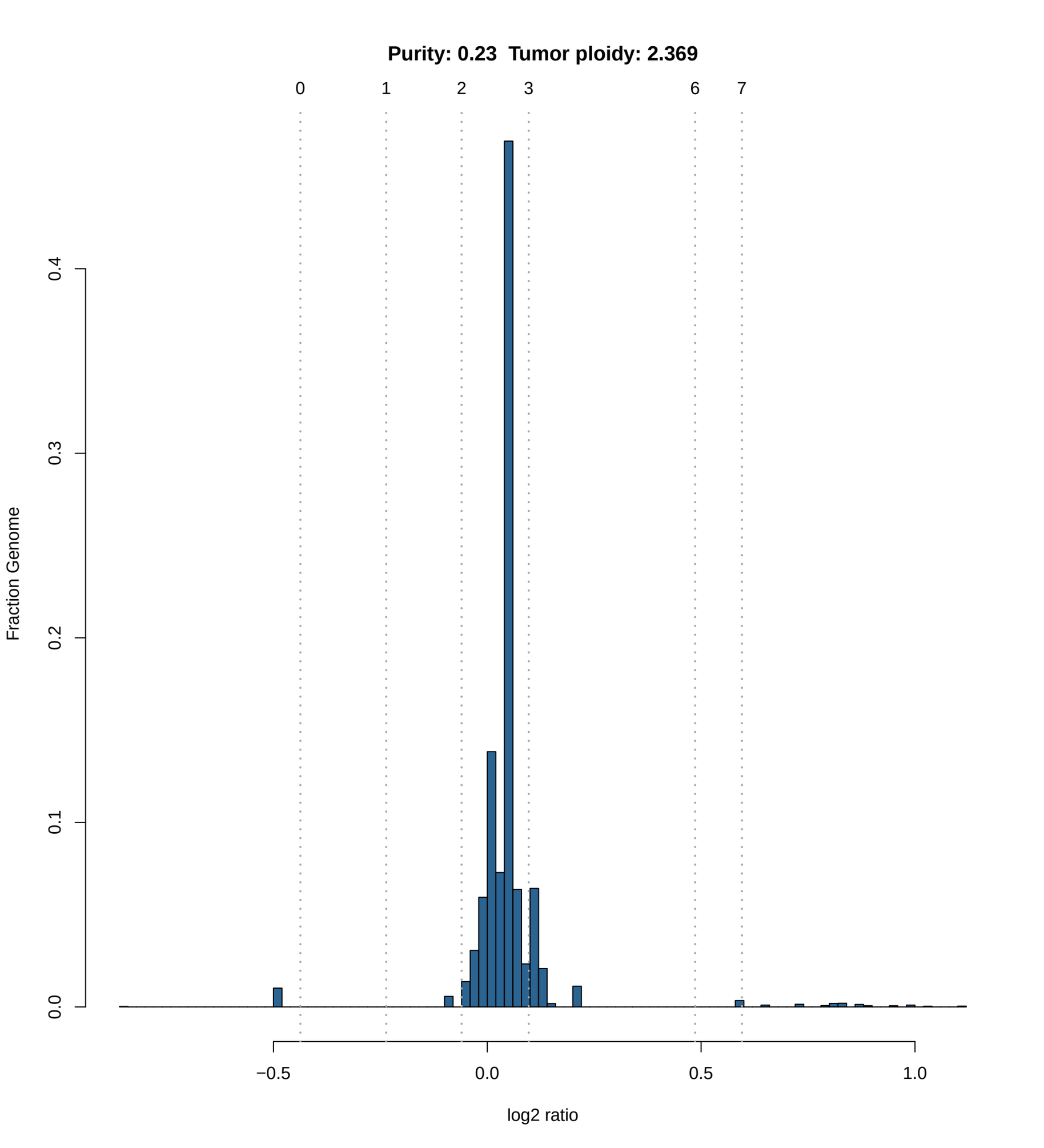
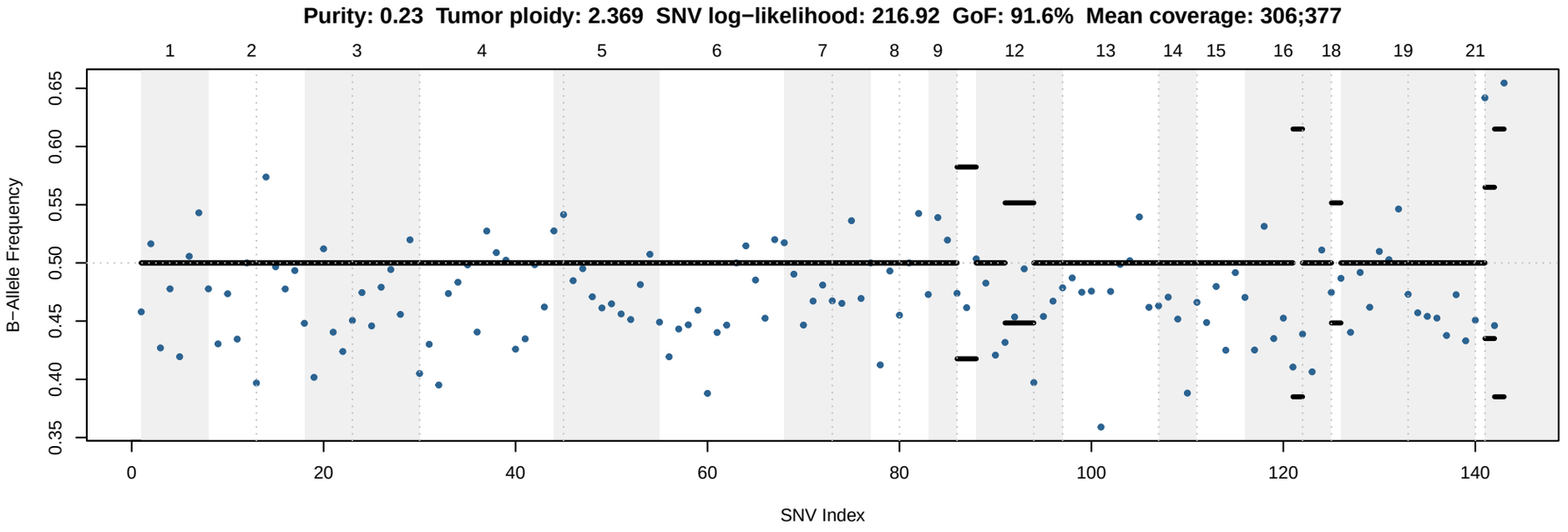
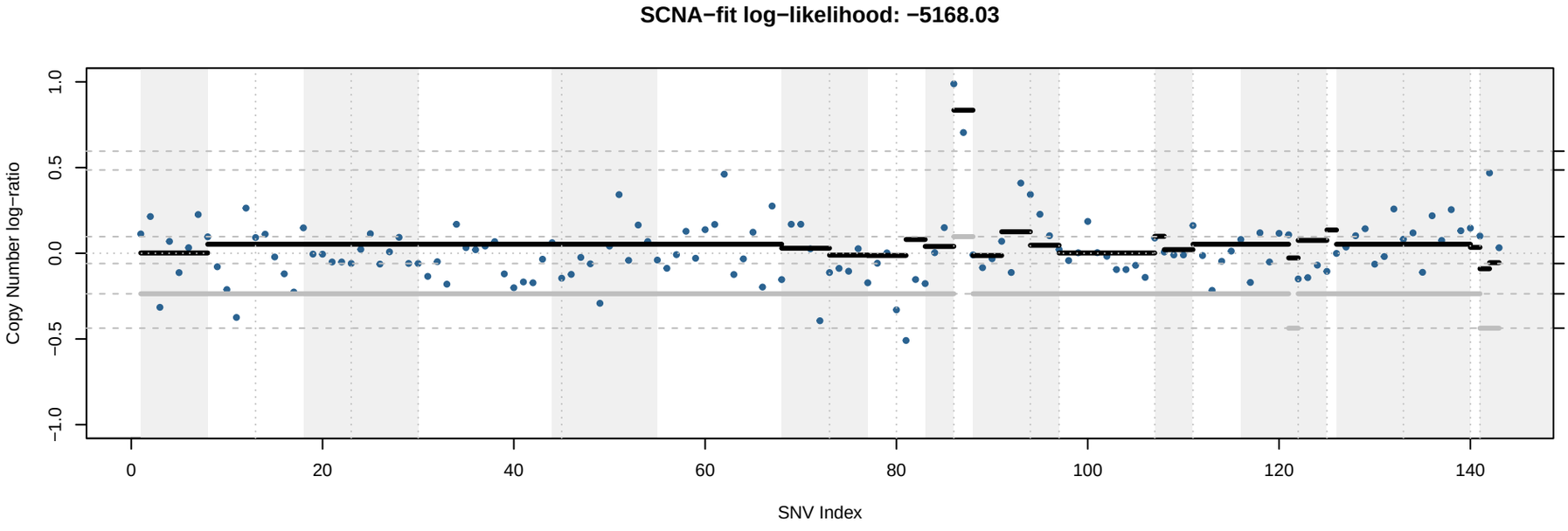
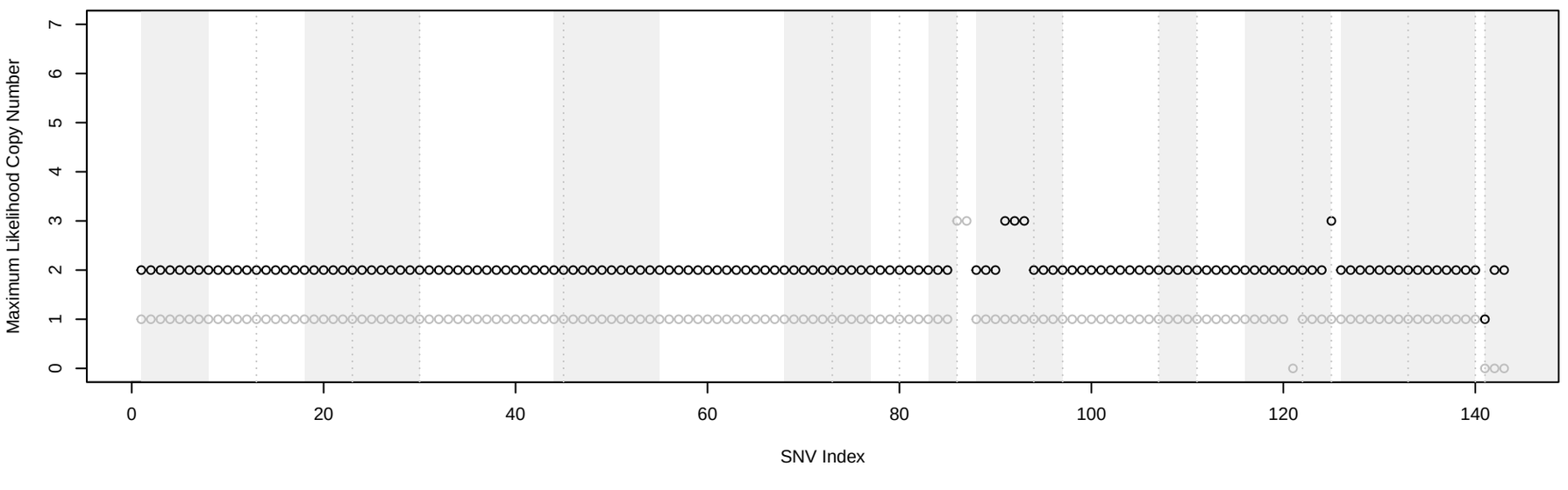
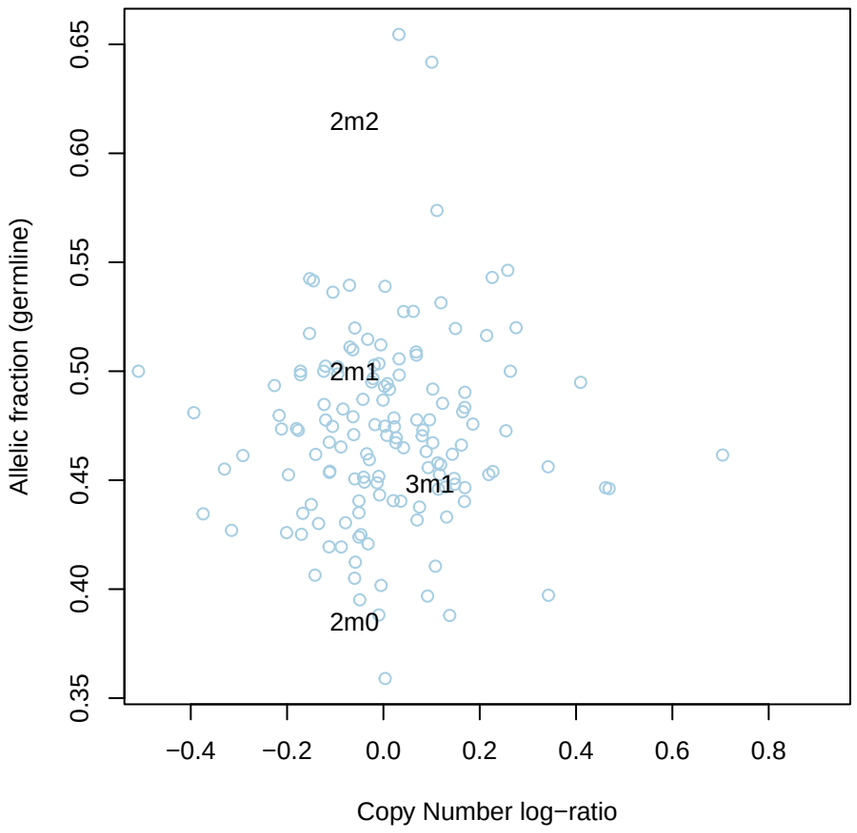
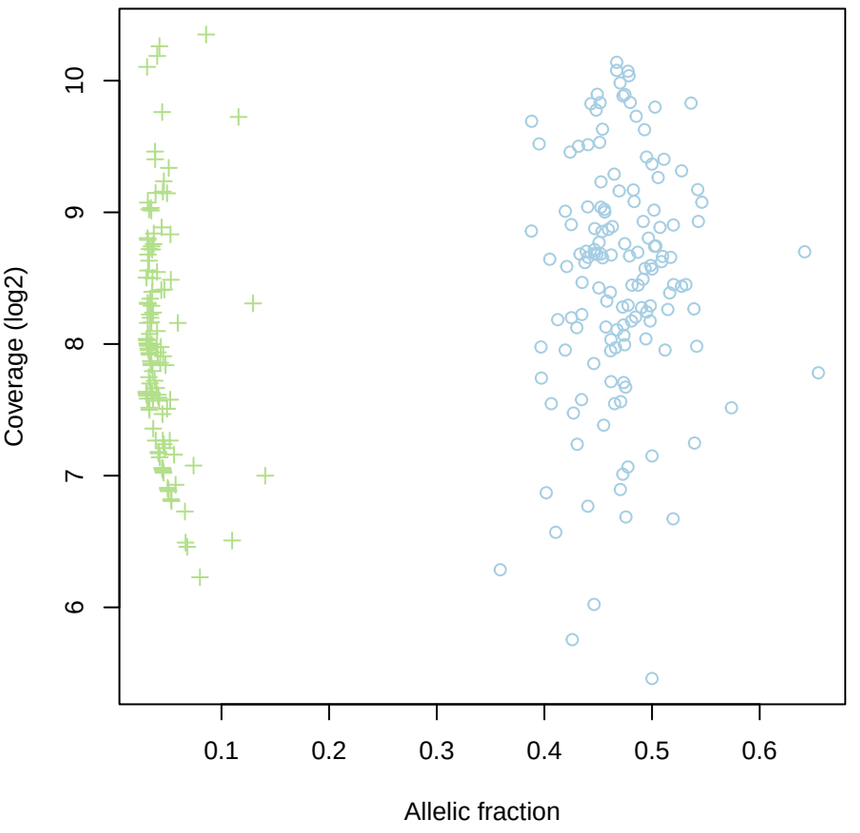

Purity: 0.23 Tumor ploidy: 2.369
0
1
2
3
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

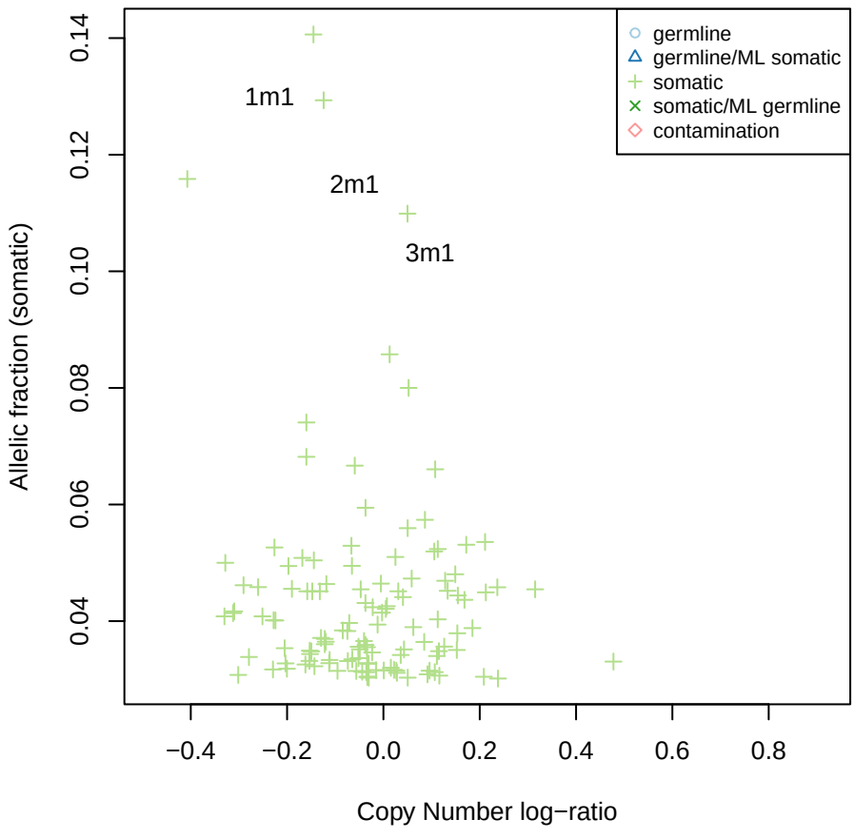

Purity: 0.23 Tumor ploidy: 2.369 SNV log−likelihood: 216.92 GoF: 91.6% Mean coverage: 306;377
1 2 3 4 5 6 7 8 9 12 13 14 15 16 18 19 21
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

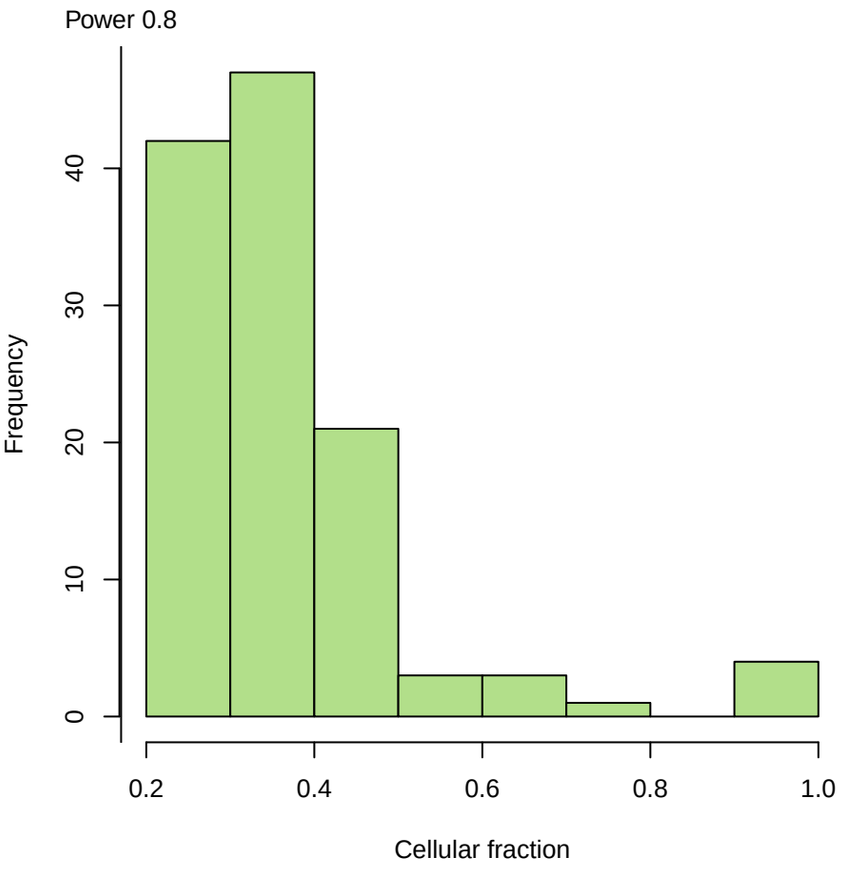

SCNA−fit log−likelihood: −5168.03
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 6
0 20 40 60 80 100 120 140
SNV Index

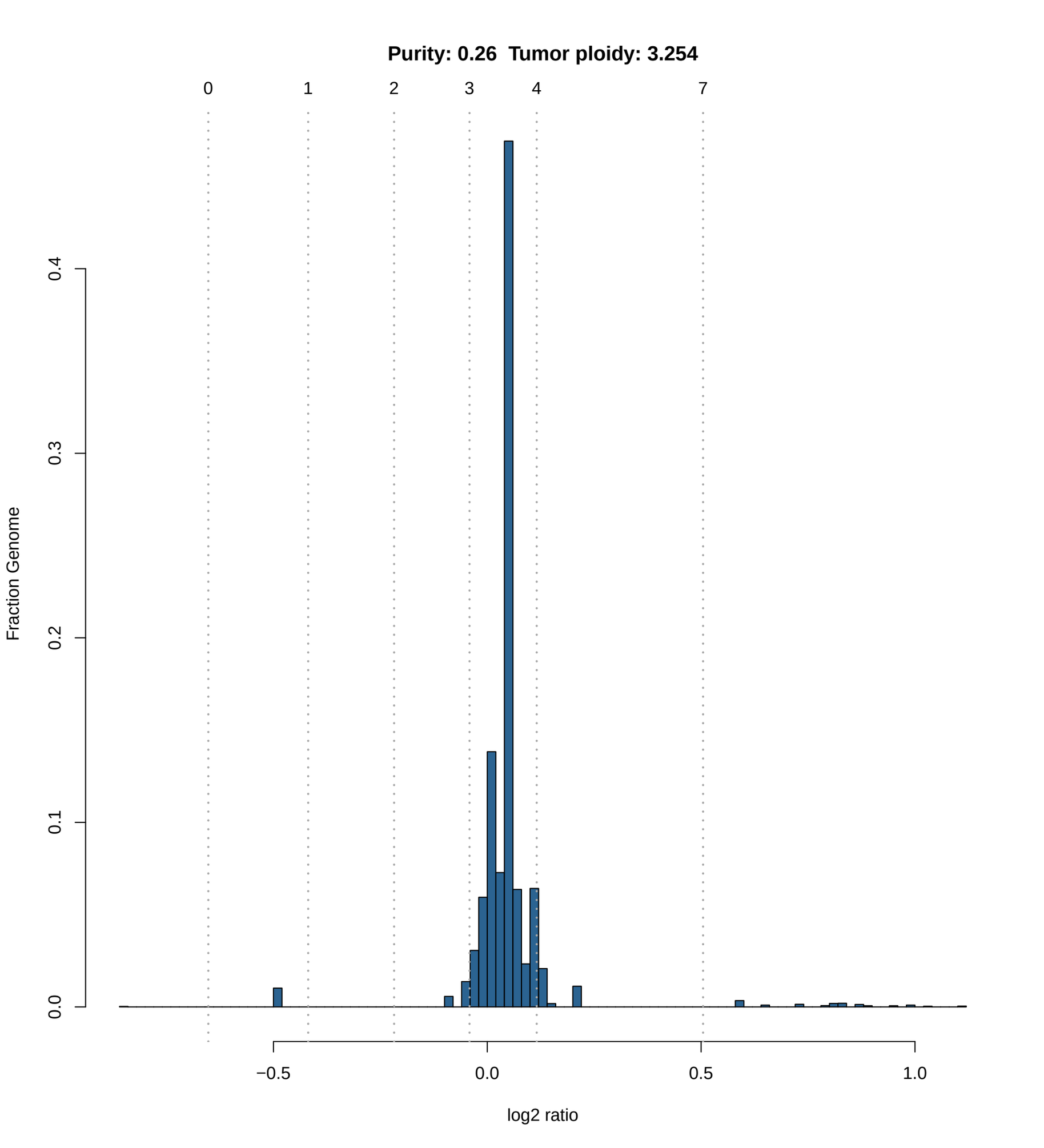

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

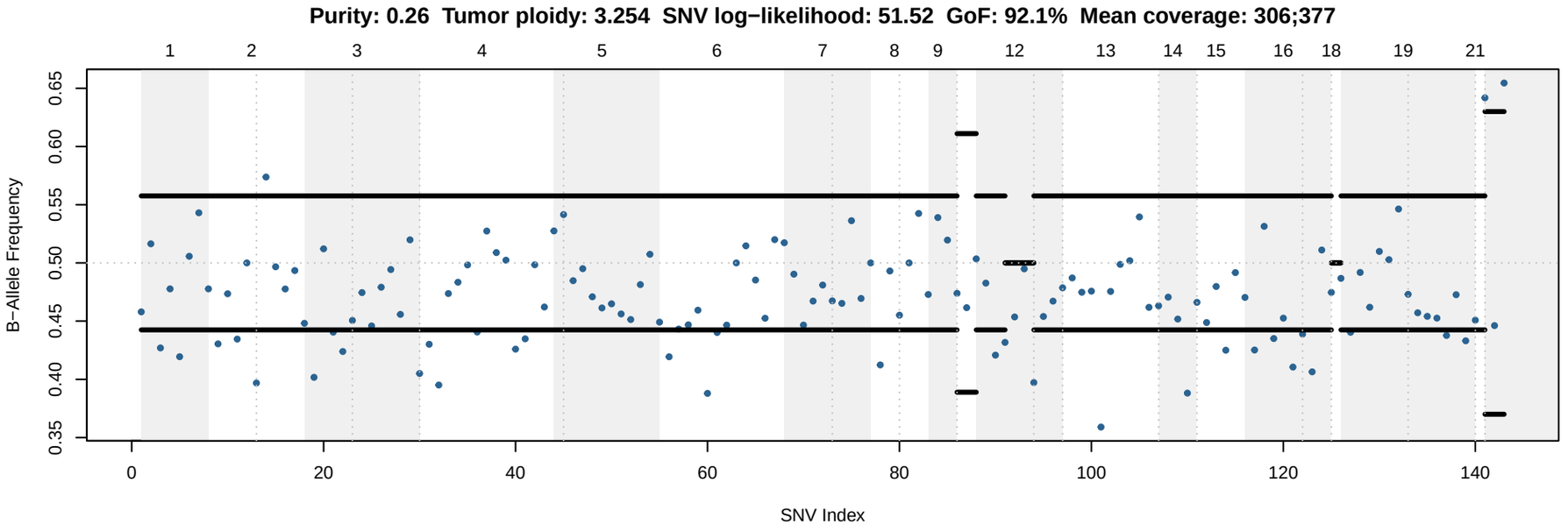

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
2m2
2m1
3m1
2m0
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

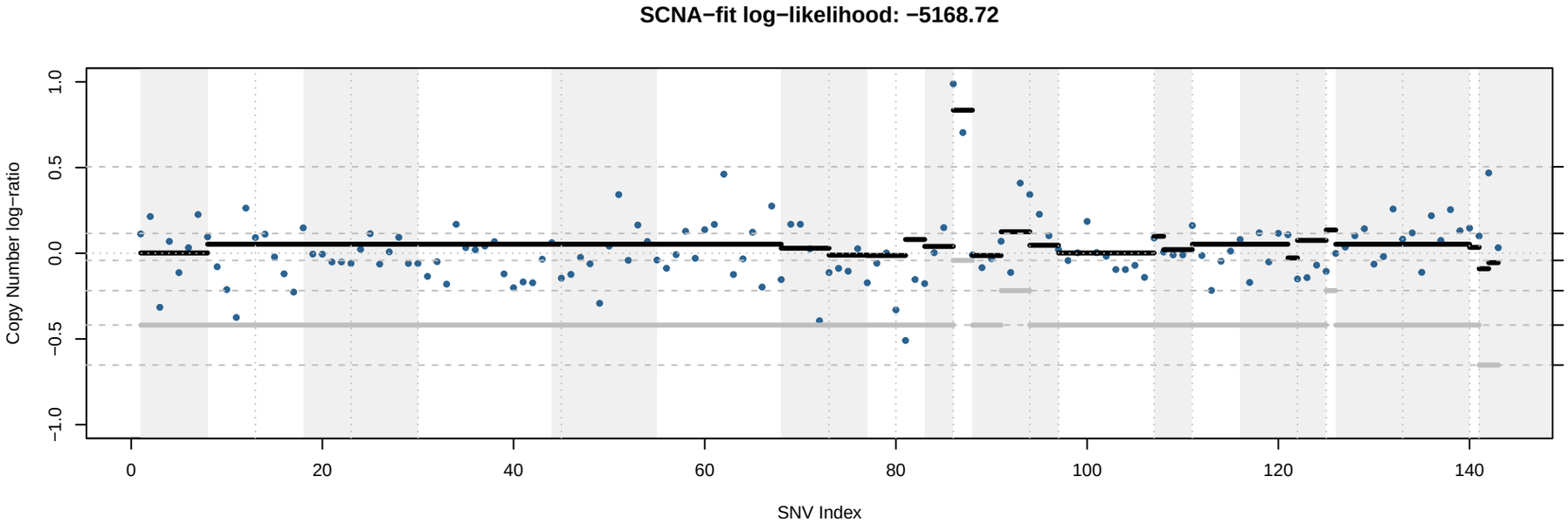

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

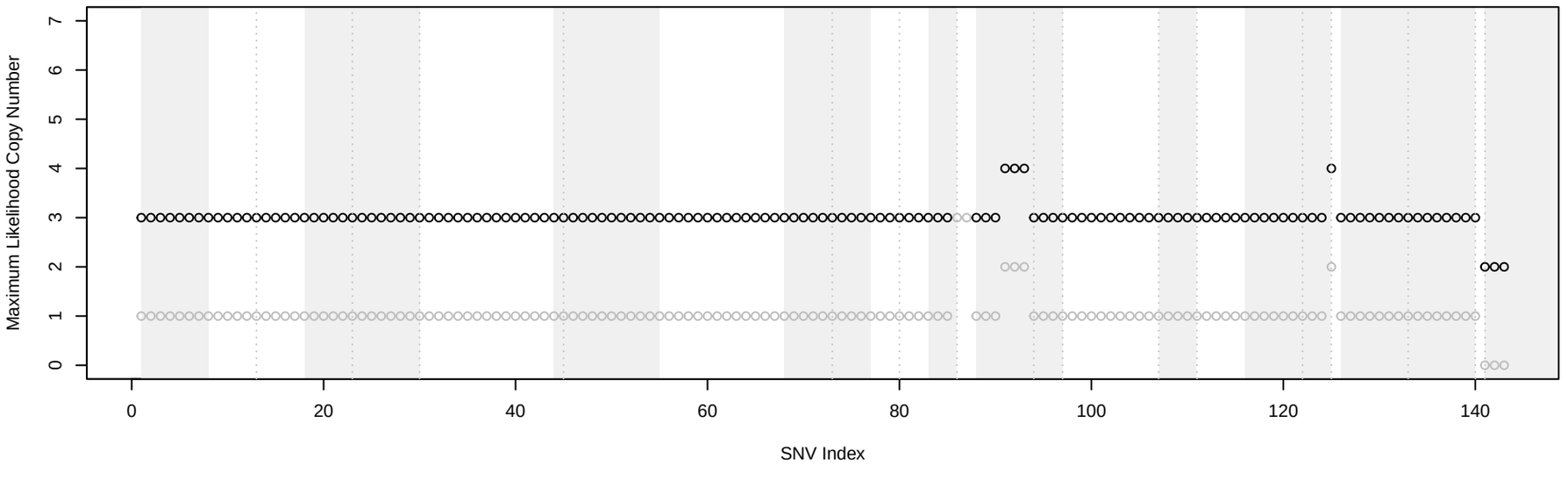

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

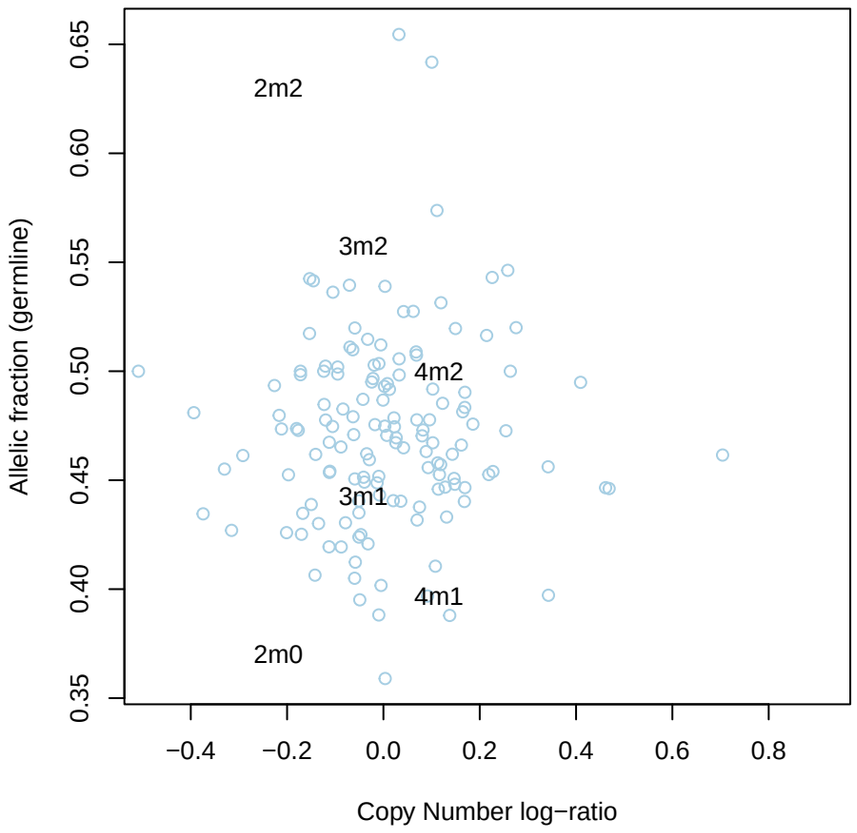

Power 0.8
Frequency
0
10
20
30
40
0.2
0.4
0.6
0.8
1.0
Cellular fraction

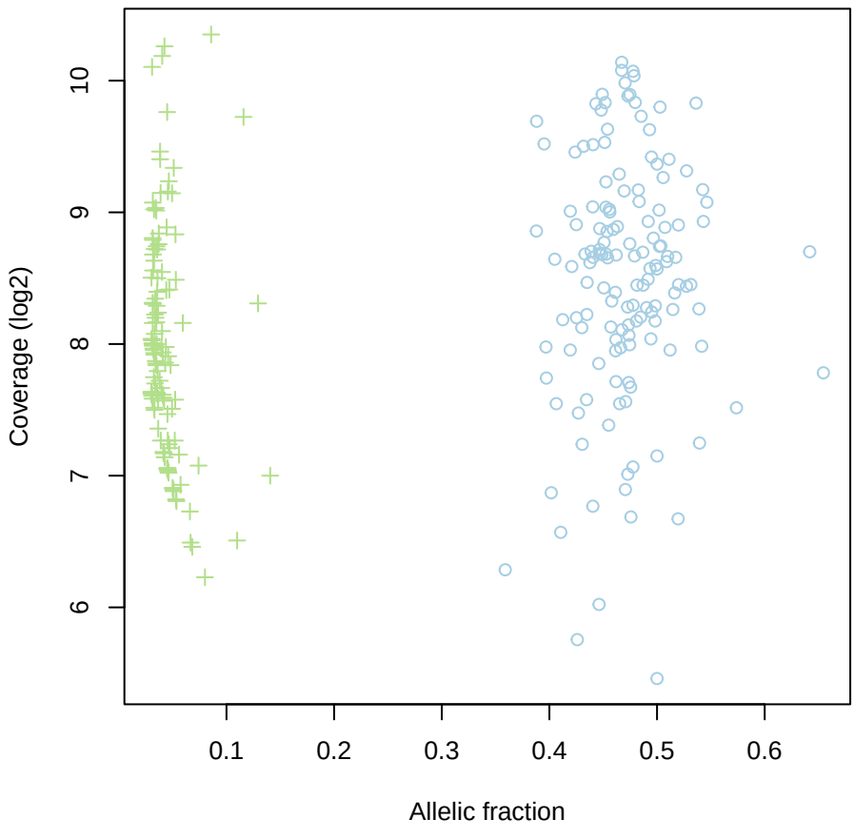

Purity: 0.26 Tumor ploidy: 3.254
0
1
2
3
4
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

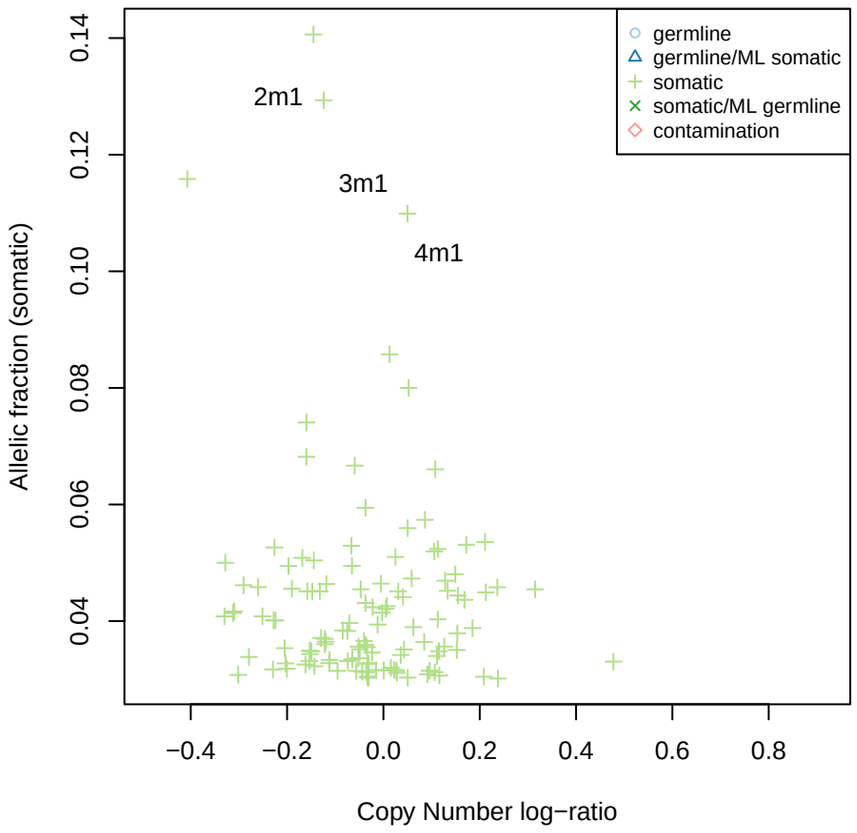

Purity: 0.26 Tumor ploidy: 3.254 SNV log−likelihood: 51.52 GoF: 92.1% Mean coverage: 306;377
1 2 3 4 5 6 7 8 9 12 13 14 15 16 18 19 21
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

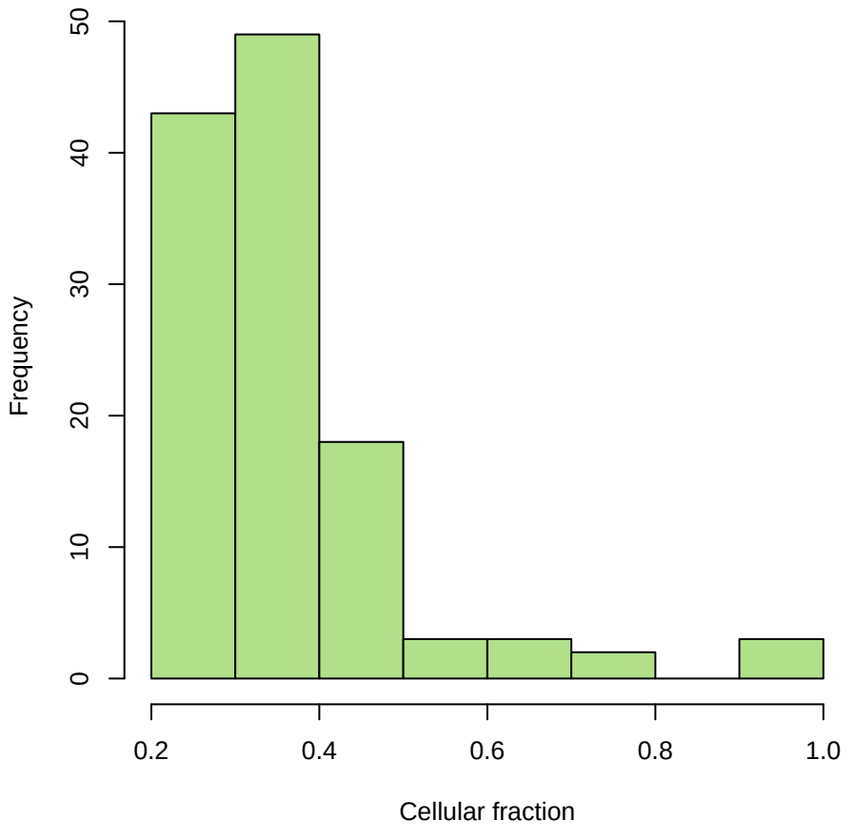

SCNA−fit log−likelihood: −5168.72
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 7
0 20 40 60 80 100 120 140
SNV Index

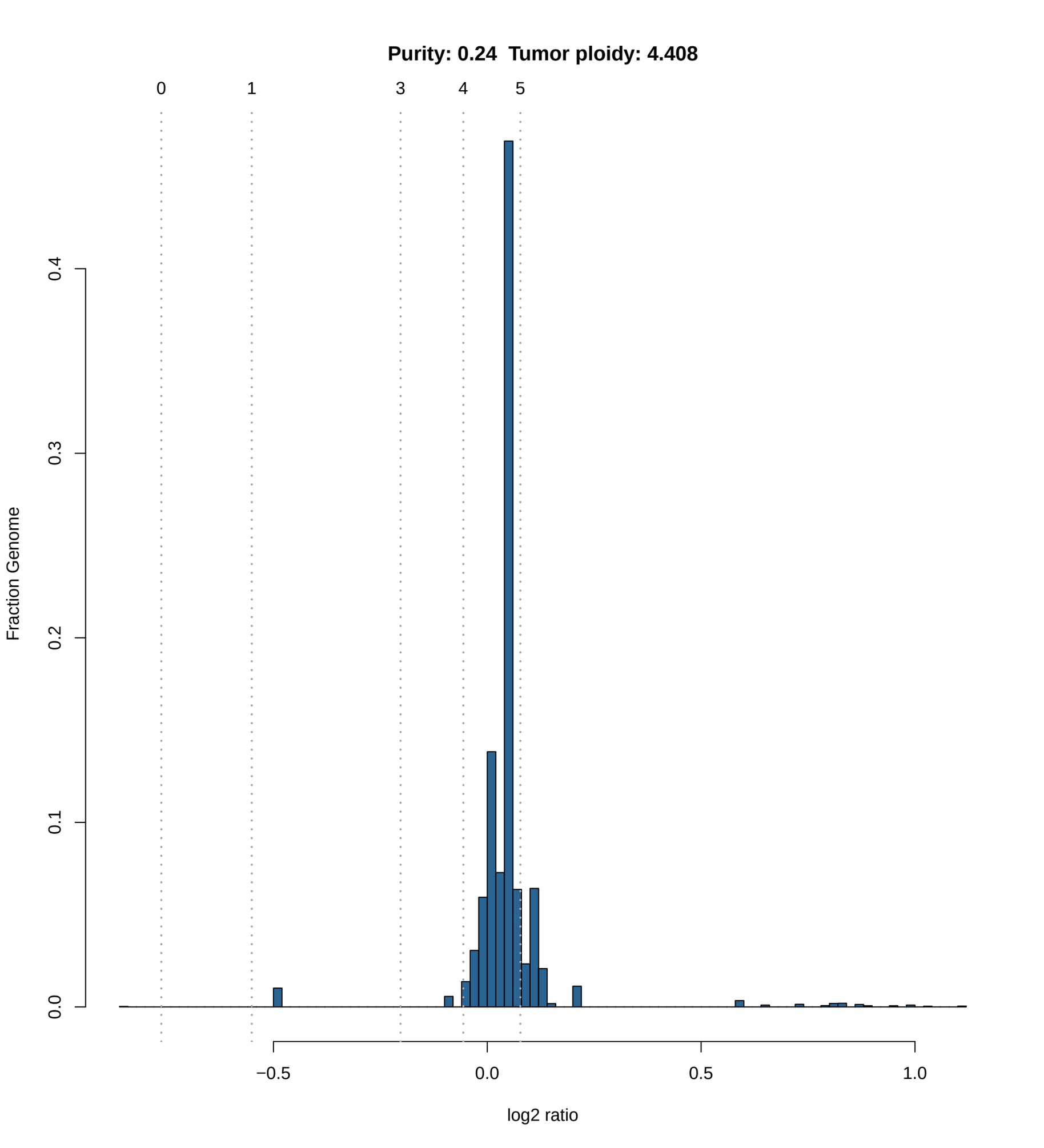

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

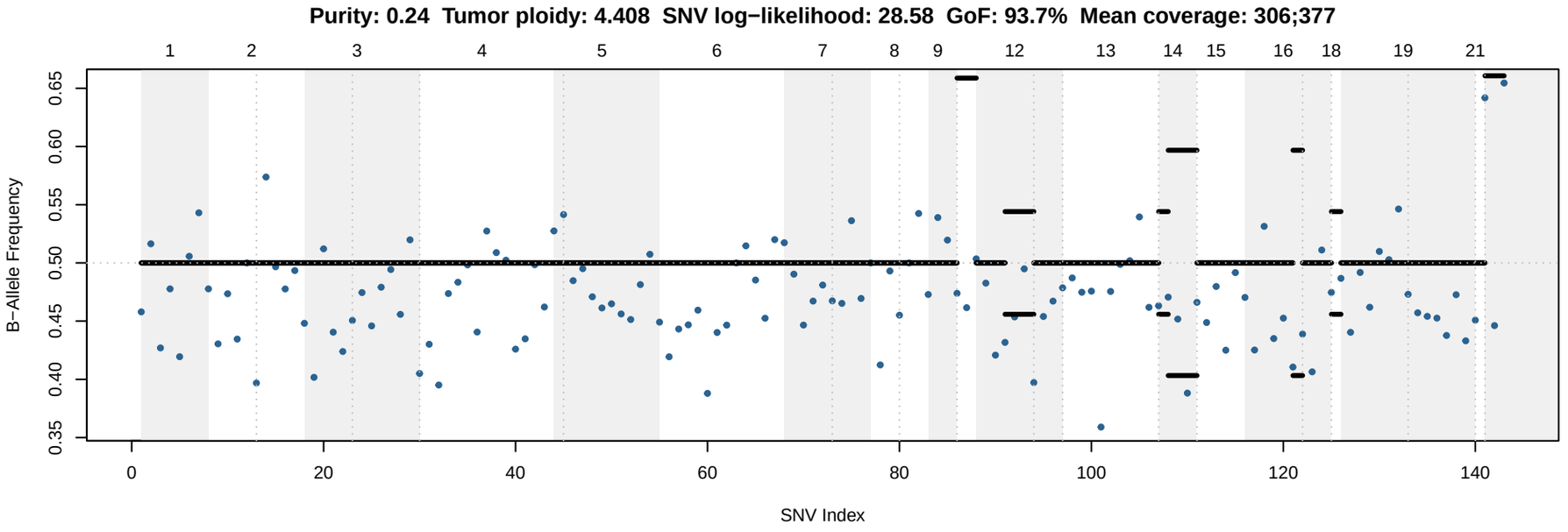

Allelic fraction (germline)
Copy Number log−ratio
2m2
3m2
4m2
3m1
4m1
2m0

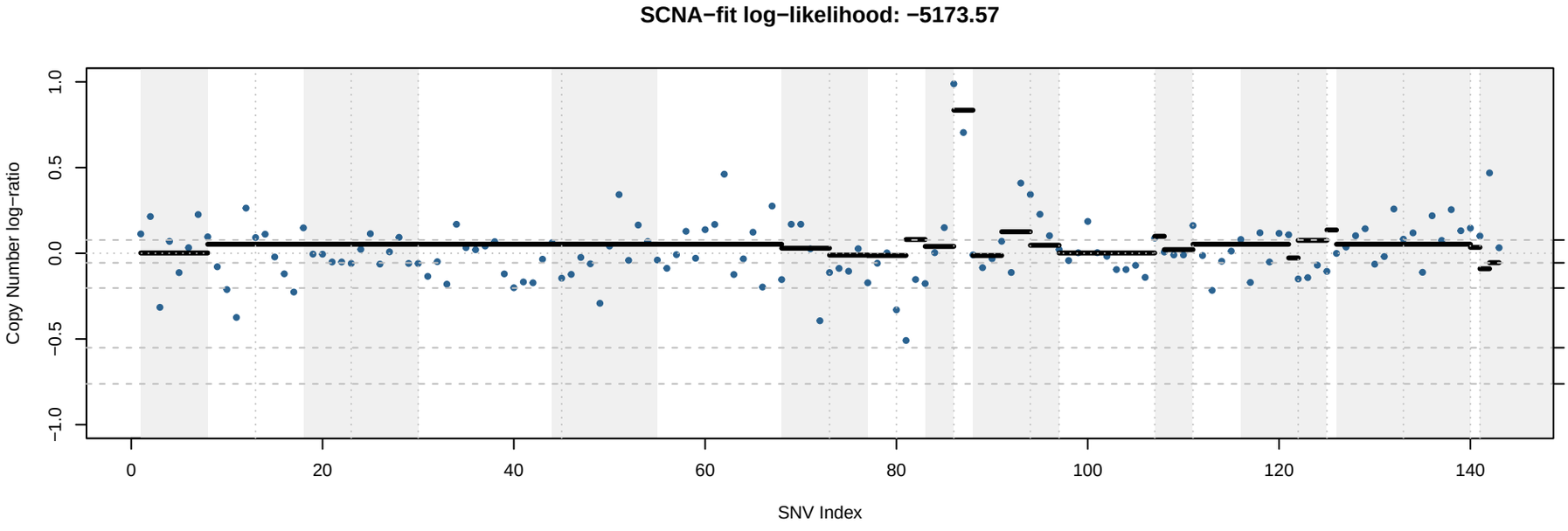

Coverage (log2)
Allelic fraction

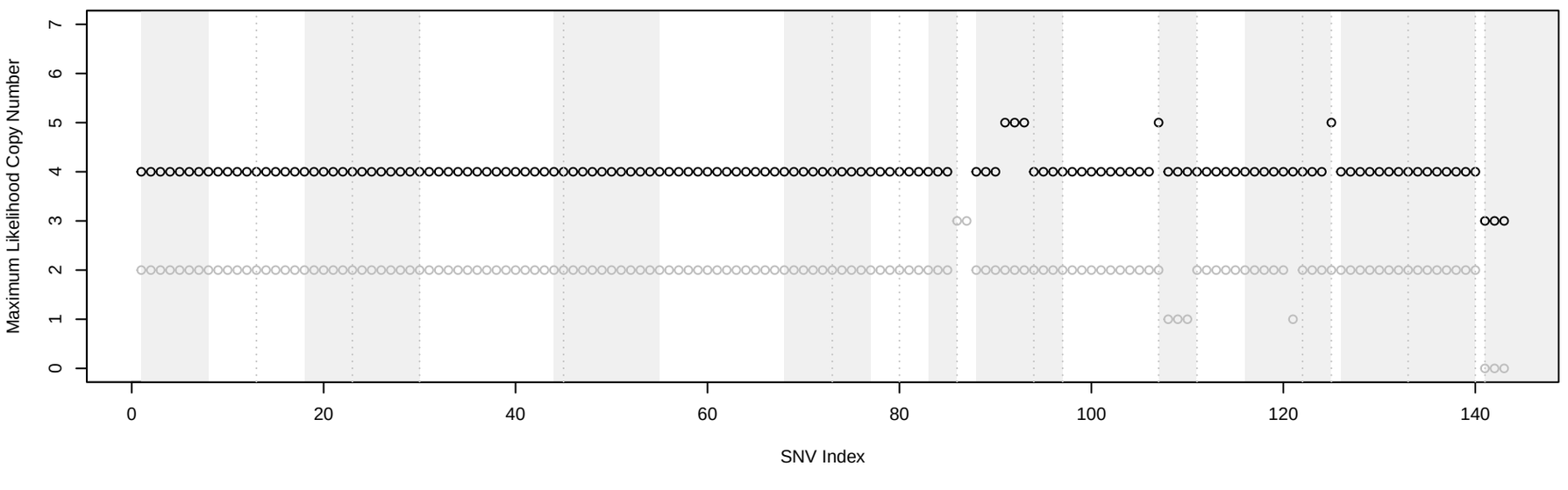

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m1
3m1
4m1

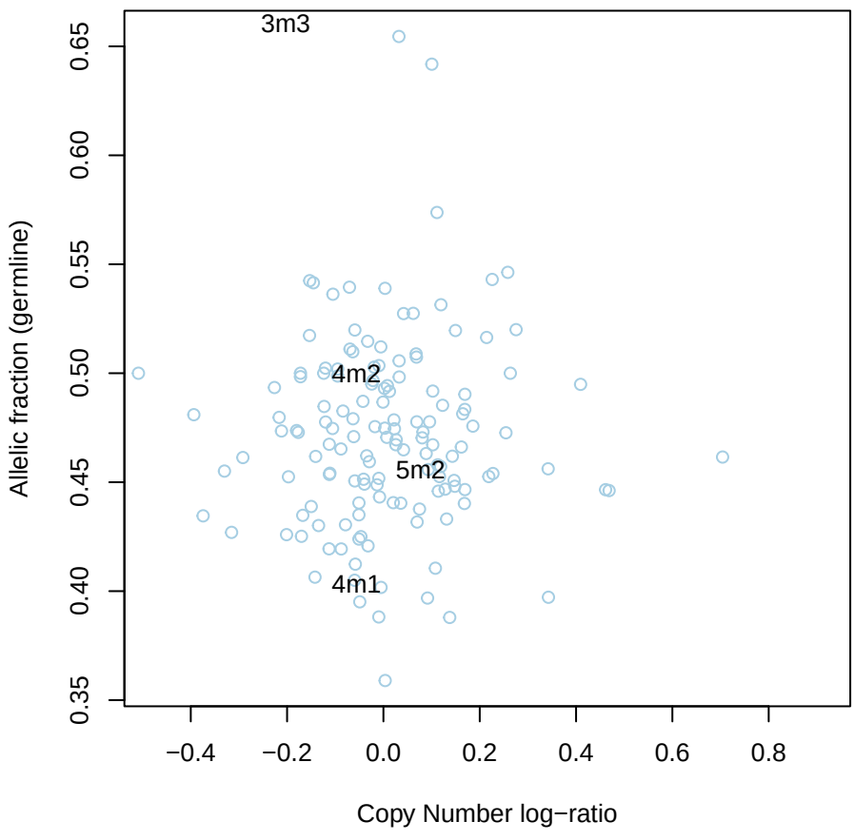

Frequency
Cellular fraction

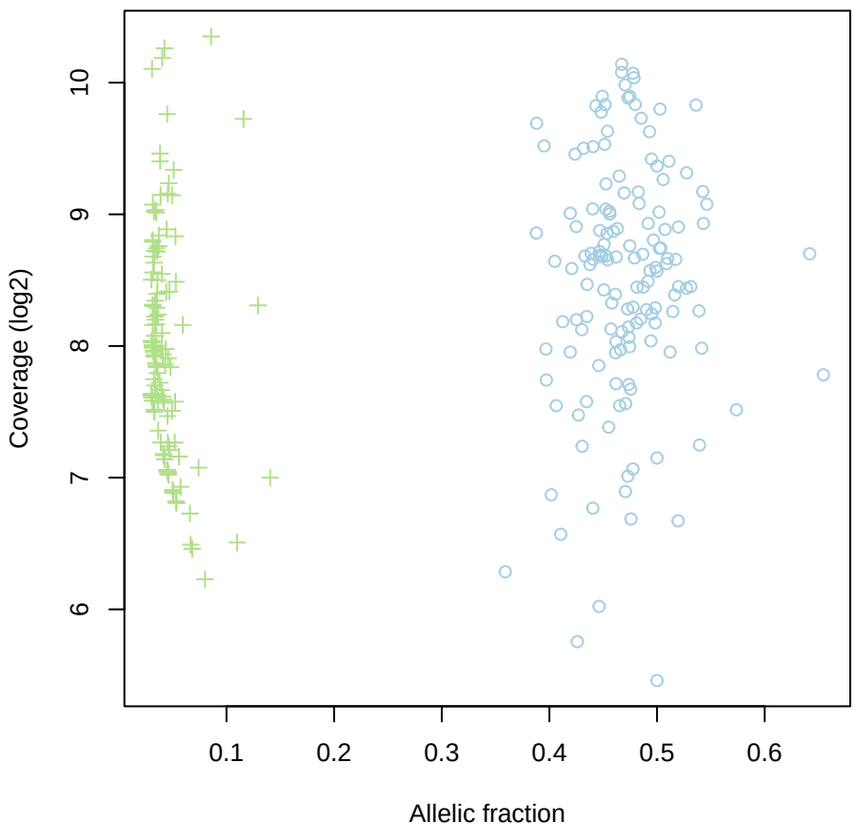

Purity: 0.24 Tumor ploidy: 4.408
0
1
3
4
5
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

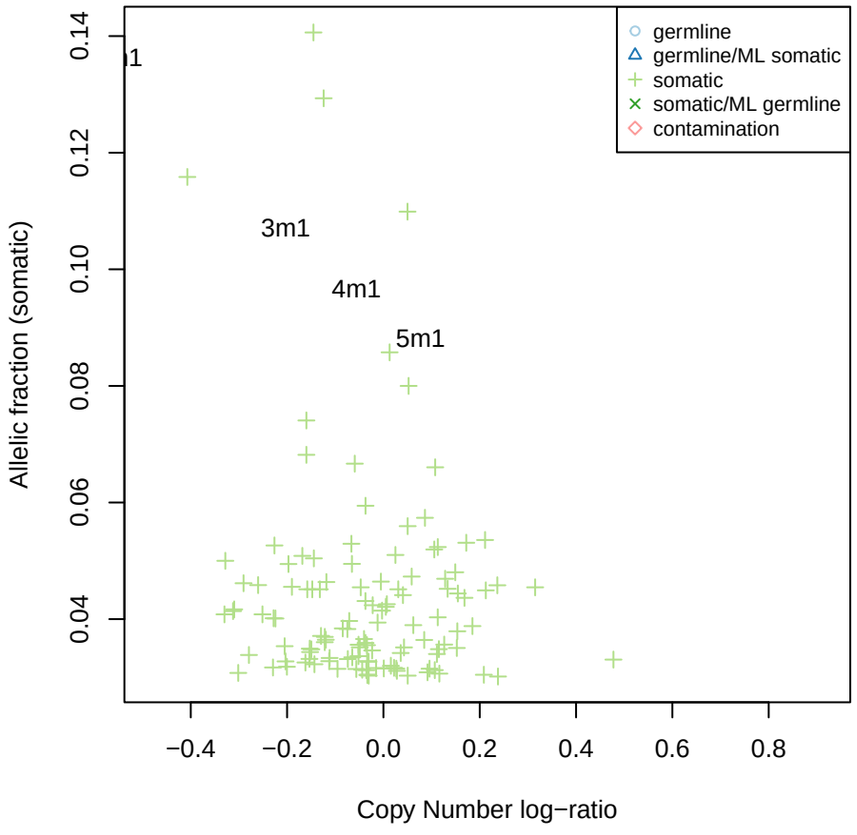

Purity: 0.24 Tumor ploidy: 4.408 SNV log−likelihood: 28.58 GoF: 93.7% Mean coverage: 306;377
1 2 3 4 5 6 7 8 9 12 13 14 15 16 18 19 21
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

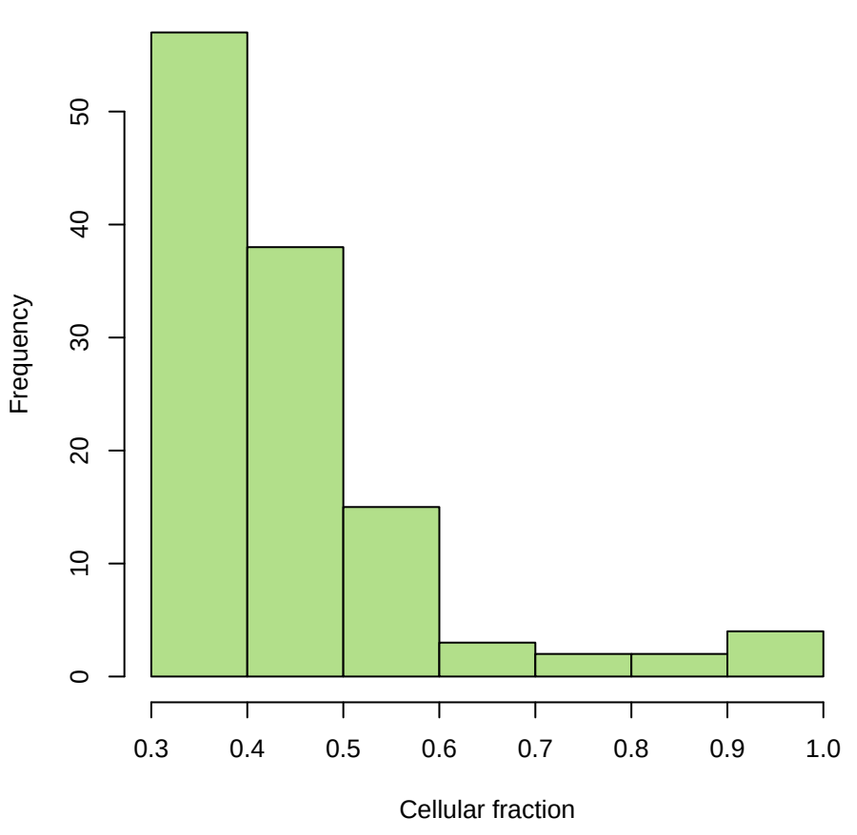

SCNA−fit log−likelihood: −5173.57
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 3 4
0 20 40 60 80 100 120 140
SNV Index

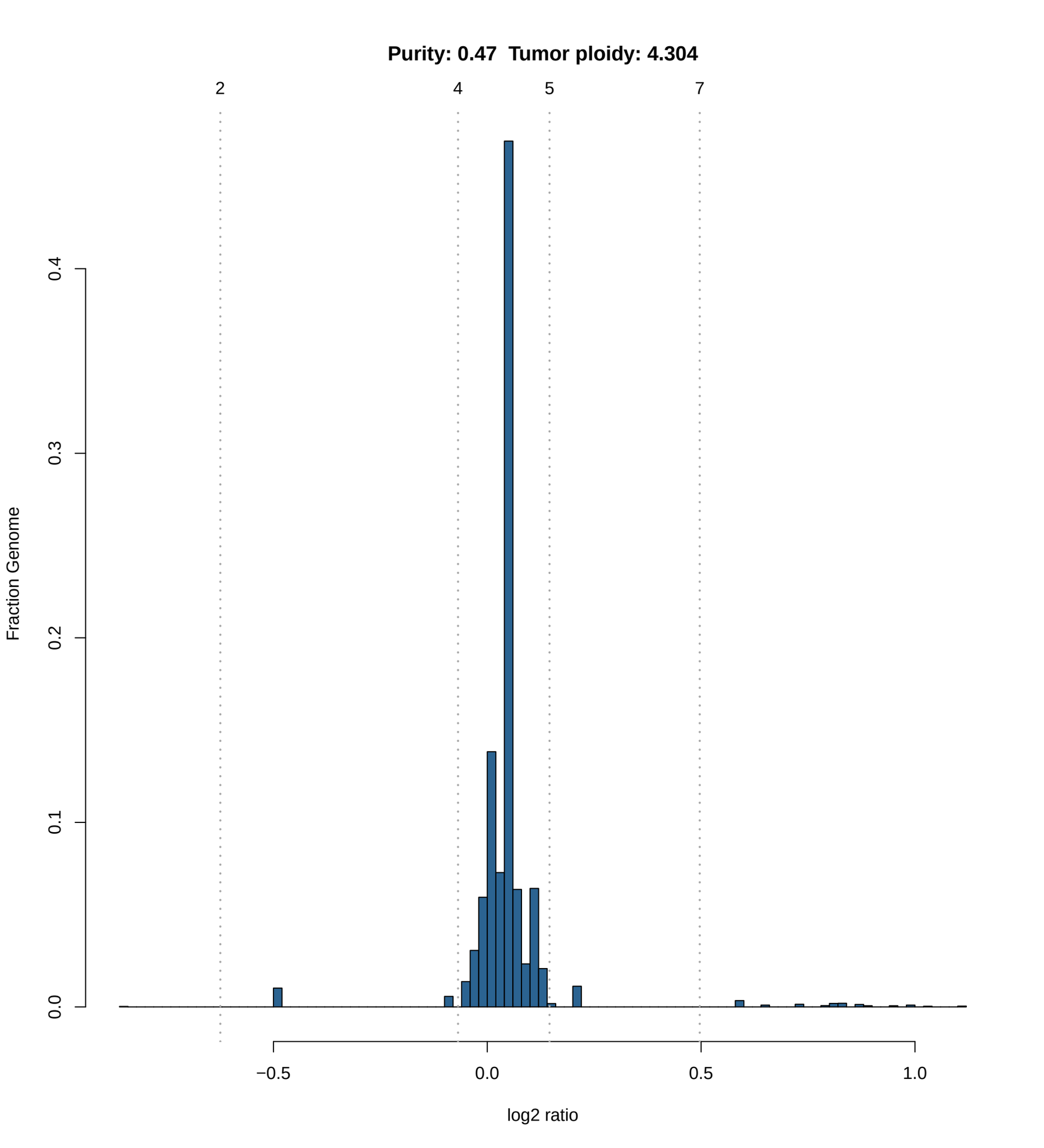

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

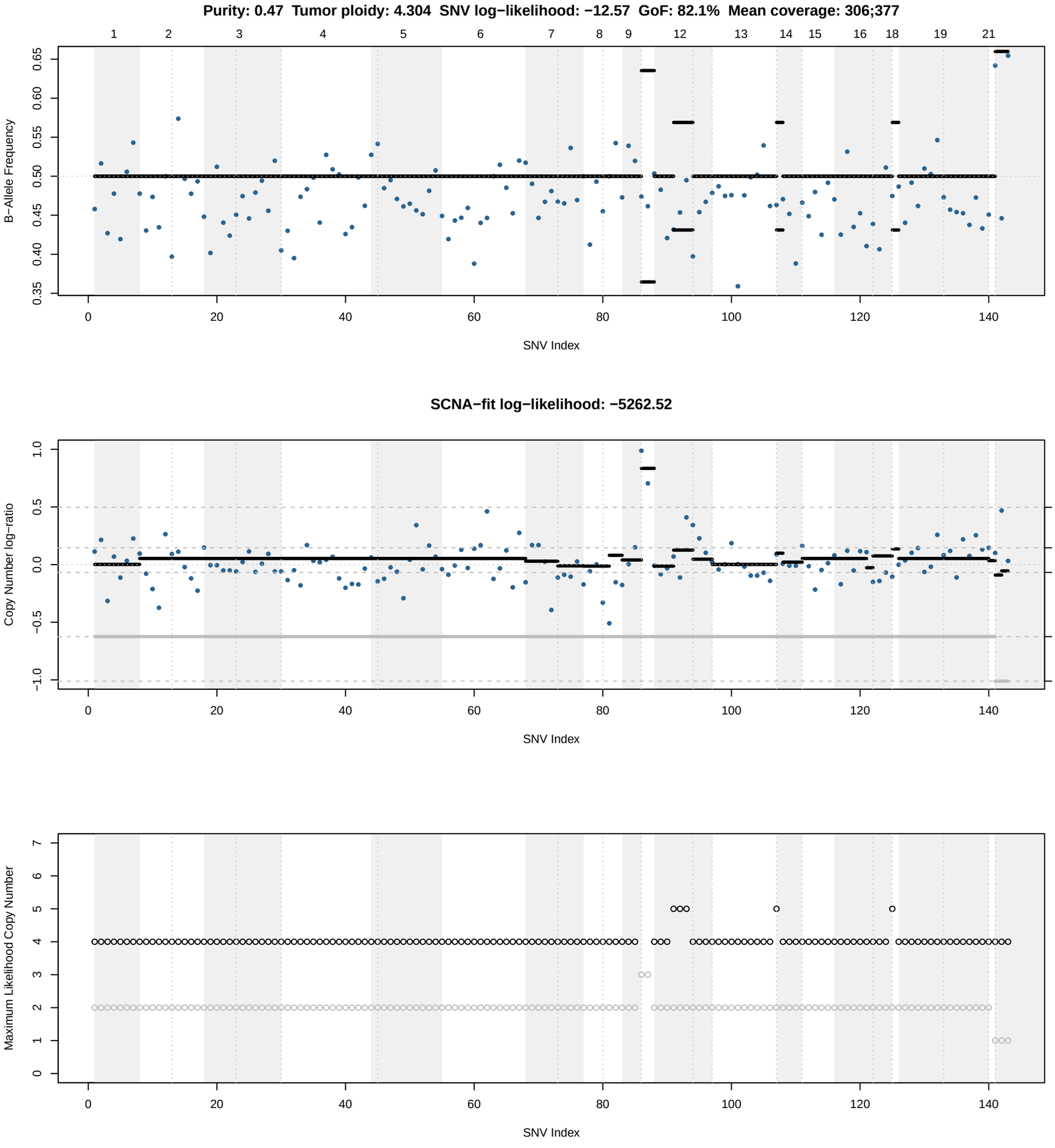

3m3
4m2
5m2
4m1
Allelic fraction (germline)
Copy Number log−ratio

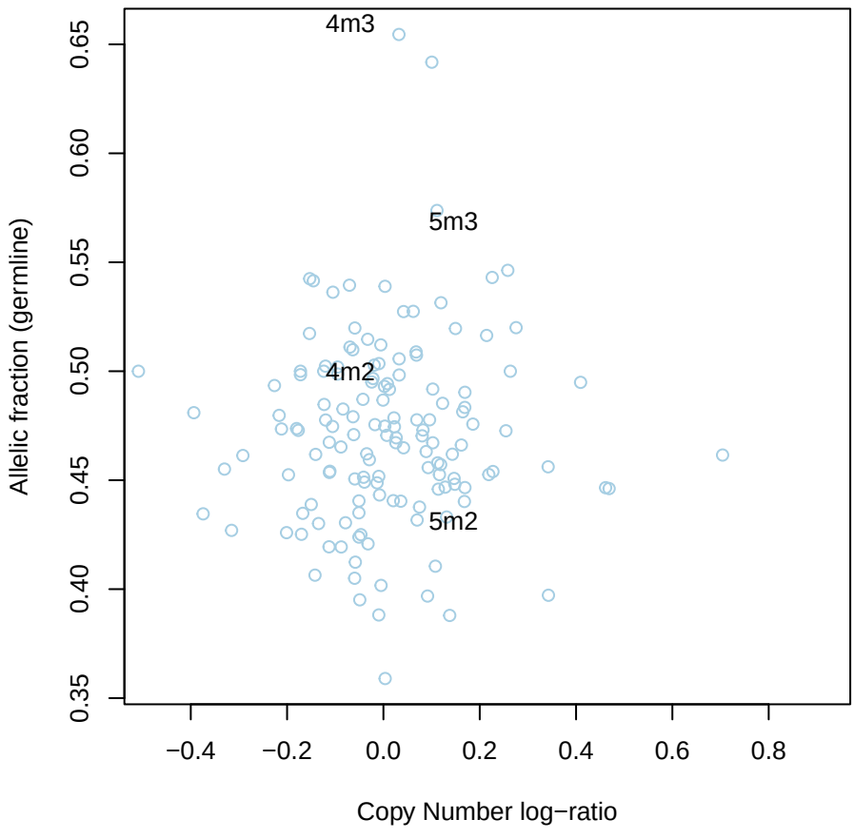

Coverage (log2)
Allelic fraction

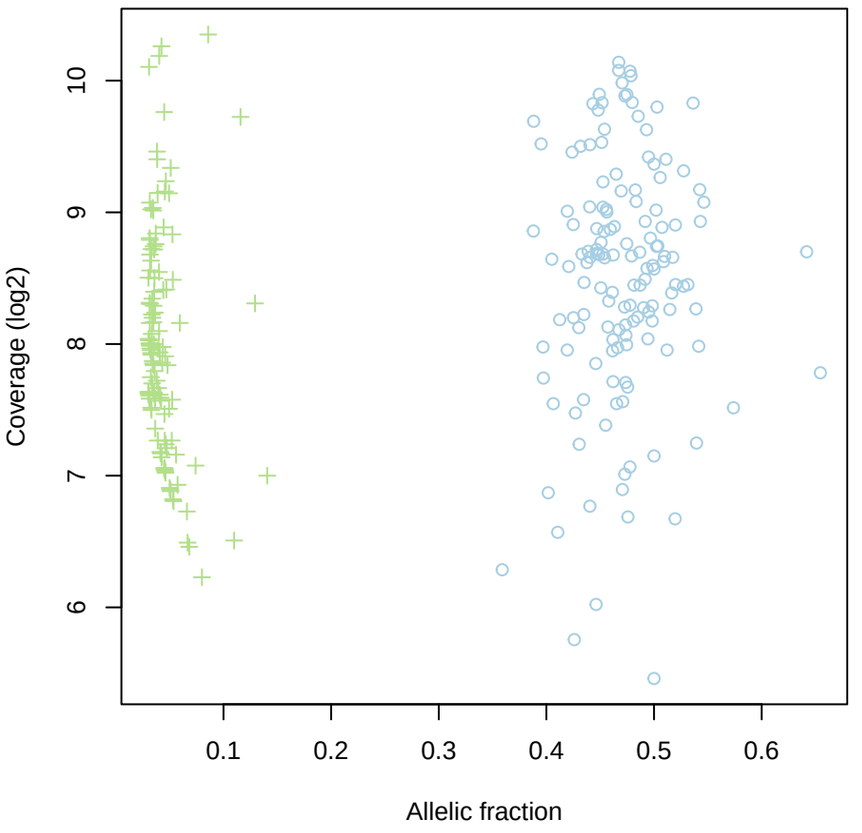

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
Allelic fraction (somatic)
Copy Number log−ratio

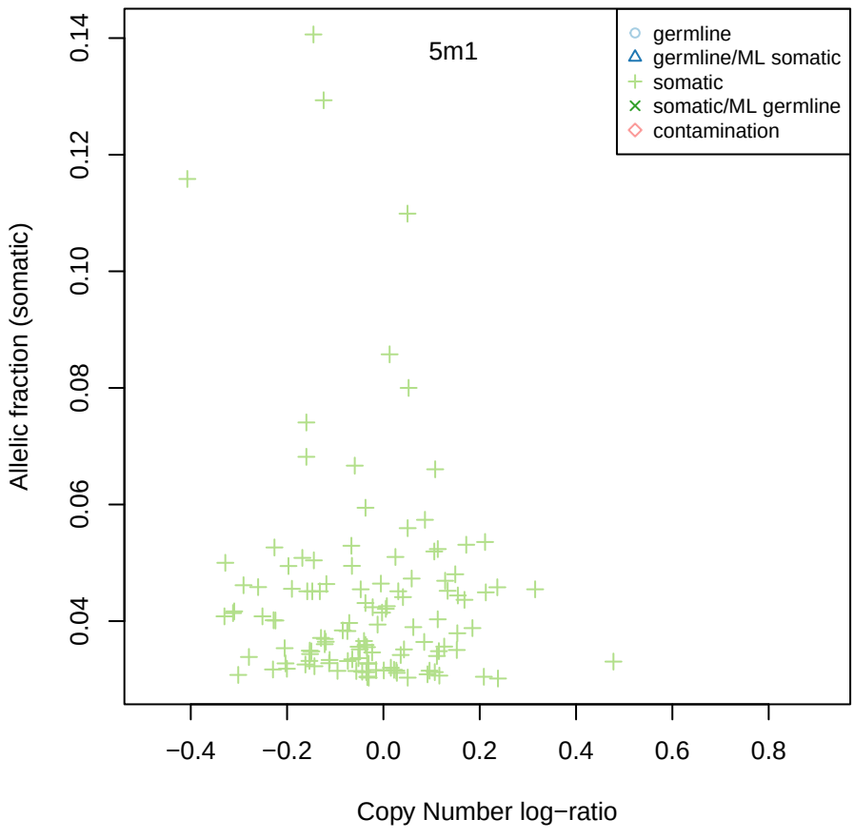

Frequency
Cellular fraction

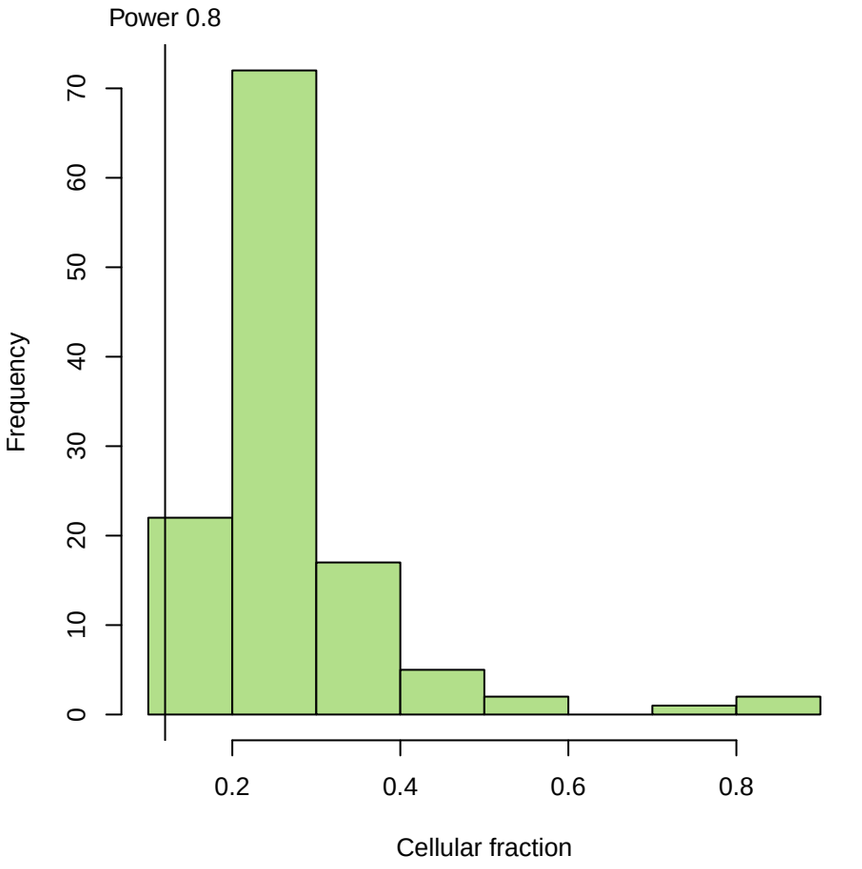

Purity: 0.47 Tumor ploidy: 4.304
2
4
5
7
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

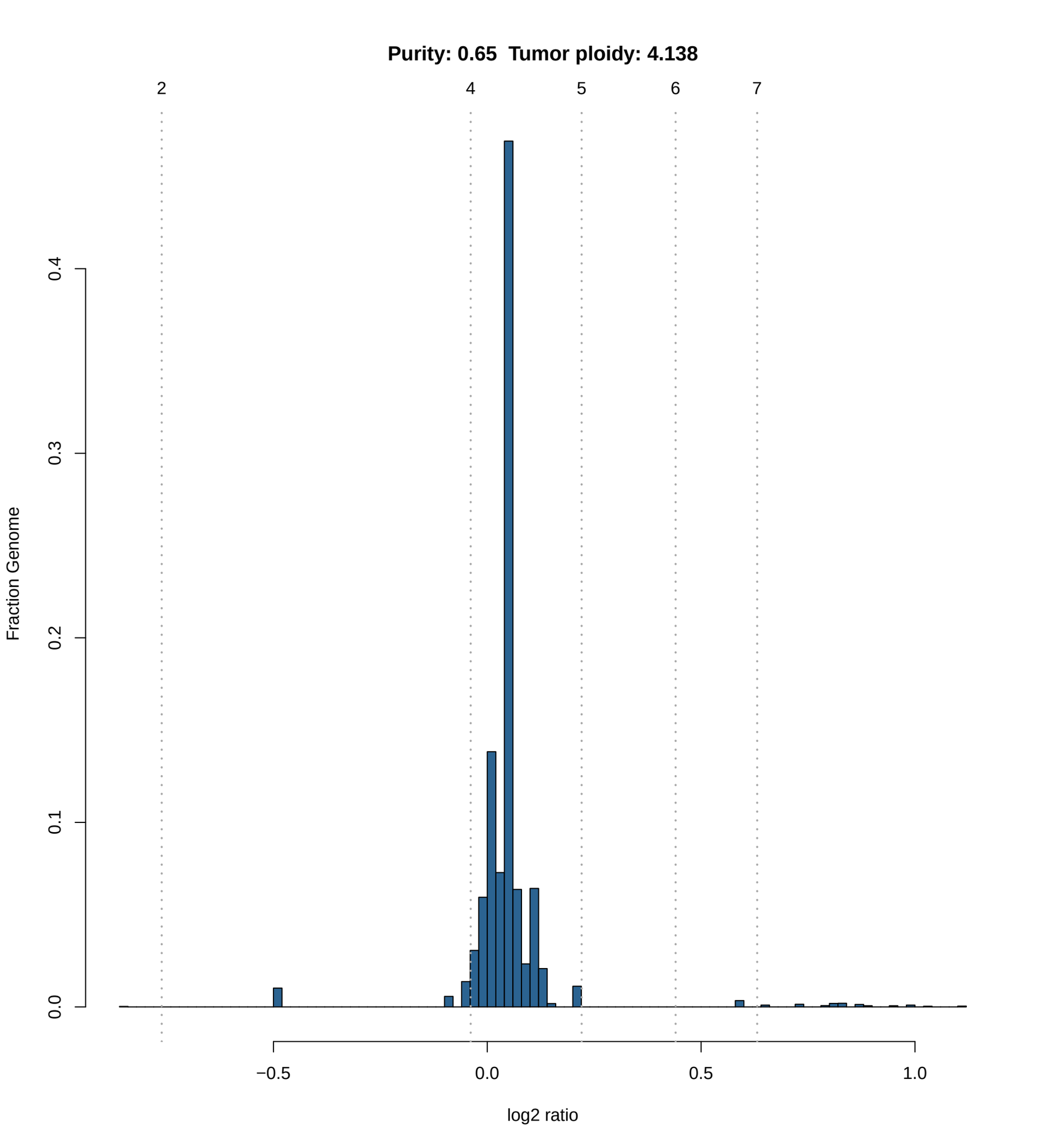

Purity: 0.47 Tumor ploidy: 4.304 SNV log−likelihood: −12.57 GoF: 82.1% Mean coverage: 306;377
1 2 3 4 5 6 7 8 9 12 13 14 15 16 18 19 21
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index
SCNA−fit log−likelihood: −5262.52
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 4 5 7
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

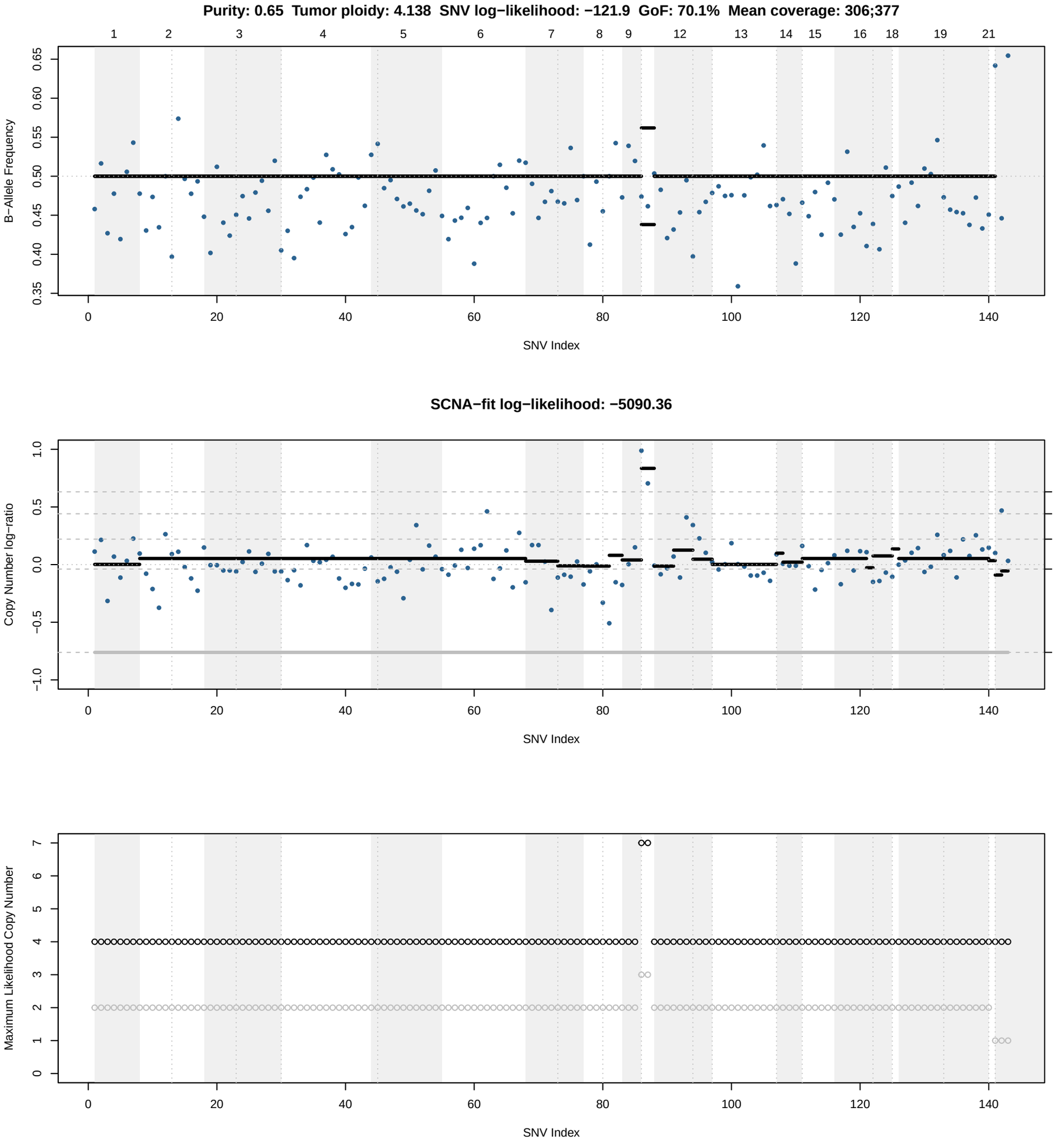

4m3
5m3
4m2
5m2
Allelic fraction (germline)
Copy Number log−ratio
0.35
0.40
0.45
0.50
0.55
0.60
0.65
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8

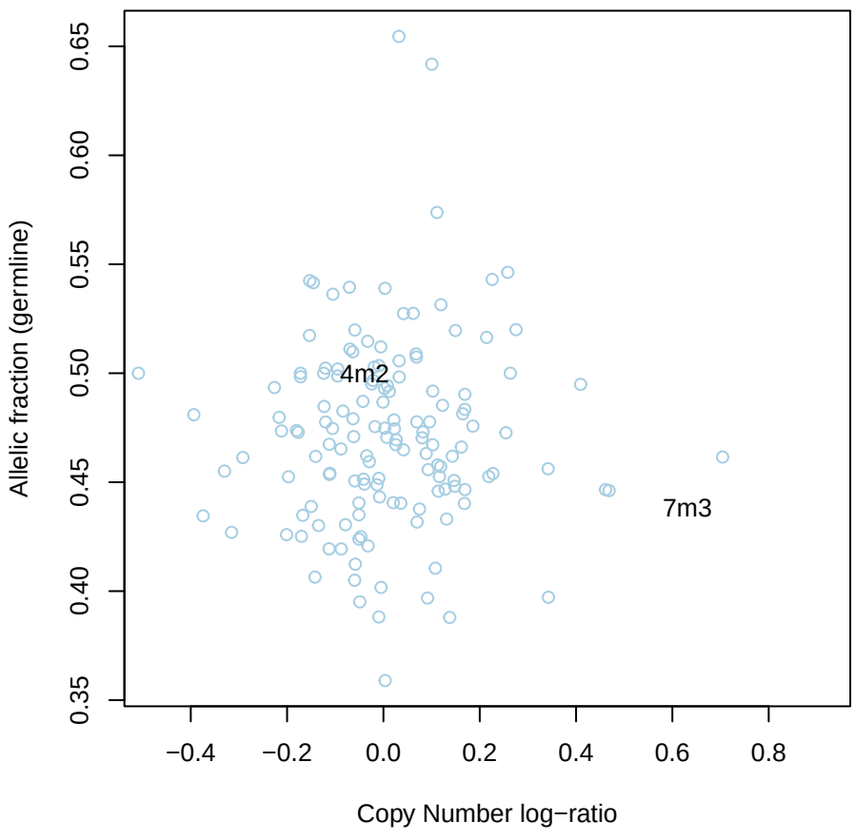

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

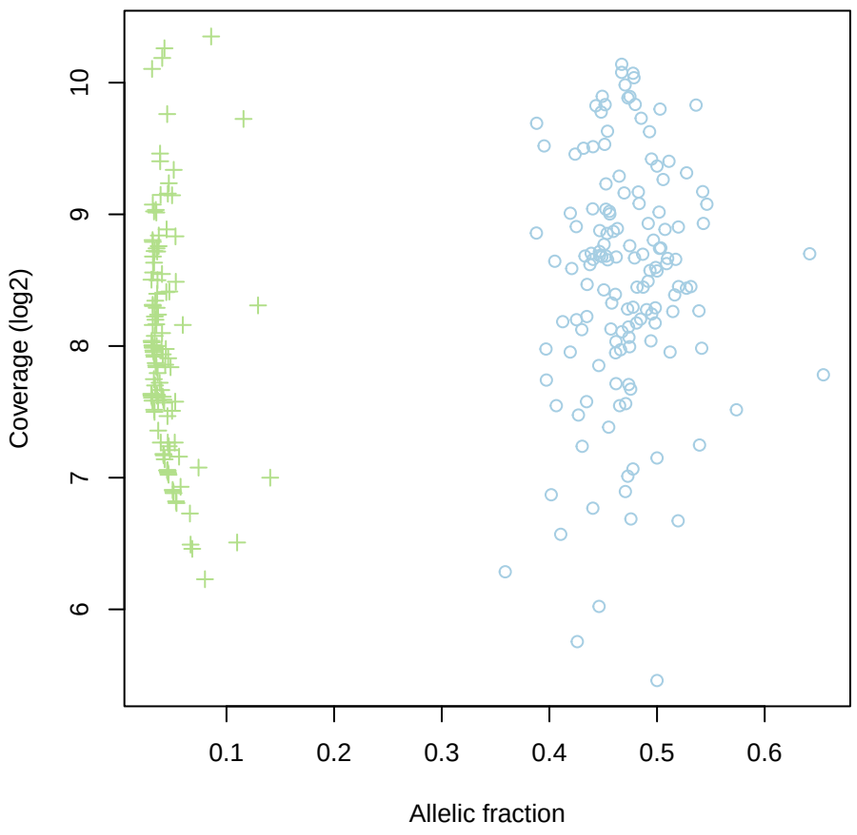

5m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
0.12
0.14
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8

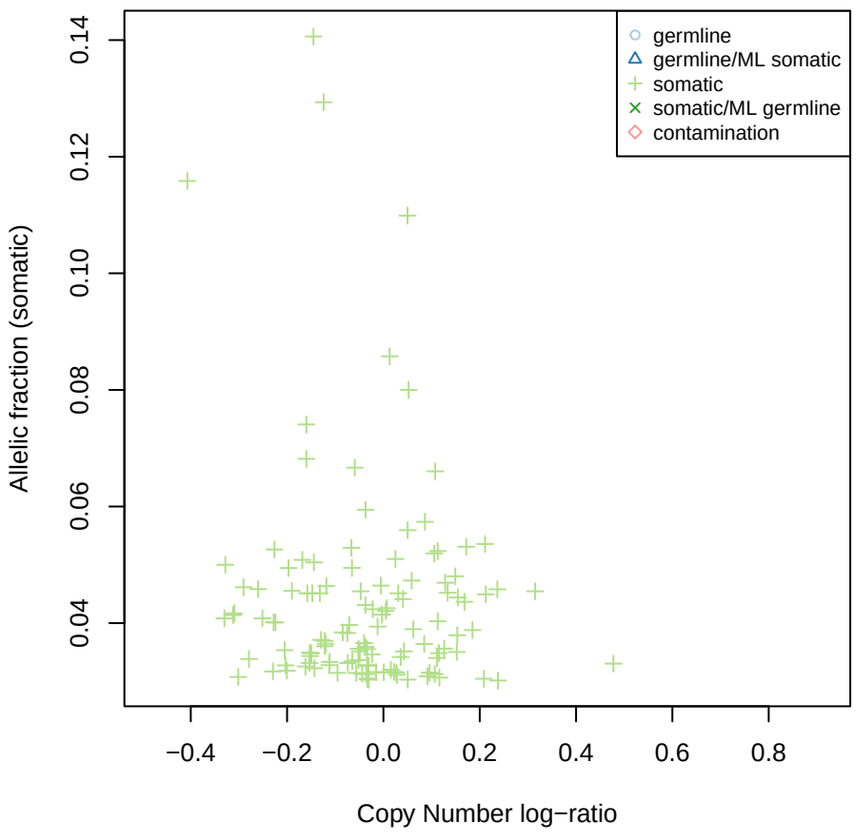

Power 0.8
Frequency
Cellular fraction
0
10
20
30
40
50
60
70
0.2
0.4
0.6
0.8

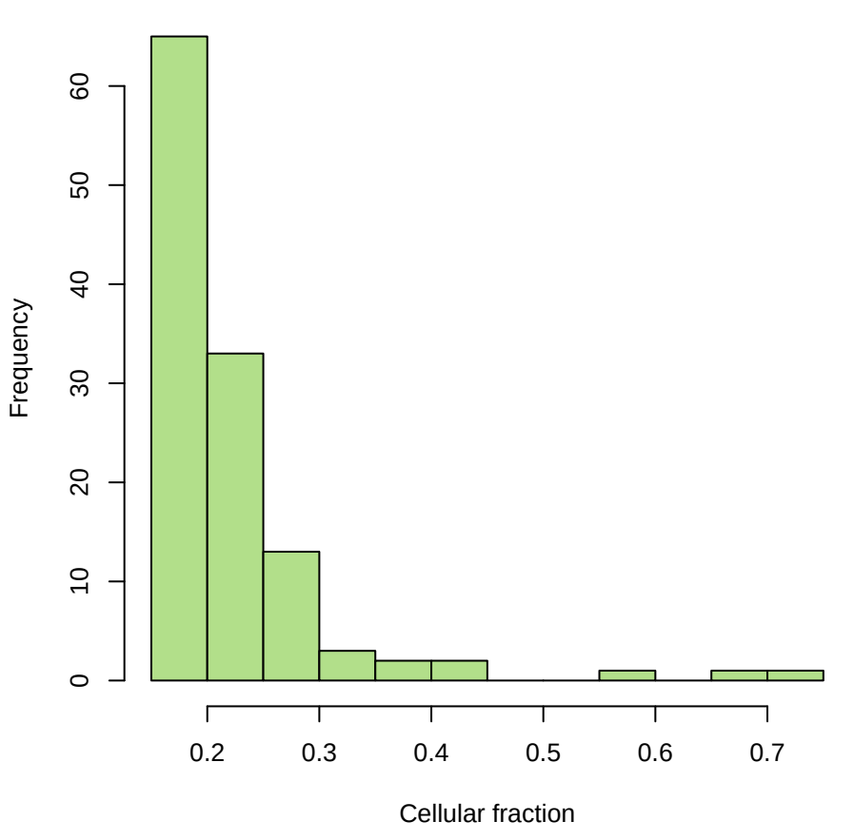

Purity: 0.65 Tumor ploidy: 4.138
2
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

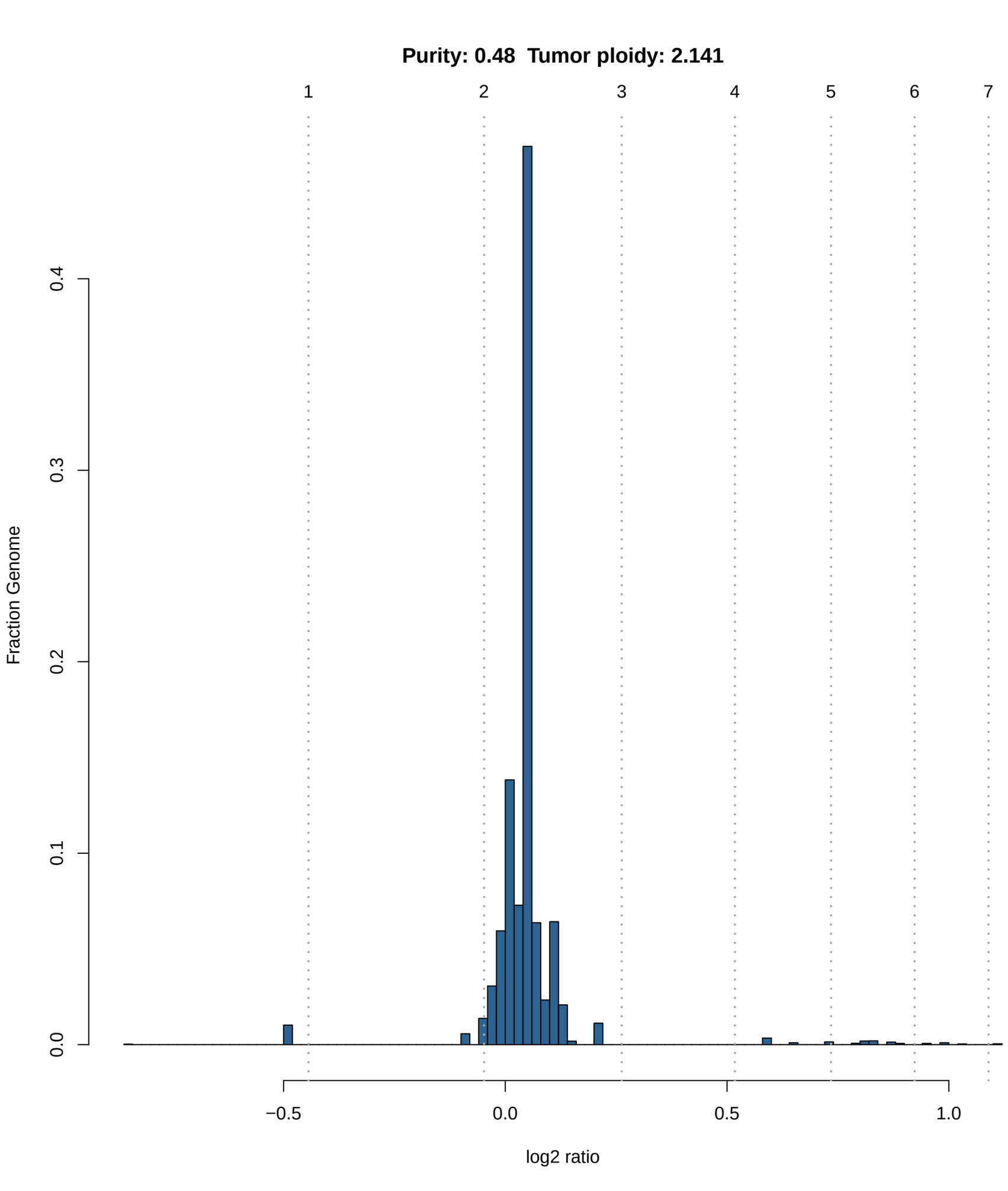

Purity: 0.65 Tumor ploidy: 4.138 SNV log−likelihood: −121.9 GoF: 70.1% Mean coverage: 306;377
1 2 3 4 5 6 7 8 9 12 13 14 15 16 18 19 21
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index
SCNA−fit log−likelihood: −5090.36
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 4 5 6 7
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

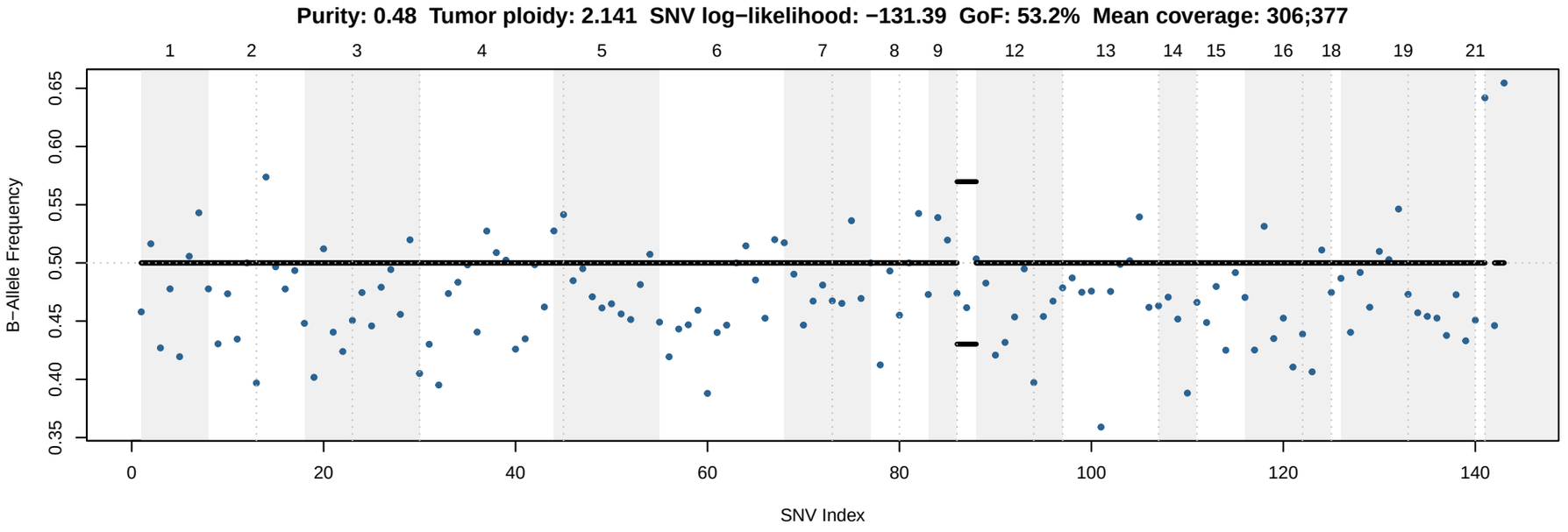

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
4m2
7m3
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

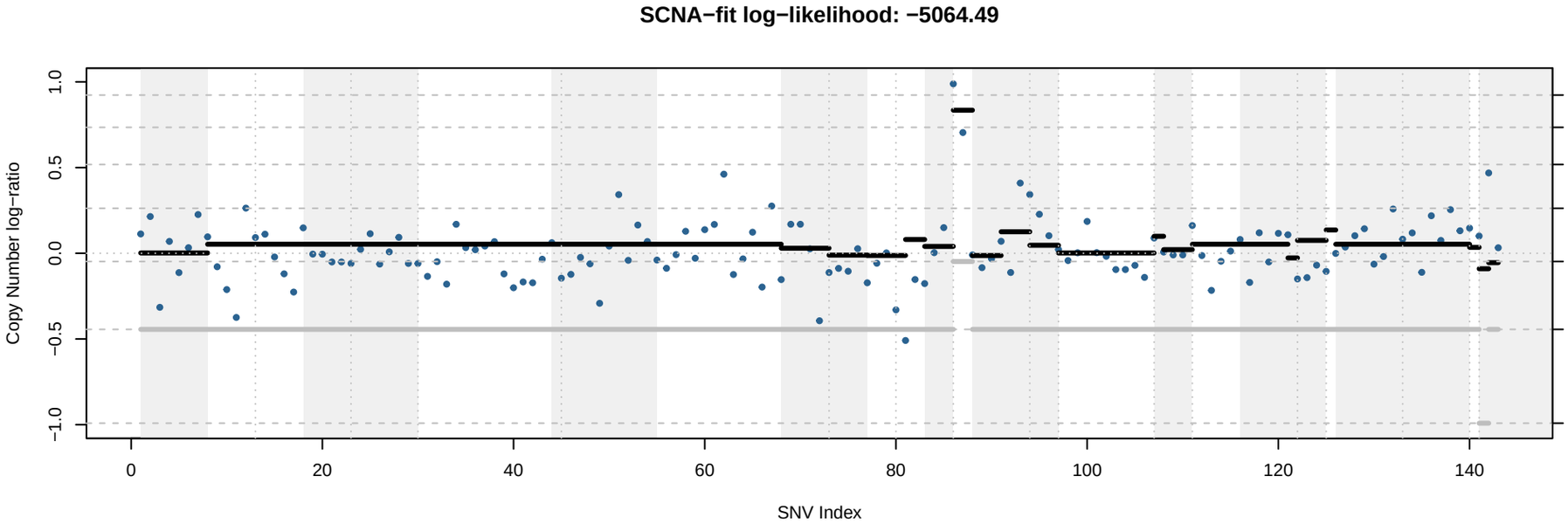

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

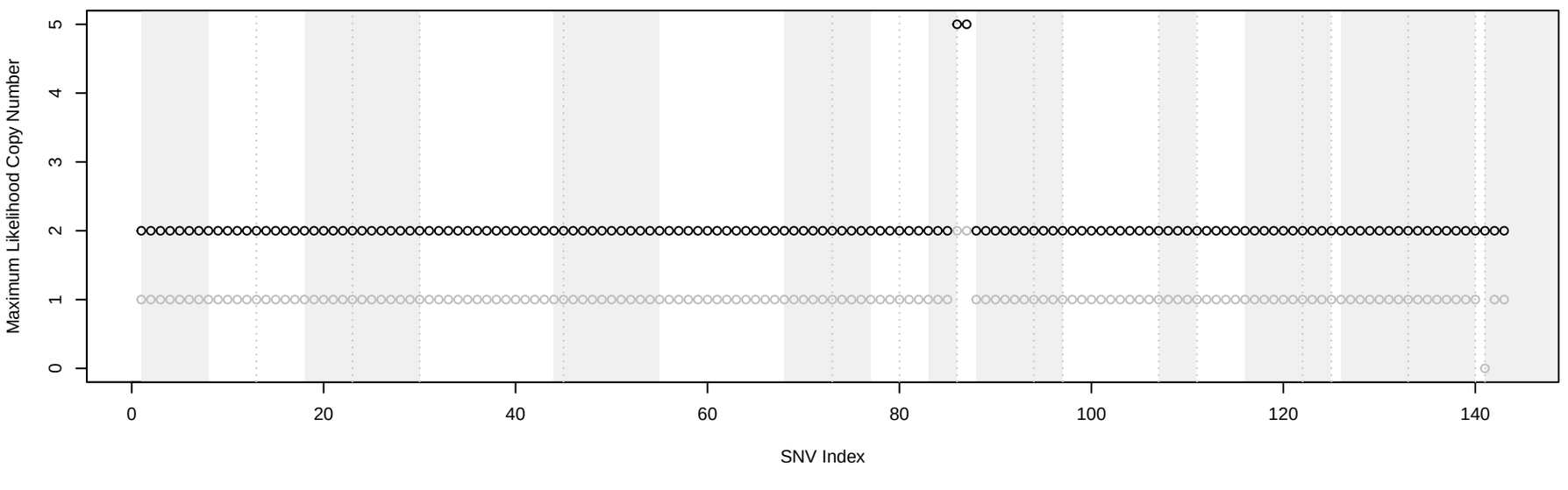

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

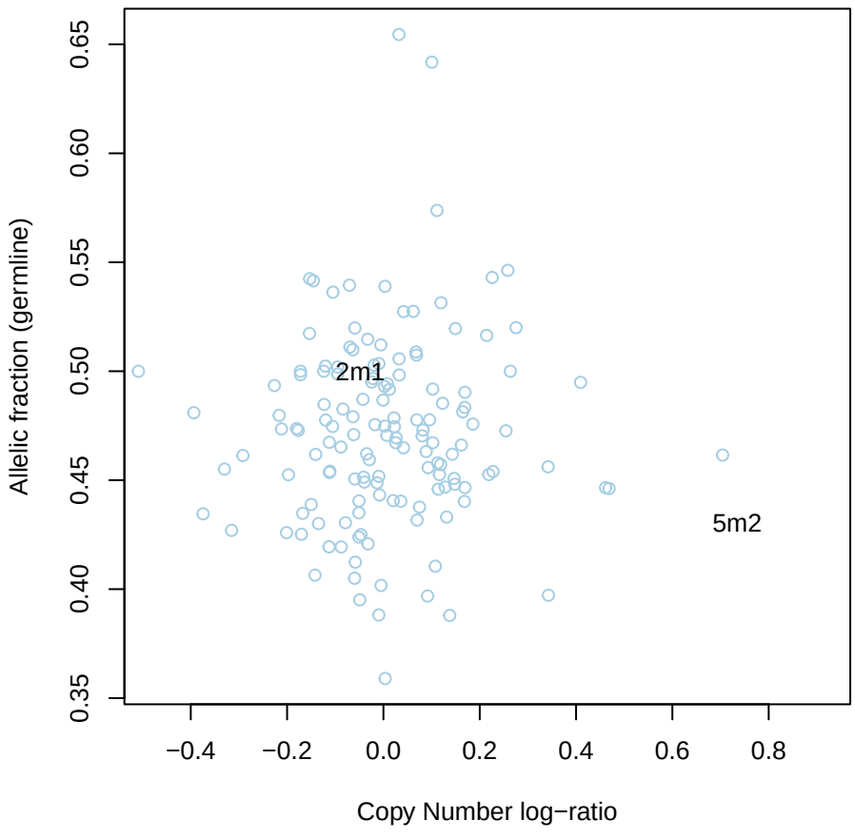

Frequency
0
10
20
30
40
50
60
0.2
0.3
0.4
0.5
0.6
0.7
Cellular fraction

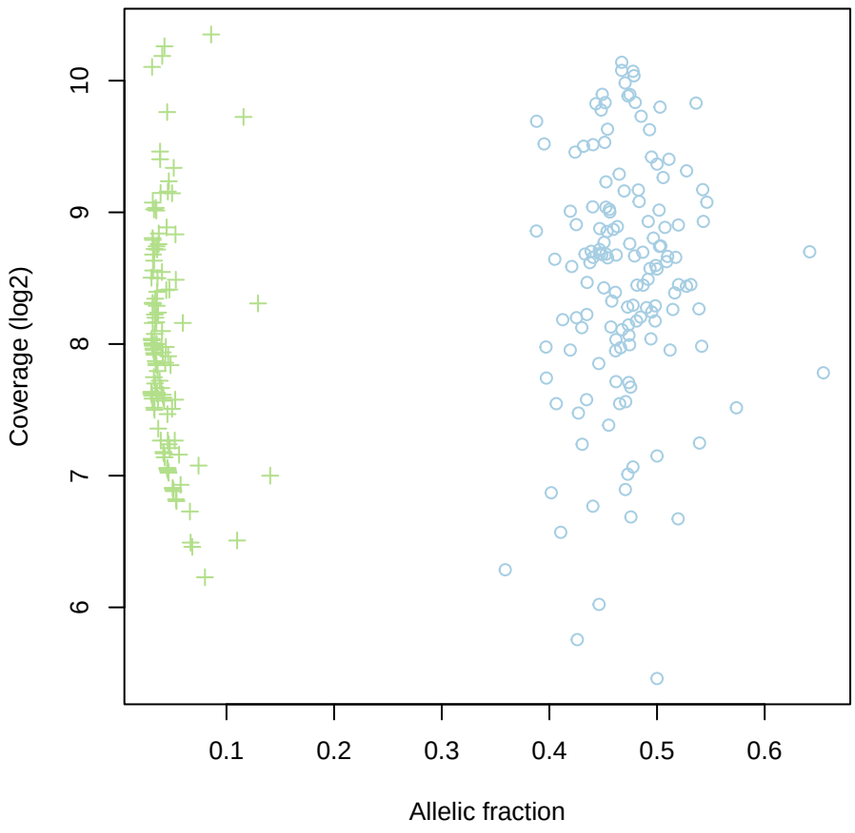

Purity: 0.48 Tumor ploidy: 2.141
1
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

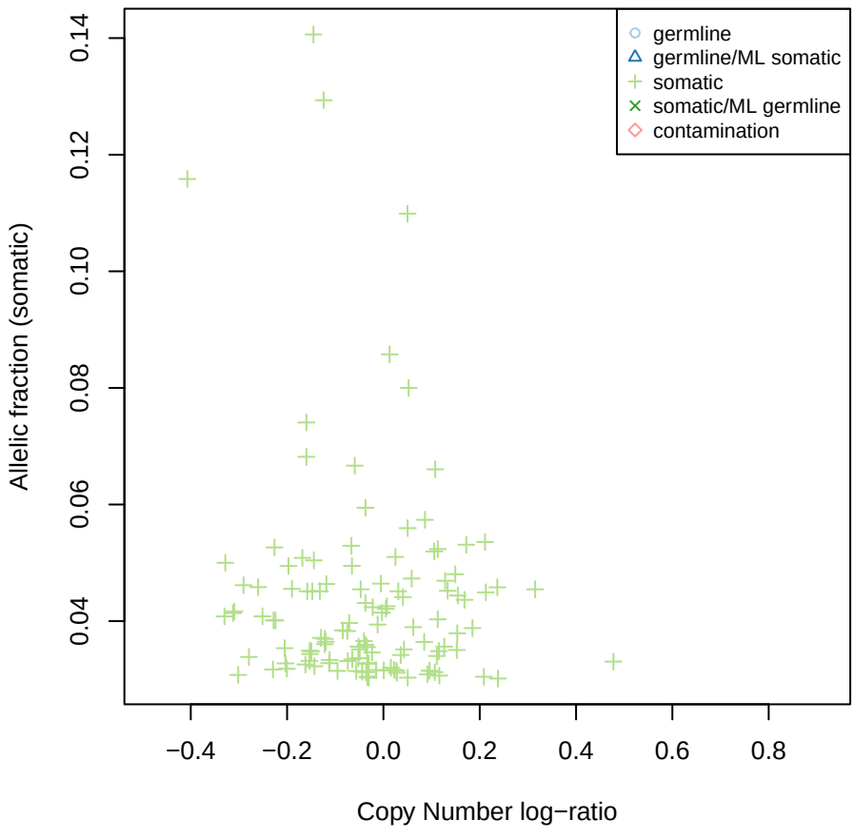

Purity: 0.48 Tumor ploidy: 2.141 SNV log−likelihood: −131.39 GoF: 53.2% Mean coverage: 306;377
1 2 3 4 5 6 7 8 9 12 13 14 15 16 18 19 21
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

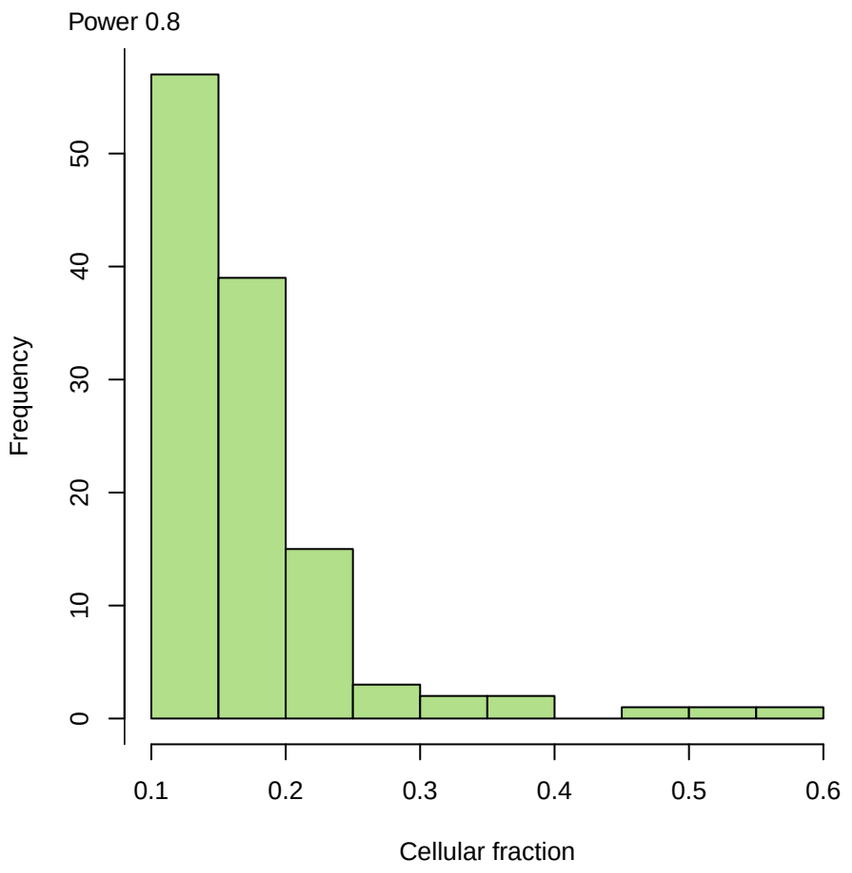

SCNA−fit log−likelihood: −5064.49
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

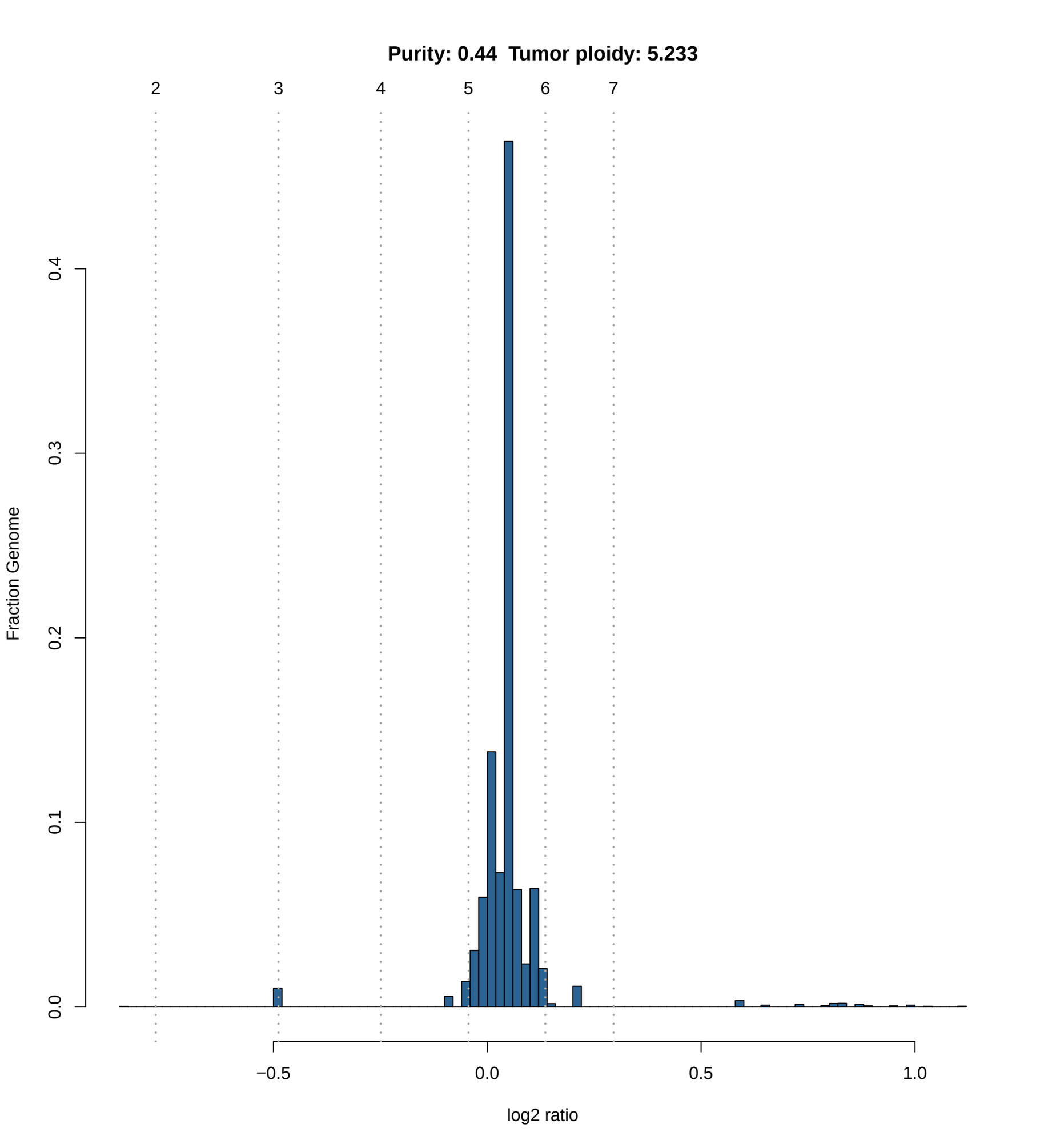

Maximum Likelihood Copy Number
0 1 2 3 4 5
∞
0 20 40 60 80 100 120 140
SNV Index

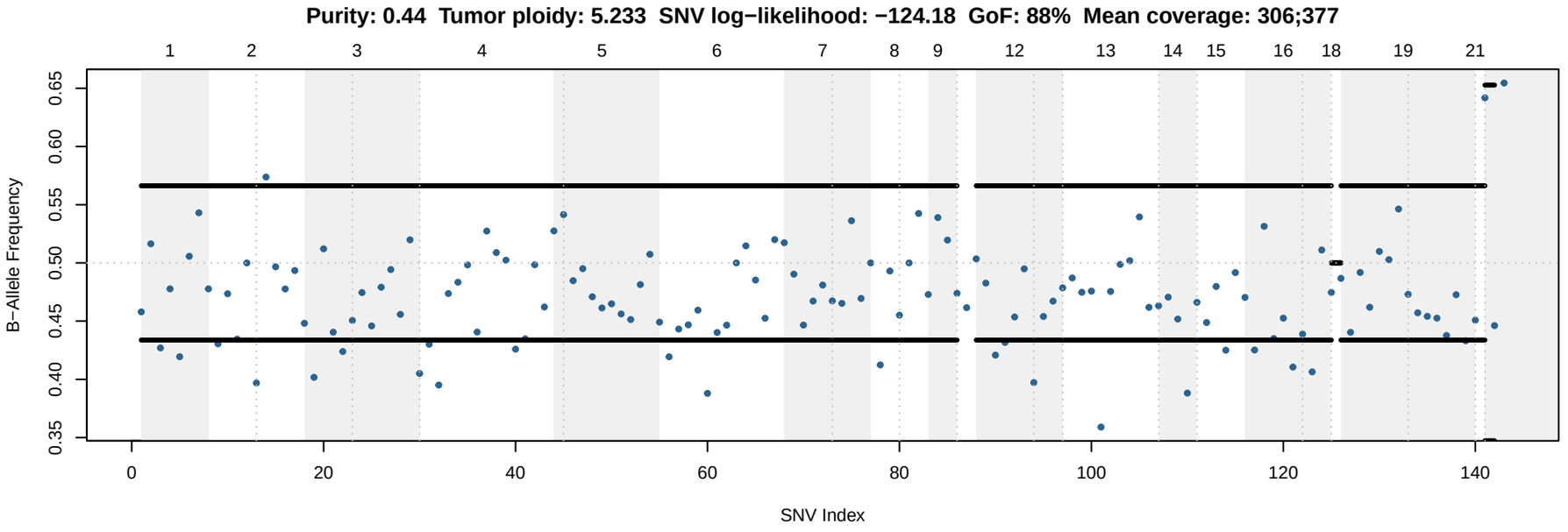

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
2m1
5m2
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

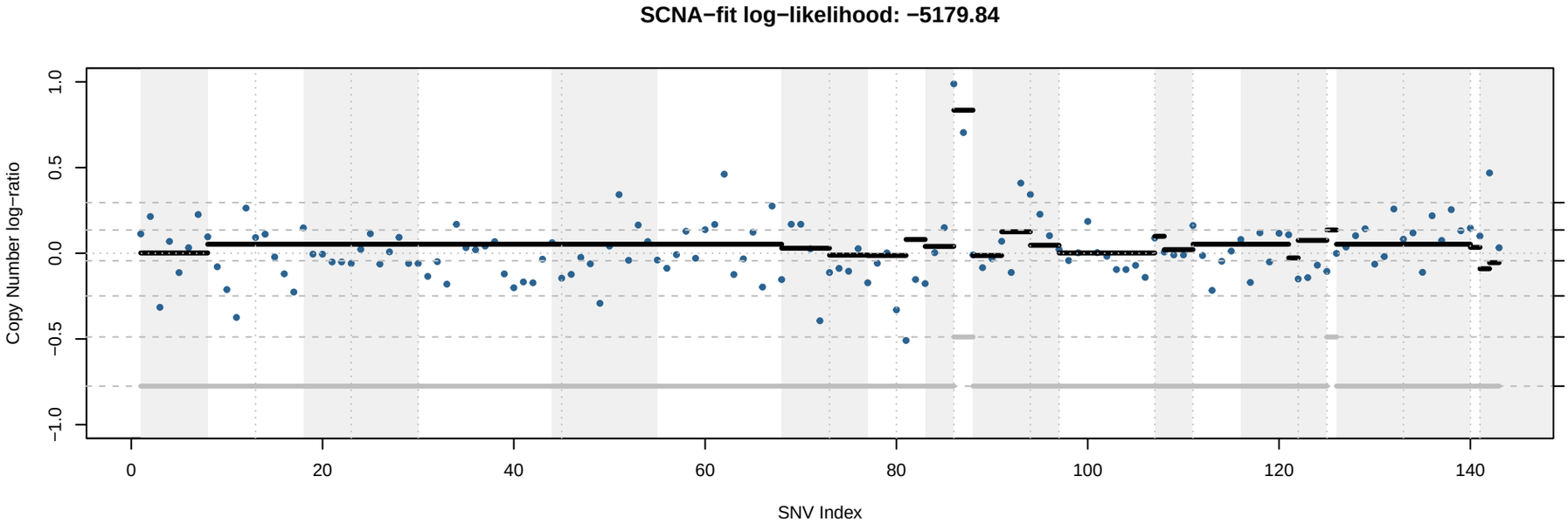

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

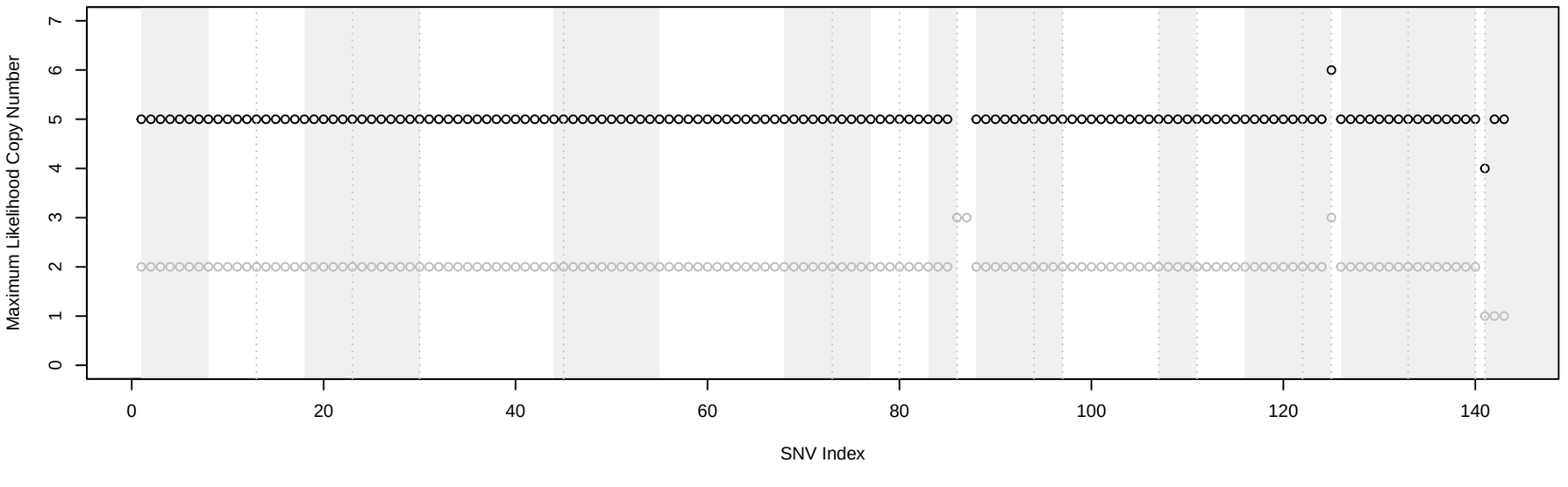

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

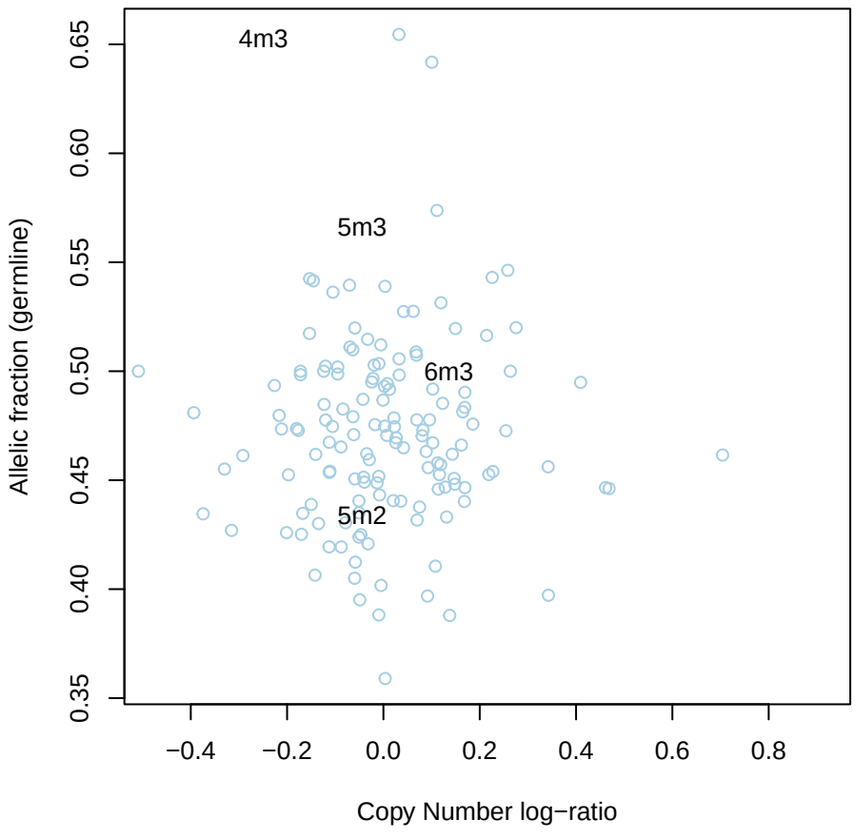

Power 0.8
Frequency
0
10
20
30
40
50
0.1
0.2
0.3
0.4
0.5
0.6
Cellular fraction

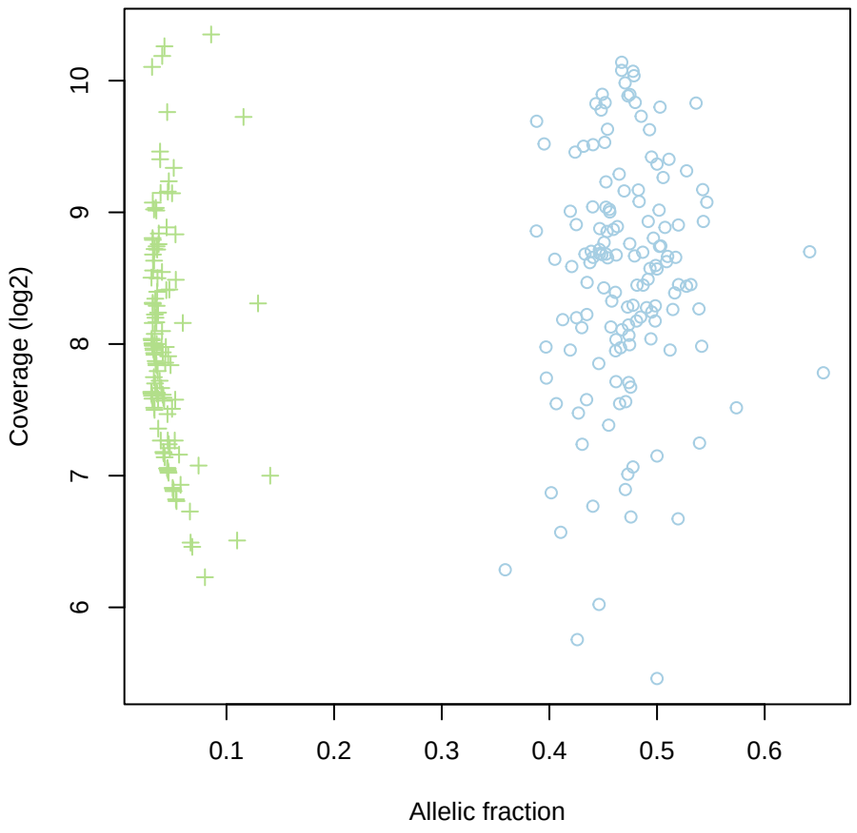

Purity: 0.44 Tumor ploidy: 5.233
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

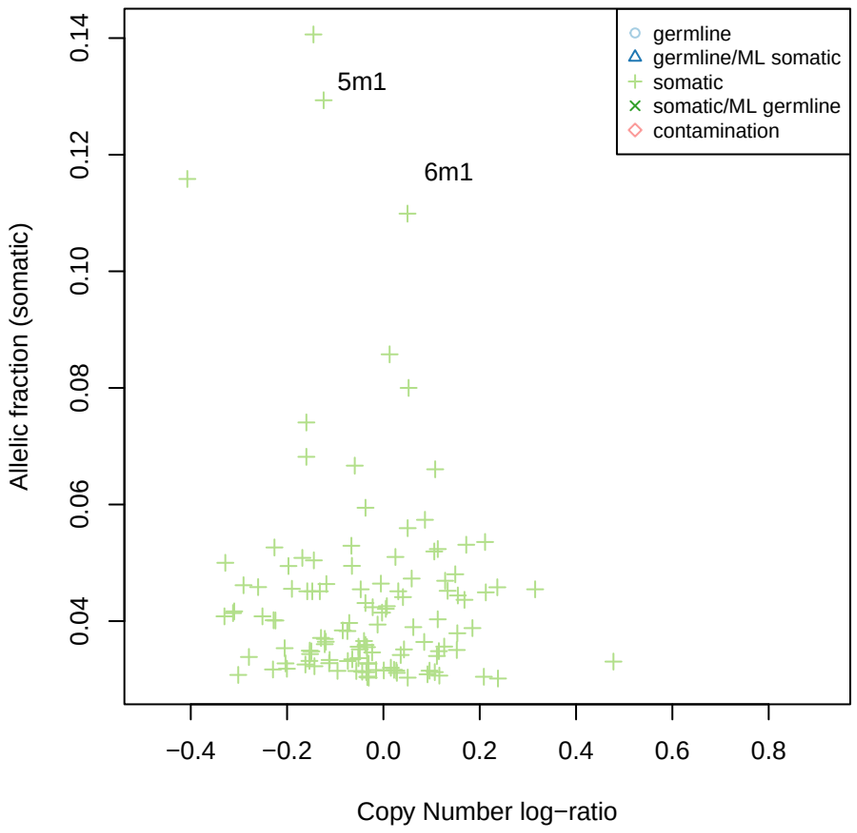

Purity: 0.44 Tumor ploidy: 5.233 SNV log−likelihood: −124.18 GoF: 88% Mean coverage: 306;377
1 2 3 4 5 6 7 8 9 12 13 14 15 16 18 19 21
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

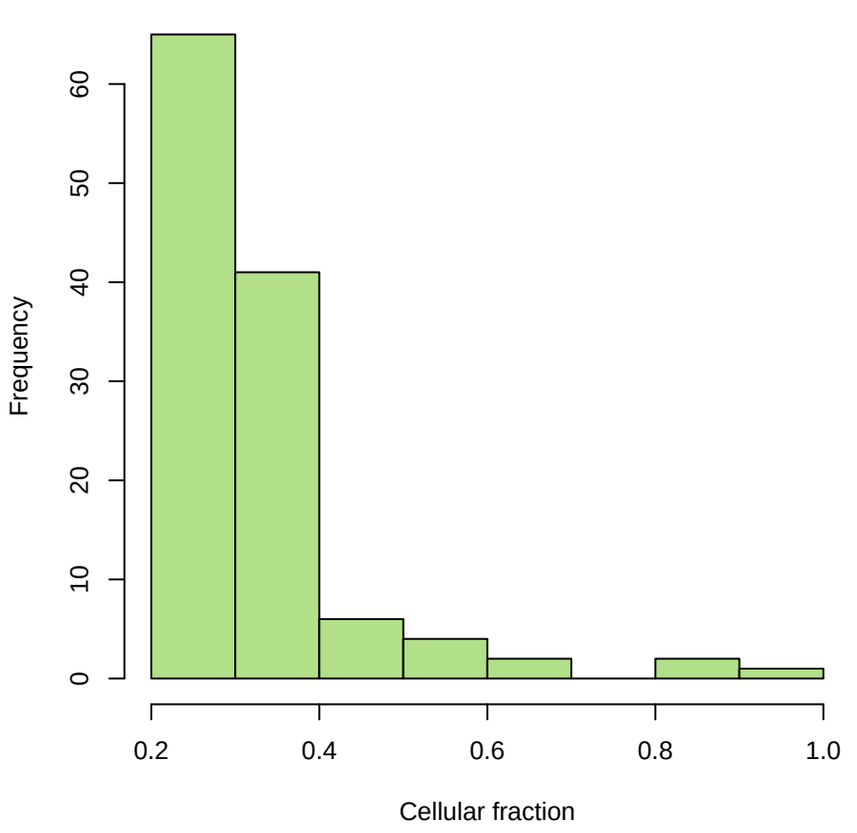

SCNA−fit log−likelihood: −5179.84
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

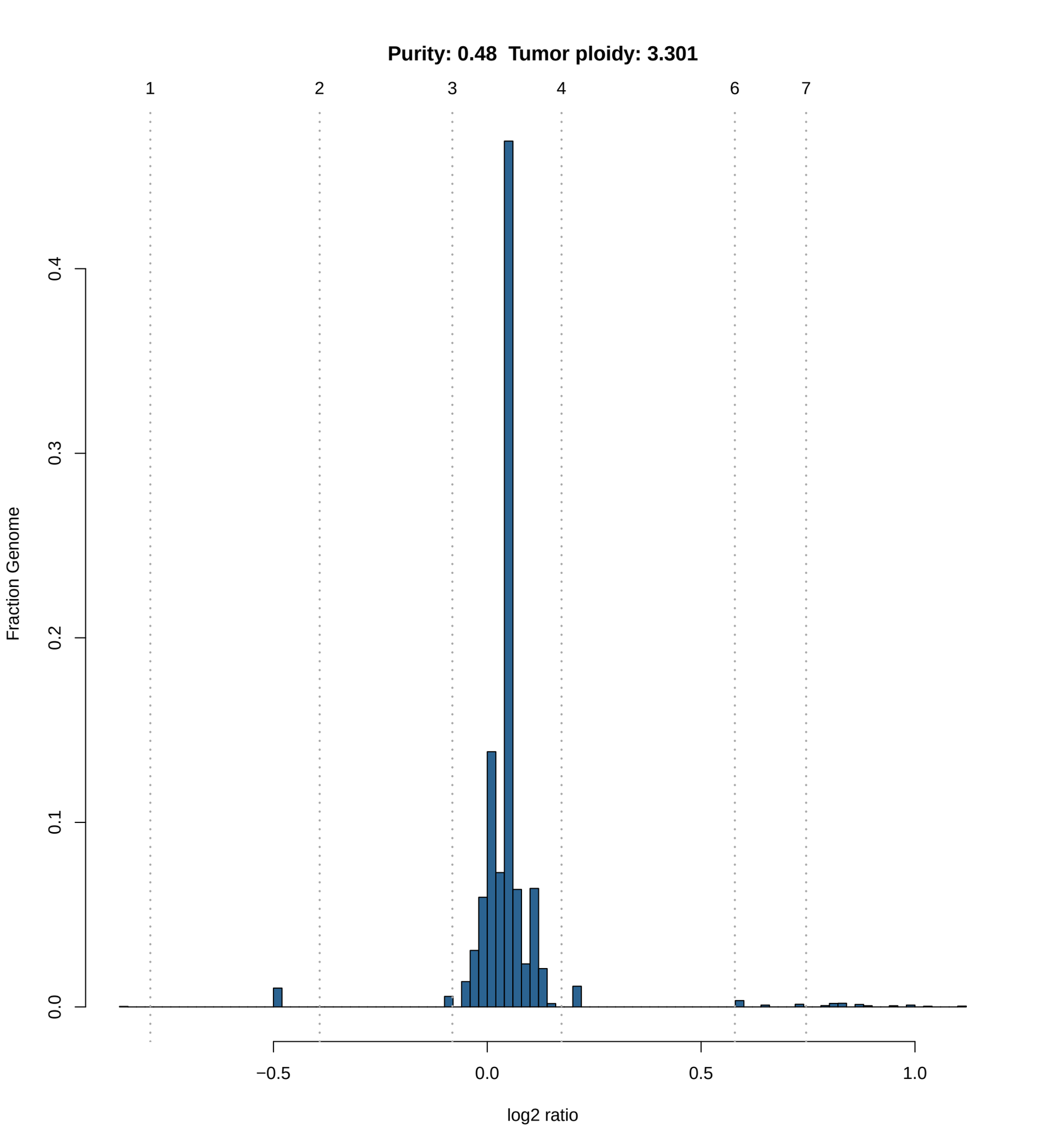

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

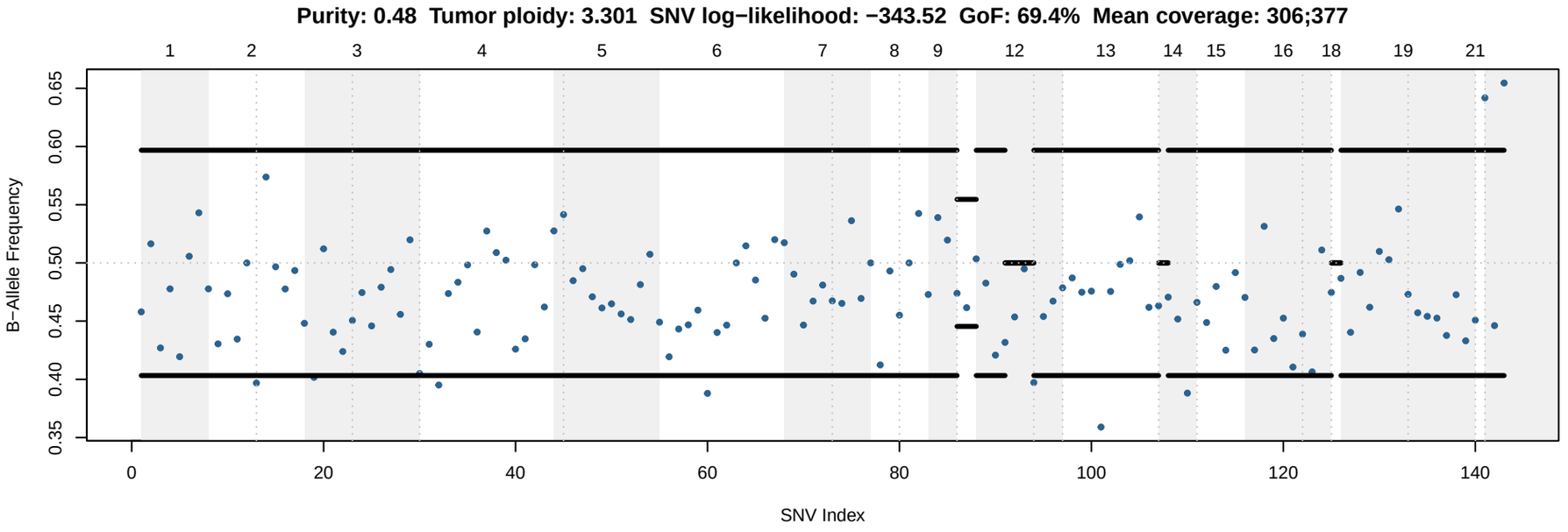

4m3
5m3
6m3
5m2
Allelic fraction (germline)
Copy Number log−ratio

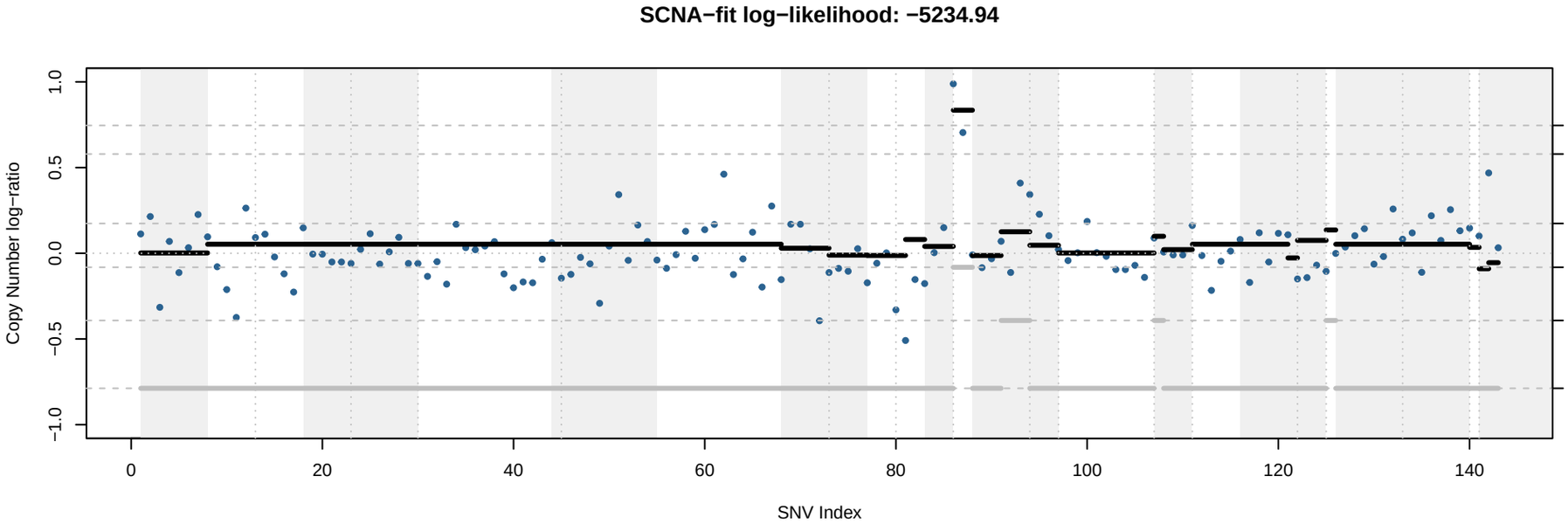

Coverage (log2)
Allelic fraction

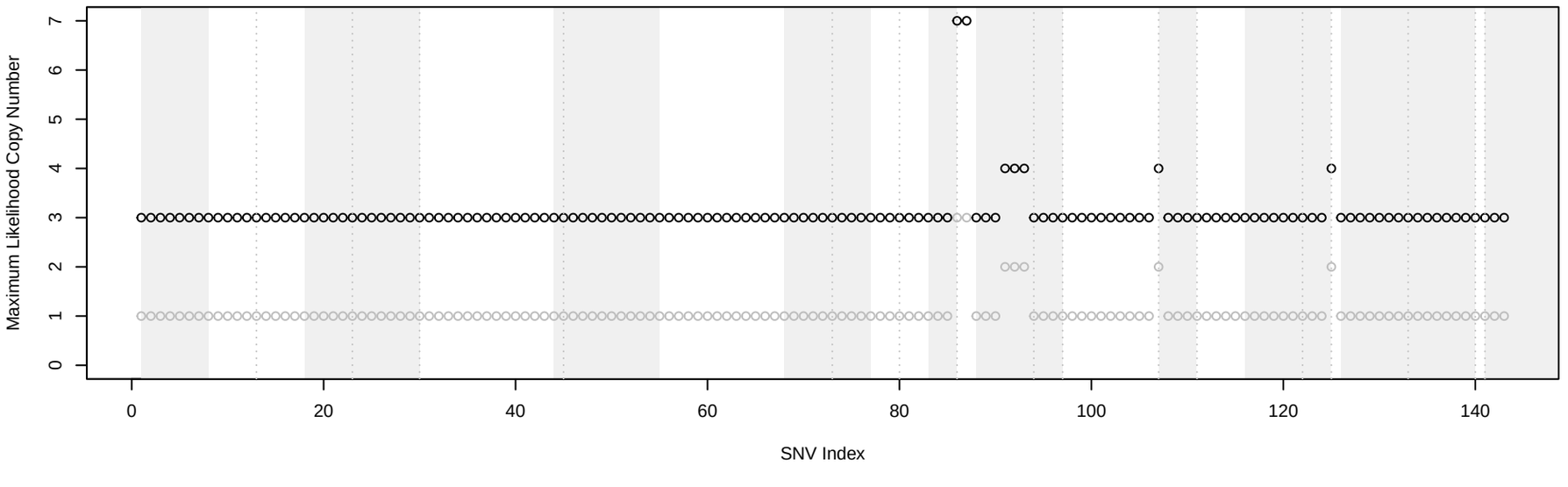

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio

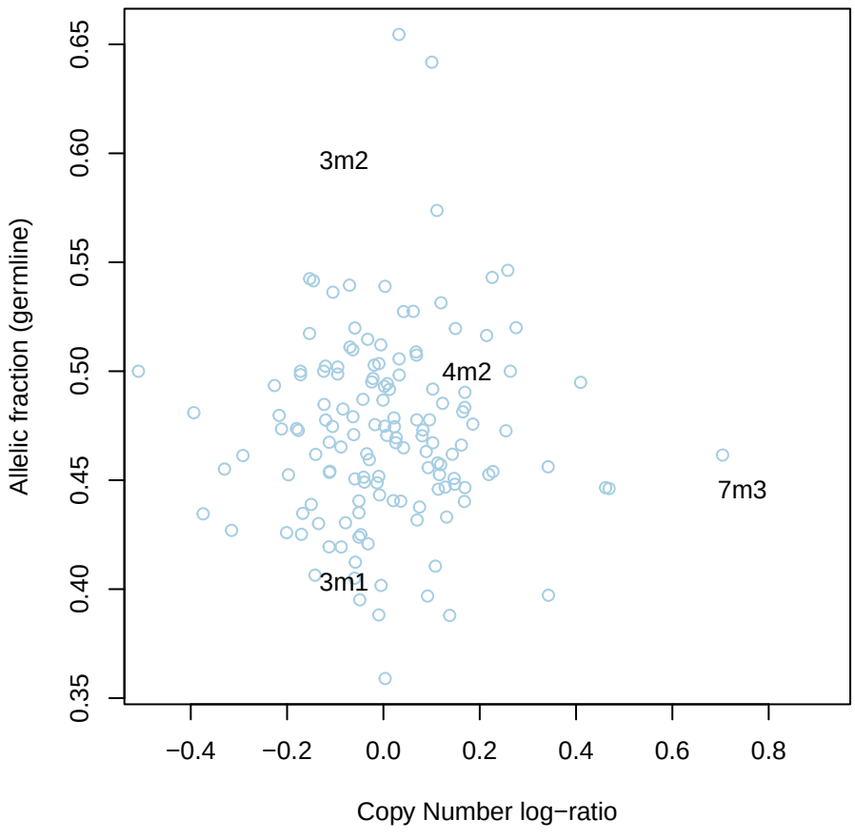

Frequency
Cellular fraction

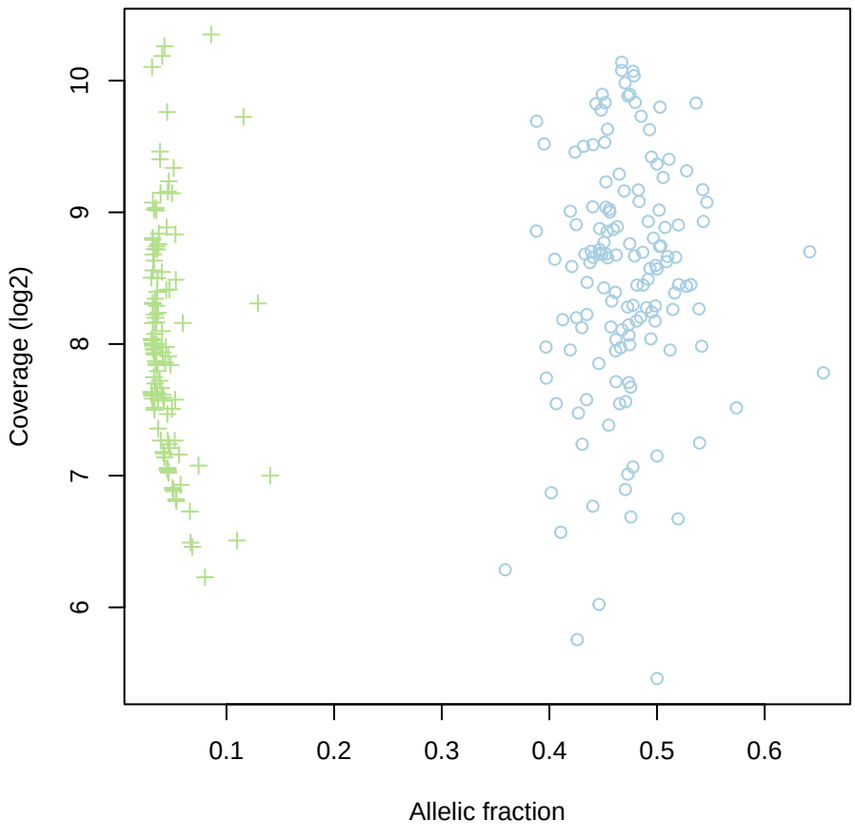

Purity: 0.48 Tumor ploidy: 3.301
1
2
3
4
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

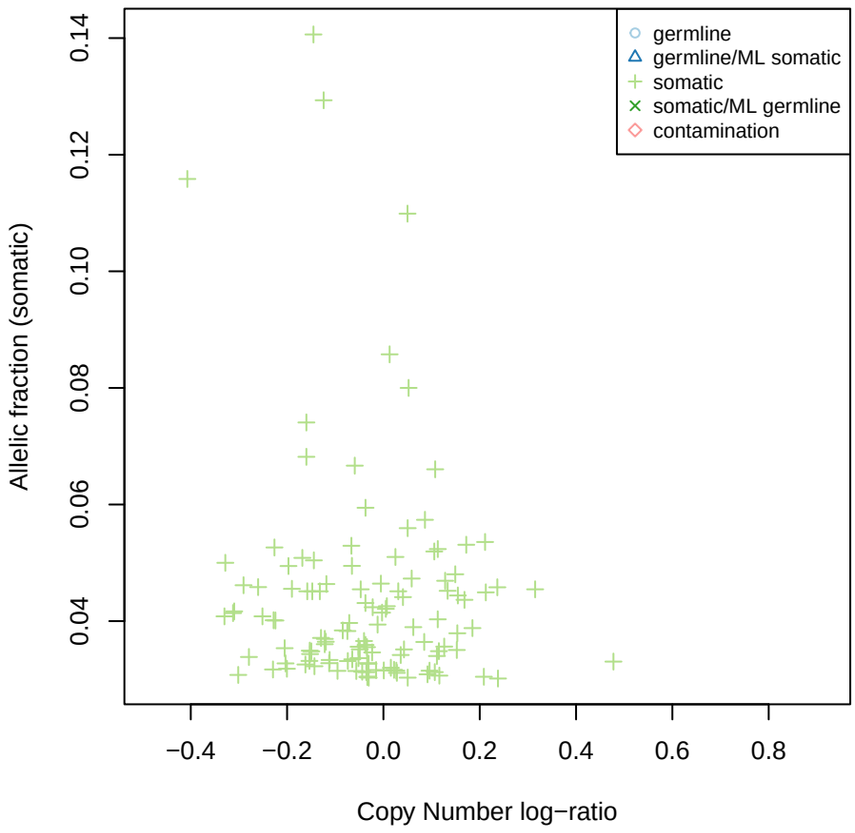

Purity: 0.48 Tumor ploidy: 3.301 SNV log−likelihood: −343.52 GoF: 69.4% Mean coverage: 306;377
1 2 3 4 5 6 7 8 9 12 13 14 15 16 18 19 21
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

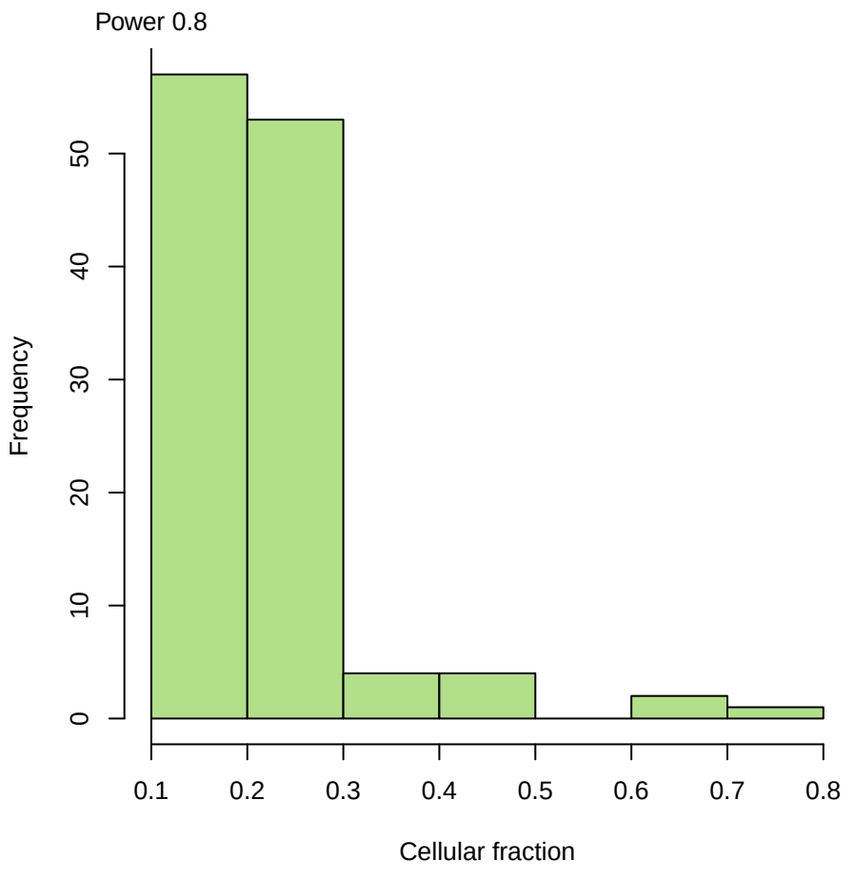

SCNA−fit log−likelihood: −5234.94
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 6 7
0 20 40 60 80 100 120 140
SNV Index

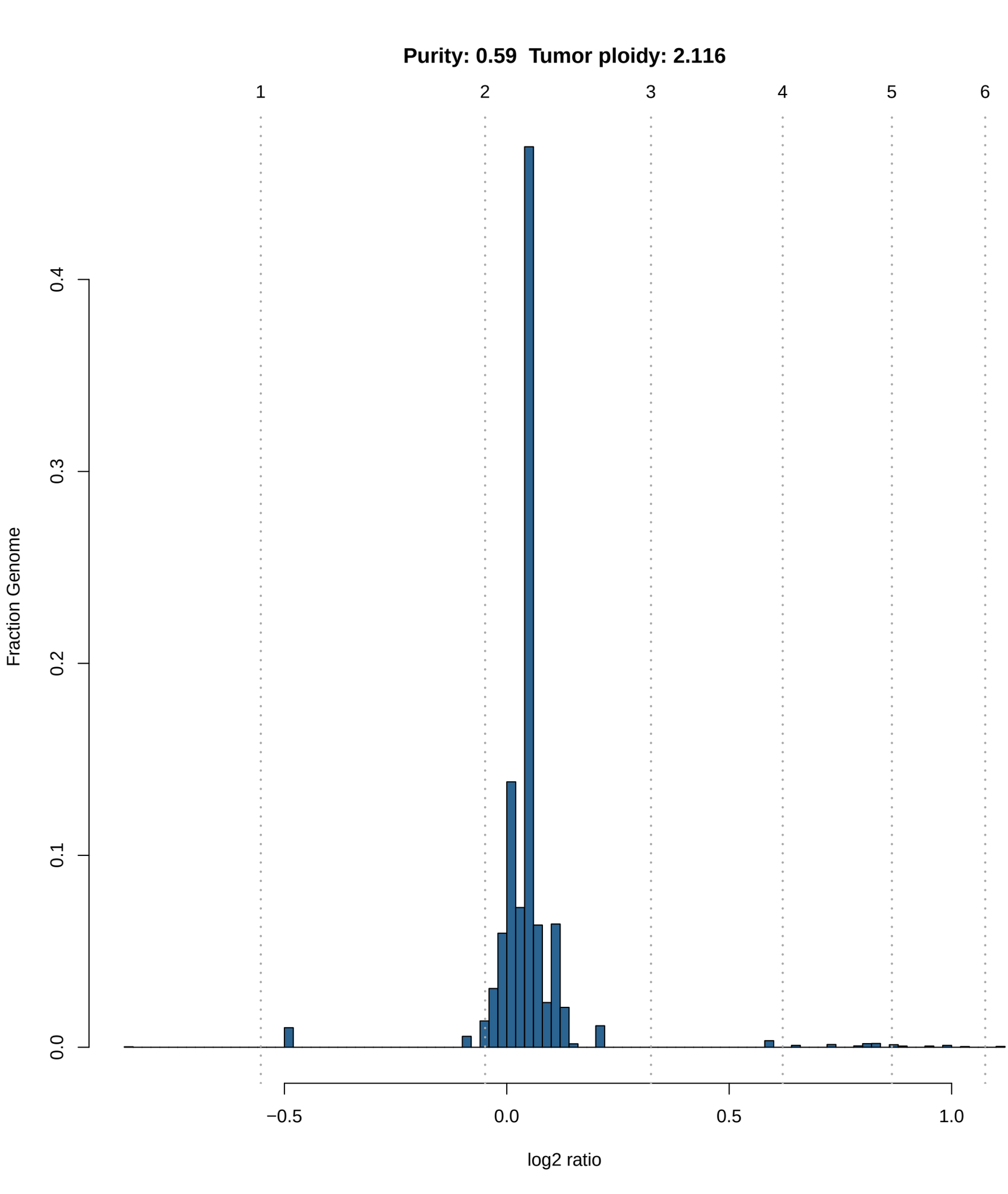

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

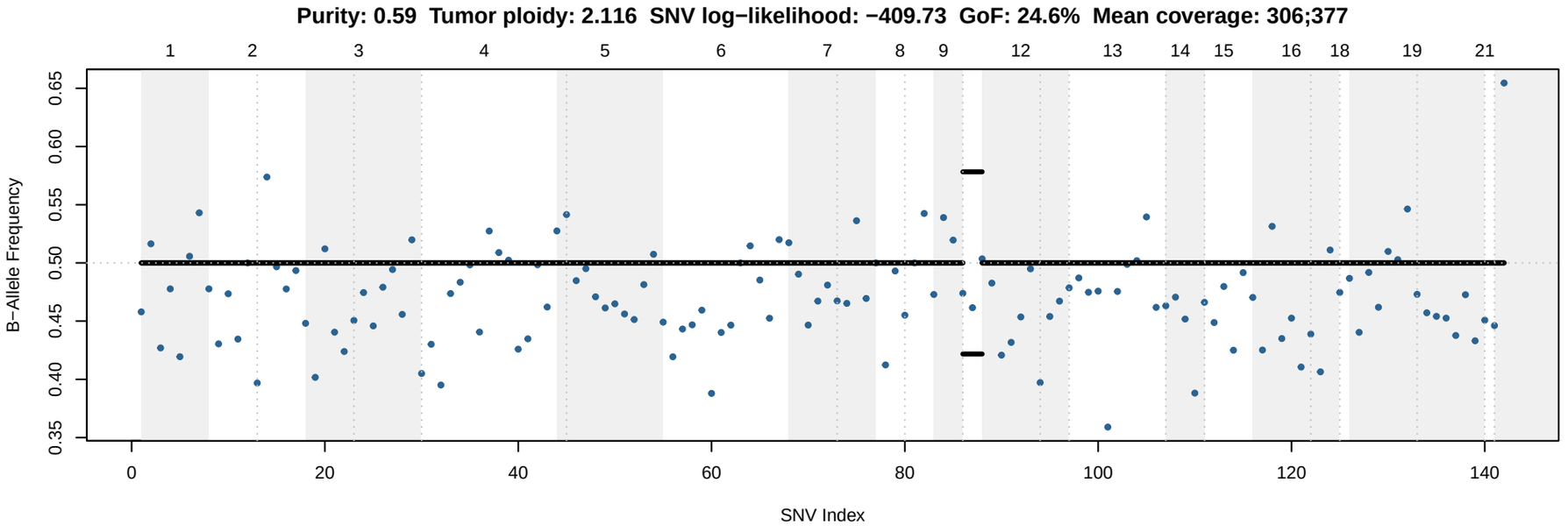

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
3m2
4m2
7m3
3m1
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

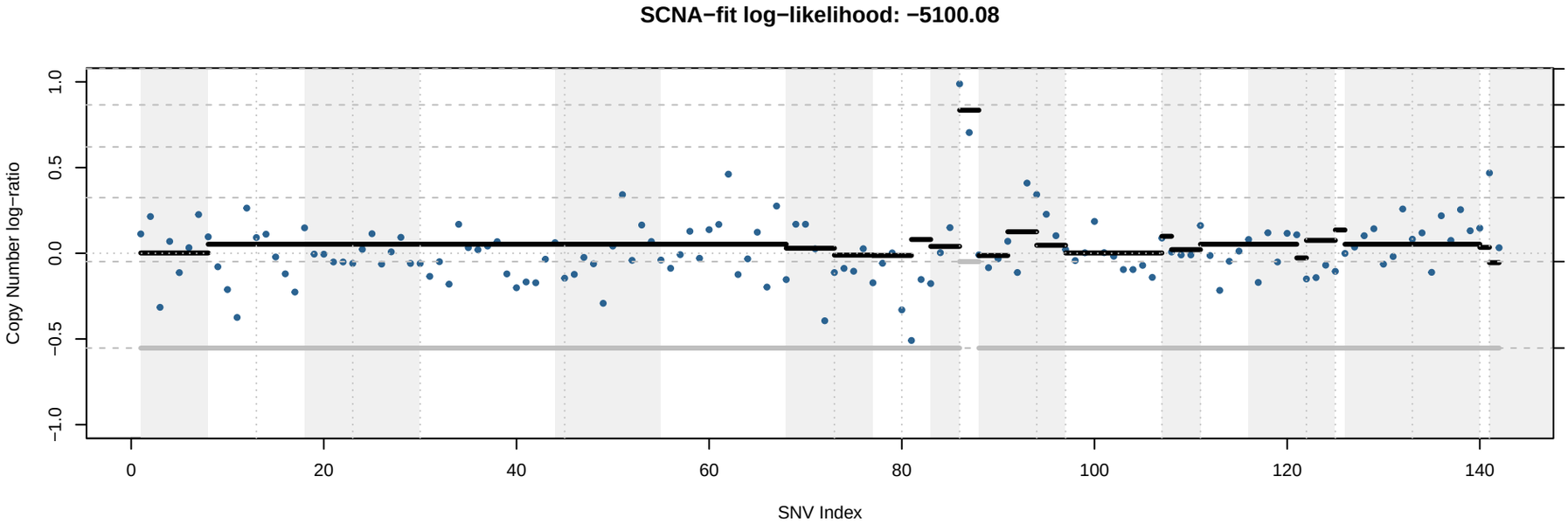

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

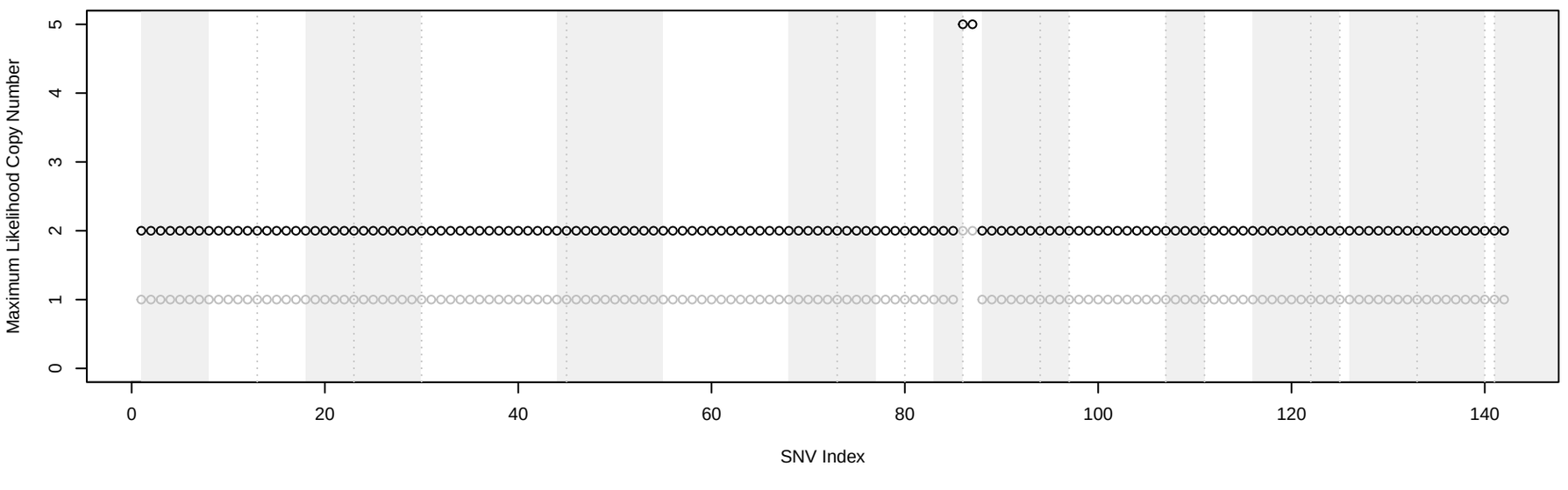

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

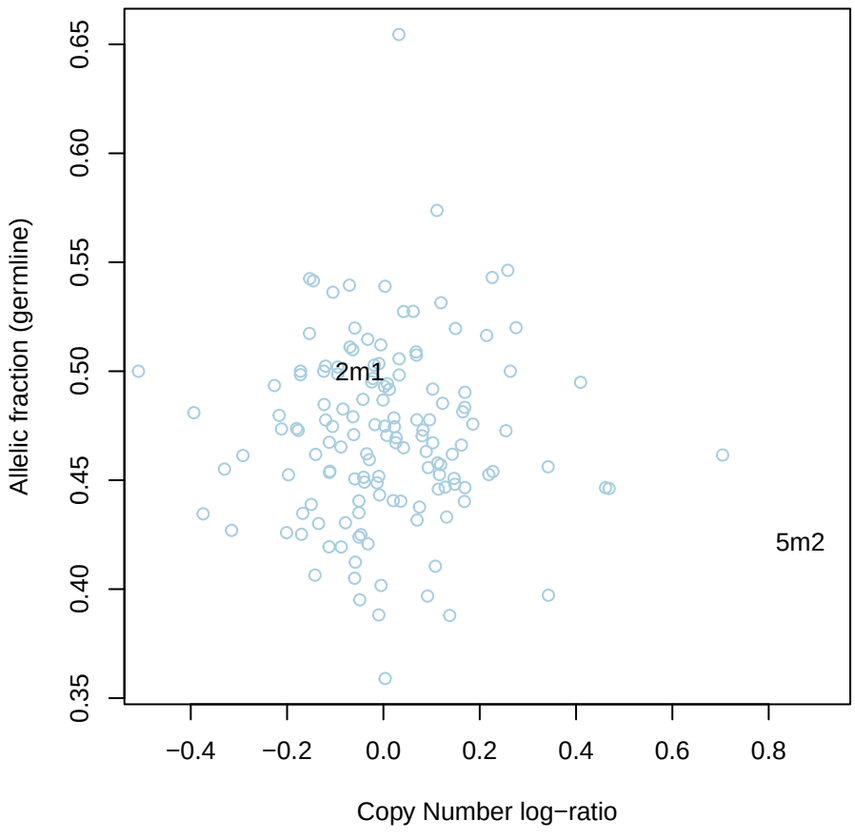

Power 0.8
Frequency
0
10
20
30
40
50
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
Cellular fraction

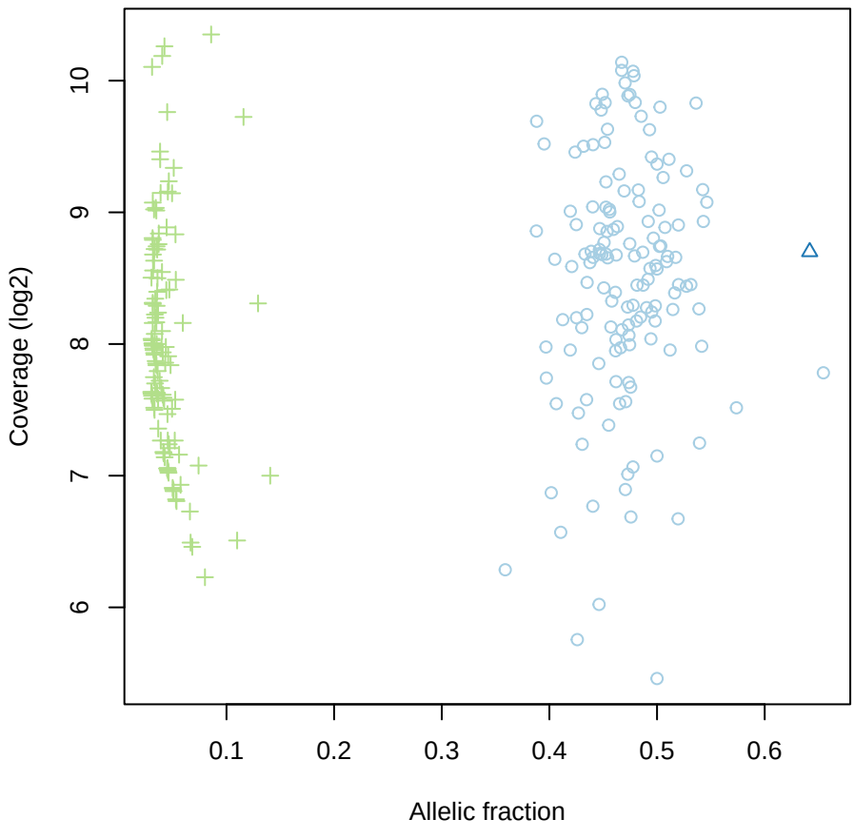

Purity: 0.59 Tumor ploidy: 2.116
1
2
3
4
5
6
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

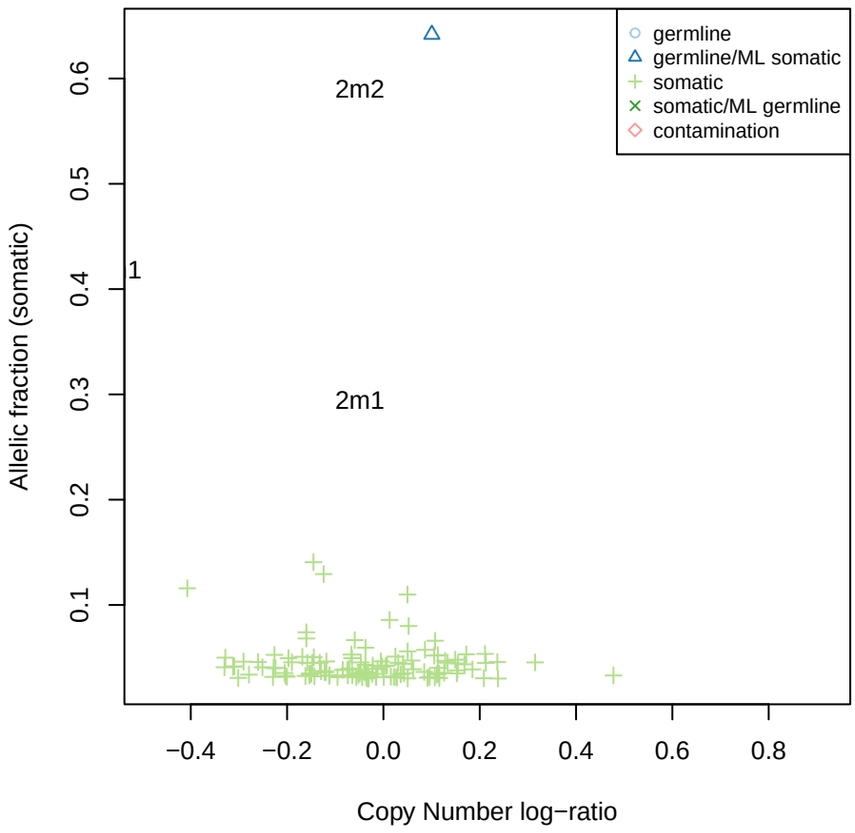

Purity: 0.59 Tumor ploidy: 2.116 SNV log−likelihood: −409.73 GoF: 24.6% Mean coverage: 306;377
1 2 3 4 5 6 7 8 9 12 13 14 15 16 18 19 21
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

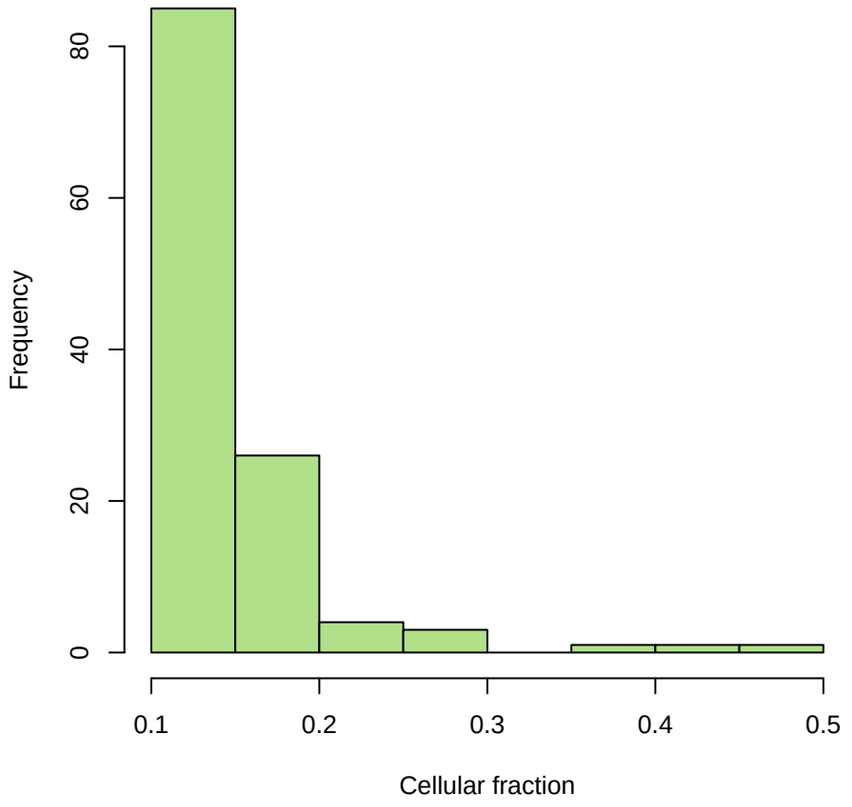

SCNA−fit log−likelihood: −5100.08
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

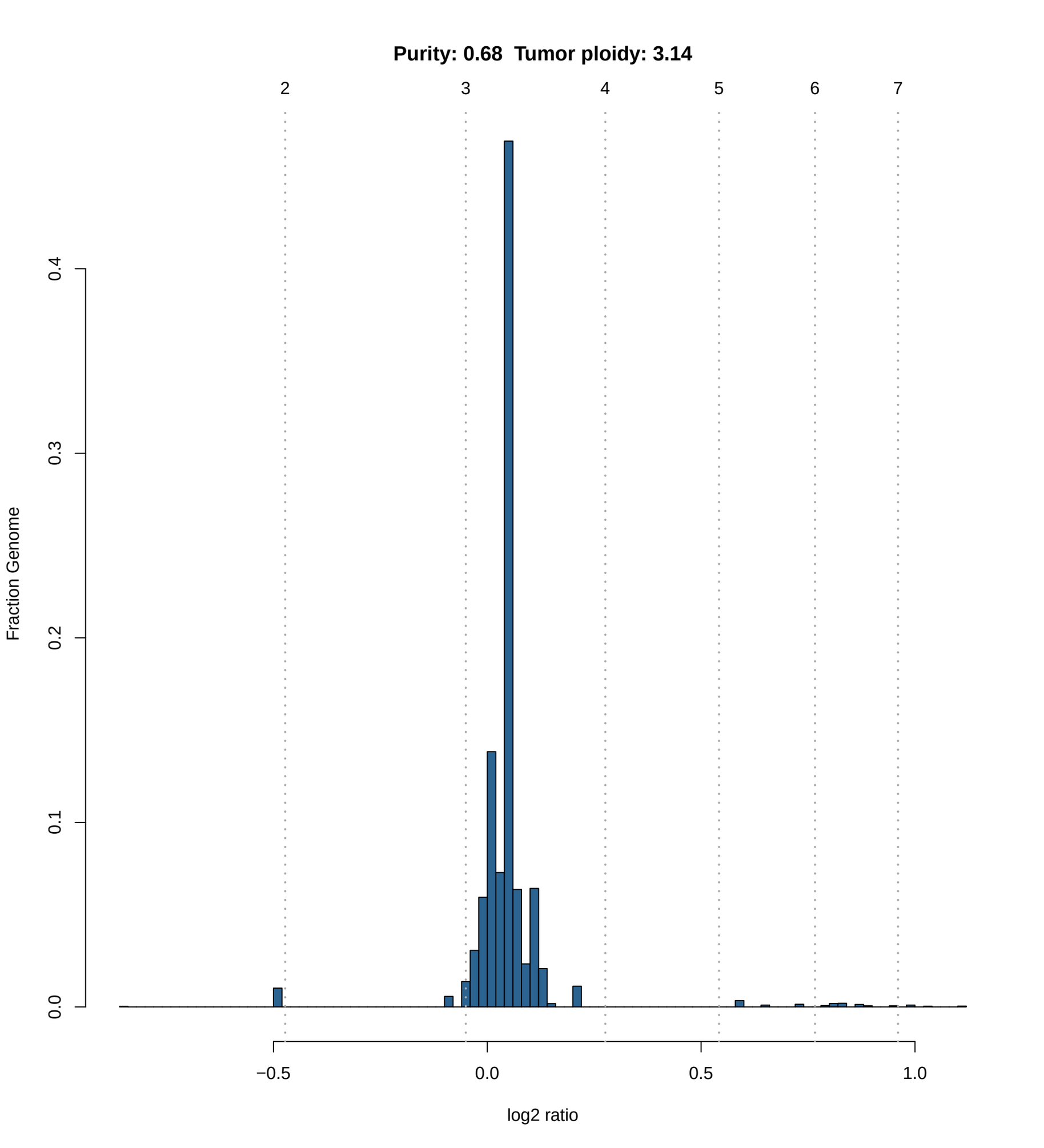

Maximum Likelihood Copy Number
0 1 2 3 4 5
∞
0 20 40 60 80 100 120 140
SNV Index

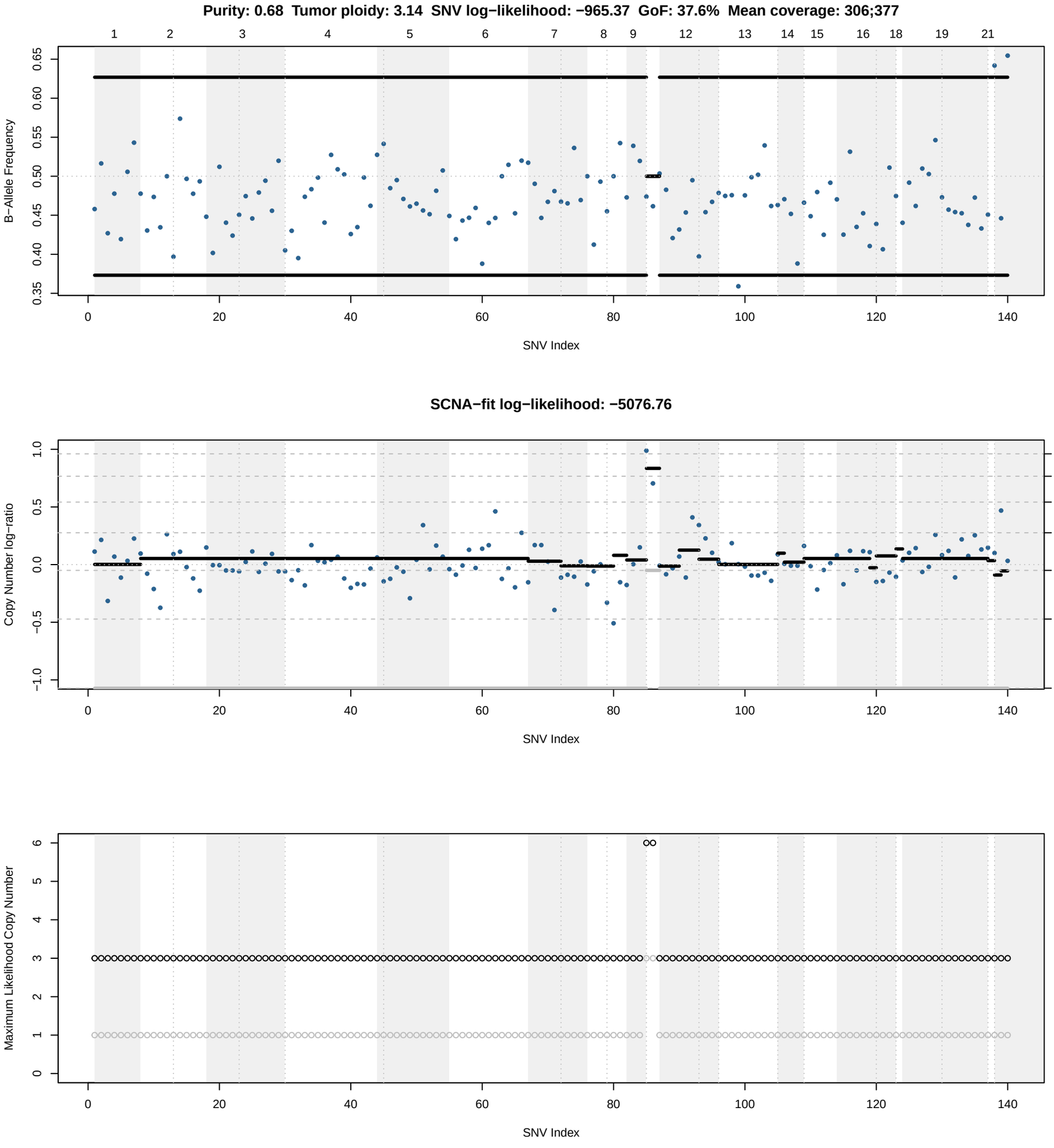

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
2m1
5m2
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

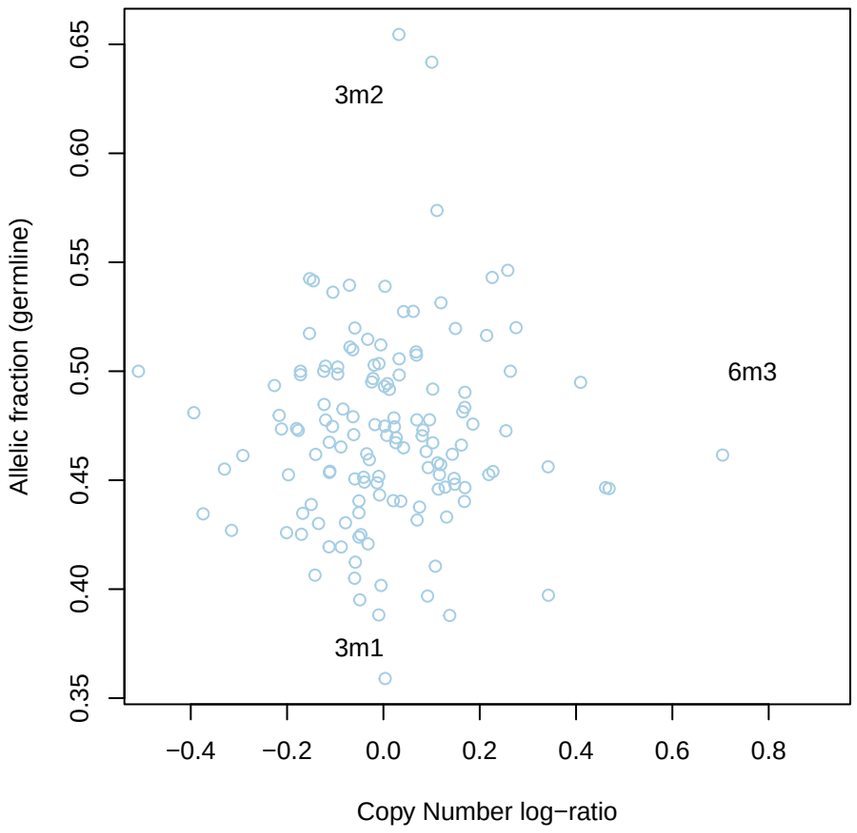

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

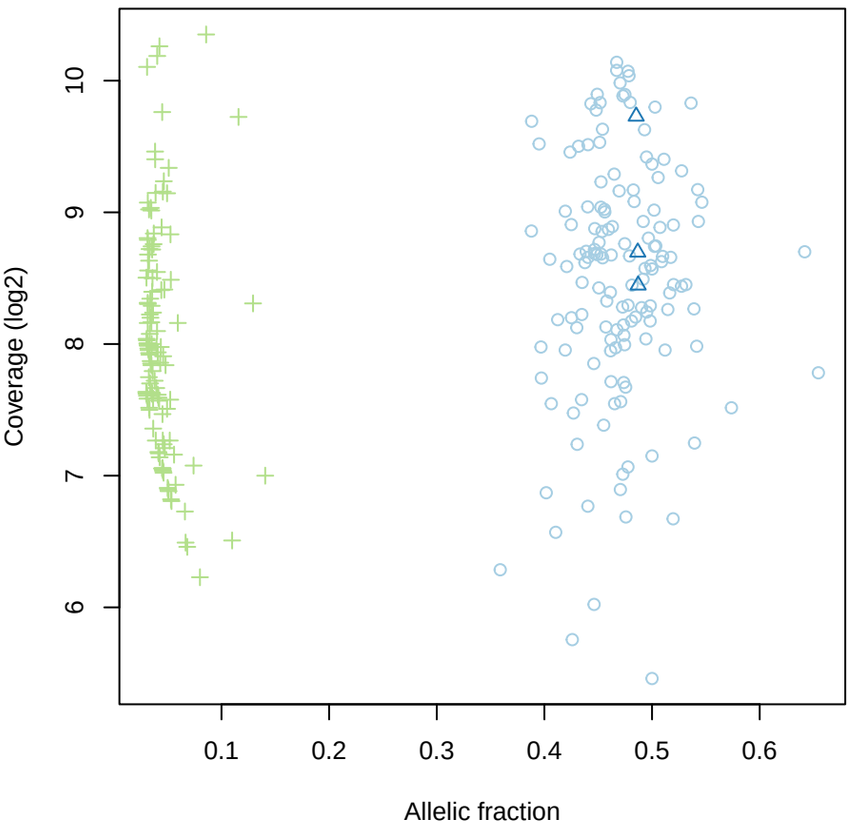

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.1
0.2
0.3
0.4
0.5
0.6
2m2
1
2m1
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

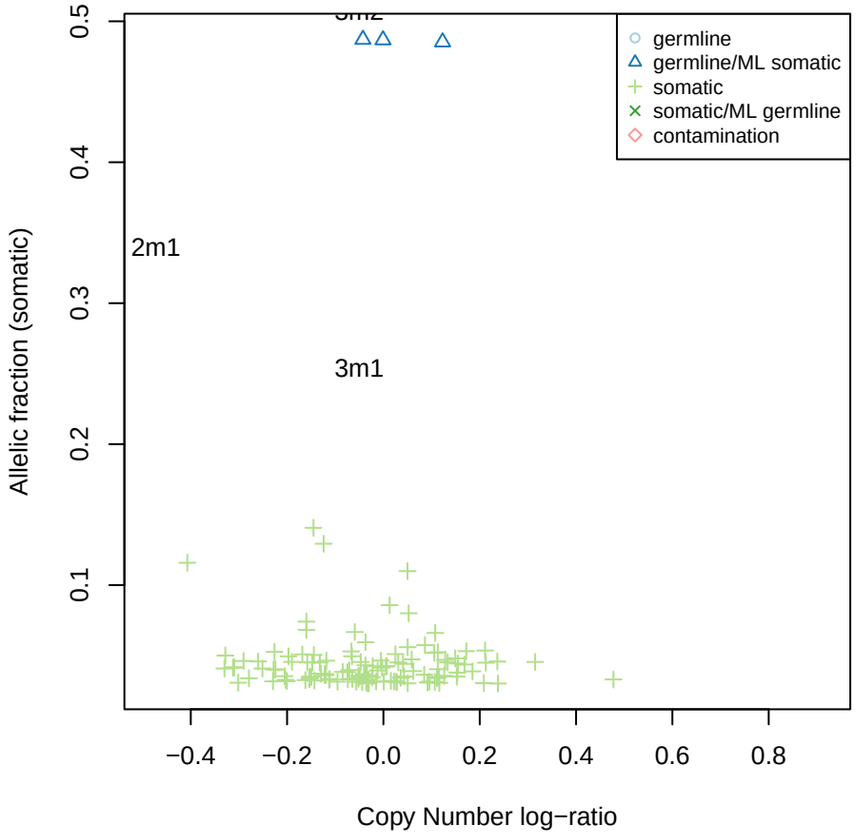

Frequency
0
20
40
60
80
0.1
0.2
0.3
0.4
0.5
Cellular fraction

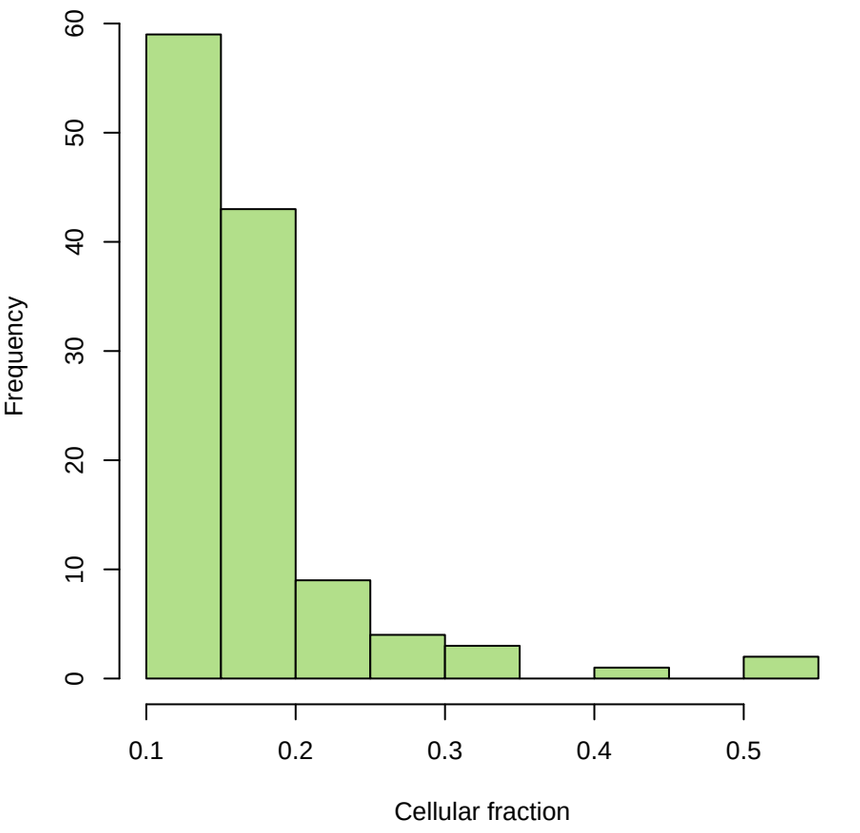

Purity: 0.68 Tumor ploidy: 3.14
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

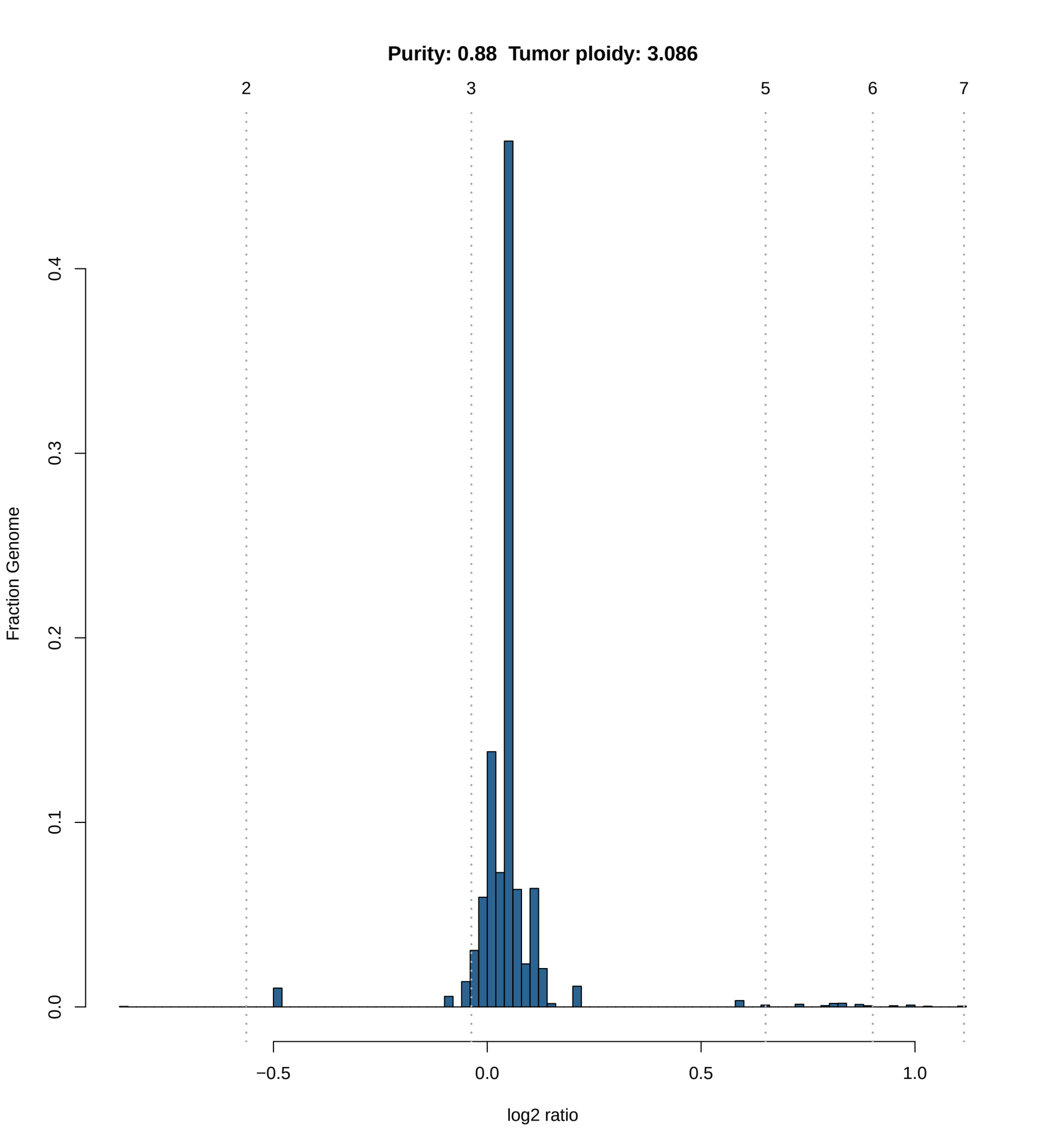

Purity: 0.68 Tumor ploidy: 3.14 SNV log−likelihood: −965.37 GoF: 37.6% Mean coverage: 306;377
1 2 3 4 5 6 7 8 9 12 13 14 15 16 18 19 21
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index
SCNA−fit log−likelihood: −5076.76
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6 7
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

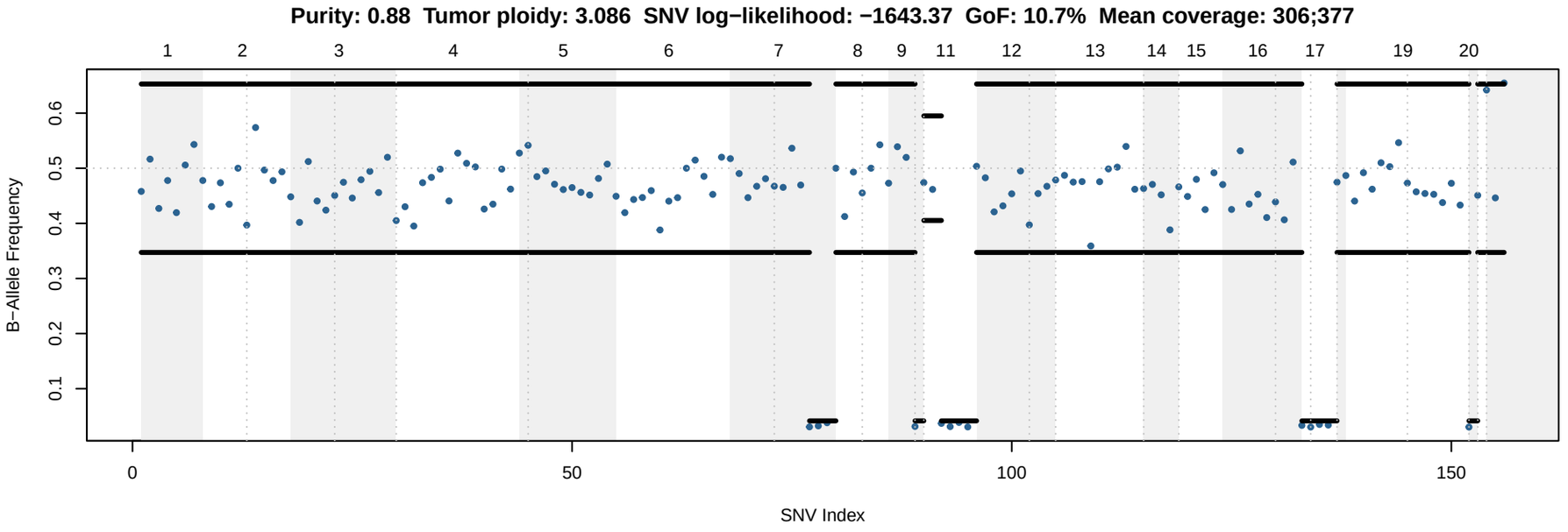

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
3m2
6m3
3m1
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

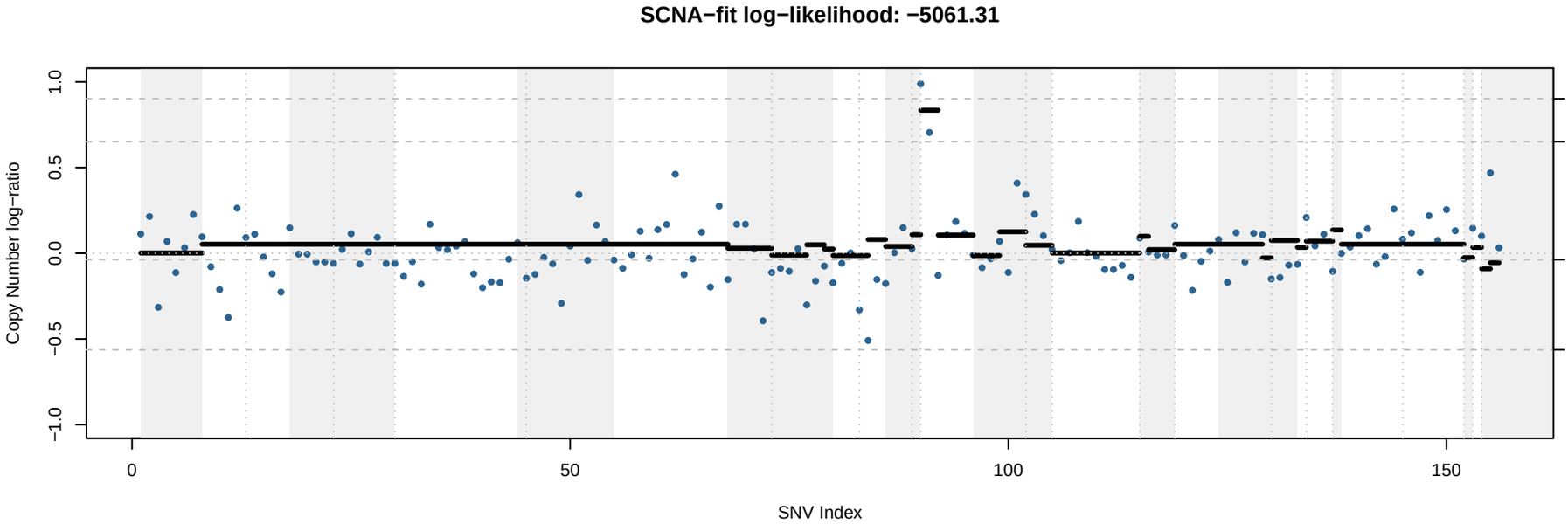

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

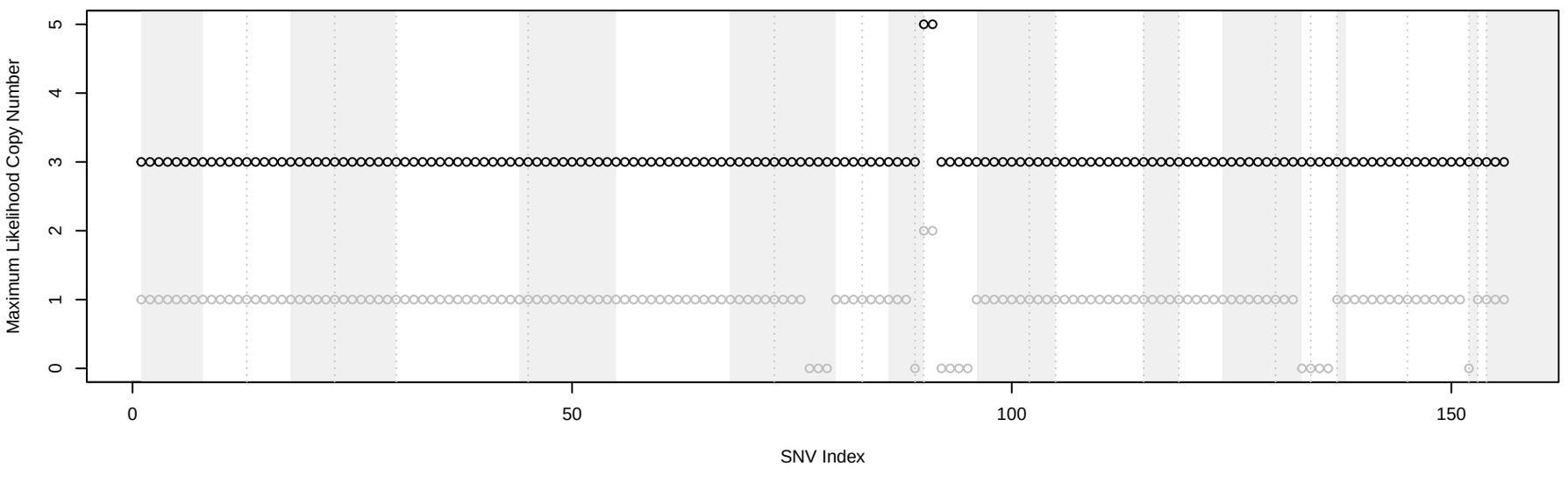

Allelic fraction (somatic)
0.1
0.2
0.3
0.4
0.5
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

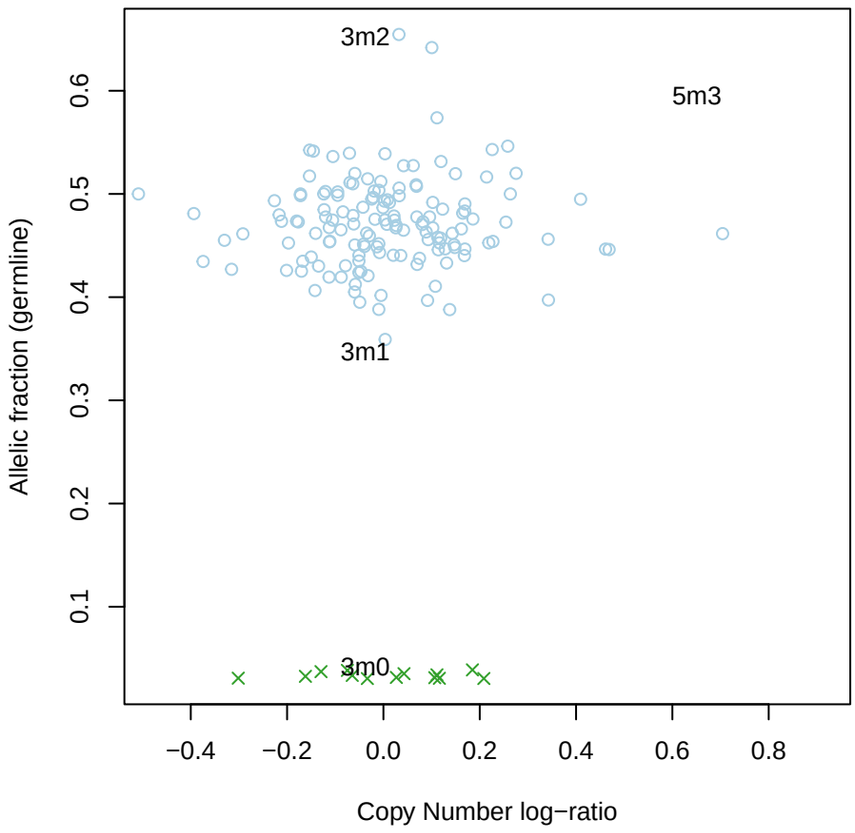

Frequency
0
10
20
30
40
50
60
0.1
0.2
0.3
0.4
0.5
Cellular fraction

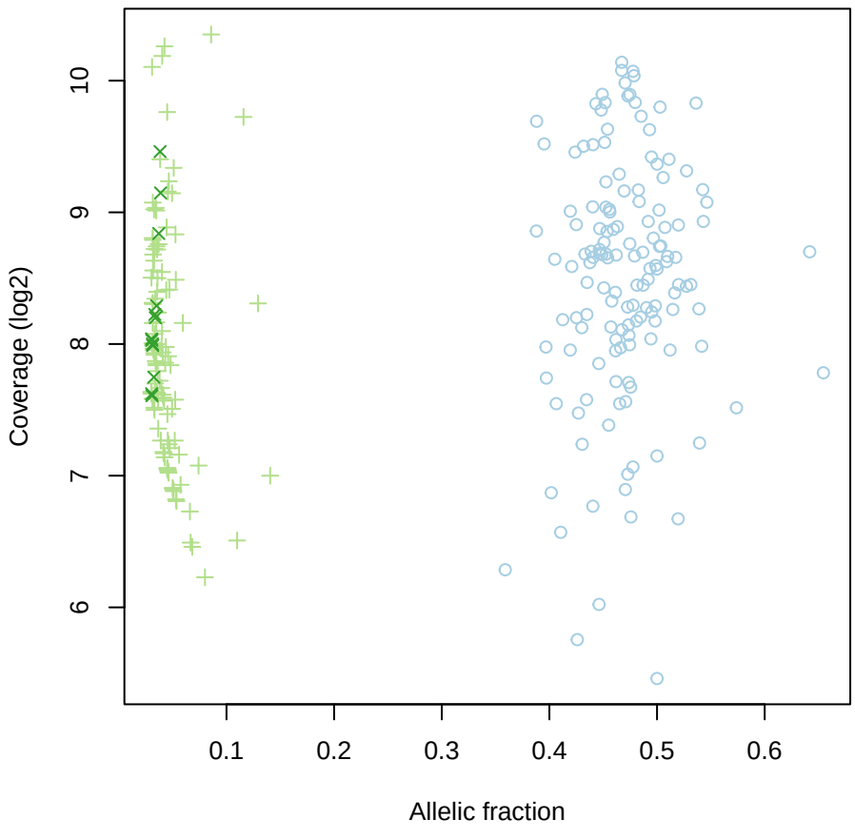

Purity: 0.88 Tumor ploidy: 3.086
2
3
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

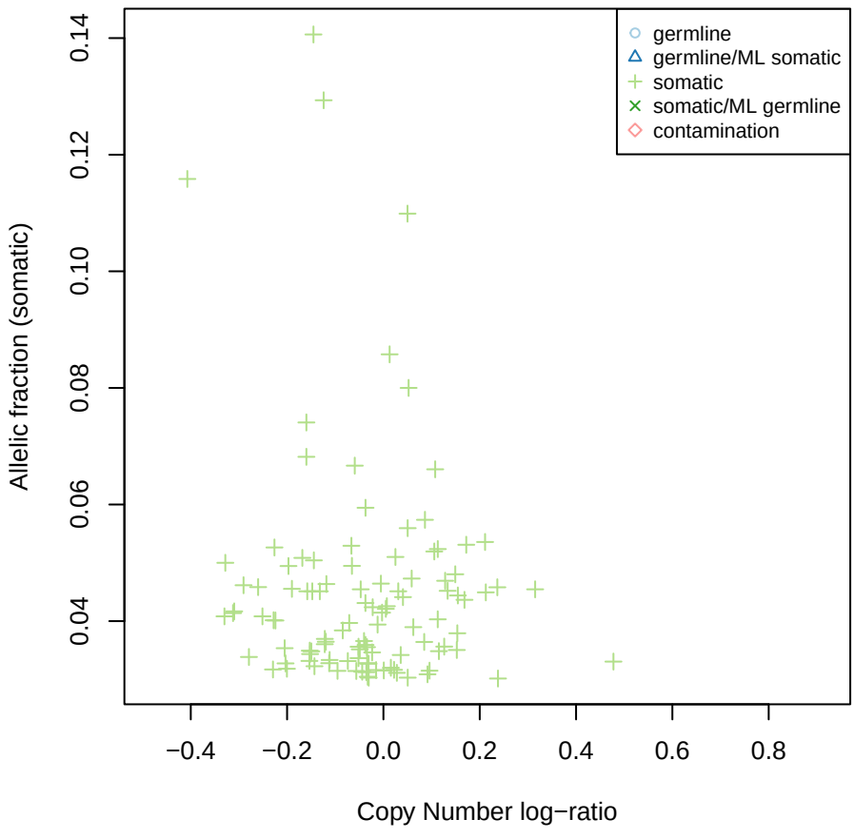

Purity: 0.88 Tumor ploidy: 3.086 SNV log−likelihood: −1643.37 GoF: 10.7% Mean coverage: 306;377
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

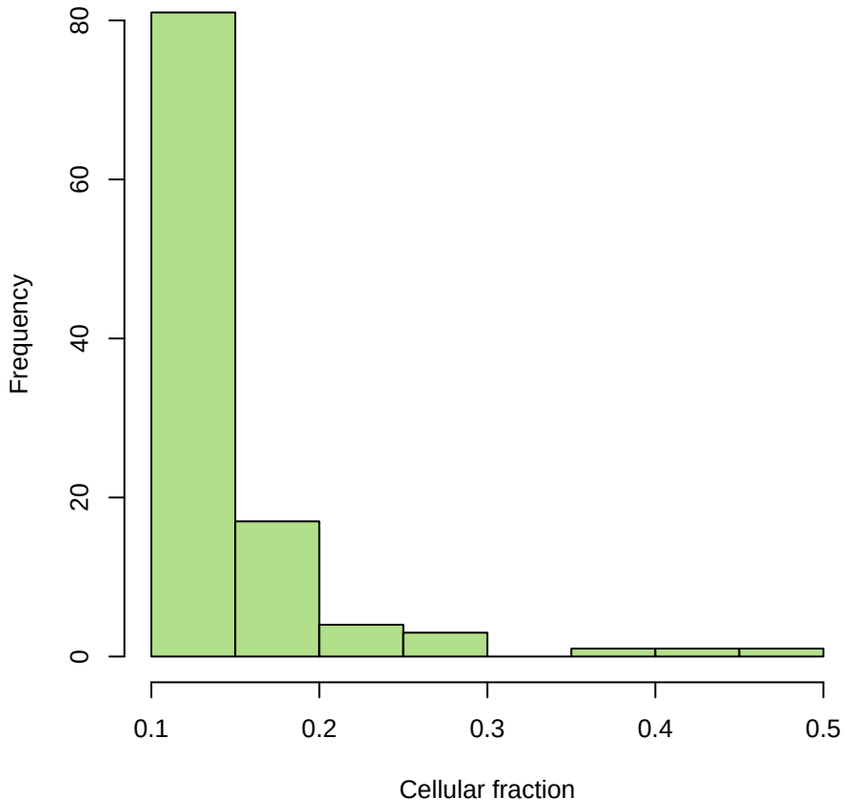

SCNA−fit log−likelihood: −5061.31
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 5 6
0 50 100 150
SNV Index


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


3m2
5m3
3m1
3m0
Allelic fraction (germline)
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
0.6
0.8


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
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
0.12
0.14
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8


Frequency
Cellular fraction
0
20
40
60
80
0.1
0.2
0.3
0.4
0.5