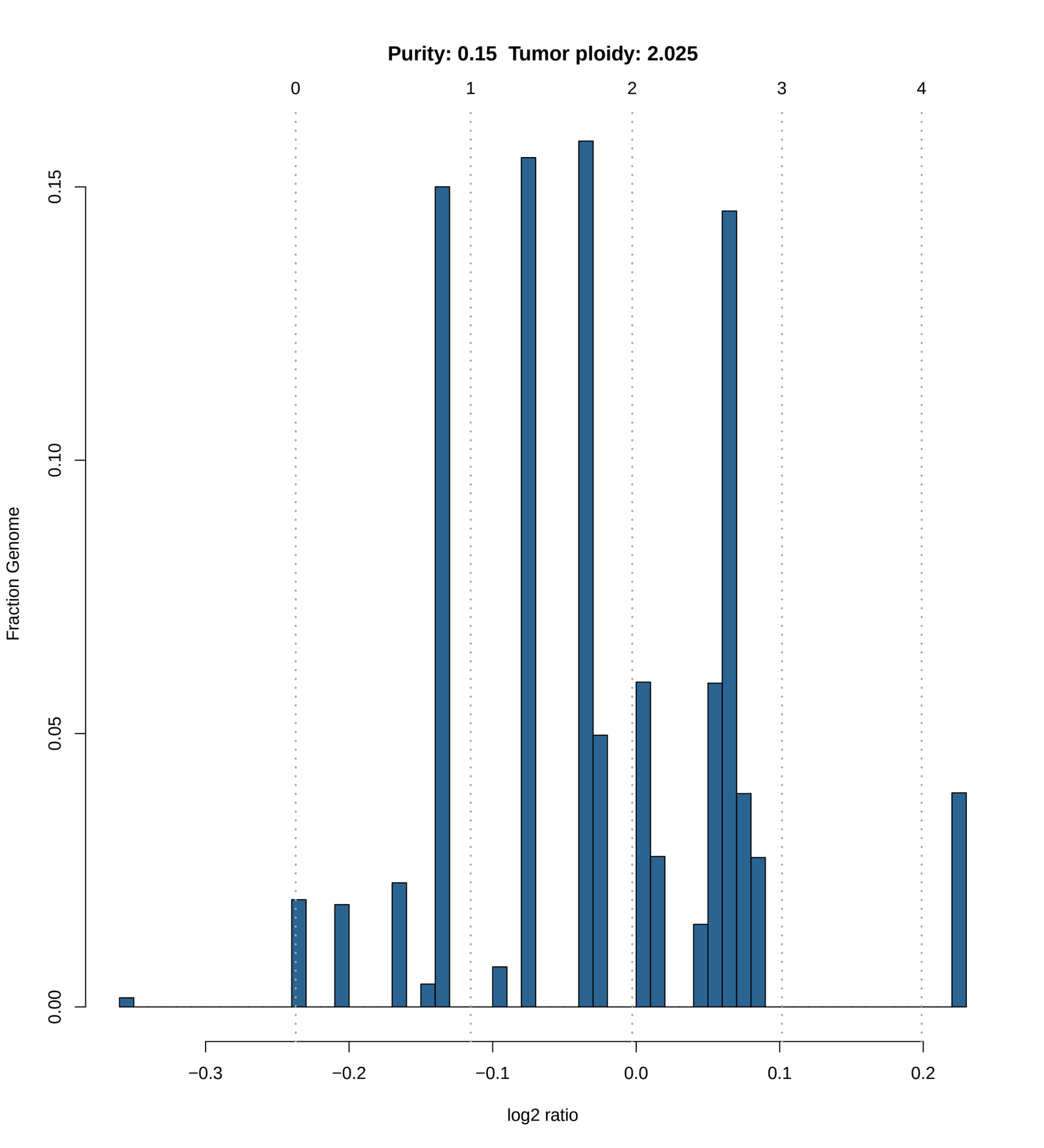
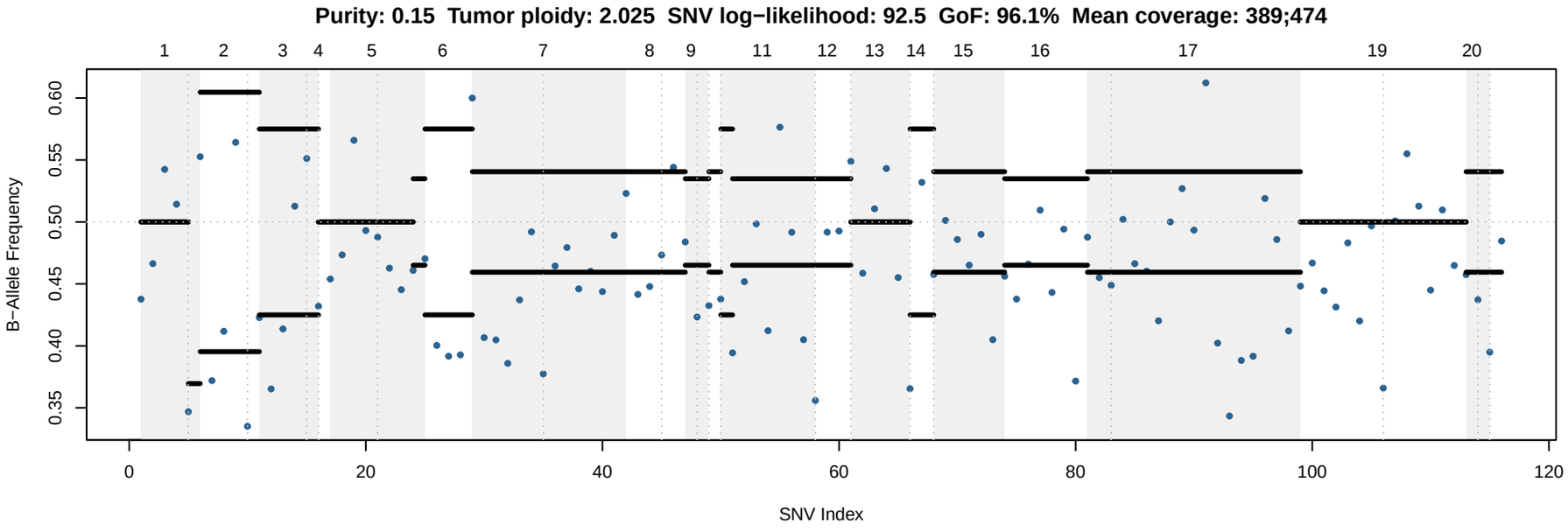
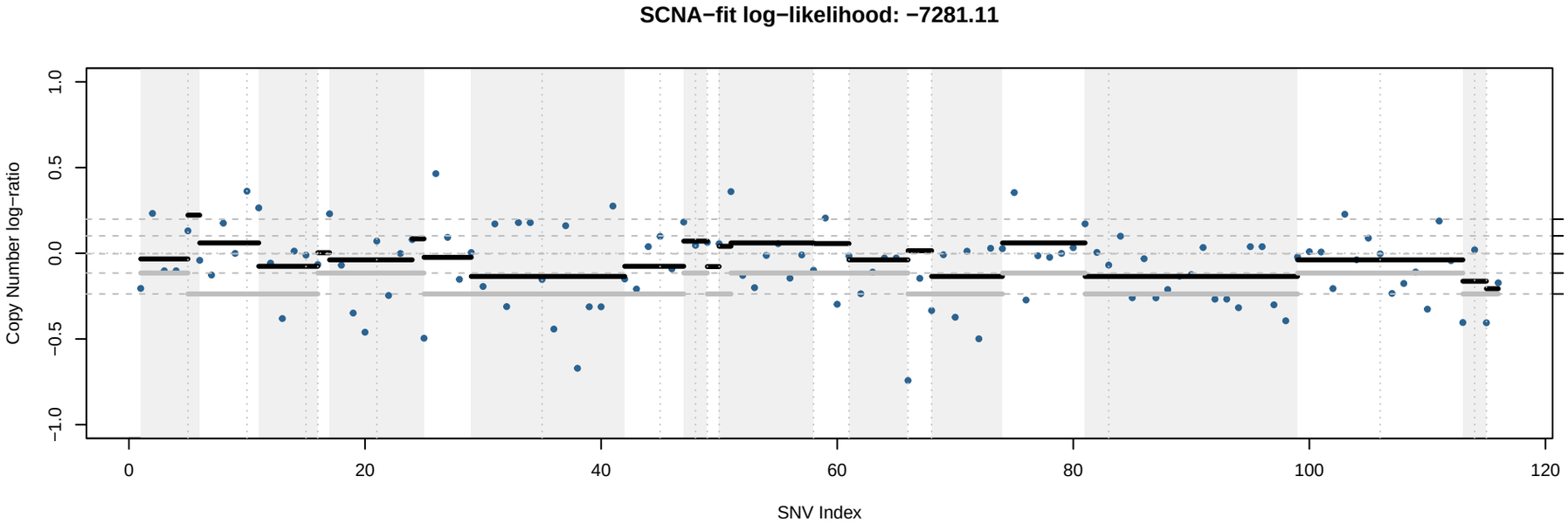
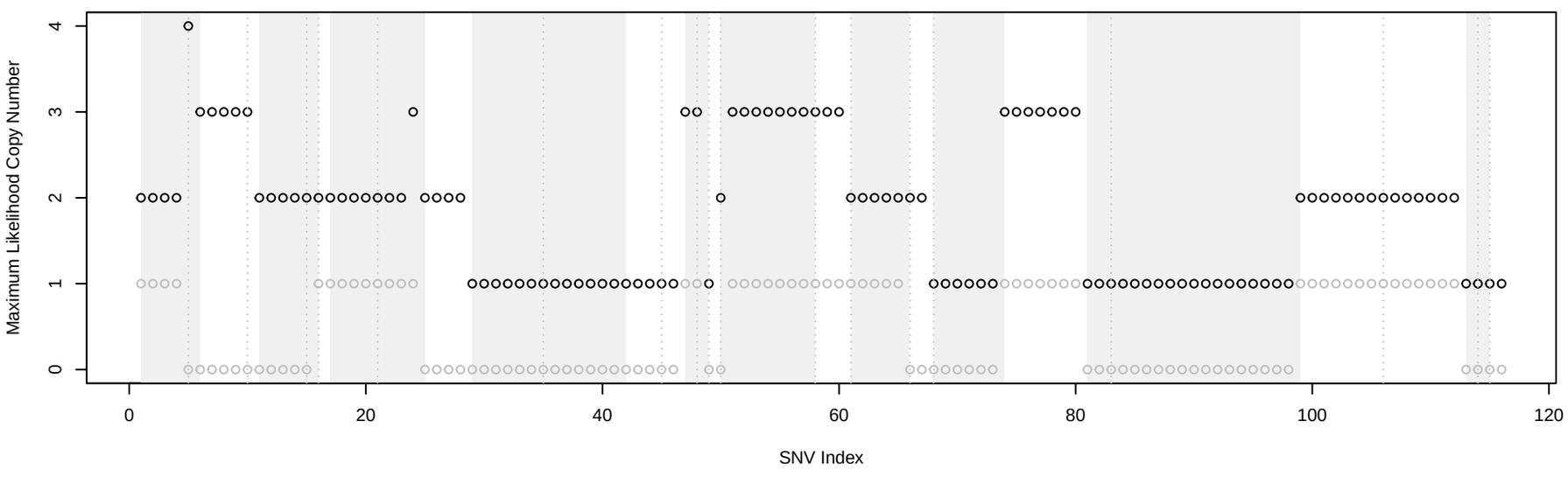
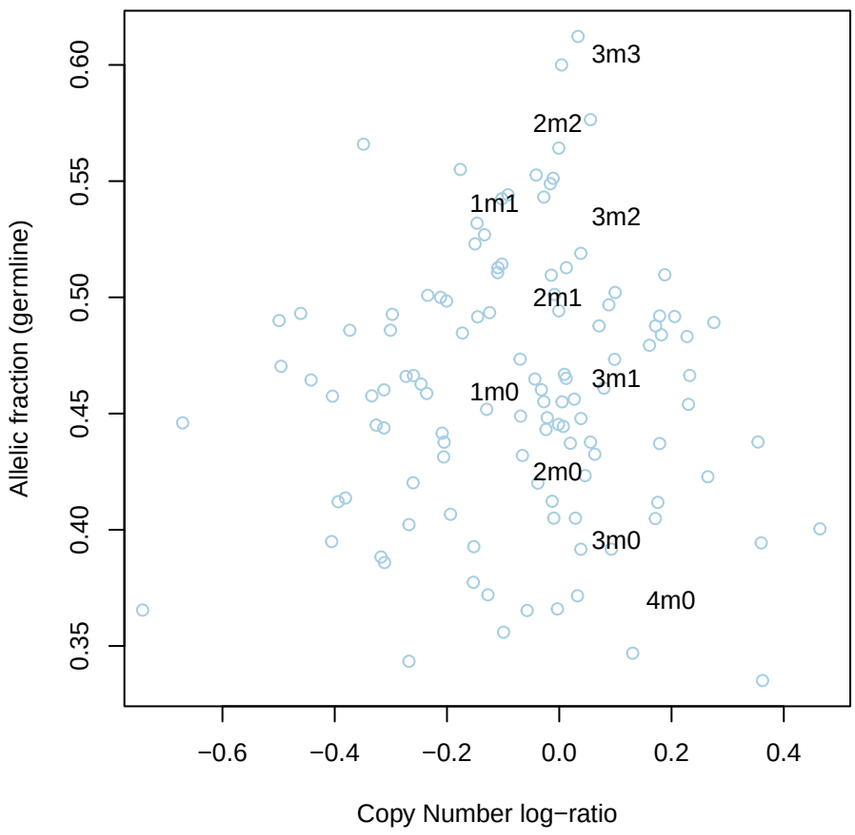
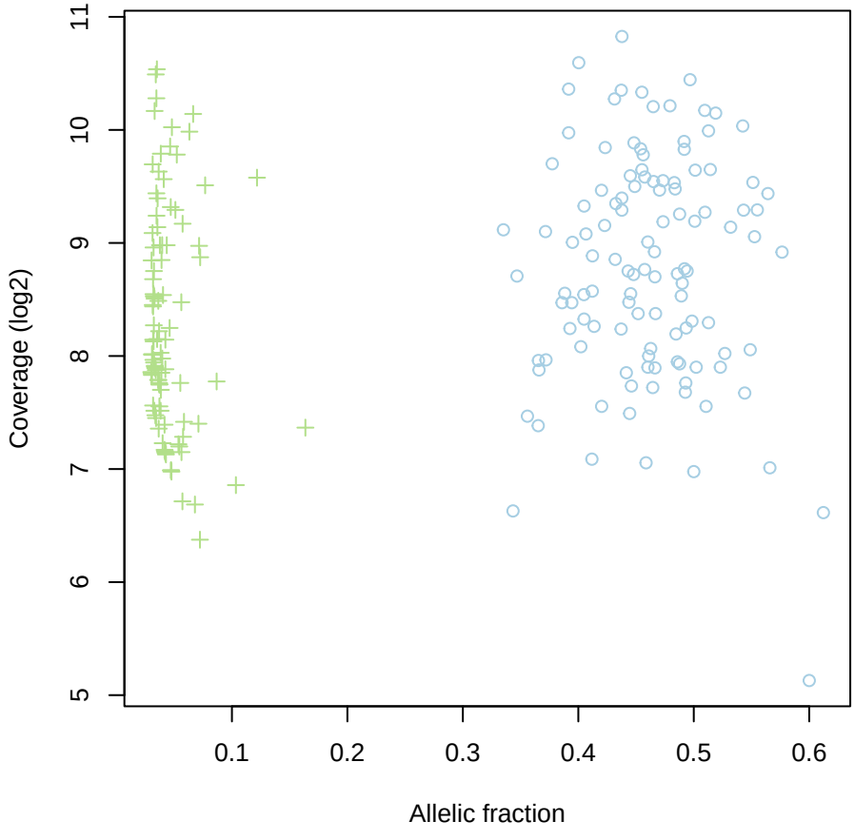

Purity: 0.15 Tumor ploidy: 2.025
0
1
2
3
4
0.15
0.10
0.05
0.00
Fraction Genome
−0.3
−0.2
−0.1
0.0
0.1
0.2
log2 ratio

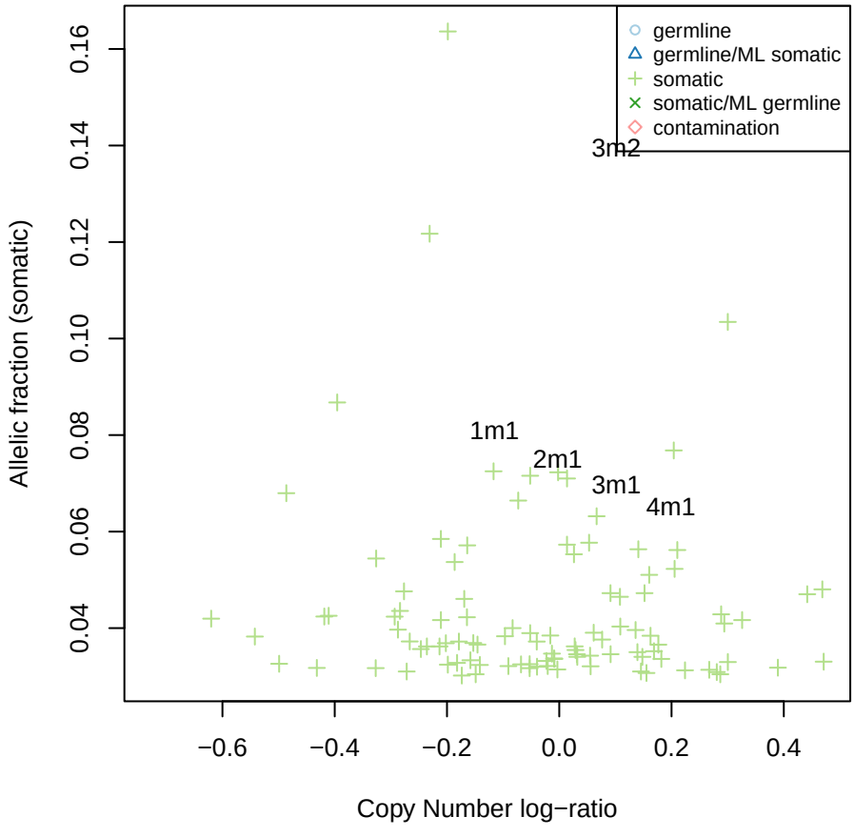

Purity: 0.15 Tumor ploidy: 2.025 SNV log−likelihood: 92.5 GoF: 96.1% Mean coverage: 389;474
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100 120
SNV Index

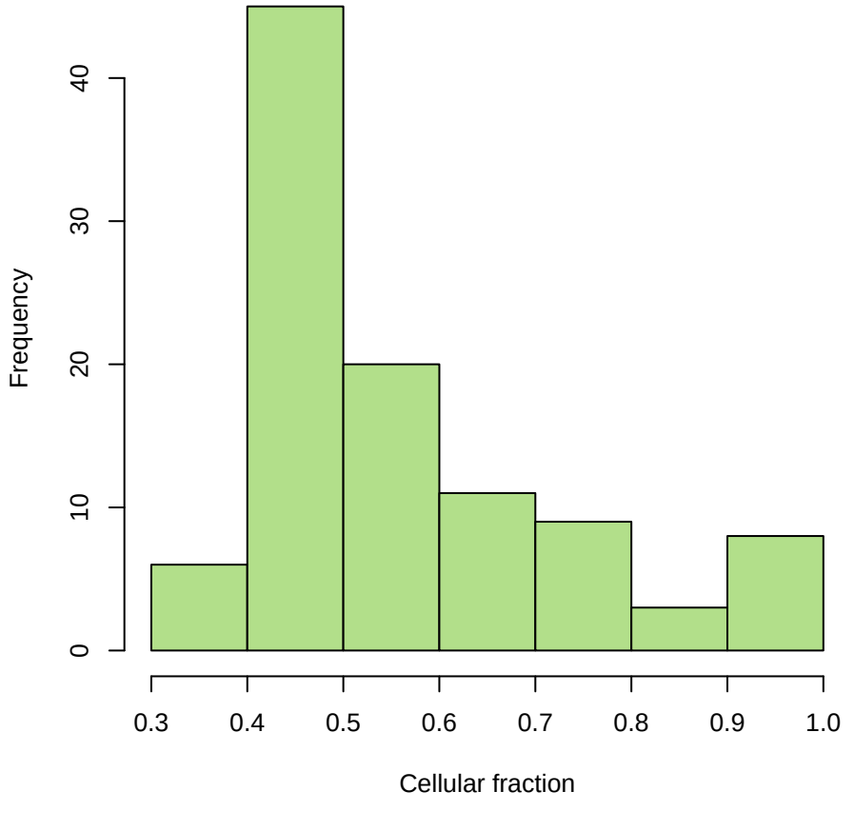

SCNA−fit log−likelihood: −7281.11
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4
0 20 40 60 80 100 120
SNV Index

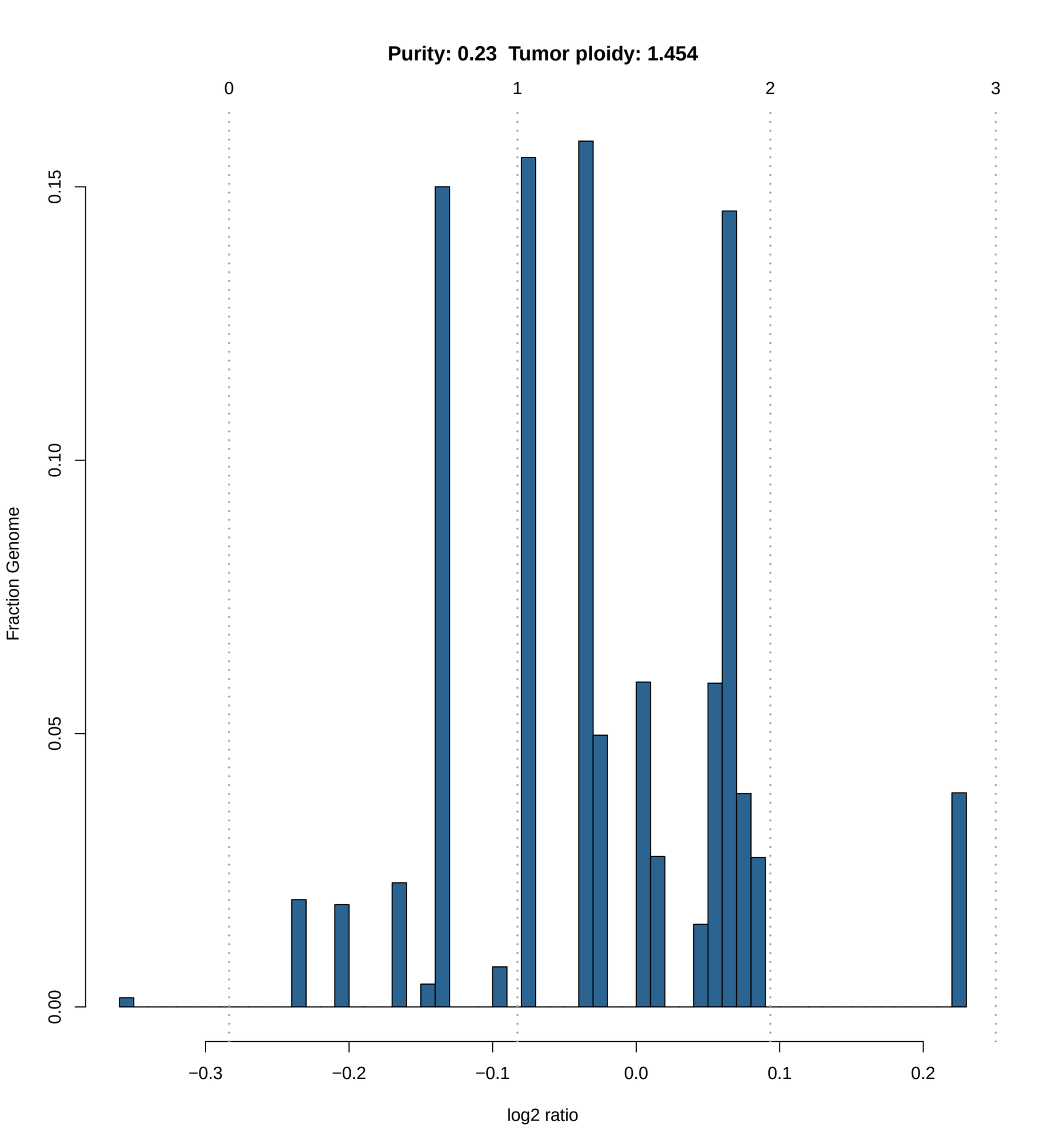

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120
SNV Index

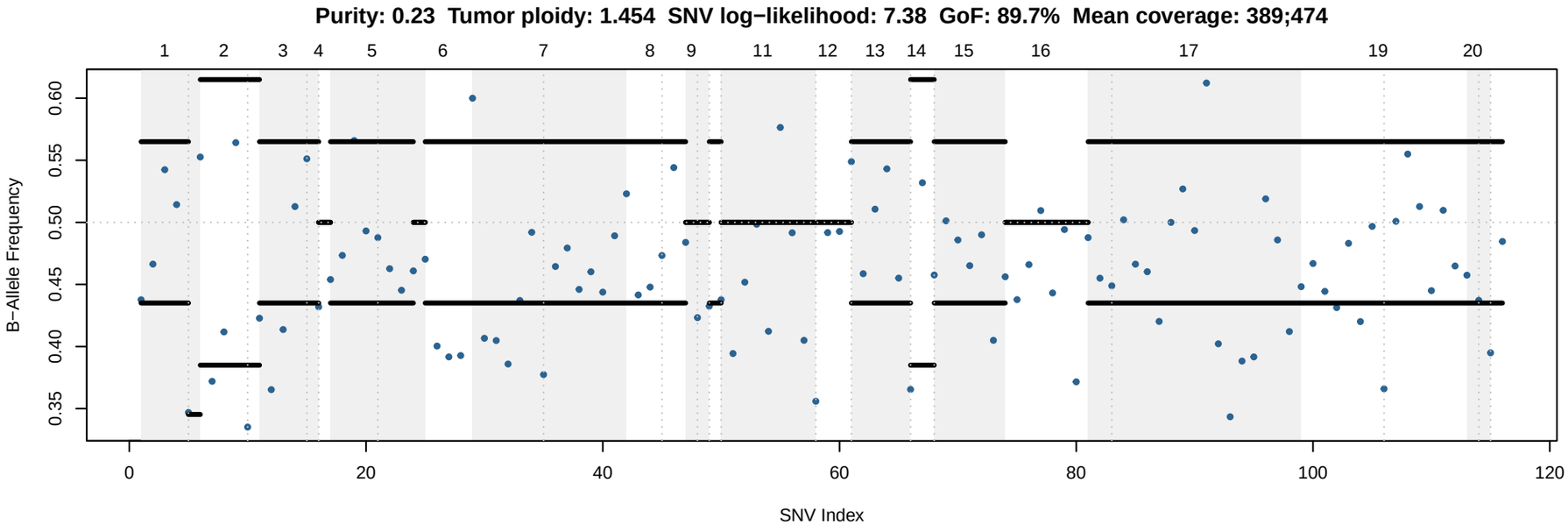

Allelic fraction (germline)
Copy Number log−ratio
3m3
2m2
1m1
3m2
2m1
3m1
1m0
2m0
3m0
4m0

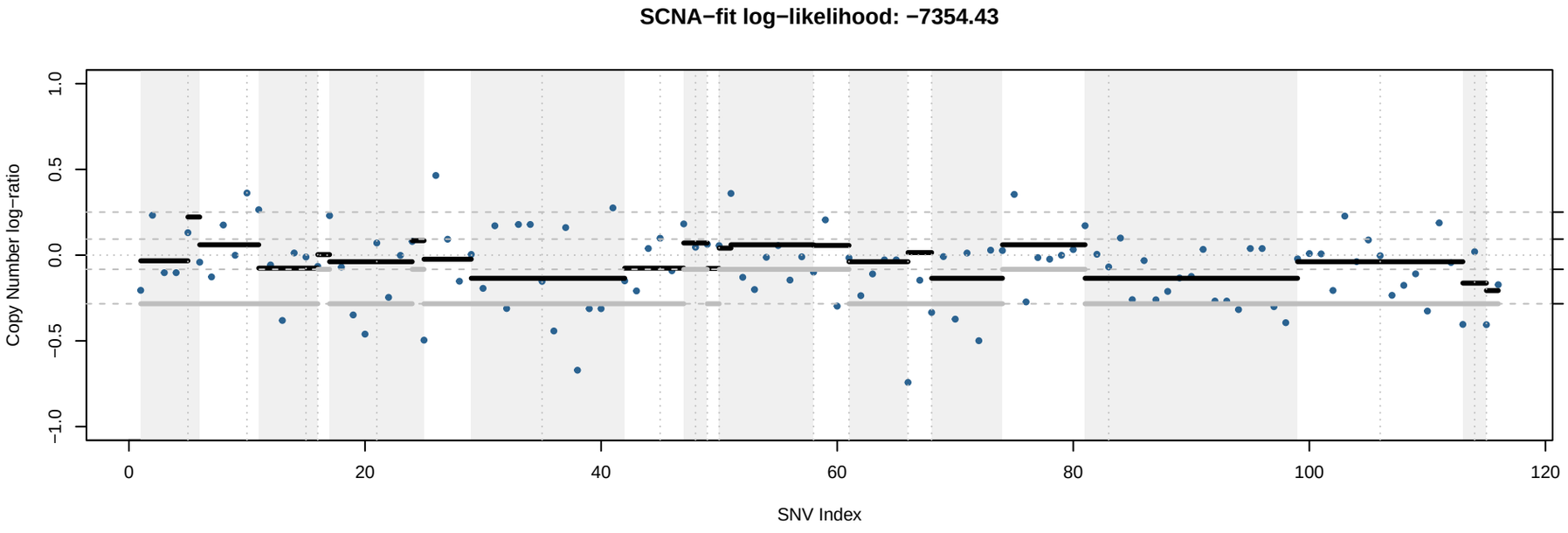

Coverage (log2)
Allelic fraction

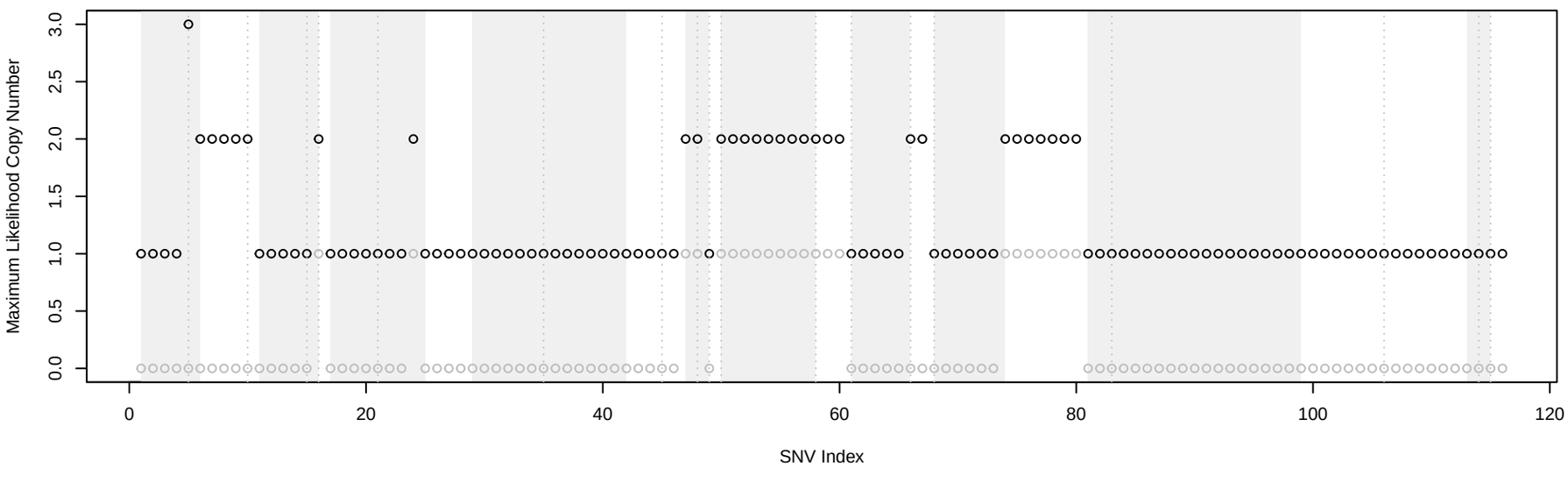

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m2
1m1
2m1
3m1
4m1

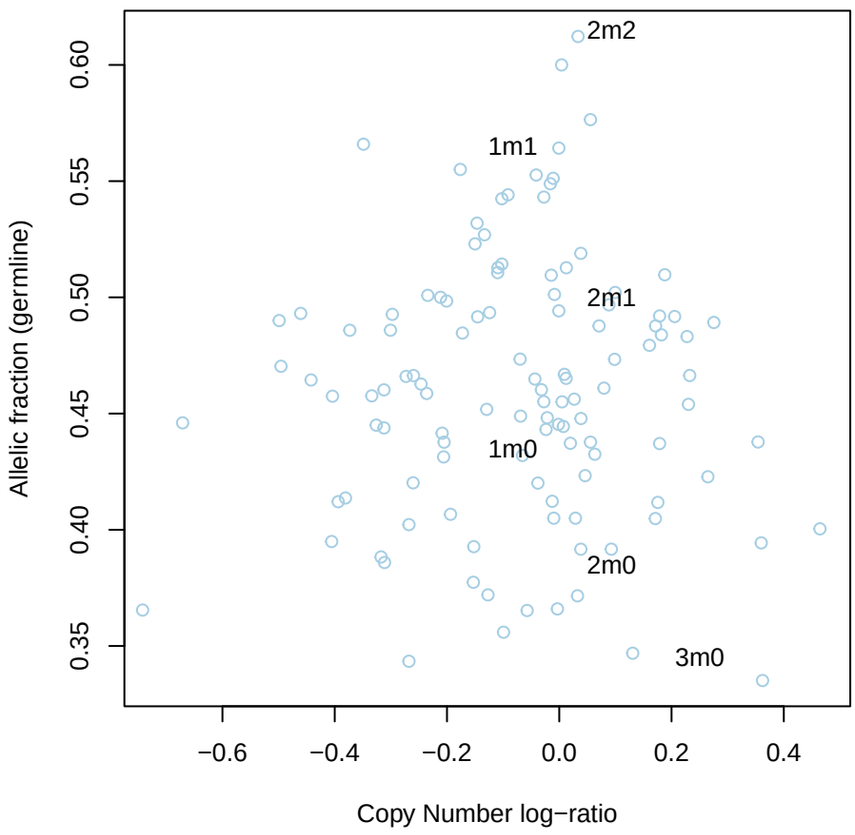

Frequency
Cellular fraction

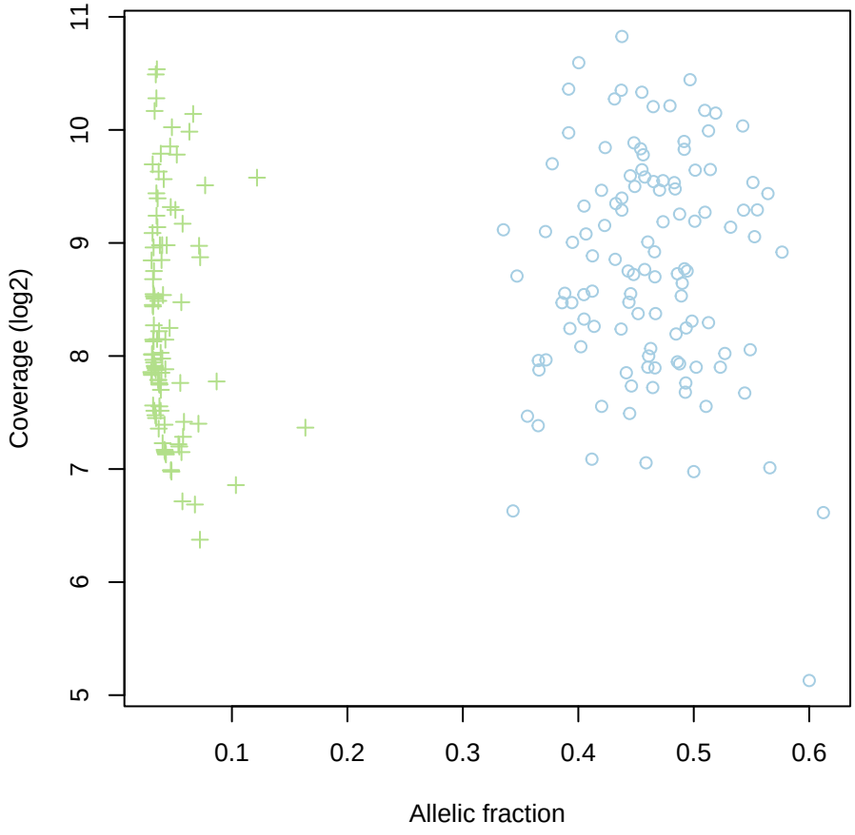

Purity: 0.23 Tumor ploidy: 1.454
0
1
2
3
0.15
0.10
0.05
0.00
Fraction Genome
−0.3
−0.2
−0.1
0.0
0.1
0.2
log2 ratio

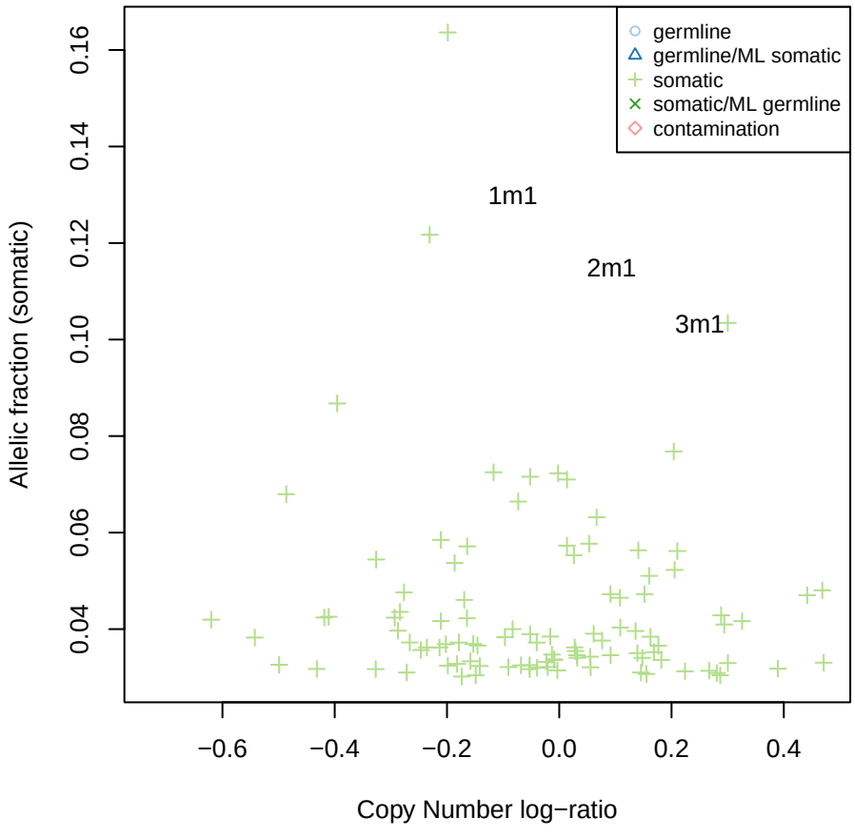

Purity: 0.23 Tumor ploidy: 1.454 SNV log−likelihood: 7.38 GoF: 89.7% Mean coverage: 389;474
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100 120
SNV Index

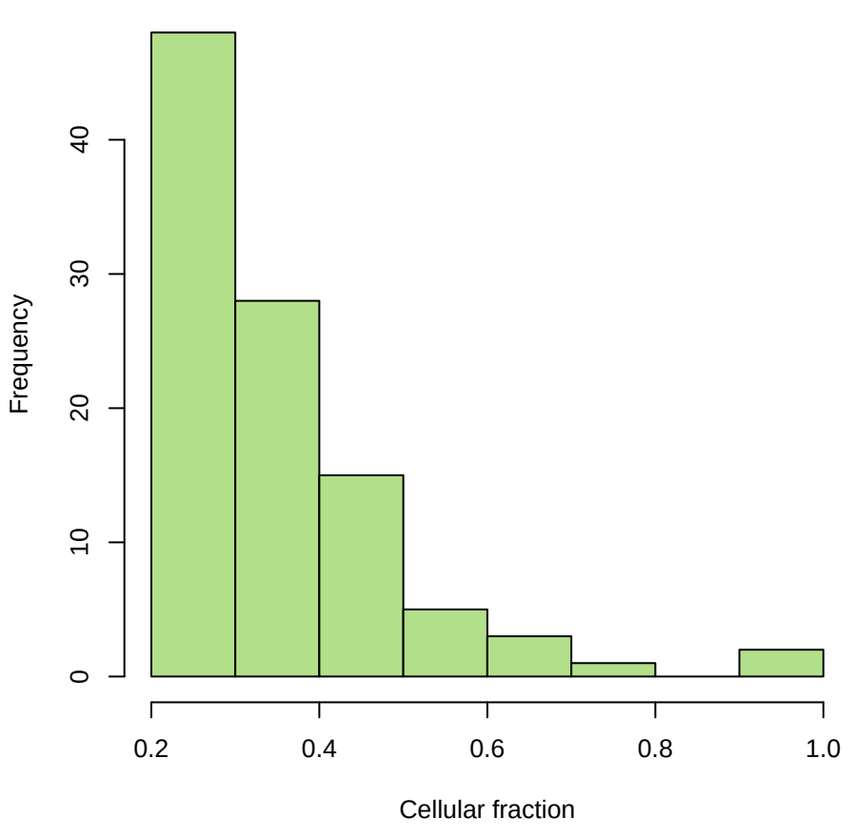

SCNA−fit log−likelihood: −7354.43
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3
0 20 40 60 80 100 120
SNV Index

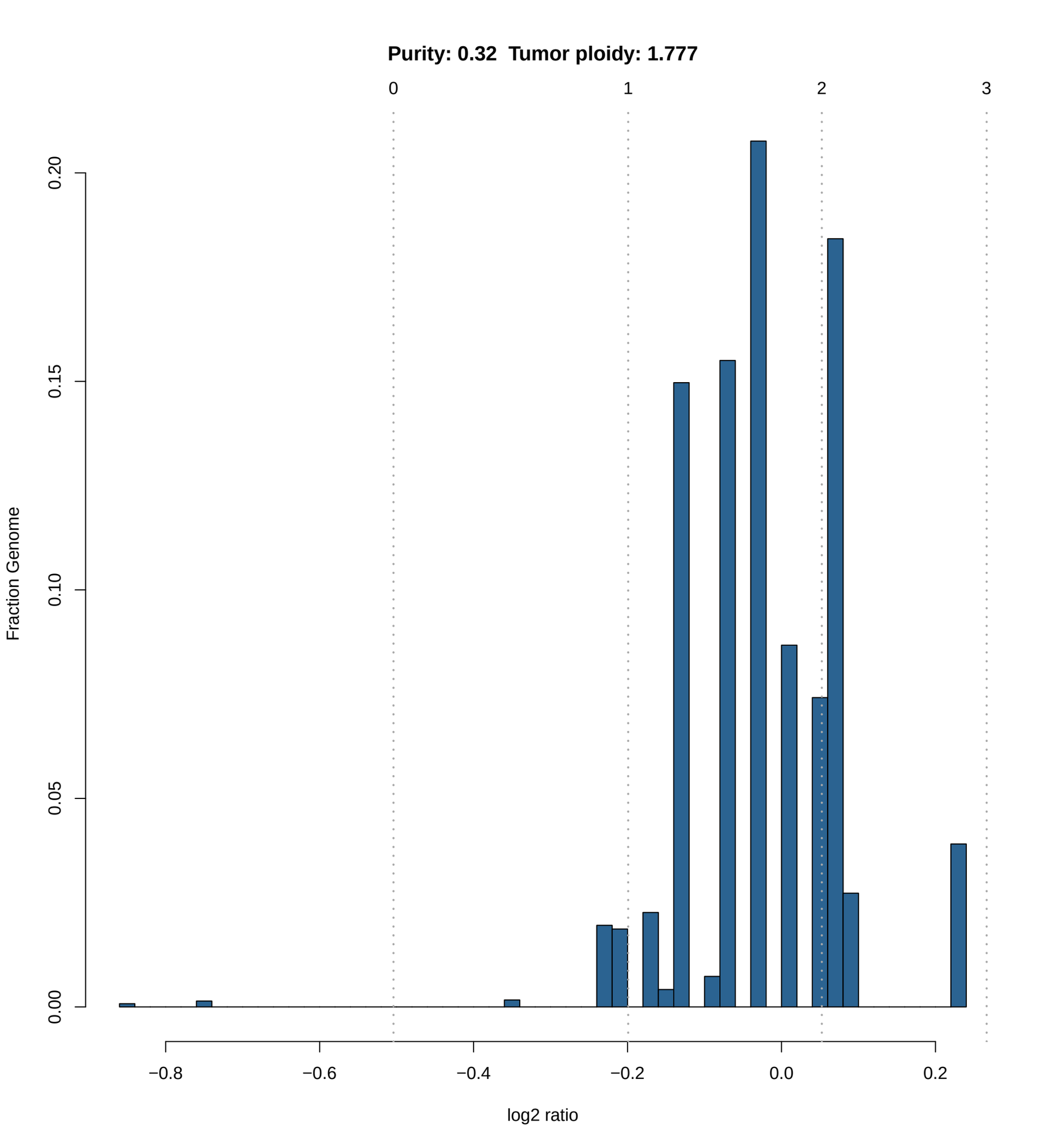

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120
SNV Index

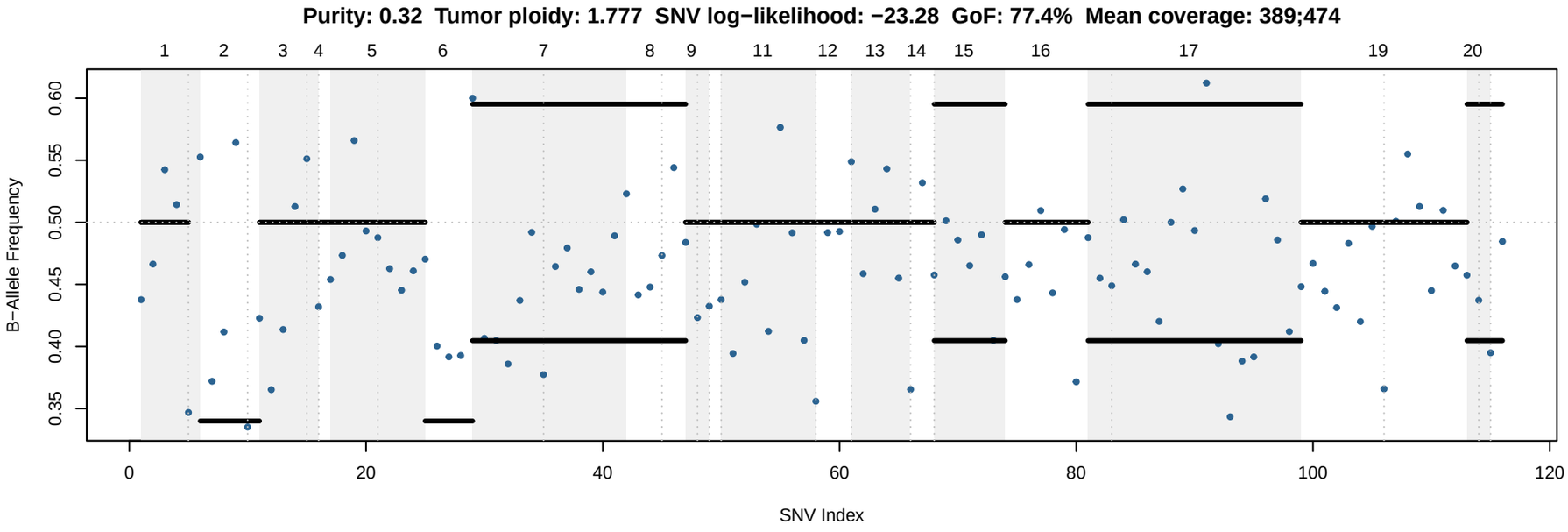

2m2
1m1
2m1
1m0
2m0
3m0
Allelic fraction (germline)
Copy Number log−ratio

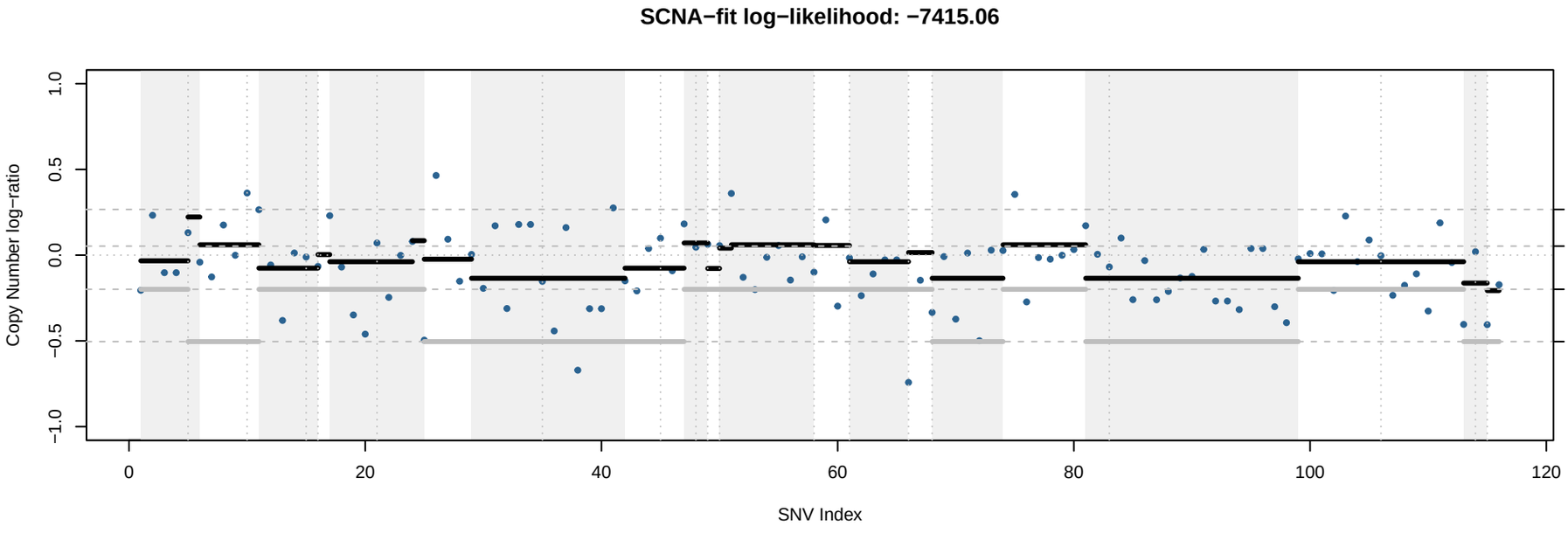

Coverage (log2)
Allelic fraction

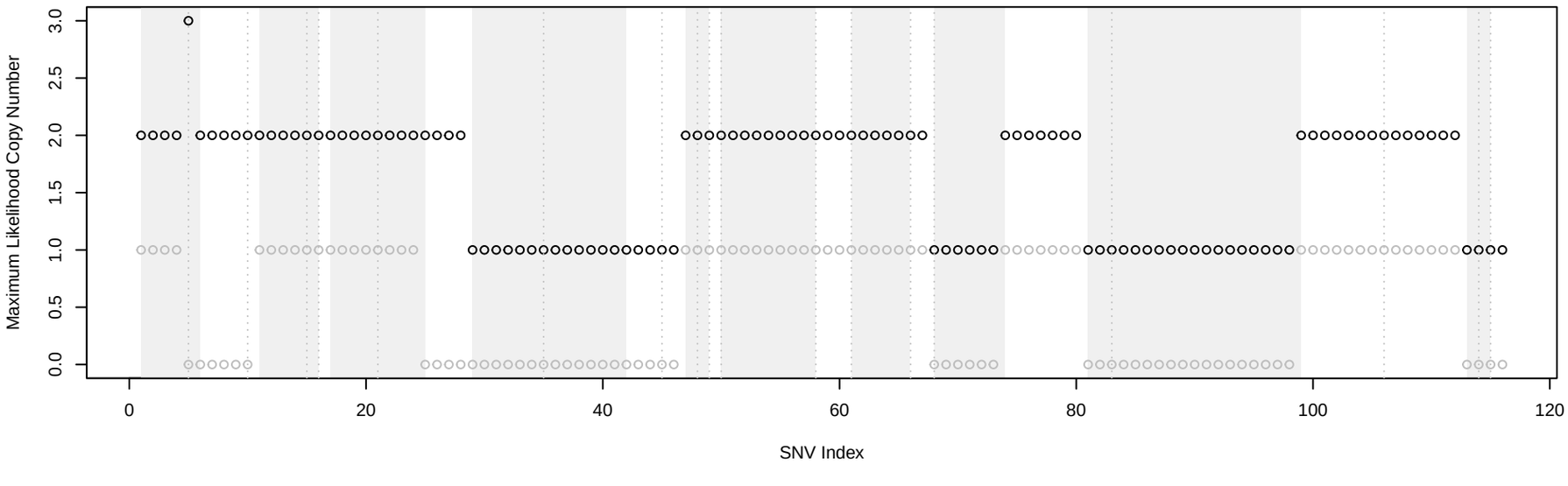

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
Allelic fraction (somatic)
Copy Number log−ratio

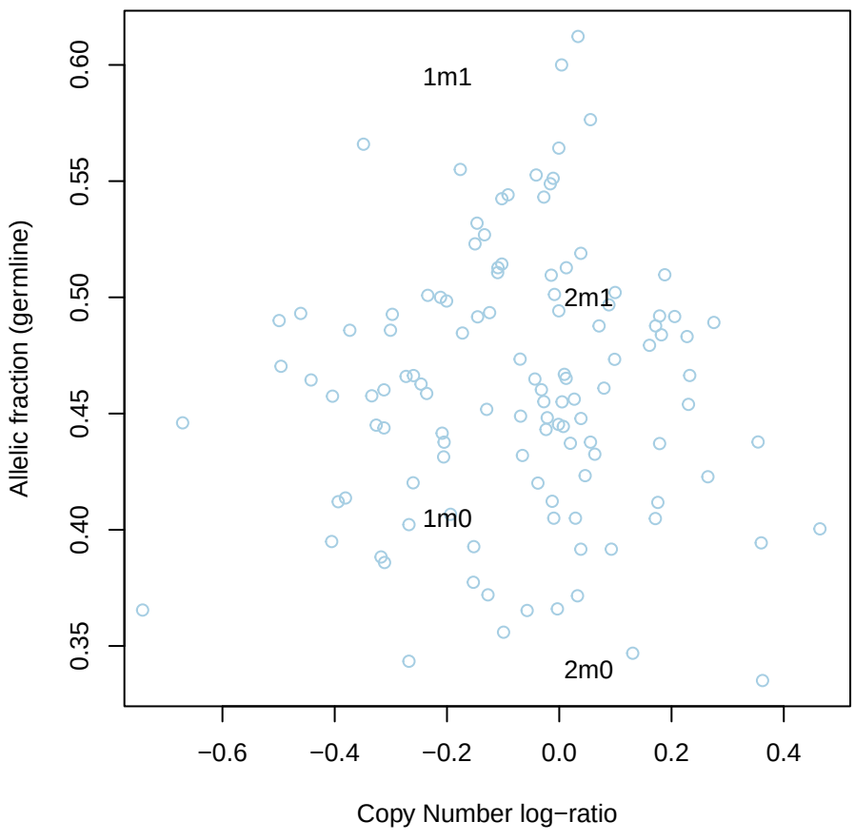

Frequency
Cellular fraction

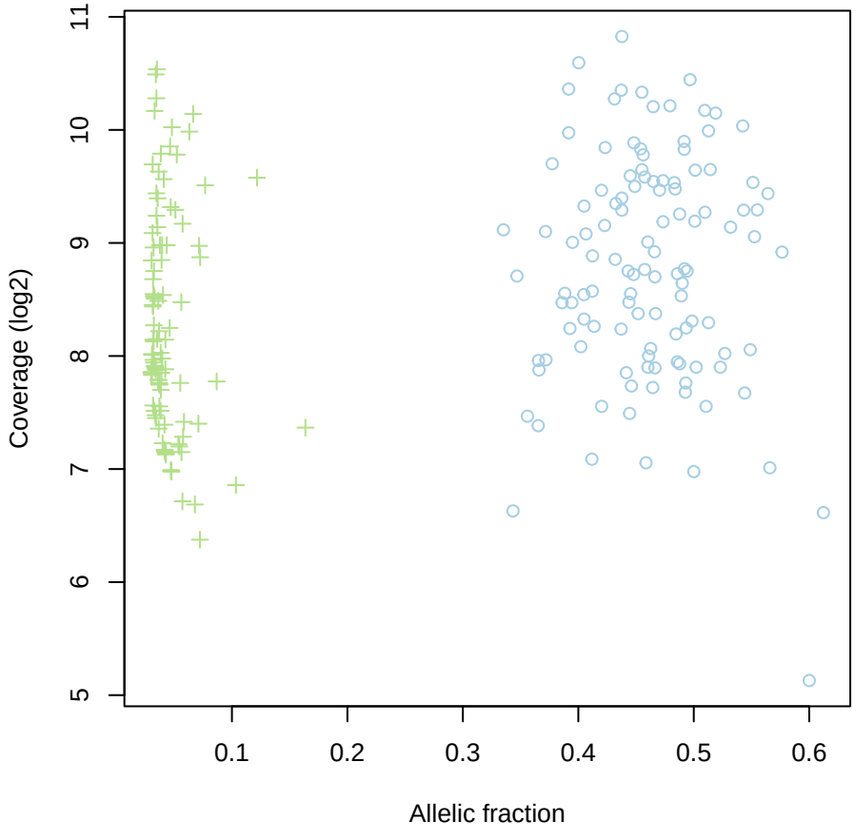

Purity: 0.32 Tumor ploidy: 1.777
0
1
2
3
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

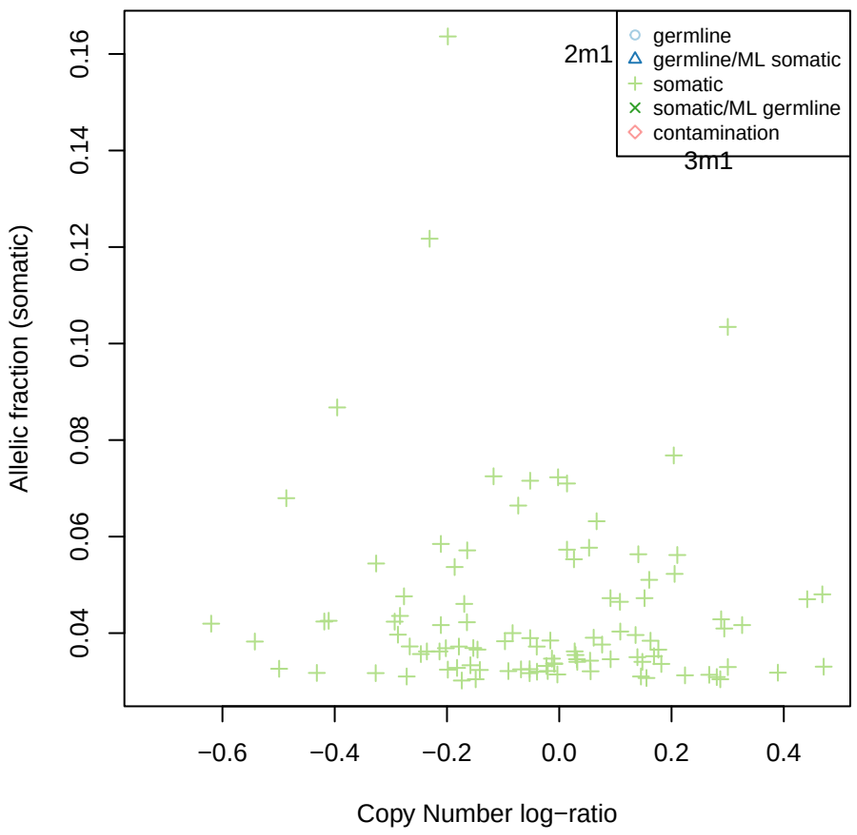

Purity: 0.32 Tumor ploidy: 1.777 SNV log−likelihood: −23.28 GoF: 77.4% Mean coverage: 389;474
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100 120
SNV Index

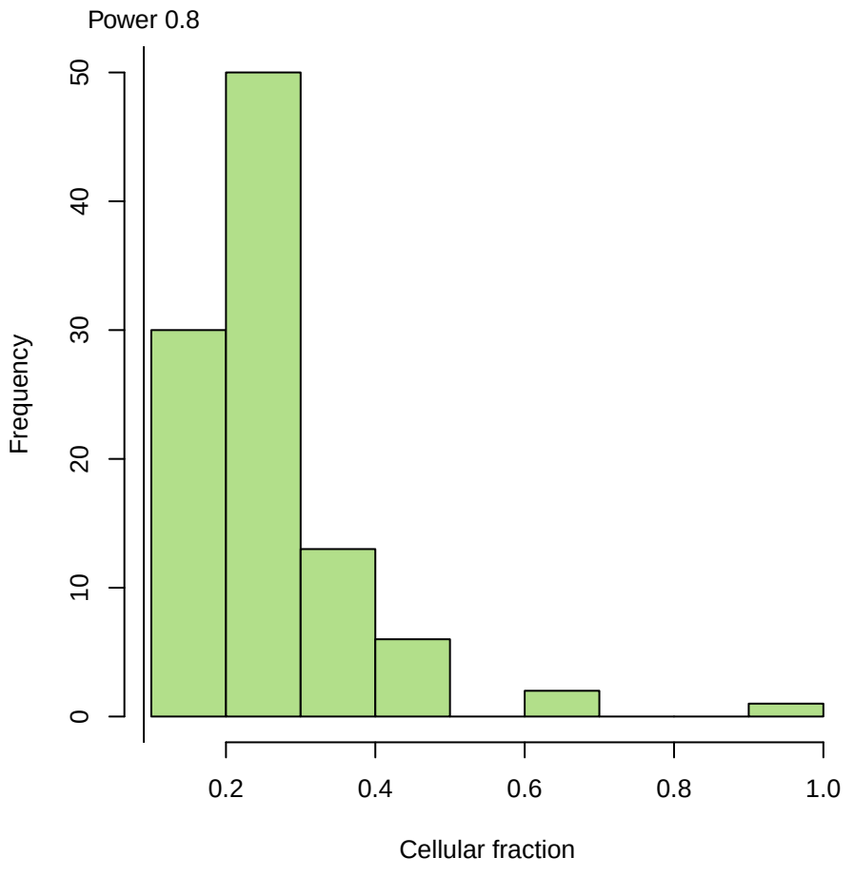

SCNA−fit log−likelihood: −7415.06
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3
0 20 40 60 80 100 120
SNV Index

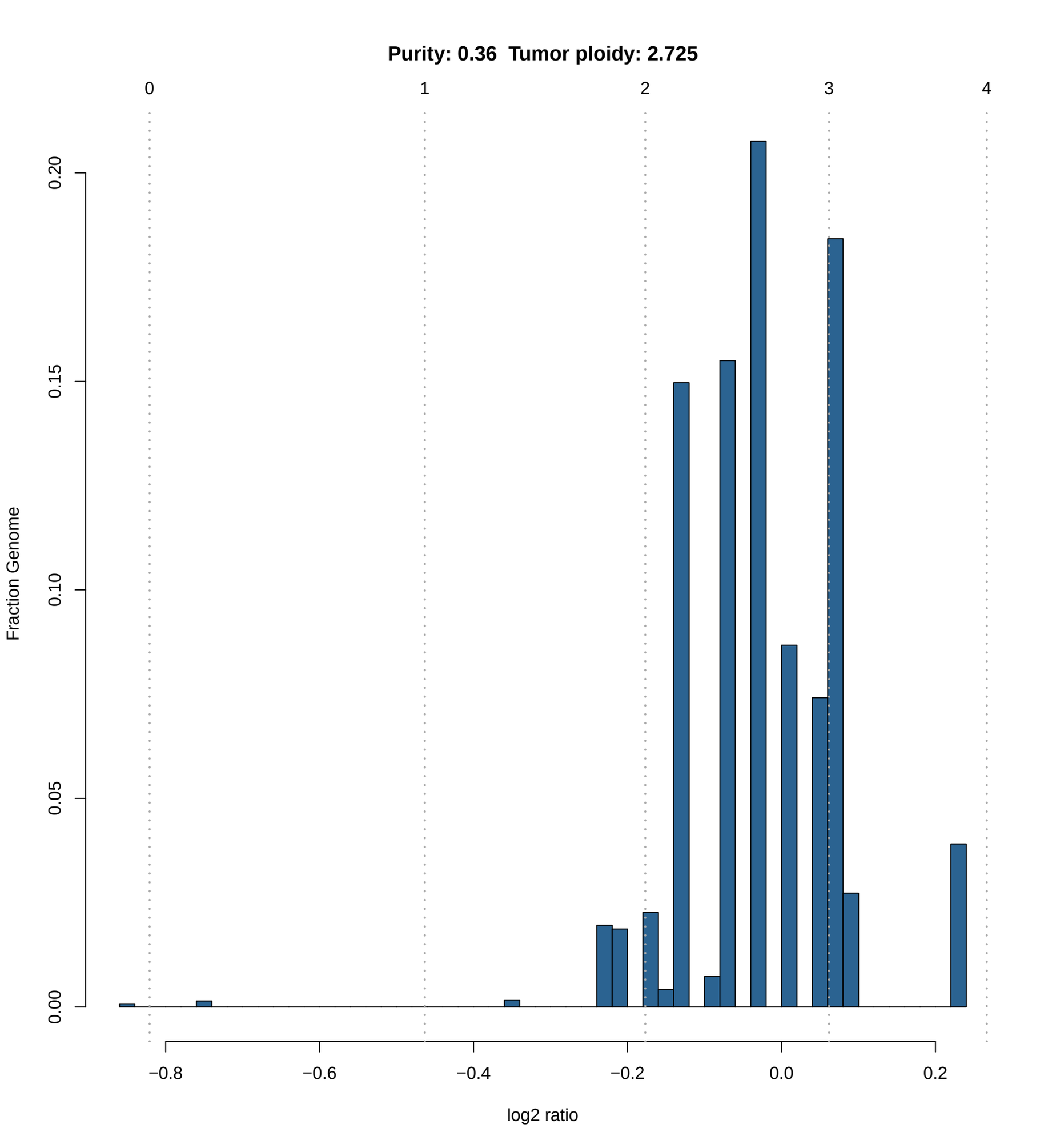

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120
SNV Index

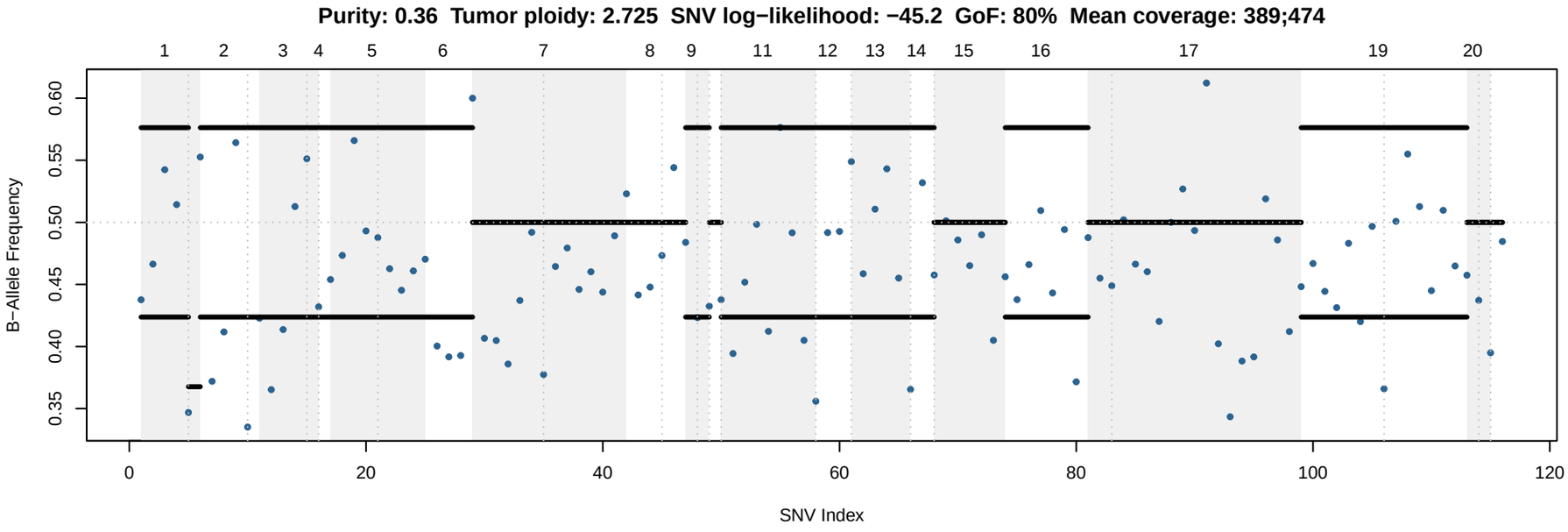

1m1
2m1
1m0
2m0
Allelic fraction (germline)
Copy Number log−ratio

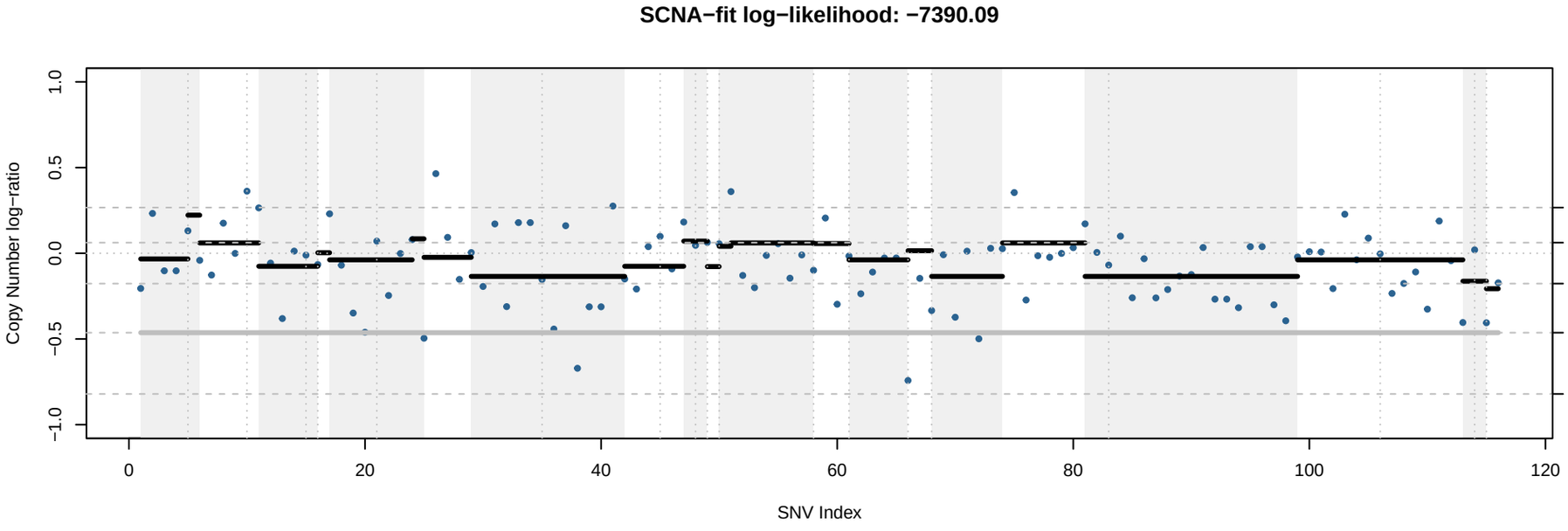

Coverage (log2)
Allelic fraction

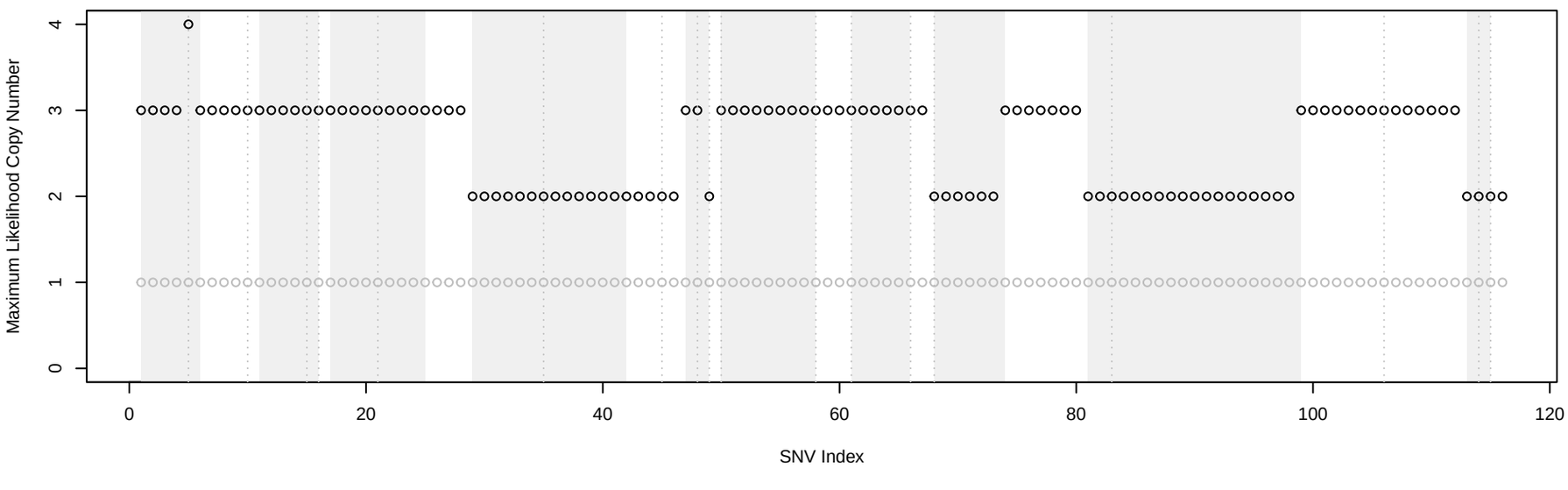

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
Allelic fraction (somatic)
Copy Number log−ratio

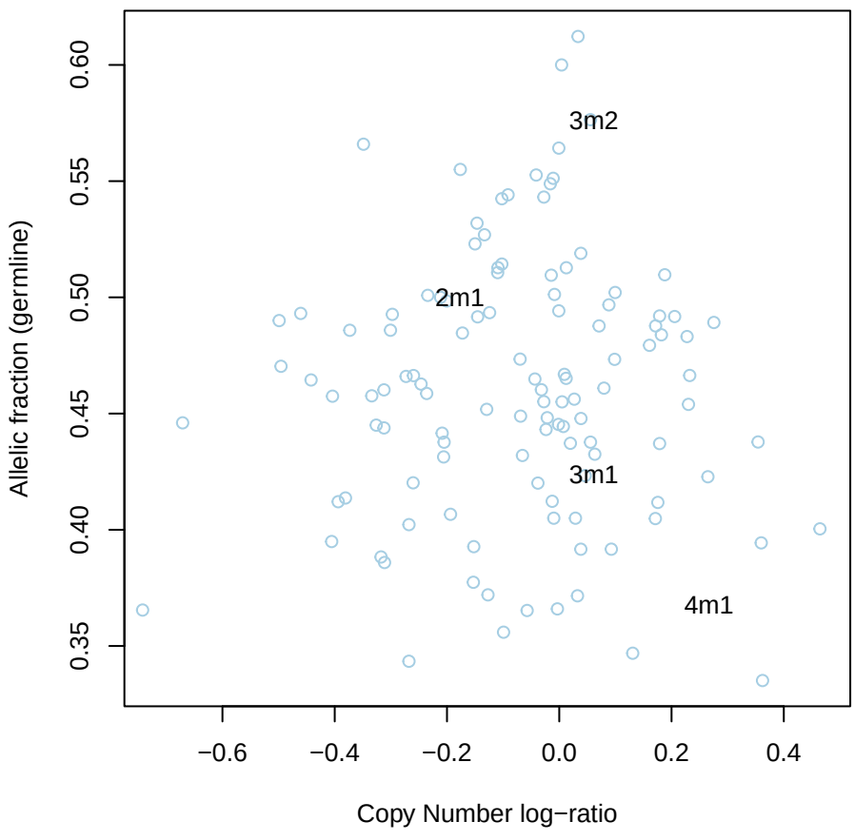

Power 0.8
Frequency
Cellular fraction

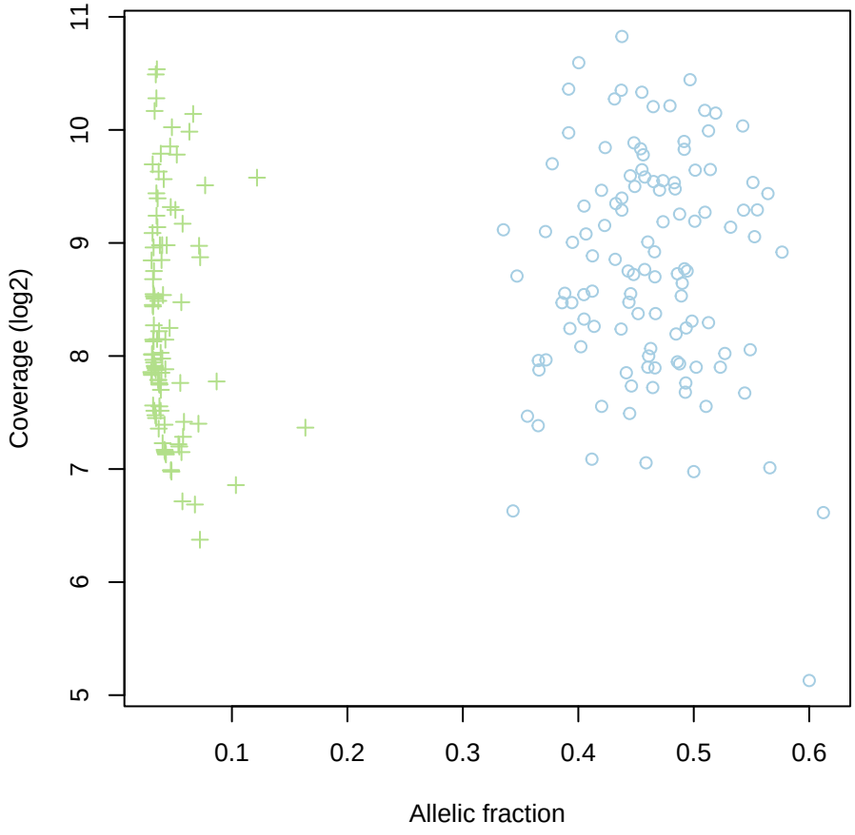

Purity: 0.36 Tumor ploidy: 2.725
0
1
2
3
4
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

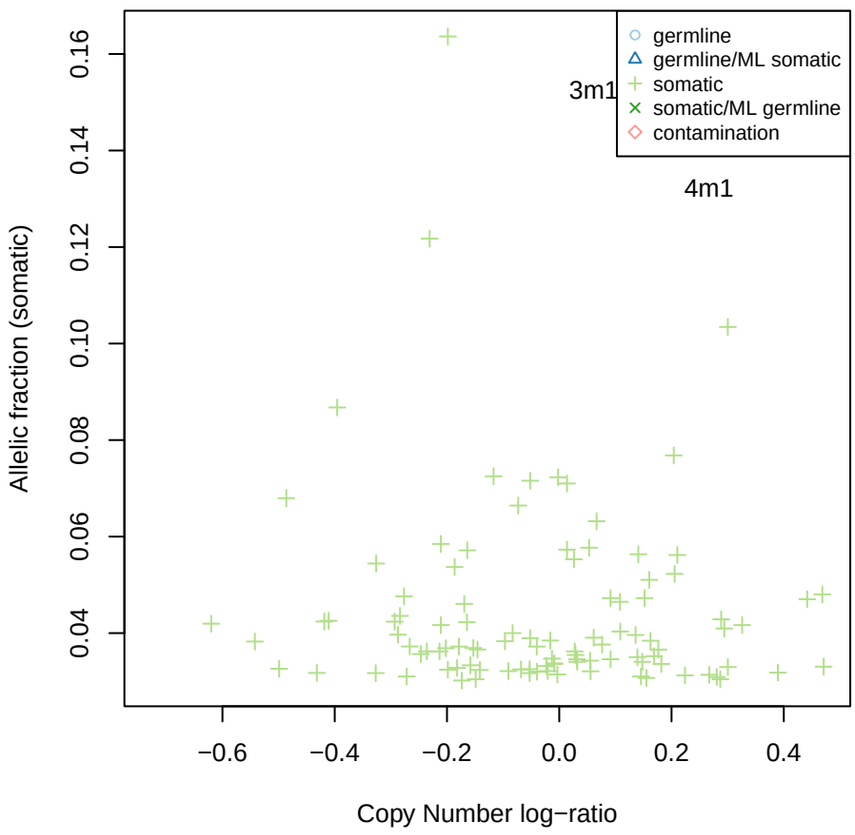

Purity: 0.36 Tumor ploidy: 2.725 SNV log−likelihood: −45.2 GoF: 80% Mean coverage: 389;474
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100 120
SNV Index

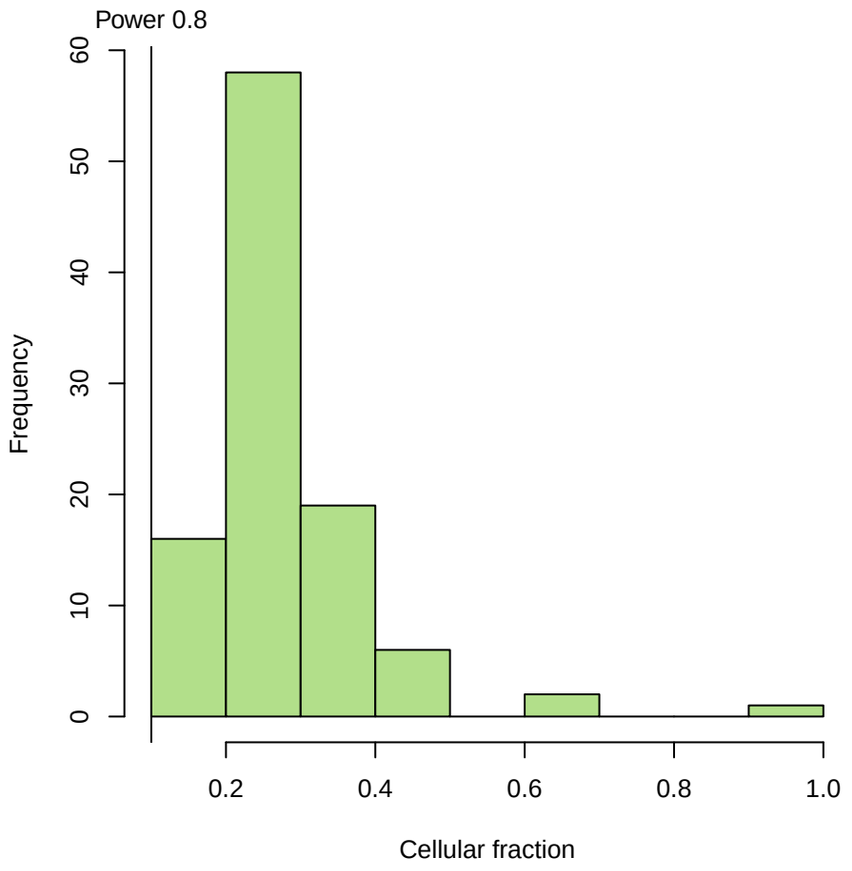

SCNA−fit log−likelihood: −7390.09
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4
0 20 40 60 80 100 120
SNV Index

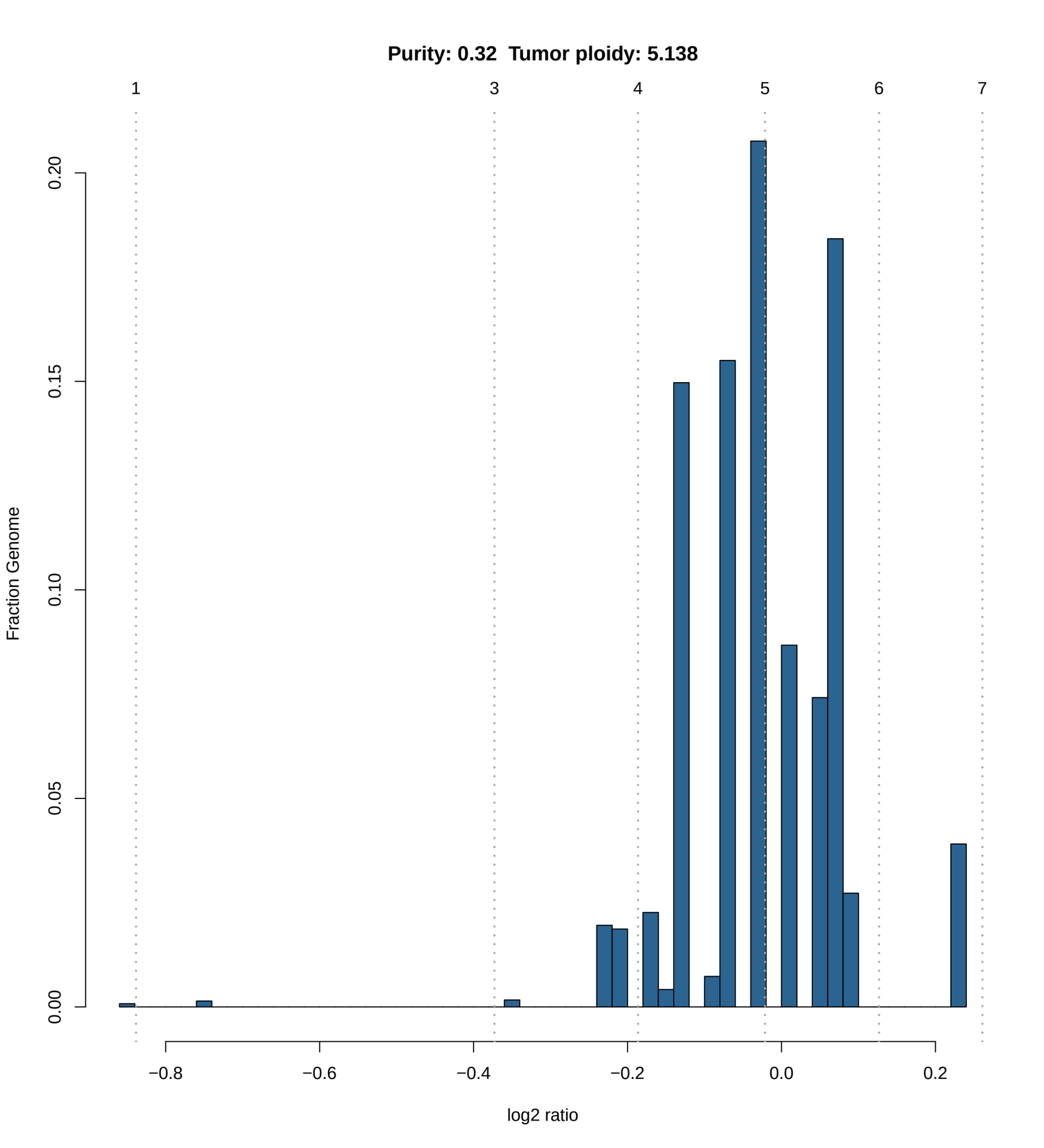

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120
SNV Index

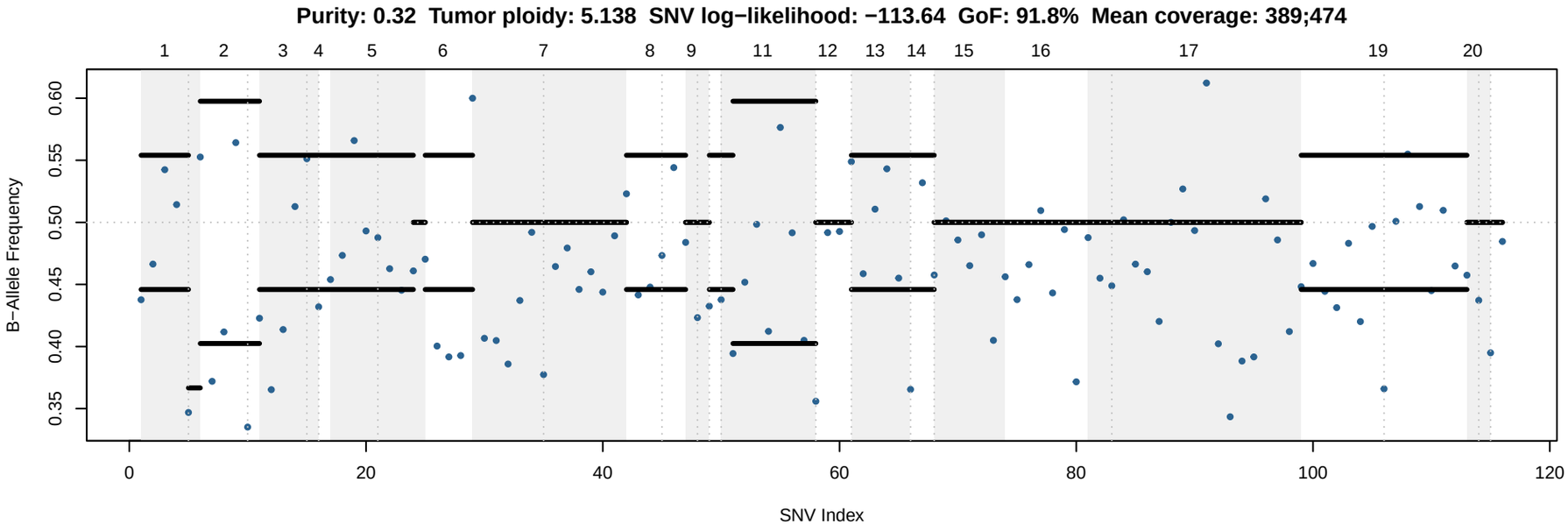

Allelic fraction (germline)
Copy Number log−ratio
3m2
2m1
3m1
4m1

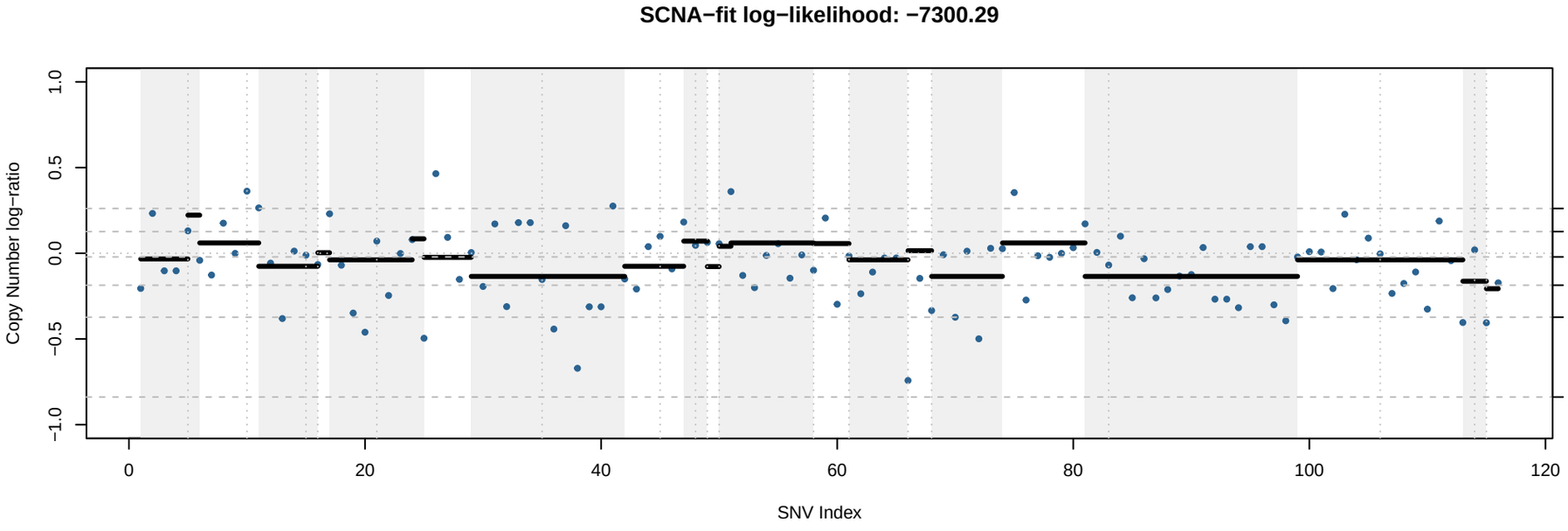

Coverage (log2)
Allelic fraction

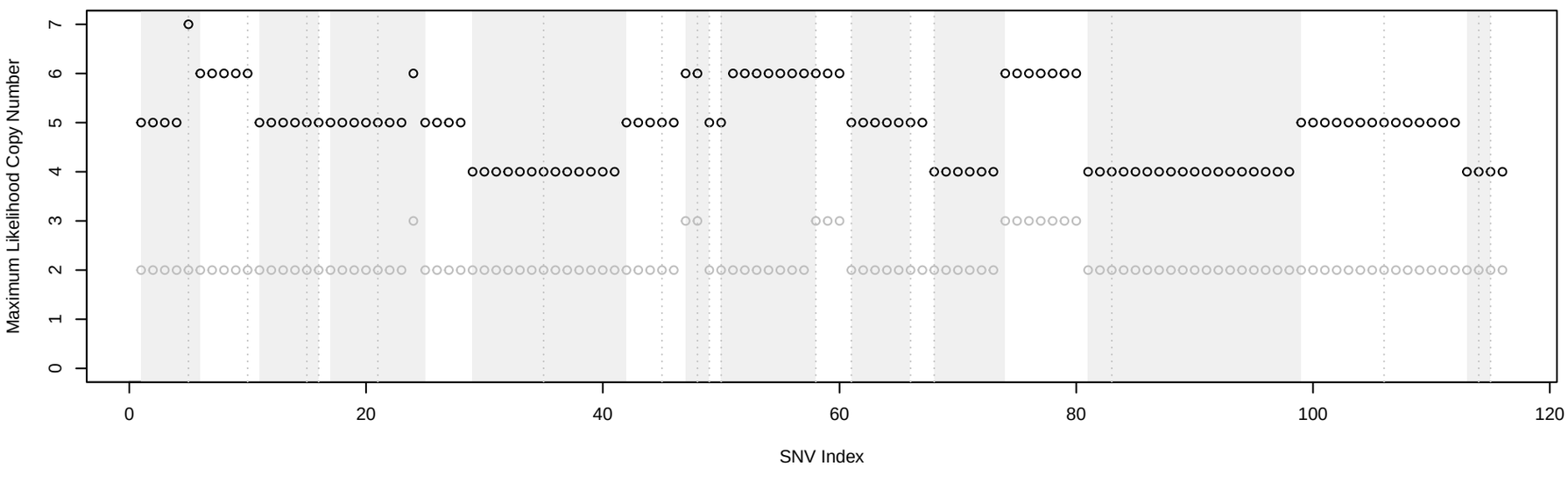

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1

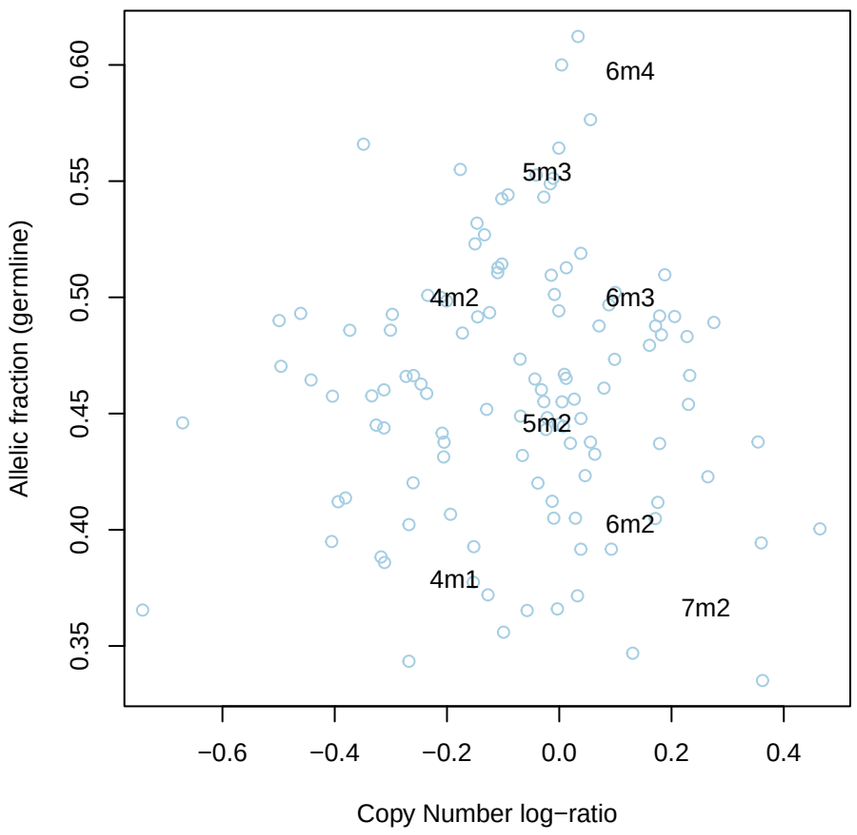

Power 0.8
Frequency
Cellular fraction

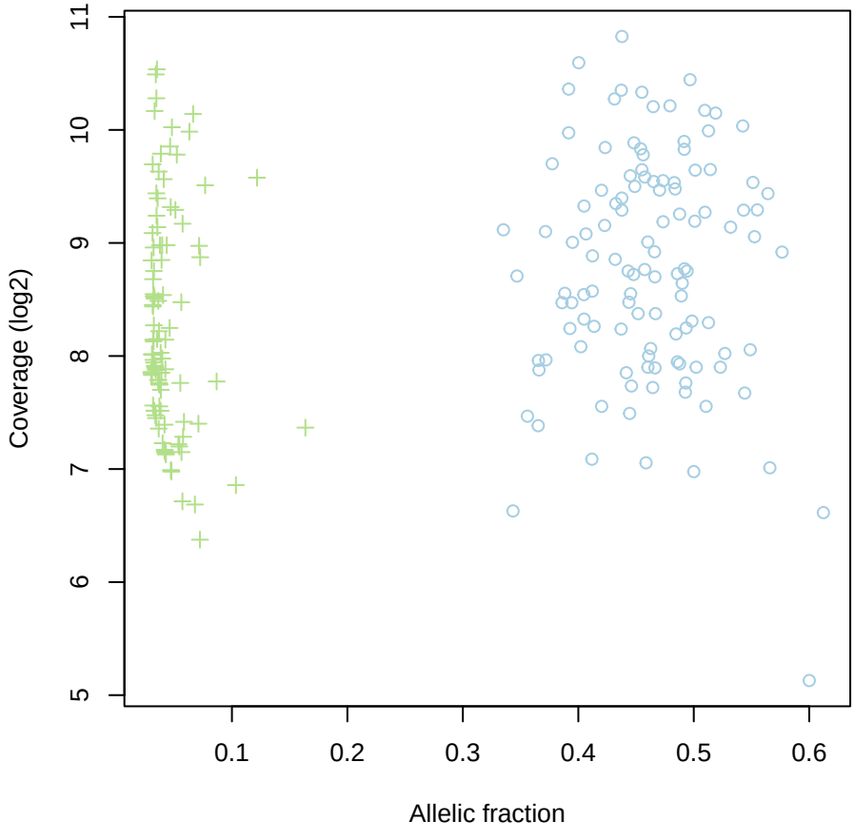

Purity: 0.32 Tumor ploidy: 5.138
1
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

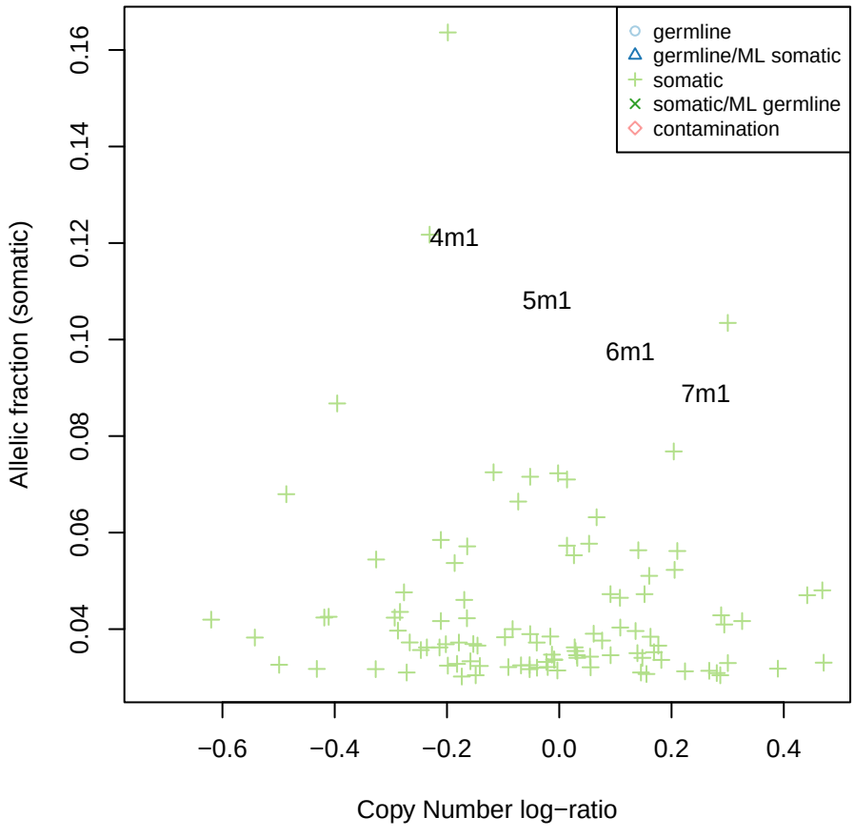

Purity: 0.32 Tumor ploidy: 5.138 SNV log−likelihood: −113.64 GoF: 91.8% Mean coverage: 389;474
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100 120
SNV Index

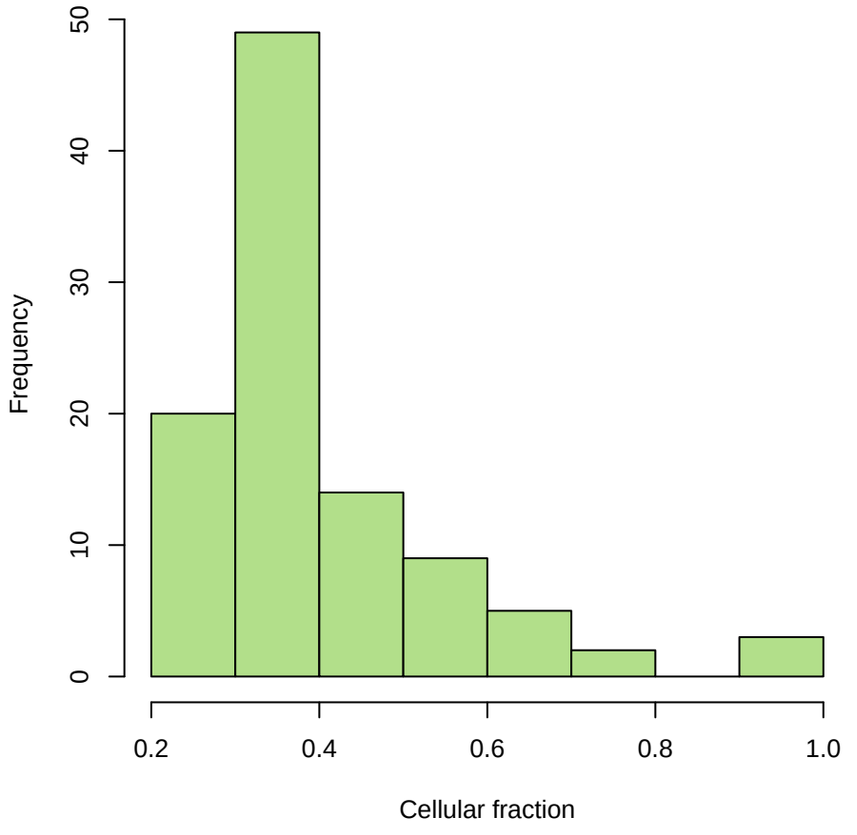

SCNA−fit log−likelihood: −7300.29
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 3 4 5 6
0 20 40 60 80 100 120
SNV Index

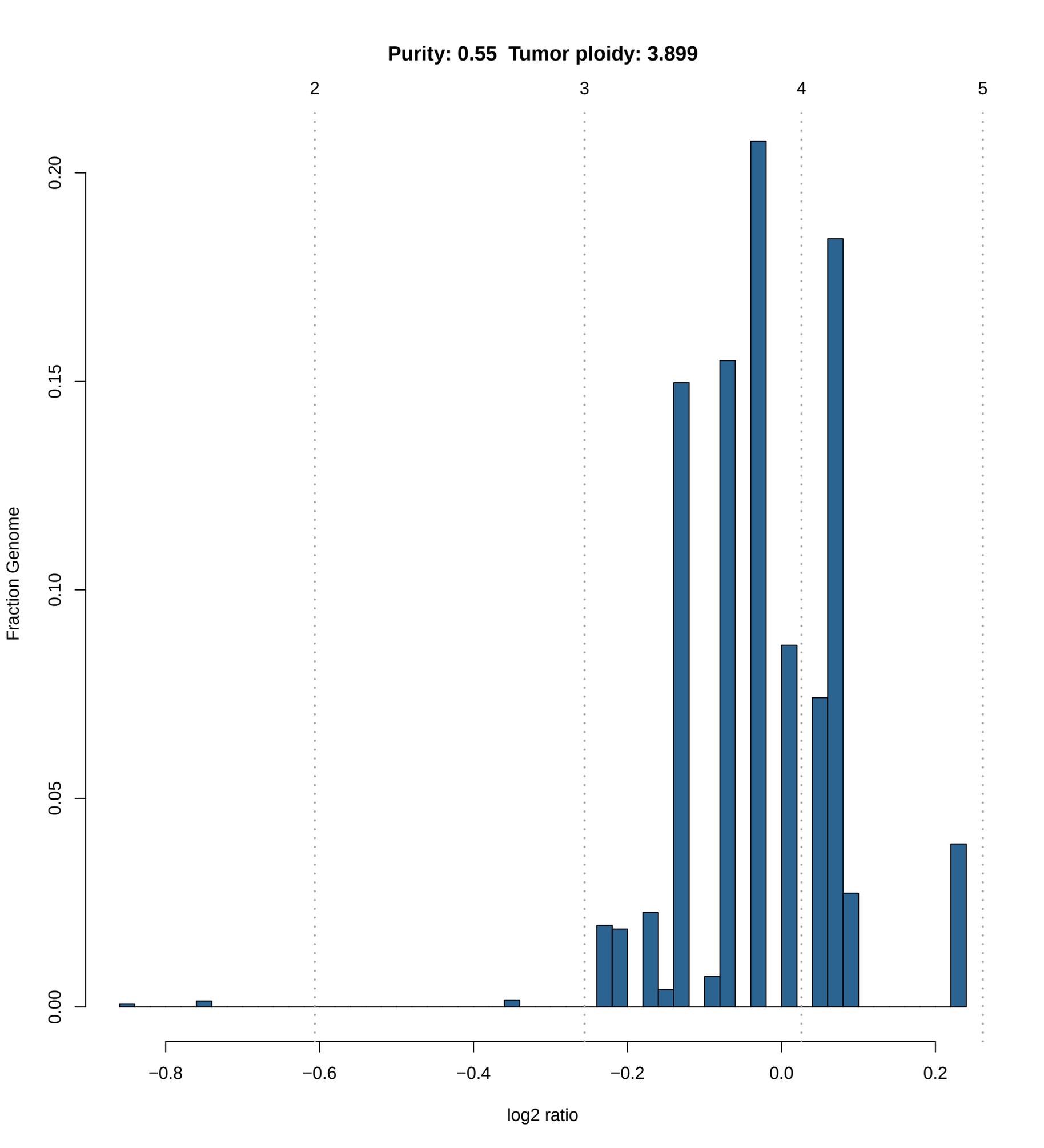

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

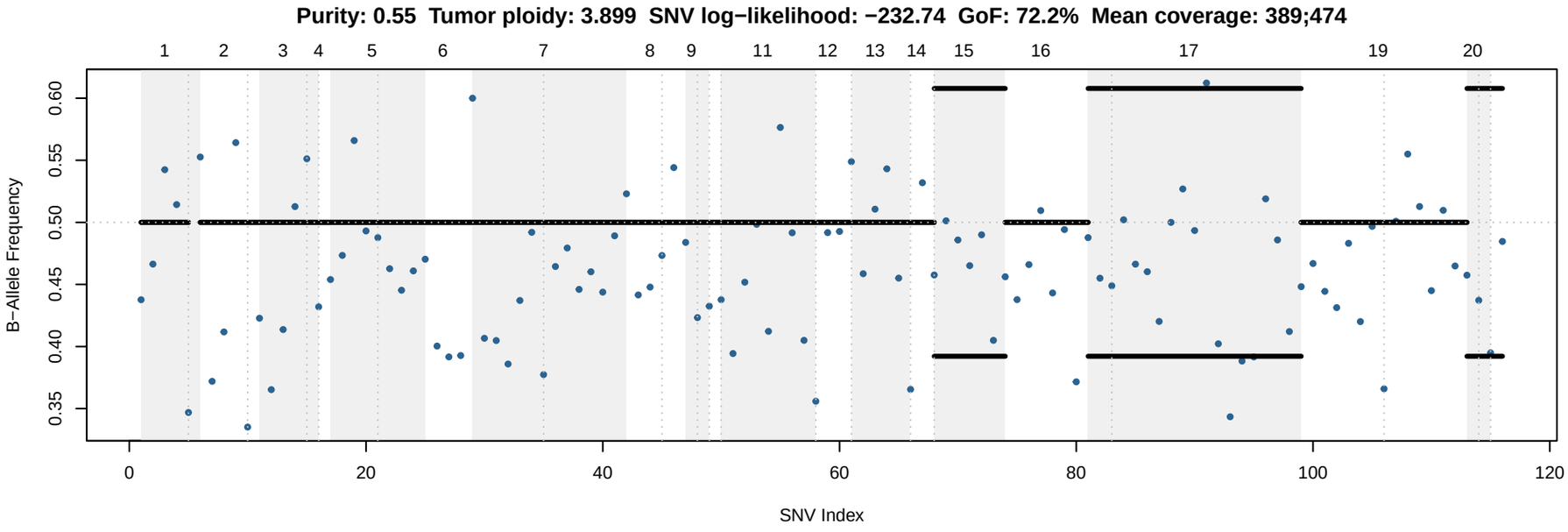

Allelic fraction (germline)
Copy Number log−ratio
6m4
5m3
4m2
6m3
5m2
6m2
4m1
7m2

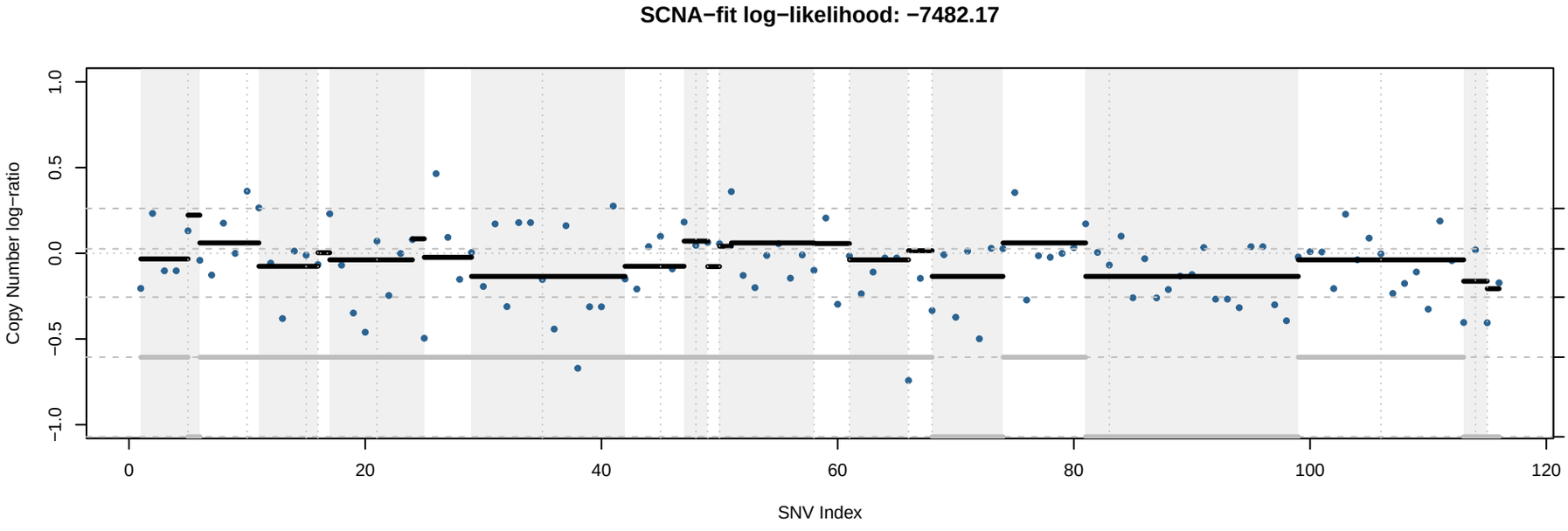

Coverage (log2)
Allelic fraction

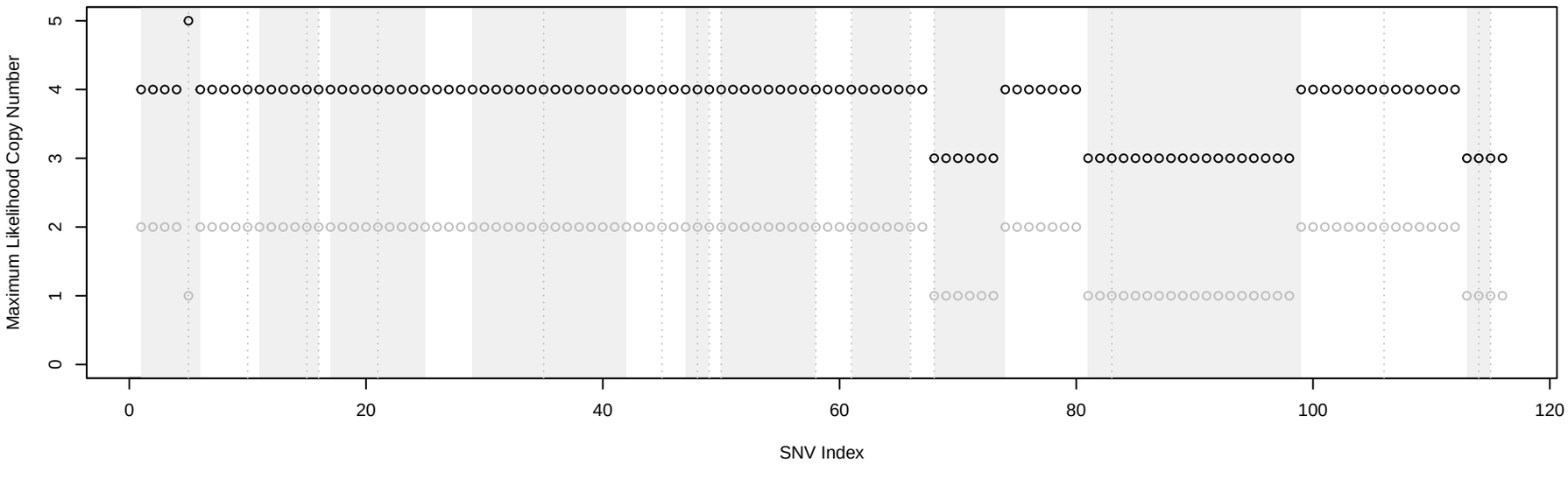

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
4m1
5m1
6m1
7m1

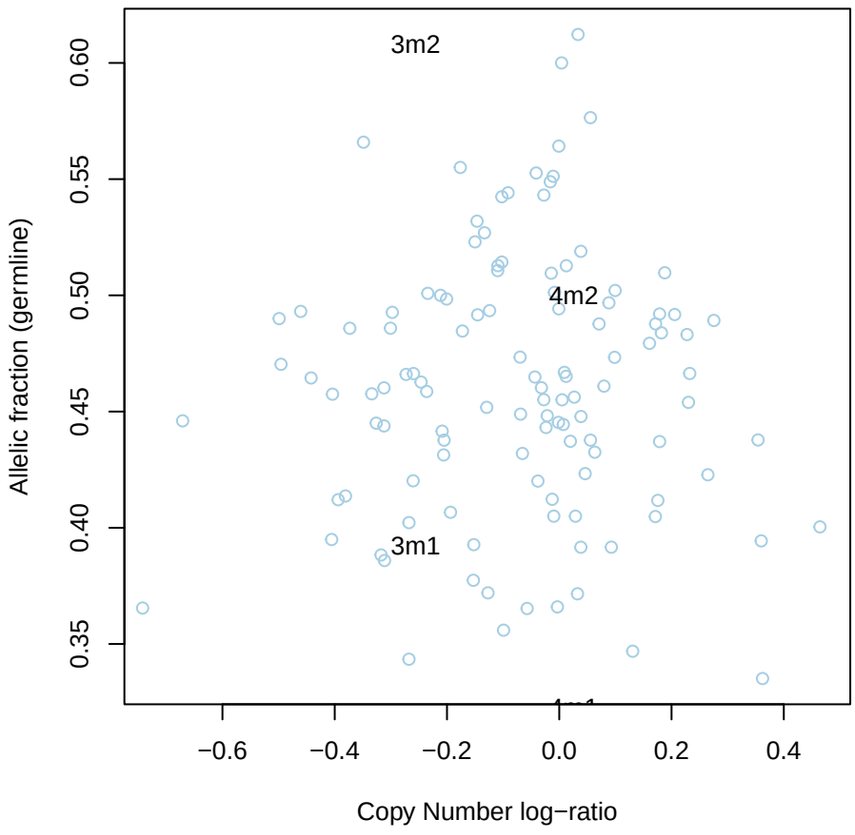

Frequency
Cellular fraction

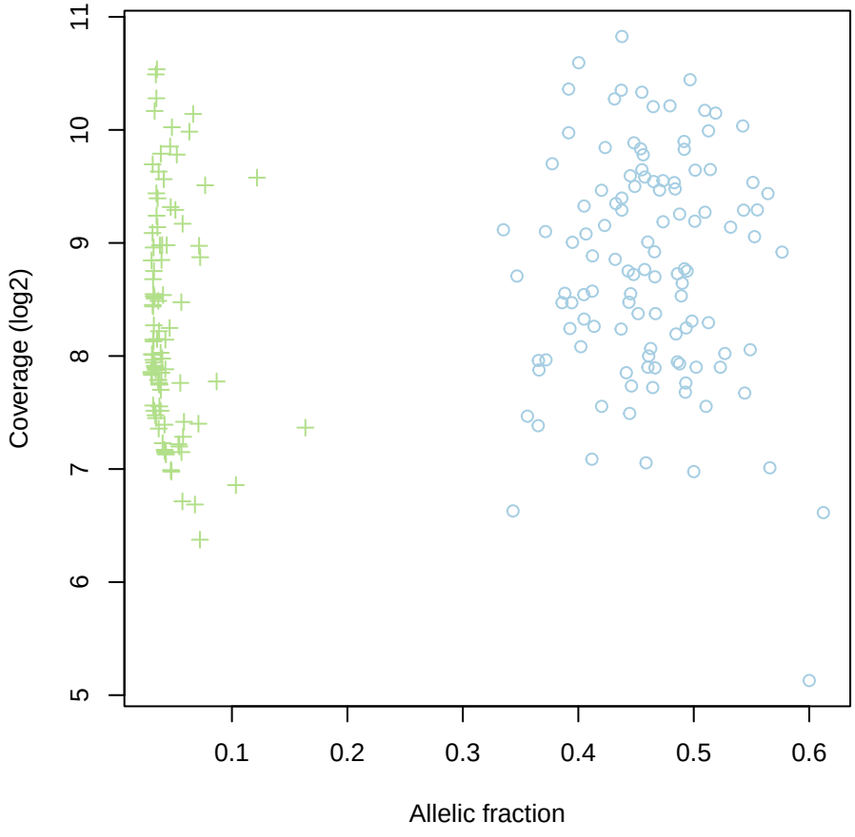

Purity: 0.55 Tumor ploidy: 3.899
2
3
4
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

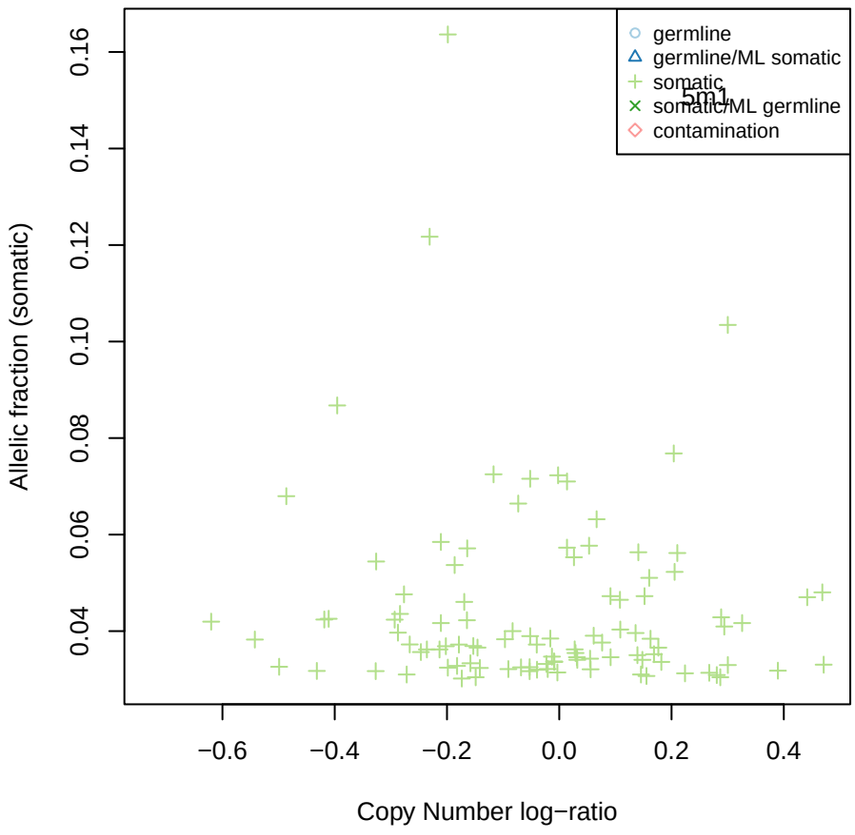

Purity: 0.55 Tumor ploidy: 3.899 SNV log−likelihood: −232.74 GoF: 72.2% Mean coverage: 389;474
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100 120
SNV Index

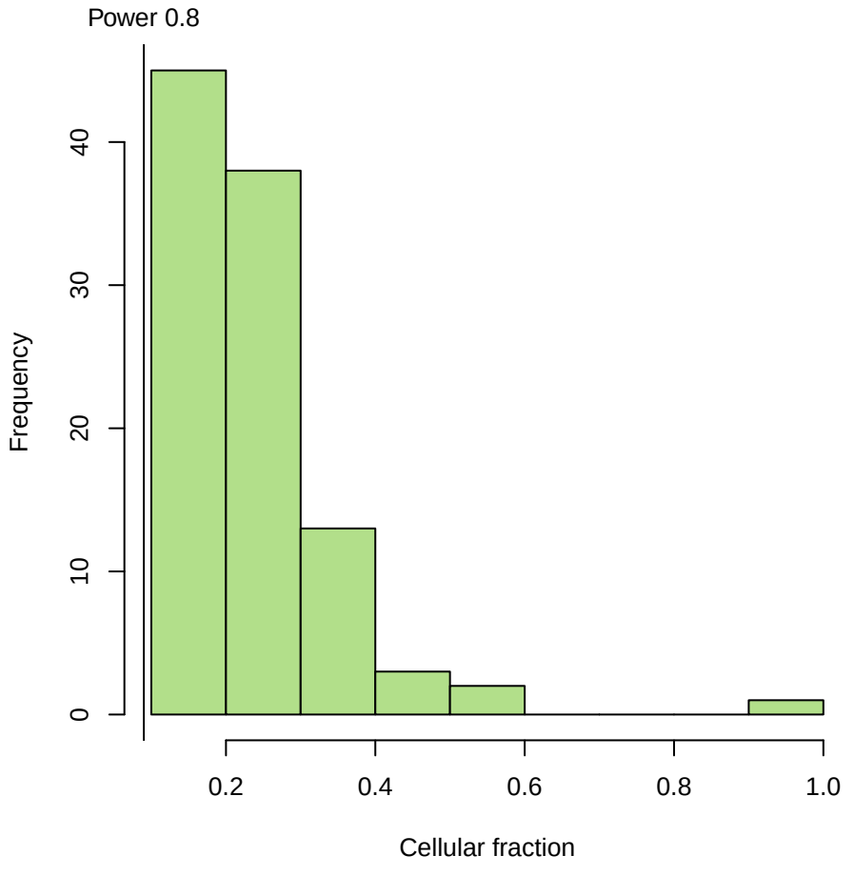

SCNA−fit log−likelihood: −7482.17
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5
0 20 40 60 80 100 120
SNV Index

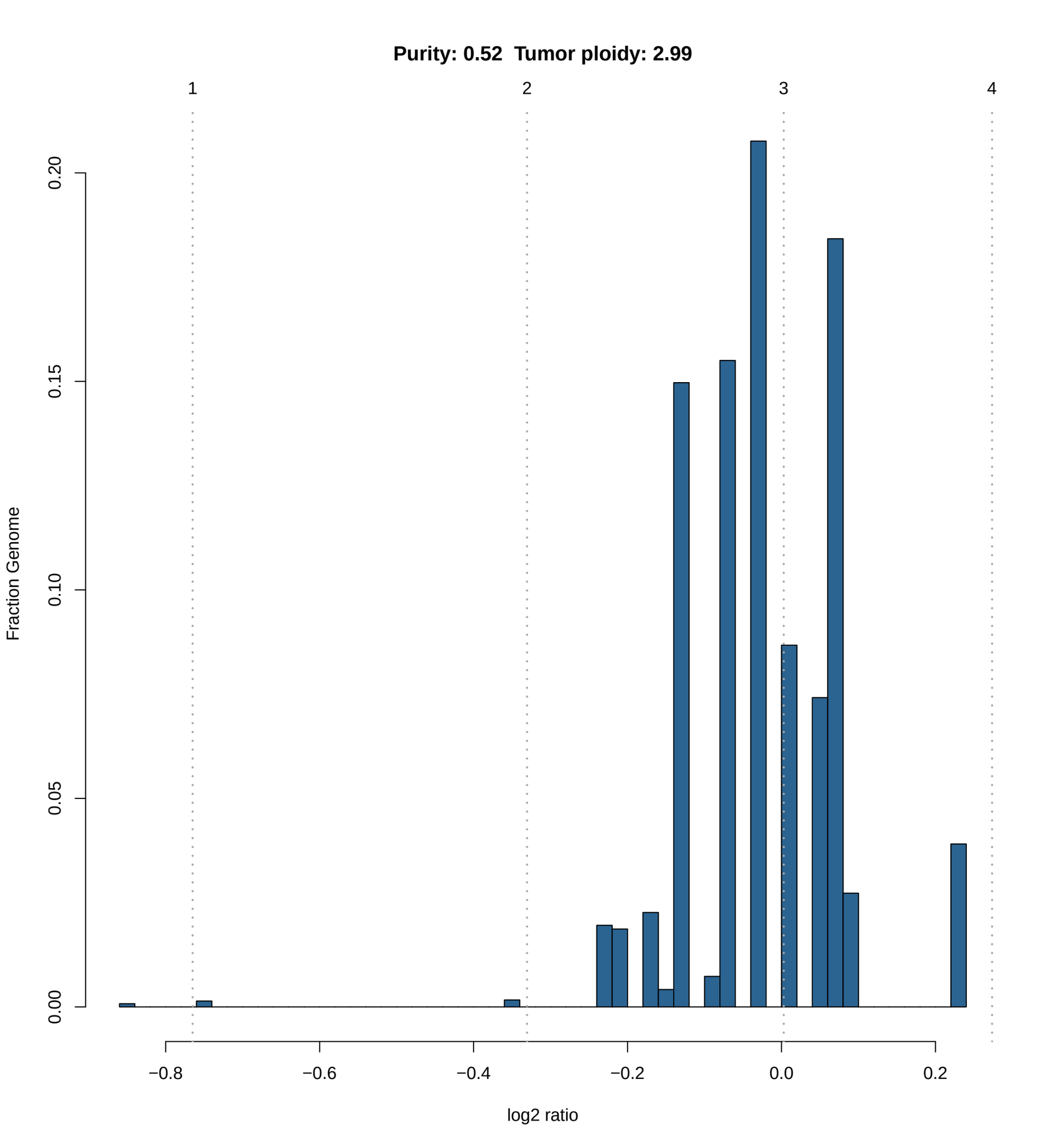

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120
SNV Index

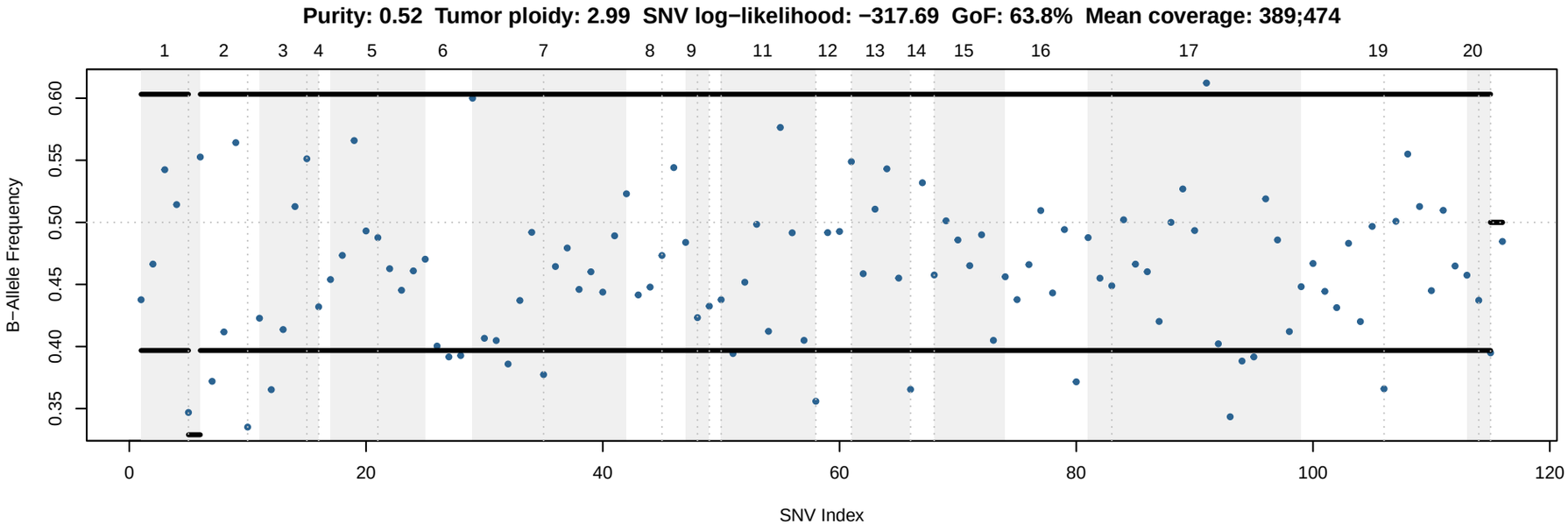

3m2
4m2
3m1
Allelic fraction (germline)
Copy Number log−ratio

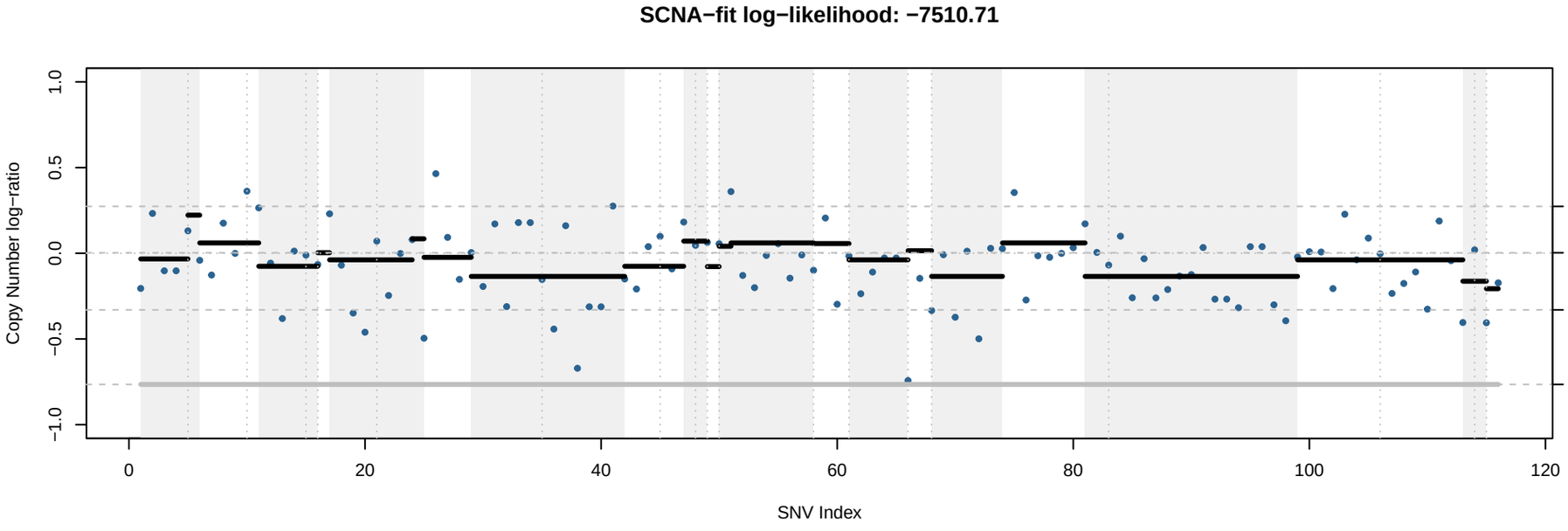

Coverage (log2)
Allelic fraction

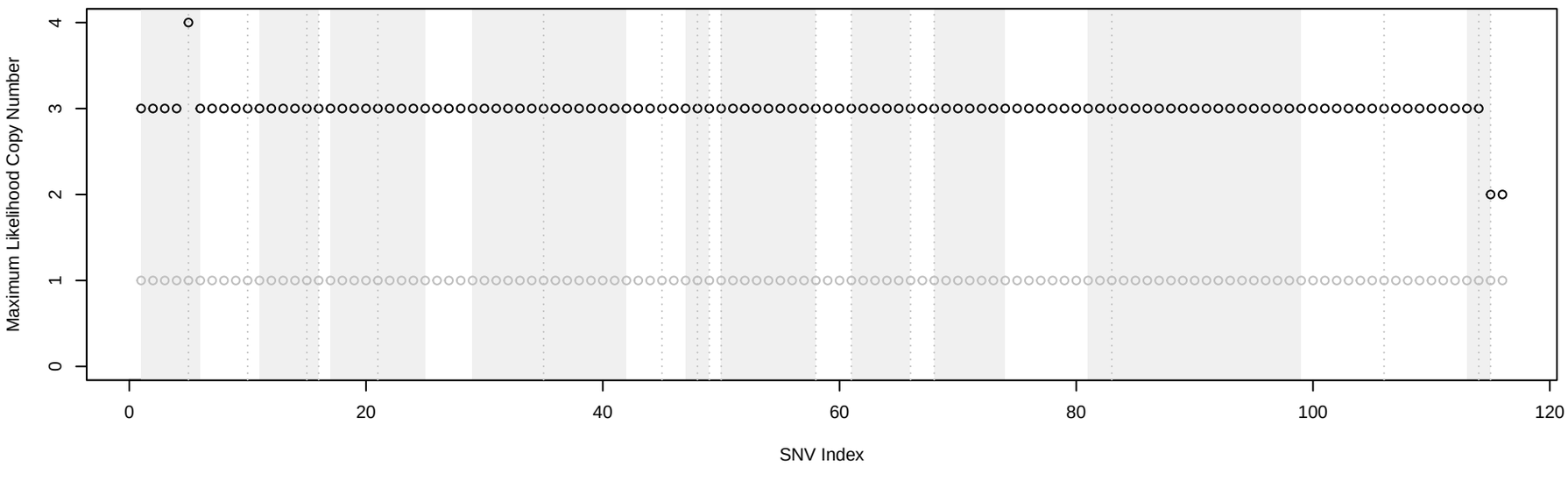

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
Allelic fraction (somatic)
Copy Number log−ratio

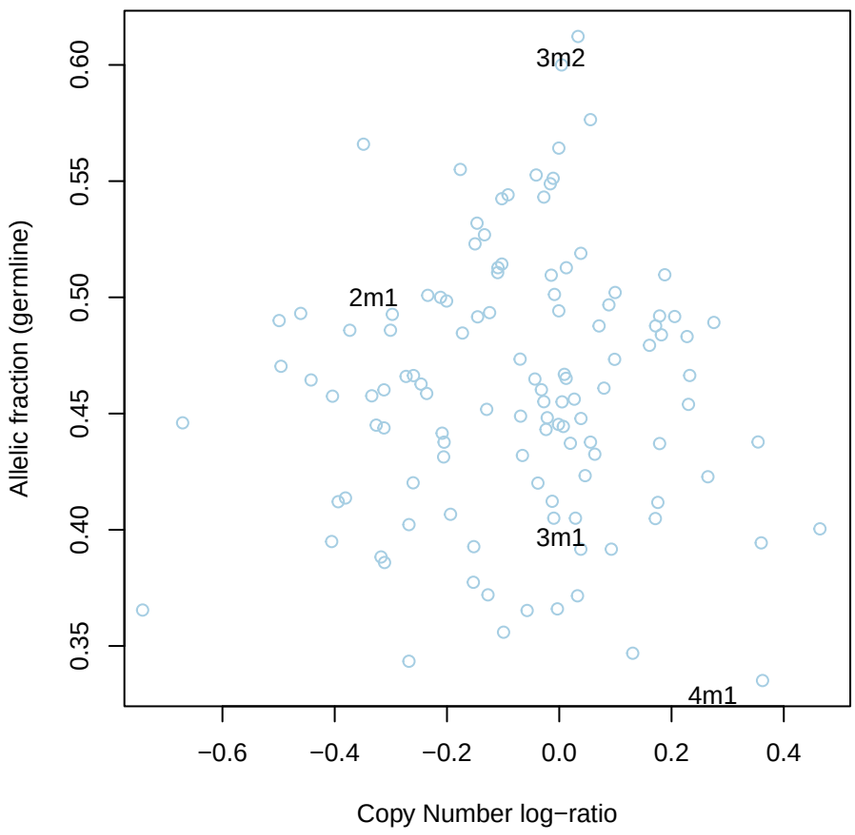

Power 0.8
Frequency
Cellular fraction

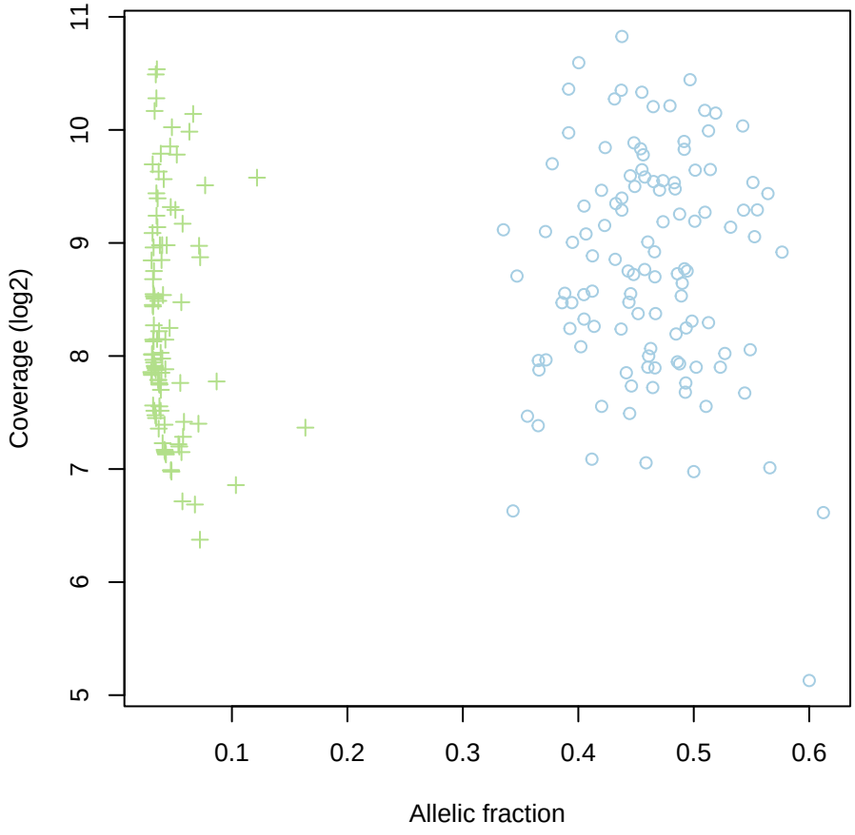

Purity: 0.52 Tumor ploidy: 2.99
1
2
3
4
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

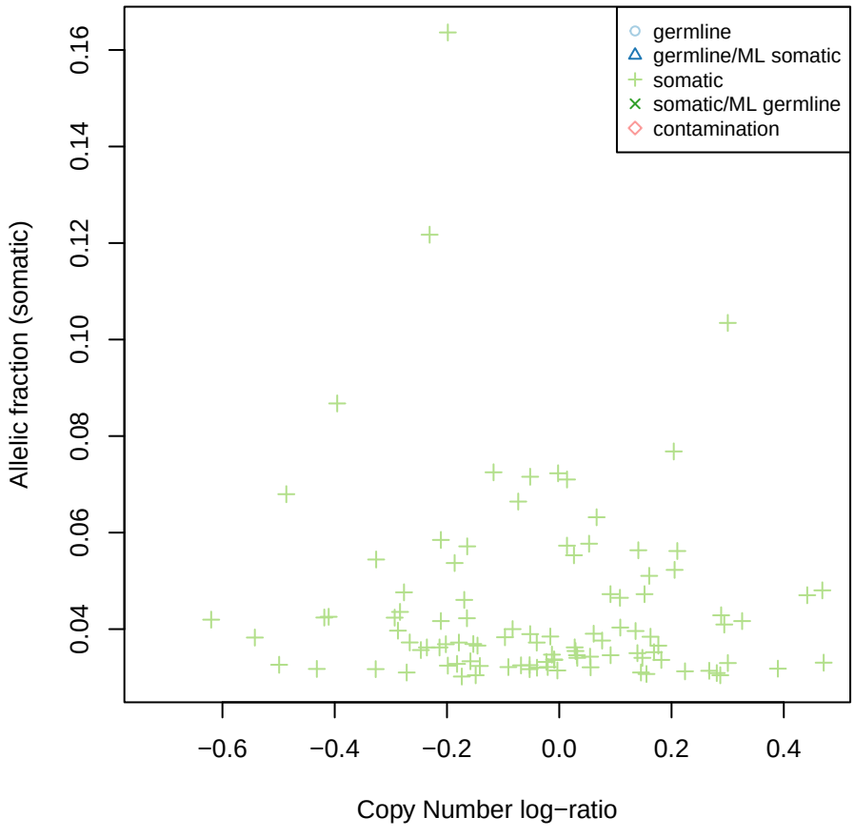

Purity: 0.52 Tumor ploidy: 2.99 SNV log−likelihood: −317.69 GoF: 63.8% Mean coverage: 389;474
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100 120
SNV Index

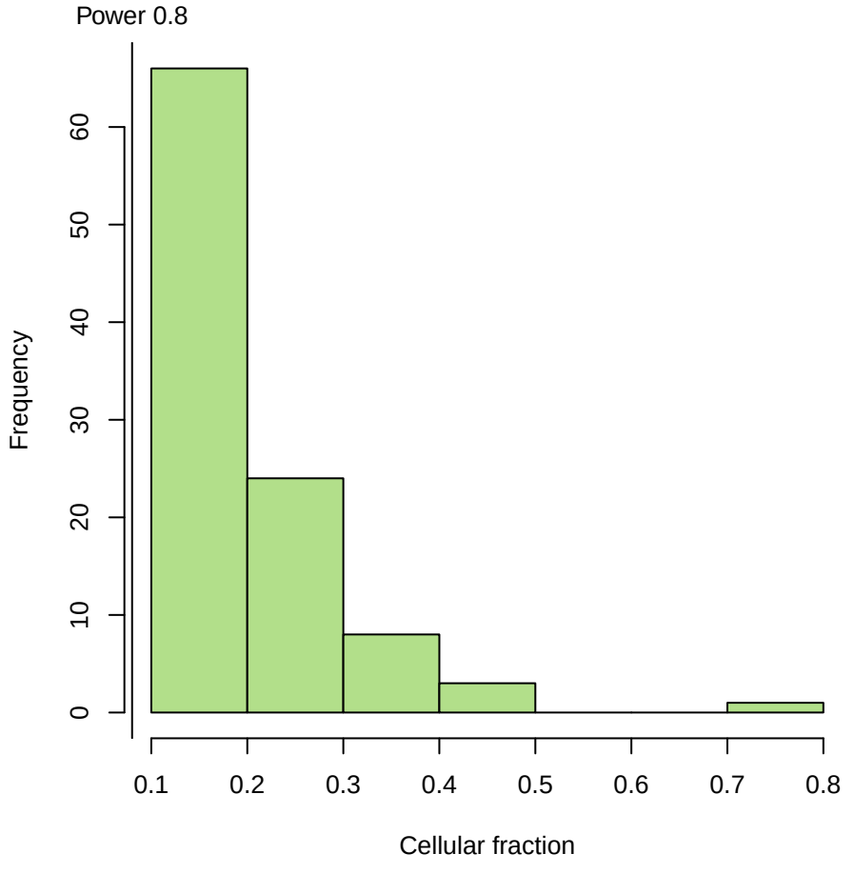

SCNA−fit log−likelihood: −7510.71
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4
0 20 40 60 80 100 120
SNV Index

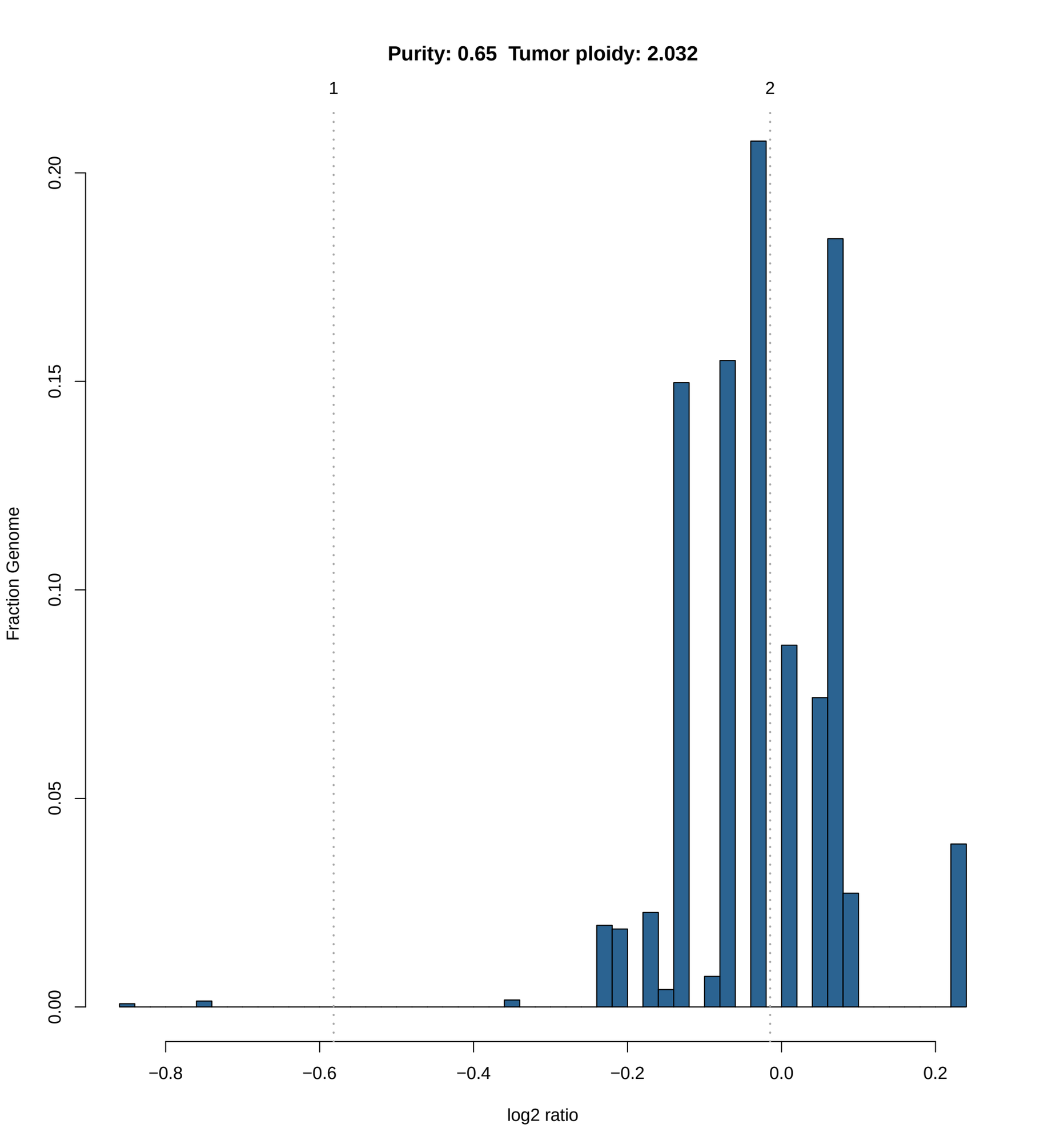

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120
SNV Index

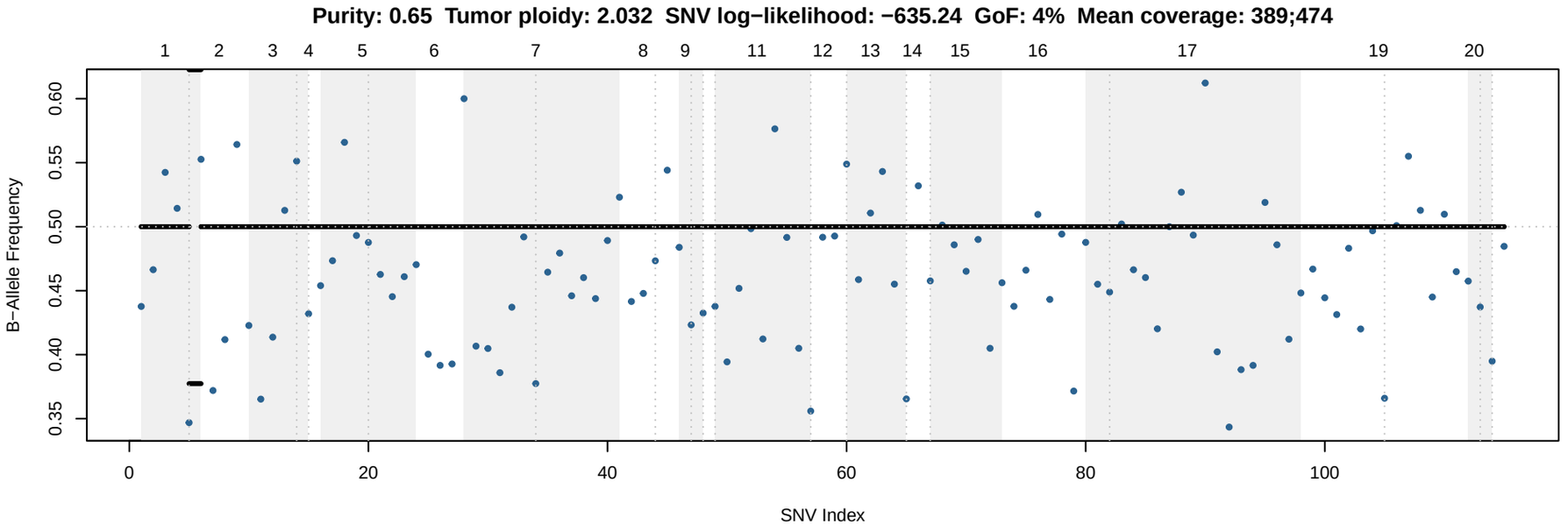

3m2
2m1
3m1
4m1
Allelic fraction (germline)
Copy Number log−ratio

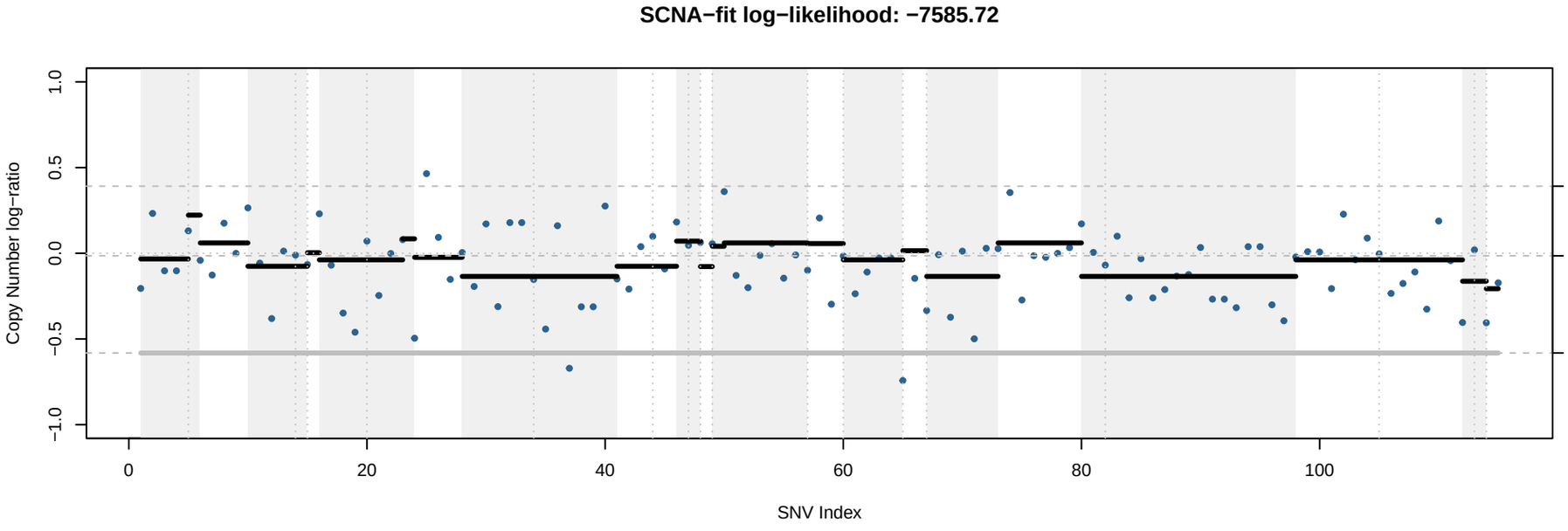

Coverage (log2)
Allelic fraction

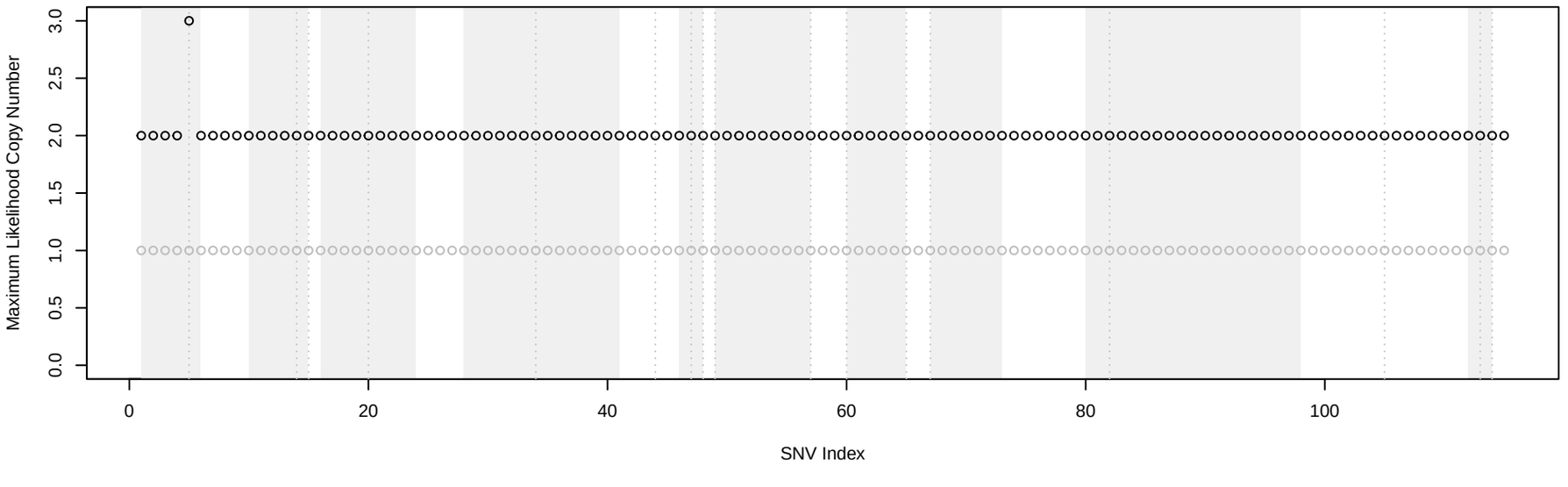

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

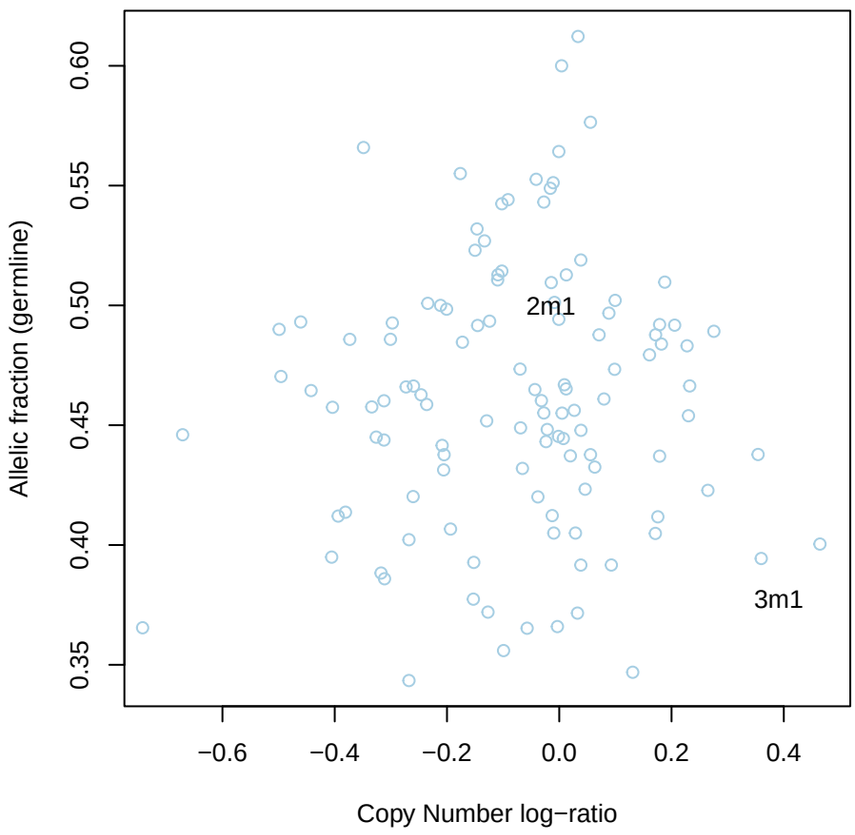

Power 0.8
Frequency
Cellular fraction

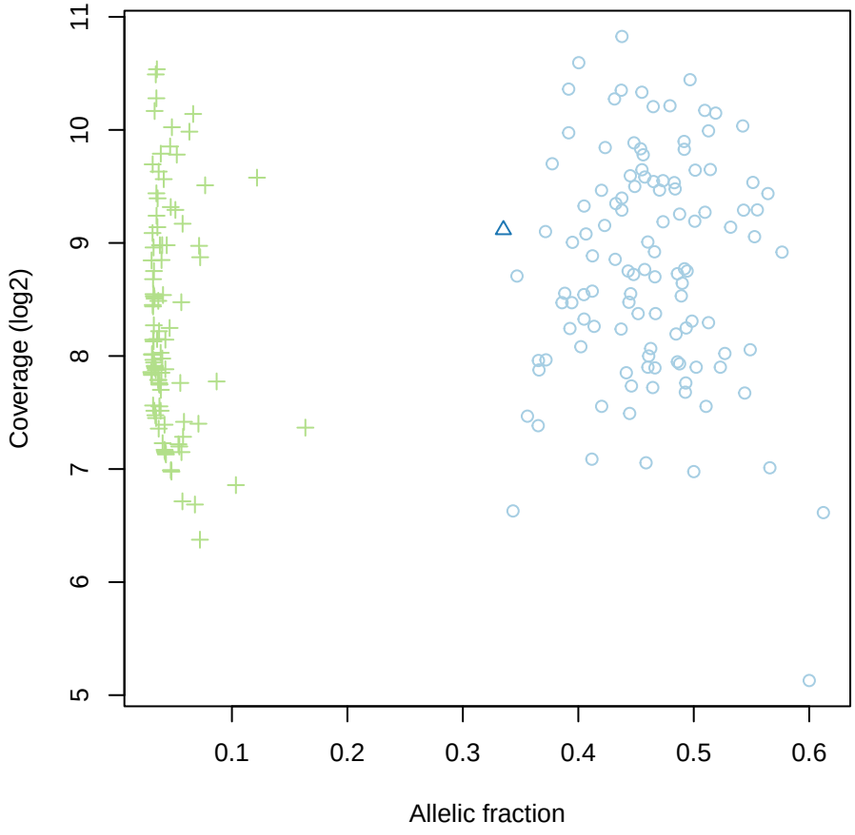

Purity: 0.65 Tumor ploidy: 2.032
1
2
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

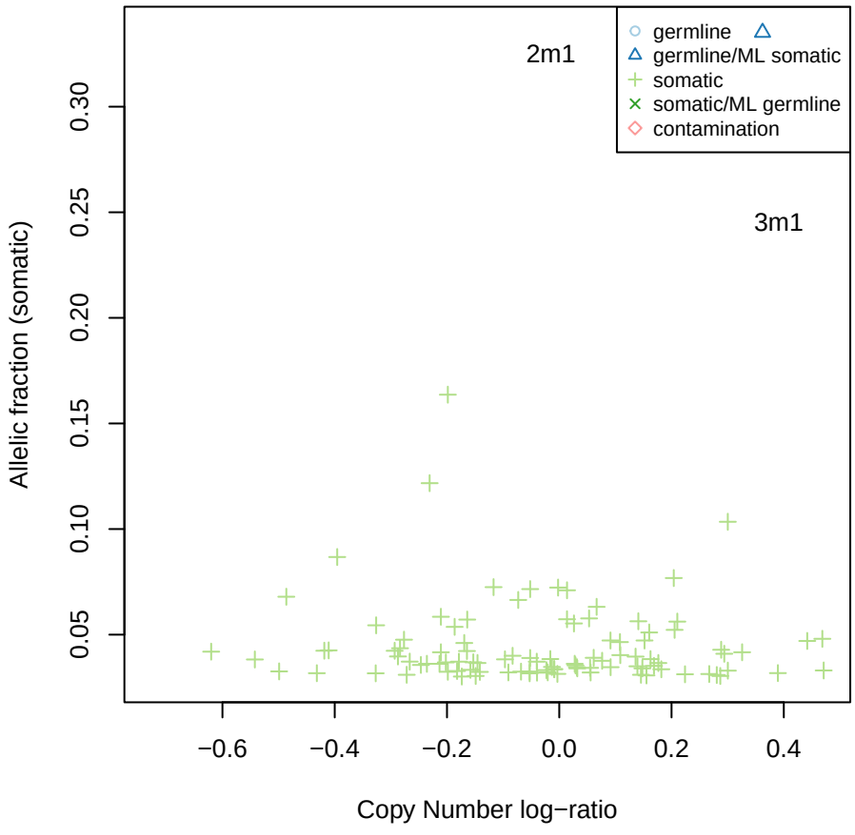

Purity: 0.65 Tumor ploidy: 2.032 SNV log−likelihood: −635.24 GoF: 4% Mean coverage: 389;474
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

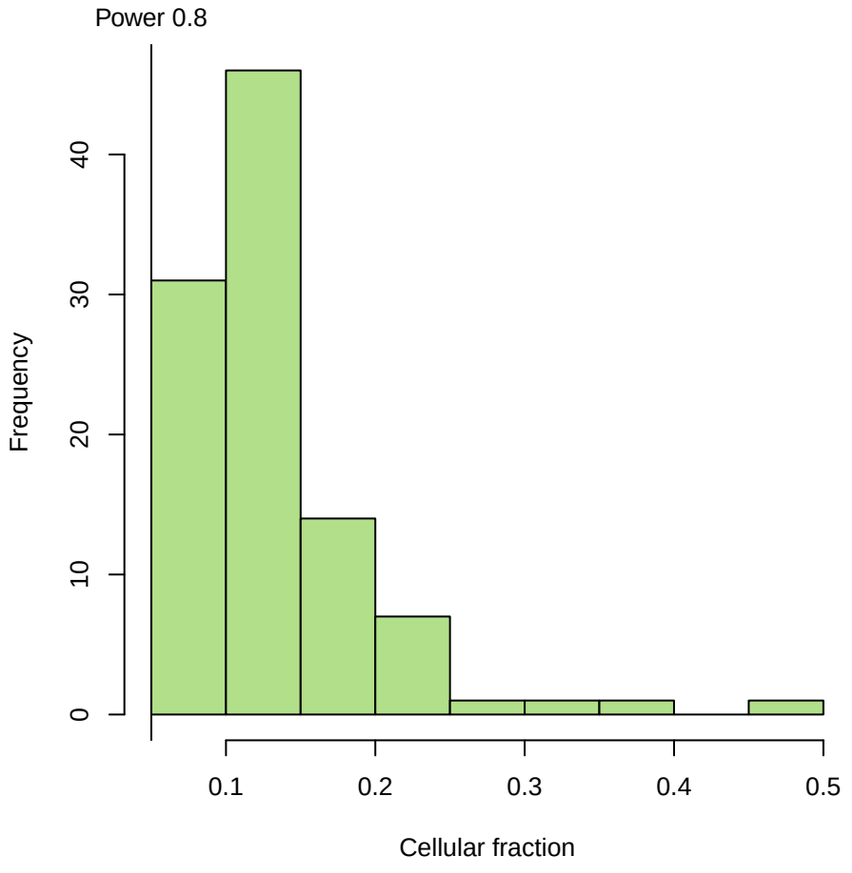

SCNA−fit log−likelihood: −7585.72
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3
0 20 40 60 80 100
SNV Index

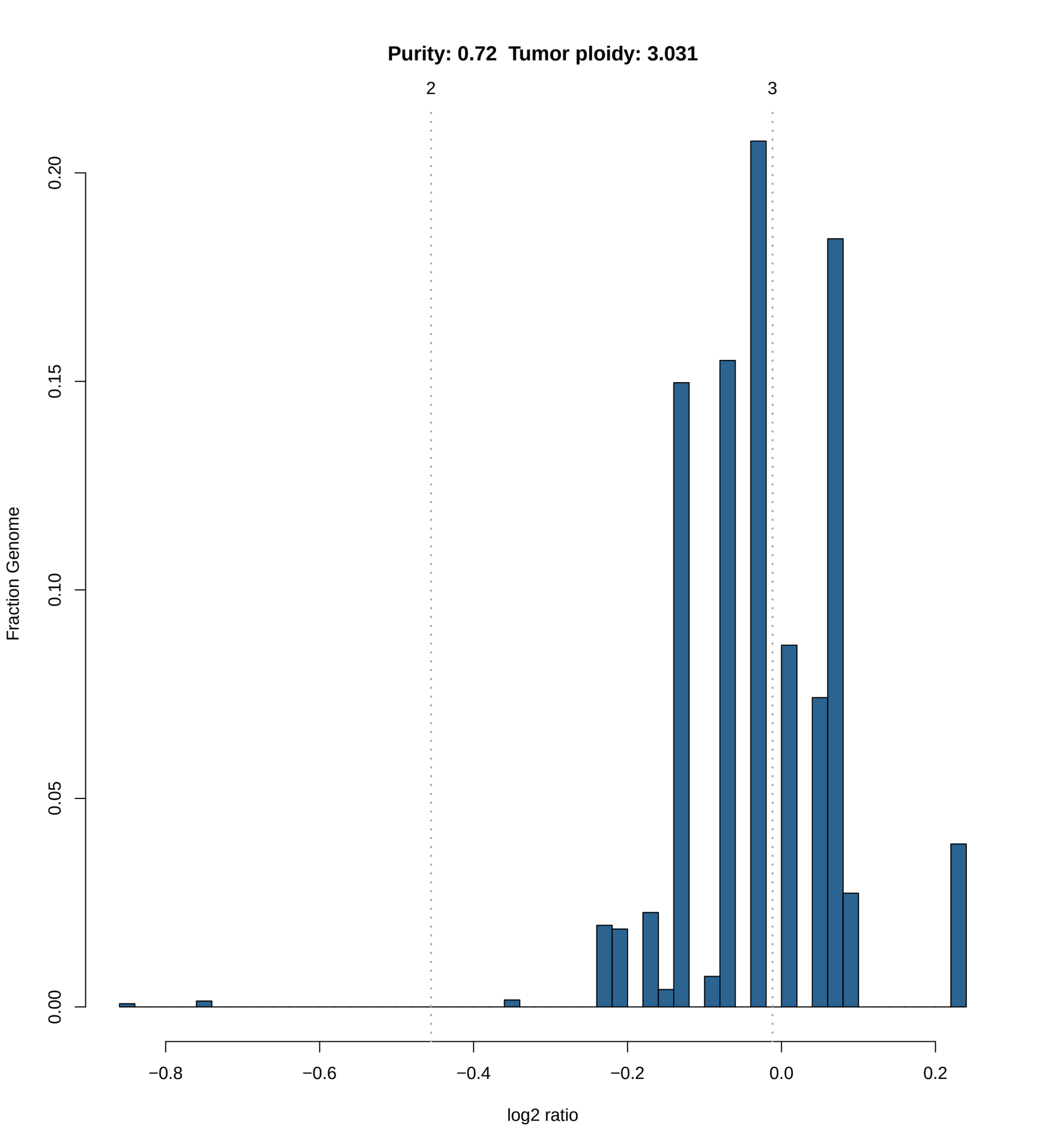

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100
SNV Index

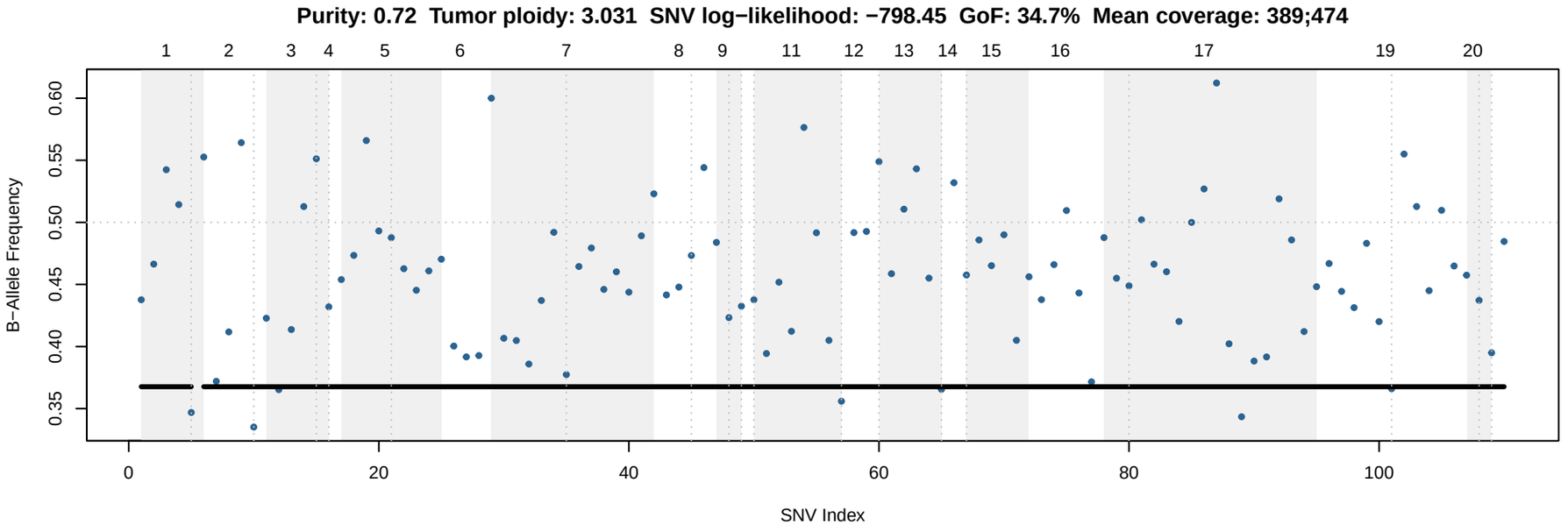

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
2m1
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

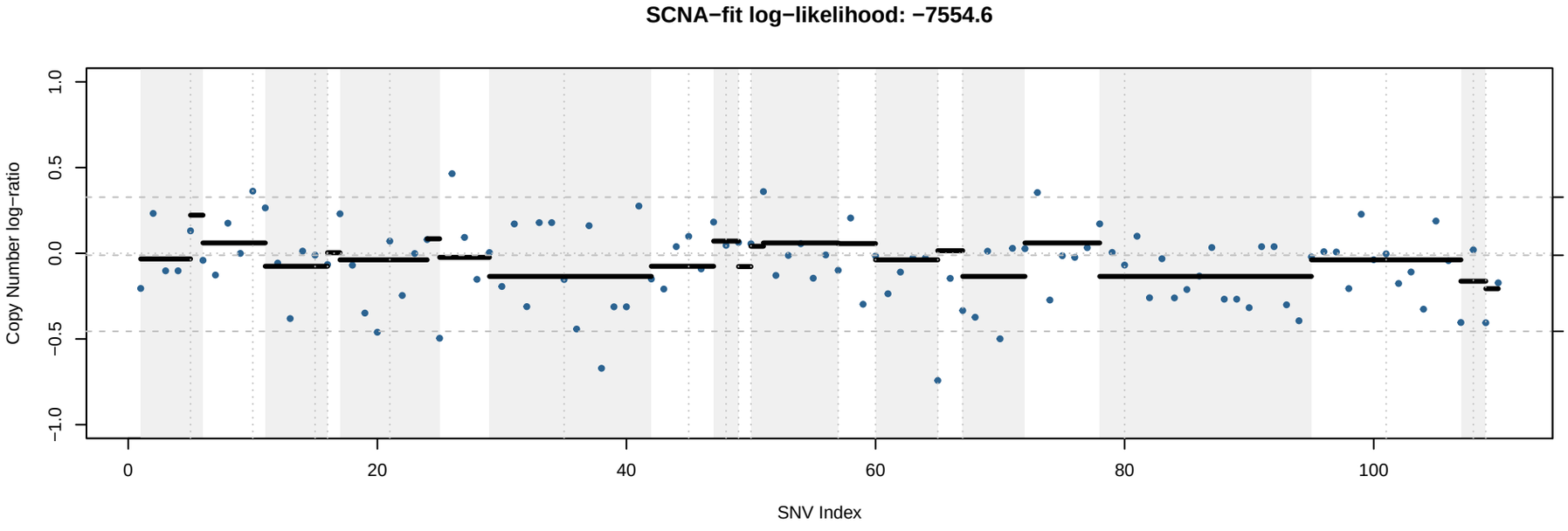

Coverage (log2)
5
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

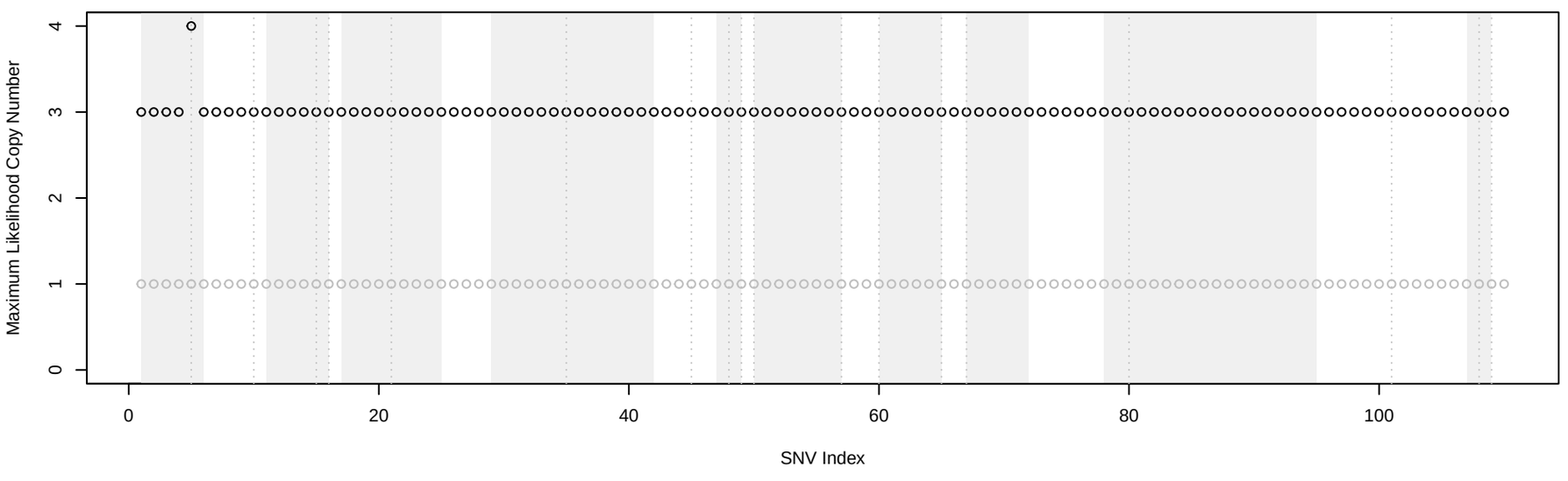

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0.30
2m1
3m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

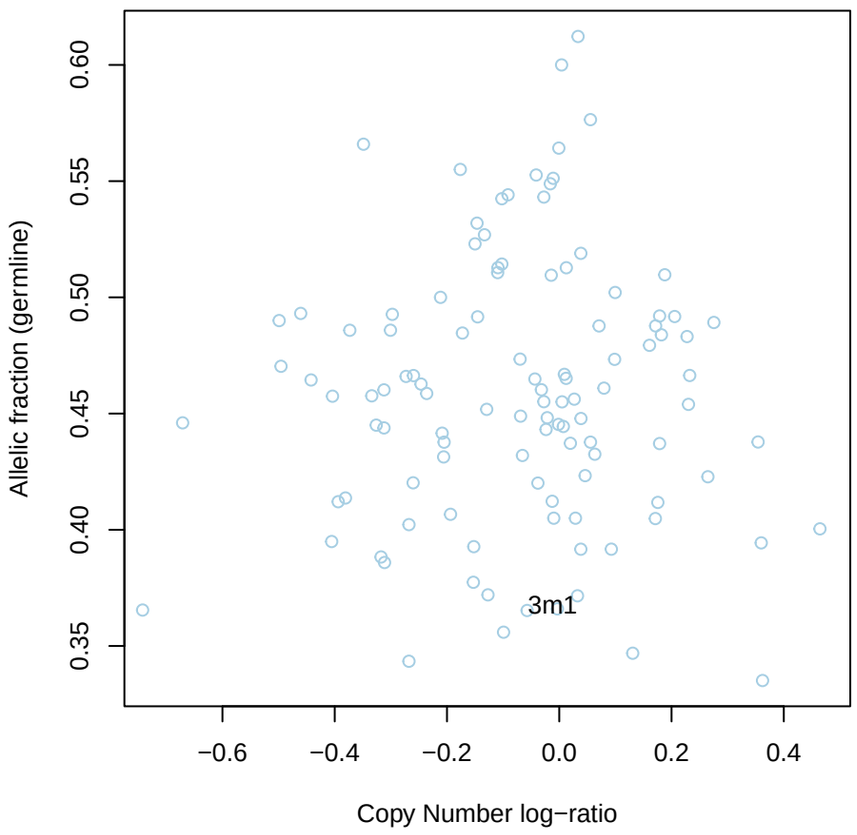

Power 0.8
Frequency
0
10
20
30
40
0.1
0.2
0.3
0.4
0.5
Cellular fraction

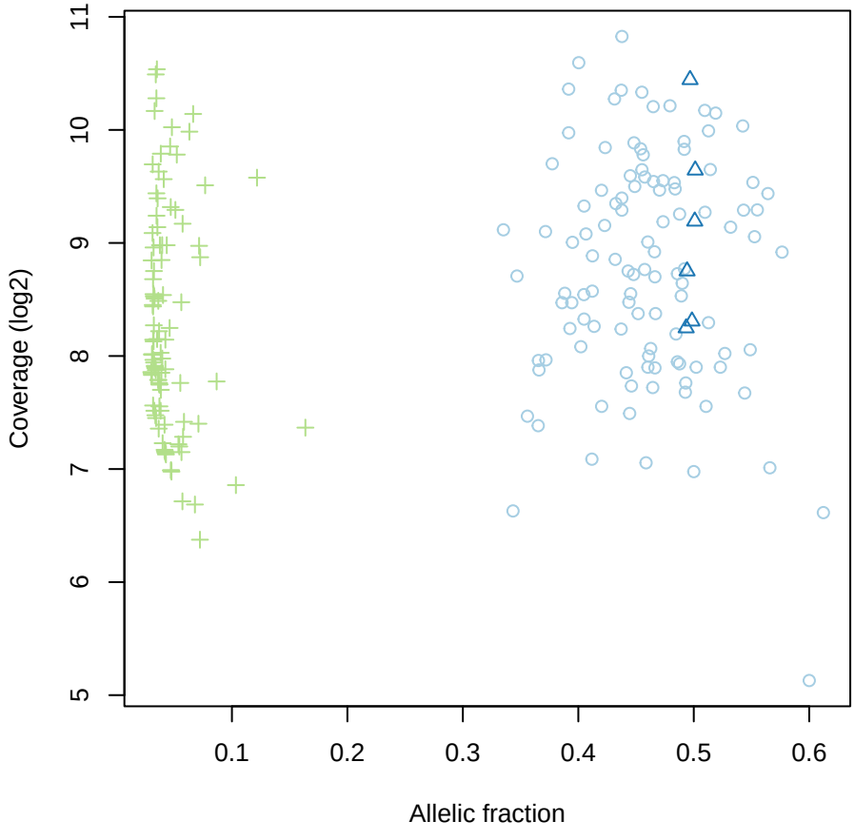

Purity: 0.72 Tumor ploidy: 3.031
2
3
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

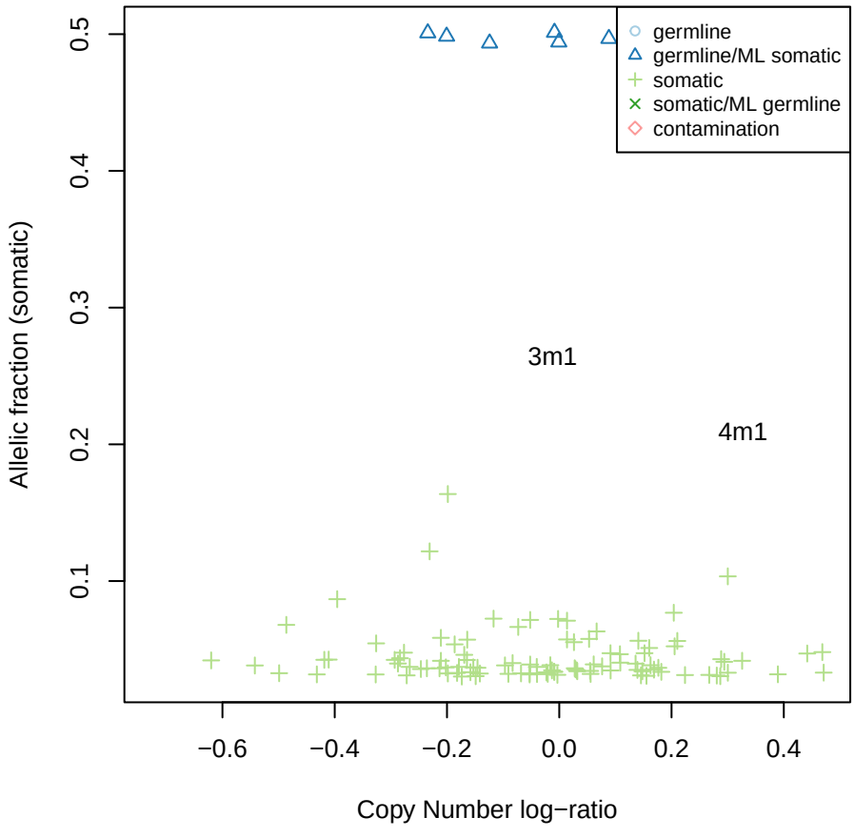

Purity: 0.72 Tumor ploidy: 3.031 SNV log−likelihood: −798.45 GoF: 34.7% Mean coverage: 389;474
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

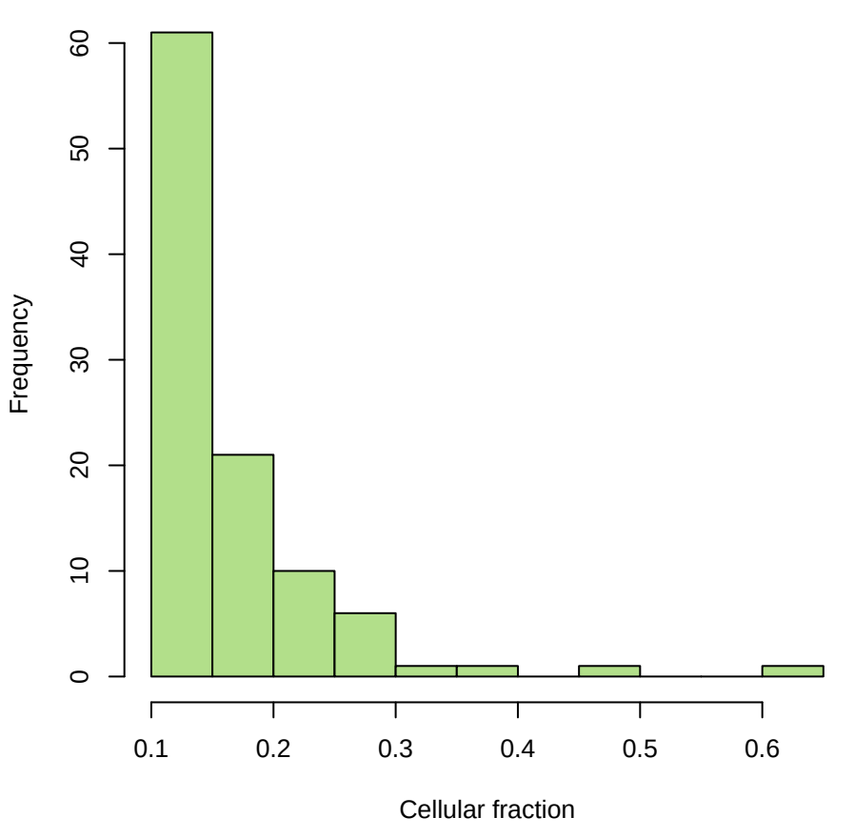

SCNA−fit log−likelihood: −7554.6
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4
0 20 40 60 80 100
SNV Index


Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100
SNV Index


Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio


Coverage (log2)
5
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction


Allelic fraction (somatic)
0.1
0.2
0.3
0.4
0.5
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio


Frequency
0
10
20
30
40
50
60
0.1
0.2
0.3
0.4
0.5
0.6
Cellular fraction