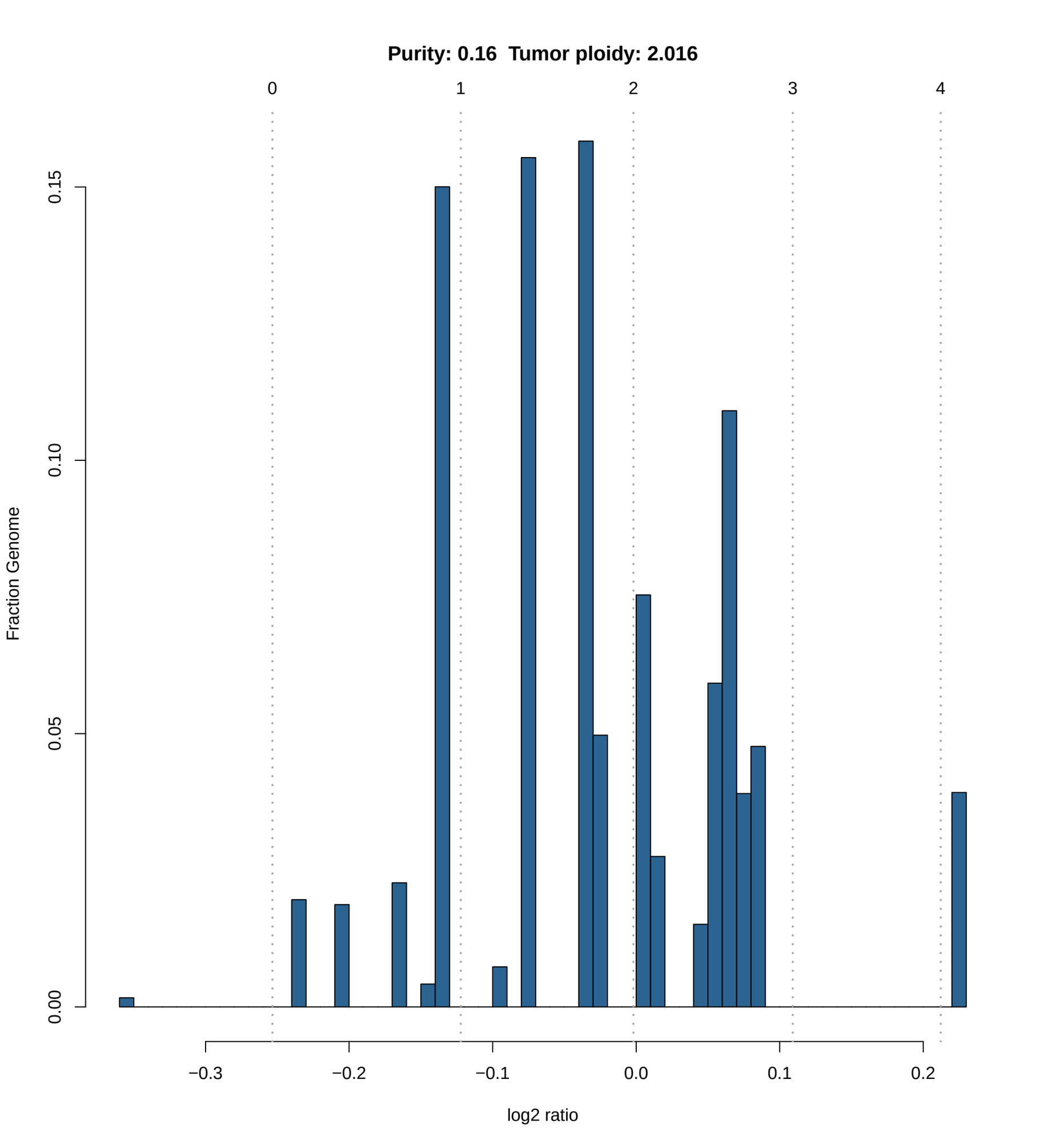
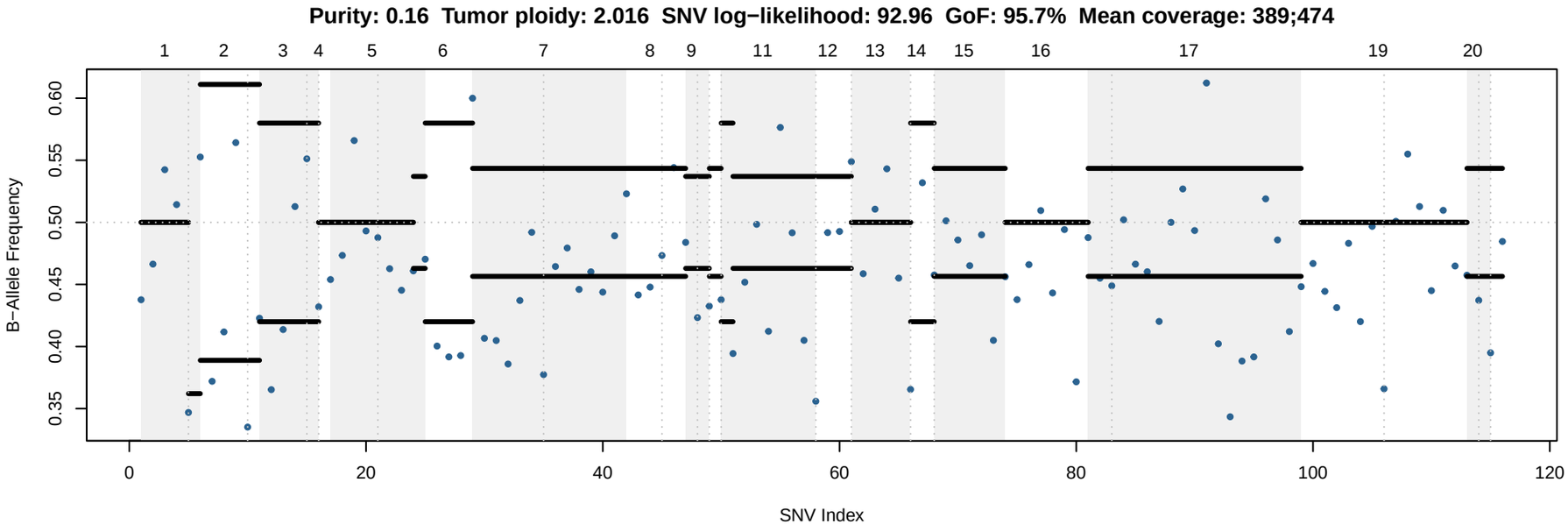
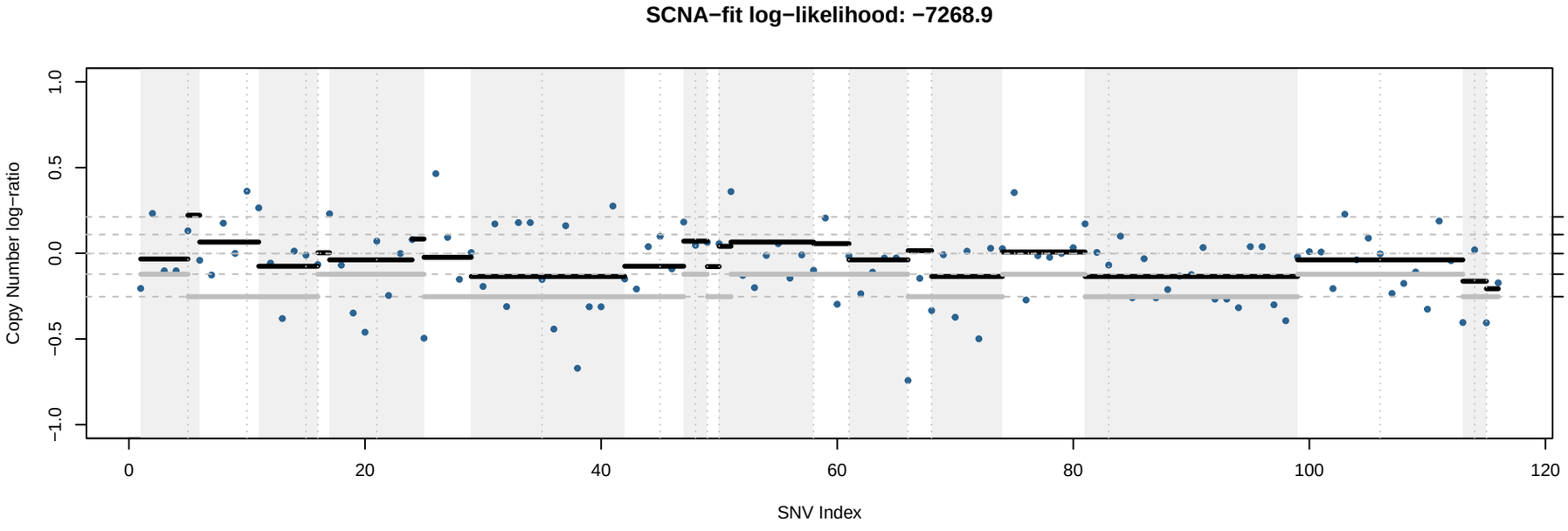
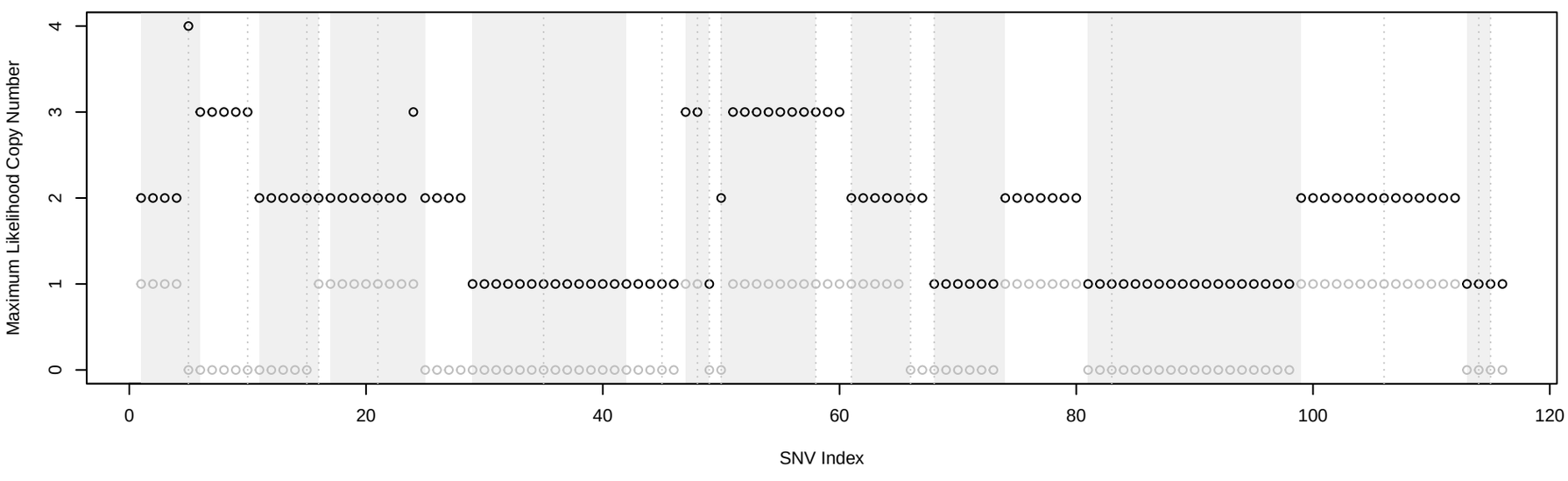
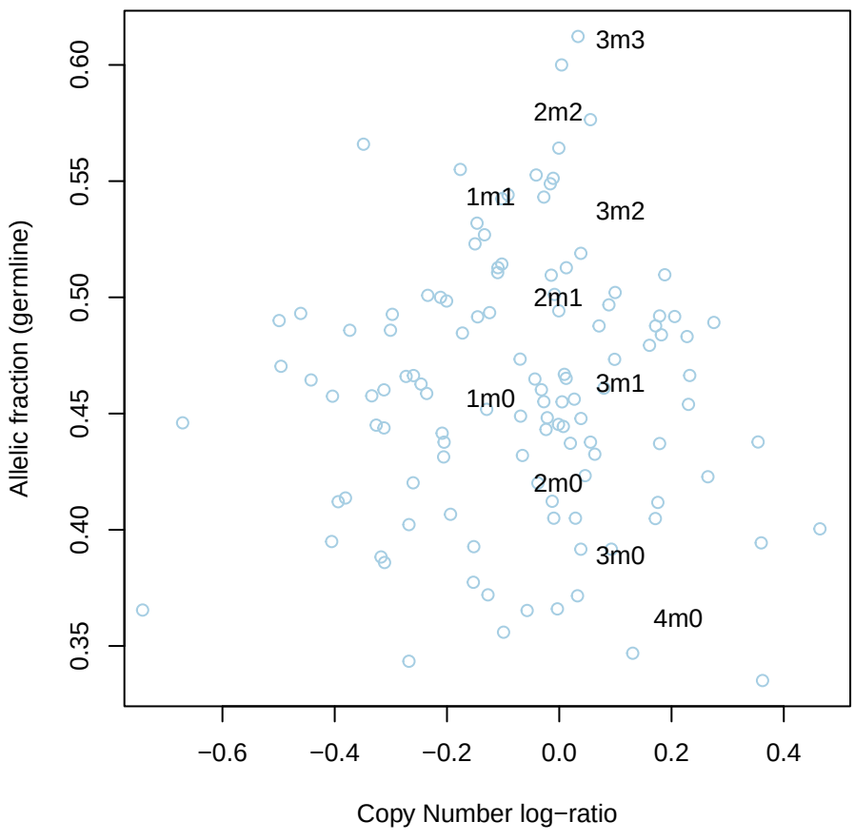
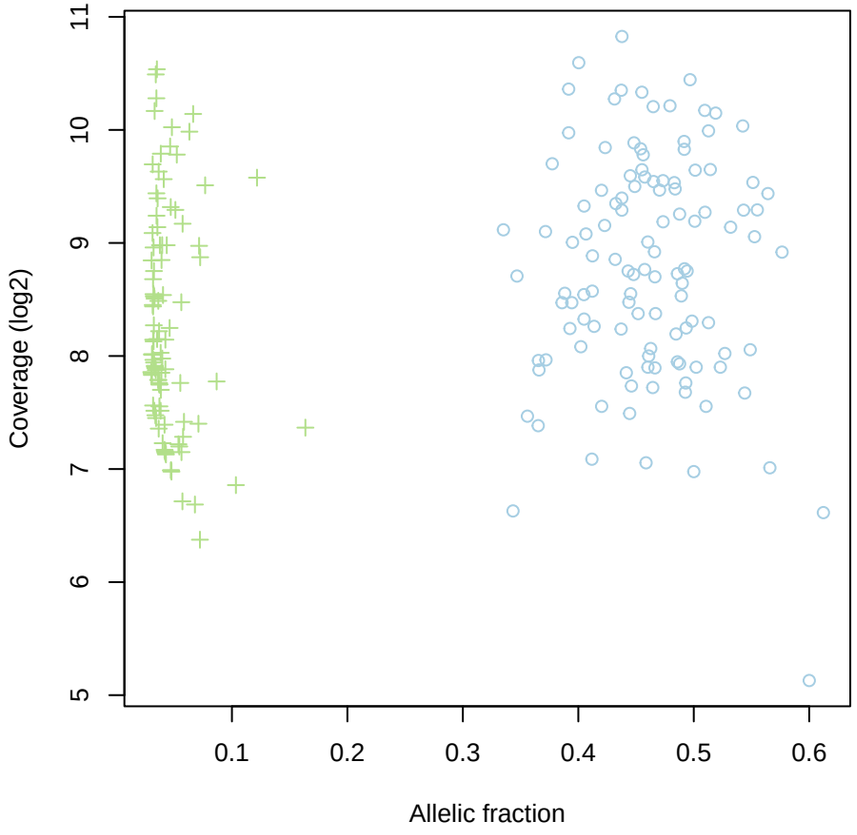

Purity: 0.16 Tumor ploidy: 2.016
0
1
2
3
4
0.15
0.10
0.05
0.00
Fraction Genome
−0.3
−0.2
−0.1
0.0
0.1
0.2
log2 ratio

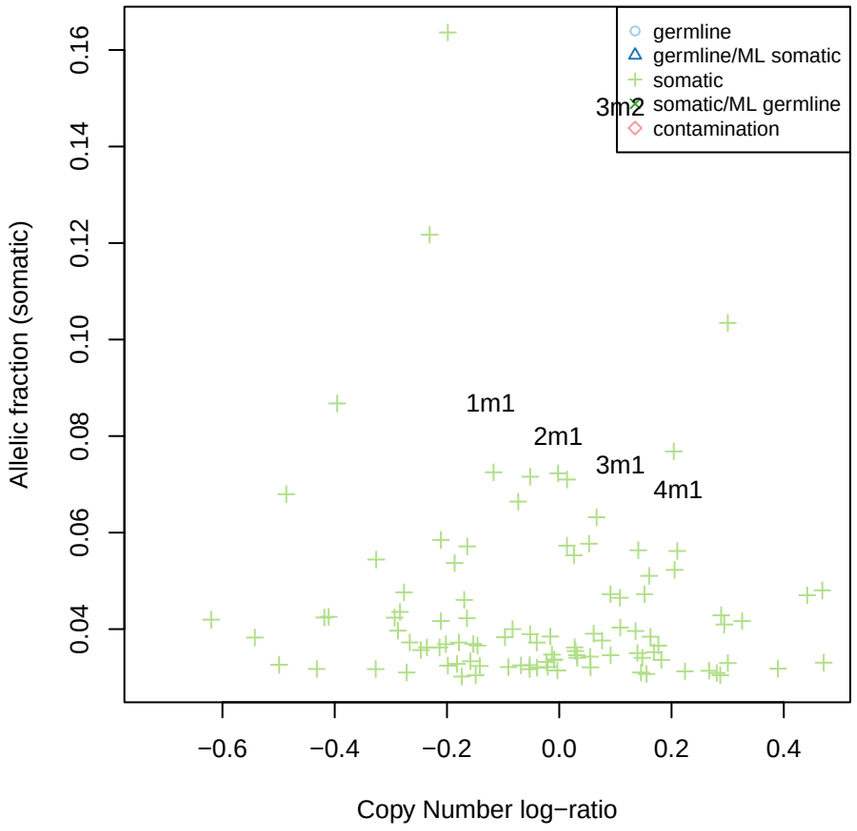

Purity: 0.16 Tumor ploidy: 2.016 SNV log−likelihood: 92.96 GoF: 95.7% Mean coverage: 389;474
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100 120
SNV Index

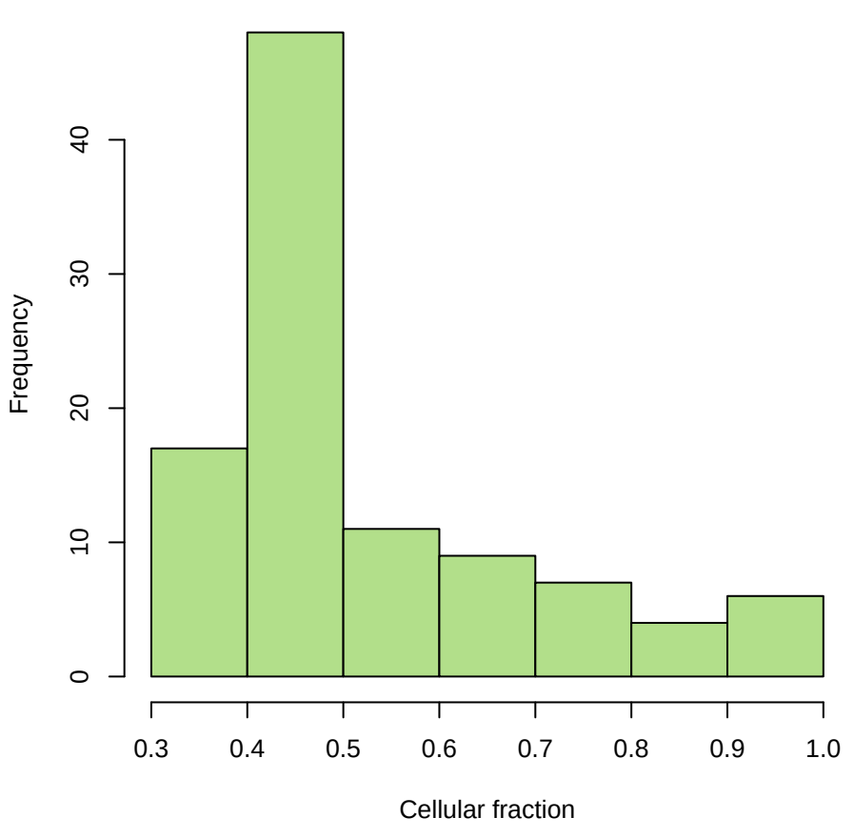

SCNA−fit log−likelihood: −7268.9
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4
0 20 40 60 80 100 120
SNV Index

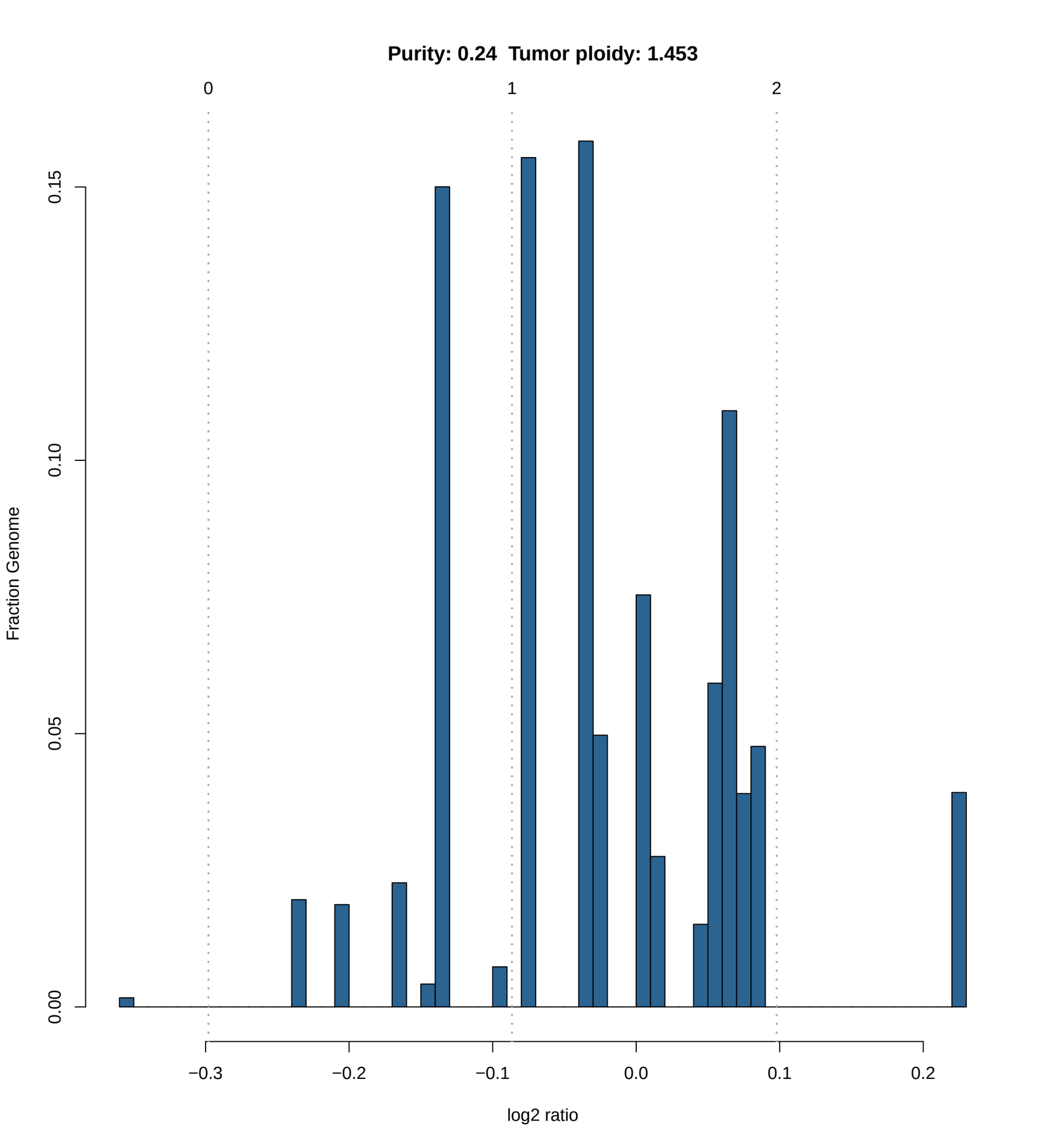

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120
SNV Index

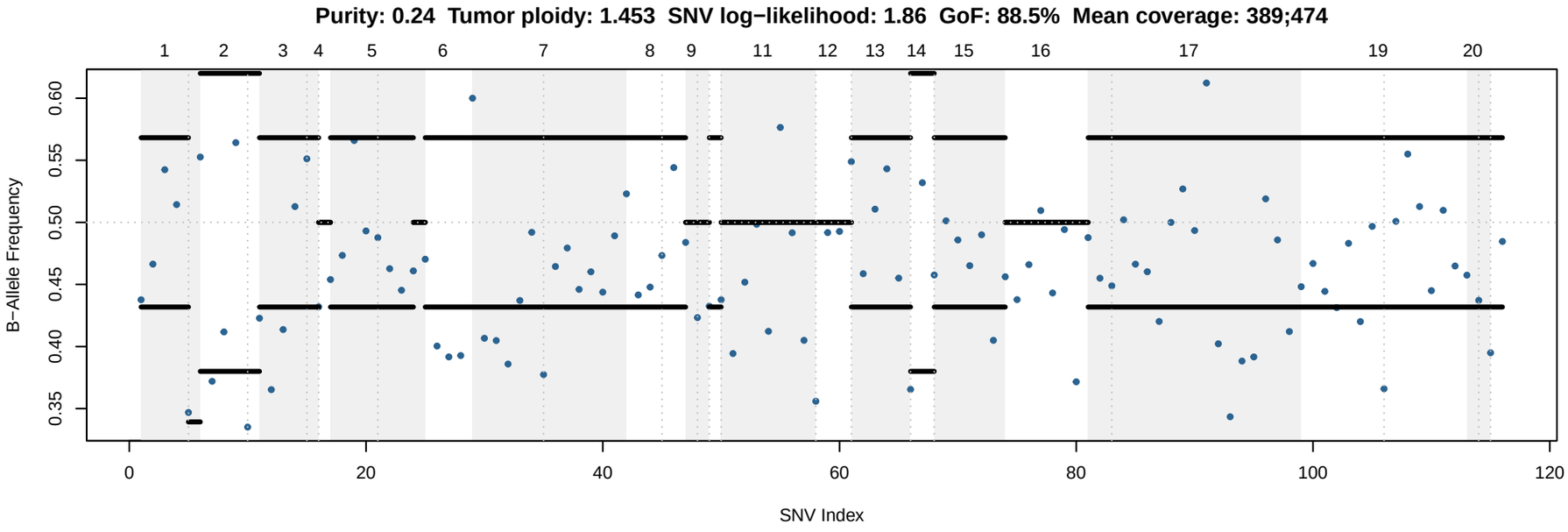

Allelic fraction (germline)
Copy Number log−ratio
3m3
2m2
1m1
3m2
2m1
3m1
1m0
2m0
3m0
4m0

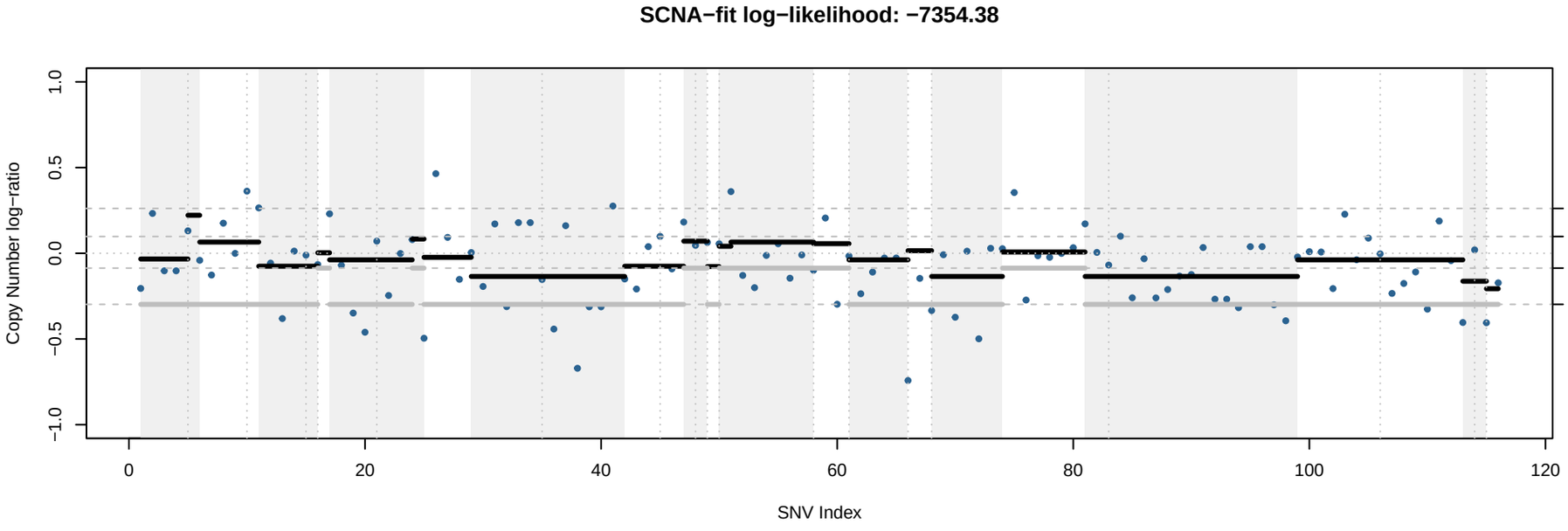

Coverage (log2)
Allelic fraction

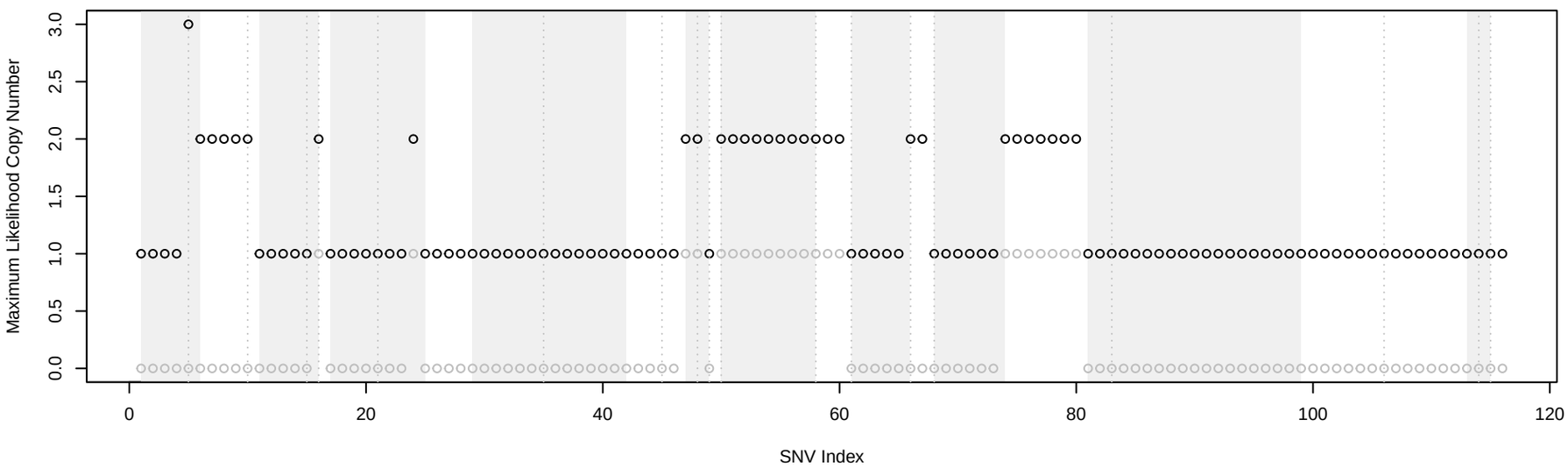

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m2
1m1
2m1
3m1
4m1

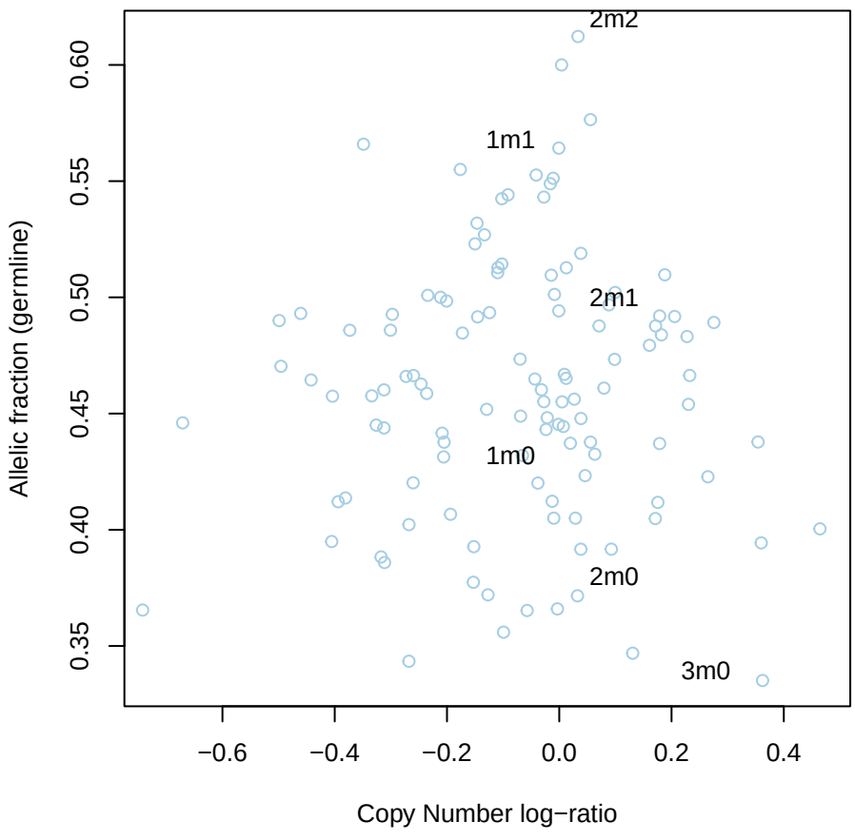

Frequency
Cellular fraction

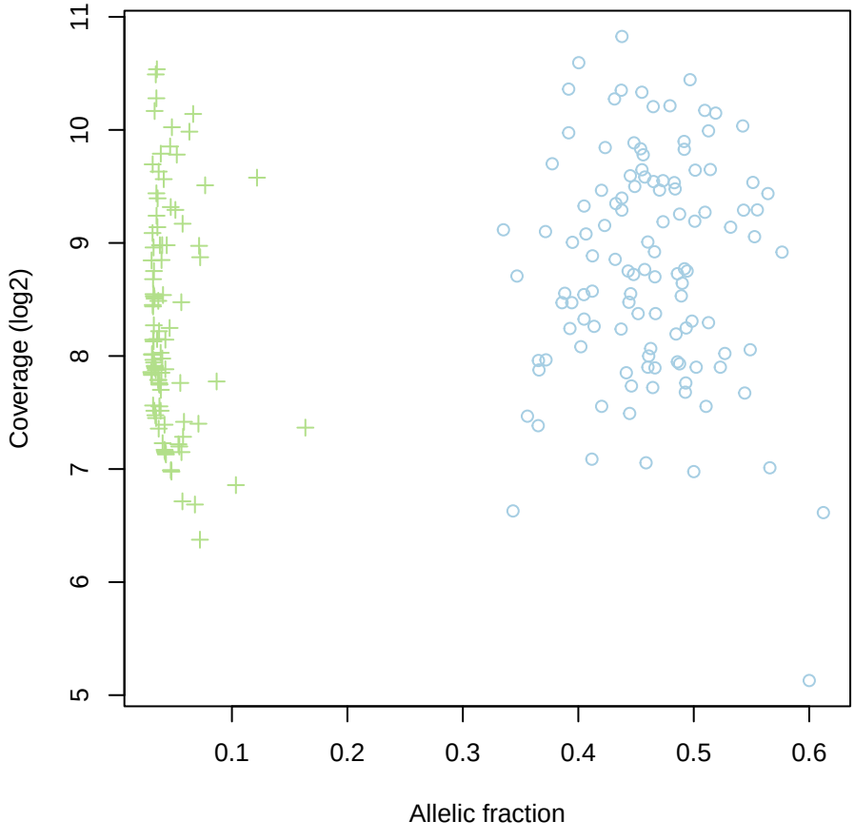

Purity: 0.24 Tumor ploidy: 1.453
0
1
2
0.15
0.10
0.05
0.00
Fraction Genome
−0.3
−0.2
−0.1
0.0
0.1
0.2
log2 ratio

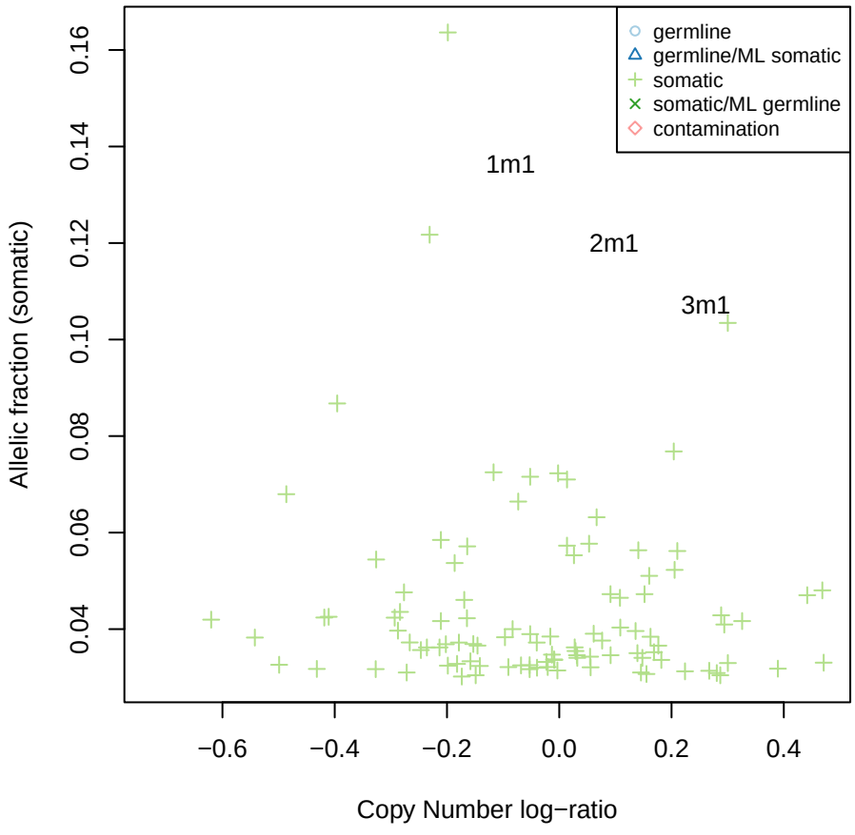

Purity: 0.24 Tumor ploidy: 1.453 SNV log−likelihood: 1.86 GoF: 88.5% Mean coverage: 389;474
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100 120
SNV Index

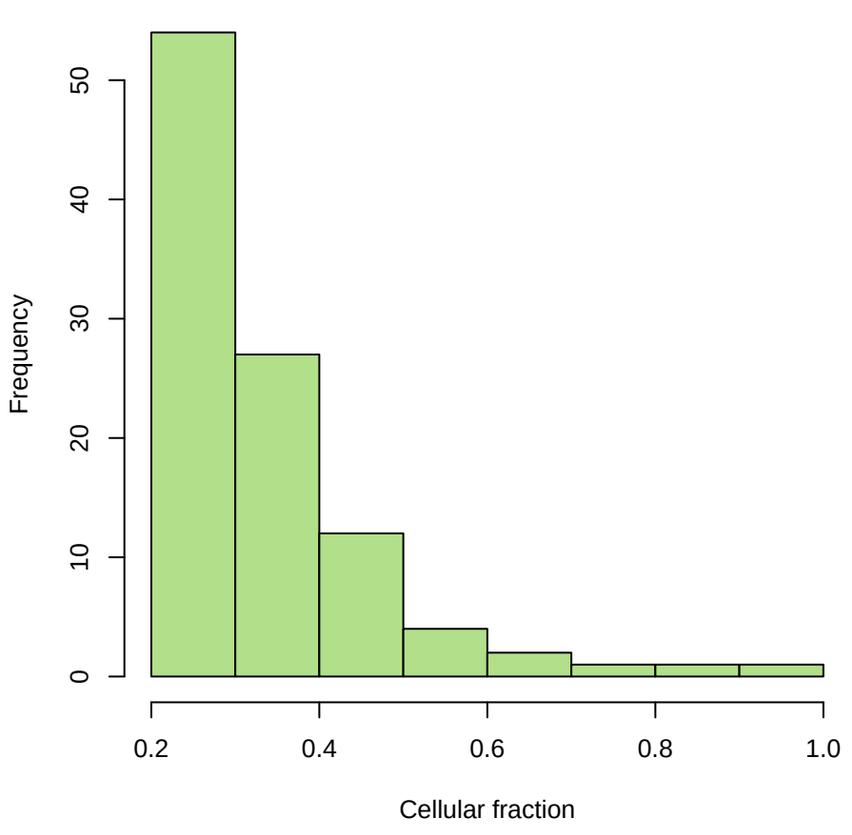

SCNA−fit log−likelihood: −7354.38
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3
0 20 40 60 80 100 120
SNV Index

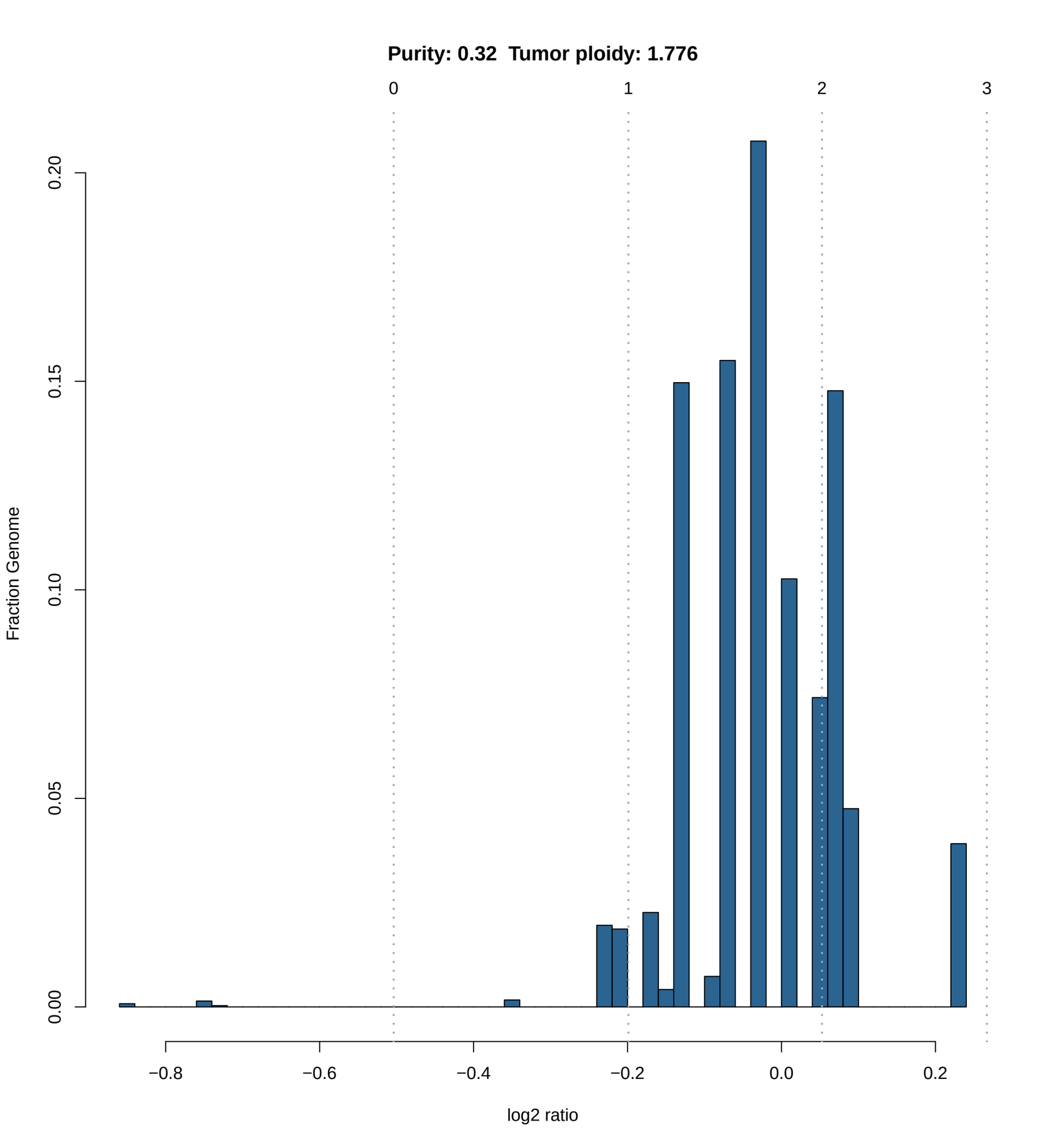

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120
SNV Index

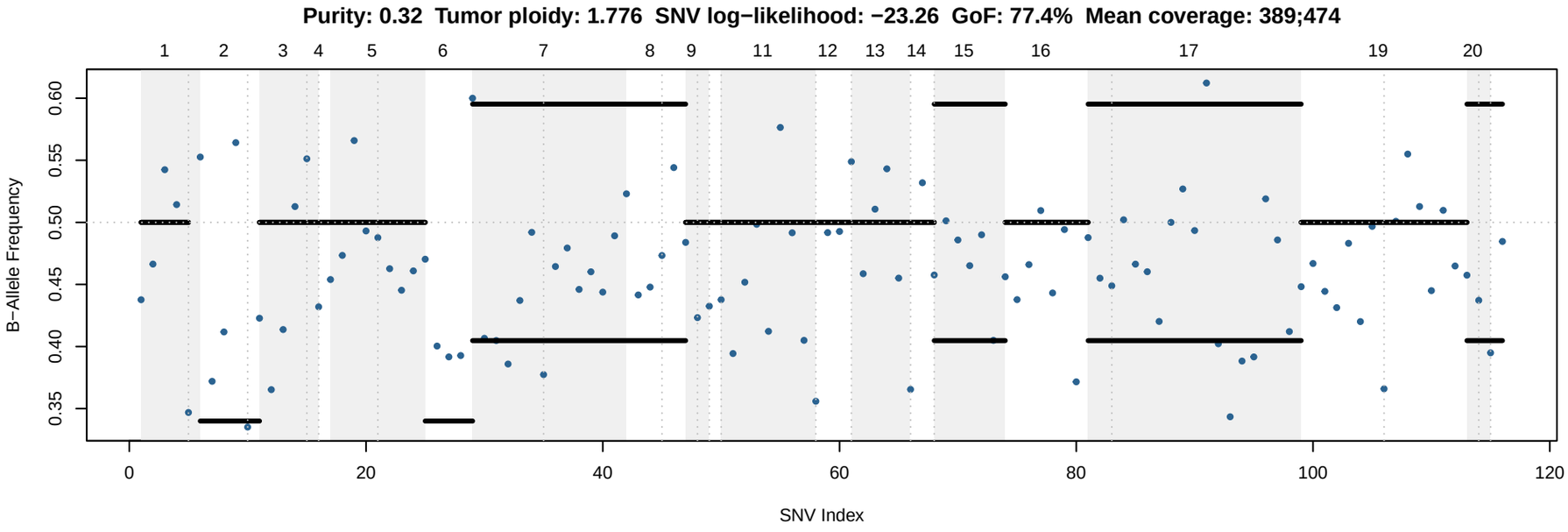

2m2
1m1
2m1
1m0
2m0
3m0
Allelic fraction (germline)
Copy Number log−ratio

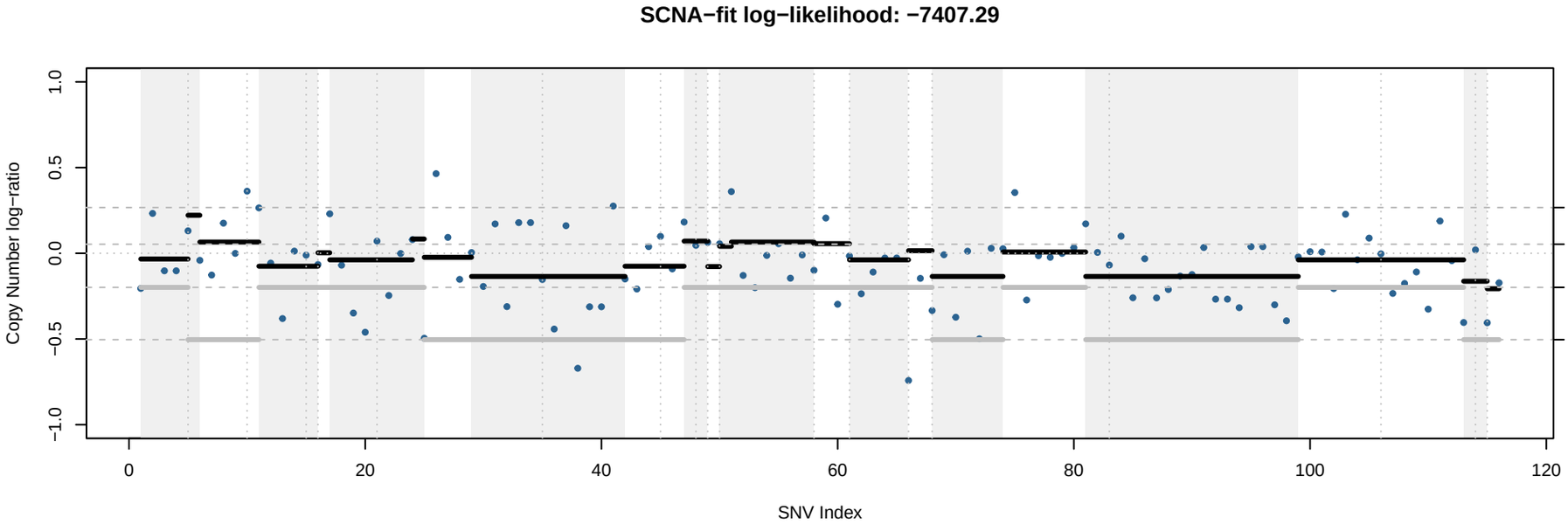

Coverage (log2)
Allelic fraction

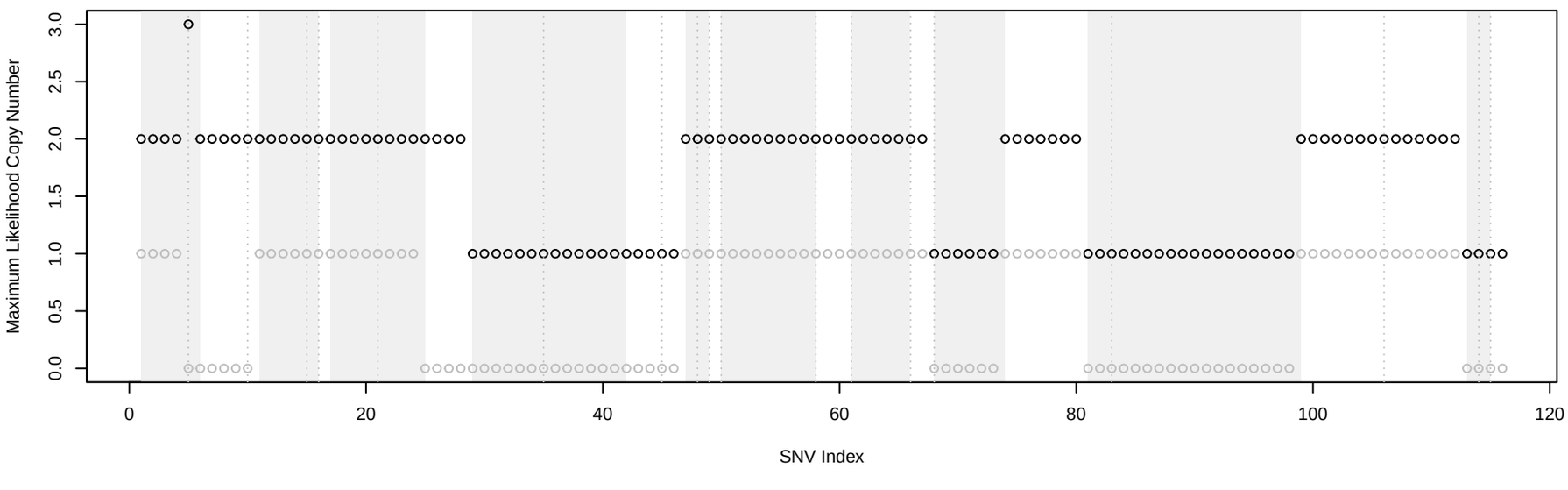

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
Allelic fraction (somatic)
Copy Number log−ratio

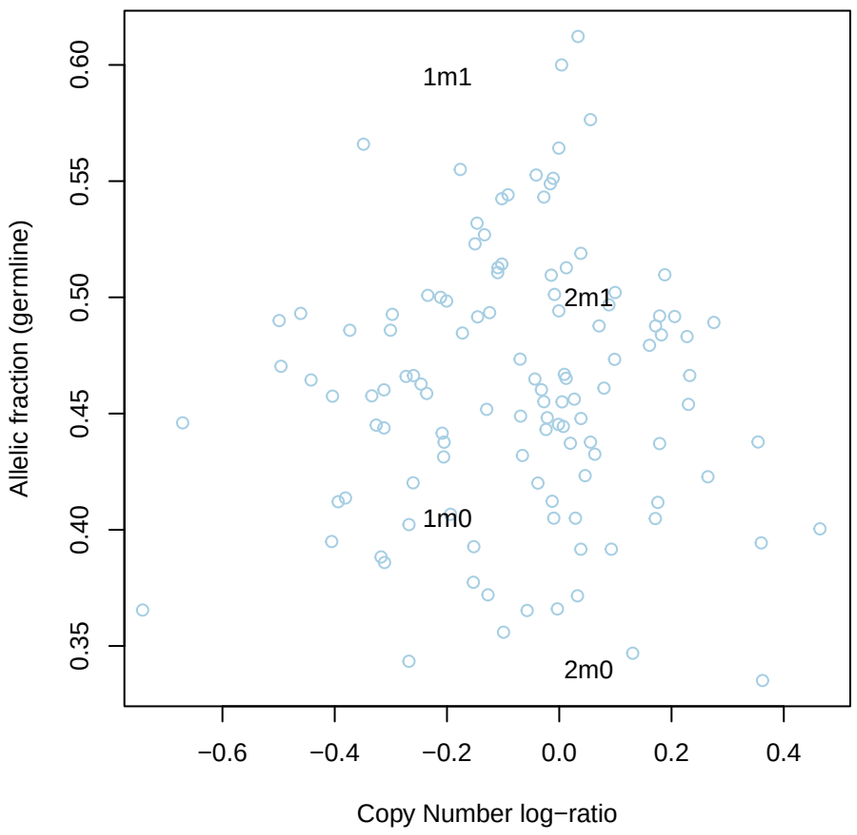

Frequency
Cellular fraction

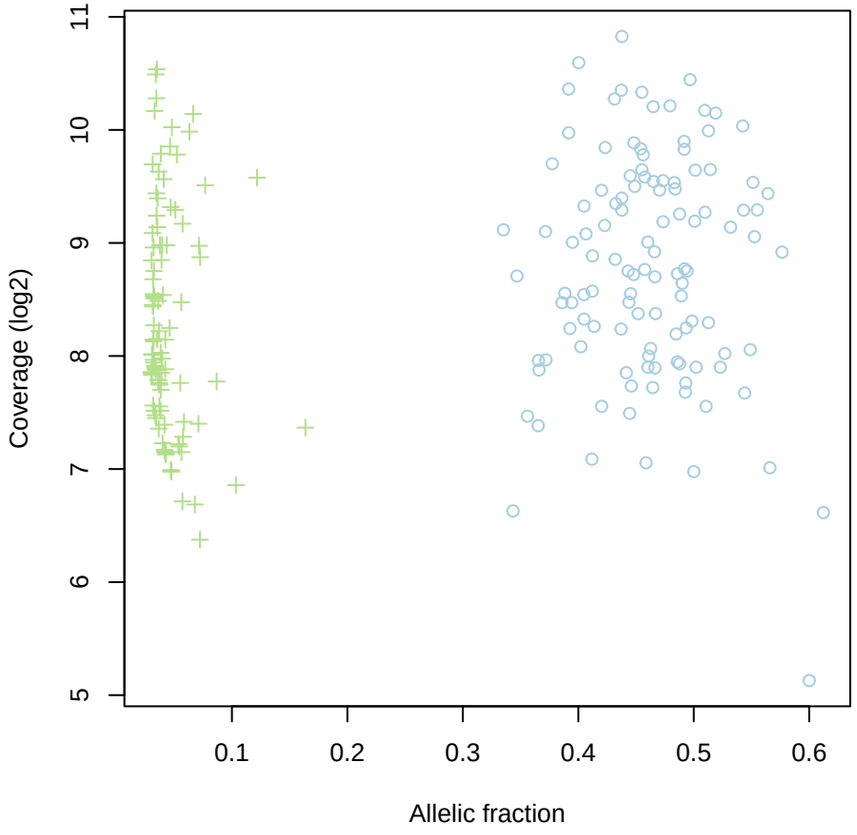

Purity: 0.32 Tumor ploidy: 1.776
0
1
2
3
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

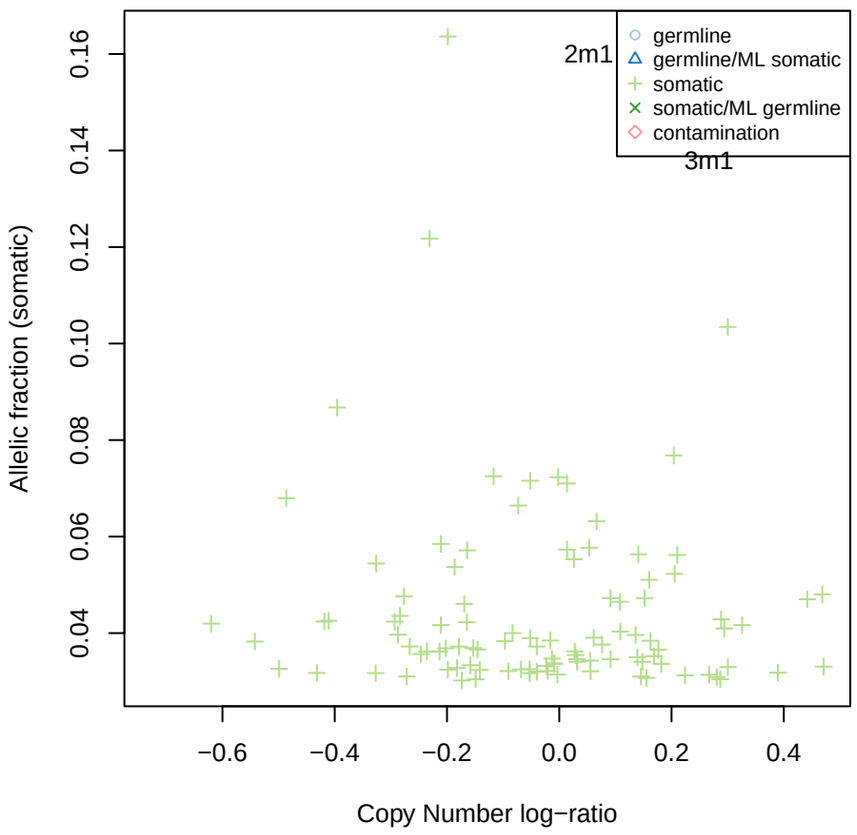

Purity: 0.32 Tumor ploidy: 1.776 SNV log−likelihood: −23.26 GoF: 77.4% Mean coverage: 389;474
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100 120
SNV Index

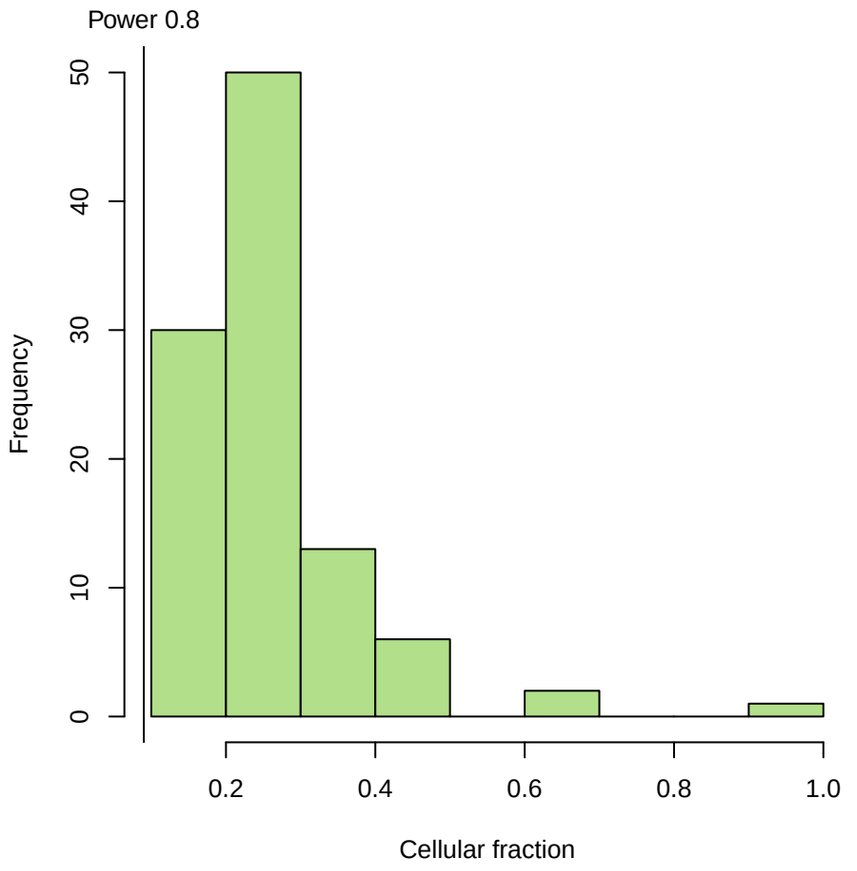

SCNA−fit log−likelihood: −7407.29
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3
0 20 40 60 80 100 120
SNV Index

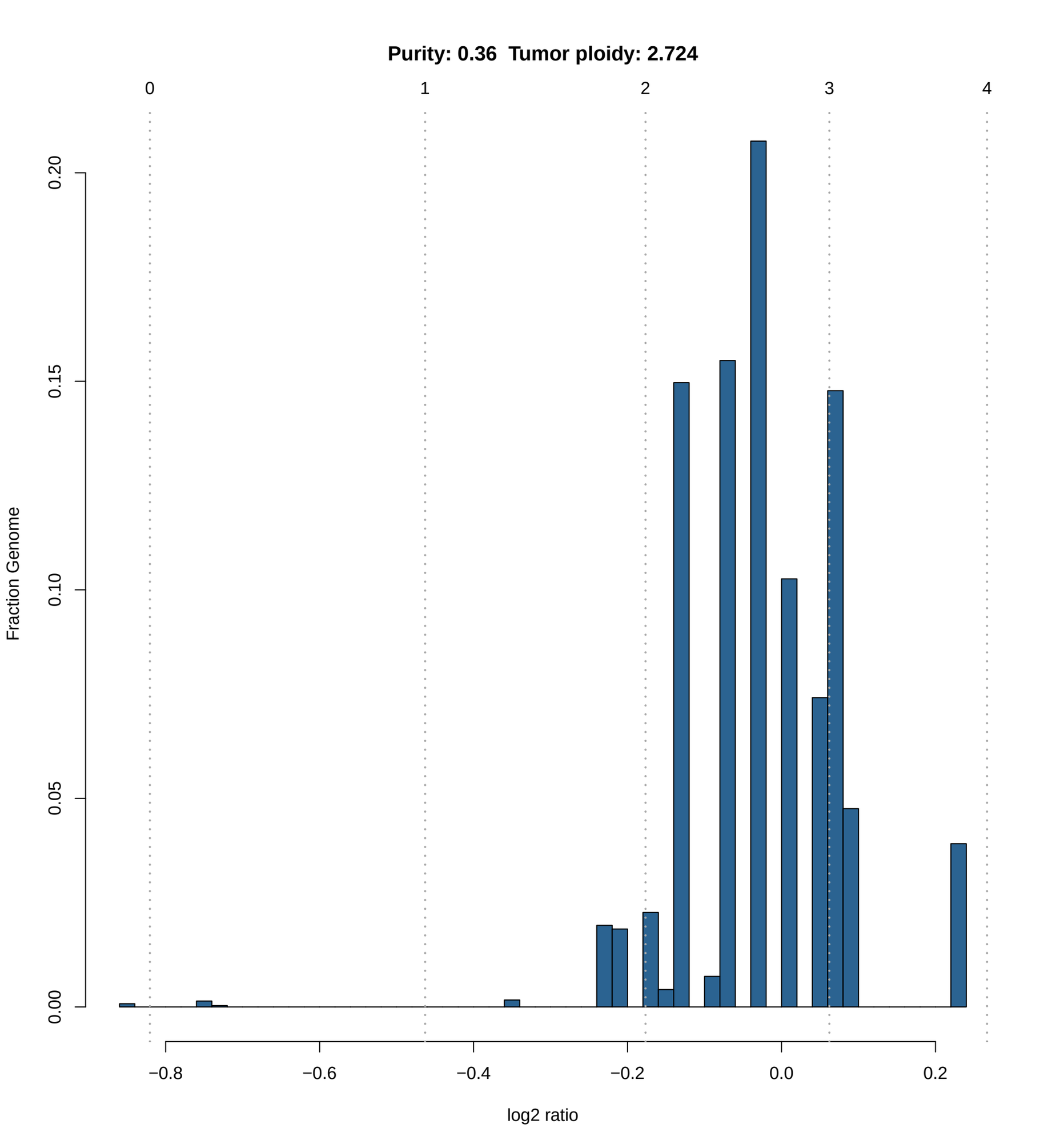

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120
SNV Index

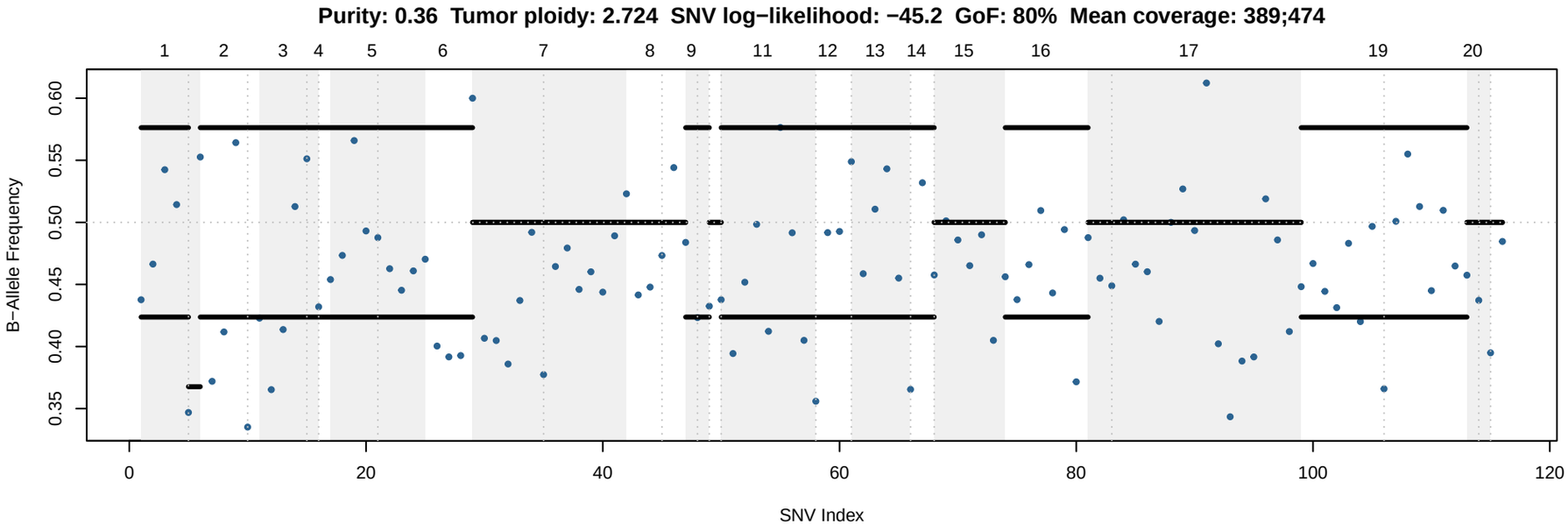

Allelic fraction (germline)
Copy Number log−ratio
1m1
2m1
1m0
2m0

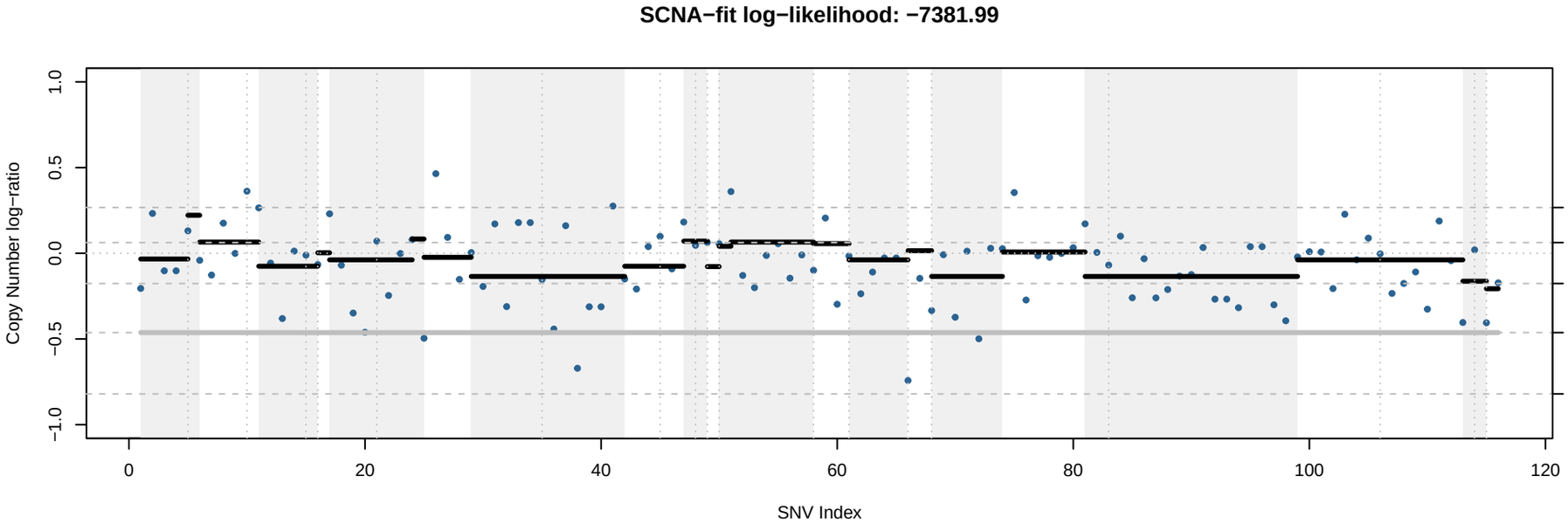

Coverage (log2)
Allelic fraction

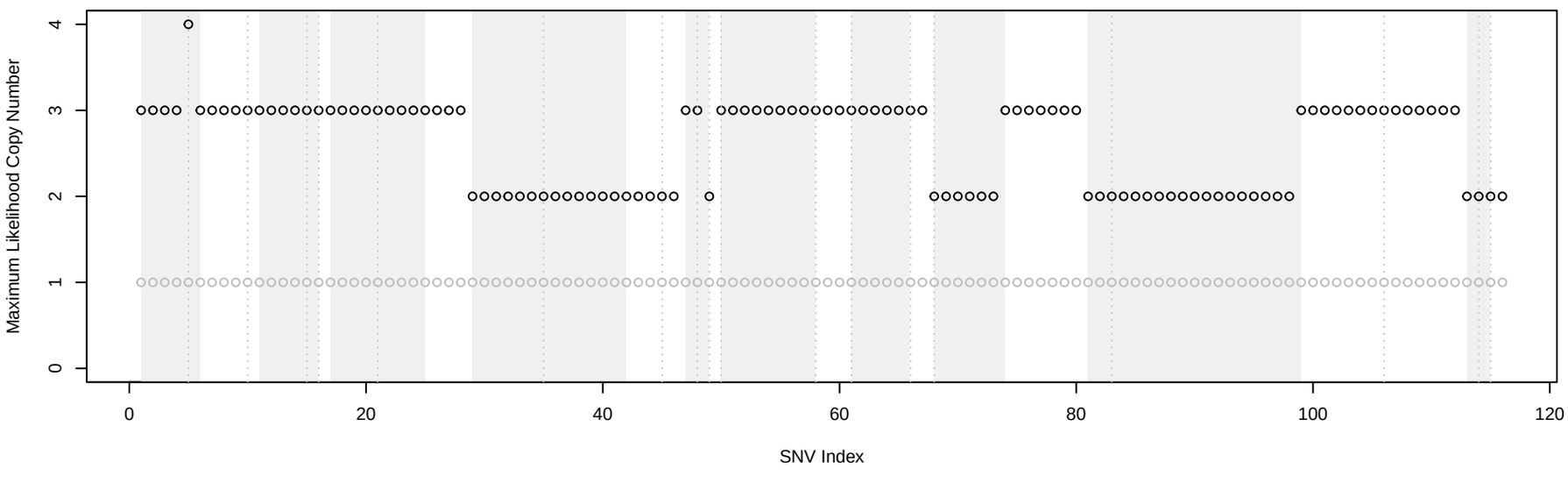

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1

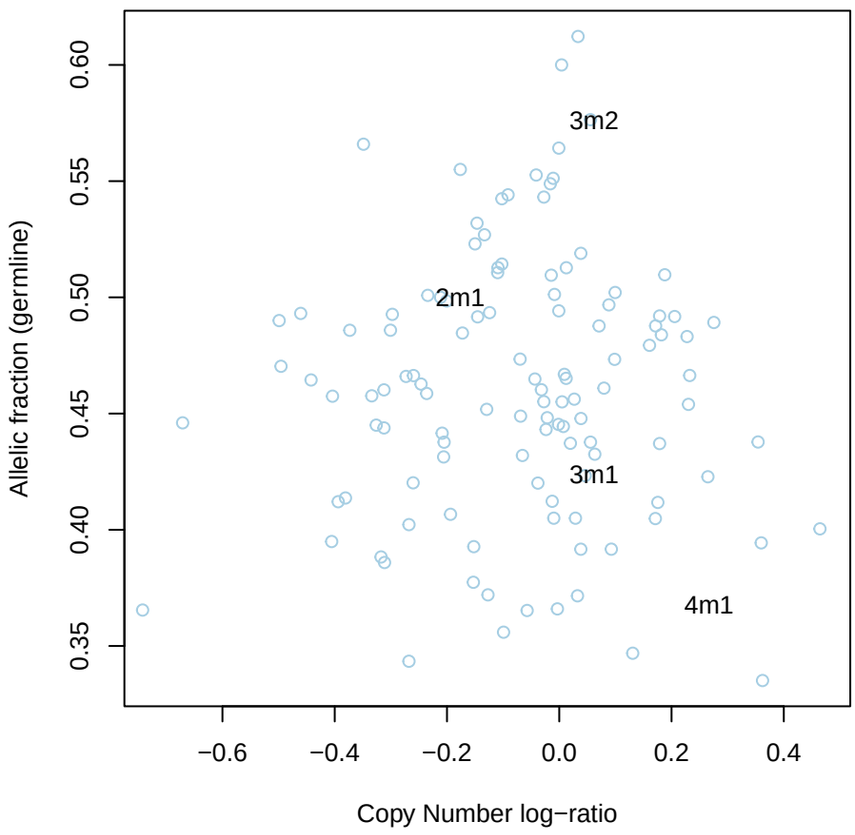

Power 0.8
Frequency
Cellular fraction

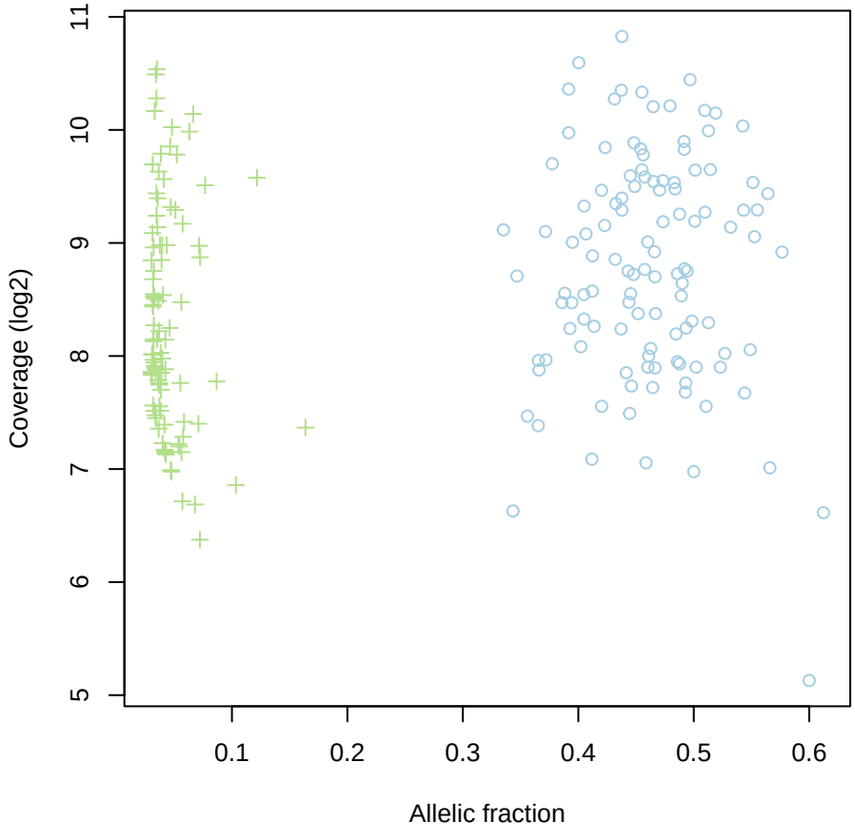

Purity: 0.36 Tumor ploidy: 2.724
0
1
2
3
4
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

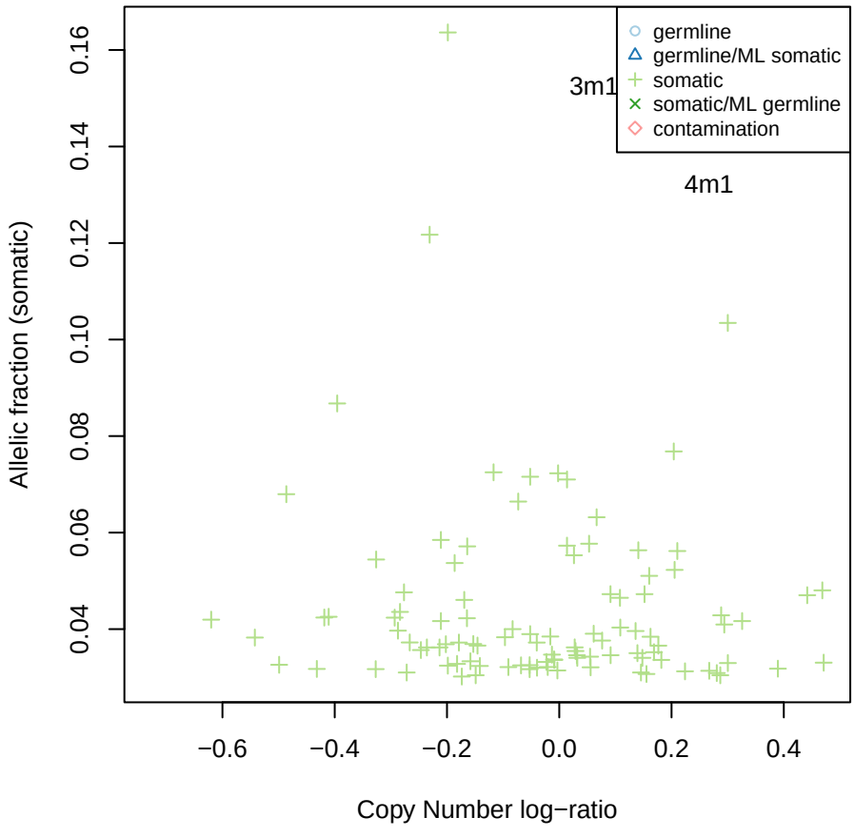

Purity: 0.36 Tumor ploidy: 2.724 SNV log−likelihood: −45.2 GoF: 80% Mean coverage: 389;474
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100 120
SNV Index

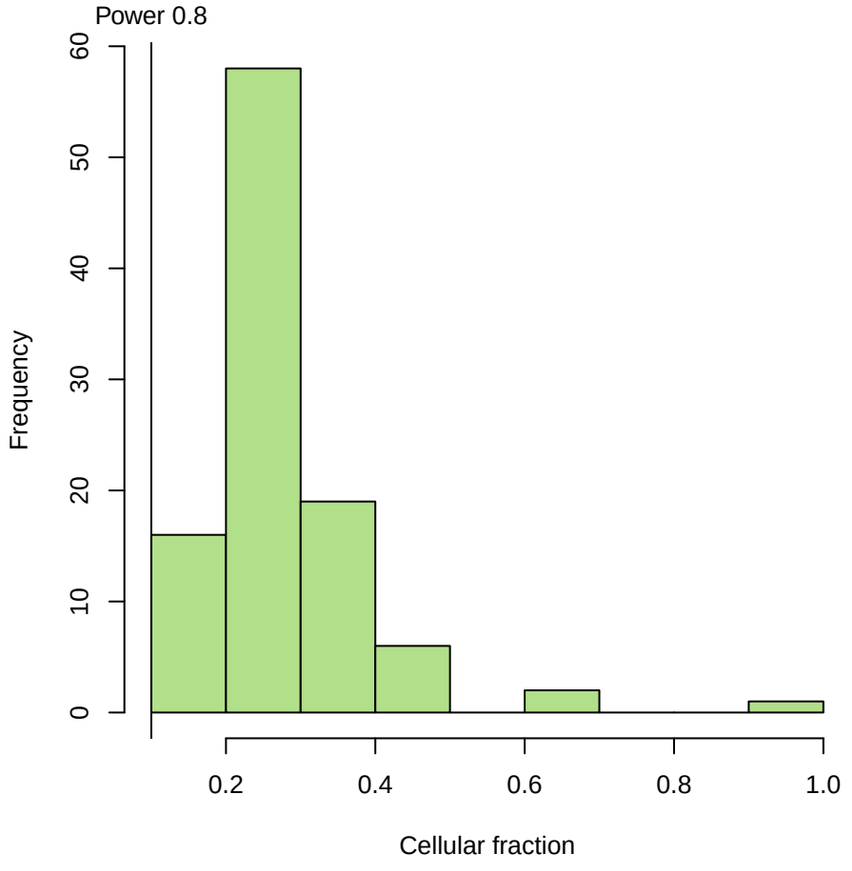

SCNA−fit log−likelihood: −7381.99
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4
0 20 40 60 80 100 120
SNV Index

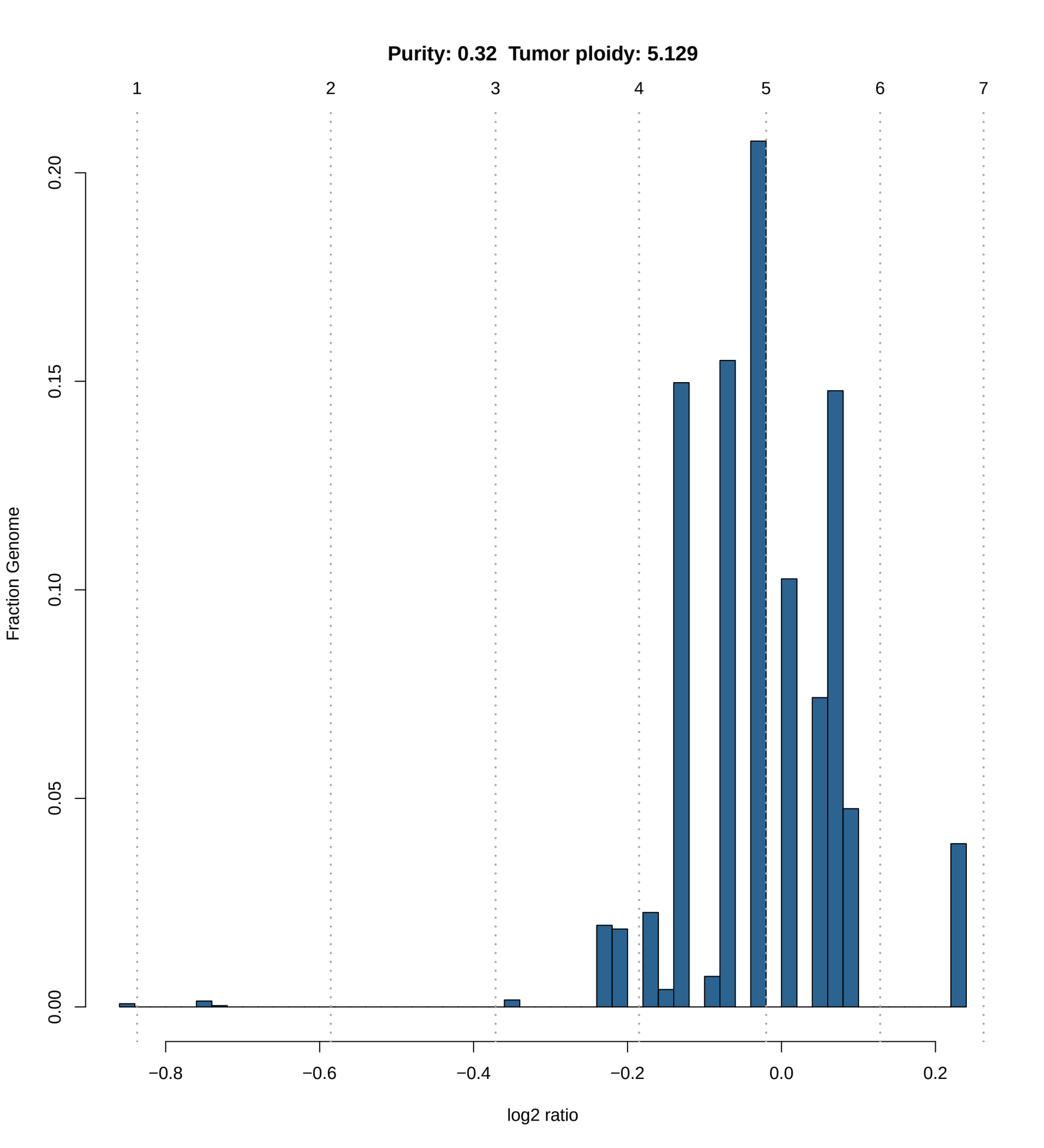

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120
SNV Index

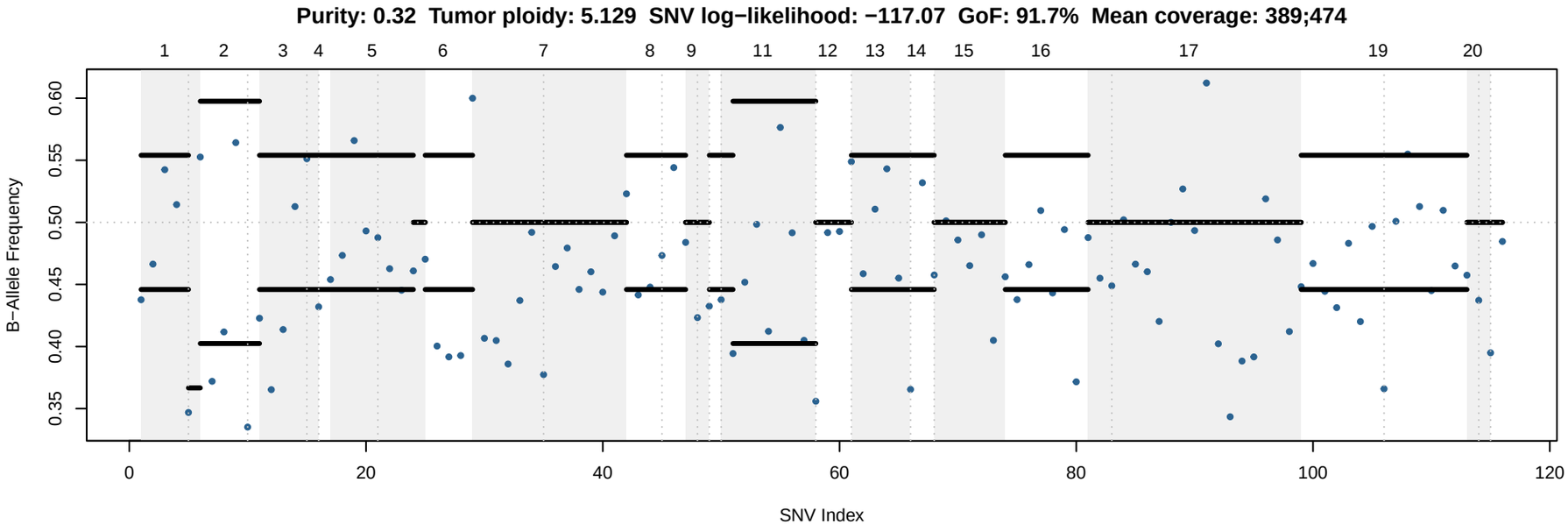

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
3m2
2m1
3m1
4m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

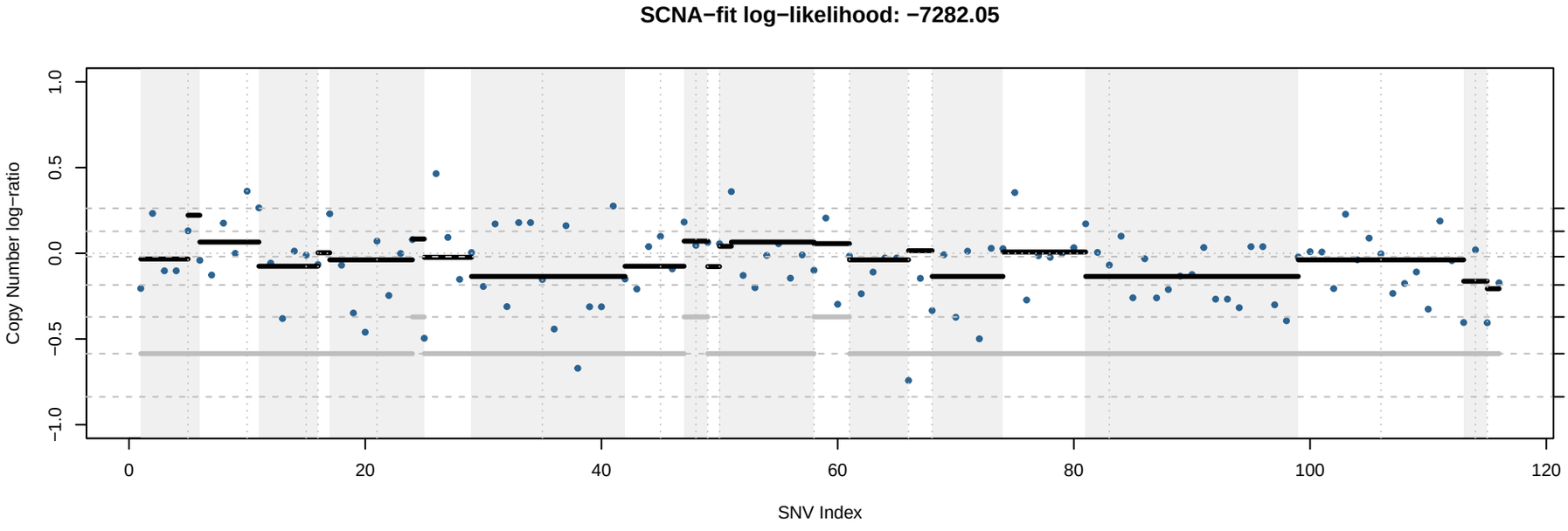

Coverage (log2)
5
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

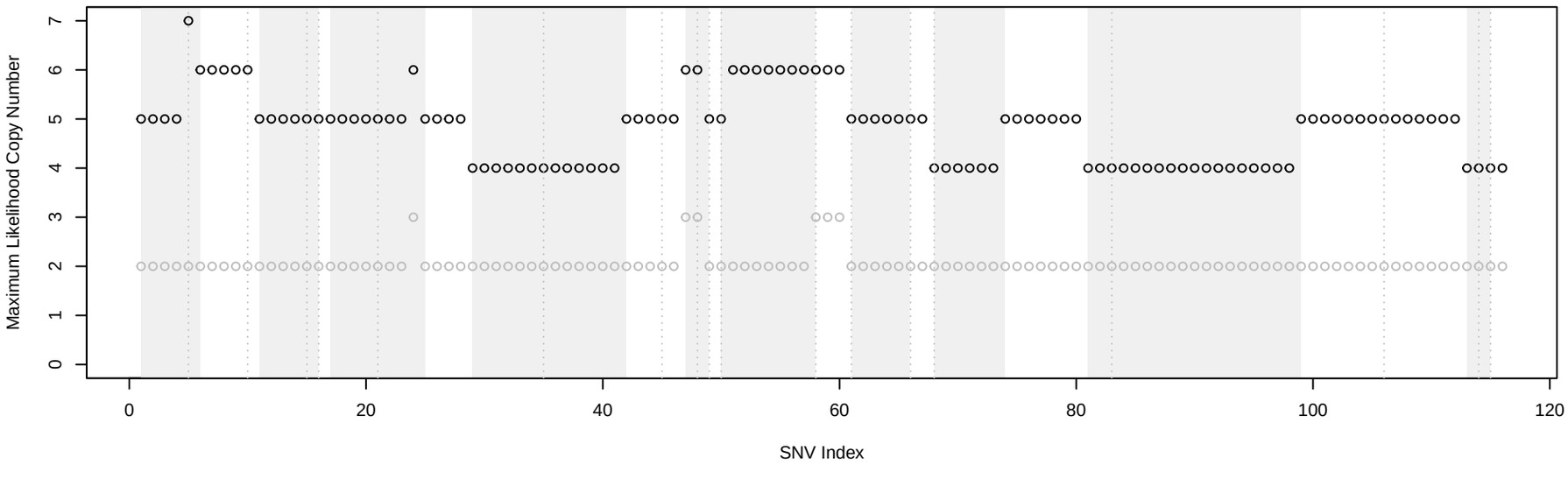

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

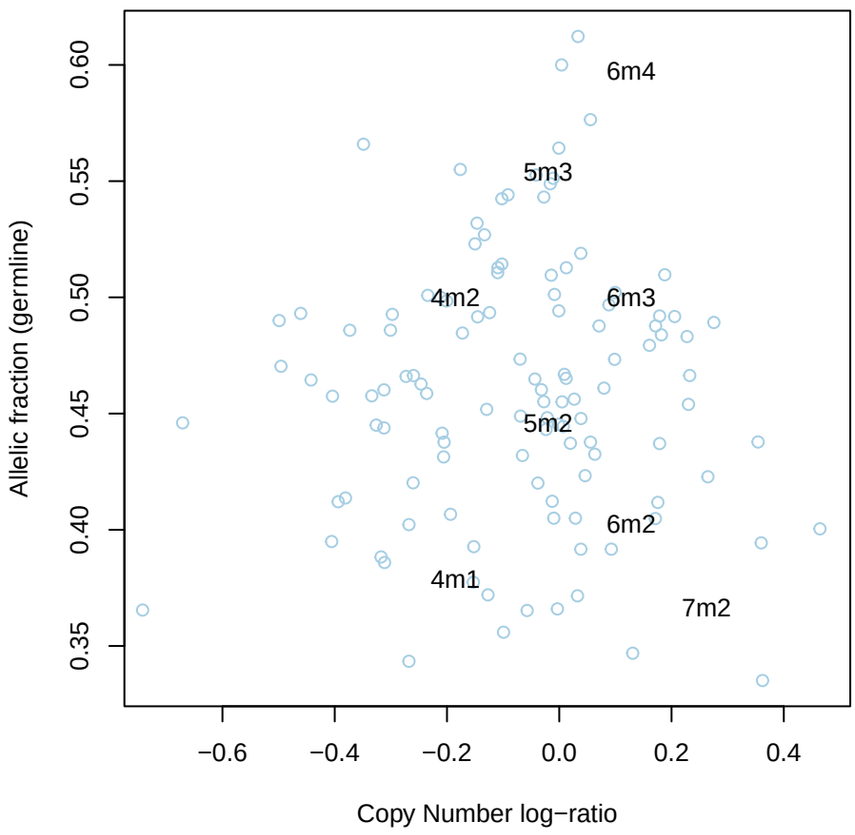

Power 0.8
Frequency
0
10
20
30
40
50
60
0.2
0.4
0.6
0.8
1.0
Cellular fraction

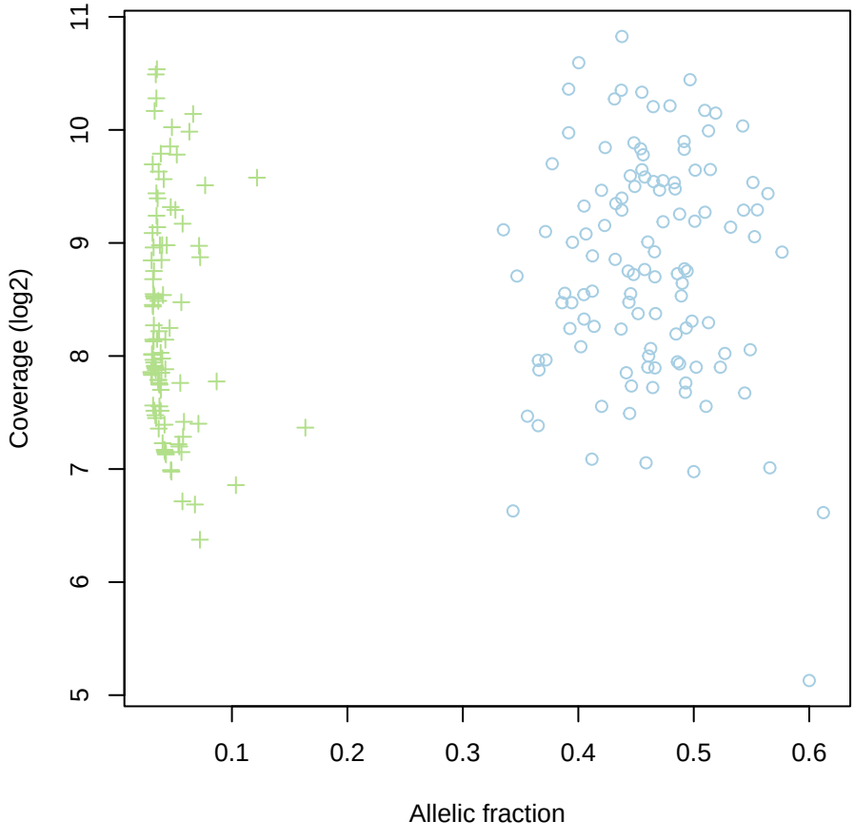

Purity: 0.32 Tumor ploidy: 5.129
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

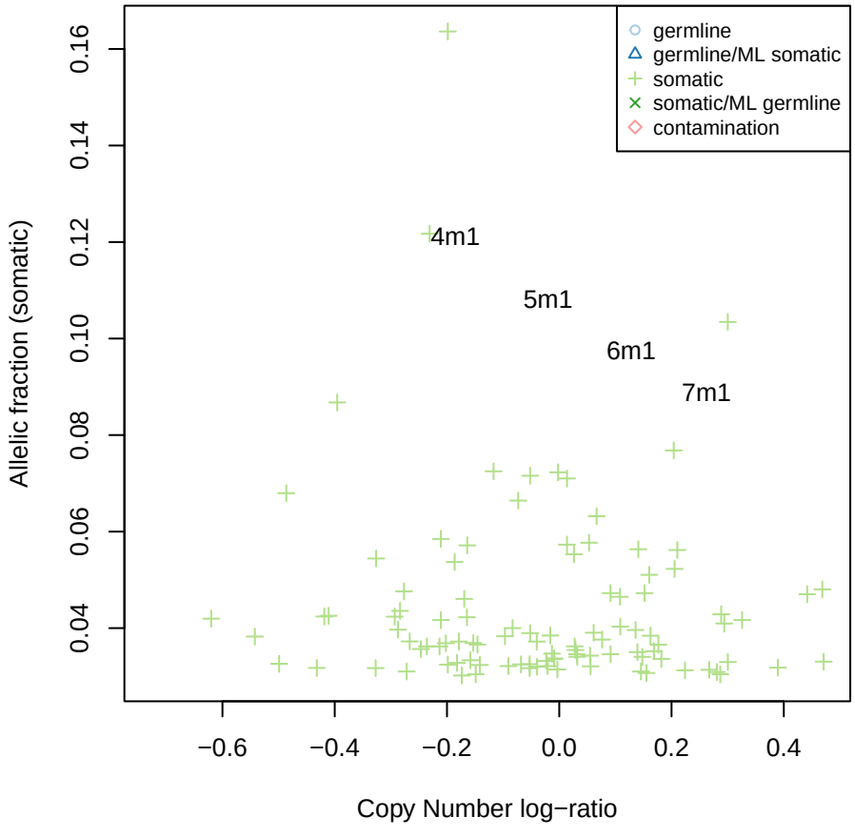

Purity: 0.32 Tumor ploidy: 5.129 SNV log−likelihood: −117.07 GoF: 91.7% Mean coverage: 389;474
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100 120
SNV Index

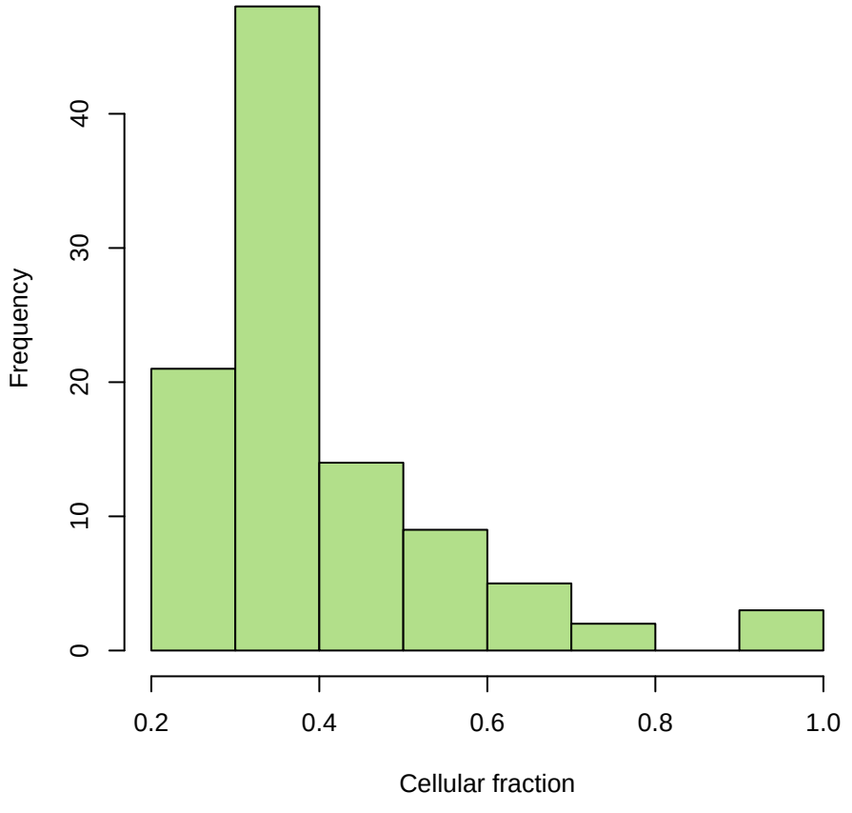

SCNA−fit log−likelihood: −7282.05
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6
0 20 40 60 80 100 120
SNV Index

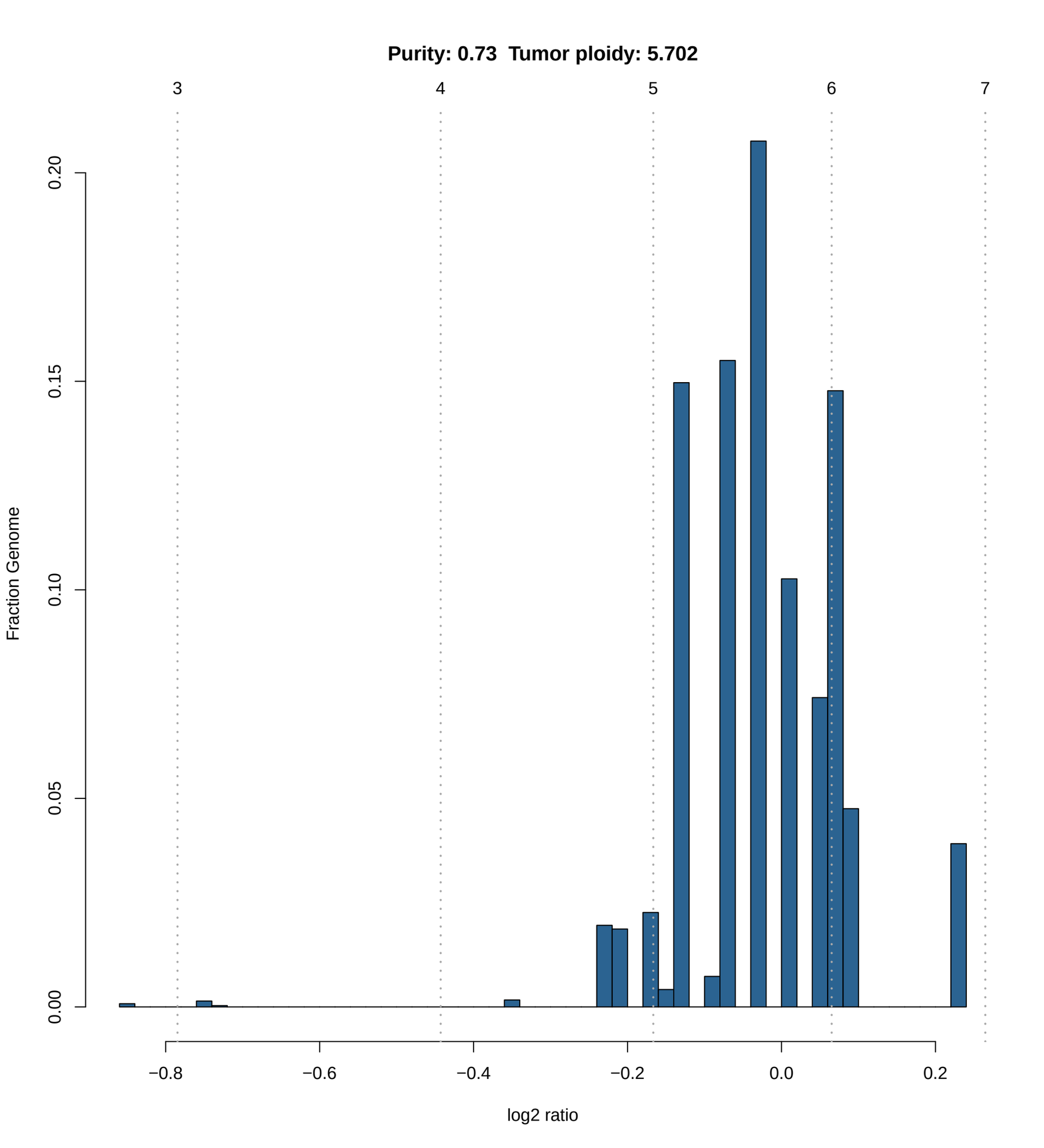

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

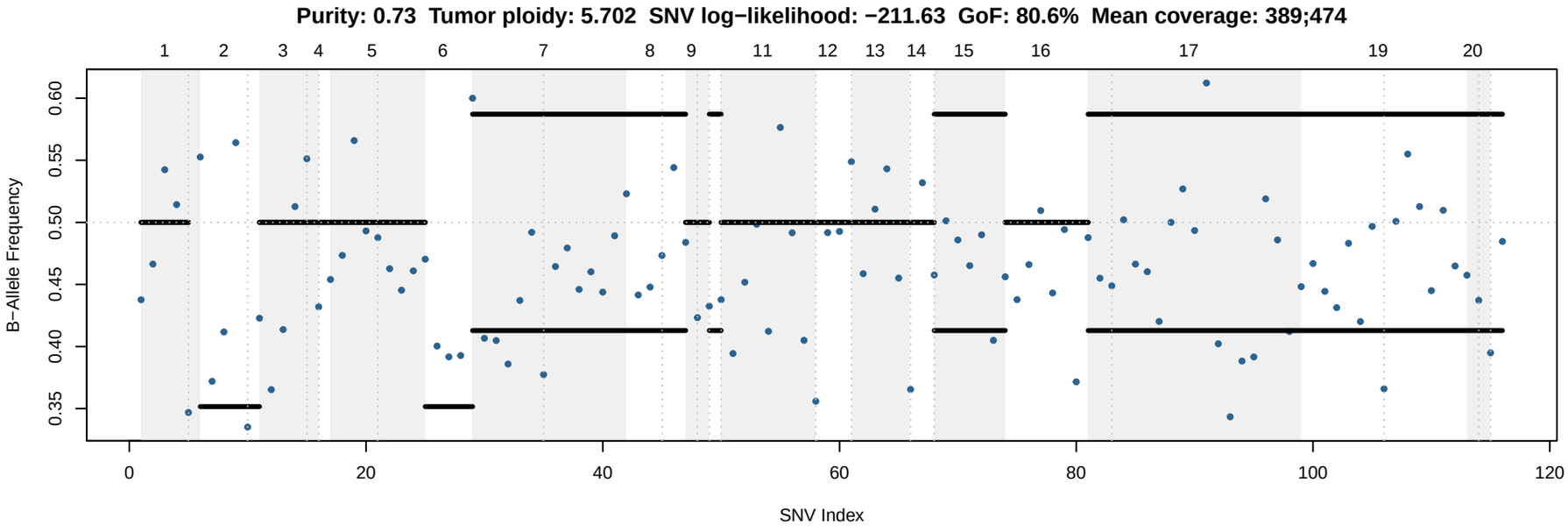

Allelic fraction (germline)
Copy Number log−ratio
6m4
5m3
4m2
6m3
5m2
6m2
4m1
7m2

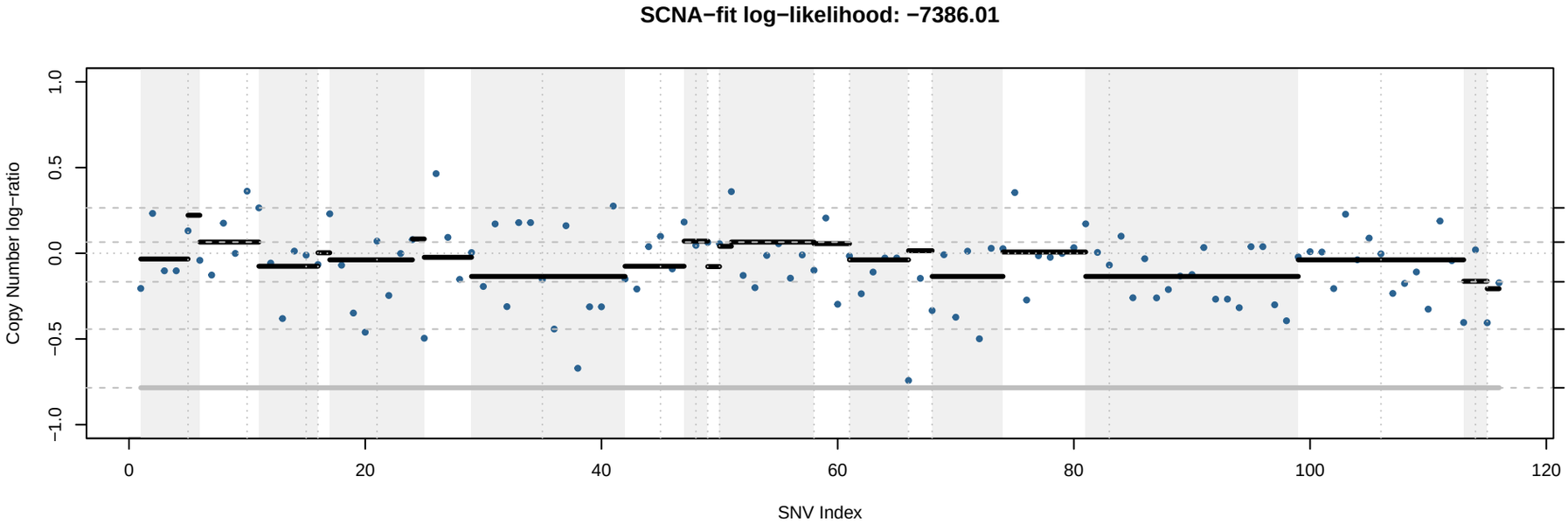

Coverage (log2)
Allelic fraction

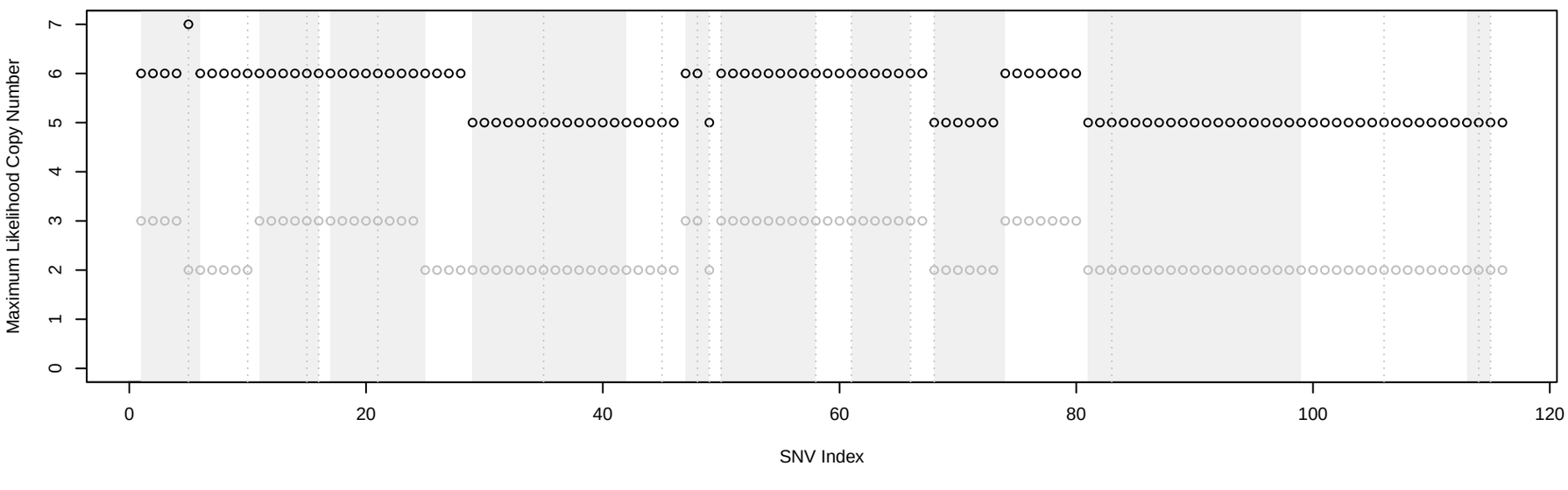

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
4m1
5m1
6m1
7m1

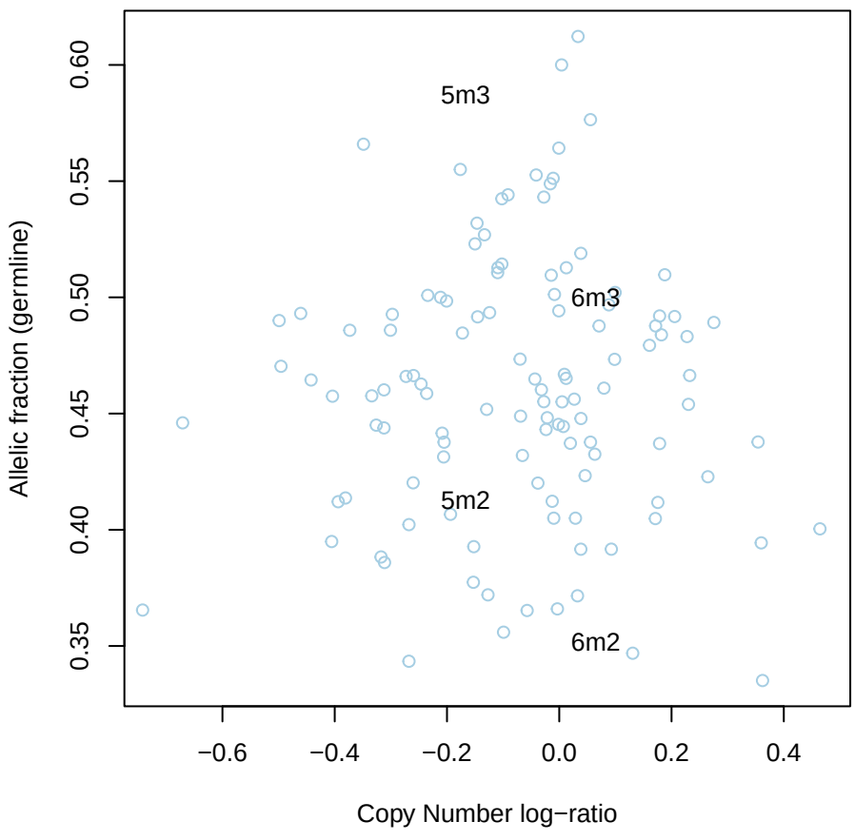

Frequency
Cellular fraction

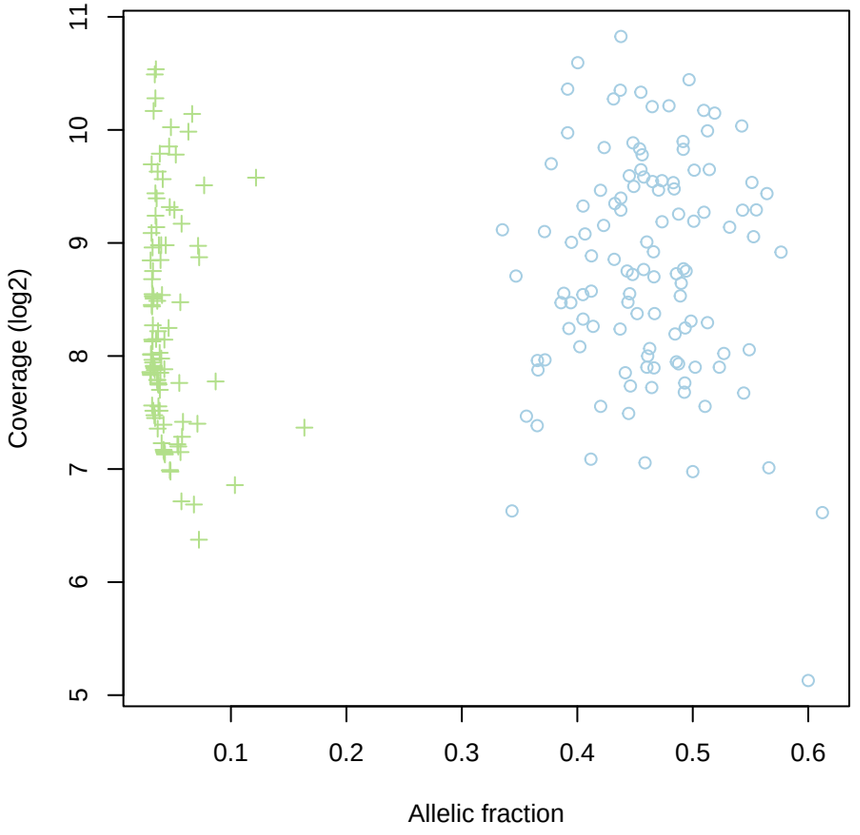

Purity: 0.73 Tumor ploidy: 5.702
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

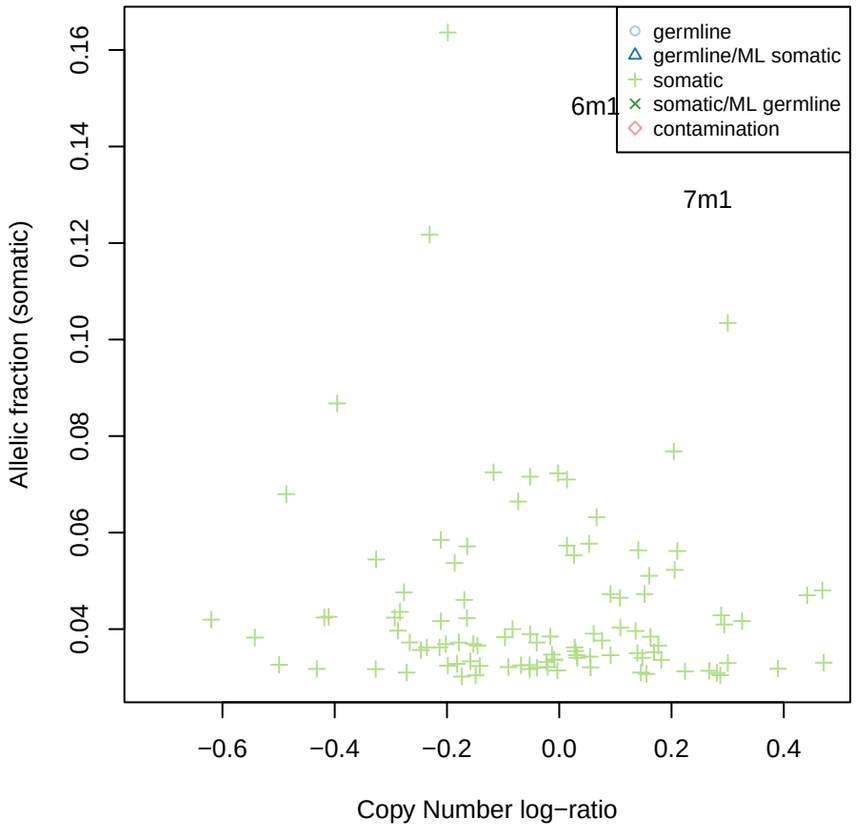

Purity: 0.73 Tumor ploidy: 5.702 SNV log−likelihood: −211.63 GoF: 80.6% Mean coverage: 389;474
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100 120
SNV Index

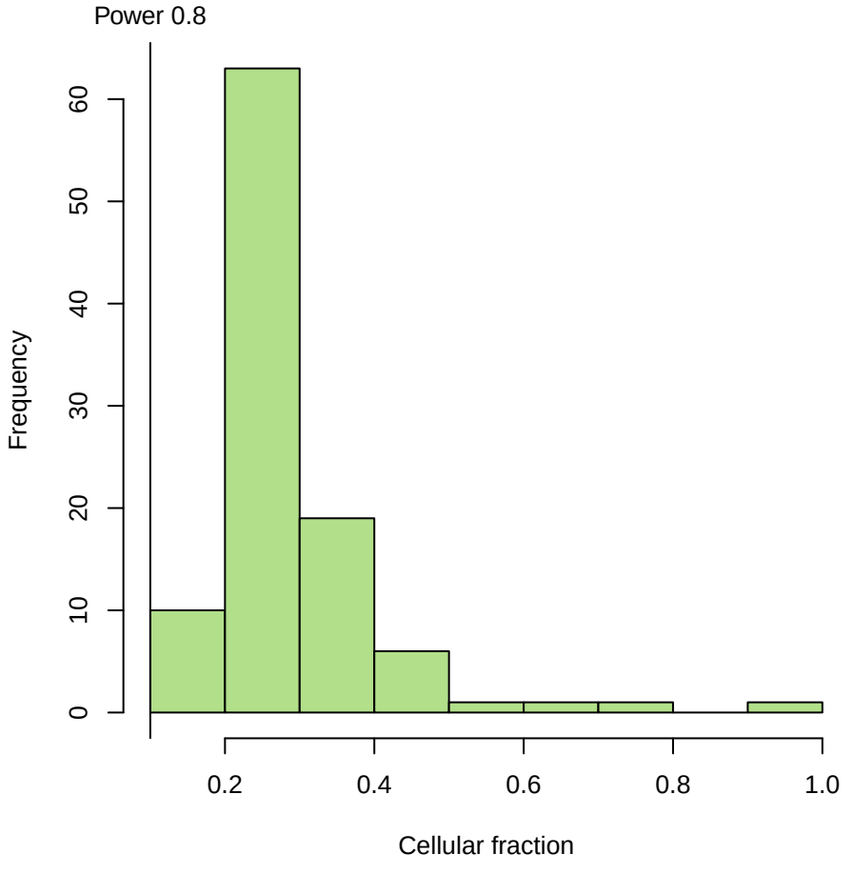

SCNA−fit log−likelihood: −7386.01
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

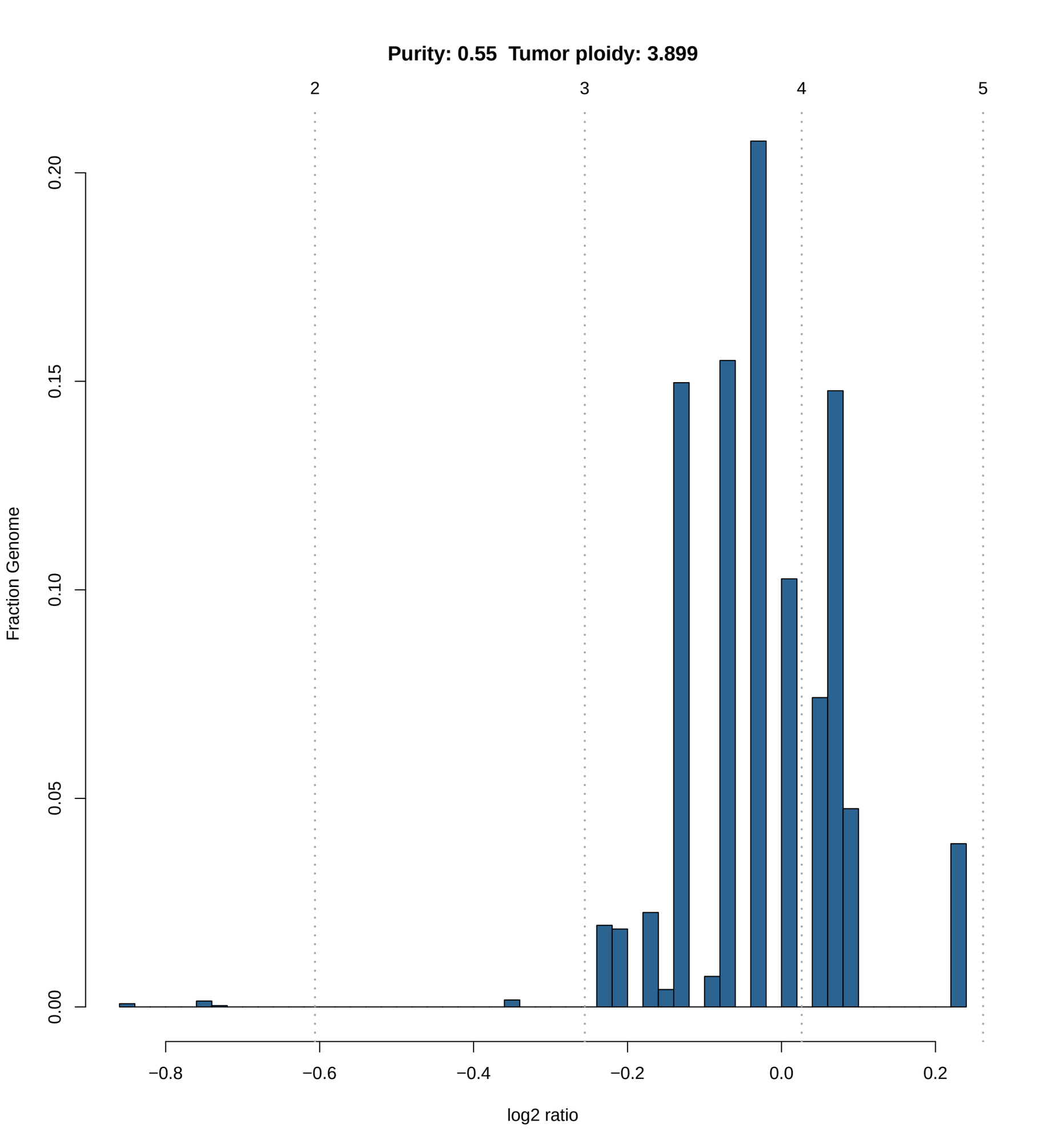

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

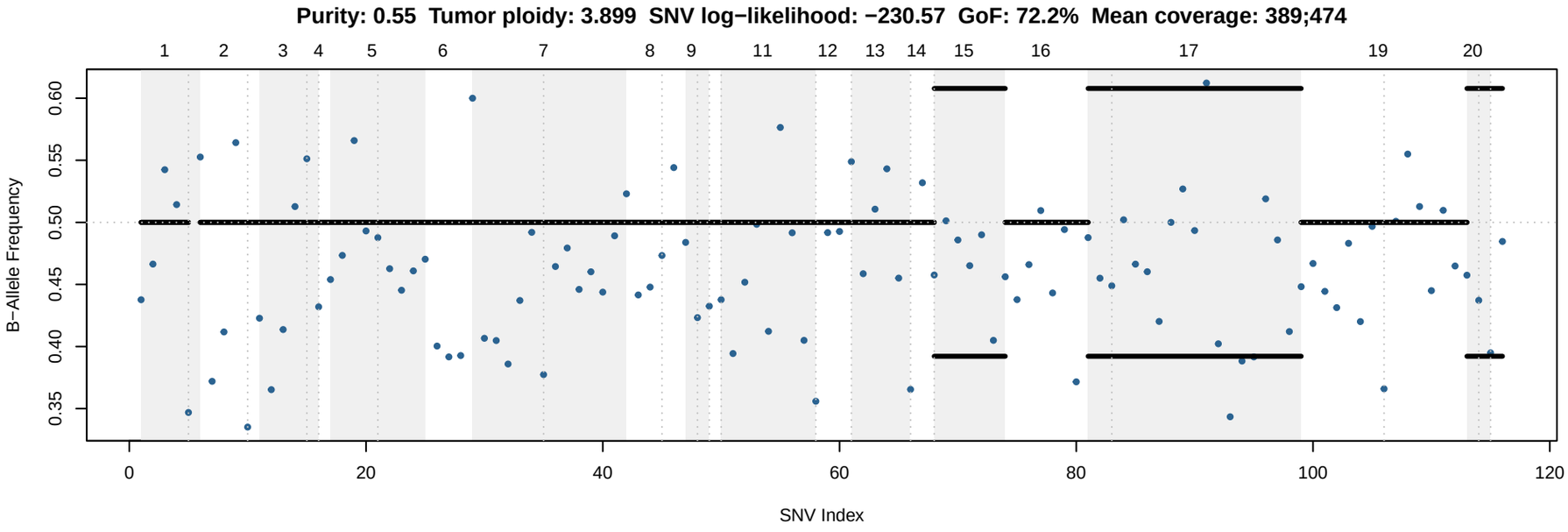

5m3
6m3
5m2
6m2
Allelic fraction (germline)
Copy Number log−ratio

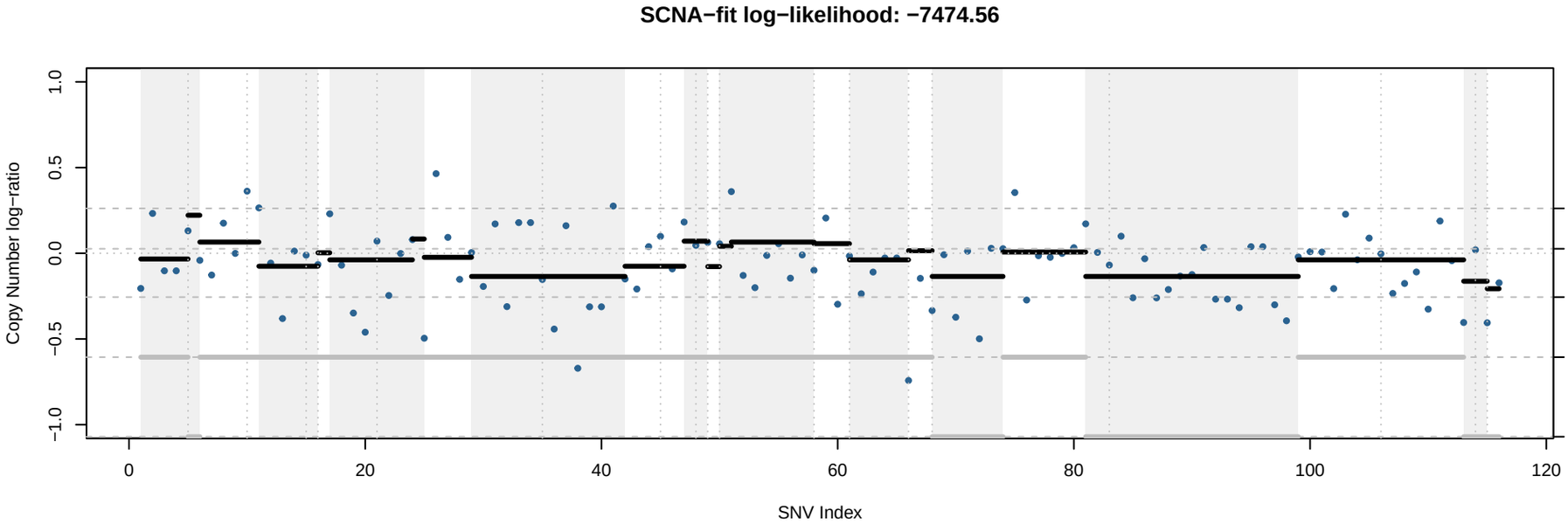

Coverage (log2)
Allelic fraction

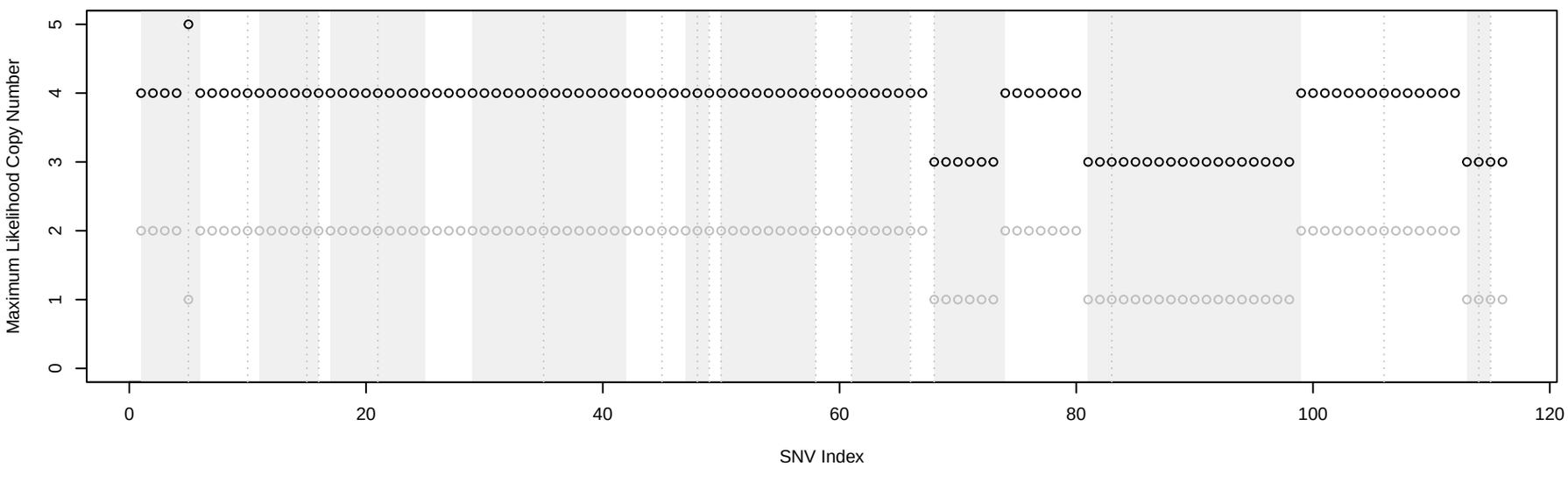

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

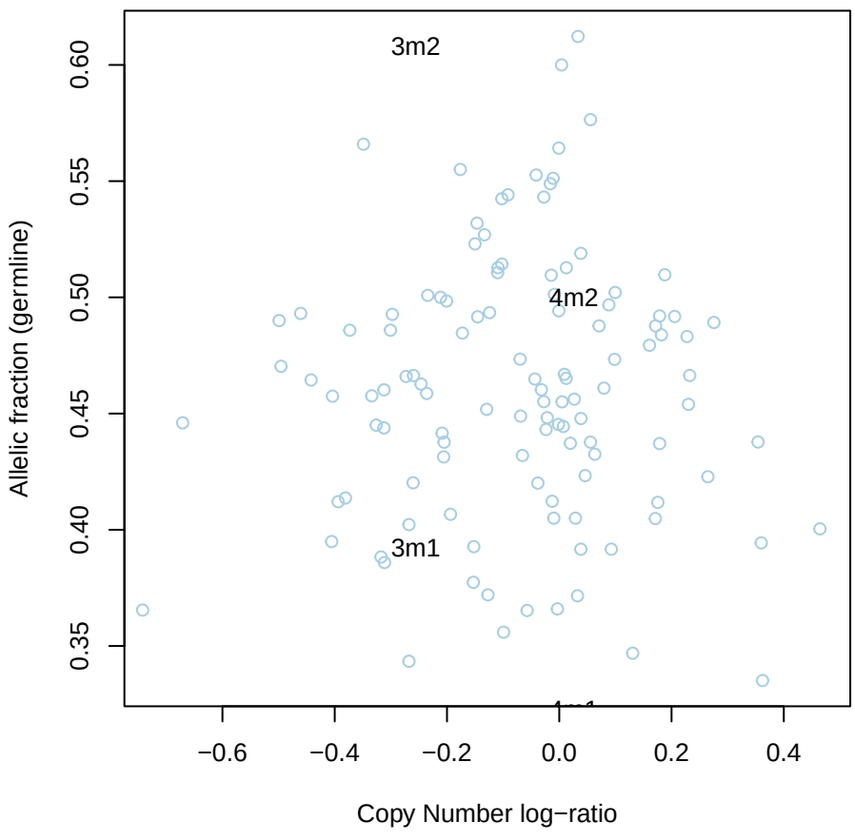

Power 0.8
Frequency
Cellular fraction

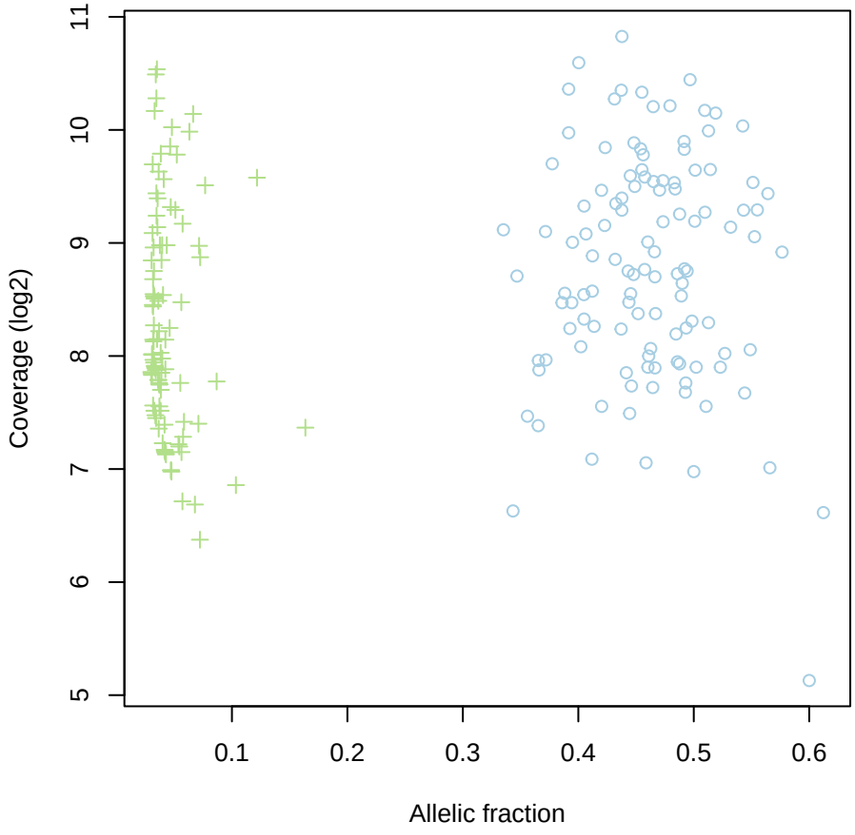

Purity: 0.55 Tumor ploidy: 3.899
2
3
4
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

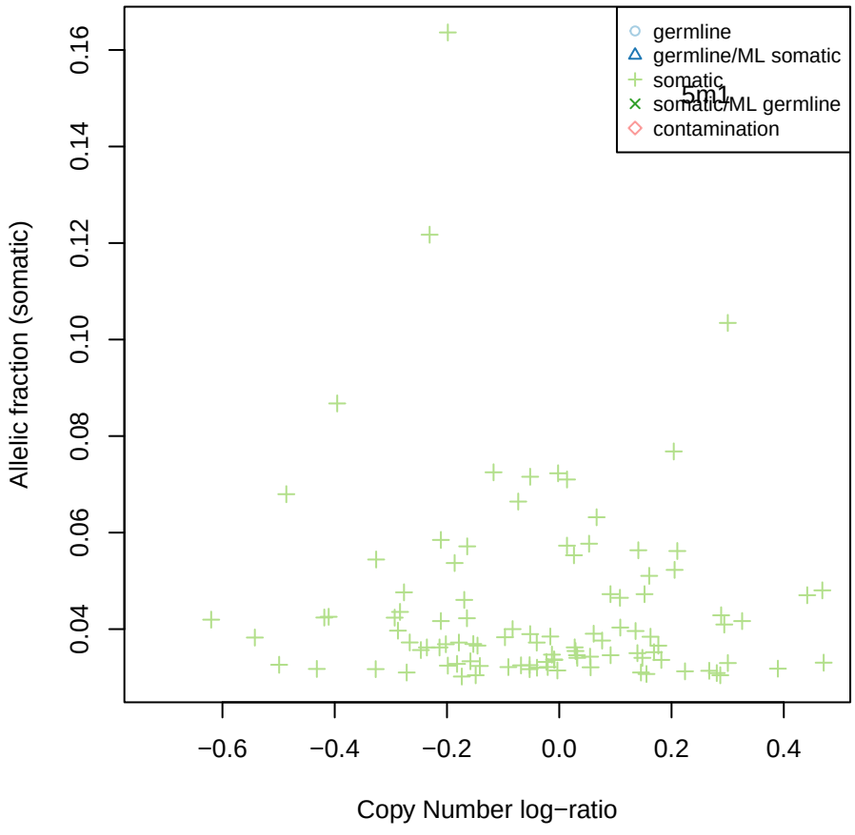

Purity: 0.55 Tumor ploidy: 3.899 SNV log−likelihood: −230.57 GoF: 72.2% Mean coverage: 389;474
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100 120
SNV Index

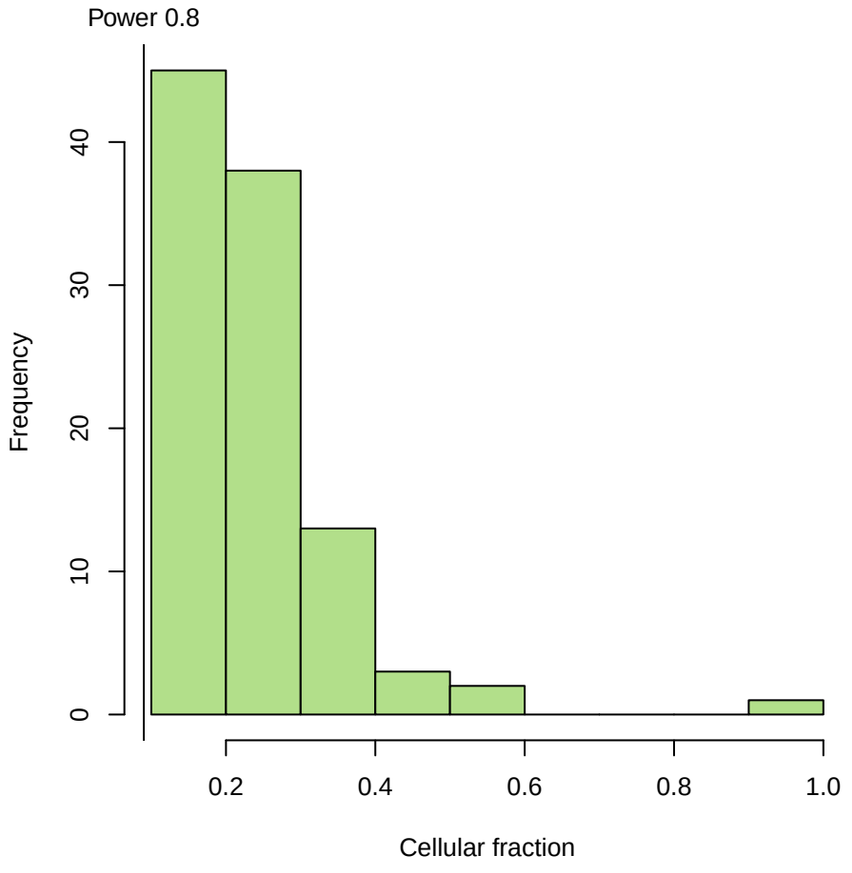

SCNA−fit log−likelihood: −7474.56
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5
0 20 40 60 80 100 120
SNV Index

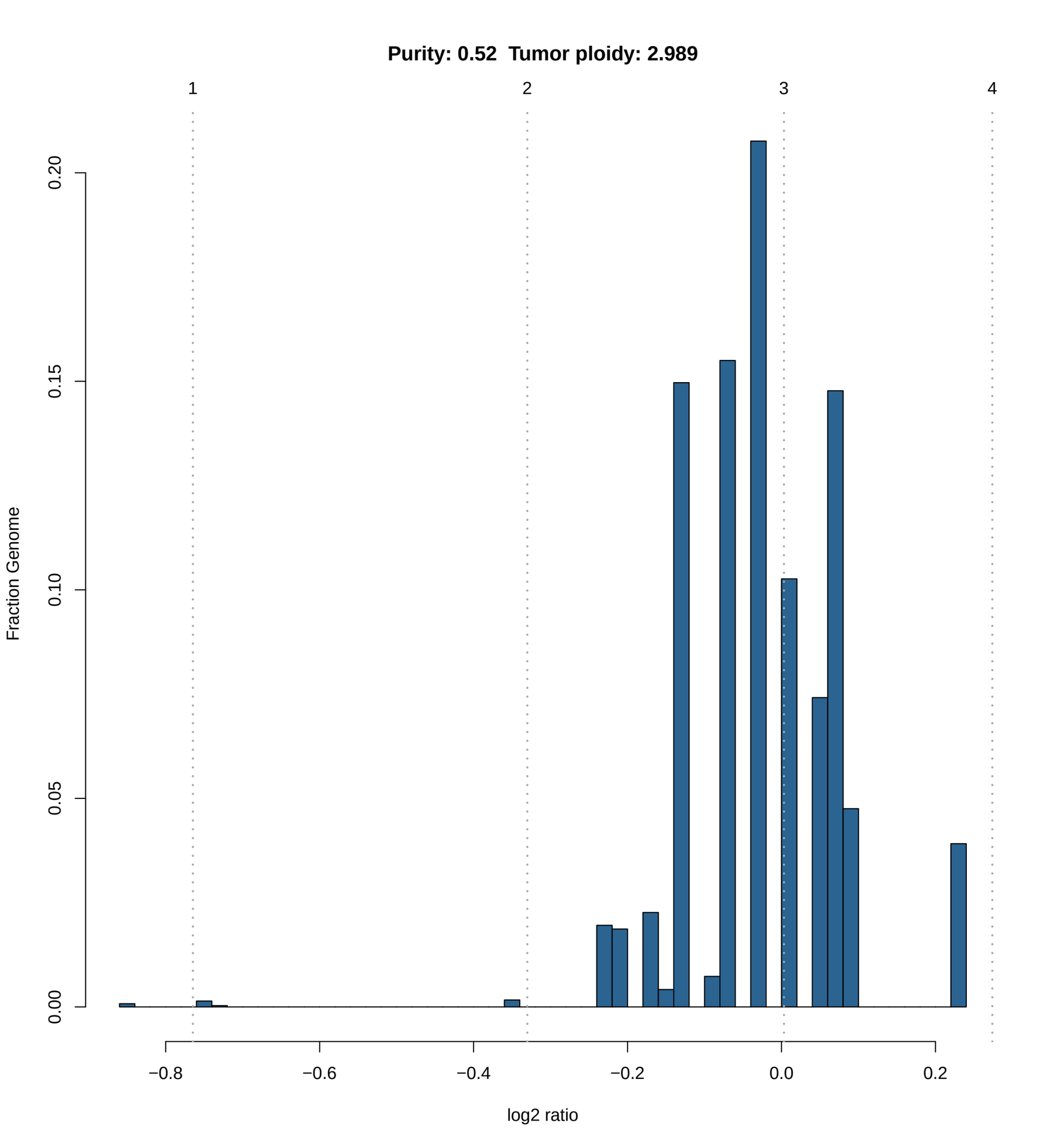

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120
SNV Index

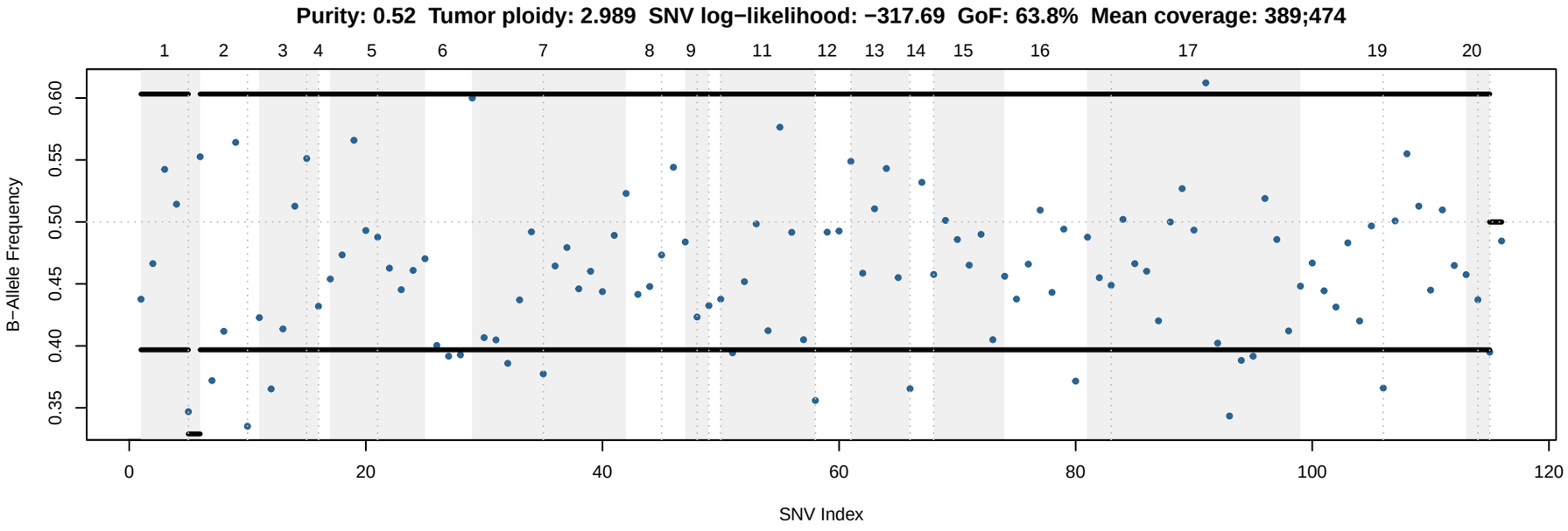

3m2
4m2
3m1
Allelic fraction (germline)
Copy Number log−ratio

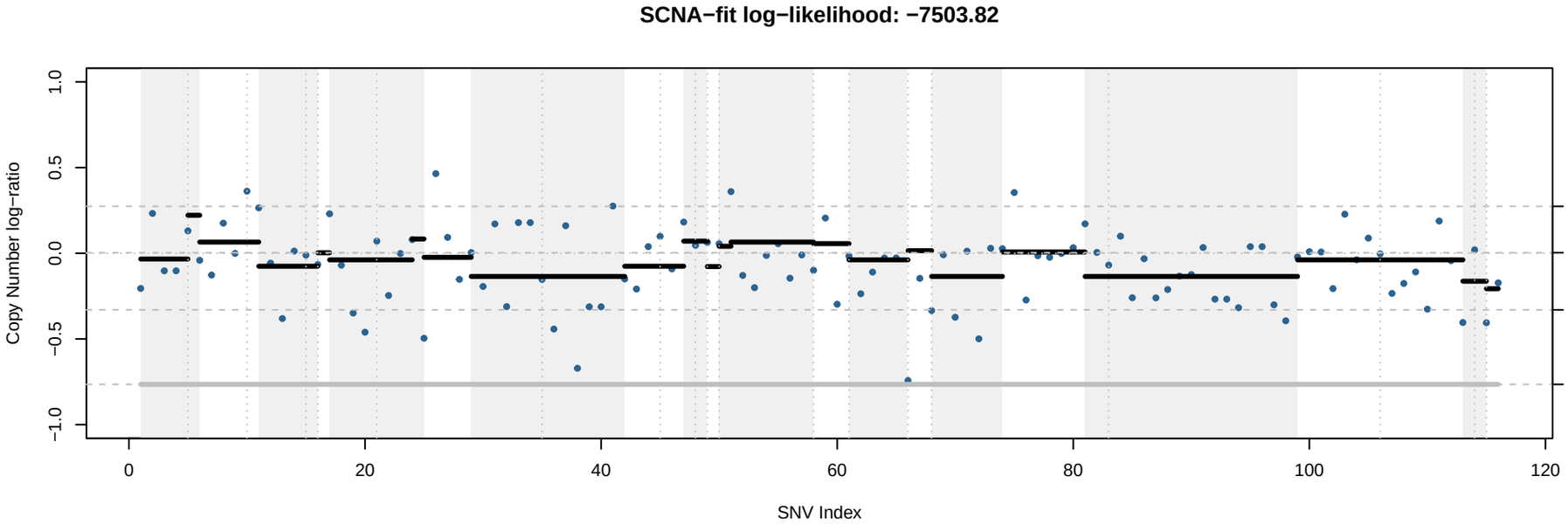

Coverage (log2)
Allelic fraction

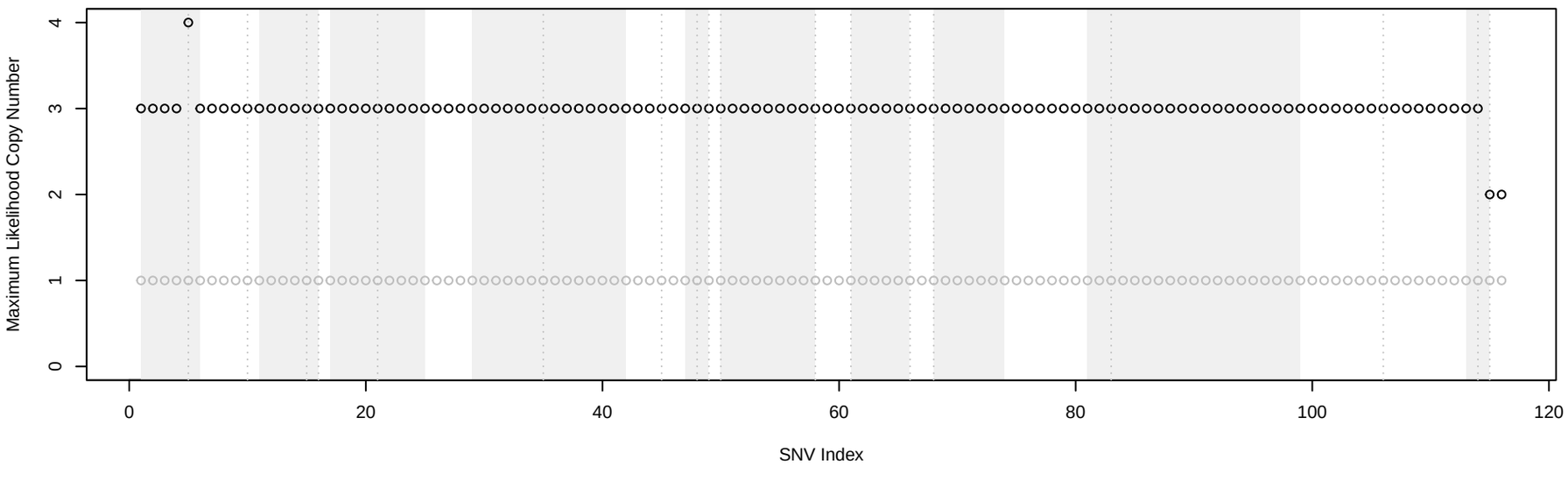

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
Allelic fraction (somatic)
Copy Number log−ratio

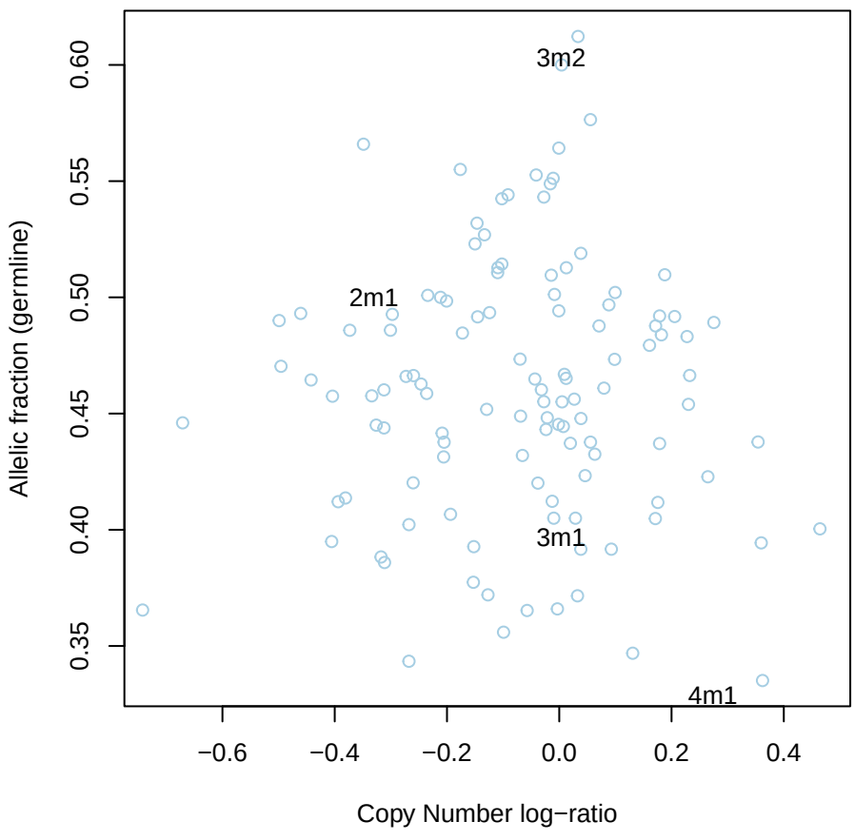

Power 0.8
Frequency
Cellular fraction

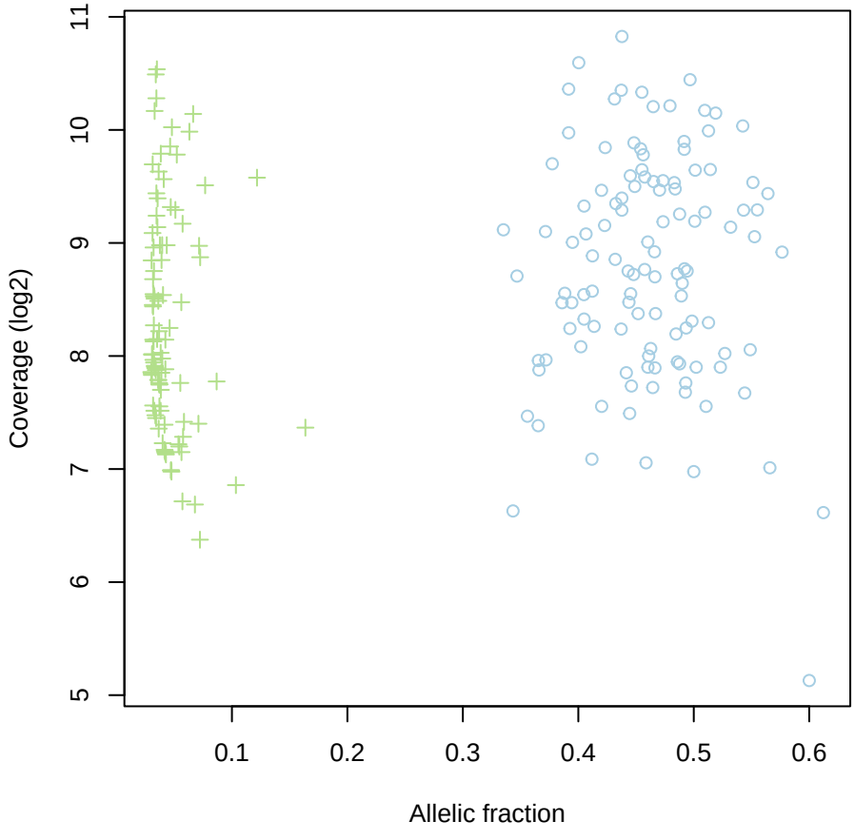

Purity: 0.52 Tumor ploidy: 2.989
1
2
3
4
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

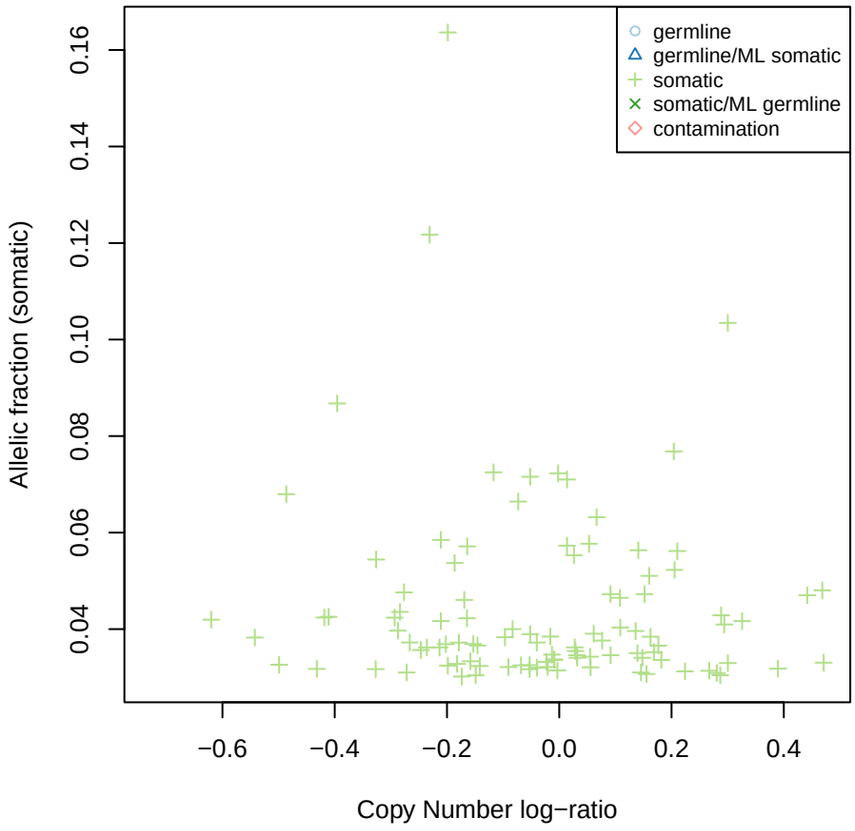

Purity: 0.52 Tumor ploidy: 2.989 SNV log−likelihood: −317.69 GoF: 63.8% Mean coverage: 389;474
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100 120
SNV Index

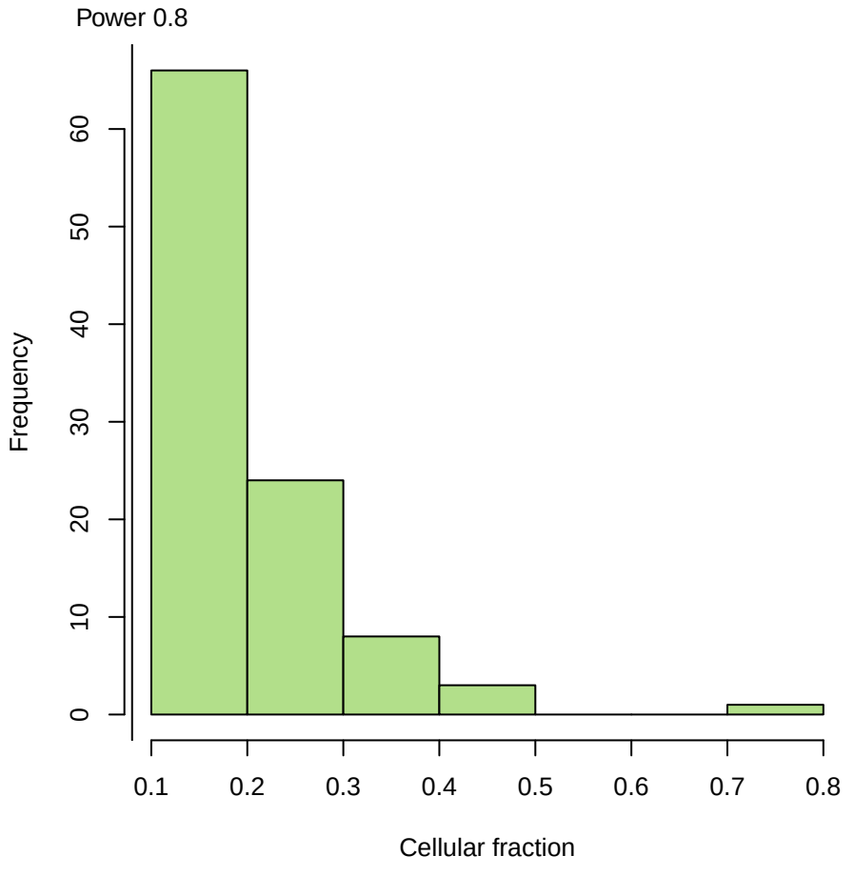

SCNA−fit log−likelihood: −7503.82
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4
0 20 40 60 80 100 120
SNV Index

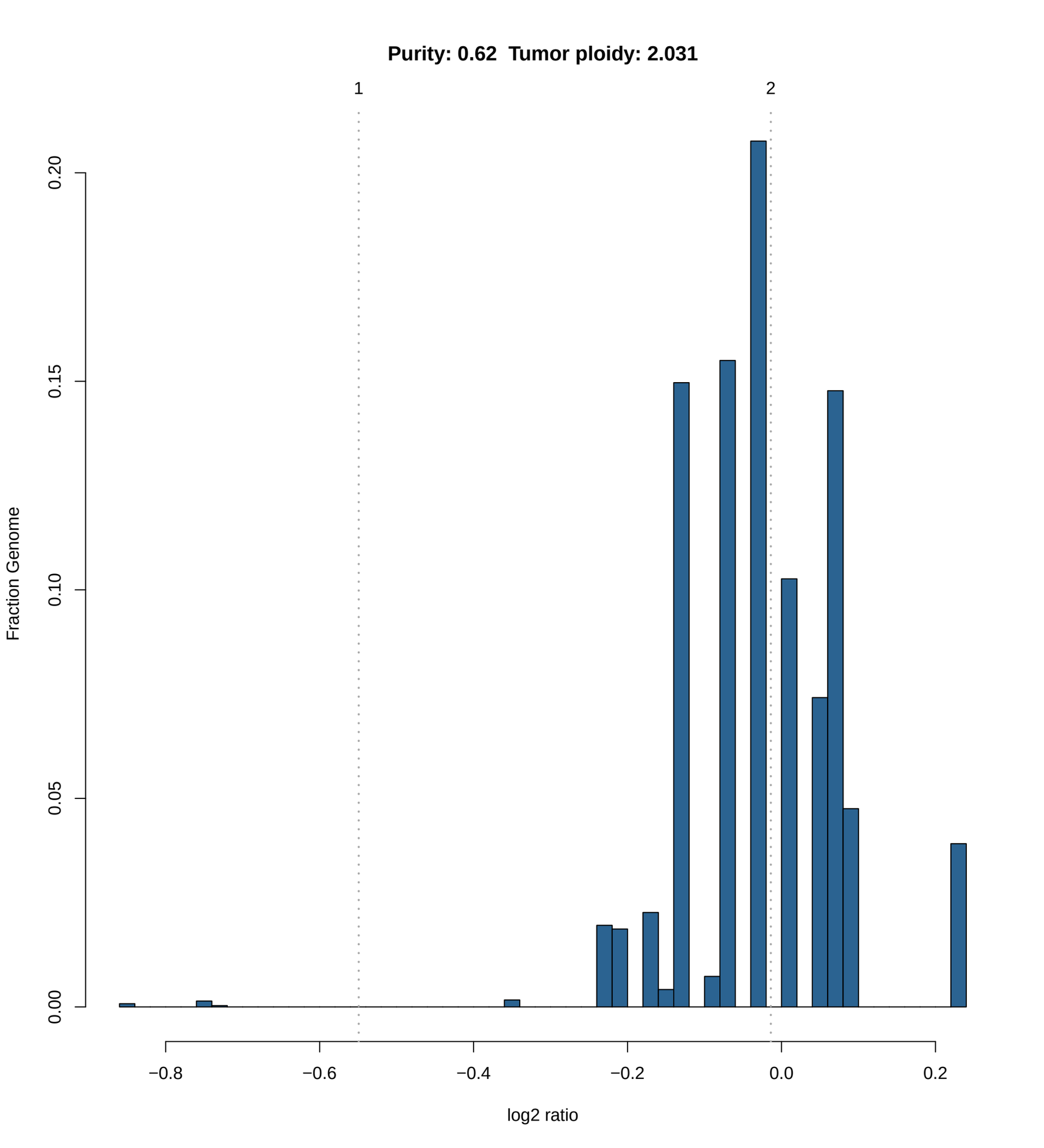

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120
SNV Index

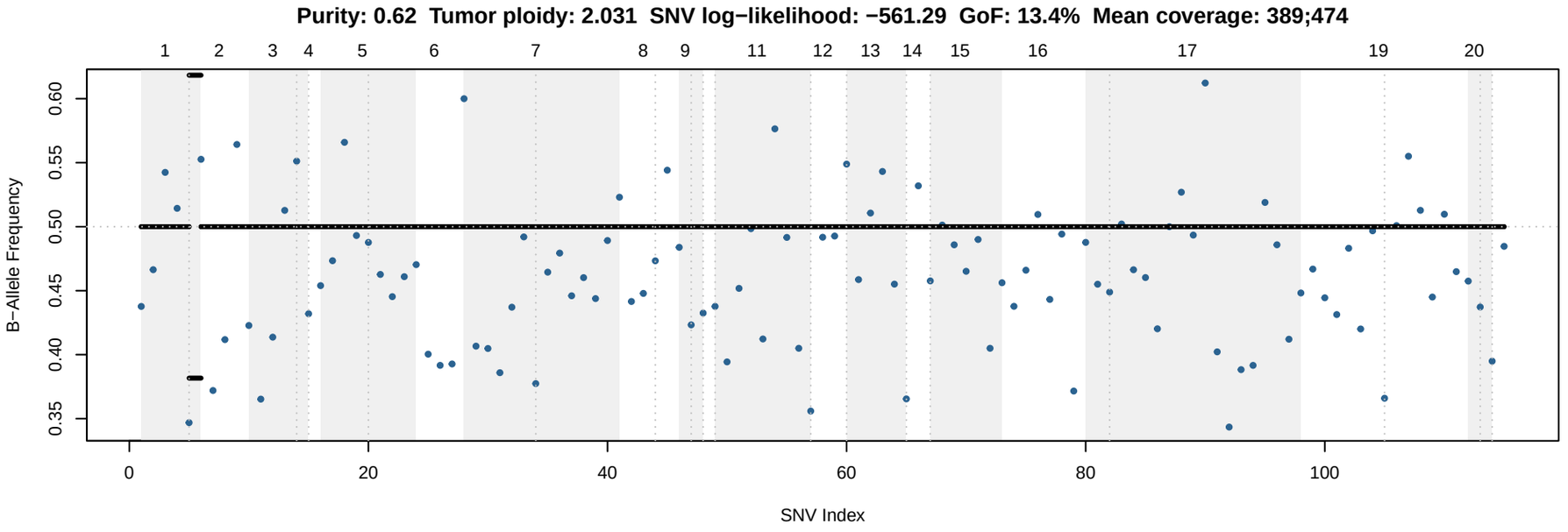

3m2
2m1
3m1
4m1
Allelic fraction (germline)
Copy Number log−ratio
0.35
0.40
0.45
0.50
0.55
0.60
−0.6
−0.4
−0.2
0.0
0.2
0.4

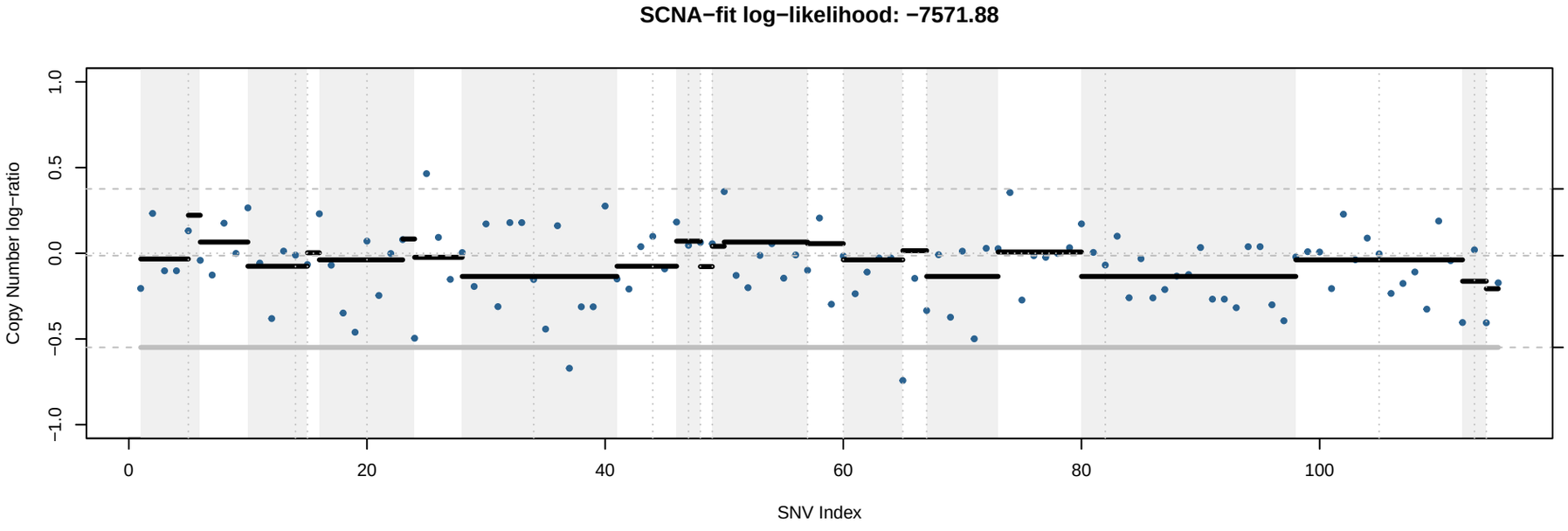

Coverage (log2)
Allelic fraction
5
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6

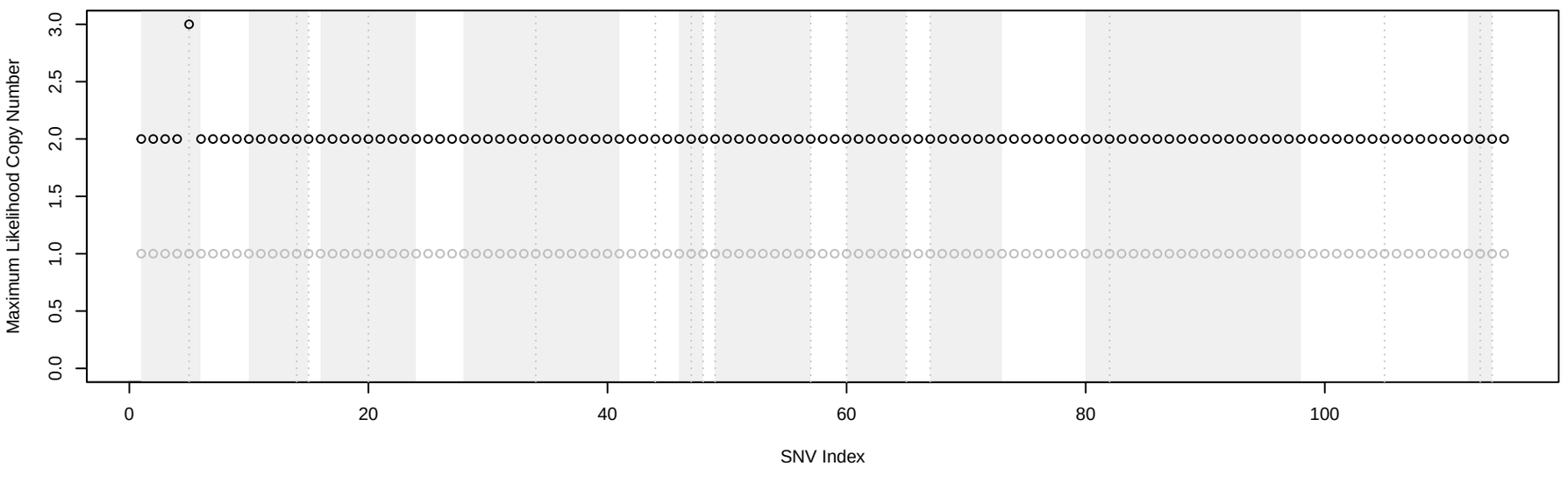

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
0.12
0.14
0.16
−0.6
−0.4
−0.2
0.0
0.2
0.4

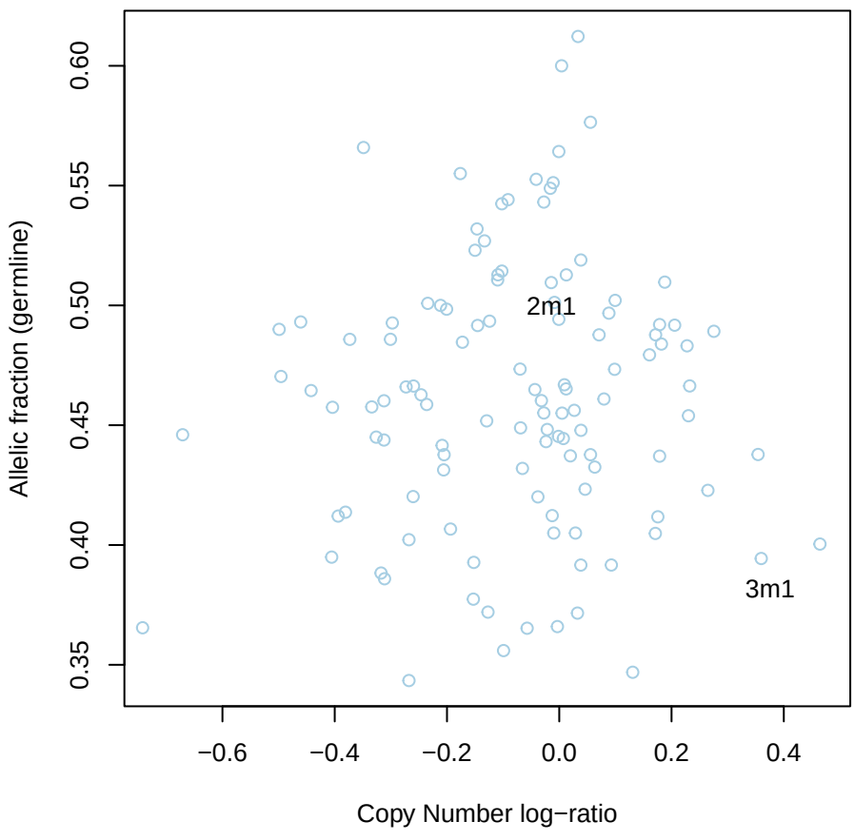

Power 0.8
Frequency
Cellular fraction
0
10
20
30
40
50
60
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8

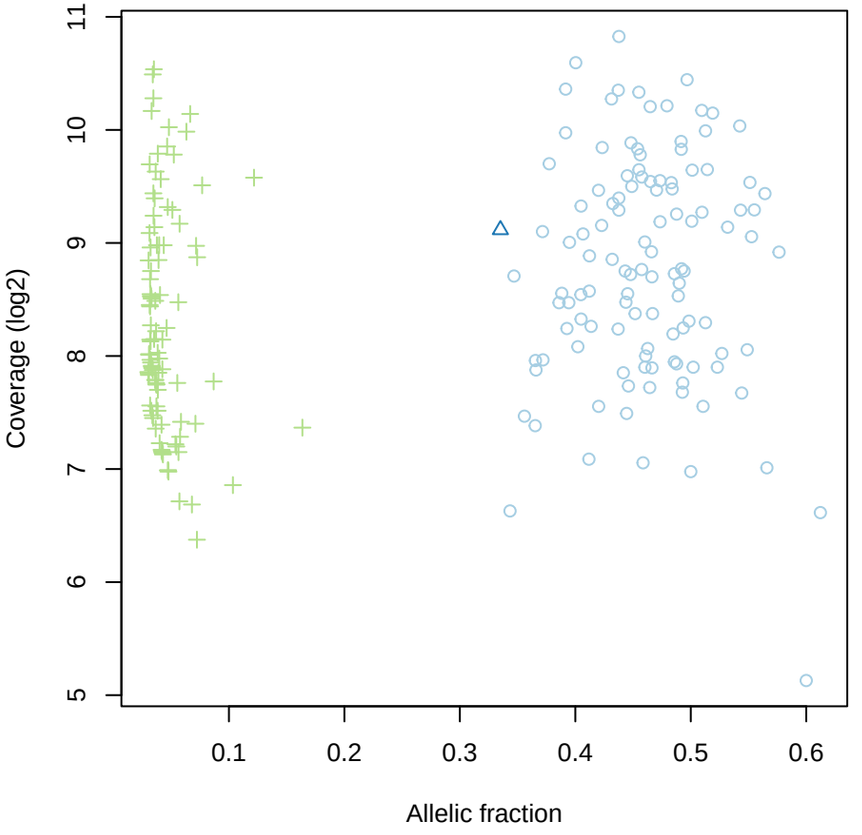

Purity: 0.62 Tumor ploidy: 2.031
1
2
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

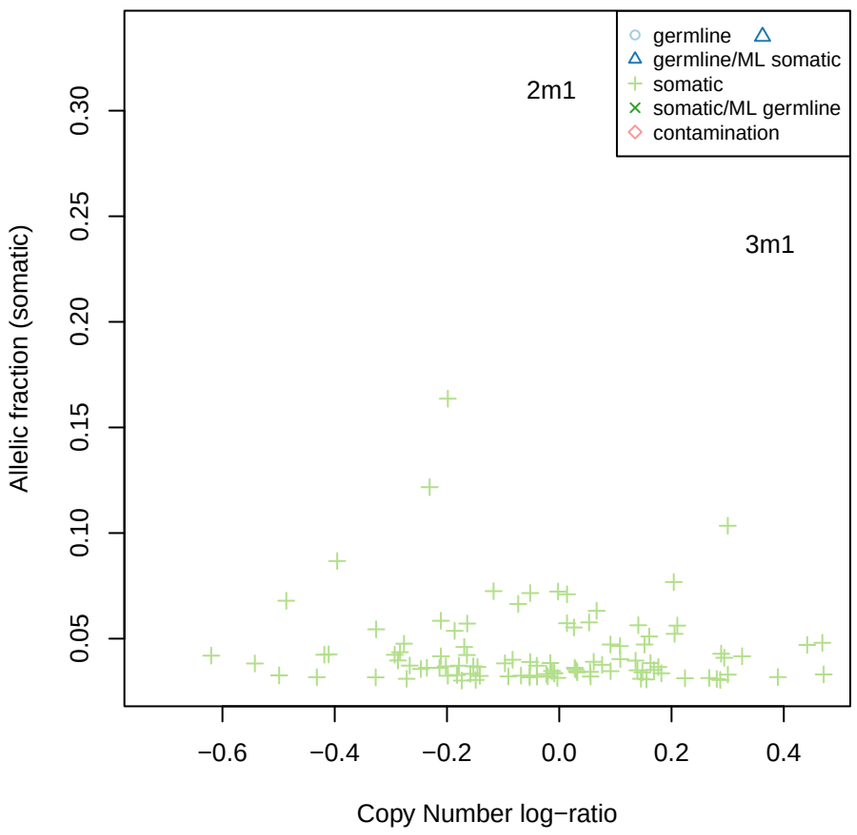

Purity: 0.62 Tumor ploidy: 2.031 SNV log−likelihood: −561.29 GoF: 13.4% Mean coverage: 389;474
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

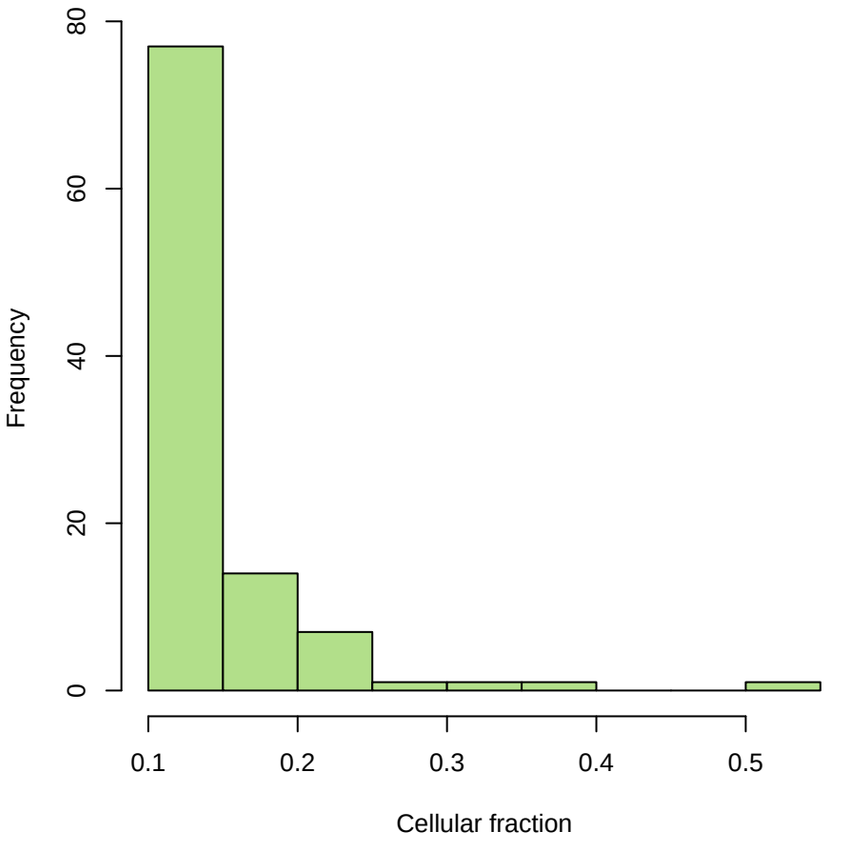

SCNA−fit log−likelihood: −7571.88
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3
0 20 40 60 80 100
SNV Index

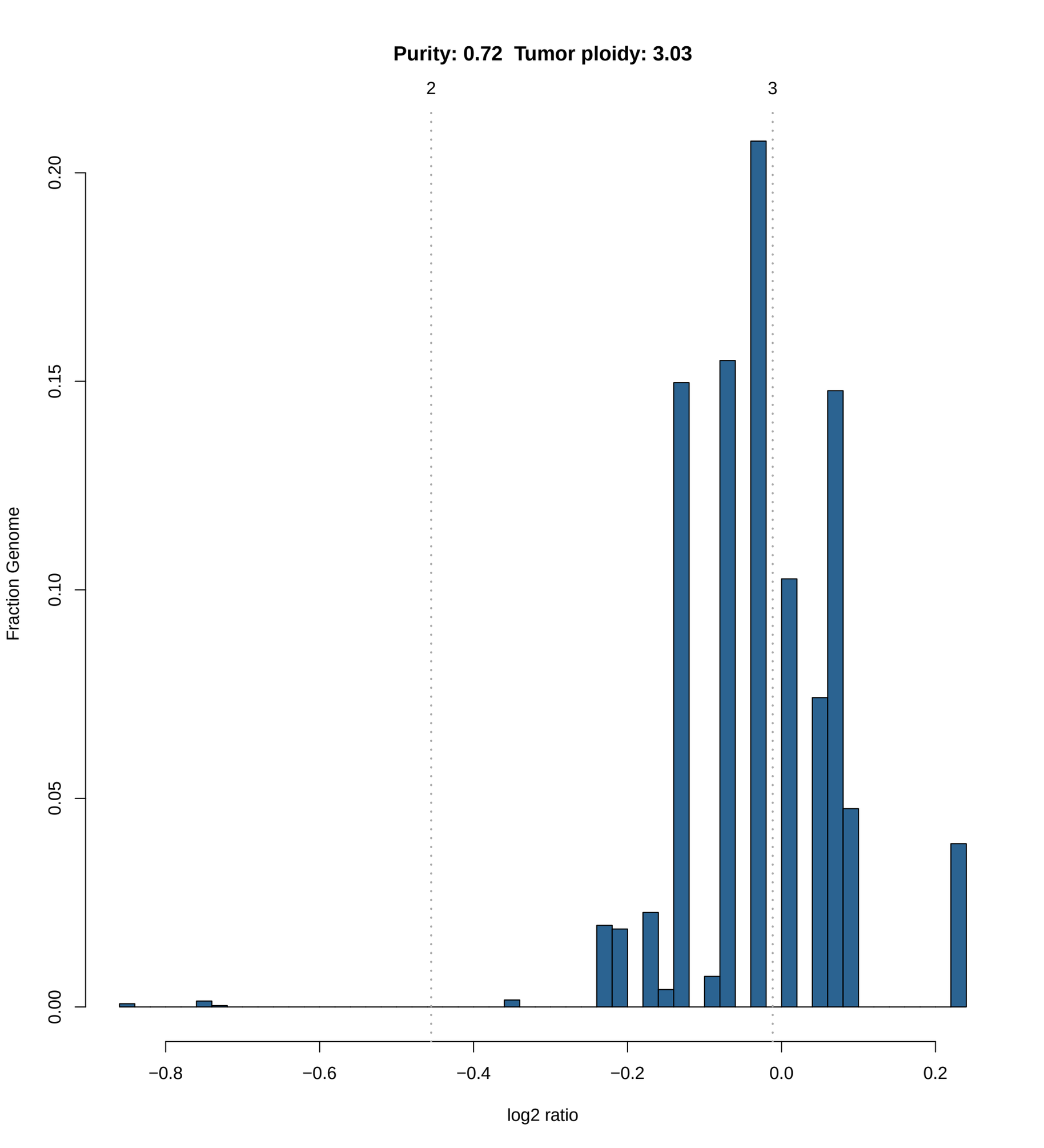

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100
SNV Index

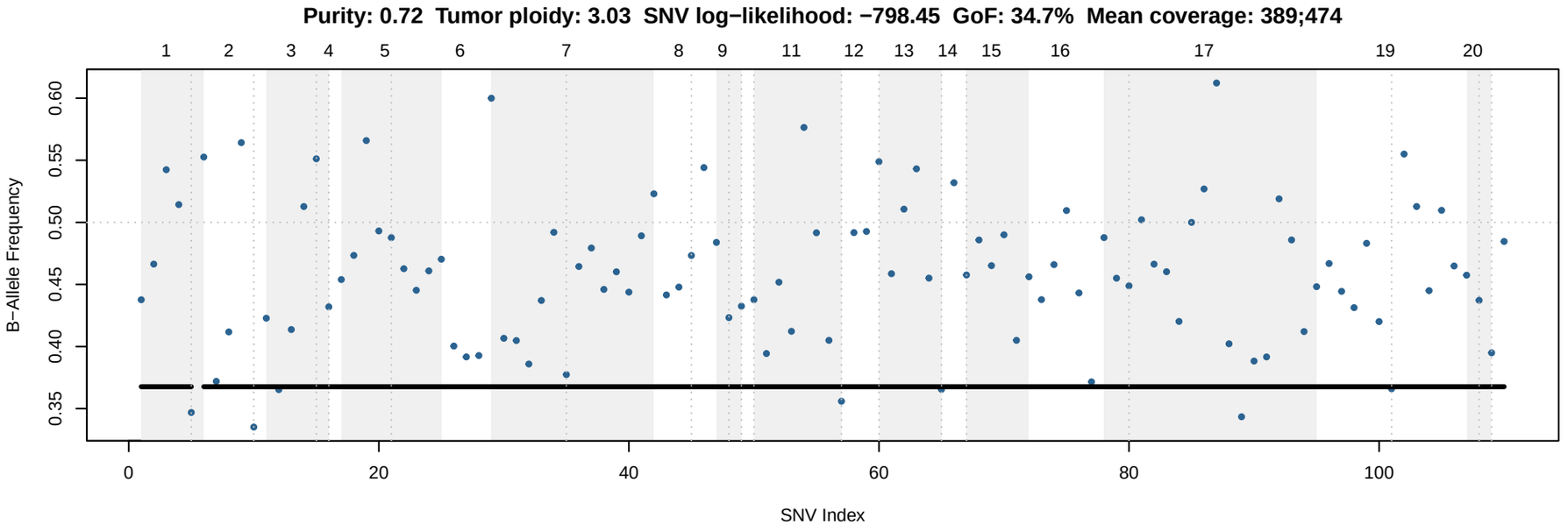

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
2m1
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

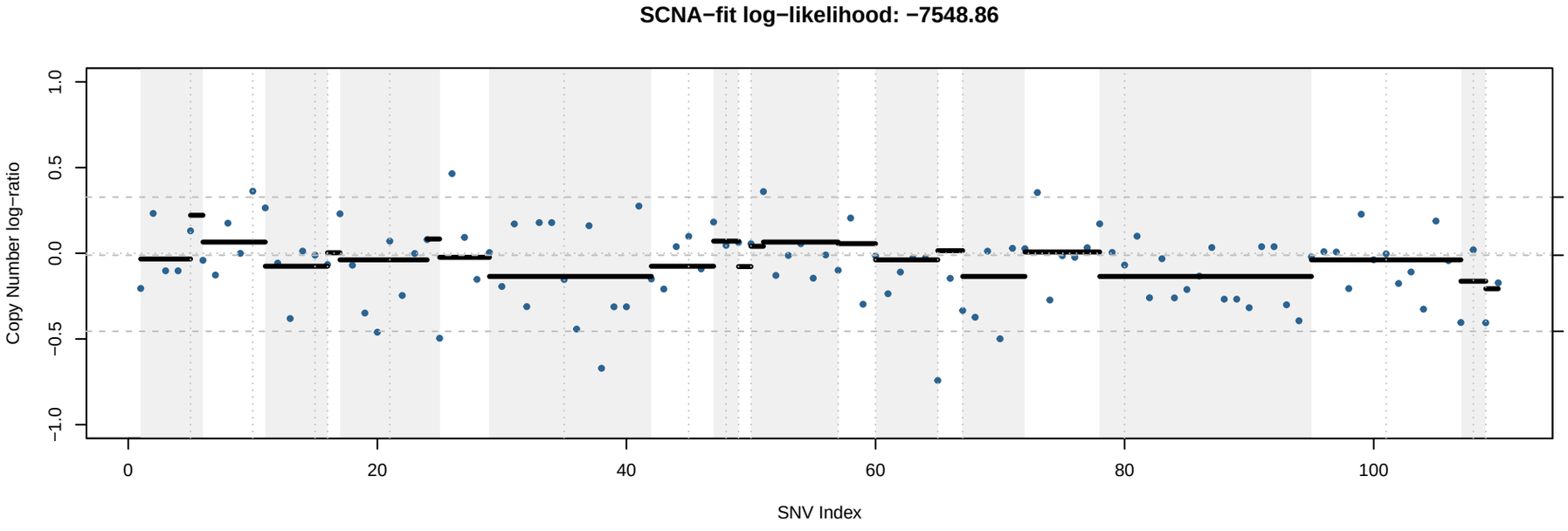

Coverage (log2)
5
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

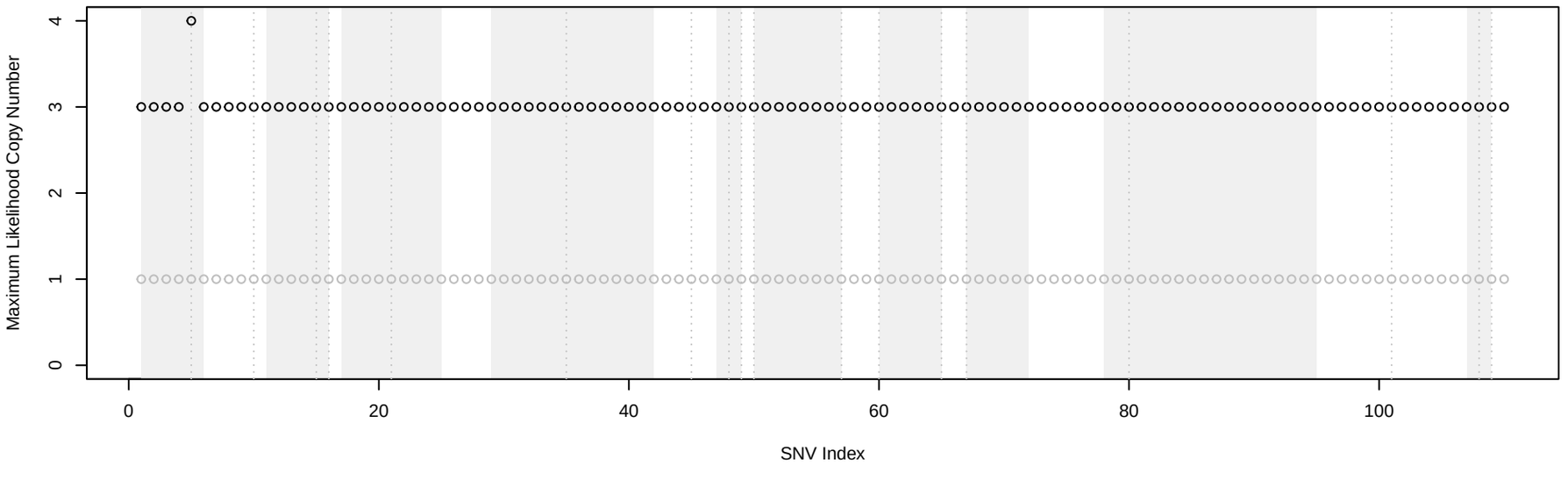

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0.30
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

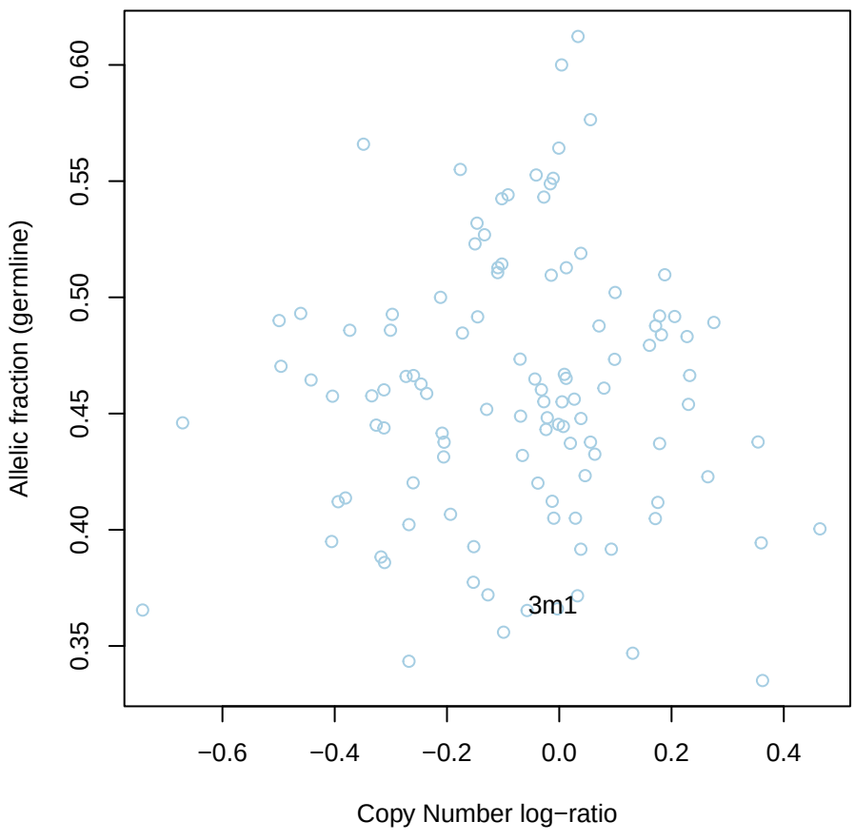

Frequency
0
20
40
60
80
0.1
0.2
0.3
0.4
0.5
Cellular fraction

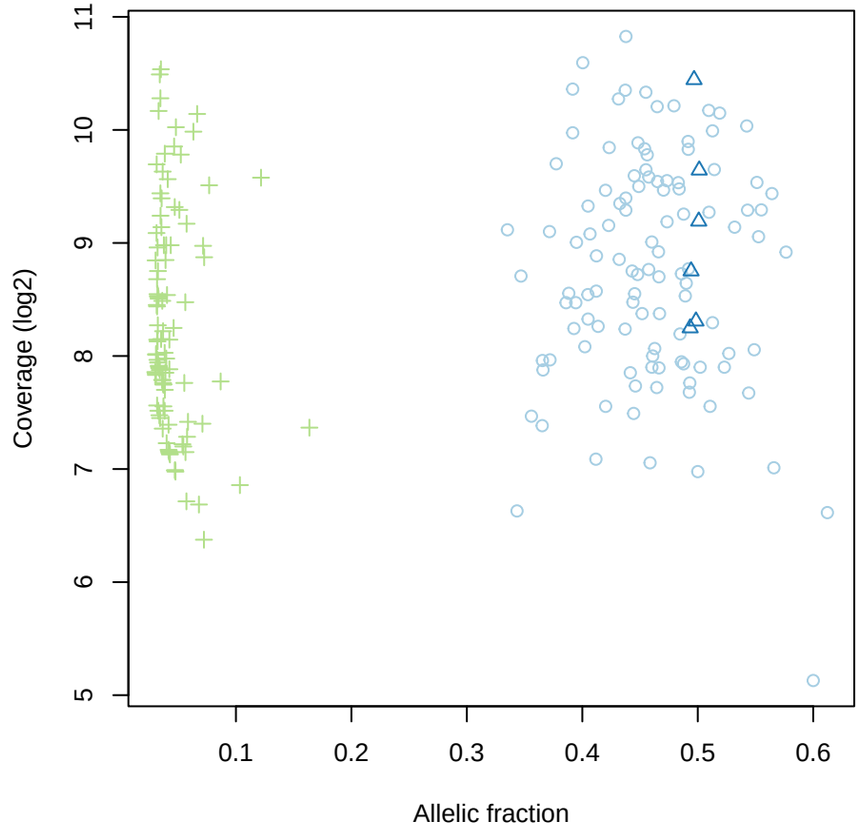

Purity: 0.72 Tumor ploidy: 3.03
2
3
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

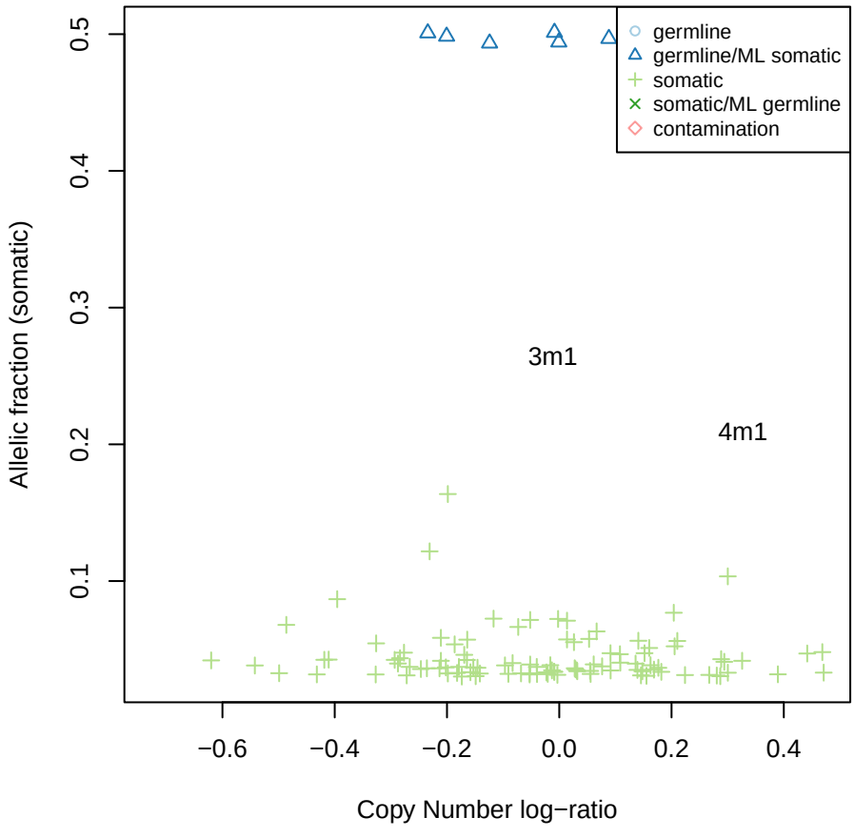

Purity: 0.72 Tumor ploidy: 3.03 SNV log−likelihood: −798.45 GoF: 34.7% Mean coverage: 389;474
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

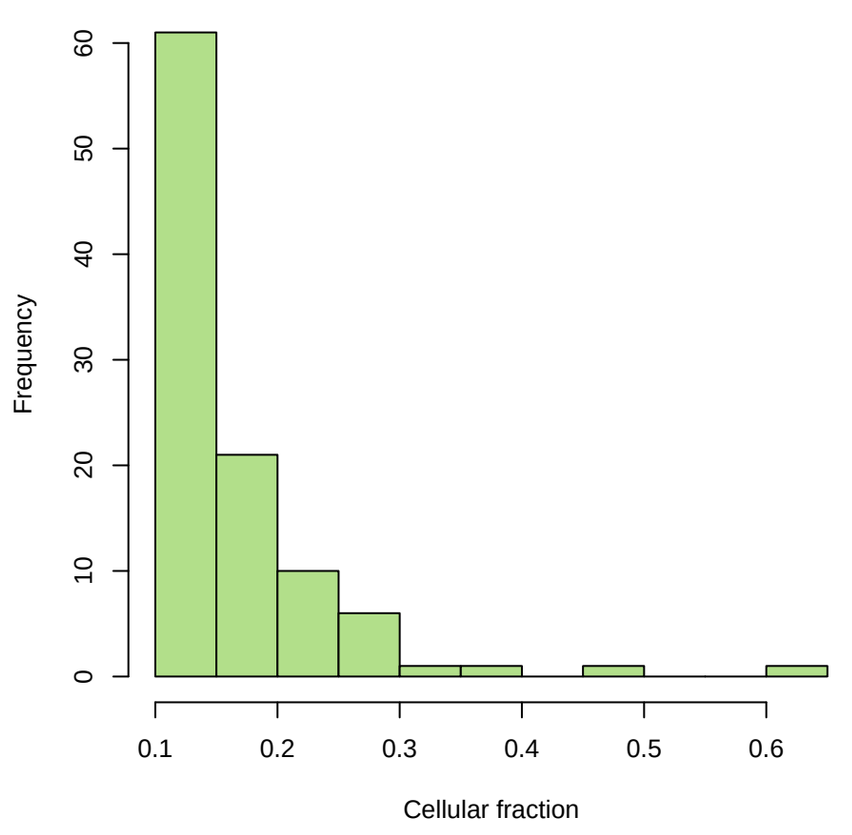

SCNA−fit log−likelihood: −7548.86
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4
0 20 40 60 80 100
SNV Index


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