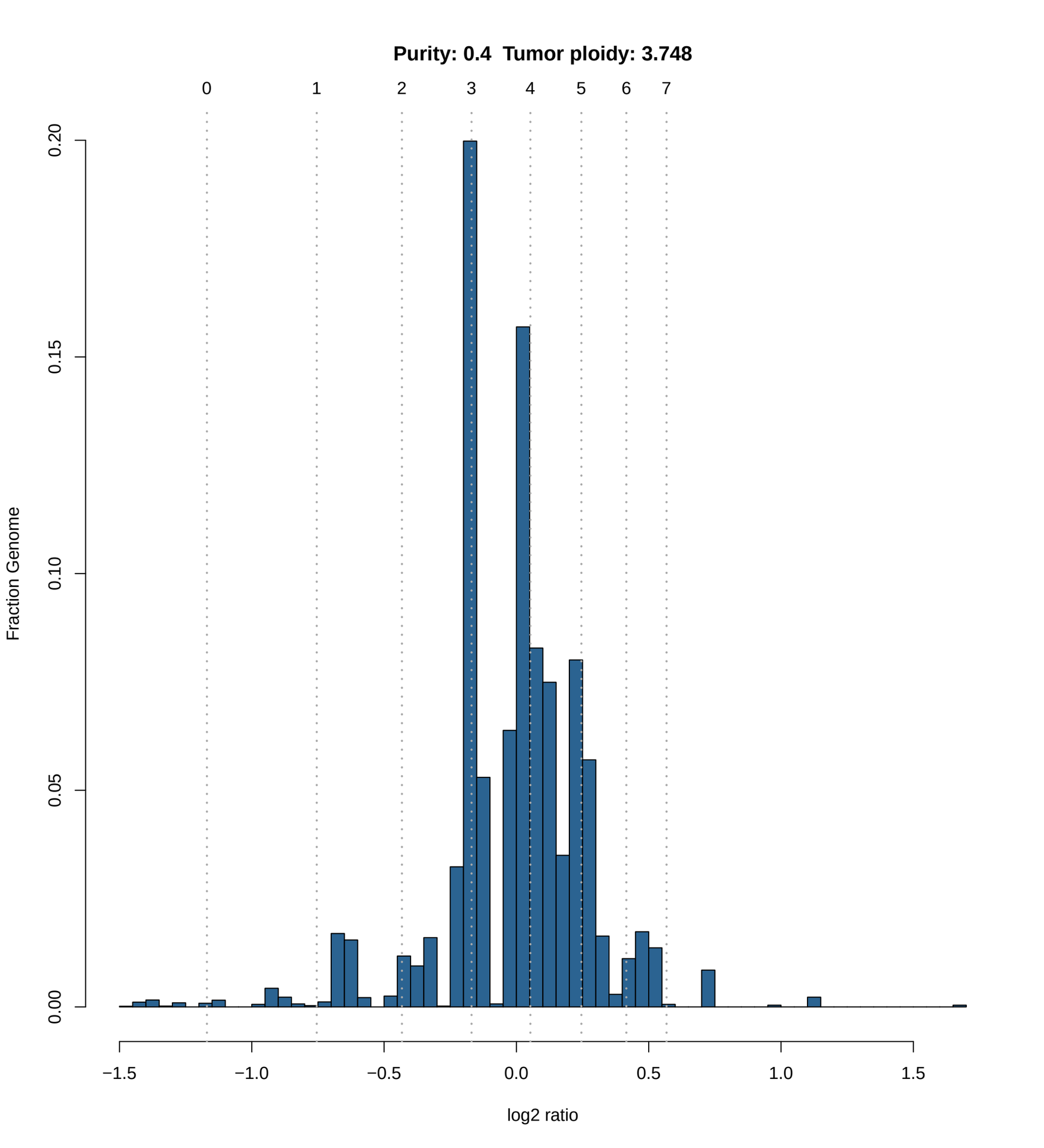
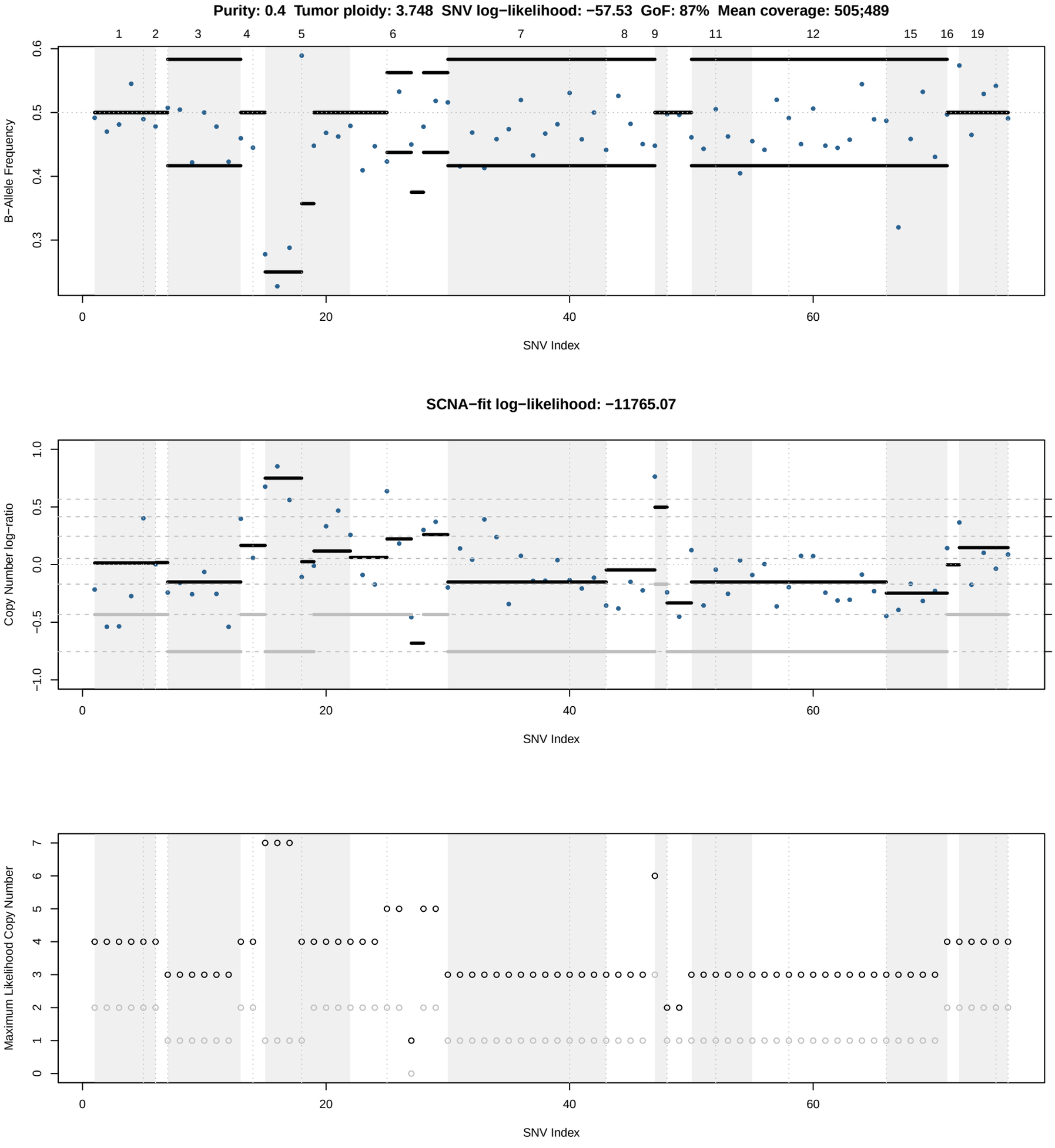
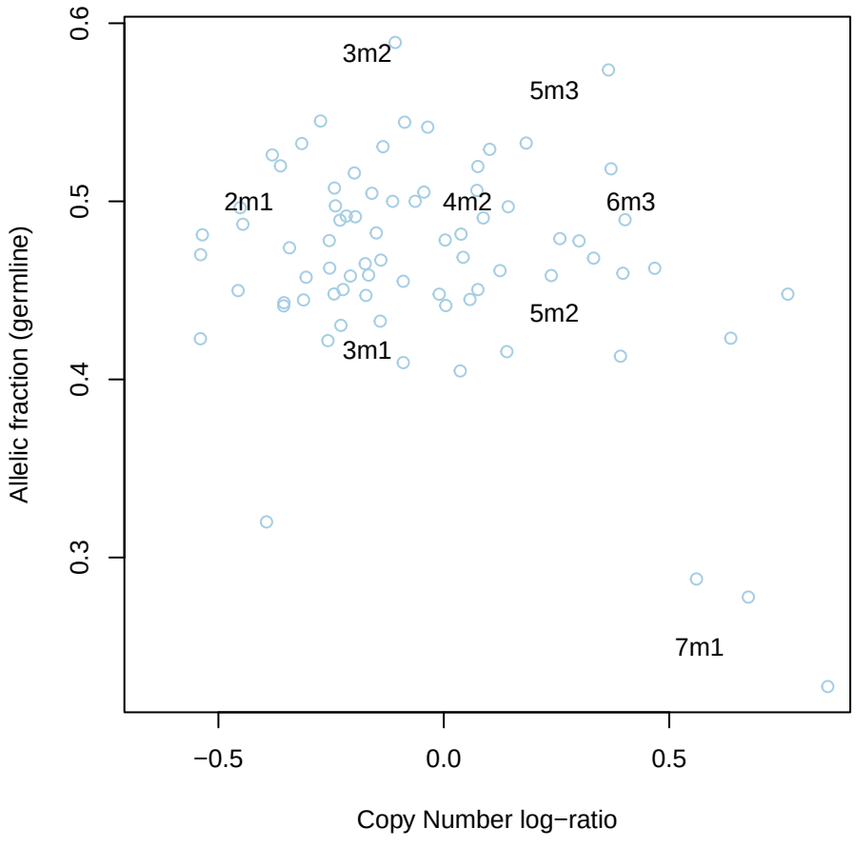
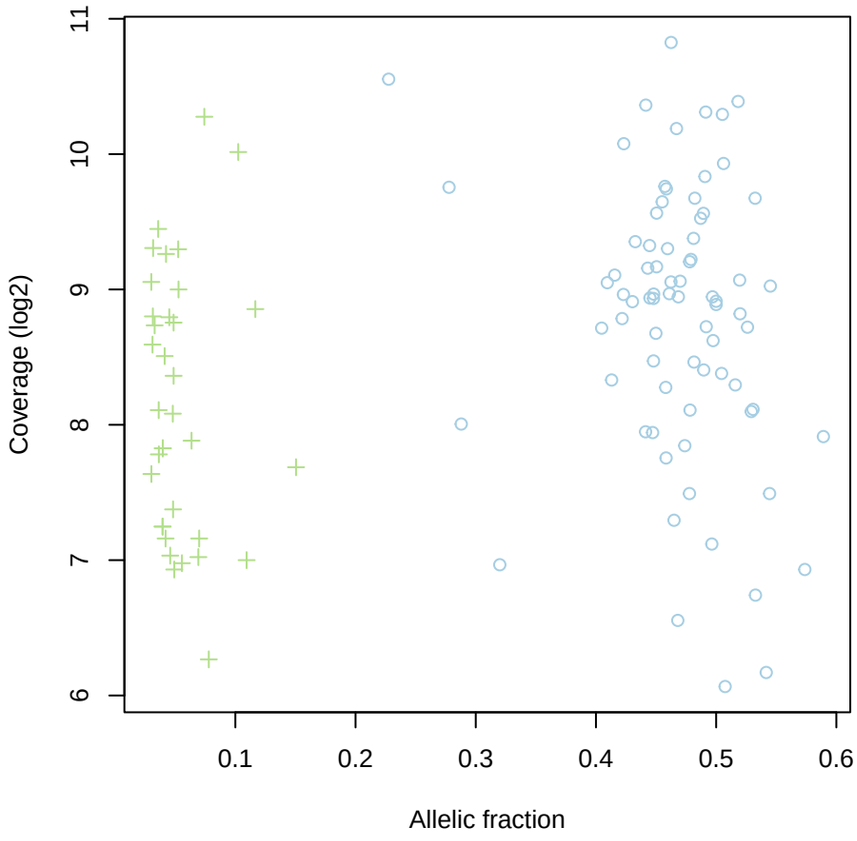
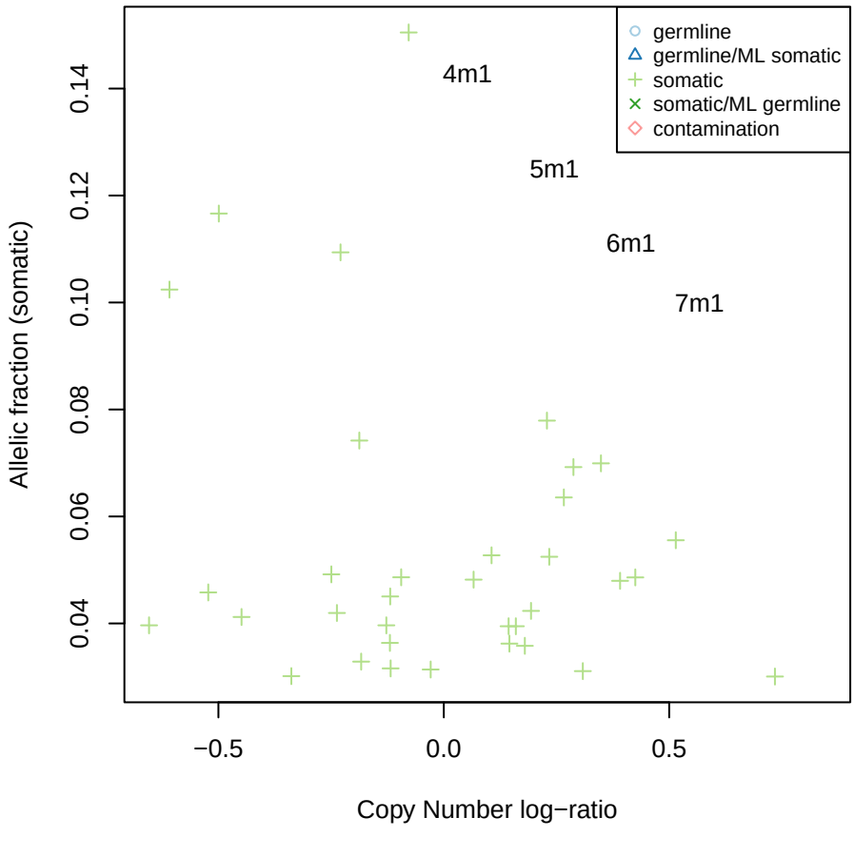
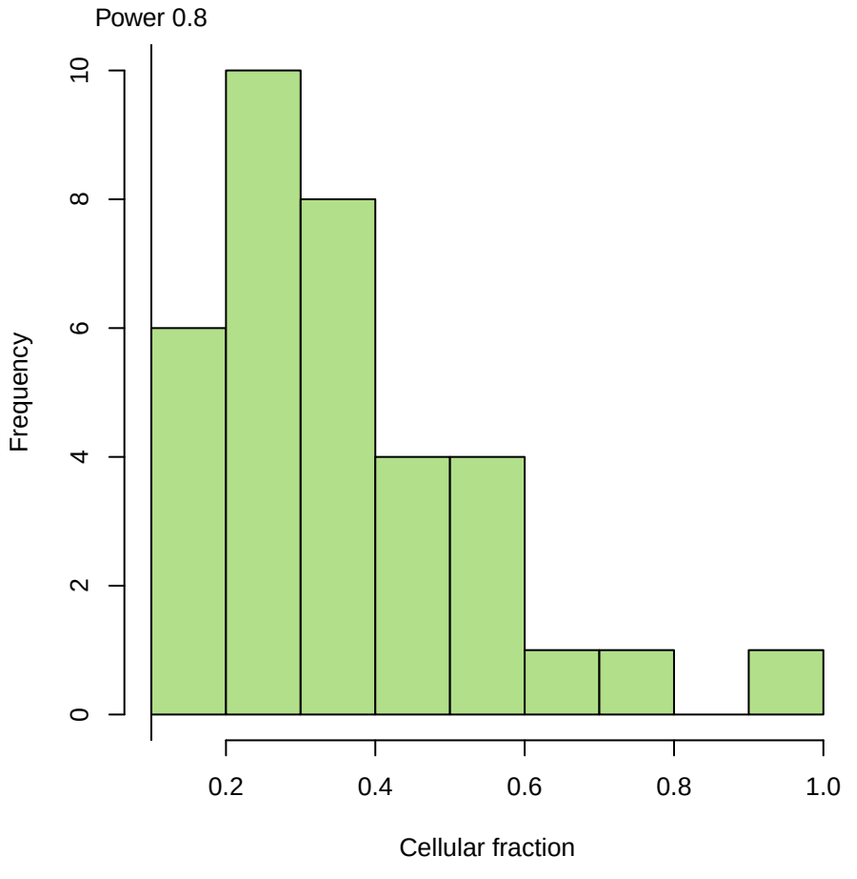

Purity: 0.4 Tumor ploidy: 3.748
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

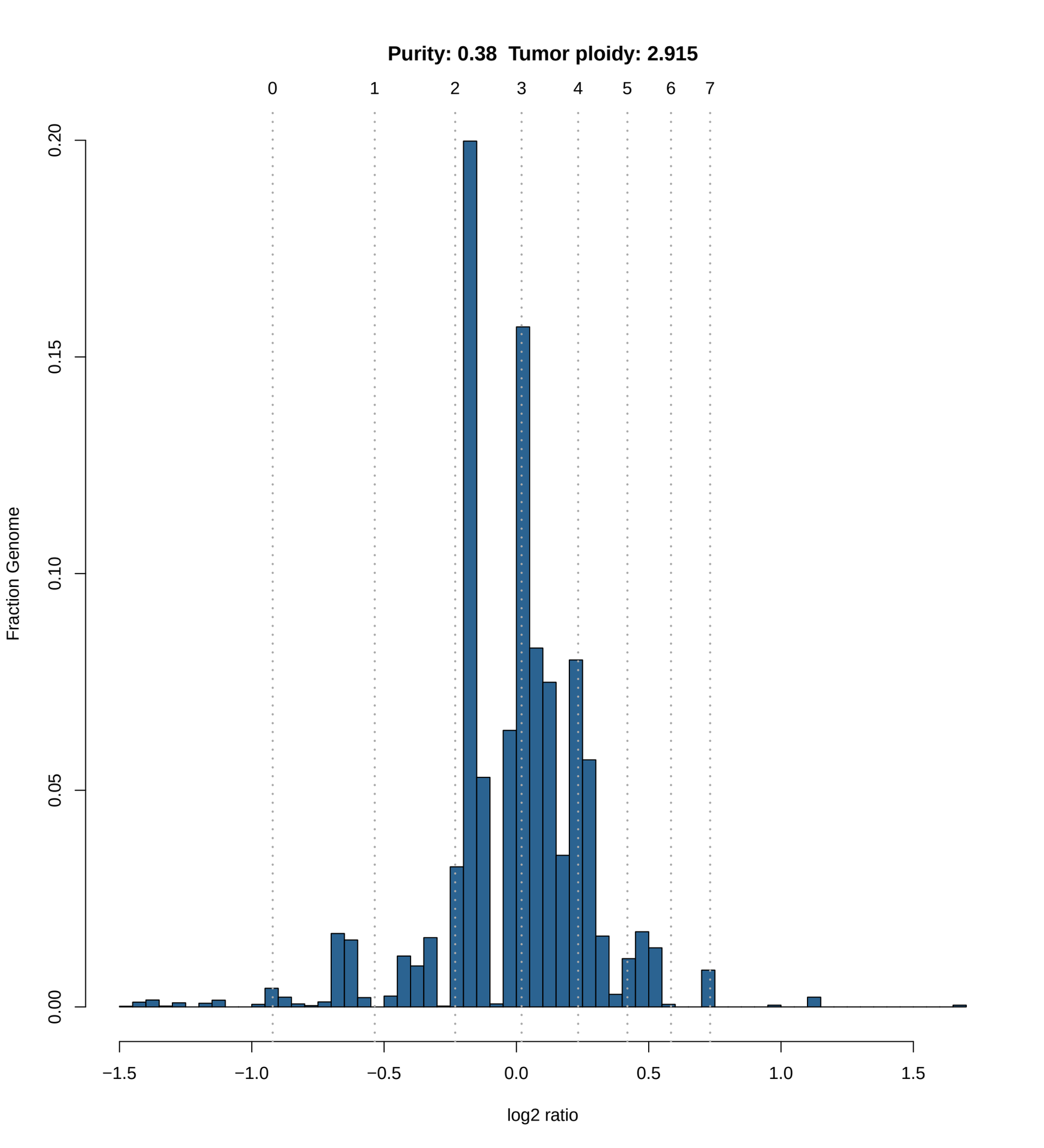

Purity: 0.4 Tumor ploidy: 3.748 SNV log−likelihood: −57.53 GoF: 87% Mean coverage: 505;489
1 2 3 4 5 6 7 8 9 11 12 15 16 19
B−Allele Frequency
0.3 0.4 0.5 0.6
0 20 40 60
SNV Index
SCNA−fit log−likelihood: −11765.07
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6 7
0 20 40 60
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60
SNV Index

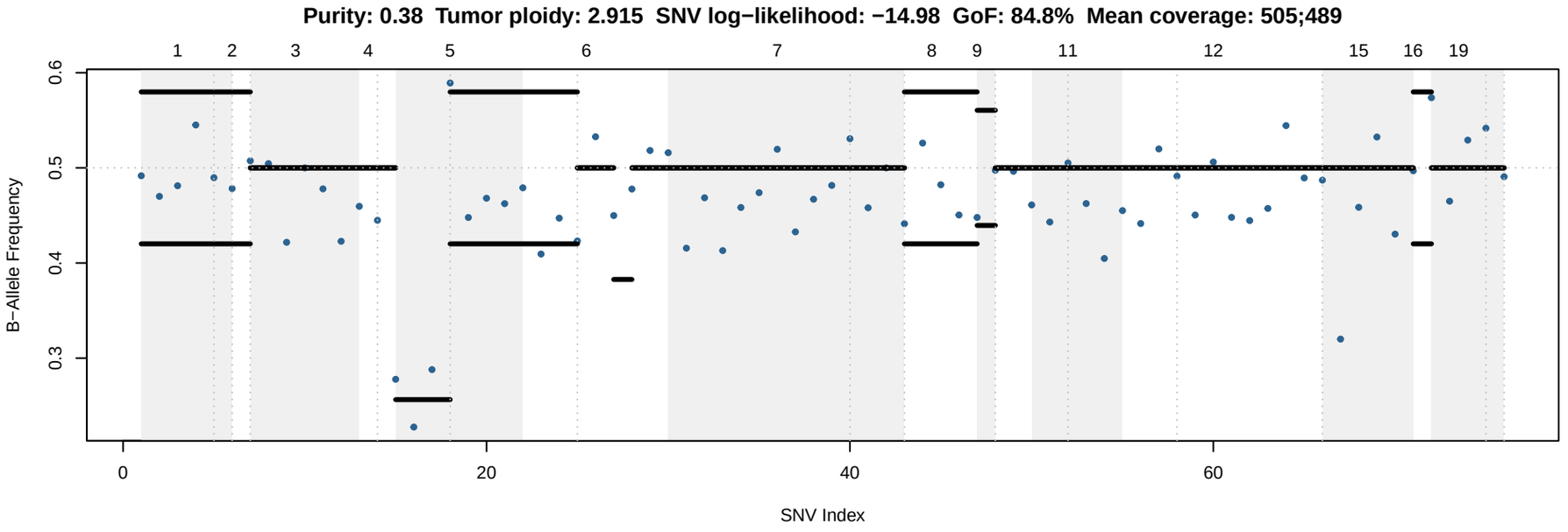

3m2
5m3
2m1
4m2
6m3
5m2
3m1
7m1
Allelic fraction (germline)
Copy Number log−ratio

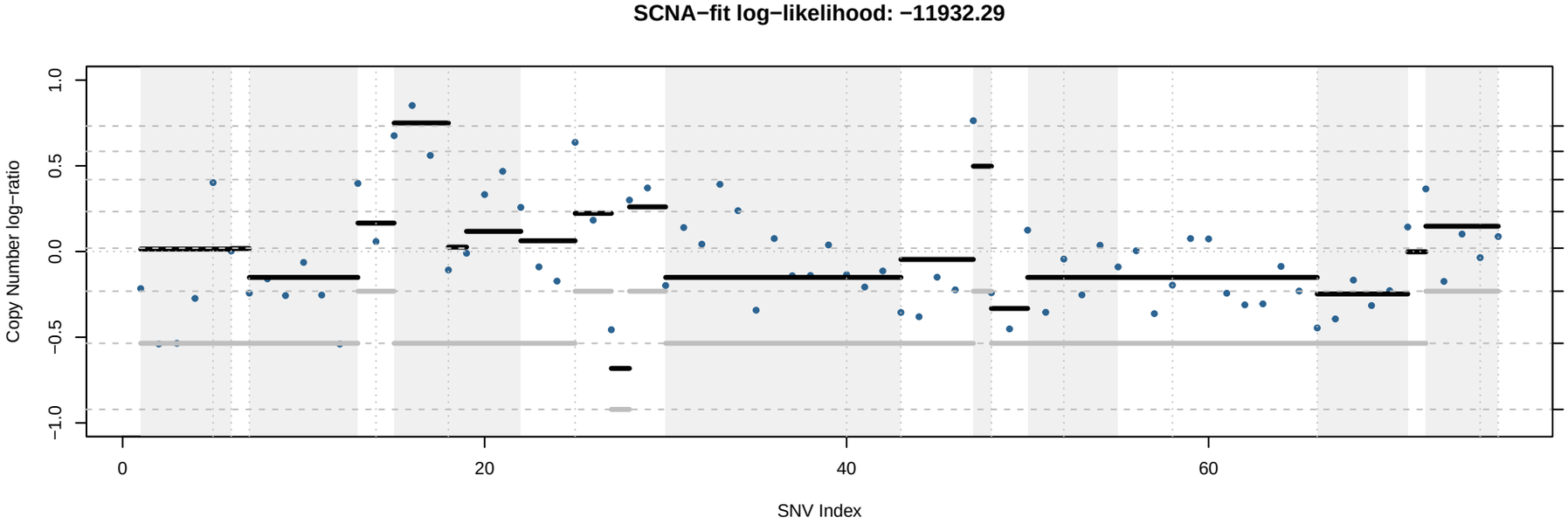

Coverage (log2)
Allelic fraction

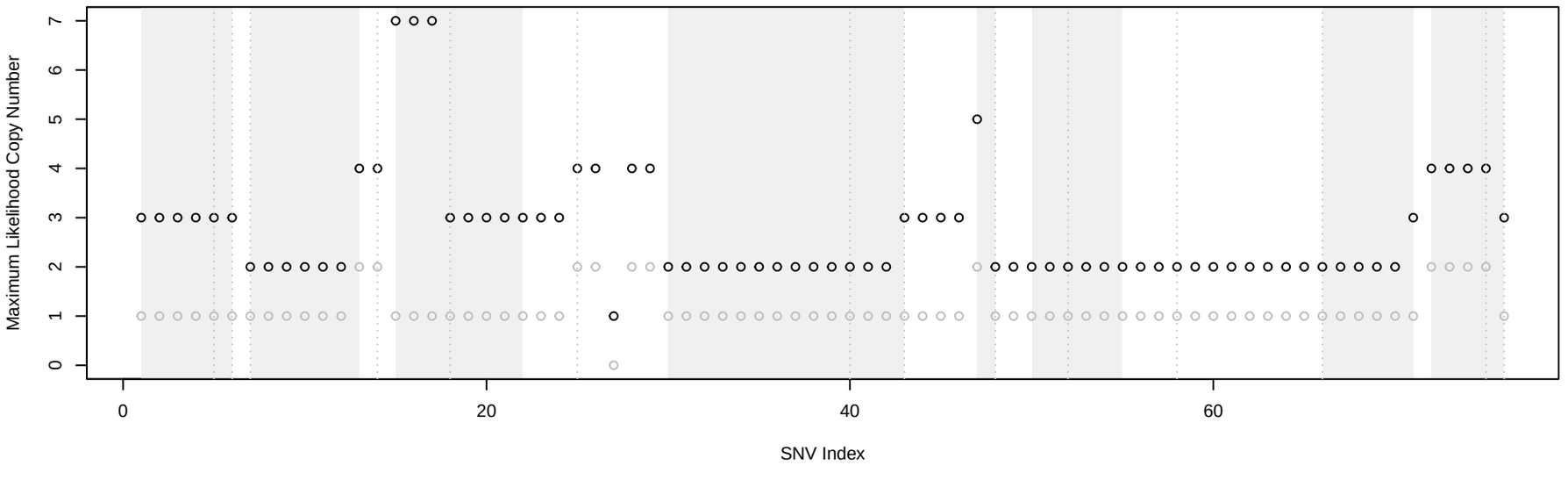

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

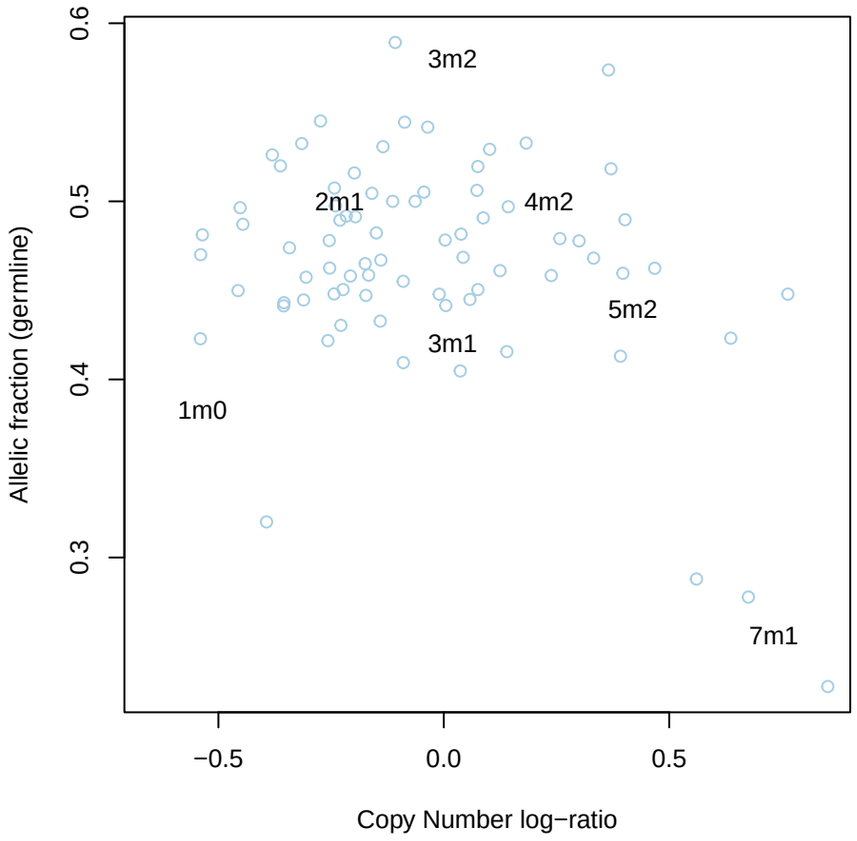

Power 0.8
Frequency
Cellular fraction

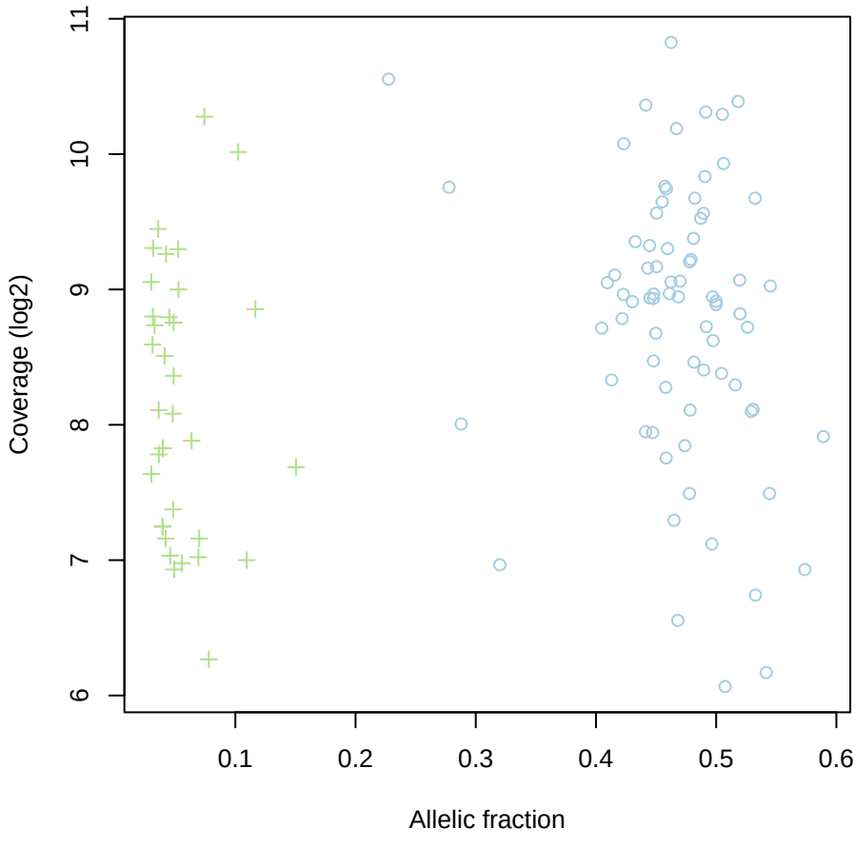

Purity: 0.38 Tumor ploidy: 2.915
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

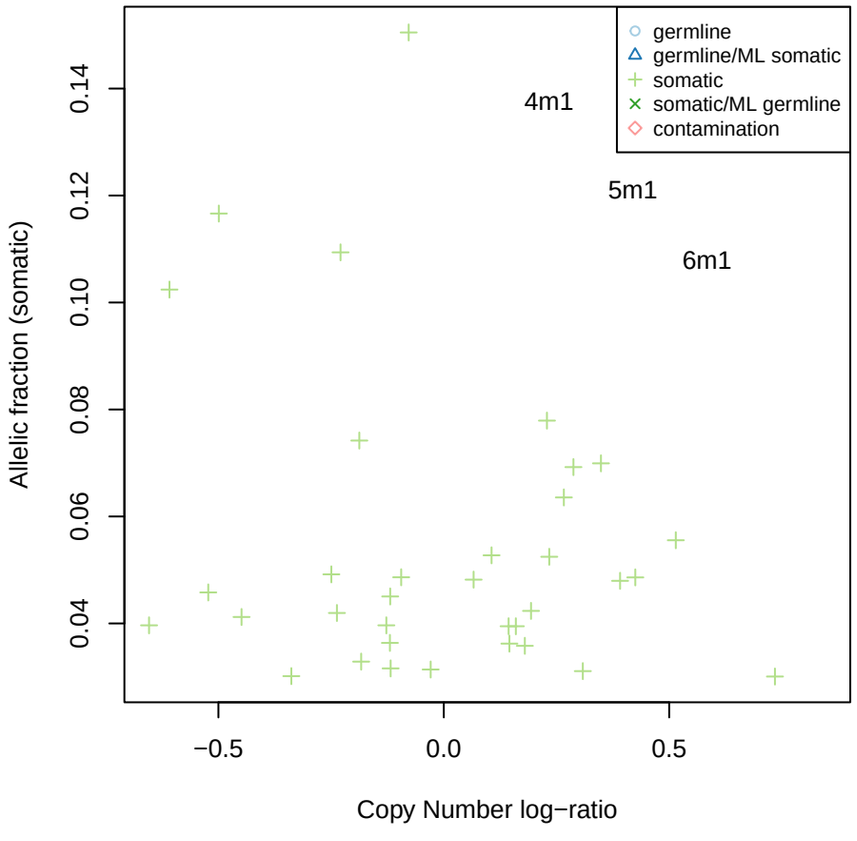

Purity: 0.38 Tumor ploidy: 2.915 SNV log−likelihood: −14.98 GoF: 84.8% Mean coverage: 505;489
1 2 3 4 5 6 7 8 9 11 12 15 16 19
B−Allele Frequency
0.3 0.4 0.5 0.6
0 20 40 60
SNV Index

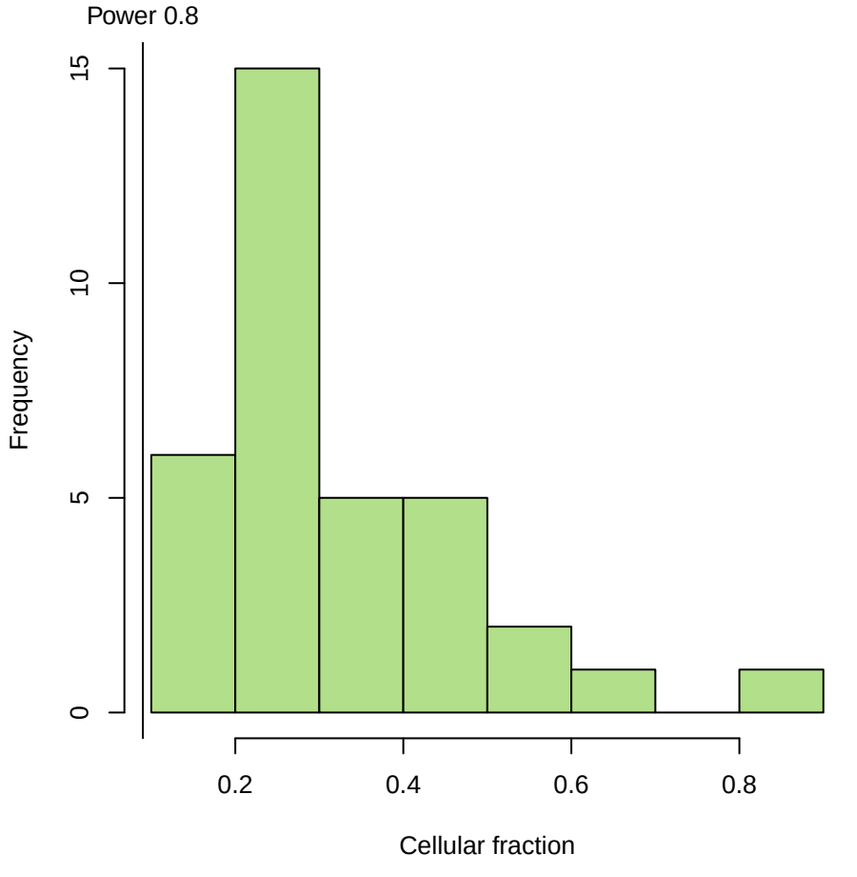

SCNA−fit log−likelihood: −11932.29
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 6 7
0 20 40 60
SNV Index

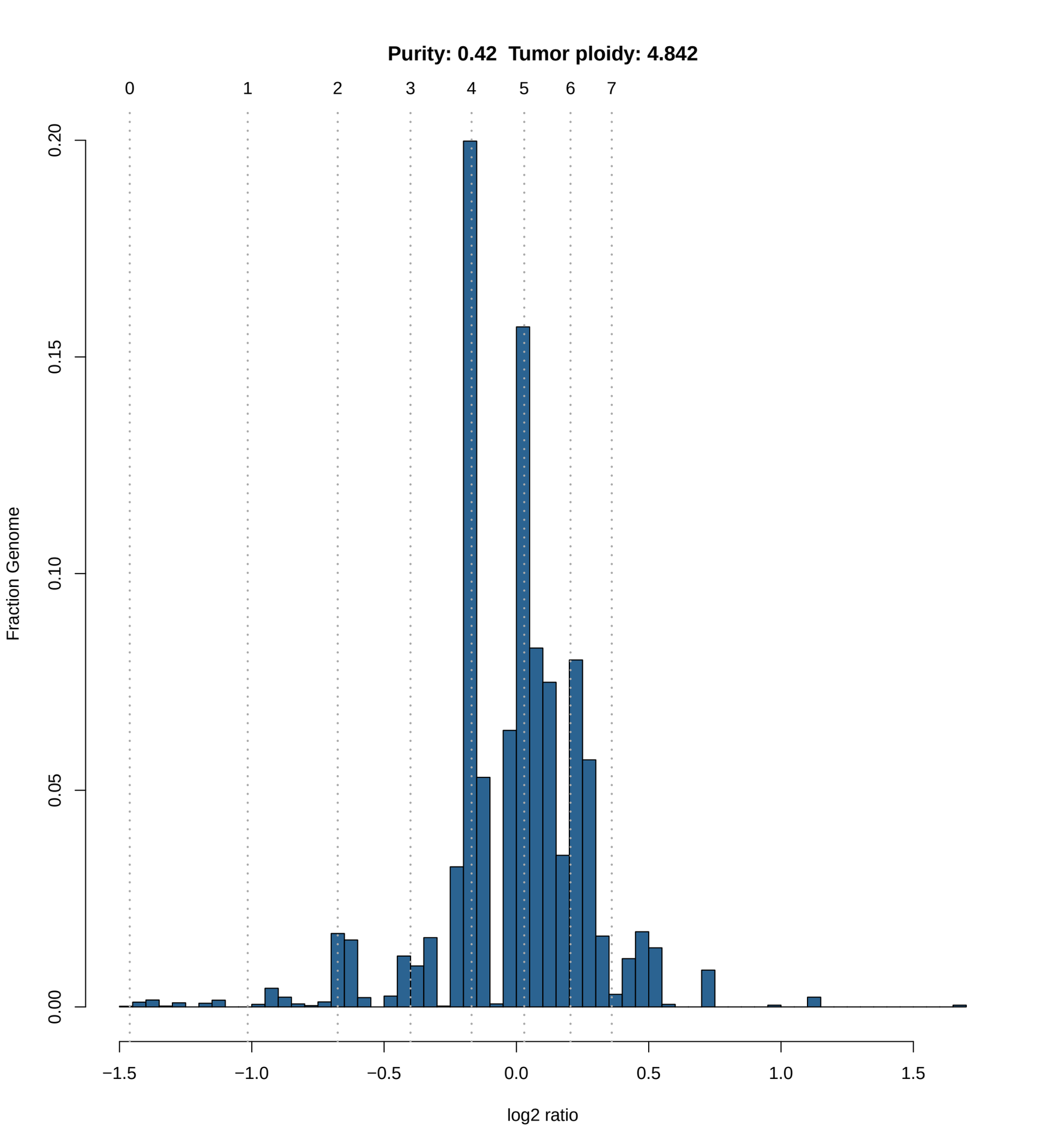

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60
SNV Index

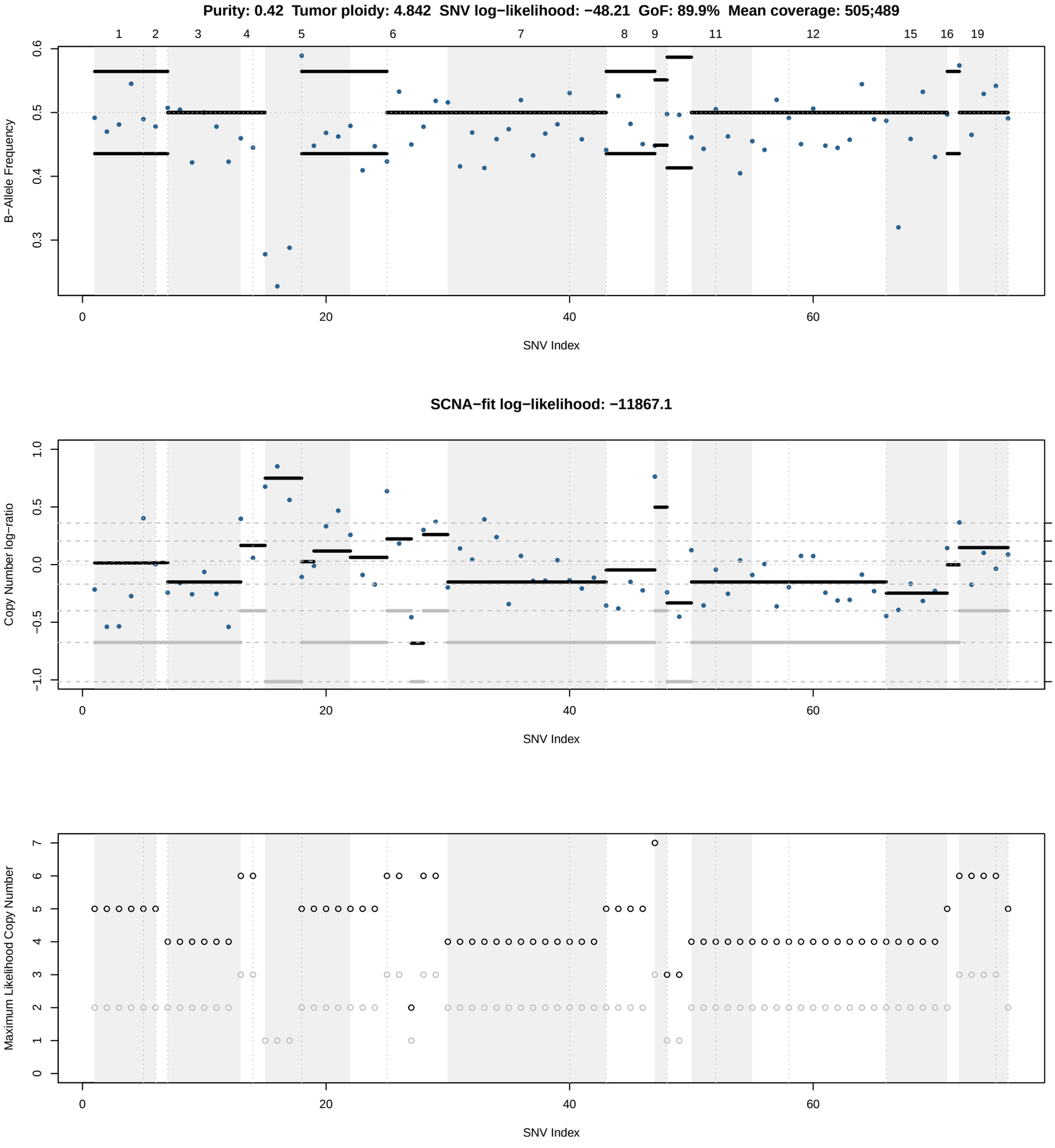

Allelic fraction (germline)
Copy Number log−ratio
3m2
2m1
4m2
5m2
3m1
1m0
7m1

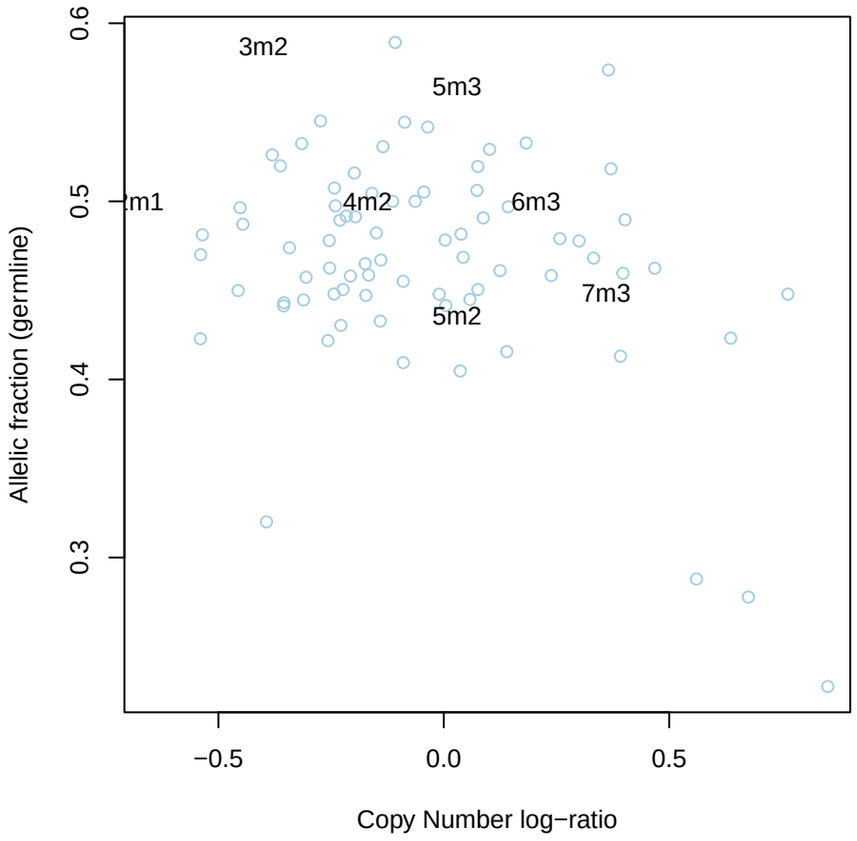

Coverage (log2)
Allelic fraction

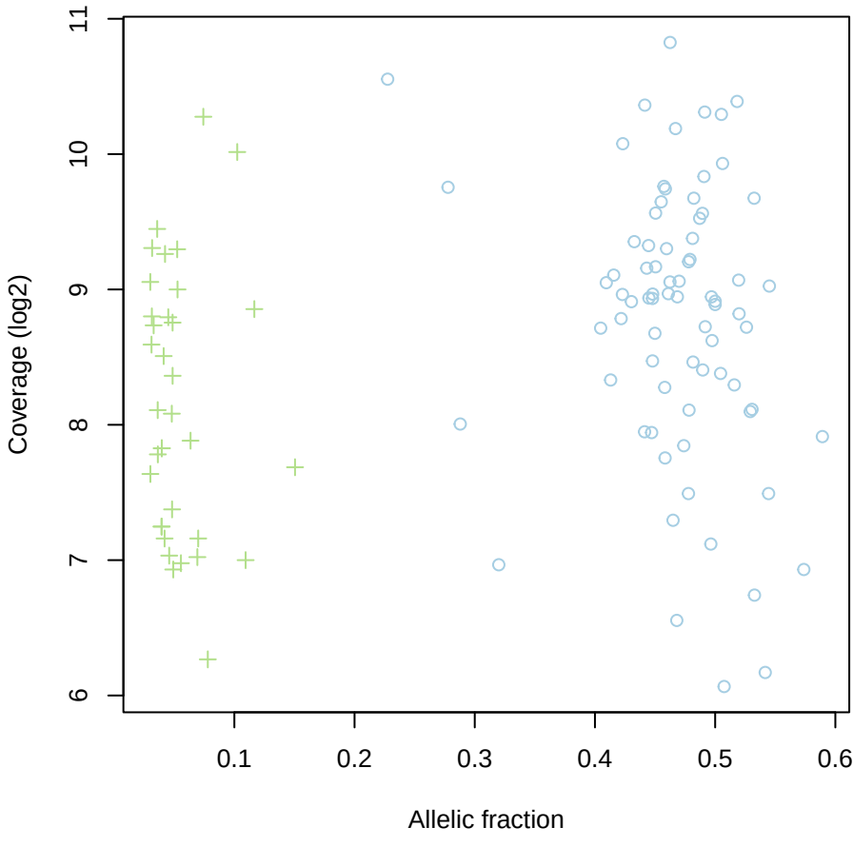

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1

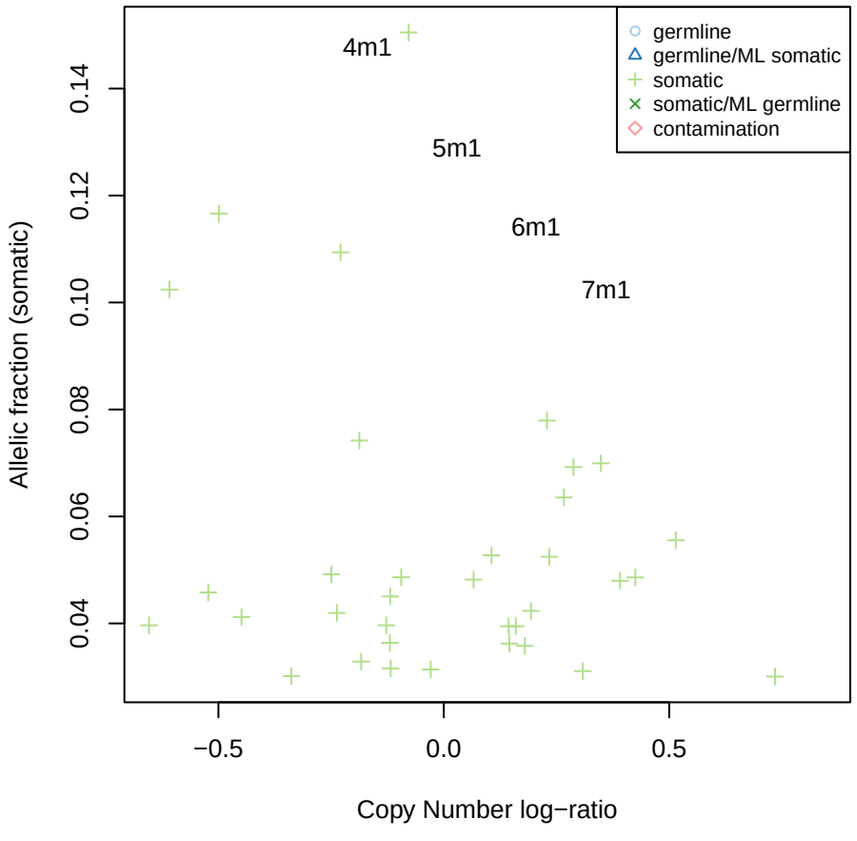

Power 0.8
Frequency
Cellular fraction

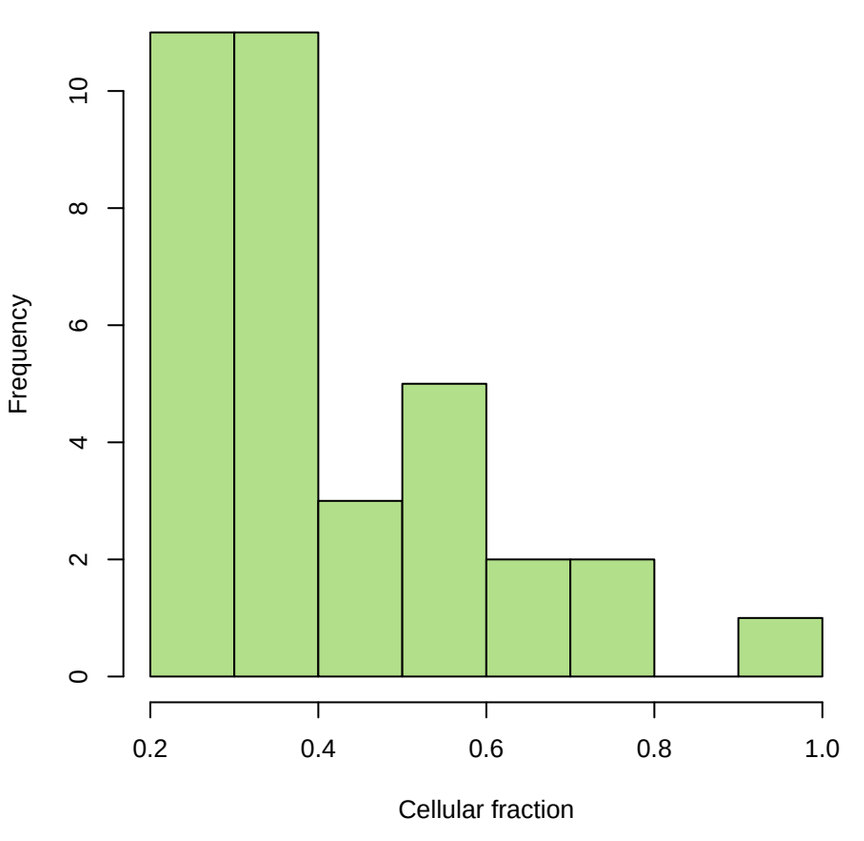

Purity: 0.42 Tumor ploidy: 4.842
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

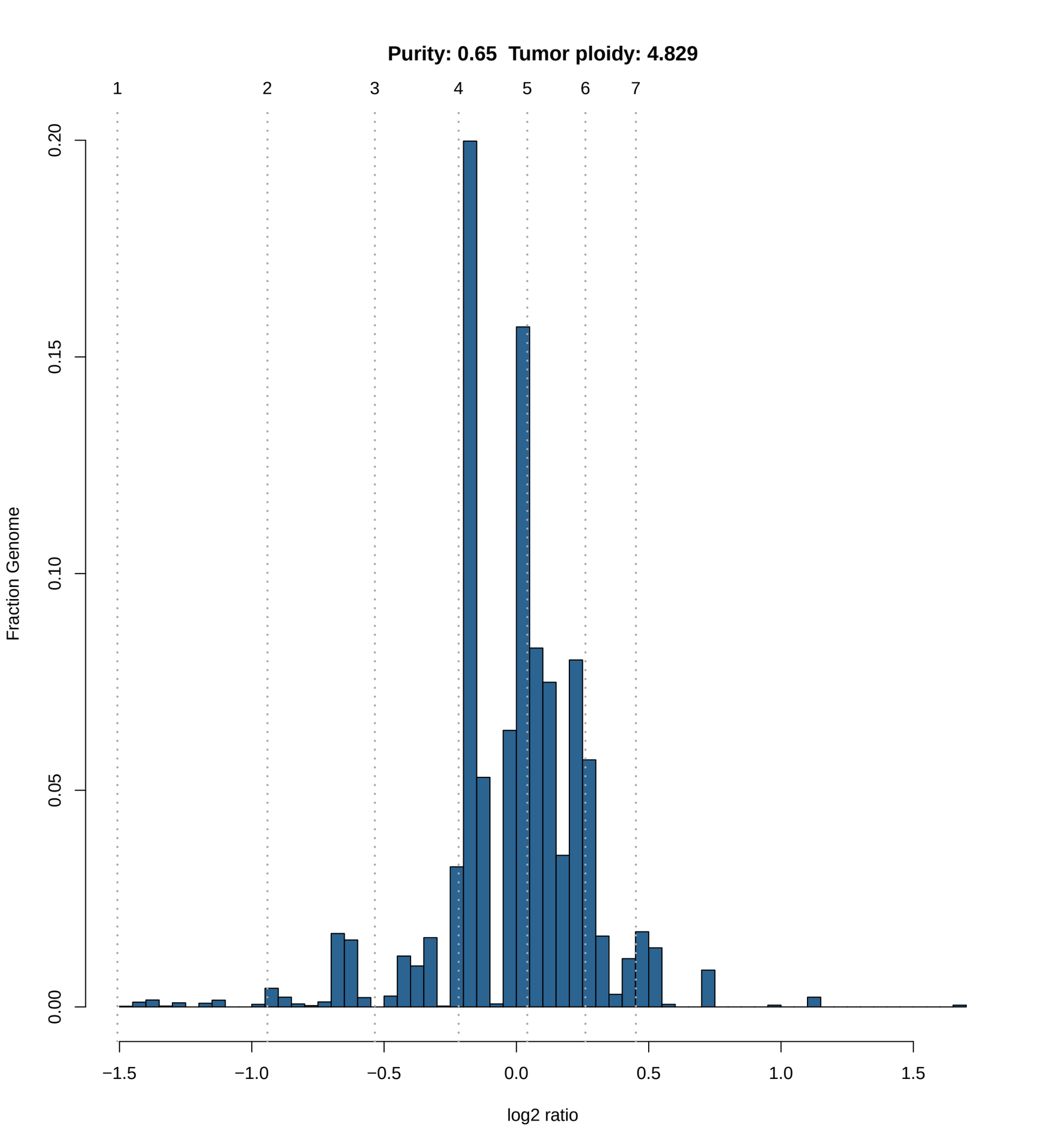

Purity: 0.42 Tumor ploidy: 4.842 SNV log−likelihood: −48.21 GoF: 89.9% Mean coverage: 505;489
1 2 3 4 5 6 7 8 9 11 12 15 16 19
B−Allele Frequency
0.3 0.4 0.5 0.6
0 20 40 60
SNV Index
SCNA−fit log−likelihood: −11867.1
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6 7
0 20 40 60
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60
SNV Index

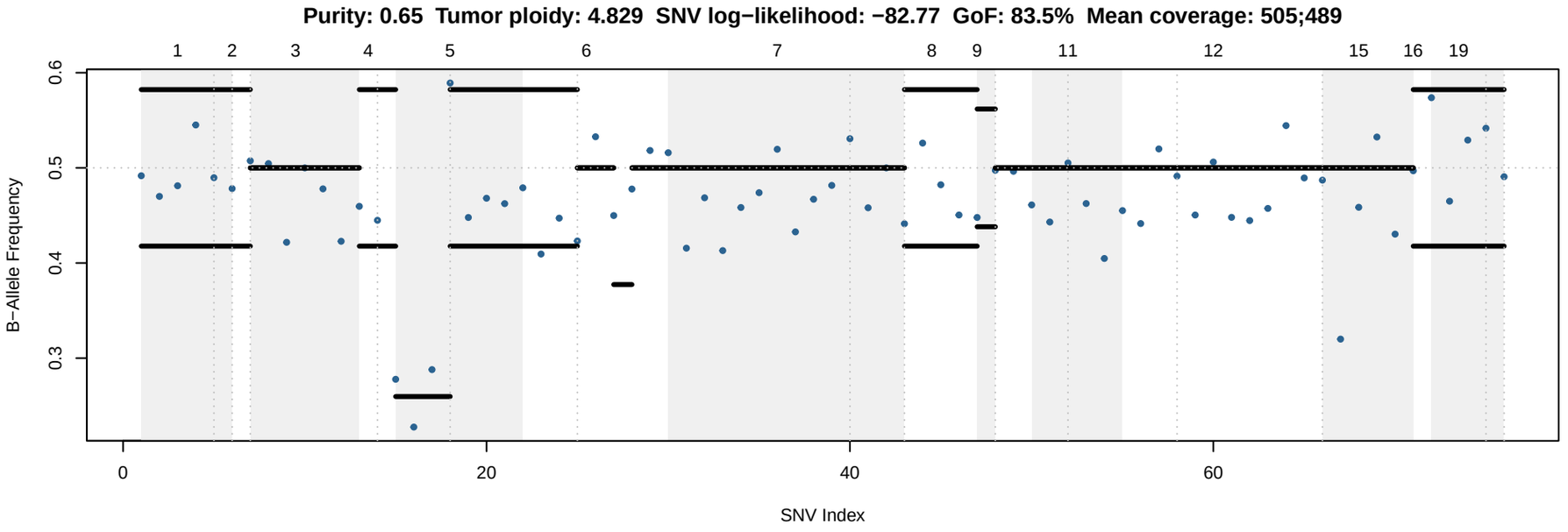

3m2
5m3
4m2
6m3
7m3
5m2
Allelic fraction (germline)
Copy Number log−ratio

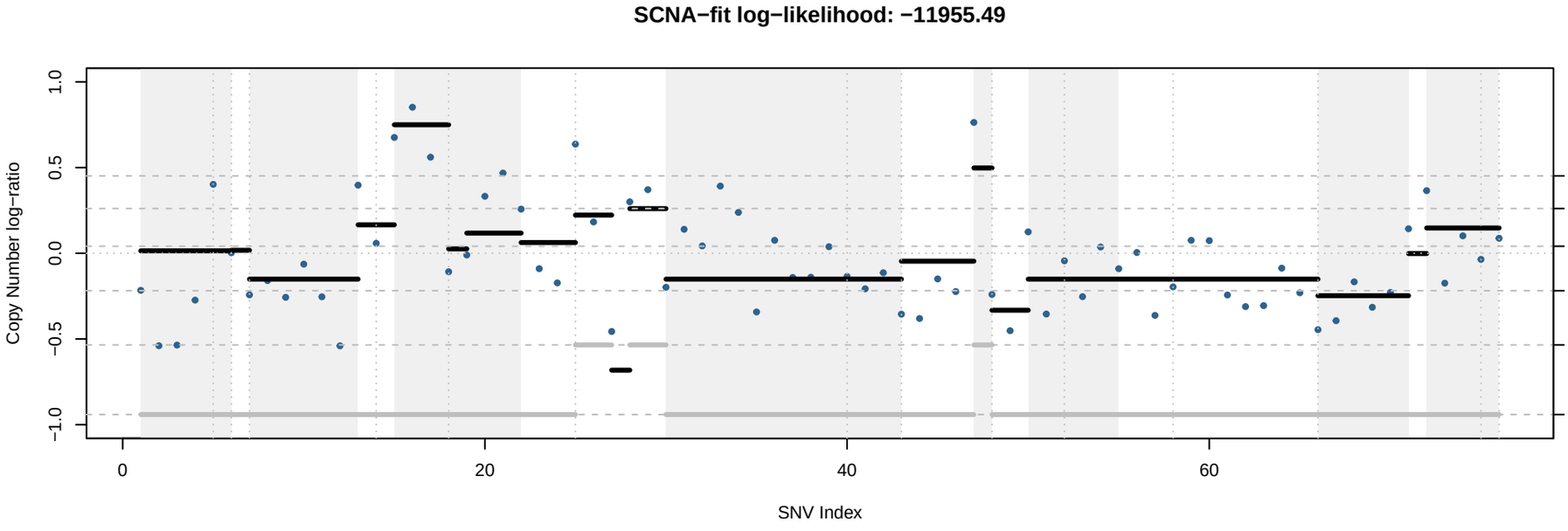

Coverage (log2)
Allelic fraction

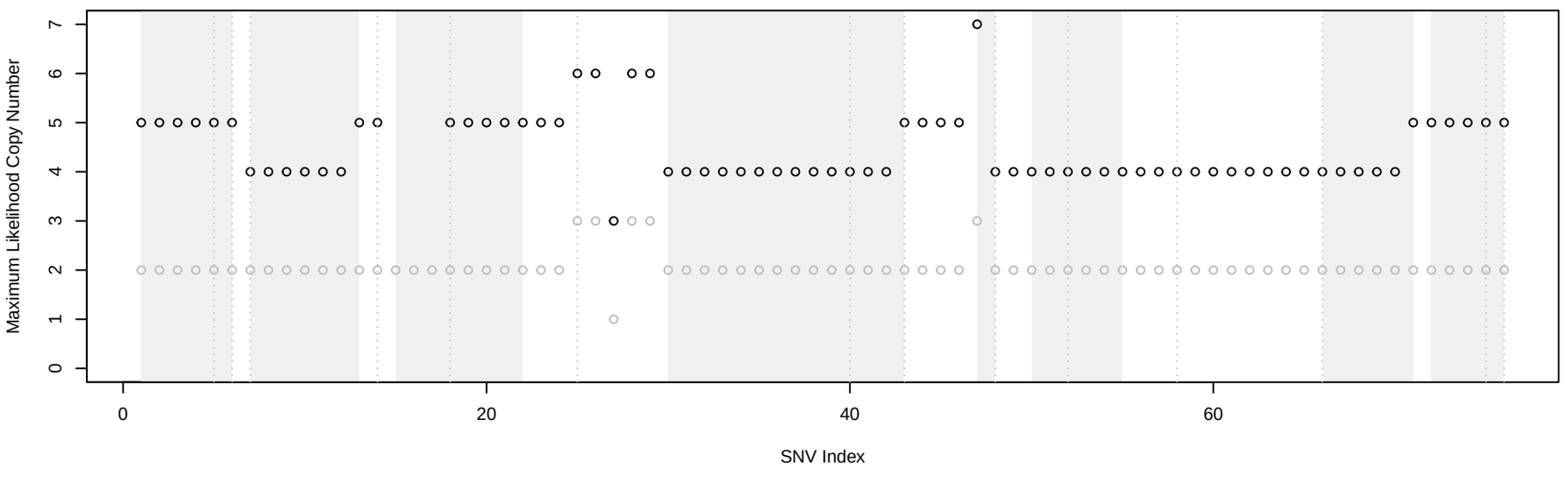

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

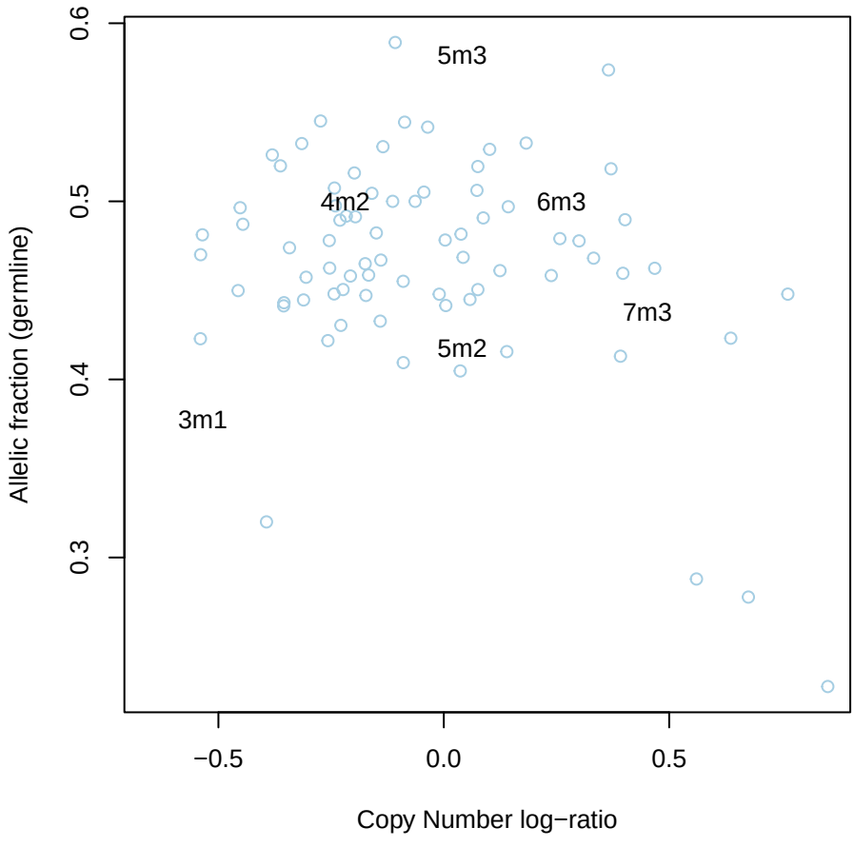

Frequency
Cellular fraction

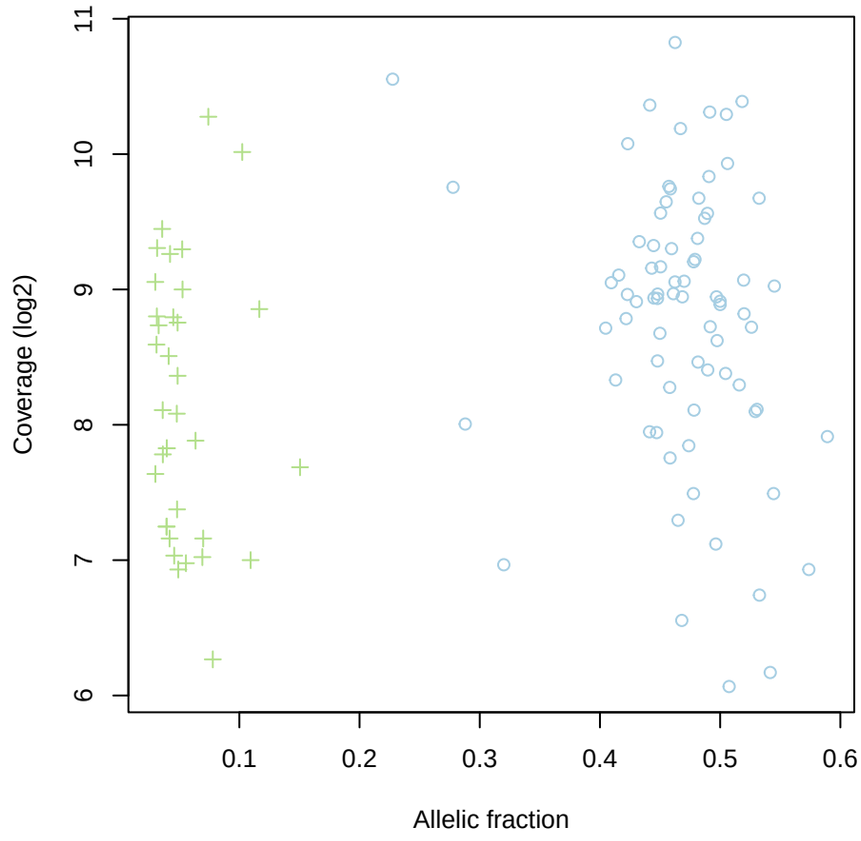

Purity: 0.65 Tumor ploidy: 4.829
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

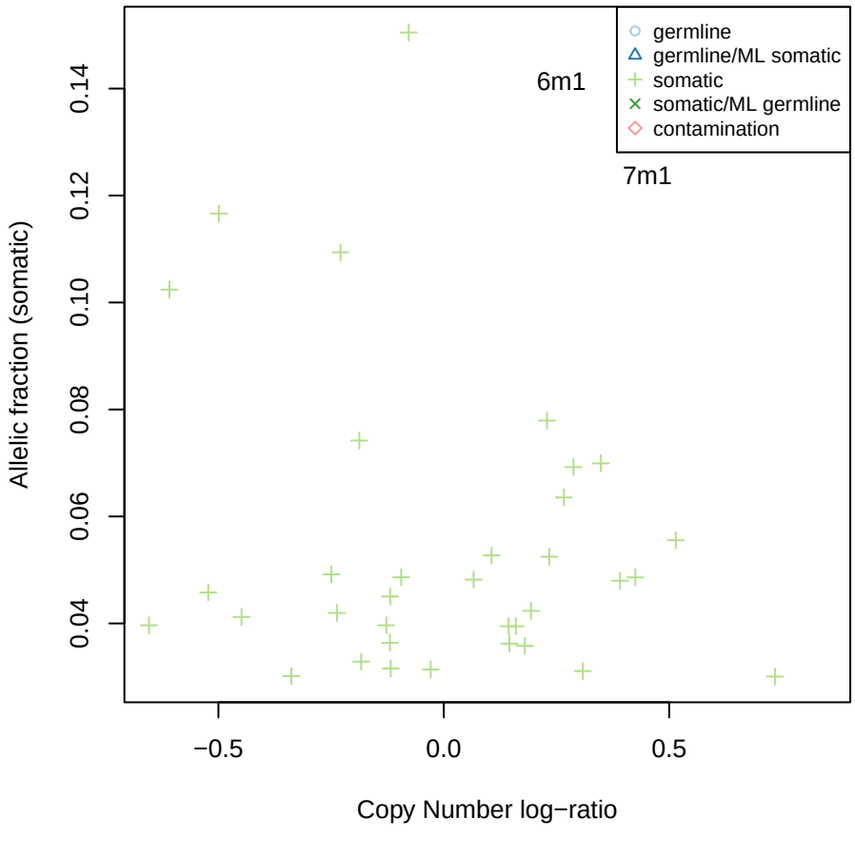

Purity: 0.65 Tumor ploidy: 4.829 SNV log−likelihood: −82.77 GoF: 83.5% Mean coverage: 505;489
1 2 3 4 5 6 7 8 9 11 12 15 16 19
B−Allele Frequency
0.3 0.4 0.5 0.6
0 20 40 60
SNV Index

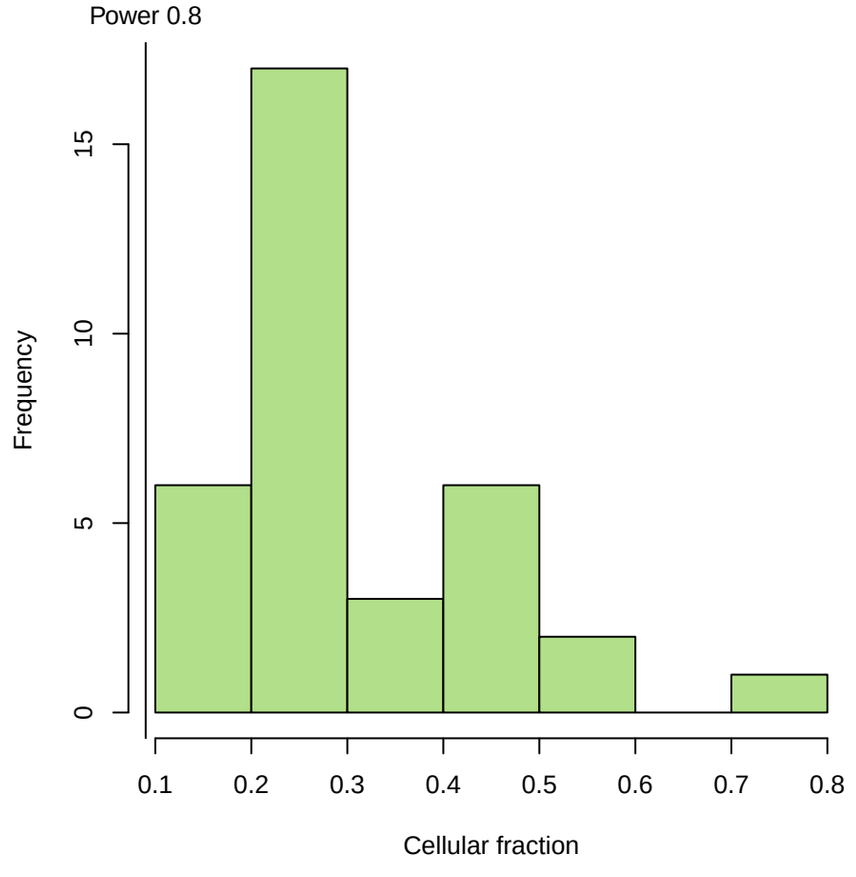

SCNA−fit log−likelihood: −11955.49
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 20 40 60
SNV Index

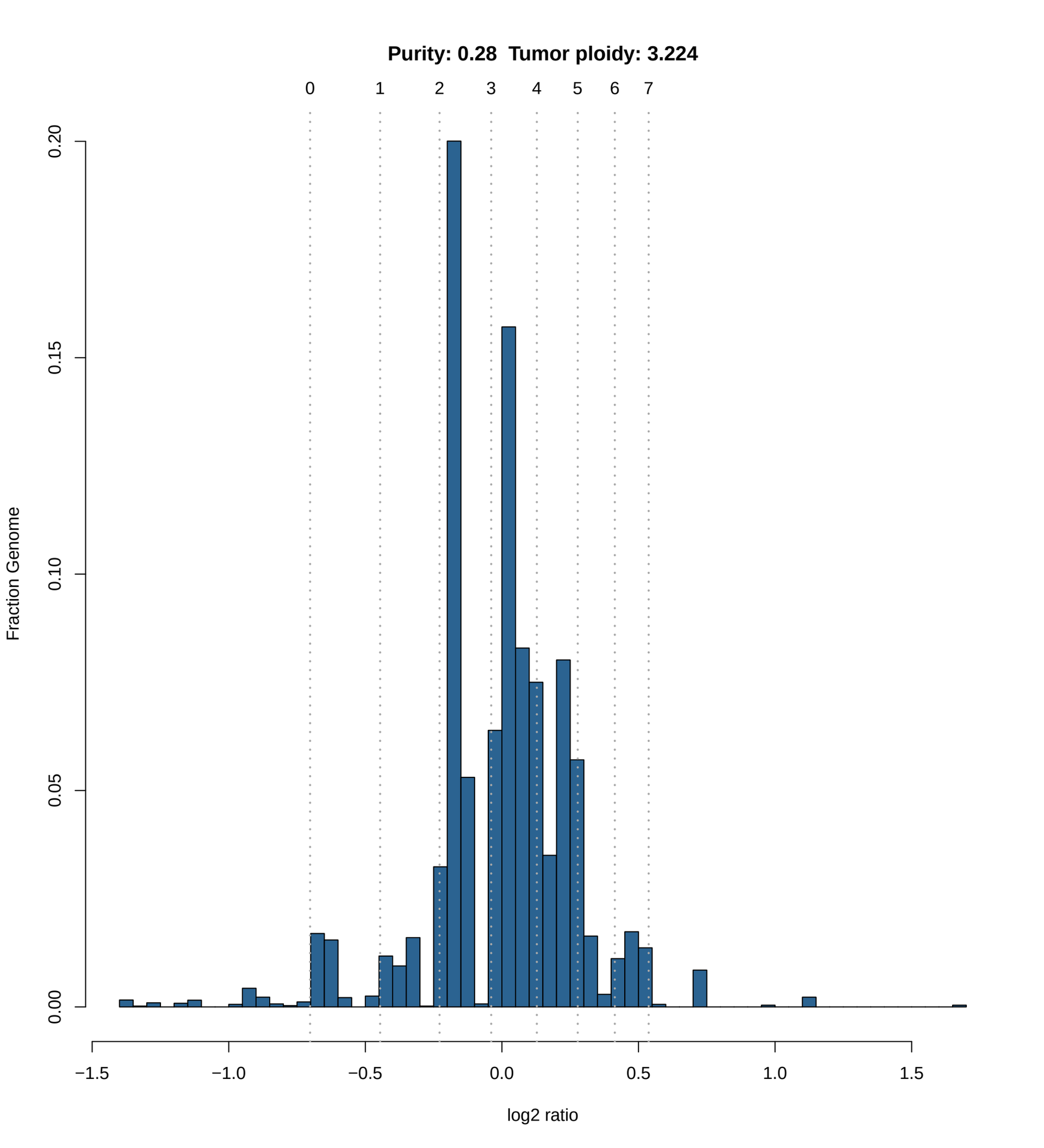

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60
SNV Index

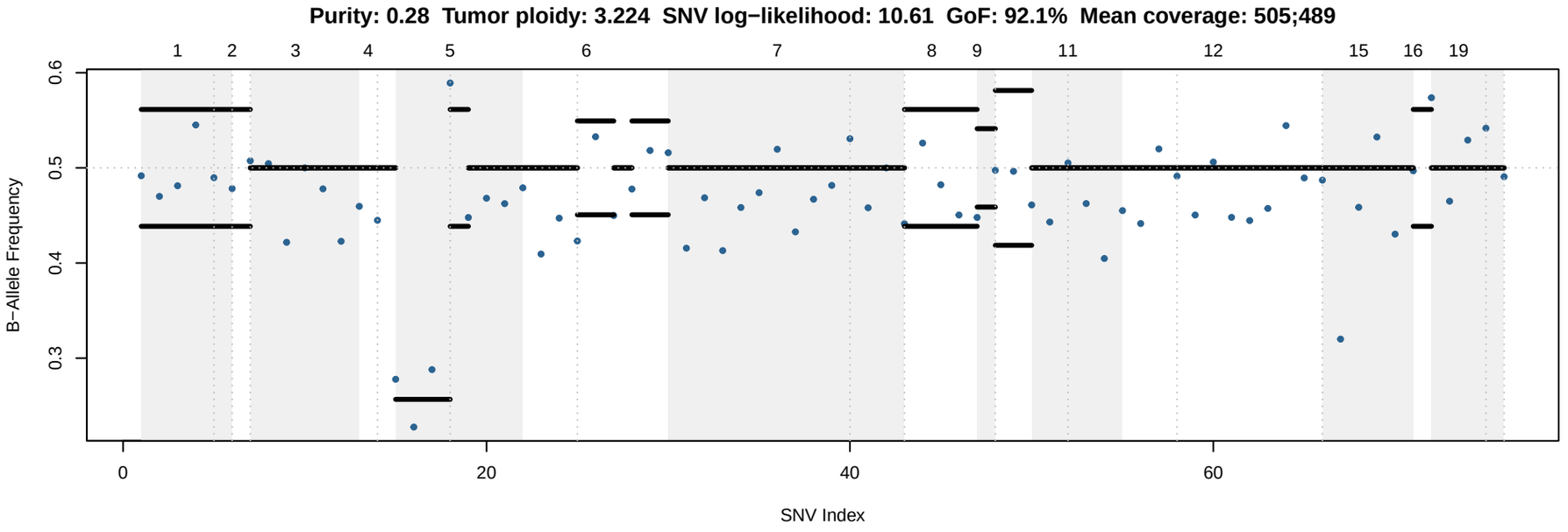

Allelic fraction (germline)
0.3
0.4
0.5
0.6
5m3
4m2
6m3
7m3
5m2
3m1
−0.5
0.0
0.5
Copy Number log−ratio

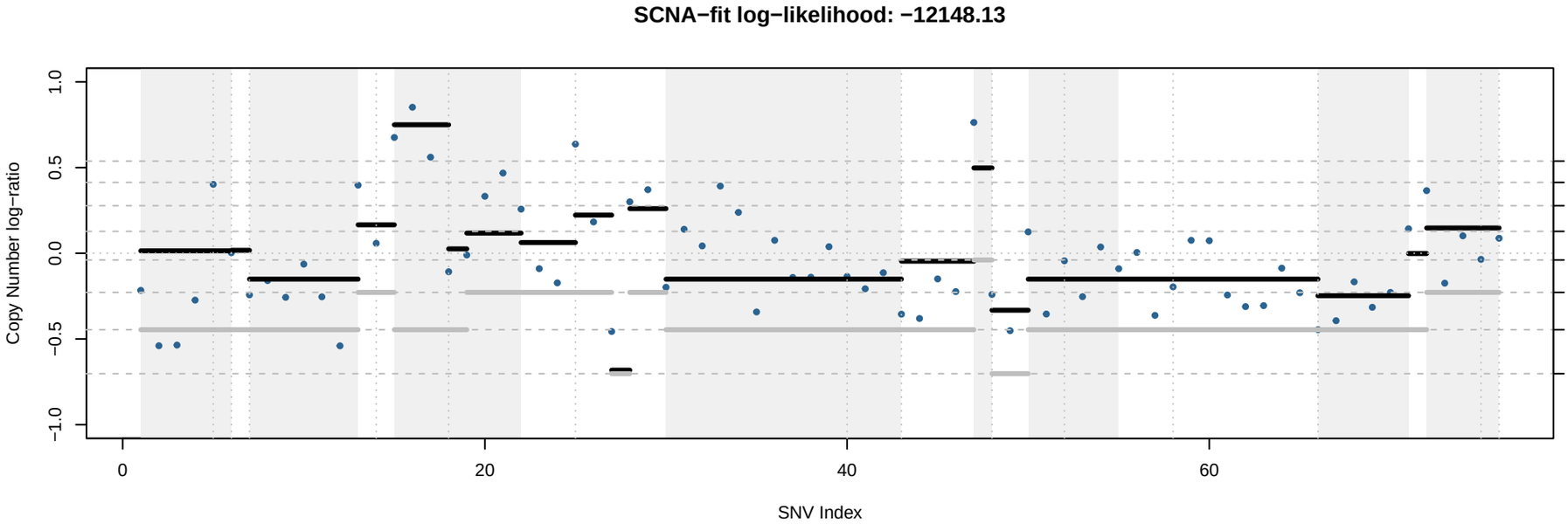

Coverage (log2)
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

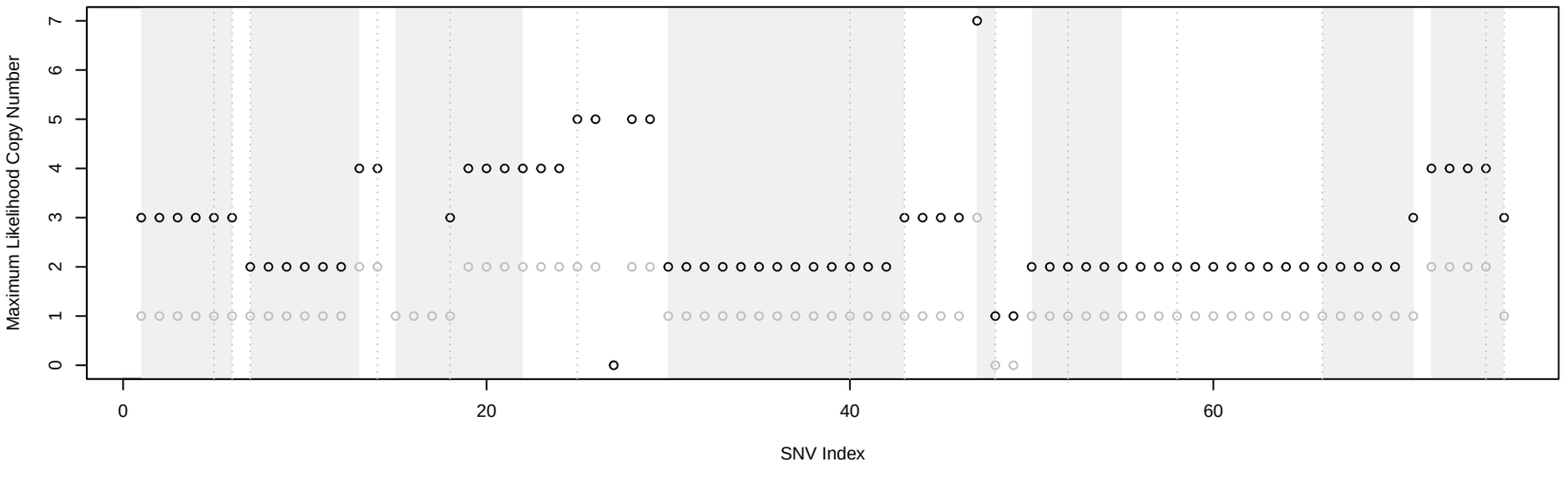

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m1
7m1
−0.5
0.0
0.5
Copy Number log−ratio

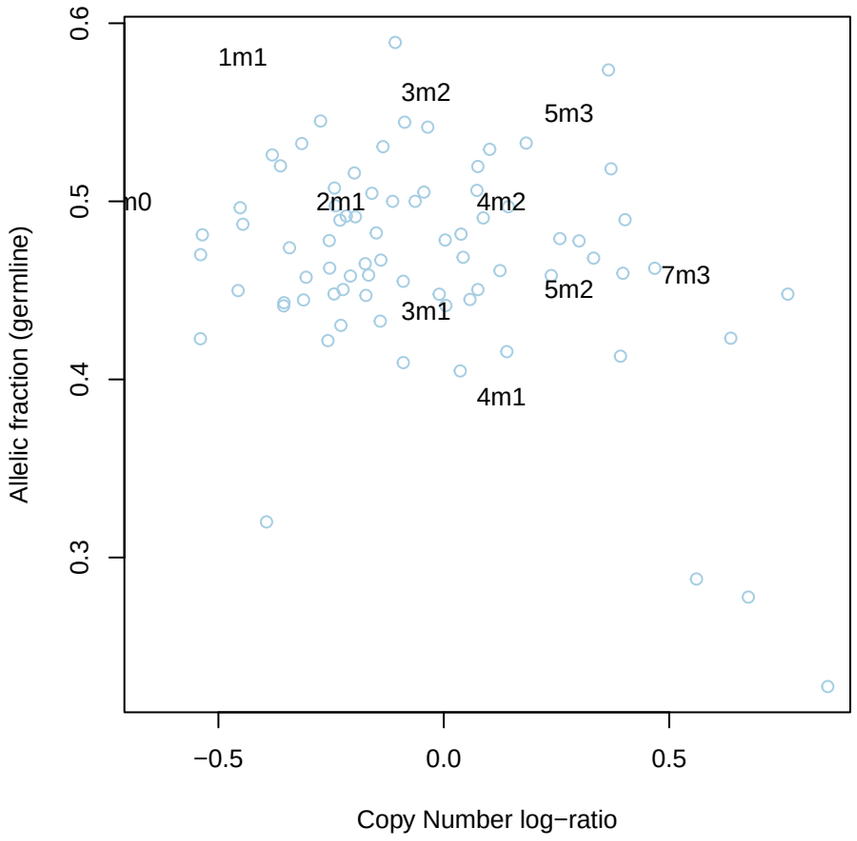

Power 0.8
Frequency
0
5
10
15
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
Cellular fraction

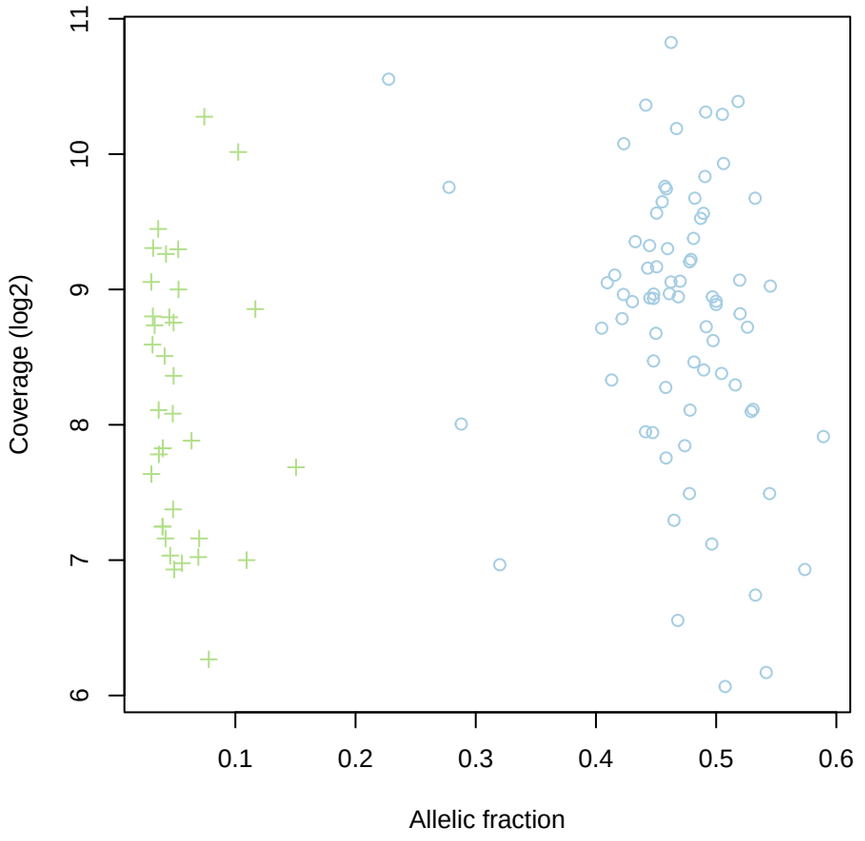

Purity: 0.28 Tumor ploidy: 3.224
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

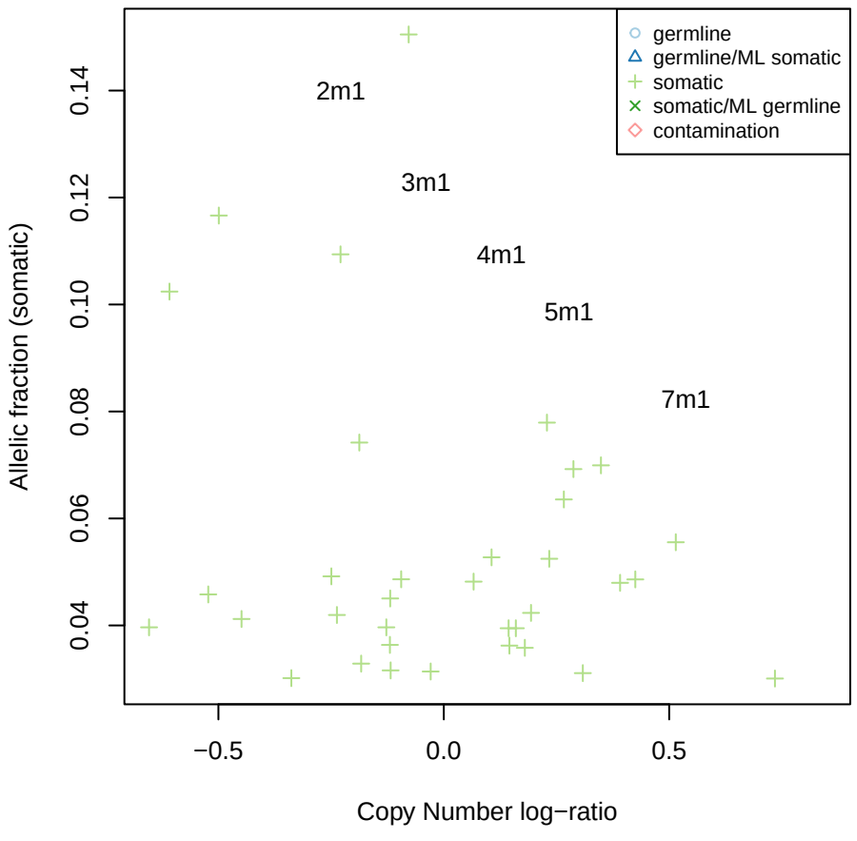

Purity: 0.28 Tumor ploidy: 3.224 SNV log−likelihood: 10.61 GoF: 92.1% Mean coverage: 505;489
1 2 3 4 5 6 7 8 9 11 12 15 16 19
B−Allele Frequency
0.3 0.4 0.5 0.6
0 20 40 60
SNV Index

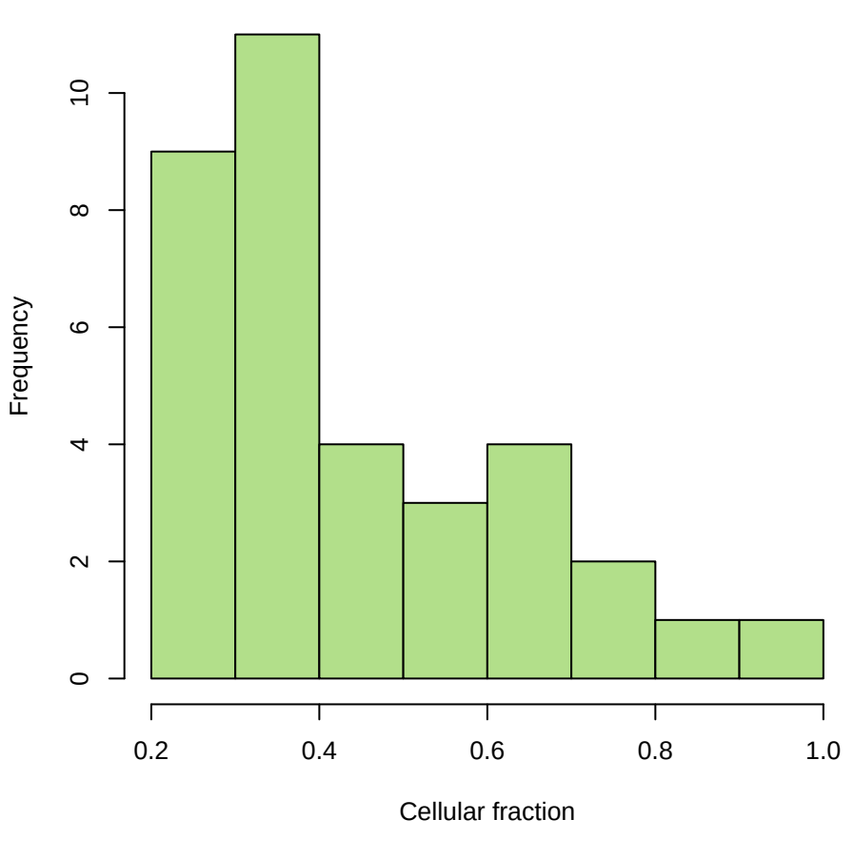

SCNA−fit log−likelihood: −12148.13
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 6 7
0 20 40 60
SNV Index

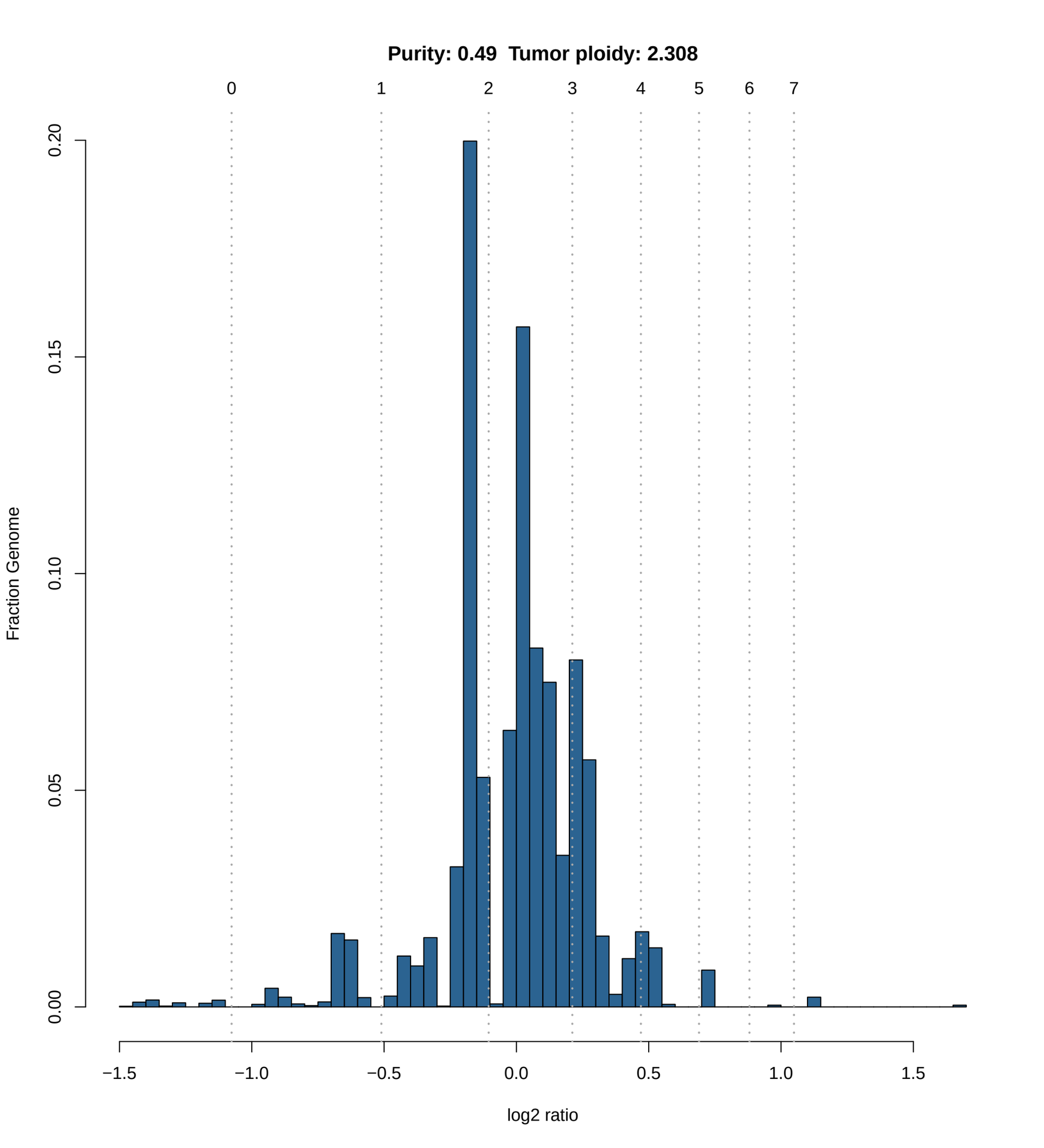

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60
SNV Index

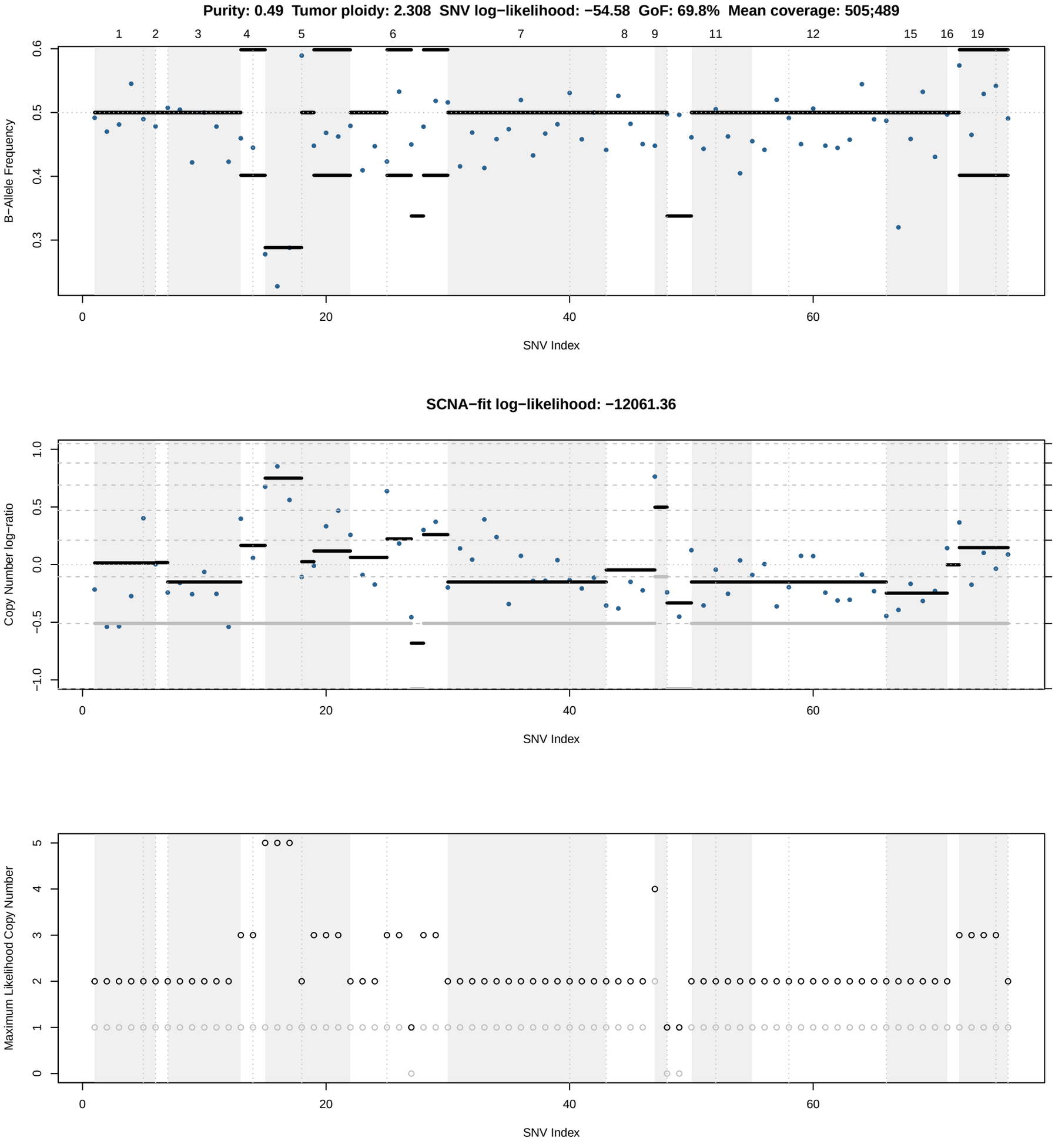

1m1
3m2
5m3
n0
2m1
4m2
7m3
5m2
3m1
4m1
Allelic fraction (germline)
Copy Number log−ratio

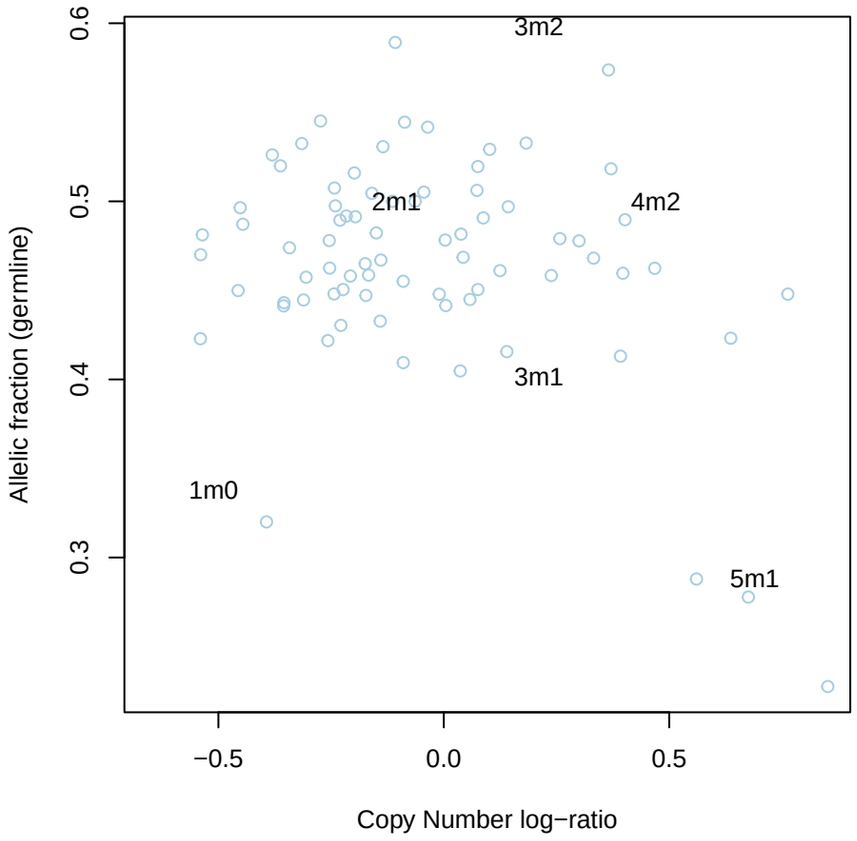

Coverage (log2)
Allelic fraction

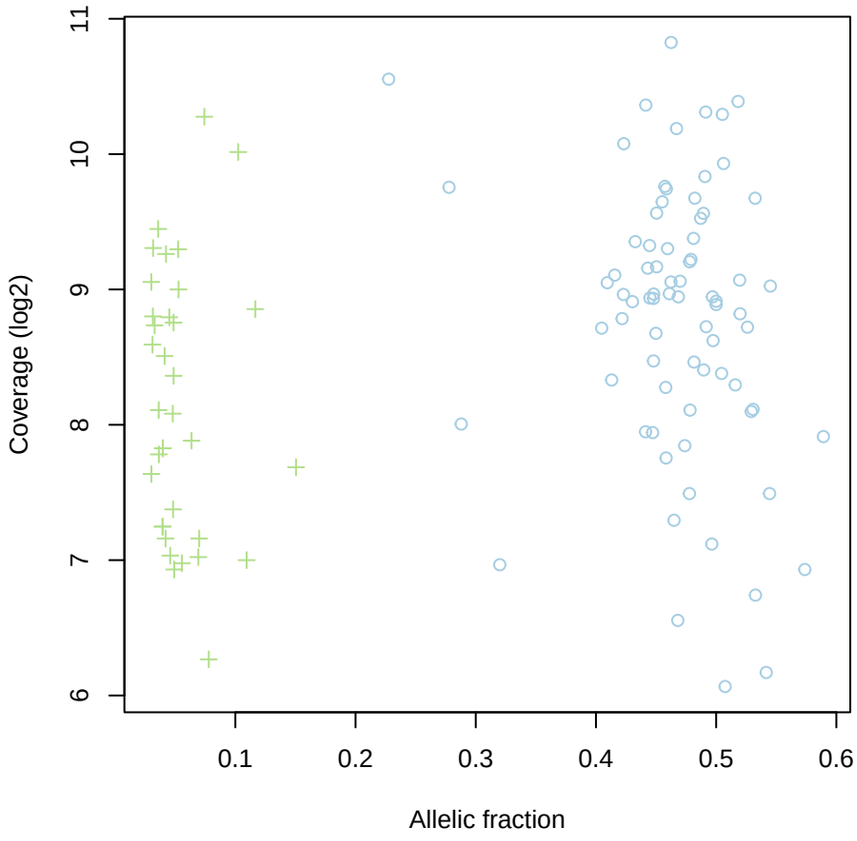

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1
5m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

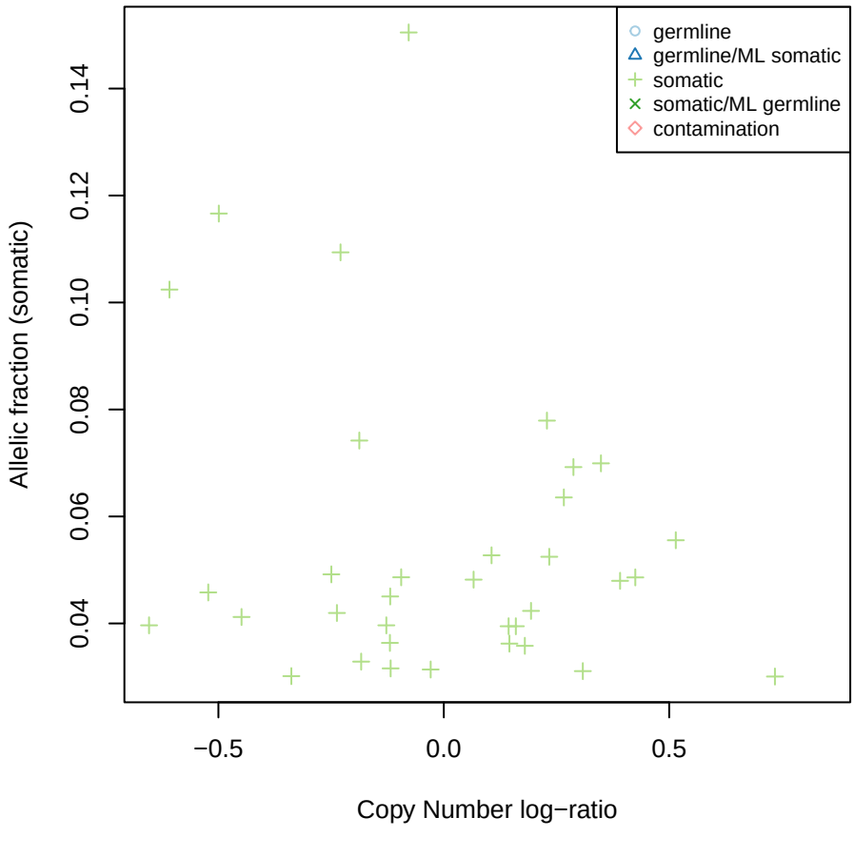

Frequency
Cellular fraction

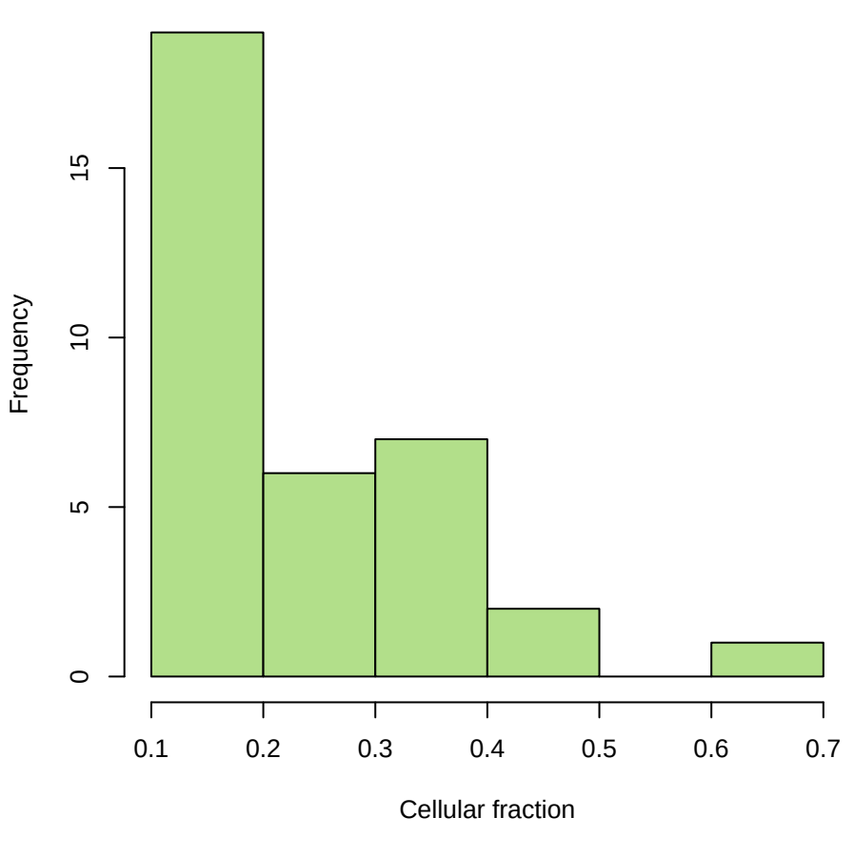

Purity: 0.49 Tumor ploidy: 2.308
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

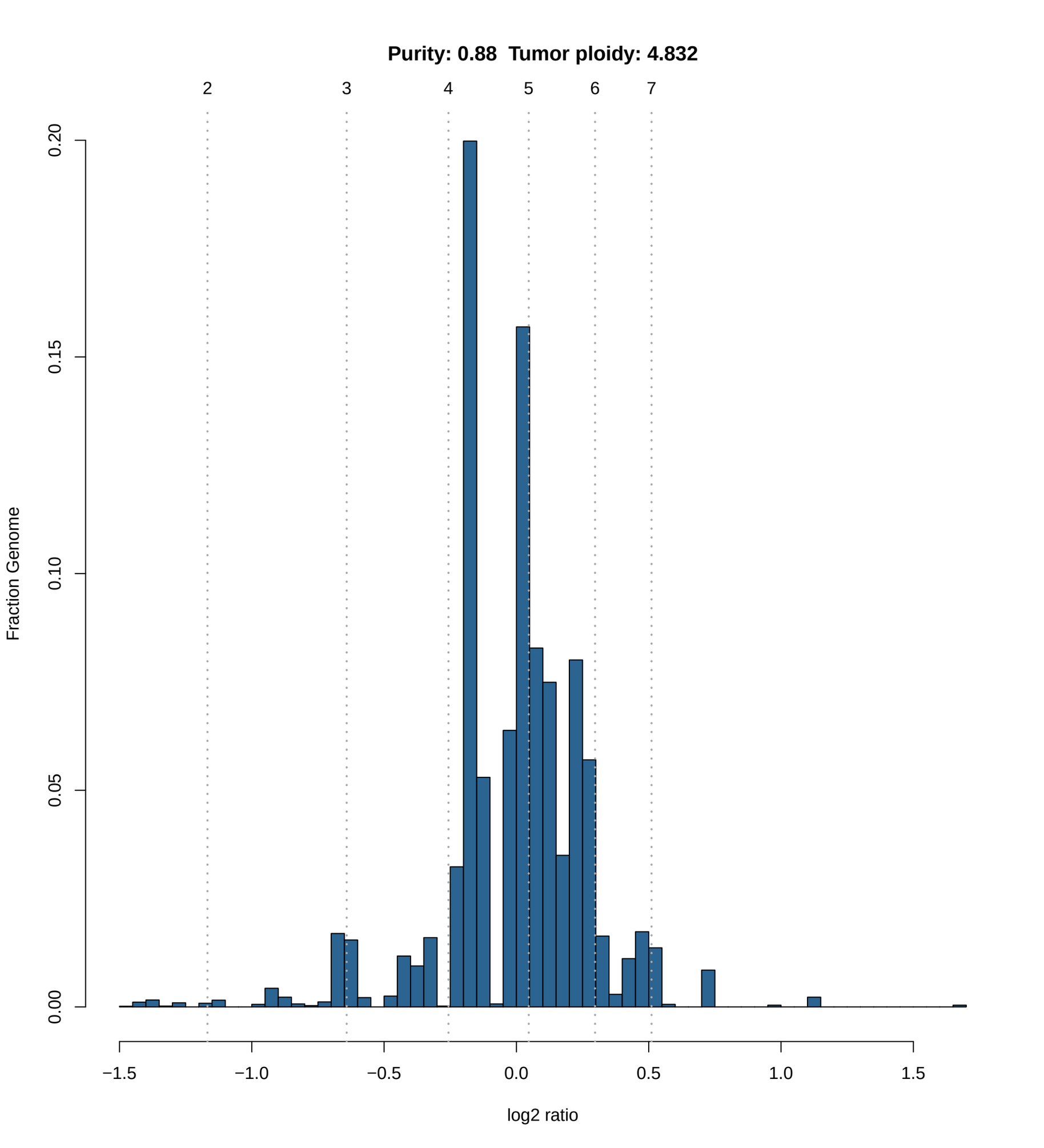

Purity: 0.49 Tumor ploidy: 2.308 SNV log−likelihood: −54.58 GoF: 69.8% Mean coverage: 505;489
1 2 3 4 5 6 7 8 9 11 12 15 16 19
B−Allele Frequency
0.3 0.4 0.5 0.6
0 20 40 60
SNV Index
SCNA−fit log−likelihood: −12061.36
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 6 7
0 20 40 60
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60
SNV Index

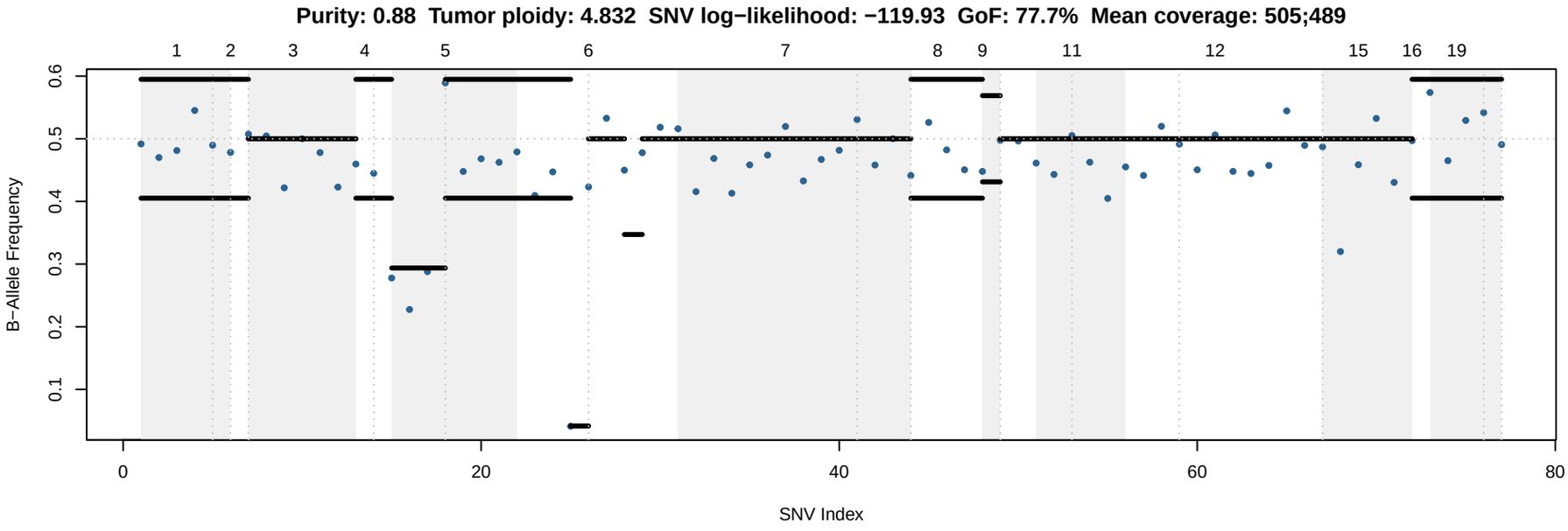

3m2
2m1
4m2
3m1
1m0
5m1
Allelic fraction (germline)
Copy Number log−ratio

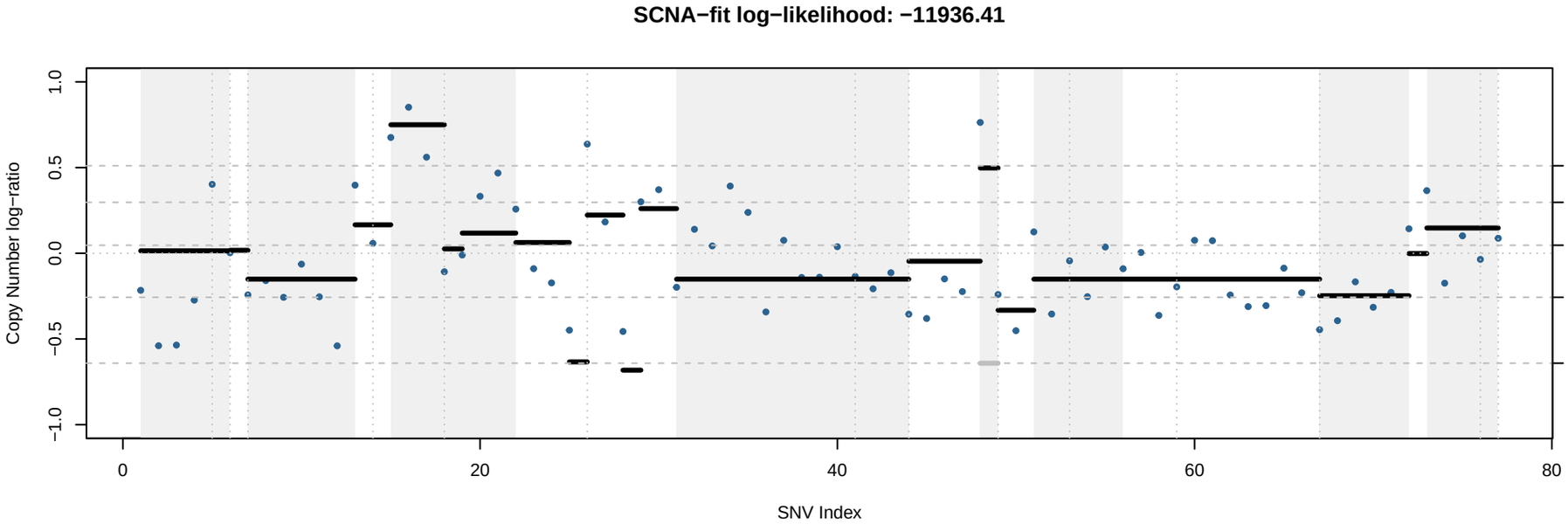

Coverage (log2)
Allelic fraction

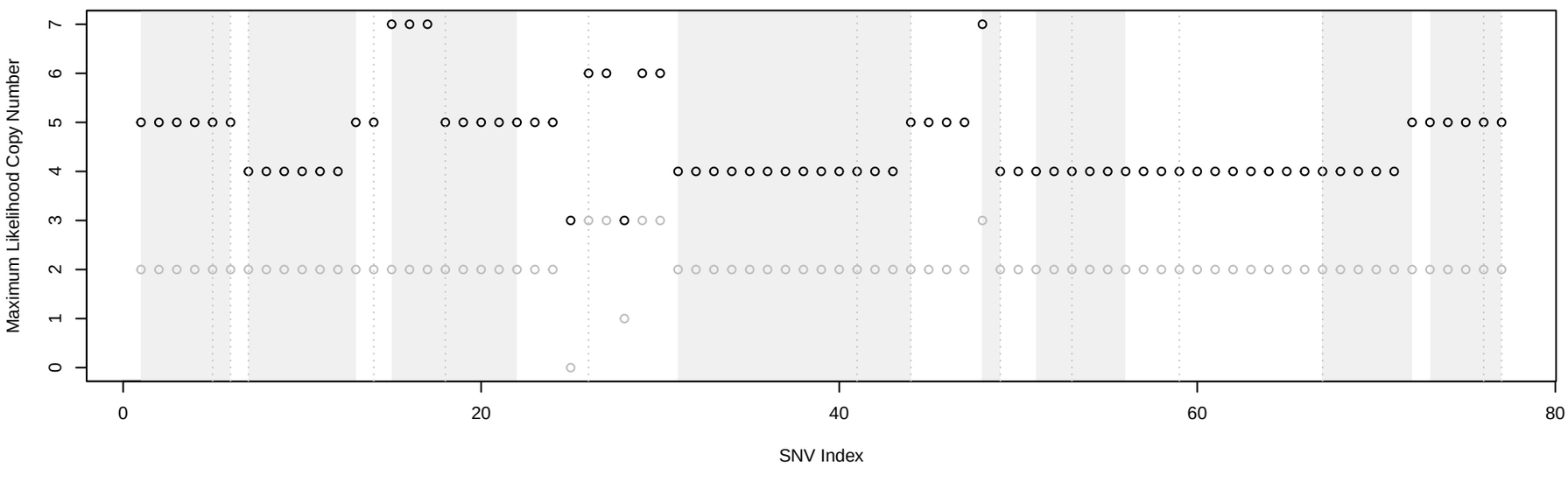

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

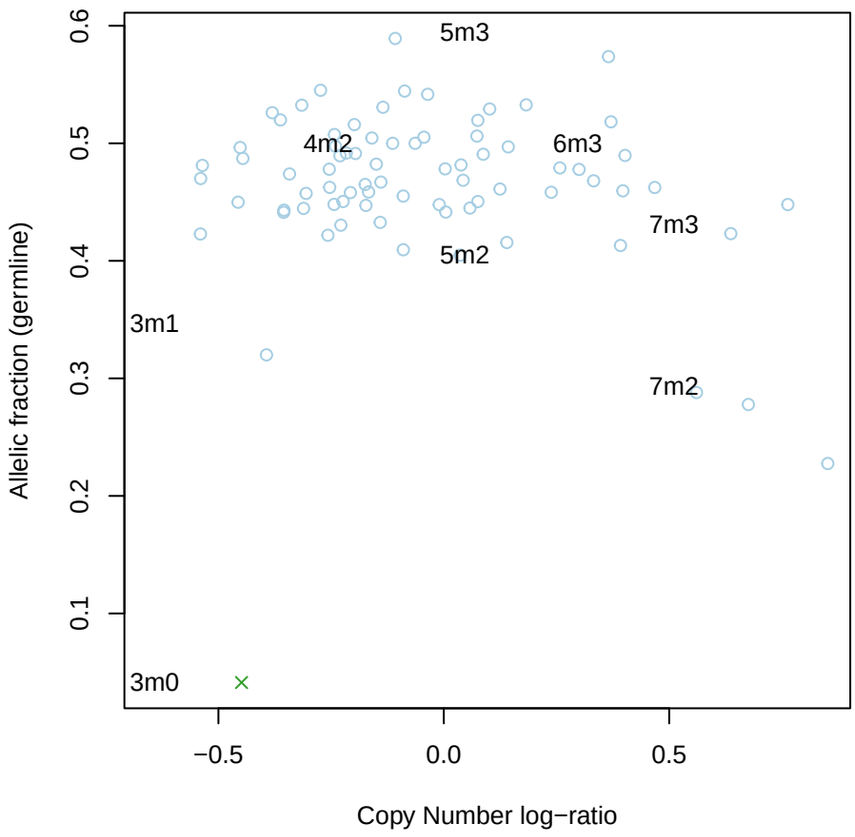

Frequency
Cellular fraction

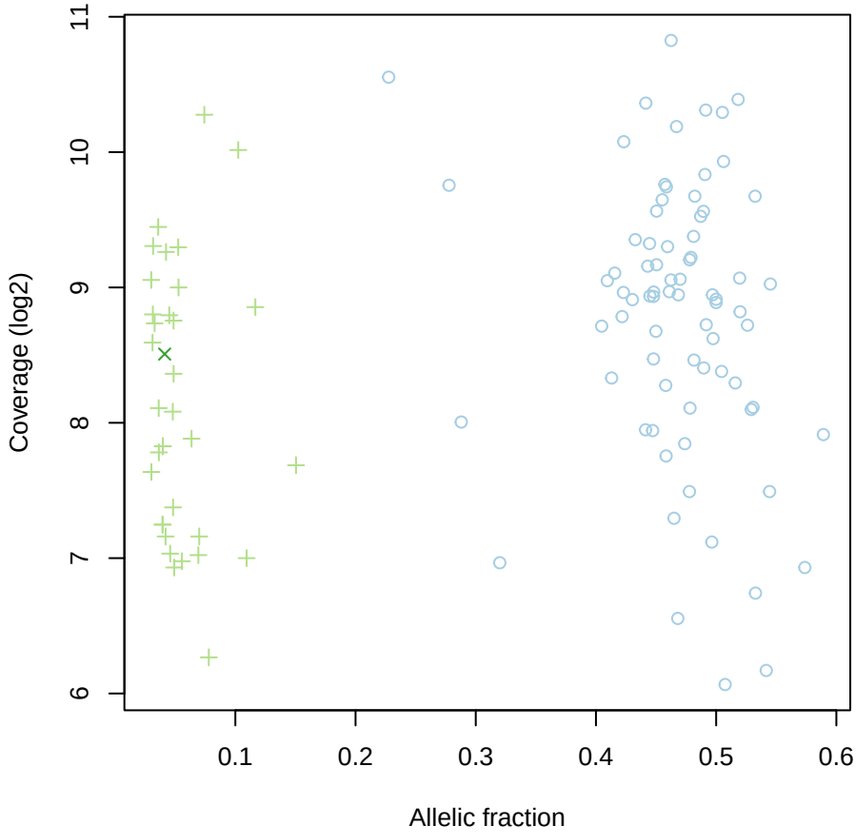

Purity: 0.88 Tumor ploidy: 4.832
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

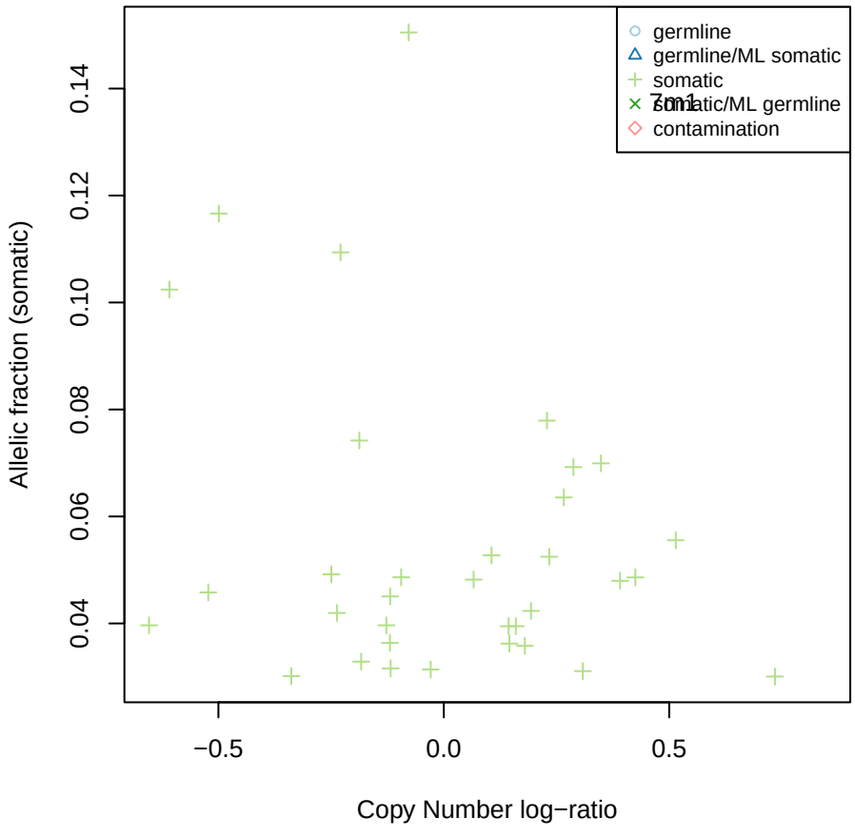

Purity: 0.88 Tumor ploidy: 4.832 SNV log−likelihood: −119.93 GoF: 77.7% Mean coverage: 505;489
1 2 3 4 5 6 7 8 9 11 12 15 16 19
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6
0 20 40 60 80
SNV Index

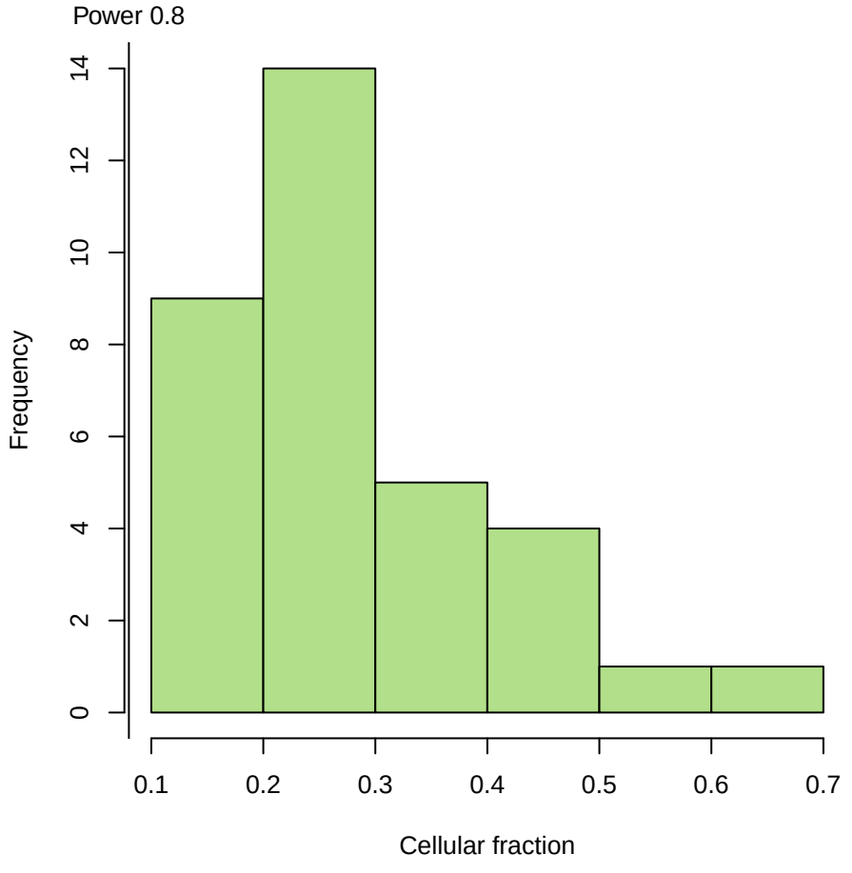

SCNA−fit log−likelihood: −11936.41
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 20 40 60 80
SNV Index


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


5m3
4m2
6m3
7m3
5m2
3m1
7m2
3m0
Allelic fraction (germline)
Copy Number log−ratio


Coverage (log2)
Allelic fraction


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


Power 0.8
Frequency
Cellular fraction