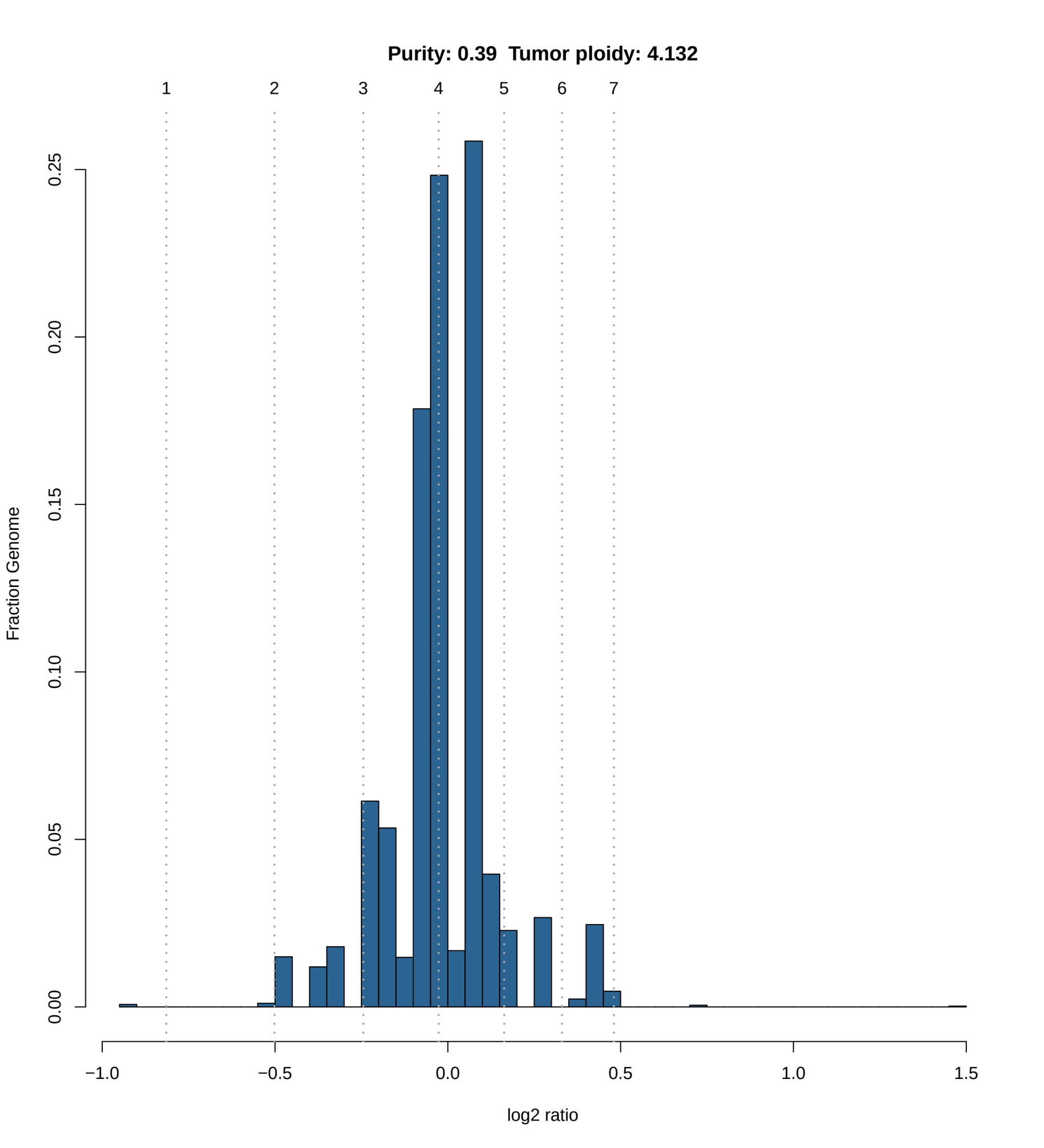
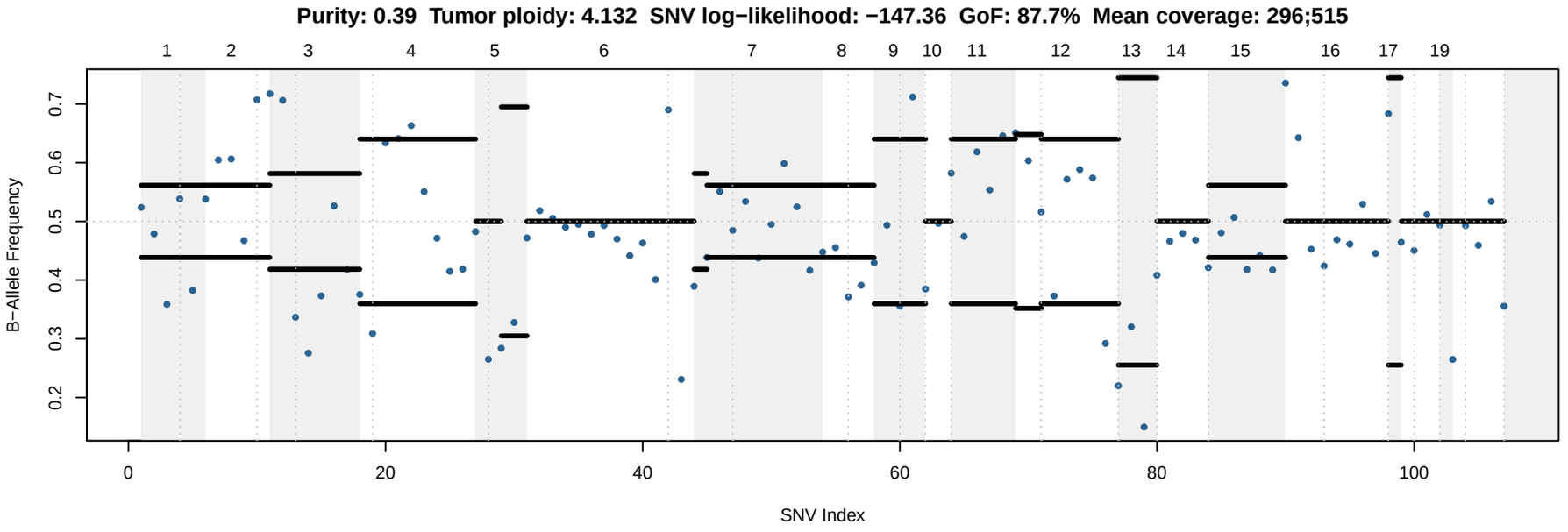
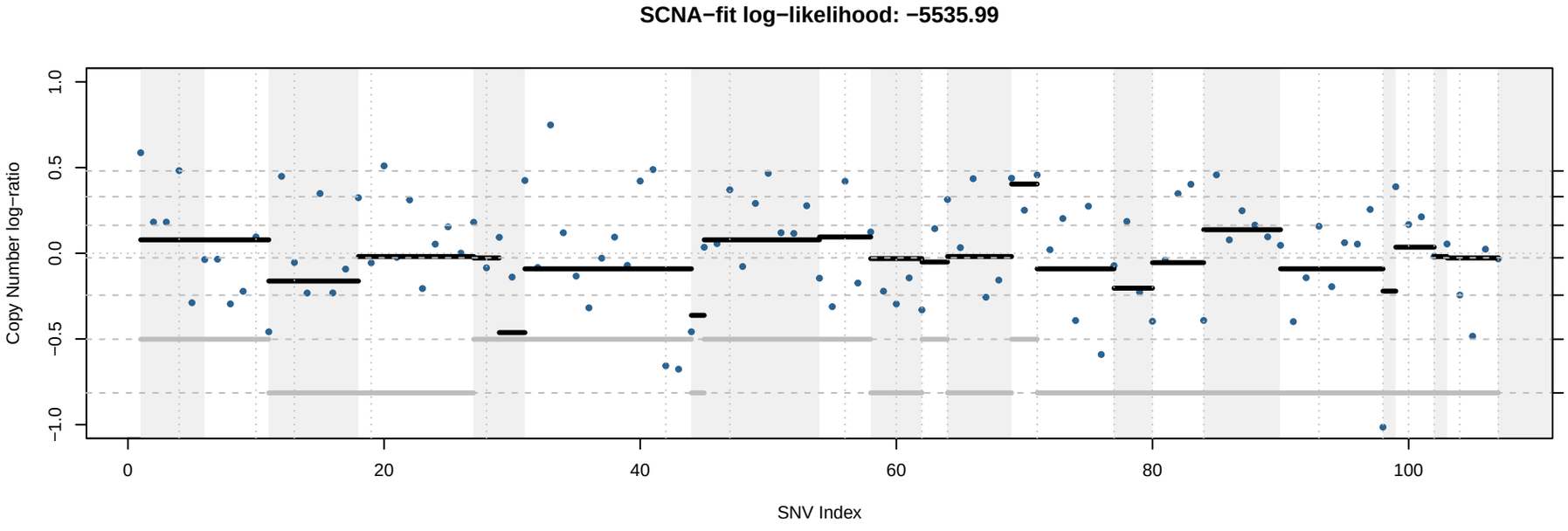
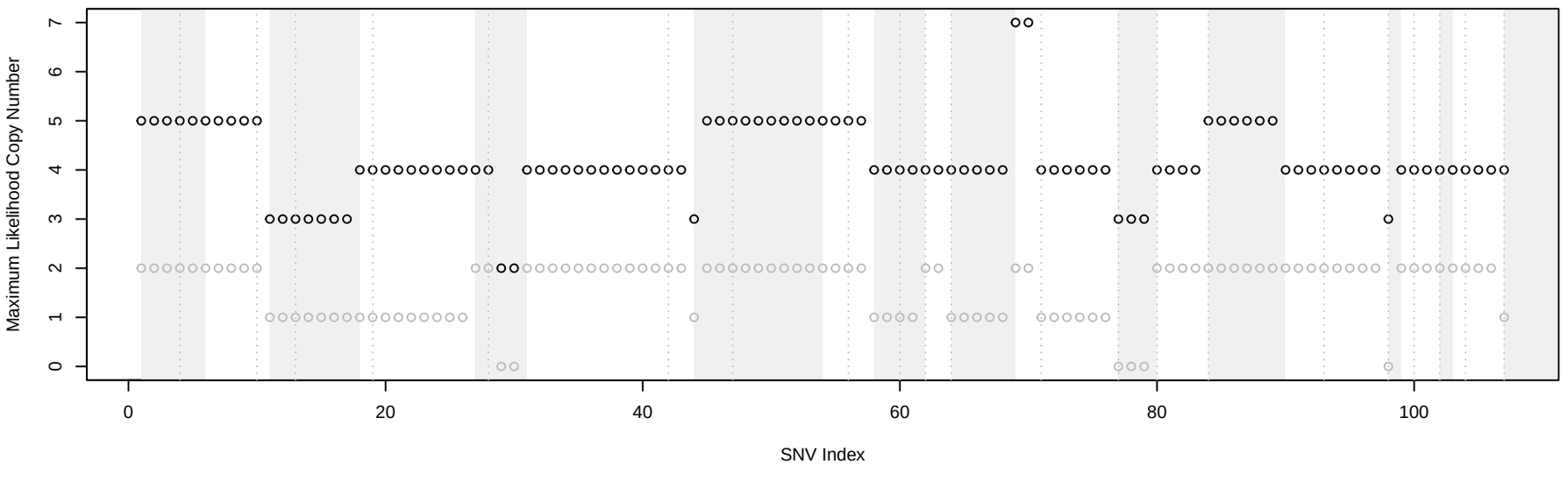
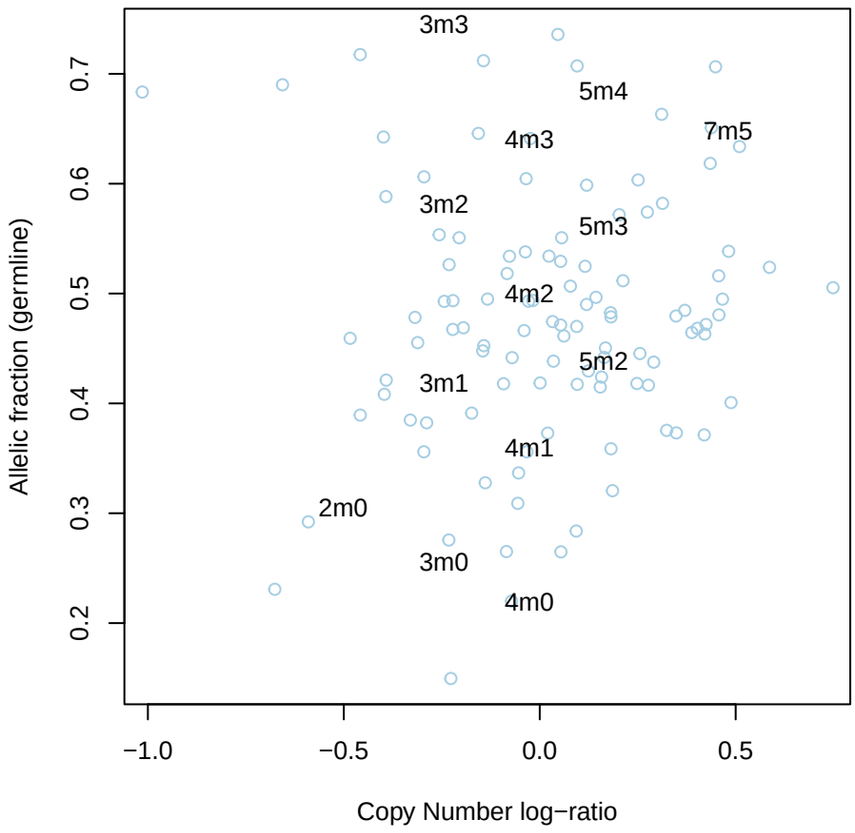
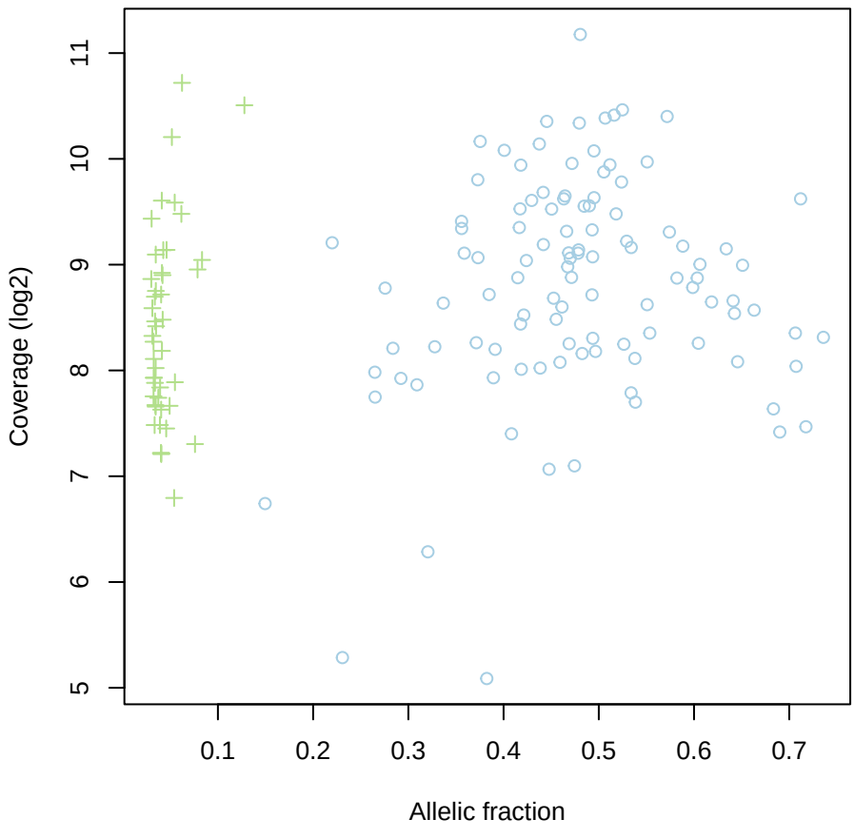

Purity: 0.39 Tumor ploidy: 4.132
1
2
3
4
5
6
7
0.00
0.05
0.10
0.15
0.20
0.25
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

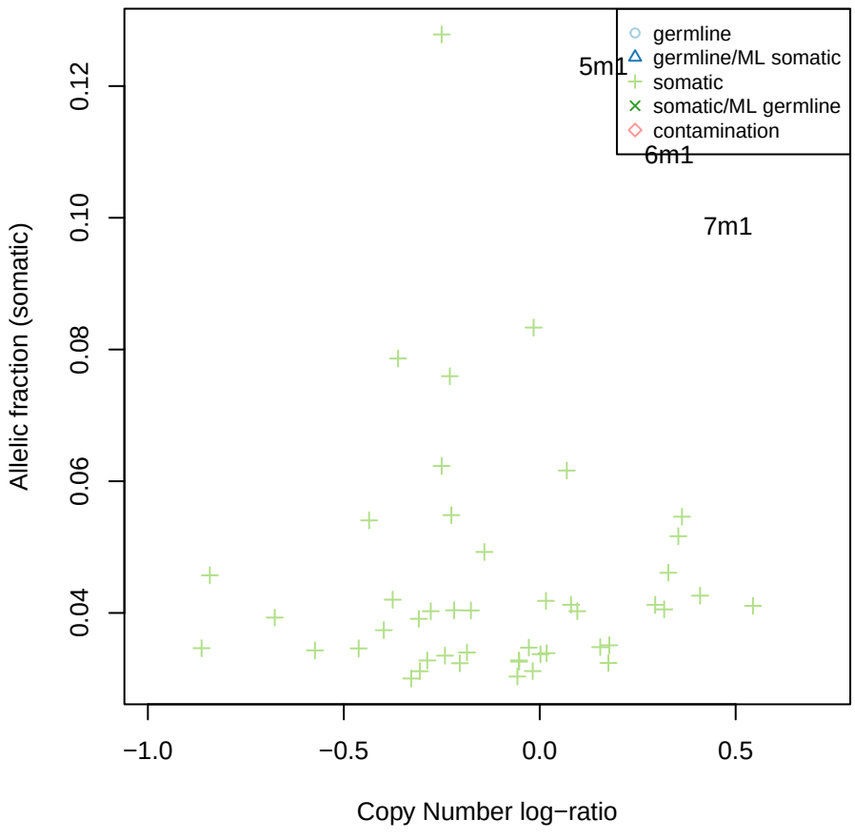

Purity: 0.39 Tumor ploidy: 4.132 SNV log−likelihood: −147.36 GoF: 87.7% Mean coverage: 296;515
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

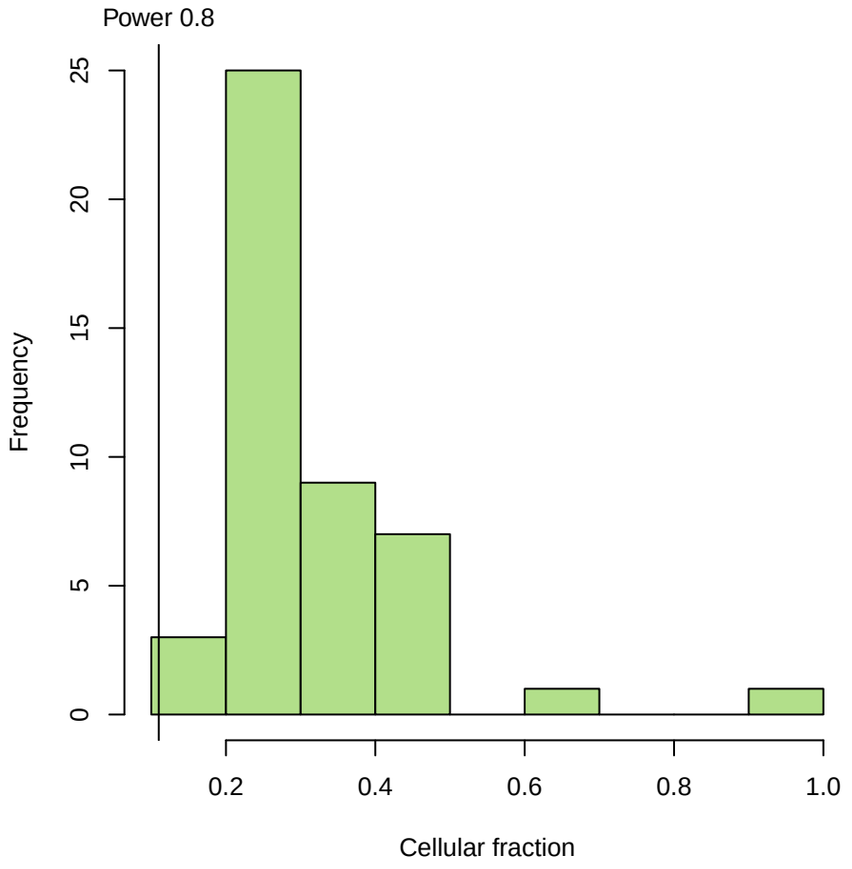

SCNA−fit log−likelihood: −5535.99
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

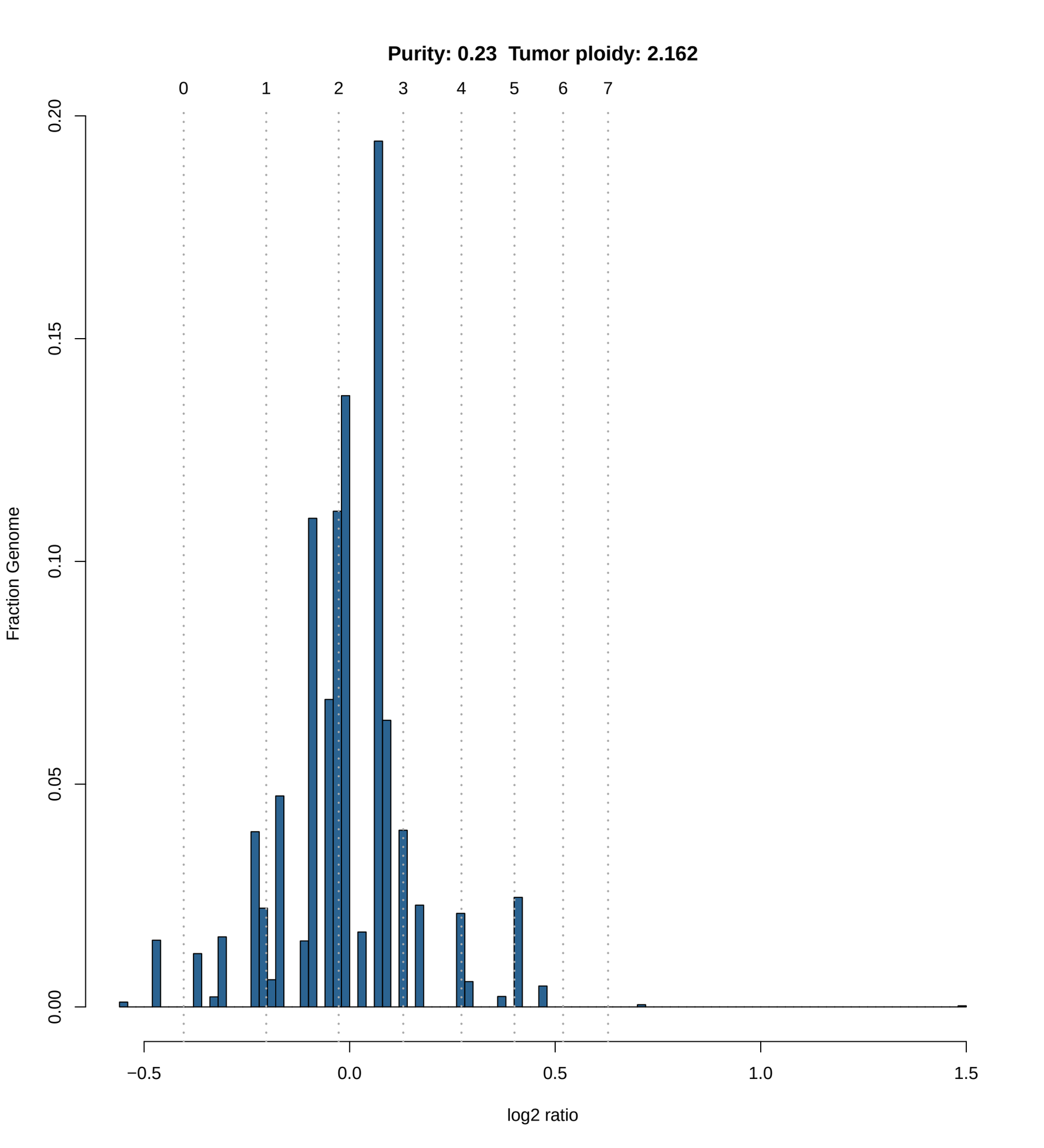

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

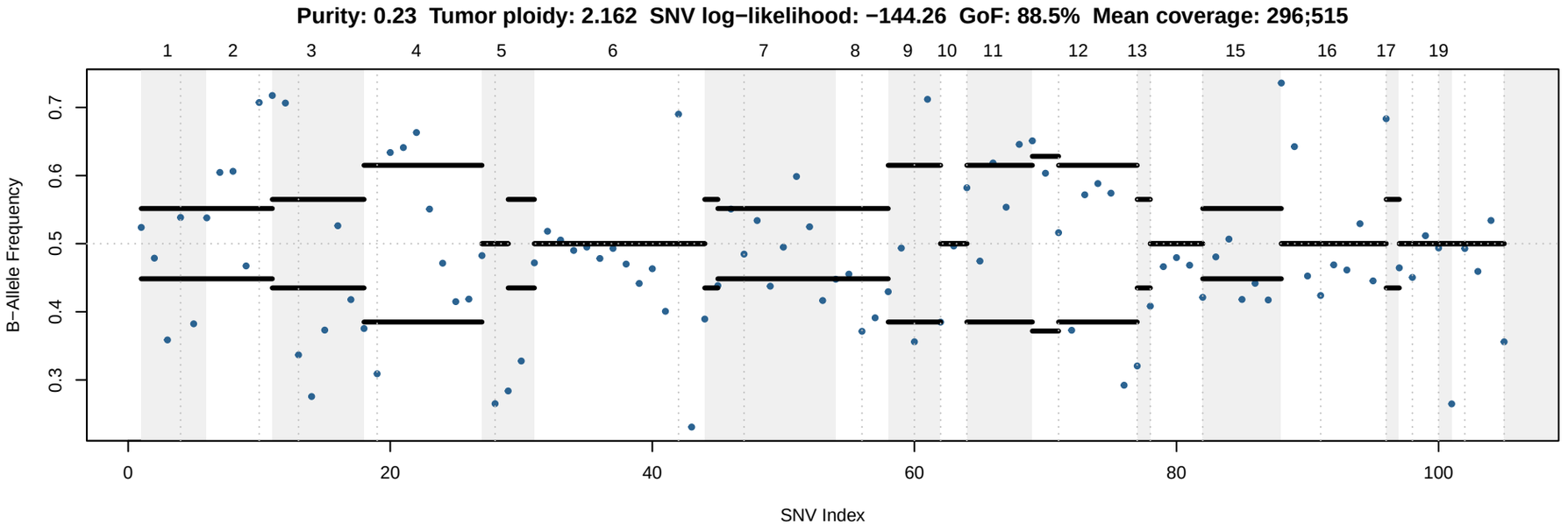

3m3
5m4
7m5
4m3
3m2
5m3
4m2
5m2
3m1
4m1
2m0
3m0
4m0
Allelic fraction (germline)
Copy Number log−ratio
0.2
0.3
0.4
0.5
0.6
0.7
−1.0
−0.5
0.0
0.5

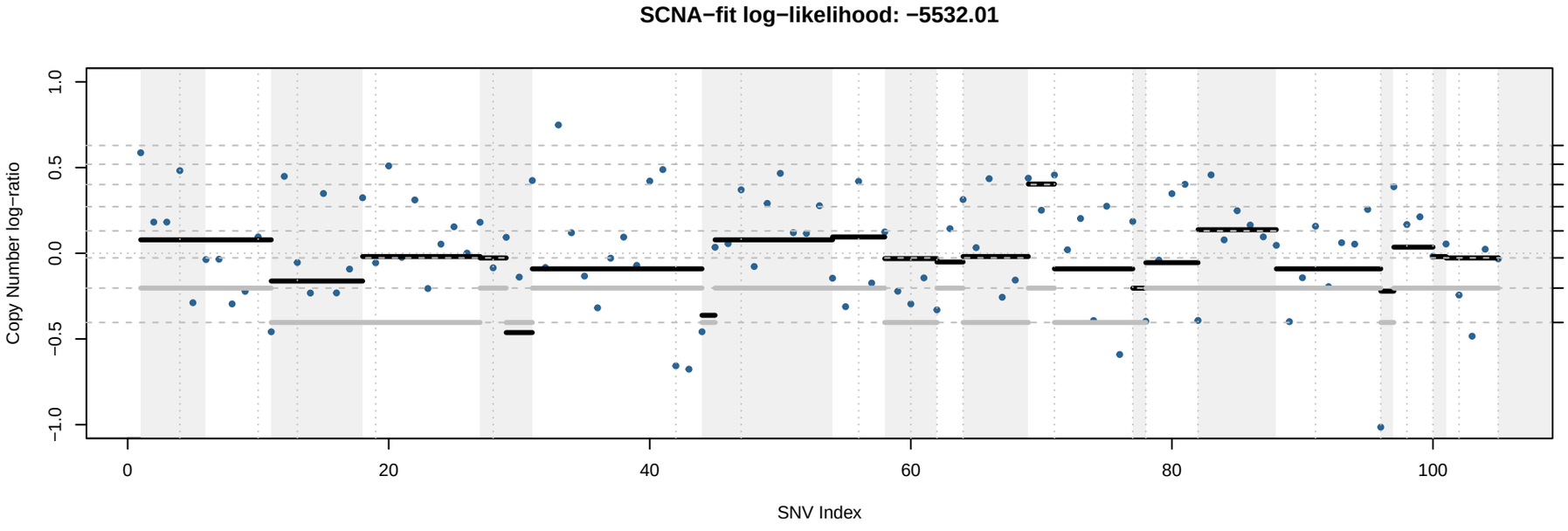

Coverage (log2)
Allelic fraction
5
6
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
0.7

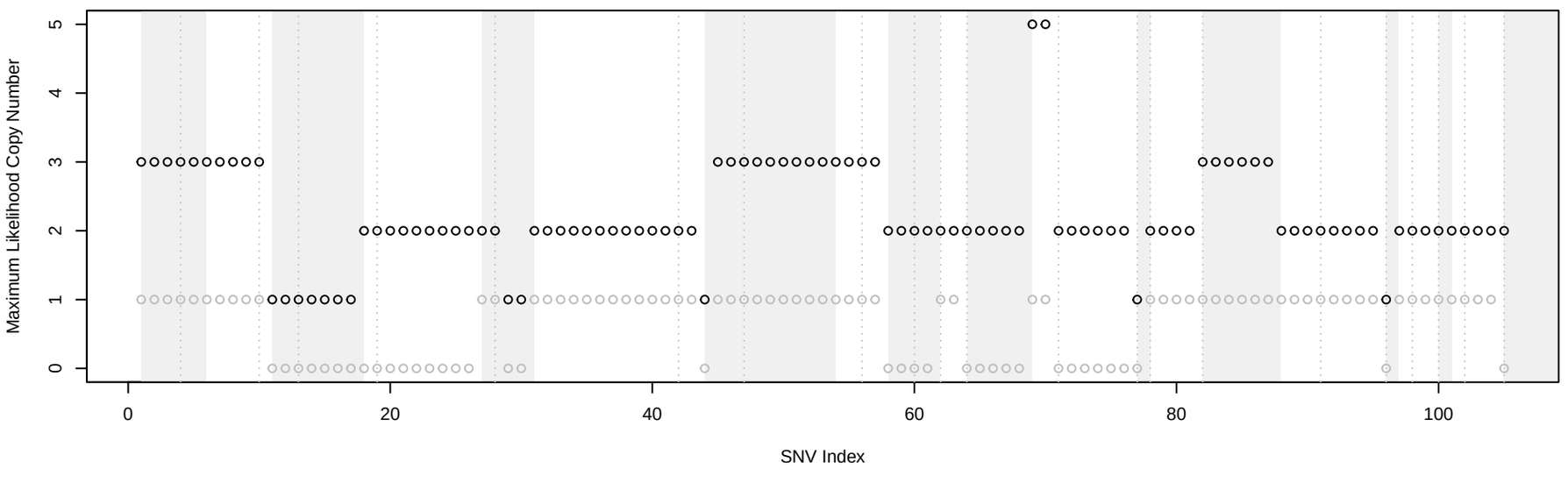

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
0.12
−1.0
−0.5
0.0
0.5

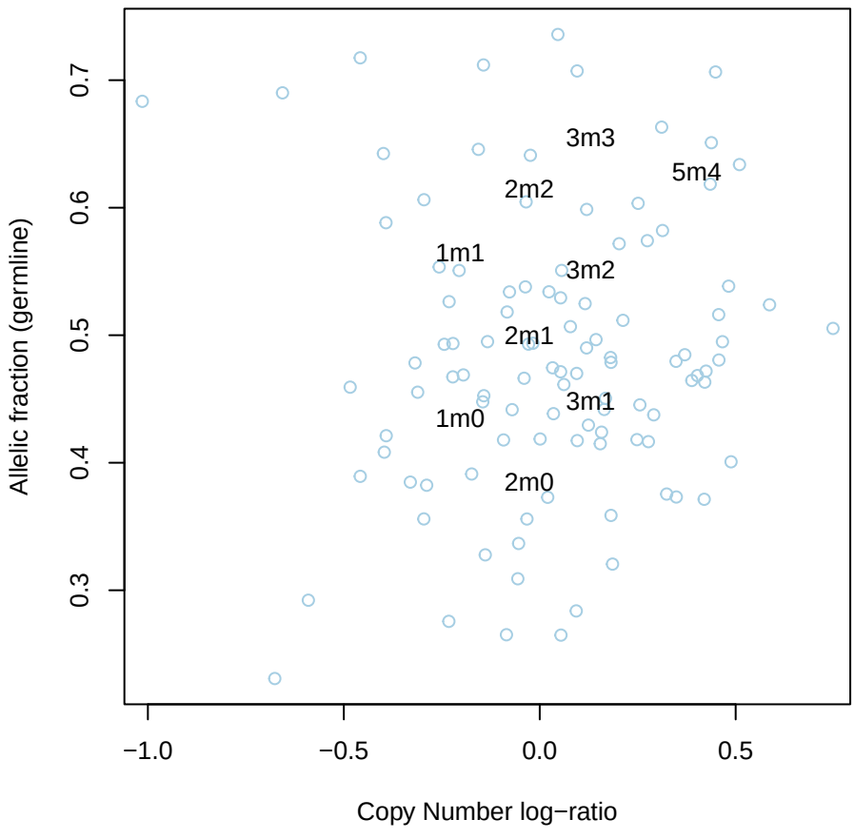

Power 0.8
Frequency
Cellular fraction
0
5
10
15
20
25
0.2
0.4
0.6
0.8
1.0

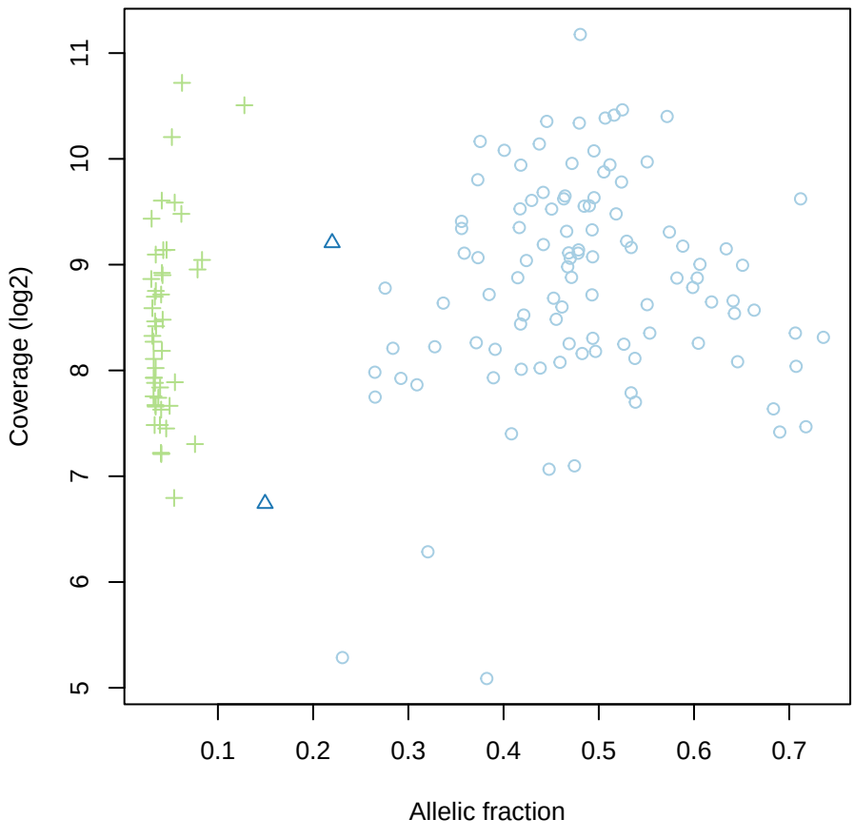

Purity: 0.23 Tumor ploidy: 2.162
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

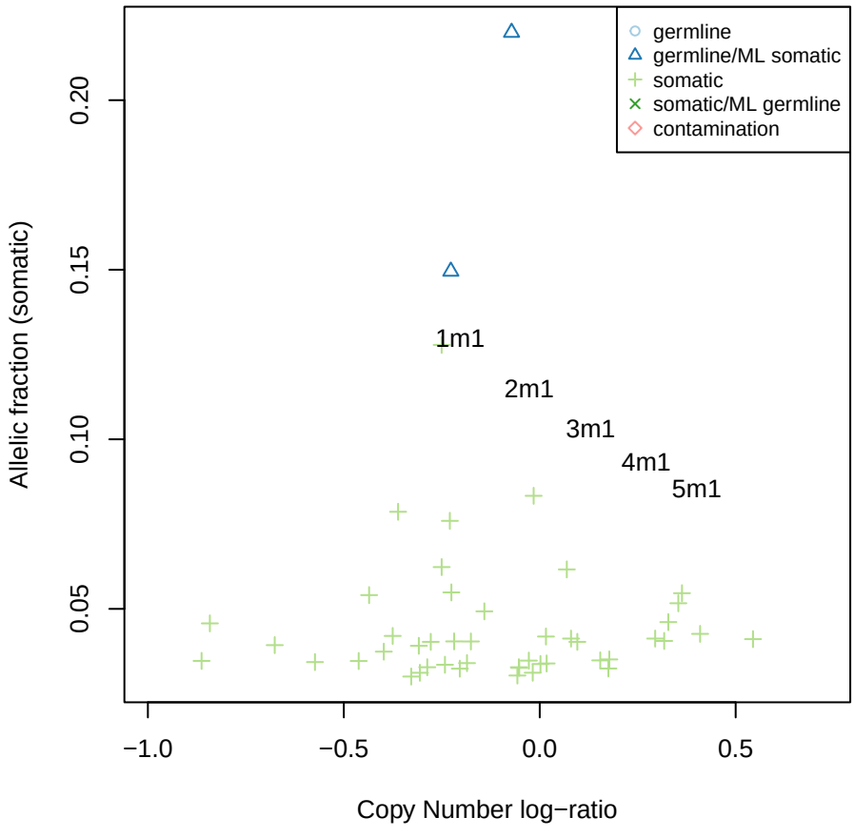

Purity: 0.23 Tumor ploidy: 2.162 SNV log−likelihood: −144.26 GoF: 88.5% Mean coverage: 296;515
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

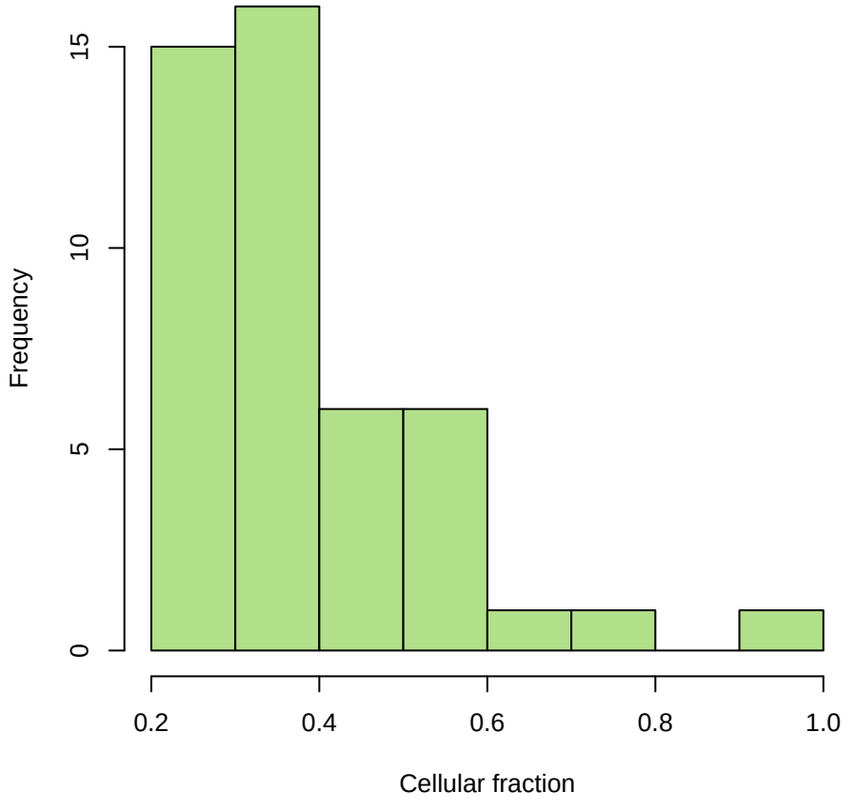

SCNA−fit log−likelihood: −5532.01
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 5 7
0 20 40 60 80 100
SNV Index

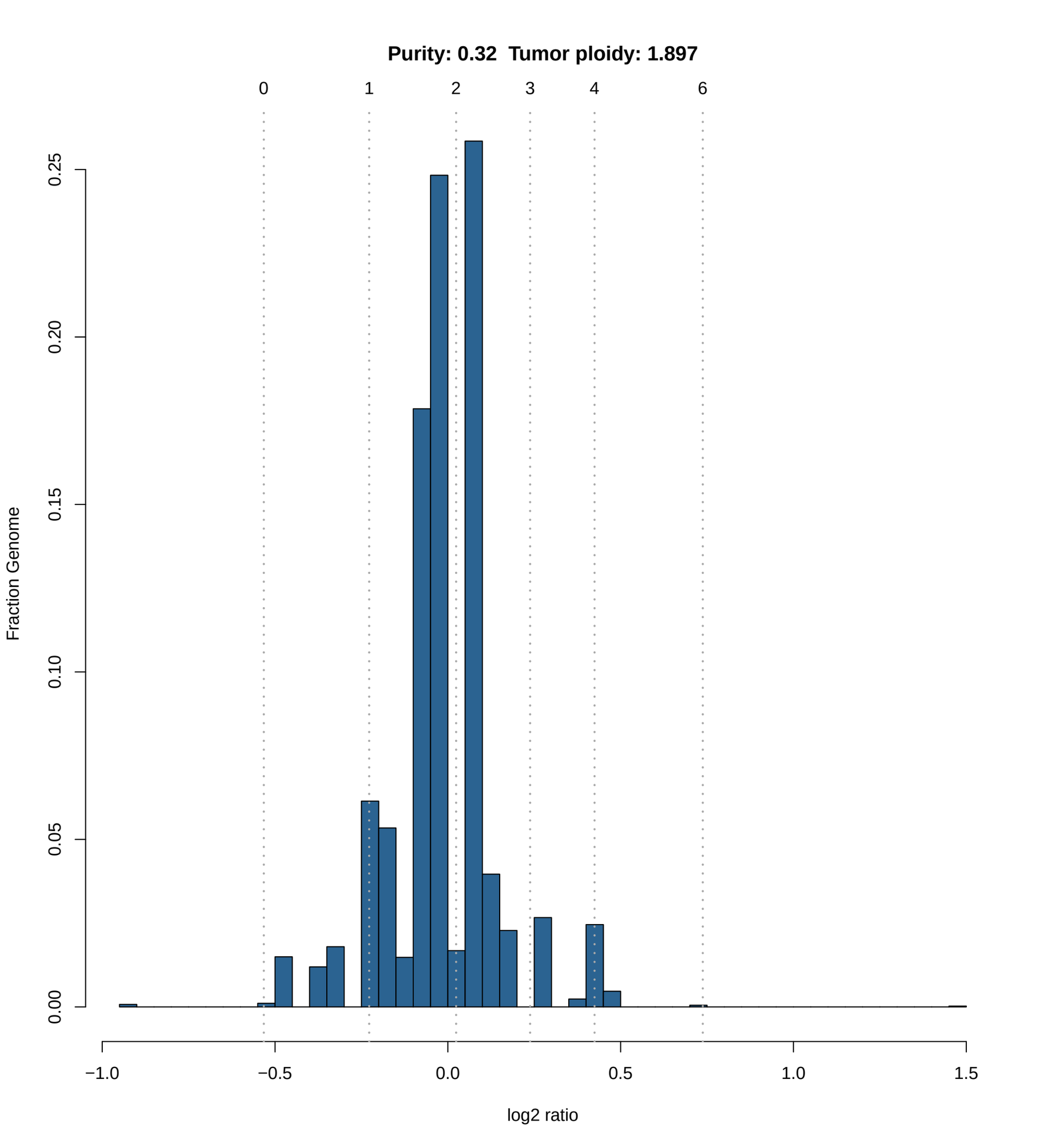

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100
SNV Index

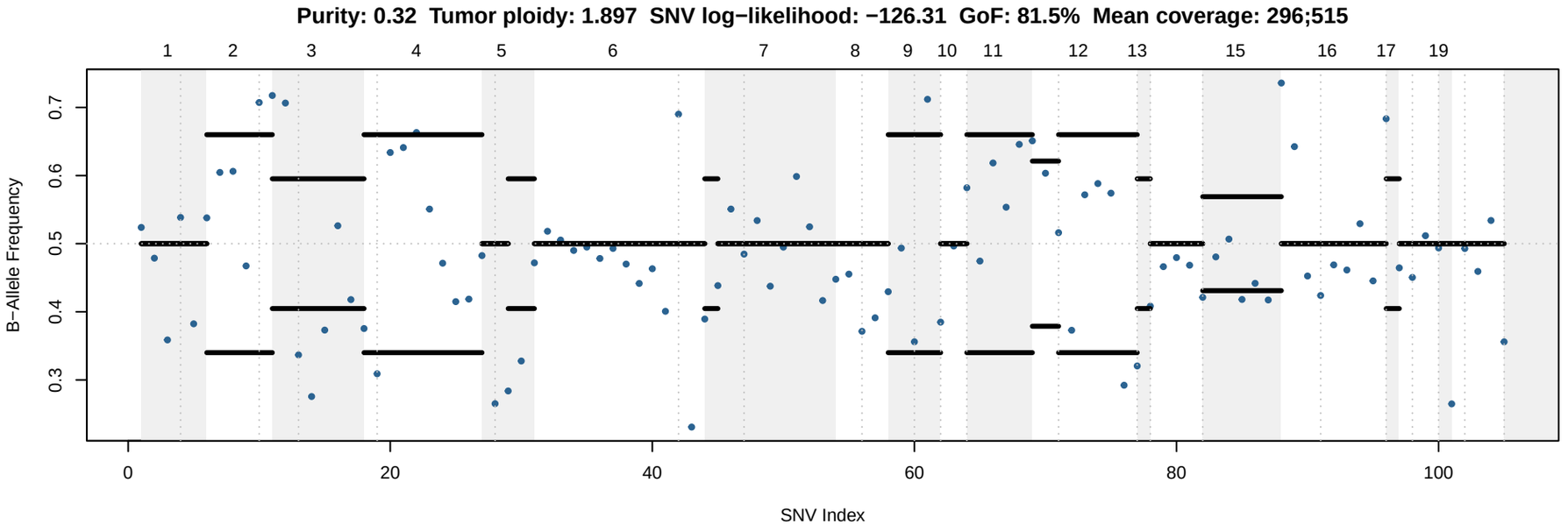

Allelic fraction (germline)
Copy Number log−ratio
3m3
5m4
2m2
1m1
3m2
2m1
3m1
1m0
2m0

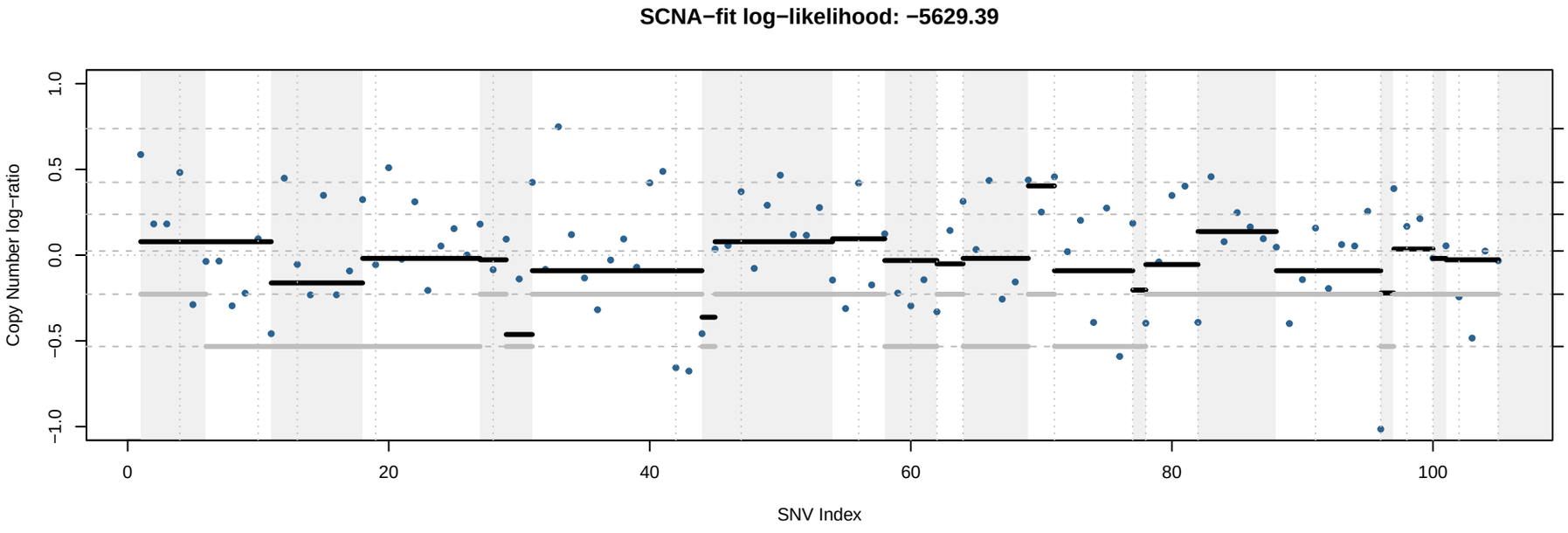

Coverage (log2)
Allelic fraction

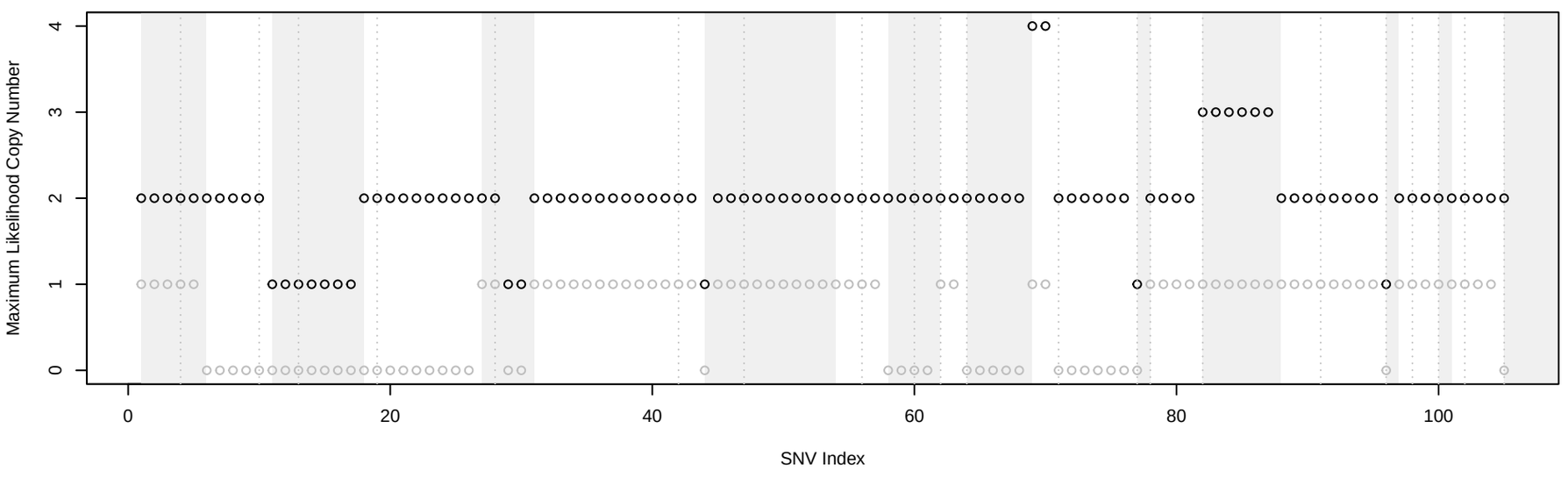

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1
3m1
4m1
5m1

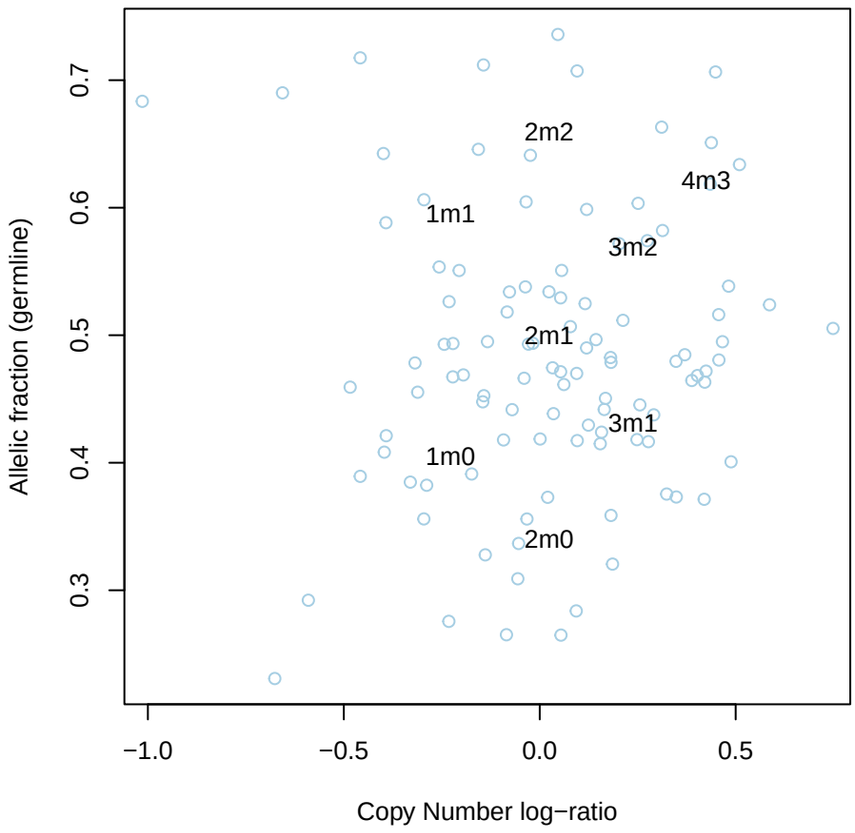

Frequency
Cellular fraction

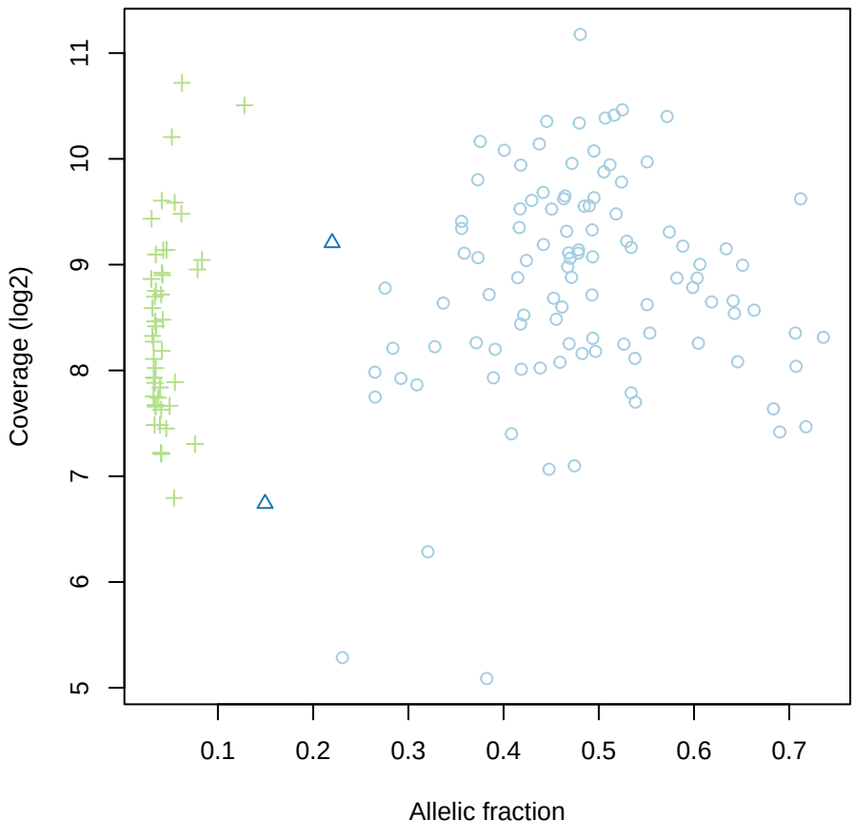

Purity: 0.32 Tumor ploidy: 1.897
0
1
2
3
4
6
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

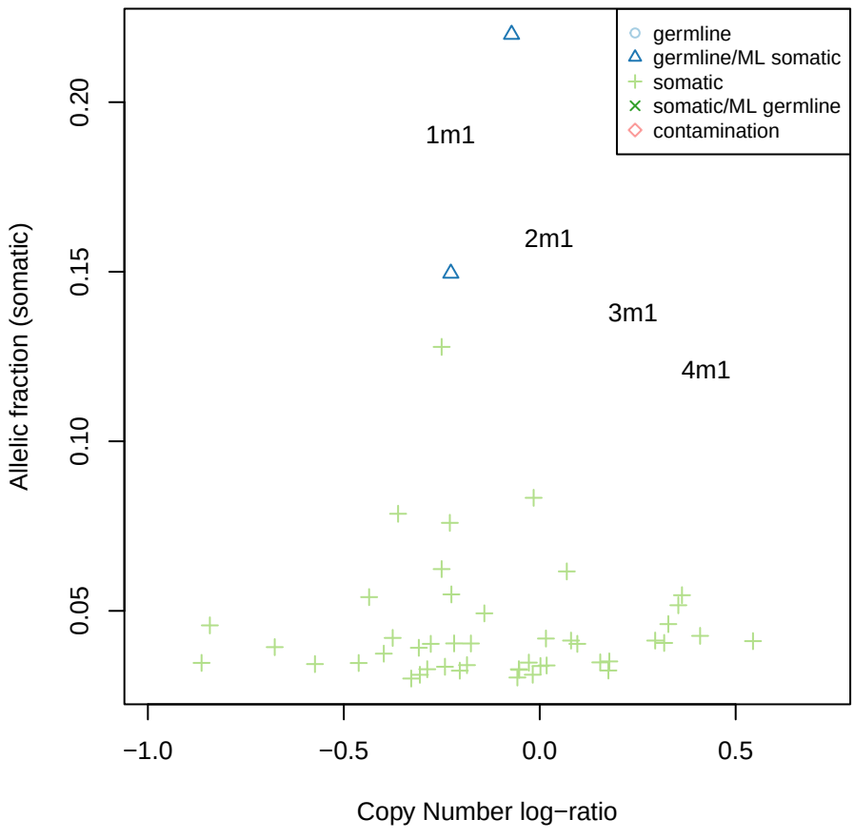

Purity: 0.32 Tumor ploidy: 1.897 SNV log−likelihood: −126.31 GoF: 81.5% Mean coverage: 296;515
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

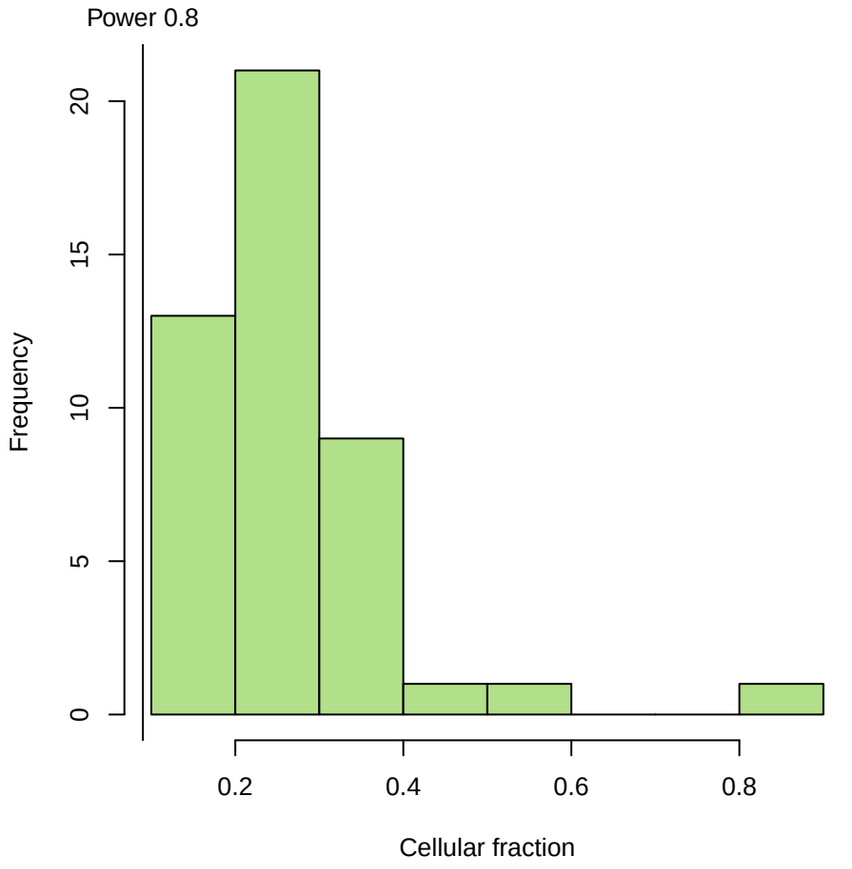

SCNA−fit log−likelihood: −5629.39
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 6
0 20 40 60 80 100
SNV Index

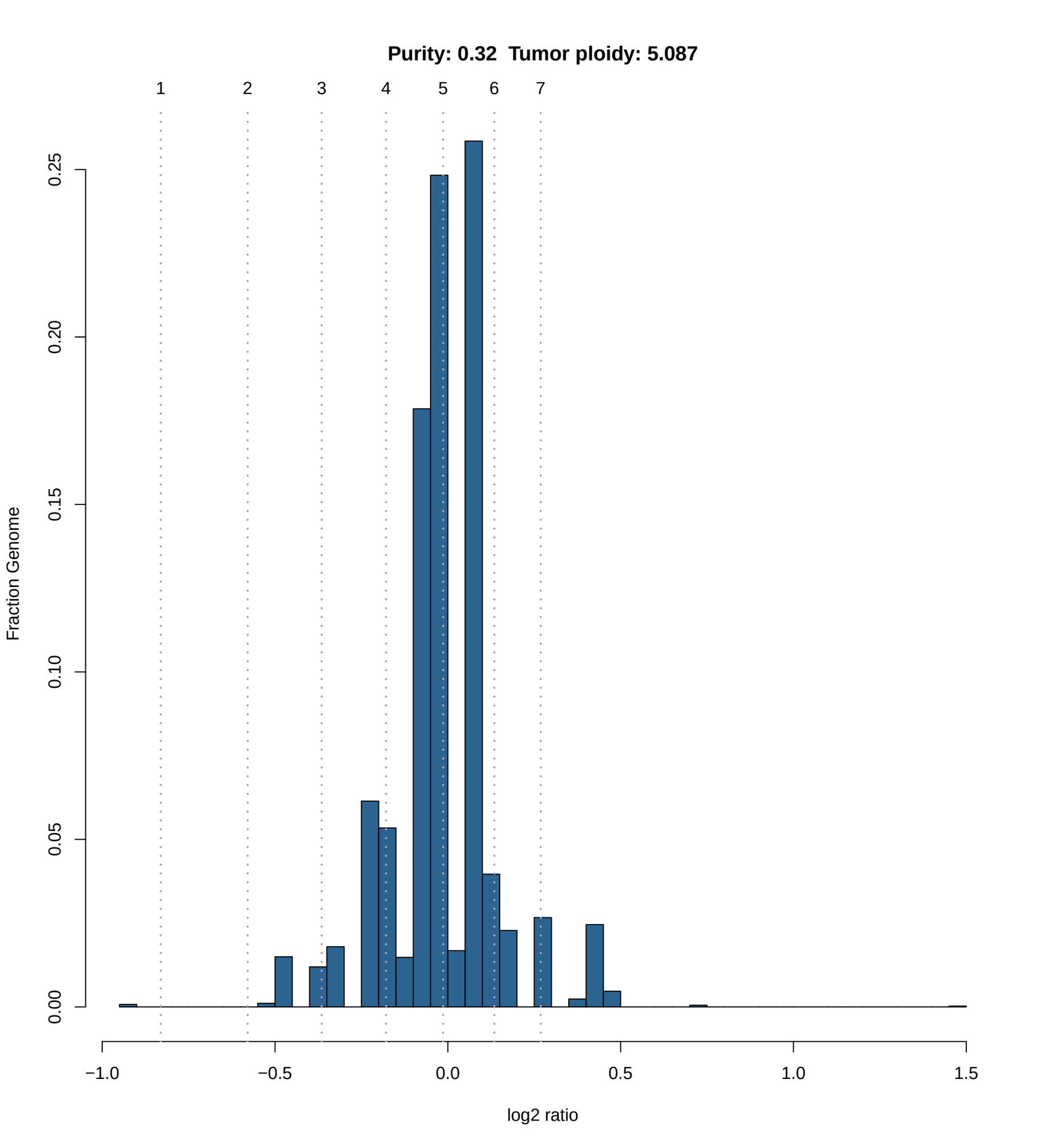

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100
SNV Index

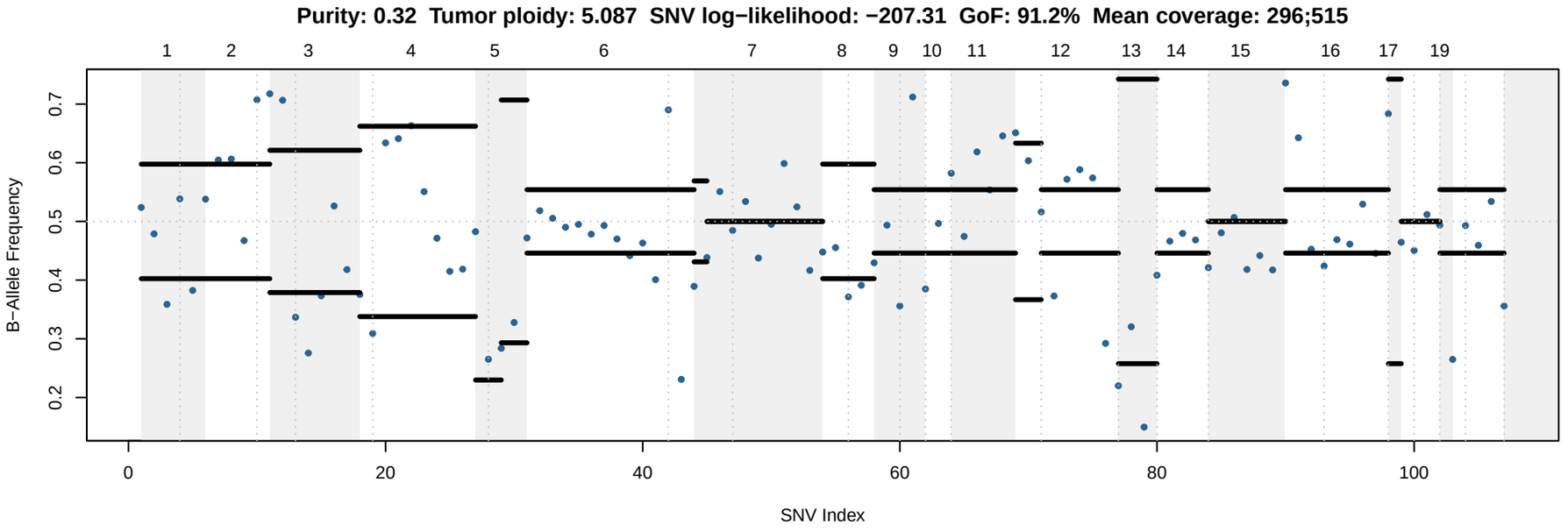

Allelic fraction (germline)
Copy Number log−ratio
2m2
4m3
1m1
3m2
2m1
3m1
1m0
2m0

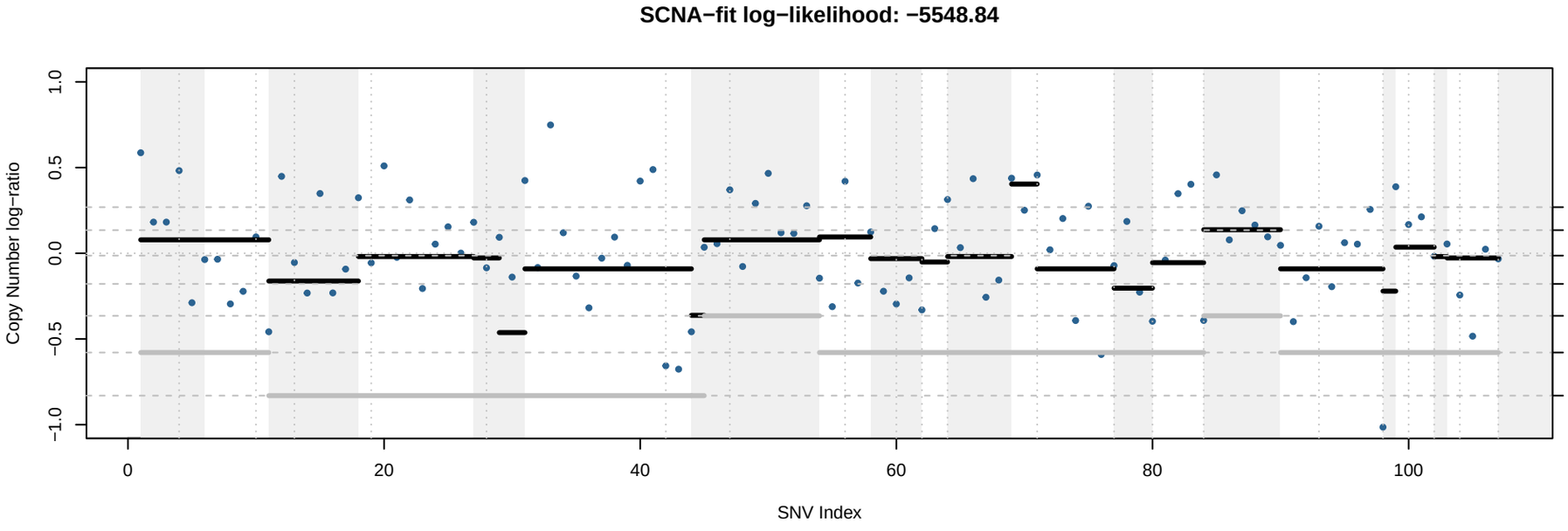

Coverage (log2)
Allelic fraction

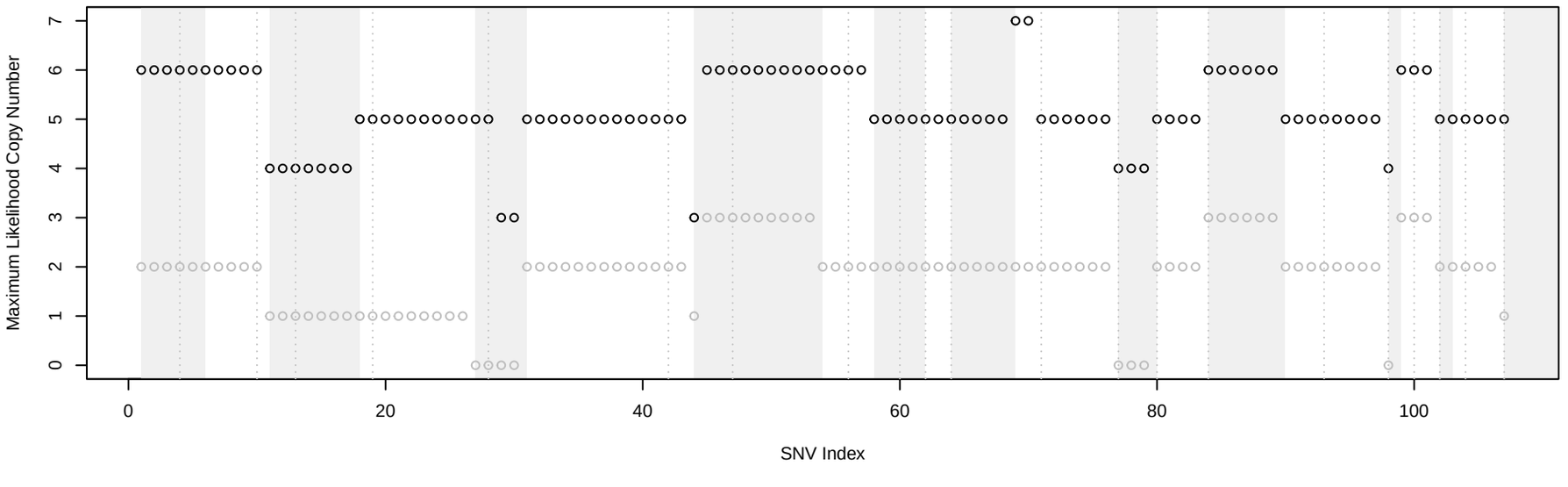

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1
3m1
4m1

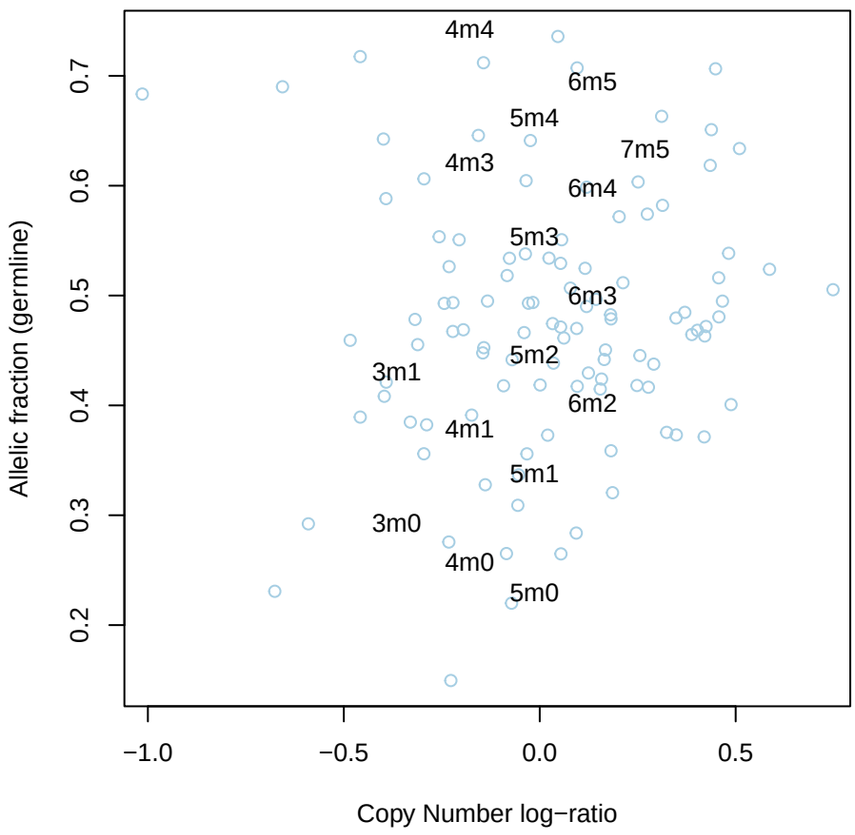

Power 0.8
Frequency
Cellular fraction

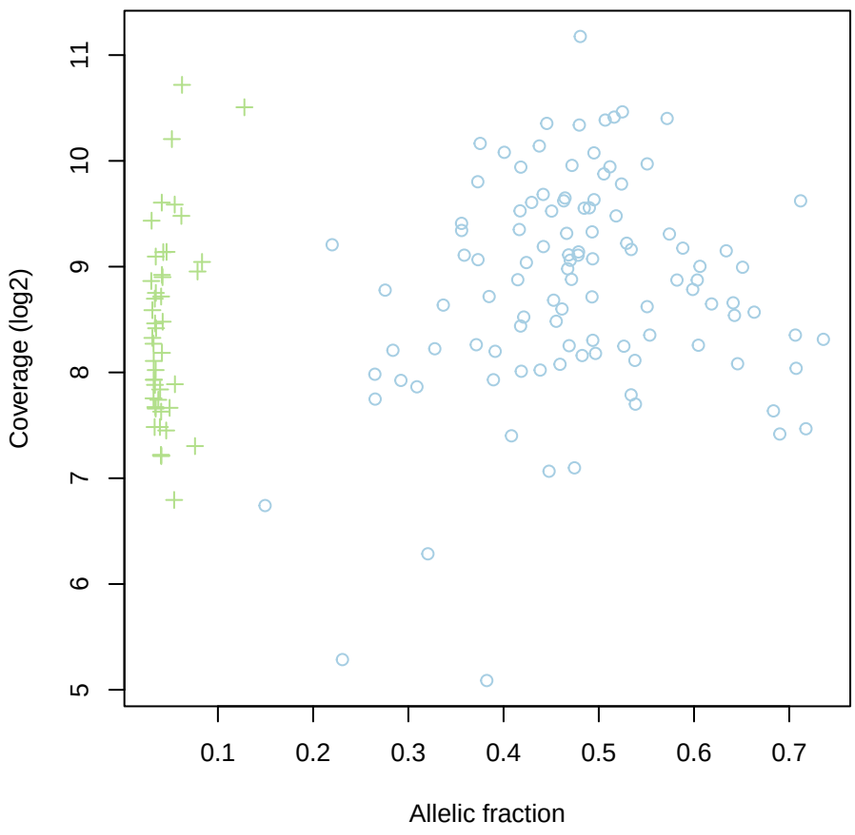

Purity: 0.32 Tumor ploidy: 5.087
1
2
3
4
5
6
7
0.00
0.05
0.10
0.15
0.20
0.25
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

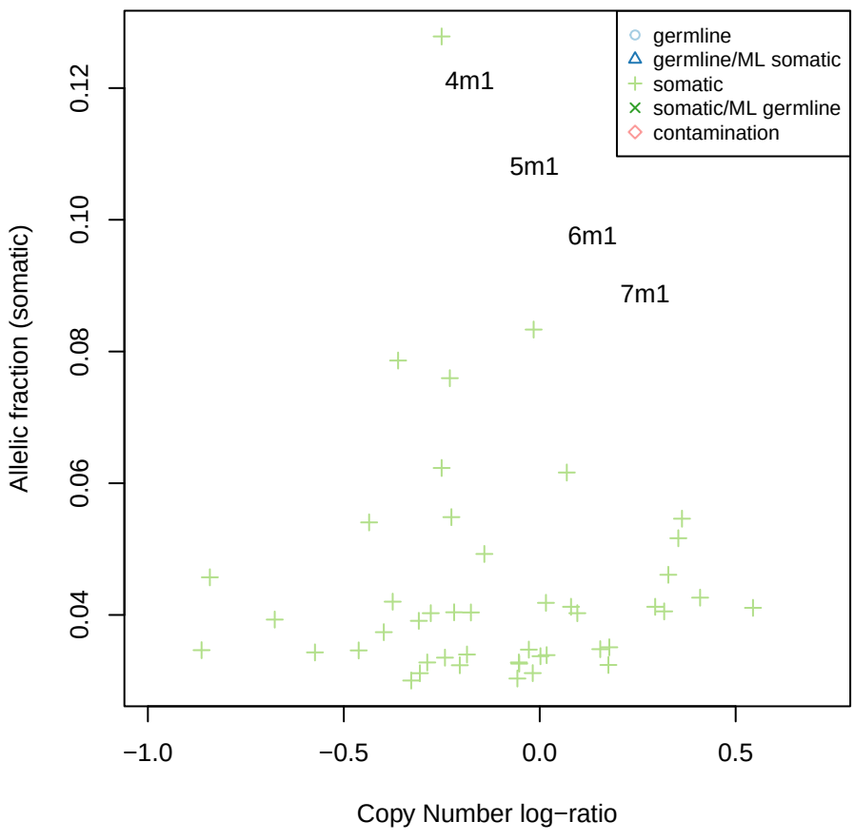

Purity: 0.32 Tumor ploidy: 5.087 SNV log−likelihood: −207.31 GoF: 91.2% Mean coverage: 296;515
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

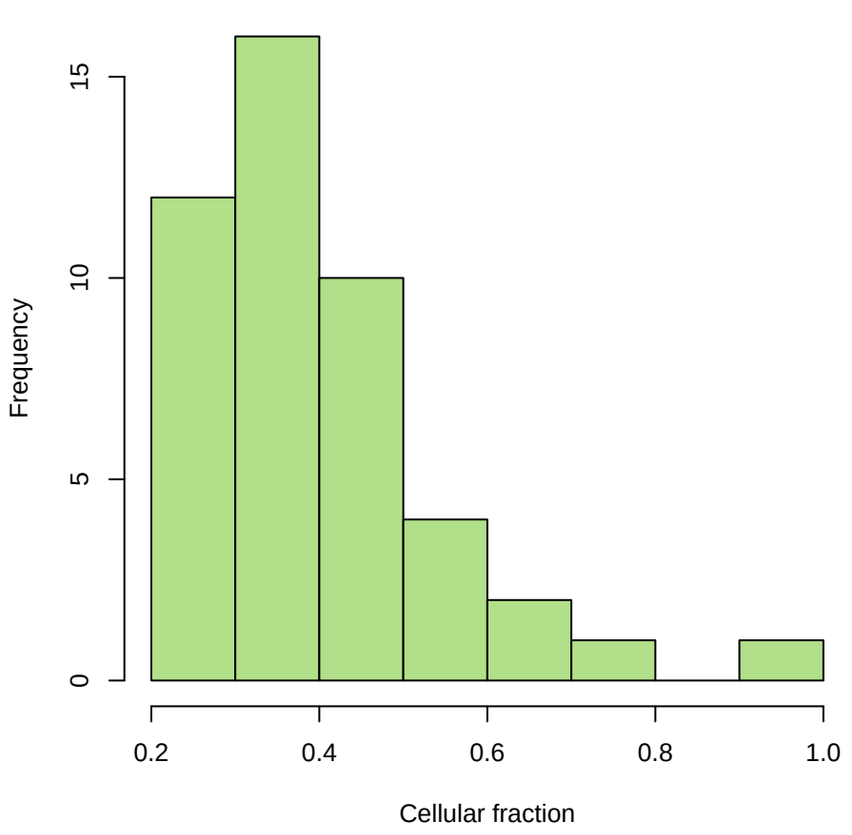

SCNA−fit log−likelihood: −5548.84
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6
0 20 40 60 80 100
SNV Index

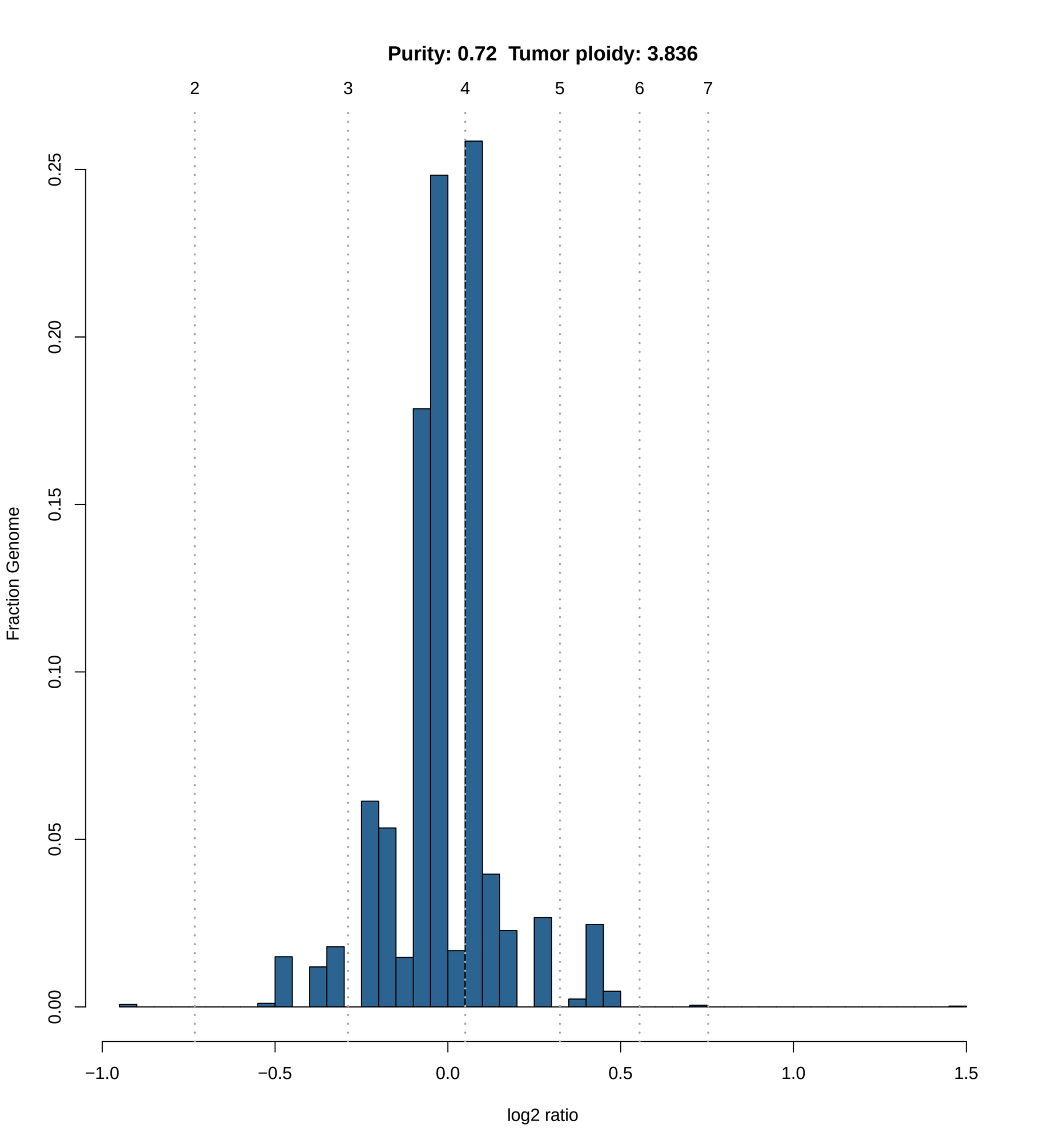

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

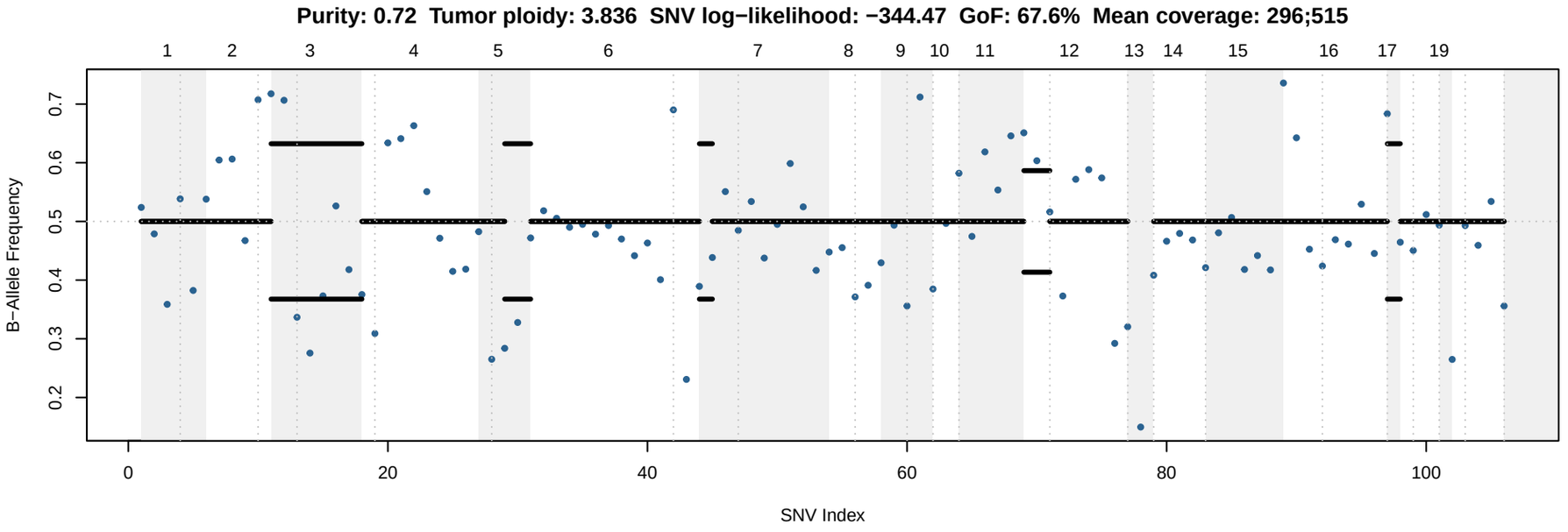

4m4
6m5
5m4
7m5
4m3
6m4
5m3
6m3
5m2
3m1
6m2
4m1
5m1
3m0
4m0
5m0
Allelic fraction (germline)
Copy Number log−ratio

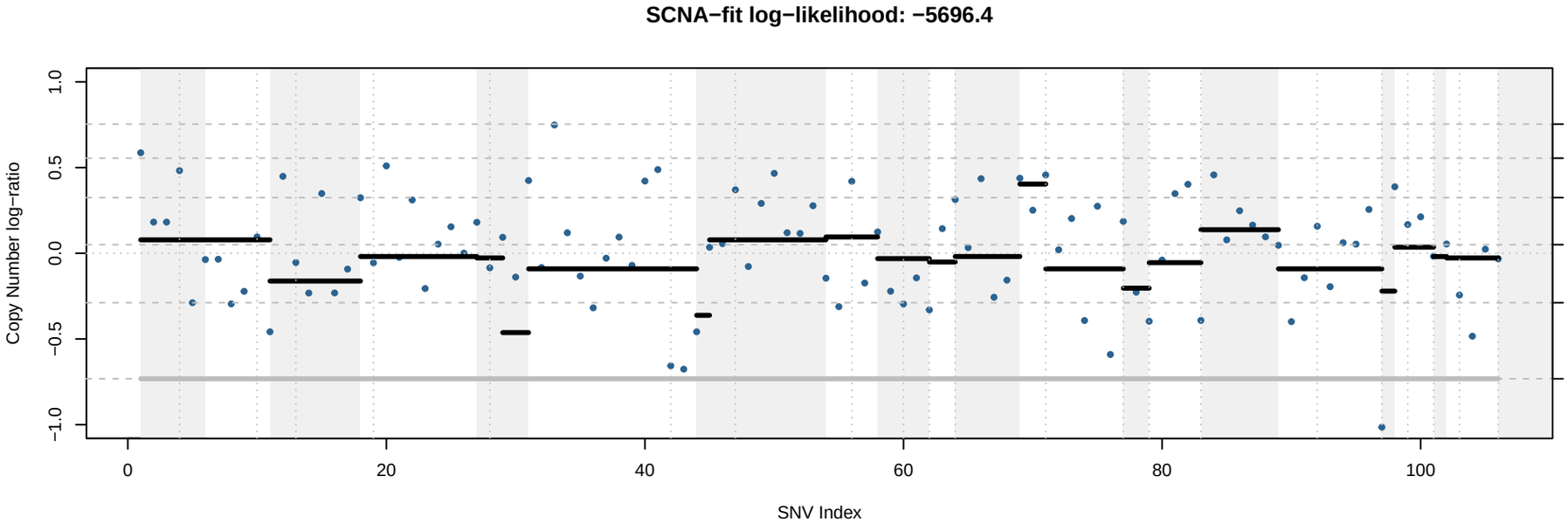

Coverage (log2)
Allelic fraction

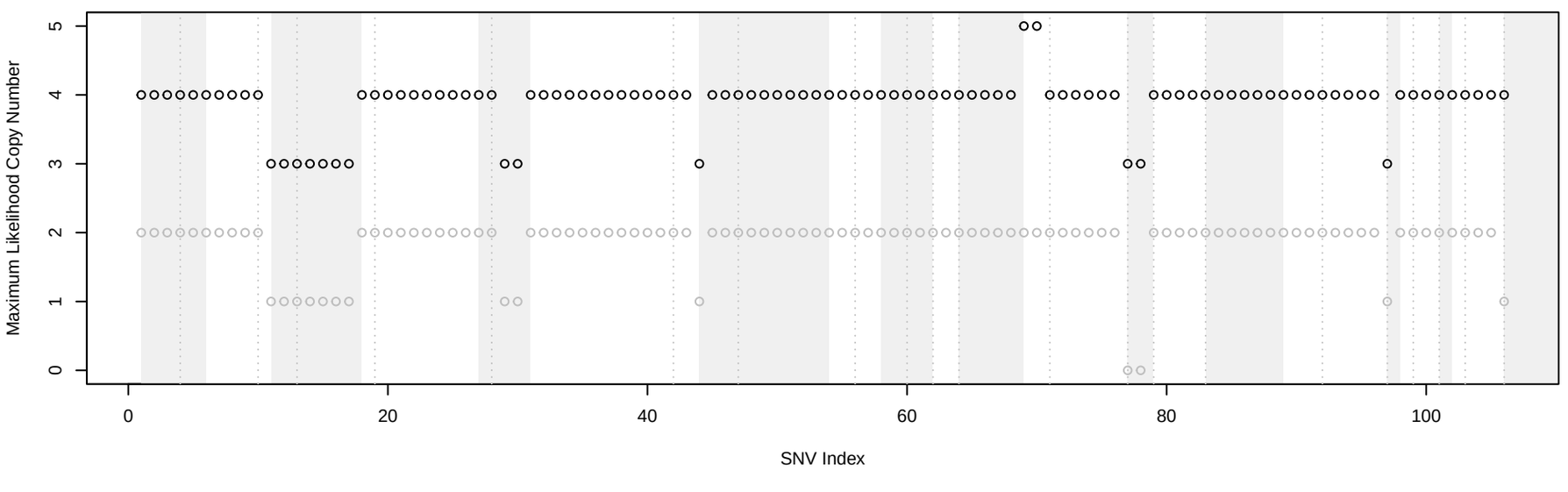

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

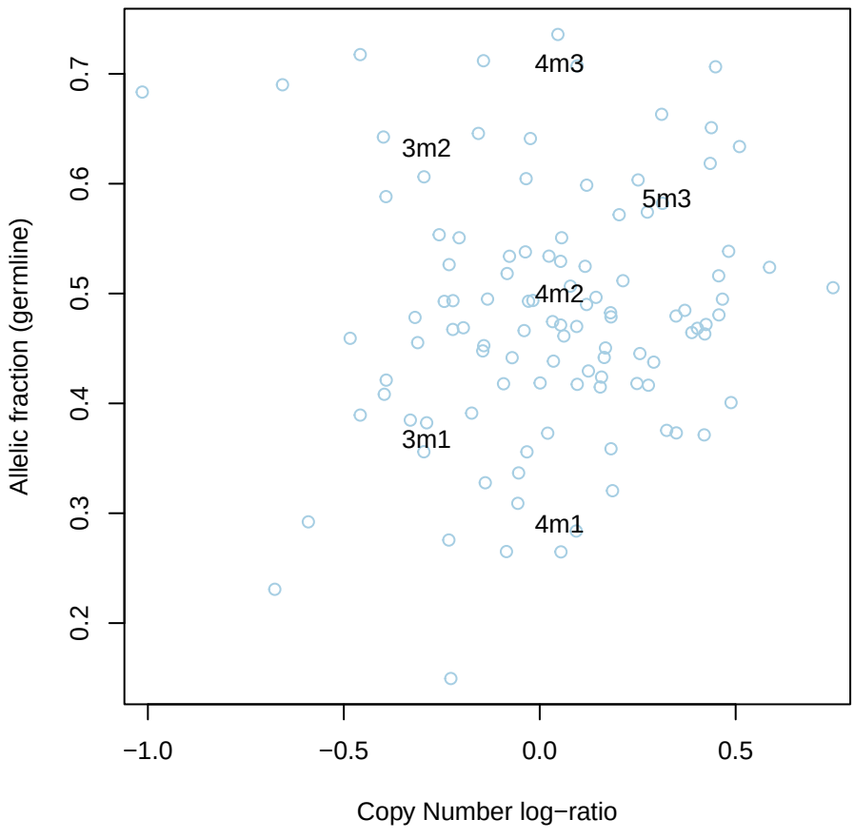

Frequency
Cellular fraction

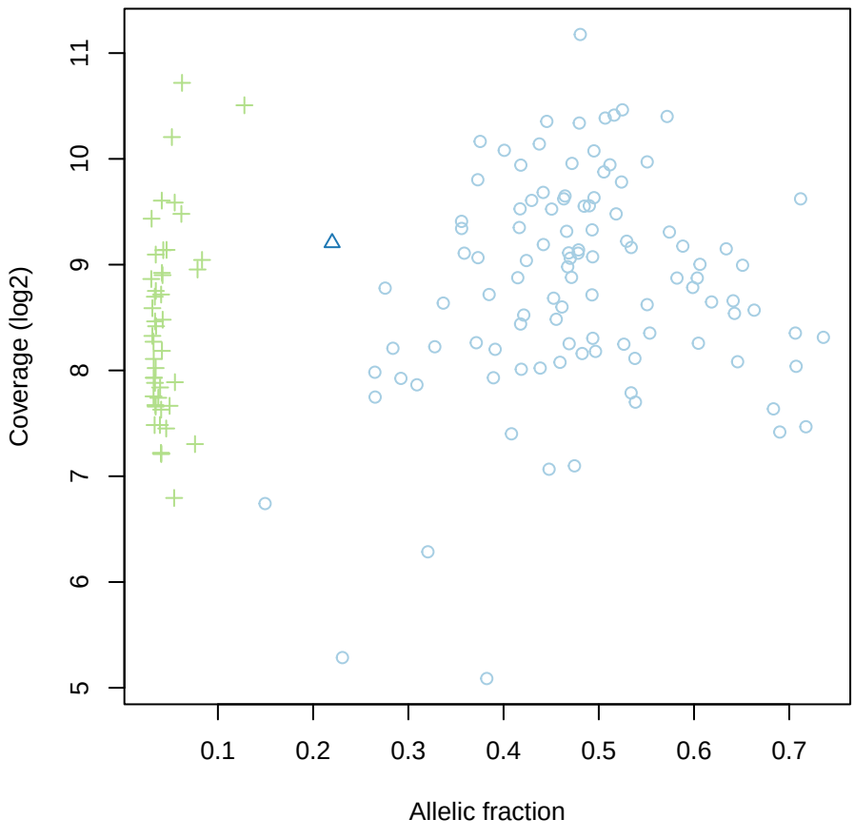

Purity: 0.72 Tumor ploidy: 3.836
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

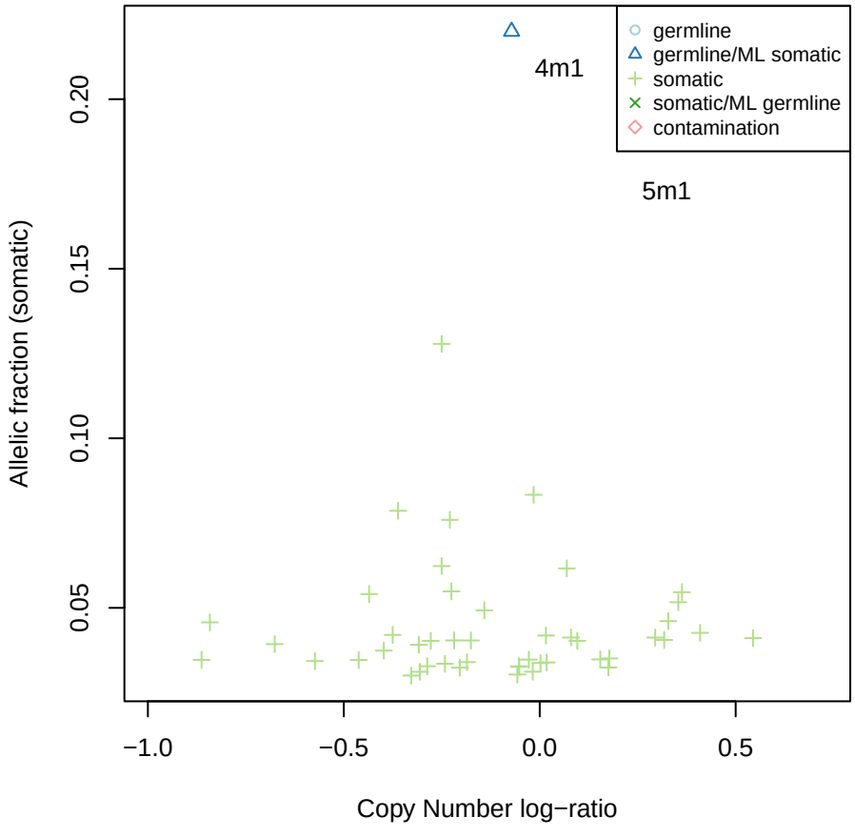

Purity: 0.72 Tumor ploidy: 3.836 SNV log−likelihood: −344.47 GoF: 67.6% Mean coverage: 296;515
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

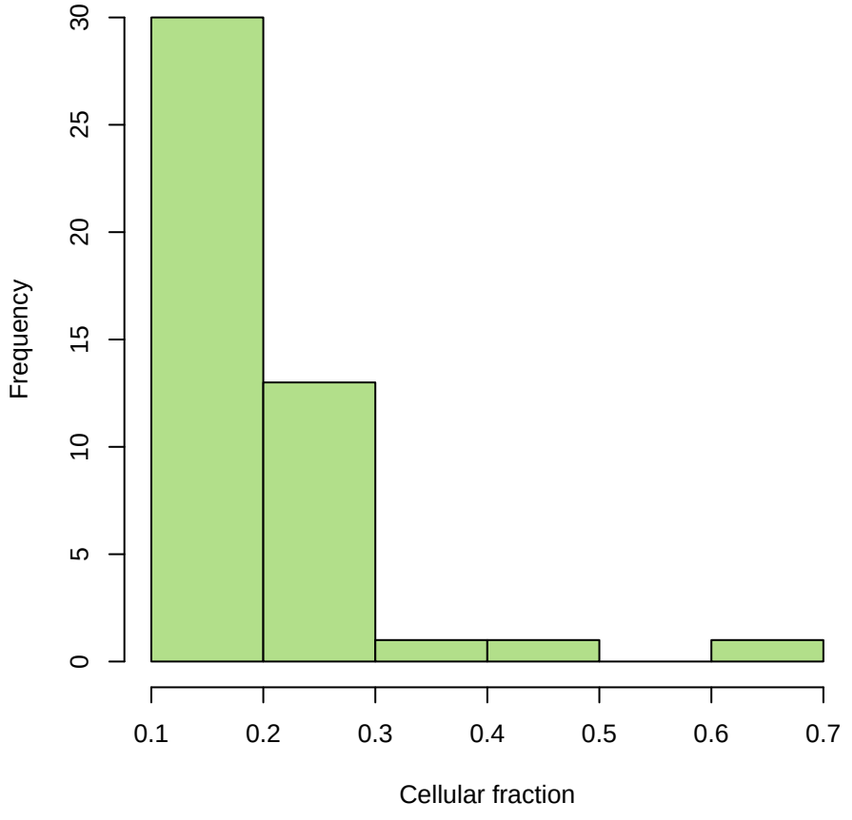

SCNA−fit log−likelihood: −5696.4
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

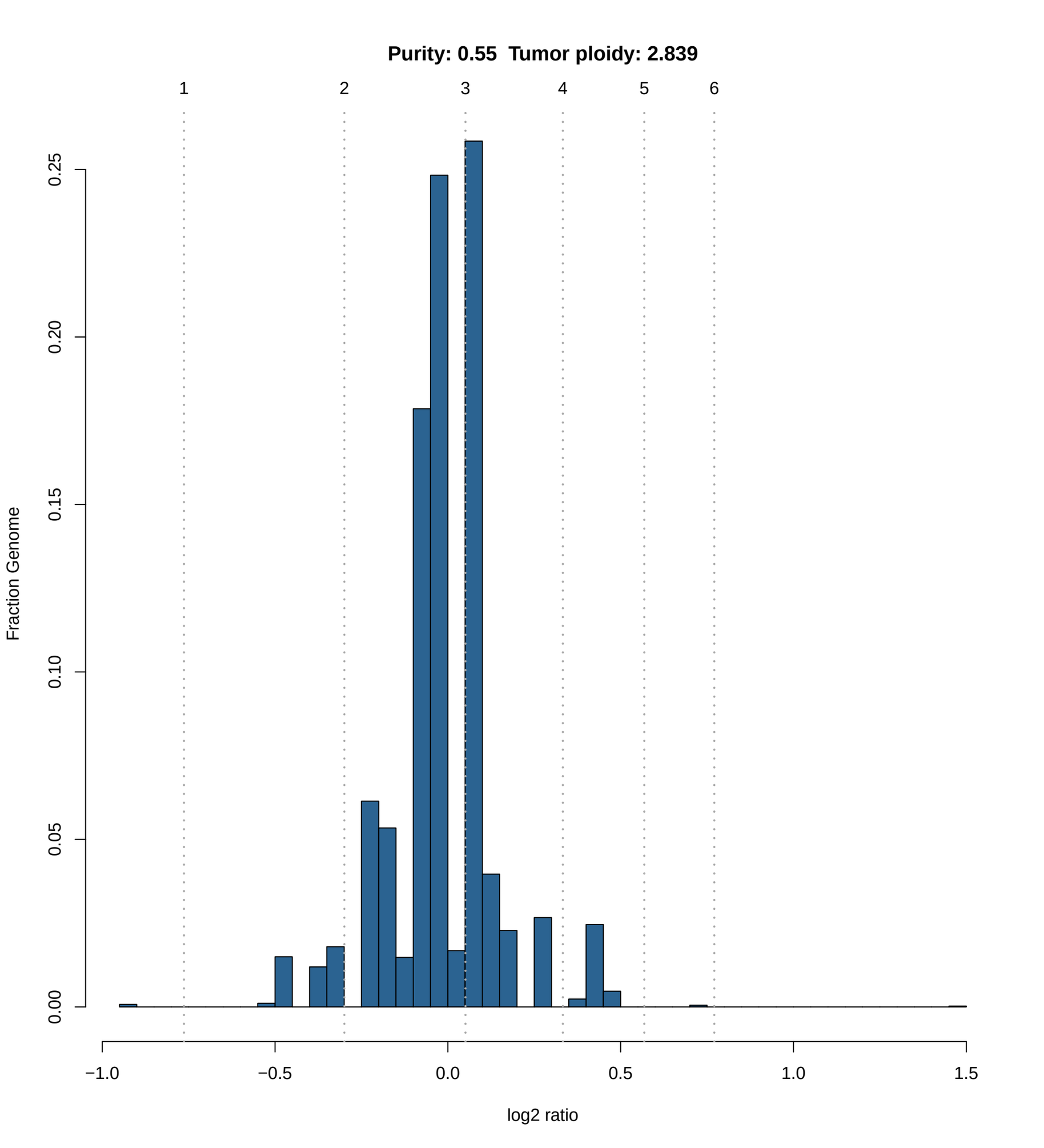

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100
SNV Index

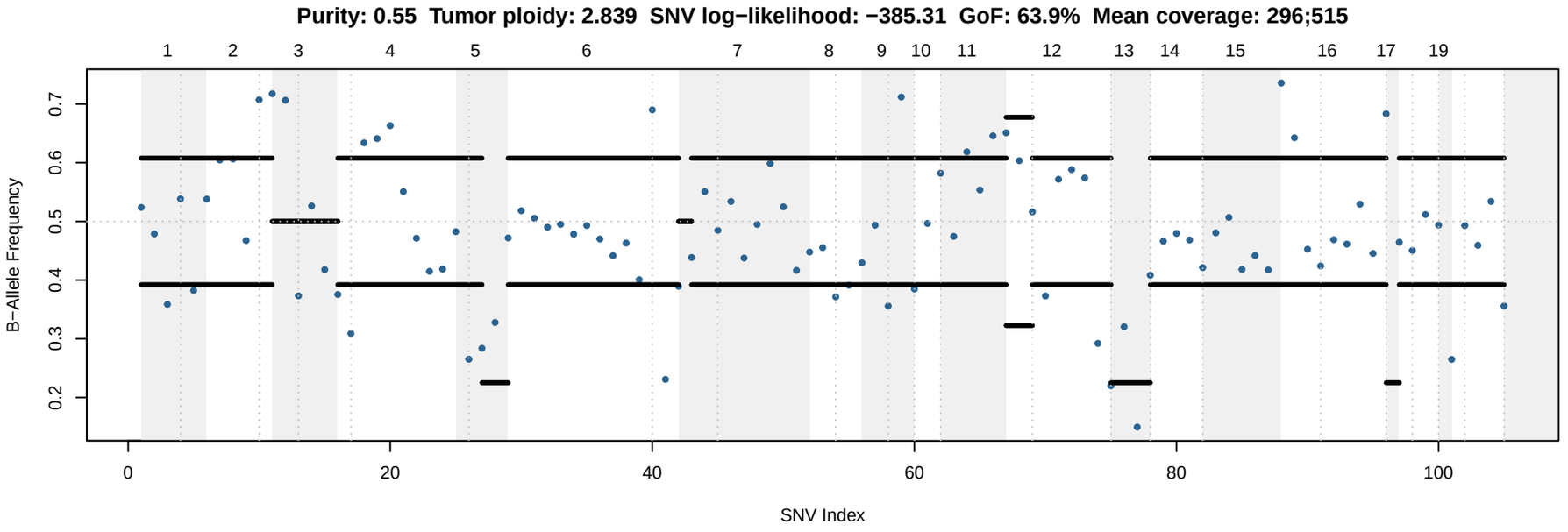

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
5m3
4m2
3m1
4m1

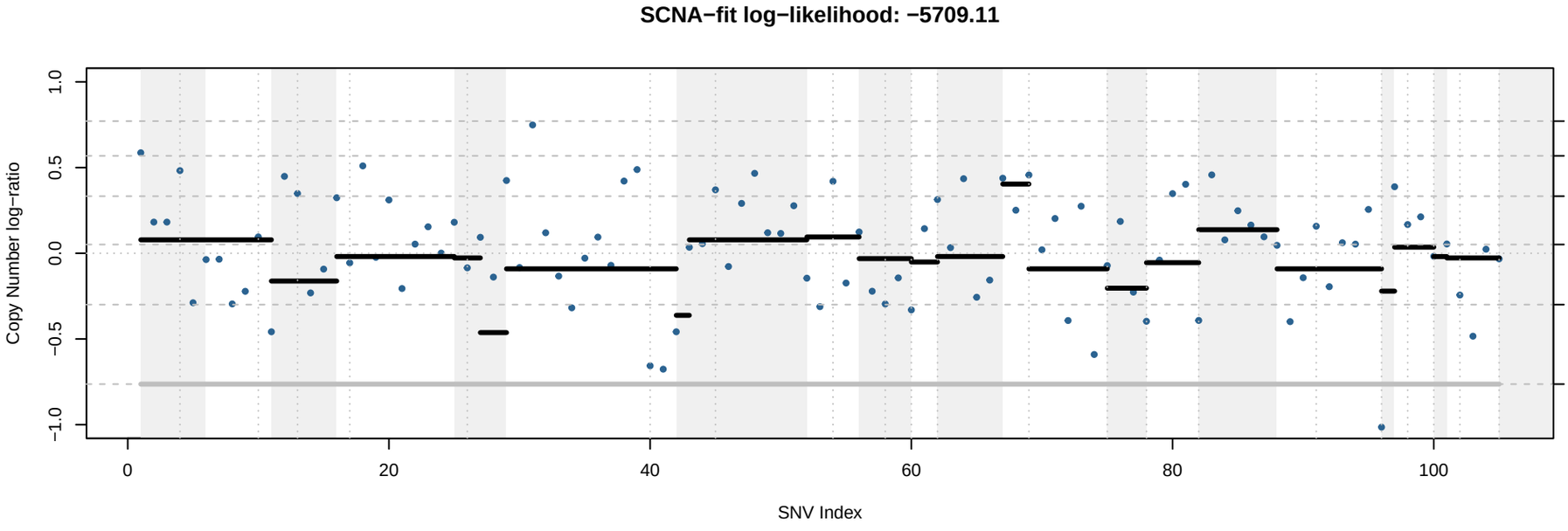

Coverage (log2)
Allelic fraction

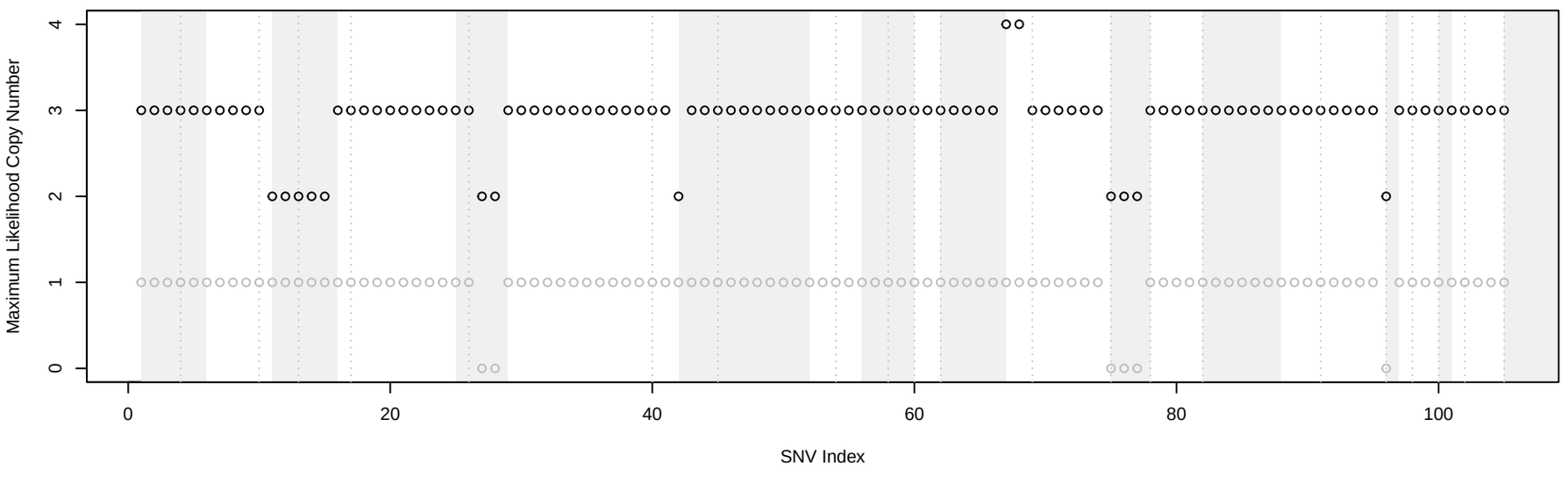

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1

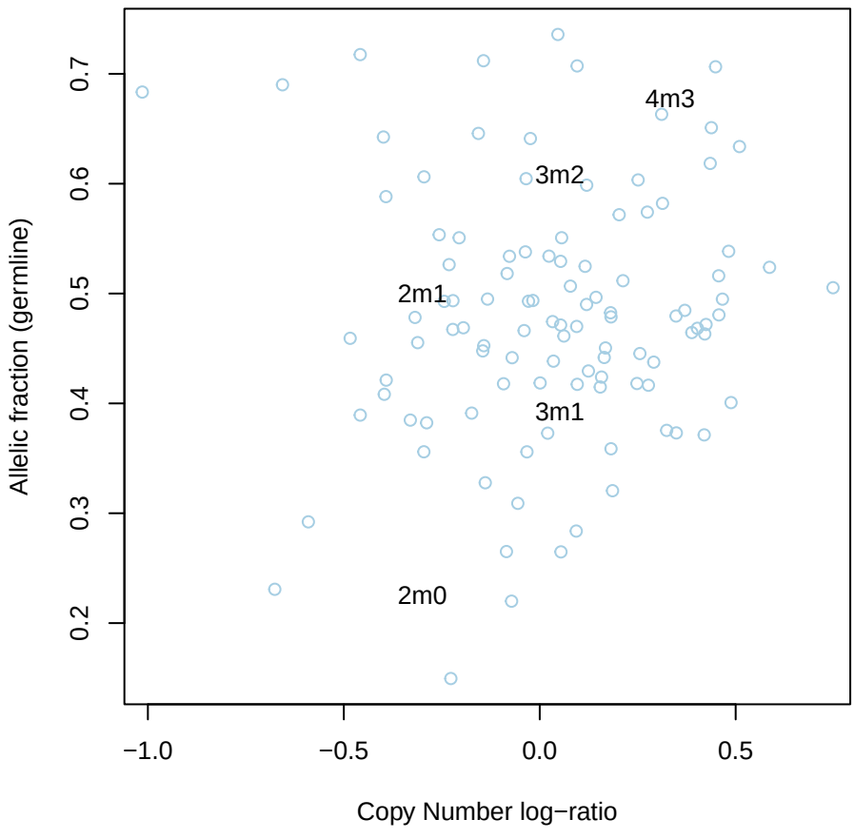

Frequency
Cellular fraction

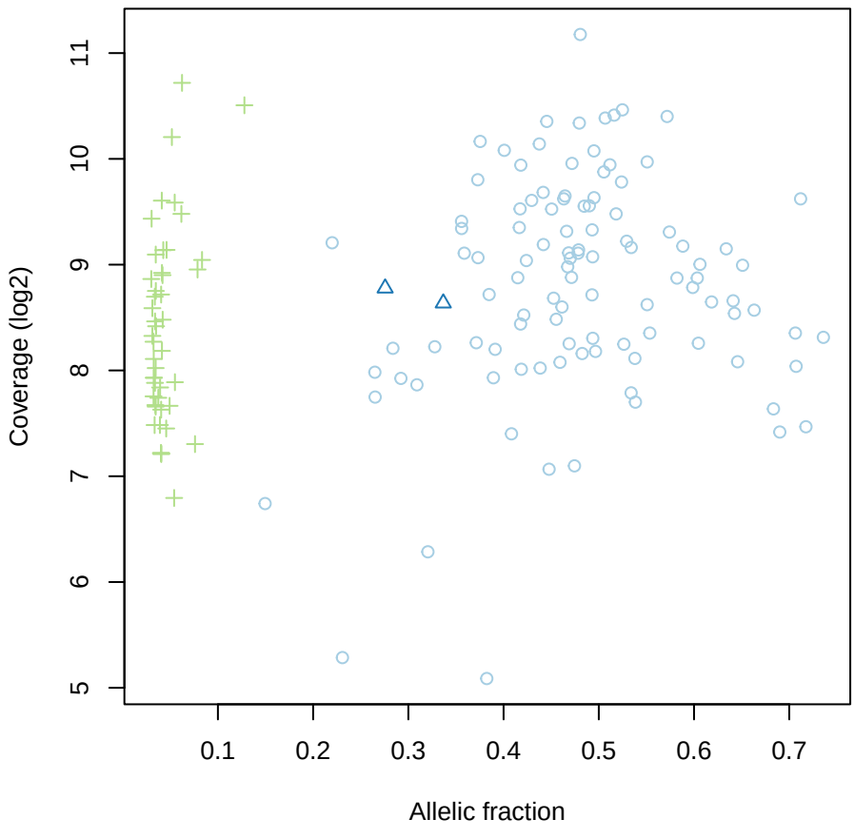

Purity: 0.55 Tumor ploidy: 2.839
1
2
3
4
5
6
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

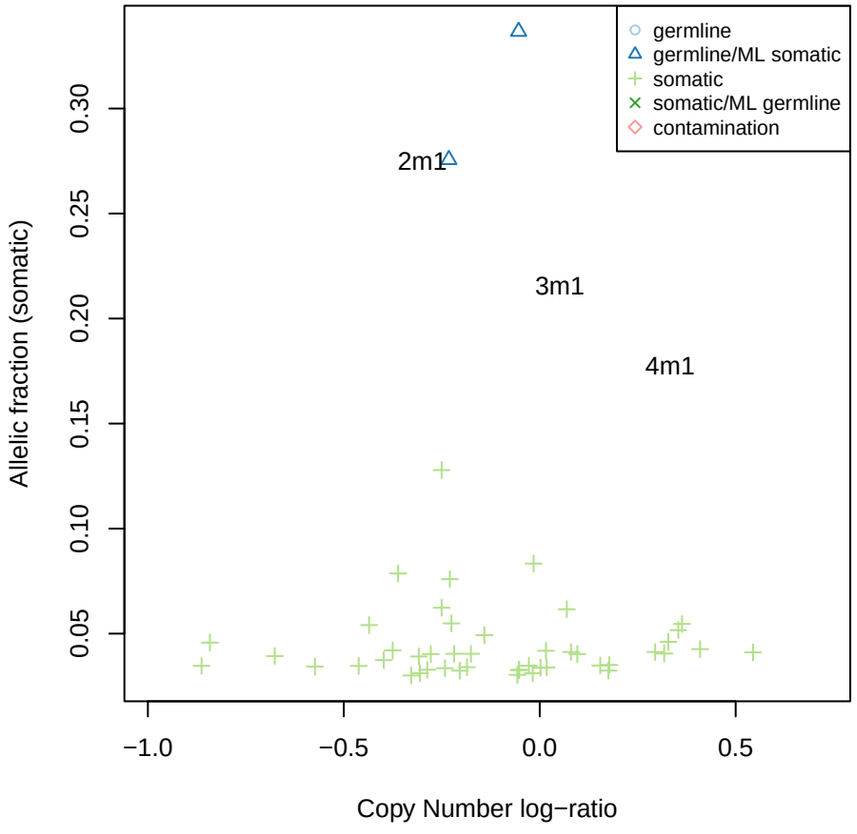

Purity: 0.55 Tumor ploidy: 2.839 SNV log−likelihood: −385.31 GoF: 63.9% Mean coverage: 296;515
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

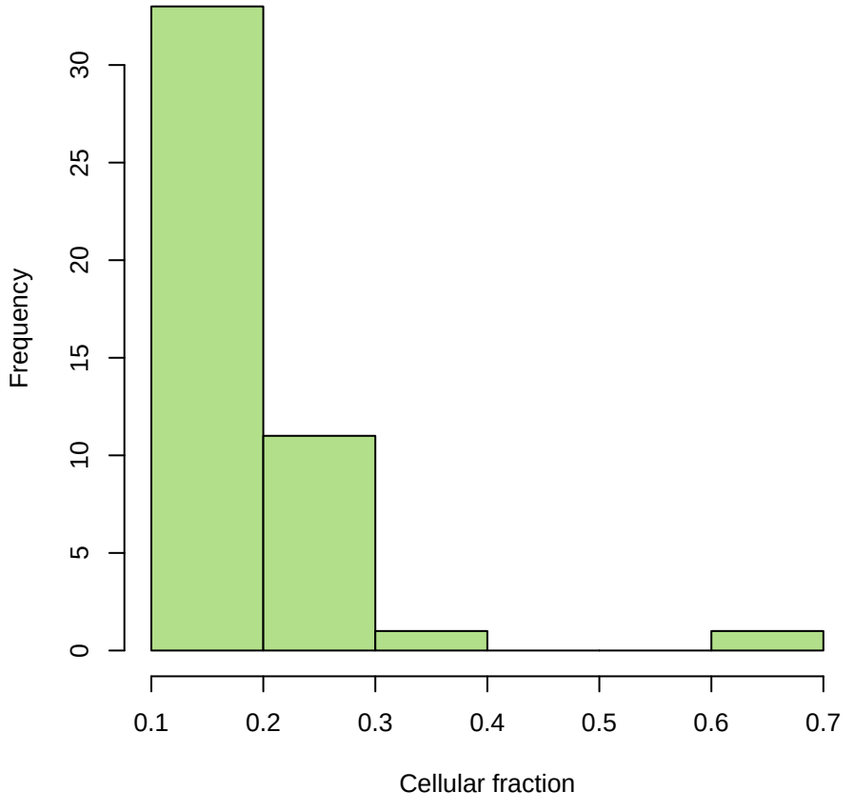

SCNA−fit log−likelihood: −5709.11
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6
0 20 40 60 80 100
SNV Index

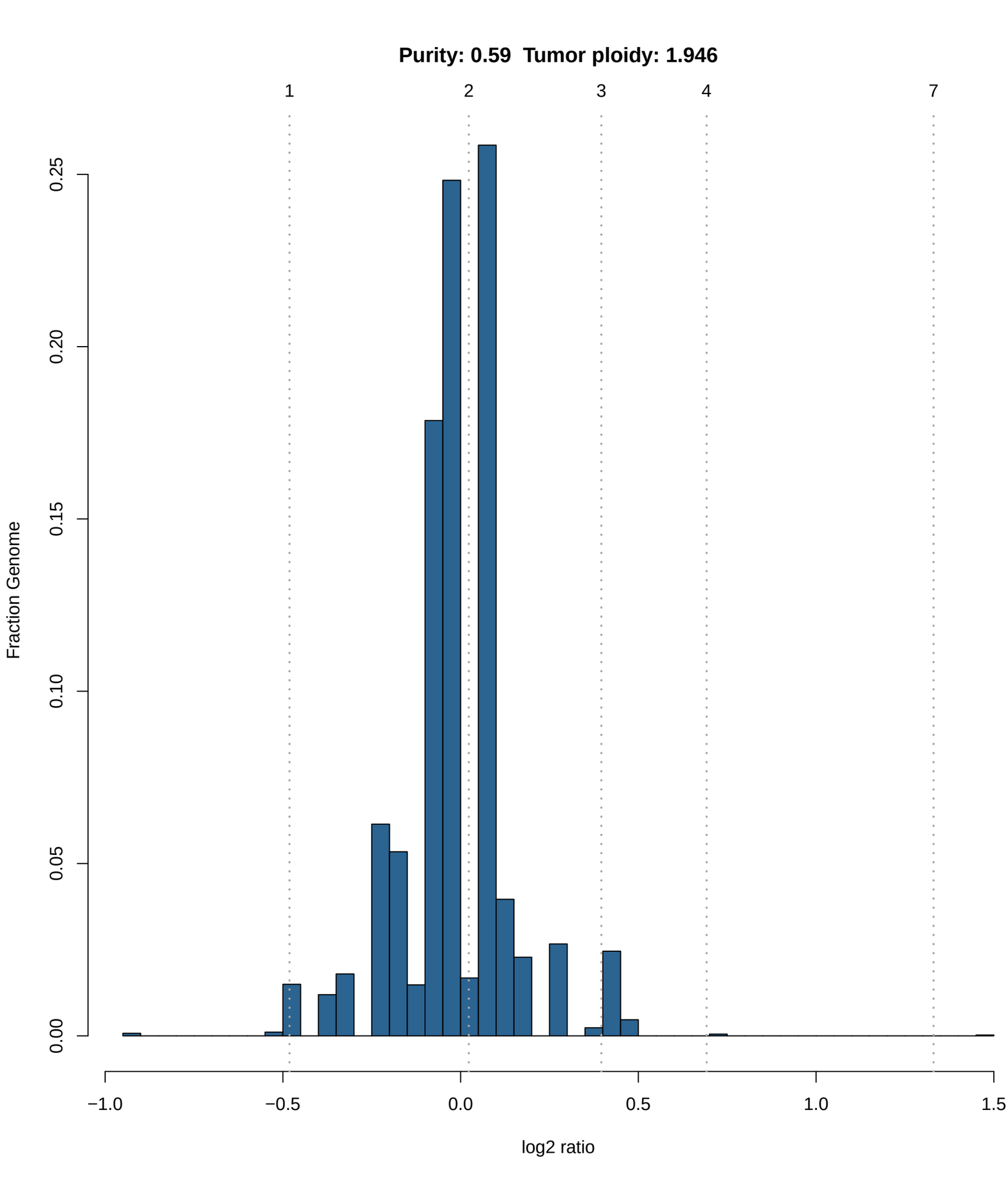

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100
SNV Index

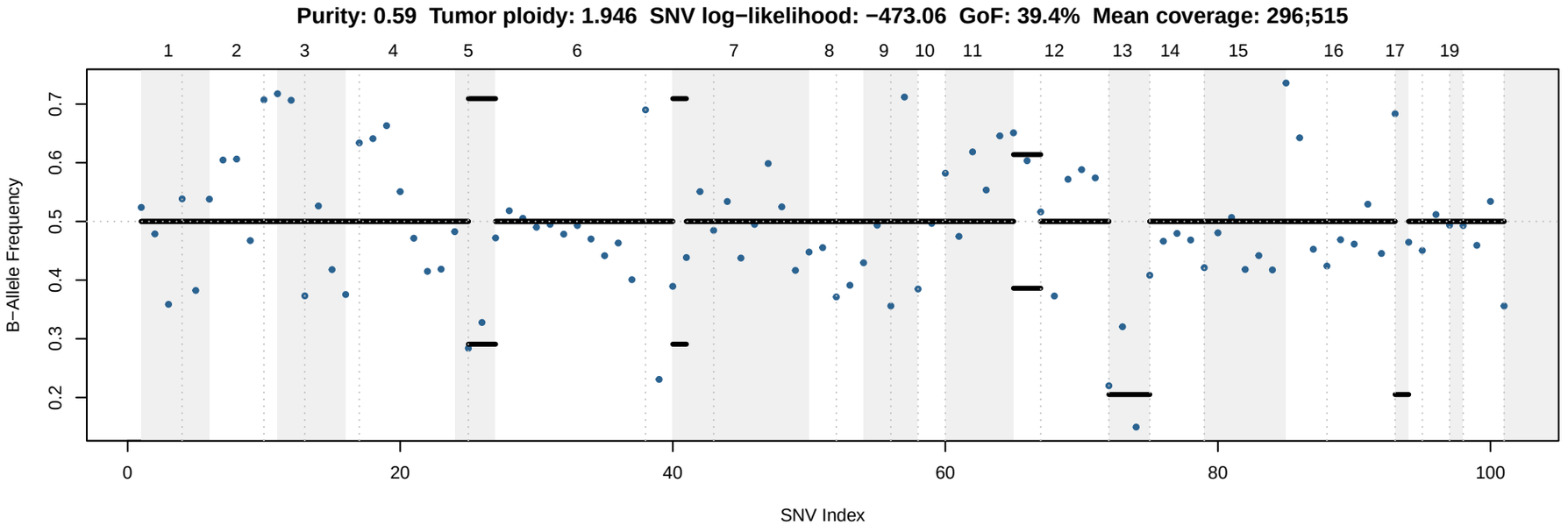

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
2m1
3m1
2m0

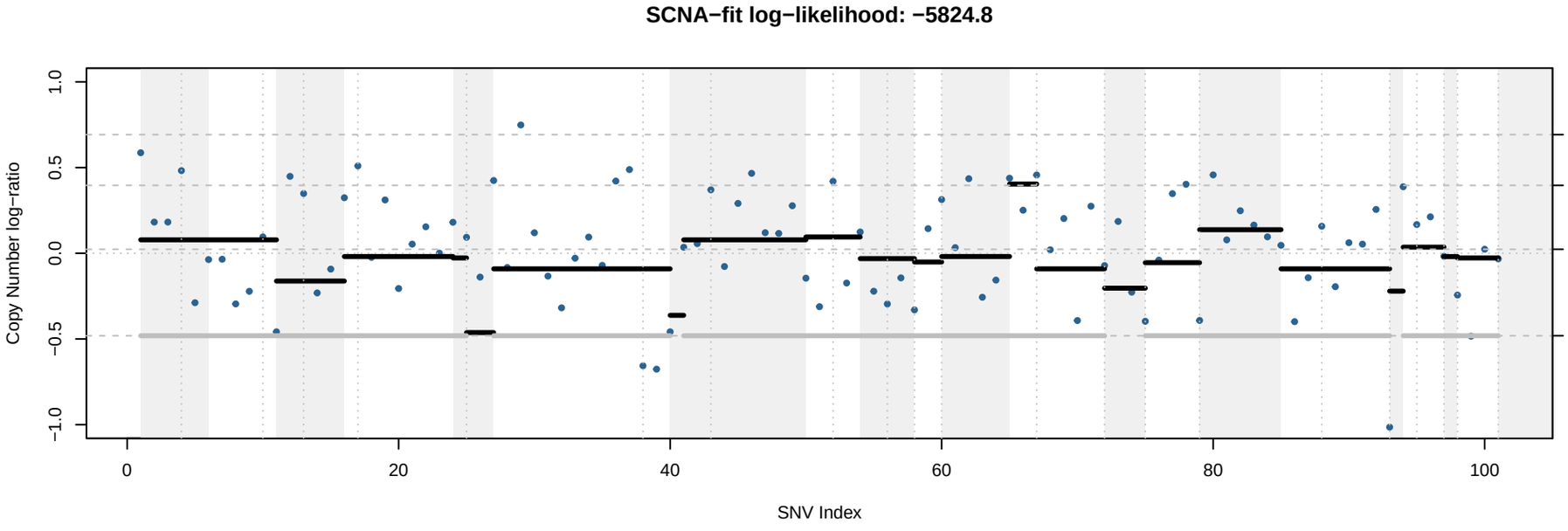

Coverage (log2)
Allelic fraction

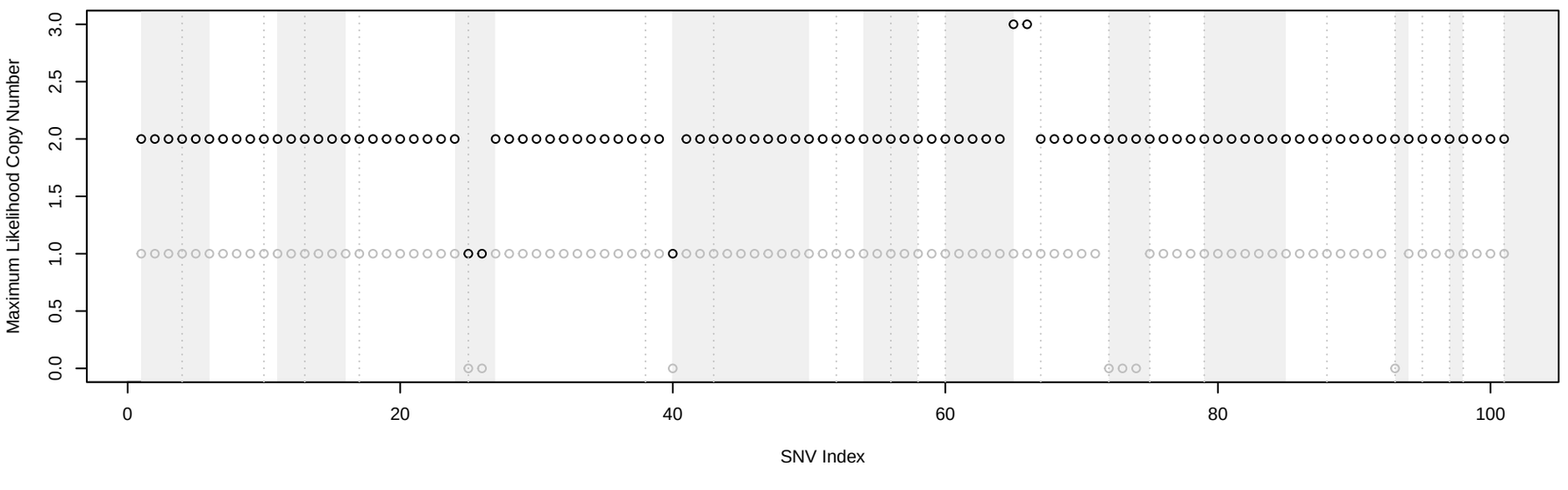

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m1
3m1
4m1

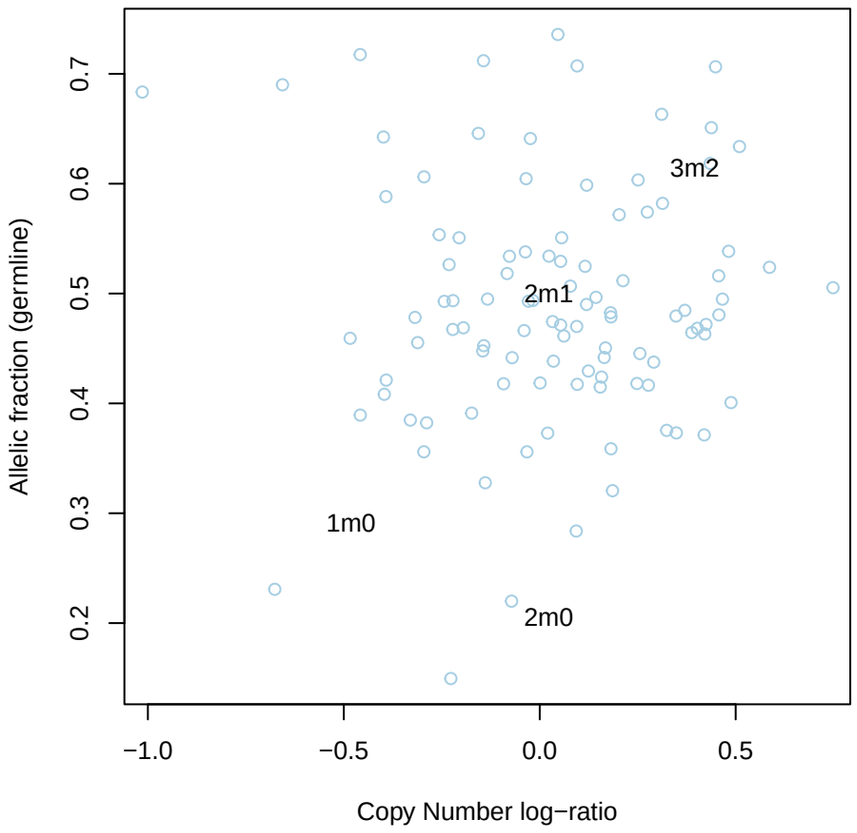

Frequency
Cellular fraction

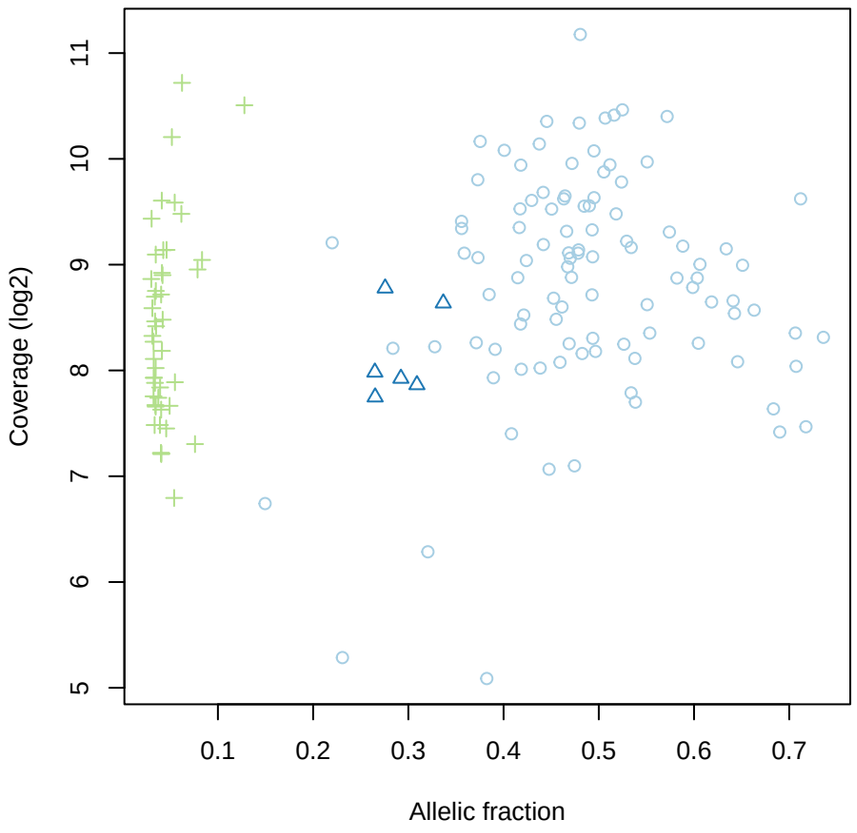

Purity: 0.59 Tumor ploidy: 1.946
1
2
3
4
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

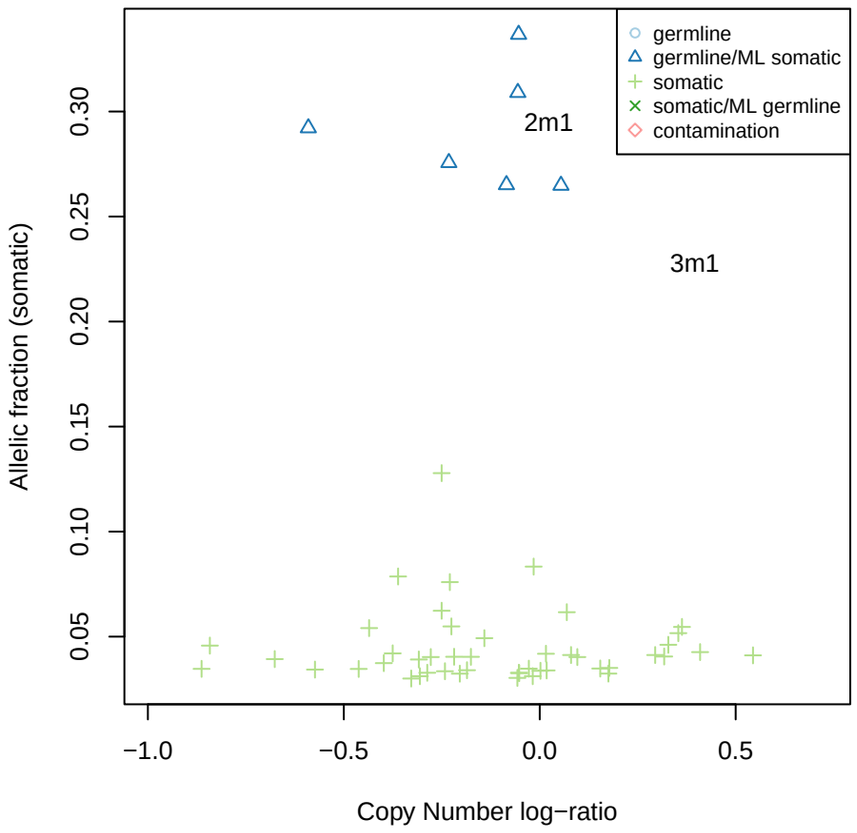

Purity: 0.59 Tumor ploidy: 1.946 SNV log−likelihood: −473.06 GoF: 39.4% Mean coverage: 296;515
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

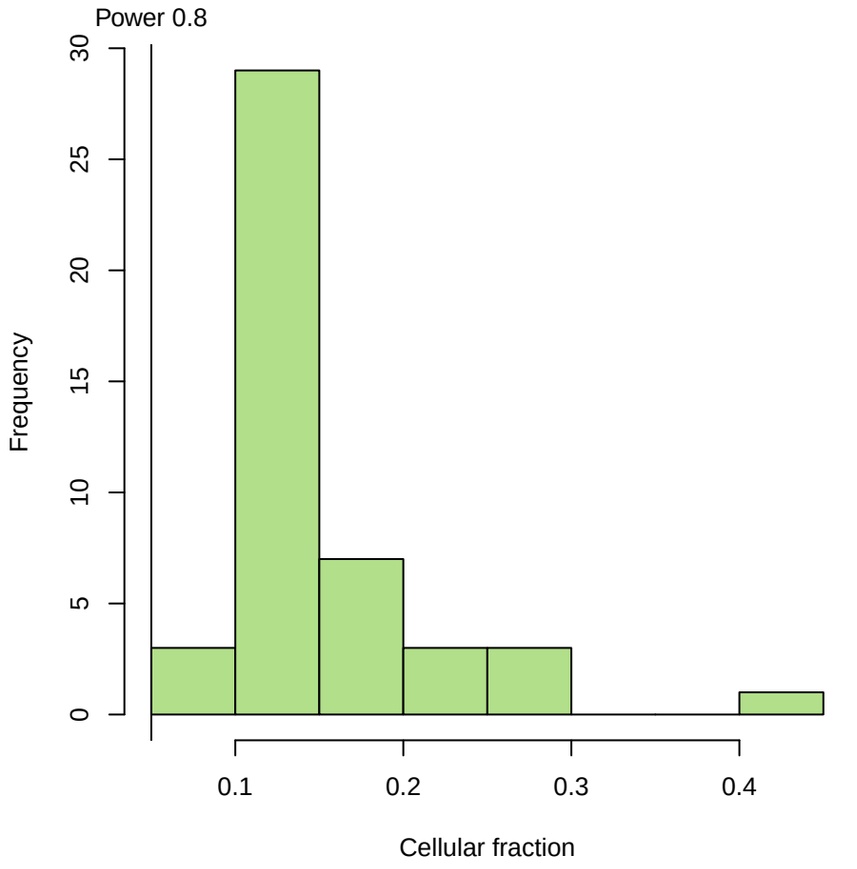

SCNA−fit log−likelihood: −5824.8
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4
0 20 40 60 80 100
SNV Index

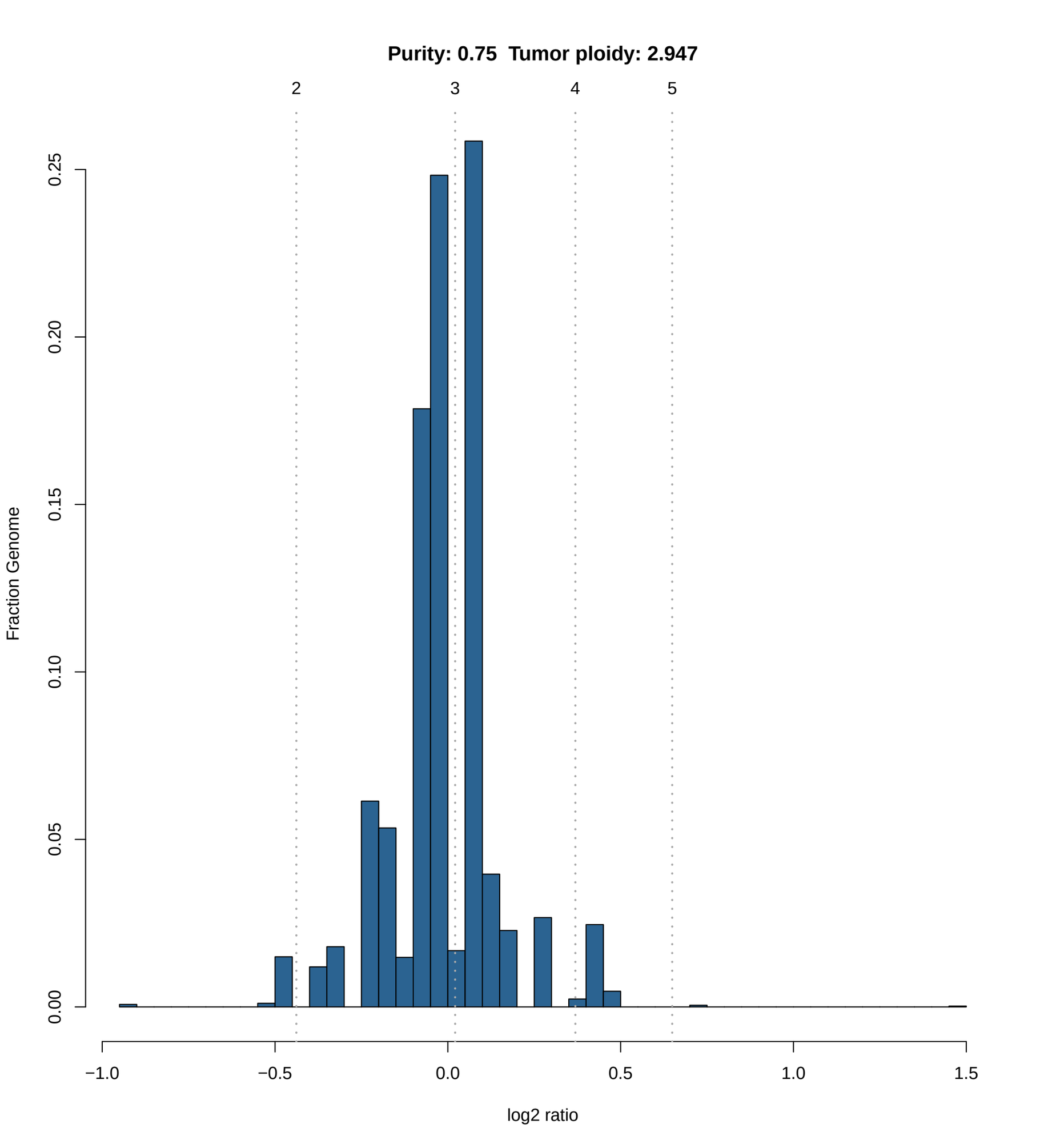

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100
SNV Index

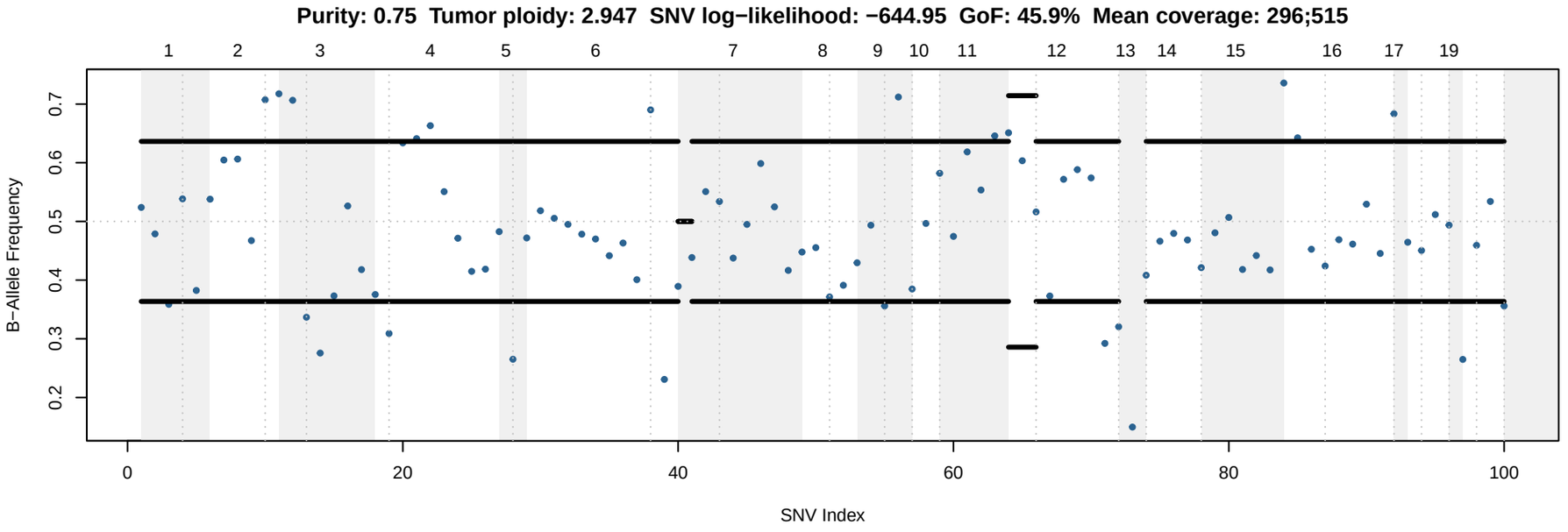

Allelic fraction (germline)
Copy Number log−ratio
3m2
2m1
1m0
2m0

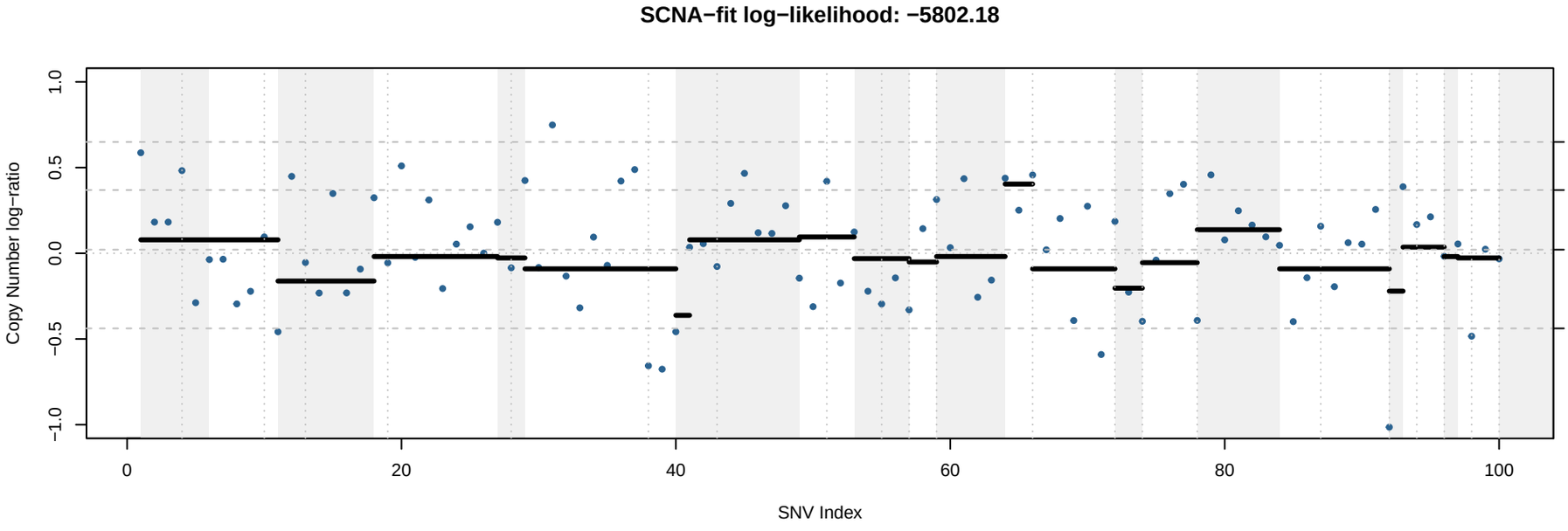

Coverage (log2)
Allelic fraction

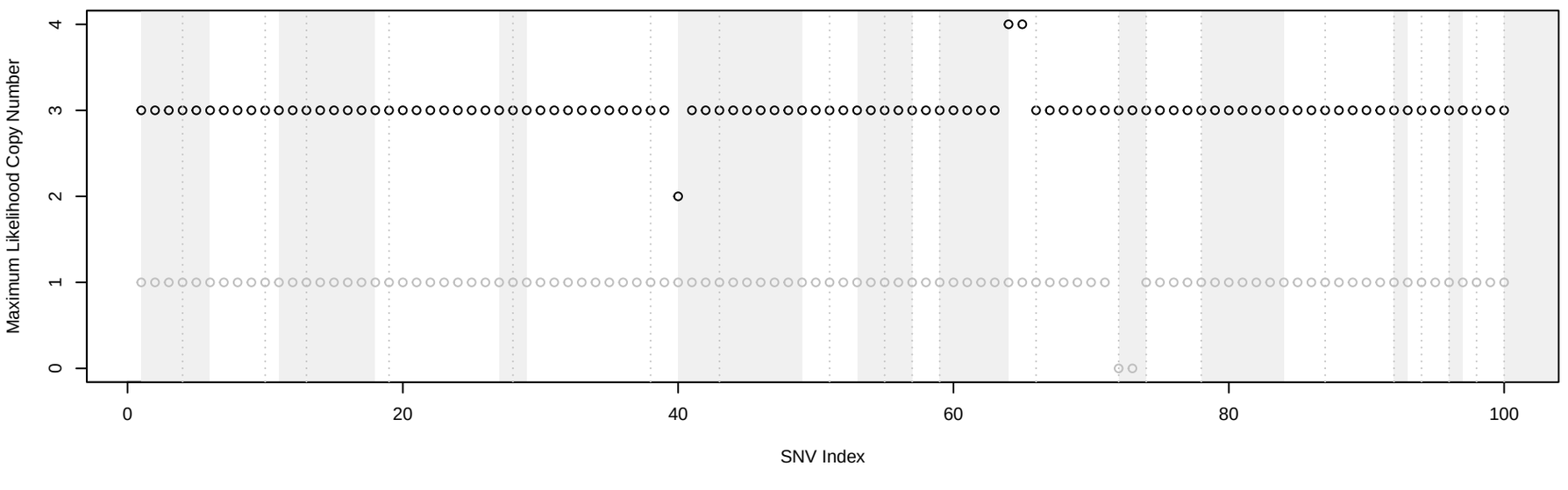

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
Allelic fraction (somatic)
Copy Number log−ratio

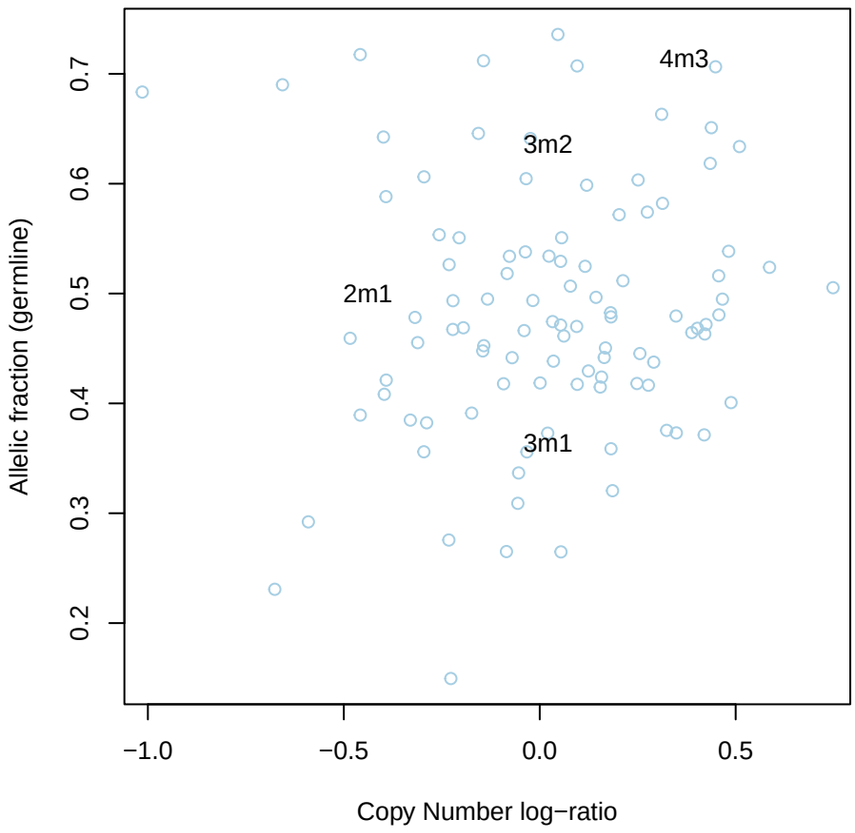

Power 0.8
Frequency
Cellular fraction

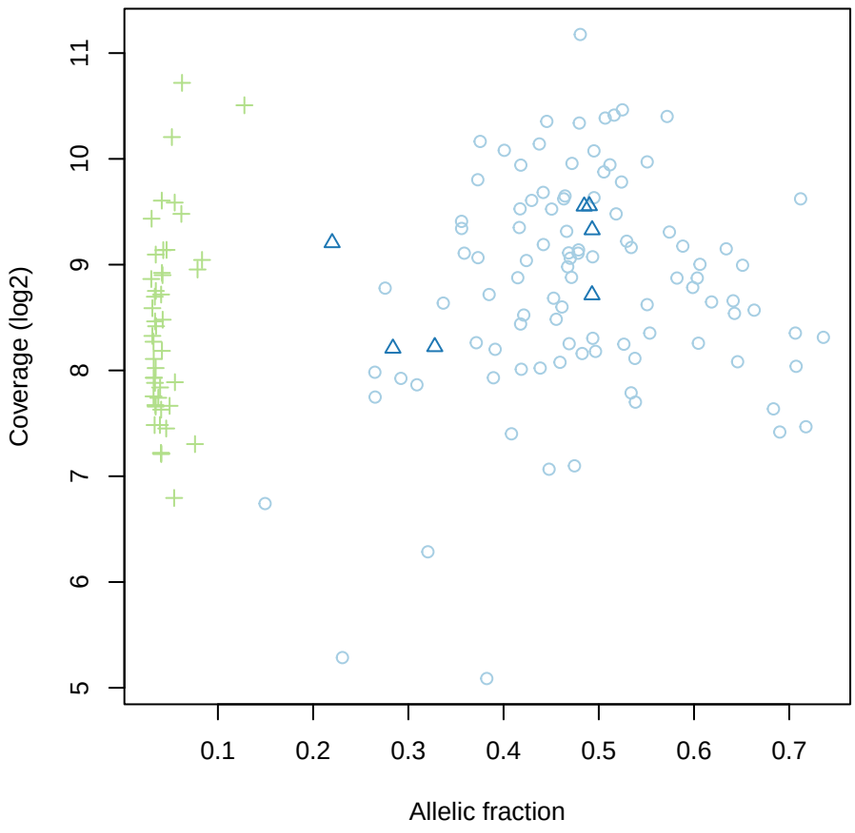

Purity: 0.75 Tumor ploidy: 2.947
2
3
4
5
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

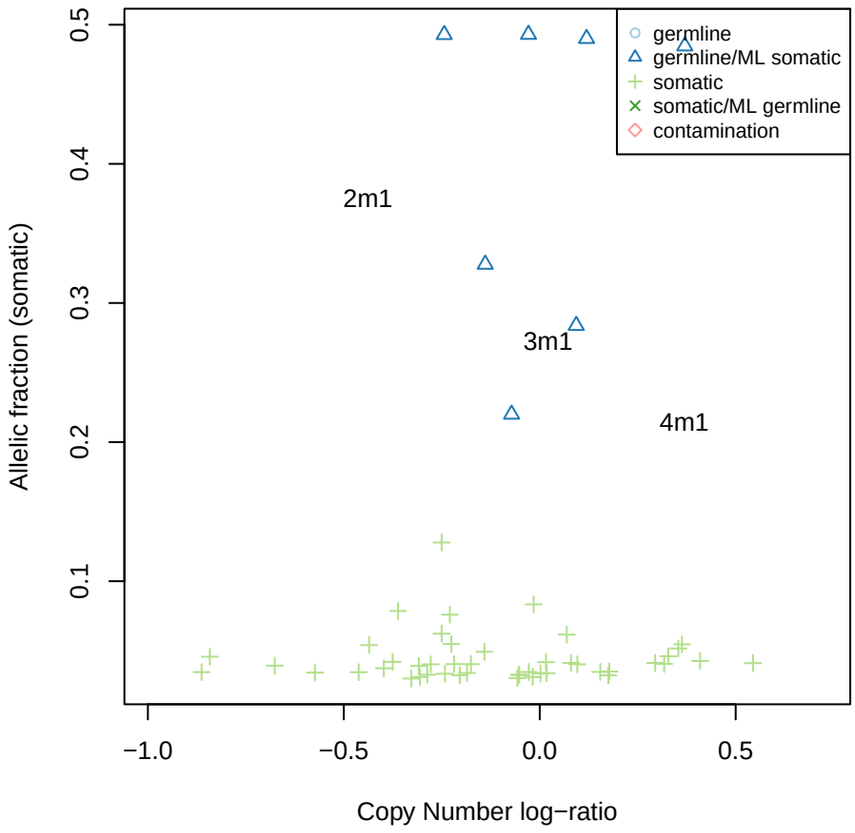

Purity: 0.75 Tumor ploidy: 2.947 SNV log−likelihood: −644.95 GoF: 45.9% Mean coverage: 296;515
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

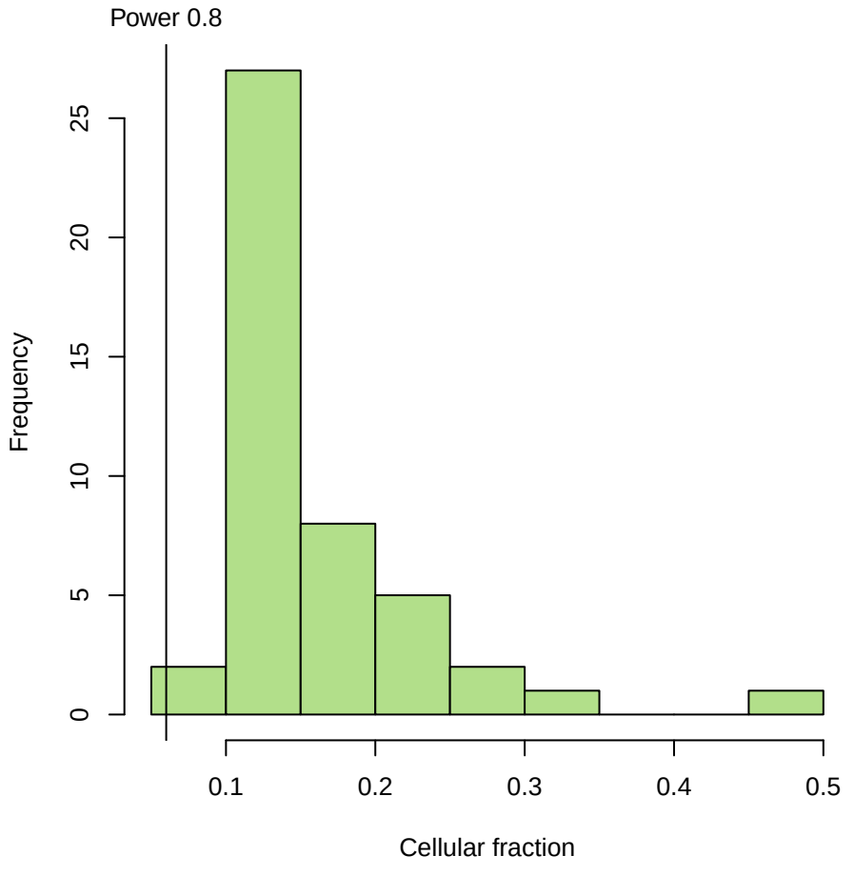

SCNA−fit log−likelihood: −5802.18
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5
0 20 40 60 80 100
SNV Index


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


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


Coverage (log2)
Allelic fraction


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


Power 0.8
Frequency
Cellular fraction