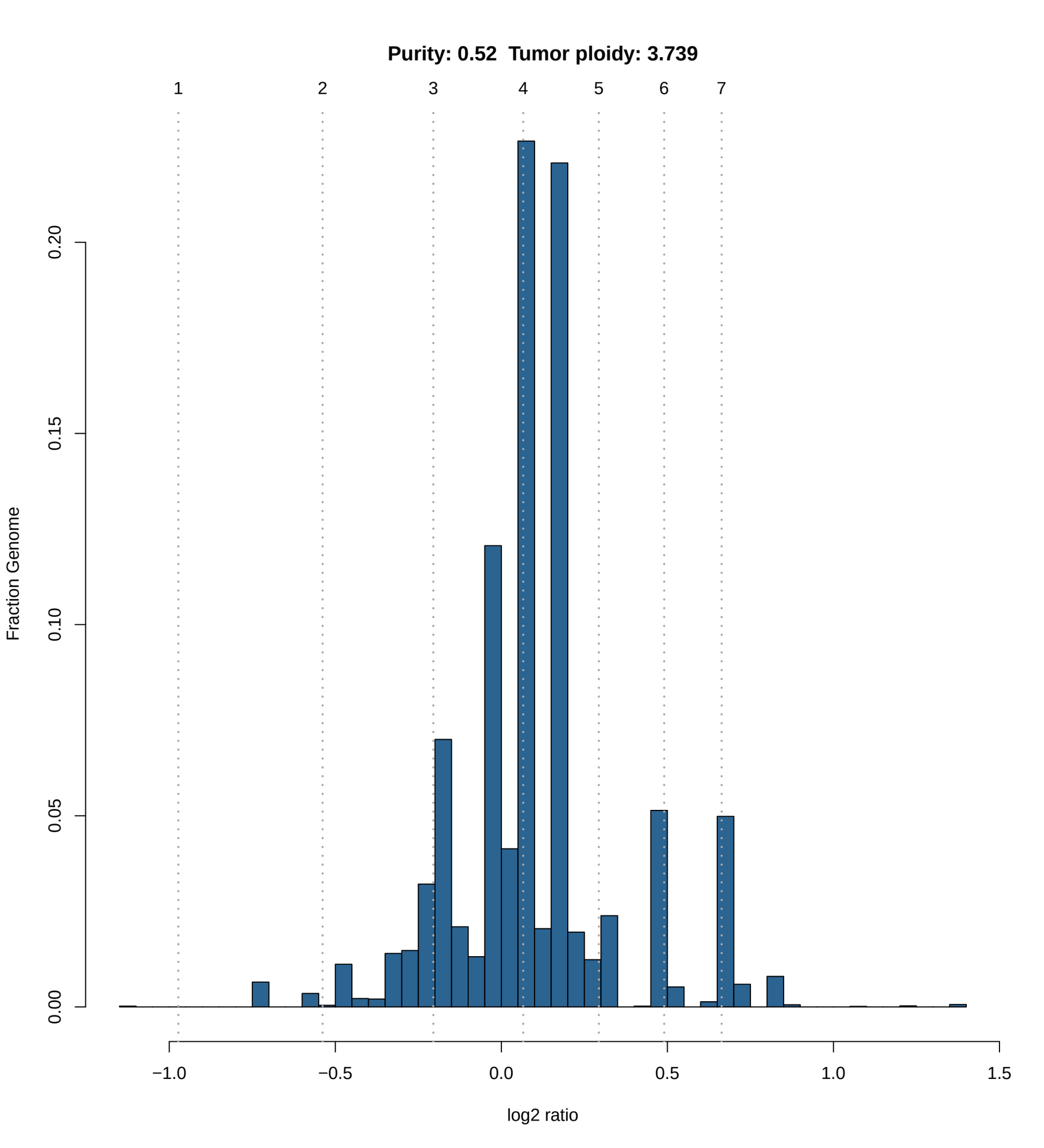
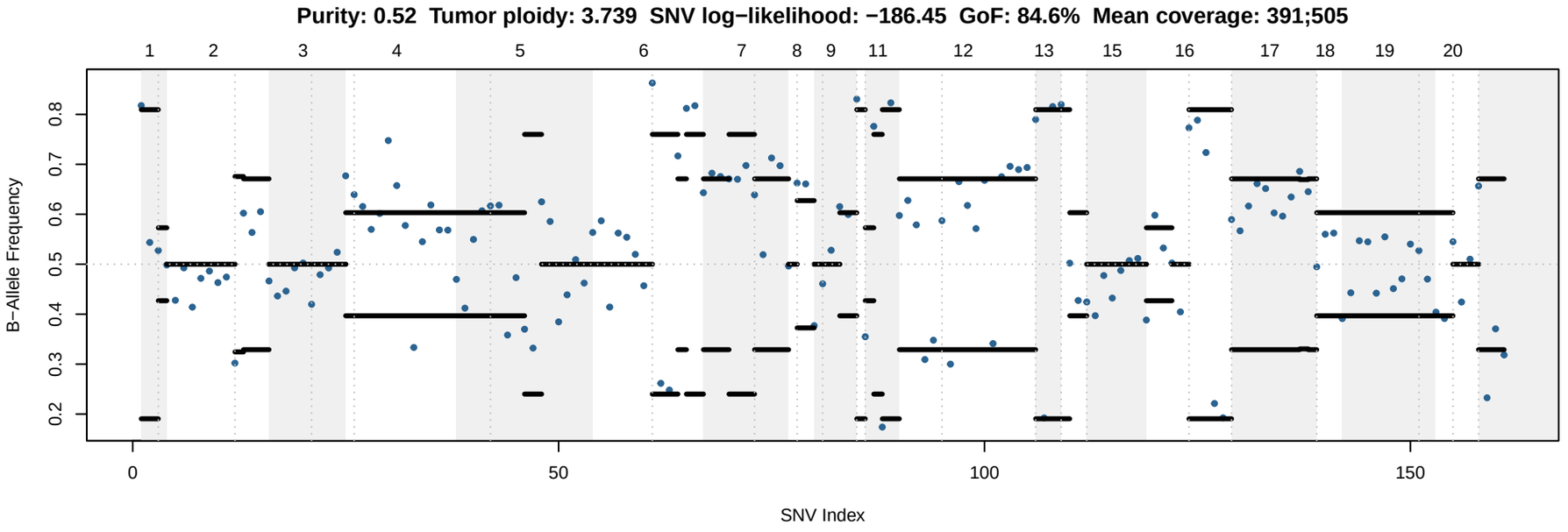
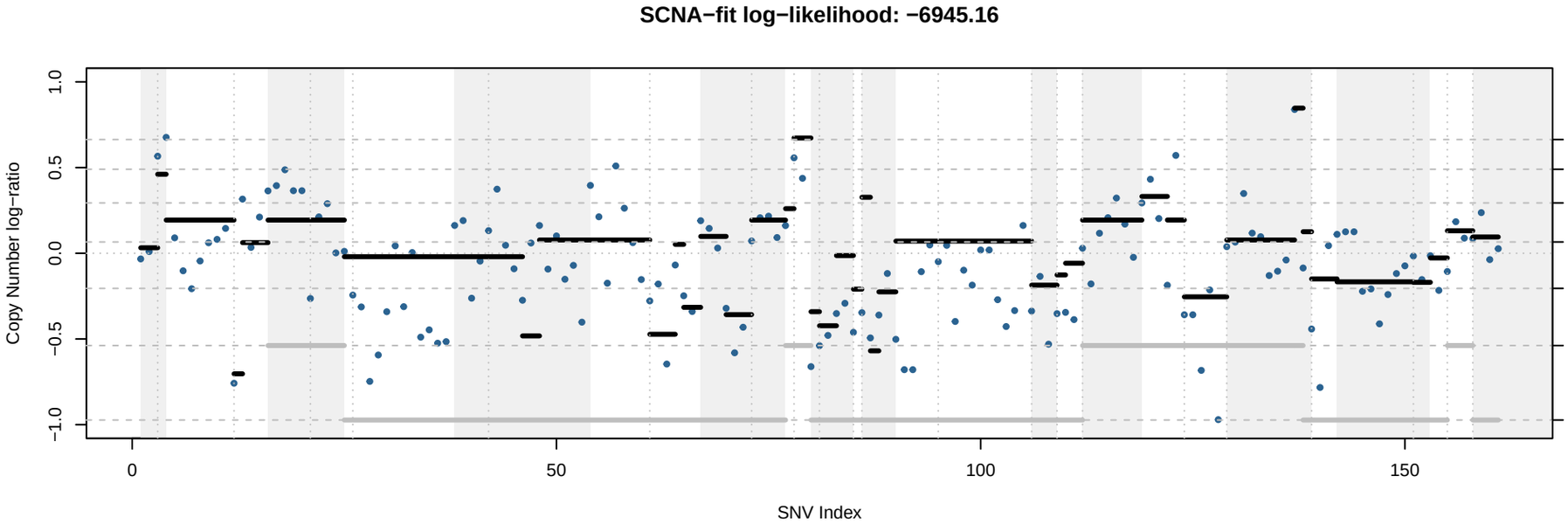
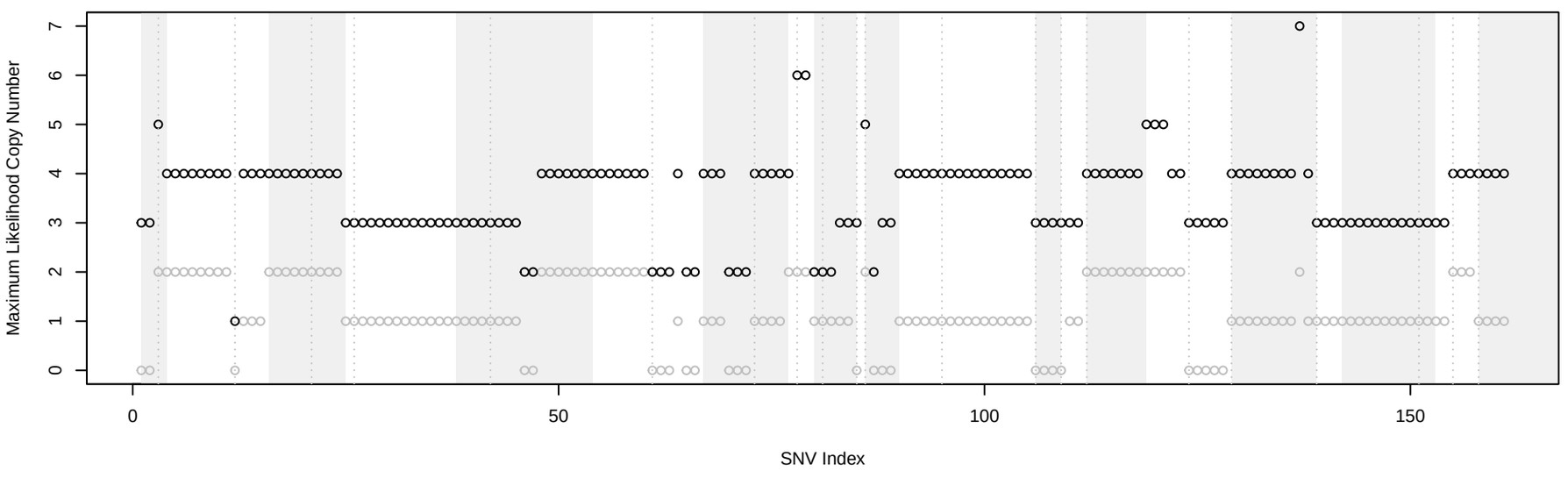
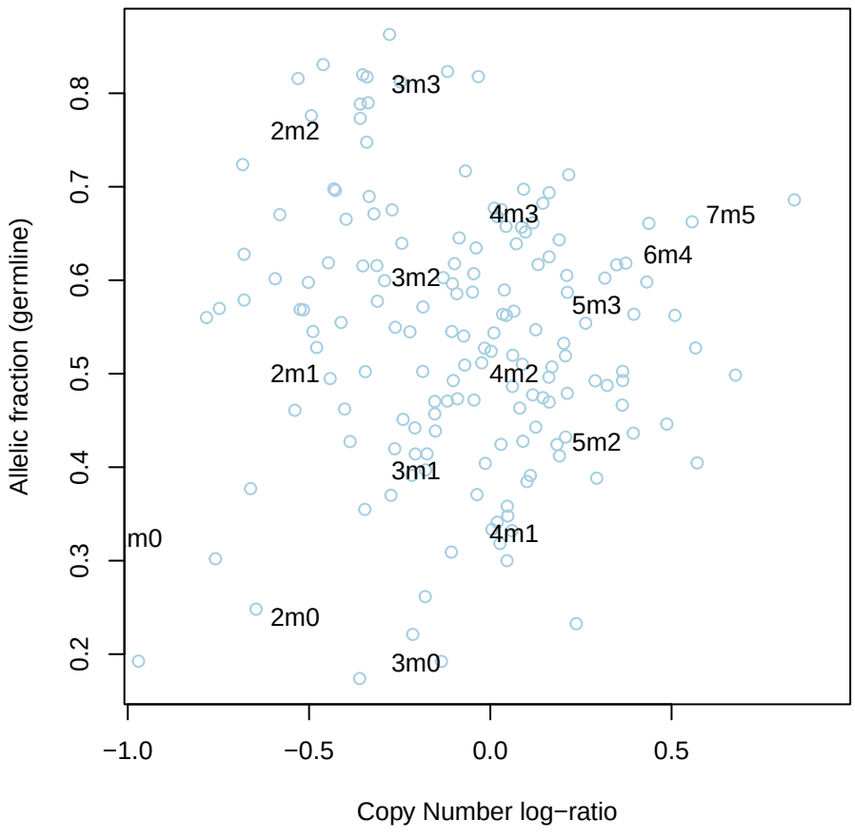
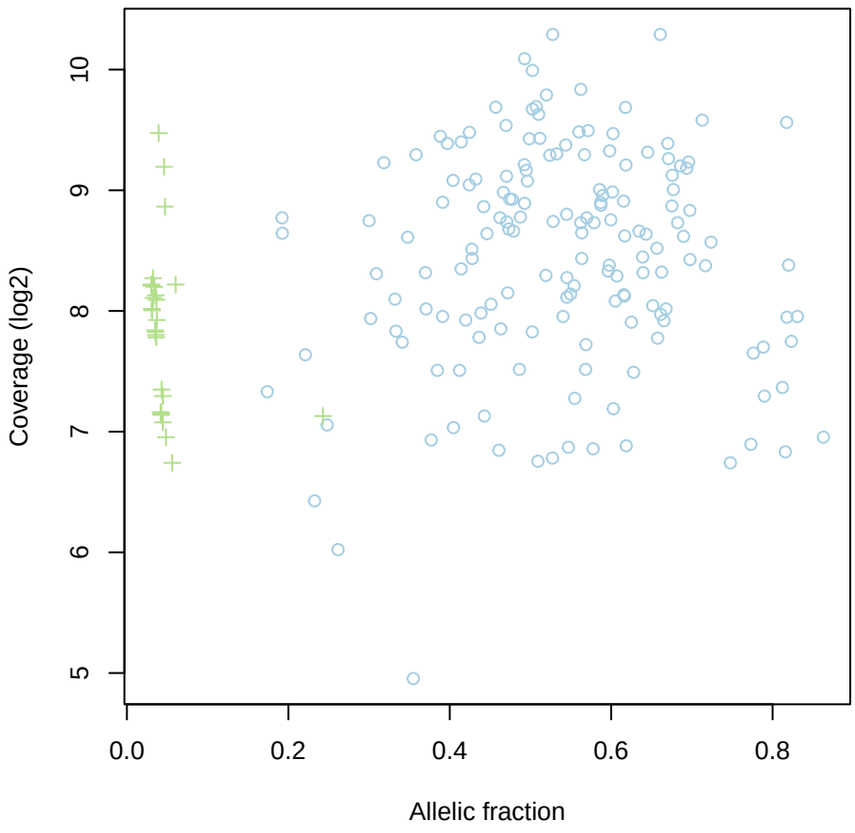

Purity: 0.52 Tumor ploidy: 3.739
1
2
3
4
5
6
7
0.00
0.05
0.10
0.15
0.20
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

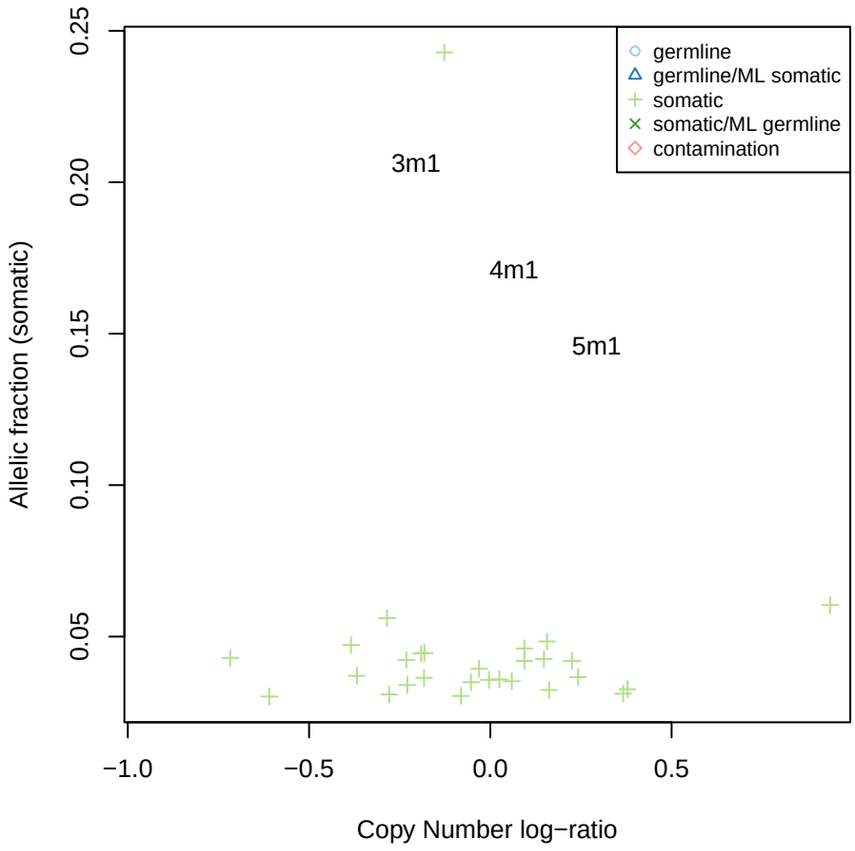

Purity: 0.52 Tumor ploidy: 3.739 SNV log−likelihood: −186.45 GoF: 84.6% Mean coverage: 391;505
1 2 3 4 5 6 7 8 9 11 12 13 15 16 17 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

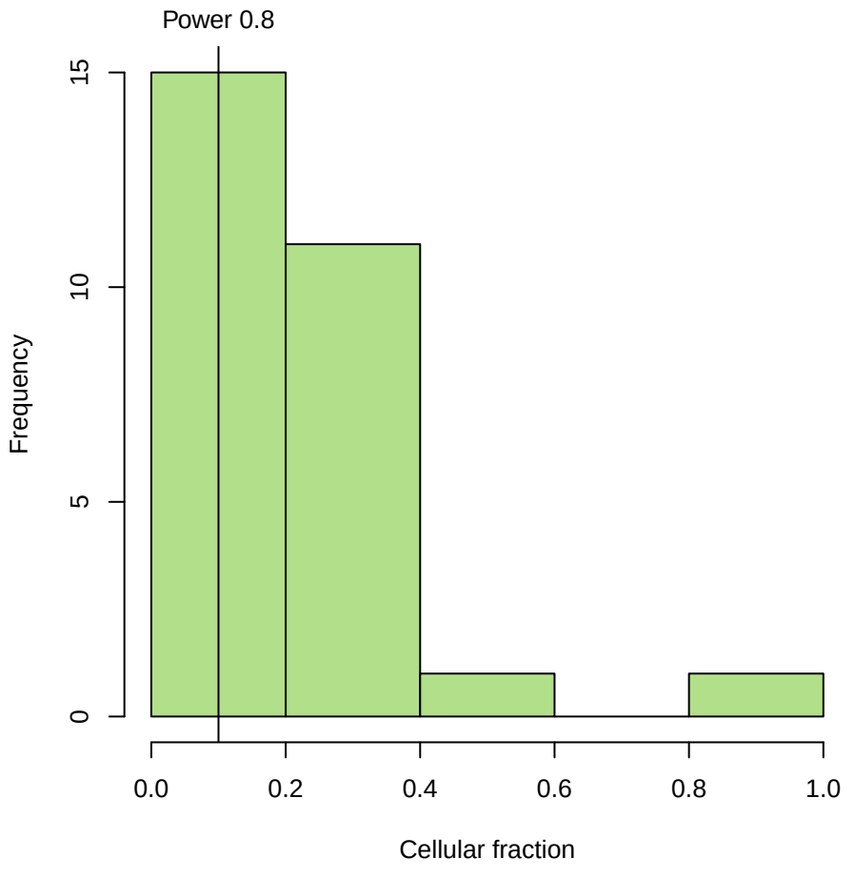

SCNA−fit log−likelihood: −6945.16
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6 7
0 50 100 150
SNV Index

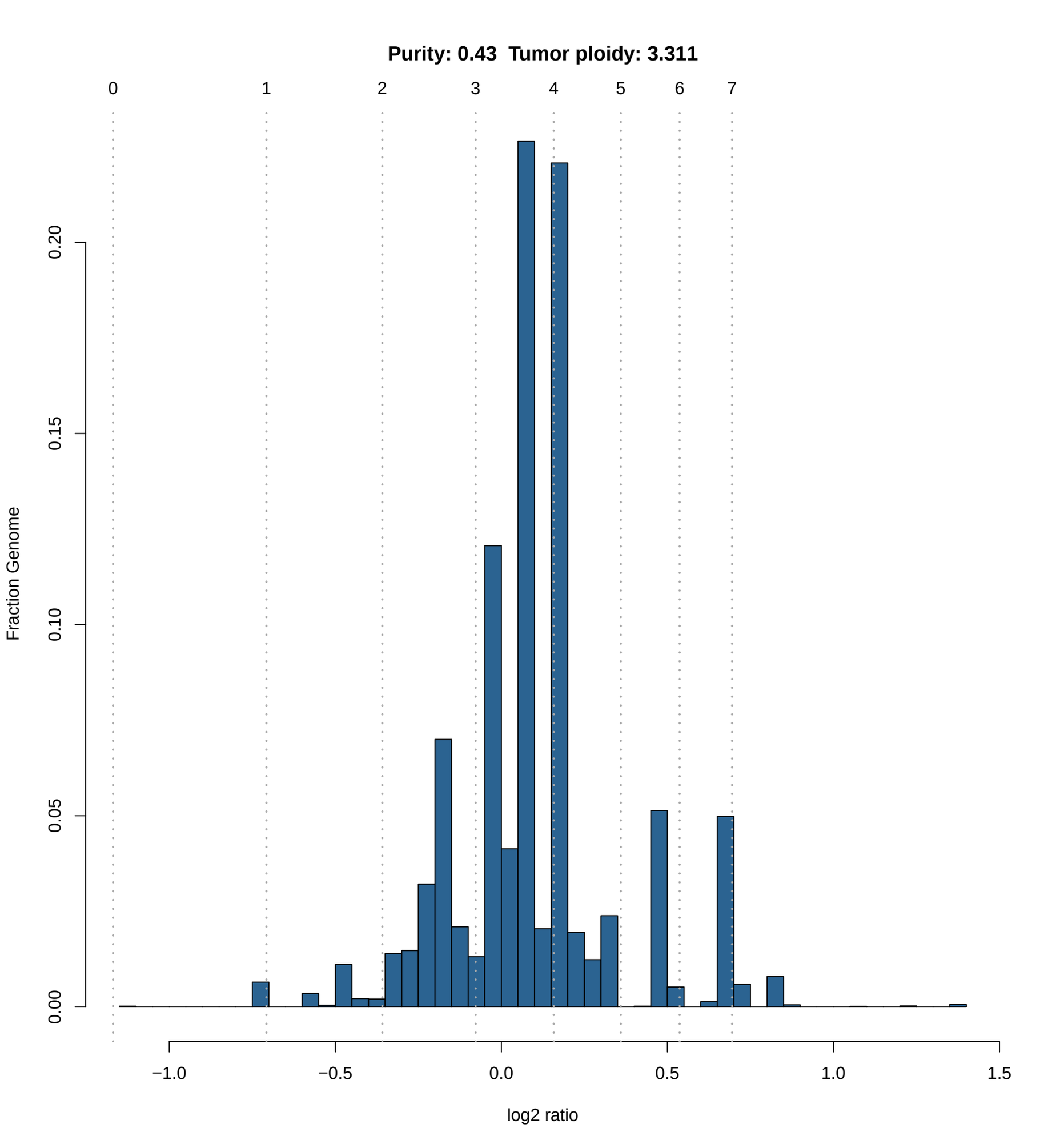

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

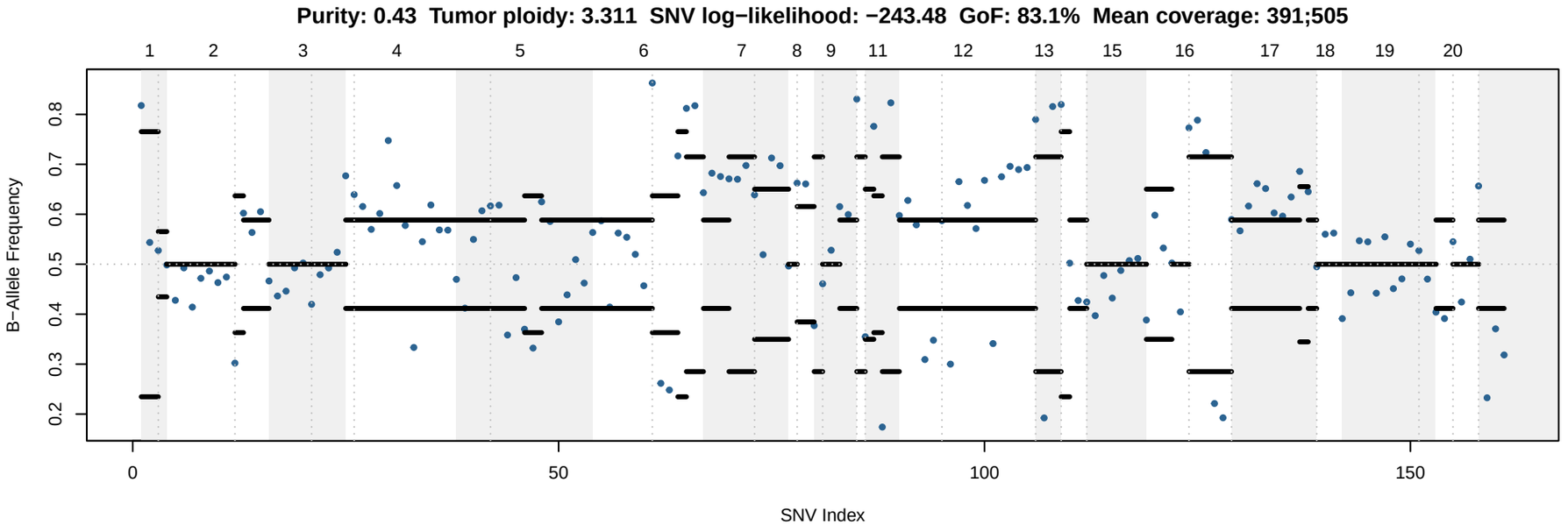

Allelic fraction (germline)
Copy Number log−ratio
3m3
2m2
4m3
7m5
6m4
3m2
5m3
2m1
4m2
5m2
3m1
m0
4m1
2m0
3m0

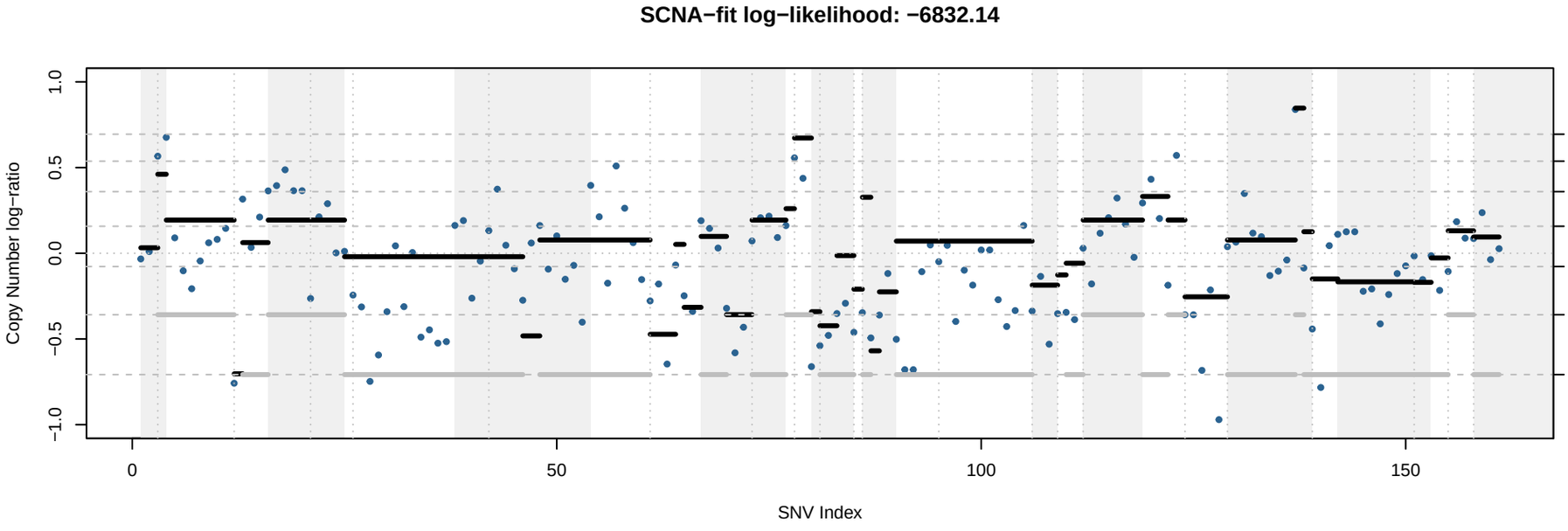

Coverage (log2)
Allelic fraction

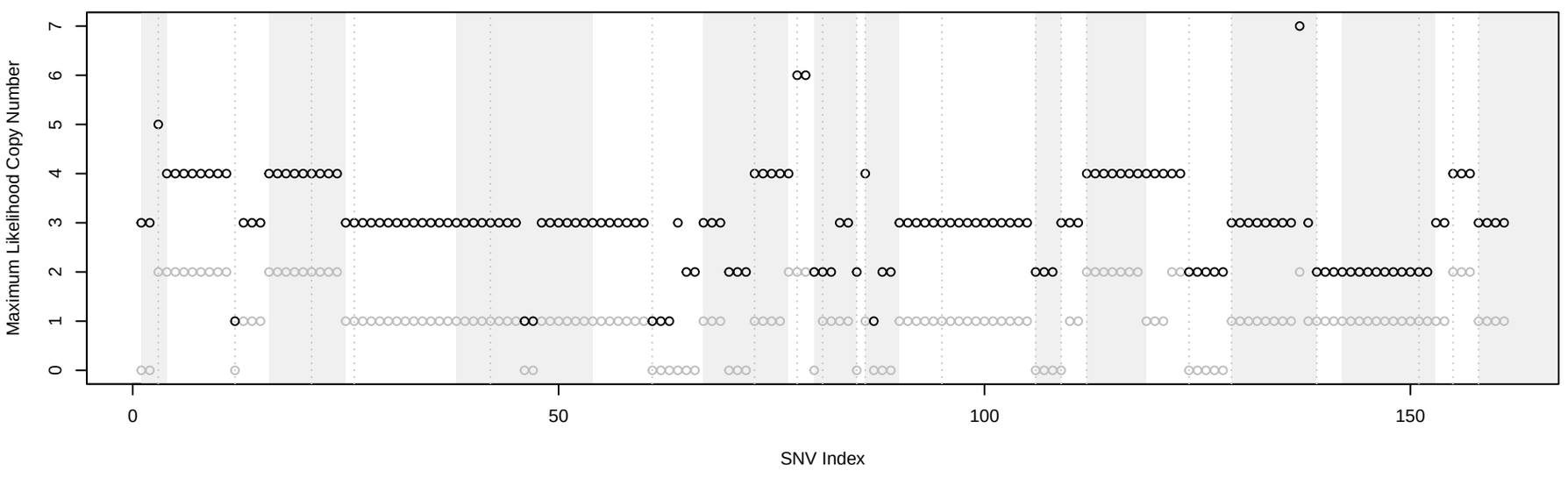

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1

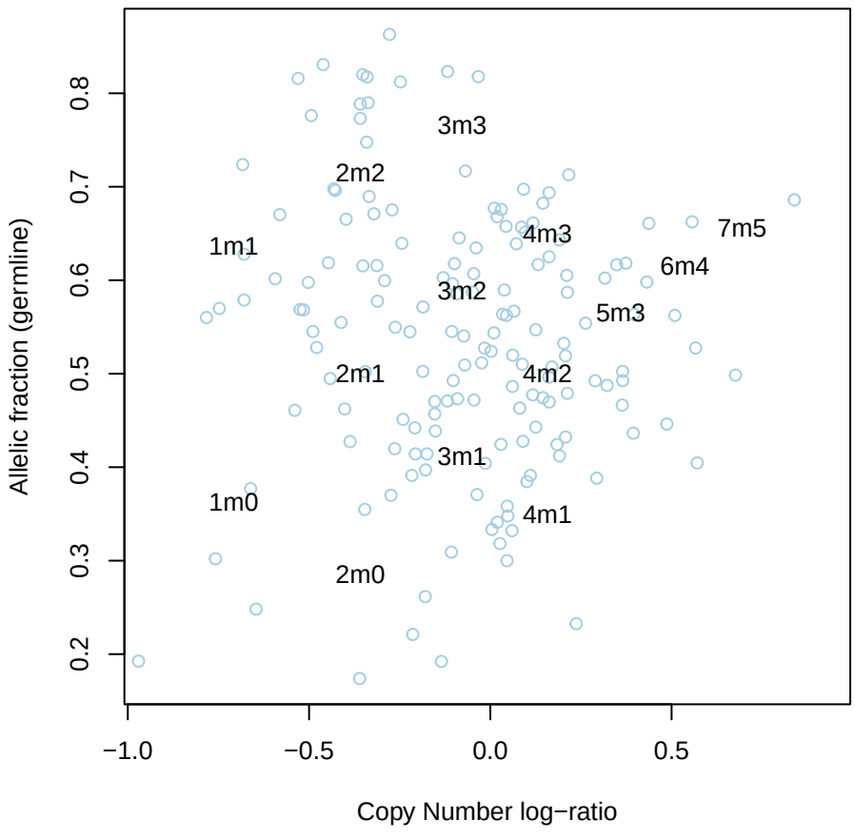

Power 0.8
Frequency
Cellular fraction

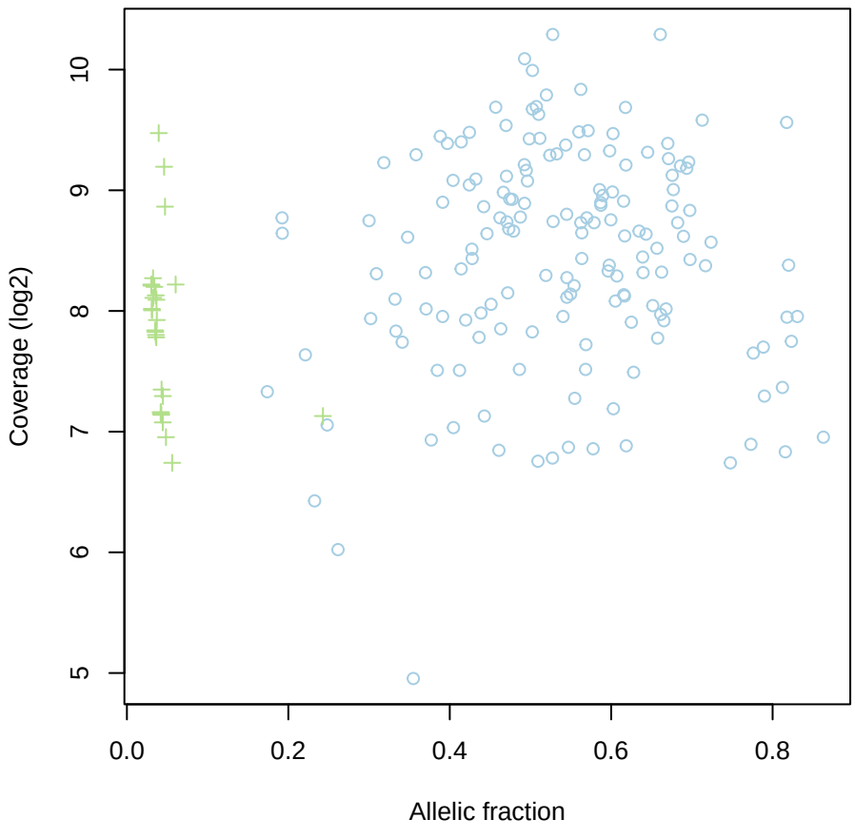

Purity: 0.43 Tumor ploidy: 3.311
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

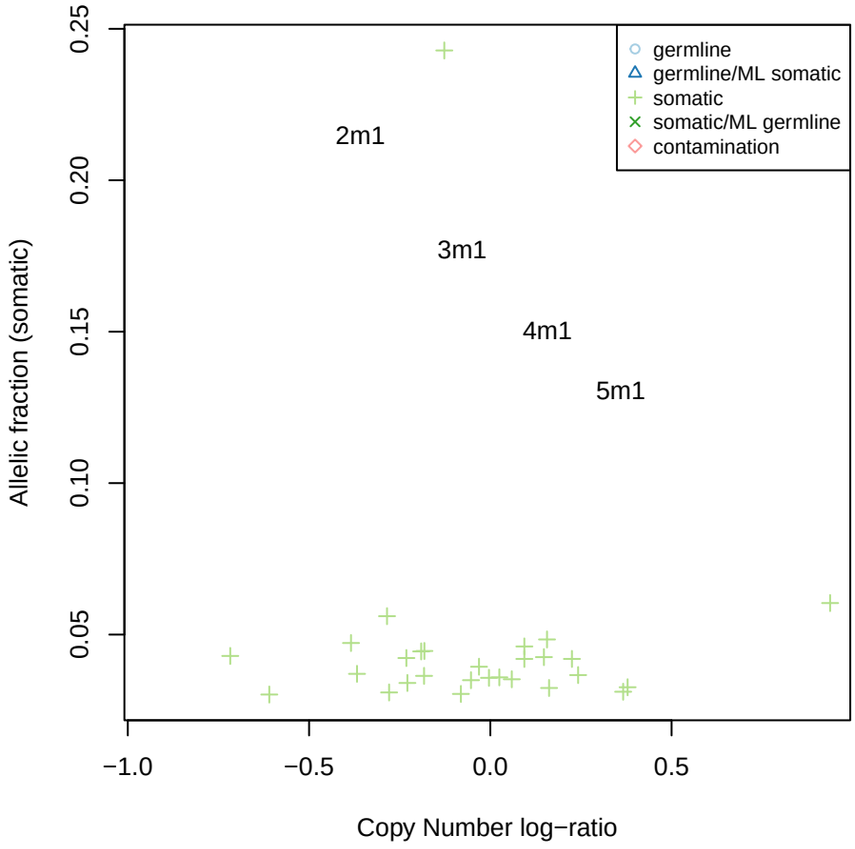

Purity: 0.43 Tumor ploidy: 3.311 SNV log−likelihood: −243.48 GoF: 83.1% Mean coverage: 391;505
1 2 3 4 5 6 7 8 9 11 12 13 15 16 17 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

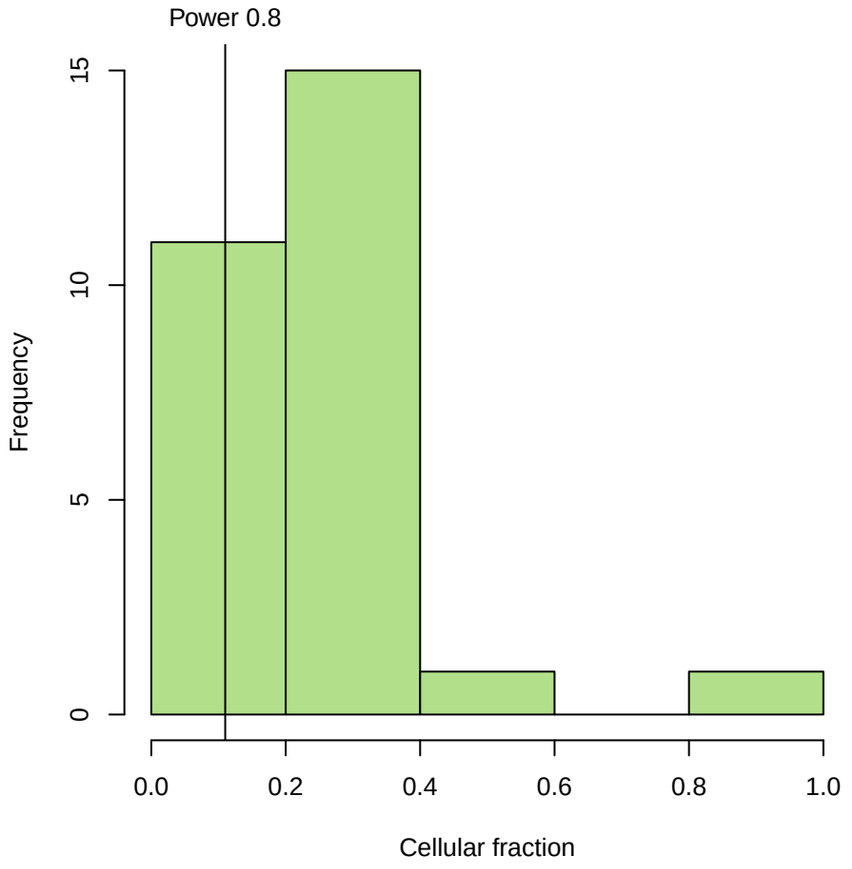

SCNA−fit log−likelihood: −6832.14
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6 7
0 50 100 150
SNV Index

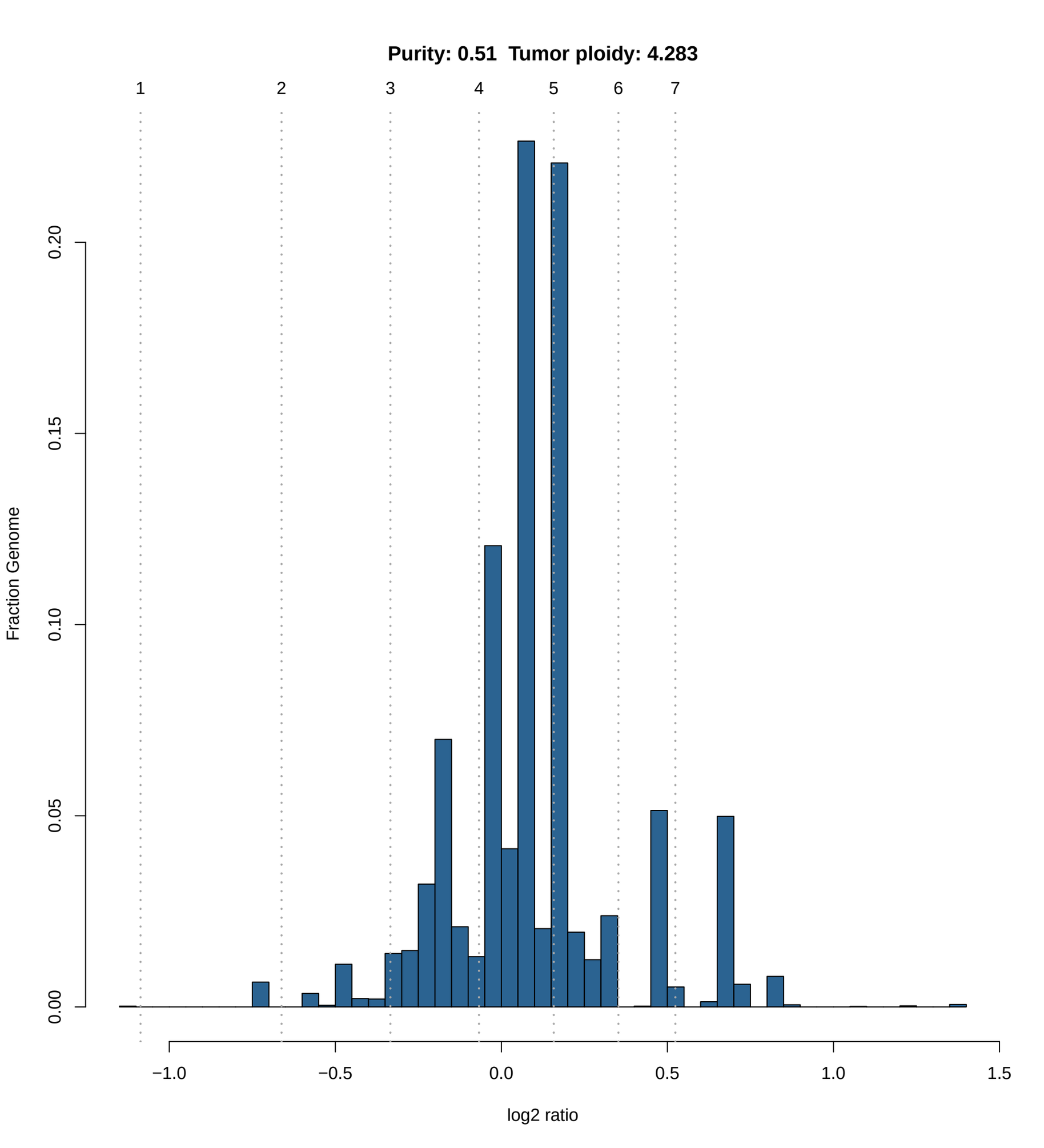

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

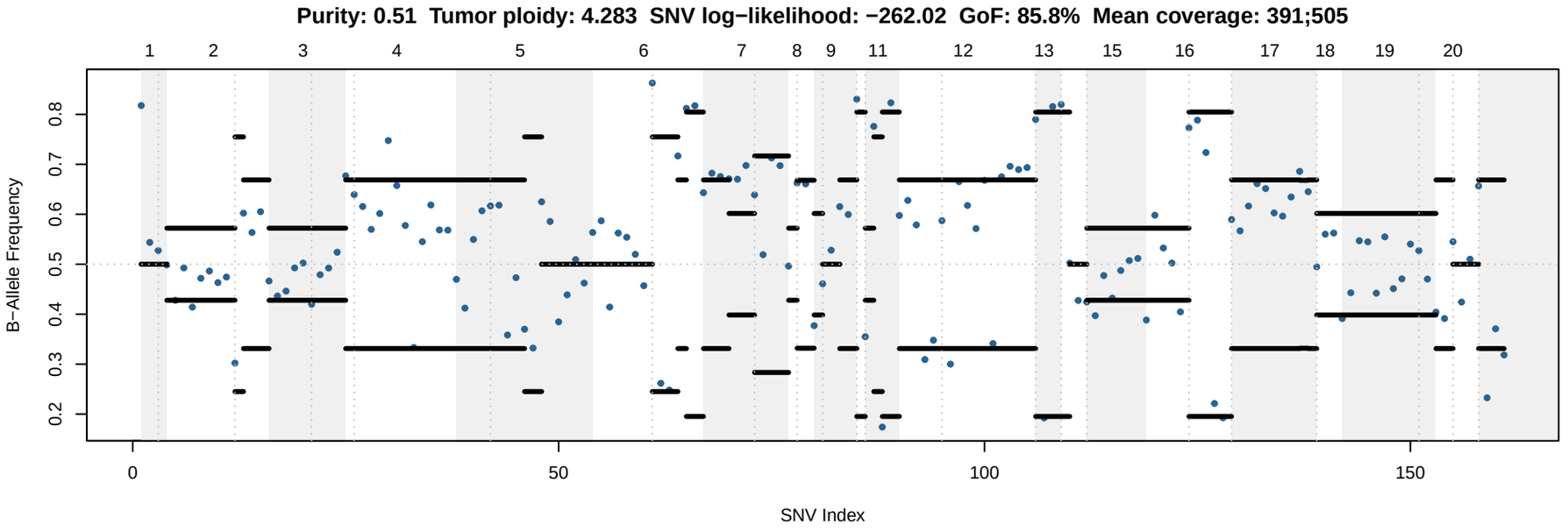

Allelic fraction (germline)
Copy Number log−ratio
1m1
2m2
3m3
4m3
7m5
6m4
3m2
5m3
2m1
4m2
3m1
1m0
4m1
2m0

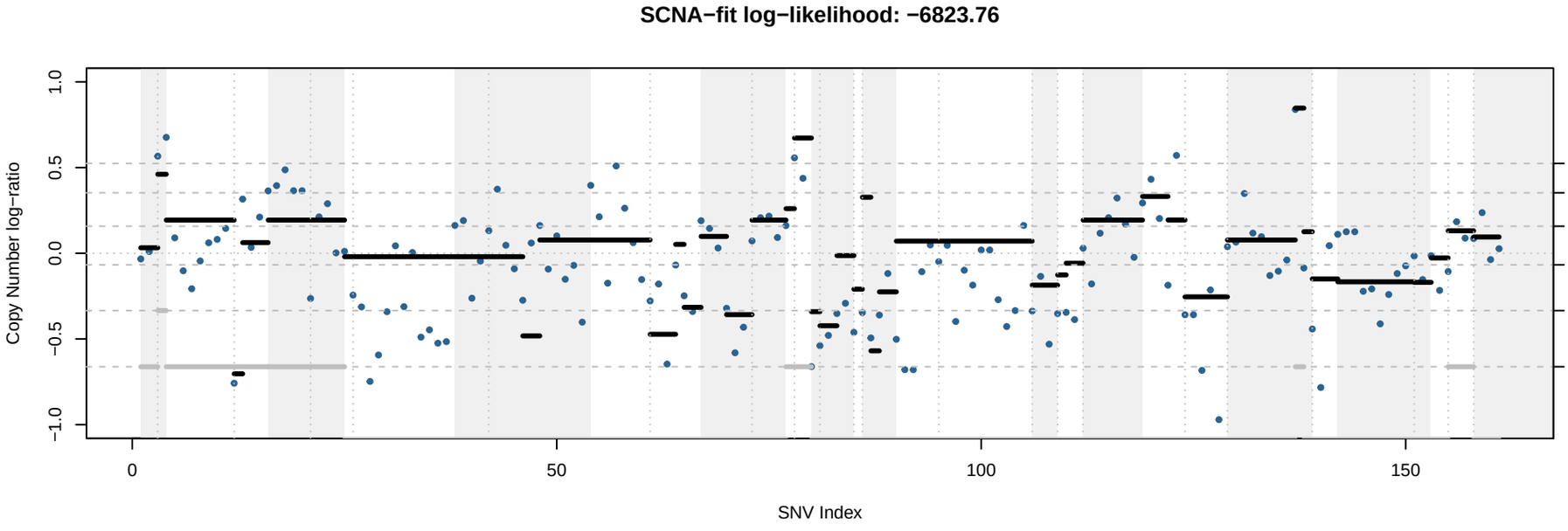

Coverage (log2)
Allelic fraction

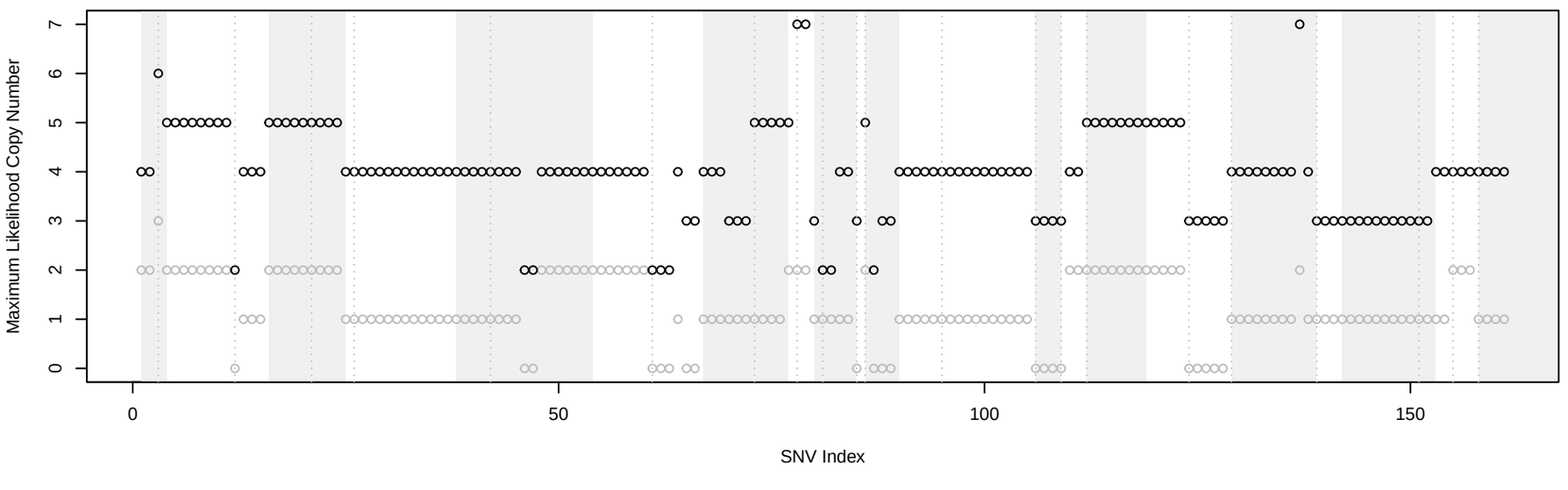

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1
5m1


Power 0.8
Frequency
Cellular fraction

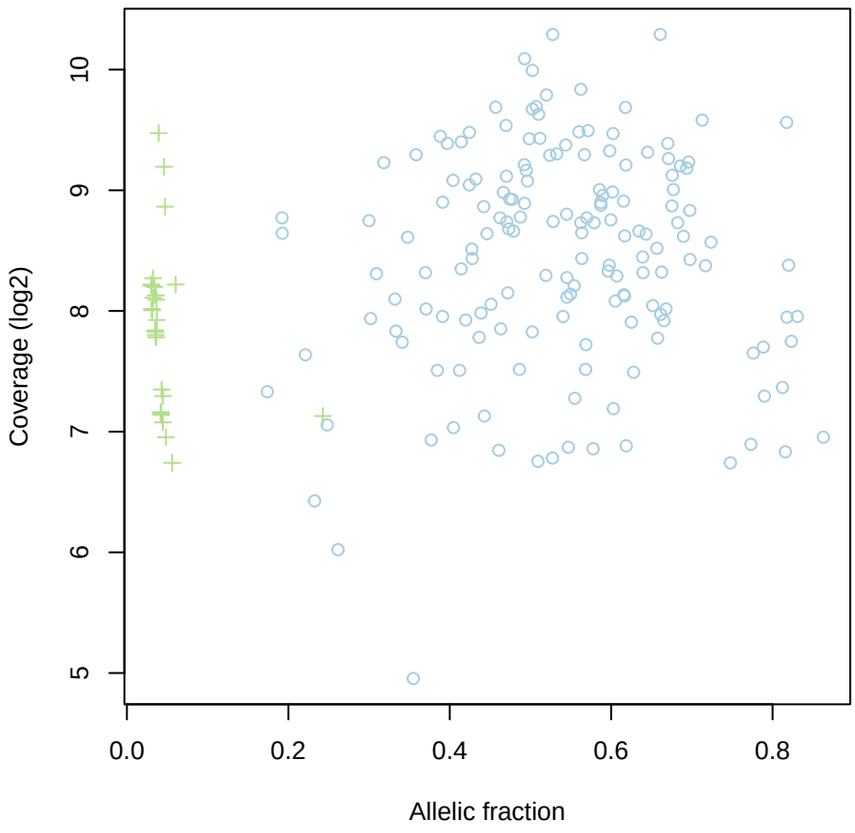

Purity: 0.51 Tumor ploidy: 4.283
1
2
3
4
5
6
7
0.00
0.05
0.10
0.15
0.20
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

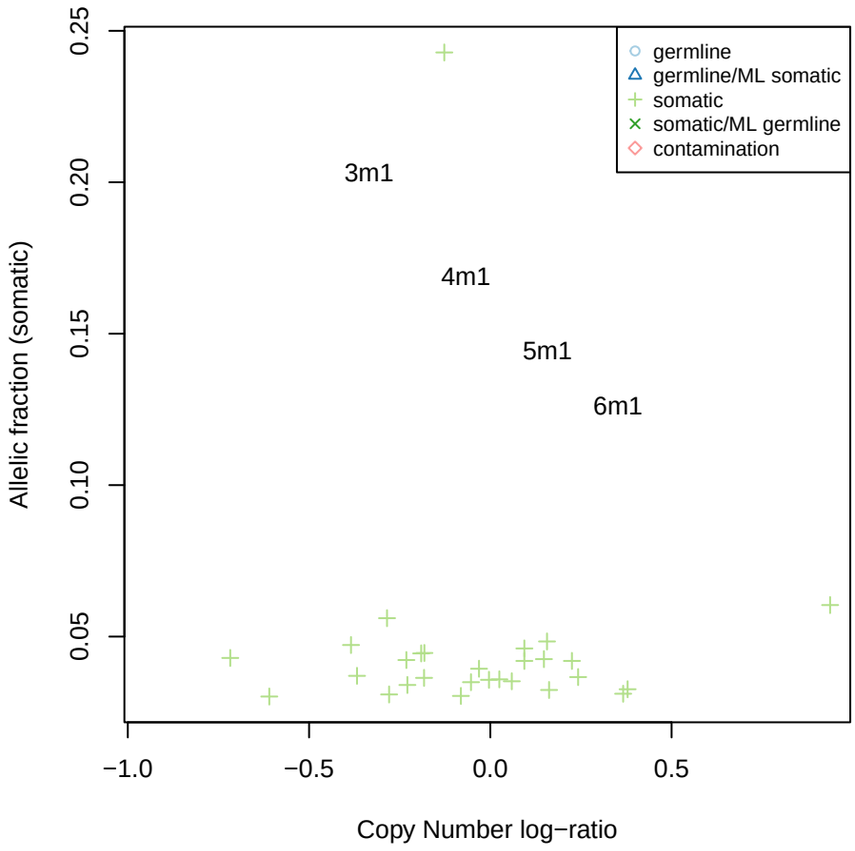

Purity: 0.51 Tumor ploidy: 4.283 SNV log−likelihood: −262.02 GoF: 85.8% Mean coverage: 391;505
1 2 3 4 5 6 7 8 9 11 12 13 15 16 17 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

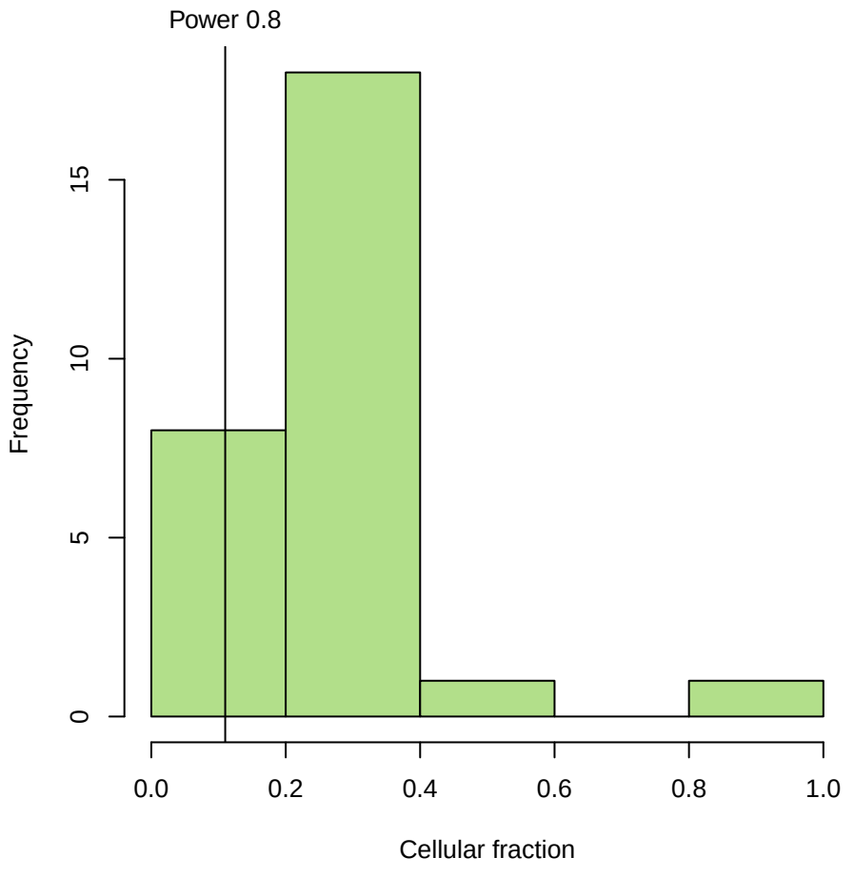

SCNA−fit log−likelihood: −6823.76
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 50 100 150
SNV Index

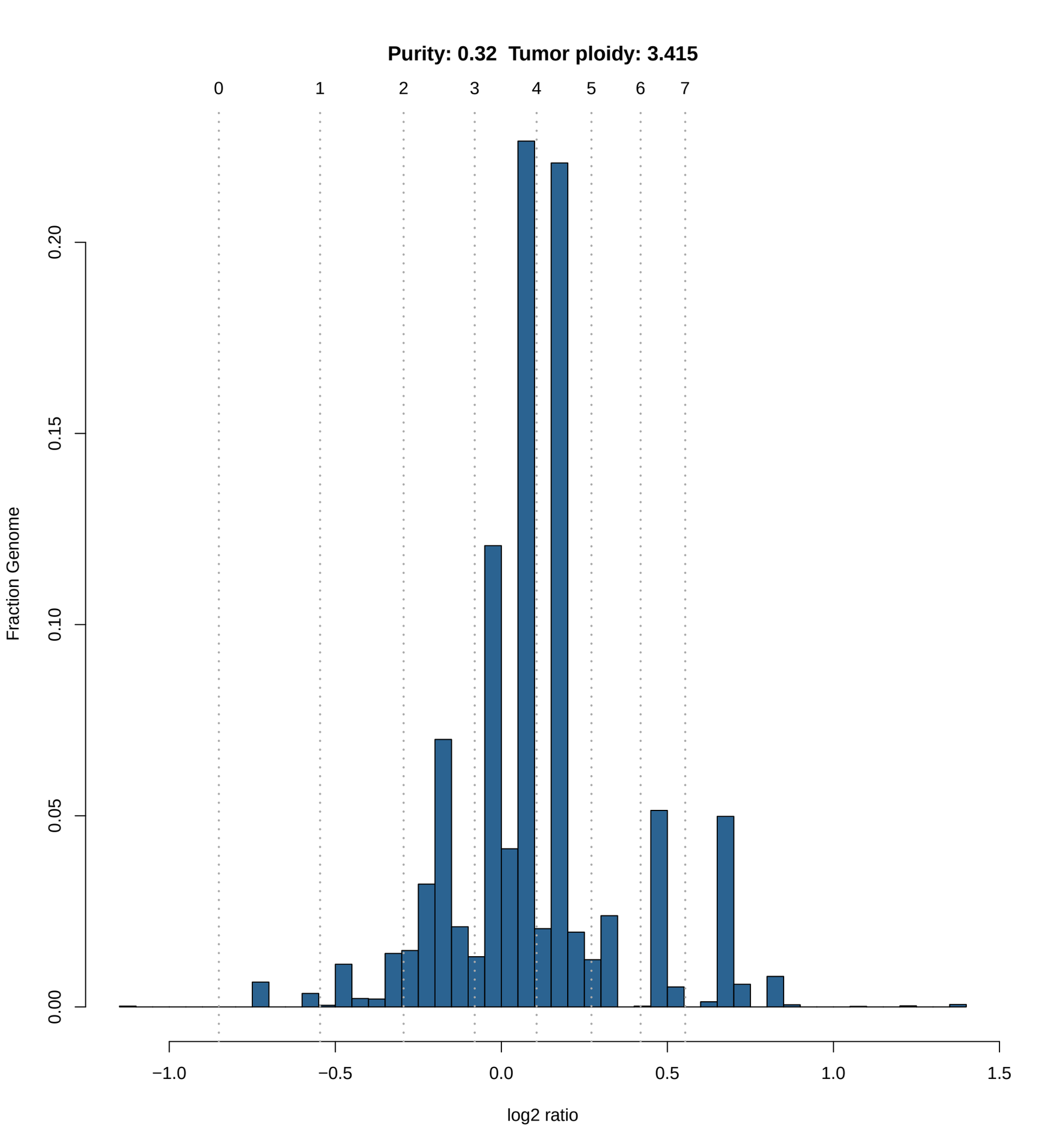

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

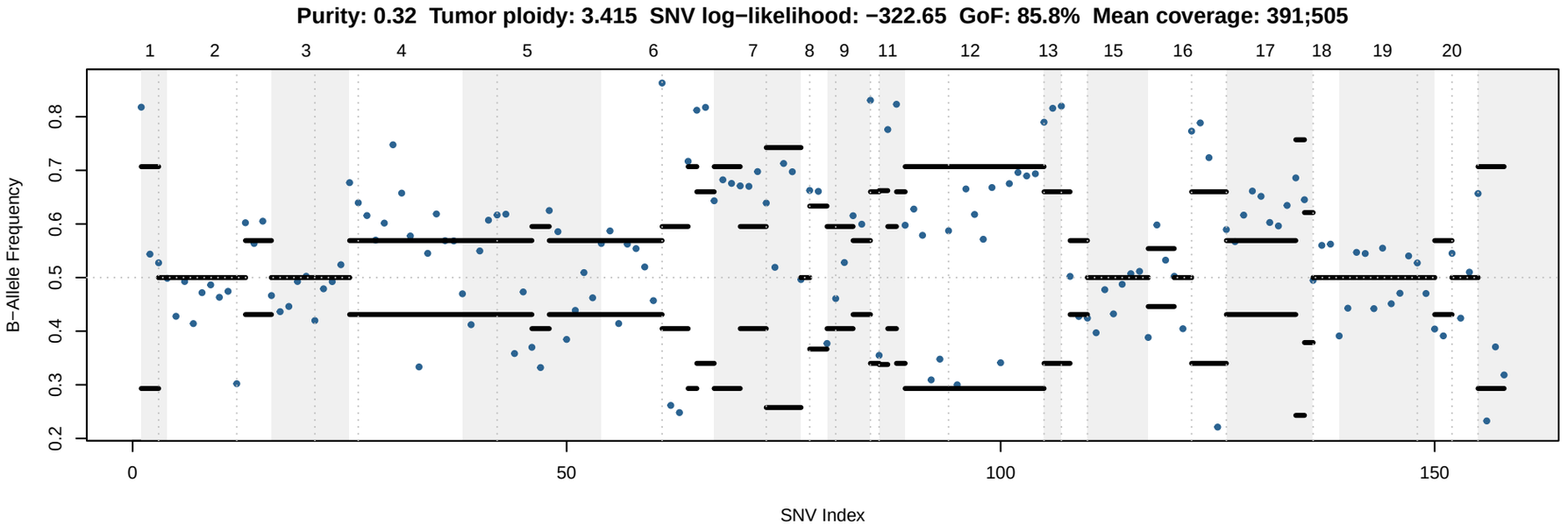
Allelic fraction (germline)
Copy Number log−ratio
4m4
3m3
2m2
5m4
4m3
7m5
3m2
5m3
2m1
4m2
6m3
5m2
3m1
4m1
2m0
3m0

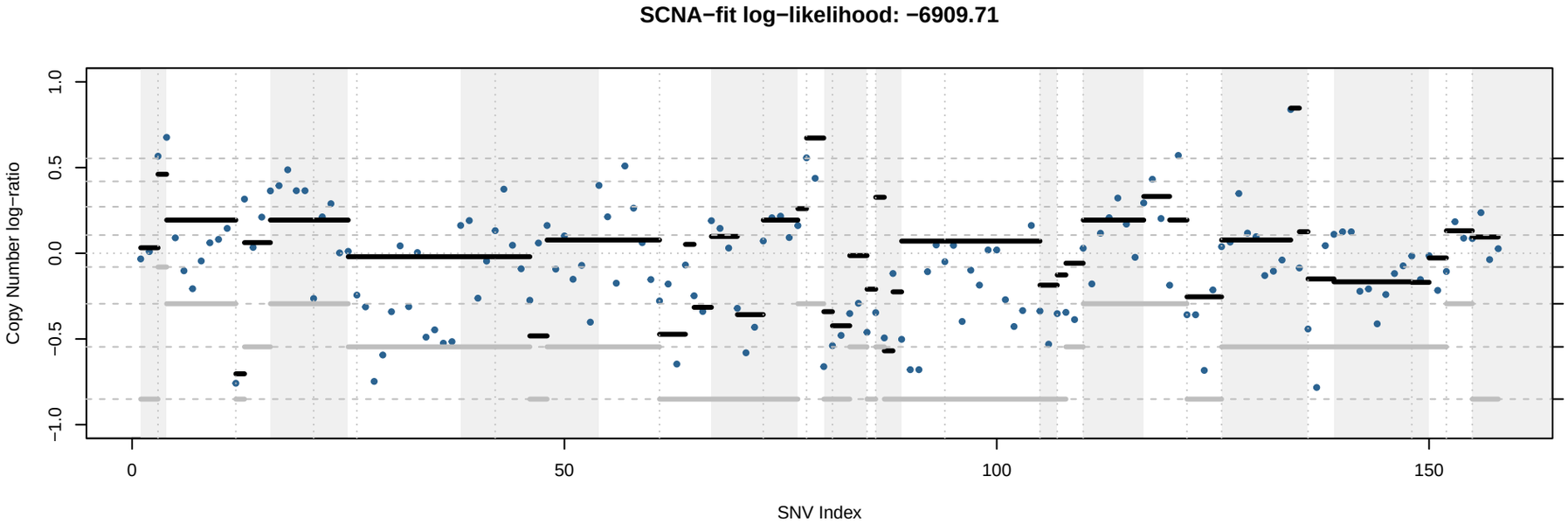

Coverage (log2)
Allelic fraction

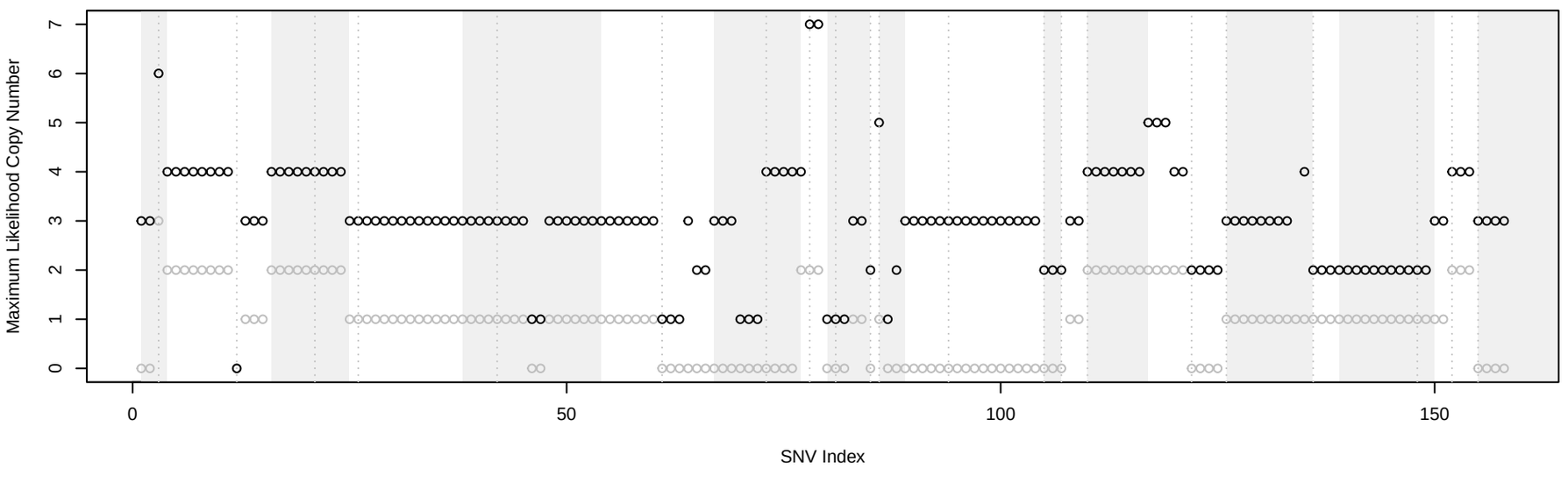

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
6m1

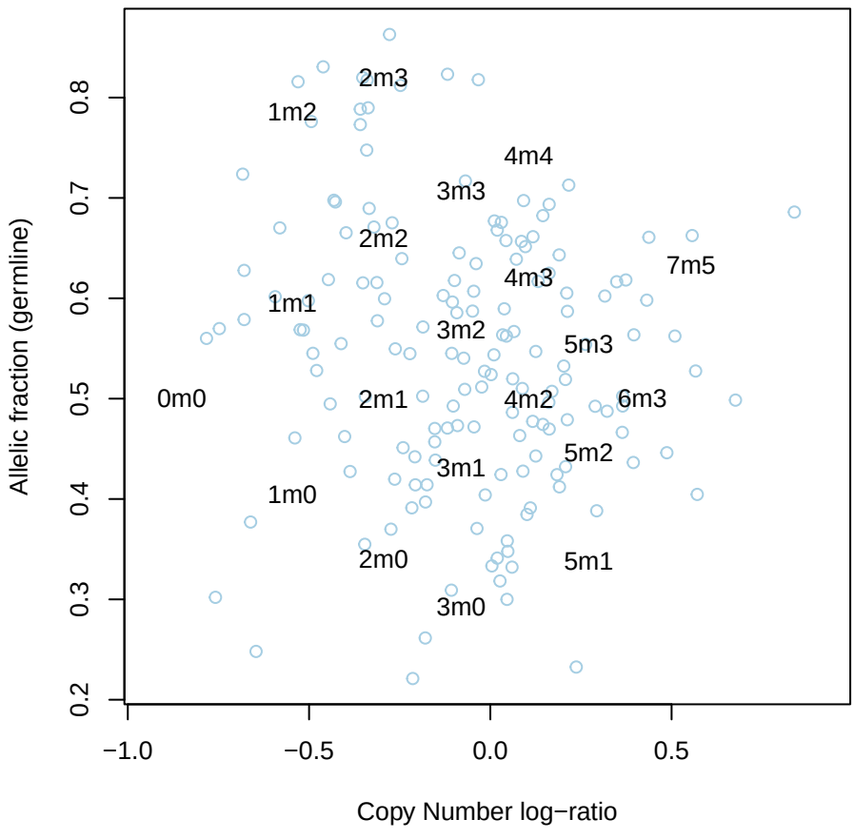

Power 0.8
Frequency
Cellular fraction

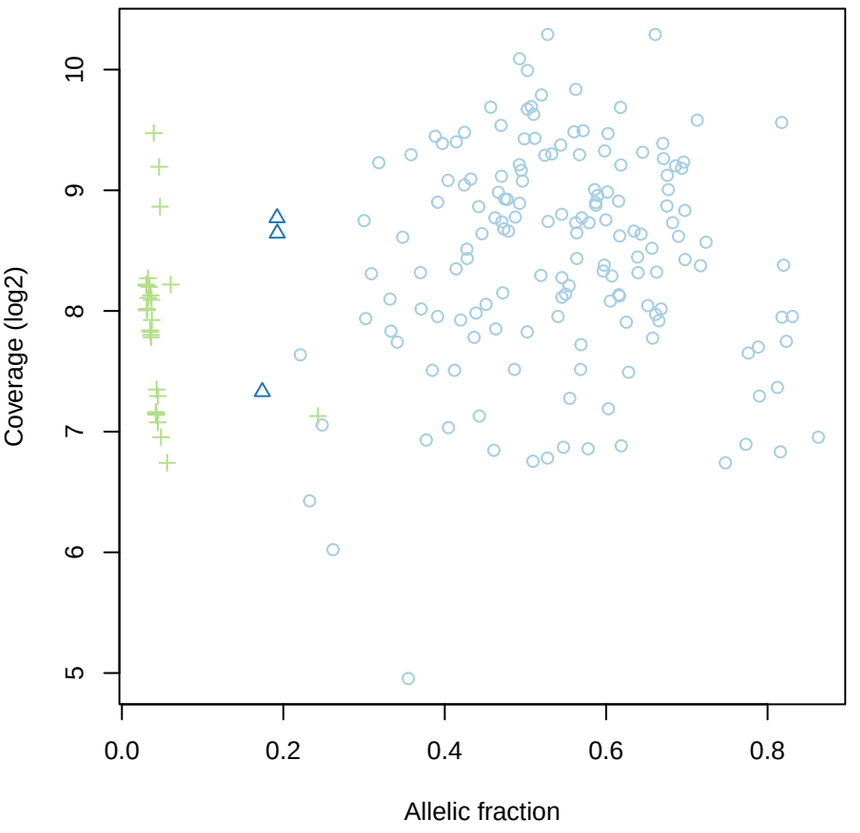

Purity: 0.32 Tumor ploidy: 3.415
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

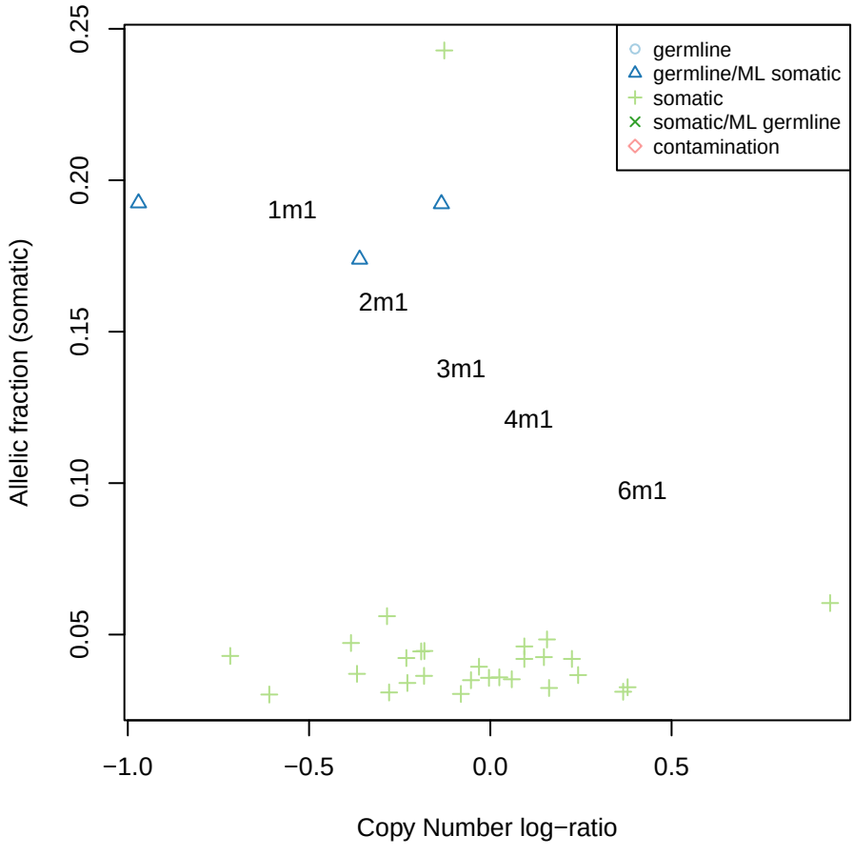

Purity: 0.32 Tumor ploidy: 3.415 SNV log−likelihood: −322.65 GoF: 85.8% Mean coverage: 391;505
1 2 3 4 5 6 7 8 9 11 12 13 15 16 17 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

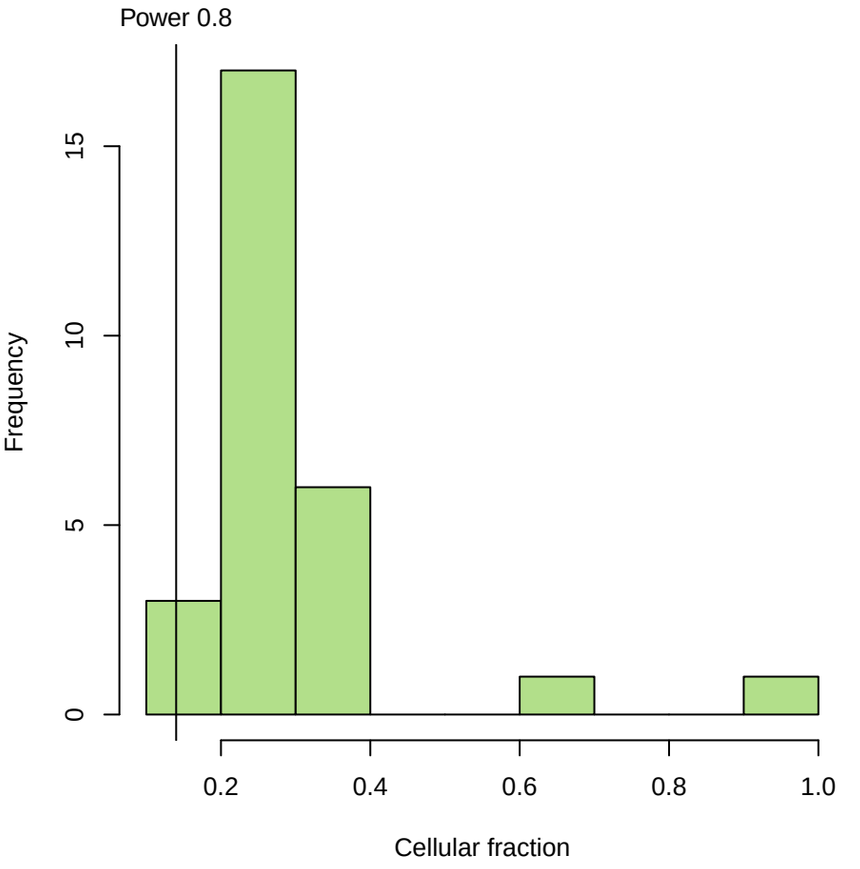

SCNA−fit log−likelihood: −6909.71
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 6
0 50 100 150
SNV Index

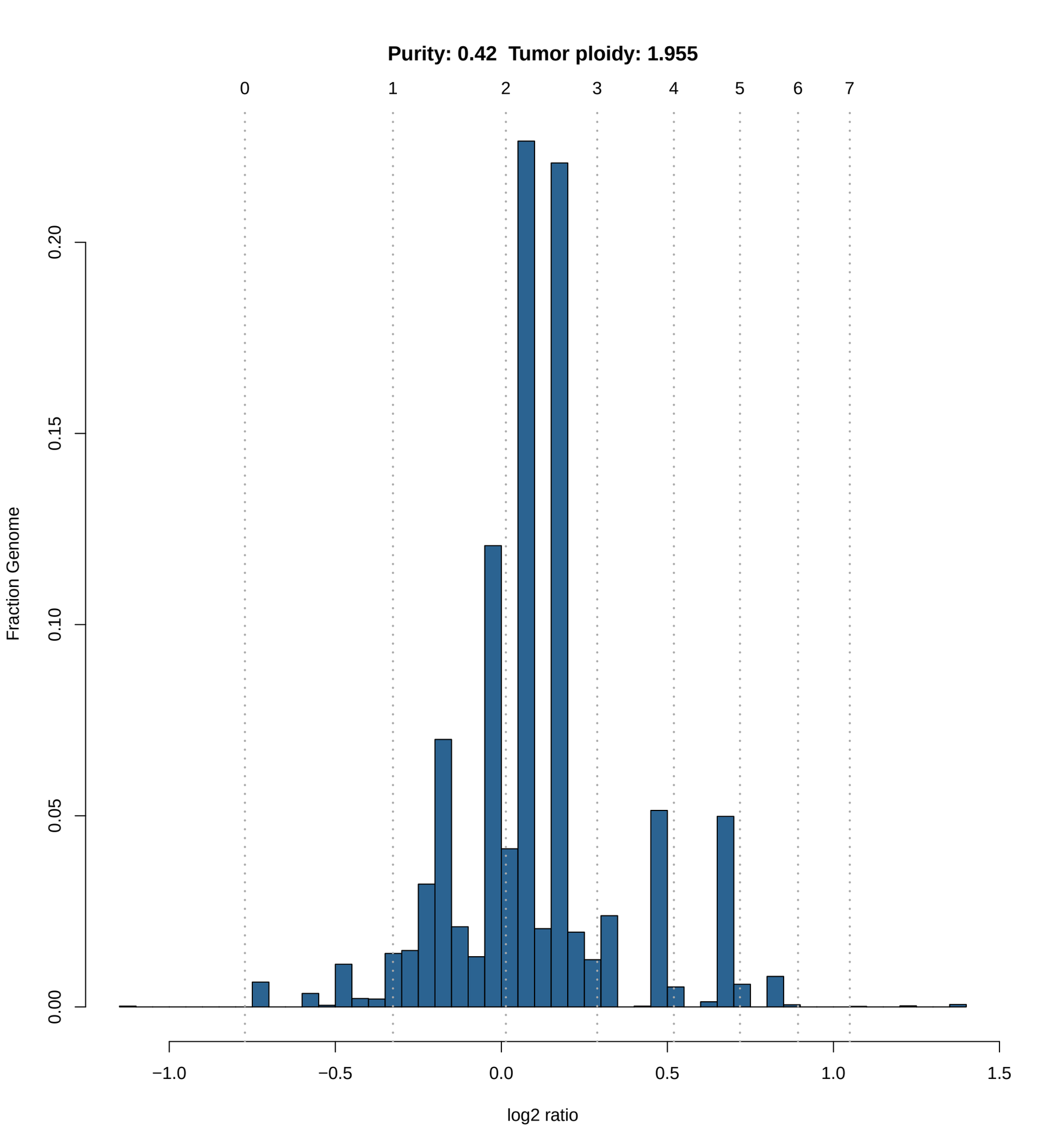

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

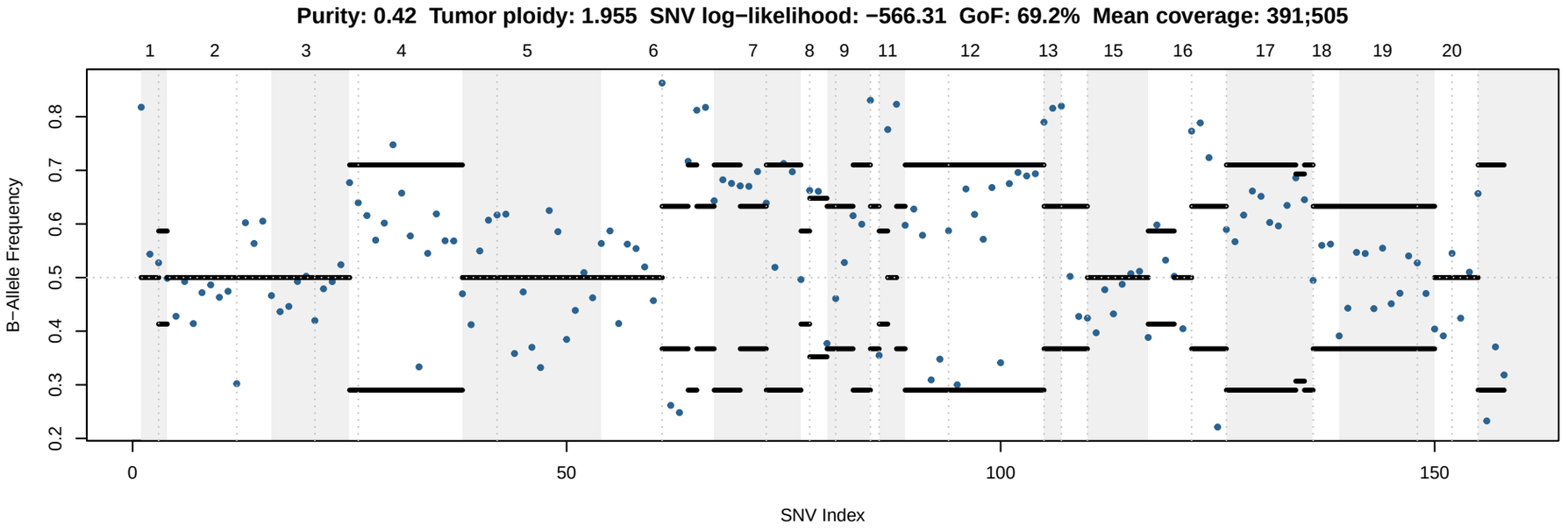

Allelic fraction (germline)
Copy Number log−ratio
0m0
1m0
1m1
1m2
2m0
2m1
2m2
2m3
3m0
3m1
3m2
3m3
4m2
4m3
4m4
5m1
5m2
5m3
6m3
7m5

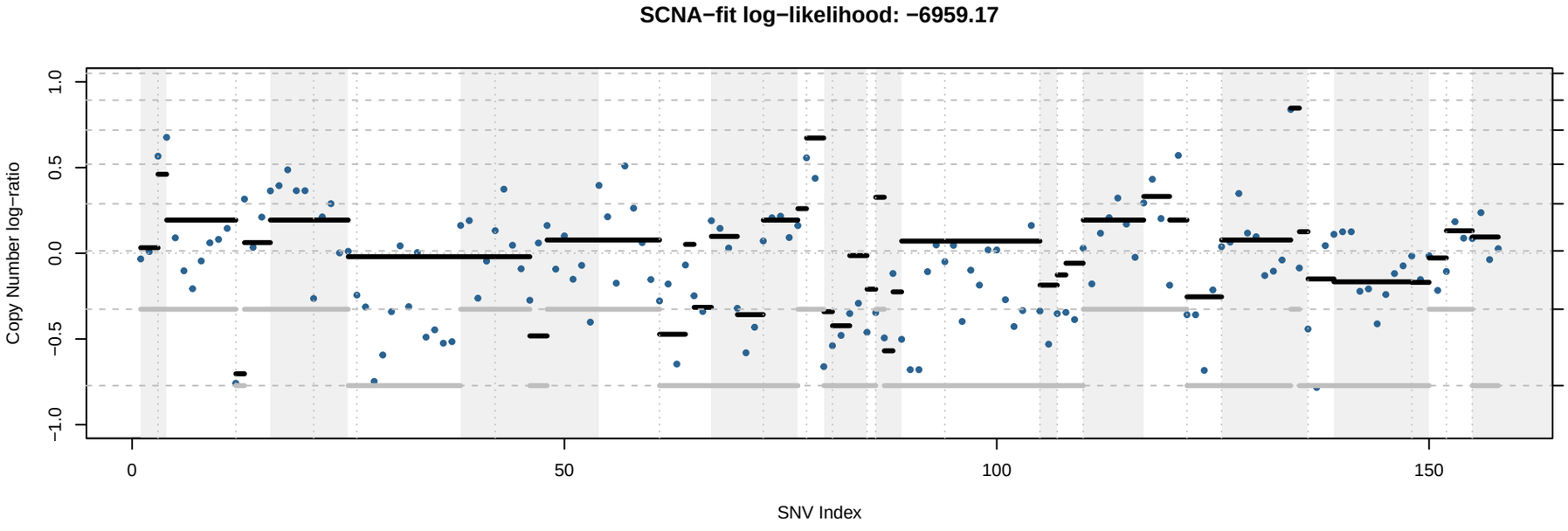

Coverage (log2)
Allelic fraction

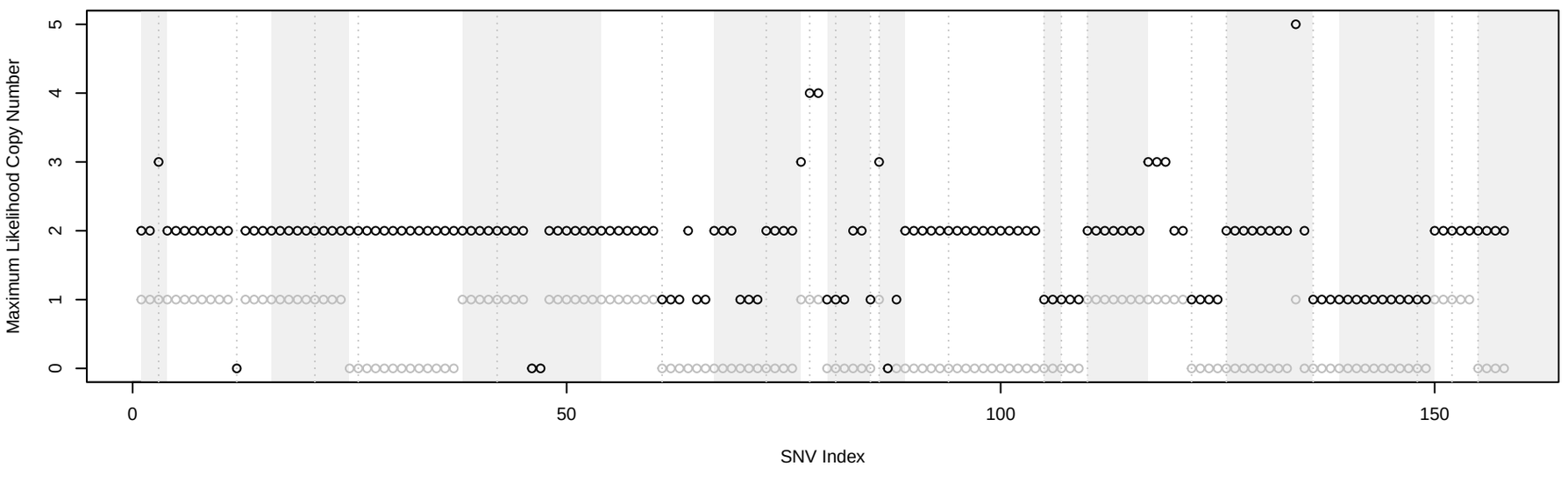

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
4m1
6m1

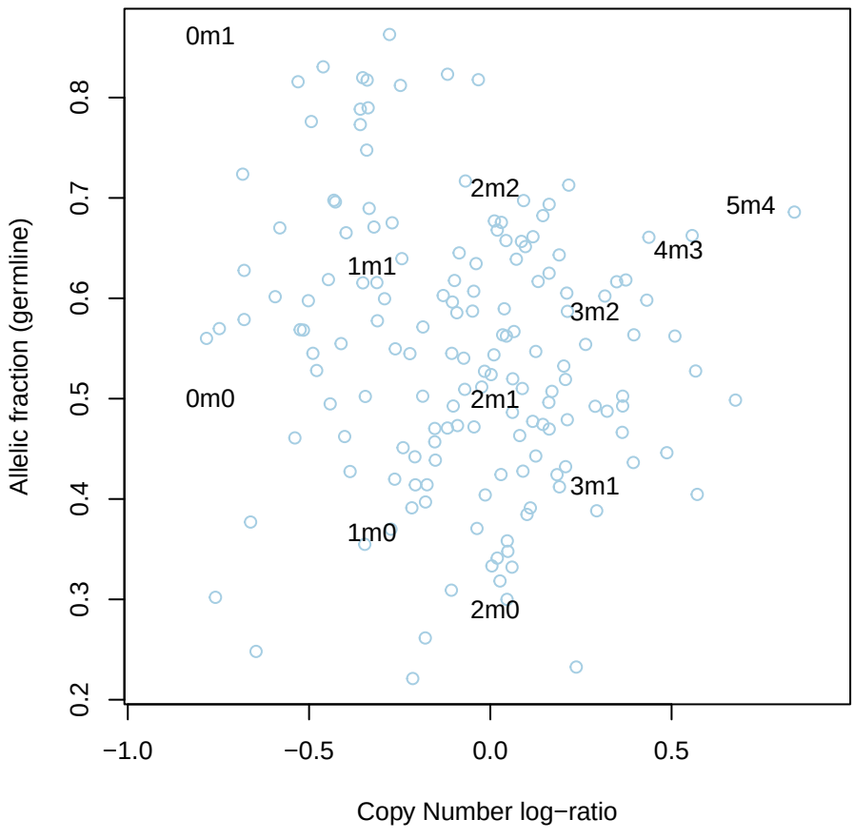

Power 0.8
Frequency
Cellular fraction

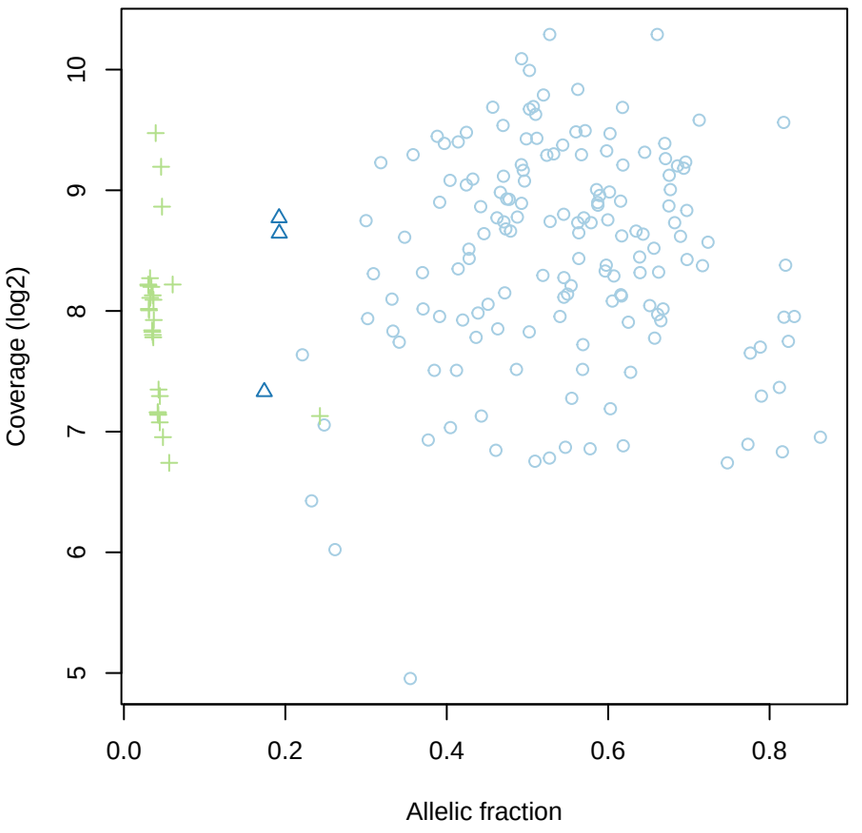

Purity: 0.42 Tumor ploidy: 1.955
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

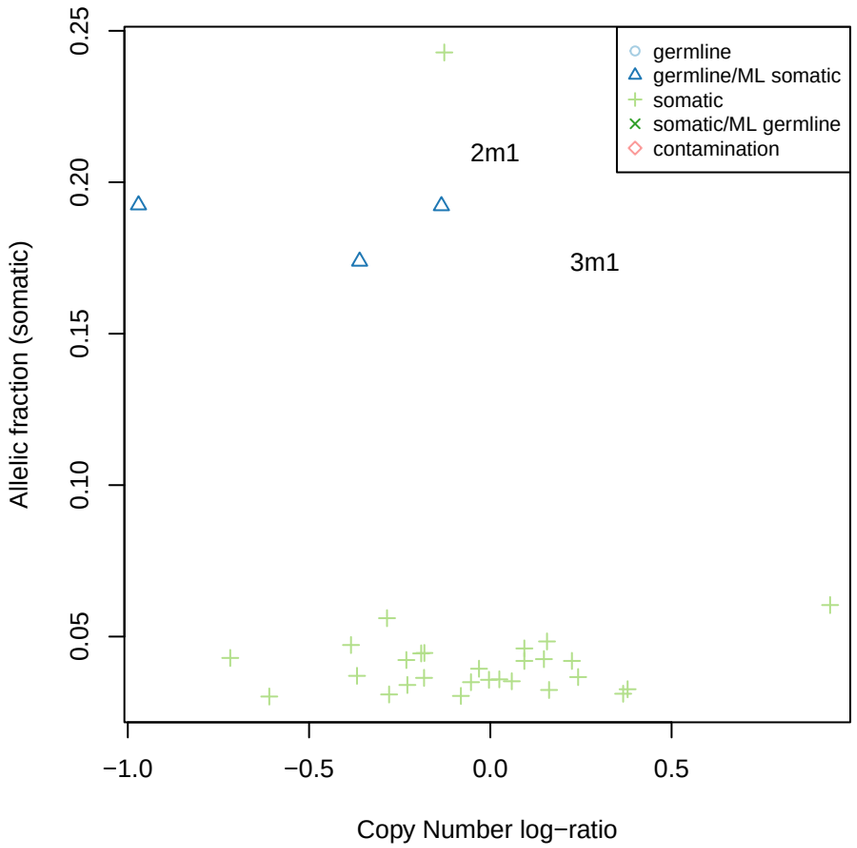

Purity: 0.42 Tumor ploidy: 1.955 SNV log−likelihood: −566.31 GoF: 69.2% Mean coverage: 391;505
1 2 3 4 5 6 7 8 9 11 12 13 15 16 17 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

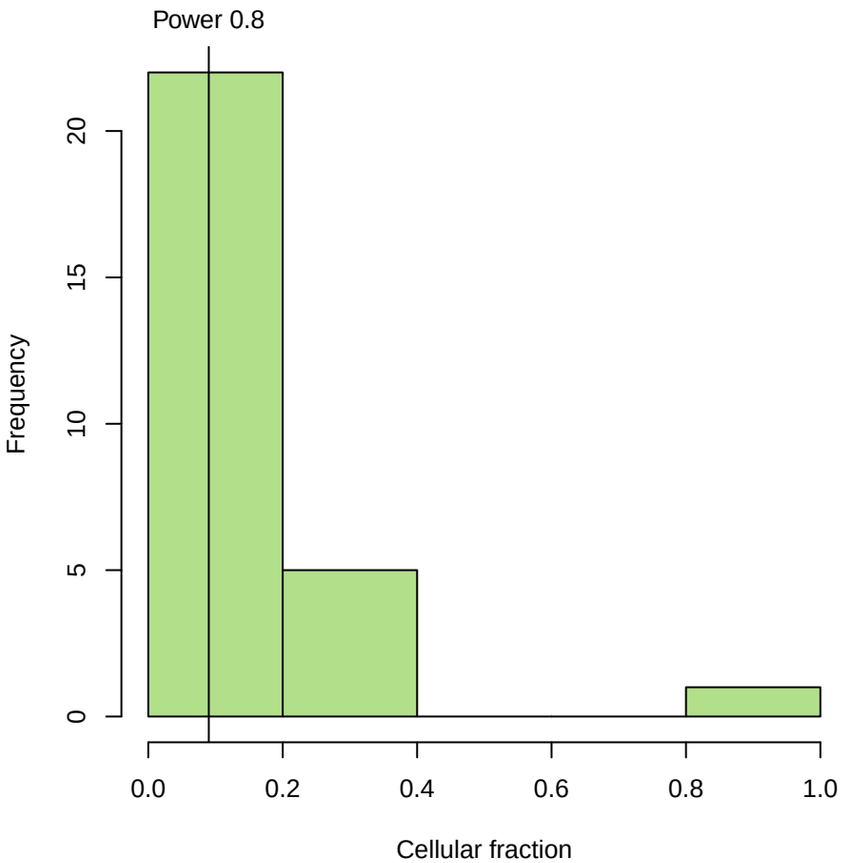

SCNA−fit log−likelihood: −6959.17
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

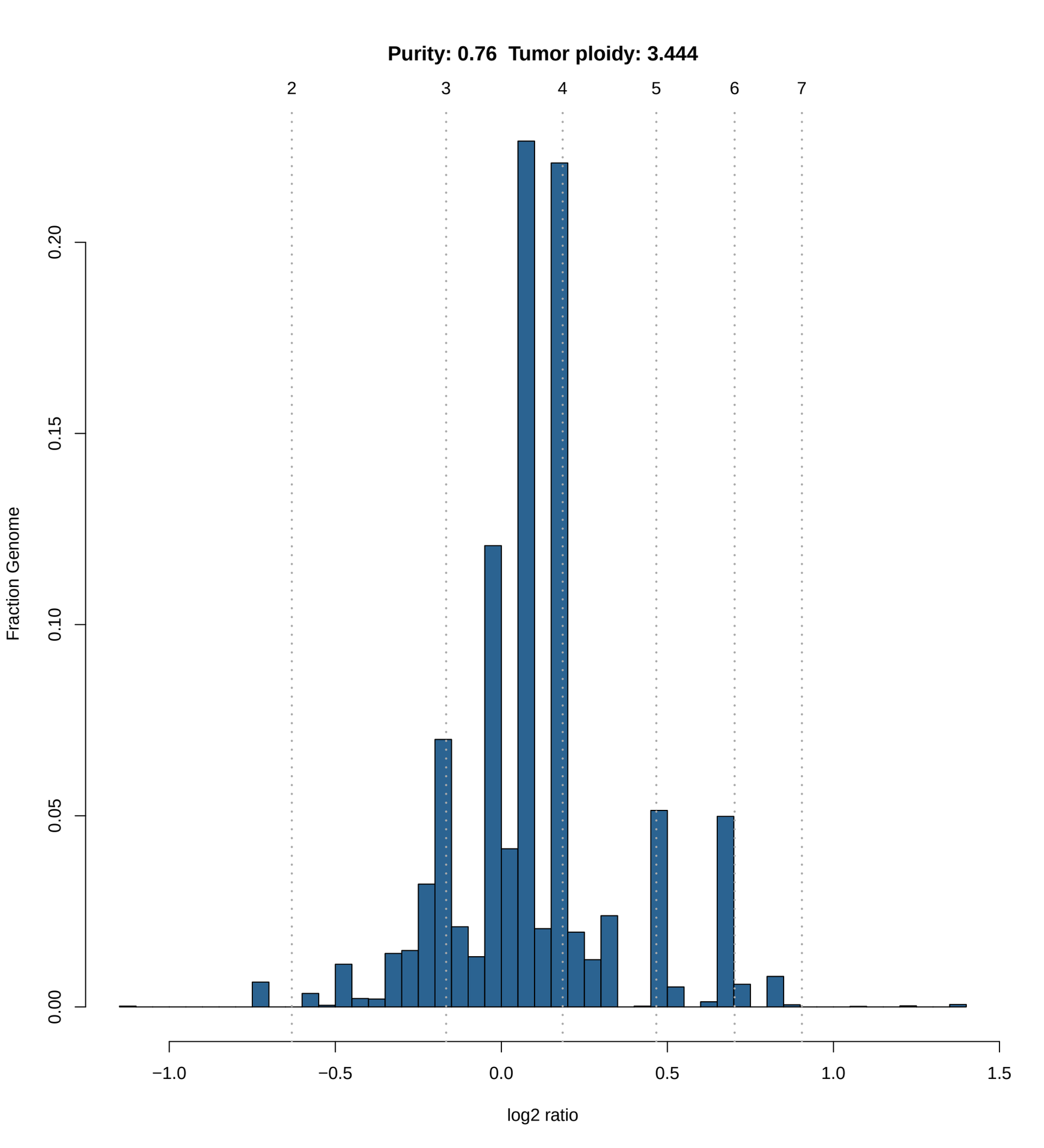

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

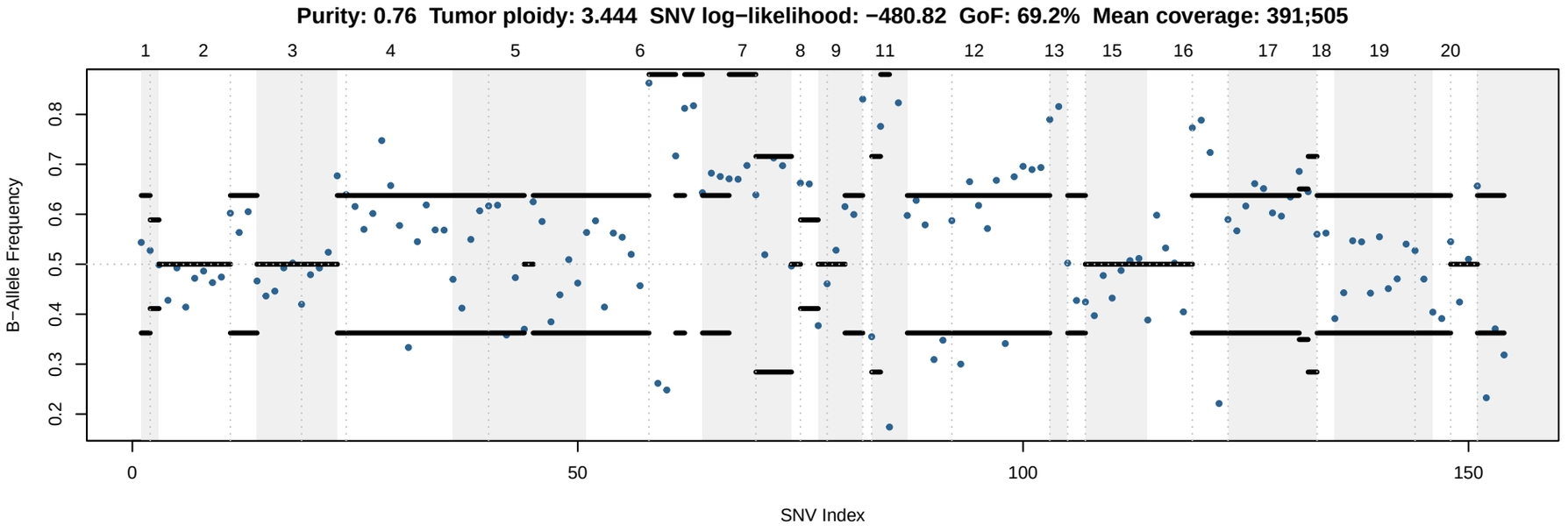

0m1
2m2
5m4
4m3
1m1
3m2
0m0
2m1
3m1
1m0
2m0
Allelic fraction (germline)
Copy Number log−ratio
0.2
0.3
0.4
0.5
0.6
0.7
0.8
−1.0
−0.5
0.0
0.5

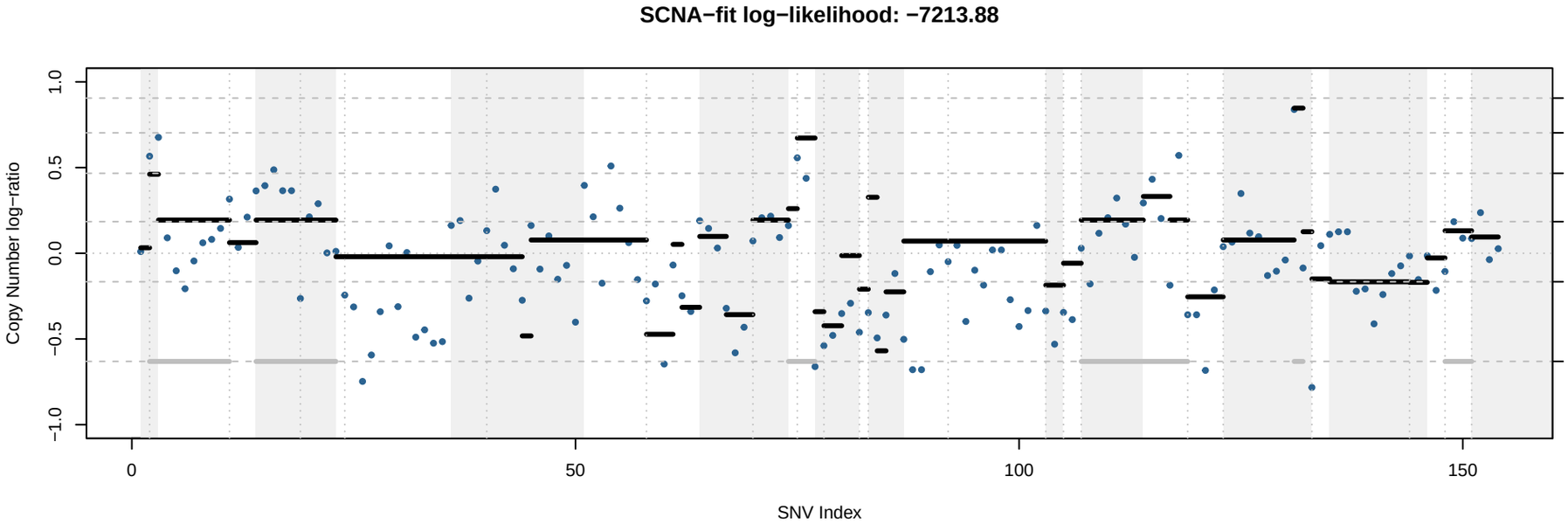

Coverage (log2)
Allelic fraction
5
6
7
8
9
10
0.0
0.2
0.4
0.6
0.8

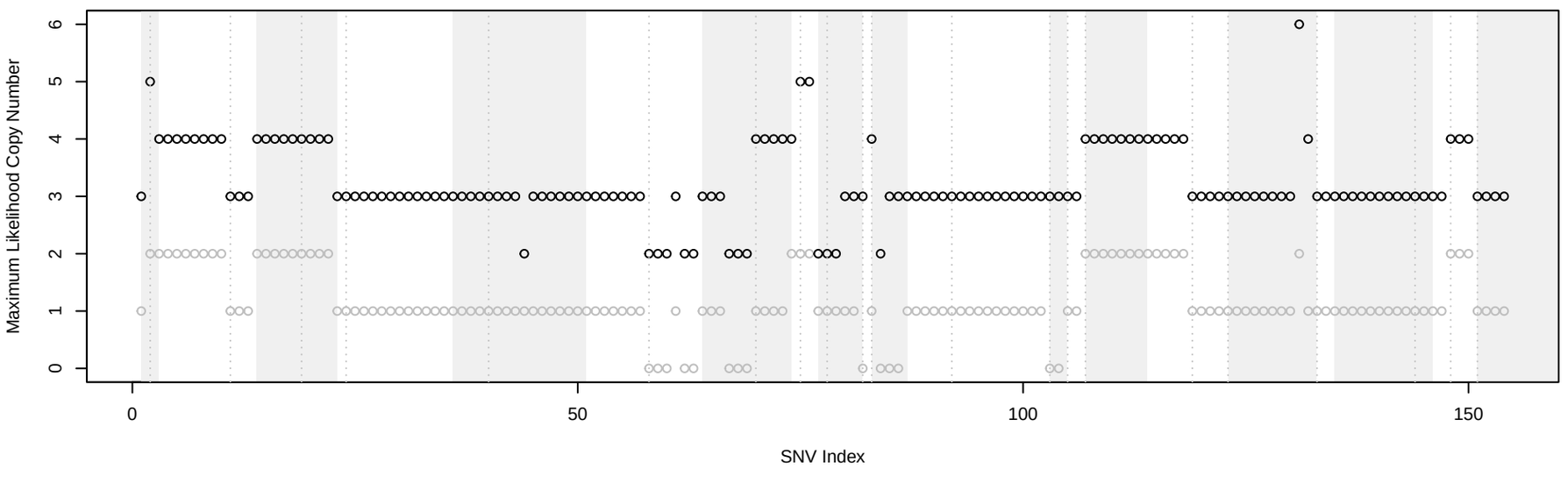

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
0.25
−1.0
−0.5
0.0
0.5

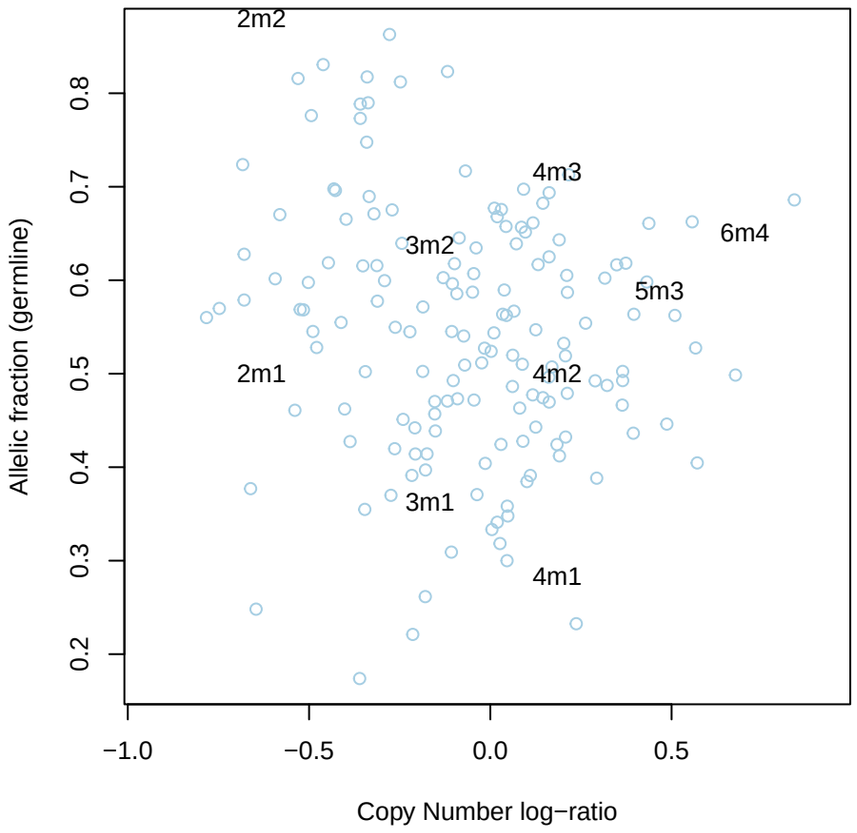

Power 0.8
Frequency
Cellular fraction
0
5
10
15
20
0.0
0.2
0.4
0.6
0.8
1.0

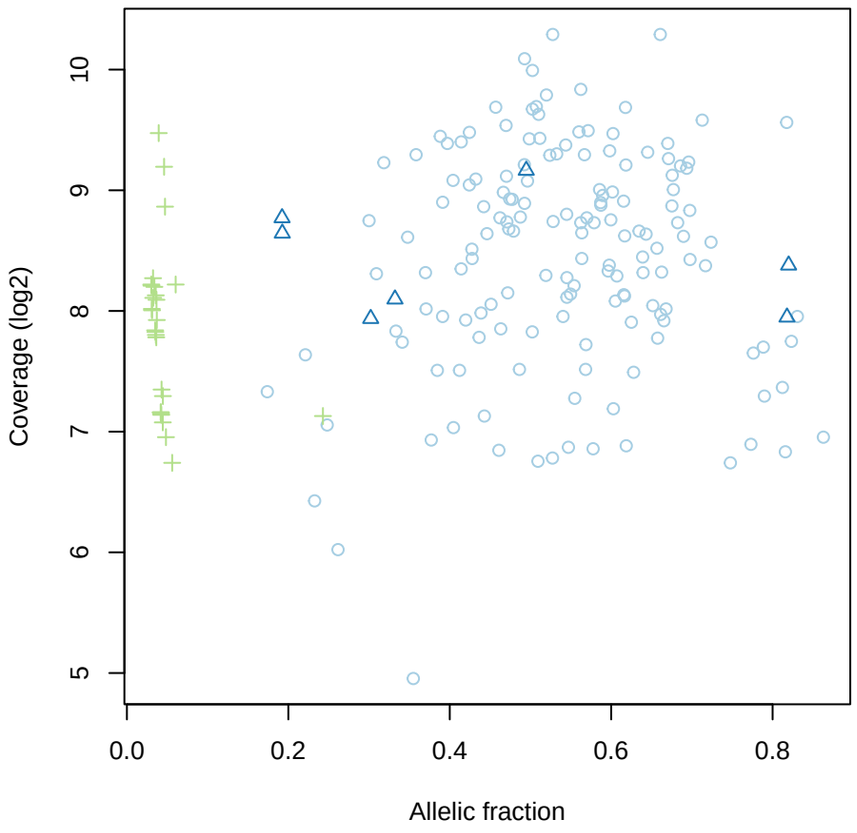

Purity: 0.76 Tumor ploidy: 3.444
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

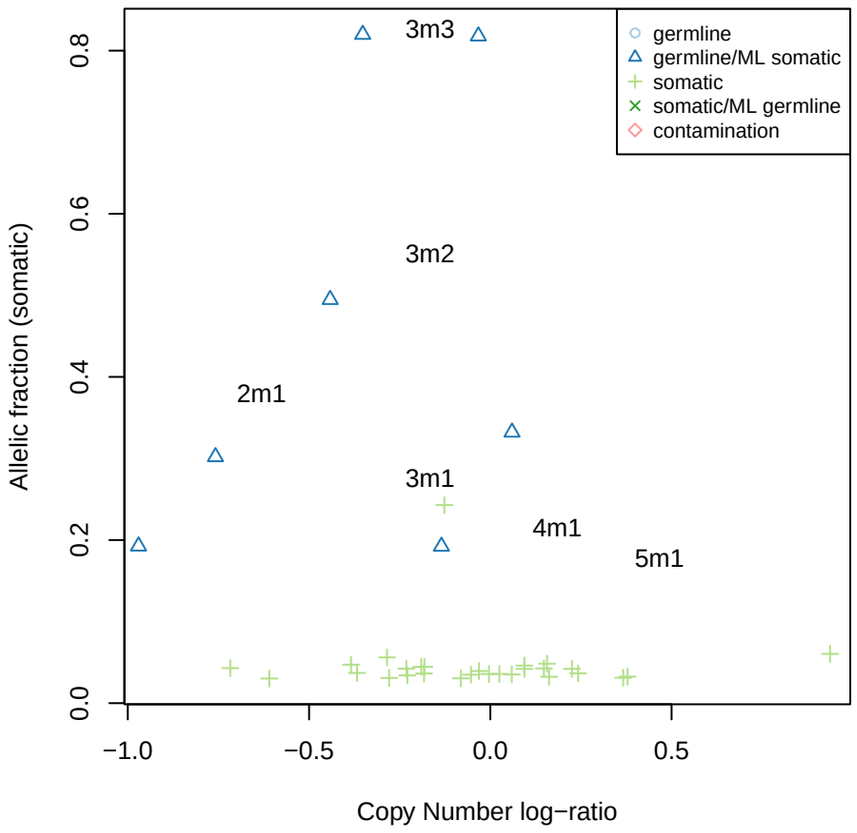

Purity: 0.76 Tumor ploidy: 3.444 SNV log−likelihood: −480.82 GoF: 69.2% Mean coverage: 391;505
1 2 3 4 5 6 7 8 9 11 12 13 15 16 17 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

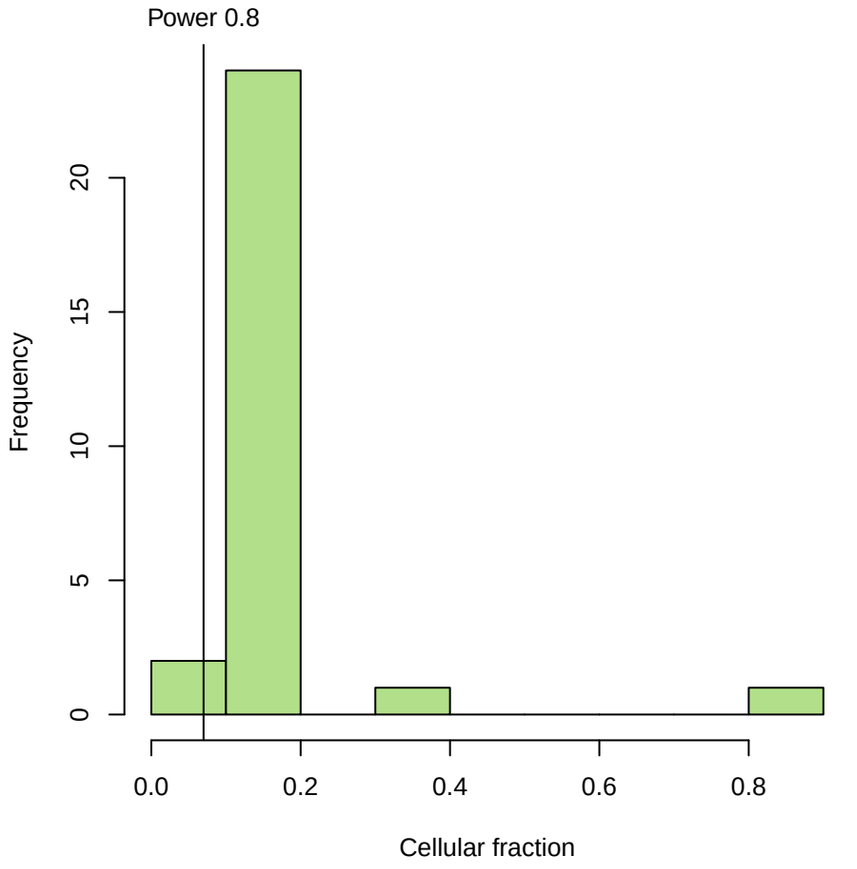

SCNA−fit log−likelihood: −7213.88
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
2 3 4 5 6 7
0 50 100 150
SNV Index

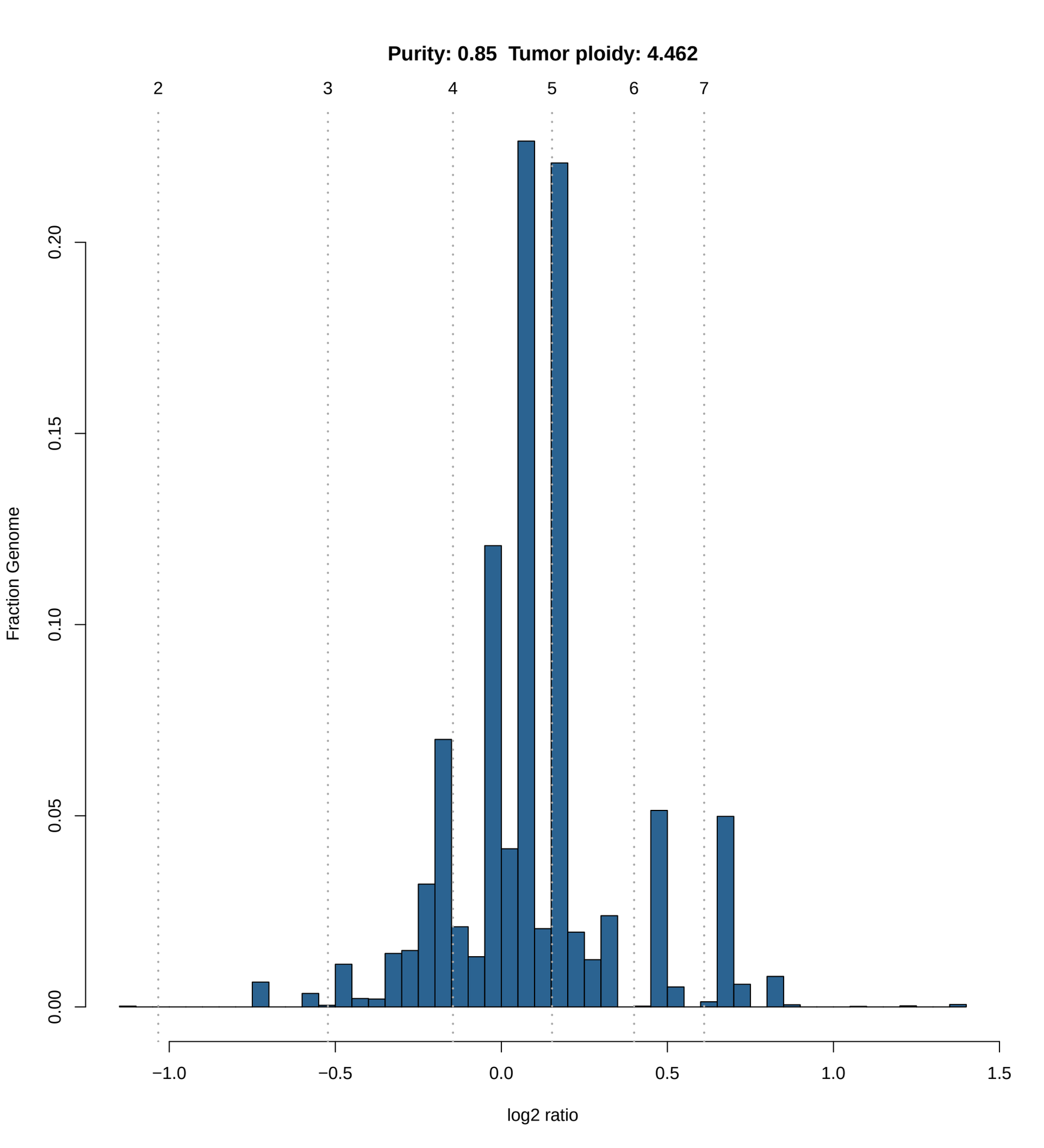

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

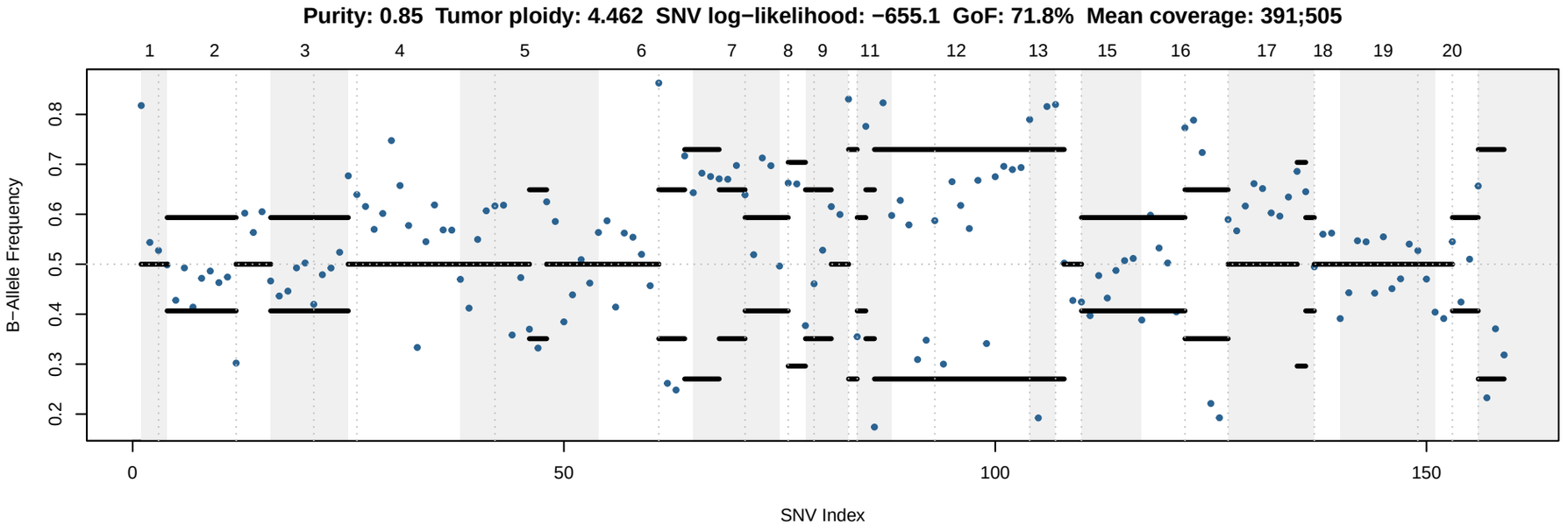

2m2
4m3
6m4
3m2
5m3
2m1
4m2
3m1
4m1
Allelic fraction (germline)
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
0.2
0.3
0.4
0.5
0.6
0.7
0.8

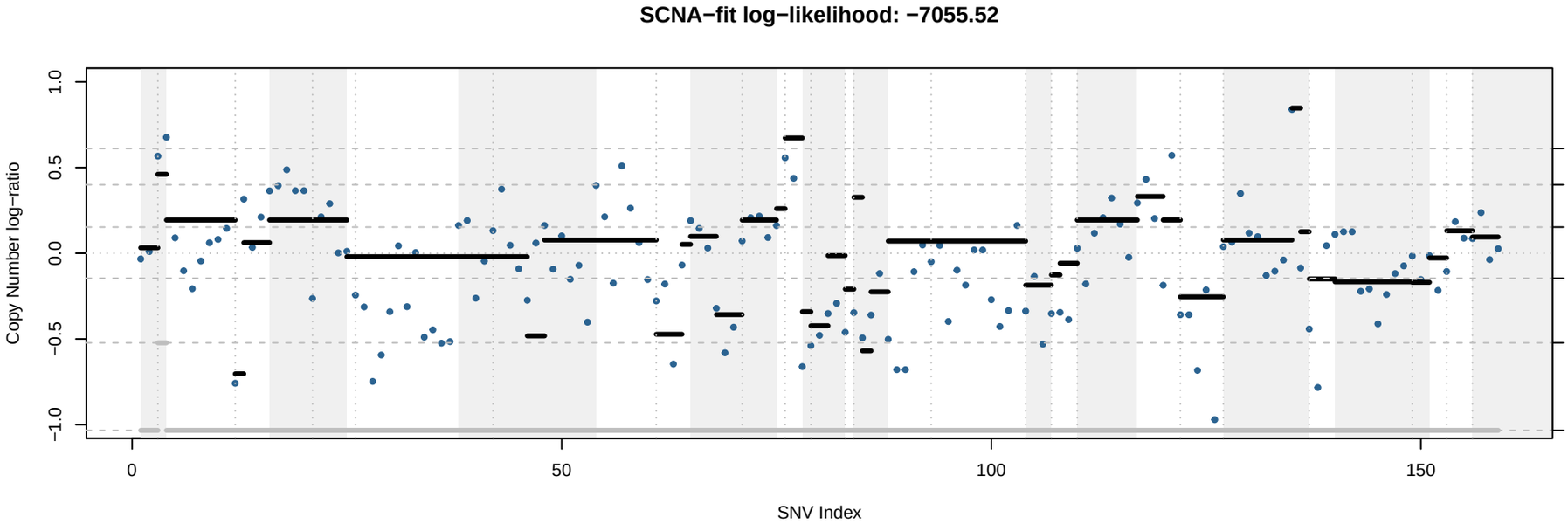

Coverage (log2)
Allelic fraction
0.0
0.2
0.4
0.6
0.8
5
6
7
8
9
10

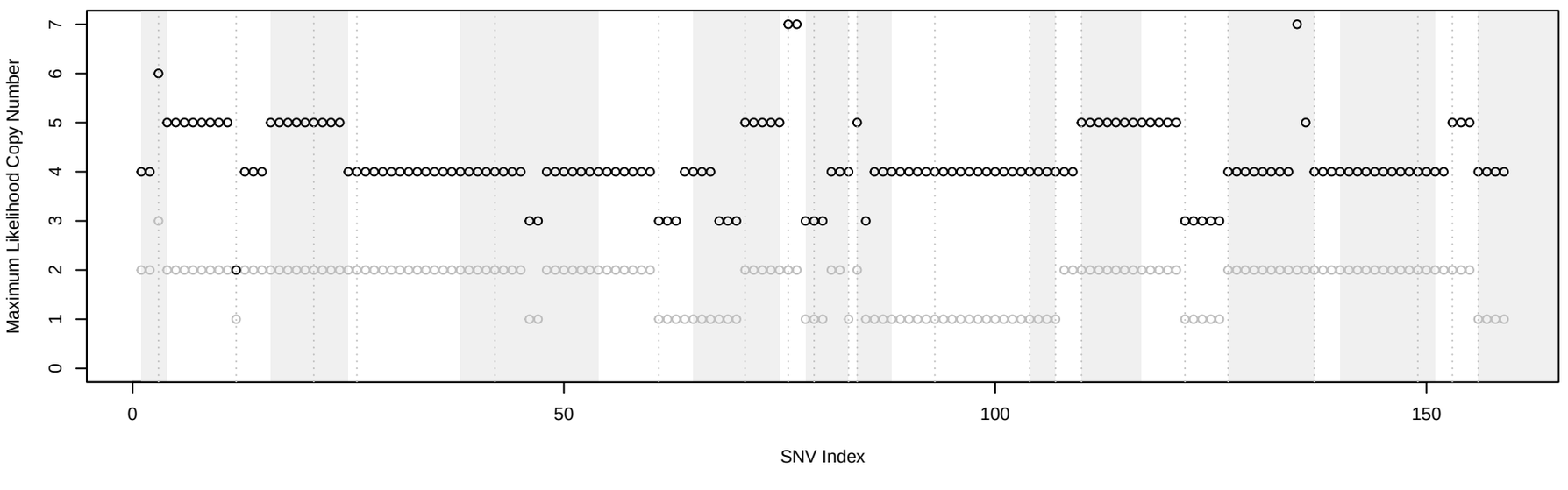

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m3
3m2
2m1
3m1
4m1
5m1
Allelic fraction (somatic)
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
0.0
0.2
0.4
0.6
0.8

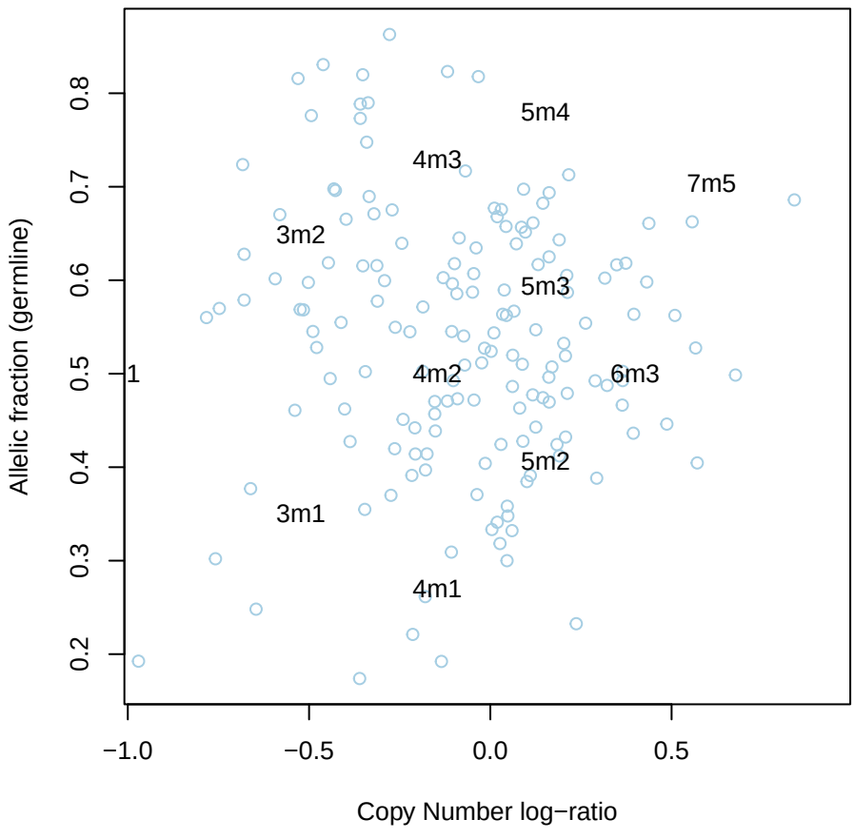

Power 0.8
Frequency
Cellular fraction
0.0
0.2
0.4
0.6
0.8
0
5
10
15
20

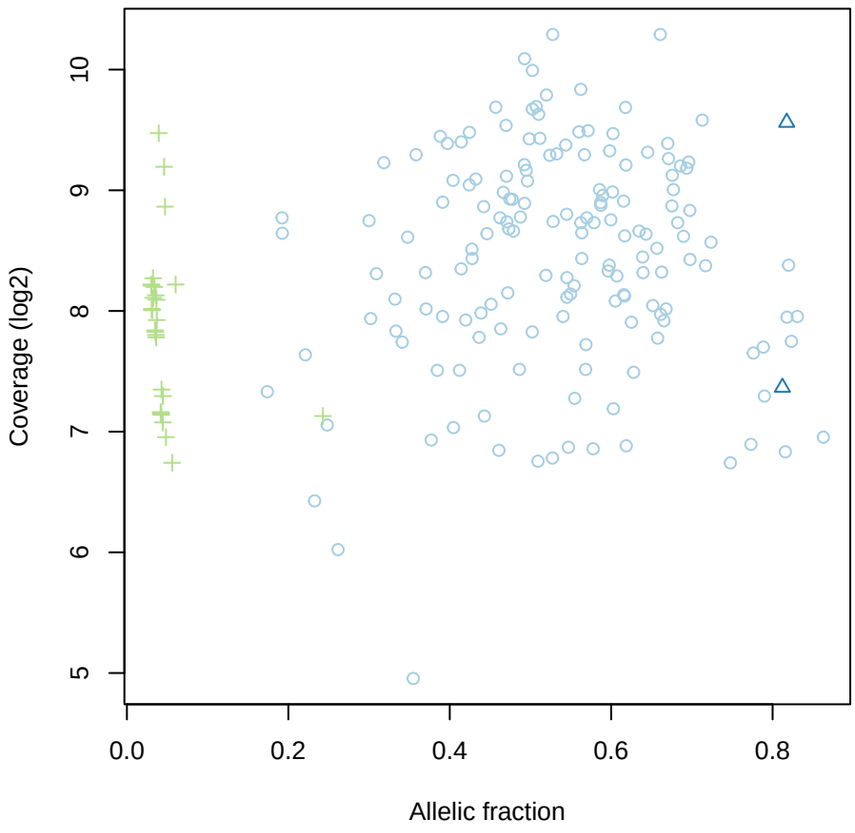

Purity: 0.85 Tumor ploidy: 4.462
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

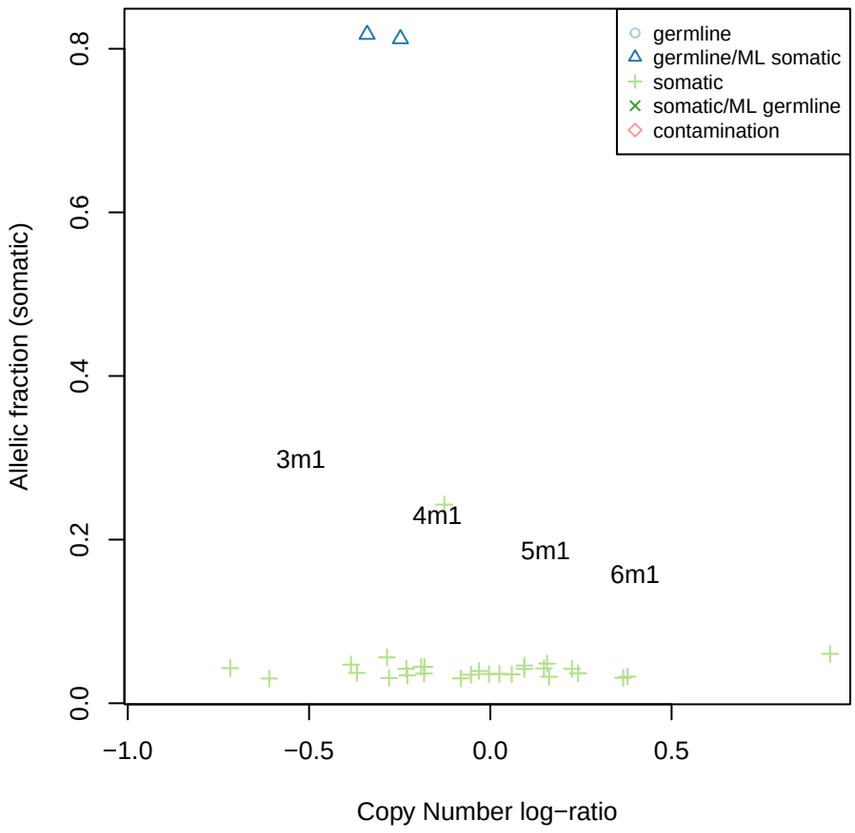

Purity: 0.85 Tumor ploidy: 4.462 SNV log−likelihood: −655.1 GoF: 71.8% Mean coverage: 391;505
1 2 3 4 5 6 7 8 9 11 12 13 15 16 17 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

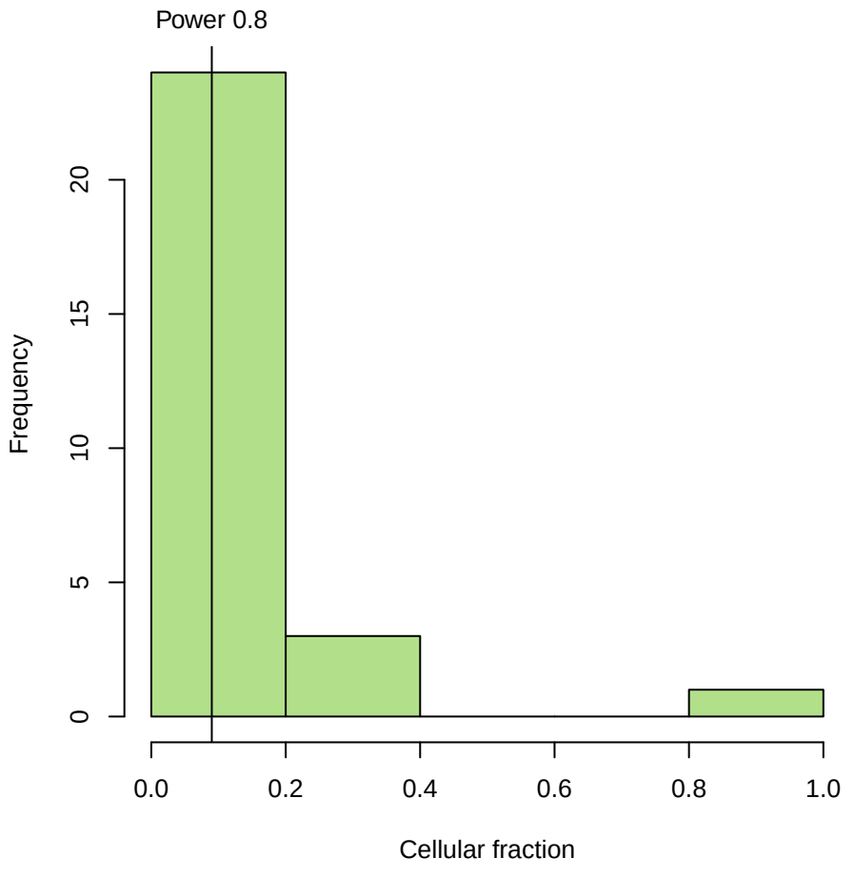

SCNA−fit log−likelihood: −7055.52
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
2 3 4 5 6 7
0 50 100 150
SNV Index

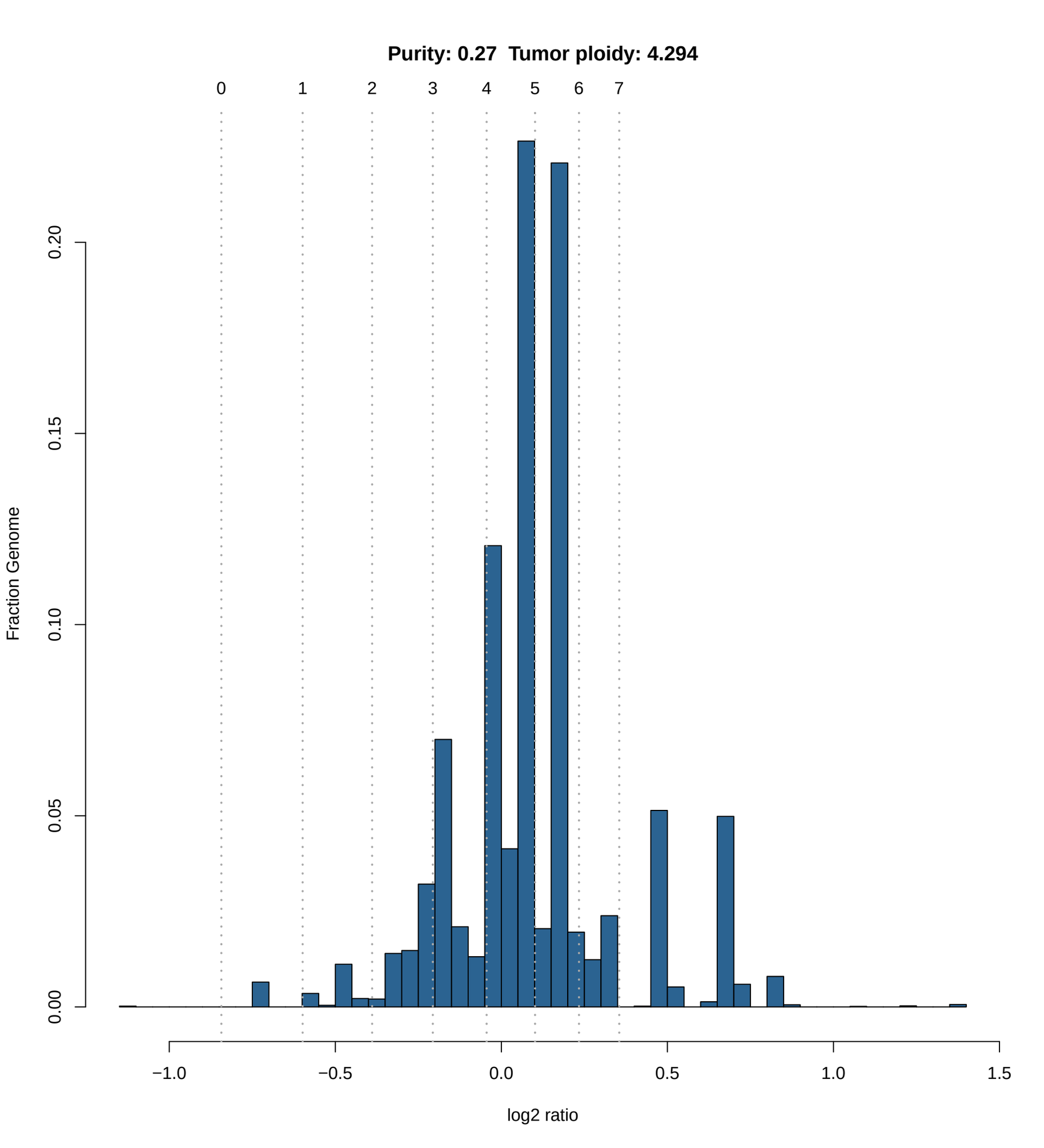

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

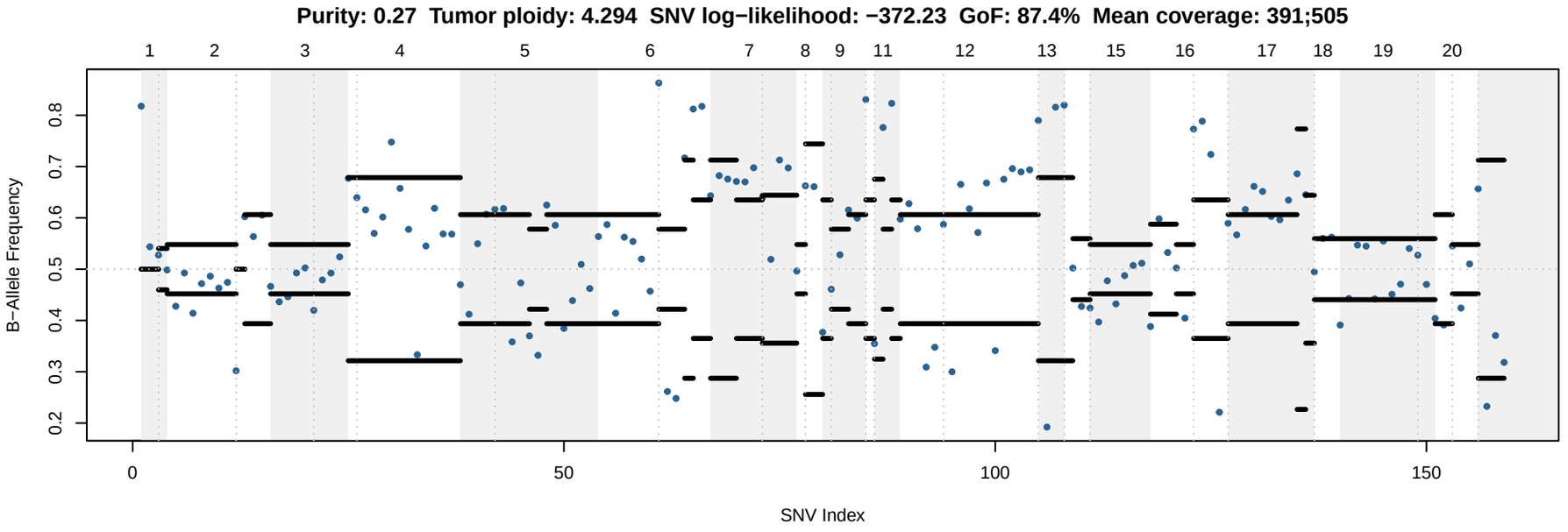

Allelic fraction (germline)
Copy Number log−ratio
5m4
4m3
7m5
3m2
5m3
1
4m2
6m3
5m2
3m1
4m1

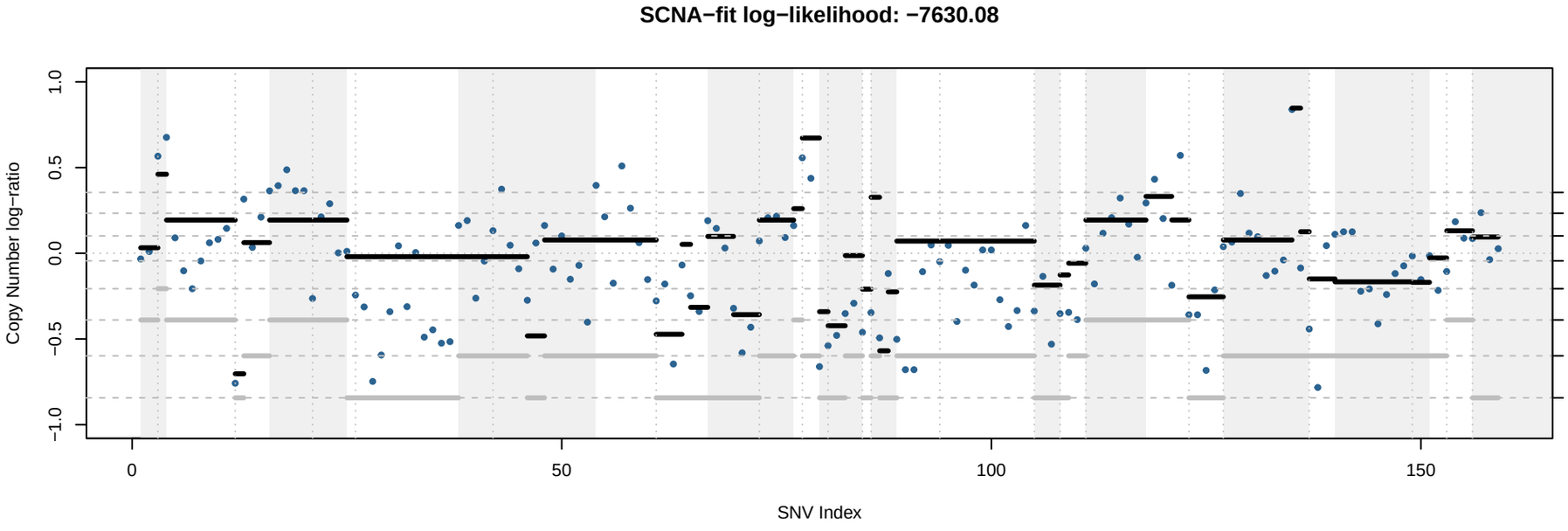

Coverage (log2)
Allelic fraction

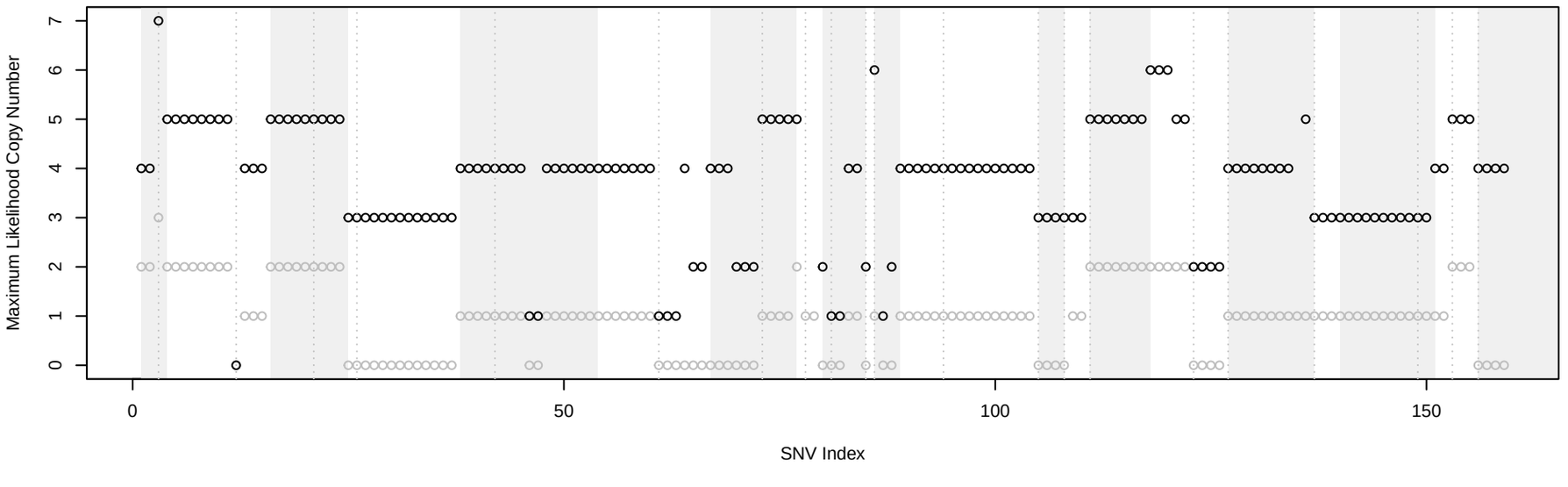

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m1
4m1
5m1
6m1

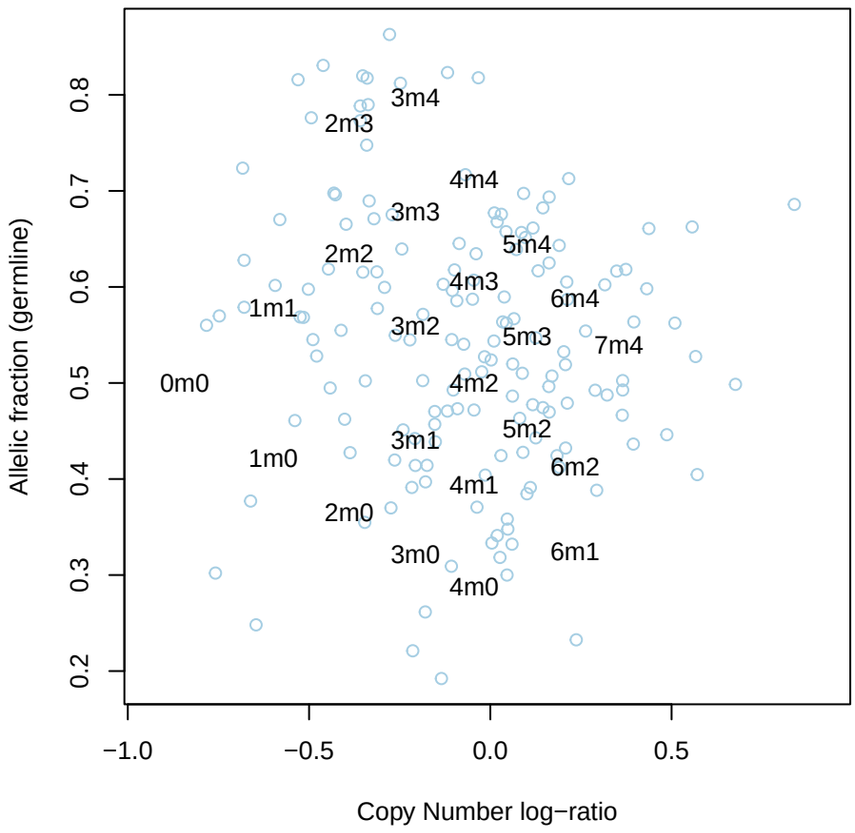

Power 0.8
Frequency
Cellular fraction

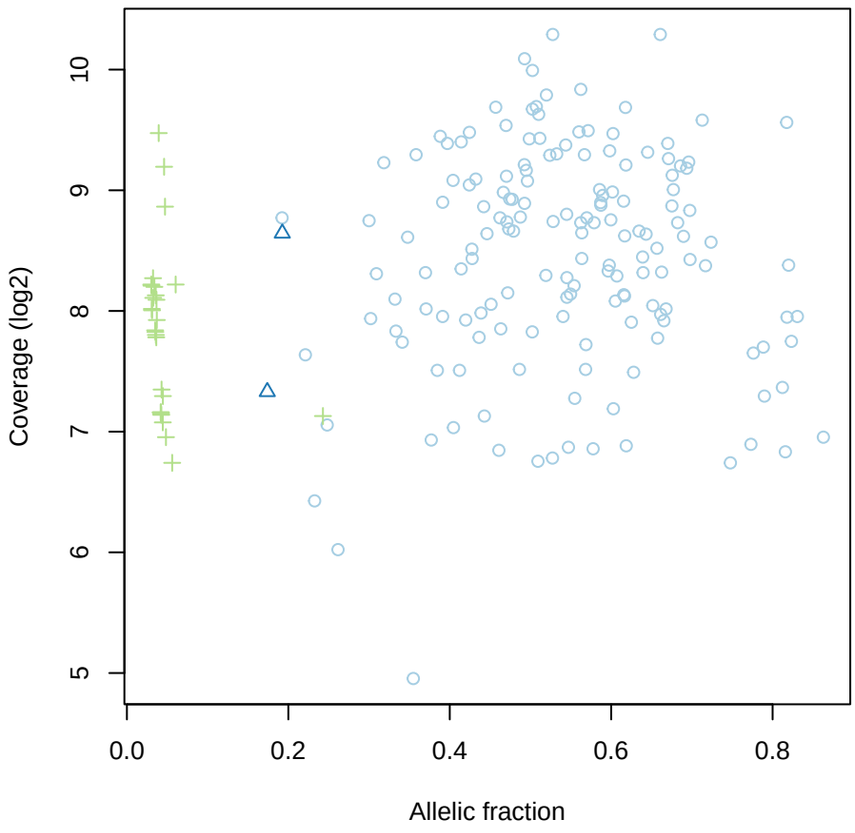

Purity: 0.27 Tumor ploidy: 4.294
0
1
2
3
4
5
6
7
0.00
0.05
0.10
0.15
0.20
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

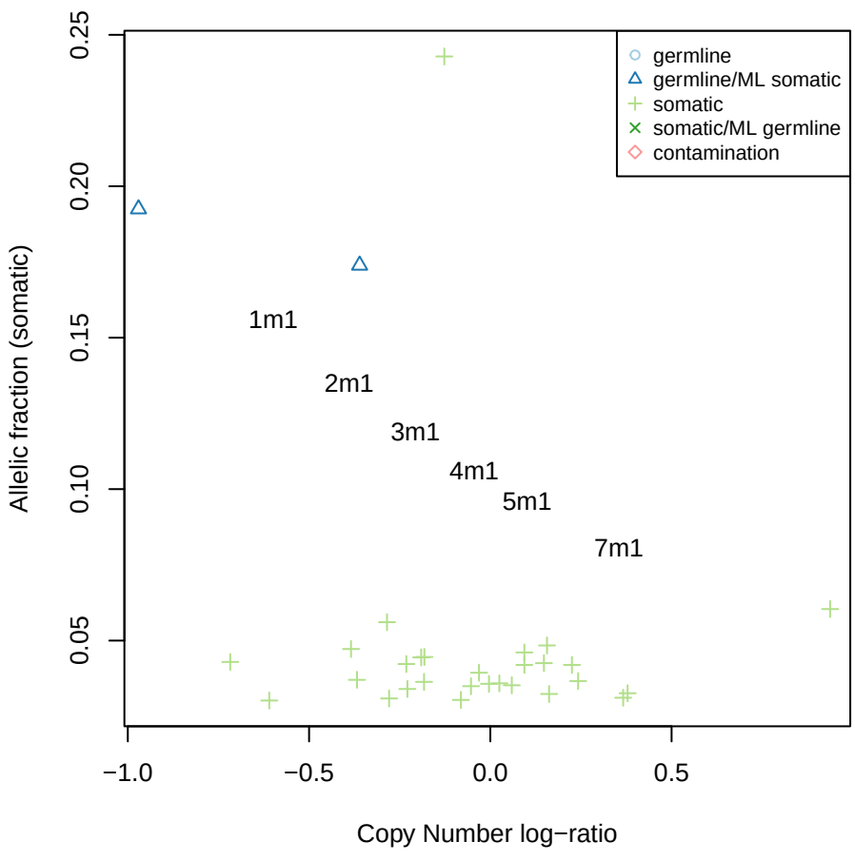

Purity: 0.27 Tumor ploidy: 4.294 SNV log−likelihood: −372.23 GoF: 87.4% Mean coverage: 391;505
1 2 3 4 5 6 7 8 9 11 12 13 15 16 17 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

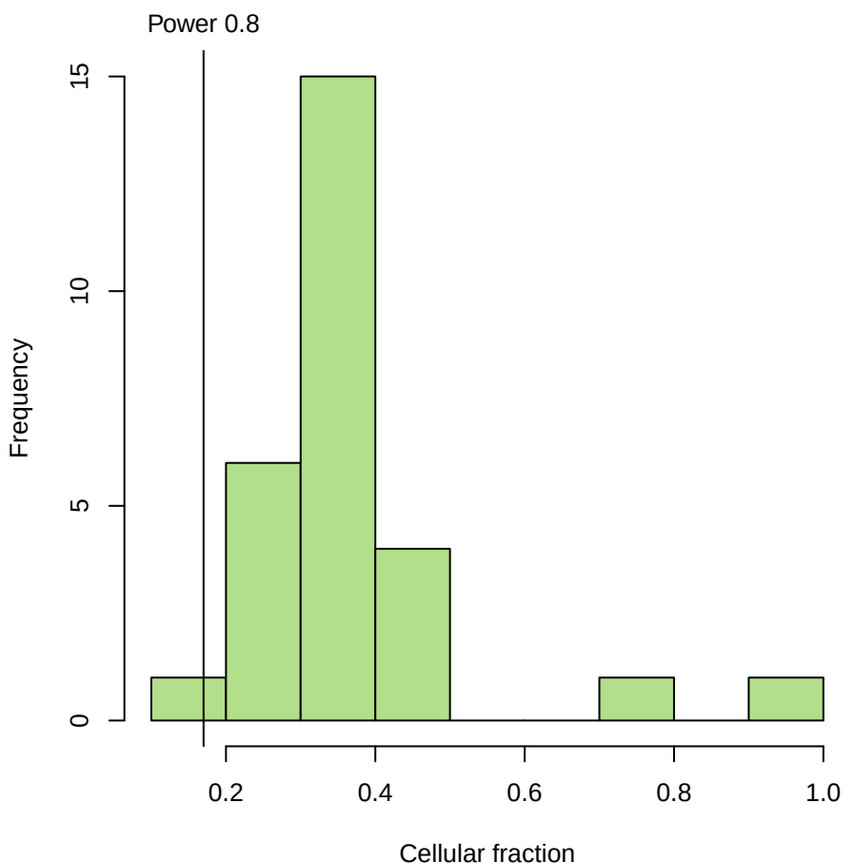

SCNA−fit log−likelihood: −7630.08
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 7
0 50 100 150
SNV Index

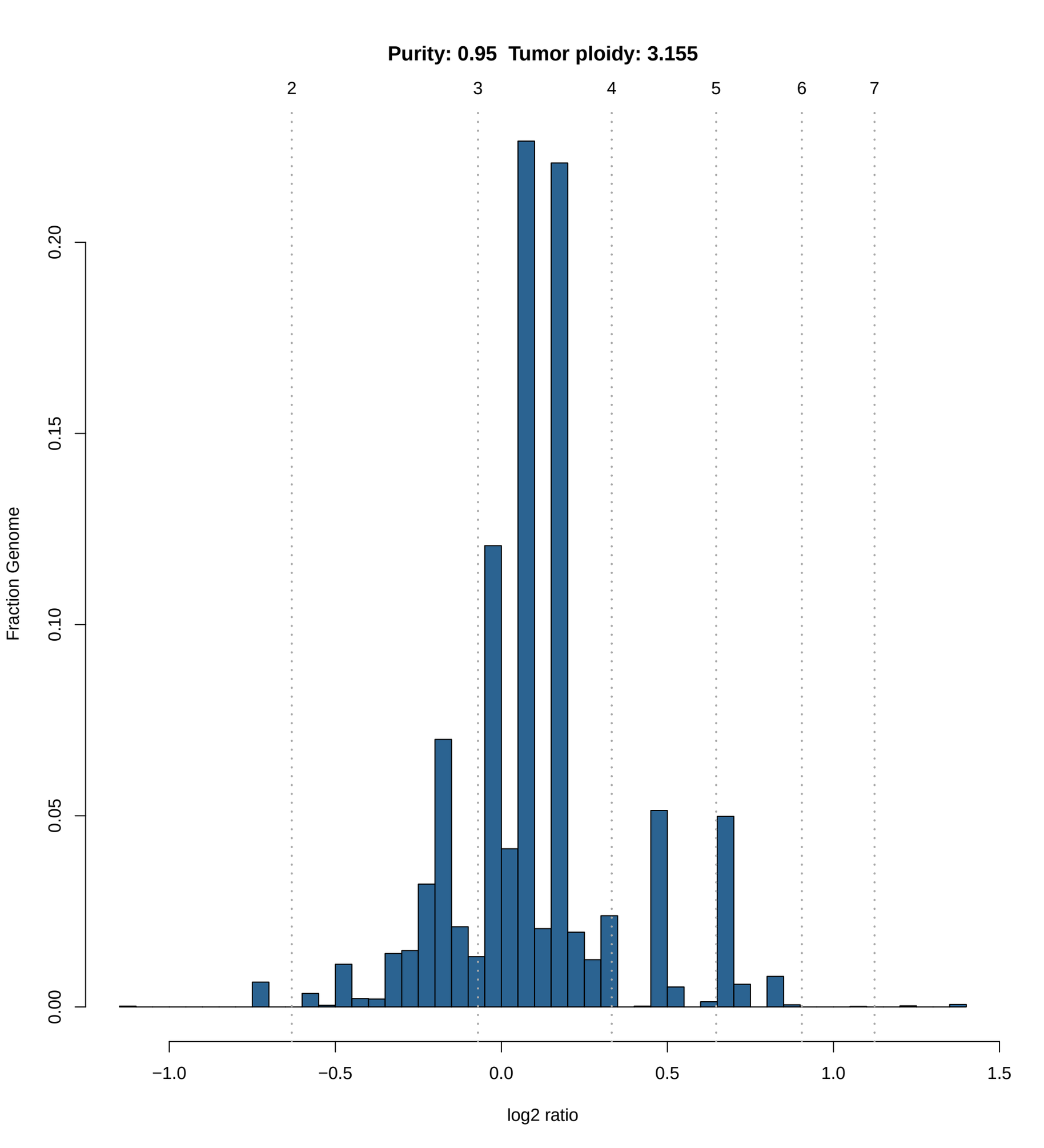

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

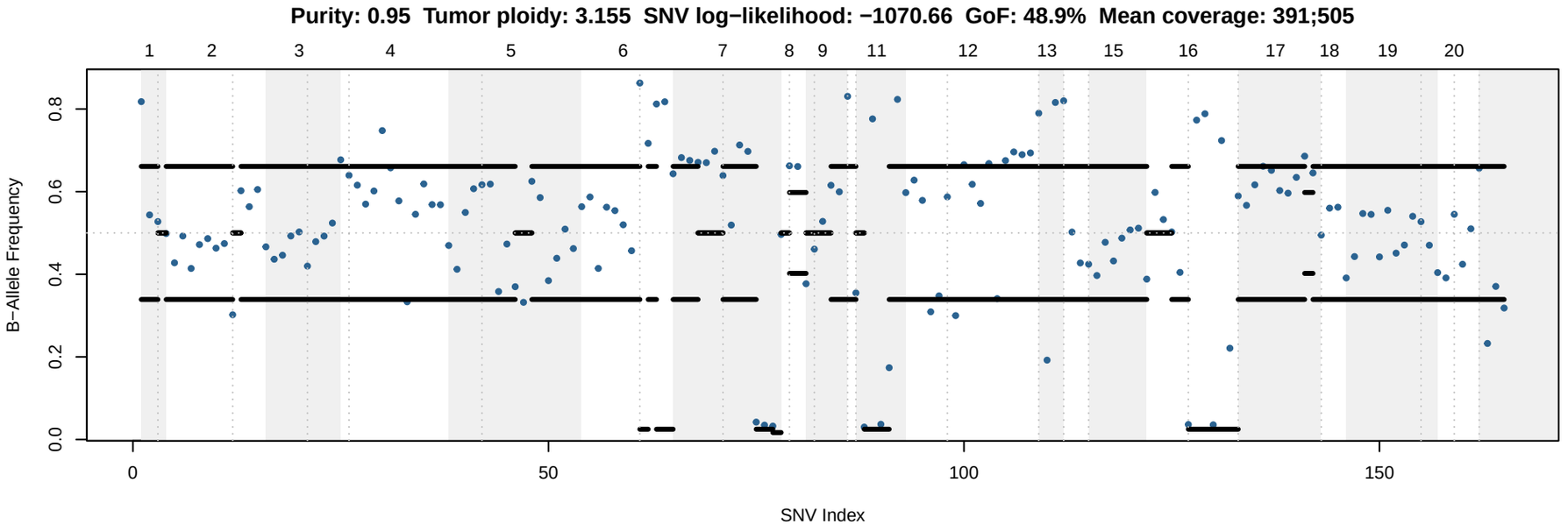

Allelic fraction (germline)
Copy Number log−ratio
0m0
1m0
1m1
2m0
2m2
2m3
3m0
3m1
3m2
3m3
3m4
4m0
4m1
4m2
4m3
4m4
5m2
5m3
5m4
6m1
6m2
6m4
7m4

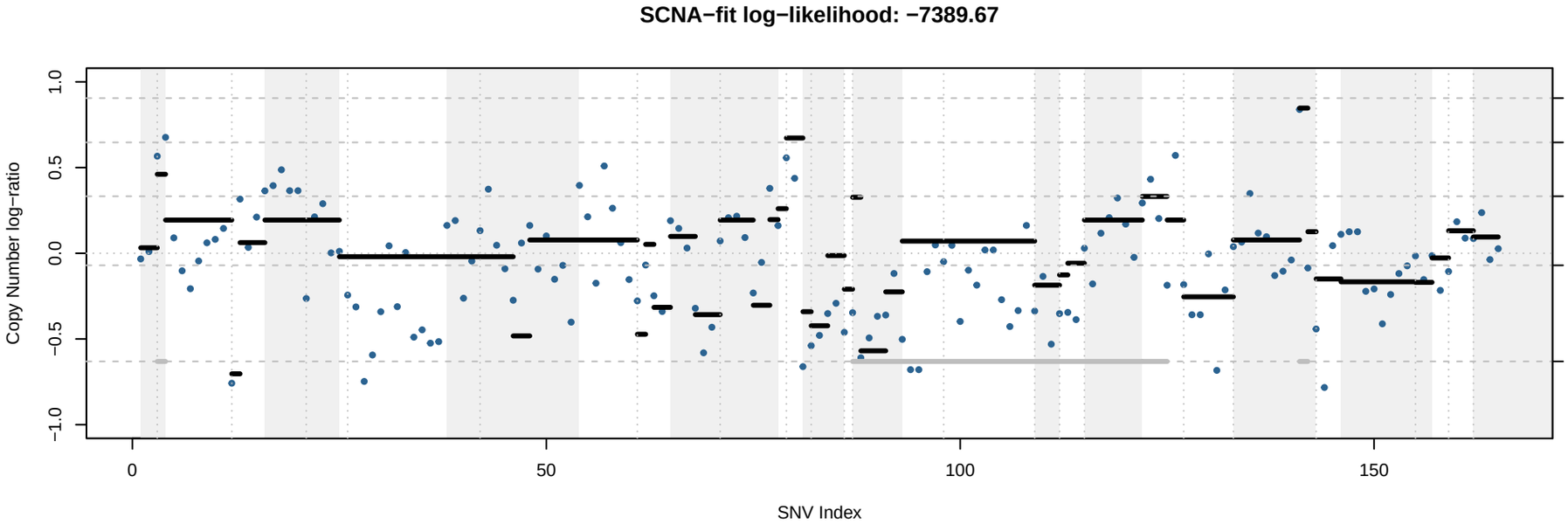

Coverage (log2)
Allelic fraction

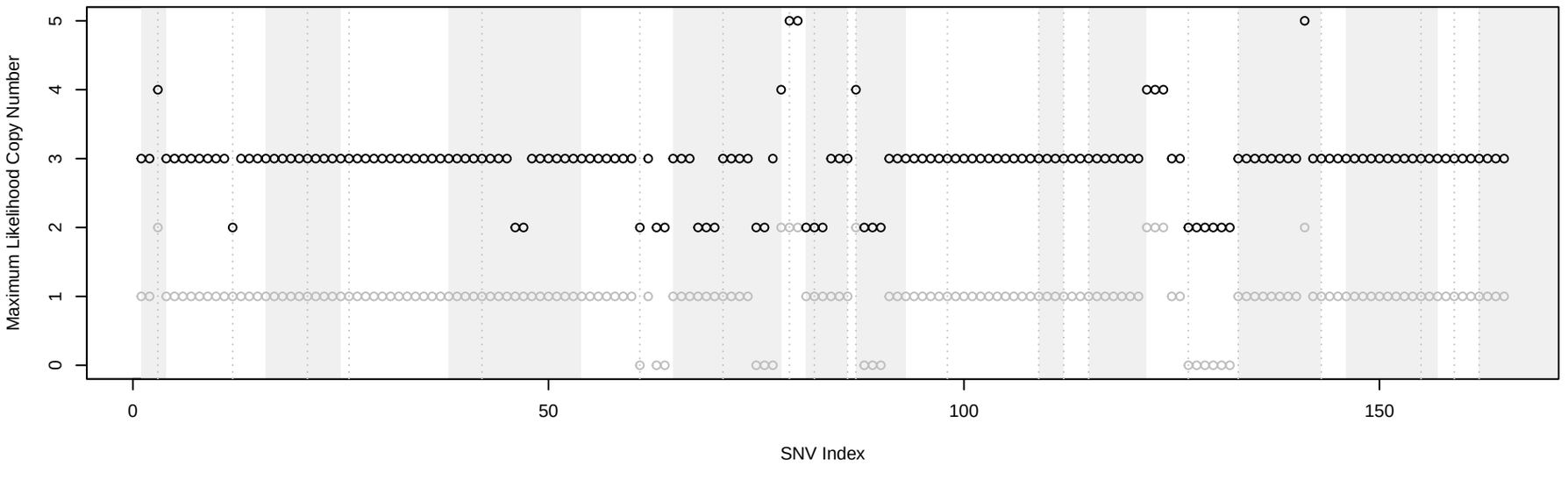

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
4m1
5m1
7m1

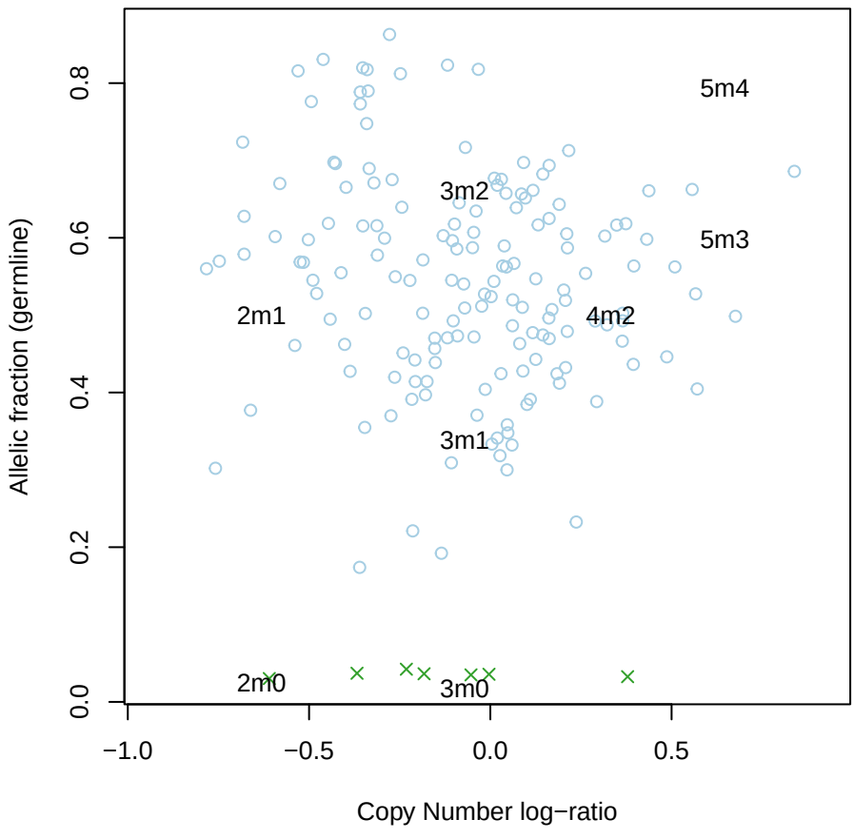

Power 0.8
Frequency
Cellular fraction

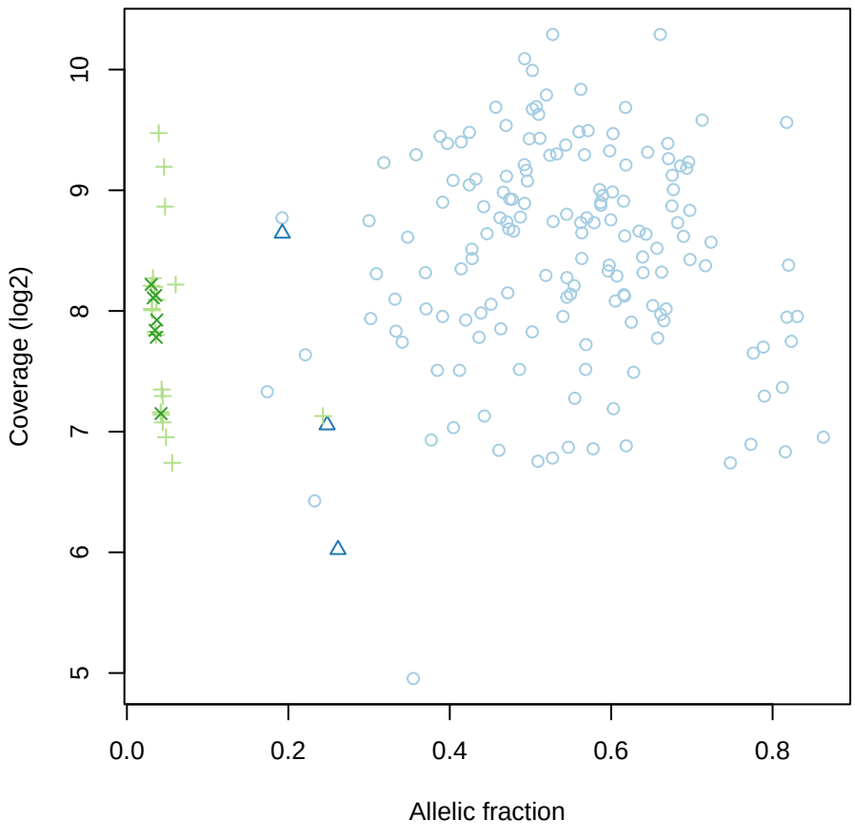

Purity: 0.95 Tumor ploidy: 3.155
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

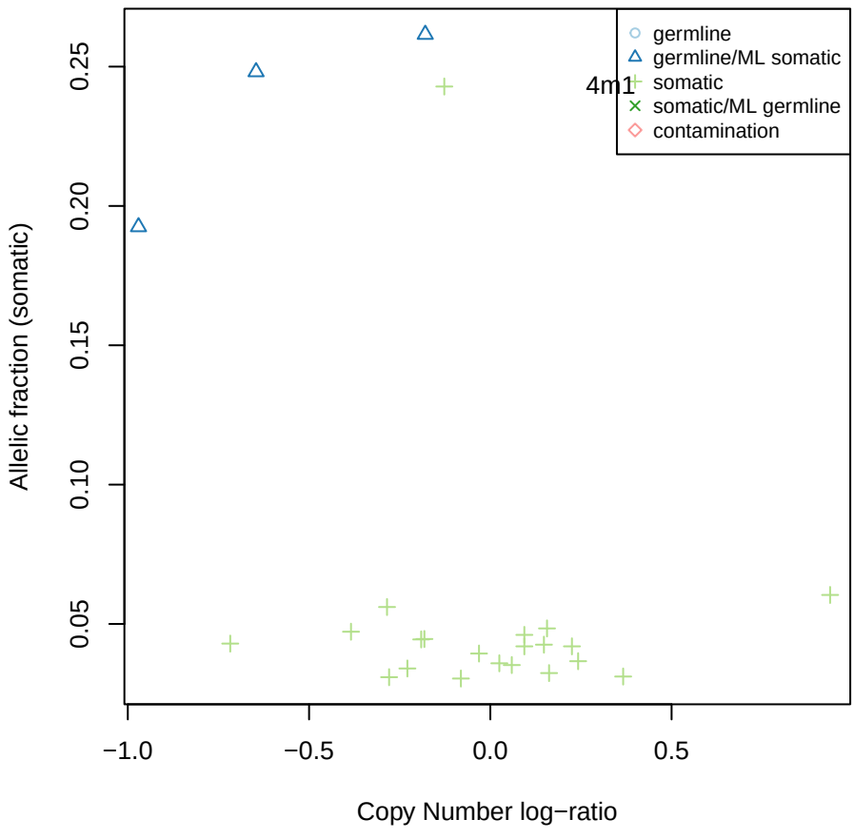

Purity: 0.95 Tumor ploidy: 3.155 SNV log−likelihood: −1070.66 GoF: 48.9% Mean coverage: 391;505
1 2 3 4 5 6 7 8 9 11 12 13 15 16 17 18 19 20
B−Allele Frequency
0.0 0.2 0.4 0.6 0.8
0 50 100 150
SNV Index

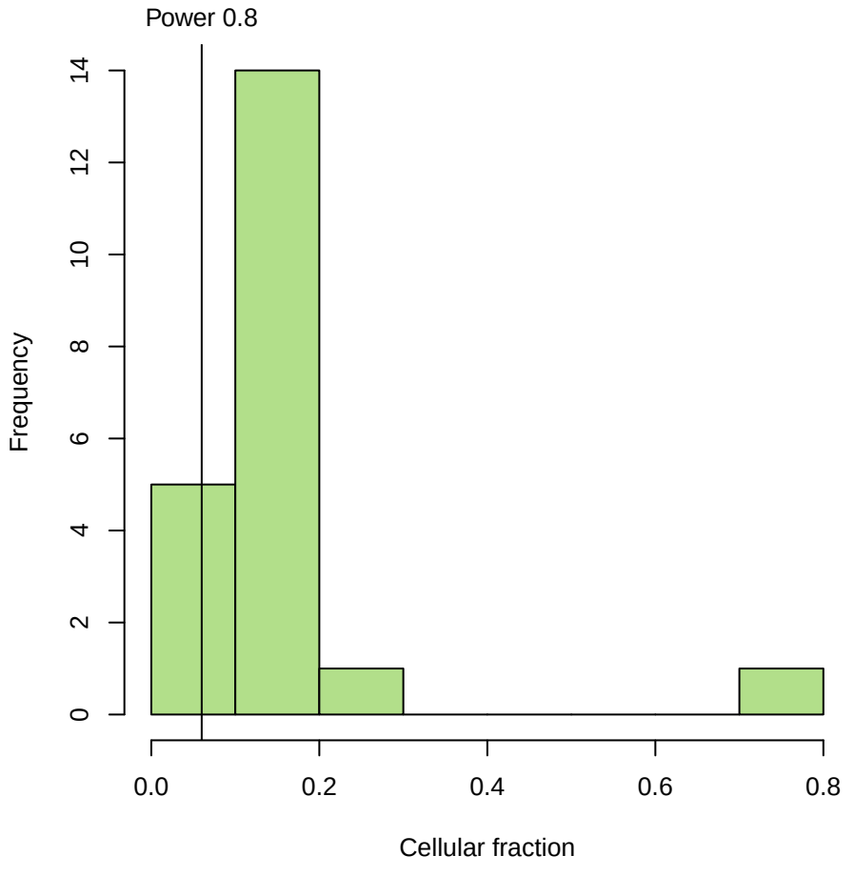

SCNA−fit log−likelihood: −7389.67
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6
0 50 100 150
SNV Index


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


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


Coverage (log2)
Allelic fraction


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


Power 0.8
Frequency
Cellular fraction