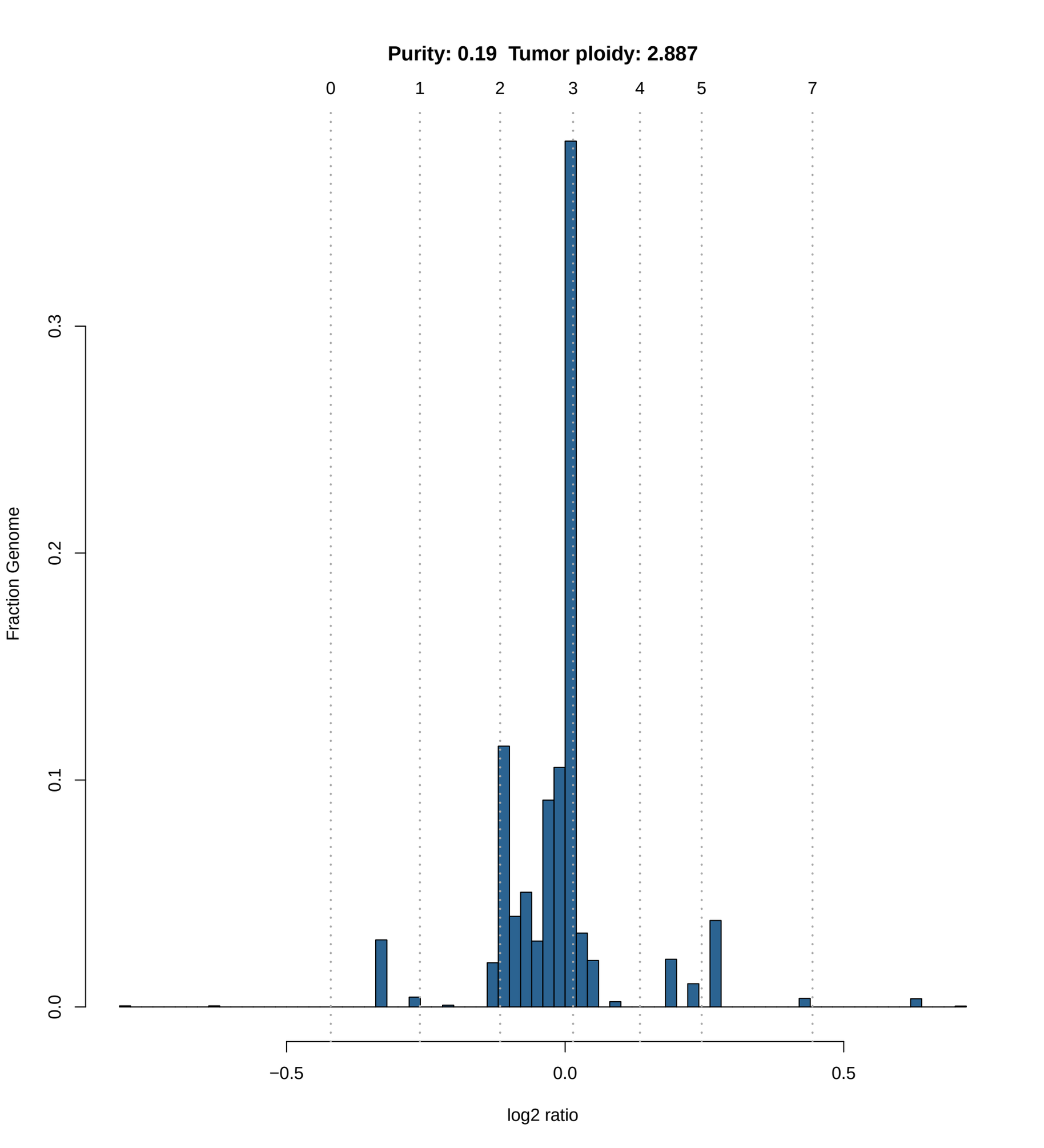
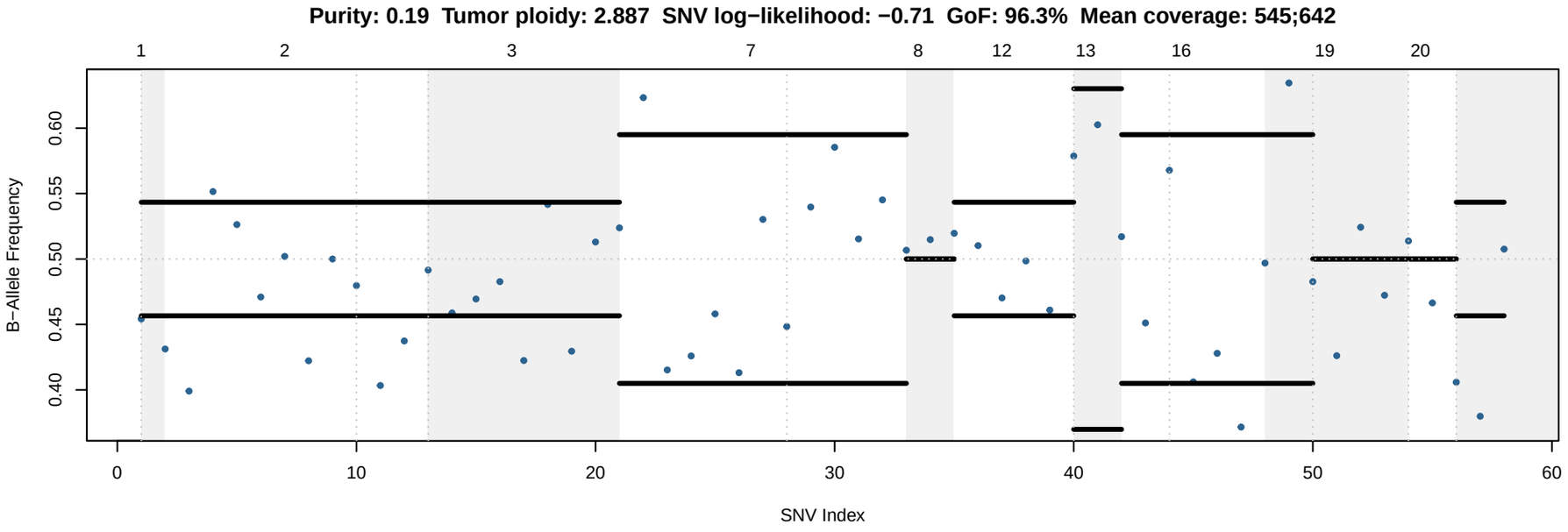
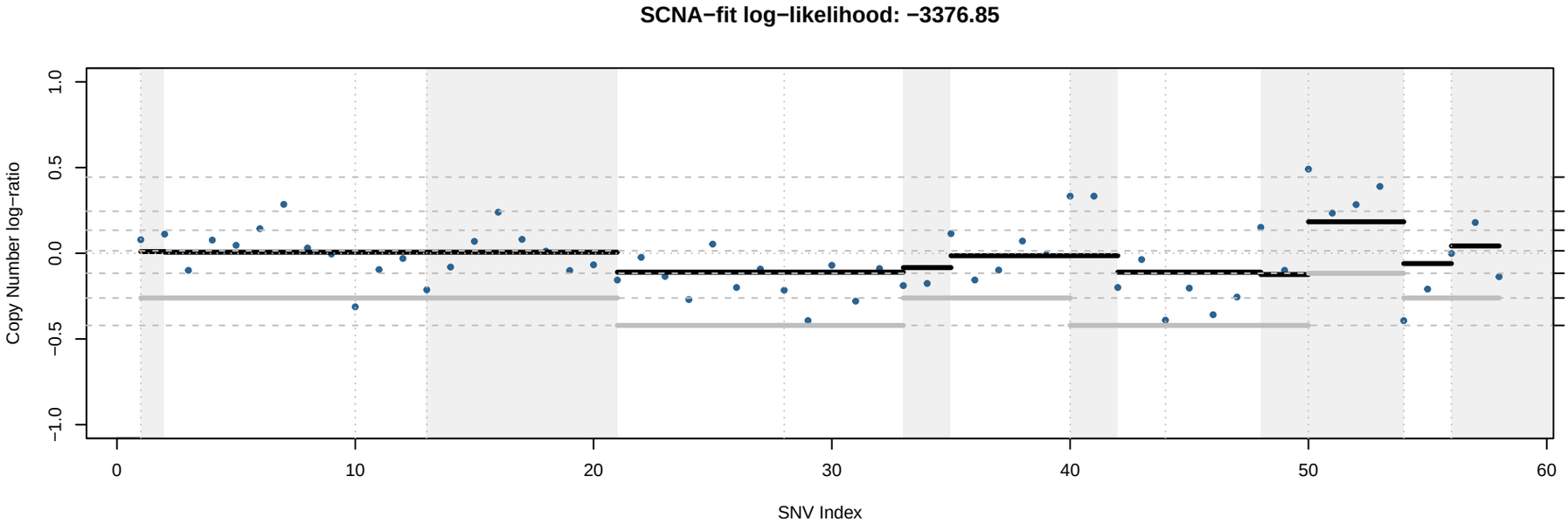
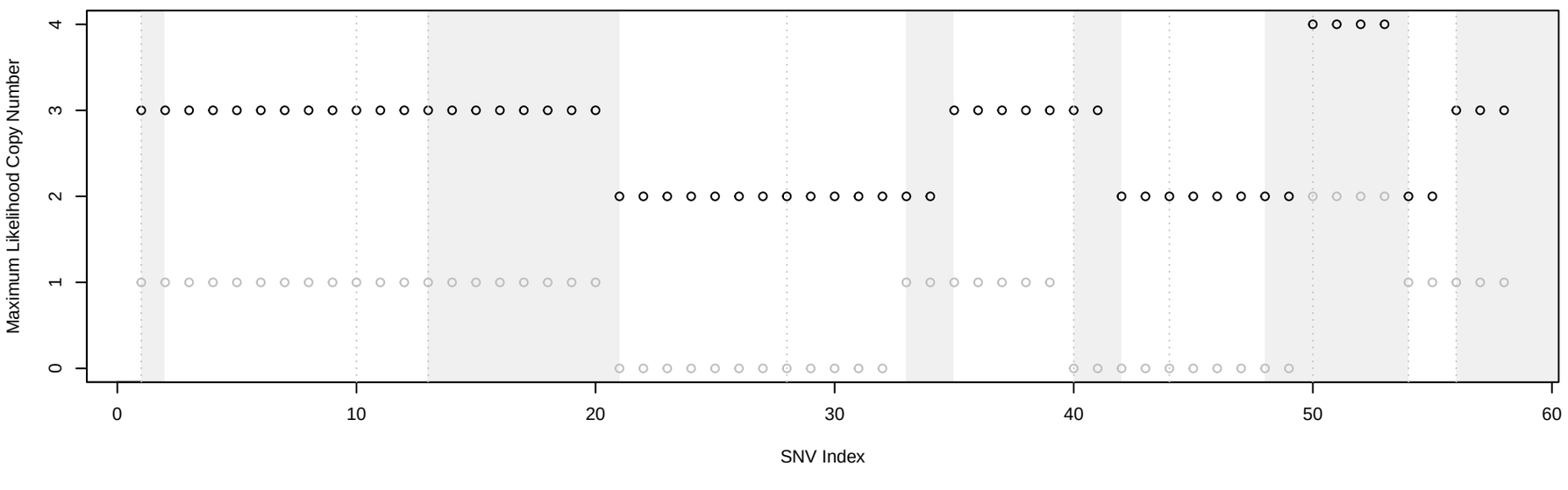
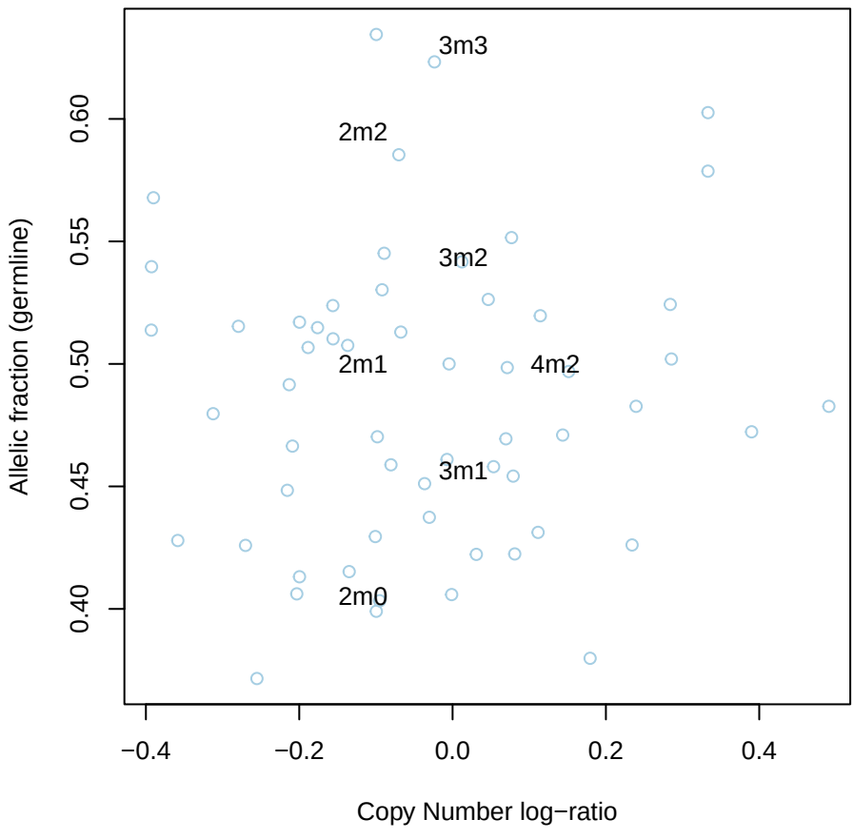
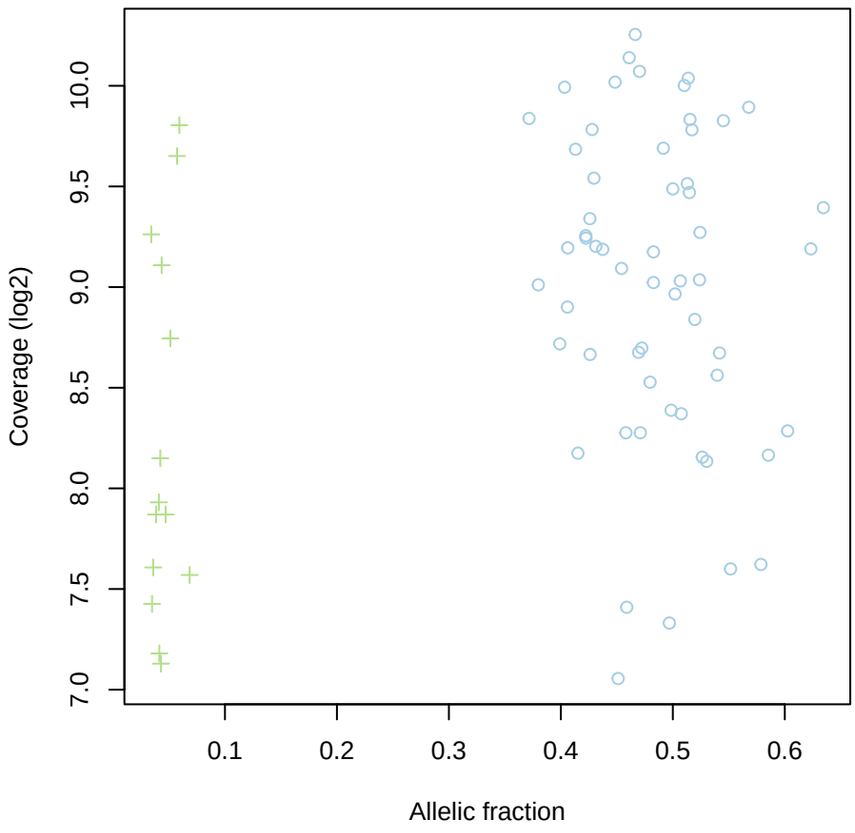

Purity: 0.19 Tumor ploidy: 2.887
0
1
2
3
4
5
7
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
log2 ratio

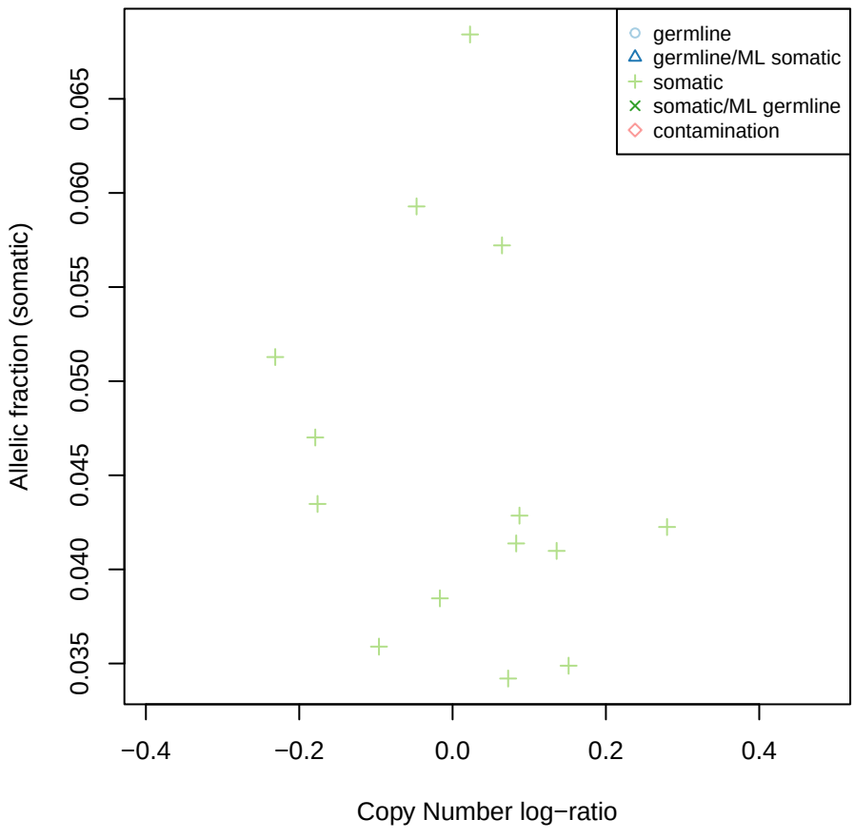

Purity: 0.19 Tumor ploidy: 2.887 SNV log−likelihood: −0.71 GoF: 96.3% Mean coverage: 545;642
1
2
3
7
8
12
13
16
19
20
B−Allele Frequency
0.40
0.45
0.50
0.55
0.60
0
10
20
30
40
50
60
SNV Index

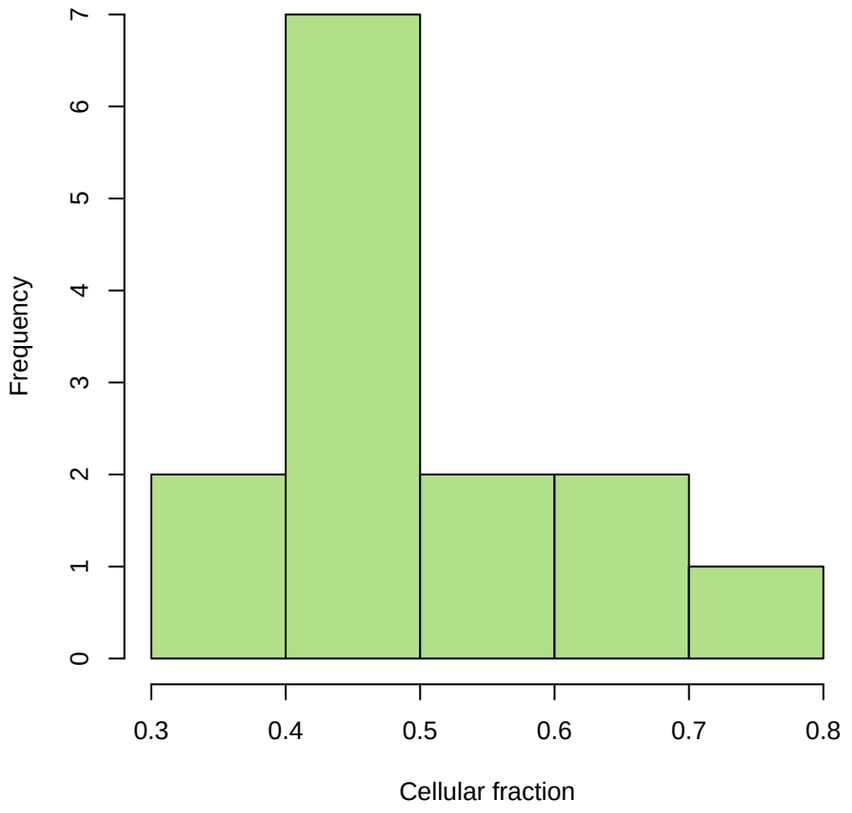

SCNA−fit log−likelihood: −3376.85
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
0
1
2
4
7
0
10
20
30
40
50
60
SNV Index

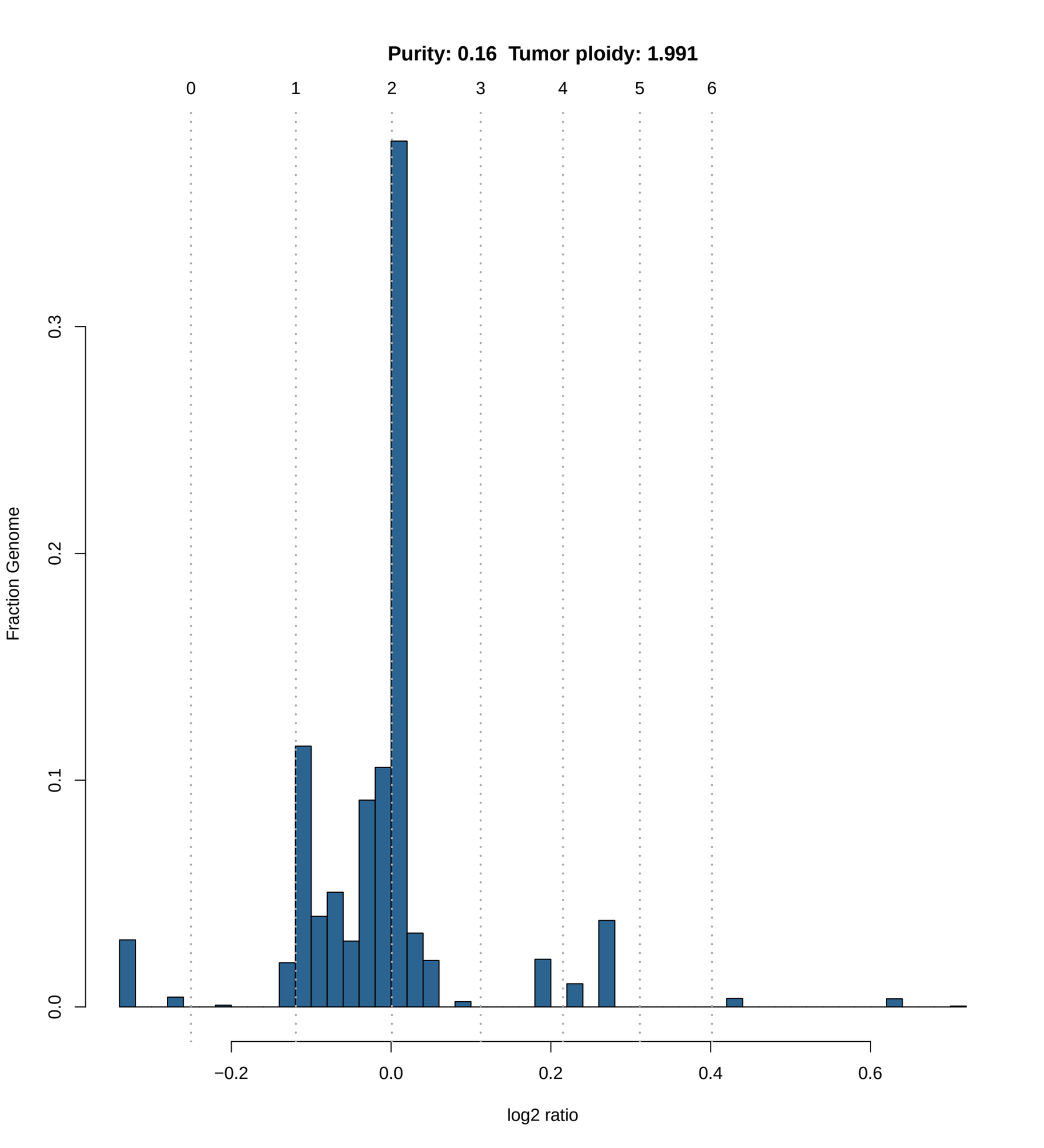

Maximum Likelihood Copy Number
0
1
2
3
4
0
10
20
30
40
50
60
SNV Index

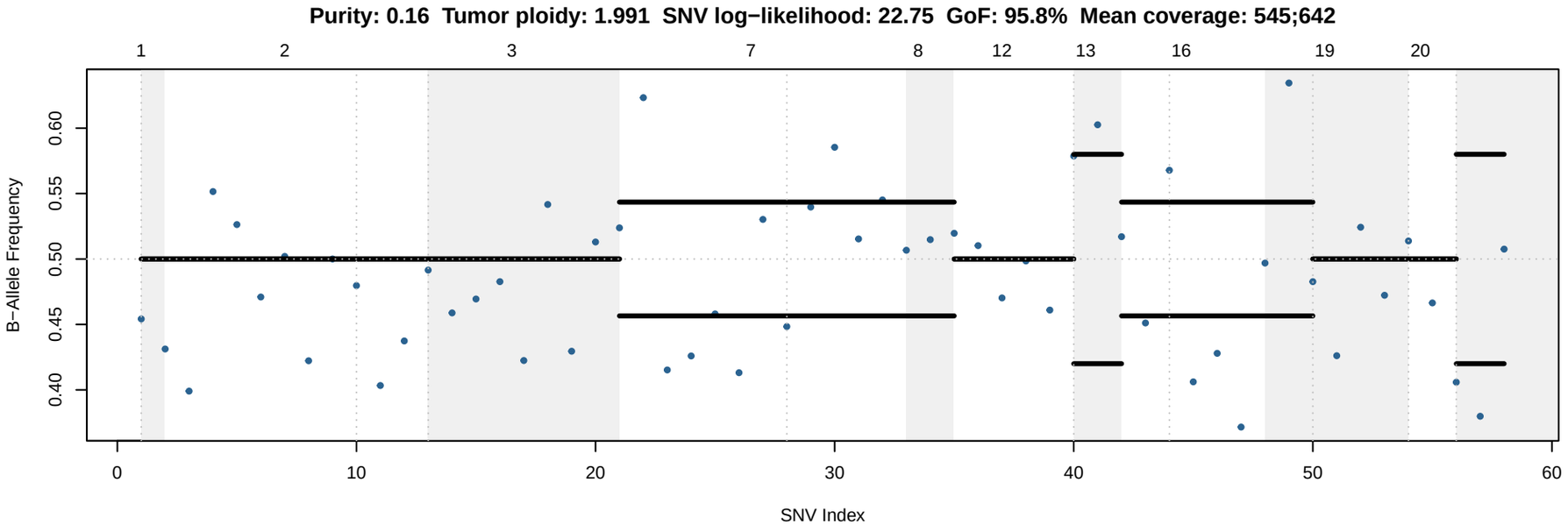

3m3
2m2
3m2
2m1
4m2
3m1
2m0
Allelic fraction (germline)
Copy Number log−ratio

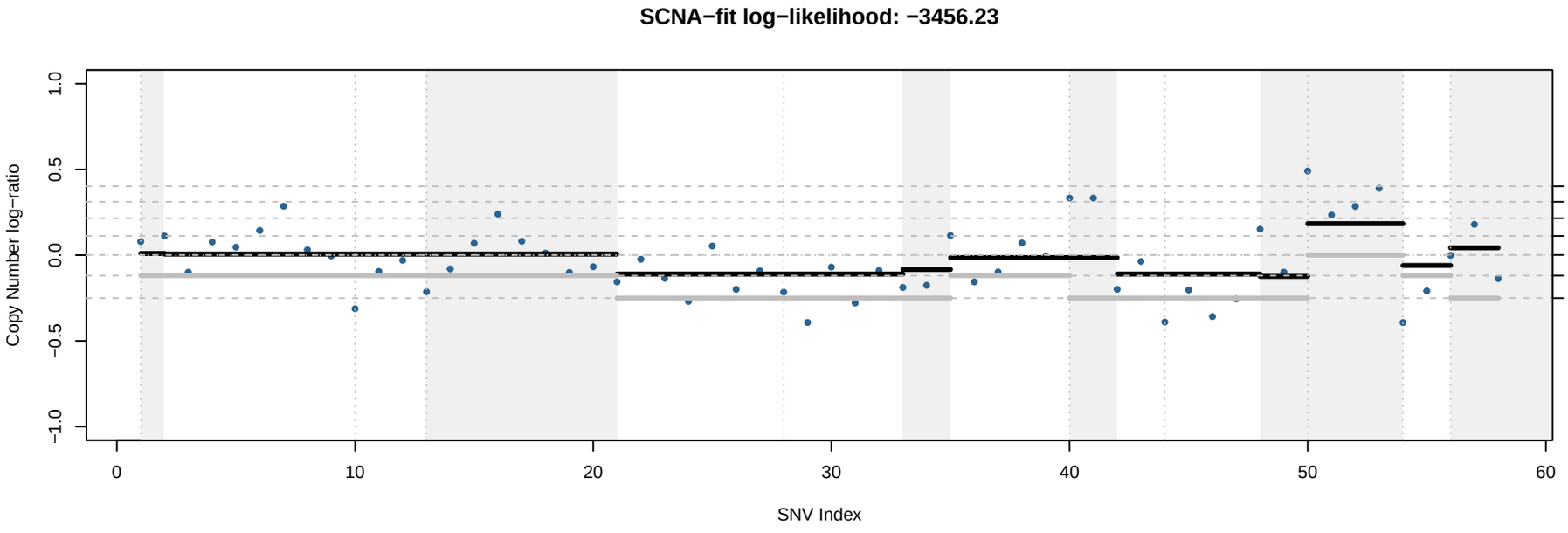

Coverage (log2)
Allelic fraction

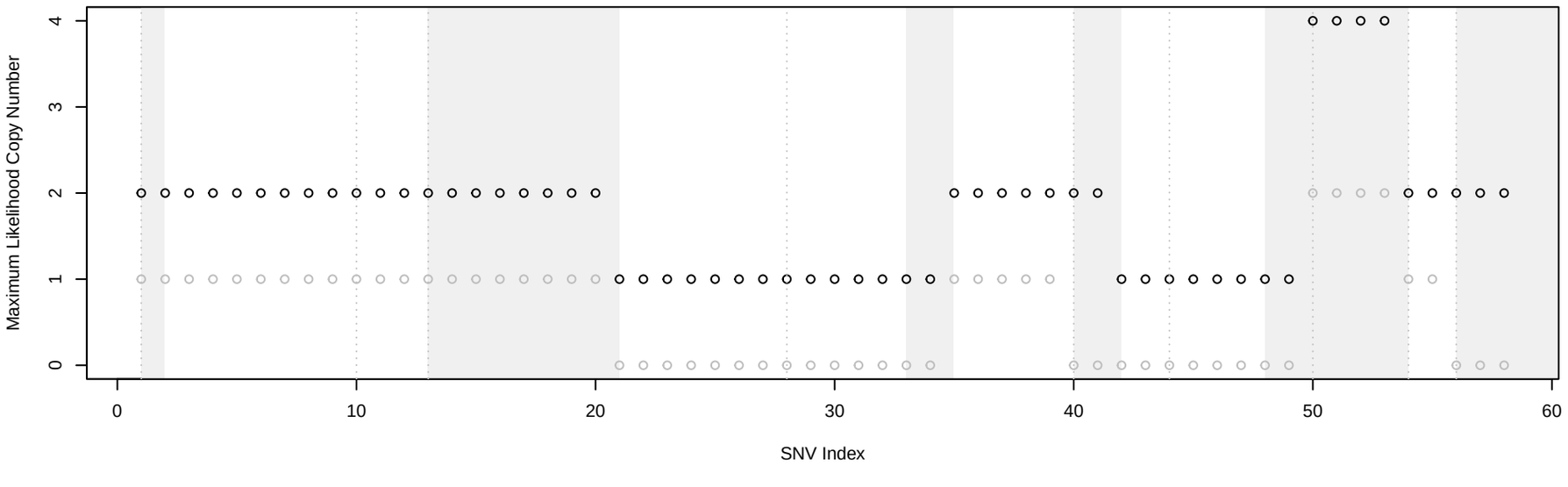

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

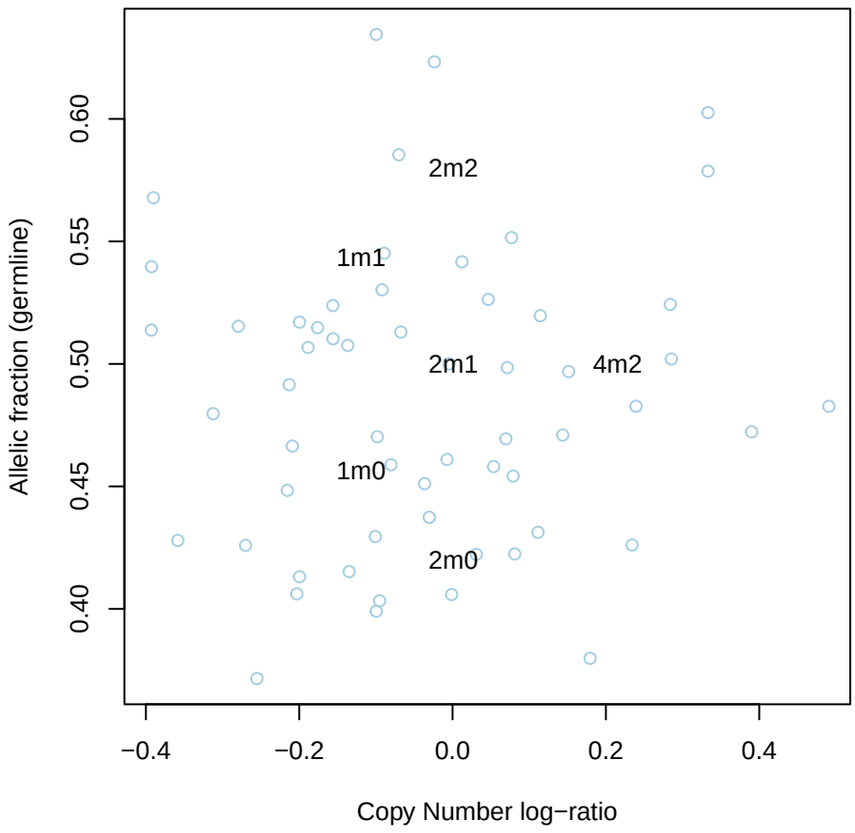

Frequency
Cellular fraction

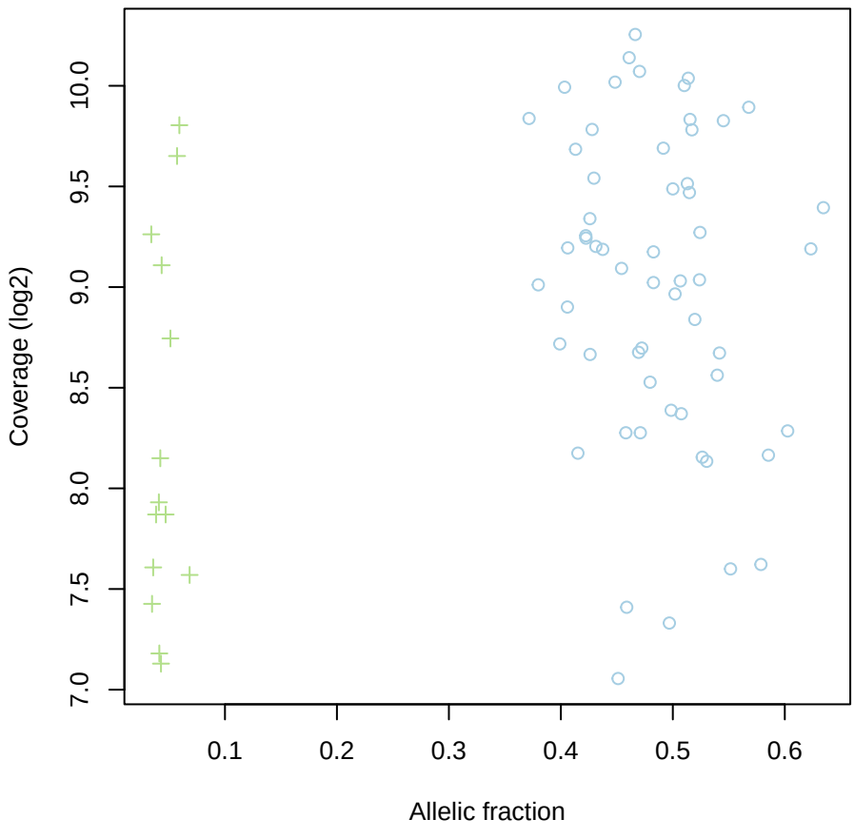

Purity: 0.16 Tumor ploidy: 1.991
0
1
2
3
4
5
6
0.0
0.1
0.2
0.3
Fraction Genome
−0.2
0.0
0.2
0.4
0.6
log2 ratio

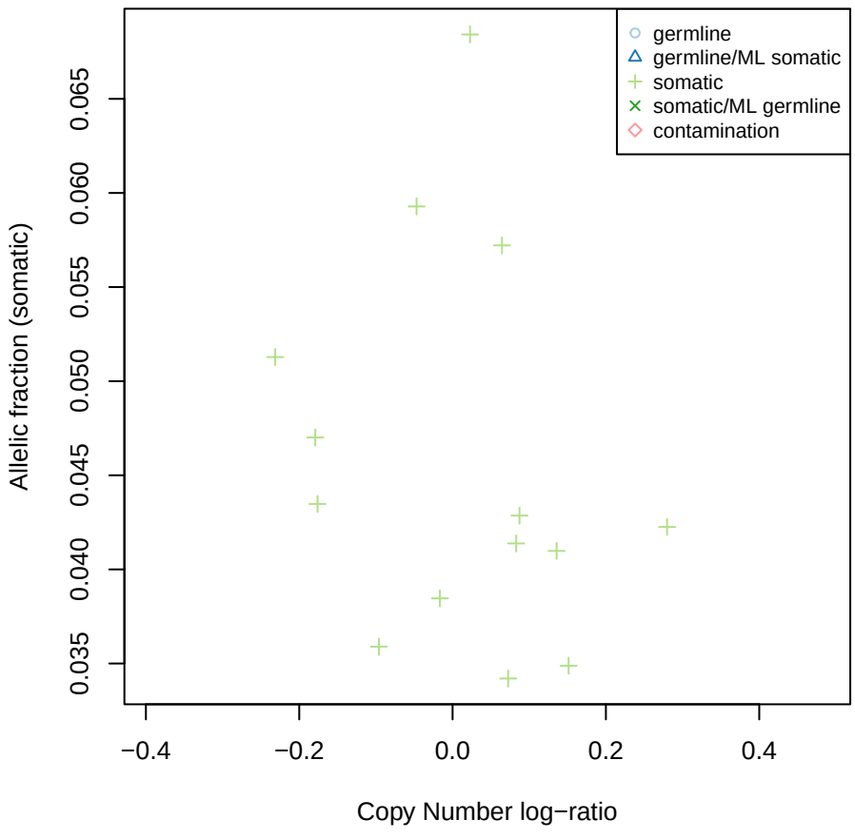

Purity: 0.16 Tumor ploidy: 1.991 SNV log−likelihood: 22.75 GoF: 95.8% Mean coverage: 545;642
1
2
3
7
8
12
13
16
19
20
B−Allele Frequency
0.40
0.45
0.50
0.55
0.60
0
10
20
30
40
50
60
SNV Index

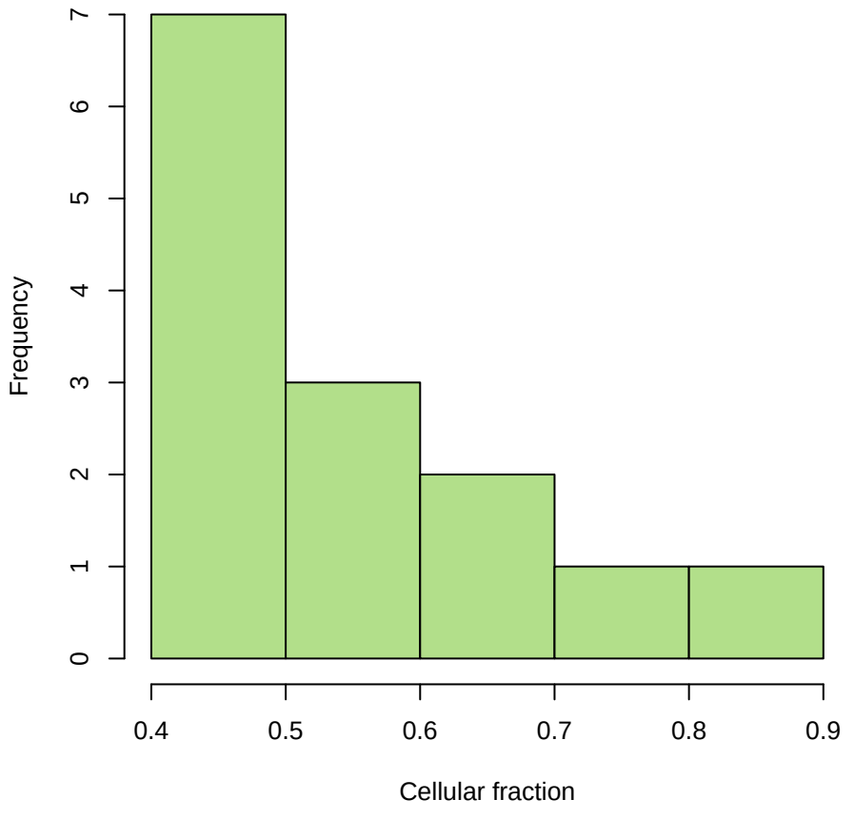

SCNA−fit log−likelihood: −3456.23
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
0
2
4
6
0
10
20
30
40
50
60
SNV Index

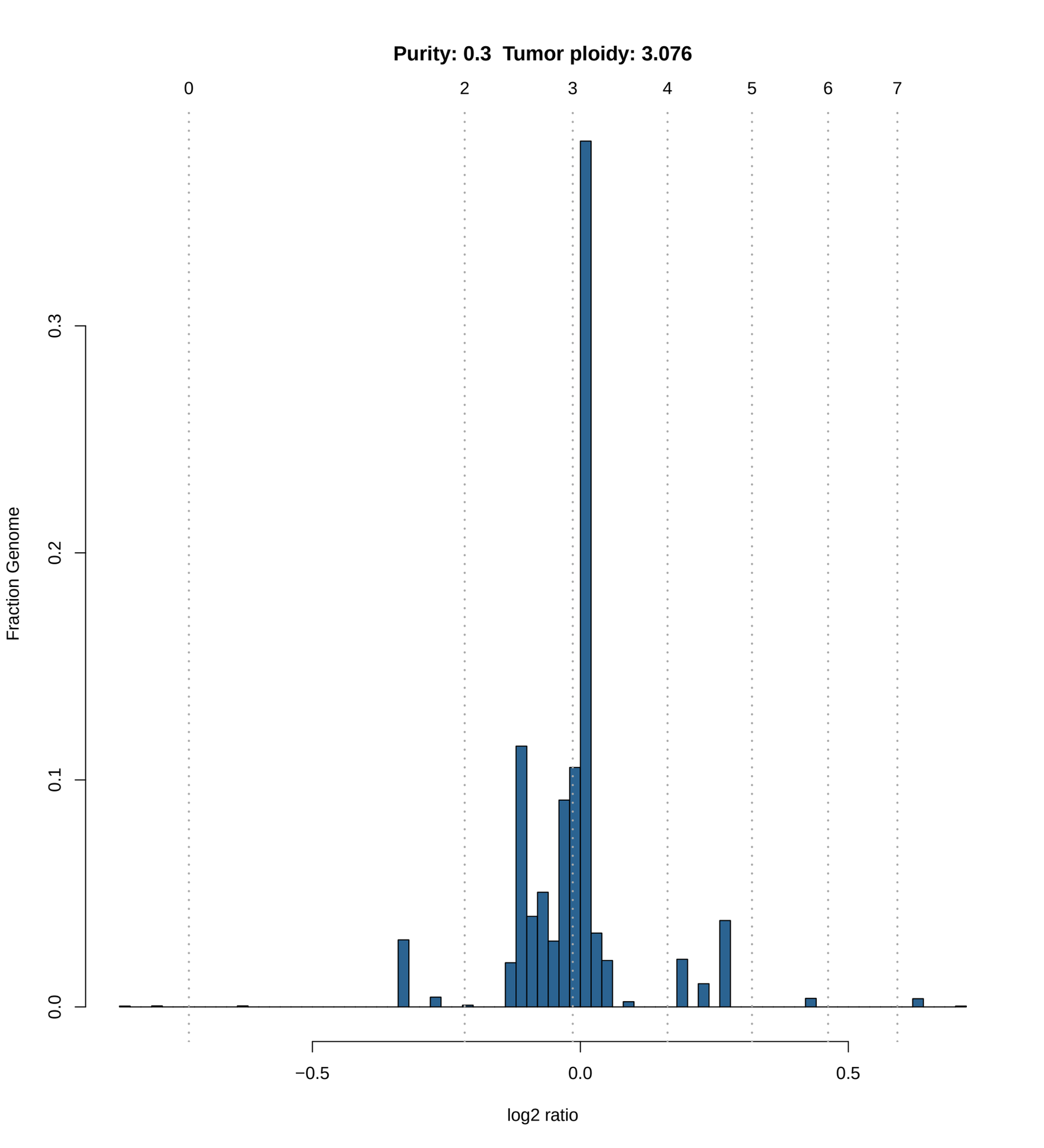

Maximum Likelihood Copy Number
0
1
2
3
4
0
10
20
30
40
50
60
SNV Index

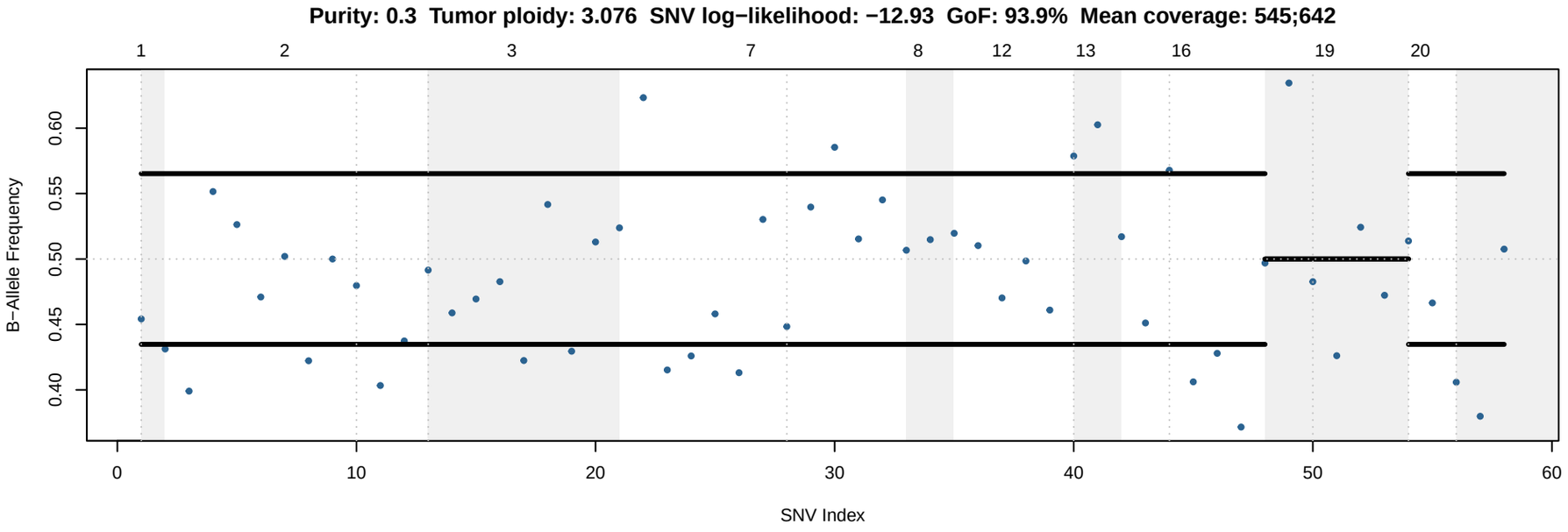

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
2m2
1m1
2m1
4m2
1m0
2m0
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

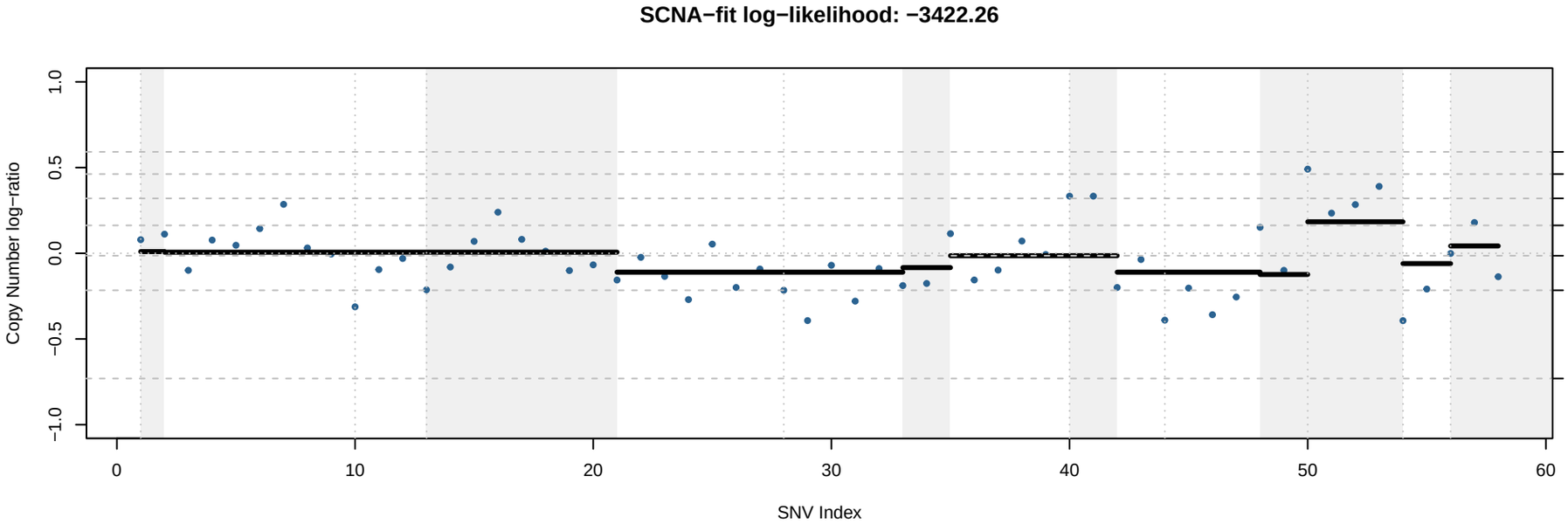

Coverage (log2)
7.0
7.5
8.0
8.5
9.0
9.5
10.0
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

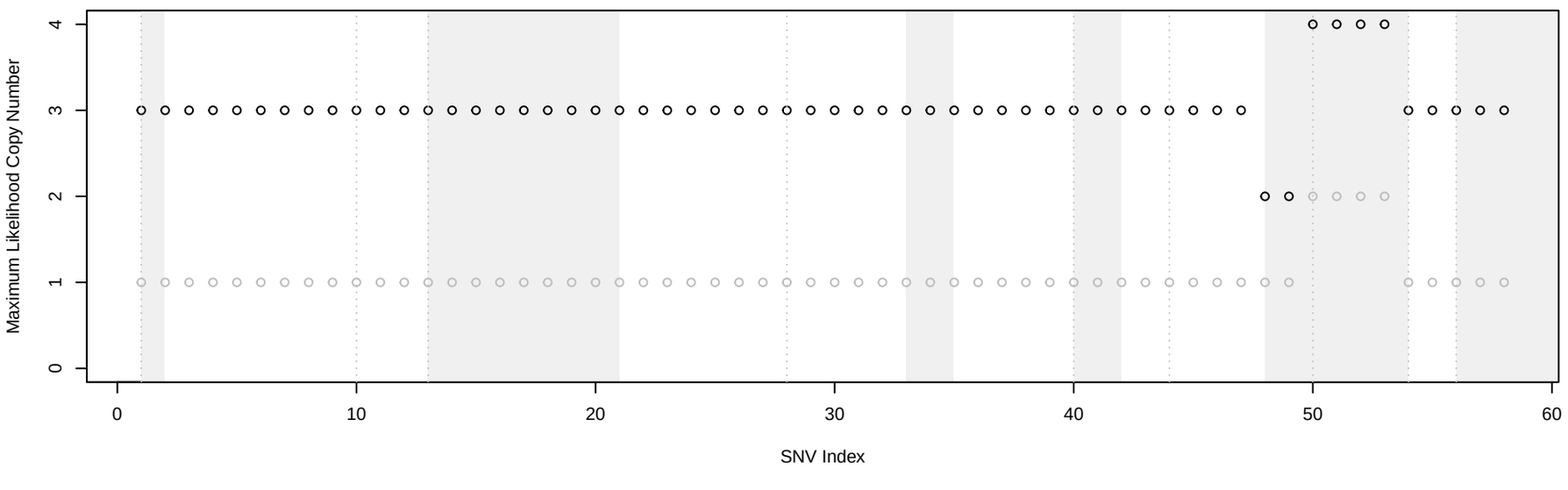

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.035
0.040
0.045
0.050
0.055
0.060
0.065
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

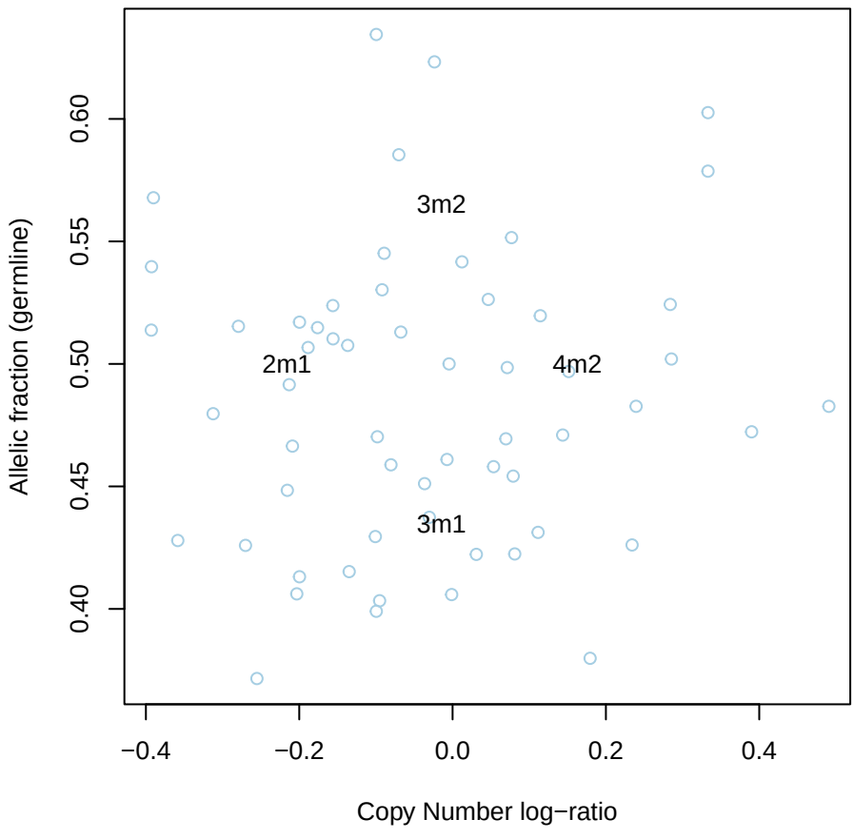

Frequency
0
1
2
3
4
5
6
7
0.4
0.5
0.6
0.7
0.8
0.9
Cellular fraction

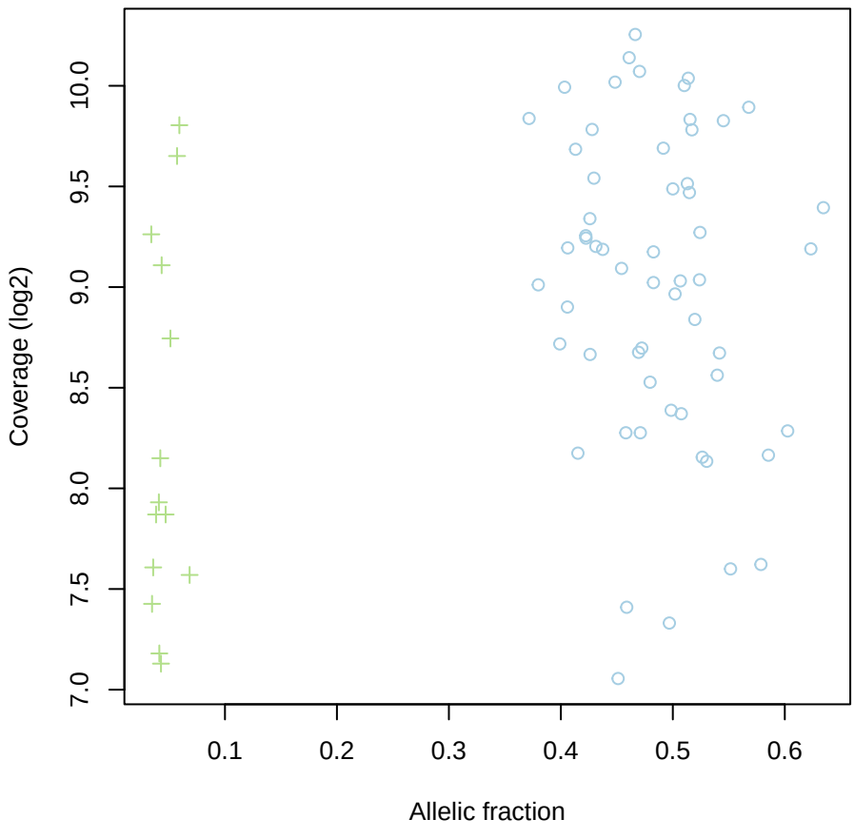

Purity: 0.3 Tumor ploidy: 3.076
0
2
3
4
5
6
7
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
log2 ratio

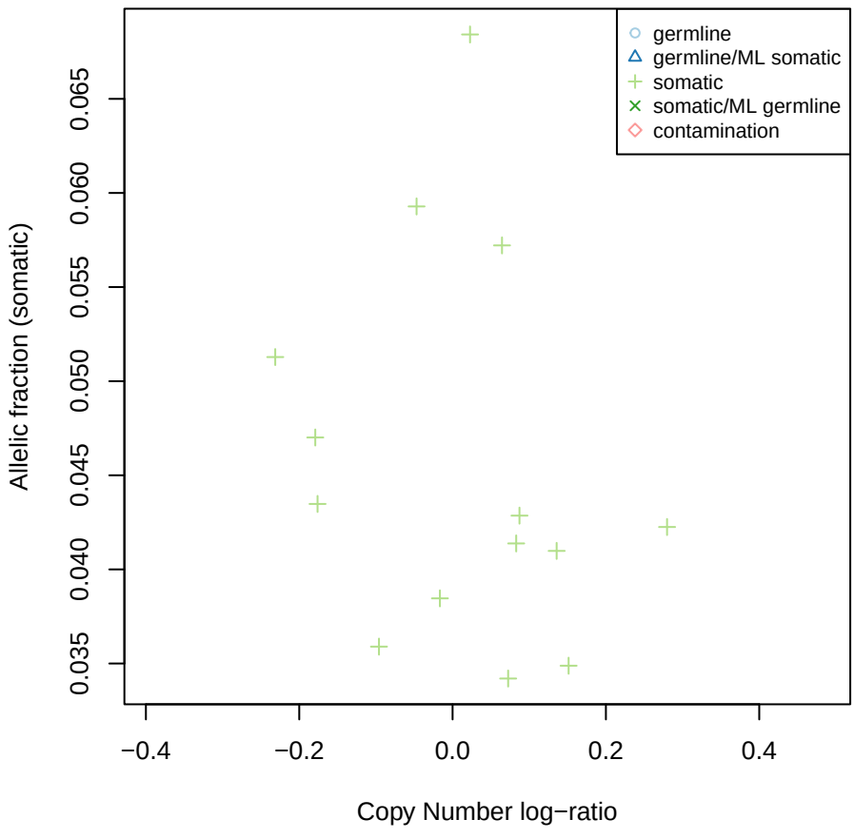

Purity: 0.3 Tumor ploidy: 3.076 SNV log−likelihood: −12.93 GoF: 93.9% Mean coverage: 545;642
1
2
3
7
8
12
13
16
19
20
B−Allele Frequency
0.40
0.45
0.50
0.55
0.60
0
10
20
30
40
50
60
SNV Index

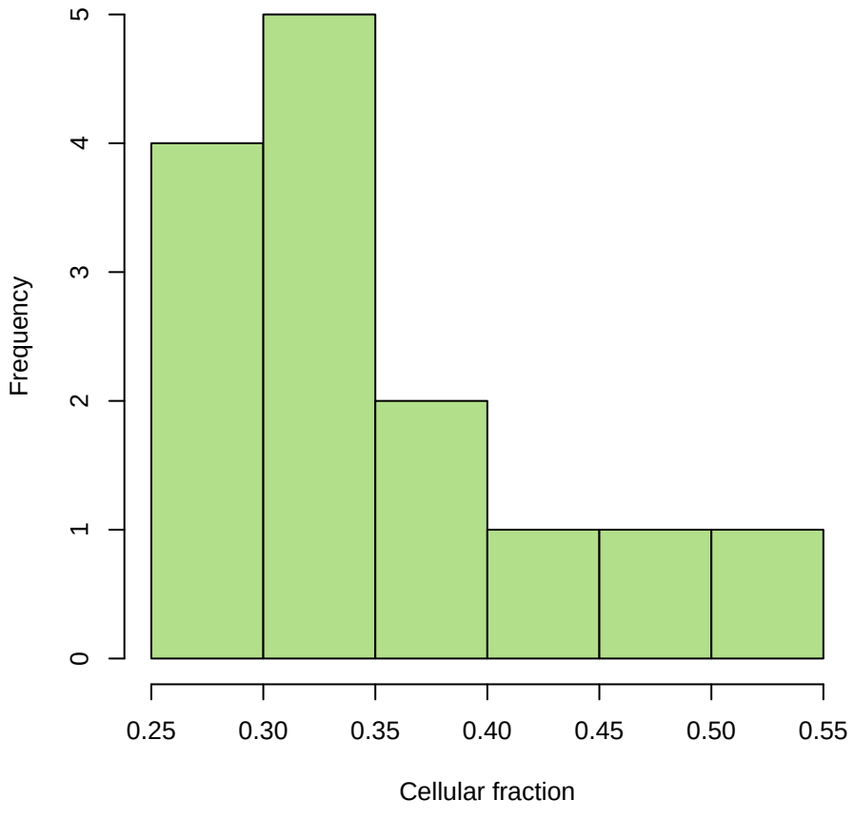

SCNA−fit log−likelihood: −3422.26
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
0
2
3
4
5
7
0
10
20
30
40
50
60
SNV Index

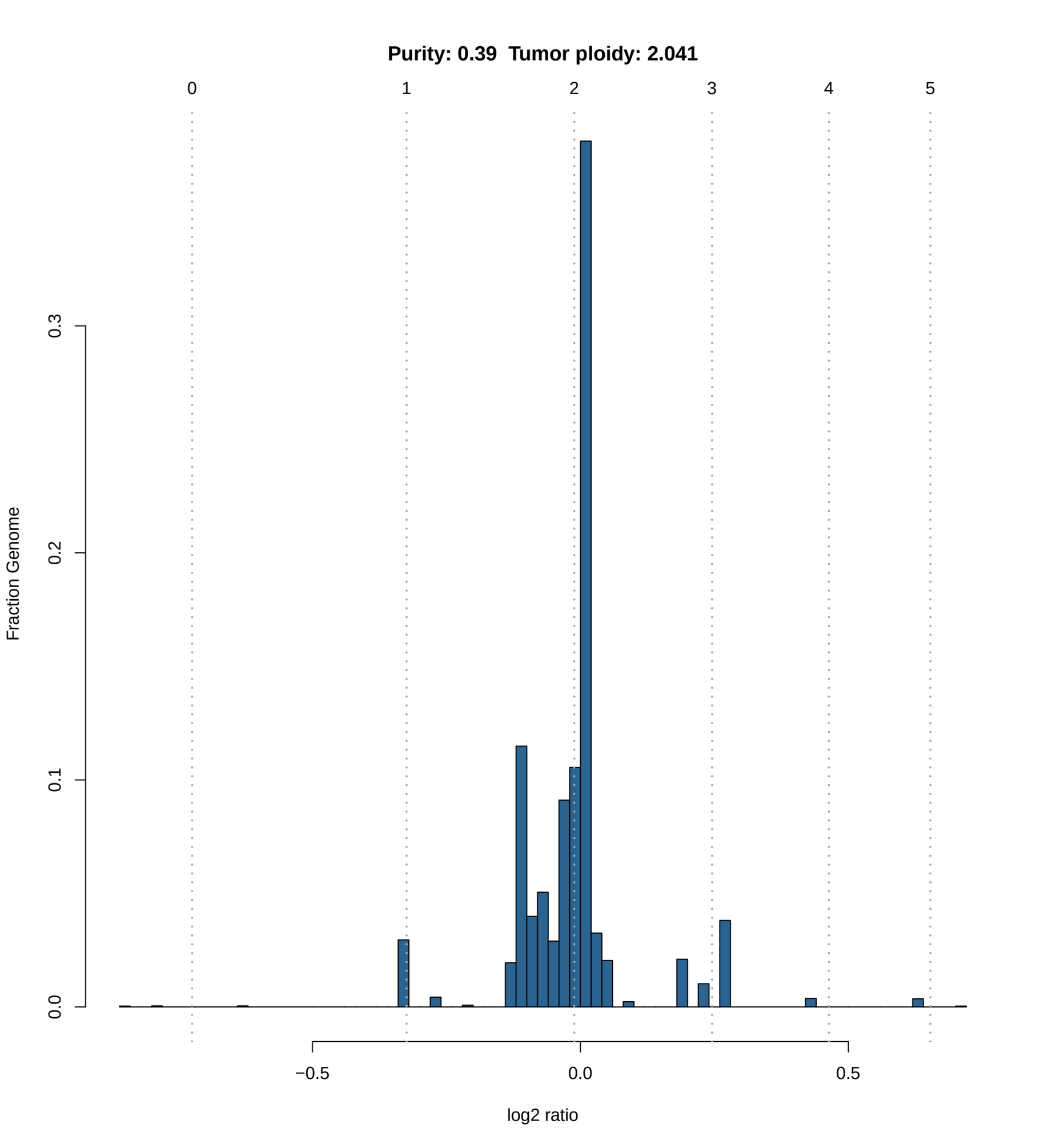

Maximum Likelihood Copy Number
0
1
2
3
4
0
10
20
30
40
50
60
SNV Index

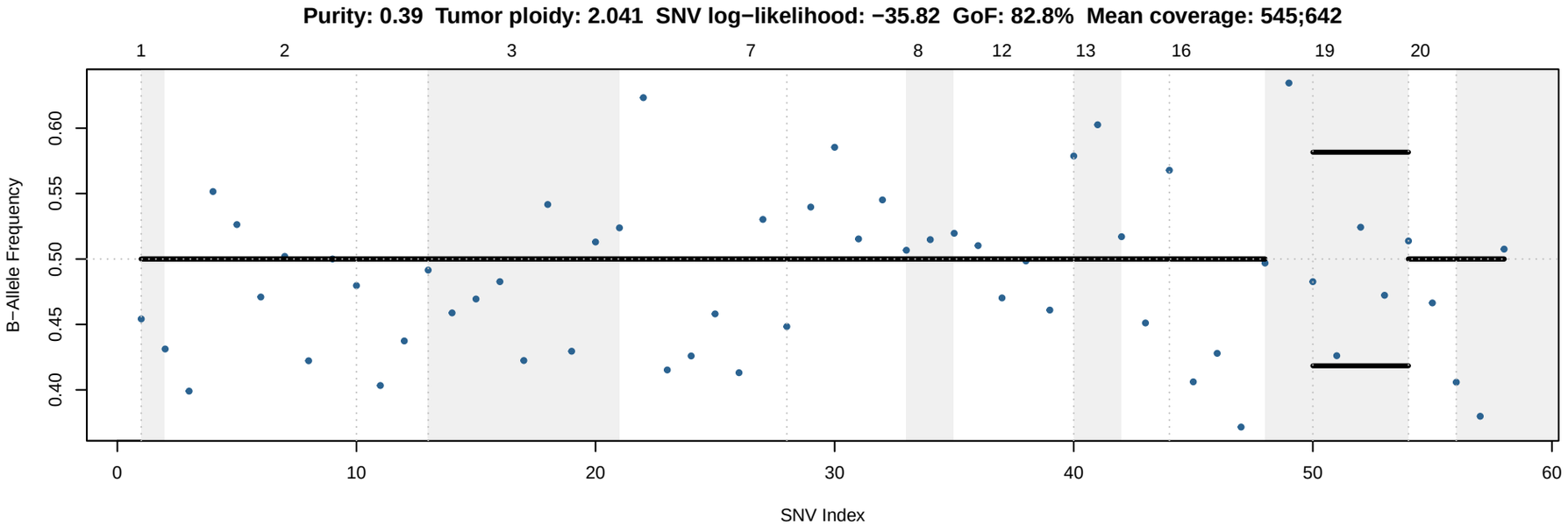

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
3m2
2m1
4m2
3m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

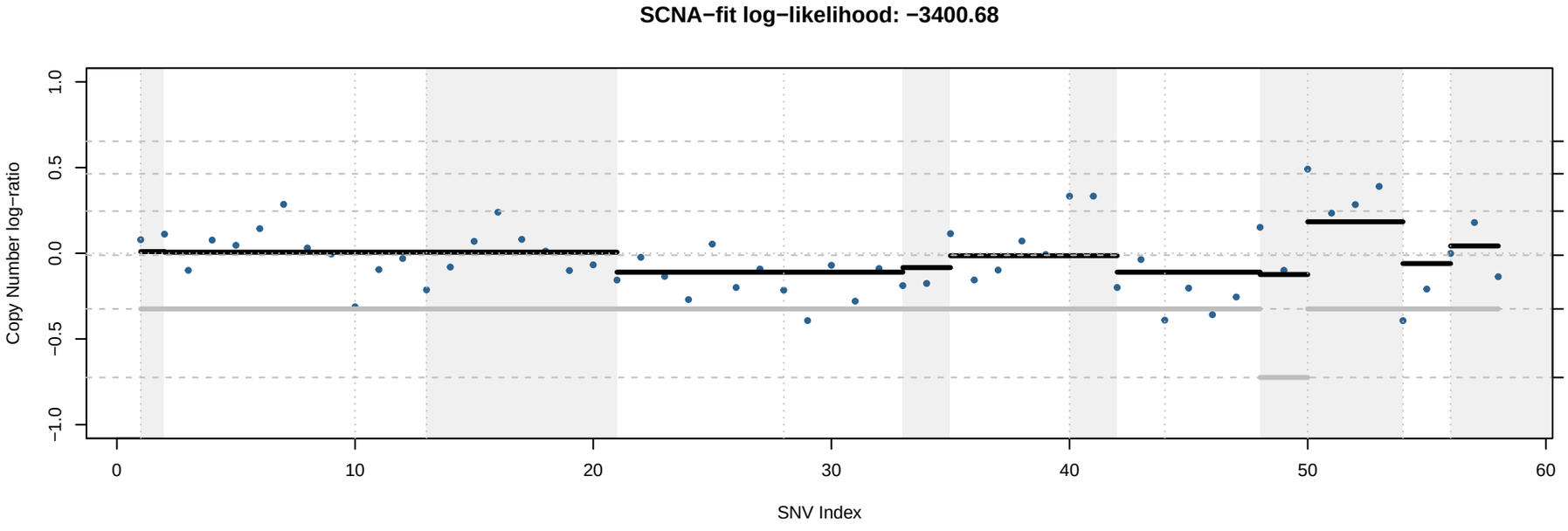

Coverage (log2)
7.0
7.5
8.0
8.5
9.0
9.5
10.0
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

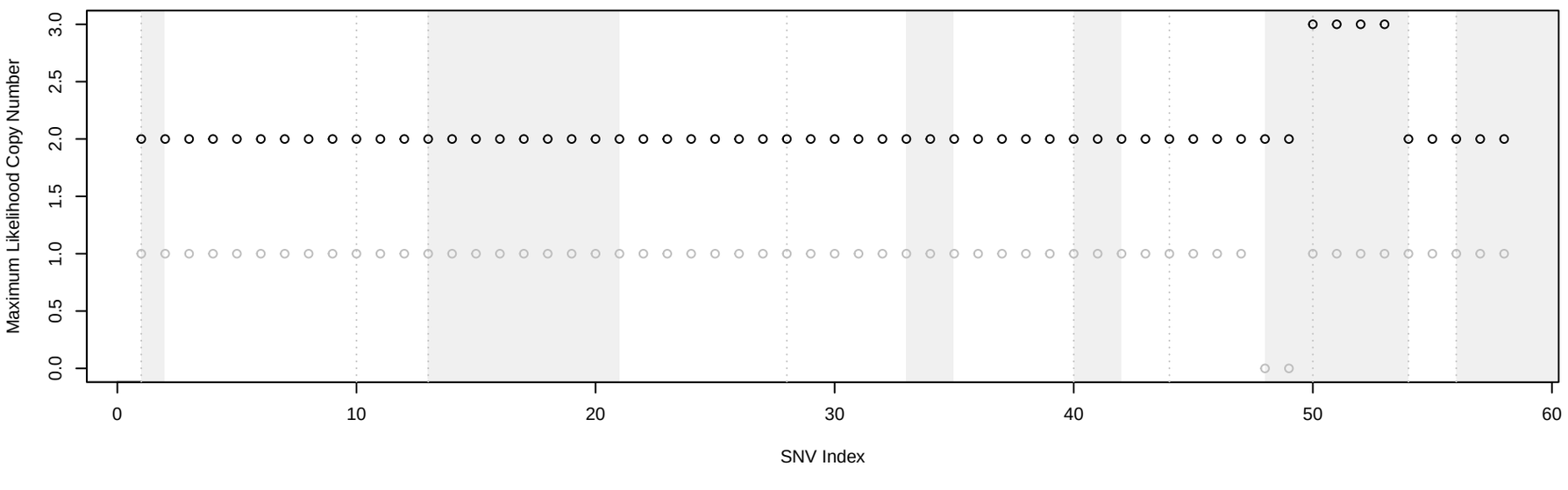

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.035
0.040
0.045
0.050
0.055
0.060
0.065
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

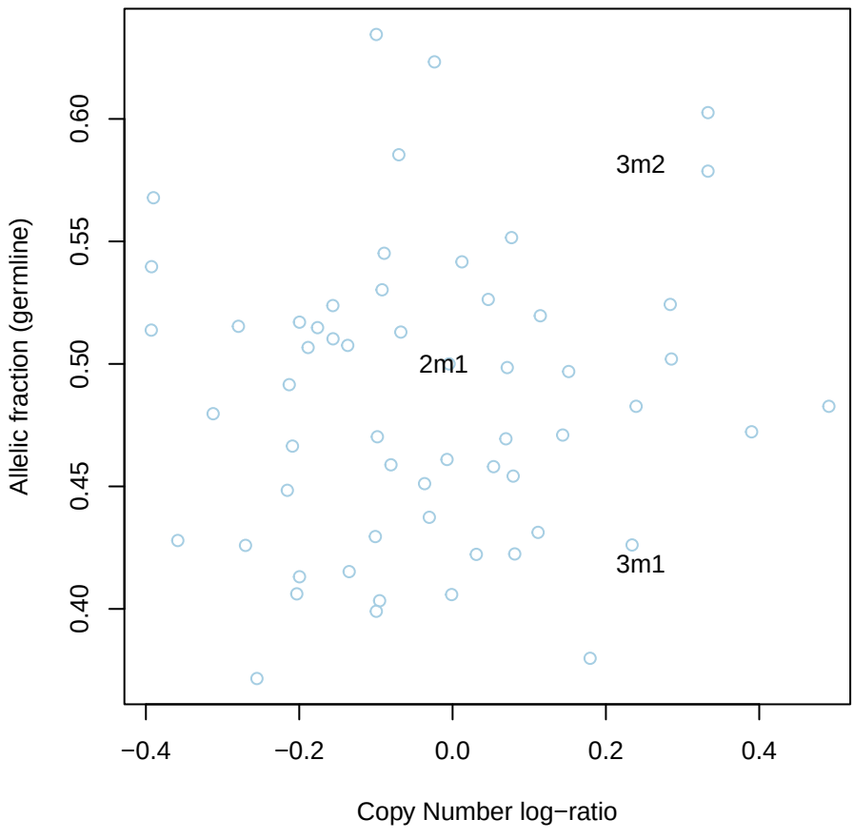

Frequency
0
1
2
3
4
5
0.25
0.30
0.35
0.40
0.45
0.50
0.55
Cellular fraction

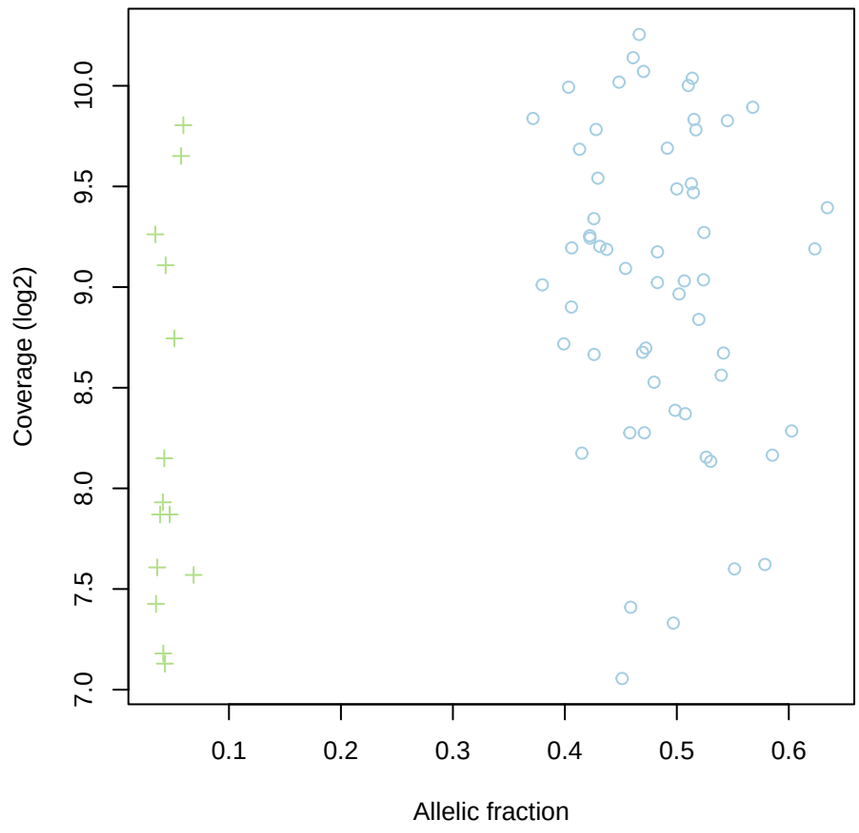

Purity: 0.39 Tumor ploidy: 2.041
0
1
2
3
4
5
0.0
0.1
0.2
0.3
Fraction Genome
−0.5
0.0
0.5
log2 ratio

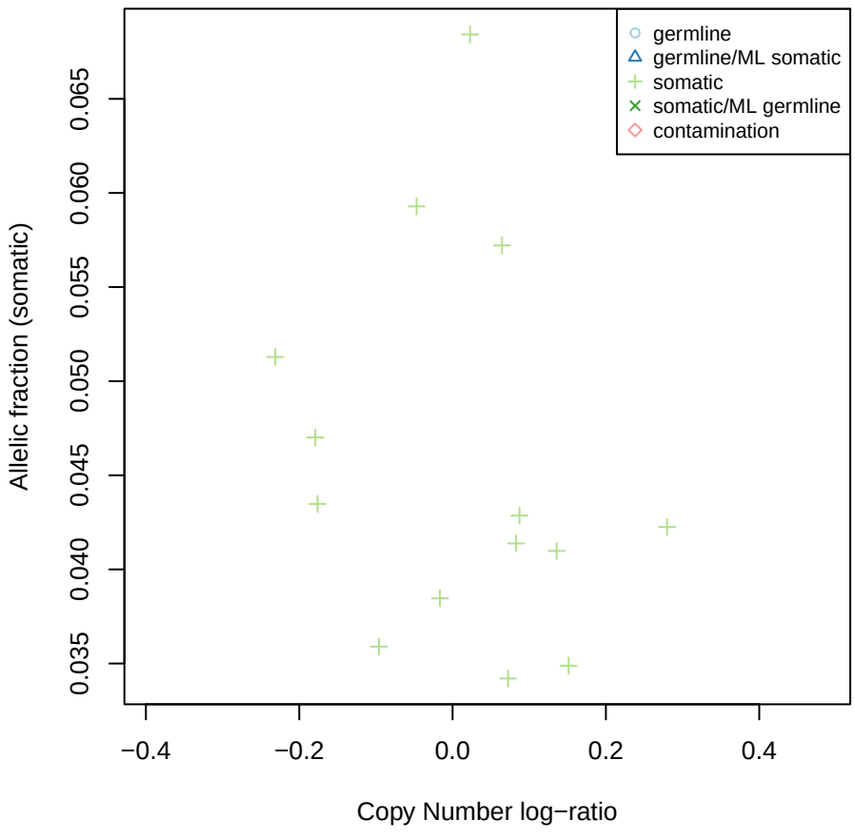

Purity: 0.39 Tumor ploidy: 2.041 SNV log−likelihood: −35.82 GoF: 82.8% Mean coverage: 545;642
1
2
3
7
8
12
13
16
19
20
B−Allele Frequency
0.40
0.45
0.50
0.55
0.60
0
10
20
30
40
50
60
SNV Index

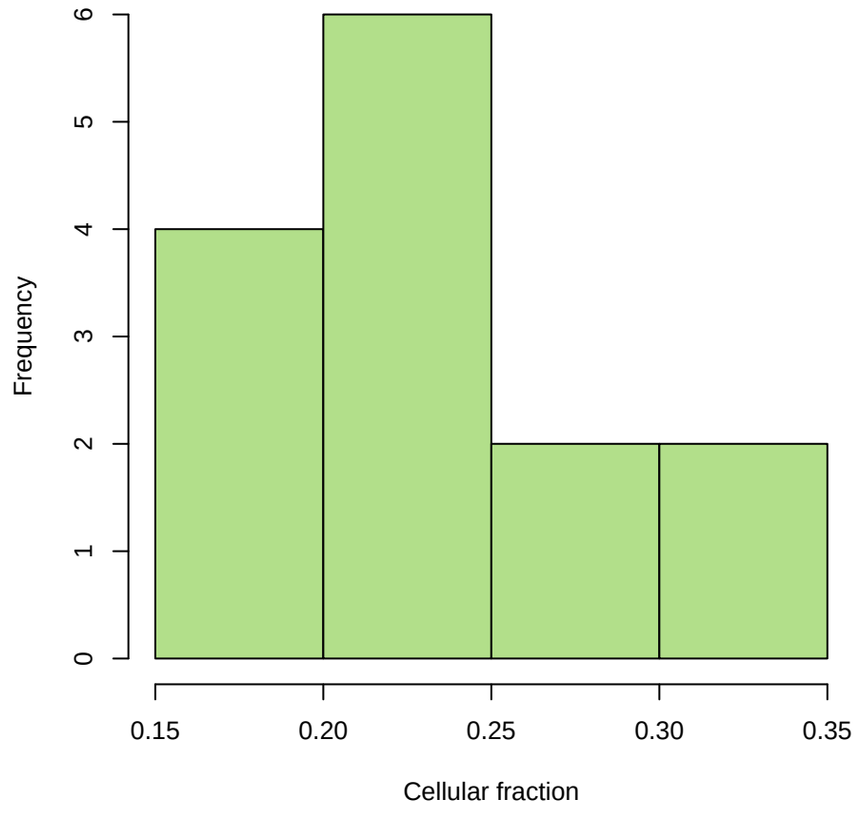

SCNA−fit log−likelihood: −3400.68
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
0
1
2
3
4
5
0
10
20
30
40
50
60
SNV Index

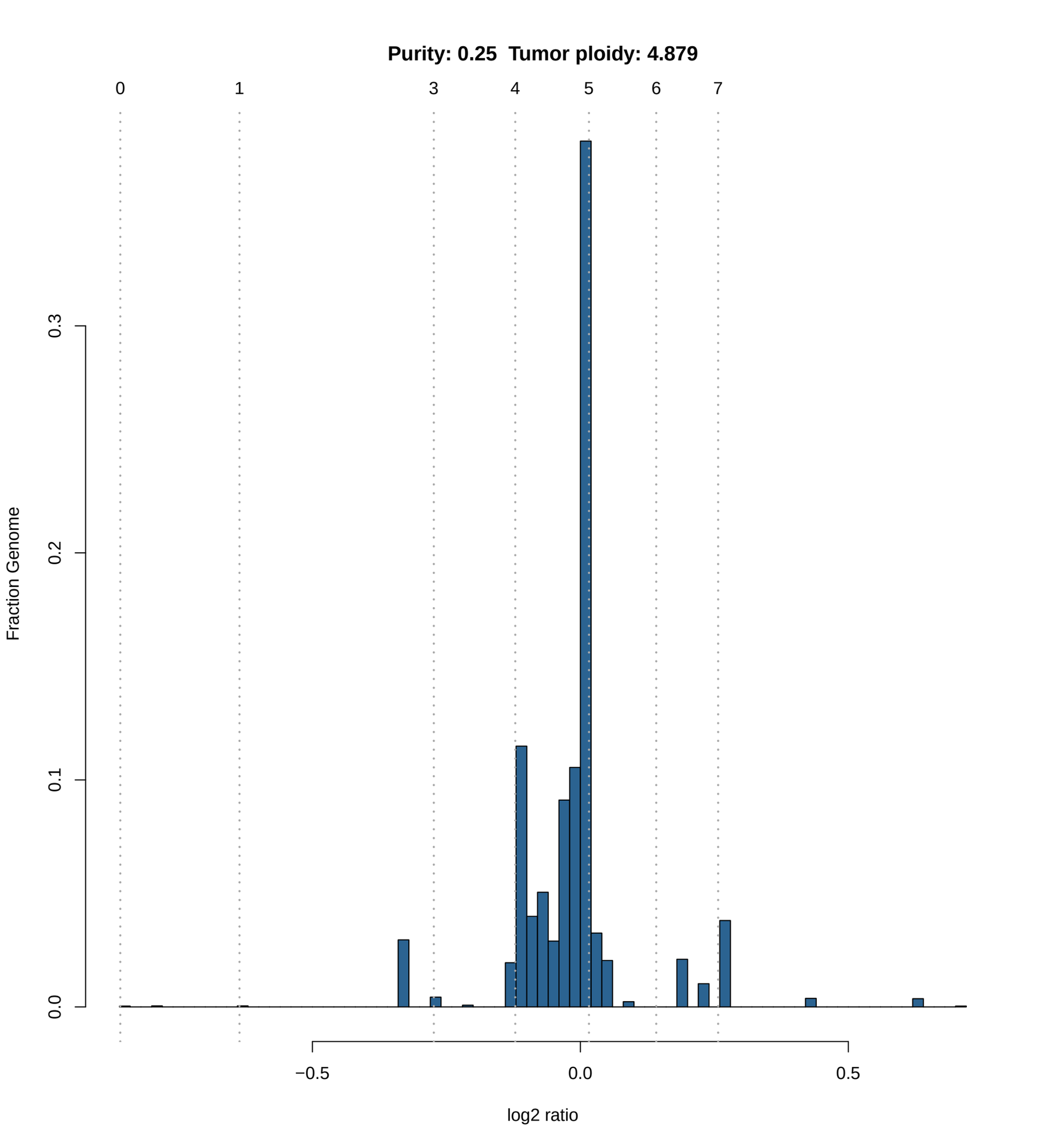

Maximum Likelihood Copy Number
0.0
0.5
1.0
1.5
2.0
2.5
3.0
0
10
20
30
40
50
60
SNV Index

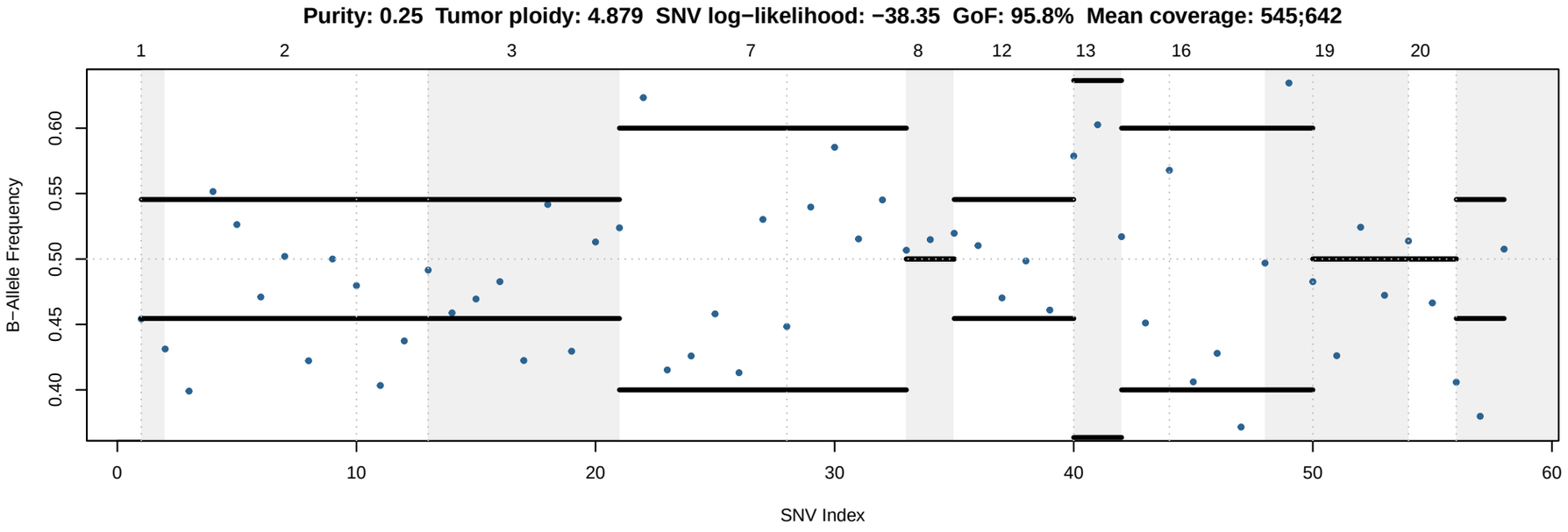

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
3m2
2m1
3m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

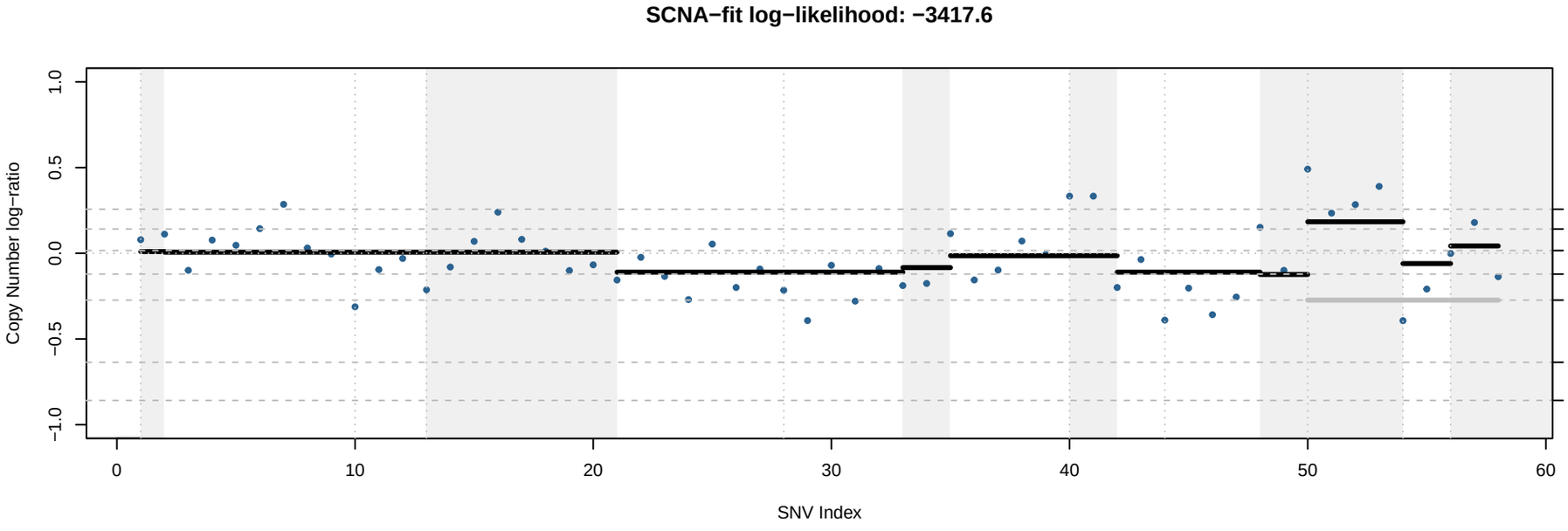

Coverage (log2)
7.0
7.5
8.0
8.5
9.0
9.5
10.0
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

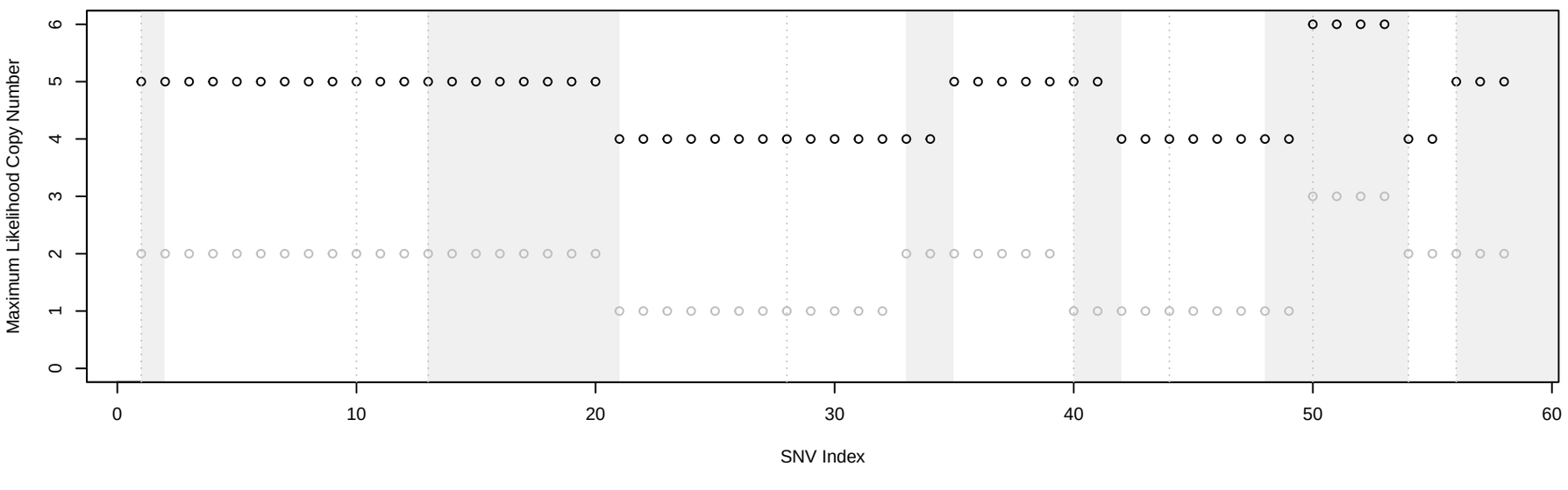

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.035
0.040
0.045
0.050
0.055
0.060
0.065
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

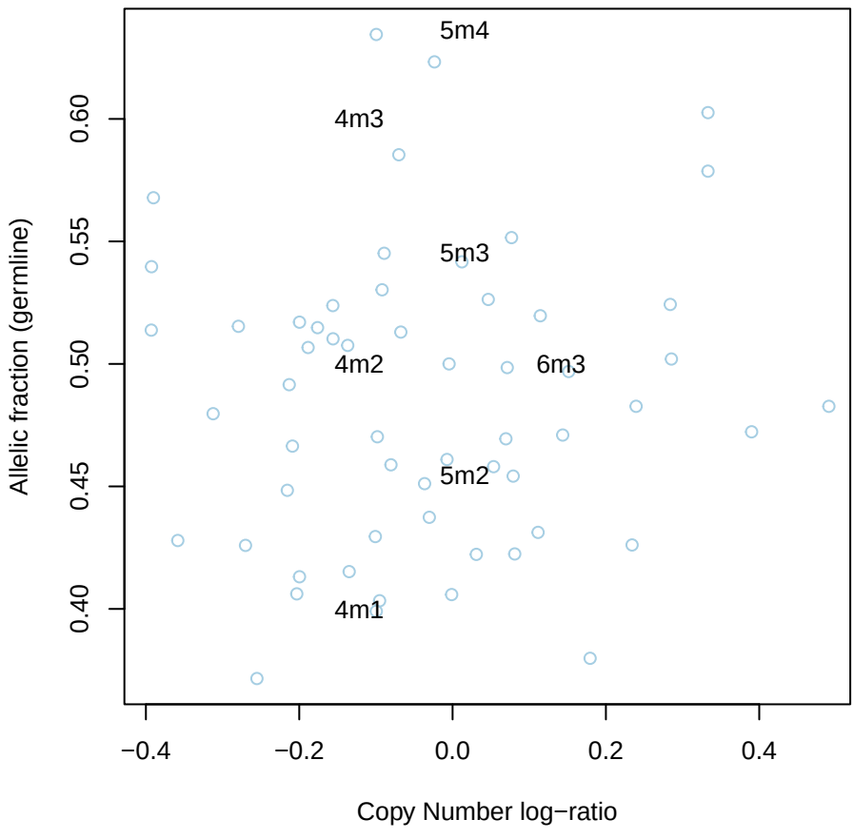

Frequency
0
1
2
3
4
5
6
0.15
0.20
0.25
0.30
0.35
Cellular fraction

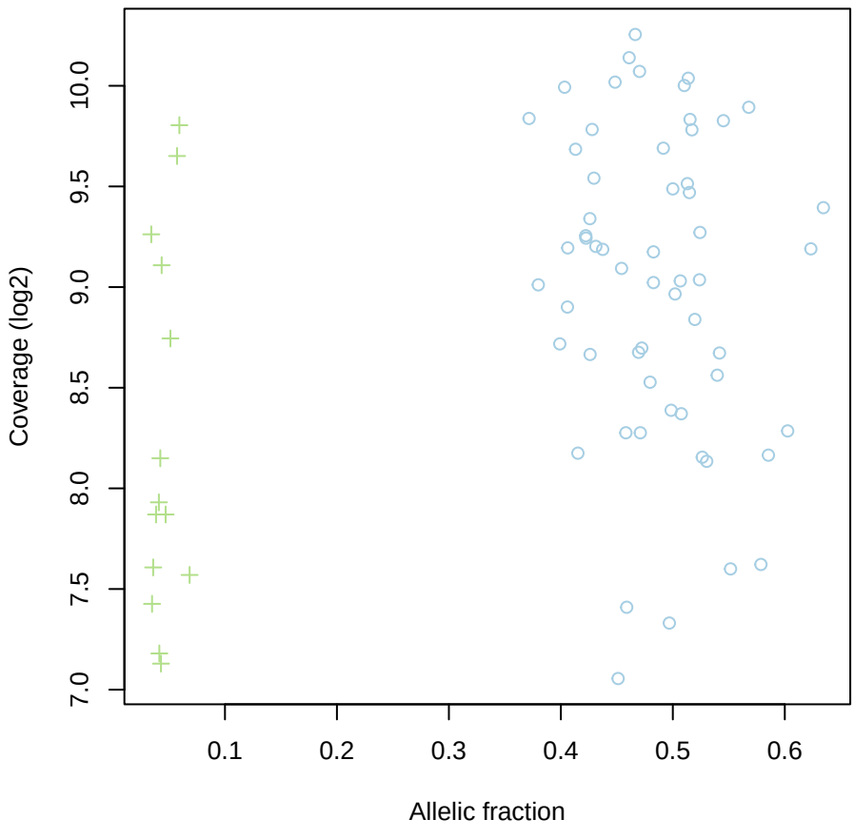

Purity: 0.25 Tumor ploidy: 4.879
0
1
3
4
5
6
7
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
log2 ratio

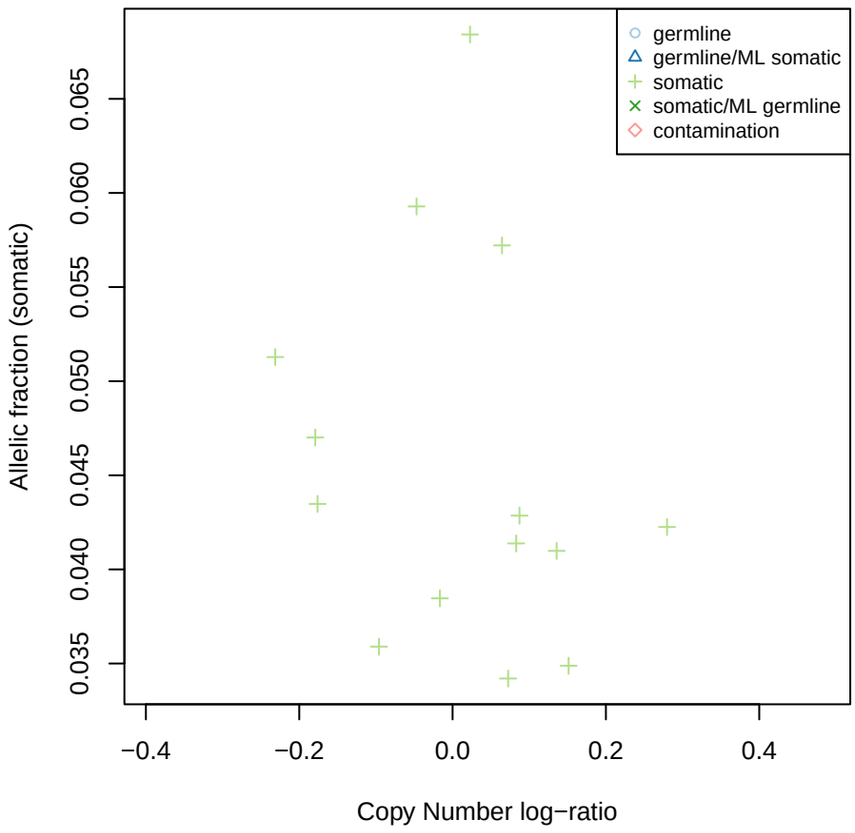

Purity: 0.25 Tumor ploidy: 4.879 SNV log−likelihood: −38.35 GoF: 95.8% Mean coverage: 545;642
1
2
3
7
8
12
13
16
19
20
B−Allele Frequency
0.40
0.45
0.50
0.55
0.60
0
10
20
30
40
50
60
SNV Index

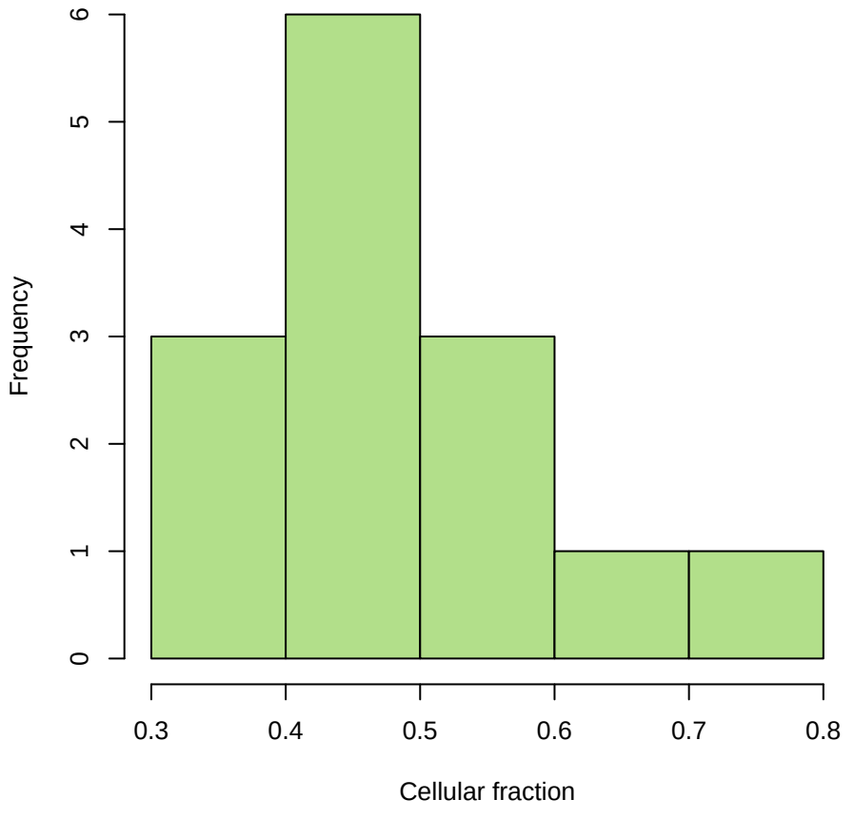

SCNA−fit log−likelihood: −3417.6
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
0
1
3
4
6
0
10
20
30
40
50
60
SNV Index

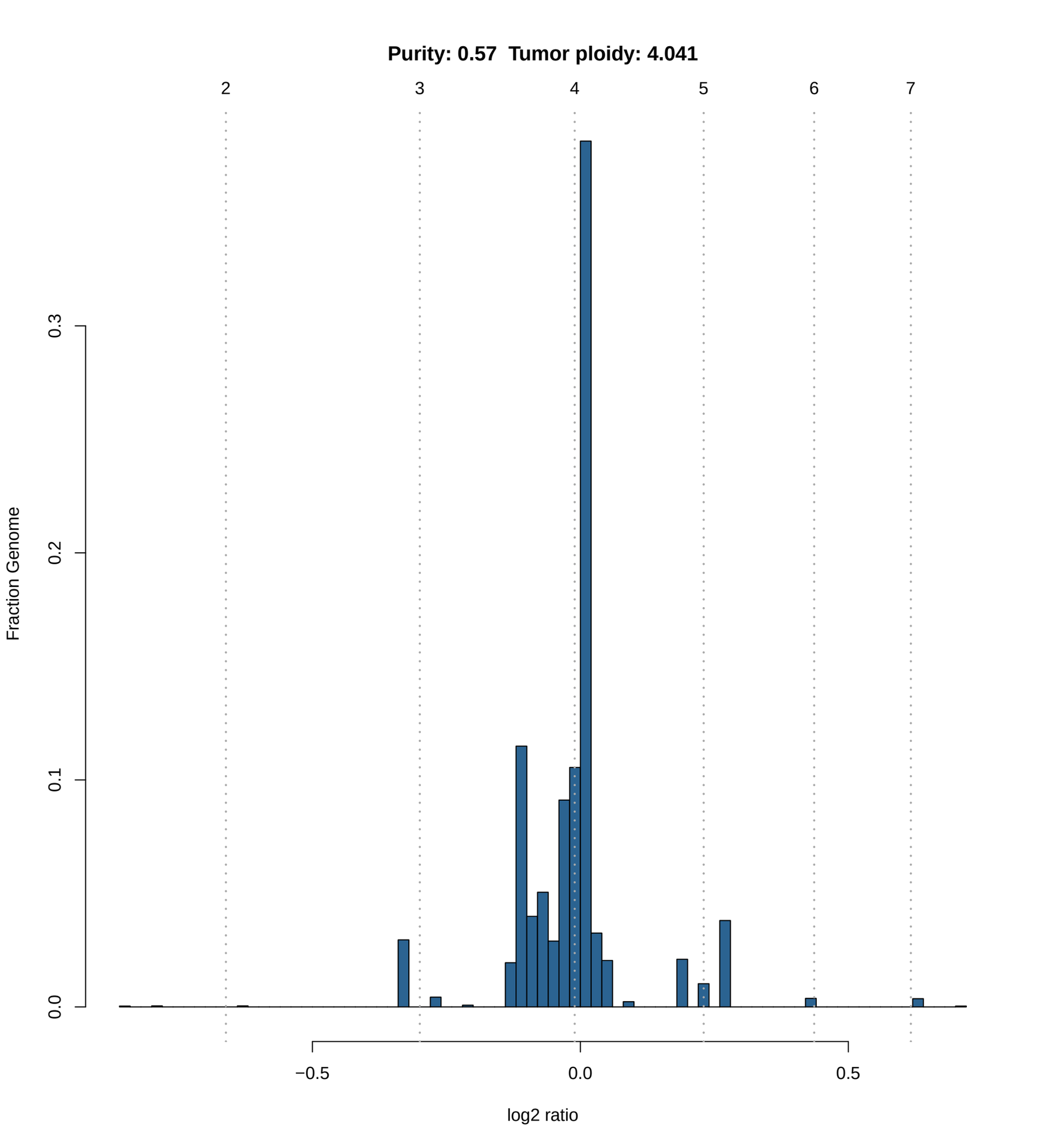

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
0
10
20
30
40
50
60
SNV Index

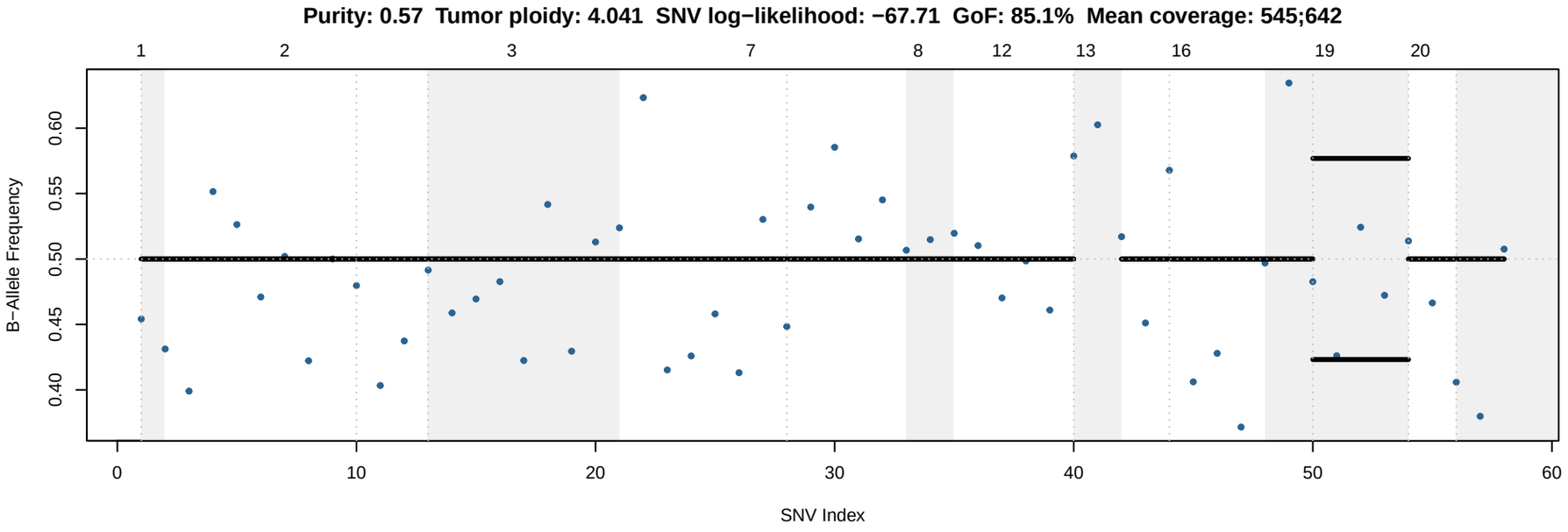

5m4
4m3
5m3
4m2
6m3
5m2
4m1
Allelic fraction (germline)
Copy Number log−ratio

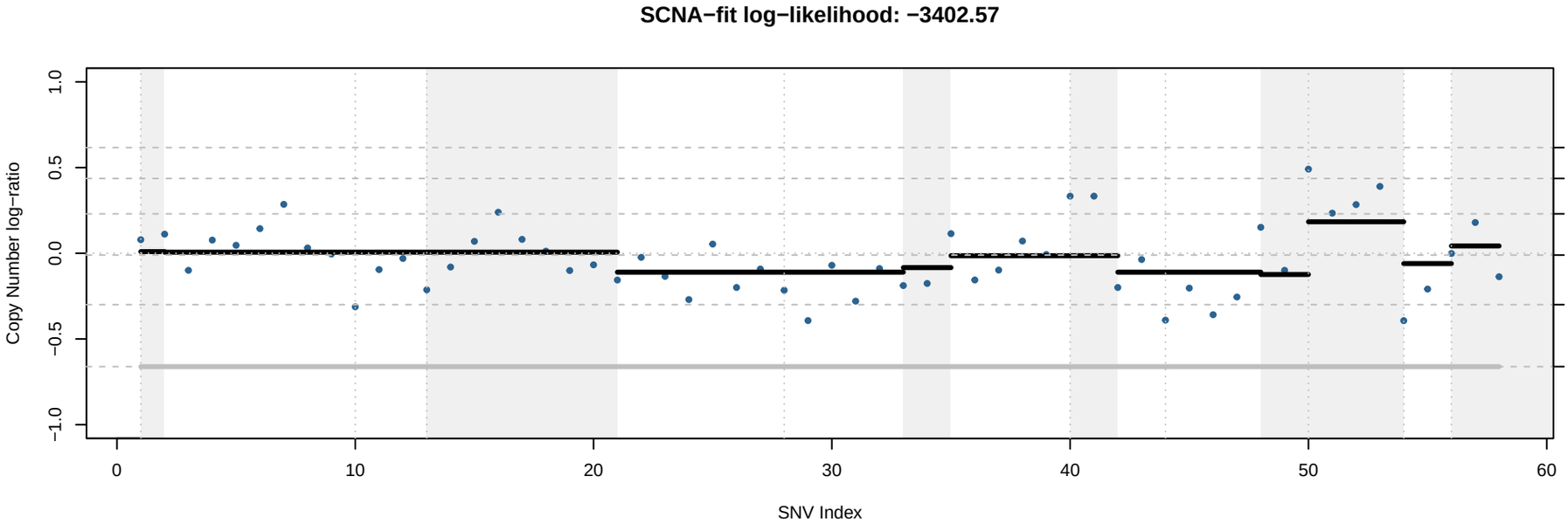

Coverage (log2)
Allelic fraction

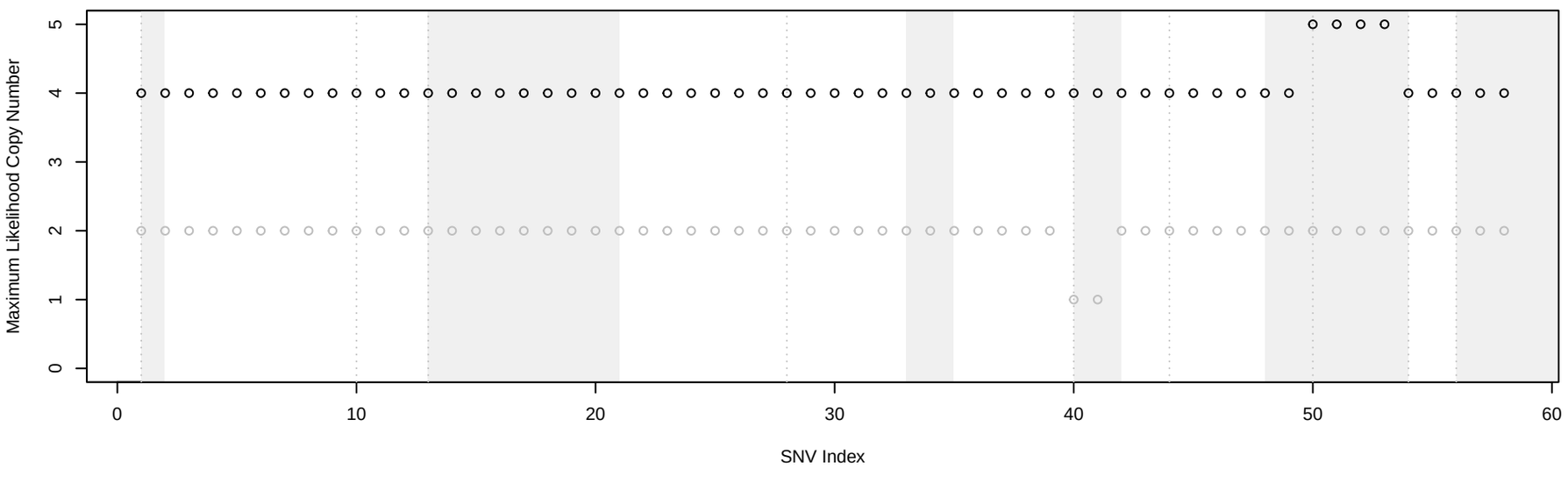

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

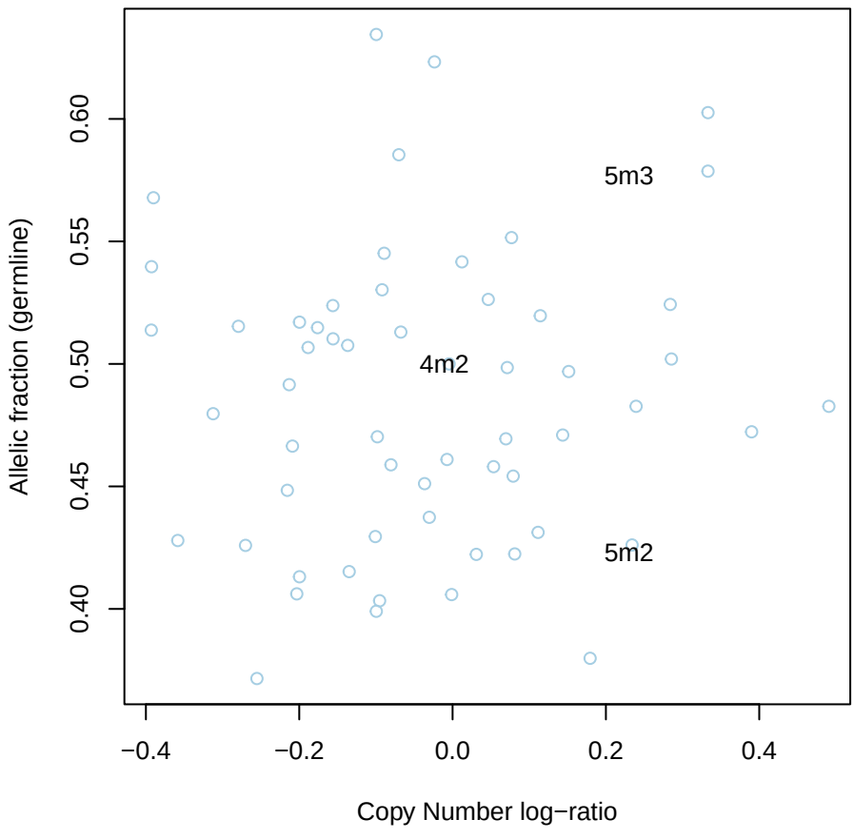

Frequency
Cellular fraction

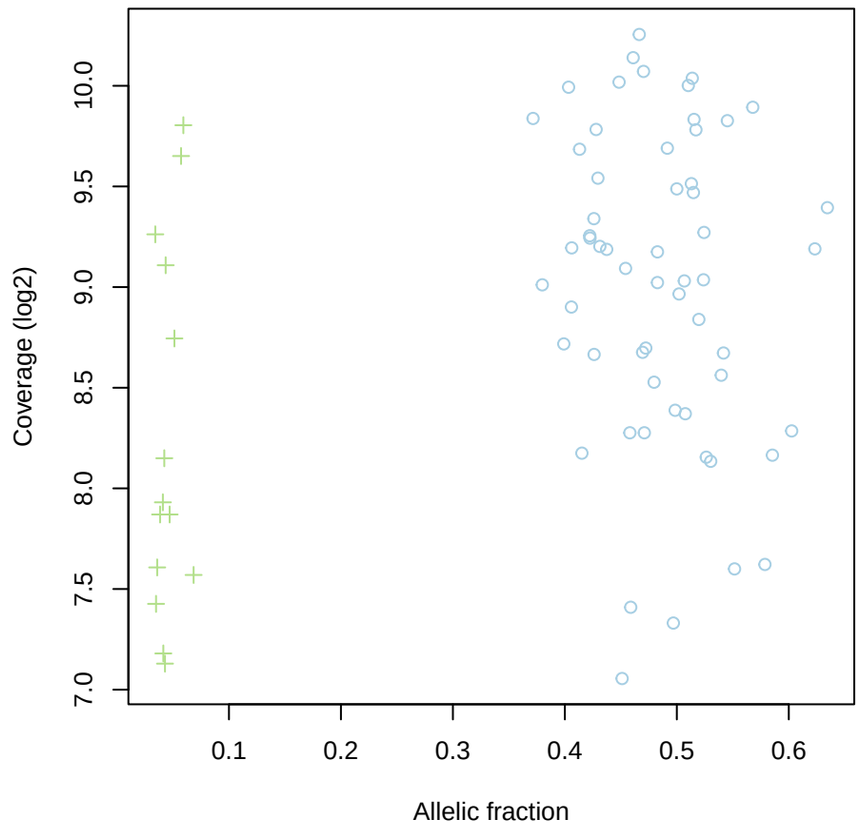

Purity: 0.57 Tumor ploidy: 4.041
2
3
4
5
6
7
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
log2 ratio

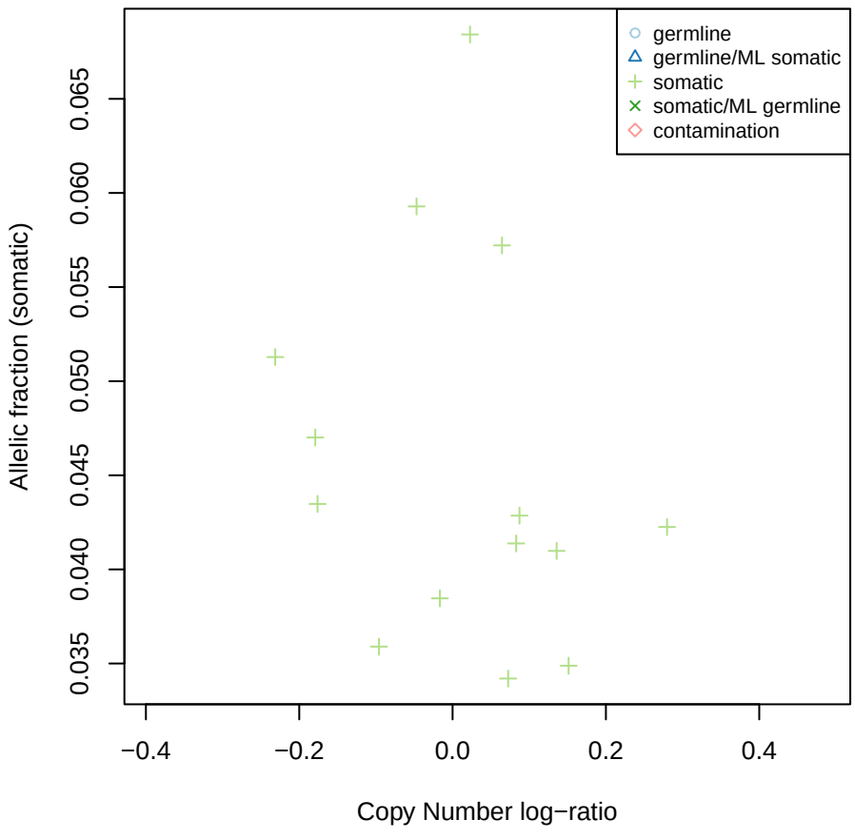

Purity: 0.57 Tumor ploidy: 4.041 SNV log−likelihood: −67.71 GoF: 85.1% Mean coverage: 545;642
1
2
3
7
8
12
13
16
19
20
B−Allele Frequency
0.40
0.45
0.50
0.55
0.60
0
10
20
30
40
50
60
SNV Index

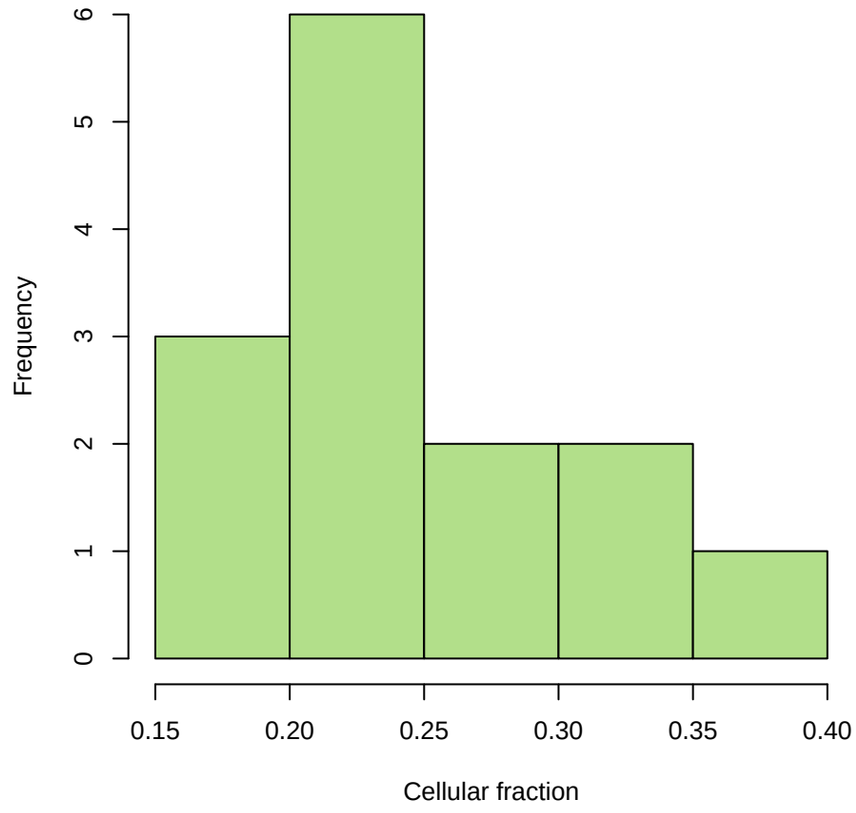

SCNA−fit log−likelihood: −3402.57
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
2
3
4
5
6
7
0
10
20
30
40
50
60
SNV Index

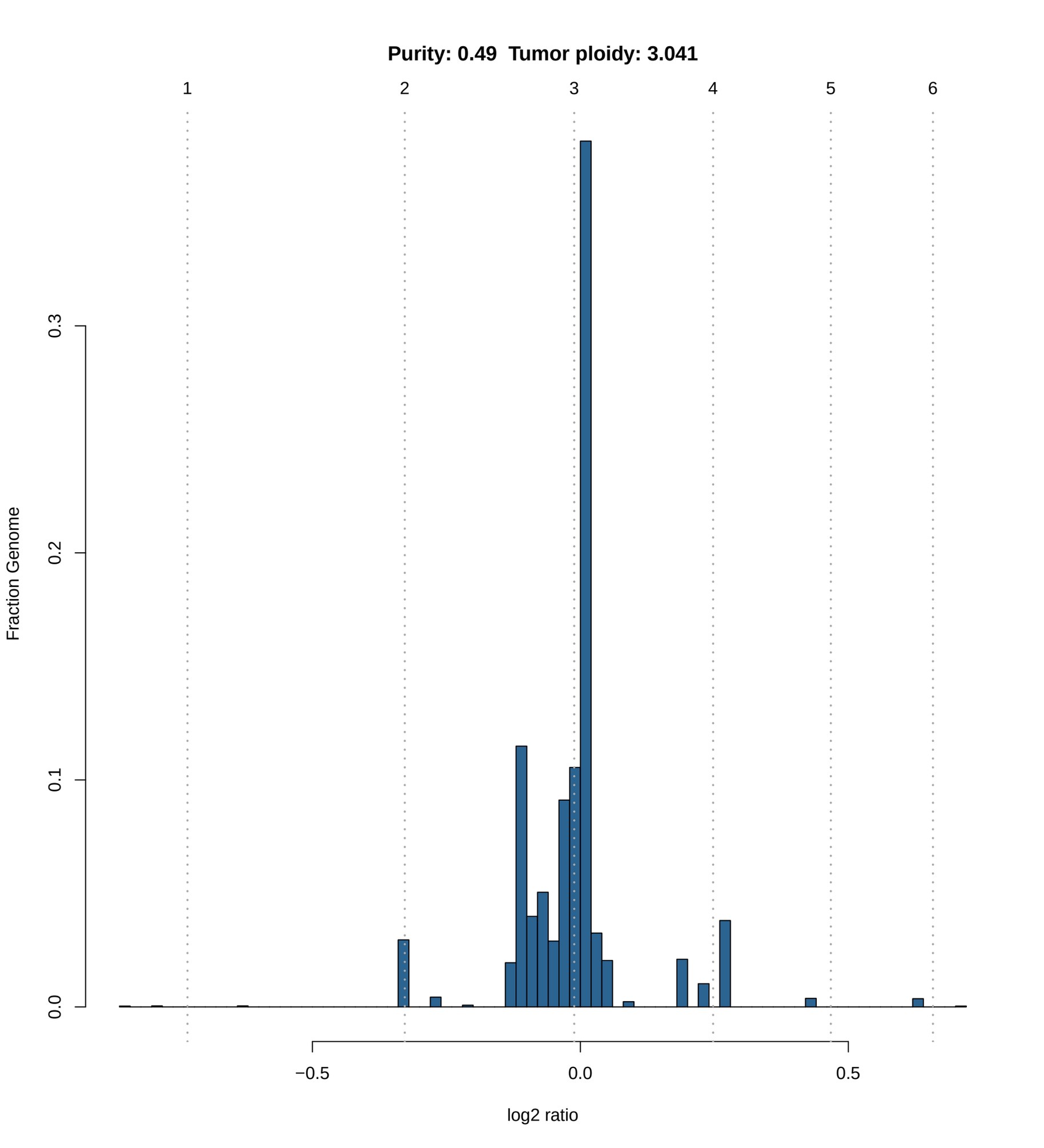

Maximum Likelihood Copy Number
0
1
2
3
4
5
0
10
20
30
40
50
60
SNV Index

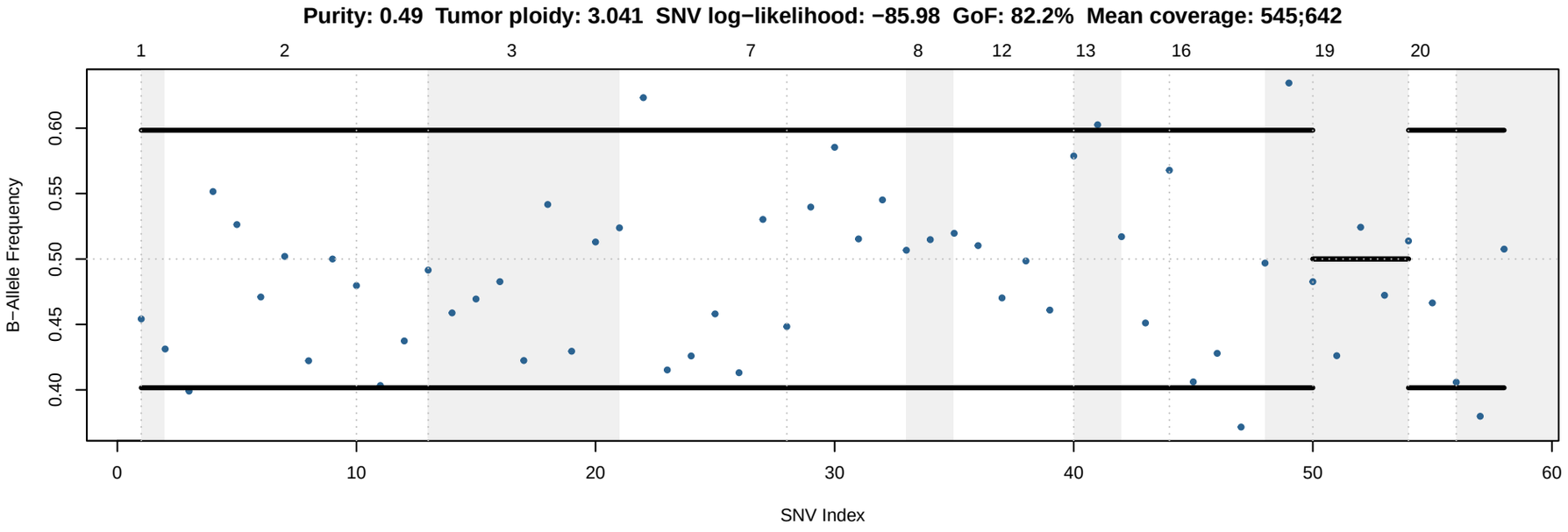

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
5m3
4m2
5m2
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

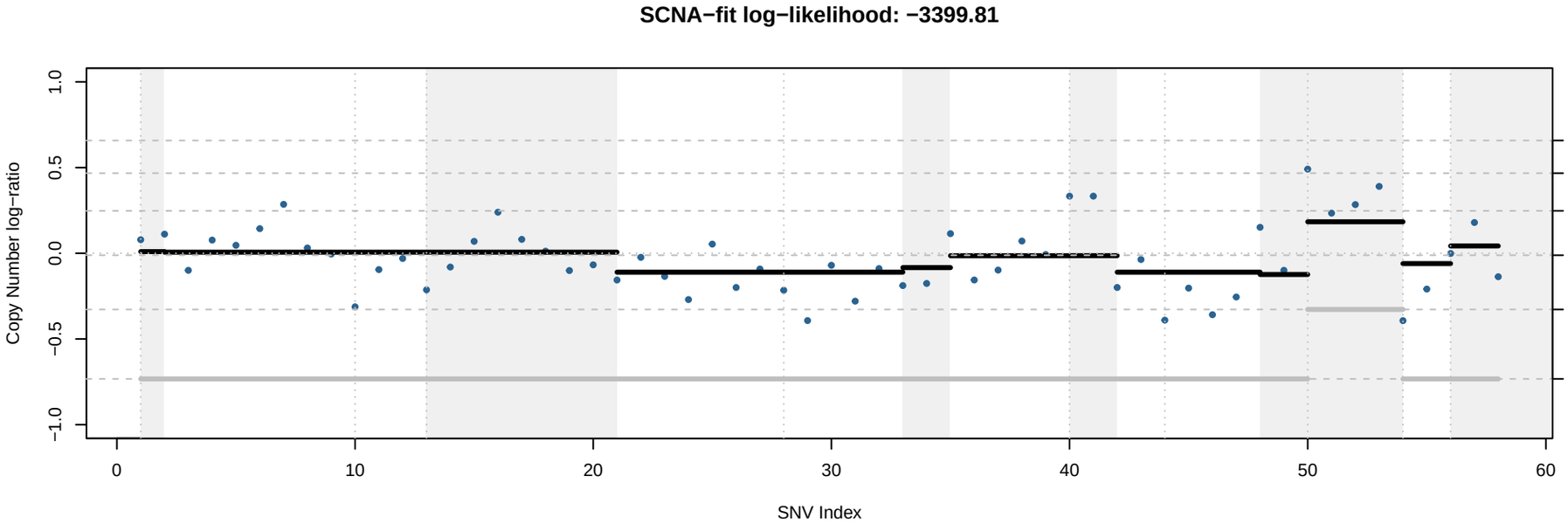

Coverage (log2)
7.0
7.5
8.0
8.5
9.0
9.5
10.0
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

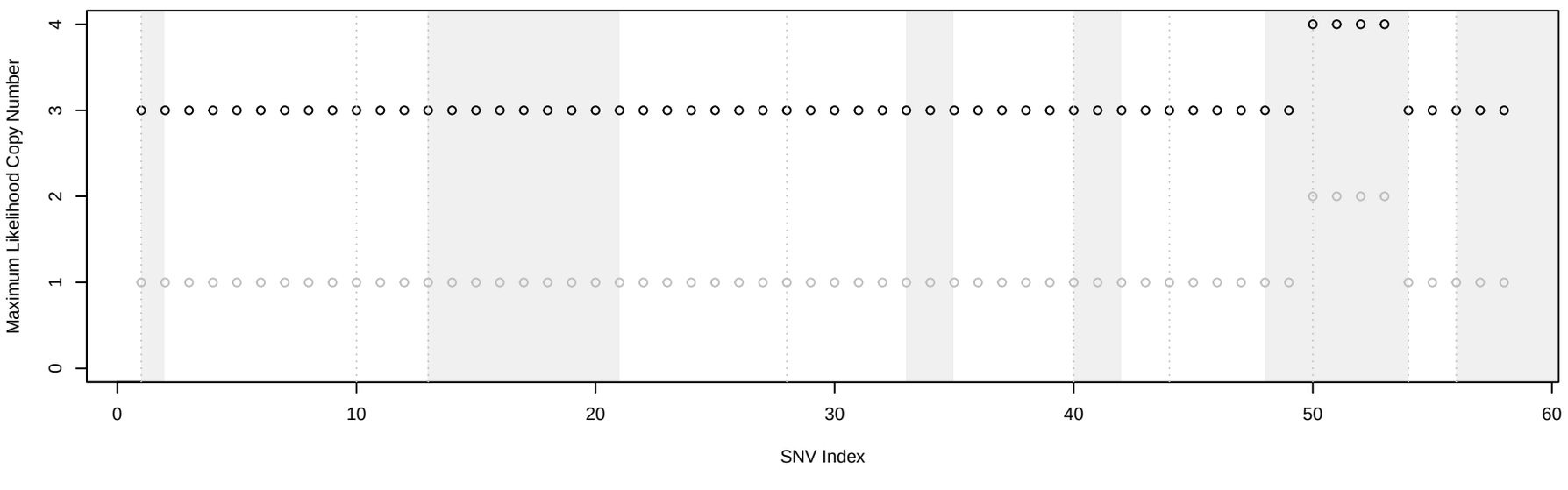

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.035
0.040
0.045
0.050
0.055
0.060
0.065
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

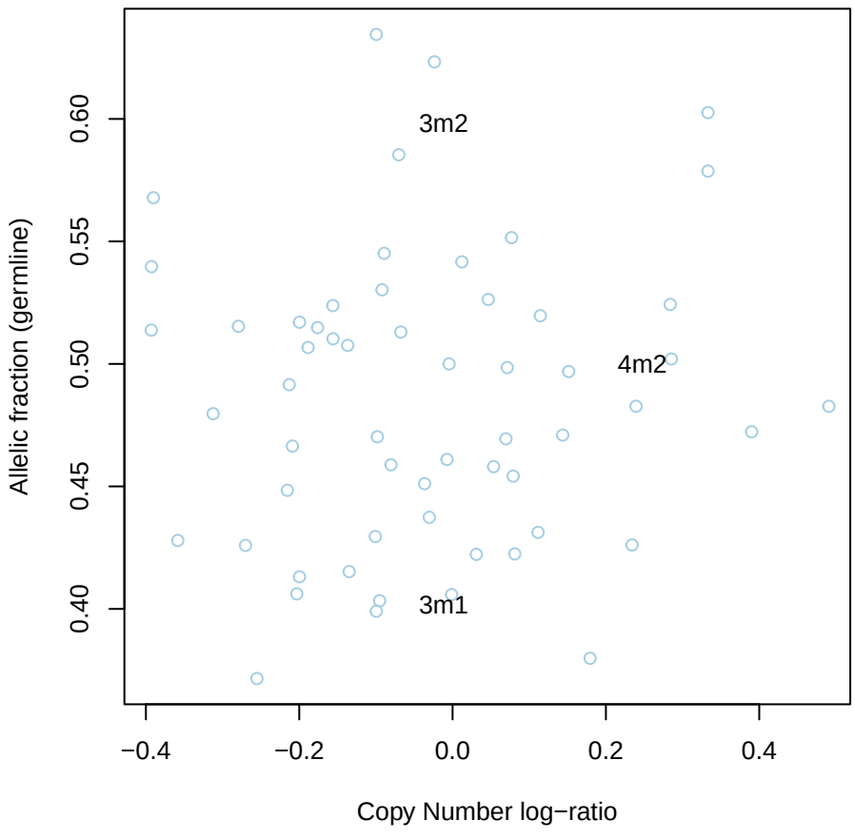

Frequency
0
1
2
3
4
5
6
0.15
0.20
0.25
0.30
0.35
0.40
Cellular fraction

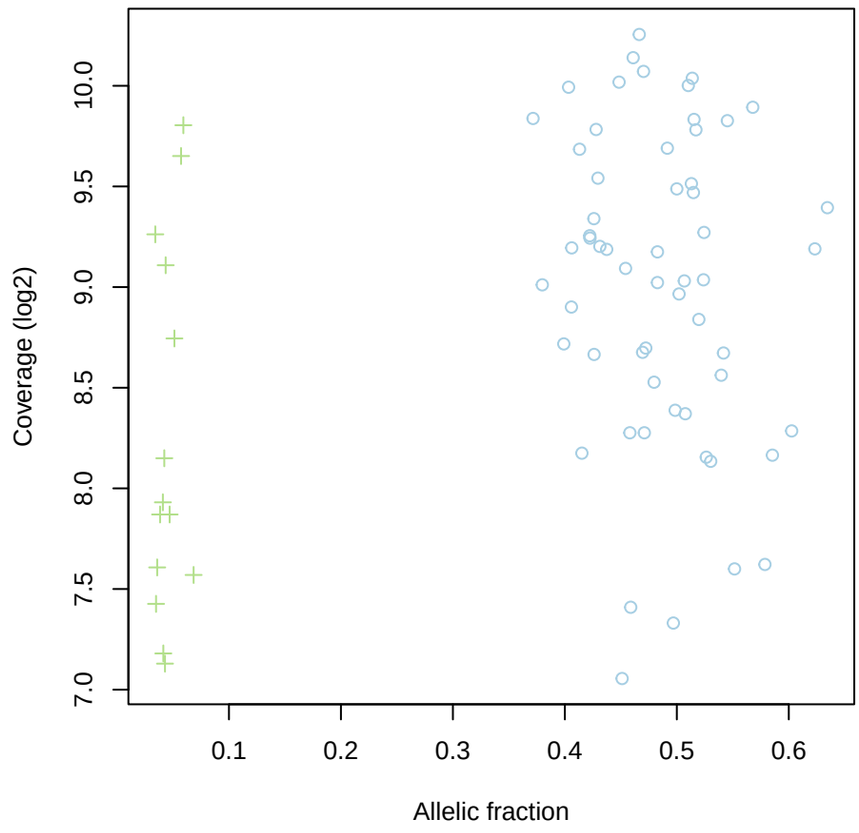

Purity: 0.49 Tumor ploidy: 3.041
1
2
3
4
5
6
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
log2 ratio

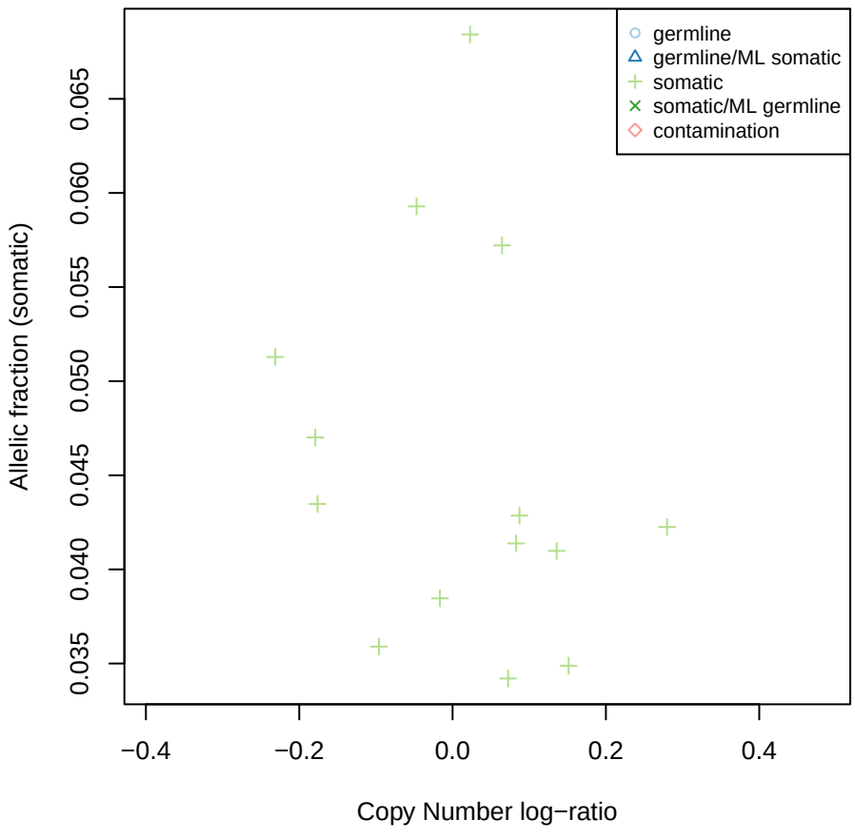

Purity: 0.49 Tumor ploidy: 3.041 SNV log−likelihood: −85.98 GoF: 82.2% Mean coverage: 545;642
1
2
3
7
8
12
13
16
19
20
B−Allele Frequency
0.40
0.45
0.50
0.55
0.60
0
10
20
30
40
50
60
SNV Index

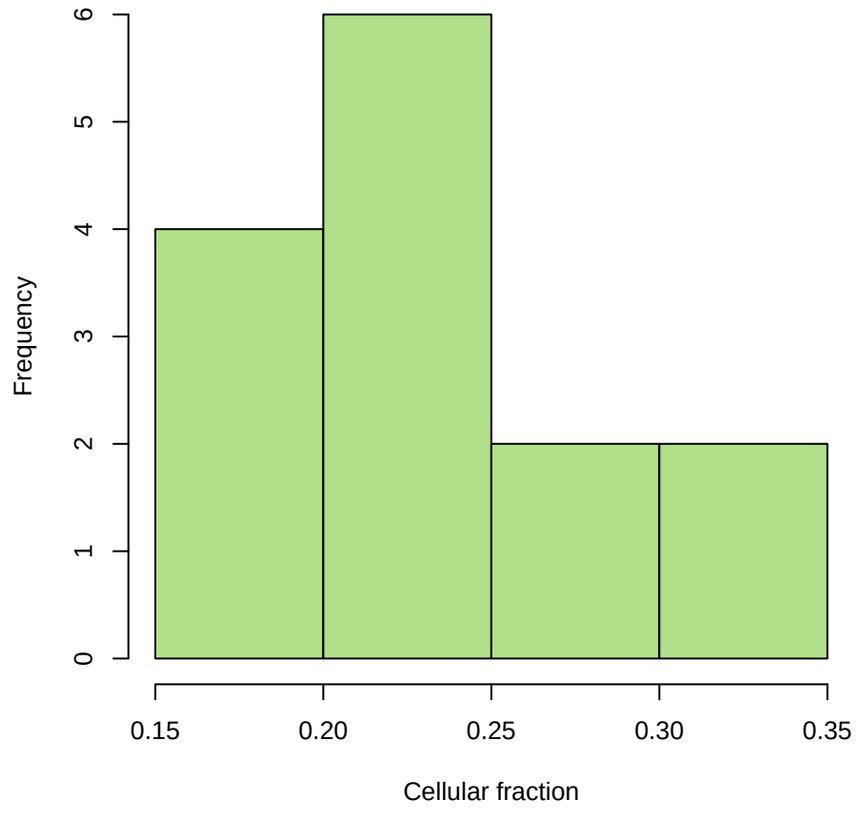

SCNA−fit log−likelihood: −3399.81
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1
2
3
4
5
6
0
10
20
30
40
50
60
SNV Index

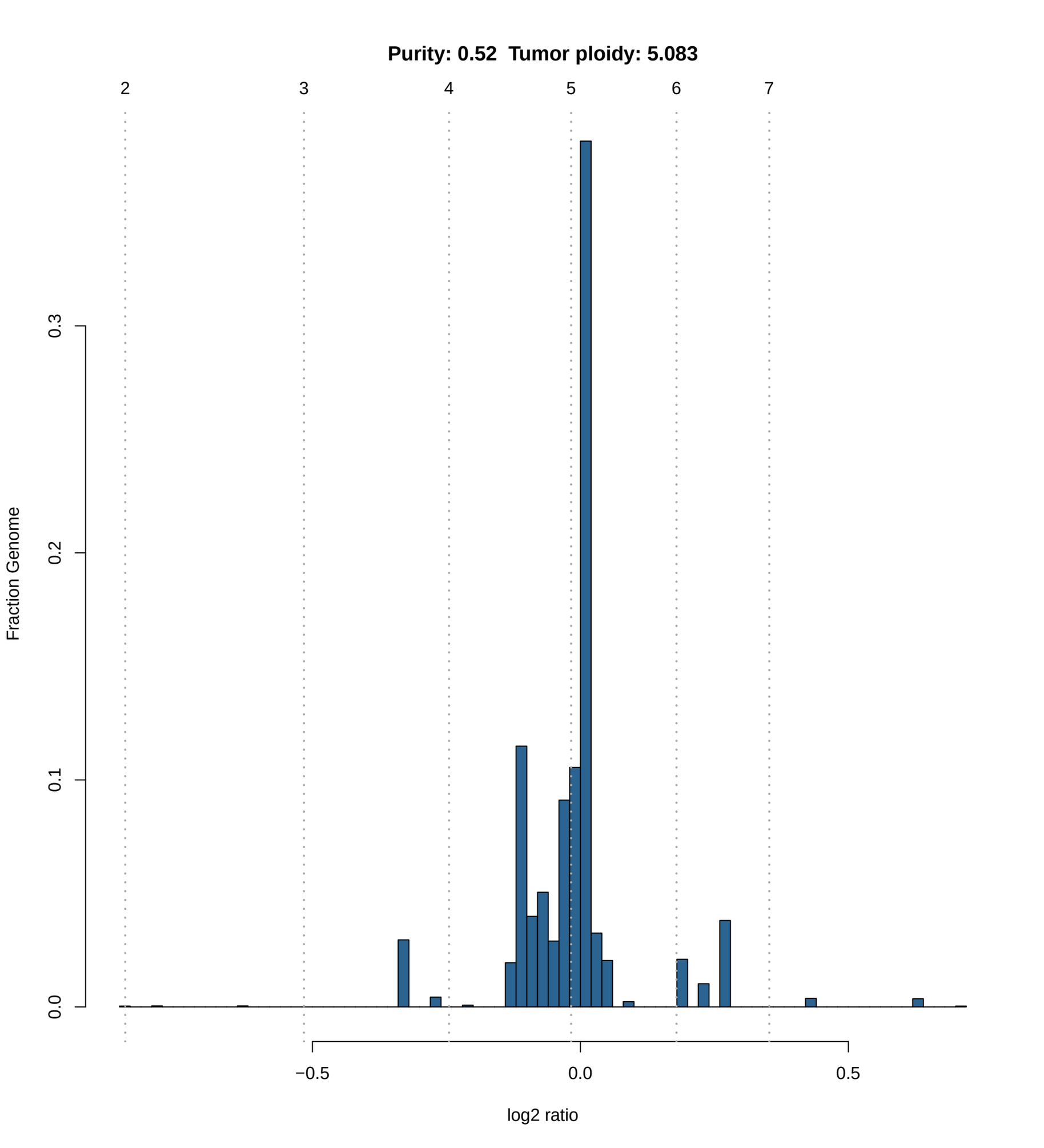

Maximum Likelihood Copy Number
0
1
2
3
4
0
10
20
30
40
50
60
SNV Index

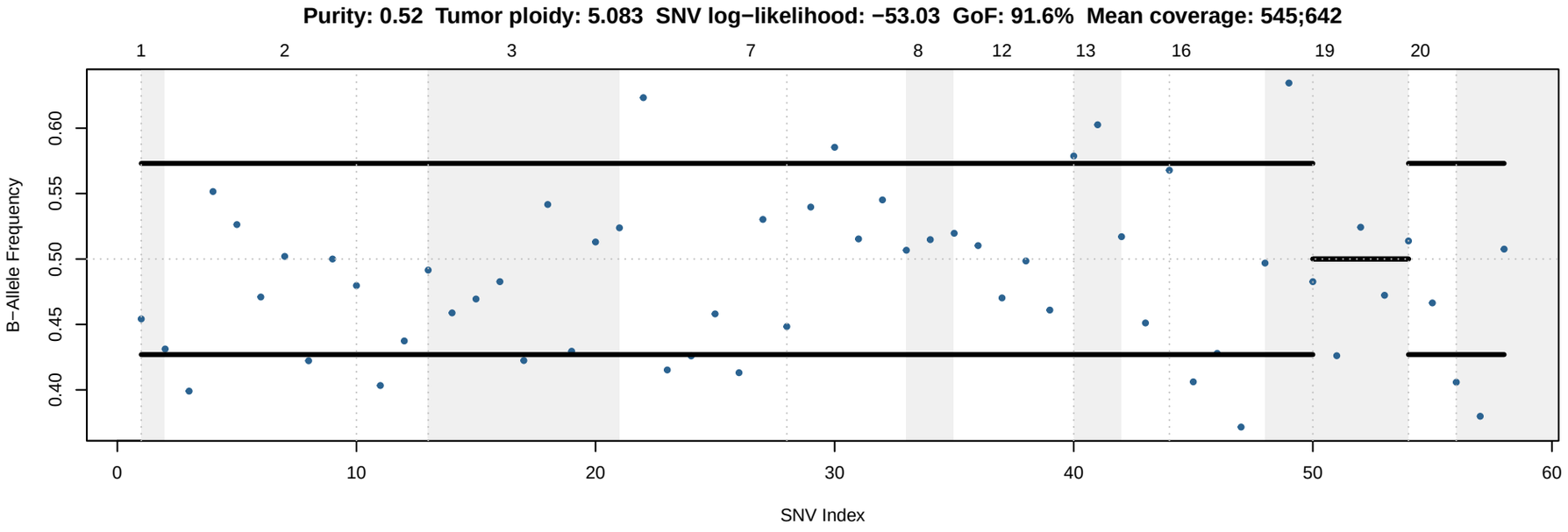

3m2
4m2
3m1
Allelic fraction (germline)
Copy Number log−ratio
0.40
0.45
0.50
0.55
0.60
−0.4
−0.2
0.0
0.2
0.4

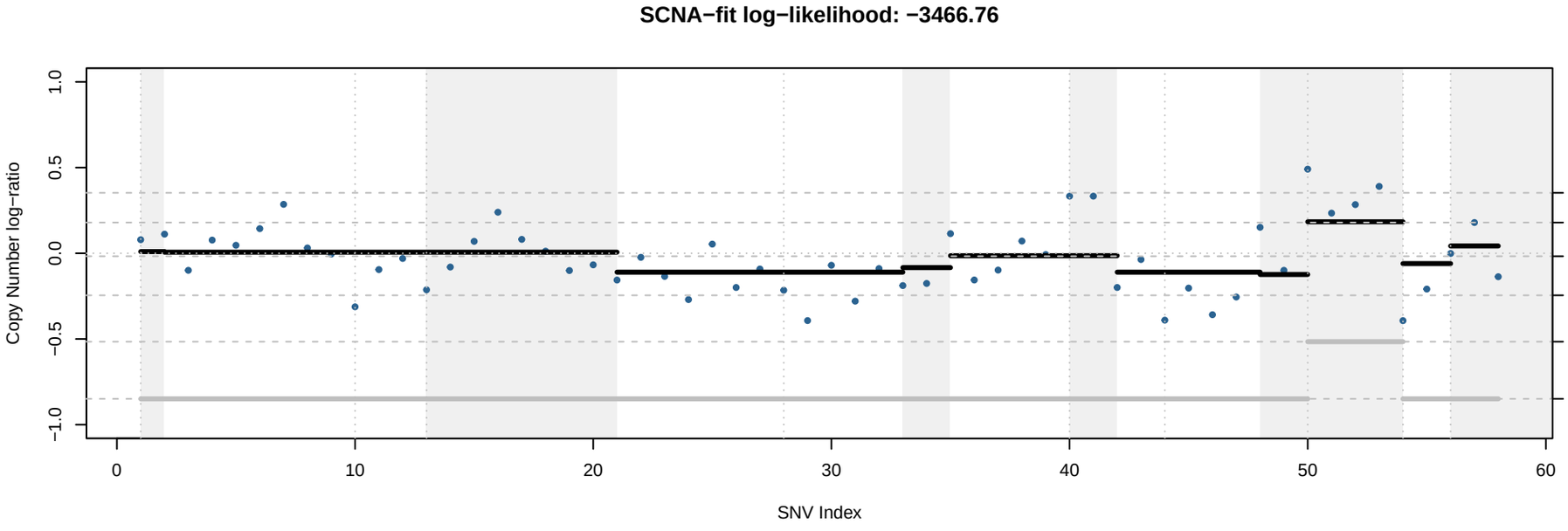

Coverage (log2)
Allelic fraction
7.0
7.5
8.0
8.5
9.0
9.5
10.0
0.1
0.2
0.3
0.4
0.5
0.6

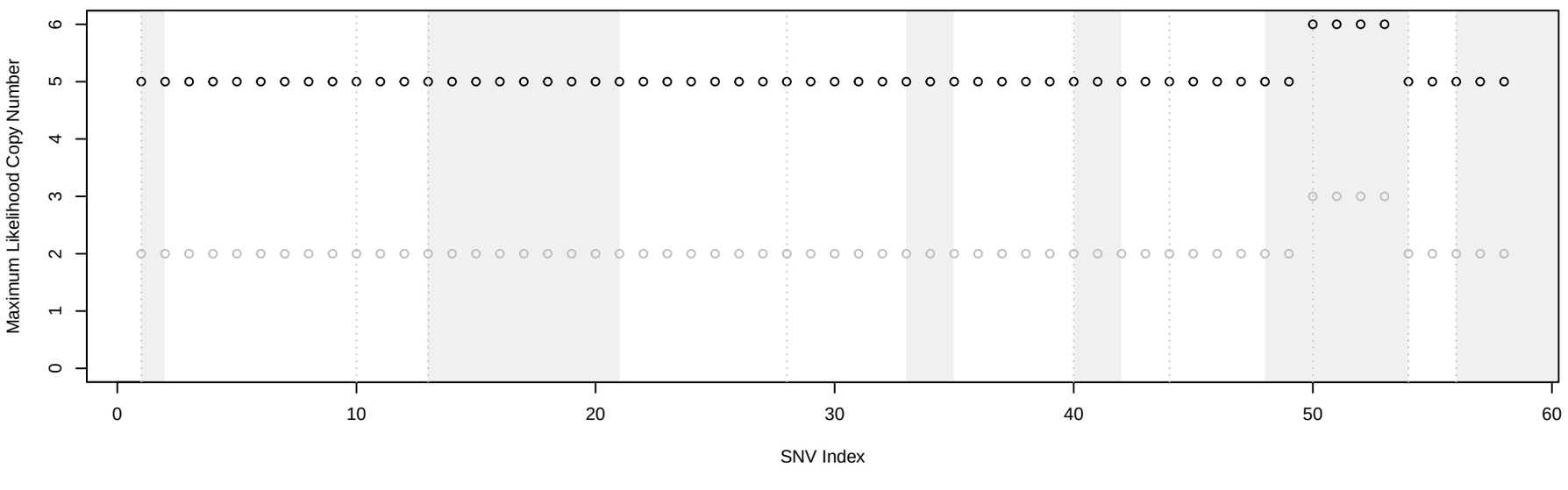

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.035
0.040
0.045
0.050
0.055
0.060
0.065
−0.4
−0.2
0.0
0.2
0.4

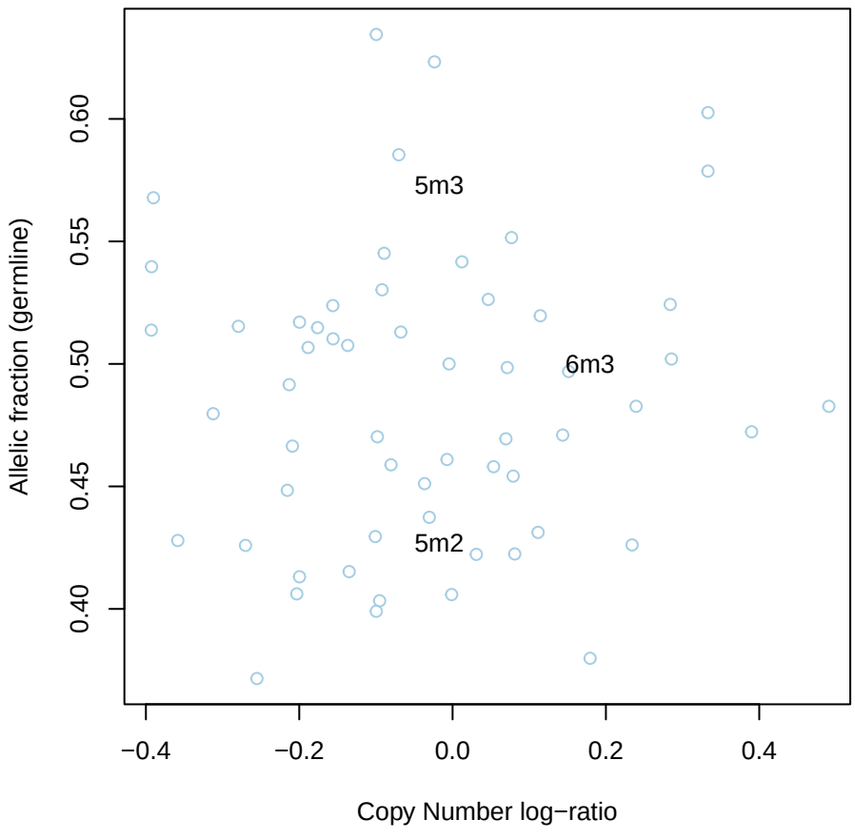

Frequency
Cellular fraction
0
1
2
3
4
5
6
0.15
0.20
0.25
0.30
0.35

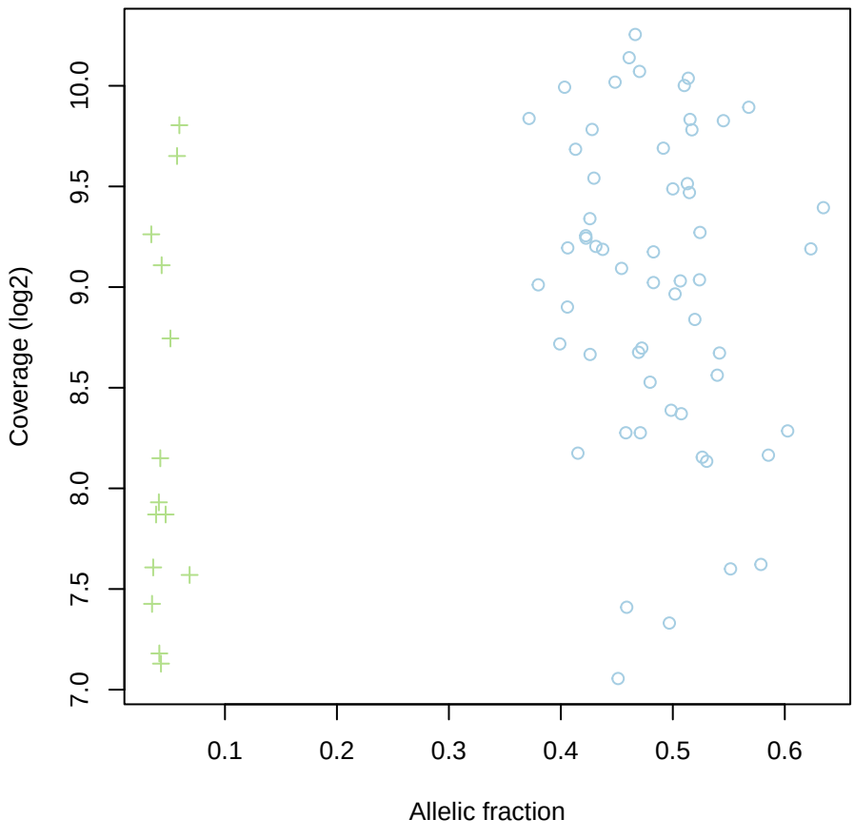

Purity: 0.52 Tumor ploidy: 5.083
2
3
4
5
6
7
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
log2 ratio

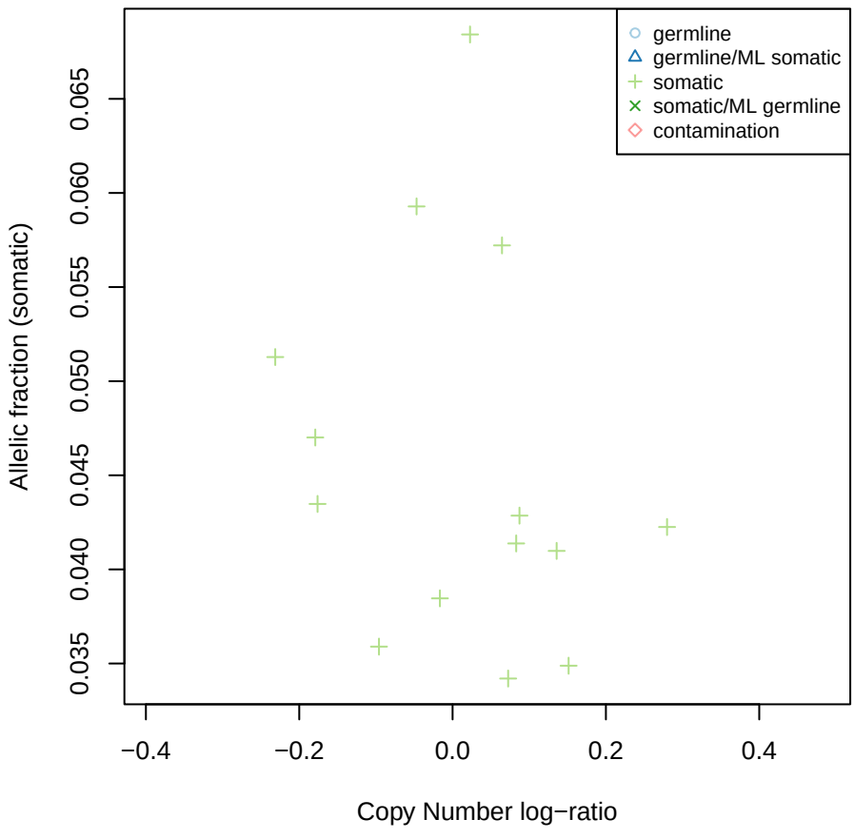

Purity: 0.52 Tumor ploidy: 5.083 SNV log−likelihood: −53.03 GoF: 91.6% Mean coverage: 545;642
1
2
3
7
8
12
13
16
19
20
B−Allele Frequency
0.40
0.45
0.50
0.55
0.60
0
10
20
30
40
50
60
SNV Index

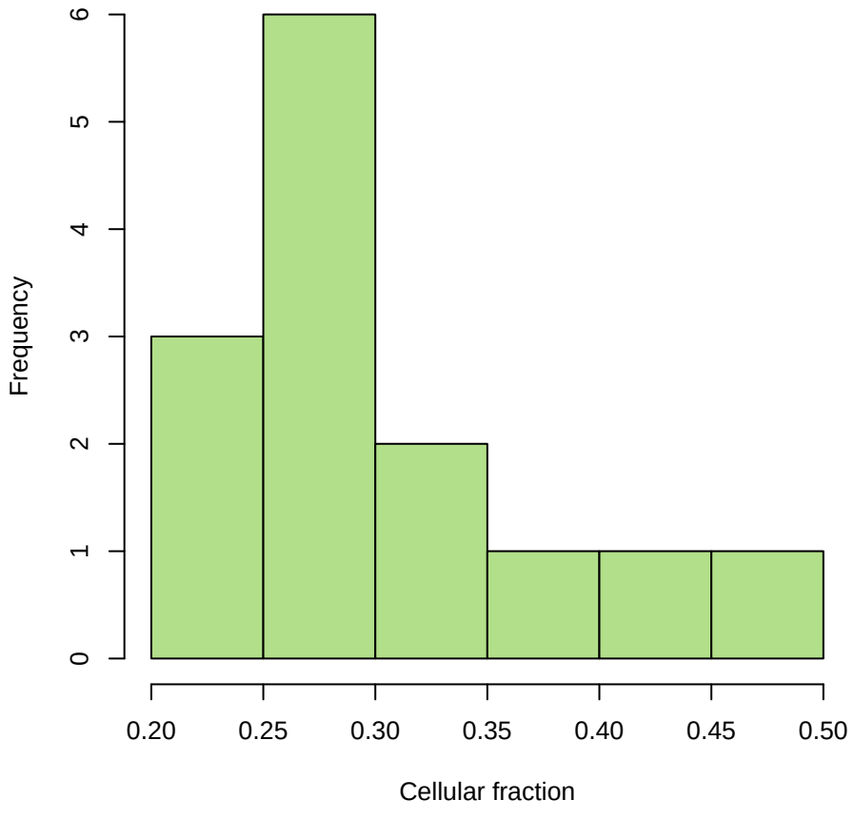

SCNA−fit log−likelihood: −3466.76
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
2
3
4
5
6
7
0
10
20
30
40
50
60
SNV Index

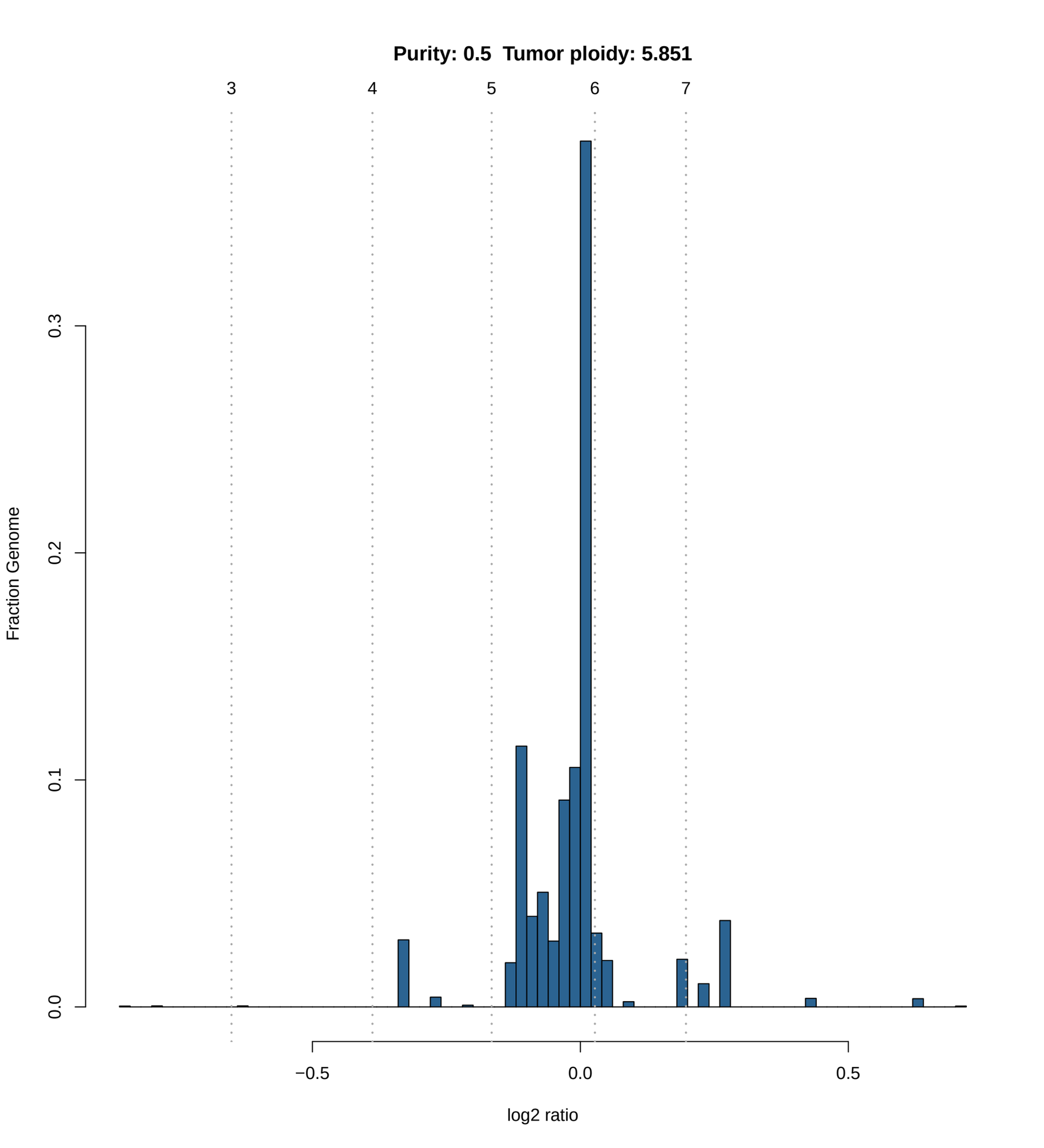

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
0
10
20
30
40
50
60
SNV Index

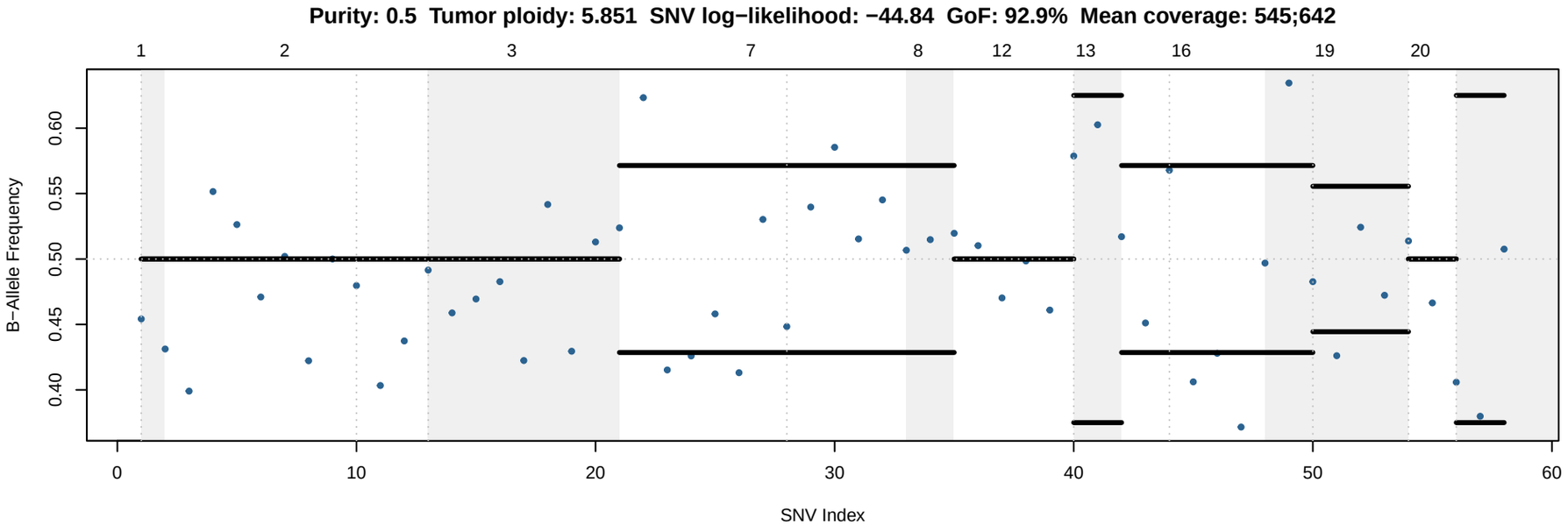

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
5m3
6m3
5m2
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

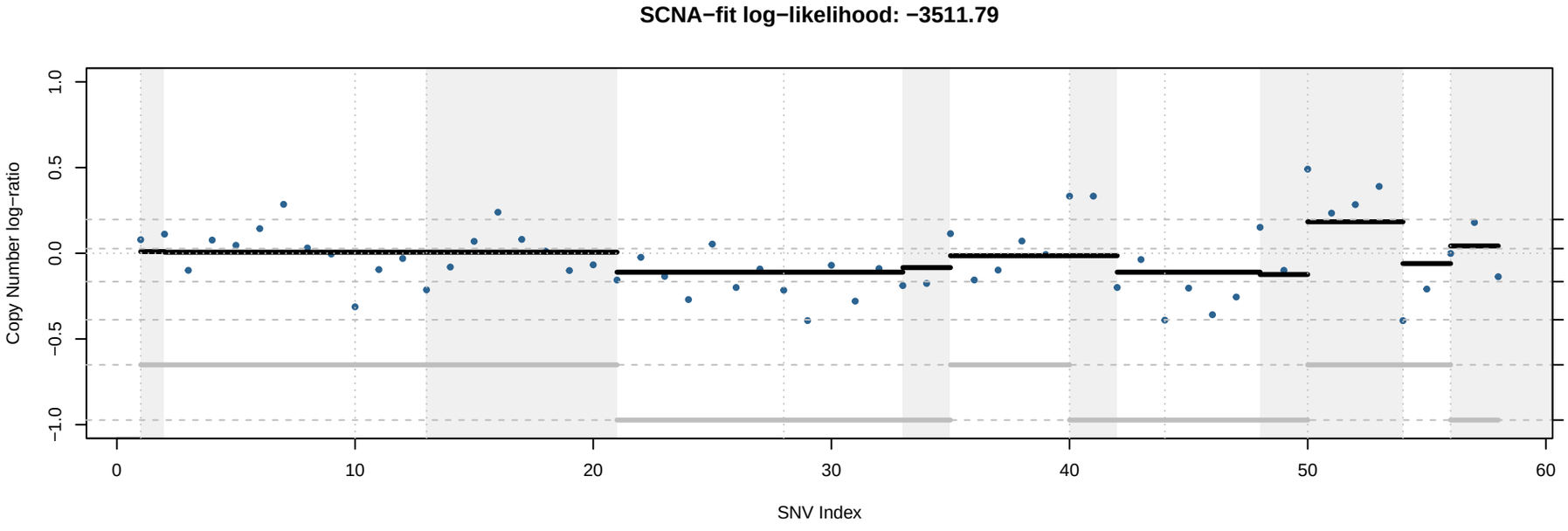

Coverage (log2)
7.0
7.5
8.0
8.5
9.0
9.5
10.0
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

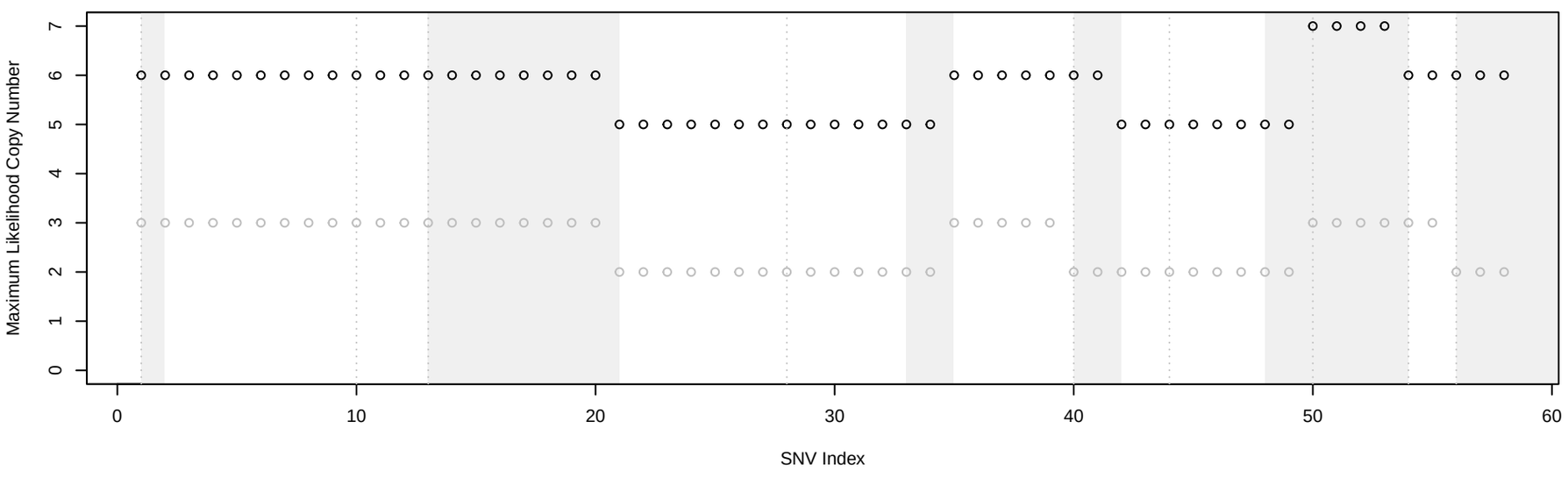

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.035
0.040
0.045
0.050
0.055
0.060
0.065
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

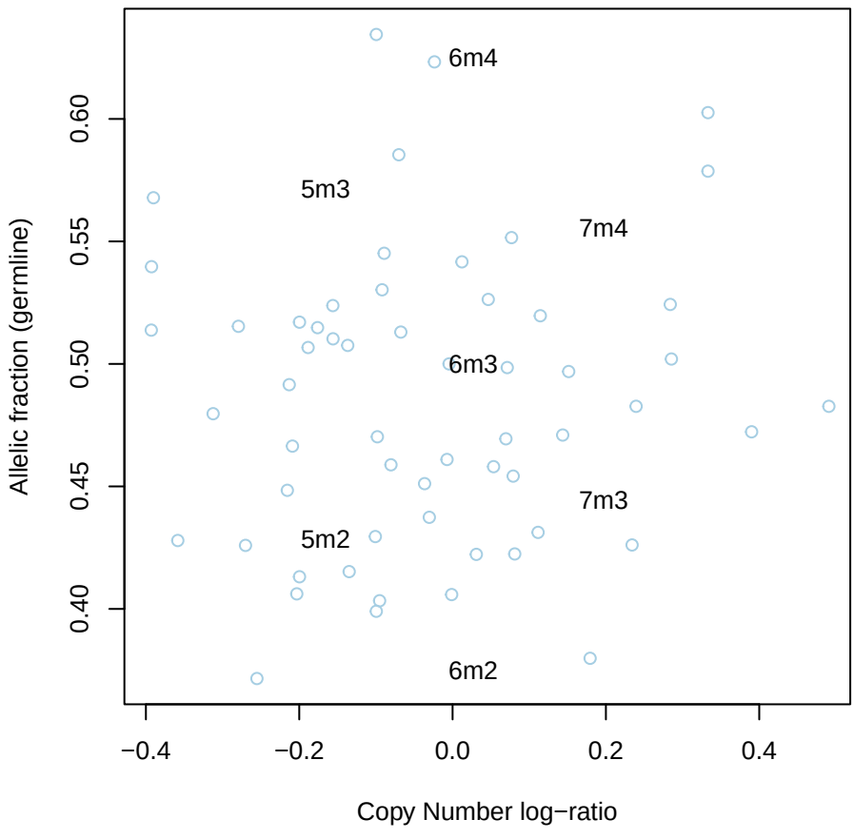

Frequency
0
1
2
3
4
5
6
0.20
0.25
0.30
0.35
0.40
0.45
0.50
Cellular fraction

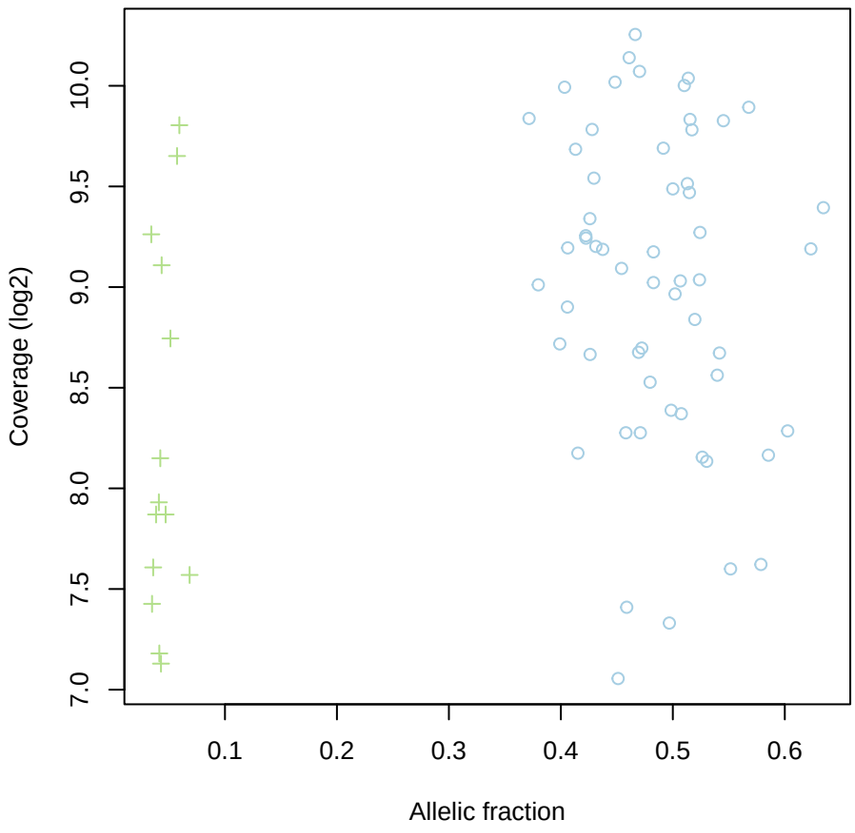

Purity: 0.5 Tumor ploidy: 5.851
3
4
5
6
7
0.0
0.1
0.2
0.3
Fraction Genome
−0.5
0.0
0.5
log2 ratio

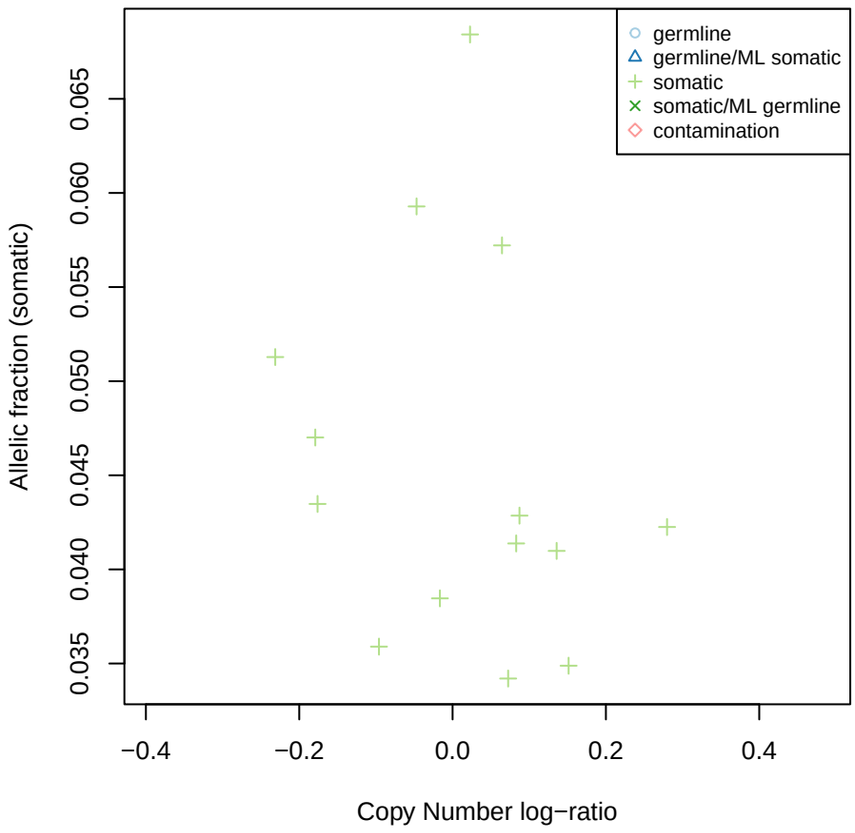

Purity: 0.5 Tumor ploidy: 5.851 SNV log−likelihood: −44.84 GoF: 92.9% Mean coverage: 545;642
1
2
3
7
8
12
13
16
19
20
B−Allele Frequency
0.40
0.45
0.50
0.55
0.60
0
10
20
30
40
50
60
SNV Index

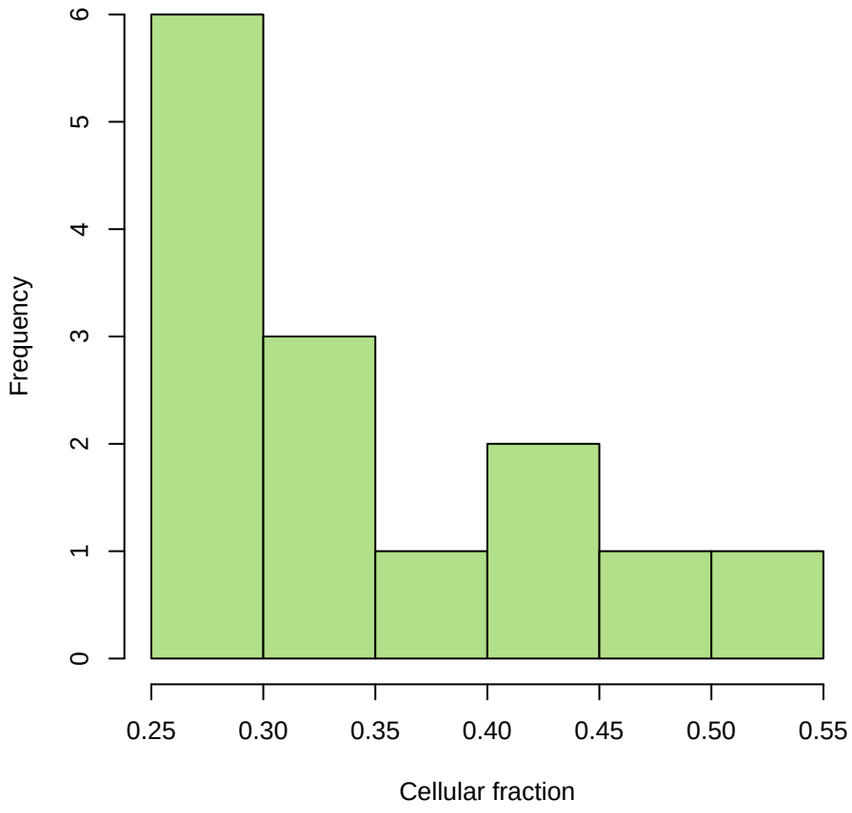

SCNA−fit log−likelihood: −3511.79
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
2
3
4
5
6
7
0
10
20
30
40
50
60
SNV Index

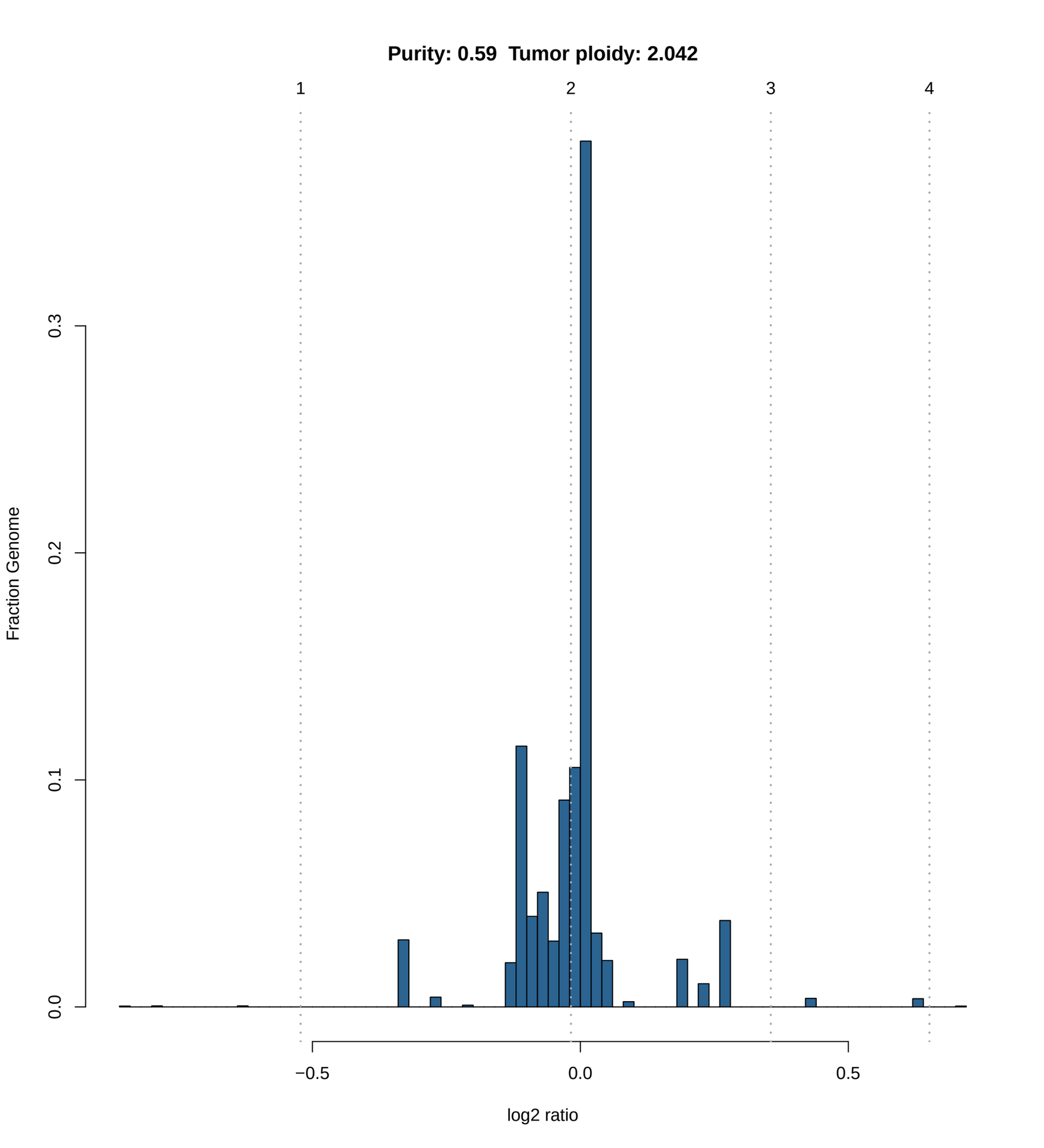

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
7
0
10
20
30
40
50
60
SNV Index

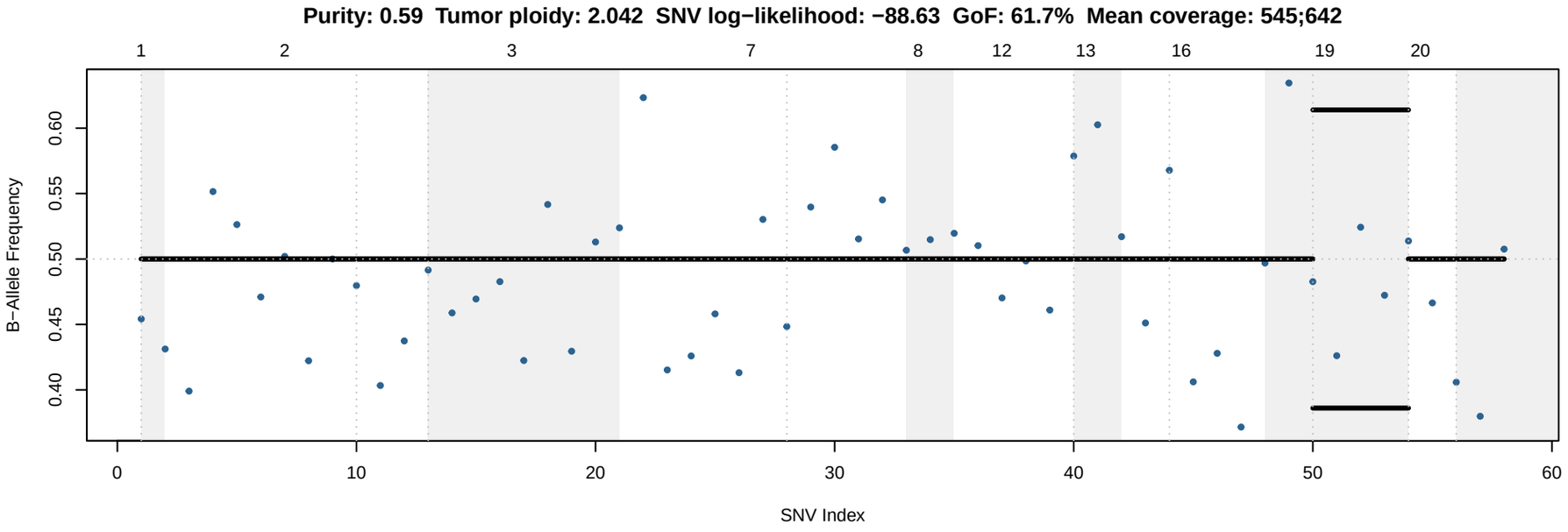

6m4
5m3
7m4
6m3
7m3
5m2
6m2
Allelic fraction (germline)
Copy Number log−ratio

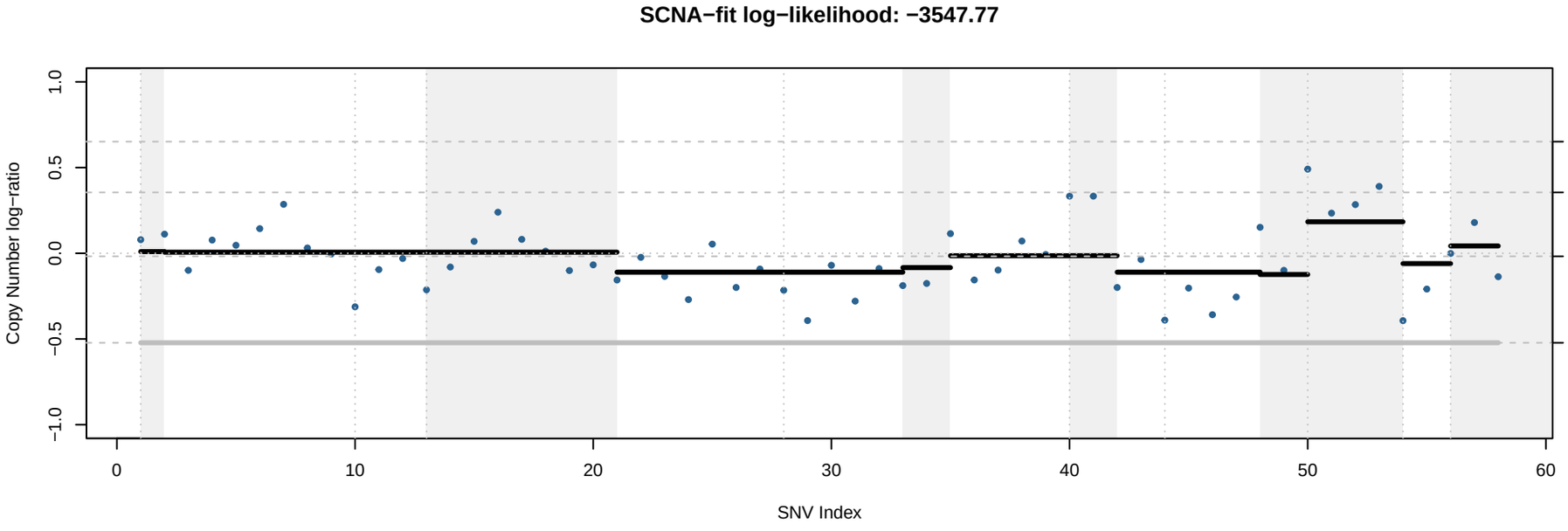

Coverage (log2)
Allelic fraction

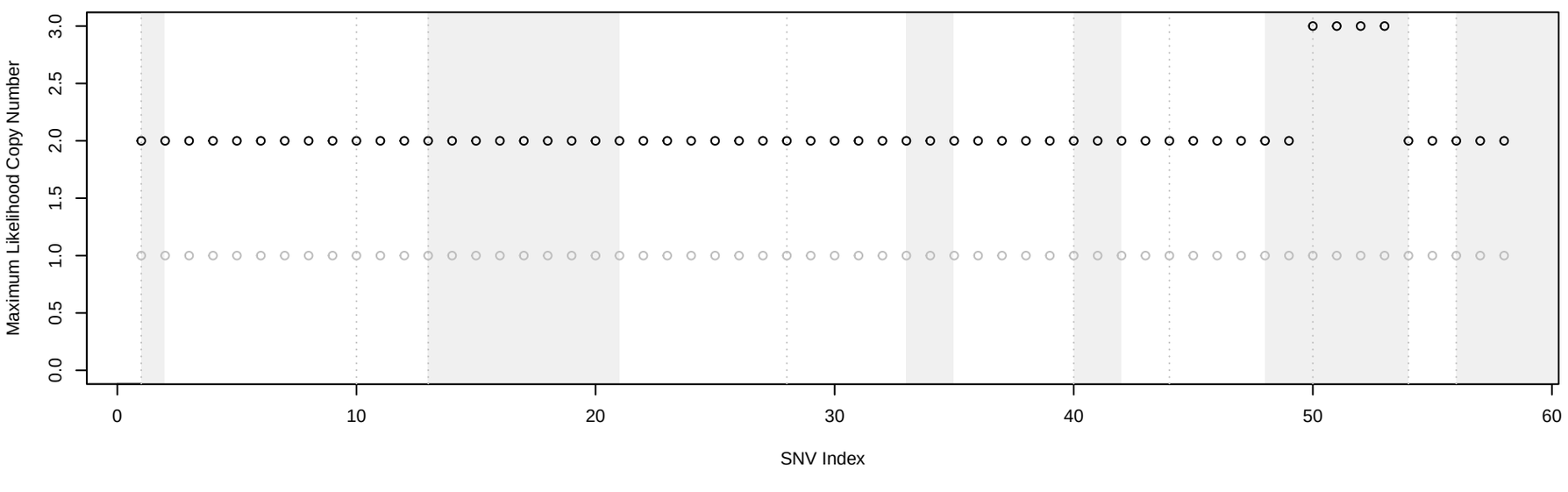

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

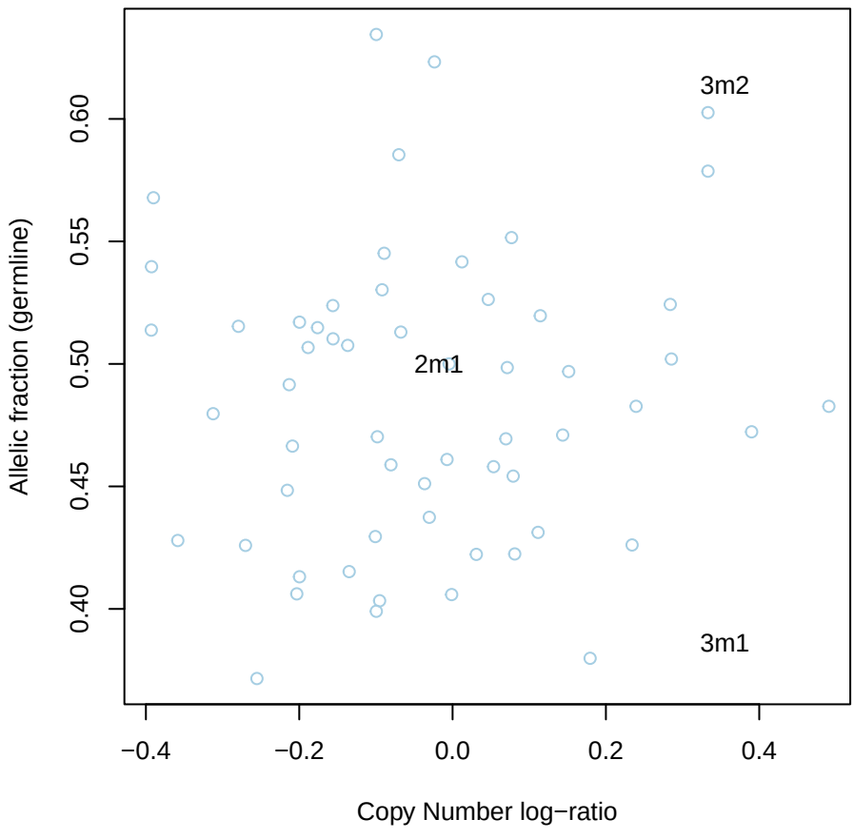

Frequency
Cellular fraction

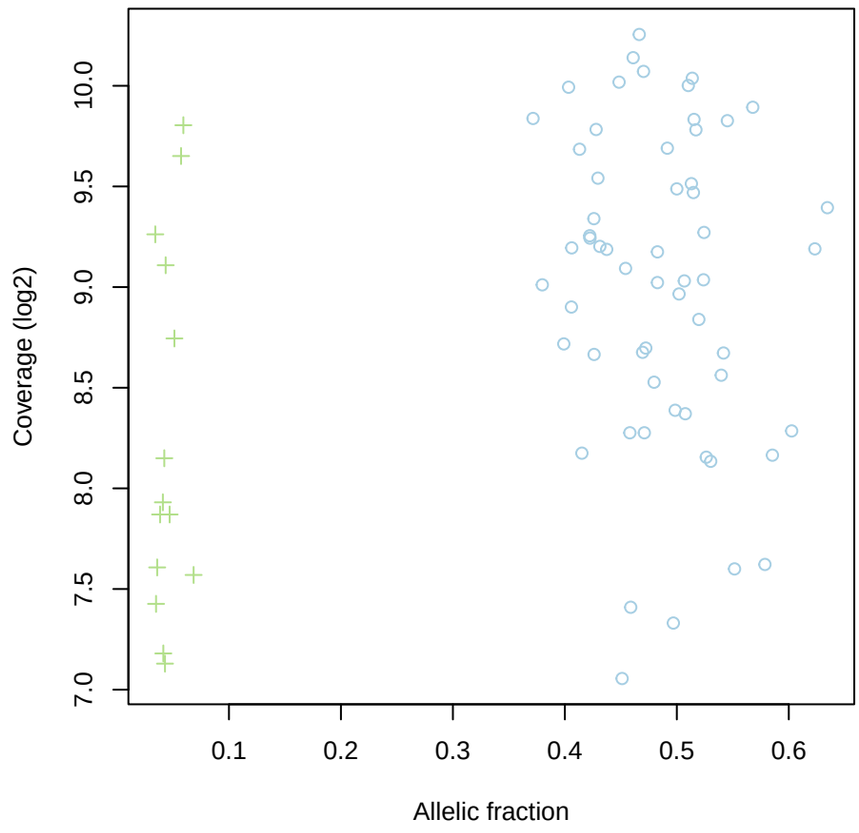

Purity: 0.59 Tumor ploidy: 2.042
1
2
3
4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
log2 ratio

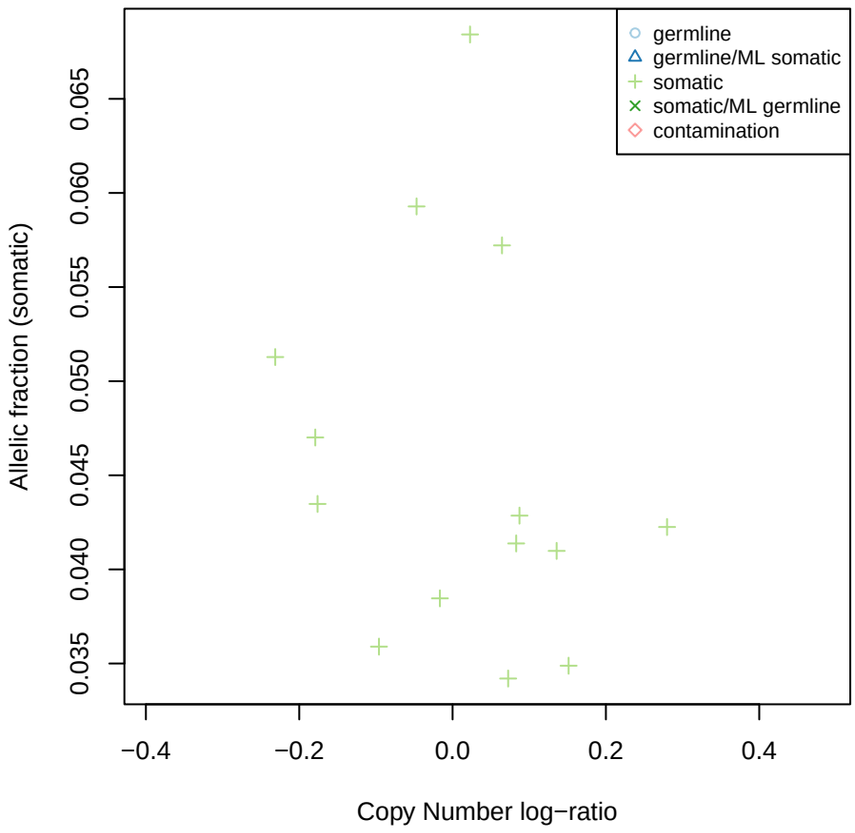

Purity: 0.59 Tumor ploidy: 2.042 SNV log−likelihood: −88.63 GoF: 61.7% Mean coverage: 545;642
1
2
3
7
8
12
13
16
19
20
B−Allele Frequency
0.40
0.45
0.50
0.55
0.60
0
10
20
30
40
50
60
SNV Index

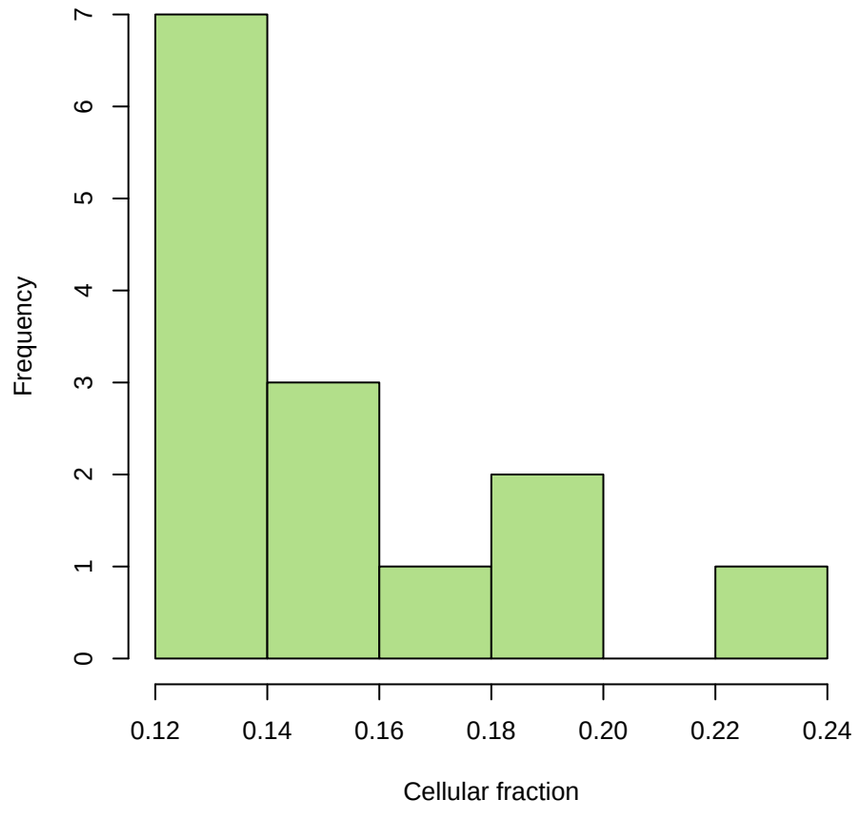

SCNA−fit log−likelihood: −3547.77
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1
2
3
4
0
10
20
30
40
50
60
SNV Index

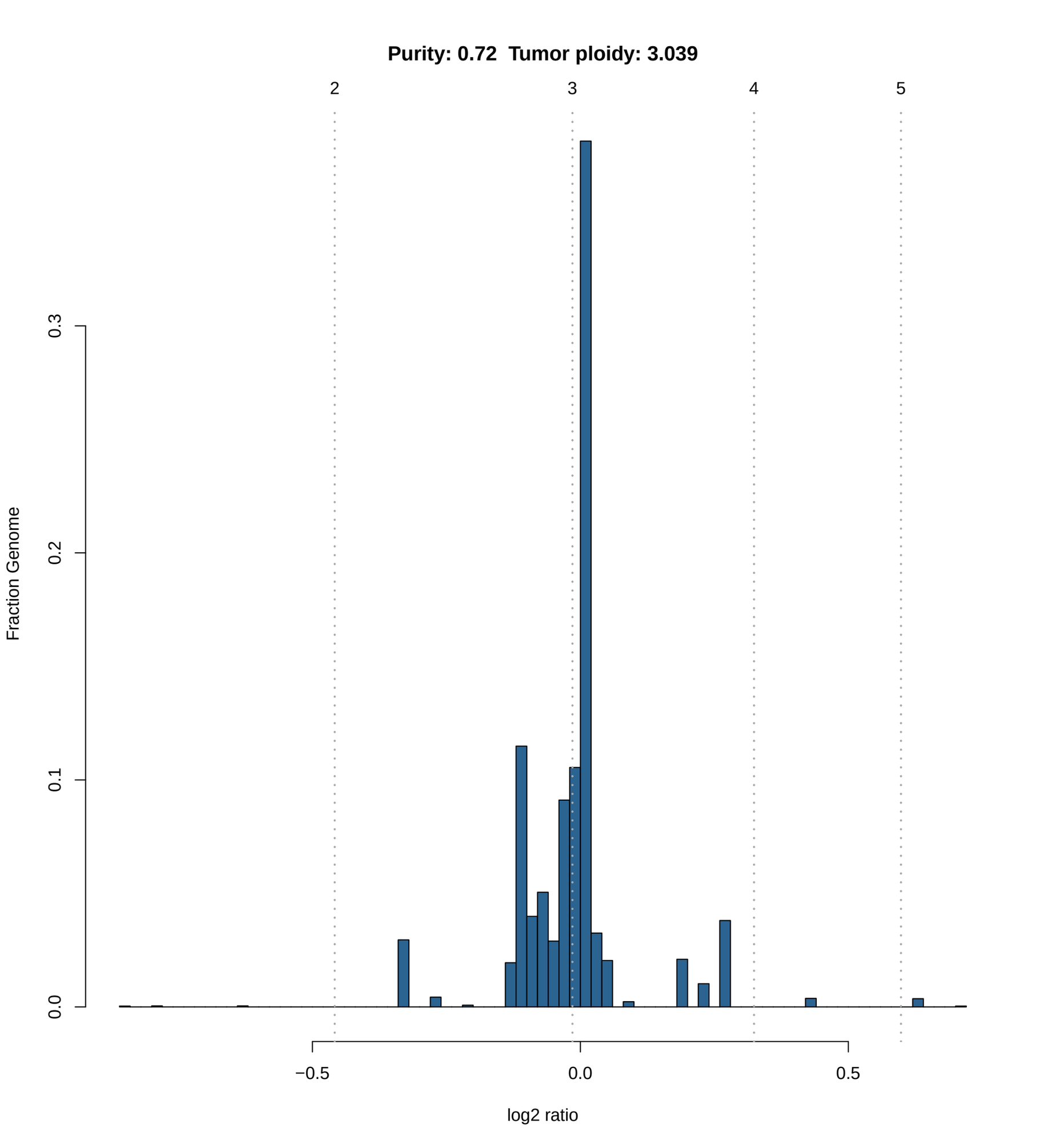

Maximum Likelihood Copy Number
0.0
0.5
1.0
1.5
2.0
2.5
3.0
0
10
20
30
40
50
60
SNV Index

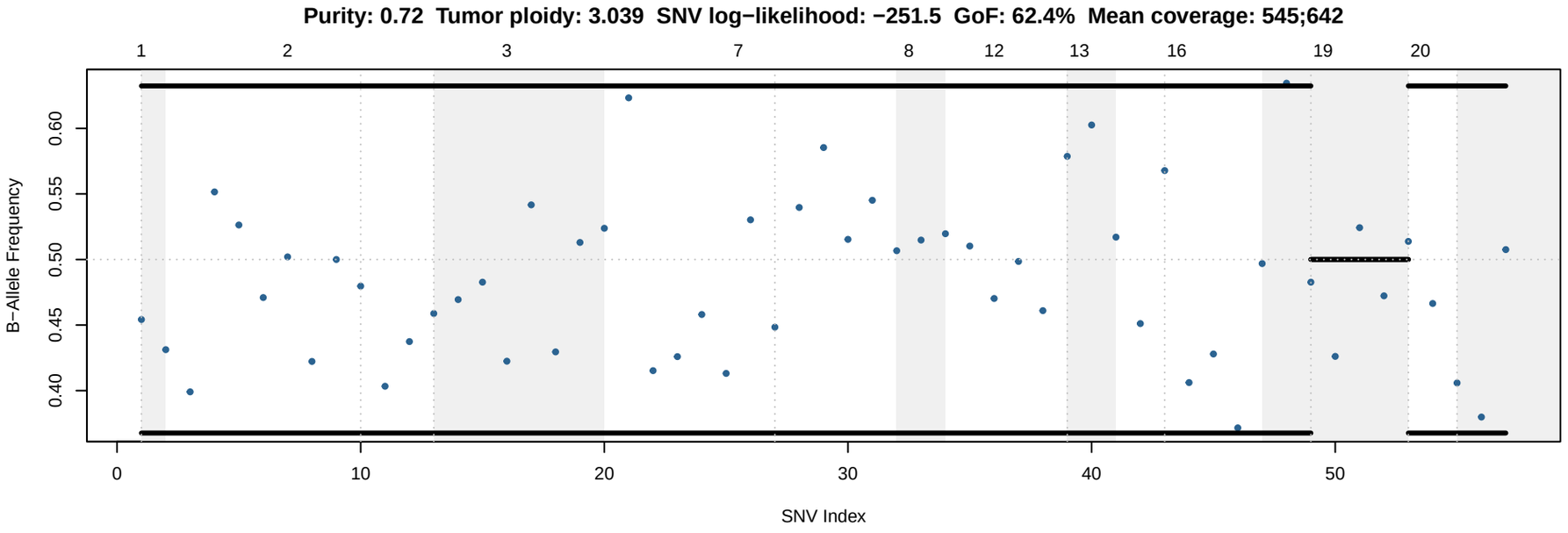

3m2
2m1
3m1
Allelic fraction (germline)
Copy Number log−ratio
0.40
0.45
0.50
0.55
0.60
−0.4
−0.2
0.0
0.2
0.4

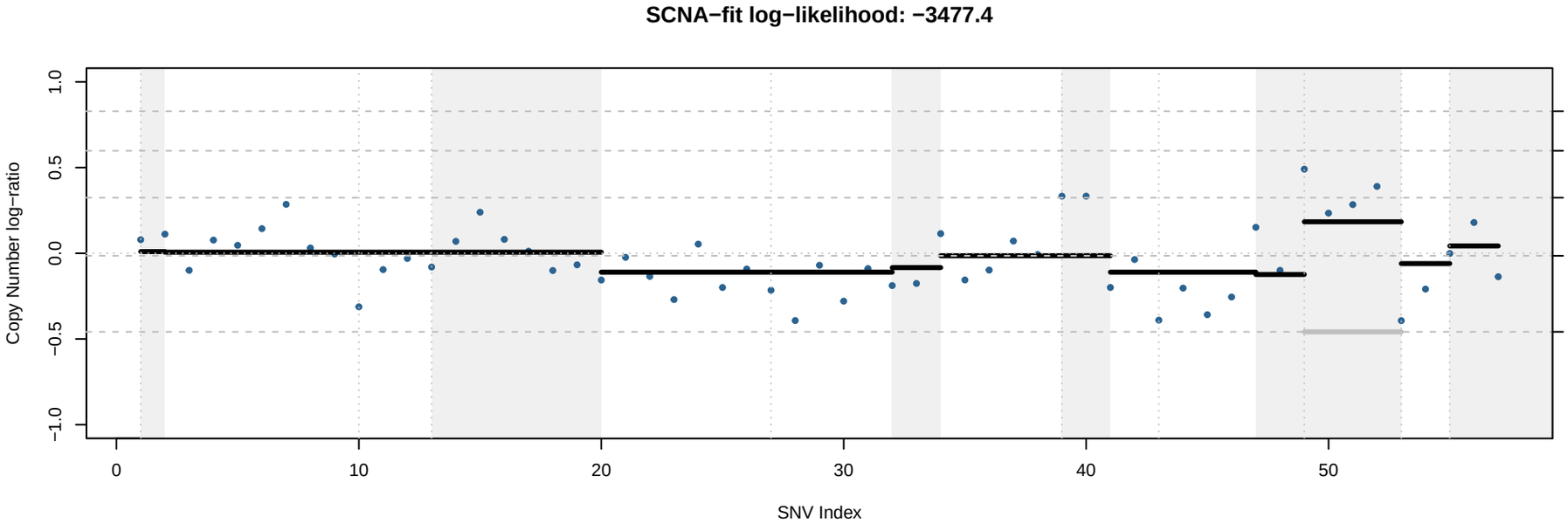

Coverage (log2)
Allelic fraction
7.0
7.5
8.0
8.5
9.0
9.5
10.0
0.1
0.2
0.3
0.4
0.5
0.6


germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.035
0.040
0.045
0.050
0.055
0.060
0.065
−0.4
−0.2
0.0
0.2
0.4


Frequency
Cellular fraction
0
1
2
3
4
5
6
7
0.12
0.14
0.16
0.18
0.20
0.22
0.24


Purity: 0.72 Tumor ploidy: 3.039
2
3
4
5
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
0.0
0.5
log2 ratio


Purity: 0.72 Tumor ploidy: 3.039 SNV log−likelihood: −251.5 GoF: 62.4% Mean coverage: 545;642
1
2
3
7
8
12
13
16
19
20
B−Allele Frequency
0.40
0.45
0.50
0.55
0.60
0
10
20
30
40
50
SNV Index


SCNA−fit log−likelihood: −3477.4
Copy Number log−ratio
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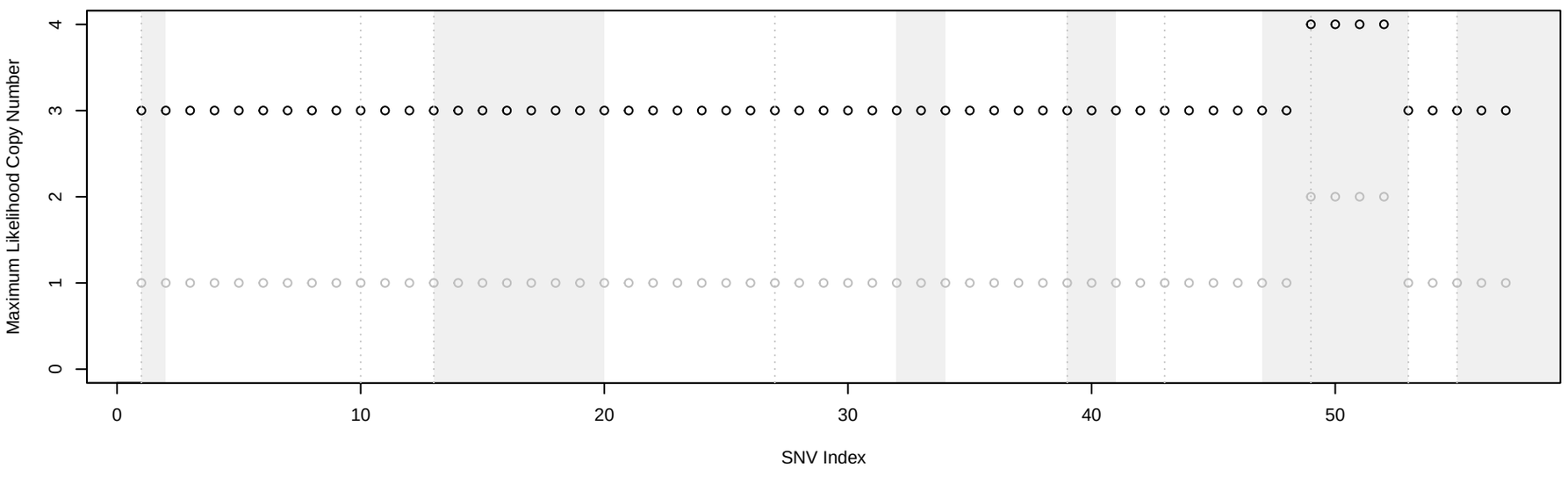
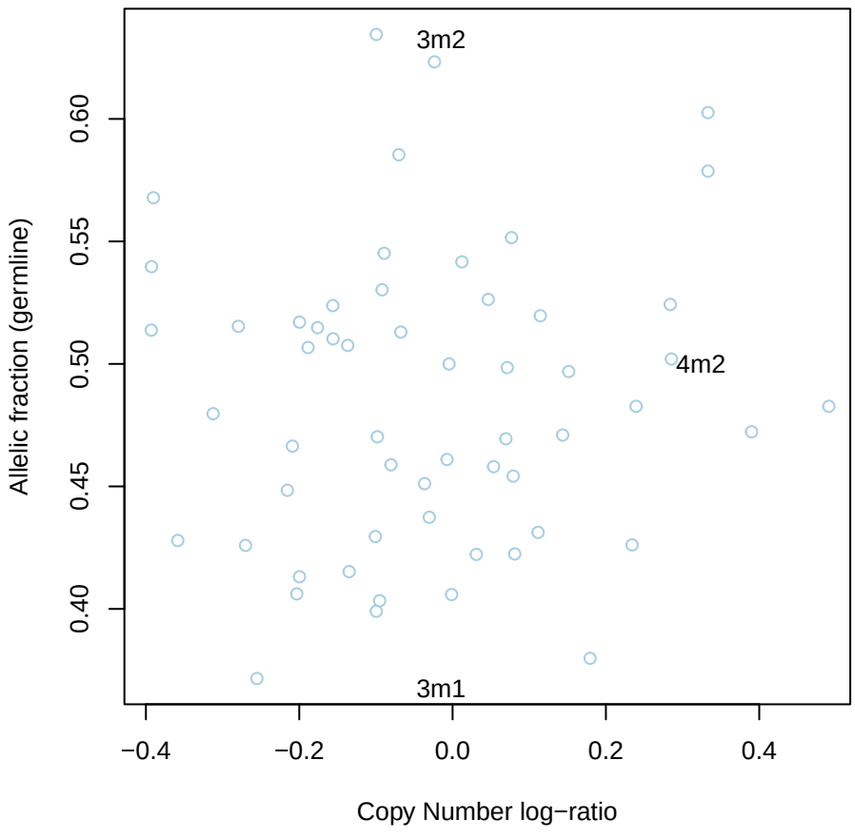
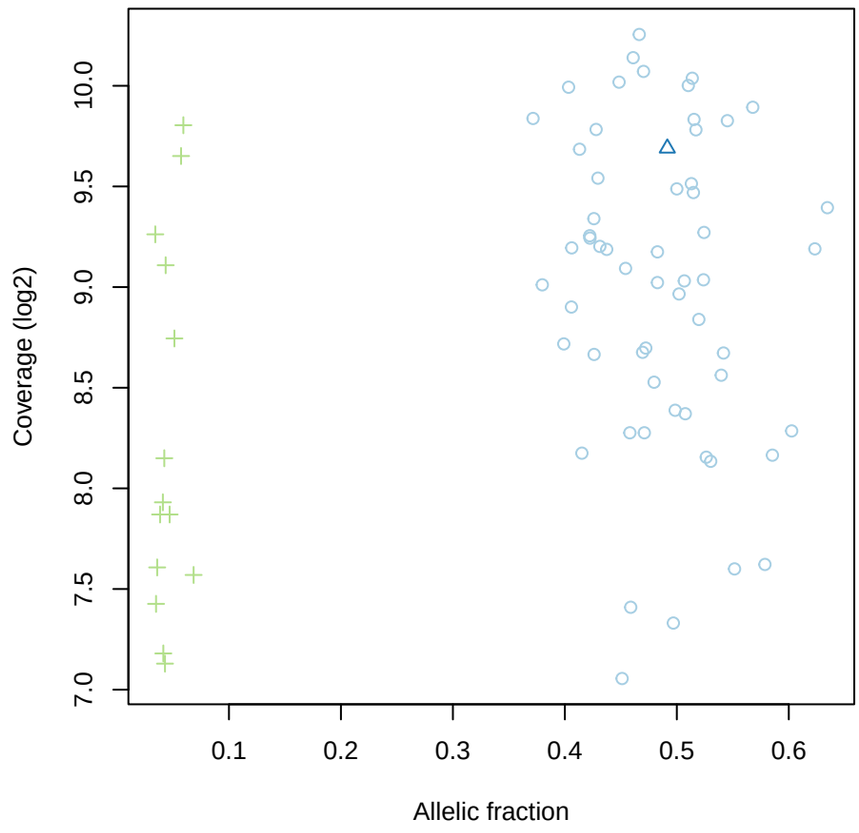
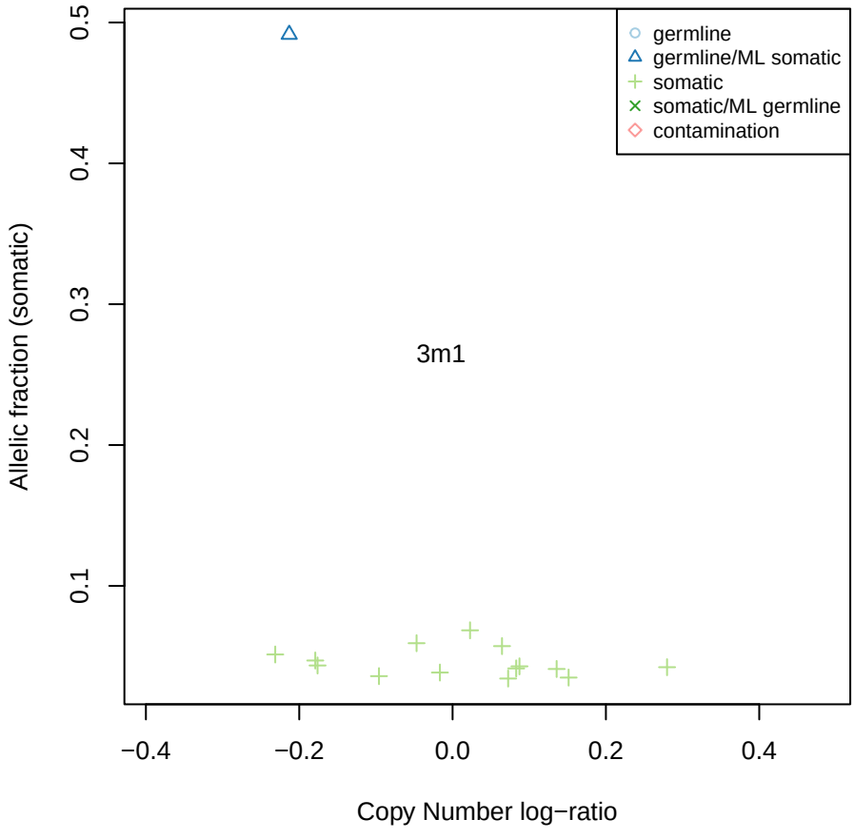
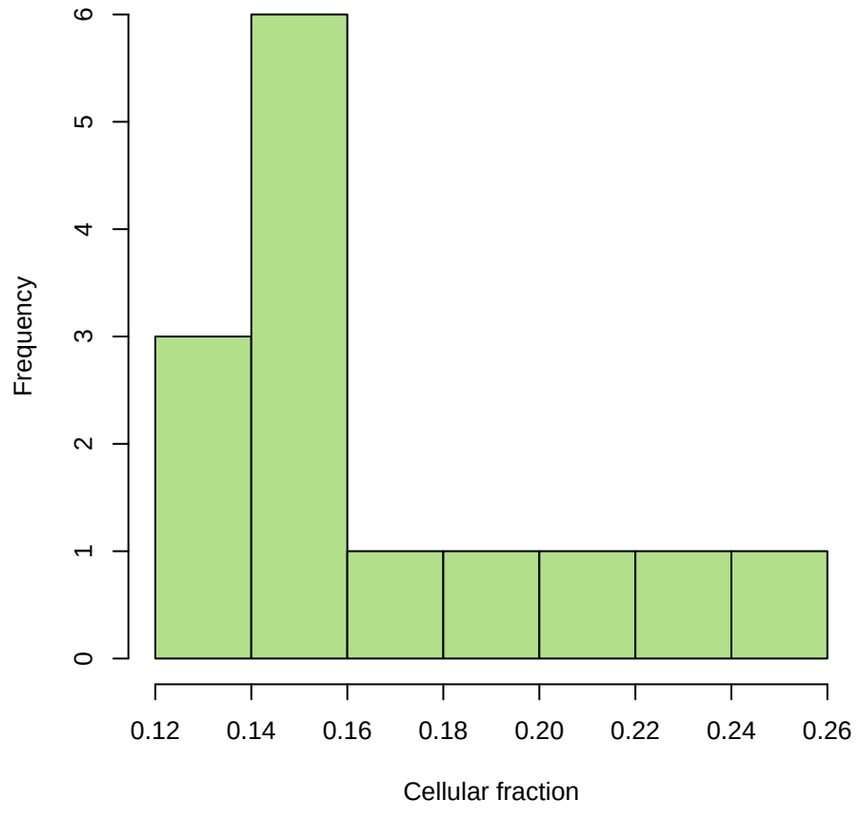
0.5
1.0
2
3
4
5
6
0
10
20
30
40
50
SNV Index


Maximum Likelihood Copy Number
0
1
2
3
4
0
10
20
30
40
50
SNV Index


3m2
4m2
3m1
Allelic fraction (germline)
Copy Number log−ratio
0.40
0.45
0.50
0.55
0.60
−0.4
−0.2
0.0
0.2
0.4


Coverage (log2)
Allelic fraction
7.0
7.5
8.0
8.5
9.0
9.5
10.0
0.1
0.2
0.3
0.4
0.5
0.6


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


Frequency
Cellular fraction
0
1
2
3
4
5
6
0.12
0.14
0.16
0.18
0.20
0.22
0.24
0.26