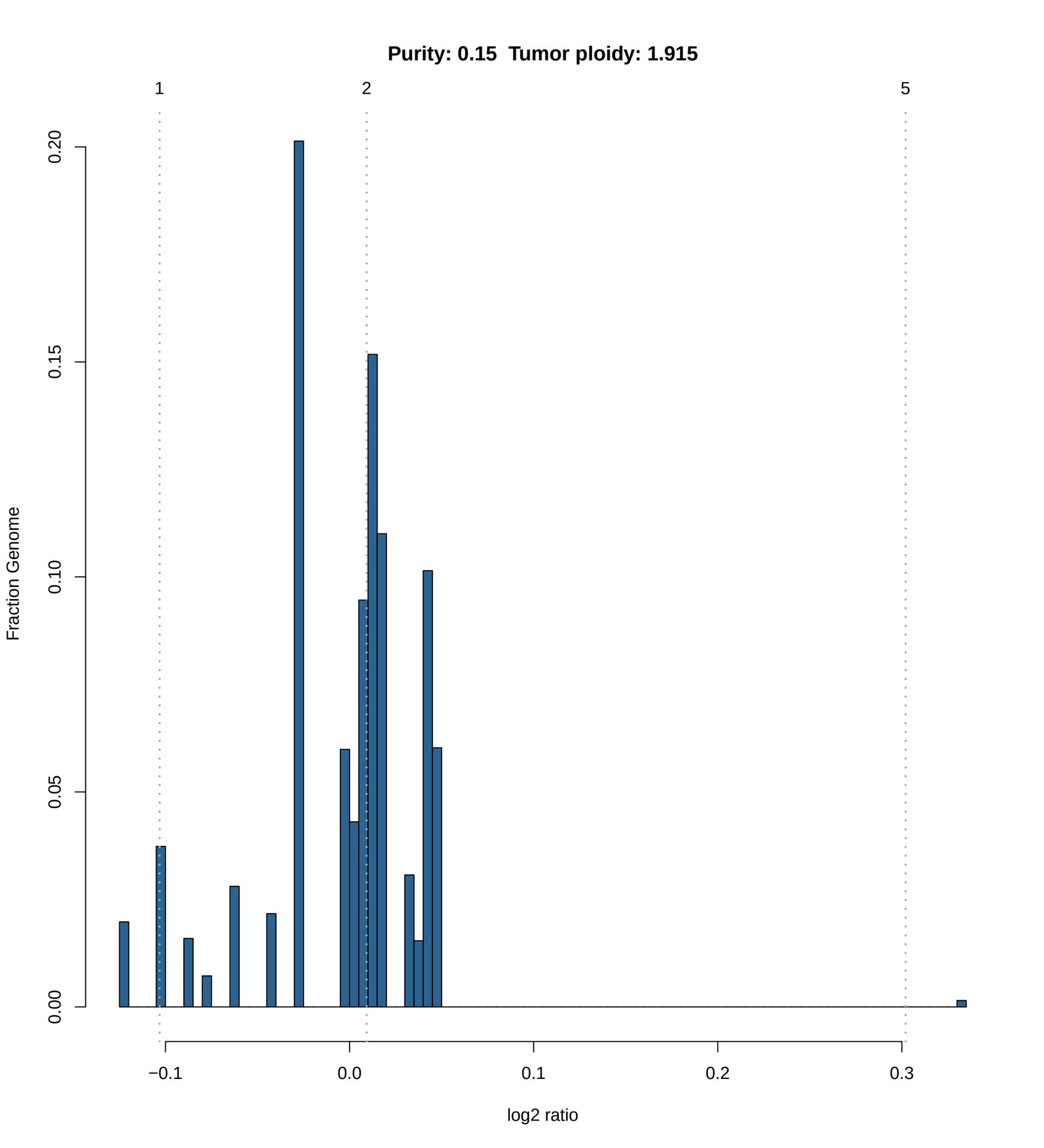
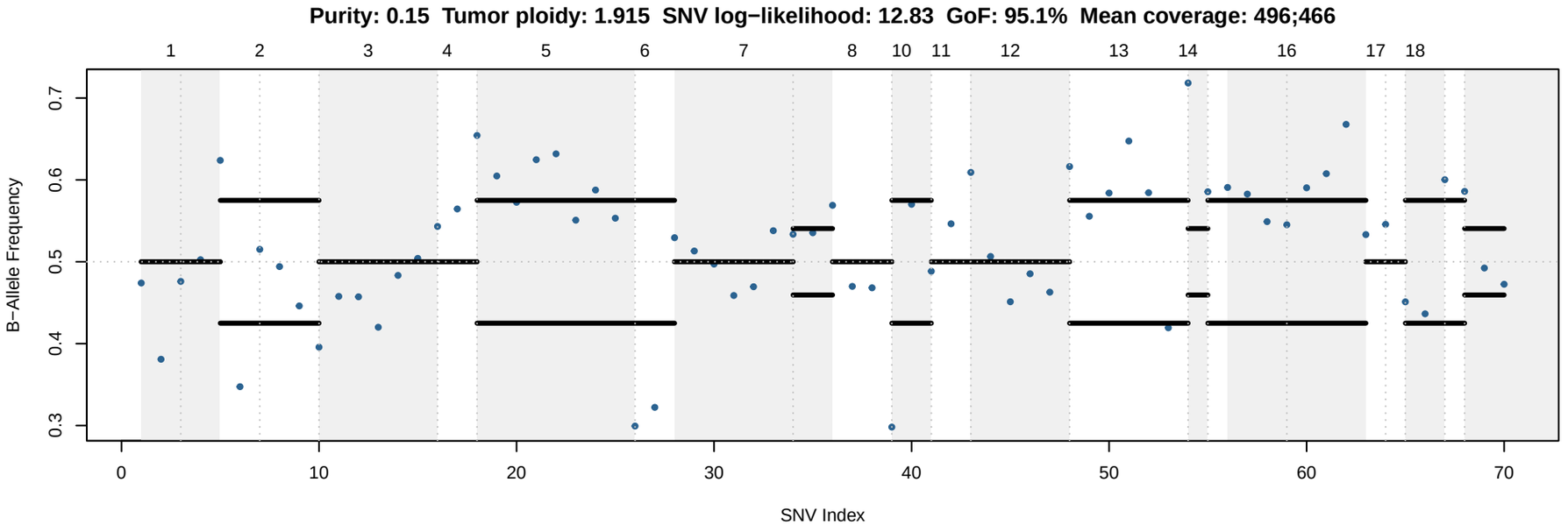
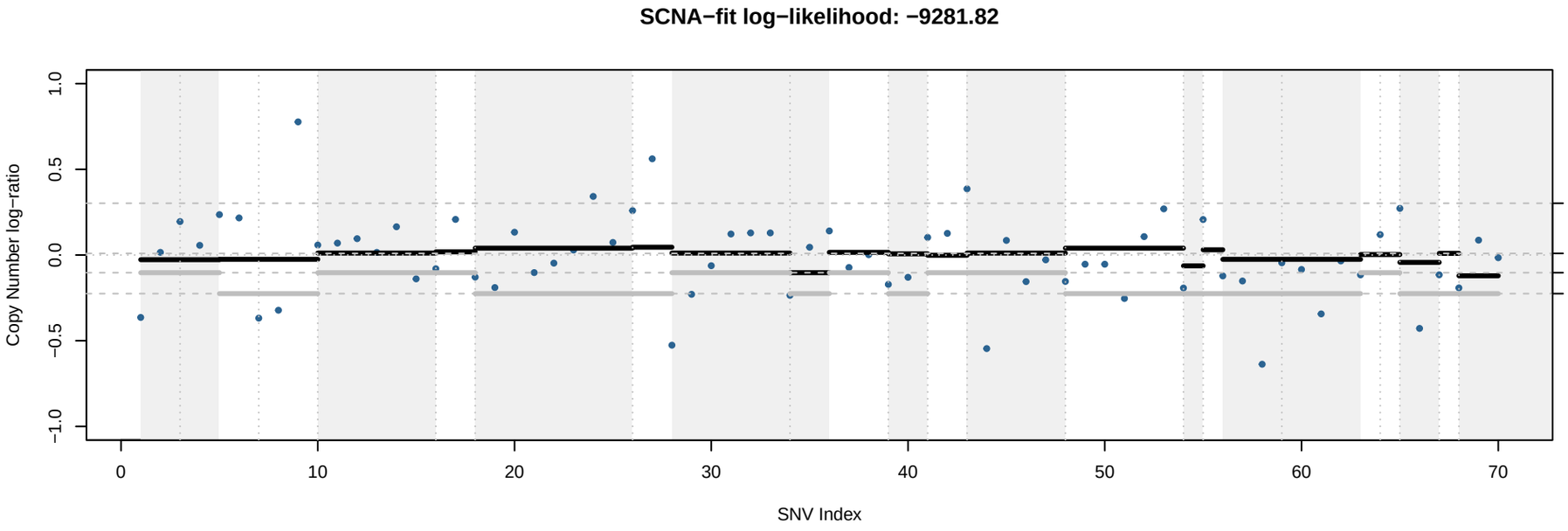
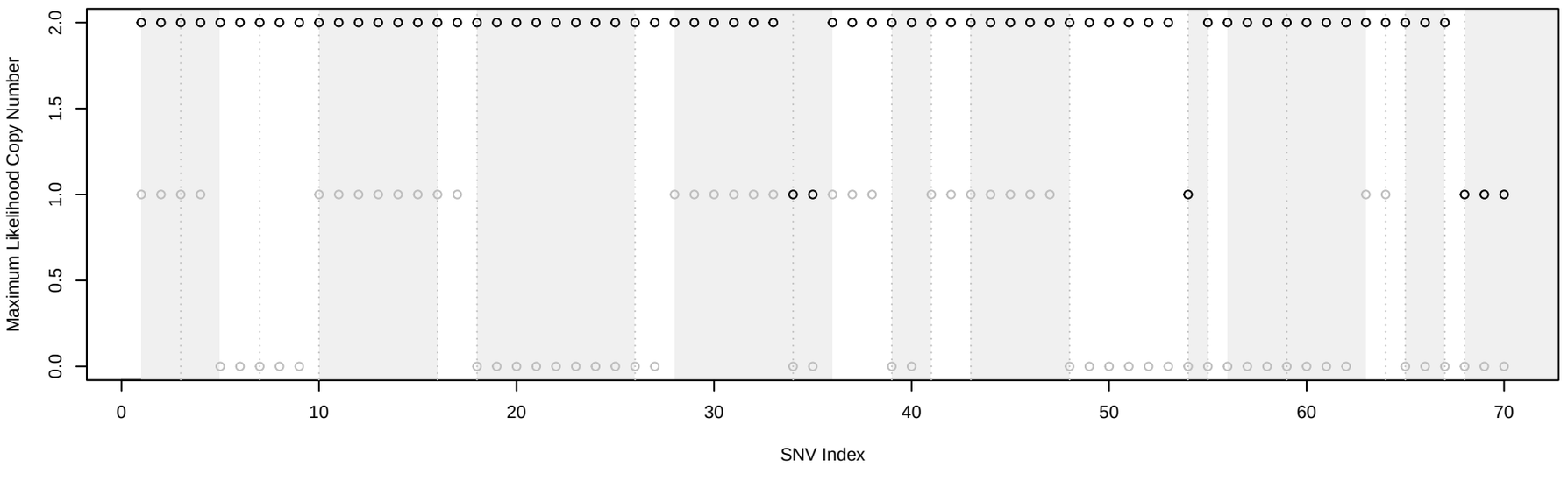
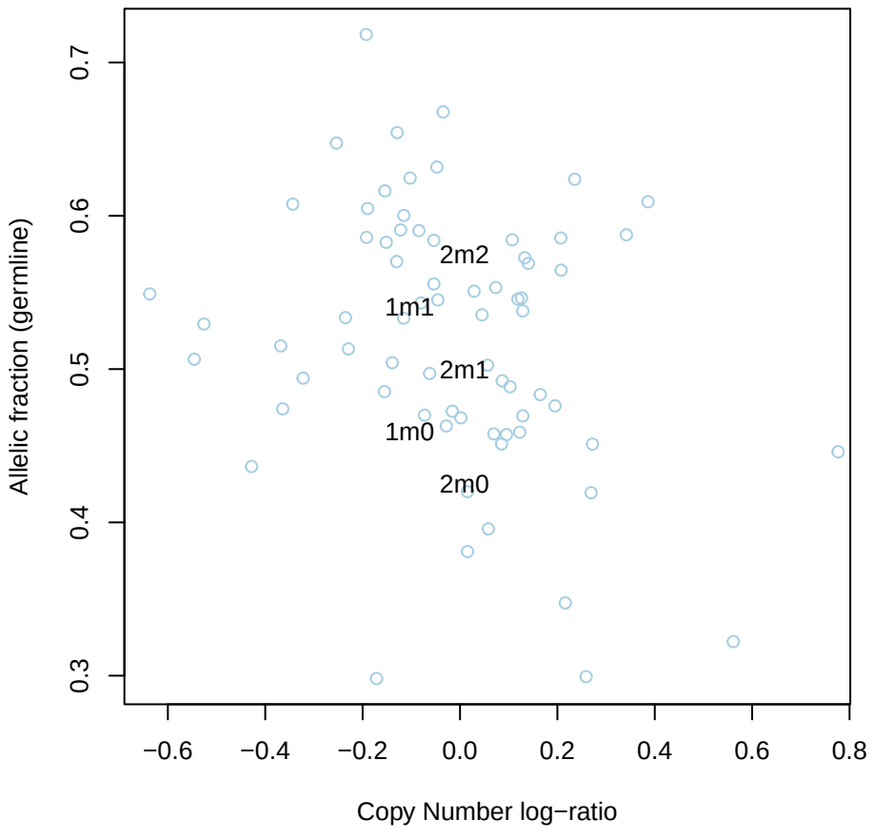
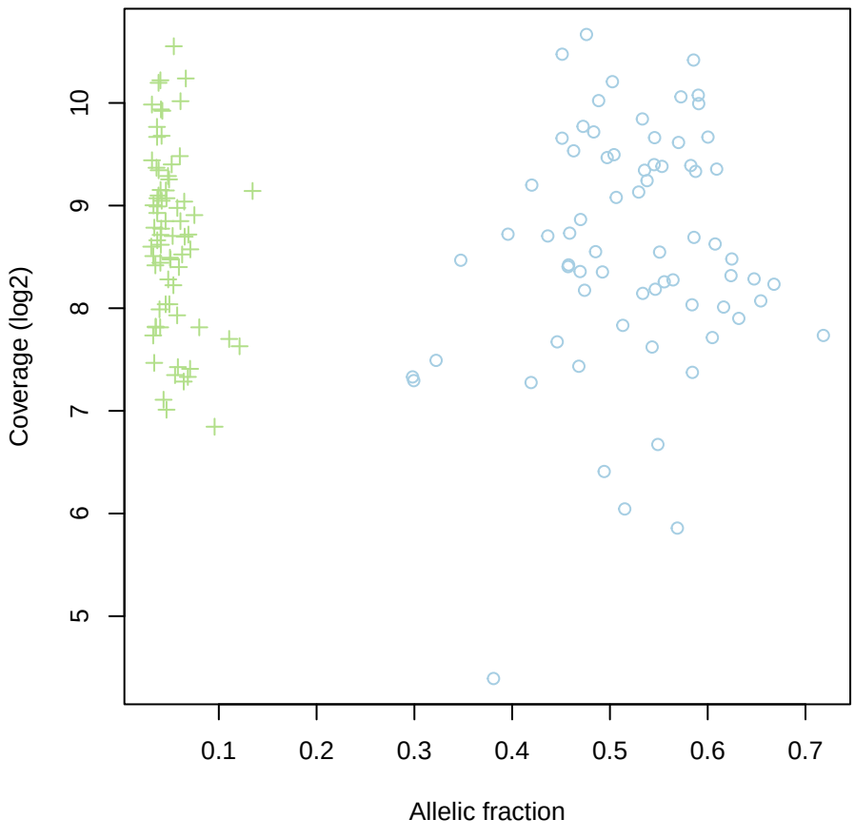

Purity: 0.15 Tumor ploidy: 1.915
1
2
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.1
0.0
0.1
0.2
0.3
log2 ratio

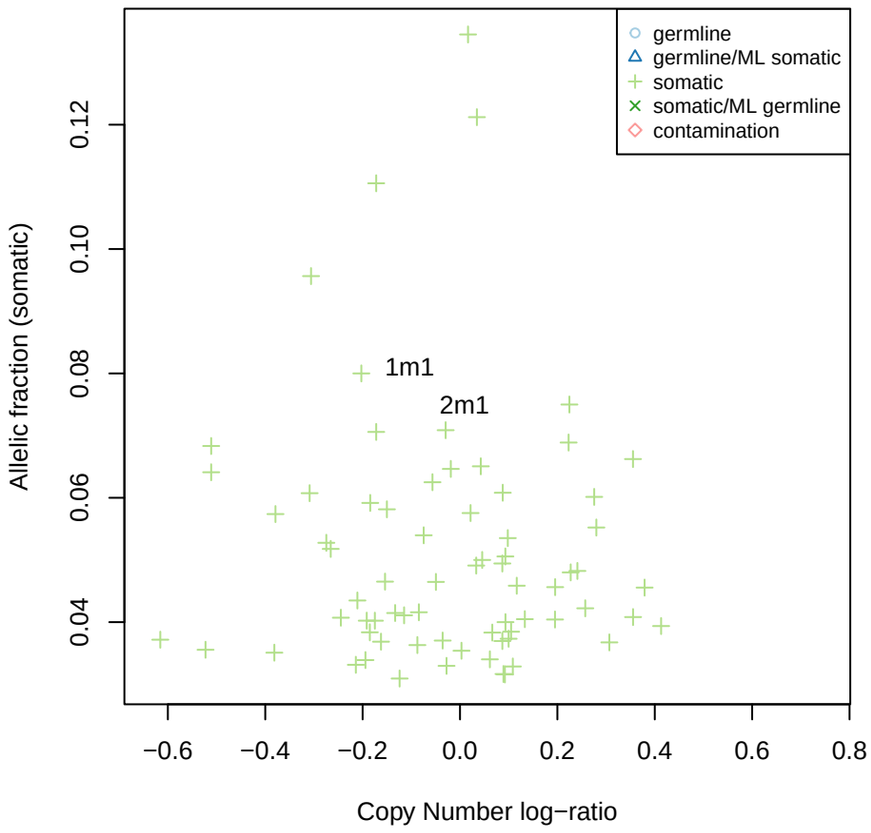

Purity: 0.15 Tumor ploidy: 1.915 SNV log−likelihood: 12.83 GoF: 95.1% Mean coverage: 496;466
1 2 3 4 5 6 7 8 10 11 12 13 14 16 17 18
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index

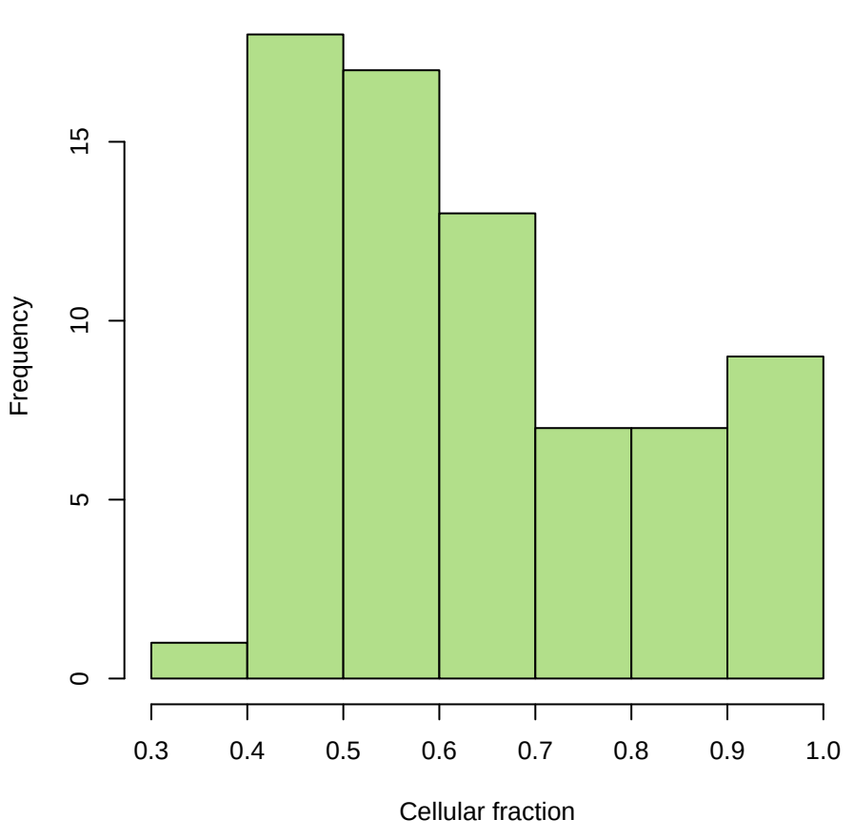

SCNA−fit log−likelihood: −9281.82
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 5
0 10 20 30 40 50 60 70
SNV Index

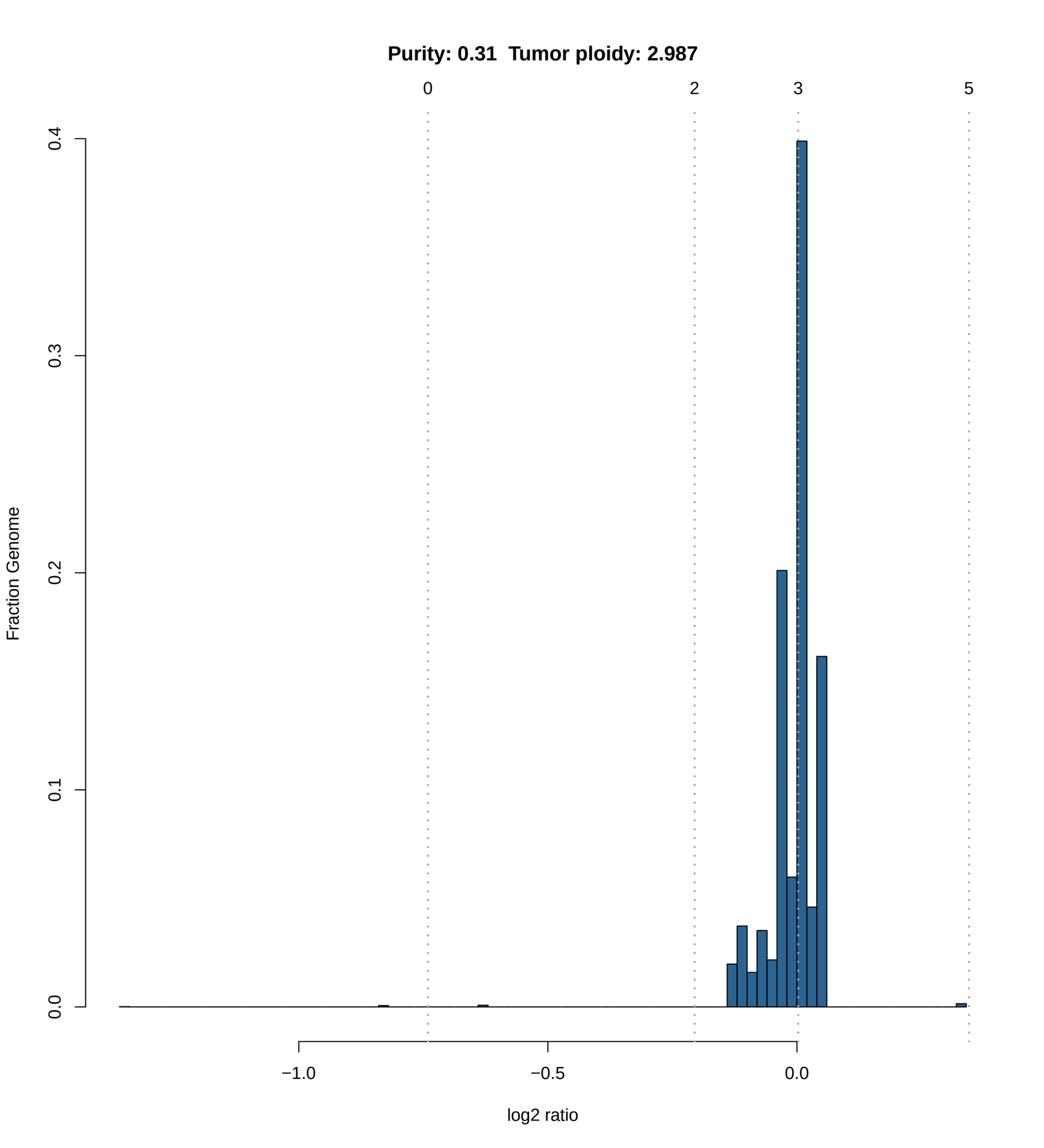

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 10 20 30 40 50 60 70
SNV Index

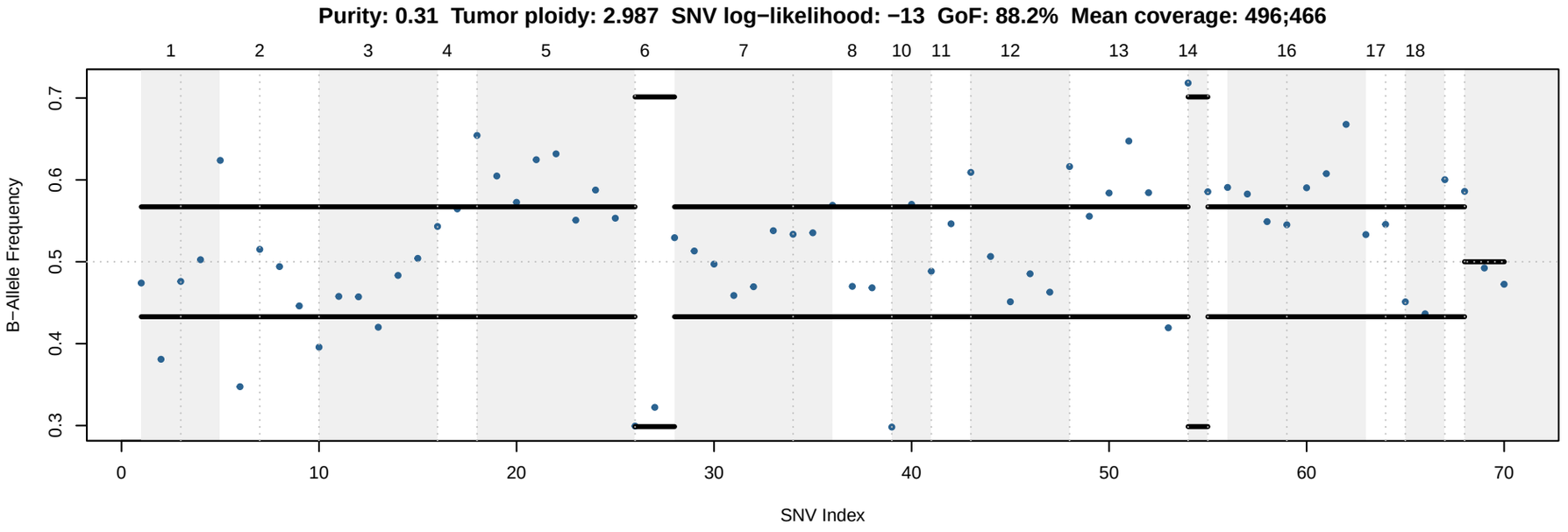

Allelic fraction (germline)
Copy Number log−ratio
2m2
1m1
2m1
1m0
2m0

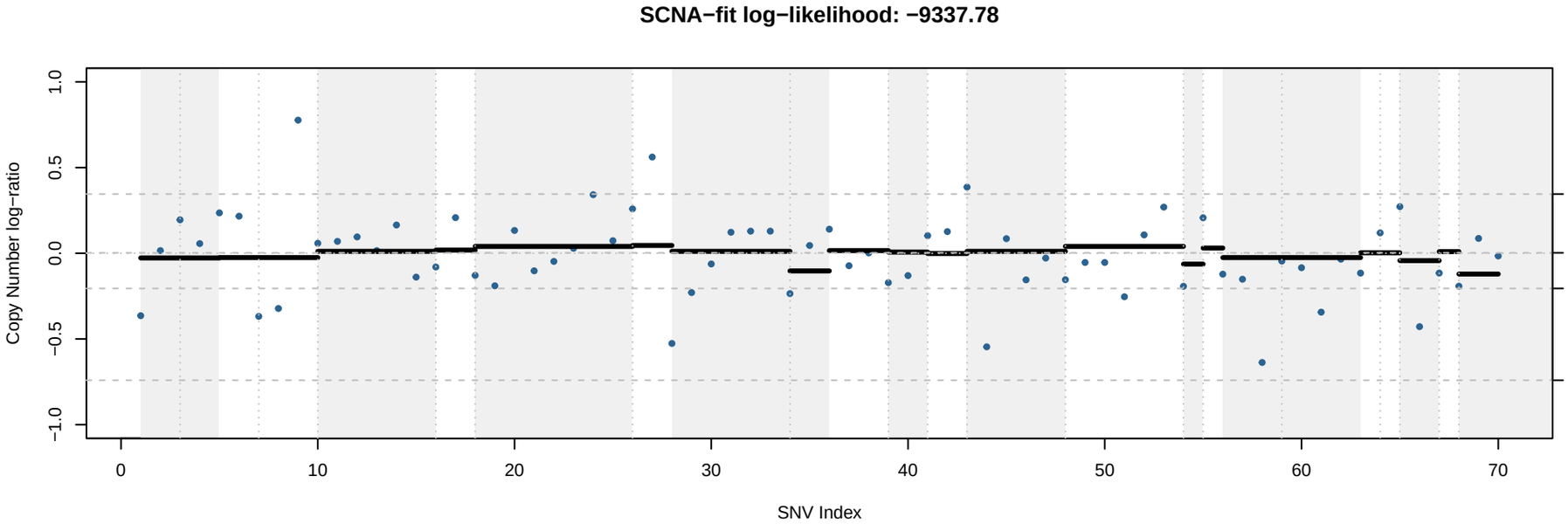

Coverage (log2)
Allelic fraction

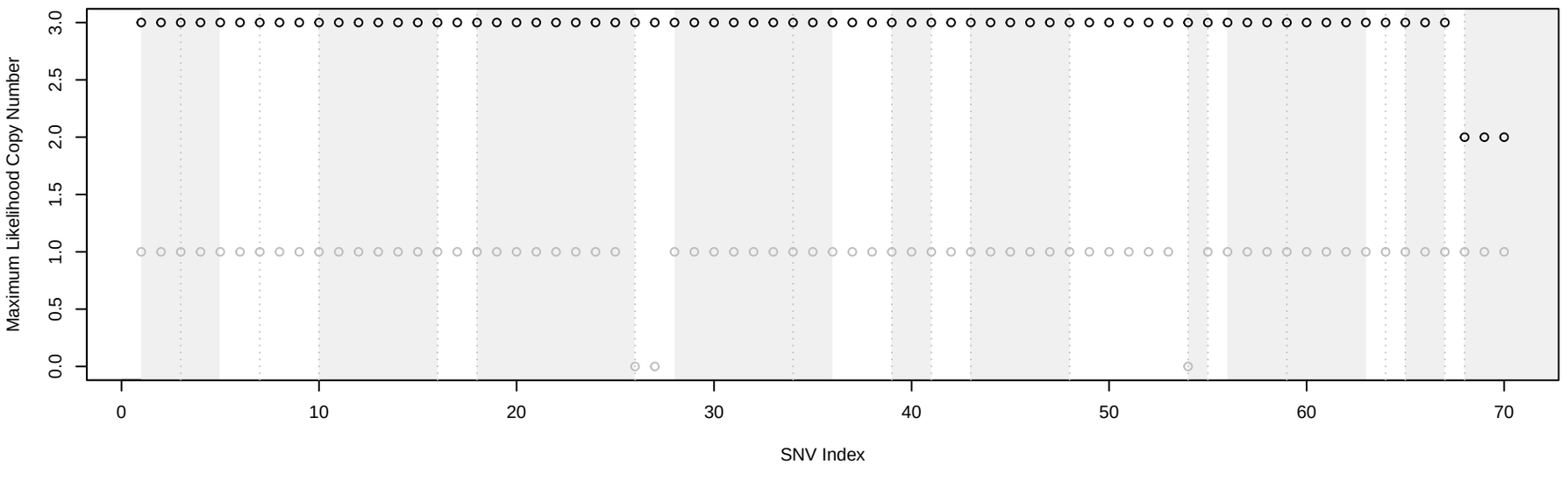

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1

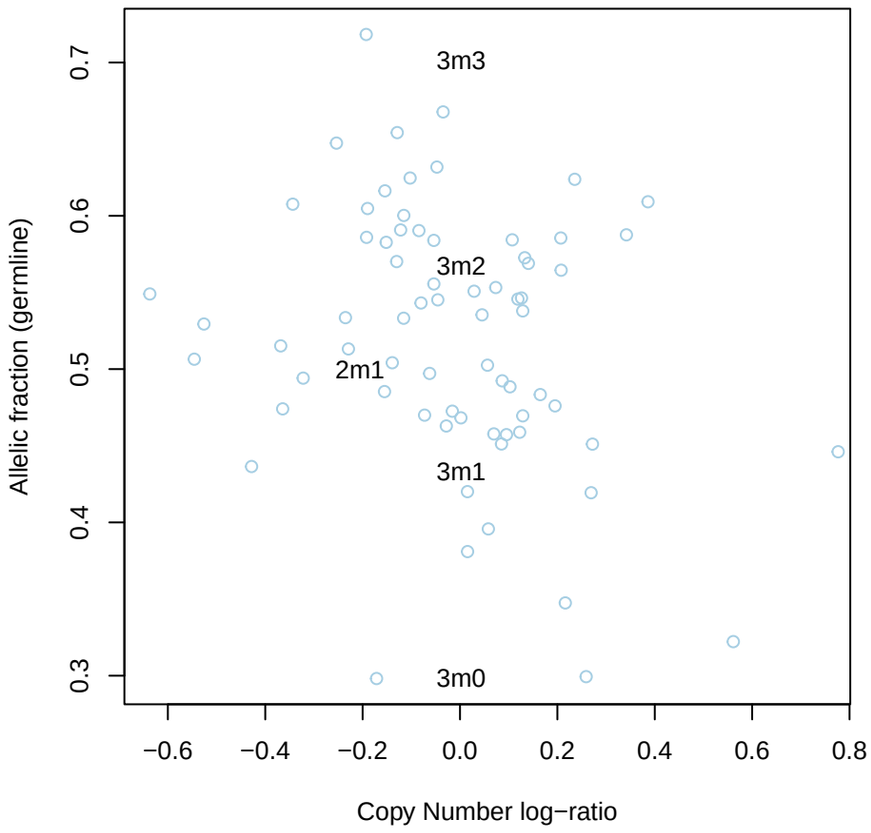

Frequency
Cellular fraction

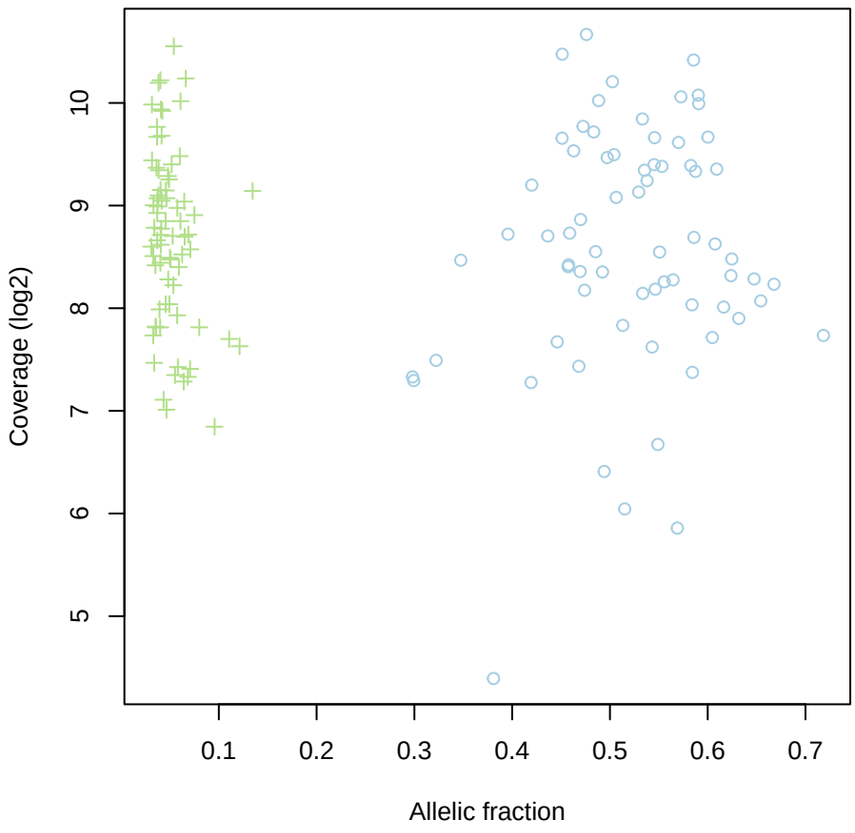

Purity: 0.31 Tumor ploidy: 2.987
0
2
3
5
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
log2 ratio

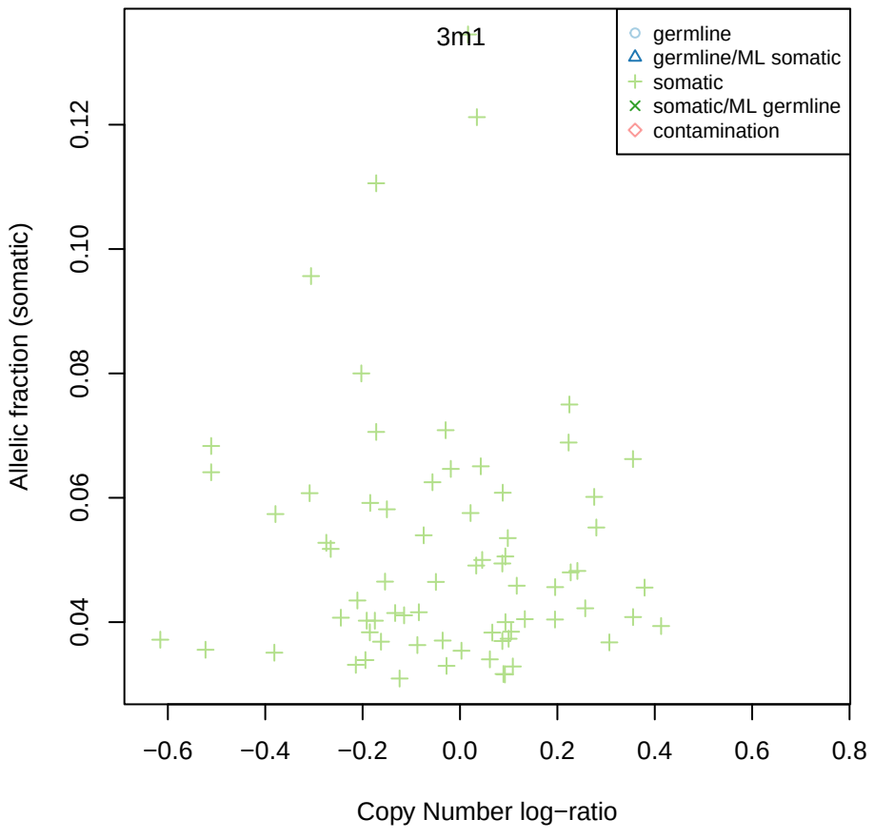

Purity: 0.31 Tumor ploidy: 2.987 SNV log−likelihood: −13 GoF: 88.2% Mean coverage: 496;466
1 2 3 4 5 6 7 8 10 11 12 13 14 16 17 18
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index

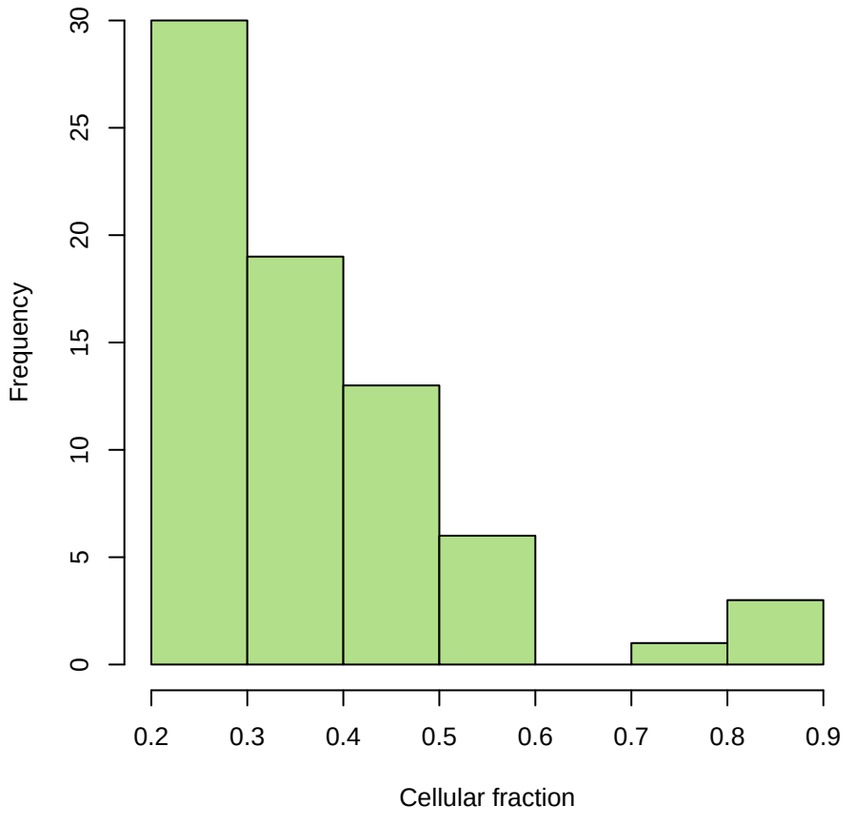

SCNA−fit log−likelihood: −9337.78
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 3 5
0 10 20 30 40 50 60 70
SNV Index

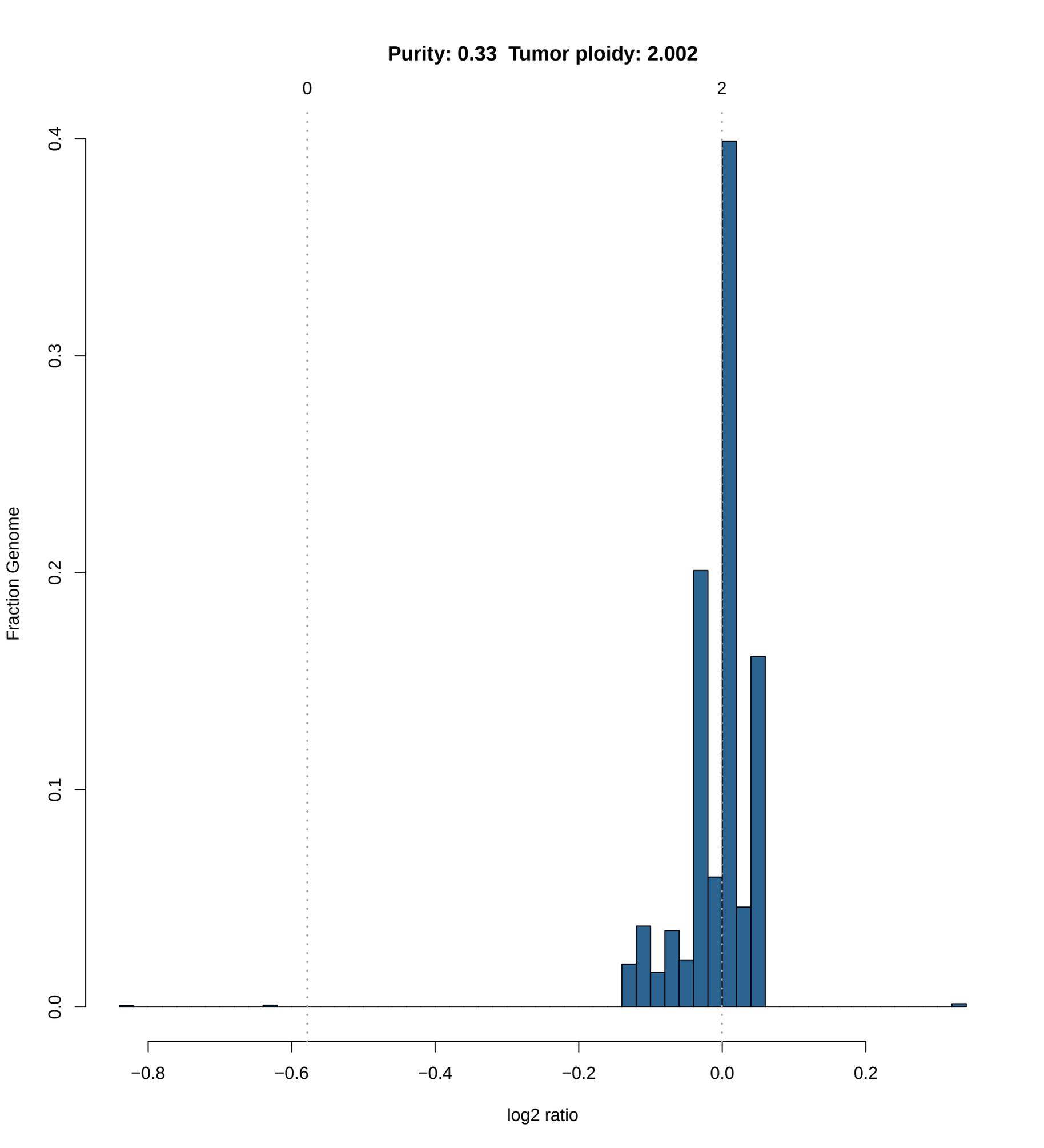

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 10 20 30 40 50 60 70
SNV Index

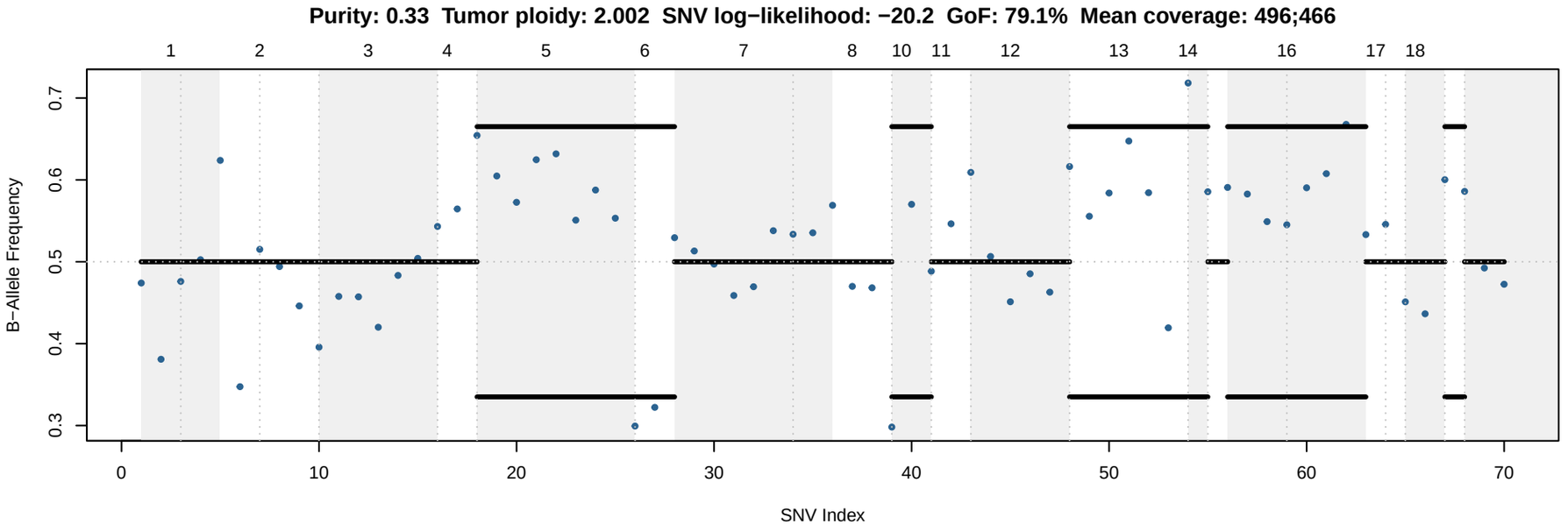

3m3
3m2
2m1
3m1
3m0
Allelic fraction (germline)
Copy Number log−ratio
0.3
0.4
0.5
0.6
0.7
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8

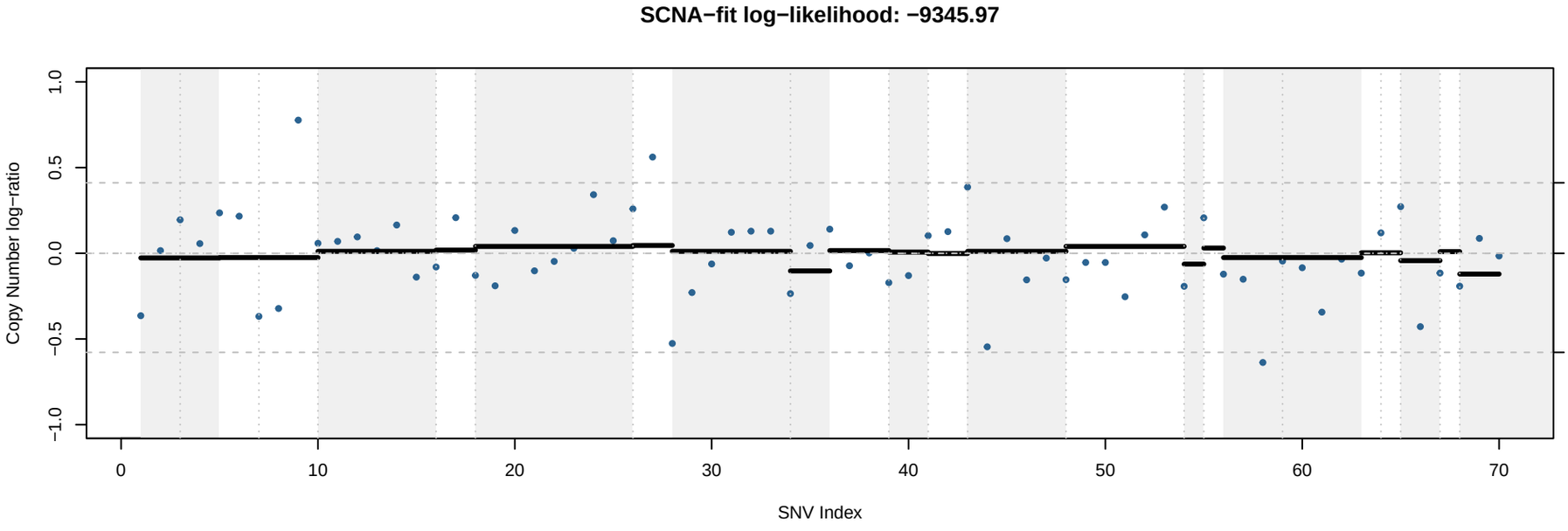

Coverage (log2)
Allelic fraction
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7

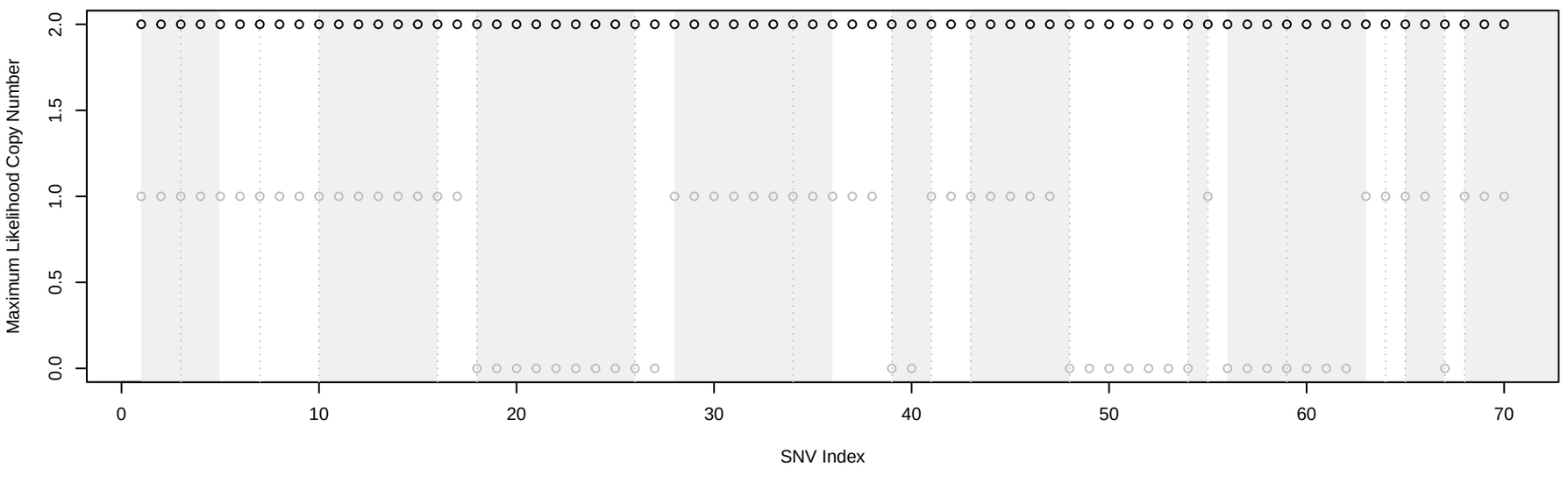

3m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
0.12
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8

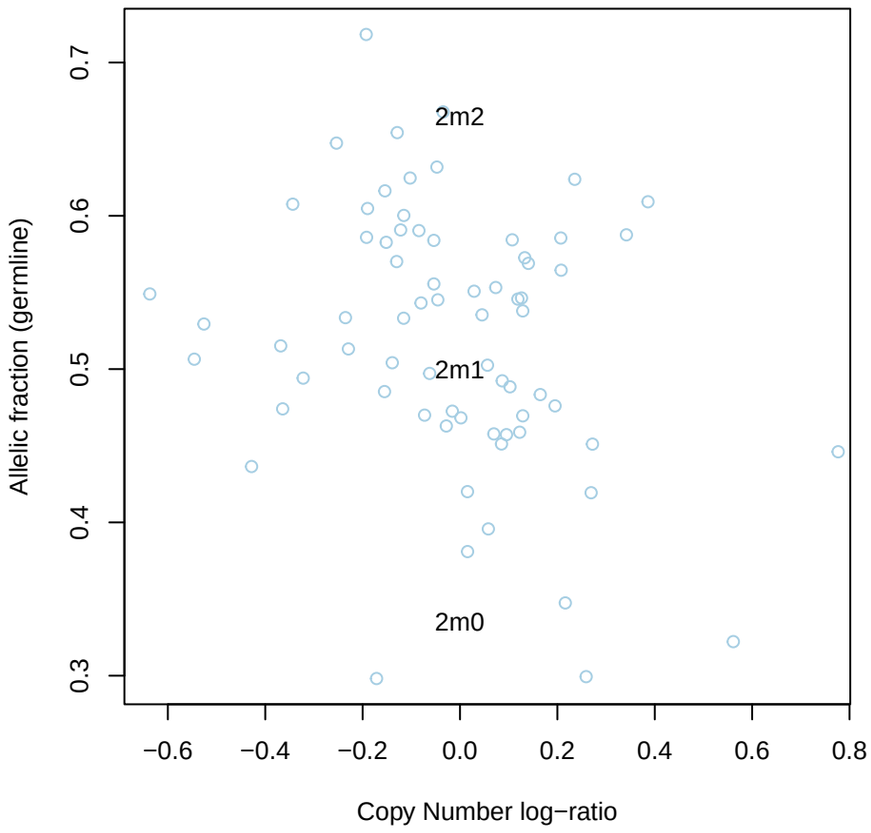

Frequency
Cellular fraction
0
5
10
15
20
25
30
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9

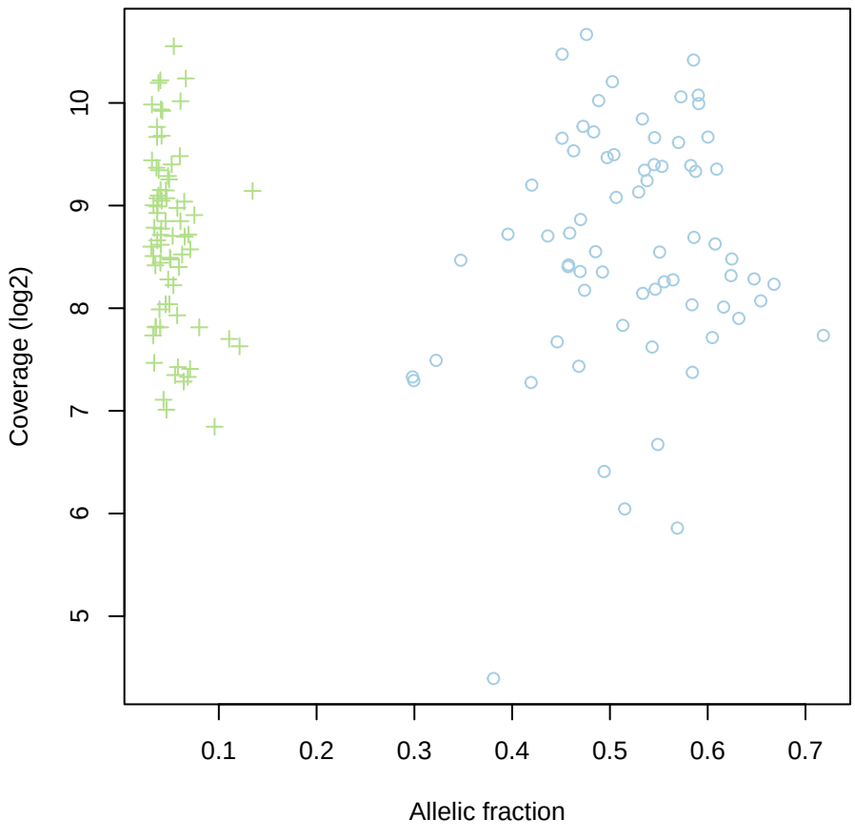

Purity: 0.33 Tumor ploidy: 2.002
0
2
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

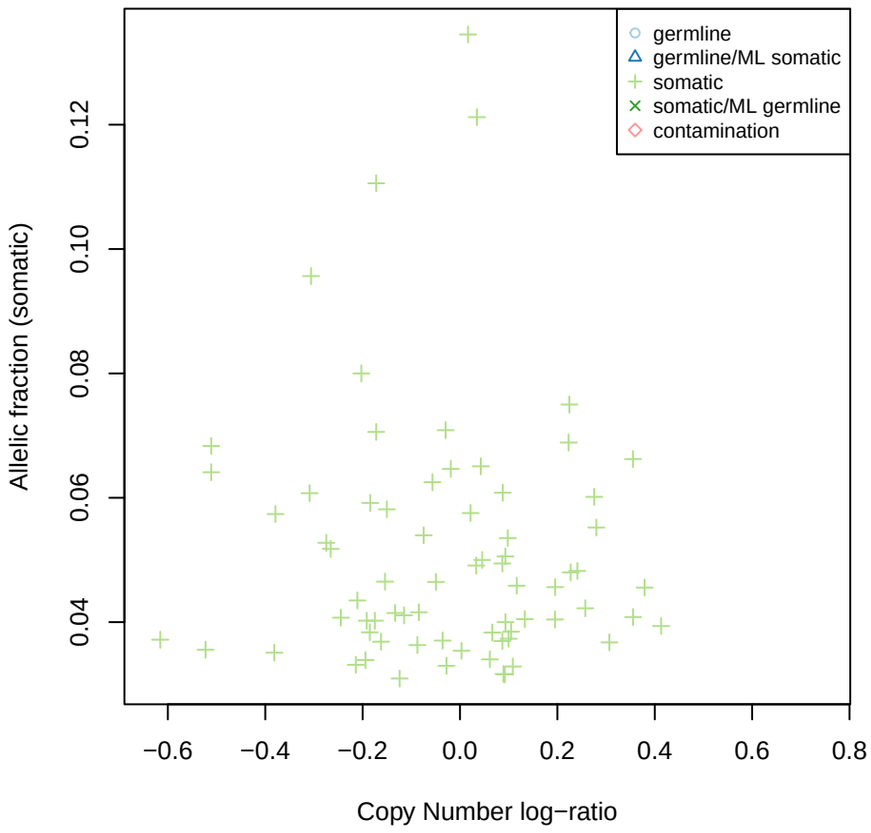

Purity: 0.33 Tumor ploidy: 2.002 SNV log−likelihood: −20.2 GoF: 79.1% Mean coverage: 496;466
1 2 3 4 5 6 7 8 10 11 12 13 14 16 17 18
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index

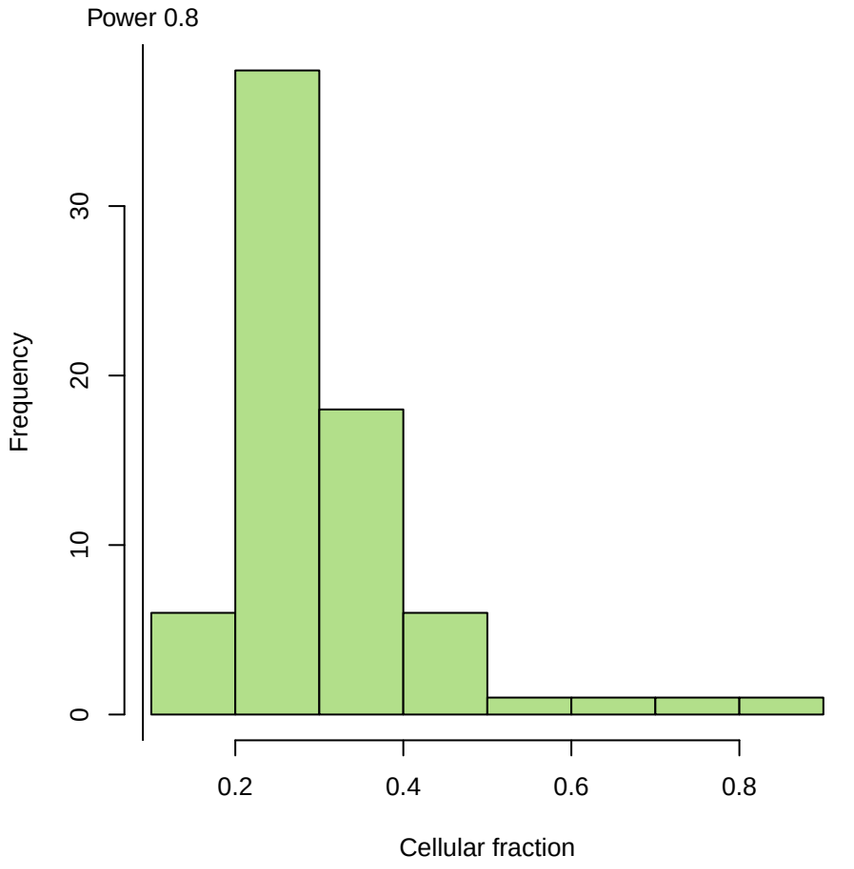

SCNA−fit log−likelihood: −9345.97
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4
0 10 20 30 40 50 60 70
SNV Index

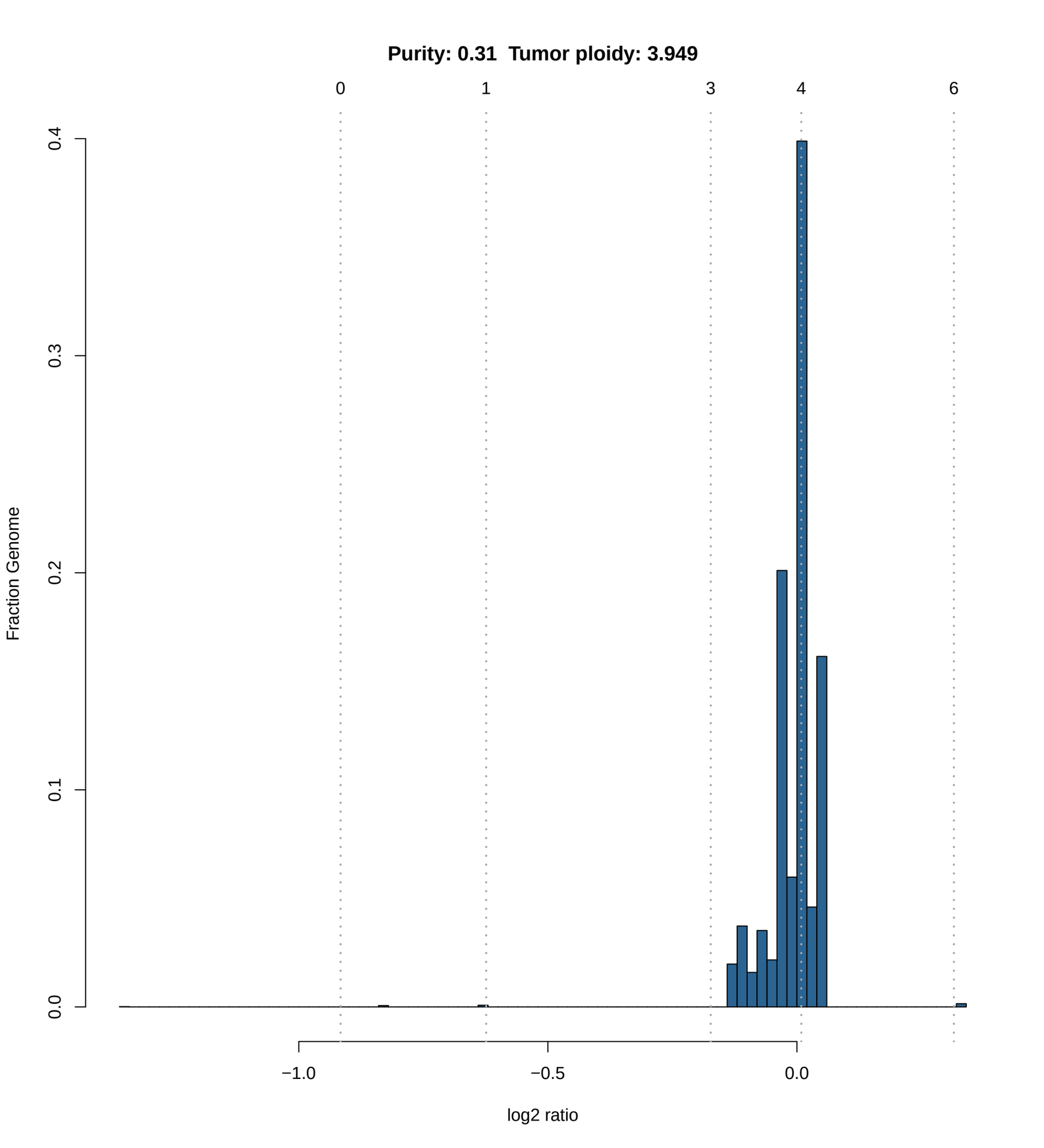

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 10 20 30 40 50 60 70
SNV Index

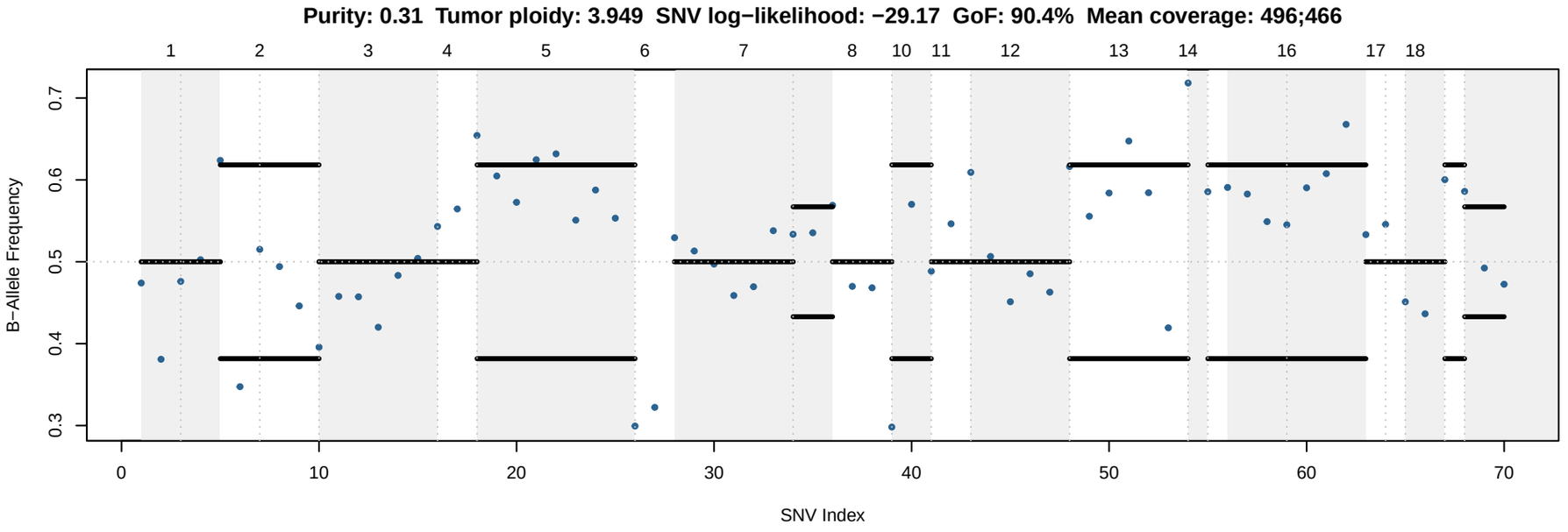

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
2m2
2m1
2m0
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

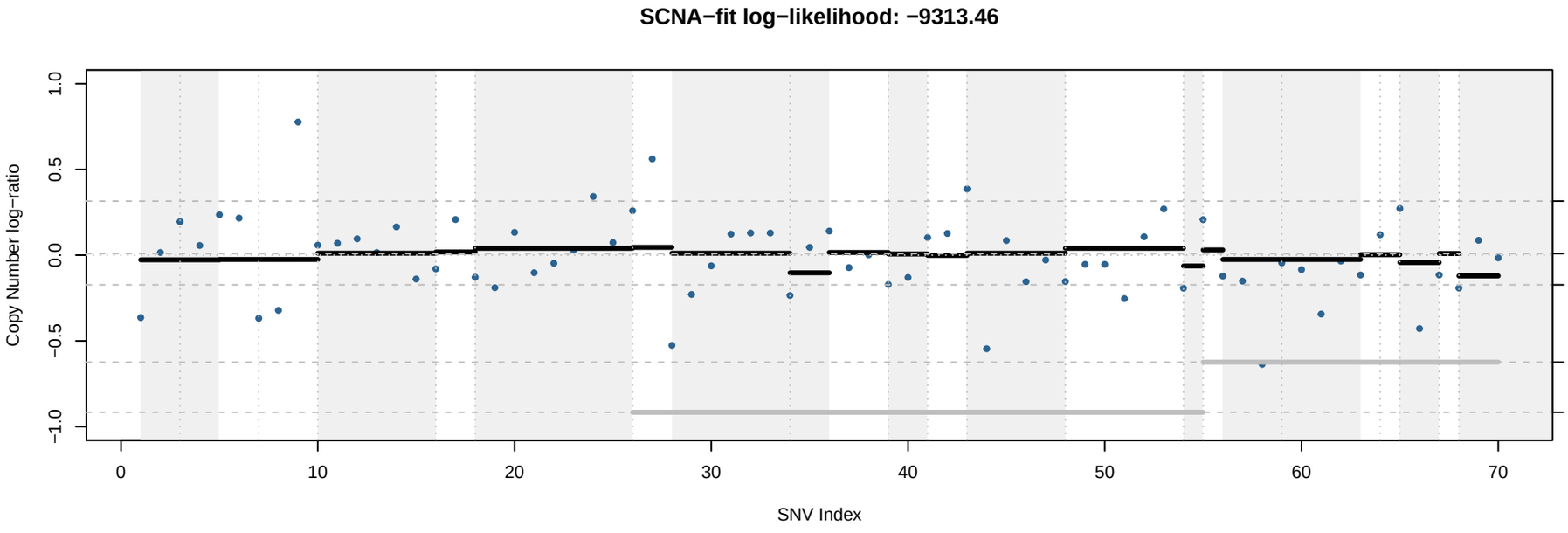

Coverage (log2)
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

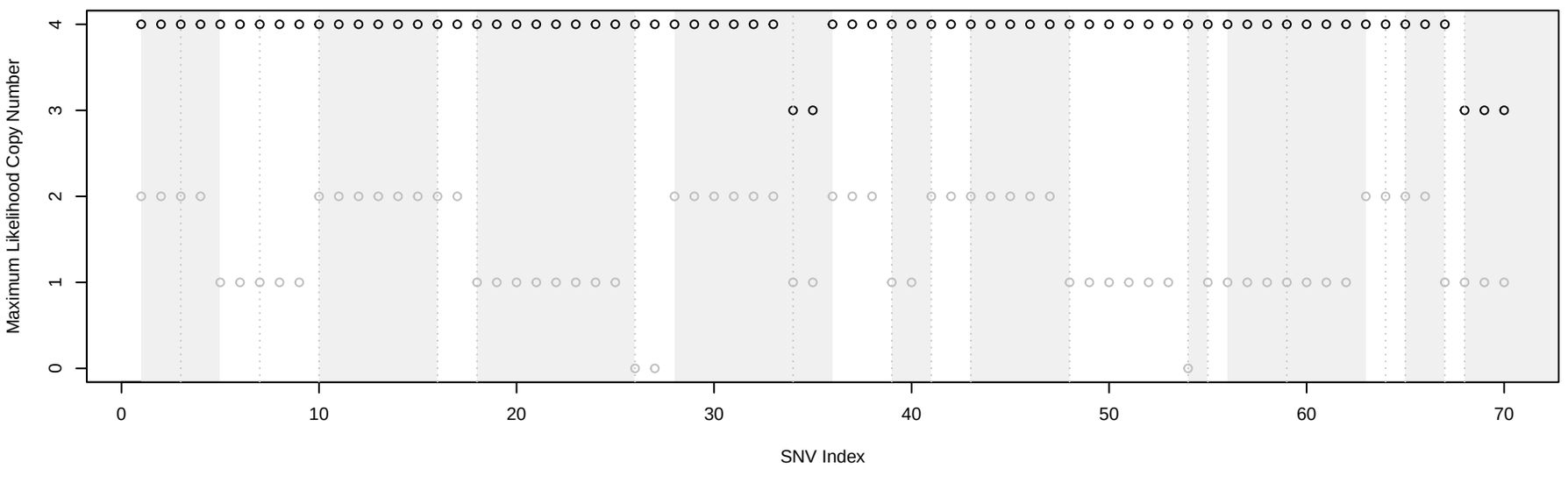

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

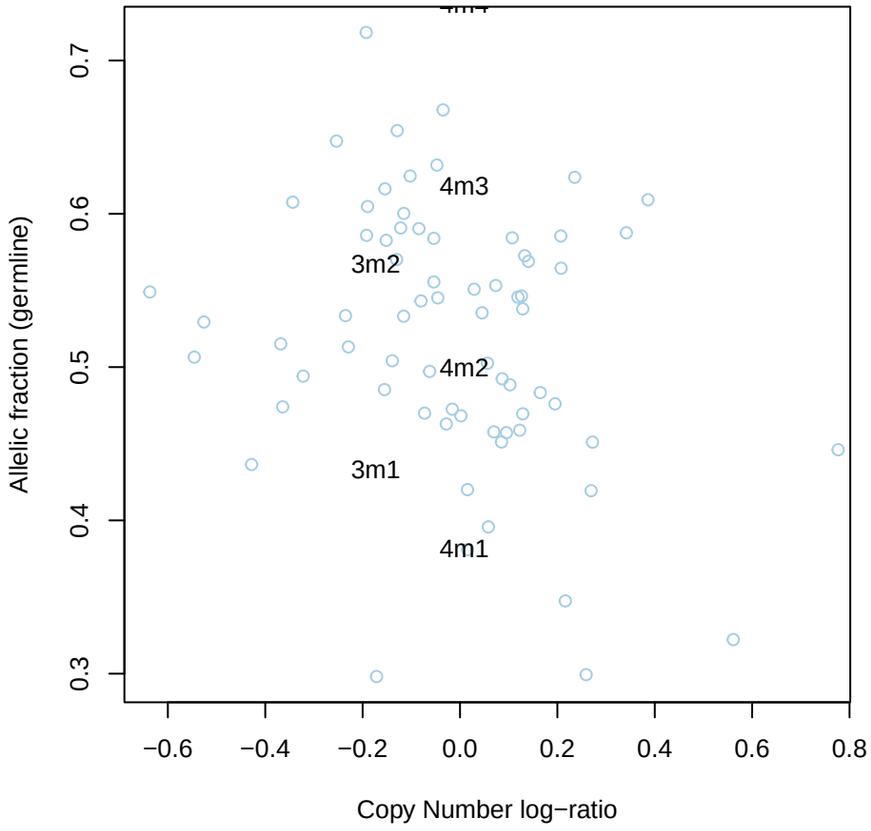

Power 0.8
Frequency
0
10
20
30
0.2
0.4
0.6
0.8
Cellular fraction

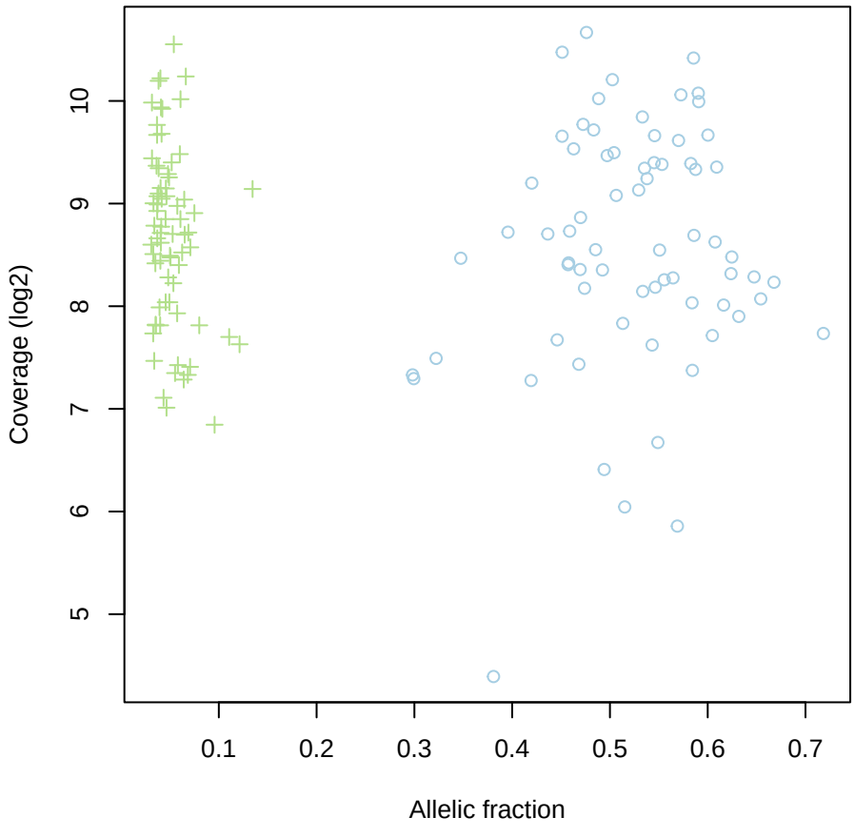

Purity: 0.31 Tumor ploidy: 3.949
0
1
3
4
6
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
log2 ratio

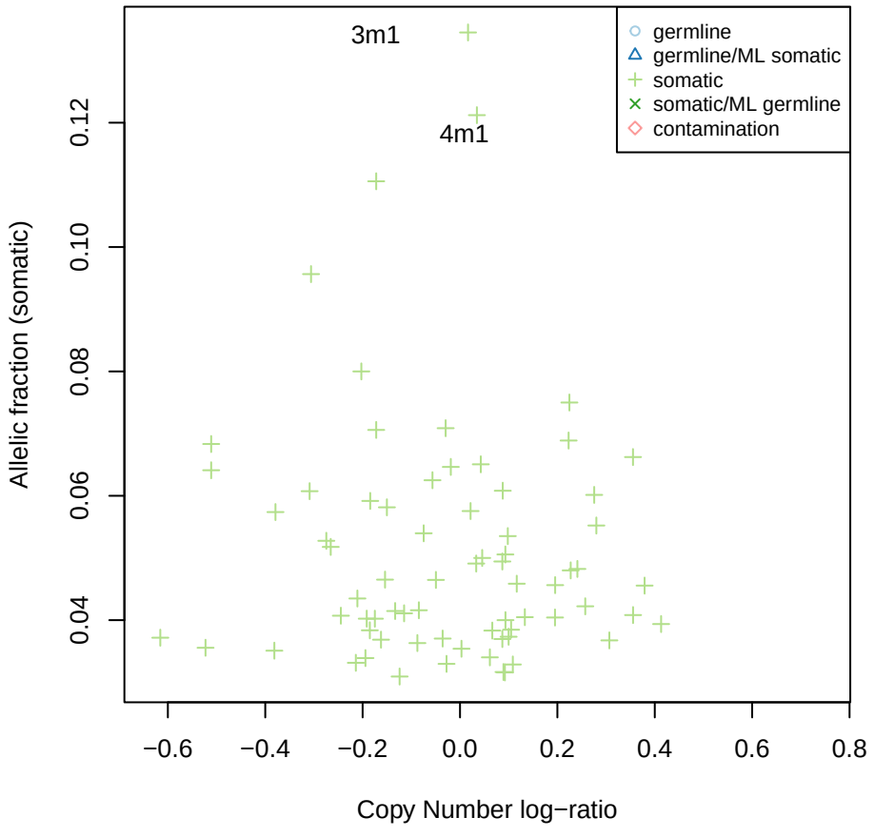

Purity: 0.31 Tumor ploidy: 3.949 SNV log−likelihood: −29.17 GoF: 90.4% Mean coverage: 496;466
1 2 3 4 5 6 7 8 10 11 12 13 14 16 17 18
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index

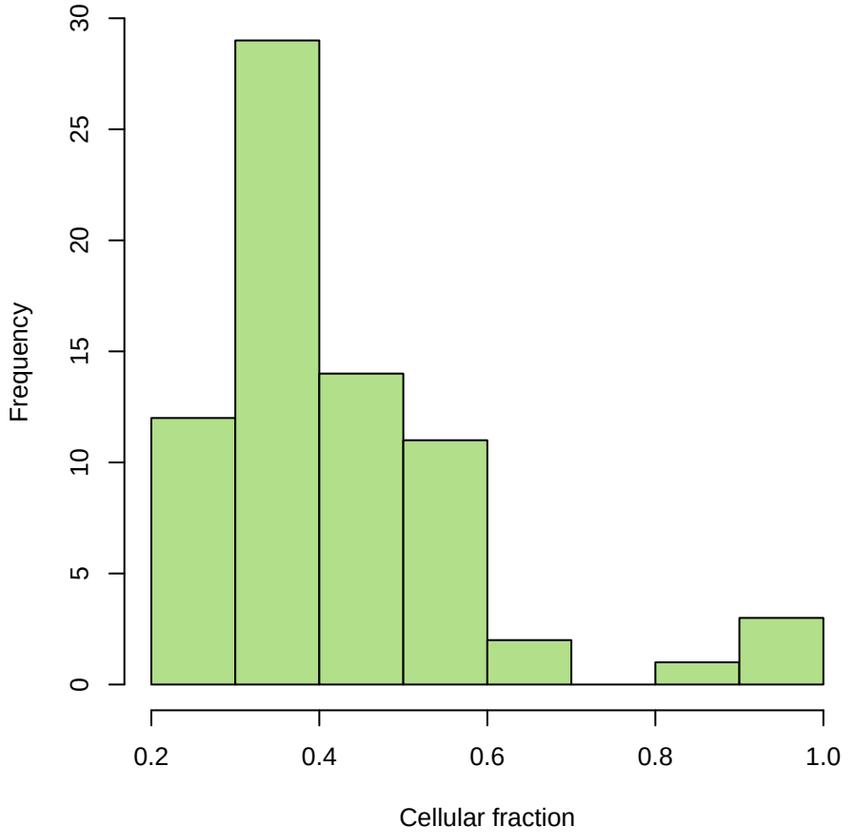

SCNA−fit log−likelihood: −9313.46
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 3 4 6
0 10 20 30 40 50 60 70
SNV Index

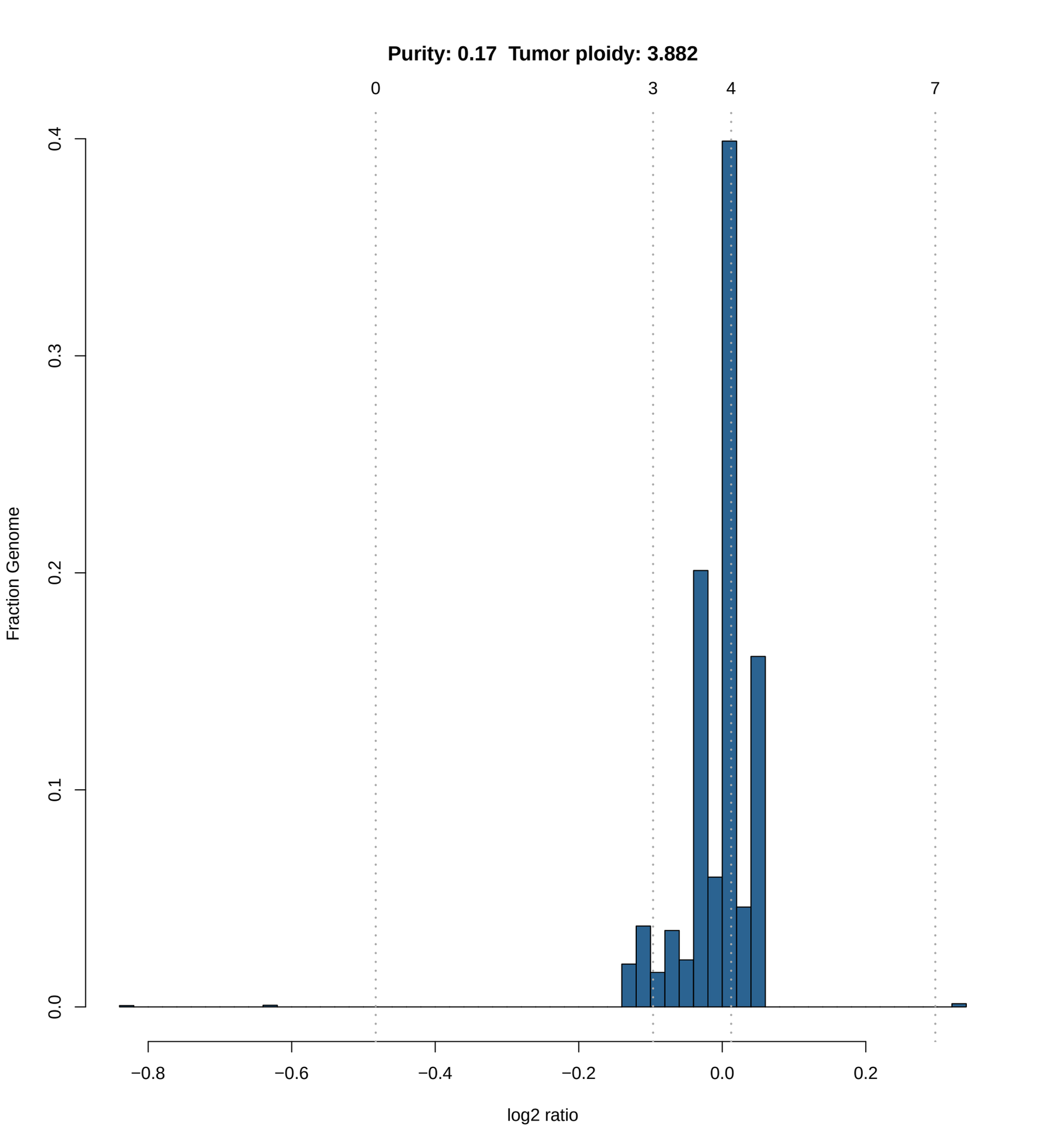

Maximum Likelihood Copy Number
0 1 2 3 4
0 10 20 30 40 50 60 70
SNV Index

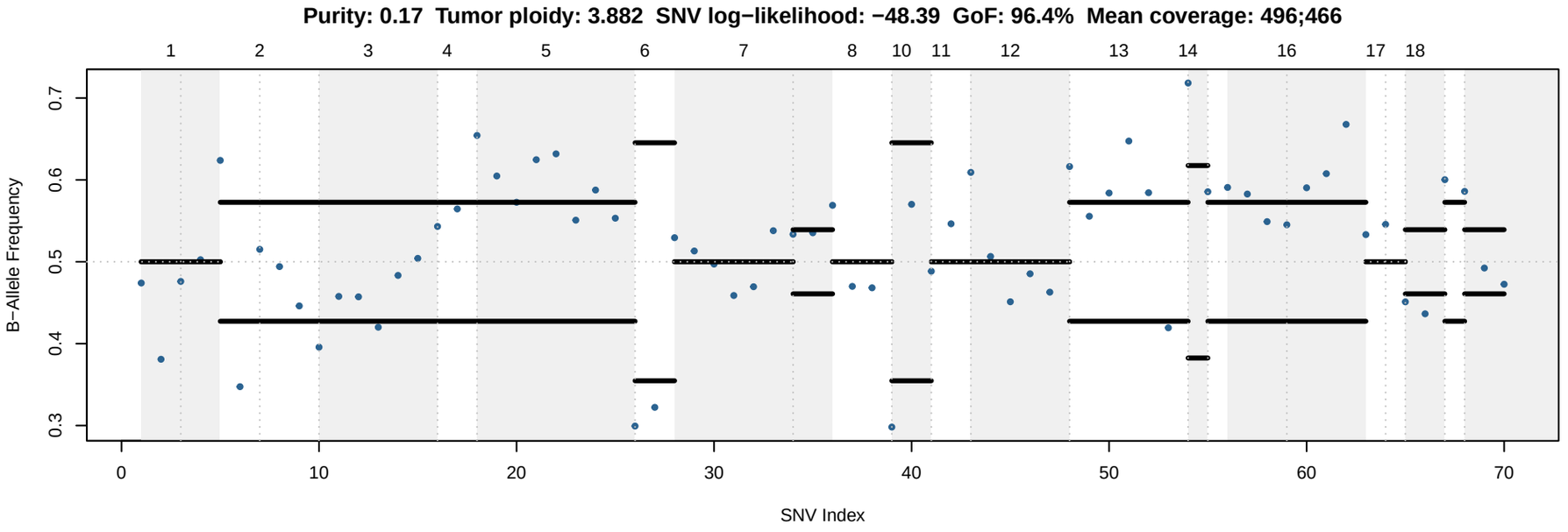

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
4m2
3m1
4m1

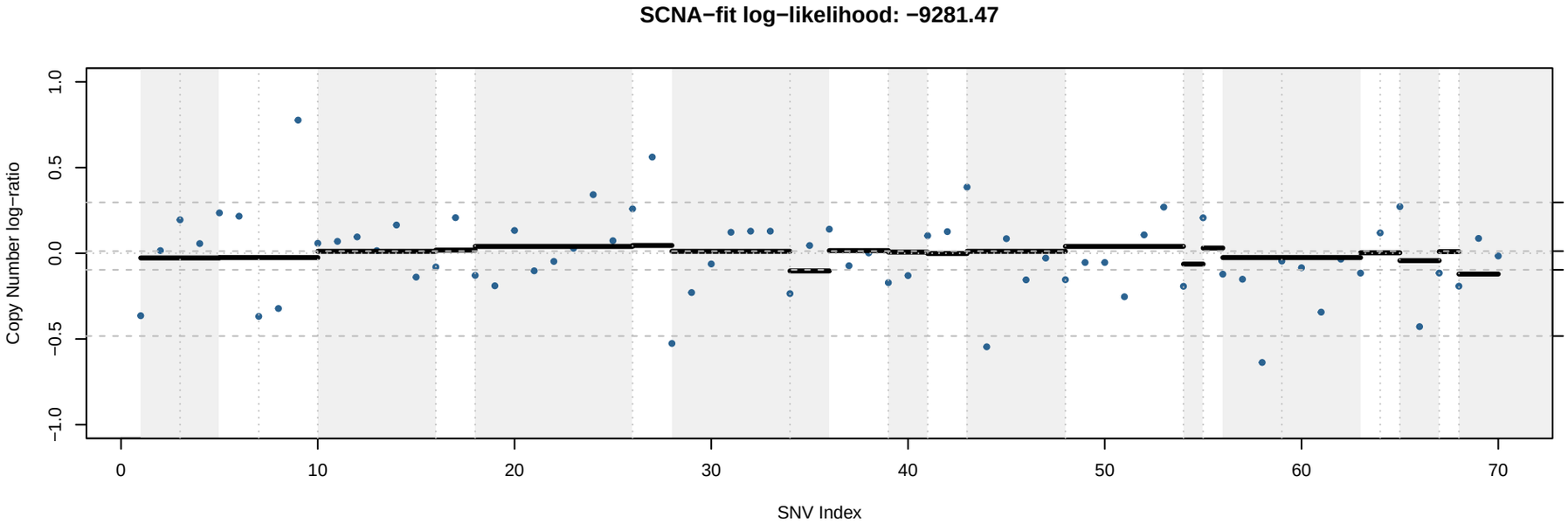

Coverage (log2)
Allelic fraction

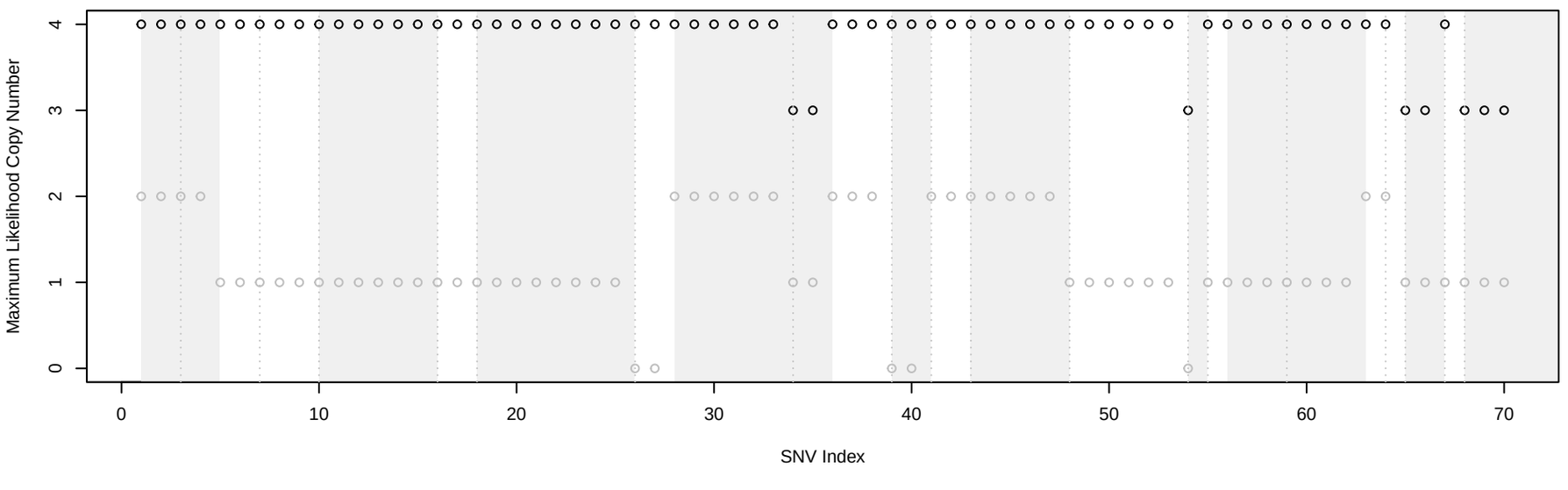

Allelic fraction (somatic)
Copy Number log−ratio
3m1
4m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

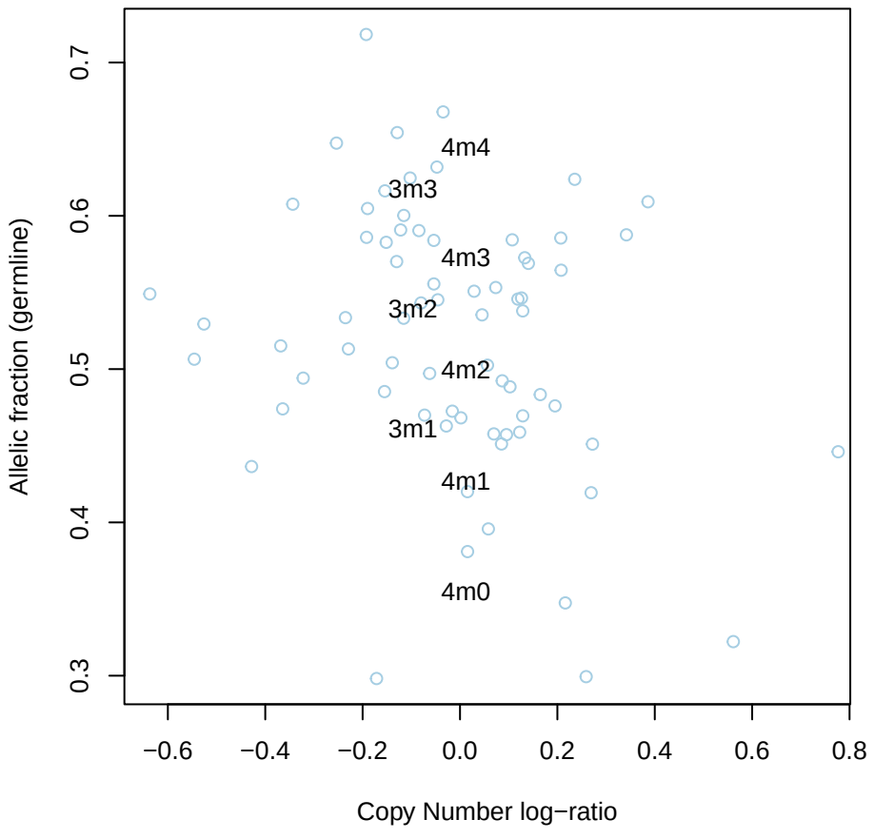

Frequency
Cellular fraction

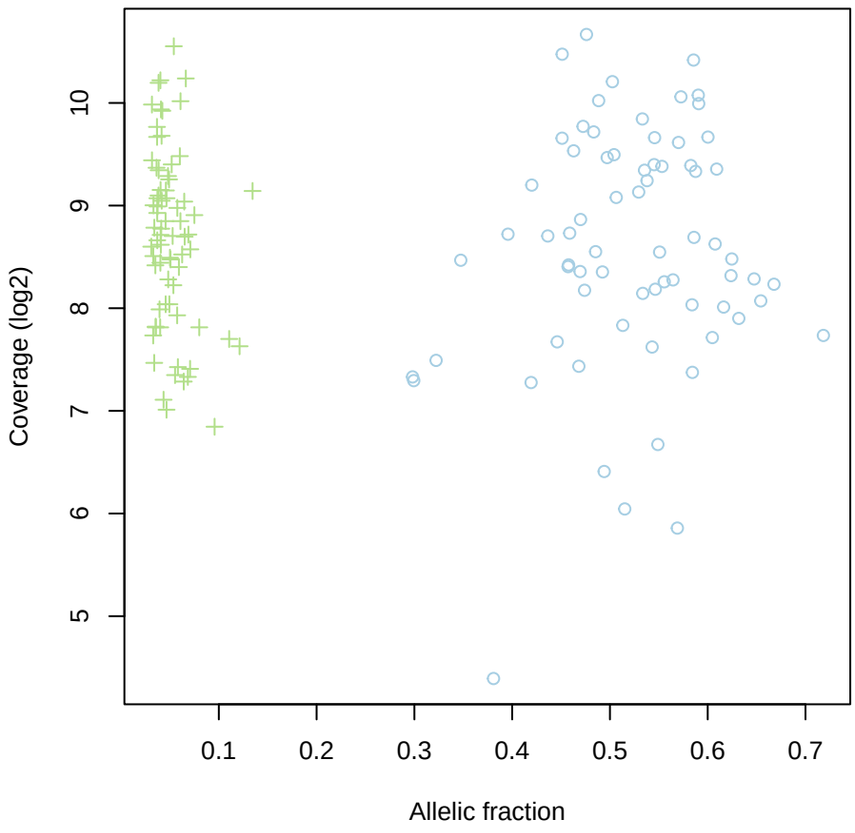

Purity: 0.17 Tumor ploidy: 3.882
0
3
4
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

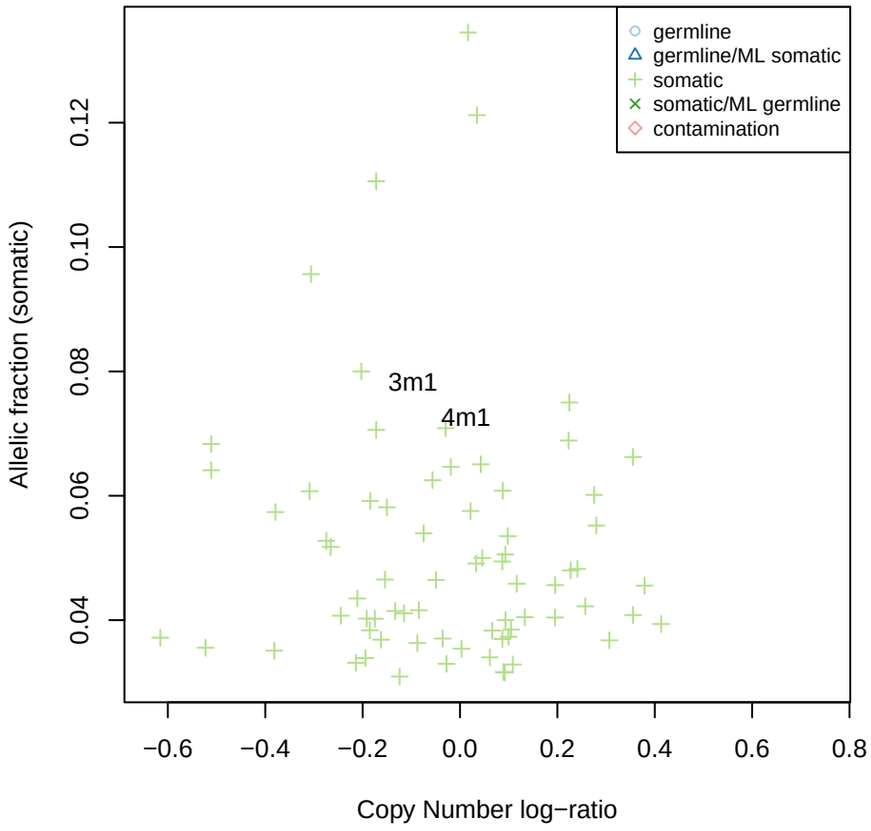

Purity: 0.17 Tumor ploidy: 3.882 SNV log−likelihood: −48.39 GoF: 96.4% Mean coverage: 496;466
1 2 3 4 5 6 7 8 10 11 12 13 14 16 17 18
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index

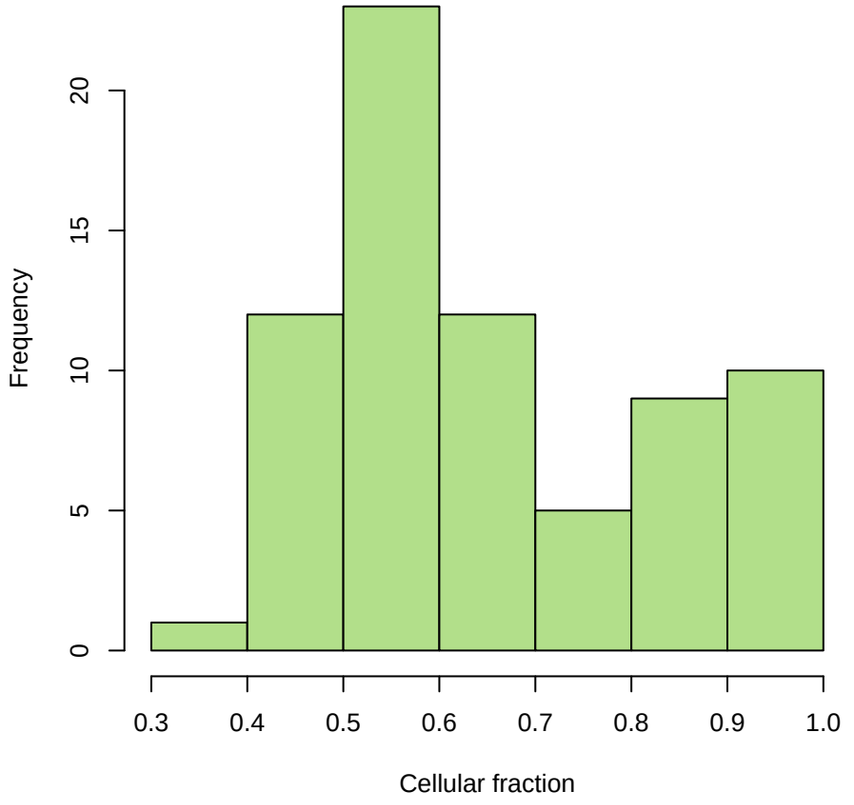

SCNA−fit log−likelihood: −9281.47
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 3 7
0 10 20 30 40 50 60 70
SNV Index

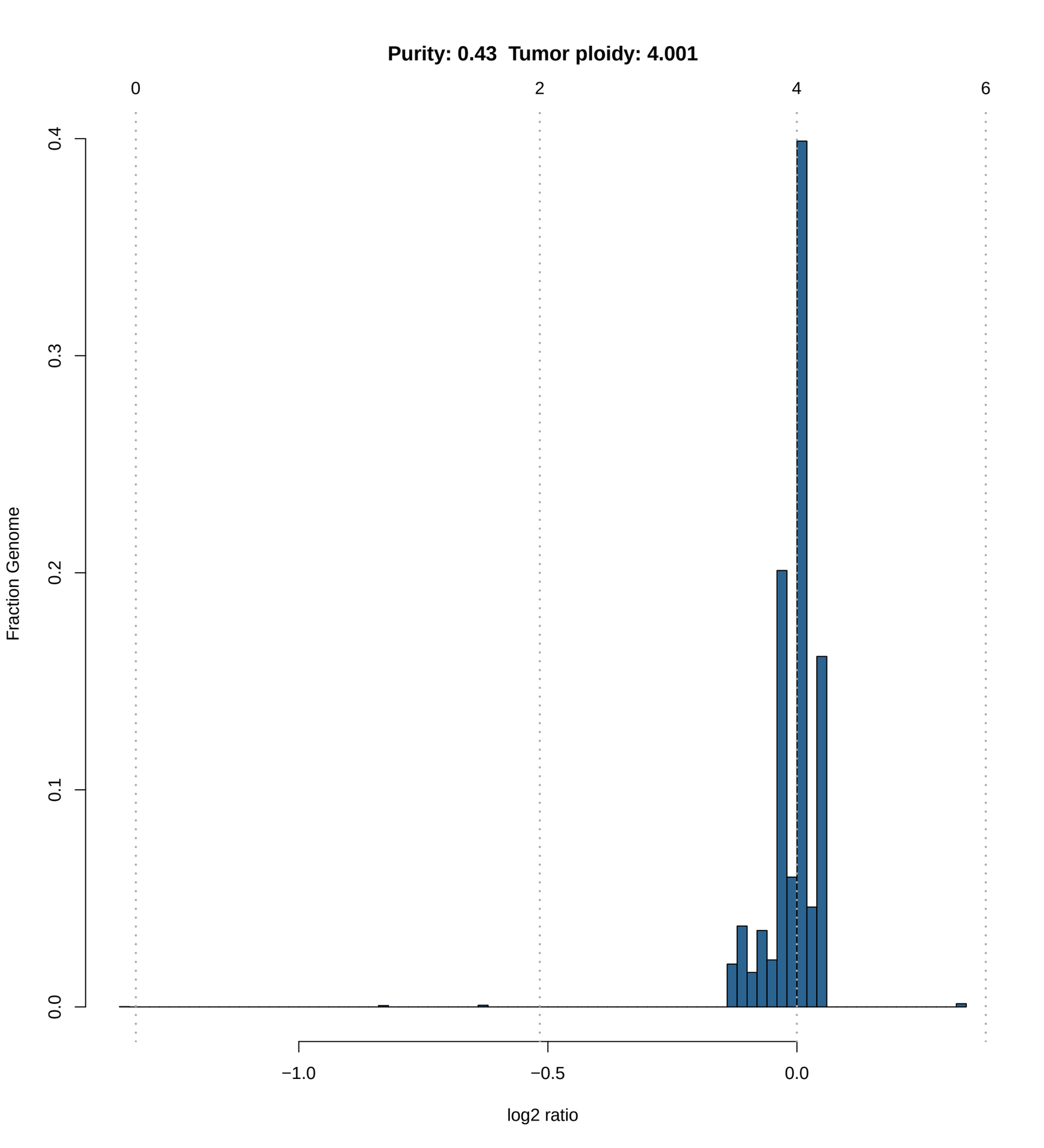

Maximum Likelihood Copy Number
0 1 2 3 4
0 10 20 30 40 50 60 70
SNV Index

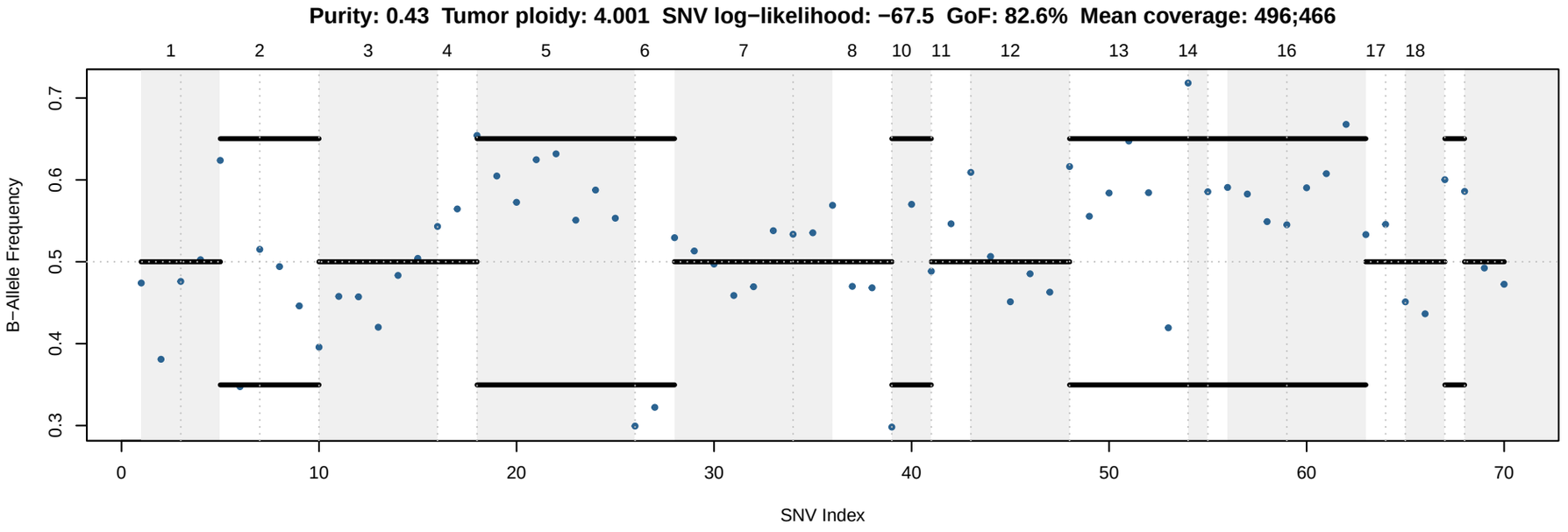

Allelic fraction (germline)
Copy Number log−ratio
4m4
3m3
4m3
3m2
4m2
3m1
4m1
4m0

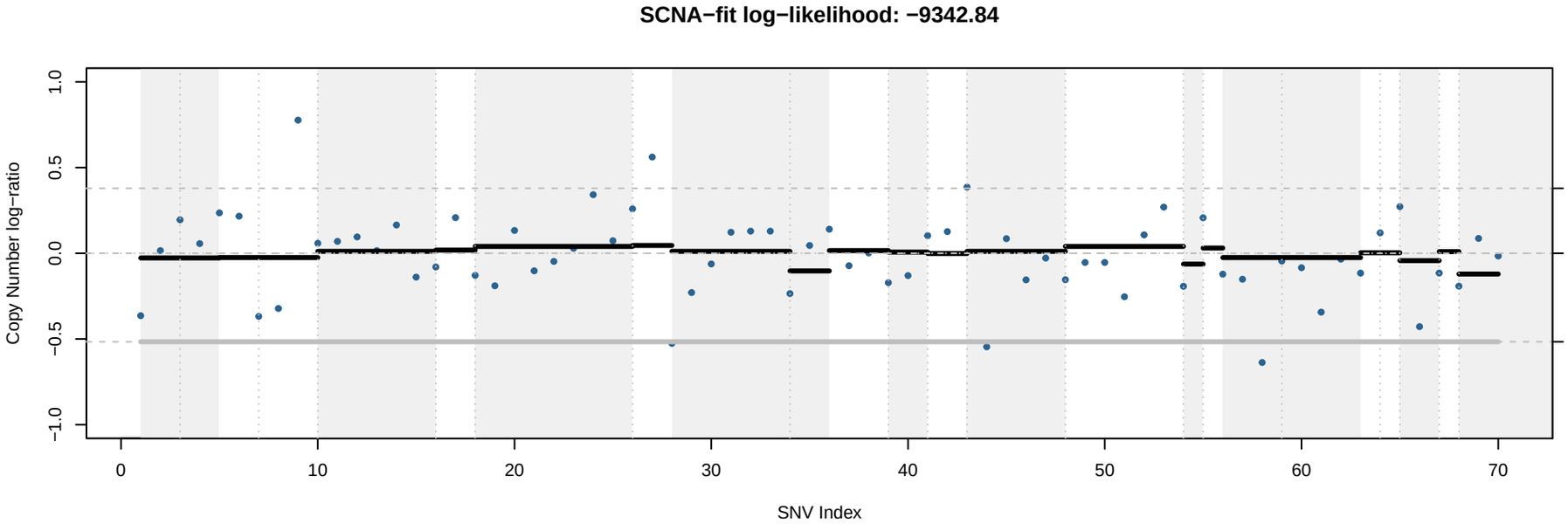

Coverage (log2)
Allelic fraction

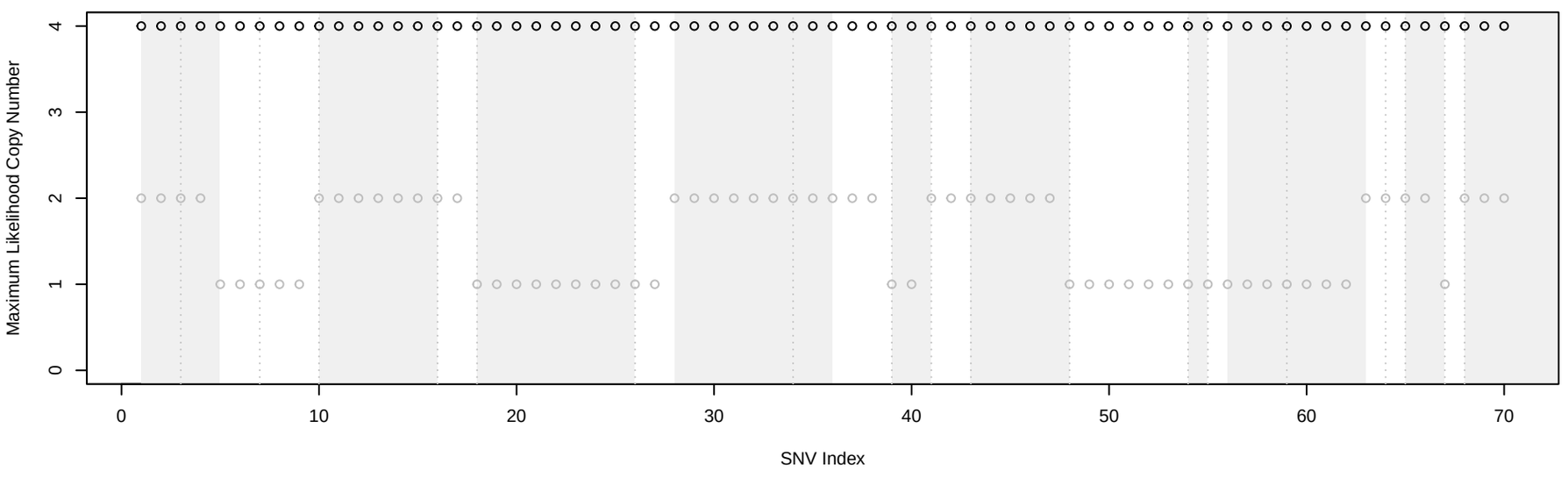

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1

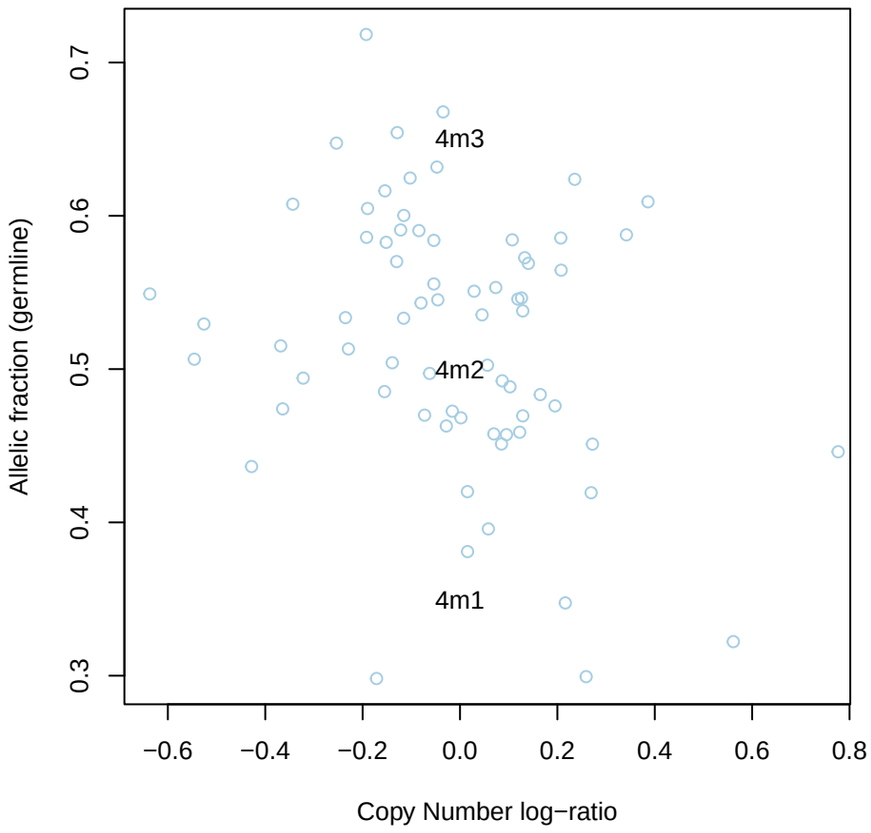

Frequency
Cellular fraction

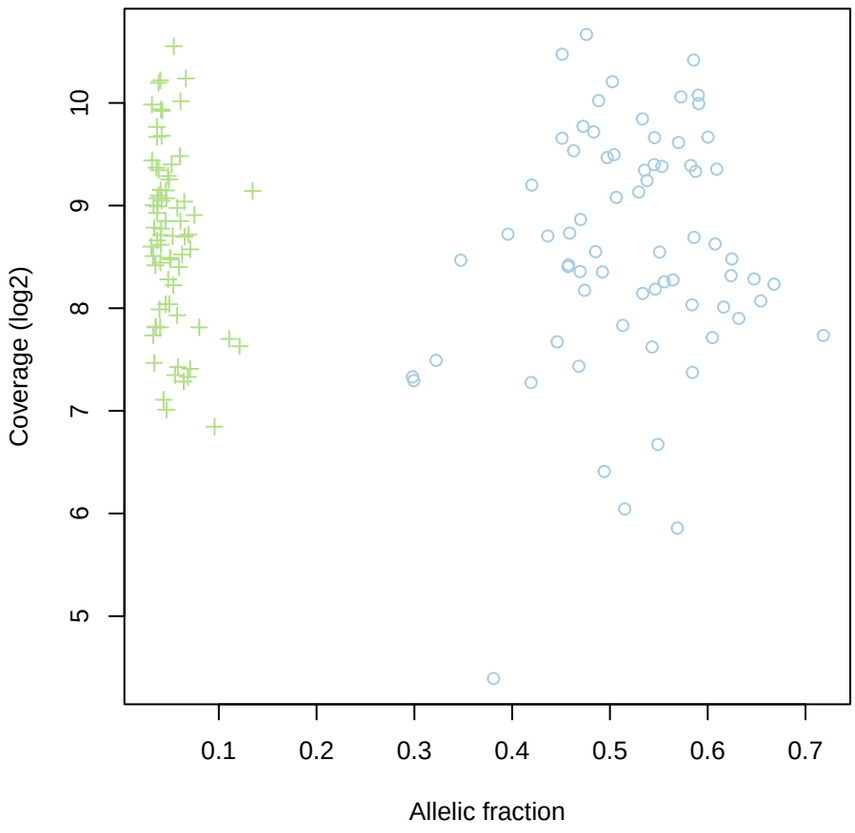

Purity: 0.43 Tumor ploidy: 4.001
0
2
4
6
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−1.0
−0.5
0.0
log2 ratio

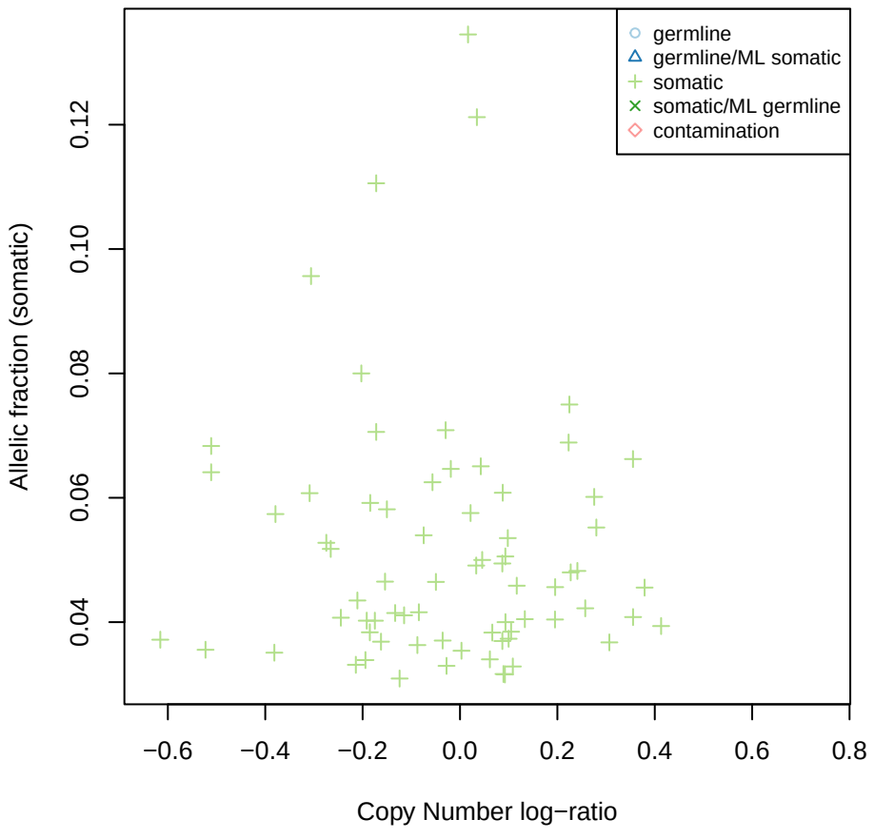

Purity: 0.43 Tumor ploidy: 4.001 SNV log−likelihood: −67.5 GoF: 82.6% Mean coverage: 496;466
1 2 3 4 5 6 7 8 10 11 12 13 14 16 17 18
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index

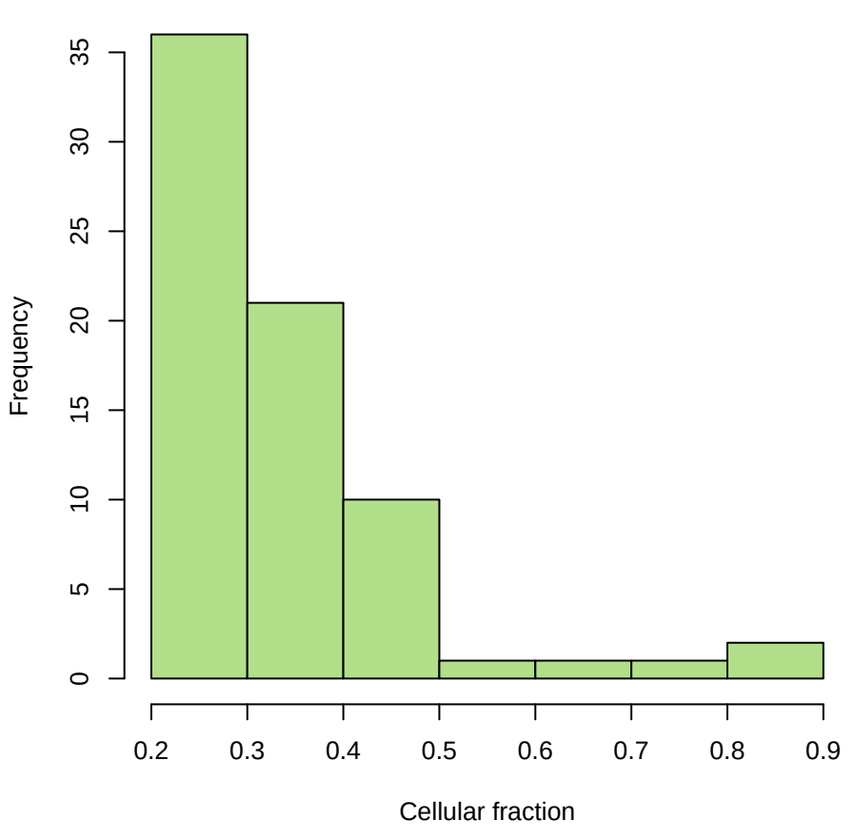

SCNA−fit log−likelihood: −9342.84
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 4 6
0 10 20 30 40 50 60 70
SNV Index

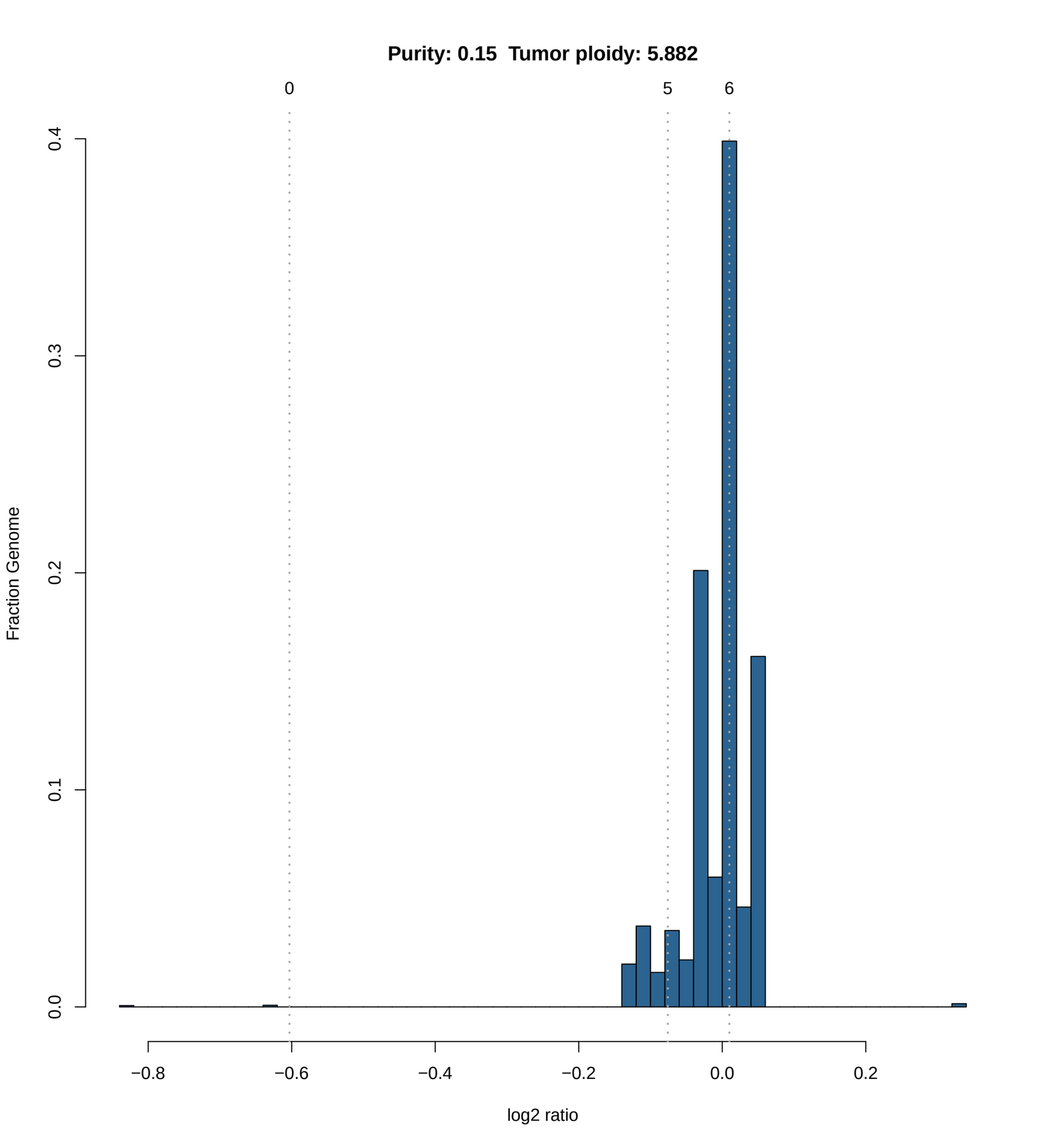

Maximum Likelihood Copy Number
0 1 2 3 4
0 10 20 30 40 50 60 70
SNV Index

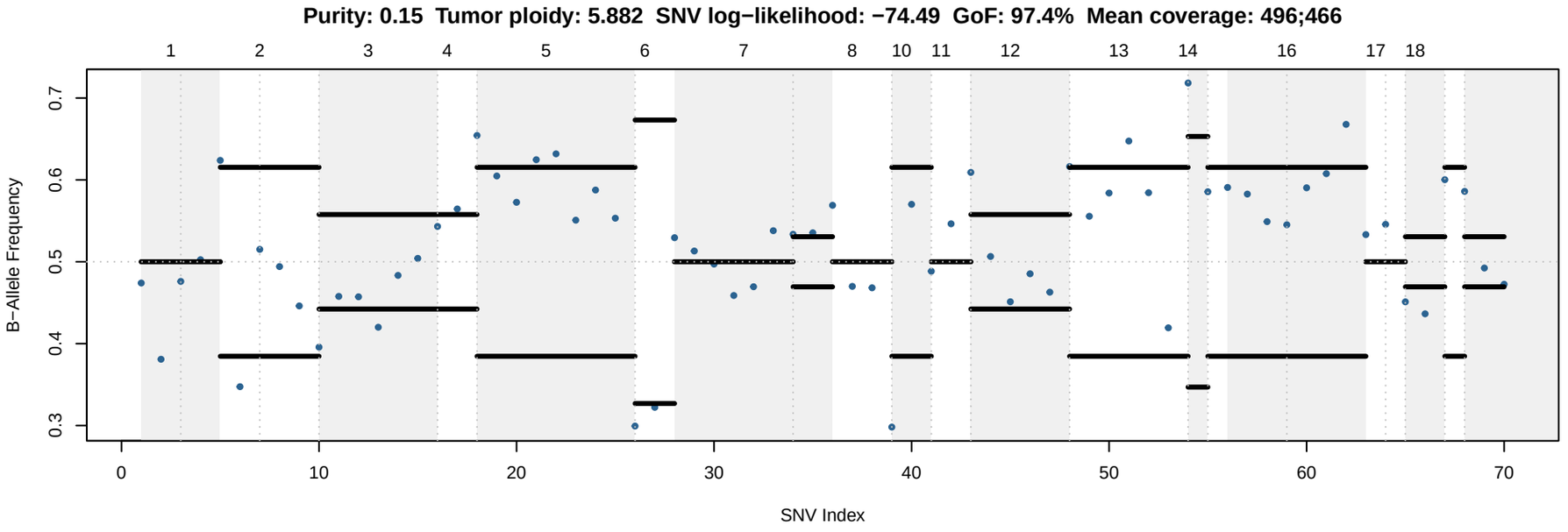

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
4m3
4m2
4m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

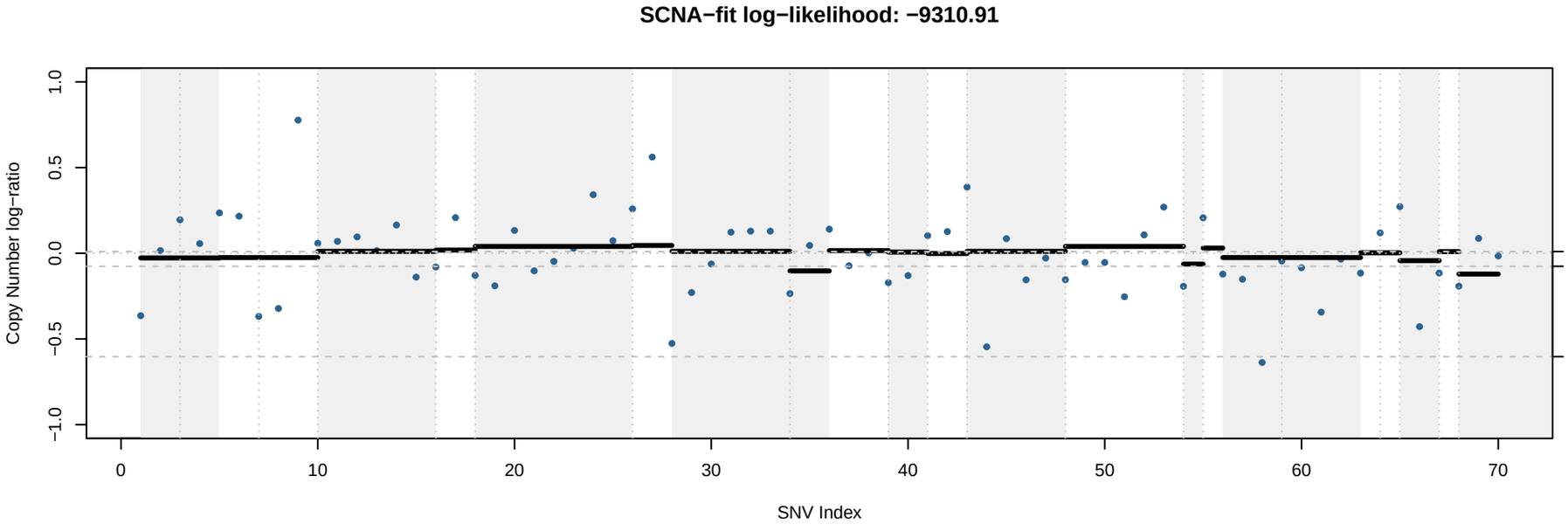

Coverage (log2)
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

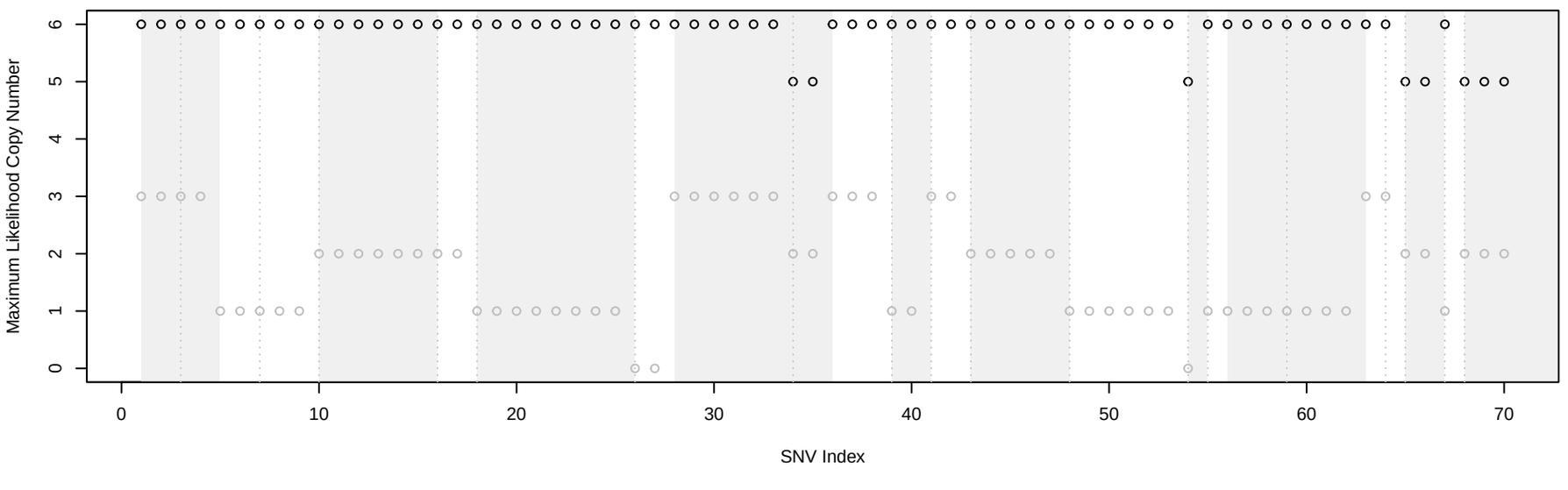

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

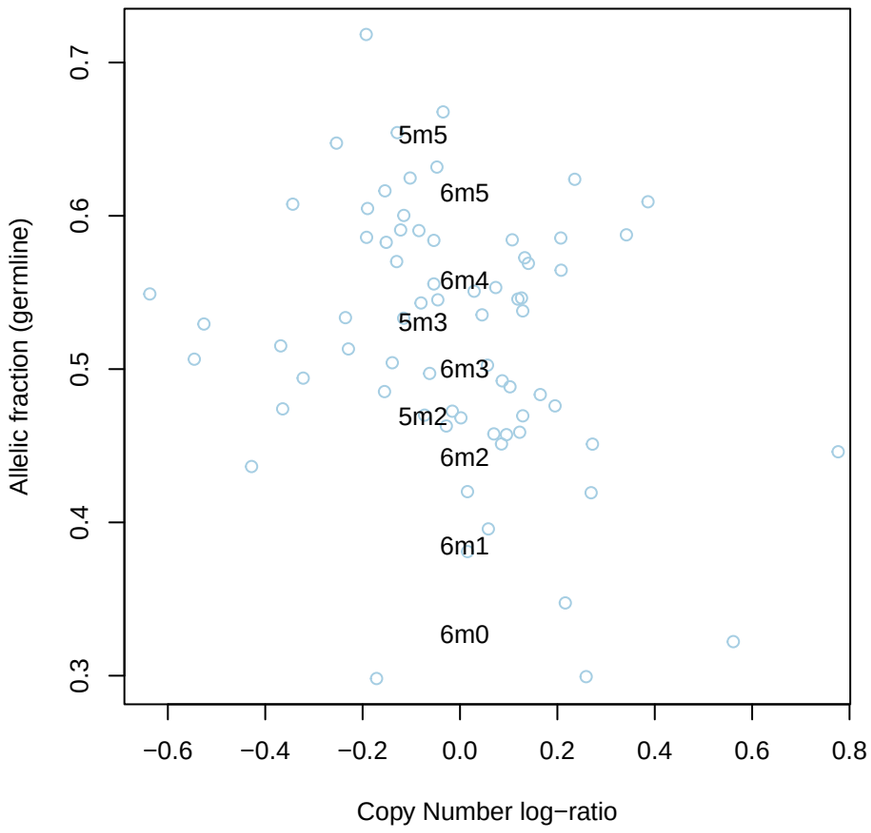

Frequency
0
5
10
15
20
25
30
35
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
Cellular fraction

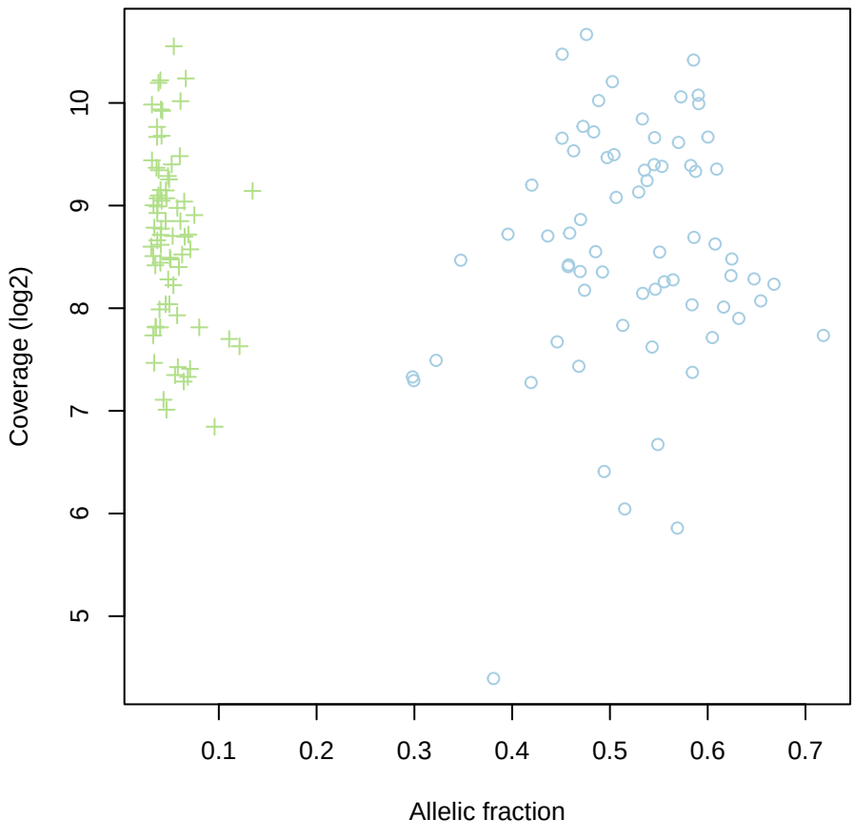

Purity: 0.15 Tumor ploidy: 5.882
0
5
6
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

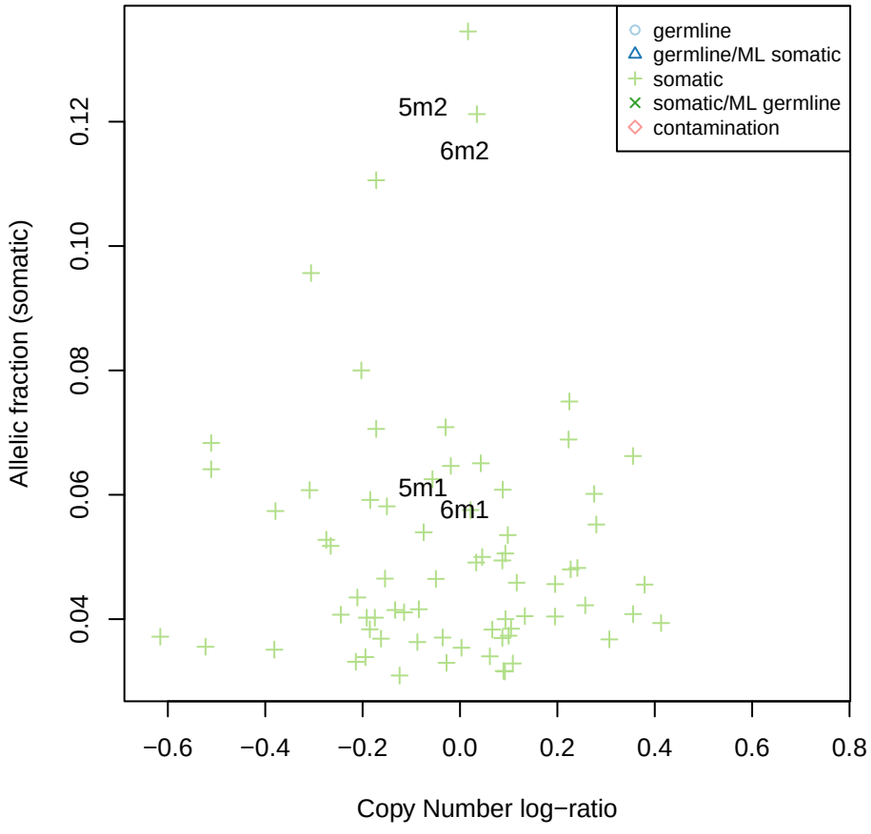

Purity: 0.15 Tumor ploidy: 5.882 SNV log−likelihood: −74.49 GoF: 97.4% Mean coverage: 496;466
1 2 3 4 5 6 7 8 10 11 12 13 14 16 17 18
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index

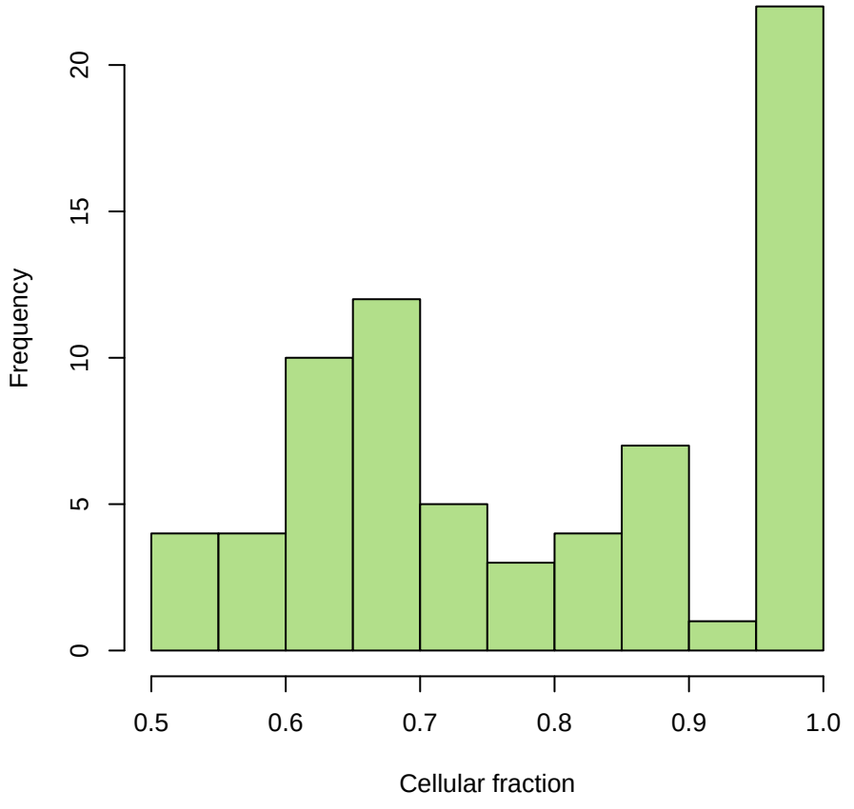

SCNA−fit log−likelihood: −9310.91
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
5
0
0 10 20 30 40 50 60 70
SNV Index

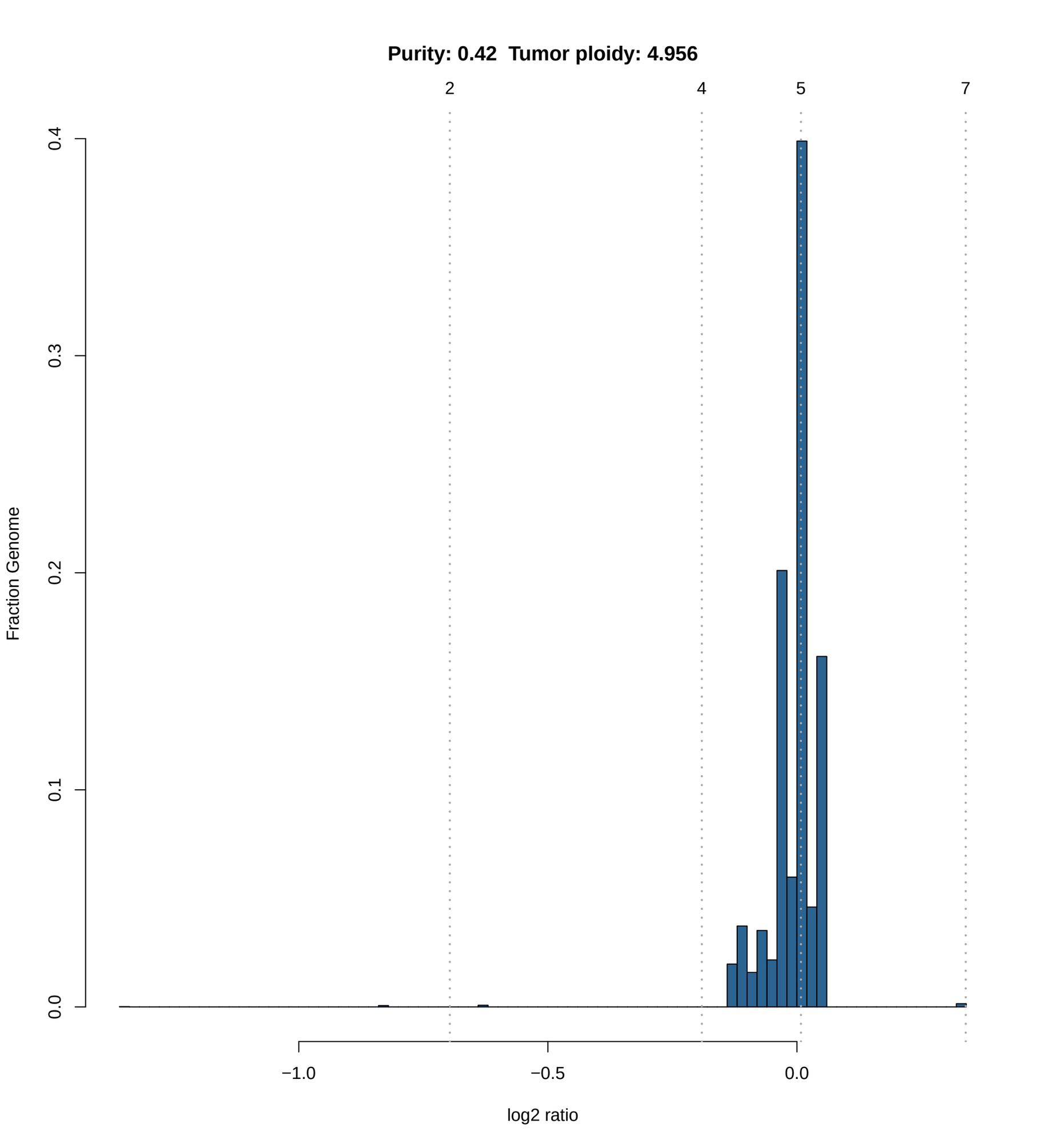

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 10 20 30 40 50 60 70
SNV Index

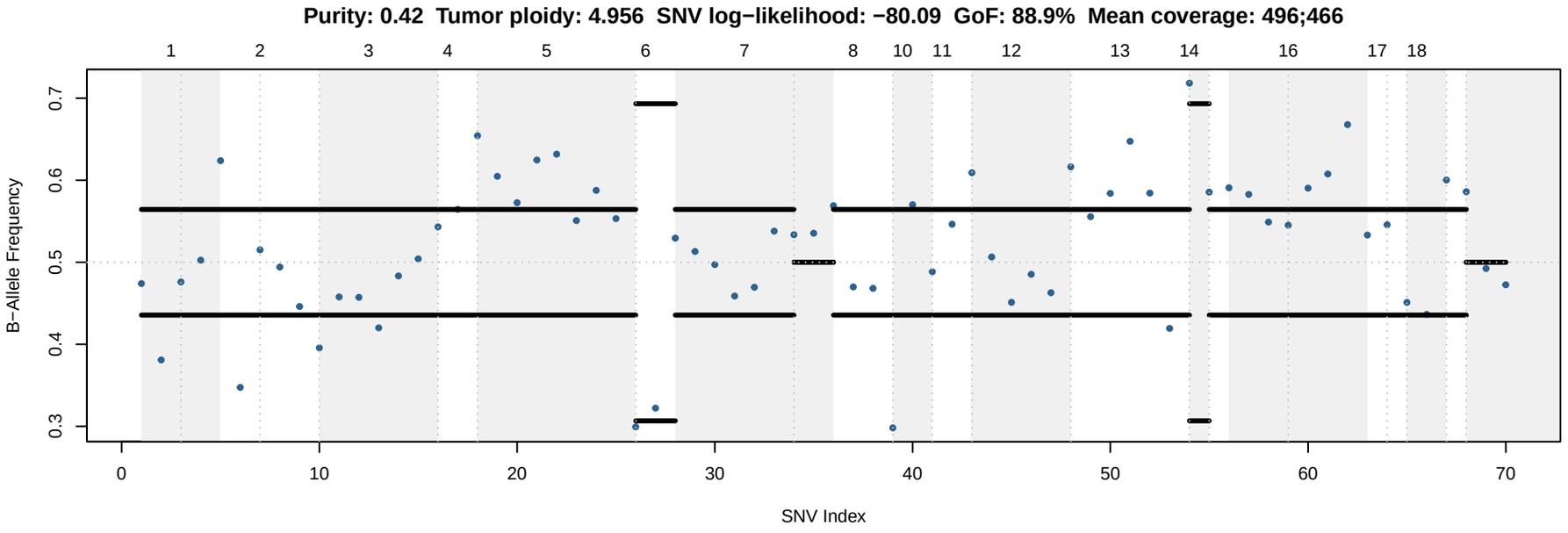

Allelic fraction (germline)
Copy Number log−ratio
5m5
6m5
6m4
5m3
6m3
5m2
6m2
6m1
6m0

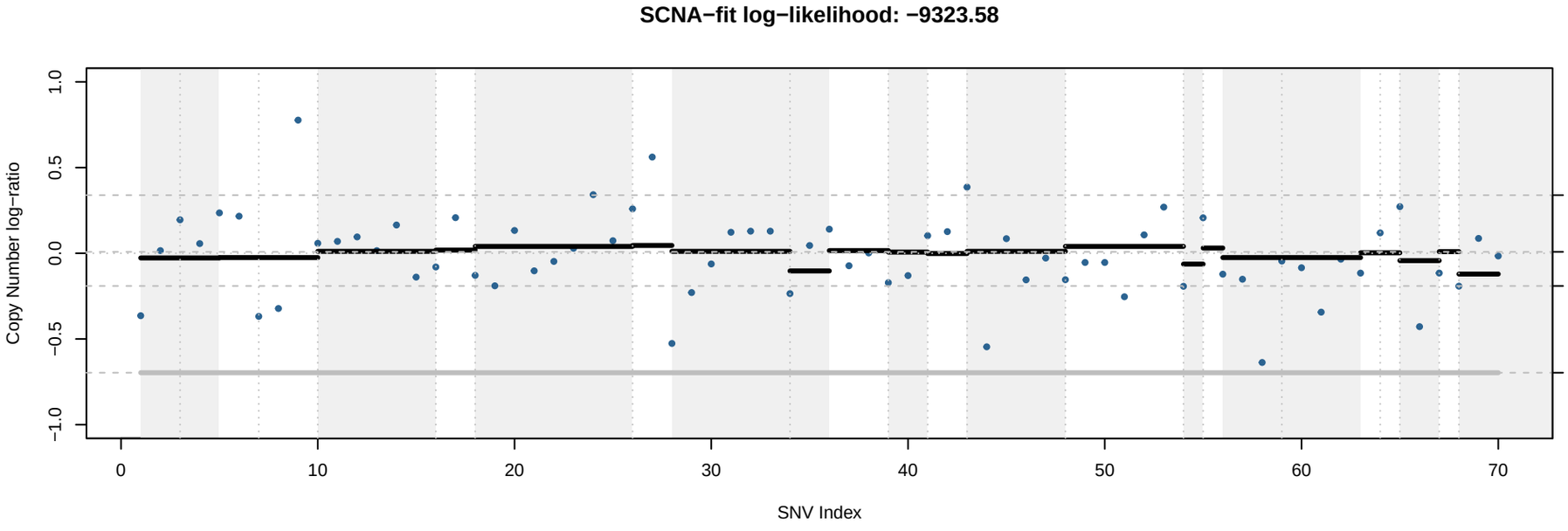

Coverage (log2)
Allelic fraction

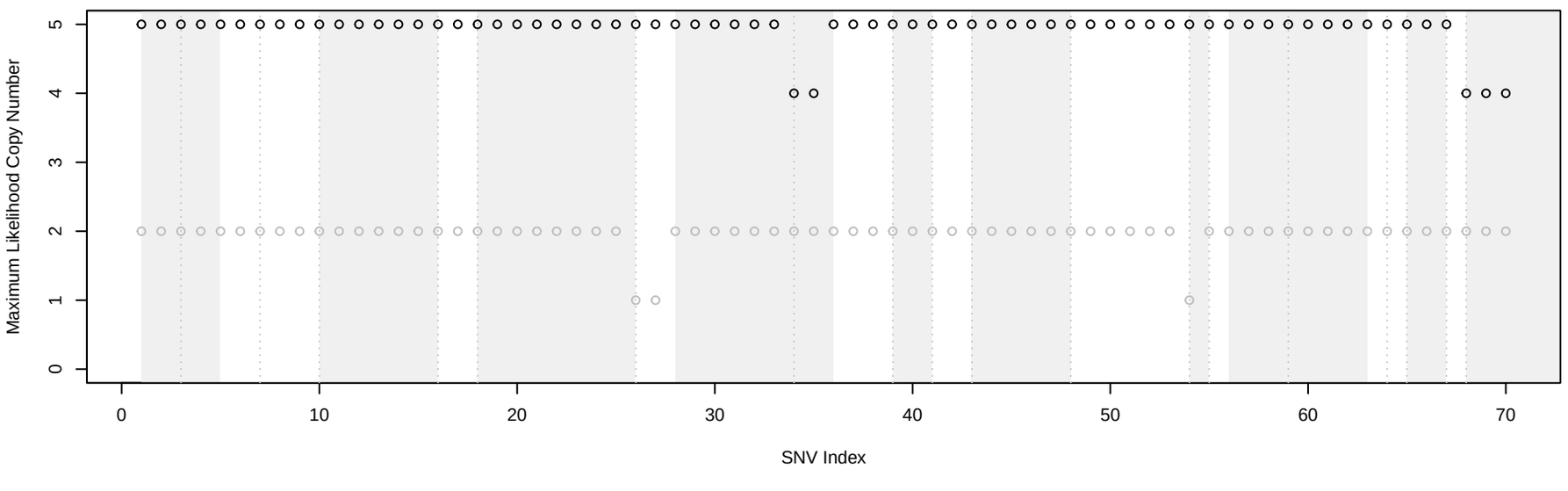

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m2
6m2
5m1
6m1

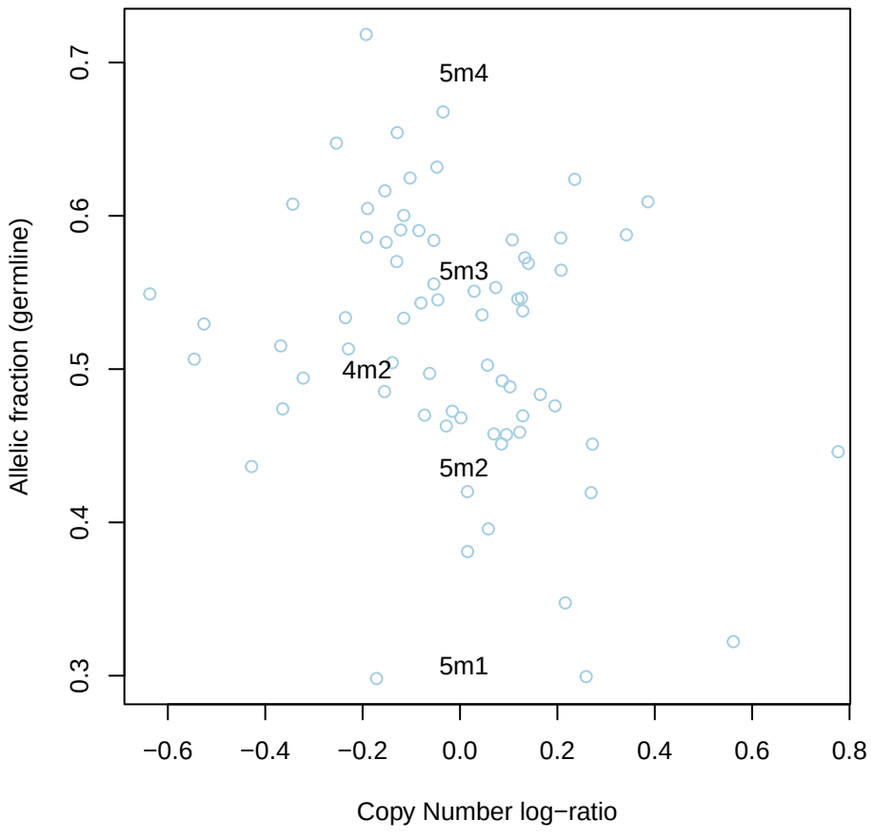

Frequency
Cellular fraction

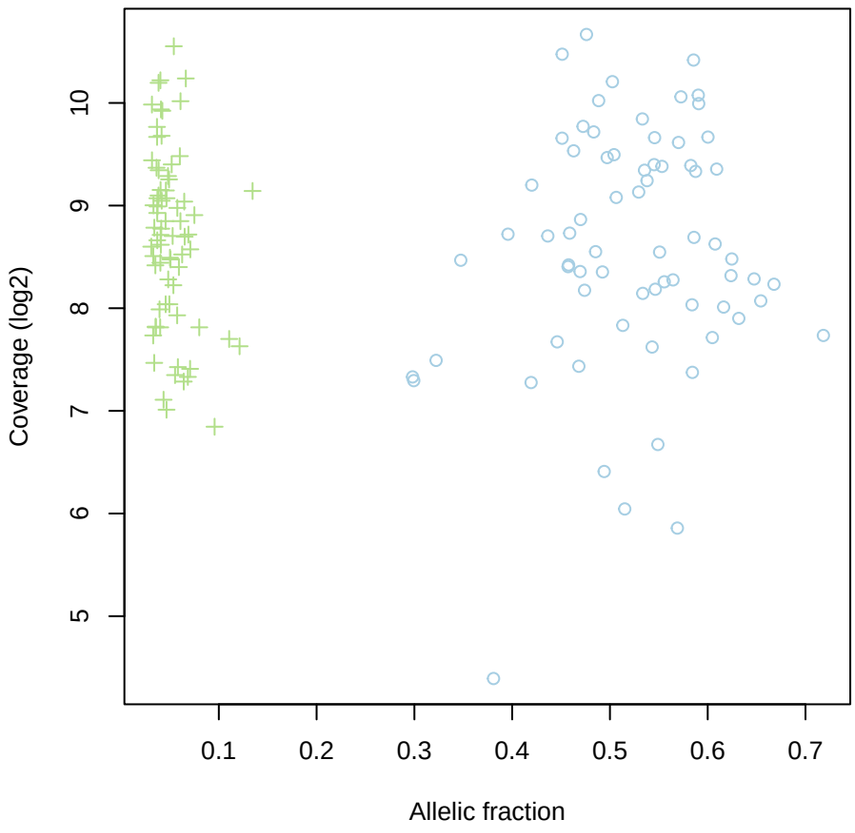

Purity: 0.42 Tumor ploidy: 4.956
2
4
5
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
log2 ratio

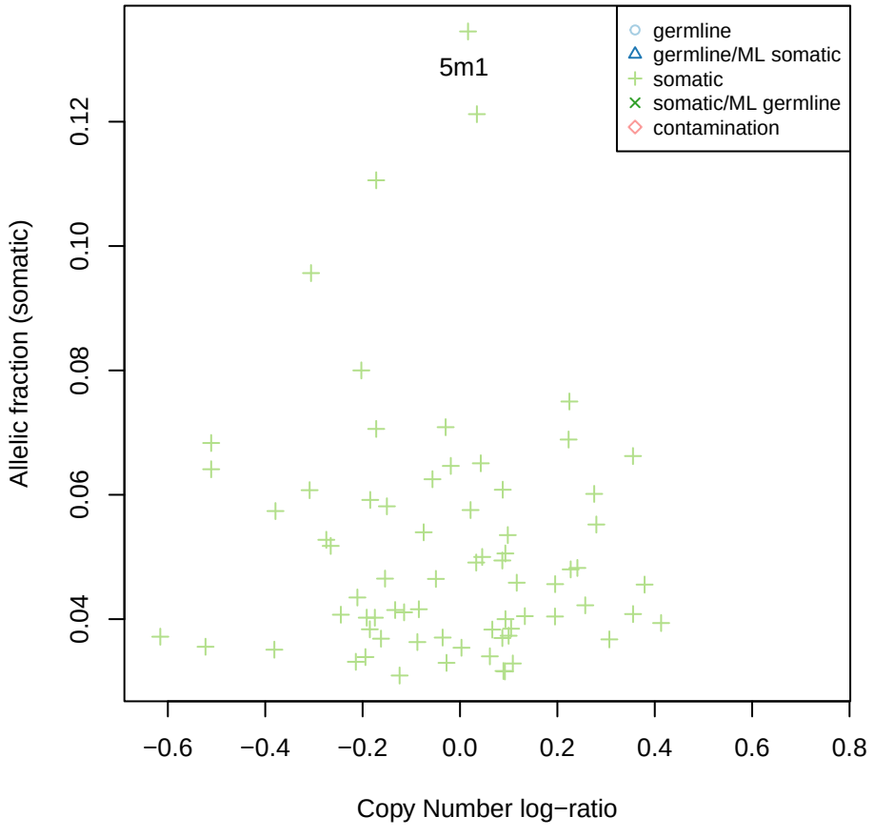

Purity: 0.42 Tumor ploidy: 4.956 SNV log−likelihood: −80.09 GoF: 88.9% Mean coverage: 496;466
1 2 3 4 5 6 7 8 10 11 12 13 14 16 17 18
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index

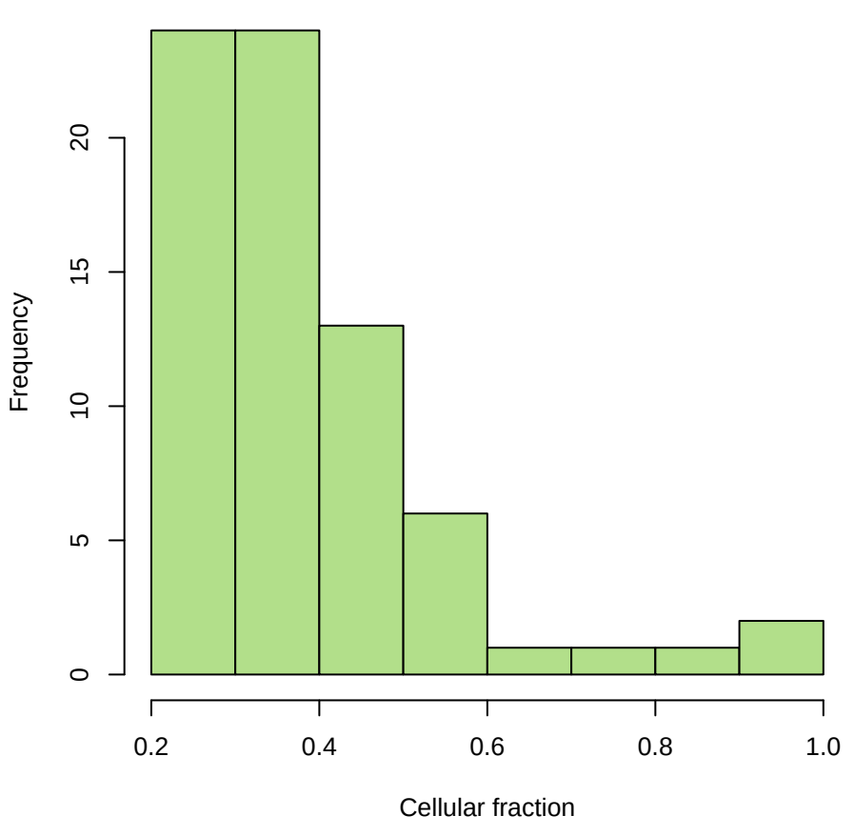

SCNA−fit log−likelihood: −9323.58
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 4 5 7
0 10 20 30 40 50 60 70
SNV Index

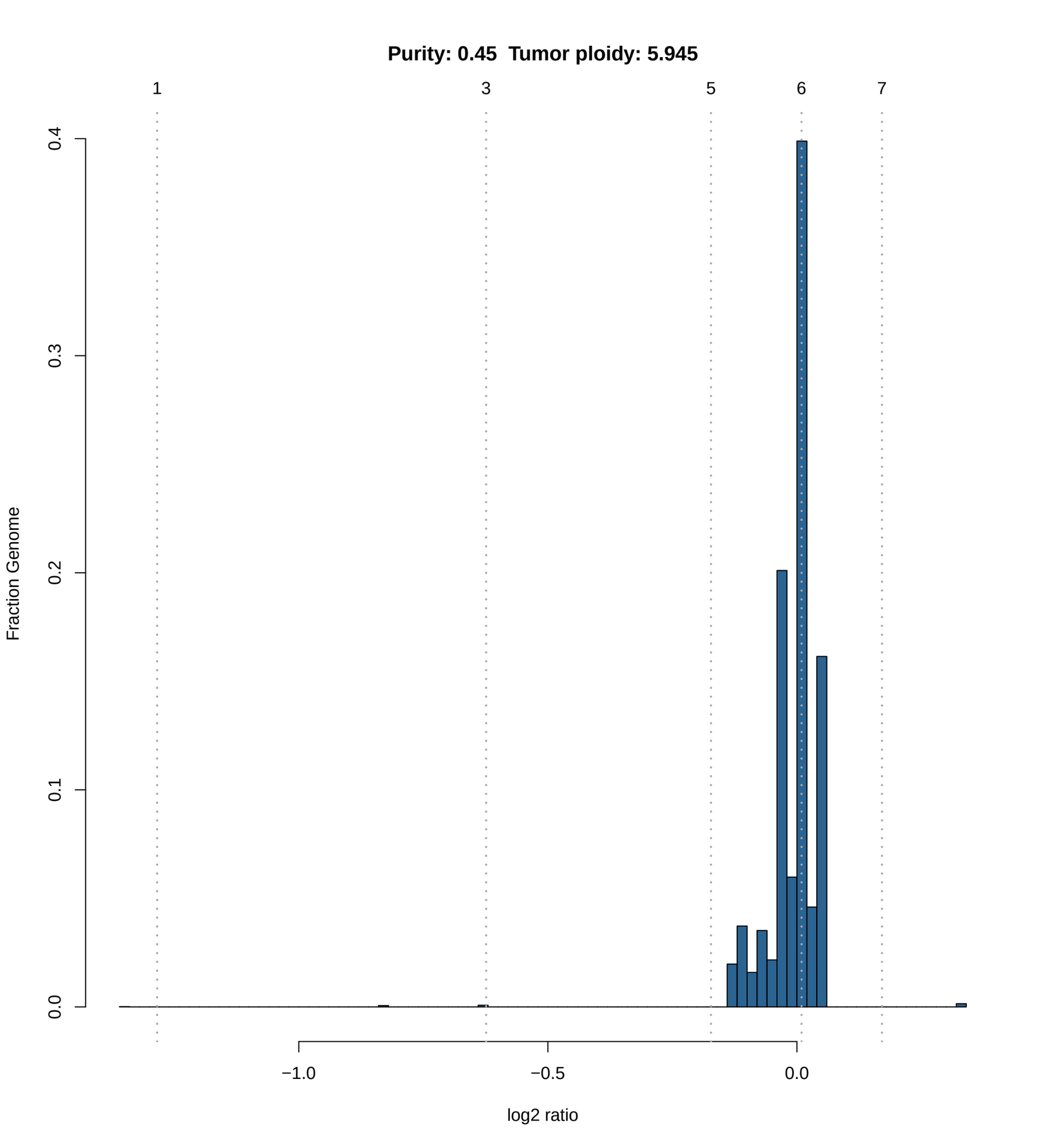

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 10 20 30 40 50 60 70
SNV Index

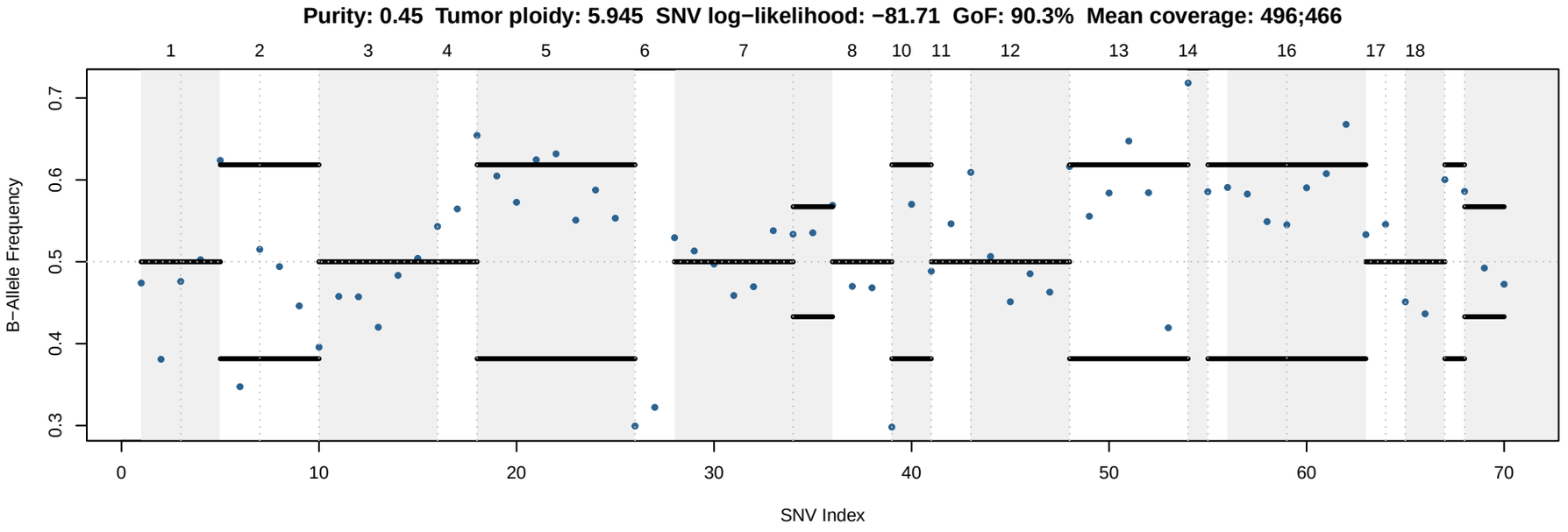

5m4
5m3
4m2
5m2
5m1
Allelic fraction (germline)
Copy Number log−ratio

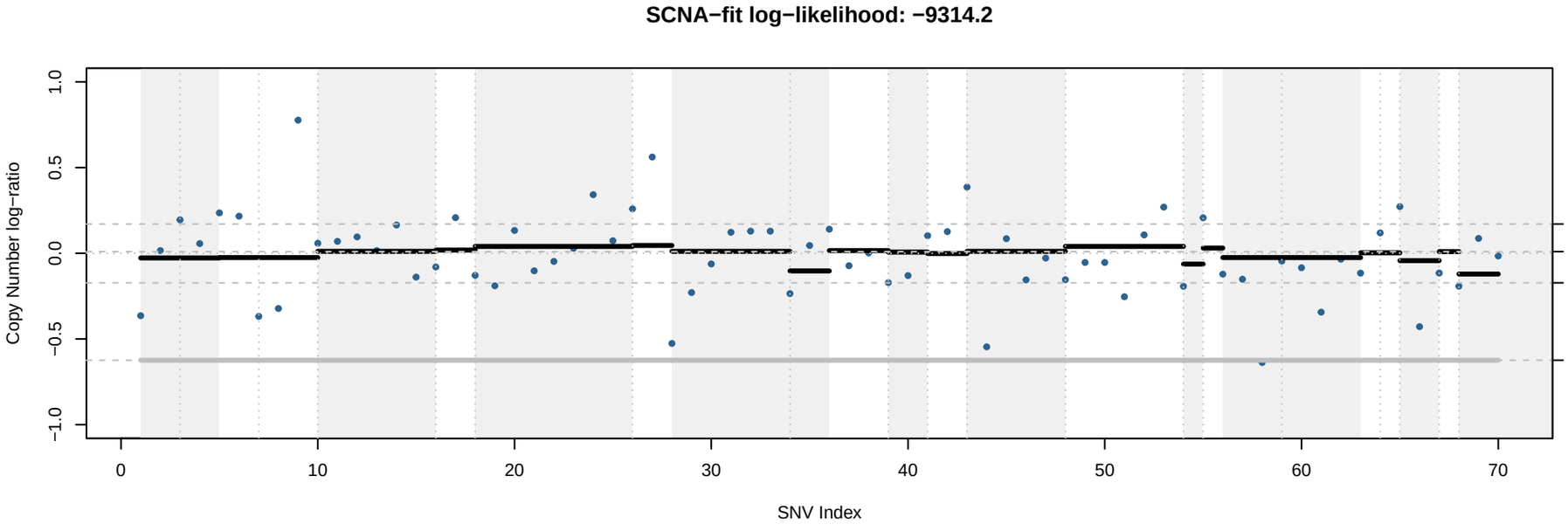

Coverage (log2)
Allelic fraction

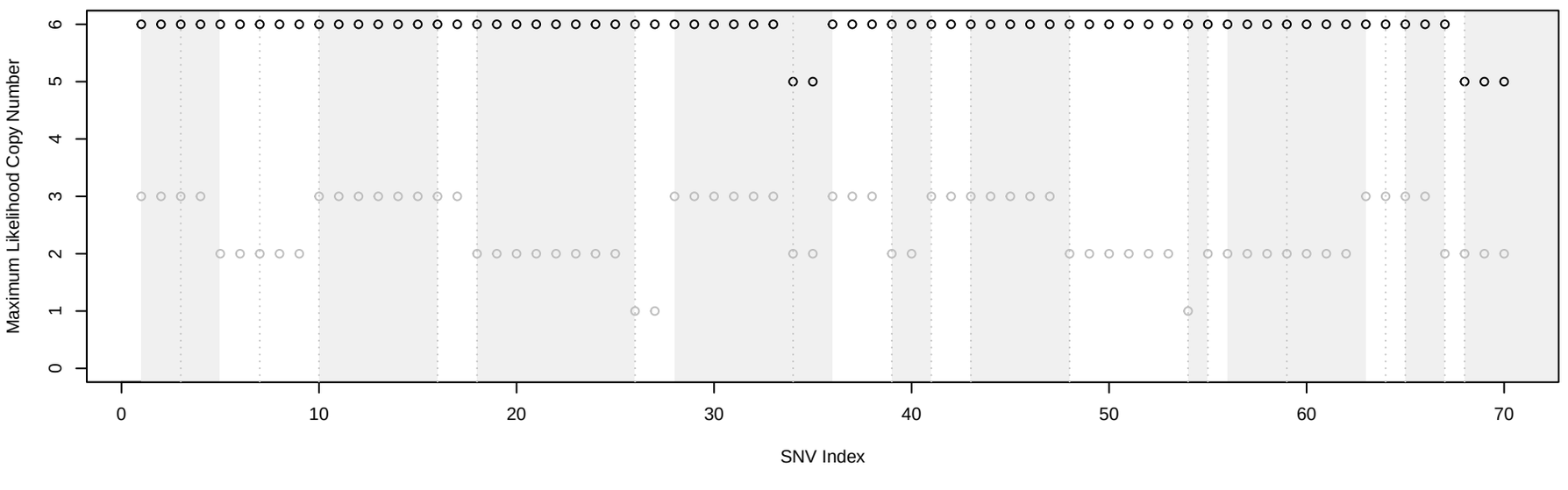

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
Allelic fraction (somatic)
Copy Number log−ratio

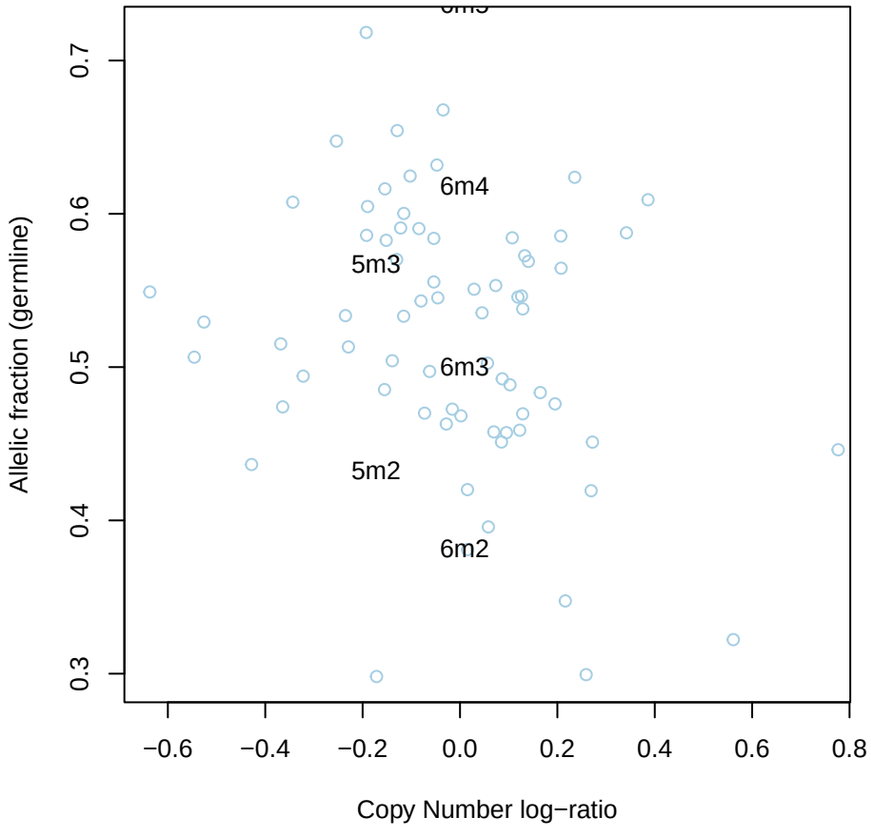

Frequency
Cellular fraction

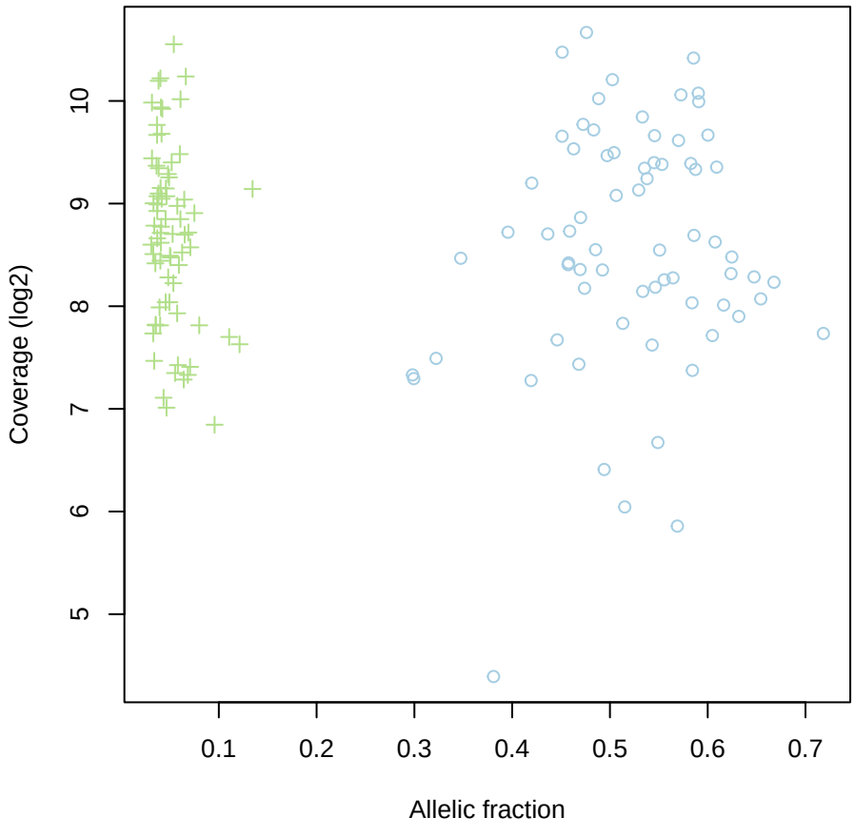

Purity: 0.45 Tumor ploidy: 5.945
1
3
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
log2 ratio

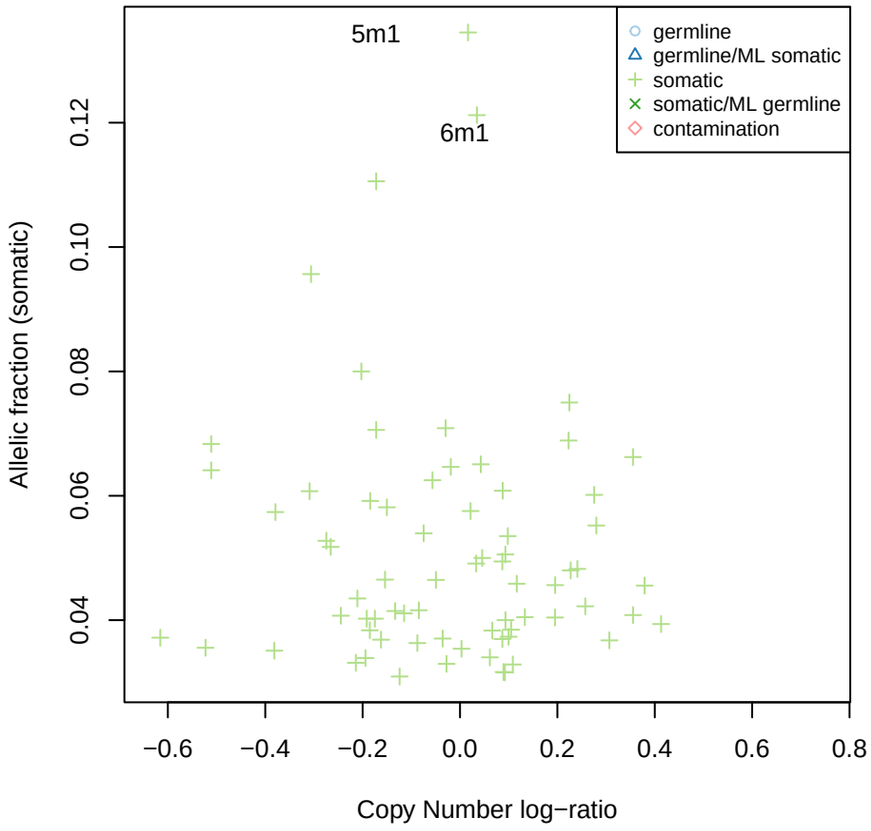

Purity: 0.45 Tumor ploidy: 5.945 SNV log−likelihood: −81.71 GoF: 90.3% Mean coverage: 496;466
1 2 3 4 5 6 7 8 10 11 12 13 14 16 17 18
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index

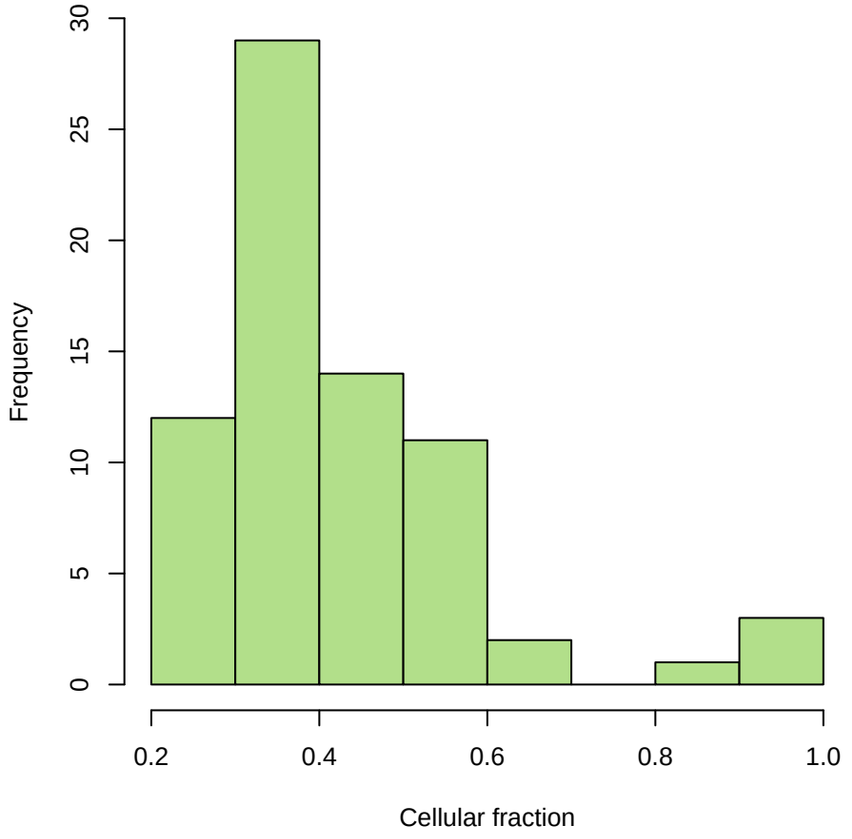

SCNA−fit log−likelihood: −9314.2
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 5 6 7
0 10 20 30 40 50 60 70
SNV Index

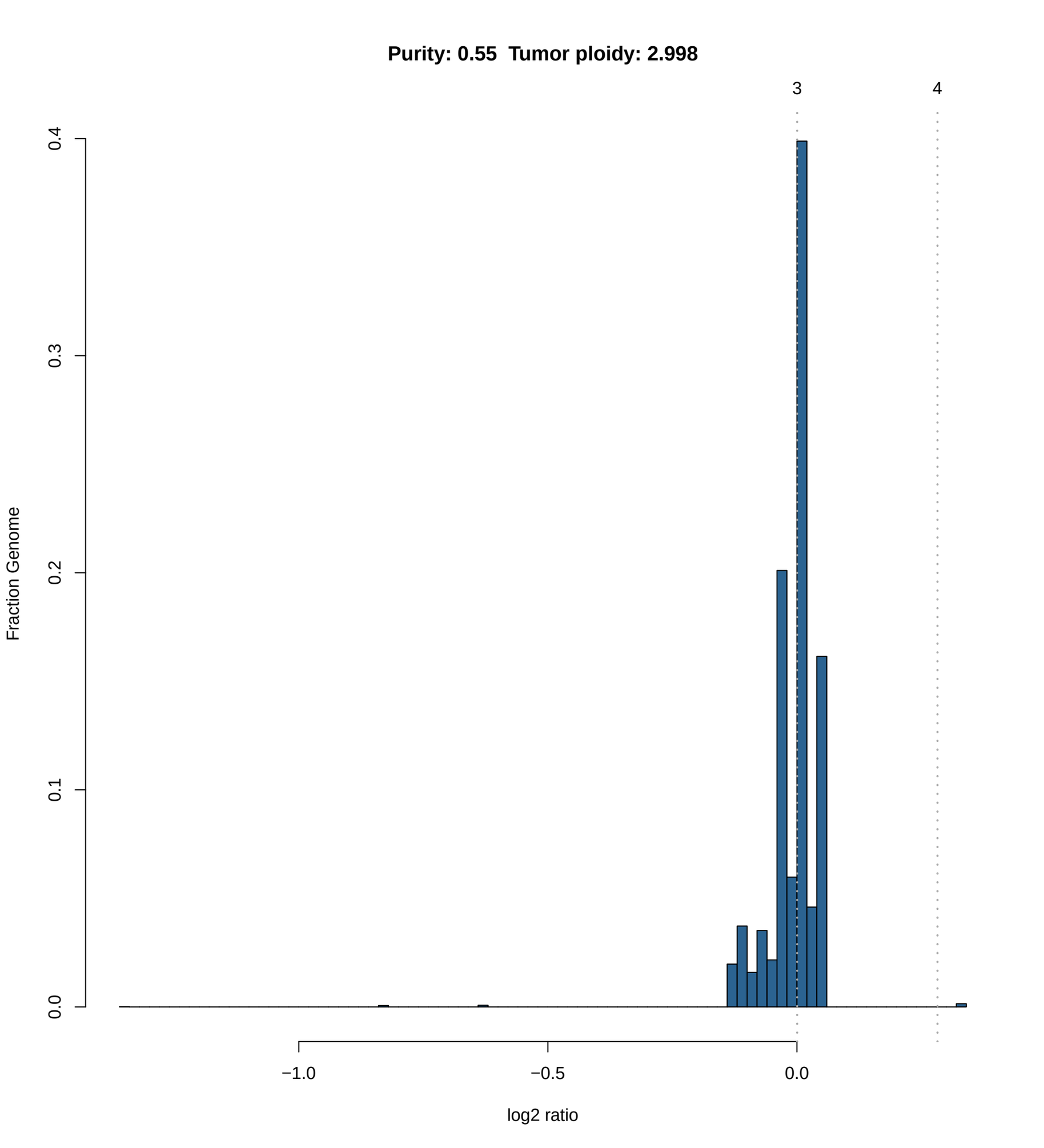

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 10 20 30 40 50 60 70
SNV Index

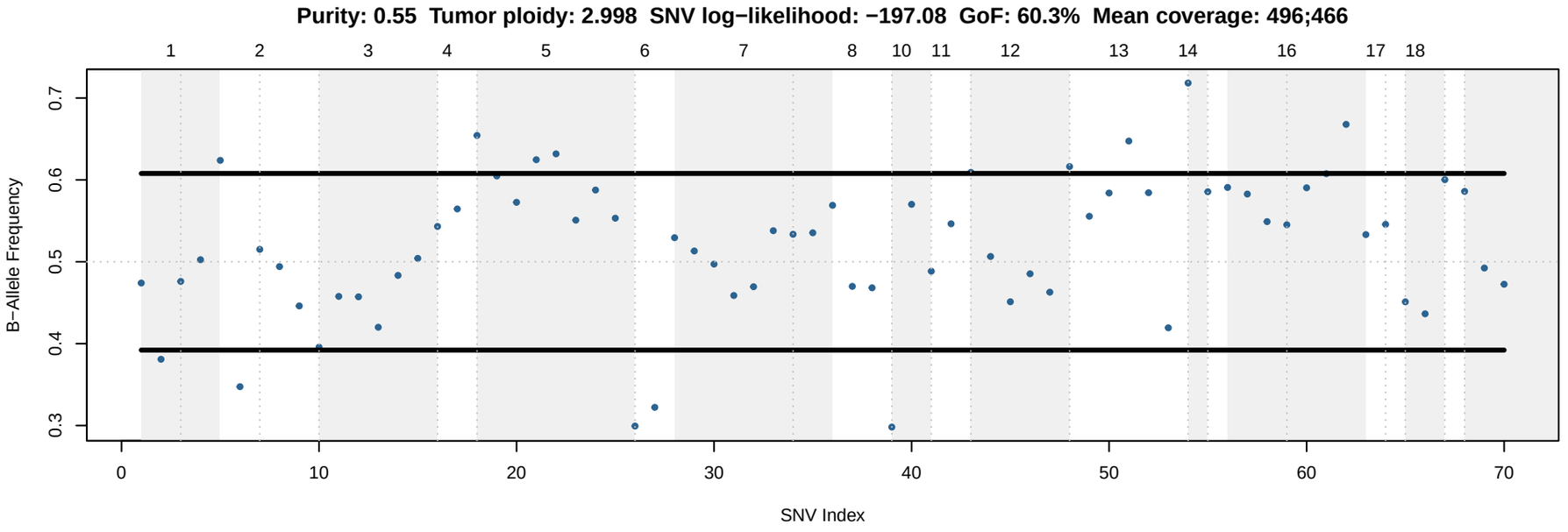

6m4
5m3
6m3
5m2
6m2
Allelic fraction (germline)
Copy Number log−ratio

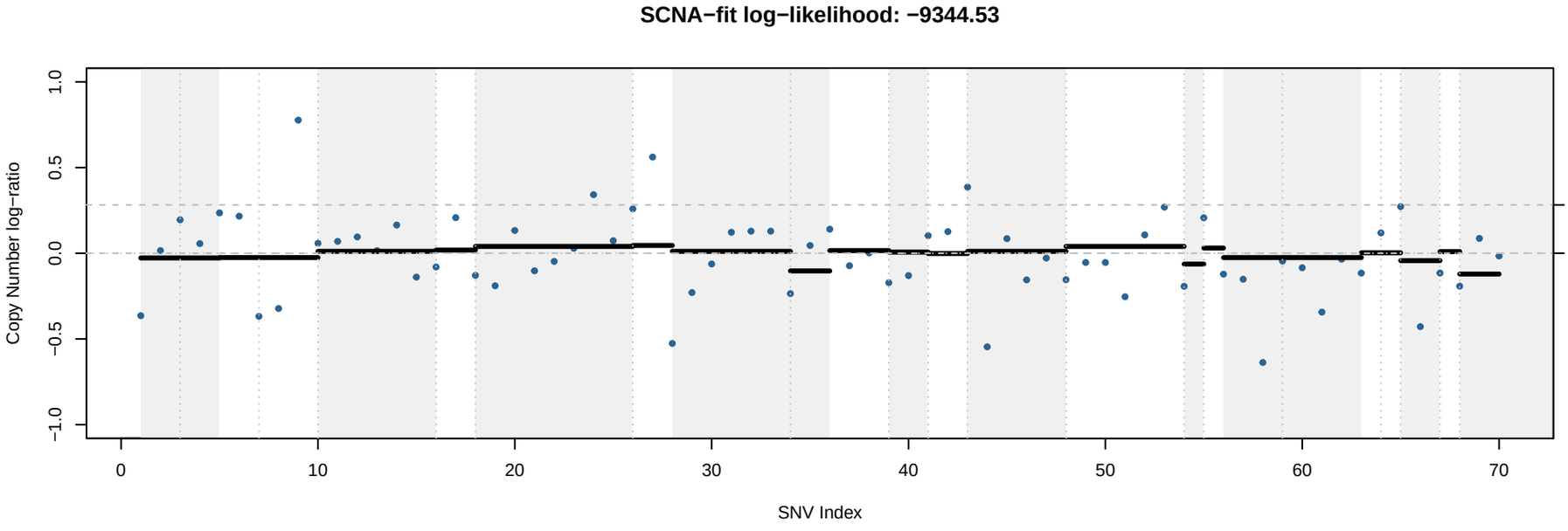

Coverage (log2)
Allelic fraction

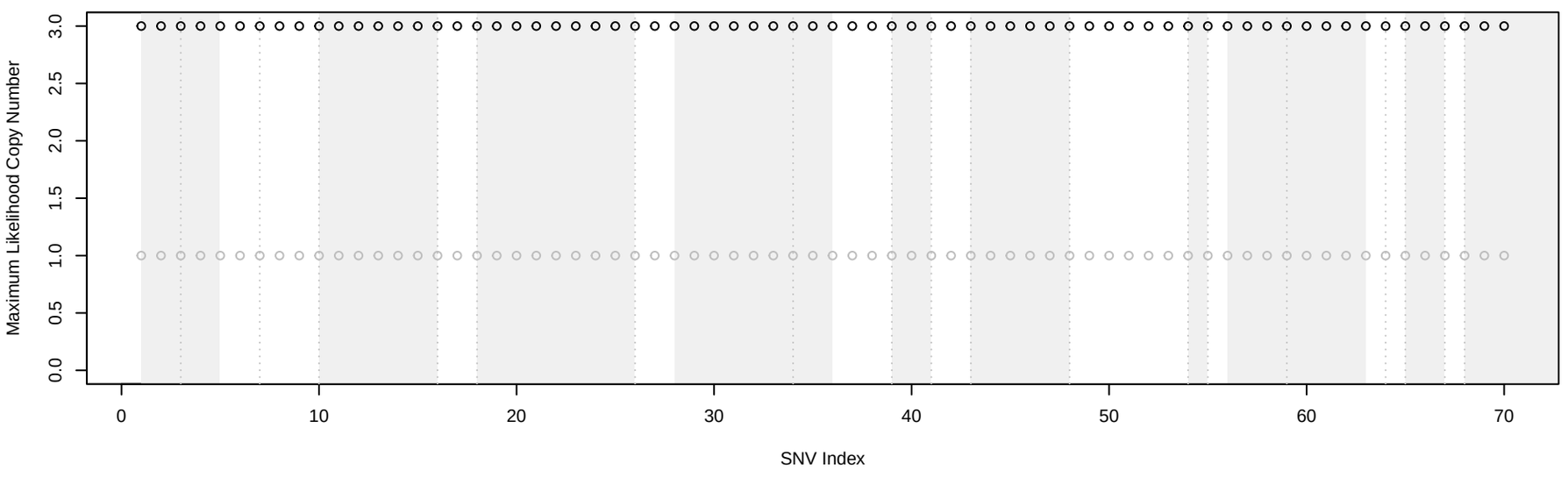

5m1
6m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

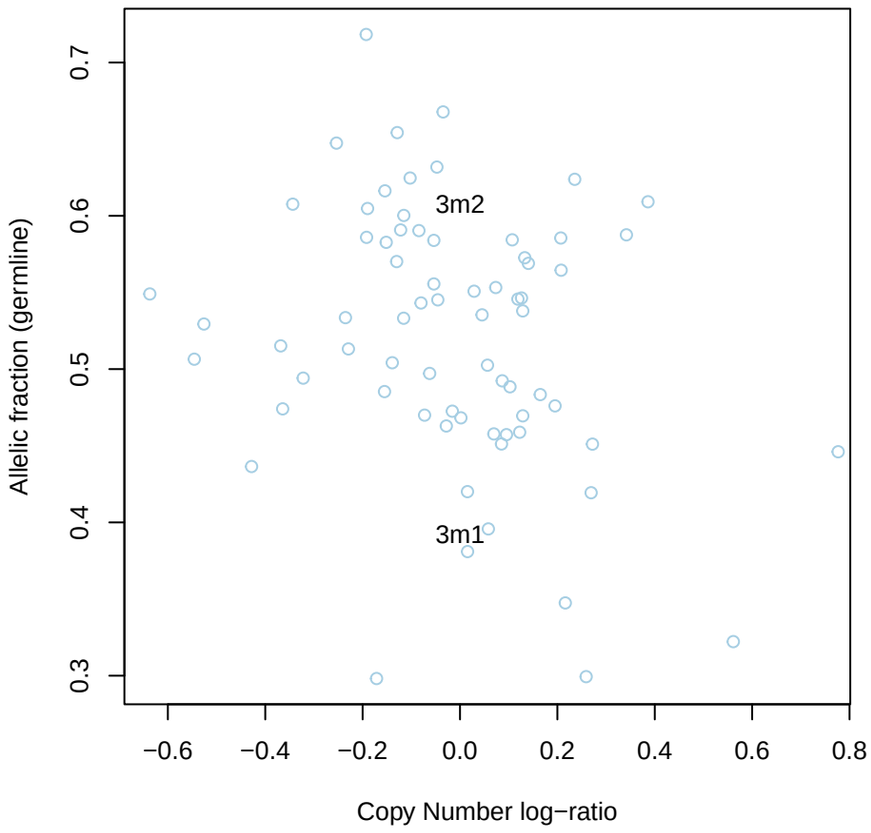

Frequency
Cellular fraction

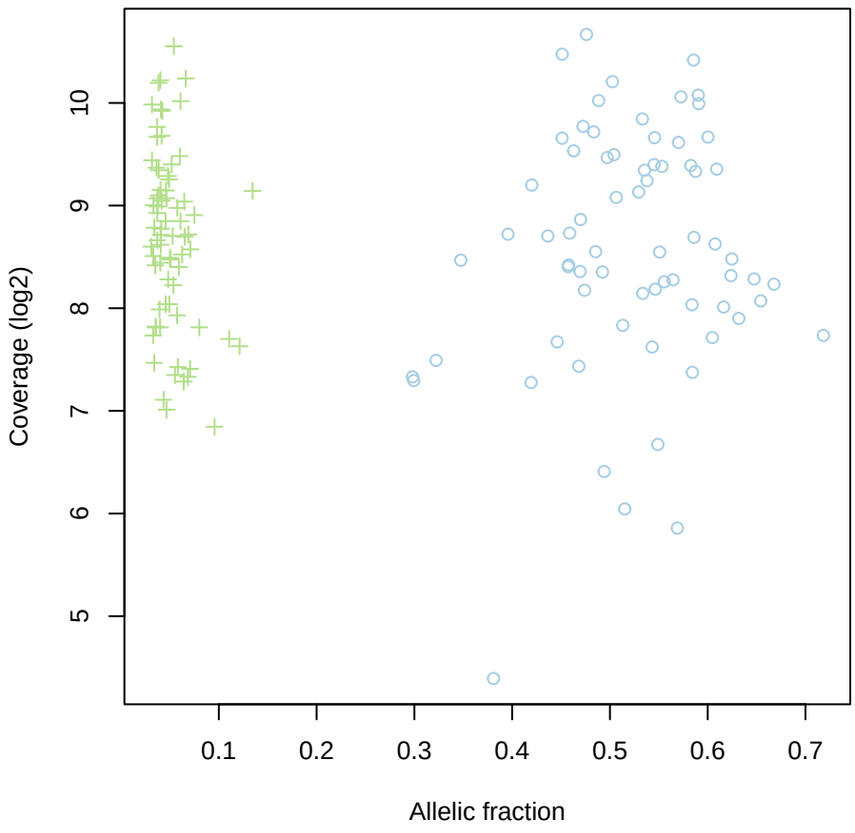

Purity: 0.55 Tumor ploidy: 2.998
3
4
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
log2 ratio

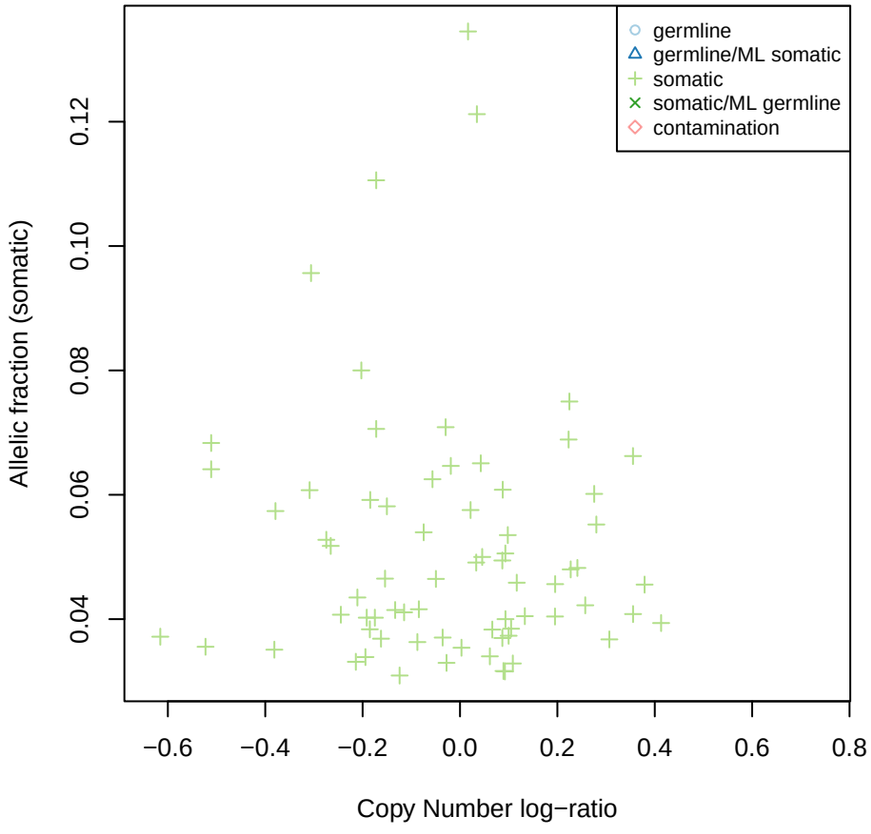

Purity: 0.55 Tumor ploidy: 2.998 SNV log−likelihood: −197.08 GoF: 60.3% Mean coverage: 496;466
1
2
3
4
5
6
7
8
10
11
12
13
14
16
17
18
B−Allele Frequency
0.3
0.4
0.5
0.6
0.7
0
10
20
30
40
50
60
70
SNV Index

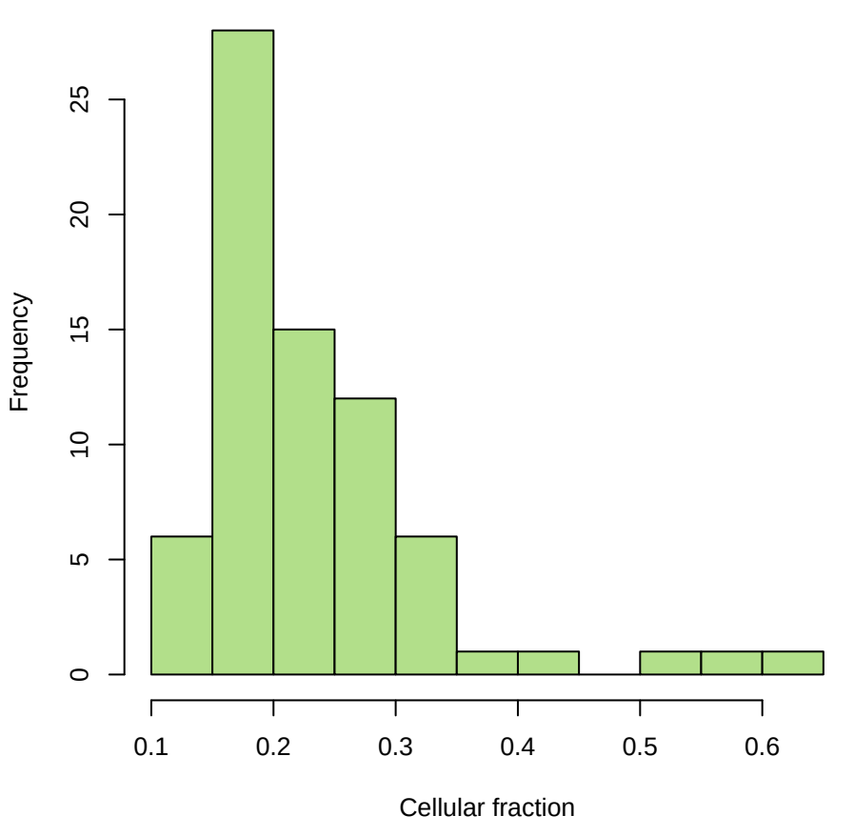

SCNA−fit log−likelihood: −9344.53
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
3
4
0
10
20
30
40
50
60
70
SNV Index

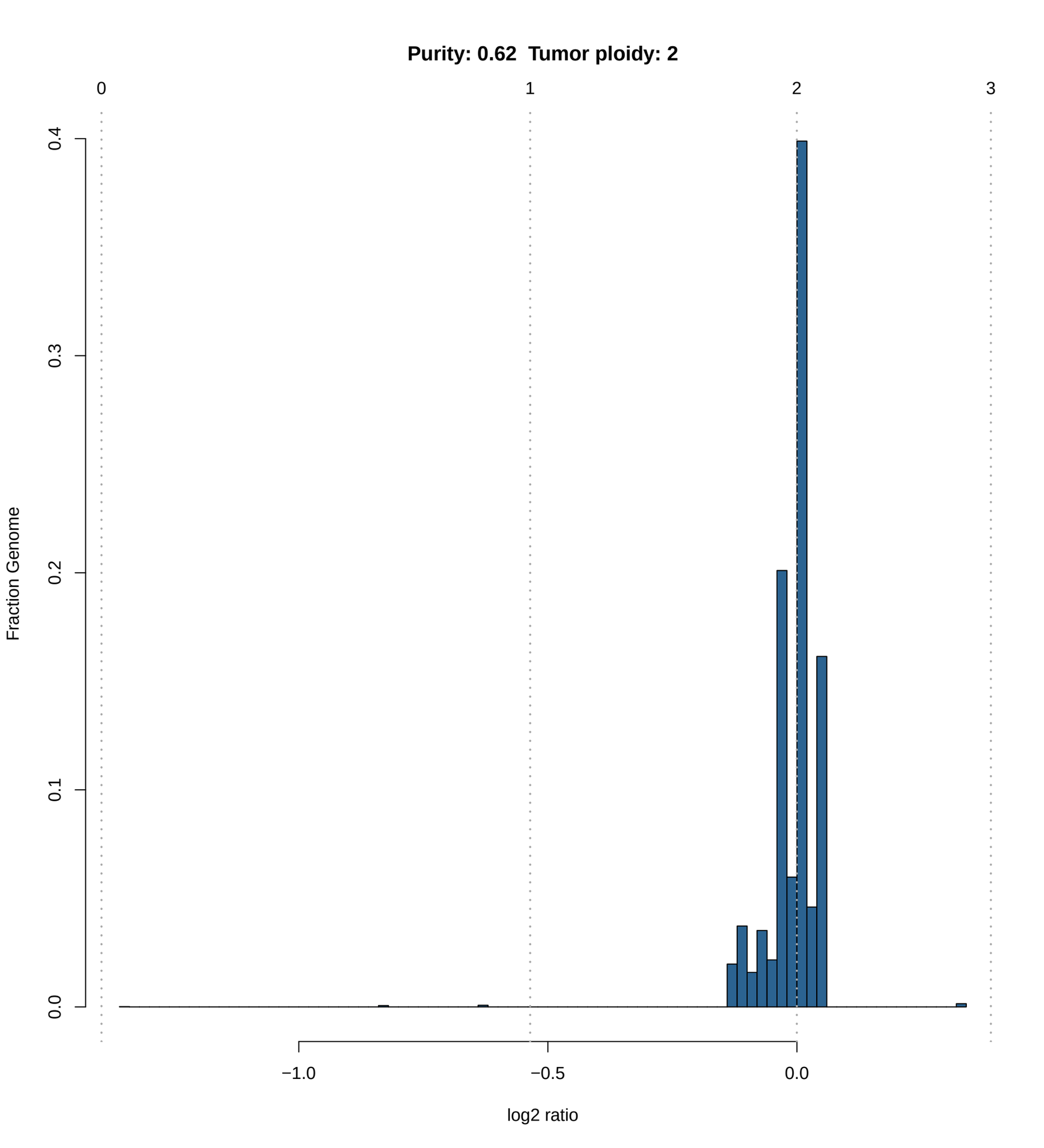

Maximum Likelihood Copy Number
0.0
0.5
1.0
1.5
2.0
2.5
3.0
0
10
20
30
40
50
60
70
SNV Index

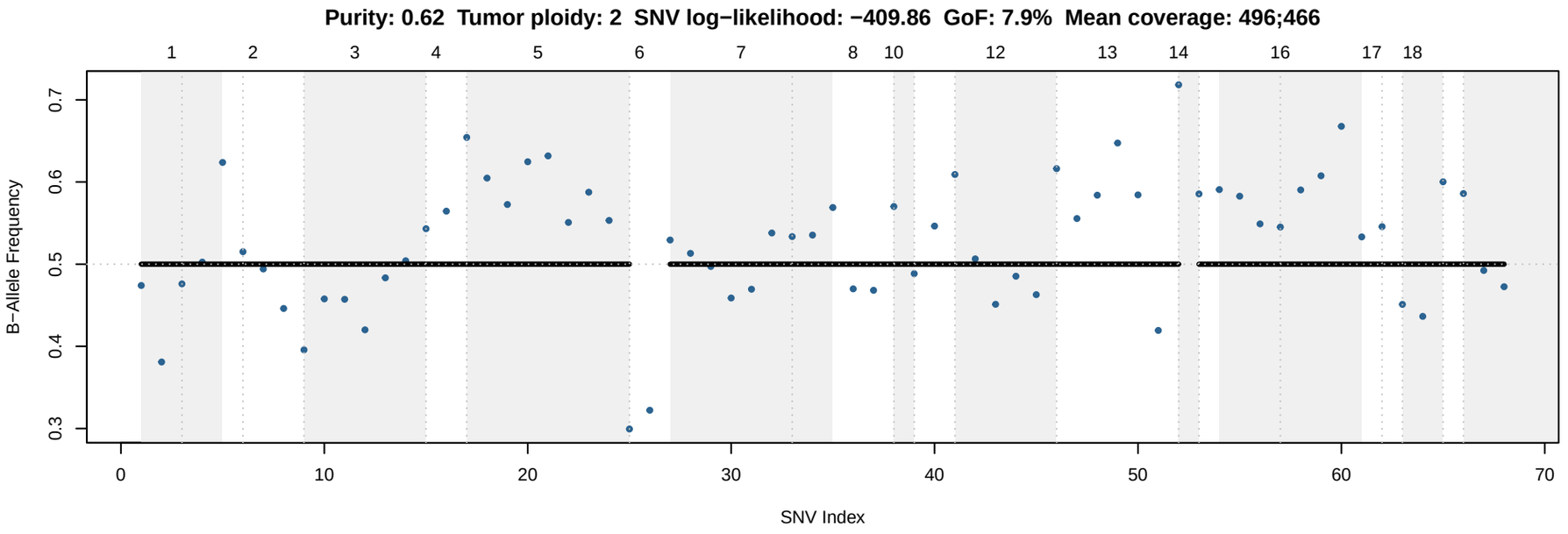

Allelic fraction (germline)
Copy Number log−ratio
3m2
3m1

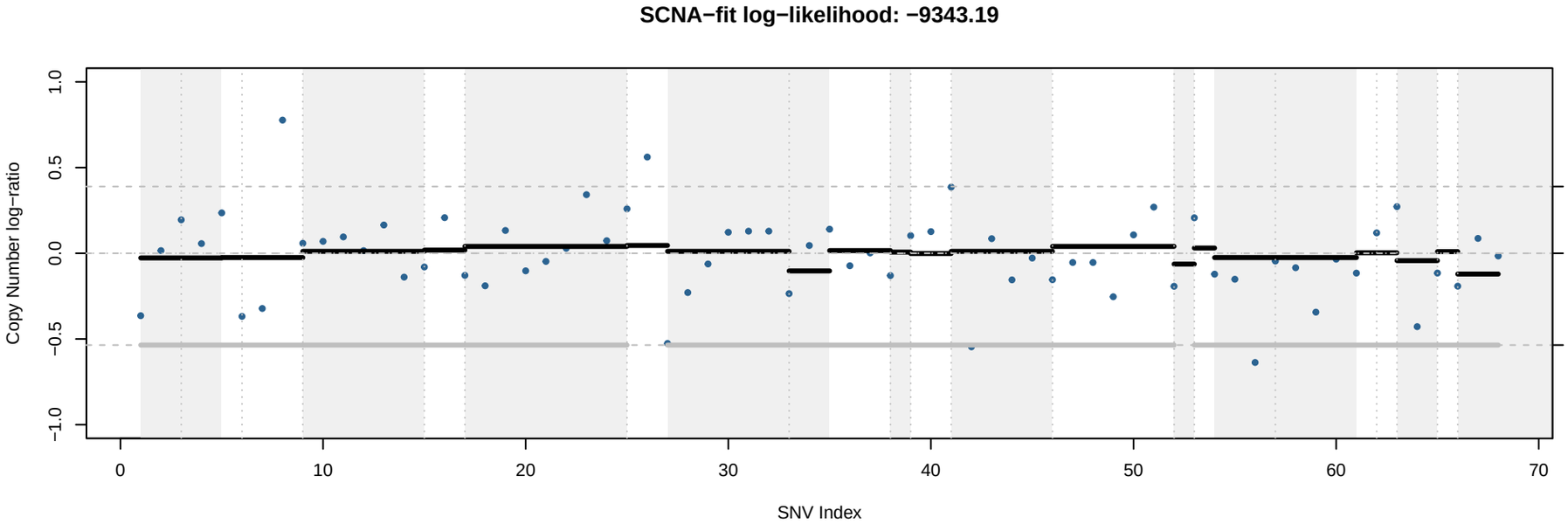

Coverage (log2)
Allelic fraction

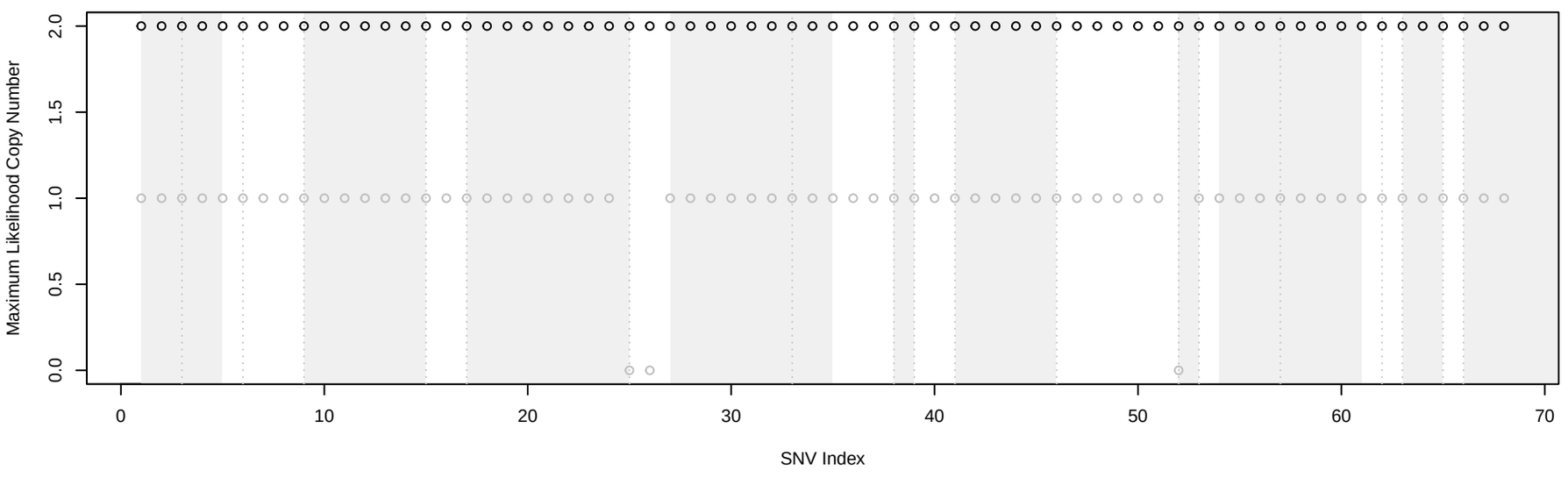

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

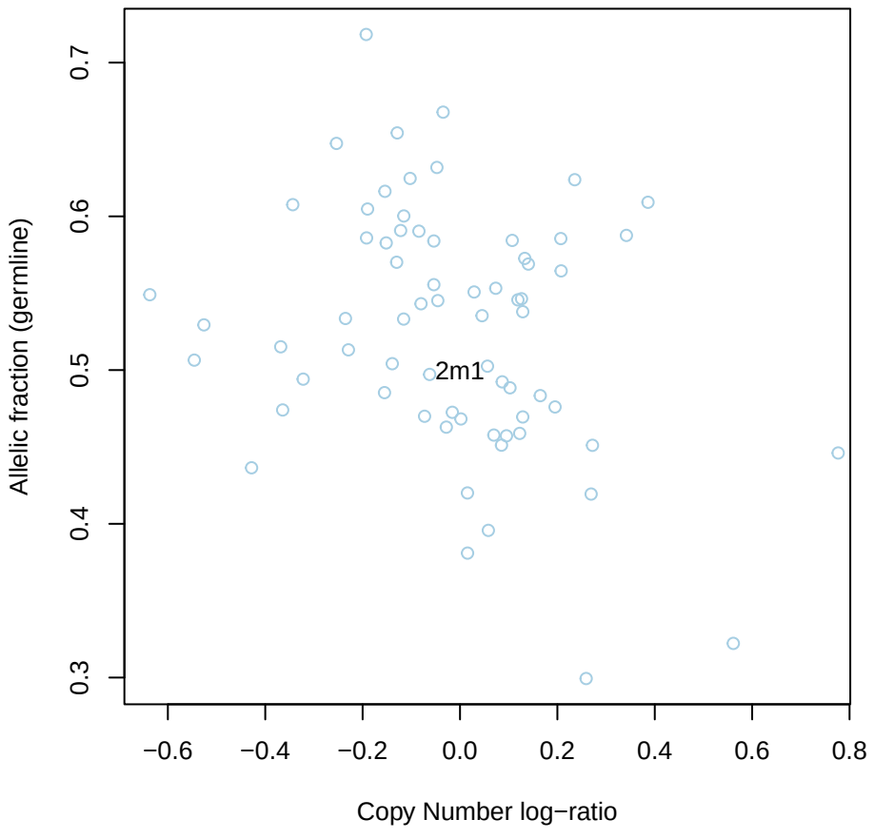

Frequency
Cellular fraction

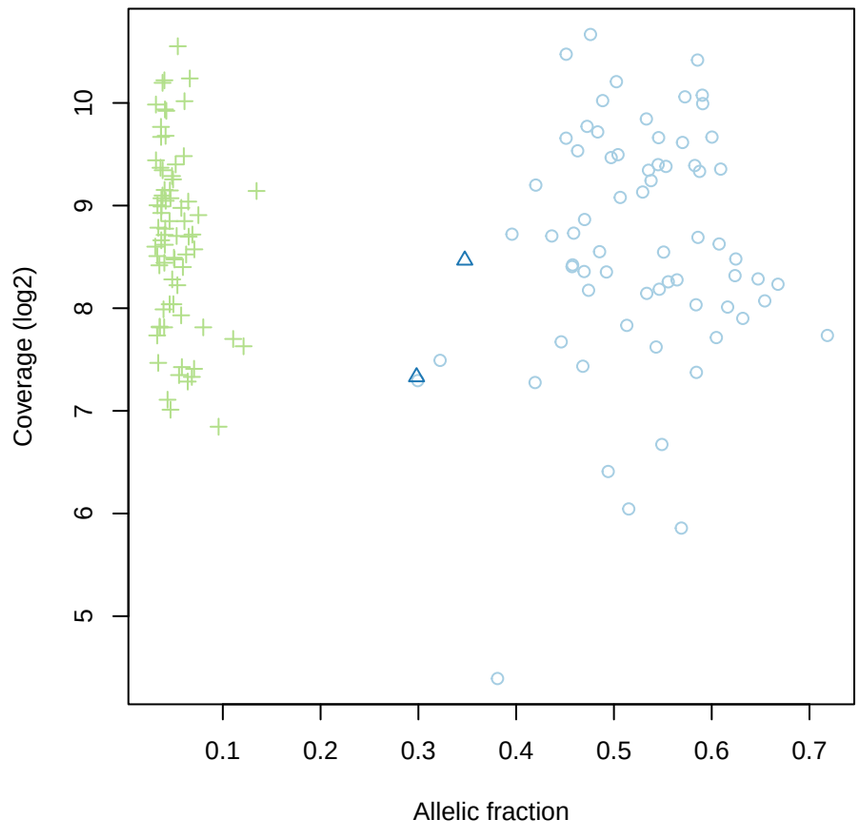

Purity: 0.62 Tumor ploidy: 2
0
1
2
3
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
log2 ratio

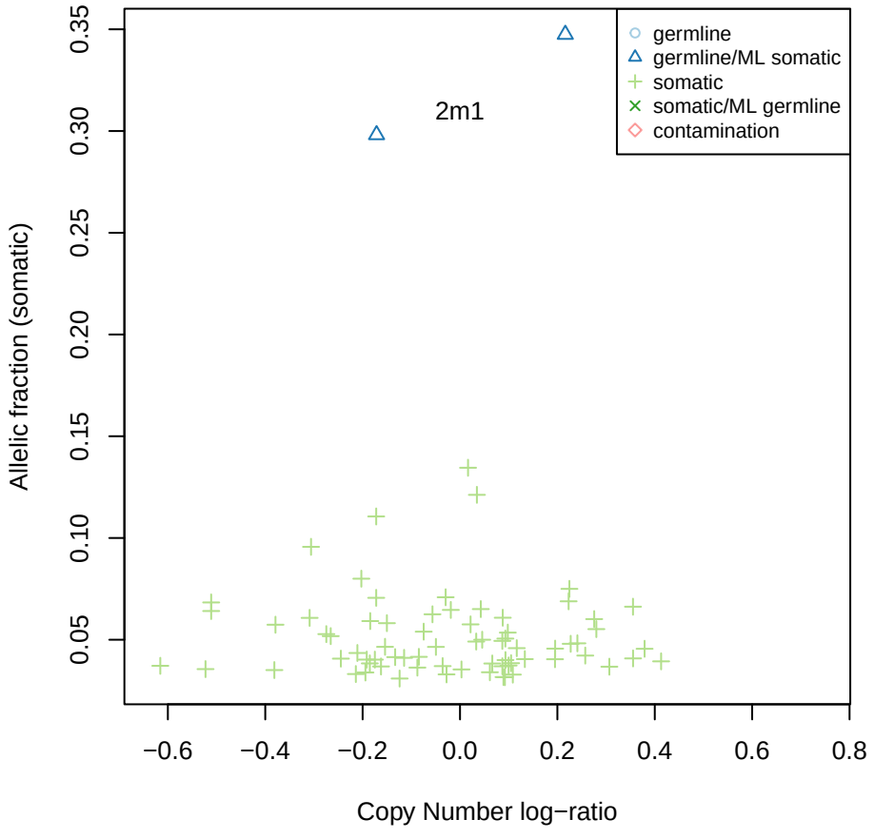

Purity: 0.62 Tumor ploidy: 2 SNV log−likelihood: −409.86 GoF: 7.9% Mean coverage: 496;466
1 2 3 4 5 6 7 8 10 12 13 14 16 17 18
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index

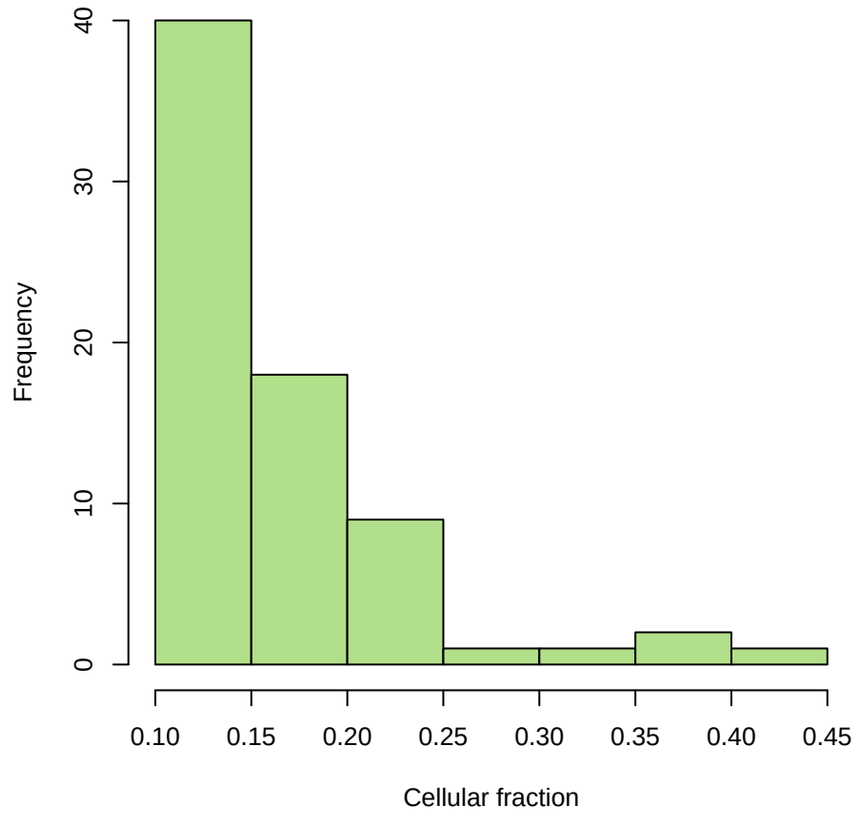

SCNA−fit log−likelihood: −9343.19
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3
0 10 20 30 40 50 60 70
SNV Index

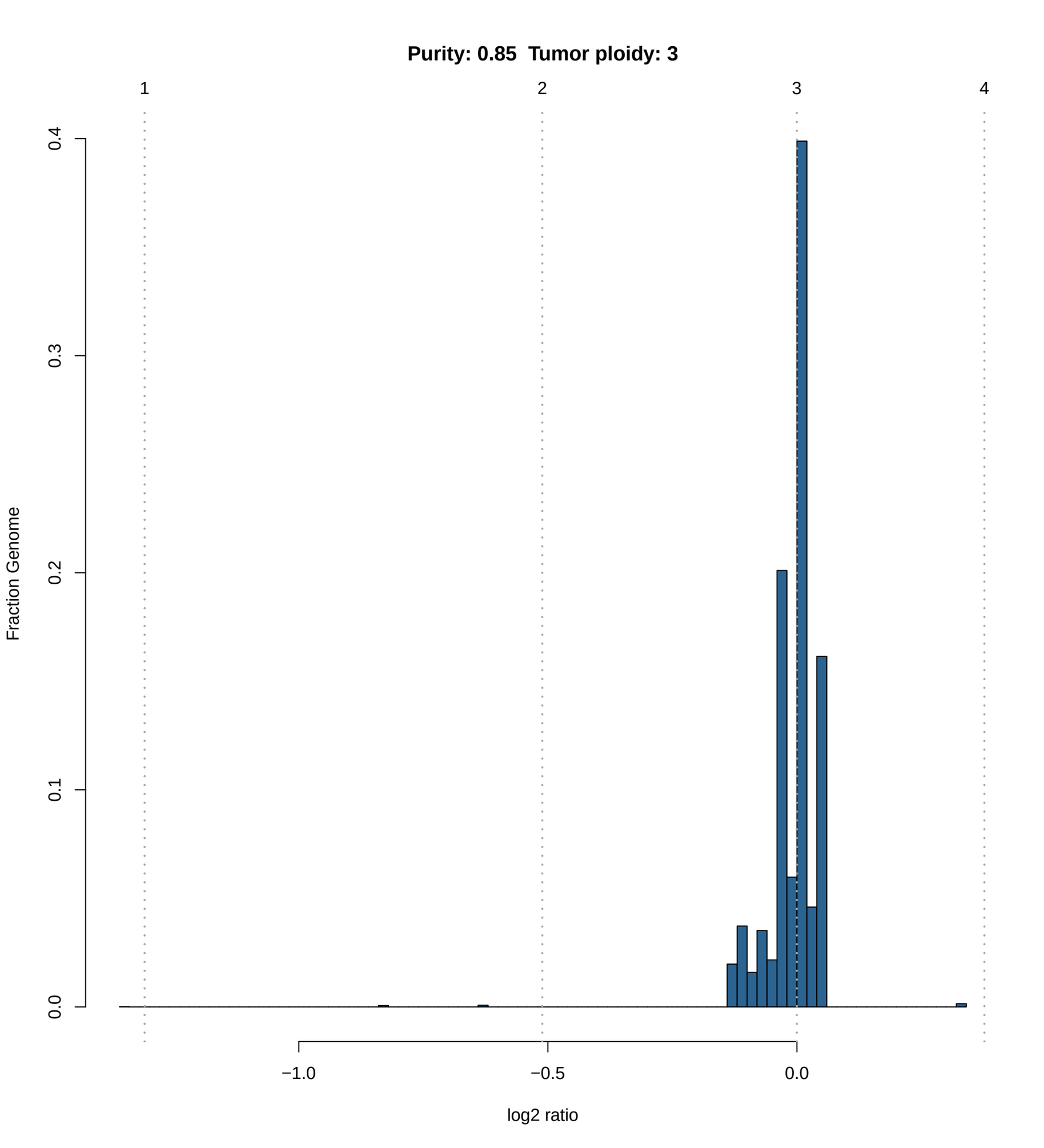

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 10 20 30 40 50 60 70
SNV Index

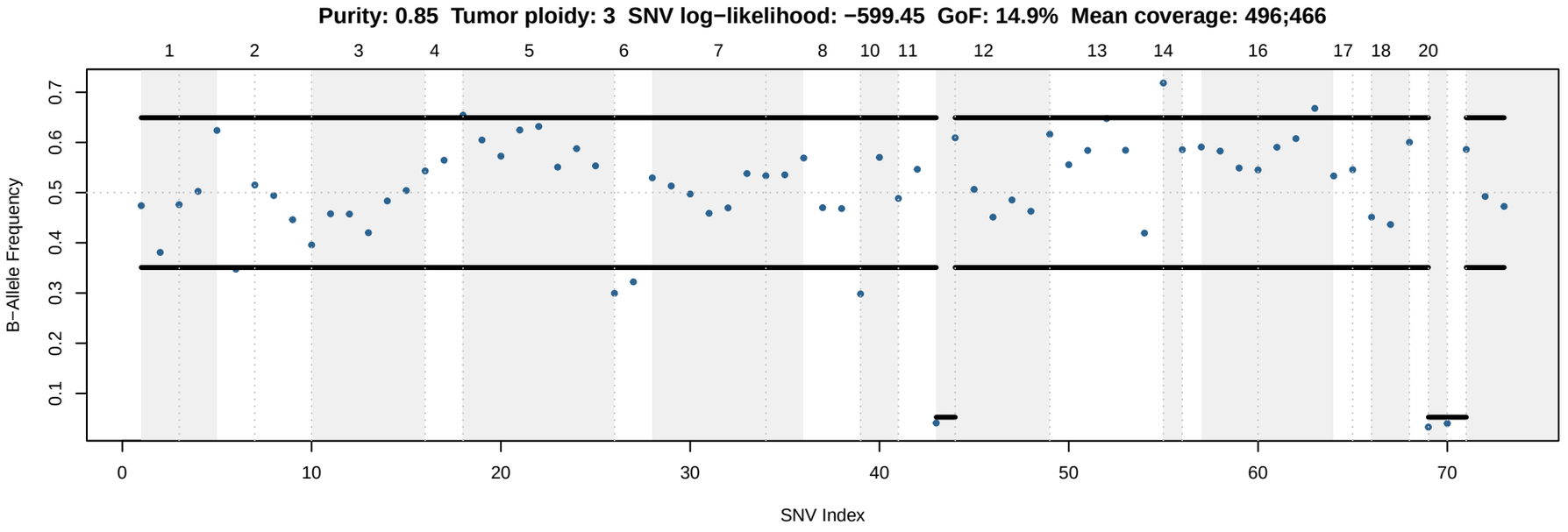

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
2m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

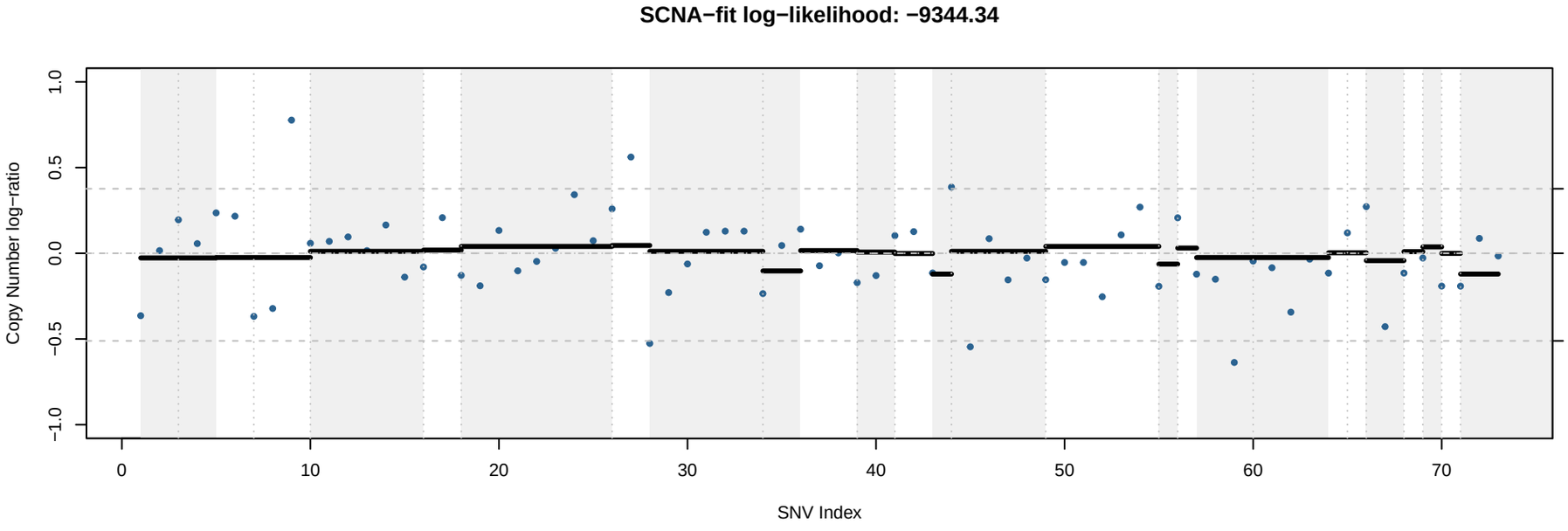

Coverage (log2)
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

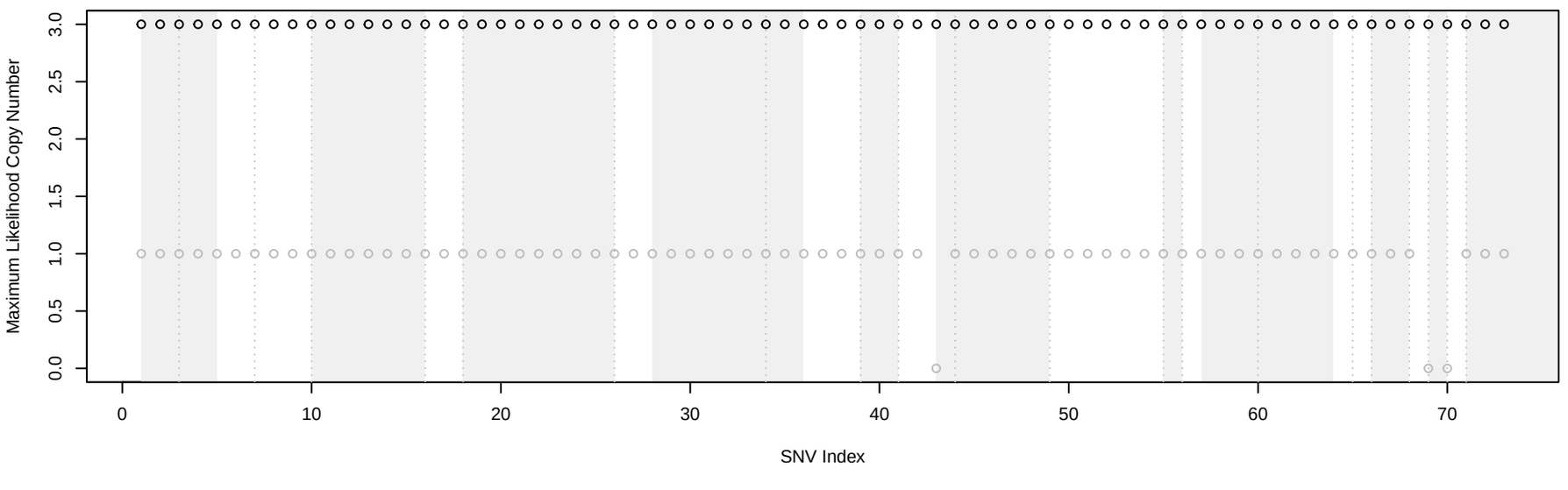

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0.30
0.35
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

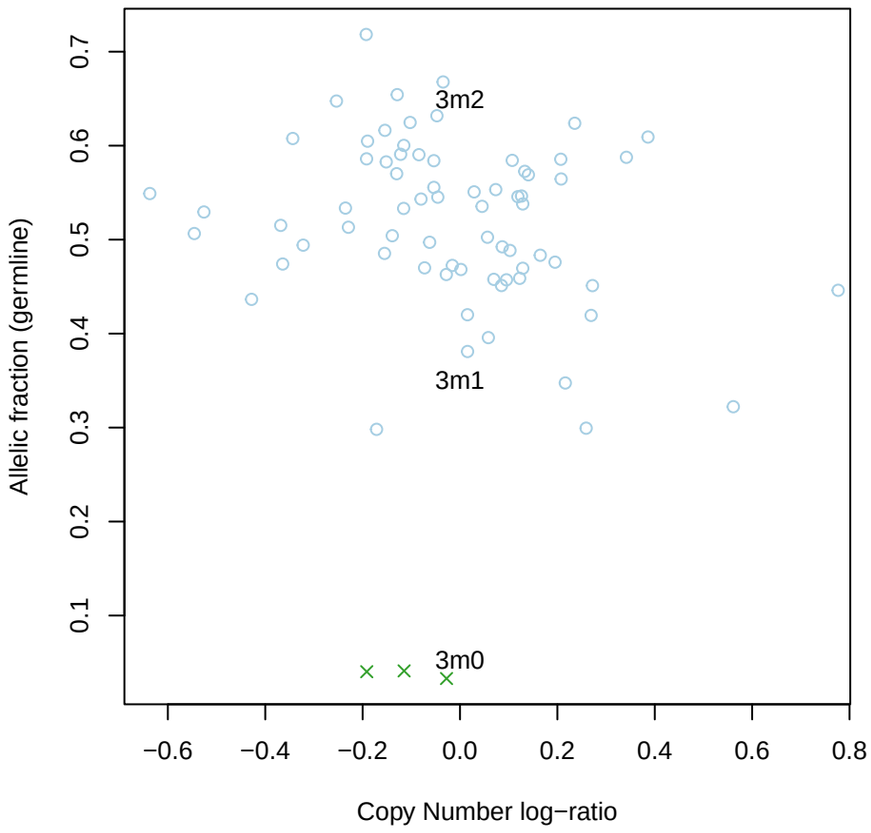

Frequency
0
10
20
30
40
0.10
0.15
0.20
0.25
0.30
0.35
0.40
0.45
Cellular fraction

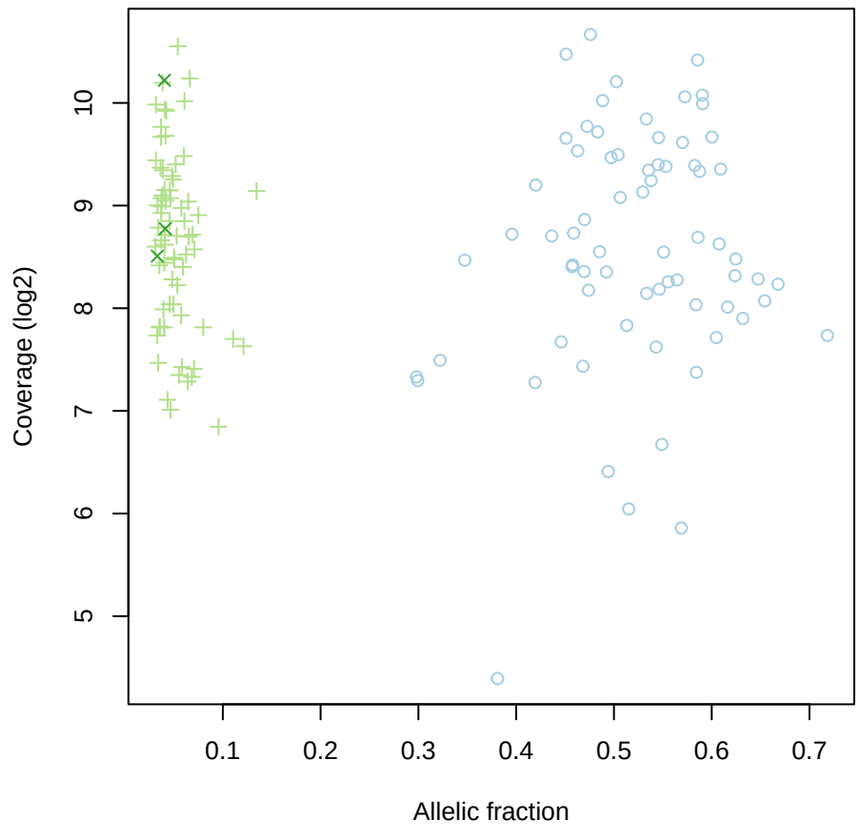

Purity: 0.85 Tumor ploidy: 3
1
2
3
4
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−1.0
−0.5
0.0
log2 ratio

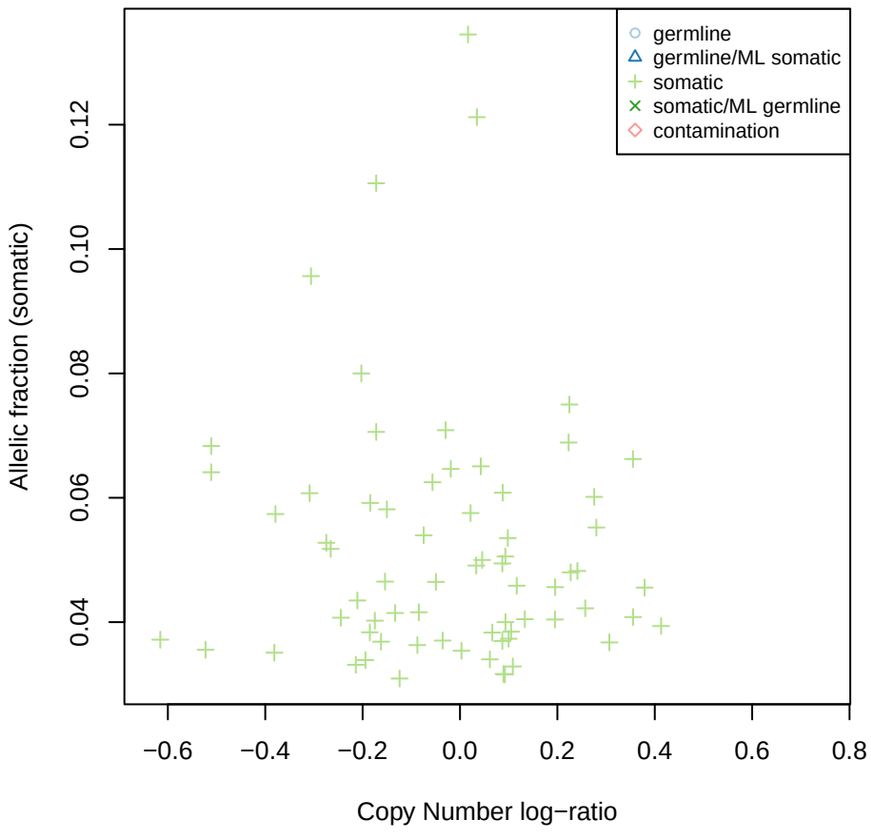

Purity: 0.85 Tumor ploidy: 3 SNV log−likelihood: −599.45 GoF: 14.9% Mean coverage: 496;466
1 2 3 4 5 6 7 8 10 11 12 13 14 16 17 18 20
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index

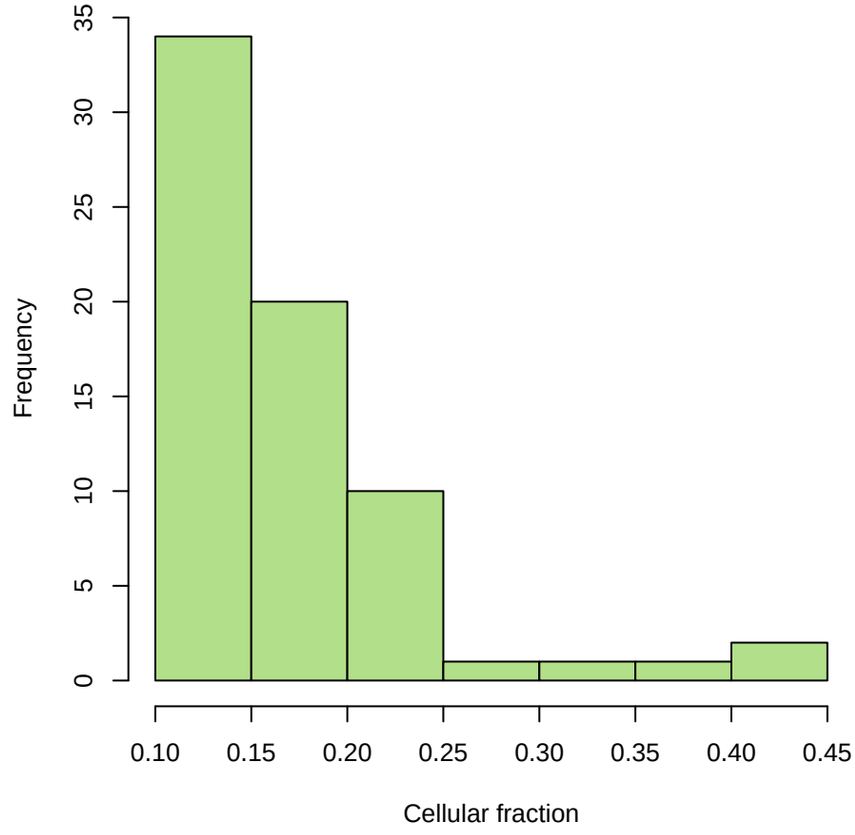

SCNA−fit log−likelihood: −9344.34
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4
0 10 20 30 40 50 60 70
SNV Index


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 70
SNV Index


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


Coverage (log2)
Allelic fraction


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


Frequency
Cellular fraction