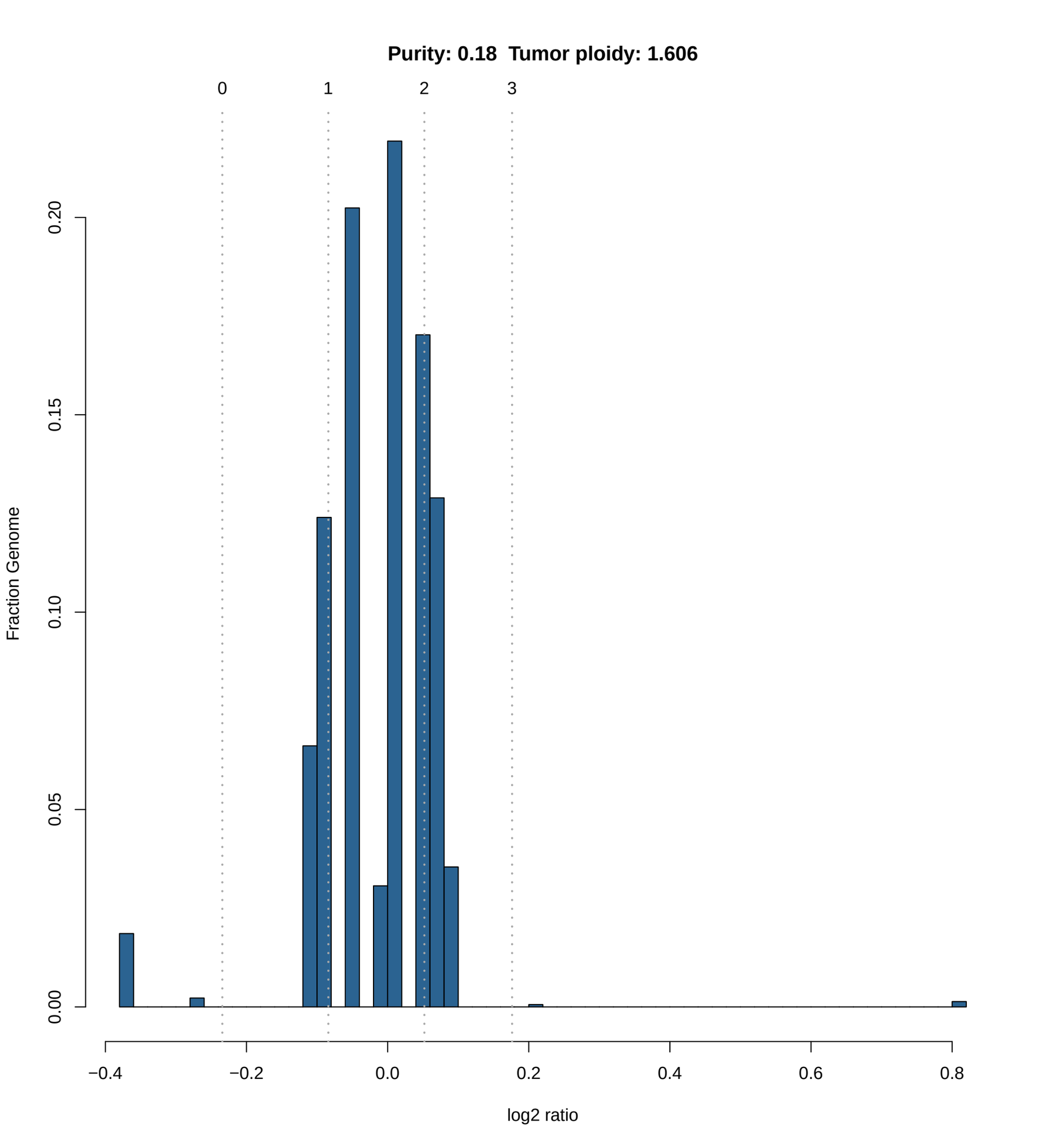
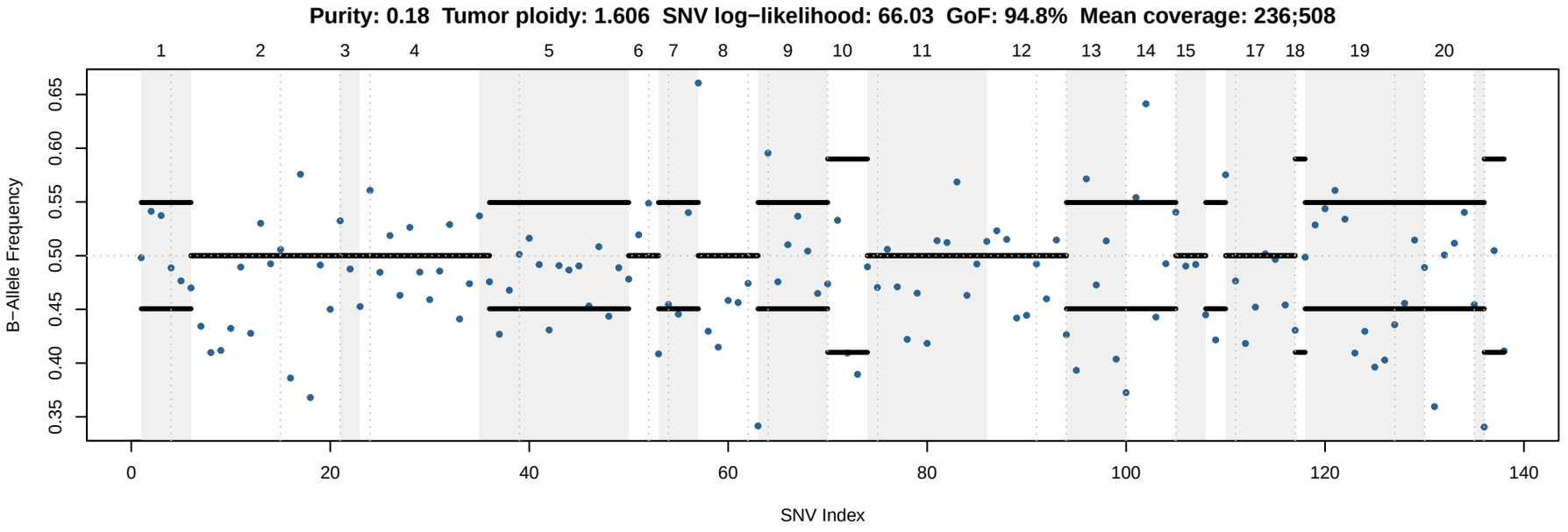
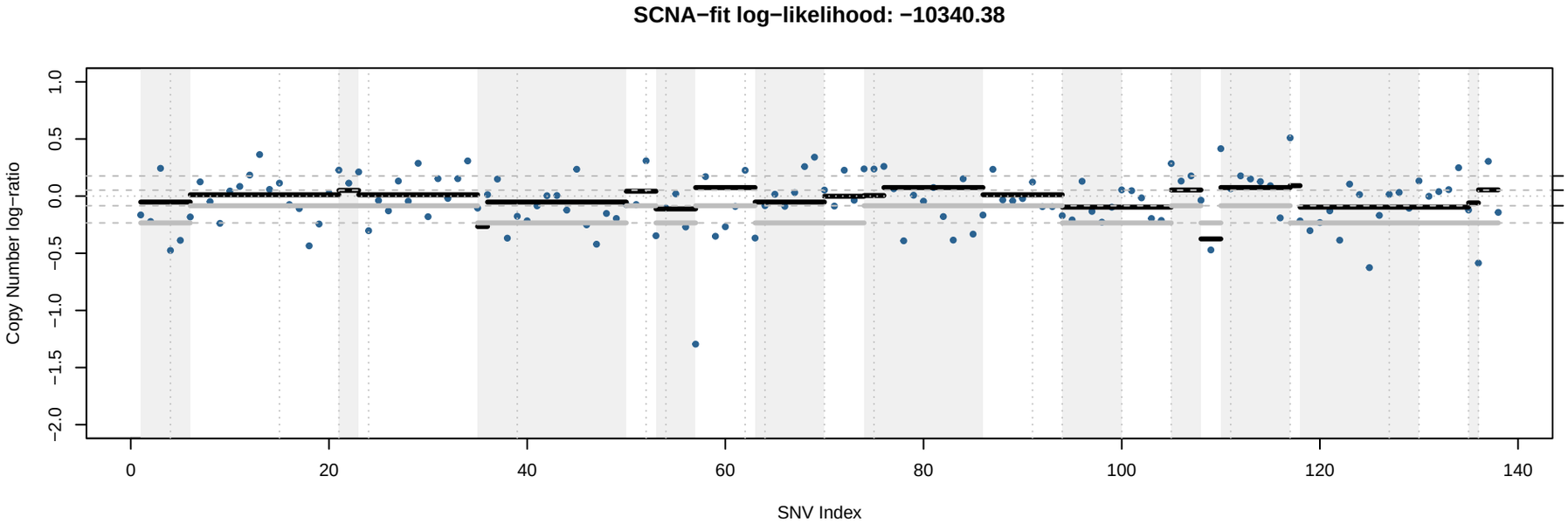
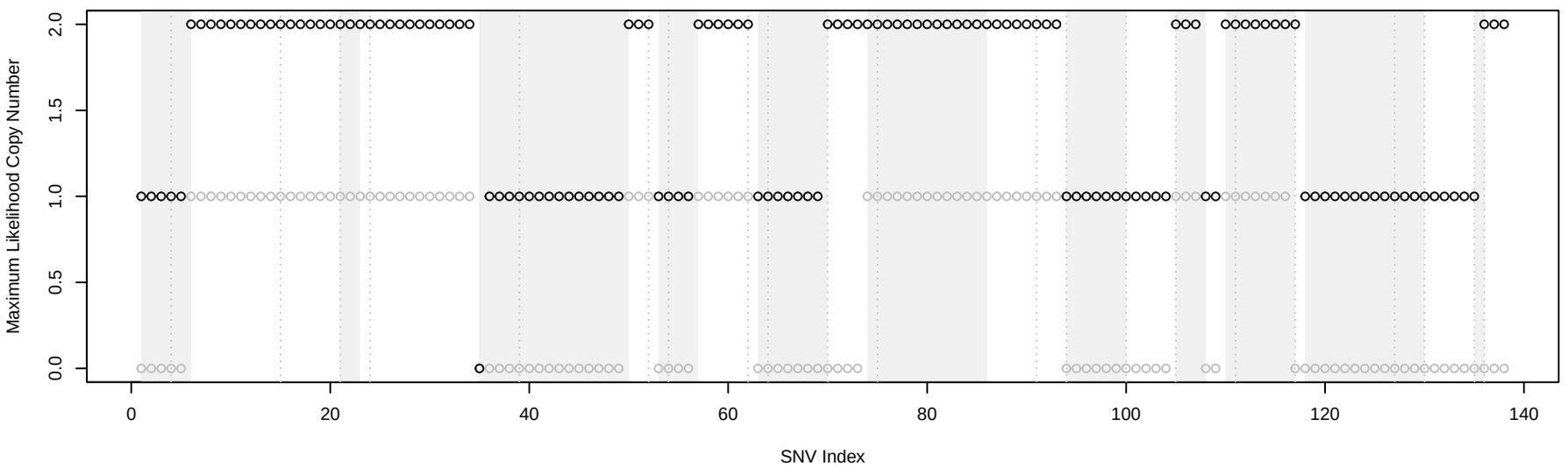
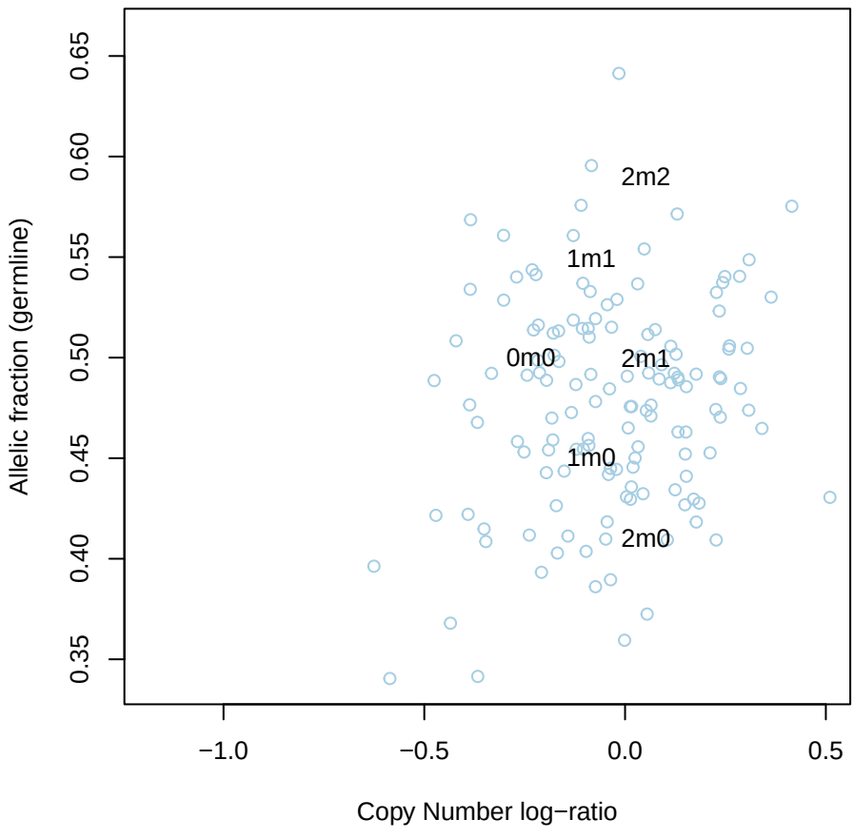
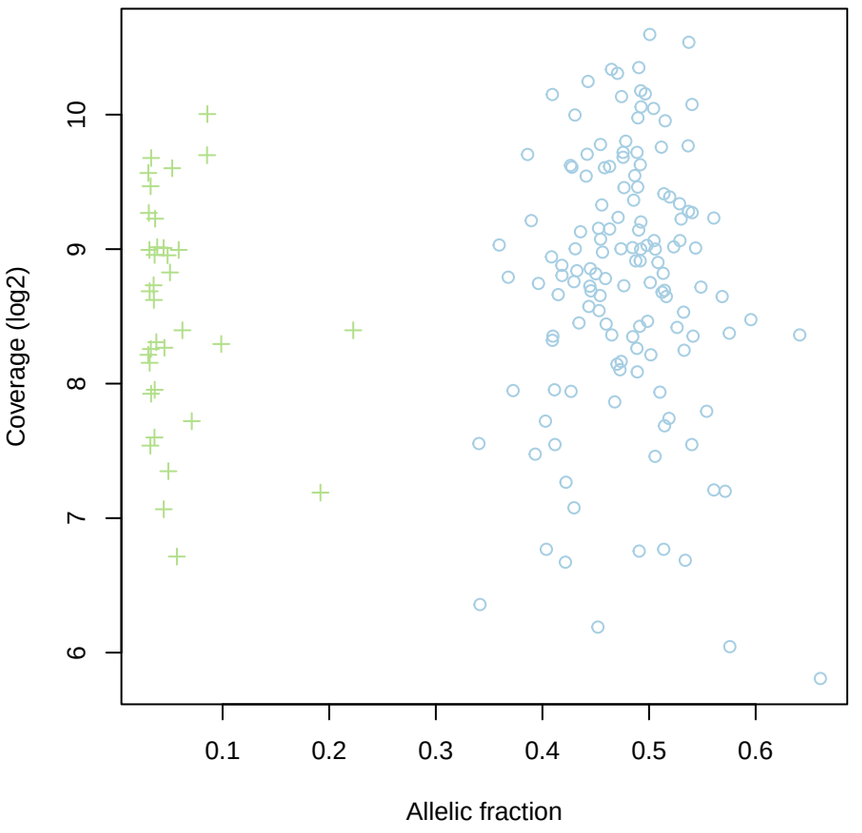

Purity: 0.18 Tumor ploidy: 1.606
0
1
2
3
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
log2 ratio

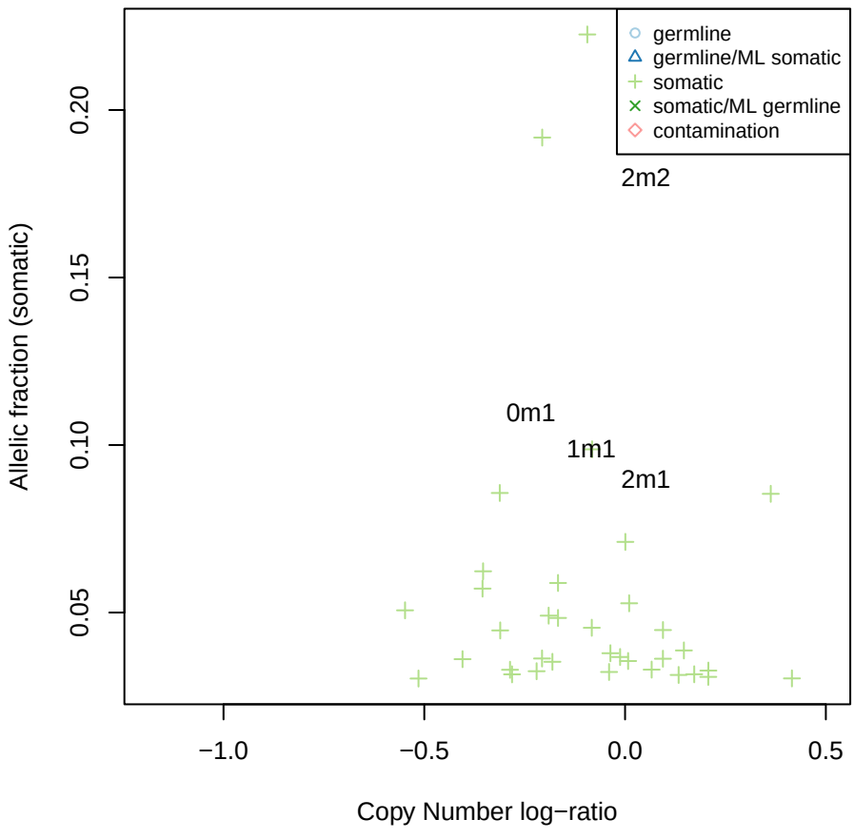

Purity: 0.18 Tumor ploidy: 1.606 SNV log−likelihood: 66.03 GoF: 94.8% Mean coverage: 236;508
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

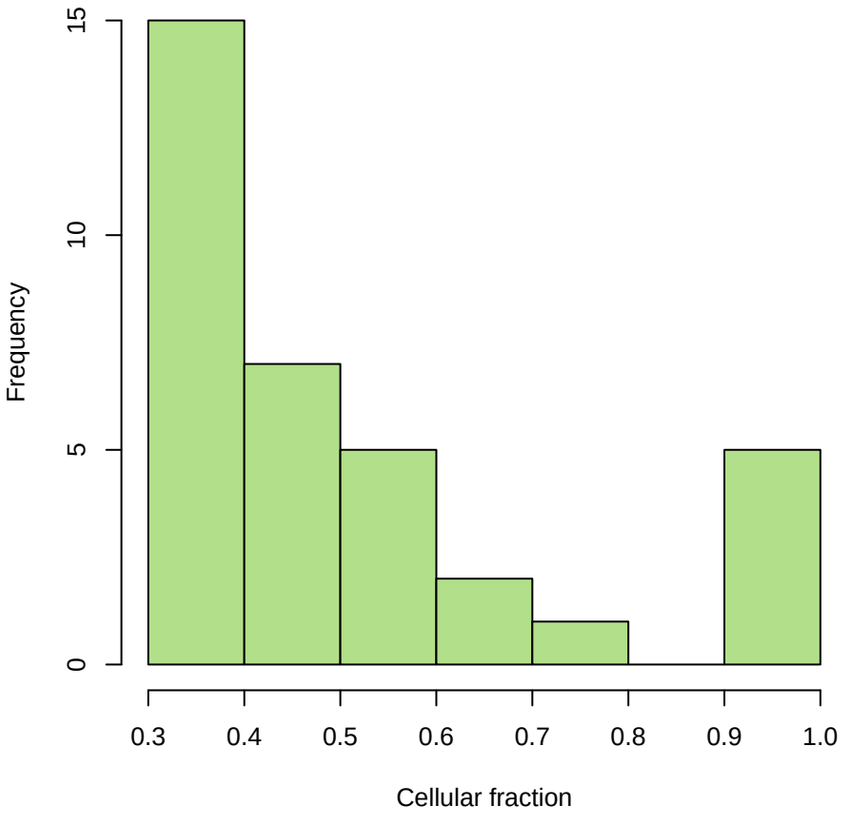

SCNA−fit log−likelihood: −10340.38
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
0 2
0 20 40 60 80 100 120 140
SNV Index

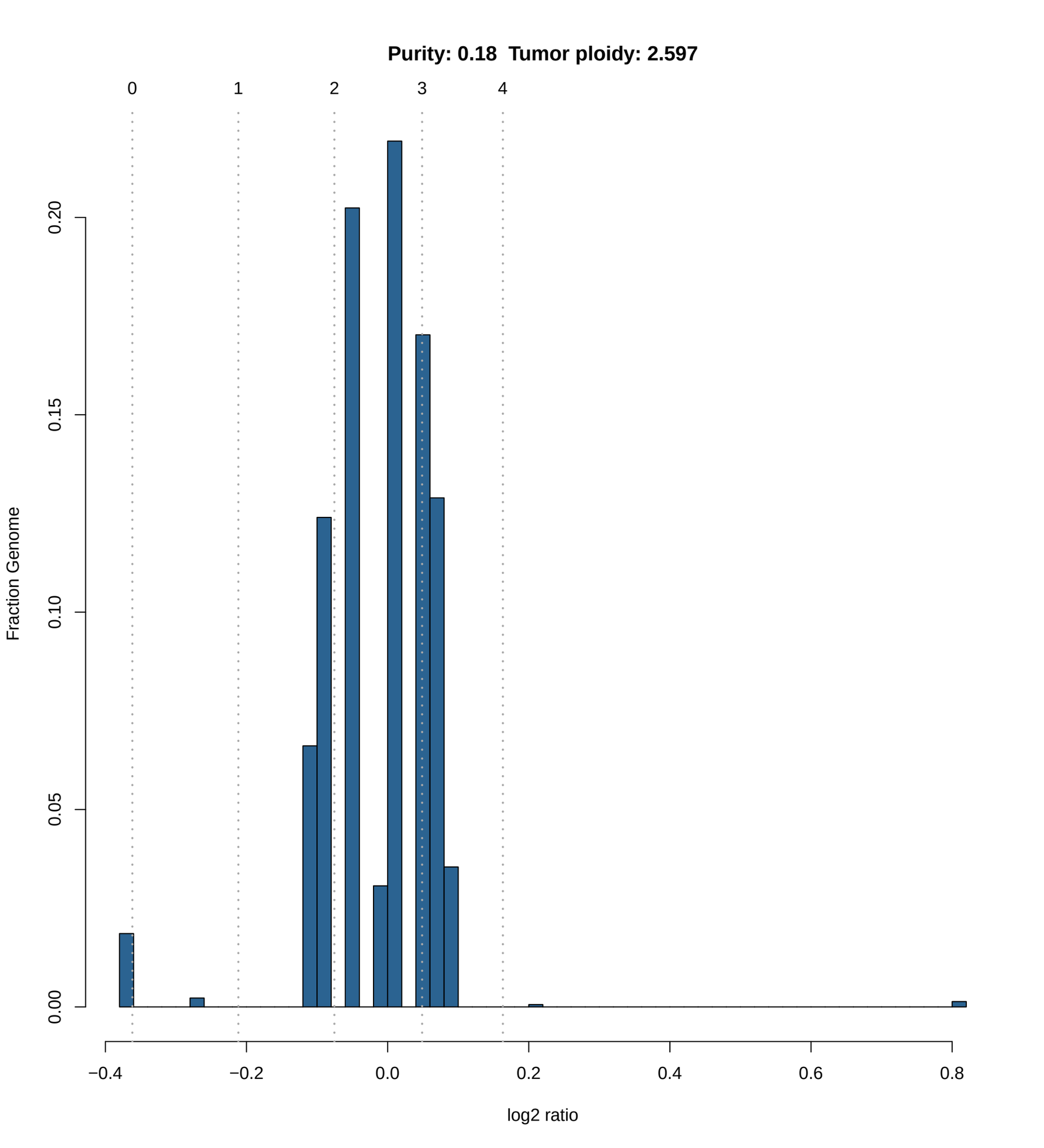

Maximum Likelihood Copy Number
2.0 1.5 1.0 0.5 0.0
0 20 40 60 80 100 120 140
SNV Index

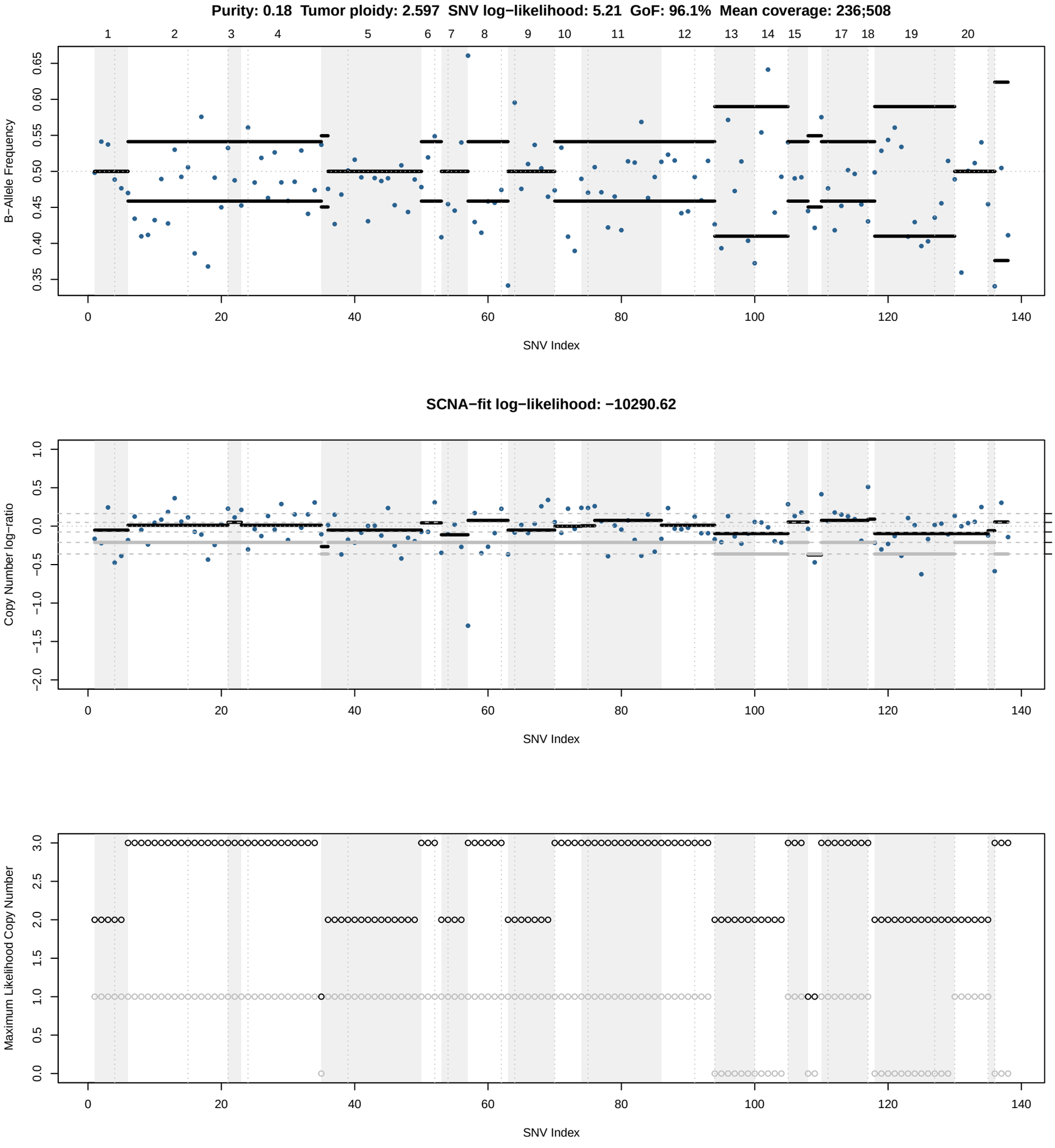

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
2m2
1m1
0m0
2m1
1m0
2m0
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

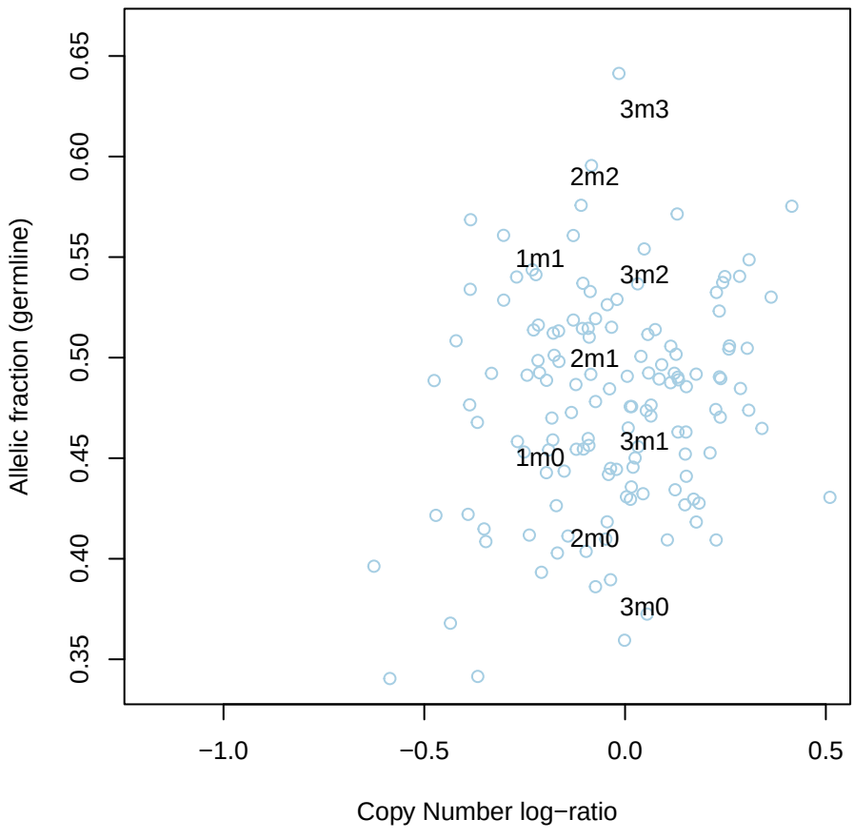

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

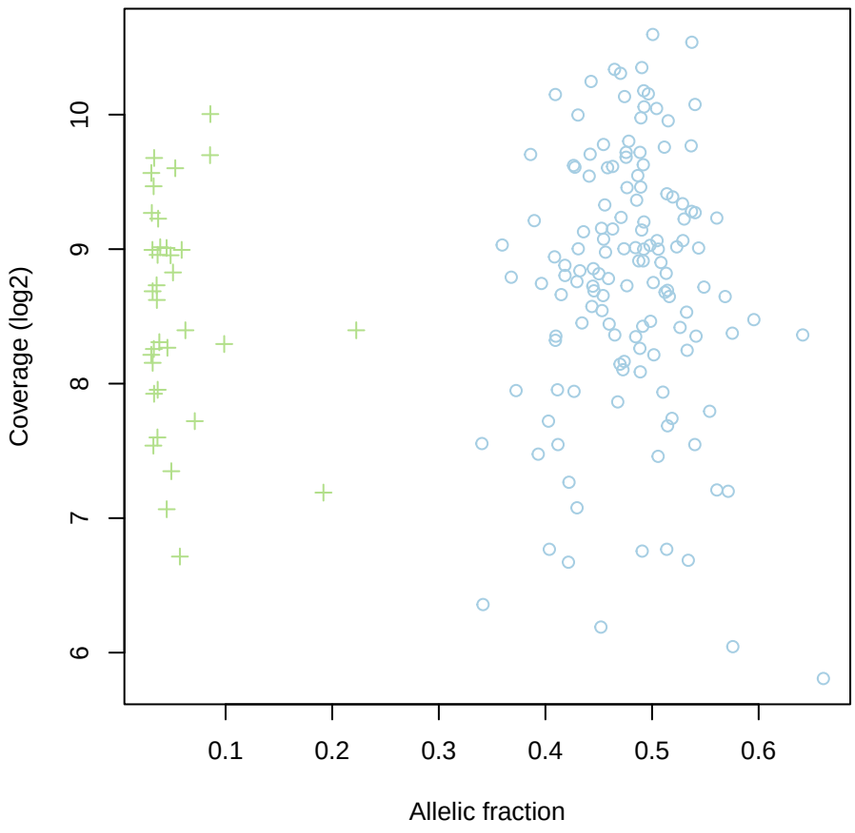

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
0m1
1m1
2m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

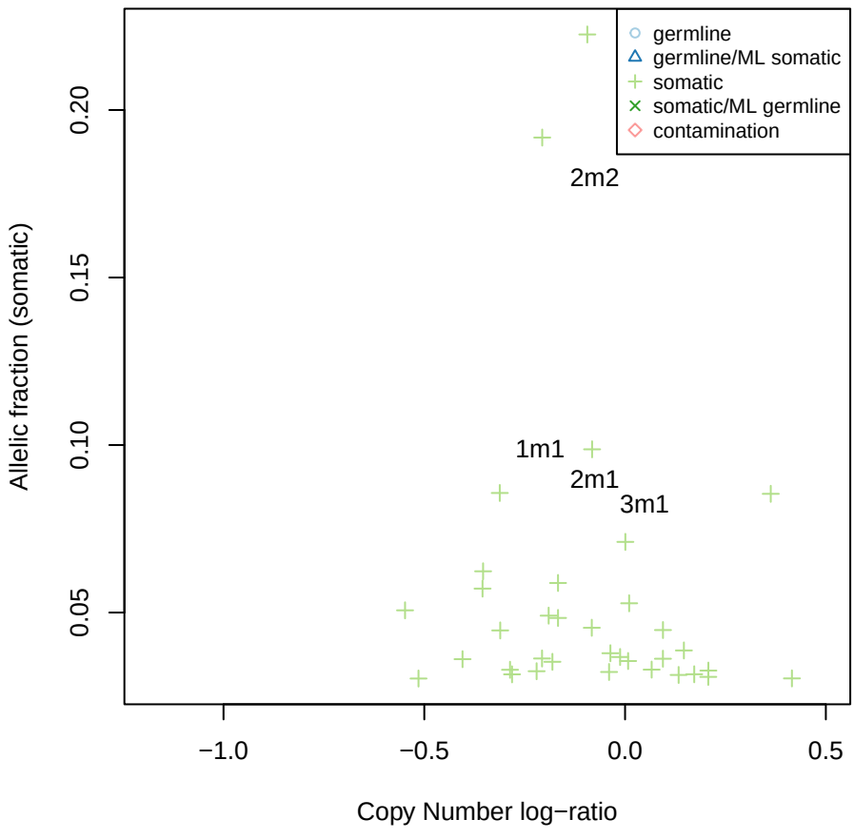

Frequency
0
5
10
15
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

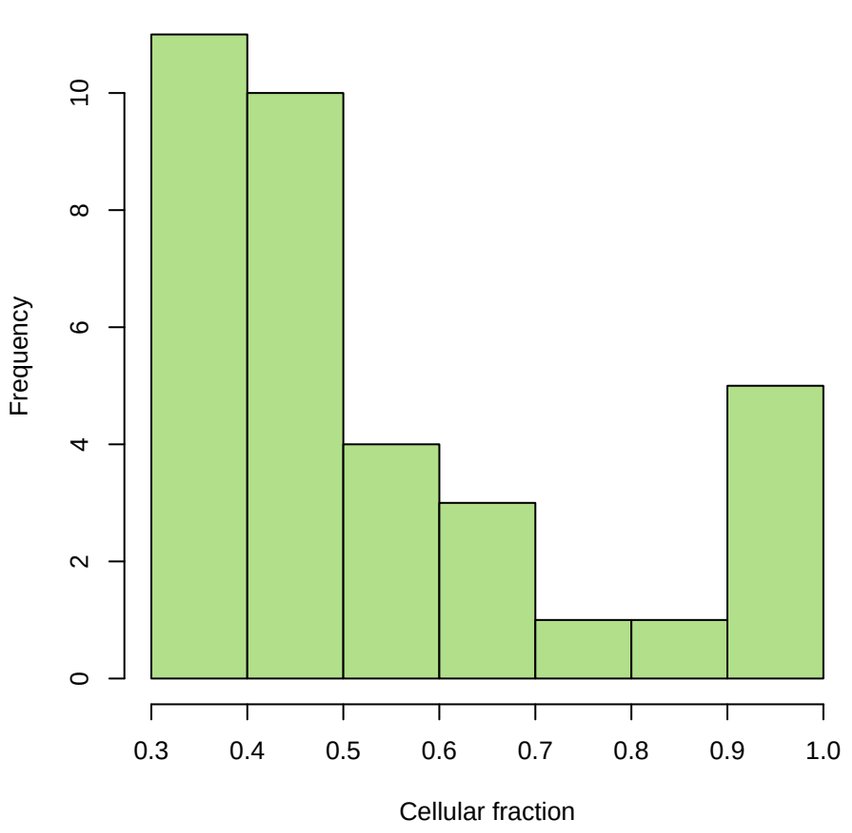

Purity: 0.18 Tumor ploidy: 2.597
0
1
2
3
4
0.00
0.05
0.10
0.15
0.20
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
log2 ratio

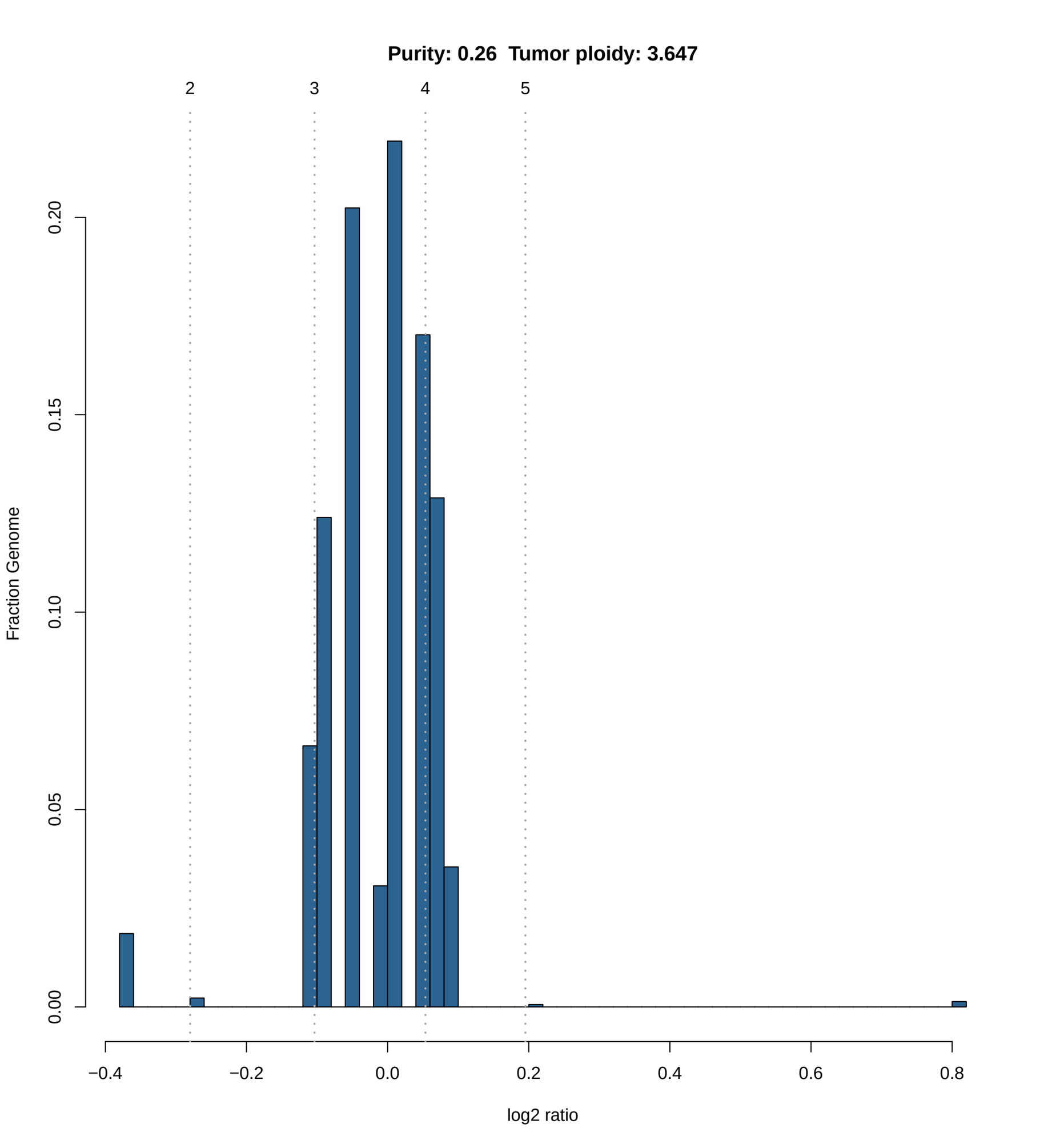

Purity: 0.18 Tumor ploidy: 2.597 SNV log−likelihood: 5.21 GoF: 96.1% Mean coverage: 236;508
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index
SCNA−fit log−likelihood: −10290.62
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 2 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

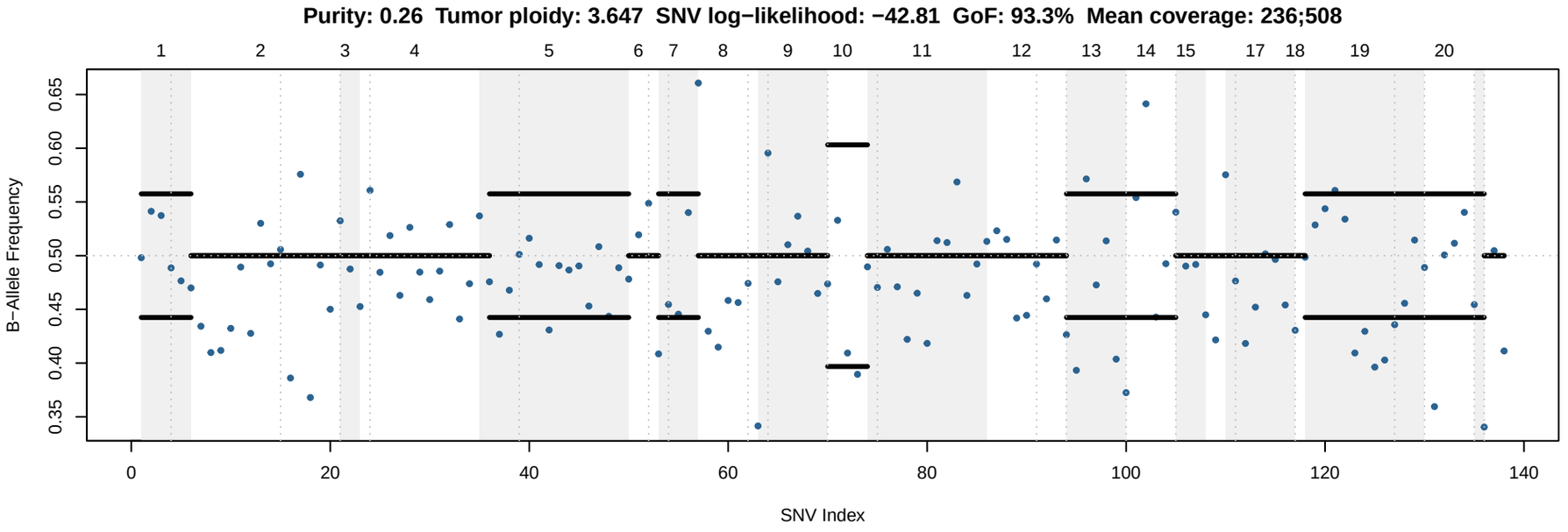

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
3m3
2m2
1m1
3m2
2m1
3m1
1m0
2m0
3m0
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

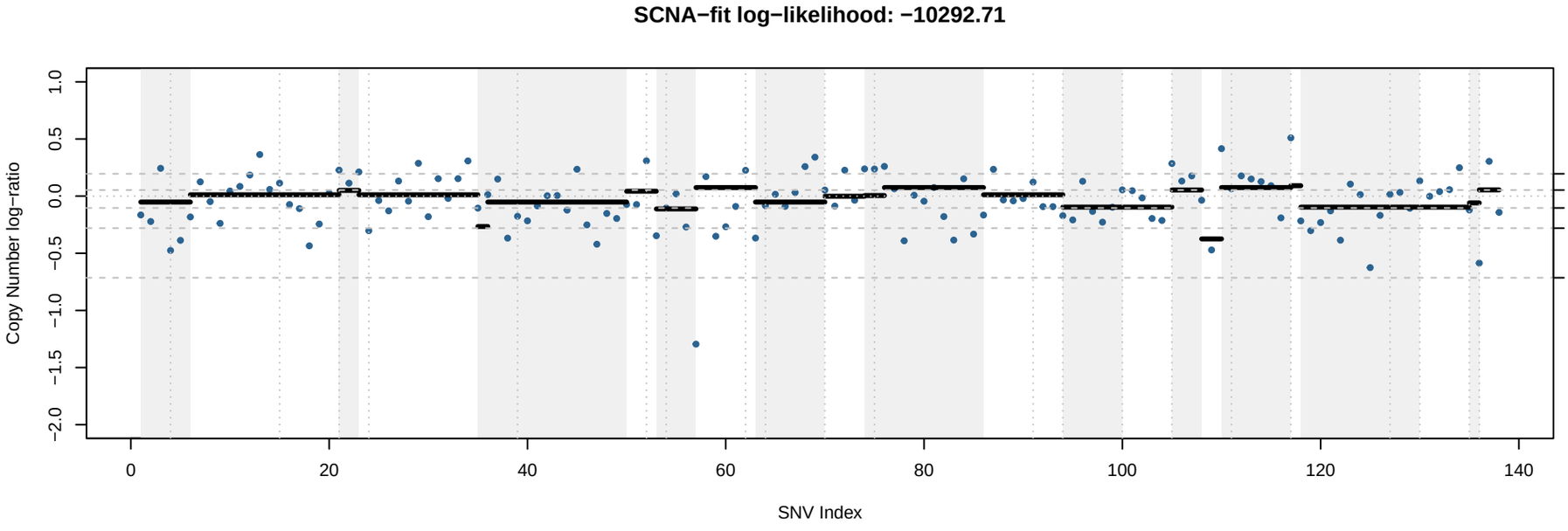

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

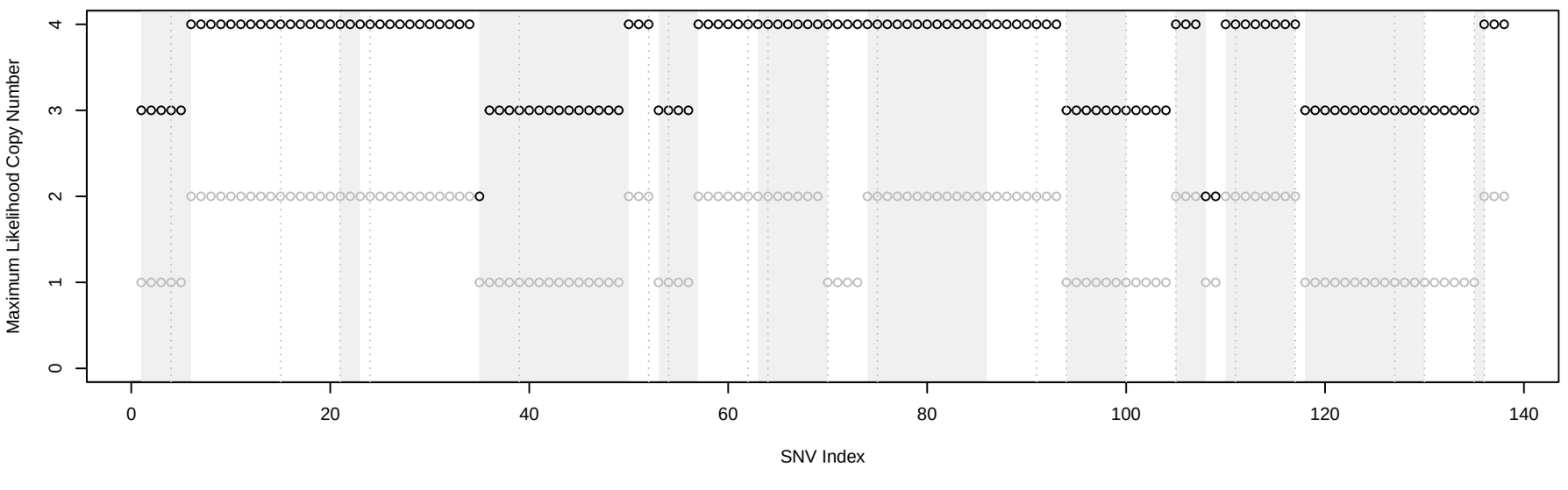

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
2m2
1m1
2m1
3m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

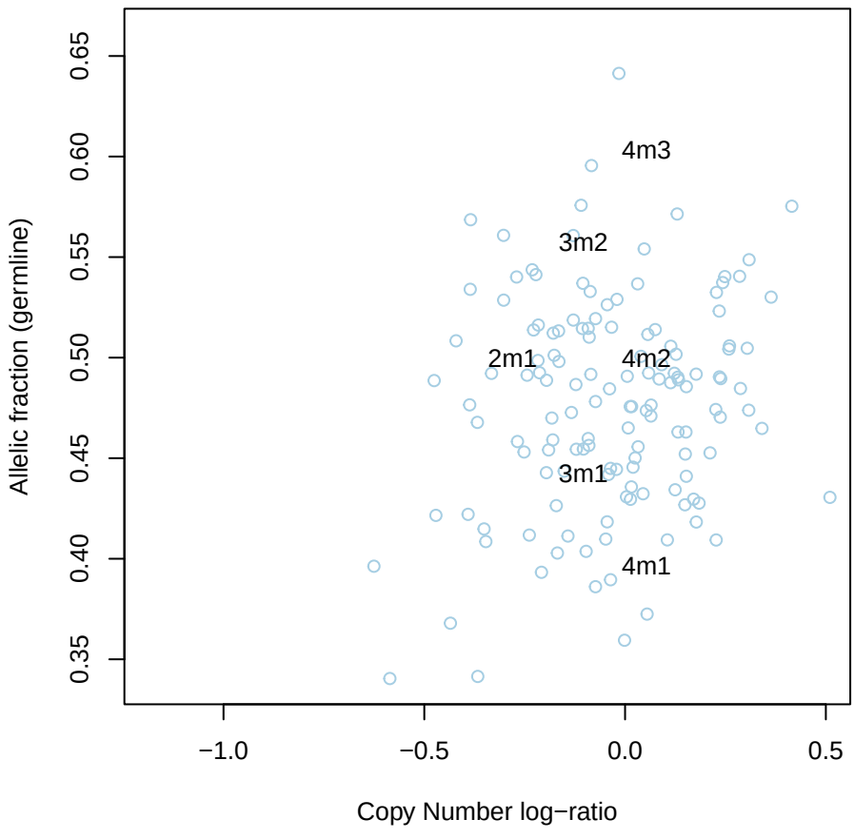

Frequency
0
2
4
6
8
10
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

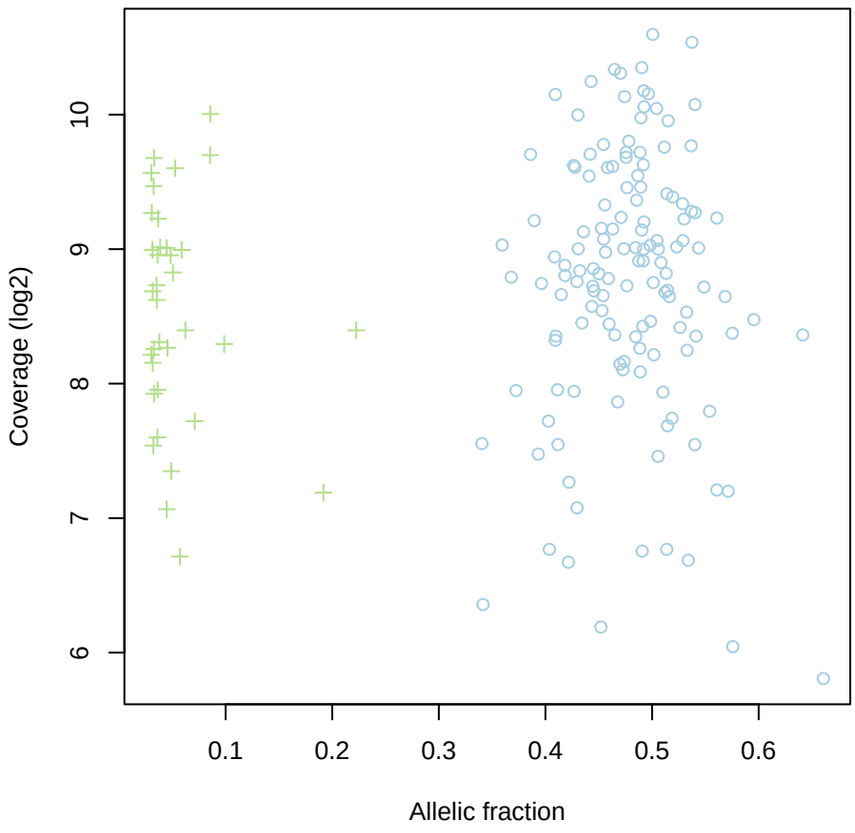

Purity: 0.26 Tumor ploidy: 3.647
2
3
4
5
0.00
0.05
0.10
0.15
0.20
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
log2 ratio

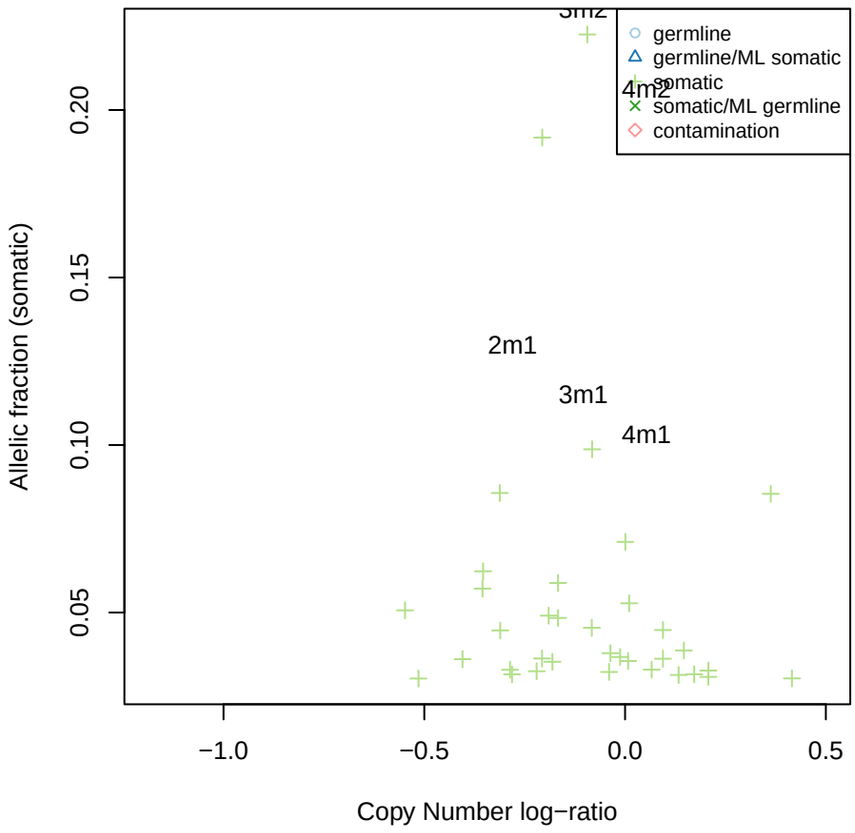

Purity: 0.26 Tumor ploidy: 3.647 SNV log−likelihood: −42.81 GoF: 93.3% Mean coverage: 236;508
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

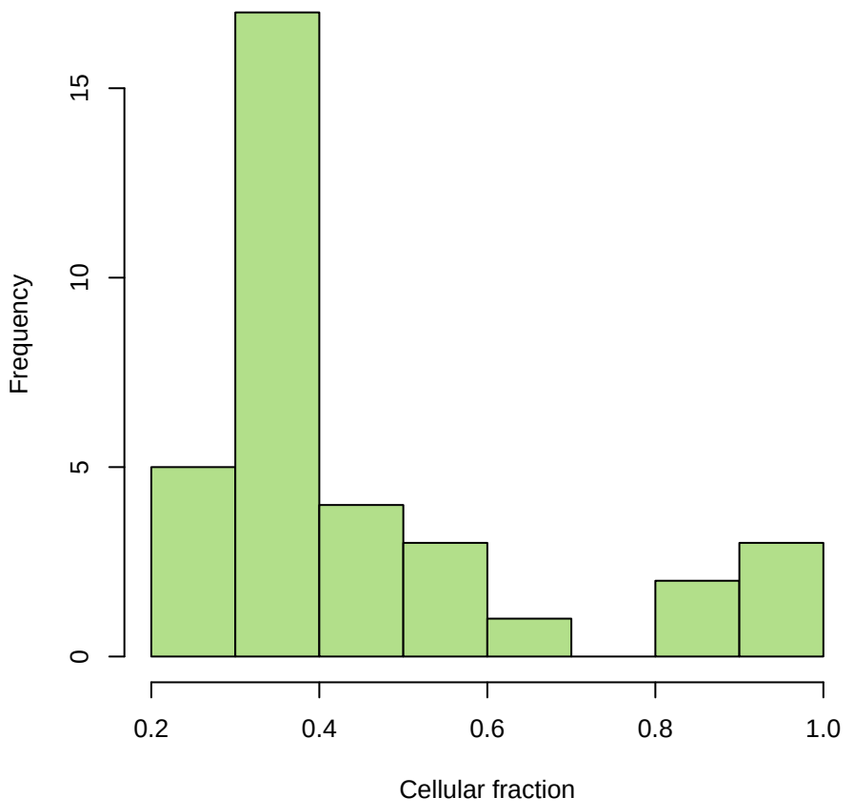

SCNA−fit log−likelihood: −10292.71
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
0 2 4
0 20 40 60 80 100 120 140
SNV Index

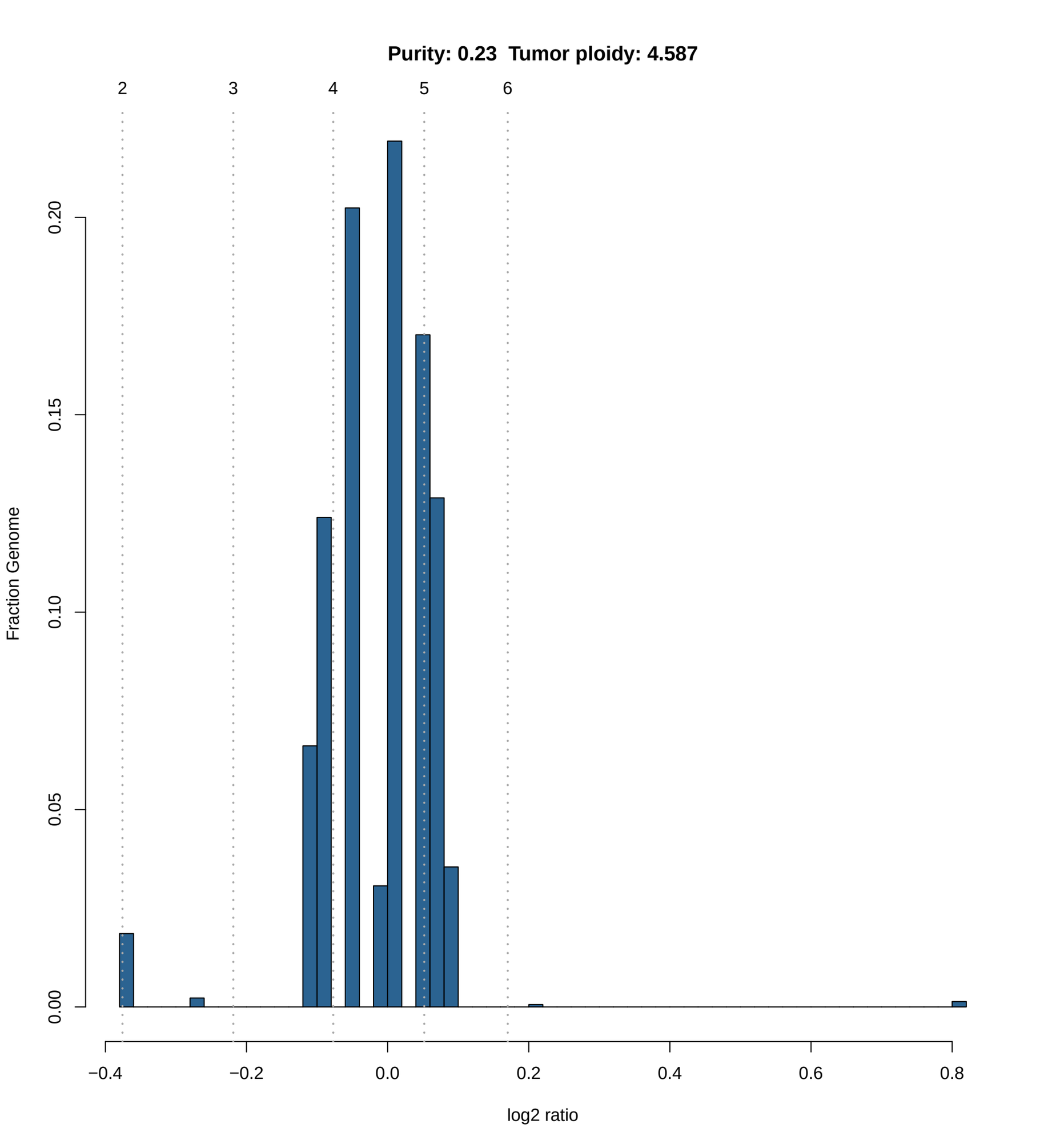

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120 140
SNV Index

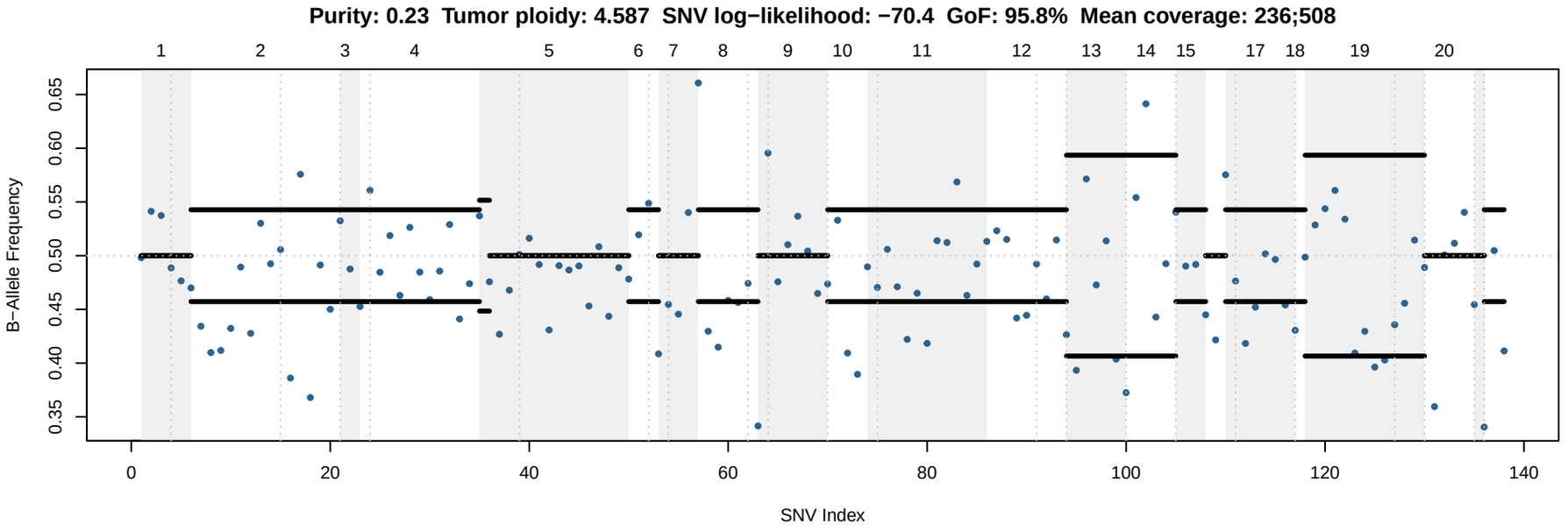

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
4m3
3m2
2m1
4m2
3m1
4m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

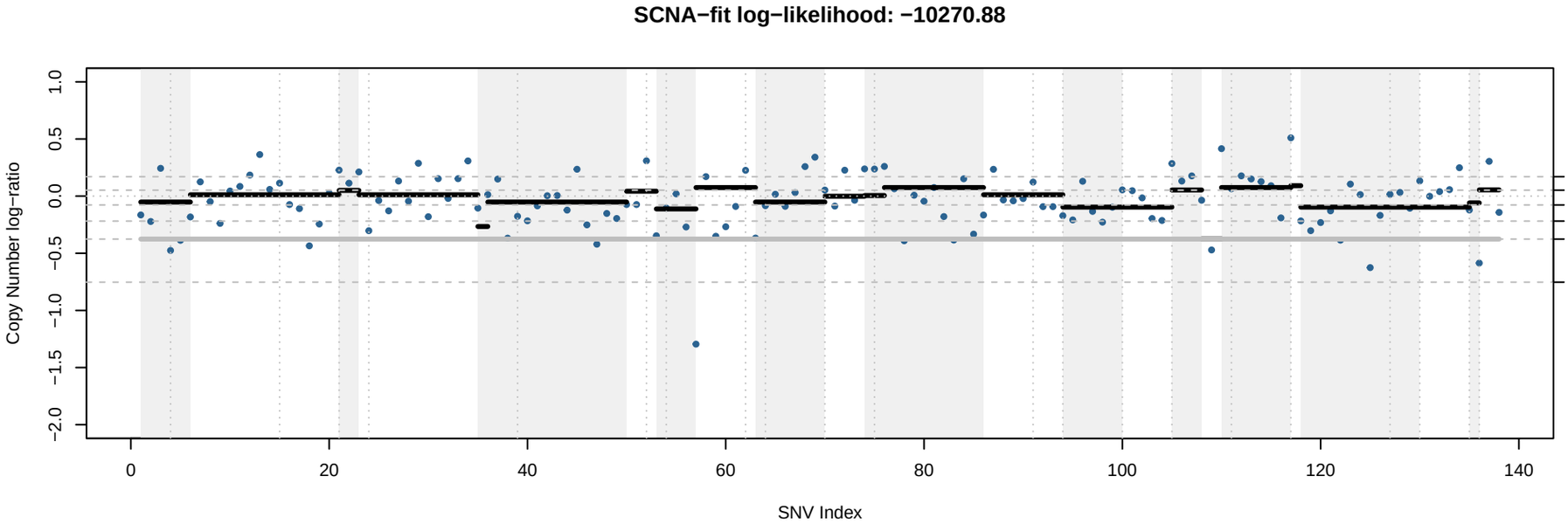

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

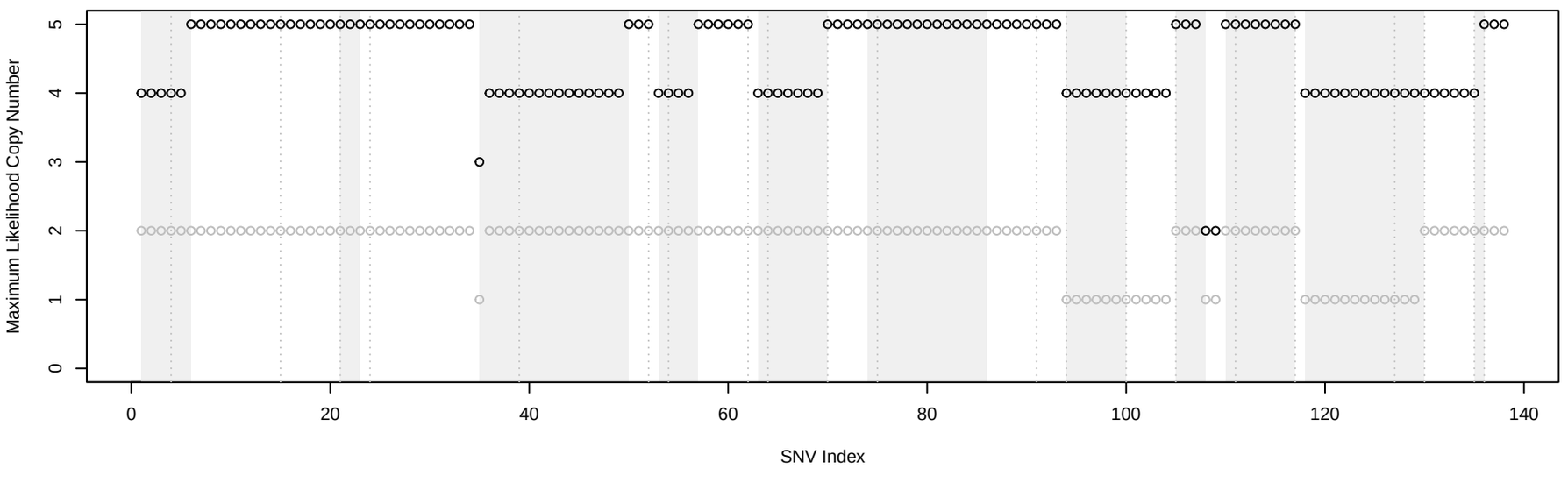

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m2
2m1
3m1
4m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

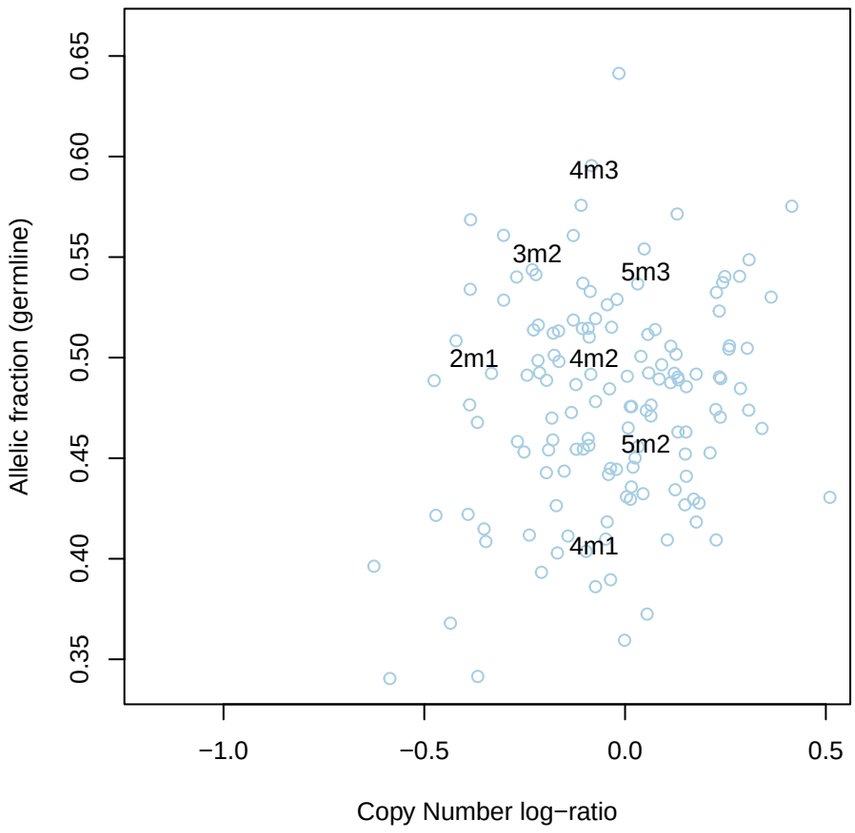

Frequency
0
5
10
15
0.2
0.4
0.6
0.8
1.0
Cellular fraction

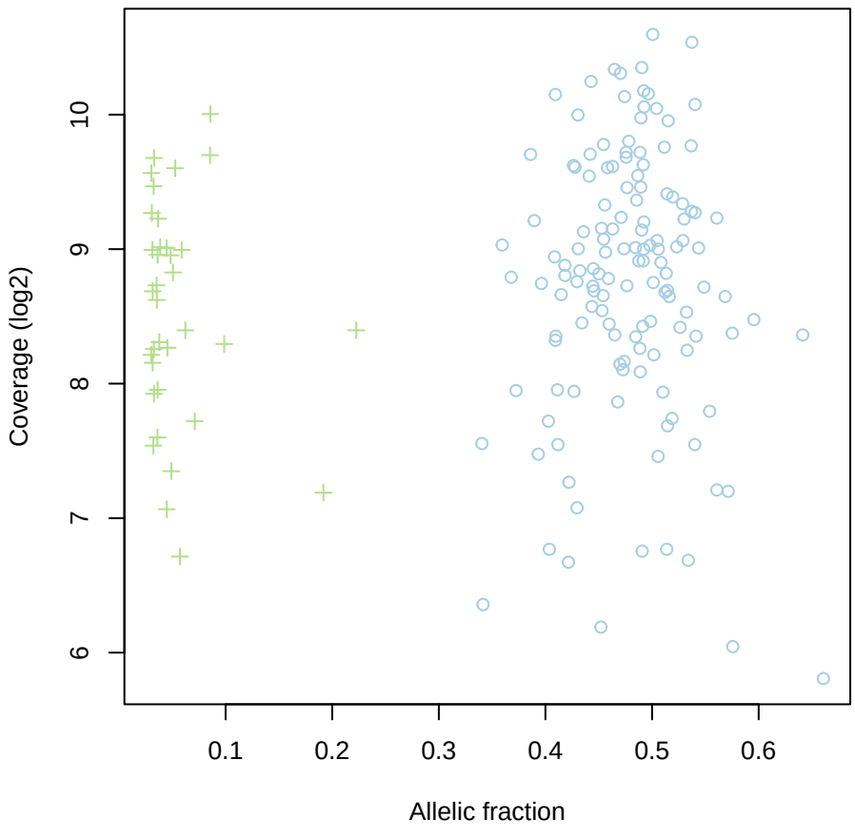

Purity: 0.23 Tumor ploidy: 4.587
2
3
4
5
6
0.00
0.05
0.10
0.15
0.20
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
log2 ratio

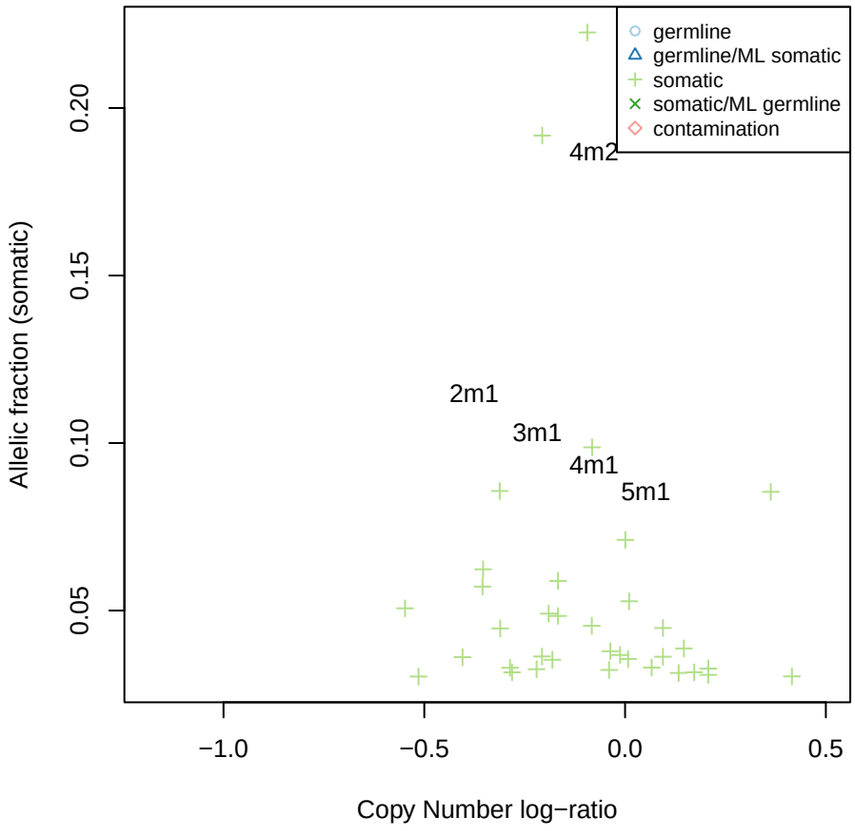

Purity: 0.23 Tumor ploidy: 4.587 SNV log−likelihood: −70.4 GoF: 95.8% Mean coverage: 236;508
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

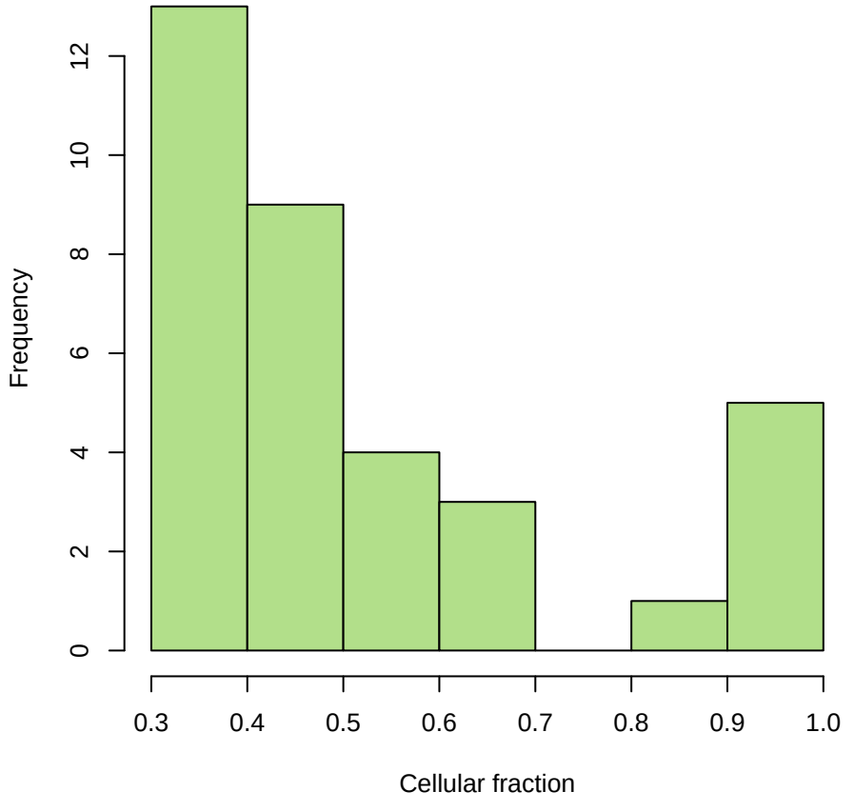

SCNA−fit log−likelihood: −10270.88
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 2 4 6
0 20 40 60 80 100 120 140
SNV Index

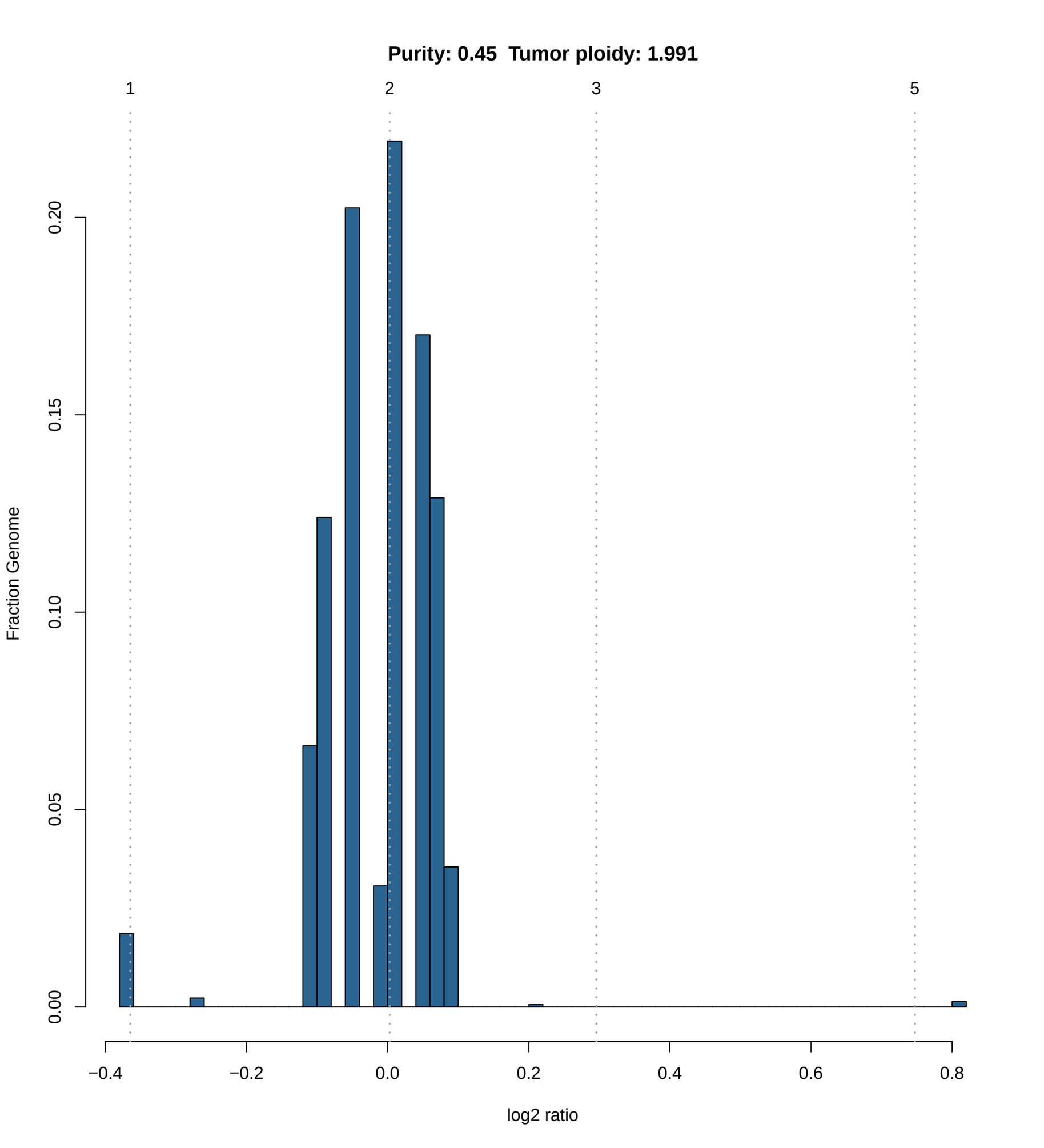

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

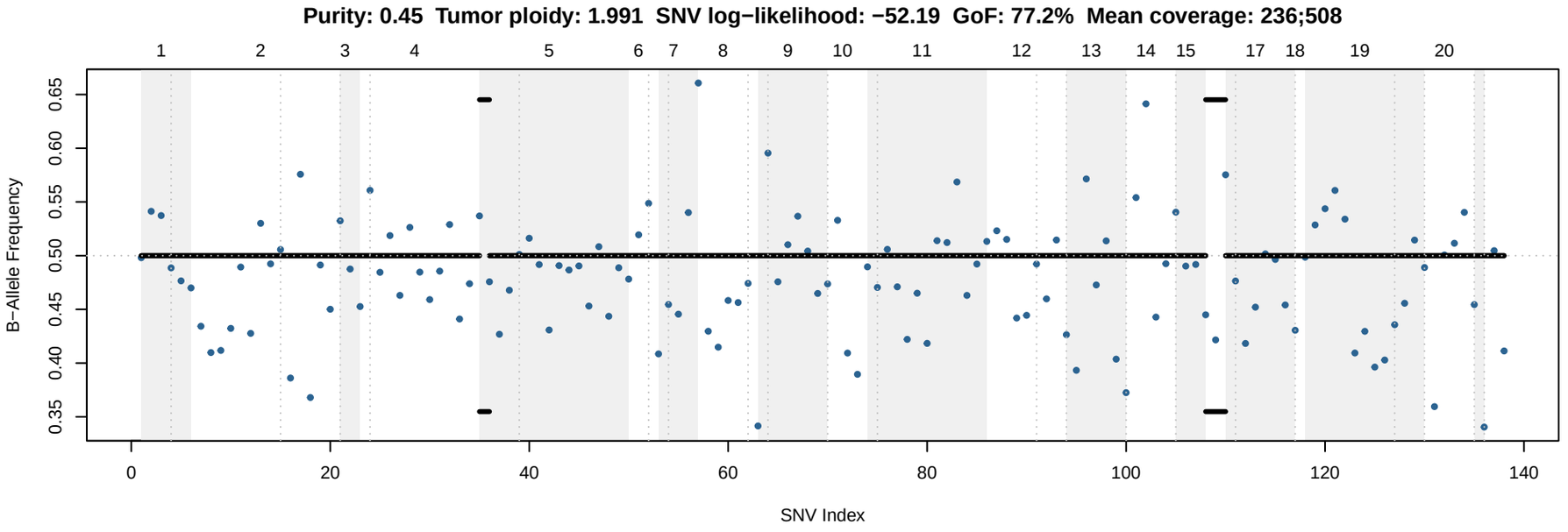

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
5m3
2m1
4m2
5m2
4m1

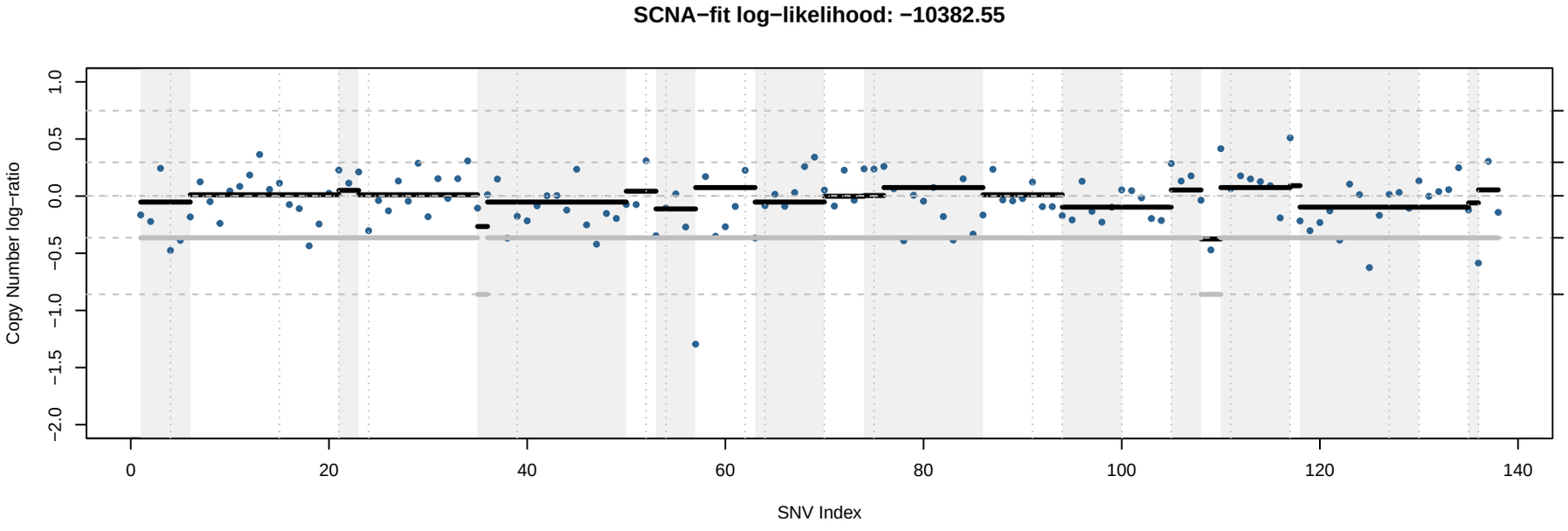

Coverage (log2)
Allelic fraction

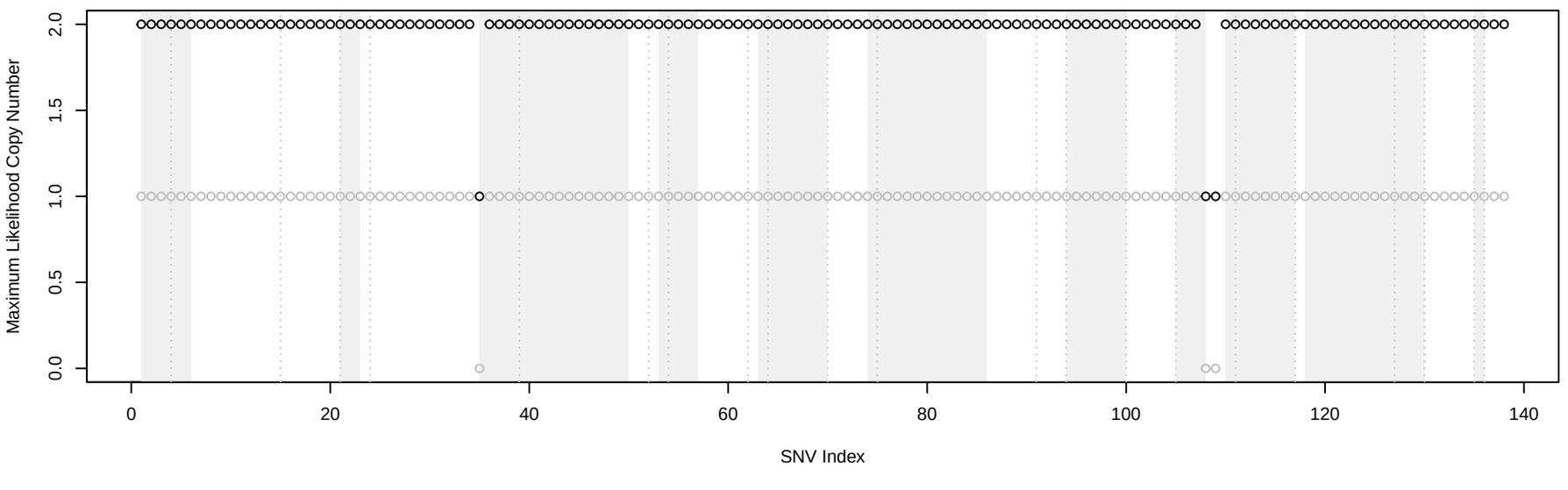

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
4m2
2m1
3m1
4m1
5m1

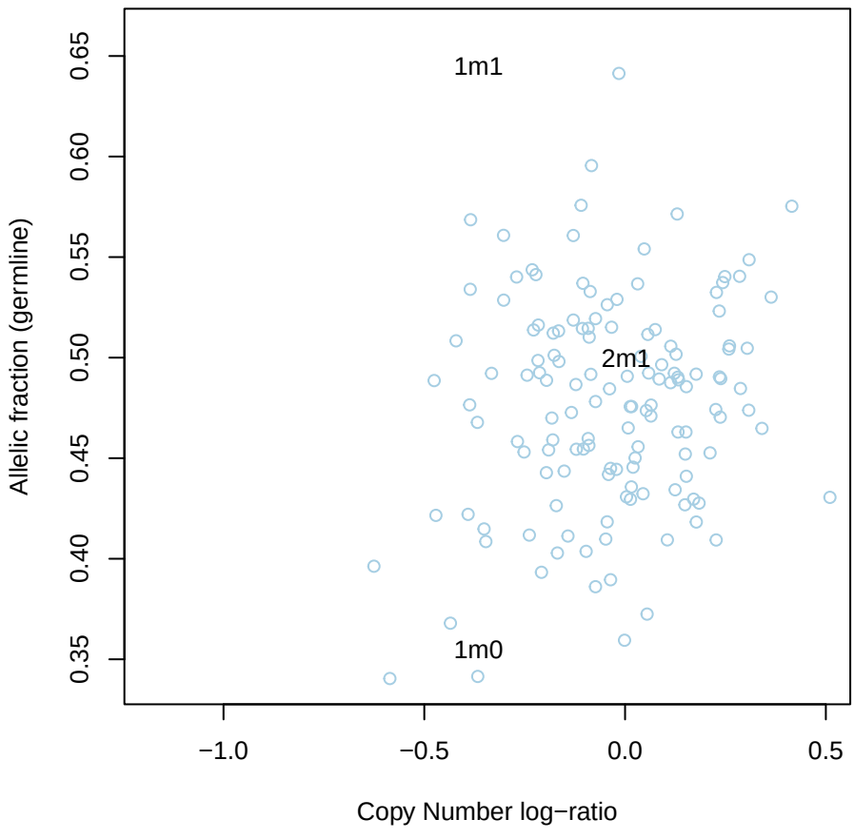

Frequency
Cellular fraction

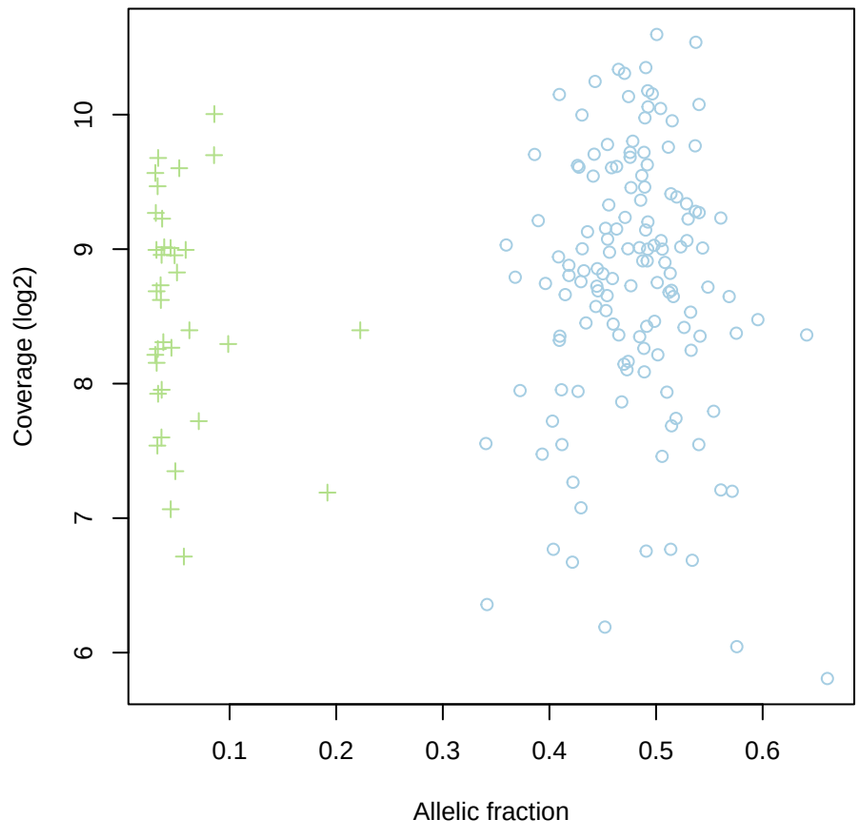

Purity: 0.45 Tumor ploidy: 1.991
1
2
3
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
log2 ratio

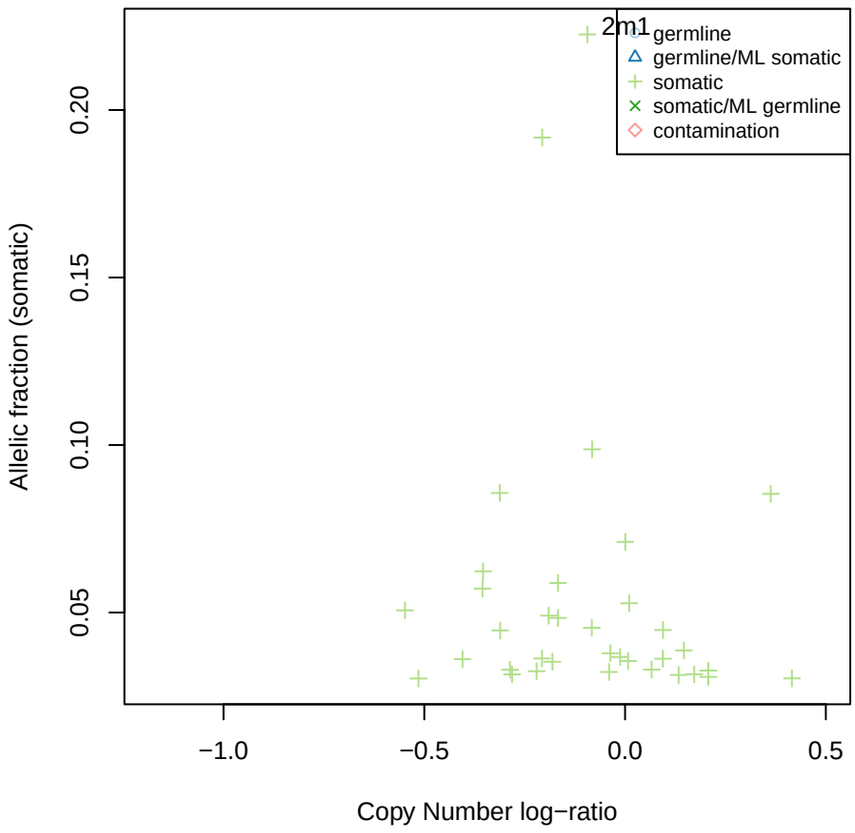

Purity: 0.45 Tumor ploidy: 1.991 SNV log−likelihood: −52.19 GoF: 77.2% Mean coverage: 236;508
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

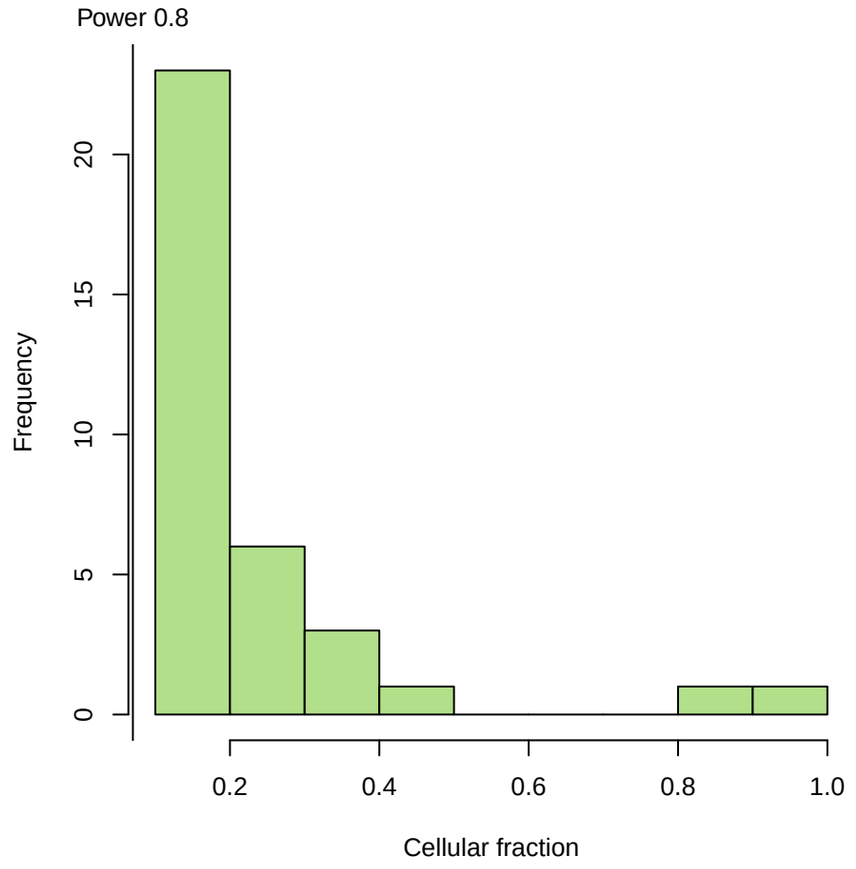

SCNA−fit log−likelihood: −10382.55
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
0 1 2 3 5
0 20 40 60 80 100 120 140
SNV Index

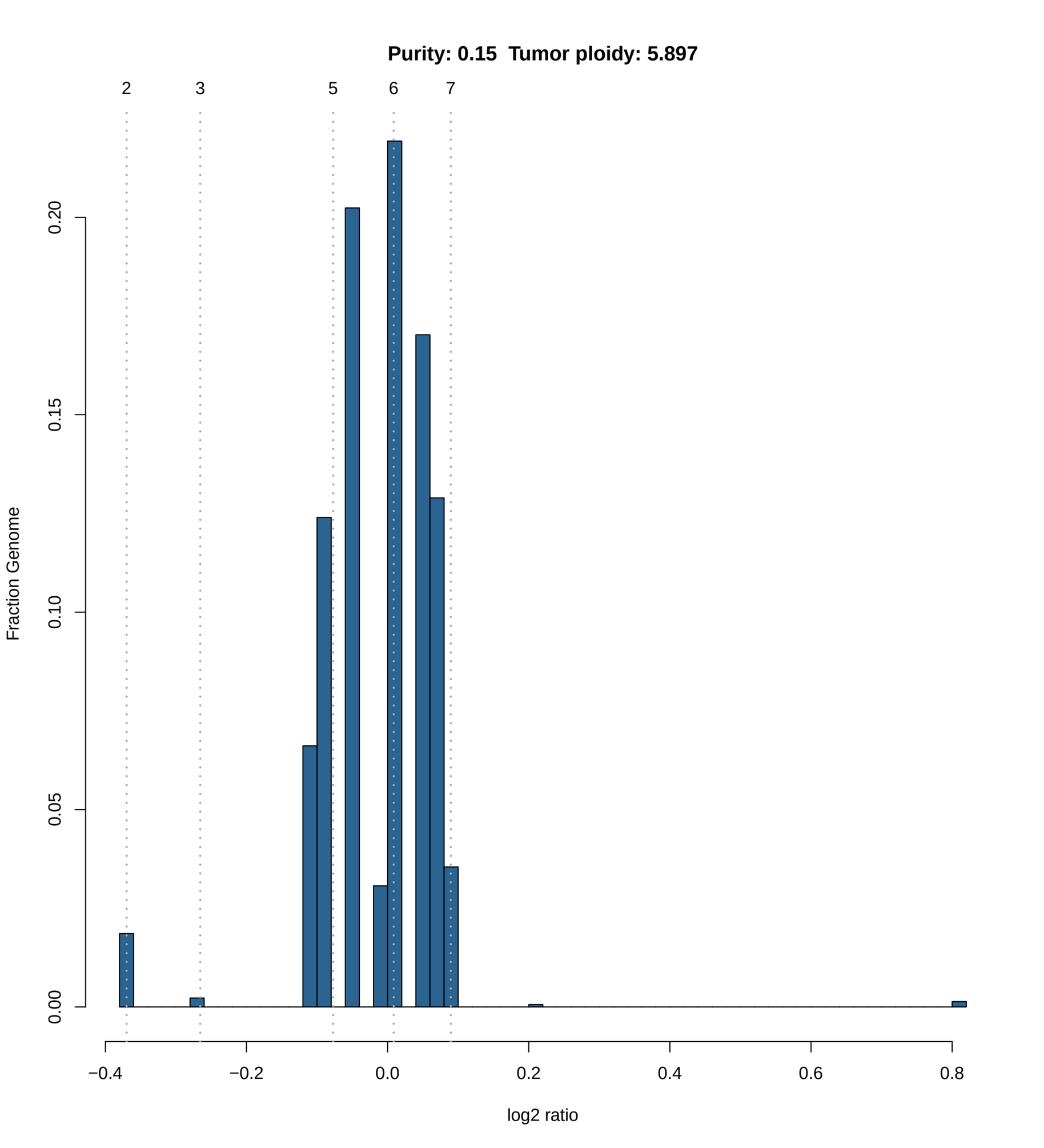

Maximum Likelihood Copy Number
2.0 1.5 1.0 0.5 0.0
0 20 40 60 80 100 120 140
SNV Index

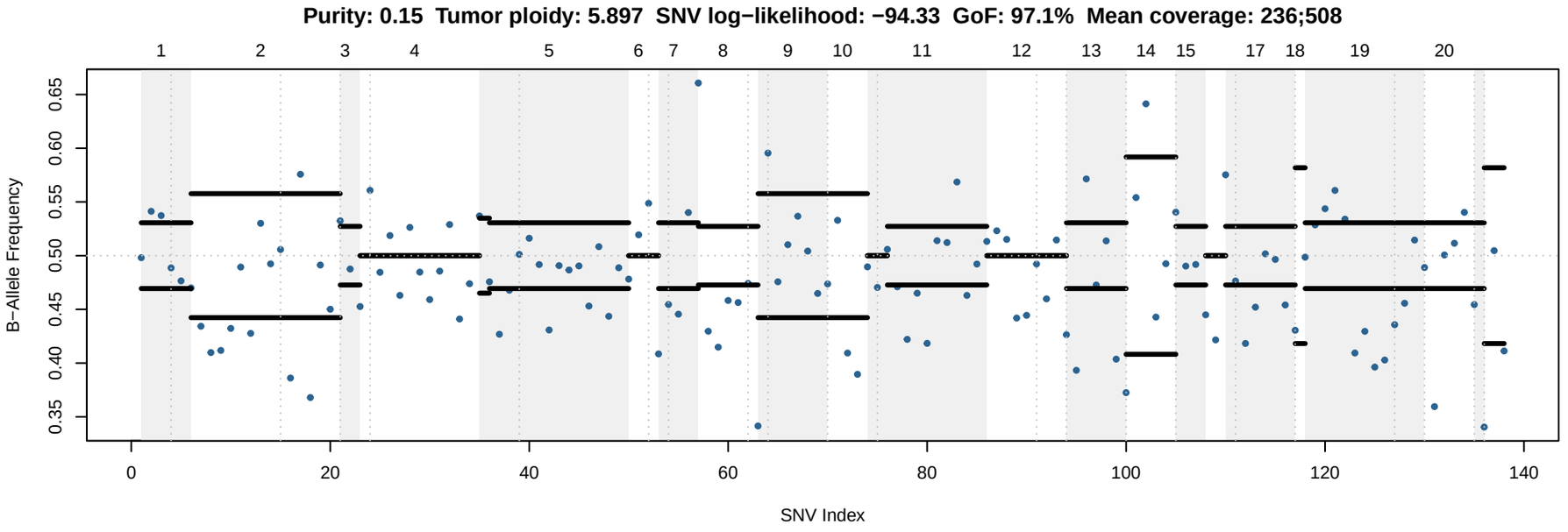

1m1
2m1
1m0
Allelic fraction (germline)
Copy Number log−ratio
0.35
0.40
0.45
0.50
0.55
0.60
0.65
−1.0
−0.5
0.0
0.5

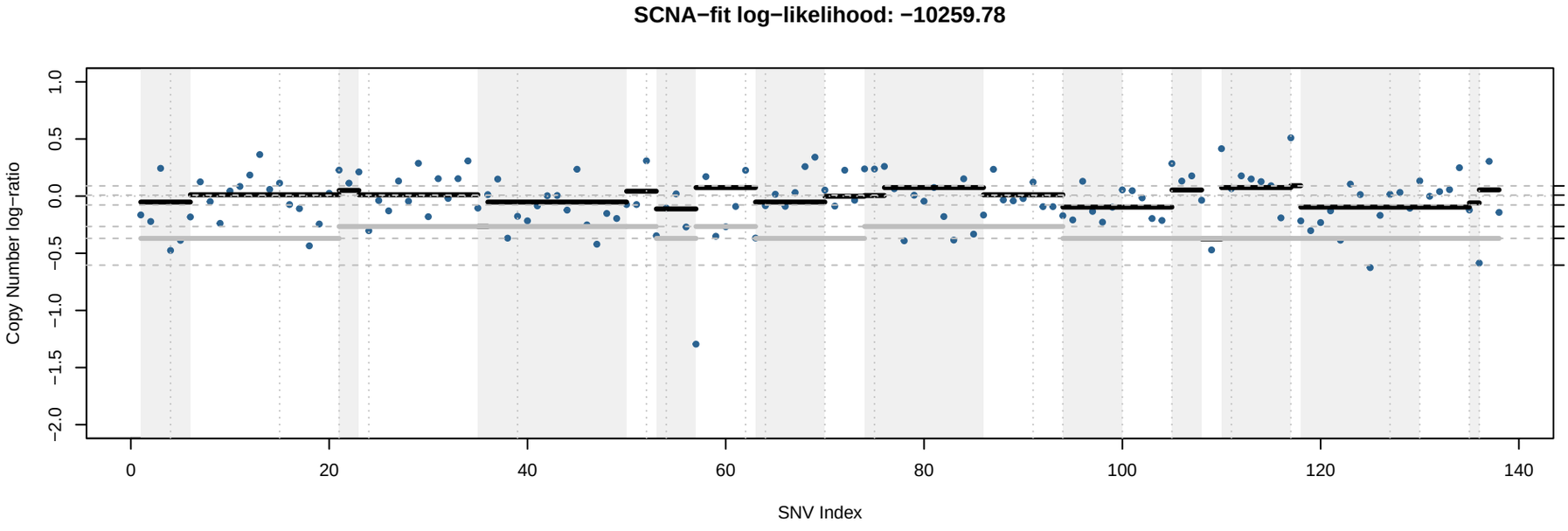

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

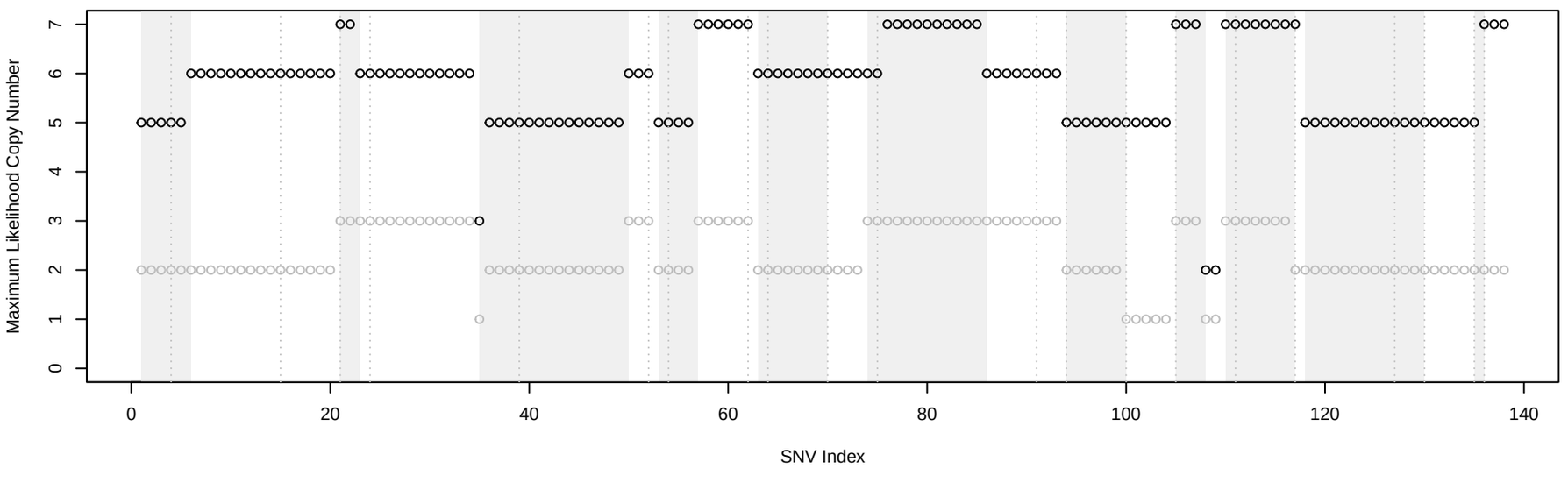

2m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
−1.0
−0.5
0.0
0.5


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

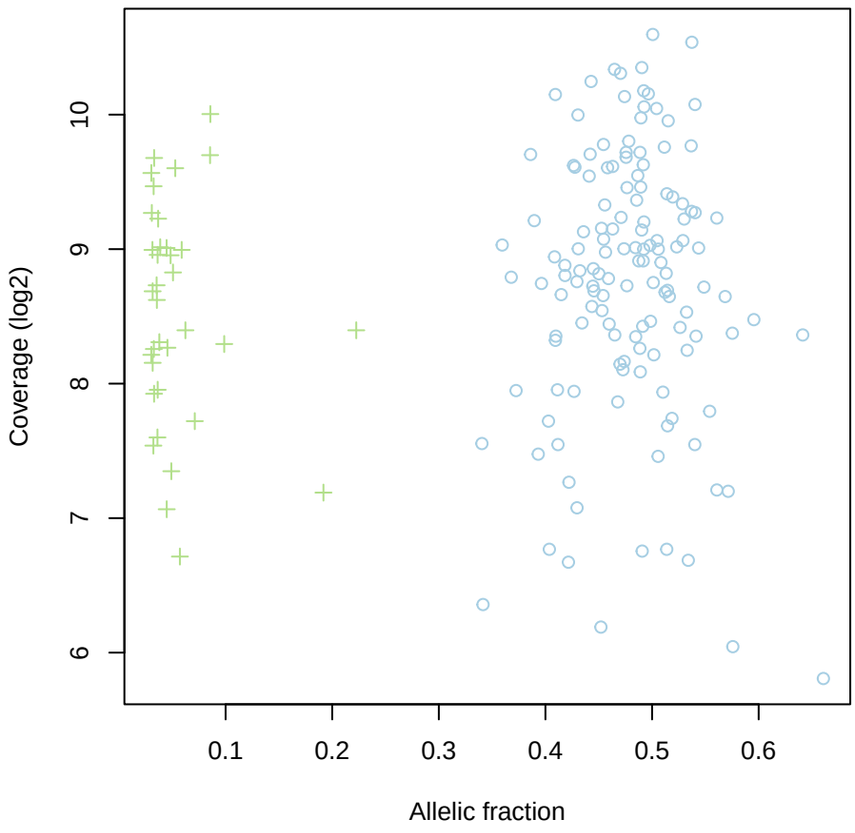

Purity: 0.15 Tumor ploidy: 5.897
2
3
5
6
7
0.00
0.05
0.10
0.15
0.20
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
log2 ratio

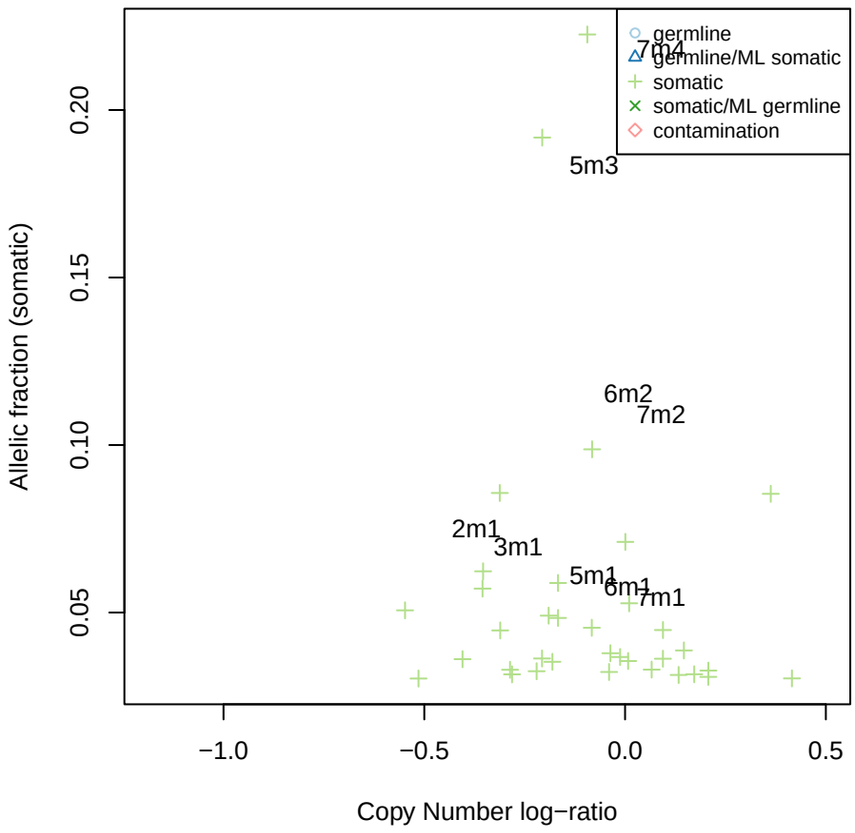

Purity: 0.15 Tumor ploidy: 5.897 SNV log−likelihood: −94.33 GoF: 97.1% Mean coverage: 236;508
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

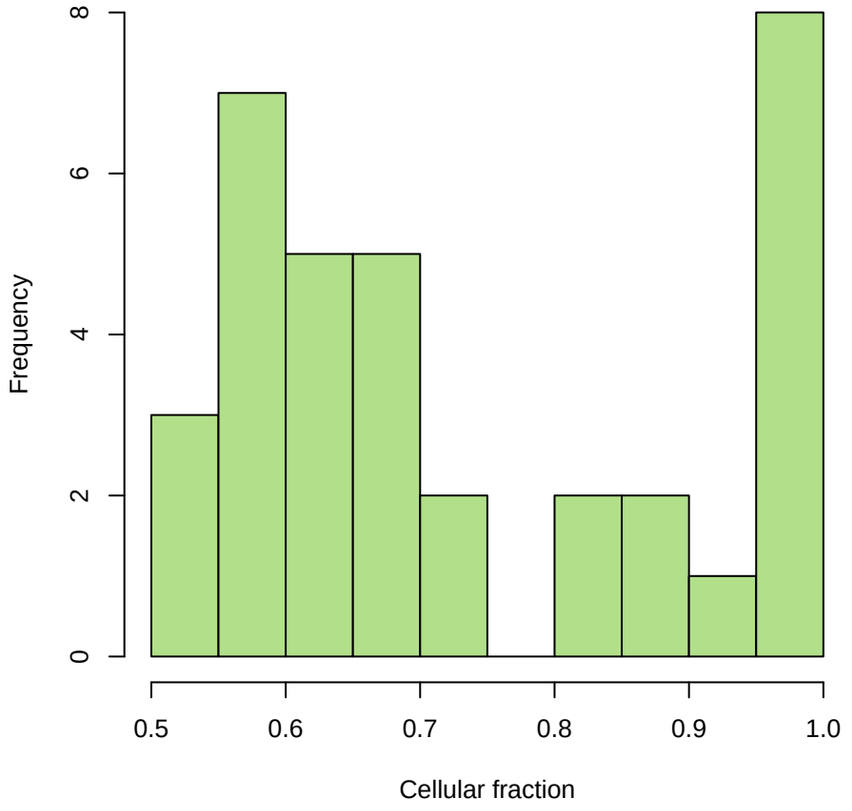

SCNA−fit log−likelihood: −10259.78
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
0 2 5
0 20 40 60 80 100 120 140
SNV Index

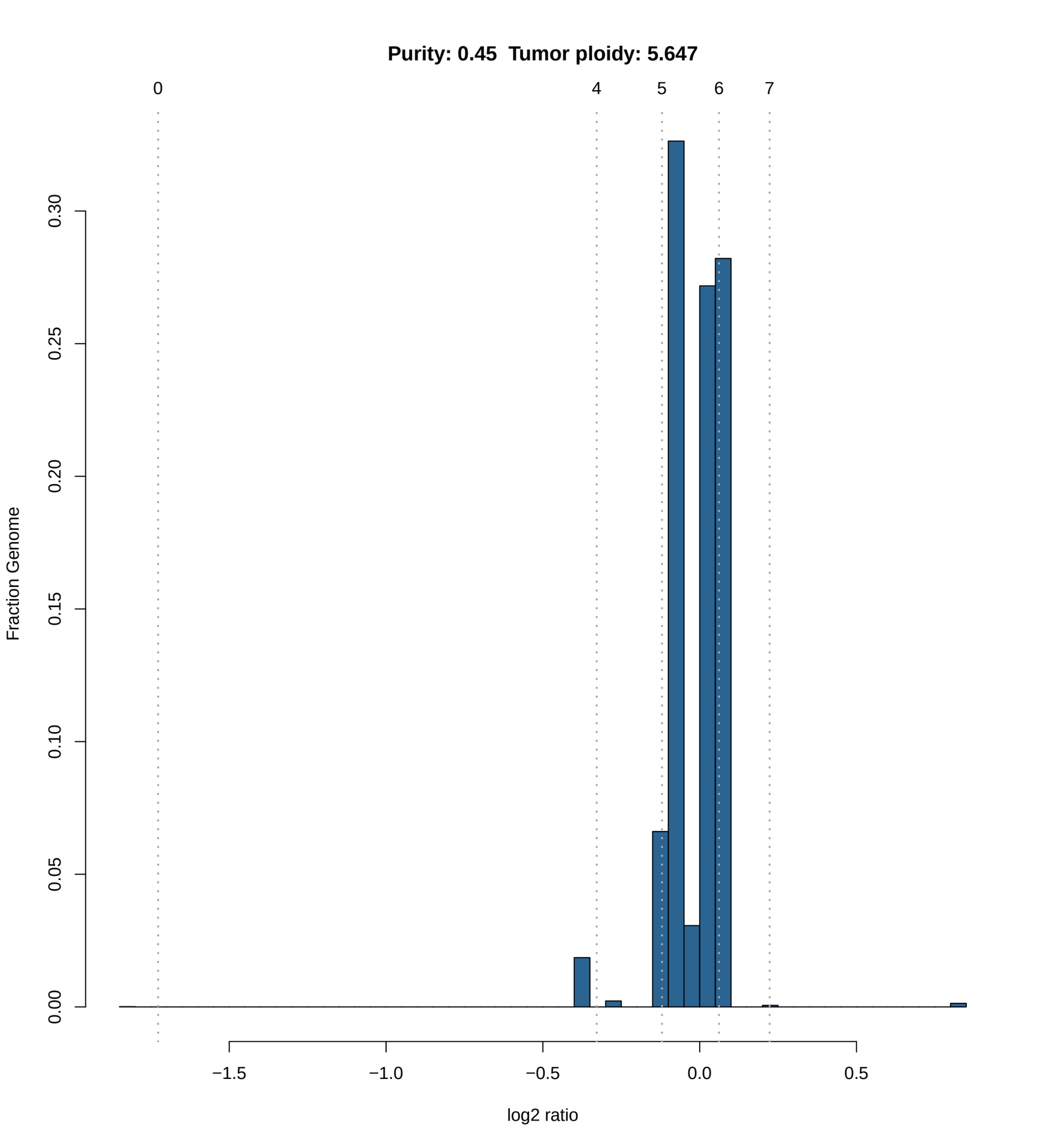

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

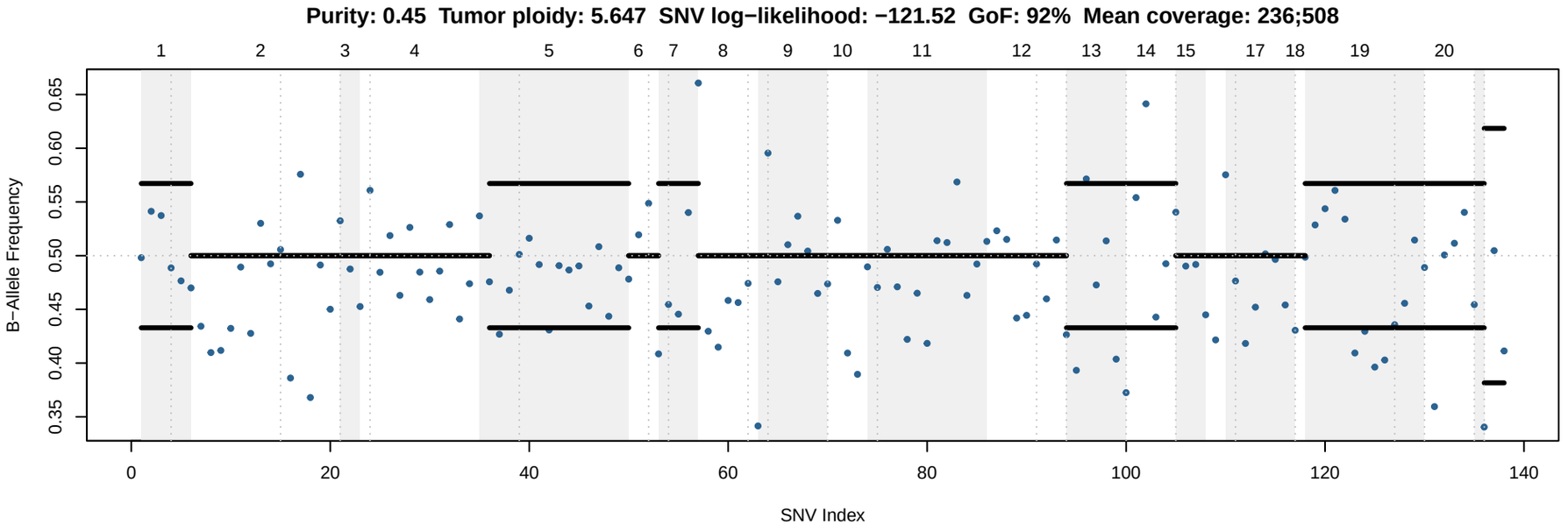
Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
5m4
6m4
3m2
5m3
7m4
2m1
6m3
5m2
7m3
6m2
7m2
5m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

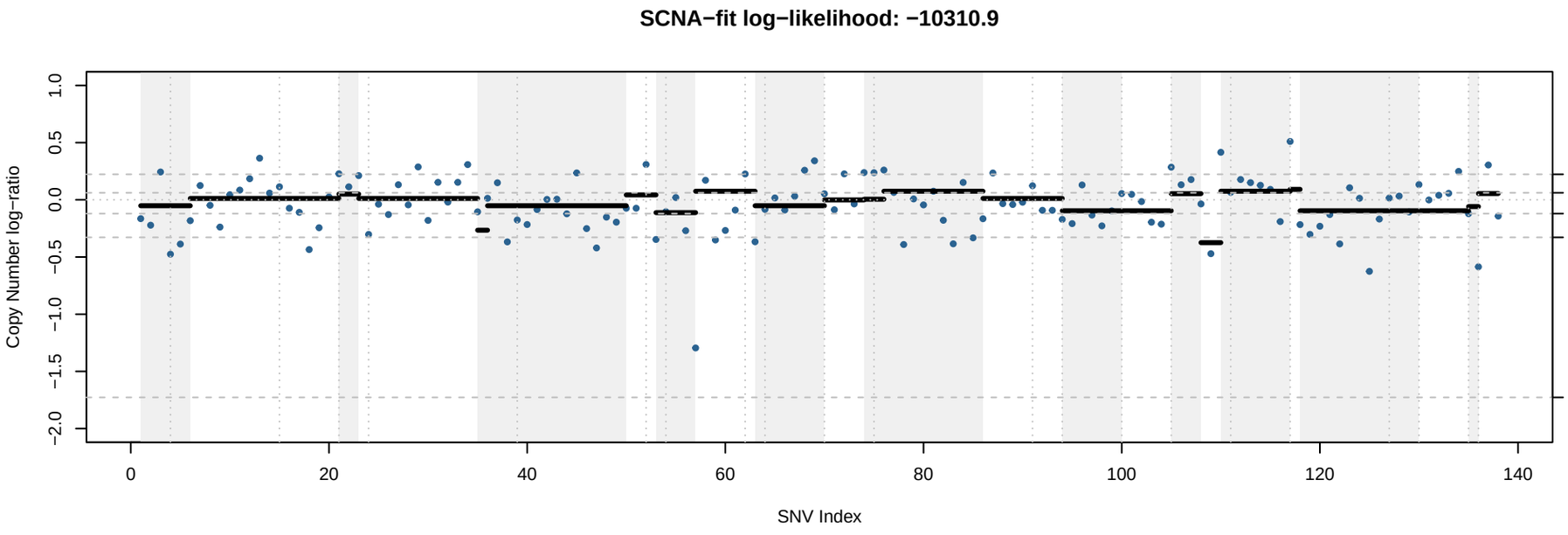

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

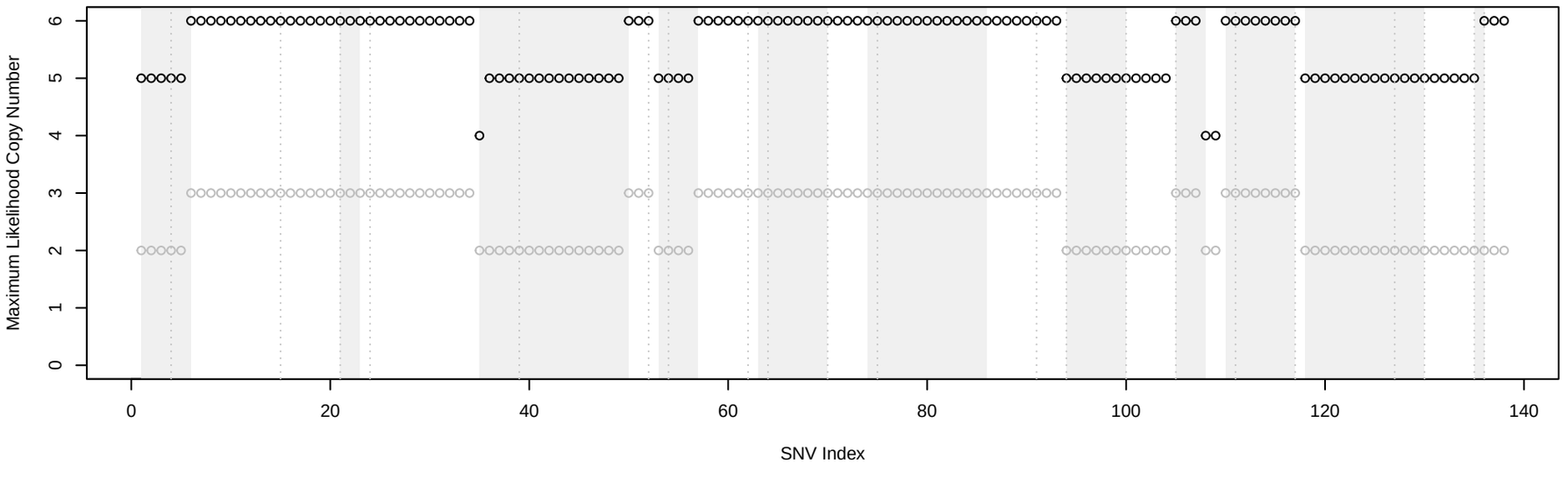

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
7m4
5m3
6m2
7m2
2m1
3m1
5m1
6m1
7m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio


Frequency
0
2
4
6
8
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

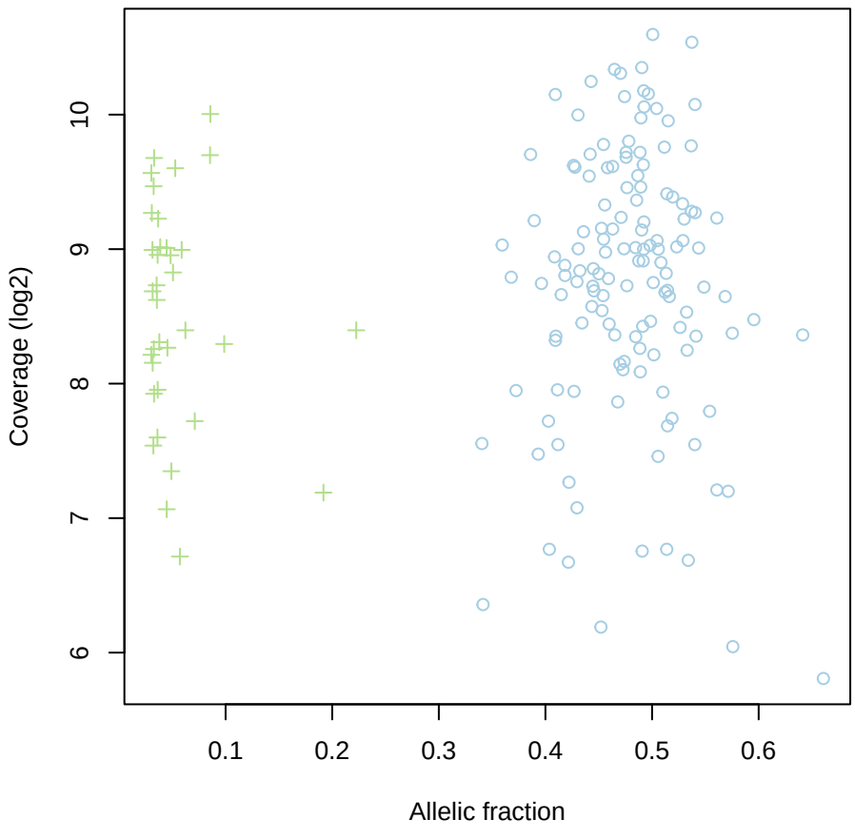

Purity: 0.45 Tumor ploidy: 5.647
0
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

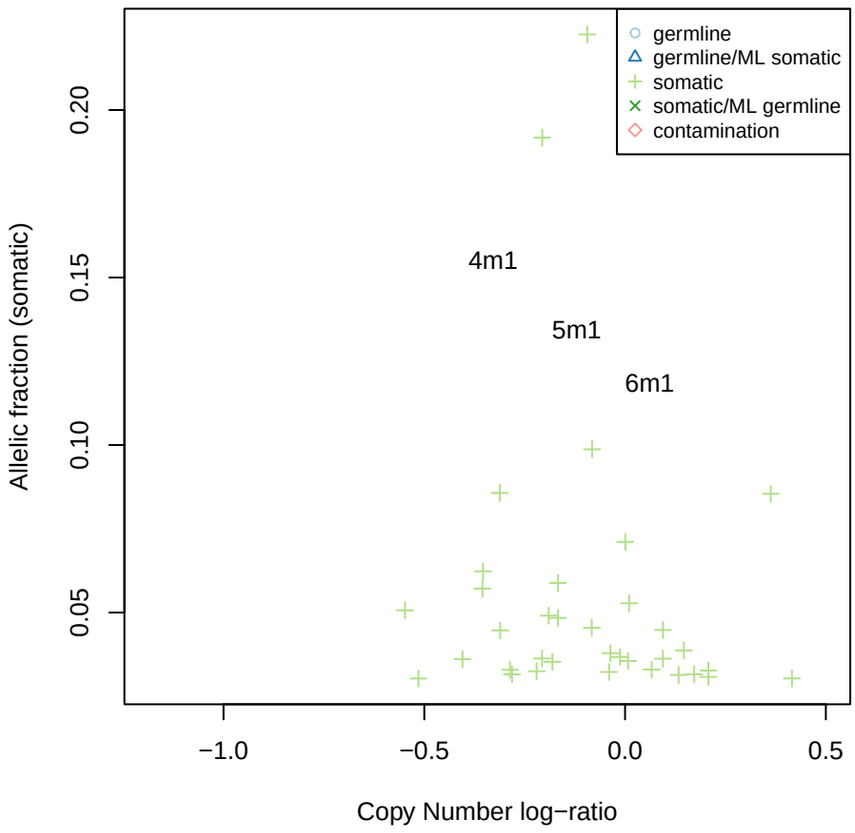

Purity: 0.45 Tumor ploidy: 5.647 SNV log−likelihood: −121.52 GoF: 92% Mean coverage: 236;508
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

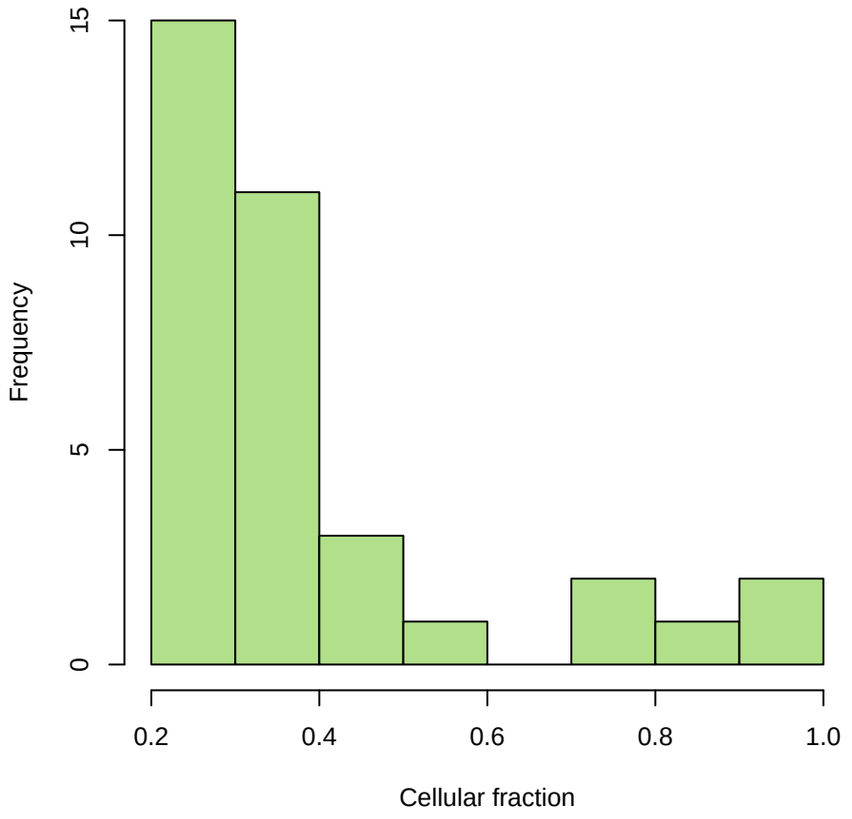

SCNA−fit log−likelihood: −10310.9
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
6 4 0
0 20 40 60 80 100 120 140
SNV Index

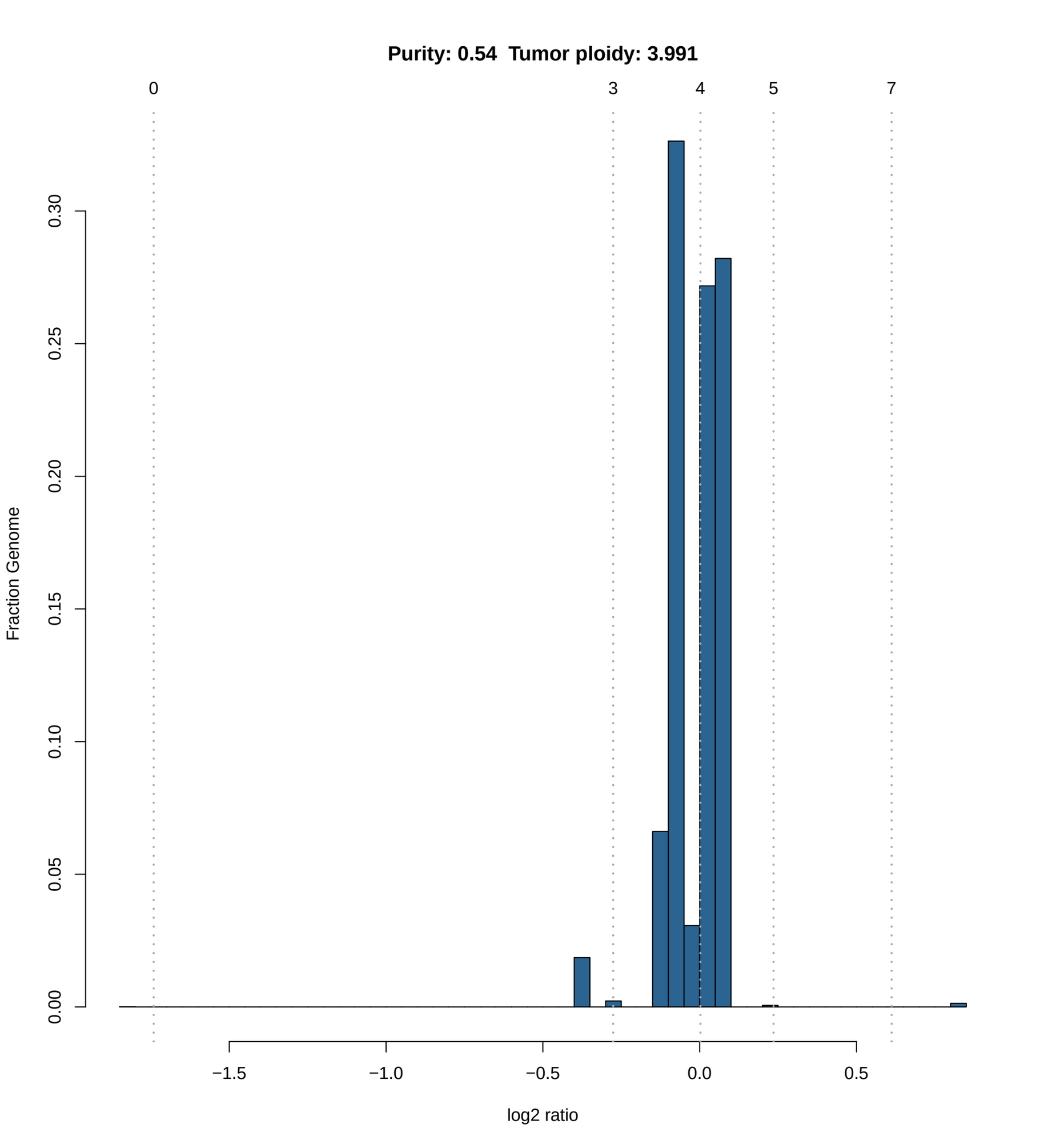

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

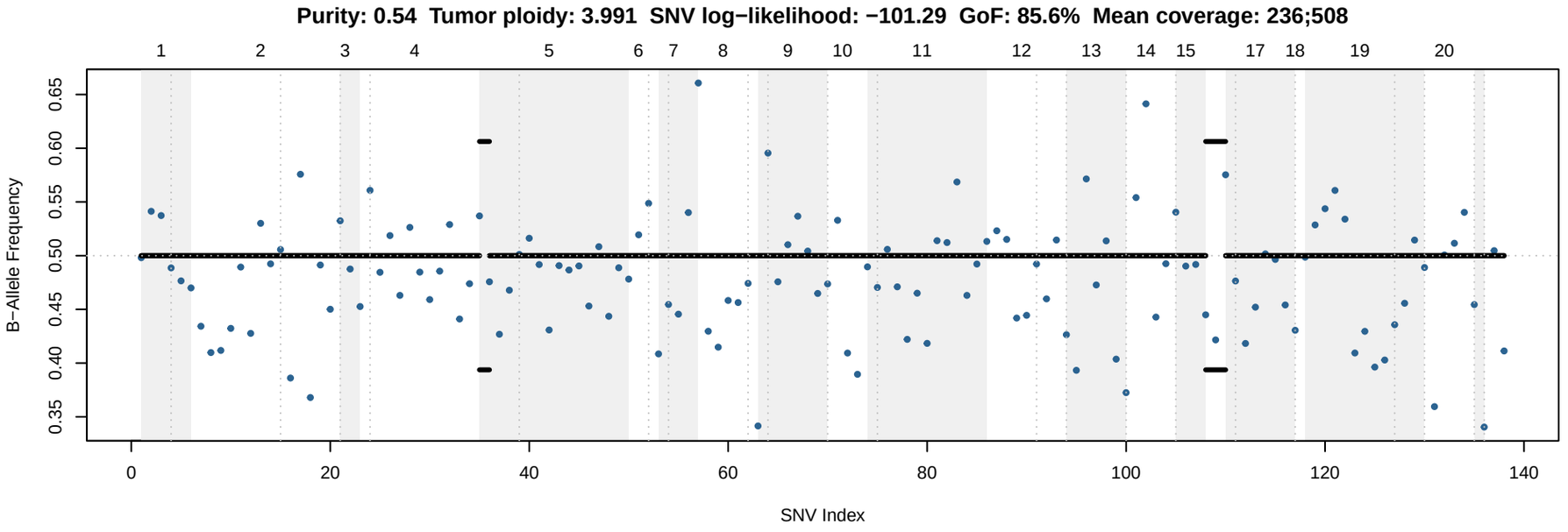
Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
6m4
5m3
4m2
6m3
5m2
6m2
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

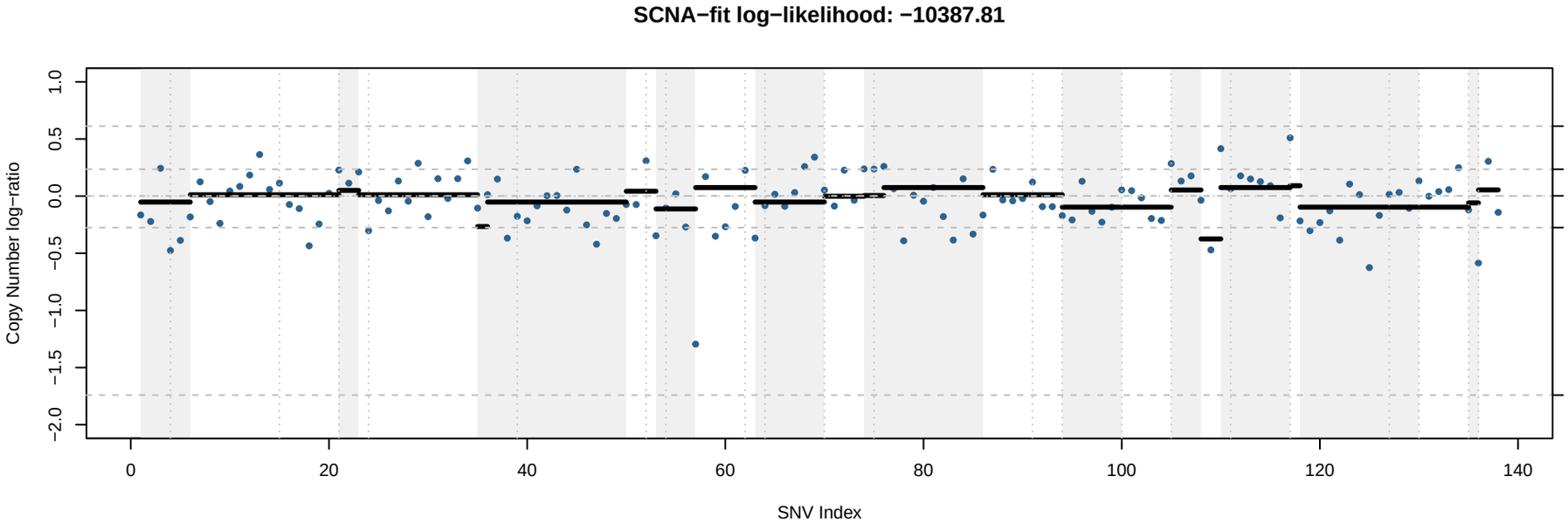

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

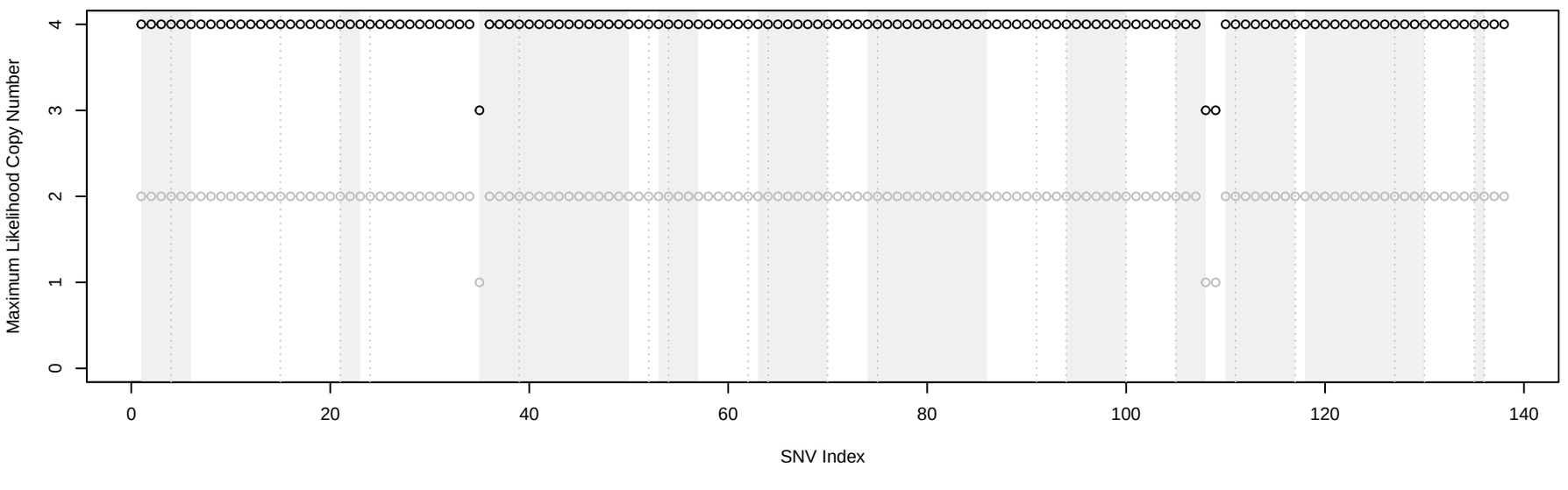

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
4m1
5m1
6m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

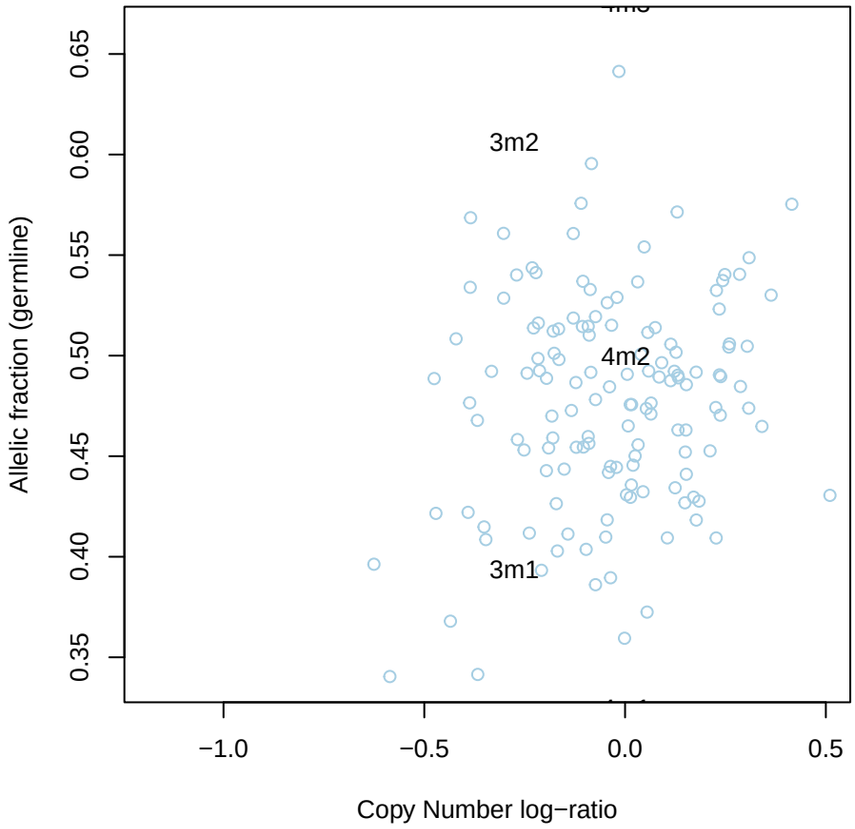

Frequency
0
5
10
15
0.2
0.4
0.6
0.8
1.0
Cellular fraction

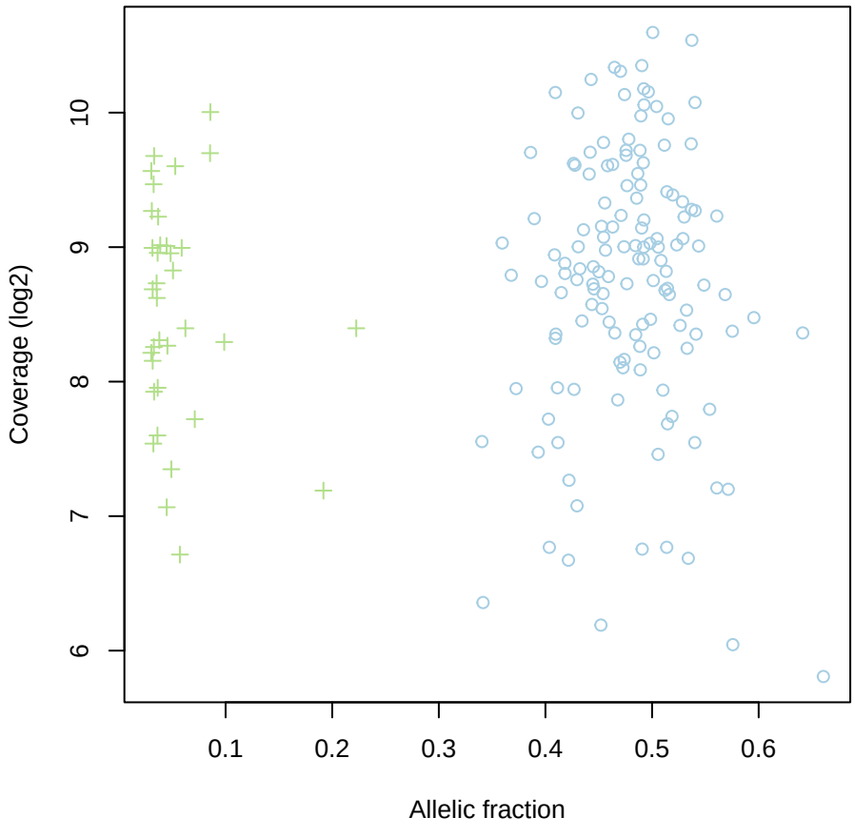

Purity: 0.54 Tumor ploidy: 3.991
0
3
4
5
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

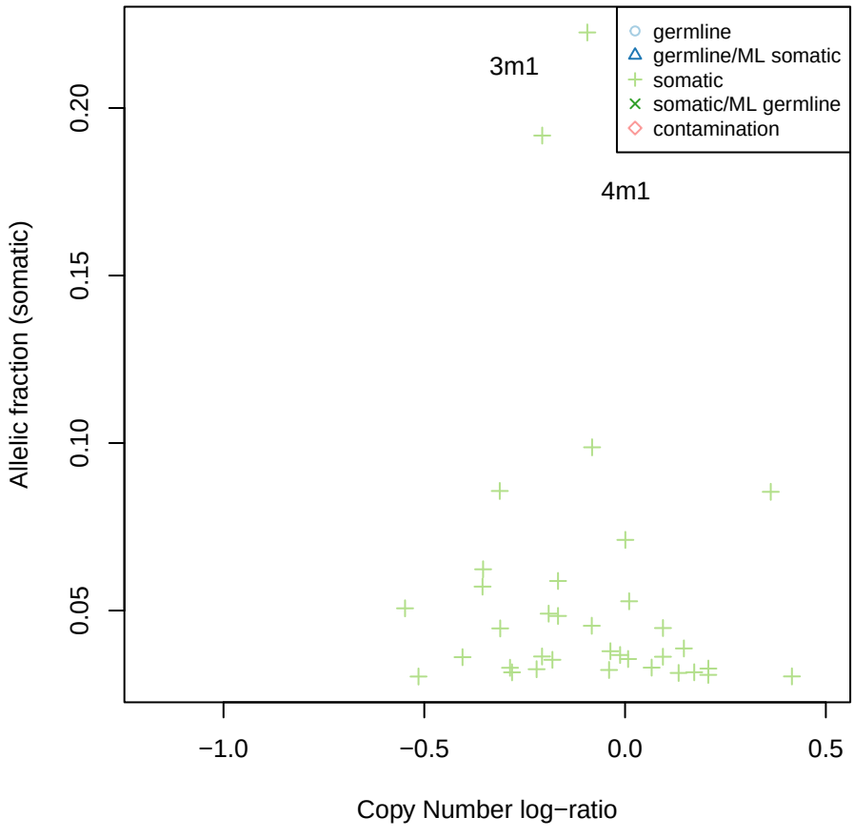

Purity: 0.54 Tumor ploidy: 3.991 SNV log−likelihood: −101.29 GoF: 85.6% Mean coverage: 236;508
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

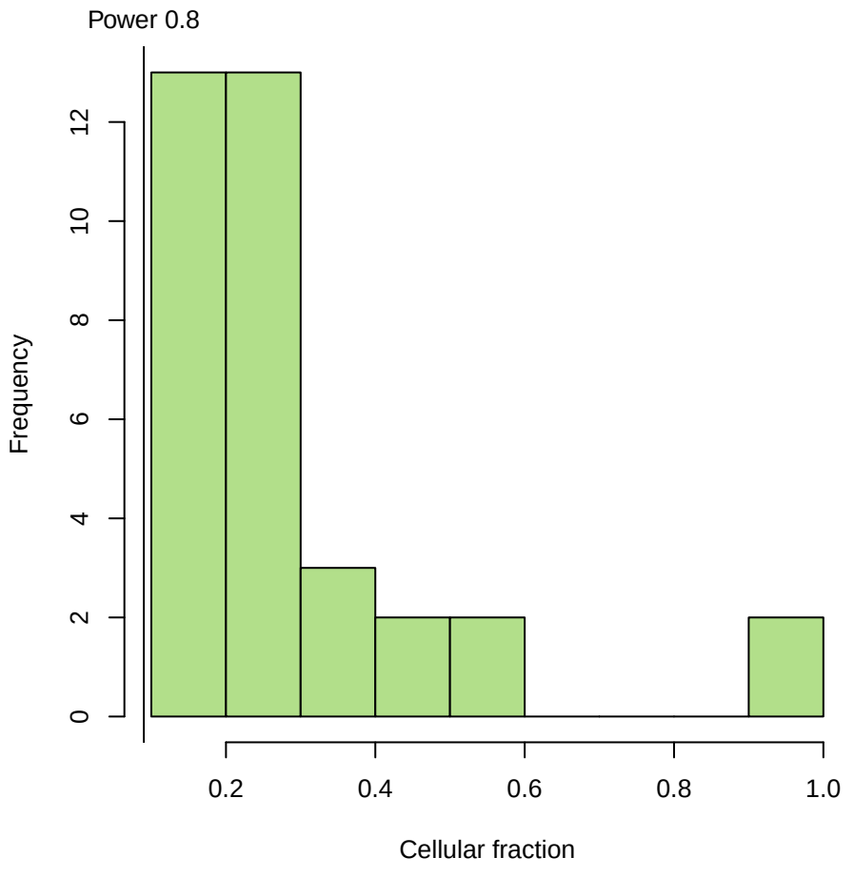

SCNA−fit log−likelihood: −10387.81
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
7 5 4 3 0
0 20 40 60 80 100 120 140
SNV Index

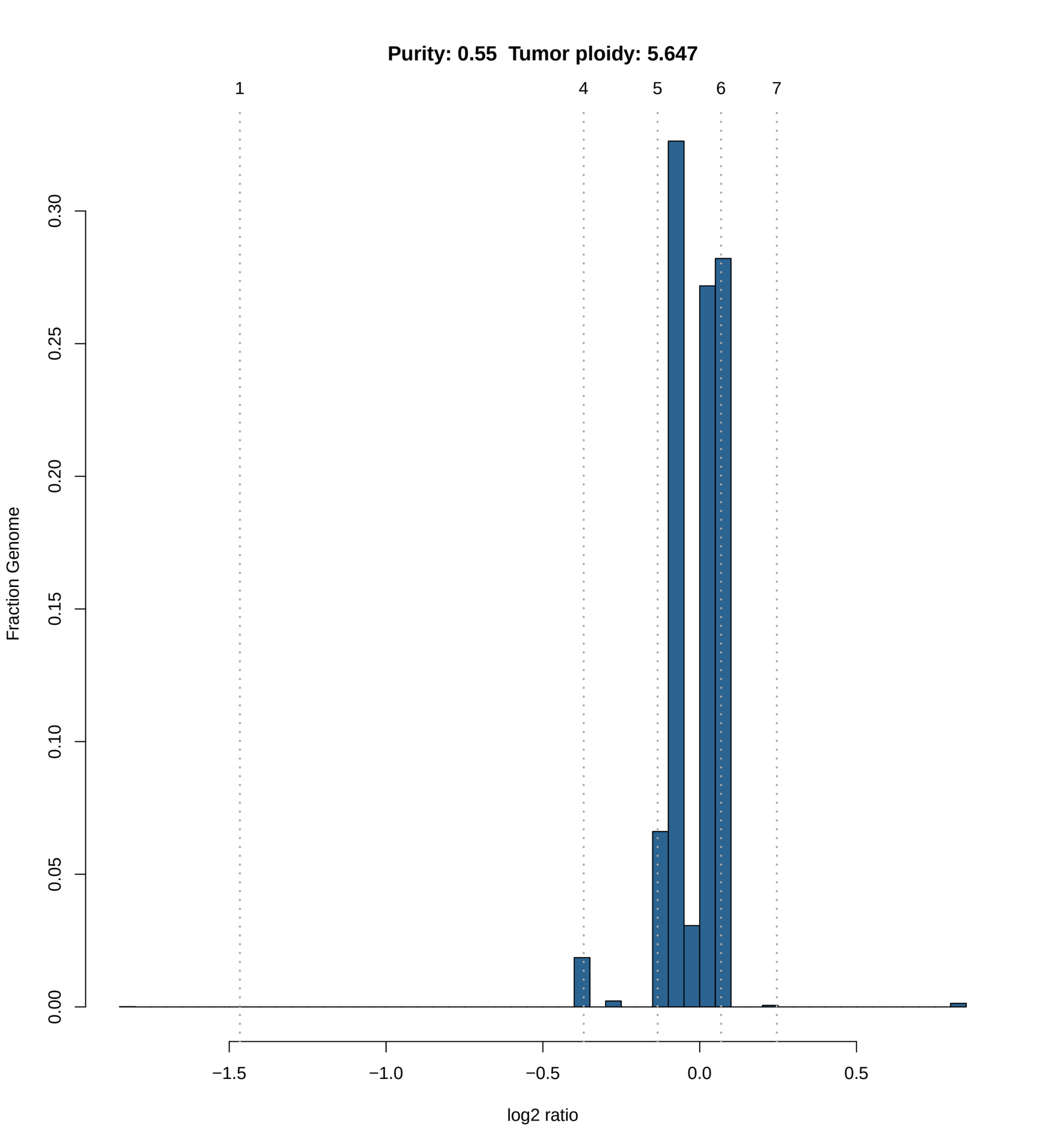

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120 140
SNV Index

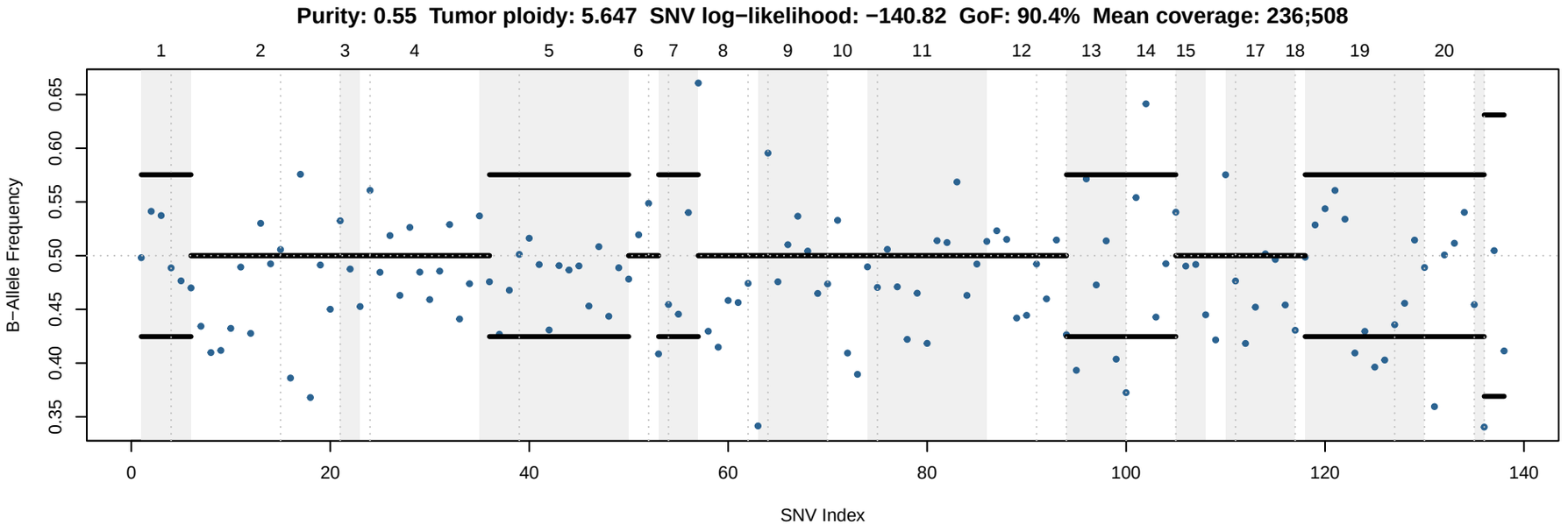

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
3m2
4m2
3m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

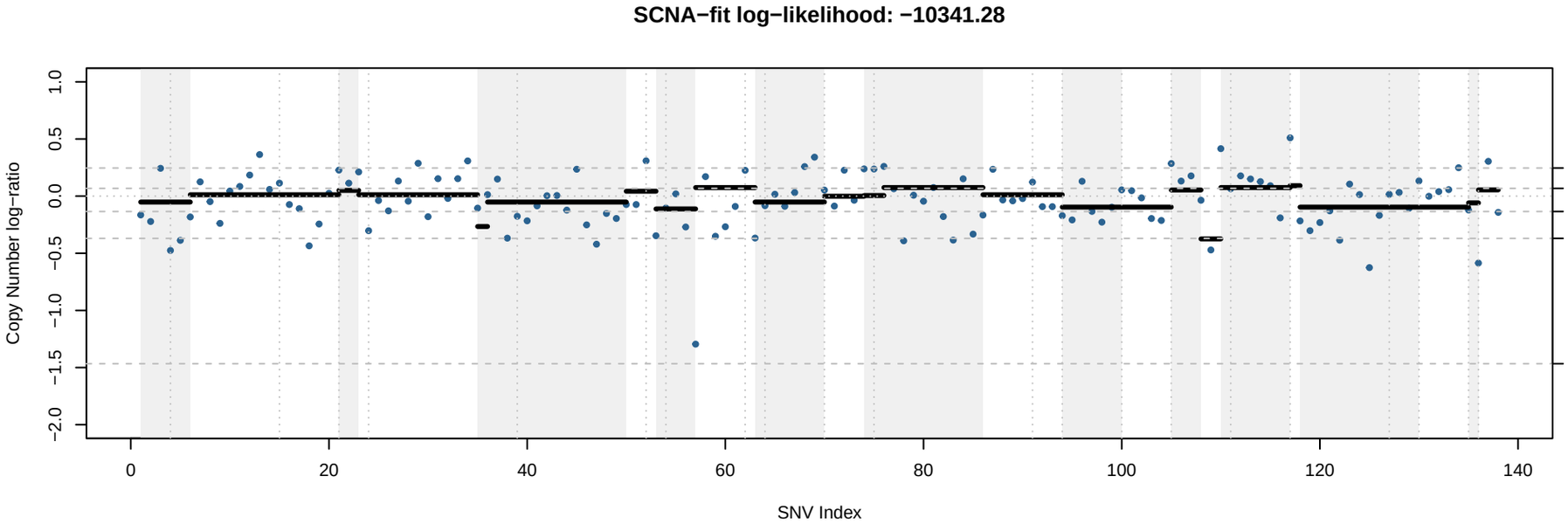

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

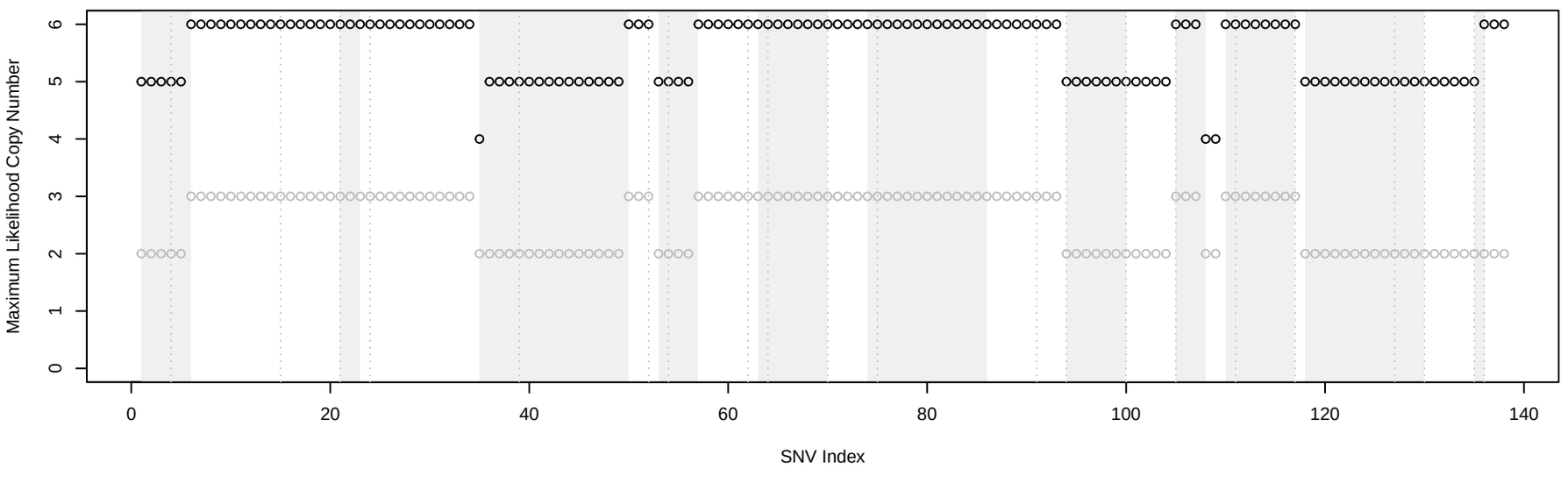

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

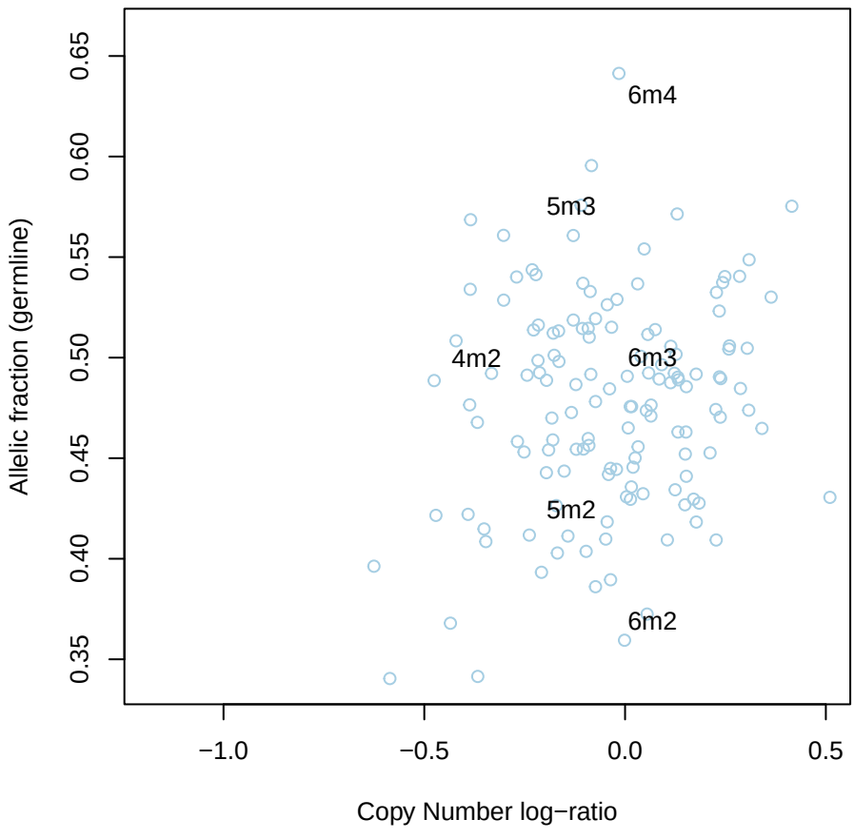

Power 0.8
Frequency
0
2
4
6
8
10
12
0.2
0.4
0.6
0.8
1.0
Cellular fraction

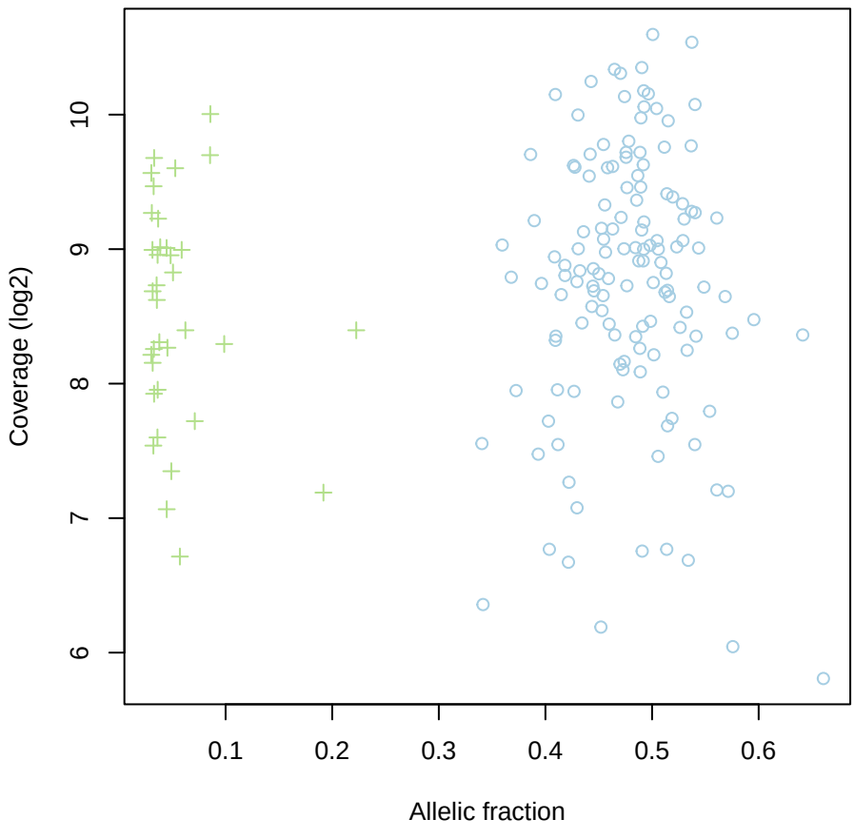

Purity: 0.55 Tumor ploidy: 5.647
1
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

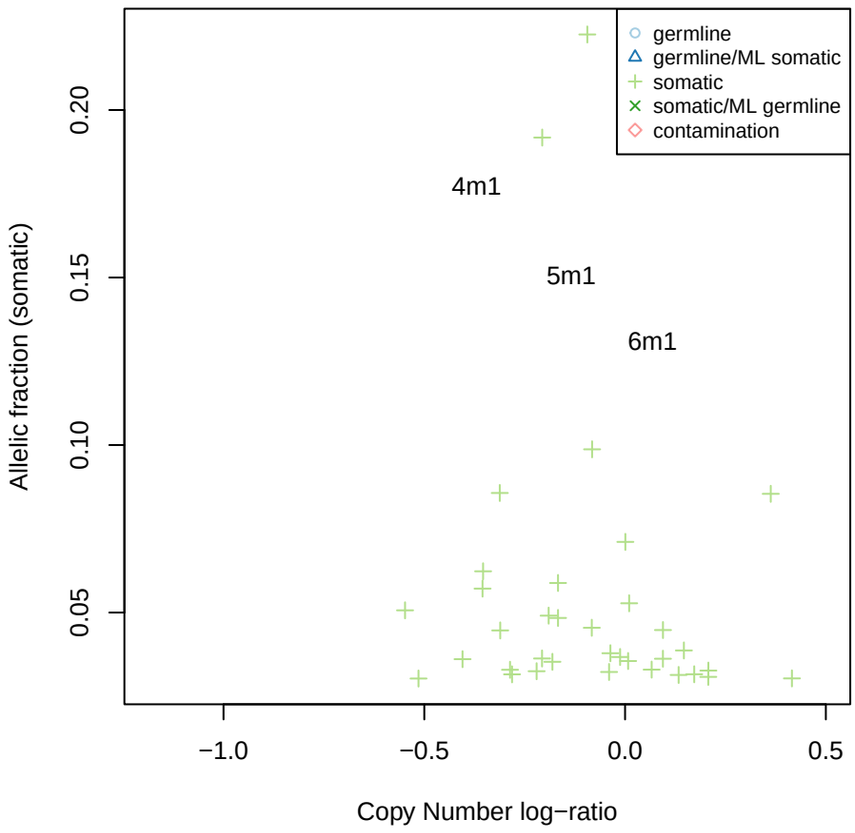

Purity: 0.55 Tumor ploidy: 5.647 SNV log−likelihood: −140.82 GoF: 90.4% Mean coverage: 236;508
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

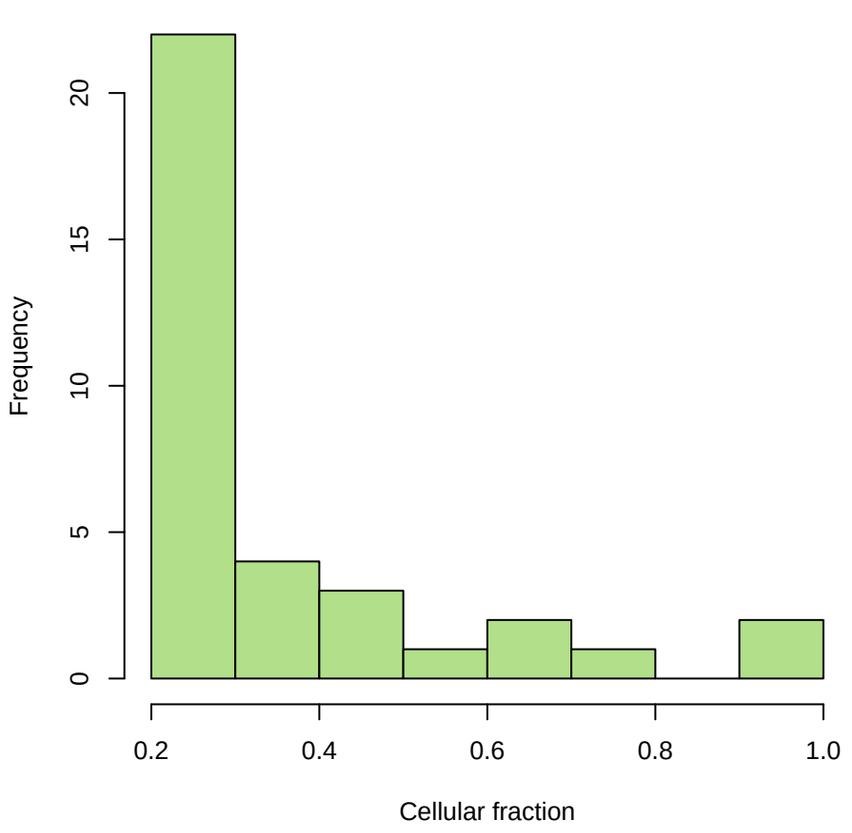

SCNA−fit log−likelihood: −10341.28
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
7 5 4 1
0 20 40 60 80 100 120 140
SNV Index

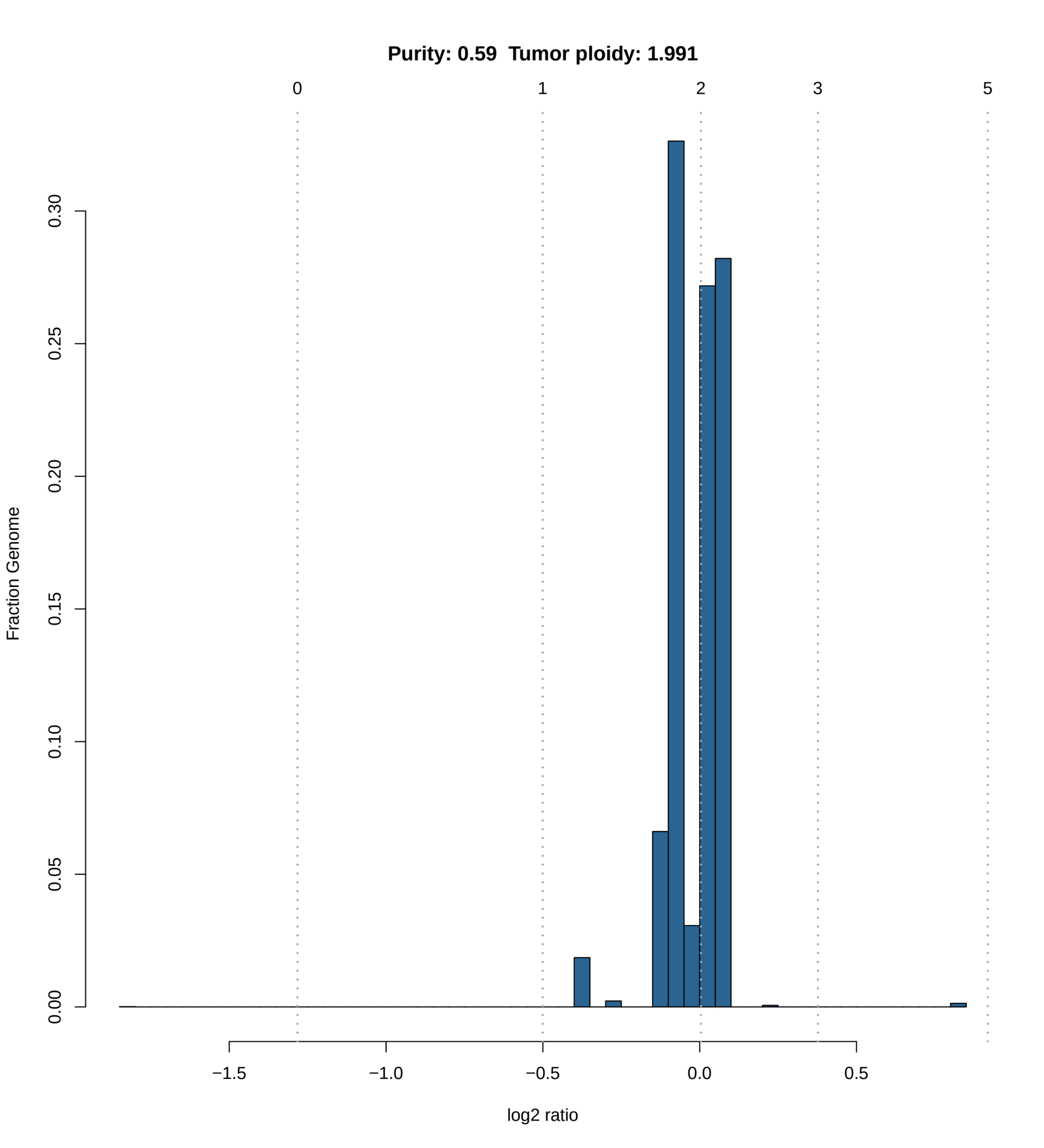

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

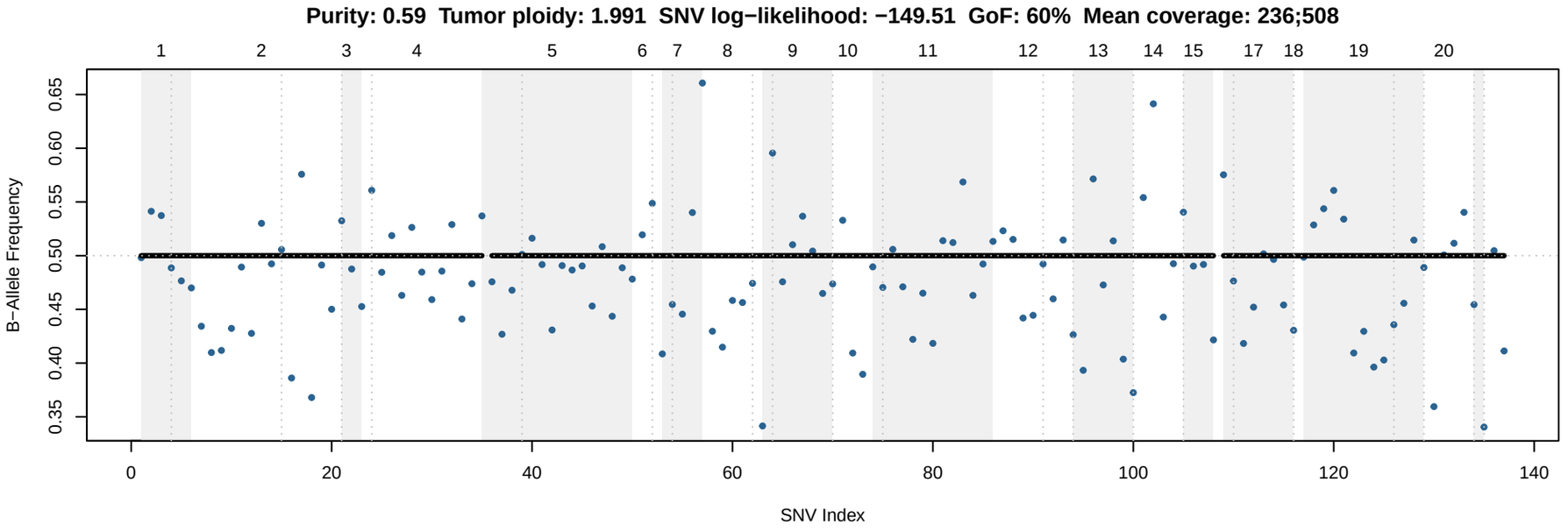

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
6m4
5m3
4m2
6m3
5m2
6m2
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

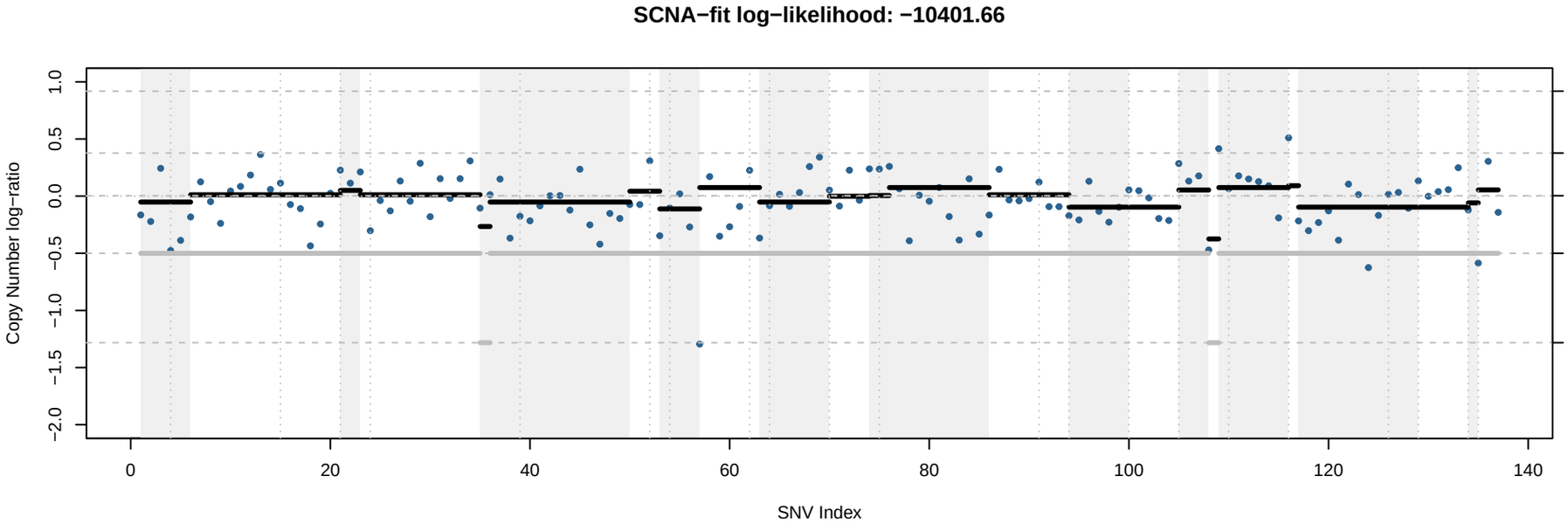

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

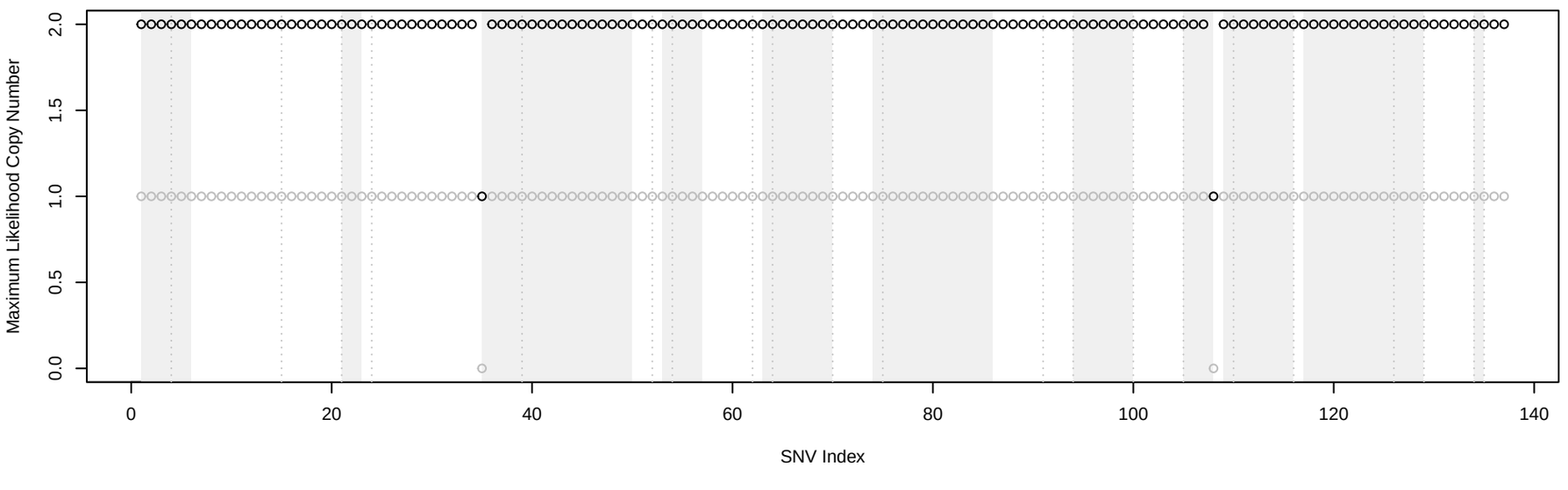

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
4m1
5m1
6m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

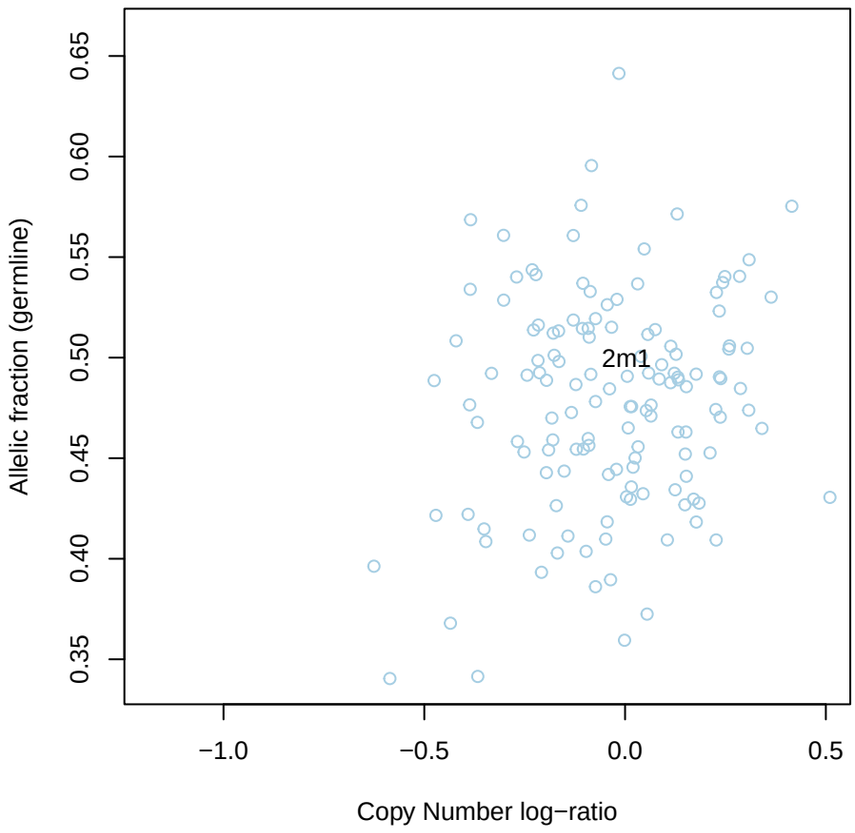

Frequency
0
5
10
15
20
0.2
0.4
0.6
0.8
1.0
Cellular fraction

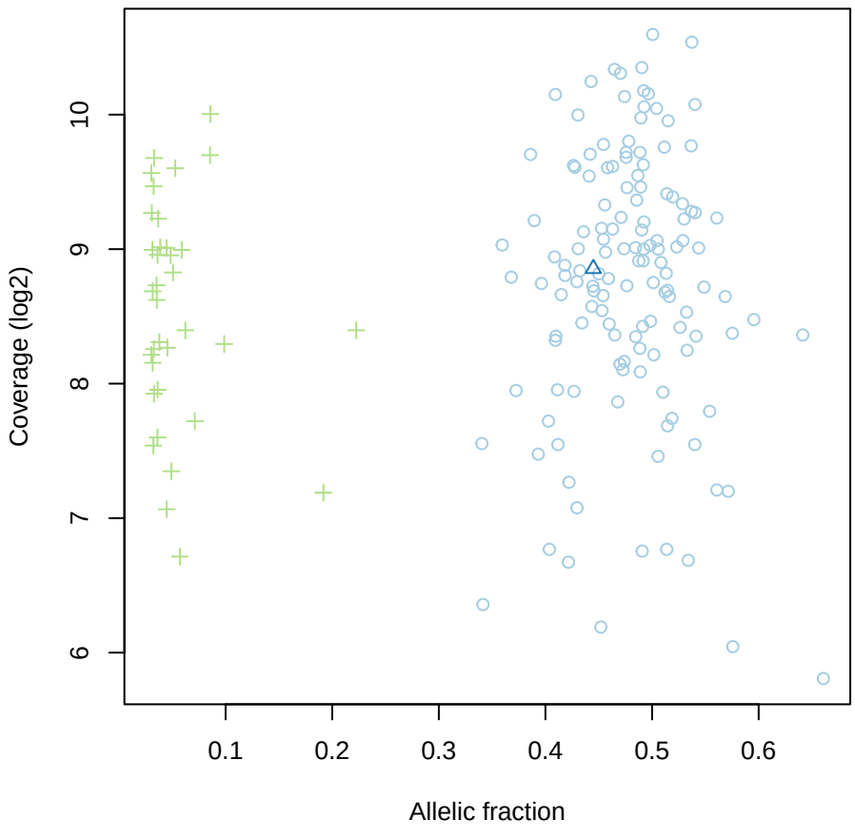

Purity: 0.59 Tumor ploidy: 1.991
0
1
2
3
5
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

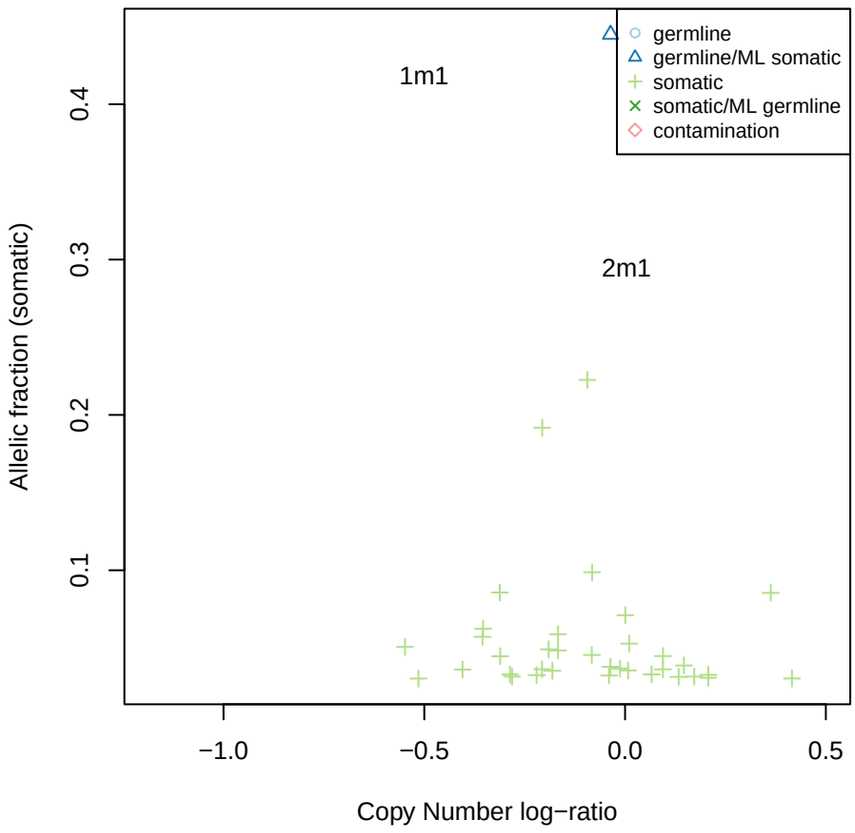

Purity: 0.59 Tumor ploidy: 1.991 SNV log−likelihood: −149.51 GoF: 60% Mean coverage: 236;508
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

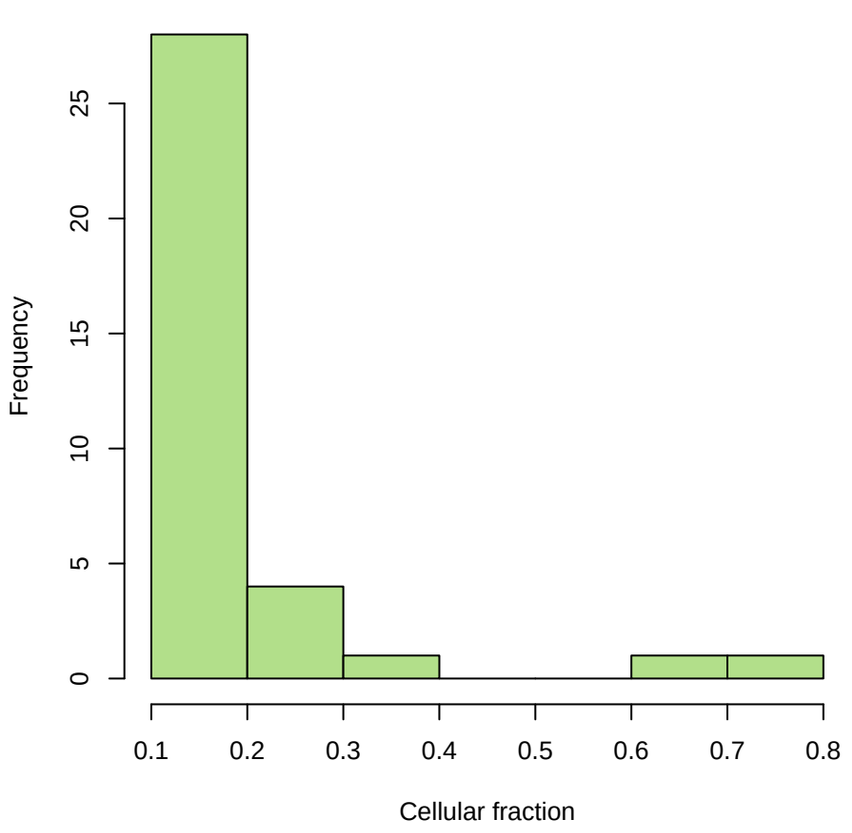

SCNA−fit log−likelihood: −10401.66
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 5
0 20 40 60 80 100 120 140
SNV Index

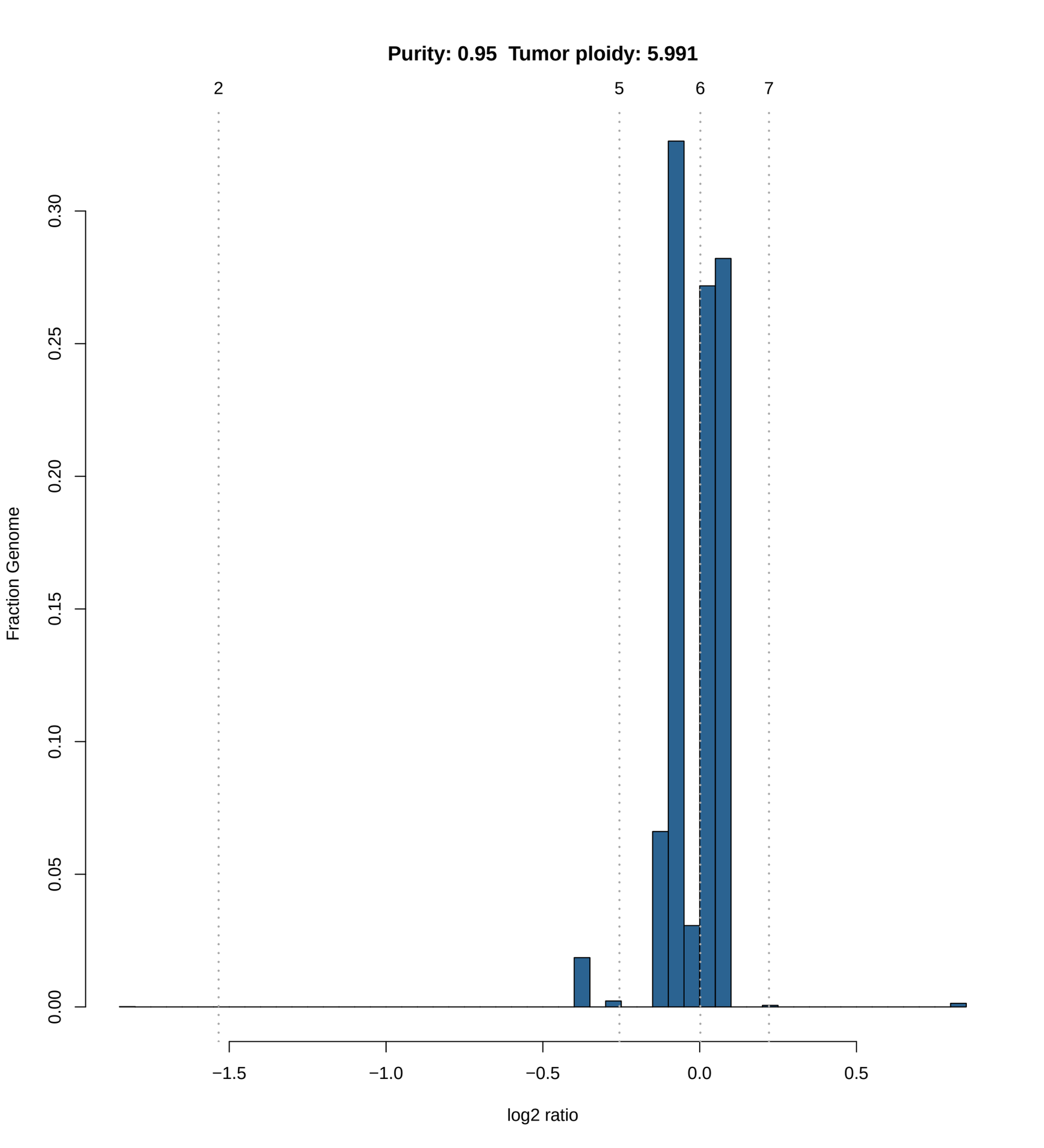

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 20 40 60 80 100 120 140
SNV Index

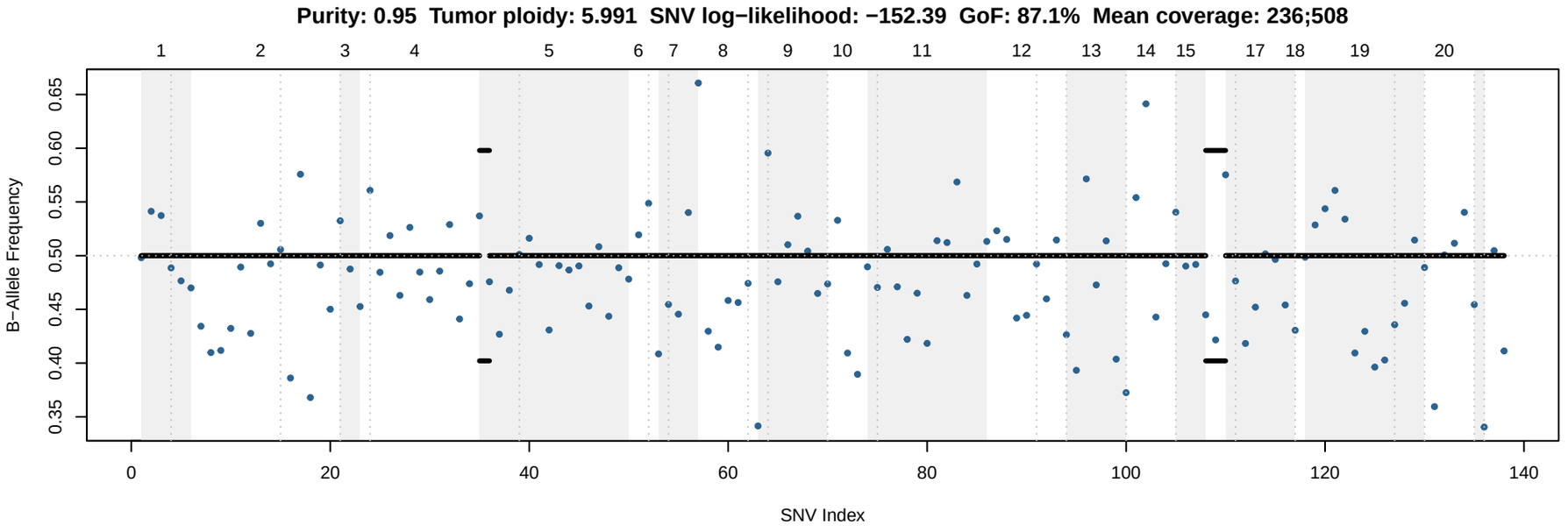

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
2m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

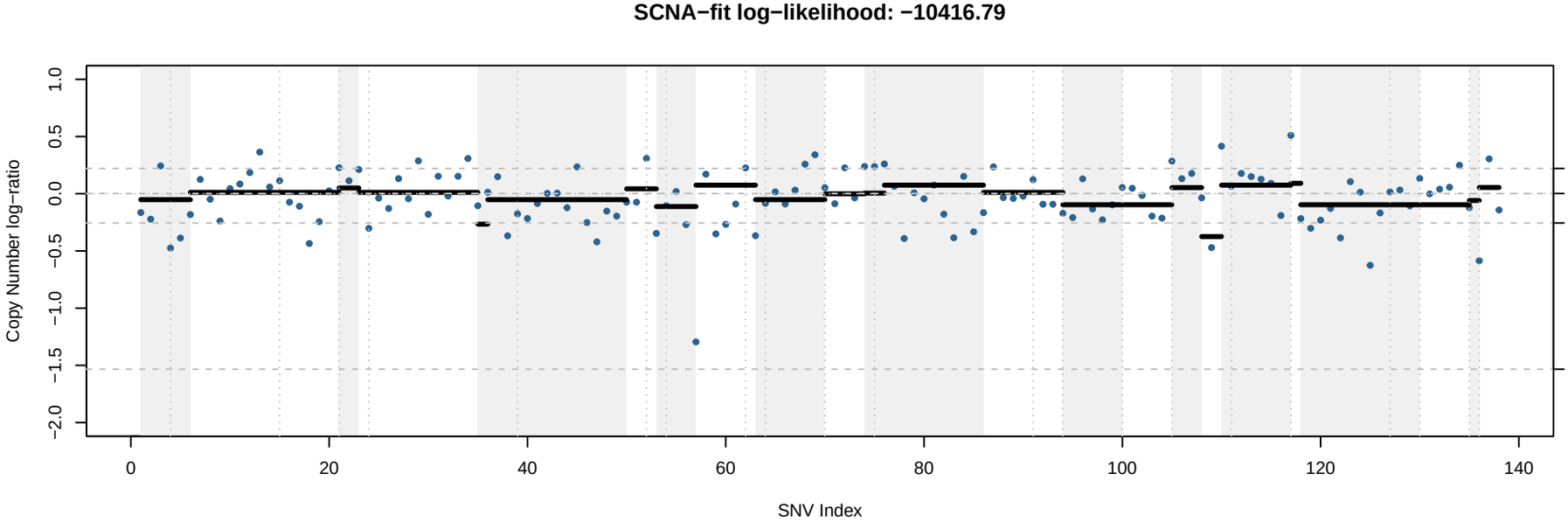

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

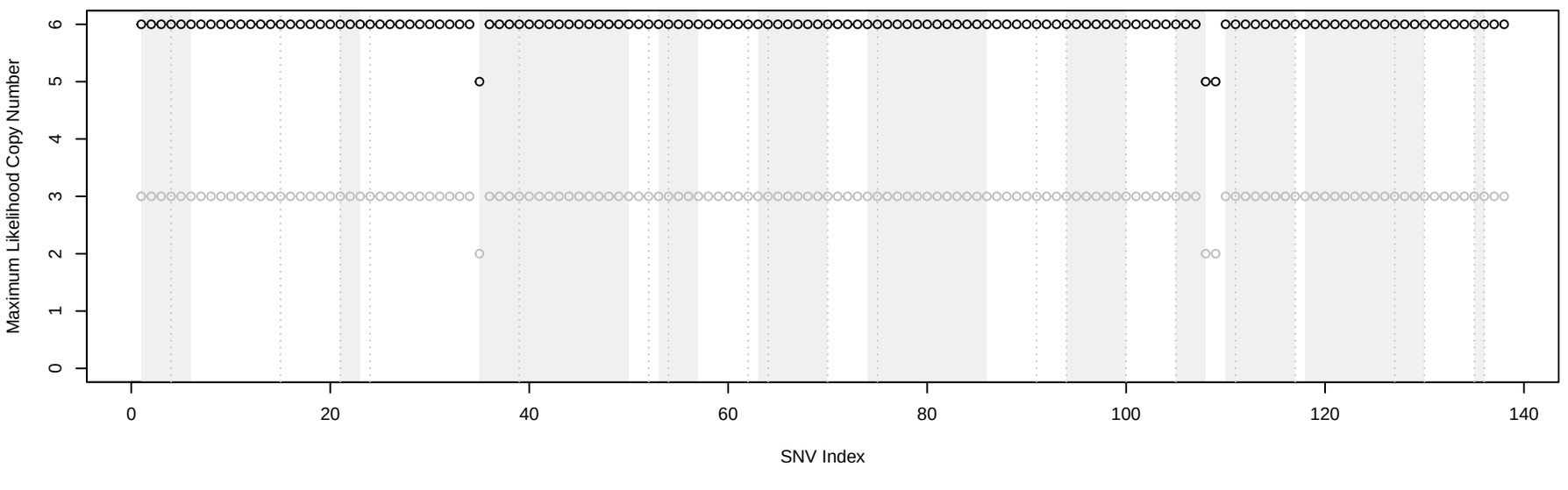

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
Allelic fraction (somatic)
0.1
0.2
0.3
0.4
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

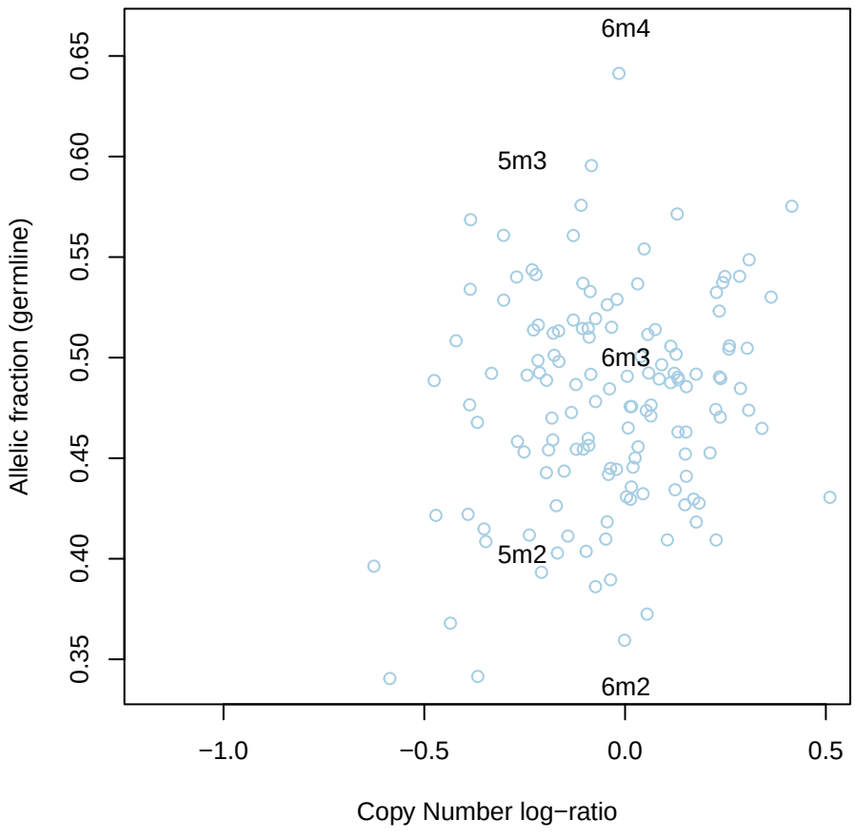

Frequency
0
5
10
15
20
25
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
Cellular fraction

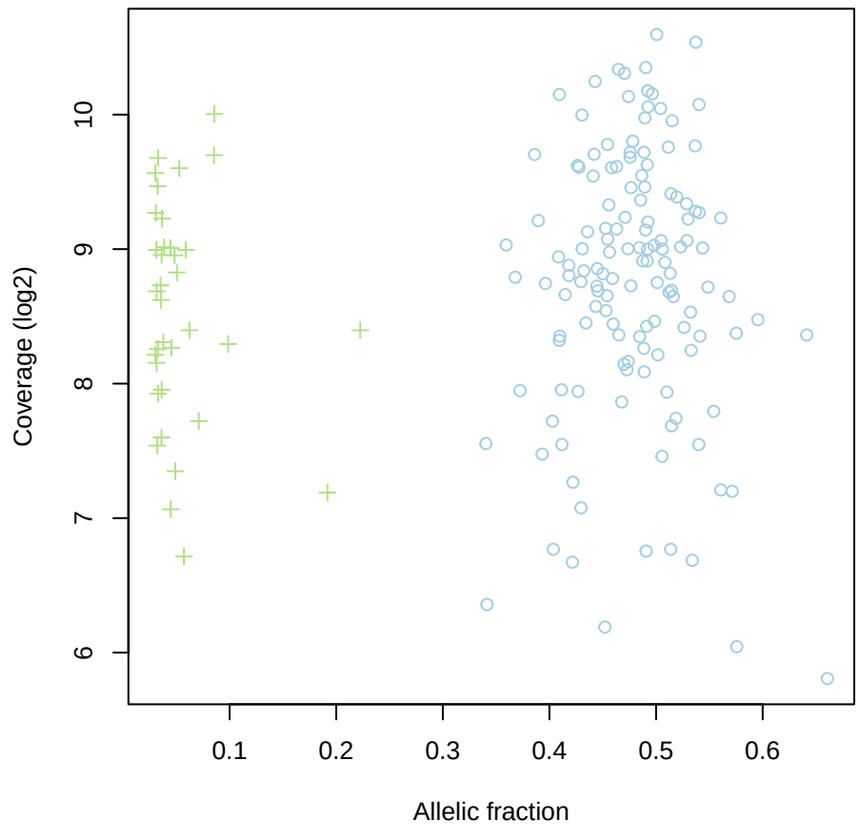

Purity: 0.95 Tumor ploidy: 5.991
2
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

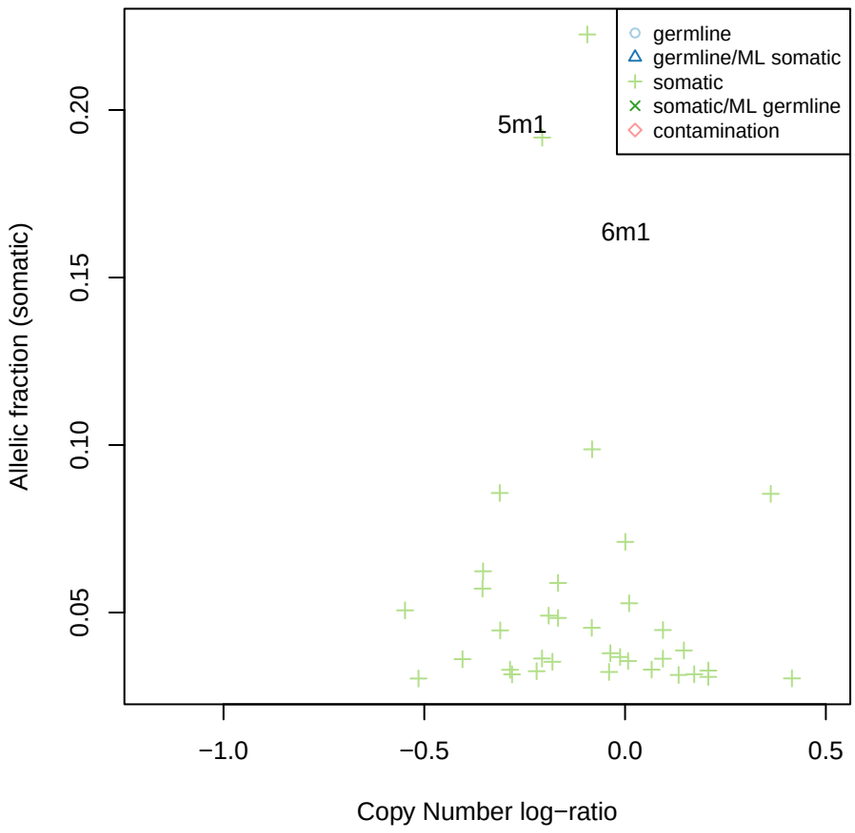

Purity: 0.95 Tumor ploidy: 5.991 SNV log−likelihood: −152.39 GoF: 87.1% Mean coverage: 236;508
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

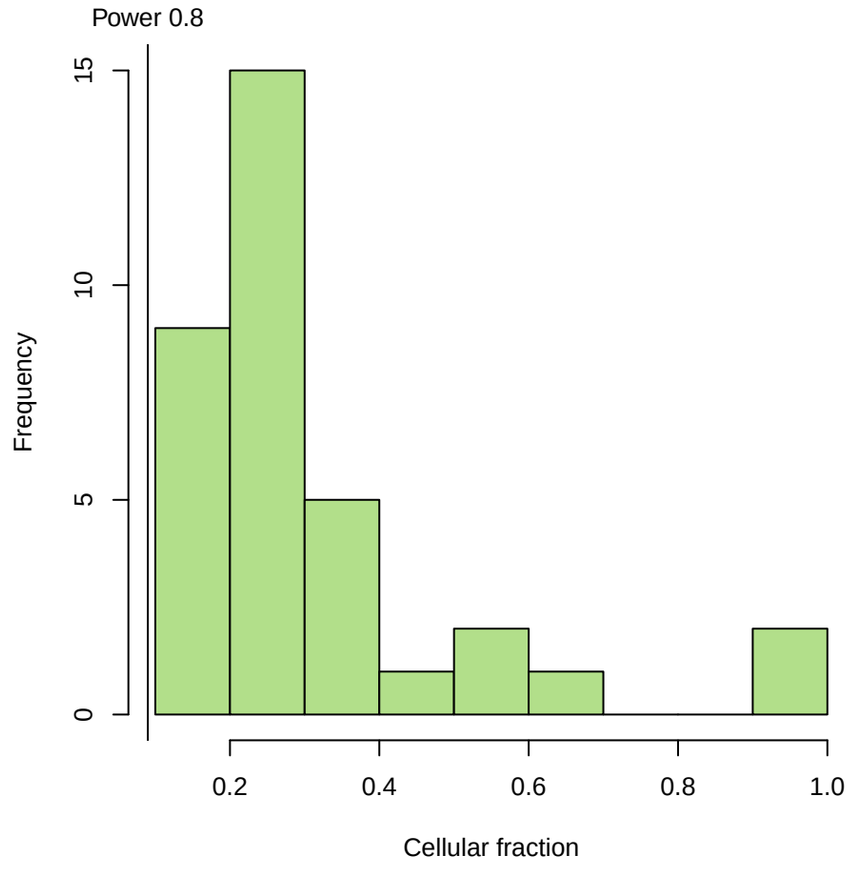

SCNA−fit log−likelihood: −10416.79
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
7 6 5 2
0 20 40 60 80 100 120 140
SNV Index

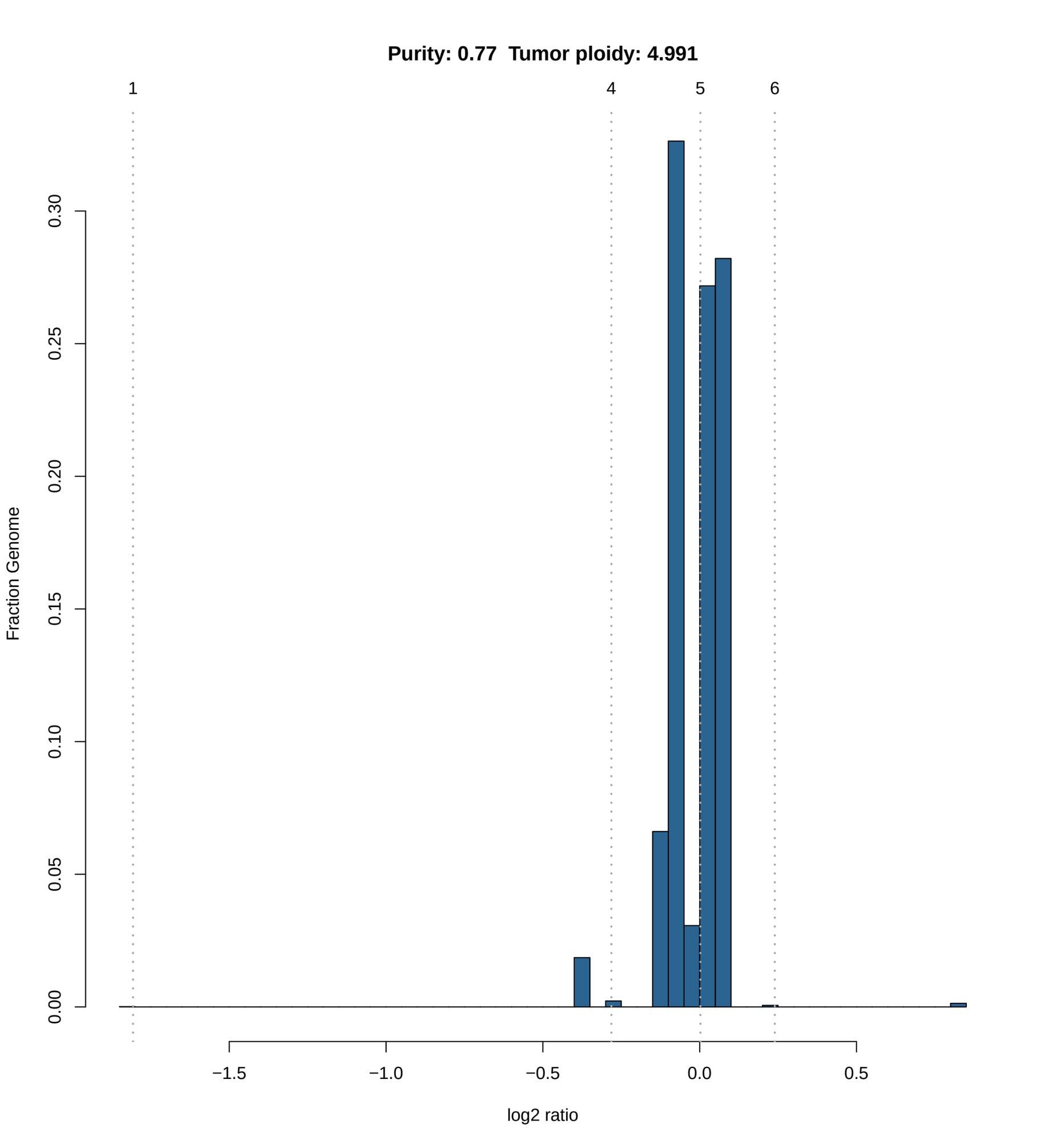

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

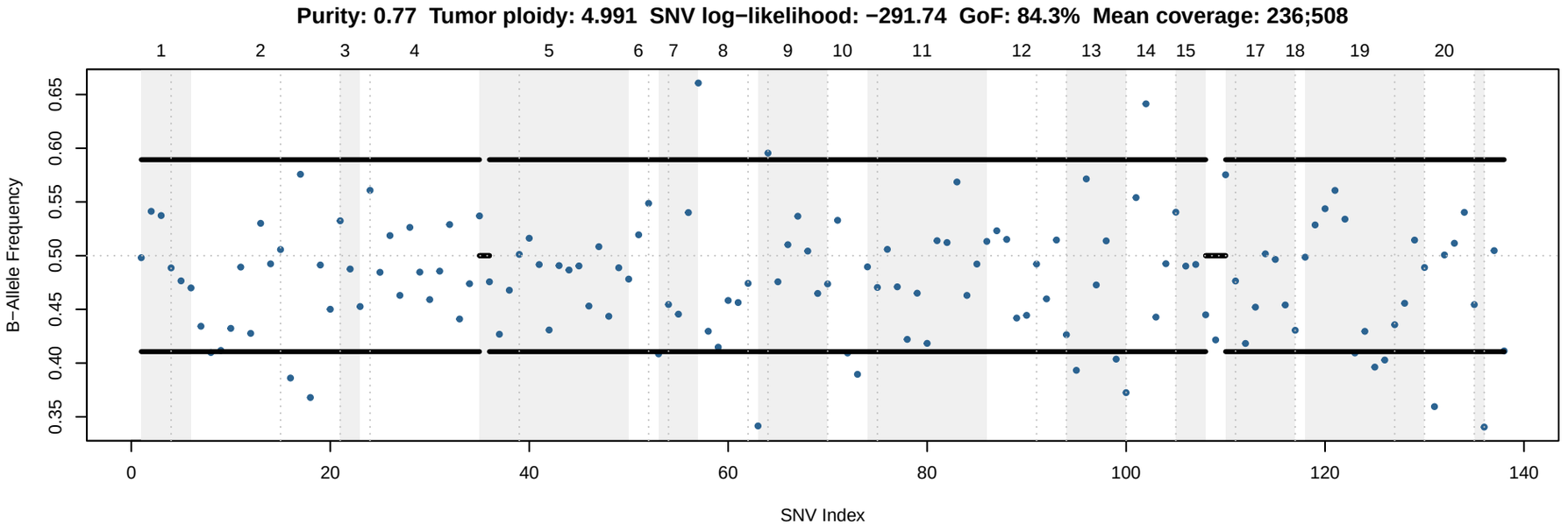

6m4
5m3
6m3
5m2
6m2
Allelic fraction (germline)
Copy Number log−ratio
0.35
0.40
0.45
0.50
0.55
0.60
0.65
−1.0
−0.5
0.0
0.5

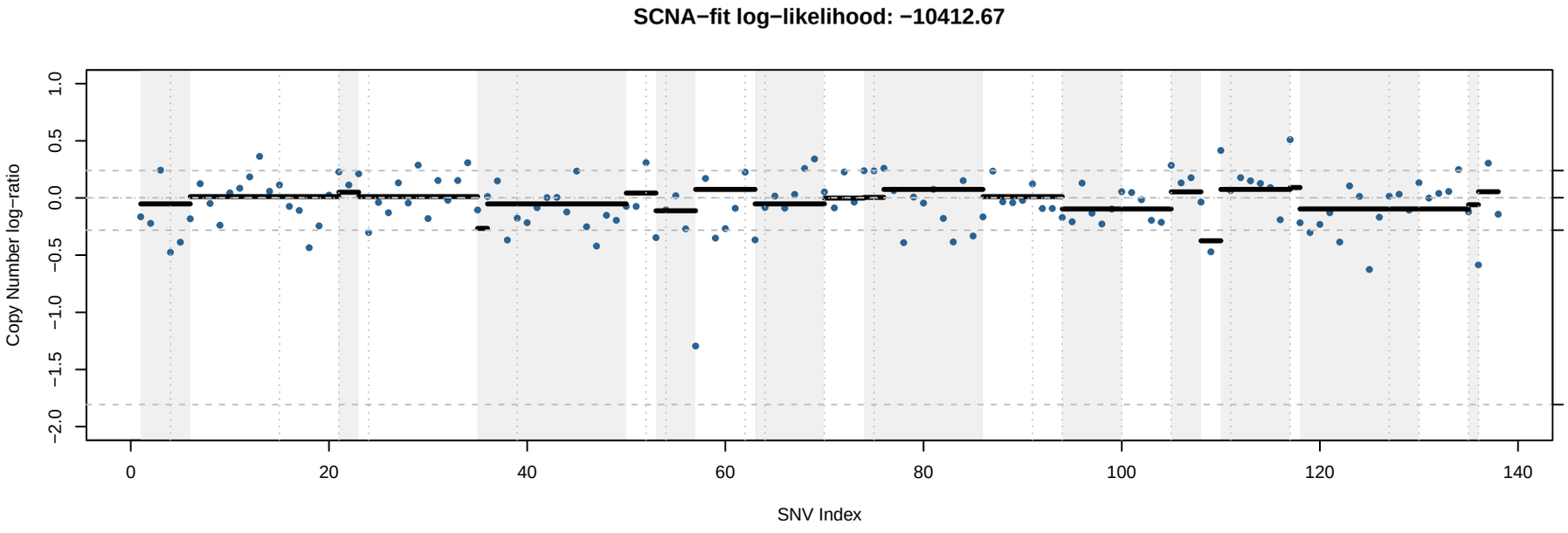

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

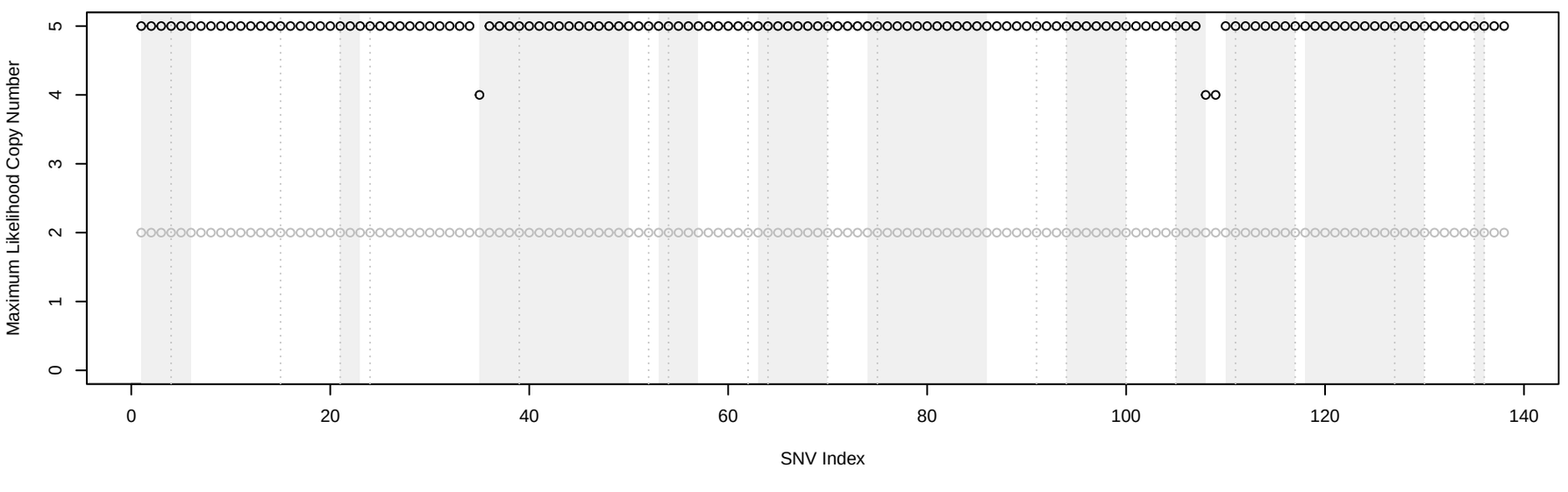

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
−1.0
−0.5
0.0
0.5

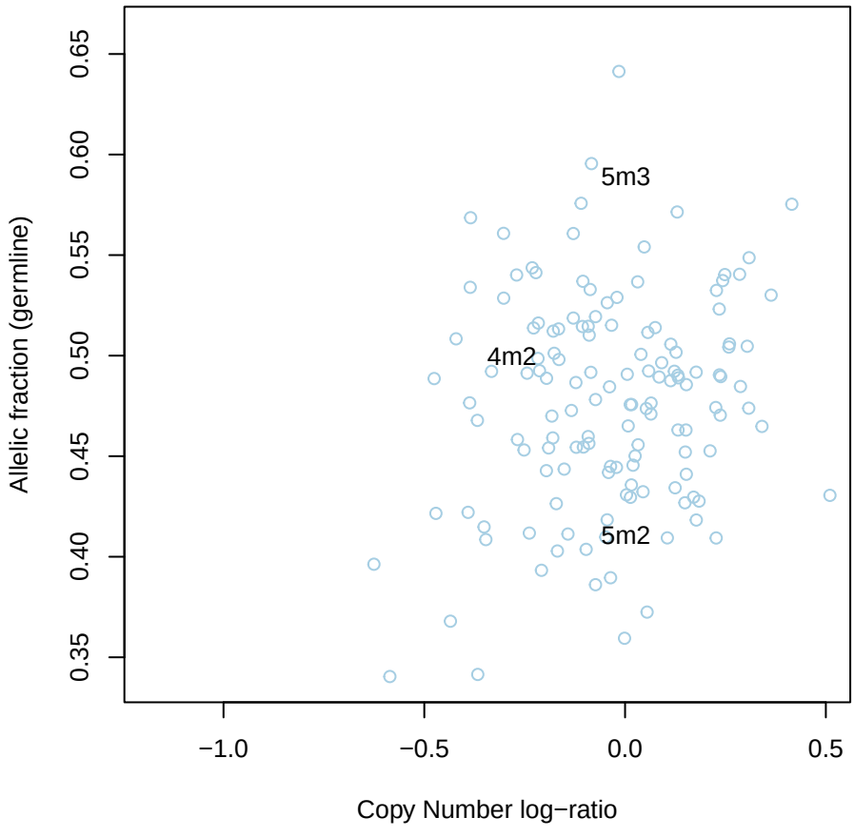

Power 0.8
Frequency
Cellular fraction
0
5
10
15
0.2
0.4
0.6
0.8
1.0

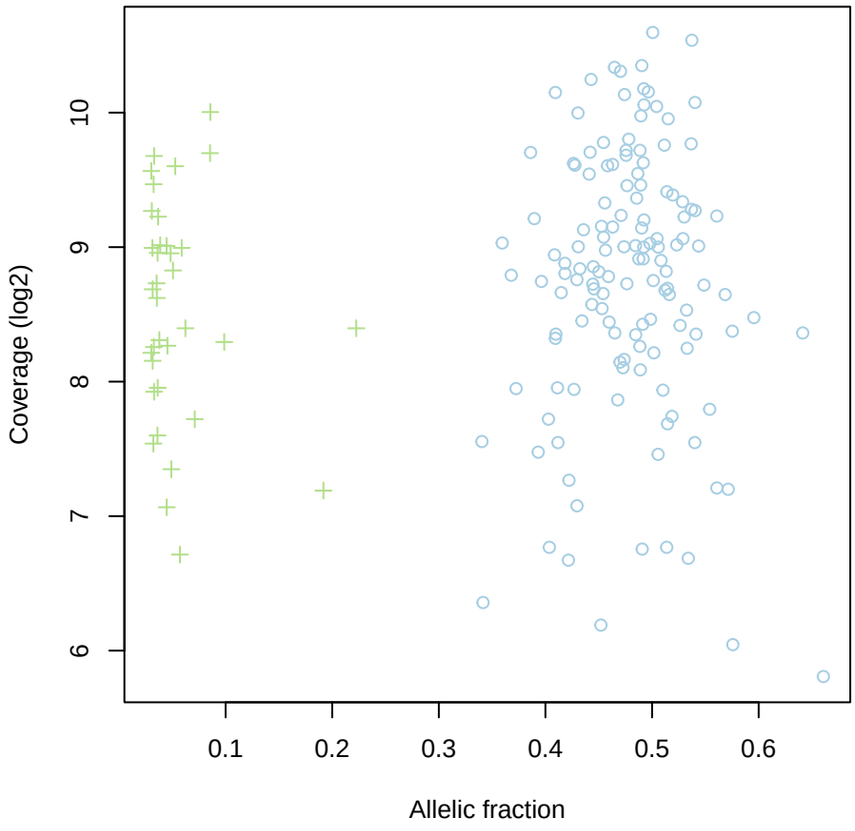

Purity: 0.77 Tumor ploidy: 4.991
1
4
5
6
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

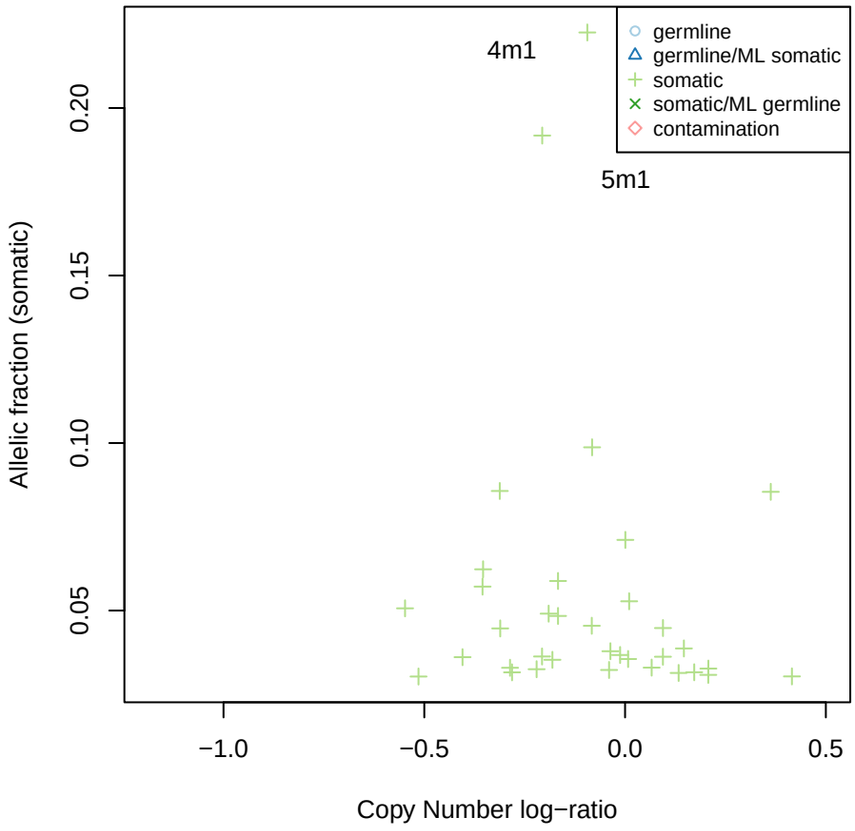

Purity: 0.77 Tumor ploidy: 4.991 SNV log−likelihood: −291.74 GoF: 84.3% Mean coverage: 236;508
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

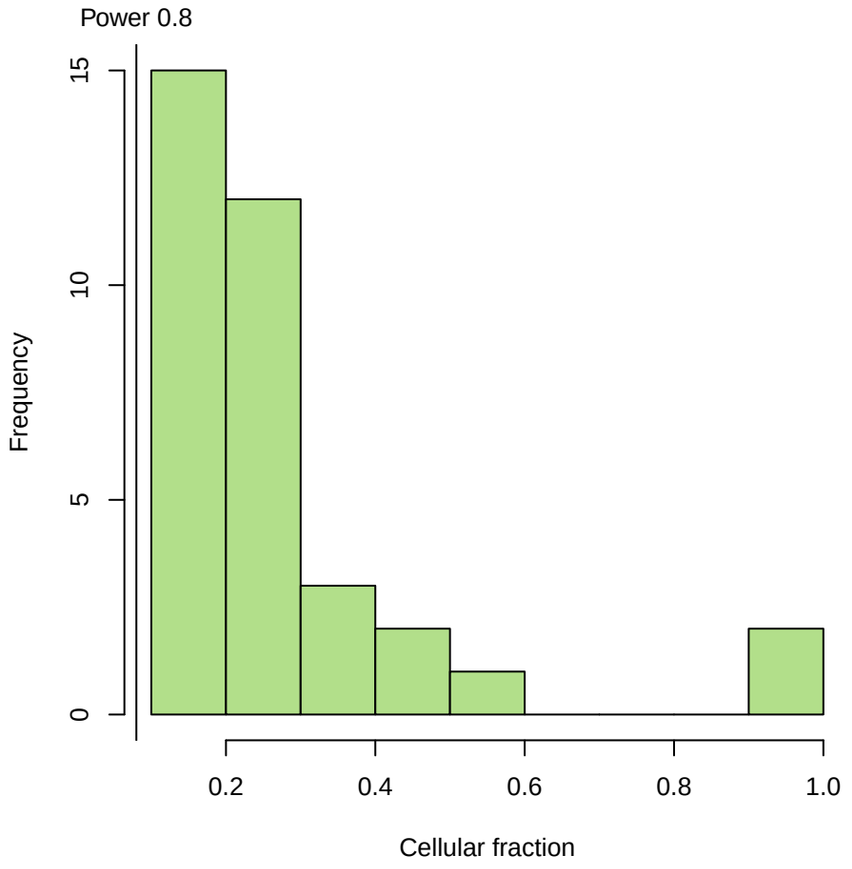

SCNA−fit log−likelihood: −10412.67
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
6 5 4 1
0 20 40 60 80 100 120 140
SNV Index

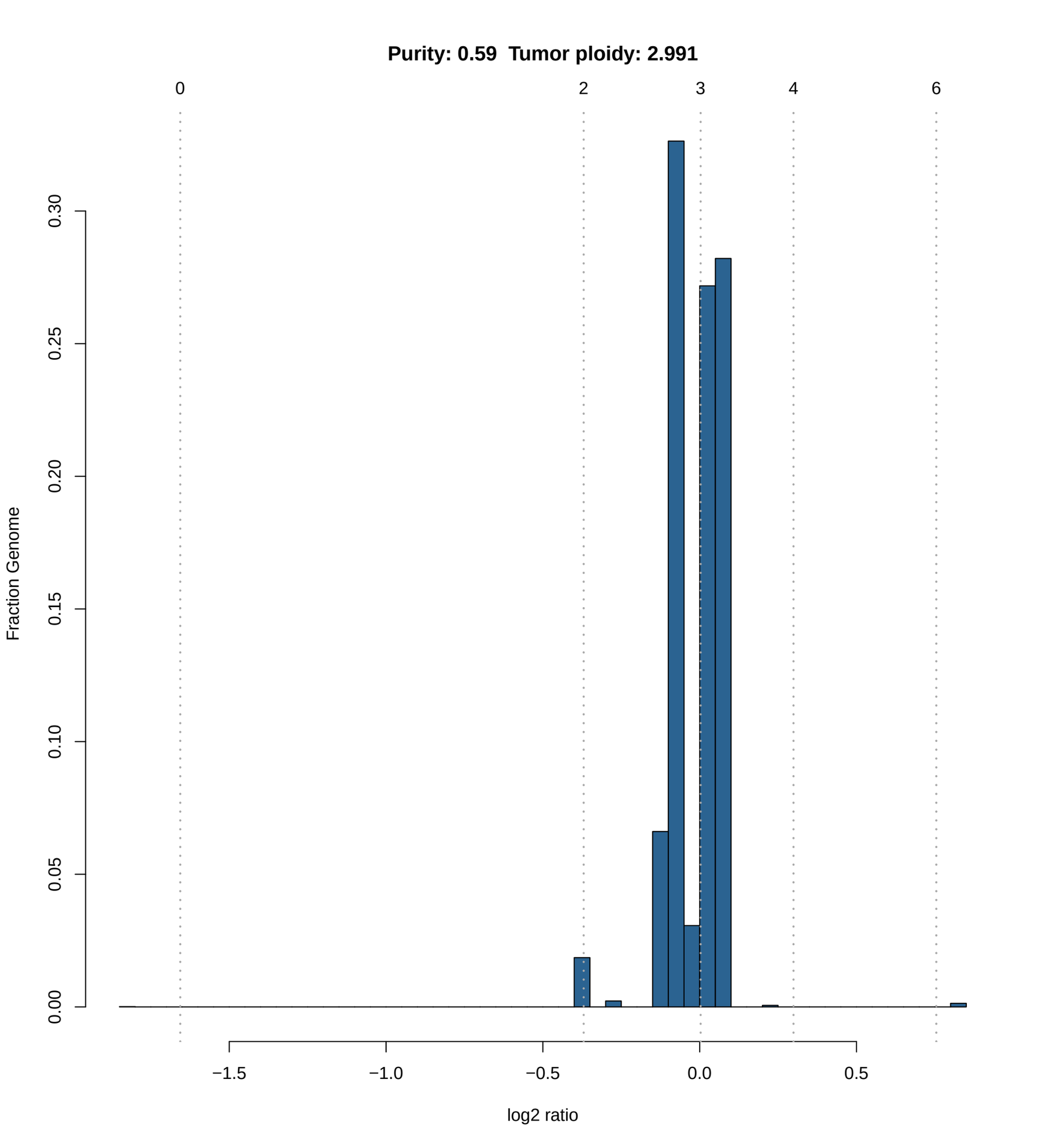

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

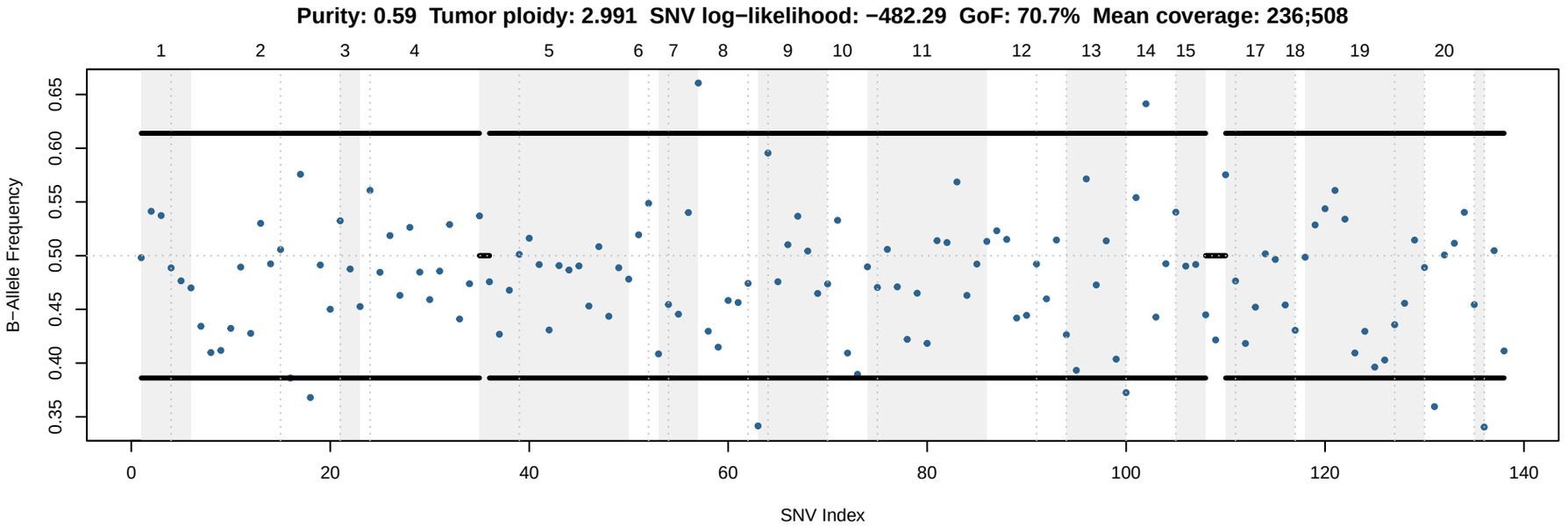

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
5m3
4m2
5m2
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

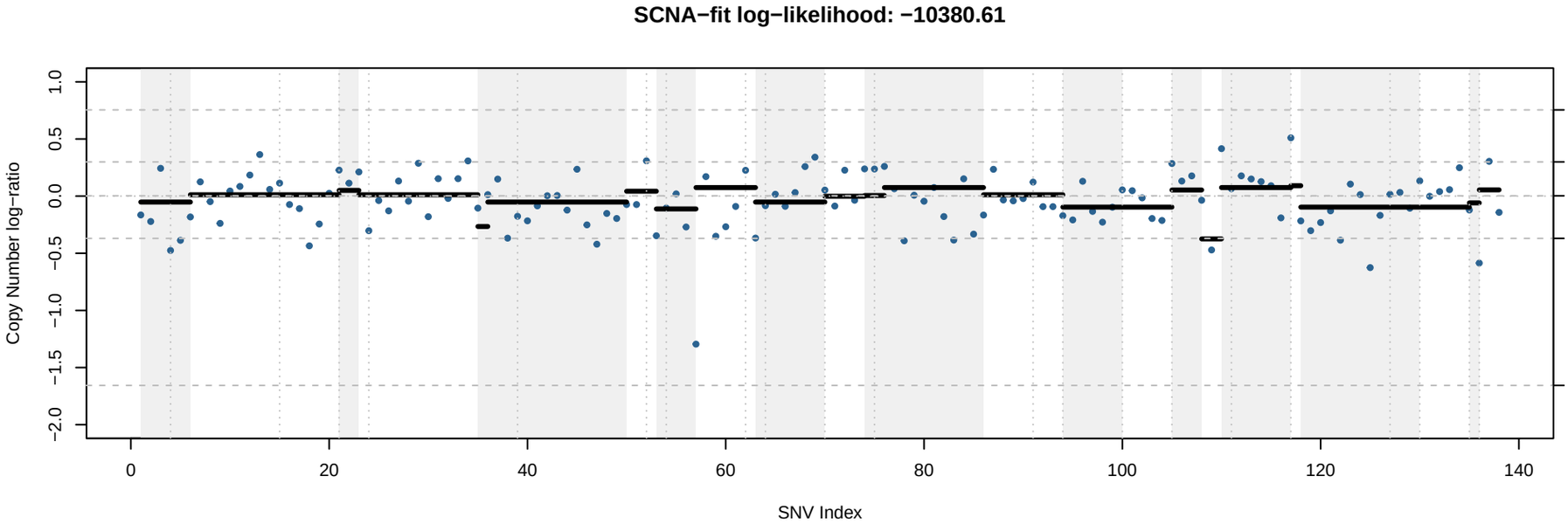

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

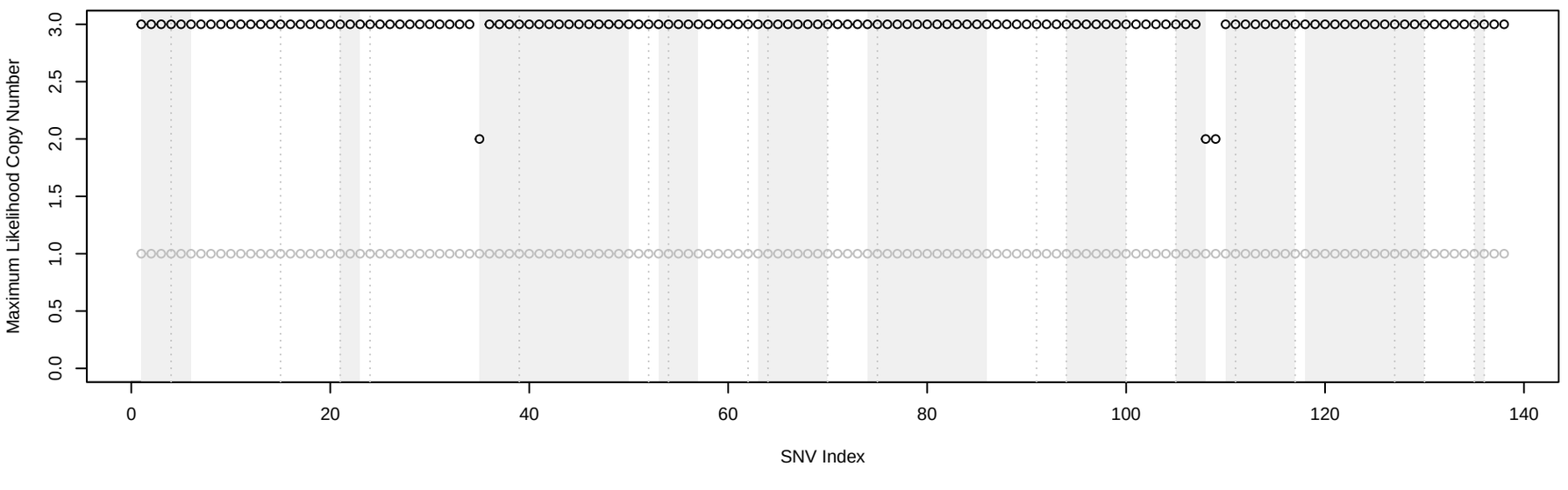

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

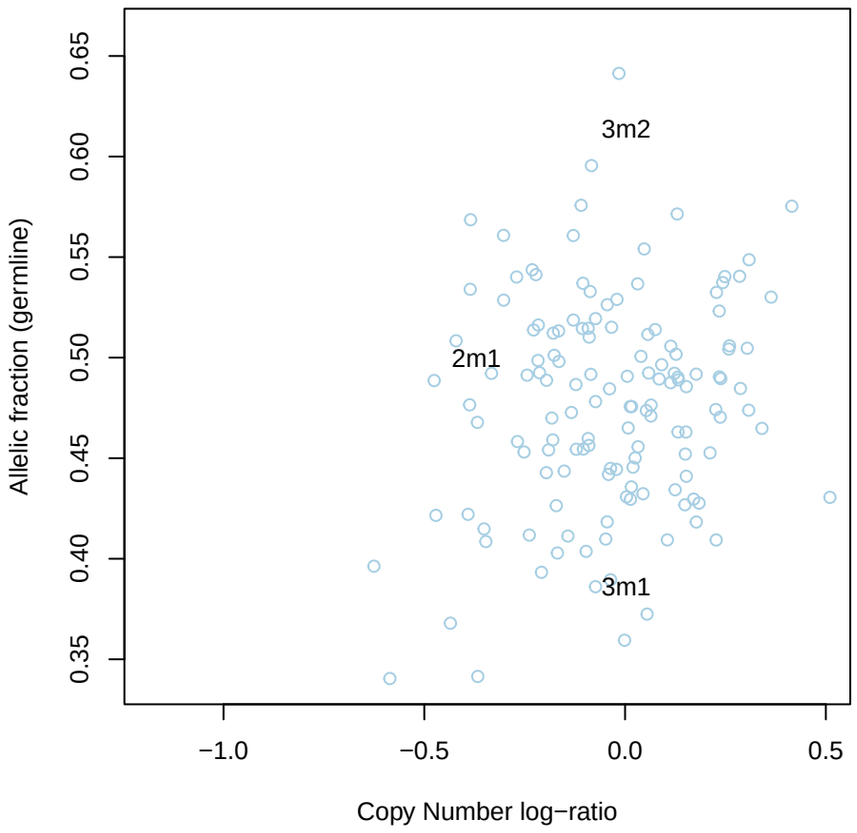

Power 0.8
Frequency
0
5
10
15
0.2
0.4
0.6
0.8
1.0
Cellular fraction

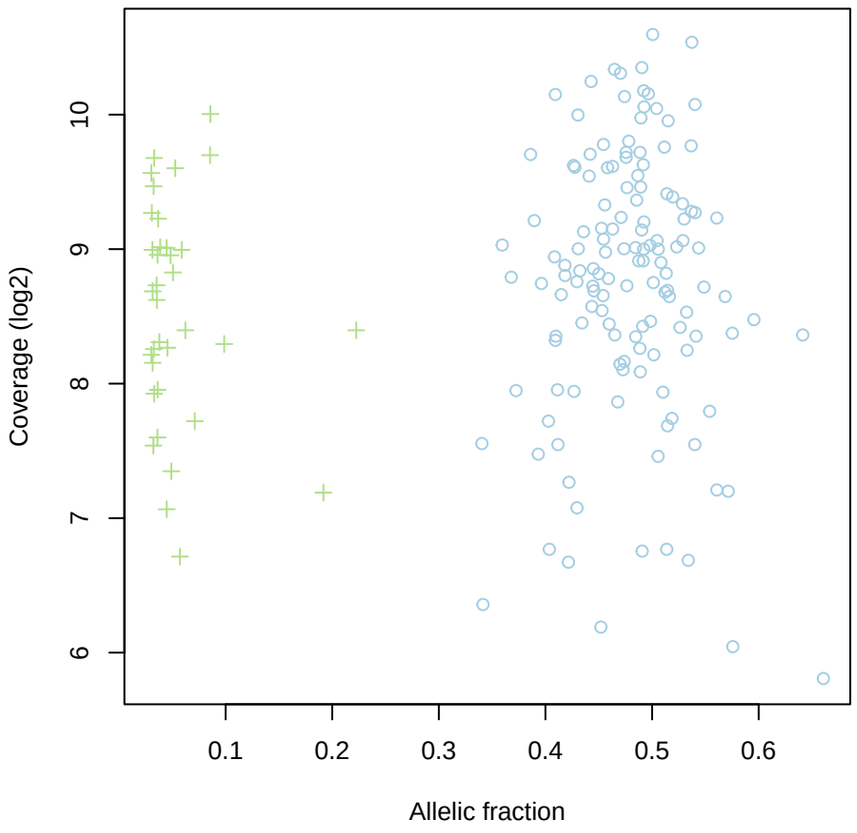

Purity: 0.59 Tumor ploidy: 2.991
0
2
3
4
6
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

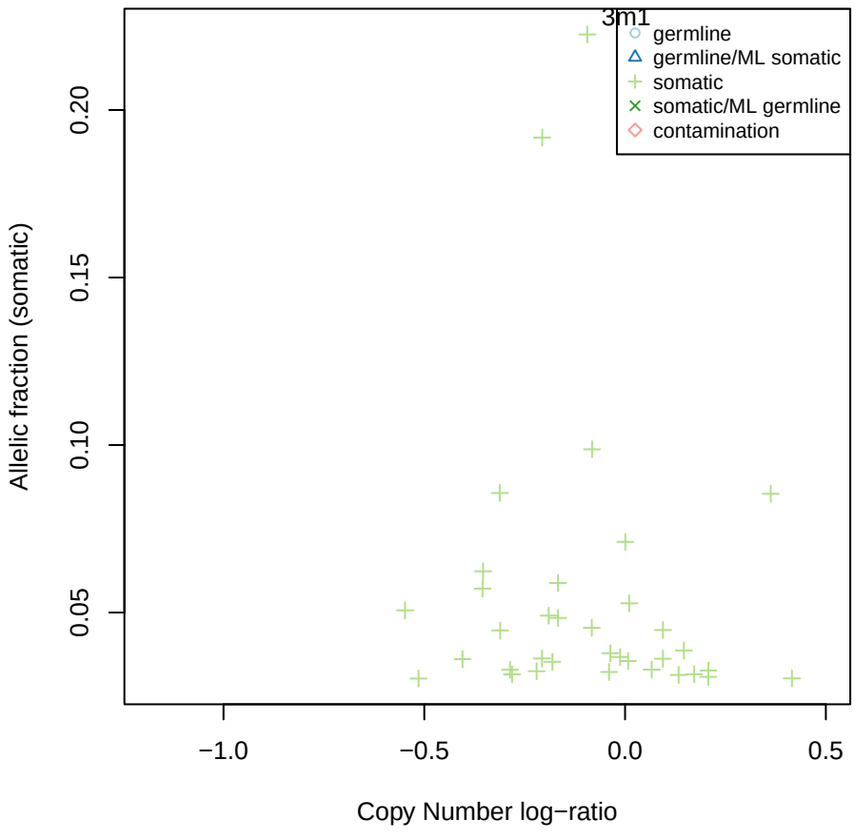

Purity: 0.59 Tumor ploidy: 2.991 SNV log−likelihood: −482.29 GoF: 70.7% Mean coverage: 236;508
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

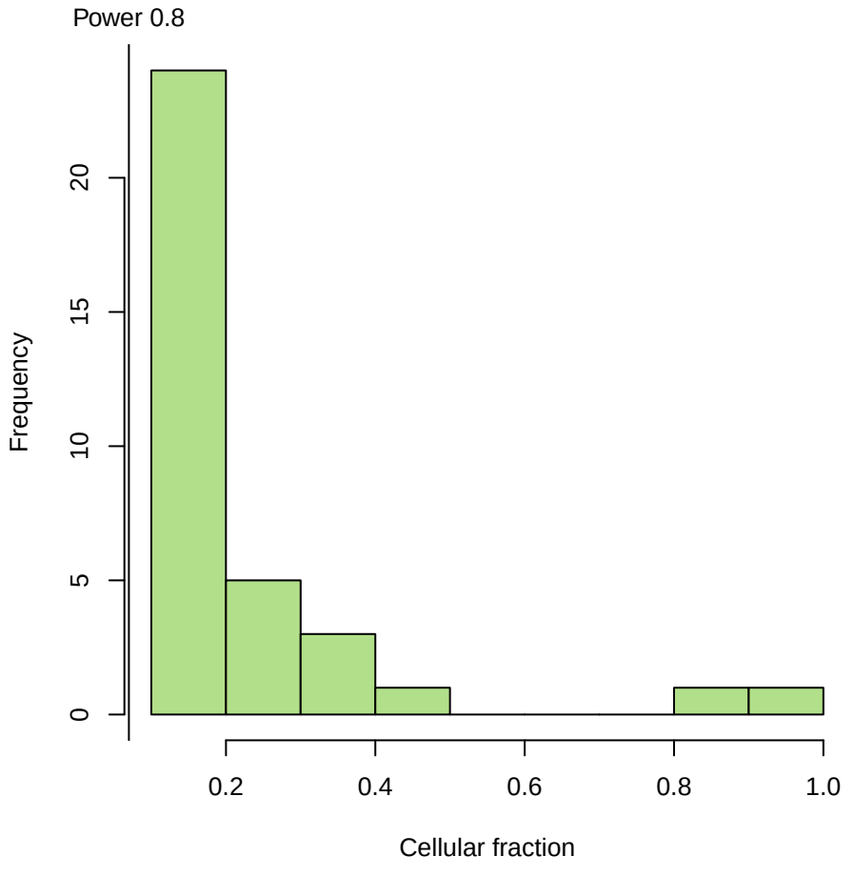

SCNA−fit log−likelihood: −10380.61
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
6 4 3 2 0
0 20 40 60 80 100 120 140
SNV Index

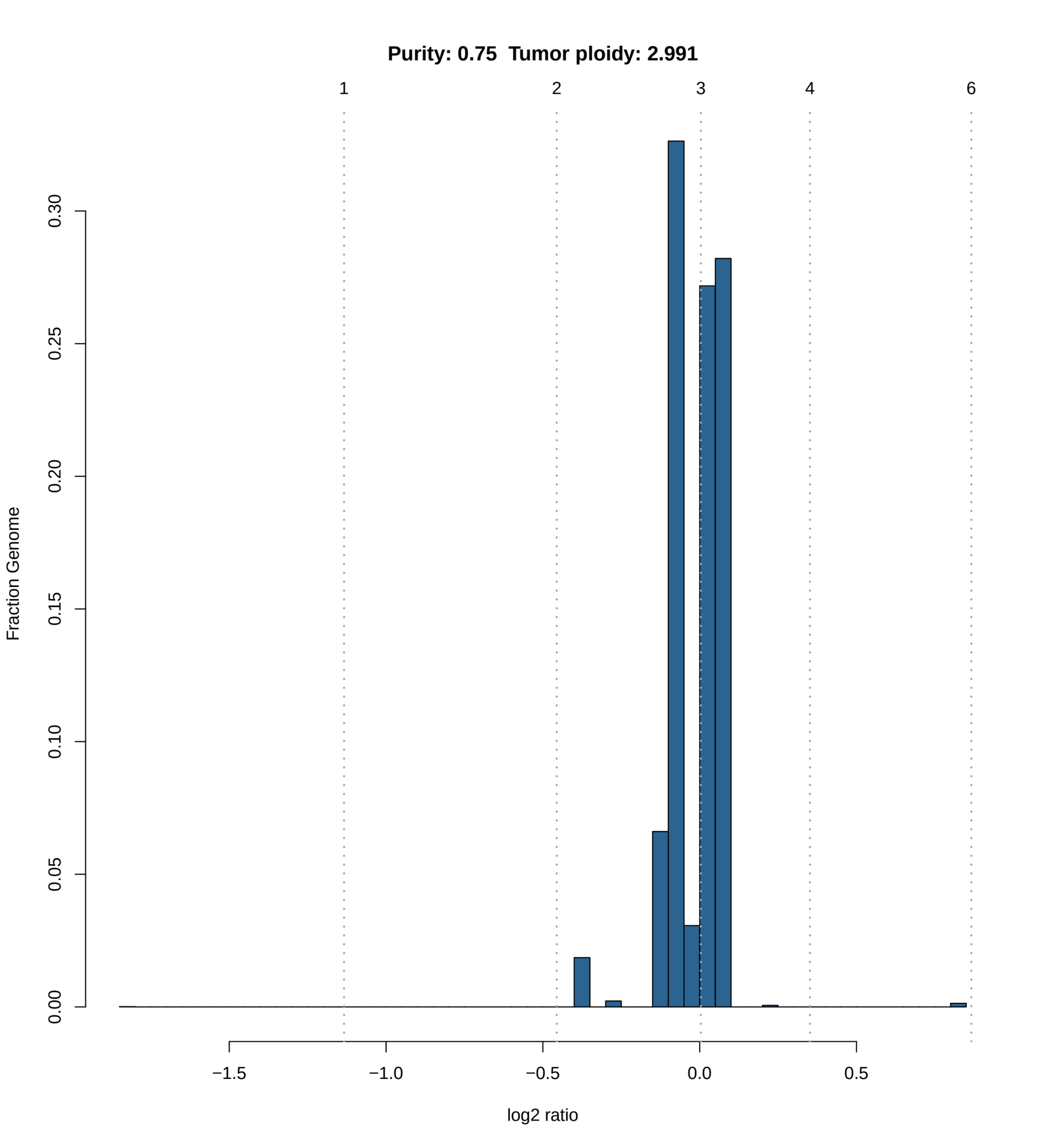

Maximum Likelihood Copy Number
3.0 2.5 2.0 1.5 1.0 0.5 0.0
0 20 40 60 80 100 120 140
SNV Index

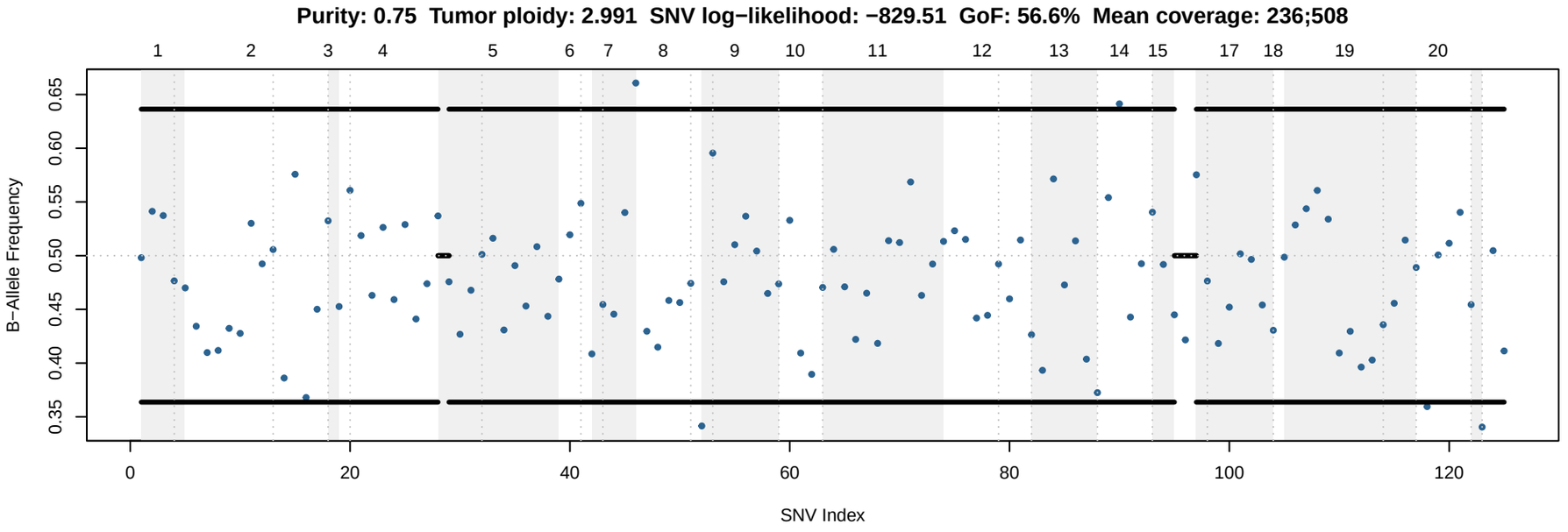

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
3m2
2m1
3m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

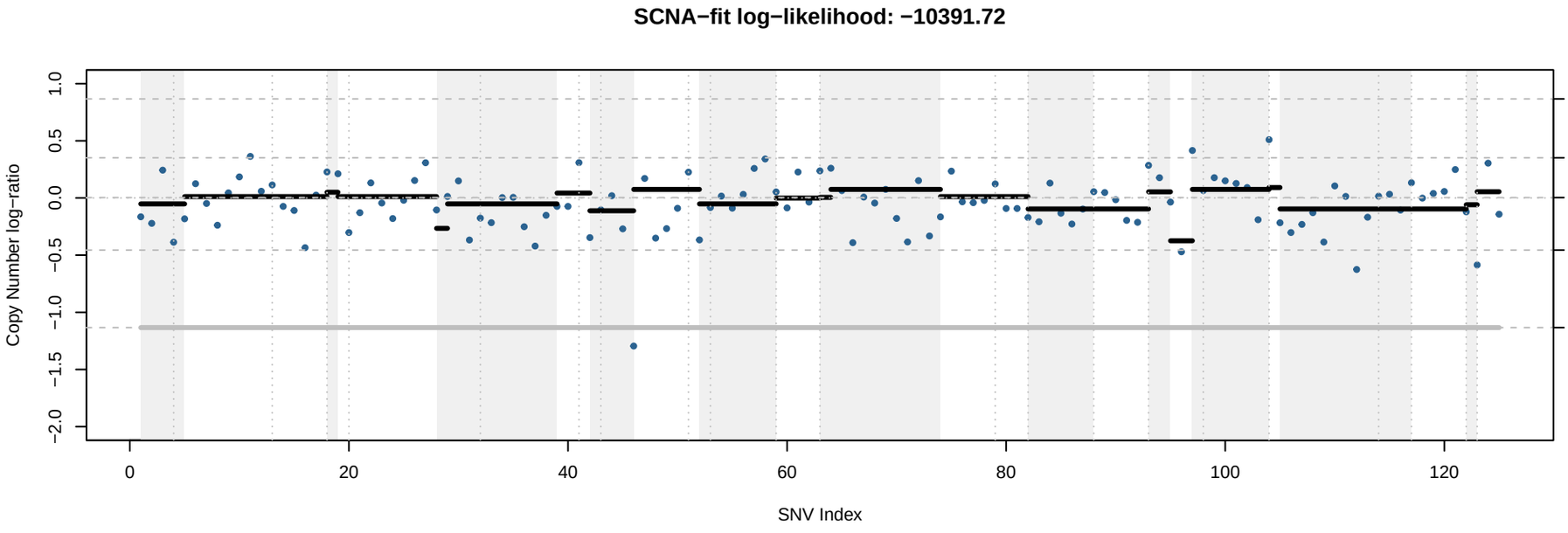

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

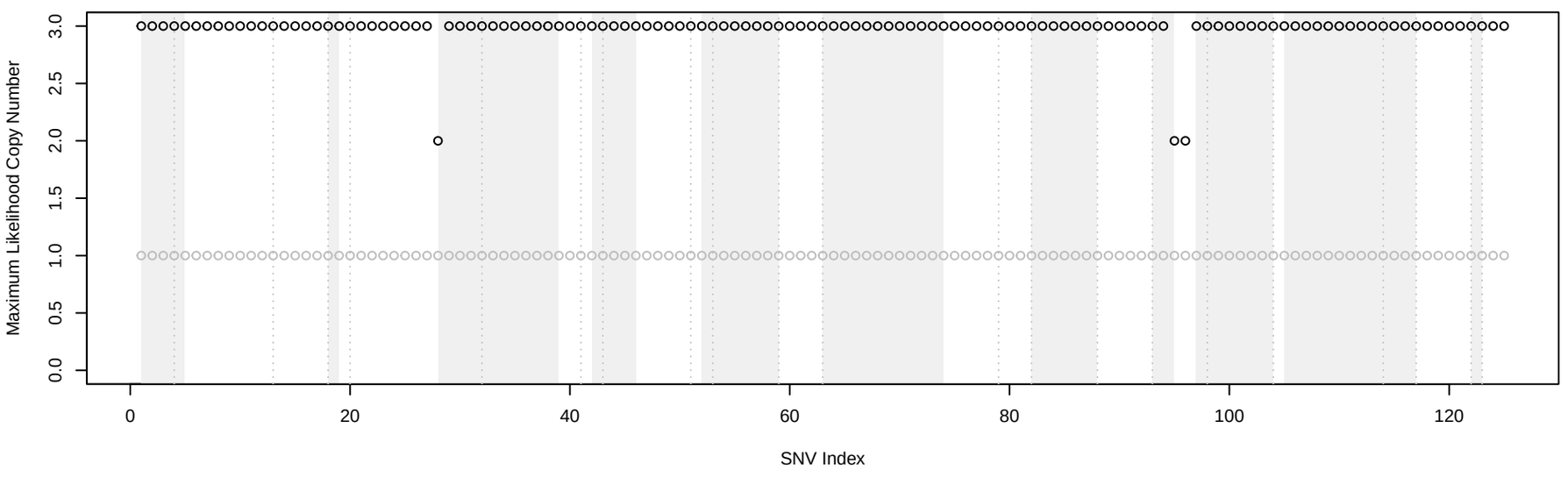

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
3m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

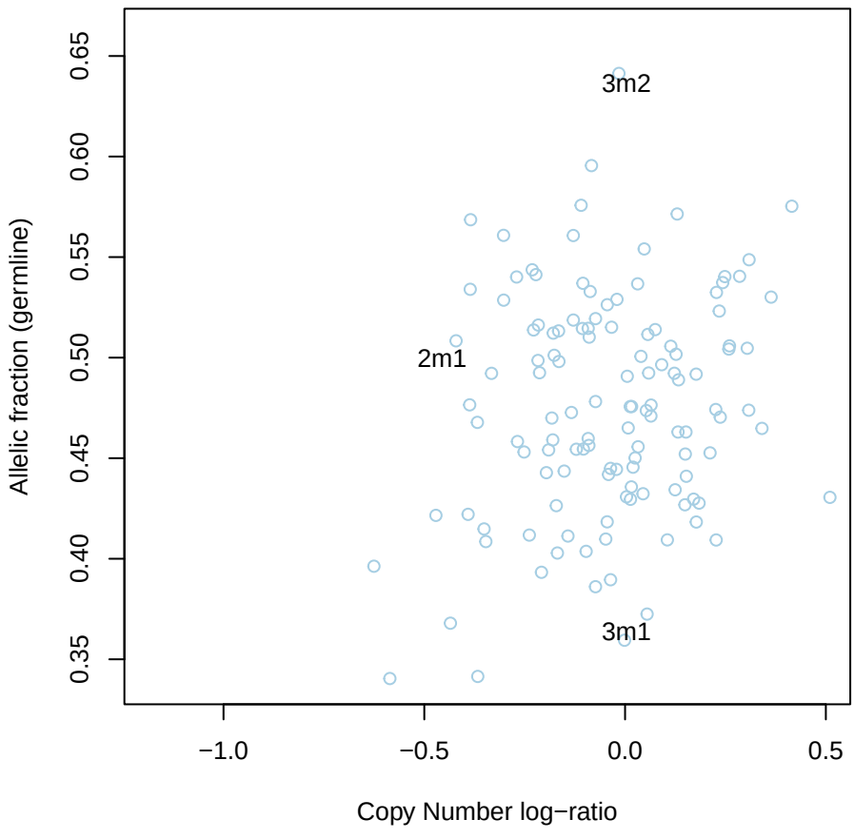

Power 0.8
Frequency
0
5
10
15
20
0.2
0.4
0.6
0.8
1.0
Cellular fraction

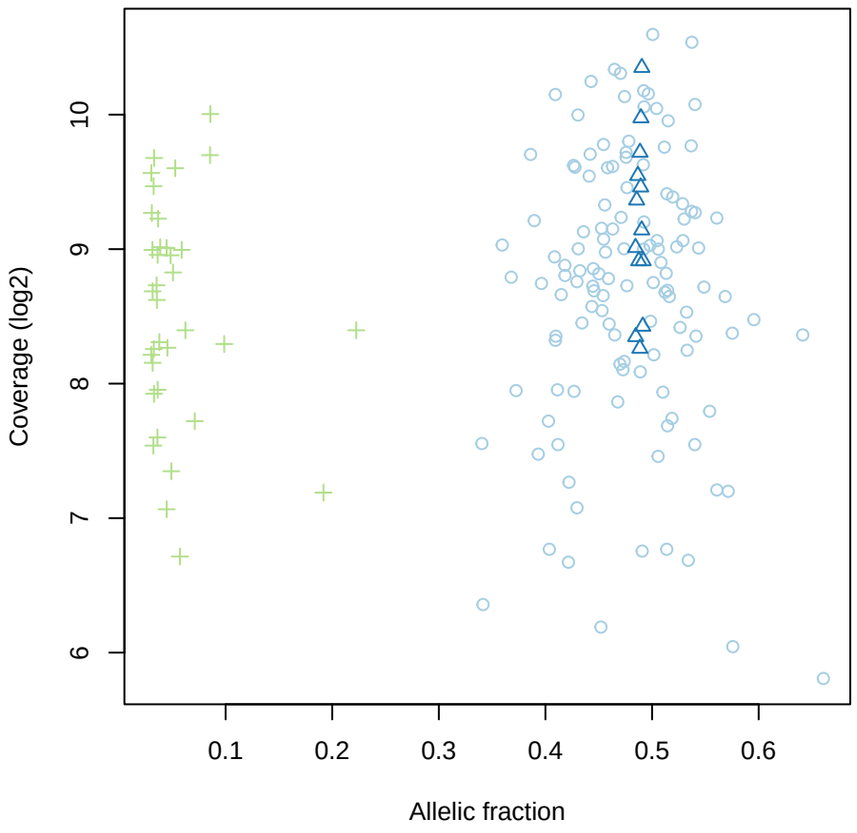

Purity: 0.75 Tumor ploidy: 2.991
1
2
3
4
6
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

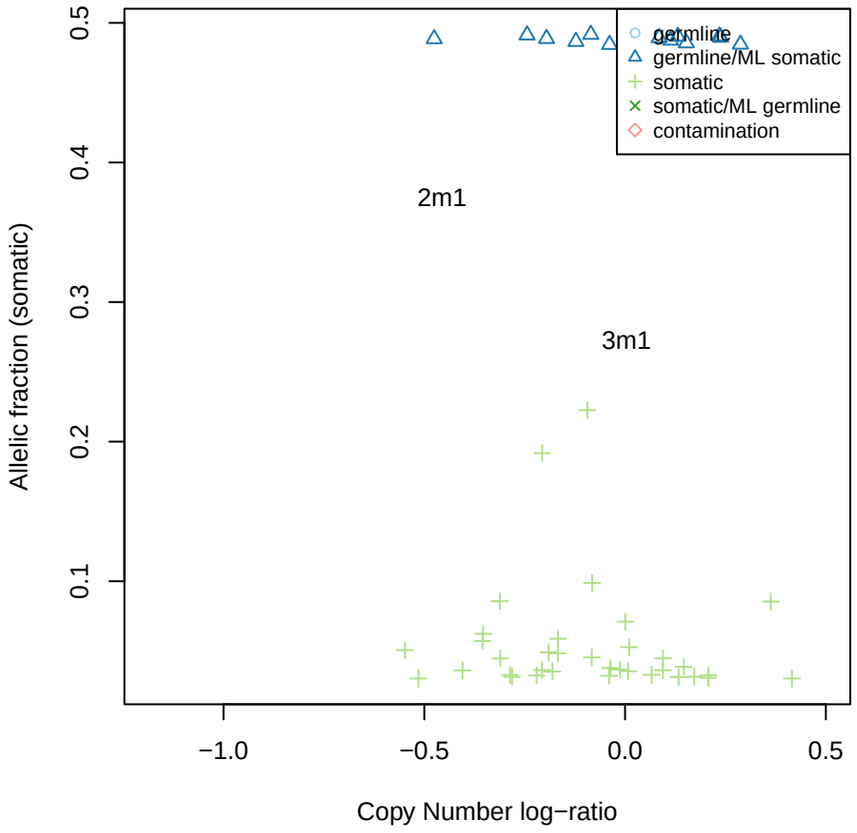

Purity: 0.75 Tumor ploidy: 2.991 SNV log−likelihood: −829.51 GoF: 56.6% Mean coverage: 236;508
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120
SNV Index

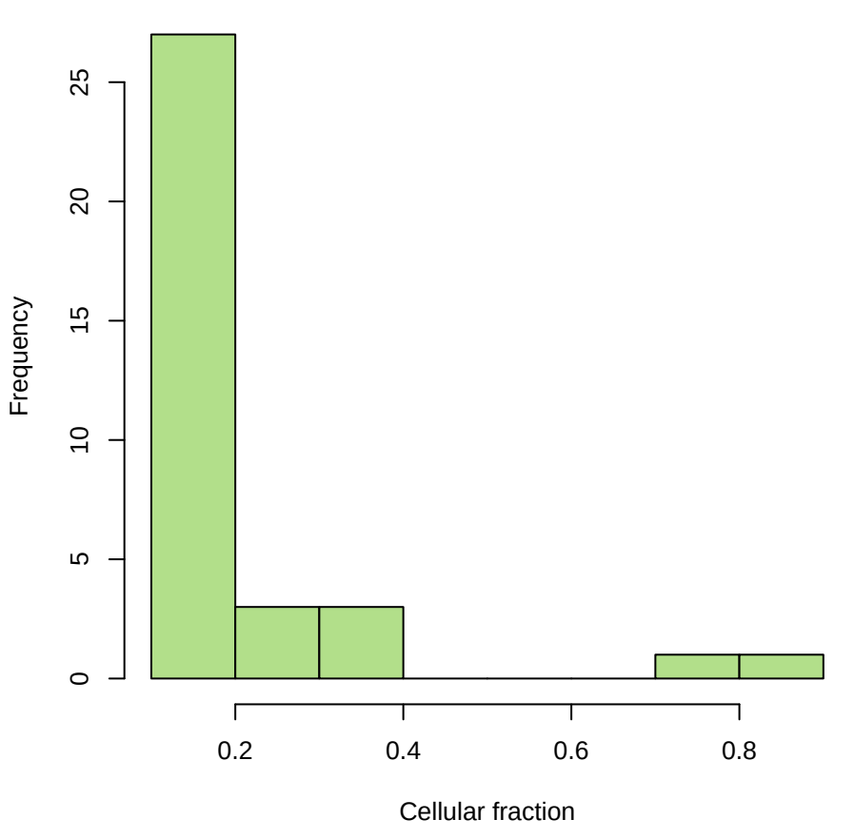

SCNA−fit log−likelihood: −10391.72
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
1 2 3 4 6
0 20 40 60 80 100 120
SNV Index


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
SNV Index


3m2
2m1
3m1
Allelic fraction (germline)
Copy Number log−ratio
0.35
0.40
0.45
0.50
0.55
0.60
0.65
−1.0
−0.5
0.0
0.5


Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6


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


Frequency
Cellular fraction
0
5
10
15
20
25
0.2
0.4
0.6
0.8