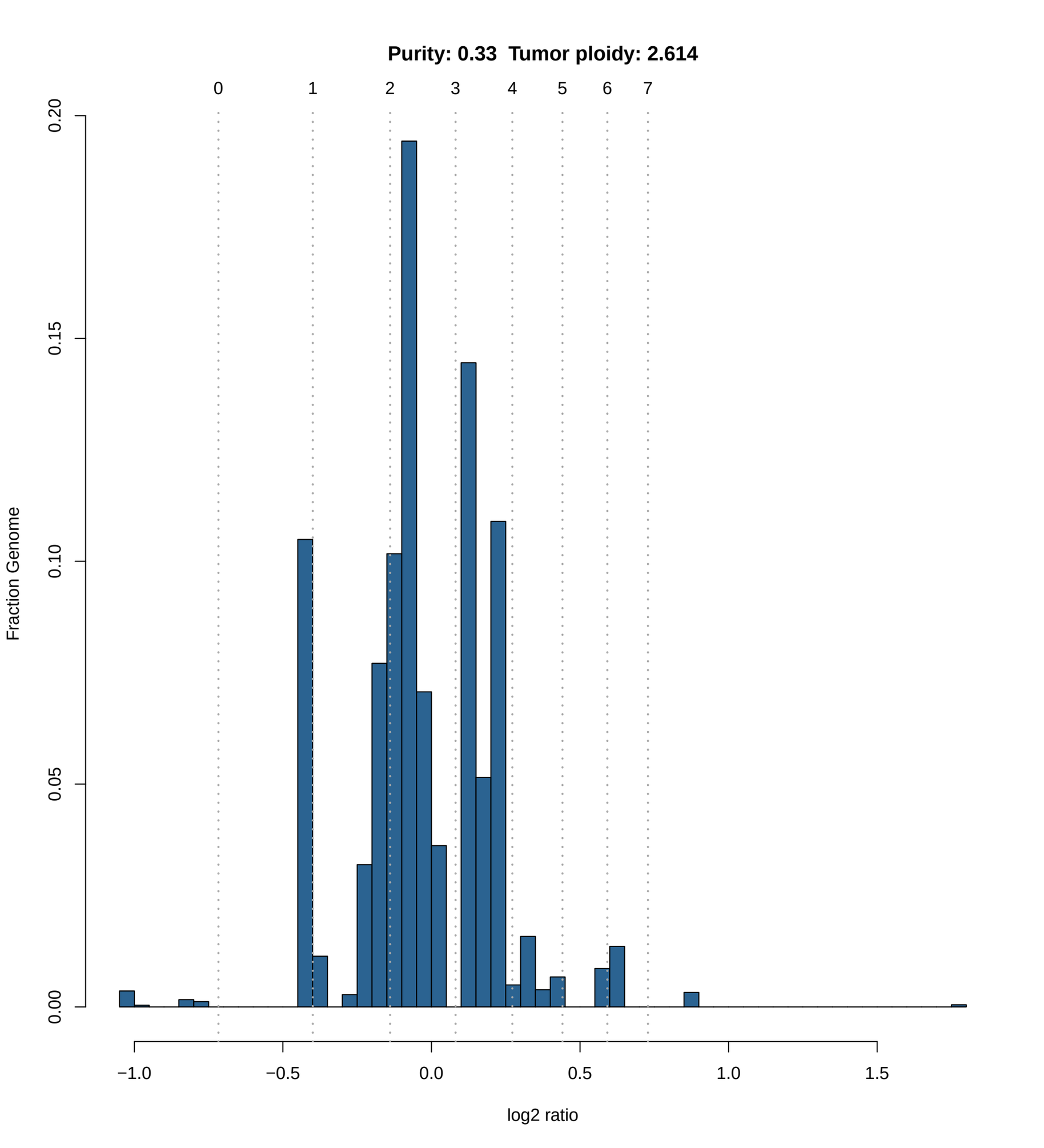
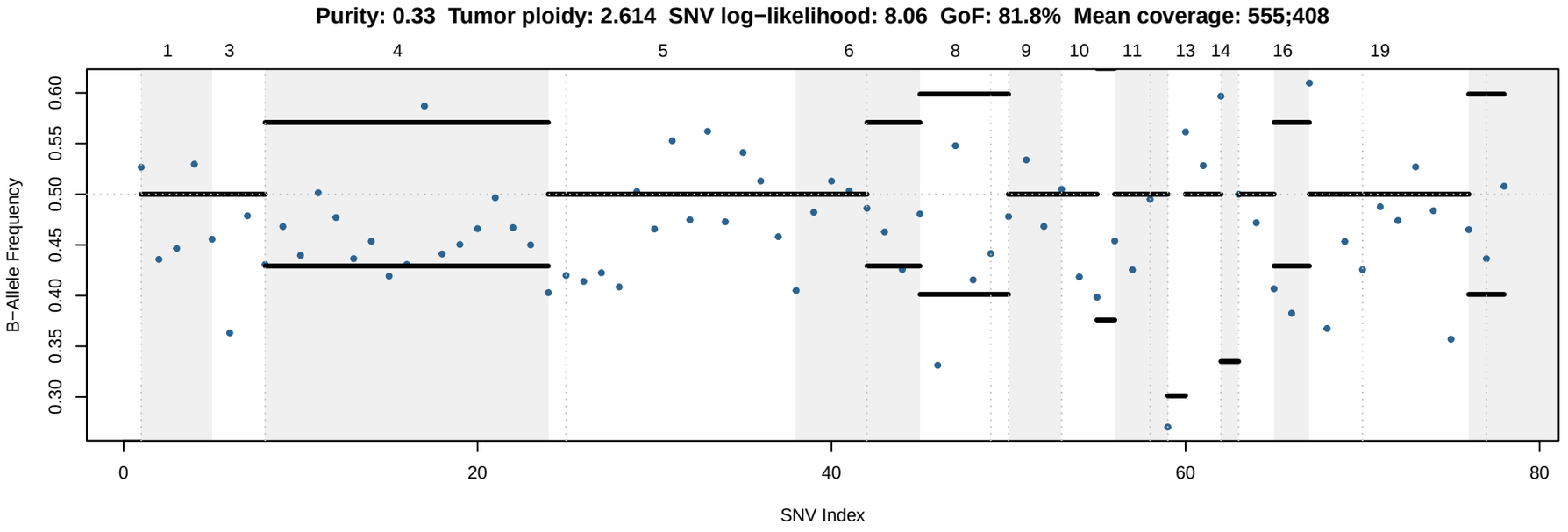
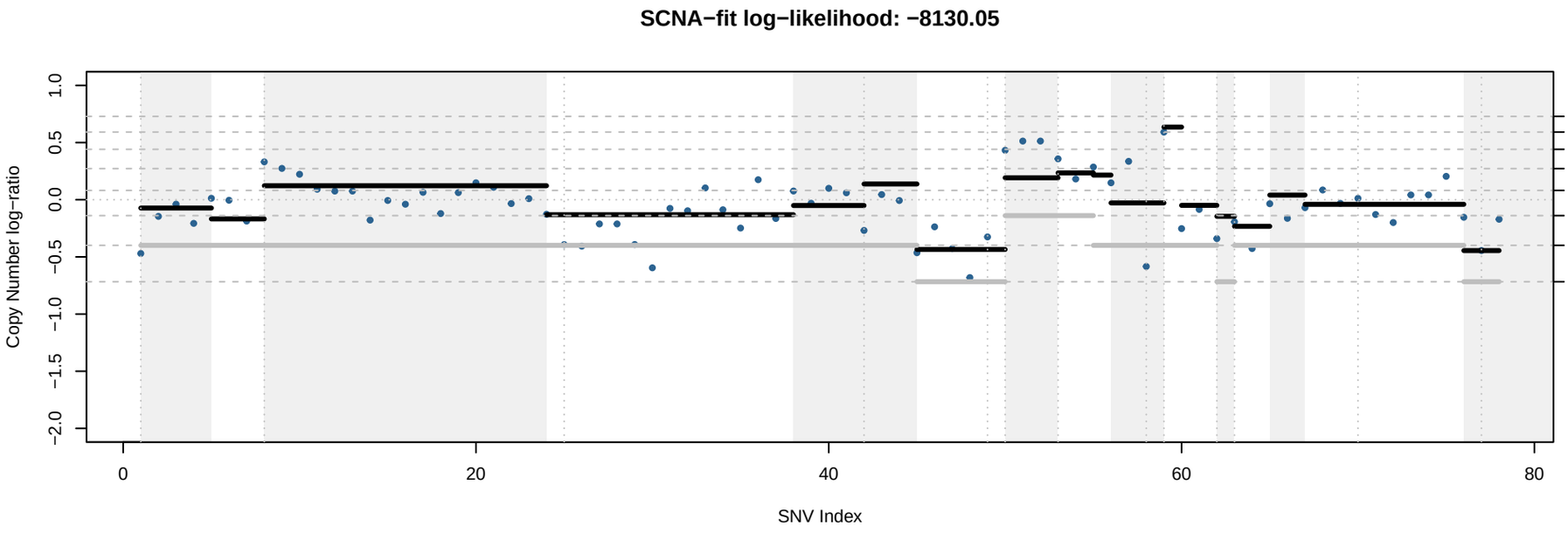
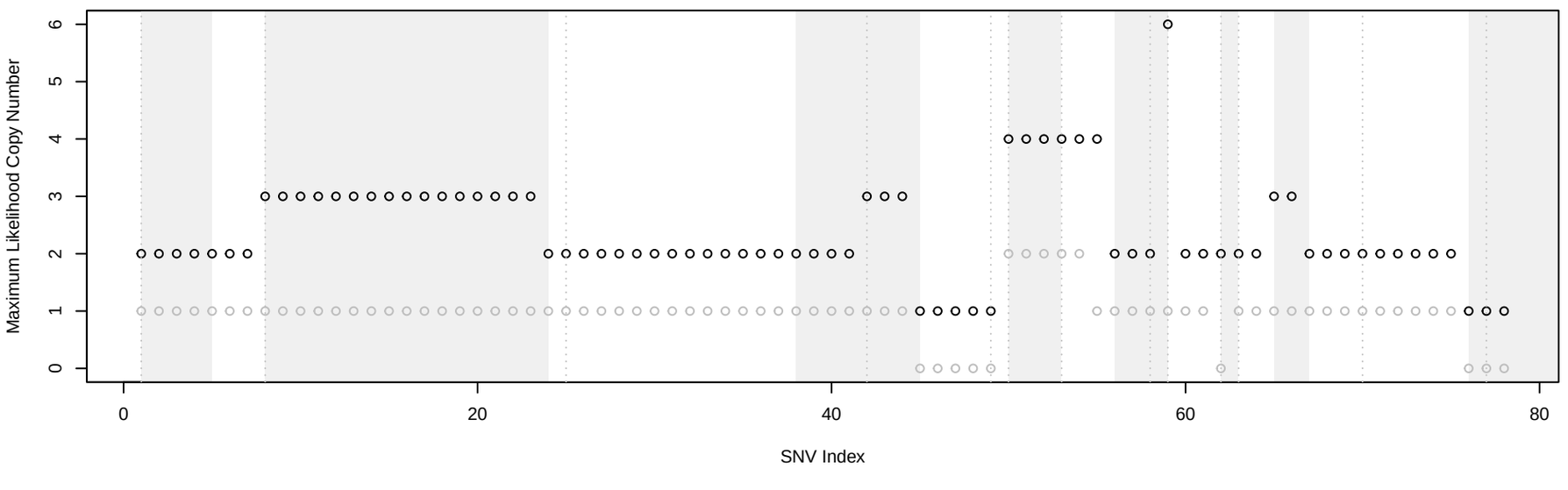
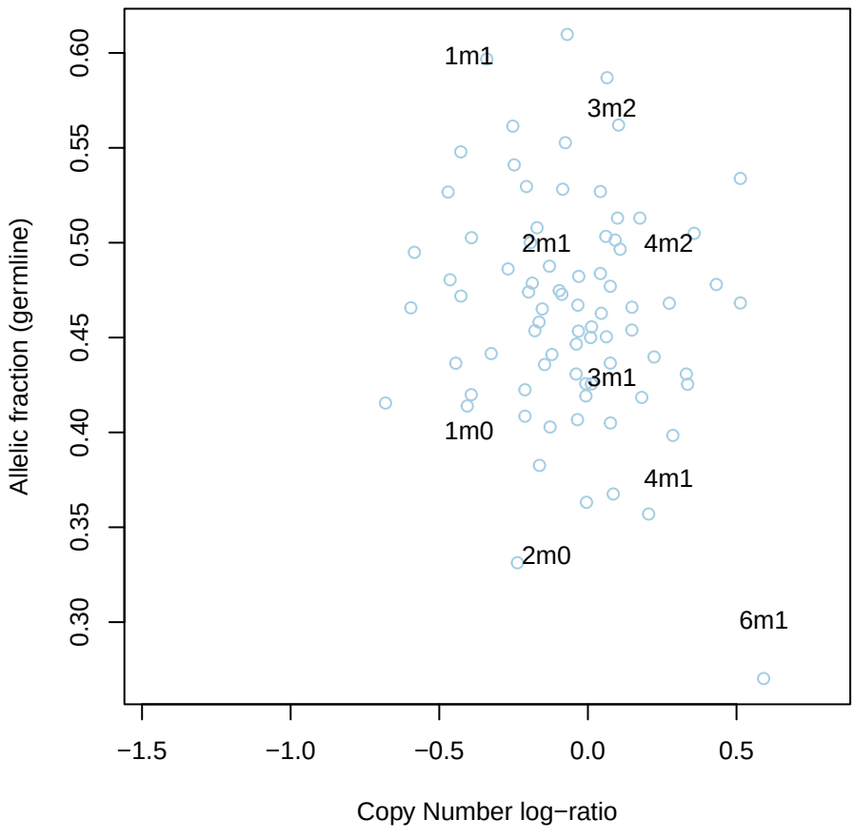
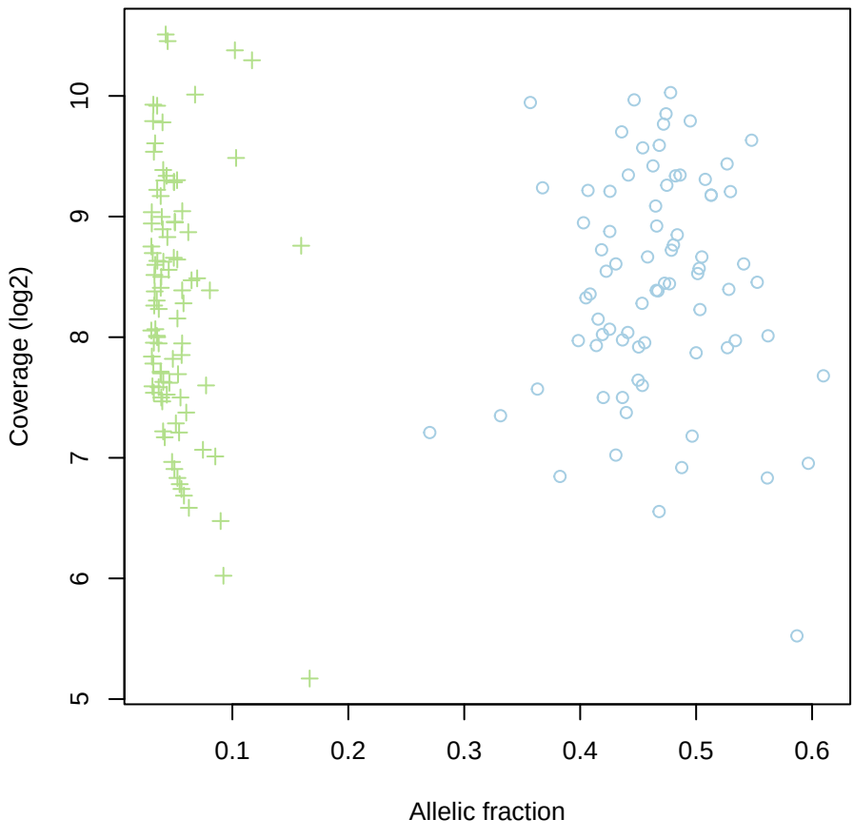

Purity: 0.33 Tumor ploidy: 2.614
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

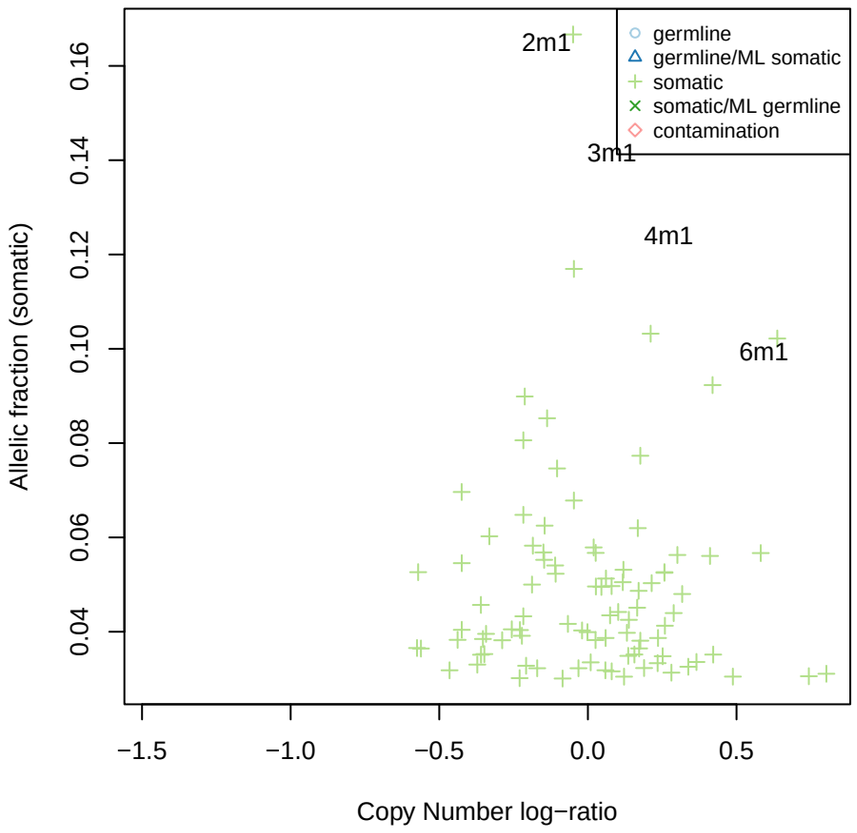

Purity: 0.33 Tumor ploidy: 2.614 SNV log−likelihood: 8.06 GoF: 81.8% Mean coverage: 555;408
1 3 4 5 6 8 9 10 11 13 14 16 19
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

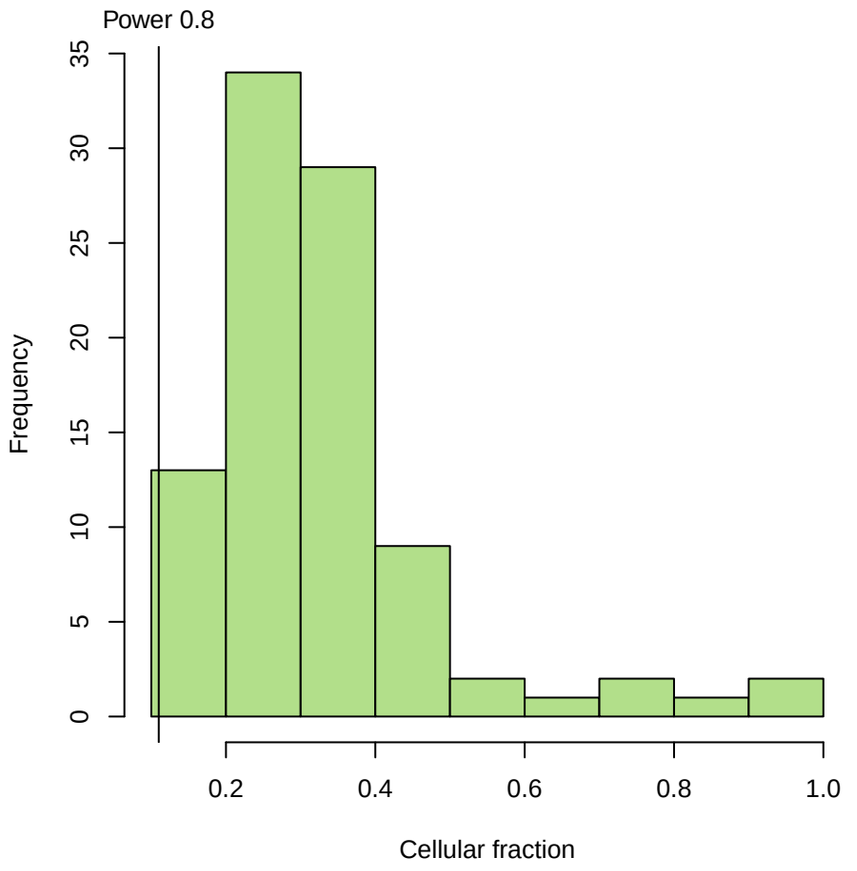

SCNA−fit log−likelihood: −8130.05
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
0 1 2 3 5 7
0 20 40 60 80
SNV Index

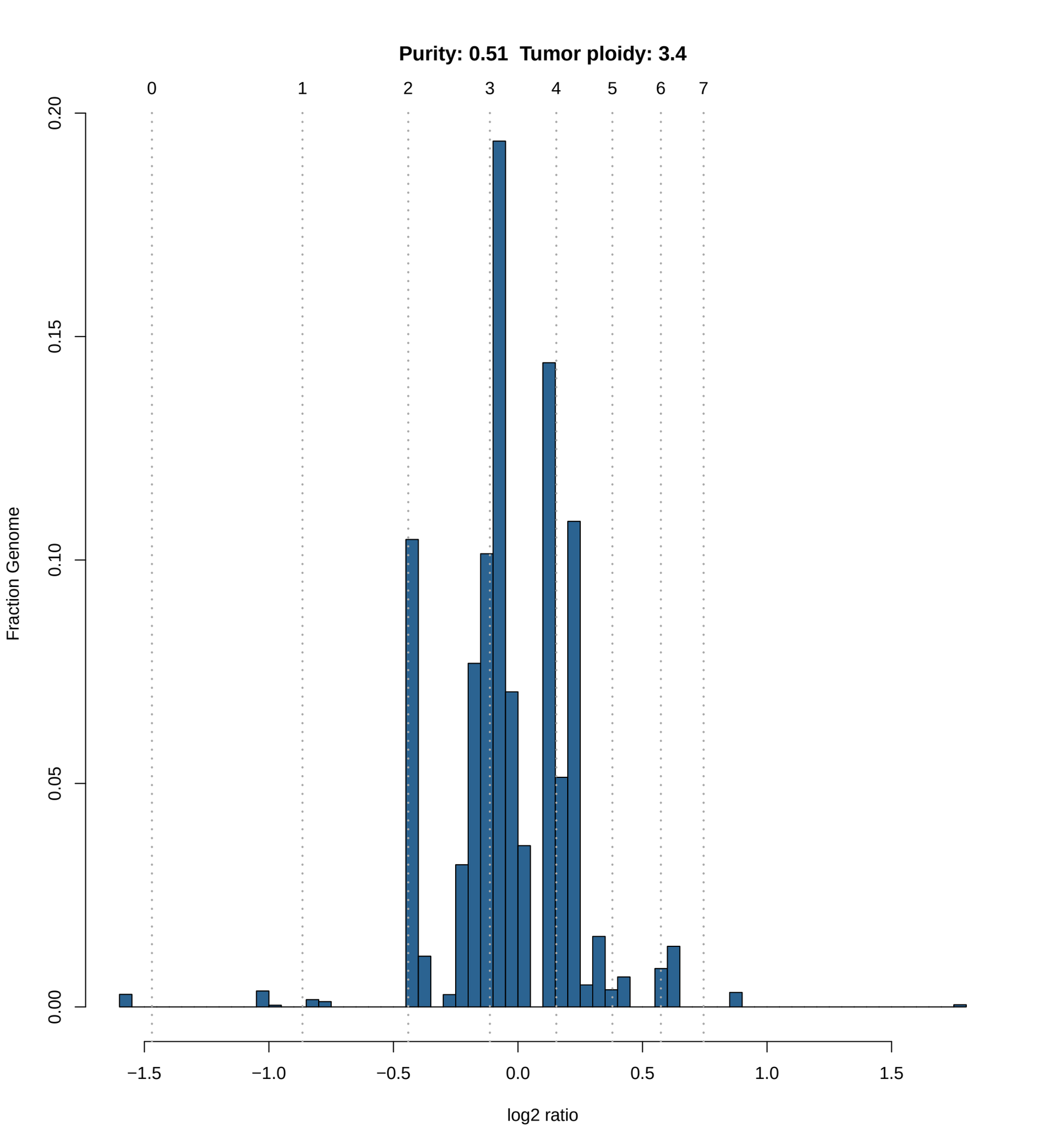

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80
SNV Index

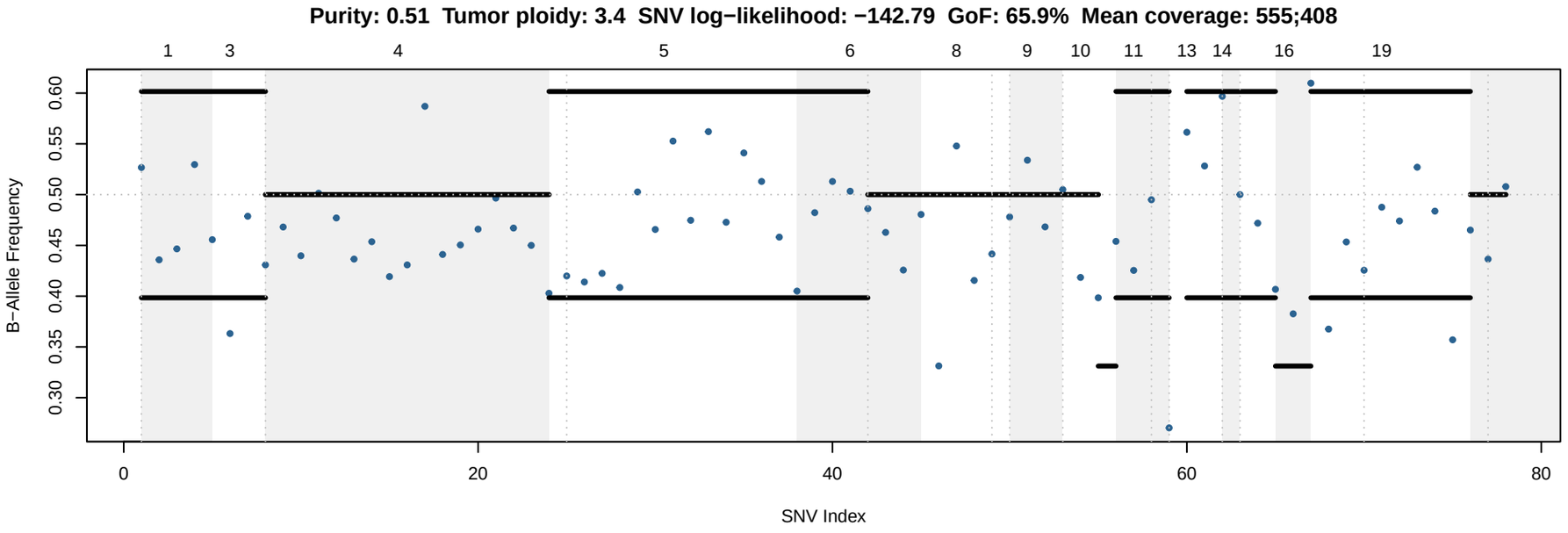

1m1
3m2
2m1
4m2
3m1
1m0
4m1
2m0
6m1
Allelic fraction (germline)
Copy Number log−ratio

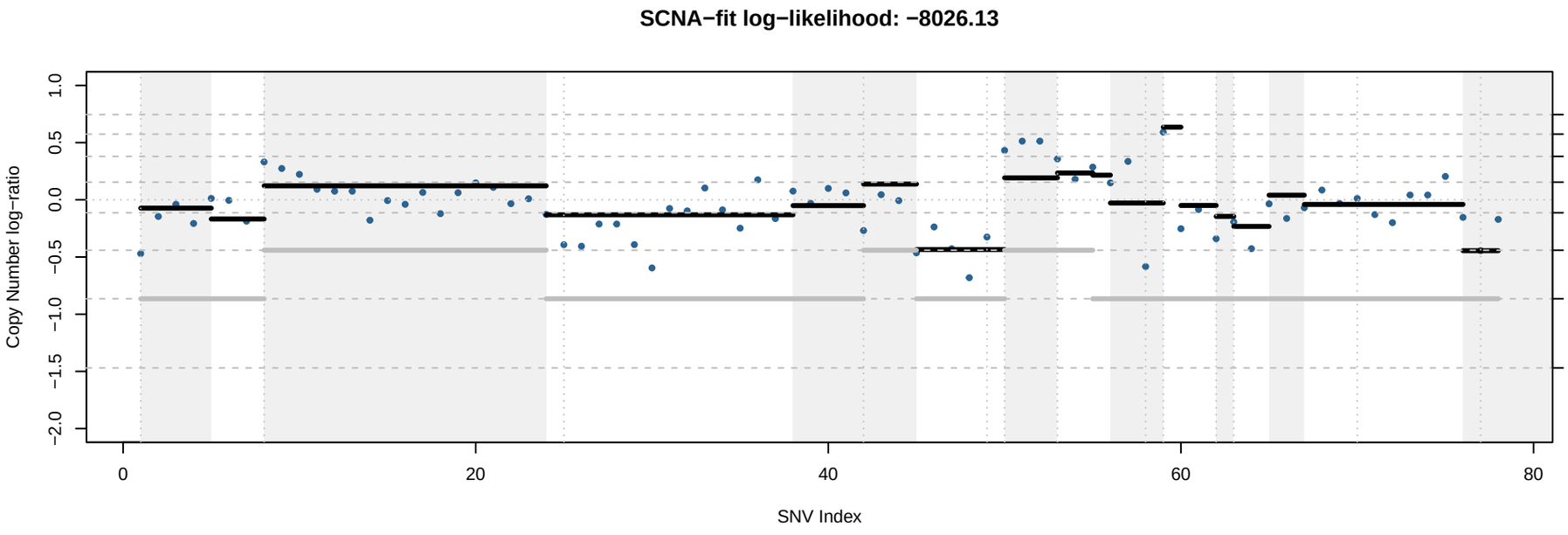

Coverage (log2)
Allelic fraction

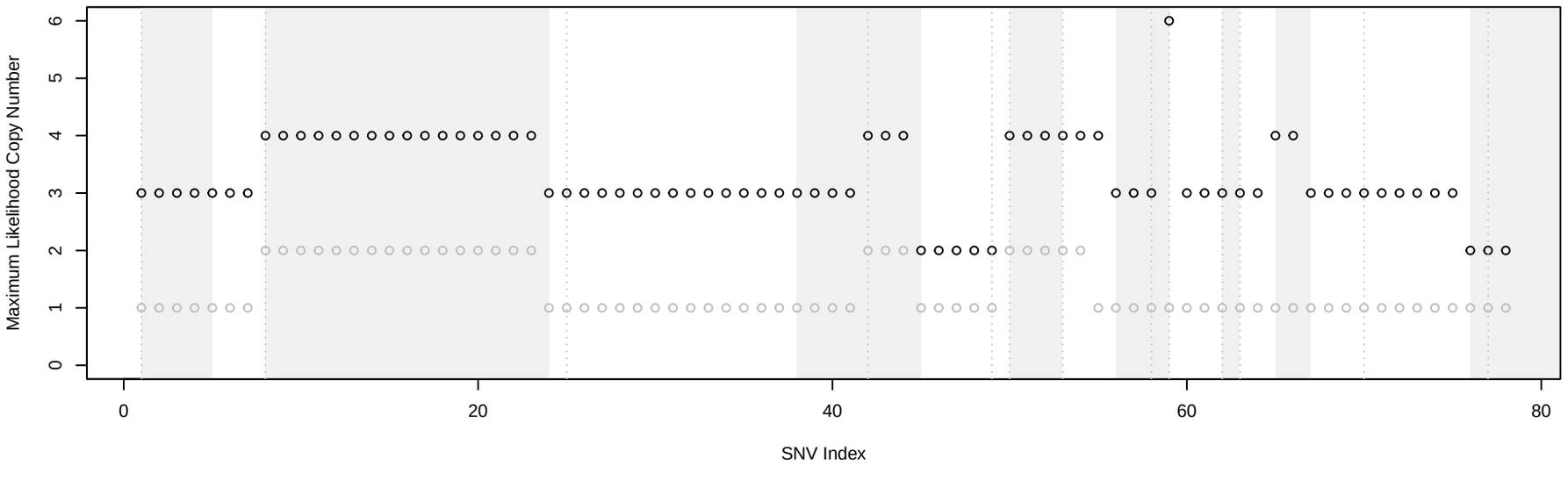

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio

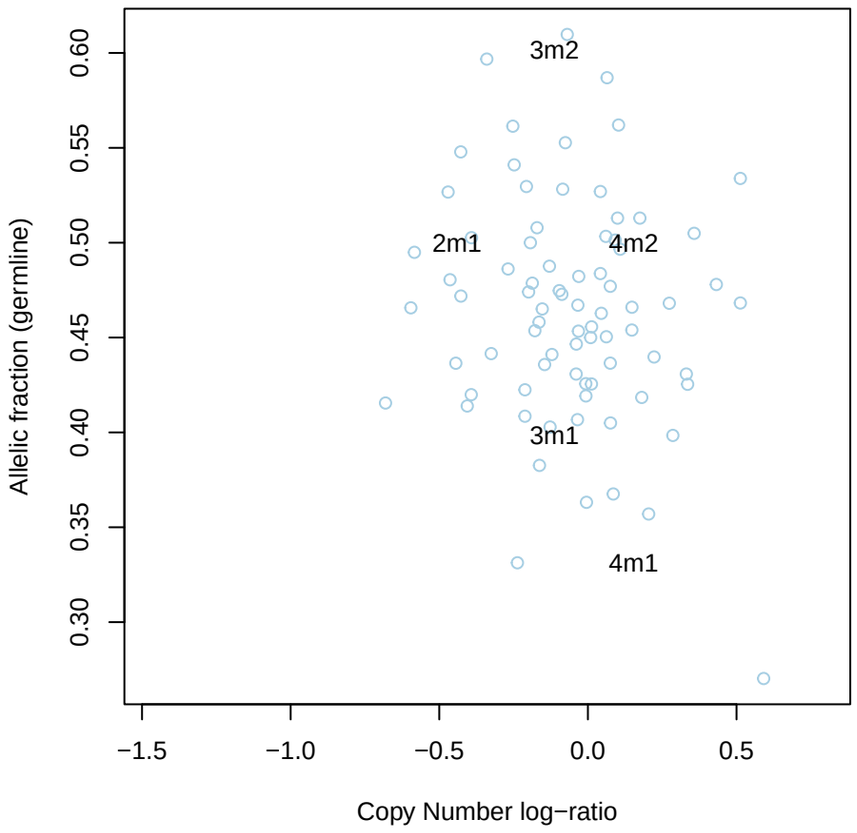

Power 0.8
Frequency
Cellular fraction

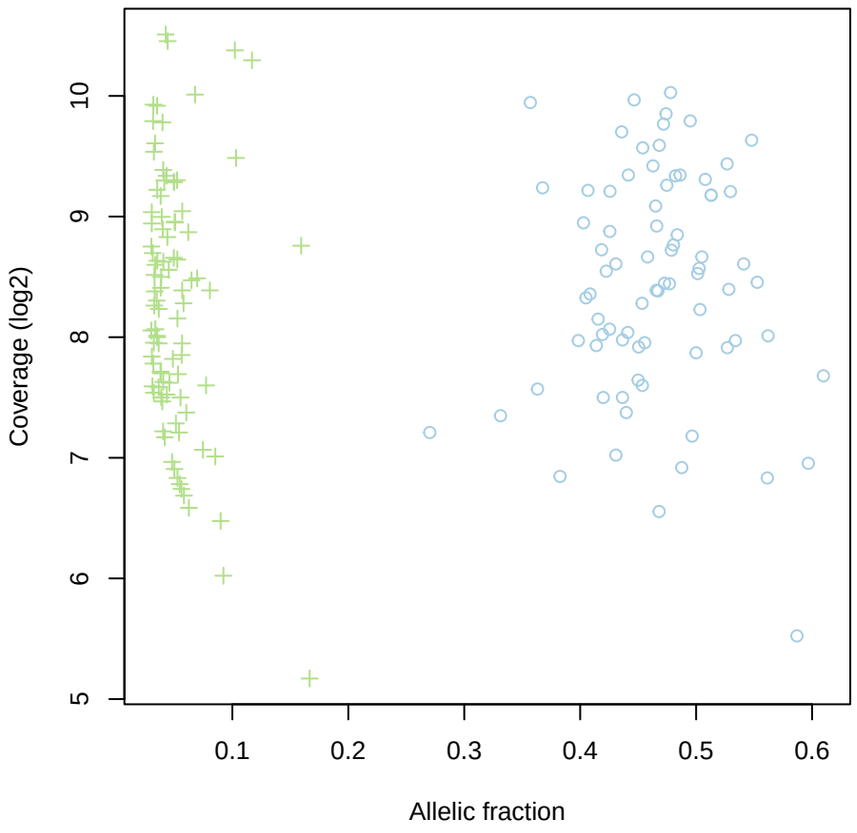

Purity: 0.51 Tumor ploidy: 3.4
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

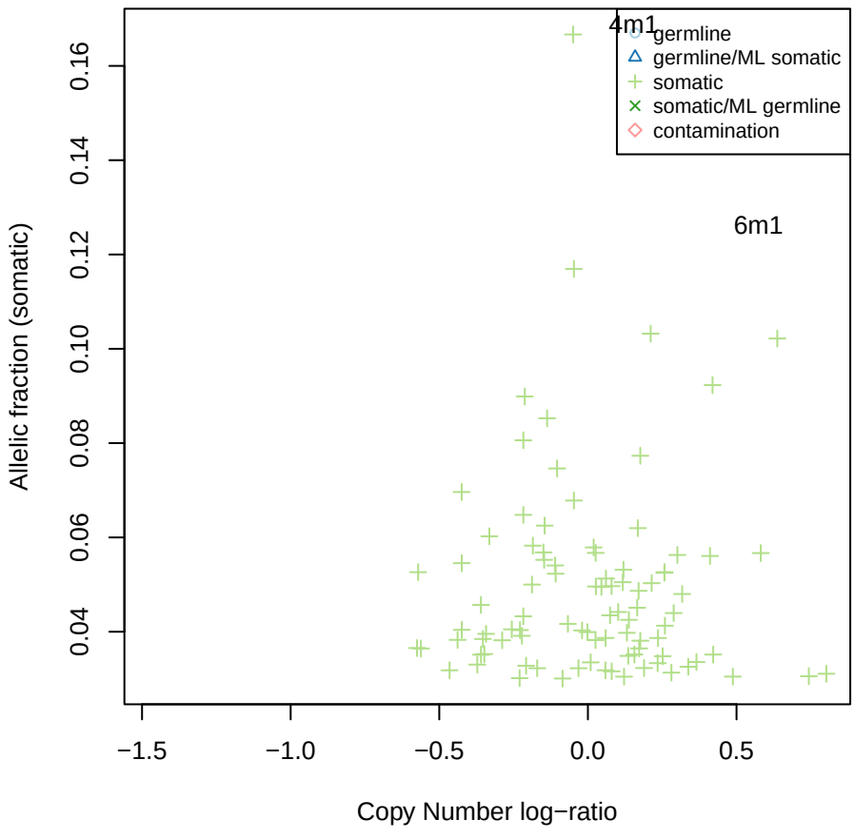

Purity: 0.51 Tumor ploidy: 3.4 SNV log−likelihood: −142.79 GoF: 65.9% Mean coverage: 555;408
1 3 4 5 6 8 9 10 11 13 14 16 19
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

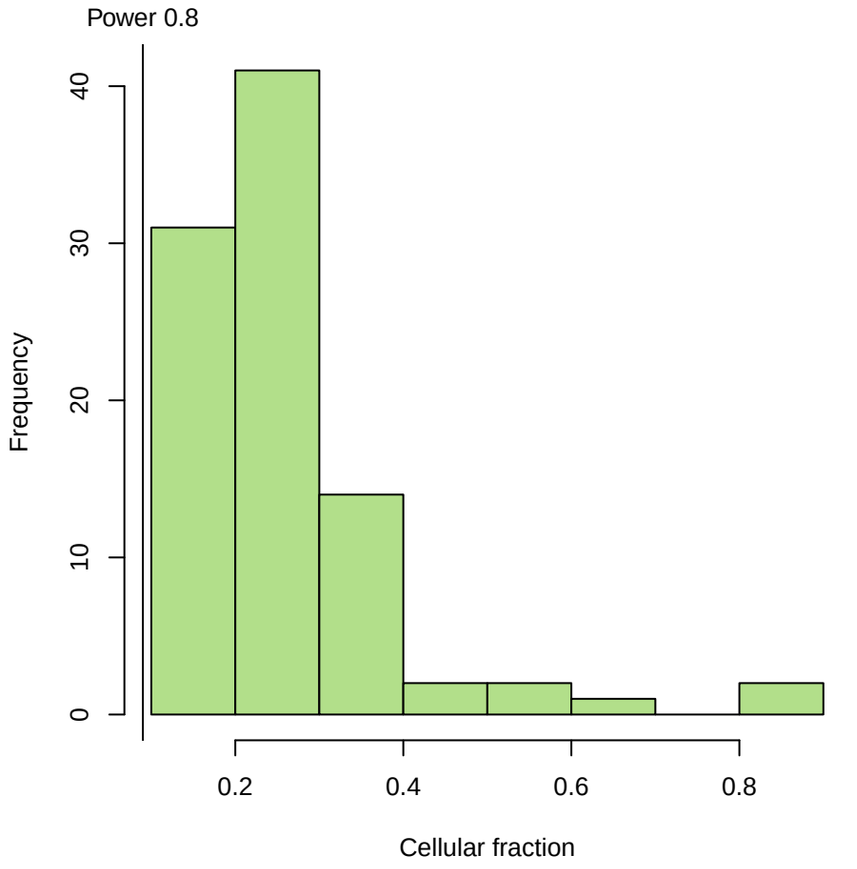

SCNA−fit log−likelihood: −8026.13
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 7
0 20 40 60 80
SNV Index

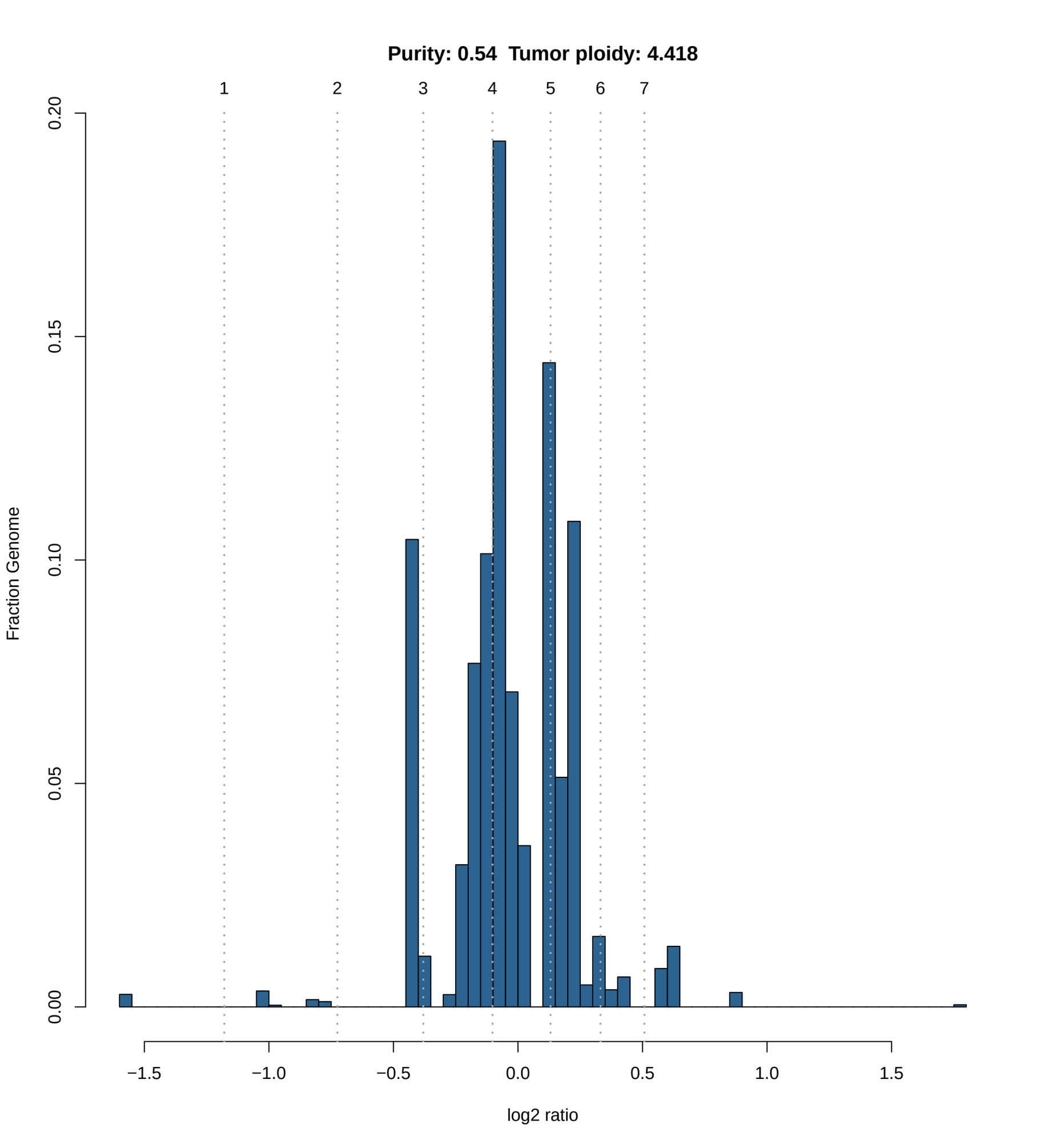

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80
SNV Index

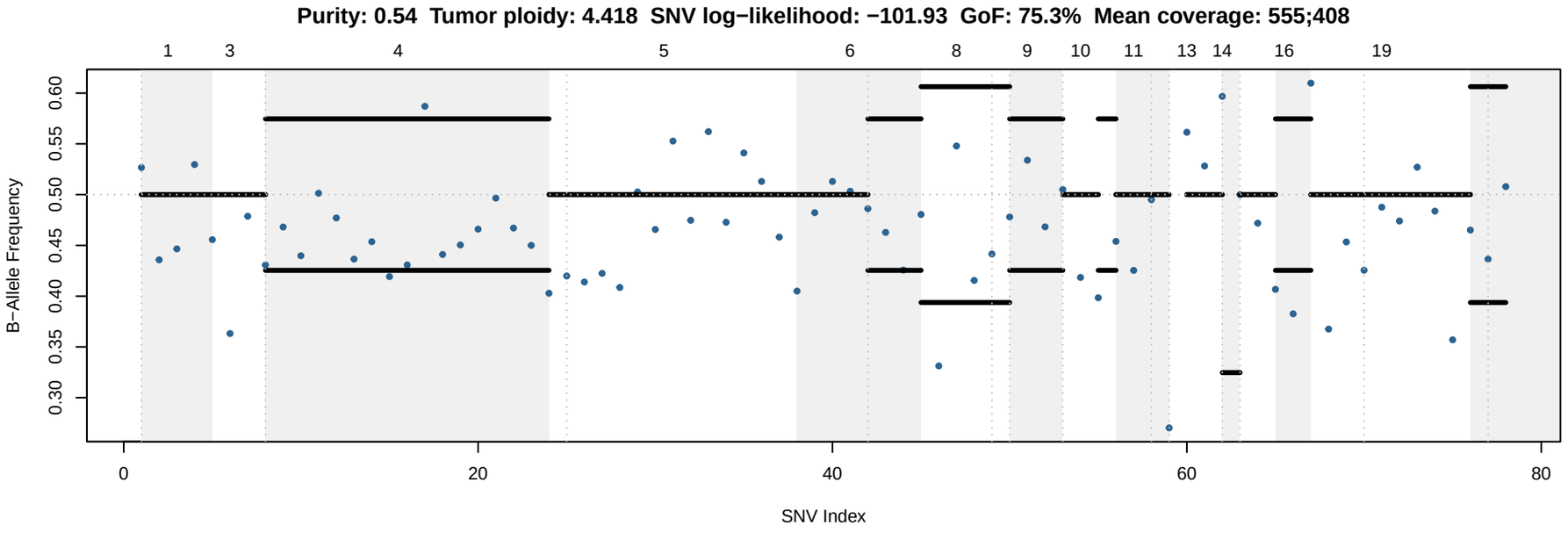

3m2
2m1
4m2
3m1
4m1
Allelic fraction (germline)
Copy Number log−ratio

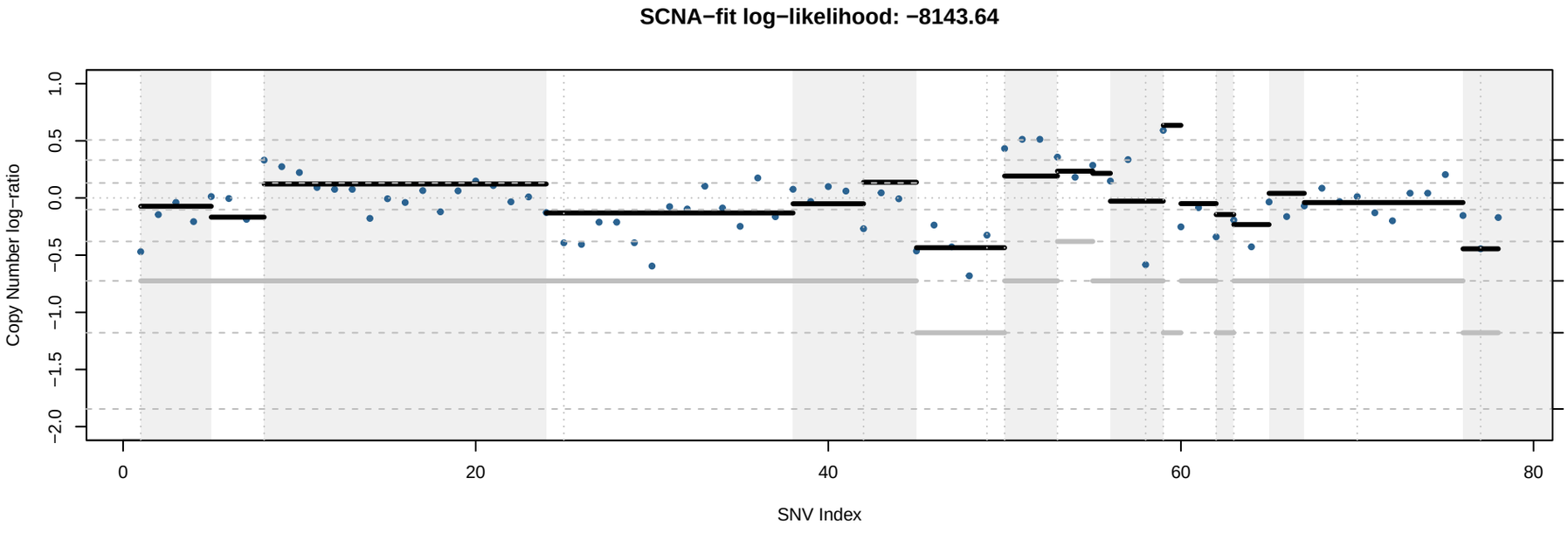

Coverage (log2)
Allelic fraction

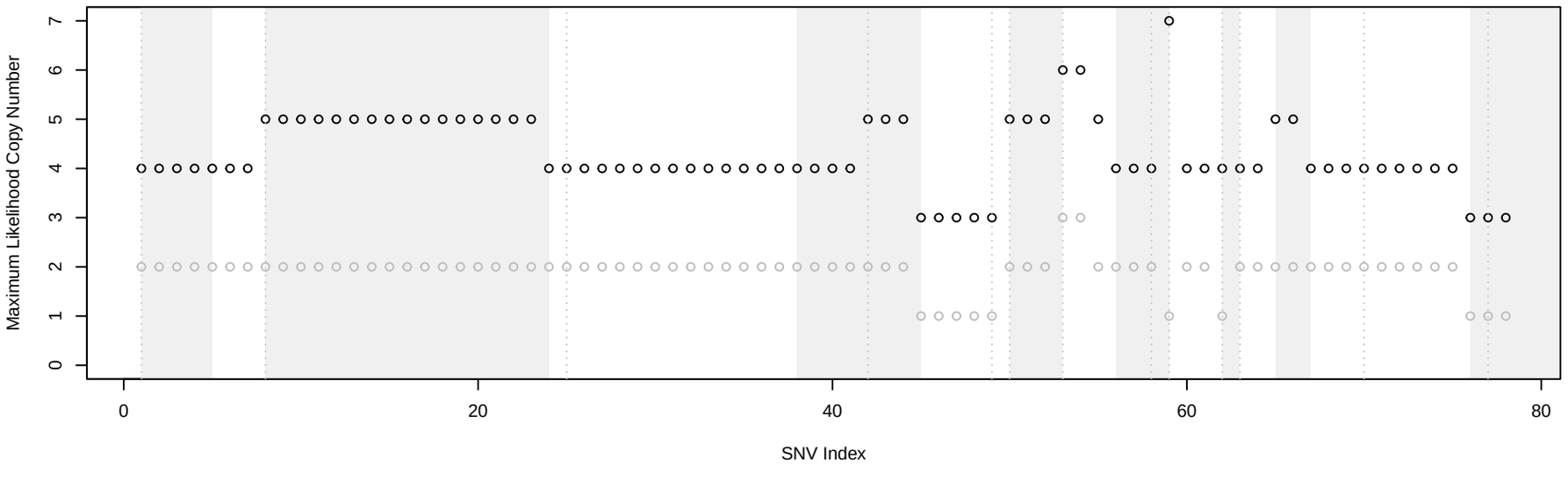

4m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m1
Allelic fraction (somatic)
Copy Number log−ratio

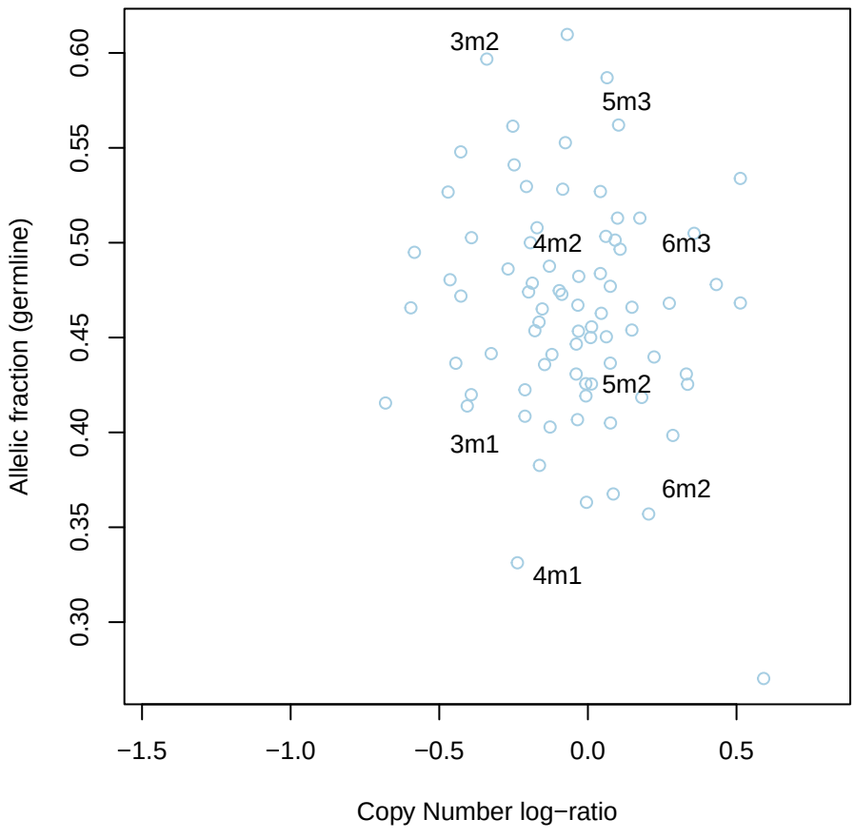

Power 0.8
Frequency
Cellular fraction

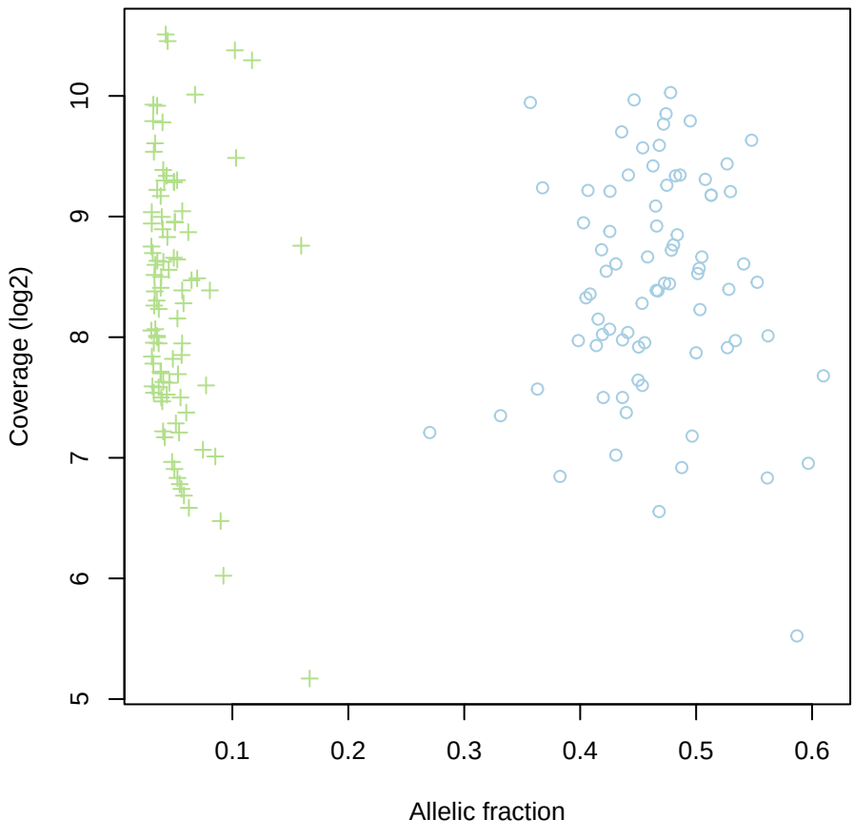

Purity: 0.54 Tumor ploidy: 4.418
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

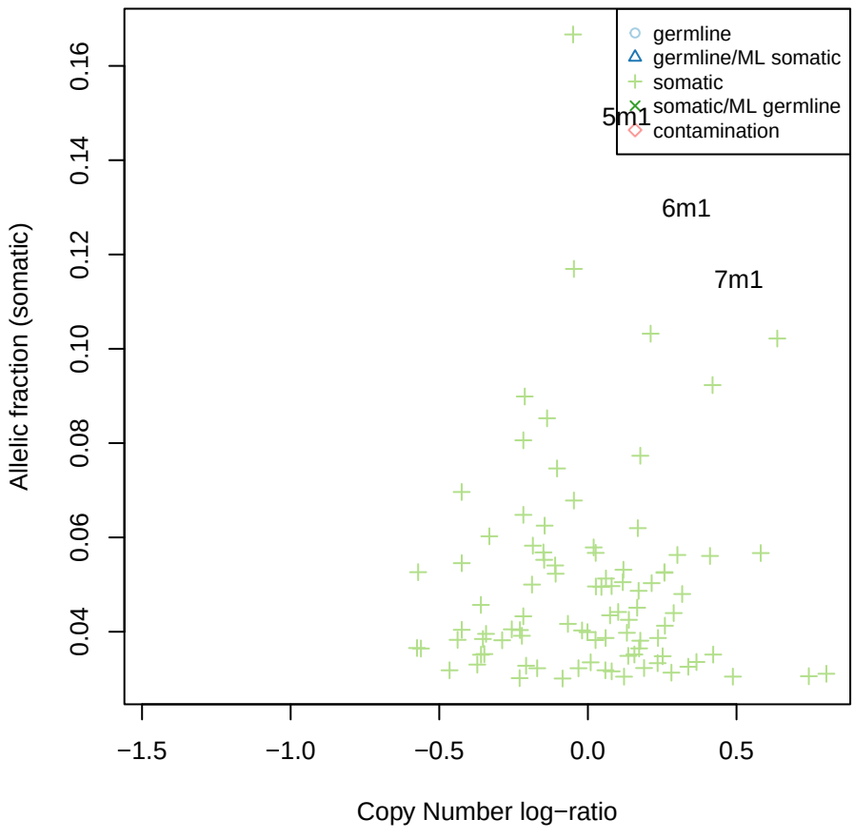

Purity: 0.54 Tumor ploidy: 4.418 SNV log−likelihood: −101.93 GoF: 75.3% Mean coverage: 555;408
1 3 4 5 6 8 9 10 11 13 14 16 19
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

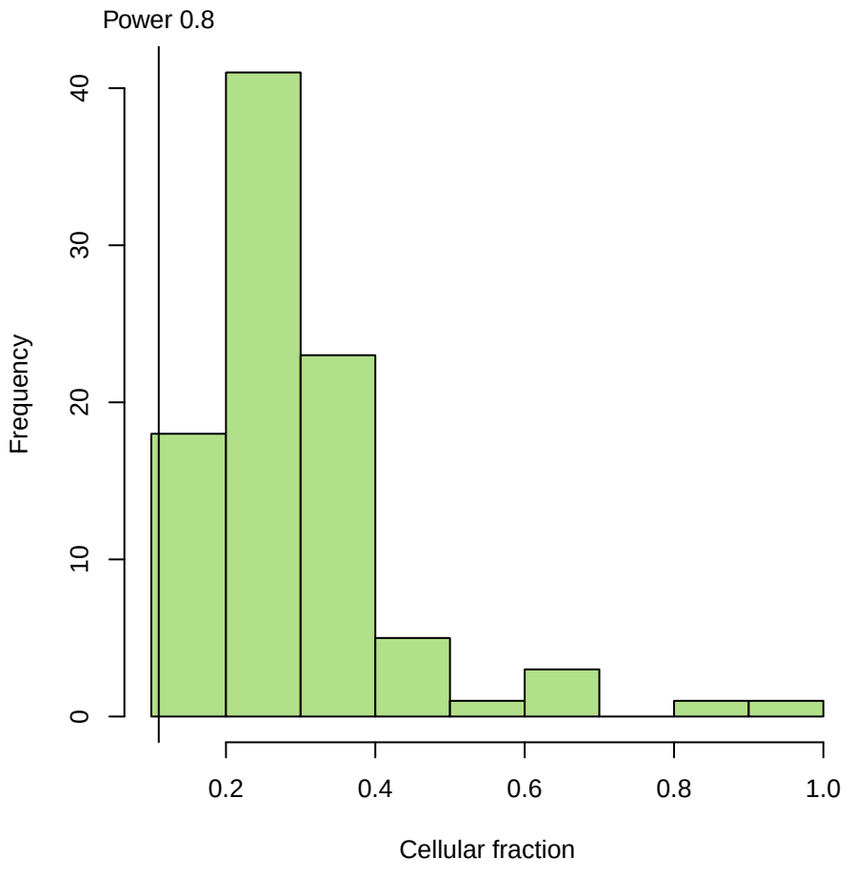

SCNA−fit log−likelihood: −8143.64
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 7
0 20 40 60 80
SNV Index

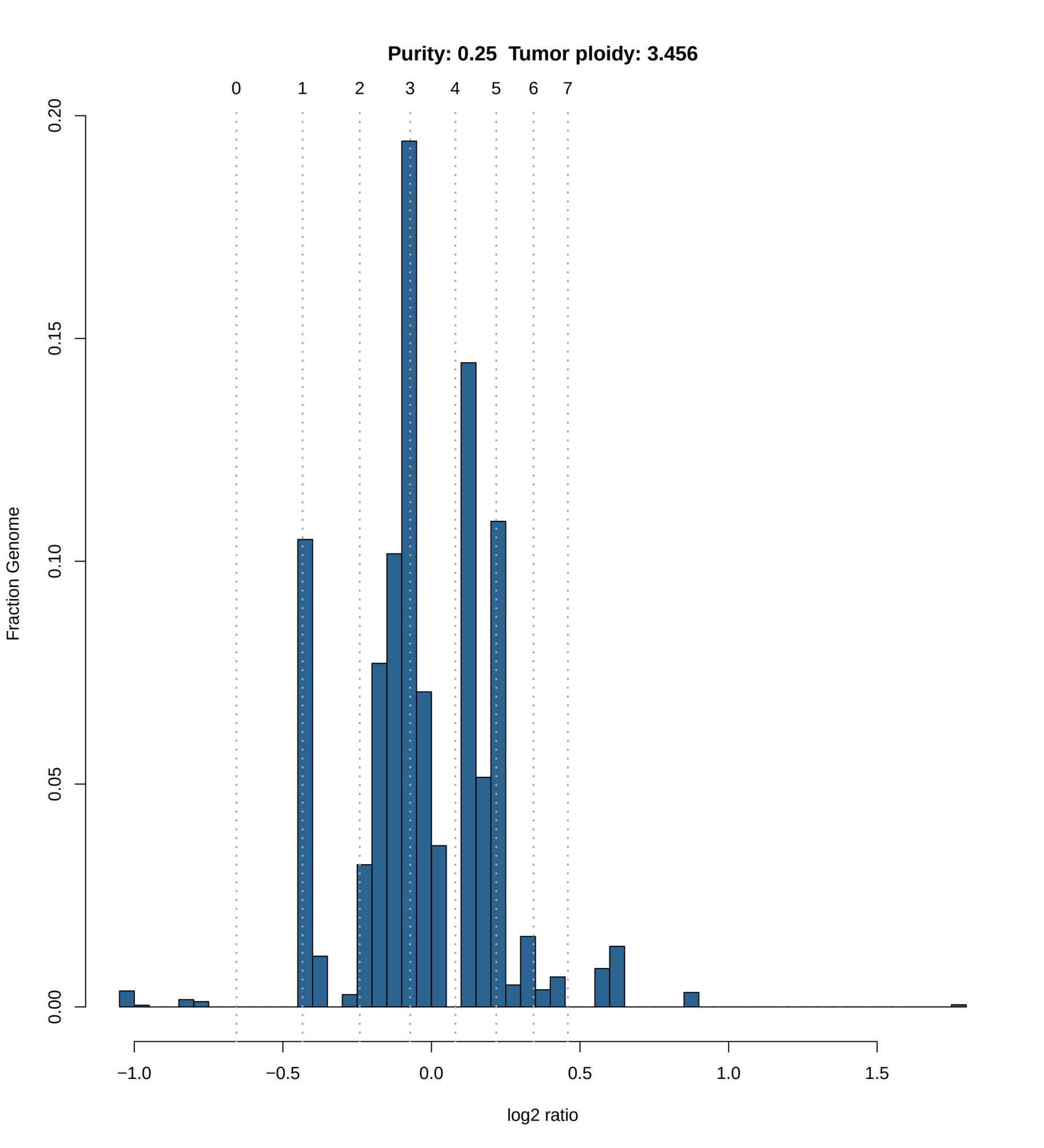

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

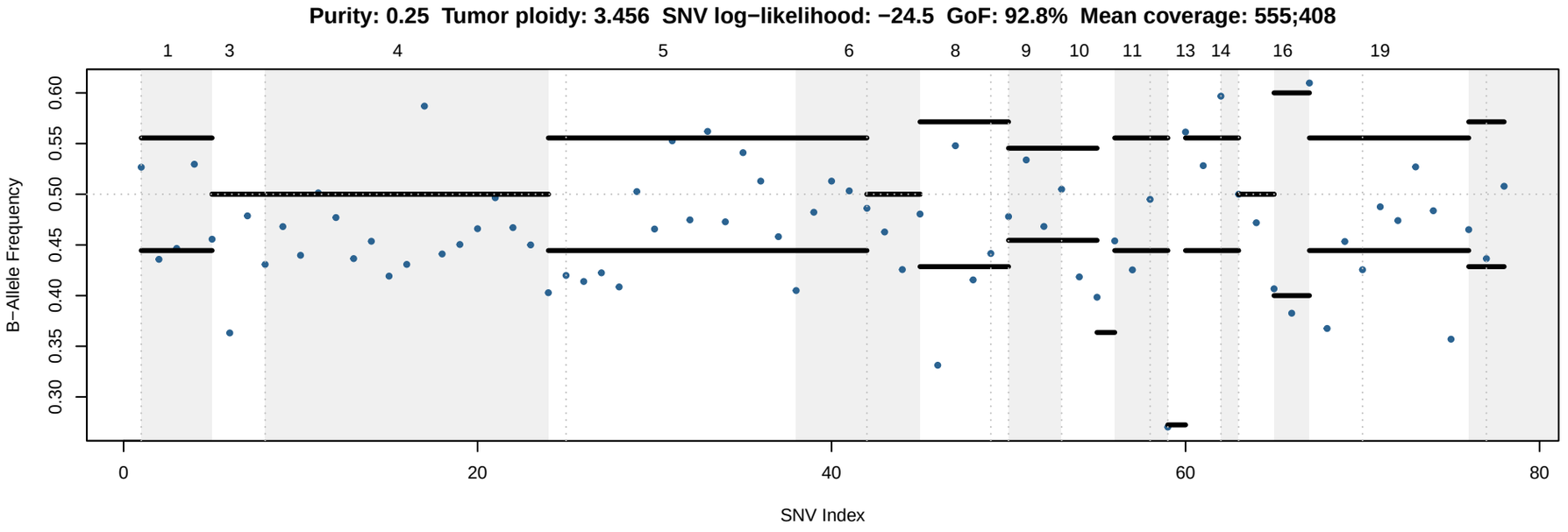

3m2
5m3
4m2
6m3
5m2
3m1
6m2
4m1
Allelic fraction (germline)
Copy Number log−ratio

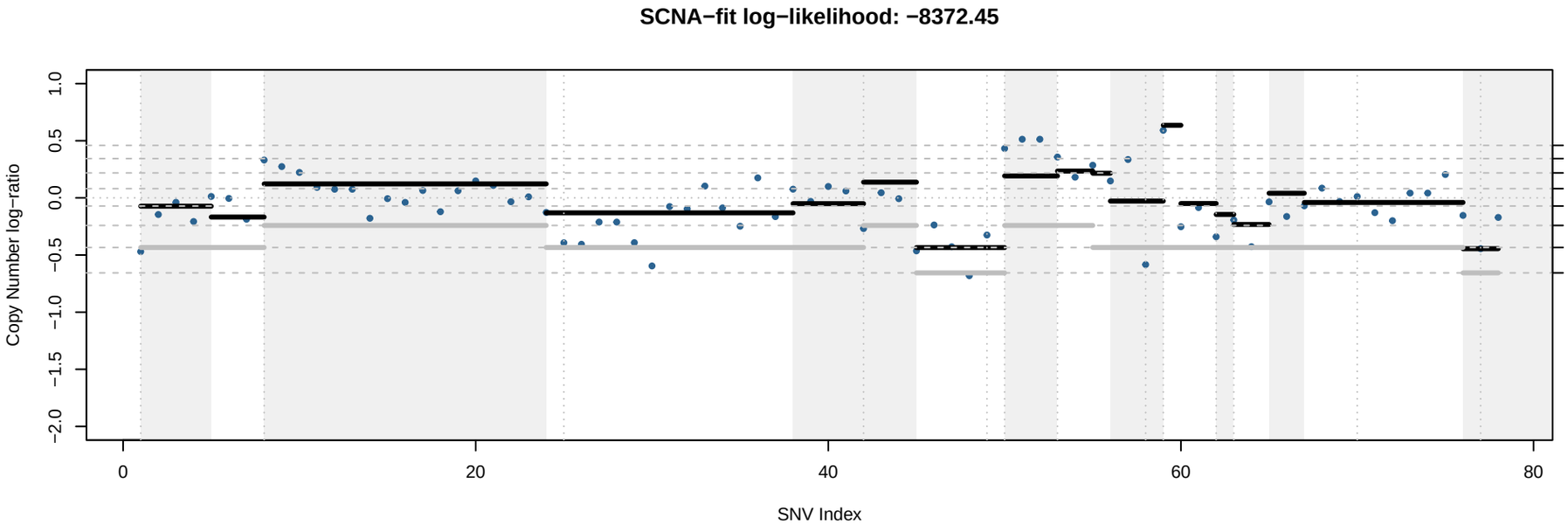

Coverage (log2)
Allelic fraction

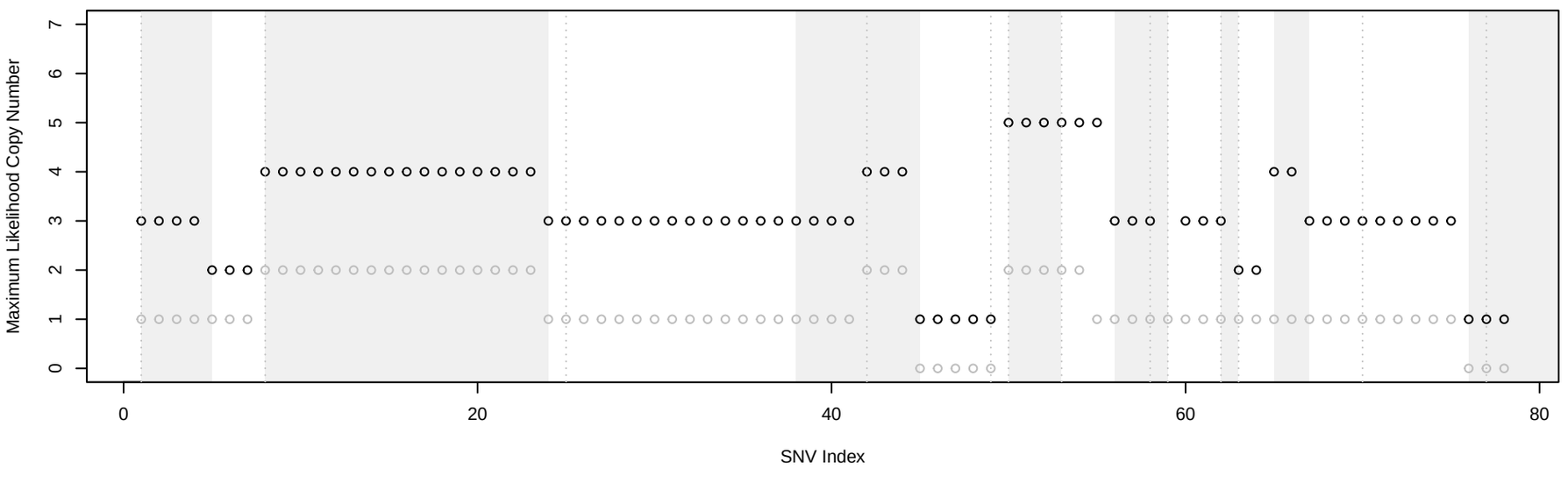

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

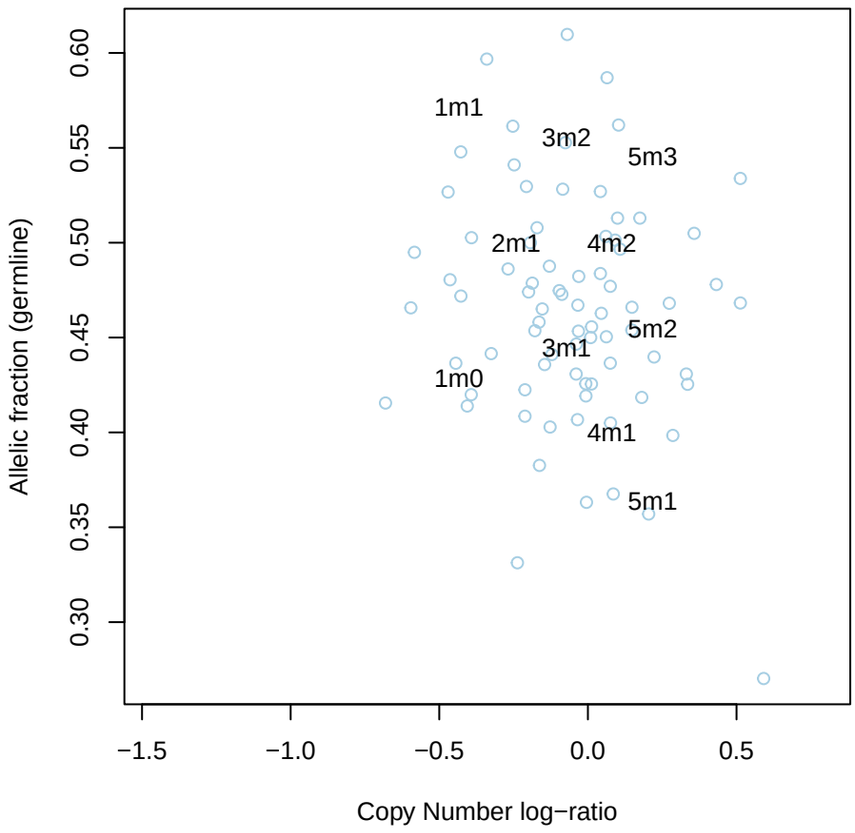

Power 0.8
Frequency
Cellular fraction

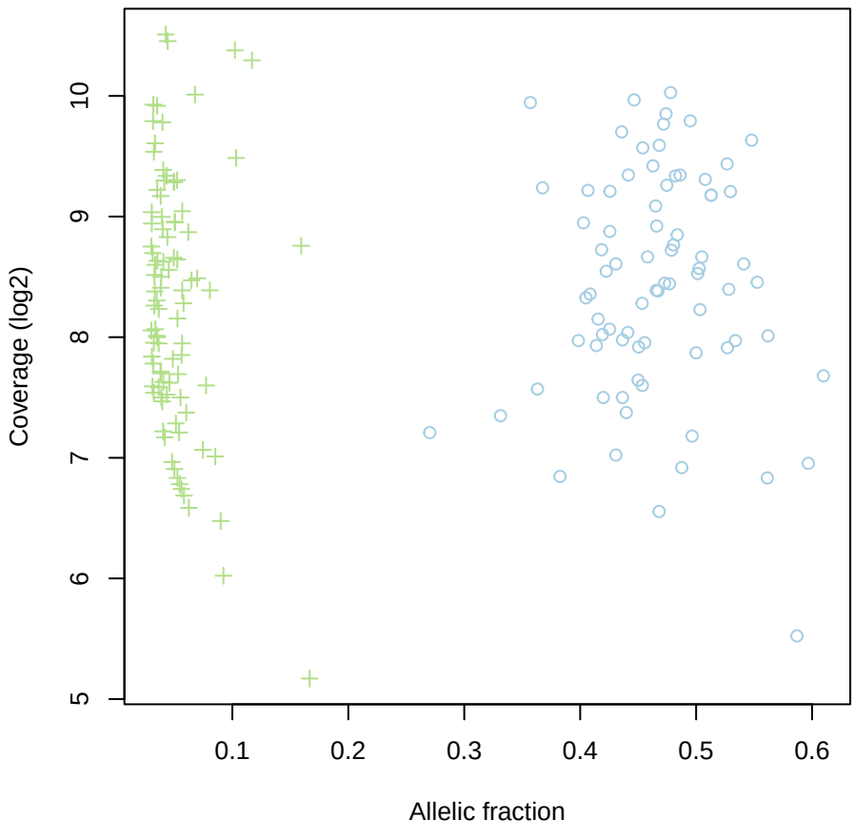

Purity: 0.25 Tumor ploidy: 3.456
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

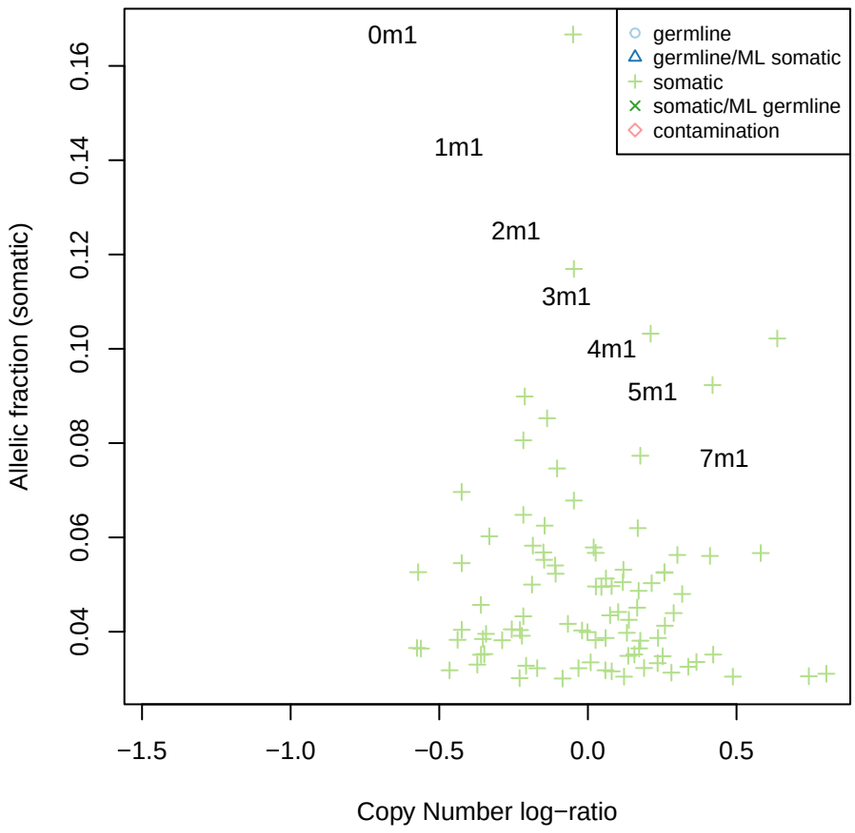

Purity: 0.25 Tumor ploidy: 3.456 SNV log−likelihood: −24.5 GoF: 92.8% Mean coverage: 555;408
1 3 4 5 6 8 9 10 11 13 14 16 19
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

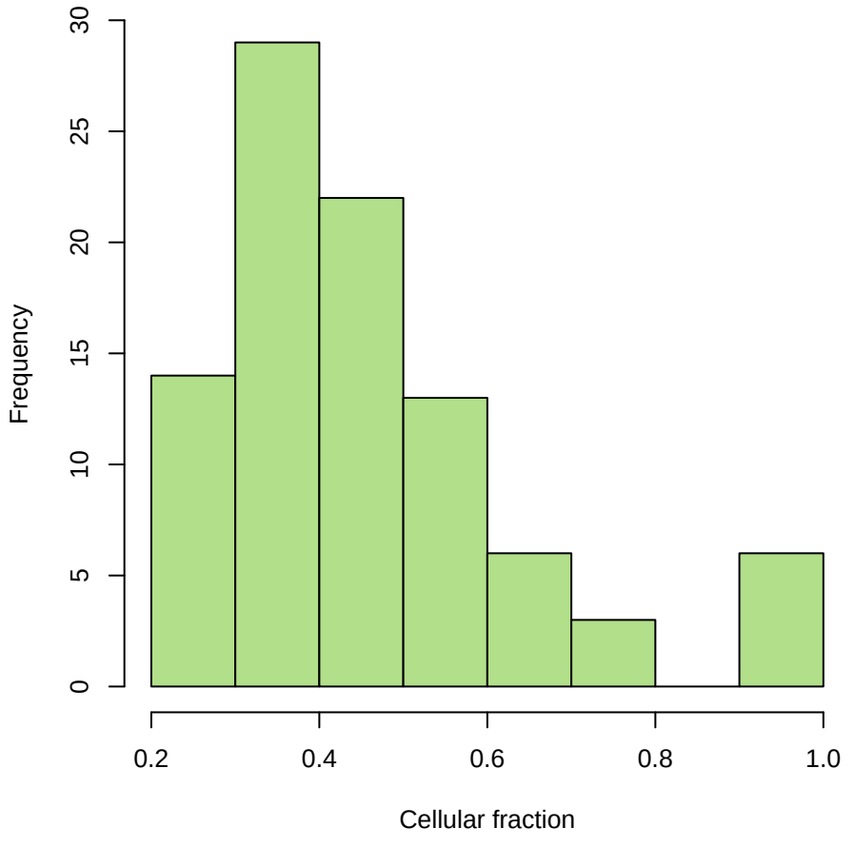

SCNA−fit log−likelihood: −8372.45
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 3 5 7
0 20 40 60 80
SNV Index

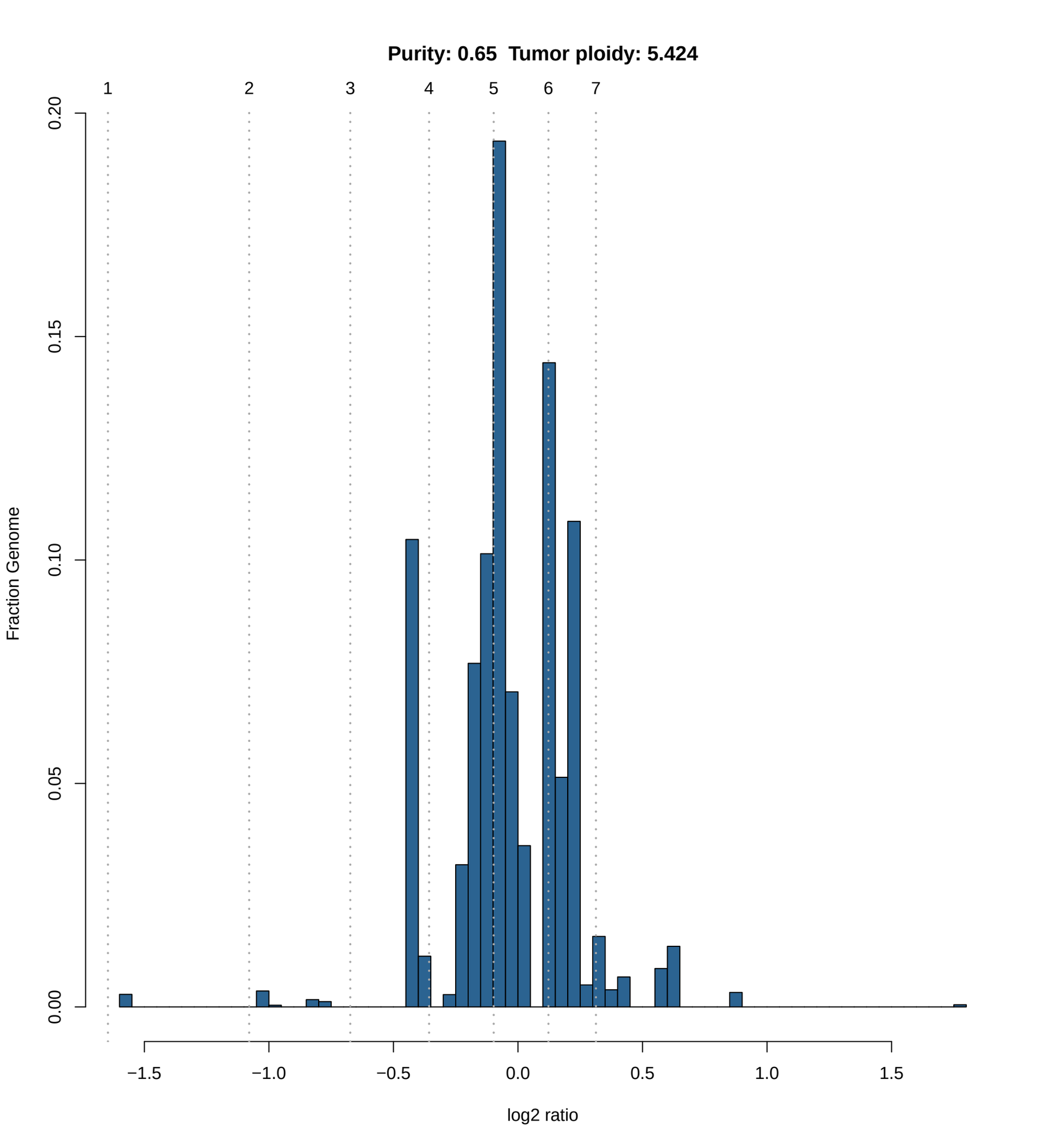

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

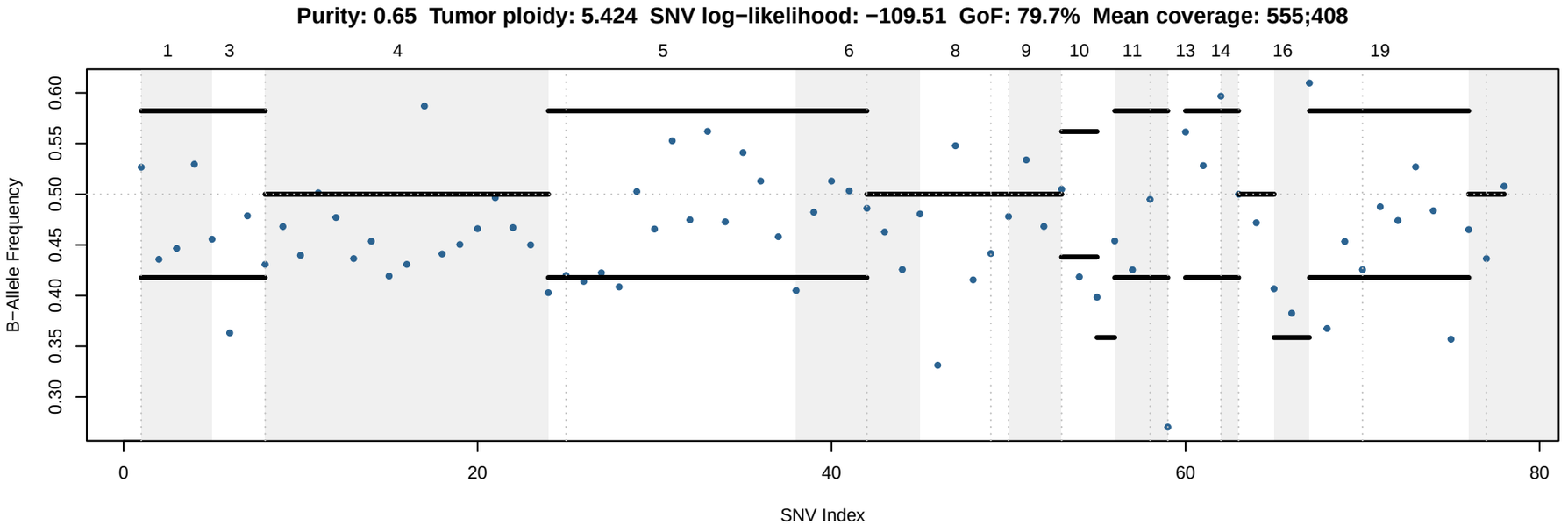

Allelic fraction (germline)
Copy Number log−ratio
1m1
3m2
5m3
2m1
4m2
5m2
3m1
1m0
4m1
5m1

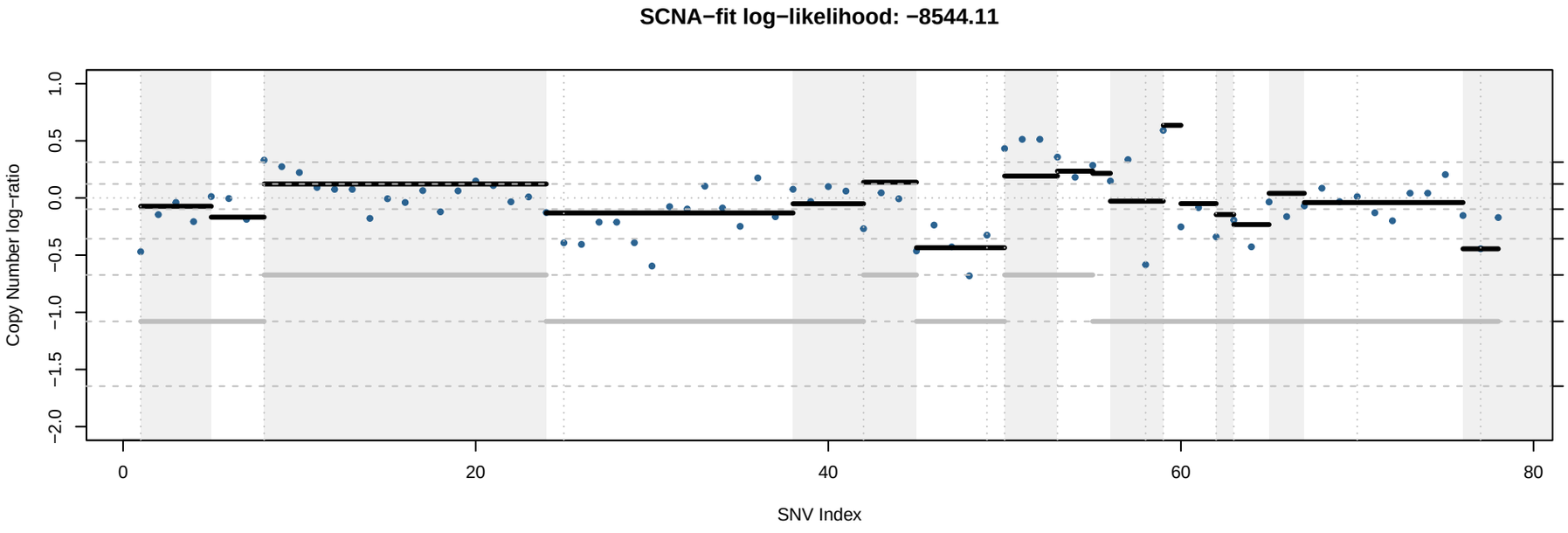

Coverage (log2)
Allelic fraction

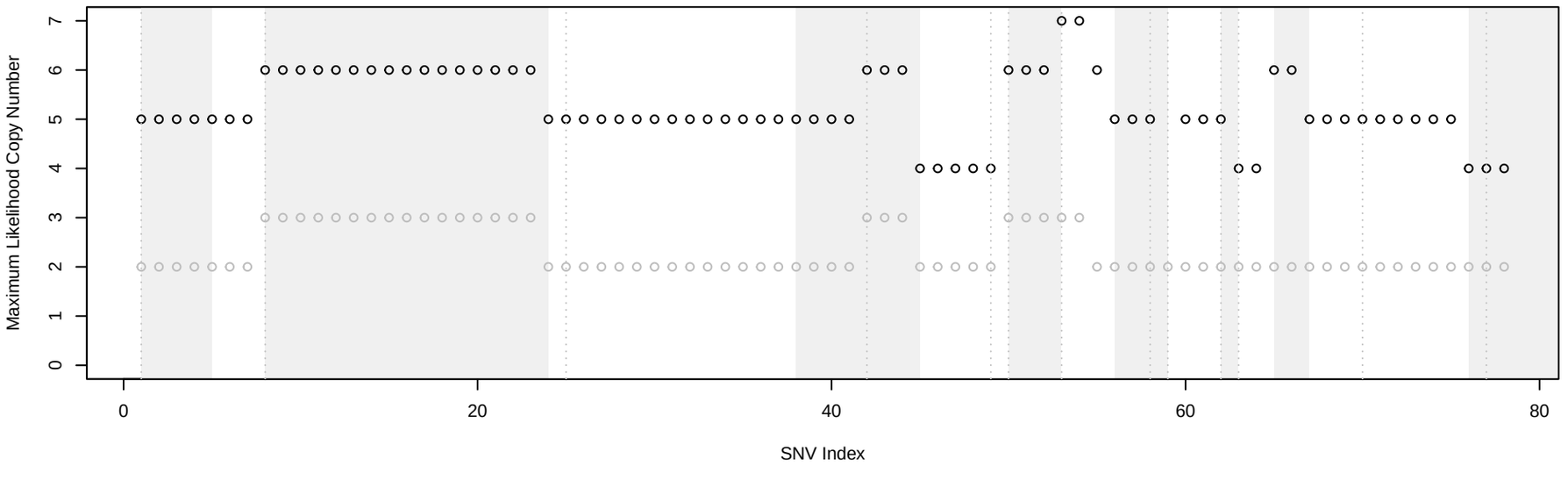

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
0m1
1m1
2m1
3m1
4m1
5m1
7m1

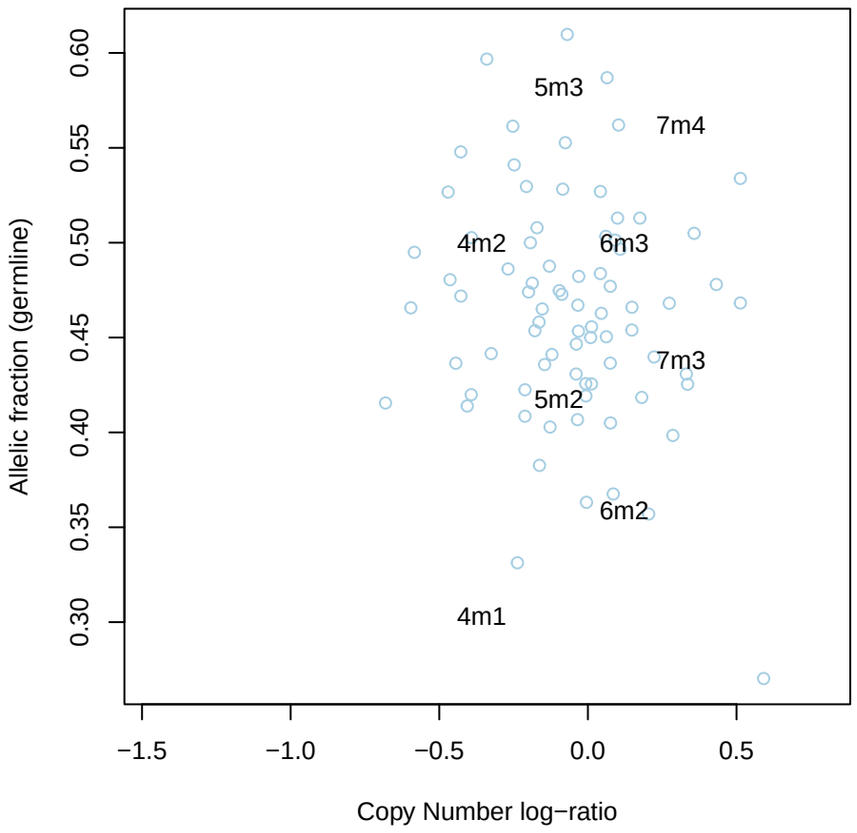

Frequency
Cellular fraction

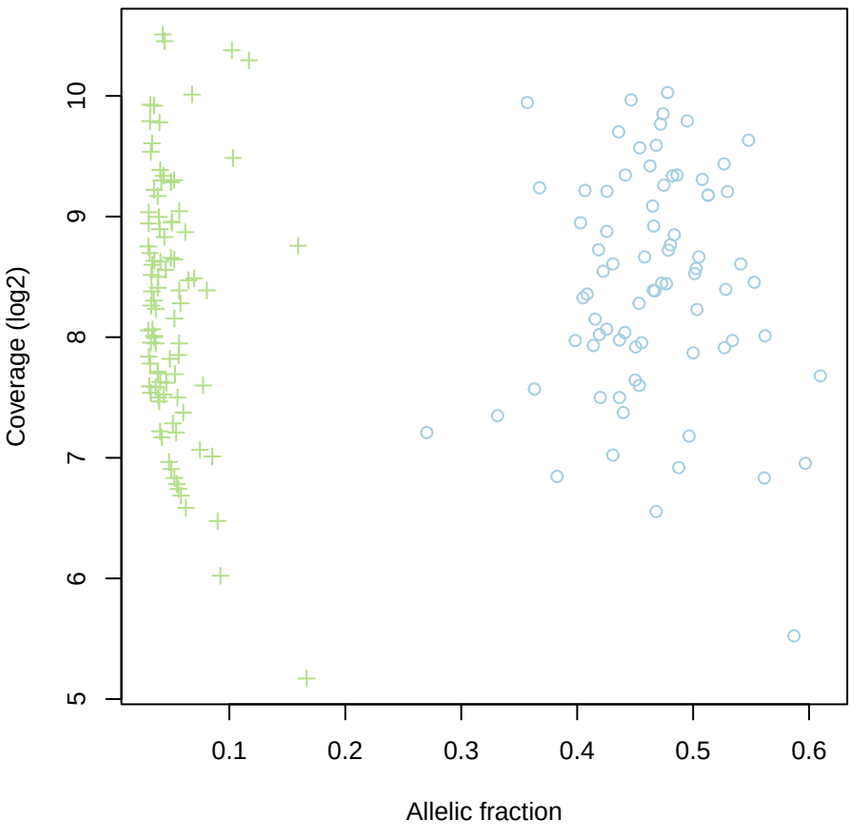

Purity: 0.65 Tumor ploidy: 5.424
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

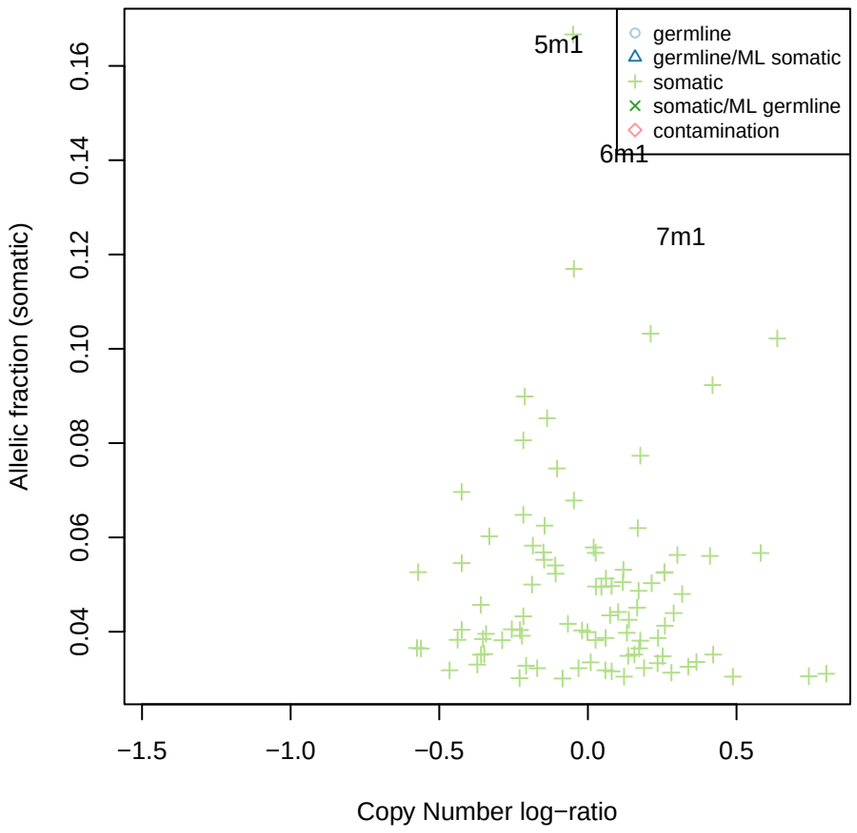

Purity: 0.65 Tumor ploidy: 5.424 SNV log−likelihood: −109.51 GoF: 79.7% Mean coverage: 555;408
1 3 4 5 6 8 9 10 11 13 14 16 19
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

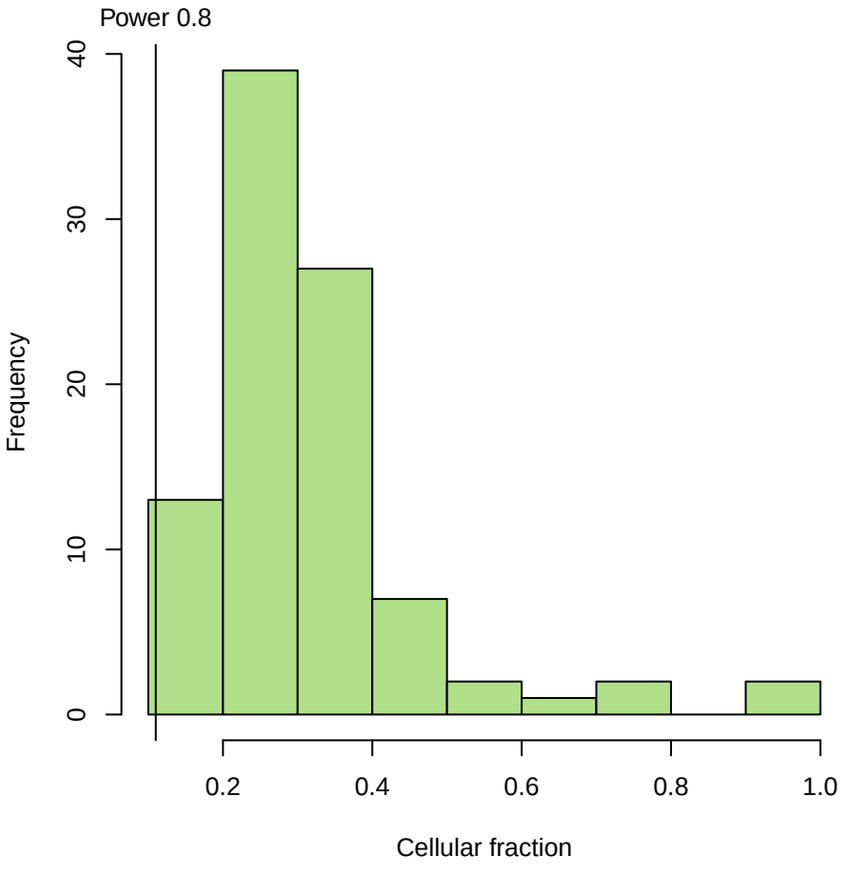

SCNA−fit log−likelihood: −8544.11
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6
0 20 40 60 80
SNV Index

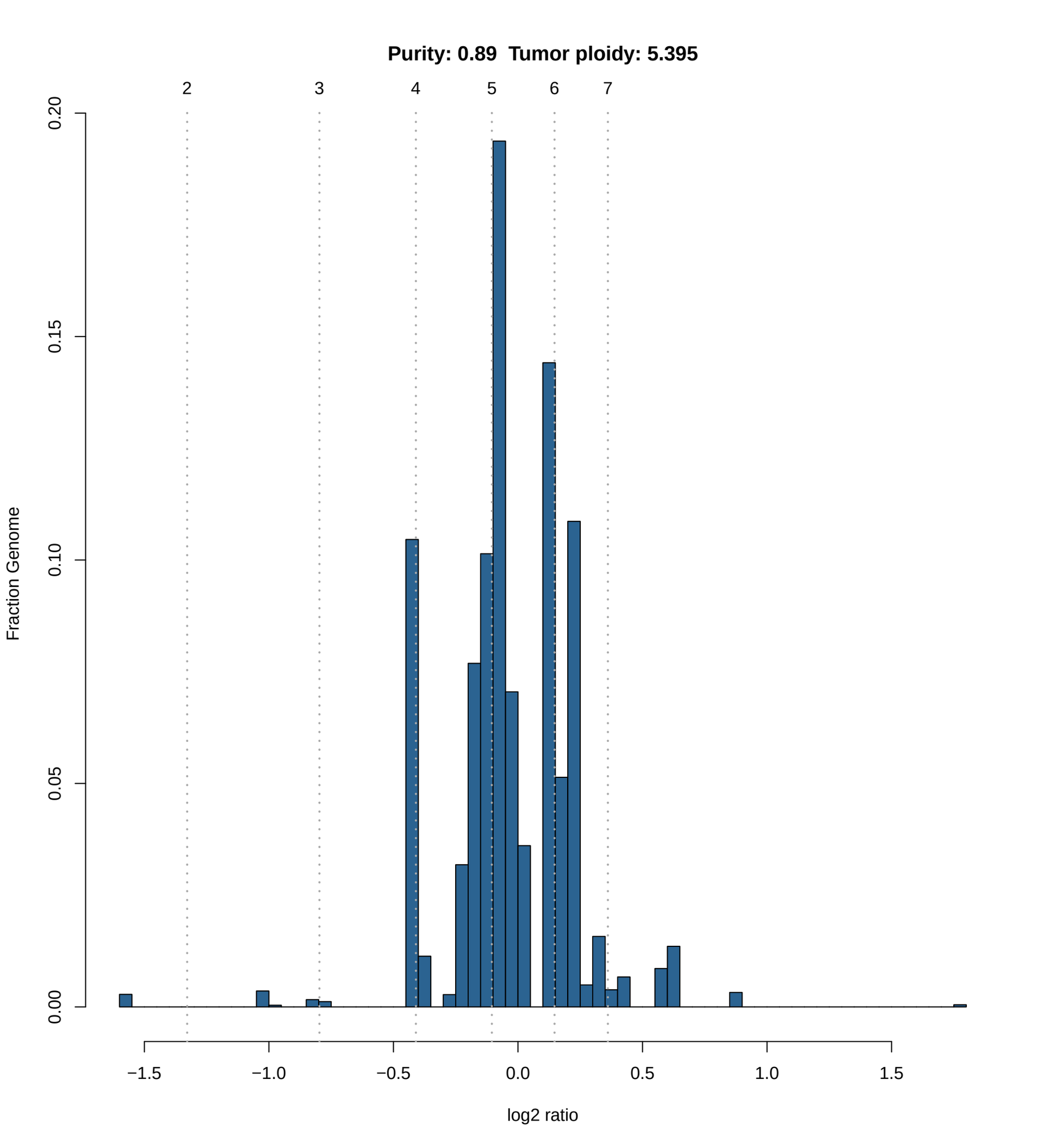

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

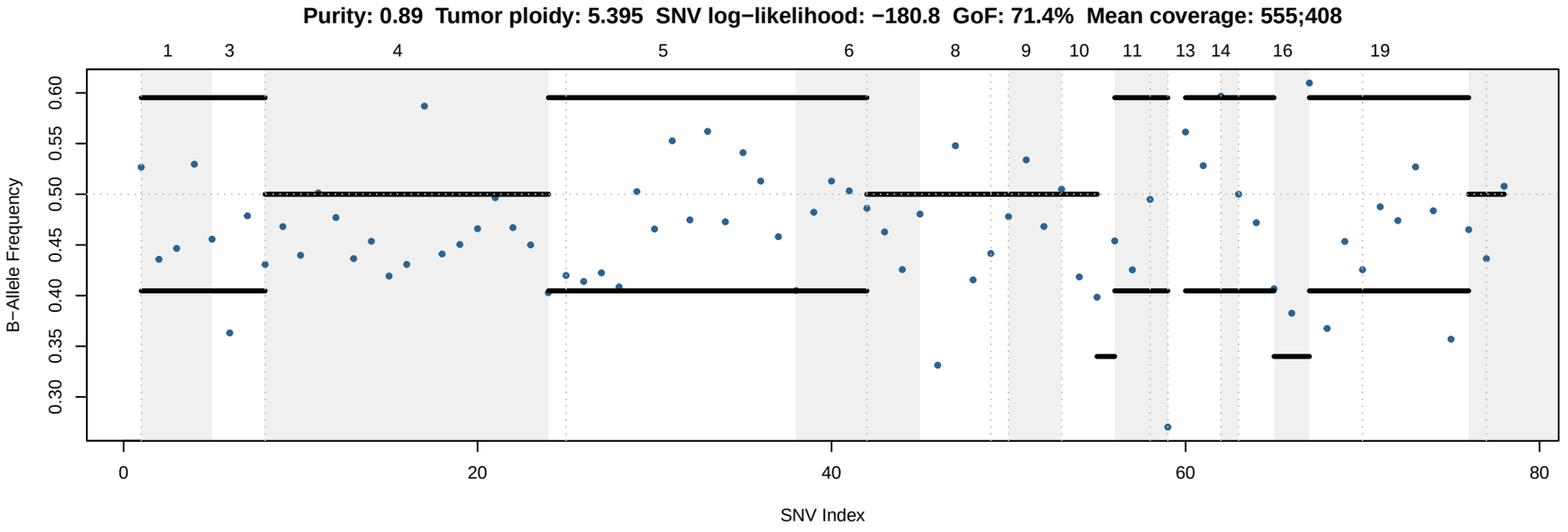

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
5m3
7m4
4m2
6m3
7m3
5m2
6m2
4m1
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

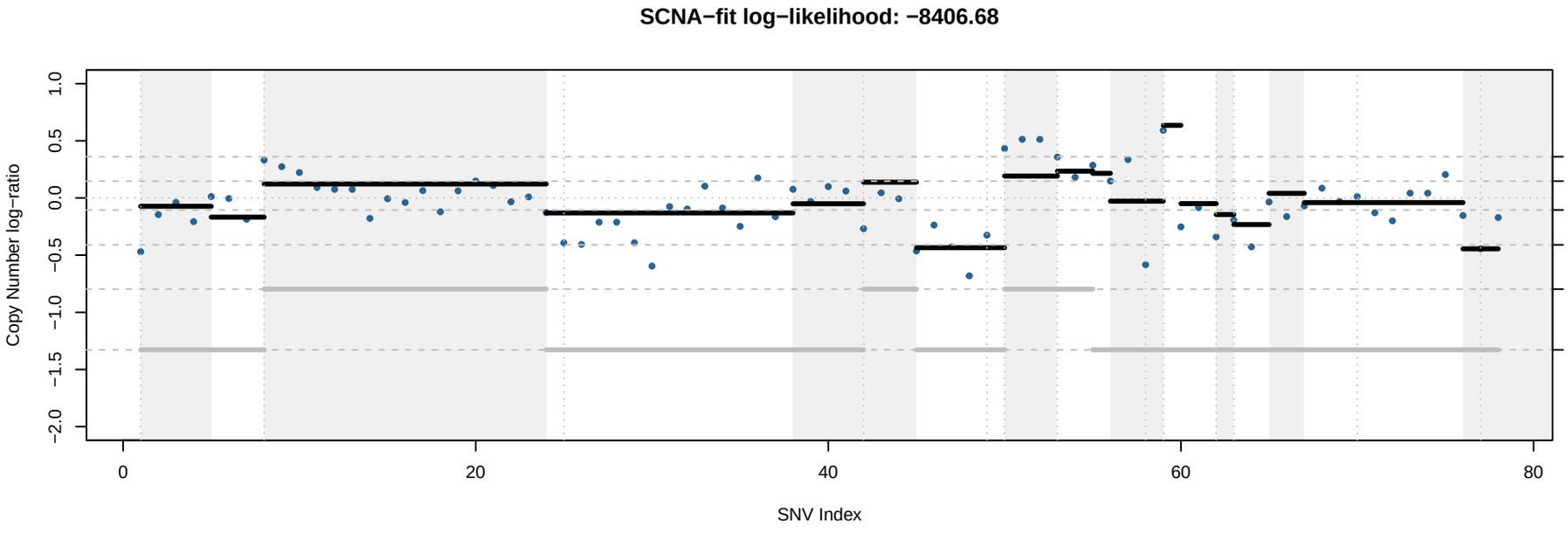

Coverage (log2)
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

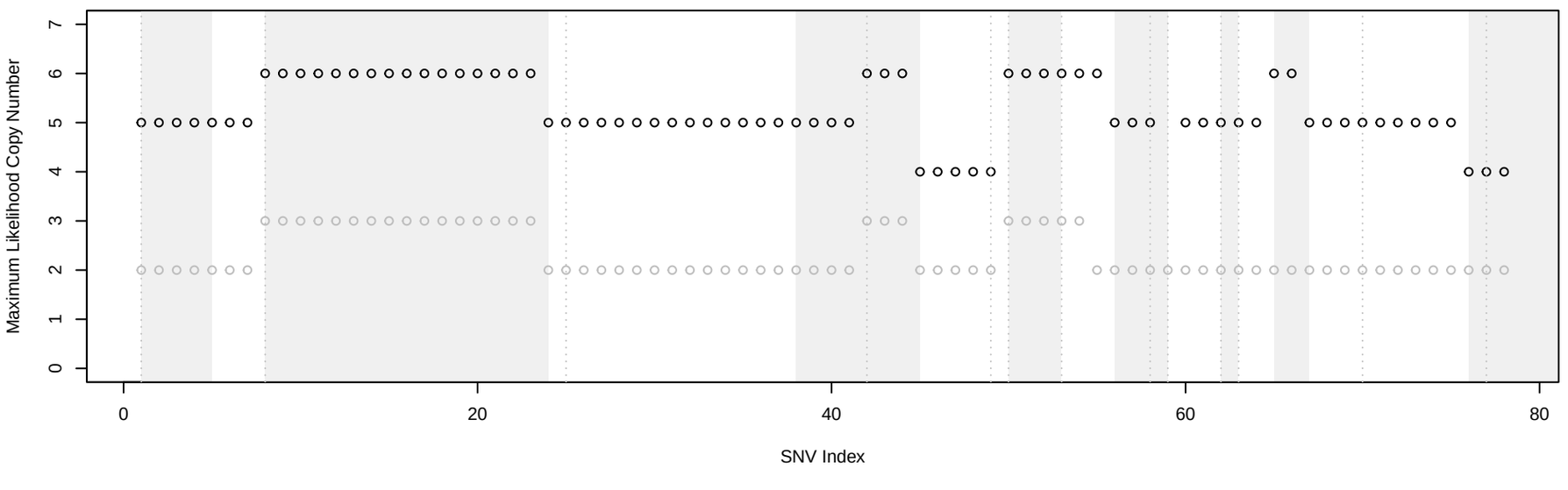

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
6m1
7m1
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

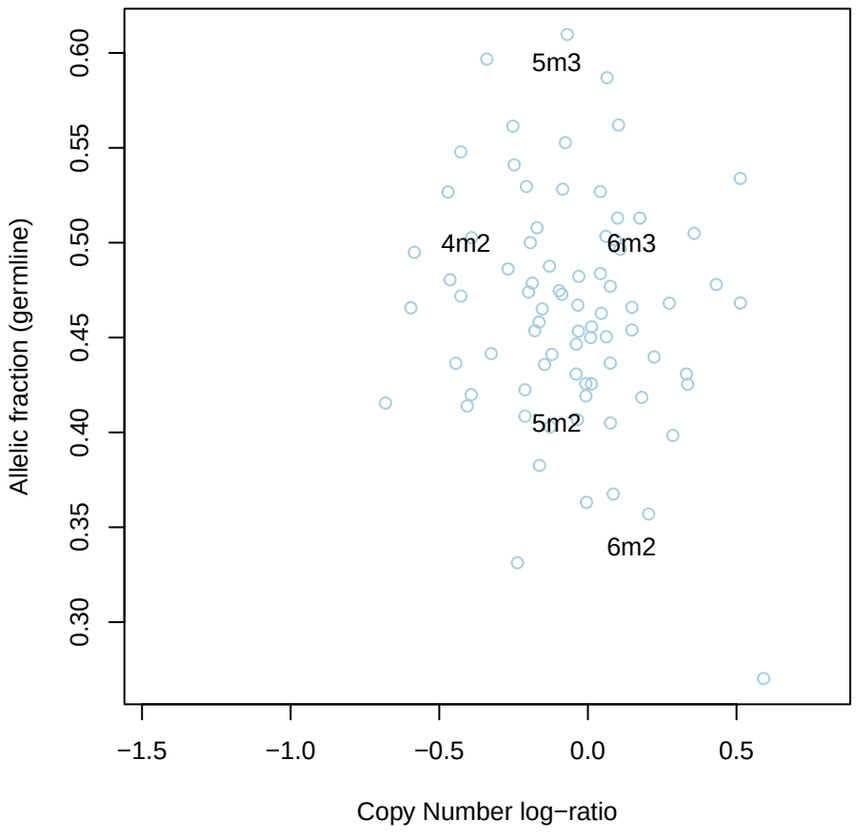

Power 0.8
Frequency
0
10
20
30
40
0.2
0.4
0.6
0.8
1.0
Cellular fraction

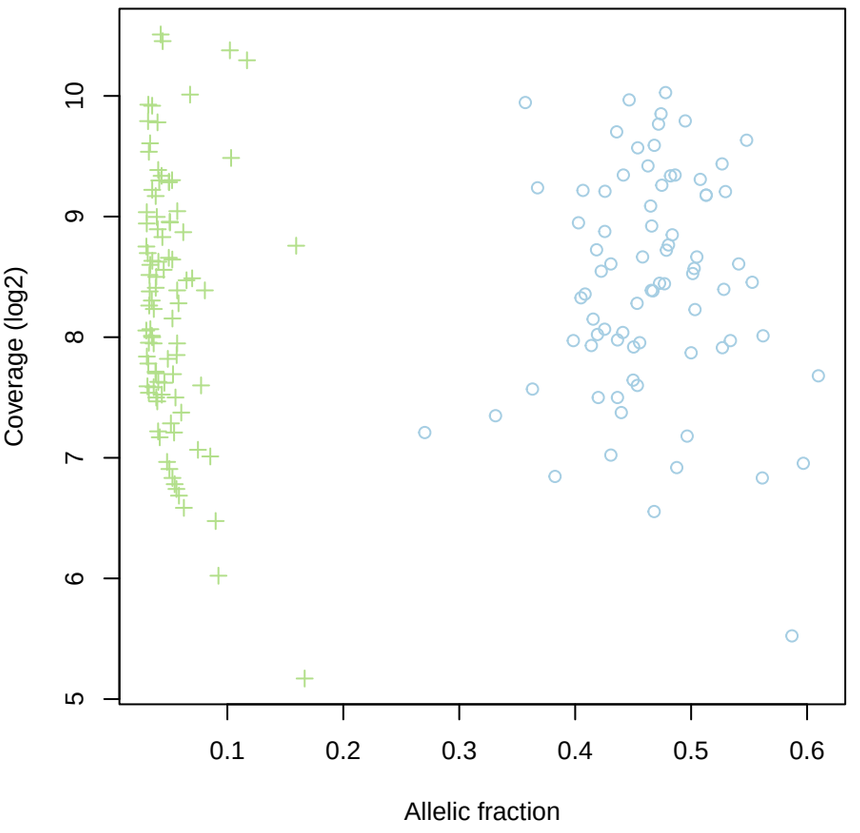

Purity: 0.89 Tumor ploidy: 5.395
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

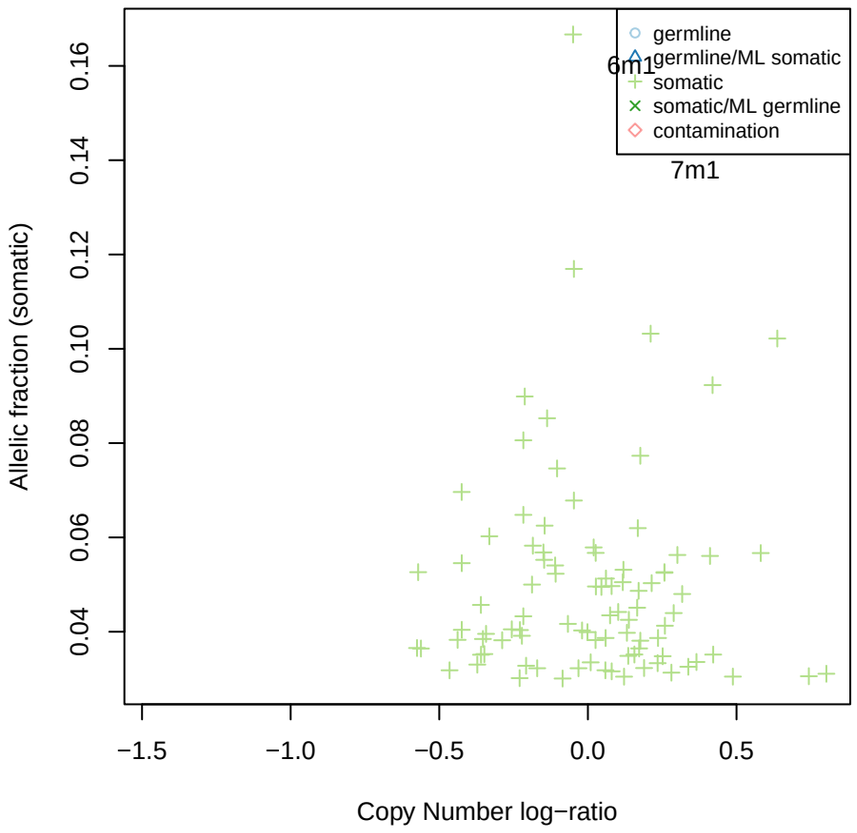

Purity: 0.89 Tumor ploidy: 5.395 SNV log−likelihood: −180.8 GoF: 71.4% Mean coverage: 555;408
1 3 4 5 6 8 9 10 11 13 14 16 19
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

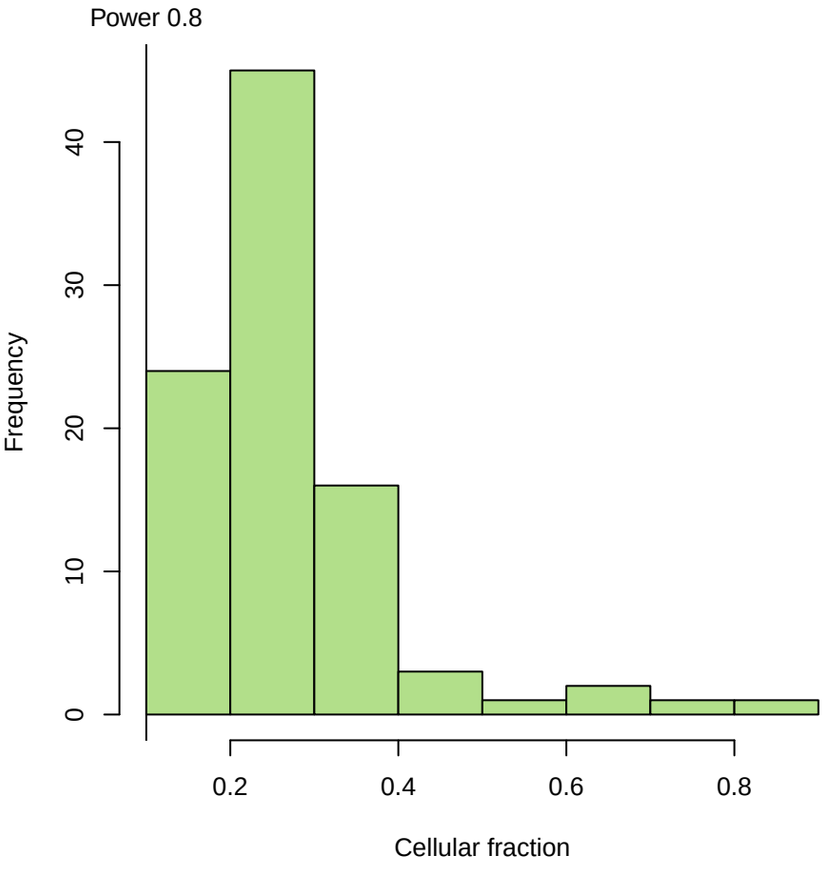

SCNA−fit log−likelihood: −8406.68
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
2 3 4 5 6
0 20 40 60 80
SNV Index

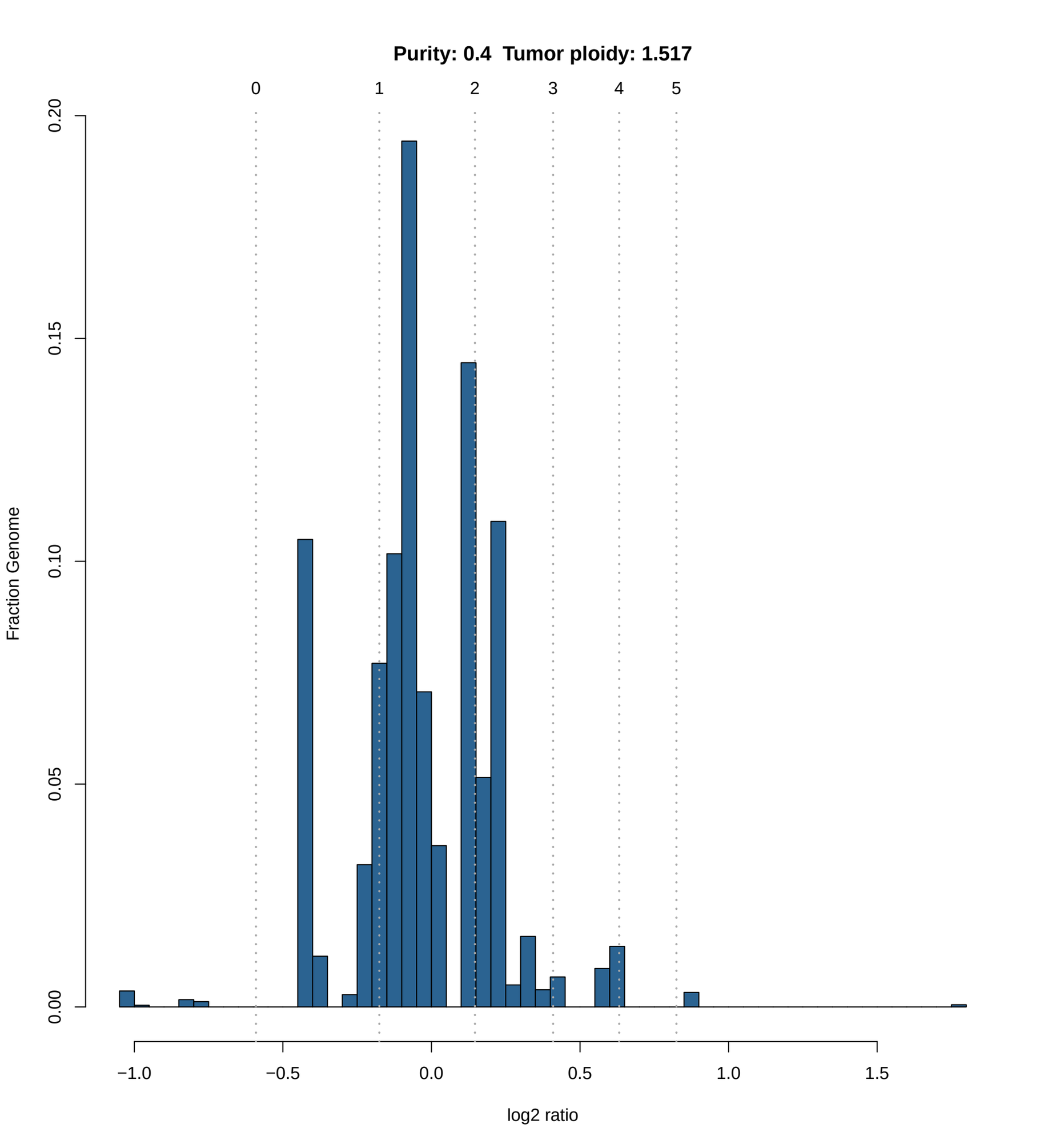

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

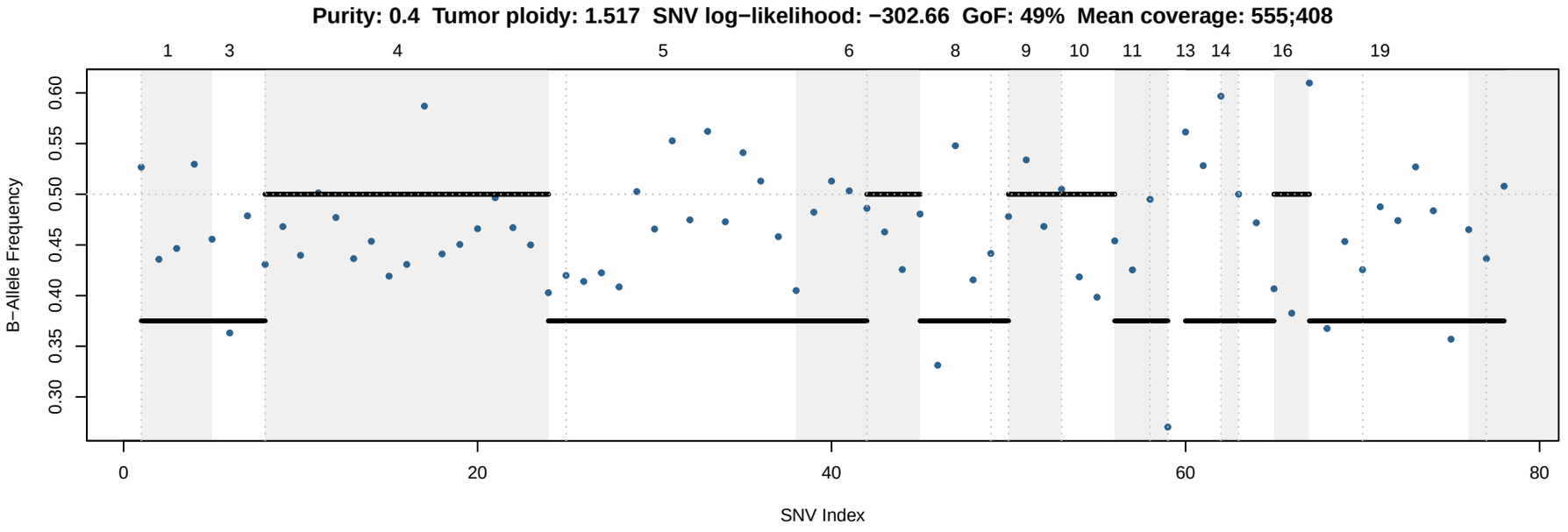

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio
5m3
4m2
6m3
5m2
6m2

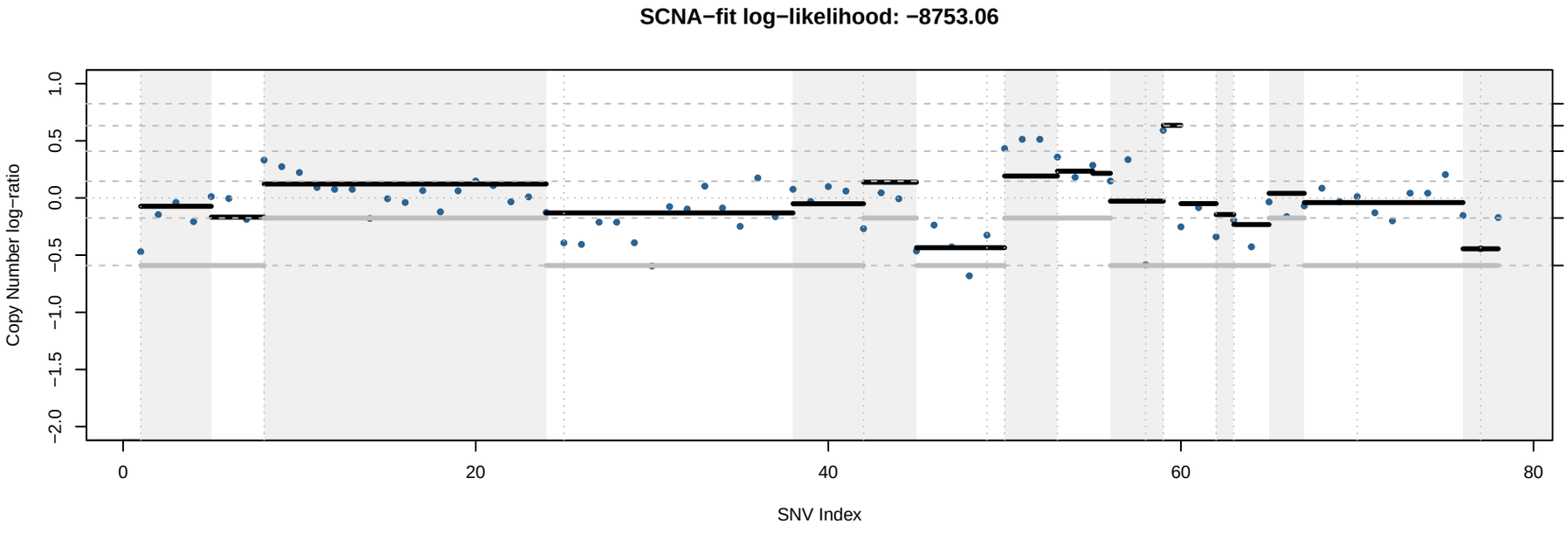

Coverage (log2)
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

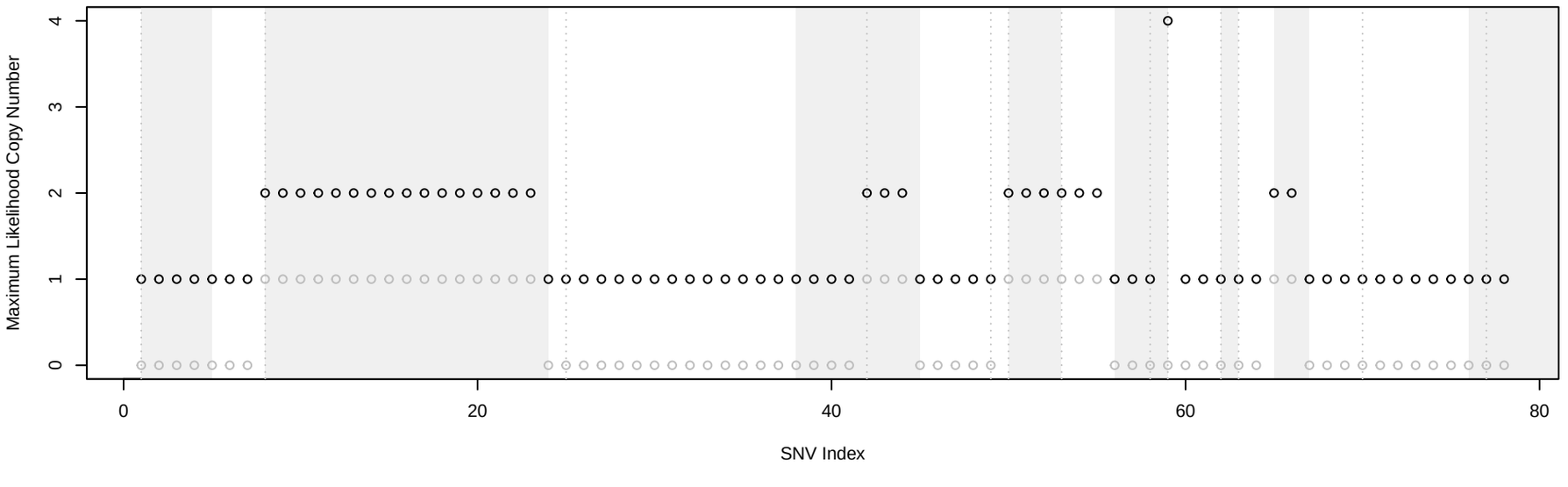

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m1
7m1

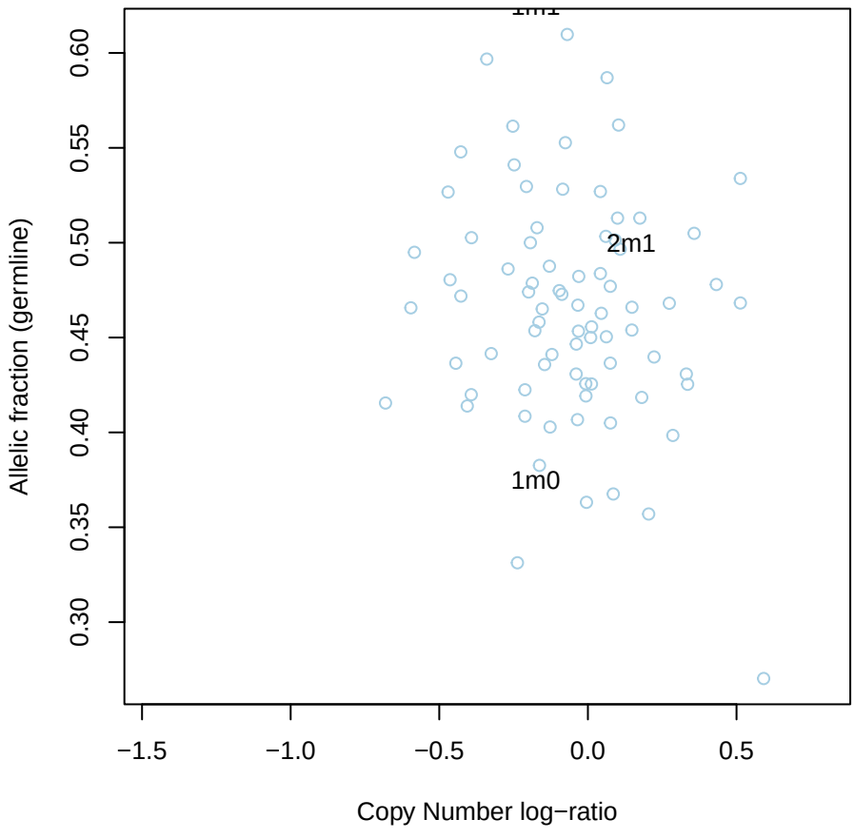

Power 0.8
Frequency
0
10
20
30
40
0.2
0.4
0.6
0.8
Cellular fraction

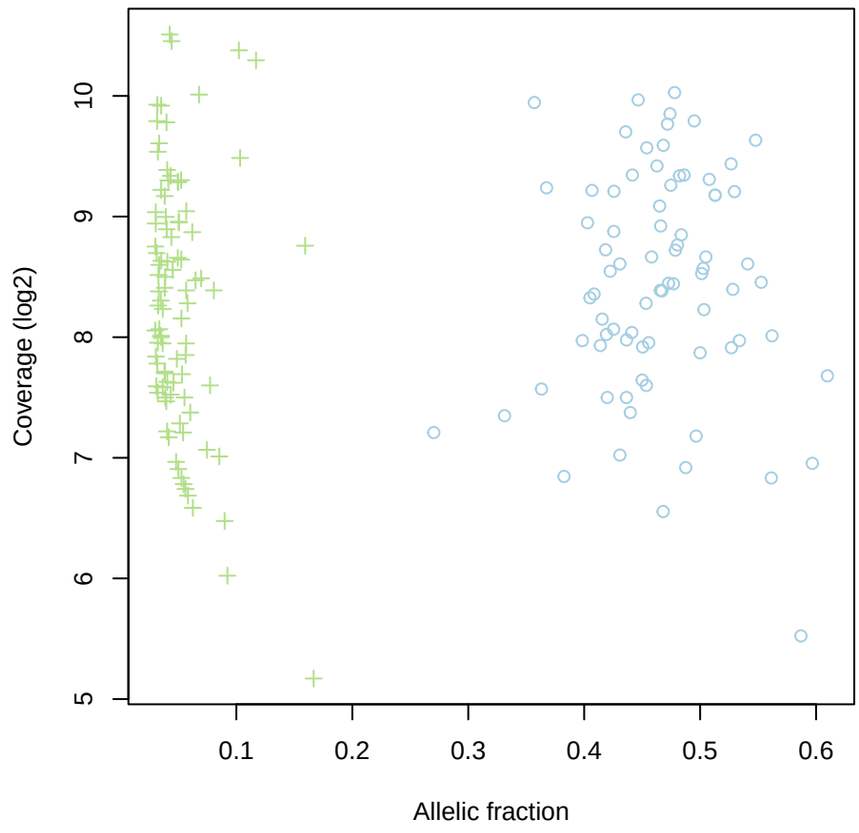

Purity: 0.4 Tumor ploidy: 1.517
0
1
2
3
4
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

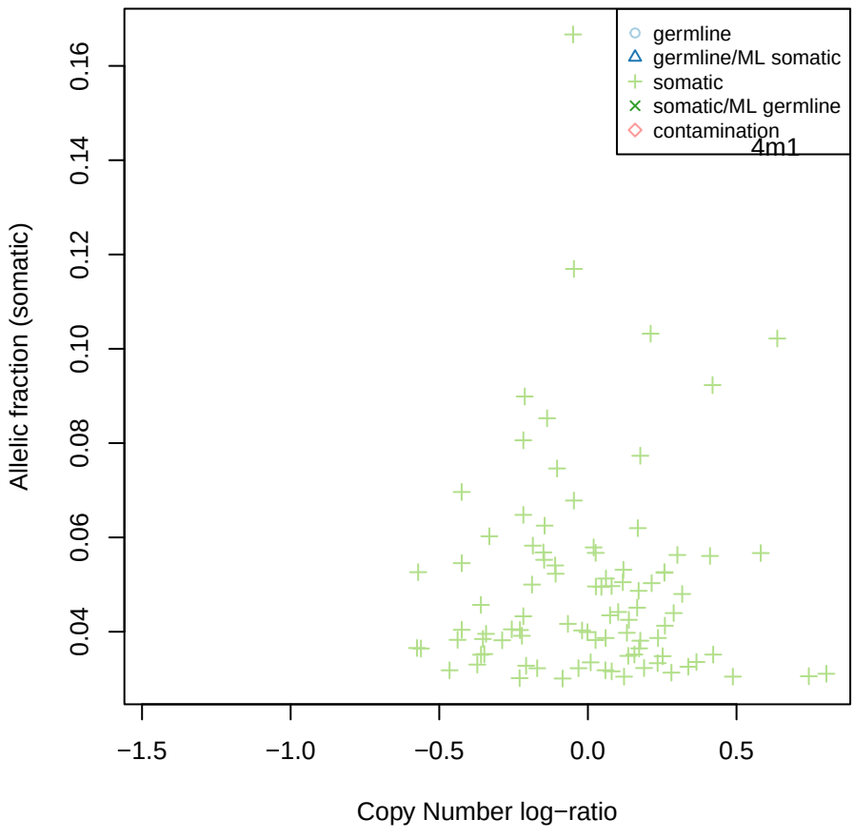

Purity: 0.4 Tumor ploidy: 1.517 SNV log−likelihood: −302.66 GoF: 49% Mean coverage: 555;408
1 3 4 5 6 8 9 10 11 13 14 16 19
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

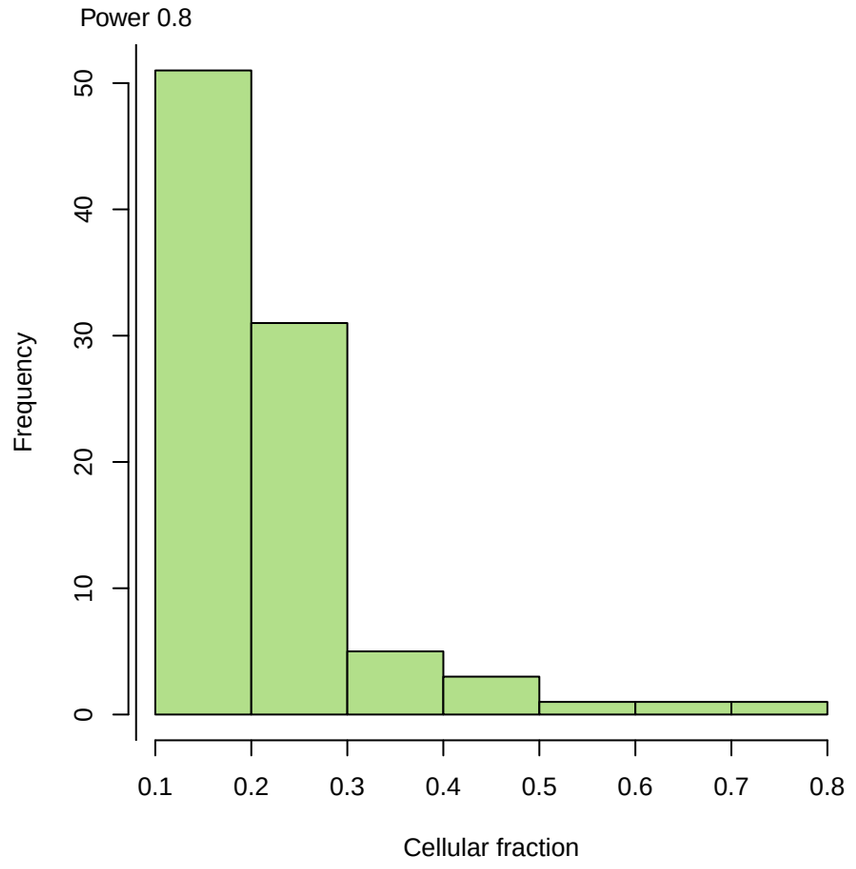

SCNA−fit log−likelihood: −8753.06
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4
0 20 40 60 80
SNV Index

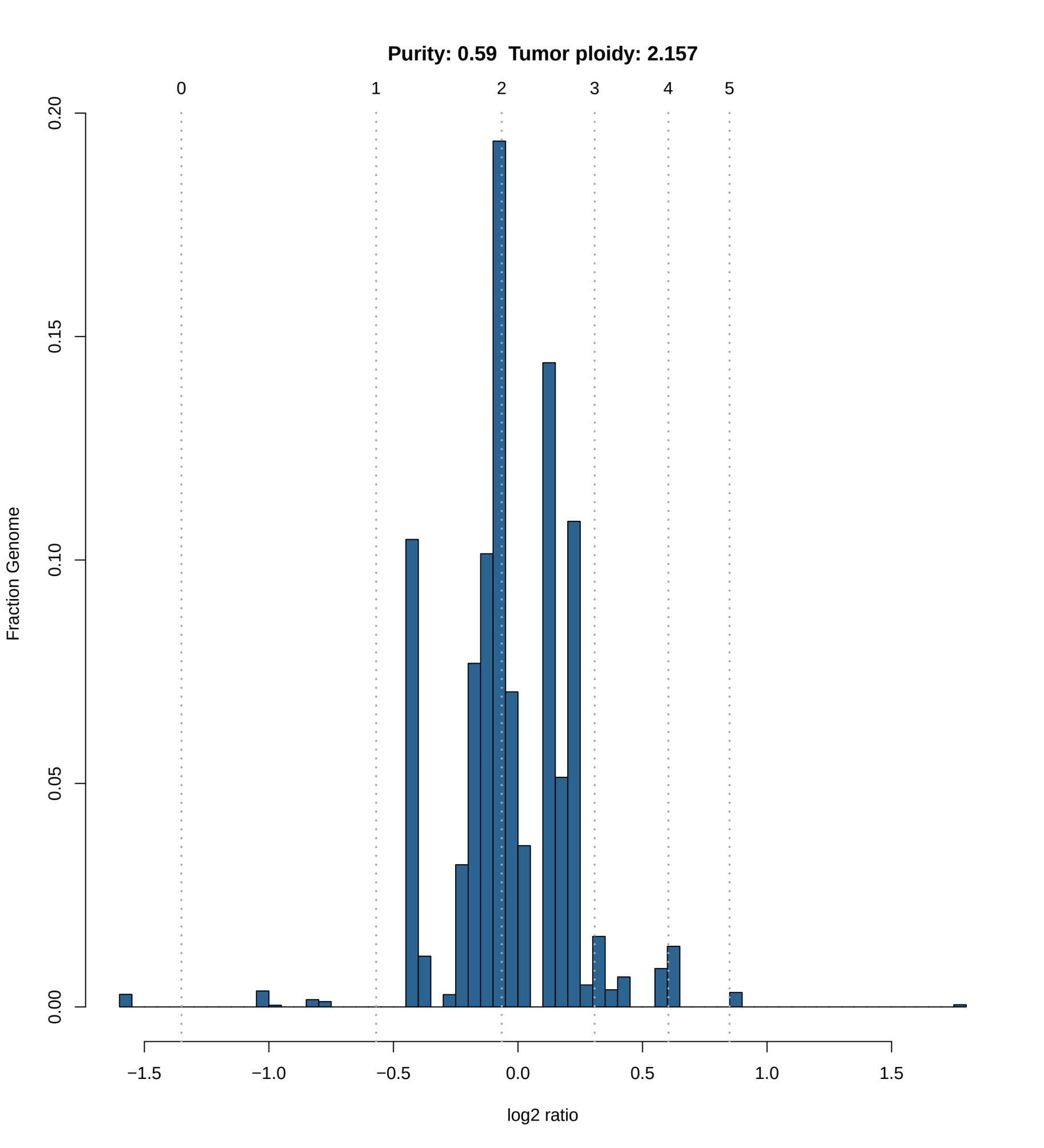

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80
SNV Index

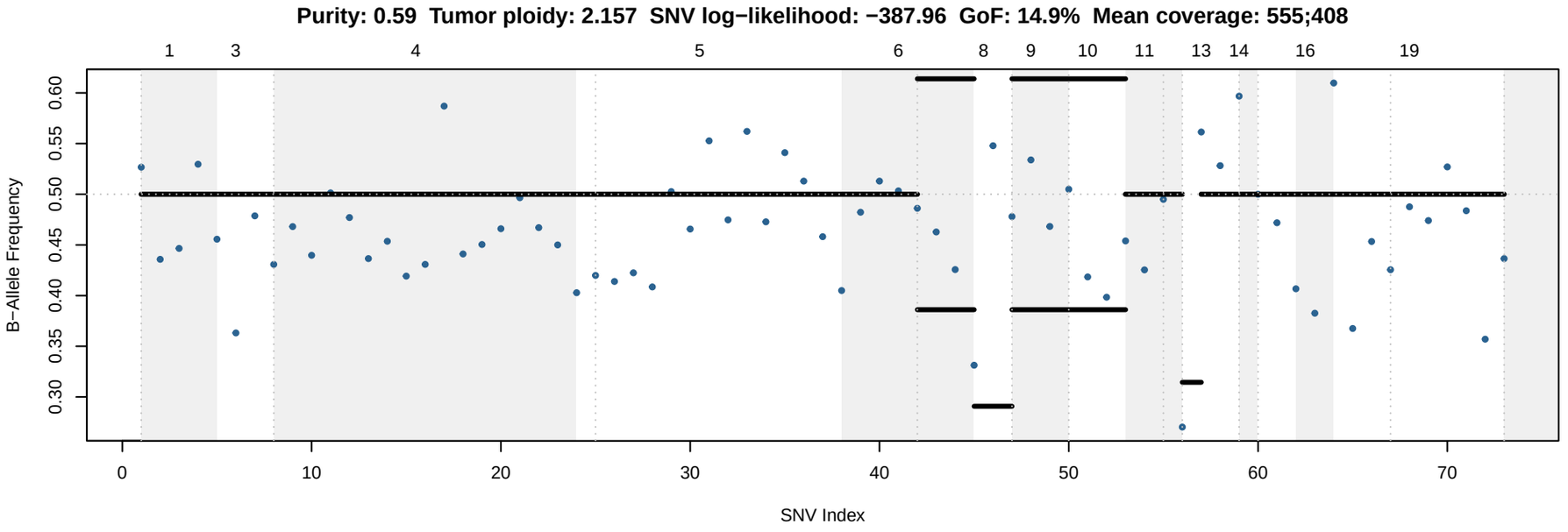

1m1
2m1
1m0
Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

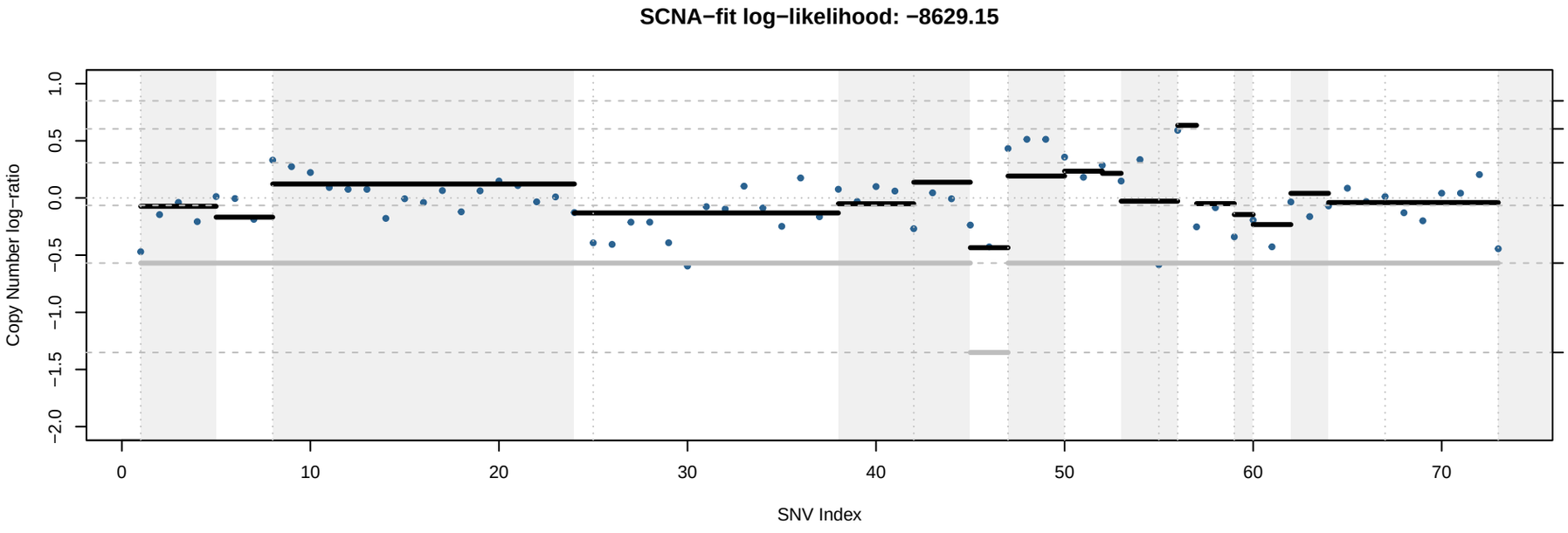

Coverage (log2)
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

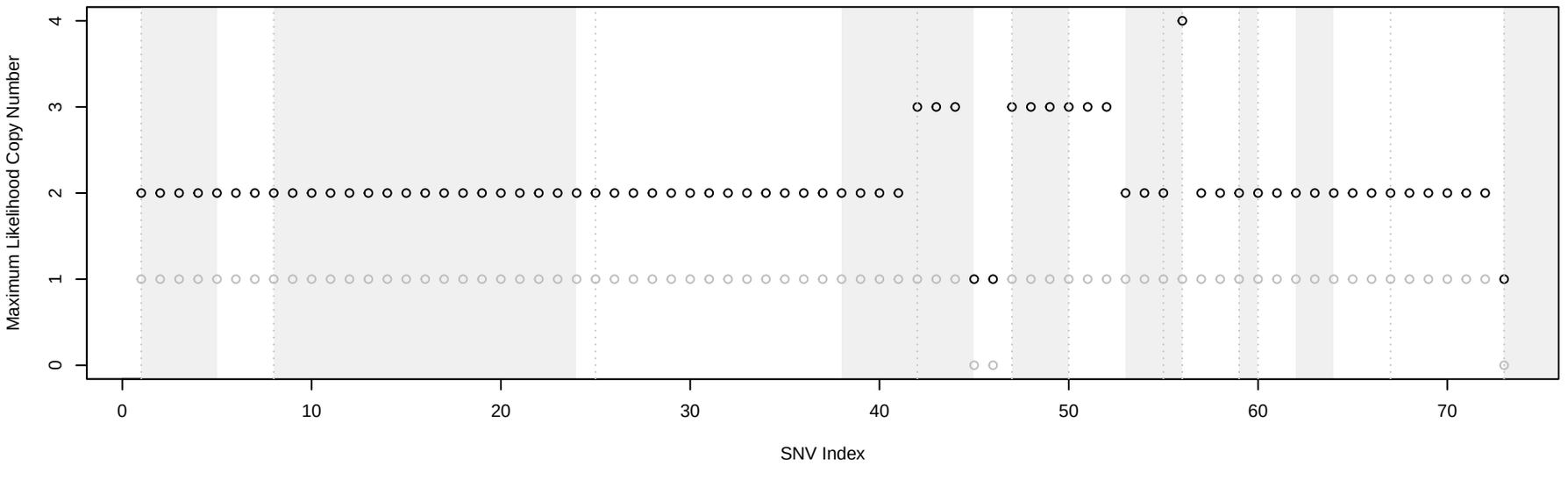

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

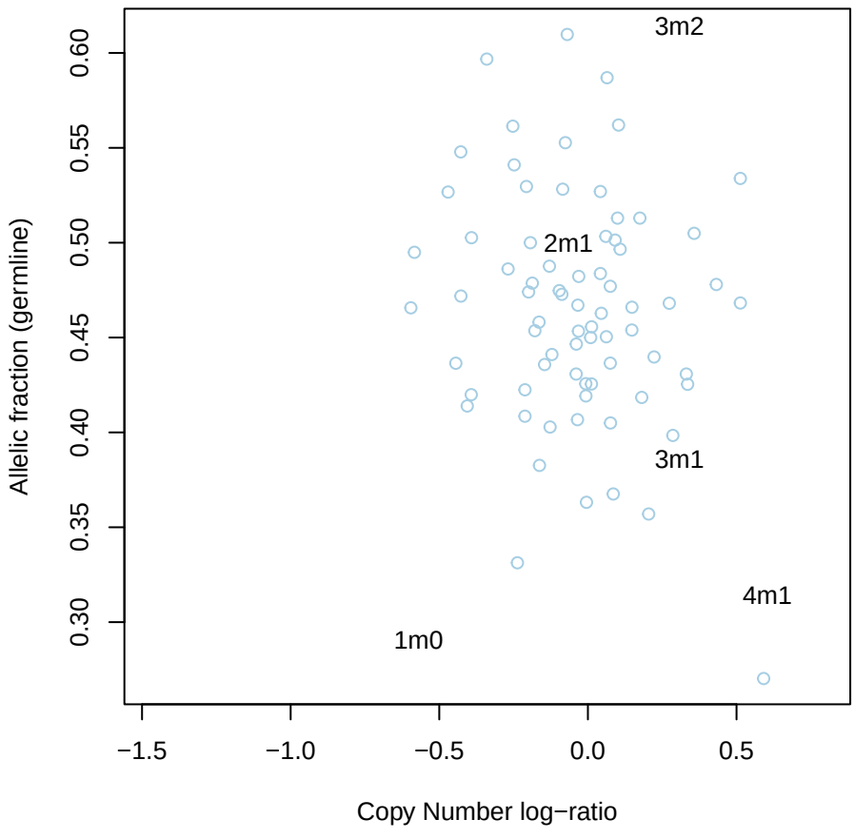

Power 0.8
Frequency
0
10
20
30
40
50
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
Cellular fraction

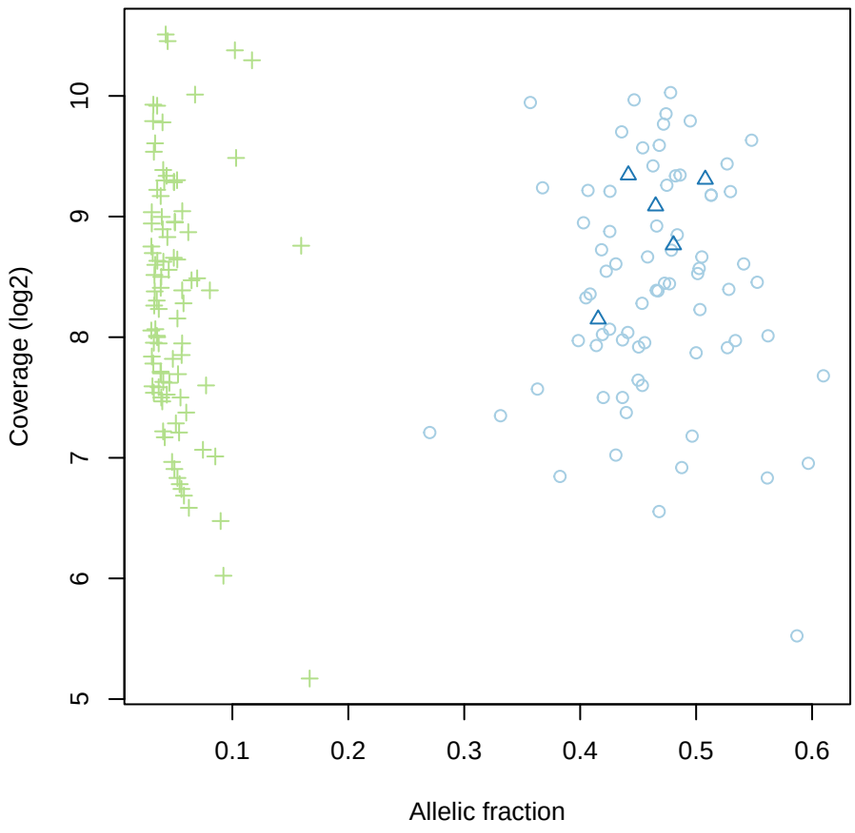

Purity: 0.59 Tumor ploidy: 2.157
0
1
2
3
4
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

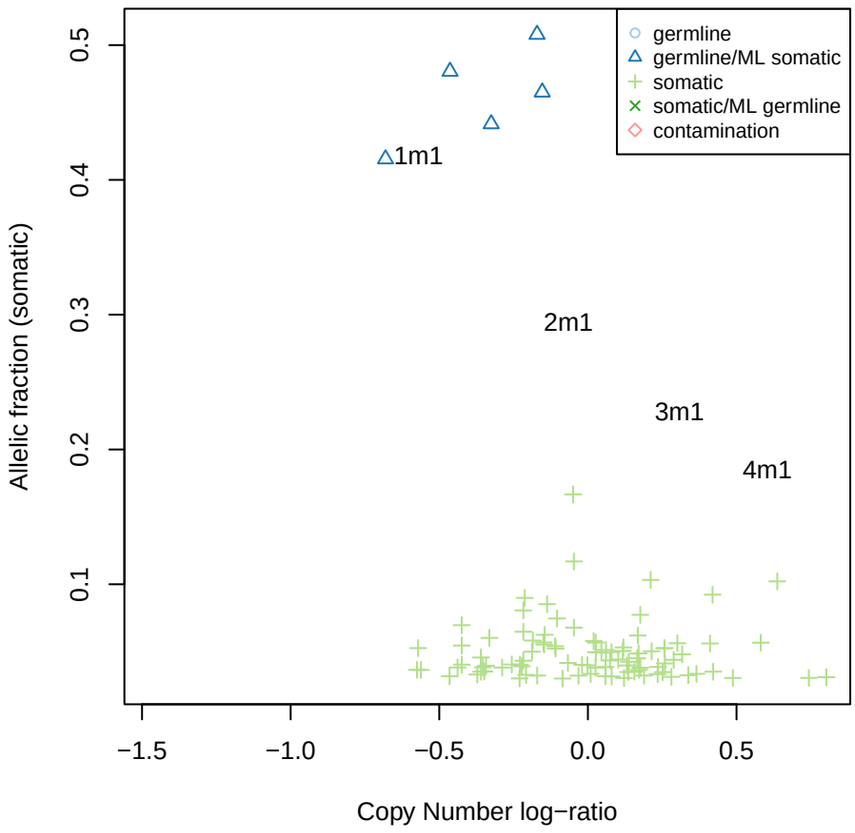

Purity: 0.59 Tumor ploidy: 2.157 SNV log−likelihood: −387.96 GoF: 14.9% Mean coverage: 555;408
1 3 4 5 6 8 9 10 11 13 14 16 19
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 10 20 30 40 50 60 70
SNV Index

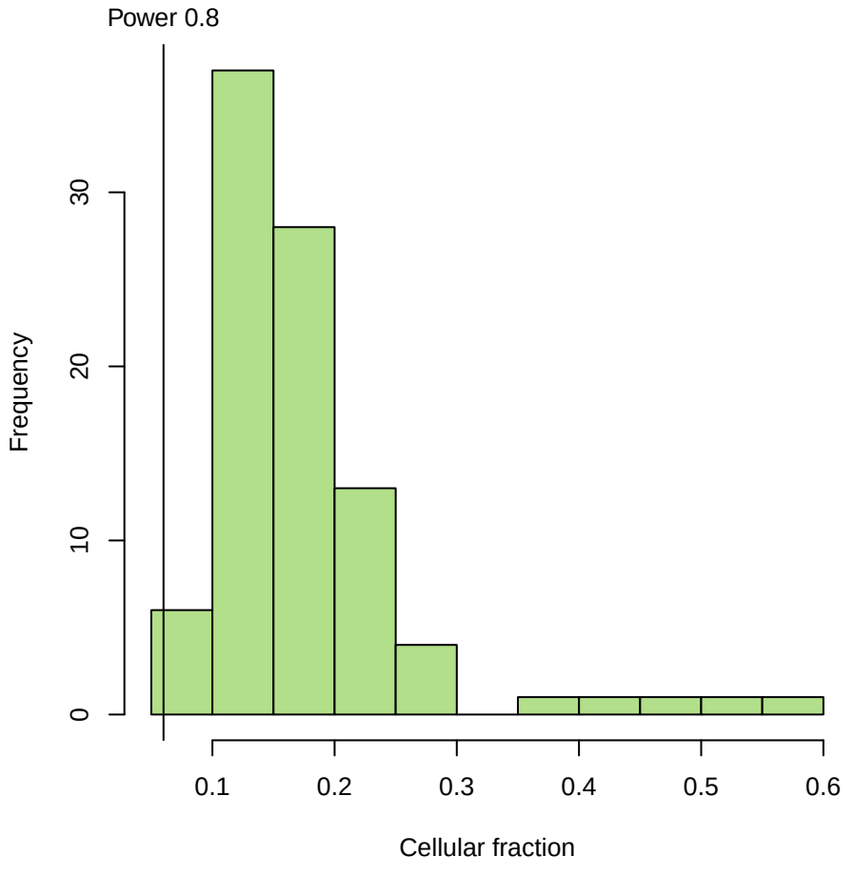

SCNA−fit log−likelihood: −8629.15
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5
0 10 20 30 40 50 60 70
SNV Index


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


3m2
2m1
3m1
4m1
1m0
Allelic fraction (germline)
Copy Number log−ratio
0.30
0.35
0.40
0.45
0.50
0.55
0.60
−1.5
−1.0
−0.5
0.0
0.5


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


germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
4m1
Allelic fraction (somatic)
Copy Number log−ratio
0.1
0.2
0.3
0.4
0.5
−1.5
−1.0
−0.5
0.0
0.5


Power 0.8
Frequency
Cellular fraction
0
10
20
30
0.1
0.2
0.3
0.4
0.5
0.6