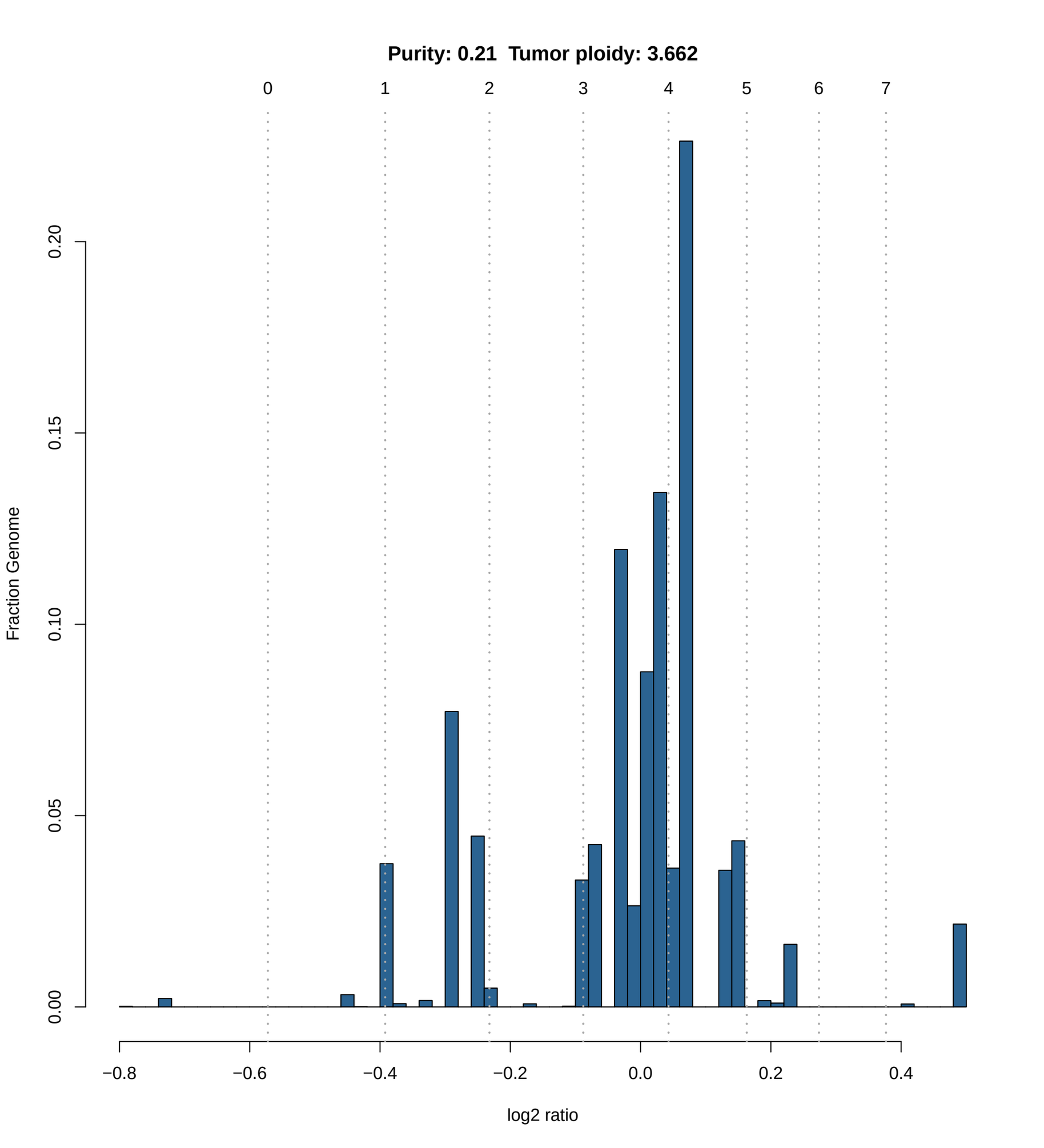
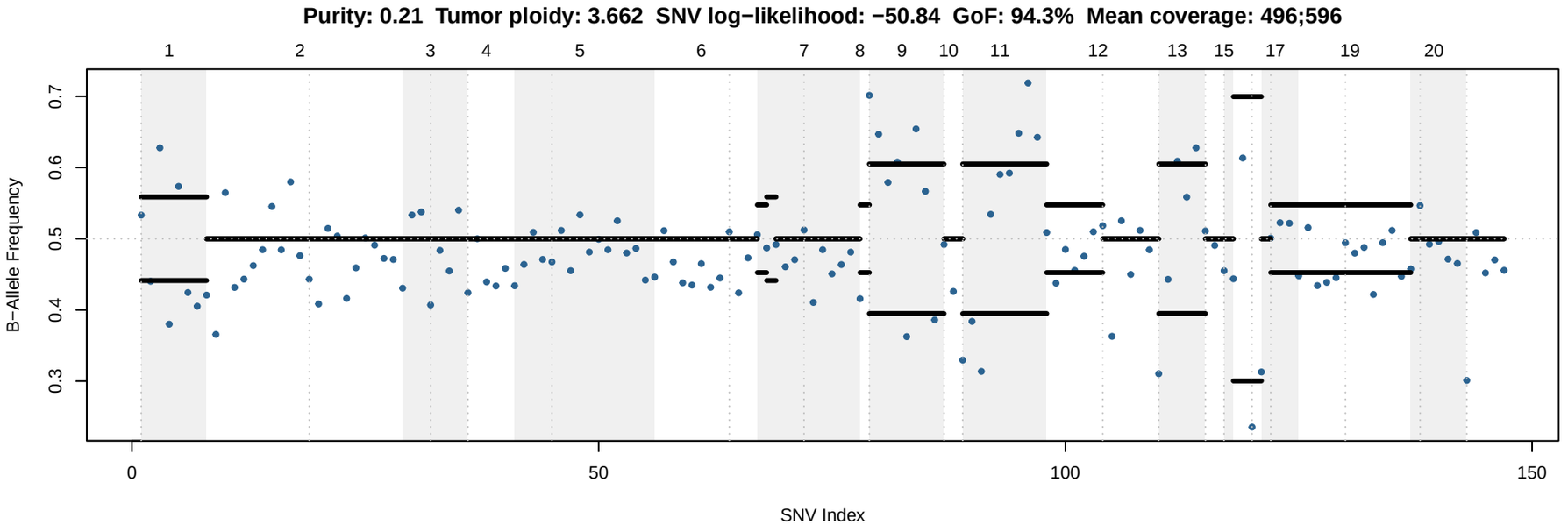
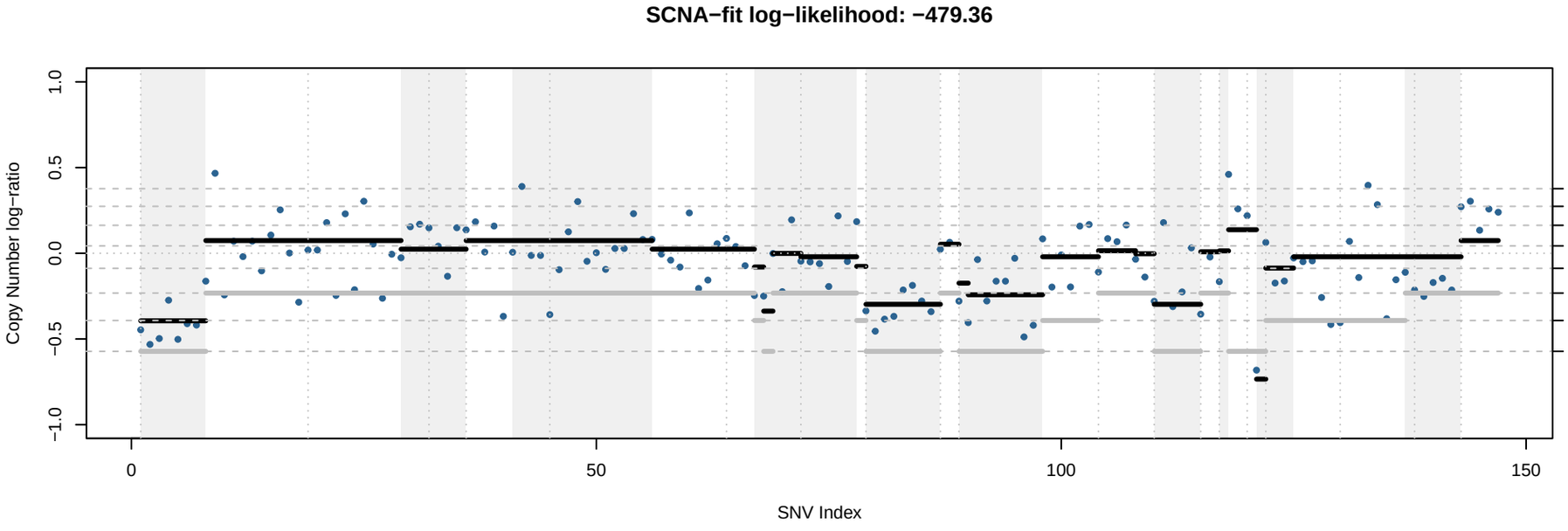
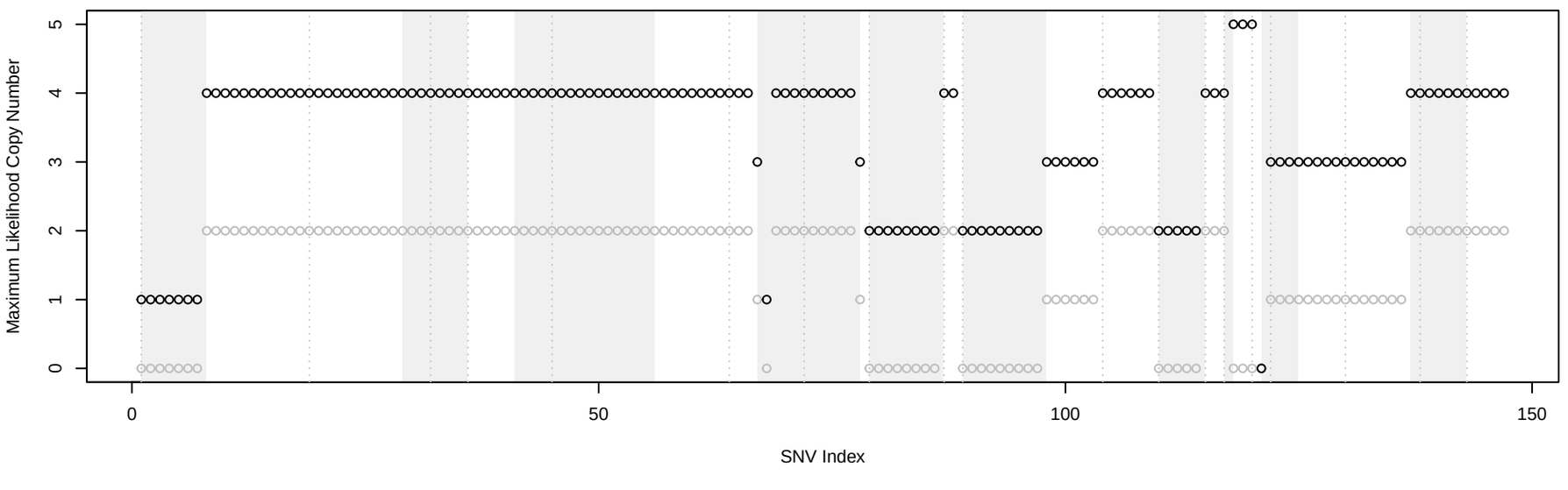
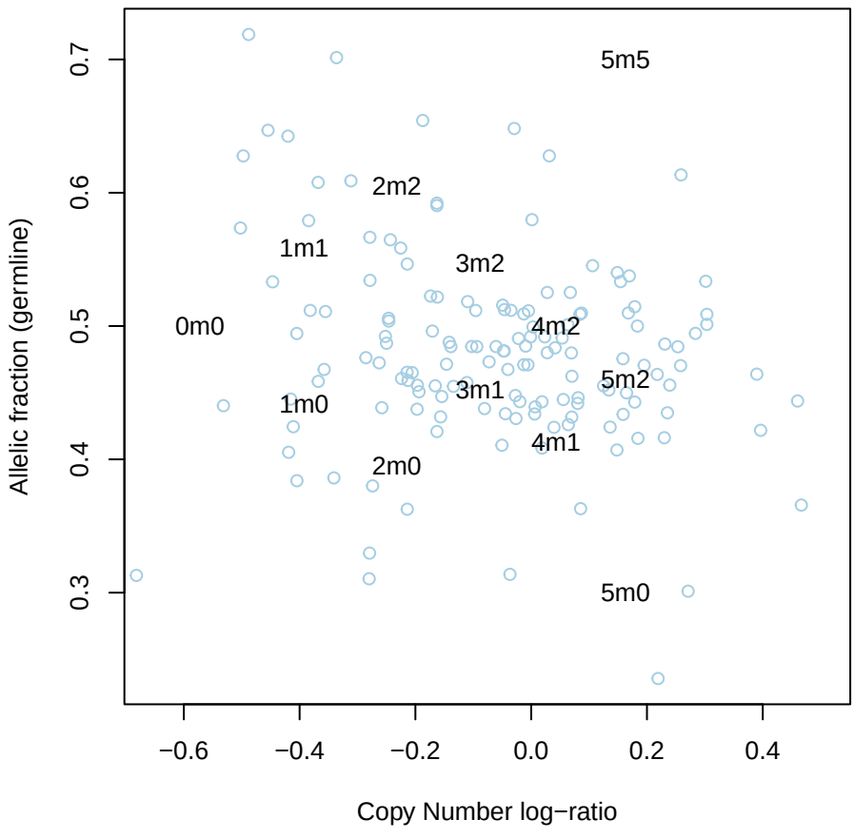
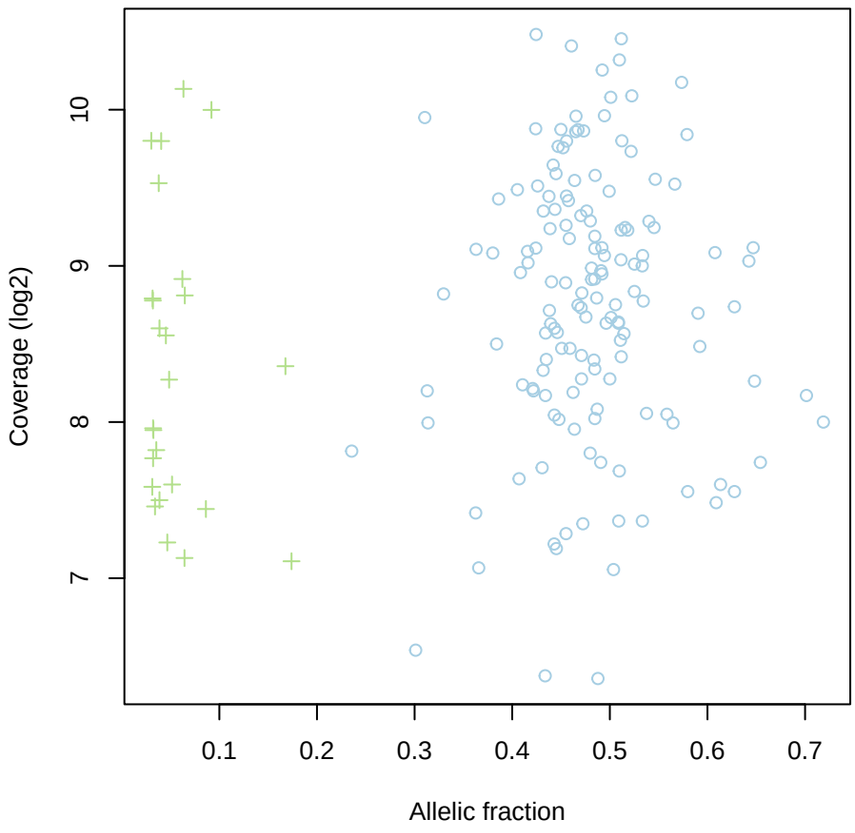

Purity: 0.21 Tumor ploidy: 3.662
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

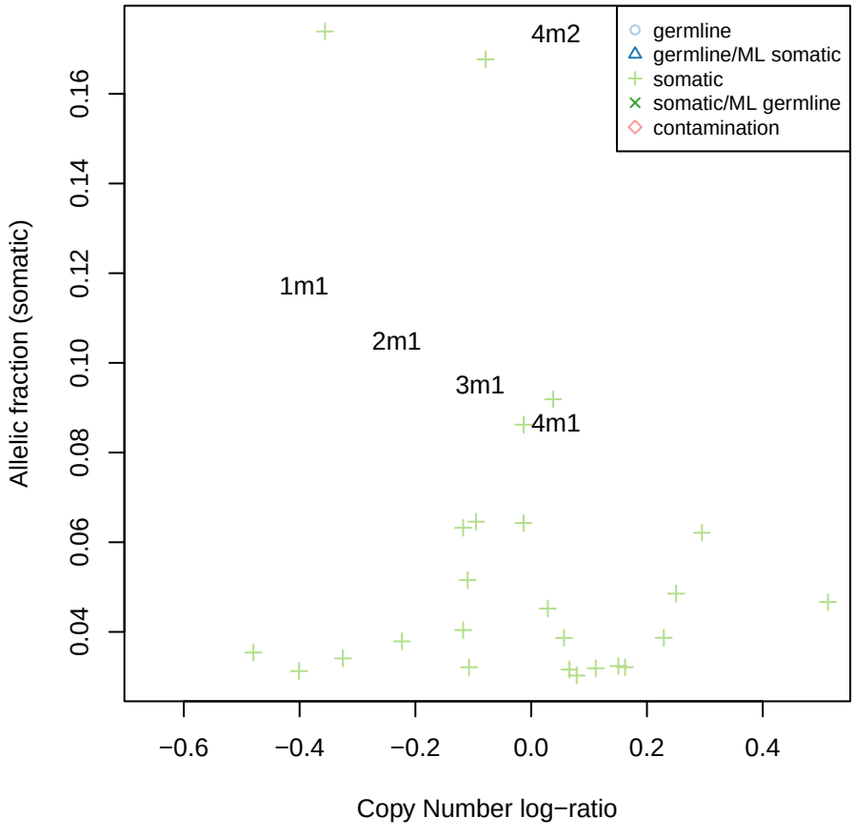

Purity: 0.21 Tumor ploidy: 3.662 SNV log−likelihood: −50.84 GoF: 94.3% Mean coverage: 496;596
1 2 3 4 5 6 7 8 9 10 11 12 13 15 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

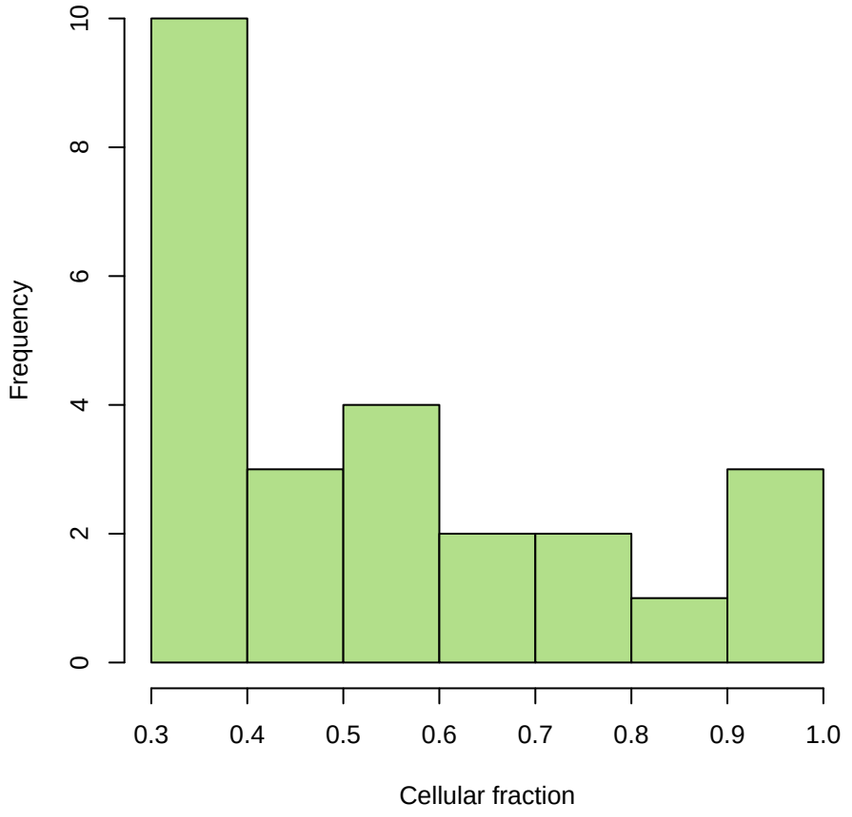

SCNA−fit log−likelihood: −479.36
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 5 7
0 50 100 150
SNV Index

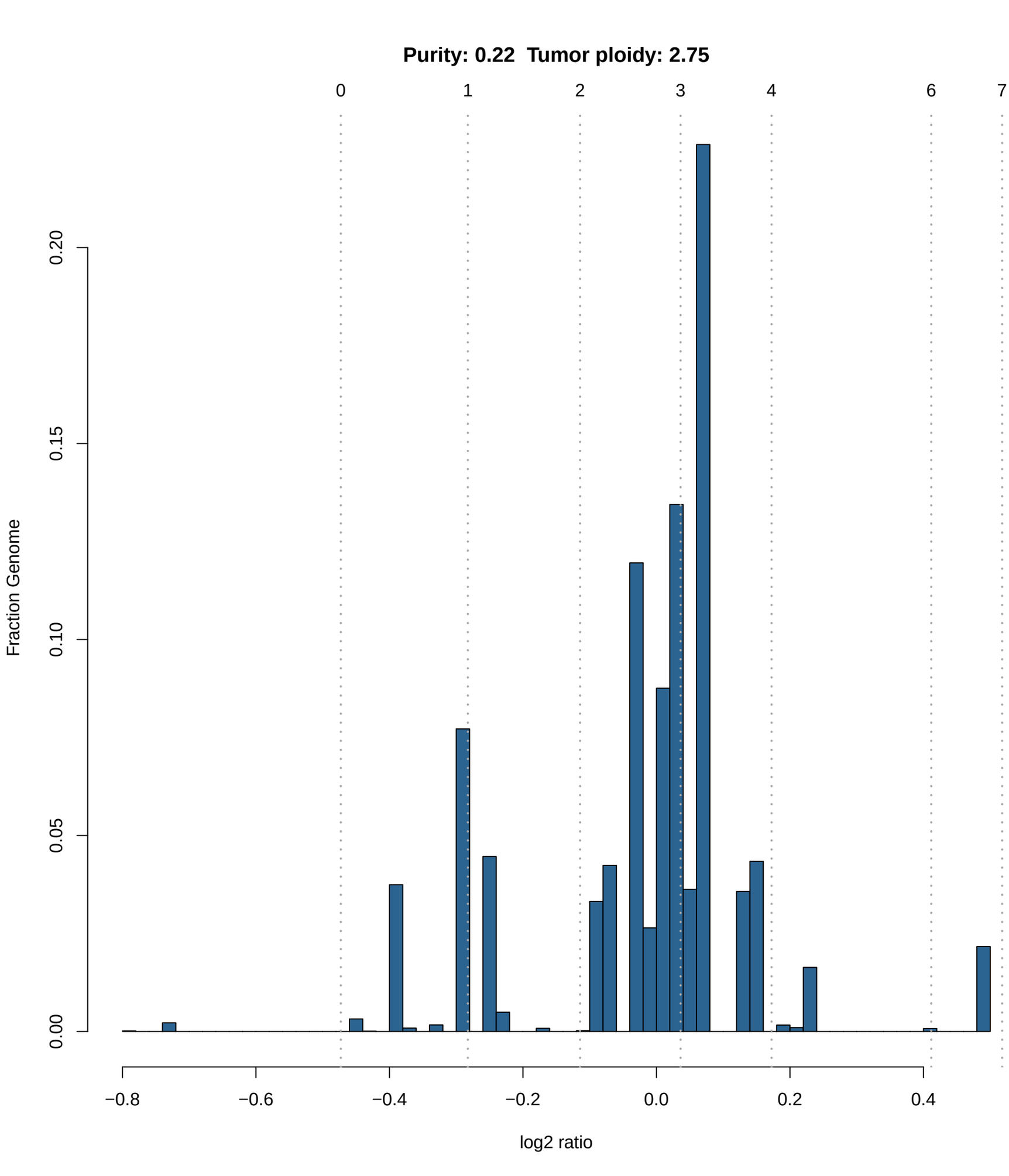

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

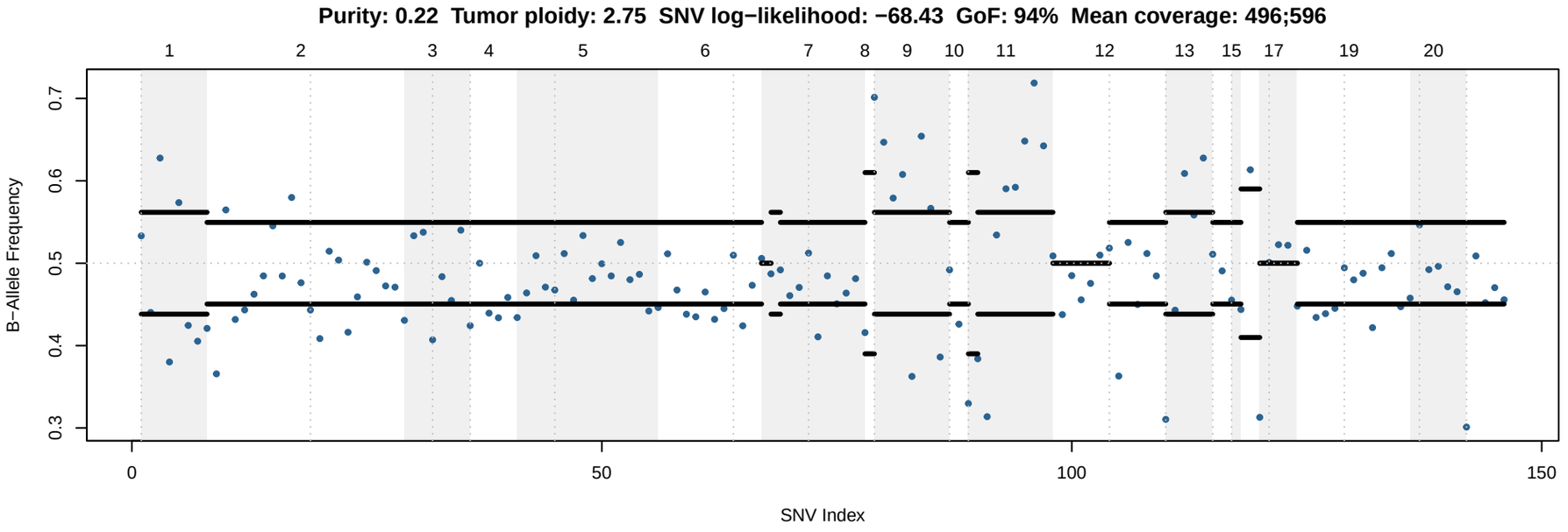

Allelic fraction (germline)
Copy Number log−ratio
0m0
1m0
1m1
2m0
2m2
3m1
3m2
4m1
4m2
5m0
5m2
5m5

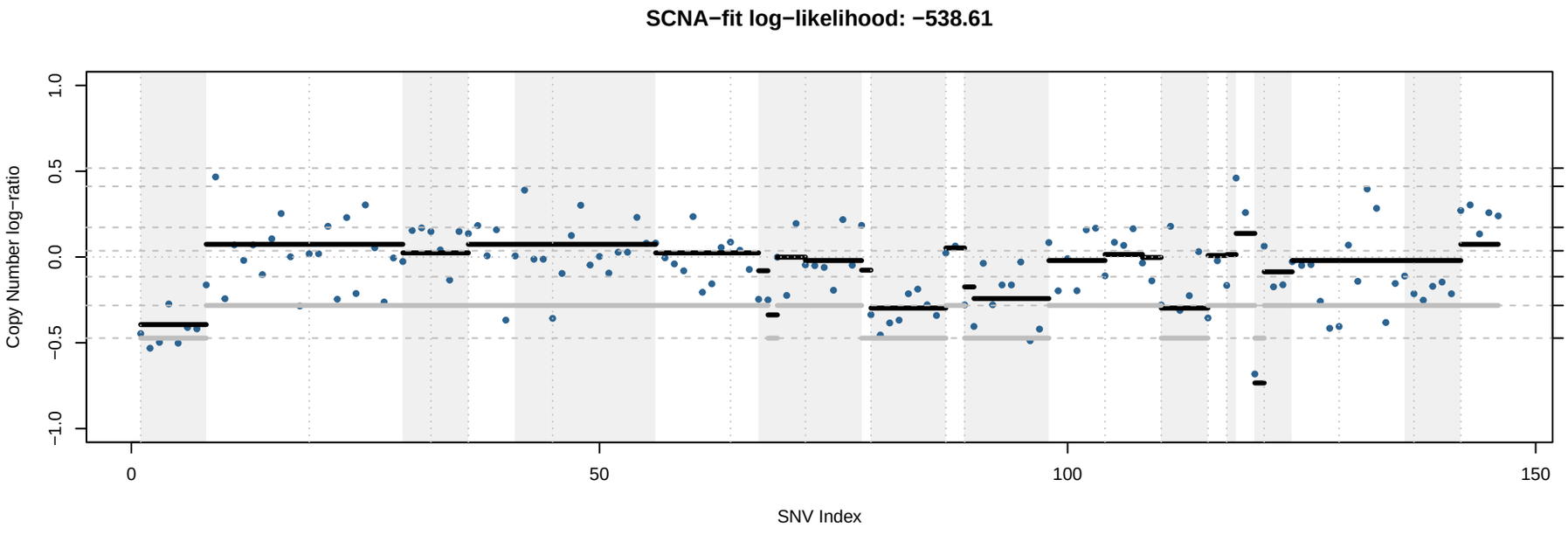

Coverage (log2)
Allelic fraction

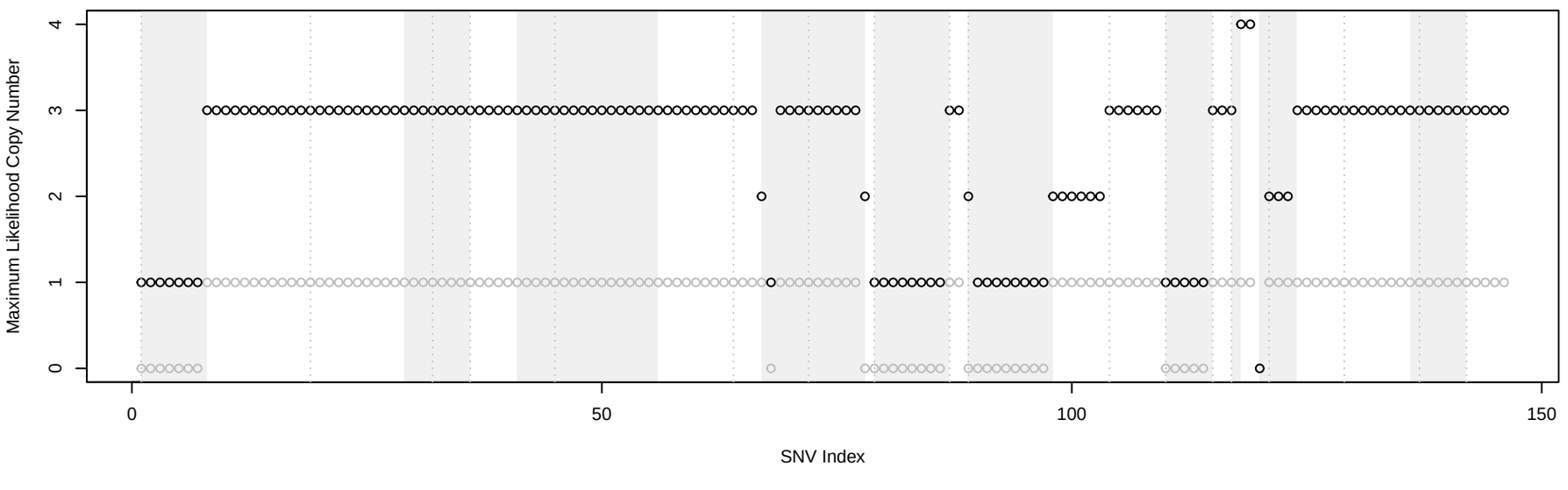

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
4m1
4m2

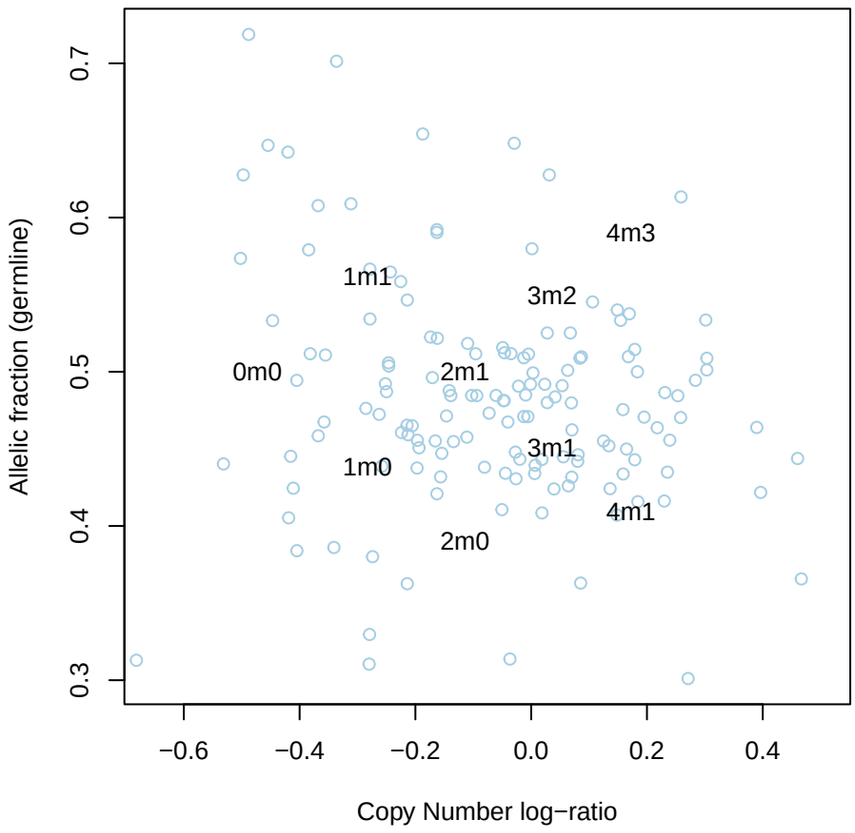

Frequency
Cellular fraction

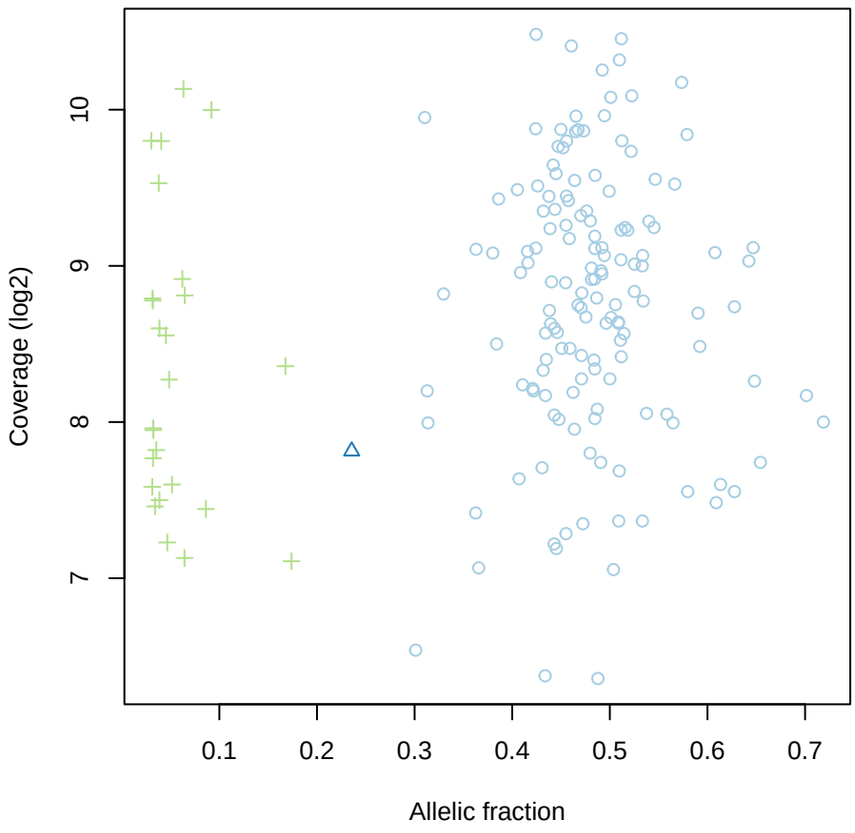

Purity: 0.22 Tumor ploidy: 2.75
0
1
2
3
4
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

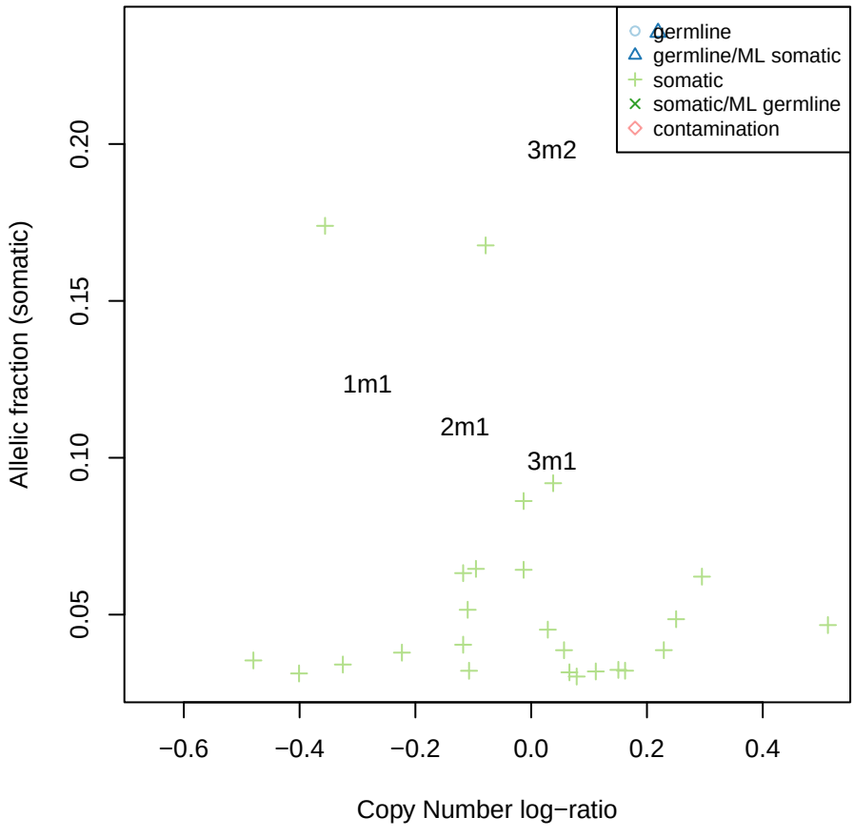

Purity: 0.22 Tumor ploidy: 2.75 SNV log−likelihood: −68.43 GoF: 94% Mean coverage: 496;596
1
2
3
4
5
6
7
8
9
10
11
12
13
15
17
19
20
B−Allele Frequency
0.3
0.4
0.5
0.6
0.7
0
50
100
150
SNV Index

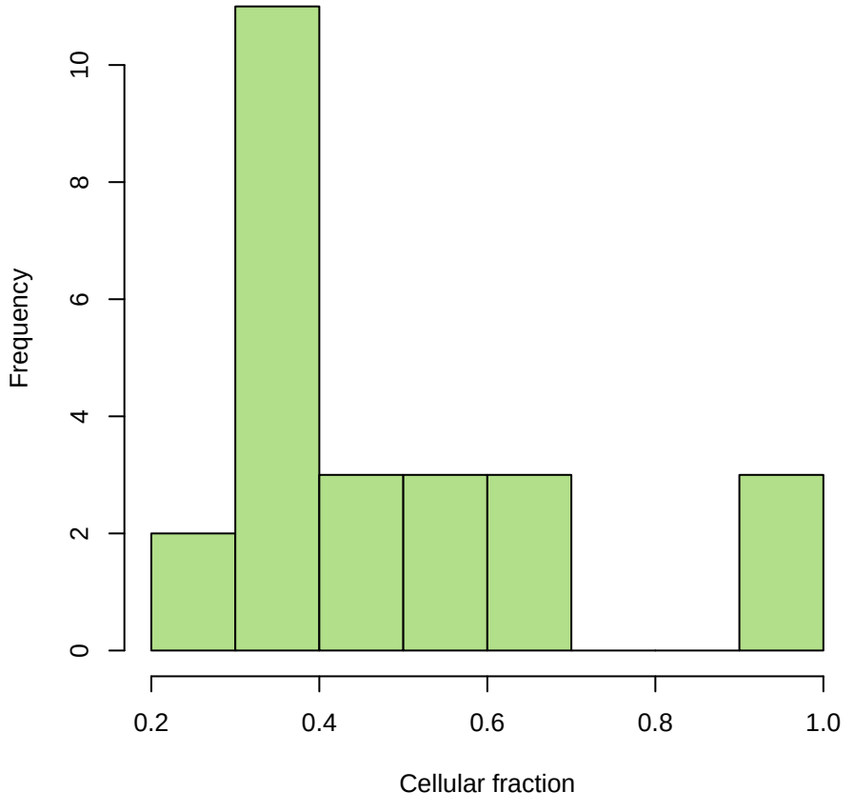

SCNA−fit log−likelihood: −538.61
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
0
1
2
3
6
0
50
100
150
SNV Index

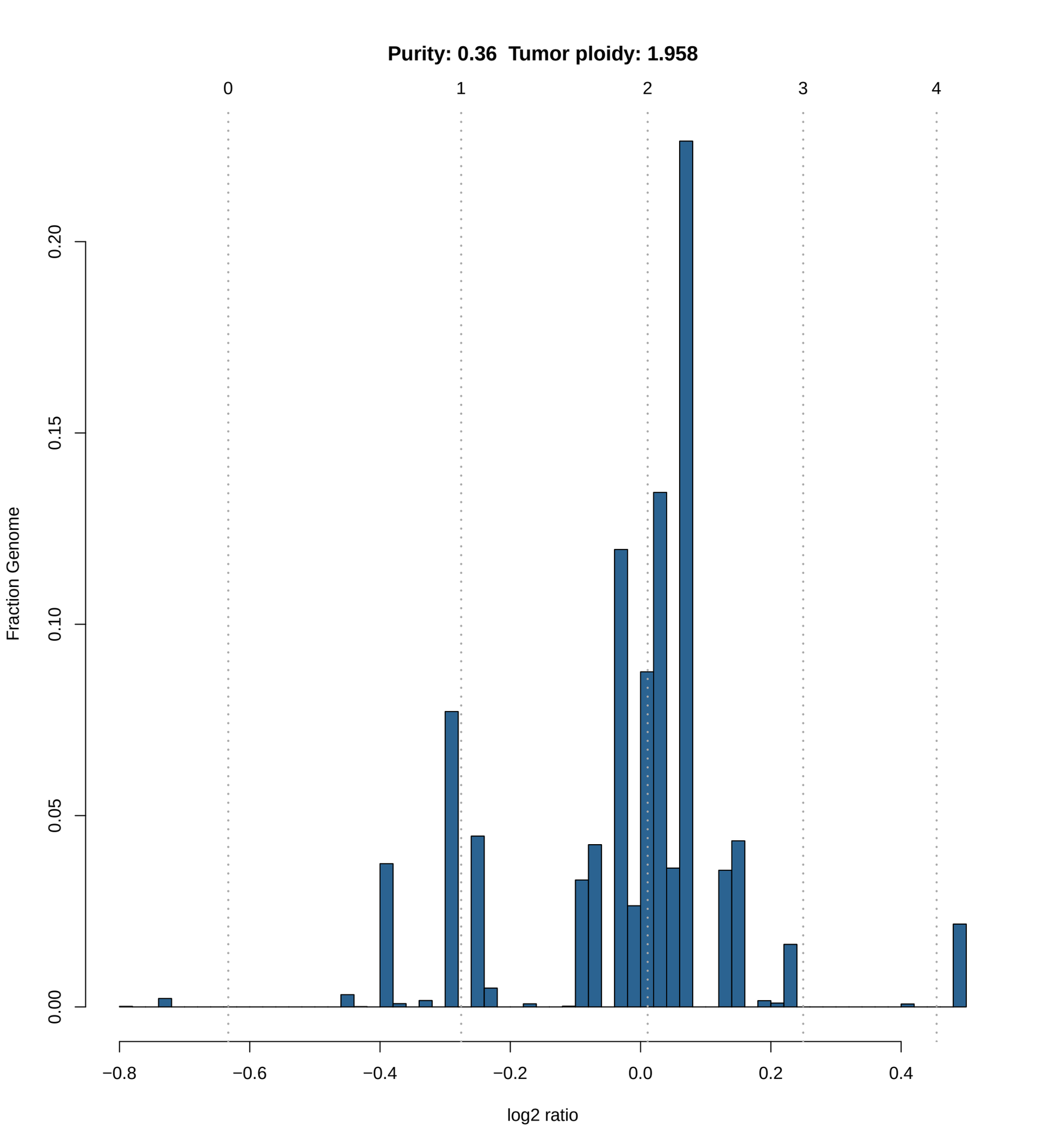

Maximum Likelihood Copy Number
0
1
2
3
4
0
50
100
150
SNV Index

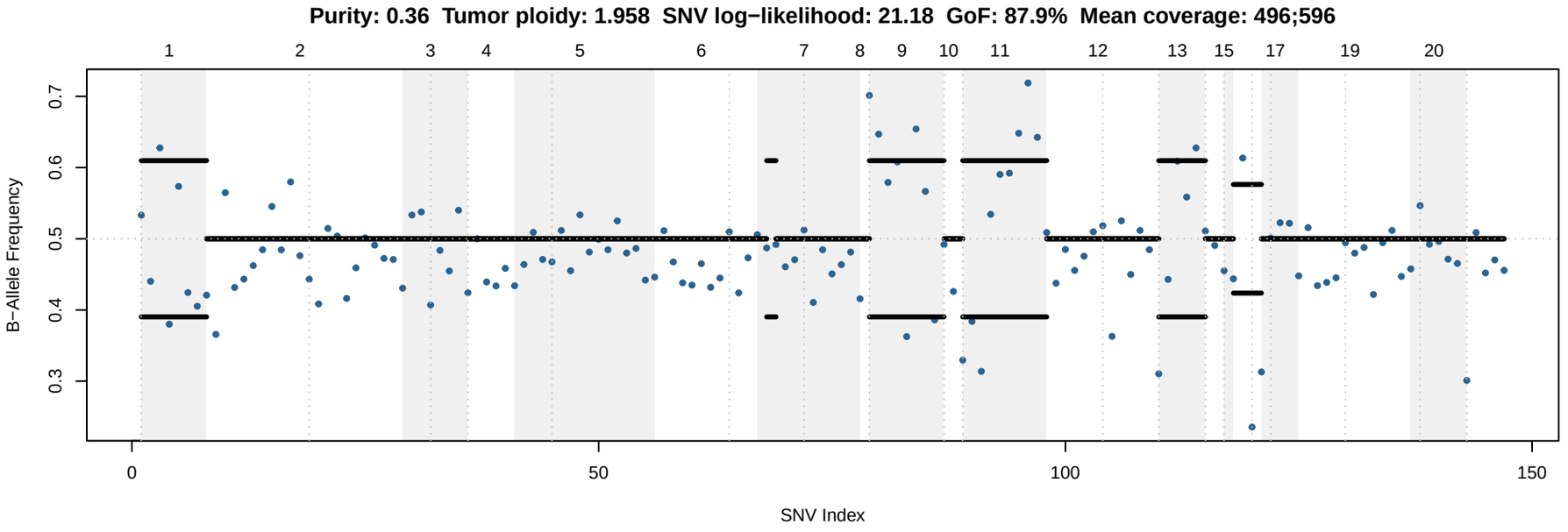

Allelic fraction (germline)
Copy Number log−ratio
0m0
1m0
1m1
2m0
2m1
3m1
3m2
4m1
4m3

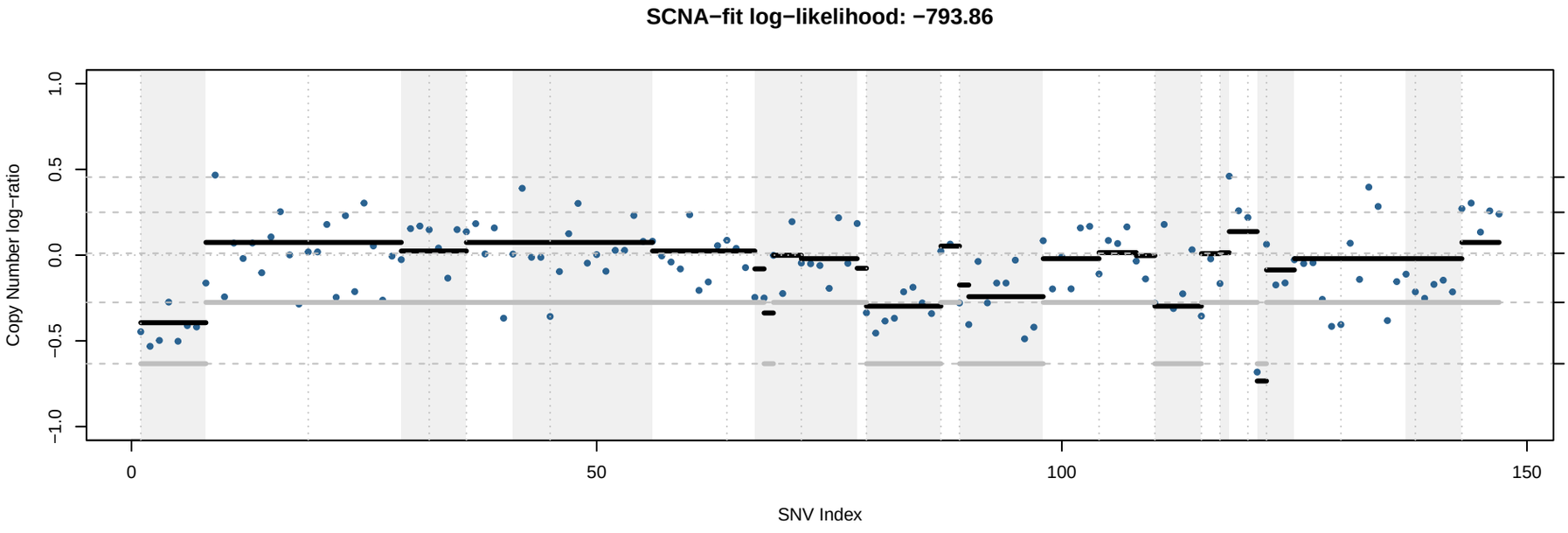

Coverage (log2)
Allelic fraction

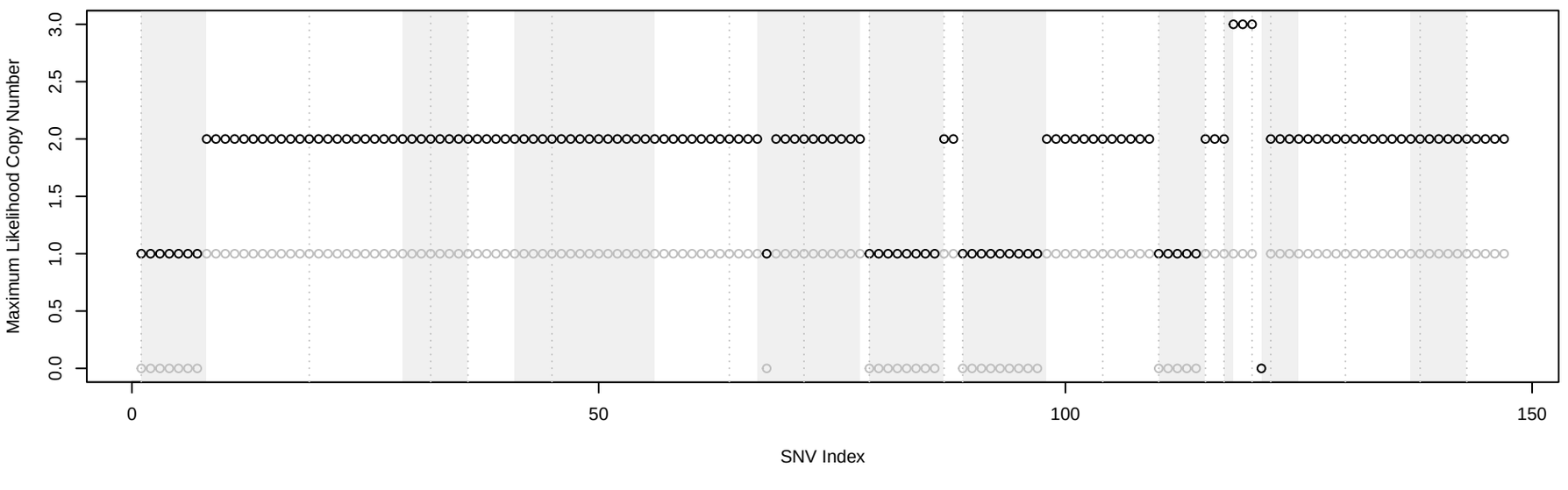

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
3m2

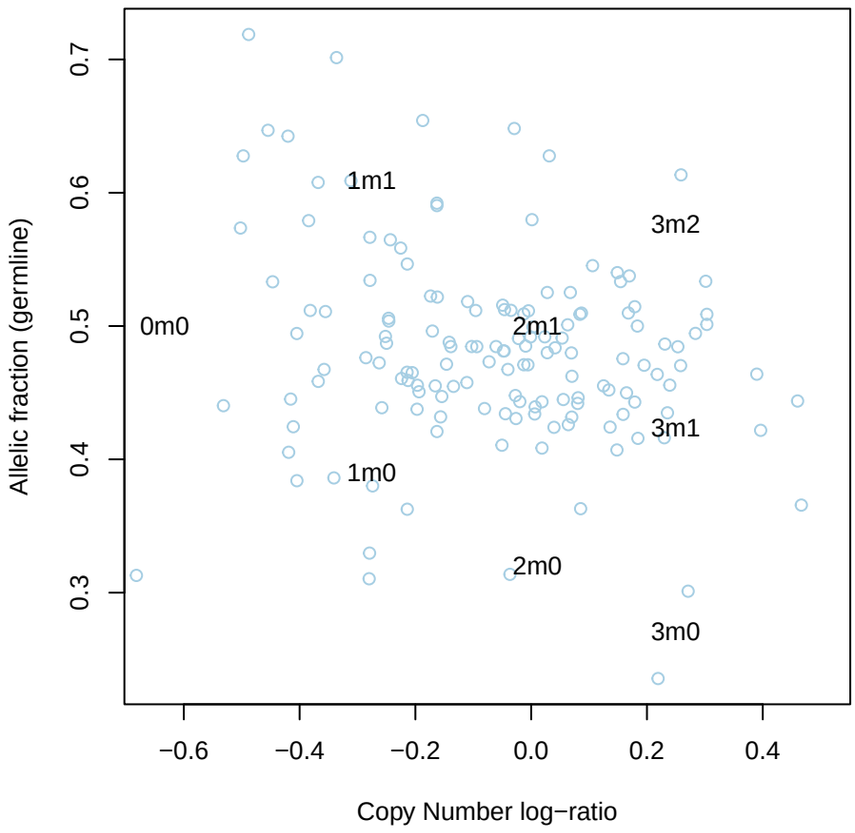

Frequency
Cellular fraction

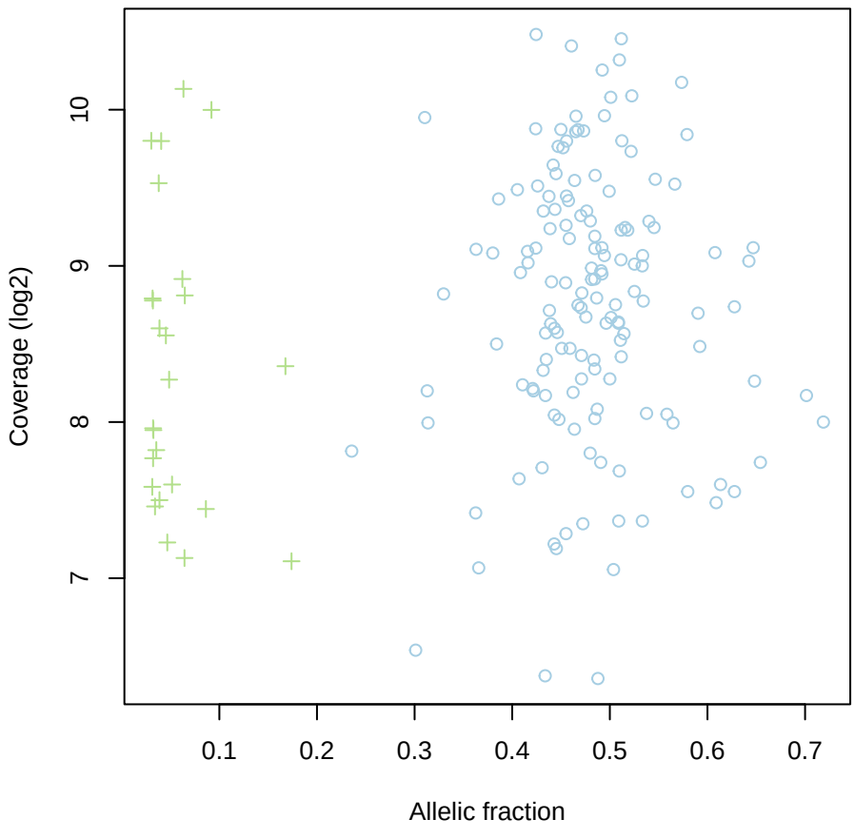

Purity: 0.36 Tumor ploidy: 1.958
0
1
2
3
4
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

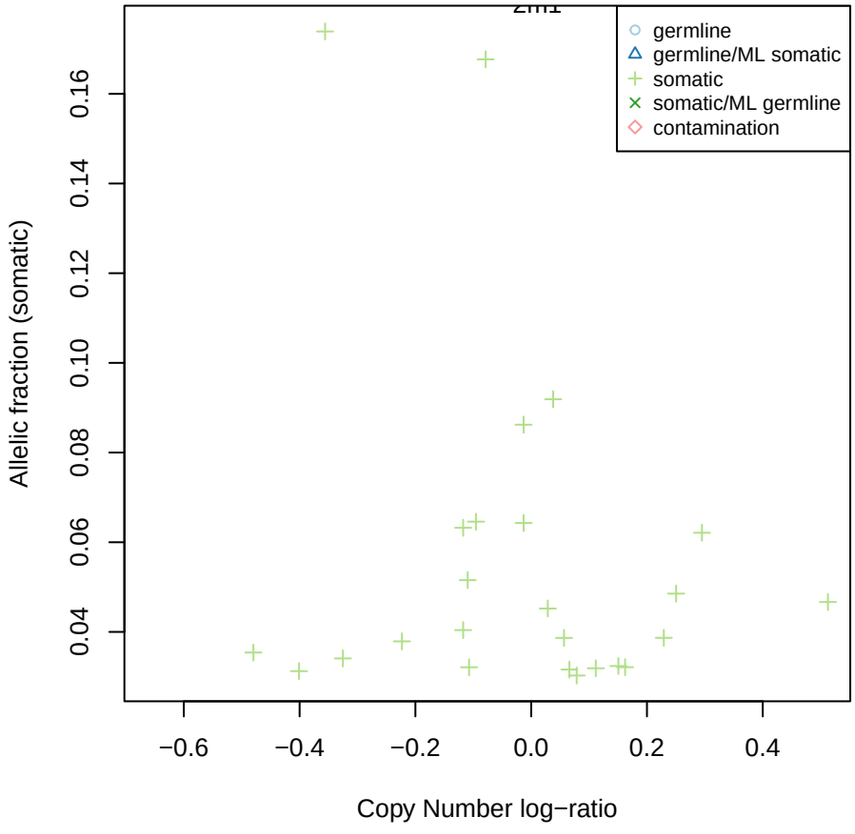

Purity: 0.36 Tumor ploidy: 1.958 SNV log−likelihood: 21.18 GoF: 87.9% Mean coverage: 496;596
1 2 3 4 5 6 7 8 9 10 11 12 13 15 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

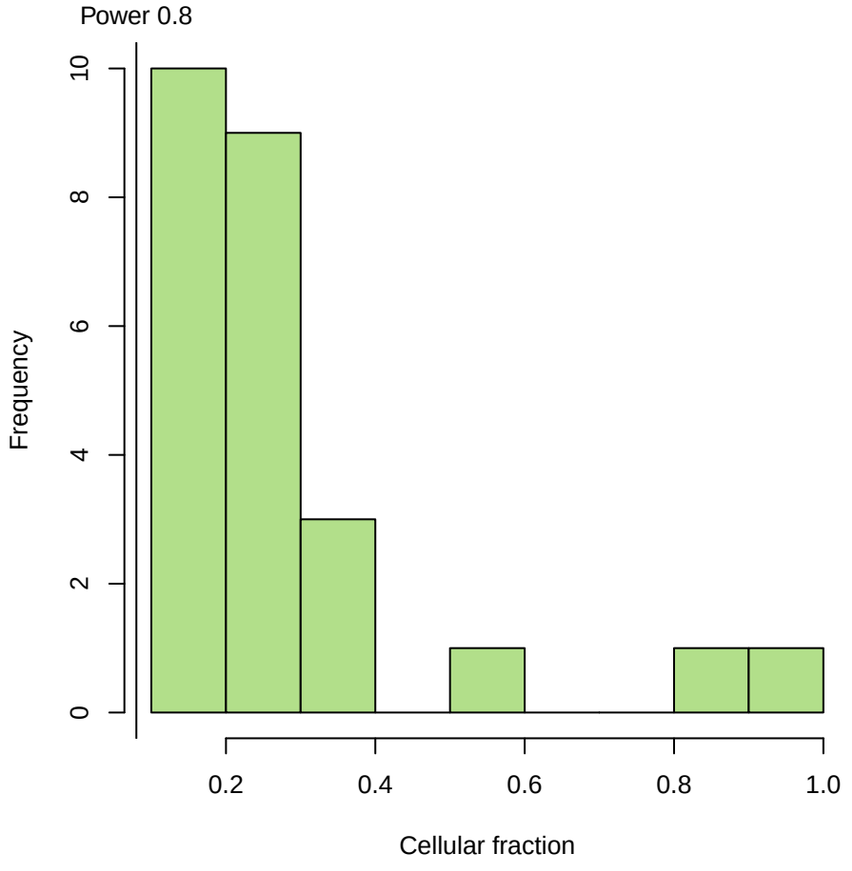

SCNA−fit log−likelihood: −793.86
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4
0 50 100 150
SNV Index

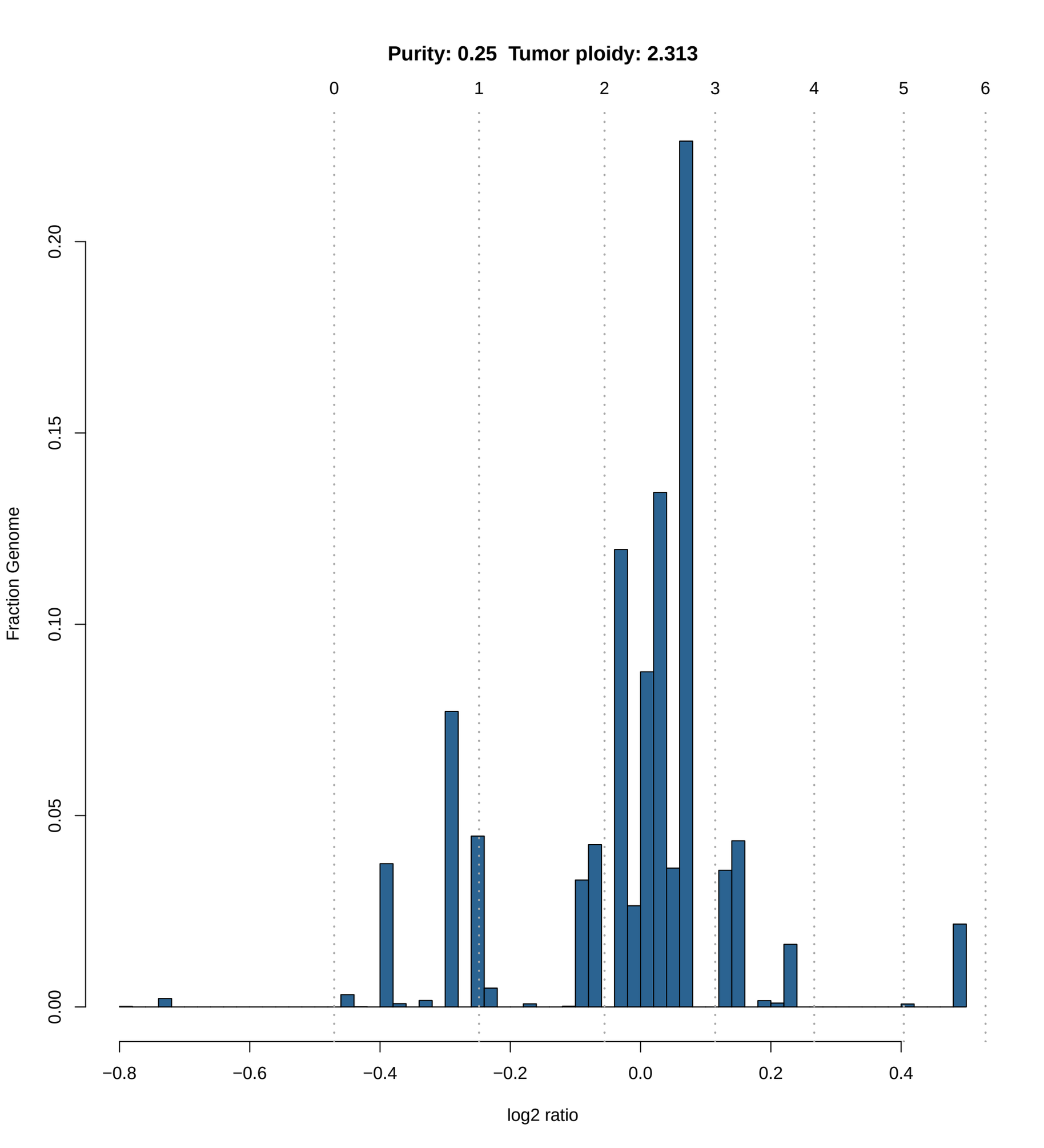

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

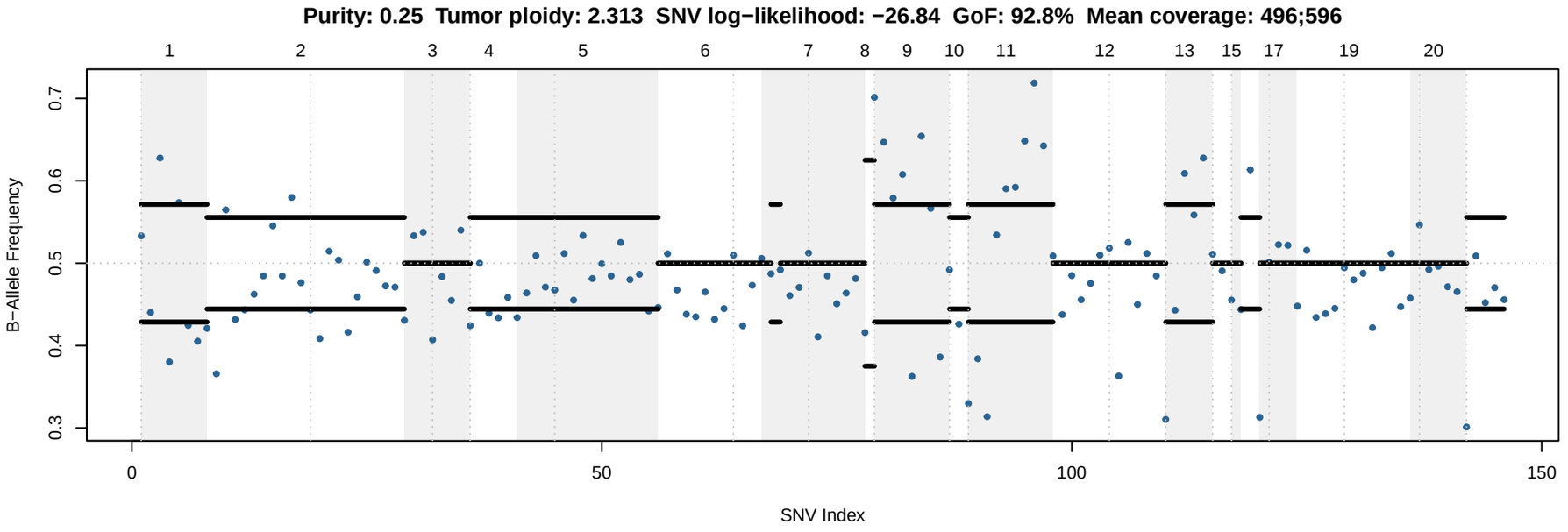

Allelic fraction (germline)
Copy Number log−ratio
0m0
1m1
2m1
3m2
3m1
1m0
2m0
3m0

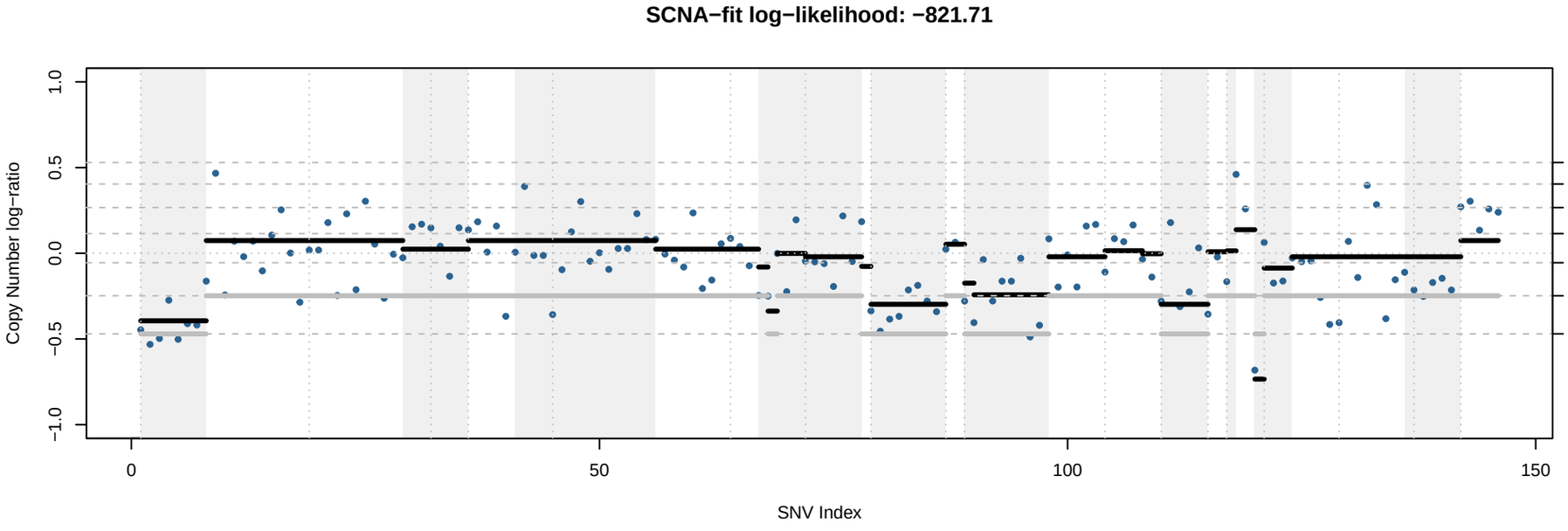

Coverage (log2)
Allelic fraction

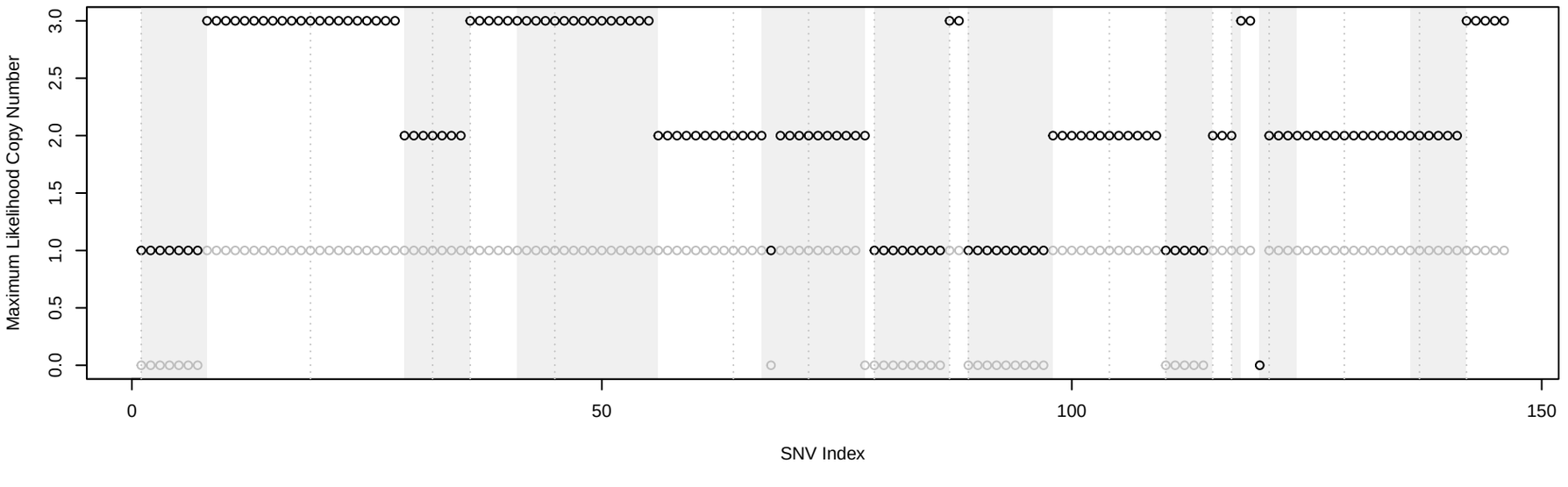

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

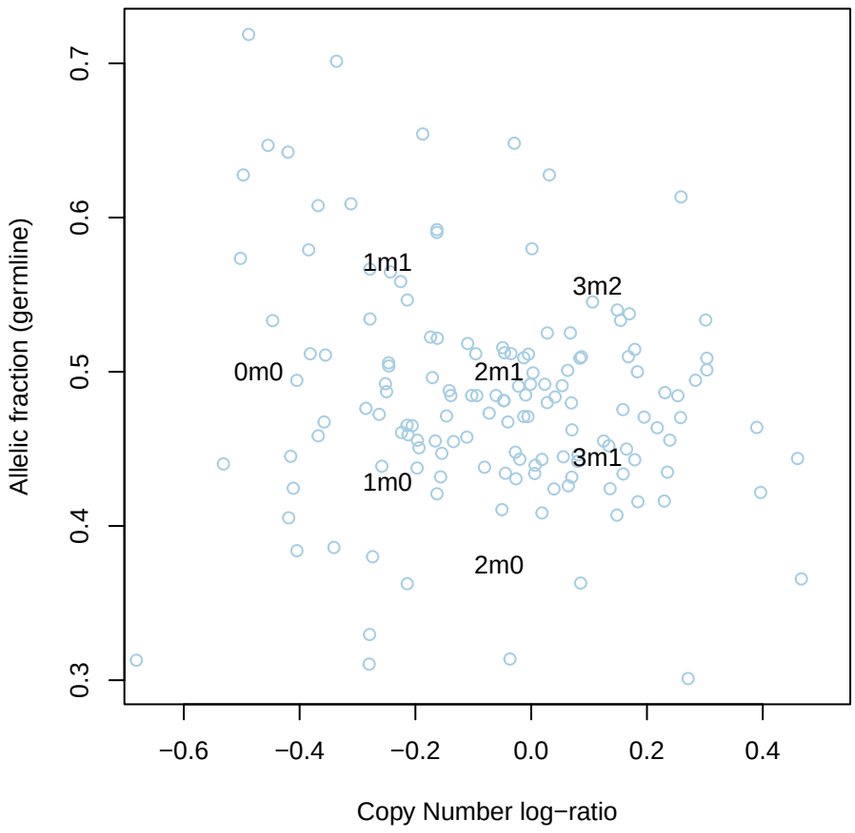

Power 0.8
Frequency
Cellular fraction

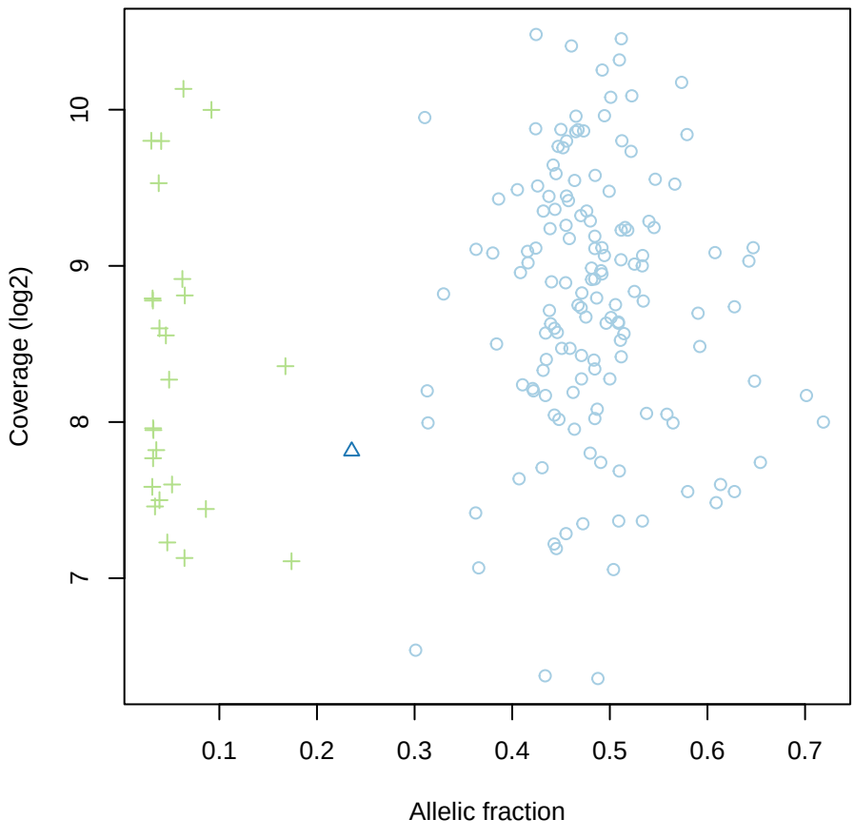

Purity: 0.25 Tumor ploidy: 2.313
0
1
2
3
4
5
6
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

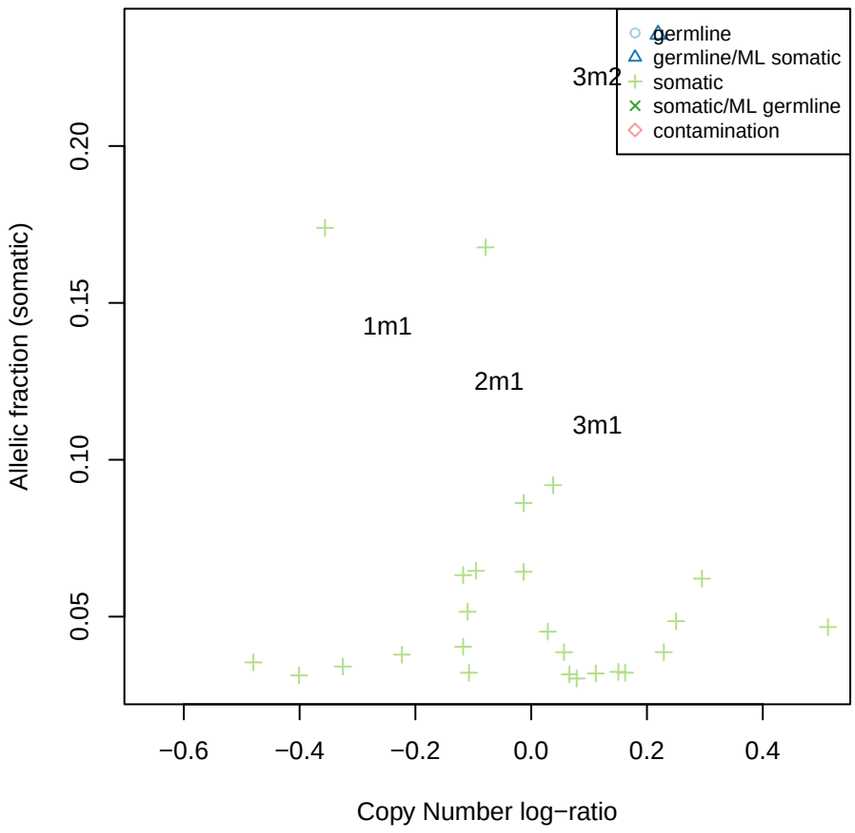

Purity: 0.25 Tumor ploidy: 2.313 SNV log−likelihood: −26.84 GoF: 92.8% Mean coverage: 496;596
1 2 3 4 5 6 7 8 9 10 11 12 13 15 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

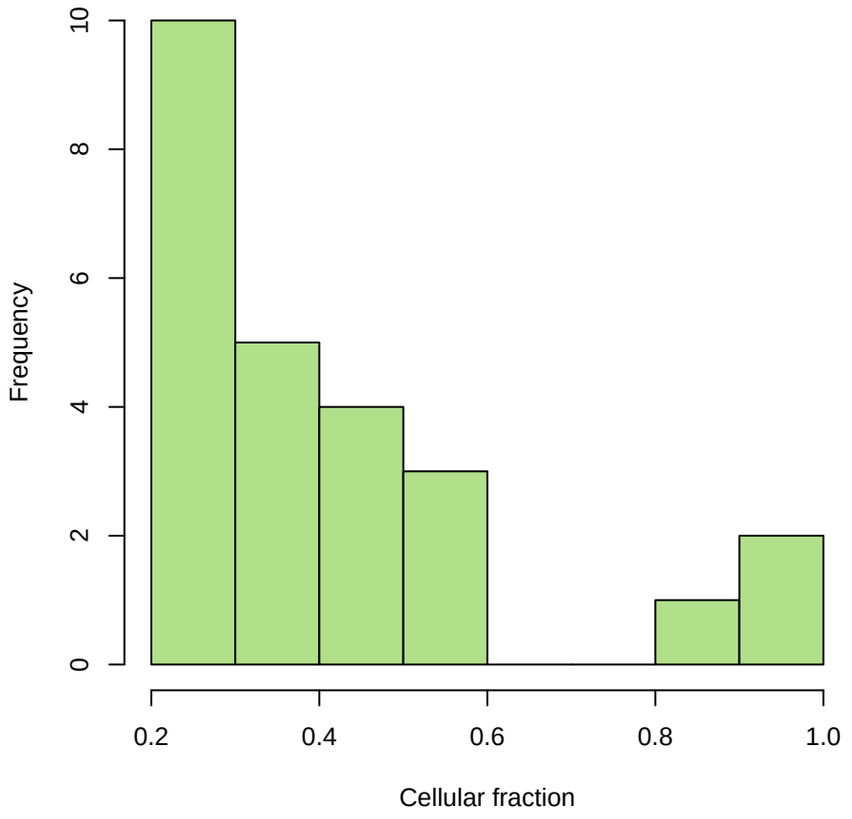

SCNA−fit log−likelihood: −821.71
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 6
0 50 100 150
SNV Index

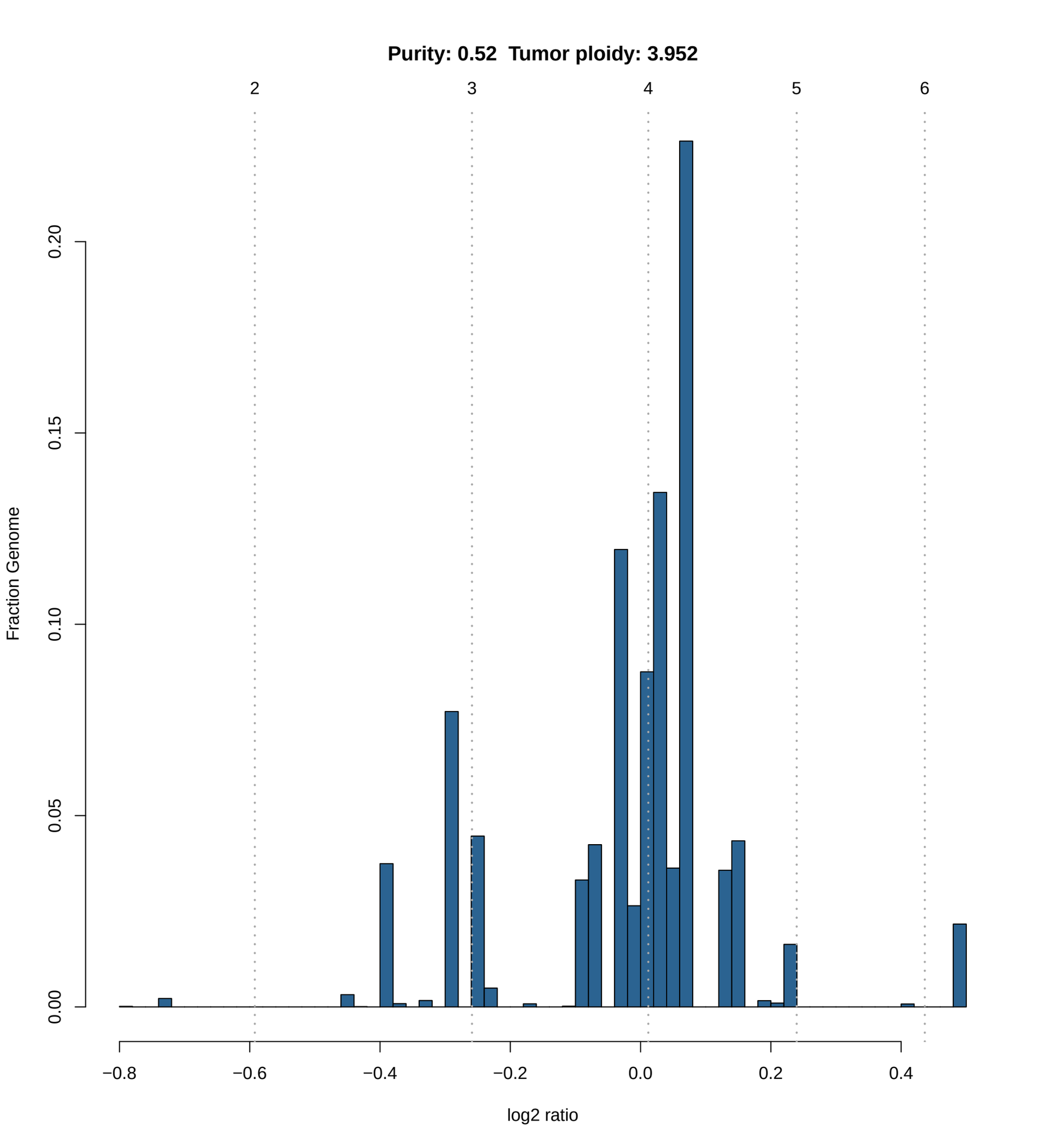

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

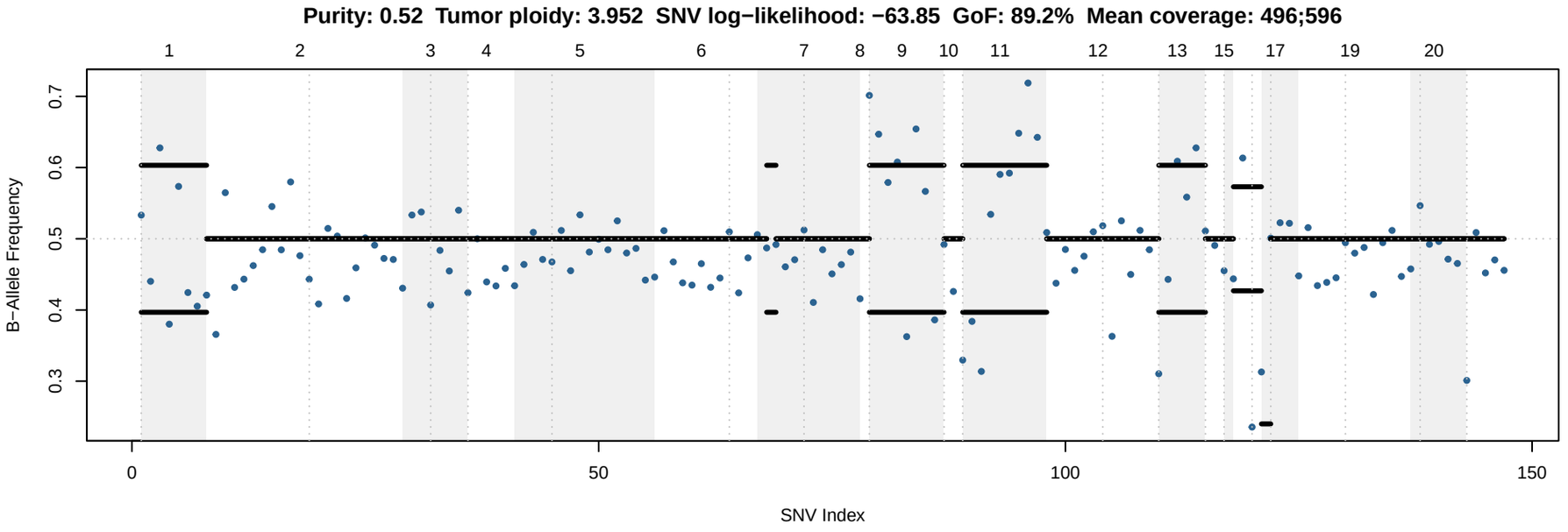

Allelic fraction (germline)
Copy Number log−ratio
0m0
1m1
2m1
3m2
1m0
3m1
2m0

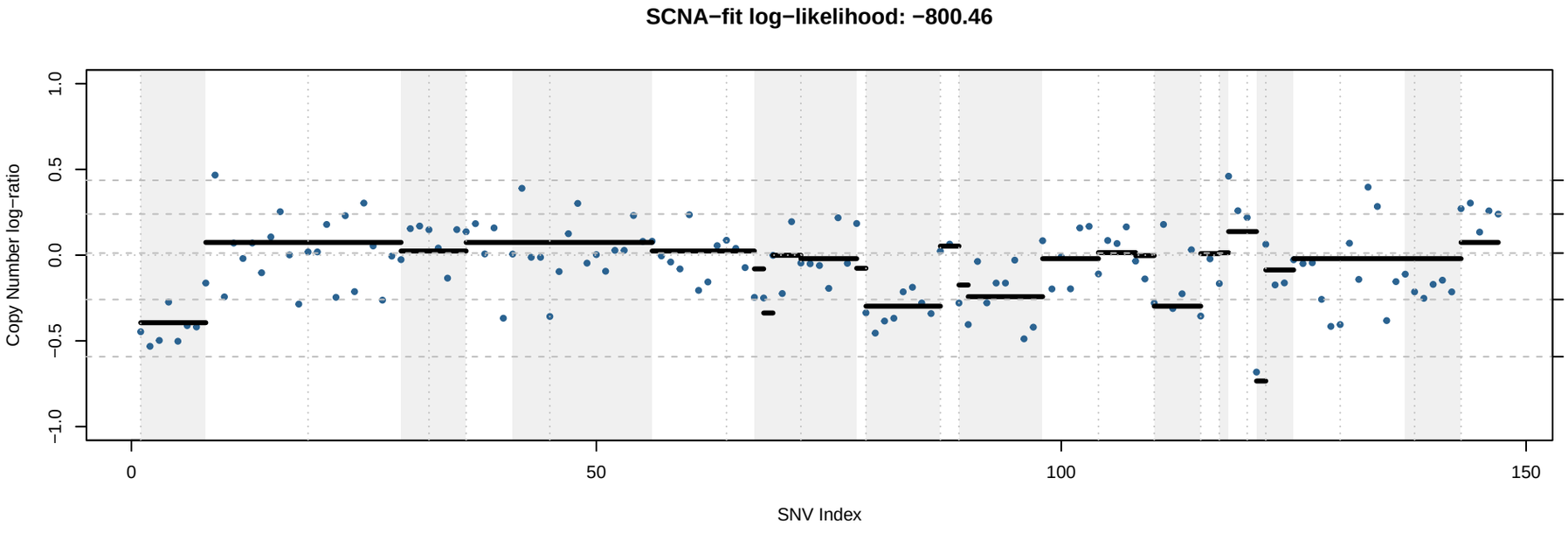

Coverage (log2)
Allelic fraction

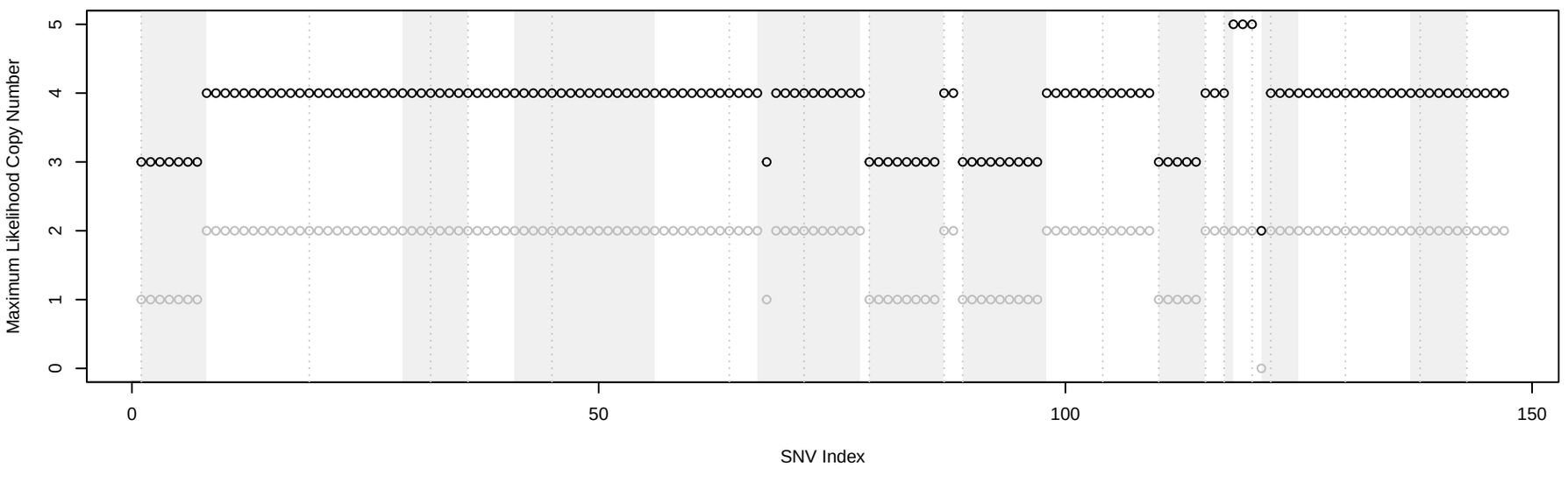

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m2
3m1

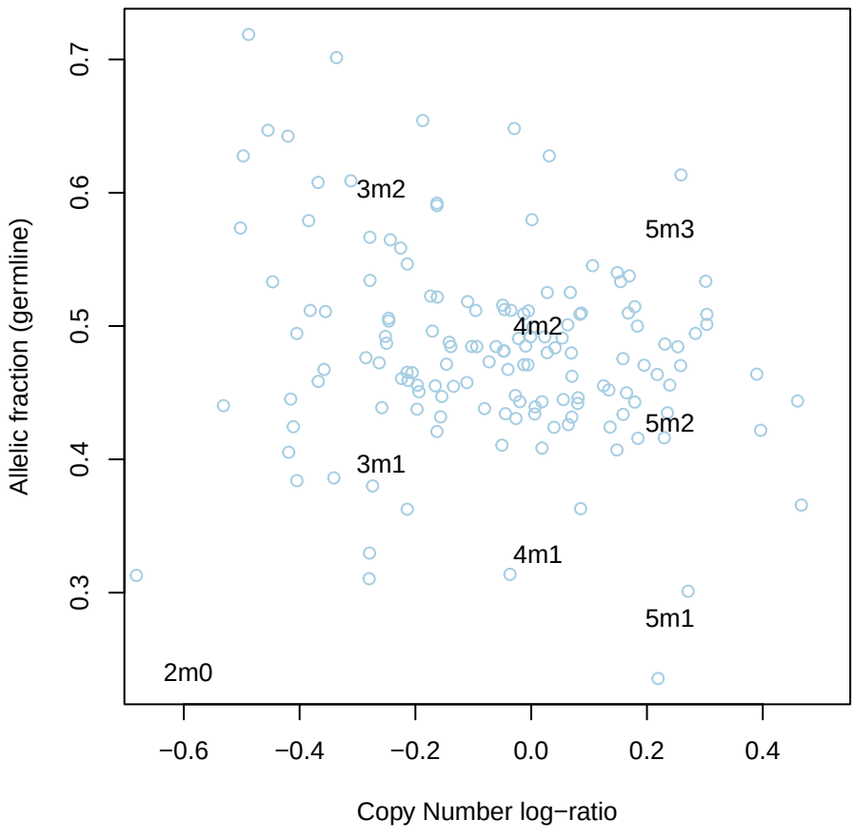

Frequency
Cellular fraction

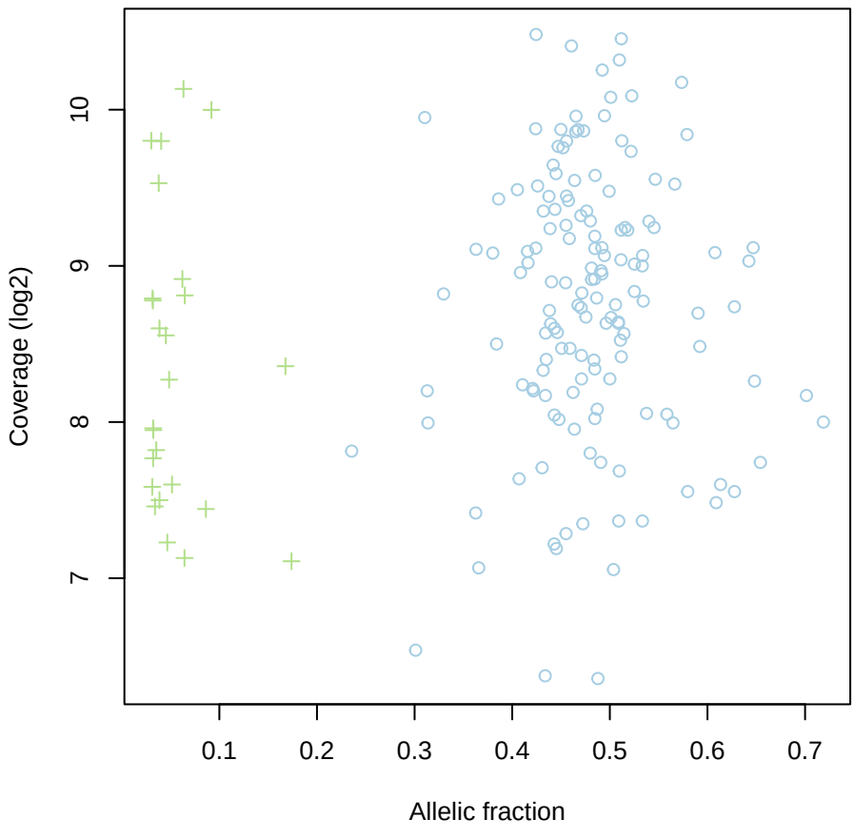

Purity: 0.52 Tumor ploidy: 3.952
2
3
4
5
6
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

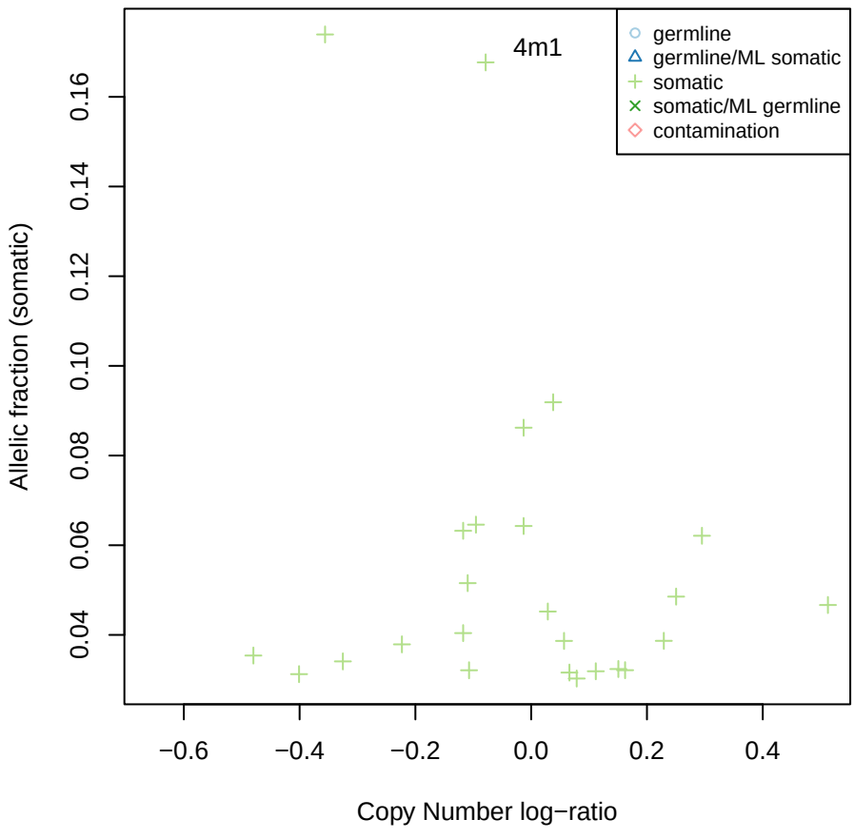

Purity: 0.52 Tumor ploidy: 3.952 SNV log−likelihood: −63.85 GoF: 89.2% Mean coverage: 496;596
1 2 3 4 5 6 7 8 9 10 11 12 13 15 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

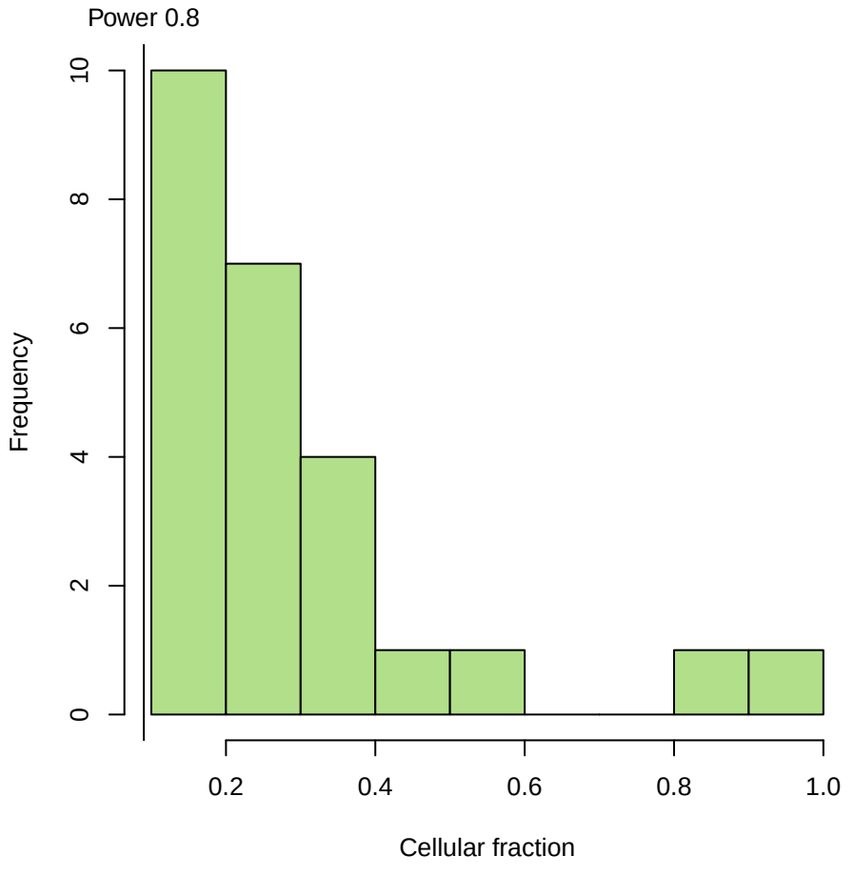

SCNA−fit log−likelihood: −800.46
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6
0 50 100 150
SNV Index

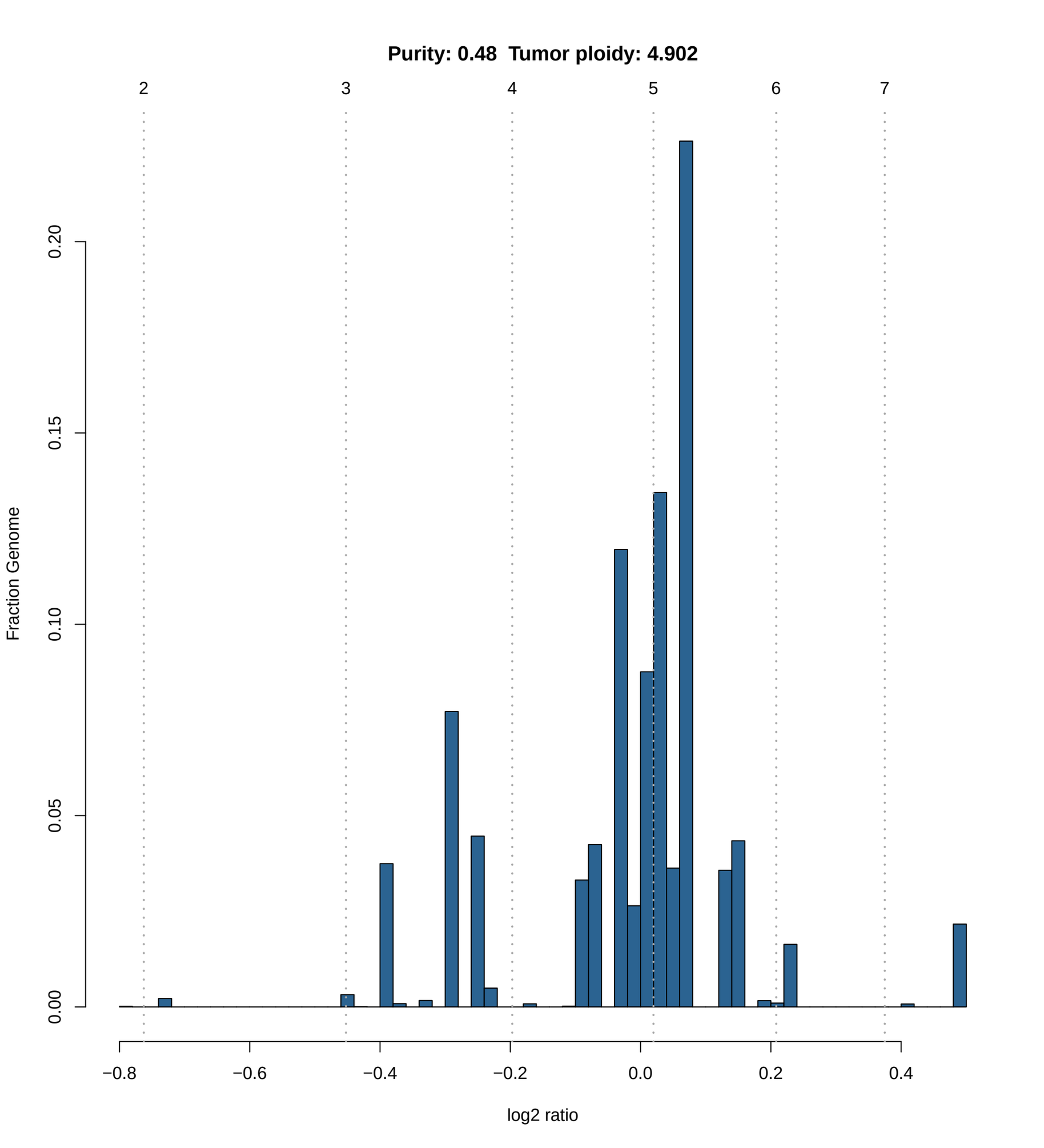

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

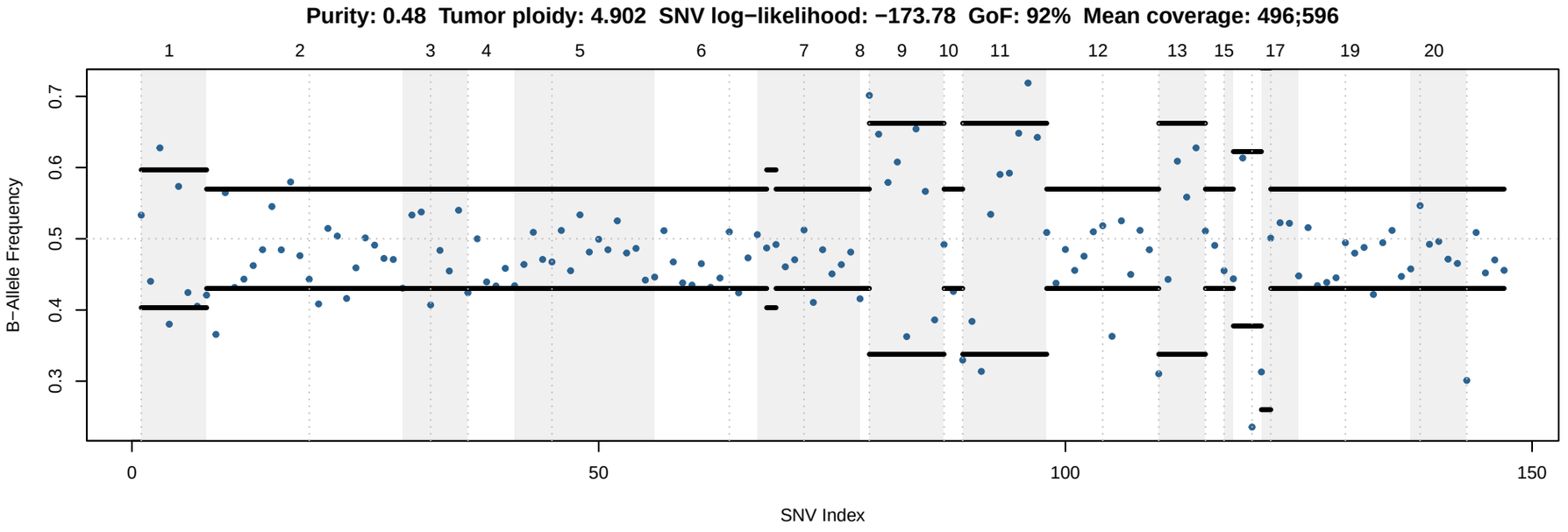

Allelic fraction (germline)
Copy Number log−ratio
3m2
5m3
4m2
5m2
3m1
4m1
5m1
2m0

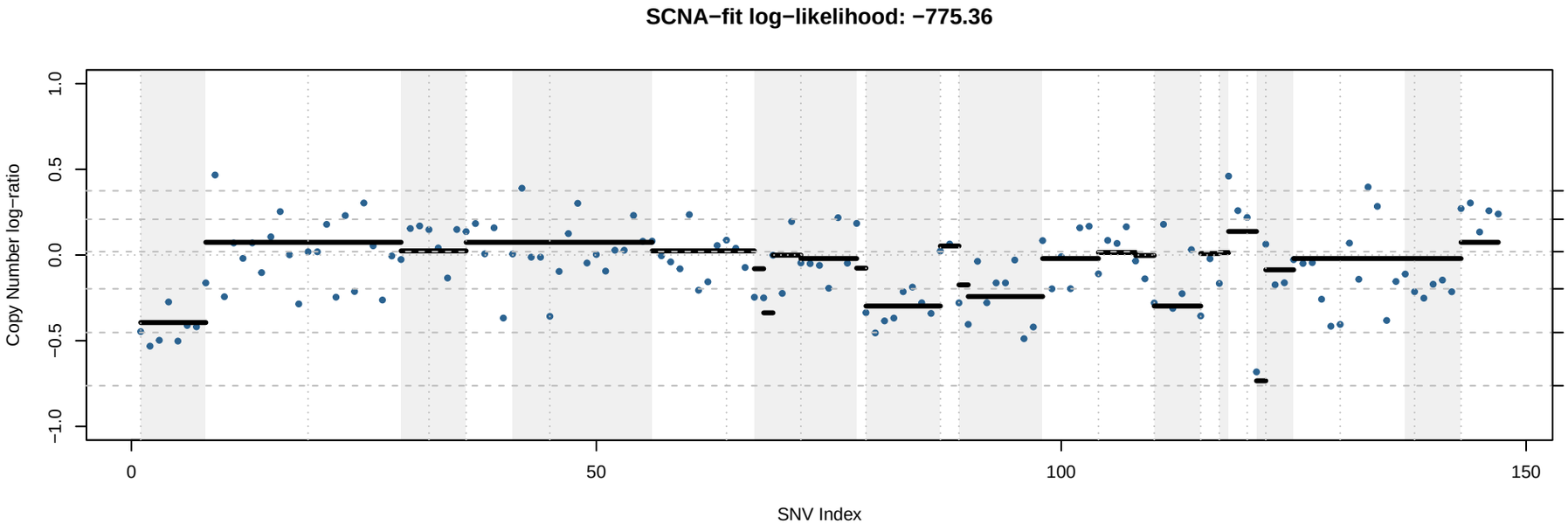

Coverage (log2)
Allelic fraction

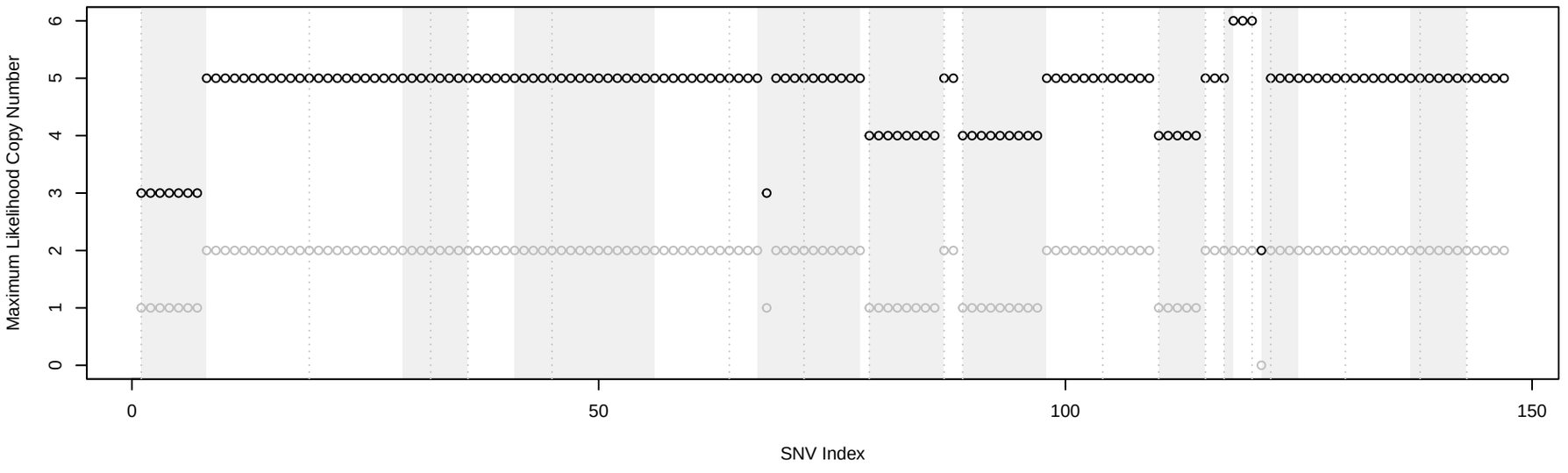

Allelic fraction (somatic)
Copy Number log−ratio
4m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

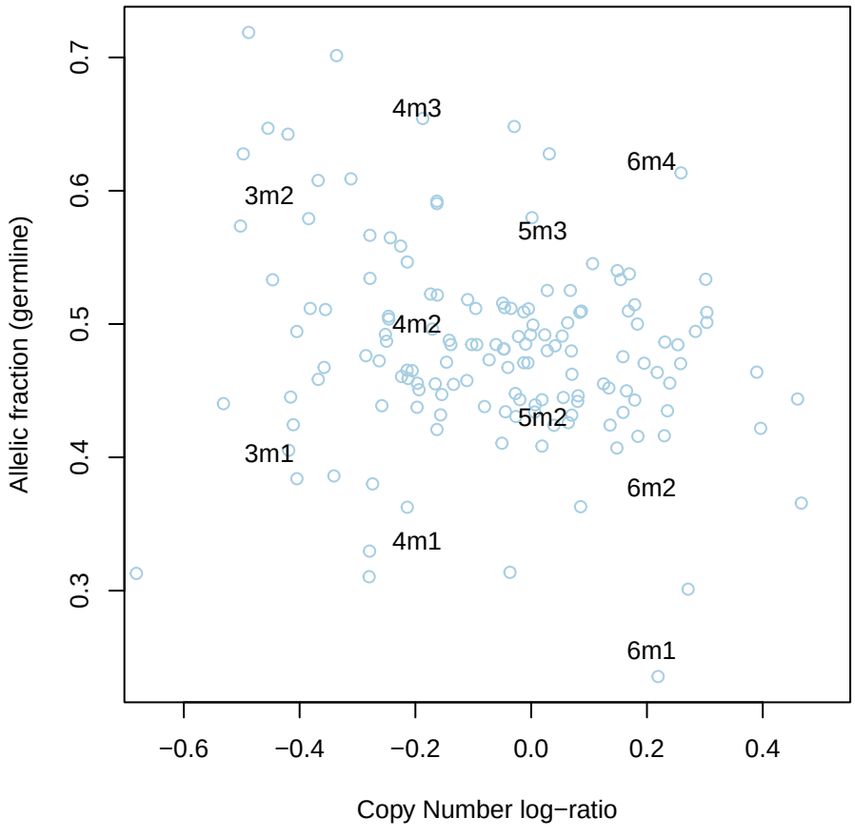

Power 0.8
Frequency
Cellular fraction

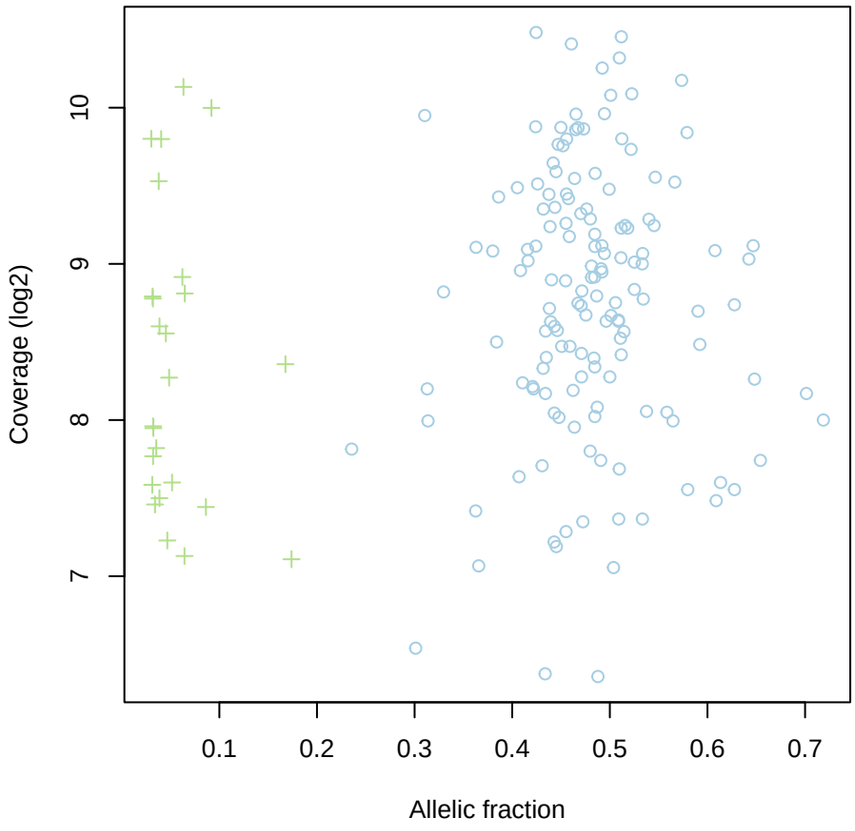

Purity: 0.48 Tumor ploidy: 4.902
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

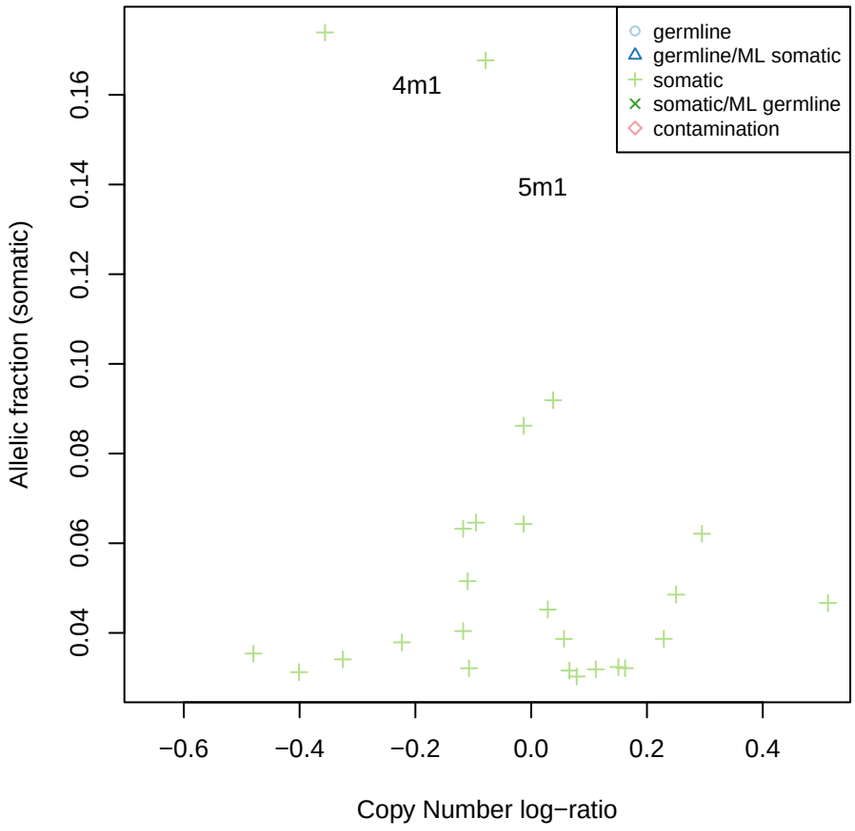

Purity: 0.48 Tumor ploidy: 4.902 SNV log−likelihood: −173.78 GoF: 92% Mean coverage: 496;596
1 2 3 4 5 6 7 8 9 10 11 12 13 15 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

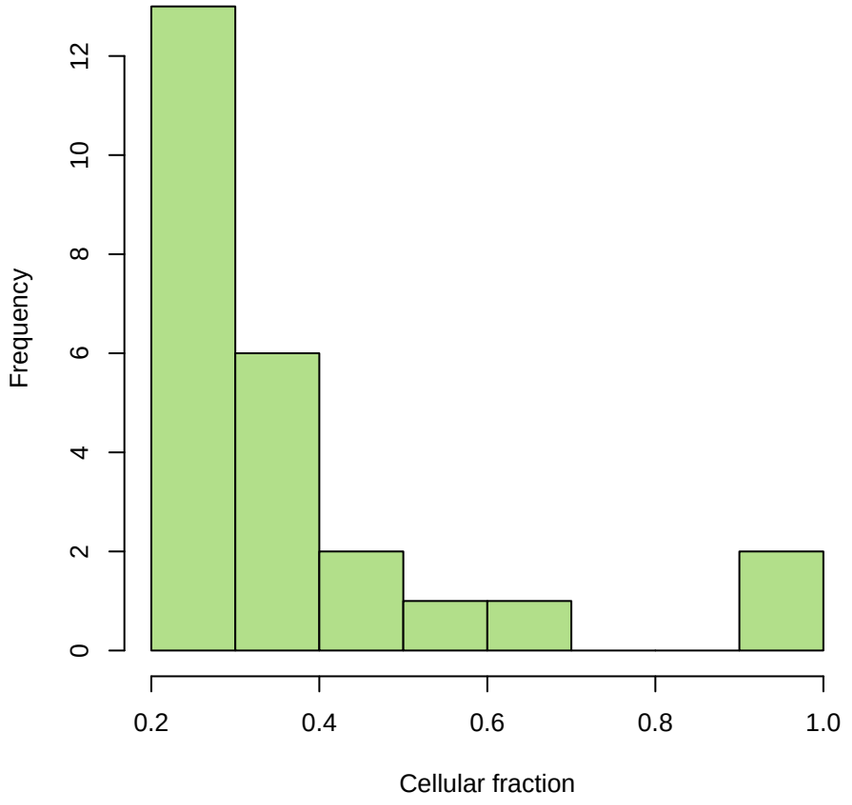

SCNA−fit log−likelihood: −775.36
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 50 100 150
SNV Index

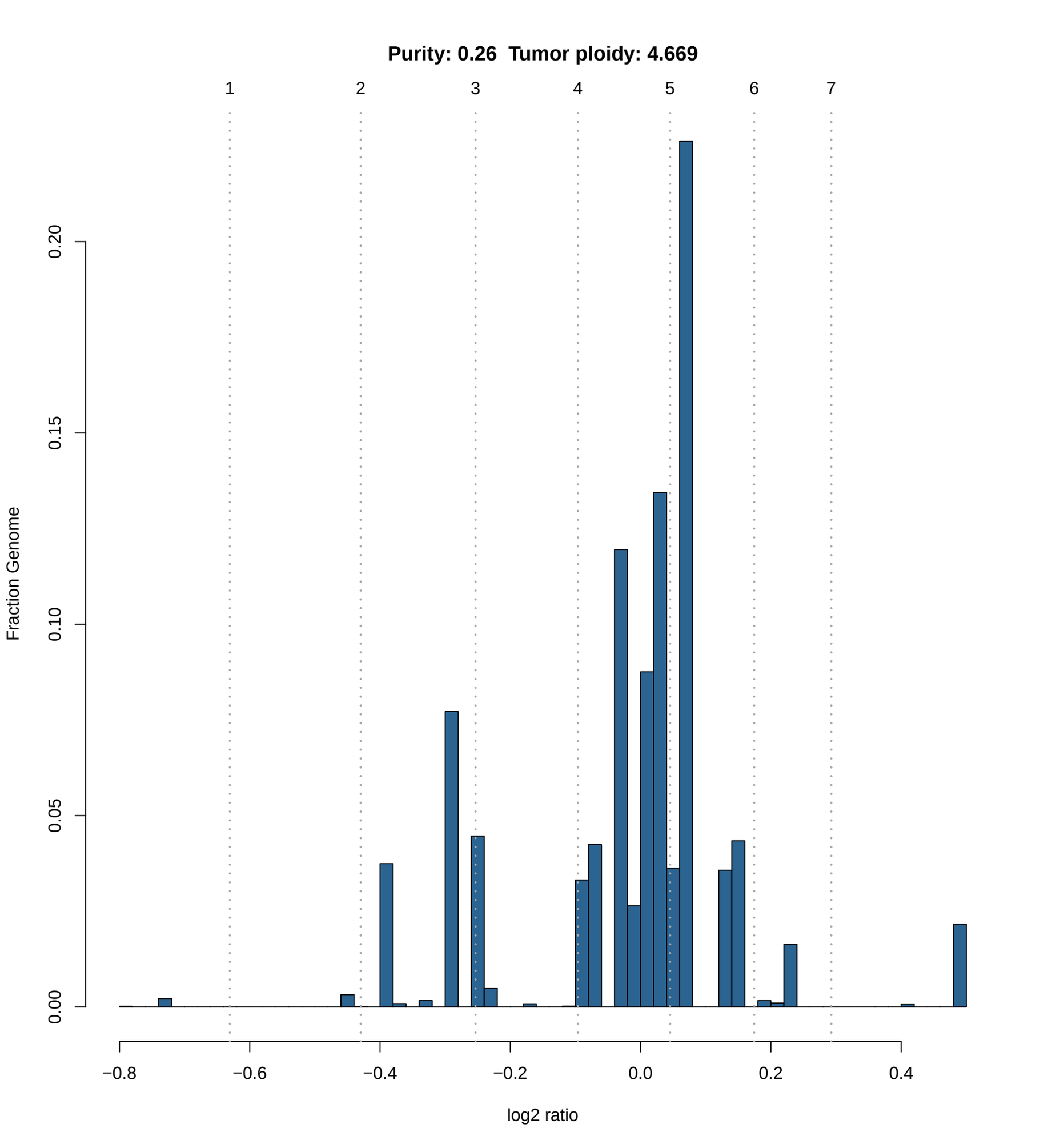

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

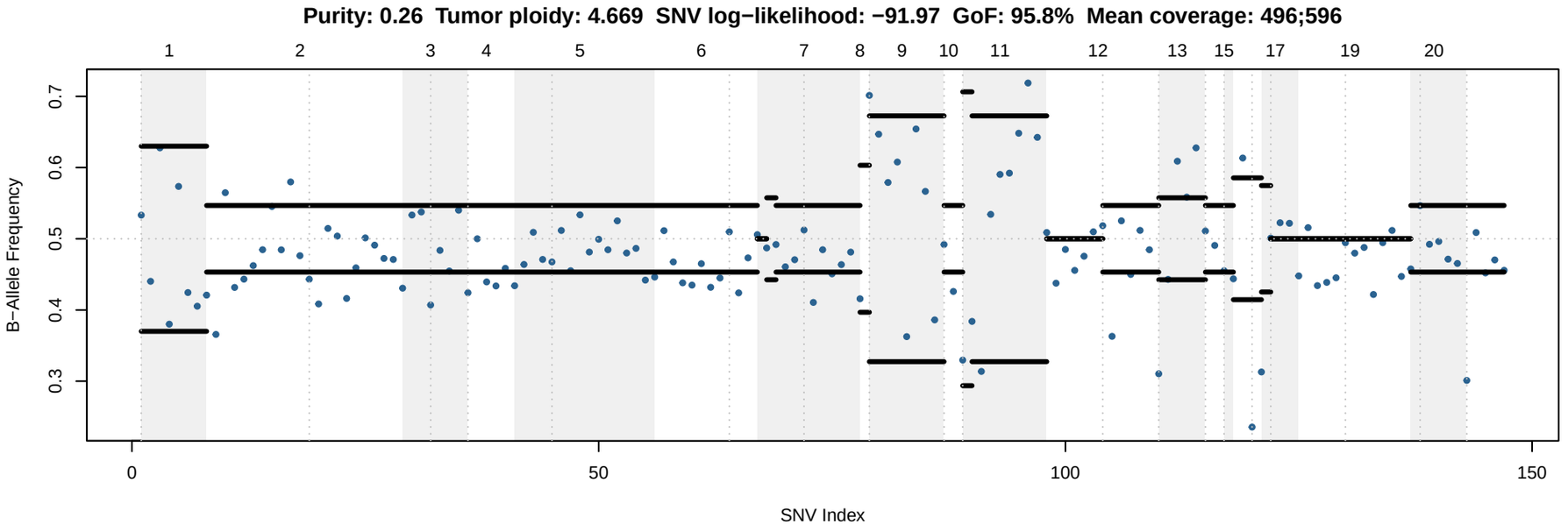

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
4m3
6m4
3m2
5m3
4m2
5m2
3m1
6m2
4m1
6m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

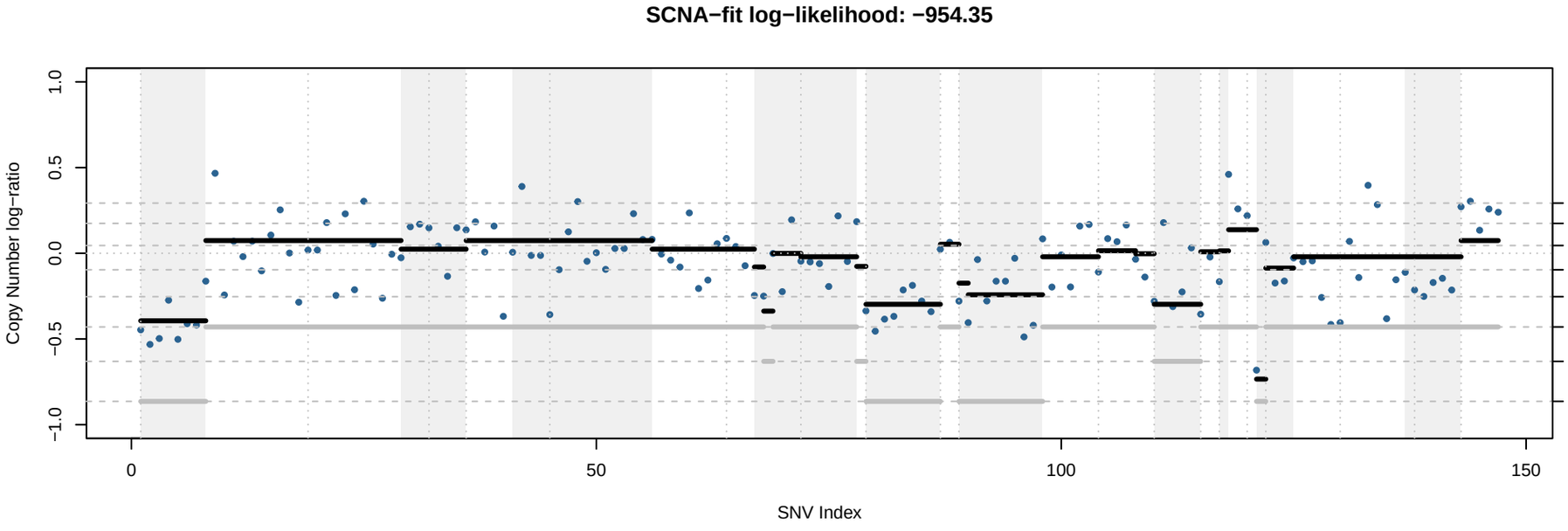

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

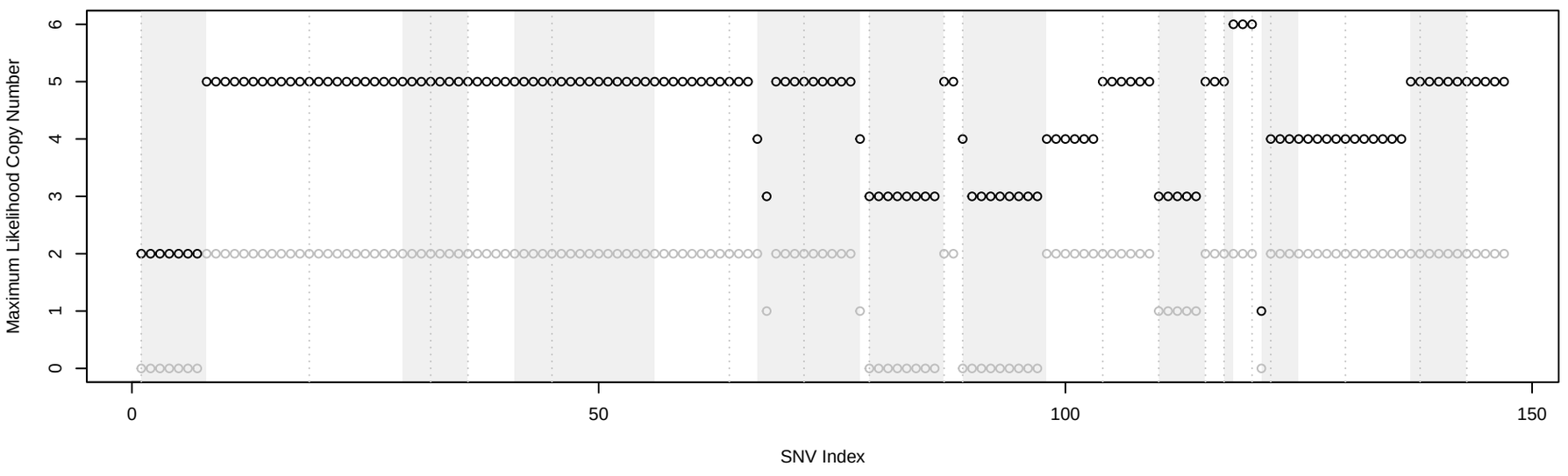

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

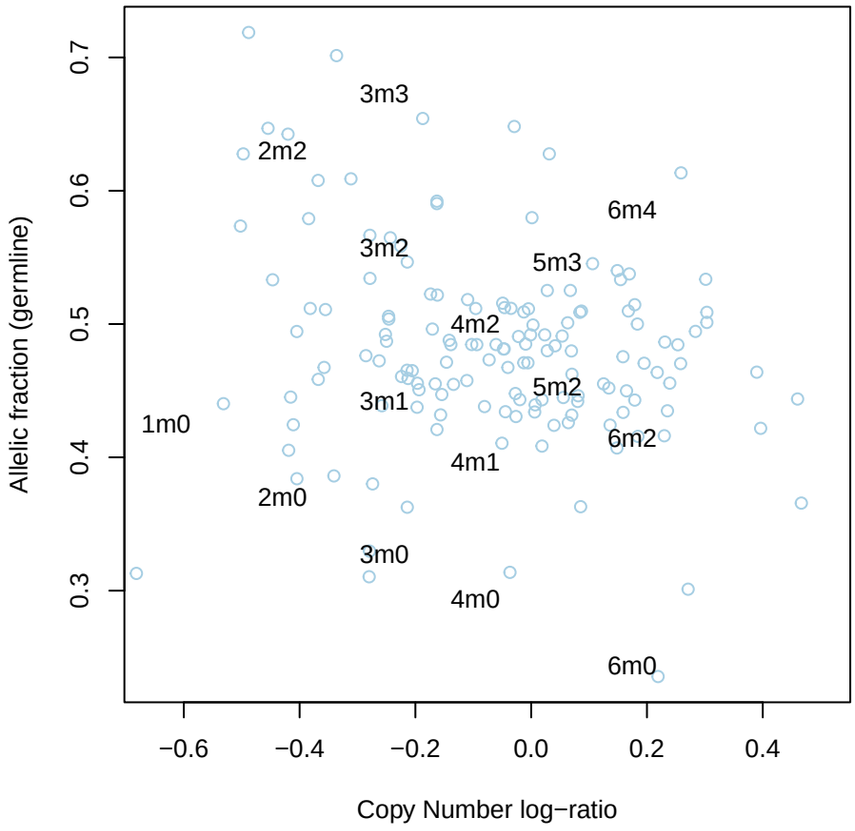

Frequency
0
2
4
6
8
10
12
0.2
0.4
0.6
0.8
1.0
Cellular fraction

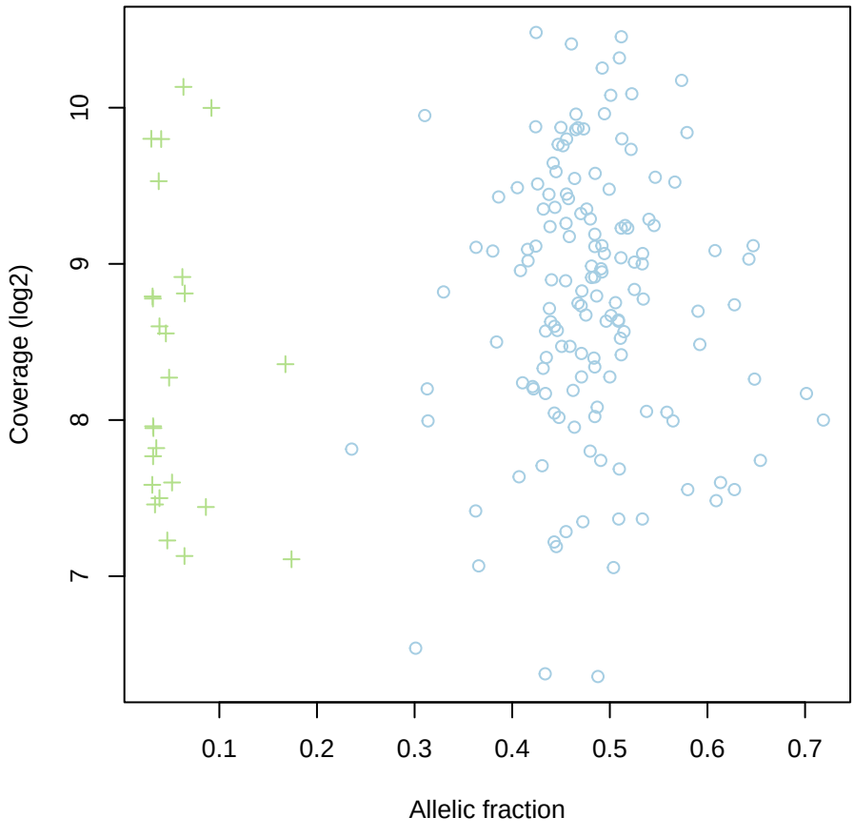

Purity: 0.26 Tumor ploidy: 4.669
1
2
3
4
5
6
7
0.00
0.05
0.10
0.15
0.20
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

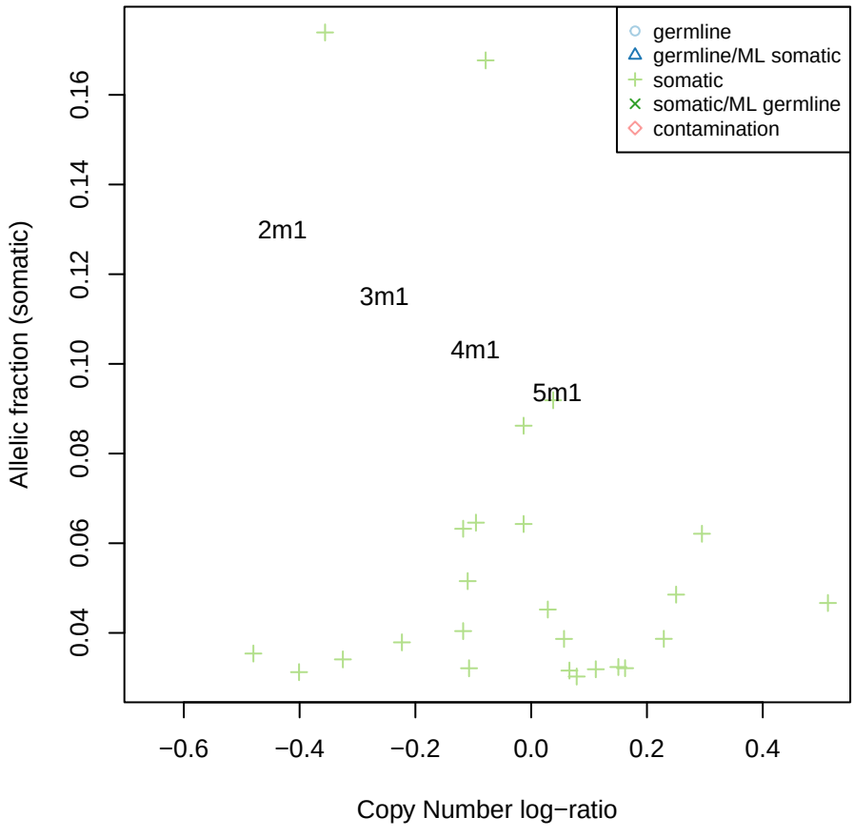

Purity: 0.26 Tumor ploidy: 4.669 SNV log−likelihood: −91.97 GoF: 95.8% Mean coverage: 496;596
1 2 3 4 5 6 7 8 9 10 11 12 13 15 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

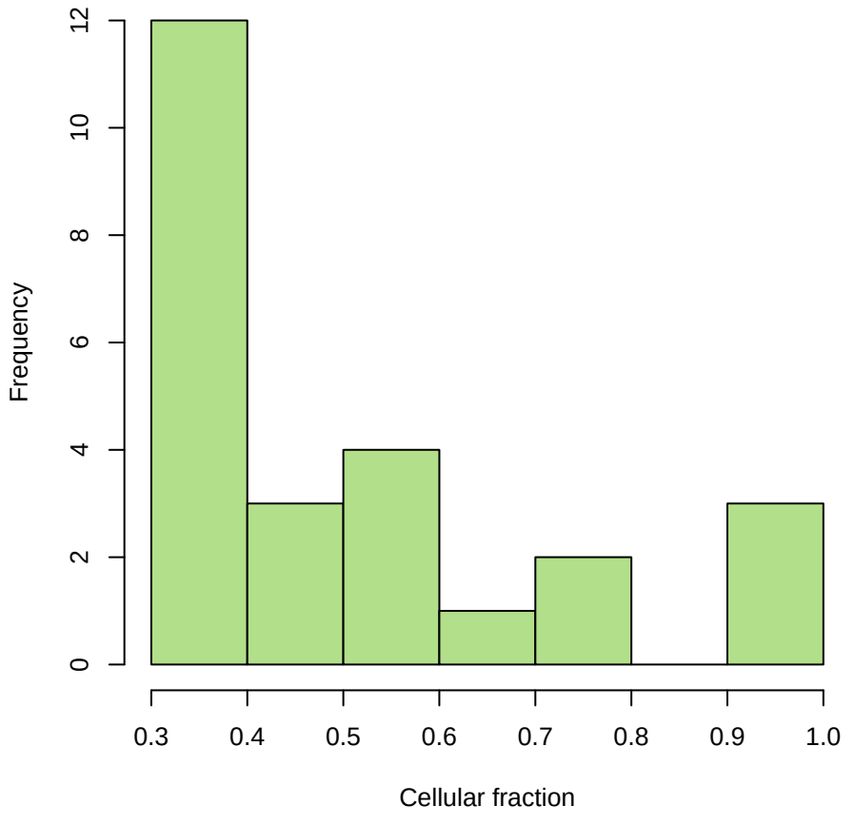

SCNA−fit log−likelihood: −954.35
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 6
0 50 100 150
SNV Index

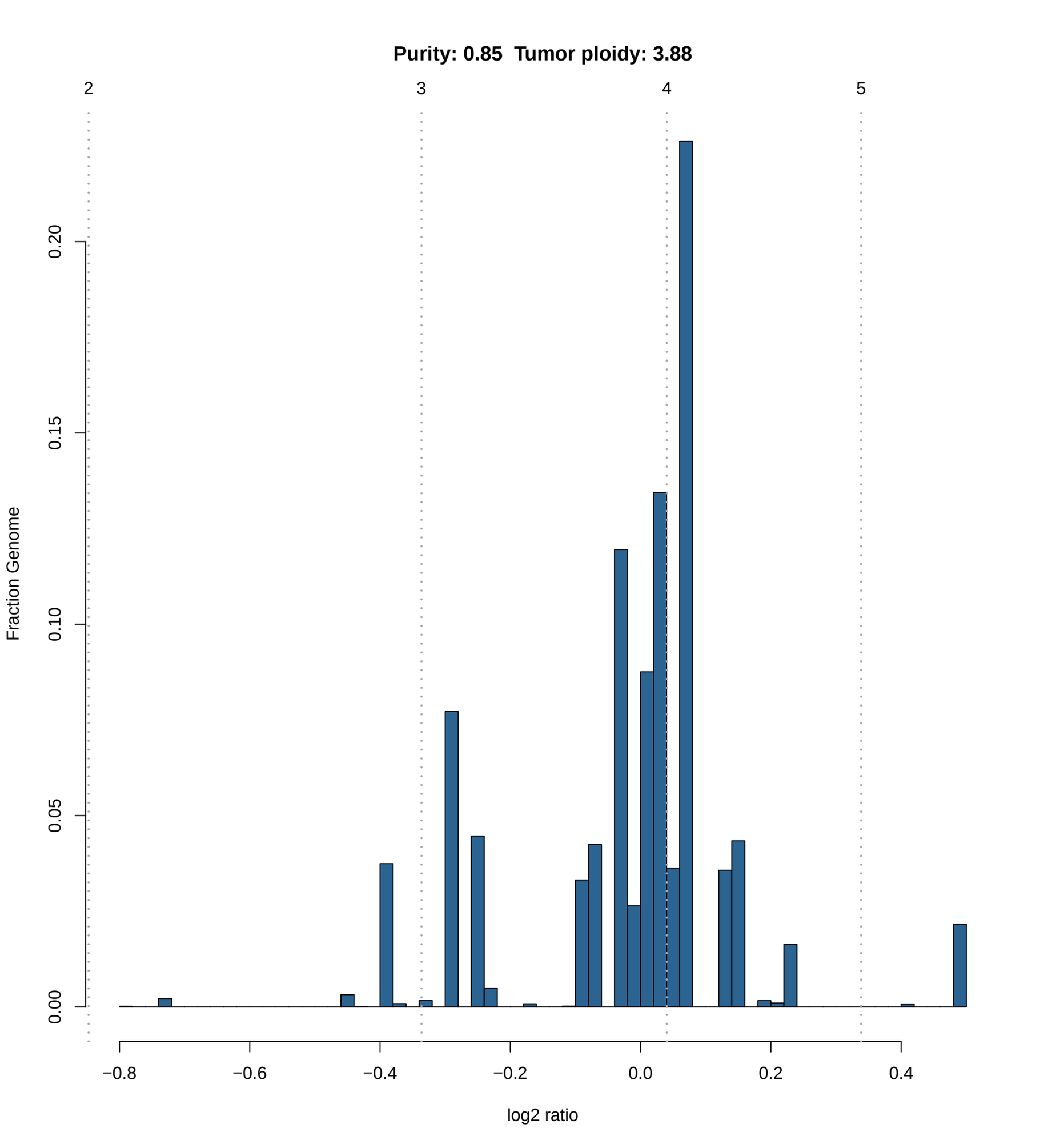

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

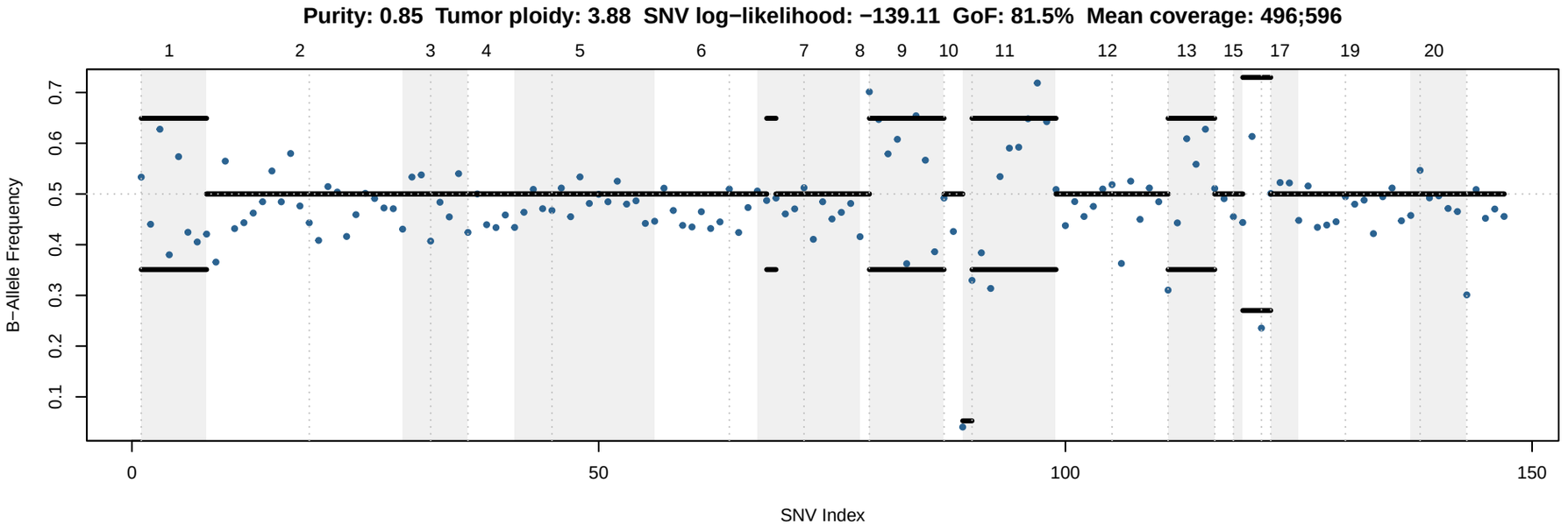

Allelic fraction (germline)
Copy Number log−ratio
1m0
2m0
2m2
3m0
3m1
3m2
3m3
4m0
4m1
4m2
5m2
5m3
6m0
6m2
6m4

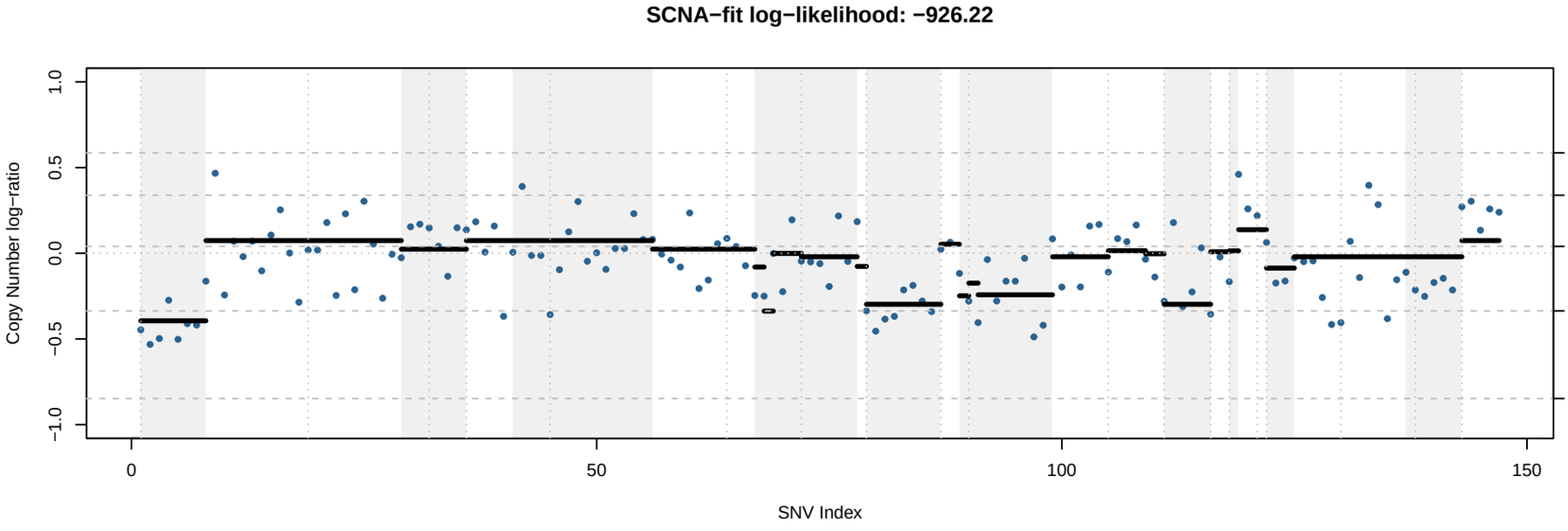

Coverage (log2)
Allelic fraction

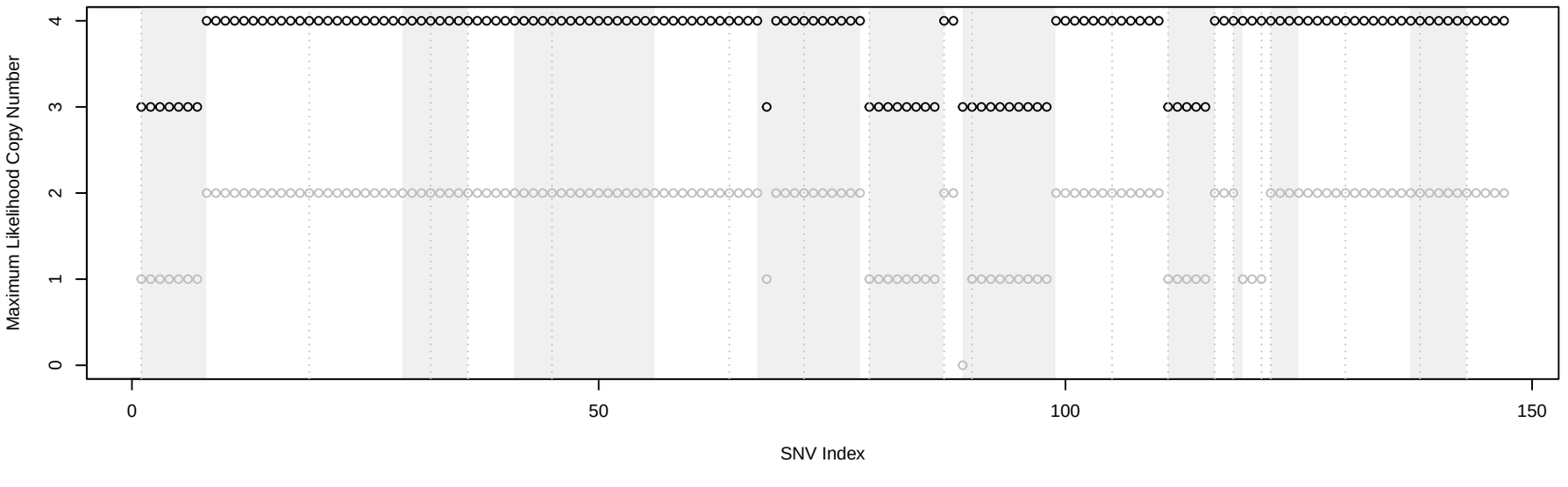

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1
5m1

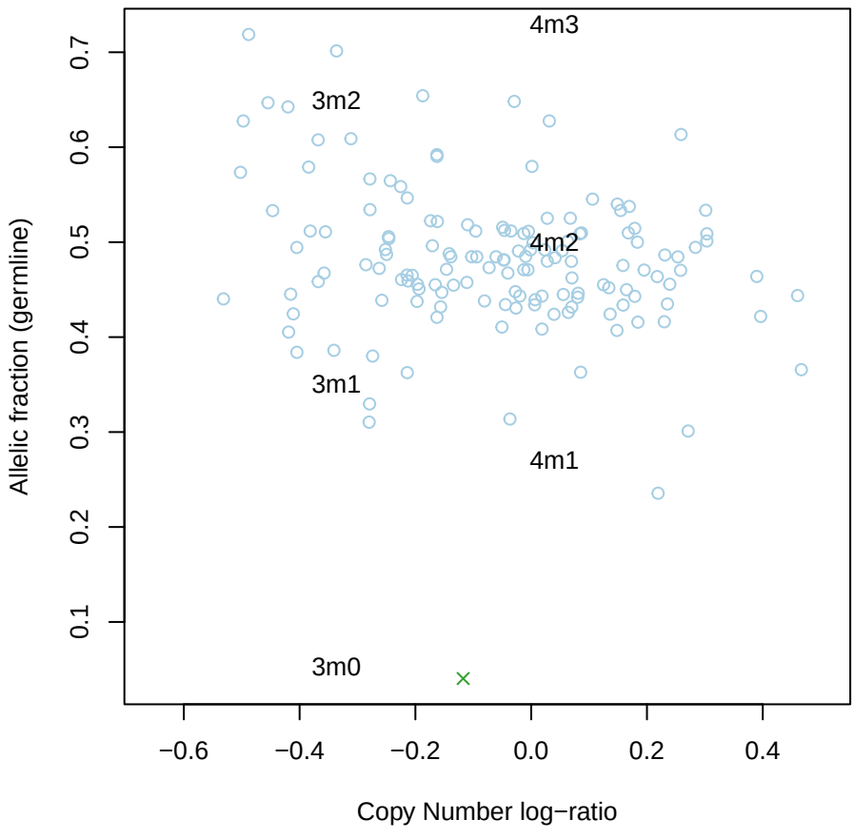

Frequency
Cellular fraction

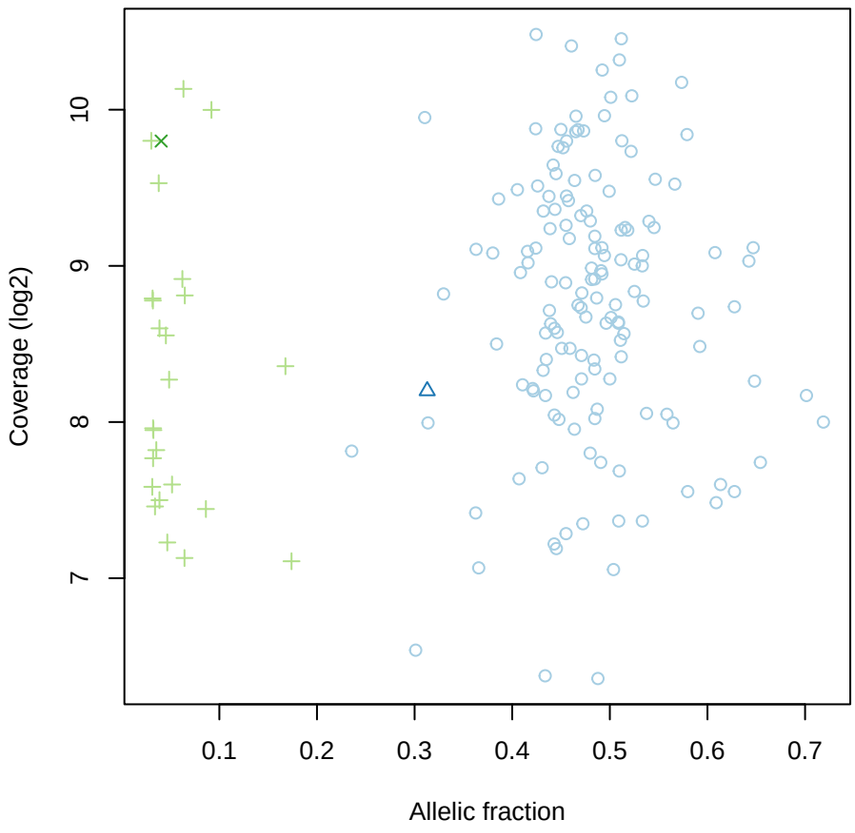

Purity: 0.85 Tumor ploidy: 3.88
2
3
4
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

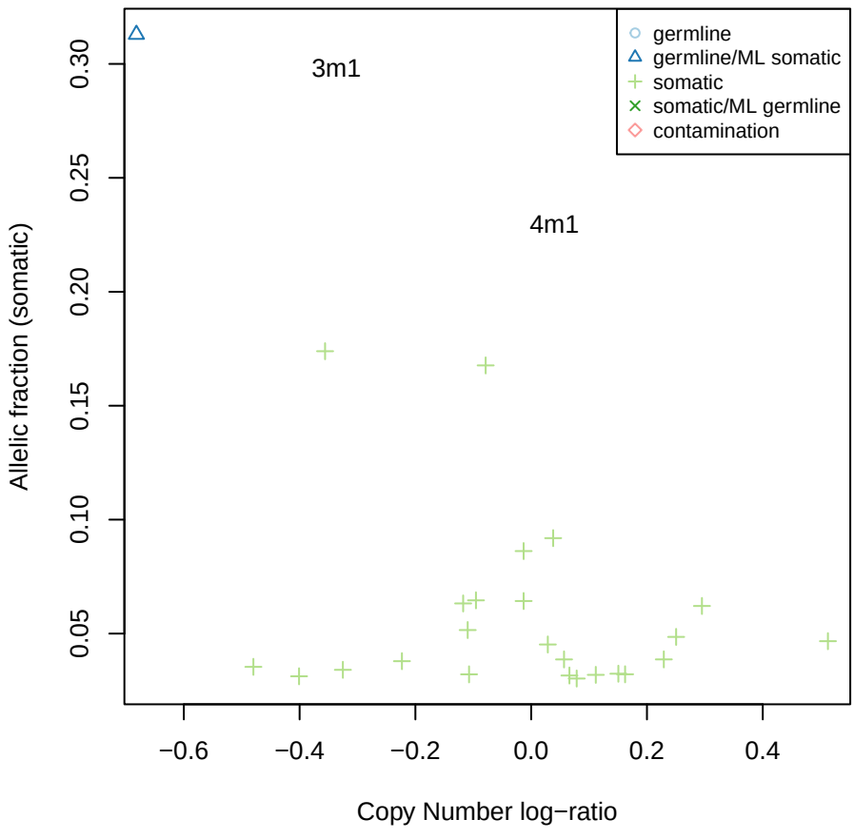

Purity: 0.85 Tumor ploidy: 3.88 SNV log−likelihood: −139.11 GoF: 81.5% Mean coverage: 496;596
1
2
3
4
5
6
7
8
9
10
11
12
13
15
17
19
20
B−Allele Frequency
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0
50
100
150
SNV Index

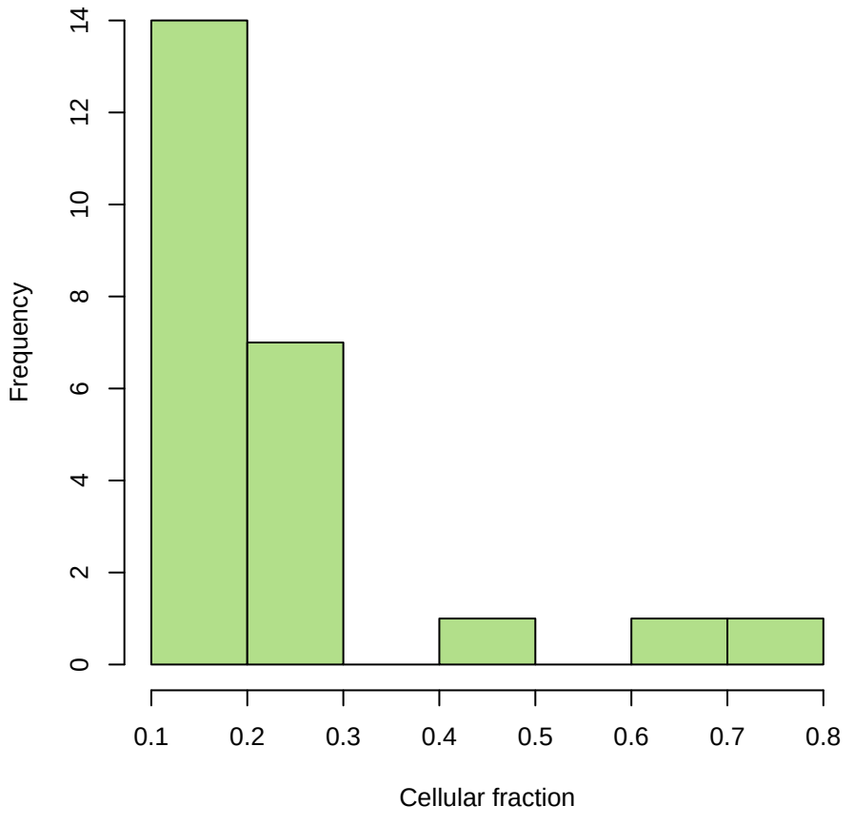

SCNA−fit log−likelihood: −926.22
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
2
3
4
5
6
0
50
100
150
SNV Index

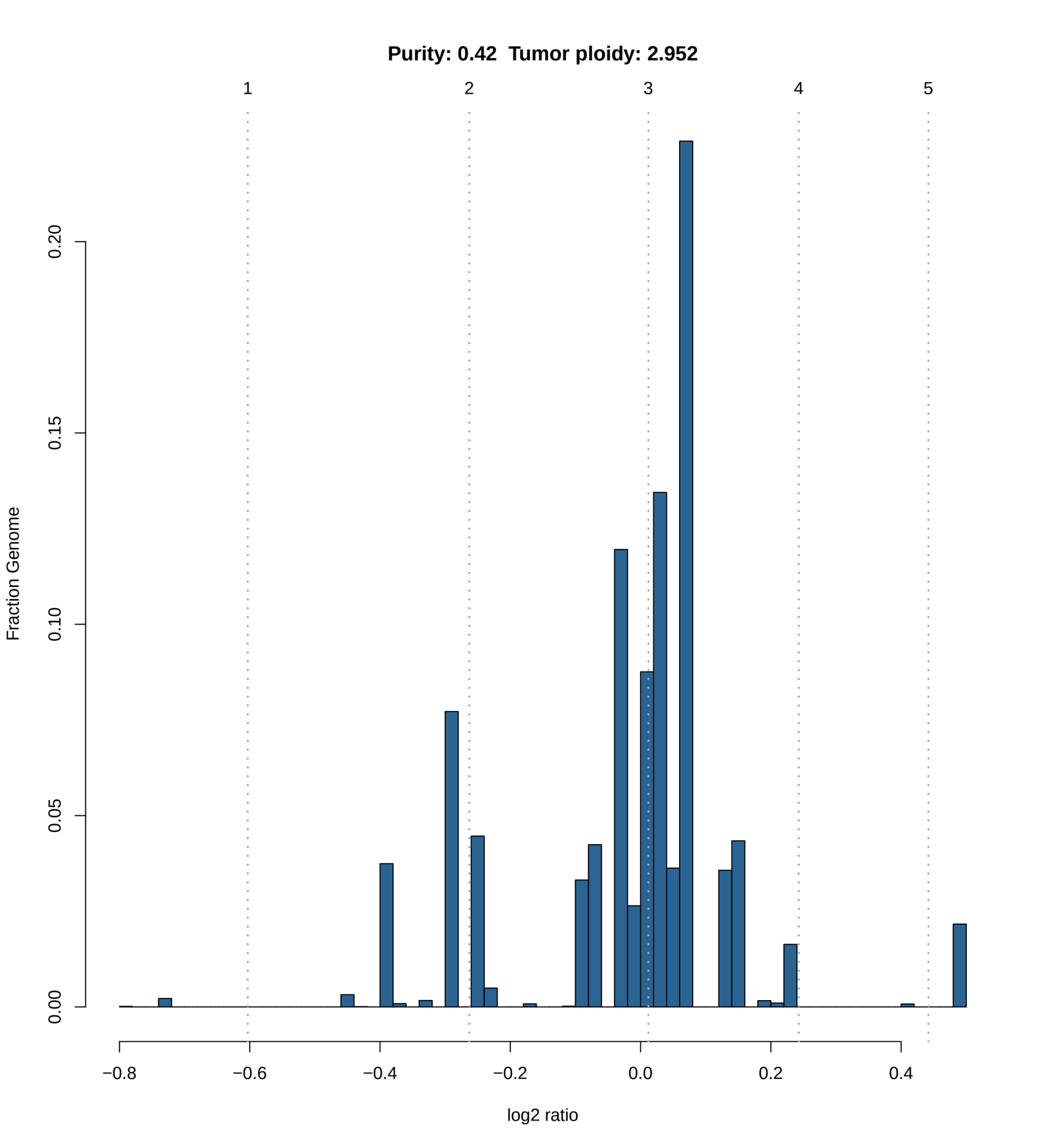

Maximum Likelihood Copy Number
0
1
2
3
4
0
50
100
150
SNV Index

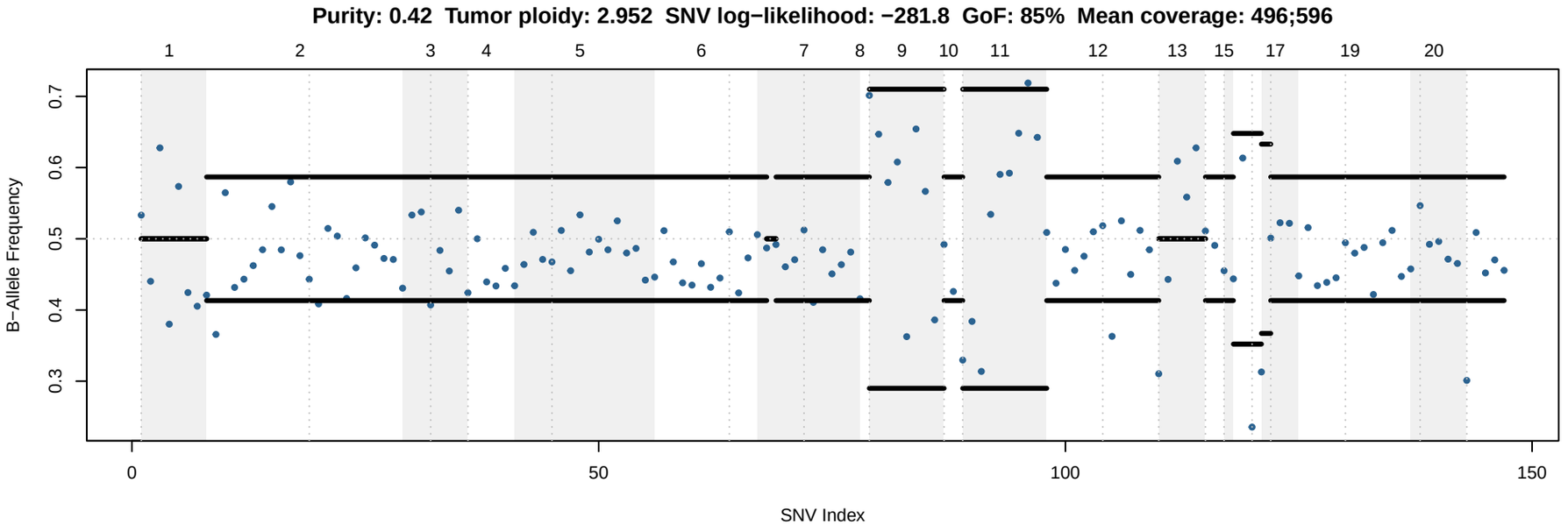

4m3
3m2
4m2
3m1
4m1
3m0
Allelic fraction (germline)
Copy Number log−ratio
0.1
0.2
0.3
0.4
0.5
0.6
0.7
−0.6
−0.4
−0.2
0.0
0.2
0.4

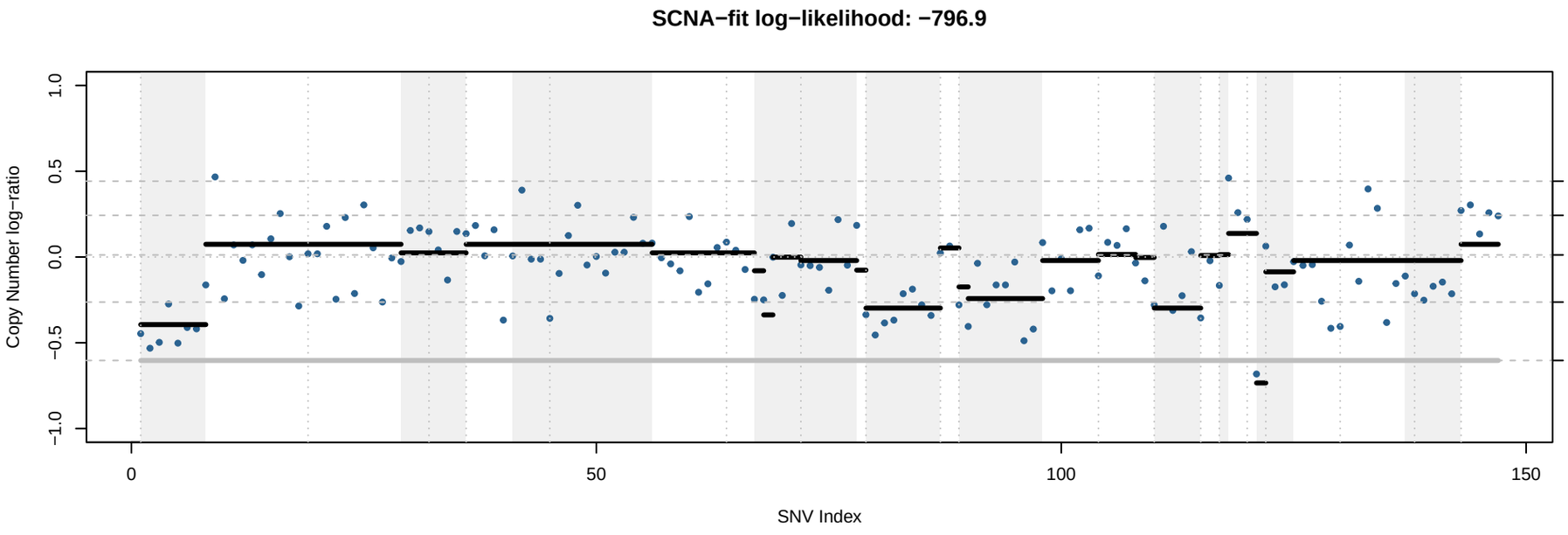

Coverage (log2)
Allelic fraction
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7

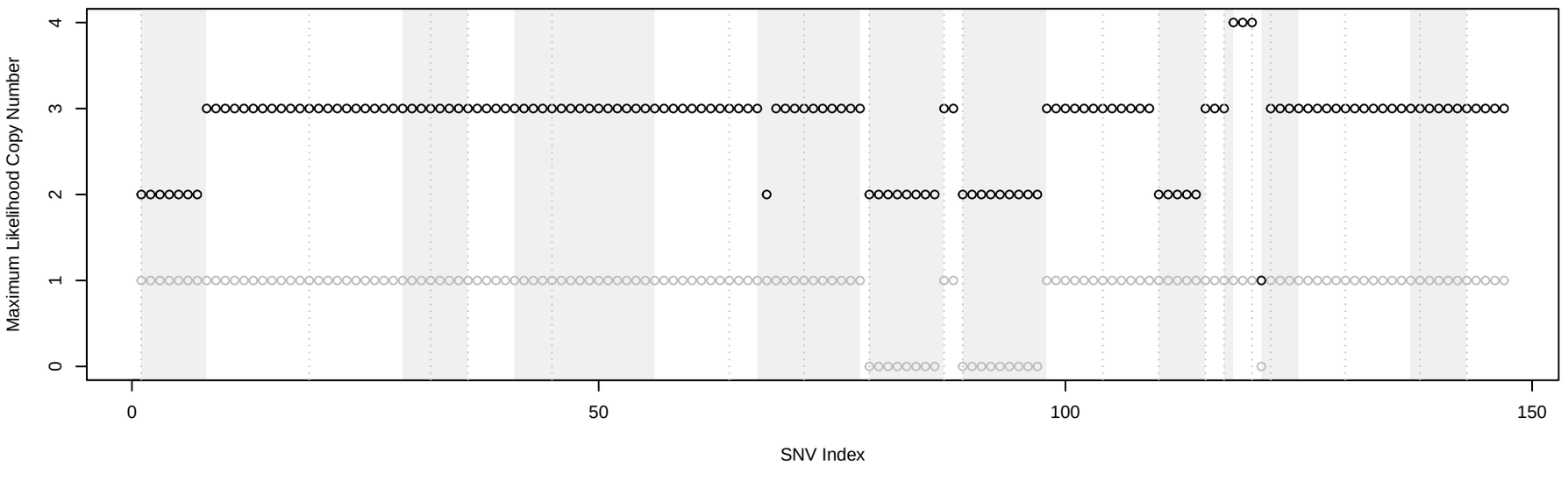

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
0.25
0.30
−0.6
−0.4
−0.2
0.0
0.2
0.4

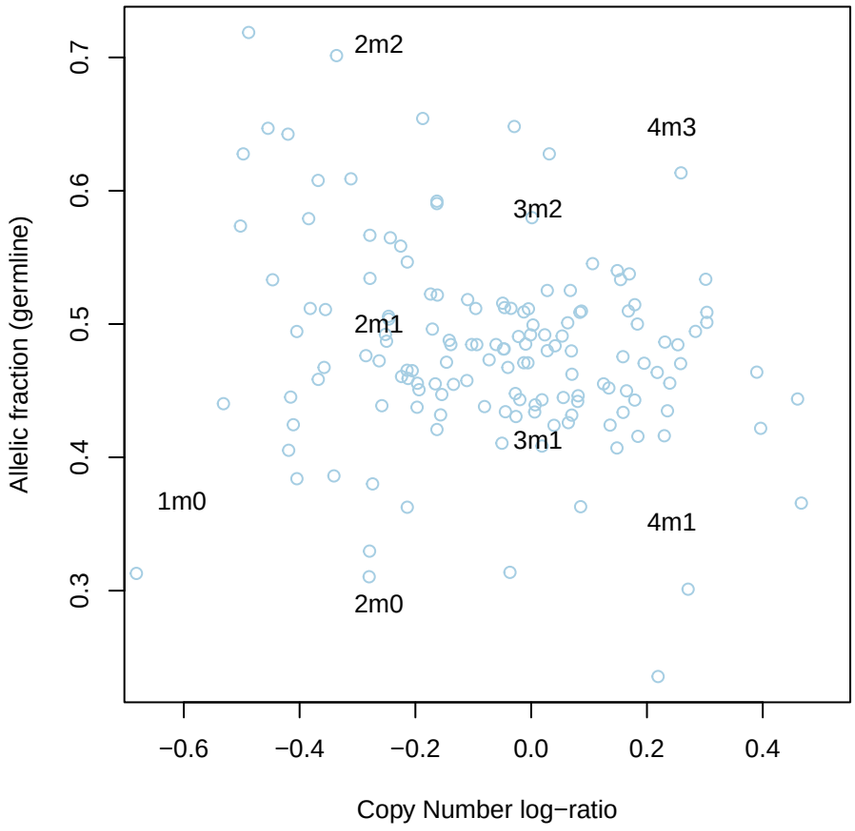

Frequency
Cellular fraction
0
2
4
6
8
10
12
14
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8

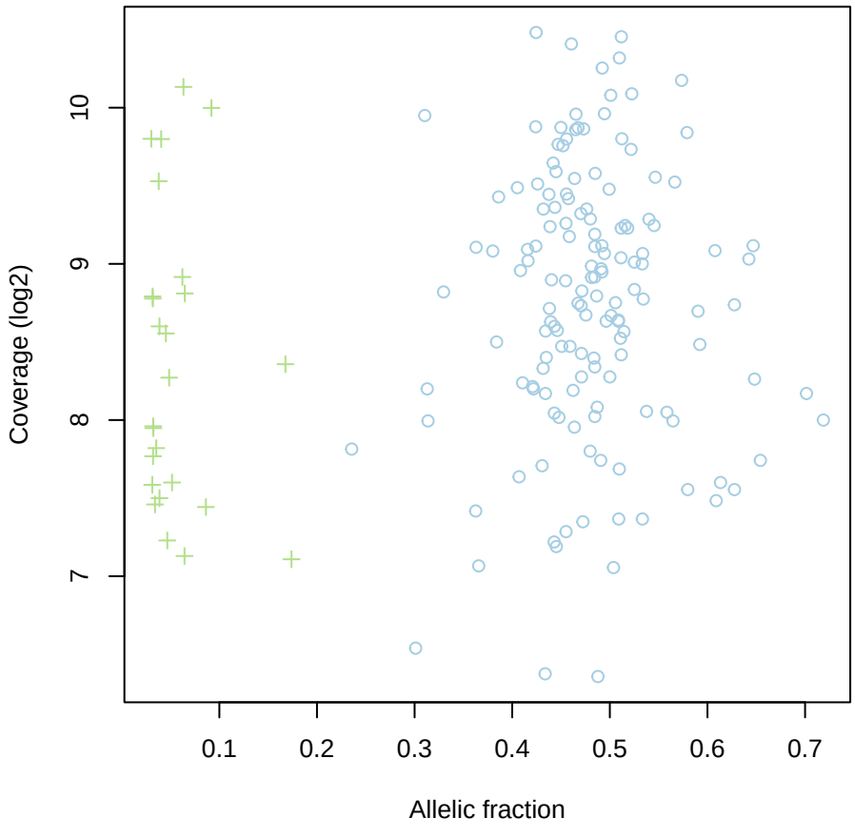

Purity: 0.42 Tumor ploidy: 2.952
1
2
3
4
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

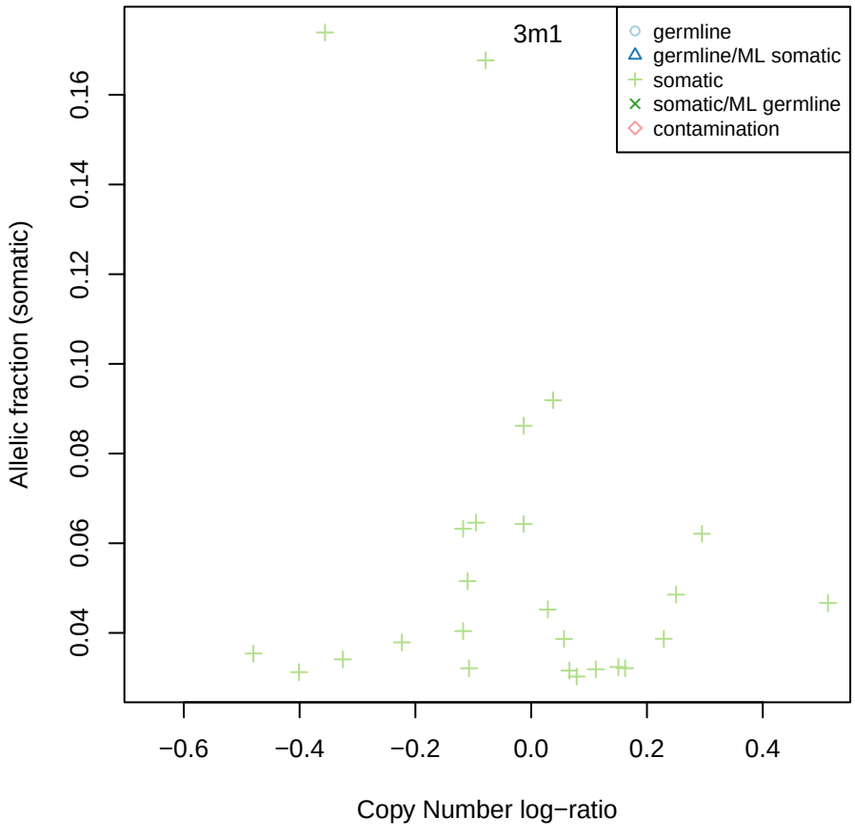

Purity: 0.42 Tumor ploidy: 2.952 SNV log−likelihood: −281.8 GoF: 85% Mean coverage: 496;596
1
2
3
4
5
6
7
8
9
10
11
12
13
15
17
19
20
B−Allele Frequency
0.3
0.4
0.5
0.6
0.7
0
50
100
150
SNV Index

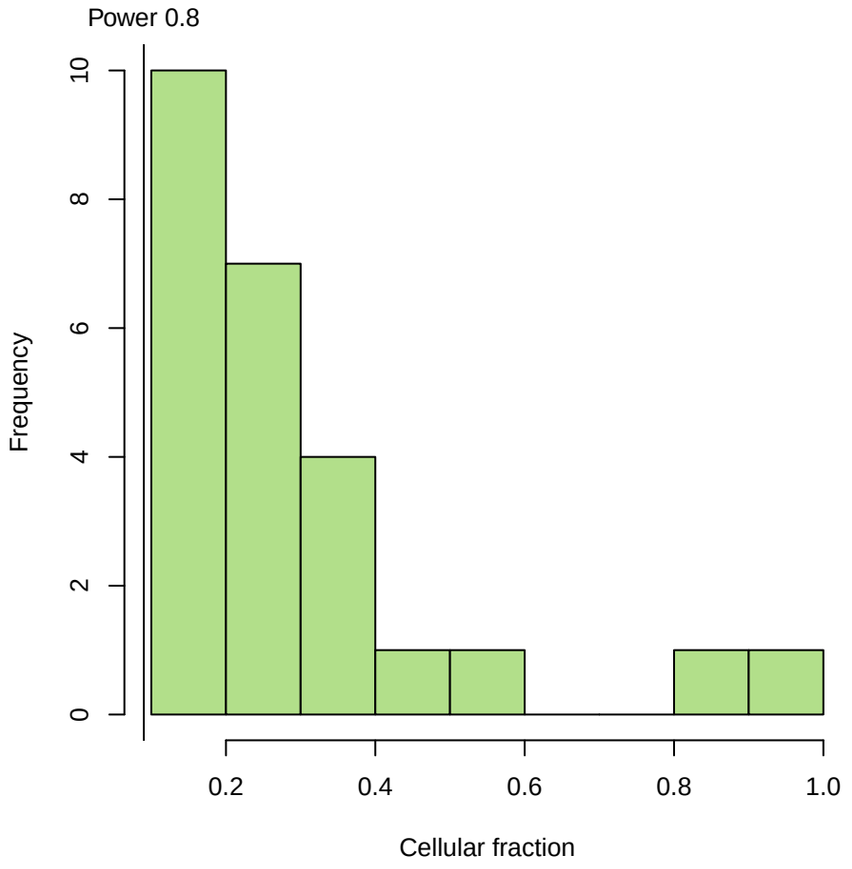

SCNA−fit log−likelihood: −796.9
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1
2
3
4
5
0
50
100
150
SNV Index

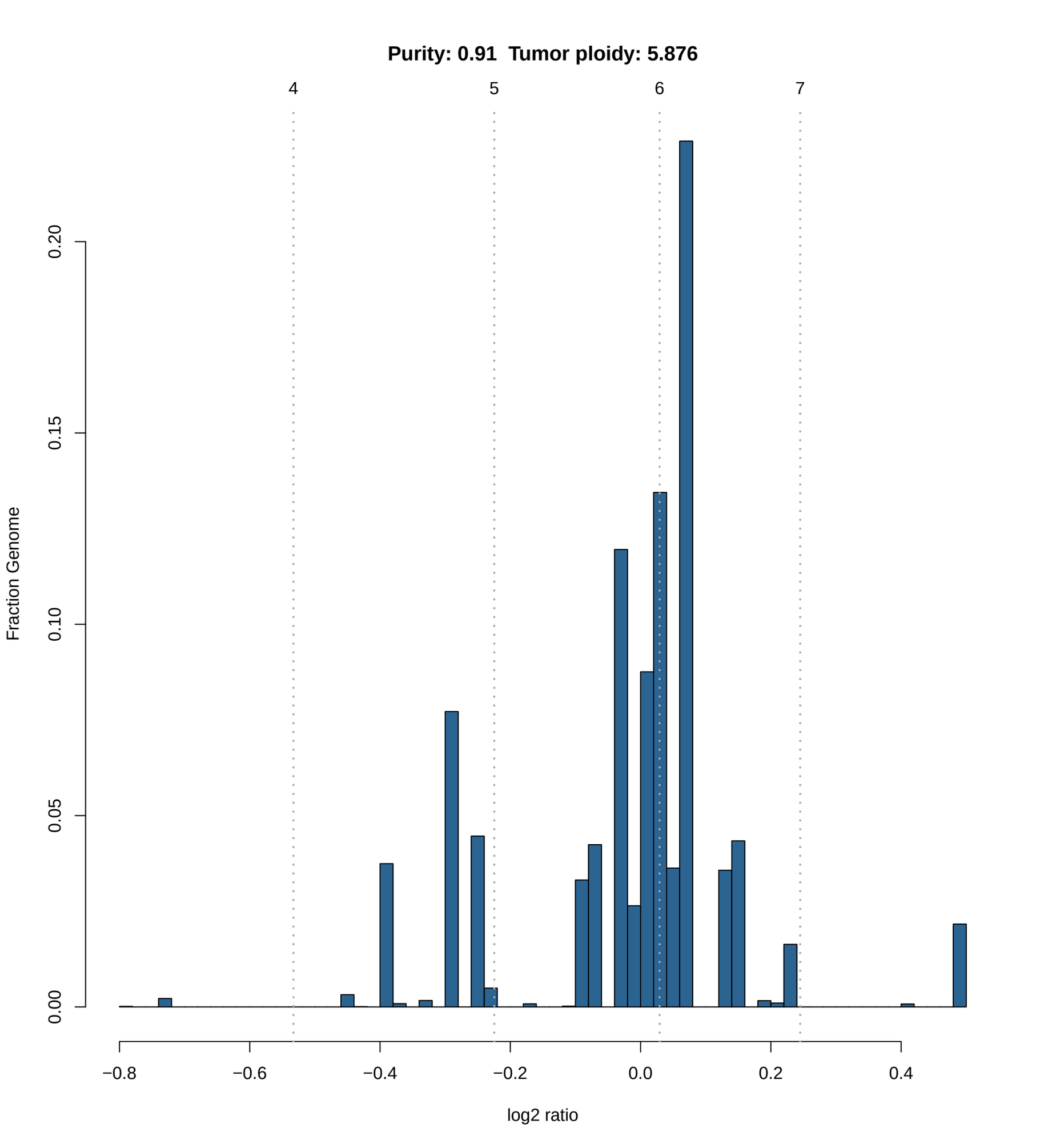

Maximum Likelihood Copy Number
0
1
2
3
4
0
50
100
150
SNV Index

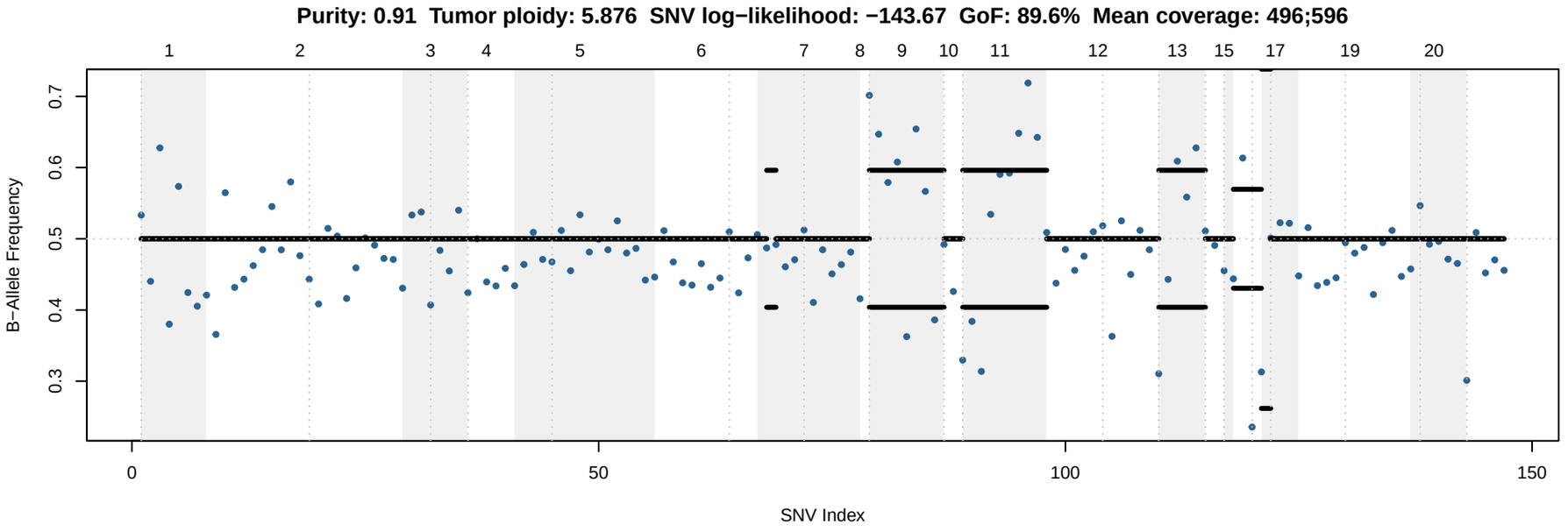

2m2
4m3
3m2
2m1
3m1
1m0
4m1
2m0
Allelic fraction (germline)
Copy Number log−ratio

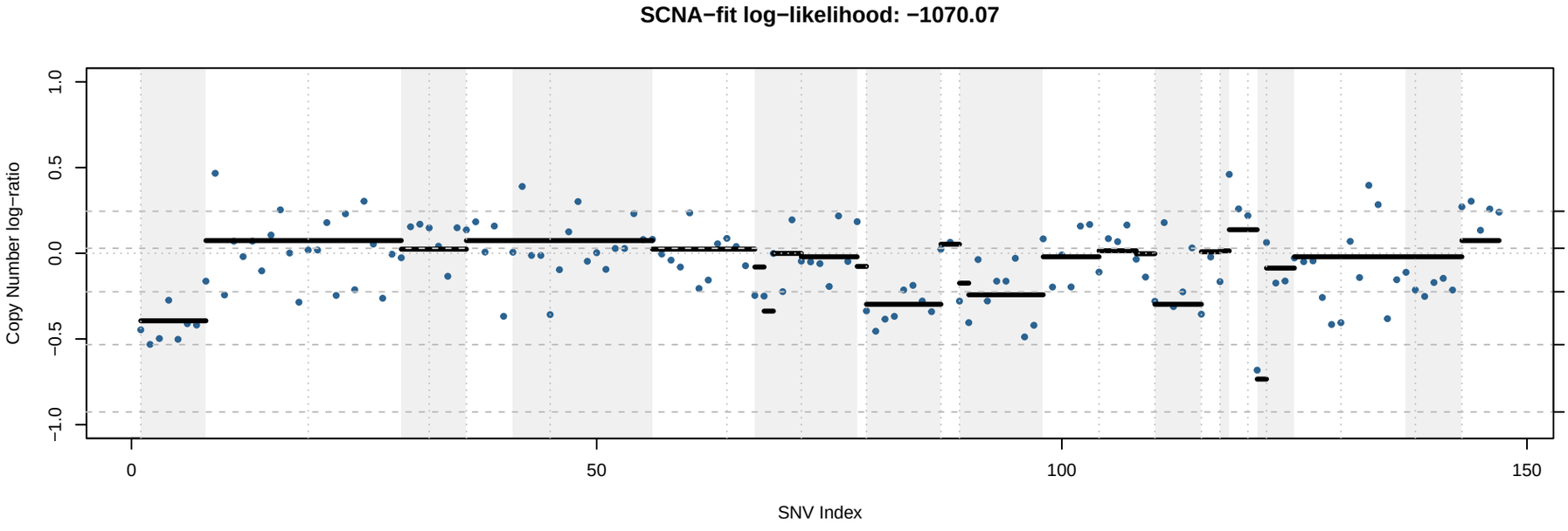

Coverage (log2)
Allelic fraction

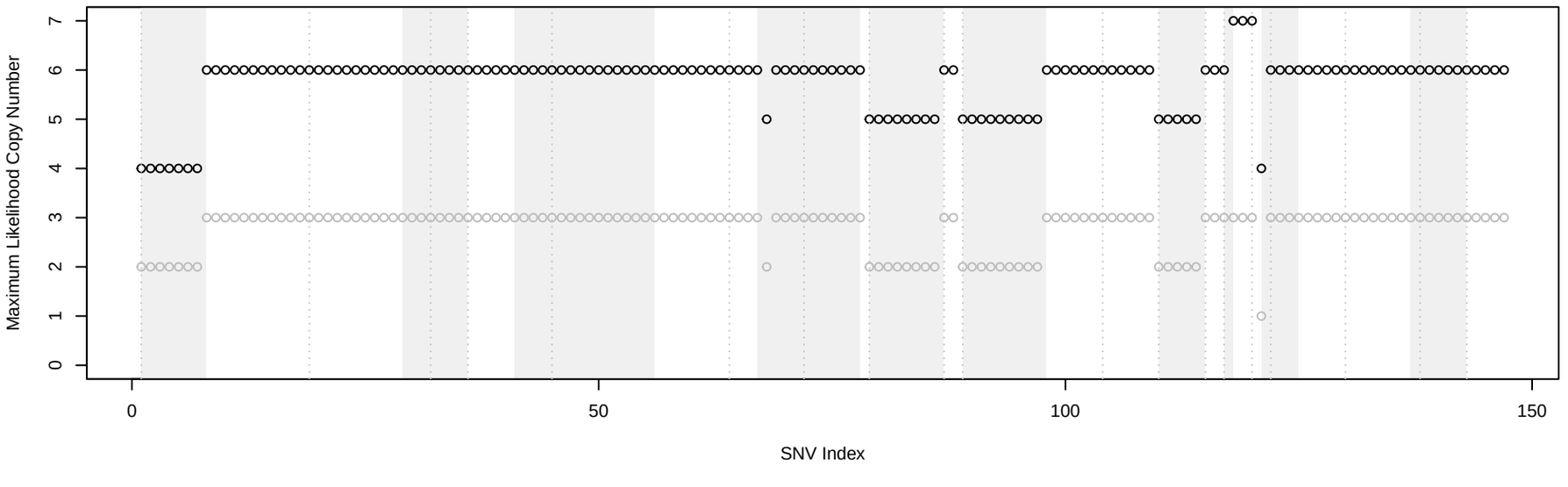

3m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

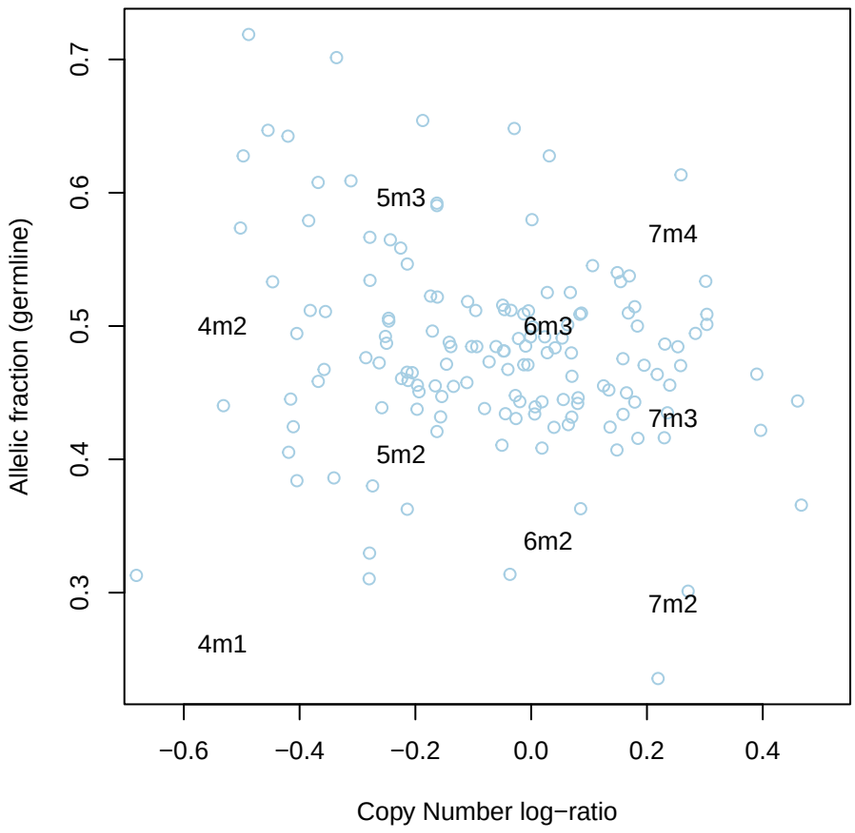

Power 0.8
Frequency
Cellular fraction

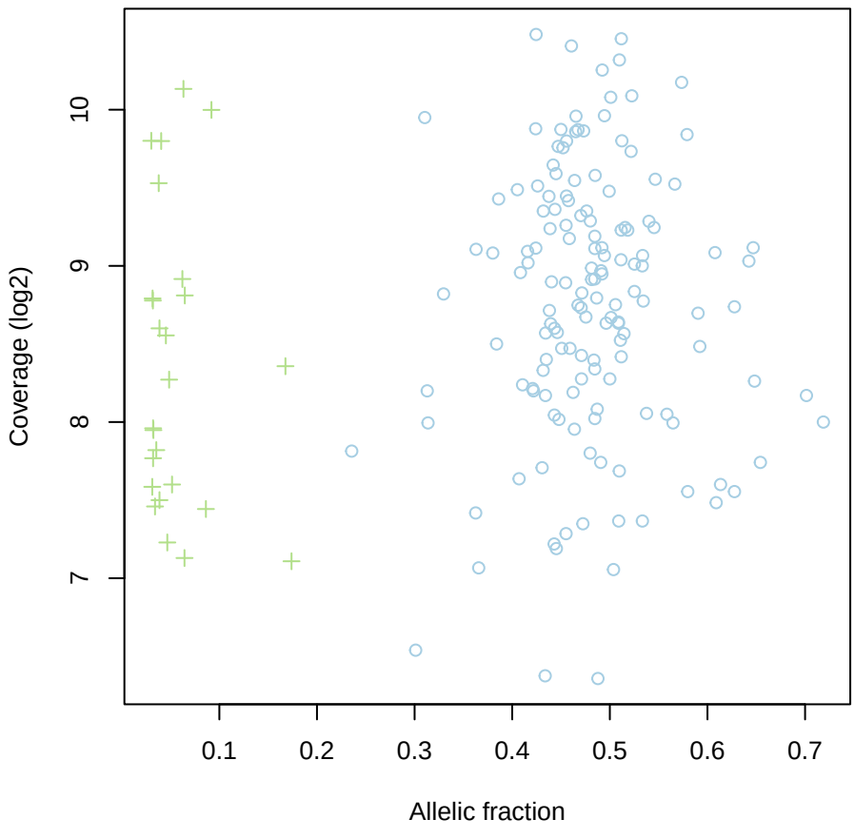

Purity: 0.91 Tumor ploidy: 5.876
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

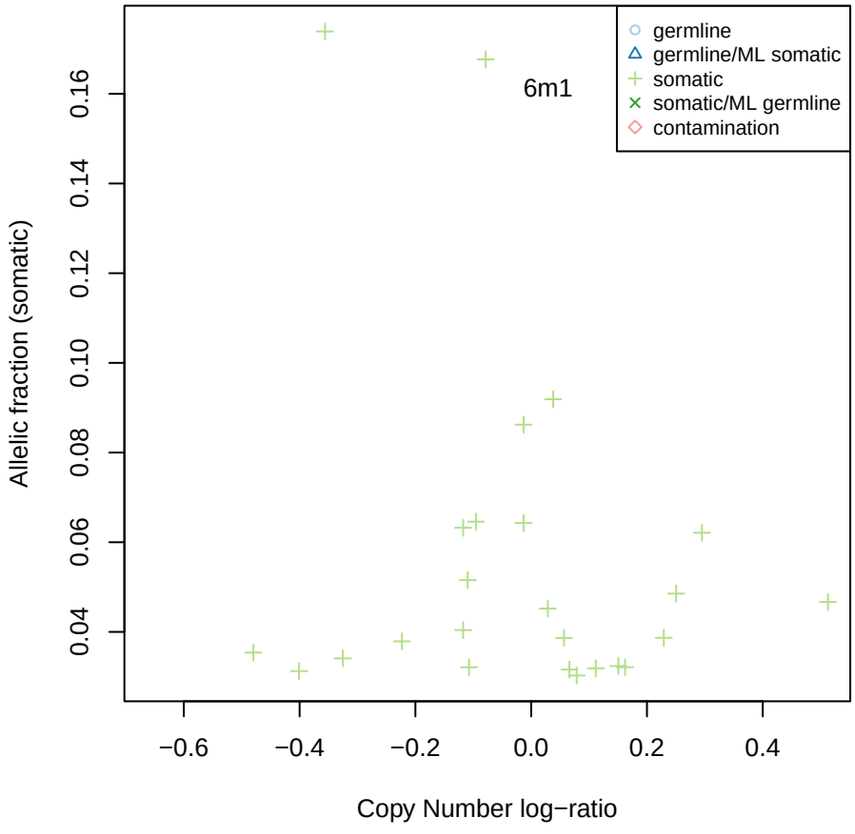

Purity: 0.91 Tumor ploidy: 5.876 SNV log−likelihood: −143.67 GoF: 89.6% Mean coverage: 496;596
1 2 3 4 5 6 7 8 9 10 11 12 13 15 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

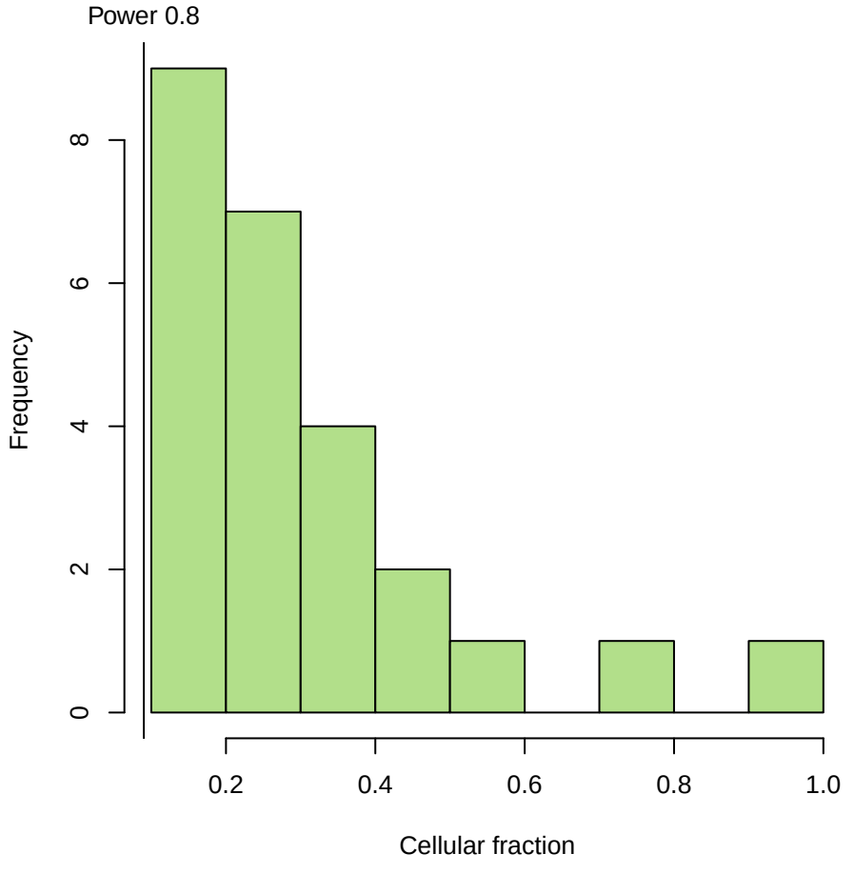

SCNA−fit log−likelihood: −1070.07
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 50 100 150
SNV Index

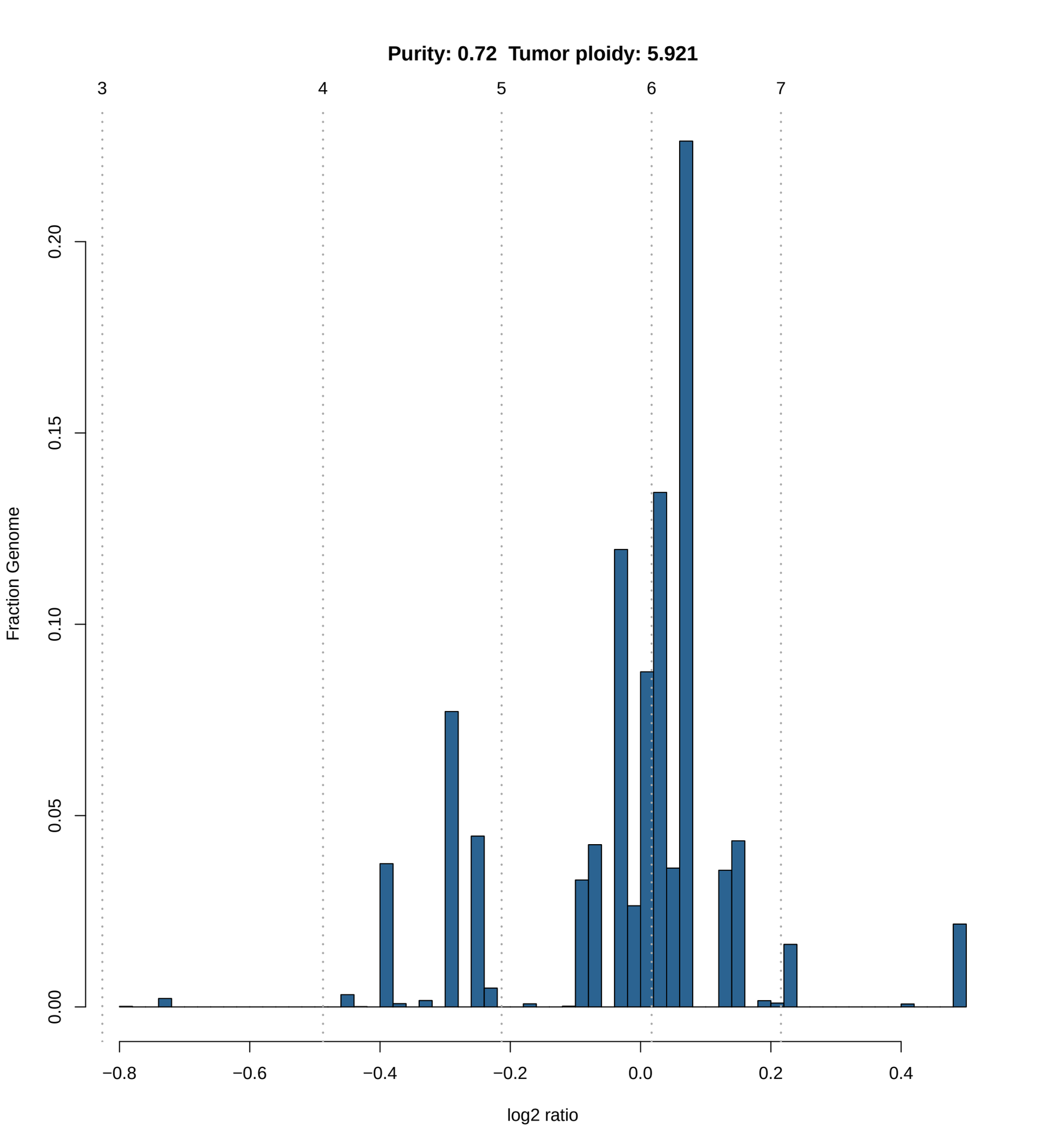

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

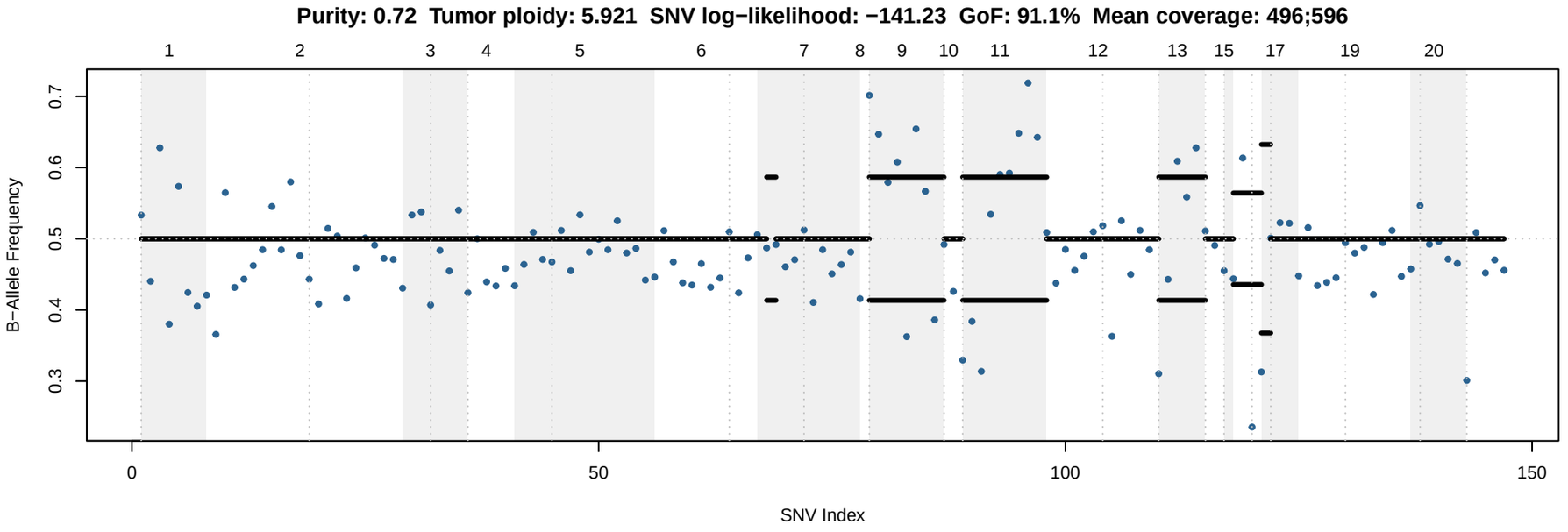

Allelic fraction (germline)
Copy Number log−ratio
5m3
7m4
4m2
6m3
7m3
5m2
6m2
7m2
4m1

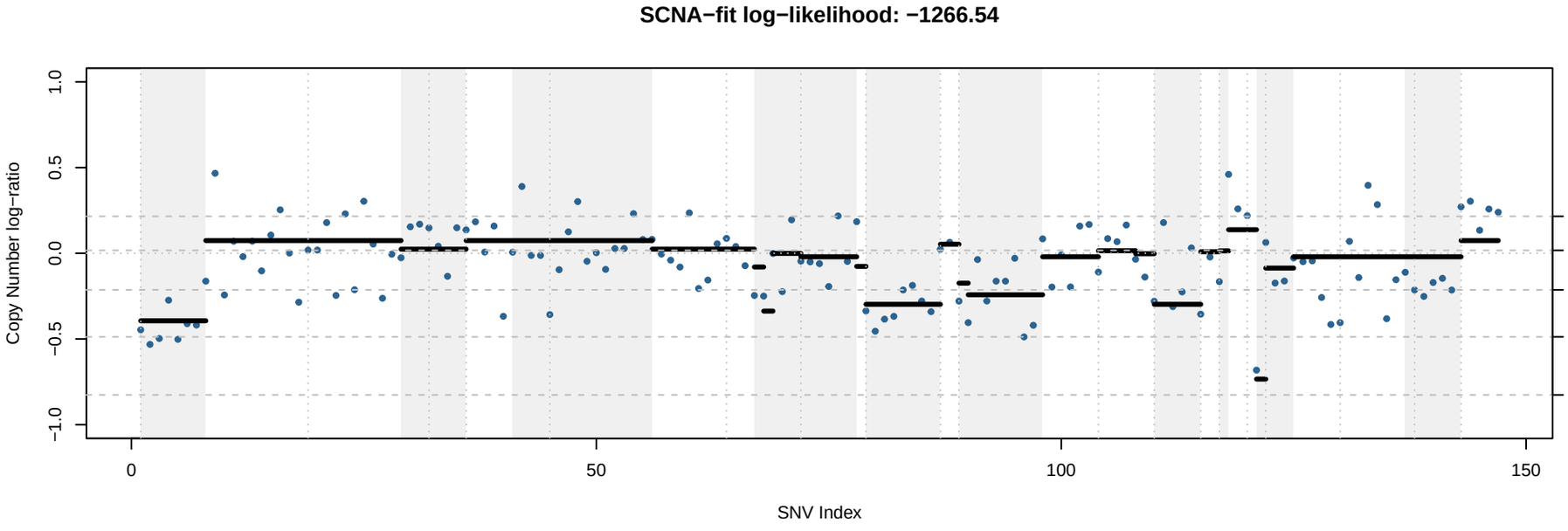

Coverage (log2)
Allelic fraction

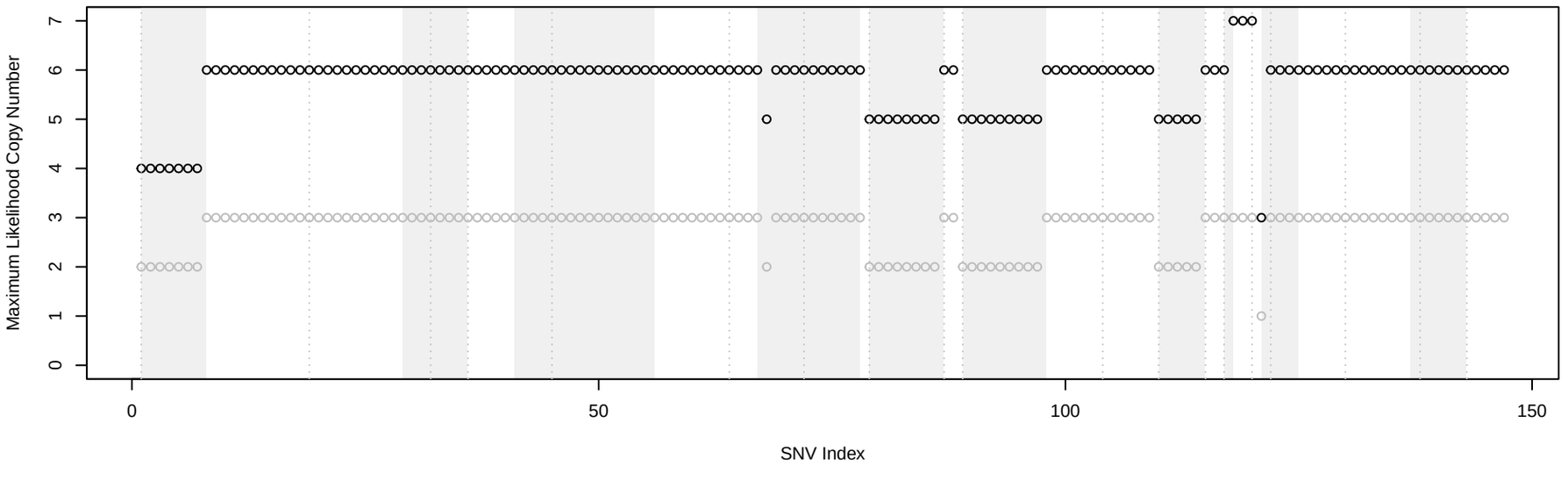

Allelic fraction (somatic)
Copy Number log−ratio
6m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

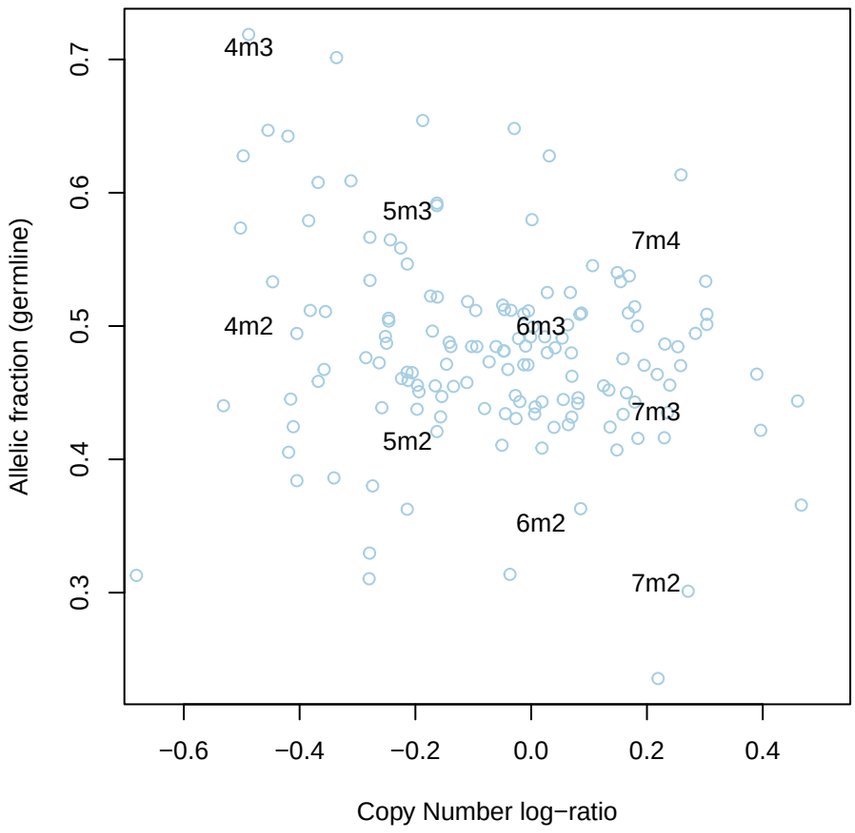

Power 0.8
Frequency
Cellular fraction

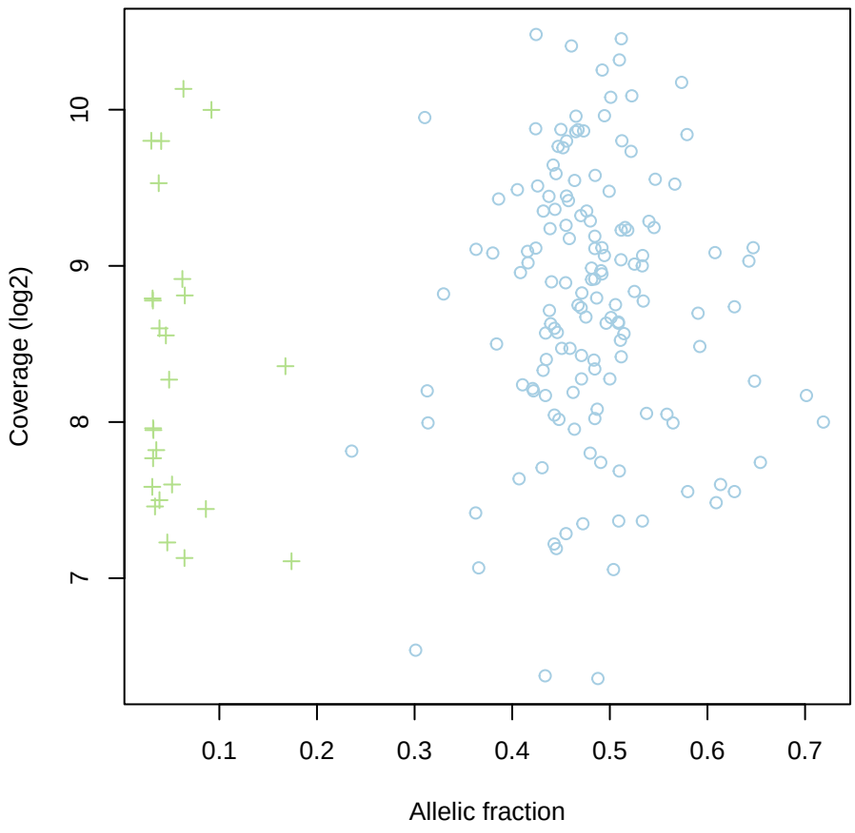

Purity: 0.72 Tumor ploidy: 5.921
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

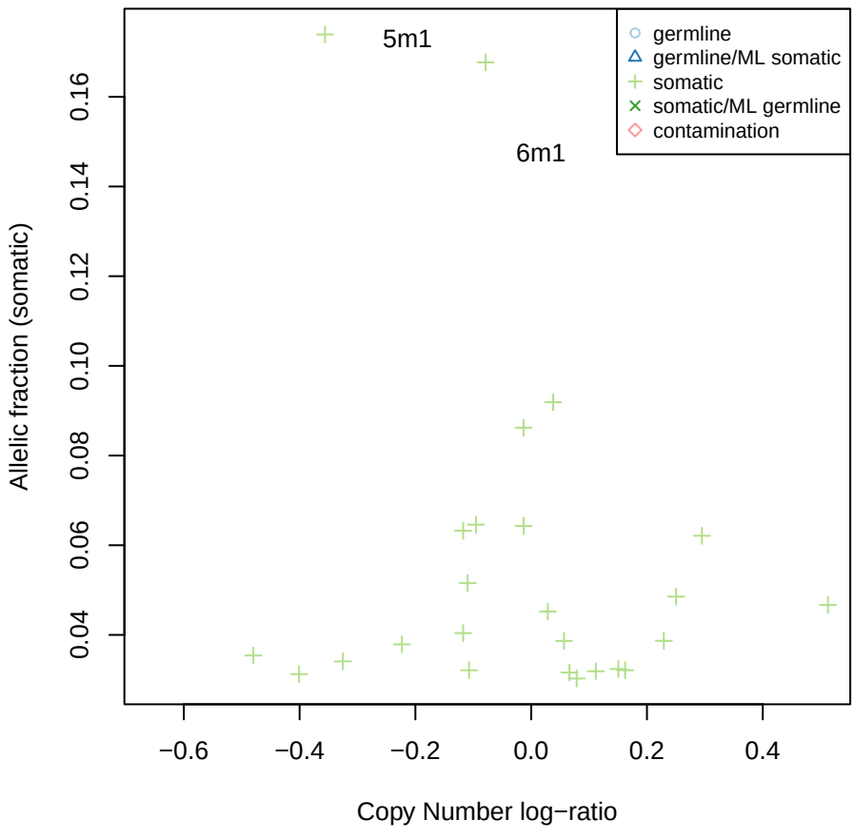

Purity: 0.72 Tumor ploidy: 5.921 SNV log−likelihood: −141.23 GoF: 91.1% Mean coverage: 496;596
1 2 3 4 5 6 7 8 9 10 11 12 13 15 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

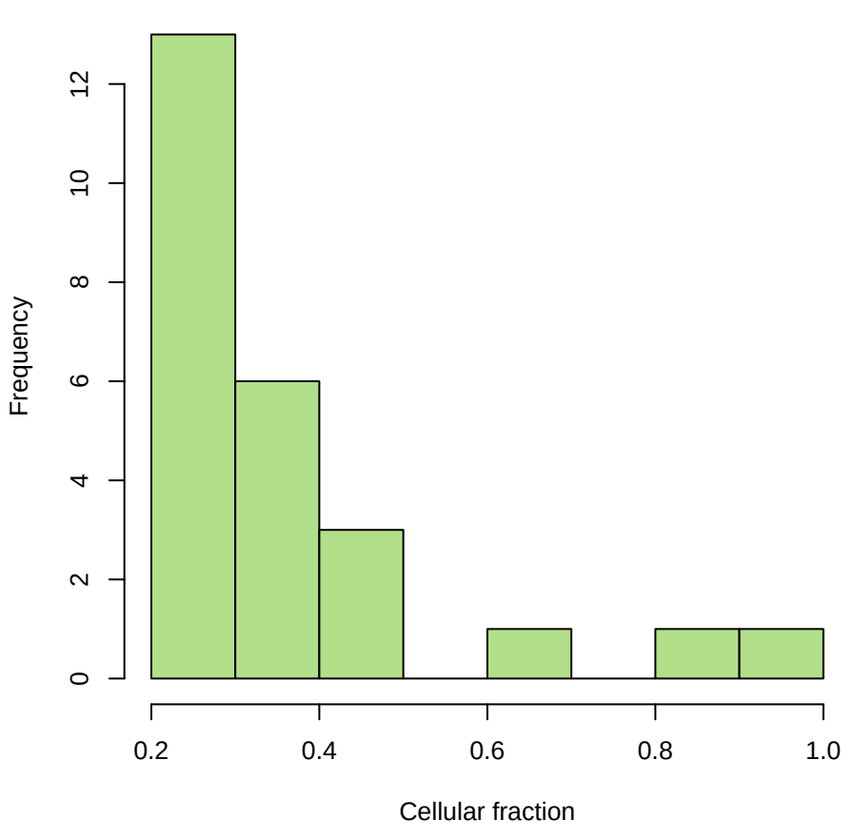

SCNA−fit log−likelihood: −1266.54
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 50 100 150
SNV Index

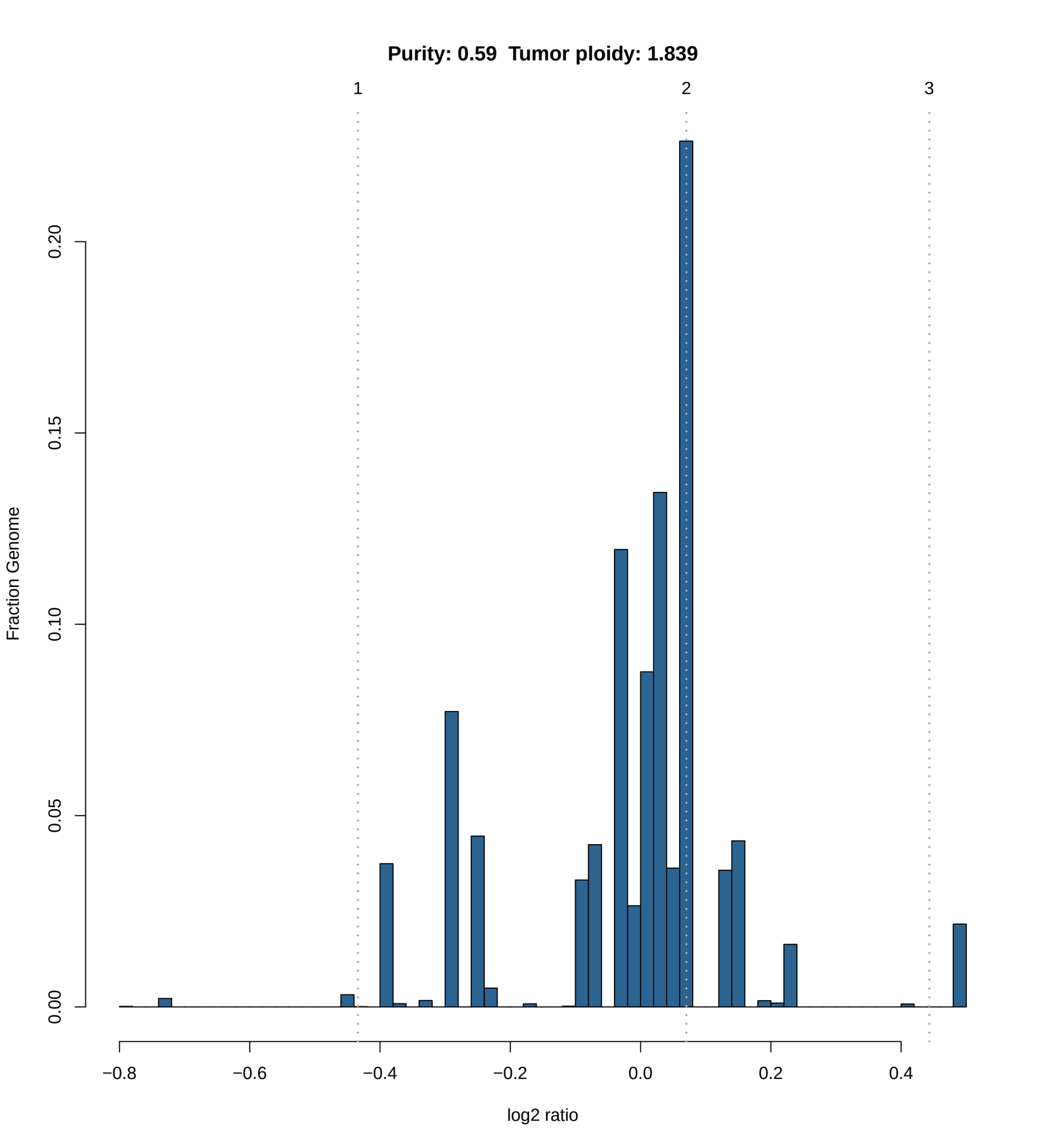

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

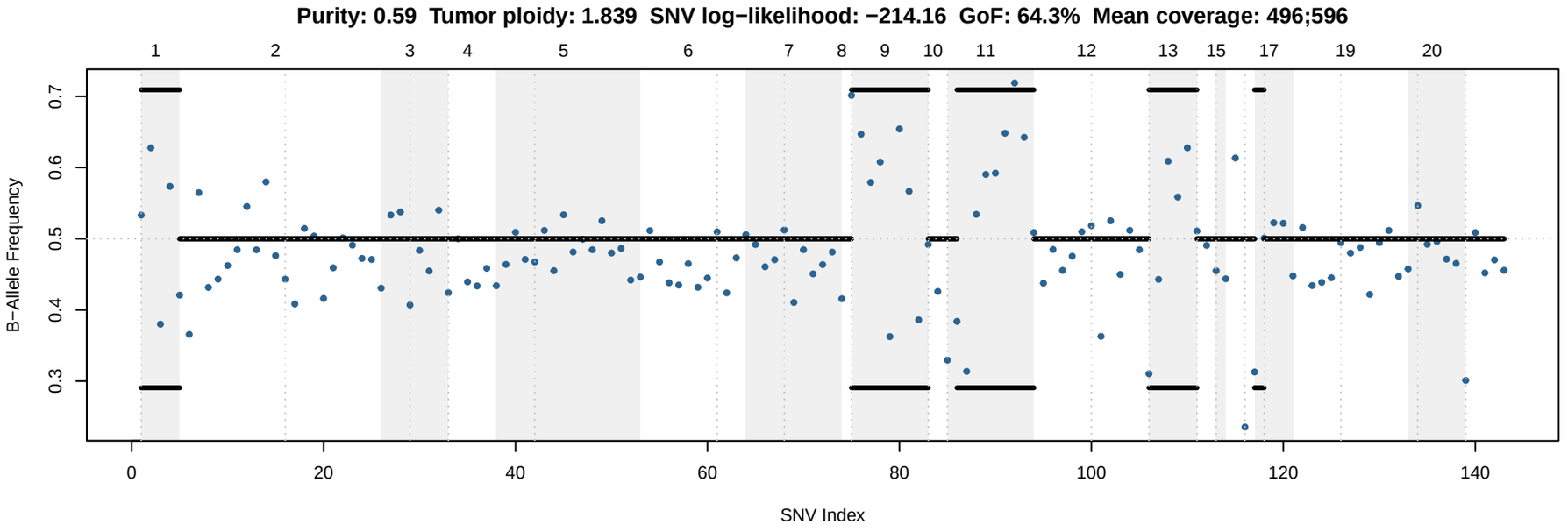

4m3
5m3
7m4
4m2
6m3
7m3
5m2
6m2
7m2
Allelic fraction (germline)
Copy Number log−ratio
0.3
0.4
0.5
0.6
0.7
−0.6
−0.4
−0.2
0.0
0.2
0.4

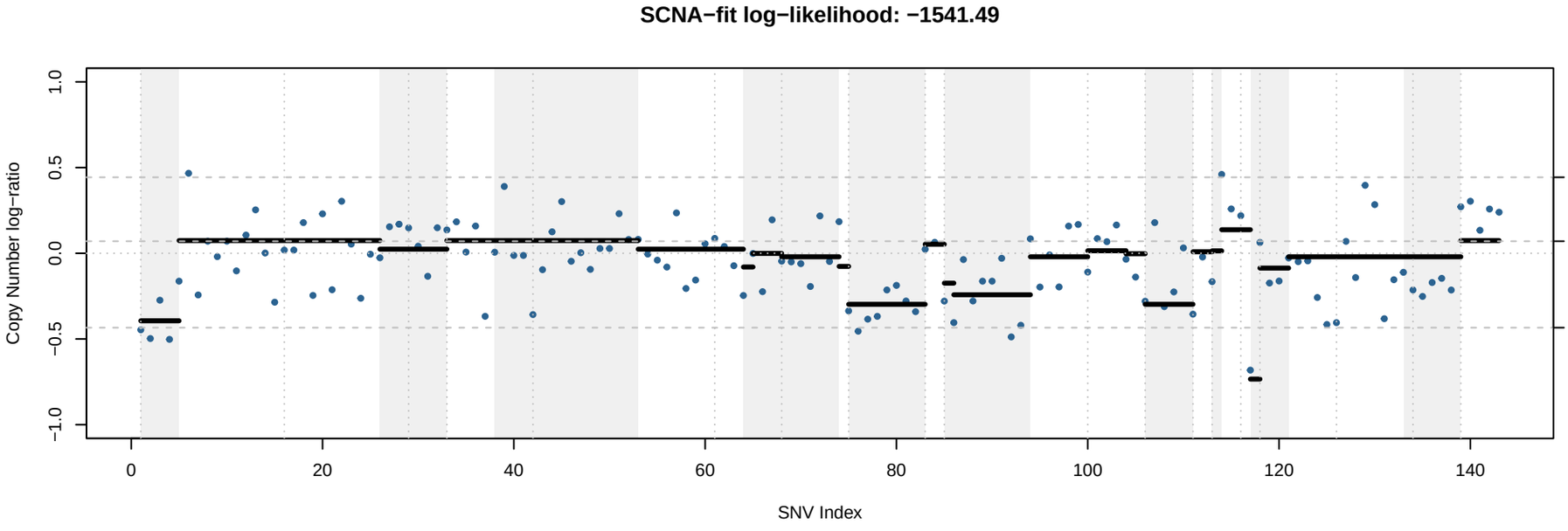

Coverage (log2)
Allelic fraction
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7

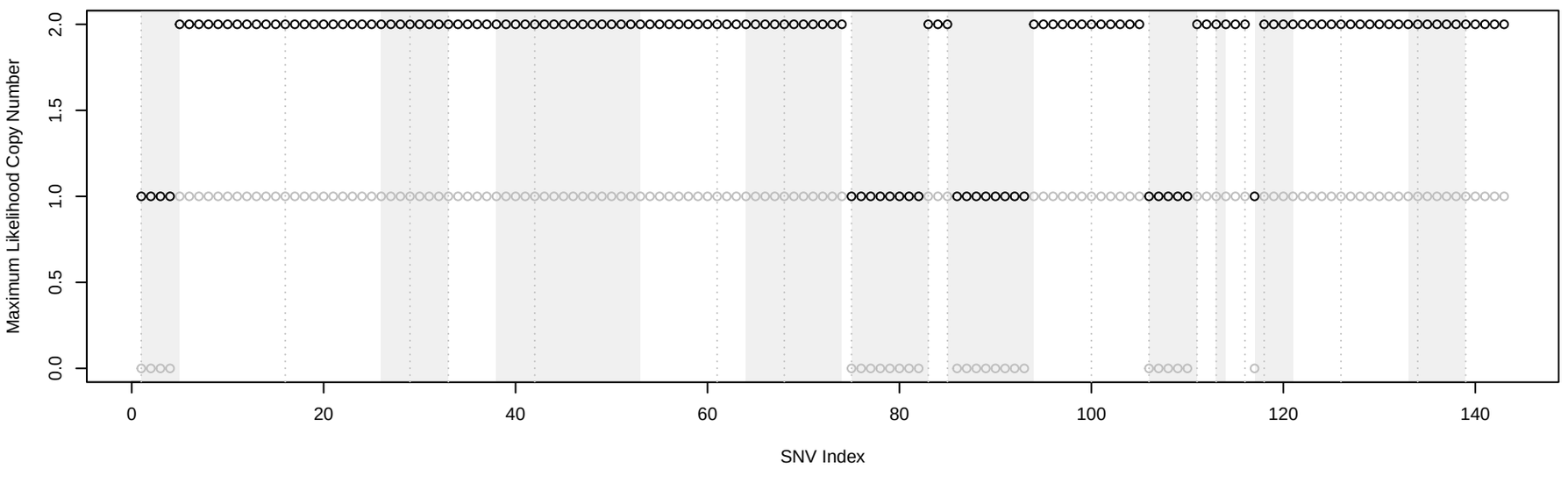

5m1
6m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
0.12
0.14
0.16
−0.6
−0.4
−0.2
0.0
0.2
0.4

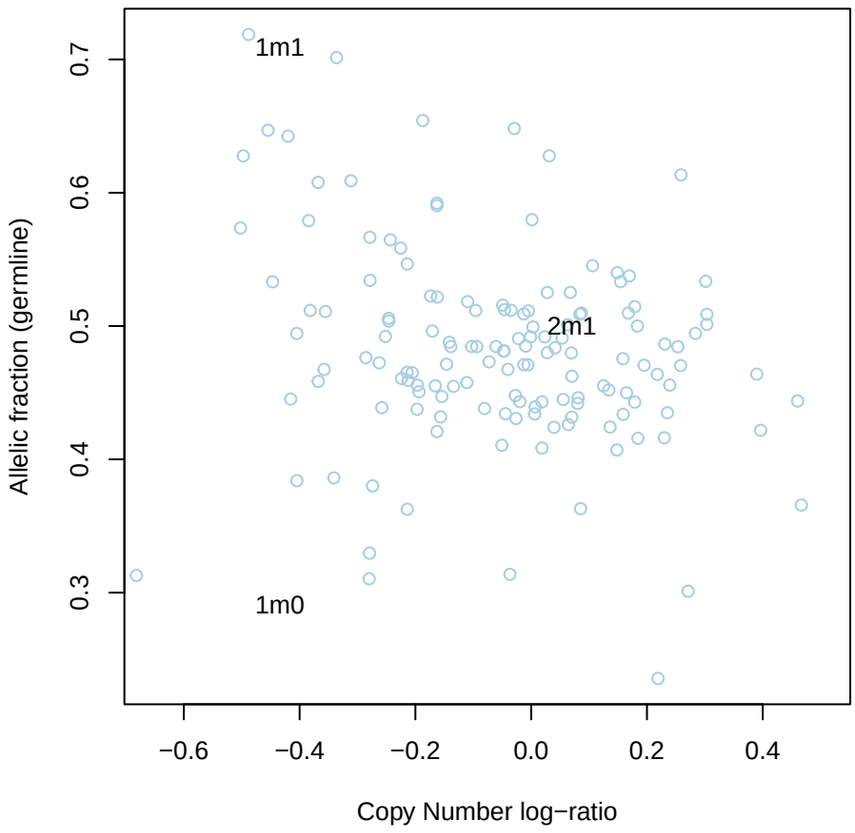

Frequency
Cellular fraction
0
2
4
6
8
10
12
0.2
0.4
0.6
0.8
1.0

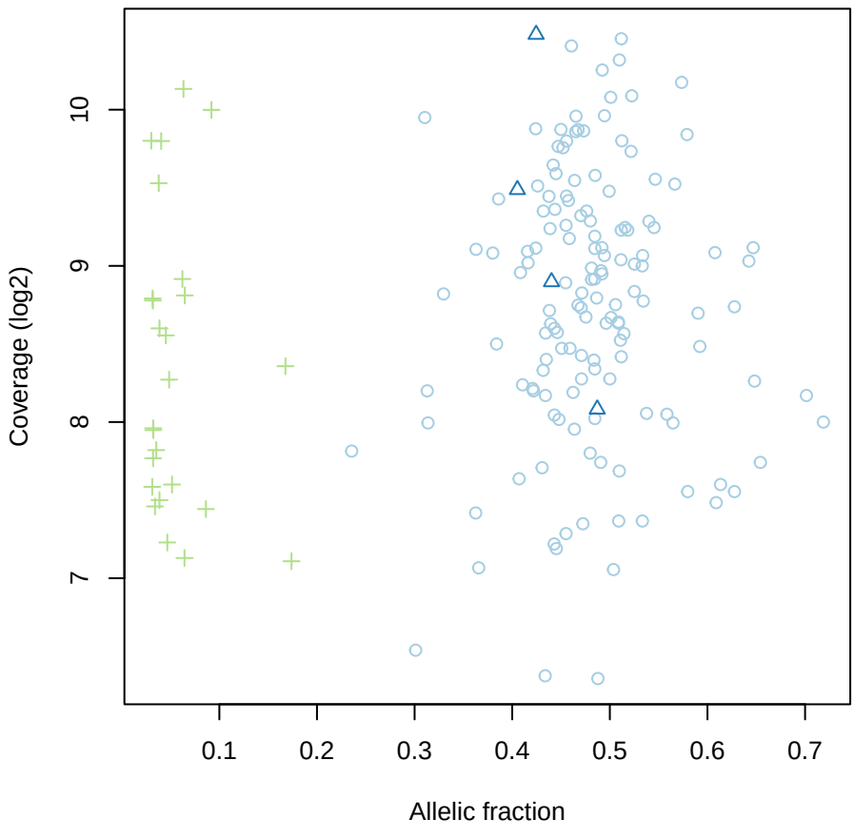

Purity: 0.59 Tumor ploidy: 1.839
1
2
3
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

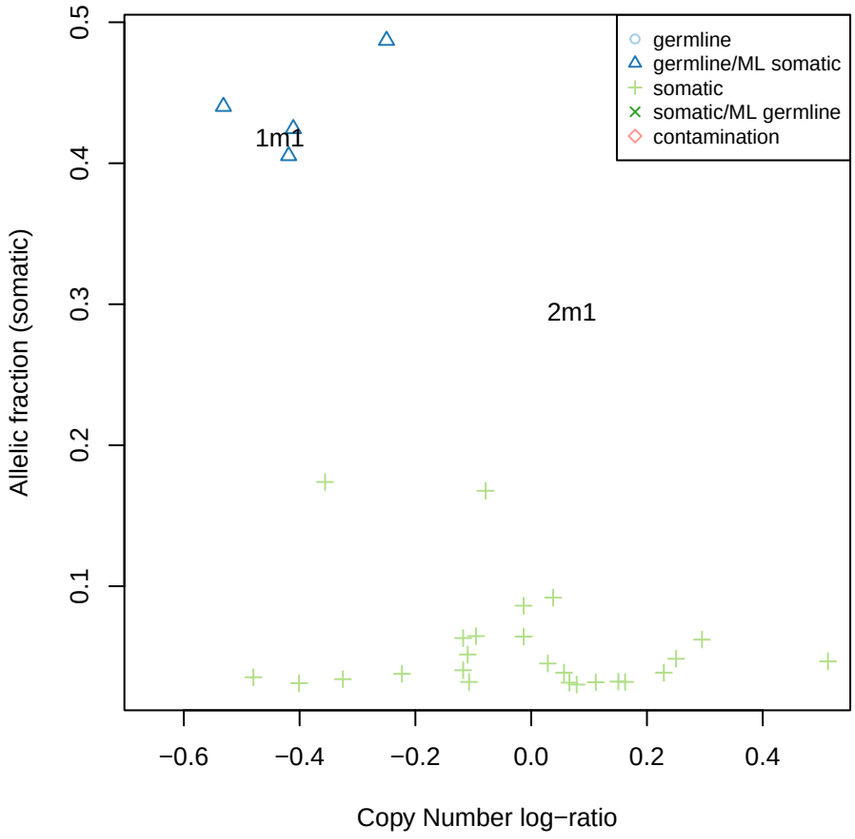

Purity: 0.59 Tumor ploidy: 1.839 SNV log−likelihood: −214.16 GoF: 64.3% Mean coverage: 496;596
1 2 3 4 5 6 7 8 9 10 11 12 13 15 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120 140
SNV Index

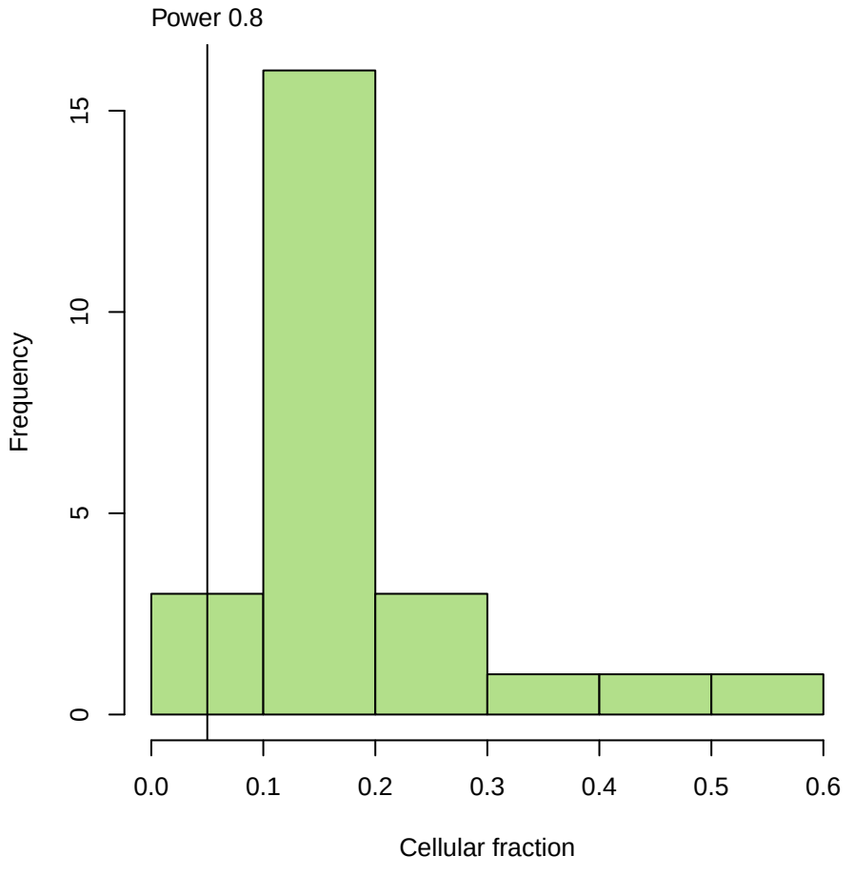

SCNA−fit log−likelihood: −1541.49
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3
0 20 40 60 80 100 120 140
SNV Index

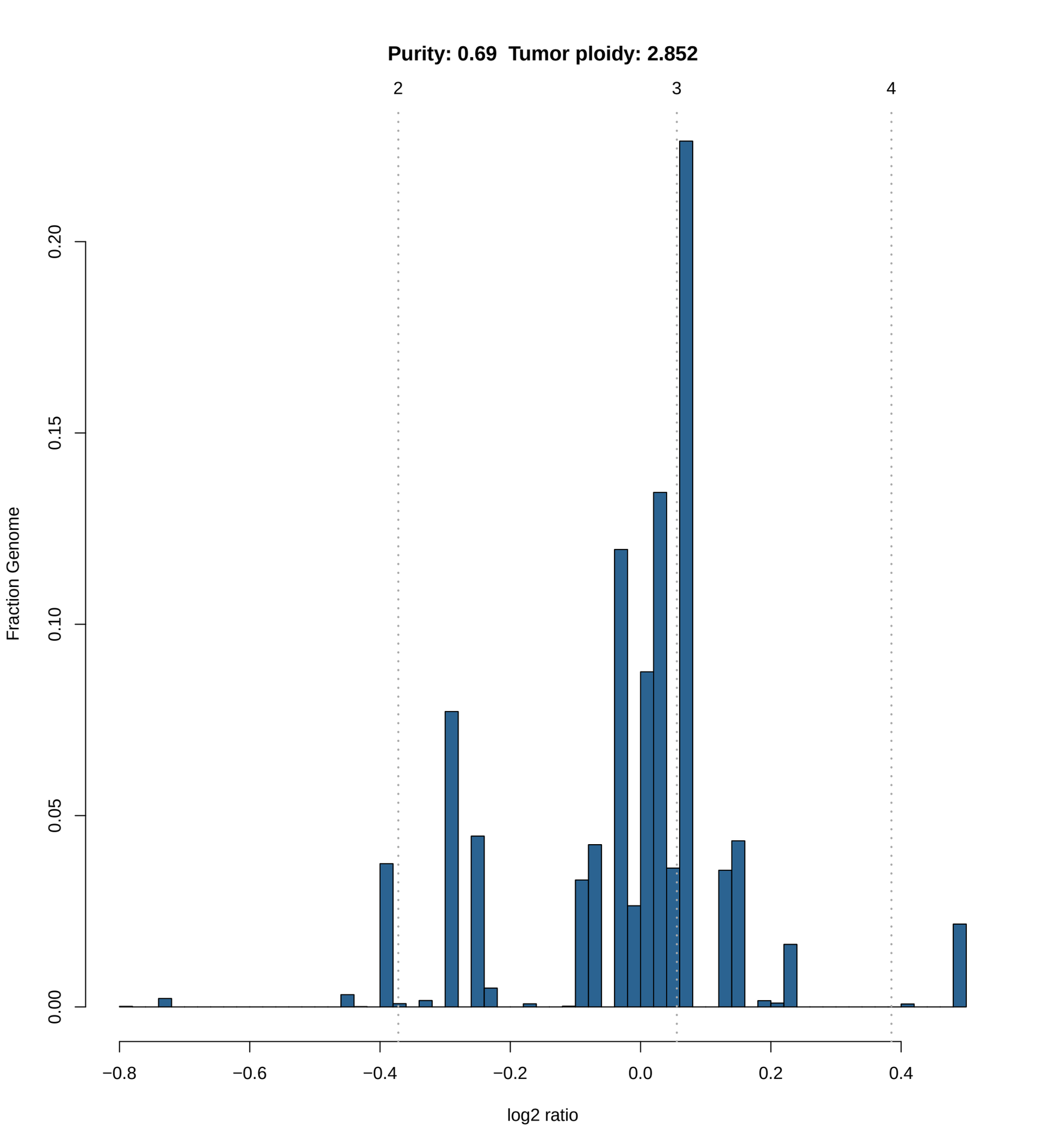

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 20 40 60 80 100 120 140
SNV Index

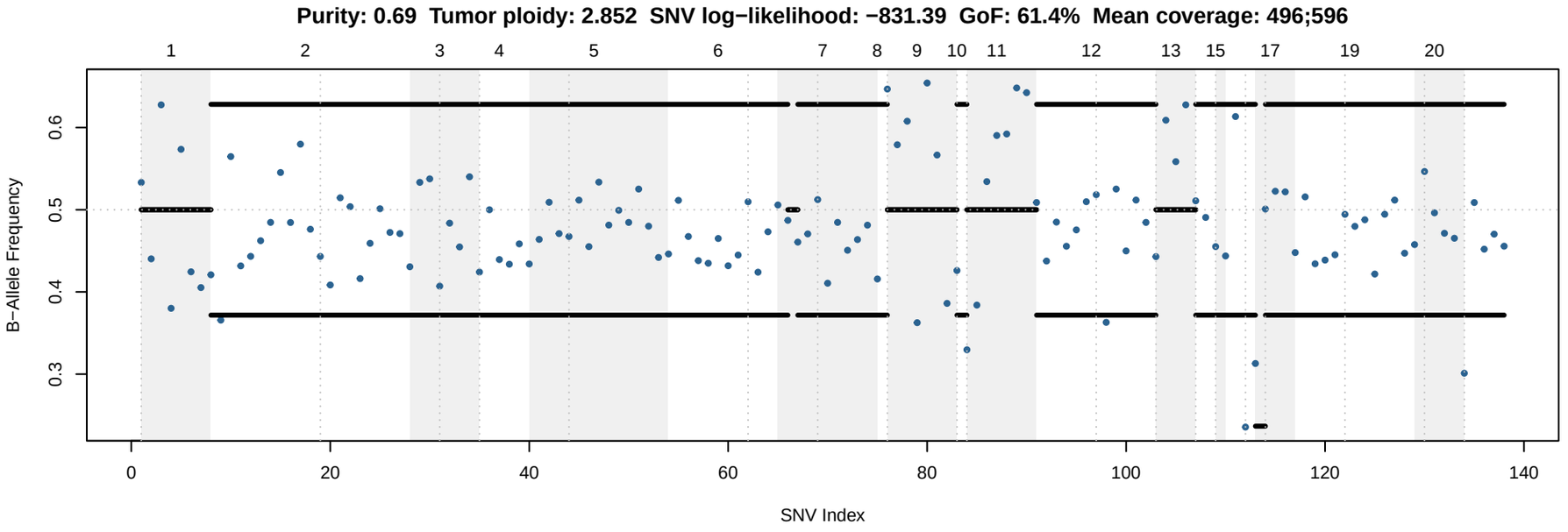

1m1
2m1
1m0
Allelic fraction (germline)
Copy Number log−ratio
0.3
0.4
0.5
0.6
0.7
−0.6
−0.4
−0.2
0.0
0.2
0.4

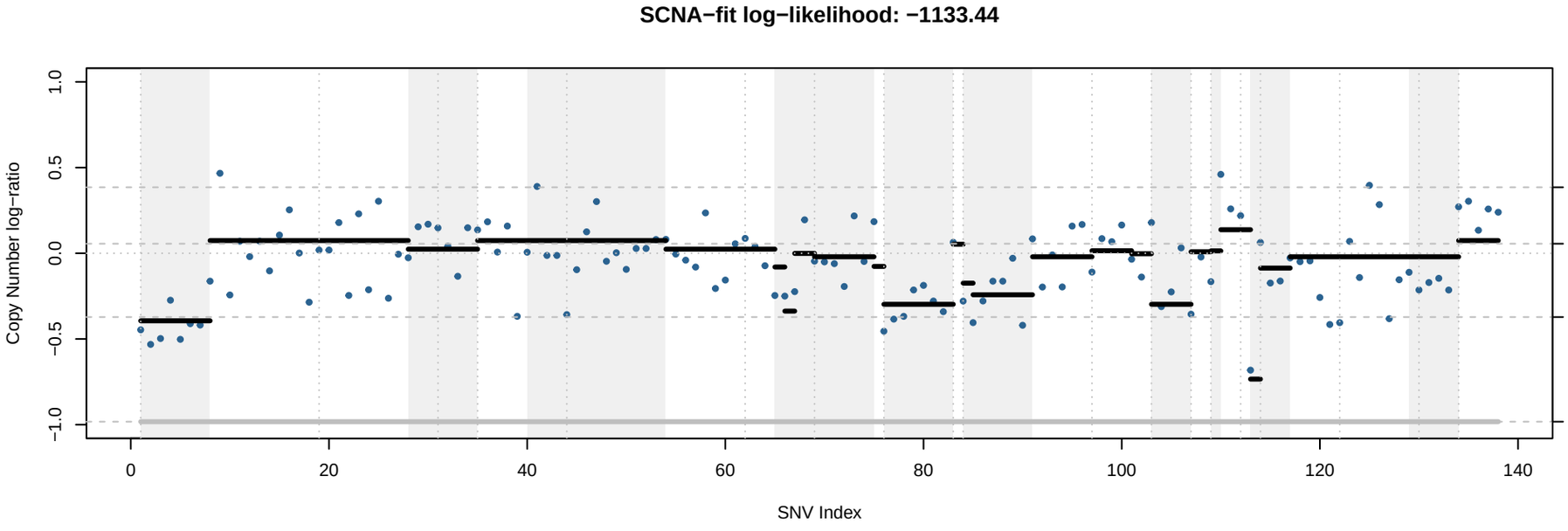

Coverage (log2)
Allelic fraction
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7

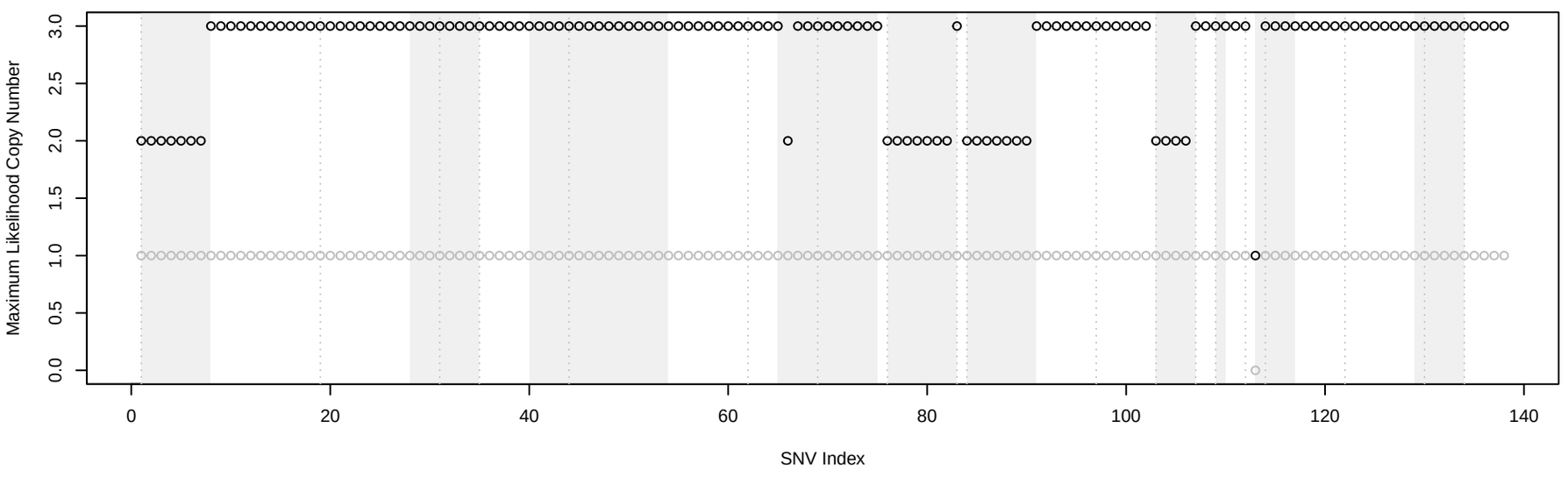

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
Allelic fraction (somatic)
Copy Number log−ratio
0.1
0.2
0.3
0.4
0.5
−0.6
−0.4
−0.2
0.0
0.2
0.4

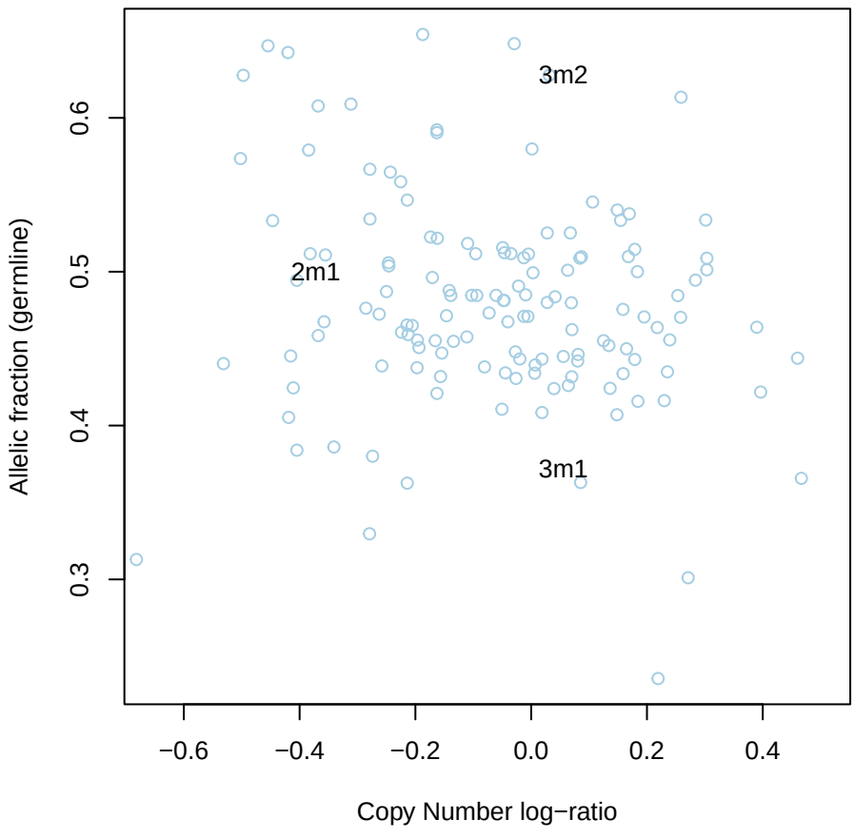

Power 0.8
Frequency
Cellular fraction
0
5
10
15
0.0
0.1
0.2
0.3
0.4
0.5
0.6

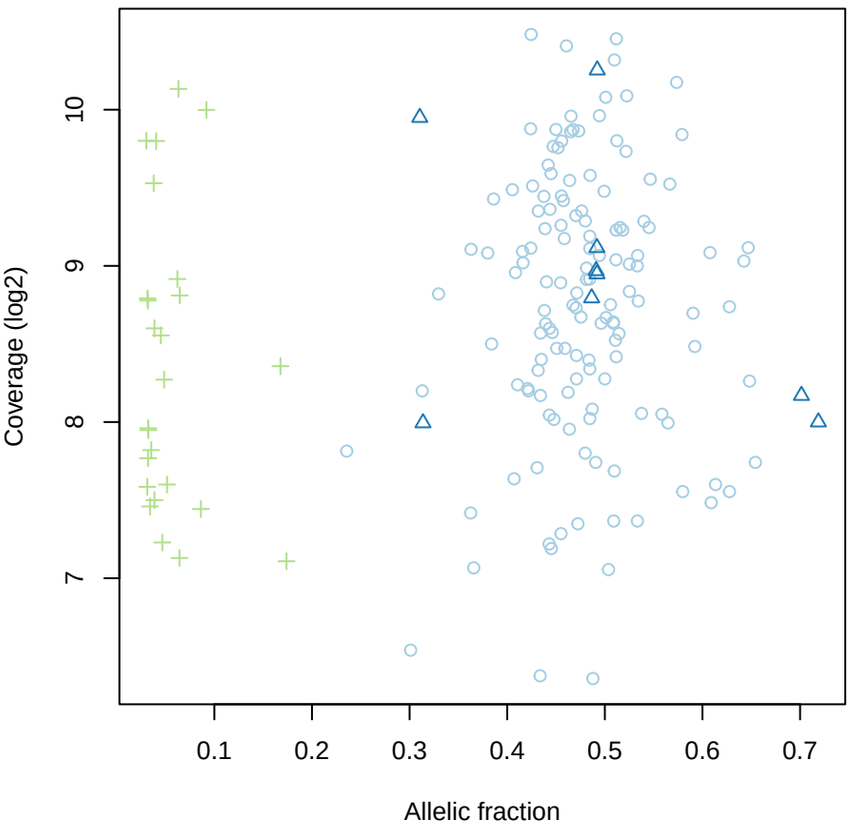

Purity: 0.69 Tumor ploidy: 2.852
2
3
4
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

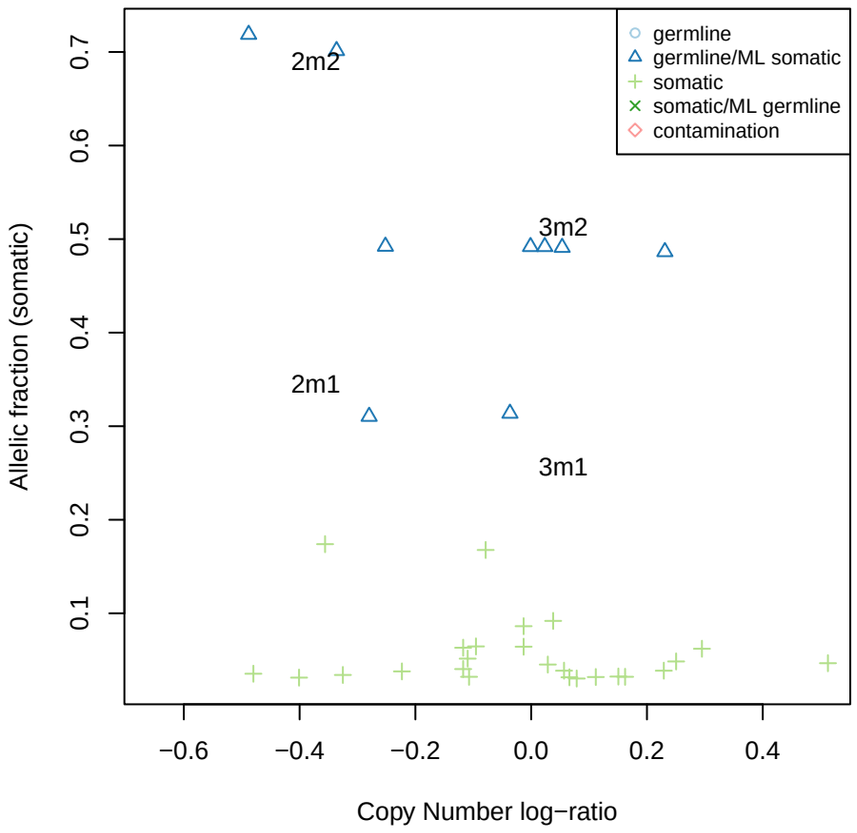

Purity: 0.69 Tumor ploidy: 2.852 SNV log−likelihood: −831.39 GoF: 61.4% Mean coverage: 496;596
1 2 3 4 5 6 7 8 9 10 11 12 13 15 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6
0 20 40 60 80 100 120 140
SNV Index

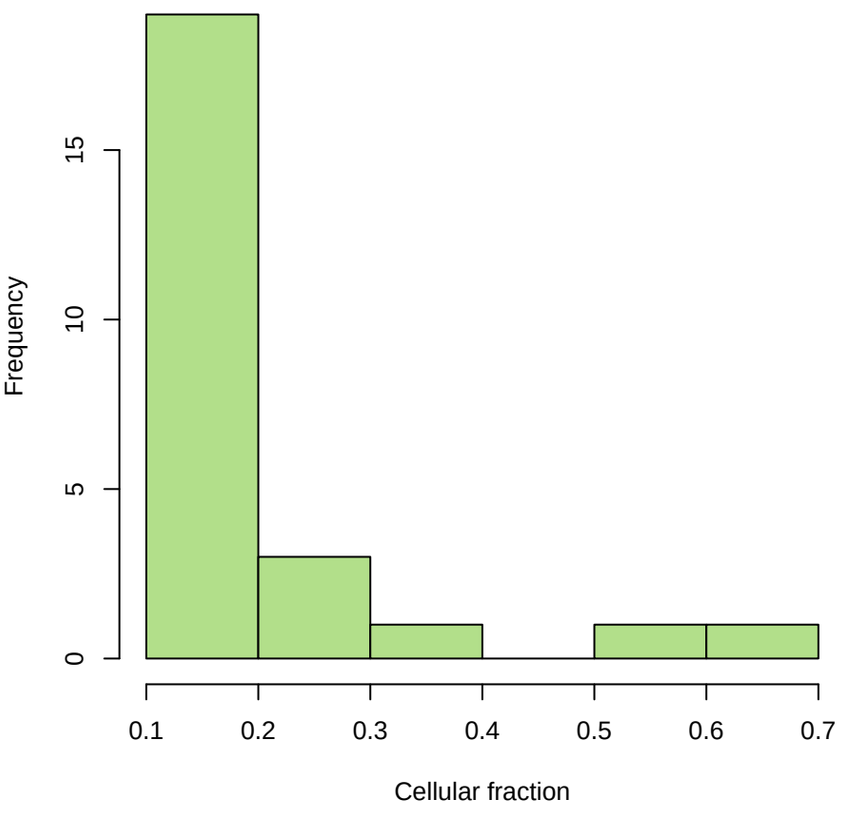

SCNA−fit log−likelihood: −1133.44
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4
0 20 40 60 80 100 120 140
SNV Index


Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120 140
SNV Index


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


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


germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
3m2
2m1
3m1
Allelic fraction (somatic)
Copy Number log−ratio
0.1
0.2
0.3
0.4
0.5
0.6
0.7
−0.6
−0.4
−0.2
0.0
0.2
0.4


Frequency
Cellular fraction
0
5
10
15
0.1
0.2
0.3
0.4
0.5
0.6
0.7