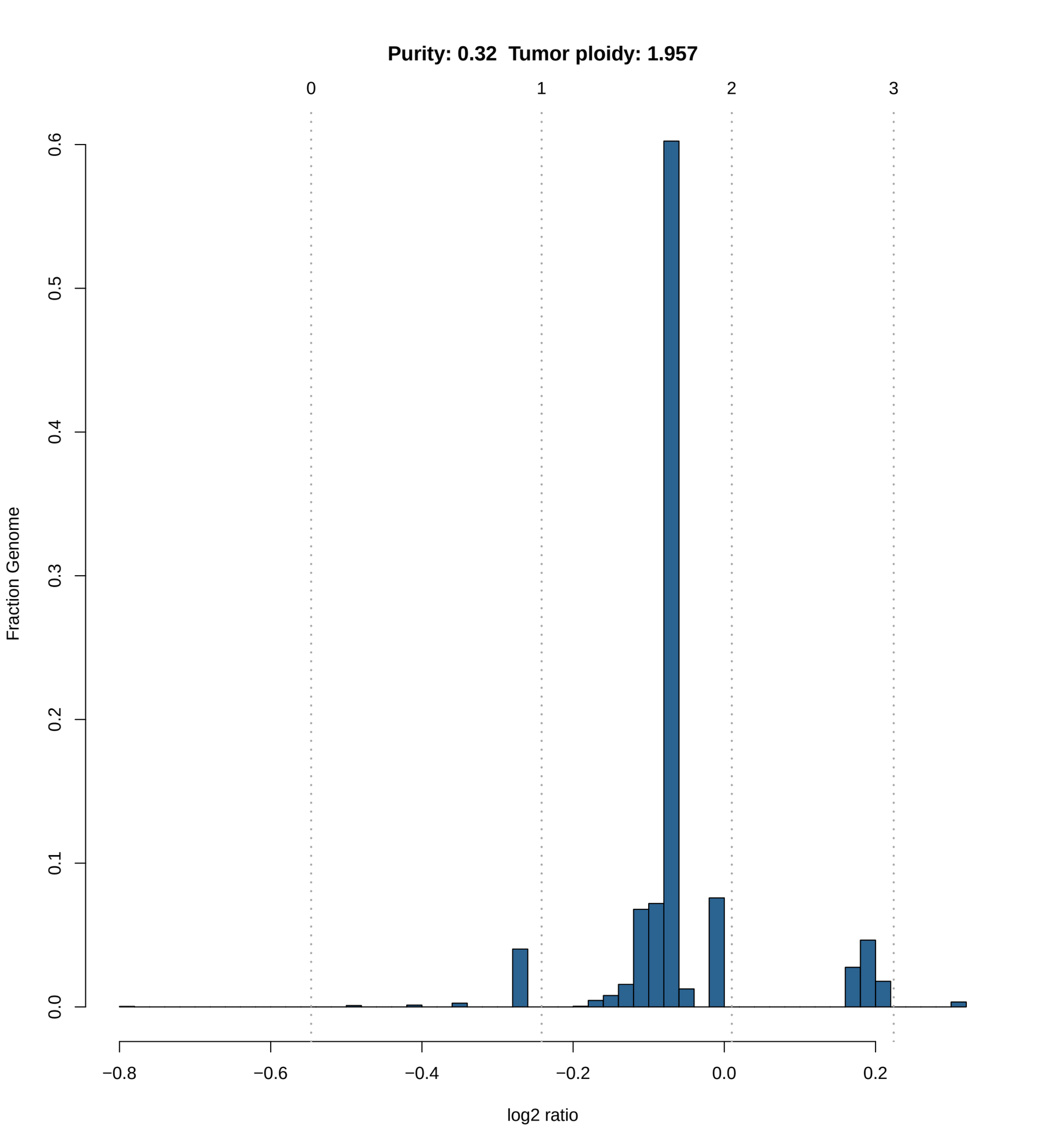
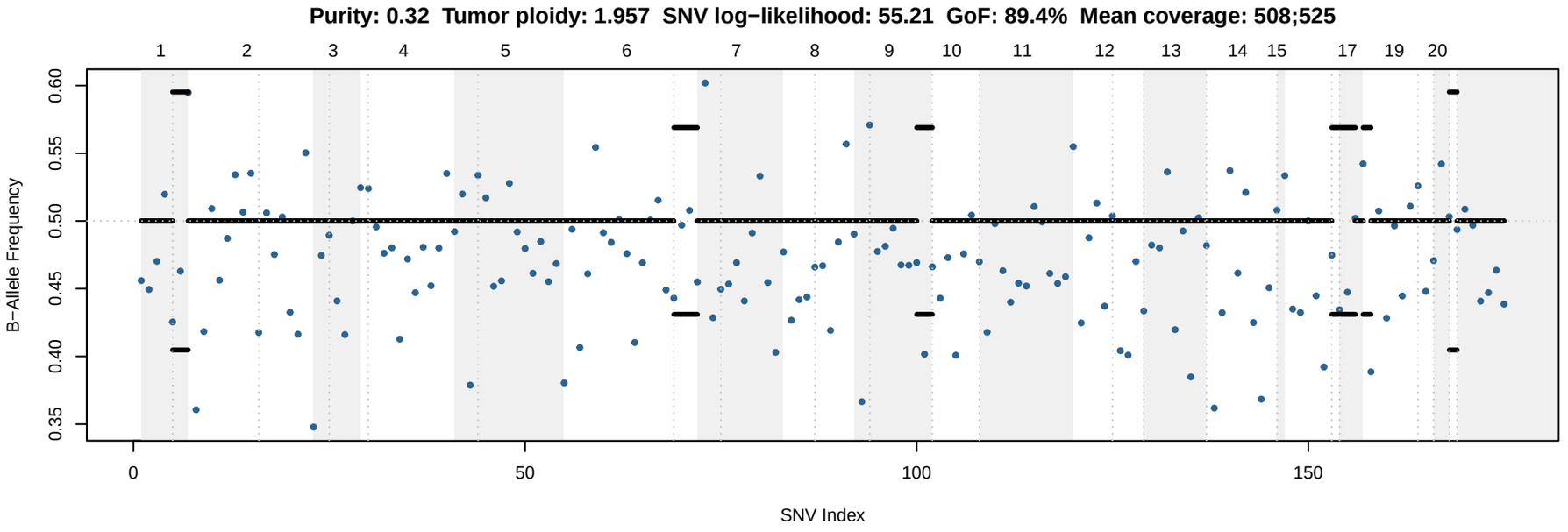
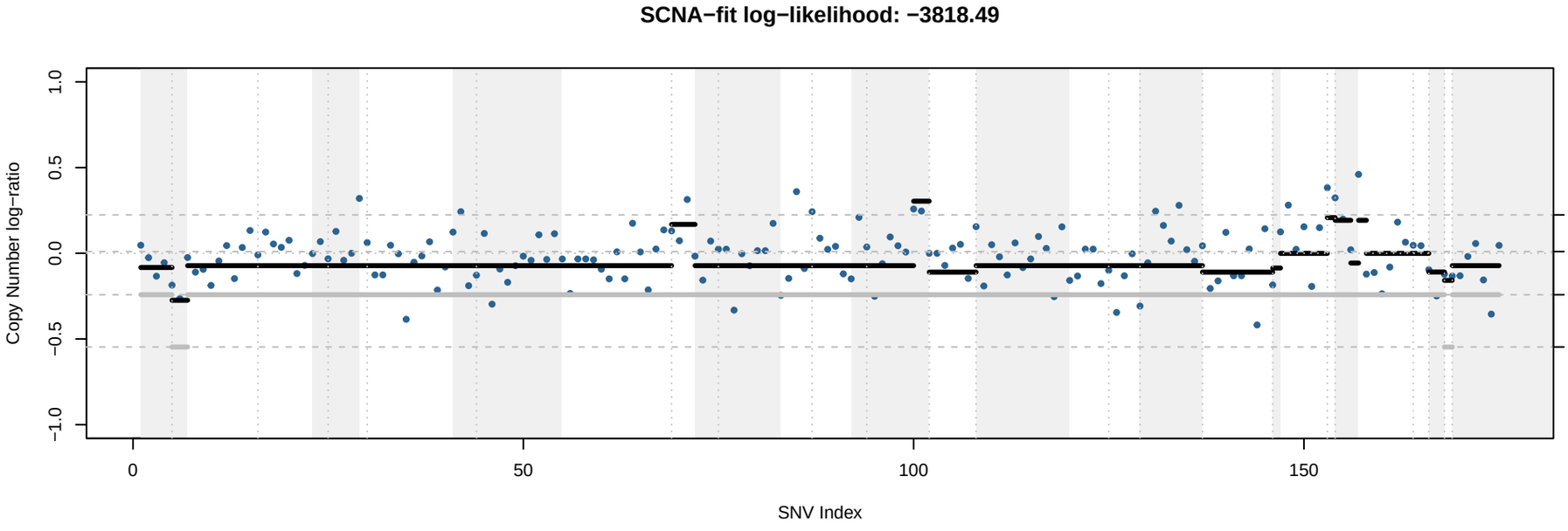
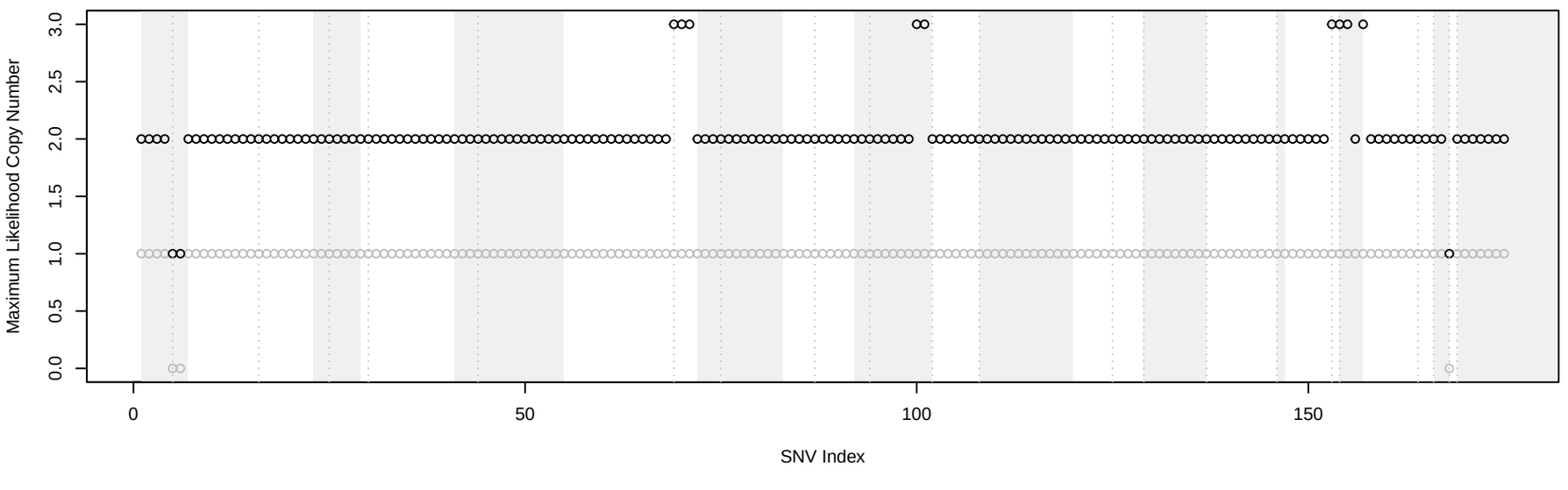
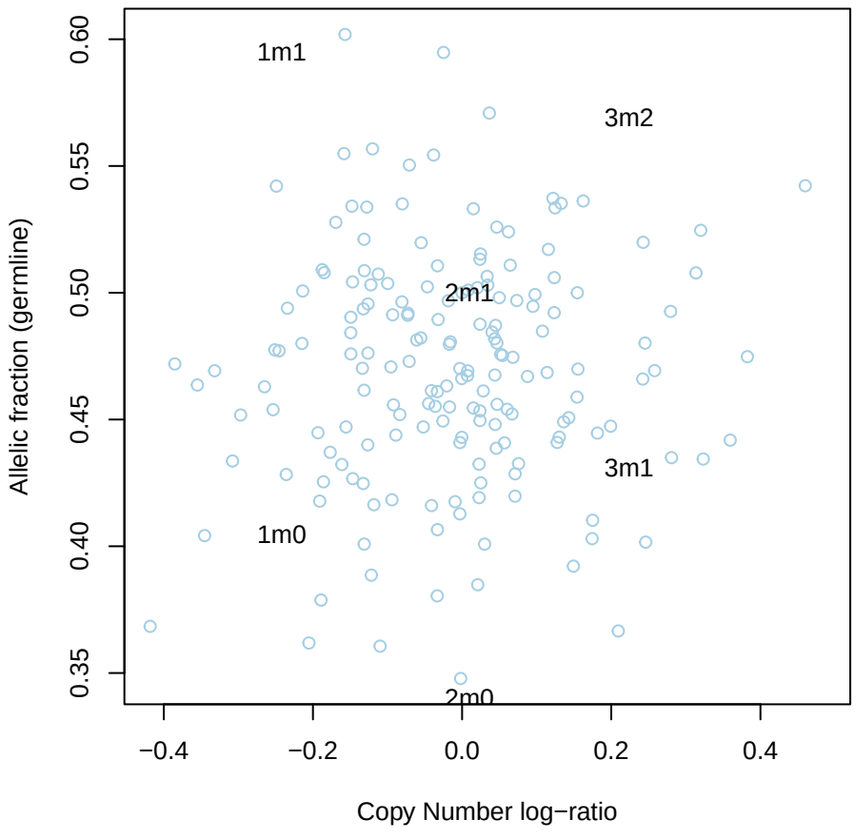
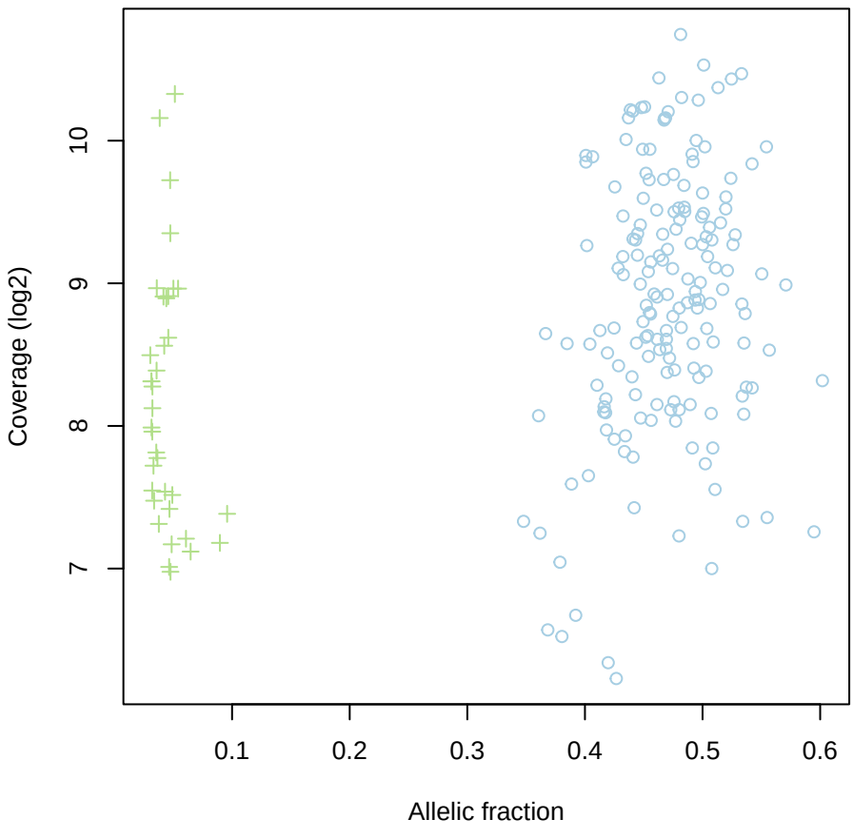

Purity: 0.32 Tumor ploidy: 1.957
0
1
2
3
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

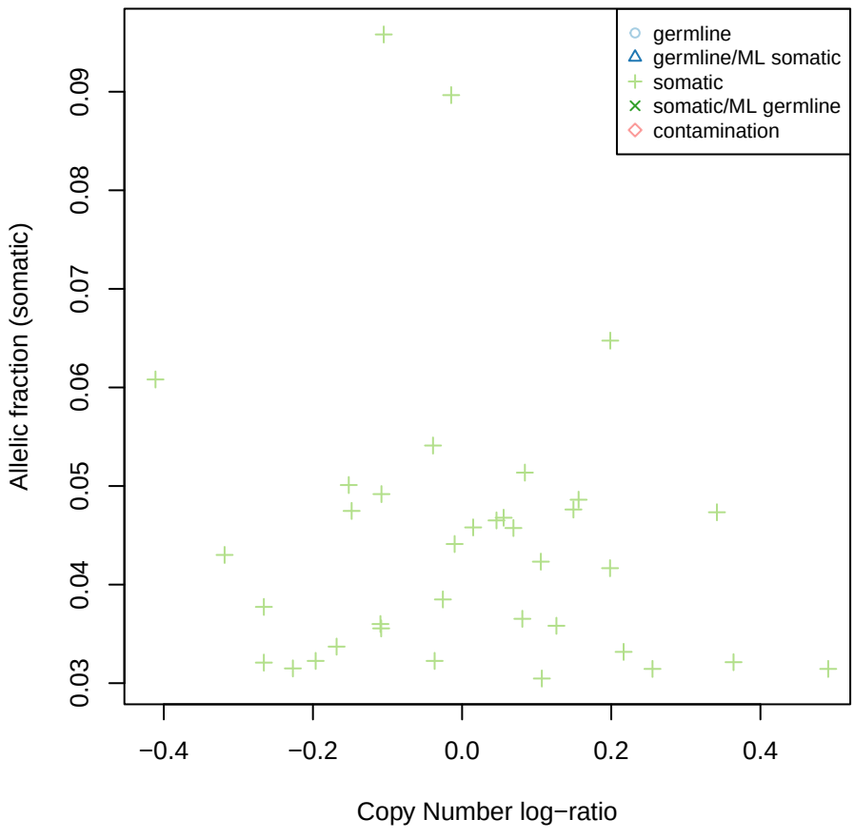

Purity: 0.32 Tumor ploidy: 1.957 SNV log−likelihood: 55.21 GoF: 89.4% Mean coverage: 508;525
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

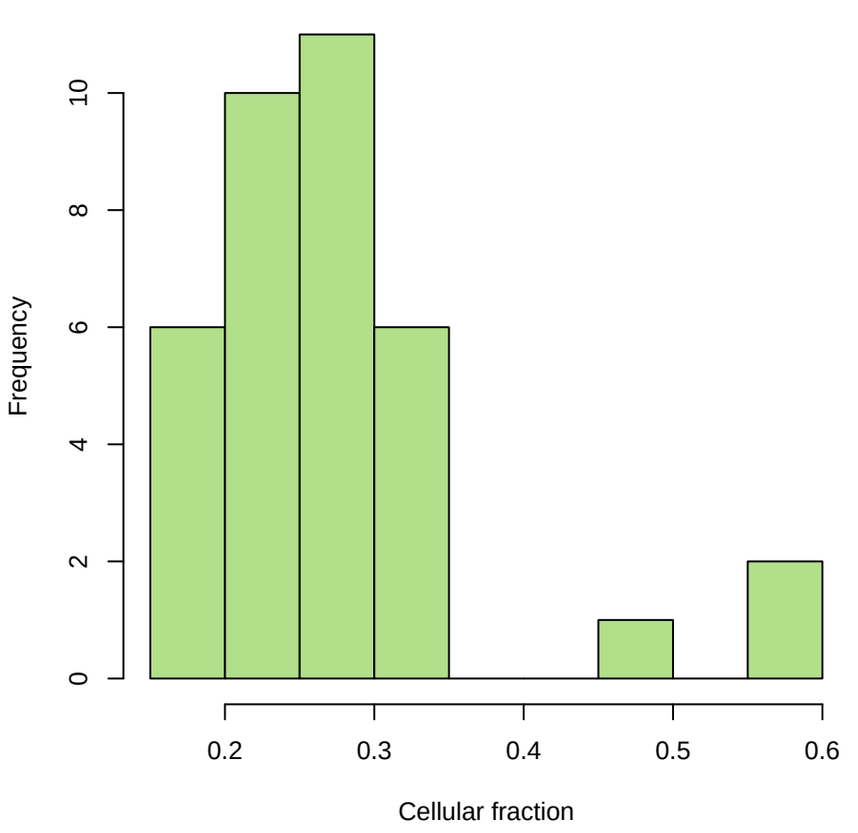

SCNA−fit log−likelihood: −3818.49
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3
0 50 100 150
SNV Index

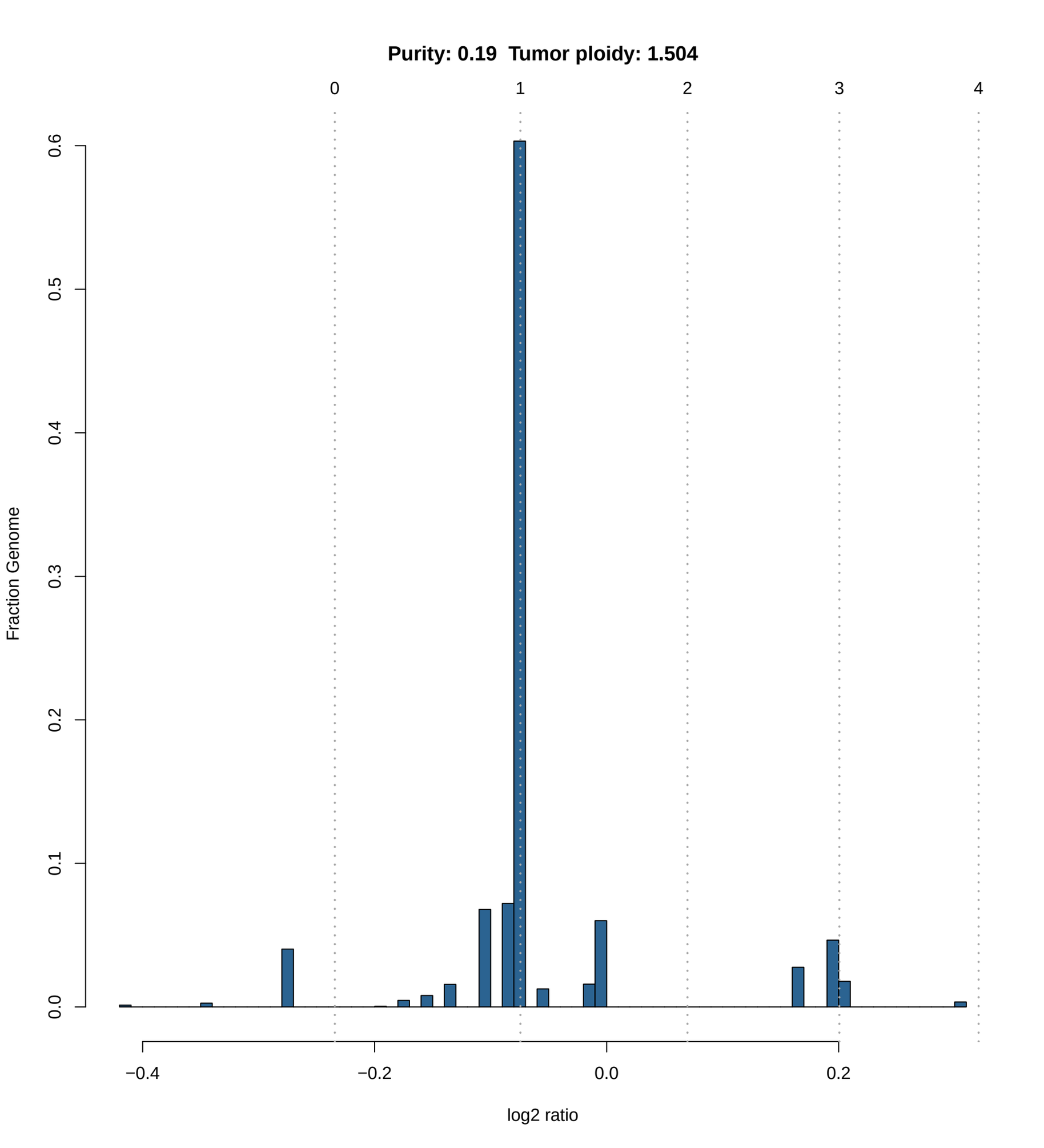

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

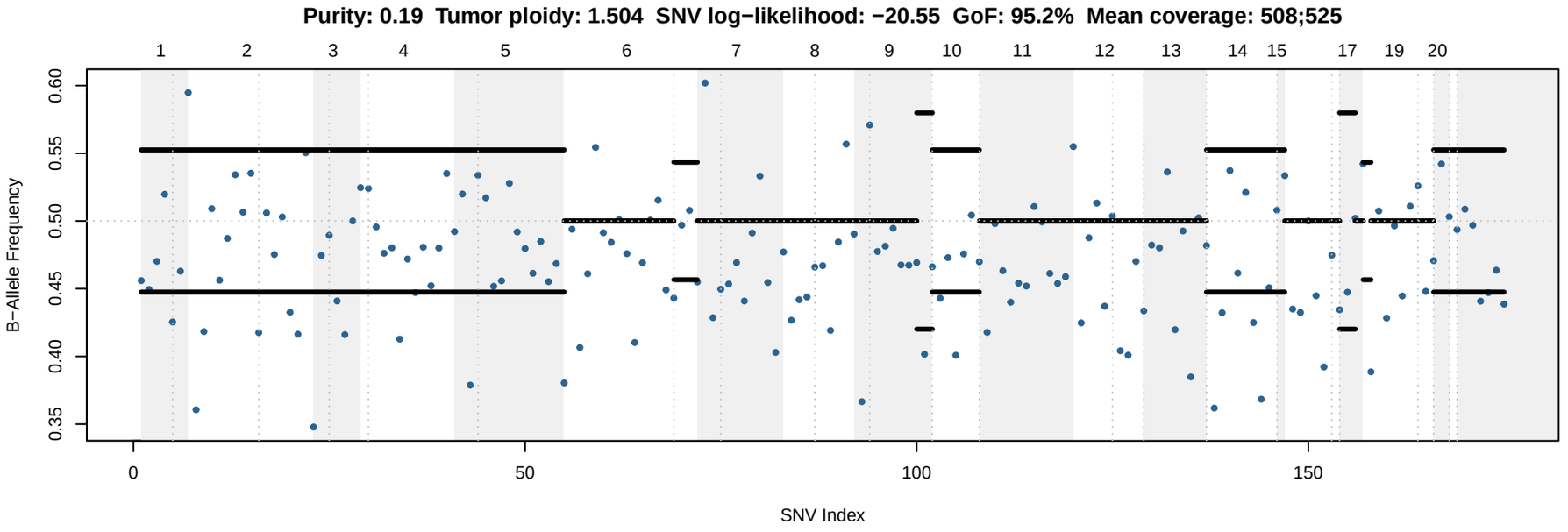

1m1
3m2
2m1
3m1
1m0
2m0
Allelic fraction (germline)
Copy Number log−ratio

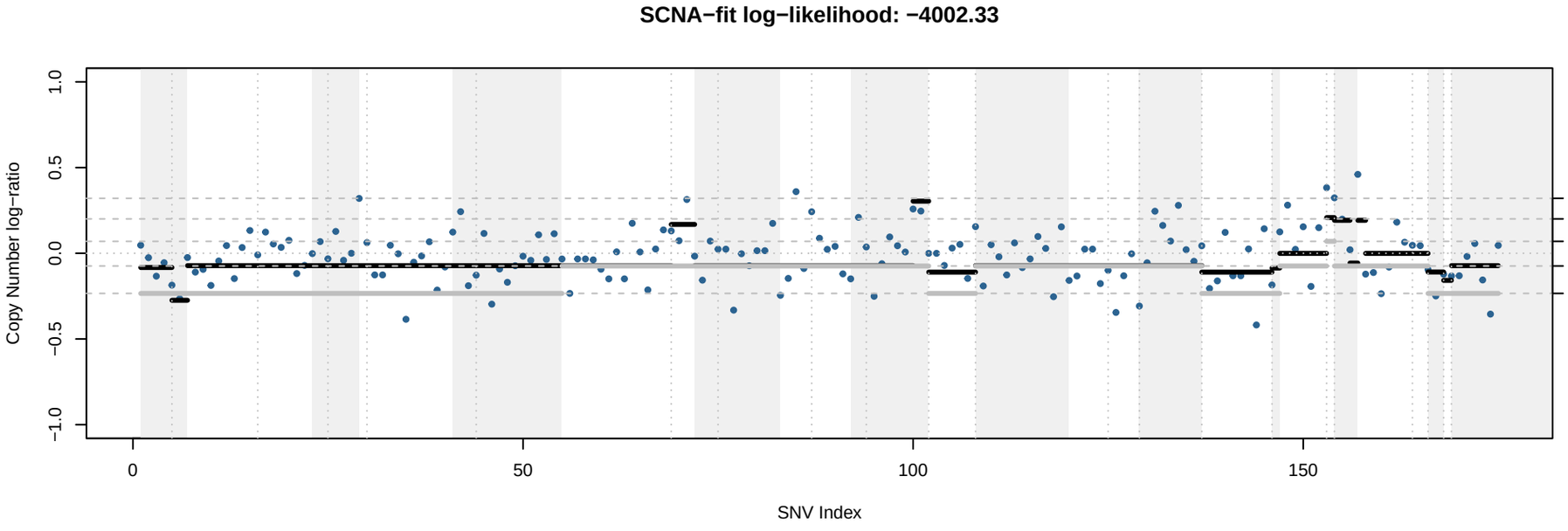

Coverage (log2)
Allelic fraction

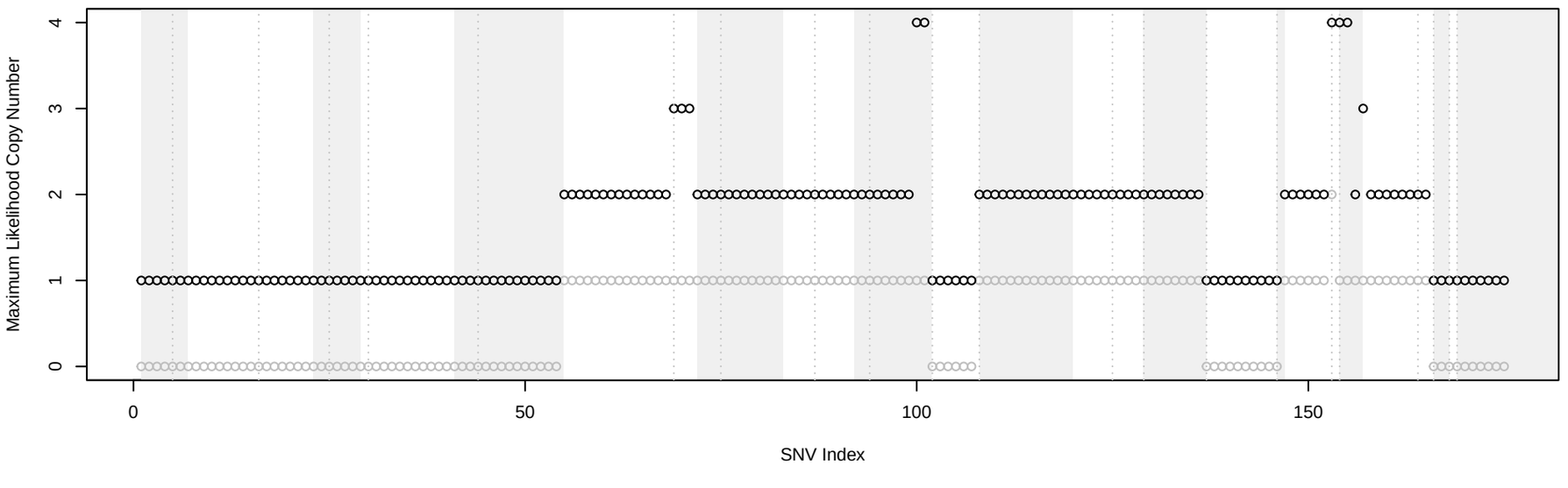

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

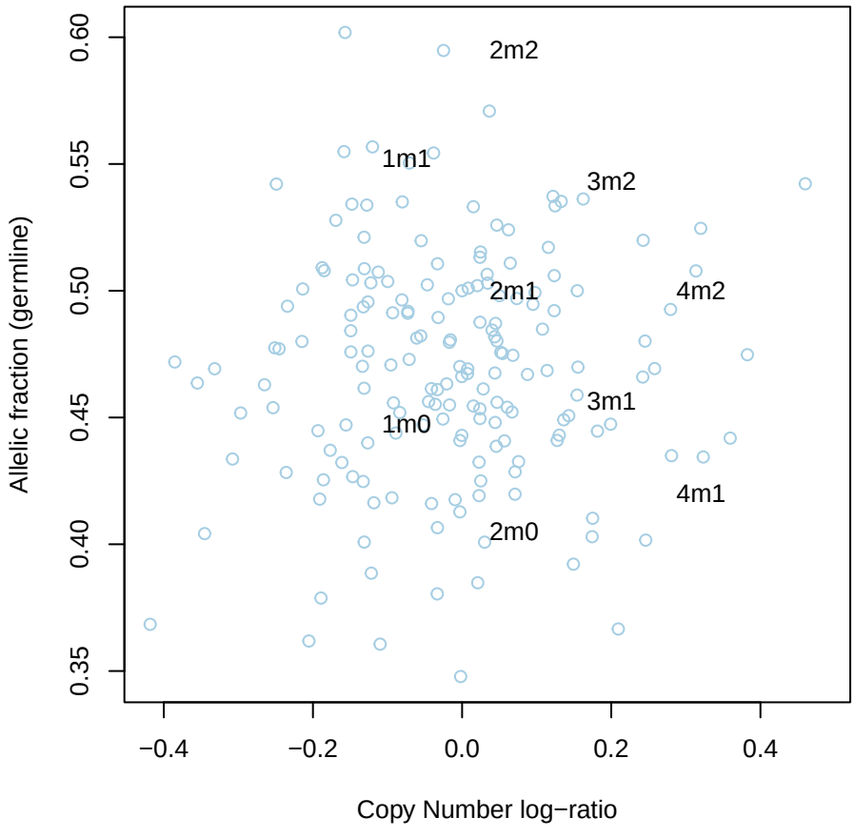

Frequency
Cellular fraction

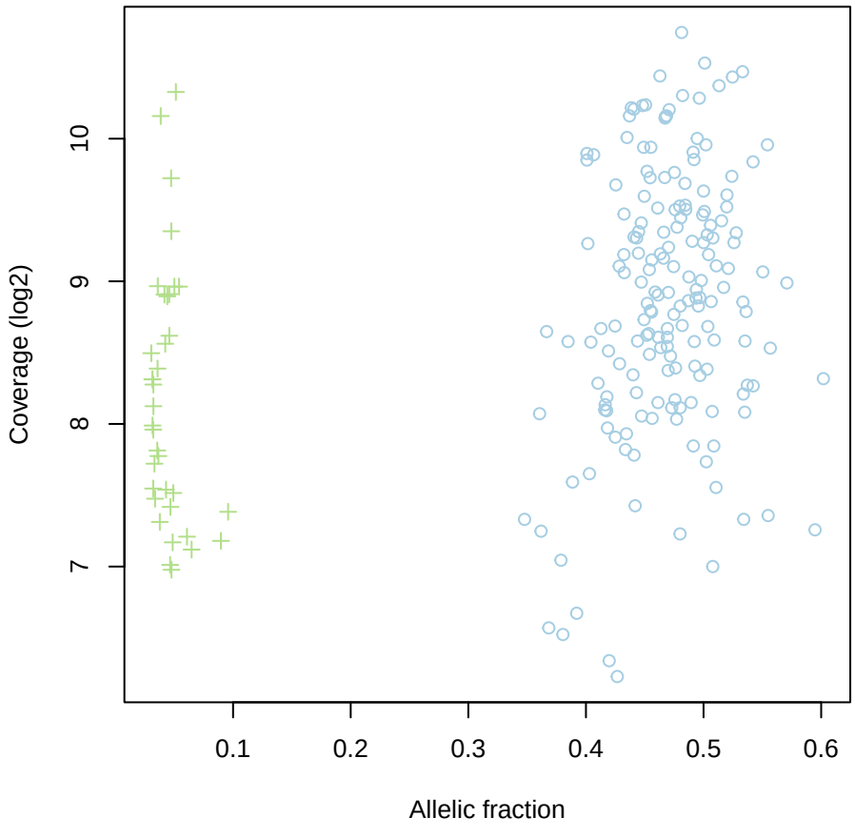

Purity: 0.19 Tumor ploidy: 1.504
0
1
2
3
4
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−0.4
−0.2
0.0
0.2
log2 ratio

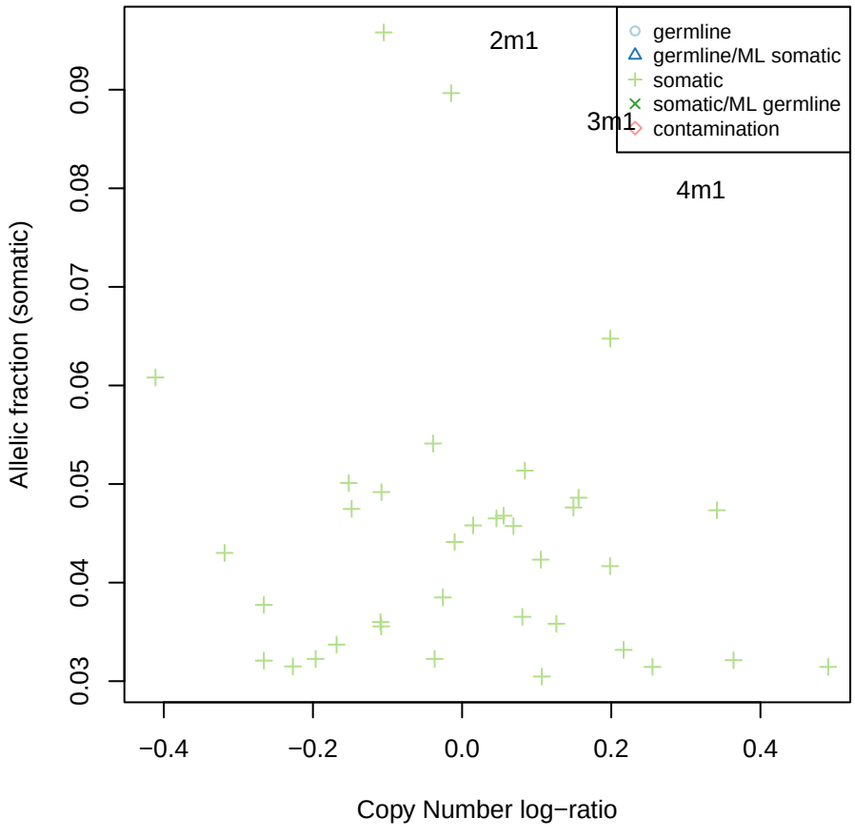

Purity: 0.19 Tumor ploidy: 1.504 SNV log−likelihood: −20.55 GoF: 95.2% Mean coverage: 508;525
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

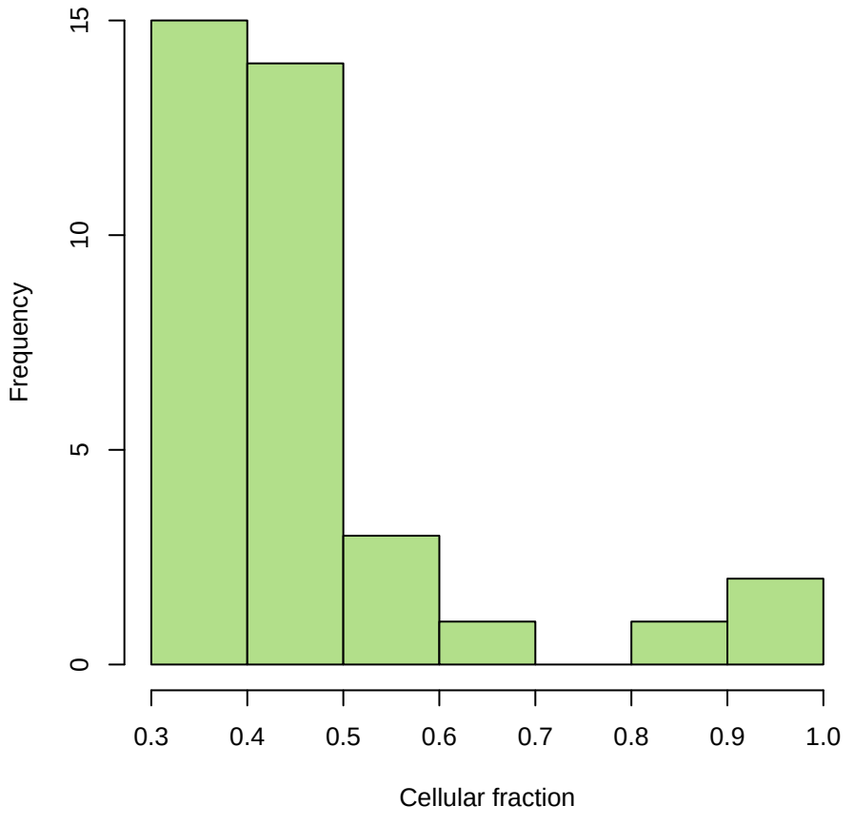

SCNA−fit log−likelihood: −4002.33
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 4
0 50 100 150
SNV Index

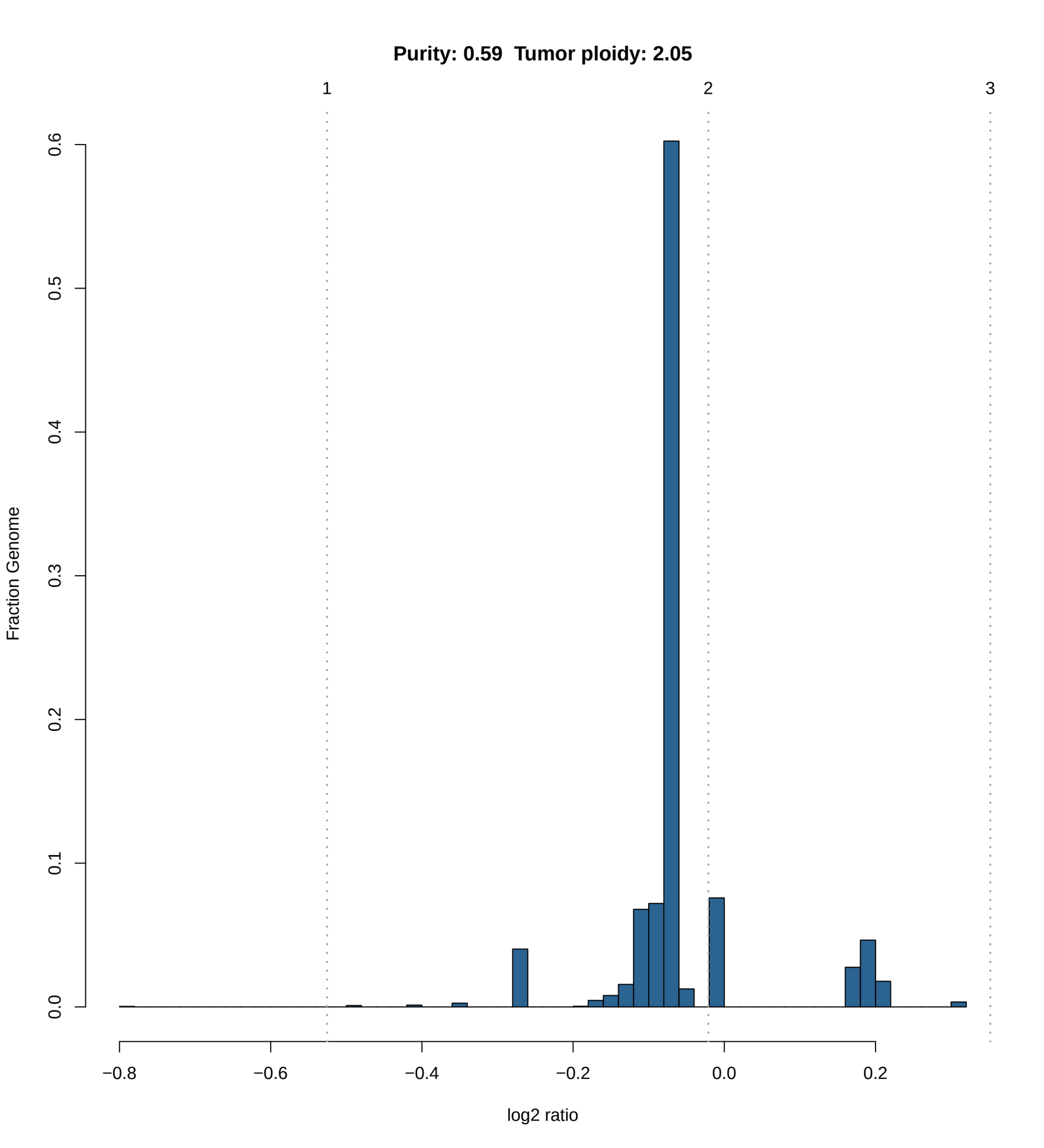

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

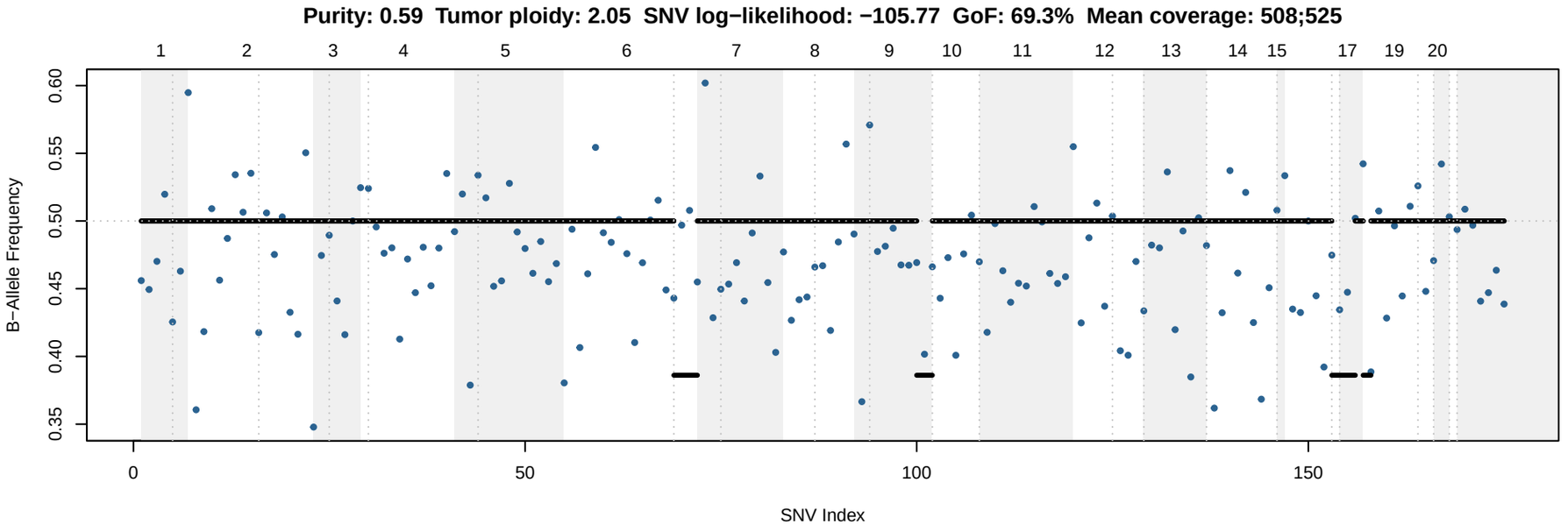

Allelic fraction (germline)
Copy Number log−ratio
2m2
1m1
3m2
2m1
4m2
3m1
1m0
4m1
2m0

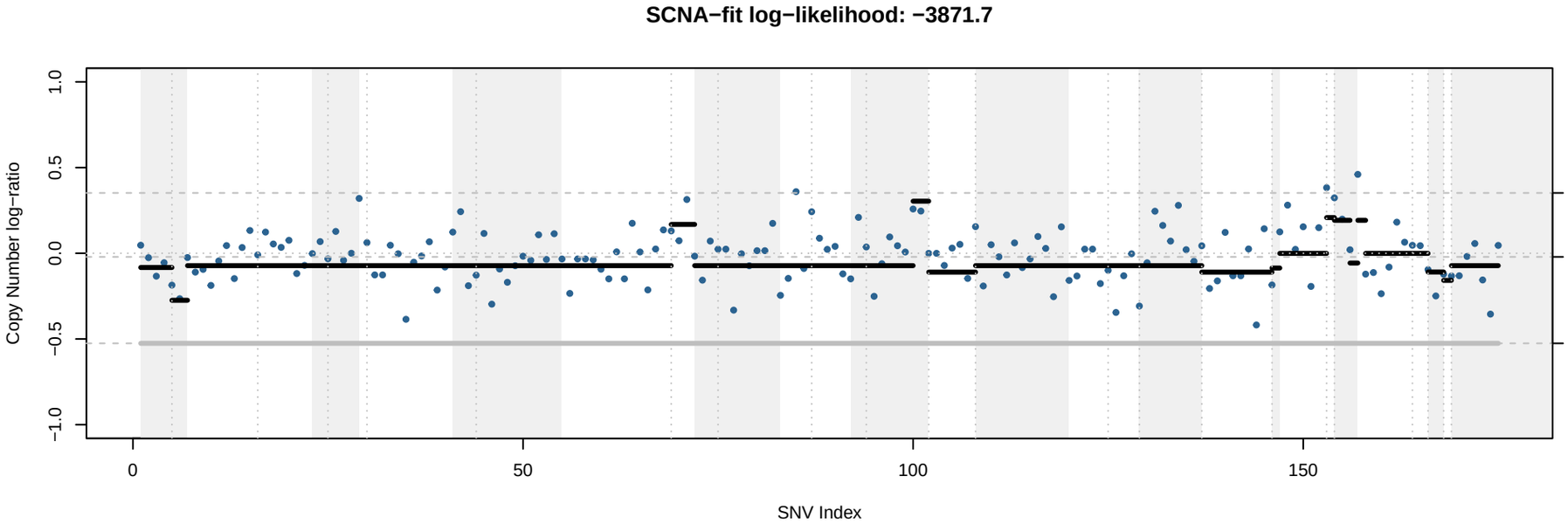

Coverage (log2)
Allelic fraction

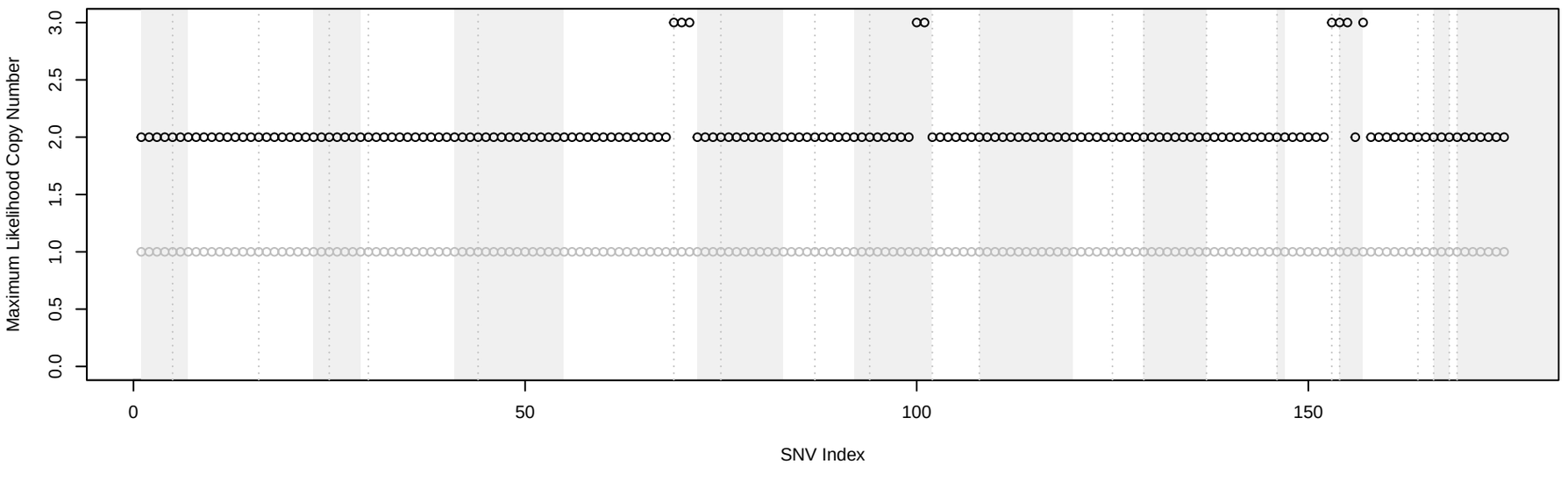

Allelic fraction (somatic)
Copy Number log−ratio
2m1
3m1
4m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

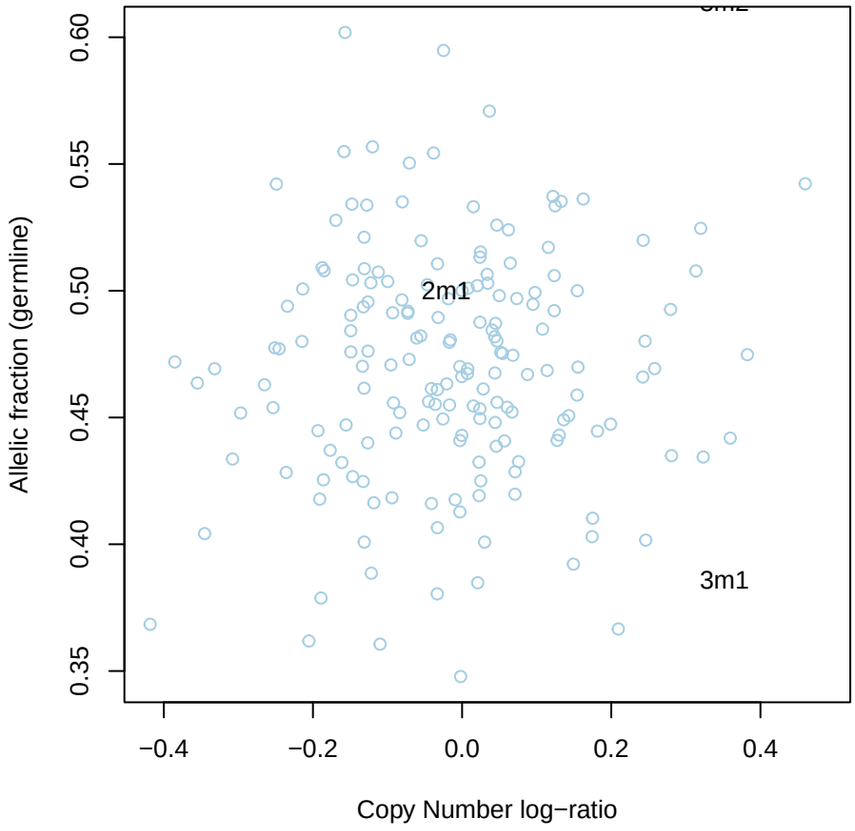

Frequency
Cellular fraction

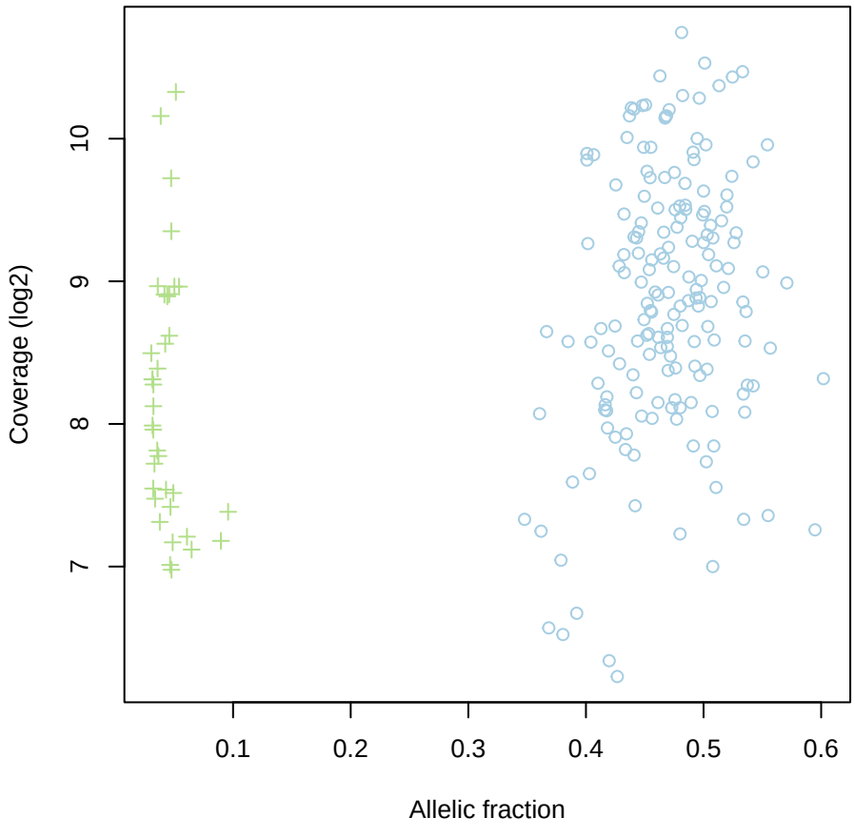

Purity: 0.59 Tumor ploidy: 2.05
1
2
3
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

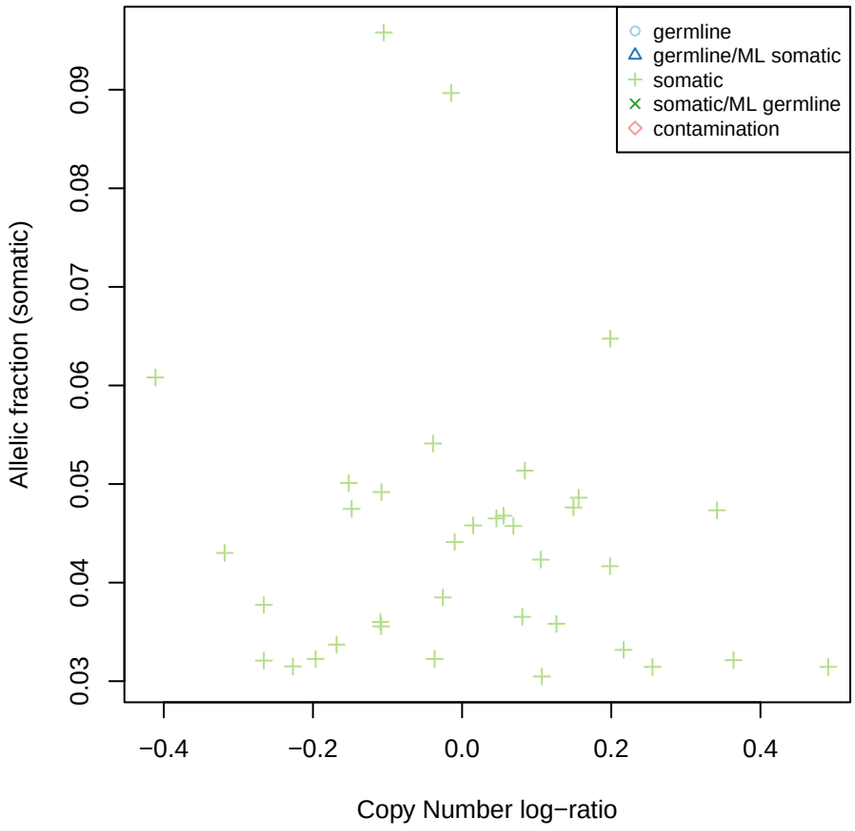

Purity: 0.59 Tumor ploidy: 2.05 SNV log−likelihood: −105.77 GoF: 69.3% Mean coverage: 508;525
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

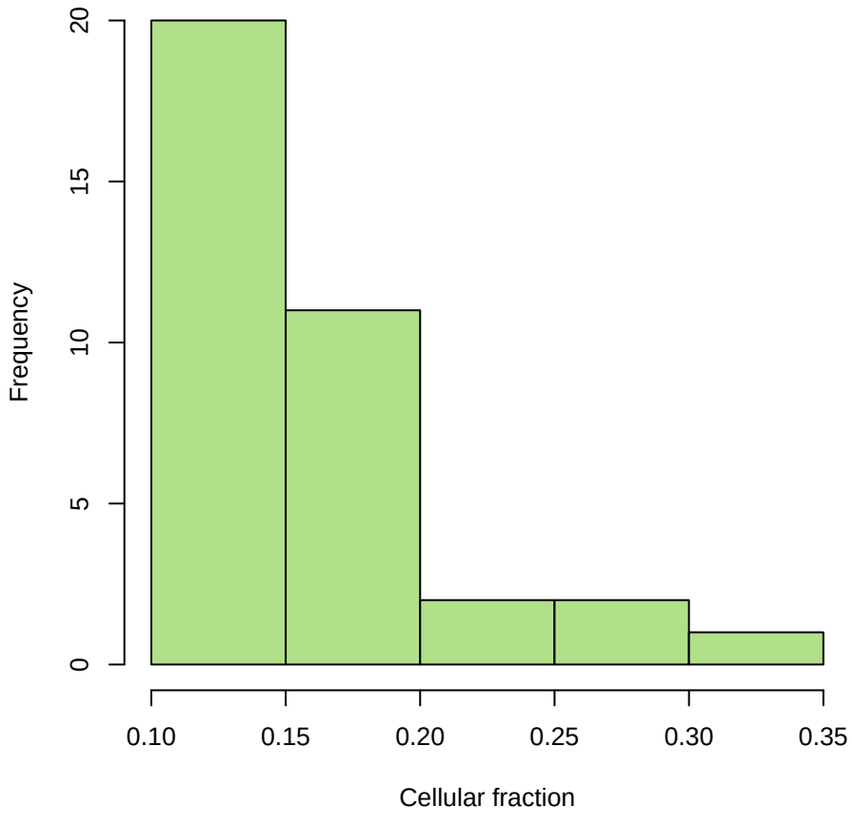

SCNA−fit log−likelihood: −3871.7
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3
0 50 100 150
SNV Index

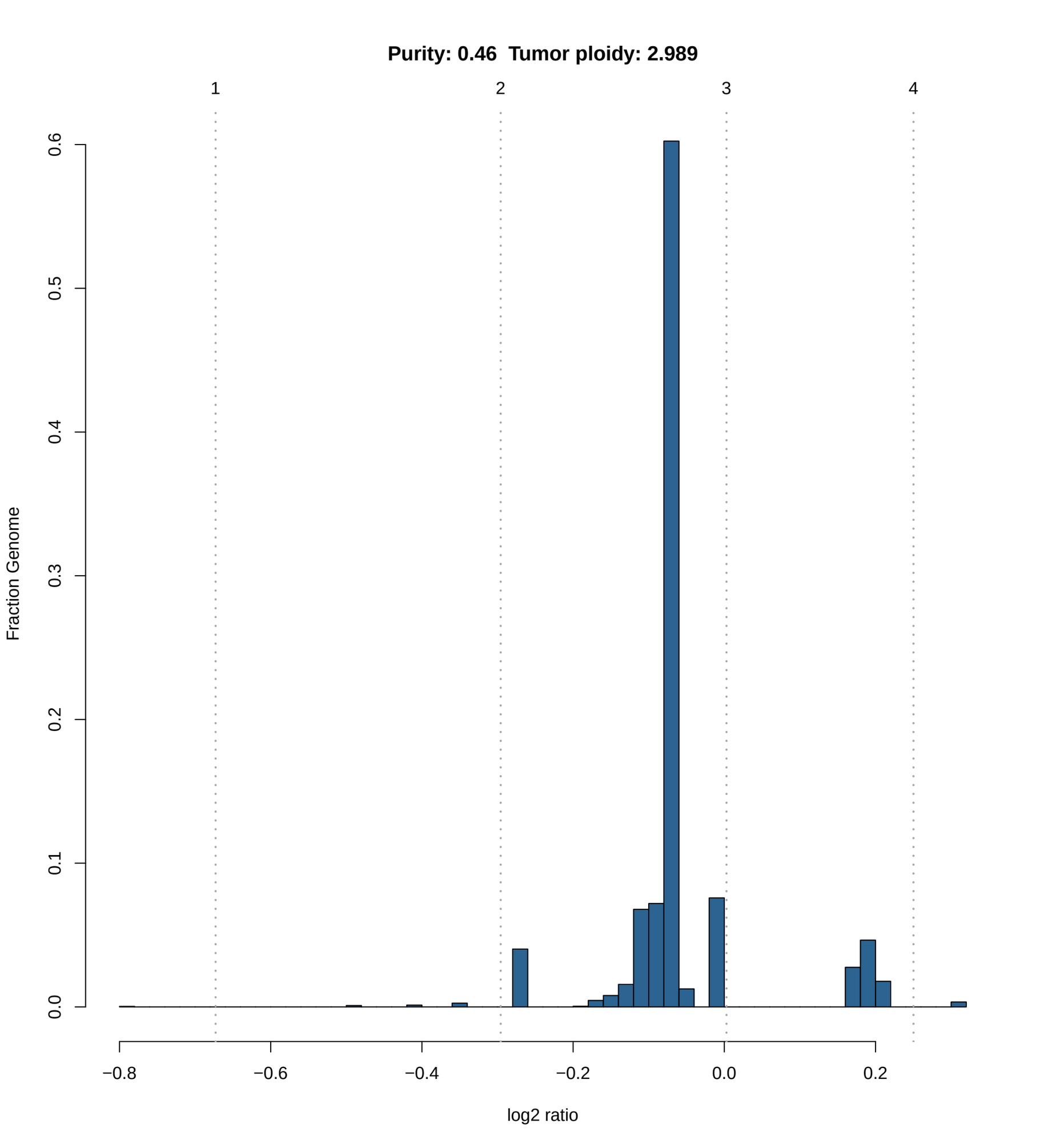

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

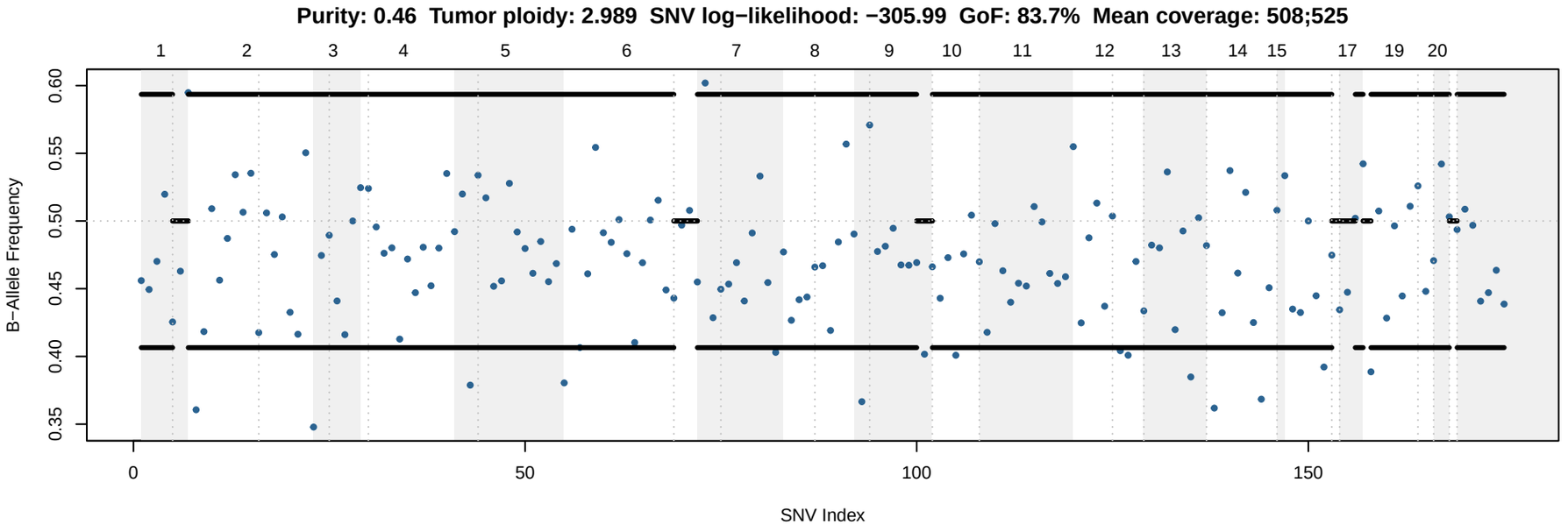

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
2m1
3m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

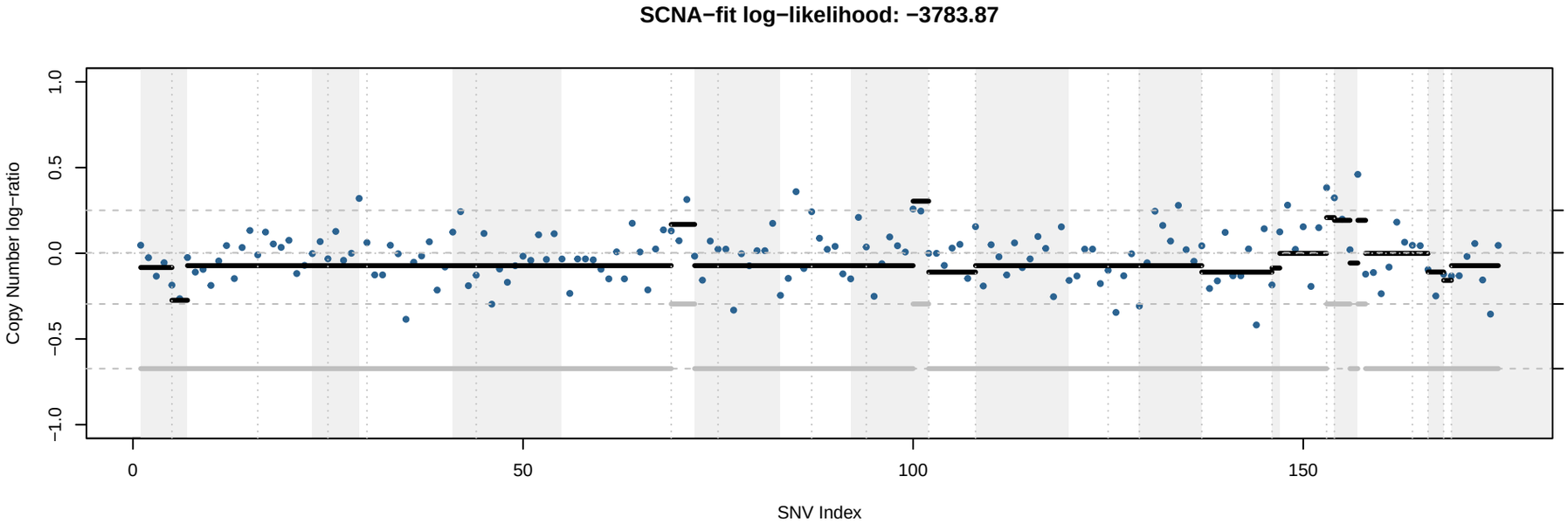

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

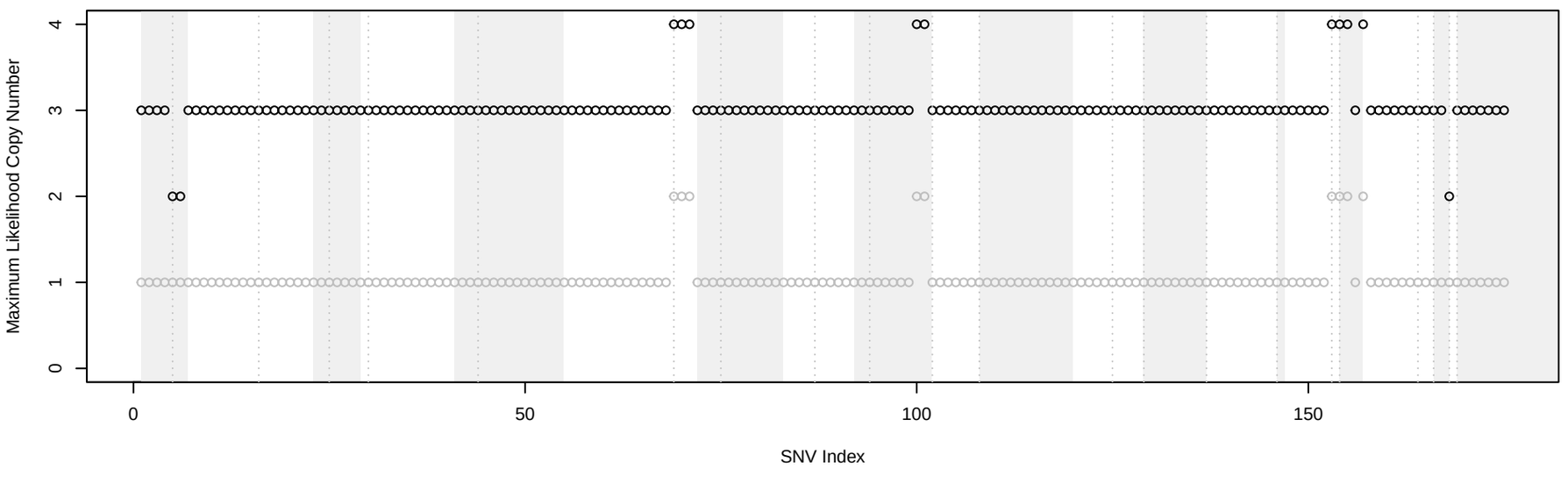

Allelic fraction (somatic)
0.03
0.04
0.05
0.06
0.07
0.08
0.09
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

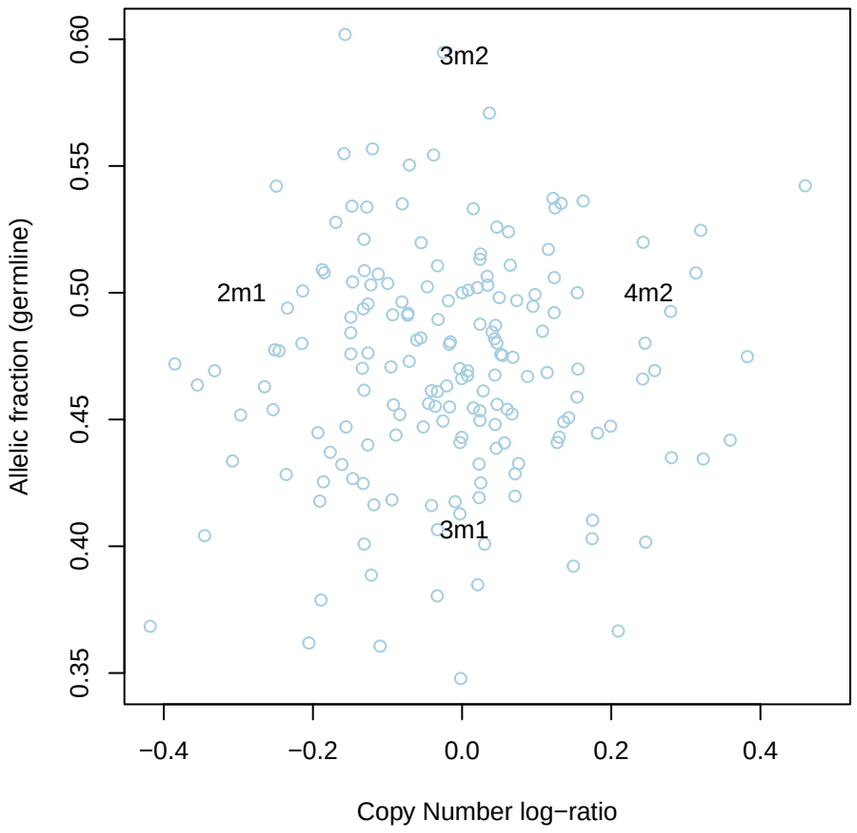

Frequency
0
5
10
15
20
0.10
0.15
0.20
0.25
0.30
0.35
Cellular fraction

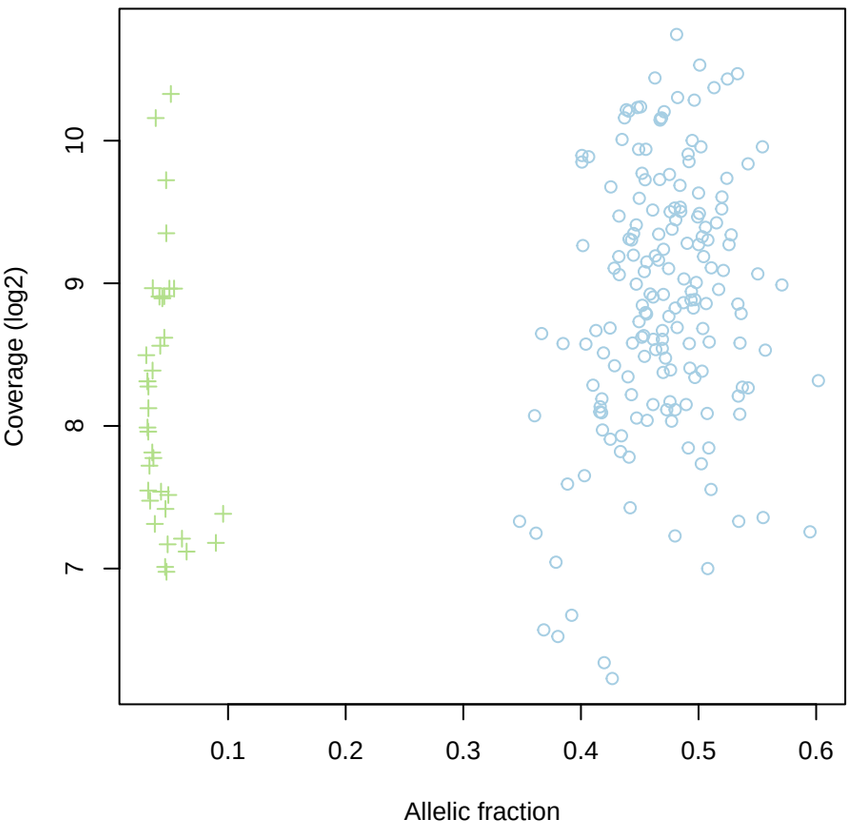

Purity: 0.46 Tumor ploidy: 2.989
1
2
3
4
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

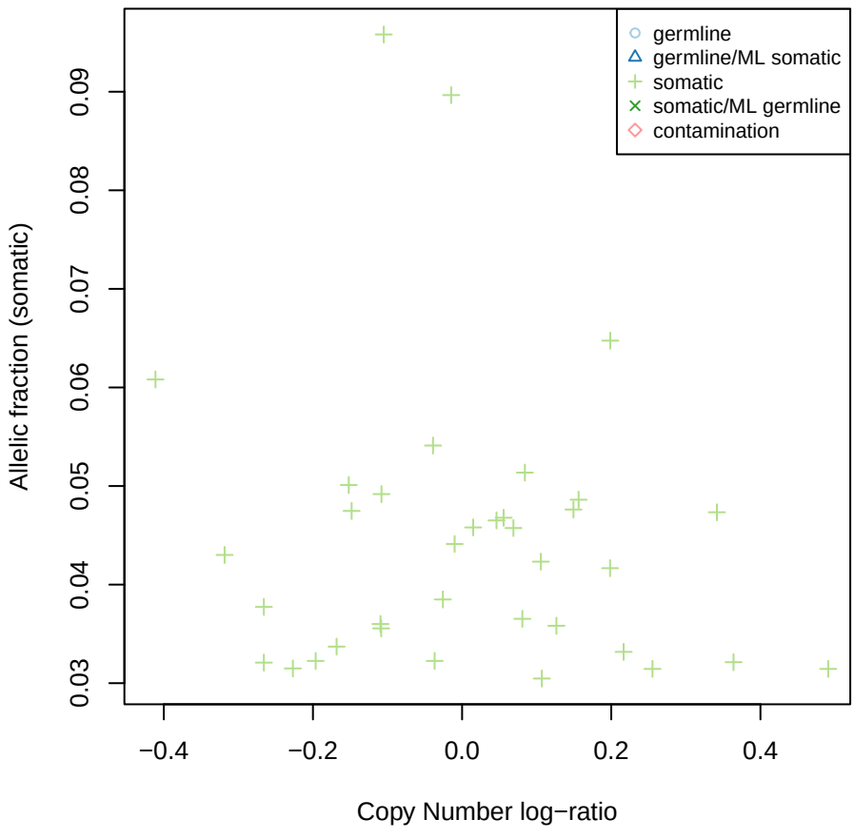

Purity: 0.46 Tumor ploidy: 2.989 SNV log−likelihood: −305.99 GoF: 83.7% Mean coverage: 508;525
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

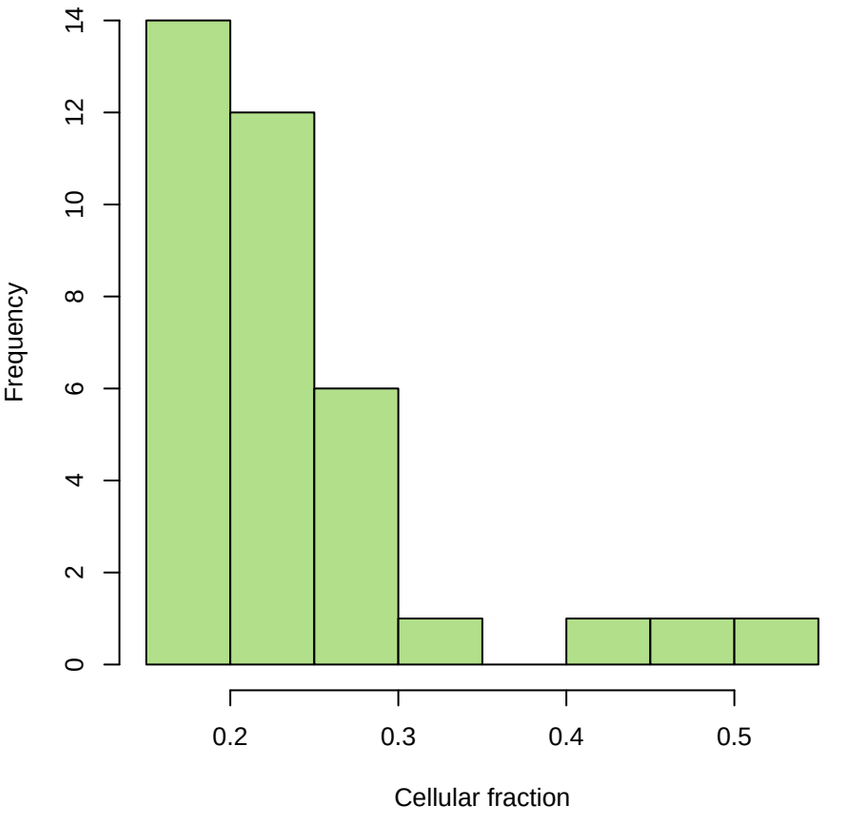

SCNA−fit log−likelihood: −3783.87
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4
0 50 100 150
SNV Index

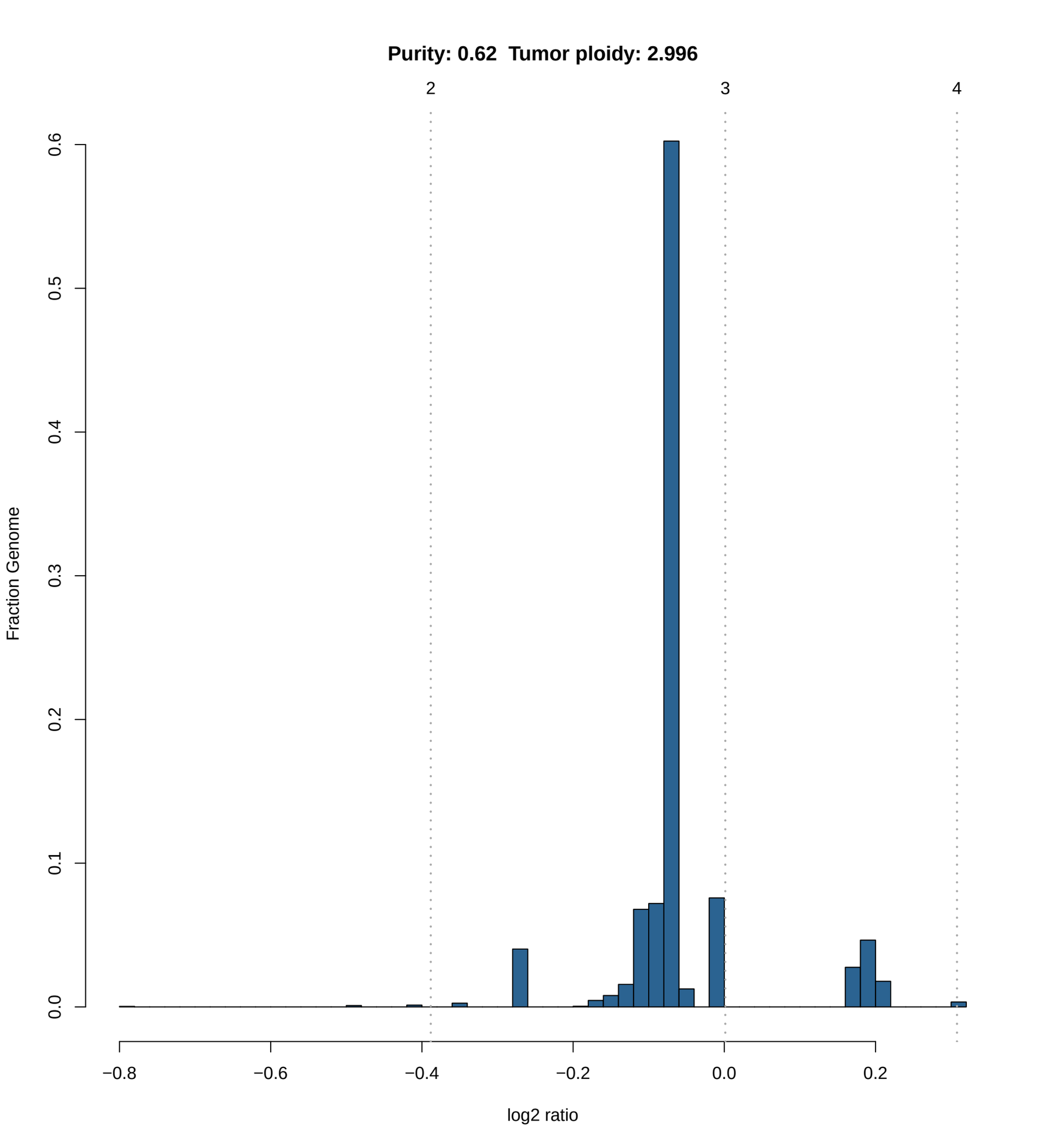

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

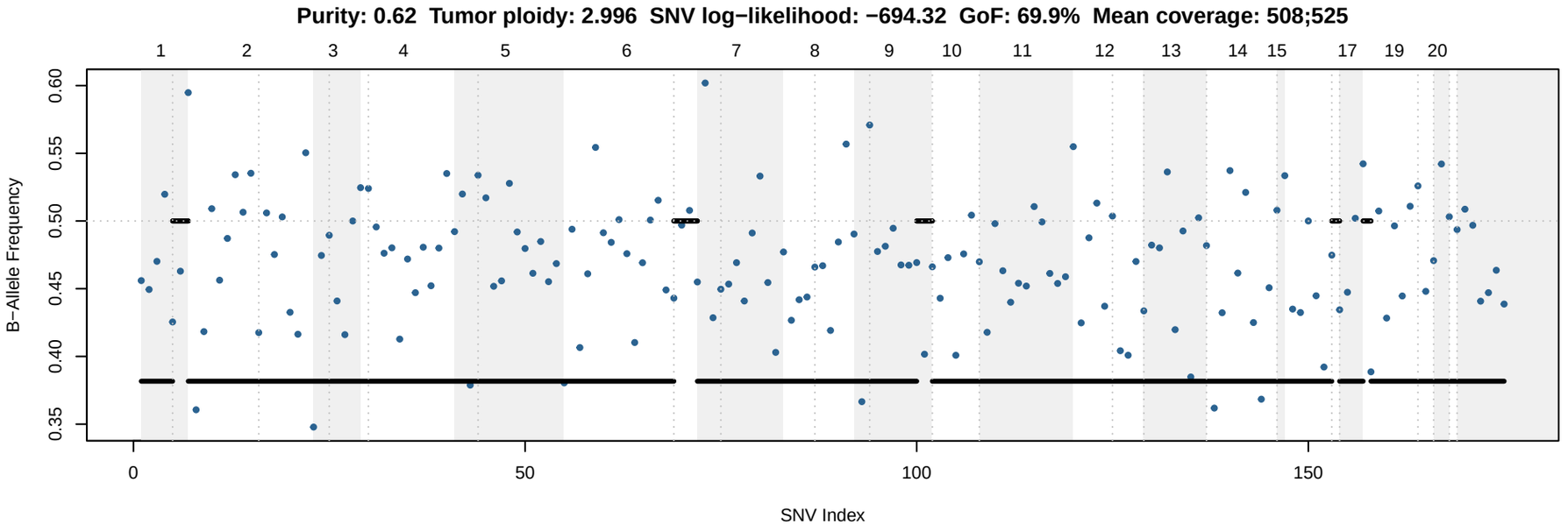

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
3m2
2m1
4m2
3m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

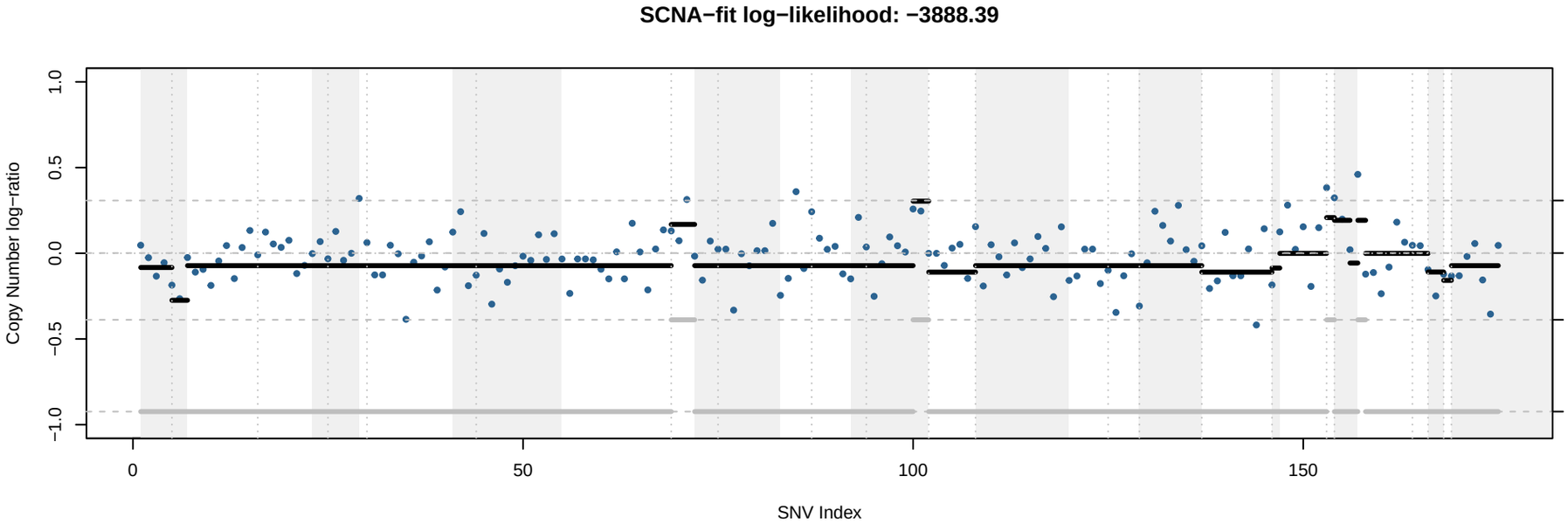

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

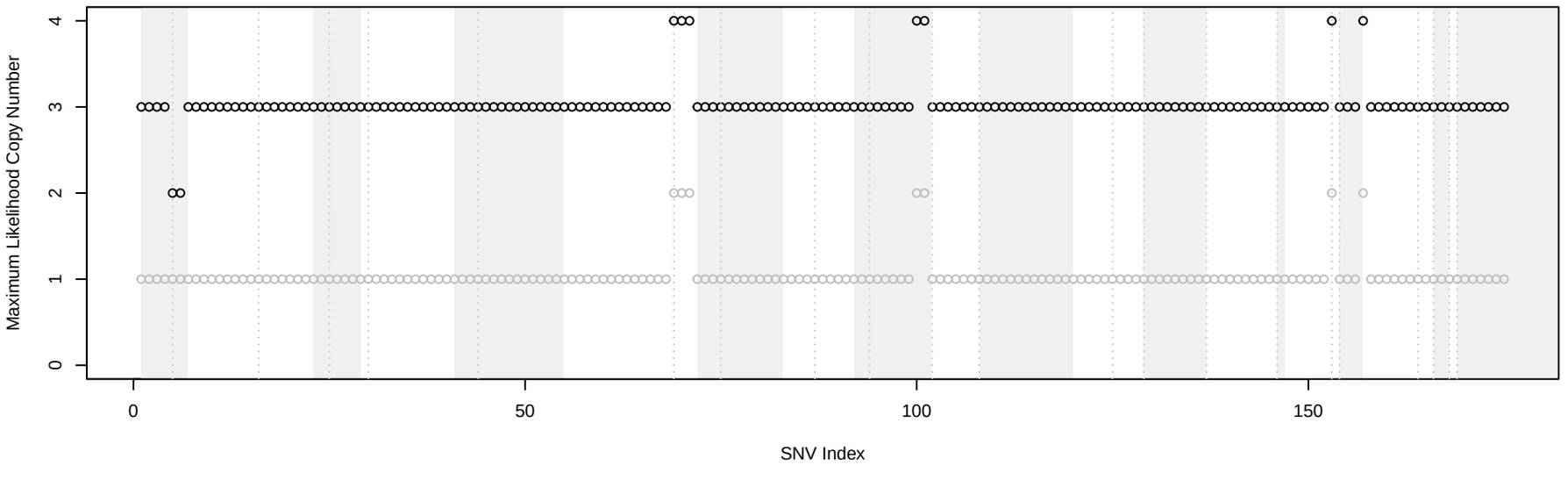

Allelic fraction (somatic)
0.03
0.04
0.05
0.06
0.07
0.08
0.09
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

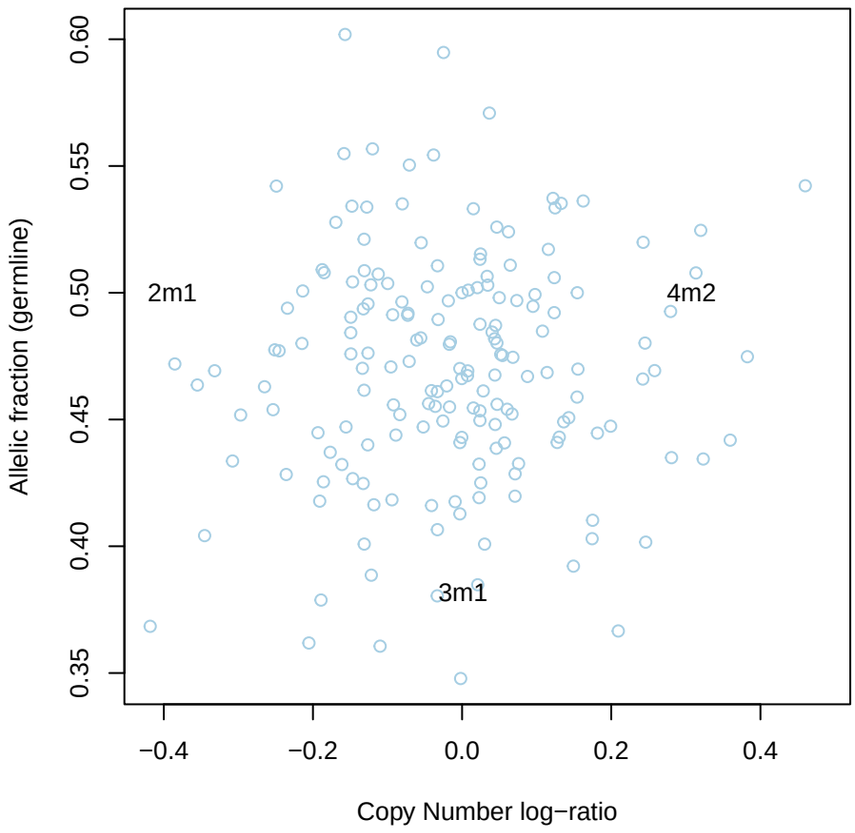

Frequency
0
2
4
6
8
10
12
14
0.2
0.3
0.4
0.5
Cellular fraction

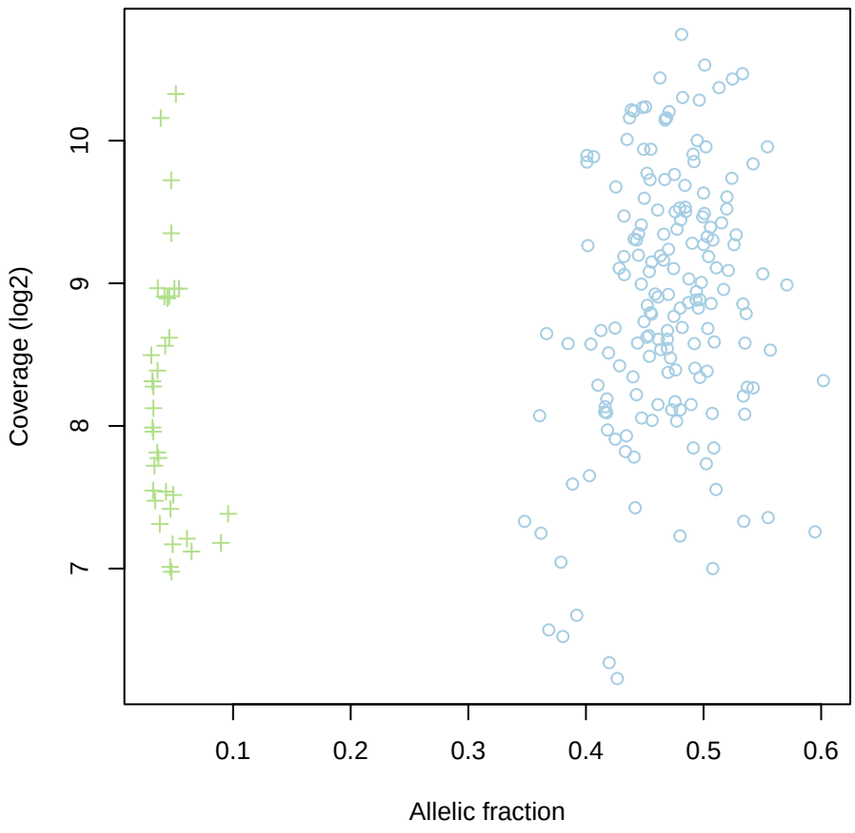

Purity: 0.62 Tumor ploidy: 2.996
2
3
4
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

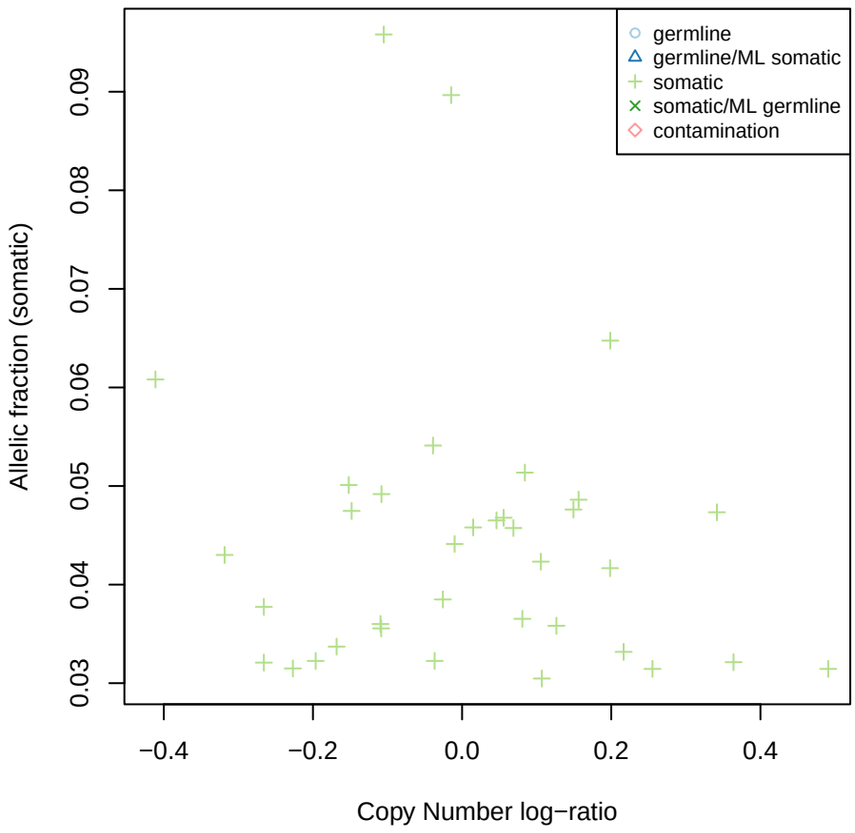

Purity: 0.62 Tumor ploidy: 2.996 SNV log−likelihood: −694.32 GoF: 69.9% Mean coverage: 508;525
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

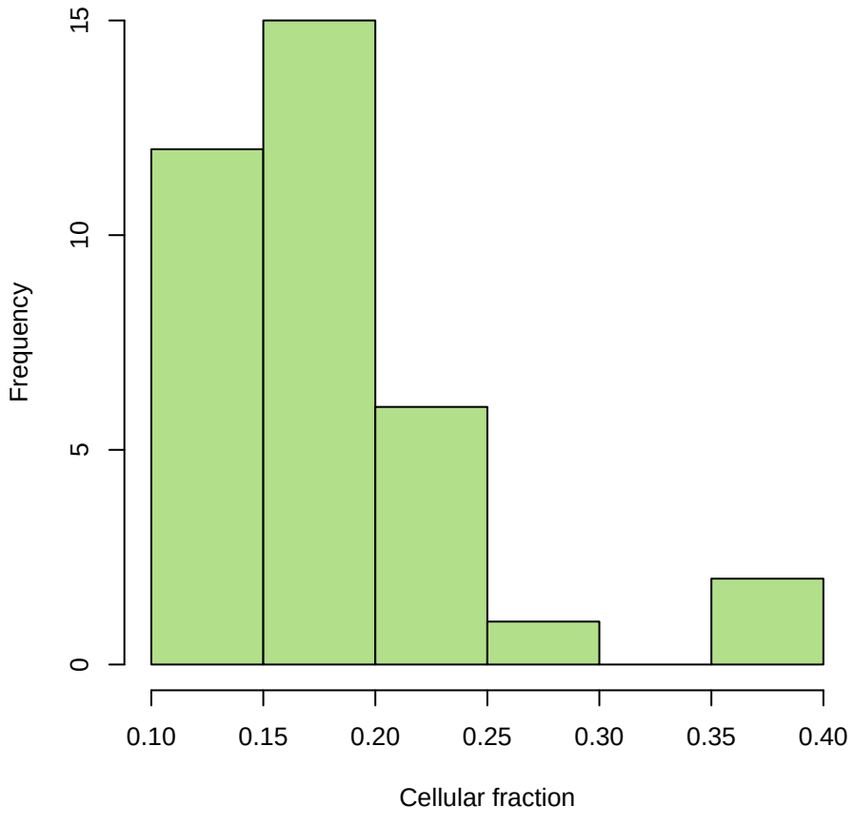

SCNA−fit log−likelihood: −3888.39
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4
0 50 100 150
SNV Index


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


Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
2m1
4m2
3m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio


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


Allelic fraction (somatic)
0.03
0.04
0.05
0.06
0.07
0.08
0.09
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio


Frequency
0
5
10
15
0.10
0.15
0.20
0.25
0.30
0.35
0.40
Cellular fraction