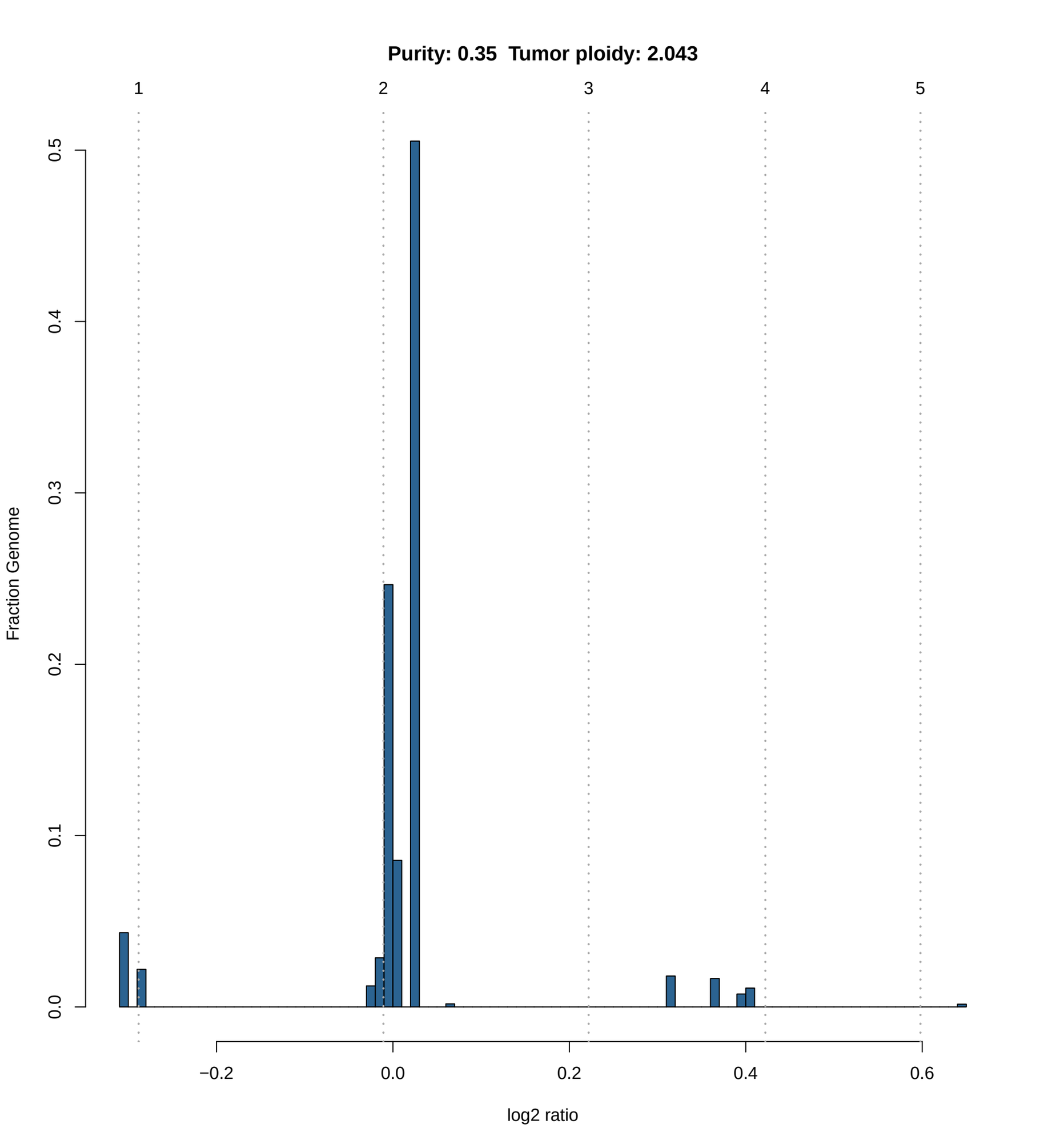
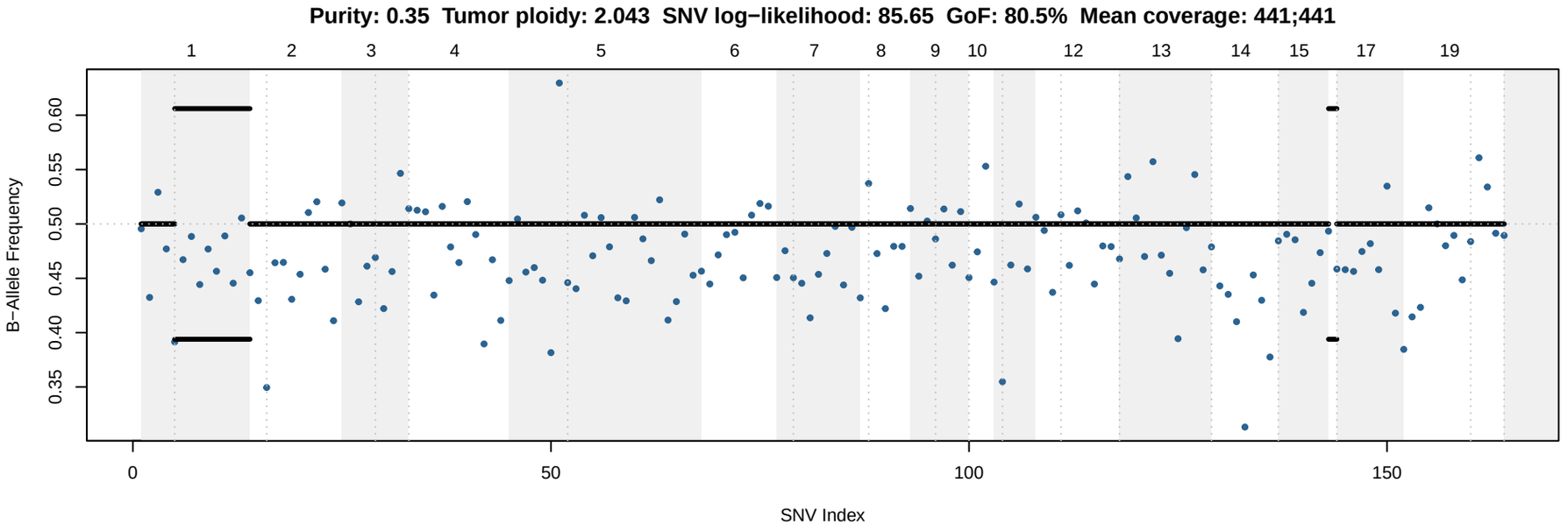
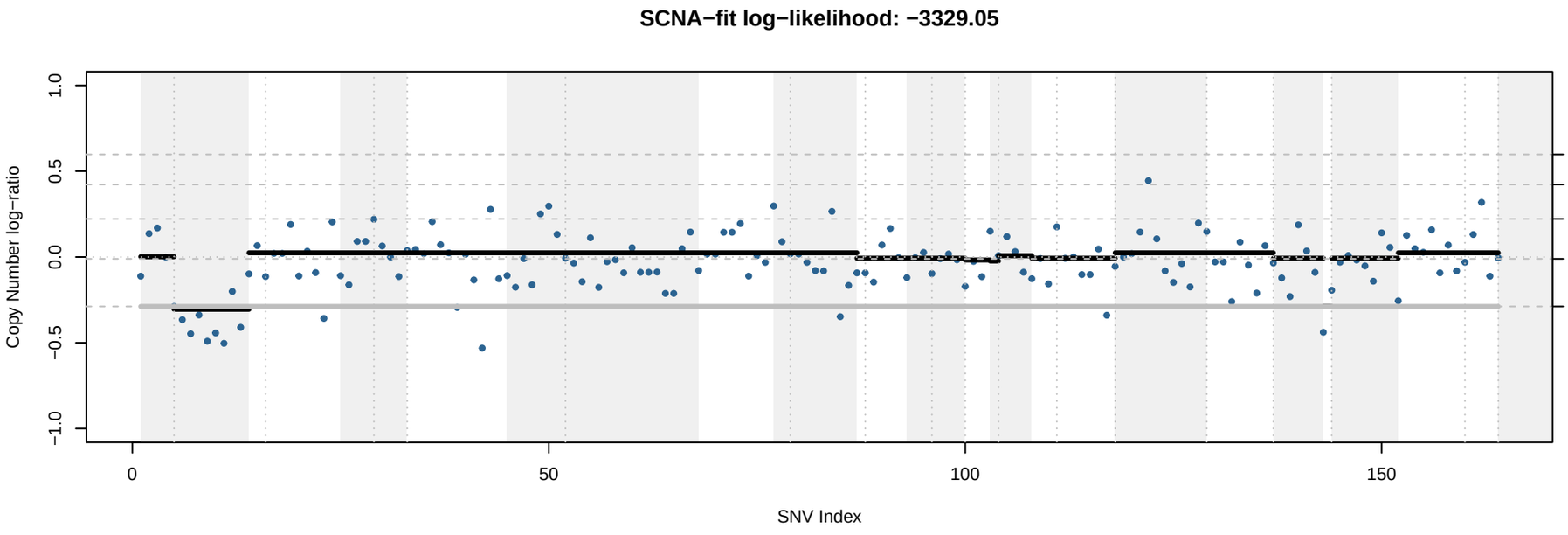
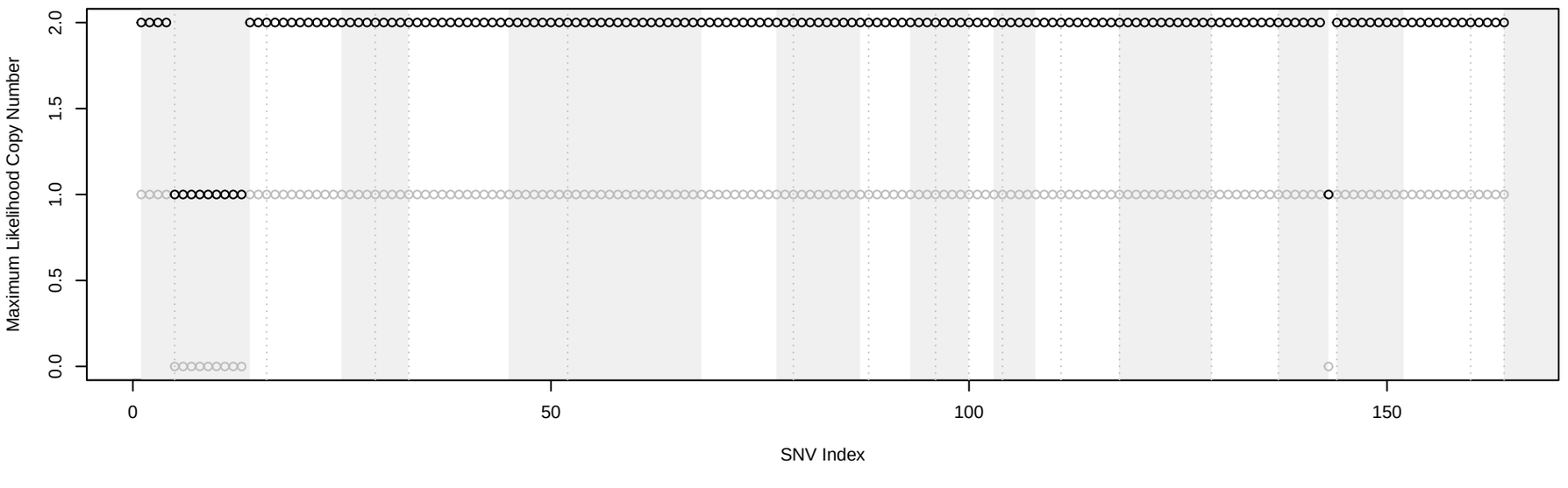
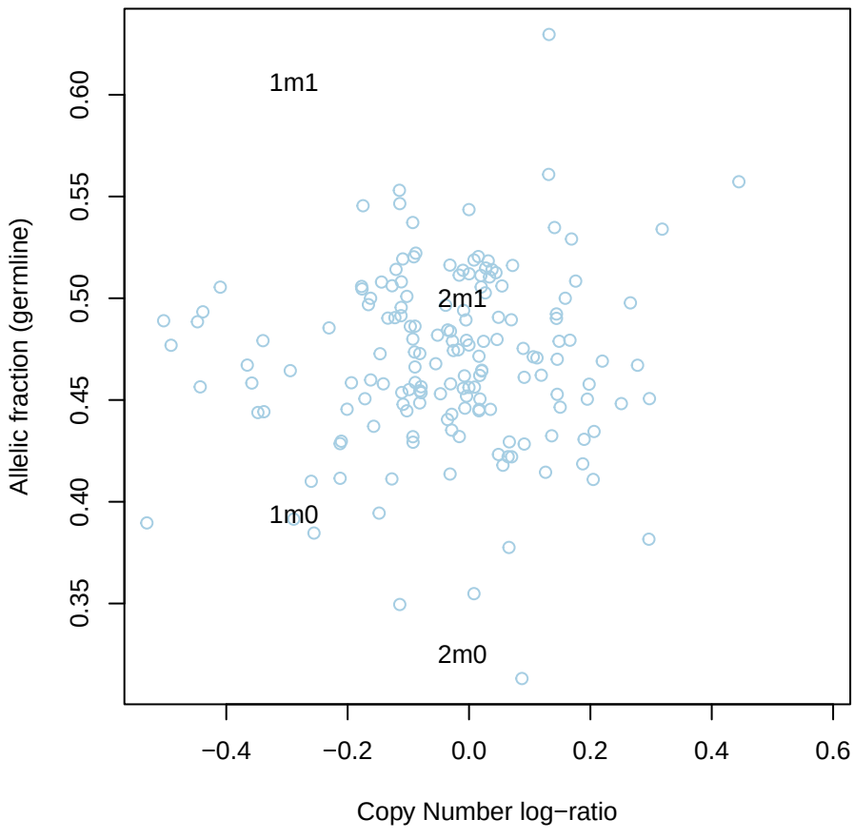
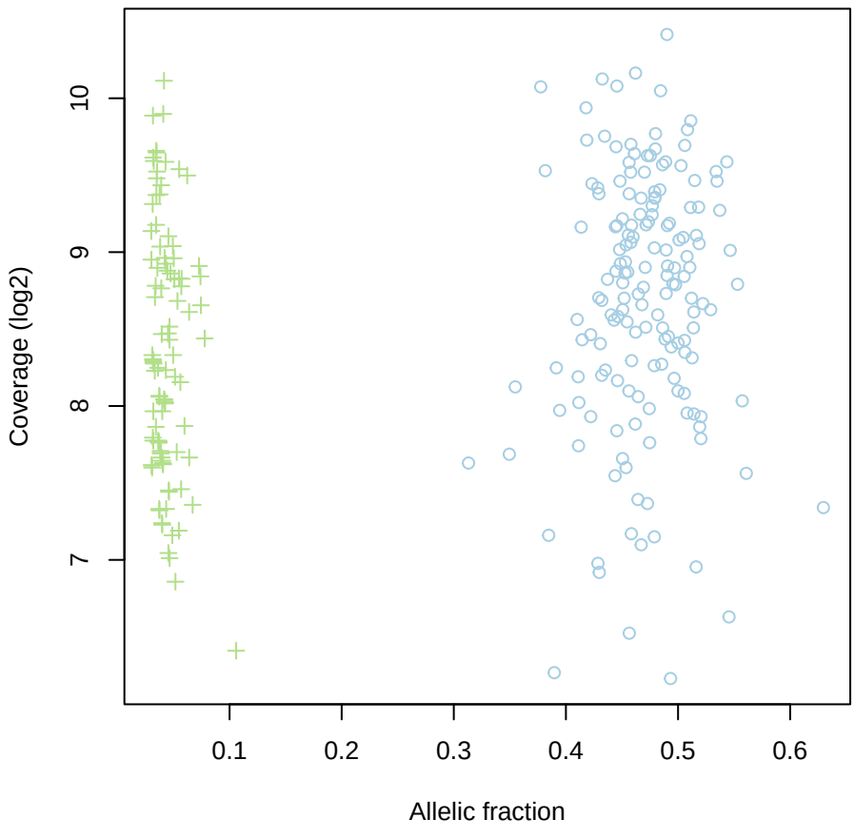

Purity: 0.35 Tumor ploidy: 2.043
1
2
3
4
5
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−0.2
0.0
0.2
0.4
0.6
log2 ratio

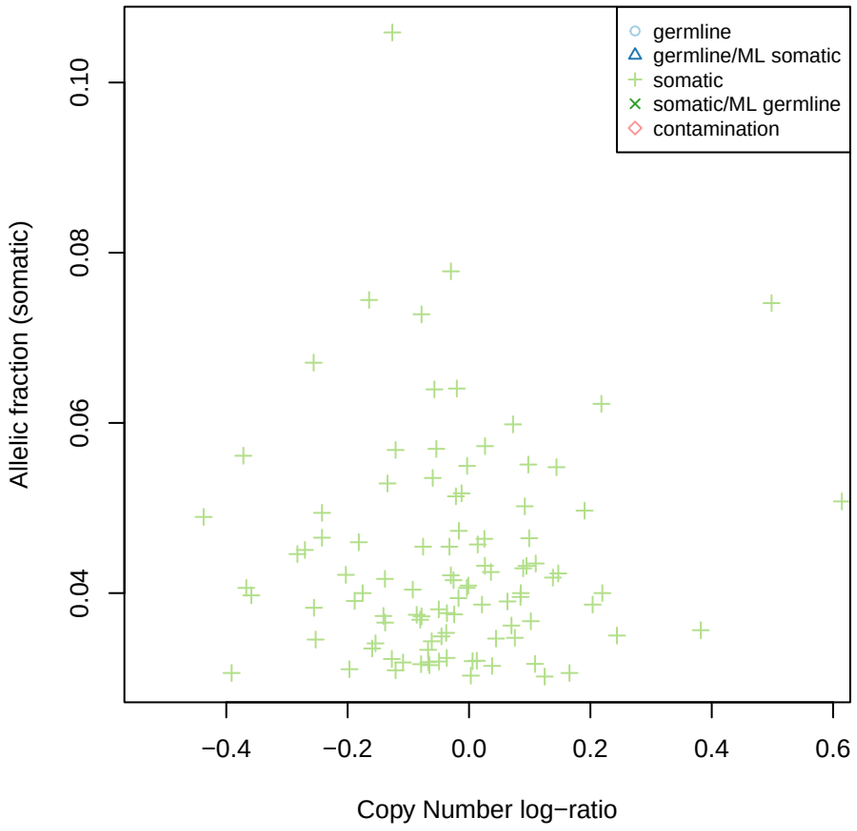

Purity: 0.35 Tumor ploidy: 2.043 SNV log−likelihood: 85.65 GoF: 80.5% Mean coverage: 441;441
1 2 3 4 5 6 7 8 9 10 12 13 14 15 17 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

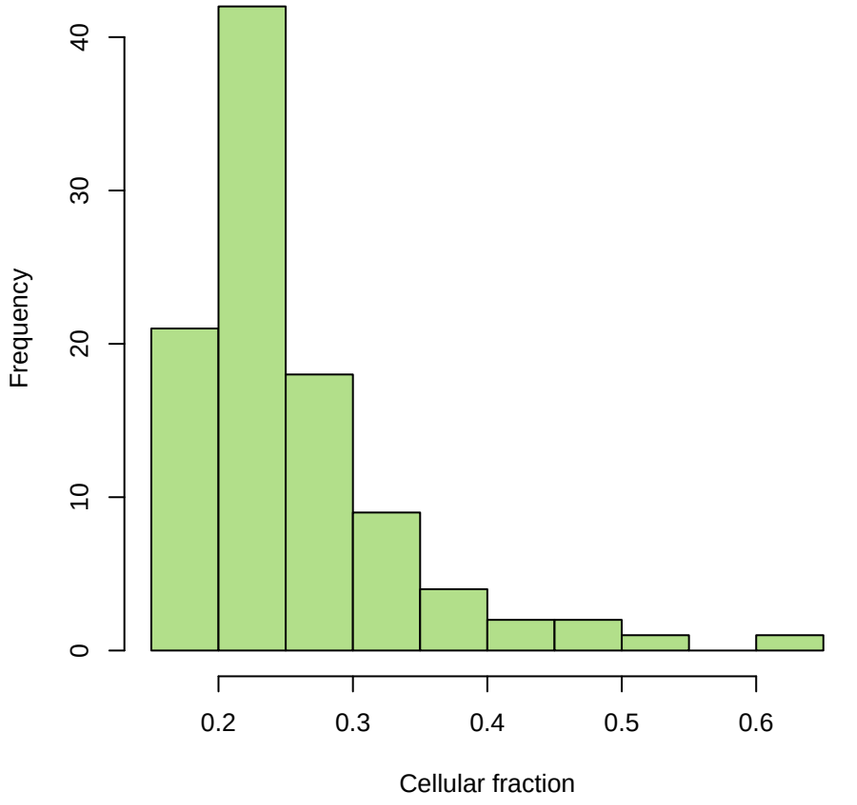

SCNA−fit log−likelihood: −3329.05
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5
0 50 100 150
SNV Index

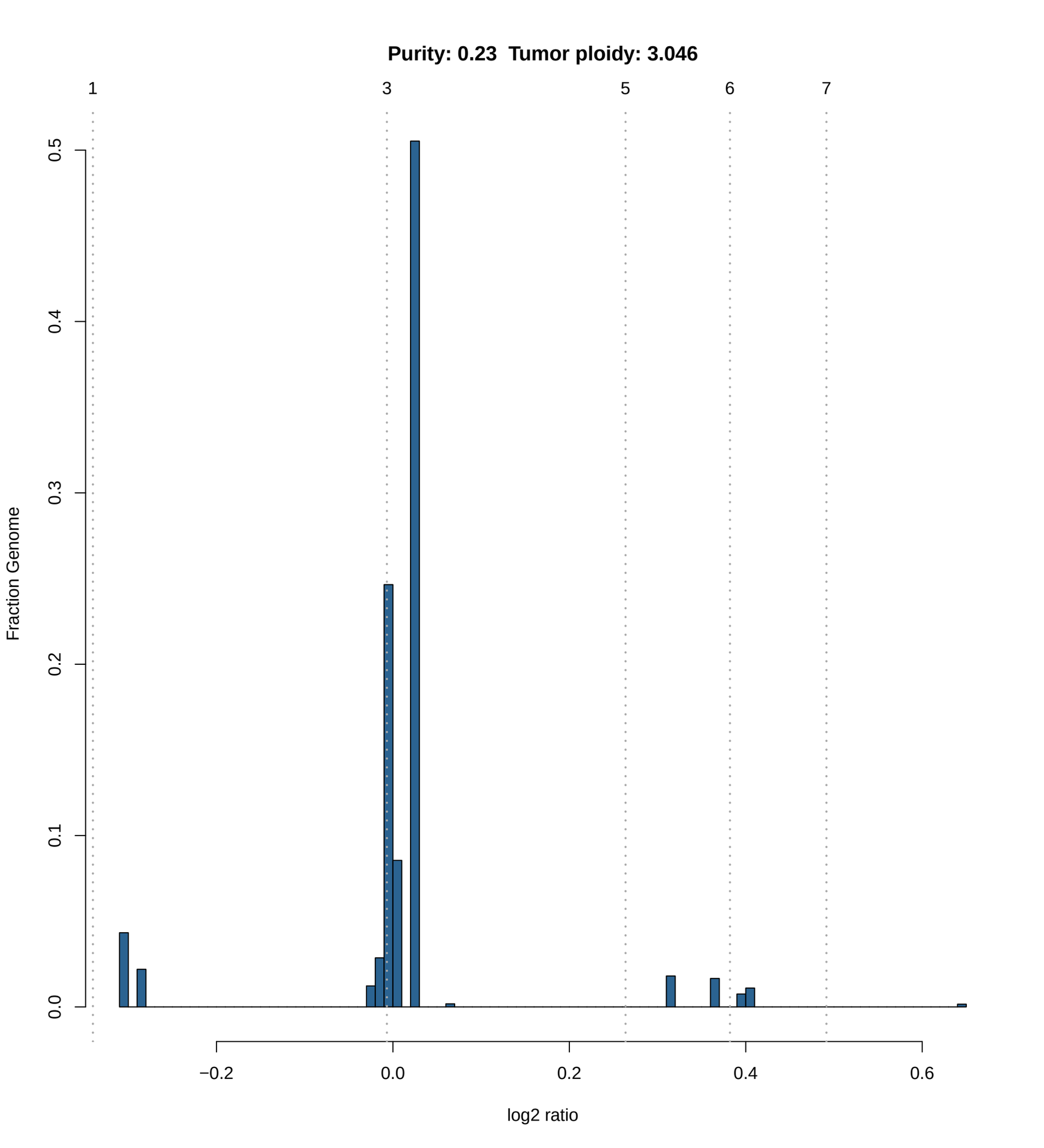

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 50 100 150
SNV Index

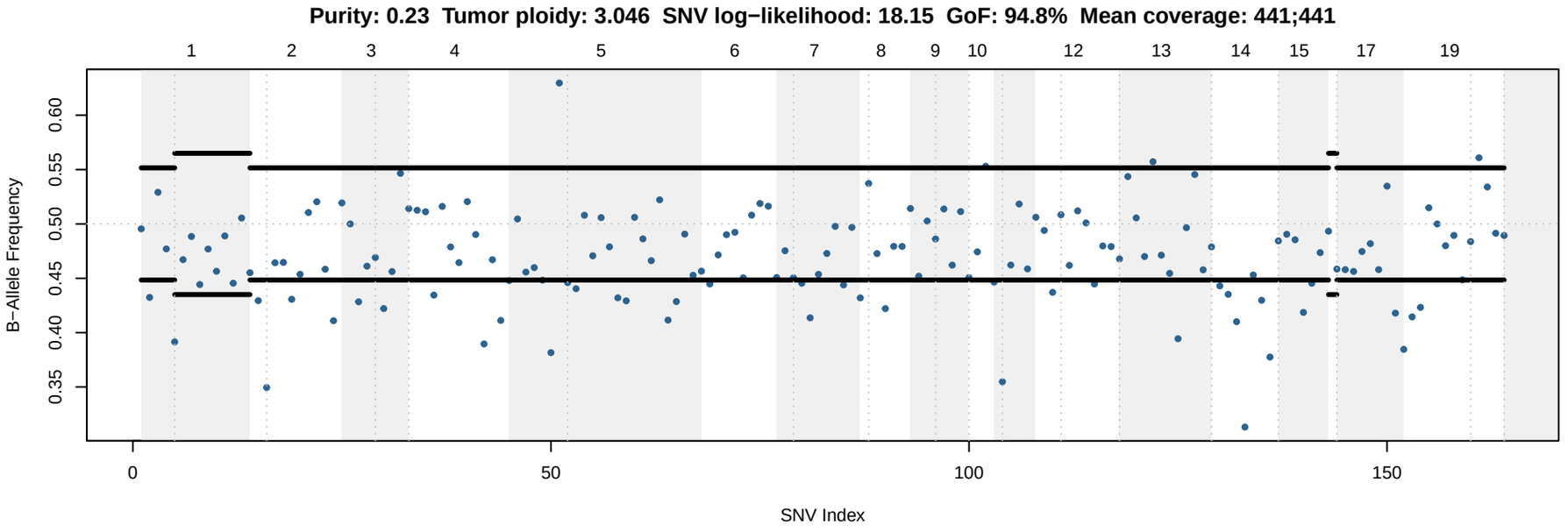

1m1
2m1
1m0
2m0
Allelic fraction (germline)
Copy Number log−ratio

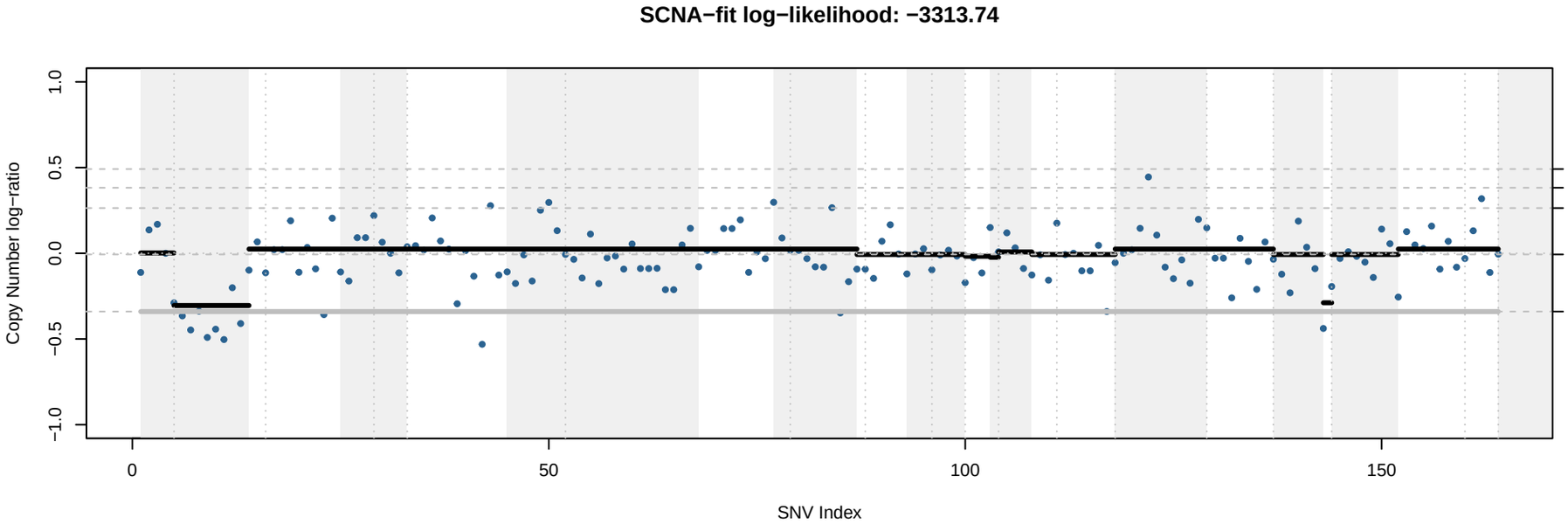

Coverage (log2)
Allelic fraction

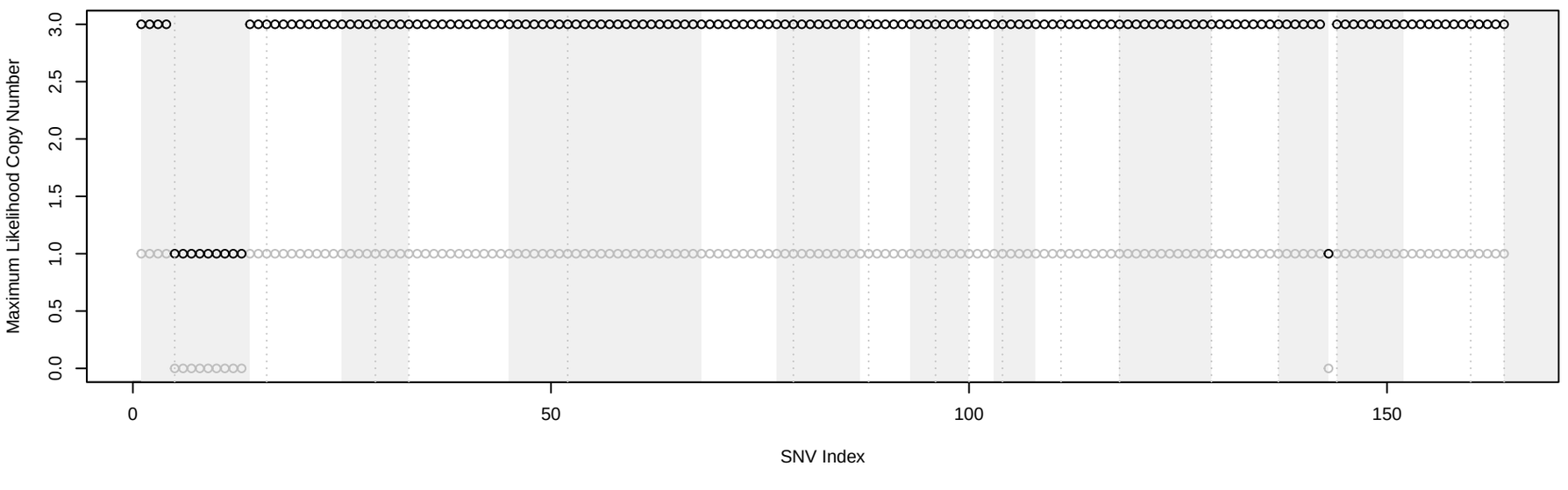

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

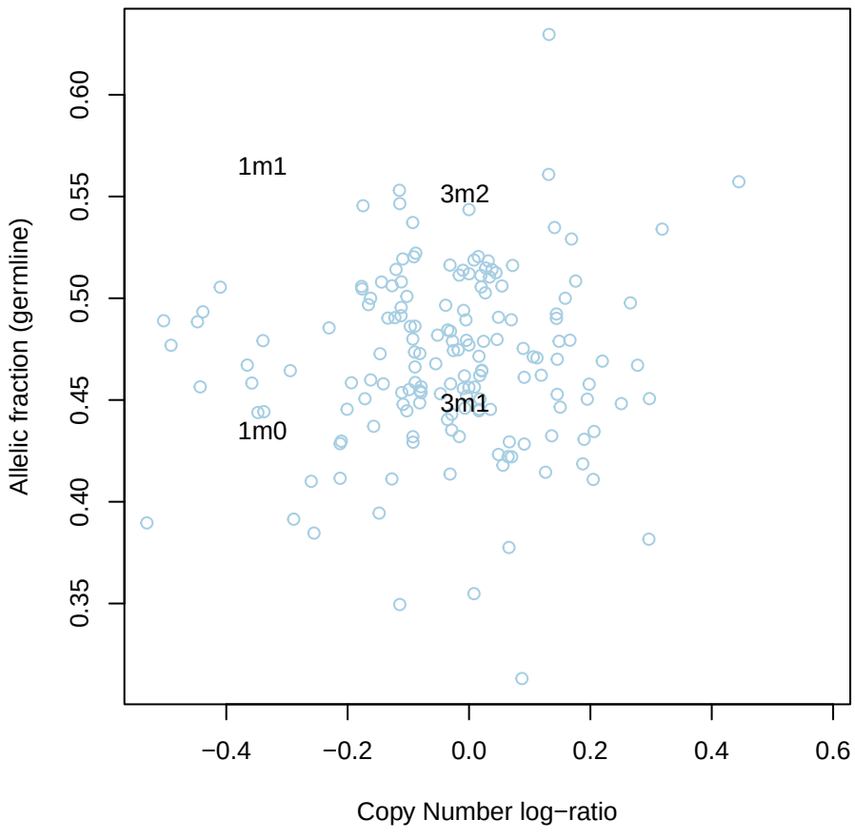

Frequency
Cellular fraction

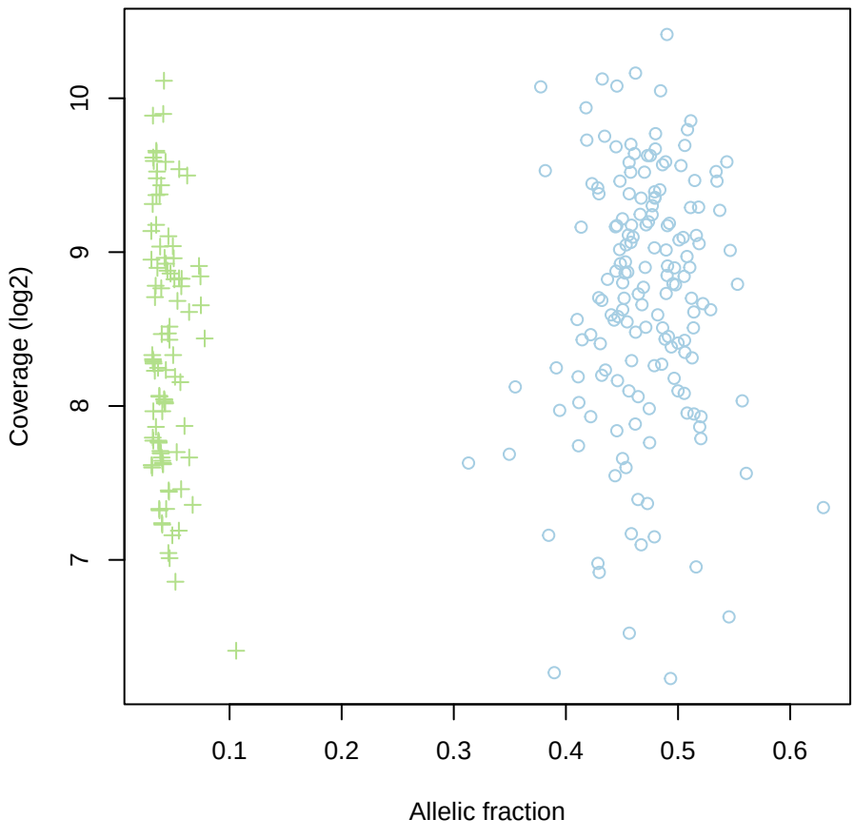

Purity: 0.23 Tumor ploidy: 3.046
1
3
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−0.2
0.0
0.2
0.4
0.6
log2 ratio

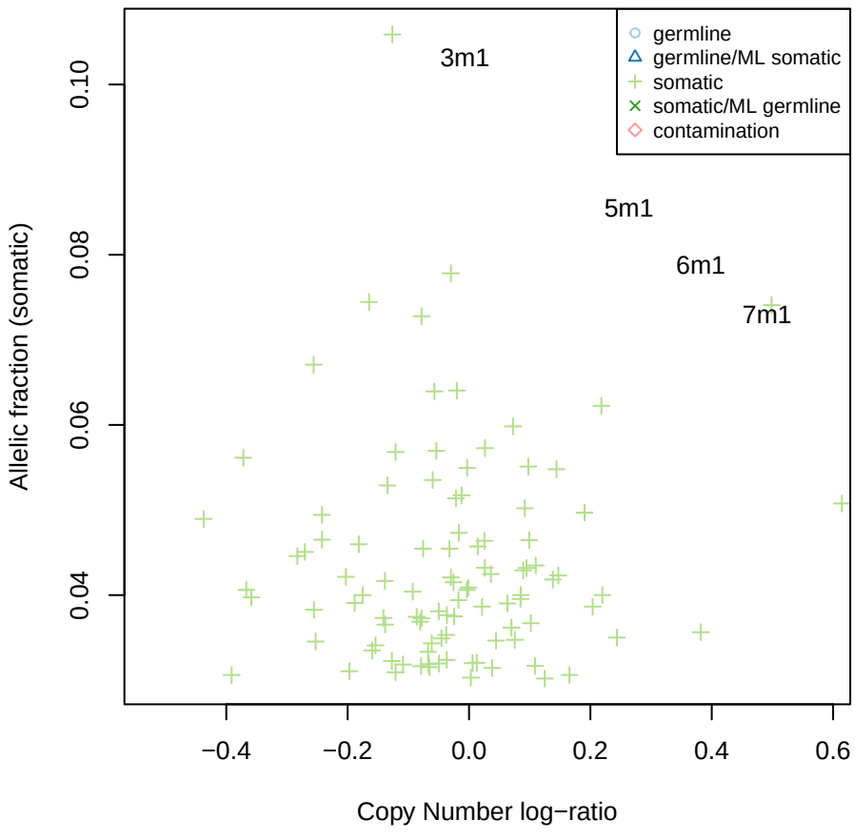

Purity: 0.23 Tumor ploidy: 3.046 SNV log−likelihood: 18.15 GoF: 94.8% Mean coverage: 441;441
1
2
3
4
5
6
7
8
9
10
12
13
14
15
17
19
B−Allele Frequency
0.35
0.40
0.45
0.50
0.55
0.60
0
50
100
150
SNV Index

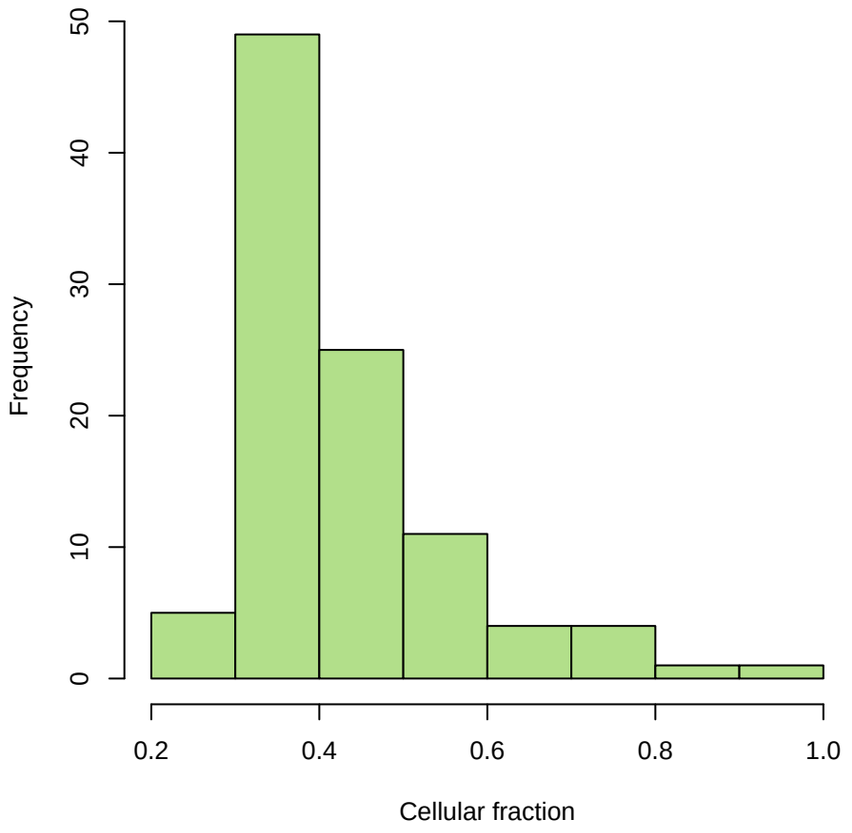

SCNA−fit log−likelihood: −3313.74
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1
3
5
7
0
50
100
150
SNV Index

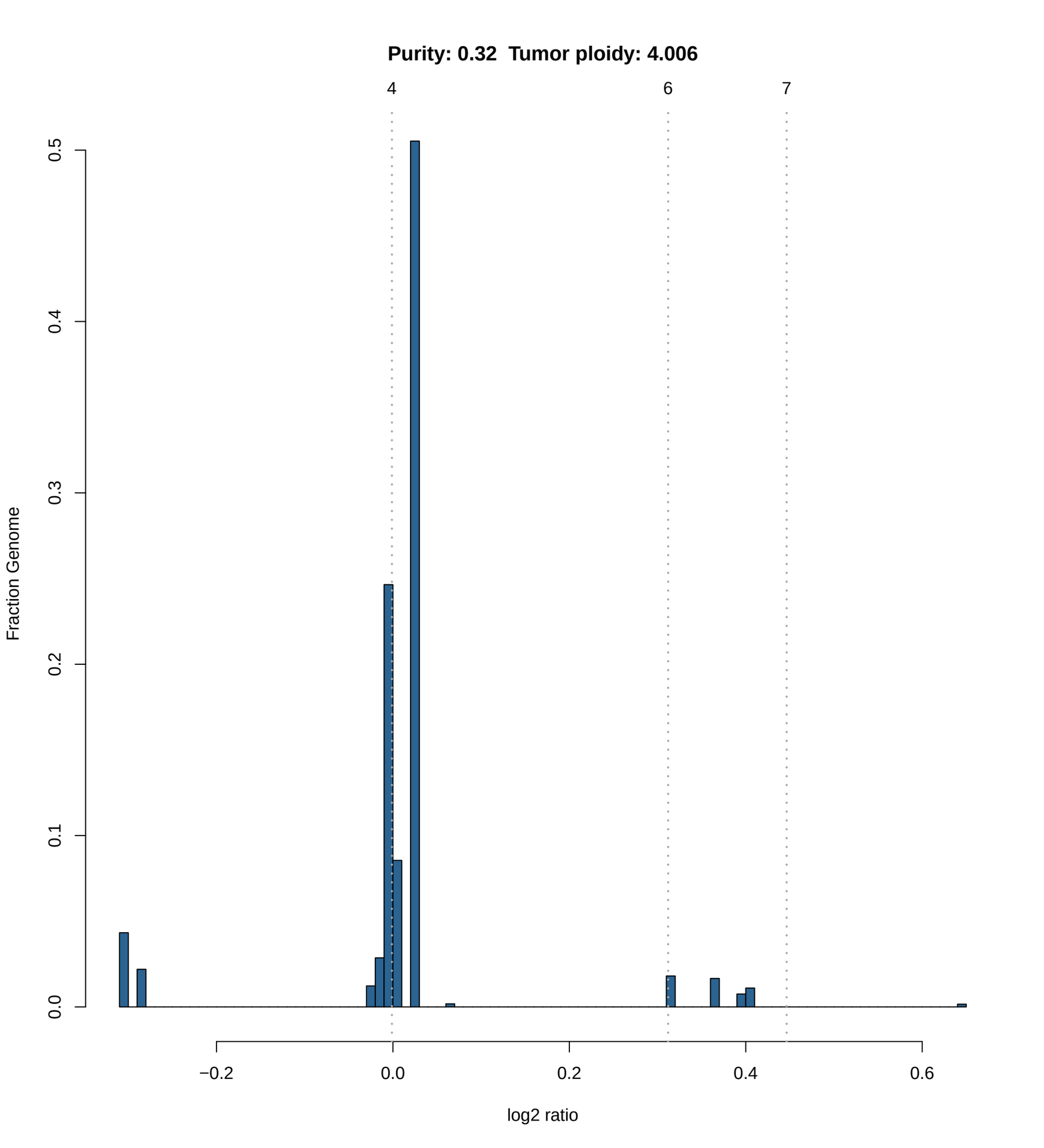

Maximum Likelihood Copy Number
0.0
0.5
1.0
1.5
2.0
2.5
3.0
0
50
100
150
SNV Index

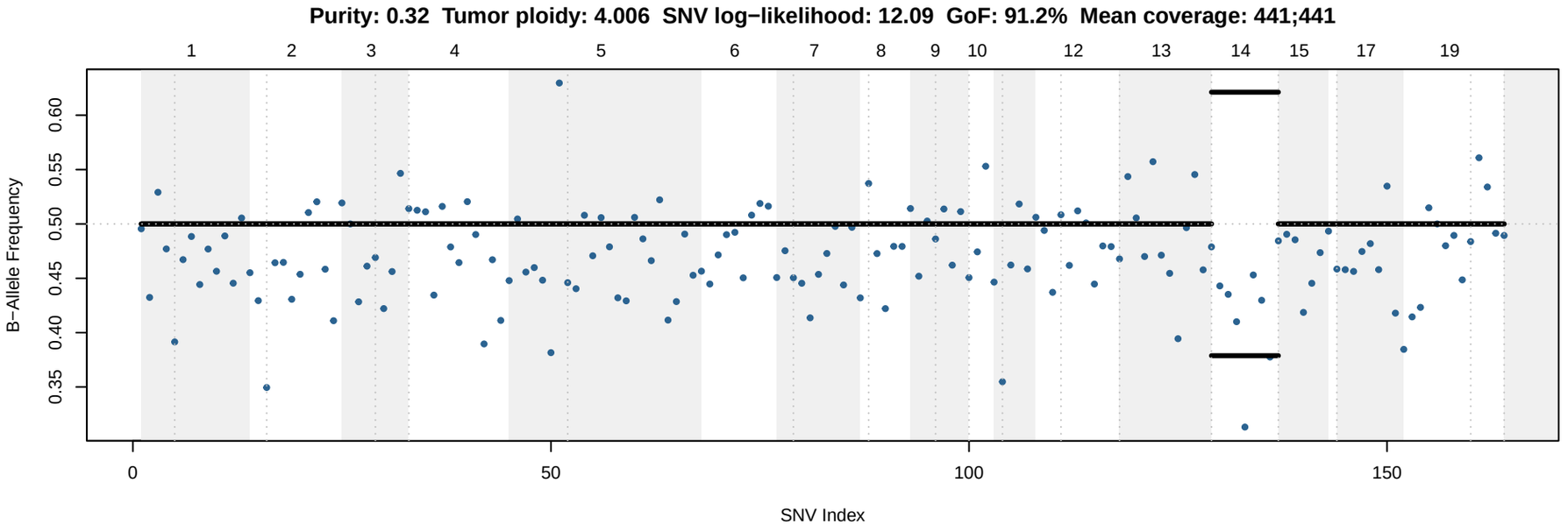

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
1m1
3m2
3m1
1m0
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

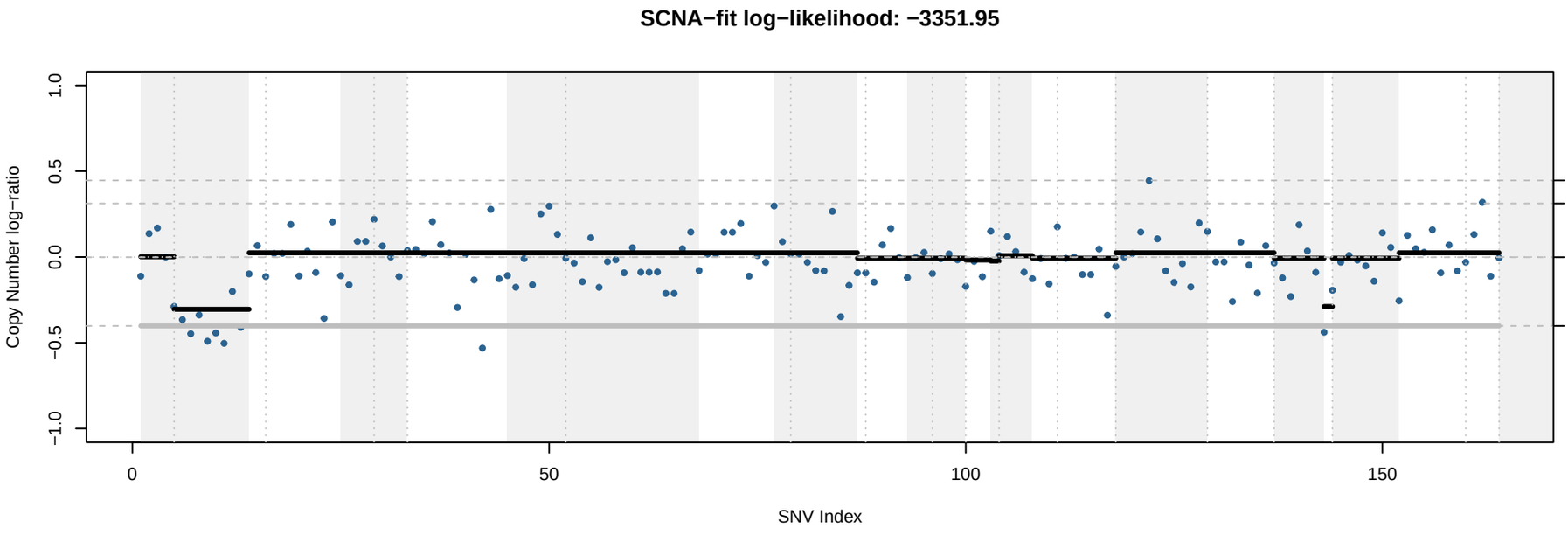

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

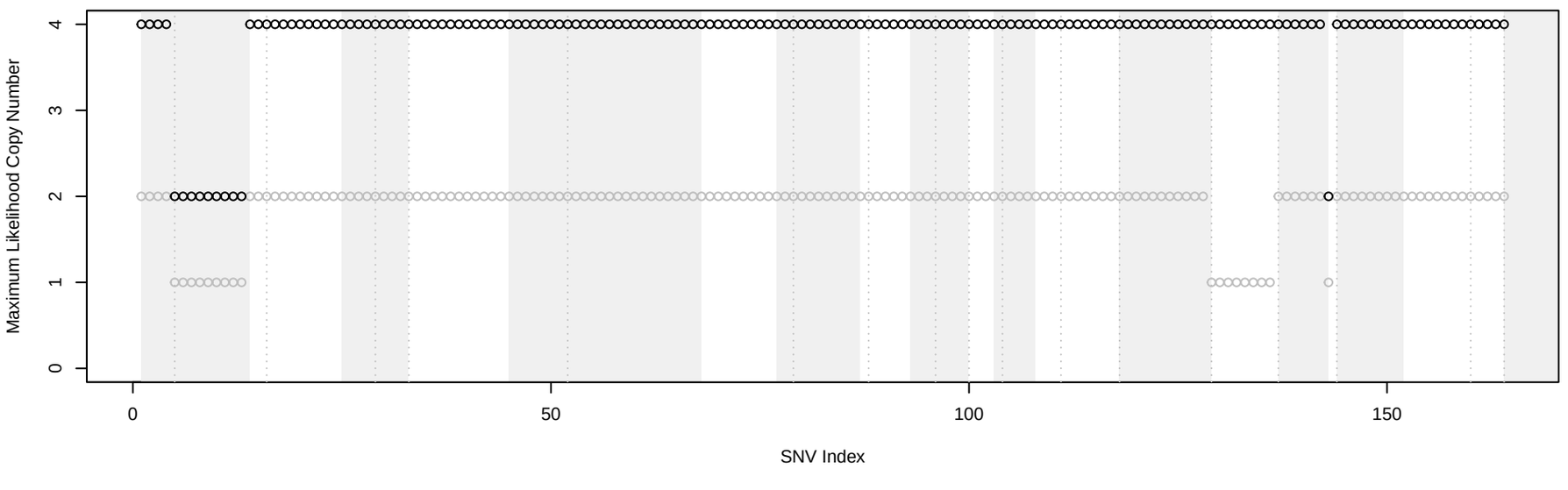

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
5m1
6m1
7m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

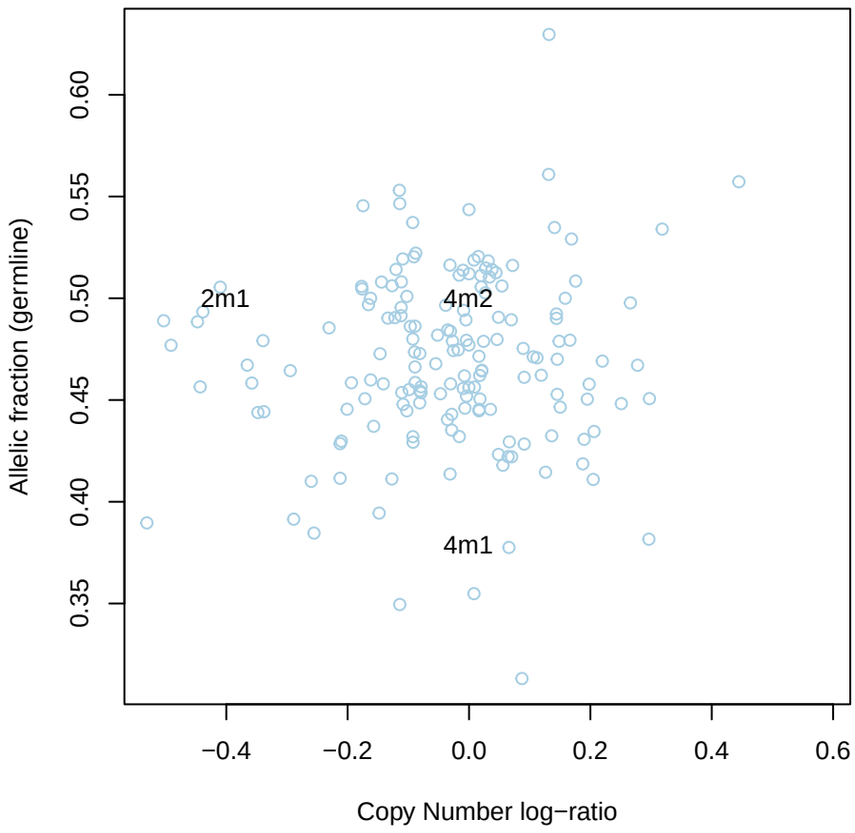

Frequency
0
10
20
30
40
50
0.2
0.4
0.6
0.8
1.0
Cellular fraction

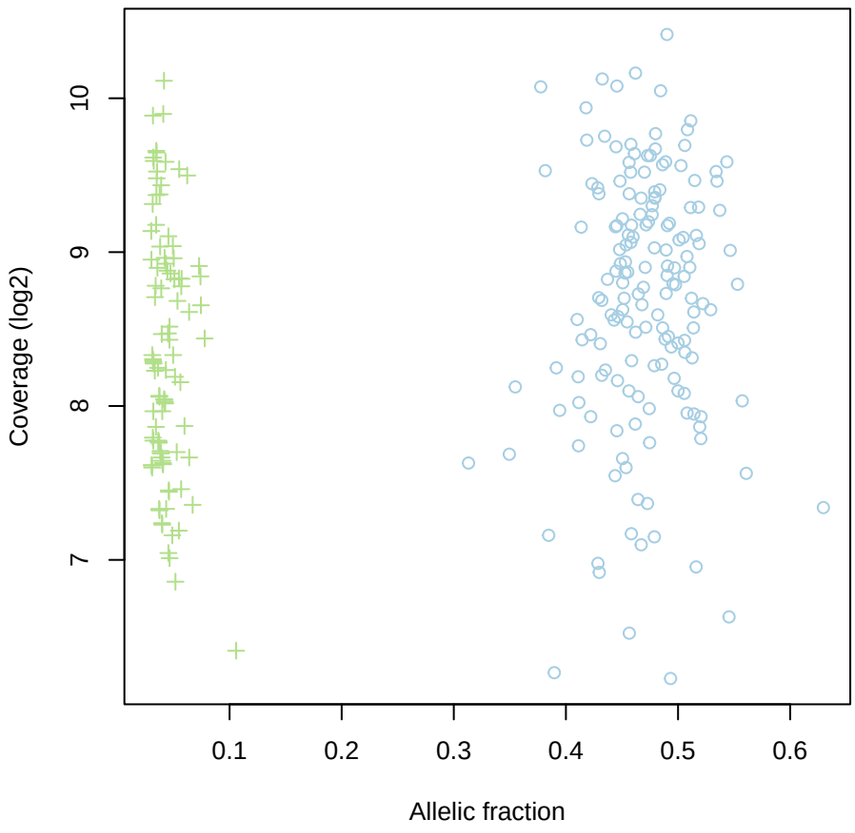

Purity: 0.32 Tumor ploidy: 4.006
4
6
7
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
−0.2
0.0
0.2
0.4
0.6
log2 ratio

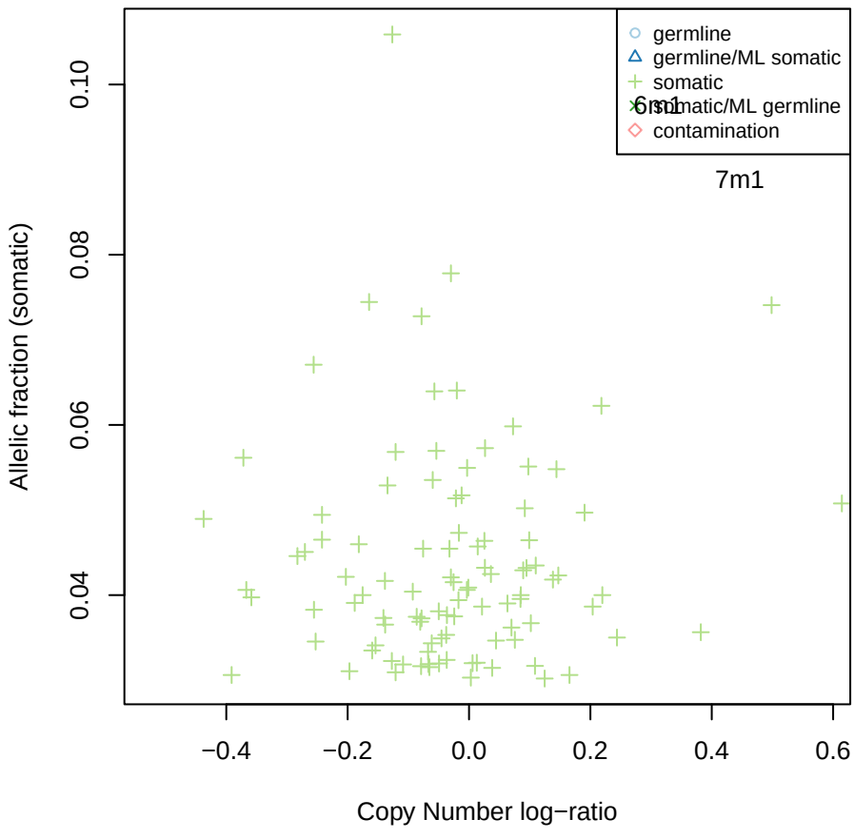

Purity: 0.32 Tumor ploidy: 4.006 SNV log−likelihood: 12.09 GoF: 91.2% Mean coverage: 441;441
1
2
3
4
5
6
7
8
9
10
12
13
14
15
17
19
B−Allele Frequency
0.35
0.40
0.45
0.50
0.55
0.60
0
50
100
150
SNV Index

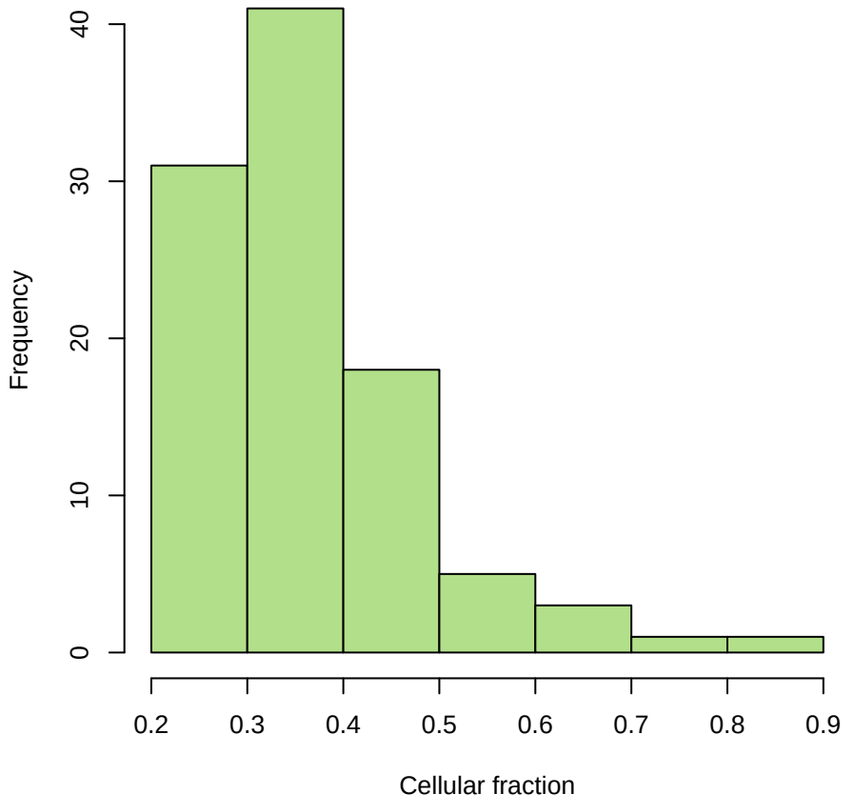

SCNA−fit log−likelihood: −3351.95
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
2
4
6
0
50
100
150
SNV Index

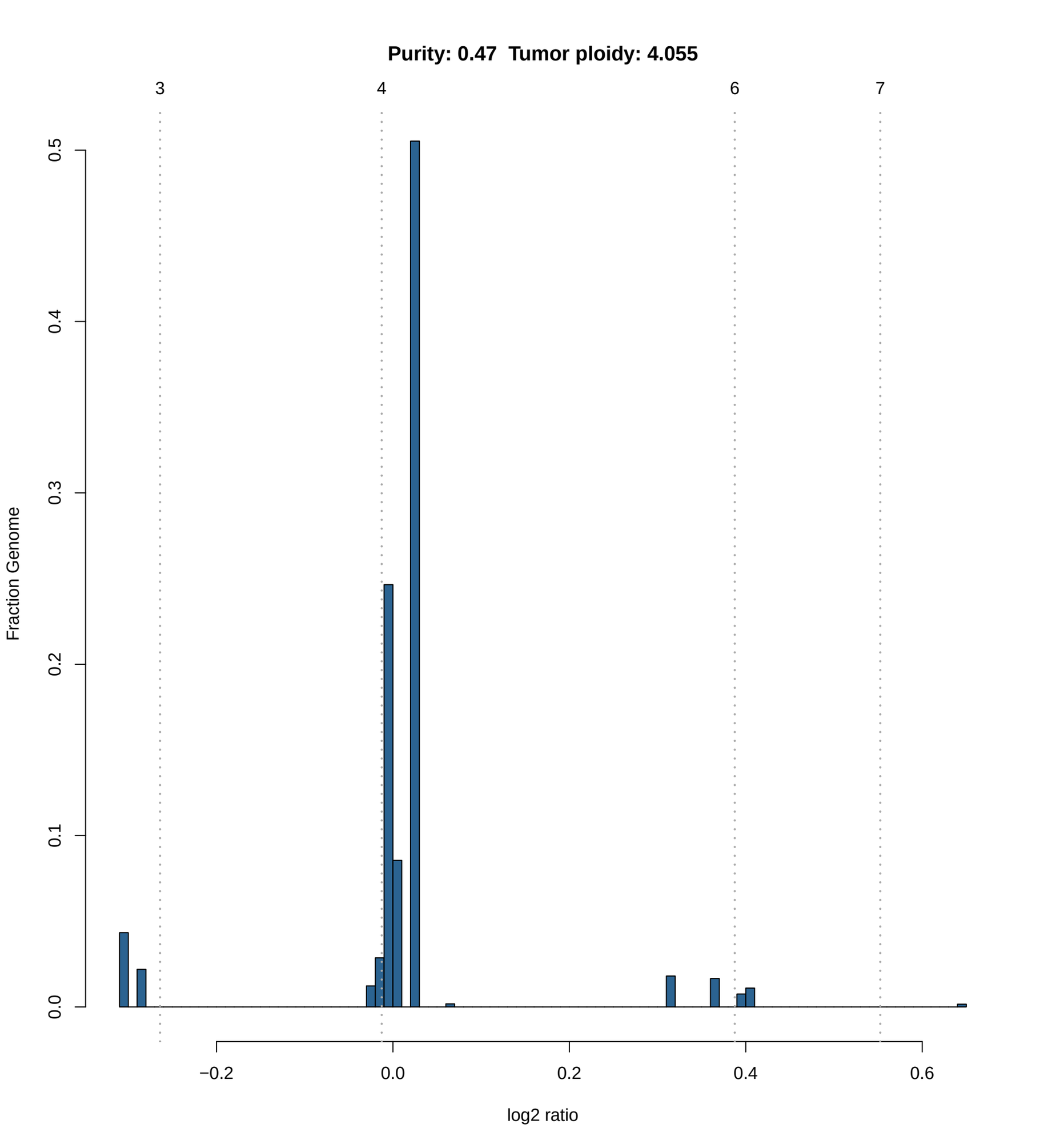

Maximum Likelihood Copy Number
0
1
2
3
4
0
50
100
150
SNV Index

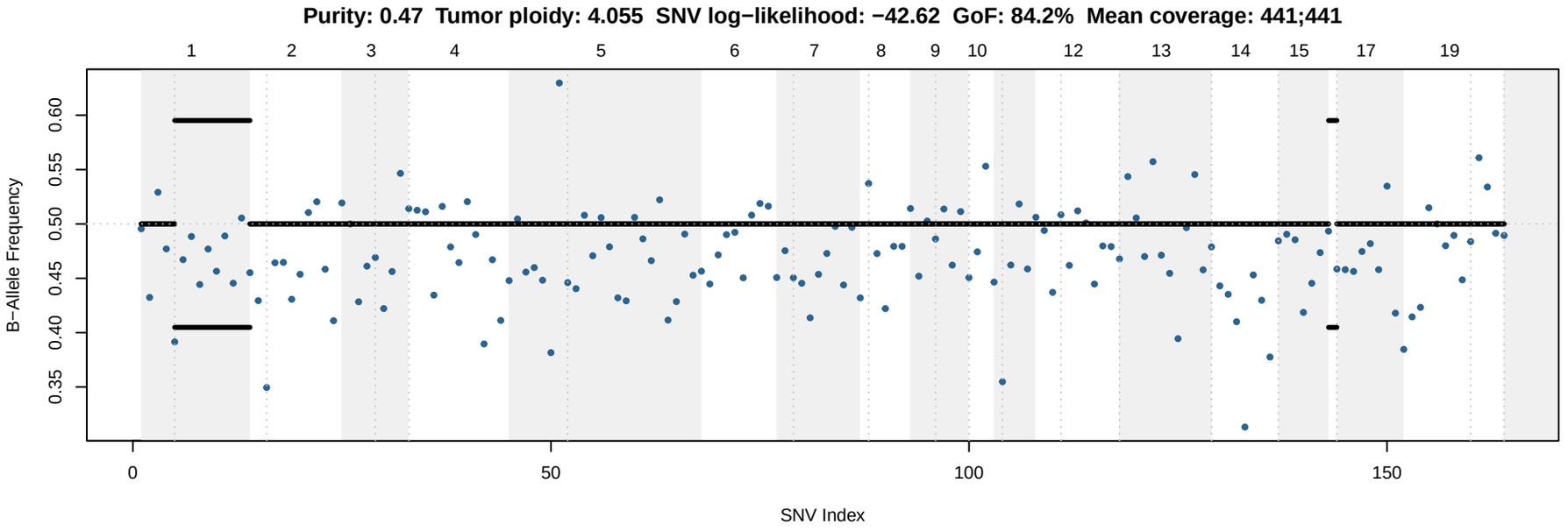

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
2m1
4m2
4m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

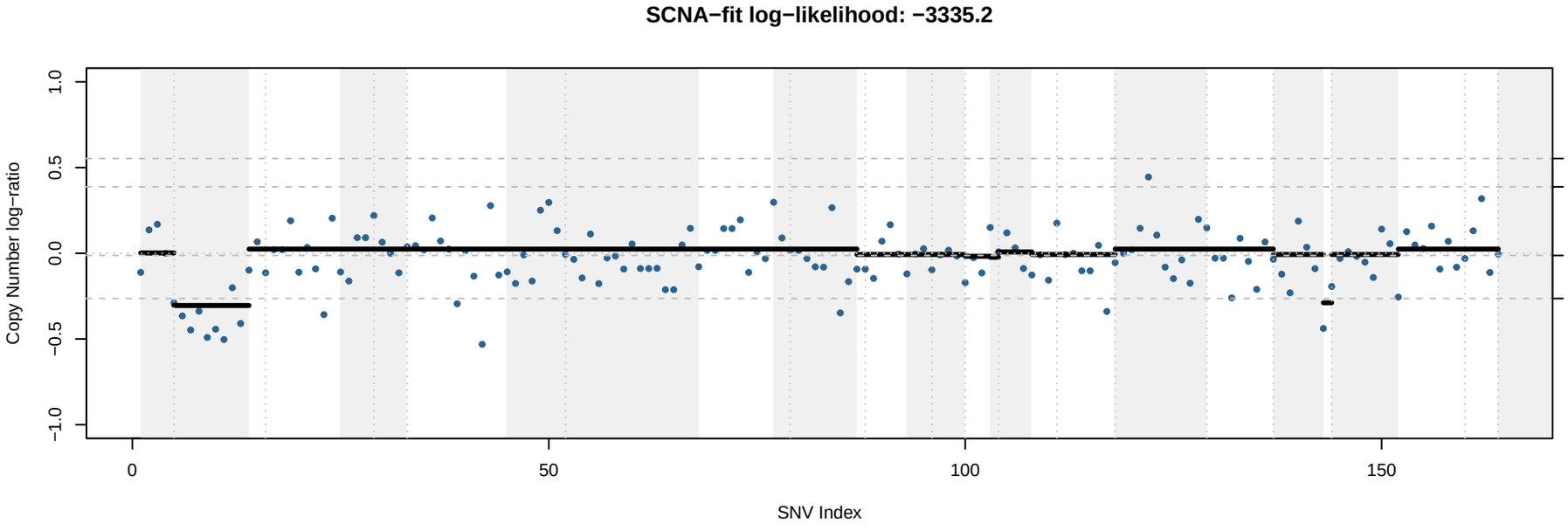

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

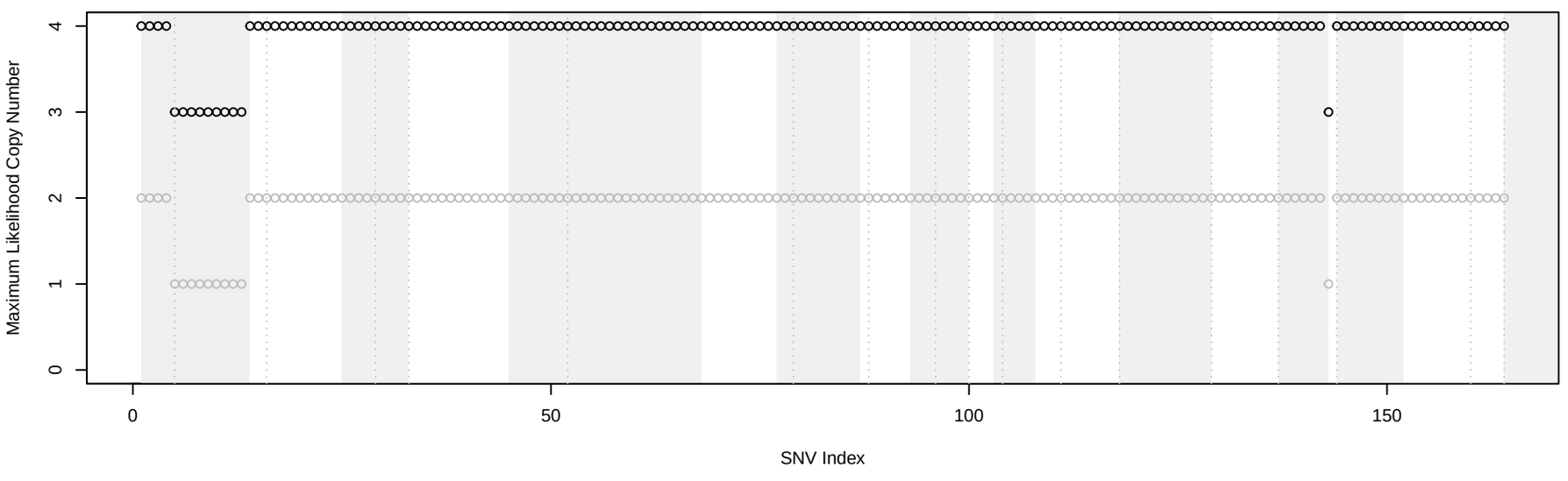

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m1
7m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

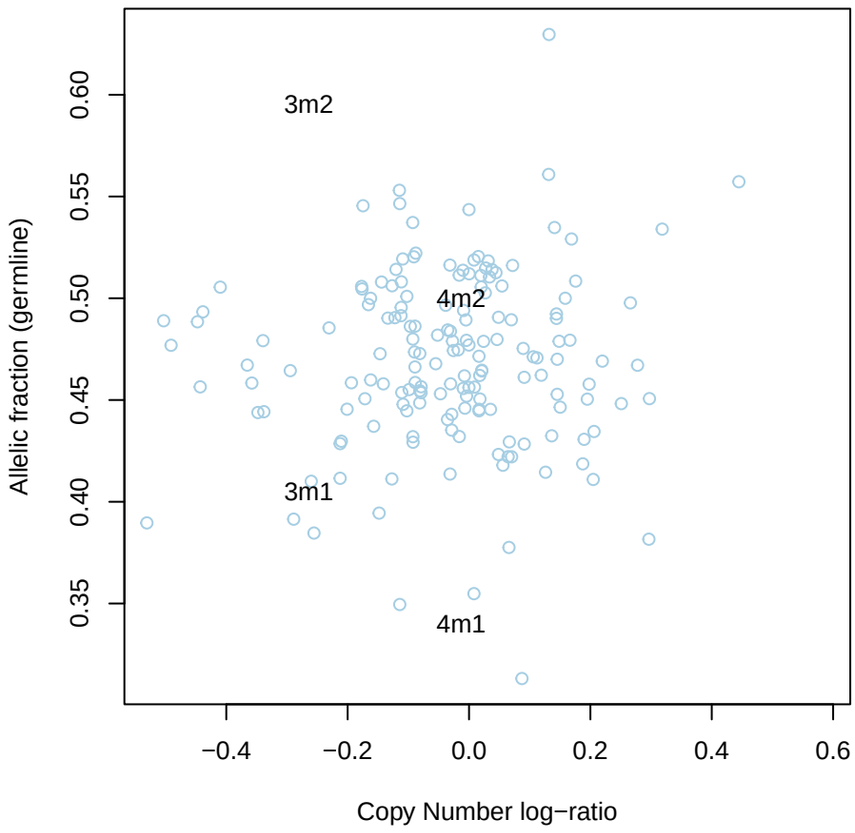

Frequency
0
10
20
30
40
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
Cellular fraction

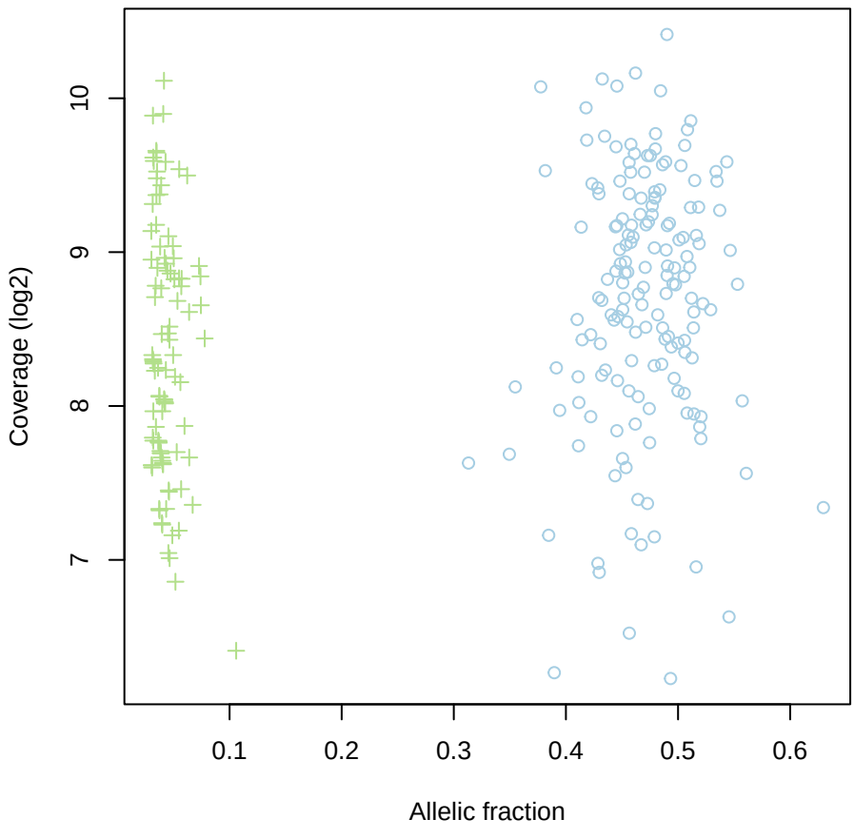

Purity: 0.47 Tumor ploidy: 4.055
3
4
6
7
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−0.2
0.0
0.2
0.4
0.6
log2 ratio

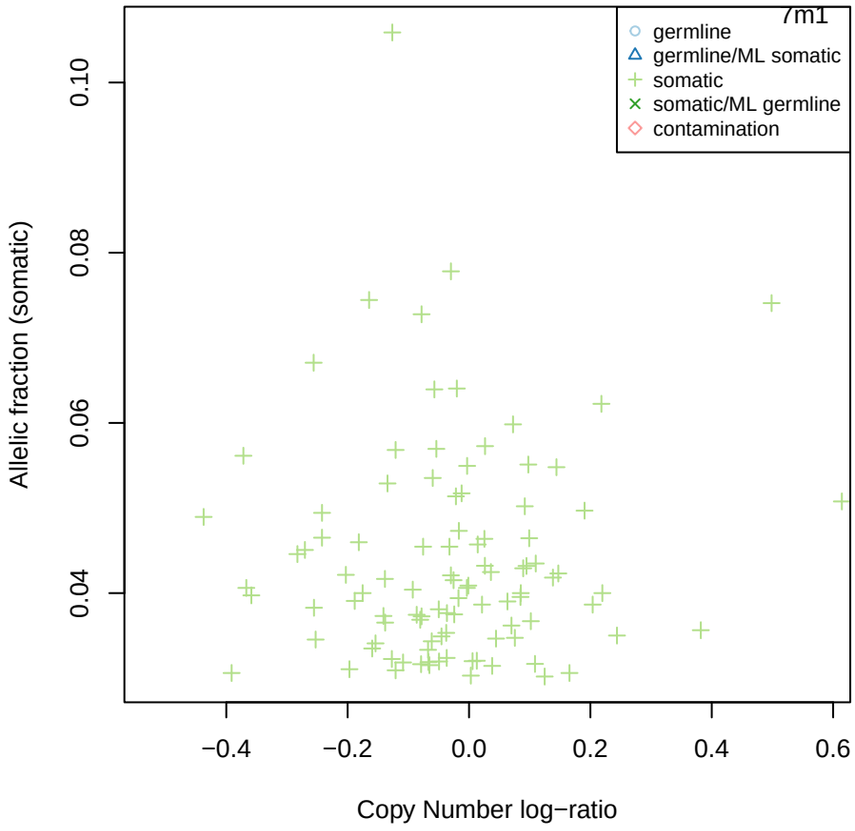

Purity: 0.47 Tumor ploidy: 4.055 SNV log−likelihood: −42.62 GoF: 84.2% Mean coverage: 441;441
1 2 3 4 5 6 7 8 9 10 12 13 14 15 17 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

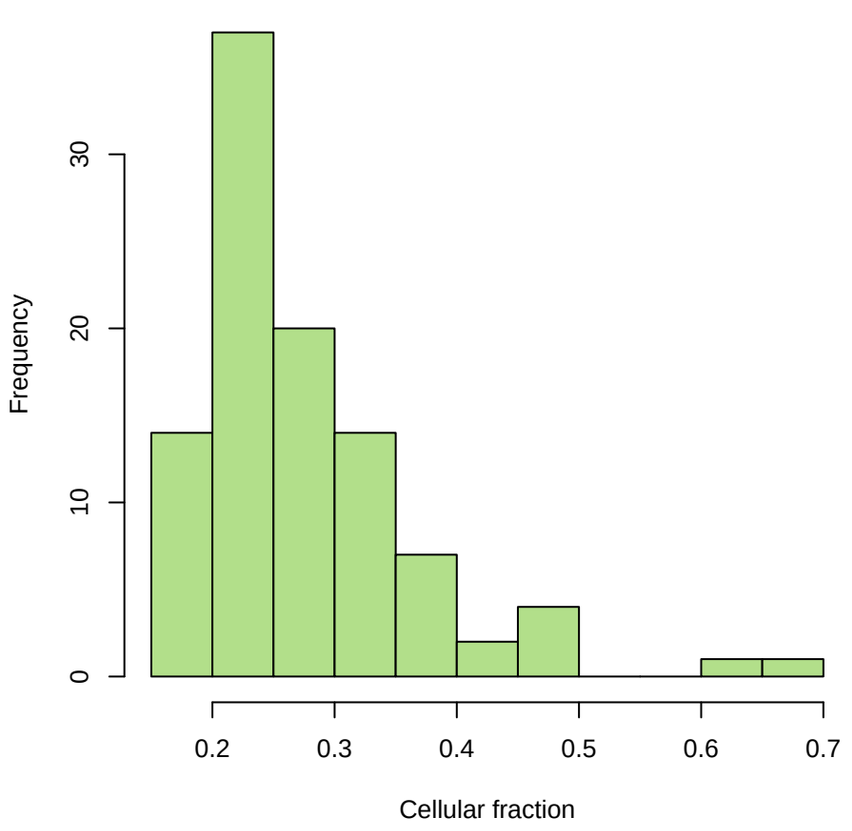

SCNA−fit log−likelihood: −3335.2
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 6 7
0 50 100 150
SNV Index

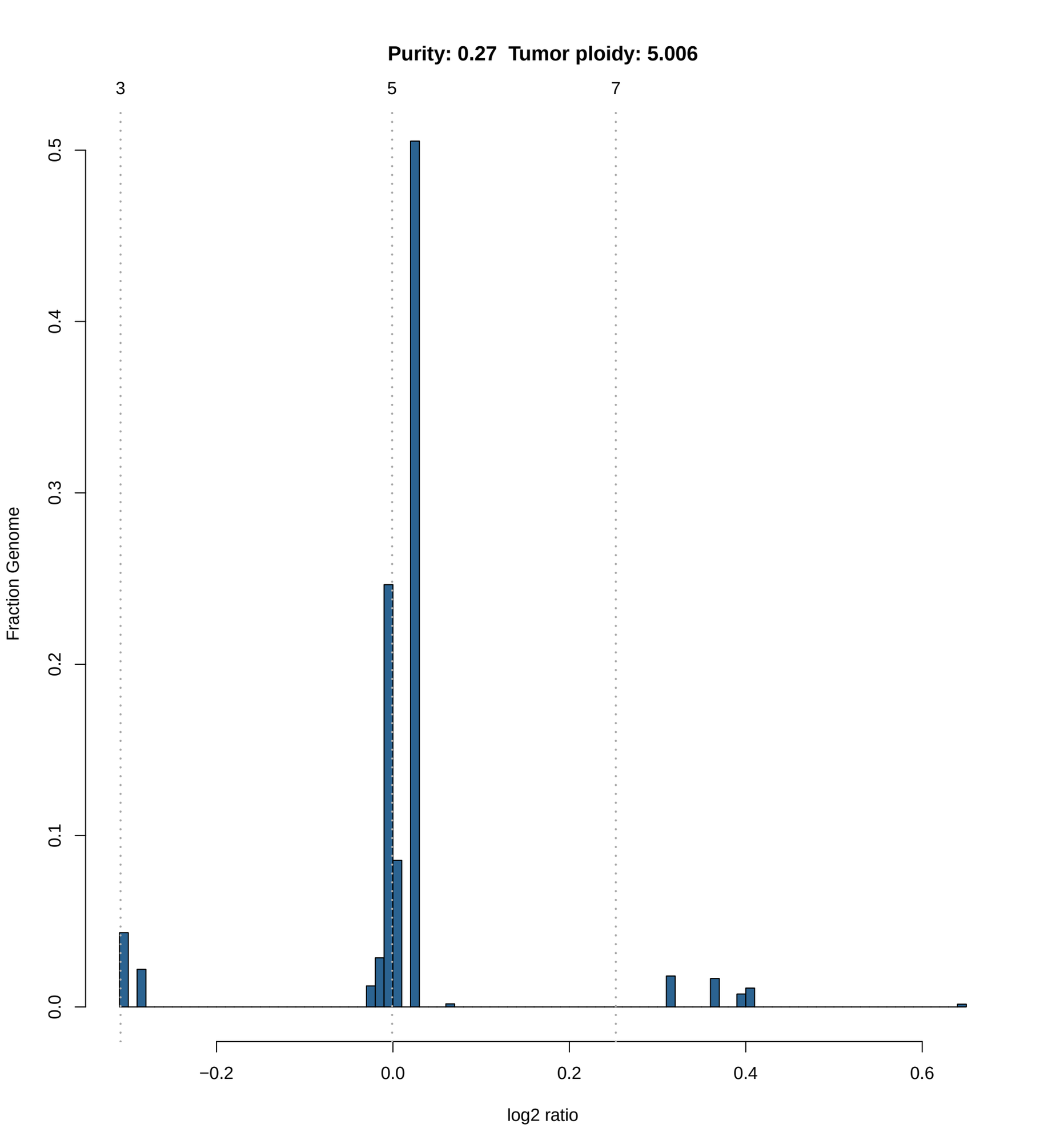

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

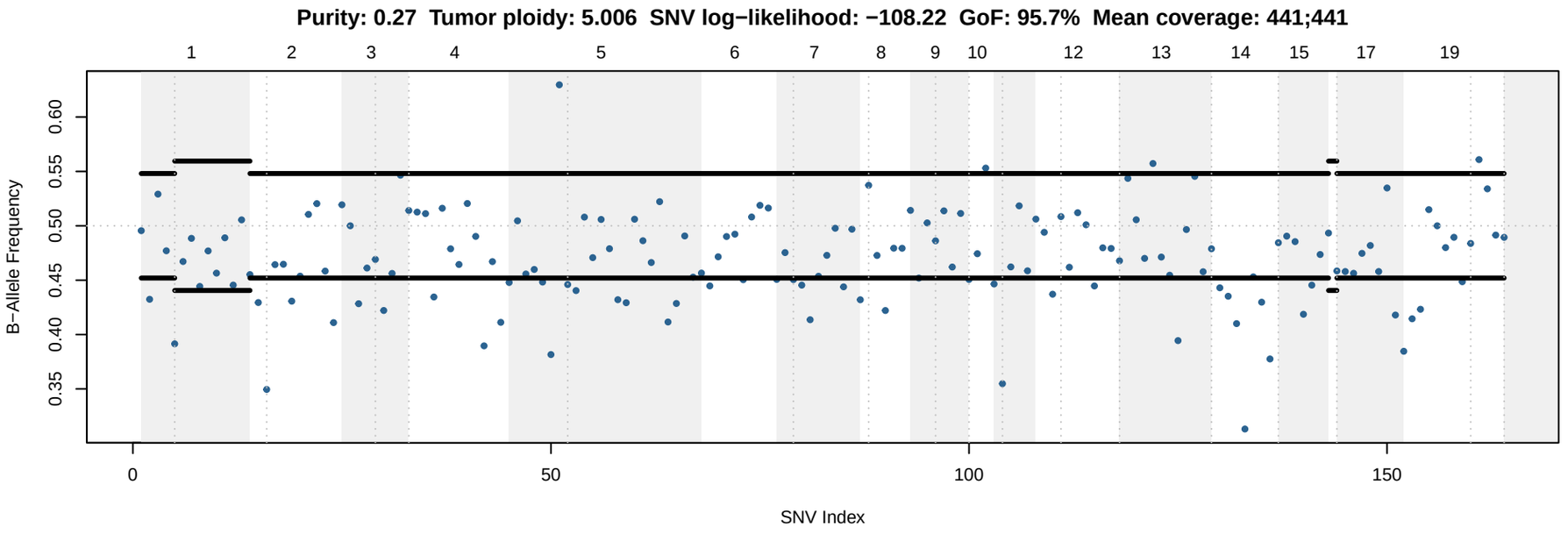

3m2
4m2
3m1
4m1
Allelic fraction (germline)
Copy Number log−ratio

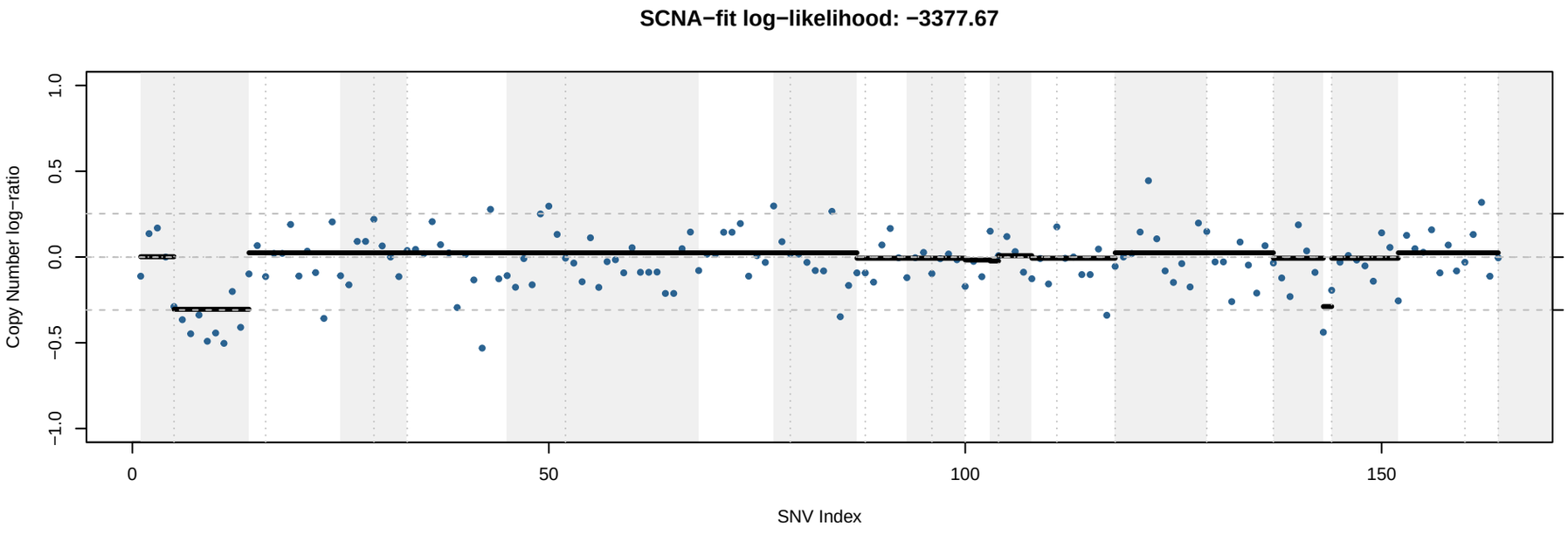

Coverage (log2)
Allelic fraction

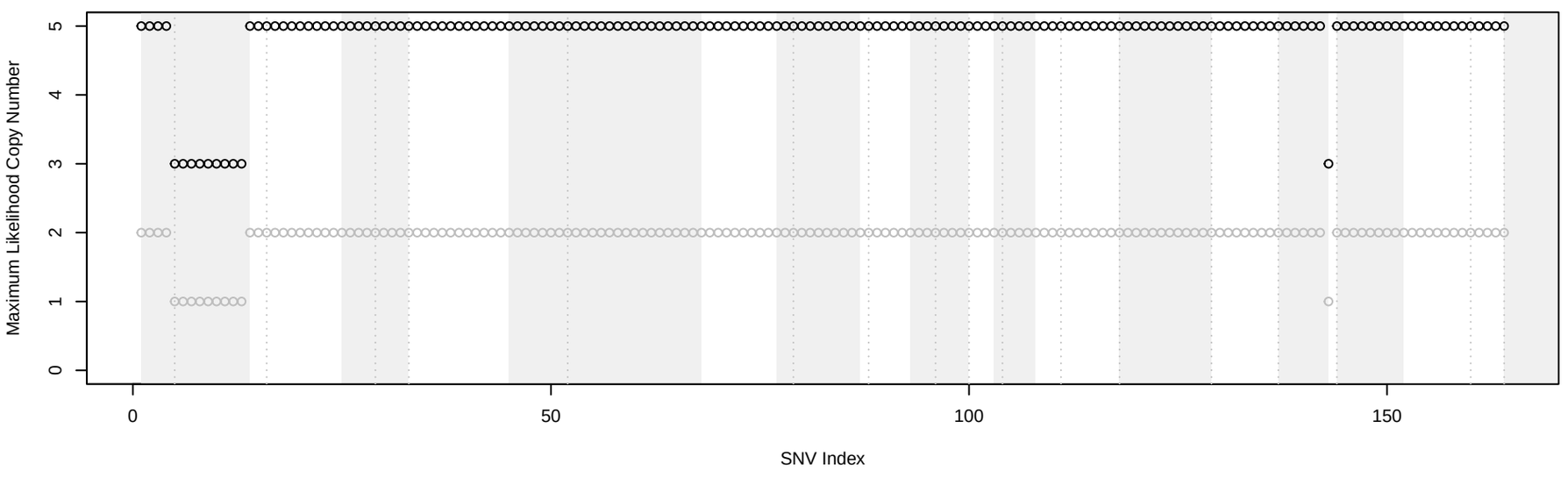

7m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

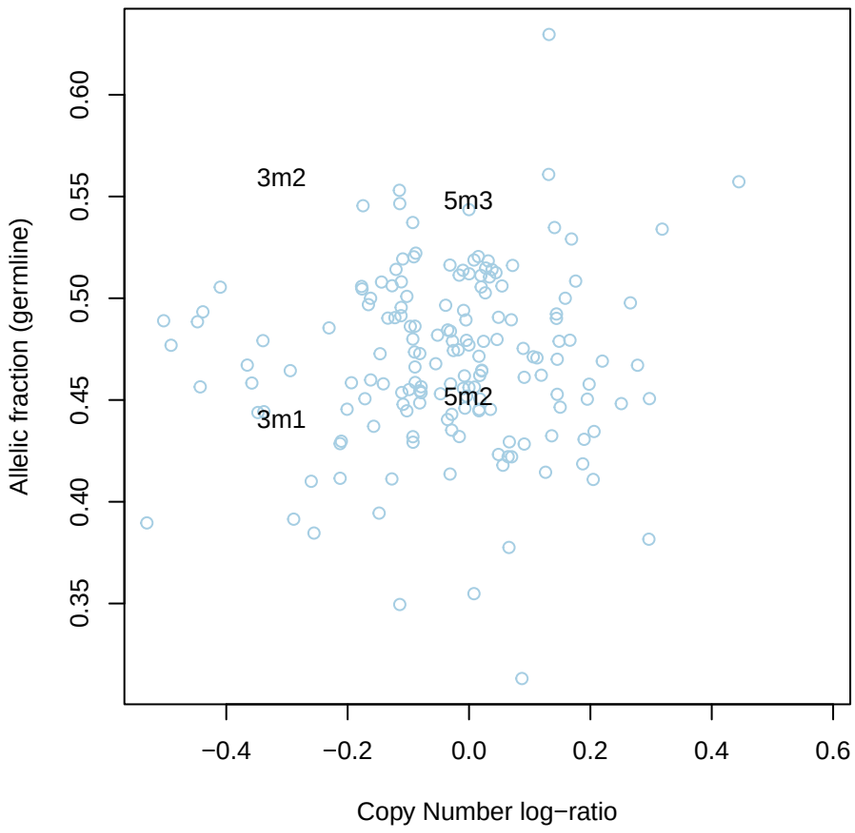

Frequency
Cellular fraction

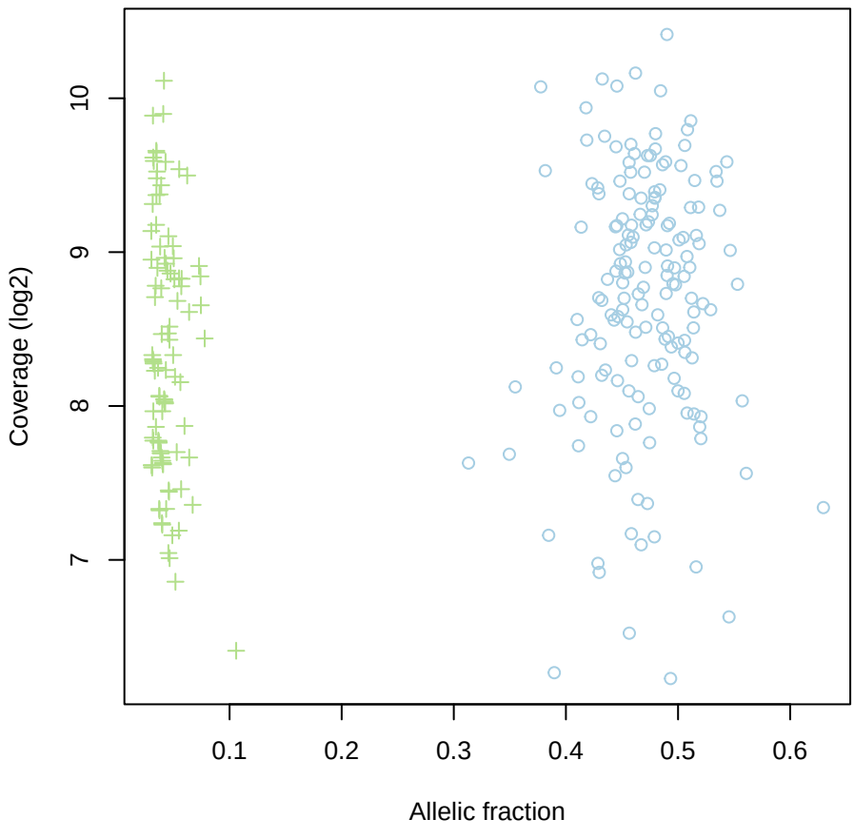

Purity: 0.27 Tumor ploidy: 5.006
3
5
7
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−0.2
0.0
0.2
0.4
0.6
log2 ratio

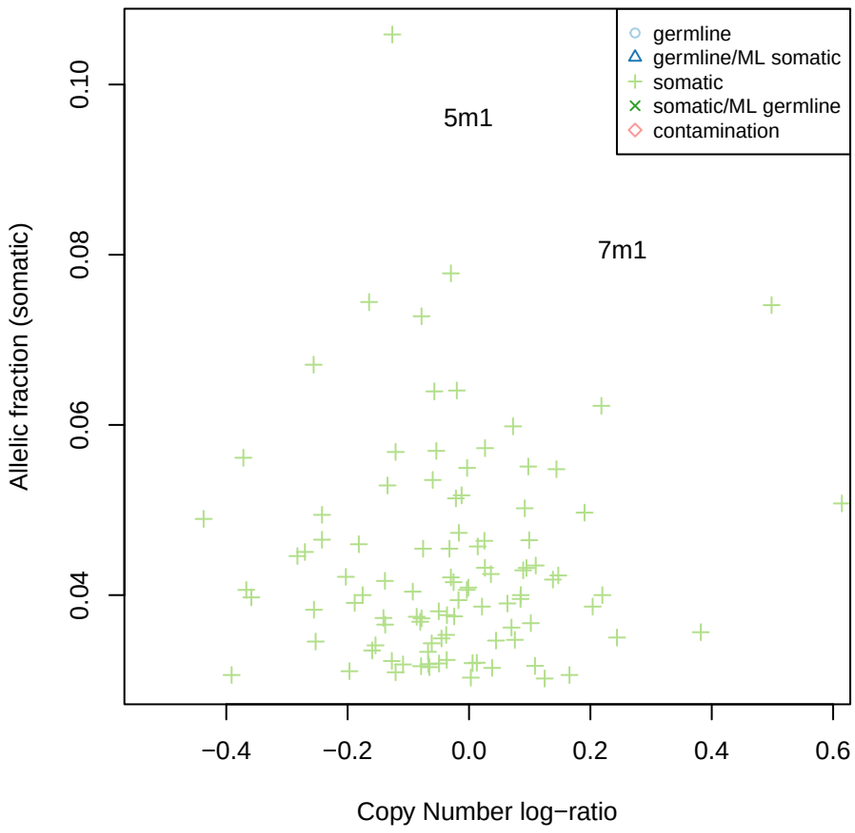

Purity: 0.27 Tumor ploidy: 5.006 SNV log−likelihood: −108.22 GoF: 95.7% Mean coverage: 441;441
1
2
3
4
5
6
7
8
9
10
12
13
14
15
17
19
B−Allele Frequency
0.35
0.40
0.45
0.50
0.55
0.60
0
50
100
150
SNV Index

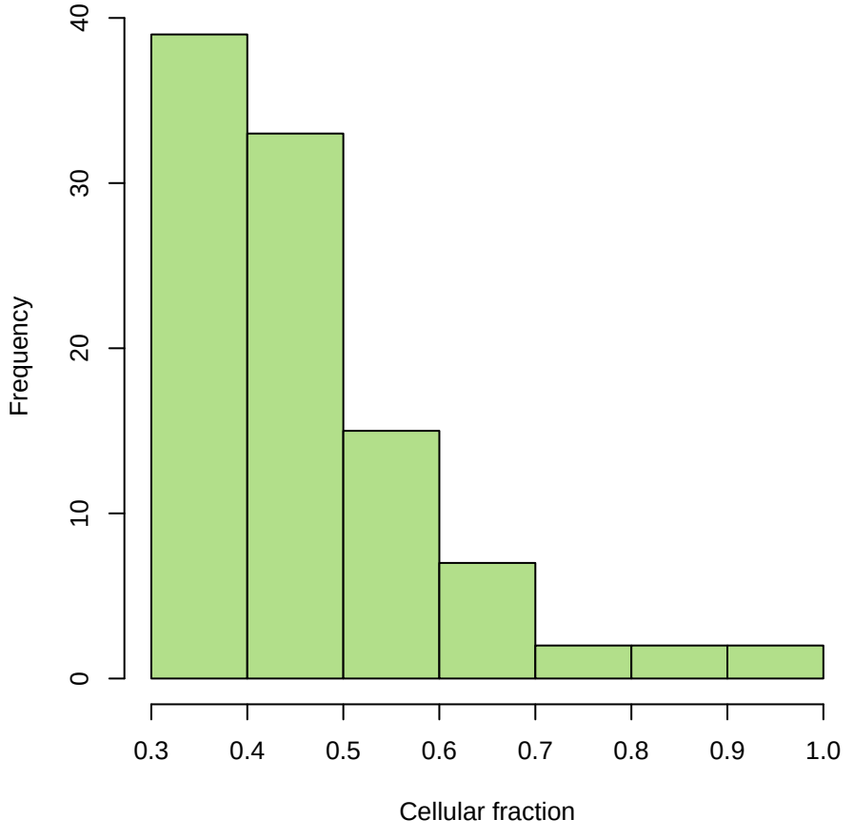

SCNA−fit log−likelihood: −3377.67
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
3
5
7
0
50
100
150
SNV Index

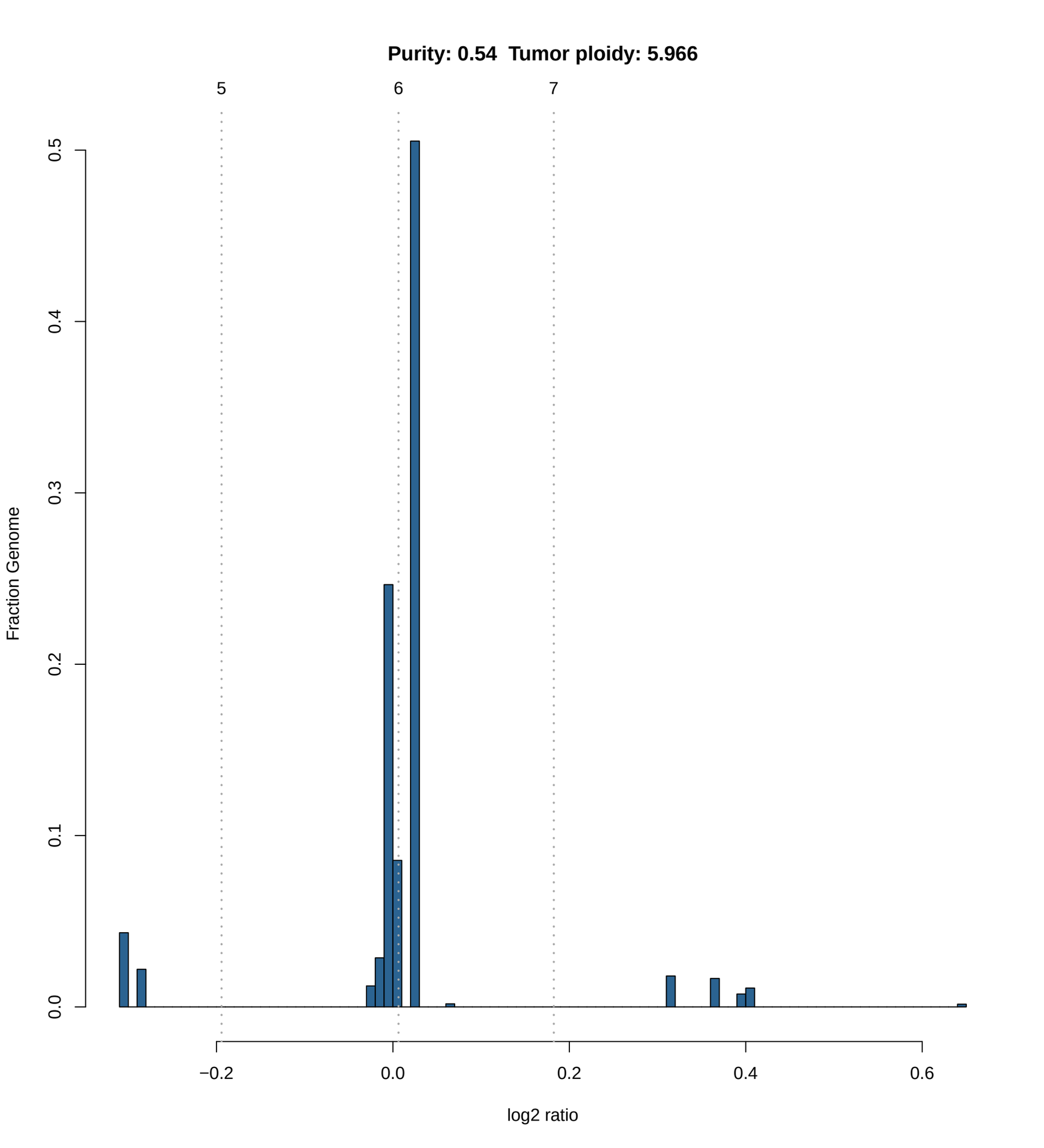

Maximum Likelihood Copy Number
0
1
2
3
4
5
0
50
100
150
SNV Index

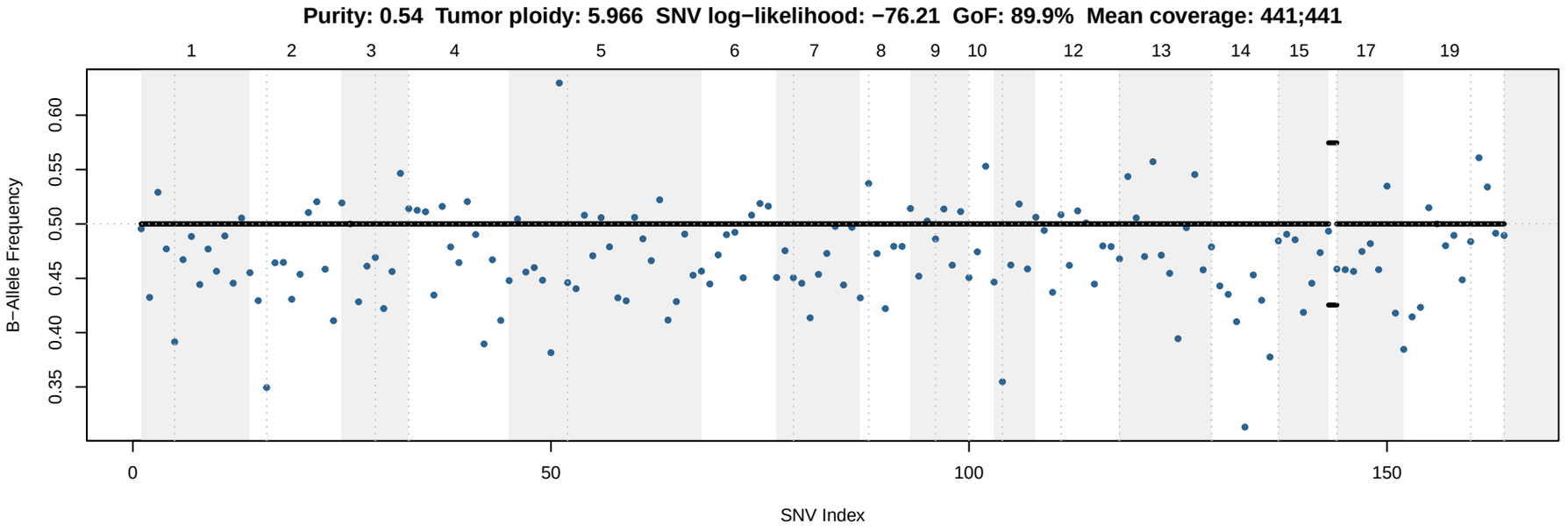

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
3m2
5m3
5m2
3m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

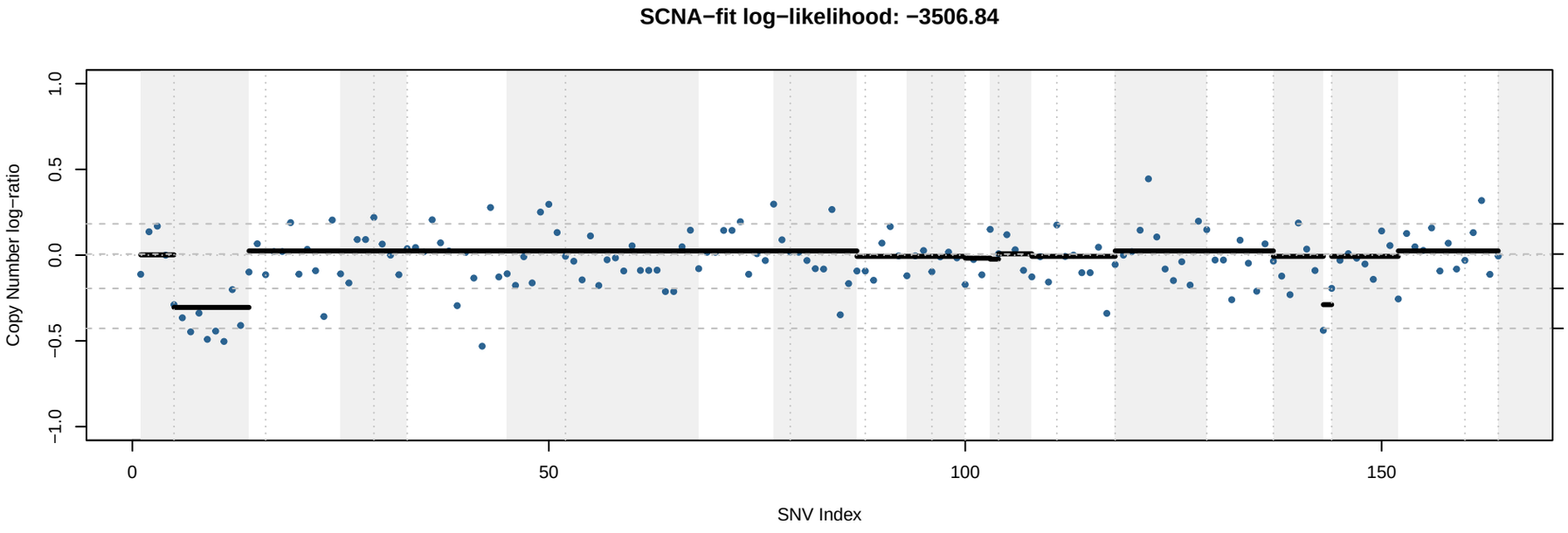

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

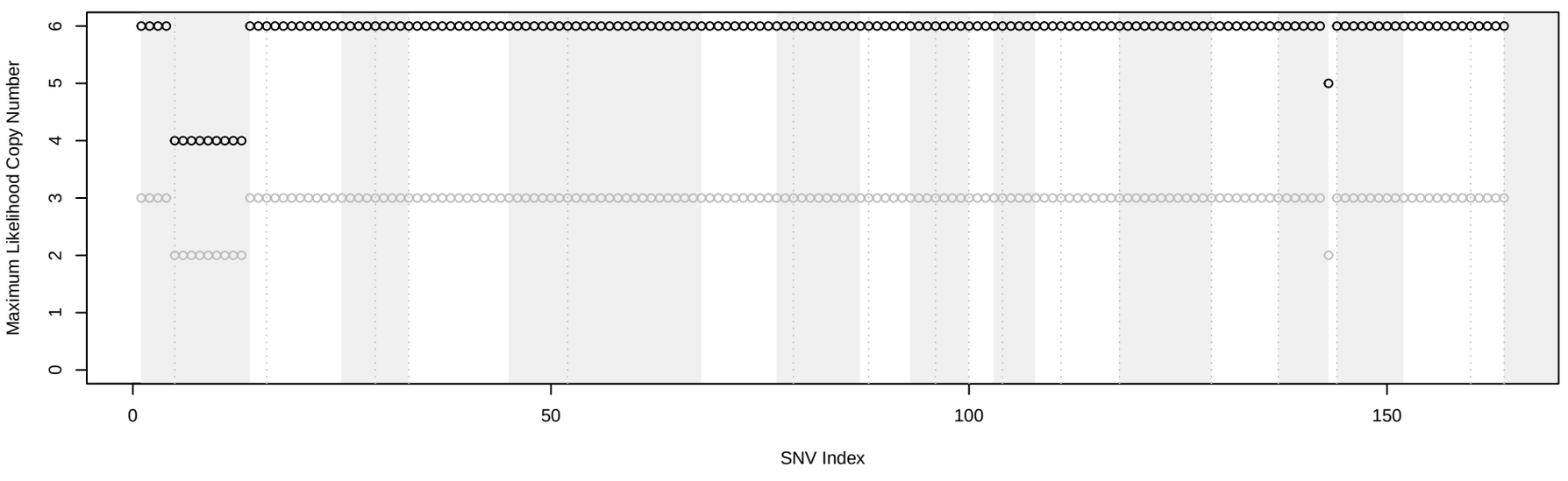

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
7m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

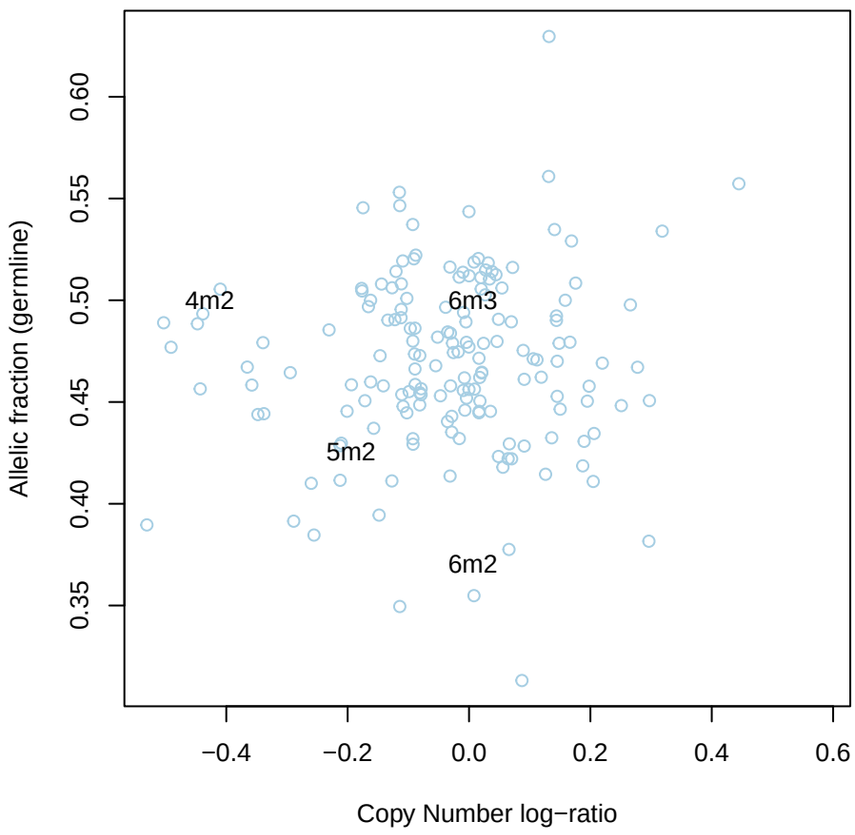

Frequency
0
10
20
30
40
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

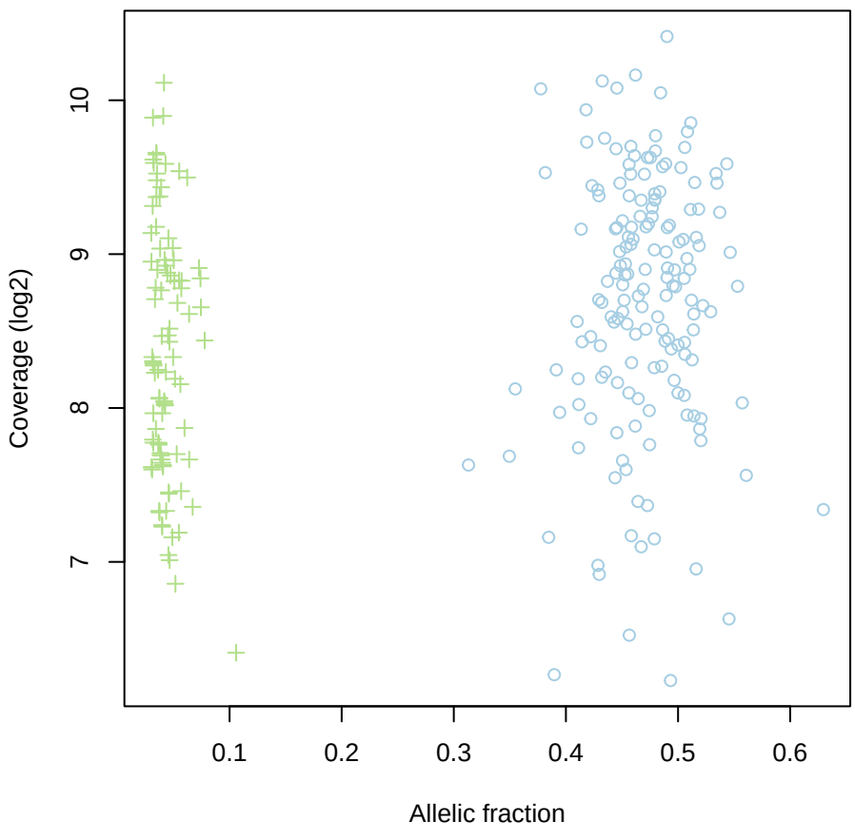

Purity: 0.54 Tumor ploidy: 5.966
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−0.2
0.0
0.2
0.4
0.6
log2 ratio

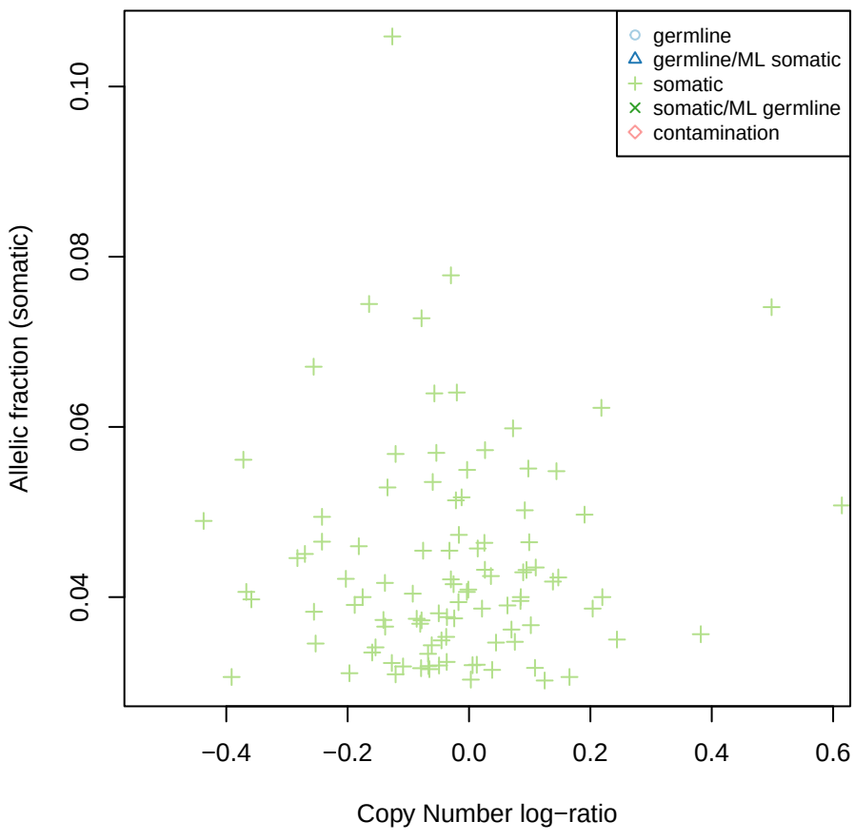

Purity: 0.54 Tumor ploidy: 5.966 SNV log−likelihood: −76.21 GoF: 89.9% Mean coverage: 441;441
1 2 3 4 5 6 7 8 9 10 12 13 14 15 17 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

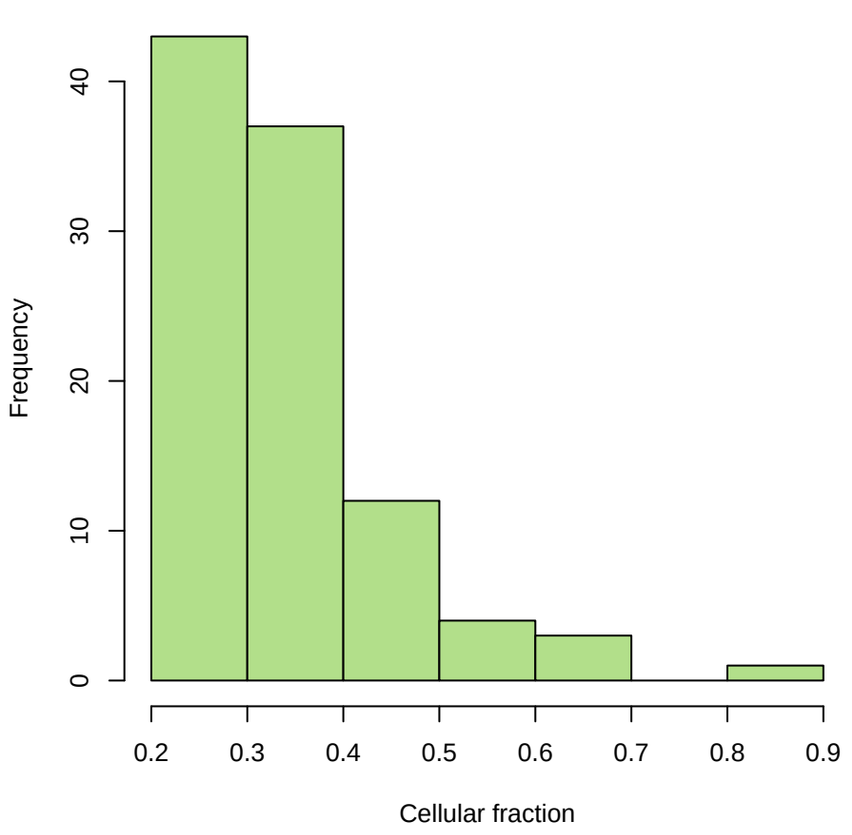

SCNA−fit log−likelihood: −3506.84
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5 6 7
0 50 100 150
SNV Index

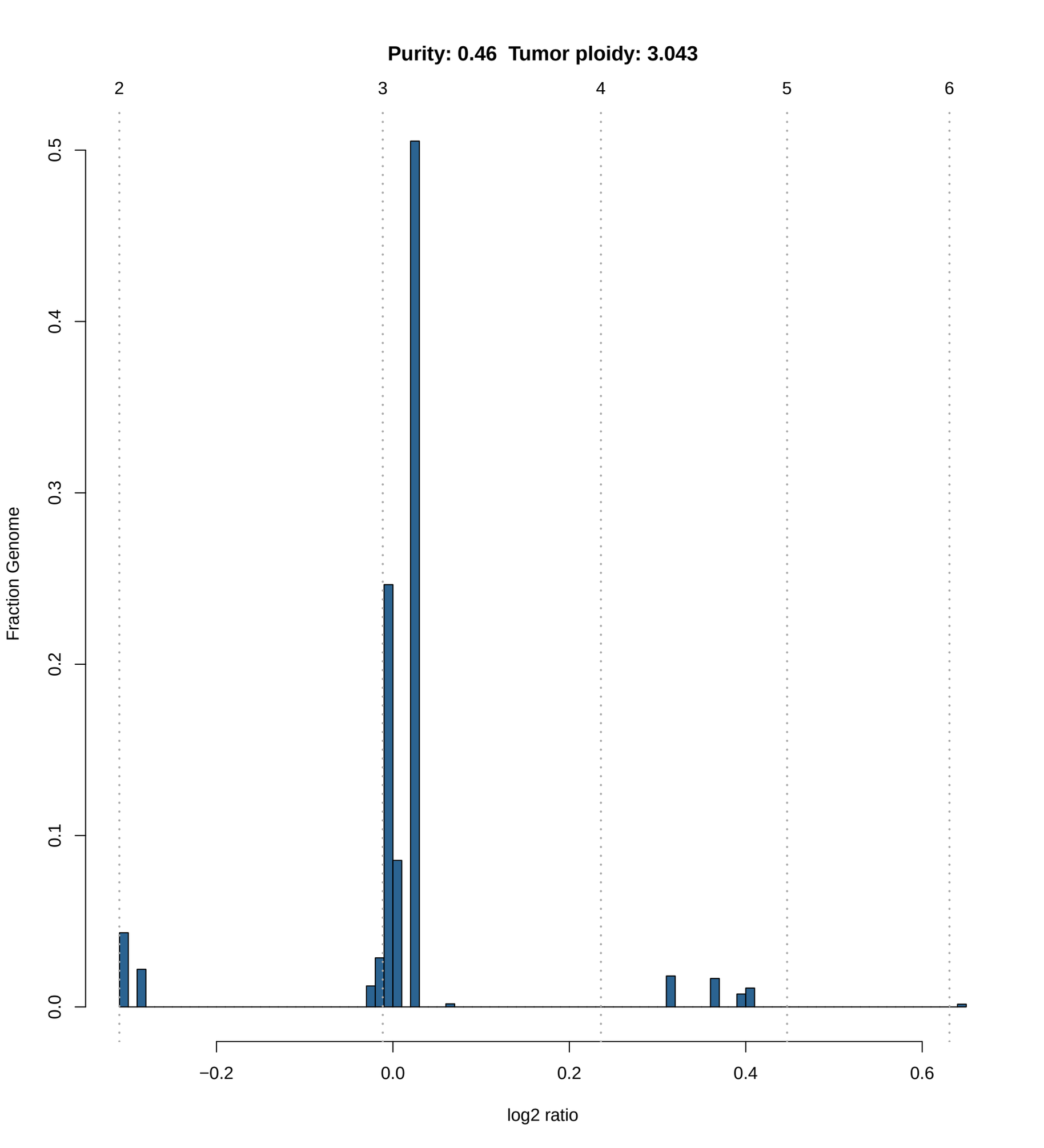

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

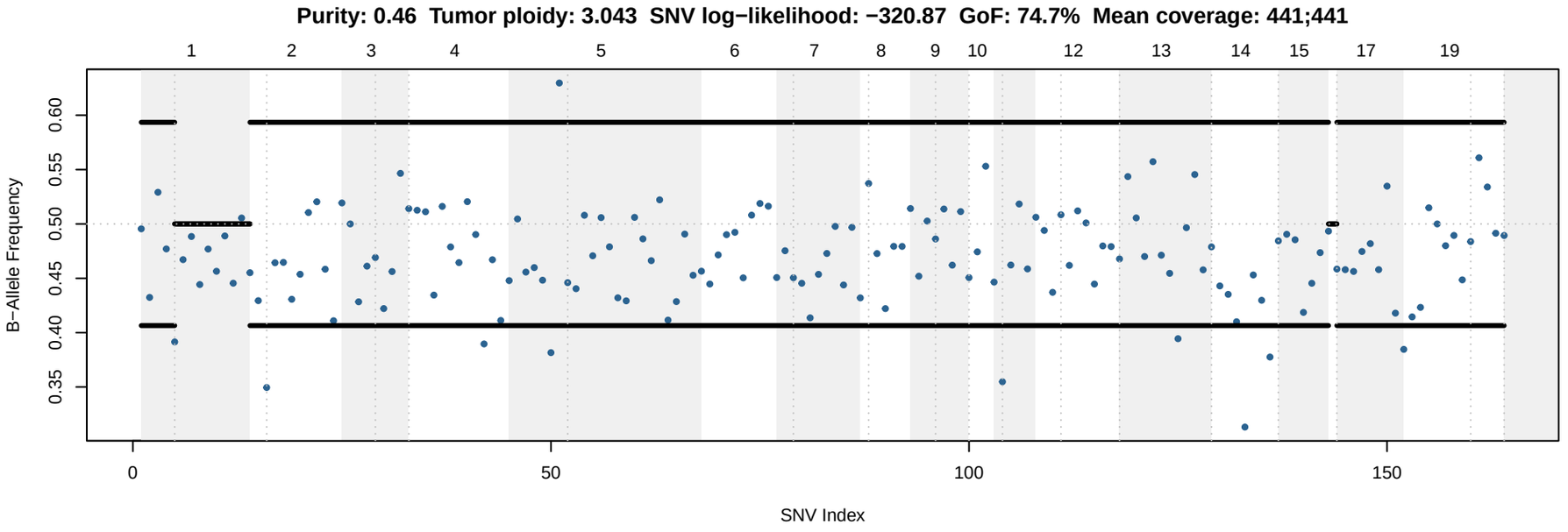

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
4m2
6m3
5m2
6m2
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

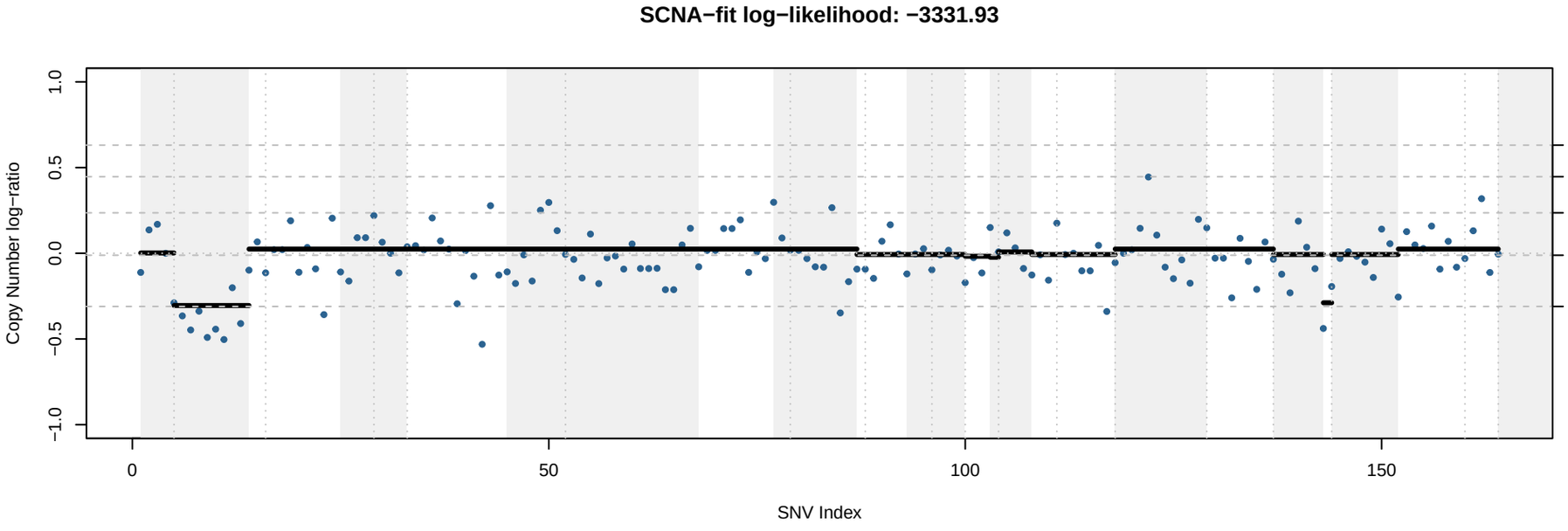

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

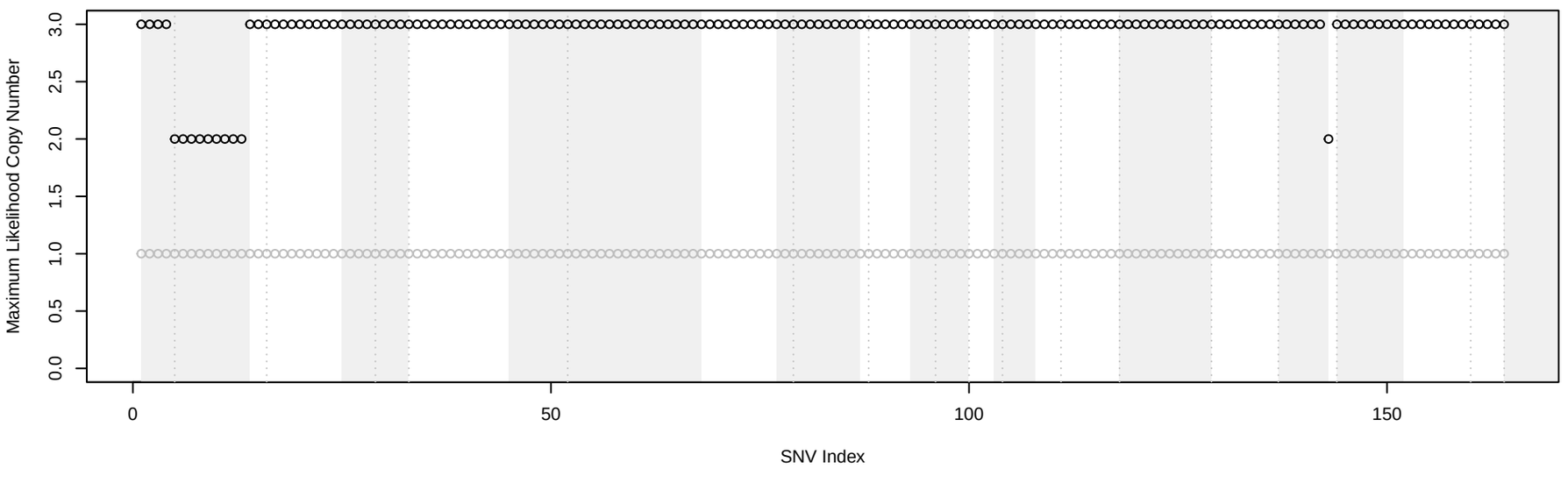

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

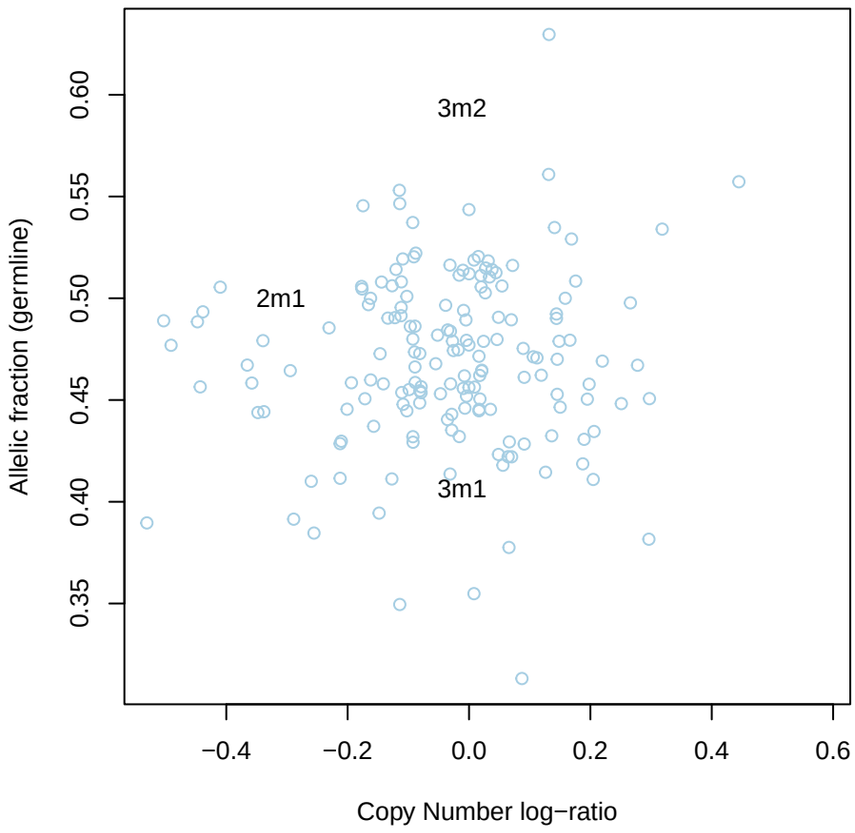

Frequency
0
10
20
30
40
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
Cellular fraction

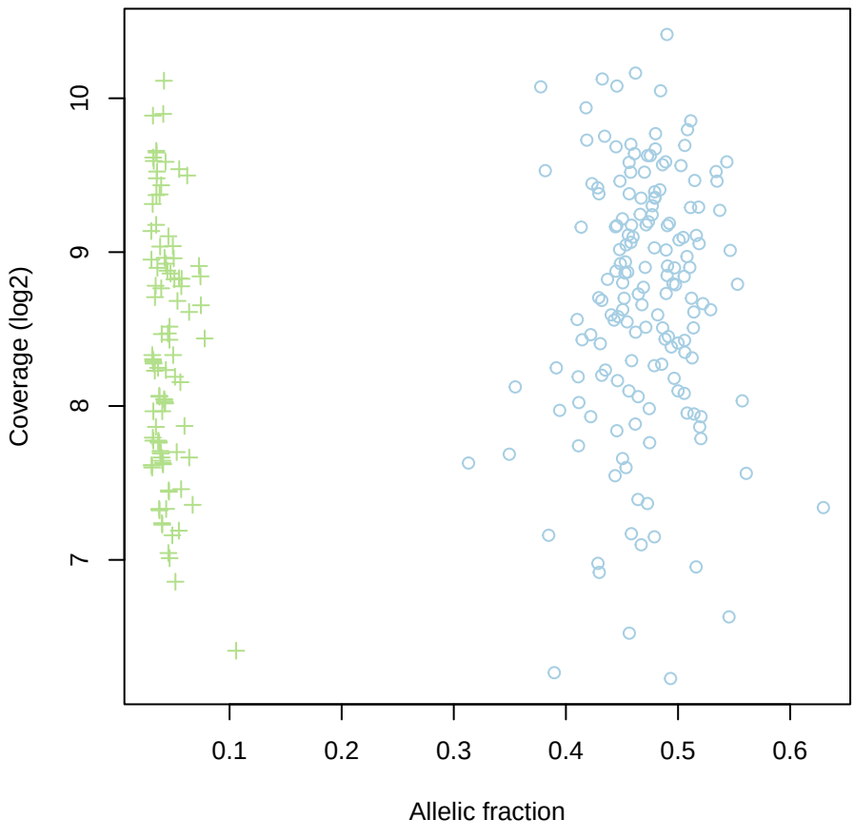

Purity: 0.46 Tumor ploidy: 3.043
2
3
4
5
6
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−0.2
0.0
0.2
0.4
0.6
log2 ratio

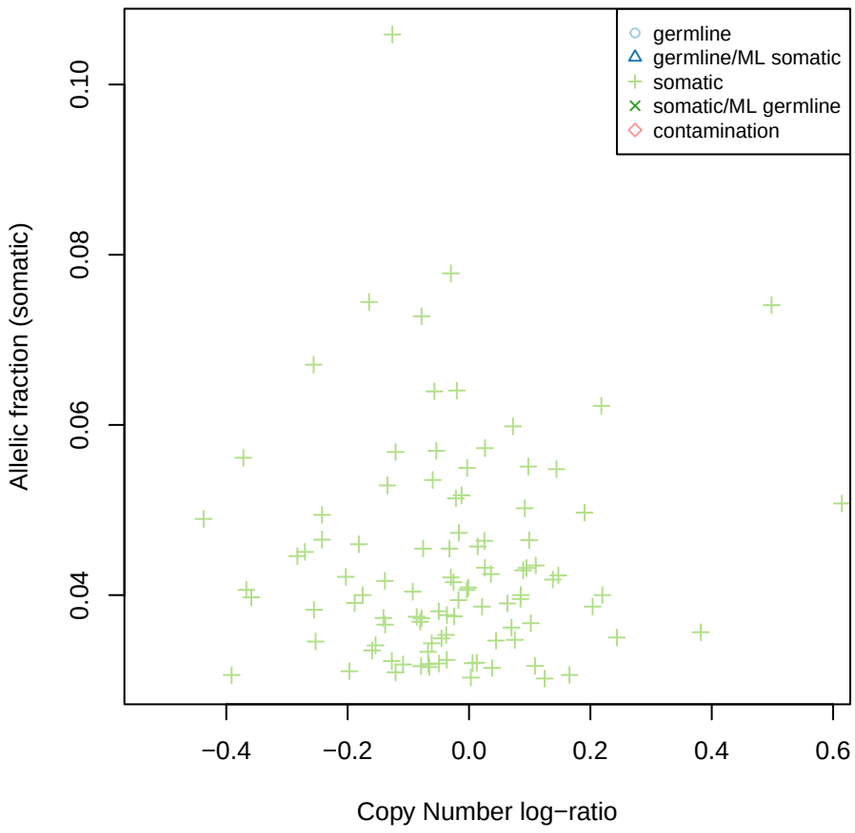

Purity: 0.46 Tumor ploidy: 3.043 SNV log−likelihood: −320.87 GoF: 74.7% Mean coverage: 441;441
1 2 3 4 5 6 7 8 9 10 12 13 14 15 17 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

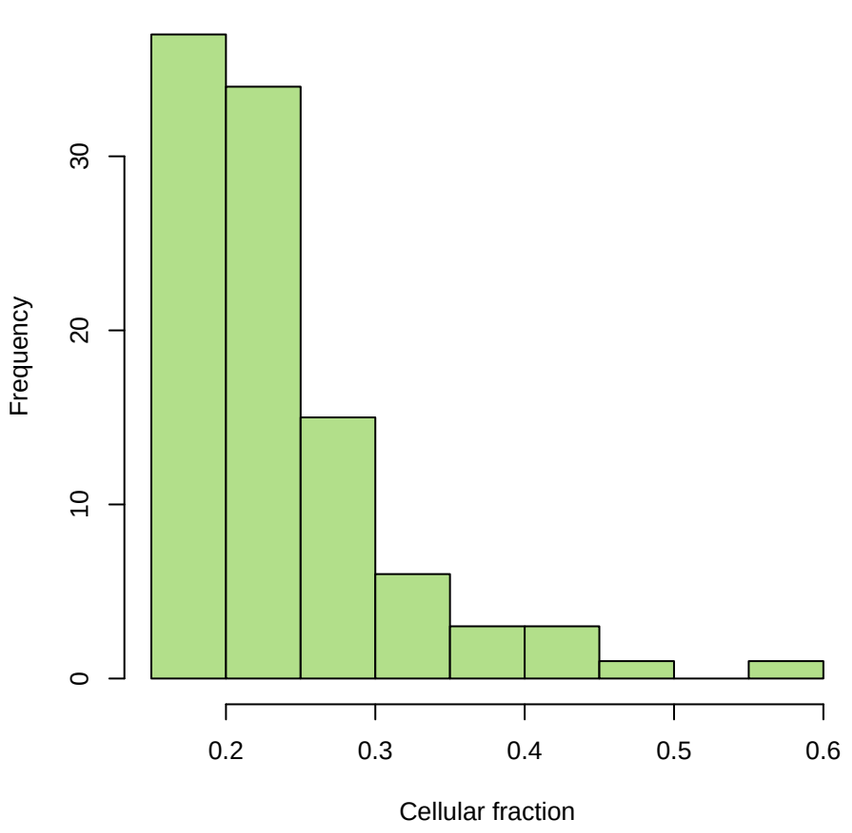

SCNA−fit log−likelihood: −3331.93
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6
0 50 100 150
SNV Index

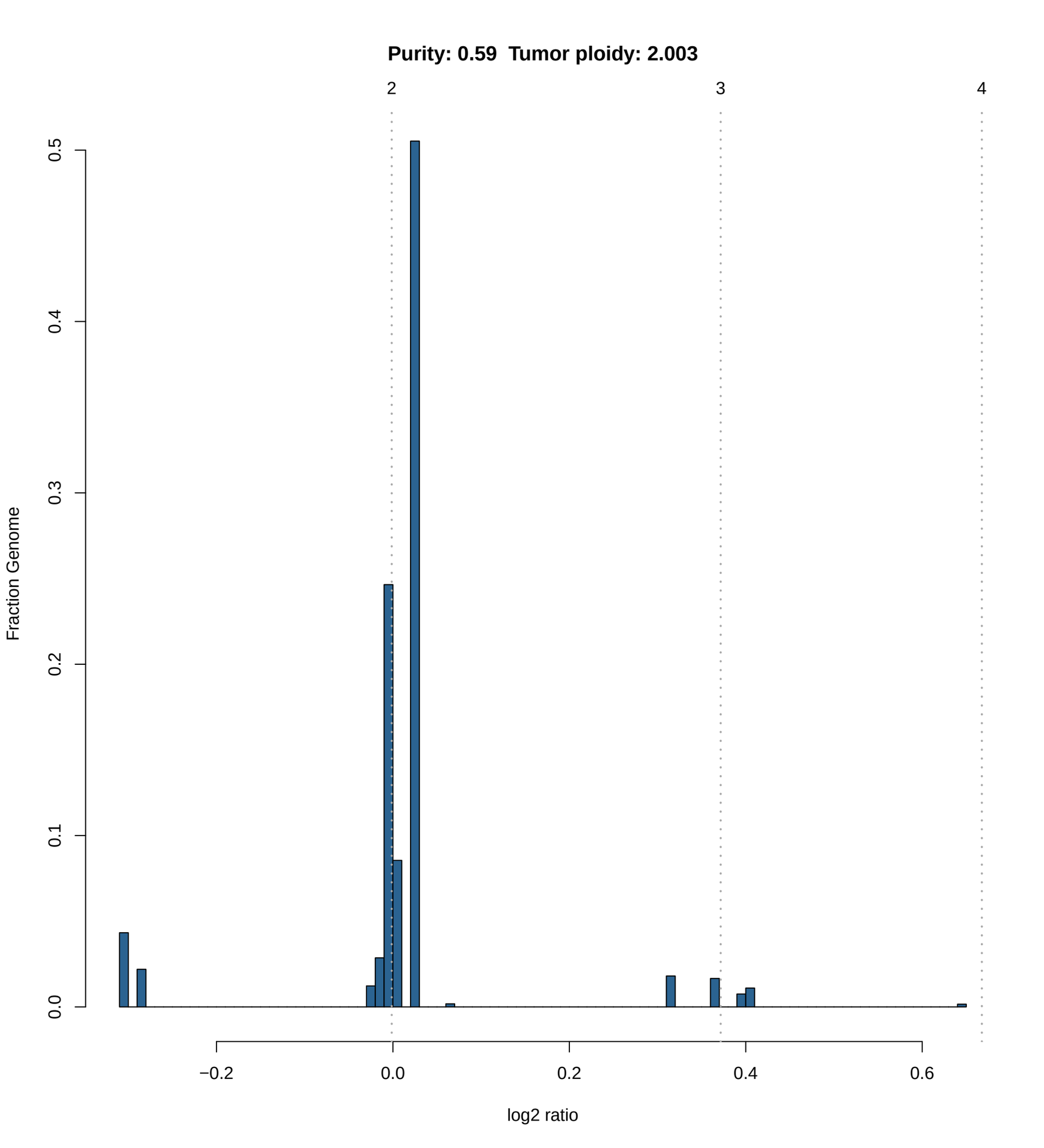

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

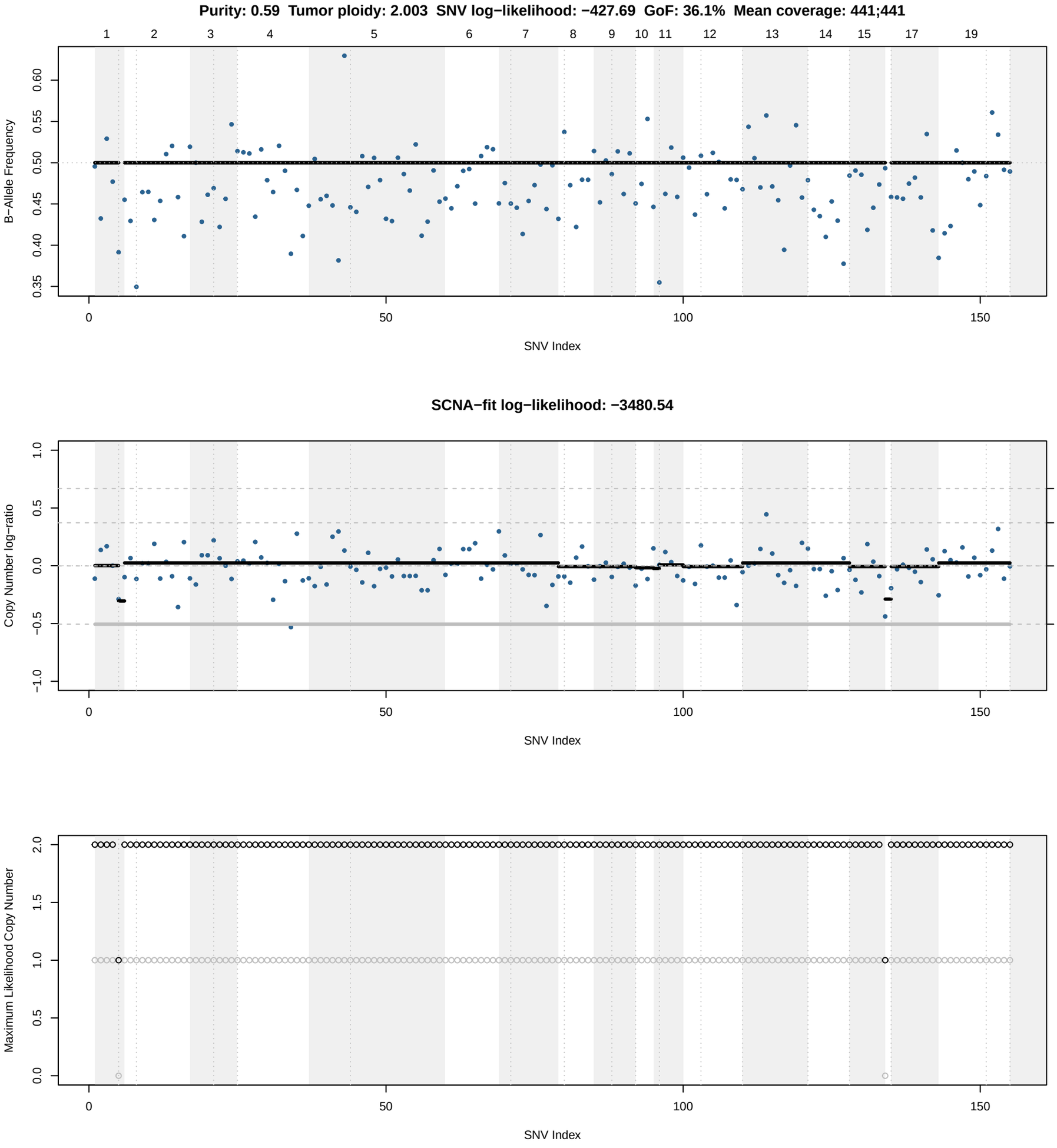

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
3m2
2m1
3m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

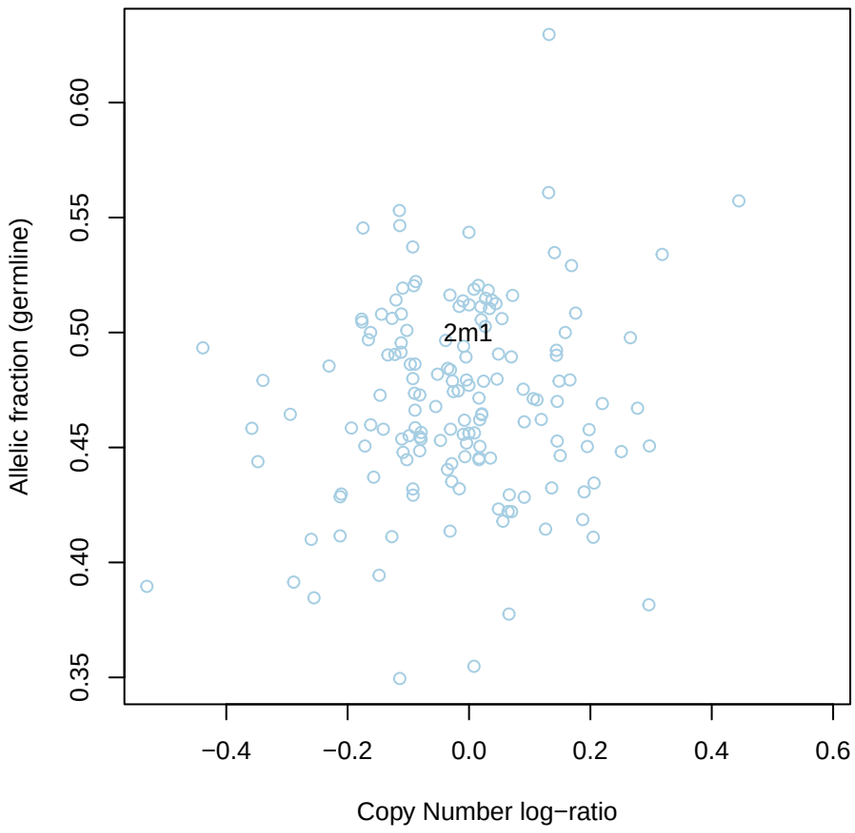

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

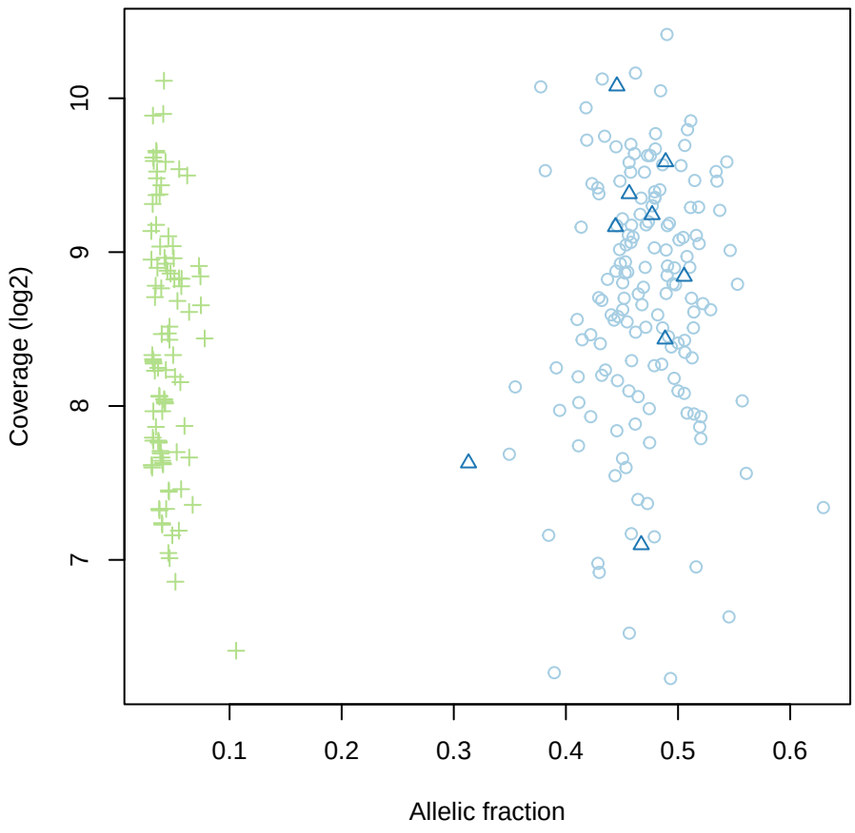

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

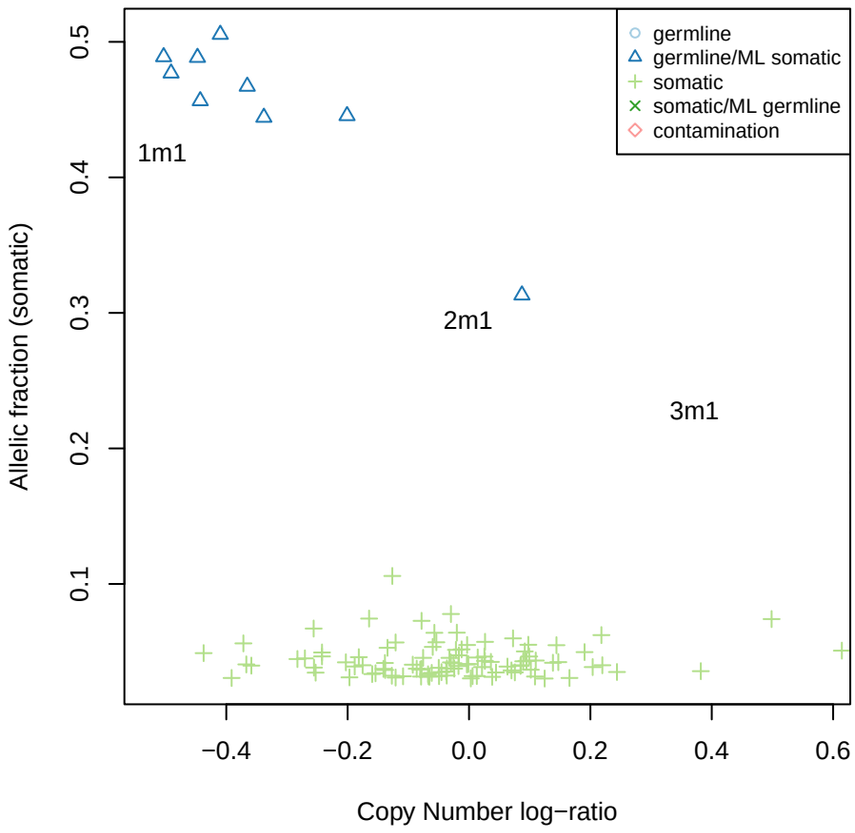

Frequency
0
10
20
30
0.2
0.3
0.4
0.5
0.6
Cellular fraction

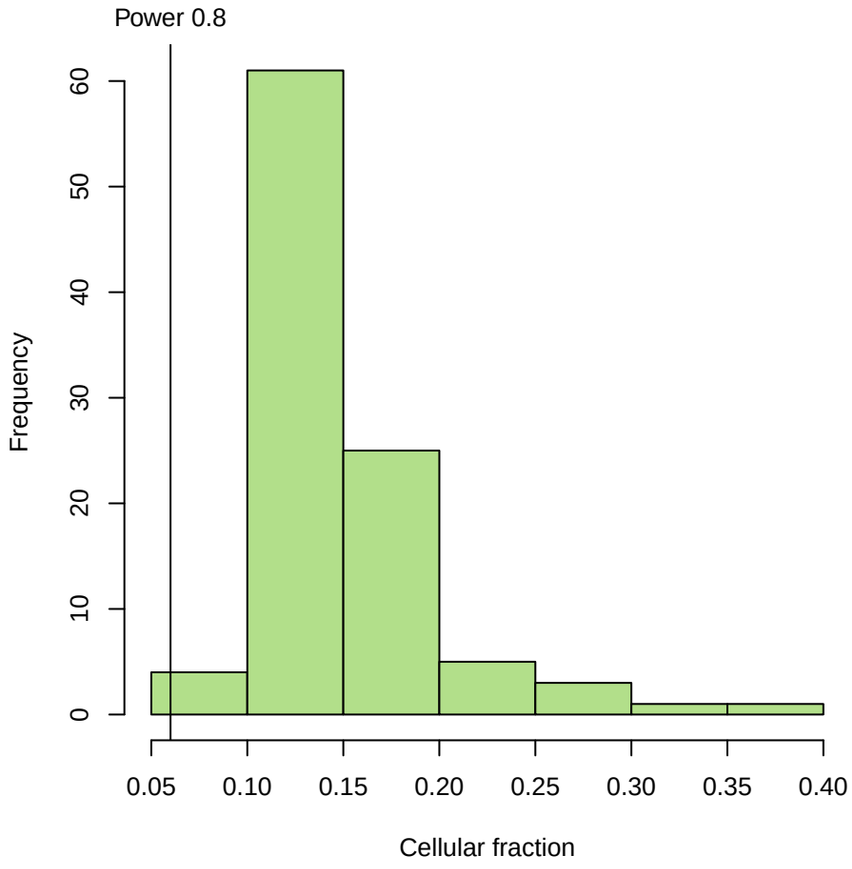

Purity: 0.59 Tumor ploidy: 2.003
2
3
4
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−0.2
0.0
0.2
0.4
0.6
log2 ratio

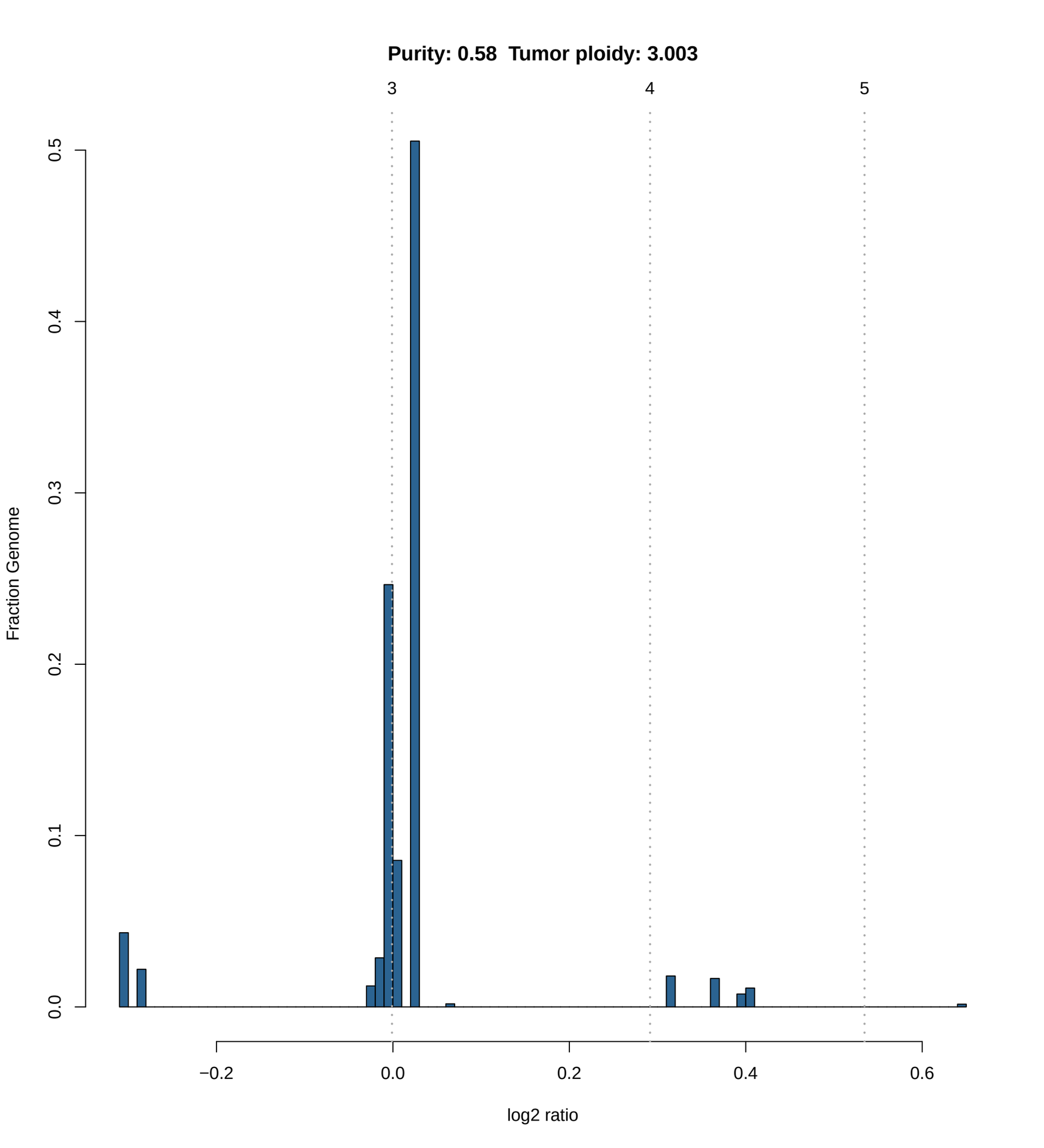

Purity: 0.59 Tumor ploidy: 2.003 SNV log−likelihood: −427.69 GoF: 36.1% Mean coverage: 441;441
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index
SCNA−fit log−likelihood: −3480.54
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4
0 50 100 150
SNV Index
Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 50 100 150
SNV Index

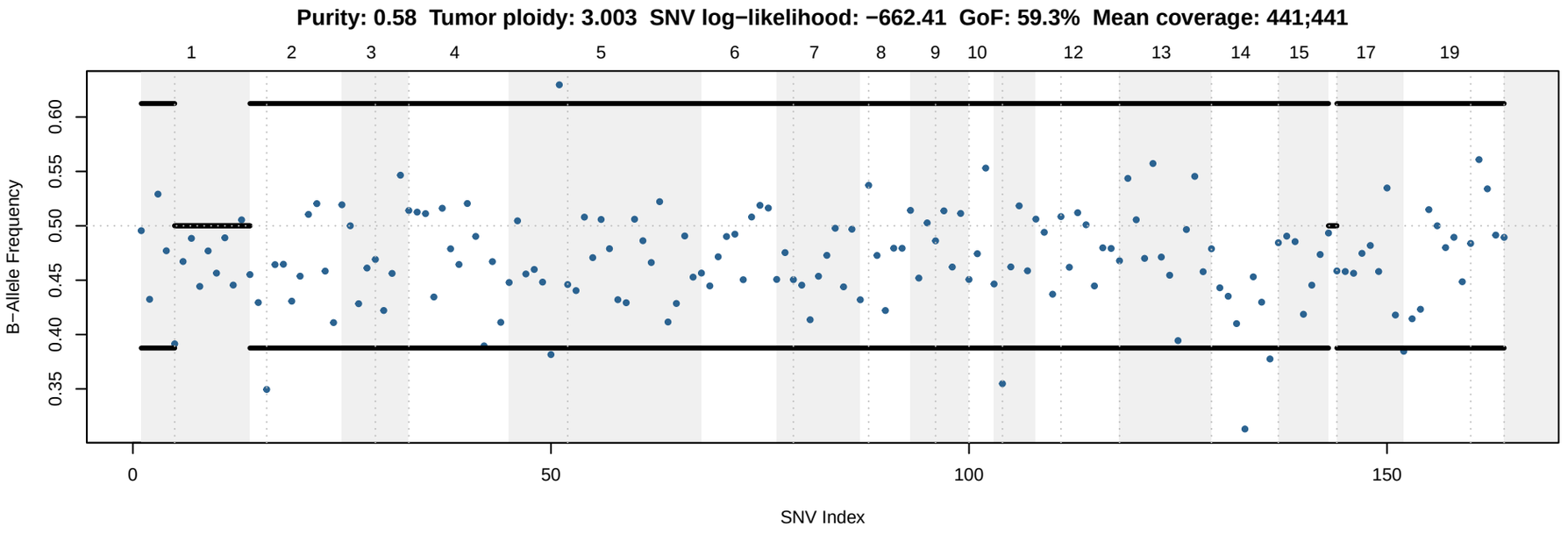

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
2m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

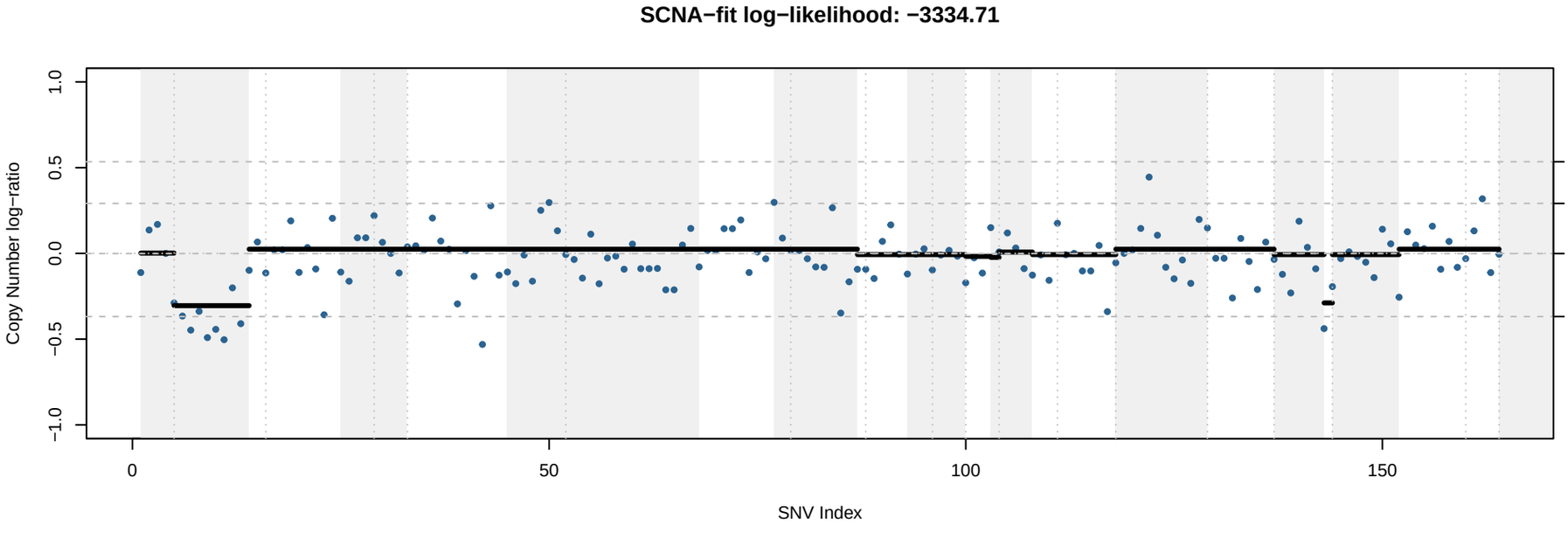

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

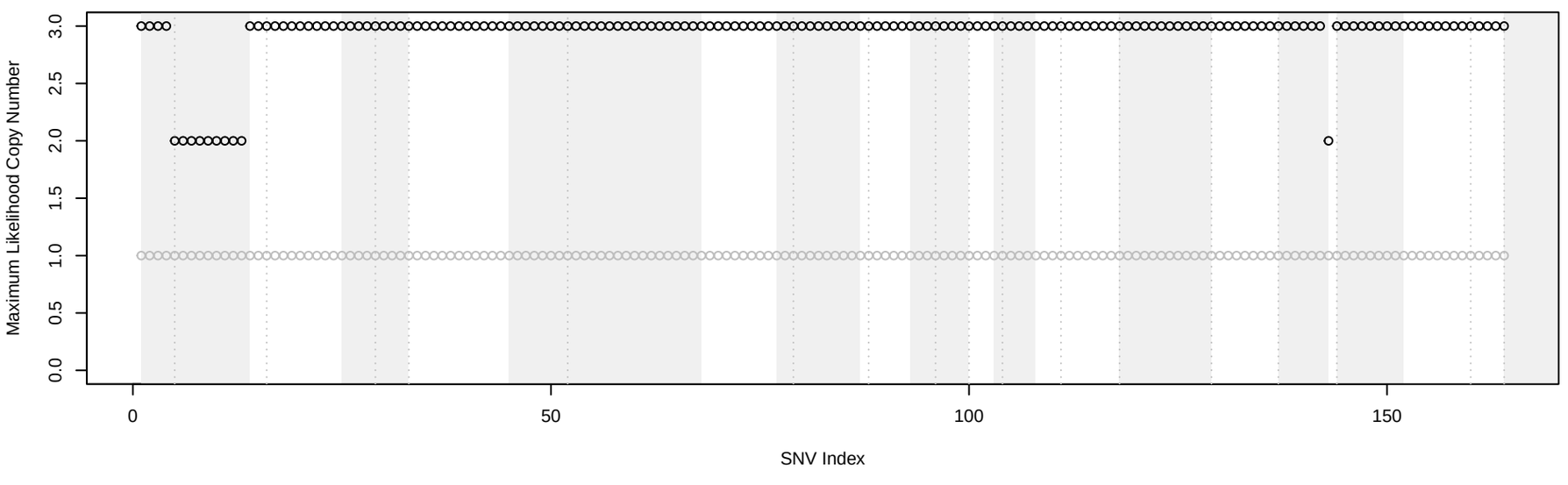

Allelic fraction (somatic)
0.1
0.2
0.3
0.4
0.5
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

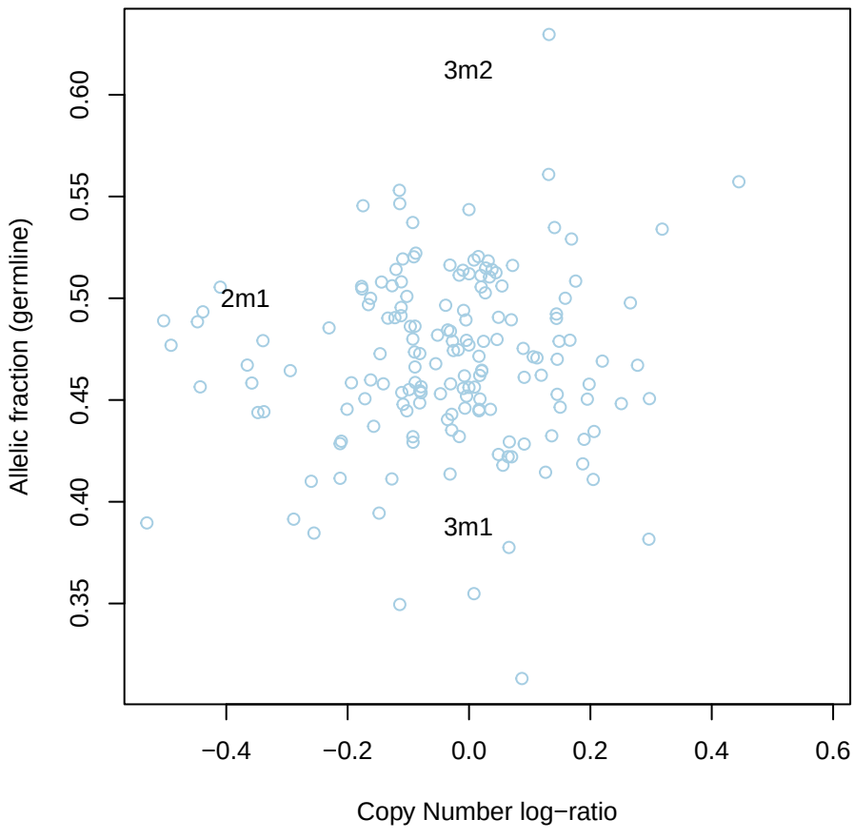

Power 0.8
Frequency
0
10
20
30
40
50
60
0.05
0.10
0.15
0.20
0.25
0.30
0.35
0.40
Cellular fraction

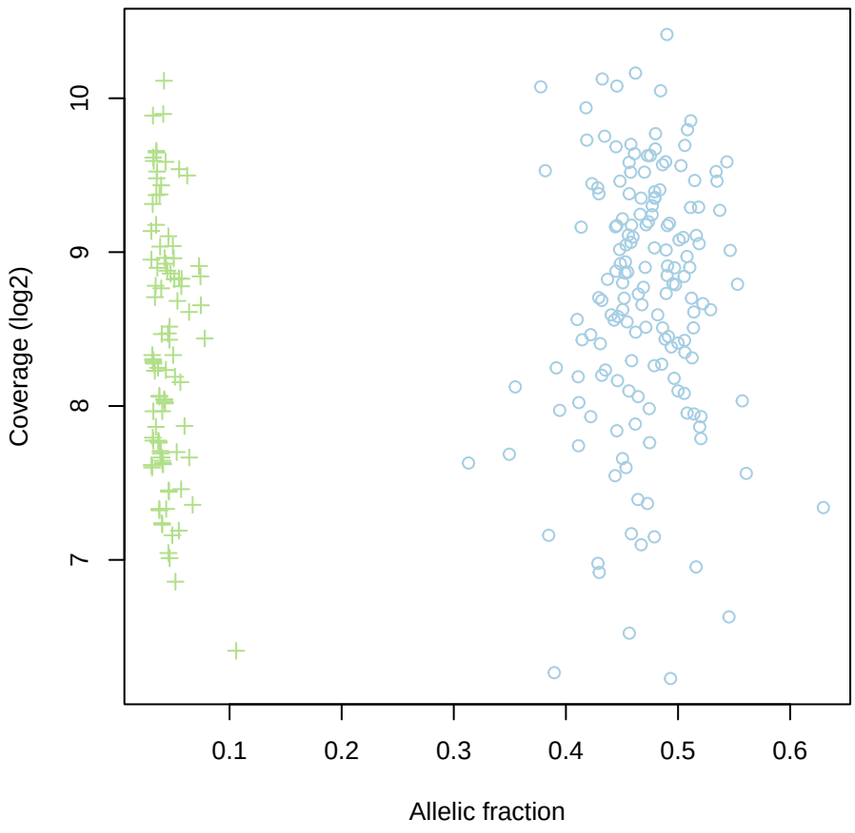

Purity: 0.58 Tumor ploidy: 3.003
3
4
5
0.0
0.1
0.2
0.3
0.4
0.5
Fraction Genome
−0.2
0.0
0.2
0.4
0.6
log2 ratio

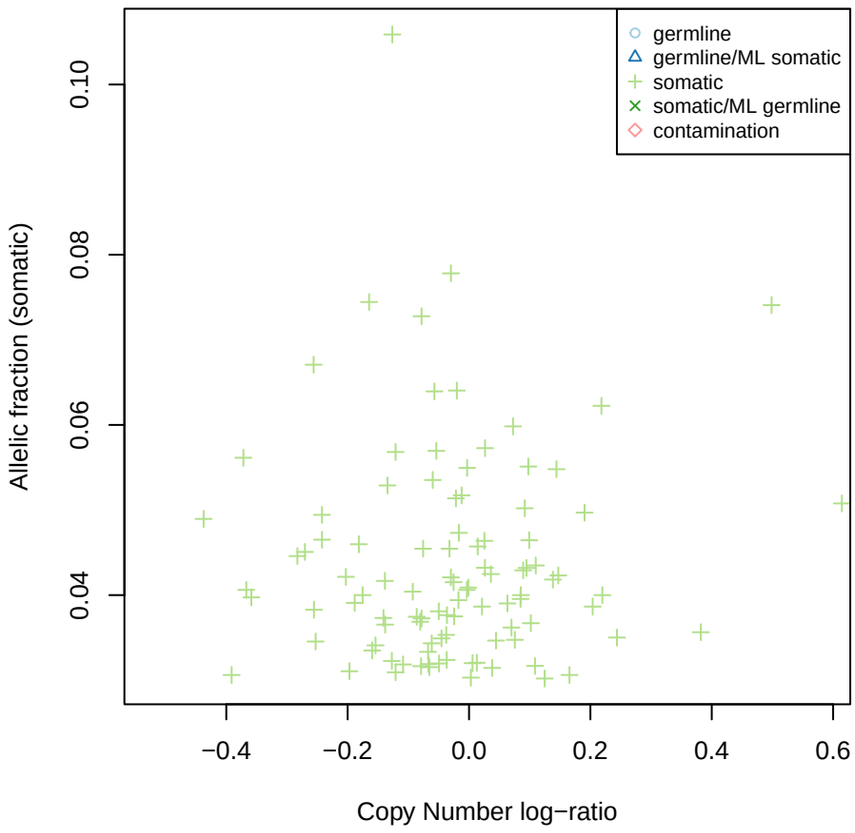

Purity: 0.58 Tumor ploidy: 3.003 SNV log−likelihood: −662.41 GoF: 59.3% Mean coverage: 441;441
1
2
3
4
5
6
7
8
9
10
12
13
14
15
17
19
B−Allele Frequency
0.35
0.40
0.45
0.50
0.55
0.60
0
50
100
150
SNV Index

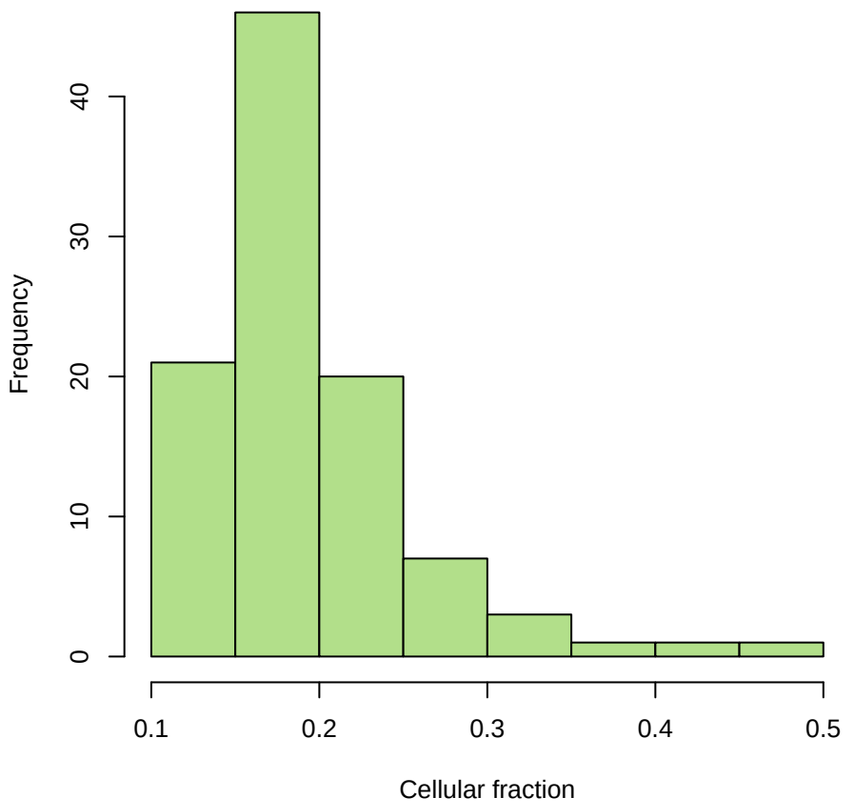

SCNA−fit log−likelihood: −3334.71
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
2
3
4
5
0
50
100
150
SNV Index


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


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


Coverage (log2)
Allelic fraction
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
−0.4
−0.2
0.0
0.2
0.4
0.6


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