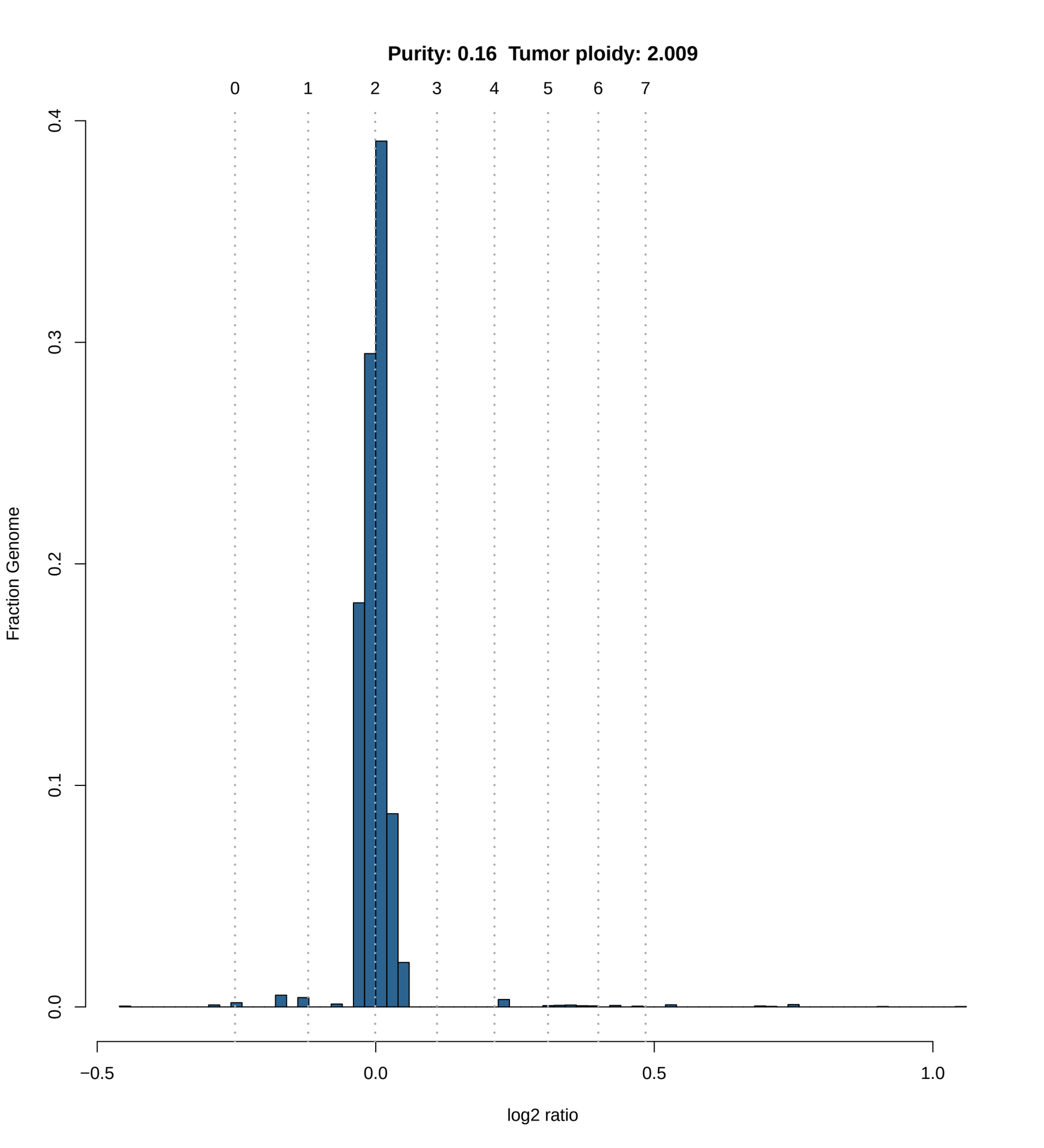
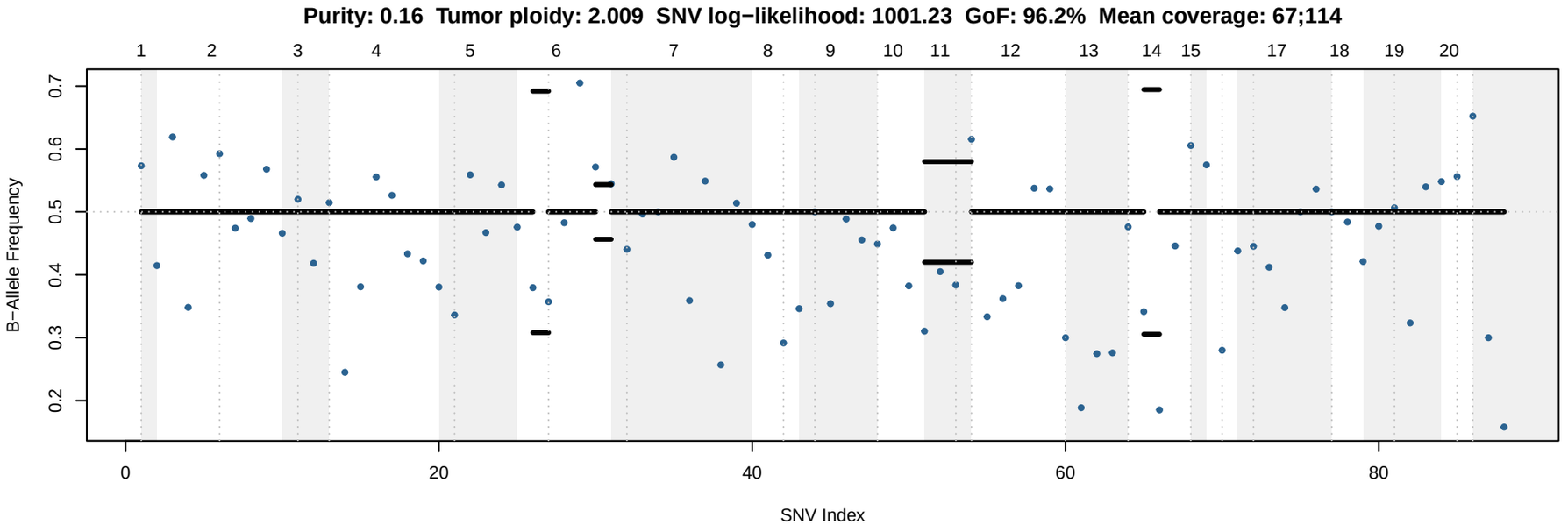
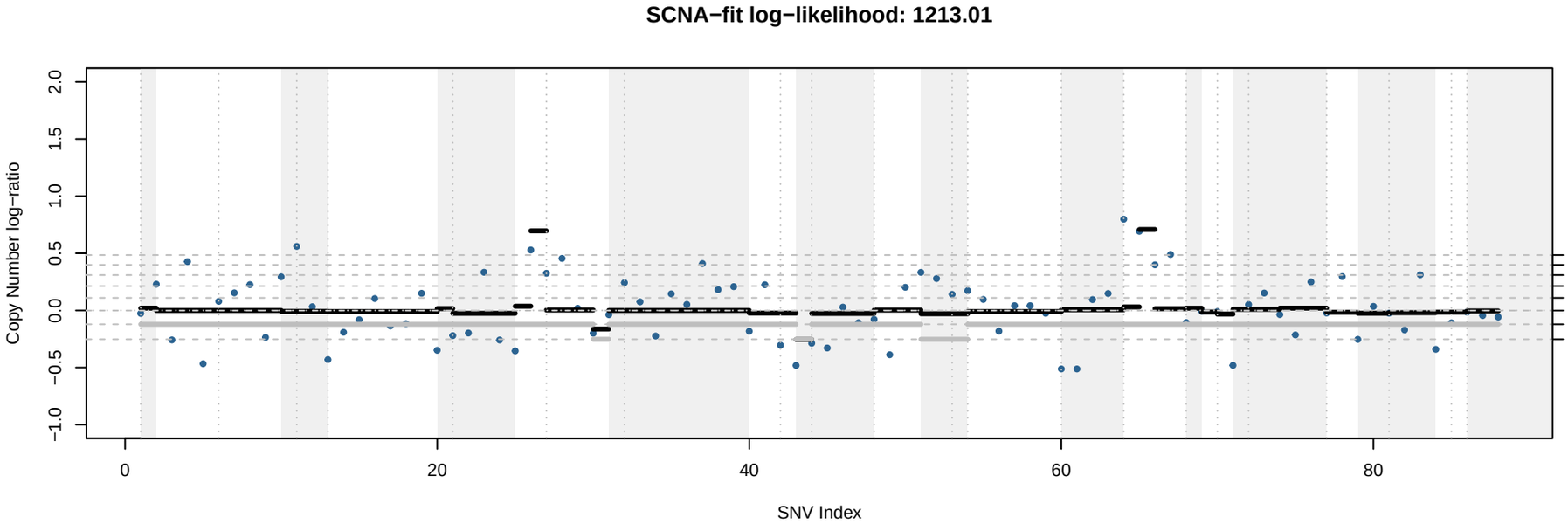
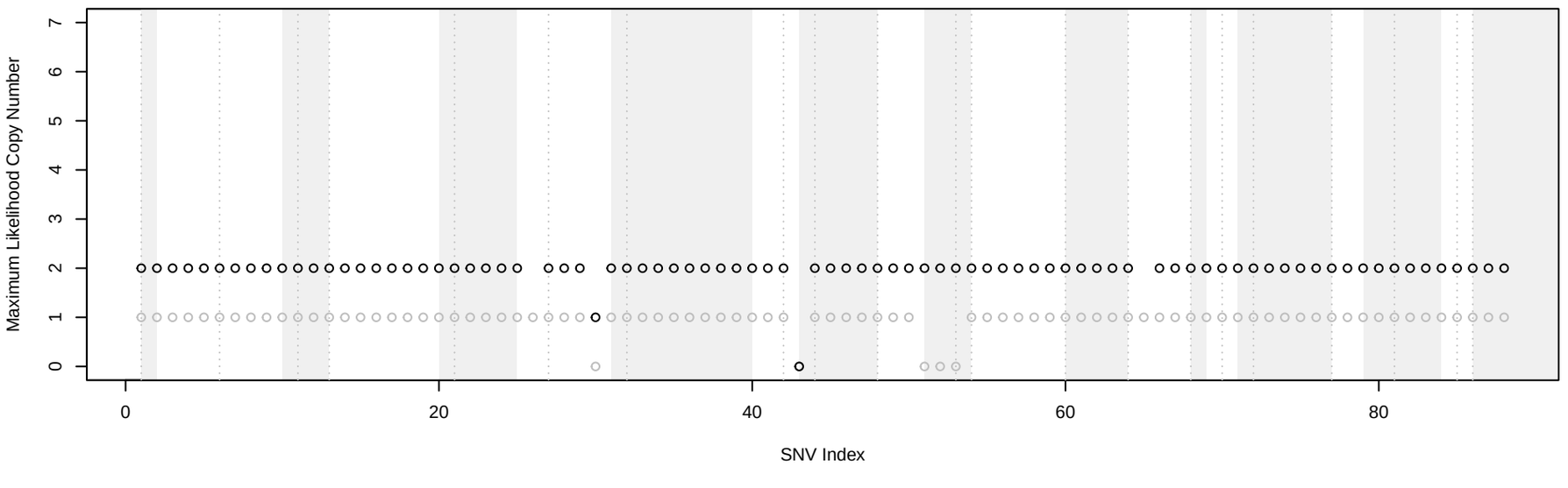
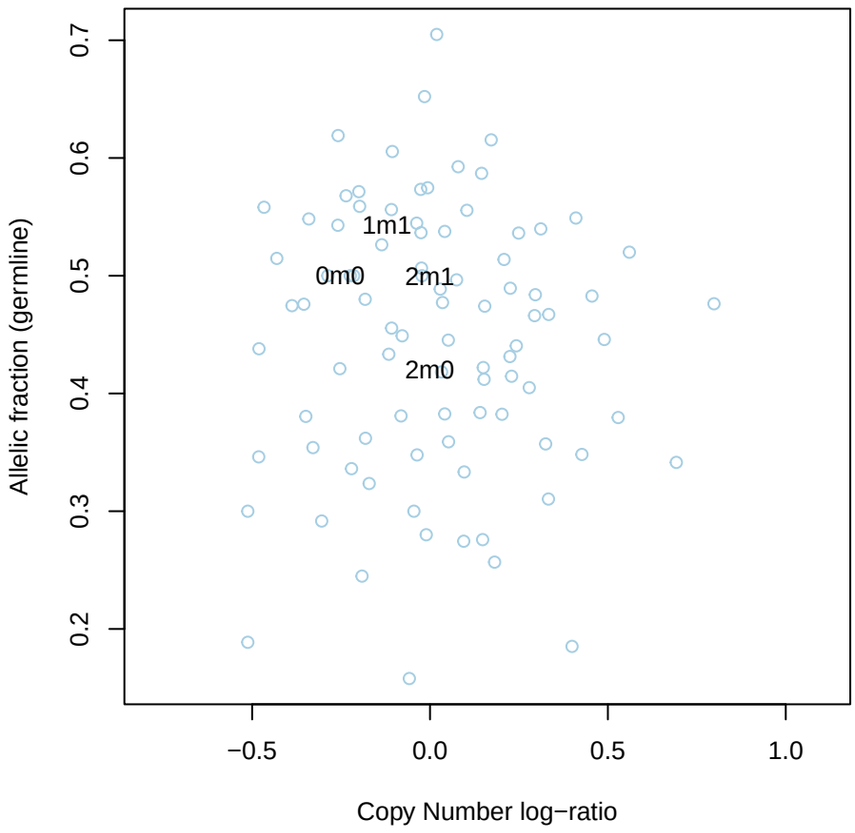
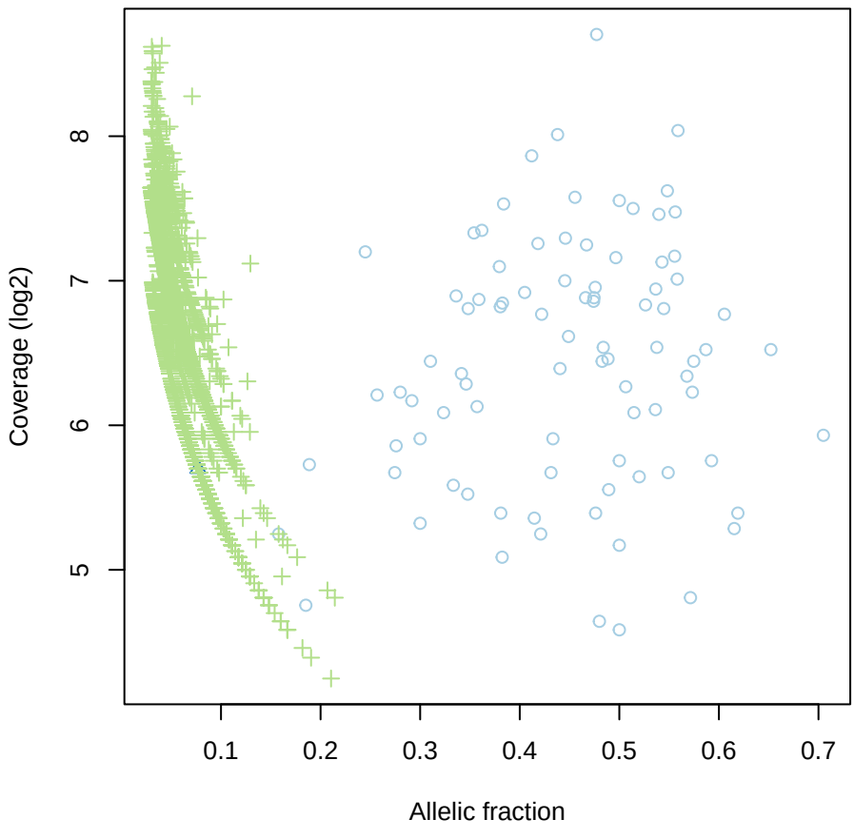

Purity: 0.16 Tumor ploidy: 2.009
0
1
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

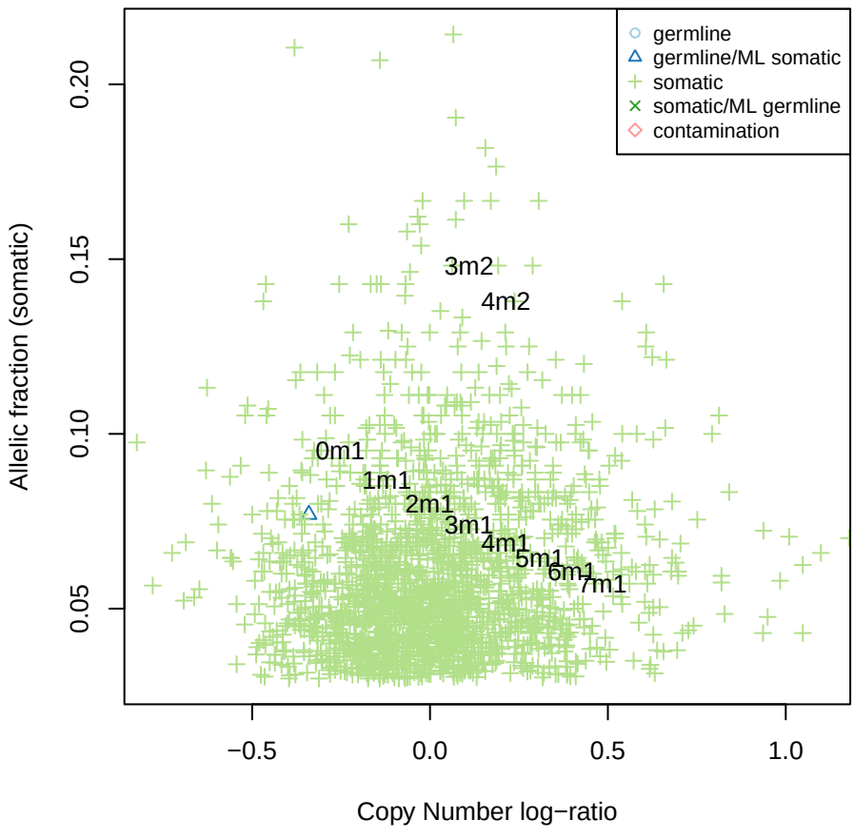

Purity: 0.16 Tumor ploidy: 2.009 SNV log−likelihood: 1001.23 GoF: 96.2% Mean coverage: 67;114
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

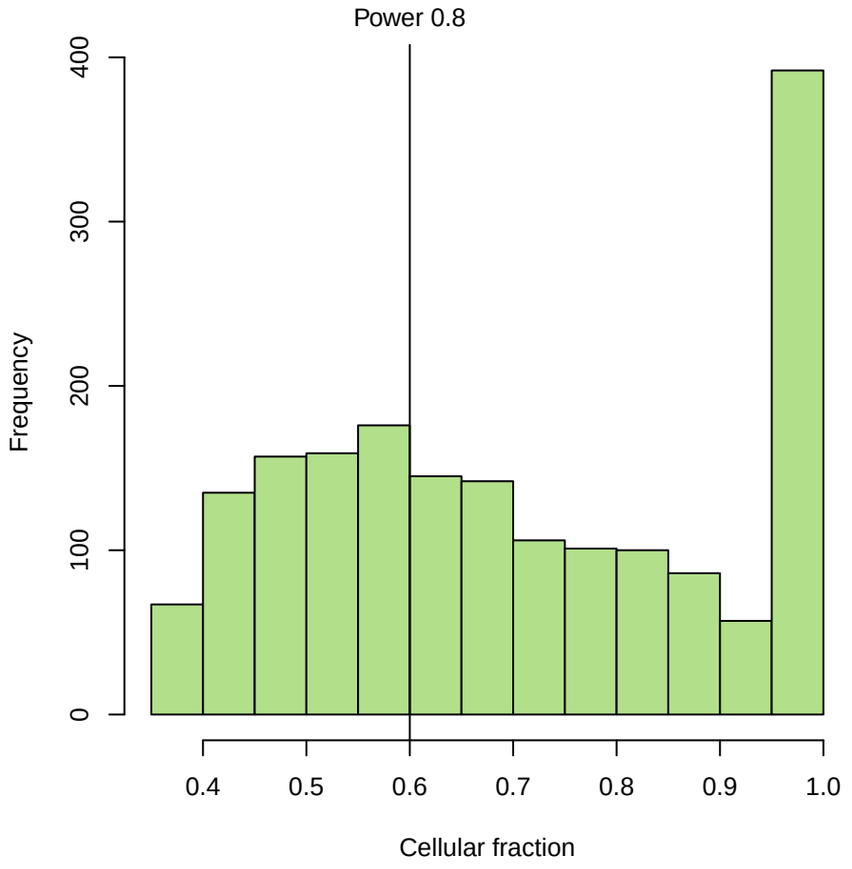

SCNA−fit log−likelihood: 1213.01
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
0 2 5
0 20 40 60 80
SNV Index

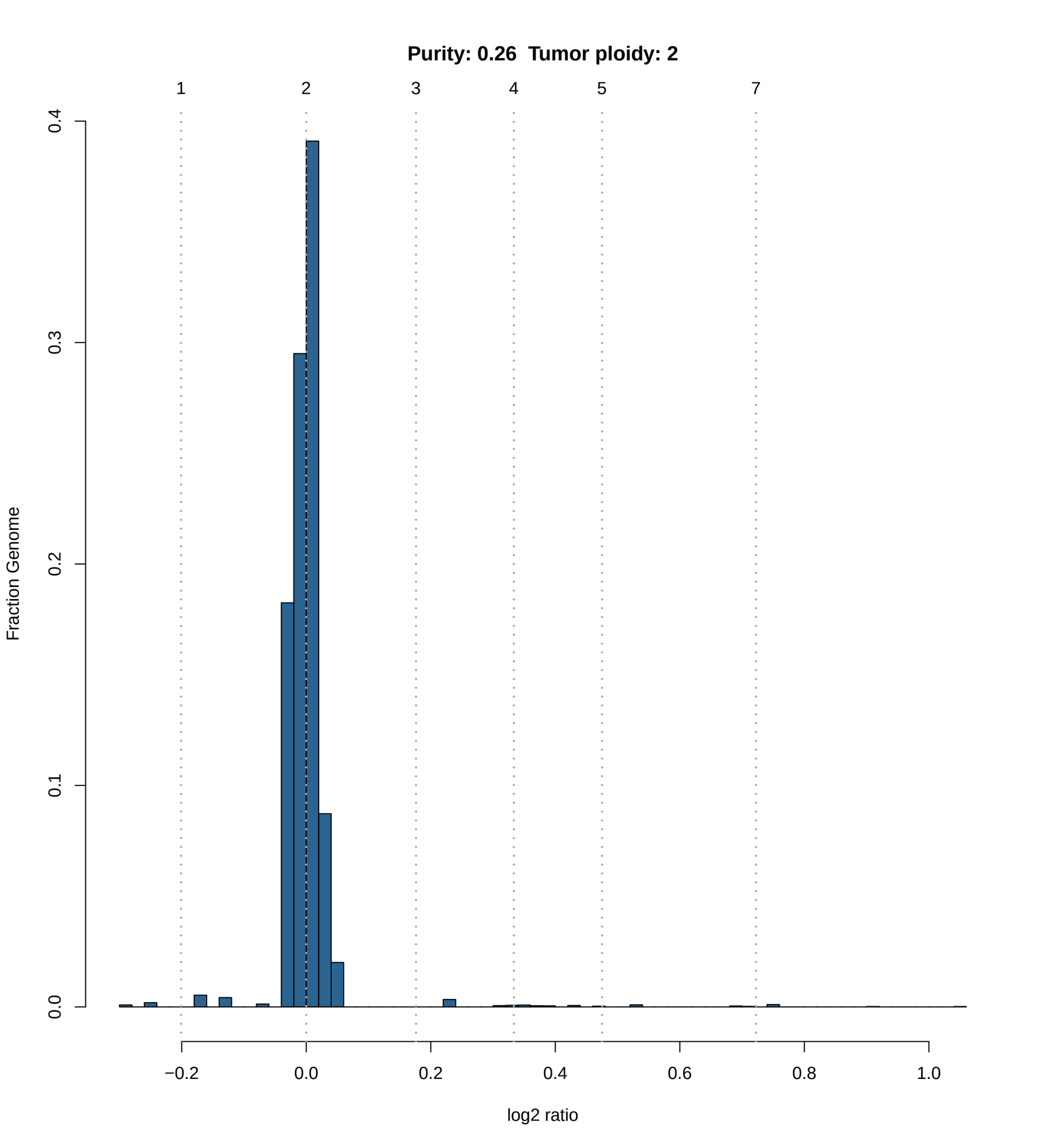

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

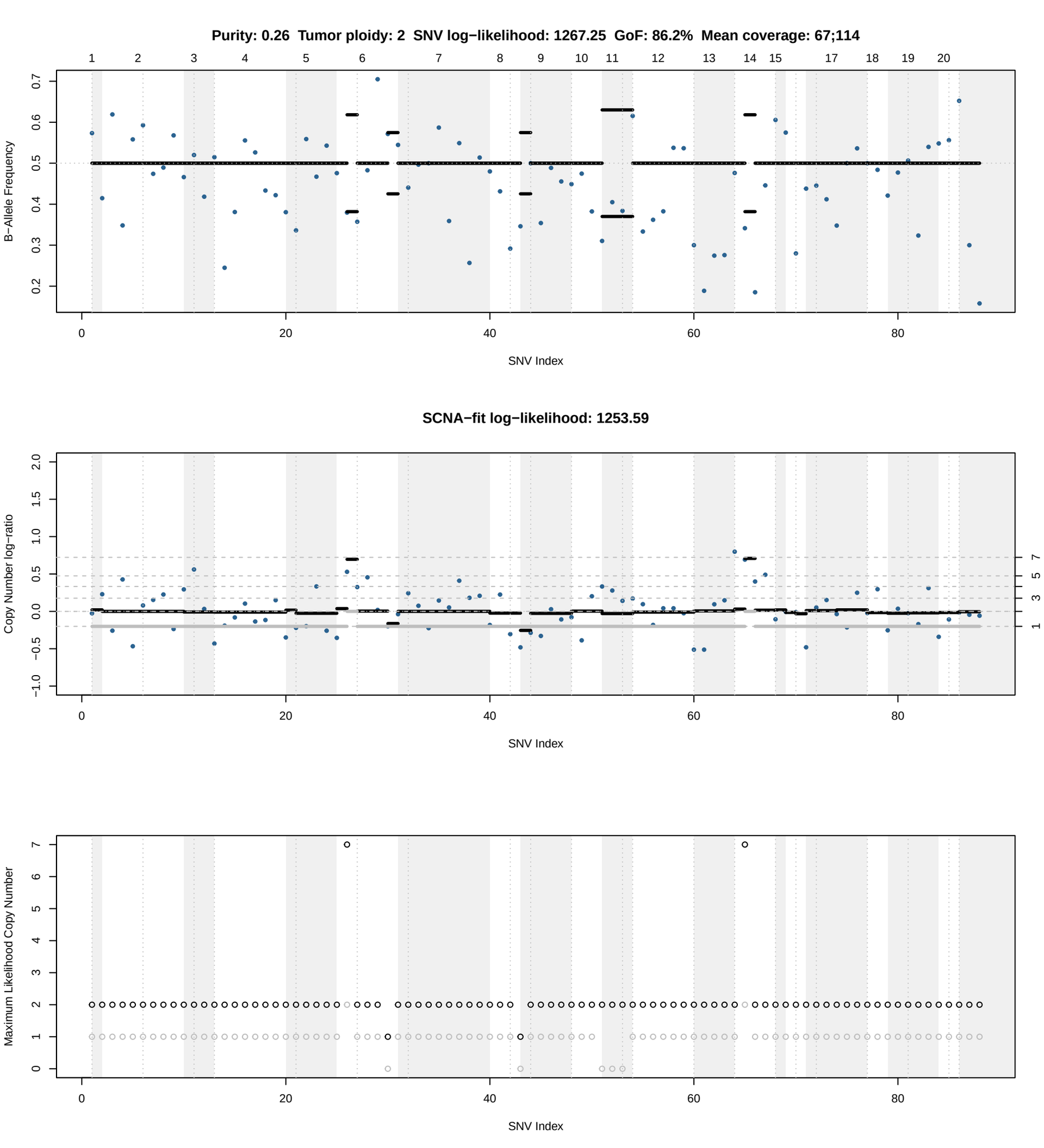

Allelic fraction (germline)
Copy Number log−ratio
1m1
0m0
2m1
2m0

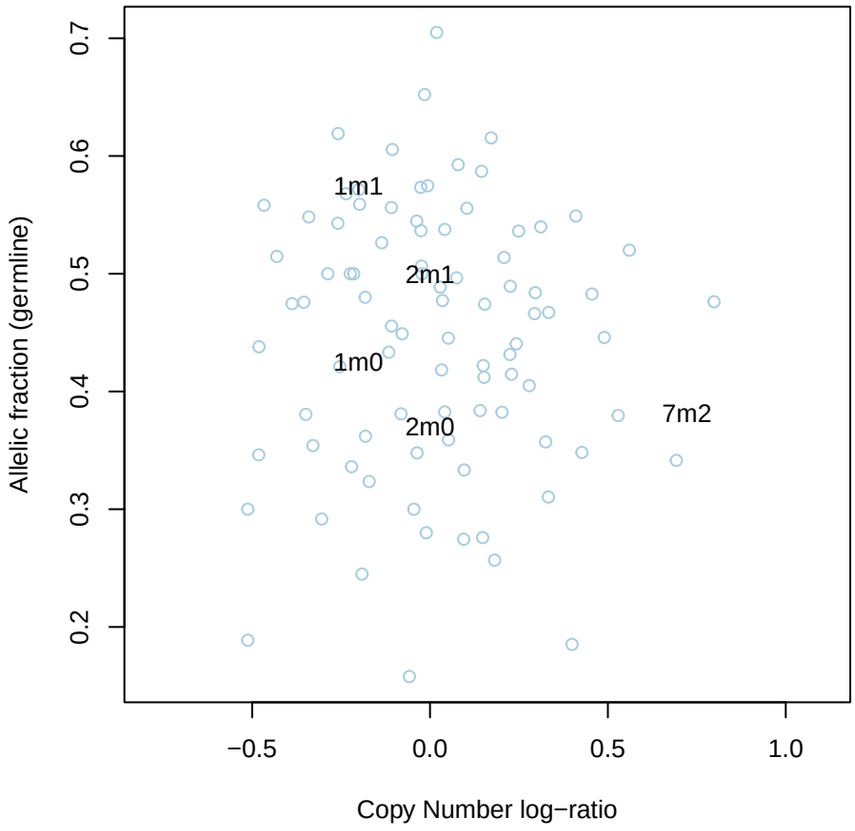

Coverage (log2)
Allelic fraction

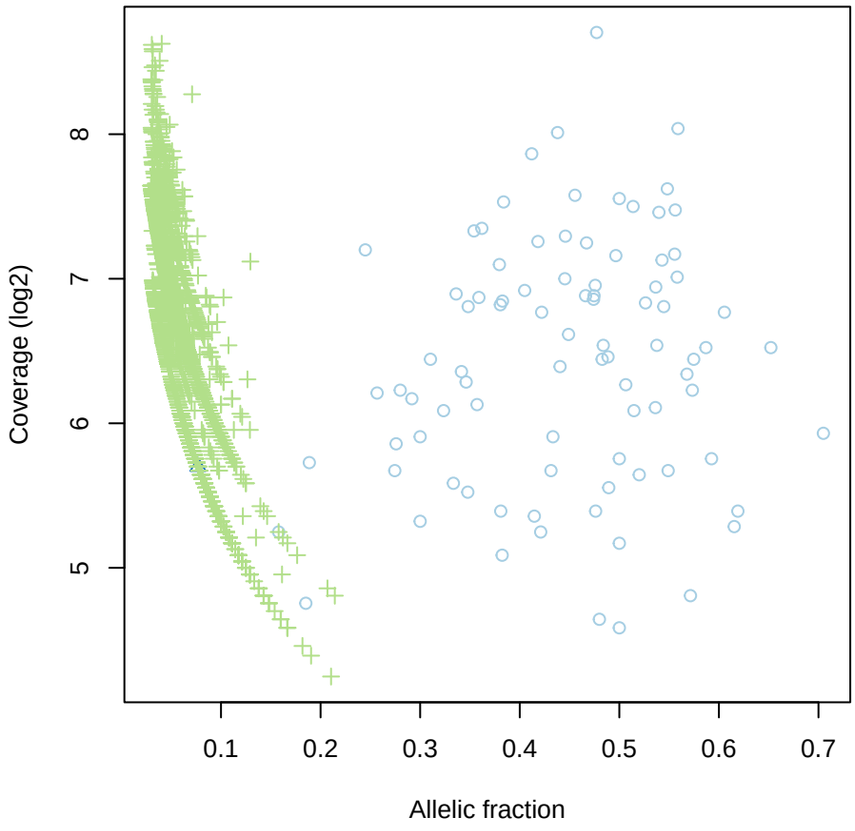

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m2
4m2
0m1
1m1
2m1
3m1
4m1
5m1
6m1
7m1

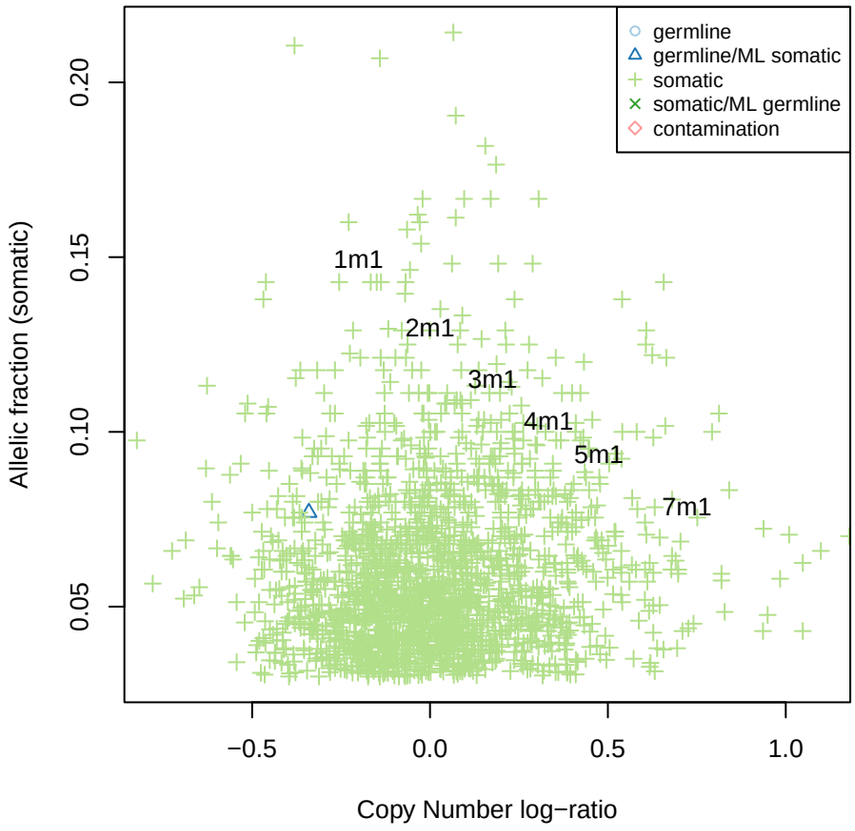

Power 0.8
Frequency
Cellular fraction

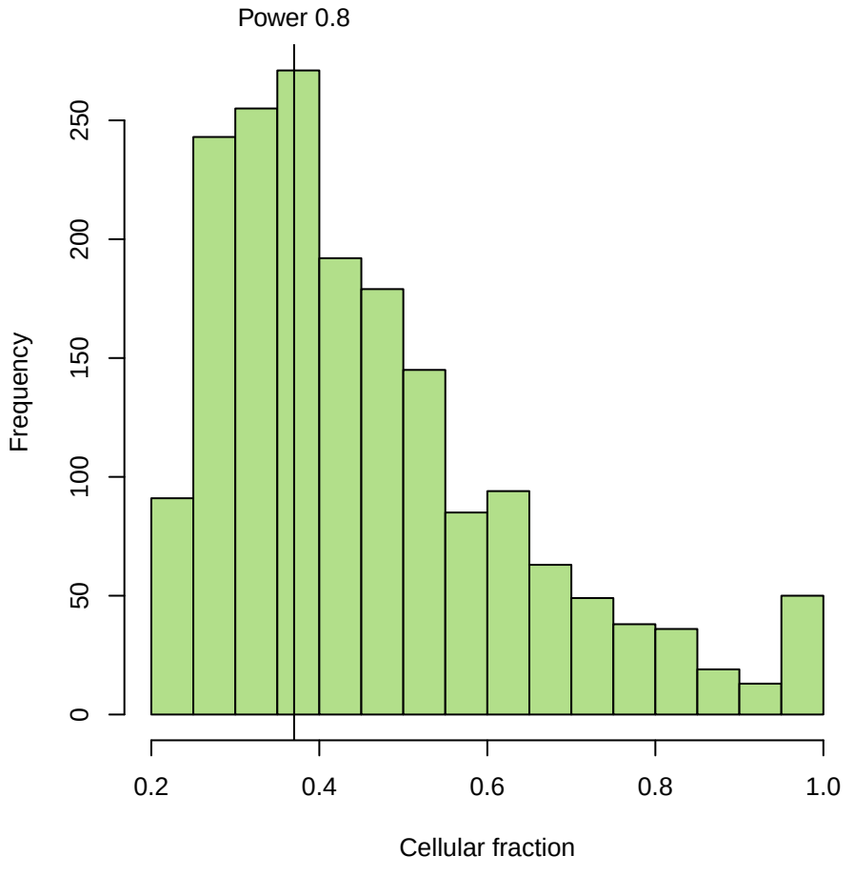

Purity: 0.26 Tumor ploidy: 2
1
2
3
4
5
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.2
0.0
0.2
0.4
0.6
0.8
1.0
log2 ratio

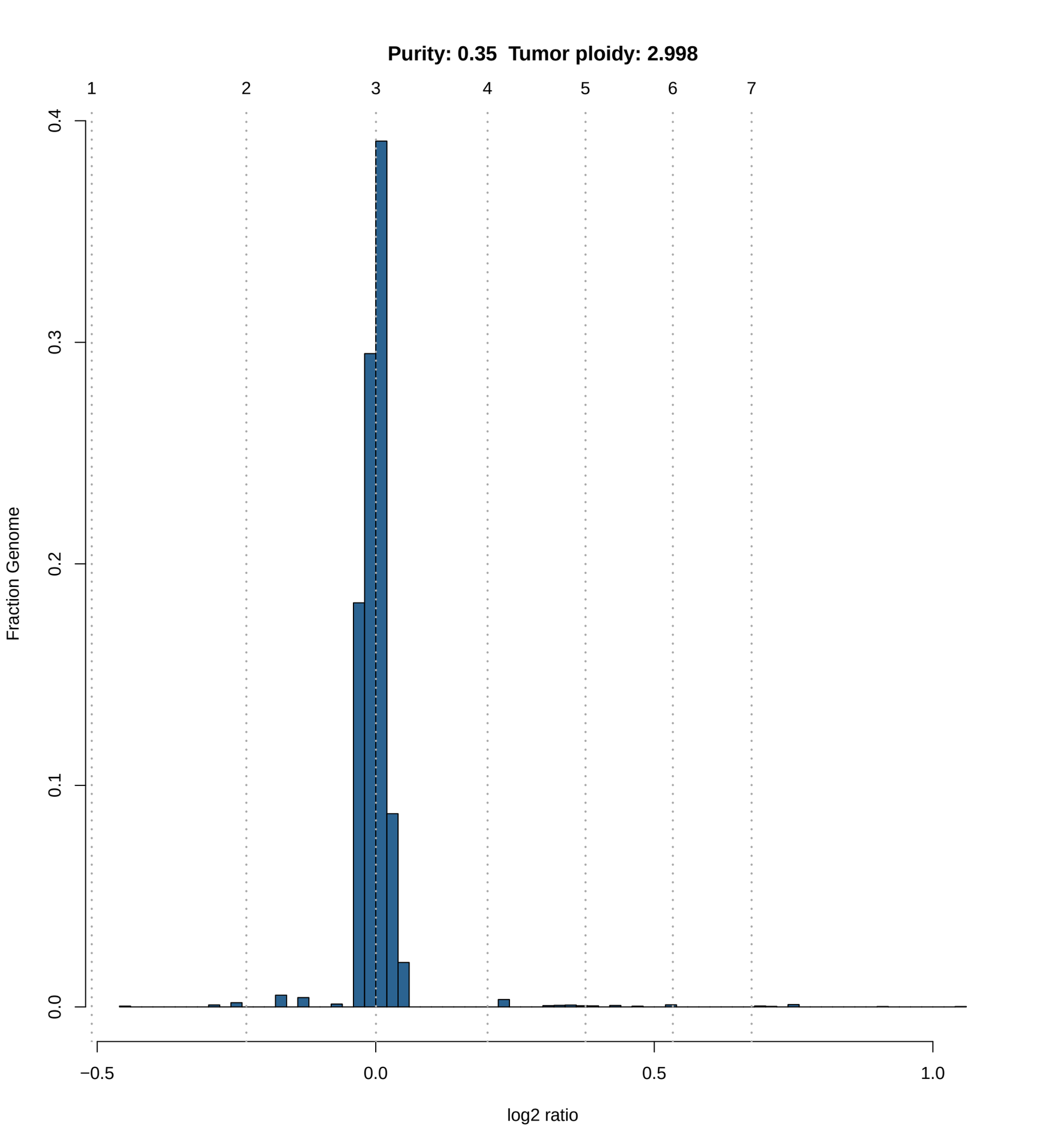

Purity: 0.26 Tumor ploidy: 2 SNV log−likelihood: 1267.25 GoF: 86.2% Mean coverage: 67;114
B−Allele Frequency
SNV Index
SCNA−fit log−likelihood: 1253.59
Copy Number log−ratio
SNV Index
Maximum Likelihood Copy Number
SNV Index

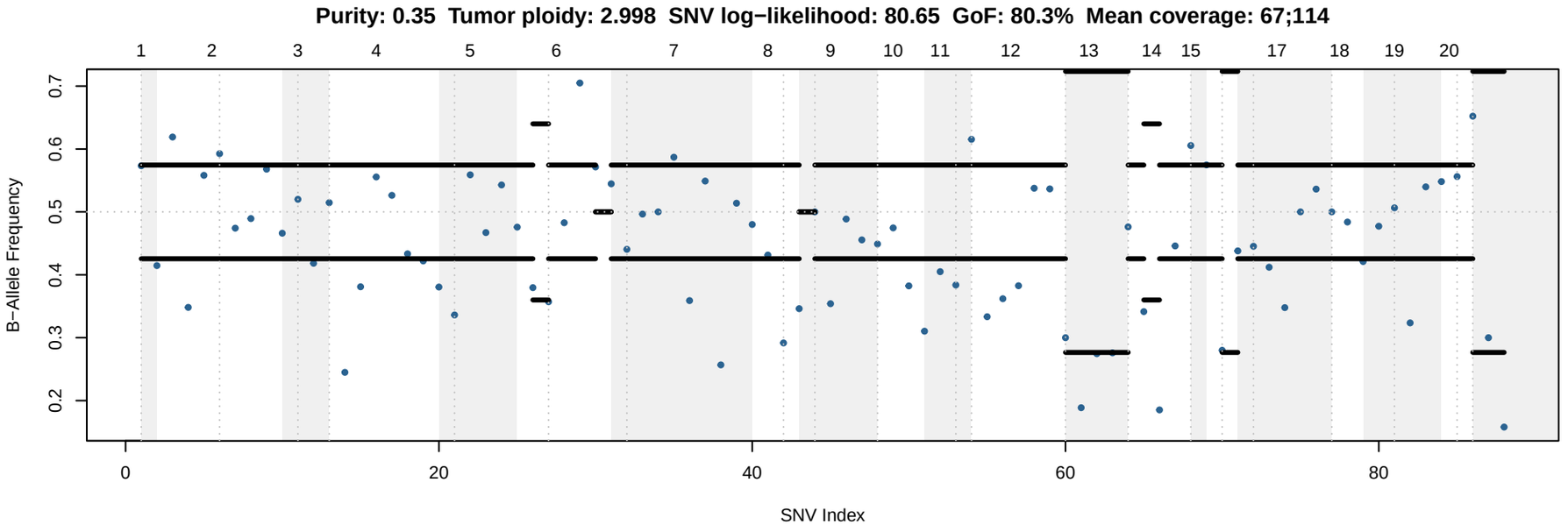

Allelic fraction (germline)
Copy Number log−ratio
1m1
2m1
1m0
2m0
7m2

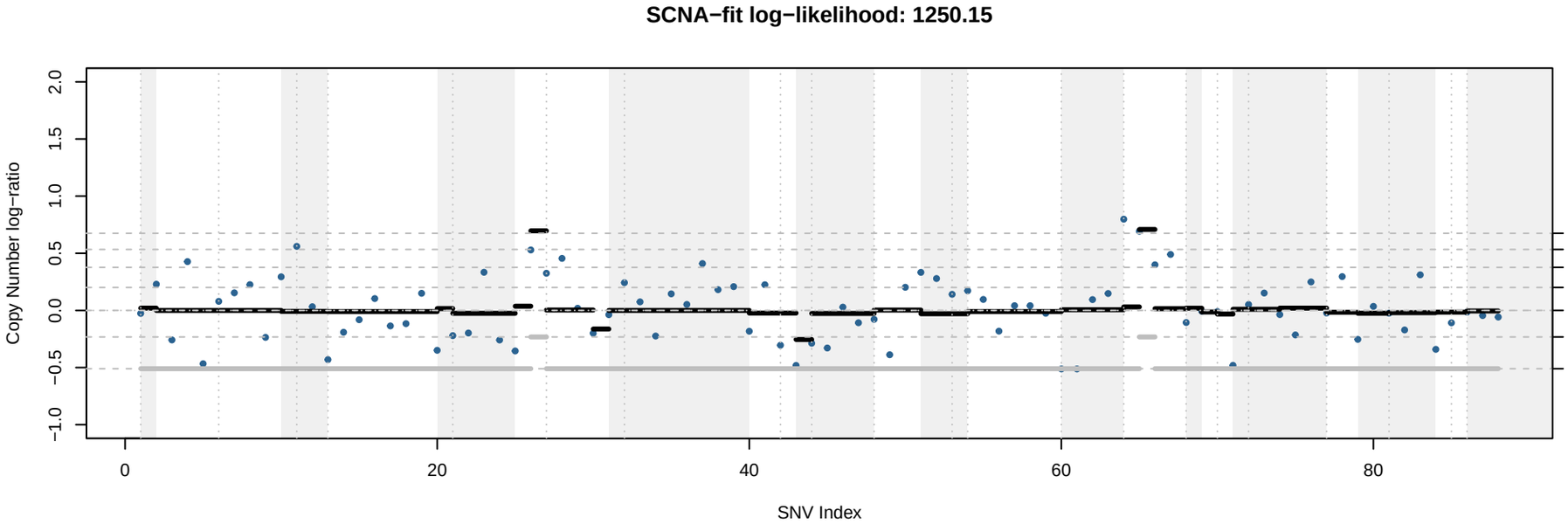

Coverage (log2)
Allelic fraction

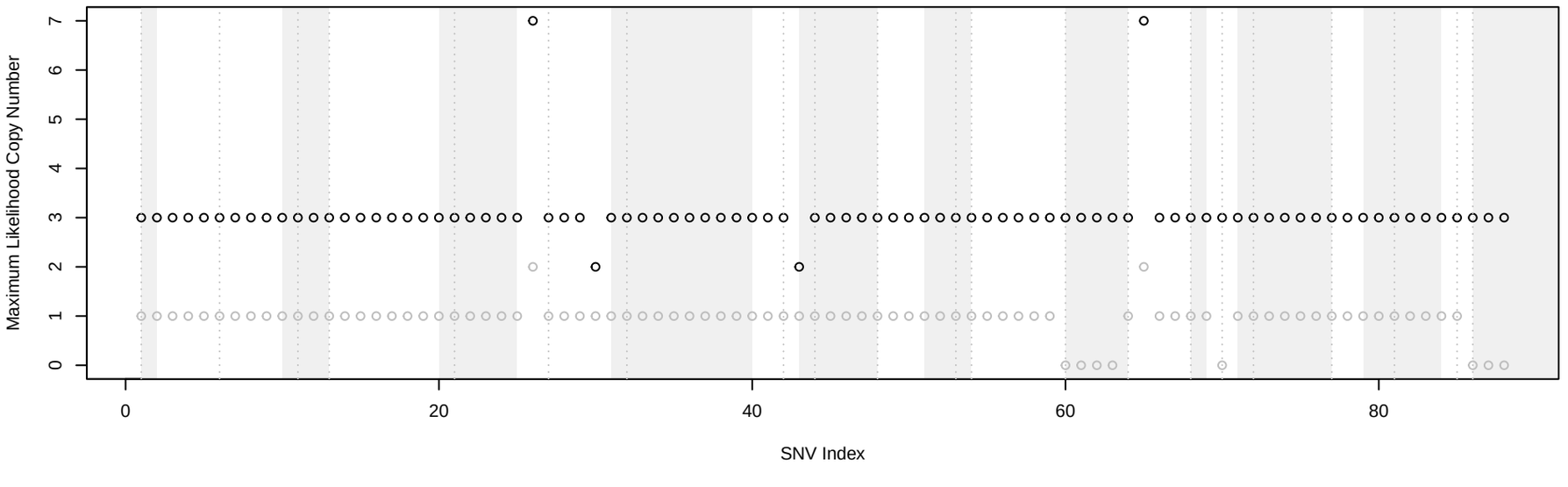

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1
3m1
4m1
5m1
7m1

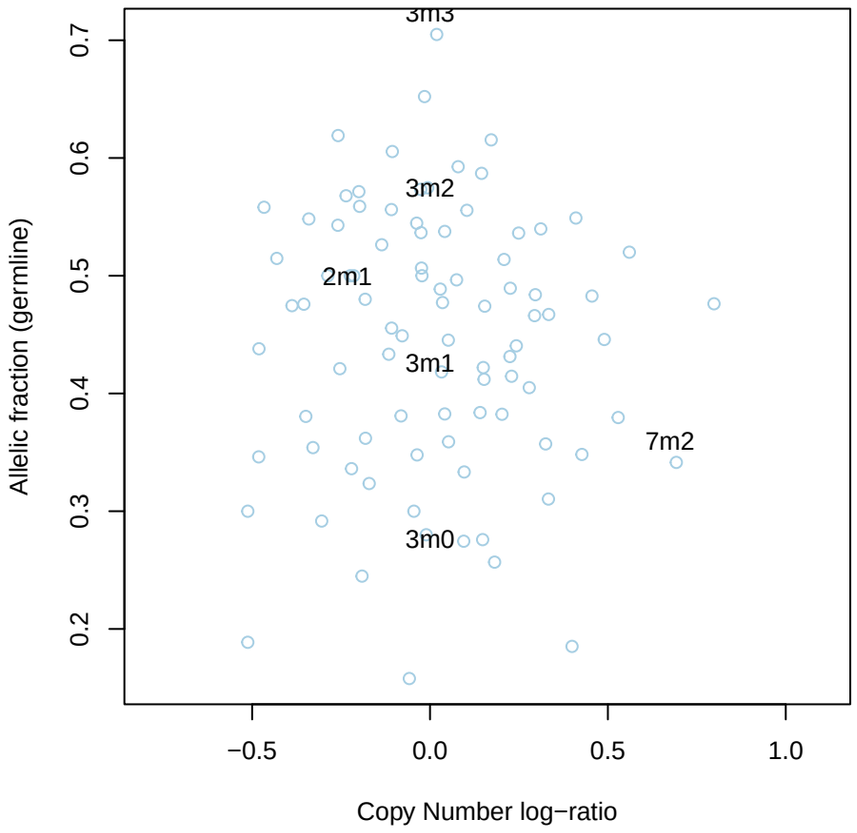

Power 0.8
Frequency
Cellular fraction

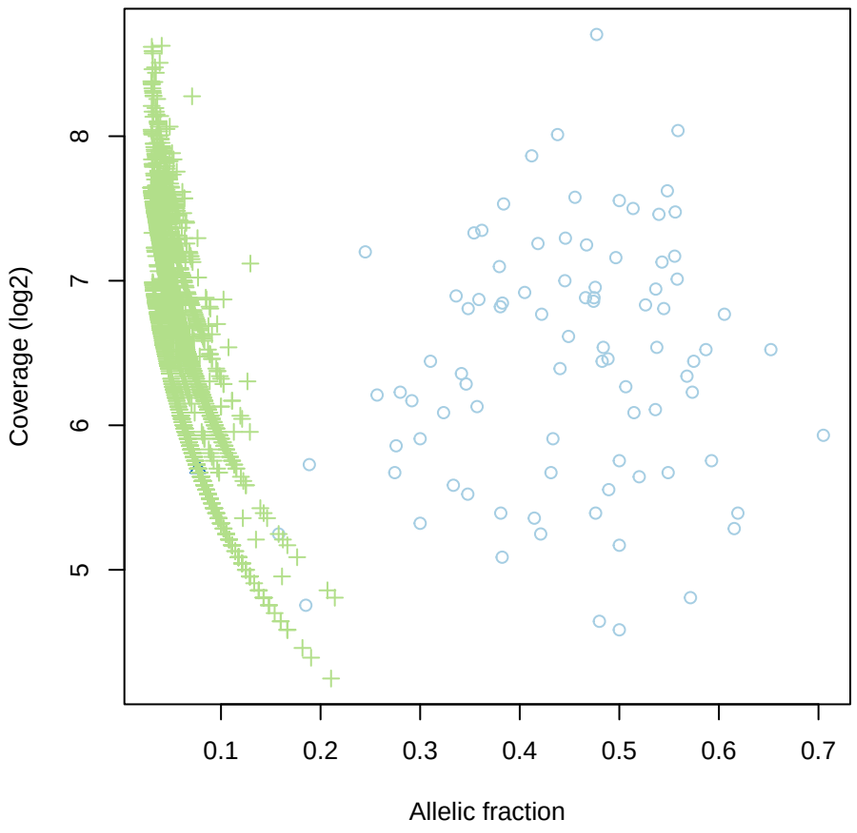

Purity: 0.35 Tumor ploidy: 2.998
1
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

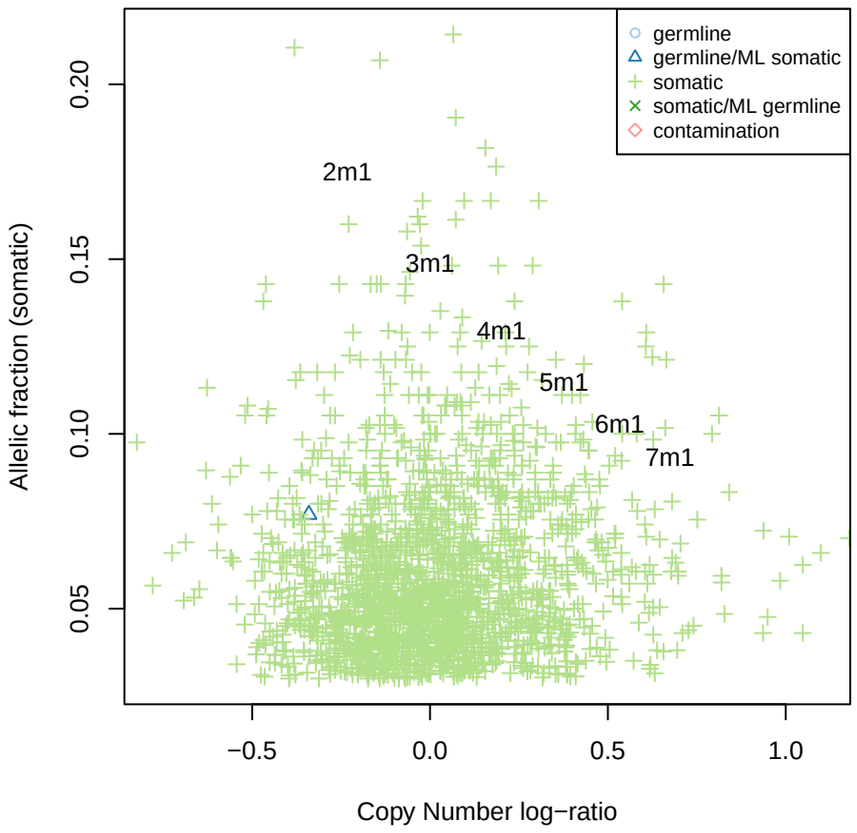

Purity: 0.35 Tumor ploidy: 2.998 SNV log−likelihood: 80.65 GoF: 80.3% Mean coverage: 67;114
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

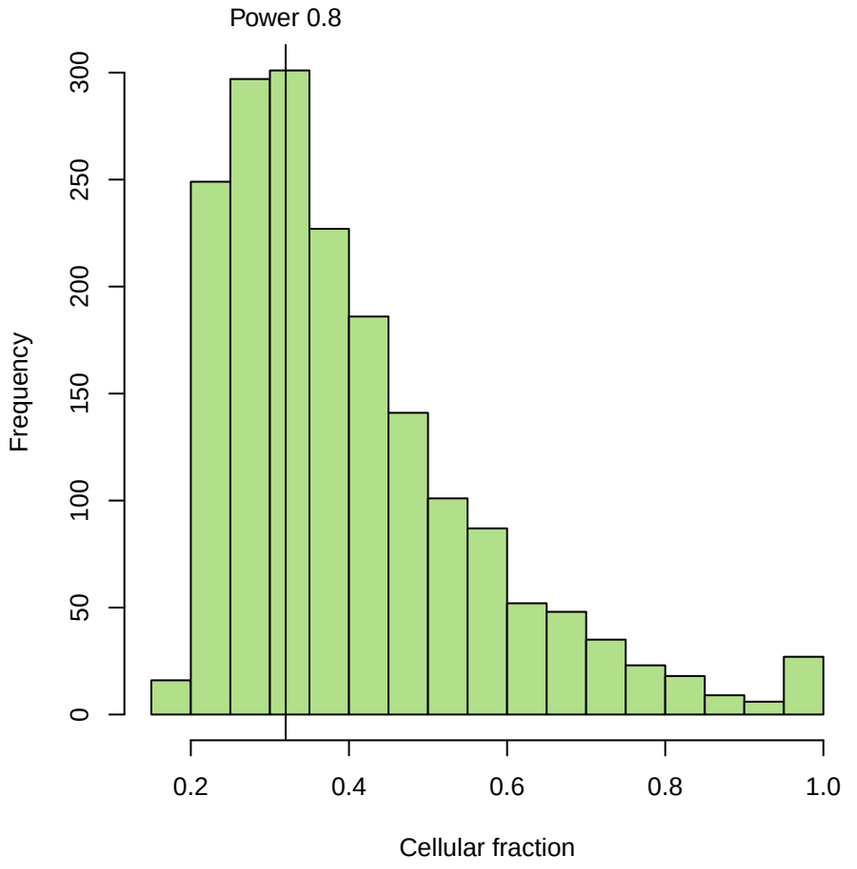

SCNA−fit log−likelihood: 1250.15
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
1 2 3 5 7
0 20 40 60 80
SNV Index

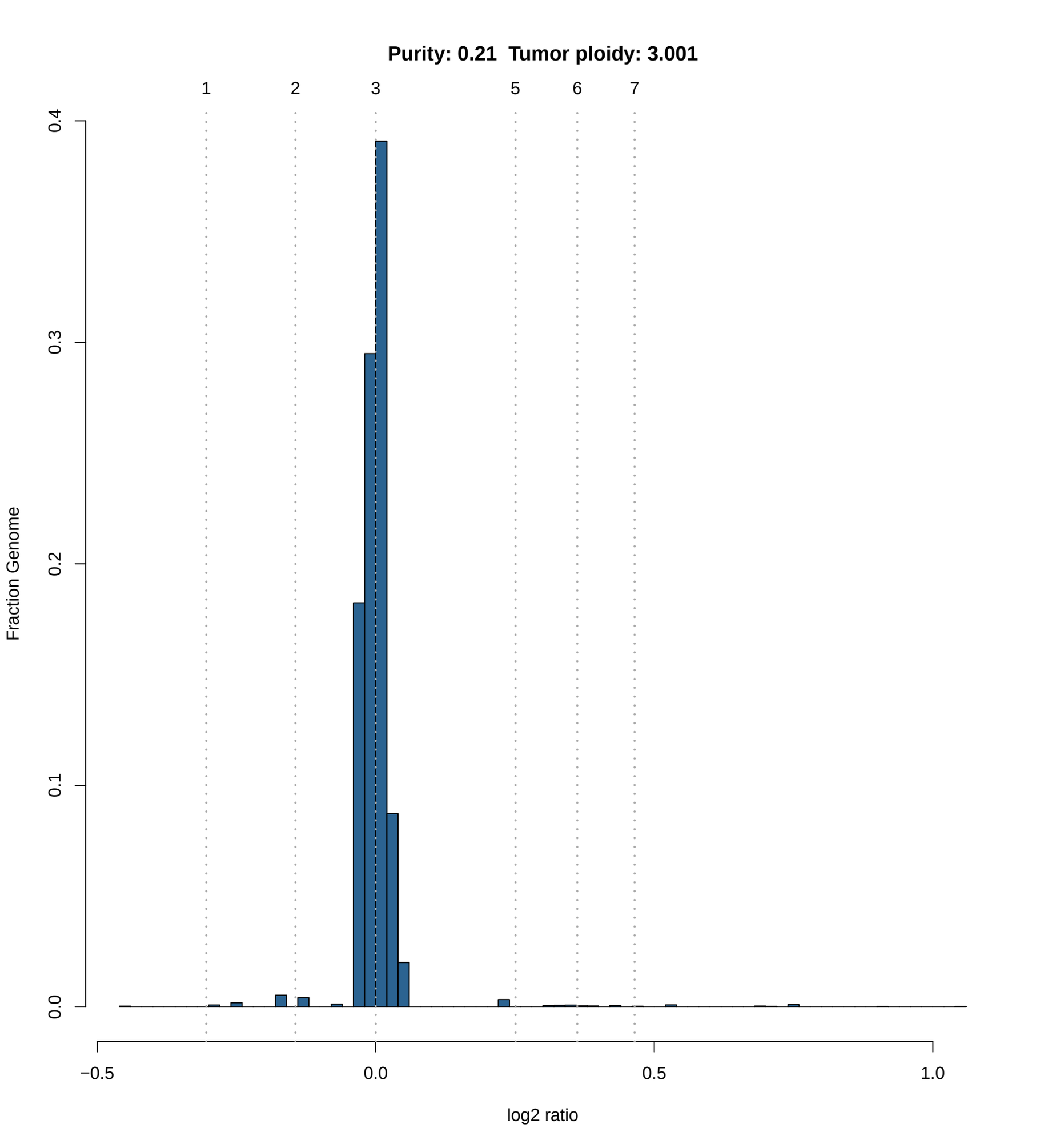

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

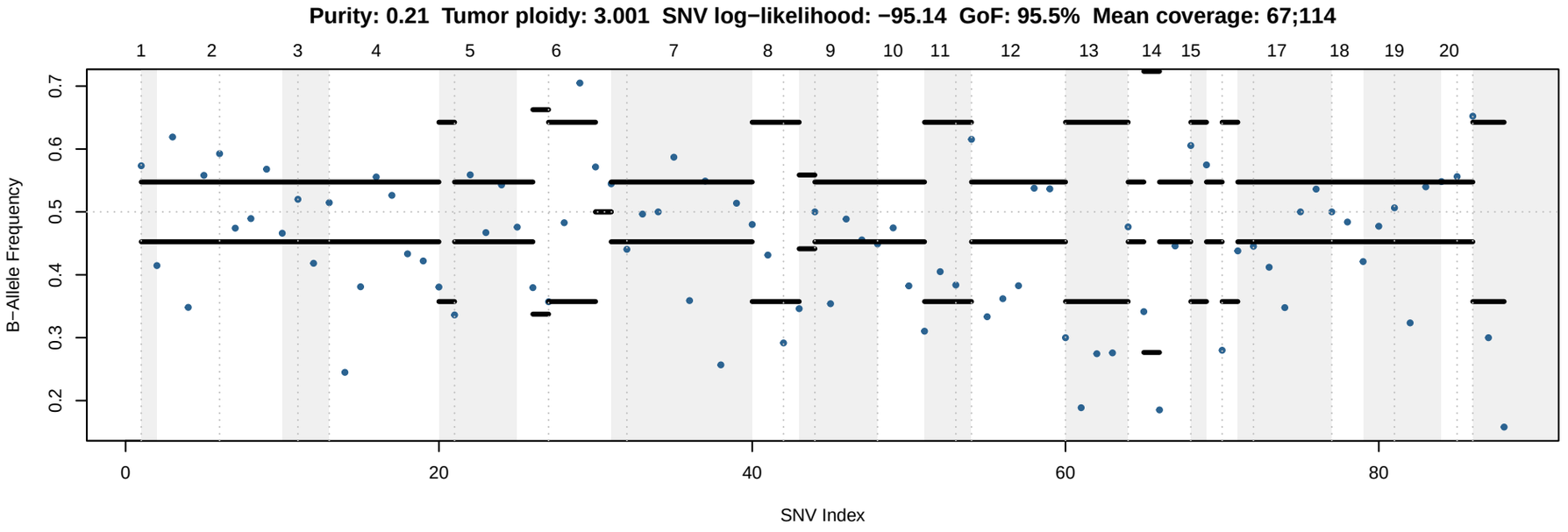

3m3
3m2
2m1
3m1
7m2
3m0
Allelic fraction (germline)
Copy Number log−ratio

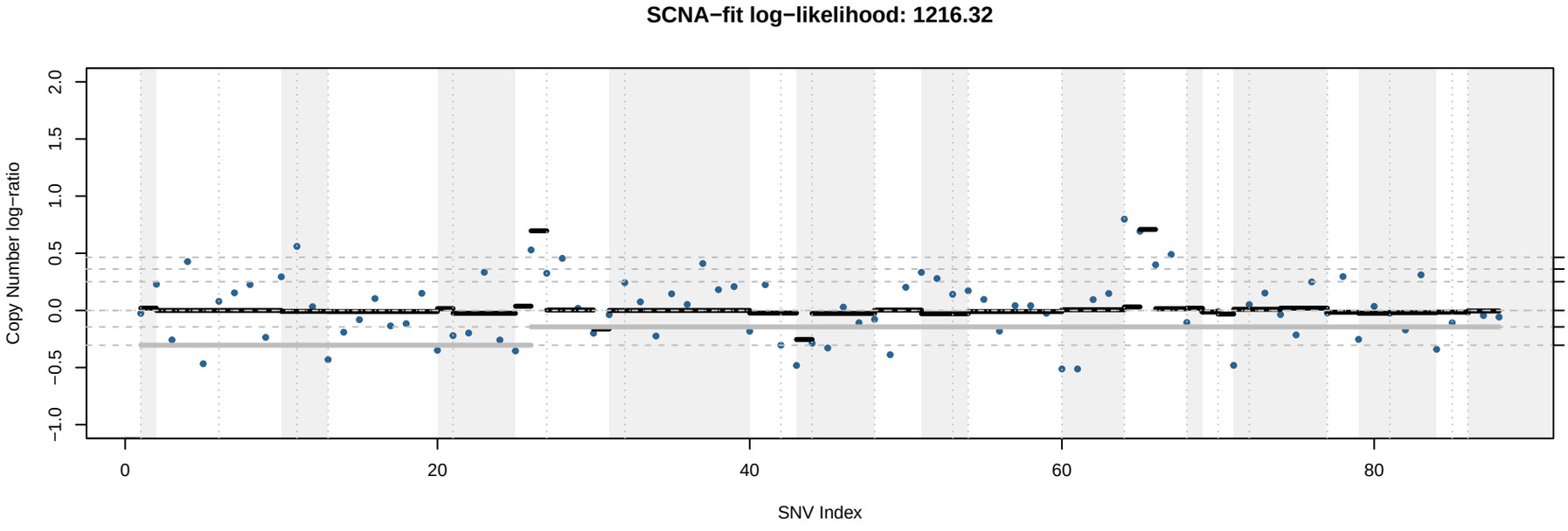

Coverage (log2)
Allelic fraction

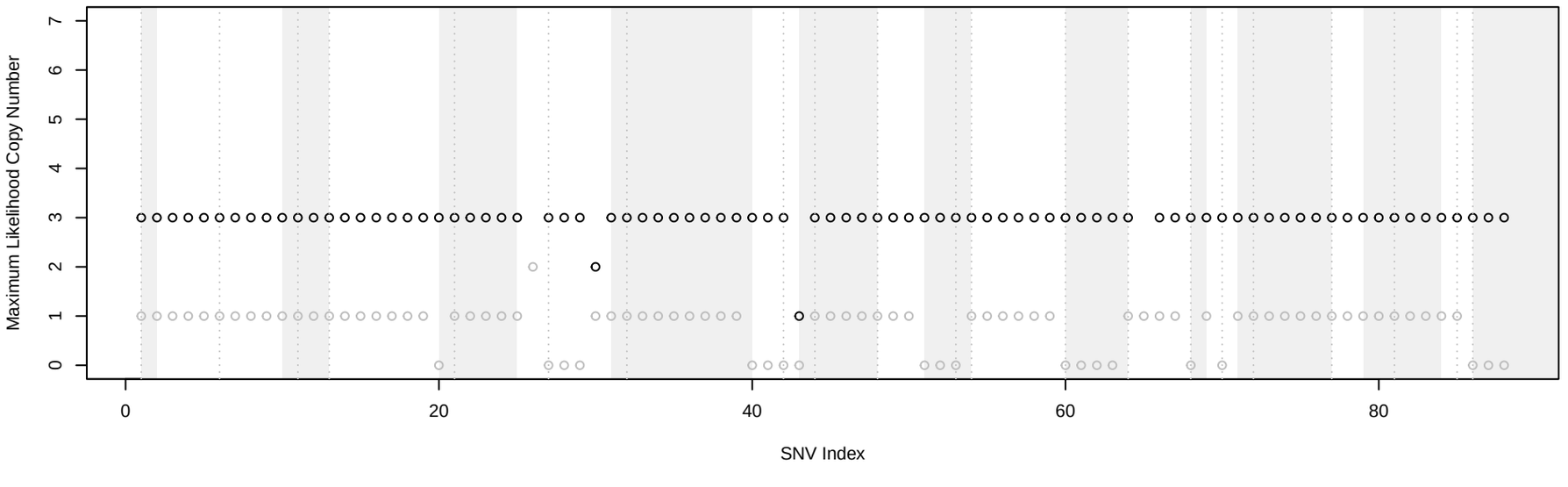

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

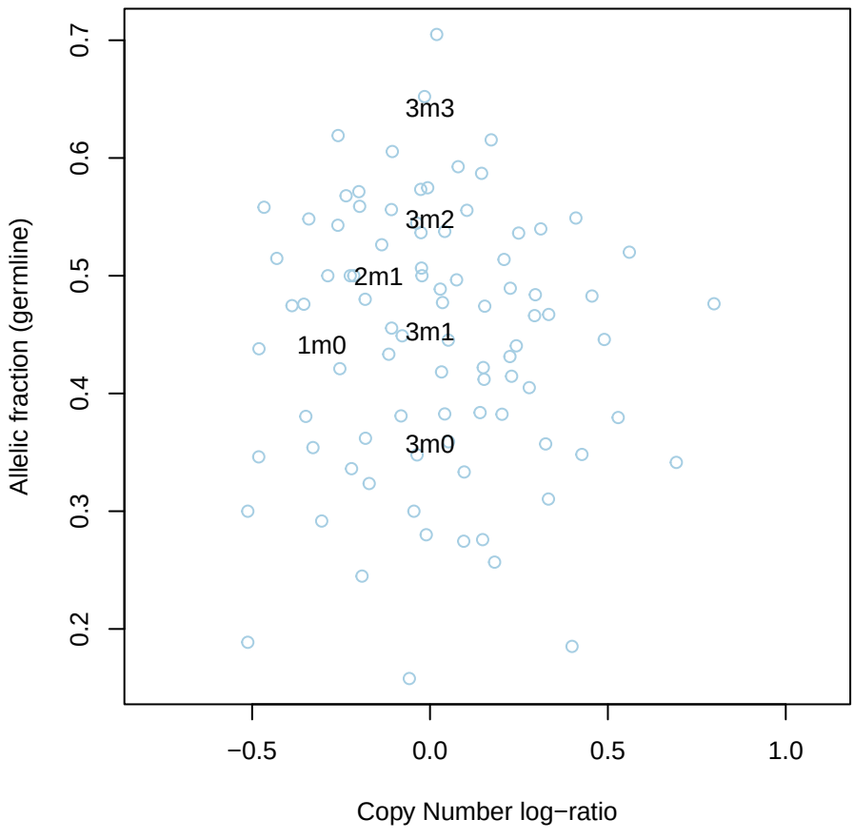

Power 0.8
Frequency
Cellular fraction

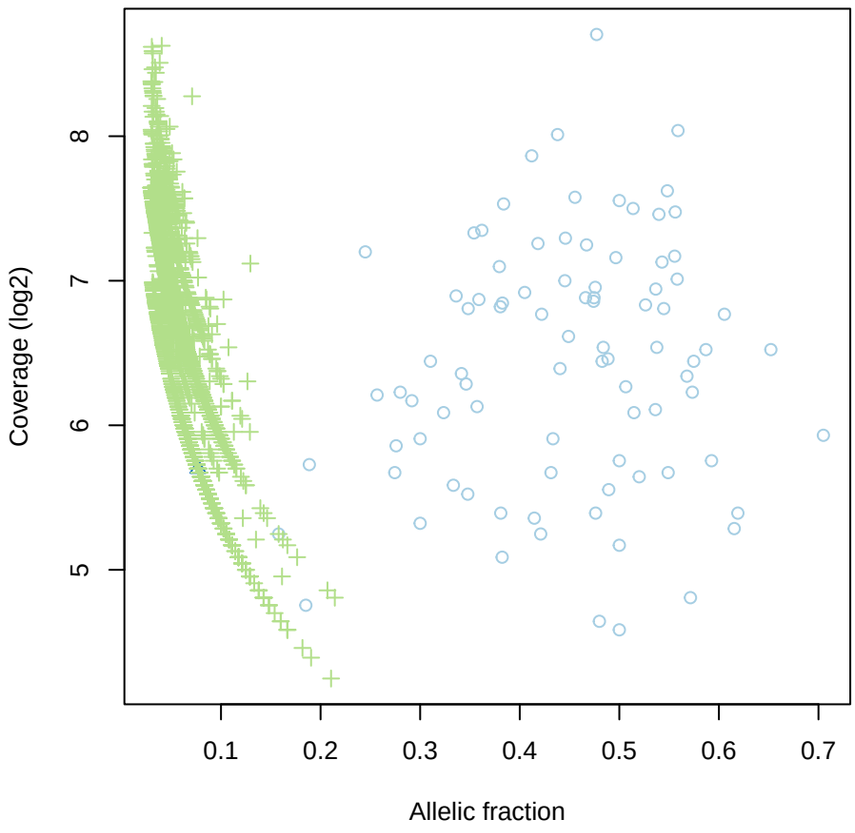

Purity: 0.21 Tumor ploidy: 3.001
1
2
3
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

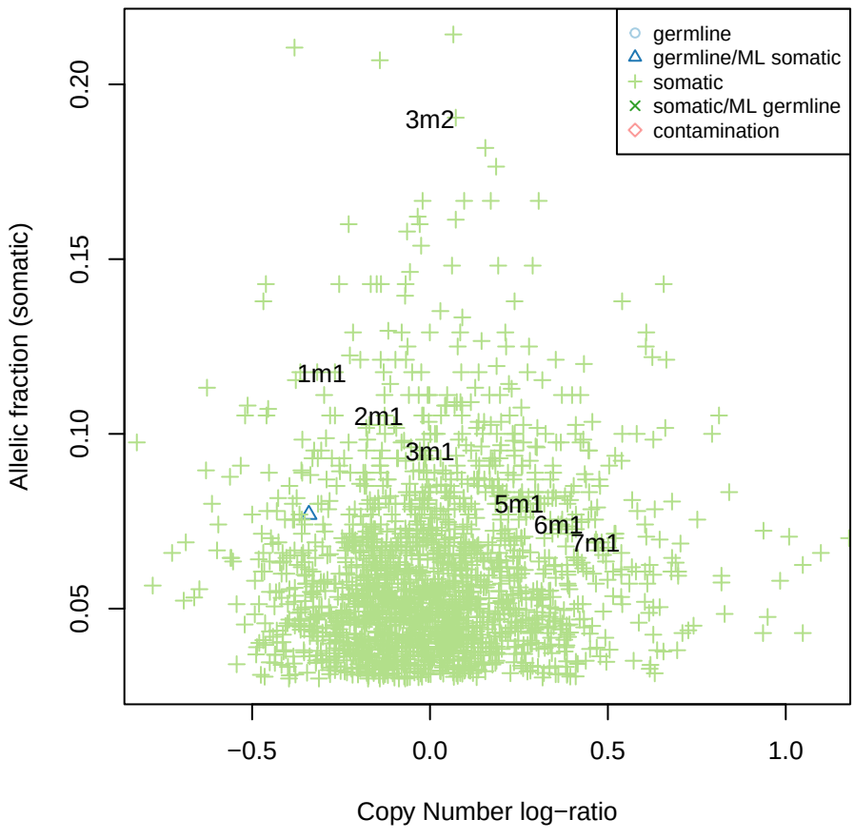

Purity: 0.21 Tumor ploidy: 3.001 SNV log−likelihood: −95.14 GoF: 95.5% Mean coverage: 67;114
B−Allele Frequency
SNV Index

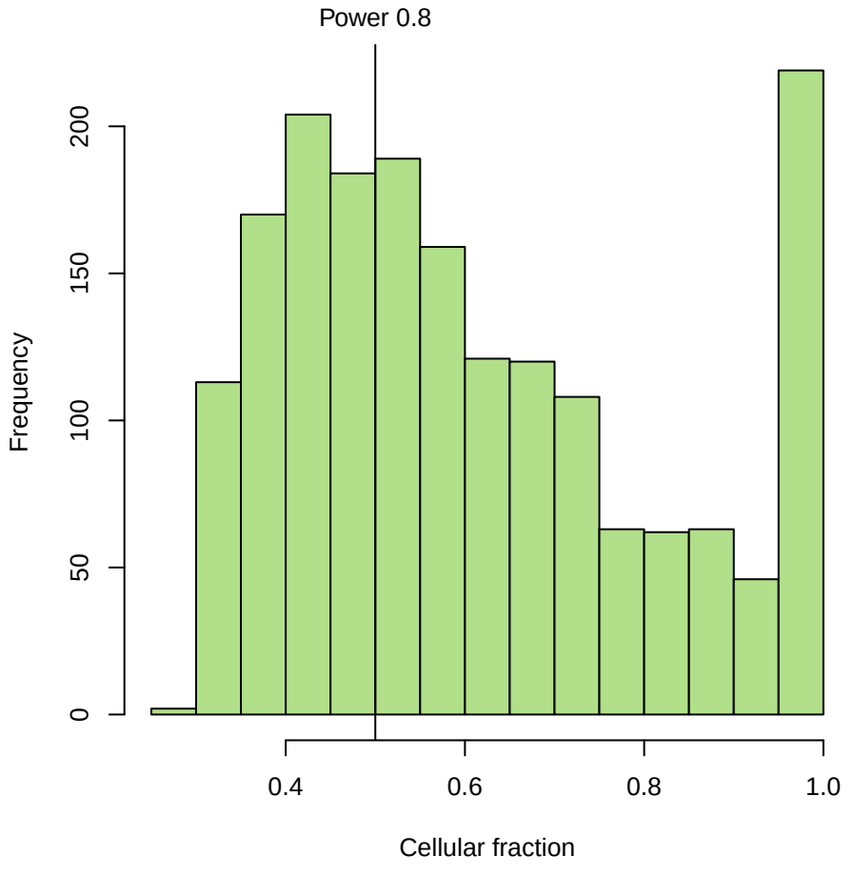

SCNA−fit log−likelihood: 1216.32
Copy Number log−ratio
SNV Index

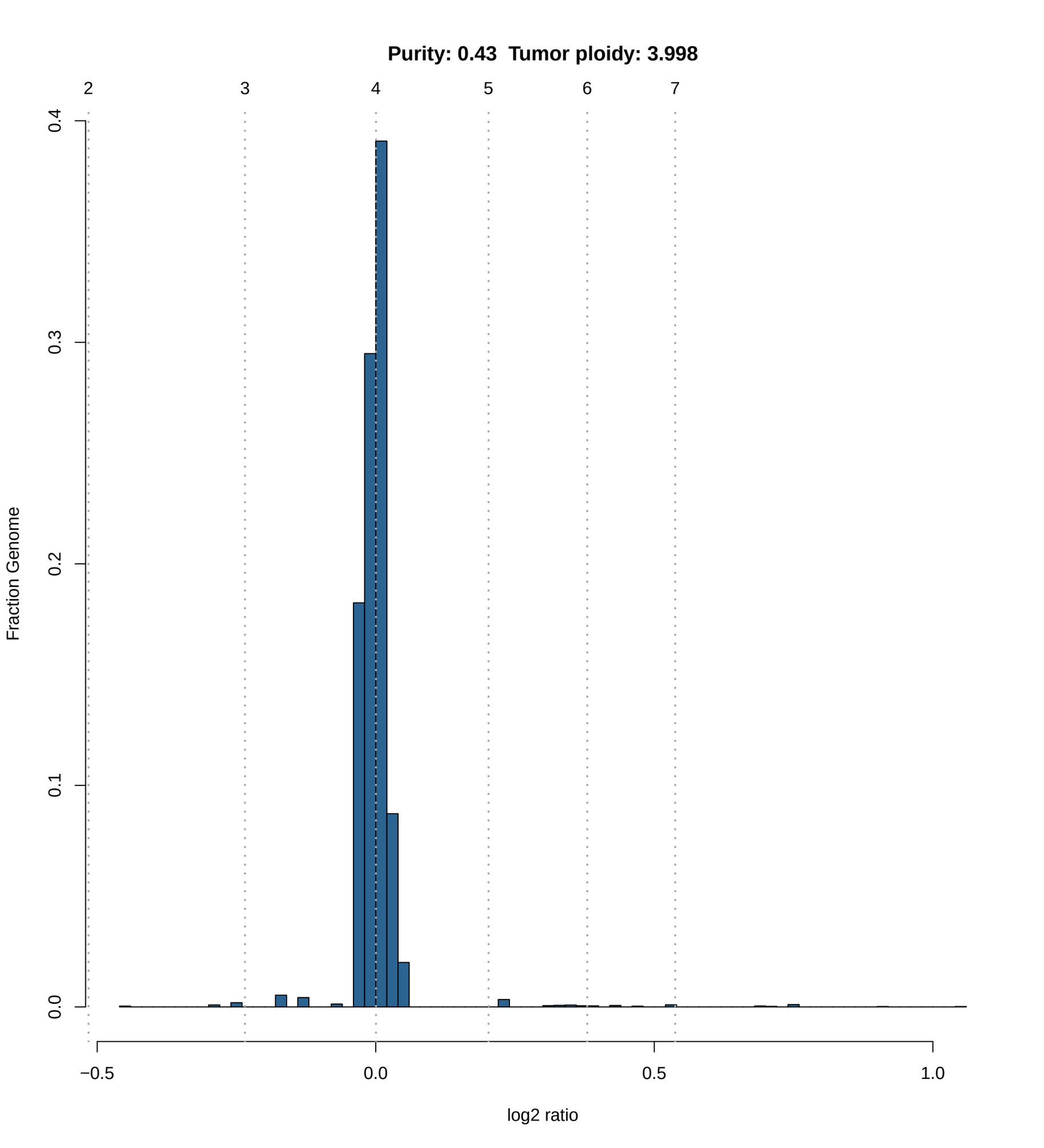

Maximum Likelihood Copy Number
SNV Index

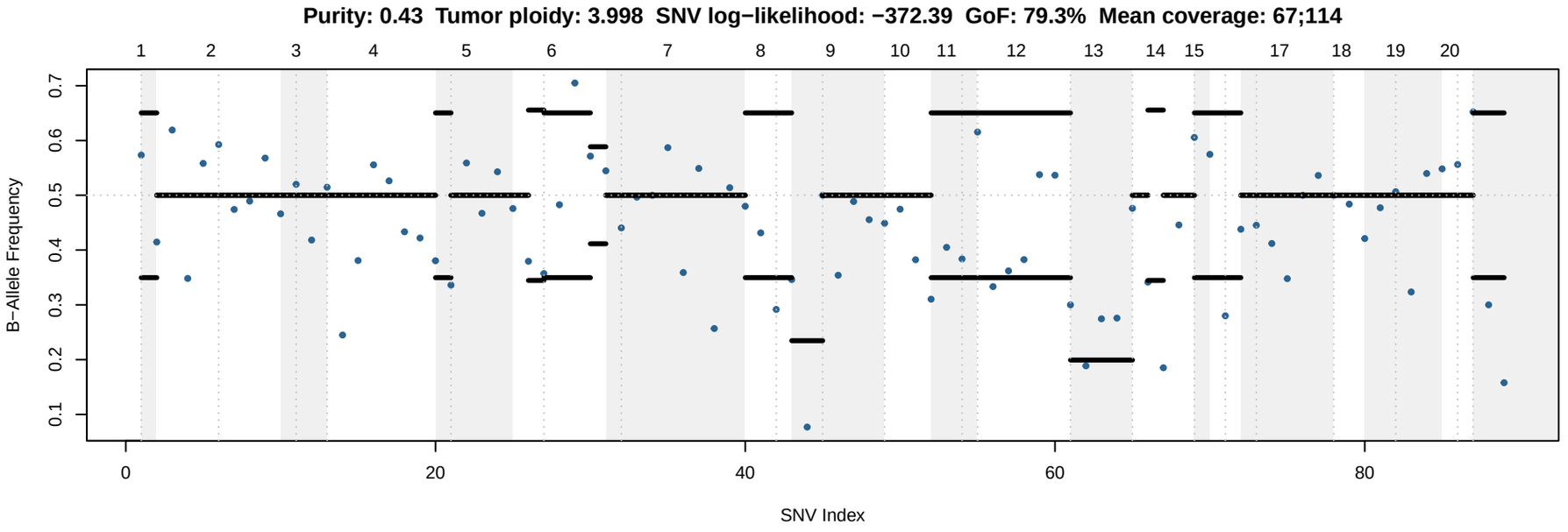

Allelic fraction (germline)
Copy Number log−ratio
3m3
3m2
2m1
3m1
1m0
3m0

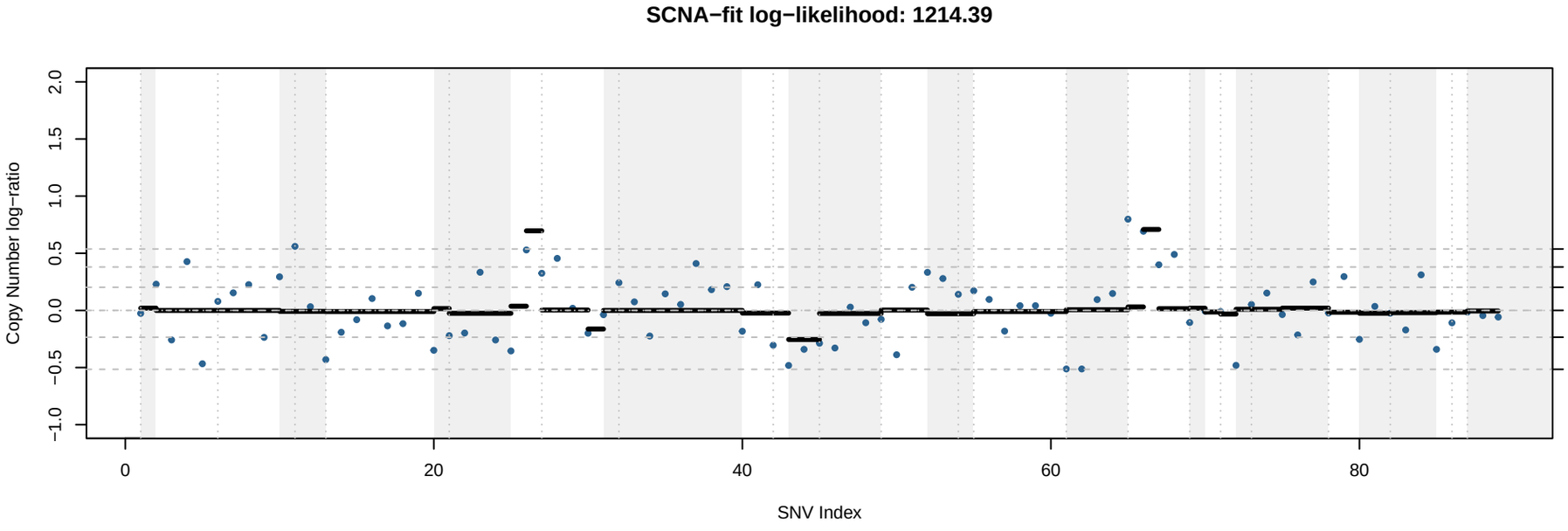

Coverage (log2)
Allelic fraction

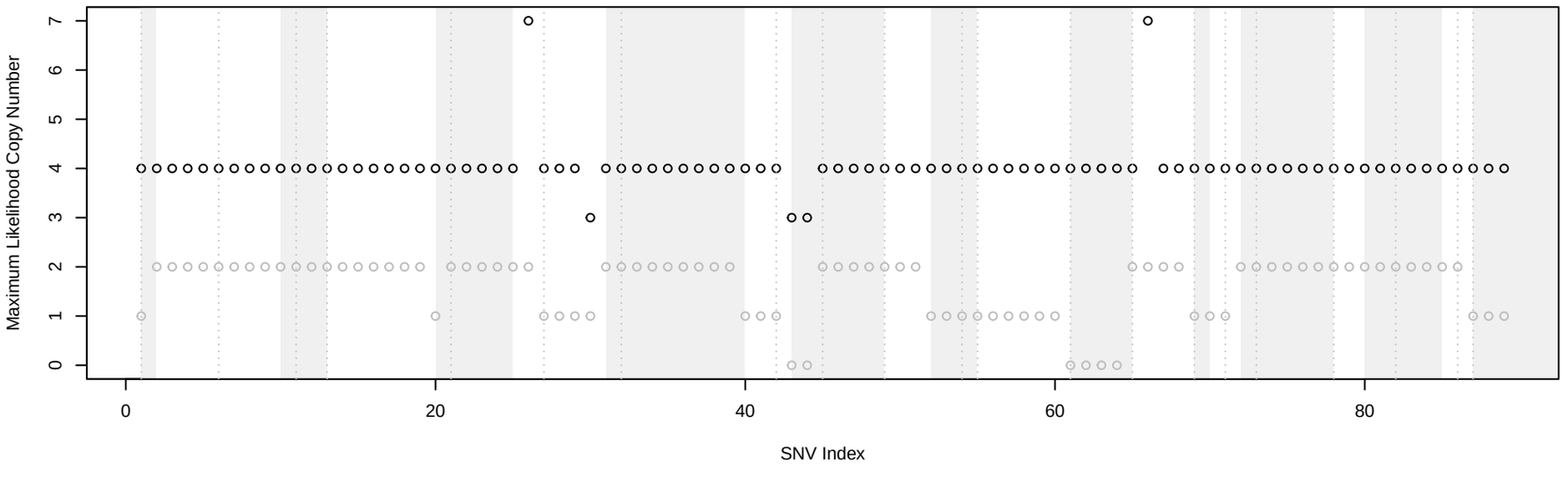

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m2
1m1
2m1
3m1
5m1
6m1
7m1

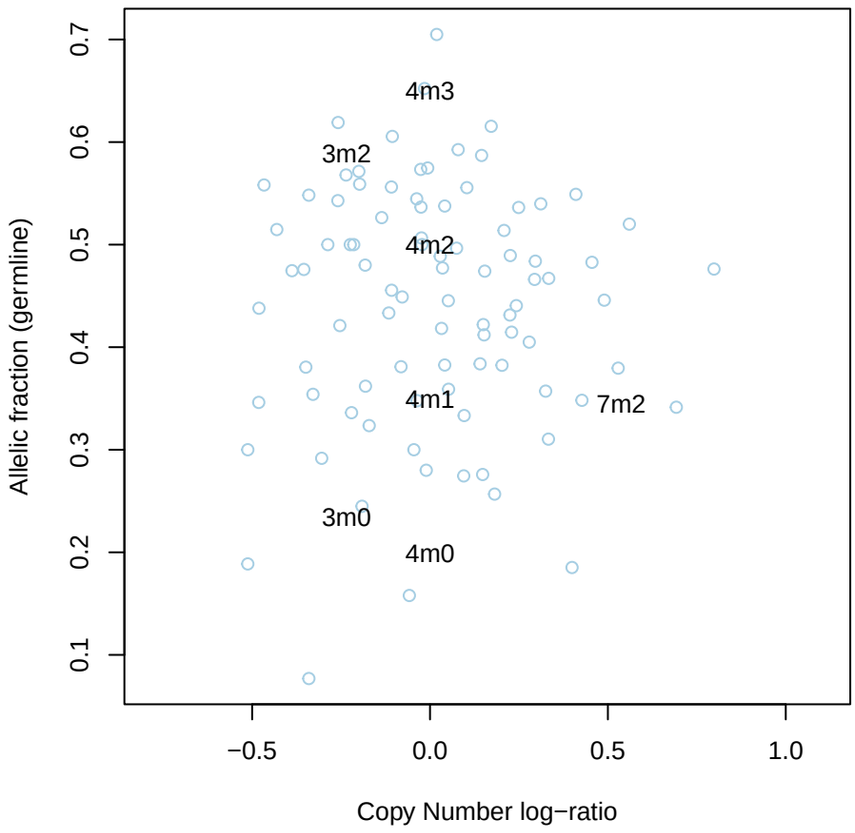

Power 0.8
Frequency
Cellular fraction

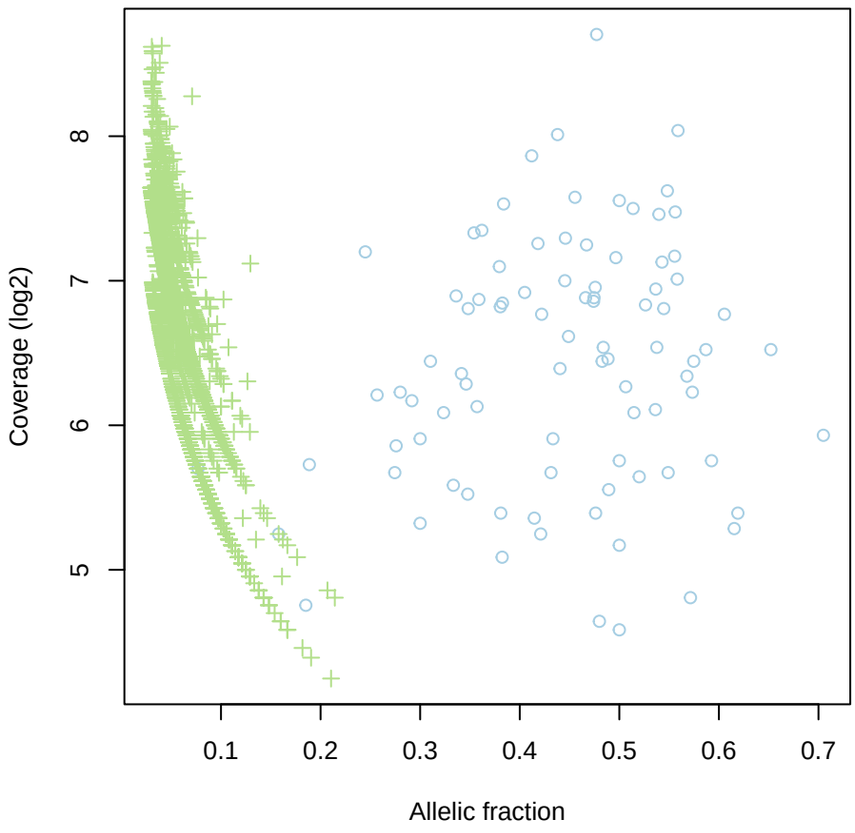

Purity: 0.43 Tumor ploidy: 3.998
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

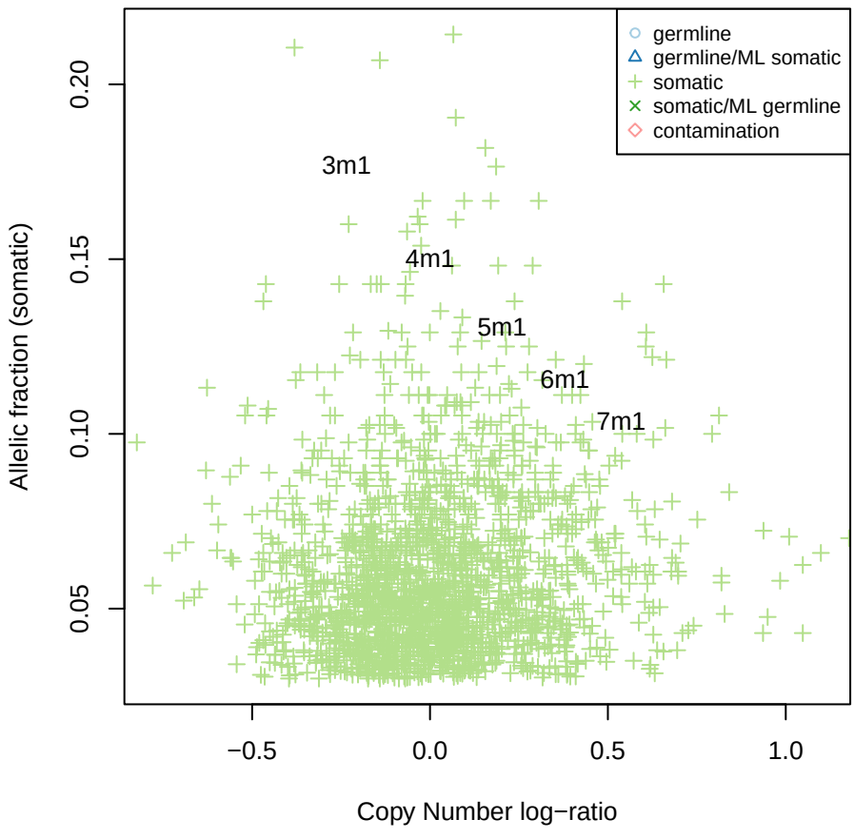

Purity: 0.43 Tumor ploidy: 3.998 SNV log−likelihood: −372.39 GoF: 79.3% Mean coverage: 67;114
B−Allele Frequency
SNV Index

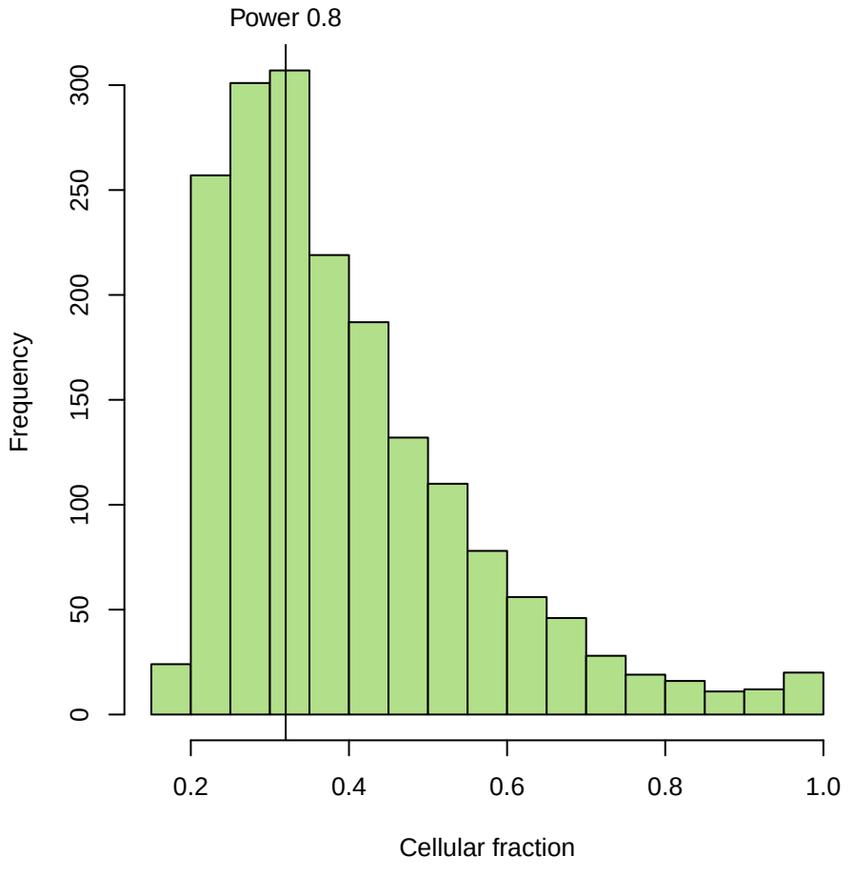

SCNA−fit log−likelihood: 1214.39
Copy Number log−ratio
SNV Index

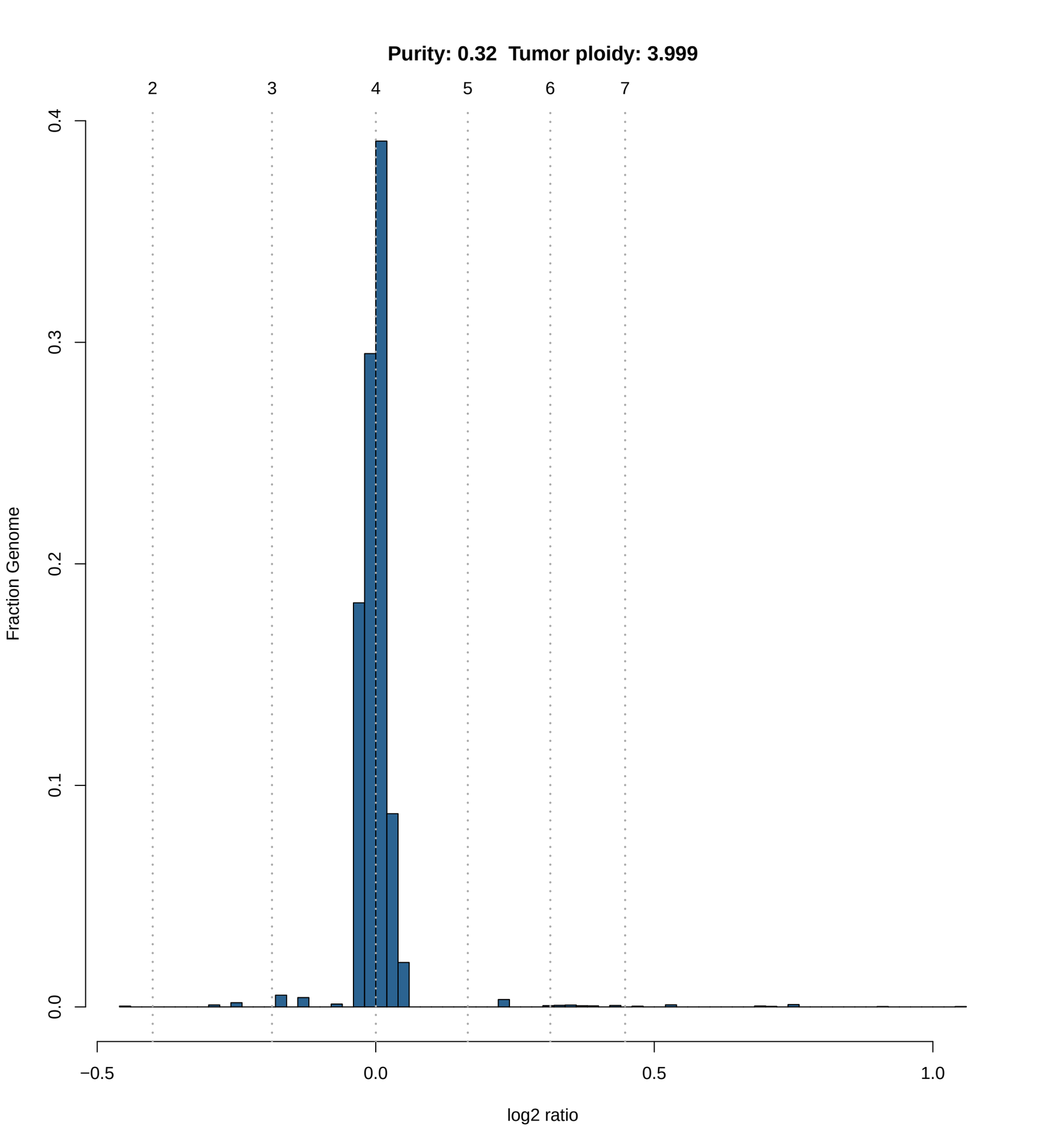

Maximum Likelihood Copy Number
SNV Index

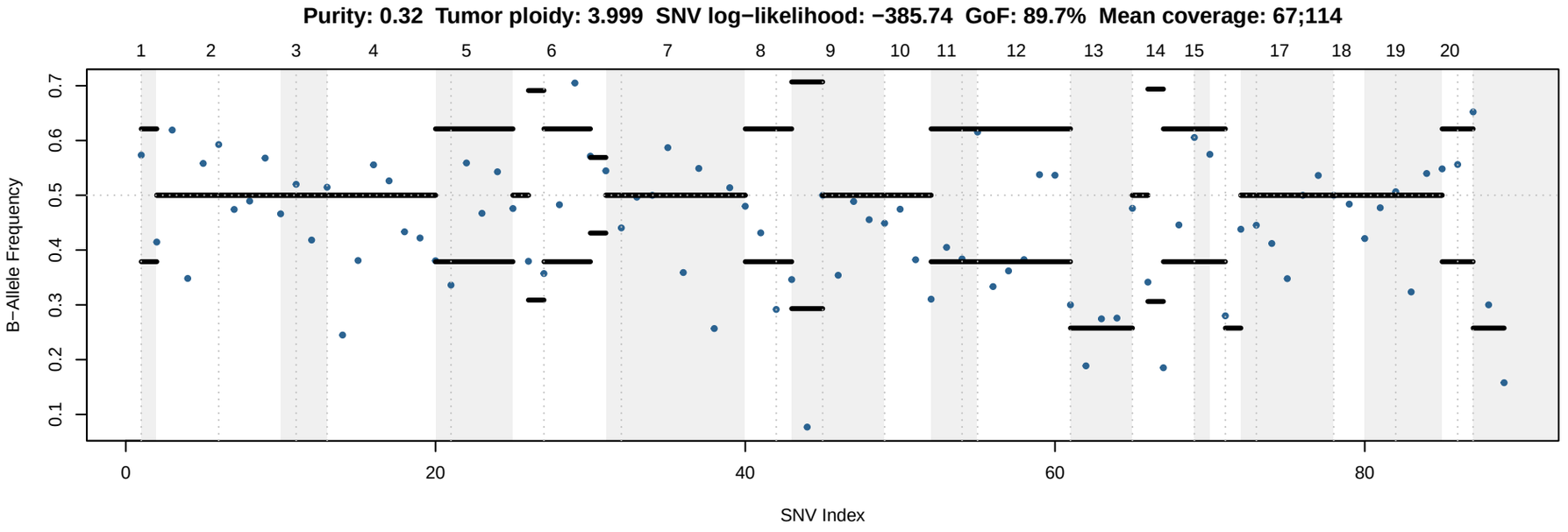

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
4m2
4m1
7m2
3m0
4m0

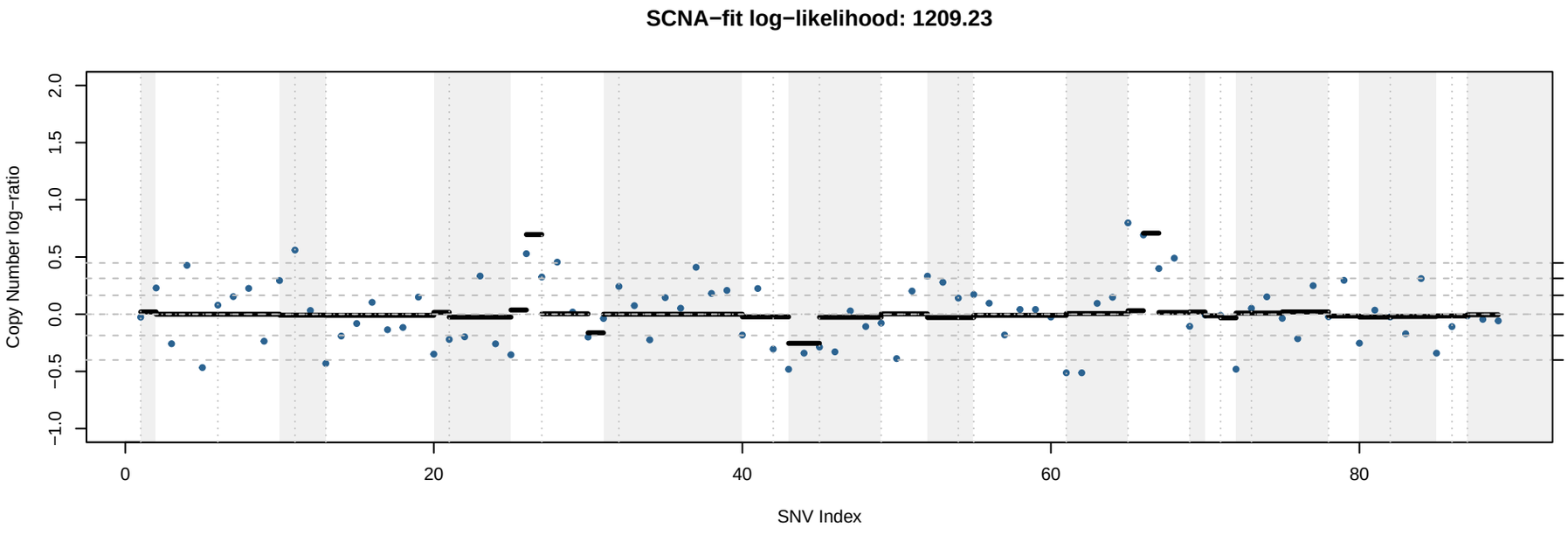

Coverage (log2)
Allelic fraction

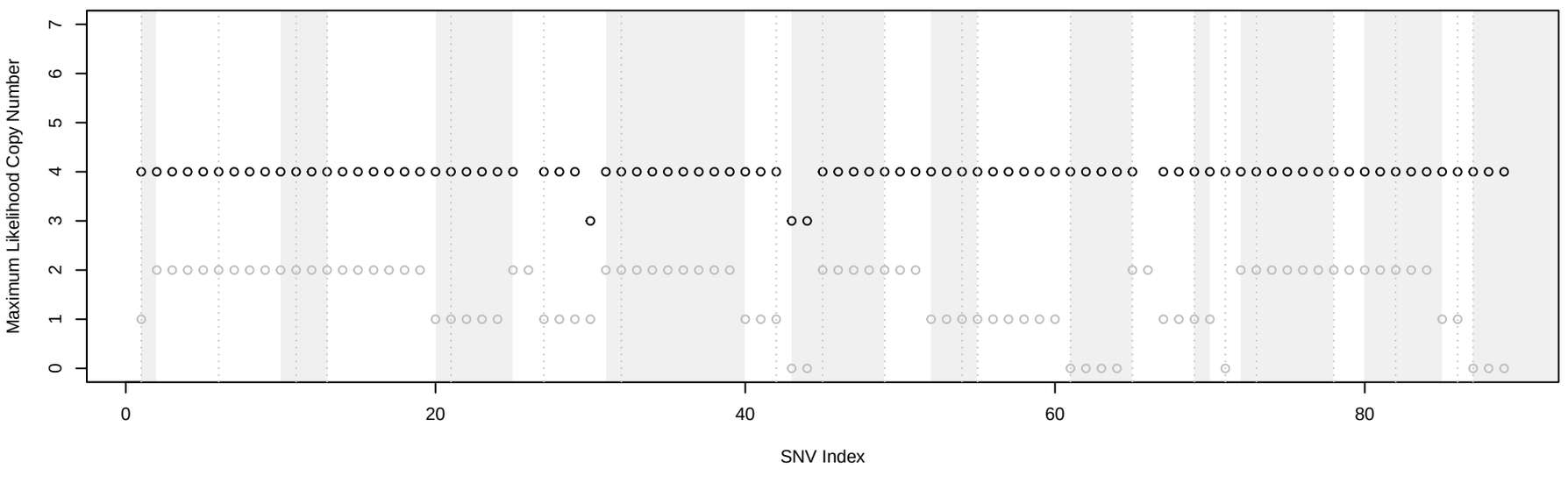

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
6m1
7m1

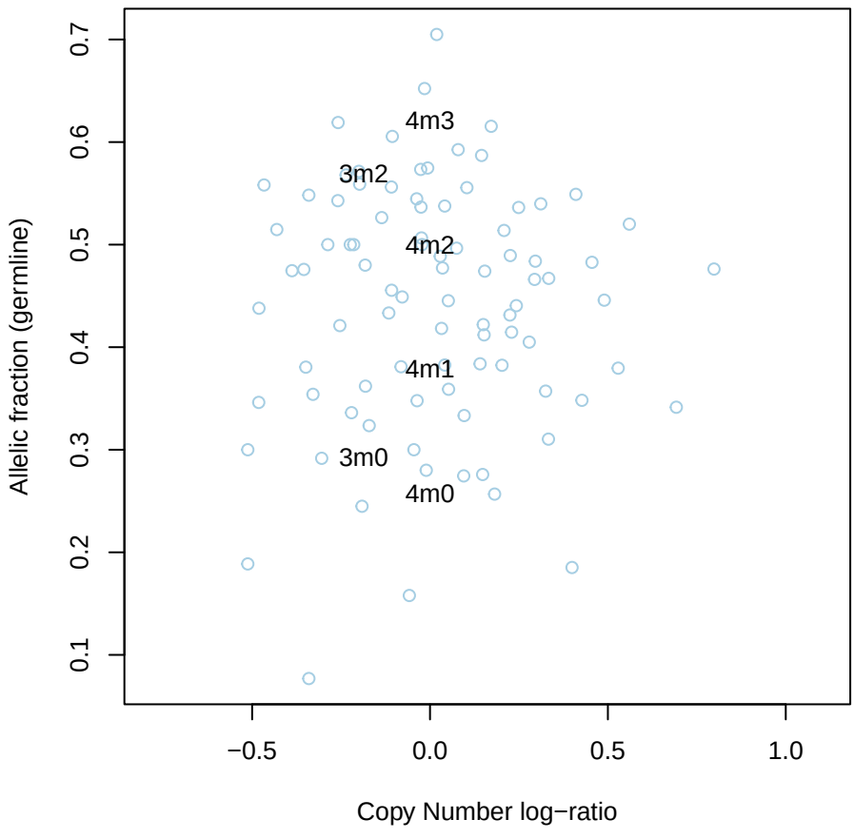

Power 0.8
Frequency
Cellular fraction

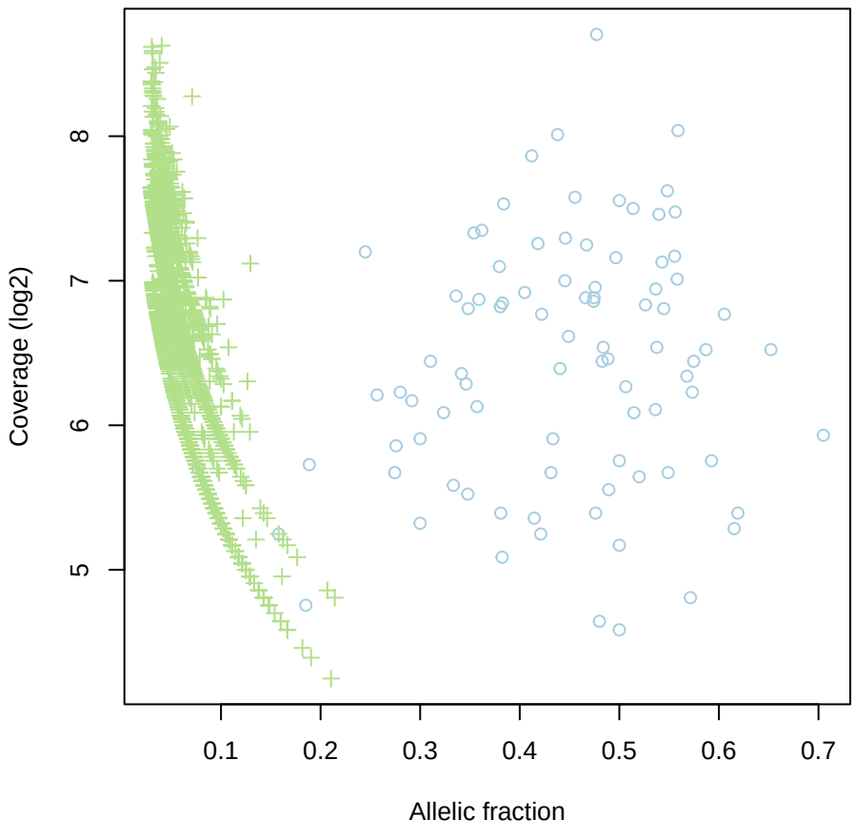

Purity: 0.32 Tumor ploidy: 3.999
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

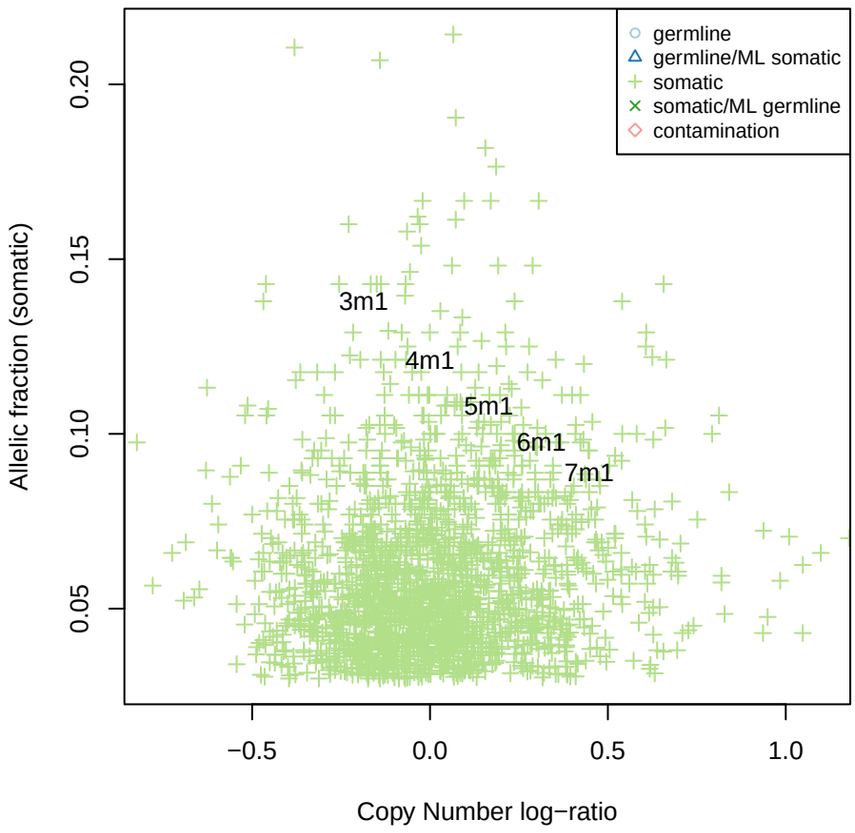

Purity: 0.32 Tumor ploidy: 3.999 SNV log−likelihood: −385.74 GoF: 89.7% Mean coverage: 67;114
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

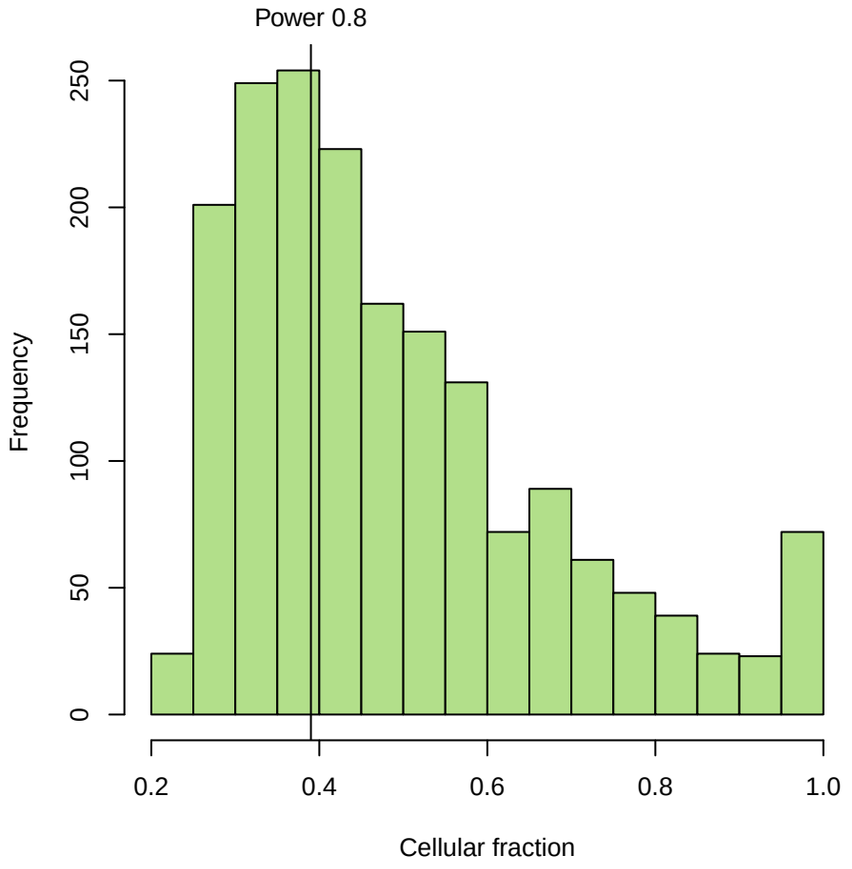

SCNA−fit log−likelihood: 1209.23
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
2 4 6
0 20 40 60 80
SNV Index

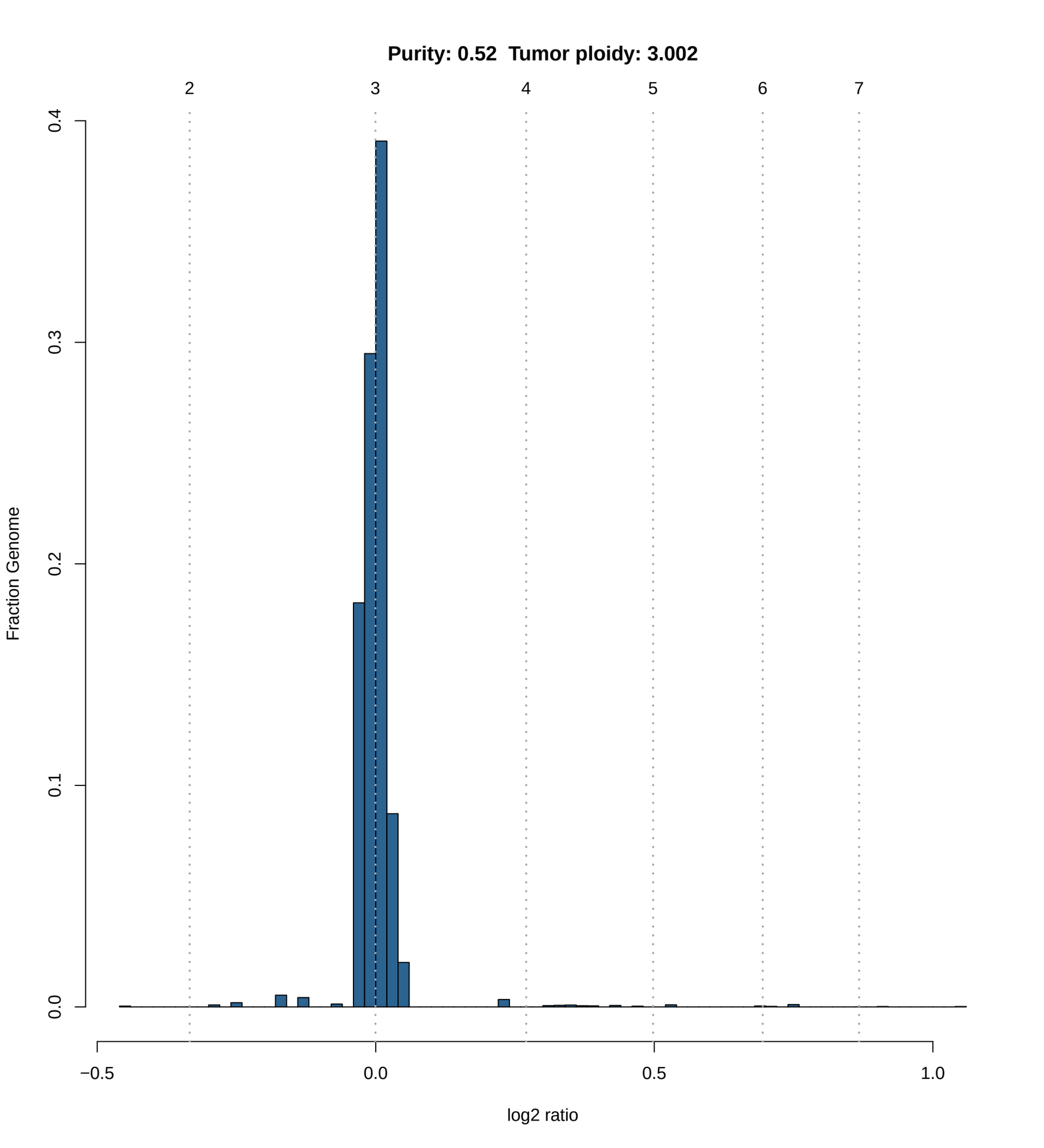

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

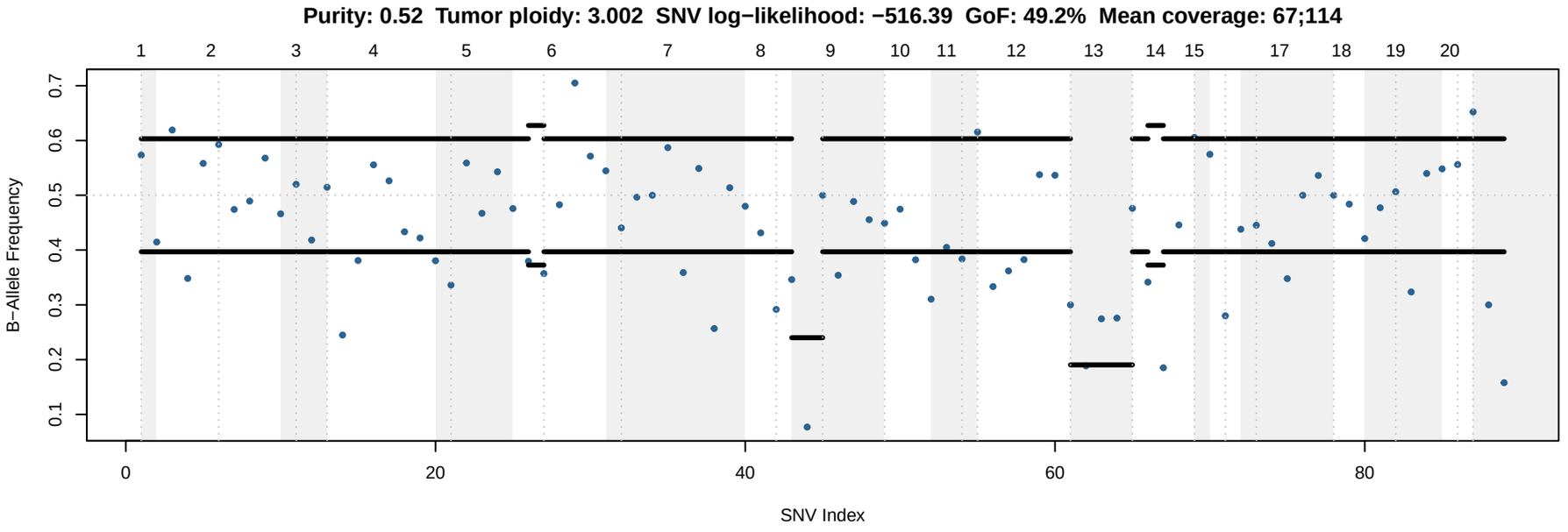

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
4m2
4m1
3m0
4m0

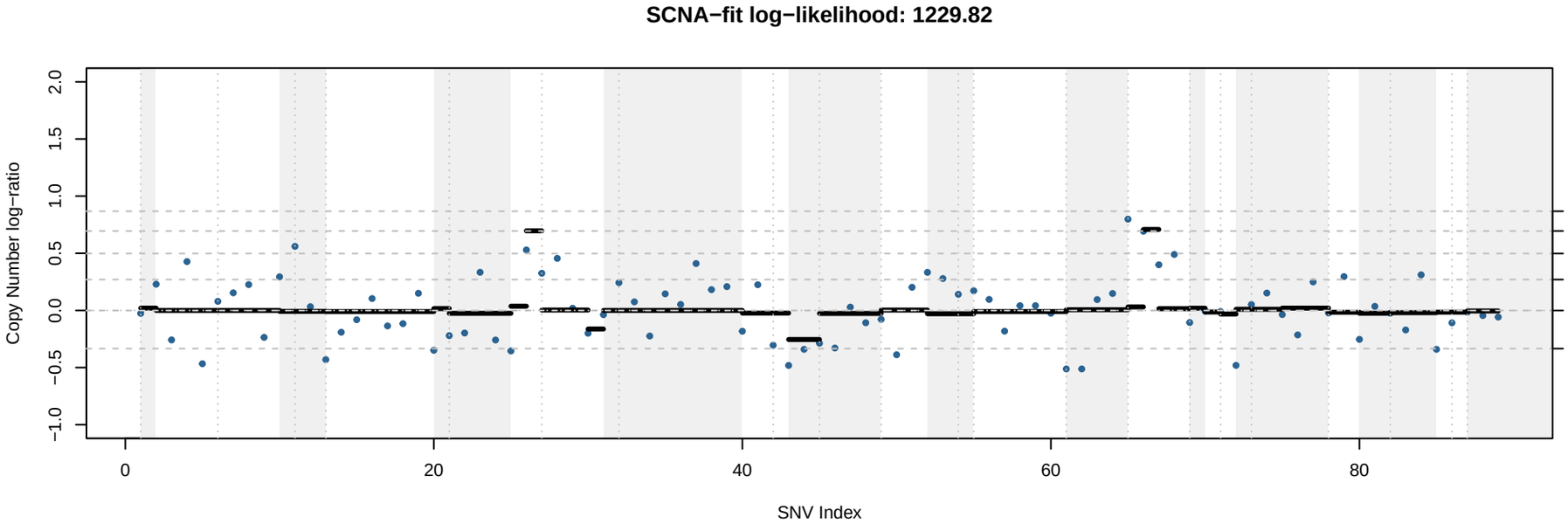

Coverage (log2)
Allelic fraction

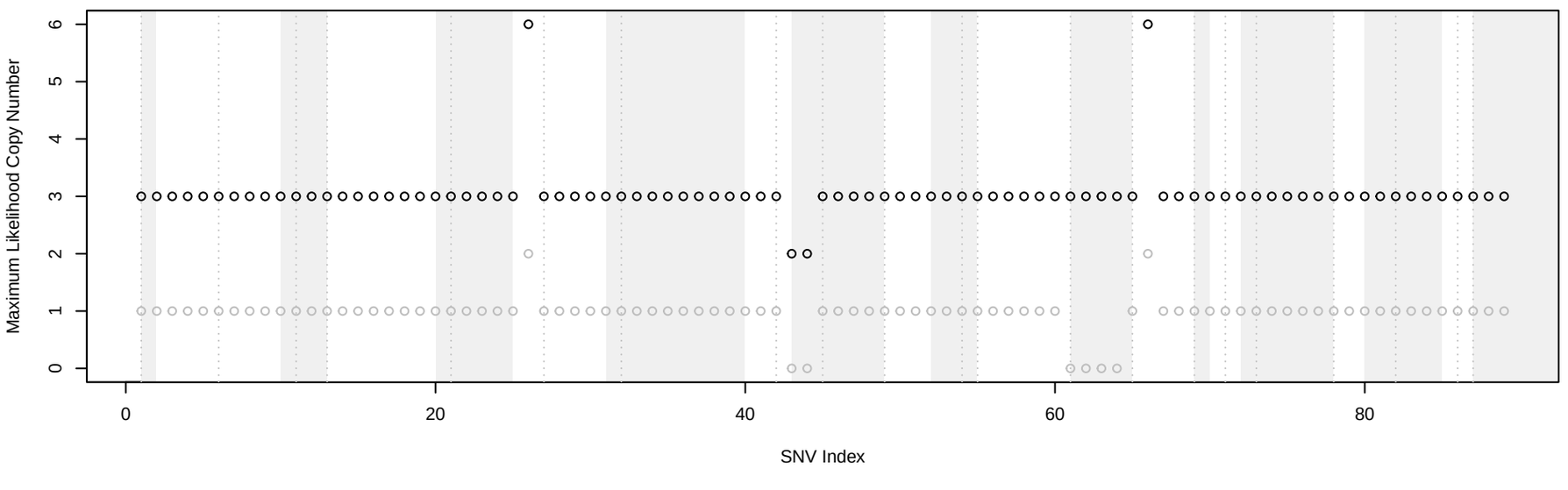

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m1
4m1
5m1
6m1
7m1

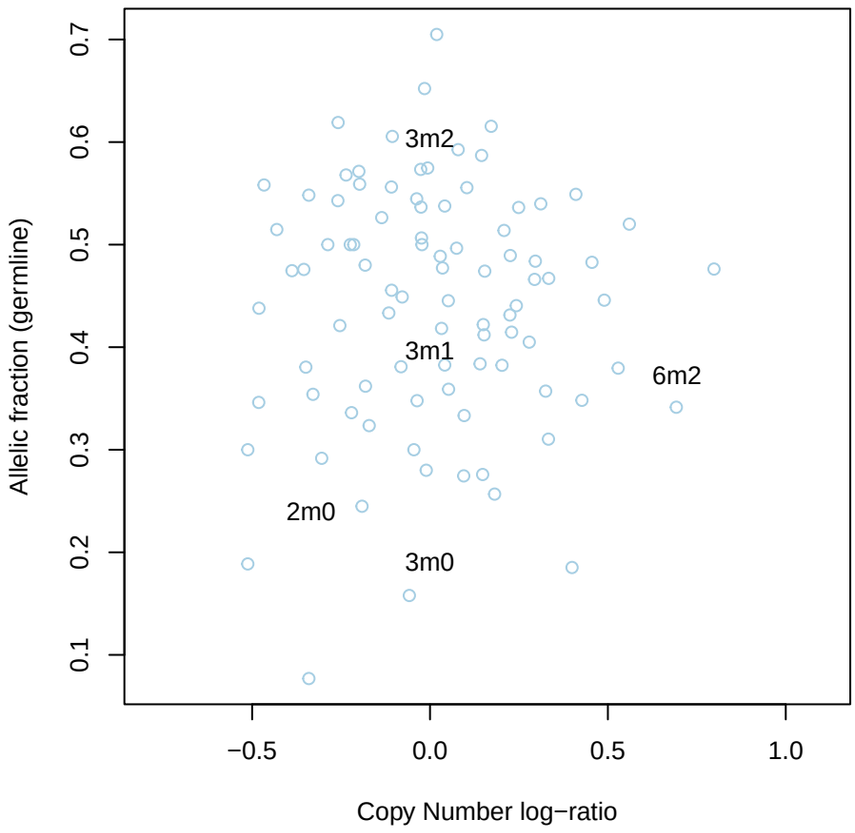

Power 0.8
Frequency
Cellular fraction

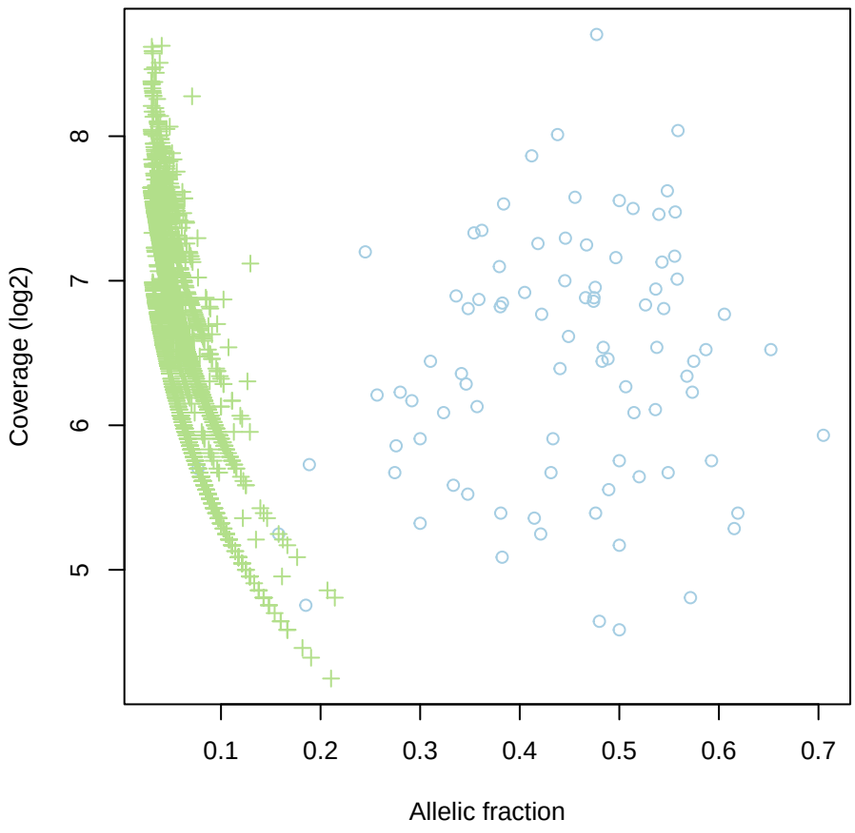

Purity: 0.52 Tumor ploidy: 3.002
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

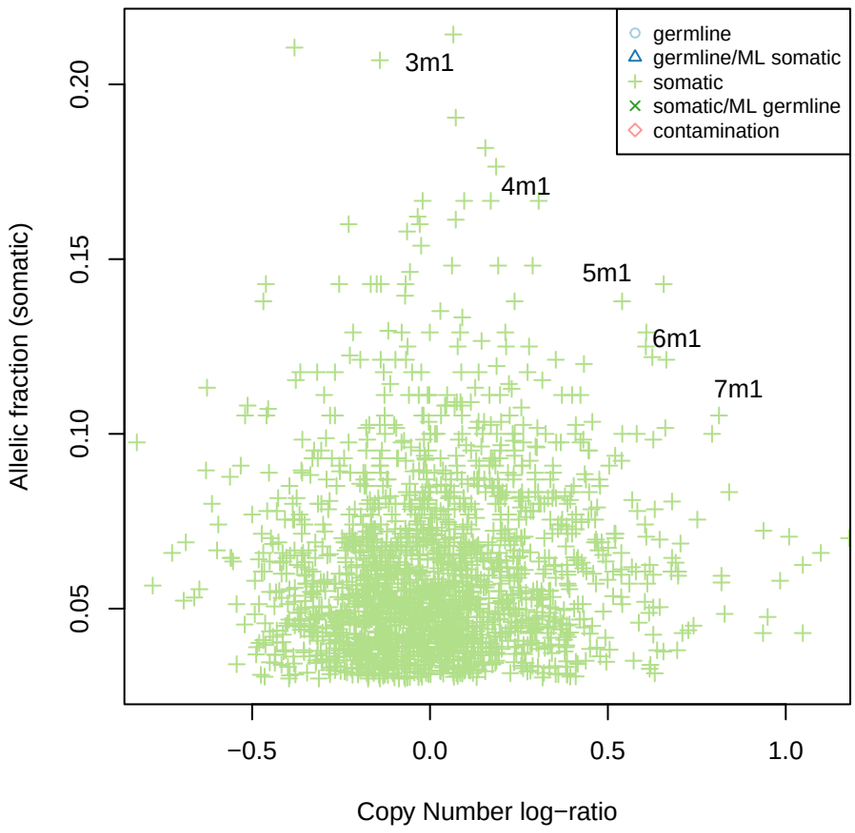

Purity: 0.52 Tumor ploidy: 3.002 SNV log−likelihood: −516.39 GoF: 49.2% Mean coverage: 67;114
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

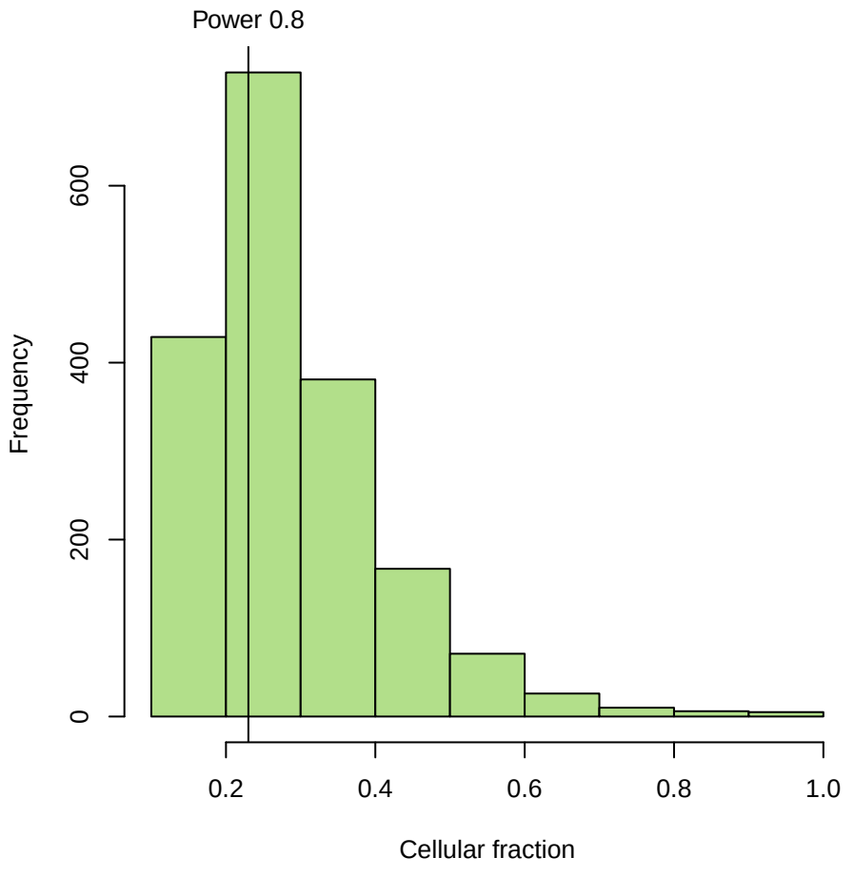

SCNA−fit log−likelihood: 1229.82
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
2 3 4 5 7
0 20 40 60 80
SNV Index

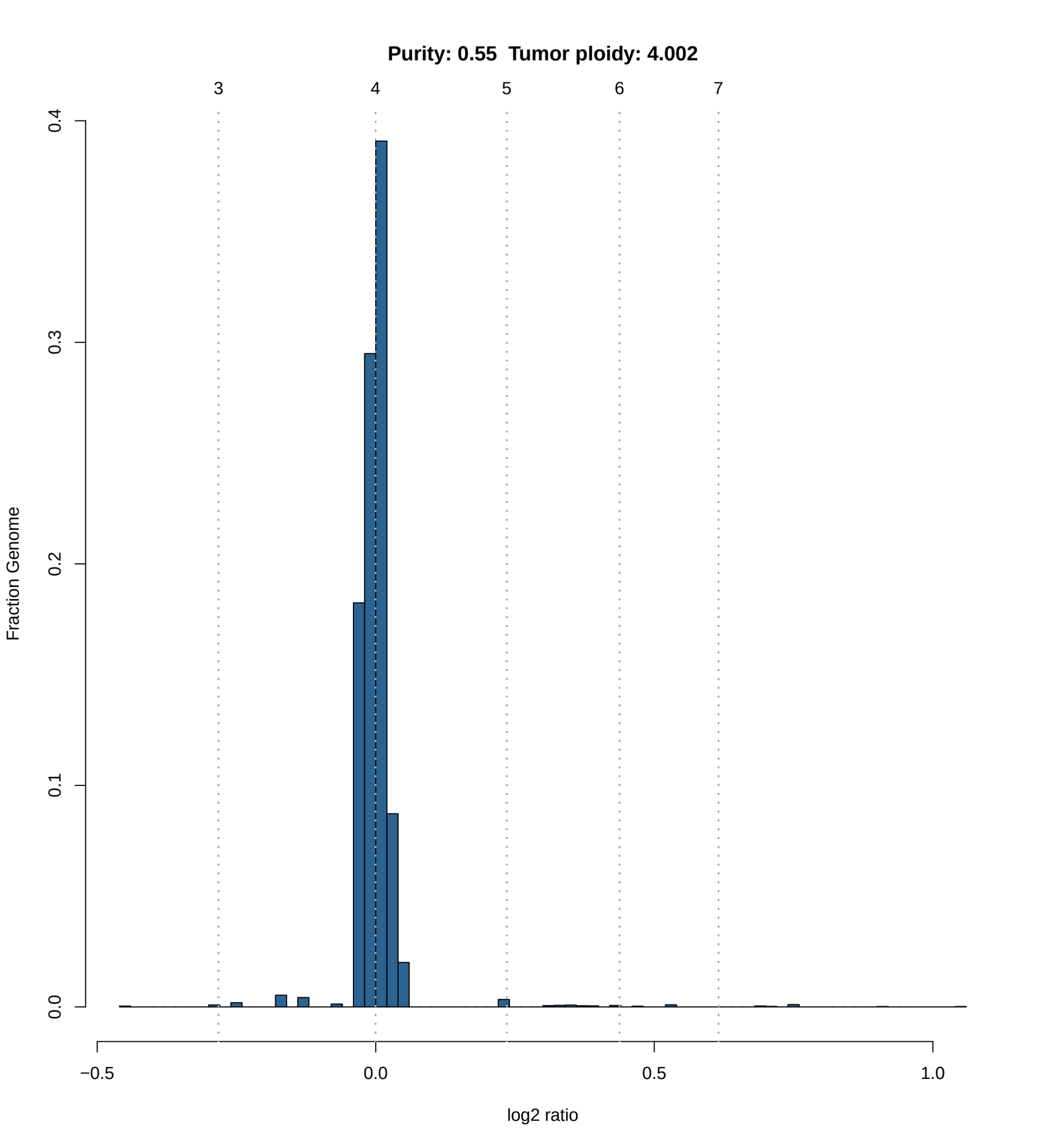

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80
SNV Index

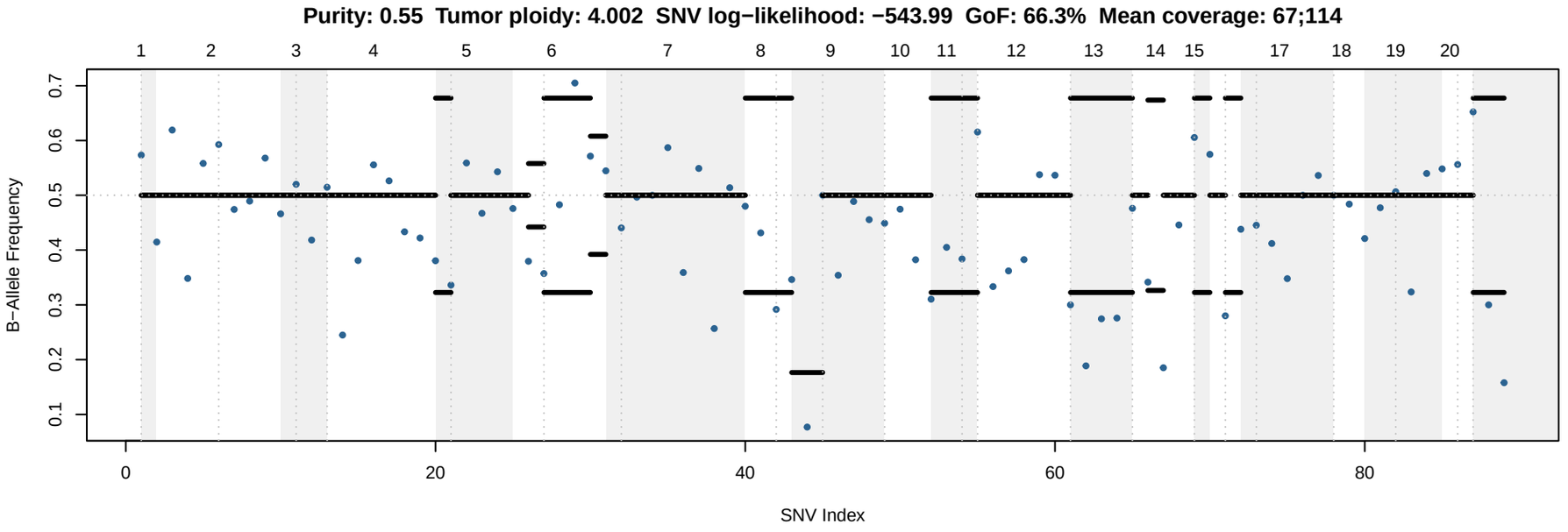

Allelic fraction (germline)
Copy Number log−ratio
3m2
3m1
6m2
2m0
3m0

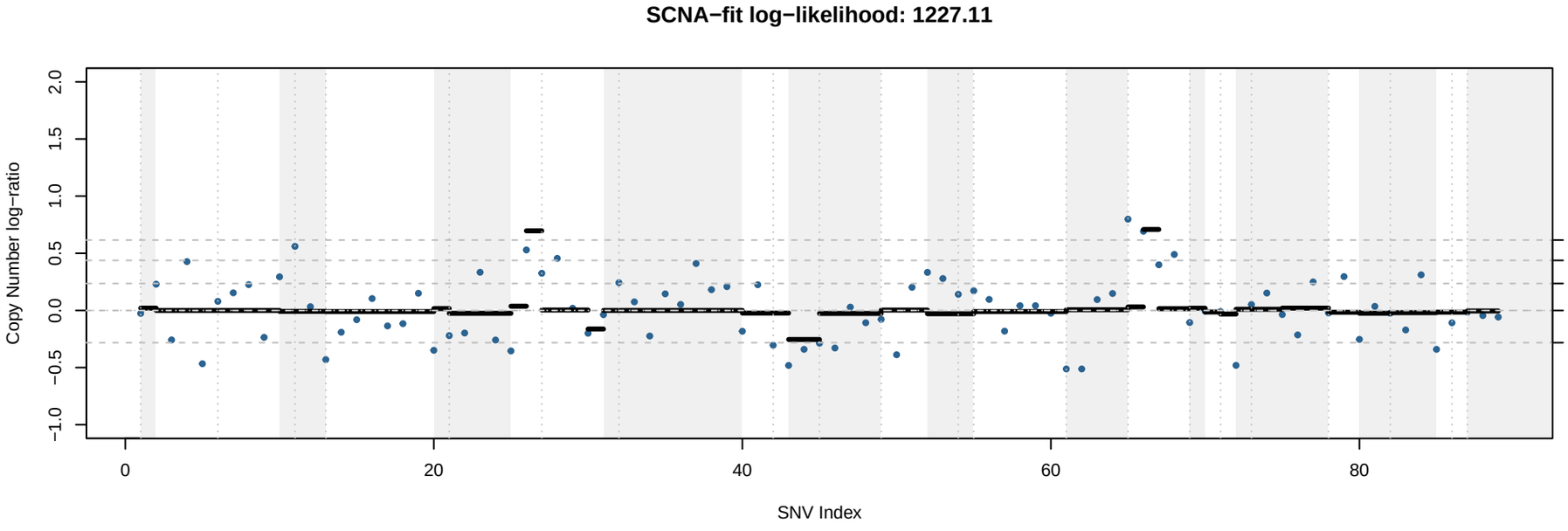

Coverage (log2)
Allelic fraction

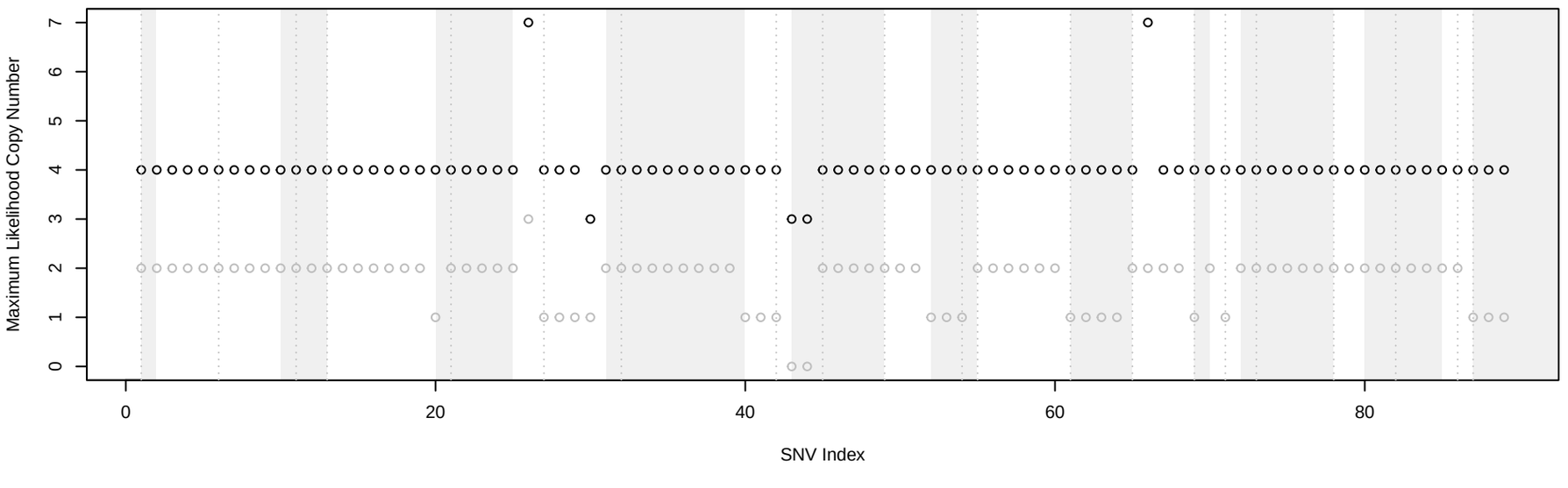

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
6m1
7m1

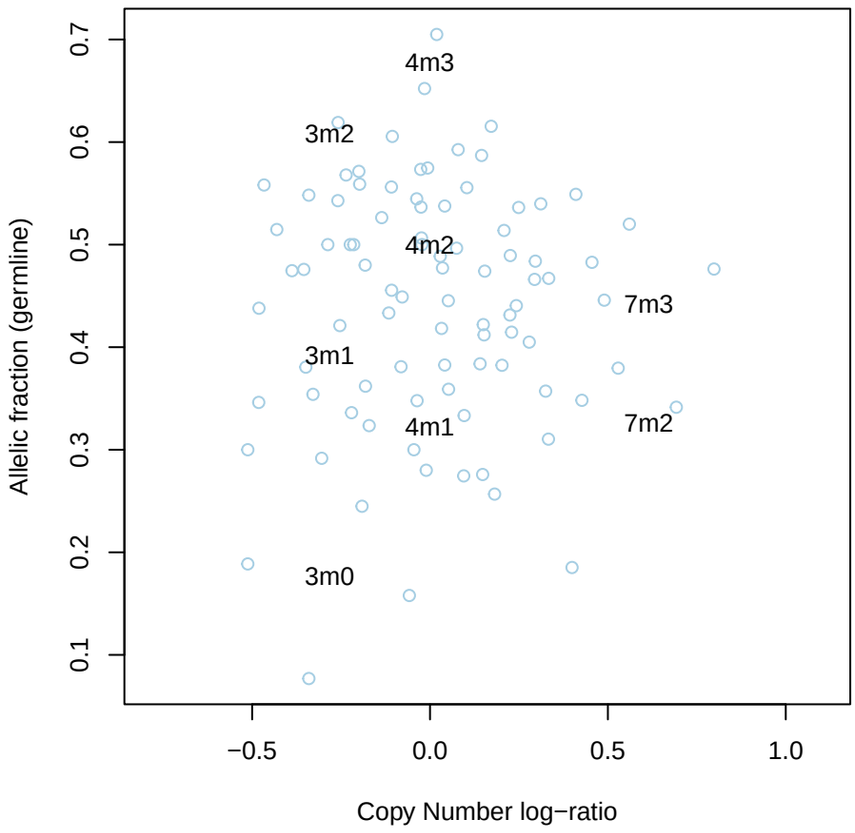

Power 0.8
Frequency
Cellular fraction

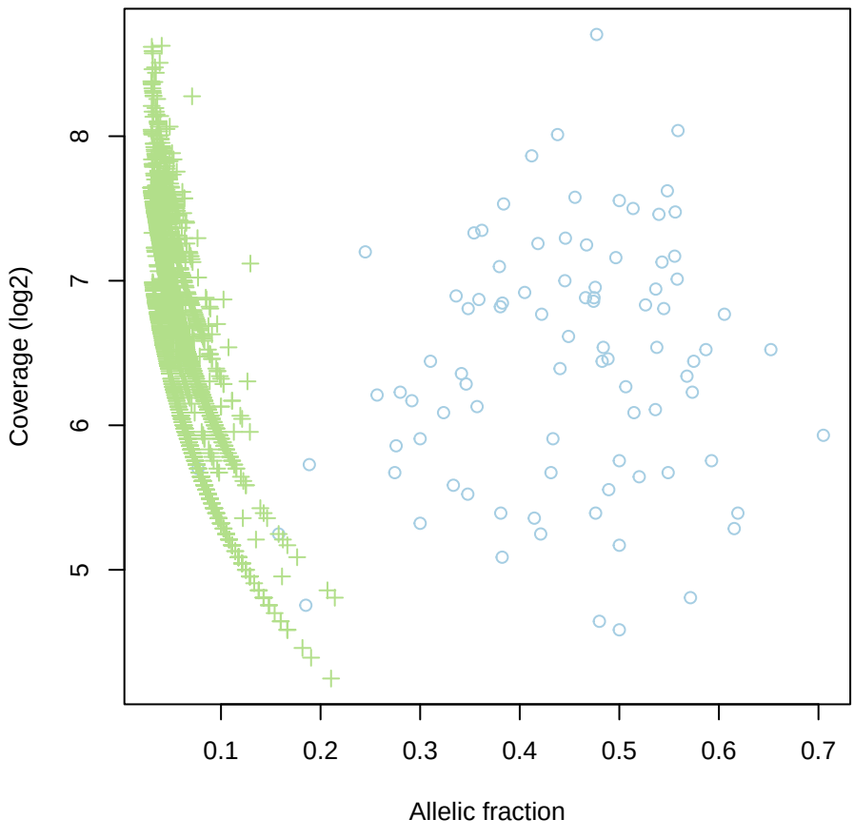

Purity: 0.55 Tumor ploidy: 4.002
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

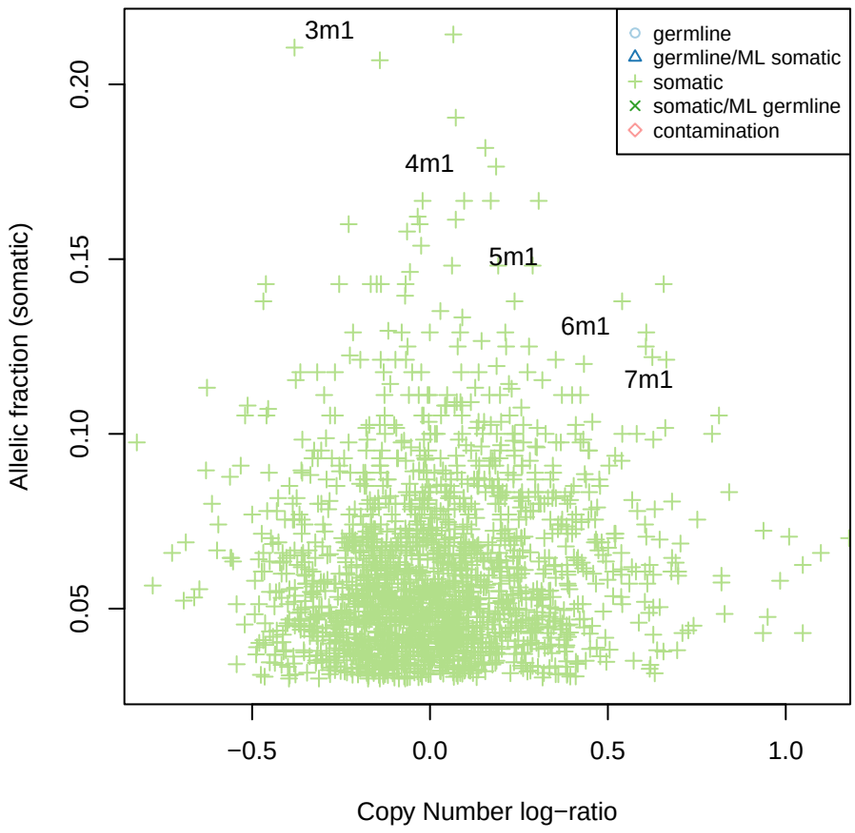

Purity: 0.55 Tumor ploidy: 4.002 SNV log−likelihood: −543.99 GoF: 66.3% Mean coverage: 67;114
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

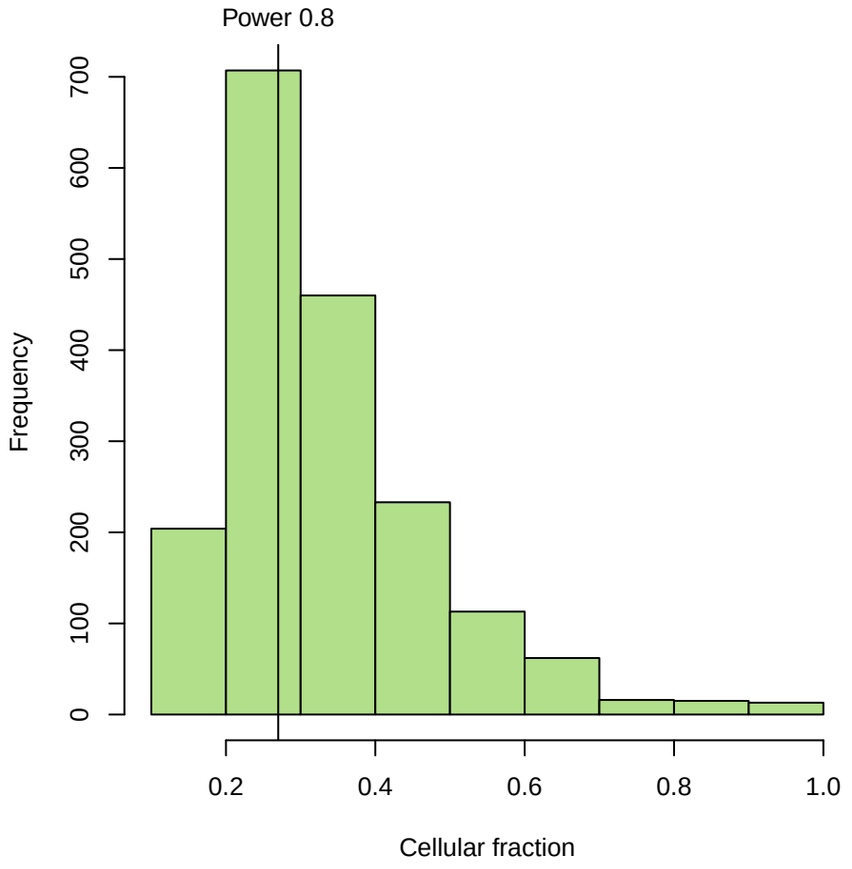

SCNA−fit log−likelihood: 1227.11
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
3 4 5 7
0 20 40 60 80
SNV Index

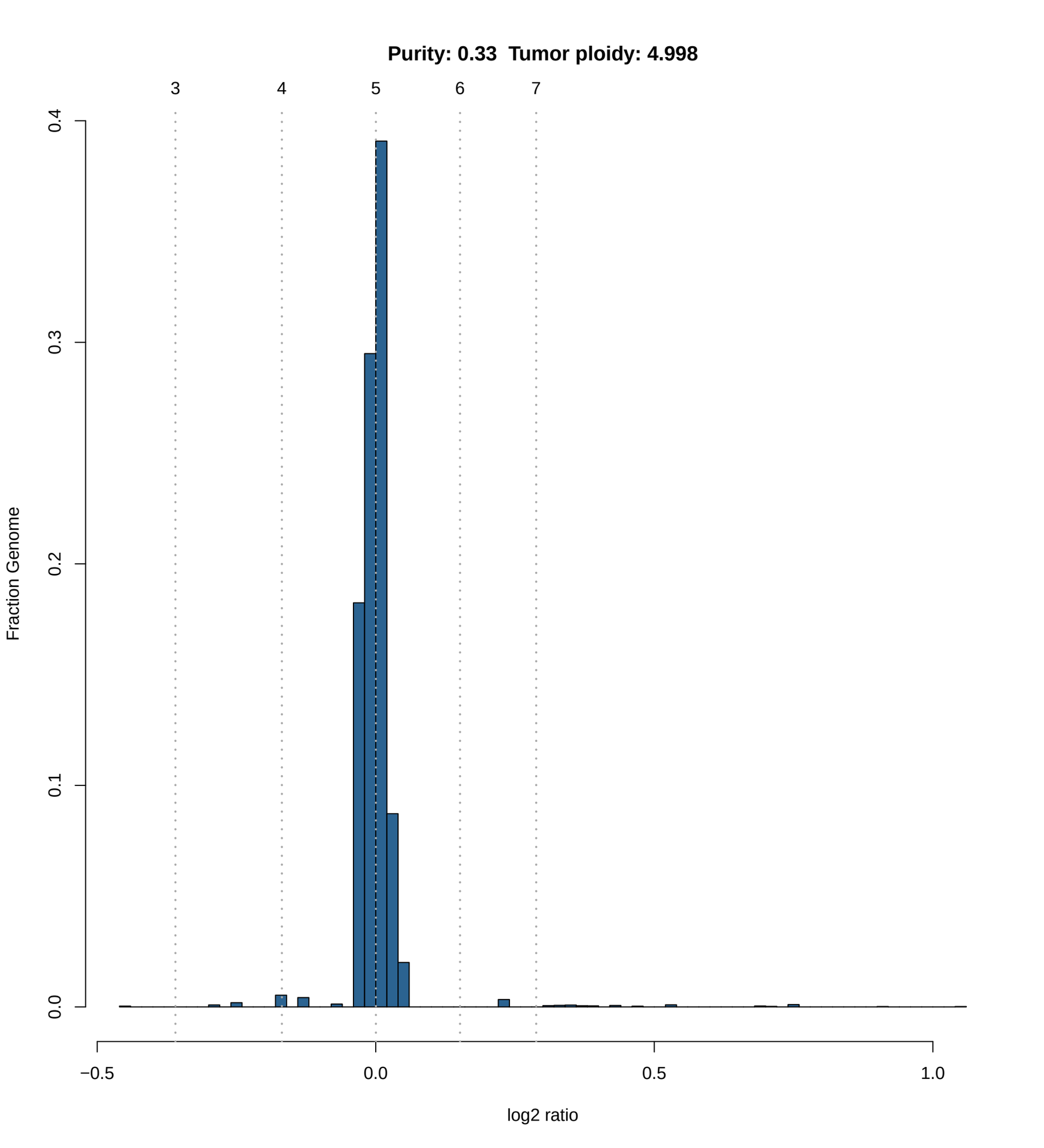

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

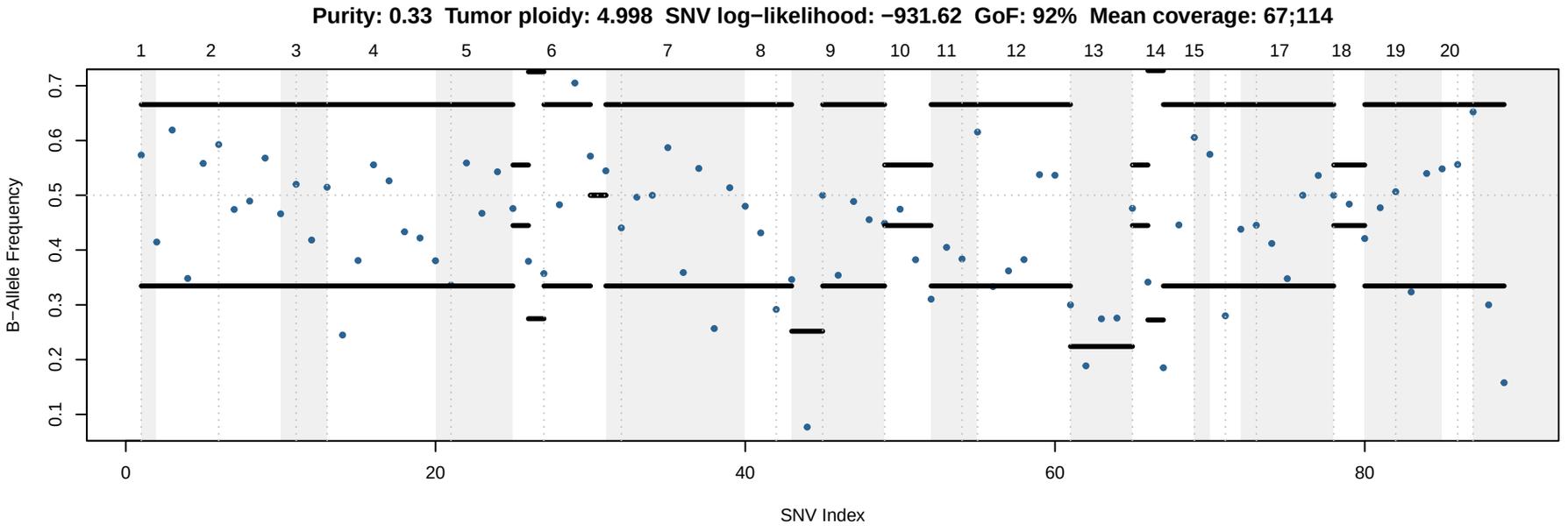

4m3
3m2
4m2
7m3
3m1
4m1
7m2
3m0
Allelic fraction (germline)
Copy Number log−ratio

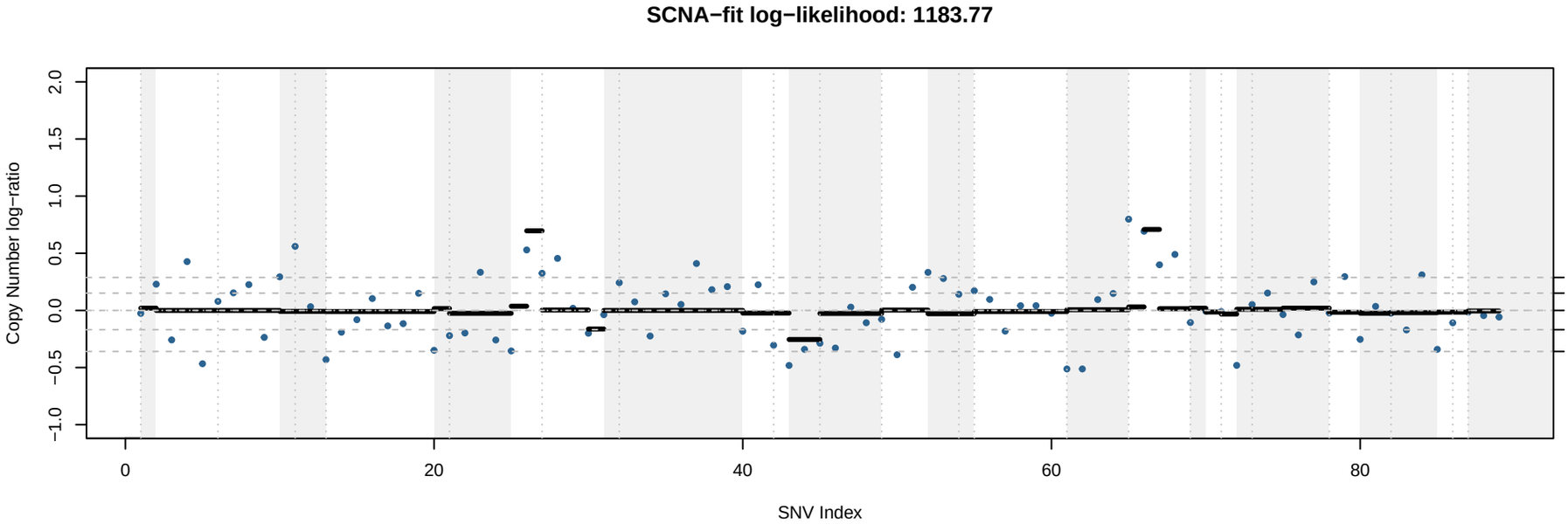

Coverage (log2)
Allelic fraction

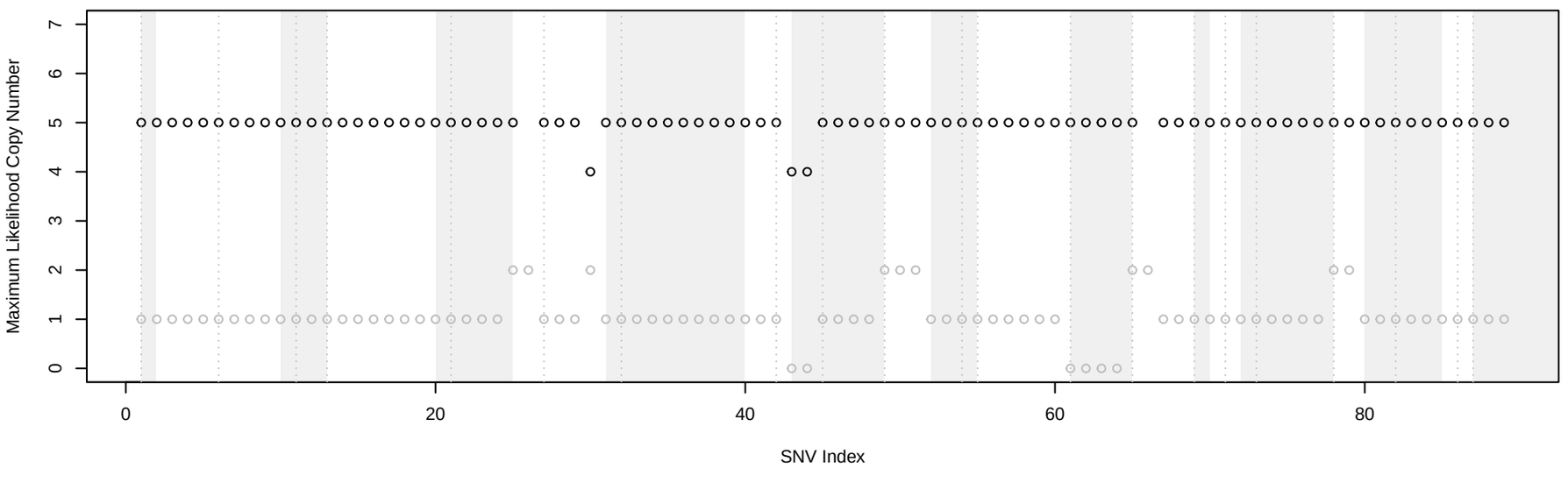

3m1
4m1
5m1
6m1
7m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

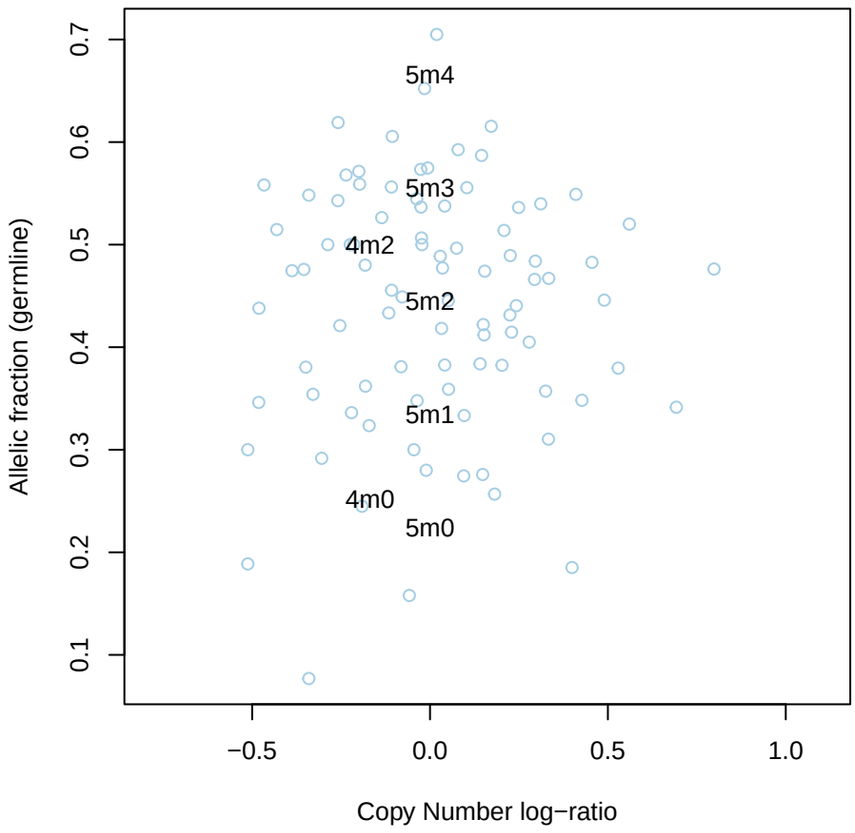

Power 0.8
Frequency
Cellular fraction

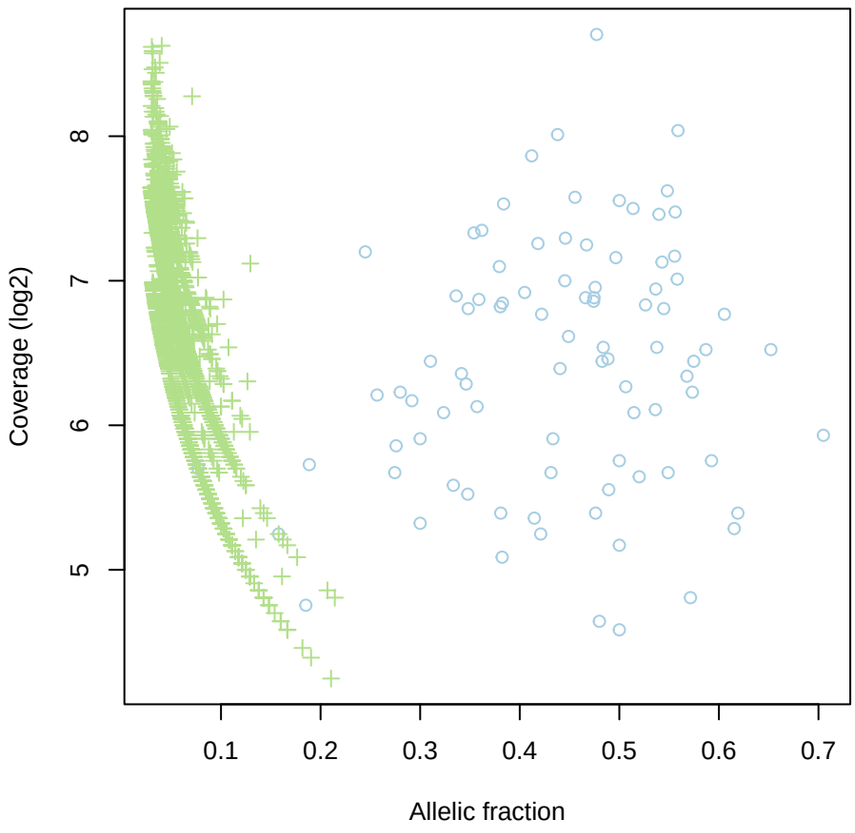

Purity: 0.33 Tumor ploidy: 4.998
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

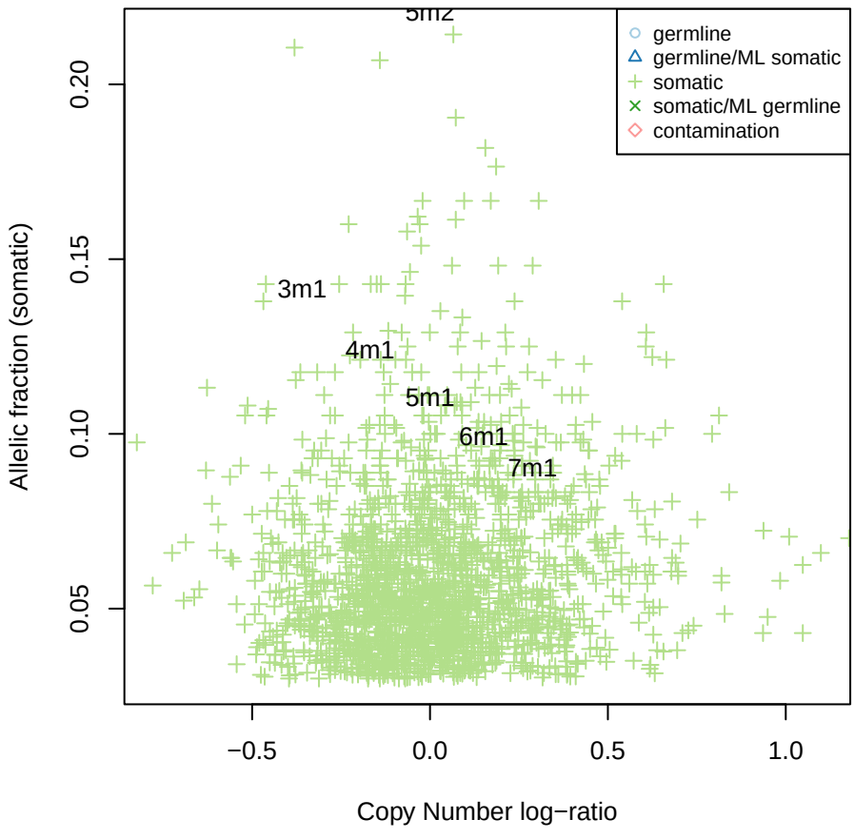

Purity: 0.33 Tumor ploidy: 4.998 SNV log−likelihood: −931.62 GoF: 92% Mean coverage: 67;114
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

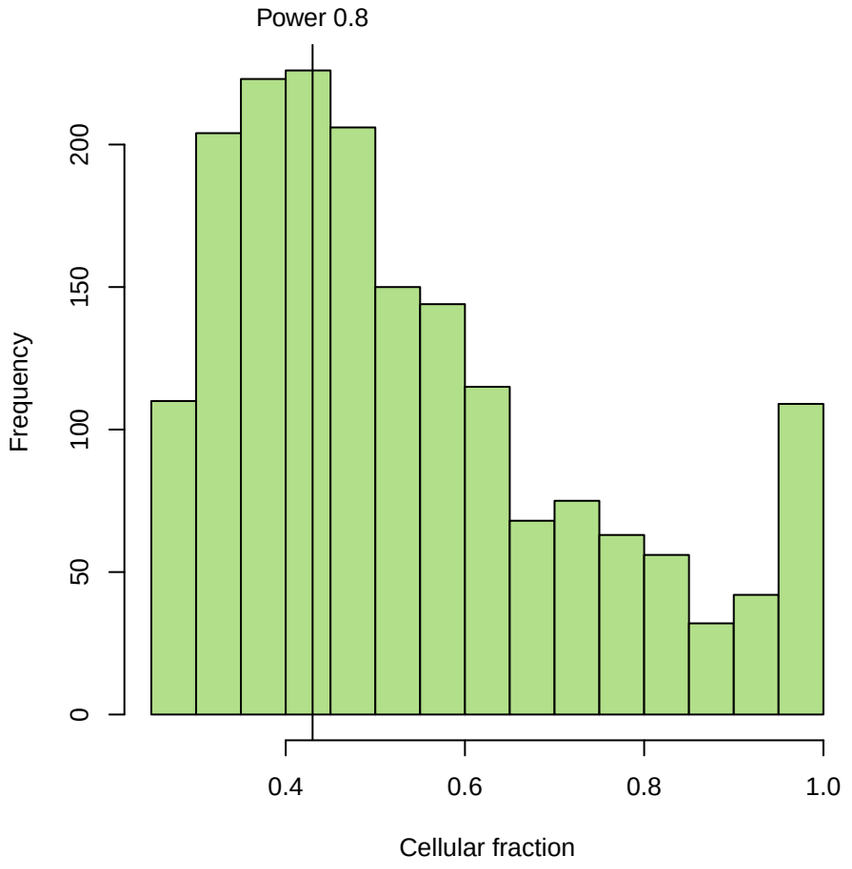

SCNA−fit log−likelihood: 1183.77
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
3 5 7
0 20 40 60 80
SNV Index

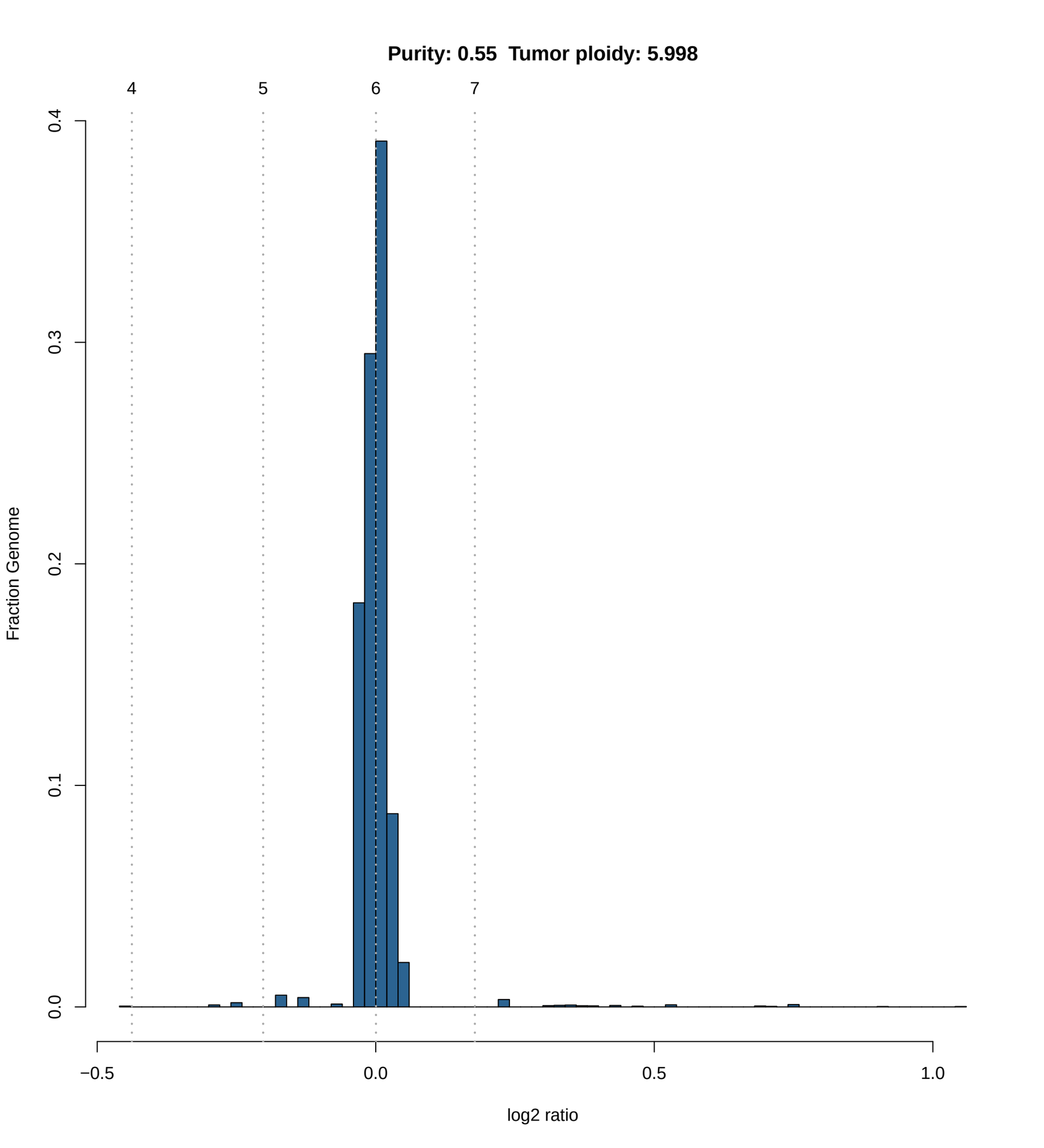

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

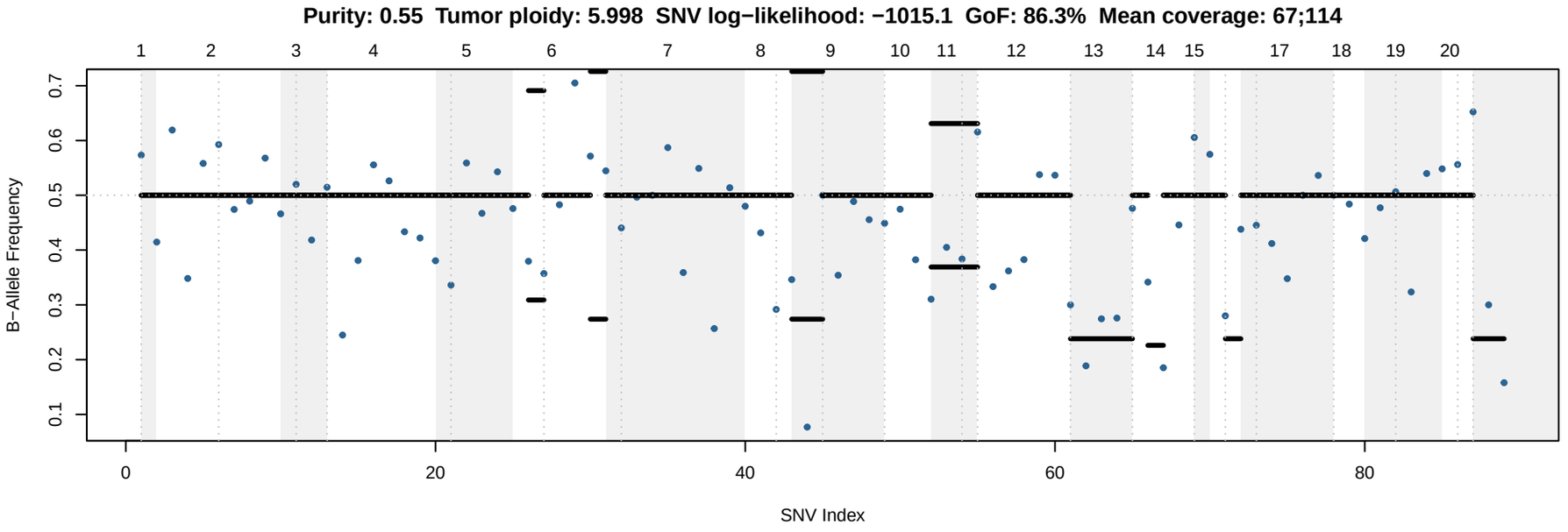

Allelic fraction (germline)
Copy Number log−ratio
5m4
5m3
4m2
5m2
5m1
4m0
5m0

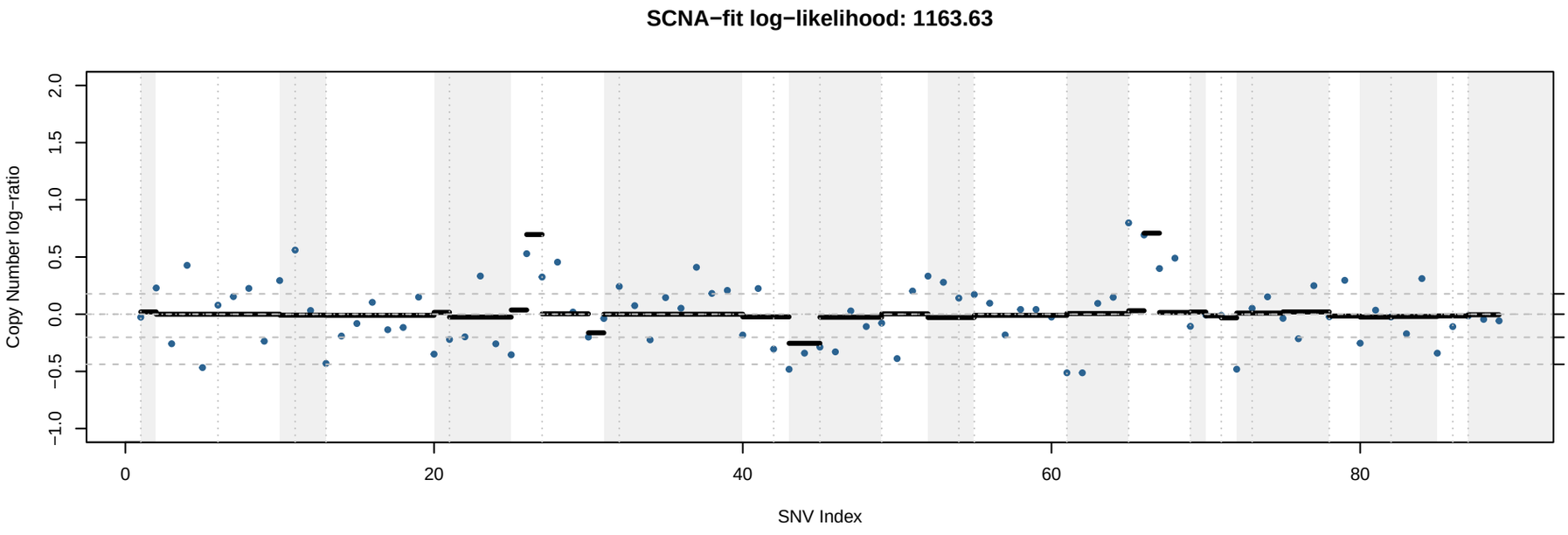

Coverage (log2)
Allelic fraction

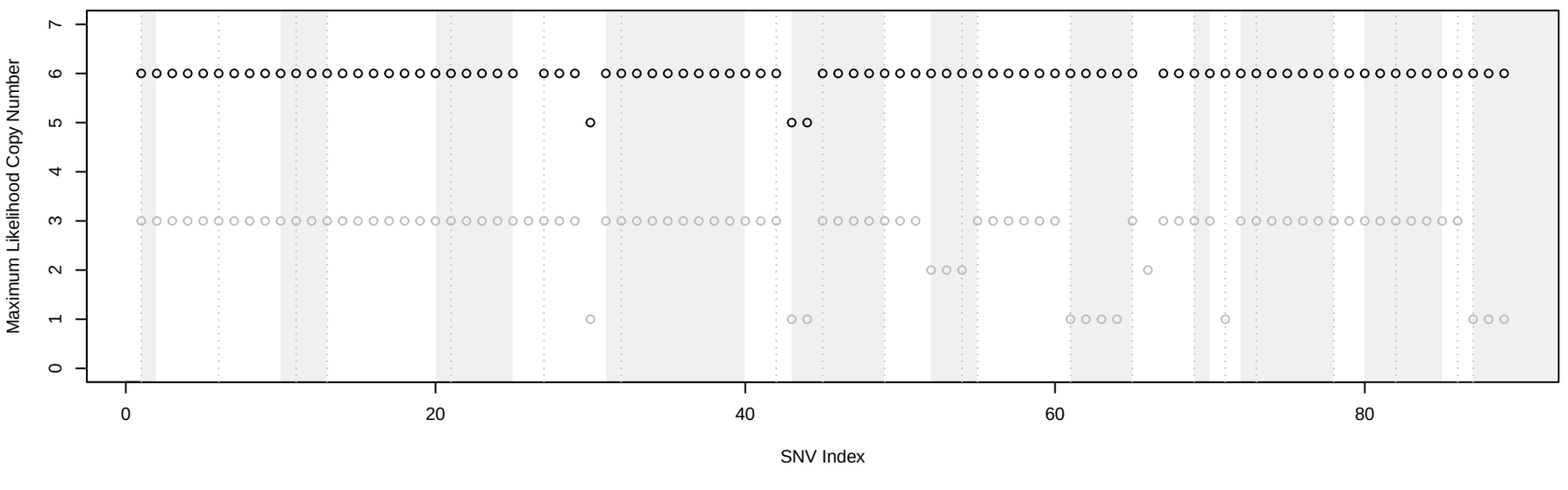

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
6m1
7m1

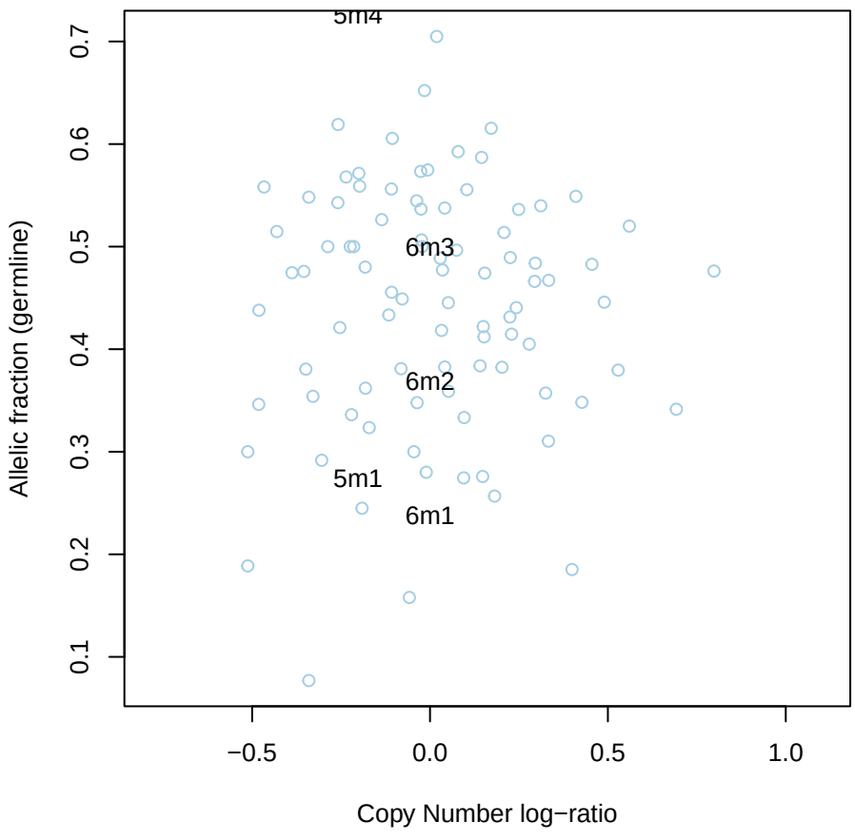

Power 0.8
Frequency
Cellular fraction

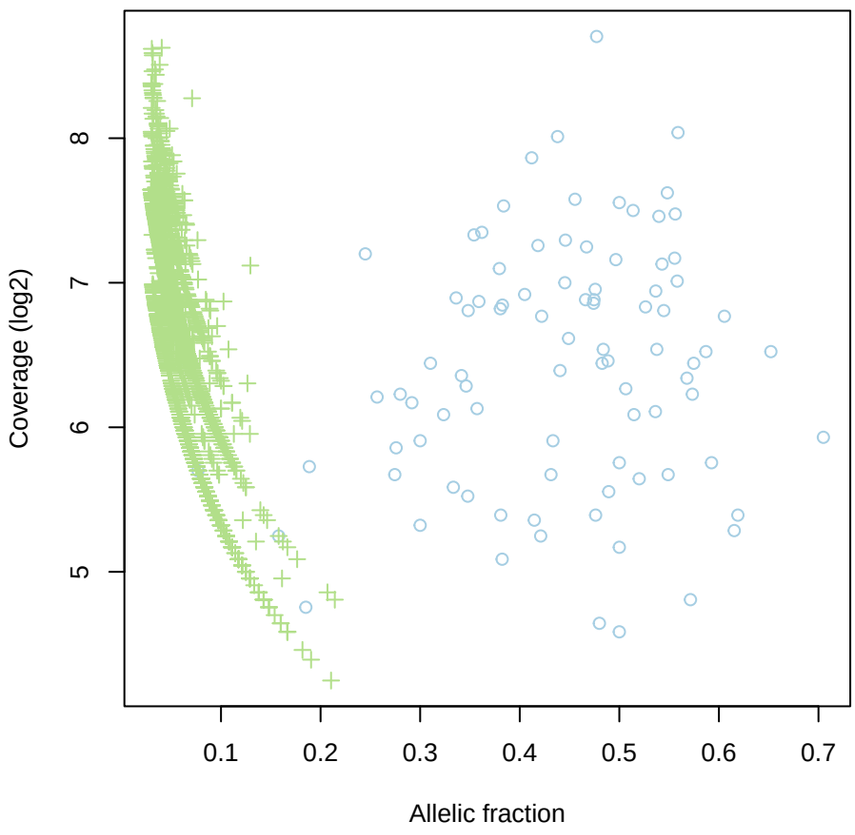

Purity: 0.55 Tumor ploidy: 5.998
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

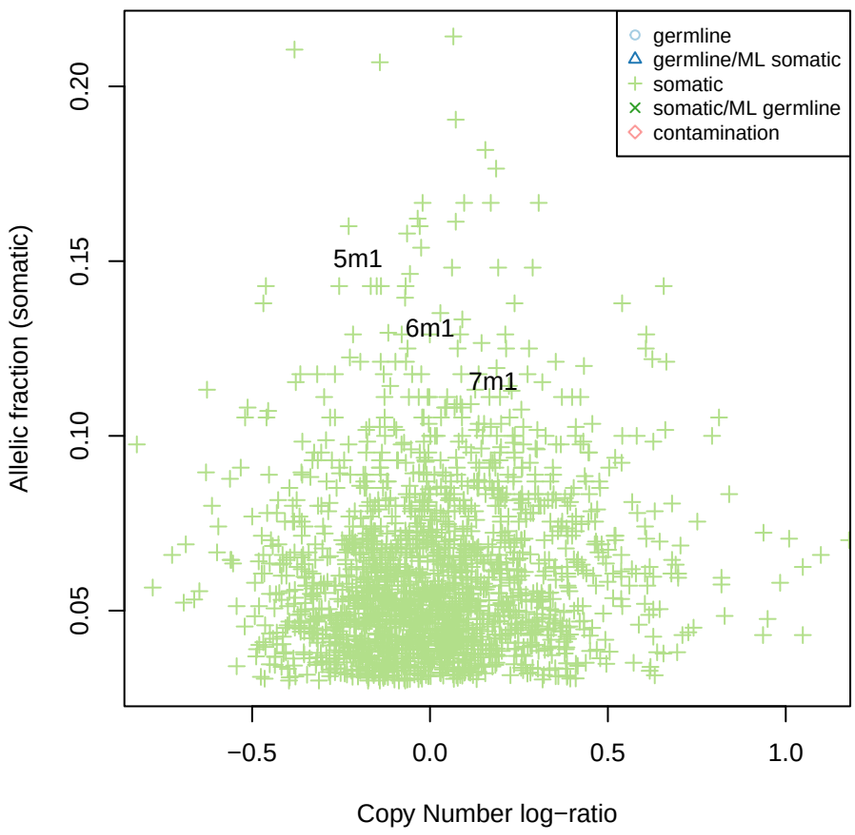

Purity: 0.55 Tumor ploidy: 5.998 SNV log−likelihood: −1015.1 GoF: 86.3% Mean coverage: 67;114
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

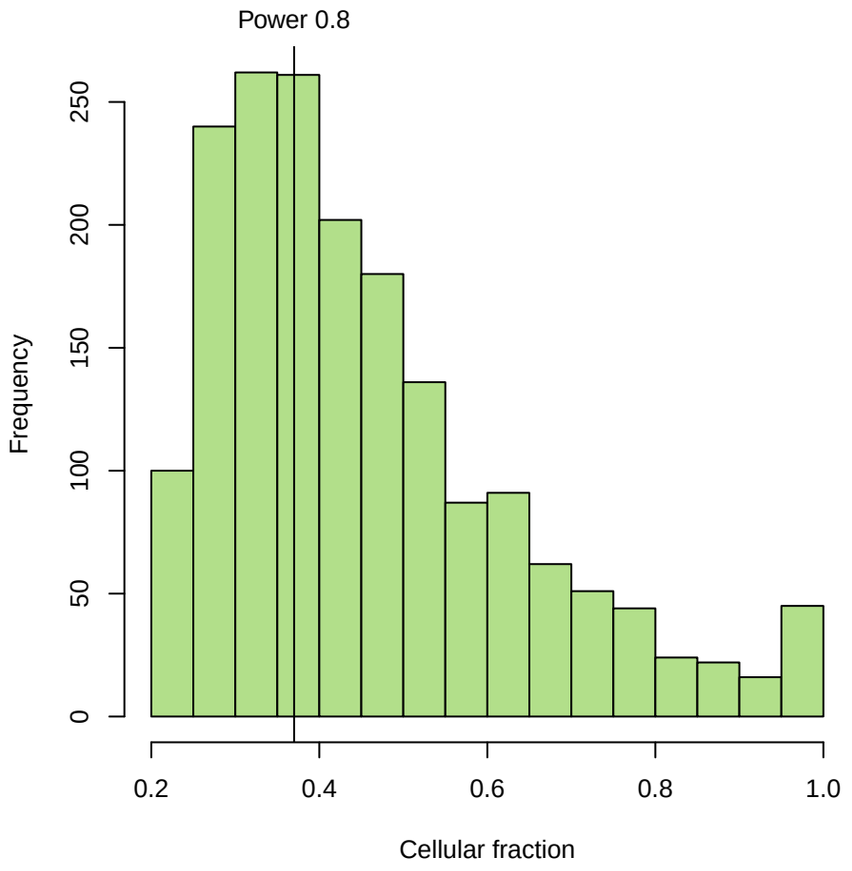

SCNA−fit log−likelihood: 1163.63
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
4 5 7
0 20 40 60 80
SNV Index

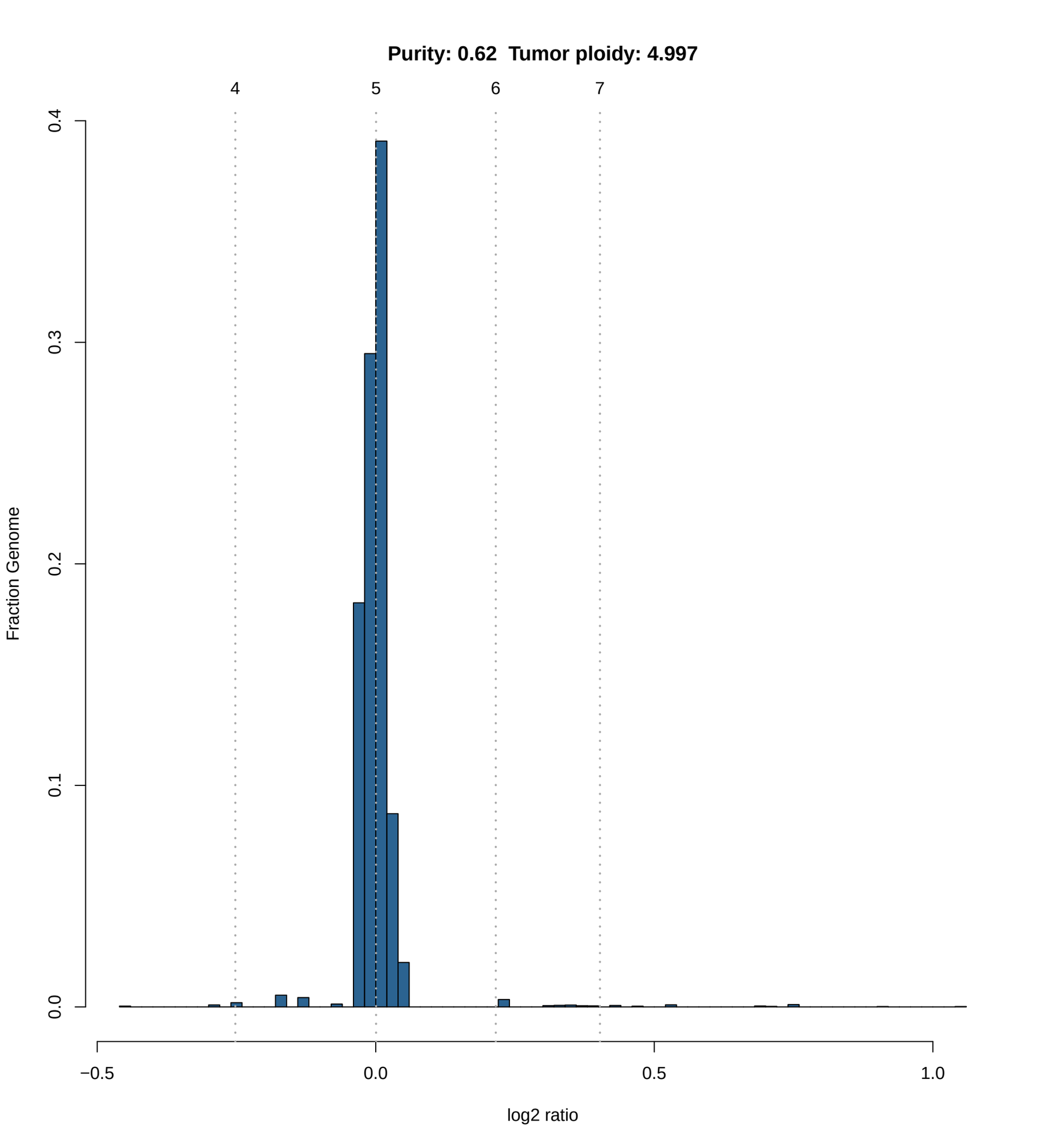

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

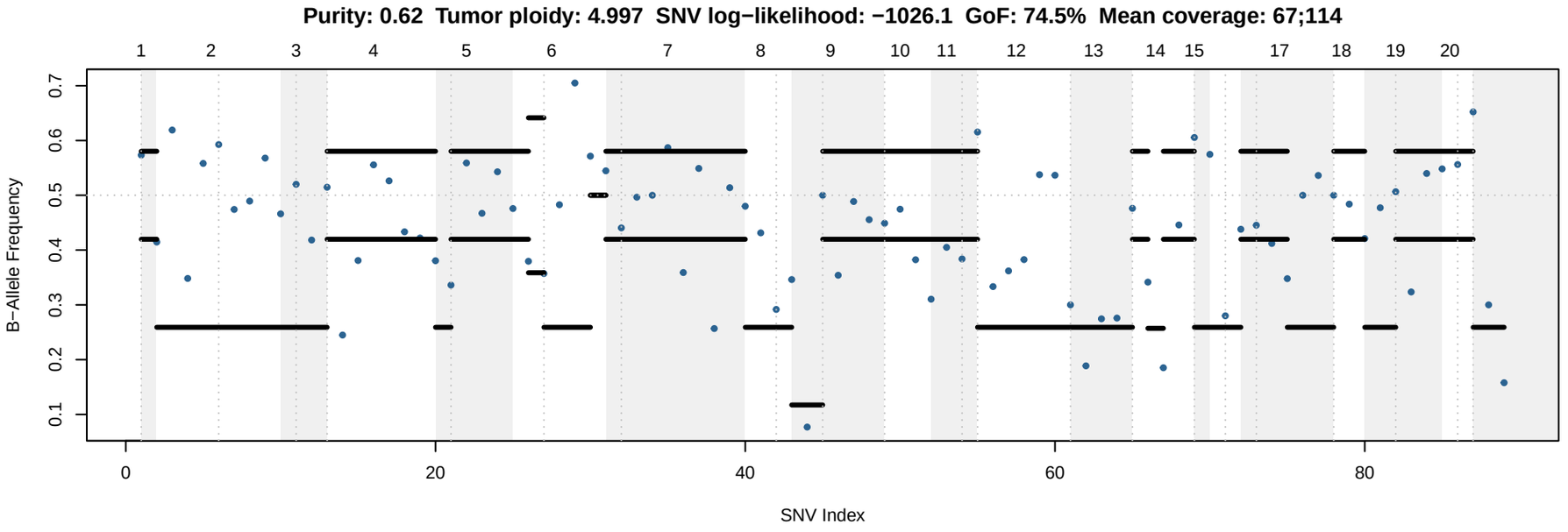

5m4
6m3
6m2
5m1
6m1
Allelic fraction (germline)
Copy Number log−ratio

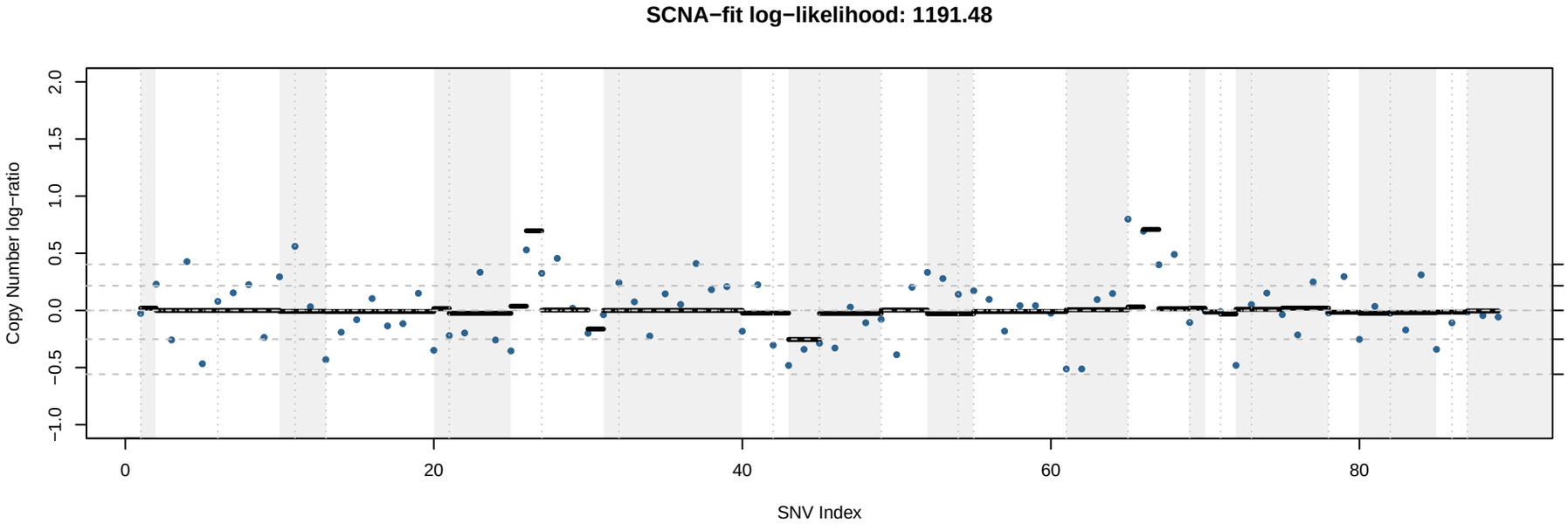

Coverage (log2)
Allelic fraction

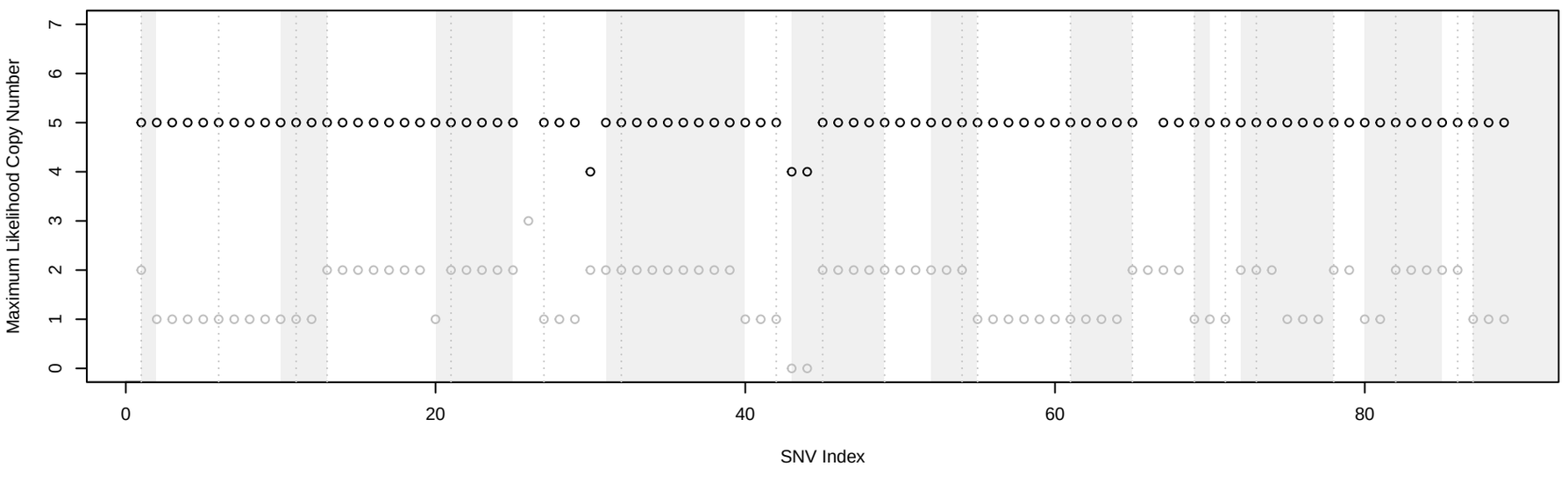

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

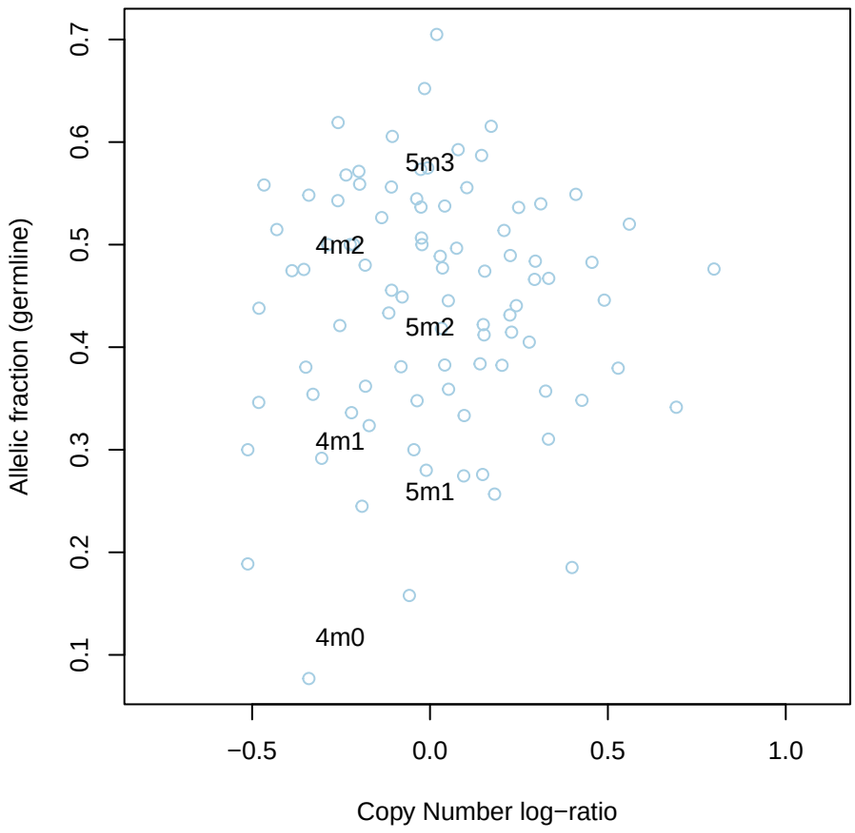

Power 0.8
Frequency
Cellular fraction

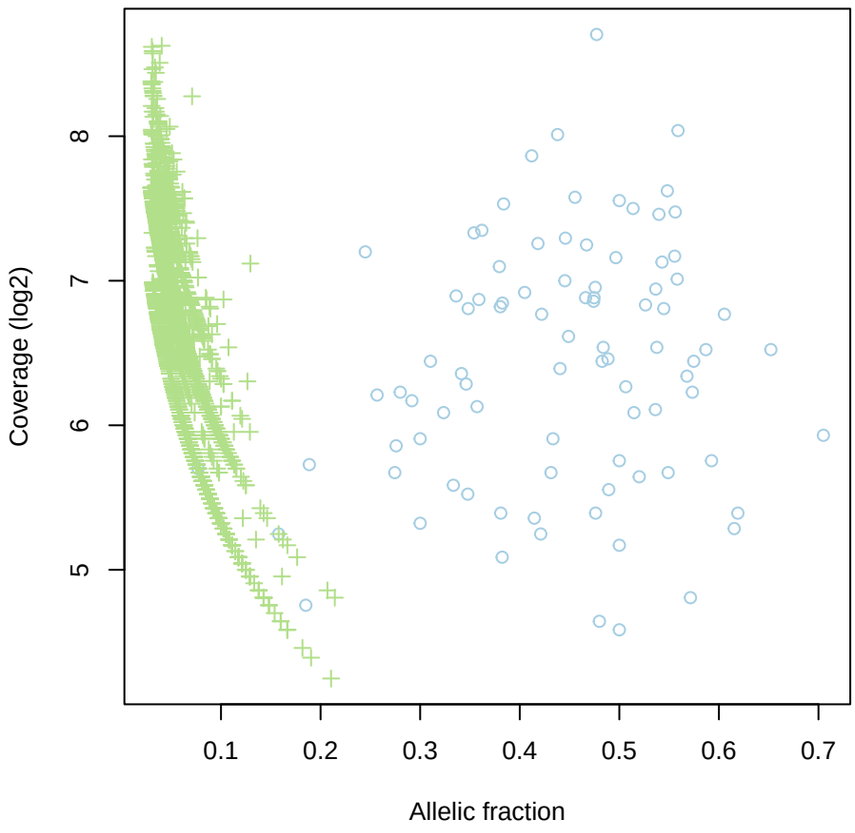

Purity: 0.62 Tumor ploidy: 4.997
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

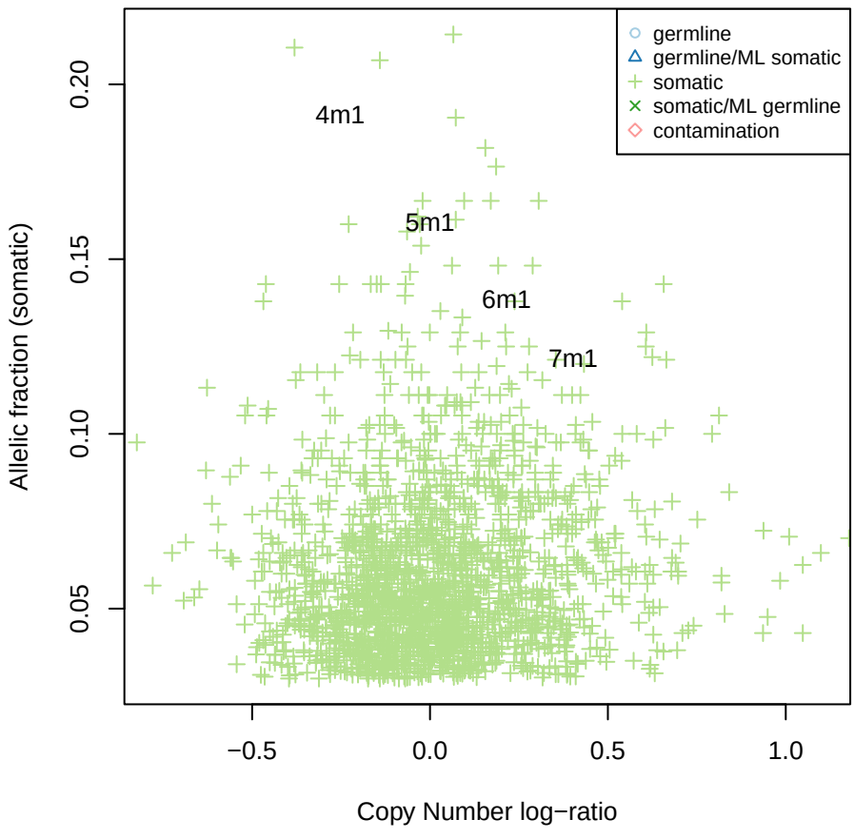

Purity: 0.62 Tumor ploidy: 4.997 SNV log−likelihood: −1026.1 GoF: 74.5% Mean coverage: 67;114
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

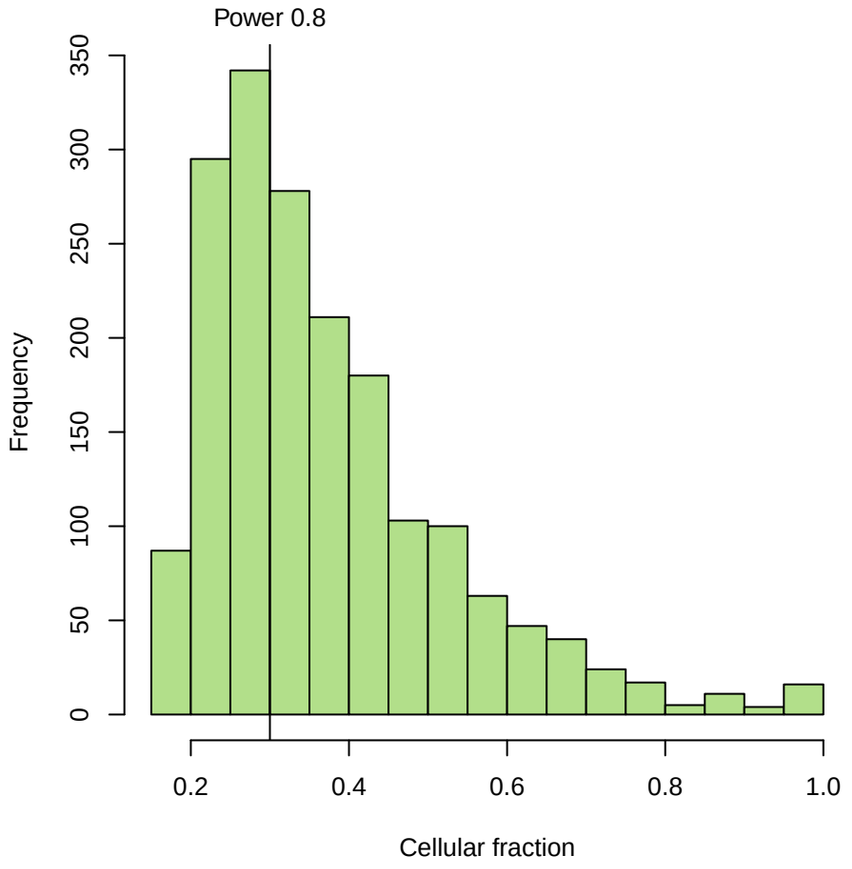

SCNA−fit log−likelihood: 1191.48
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
3 4 5 7
0 20 40 60 80
SNV Index

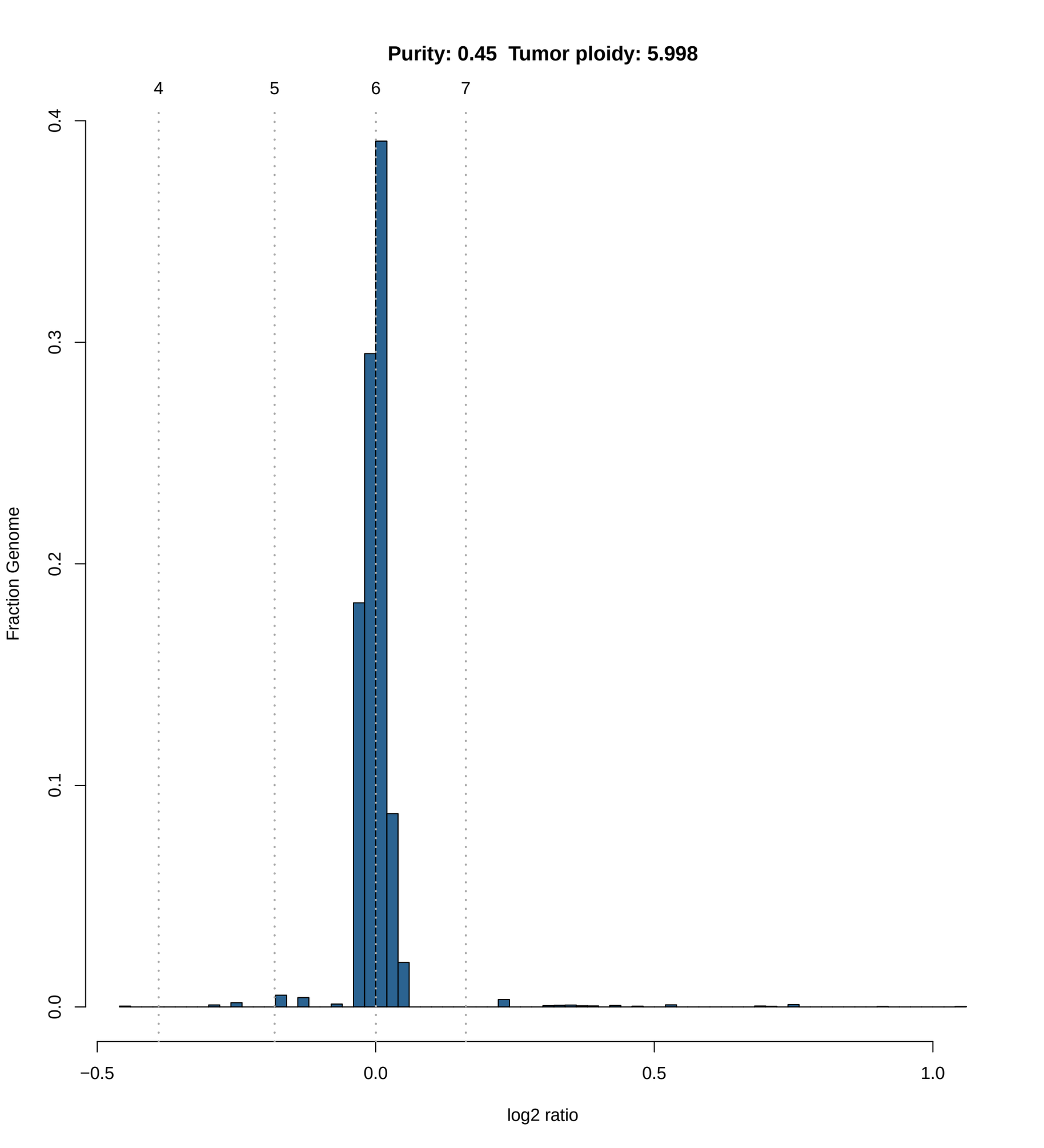

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

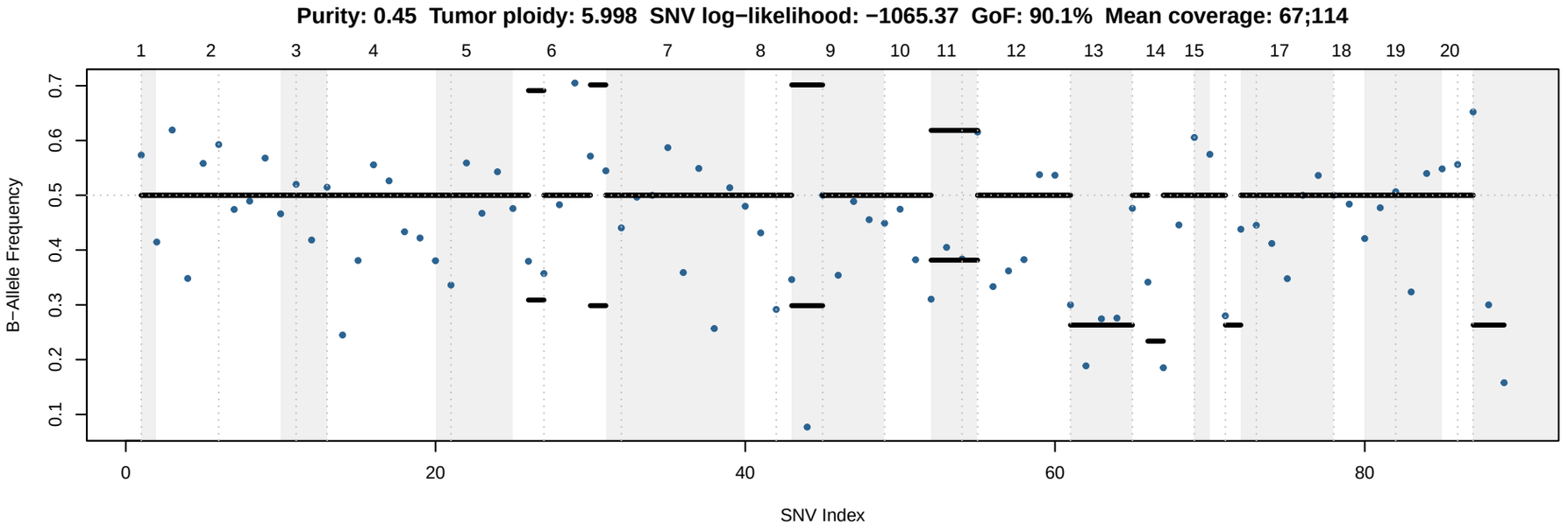

Allelic fraction (germline)
Copy Number log−ratio
5m3
4m2
5m2
4m1
5m1
4m0

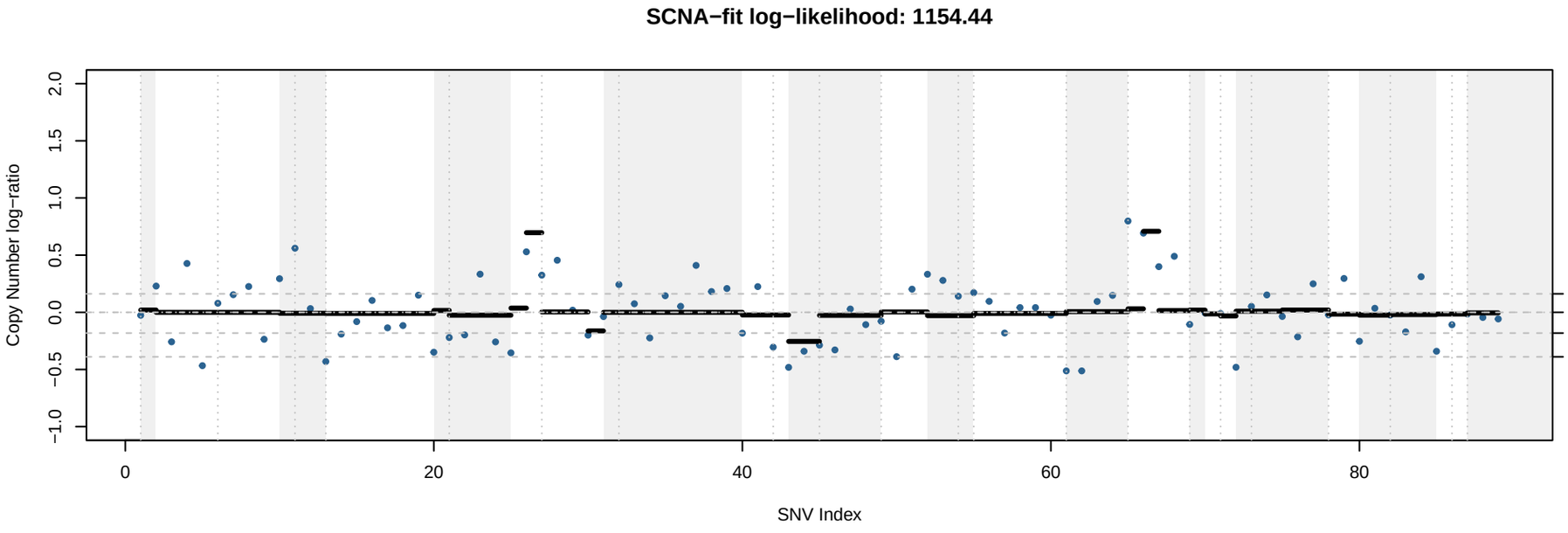

Coverage (log2)
Allelic fraction

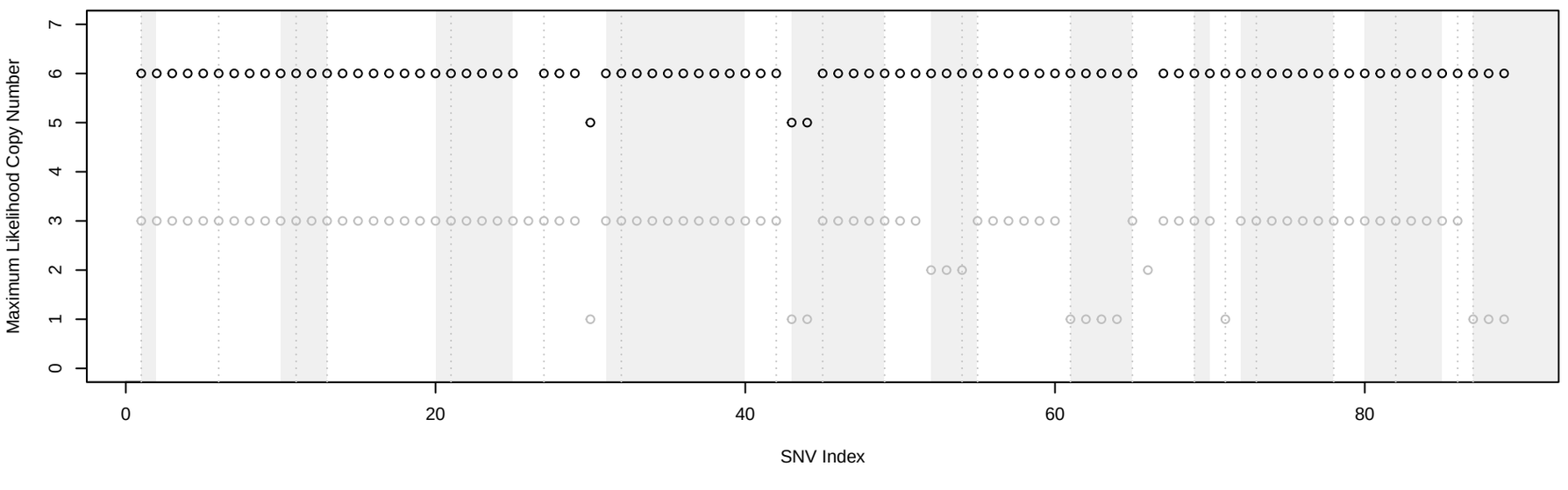

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
7m1

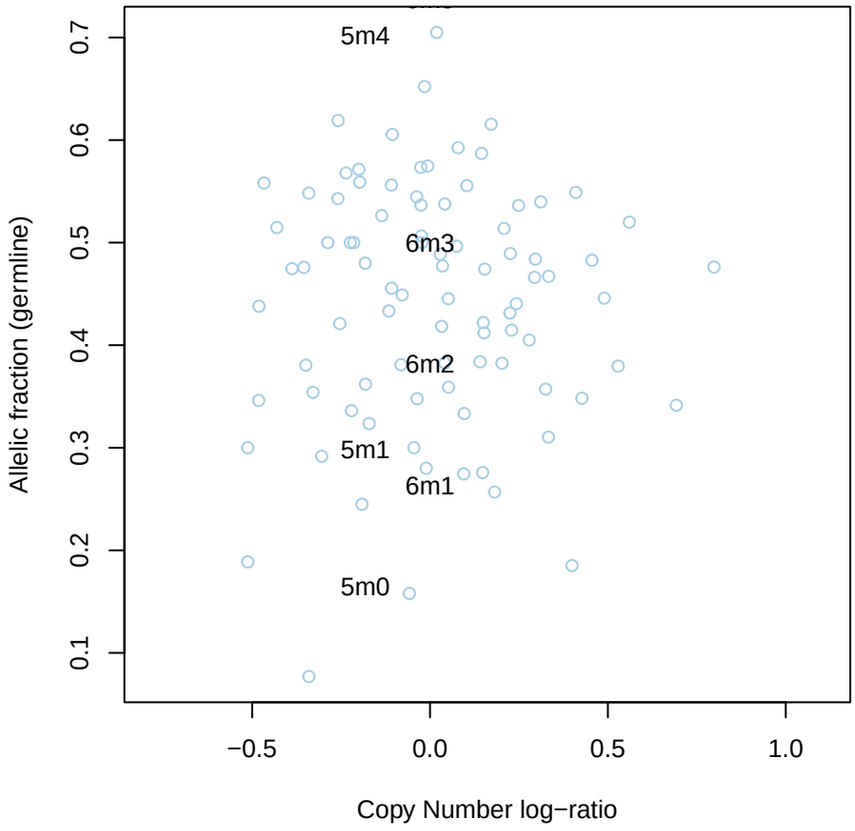

Power 0.8
Frequency
Cellular fraction

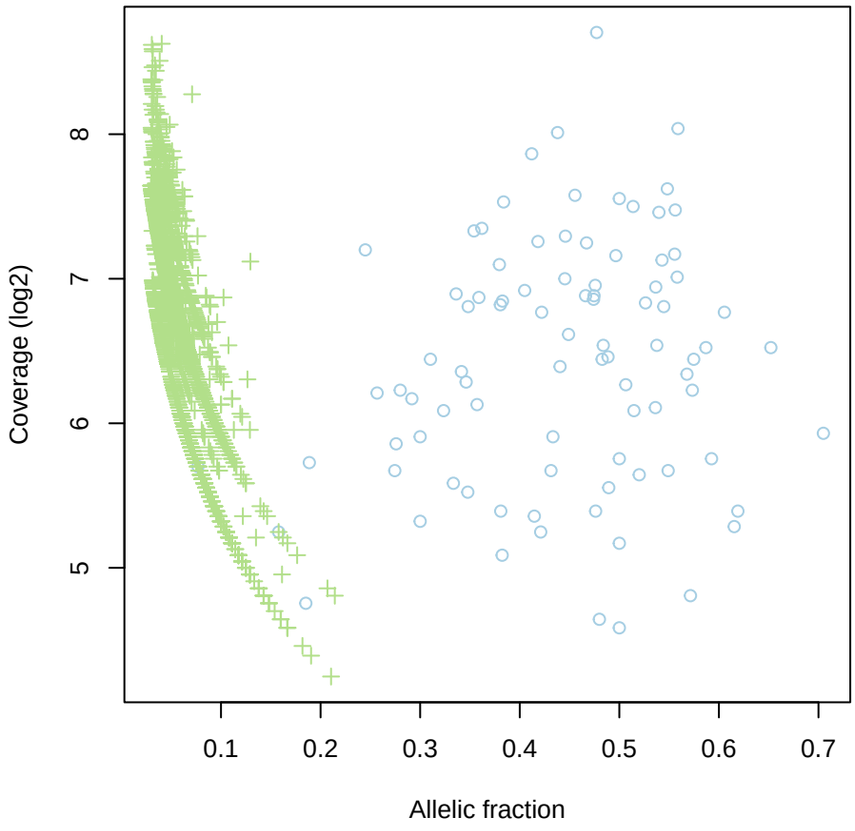

Purity: 0.45 Tumor ploidy: 5.998
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

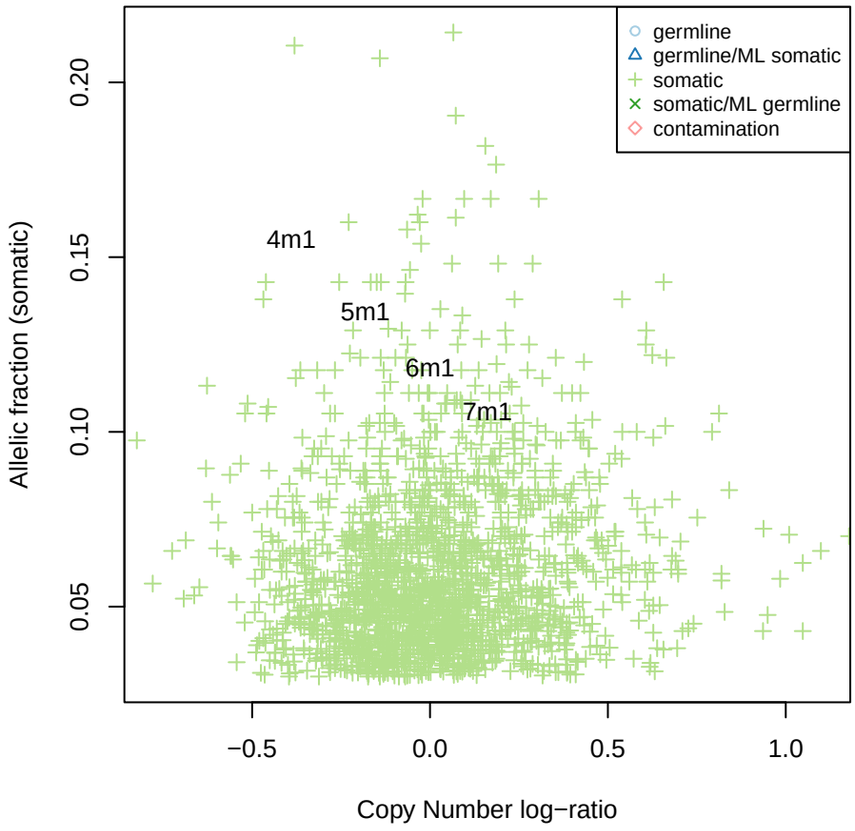

Purity: 0.45 Tumor ploidy: 5.998 SNV log−likelihood: −1065.37 GoF: 90.1% Mean coverage: 67;114
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

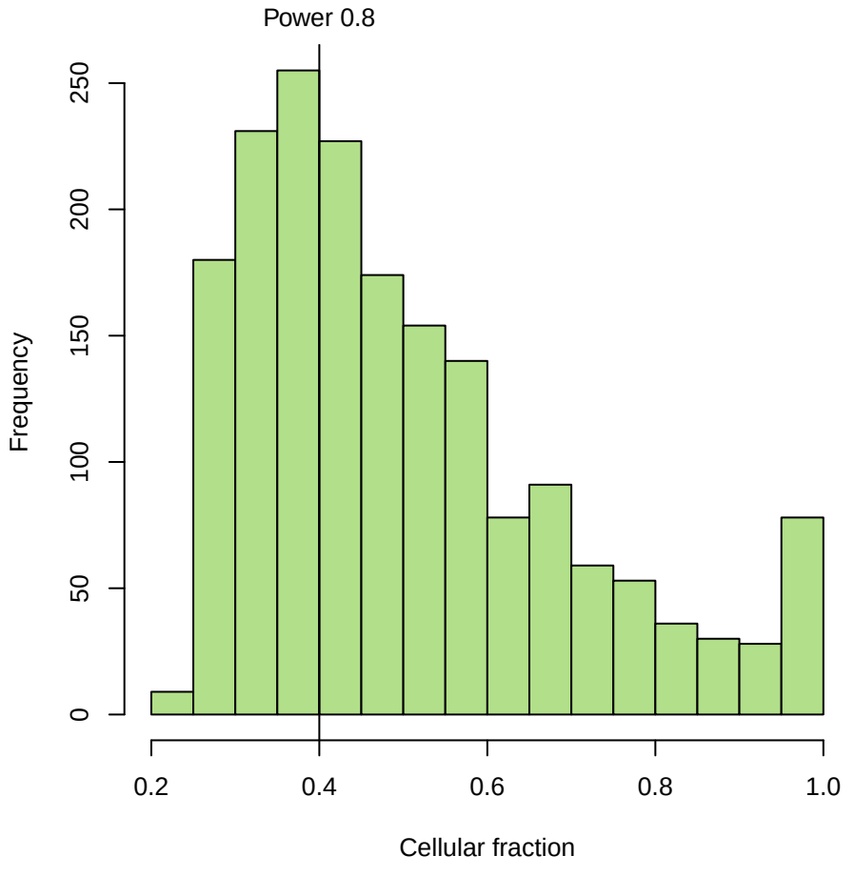

SCNA−fit log−likelihood: 1154.44
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
4 6
0 20 40 60 80
SNV Index

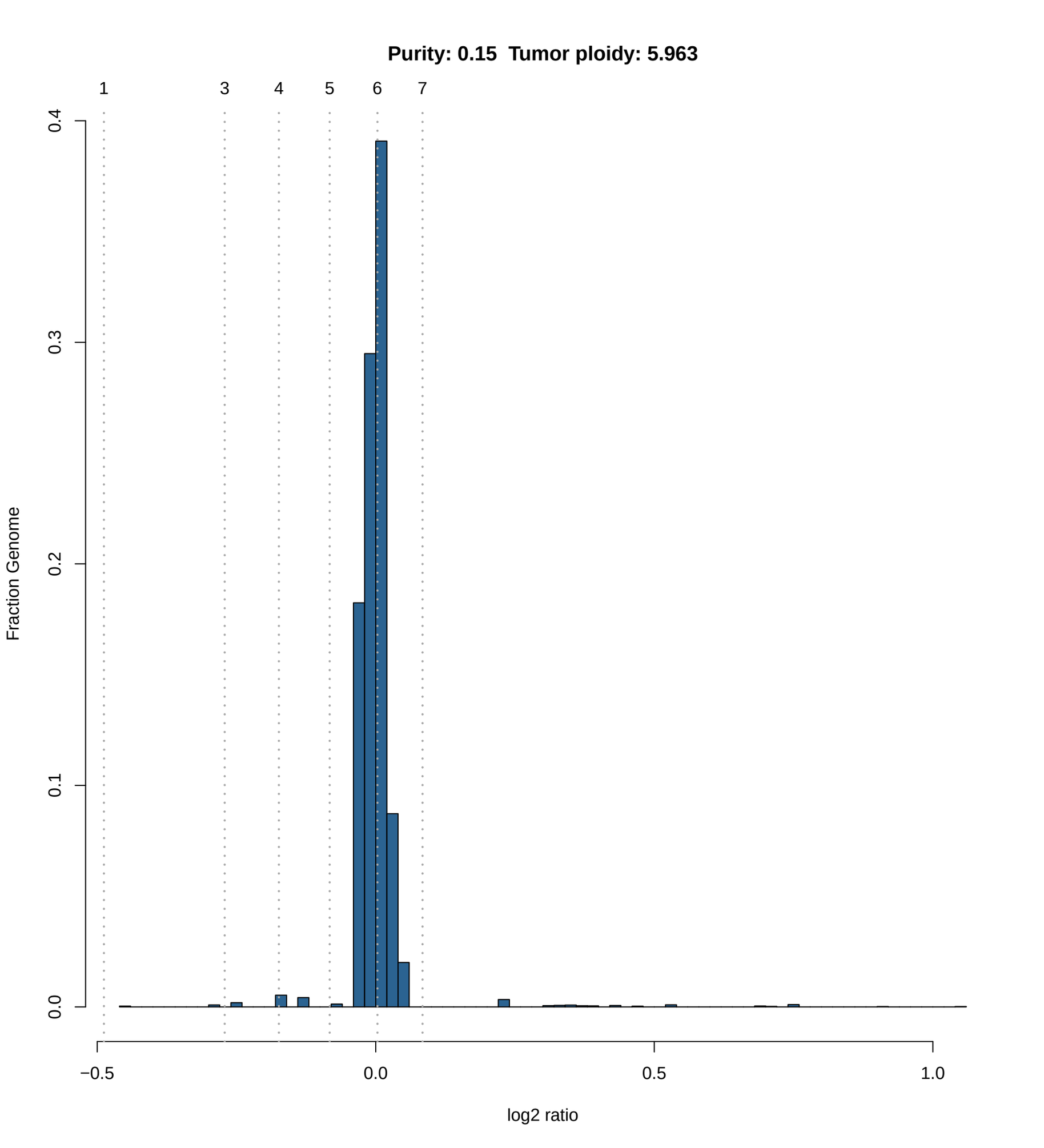

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

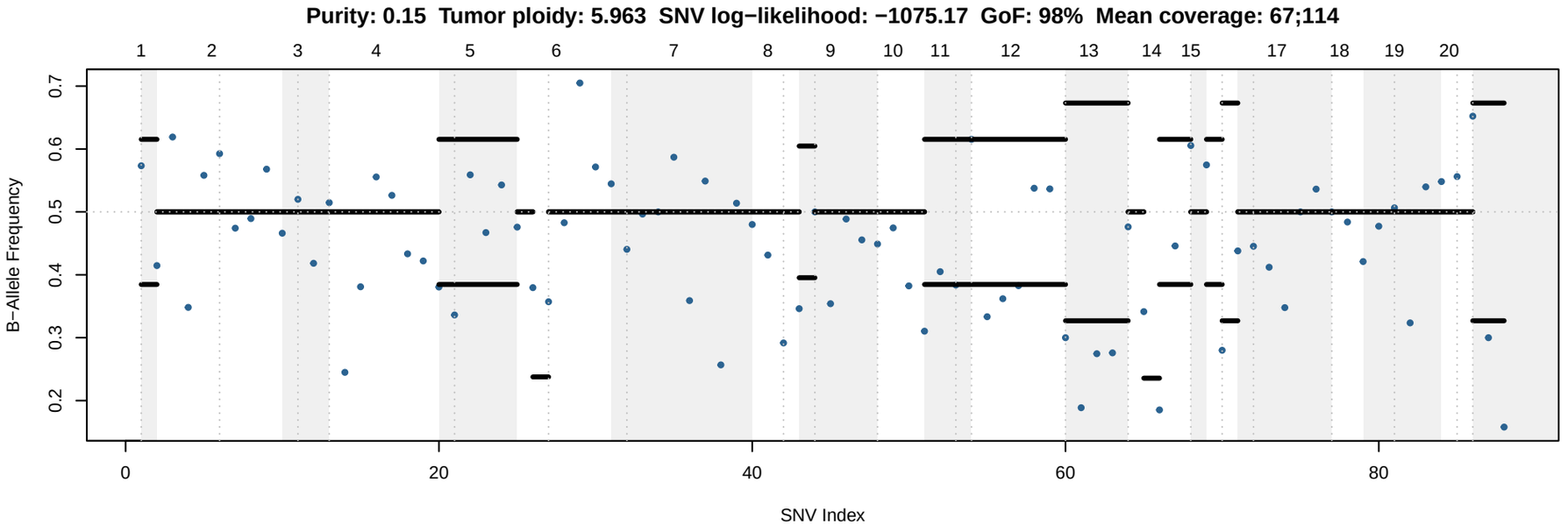

5m4
6m3
6m2
5m1
6m1
5m0
Allelic fraction (germline)
Copy Number log−ratio

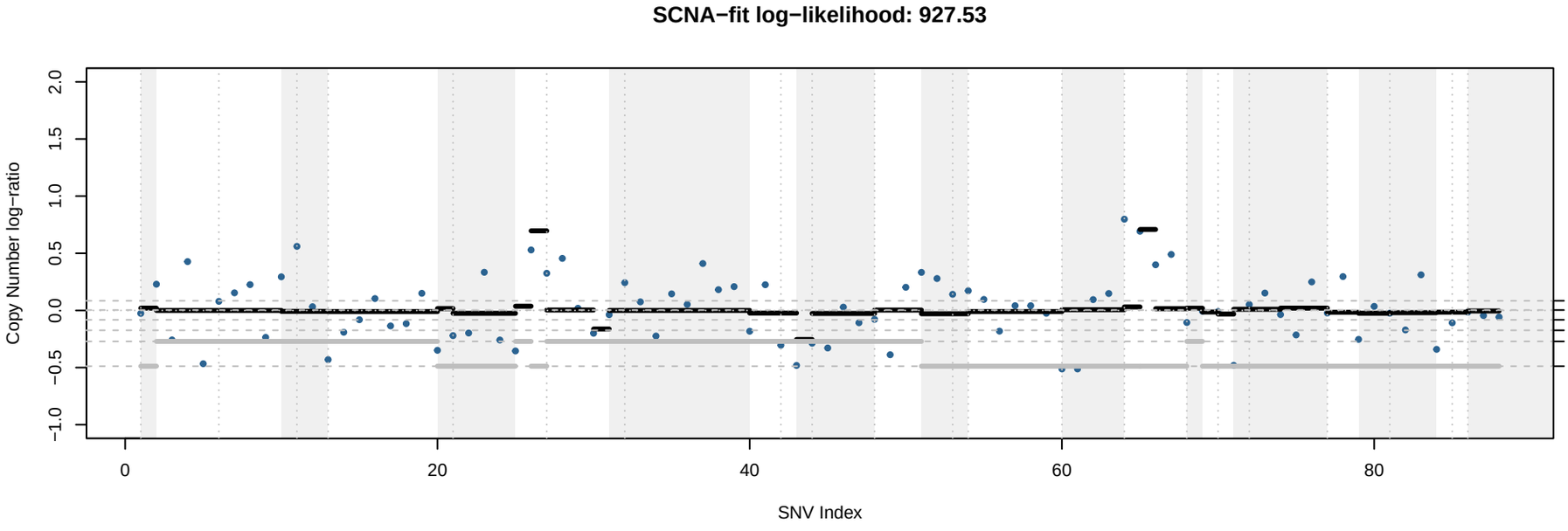

Coverage (log2)
Allelic fraction

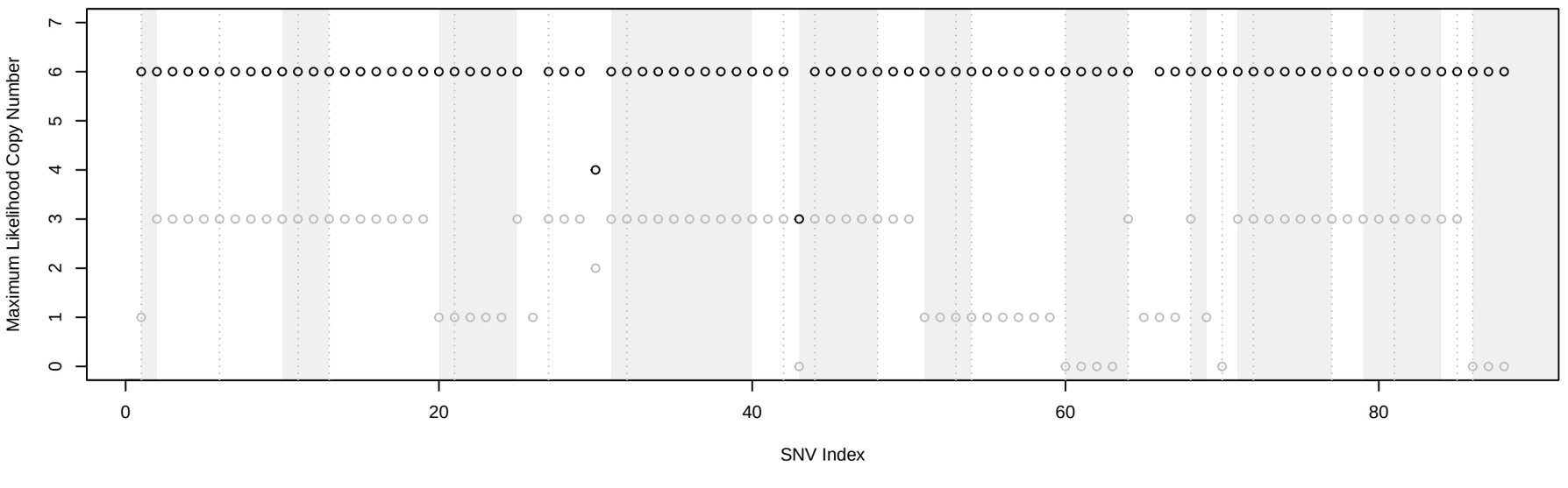

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

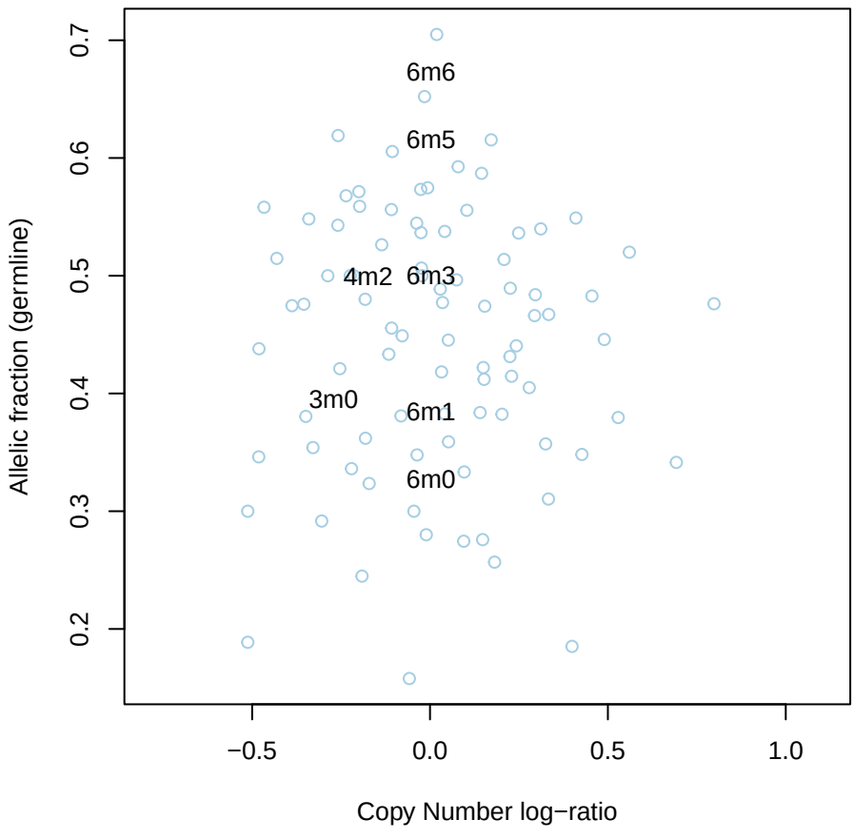

Power 0.8
Frequency
Cellular fraction

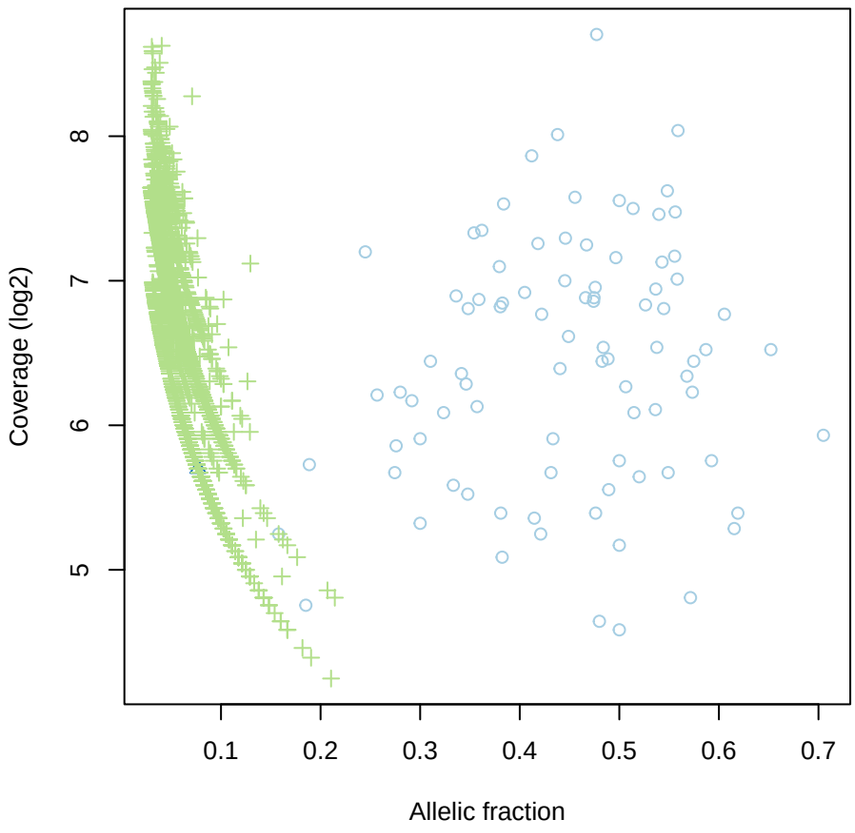

Purity: 0.15 Tumor ploidy: 5.963
1
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

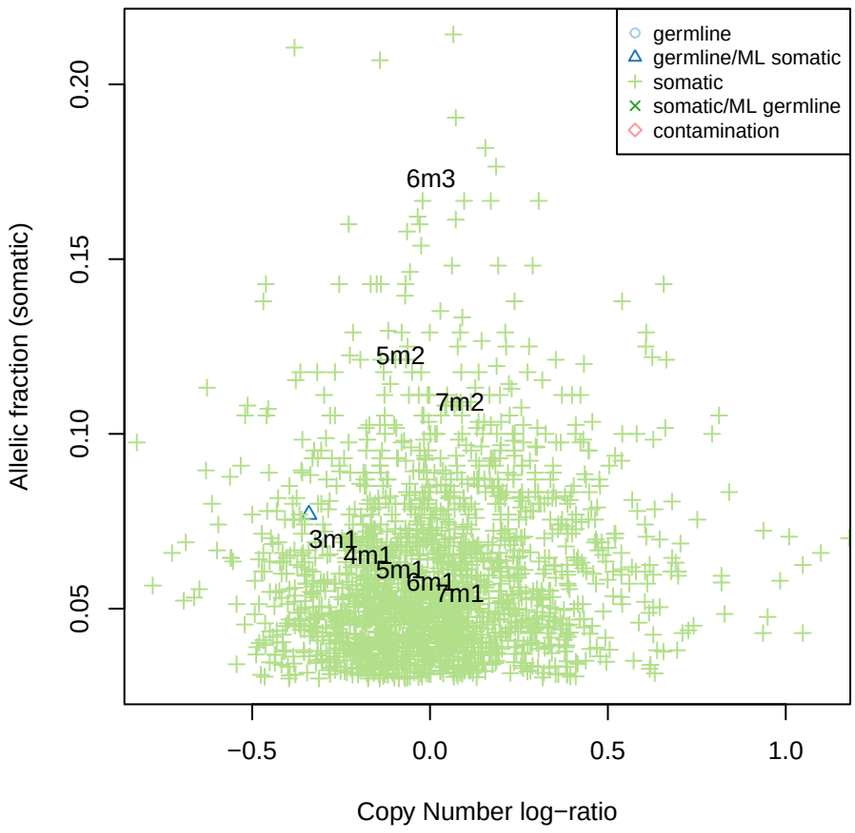

Purity: 0.15 Tumor ploidy: 5.963 SNV log−likelihood: −1075.17 GoF: 98% Mean coverage: 67;114
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

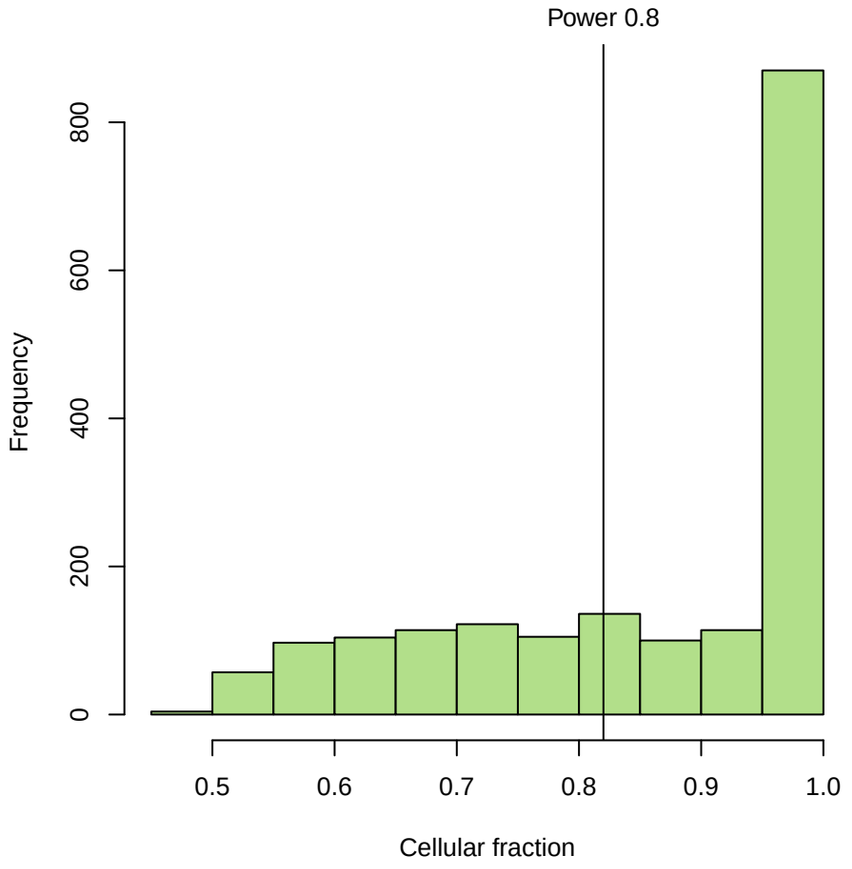

SCNA−fit log−likelihood: 927.53
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
1 3 6
0 20 40 60 80
SNV Index

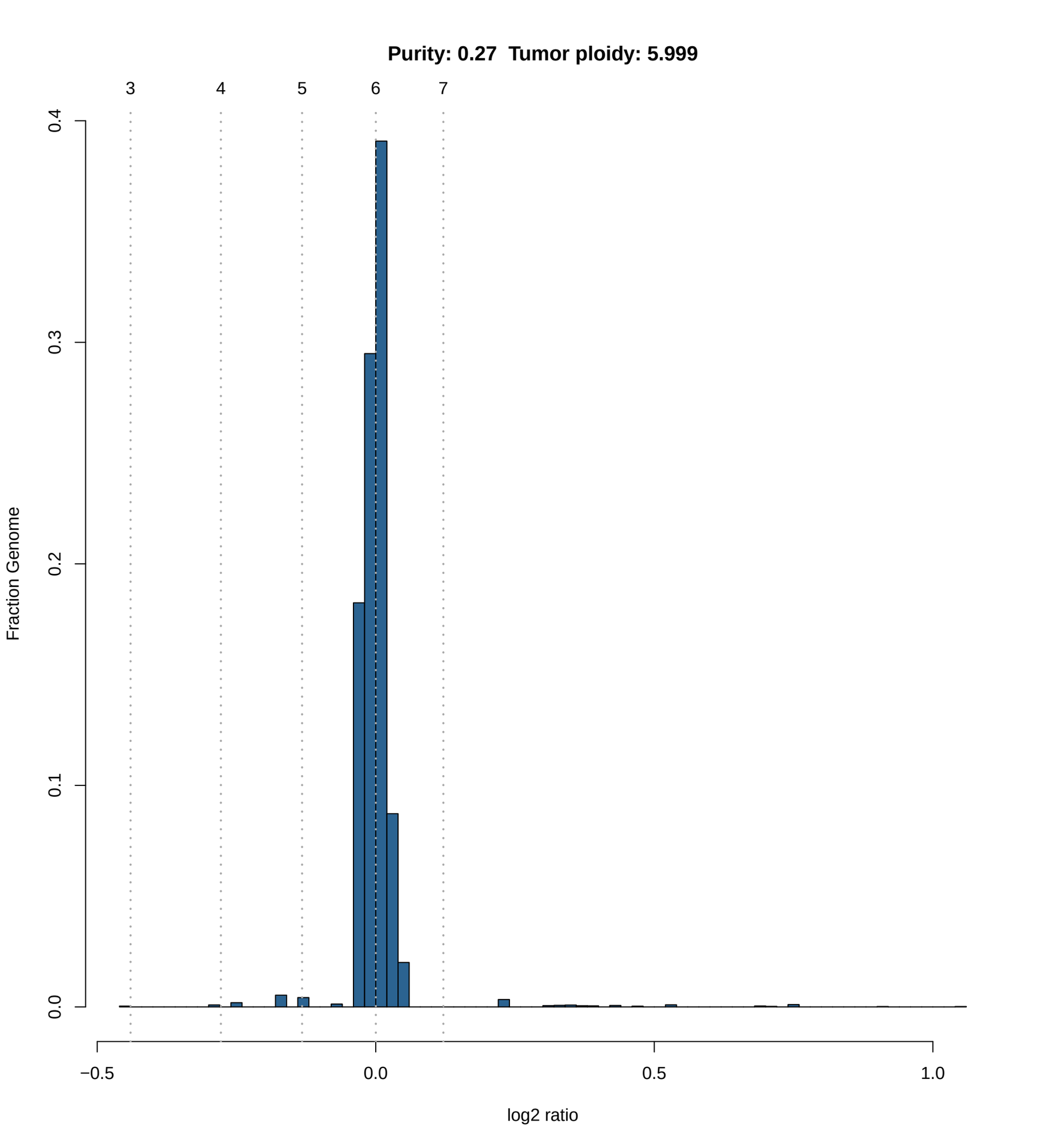

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

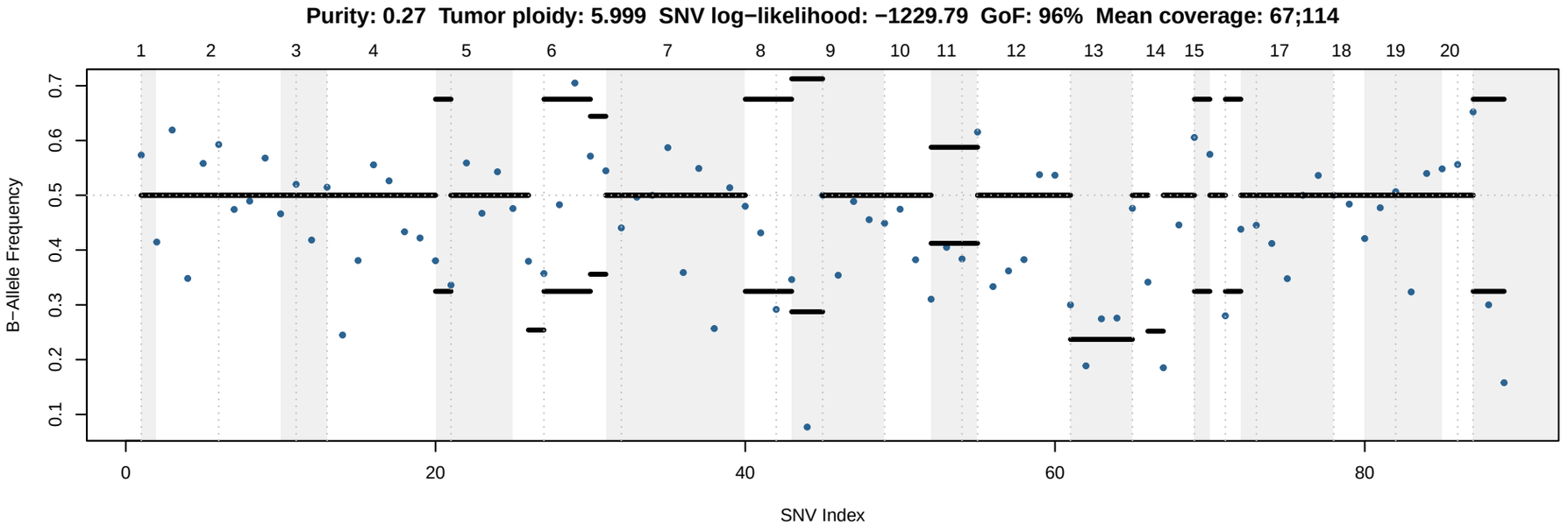

Allelic fraction (germline)
Copy Number log−ratio
6m6
6m5
4m2
6m3
3m0
6m1
6m0

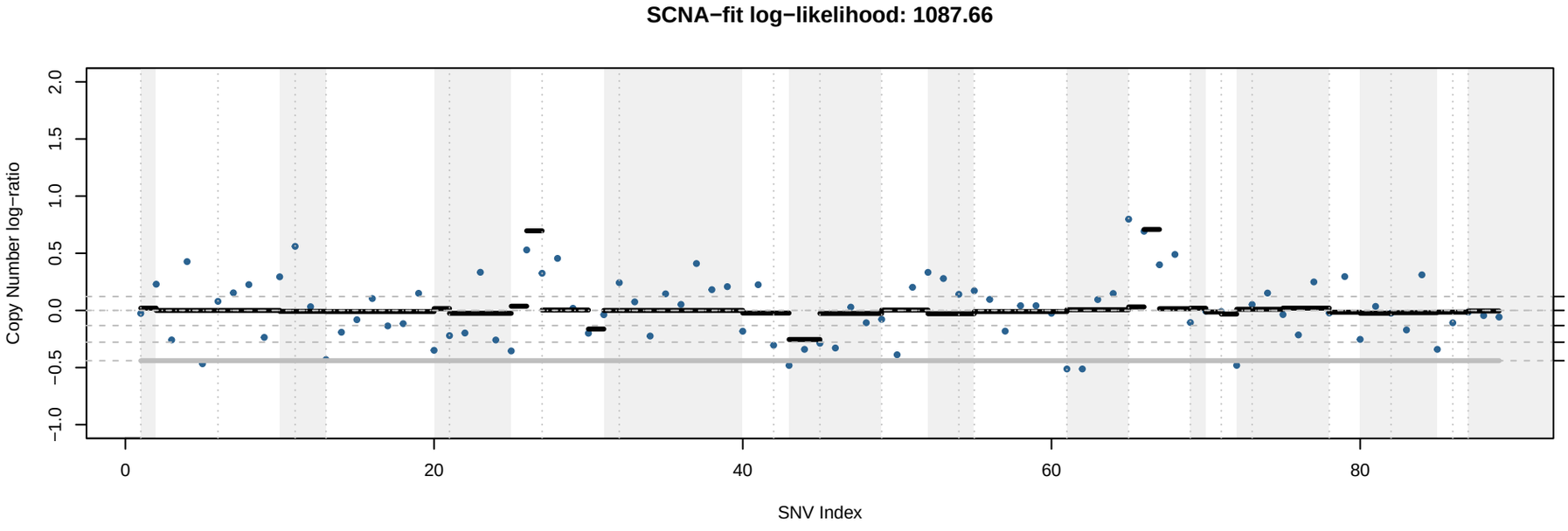

Coverage (log2)
Allelic fraction

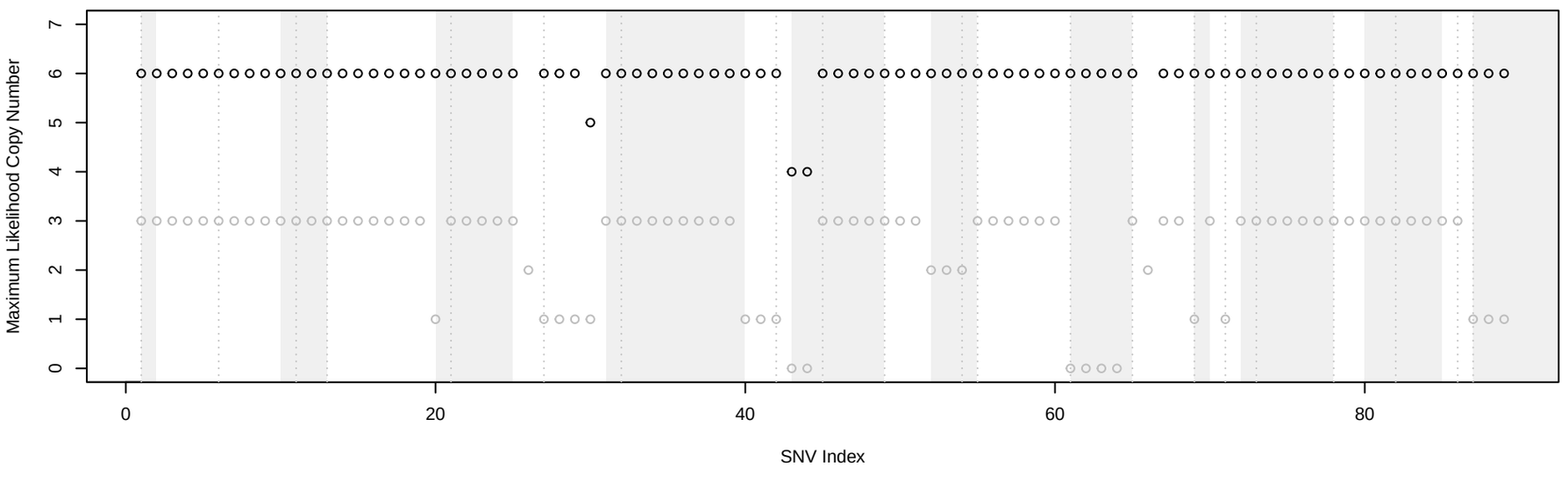

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
6m3
5m2
7m2
3m1
4m1
5m1
6m1
7m1

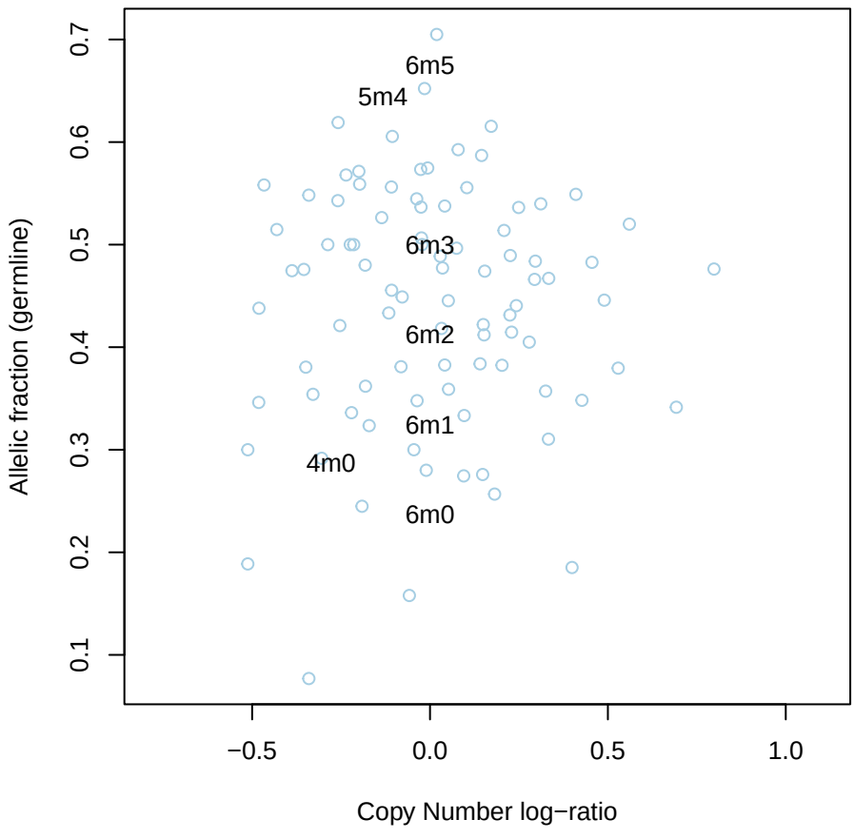

Power 0.8
Frequency
Cellular fraction

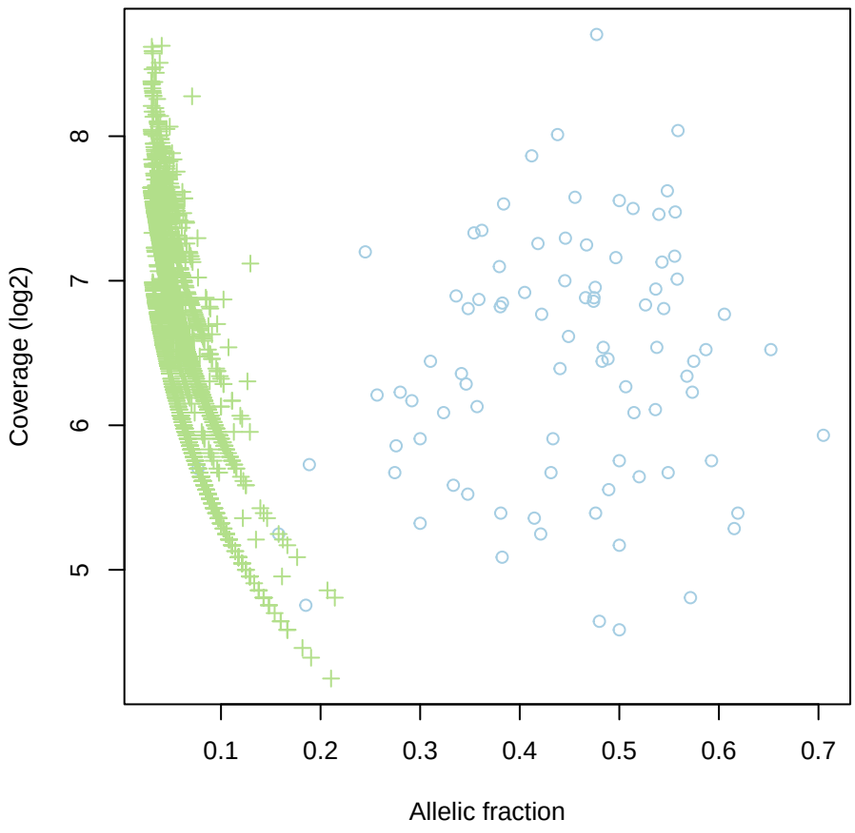

Purity: 0.27 Tumor ploidy: 5.999
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

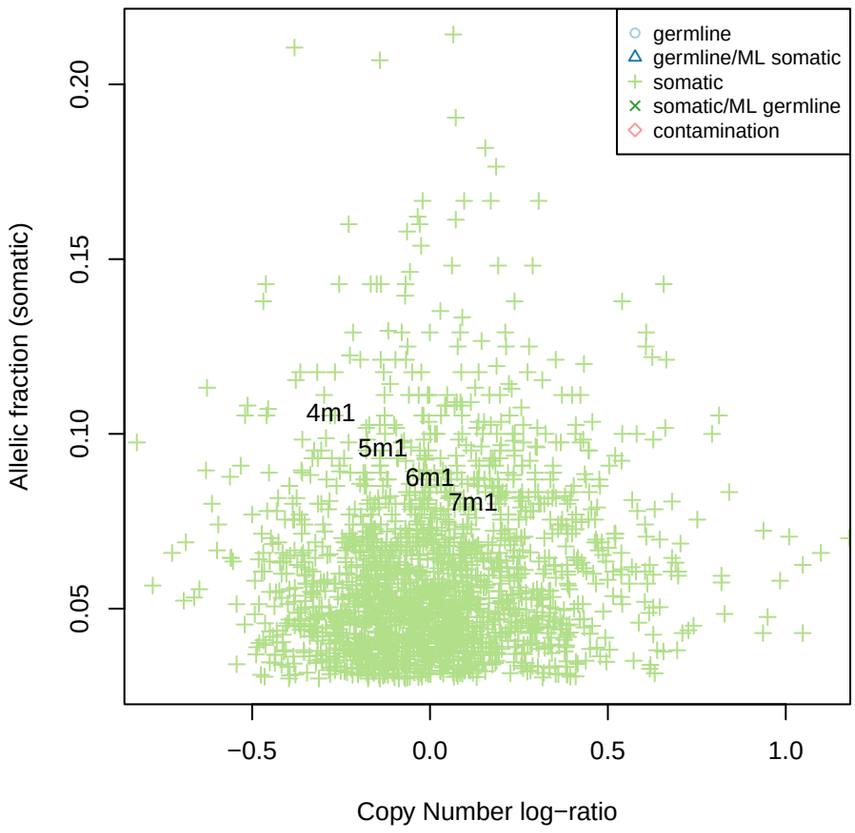

Purity: 0.27 Tumor ploidy: 5.999 SNV log−likelihood: −1229.79 GoF: 96% Mean coverage: 67;114
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

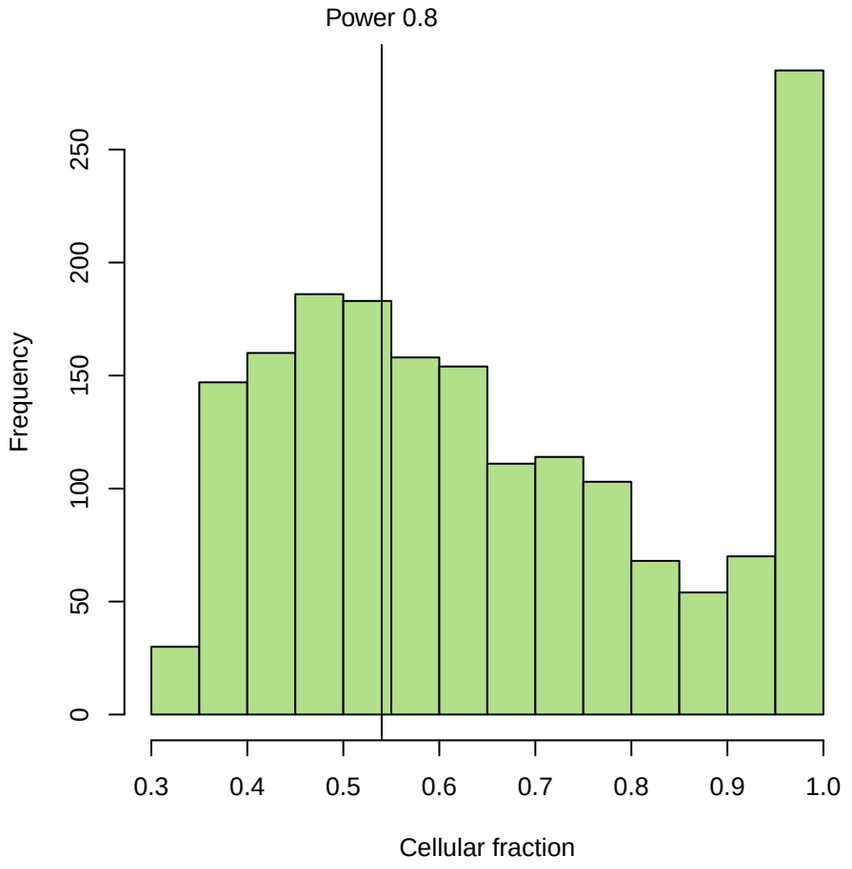

SCNA−fit log−likelihood: 1087.66
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
3 5 7
0 20 40 60 80
SNV Index

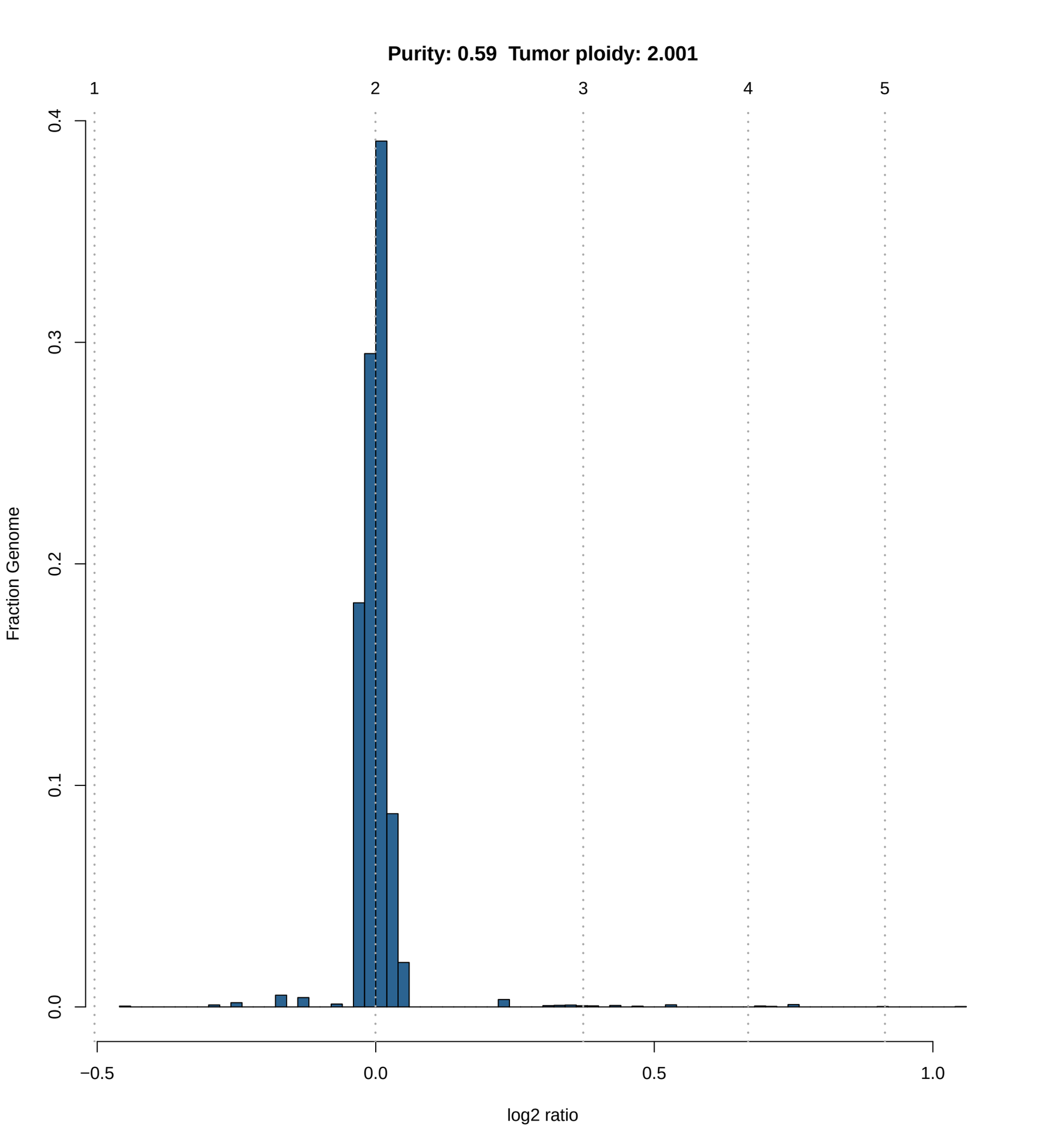

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

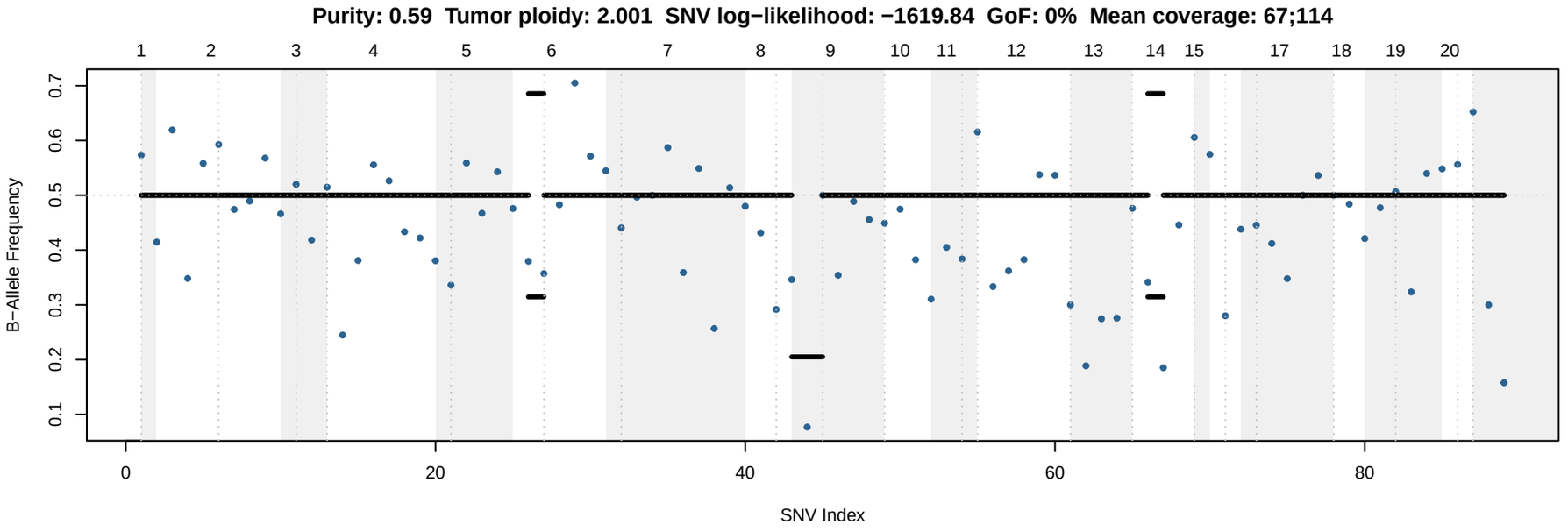

6m5
5m4
6m3
6m2
6m1
4m0
6m0
Allelic fraction (germline)
Copy Number log−ratio

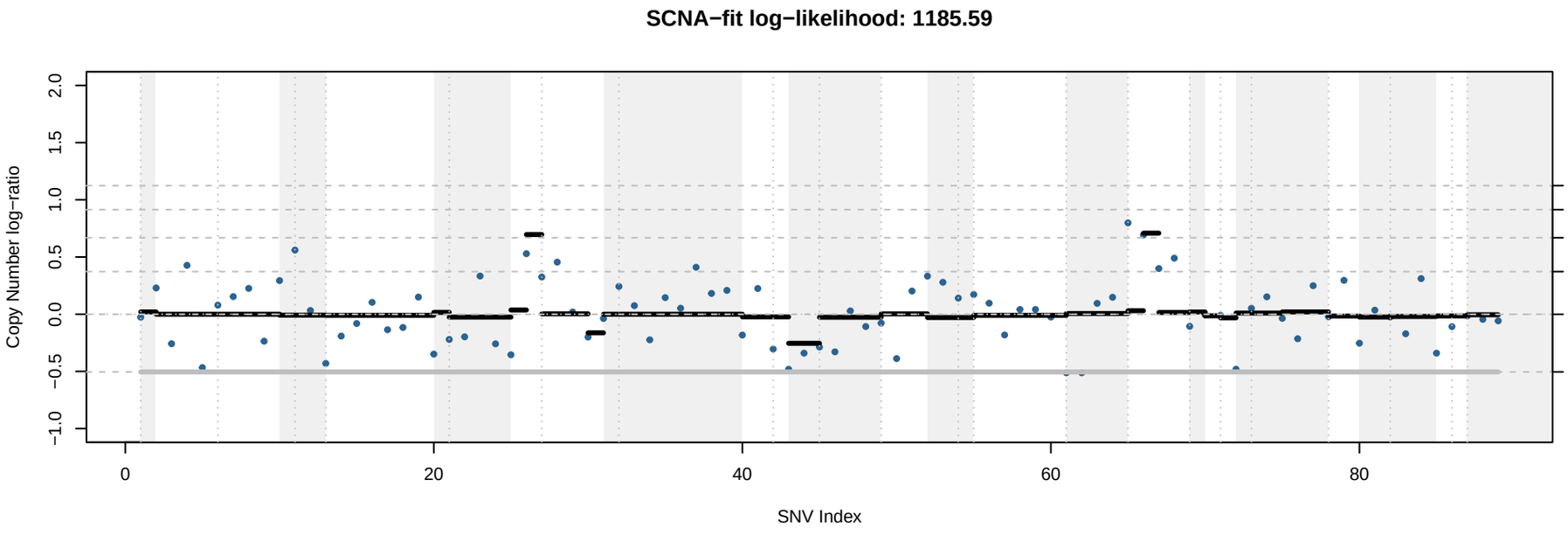

Coverage (log2)
Allelic fraction

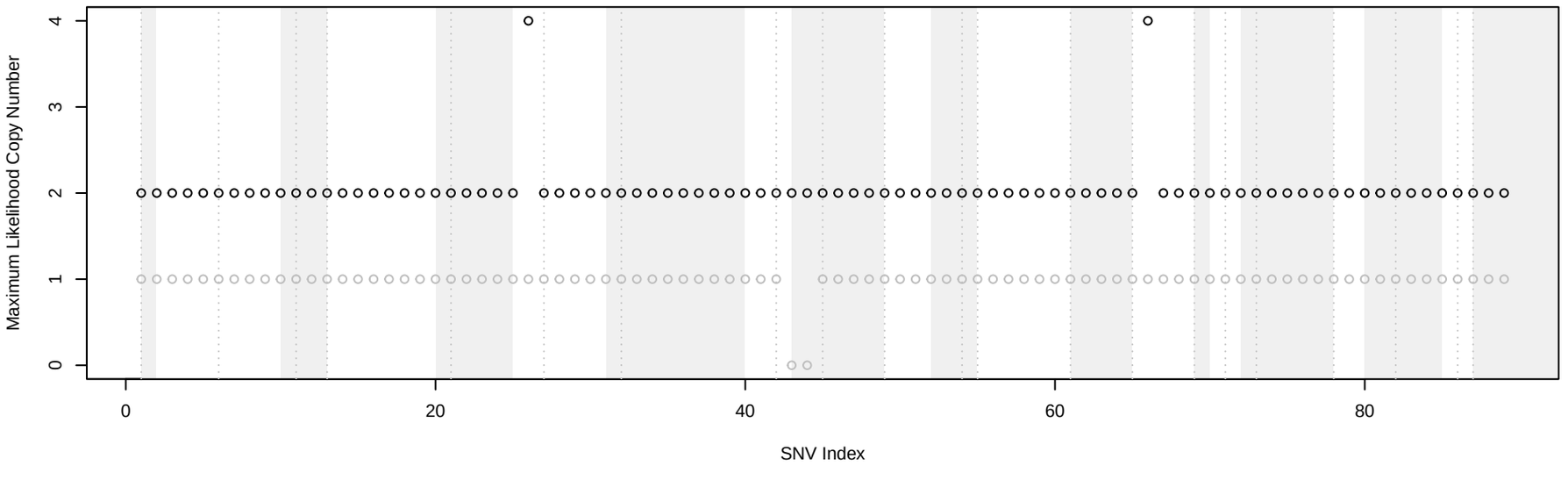

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

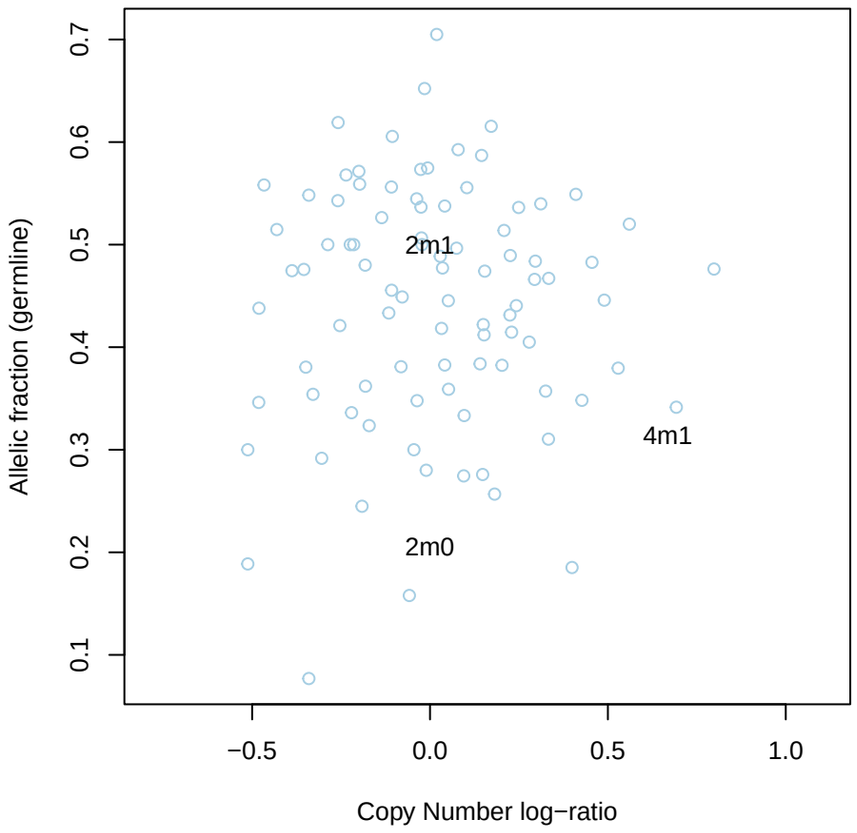

Power 0.8
Frequency
Cellular fraction

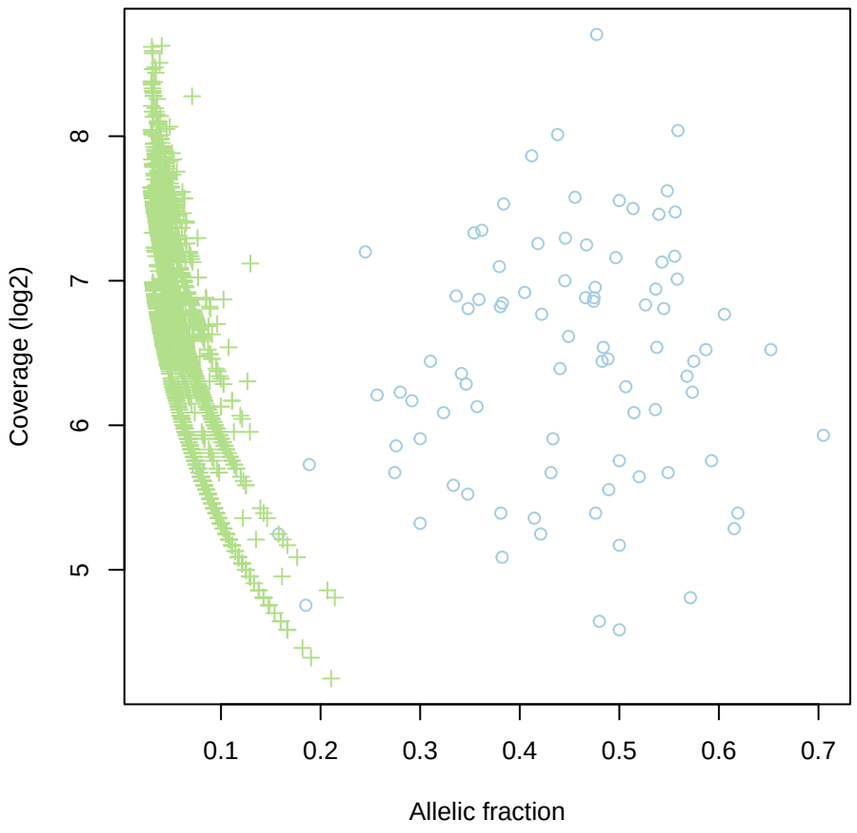

Purity: 0.59 Tumor ploidy: 2.001
1
2
3
4
5
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

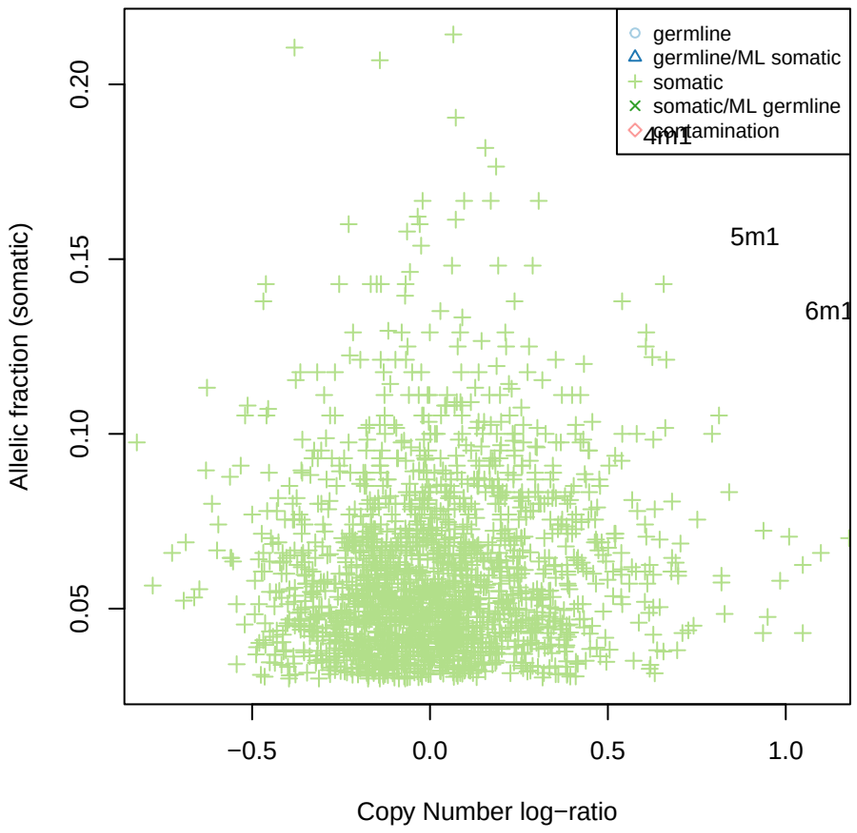

Purity: 0.59 Tumor ploidy: 2.001 SNV log−likelihood: −1619.84 GoF: 0% Mean coverage: 67;114
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

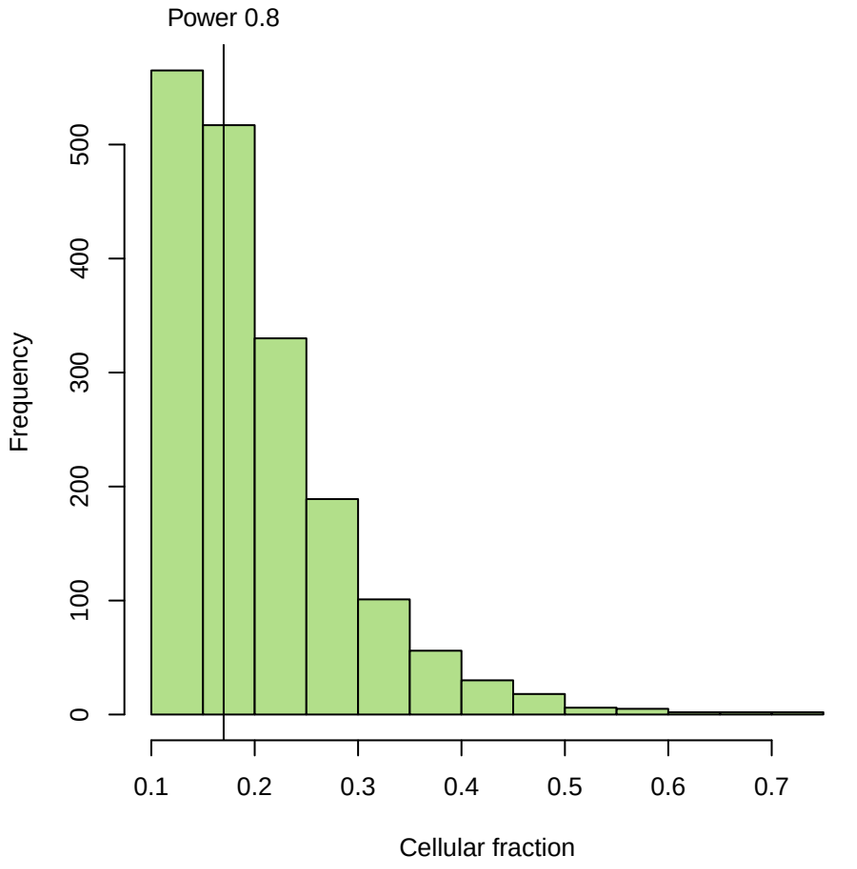

SCNA−fit log−likelihood: 1185.59
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
1 2 3 4 5
0 20 40 60 80
SNV Index

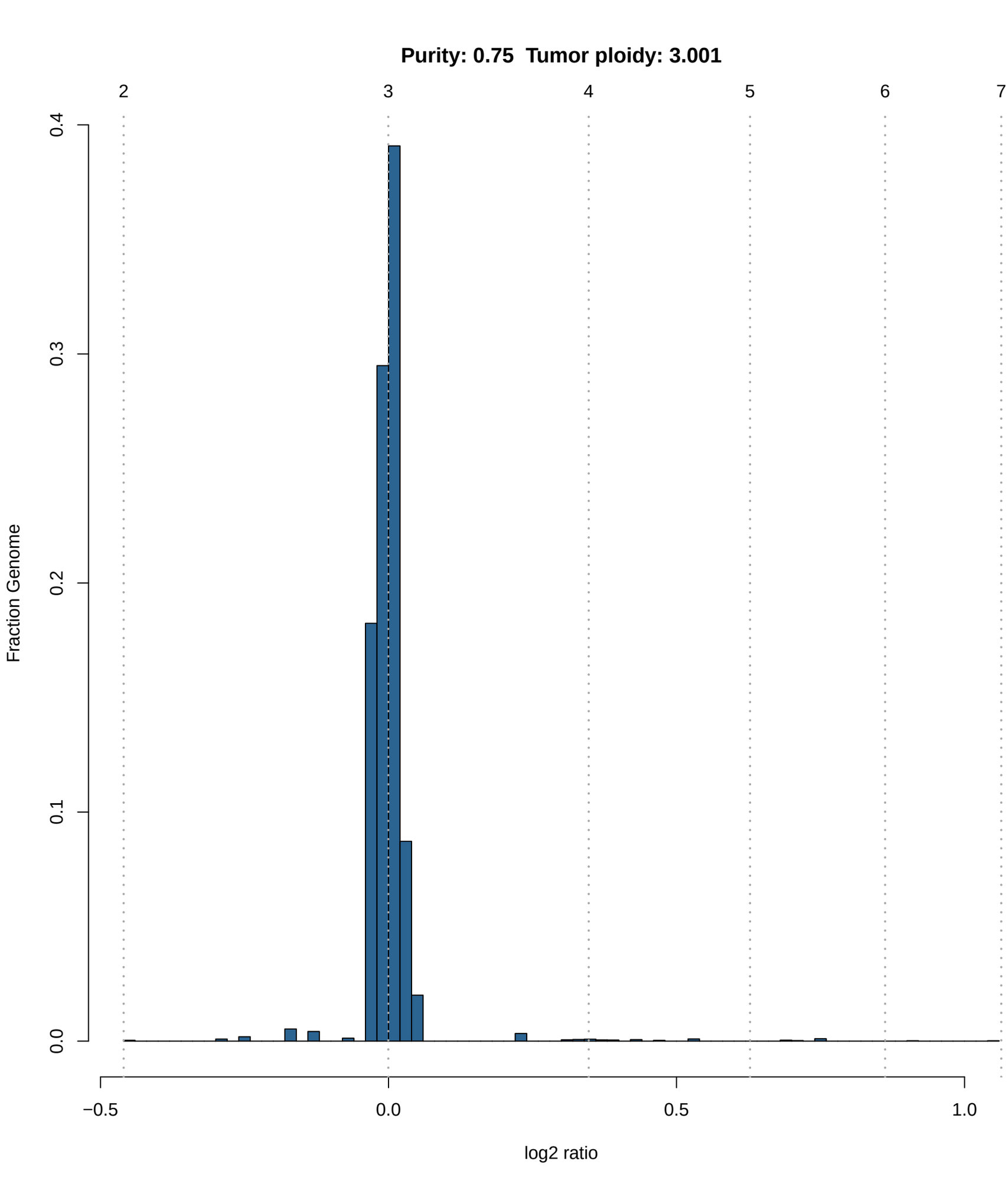

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80
SNV Index

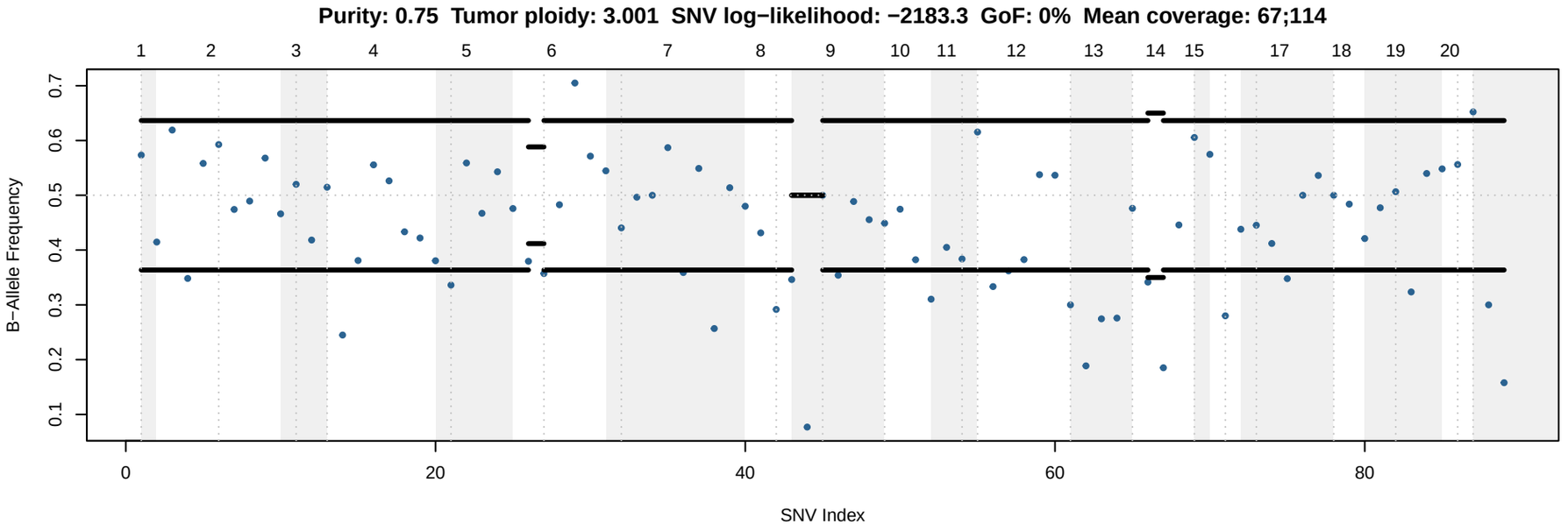

Allelic fraction (germline)
Copy Number log−ratio
2m1
4m1
2m0

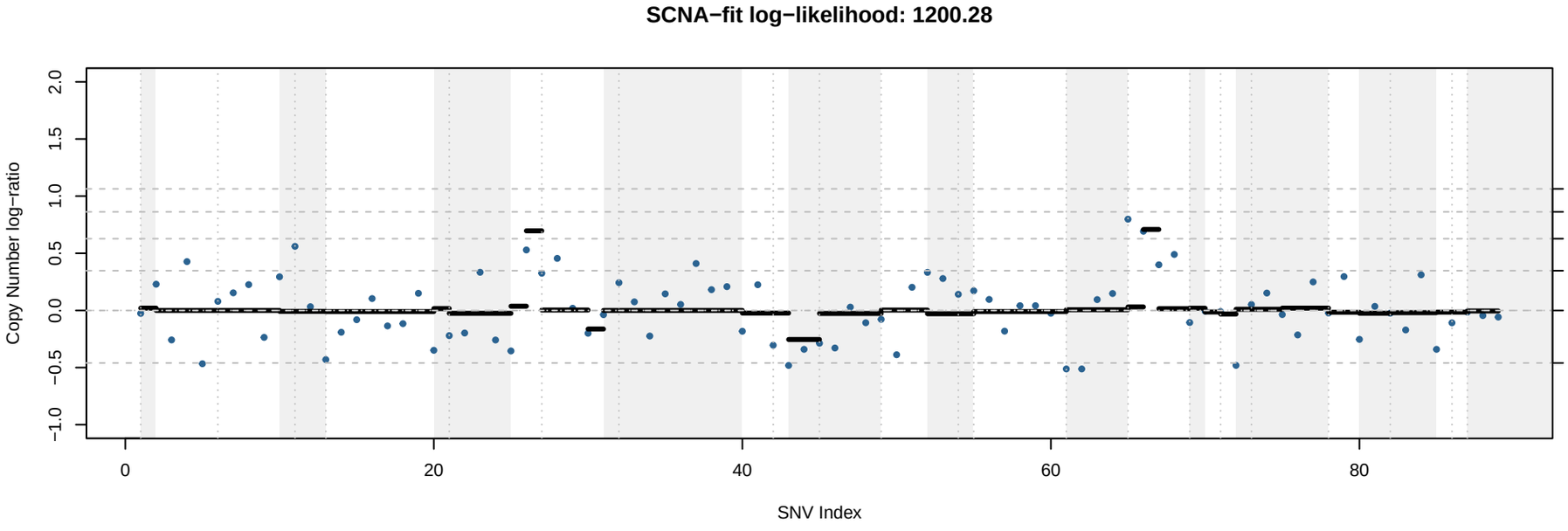

Coverage (log2)
Allelic fraction

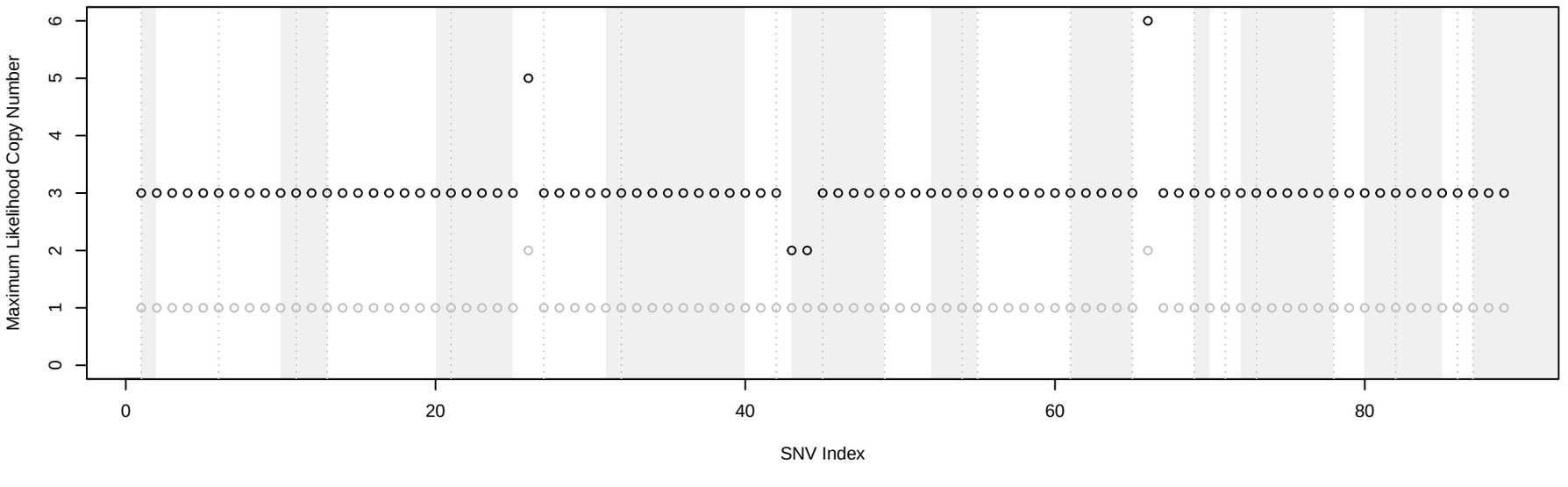

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1

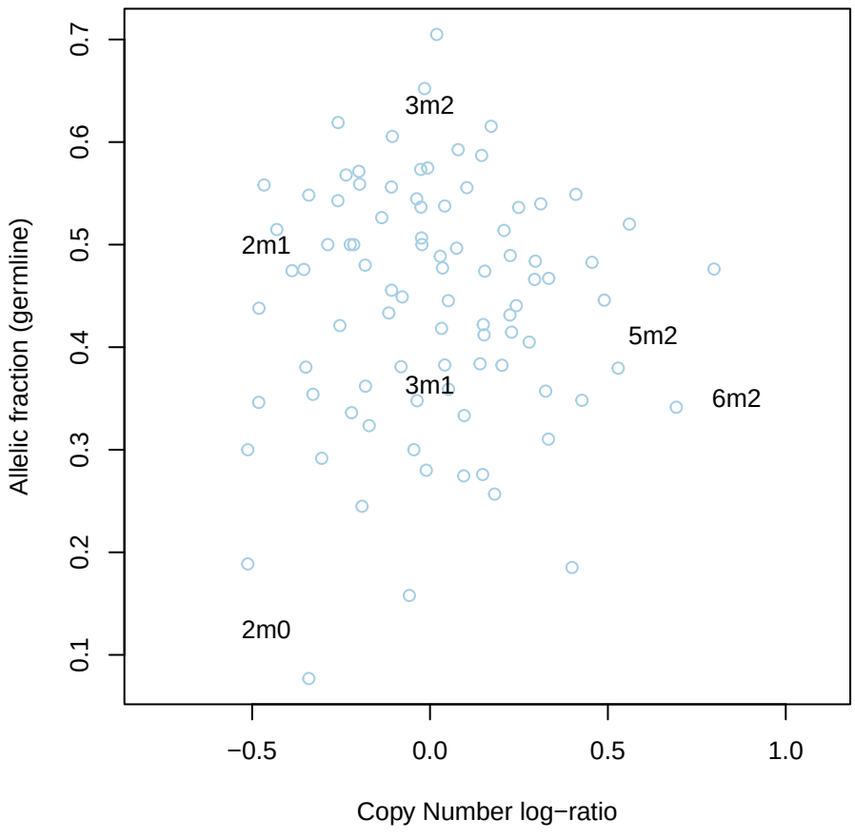

Power 0.8
Frequency
Cellular fraction

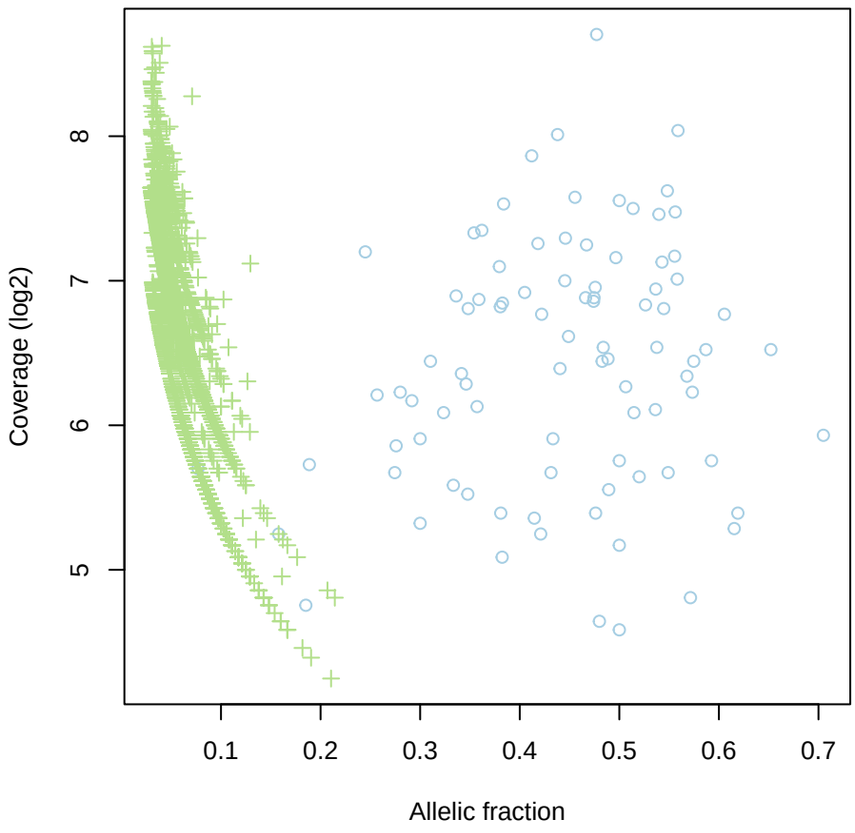

Purity: 0.75 Tumor ploidy: 3.001
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

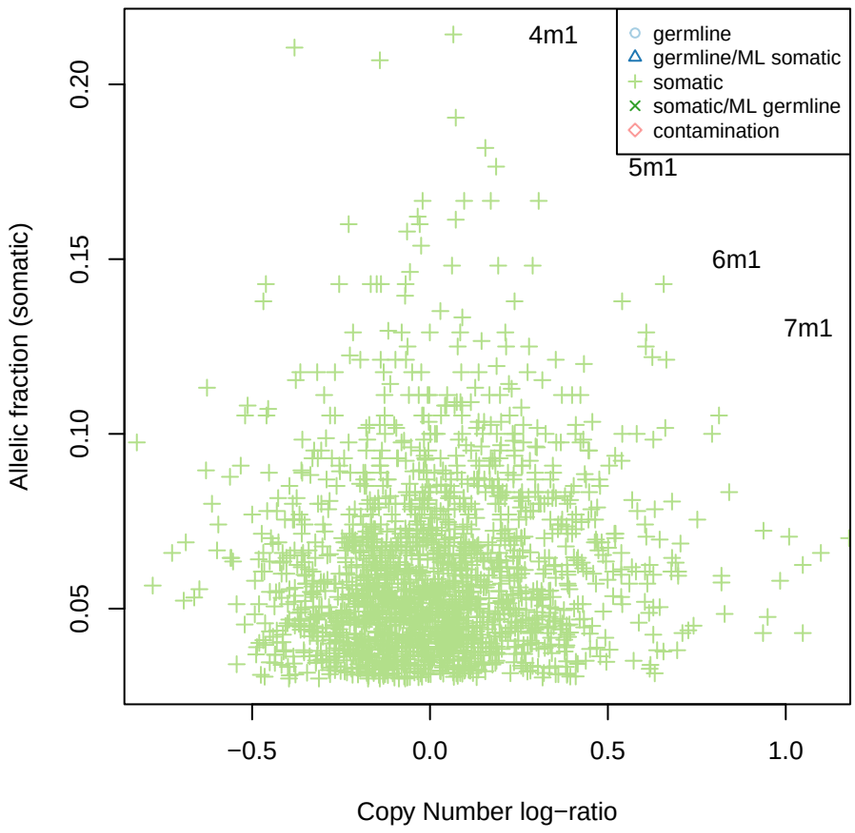

Purity: 0.75 Tumor ploidy: 3.001 SNV log−likelihood: −2183.3 GoF: 0% Mean coverage: 67;114
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80
SNV Index

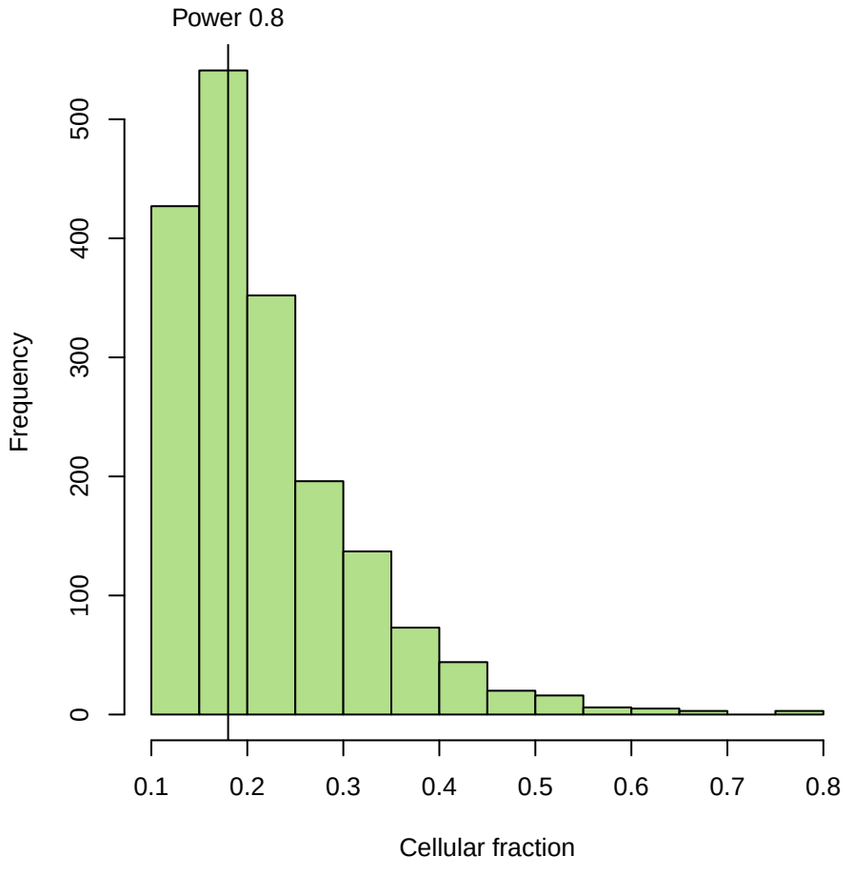

SCNA−fit log−likelihood: 1200.28
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
2 3 4 5 6
0 20 40 60 80
SNV Index


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


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


Coverage (log2)
Allelic fraction


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


Power 0.8
Frequency
Cellular fraction