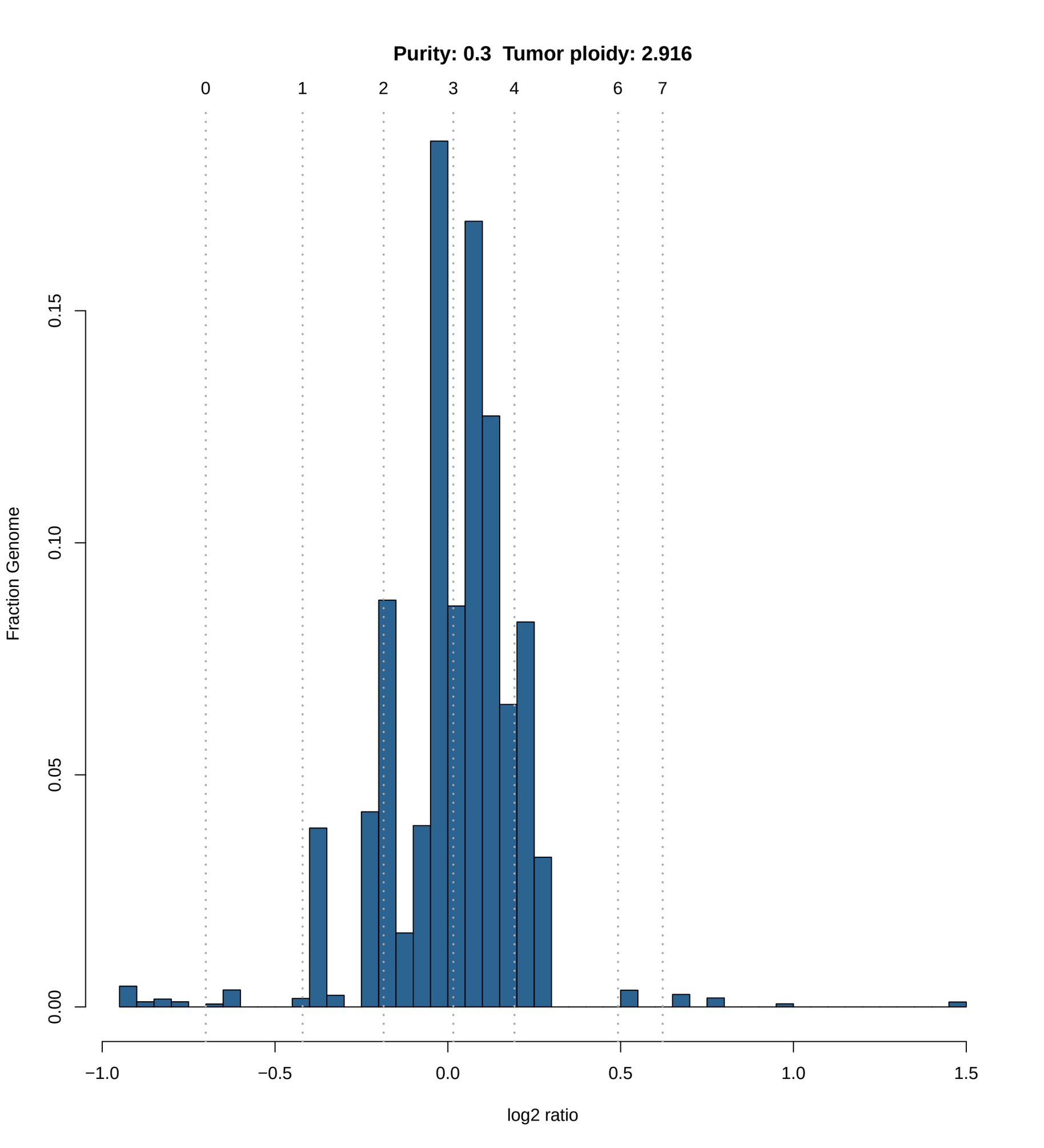
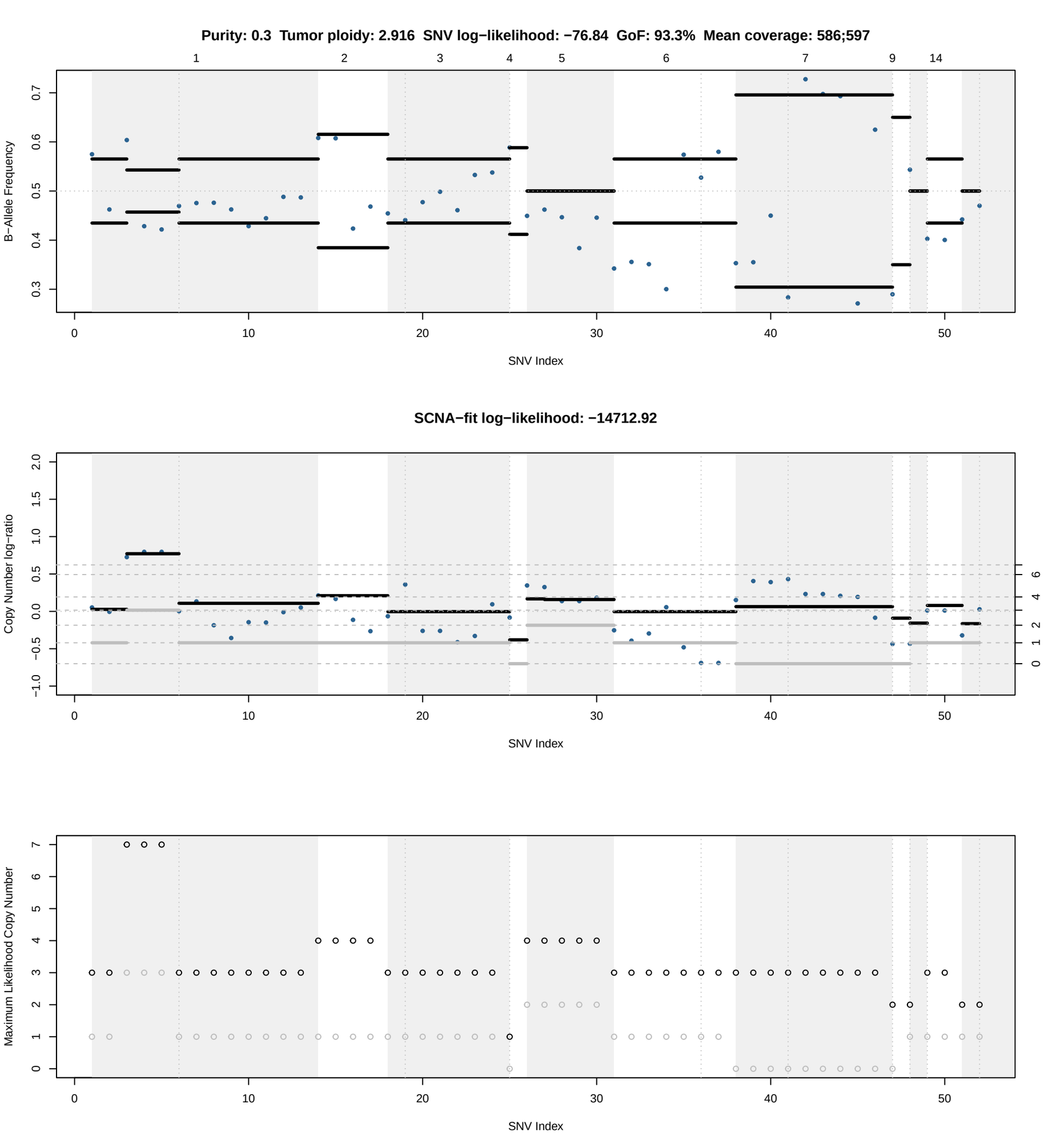
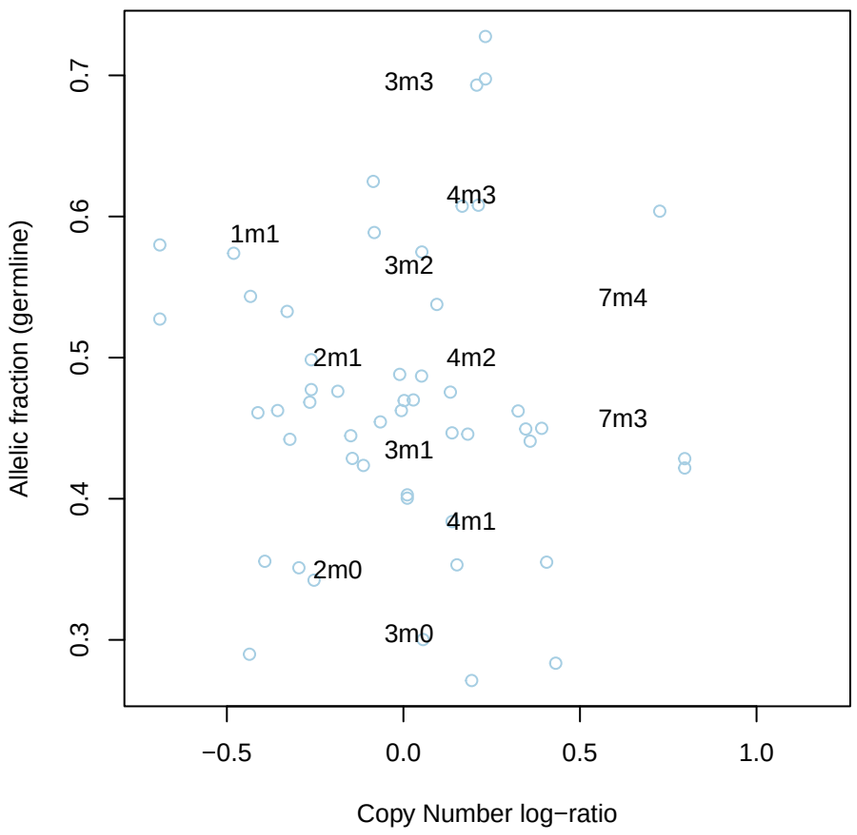
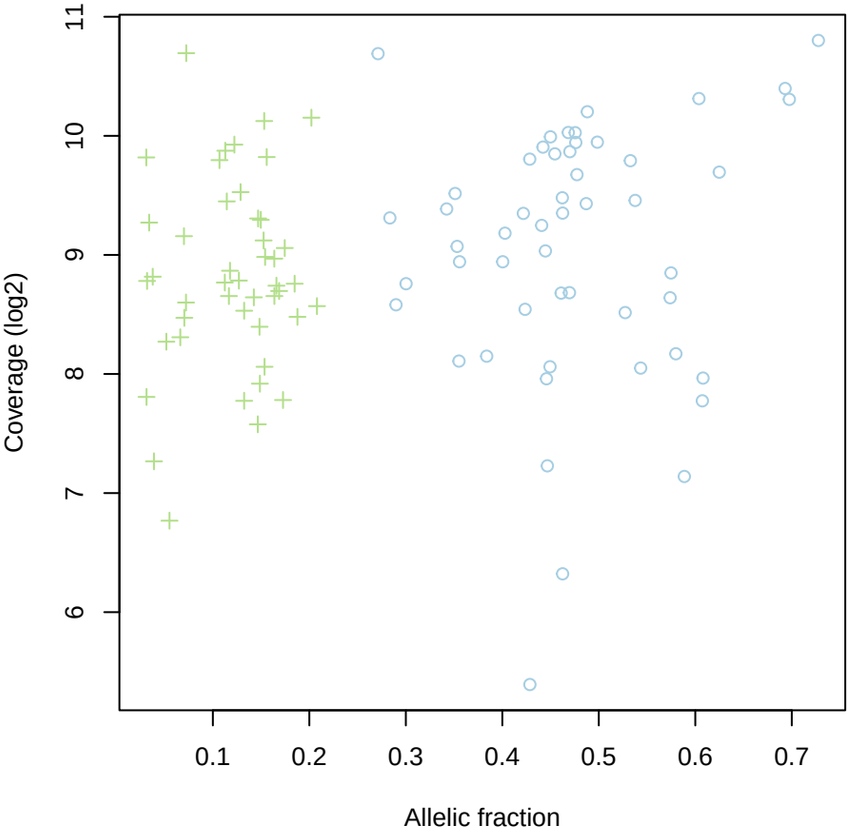
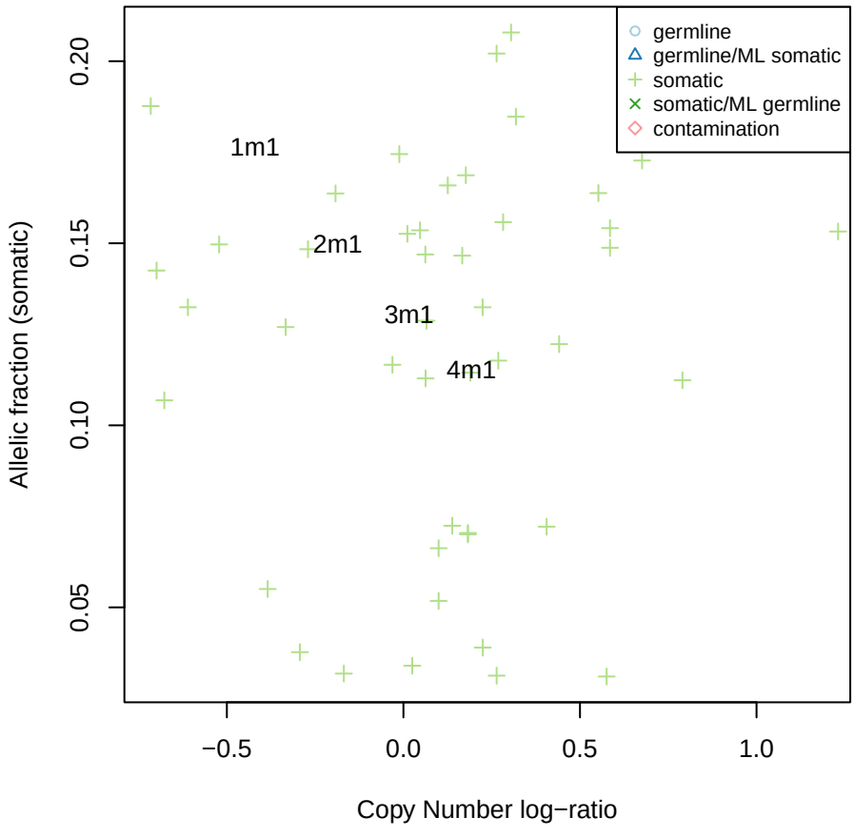
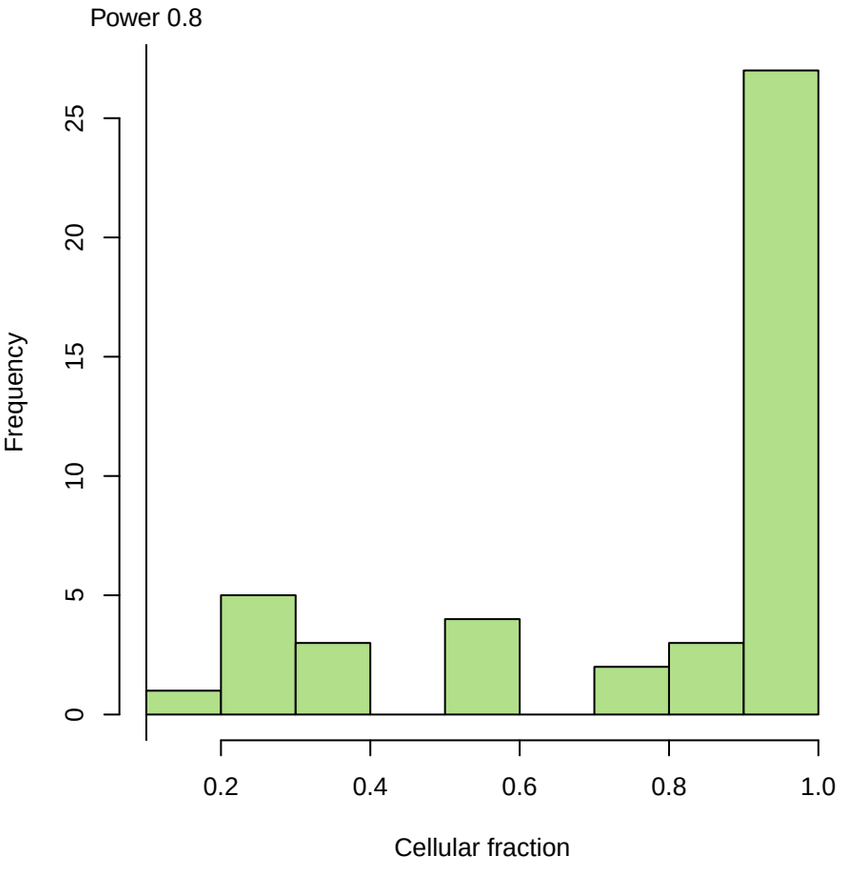

Purity: 0.3 Tumor ploidy: 2.916
0
1
2
3
4
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

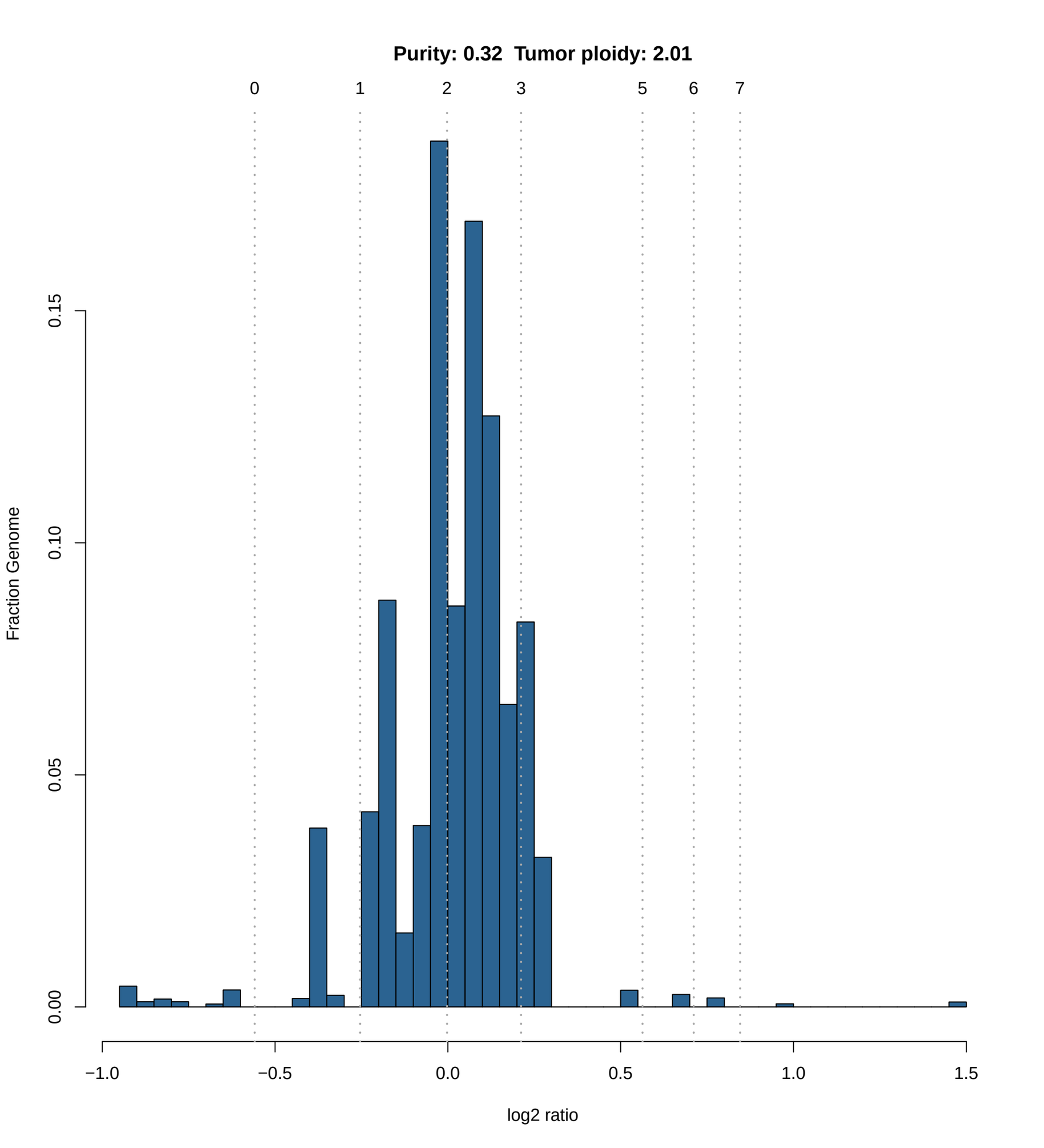

Purity: 0.3 Tumor ploidy: 2.916 SNV log−likelihood: −76.84 GoF: 93.3% Mean coverage: 586;597
1
2
3
4
5
6
7
9
14
B−Allele Frequency
0.3
0.4
0.5
0.6
0.7
0
10
20
30
40
50
SNV Index
SCNA−fit log−likelihood: −14712.92
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
0
1
2
4
6
0
10
20
30
40
50
SNV Index
Maximum Likelihood Copy Number
0
1
2
3
4
5
6
7
0
10
20
30
40
50
SNV Index

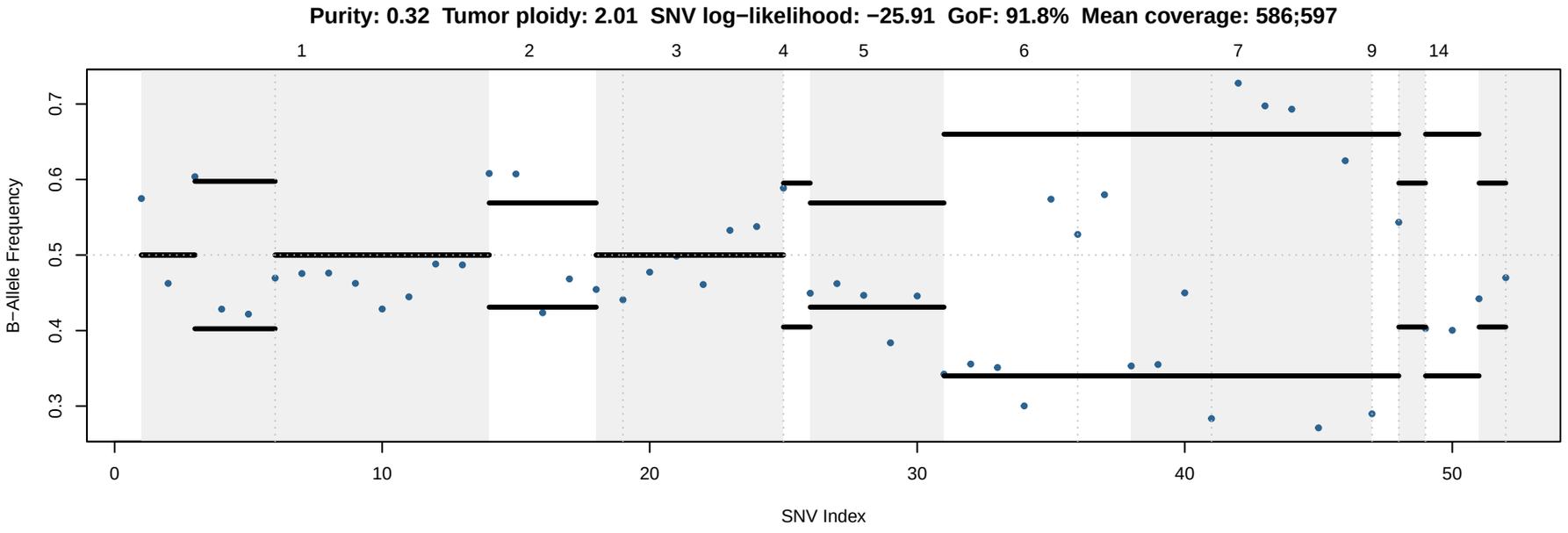

Allelic fraction (germline)
Copy Number log−ratio
1m1
2m1
3m1
4m1
3m2
4m2
3m3
4m3
7m4
7m3
2m0
3m0

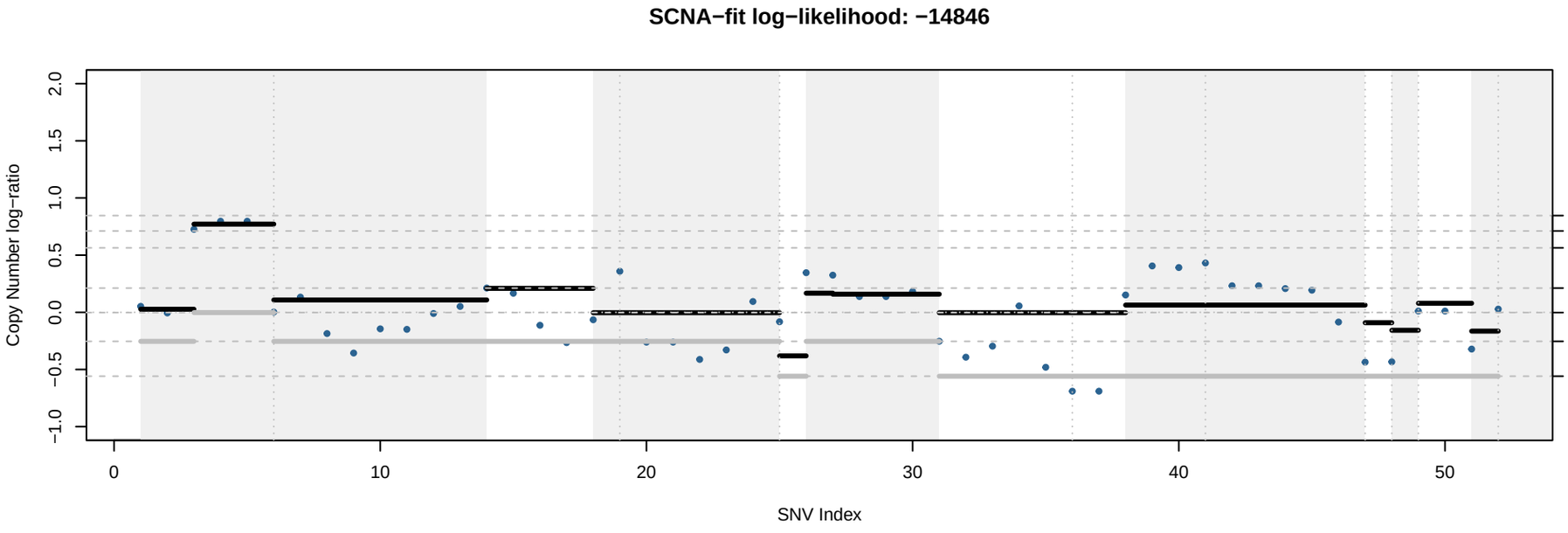

Coverage (log2)
Allelic fraction

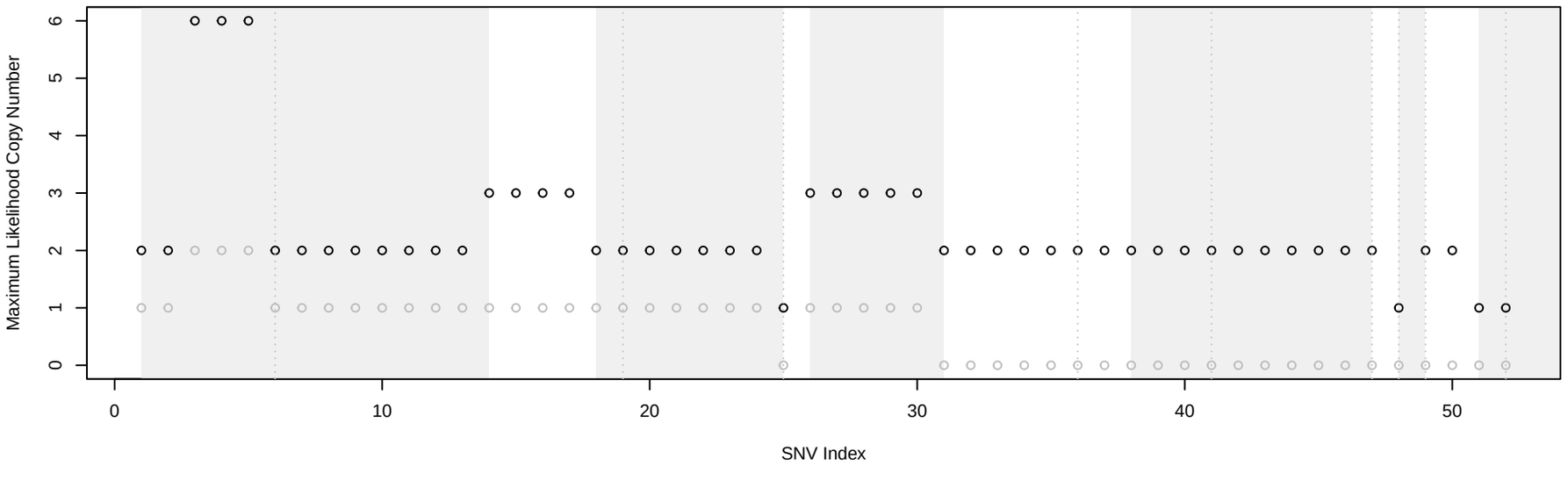

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1
3m1
4m1

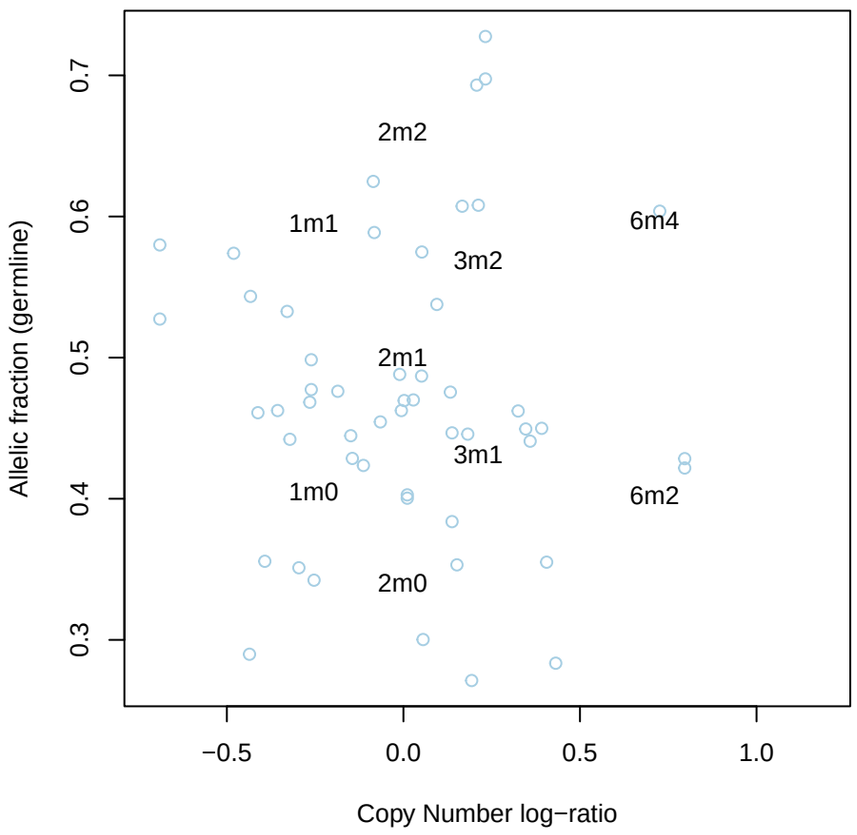

Power 0.8
Frequency
Cellular fraction

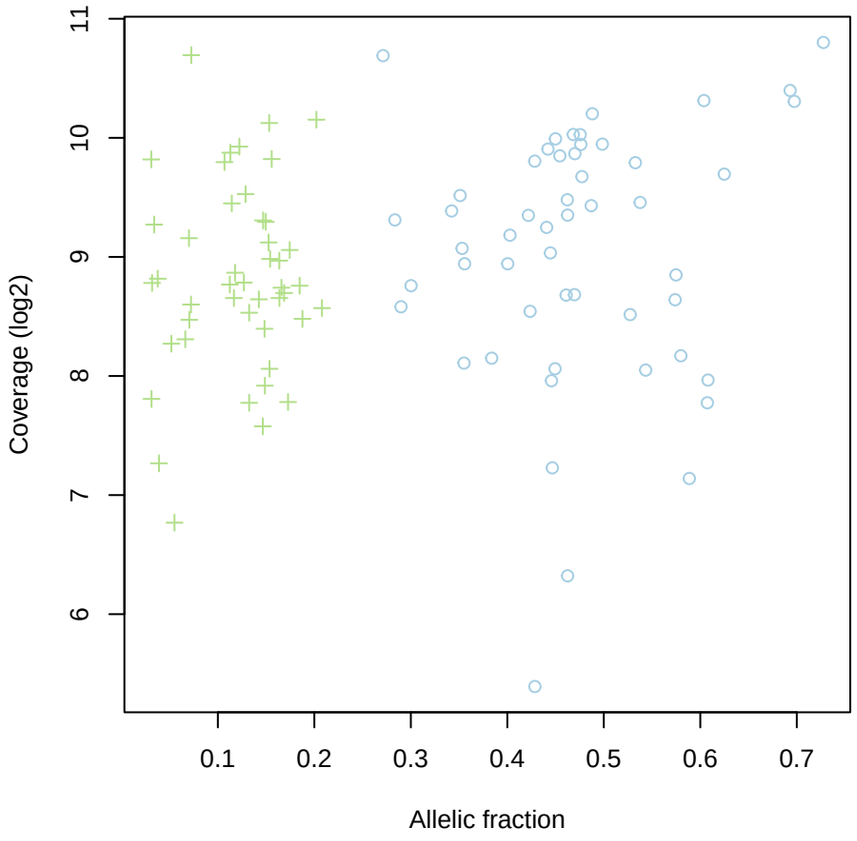

Purity: 0.32 Tumor ploidy: 2.01
0
1
2
3
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

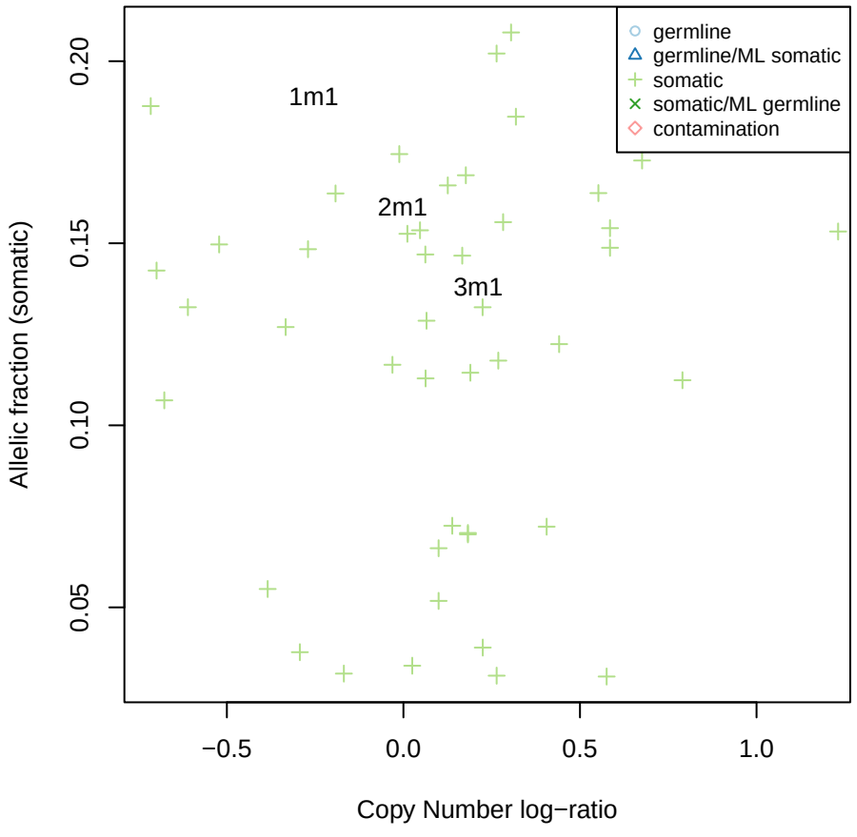

Purity: 0.32 Tumor ploidy: 2.01 SNV log−likelihood: −25.91 GoF: 91.8% Mean coverage: 586;597
1
2
3
4
5
6
7
9
14
B−Allele Frequency
0.3
0.4
0.5
0.6
0.7
0
10
20
30
40
50
SNV Index

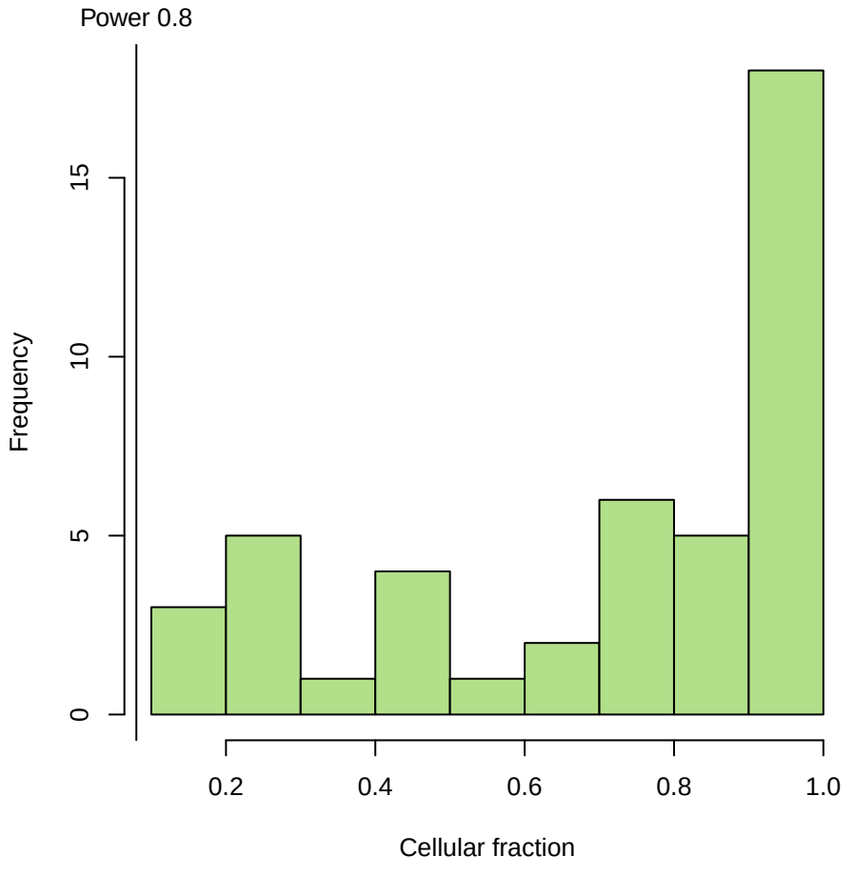

SCNA−fit log−likelihood: −14846
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
0
1
2
5
7
0
10
20
30
40
50
SNV Index

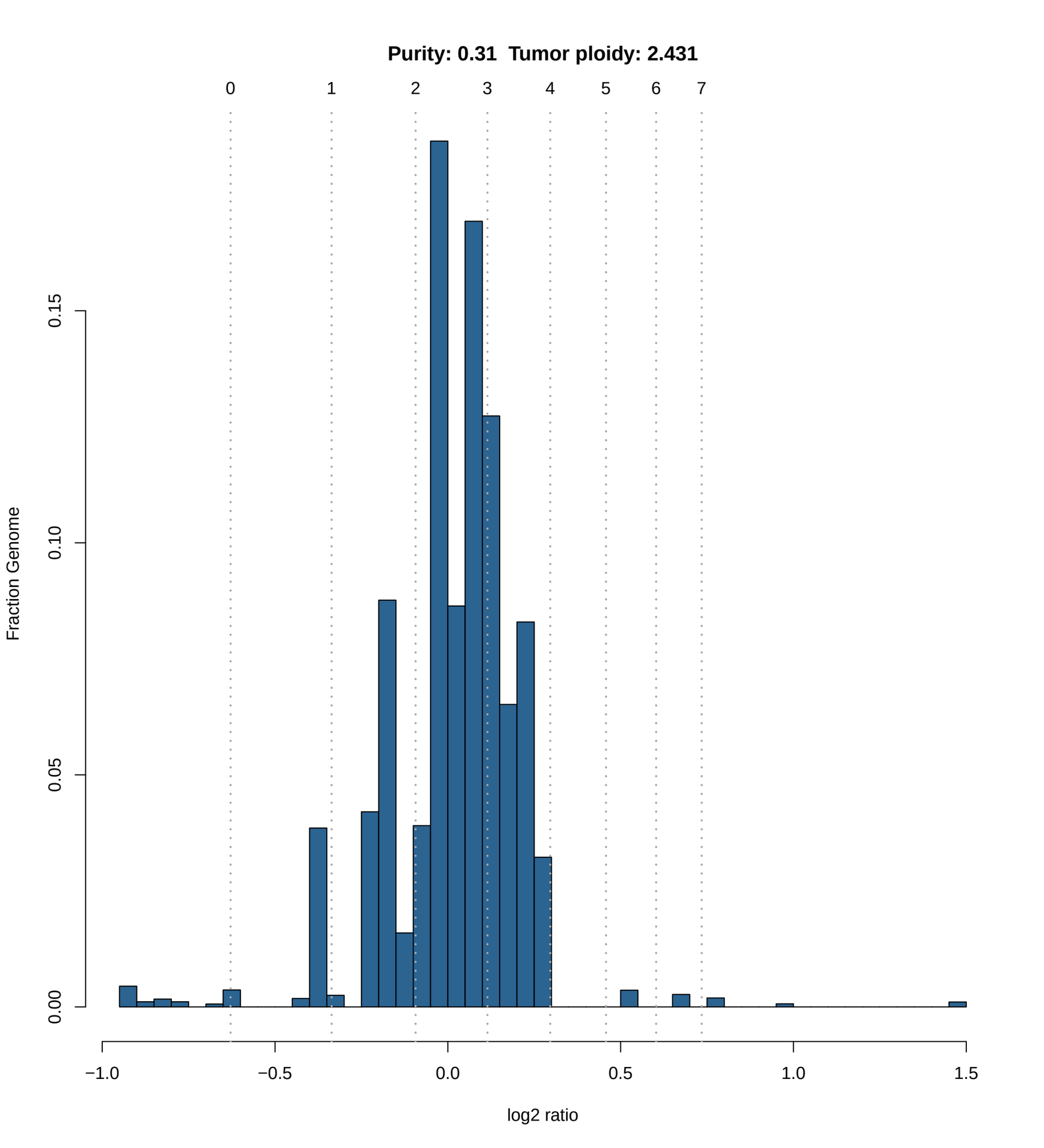

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
0
10
20
30
40
50
SNV Index

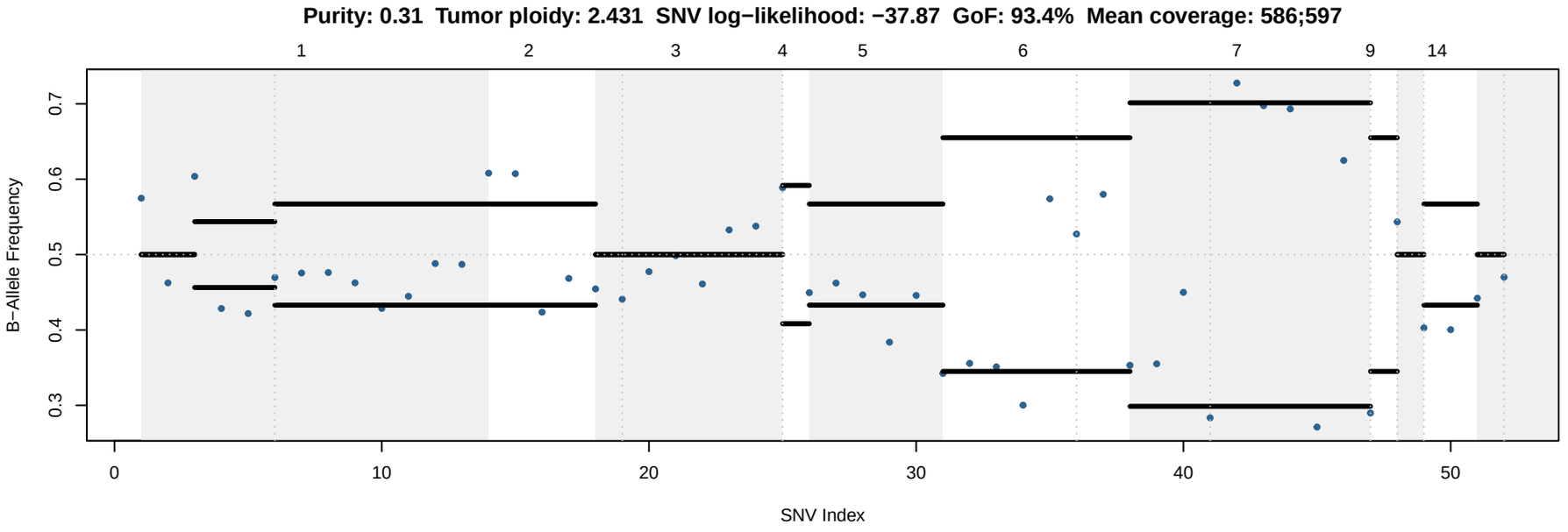

Allelic fraction (germline)
Copy Number log−ratio
2m2
1m1
6m4
3m2
2m1
3m1
1m0
6m2
2m0

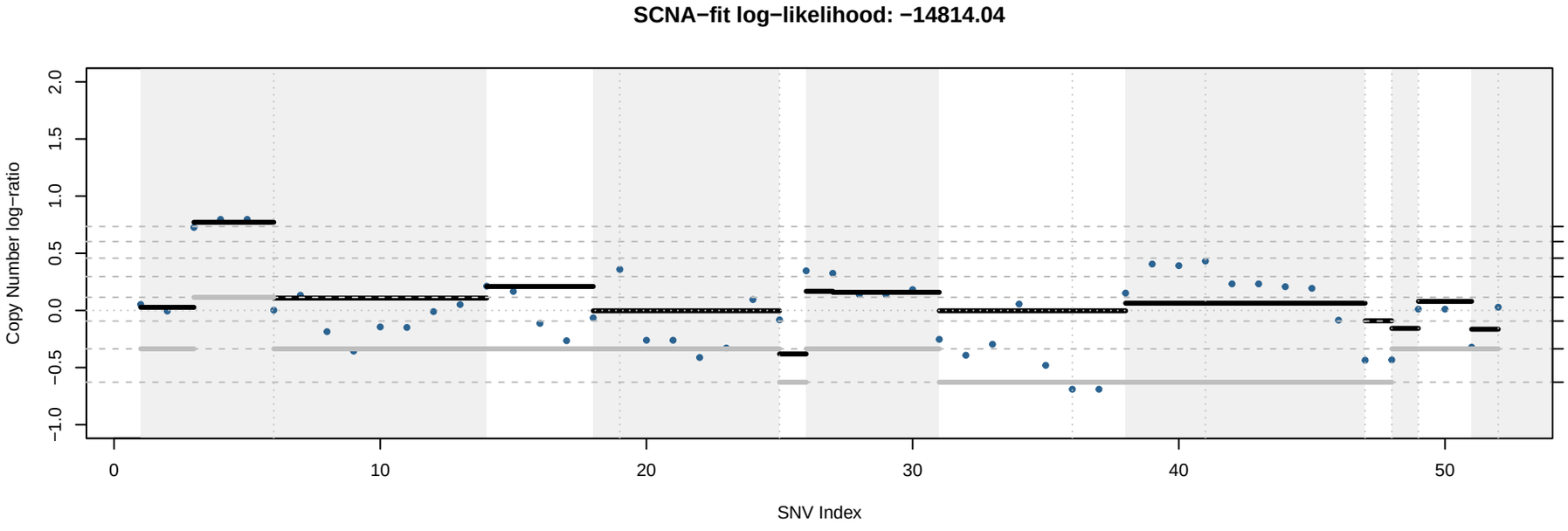

Coverage (log2)
Allelic fraction

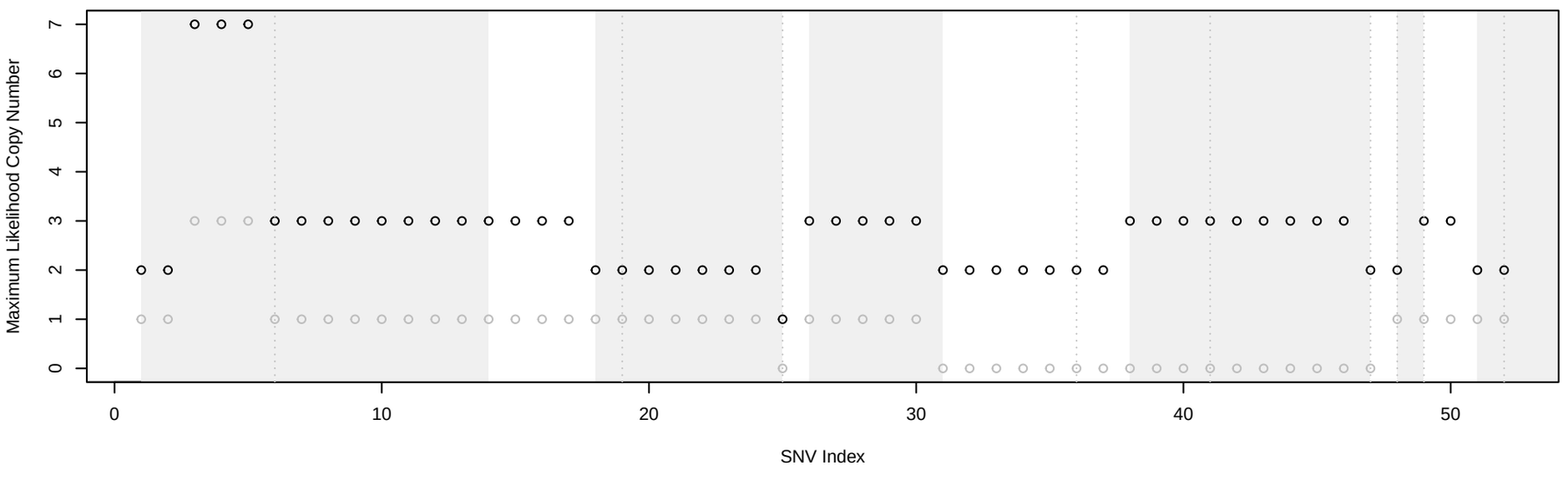

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1

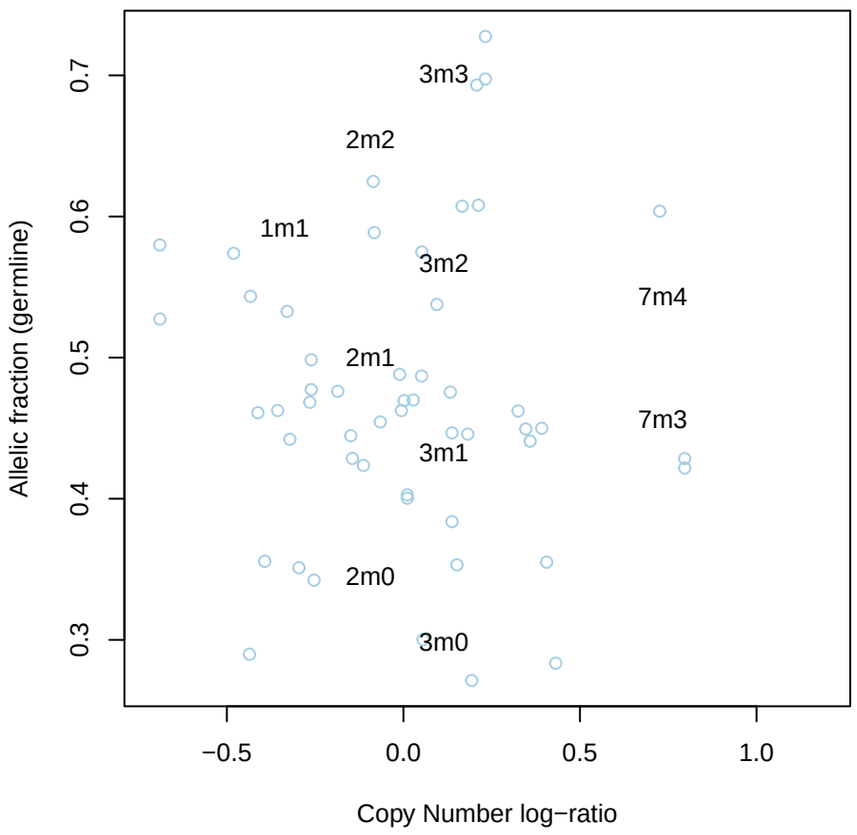

Power 0.8
Frequency
Cellular fraction

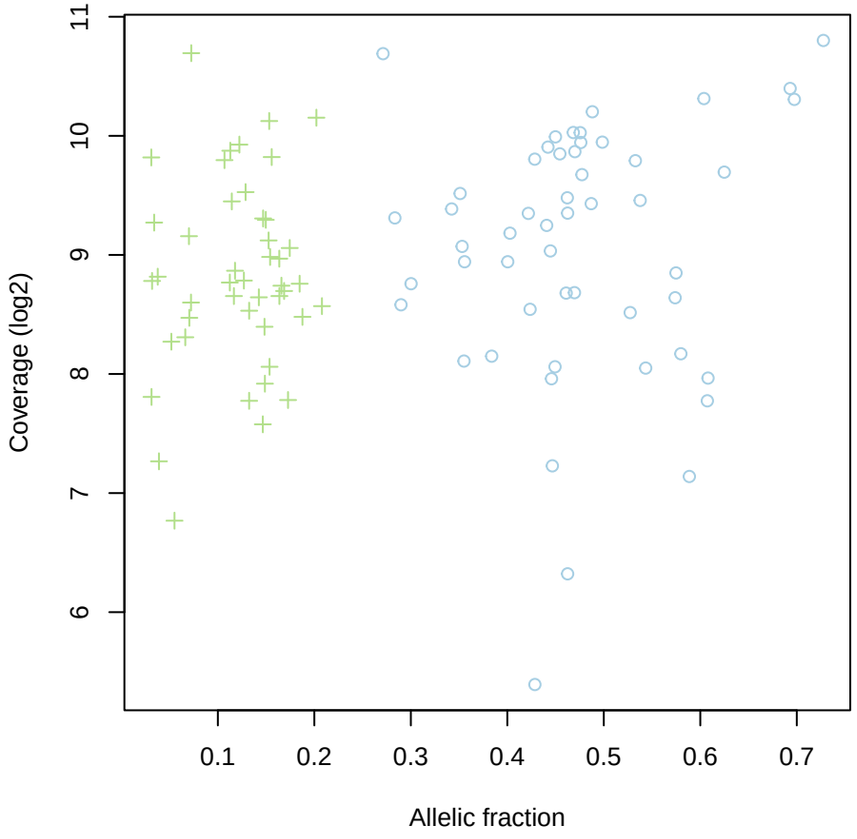

Purity: 0.31 Tumor ploidy: 2.431
0
1
2
3
4
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

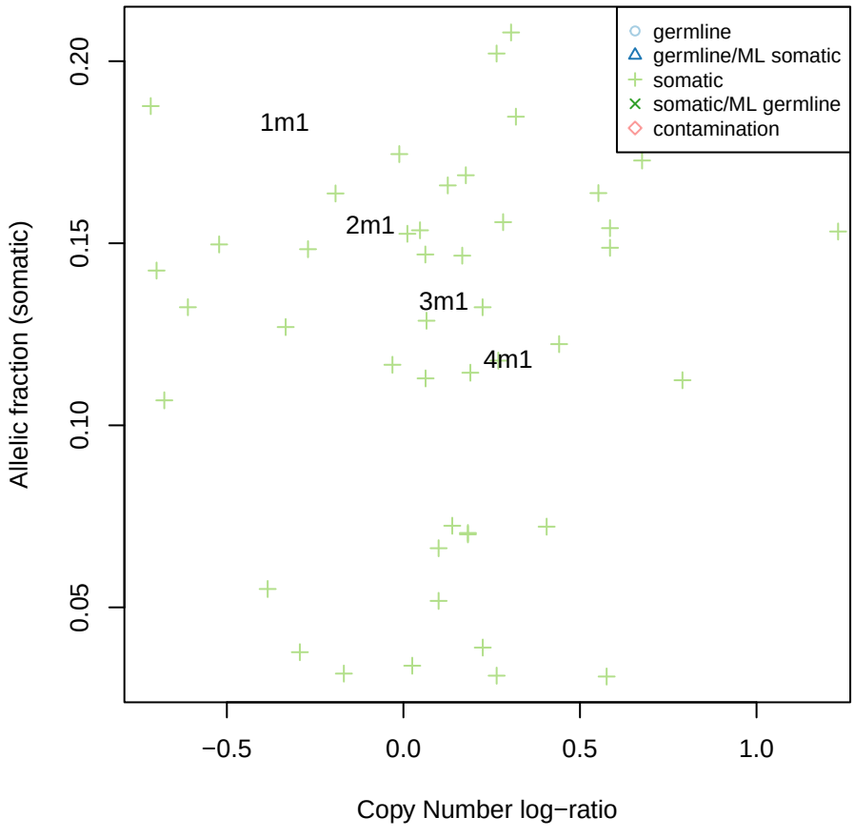

Purity: 0.31 Tumor ploidy: 2.431 SNV log−likelihood: −37.87 GoF: 93.4% Mean coverage: 586;597
1
2
3
4
5
6
7
9
14
B−Allele Frequency
0.3
0.4
0.5
0.6
0.7
0
10
20
30
40
50
SNV Index

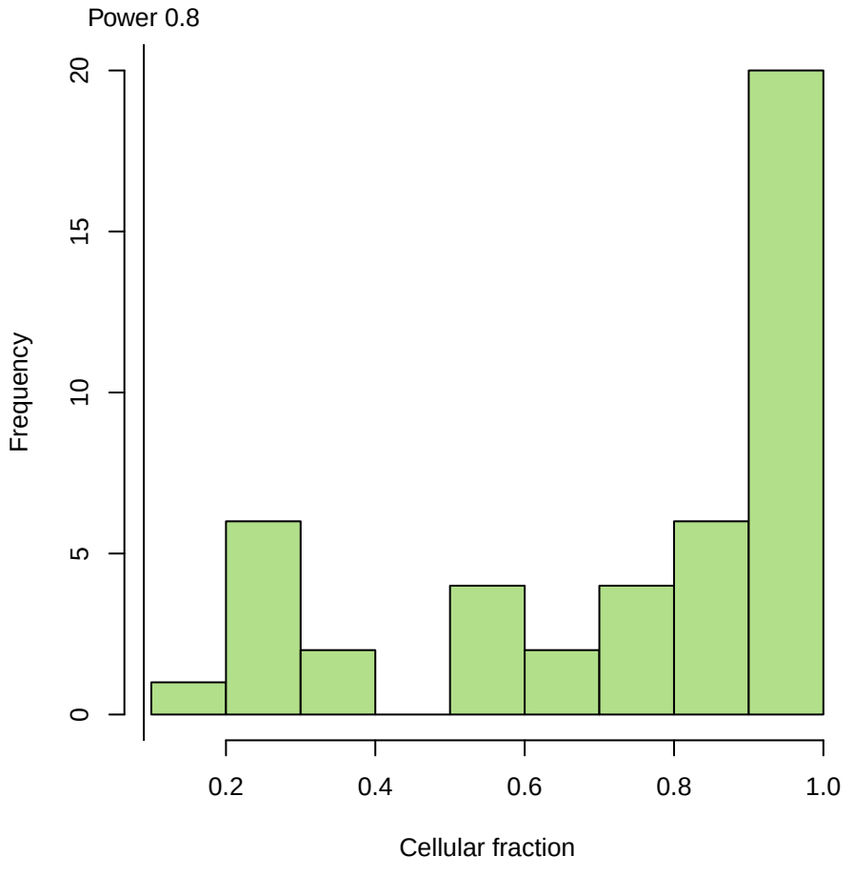

SCNA−fit log−likelihood: −14814.04
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
0
1
2
4
6
0
10
20
30
40
50
SNV Index

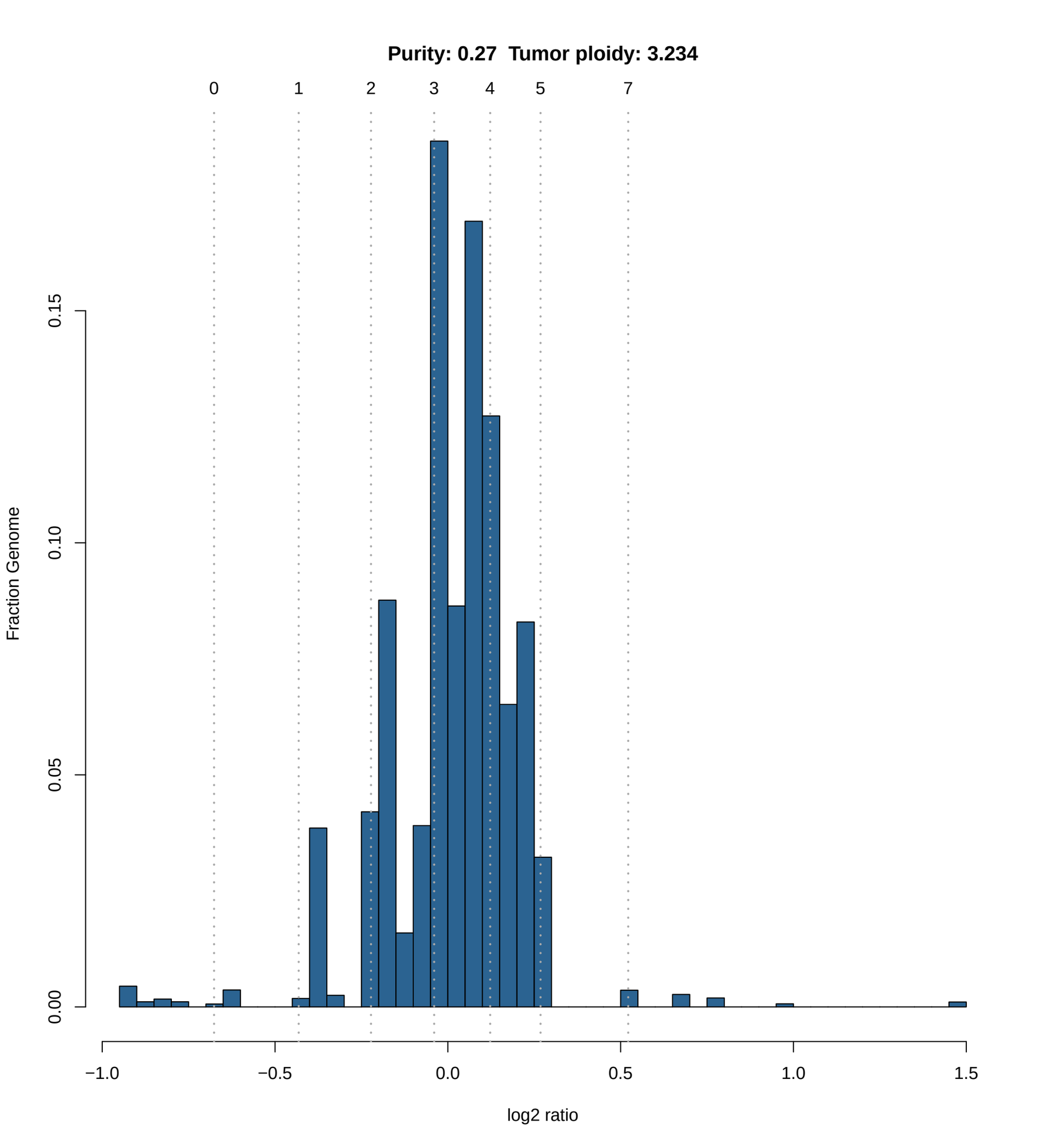

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
7
0
10
20
30
40
50
SNV Index

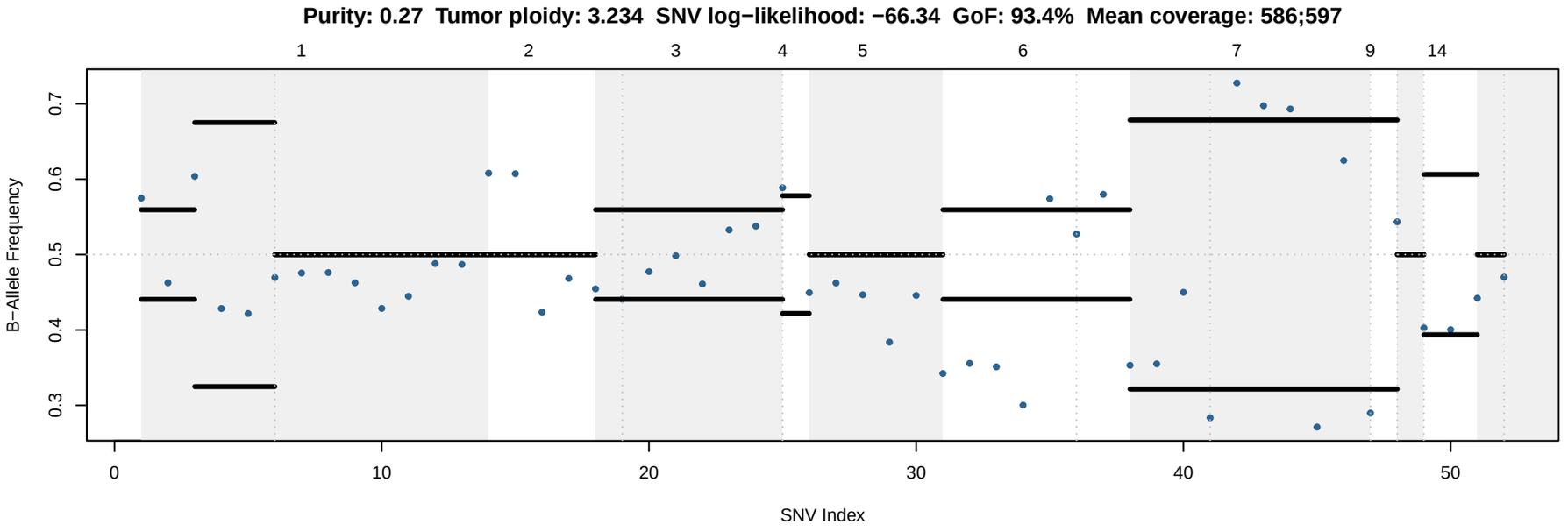

Allelic fraction (germline)
Copy Number log−ratio
3m3
2m2
1m1
3m2
7m4
2m1
7m3
3m1
2m0
3m0

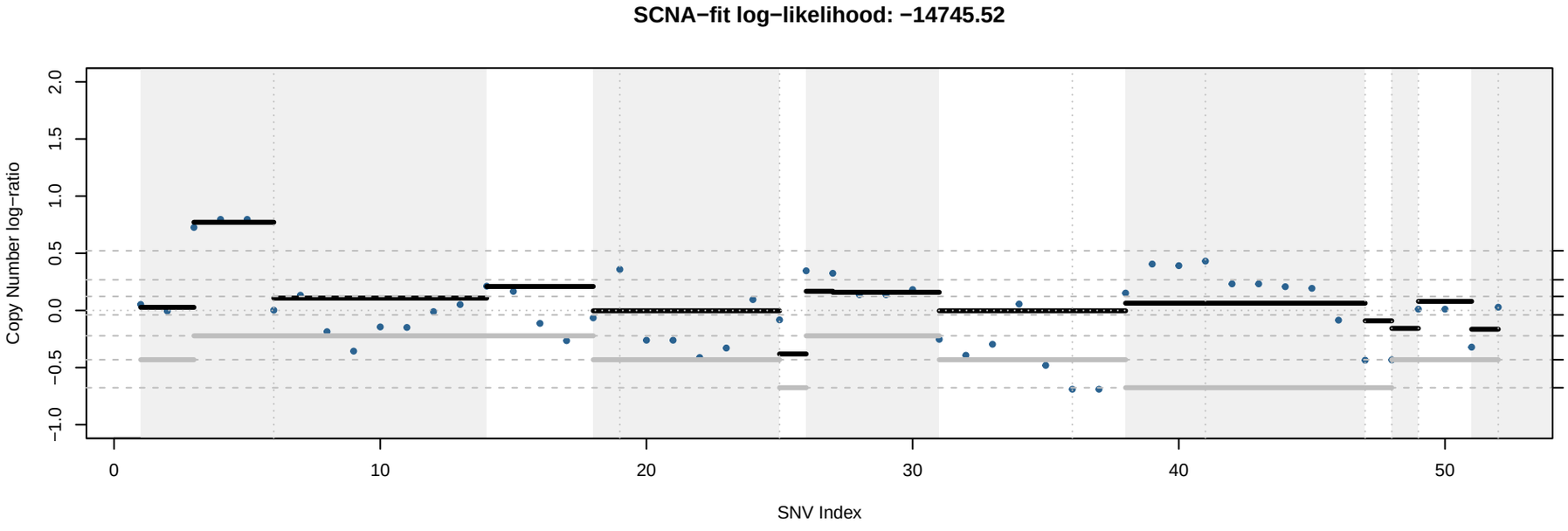

Coverage (log2)
Allelic fraction

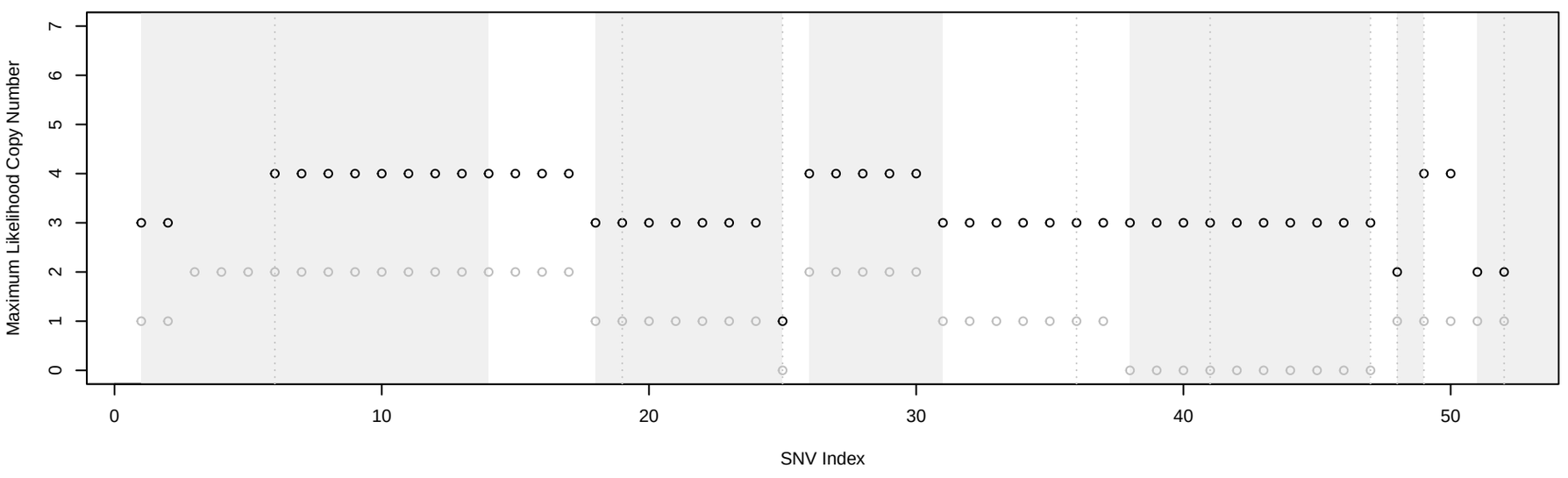

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1
3m1
4m1

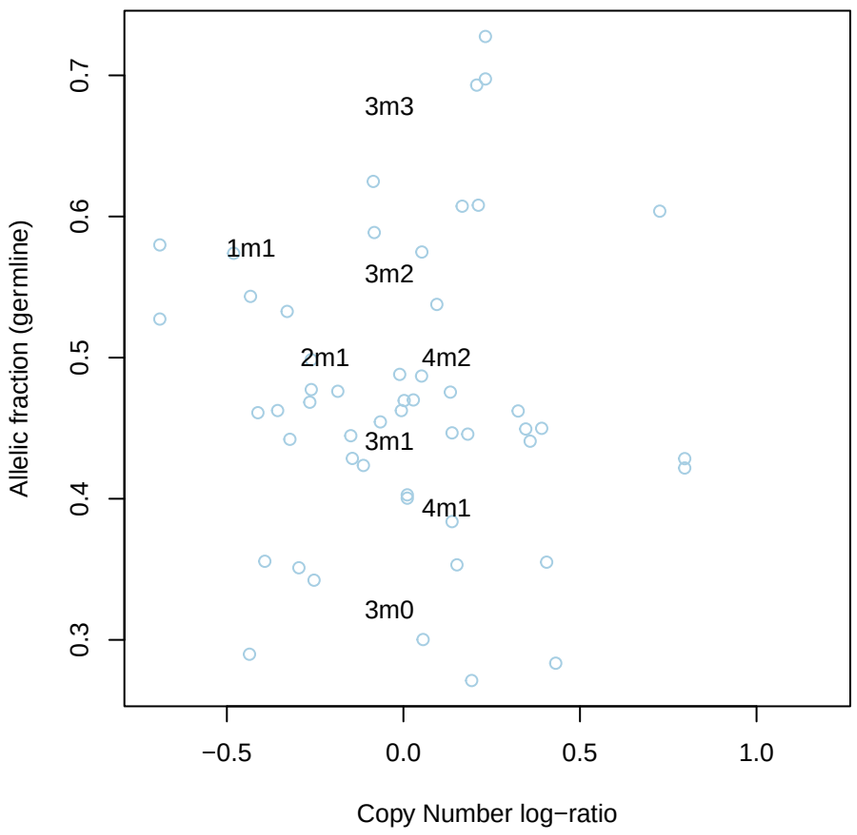

Power 0.8
Frequency
Cellular fraction

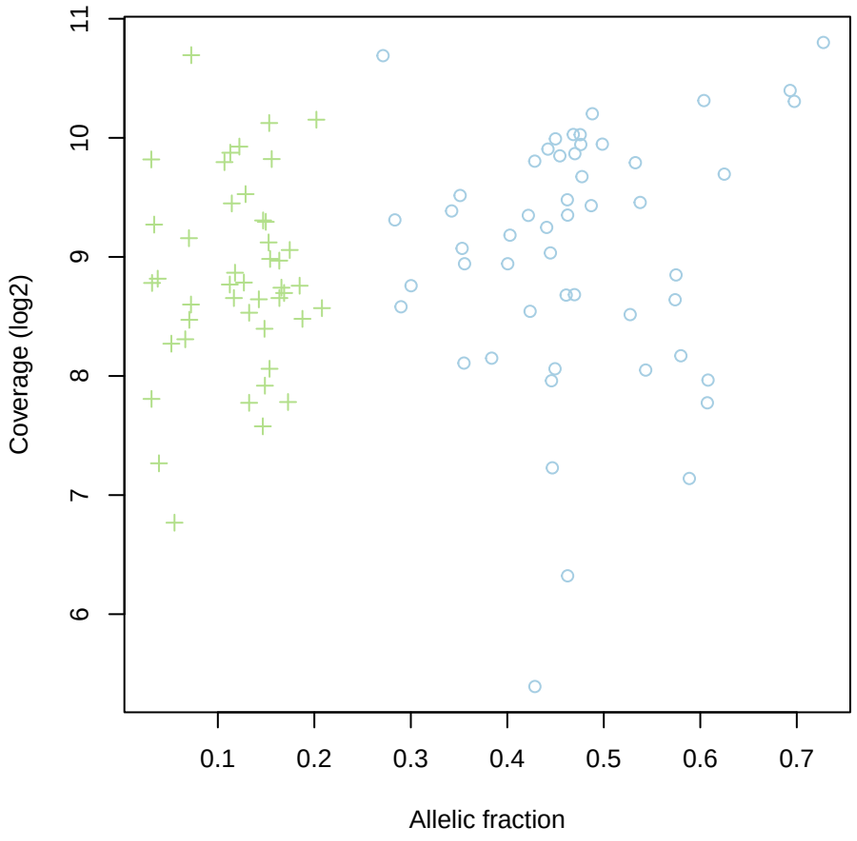

Purity: 0.27 Tumor ploidy: 3.234
0
1
2
3
4
5
7
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

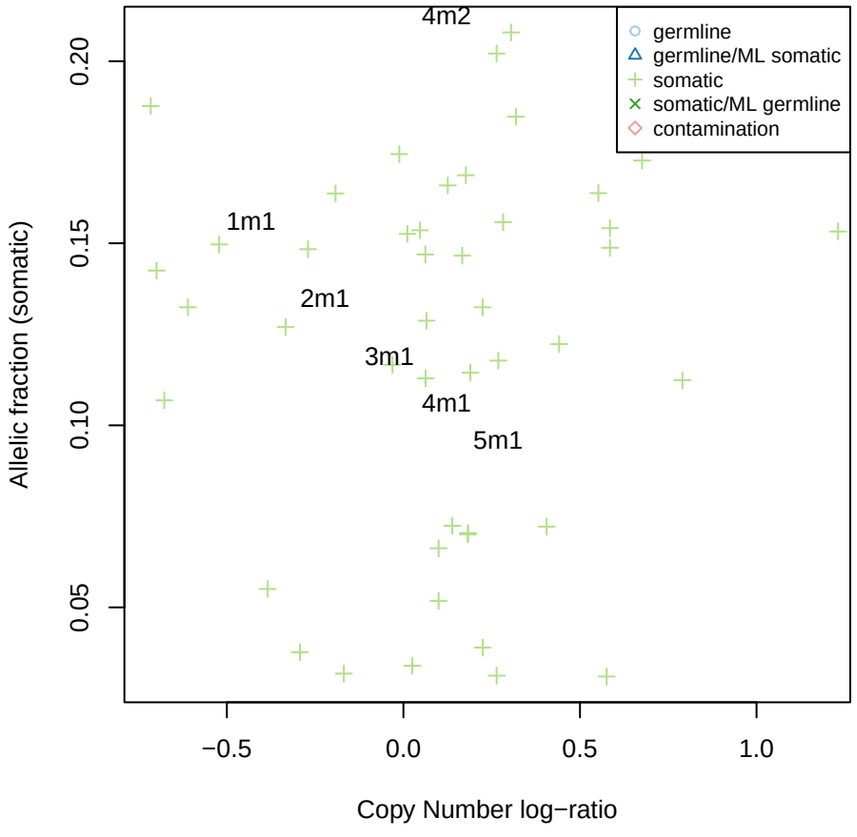

Purity: 0.27 Tumor ploidy: 3.234 SNV log−likelihood: −66.34 GoF: 93.4% Mean coverage: 586;597
1
2
3
4
5
6
7
9
14
B−Allele Frequency
0.3
0.4
0.5
0.6
0.7
0
10
20
30
40
50
SNV Index

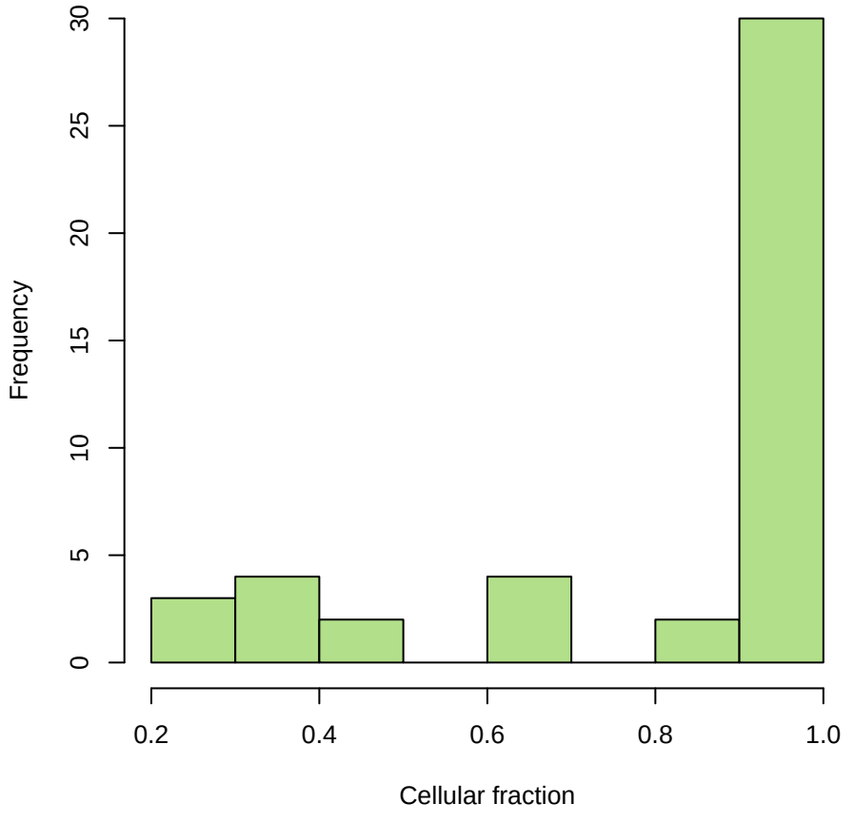

SCNA−fit log−likelihood: −14745.52
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
0
1
3
5
7
0
10
20
30
40
50
SNV Index

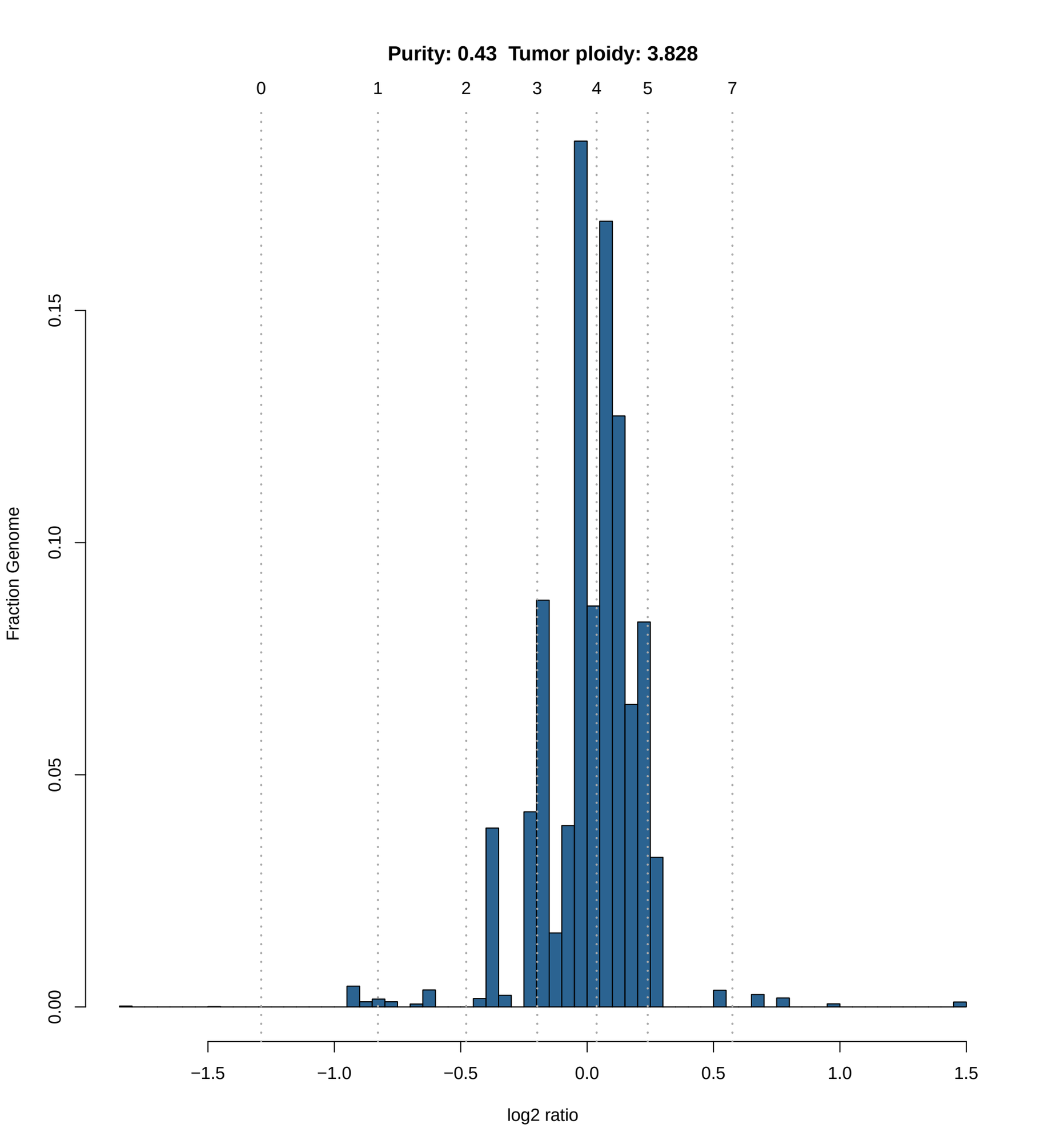

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
7
0
10
20
30
40
50
SNV Index

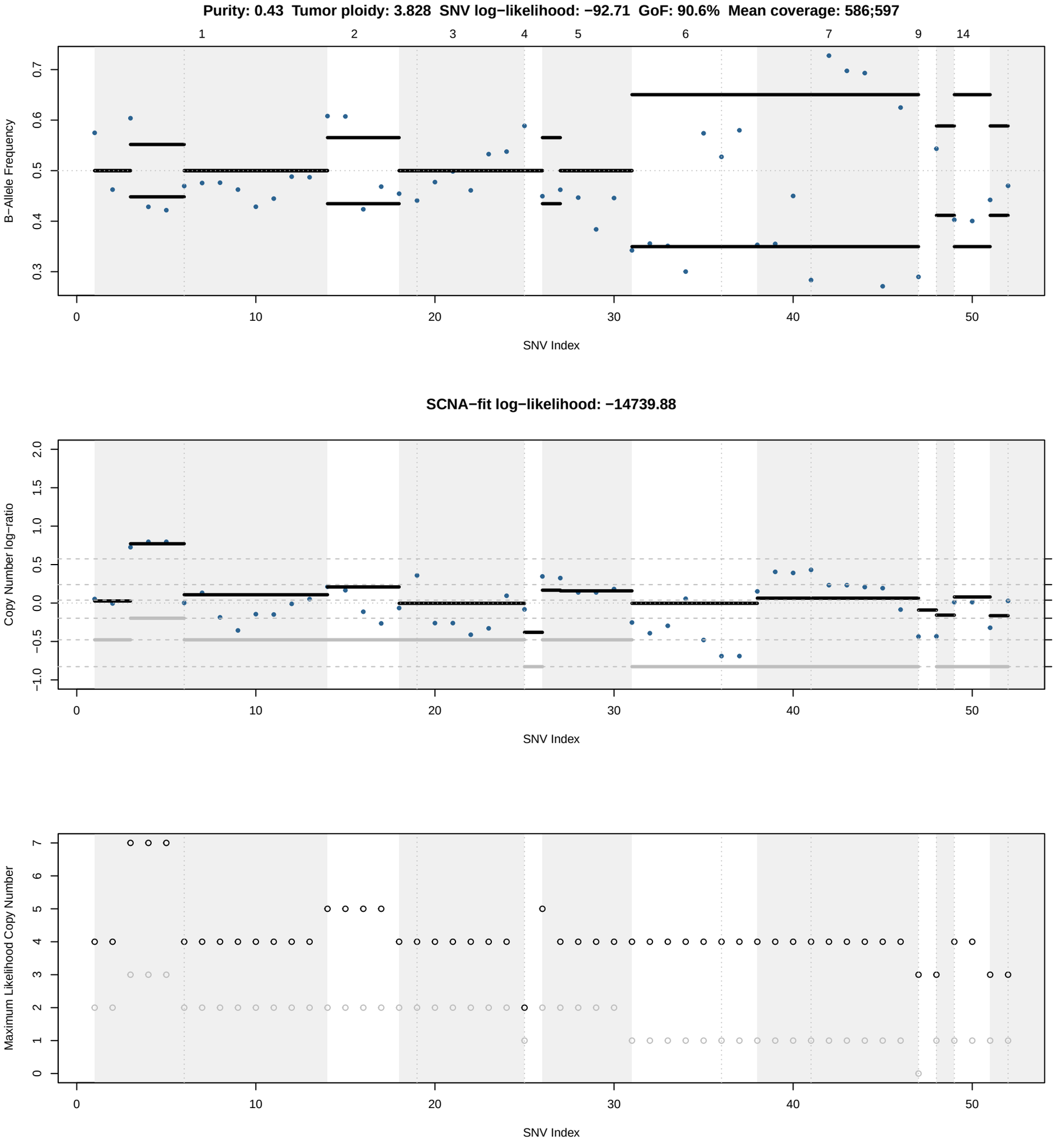

Allelic fraction (germline)
Copy Number log−ratio
3m3
1m1
3m2
2m1
4m2
3m1
4m1
3m0

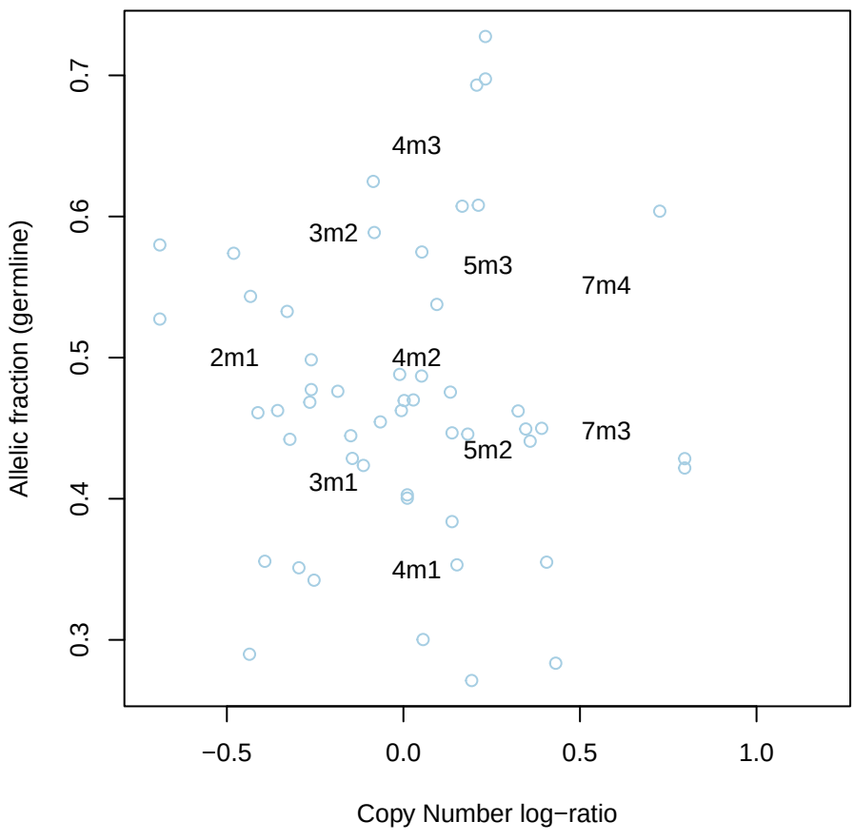

Coverage (log2)
Allelic fraction

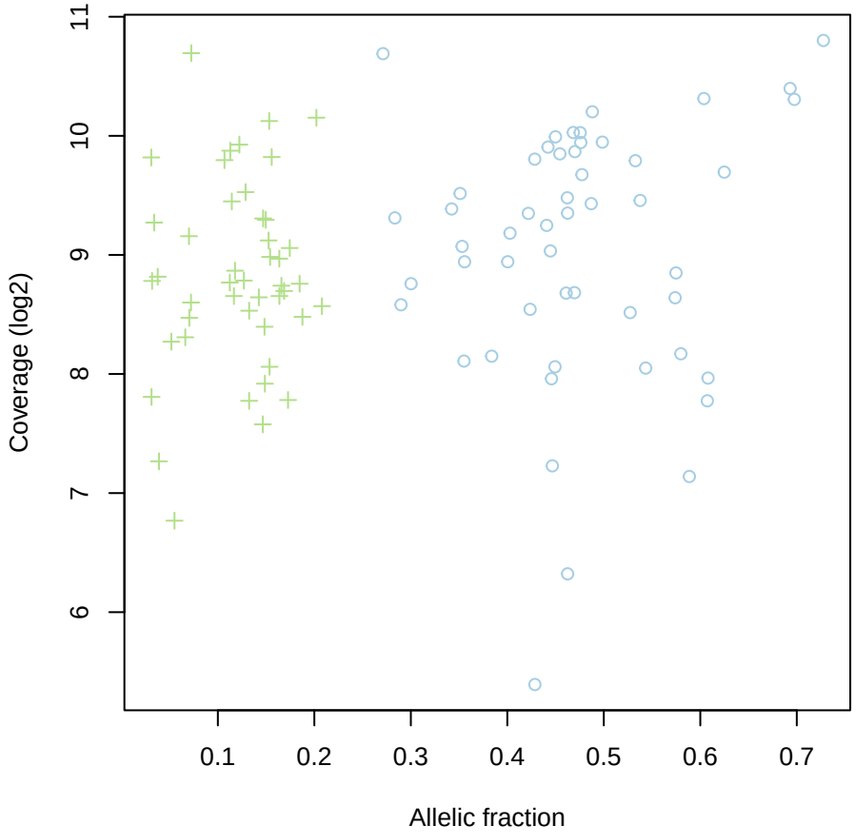

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m2
1m1
2m1
3m1
4m1
5m1

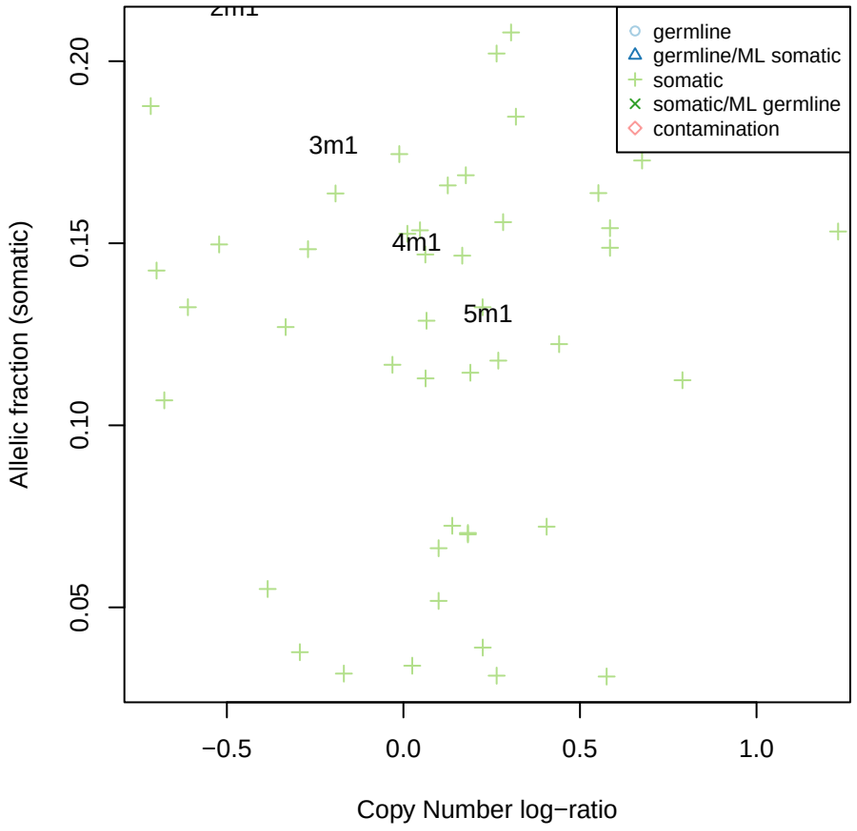

Frequency
Cellular fraction

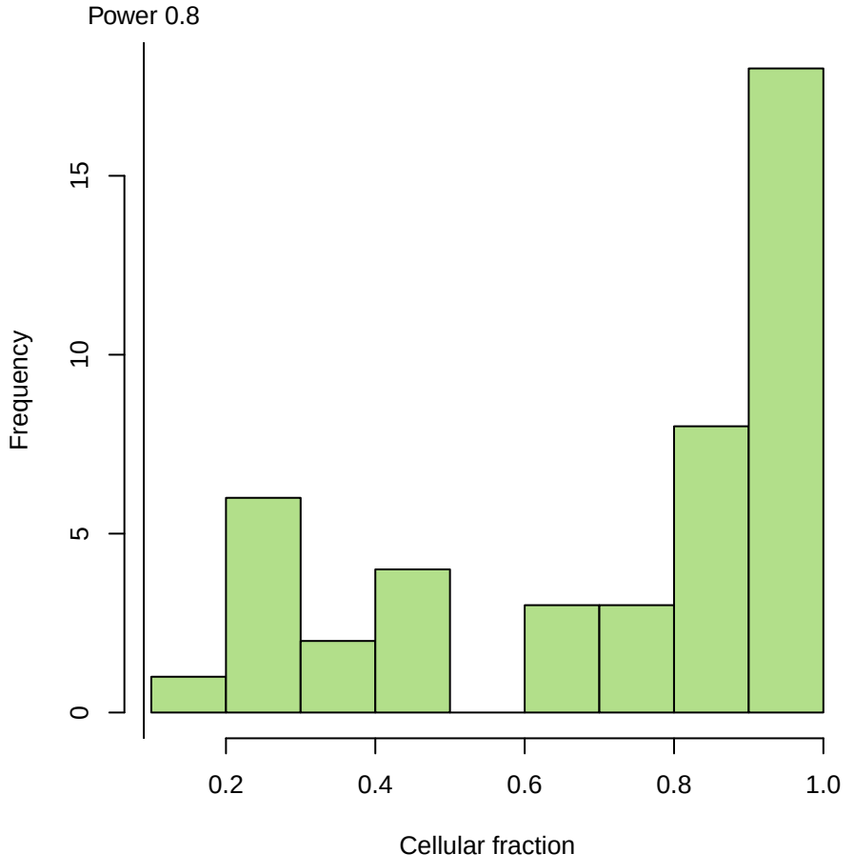

Purity: 0.43 Tumor ploidy: 3.828
0
1
2
3
4
5
7
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

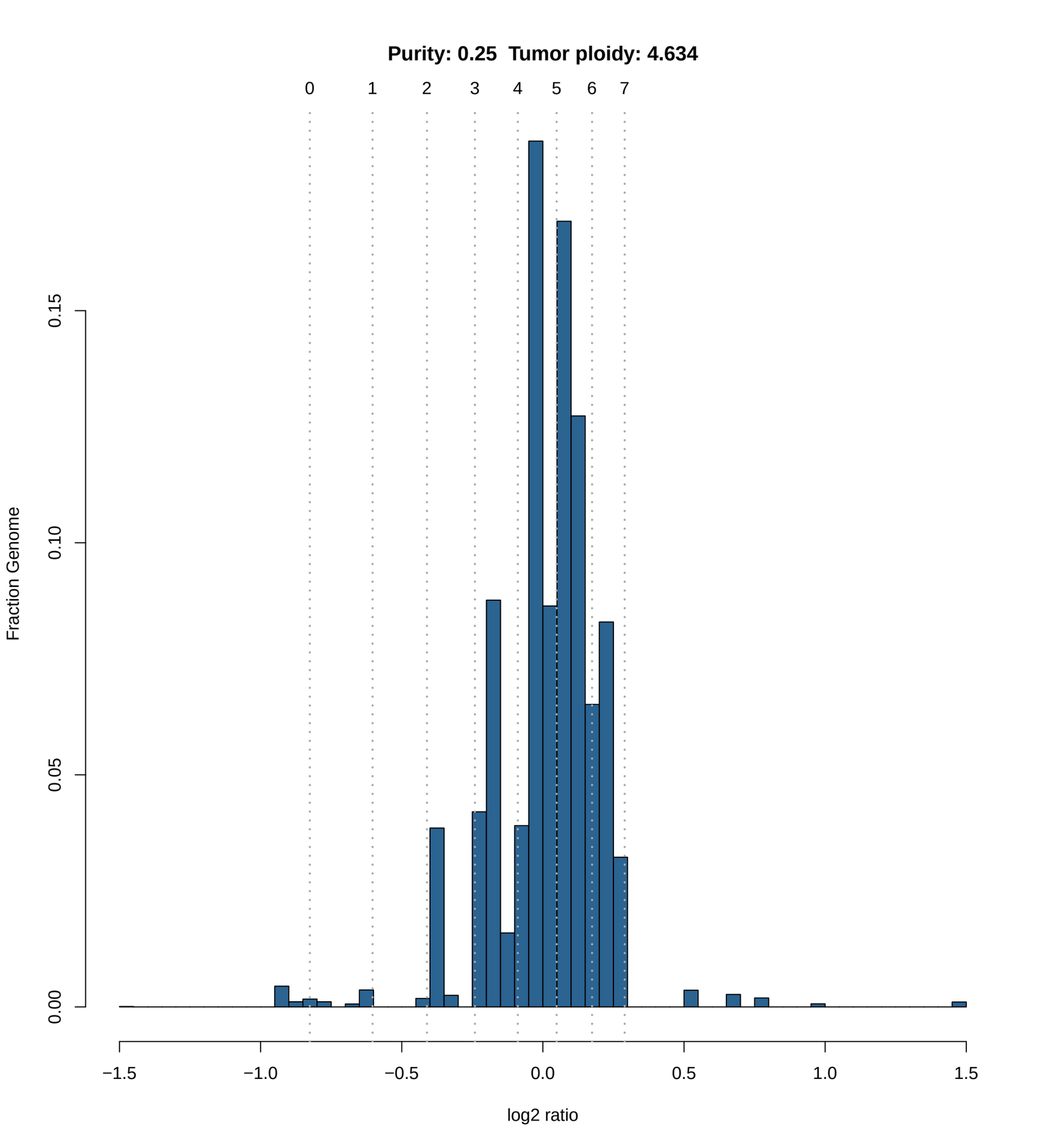

Purity: 0.43 Tumor ploidy: 3.828 SNV log−likelihood: −92.71 GoF: 90.6% Mean coverage: 586;597
1
2
3
4
5
6
7
9
14
B−Allele Frequency
0.3
0.4
0.5
0.6
0.7
0
10
20
30
40
50
SNV Index
SCNA−fit log−likelihood: −14739.88
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
1
2
3
4
7
0
10
20
30
40
50
SNV Index
Maximum Likelihood Copy Number
0
1
2
3
4
5
6
7
0
10
20
30
40
50
SNV Index

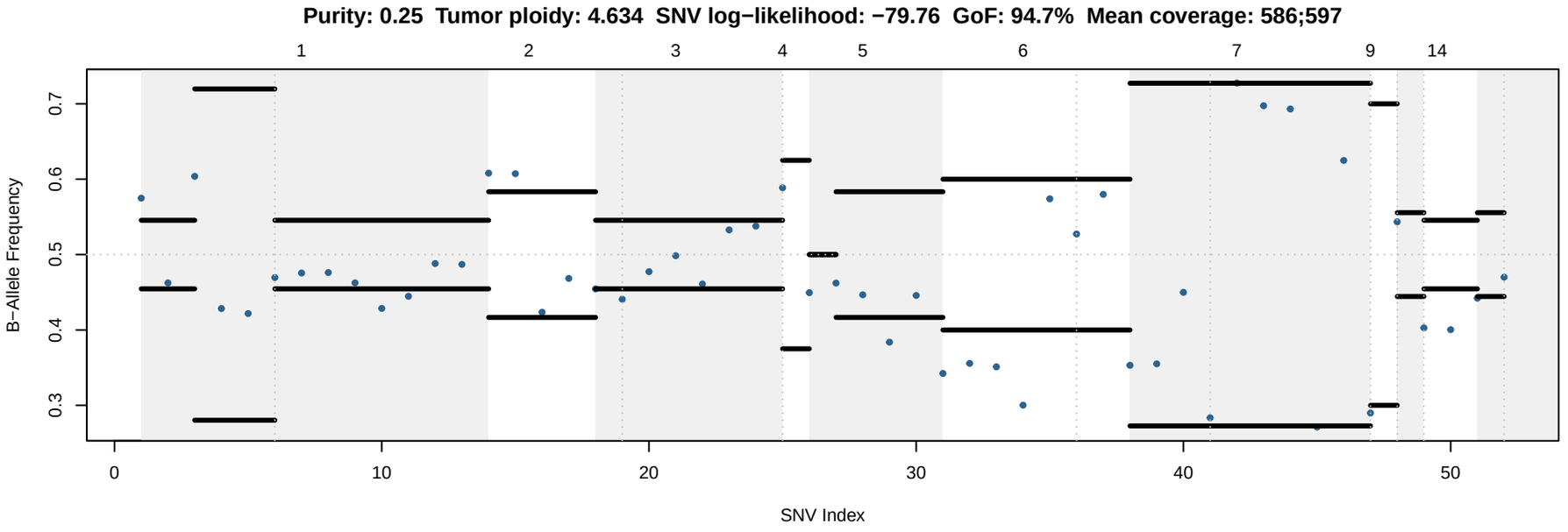

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
5m3
7m4
2m1
4m2
7m3
5m2
3m1
4m1

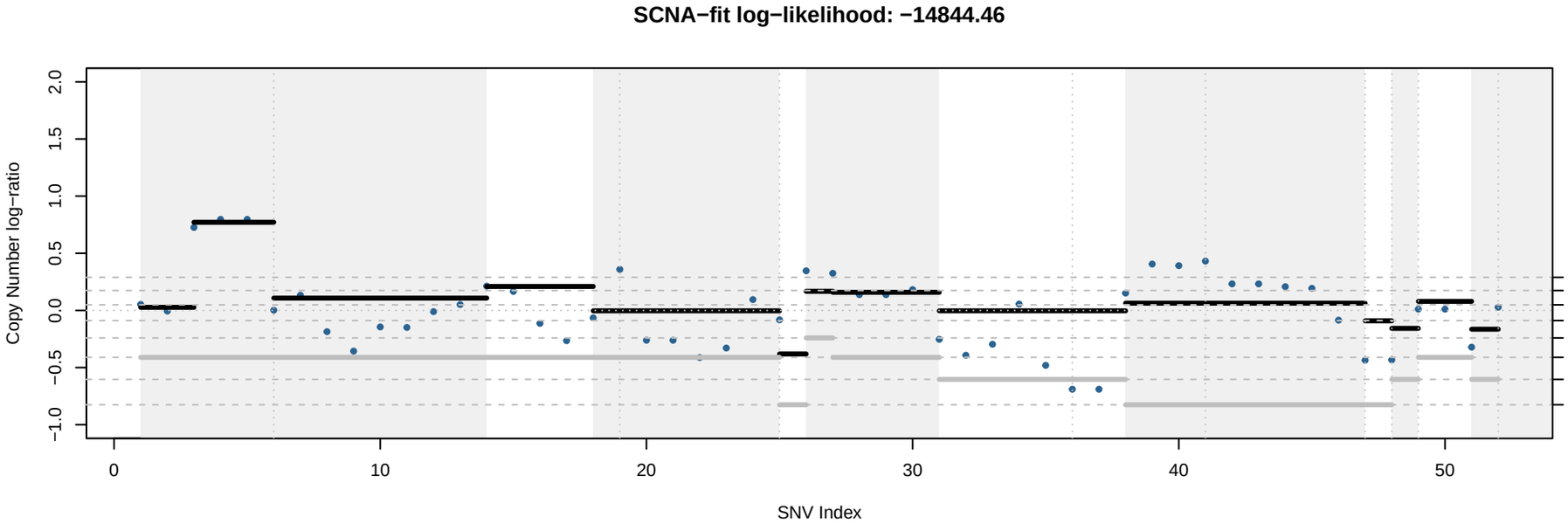

Coverage (log2)
Allelic fraction

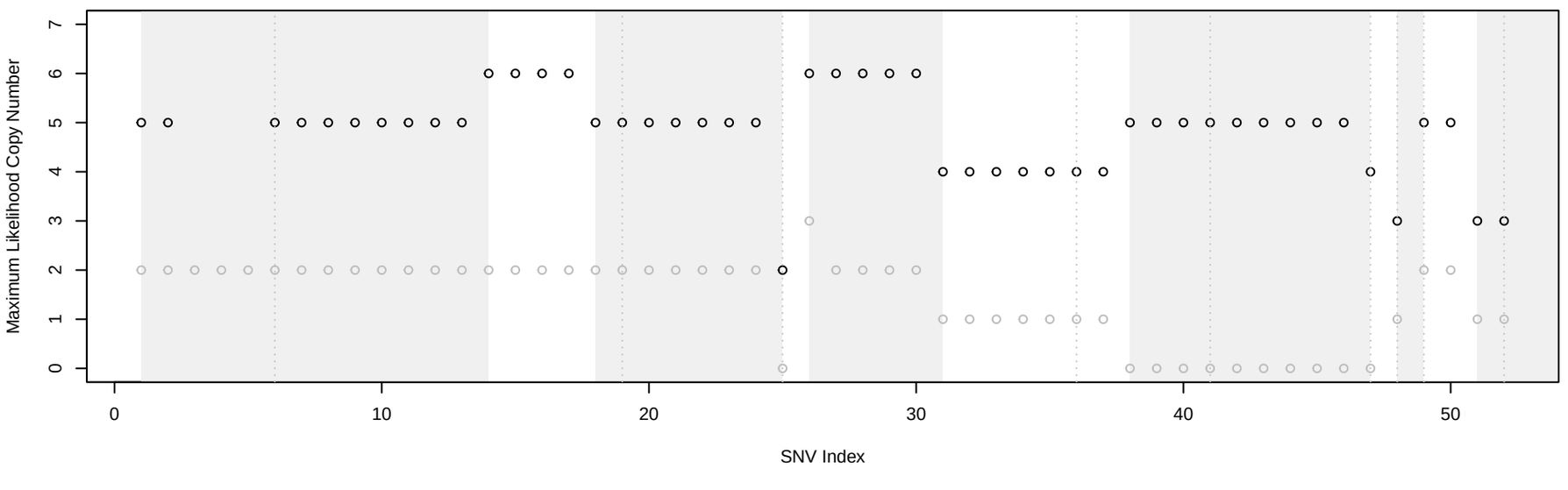

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1

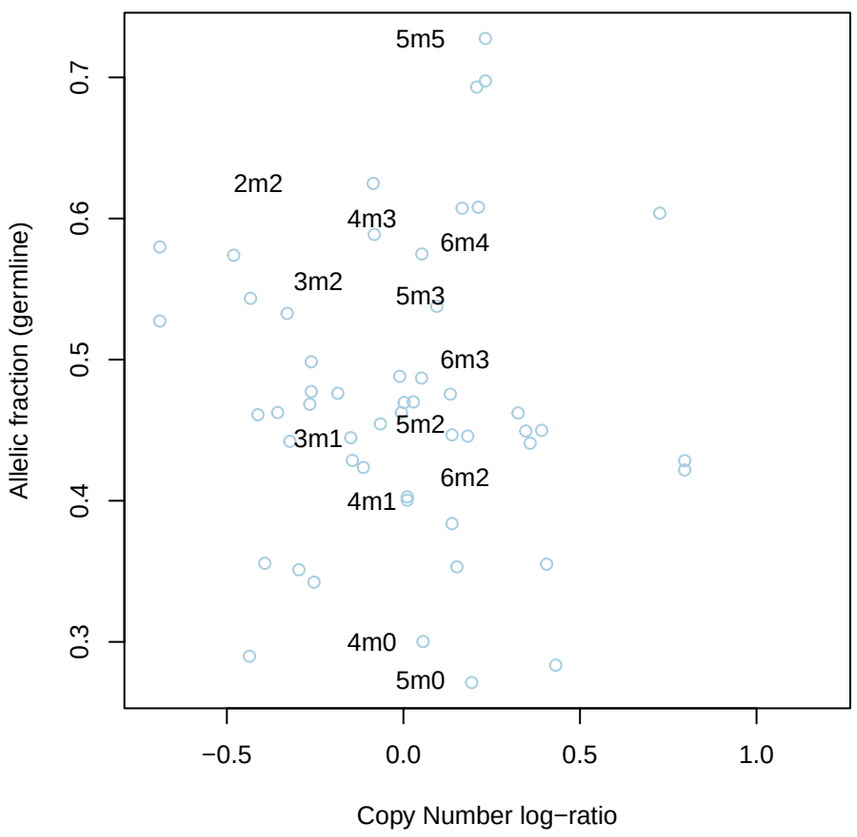

Power 0.8
Frequency
Cellular fraction

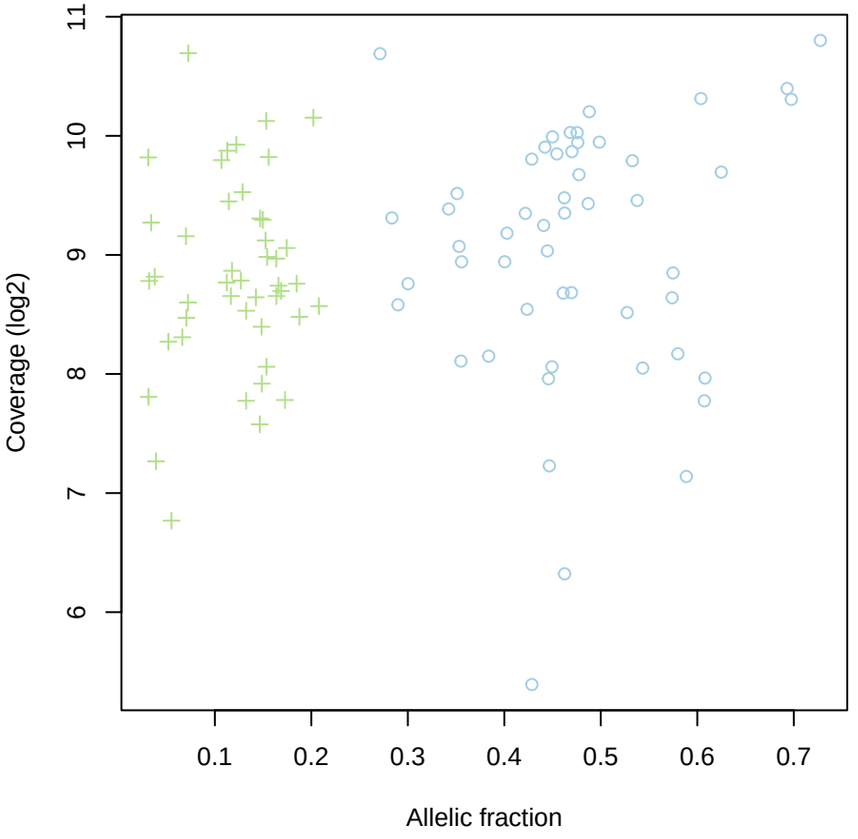

Purity: 0.25 Tumor ploidy: 4.634
0
1
2
3
4
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

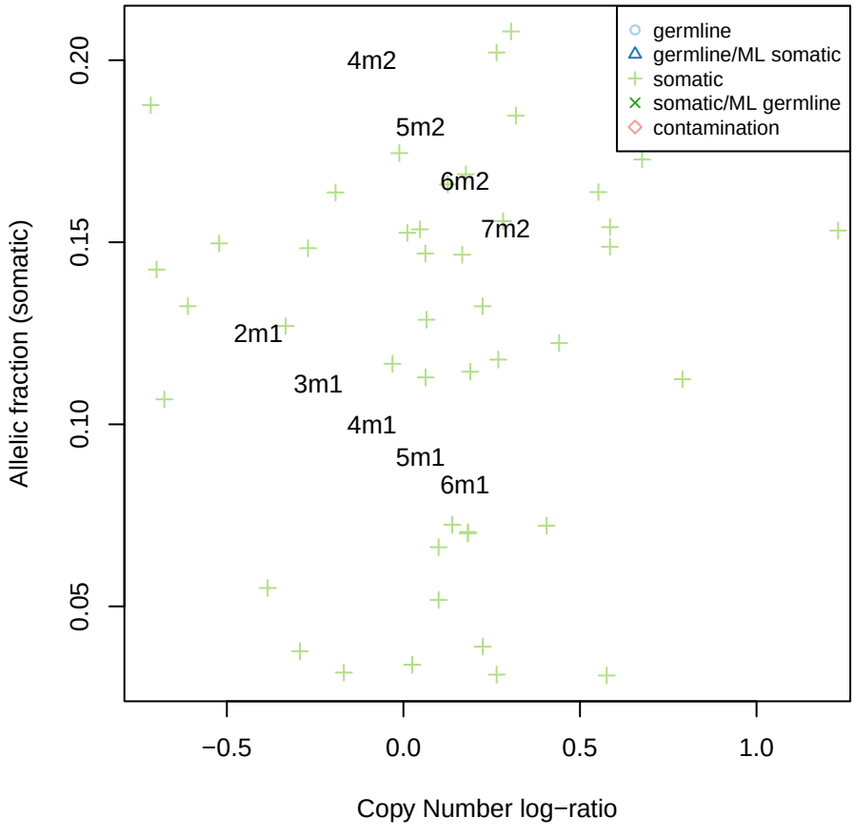

Purity: 0.25 Tumor ploidy: 4.634 SNV log−likelihood: −79.76 GoF: 94.7% Mean coverage: 586;597
1
2
3
4
5
6
7
9
14
B−Allele Frequency
0.3
0.4
0.5
0.6
0.7
0
10
20
30
40
50
SNV Index

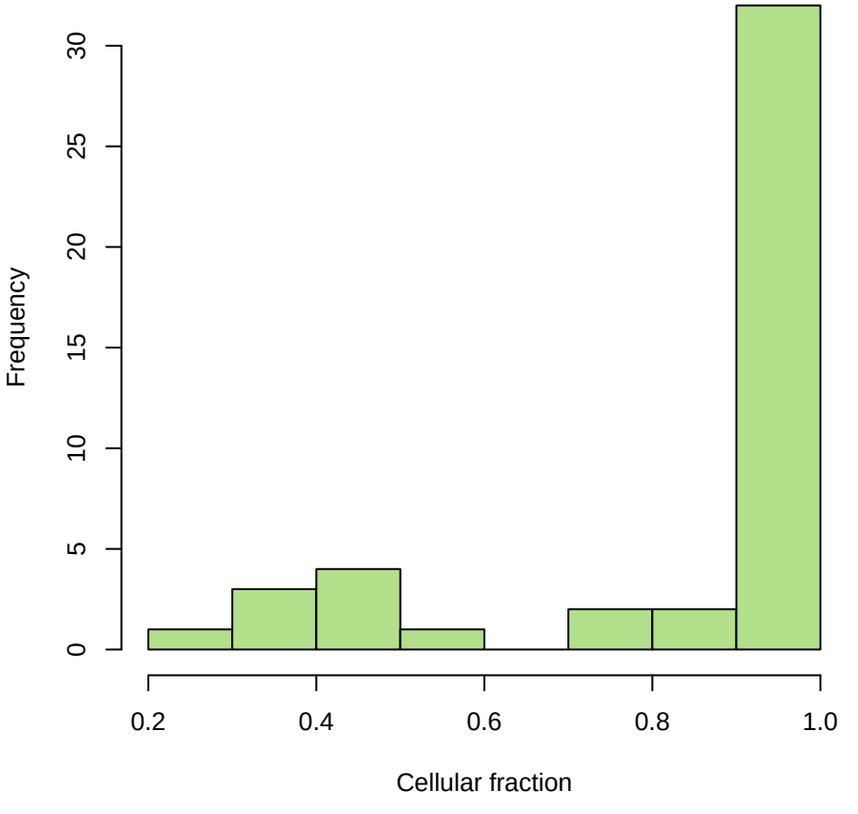

SCNA−fit log−likelihood: −14844.46
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
0
1
3
5
7
0
10
20
30
40
50
SNV Index

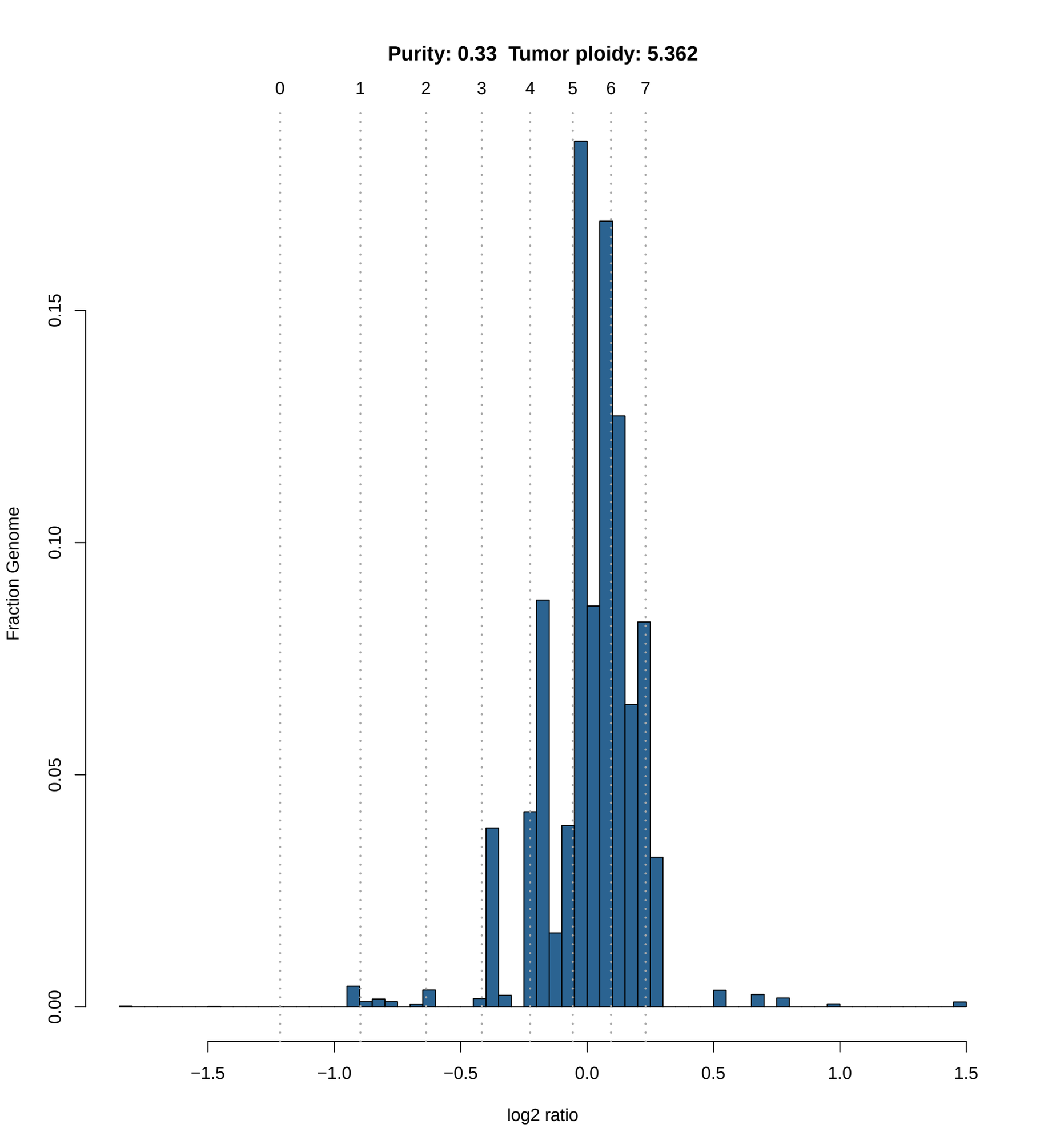

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
7
0
10
20
30
40
50
SNV Index

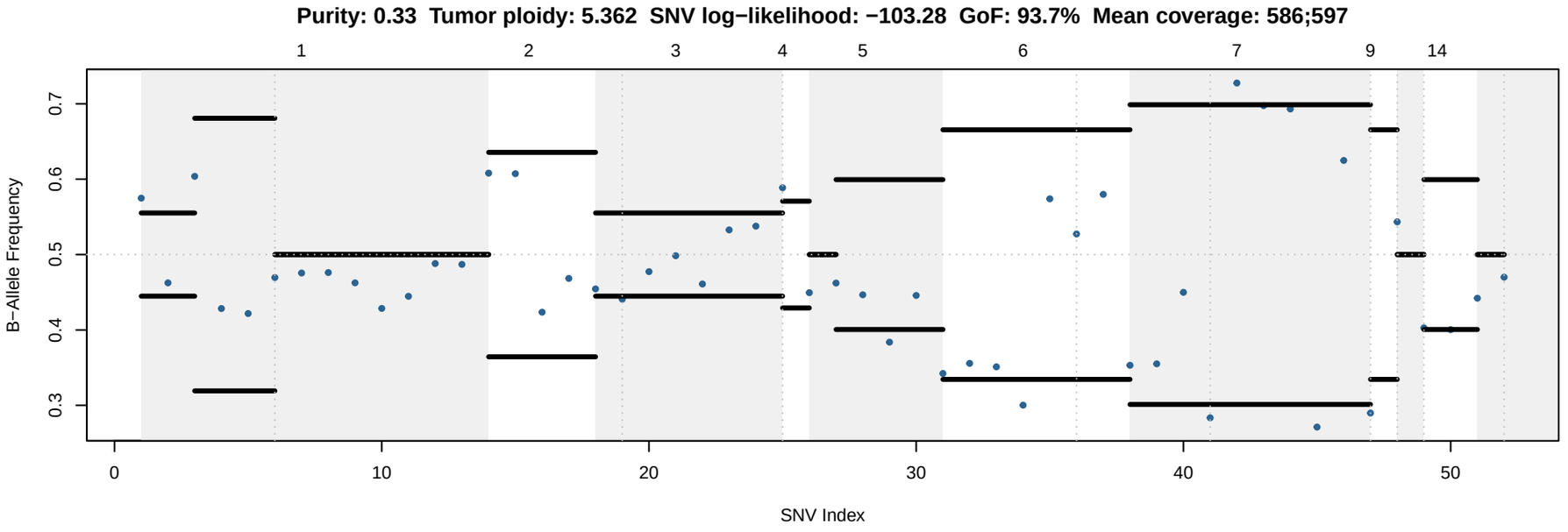

5m5
2m2
4m3
6m4
3m2
5m3
6m3
5m2
3m1
6m2
4m1
4m0
5m0
Allelic fraction (germline)
Copy Number log−ratio

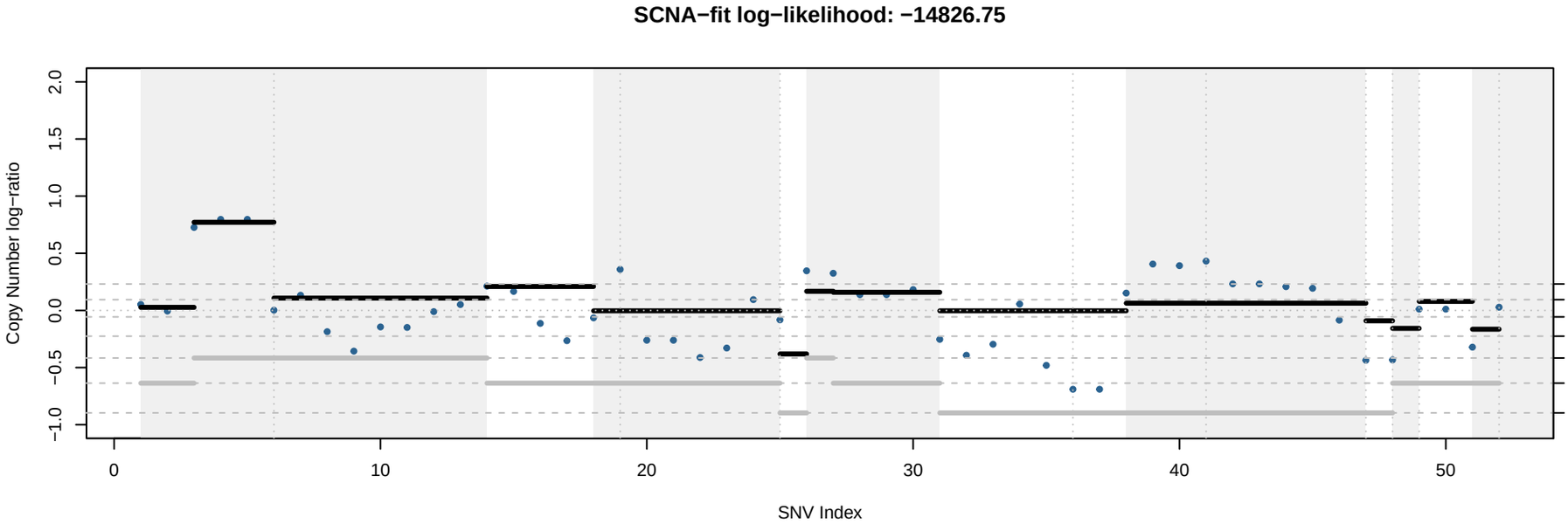

Coverage (log2)
Allelic fraction

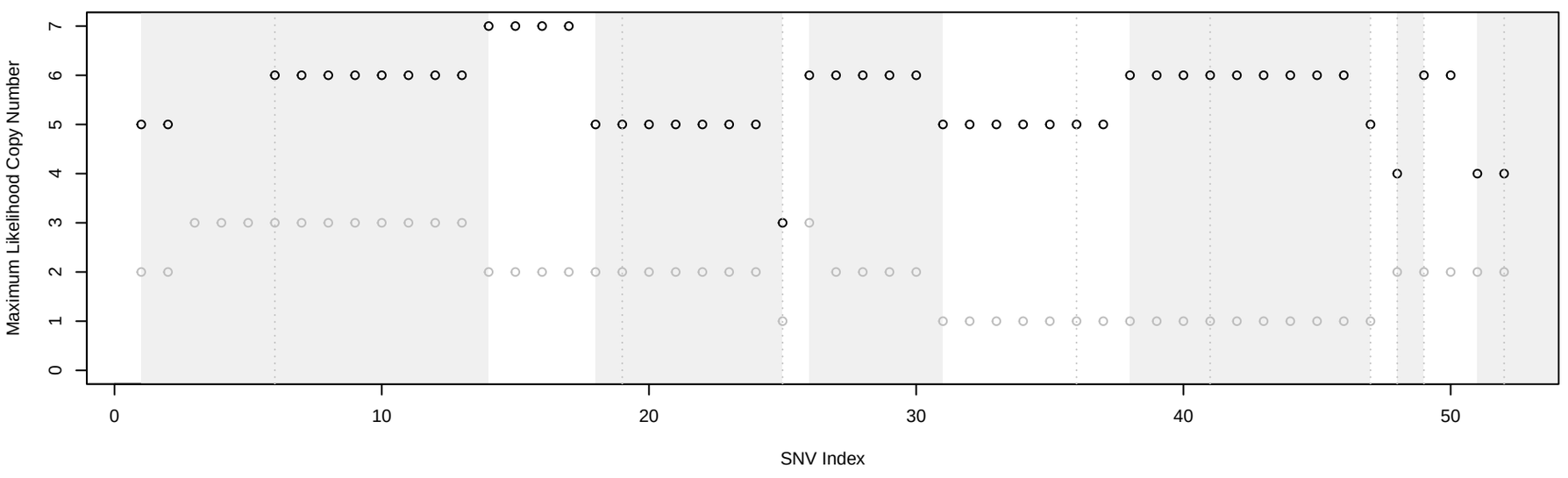

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m2
5m2
6m2
7m2
2m1
3m1
4m1
5m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio

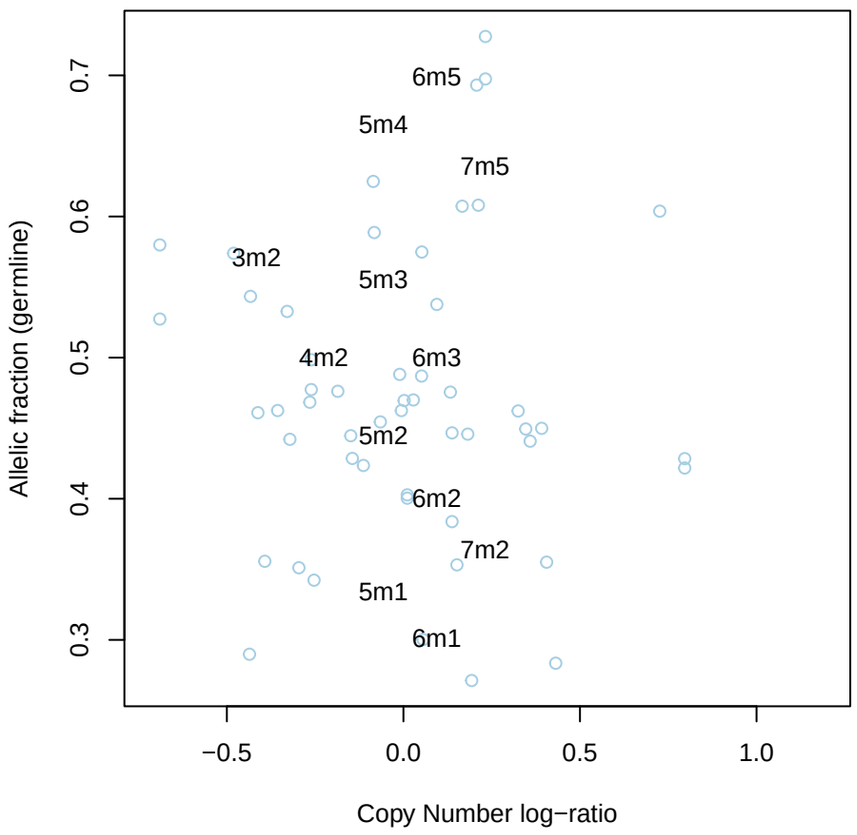

Frequency
Cellular fraction

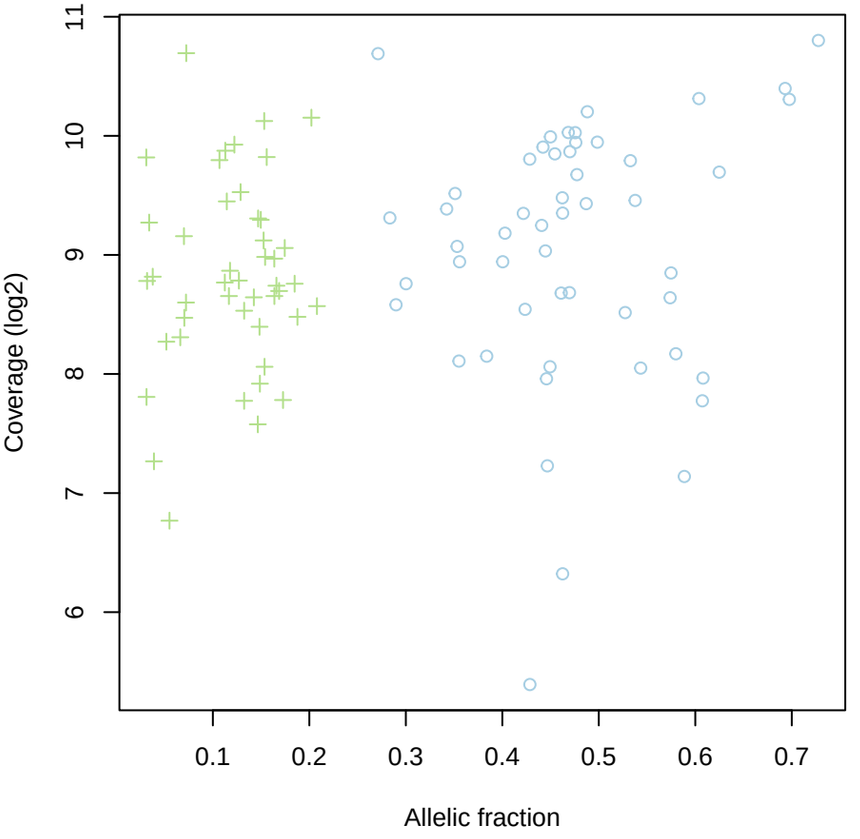

Purity: 0.33 Tumor ploidy: 5.362
0
1
2
3
4
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

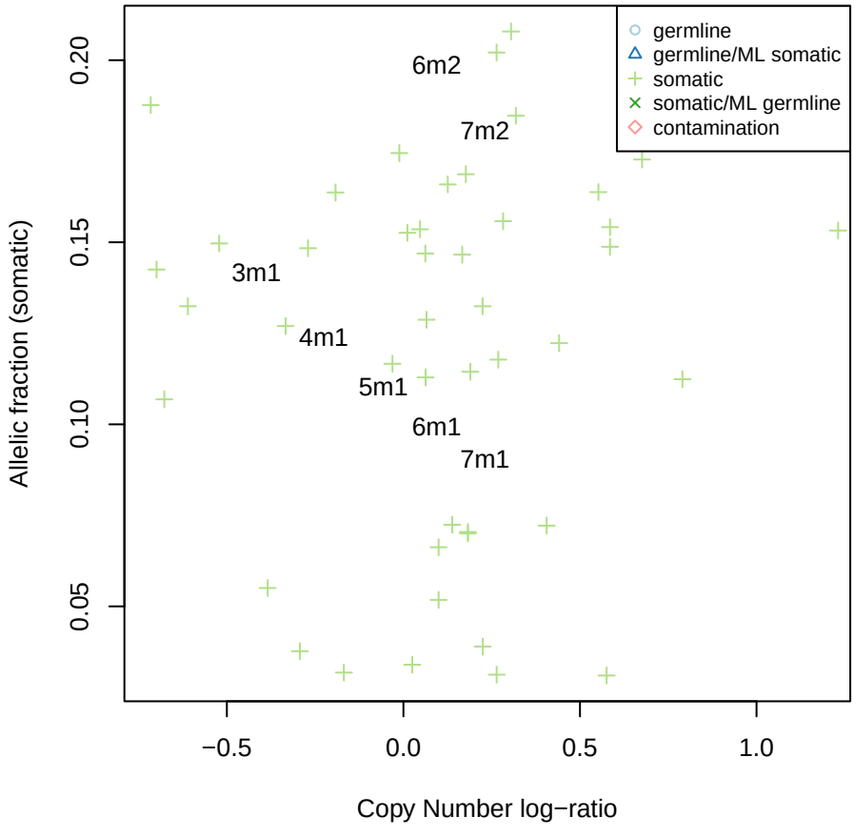

Purity: 0.33 Tumor ploidy: 5.362 SNV log−likelihood: −103.28 GoF: 93.7% Mean coverage: 586;597
1
2
3
4
5
6
7
9
14
B−Allele Frequency
0.3
0.4
0.5
0.6
0.7
0
10
20
30
40
50
SNV Index

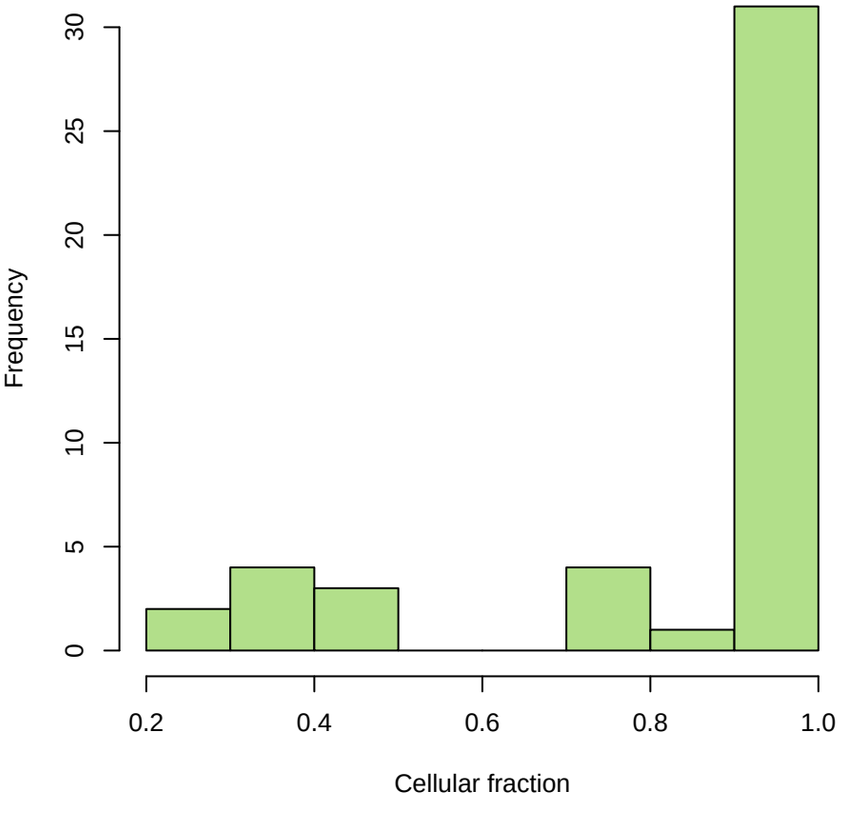

SCNA−fit log−likelihood: −14826.75
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
1
2
3
5
7
0
10
20
30
40
50
SNV Index

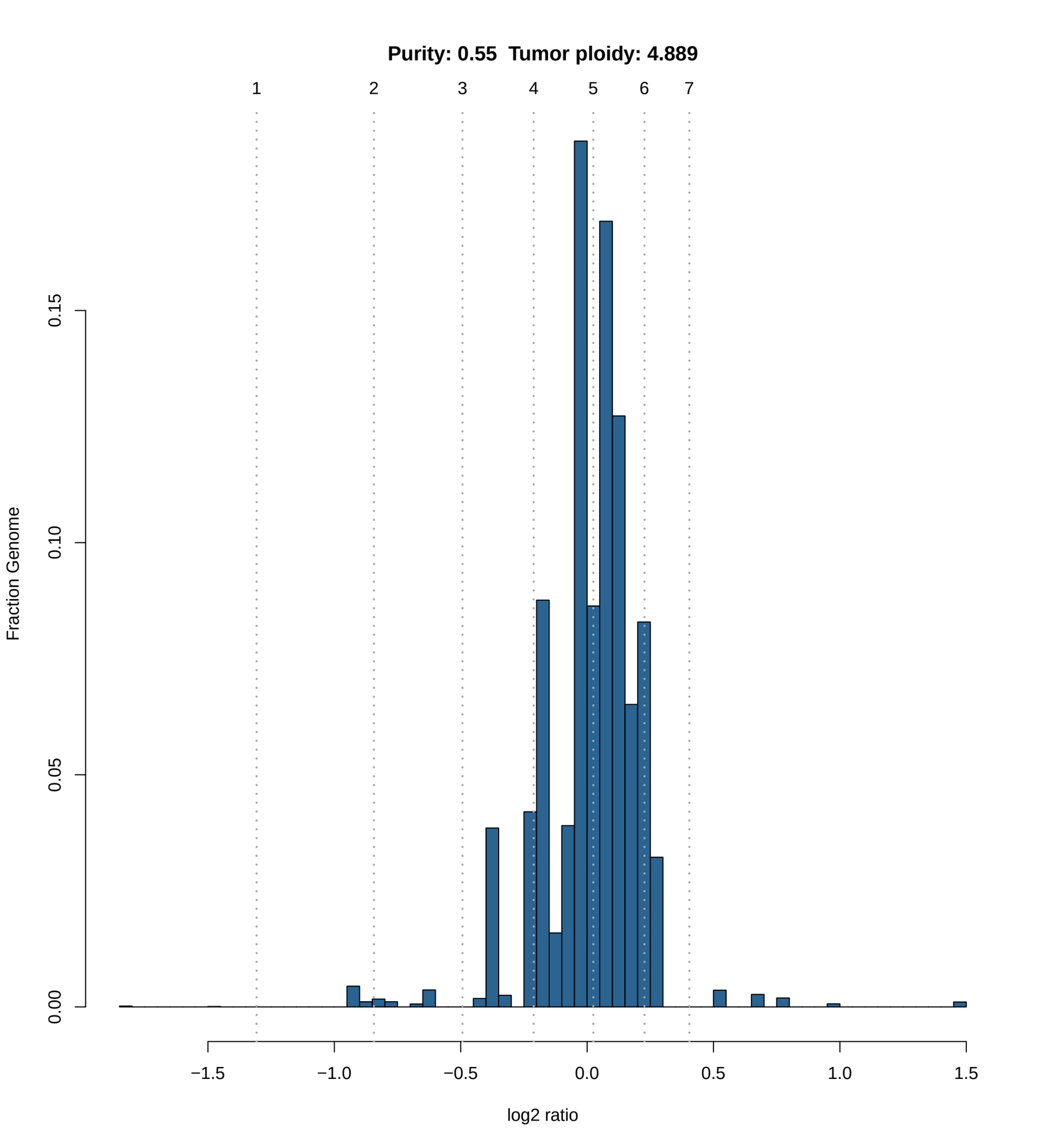

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
7
0
10
20
30
40
50
SNV Index

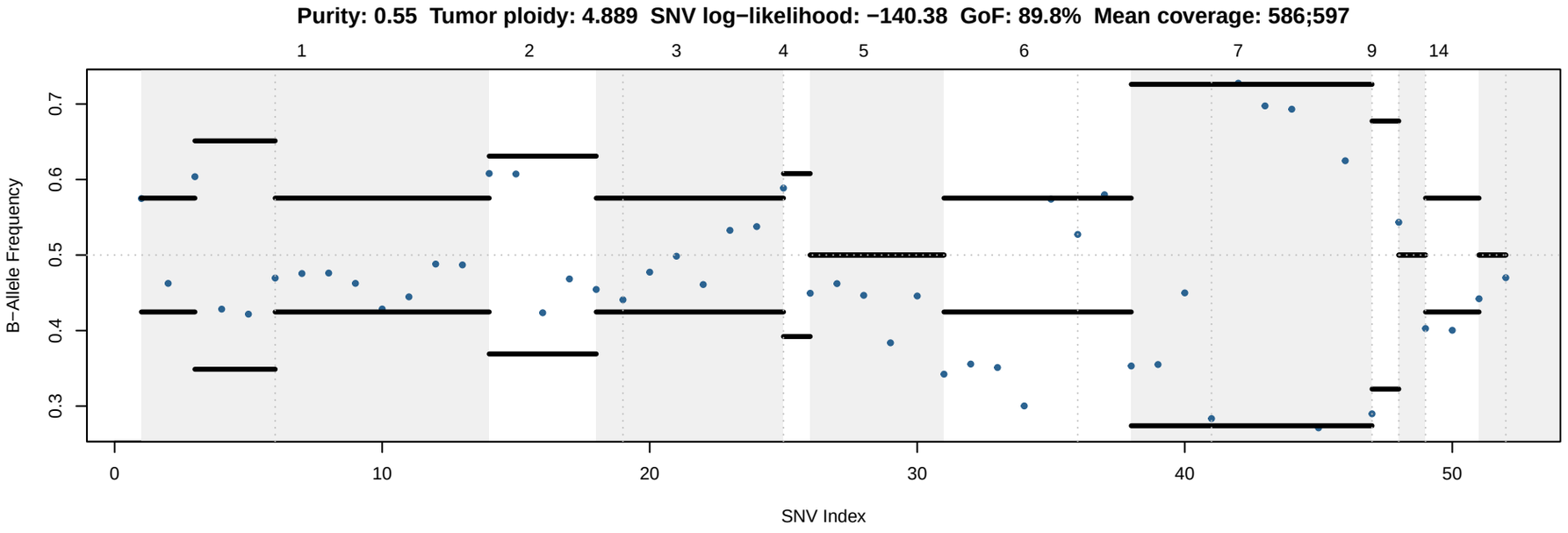

Allelic fraction (germline)
Copy Number log−ratio
6m5
5m4
7m5
3m2
5m3
4m2
6m3
5m2
6m2
7m2
5m1
6m1

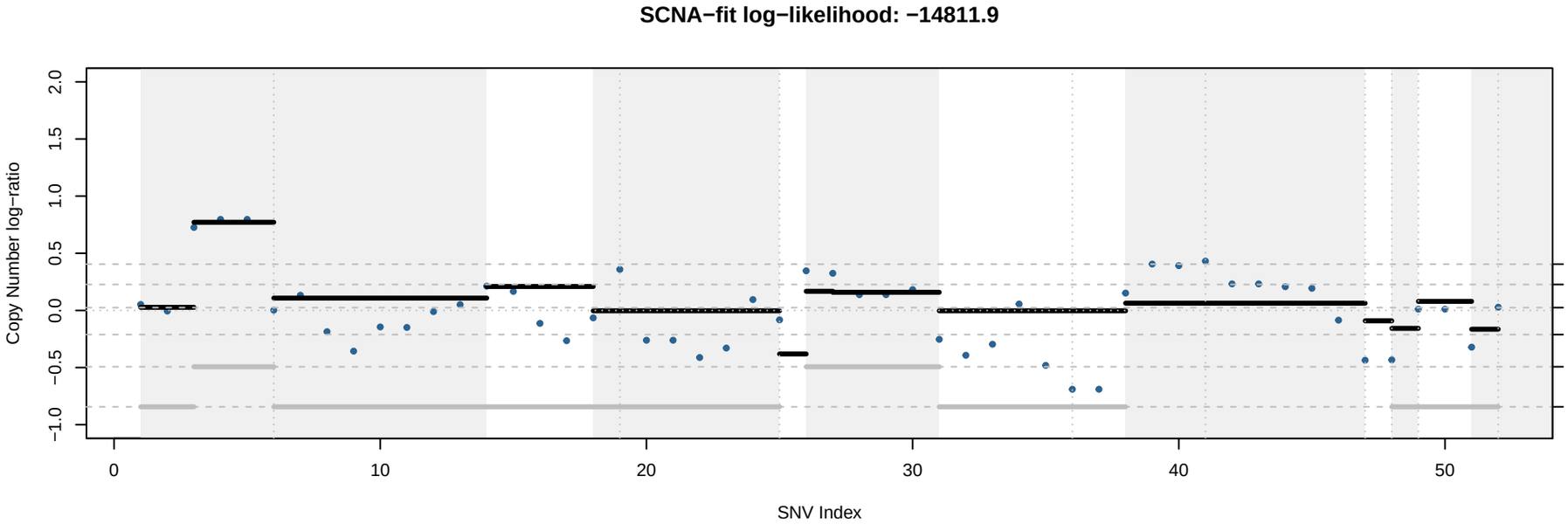

Coverage (log2)
Allelic fraction

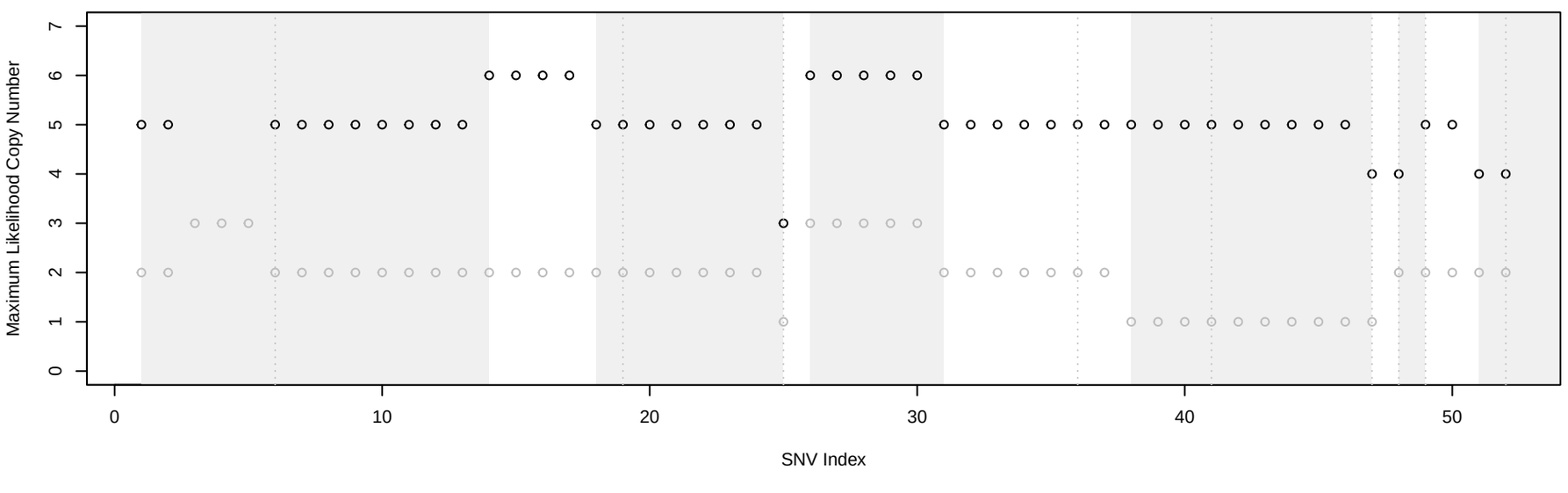

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
6m2
7m2
3m1
4m1
5m1
6m1
7m1

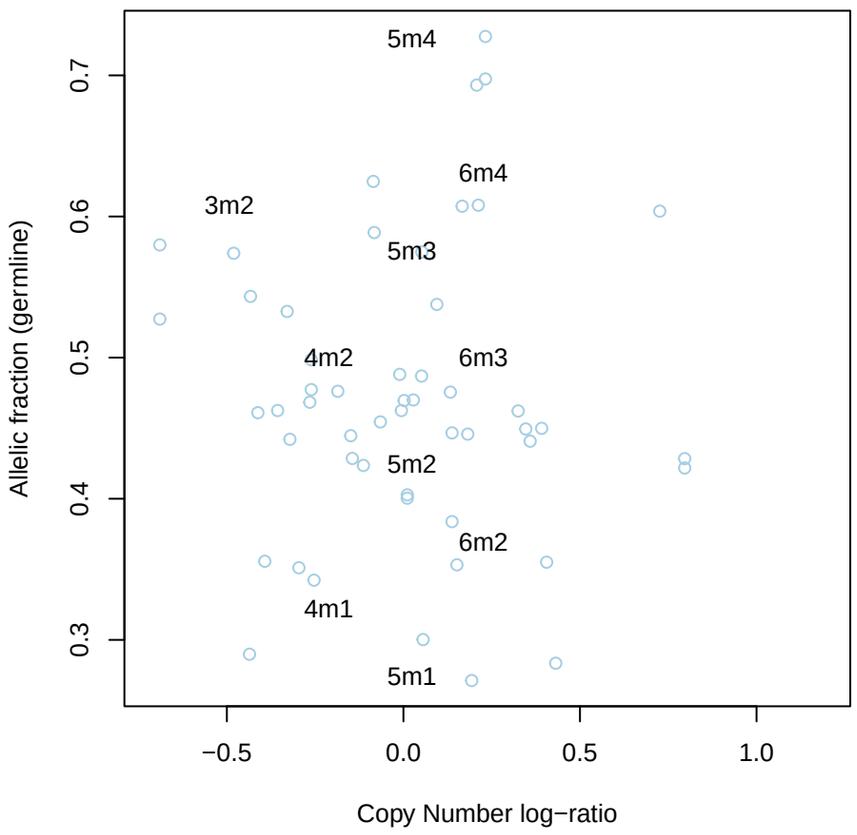

Frequency
Cellular fraction

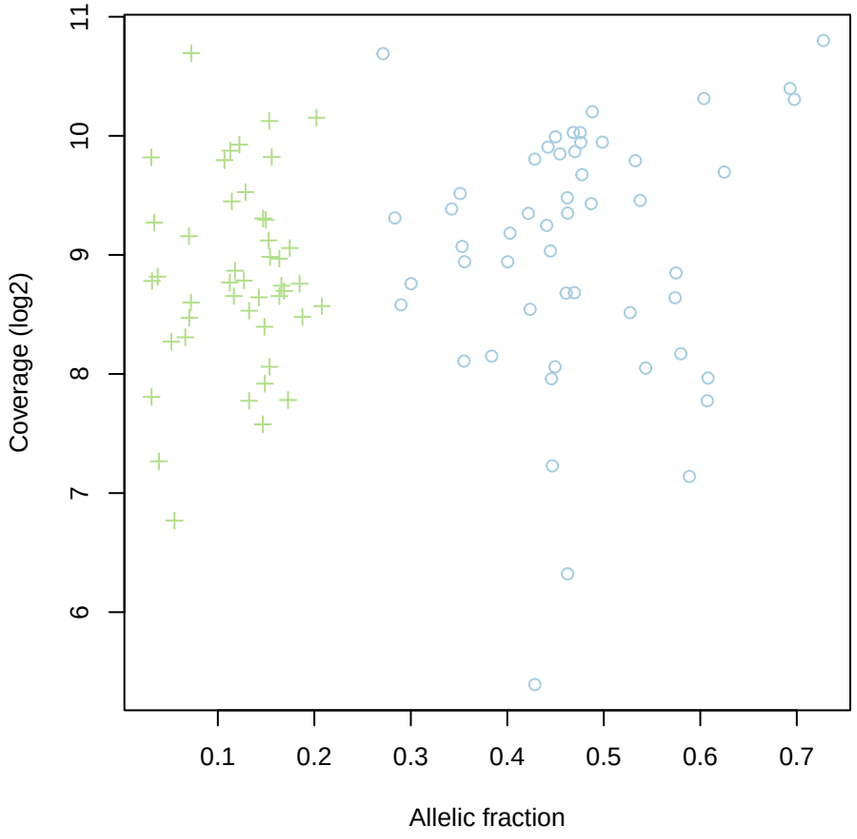

Purity: 0.55 Tumor ploidy: 4.889
1
2
3
4
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

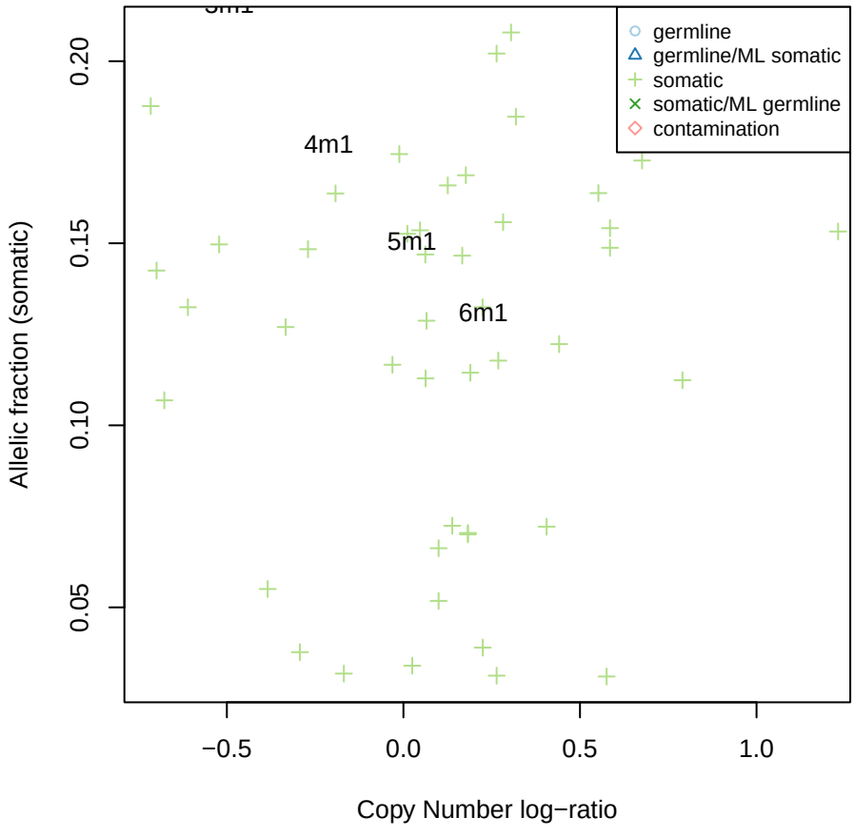

Purity: 0.55 Tumor ploidy: 4.889 SNV log−likelihood: −140.38 GoF: 89.8% Mean coverage: 586;597
1
2
3
4
5
6
7
9
14
B−Allele Frequency
0.3
0.4
0.5
0.6
0.7
0
10
20
30
40
50
SNV Index

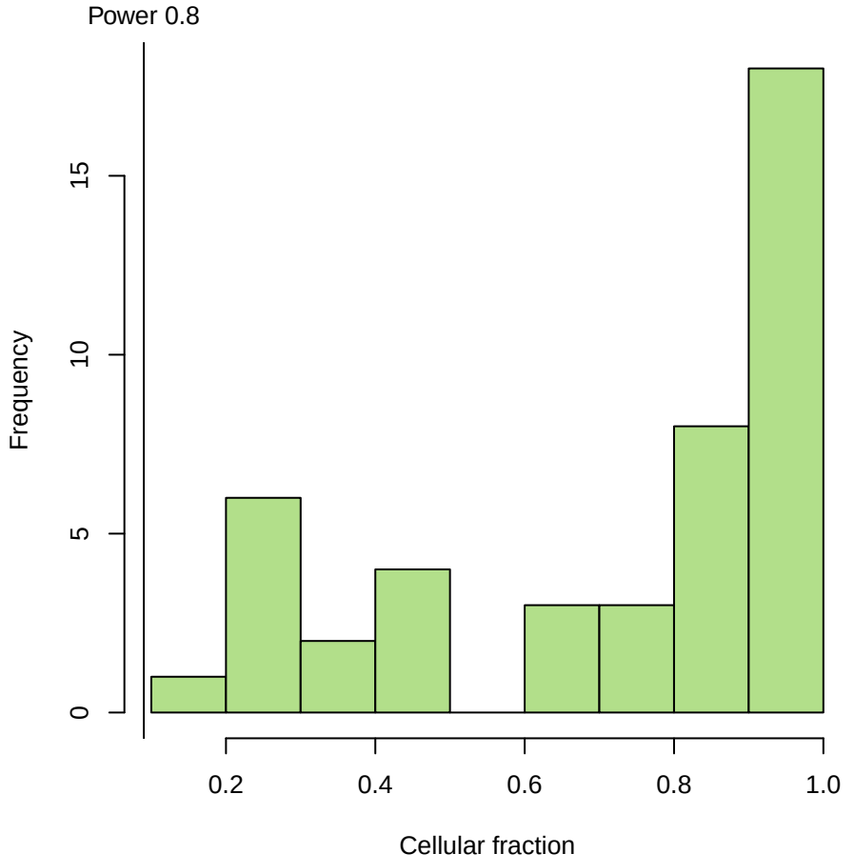

SCNA−fit log−likelihood: −14811.9
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
2
3
4
5
7
0
10
20
30
40
50
SNV Index

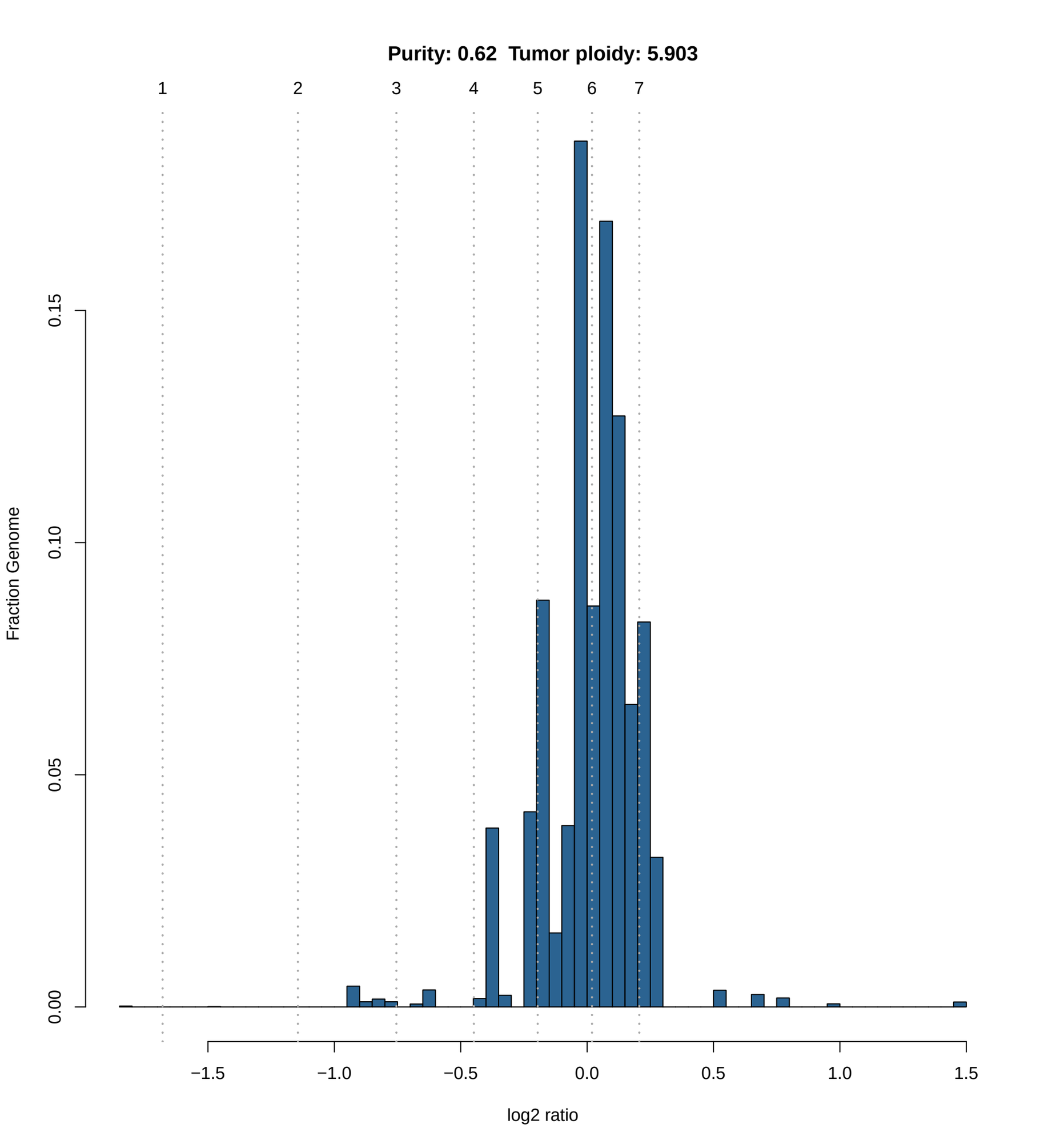

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
7
0
10
20
30
40
50
SNV Index

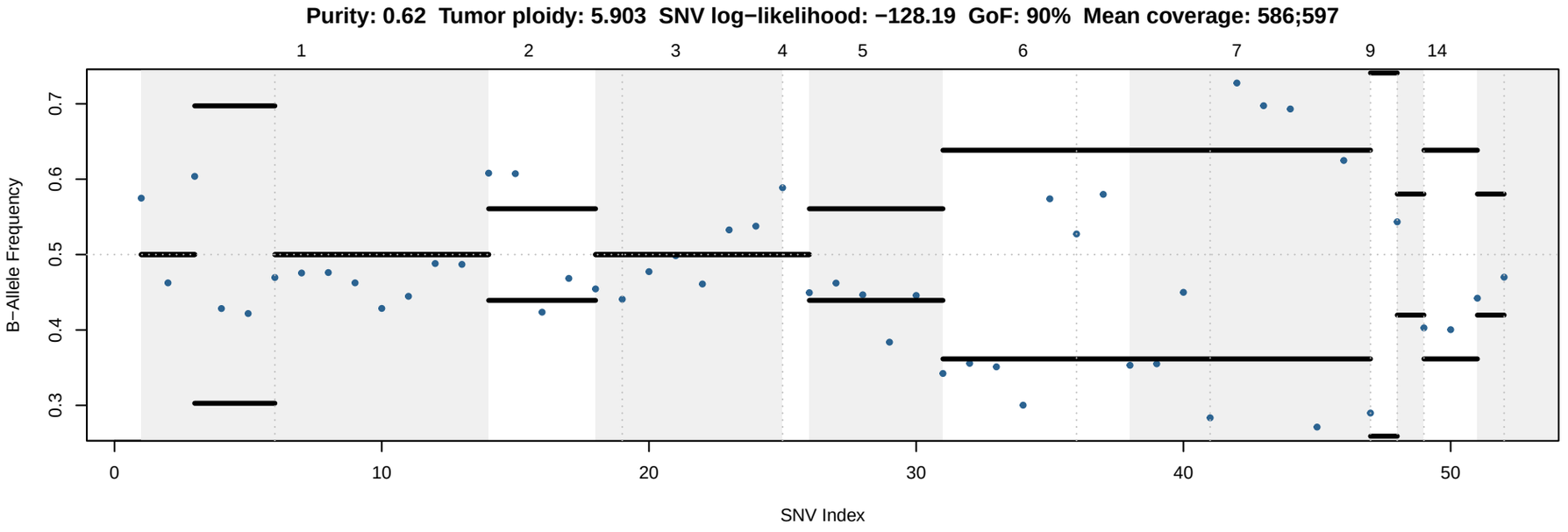

5m4
6m4
3m2
5m3
4m2
6m3
5m2
6m2
4m1
5m1
Allelic fraction (germline)
Copy Number log−ratio

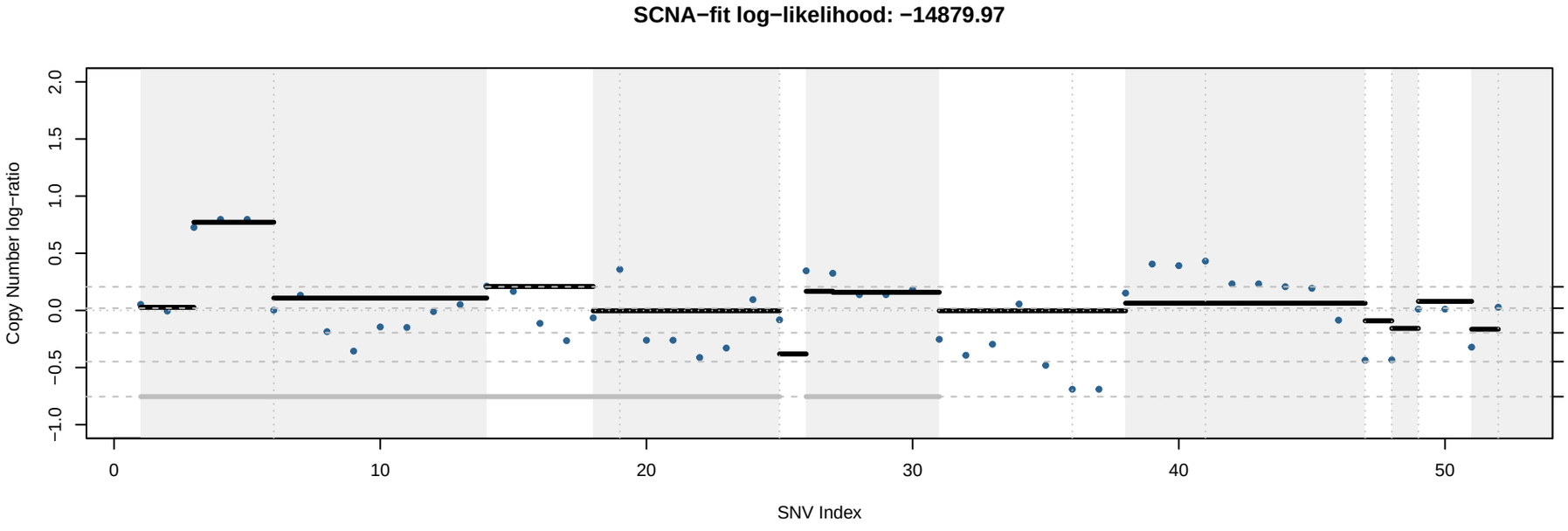

Coverage (log2)
Allelic fraction

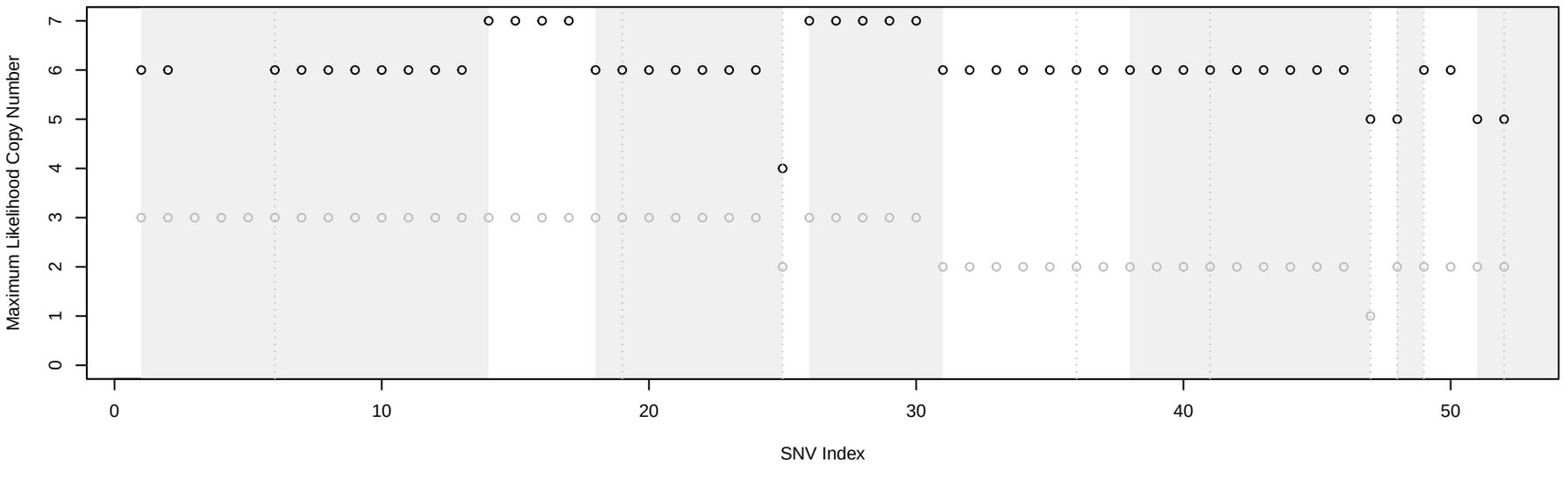

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio

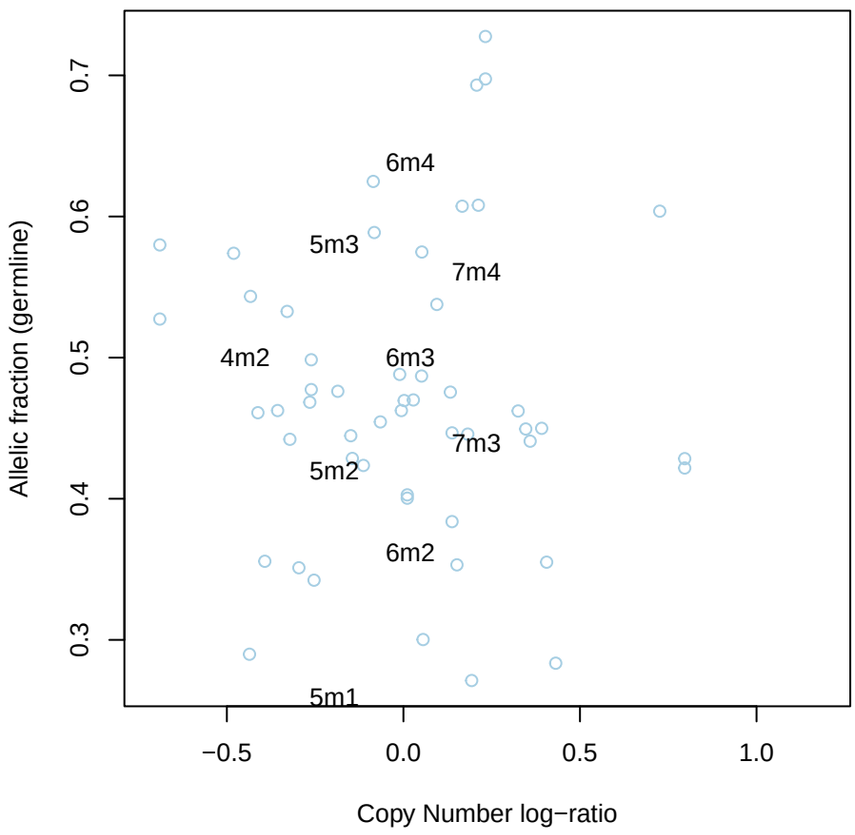

Power 0.8
Frequency
Cellular fraction

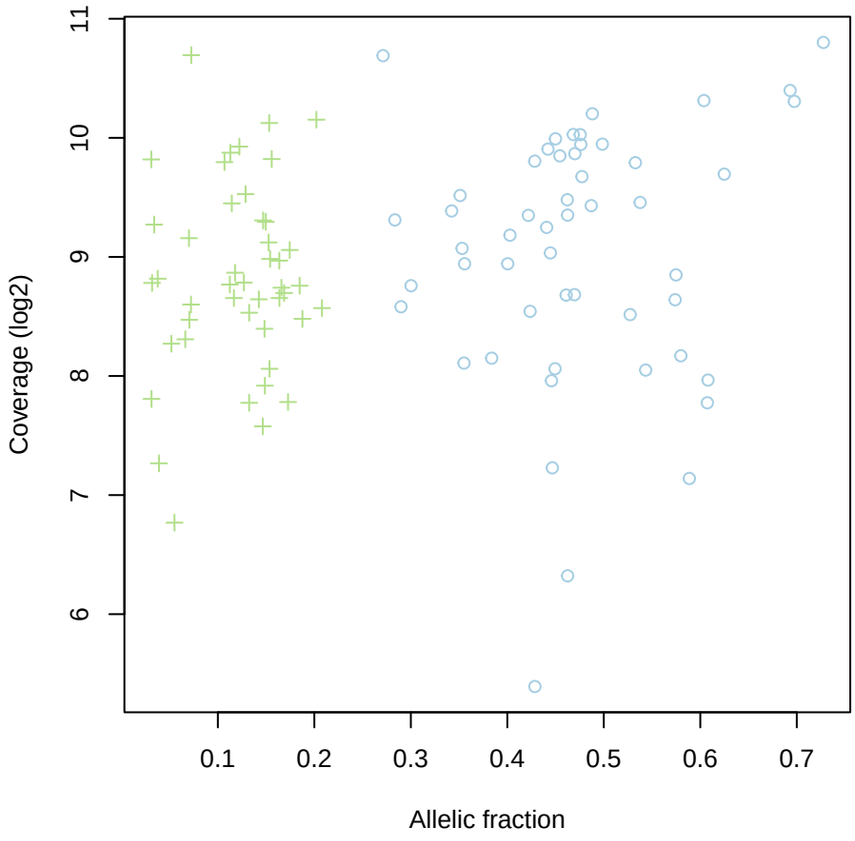

Purity: 0.62 Tumor ploidy: 5.903
1
2
3
4
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

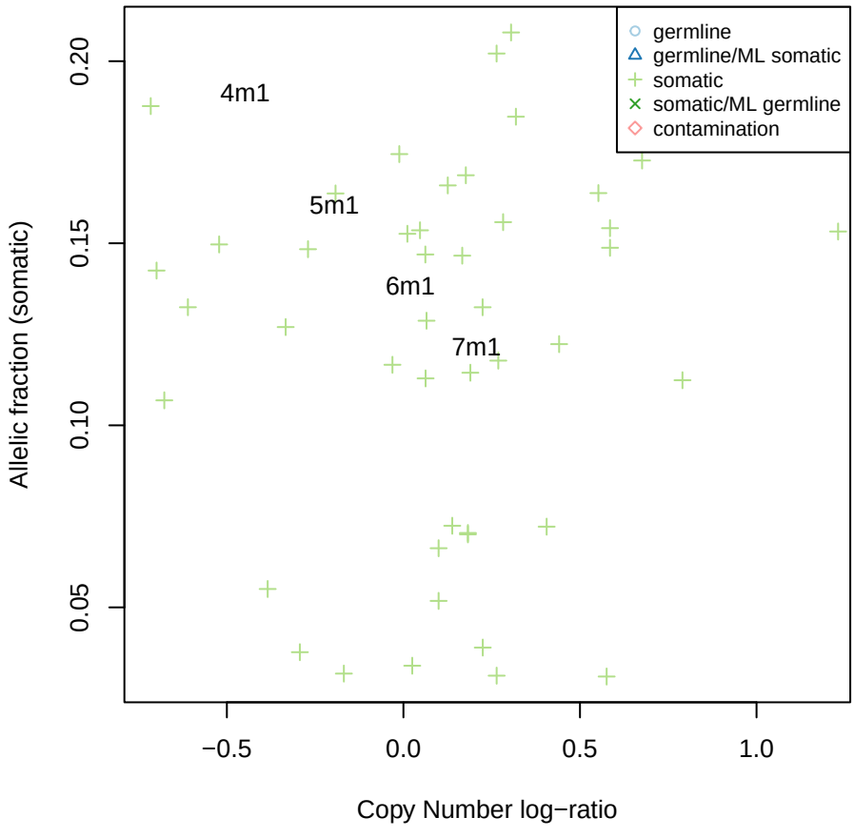

Purity: 0.62 Tumor ploidy: 5.903 SNV log−likelihood: −128.19 GoF: 90% Mean coverage: 586;597
1
2
3
4
5
6
7
9
14
B−Allele Frequency
0.3
0.4
0.5
0.6
0.7
0
10
20
30
40
50
SNV Index

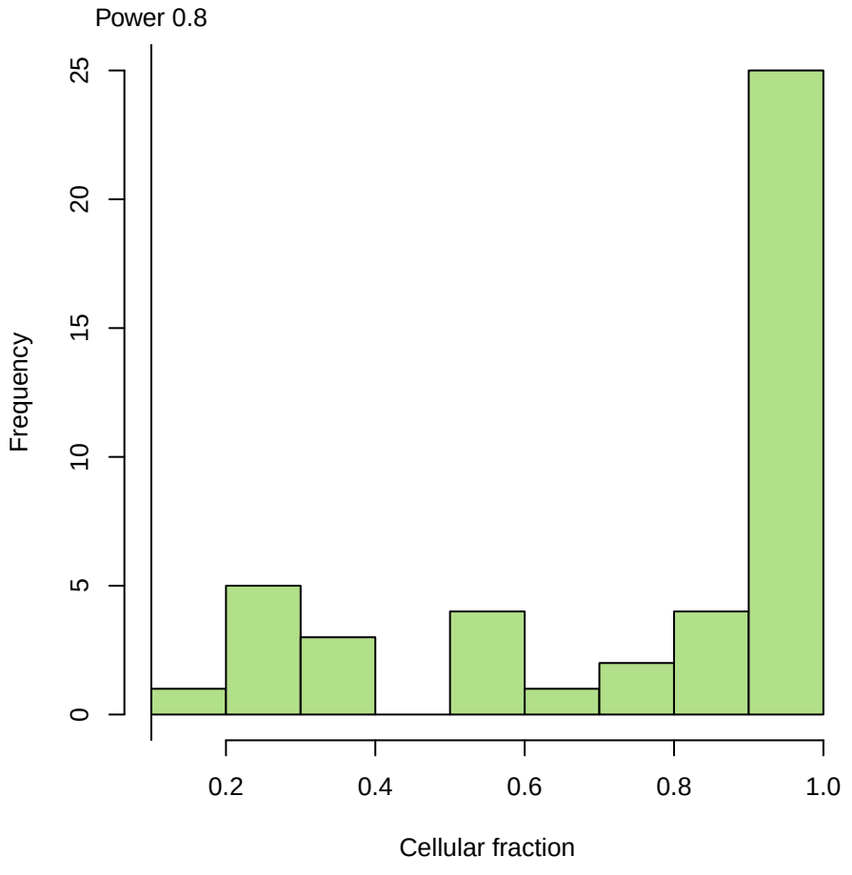

SCNA−fit log−likelihood: −14879.97
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
3
4
5
7
0
10
20
30
40
50
SNV Index

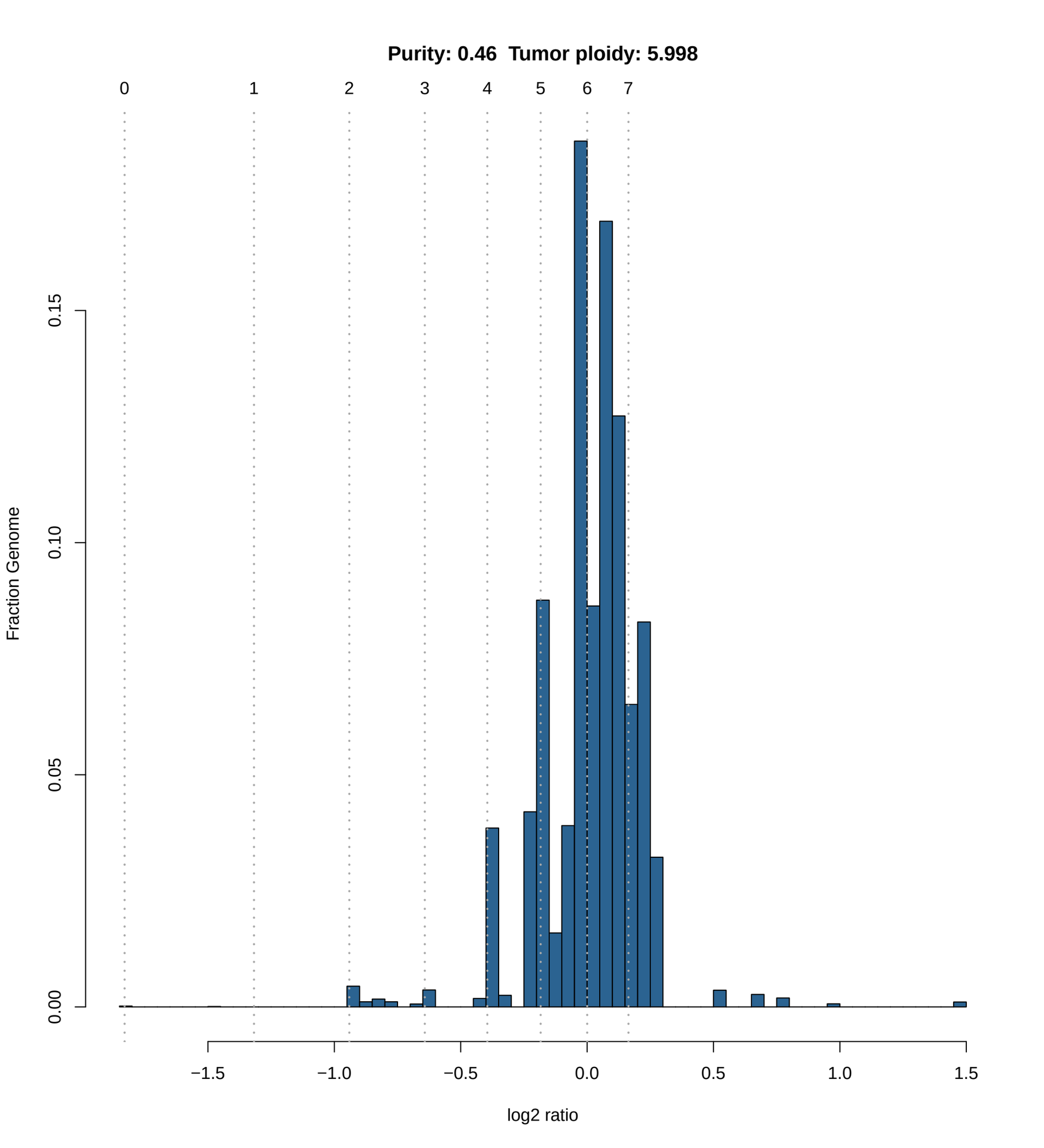

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
7
0
10
20
30
40
50
SNV Index

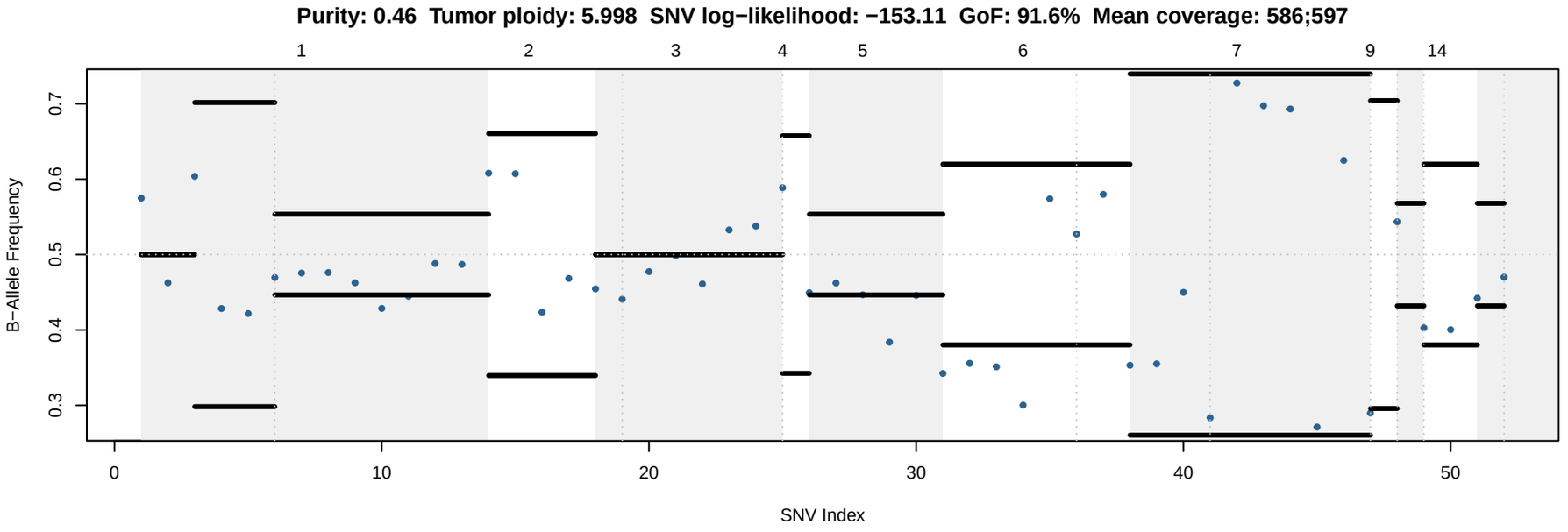

Allelic fraction (germline)
Copy Number log−ratio
6m4
5m3
7m4
4m2
6m3
7m3
5m2
6m2
5m1

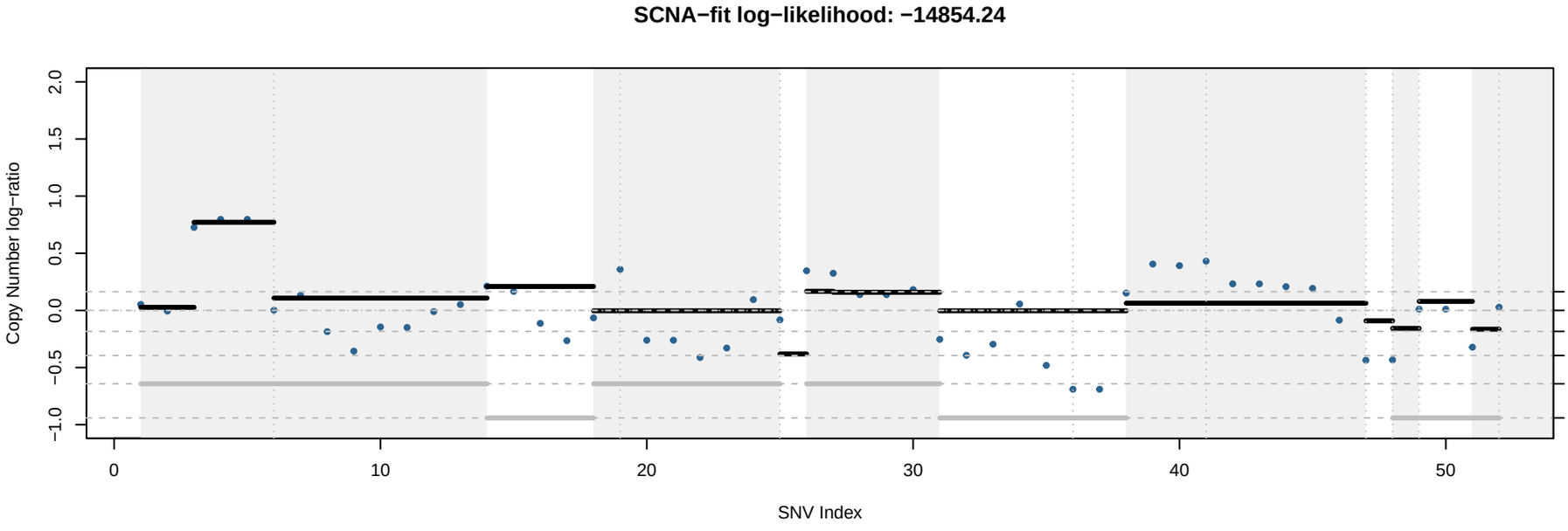

Coverage (log2)
Allelic fraction

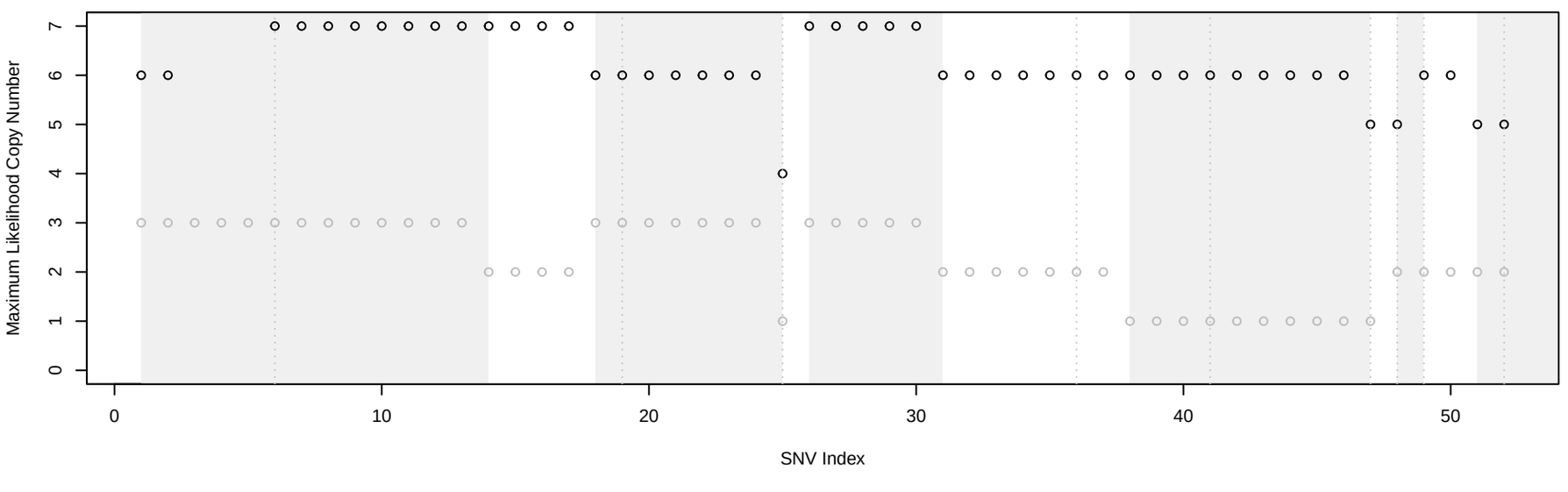

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
4m1
5m1
6m1
7m1

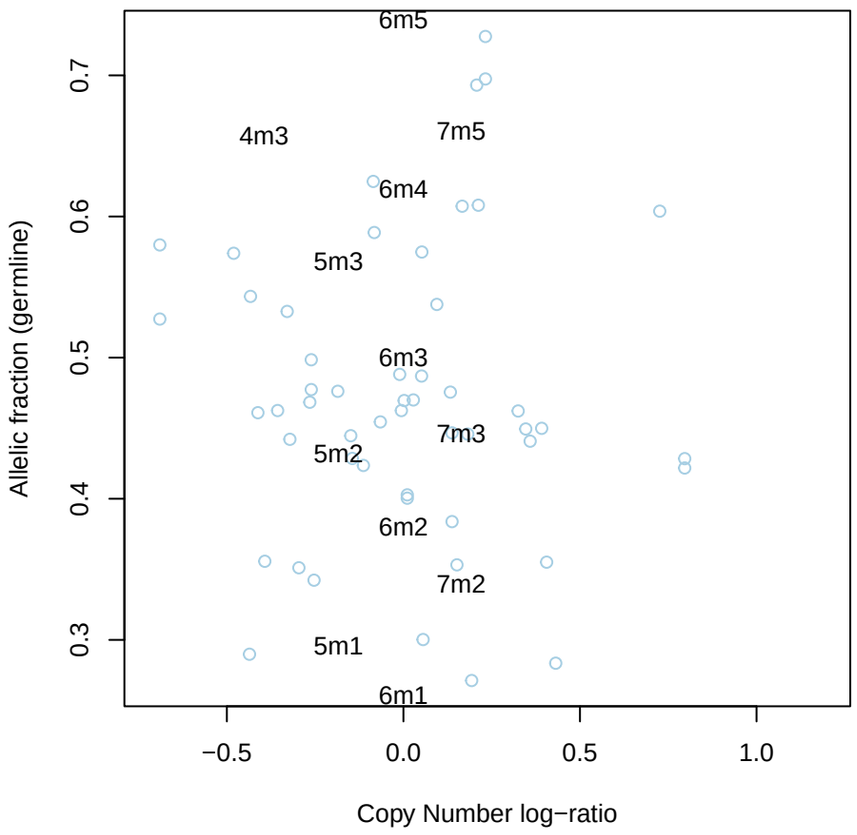

Power 0.8
Frequency
Cellular fraction

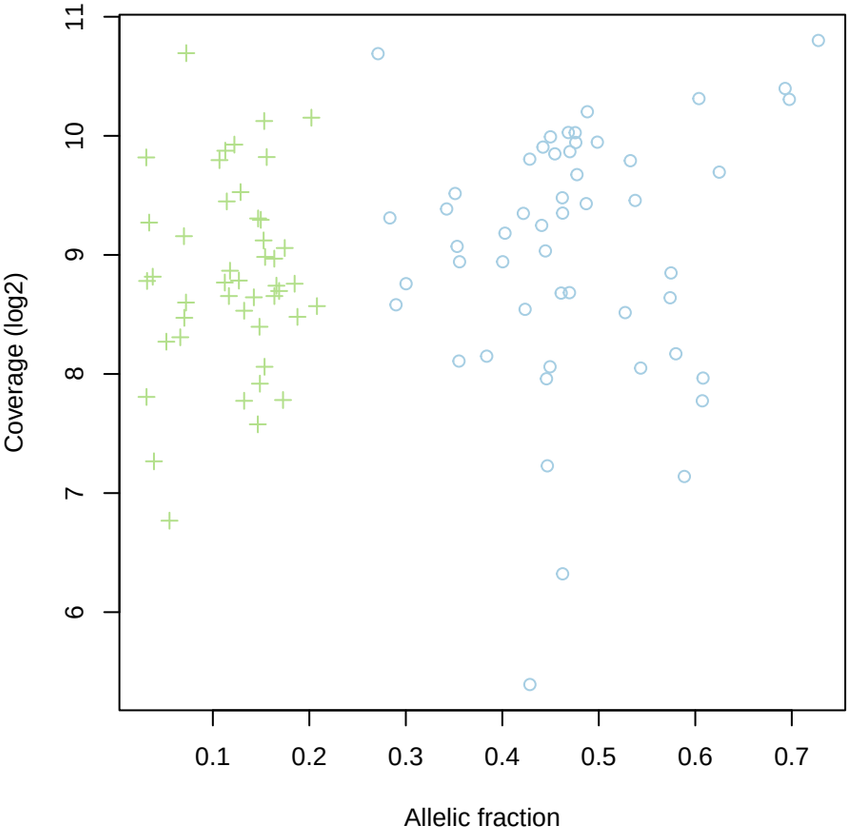

Purity: 0.46 Tumor ploidy: 5.998
0
1
2
3
4
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

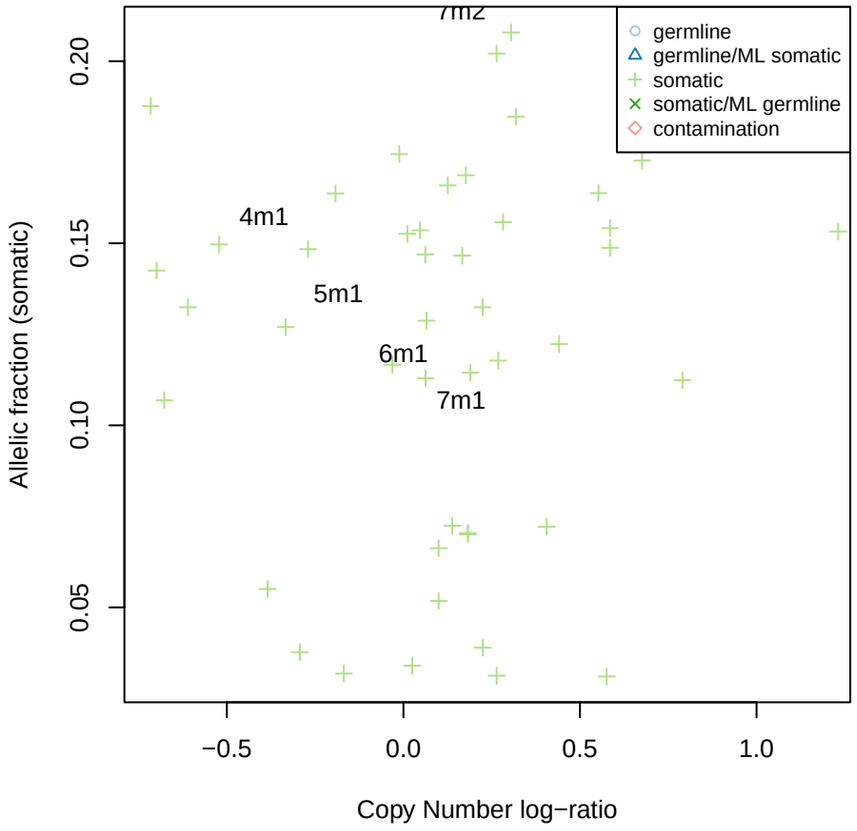

Purity: 0.46 Tumor ploidy: 5.998 SNV log−likelihood: −153.11 GoF: 91.6% Mean coverage: 586;597
1
2
3
4
5
6
7
9
14
B−Allele Frequency
0.3
0.4
0.5
0.6
0.7
0
10
20
30
40
50
SNV Index

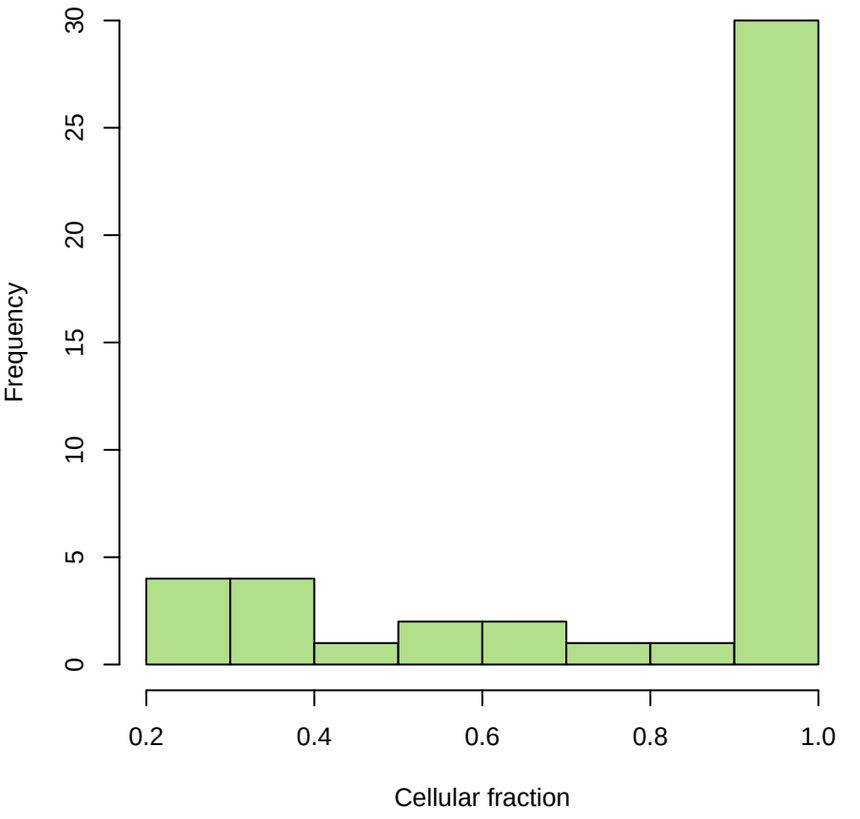

SCNA−fit log−likelihood: −14854.24
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
2
3
4
6
0
10
20
30
40
50
SNV Index

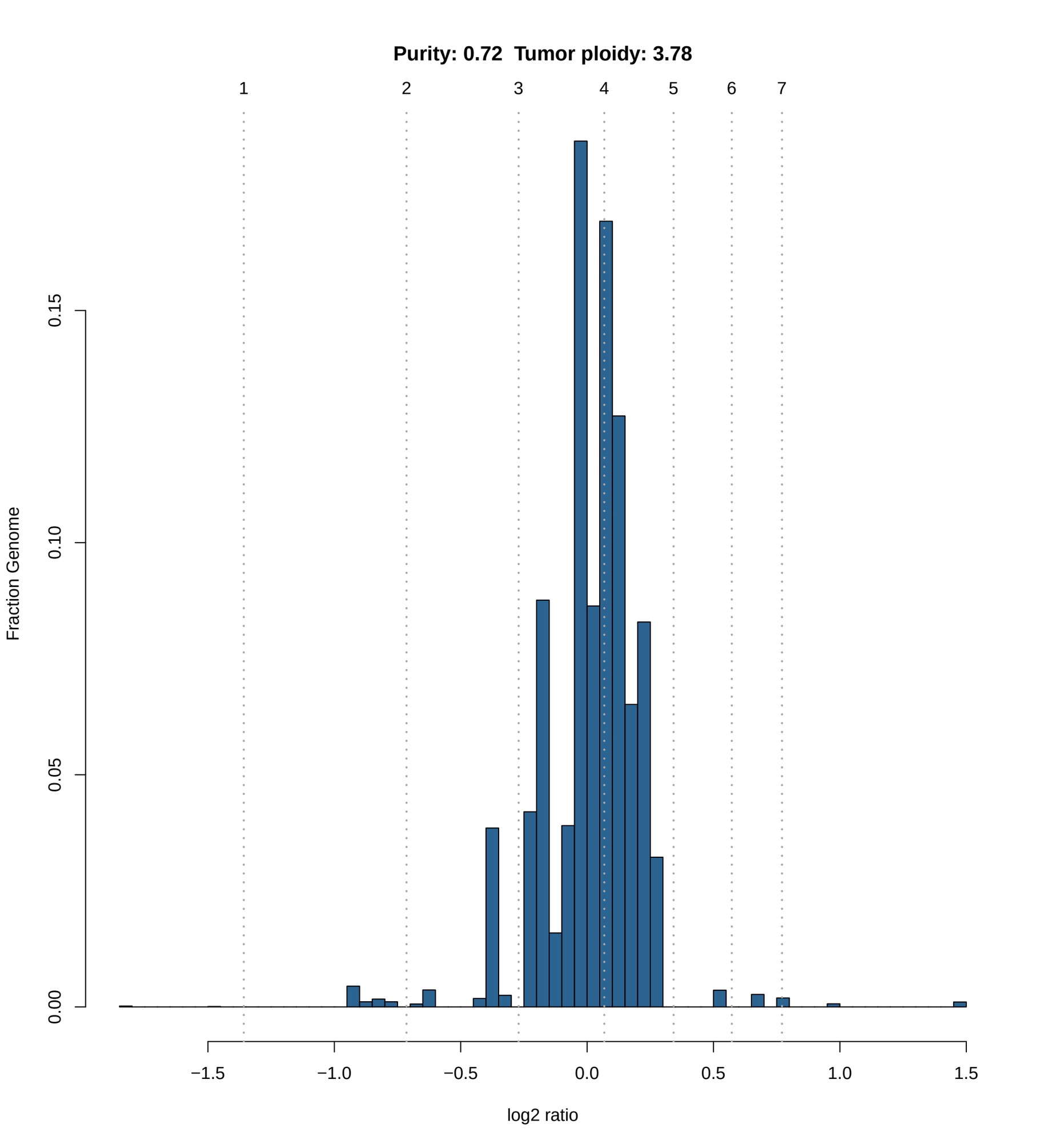

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
7
0
10
20
30
40
50
SNV Index

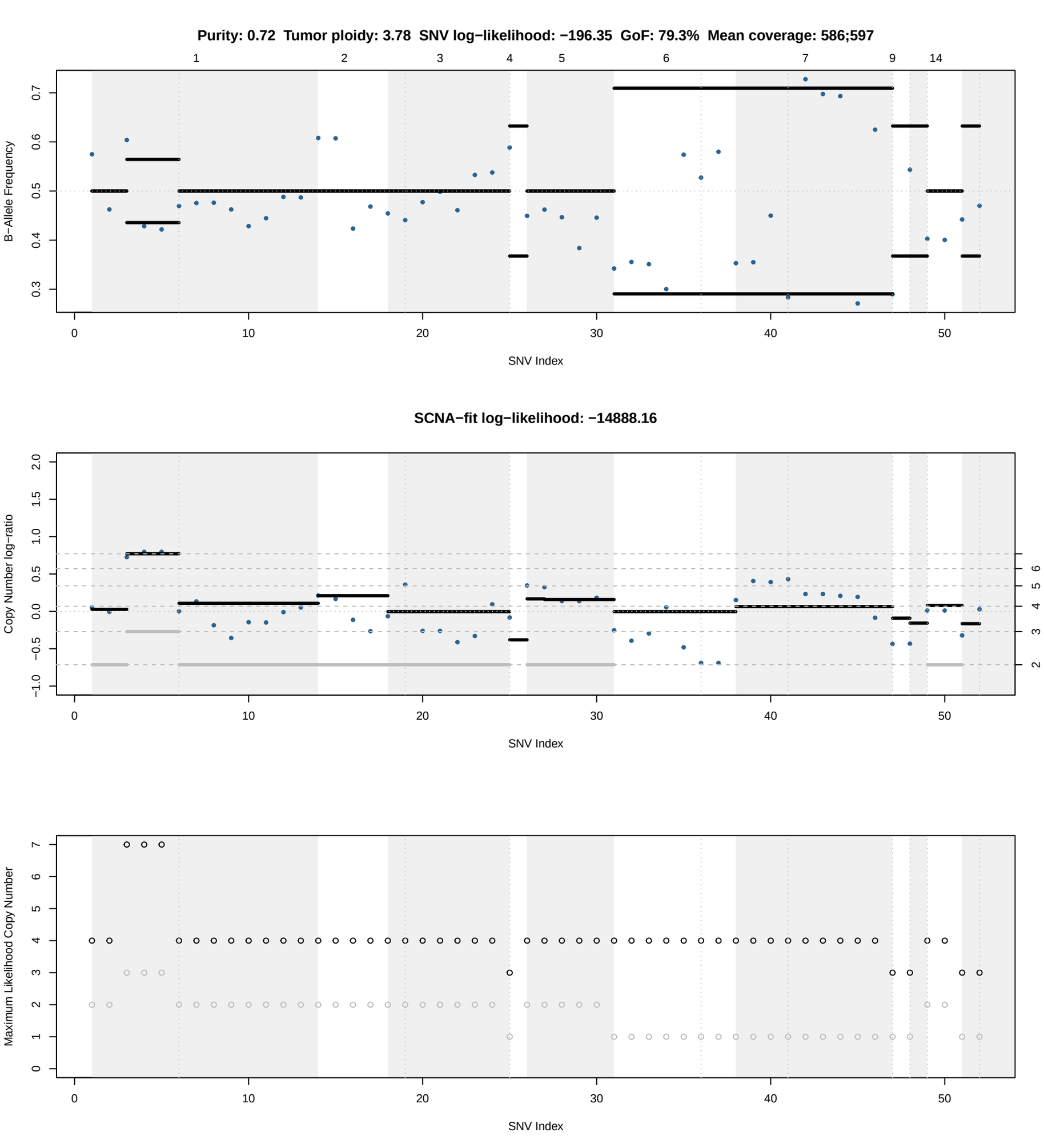

6m5
4m3
7m5
6m4
5m3
6m3
7m3
5m2
6m2
7m2
5m1
6m1
Allelic fraction (germline)
Copy Number log−ratio

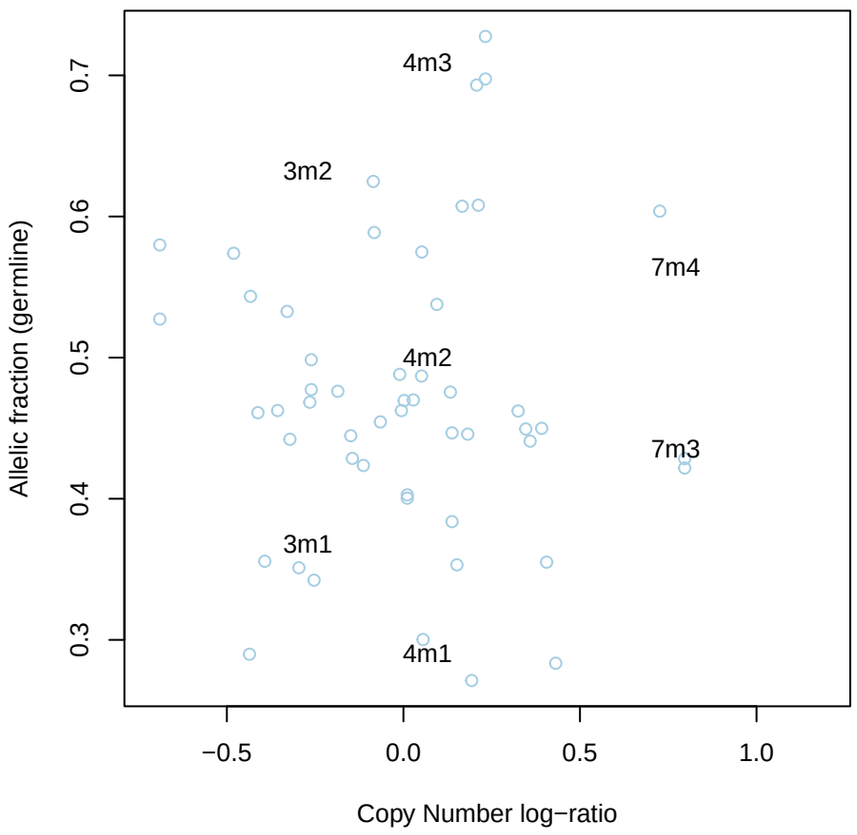

Coverage (log2)
Allelic fraction

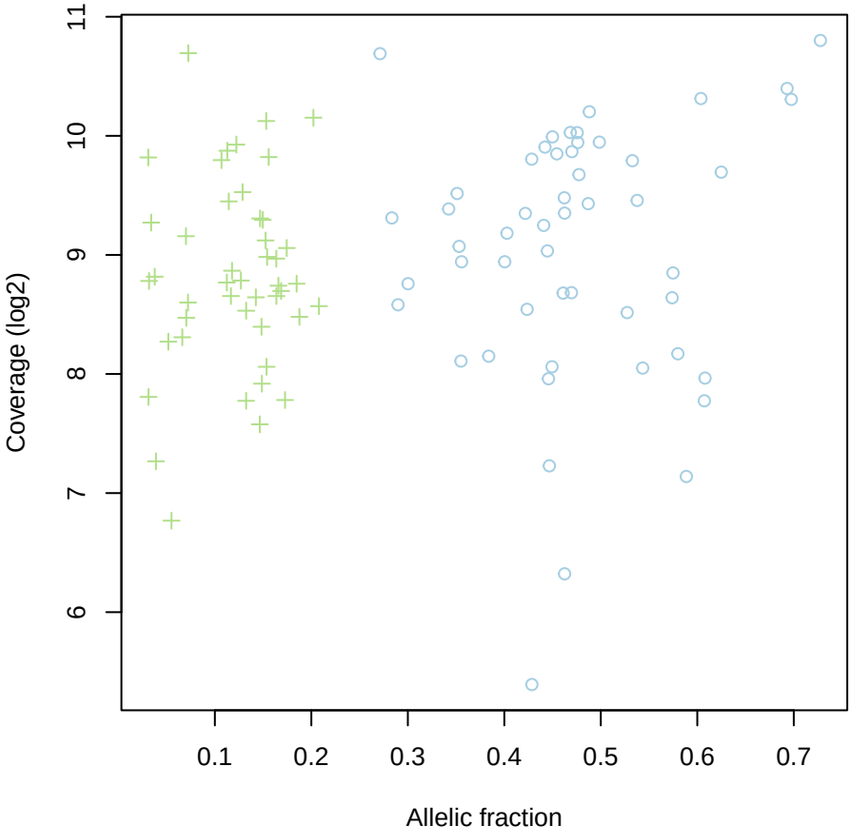

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

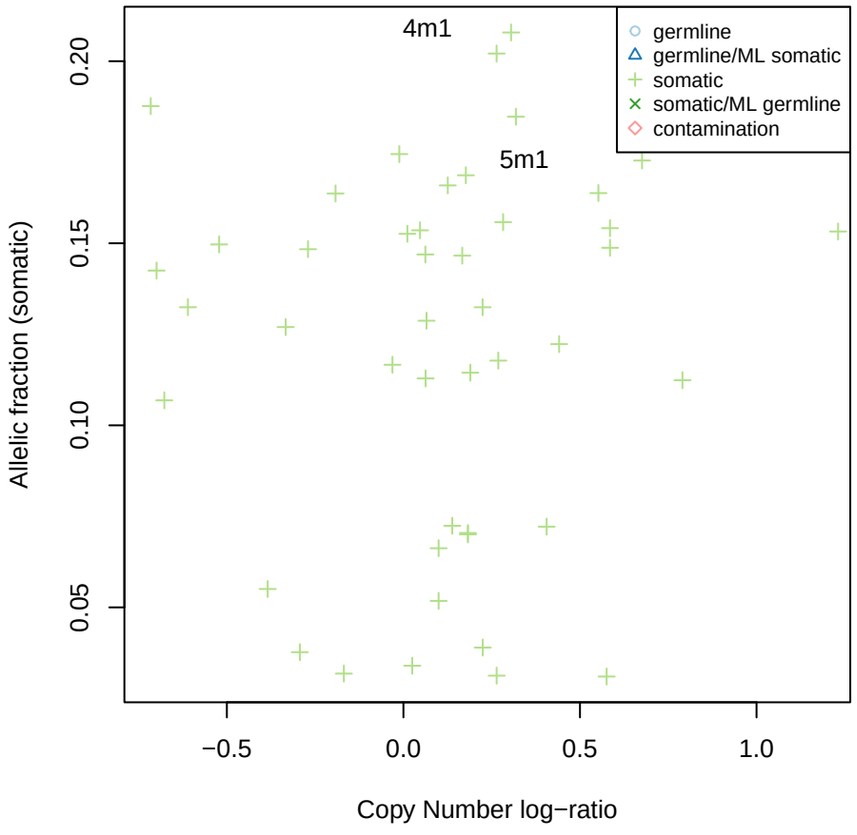

Frequency
Cellular fraction

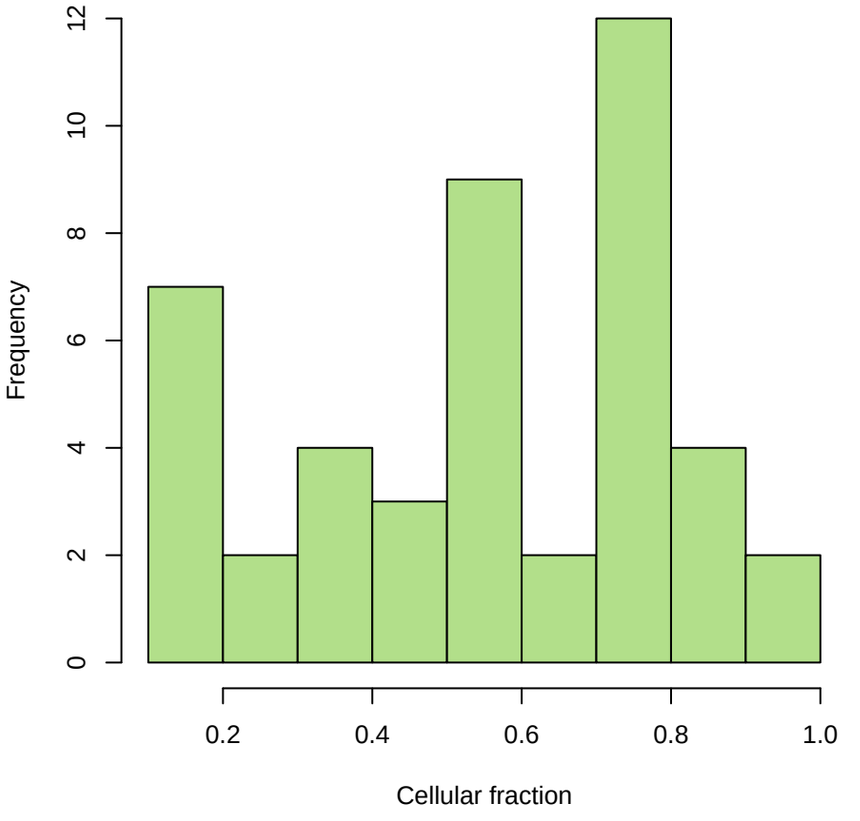

Purity: 0.72 Tumor ploidy: 3.78
1
2
3
4
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

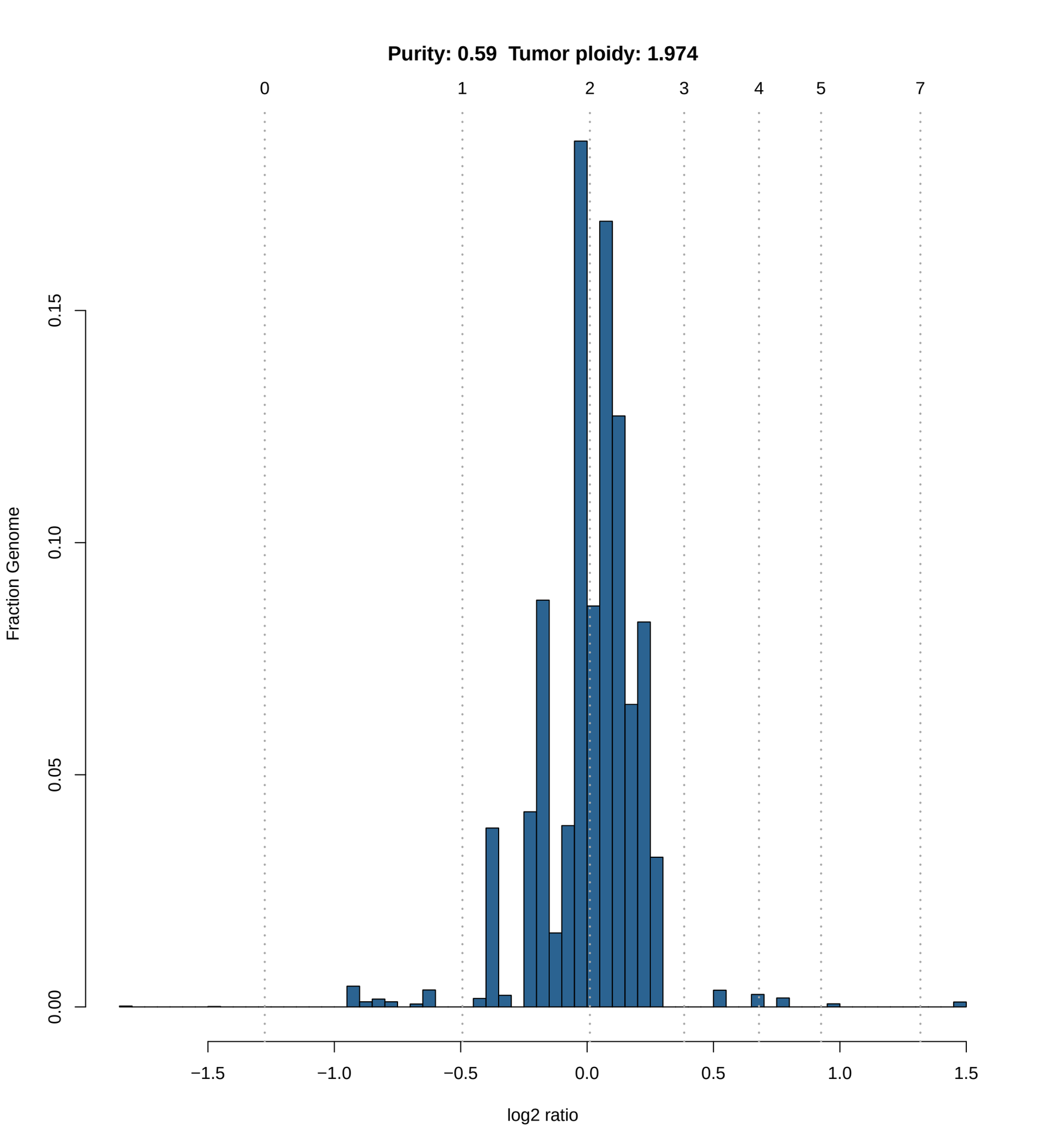

Purity: 0.72 Tumor ploidy: 3.78 SNV log−likelihood: −196.35 GoF: 79.3% Mean coverage: 586;597
1
2
3
4
5
6
7
9
14
B−Allele Frequency
0.3
0.4
0.5
0.6
0.7
0
10
20
30
40
50
SNV Index
SCNA−fit log−likelihood: −14888.16
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
2
3
4
5
6
0
10
20
30
40
50
SNV Index
Maximum Likelihood Copy Number
0
1
2
3
4
5
6
7
0
10
20
30
40
50
SNV Index

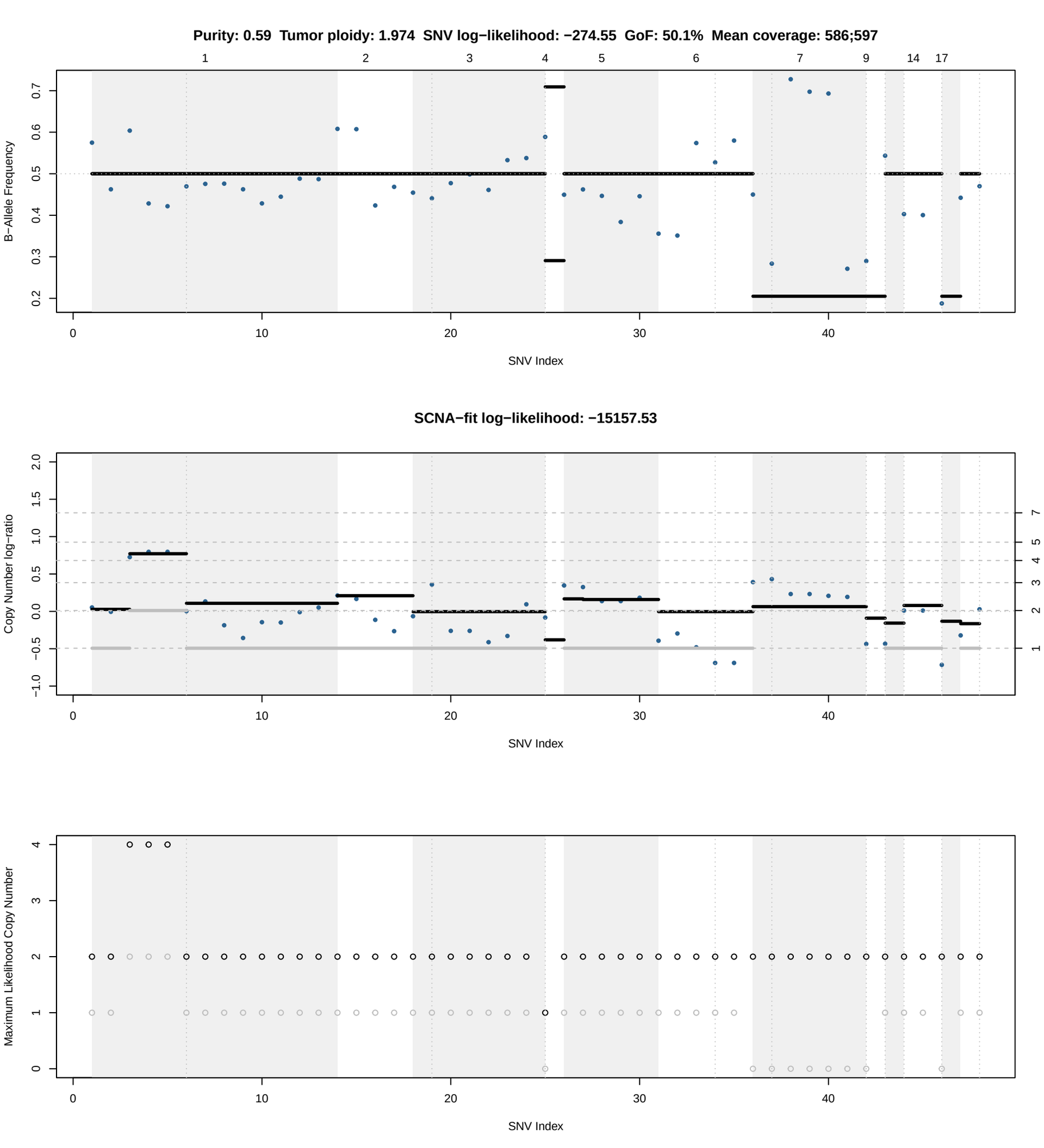

4m3
3m2
7m4
4m2
7m3
3m1
4m1
Allelic fraction (germline)
Copy Number log−ratio

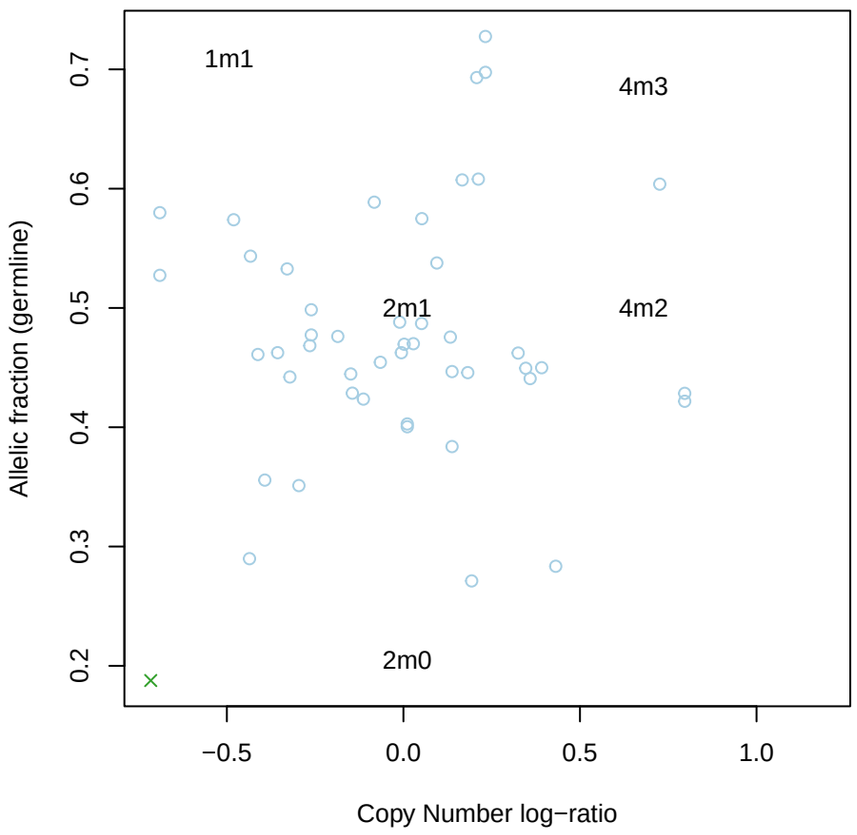

Coverage (log2)
Allelic fraction

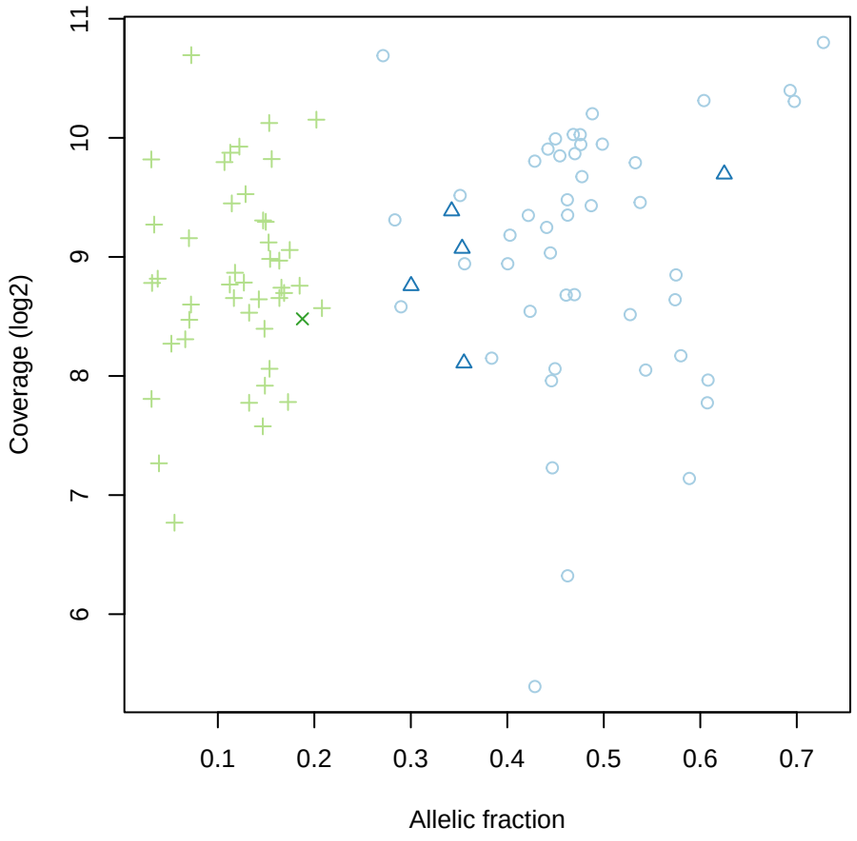

4m1
5m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

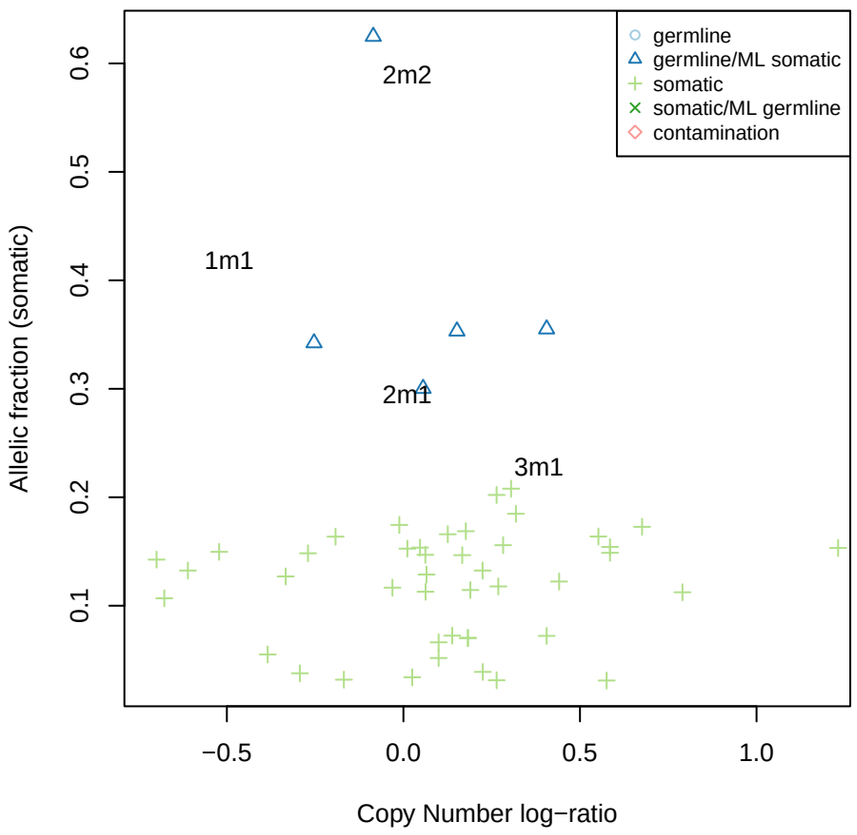

Frequency
Cellular fraction

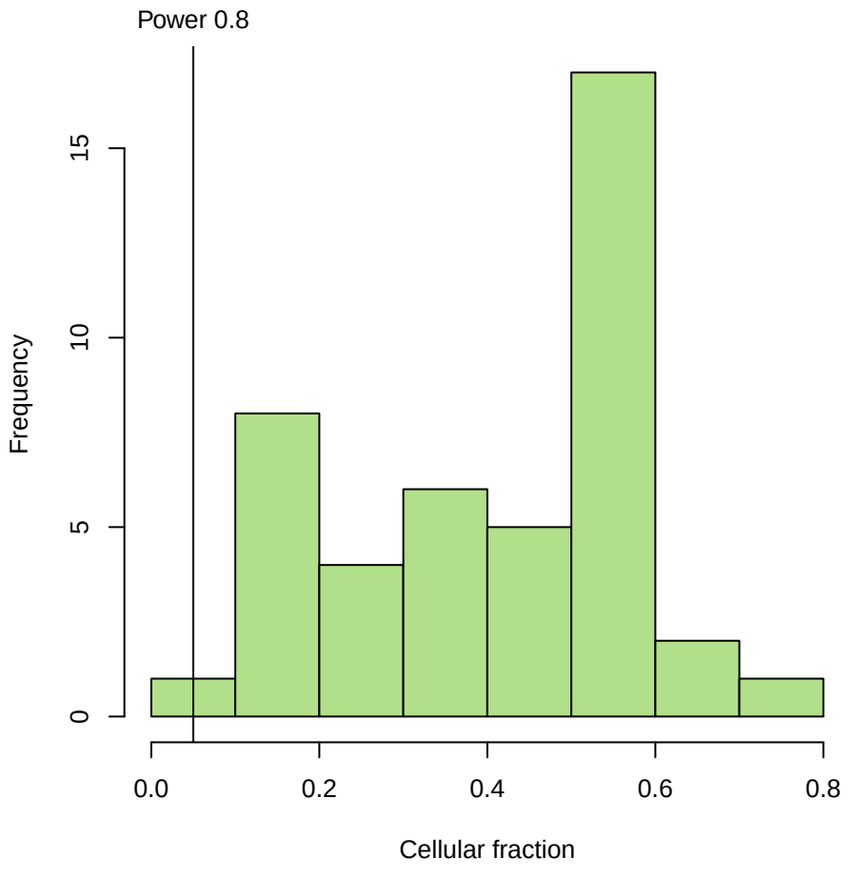

Purity: 0.59 Tumor ploidy: 1.974
0
1
2
3
4
5
7
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio


Purity: 0.59 Tumor ploidy: 1.974 SNV log−likelihood: −274.55 GoF: 50.1% Mean coverage: 586;597
1 2 3 4 5 6 7 9 14 17
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 10 20 30 40
SNV Index
SCNA−fit log−likelihood: −15157.53
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0 1.5 2.0
1 2 3 4 5 7
0 10 20 30 40
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4
0 10 20 30 40
SNV Index


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


Coverage (log2)
Allelic fraction


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


Power 0.8
Frequency
Cellular fraction