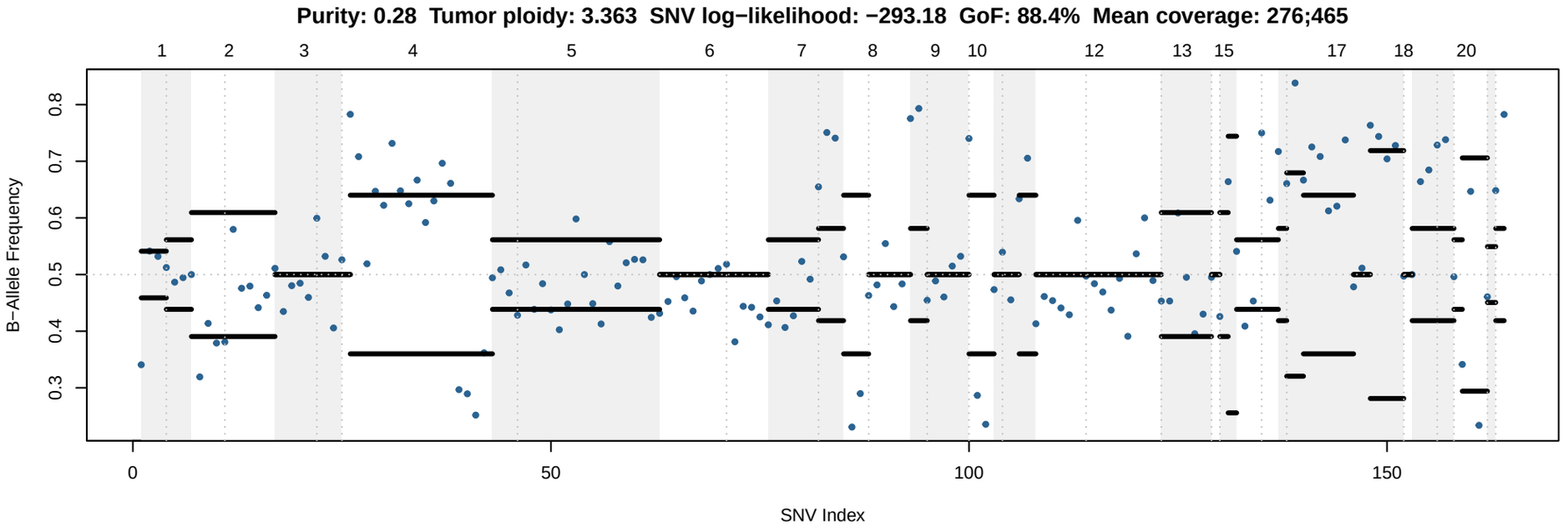

3m3
5m4
4m3
7m5
3m2
5m3
7m4
4m2
6m3
7m3
5m2
3m1
7m2
4m1
Allelic fraction (germline)
Copy Number log−ratio

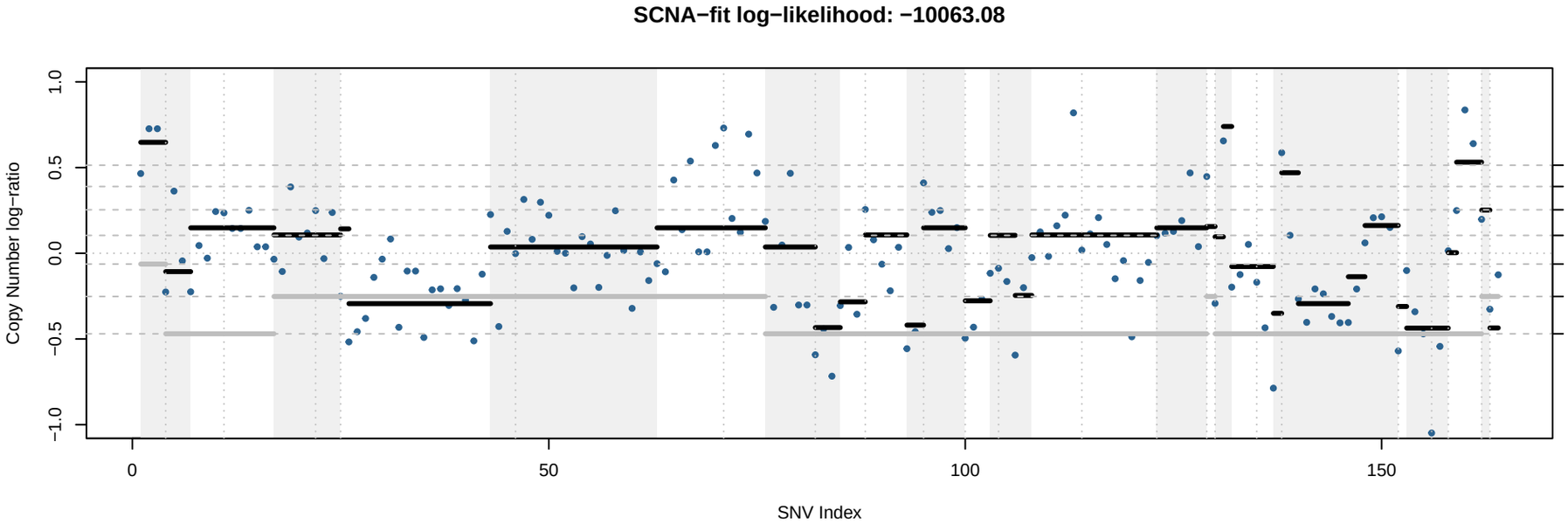

Coverage (log2)
Allelic fraction

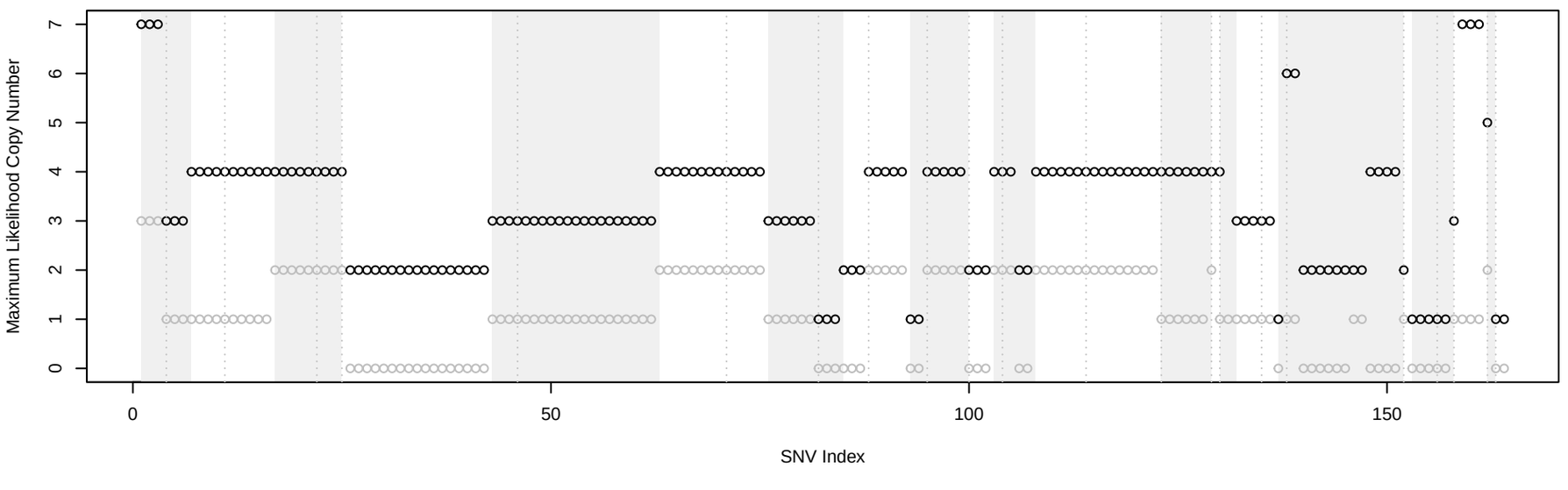

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m2
5m2
3m1
4m1
5m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio

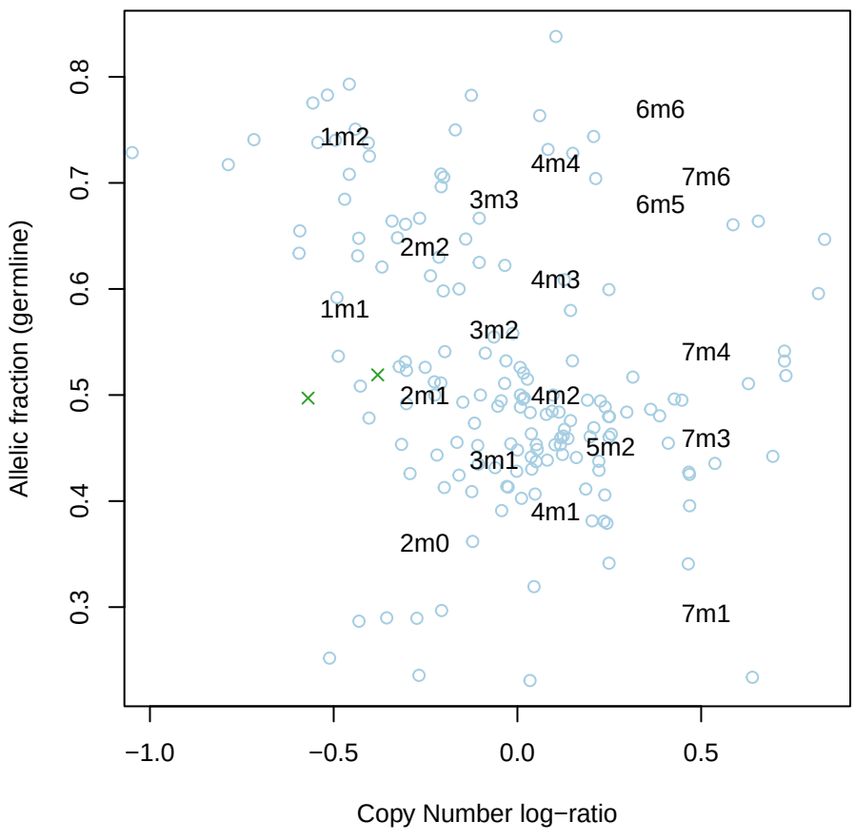

Power 0.8
Frequency
Cellular fraction

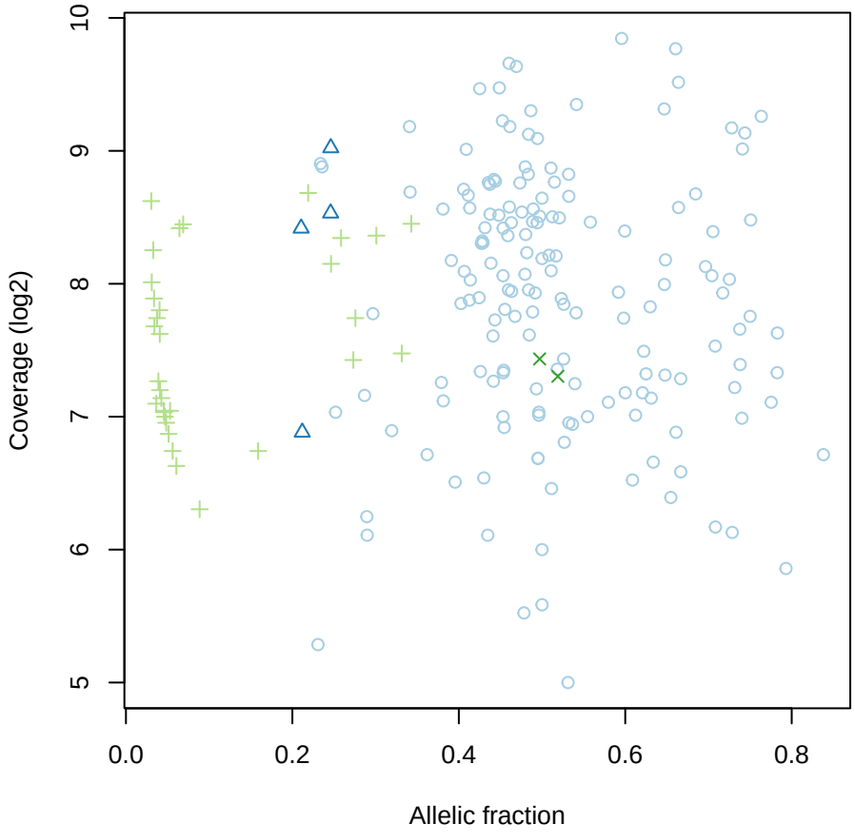

Purity: 0.28 Tumor ploidy: 3.363
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

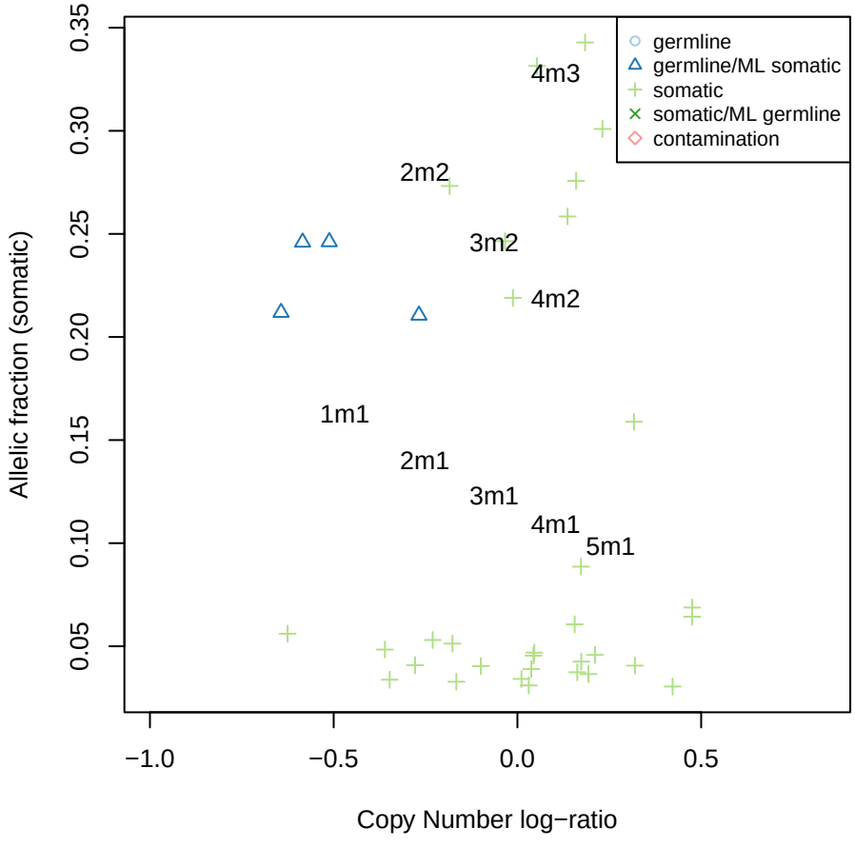

Purity: 0.28 Tumor ploidy: 3.363 SNV log−likelihood: −293.18 GoF: 88.4% Mean coverage: 276;465
1 2 3 4 5 6 7 8 9 10 12 13 15 17 18 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

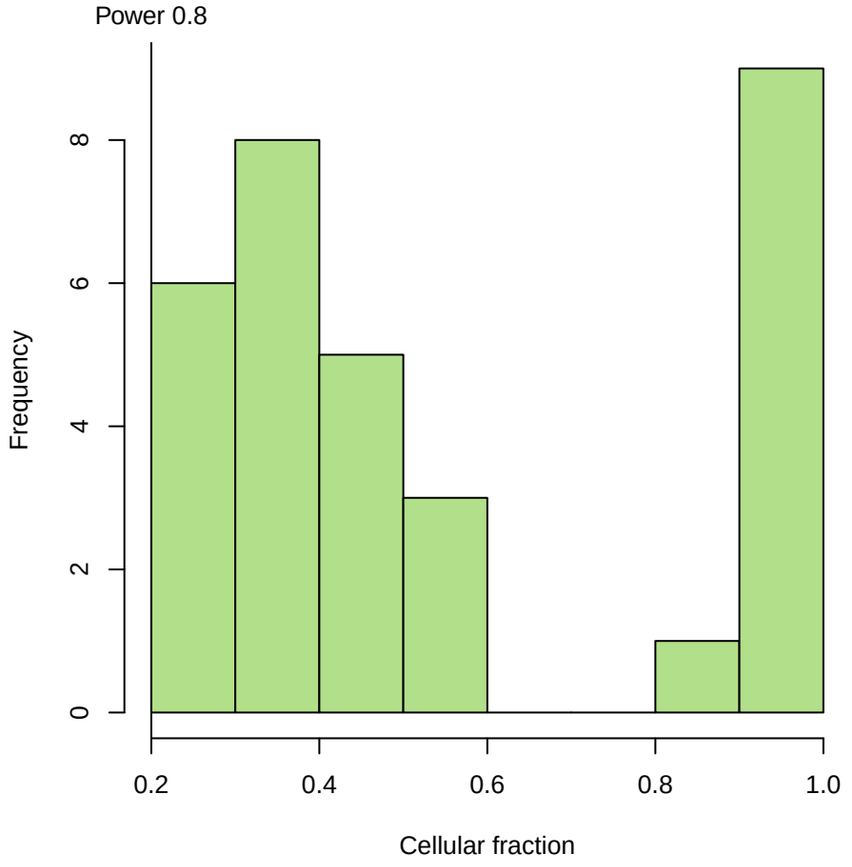

SCNA−fit log−likelihood: −10063.08
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 7
0 50 100 150
SNV Index

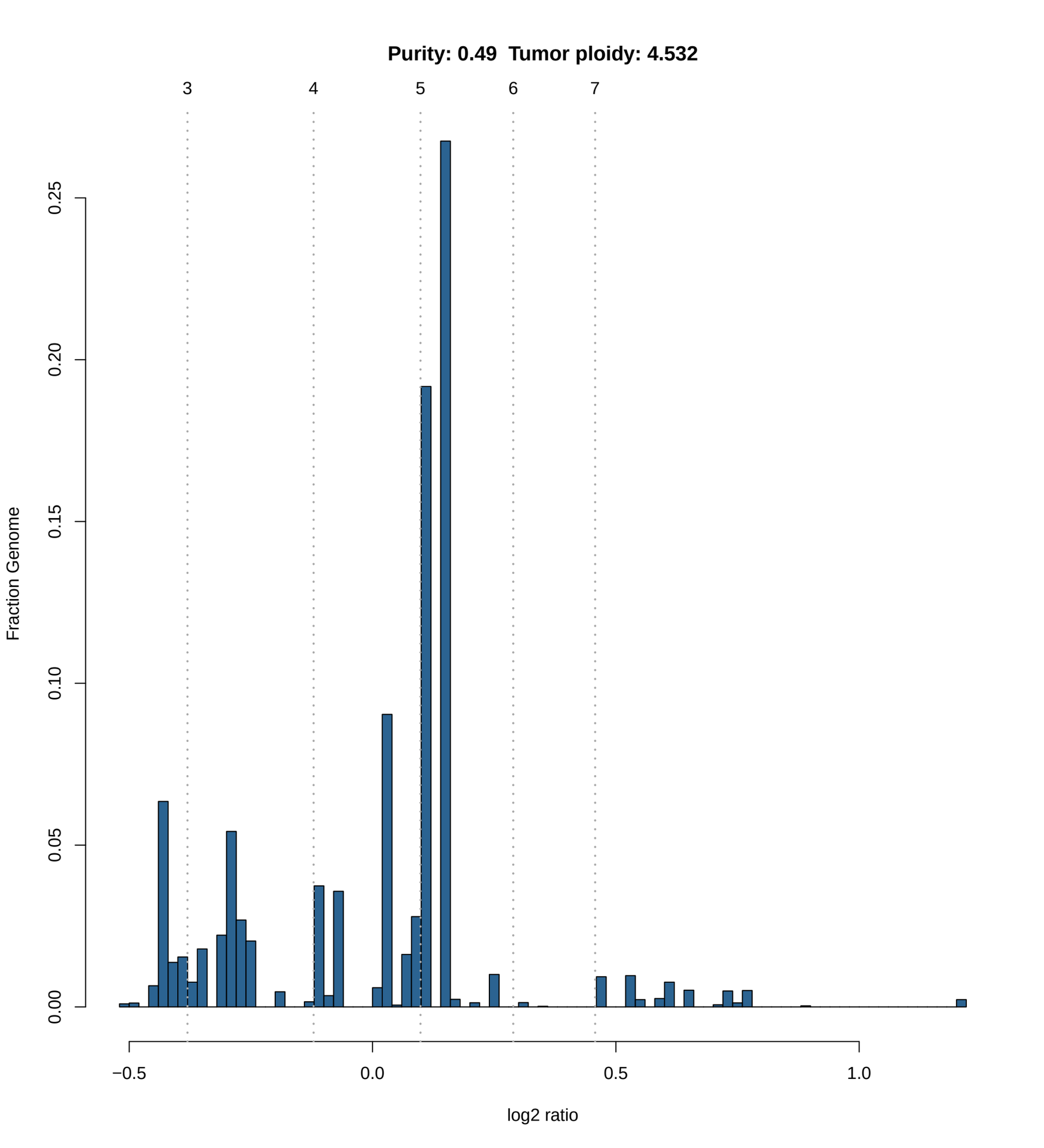

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

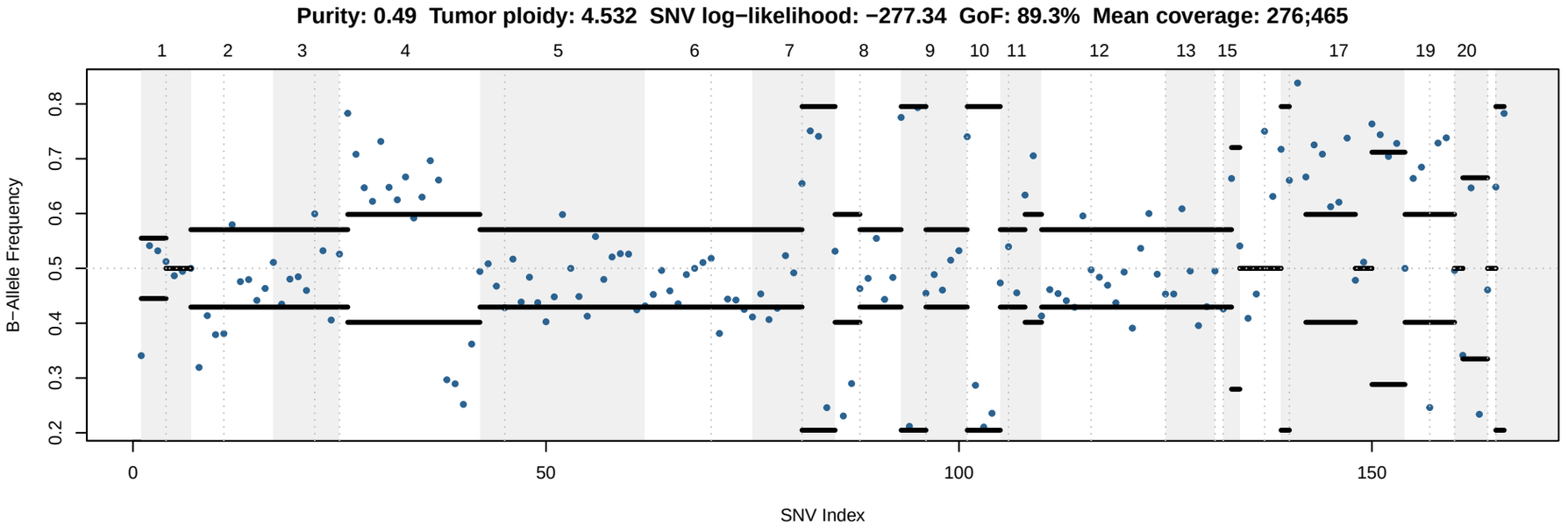

Allelic fraction (germline)
Copy Number log−ratio
1m2
6m6
4m4
7m6
3m3
6m5
2m2
4m3
1m1
3m2
7m4
2m1
4m2
5m2
7m3
3m1
4m1
2m0
7m1

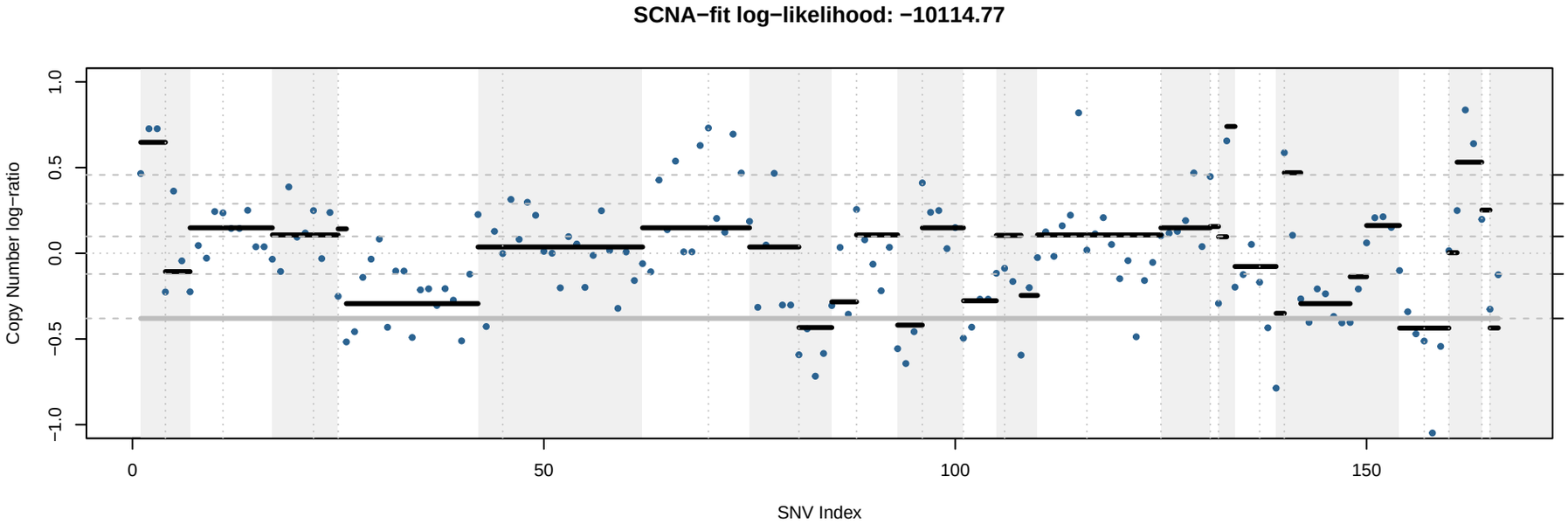

Coverage (log2)
Allelic fraction

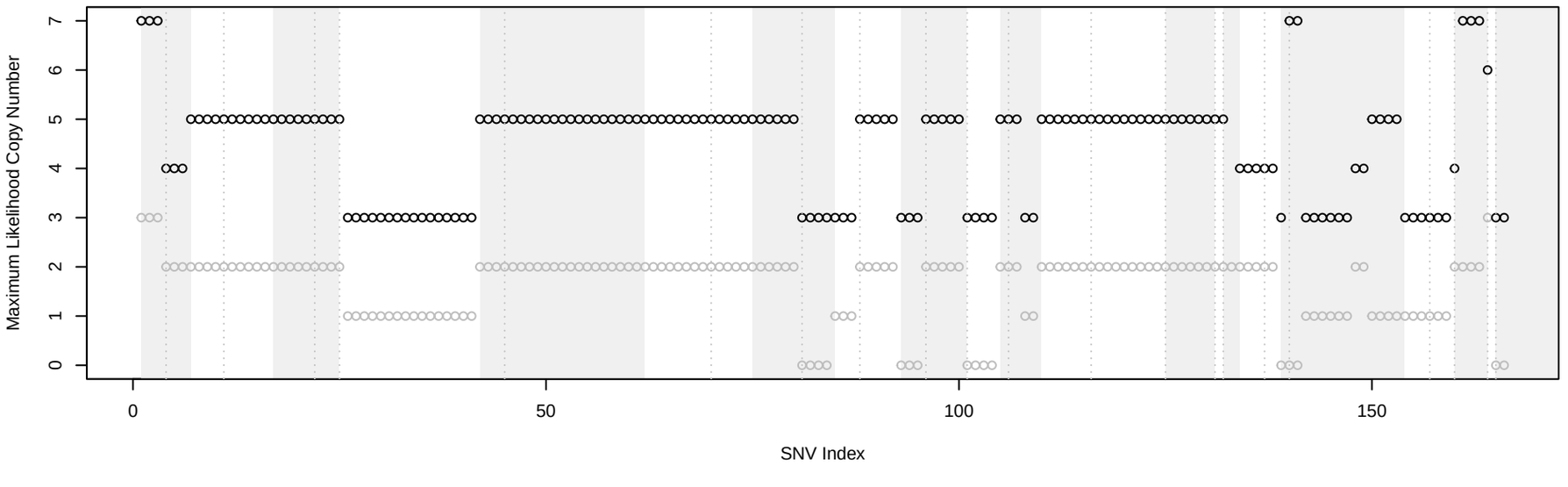

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
4m3
2m2
3m2
4m2
1m1
2m1
3m1
4m1
5m1

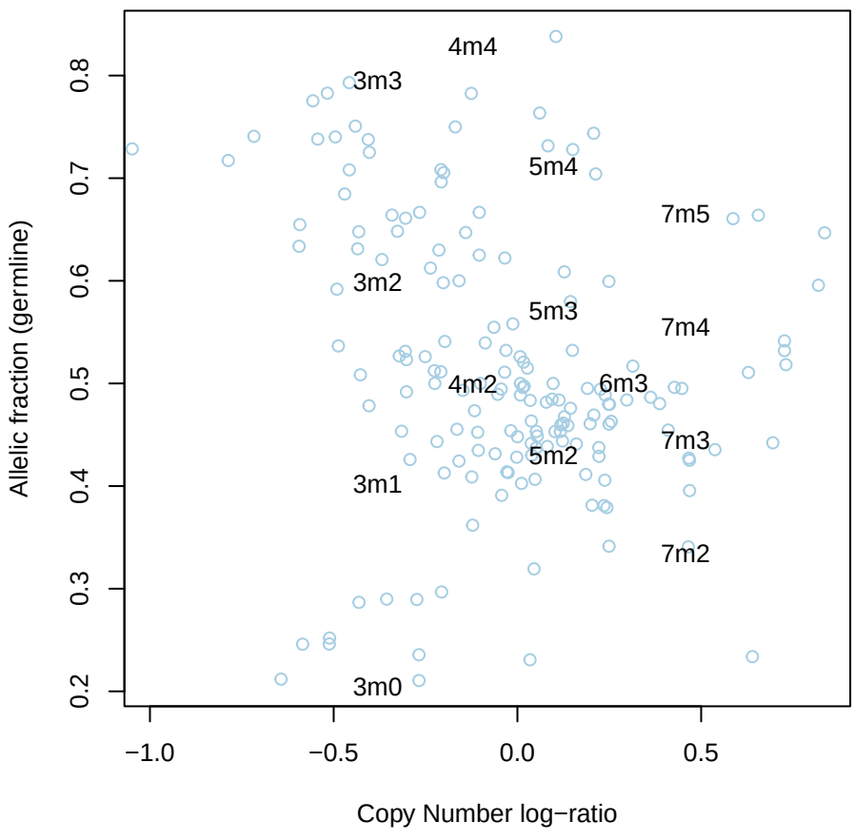

Power 0.8
Frequency
Cellular fraction

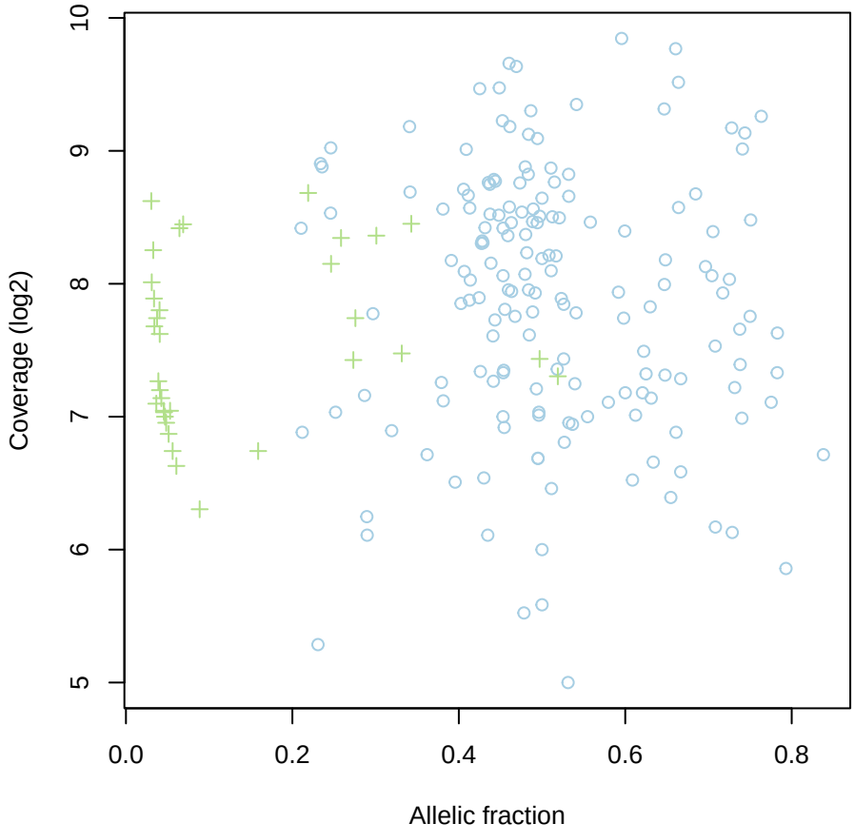

Purity: 0.49 Tumor ploidy: 4.532
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

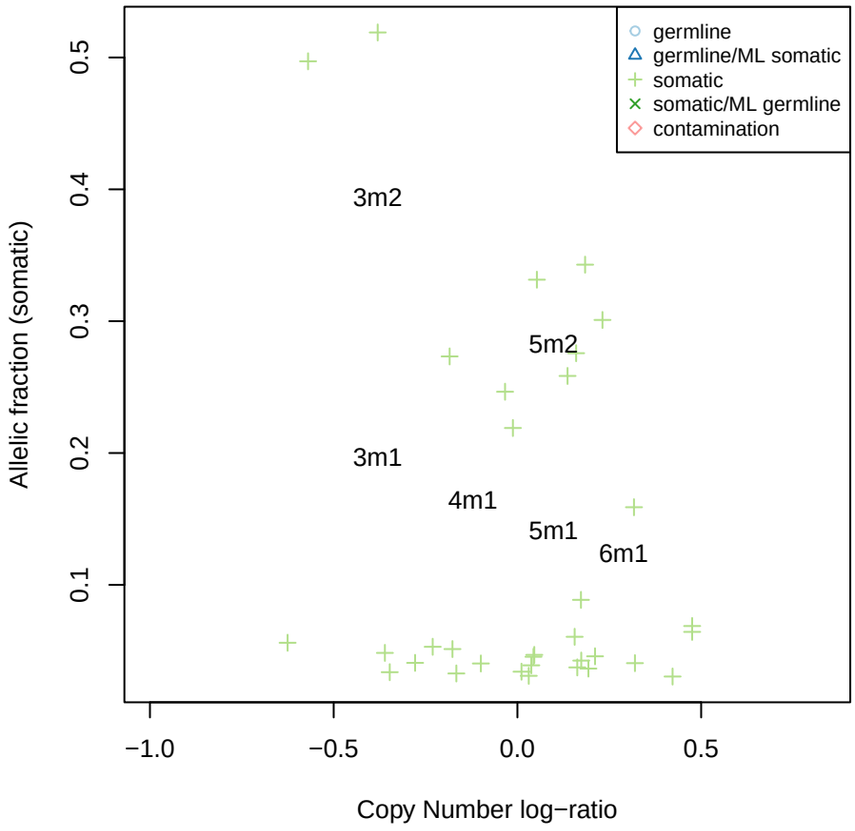

Purity: 0.49 Tumor ploidy: 4.532 SNV log−likelihood: −277.34 GoF: 89.3% Mean coverage: 276;465
1 2 3 4 5 6 7 8 9 10 11 12 13 15 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

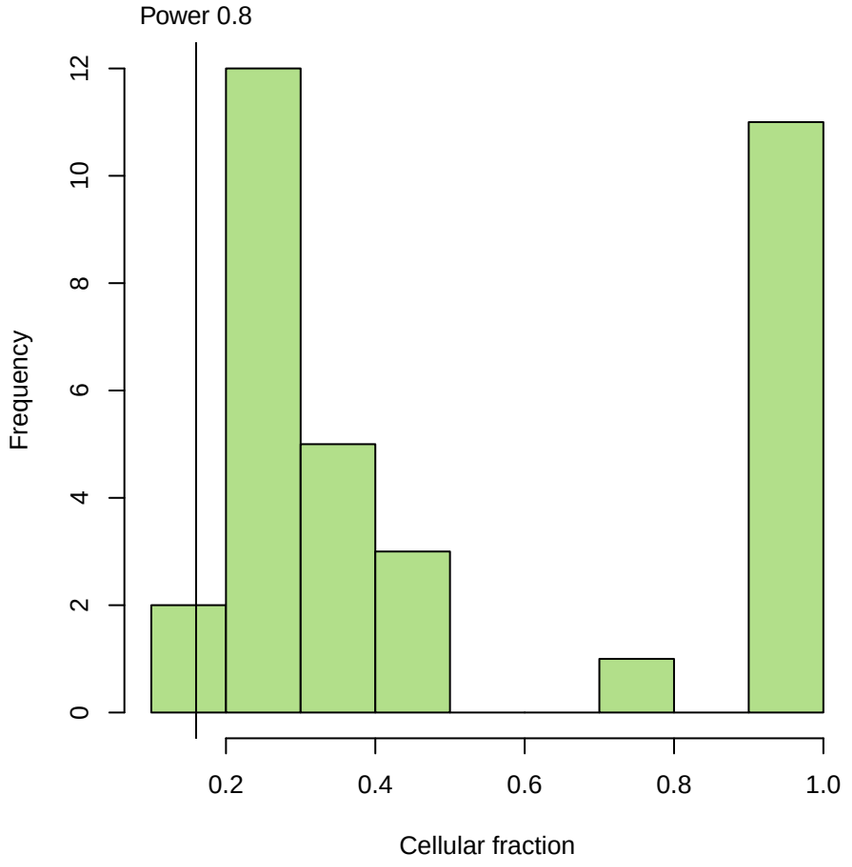

SCNA−fit log−likelihood: −10114.77
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 50 100 150
SNV Index

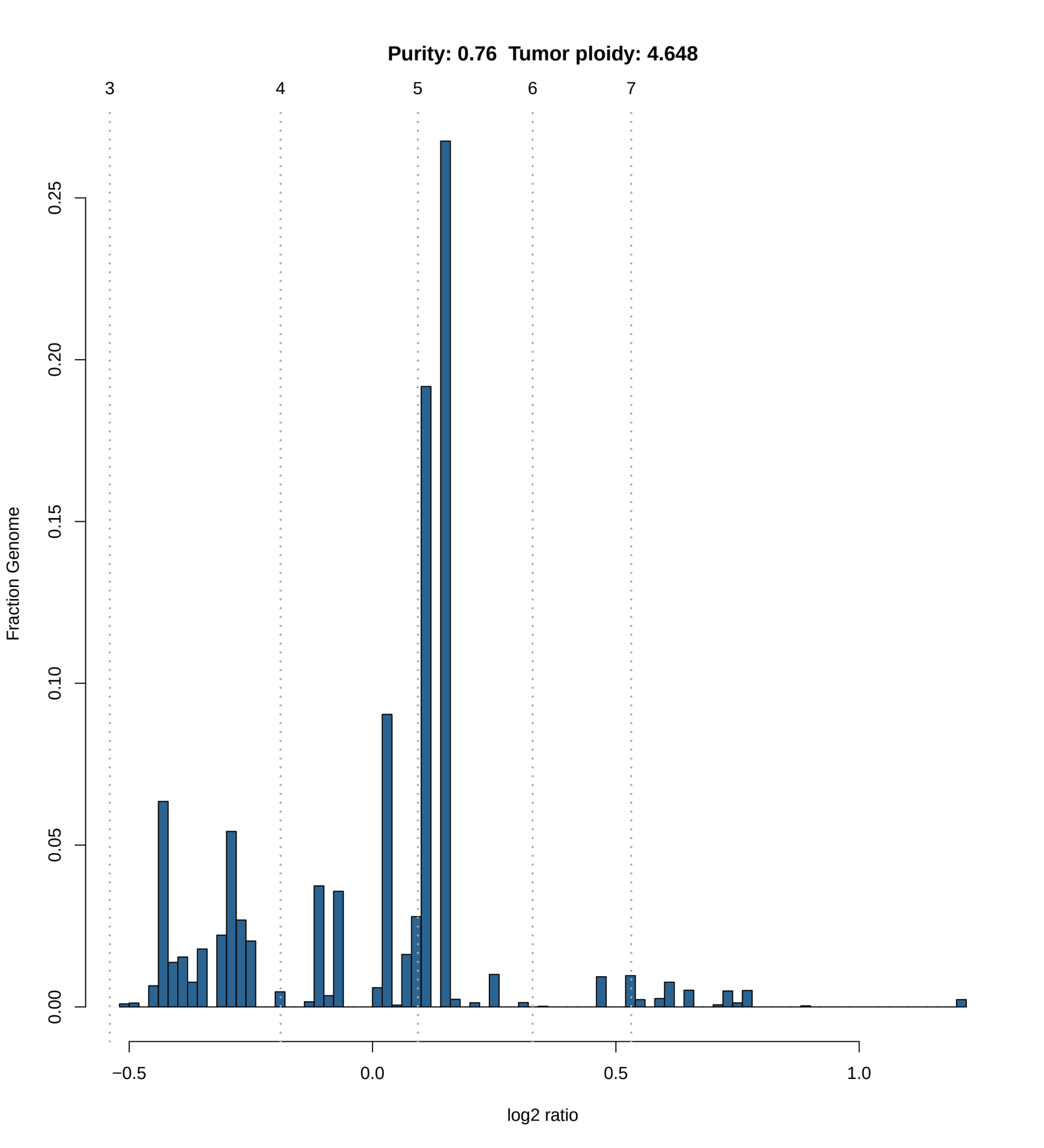

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

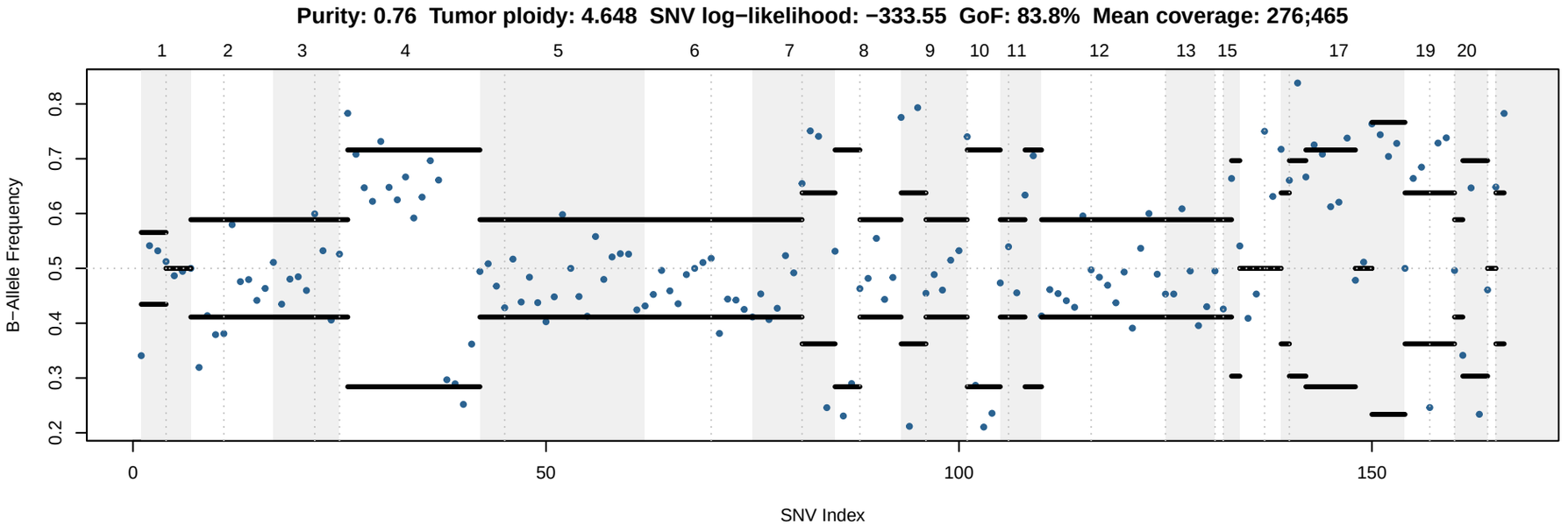

4m4
3m3
5m4
7m5
3m2
5m3
7m4
4m2
6m3
7m3
5m2
3m1
7m2
3m0
Allelic fraction (germline)
Copy Number log−ratio

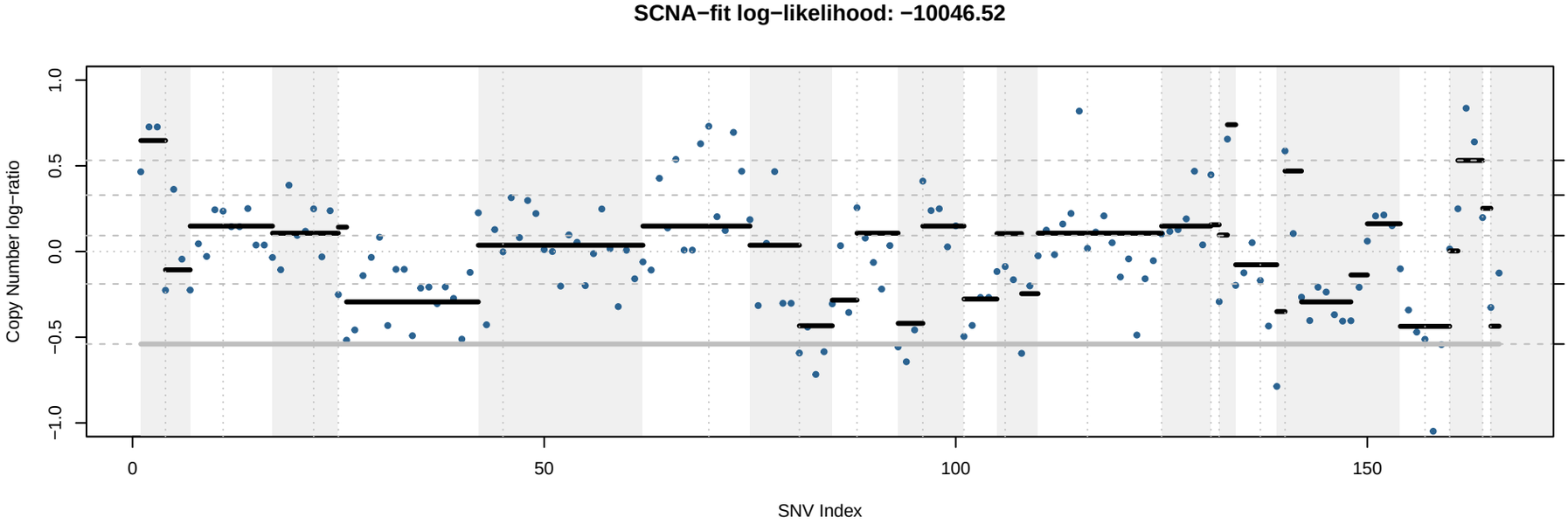

Coverage (log2)
Allelic fraction

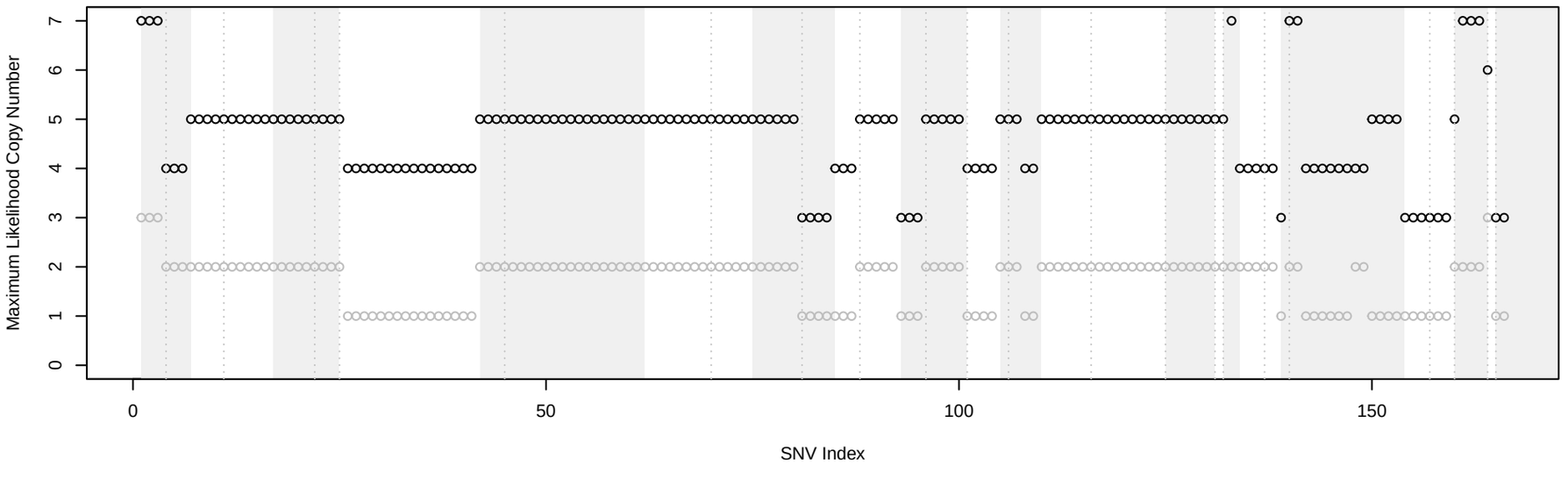

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m2
5m2
3m1
4m1
5m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio

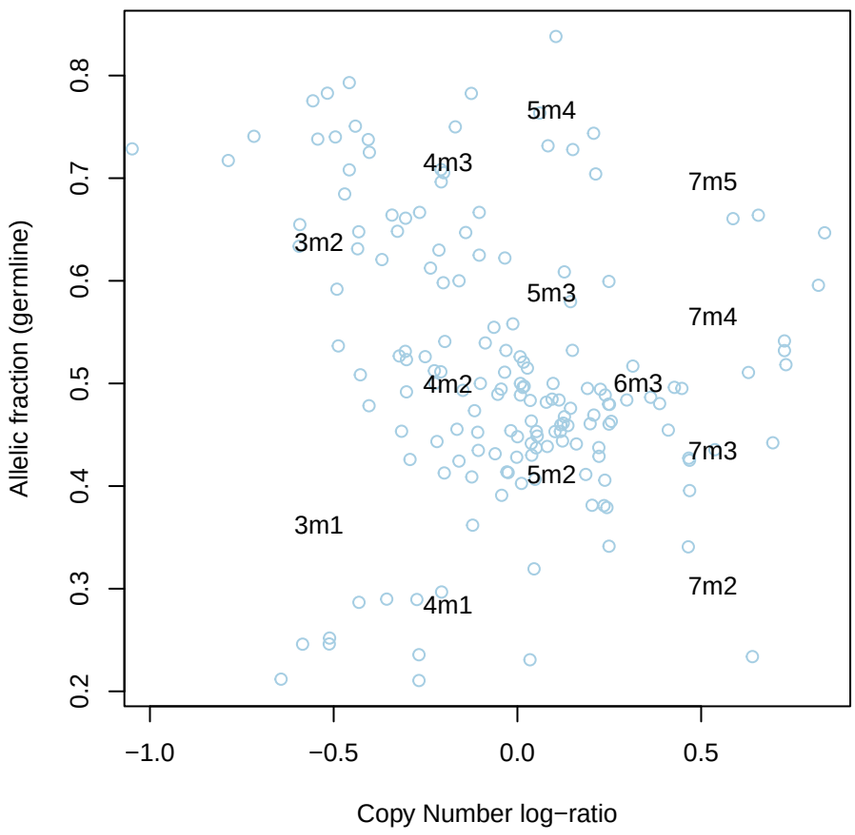

Power 0.8
Frequency
Cellular fraction

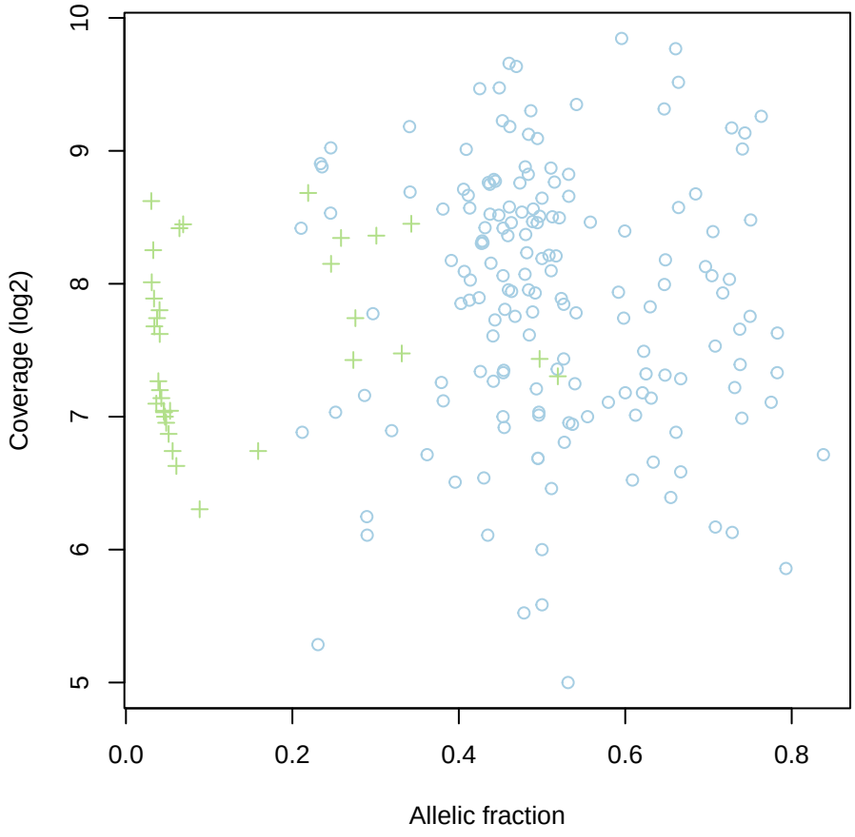

Purity: 0.76 Tumor ploidy: 4.648
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

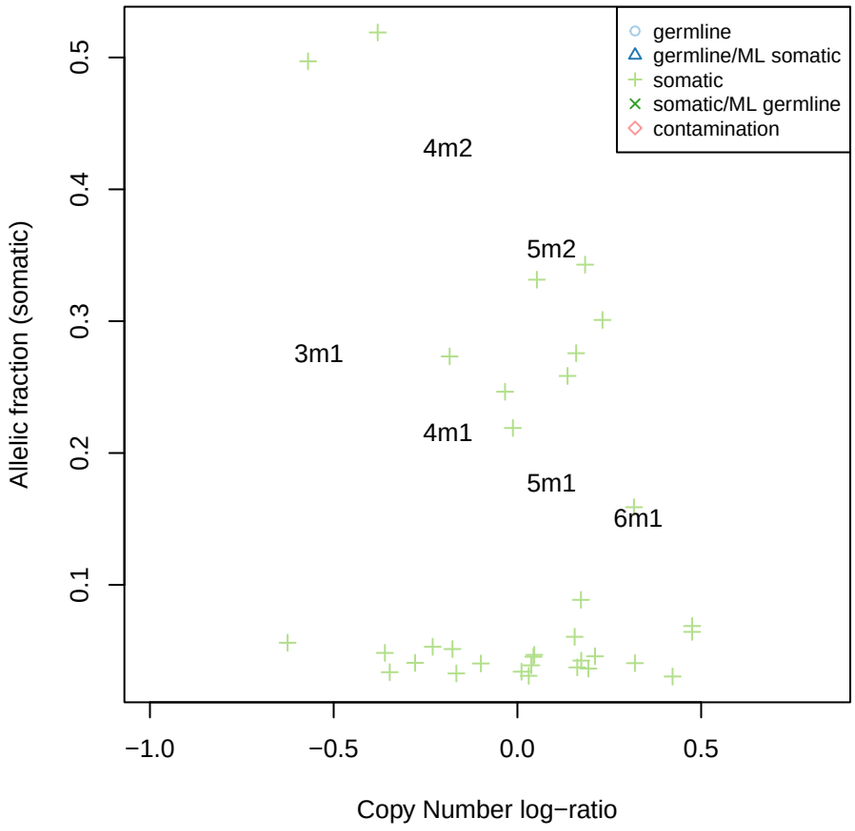

Purity: 0.76 Tumor ploidy: 4.648 SNV log−likelihood: −333.55 GoF: 83.8% Mean coverage: 276;465
1 2 3 4 5 6 7 8 9 10 11 12 13 15 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

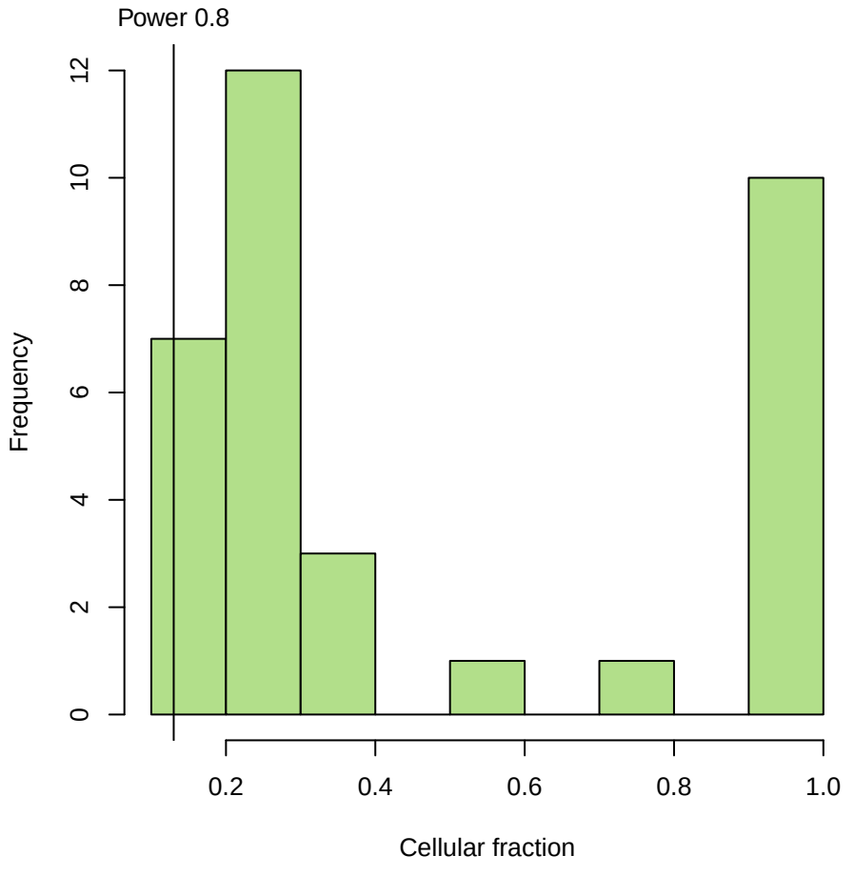

SCNA−fit log−likelihood: −10046.52
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 50 100 150
SNV Index

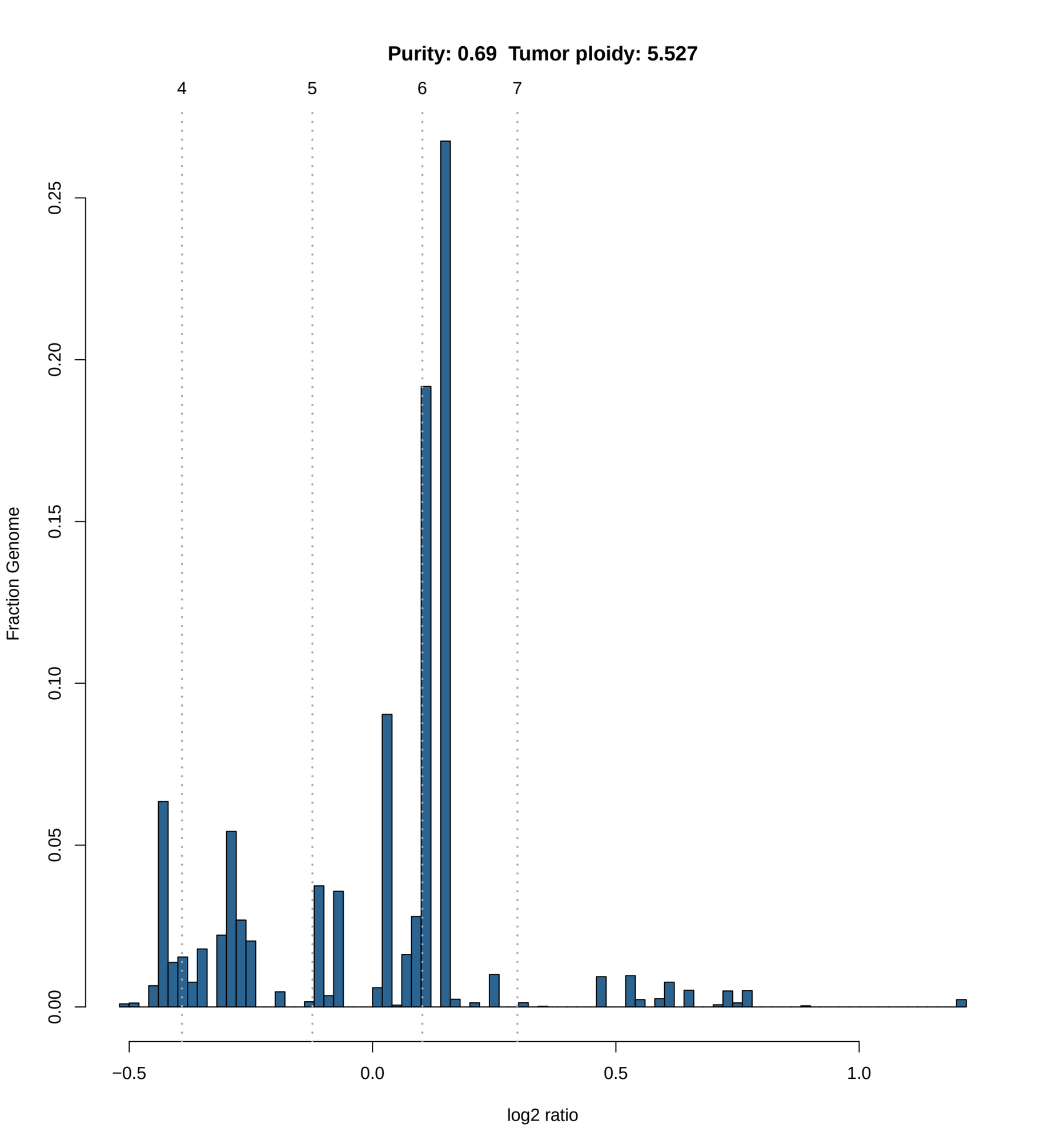

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

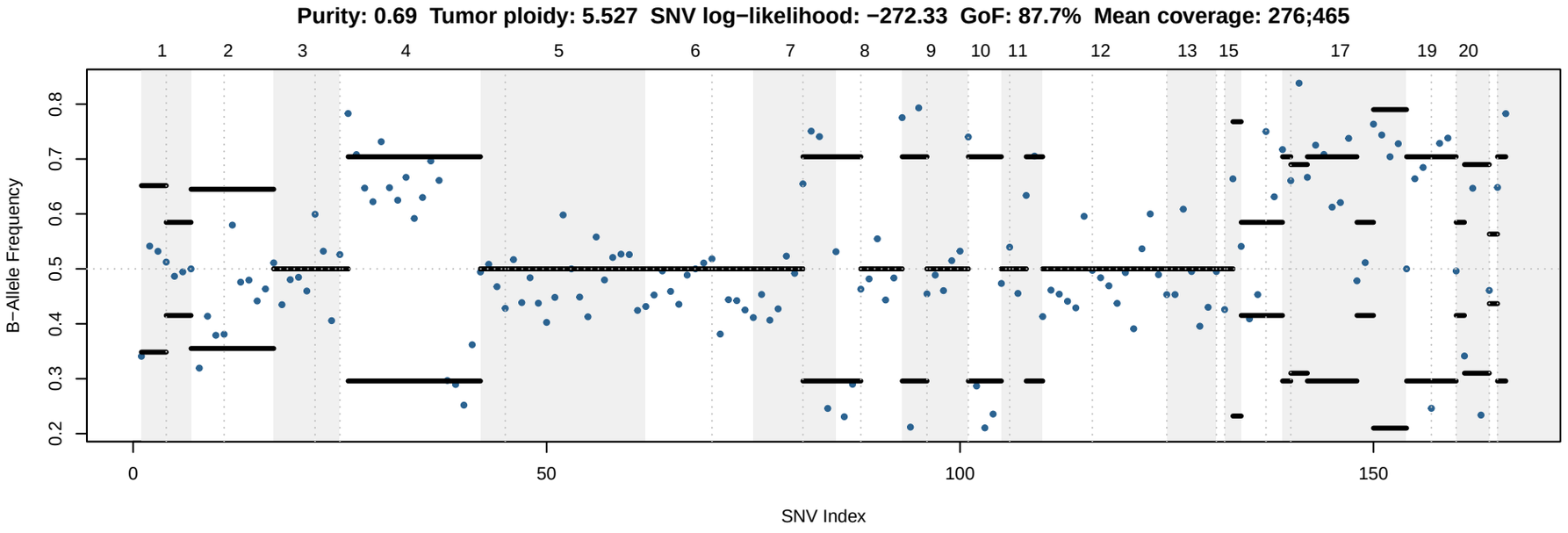

Allelic fraction (germline)
Copy Number log−ratio
5m4
4m3
7m5
3m2
5m3
7m4
4m2
6m3
7m3
5m2
3m1
7m2
4m1

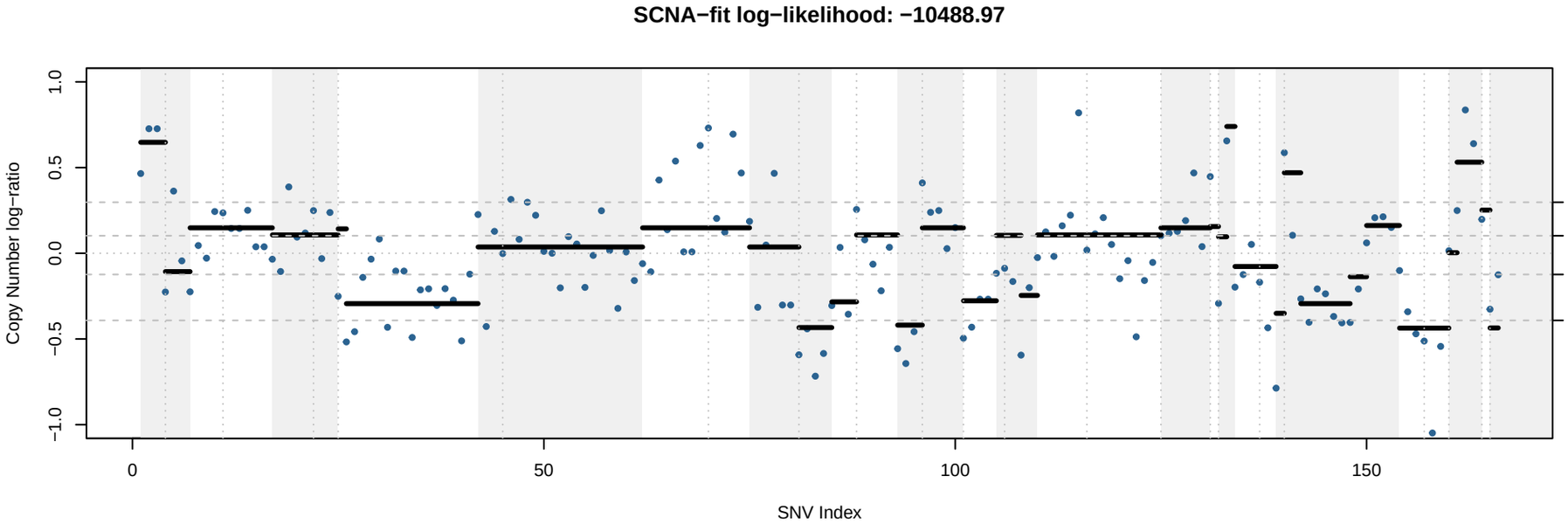

Coverage (log2)
Allelic fraction

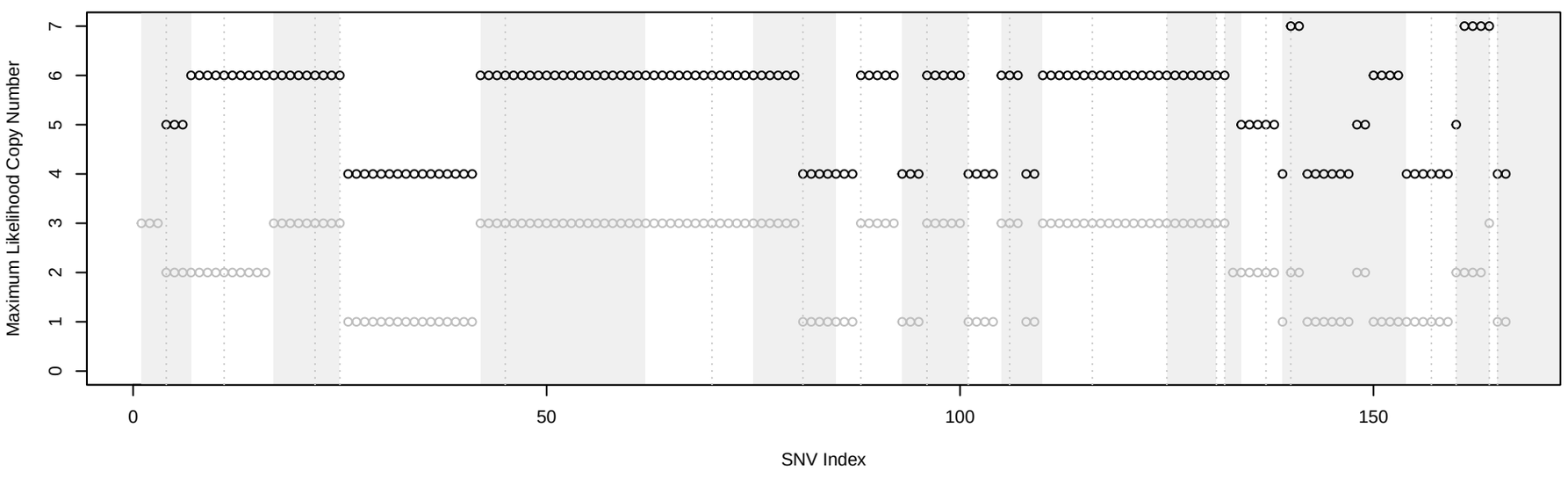

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
4m2
5m2
3m1
4m1
5m1
6m1

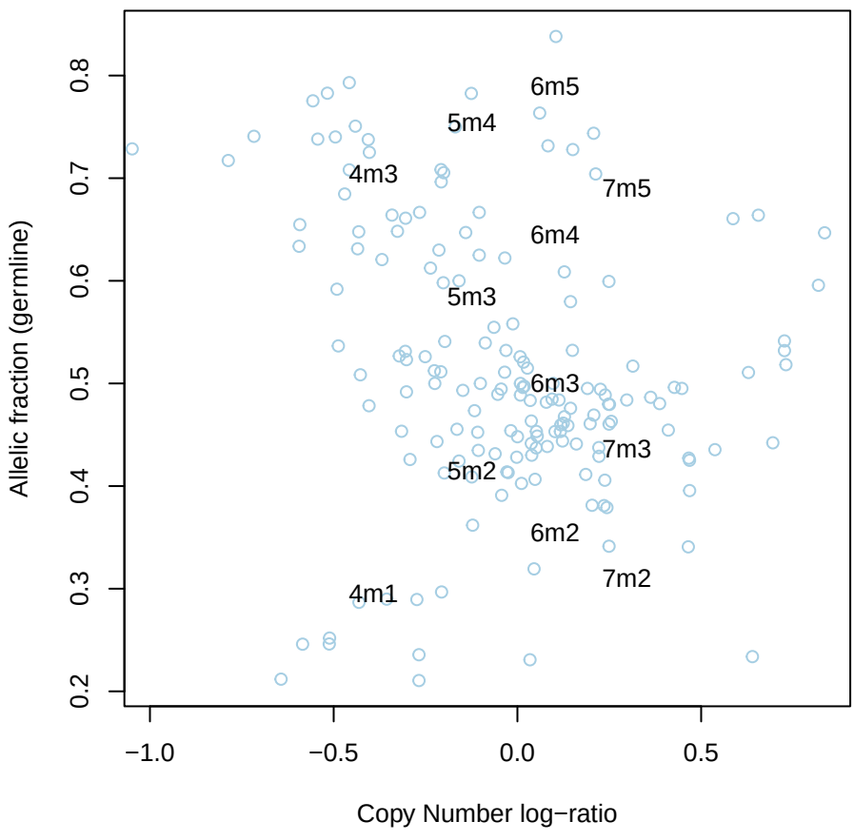

Power 0.8
Frequency
Cellular fraction

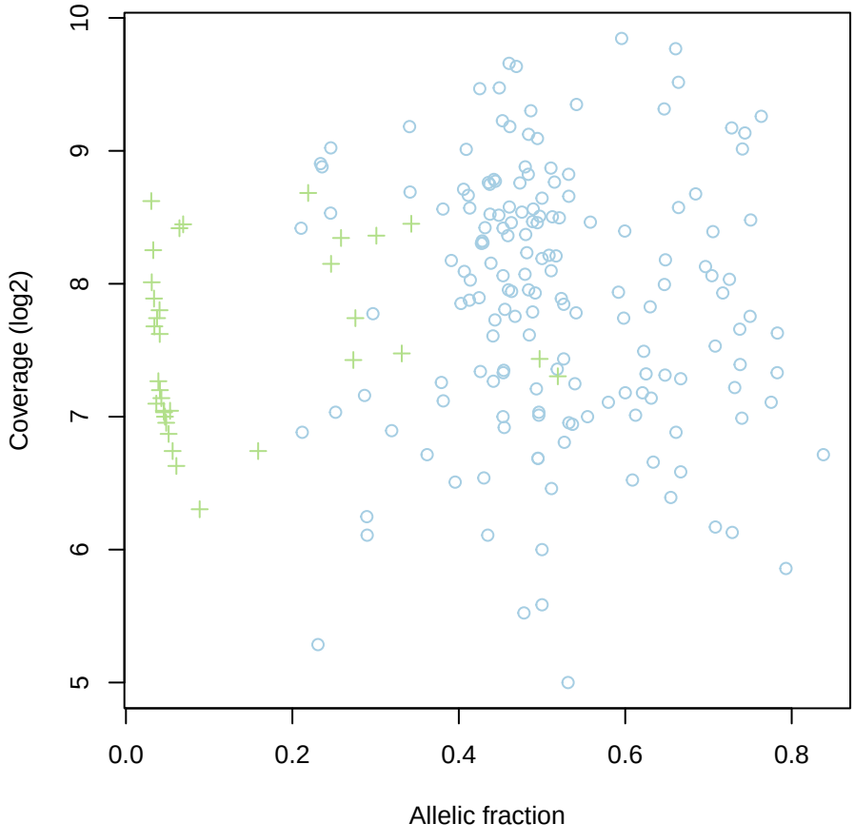

Purity: 0.69 Tumor ploidy: 5.527
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

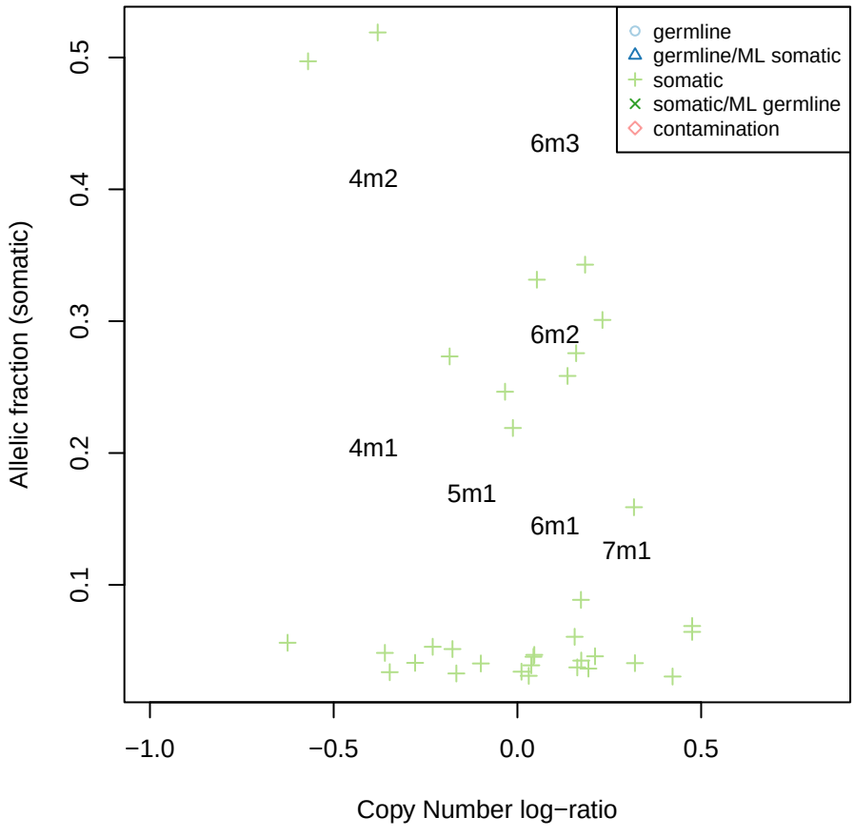

Purity: 0.69 Tumor ploidy: 5.527 SNV log−likelihood: −272.33 GoF: 87.7% Mean coverage: 276;465
1 2 3 4 5 6 7 8 9 10 11 12 13 15 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

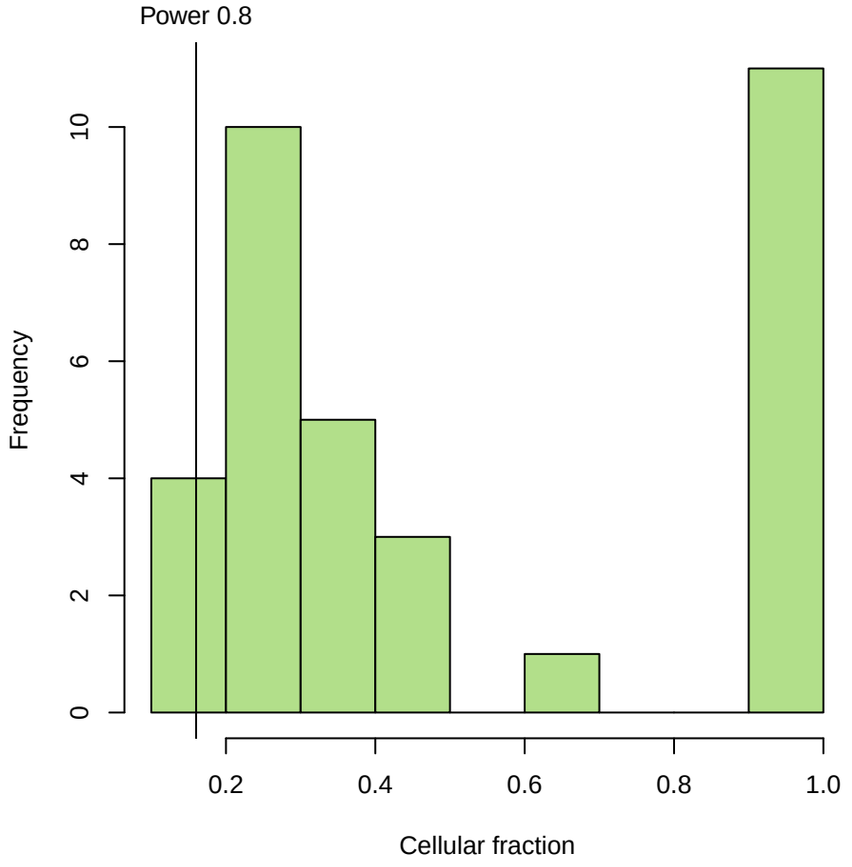

SCNA−fit log−likelihood: −10488.97
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
4 5 6 7
0 50 100 150
SNV Index

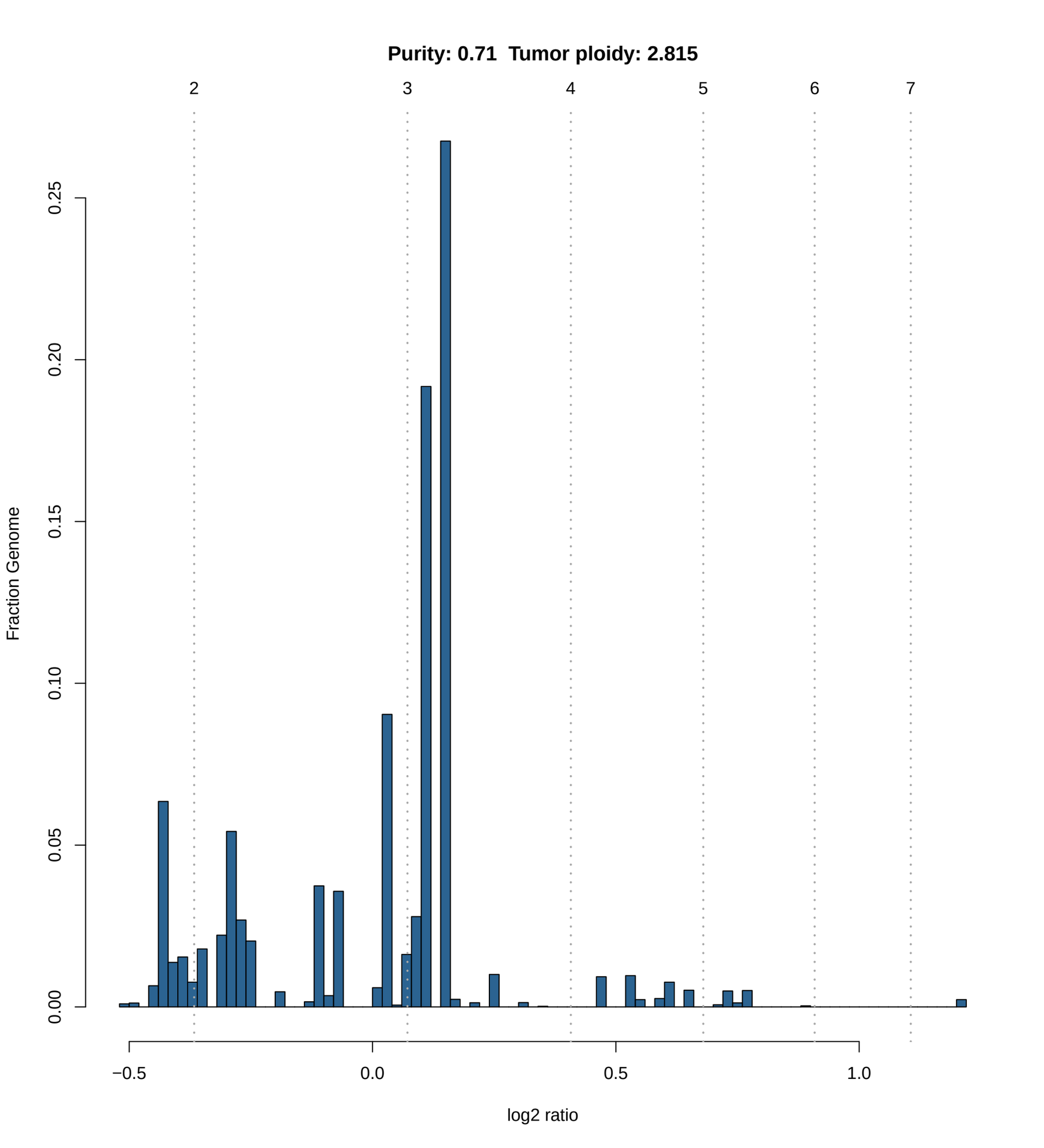

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

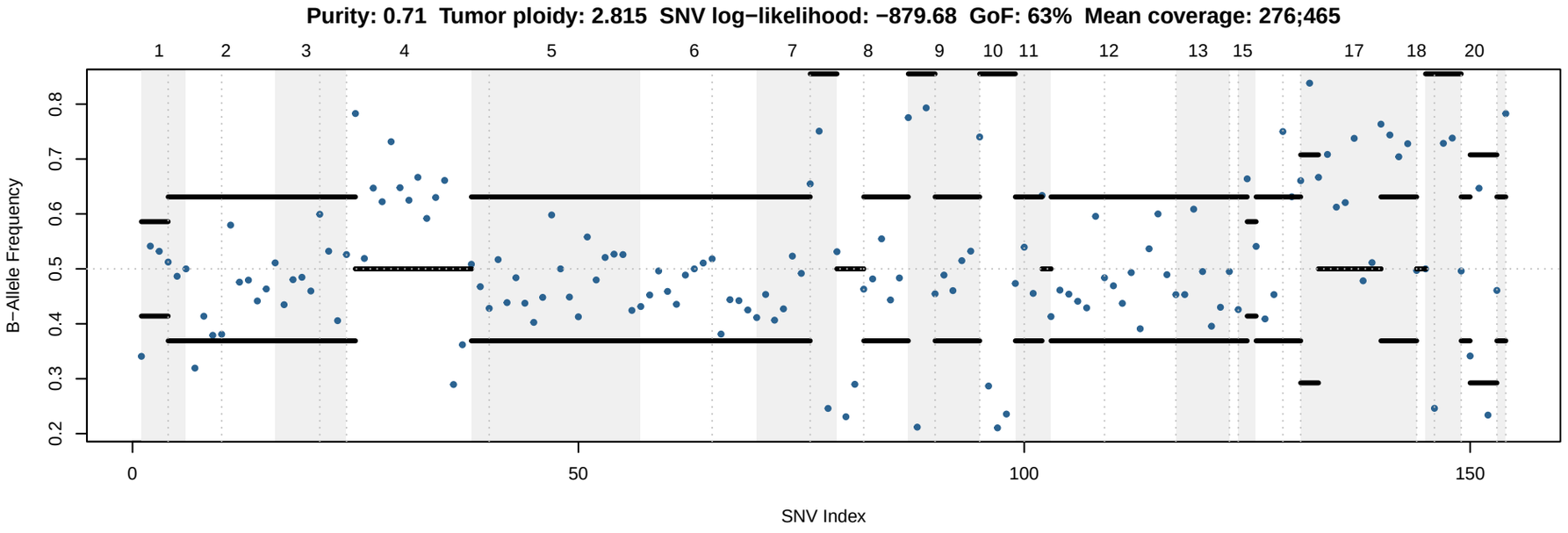

Allelic fraction (germline)
Copy Number log−ratio
6m5
5m4
4m3
7m5
6m4
5m3
6m3
7m3
5m2
6m2
7m2
4m1

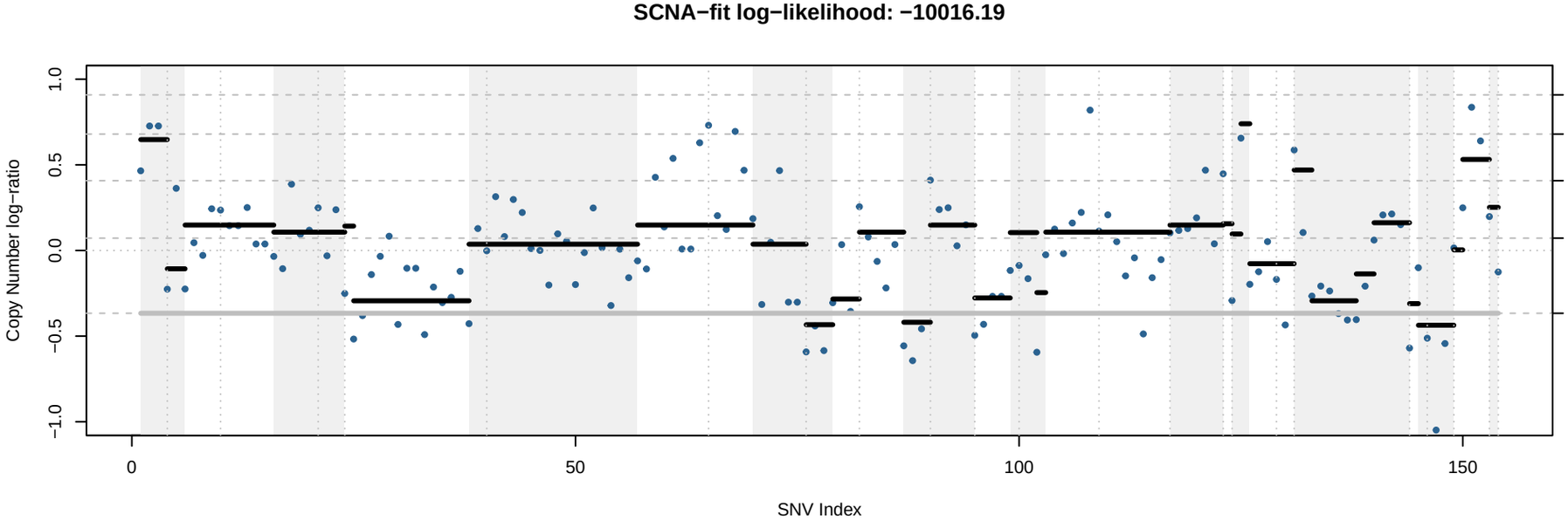

Coverage (log2)
Allelic fraction

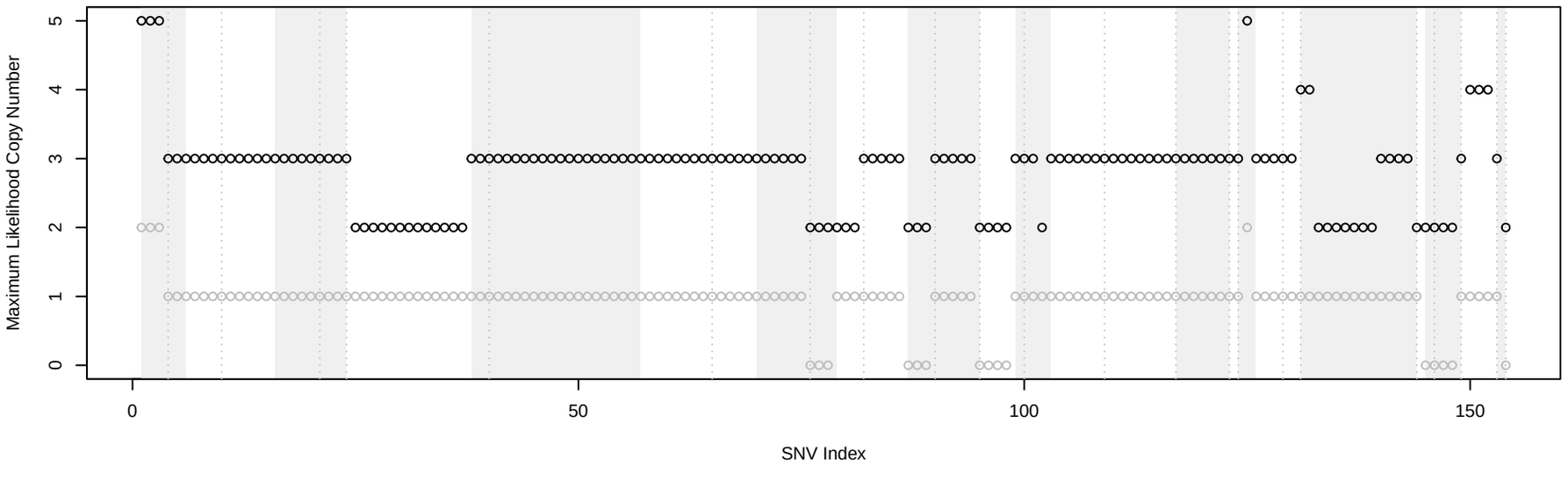

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
6m3
4m2
6m2
4m1
5m1
6m1
7m1

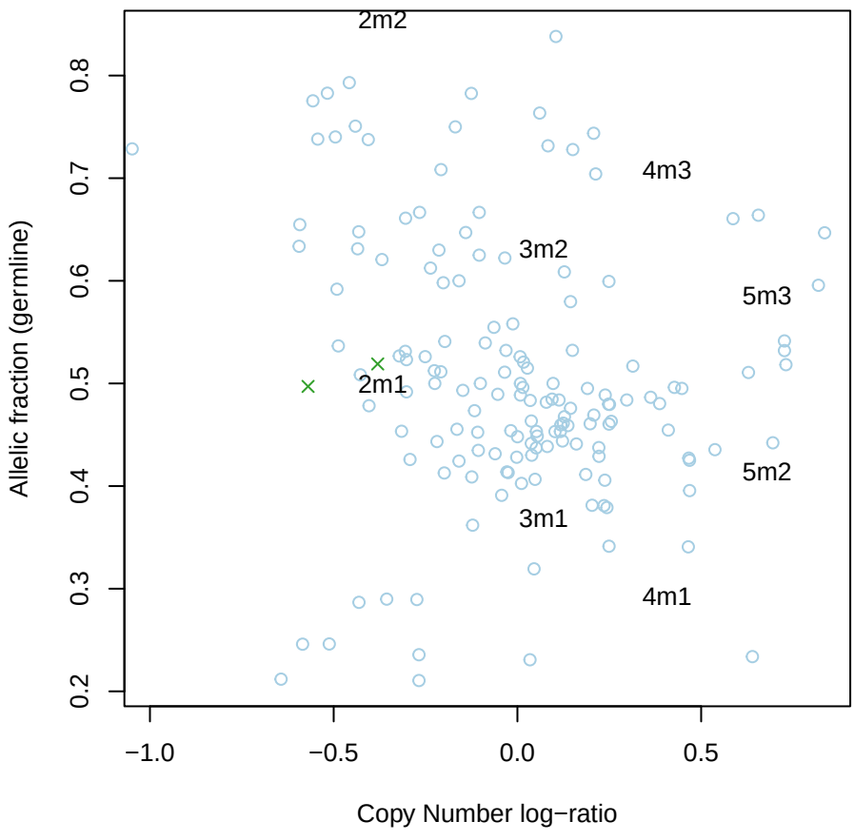

Power 0.8
Frequency
Cellular fraction

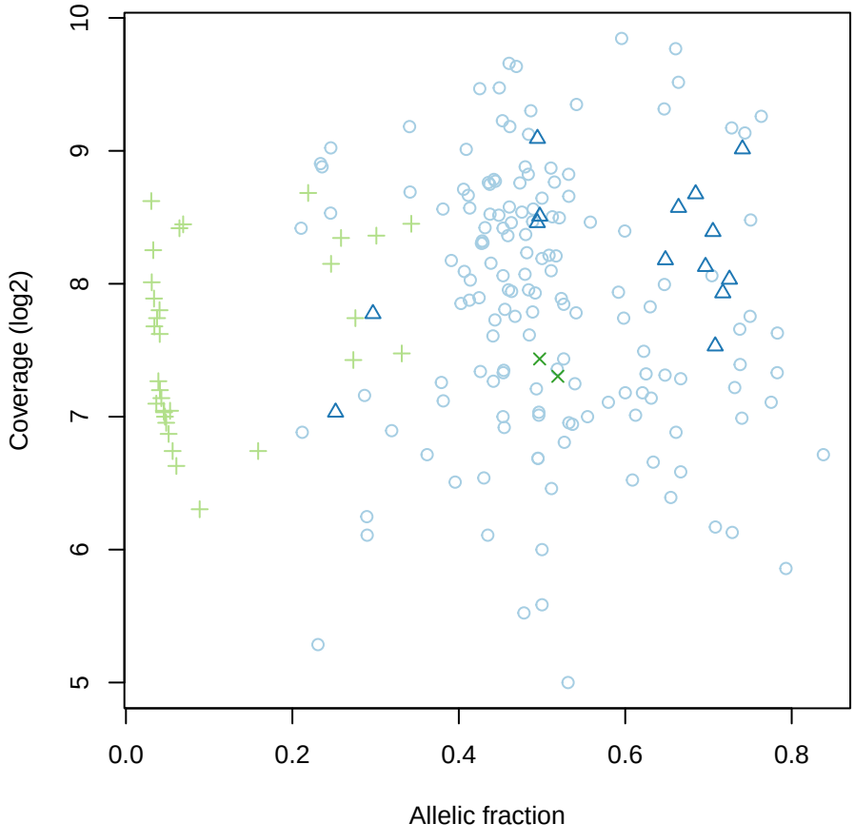

Purity: 0.71 Tumor ploidy: 2.815
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

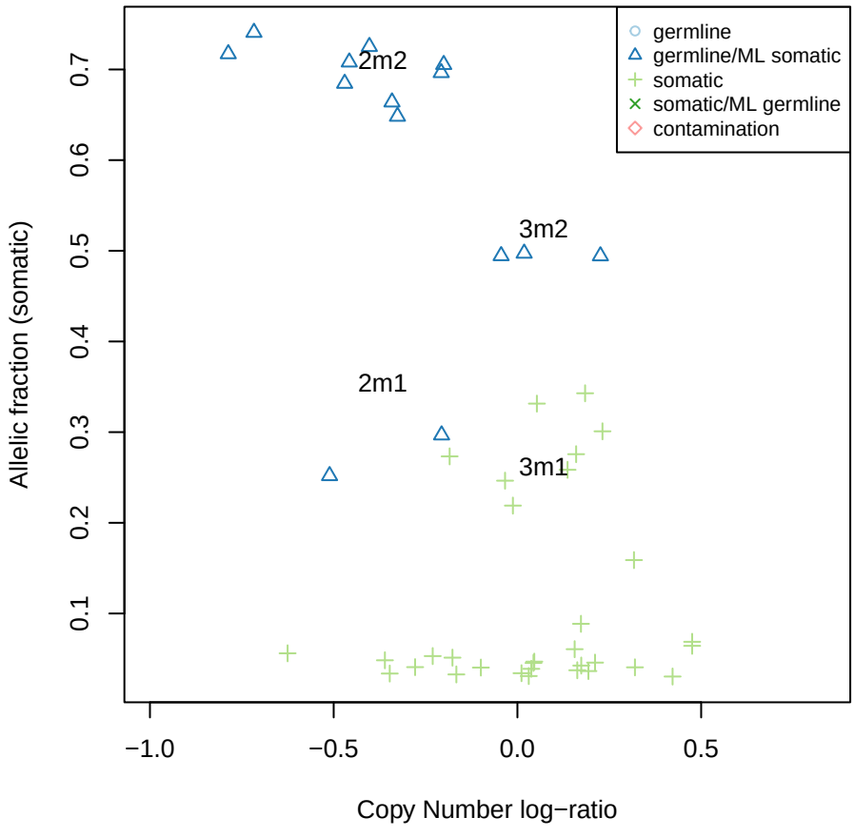

Purity: 0.71 Tumor ploidy: 2.815 SNV log−likelihood: −879.68 GoF: 63% Mean coverage: 276;465
1 2 3 4 5 6 7 8 9 10 11 12 13 15 17 18 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

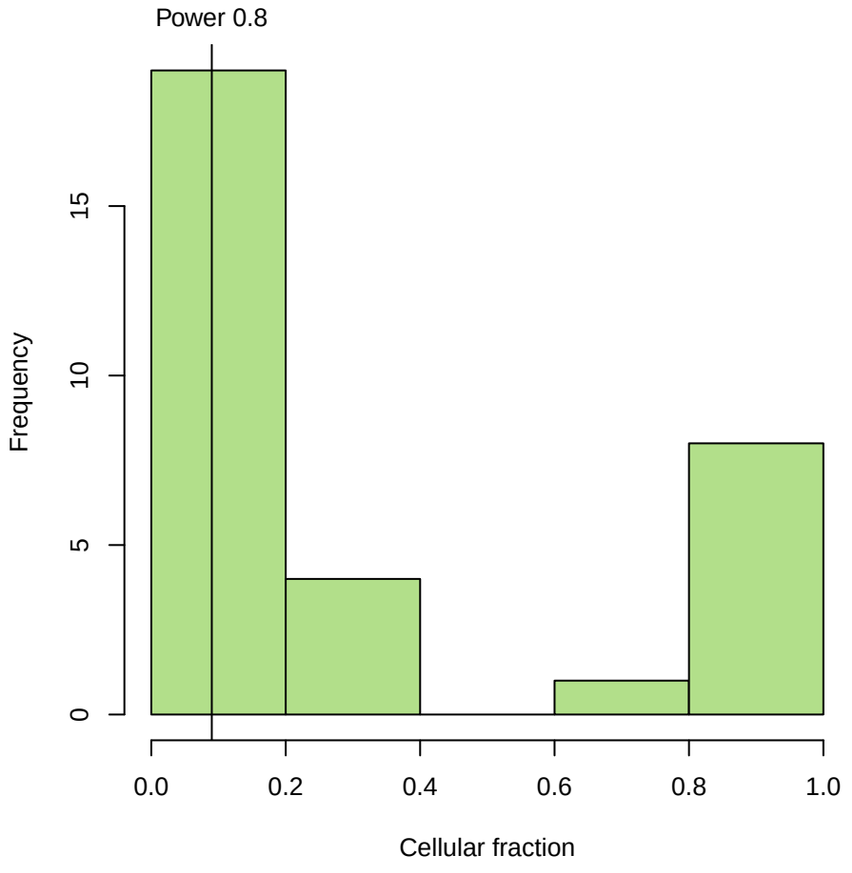

SCNA−fit log−likelihood: −10016.19
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6
0 50 100 150
SNV Index


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


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


Coverage (log2)
Allelic fraction


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


Power 0.8
Frequency
Cellular fraction