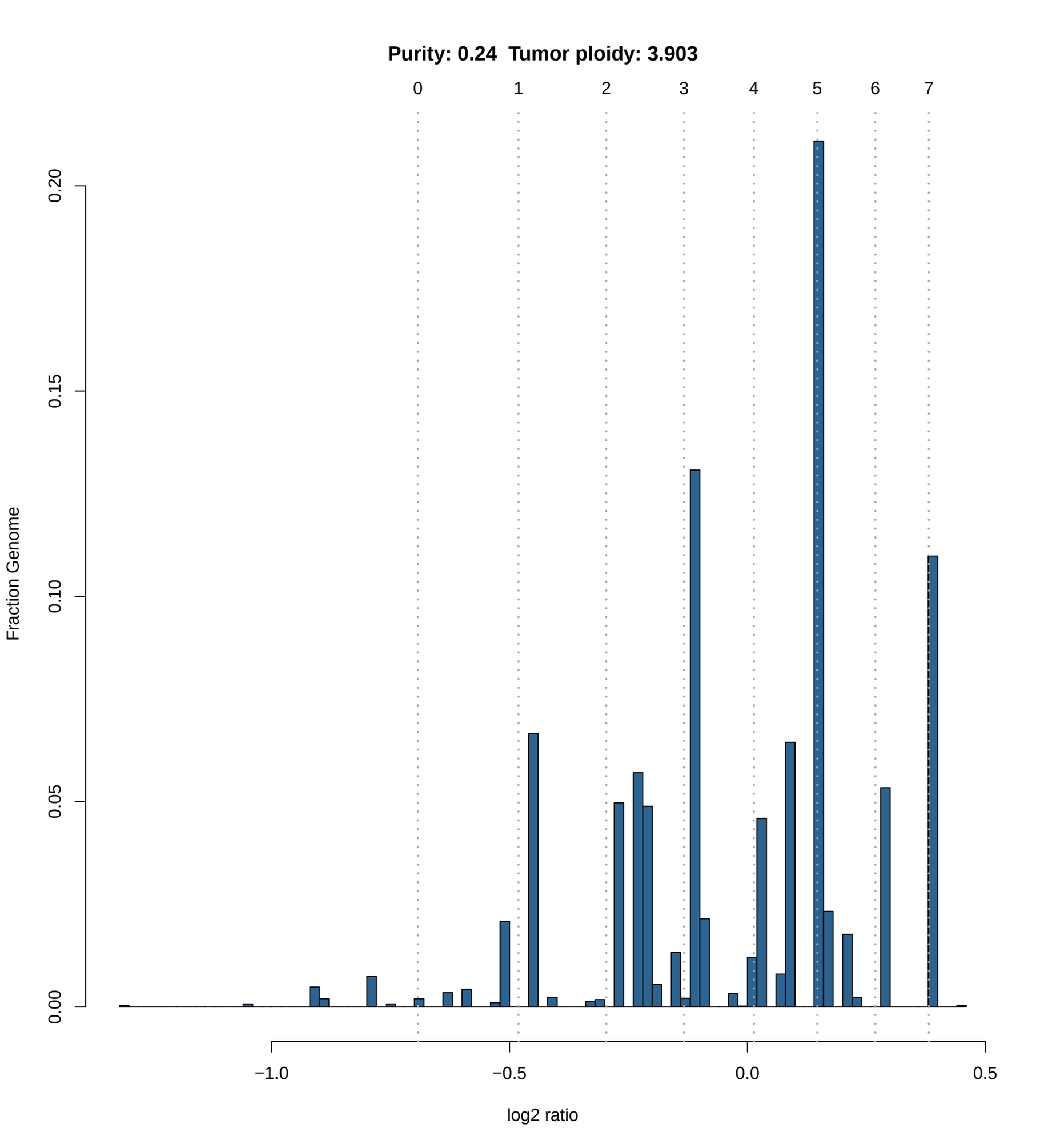
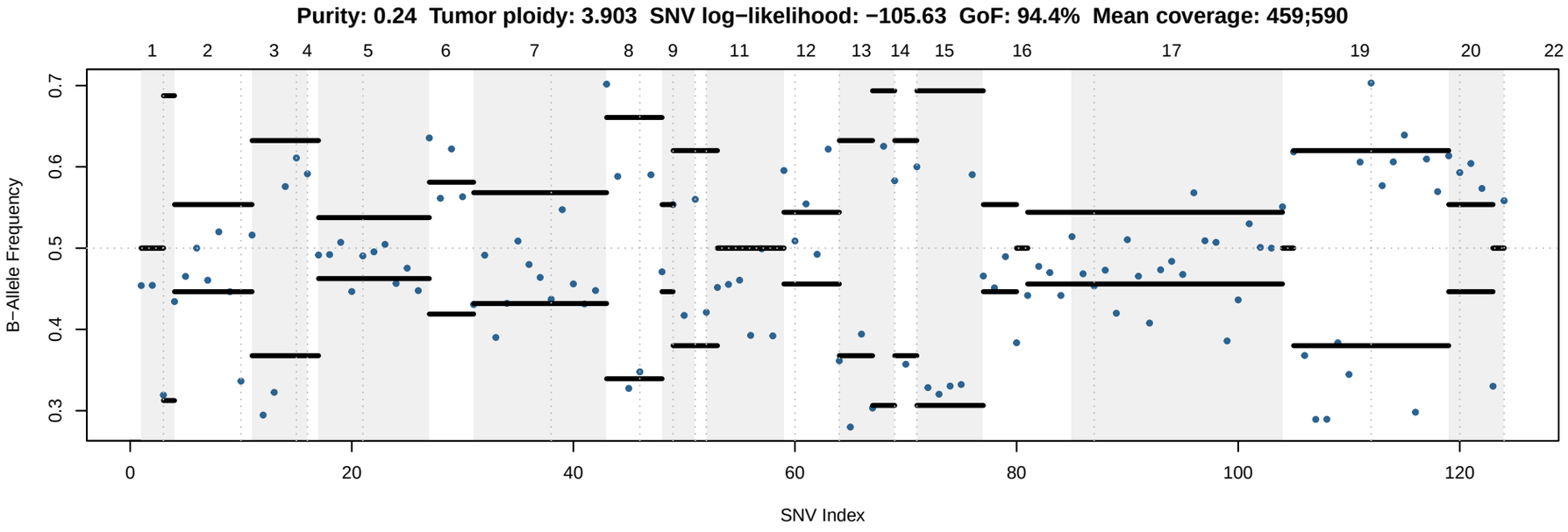
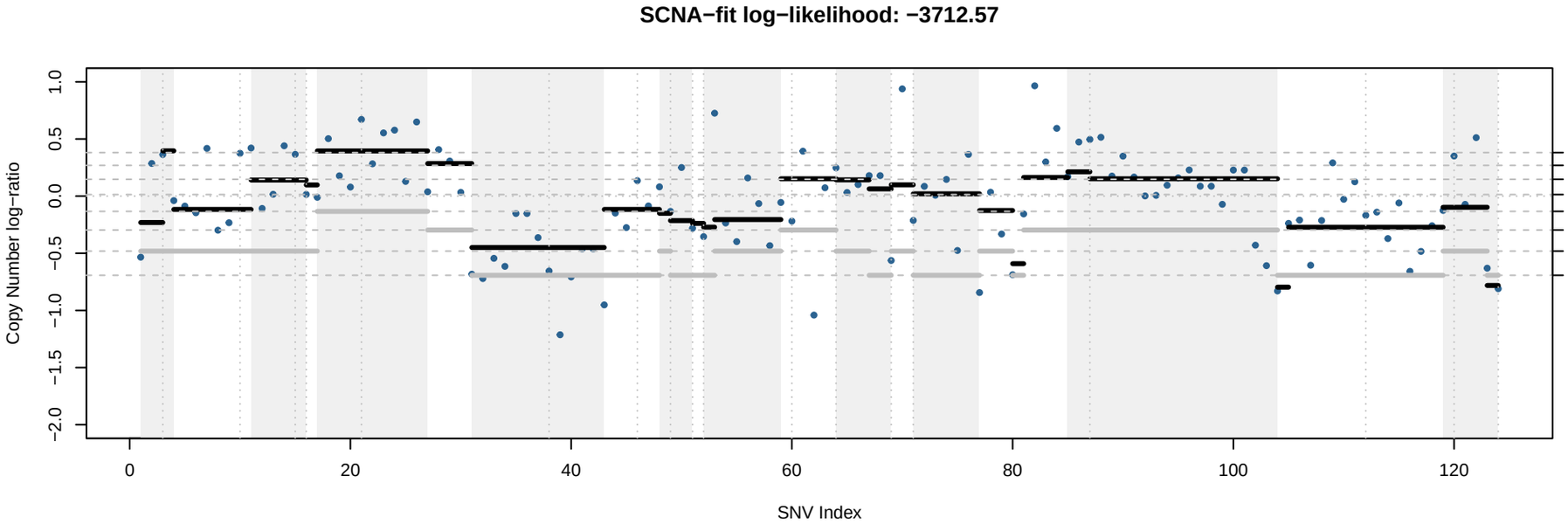
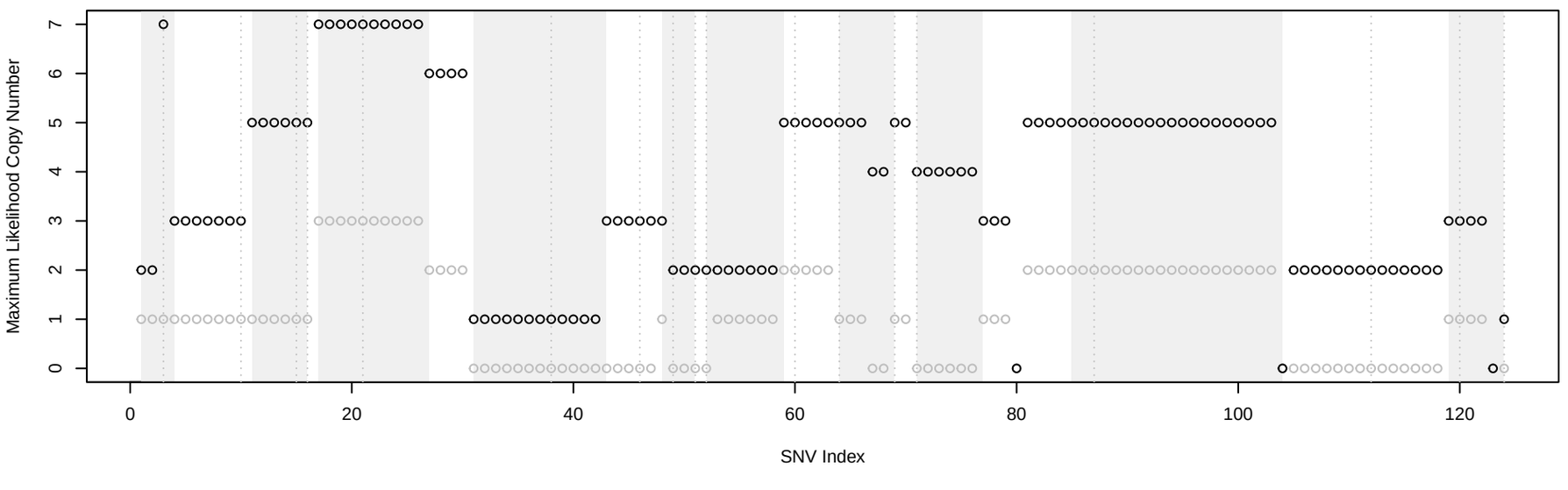
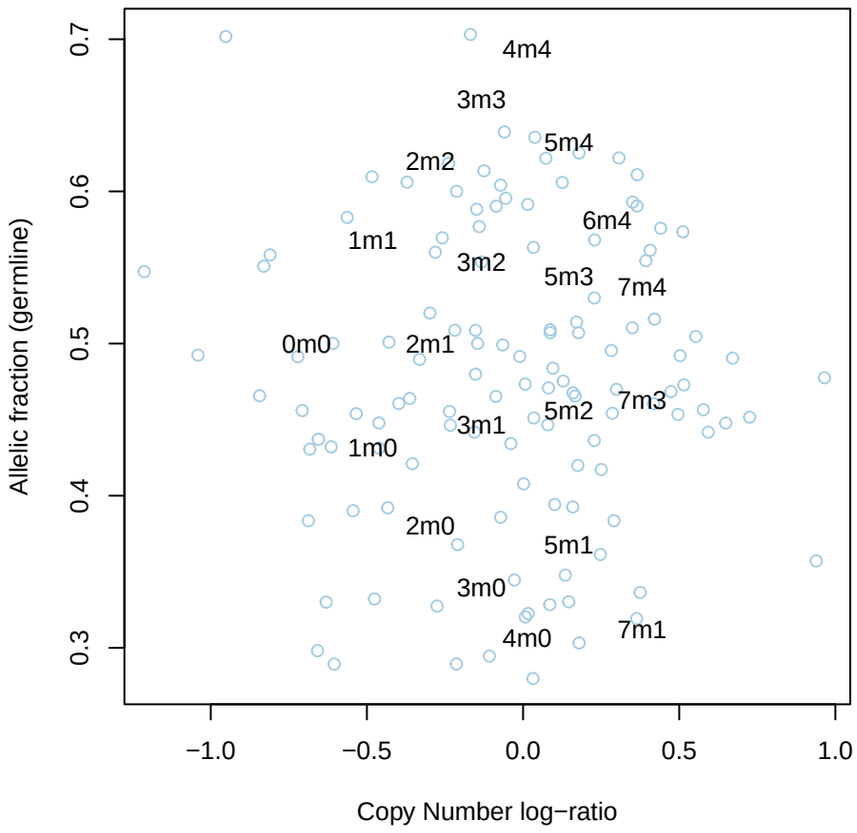
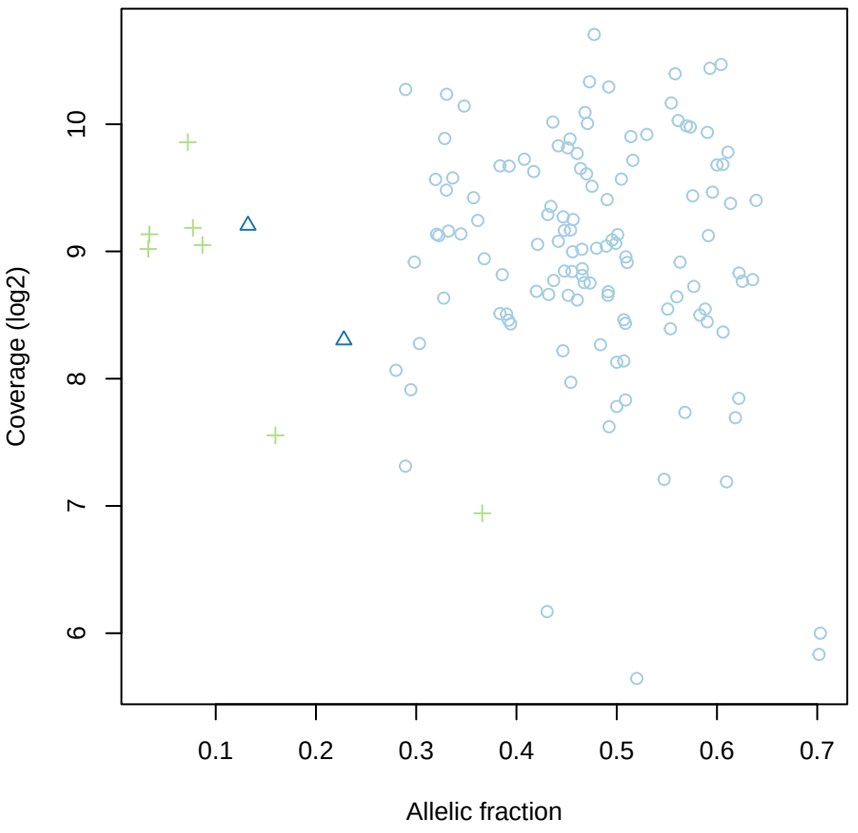

Purity: 0.24  Tumor ploidy: 3.903
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

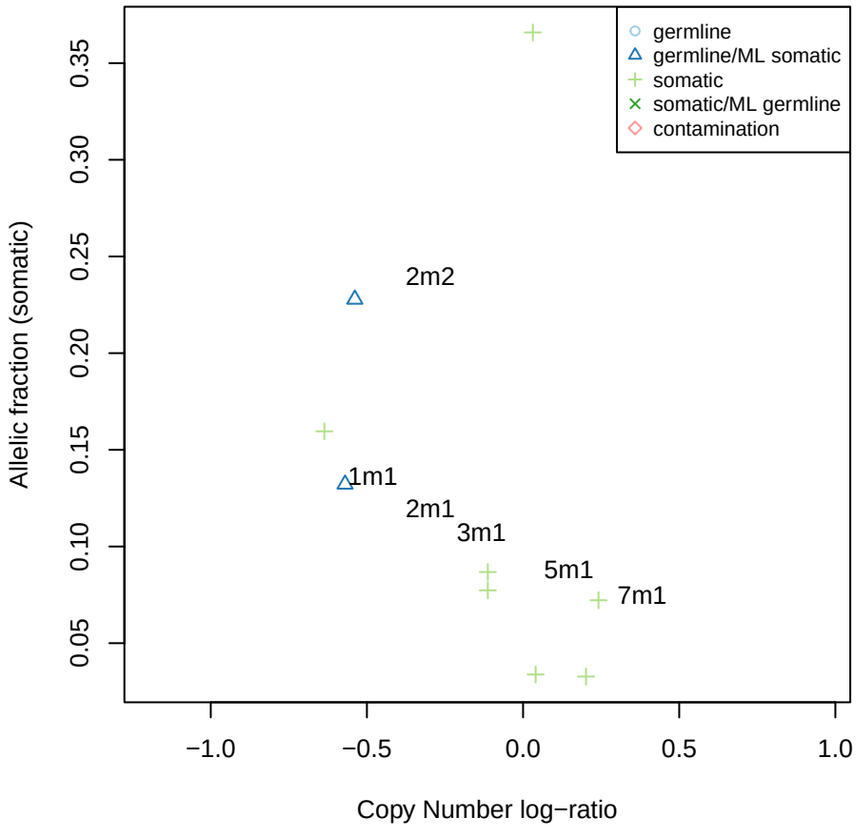

Purity: 0.24 Tumor ploidy: 3.903 SNV log−likelihood: −105.63 GoF: 94.4% Mean coverage: 459;590
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20 22
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

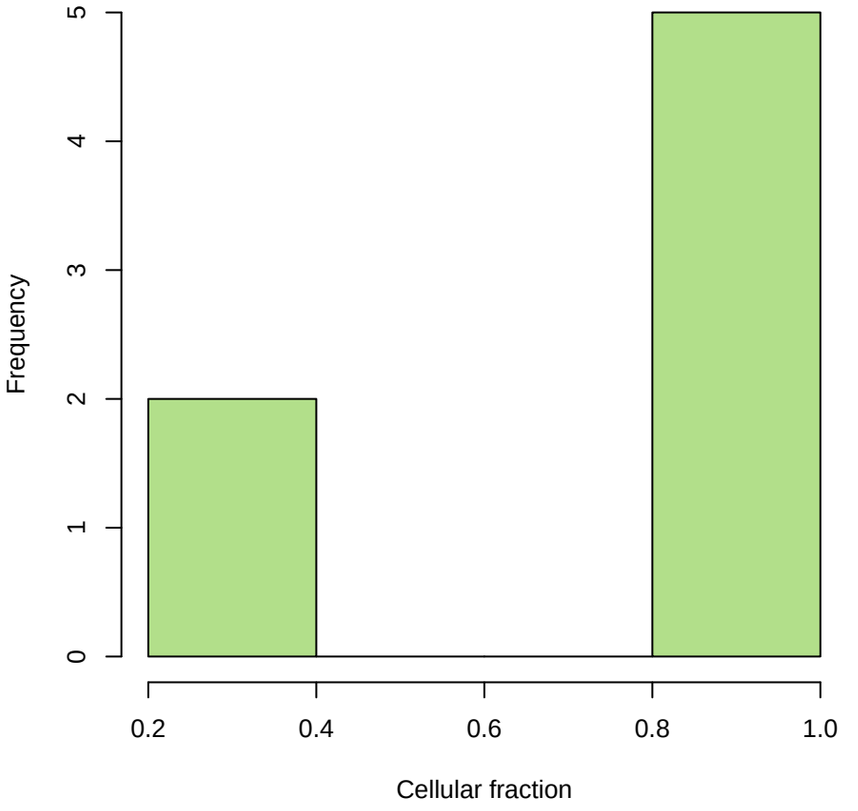

SCNA−fit log−likelihood: −3712.57
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 2 4 6
0 20 40 60 80 100 120
SNV Index

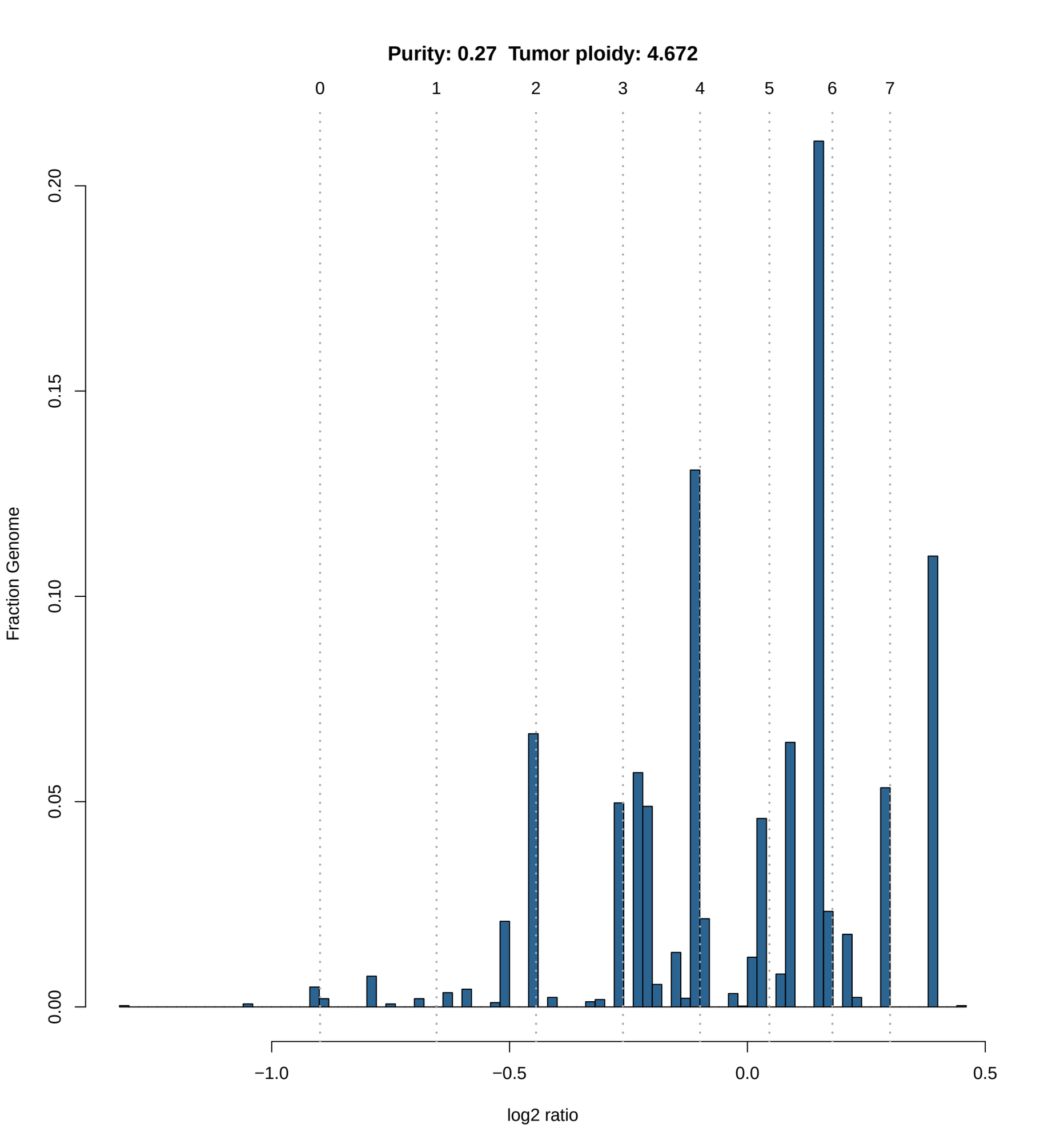

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

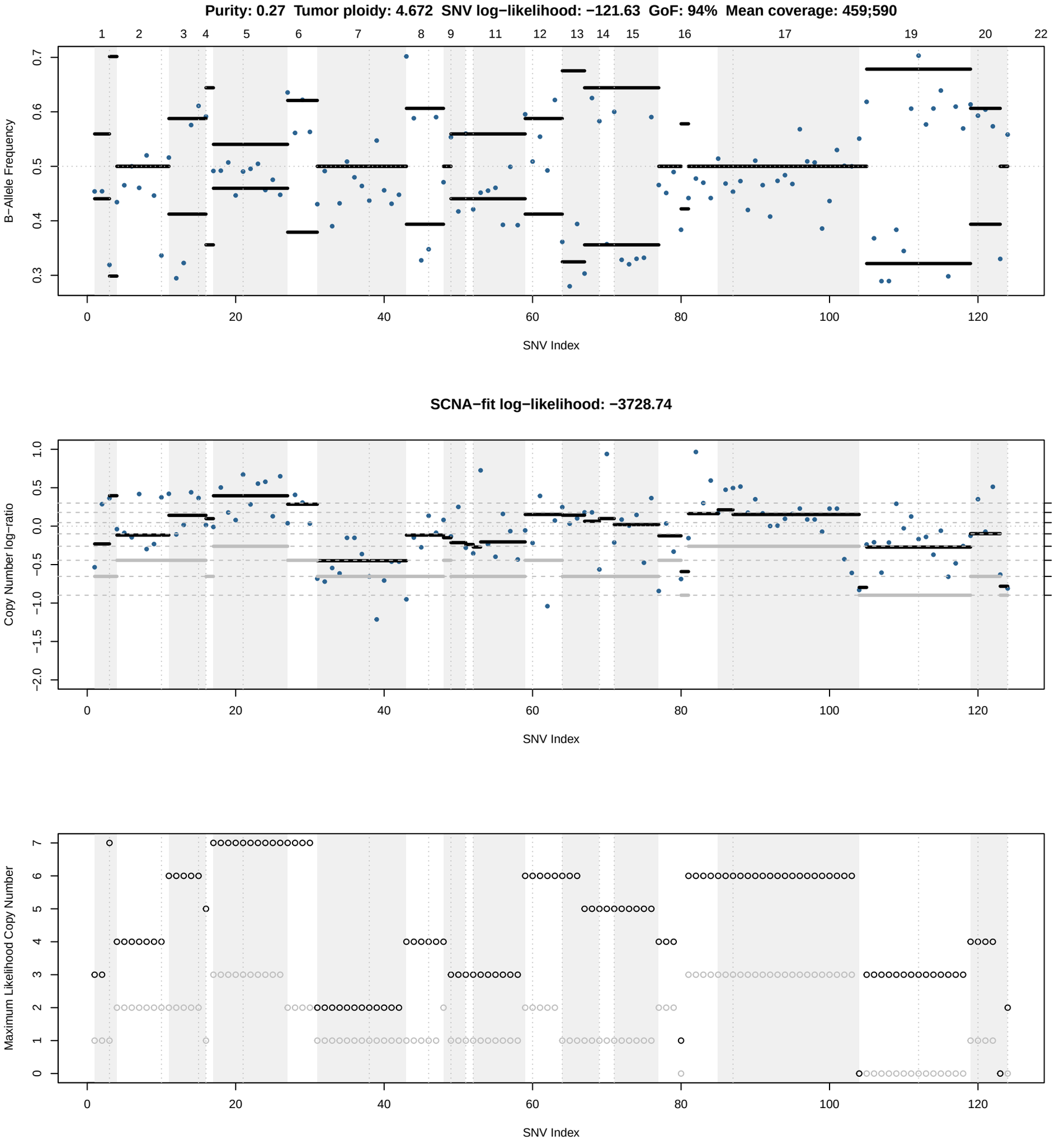

Allelic fraction (germline)
Copy Number log−ratio
4m4
3m3
5m4
2m2
6m4
1m1
3m2
5m3
7m4
0m0
2m1
7m3
5m2
3m1
1m0
2m0
5m1
3m0
7m1
4m0

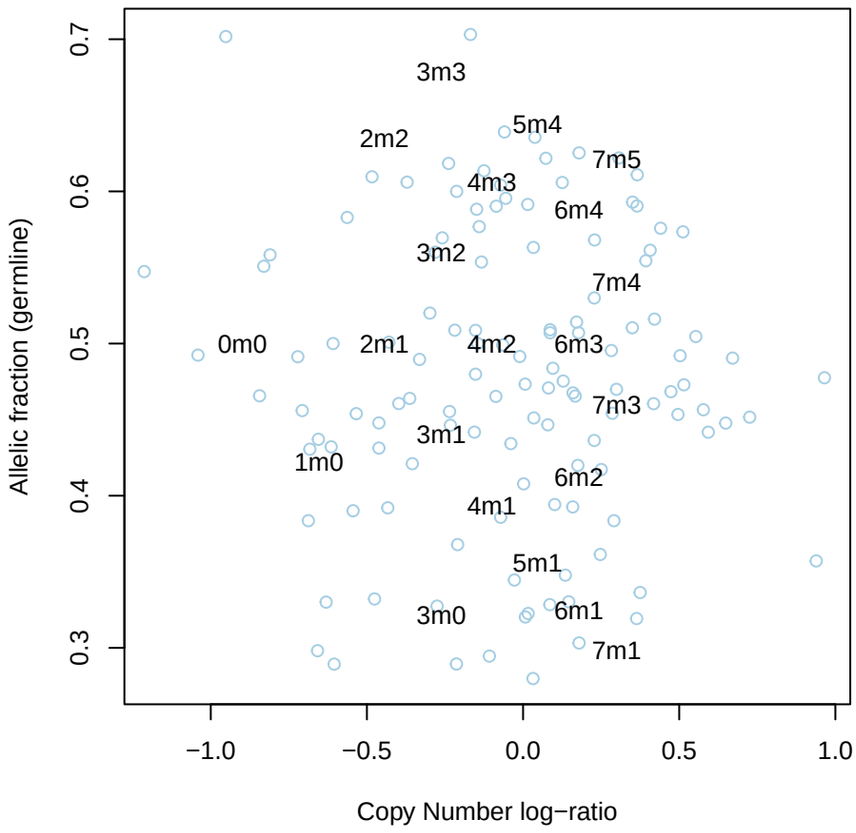

Coverage (log2)
Allelic fraction

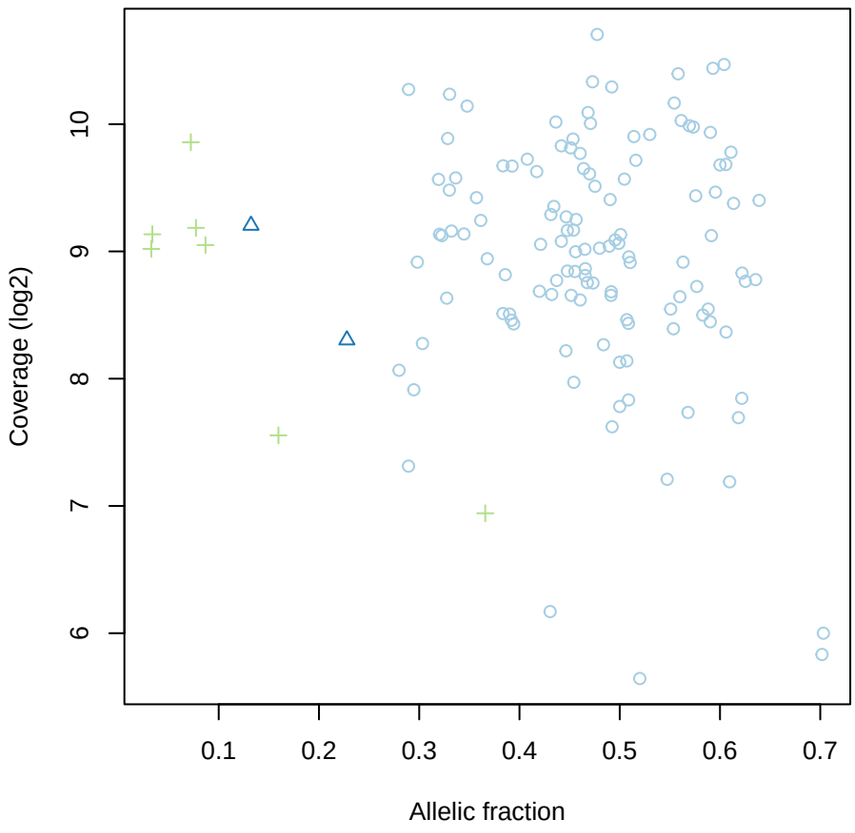

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m2
1m1
2m1
3m1
5m1
7m1

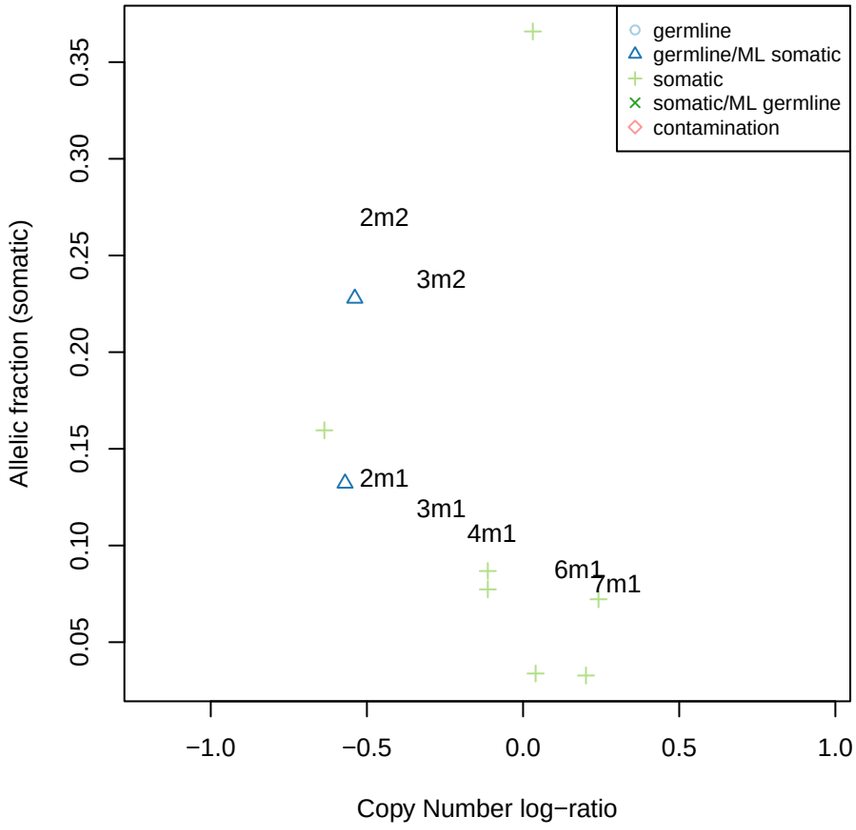

Frequency
Cellular fraction

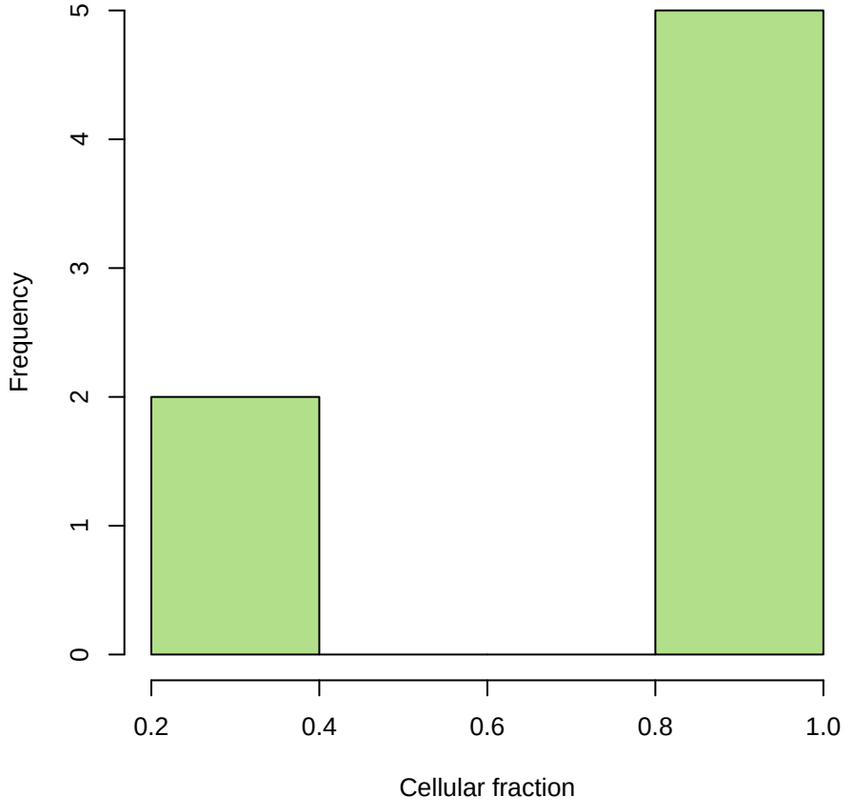

Purity: 0.27  Tumor ploidy: 4.672
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

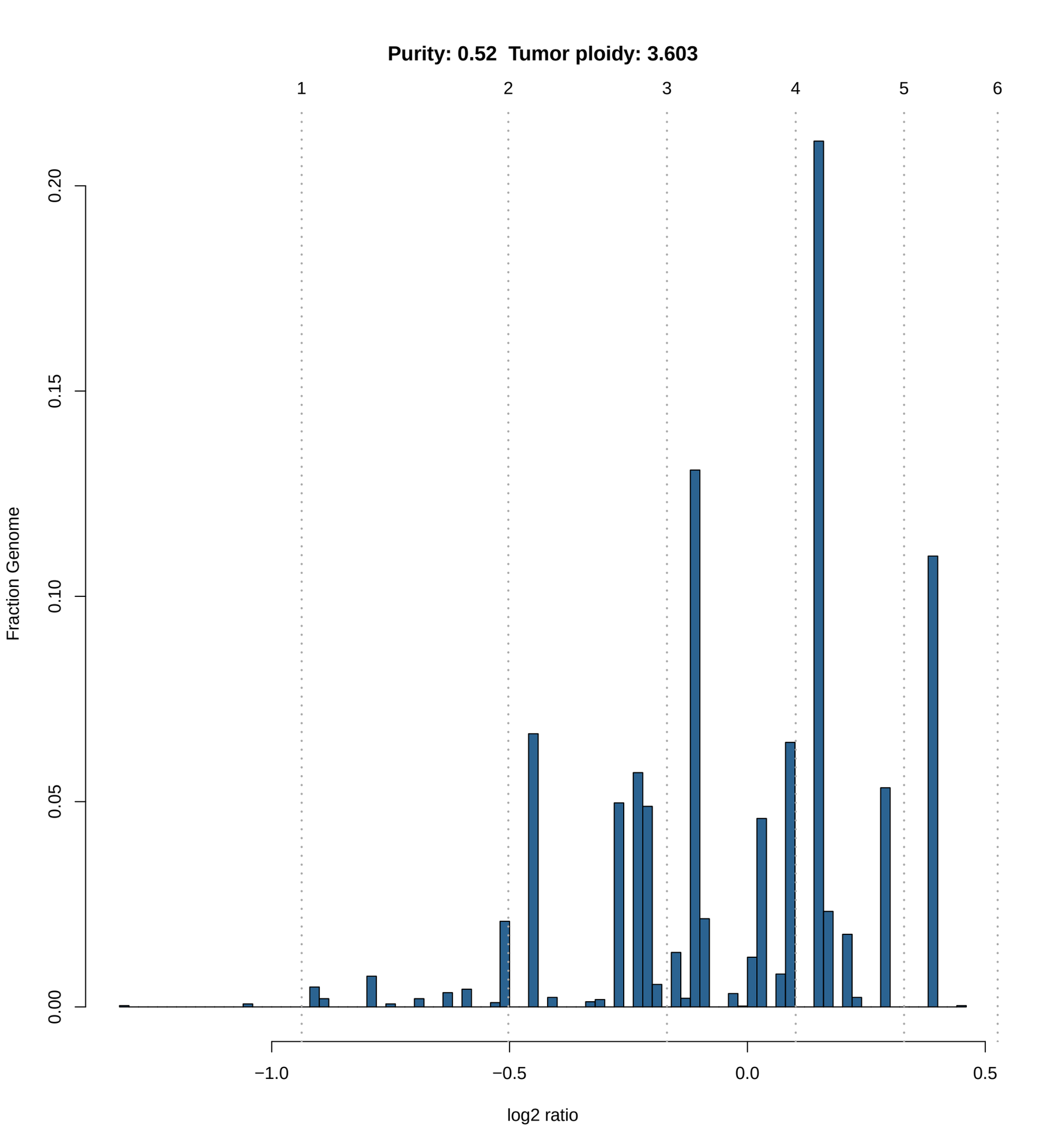

Purity: 0.27 Tumor ploidy: 4.672 SNV log−likelihood: −121.63 GoF: 94% Mean coverage: 459;590
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20 22
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index
SCNA−fit log−likelihood: −3728.74
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 3 5 7
0 20 40 60 80 100 120
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

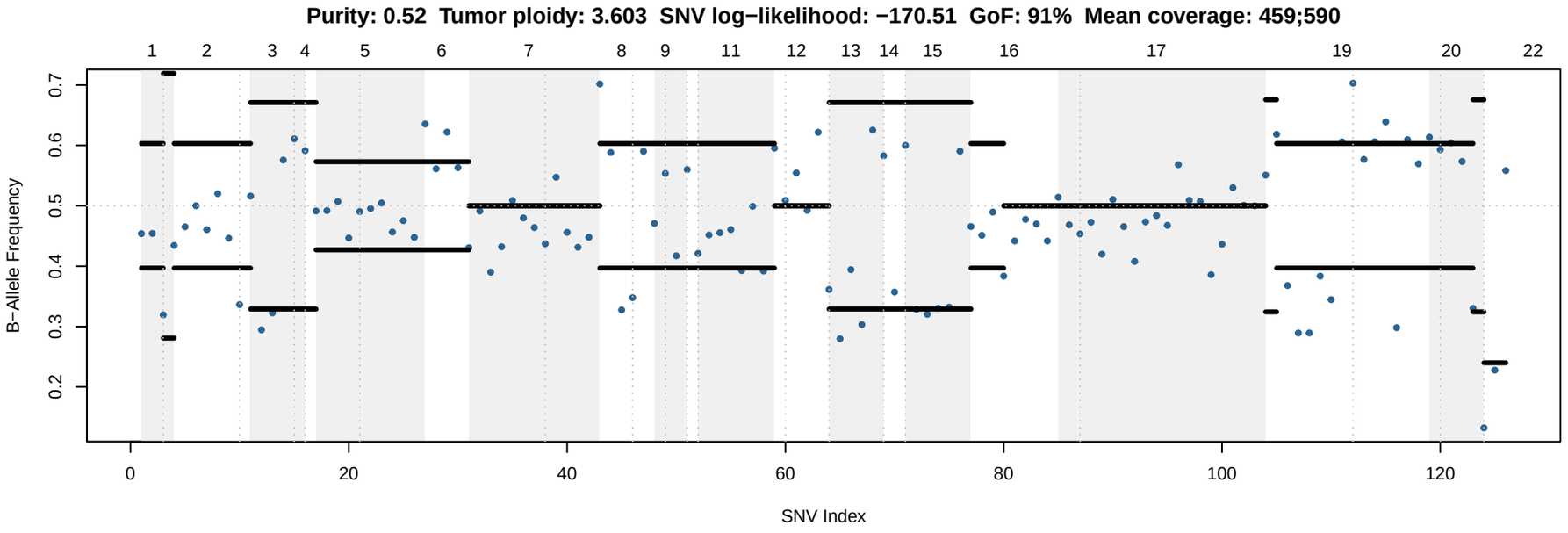

Allelic fraction (germline)
Copy Number log−ratio
3m3
5m4
2m2
7m5
4m3
6m4
3m2
7m4
0m0
2m1
4m2
6m3
7m3
3m1
1m0
6m2
4m1
5m1
3m0
6m1
7m1

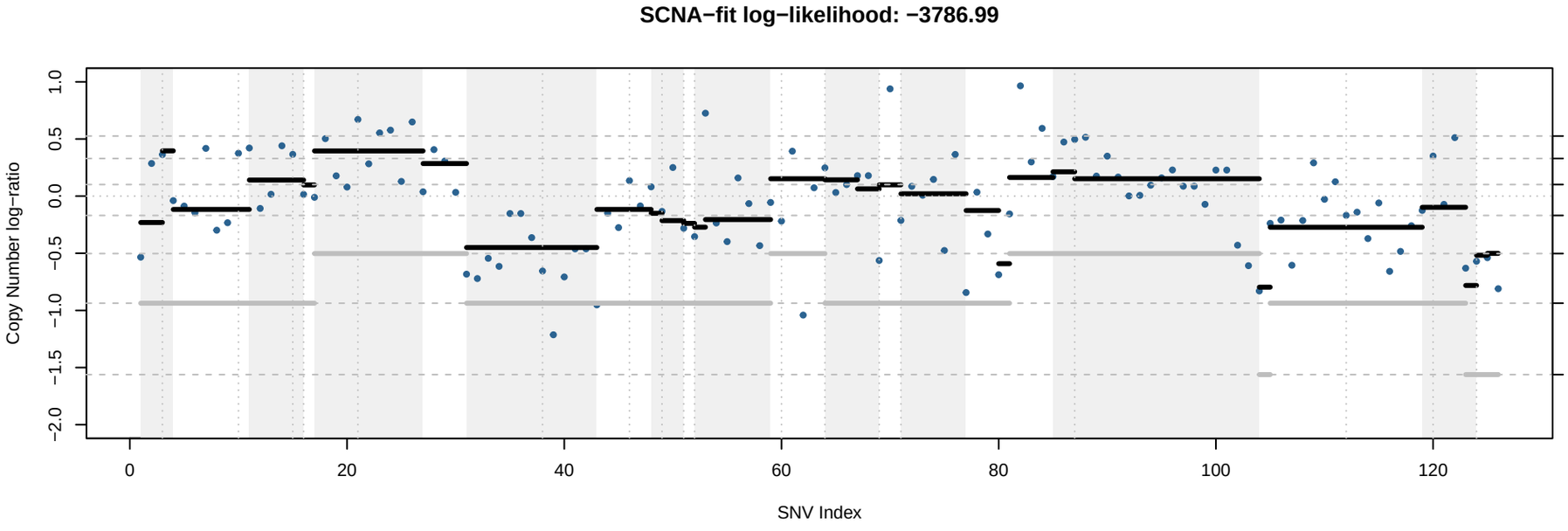

Coverage (log2)
Allelic fraction

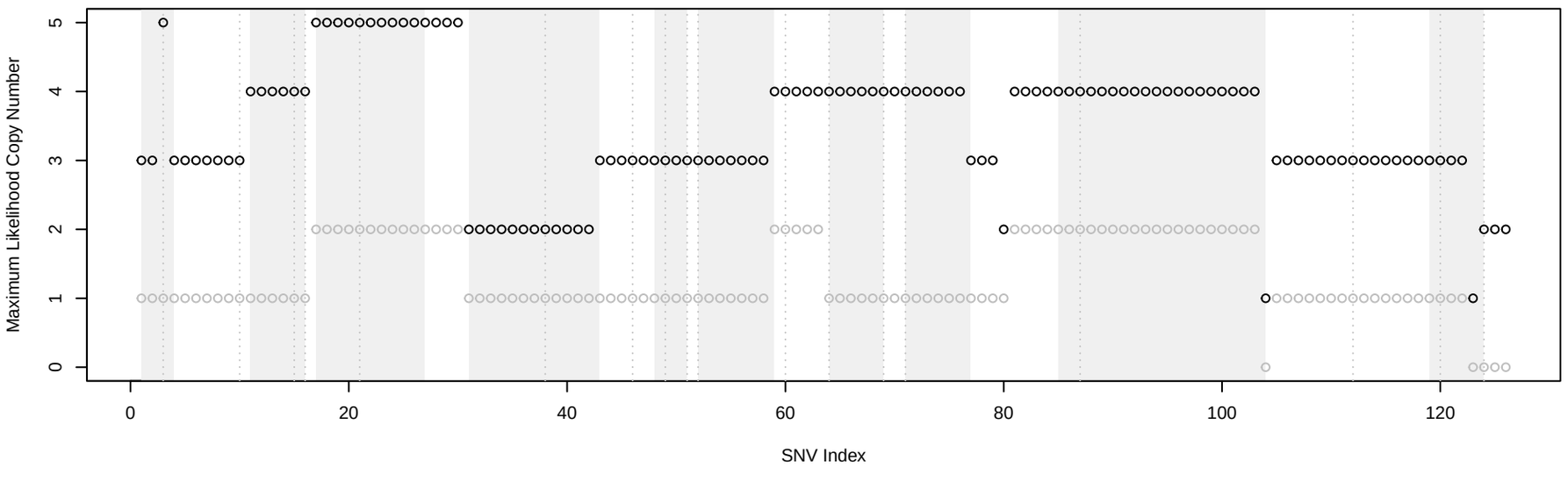

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m2
3m2
2m1
3m1
4m1
6m1
7m1

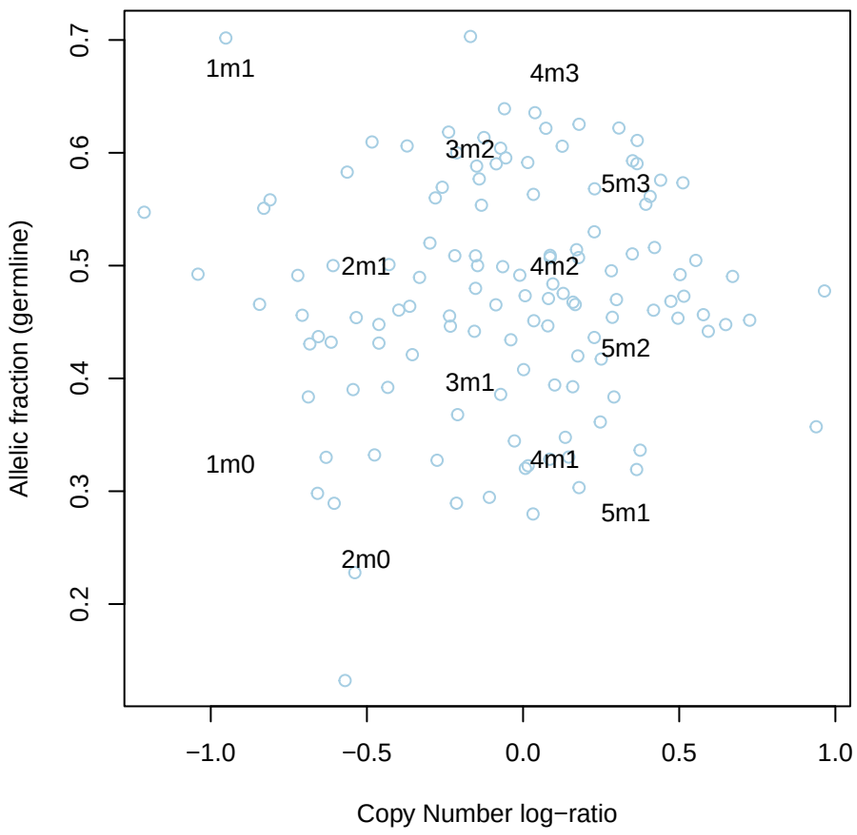

Frequency
Cellular fraction

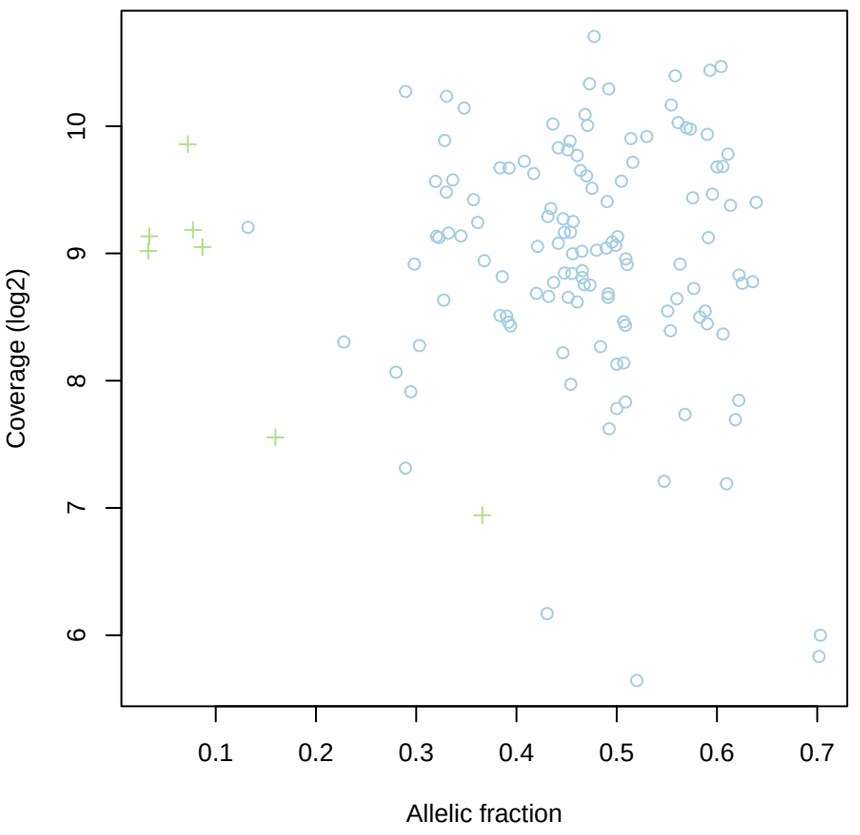

Purity: 0.52  Tumor ploidy: 3.603
1
2
3
4
5
6
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

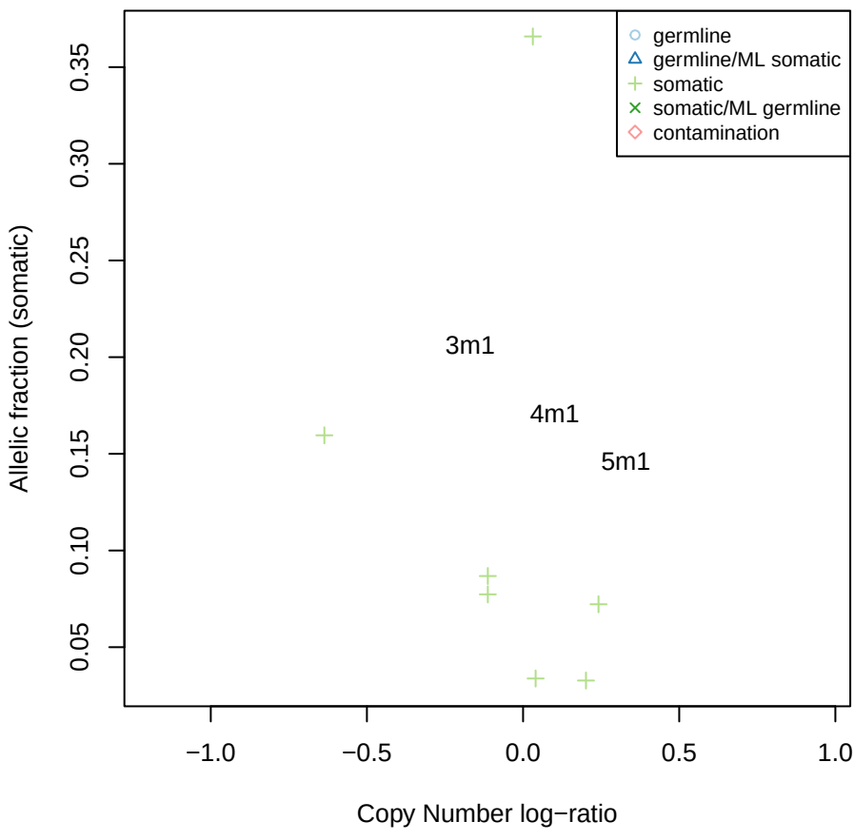

Purity: 0.52 Tumor ploidy: 3.603 SNV log−likelihood: −170.51 GoF: 91% Mean coverage: 459;590
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20 22
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

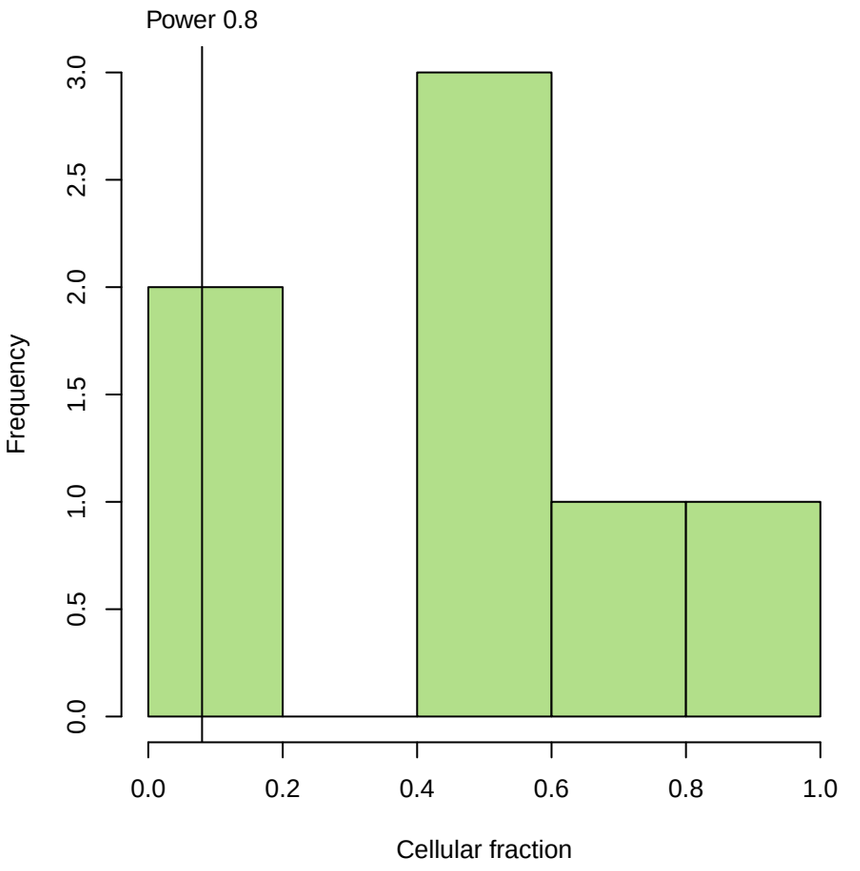

SCNA−fit log−likelihood: −3786.99
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5
0 20 40 60 80 100 120
SNV Index

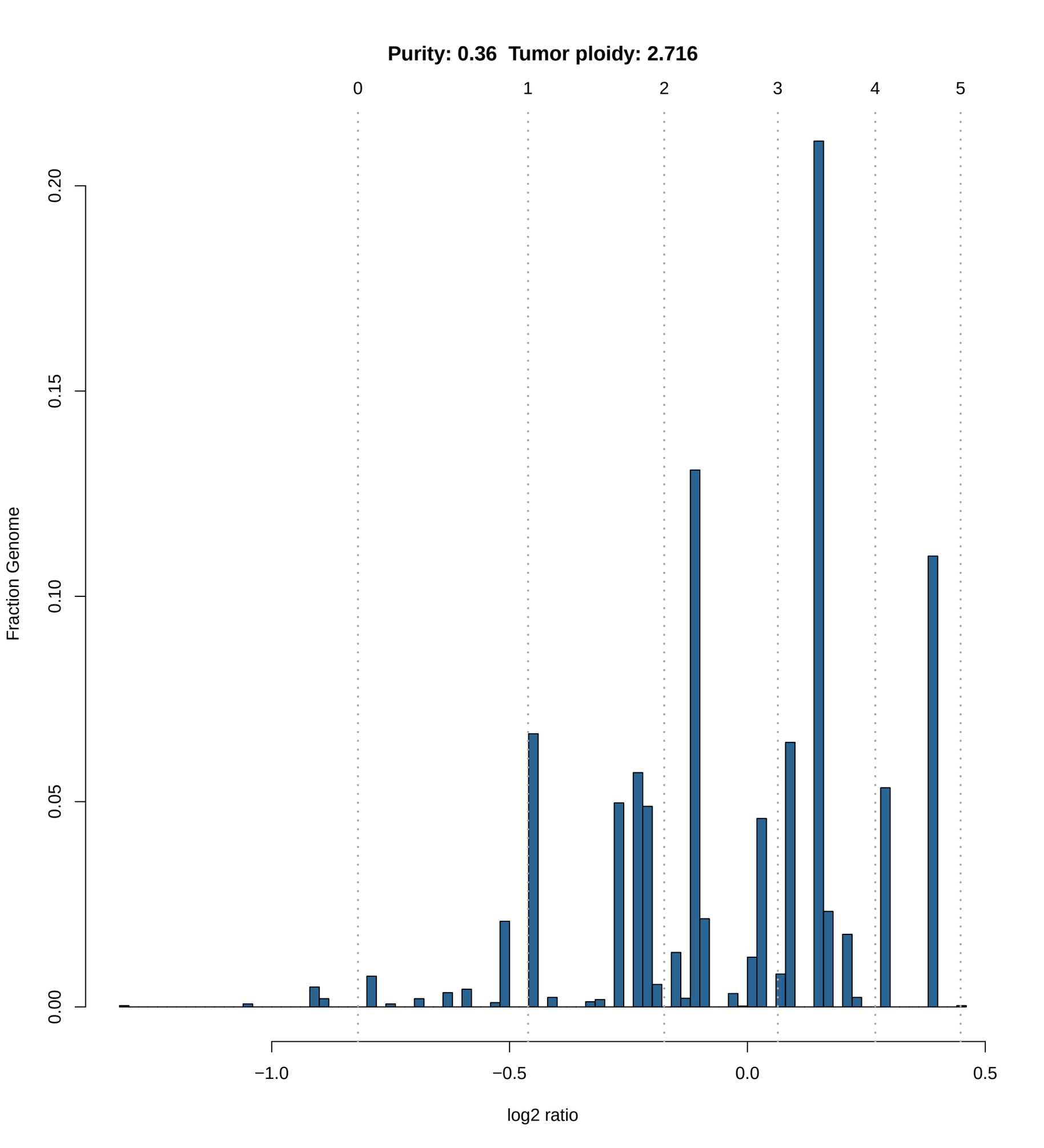

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120
SNV Index

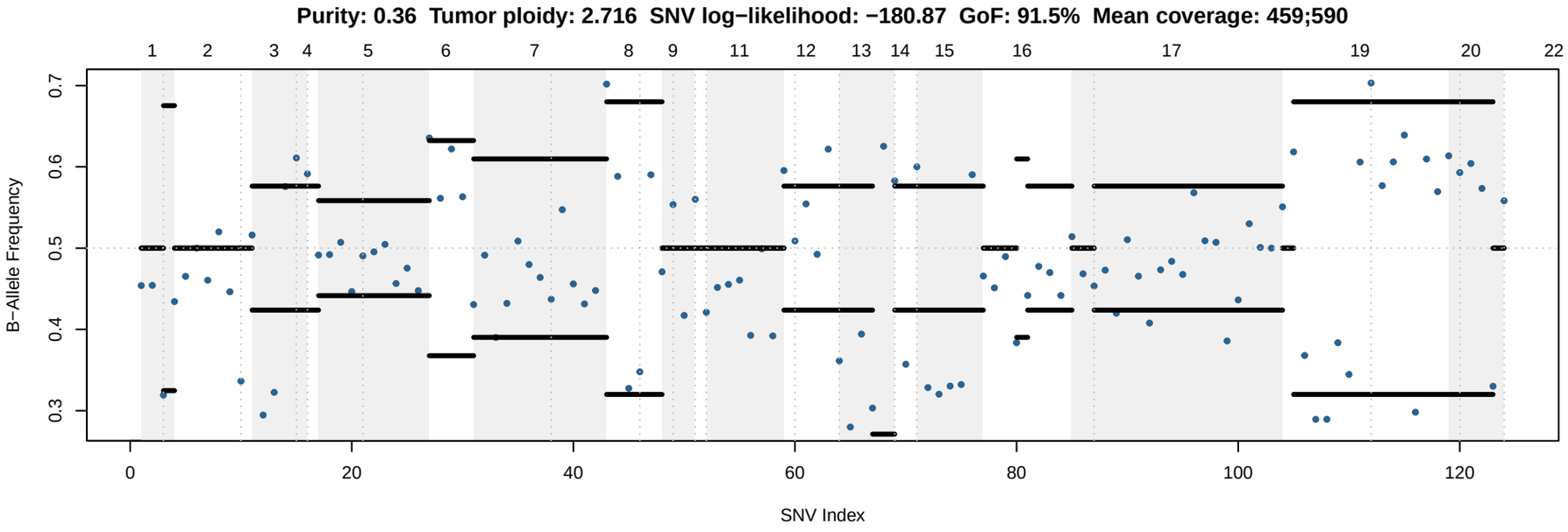

1m1
4m3
3m2
5m3
2m1
4m2
5m2
3m1
1m0
4m1
5m1
2m0
Allelic fraction (germline)
Copy Number log−ratio

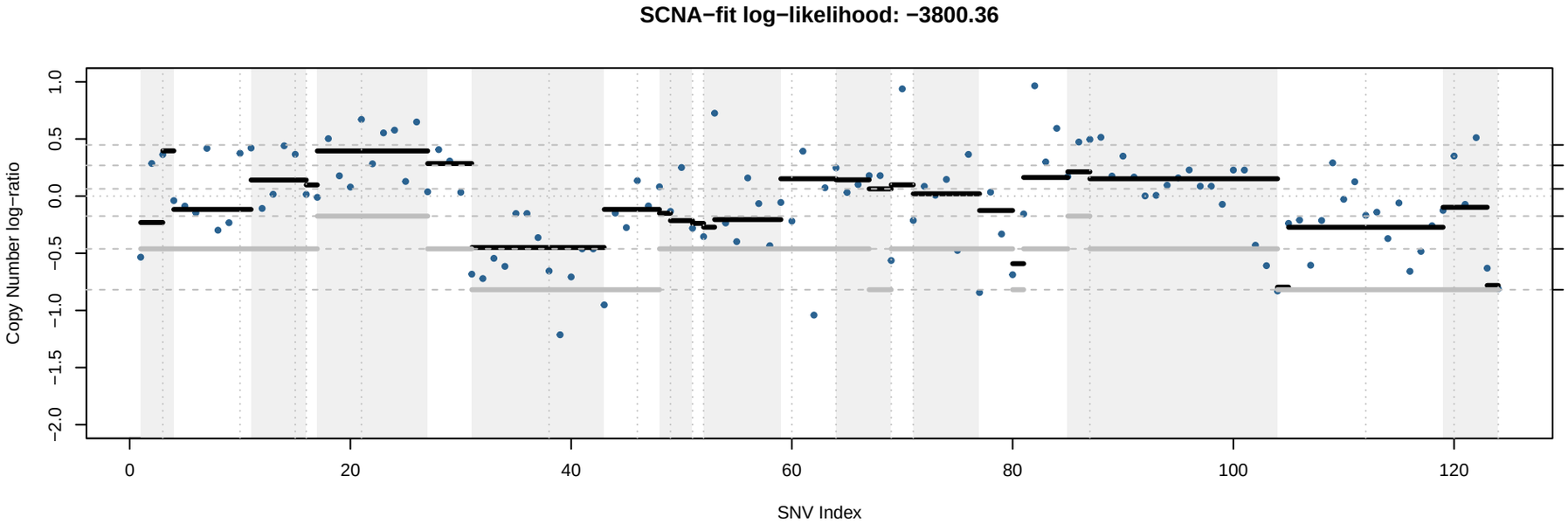

Coverage (log2)
Allelic fraction

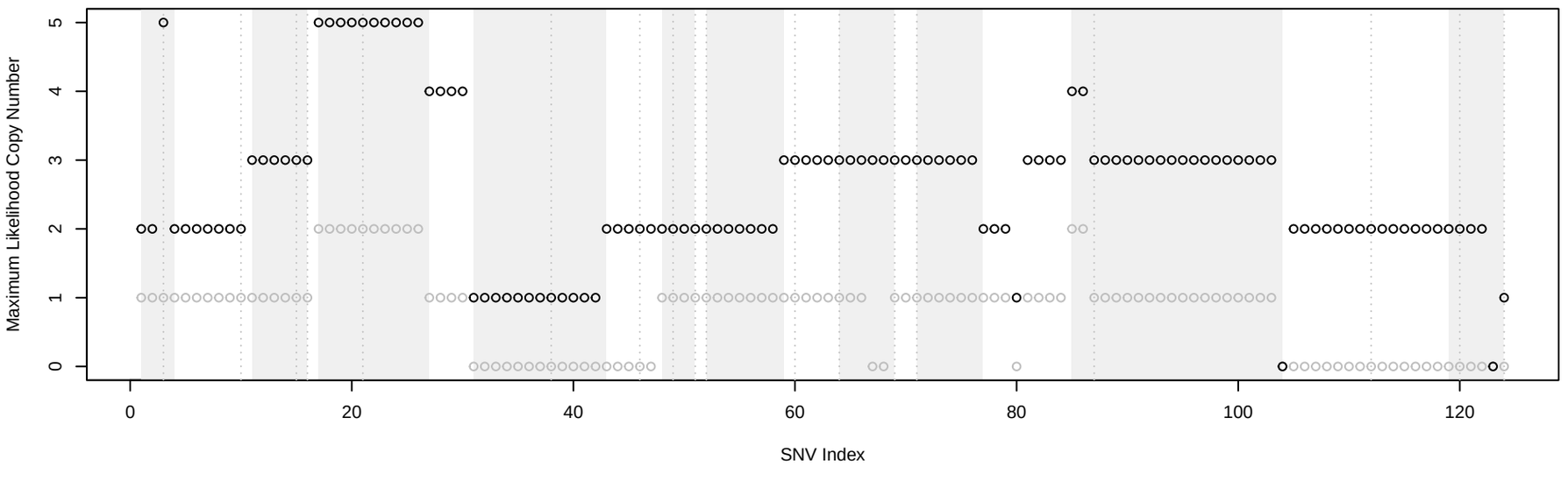

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
Allelic fraction (somatic)
Copy Number log−ratio

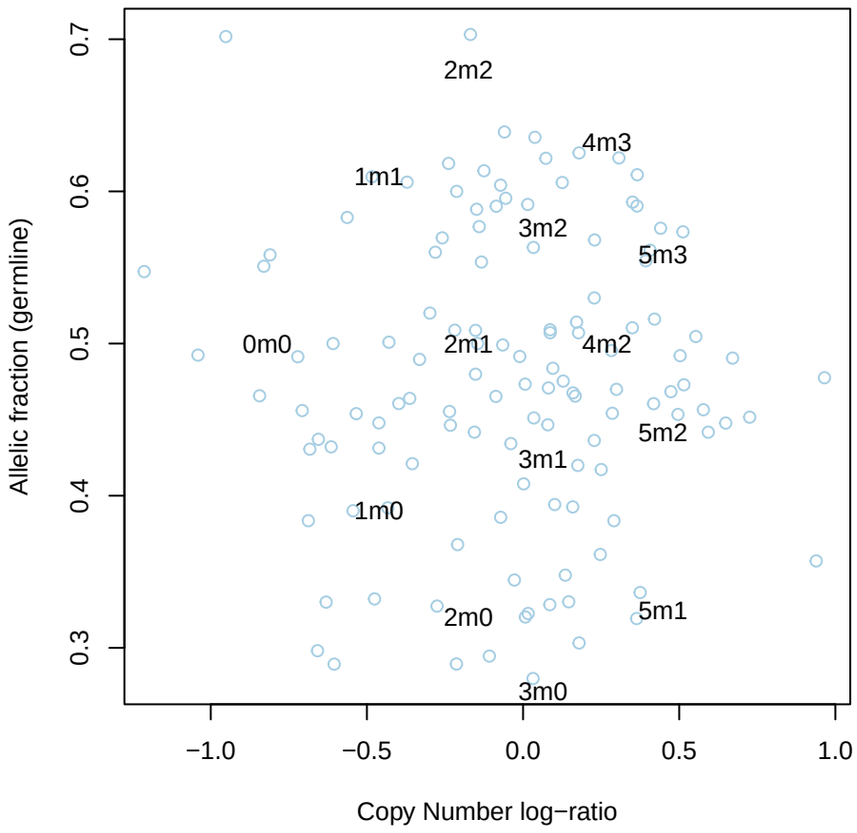

Power 0.8
Frequency
Cellular fraction

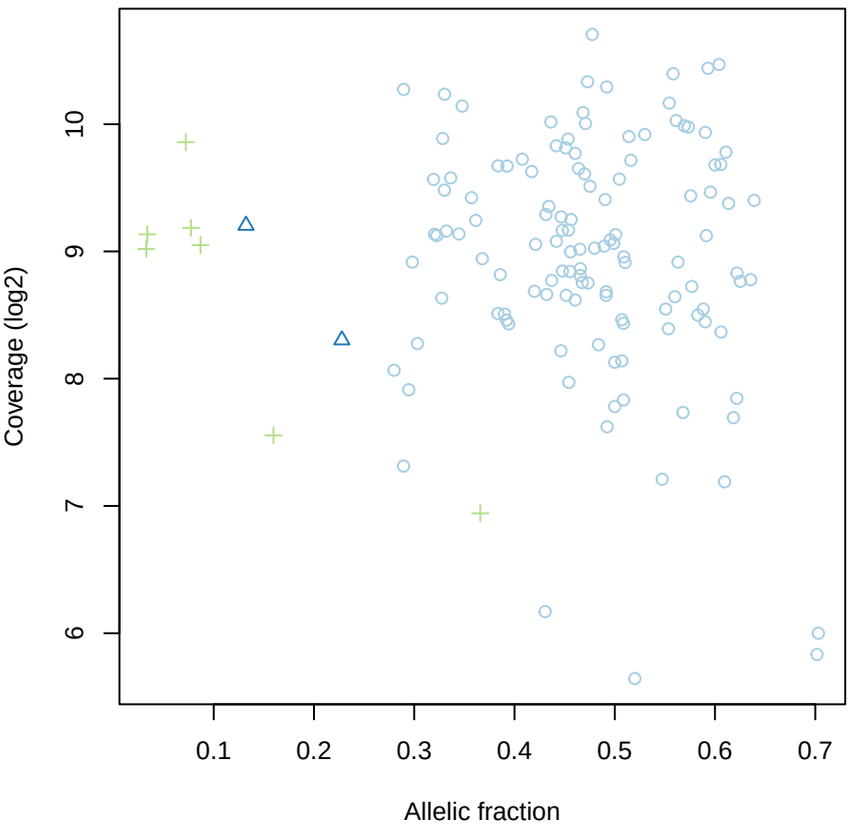

Purity: 0.36  Tumor ploidy: 2.716
0
1
2
3
4
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

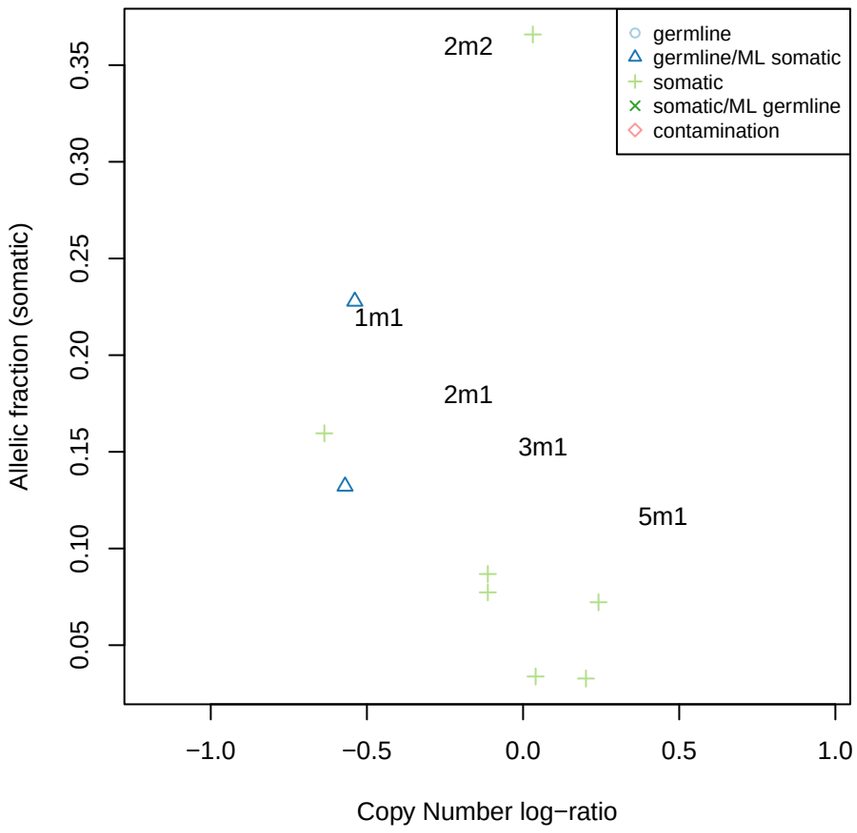

Purity: 0.36 Tumor ploidy: 2.716 SNV log−likelihood: −180.87 GoF: 91.5% Mean coverage: 459;590
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20 22
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

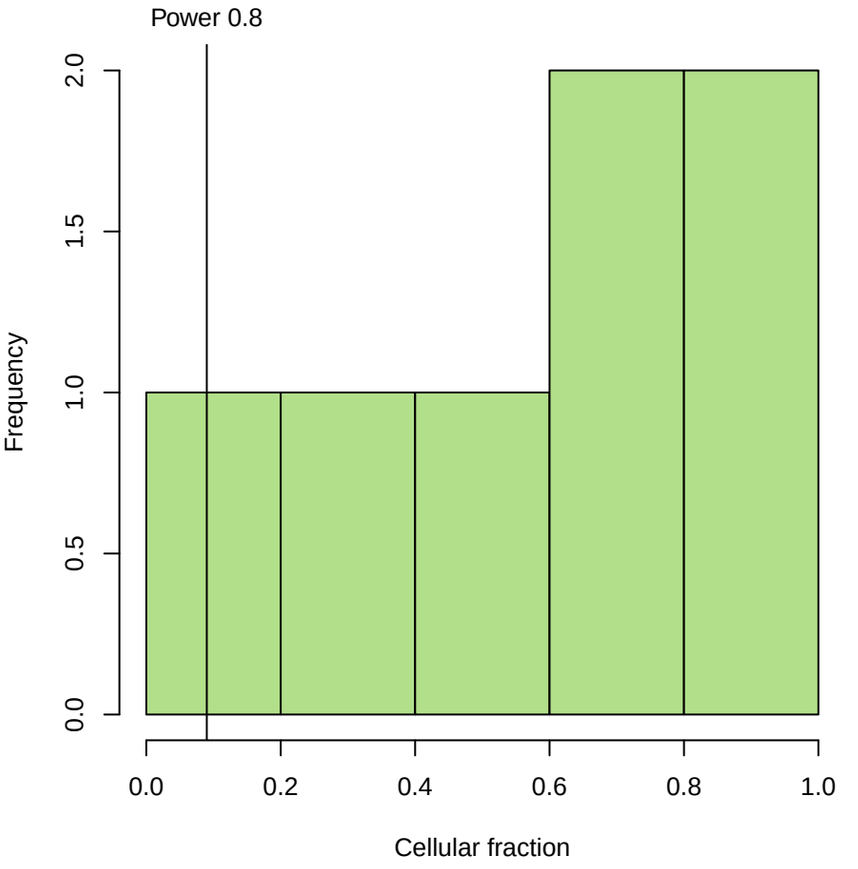

SCNA−fit log−likelihood: −3800.36
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 5
0 20 40 60 80 100 120
SNV Index

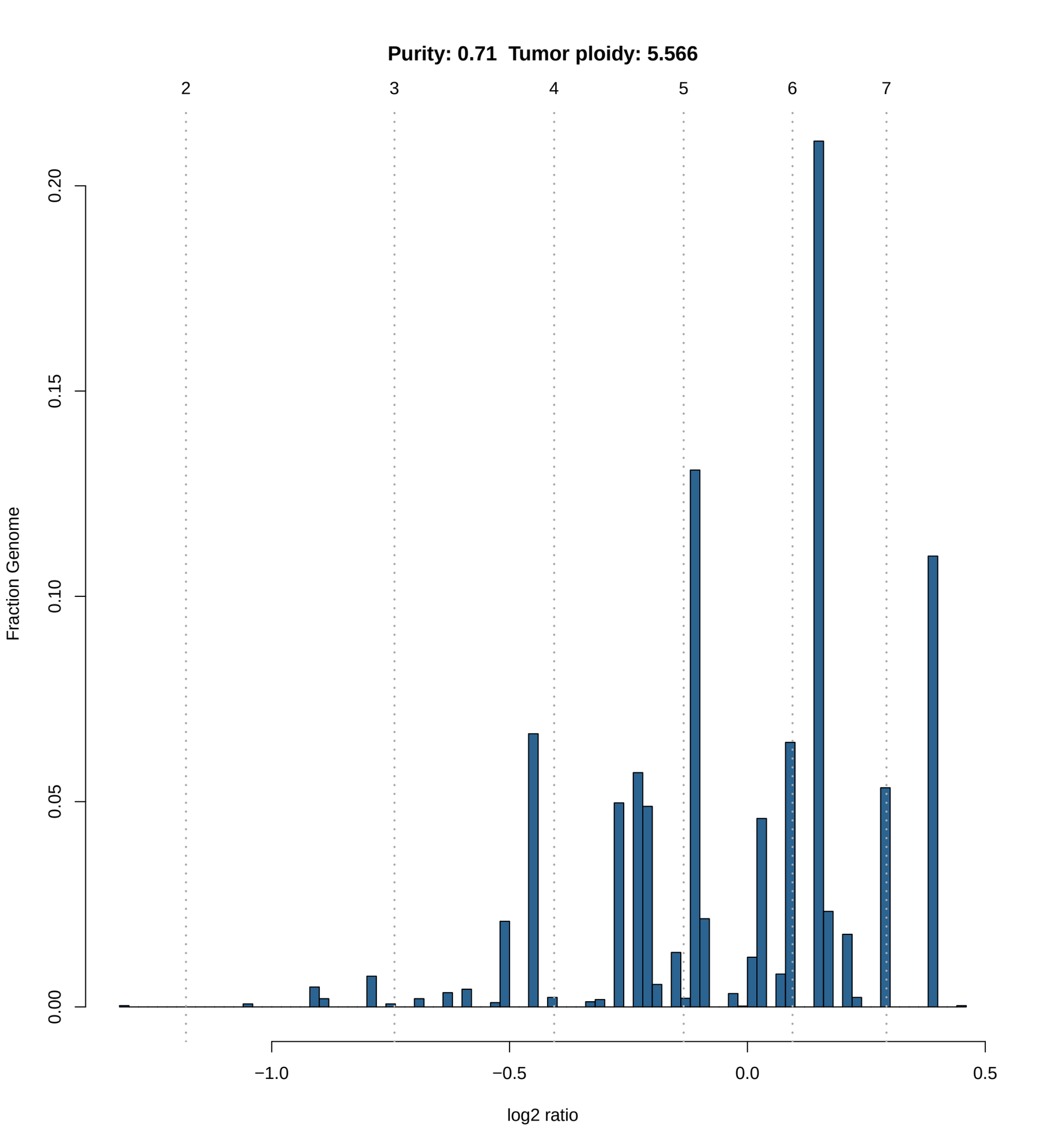

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120
SNV Index

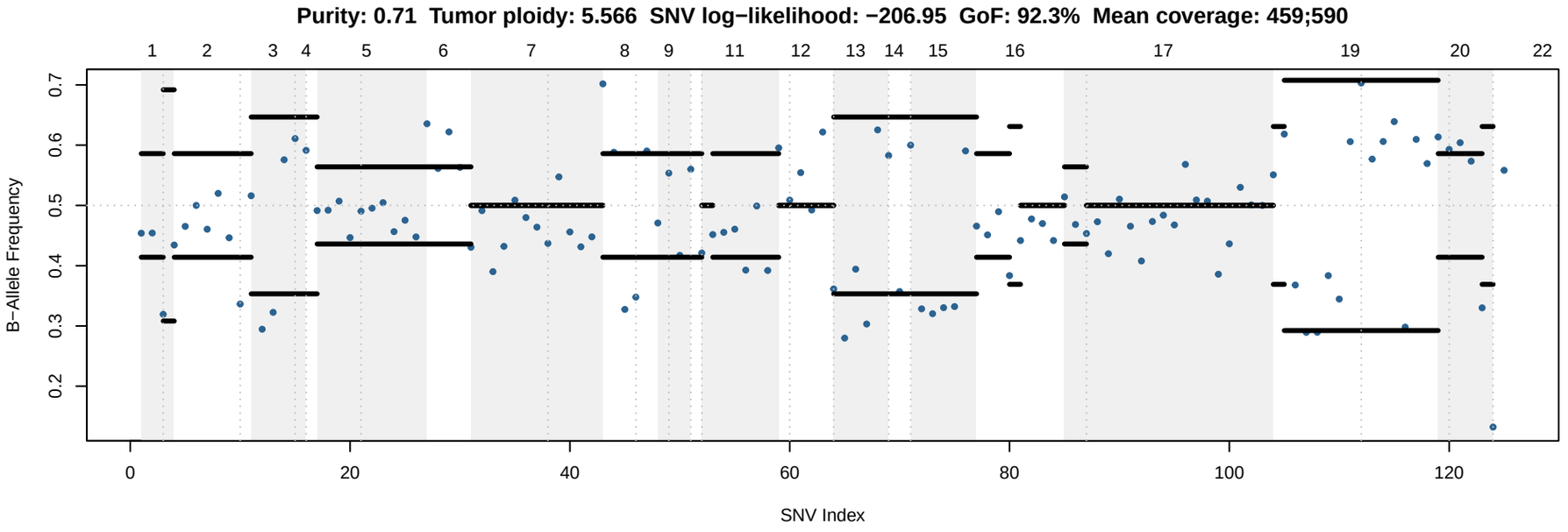

Allelic fraction (germline)
Copy Number log−ratio
0m0
1m0
2m0
3m0
1m1
2m1
3m1
4m2
5m1
5m2
2m2
3m2
4m3
5m3

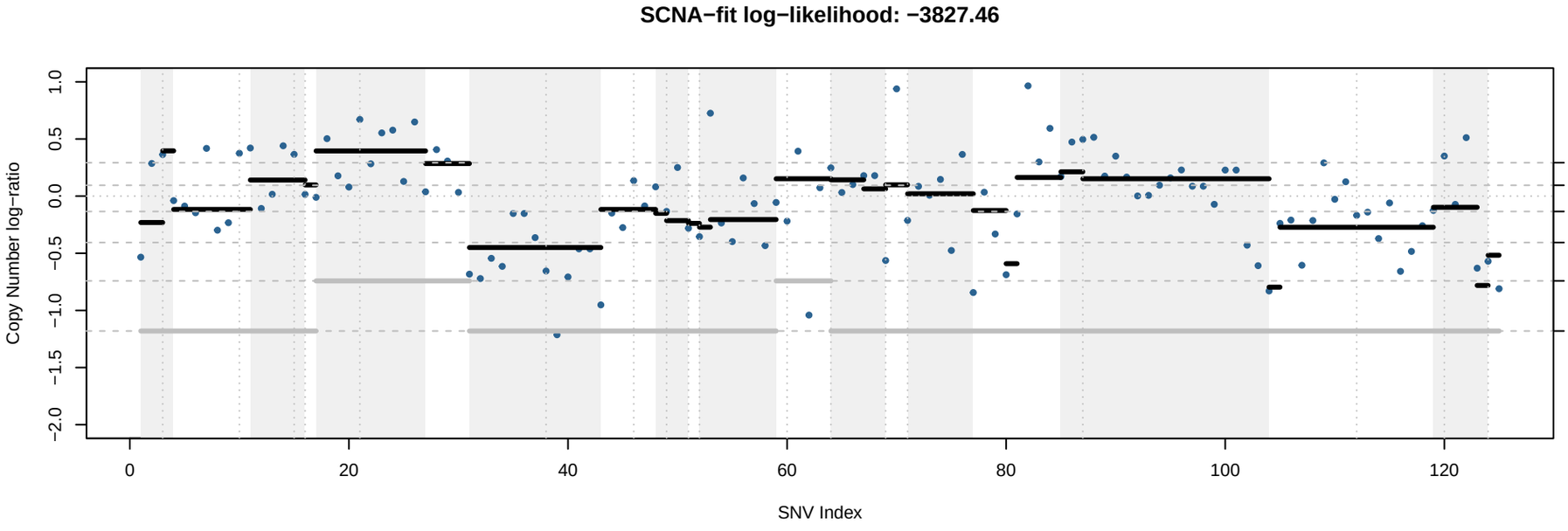

Coverage (log2)
Allelic fraction

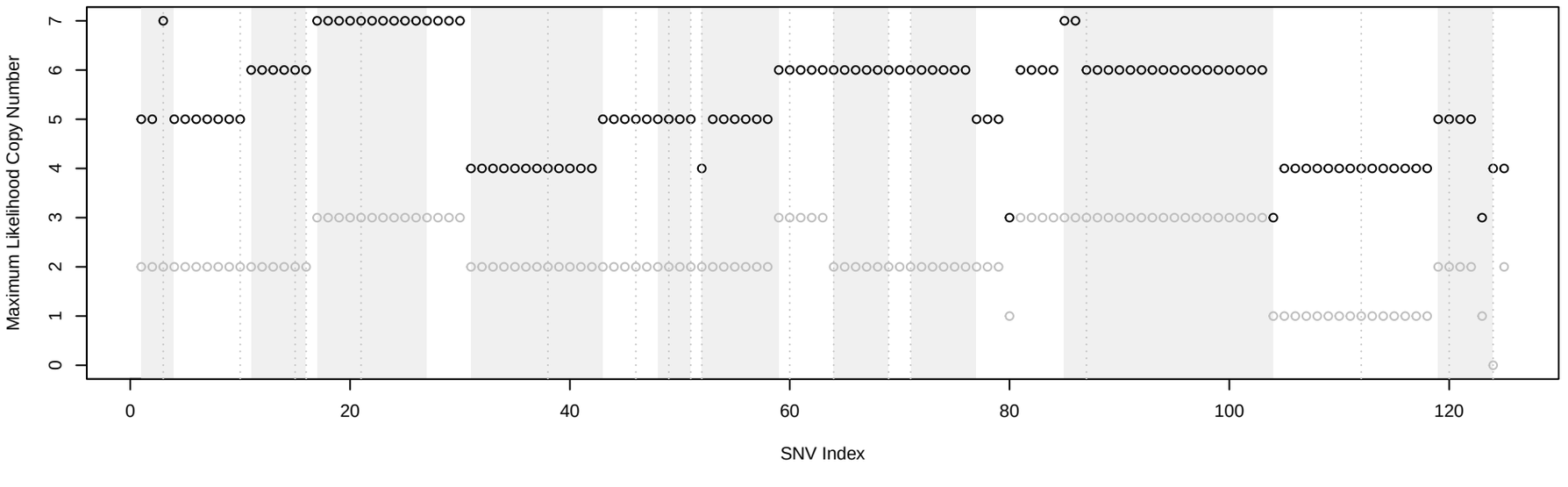

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
5m1
2m2

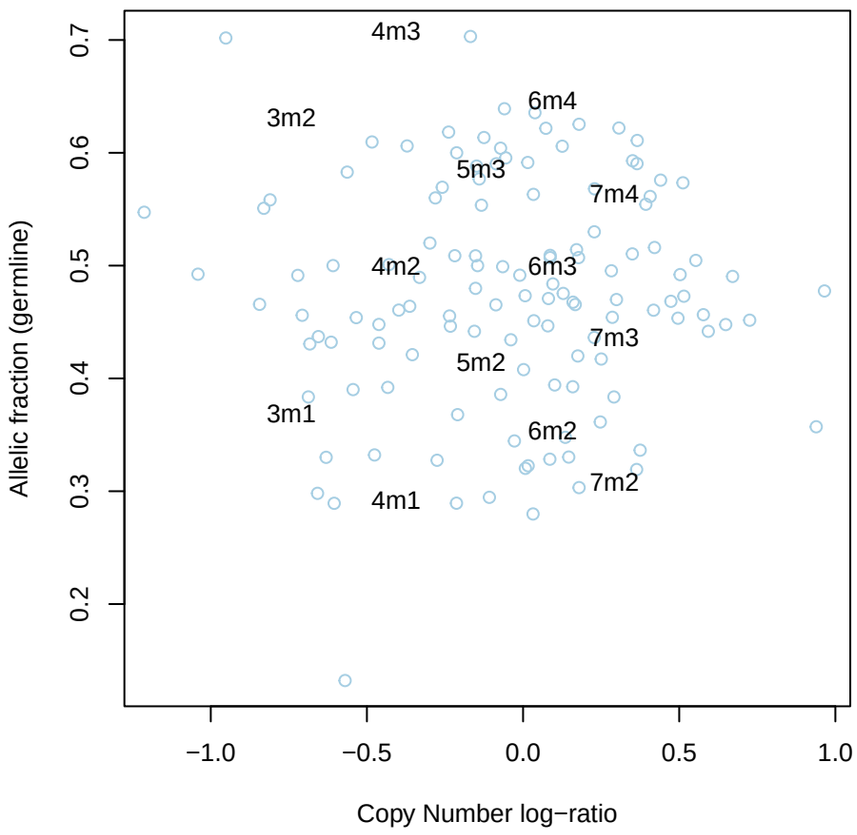

Power 0.8
Frequency
Cellular fraction

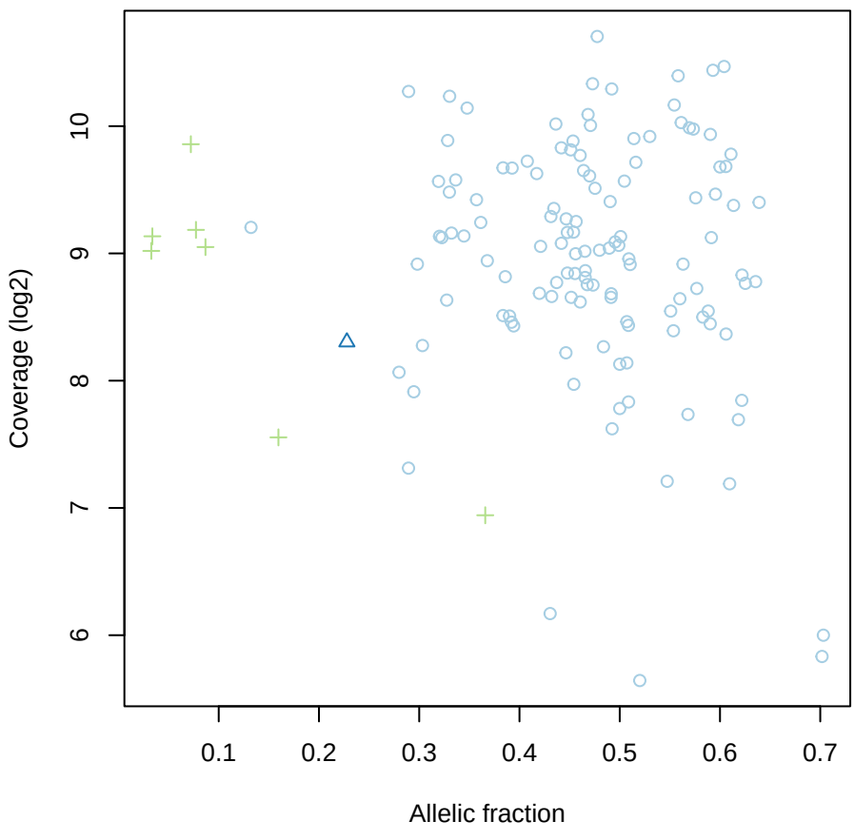

Purity: 0.71  Tumor ploidy: 5.566
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

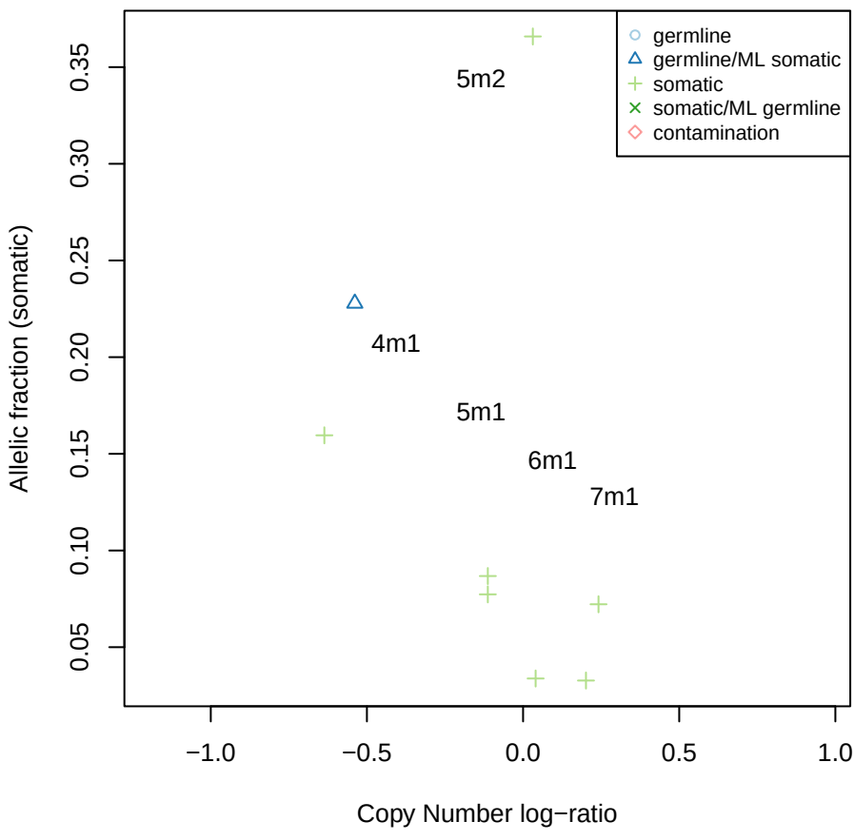

Purity: 0.71 Tumor ploidy: 5.566 SNV log−likelihood: −206.95 GoF: 92.3% Mean coverage: 459;590
B−Allele Frequency
SNV Index

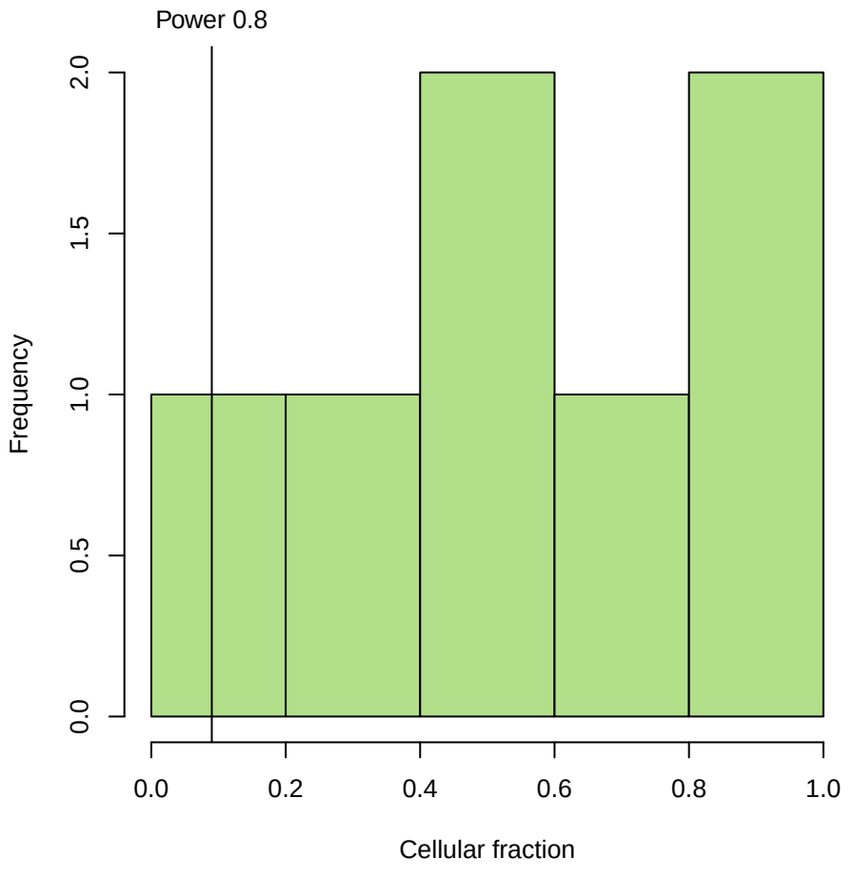

SCNA−fit log−likelihood: −3827.46
Copy Number log−ratio
SNV Index

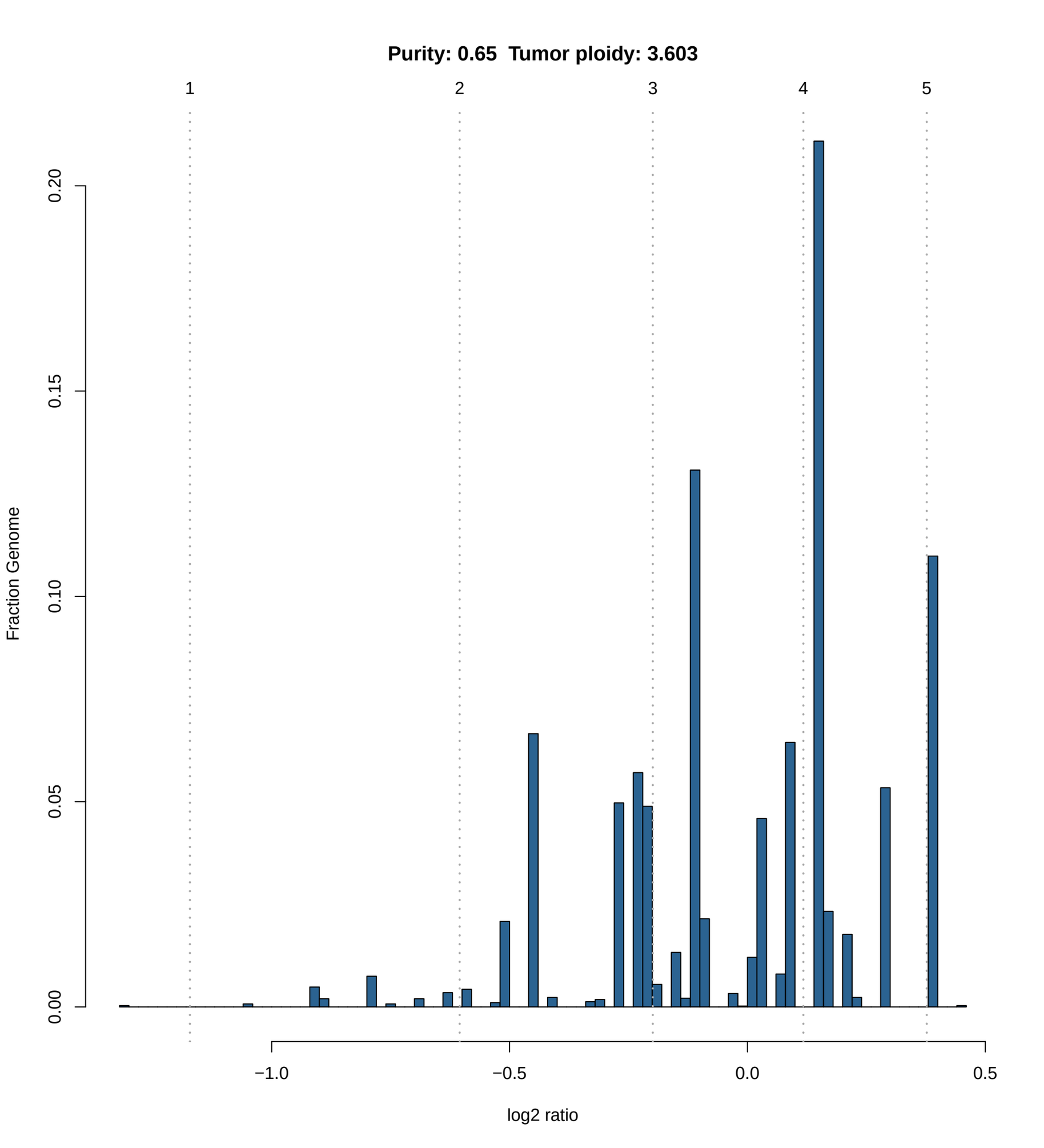

Maximum Likelihood Copy Number
SNV Index

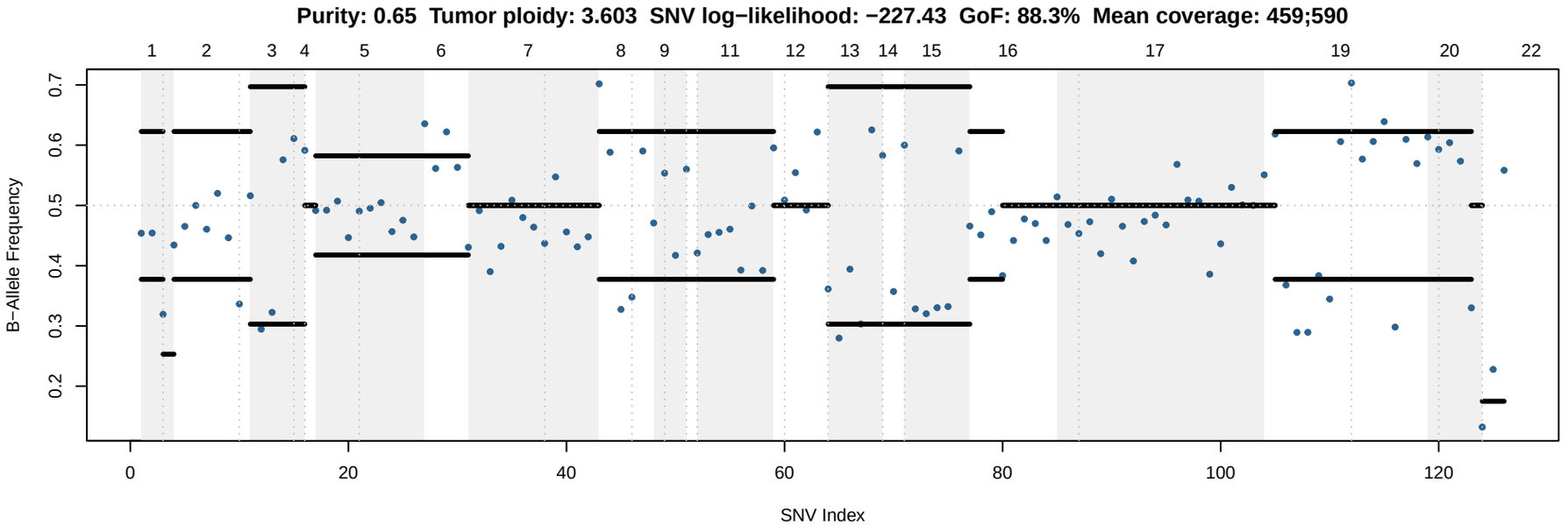

4m3
6m4
3m2
5m3
7m4
4m2
6m3
7m3
5m2
3m1
6m2
7m2
4m1
Allelic fraction (germline)
Copy Number log−ratio

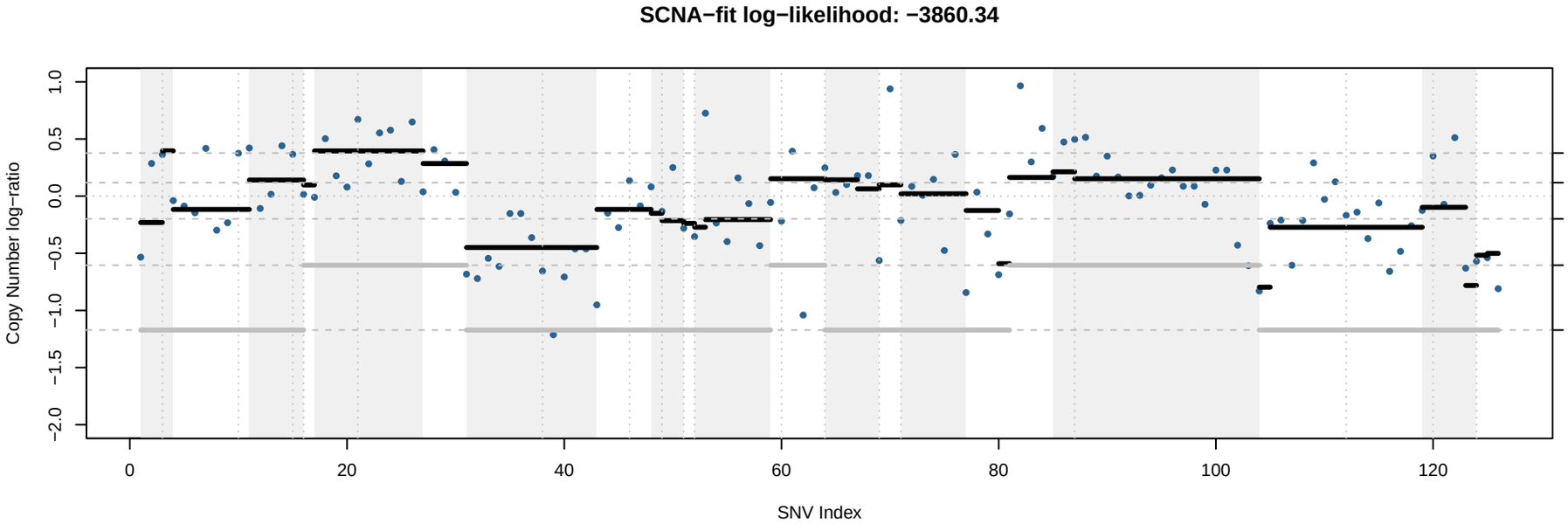

Coverage (log2)
Allelic fraction

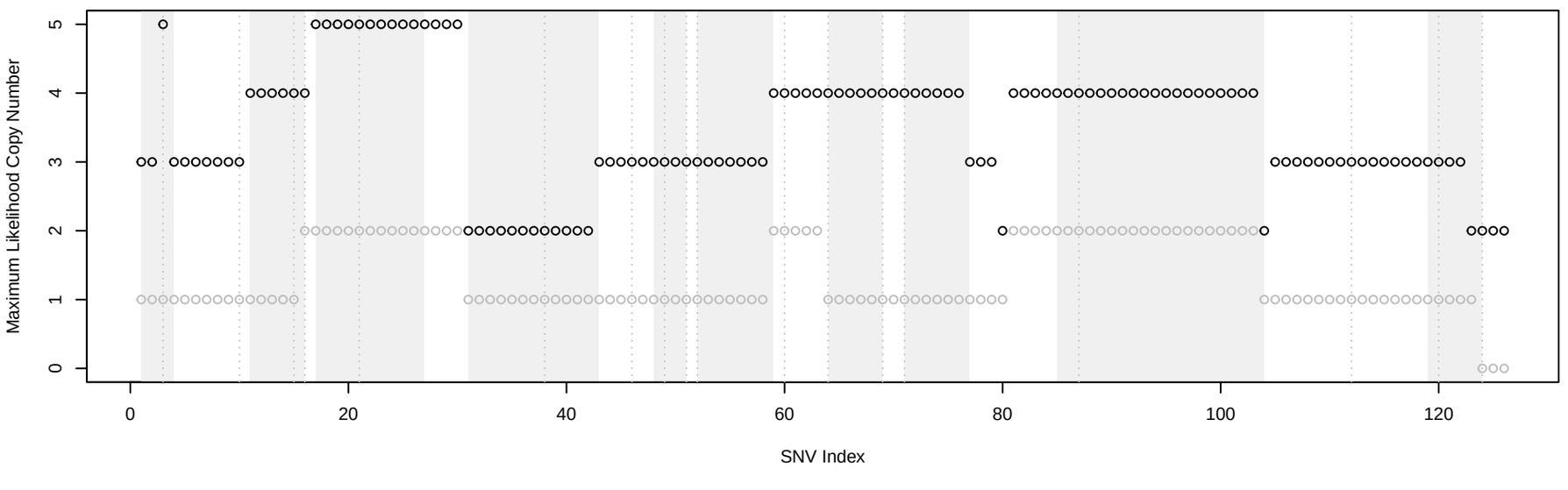

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m2
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

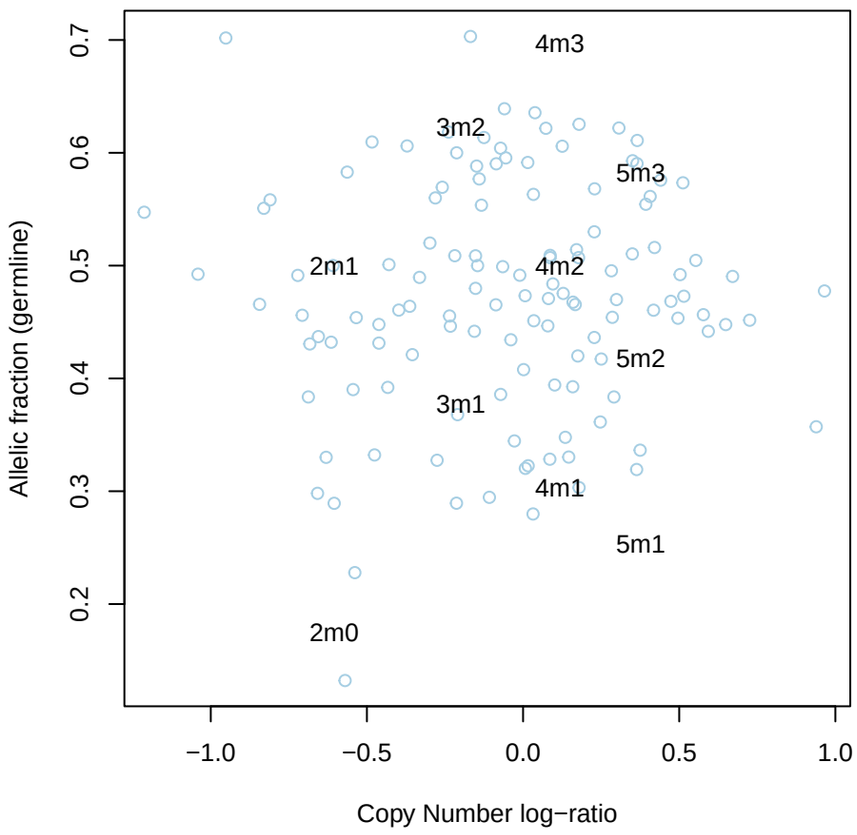

Power 0.8
Frequency
Cellular fraction

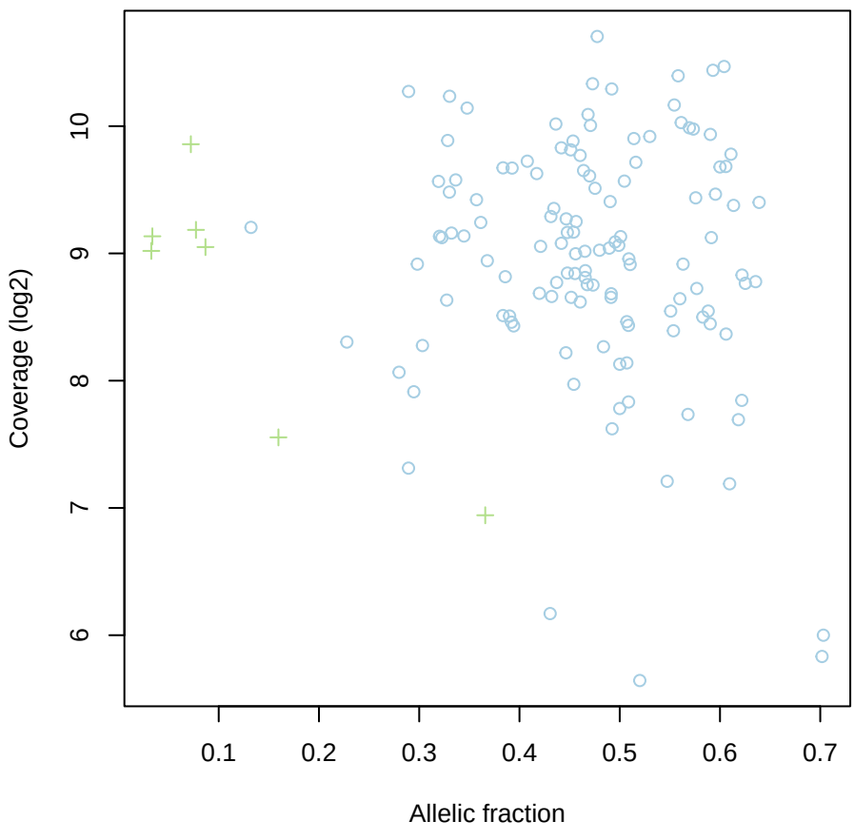

Purity: 0.65  Tumor ploidy: 3.603
1
2
3
4
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

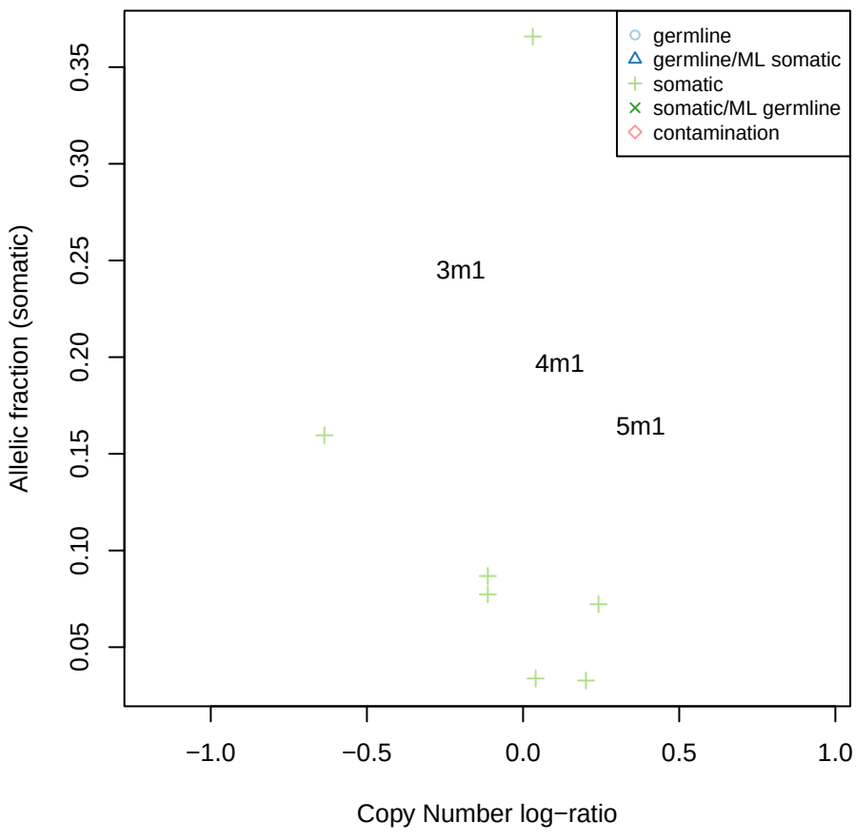

Purity: 0.65 Tumor ploidy: 3.603 SNV log−likelihood: −227.43 GoF: 88.3% Mean coverage: 459;590
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20 22
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

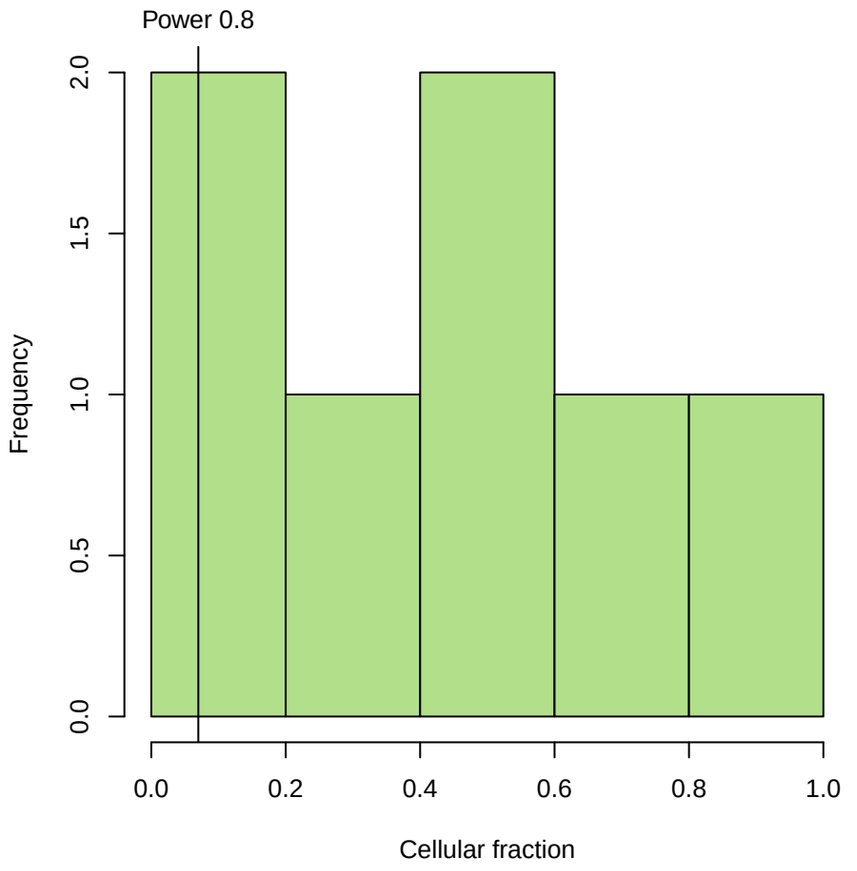

SCNA−fit log−likelihood: −3860.34
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5
0 20 40 60 80 100 120
SNV Index

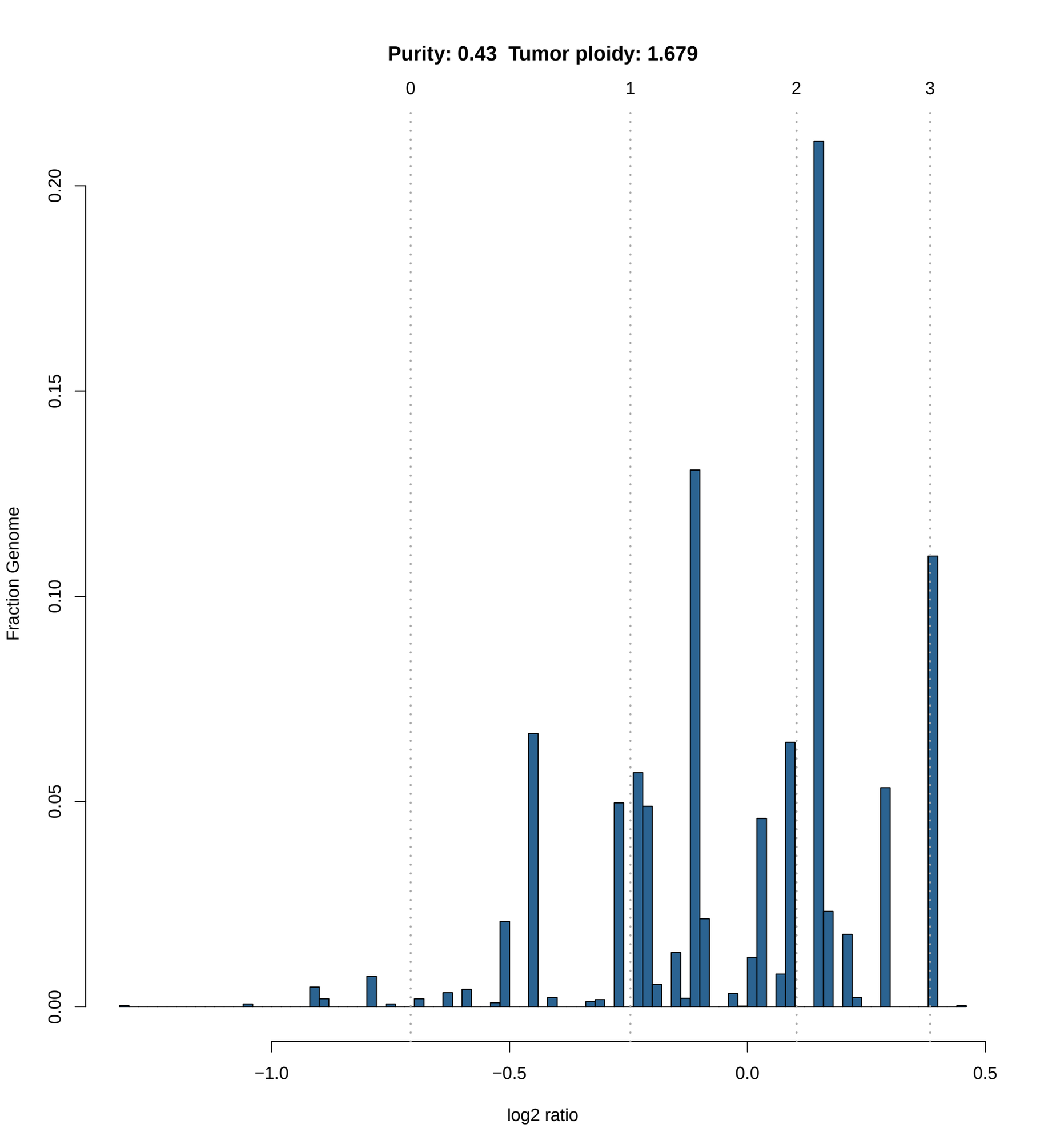

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120
SNV Index

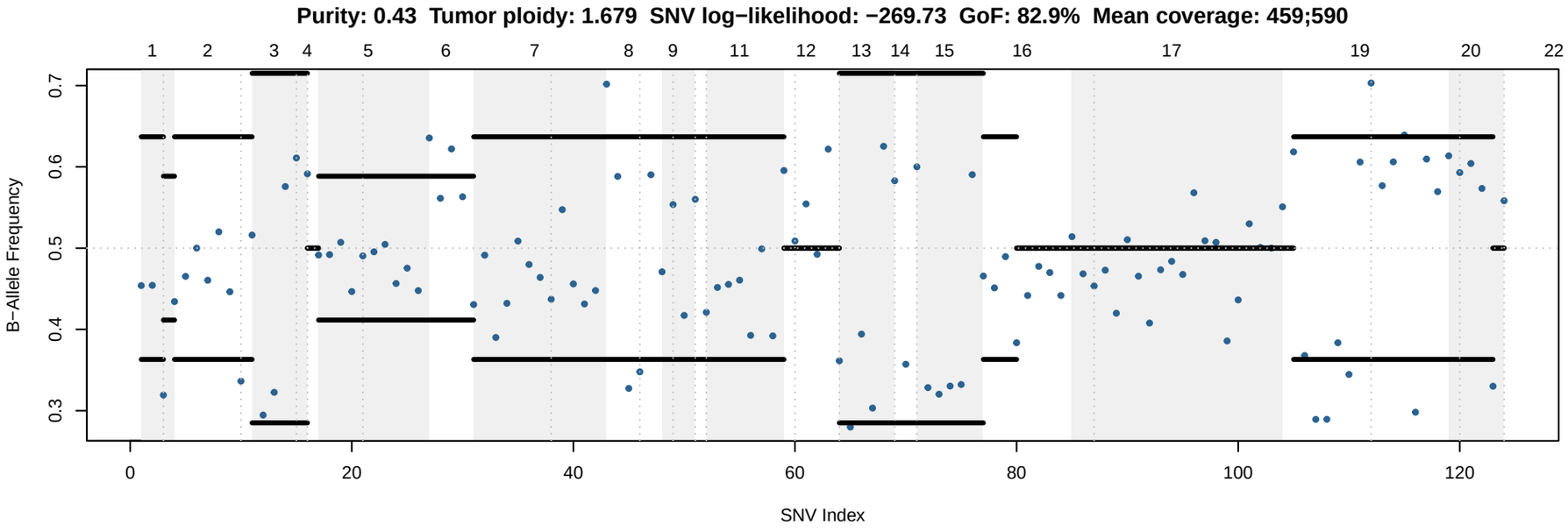

4m3
3m2
5m3
2m1
4m2
5m2
3m1
4m1
5m1
2m0
Allelic fraction (germline)
Copy Number log−ratio

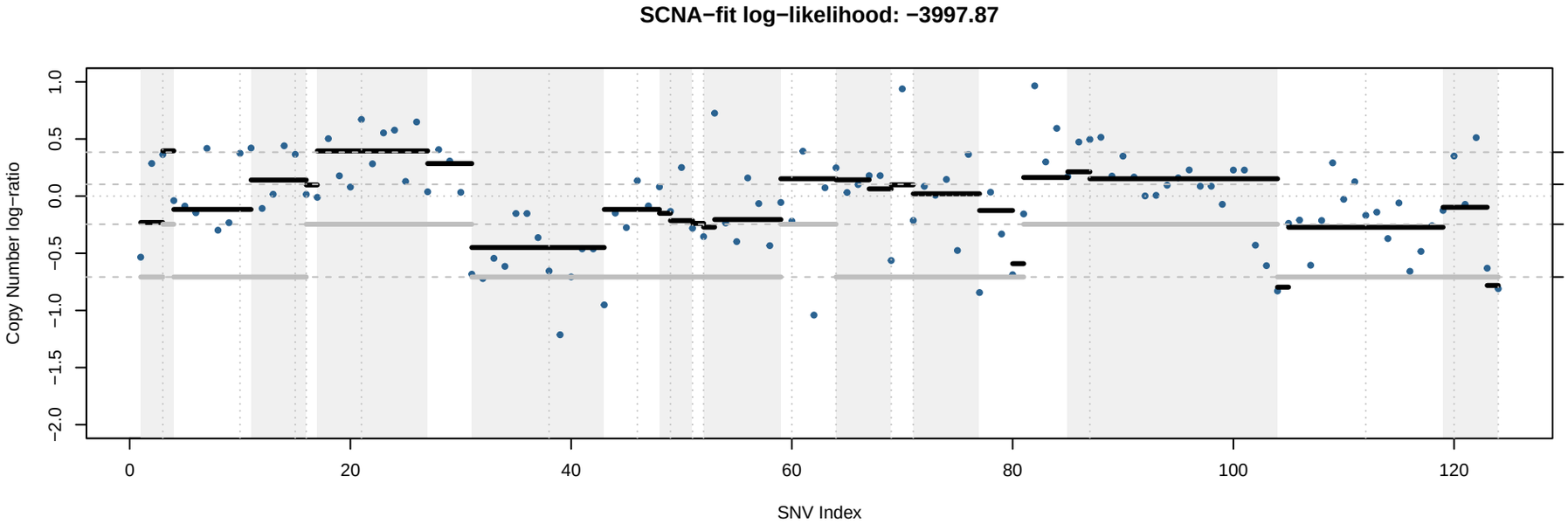

Coverage (log2)
Allelic fraction

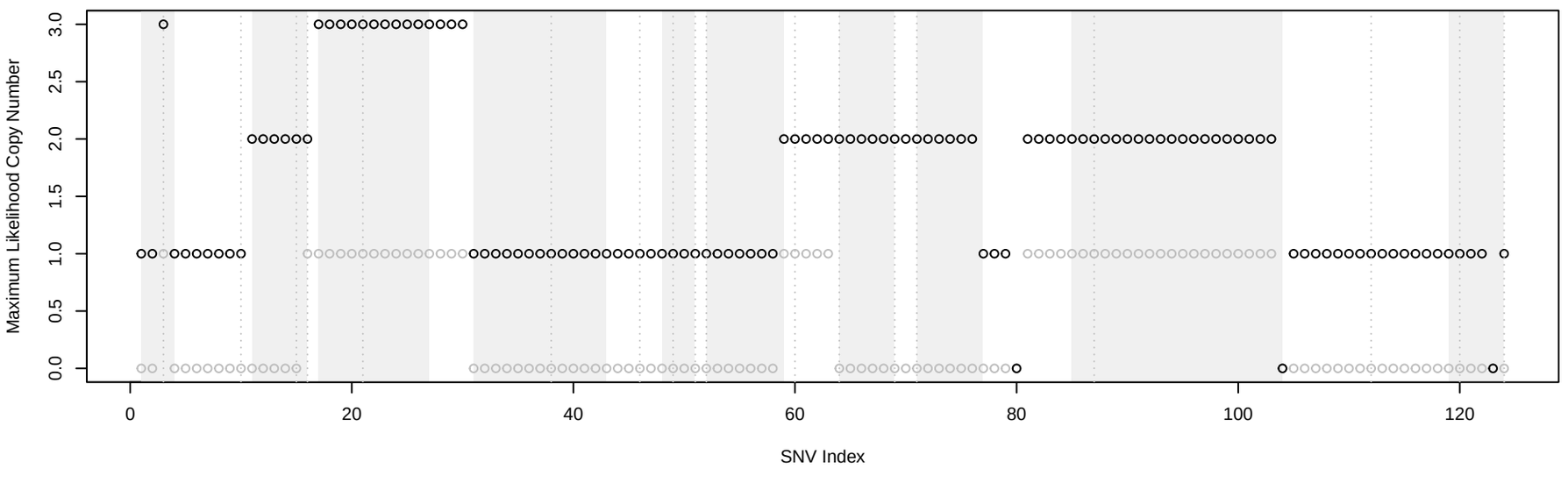

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
Allelic fraction (somatic)
Copy Number log−ratio

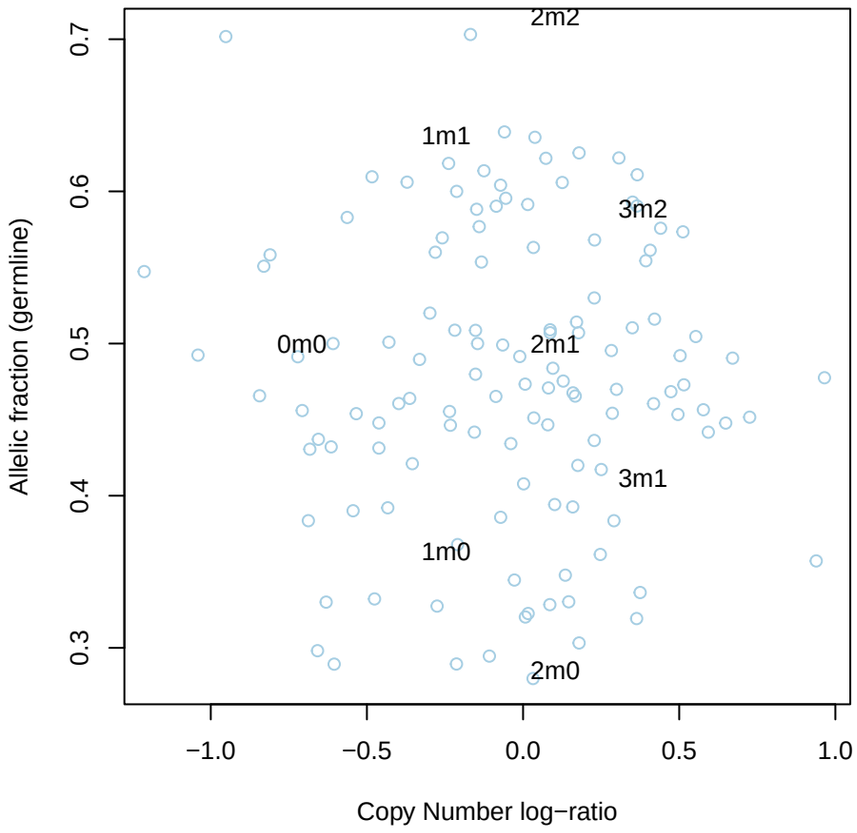

Power 0.8
Frequency
Cellular fraction

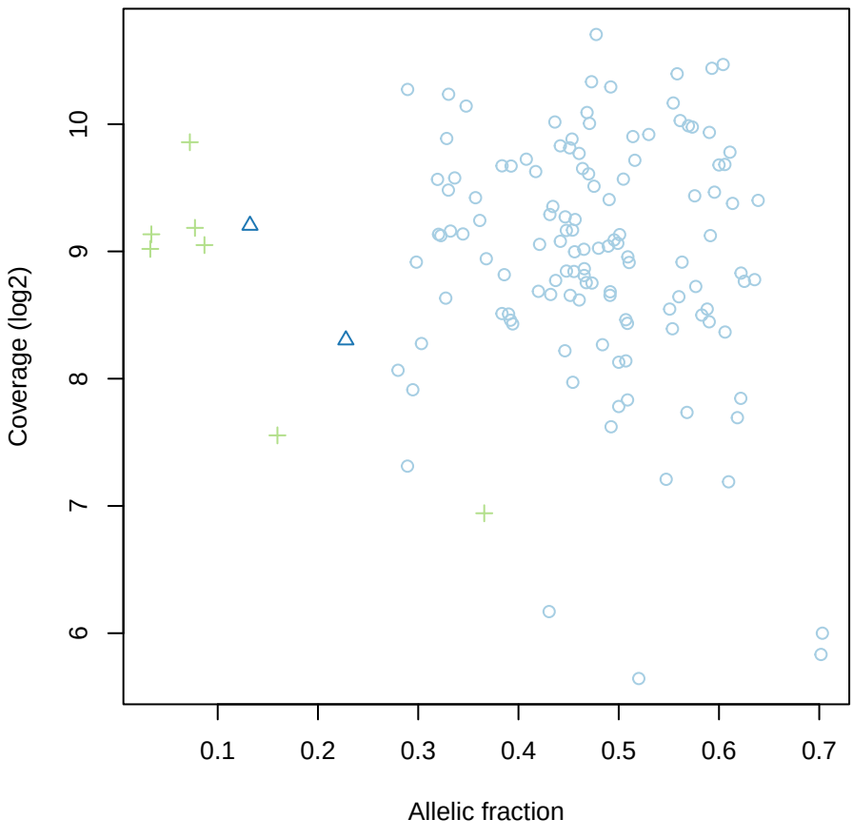

Purity: 0.43  Tumor ploidy: 1.679
0
1
2
3
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

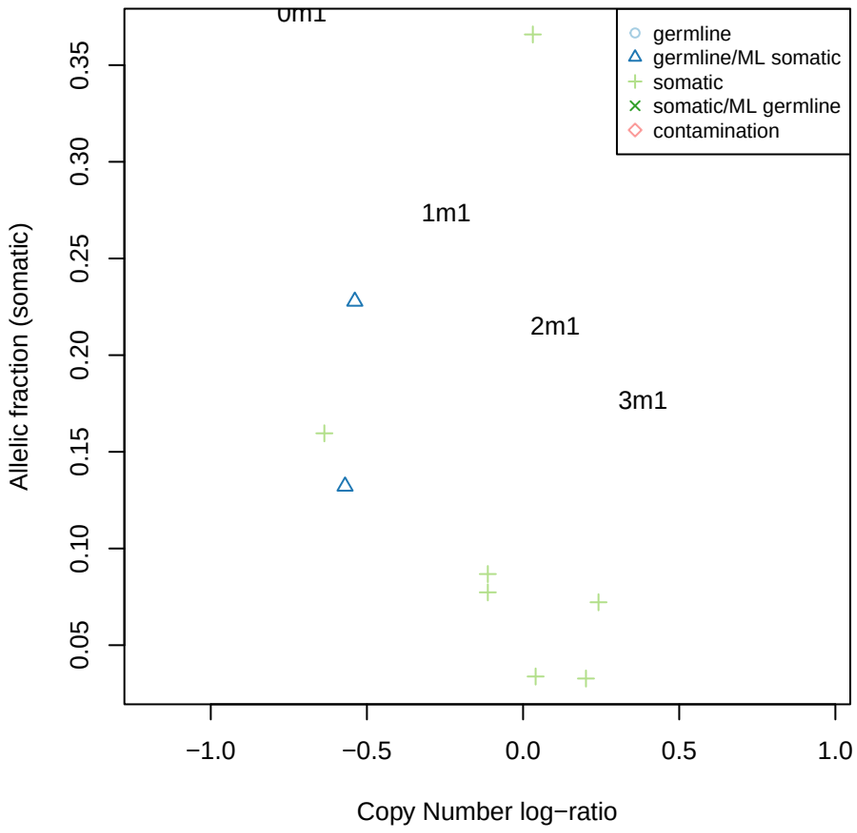

Purity: 0.43 Tumor ploidy: 1.679 SNV log−likelihood: −269.73 GoF: 82.9% Mean coverage: 459;590
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20 22
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

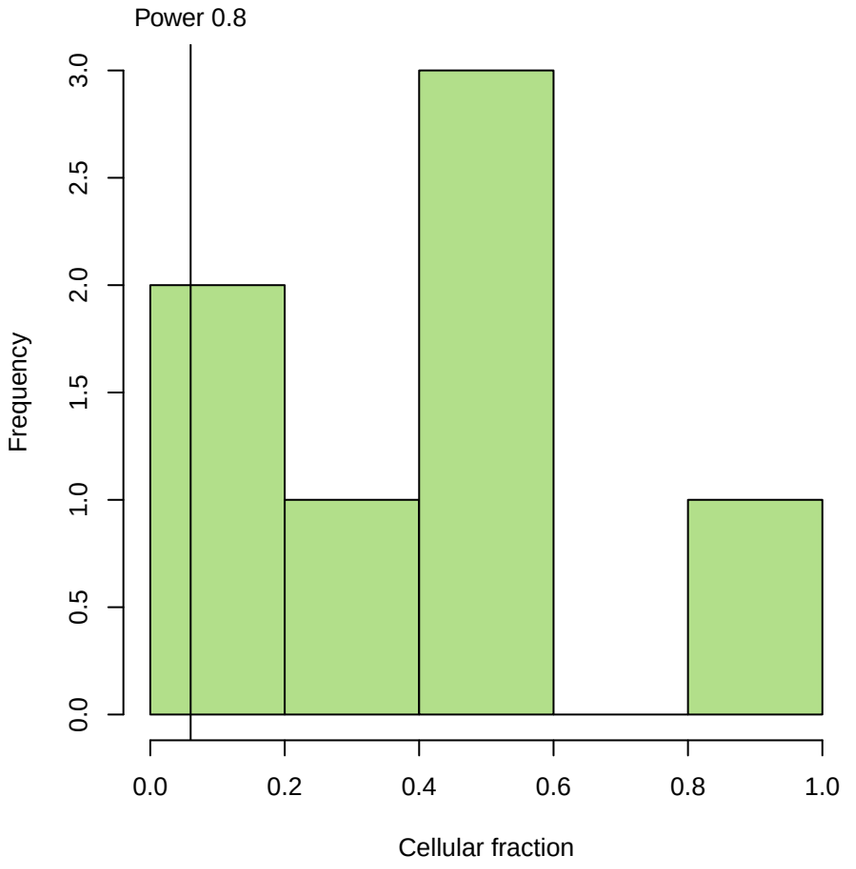

SCNA−fit log−likelihood: −3997.87
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3
0 20 40 60 80 100 120
SNV Index

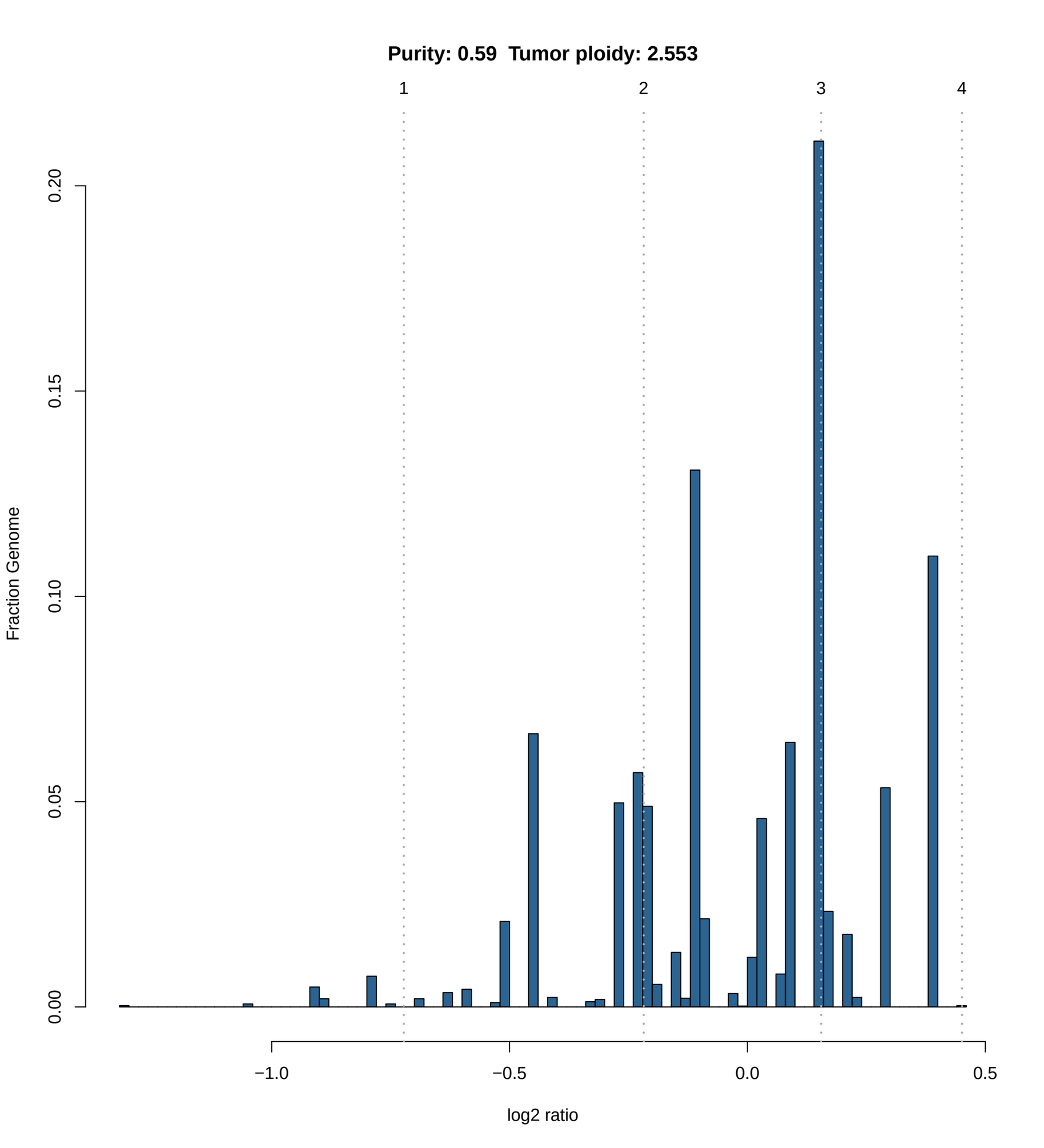

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120
SNV Index

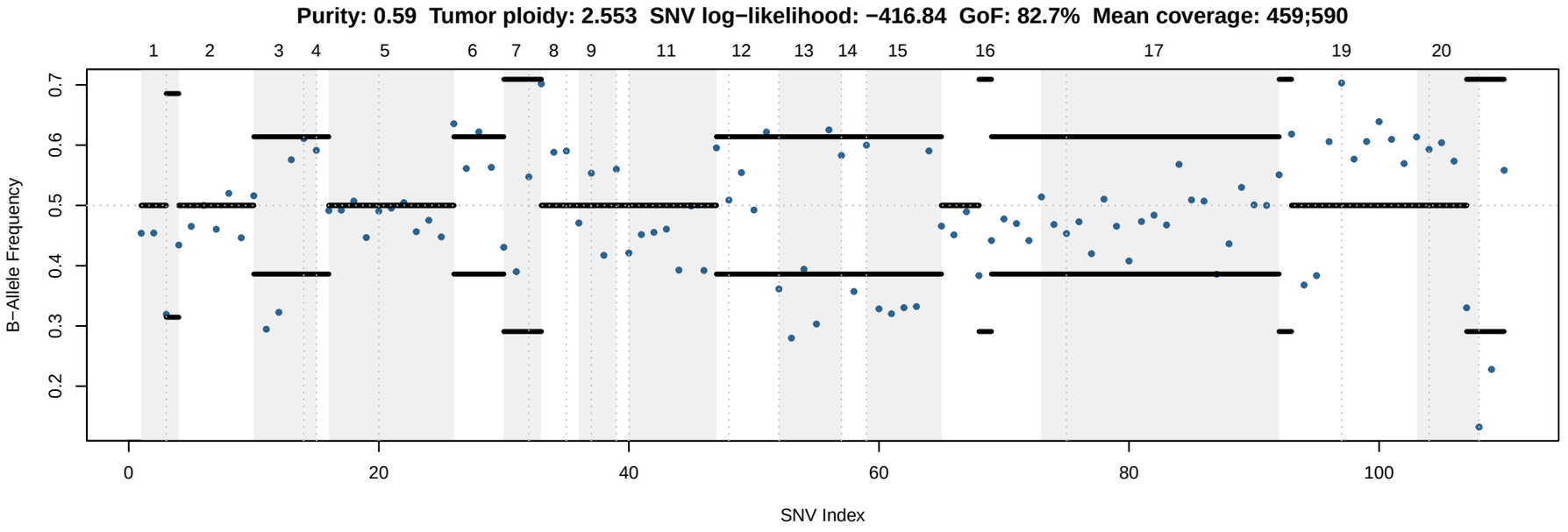

2m2
1m1
3m2
0m0
2m1
3m1
1m0
2m0
Allelic fraction (germline)
Copy Number log−ratio

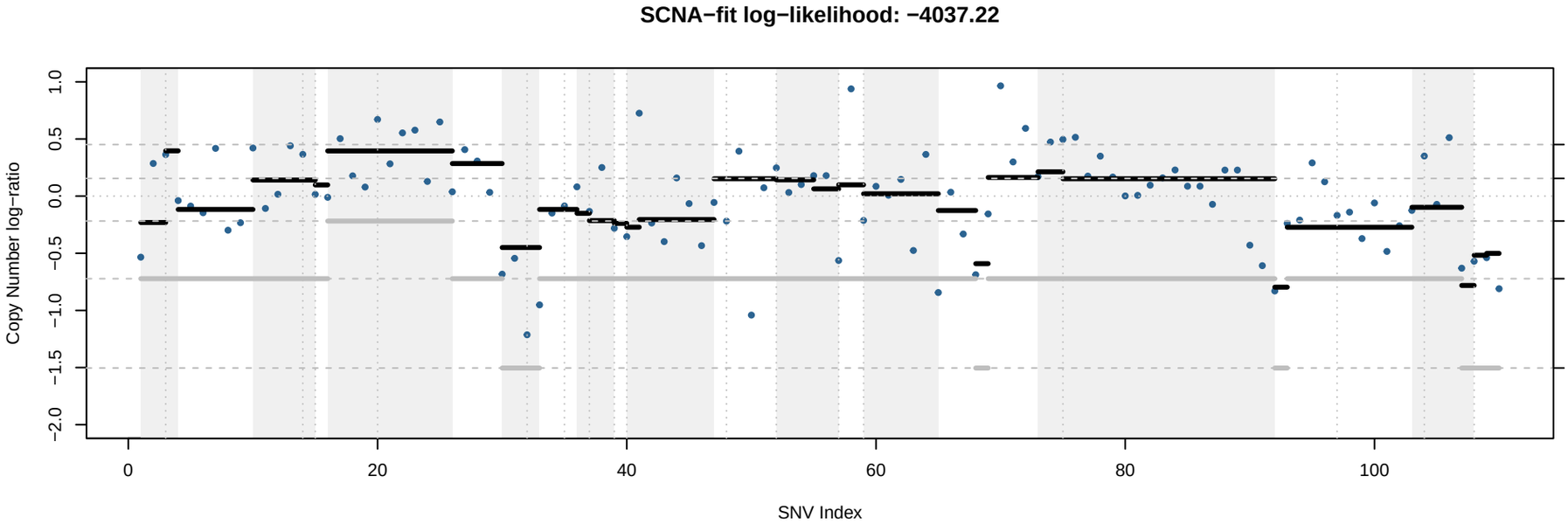

Coverage (log2)
Allelic fraction

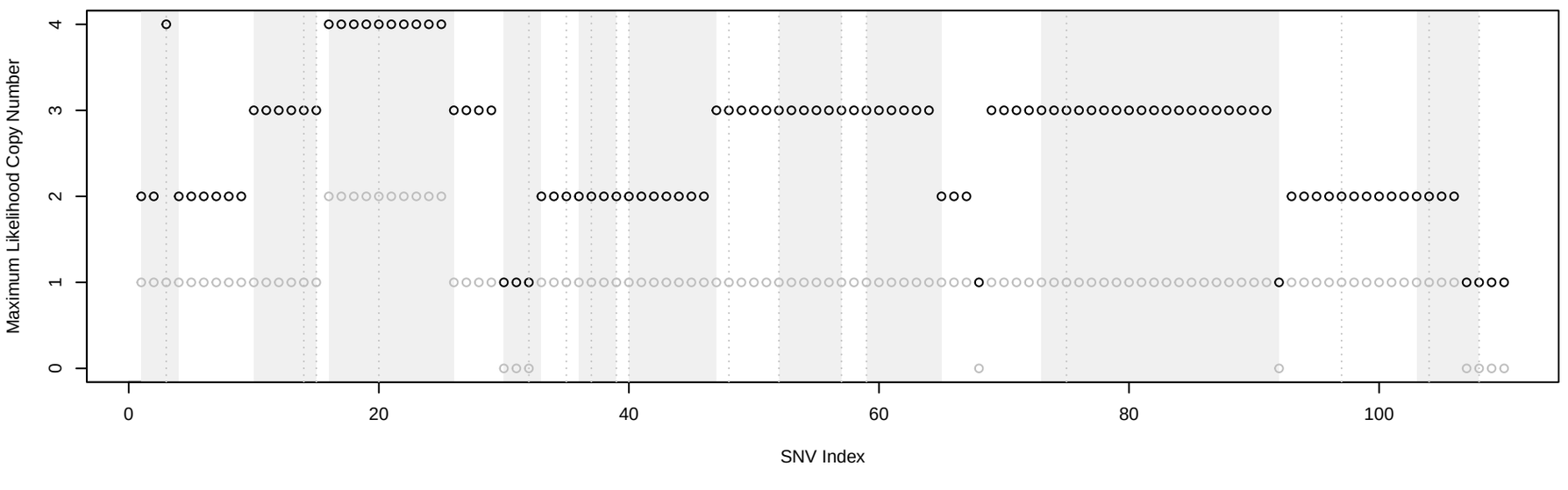

0m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
Allelic fraction (somatic)
Copy Number log−ratio

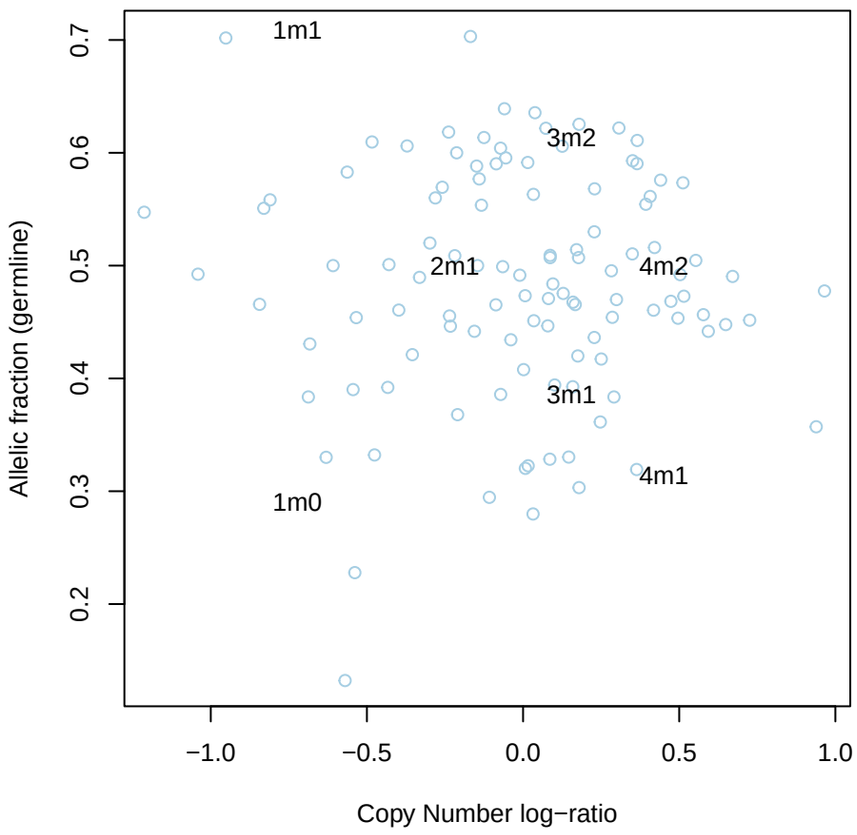

Power 0.8
Frequency
Cellular fraction

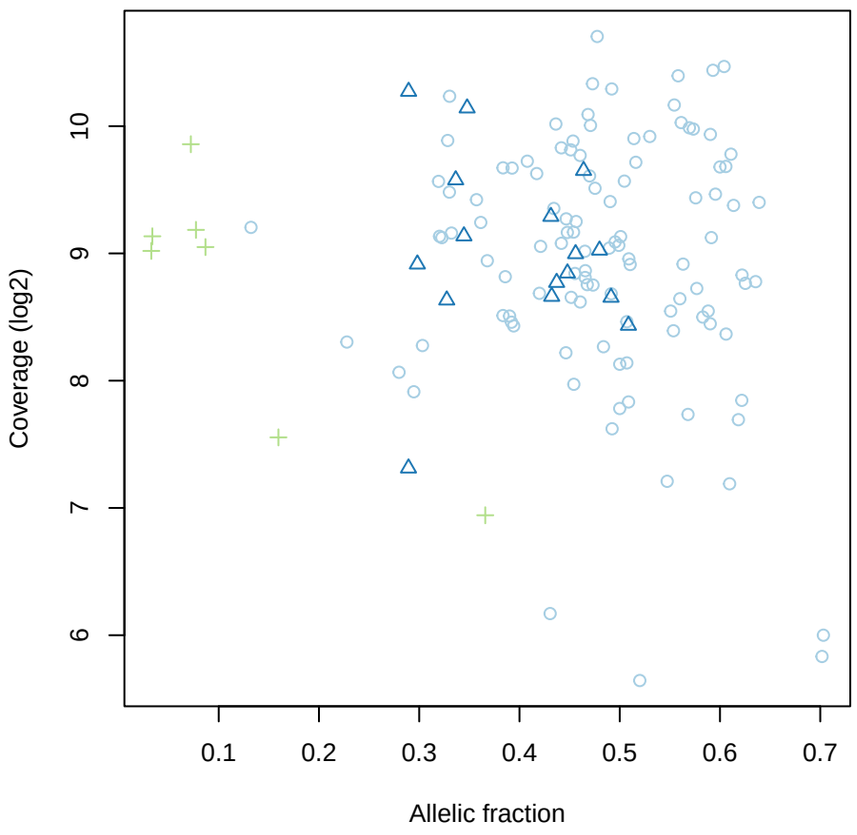

Purity: 0.59  Tumor ploidy: 2.553
1
2
3
4
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

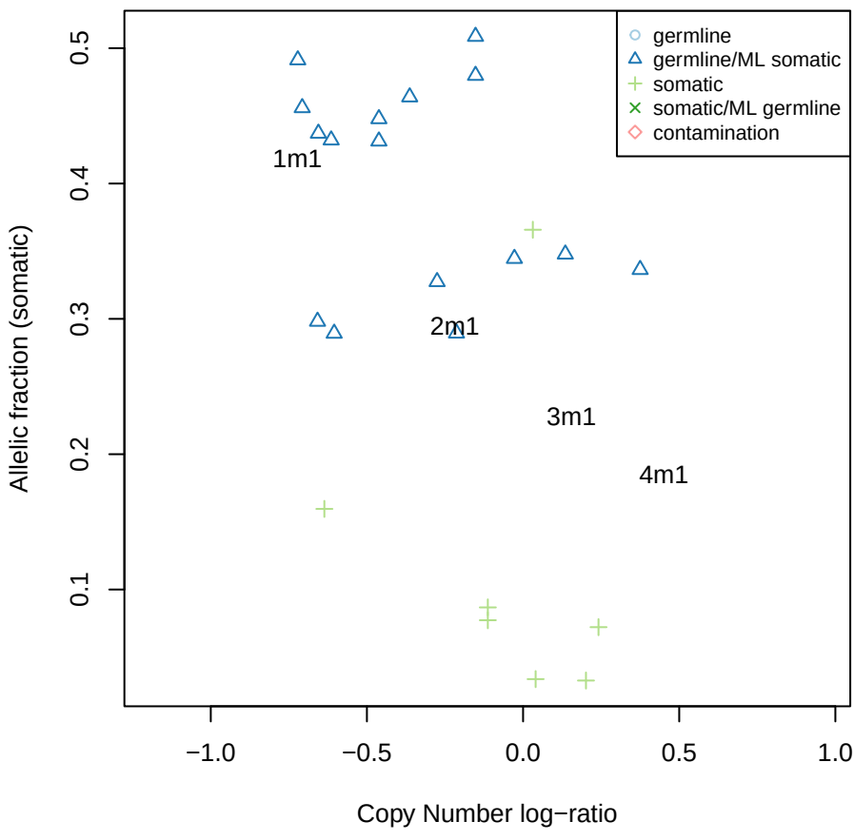

Purity: 0.59 Tumor ploidy: 2.553 SNV log−likelihood: −416.84 GoF: 82.7% Mean coverage: 459;590
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

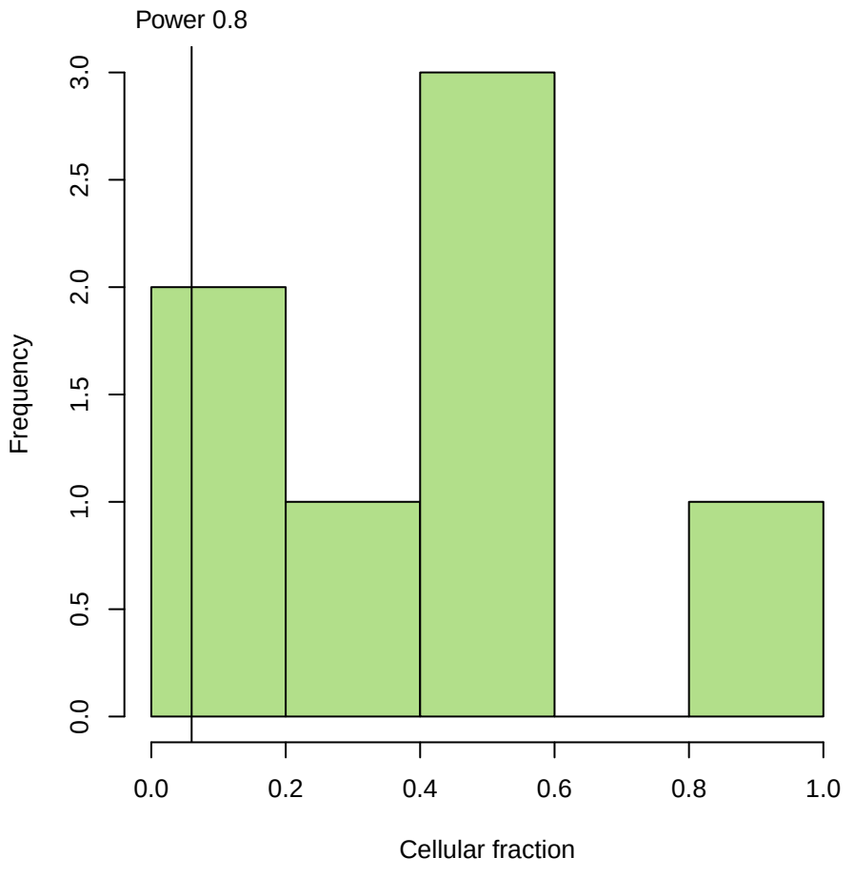

SCNA−fit log−likelihood: −4037.22
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4
0 20 40 60 80 100
SNV Index


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


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


Coverage (log2)
Allelic fraction


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


Power 0.8
Frequency
Cellular fraction