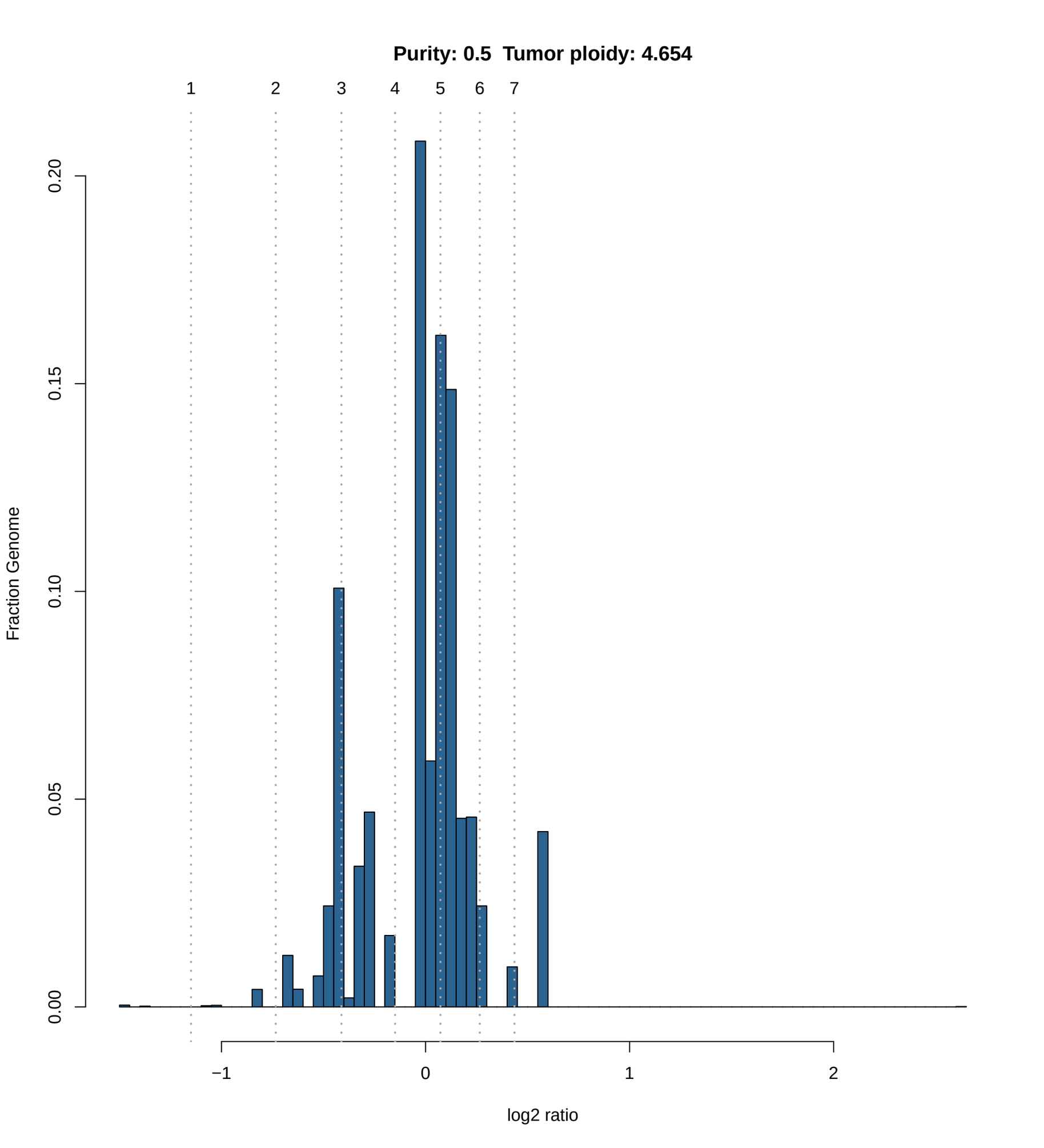
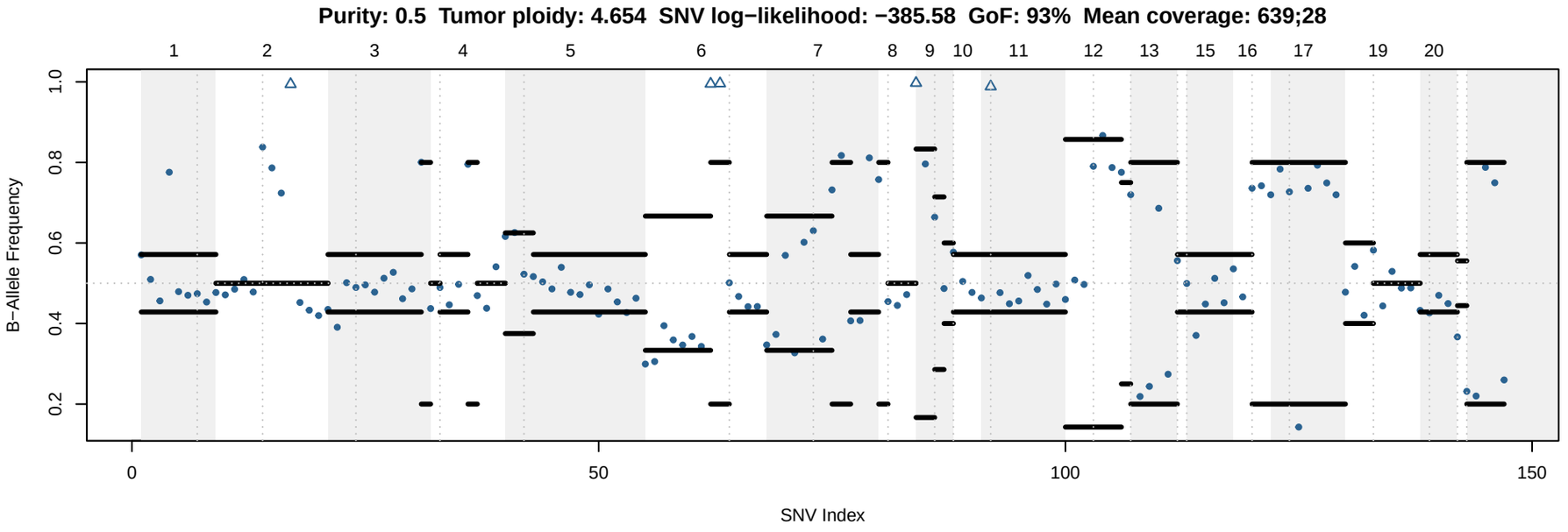
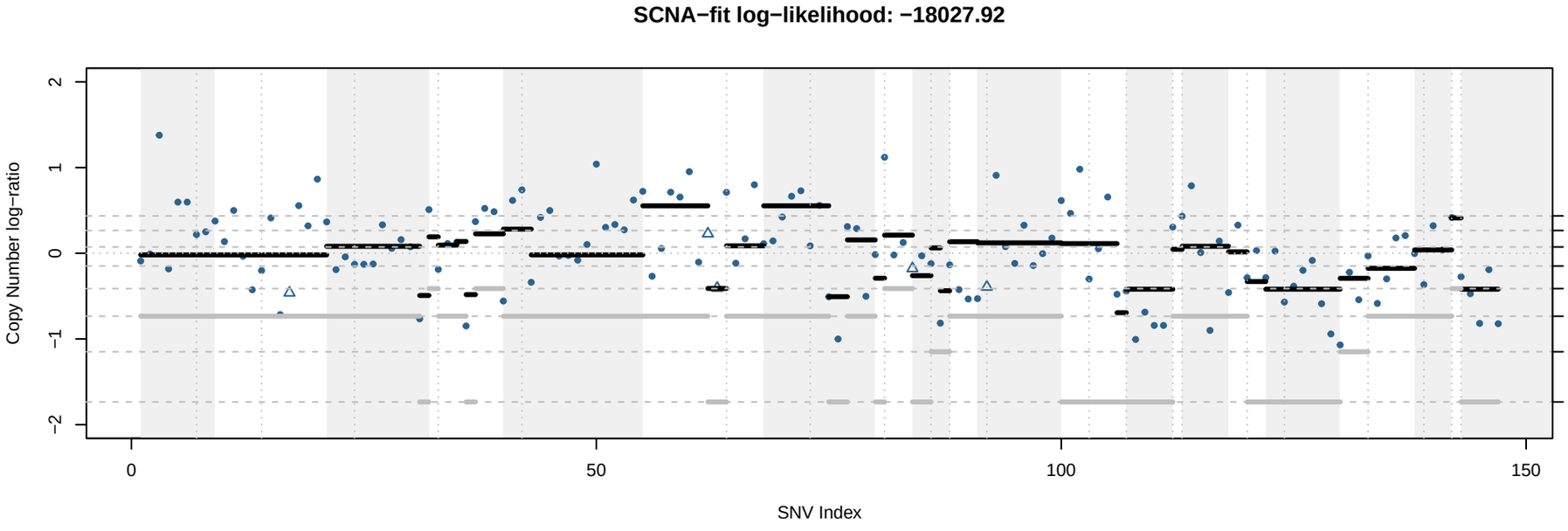
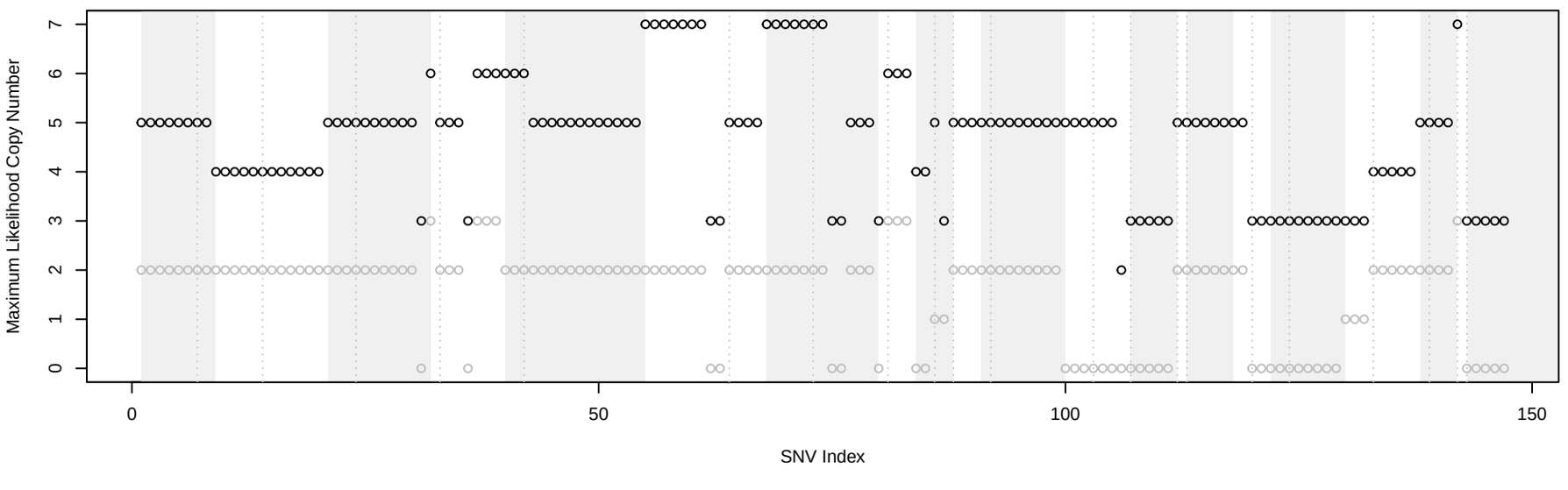
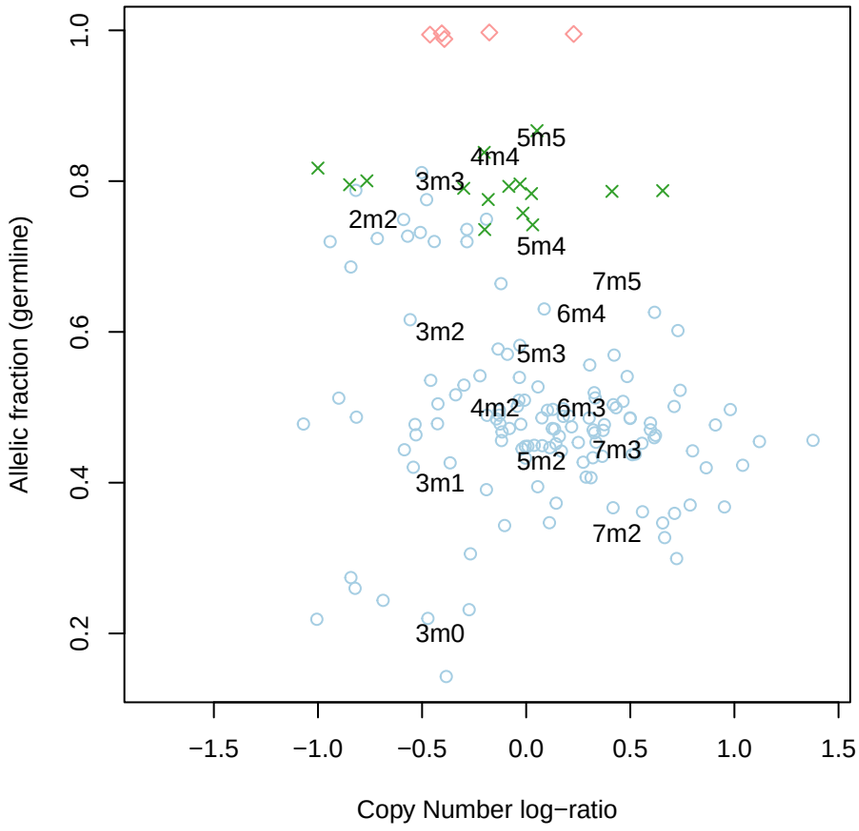
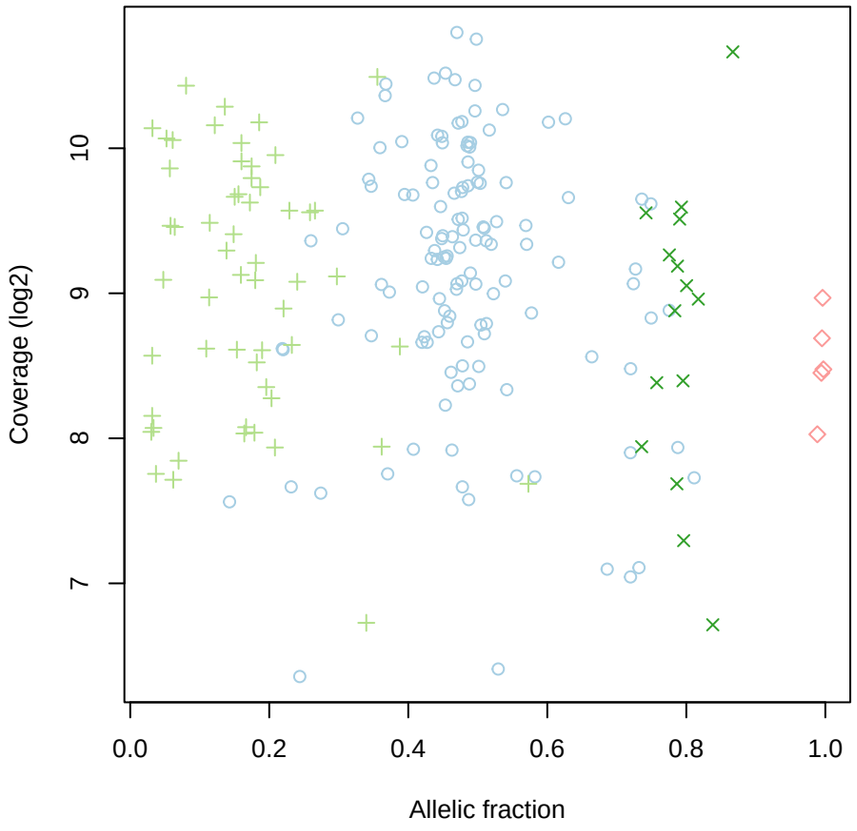

Purity: 0.5 Tumor ploidy: 4.654
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1
0
1
2
log2 ratio

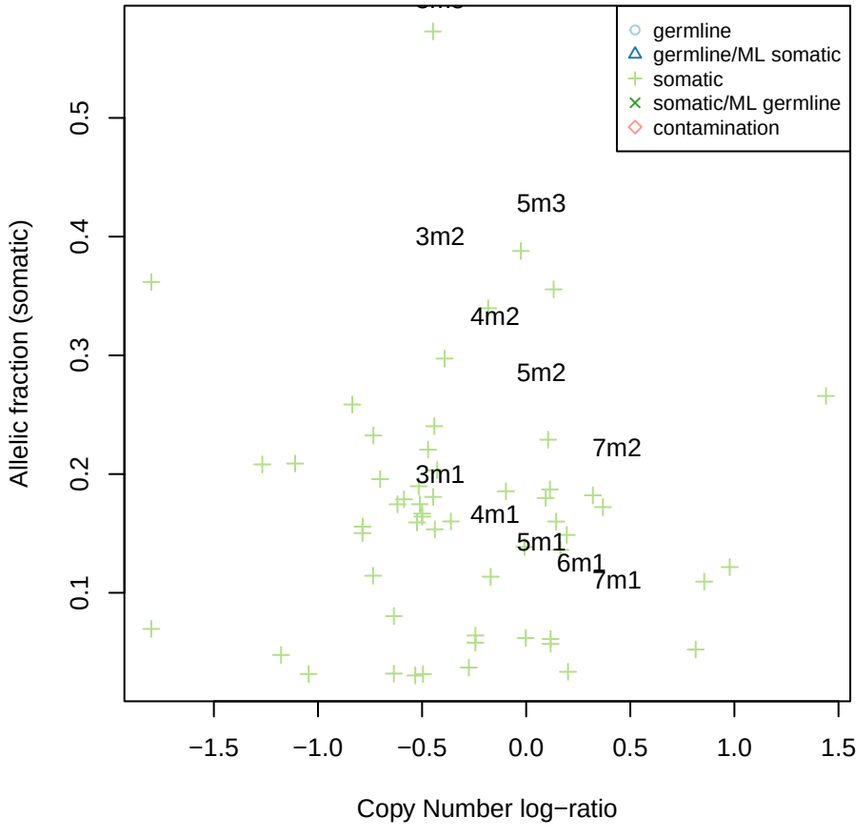

Purity: 0.5 Tumor ploidy: 4.654 SNV log−likelihood: −385.58 GoF: 93% Mean coverage: 639;28
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.2 0.4 0.6 0.8 1.0
0 50 100 150
SNV Index

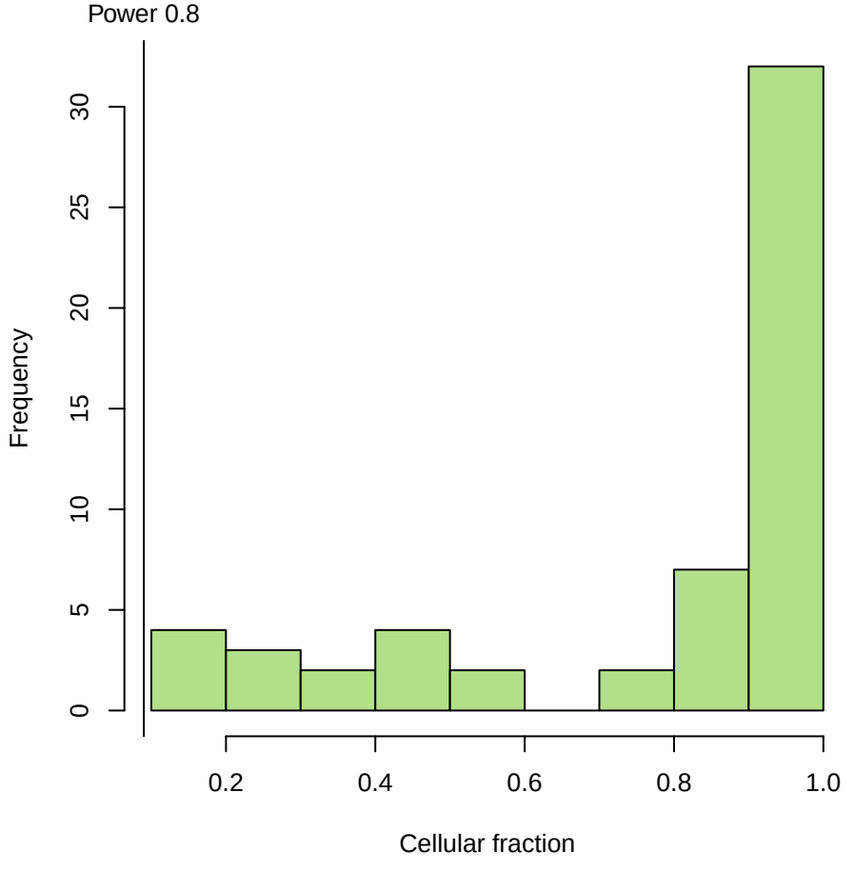

SCNA−fit log−likelihood: −18027.92
Copy Number log−ratio
−2 −1 0 1 2
0 1 2 3 4 5 7
0 50 100 150
SNV Index

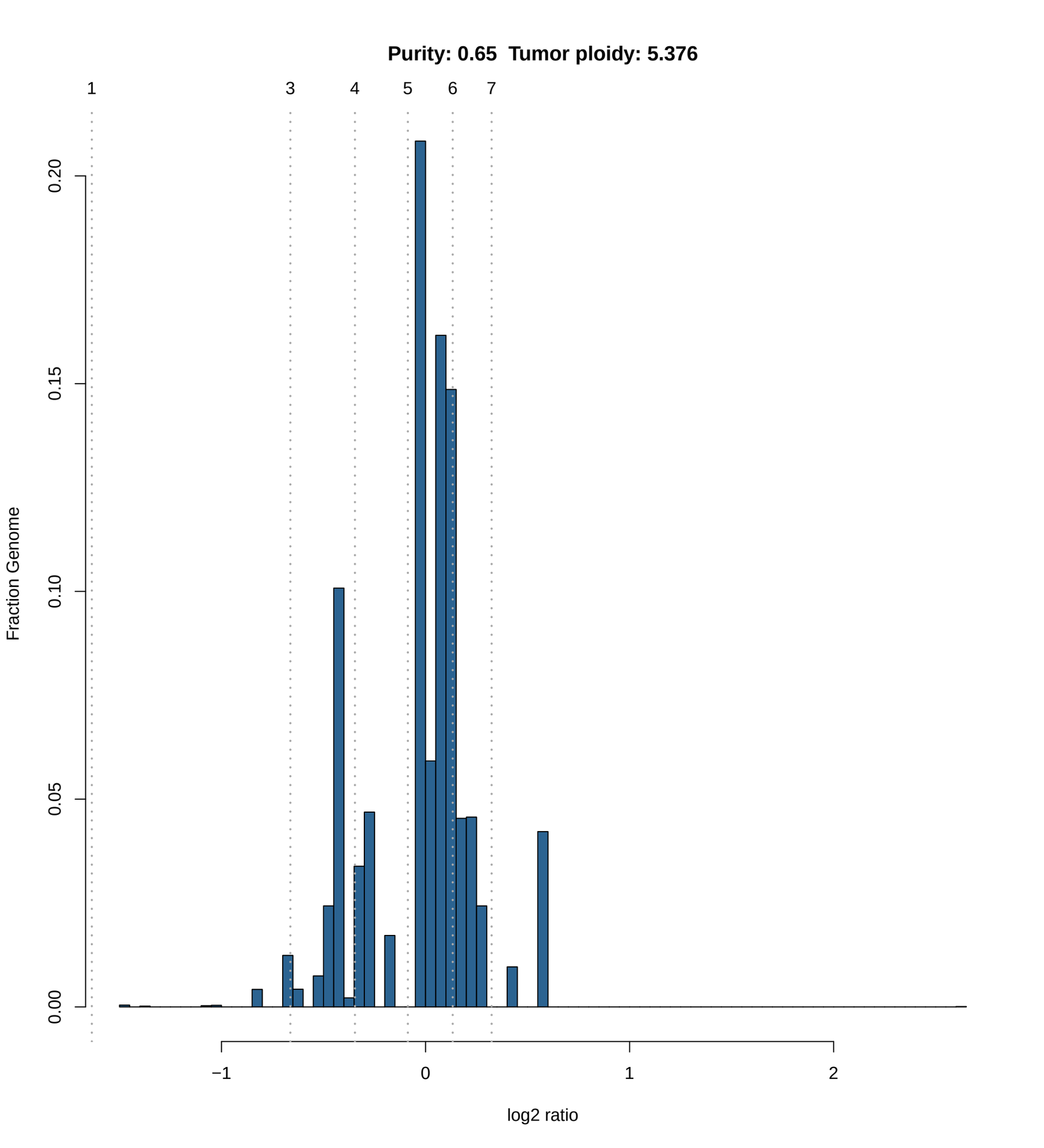

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

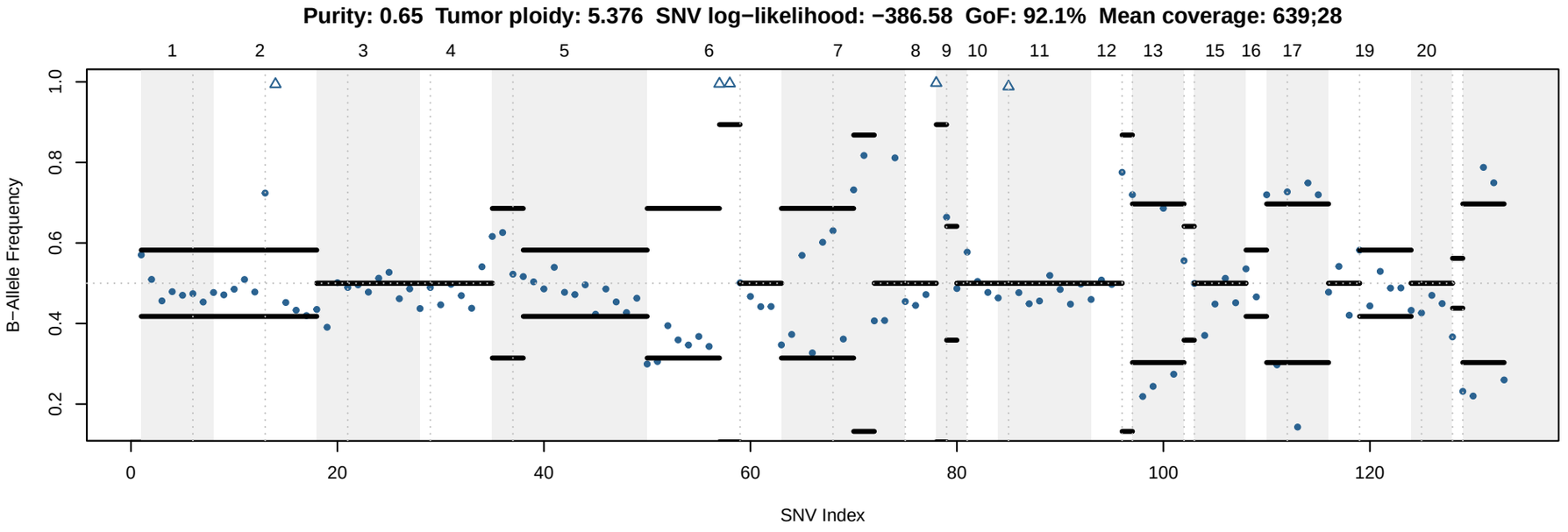

Allelic fraction (germline)
Copy Number log−ratio
5m5
4m4
3m3
2m2
5m4
7m5
6m4
3m2
5m3
4m2
6m3
7m3
5m2
3m1
7m2
3m0

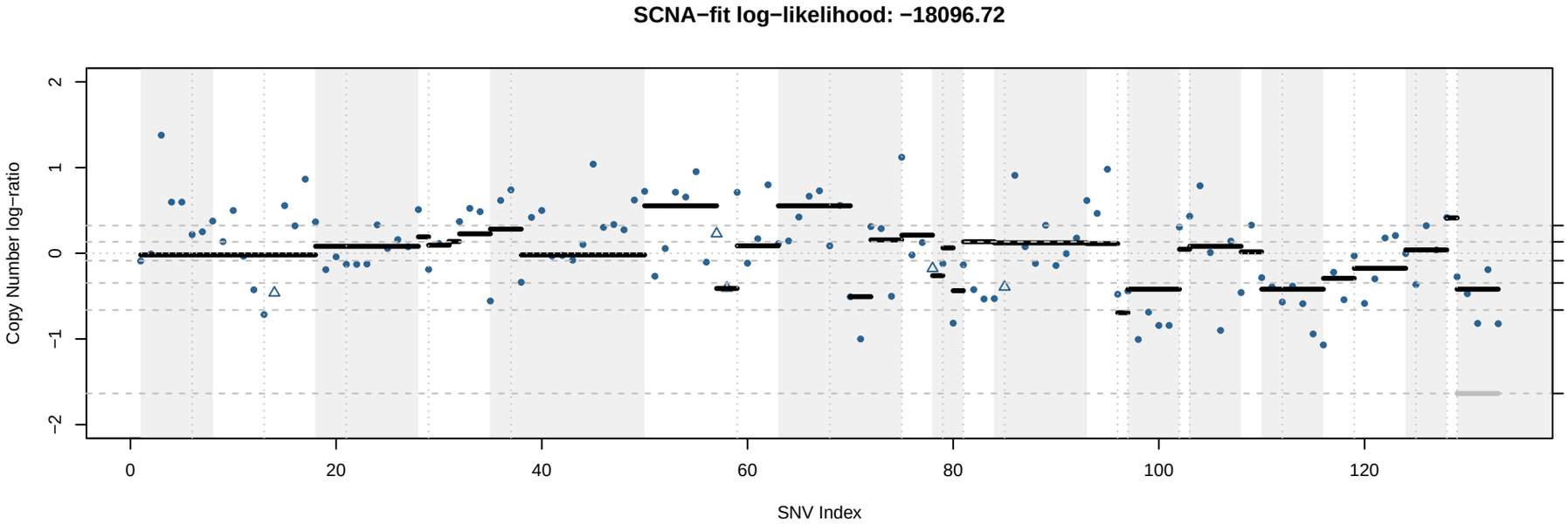

Coverage (log2)
Allelic fraction

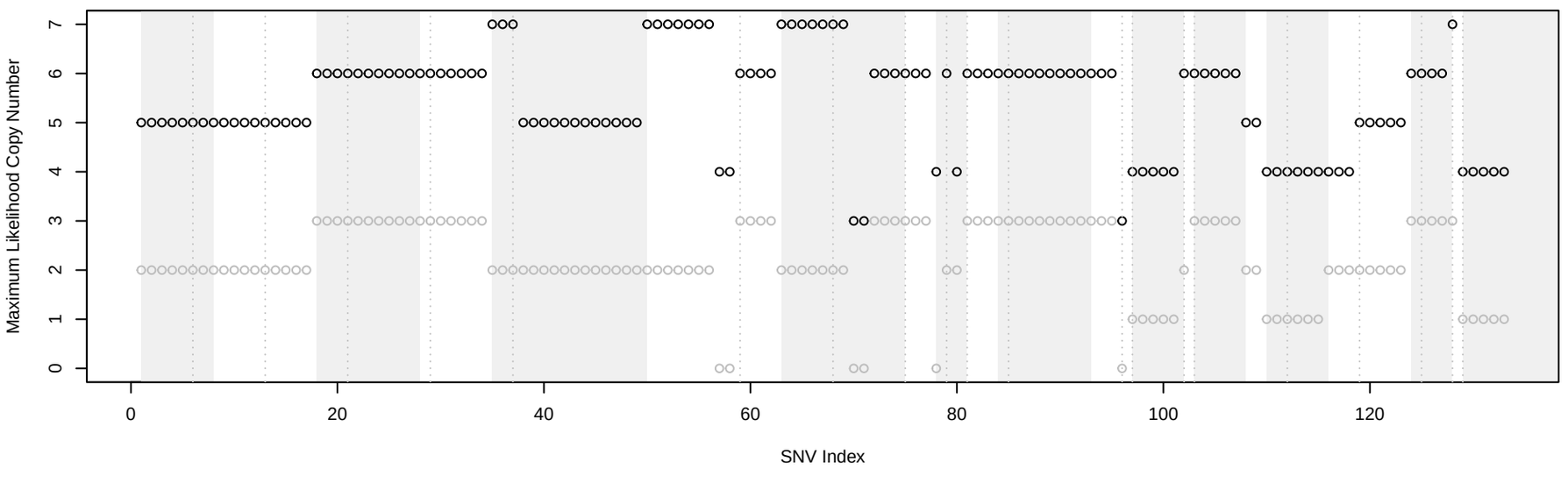

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
5m3
3m2
4m2
5m2
7m2
3m1
4m1
5m1
6m1
7m1

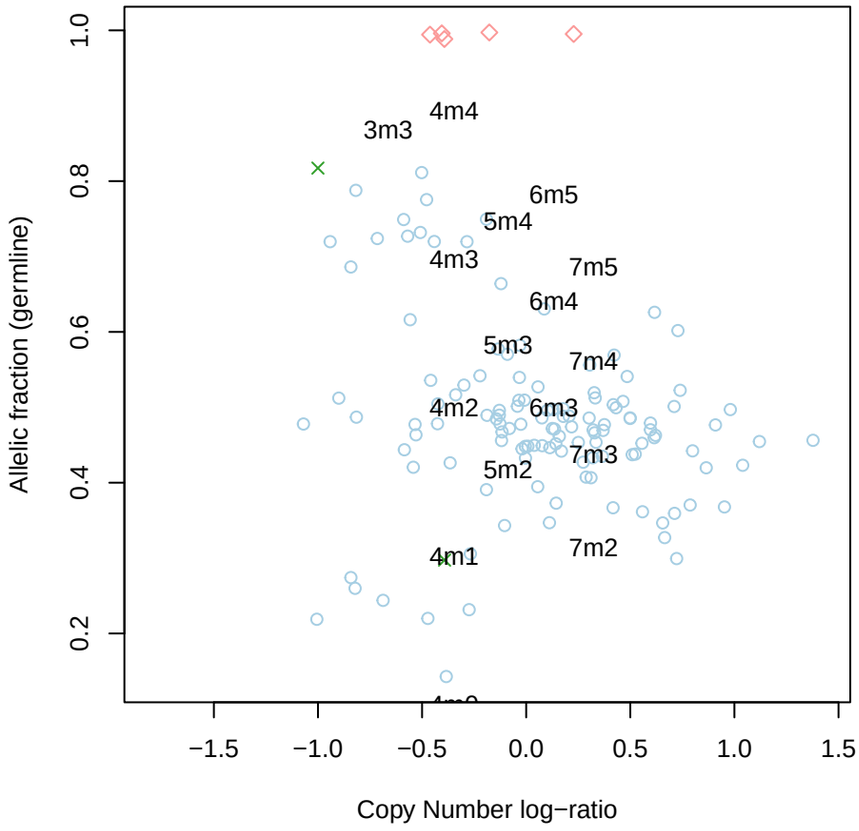

Power 0.8
Frequency
Cellular fraction

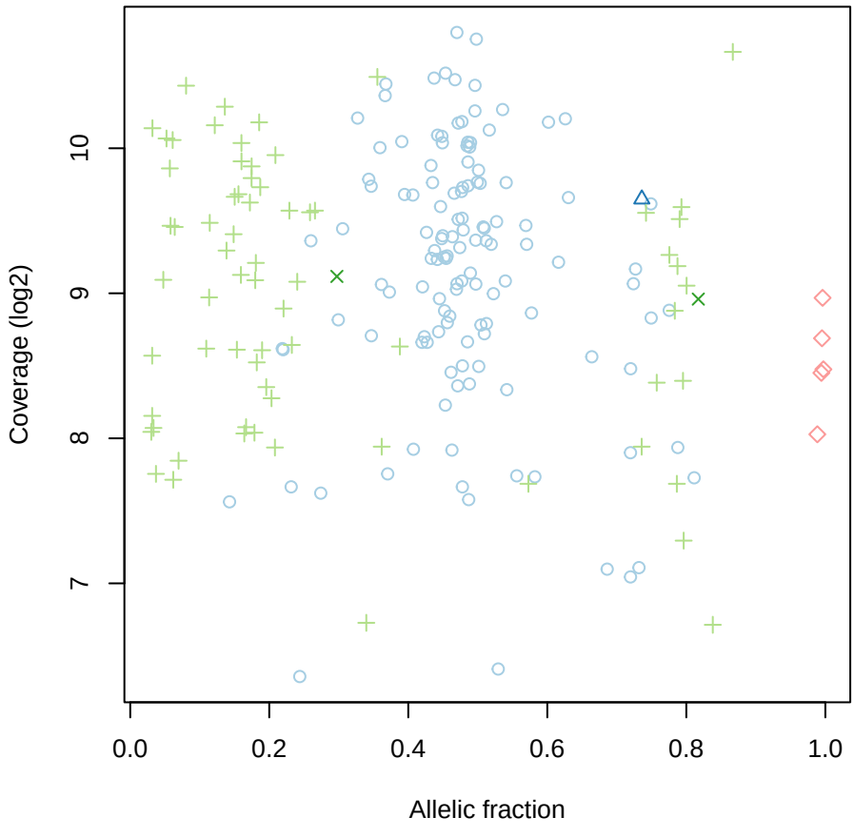

Purity: 0.65 Tumor ploidy: 5.376
1
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1
0
1
2
log2 ratio

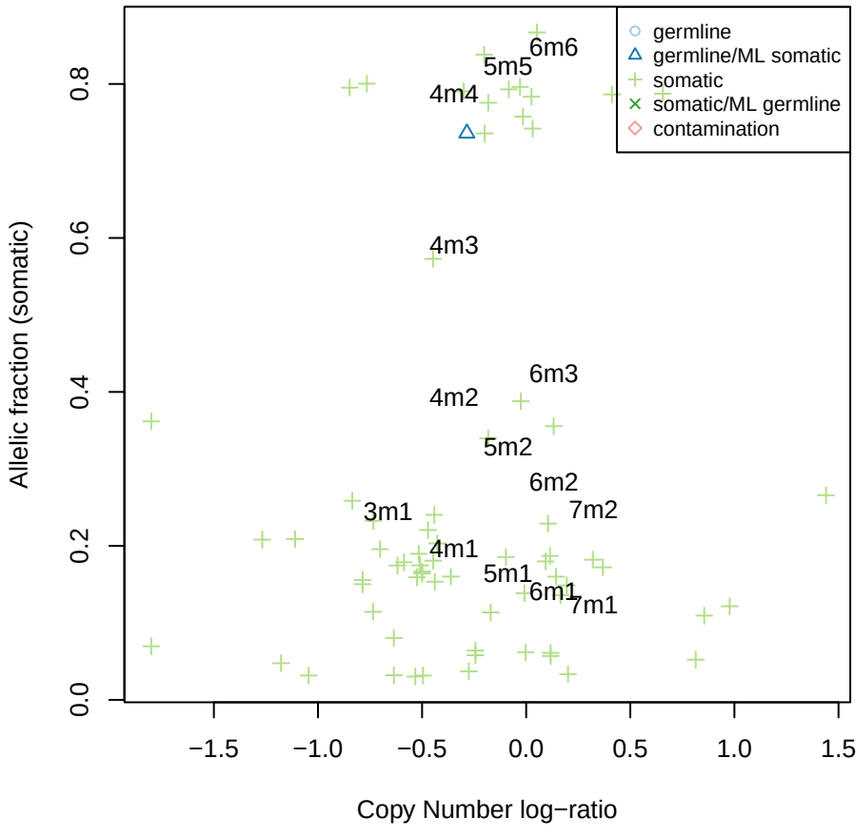

Purity: 0.65 Tumor ploidy: 5.376 SNV log−likelihood: −386.58 GoF: 92.1% Mean coverage: 639;28
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.2 0.4 0.6 0.8 1.0
0 20 40 60 80 100 120
SNV Index

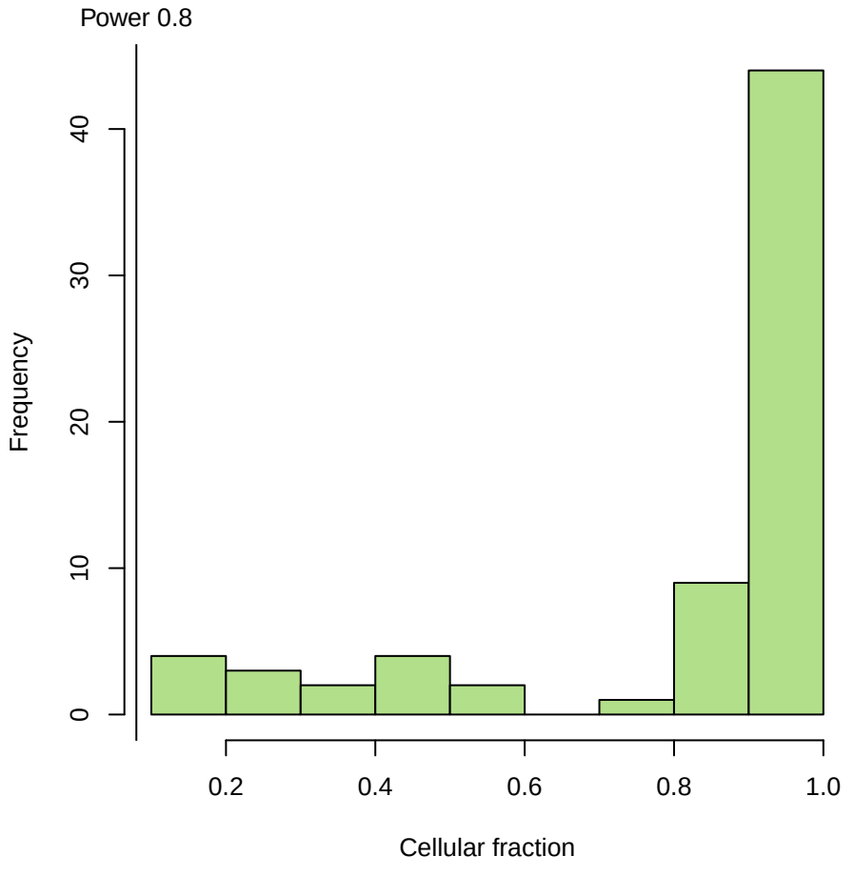

SCNA−fit log−likelihood: −18096.72
Copy Number log−ratio
−2 −1 0 1 2
1 3 4 6
0 20 40 60 80 100 120
SNV Index

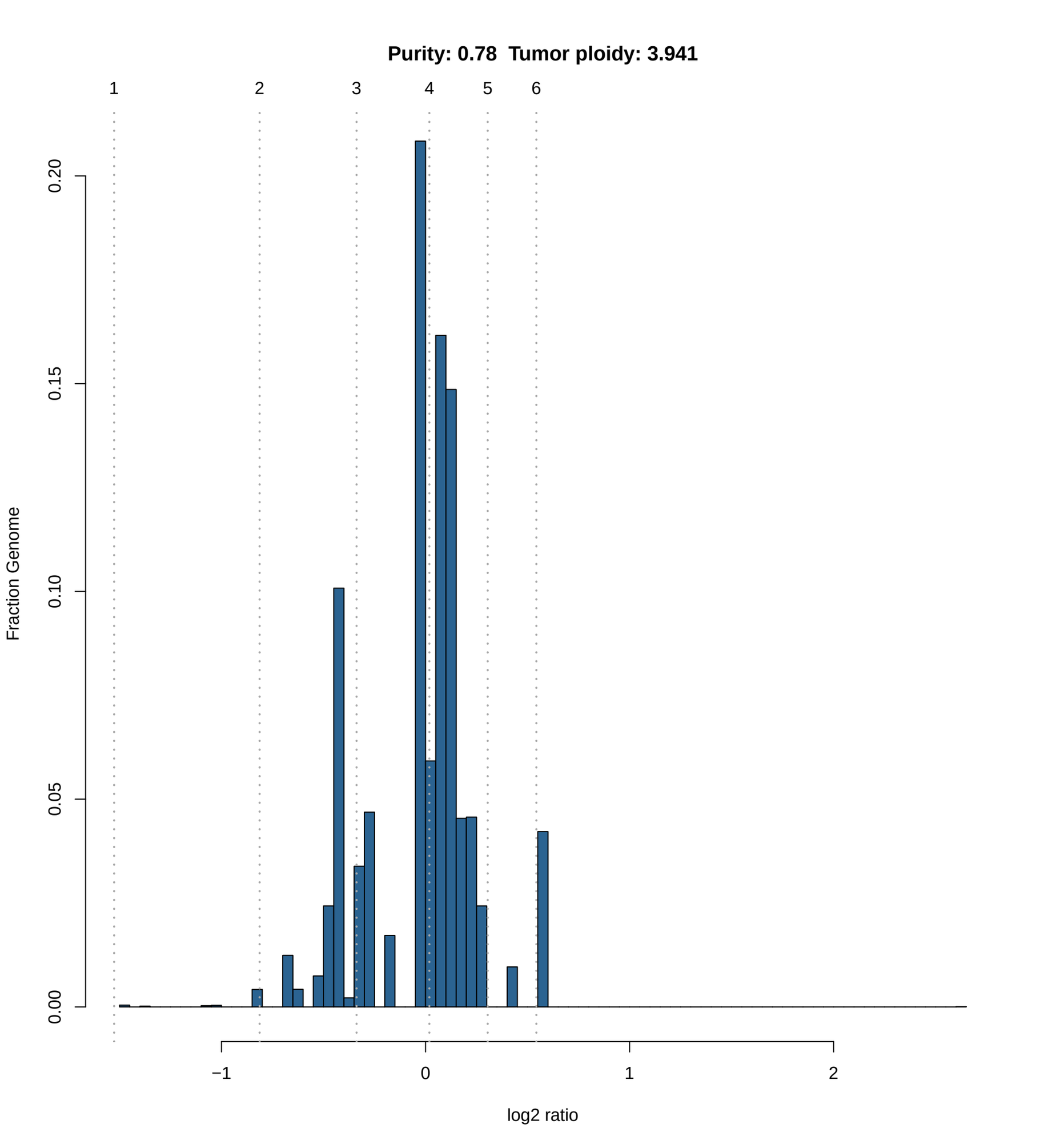

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

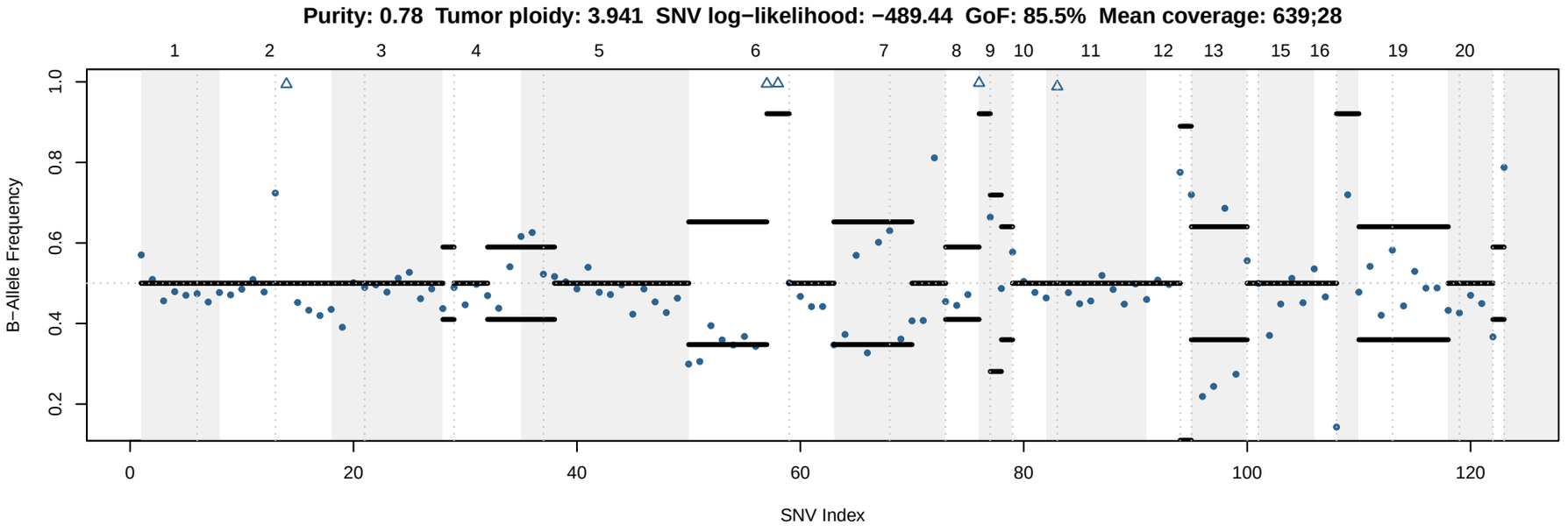

Allelic fraction (germline)
Copy Number log−ratio
3m3
4m4
6m5
5m4
4m3
7m5
6m4
5m3
7m4
4m2
6m3
7m3
5m2
7m2
4m1

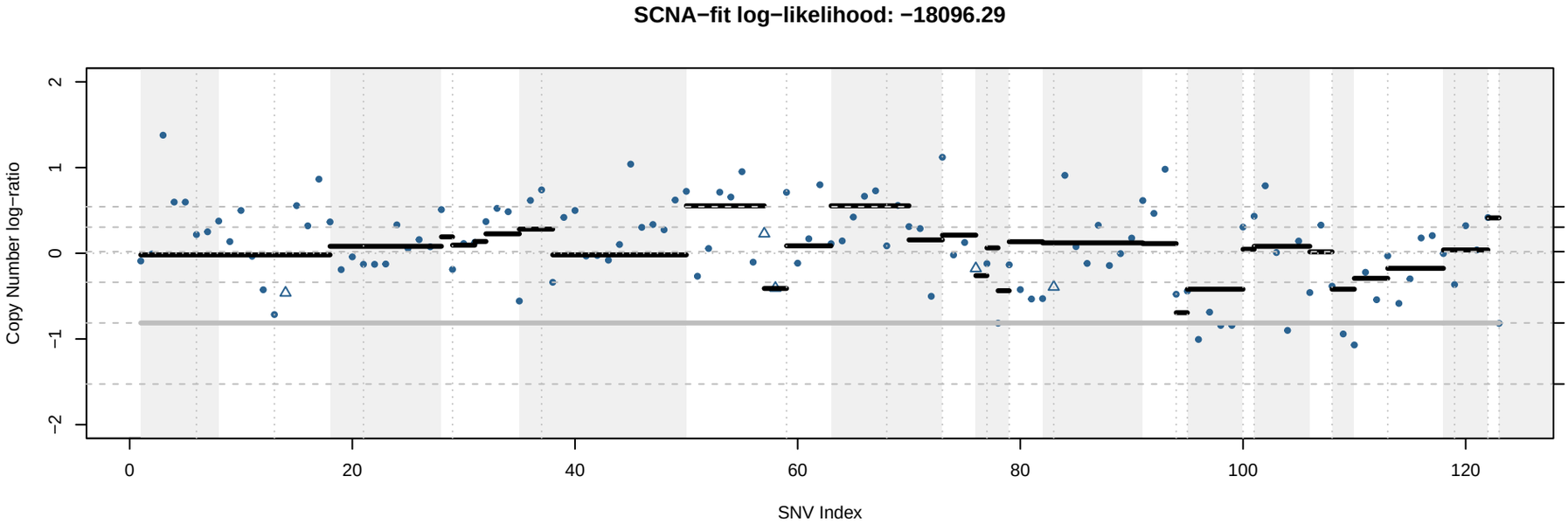

Coverage (log2)
Allelic fraction

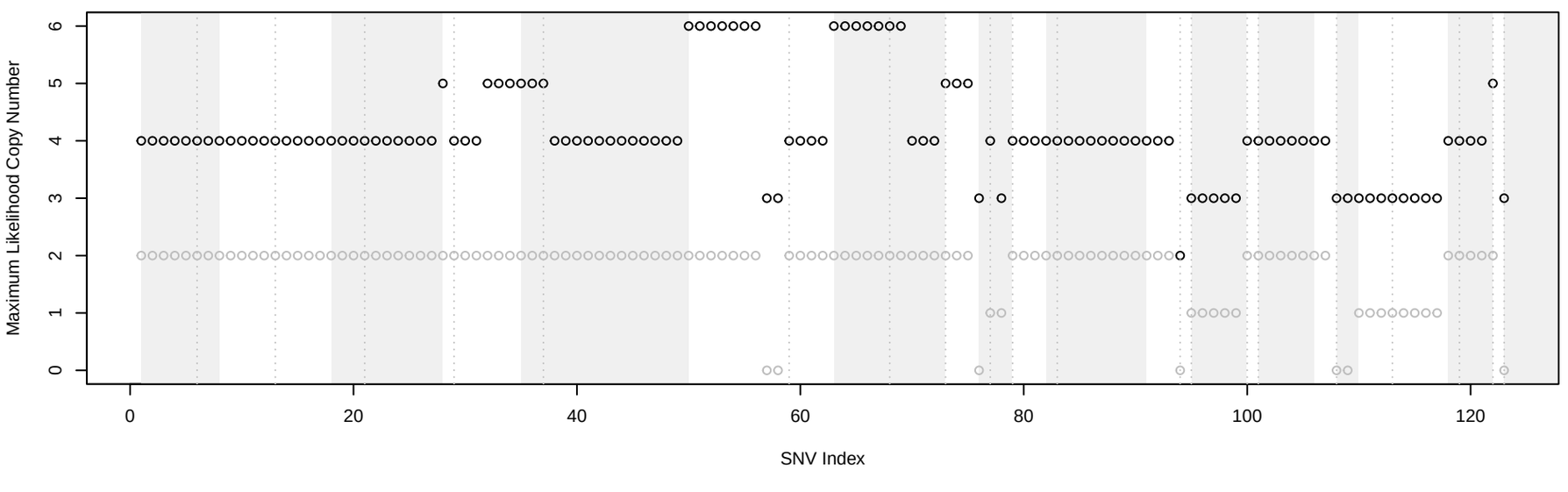

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
6m6
5m5
4m4
4m3
6m3
4m2
5m2
6m2
3m1
7m2
4m1
5m1
6m1
7m1

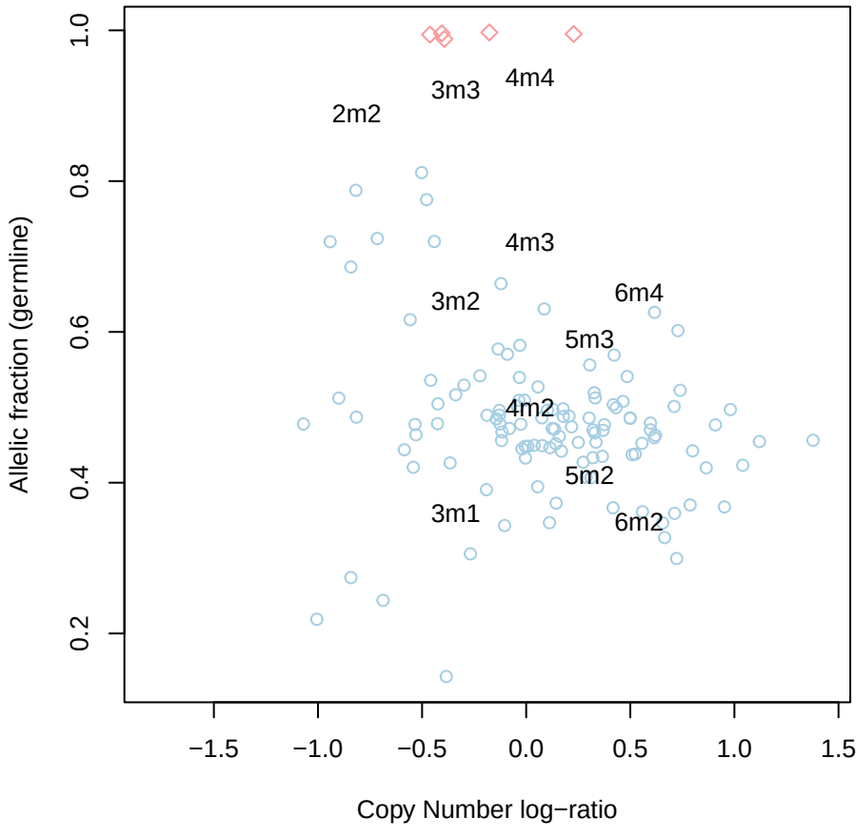

Power 0.8
Frequency
Cellular fraction

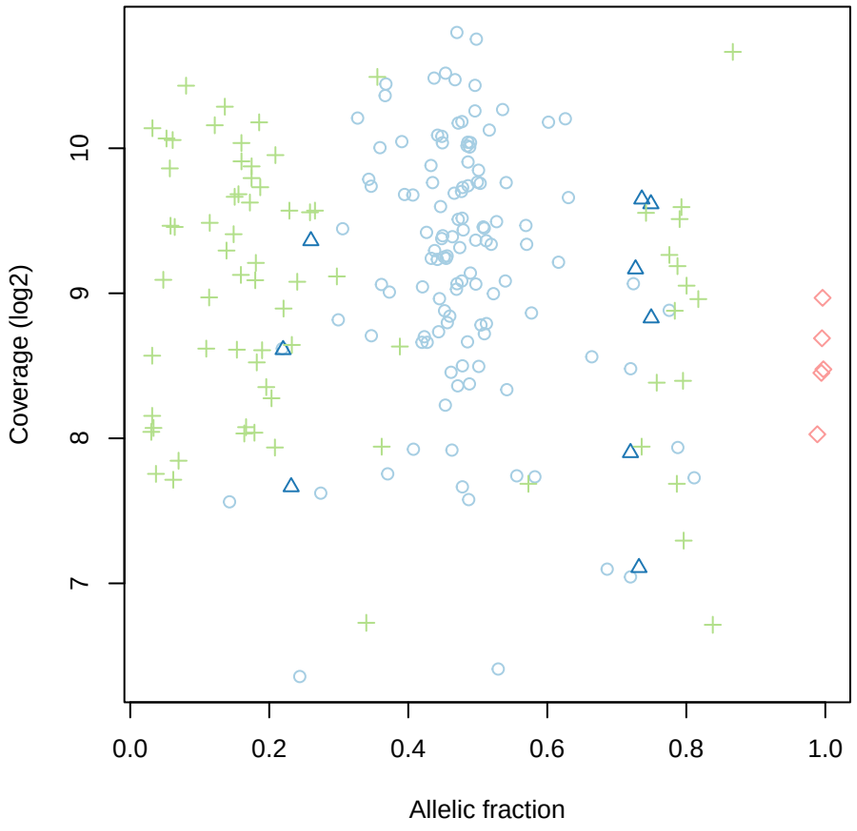

Purity: 0.78 Tumor ploidy: 3.941
1
2
3
4
5
6
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1
0
1
2
log2 ratio

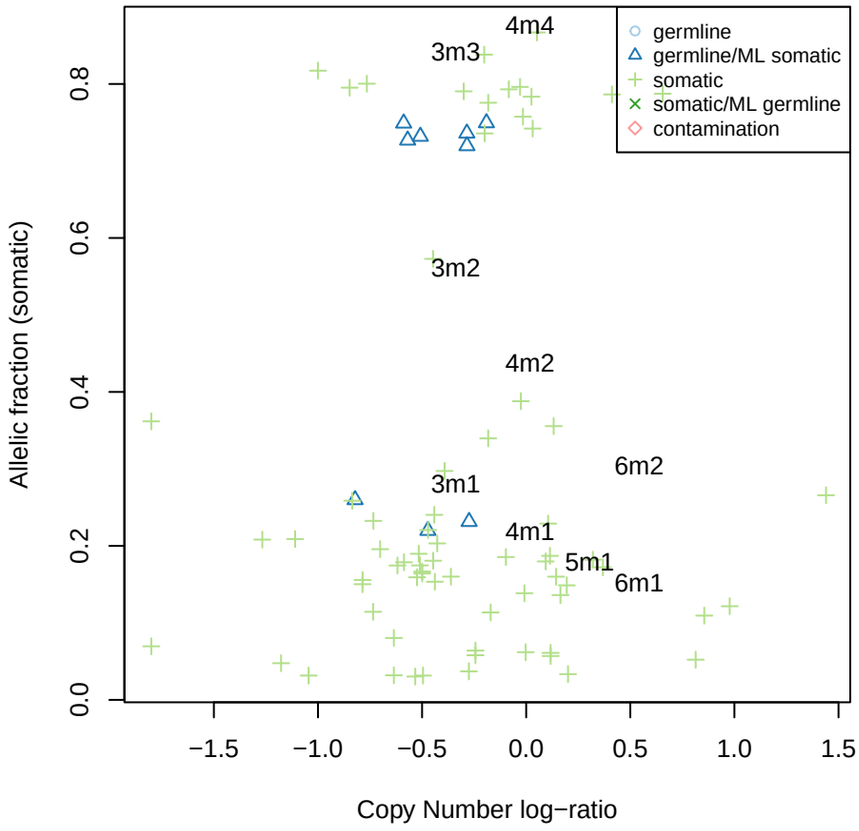

Purity: 0.78 Tumor ploidy: 3.941 SNV log−likelihood: −489.44 GoF: 85.5% Mean coverage: 639;28
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 19 20
B−Allele Frequency
0.2 0.4 0.6 0.8 1.0
0 20 40 60 80 100 120
SNV Index

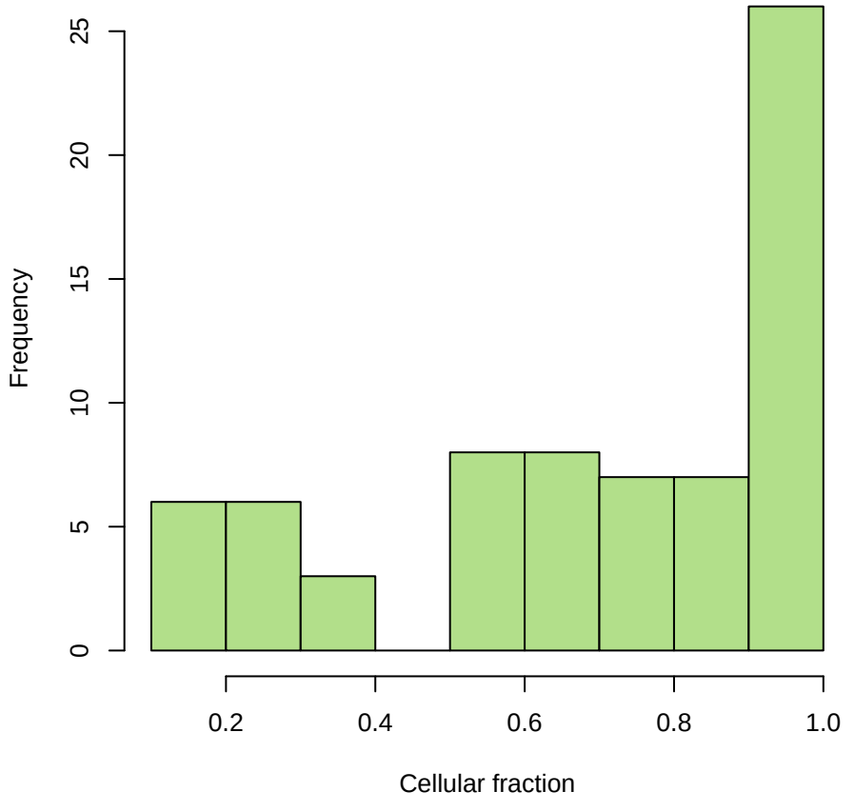

SCNA−fit log−likelihood: −18096.29
Copy Number log−ratio
−2 −1 0 1 2
1 2 3 4 6
0 20 40 60 80 100 120
SNV Index

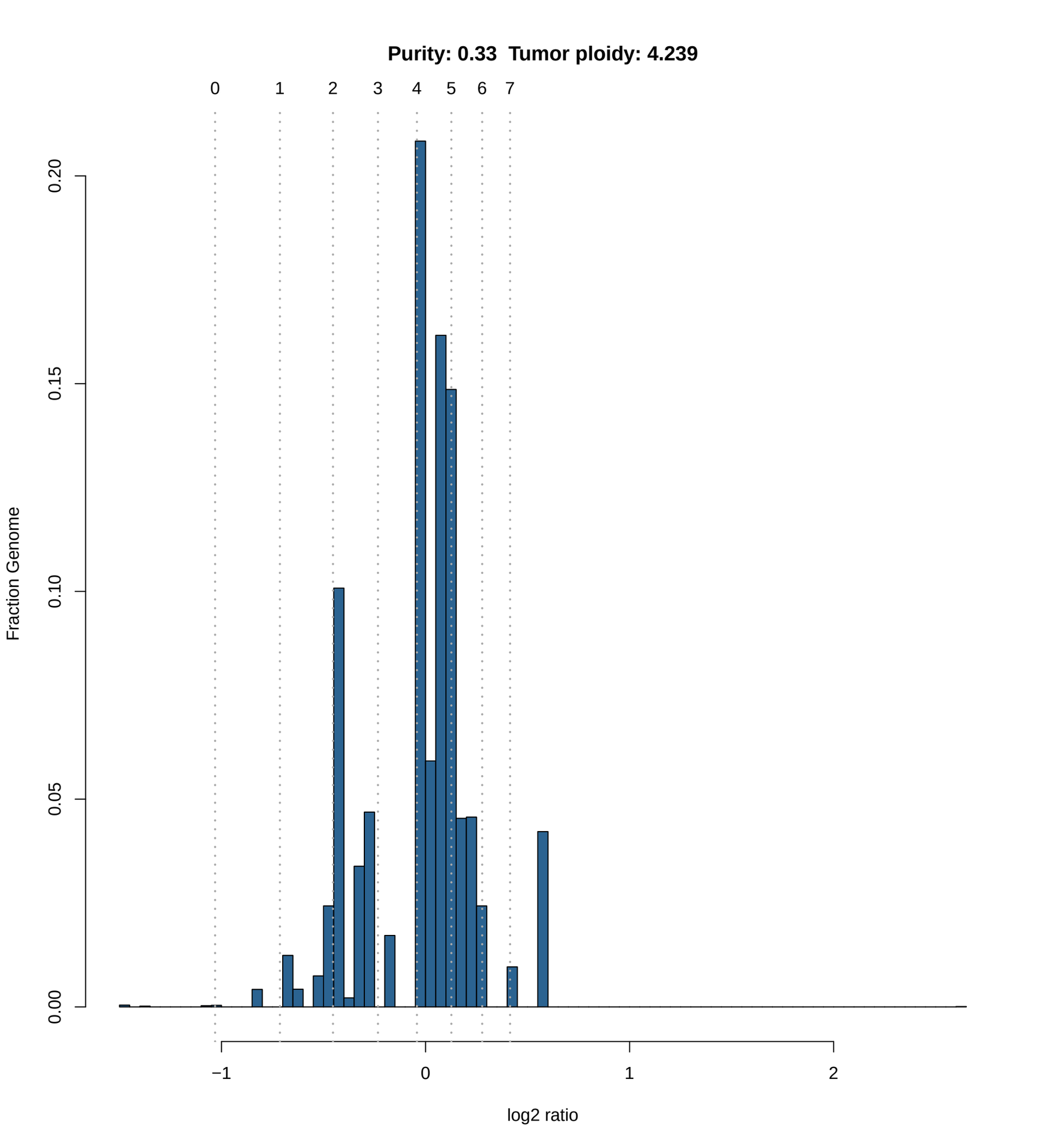

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120
SNV Index

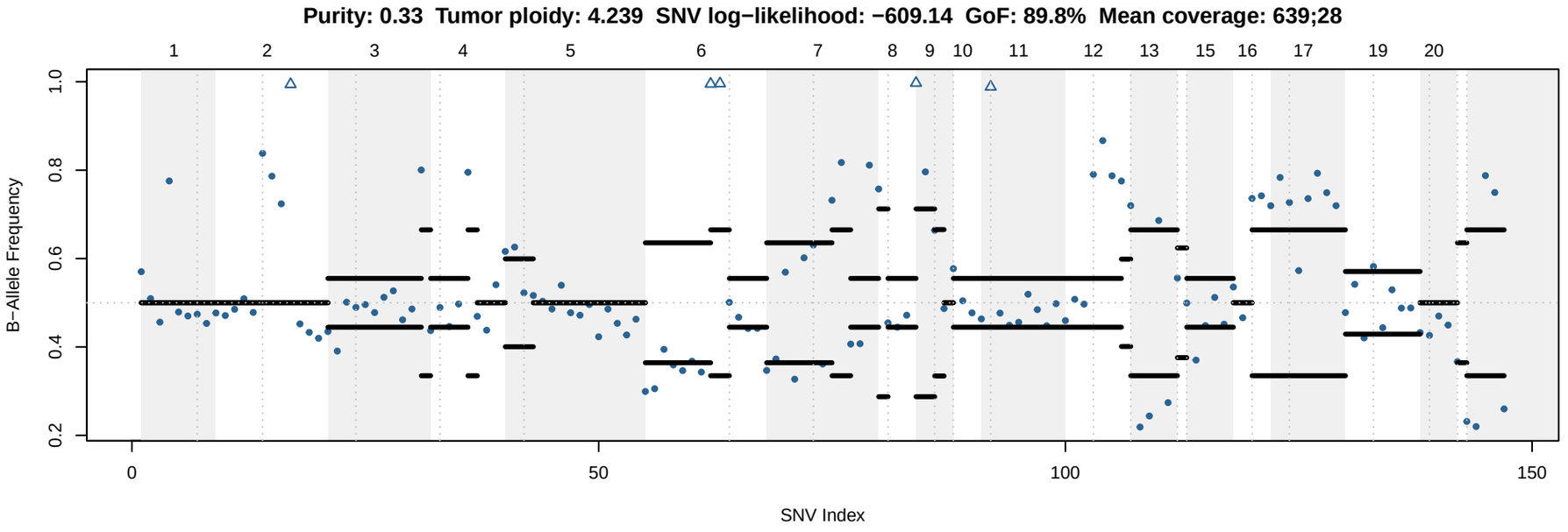

Allelic fraction (germline)
Copy Number log−ratio
2m2
3m3
4m4
4m3
3m2
6m4
5m3
4m2
5m2
3m1
6m2

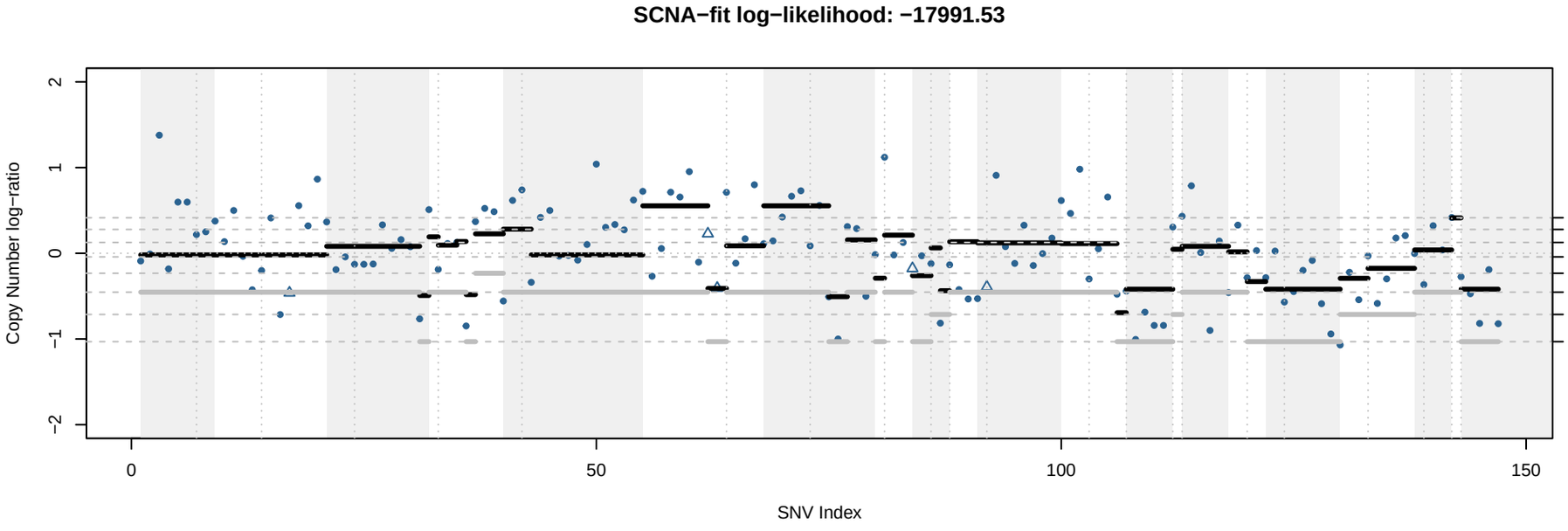

Coverage (log2)
Allelic fraction

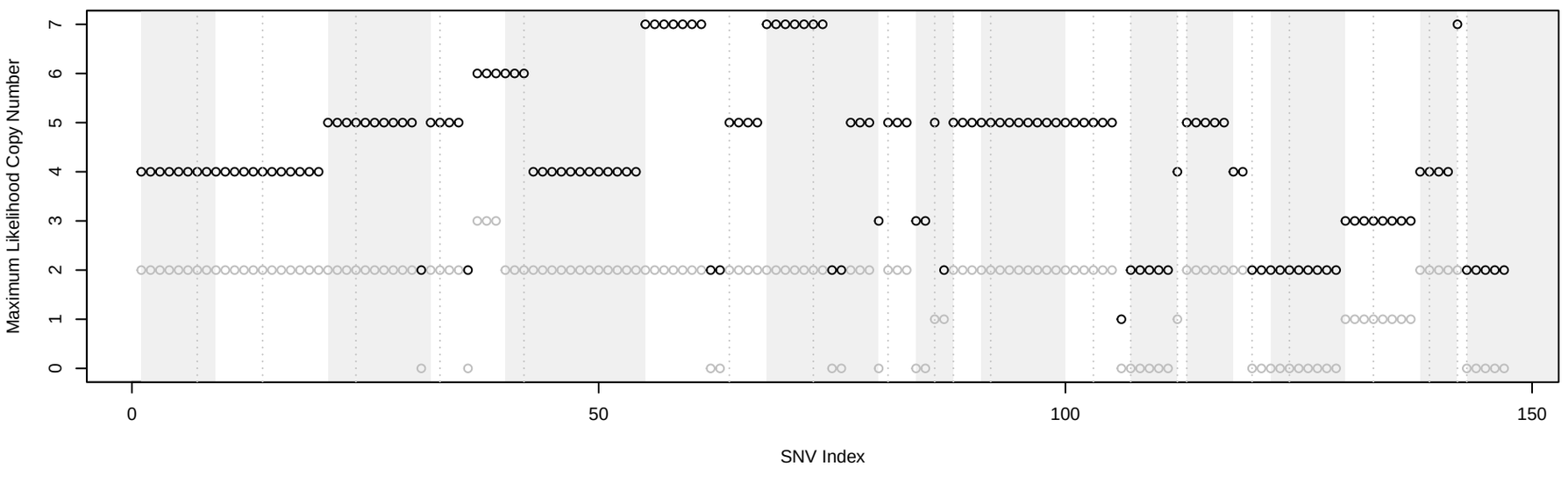

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m4
3m3
3m2
4m2
6m2
3m1
4m1
5m1
6m1

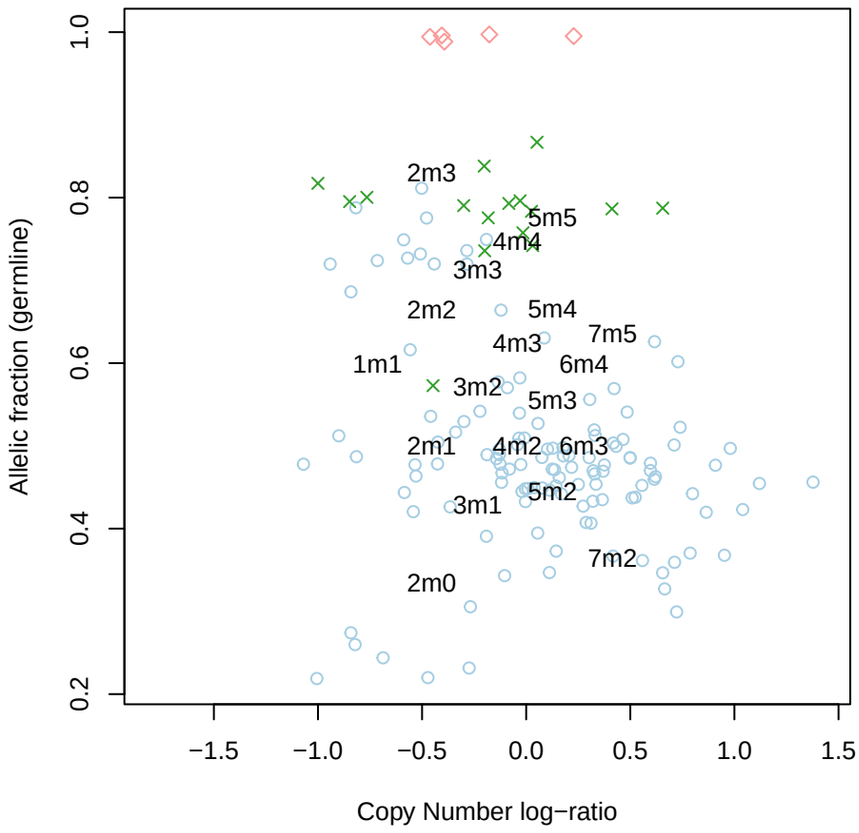

Frequency
Cellular fraction

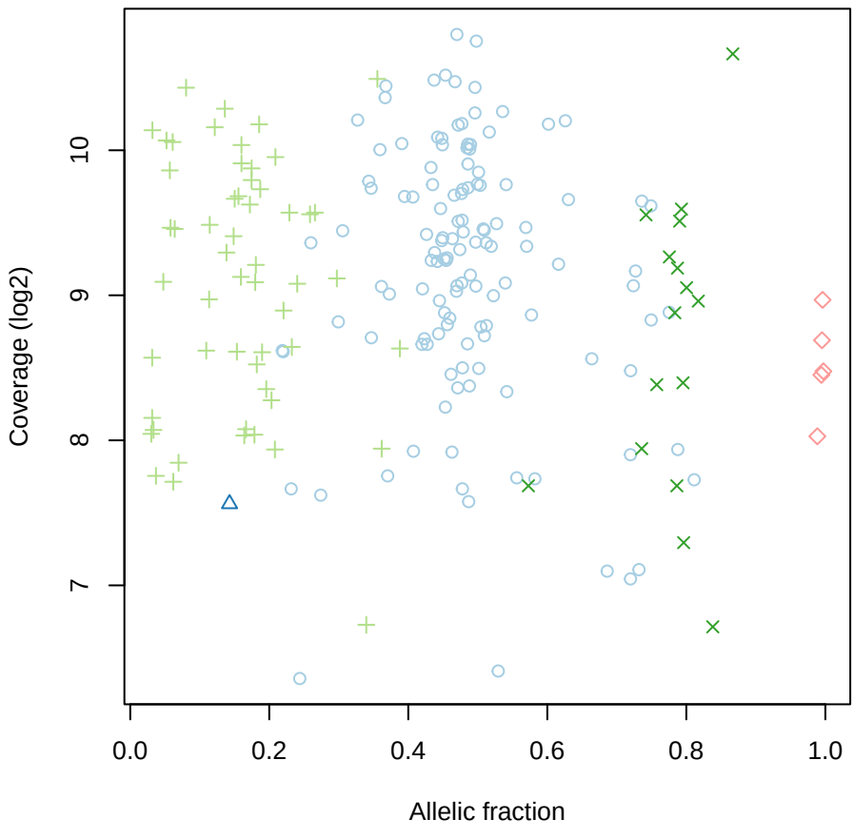

Purity: 0.33 Tumor ploidy: 4.239
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1
0
1
2
log2 ratio

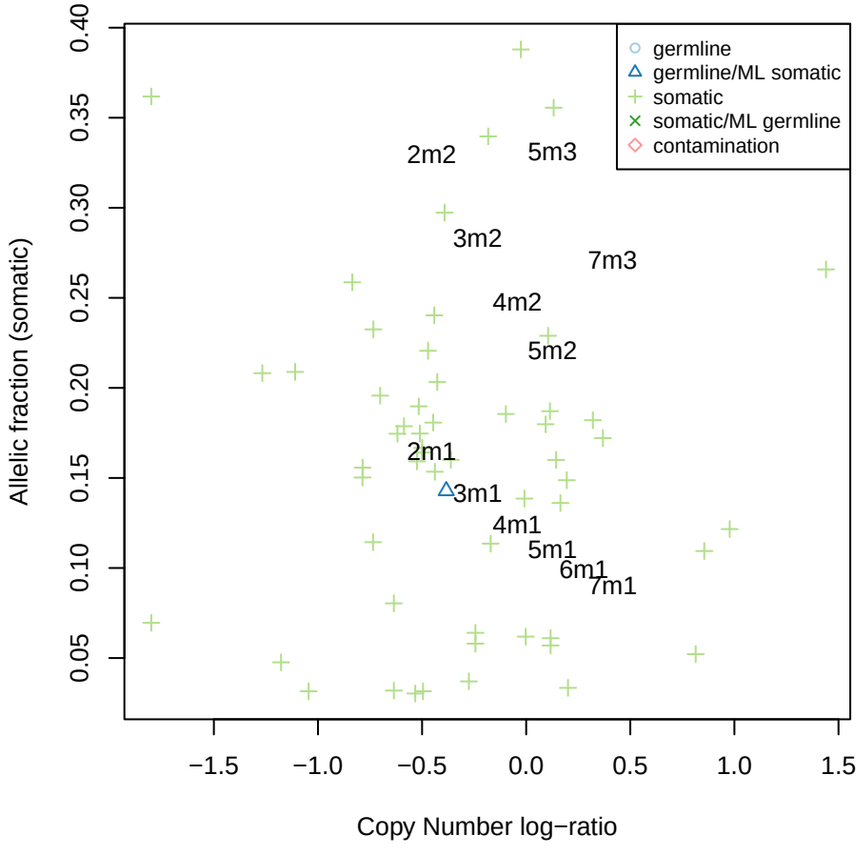

Purity: 0.33 Tumor ploidy: 4.239 SNV log−likelihood: −609.14 GoF: 89.8% Mean coverage: 639;28
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.2 0.4 0.6 0.8 1.0
0 50 100 150
SNV Index

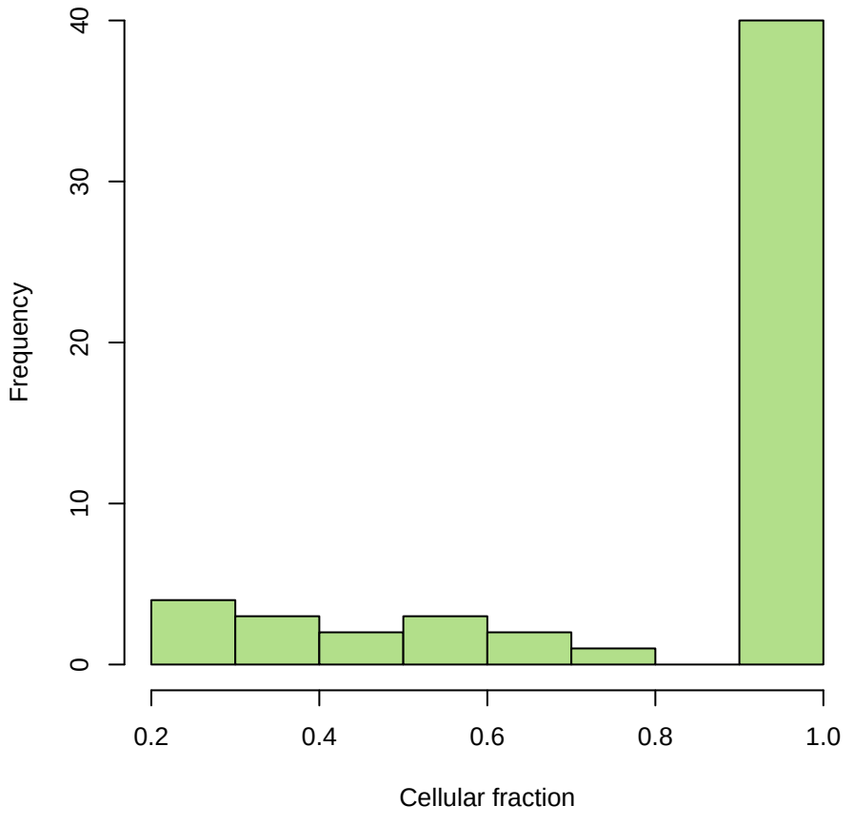

SCNA−fit log−likelihood: −17991.53
Copy Number log−ratio
−2 −1 0 1 2
0 1 3 5 7
0 50 100 150
SNV Index

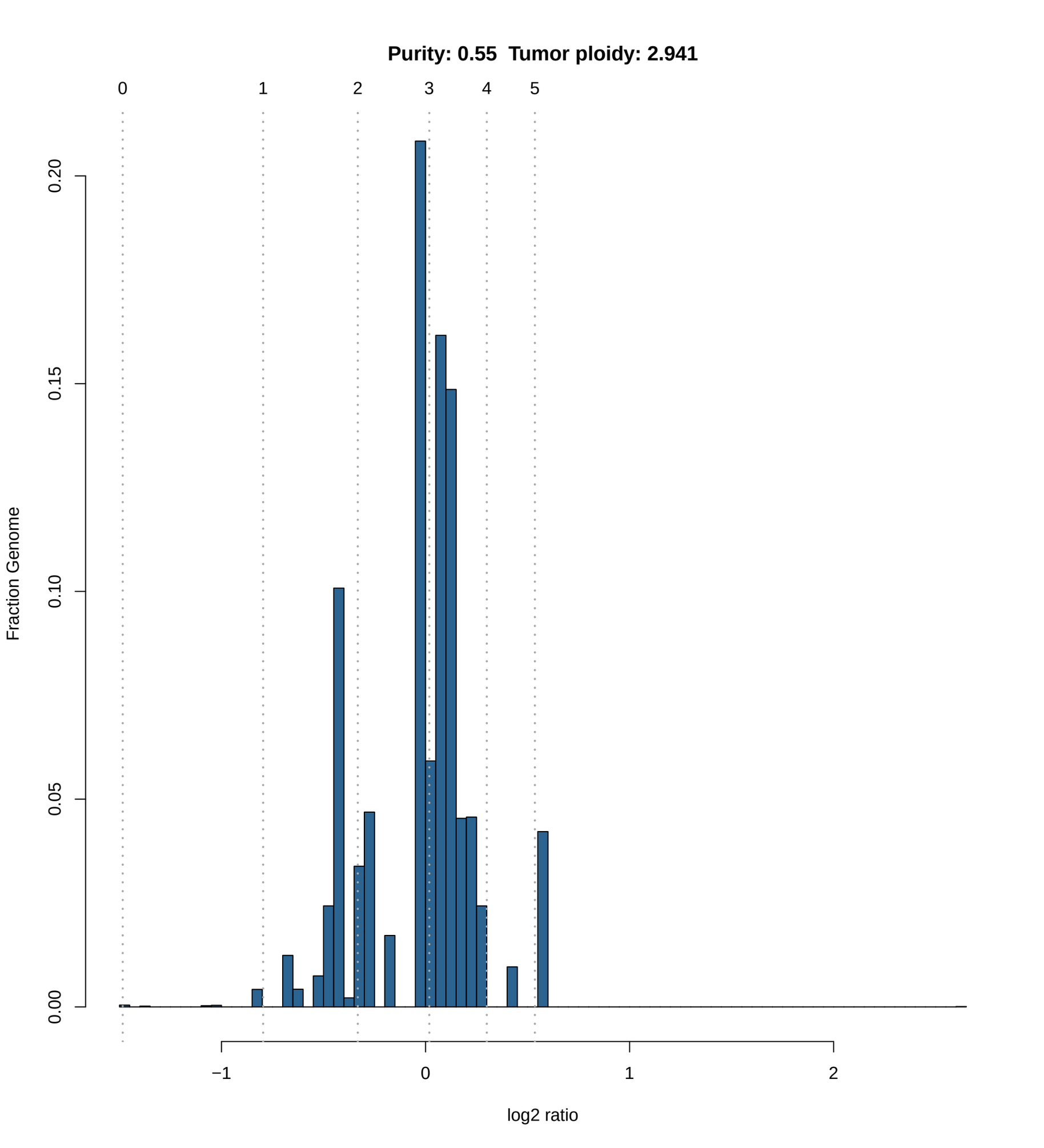

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

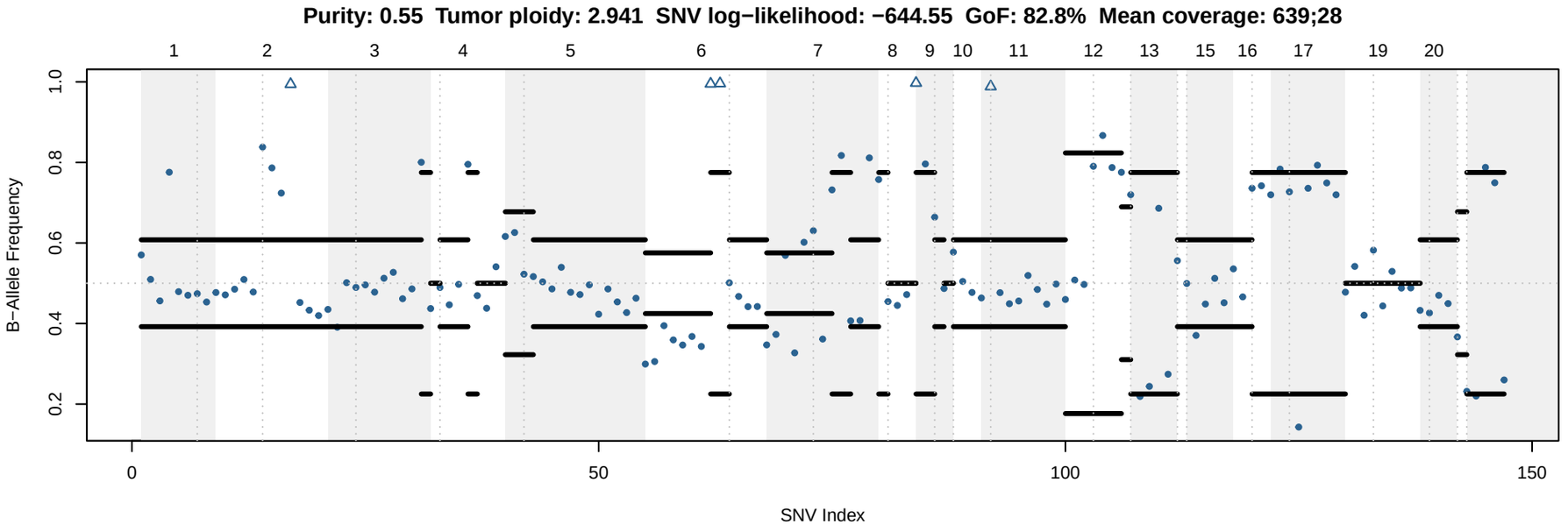

Allelic fraction (germline)
Copy Number log−ratio
2m3
5m5
4m4
3m3
2m2
5m4
7m5
4m3
1m1
6m4
3m2
5m3
2m1
4m2
6m3
5m2
3m1
7m2
2m0

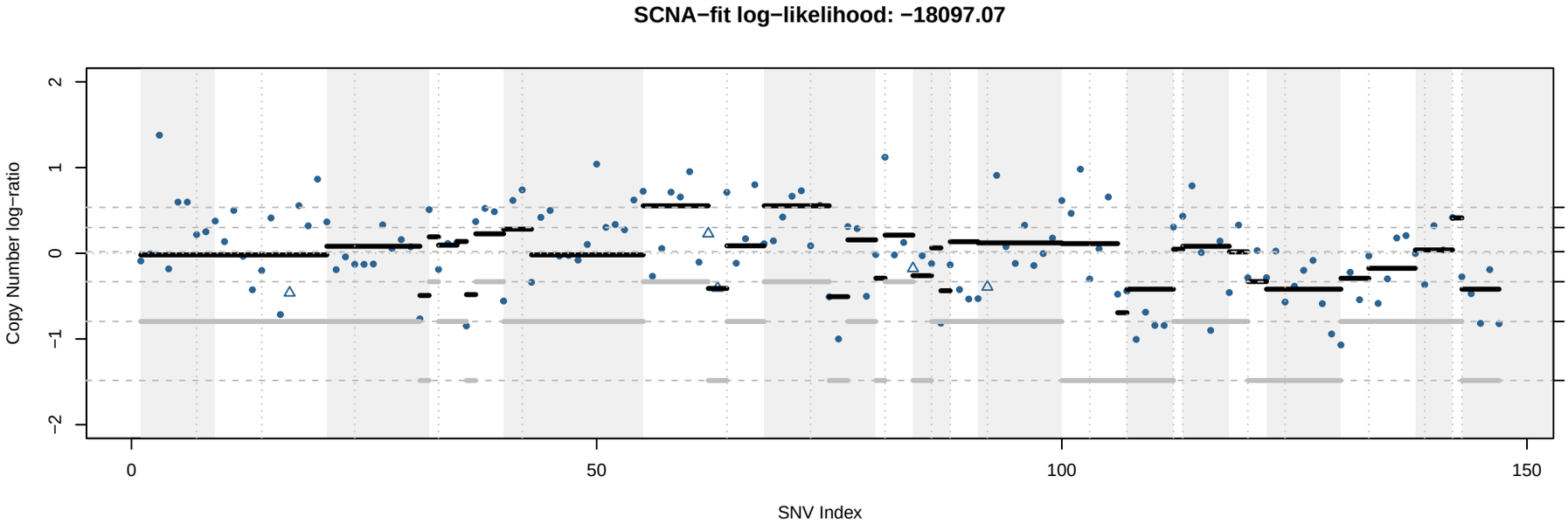

Coverage (log2)
Allelic fraction

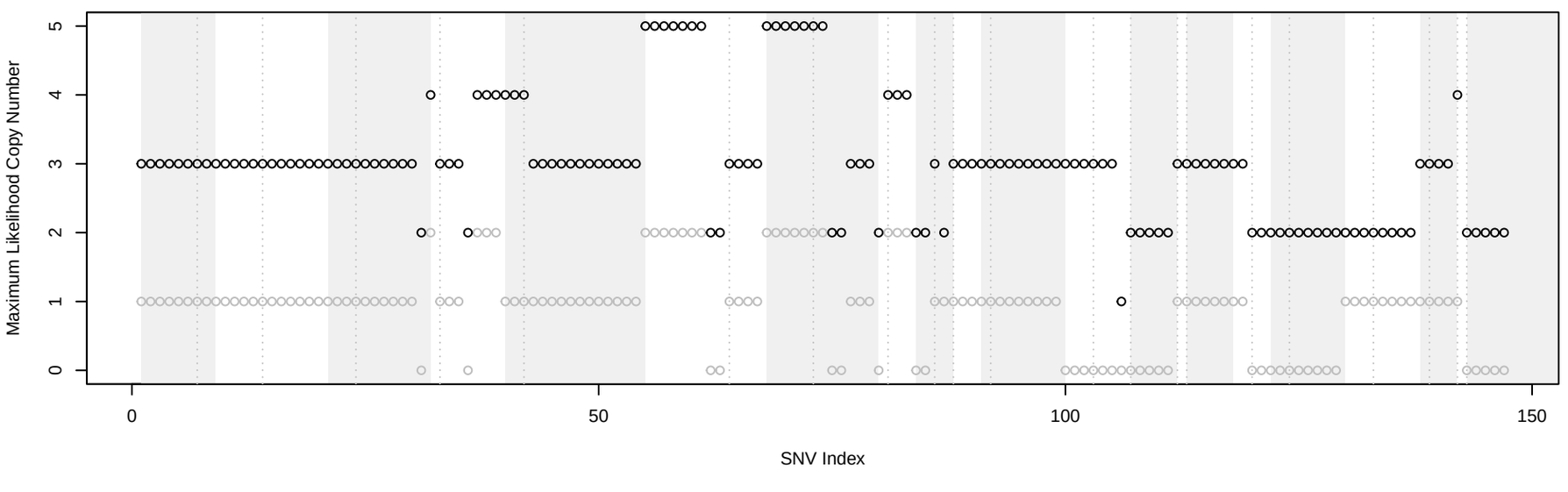

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m2
5m3
3m2
7m3
4m2
5m2
2m1
3m1
4m1
5m1
6m1
7m1

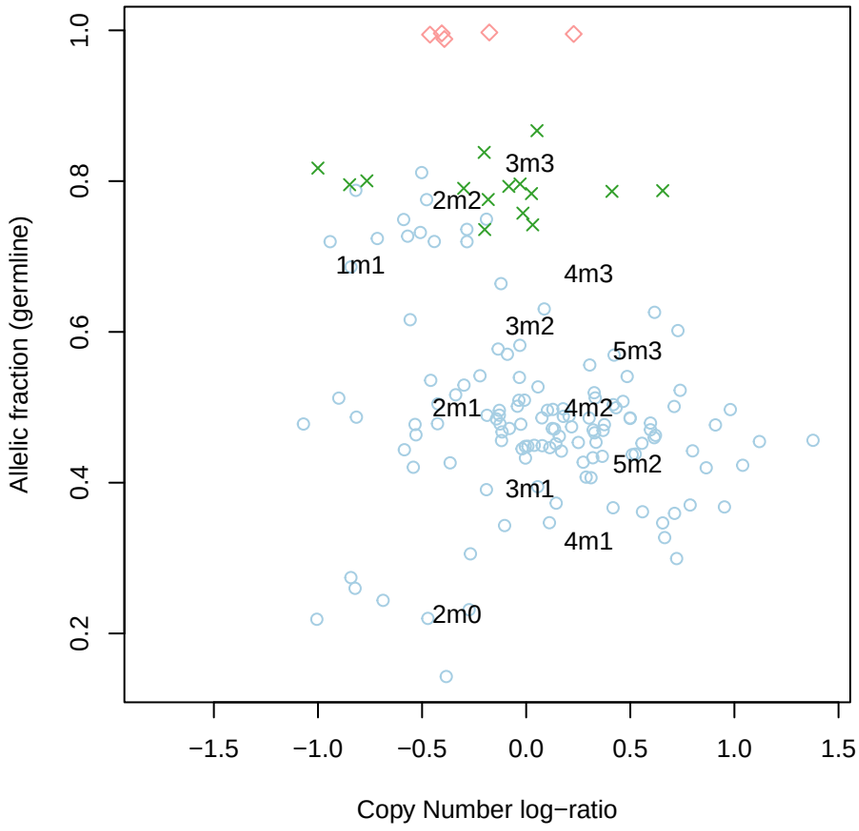

Frequency
Cellular fraction

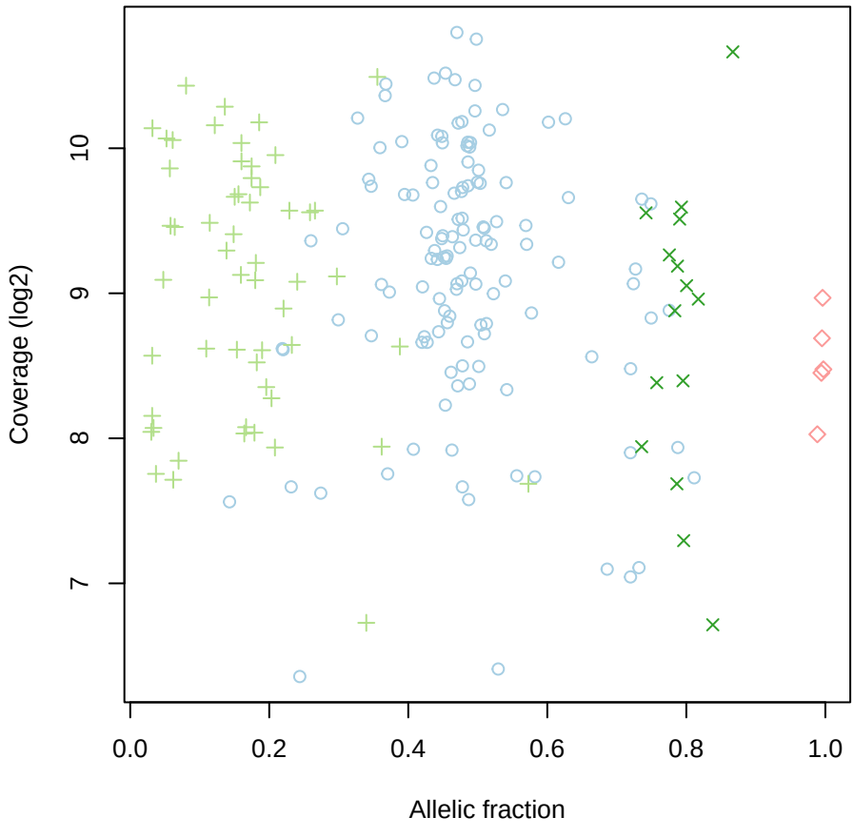

Purity: 0.55 Tumor ploidy: 2.941
0
1
2
3
4
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1
0
1
2
log2 ratio

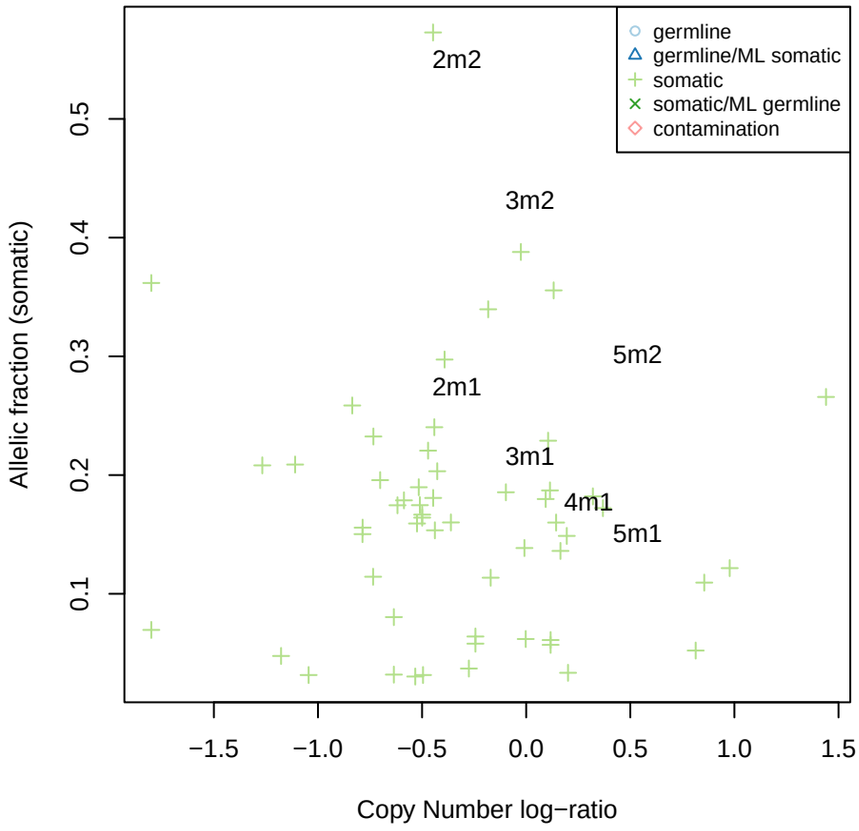

Purity: 0.55 Tumor ploidy: 2.941 SNV log−likelihood: −644.55 GoF: 82.8% Mean coverage: 639;28
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.2 0.4 0.6 0.8 1.0
0 50 100 150
SNV Index

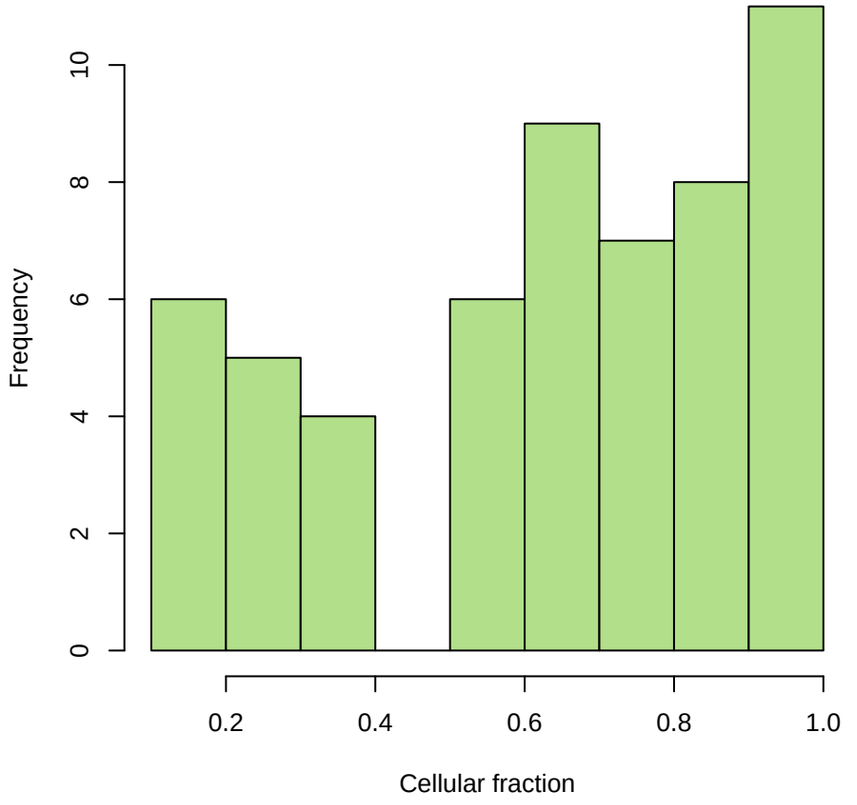

SCNA−fit log−likelihood: −18097.07
Copy Number log−ratio
−2 −1 0 1 2
0 1 2 3 4 5
0 50 100 150
SNV Index

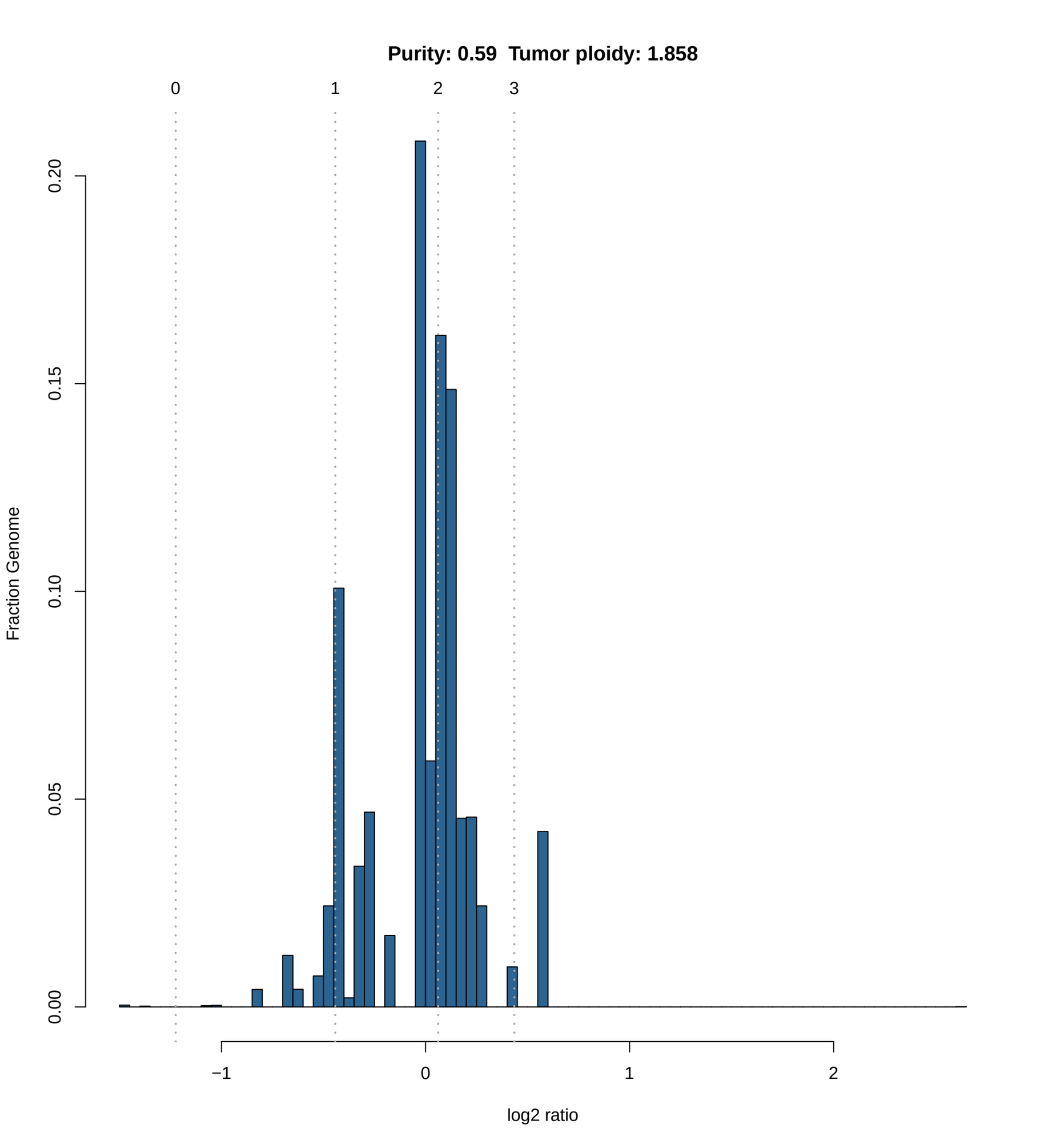

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

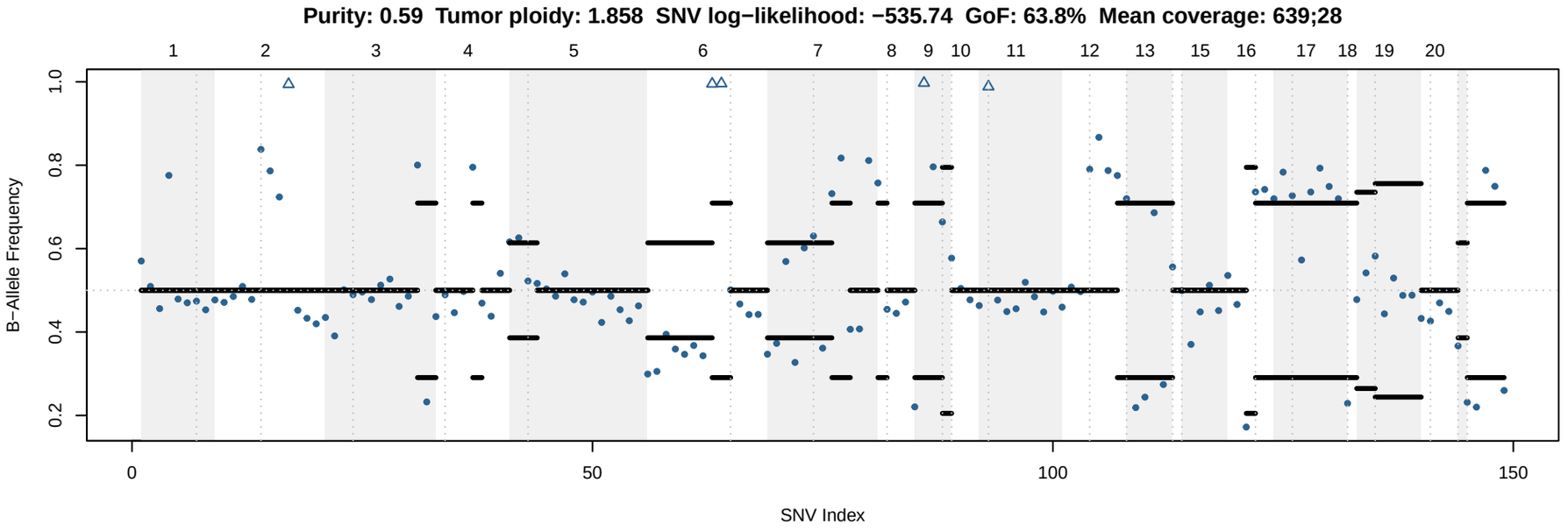

Allelic fraction (germline)
Copy Number log−ratio
1m1
2m2
3m3
4m3
3m2
5m3
2m1
4m2
5m2
3m1
4m1
2m0

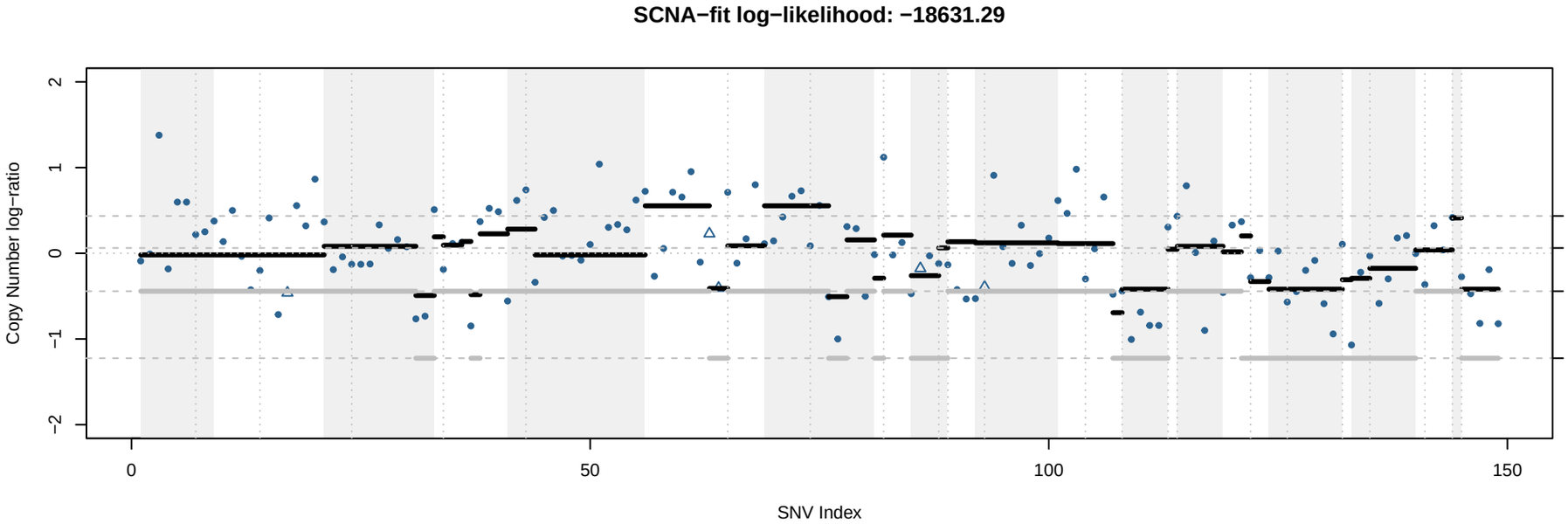

Coverage (log2)
Allelic fraction

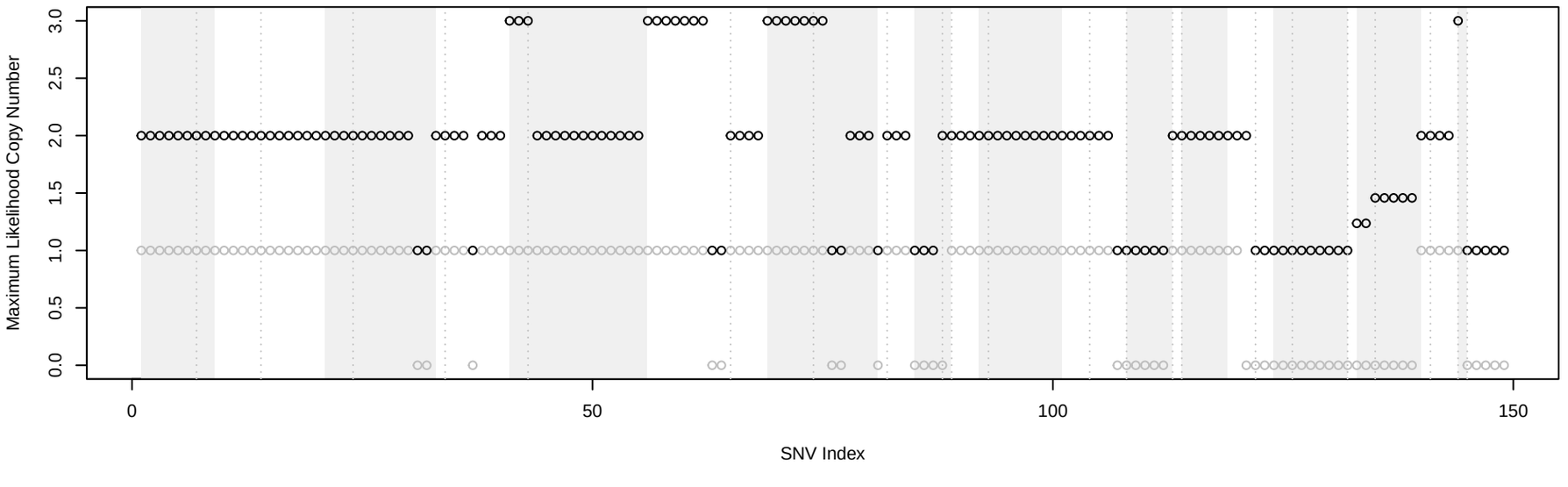

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m2
3m2
5m2
2m1
3m1
4m1
5m1

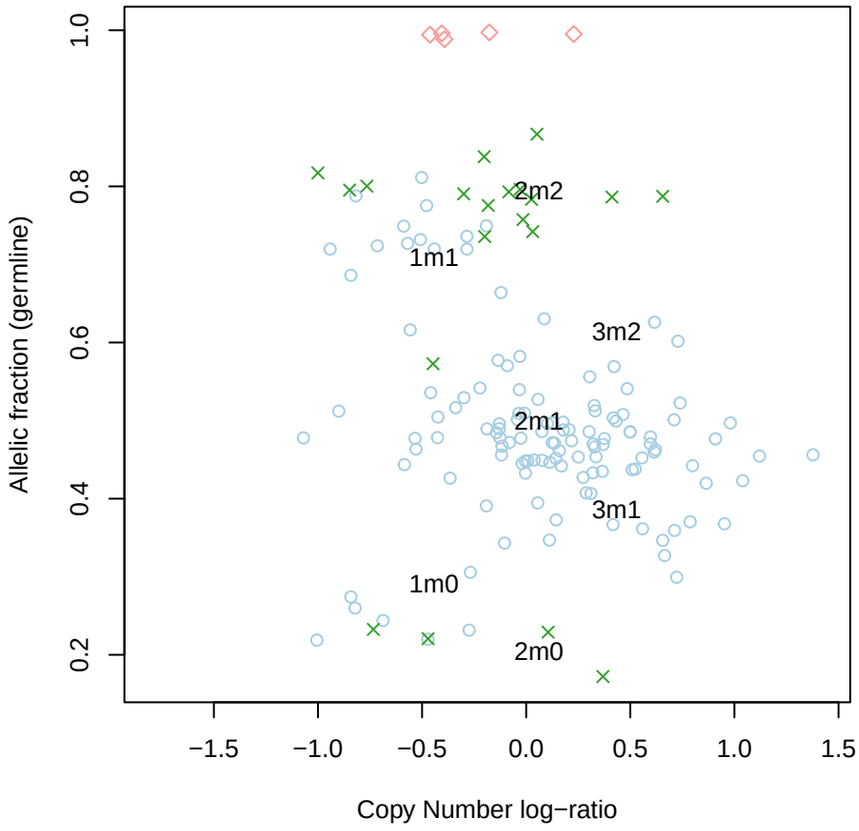

Frequency
Cellular fraction

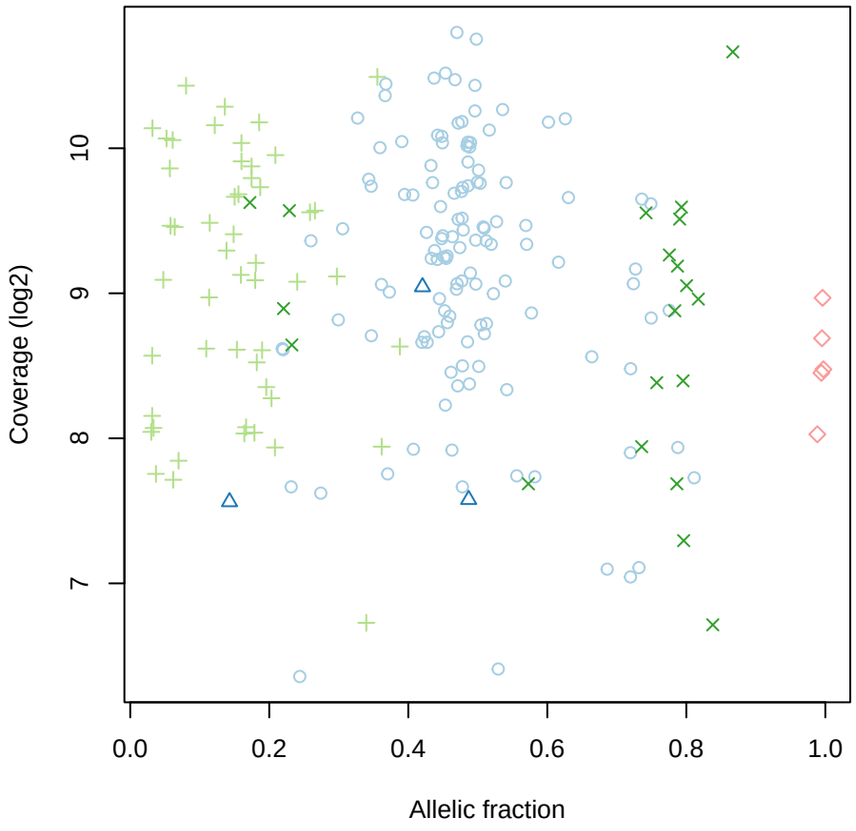

Purity: 0.59 Tumor ploidy: 1.858
0
1
2
3
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1
0
1
2
log2 ratio

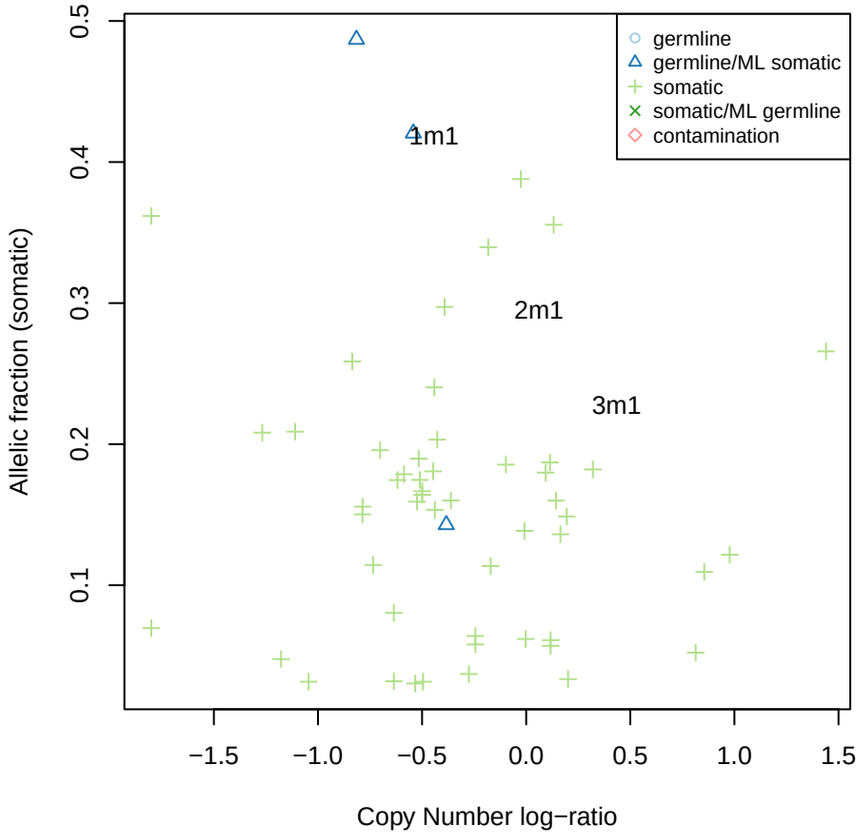

Purity: 0.59 Tumor ploidy: 1.858 SNV log−likelihood: −535.74 GoF: 63.8% Mean coverage: 639;28
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 18 19 20
B−Allele Frequency
0.2 0.4 0.6 0.8 1.0
0 50 100 150
SNV Index

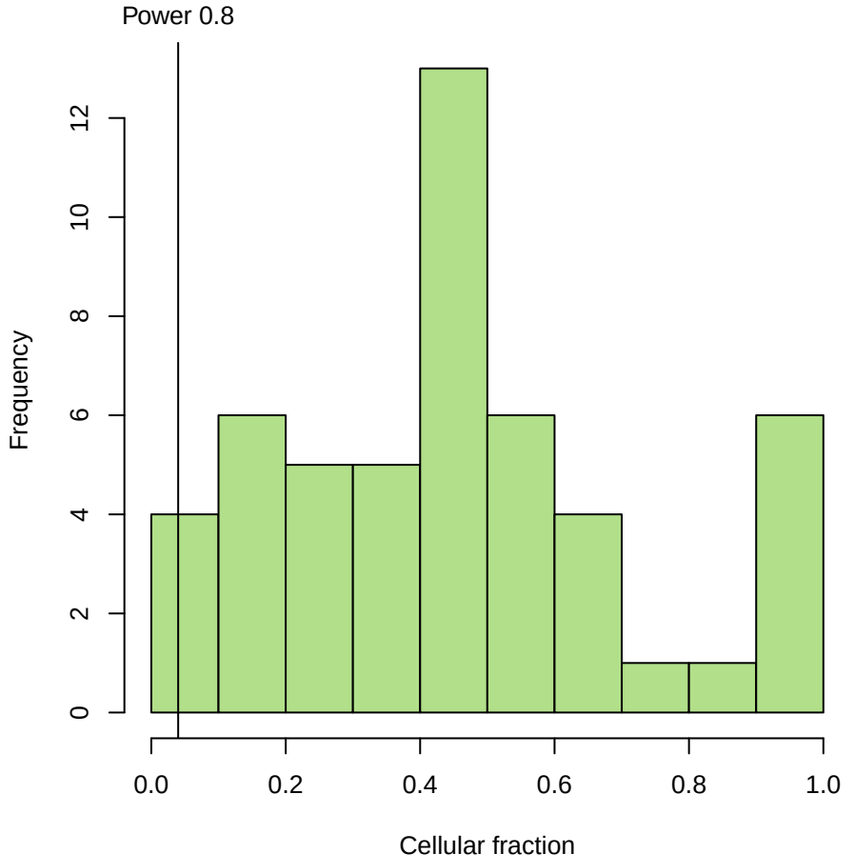

SCNA−fit log−likelihood: −18631.29
Copy Number log−ratio
−2 −1 0 1 2
0 1 2 3
0 50 100 150
SNV Index

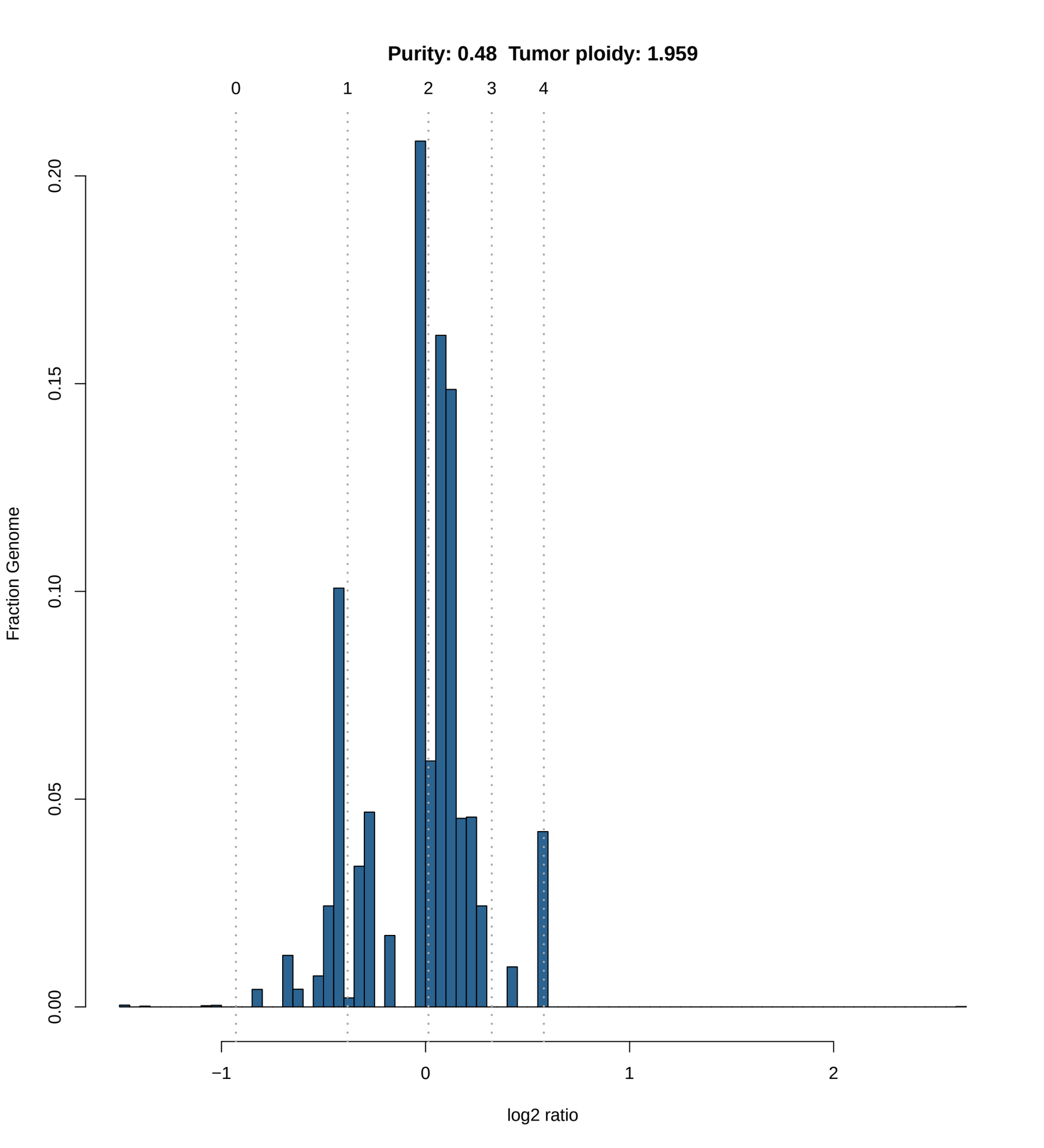

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

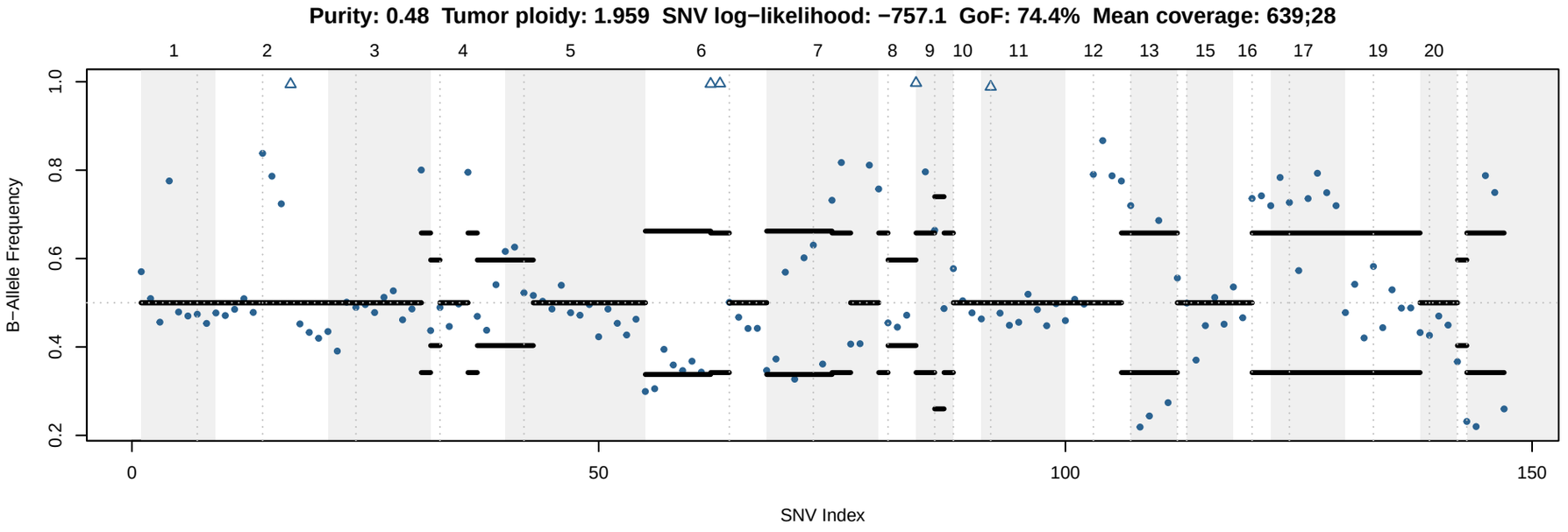

Allelic fraction (germline)
Copy Number log−ratio
1m1
2m2
3m2
2m1
3m1
1m0
2m0

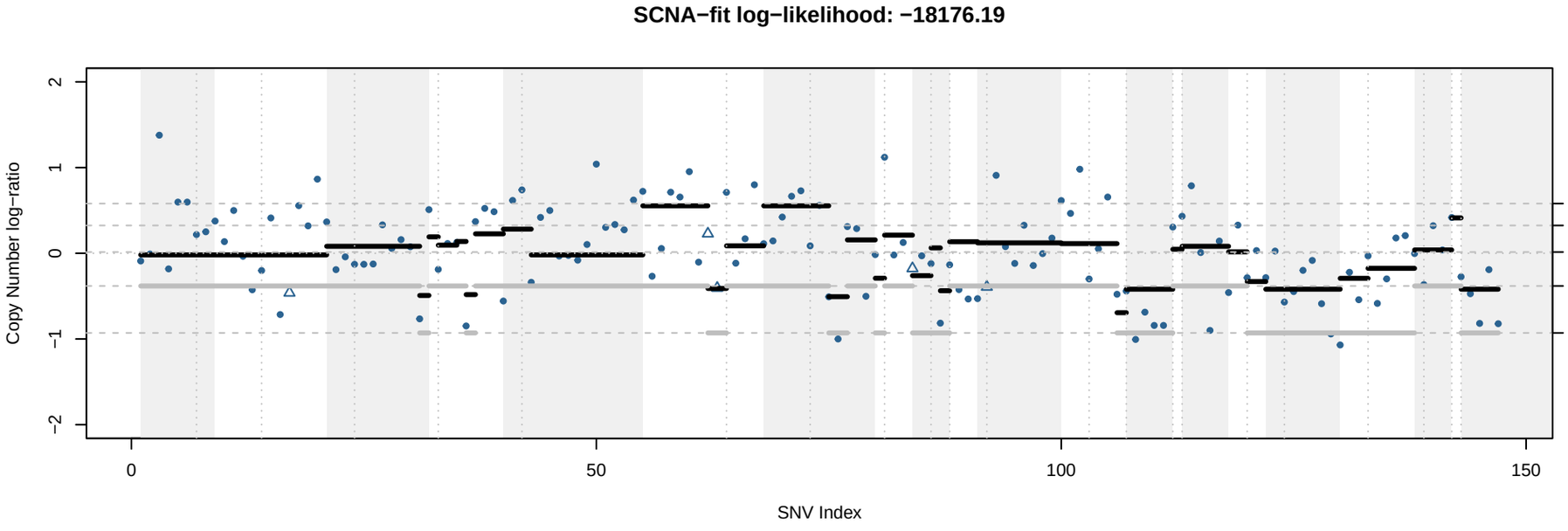

Coverage (log2)
Allelic fraction

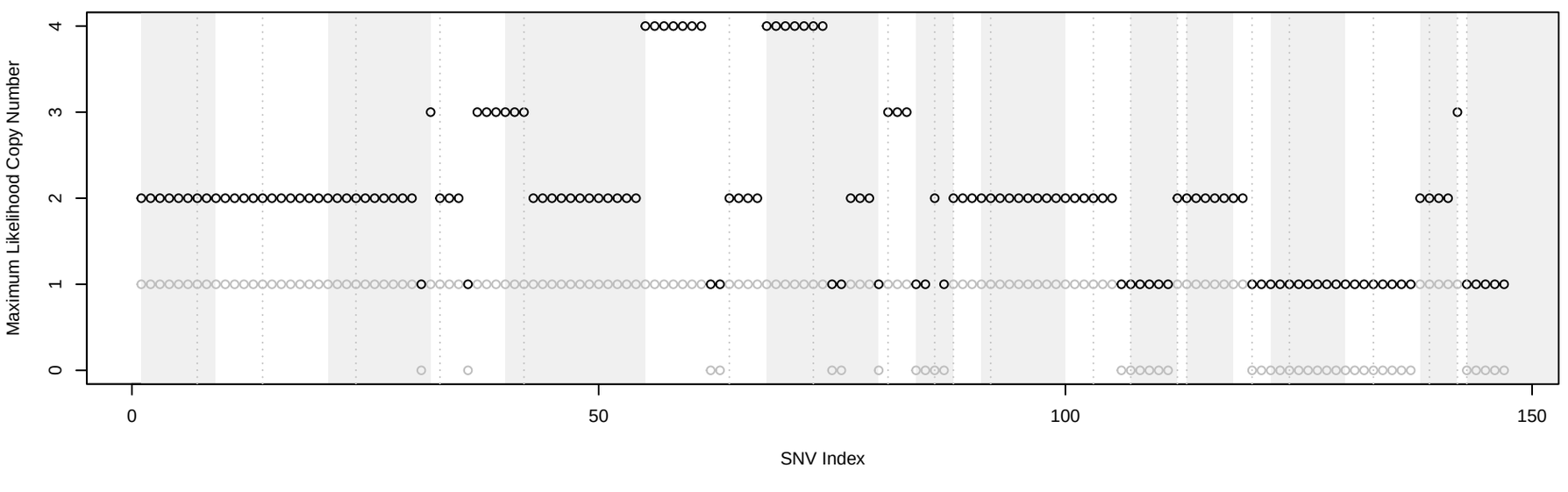

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1
3m1

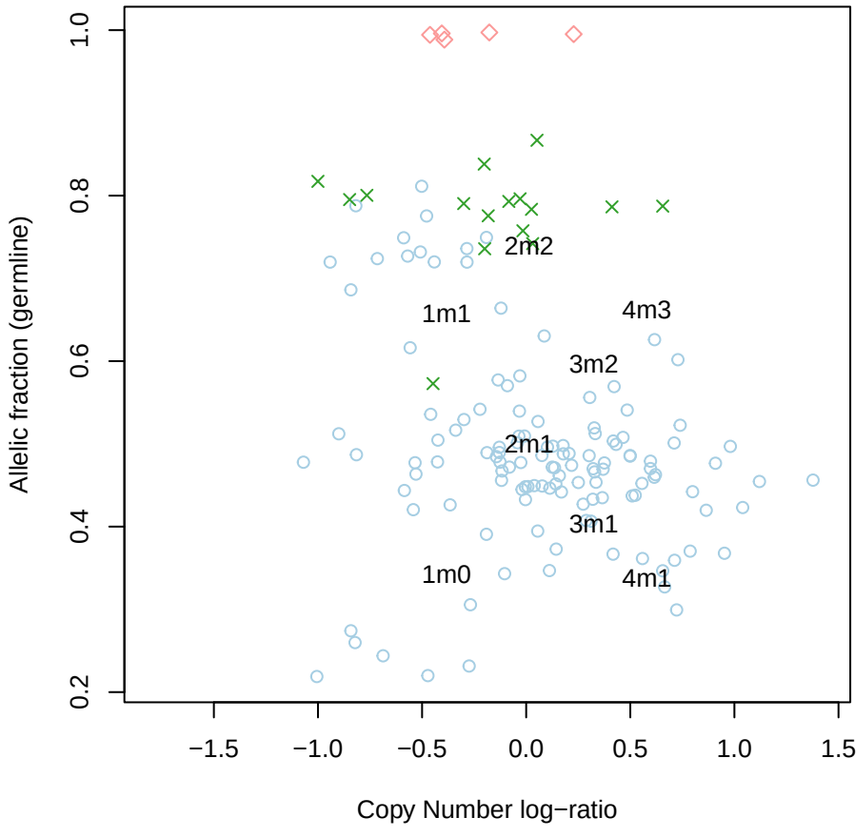

Power 0.8
Frequency
Cellular fraction

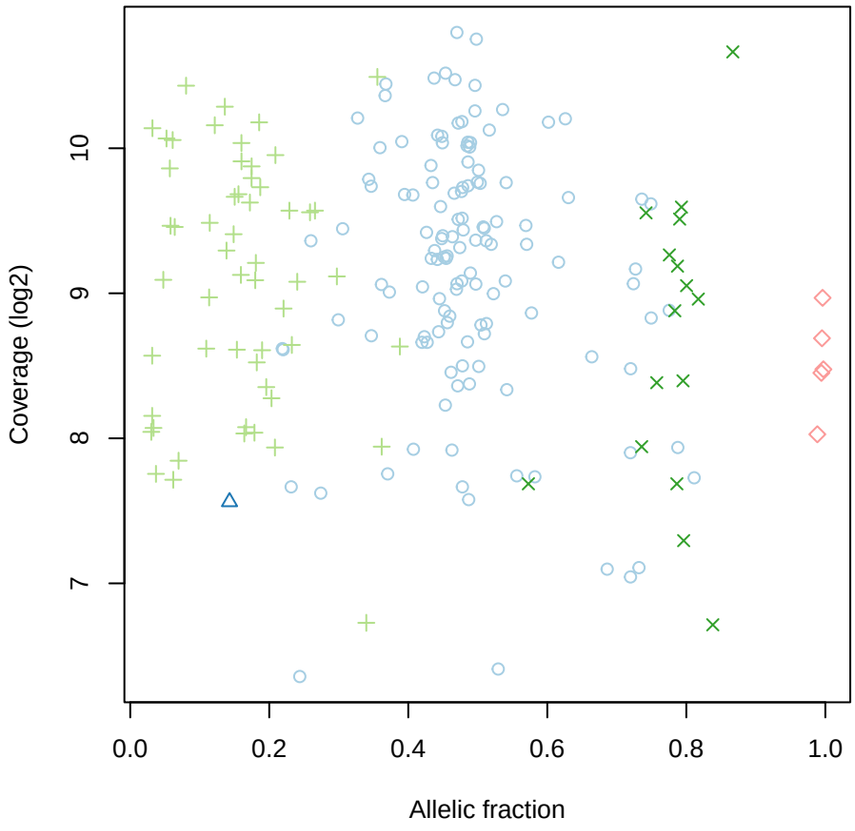

Purity: 0.48 Tumor ploidy: 1.959
0
1
2
3
4
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1
0
1
2
log2 ratio

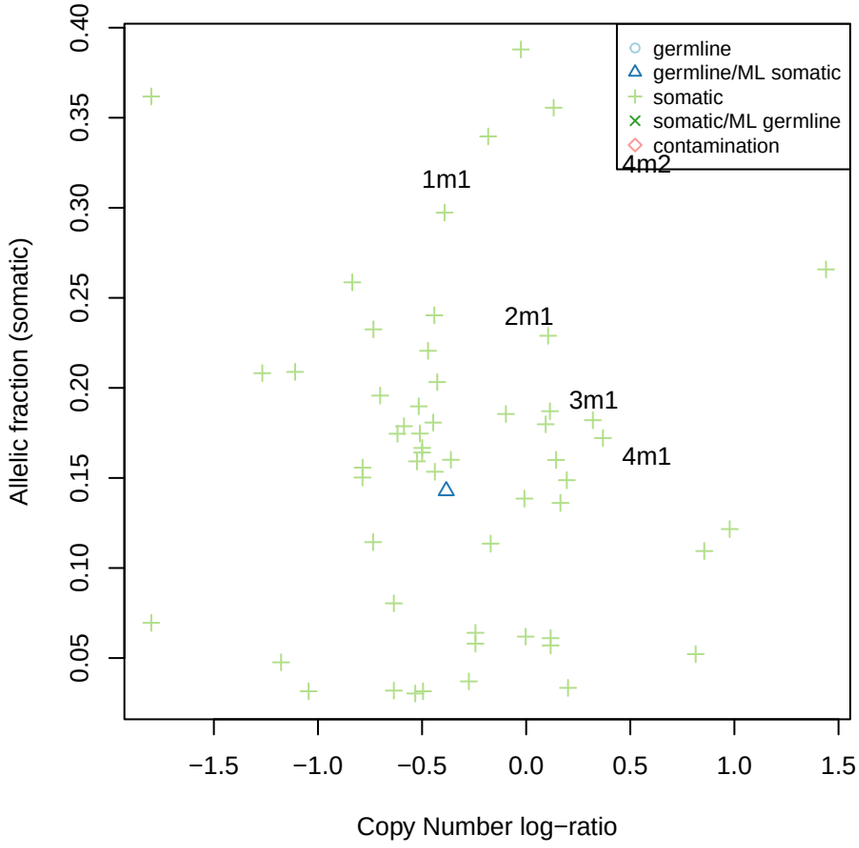

Purity: 0.48 Tumor ploidy: 1.959 SNV log−likelihood: −757.1 GoF: 74.4% Mean coverage: 639;28
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.2 0.4 0.6 0.8 1.0
0 50 100 150
SNV Index

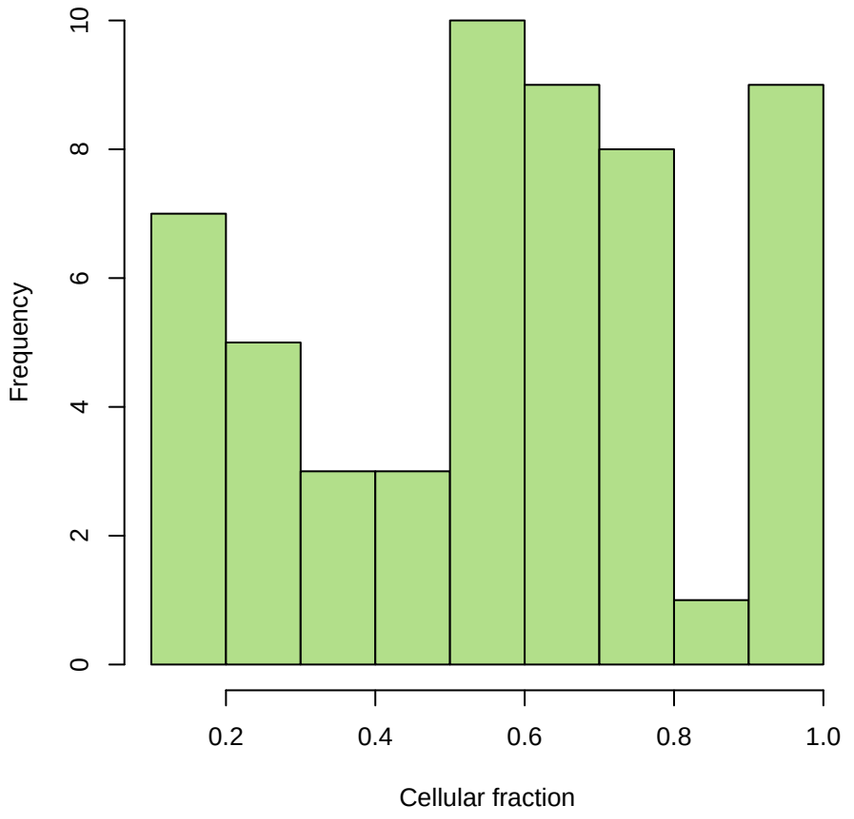

SCNA−fit log−likelihood: −18176.19
Copy Number log−ratio
−2 −1 0 1 2
0 1 2 3
0 50 100 150
SNV Index

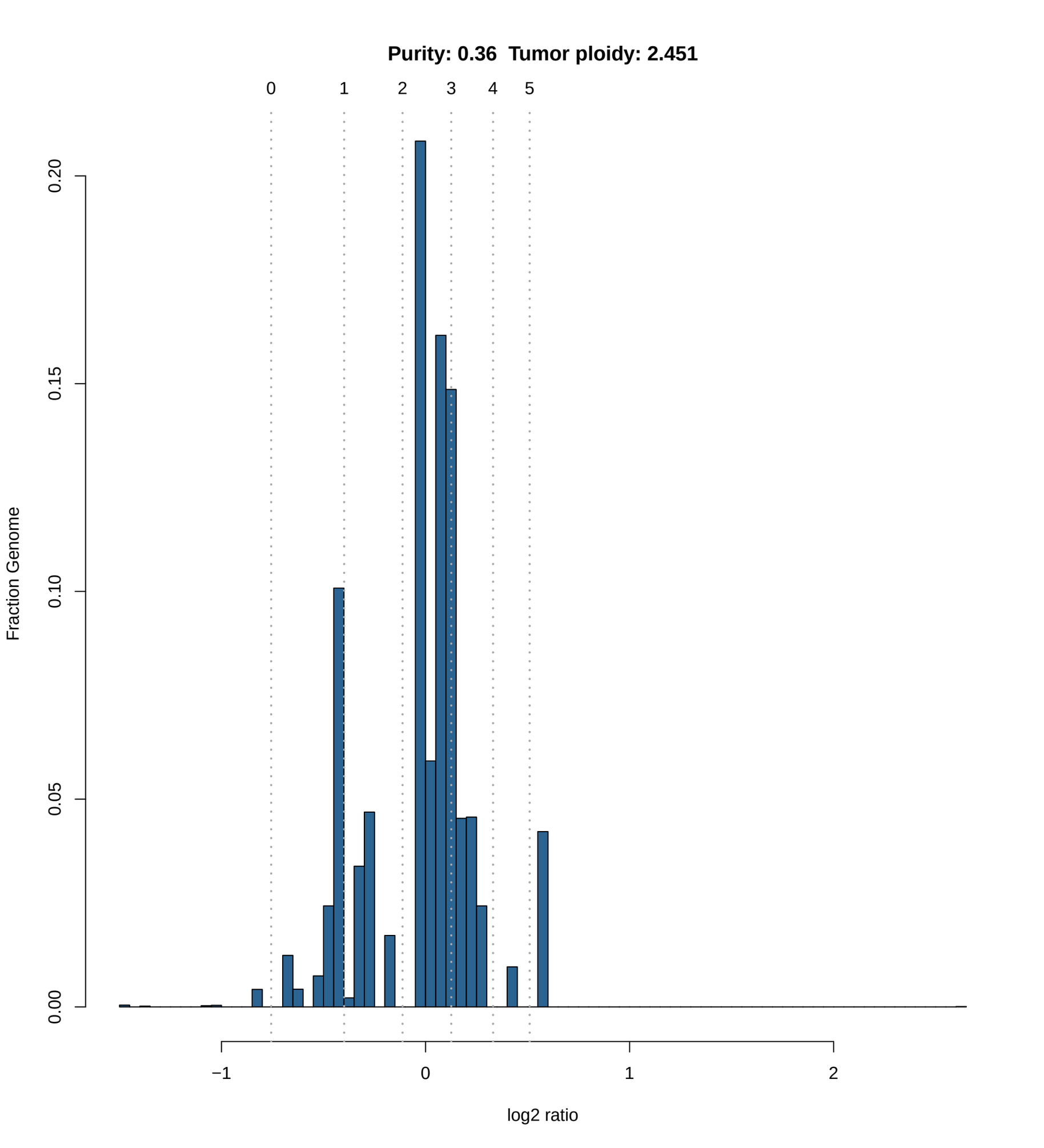

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

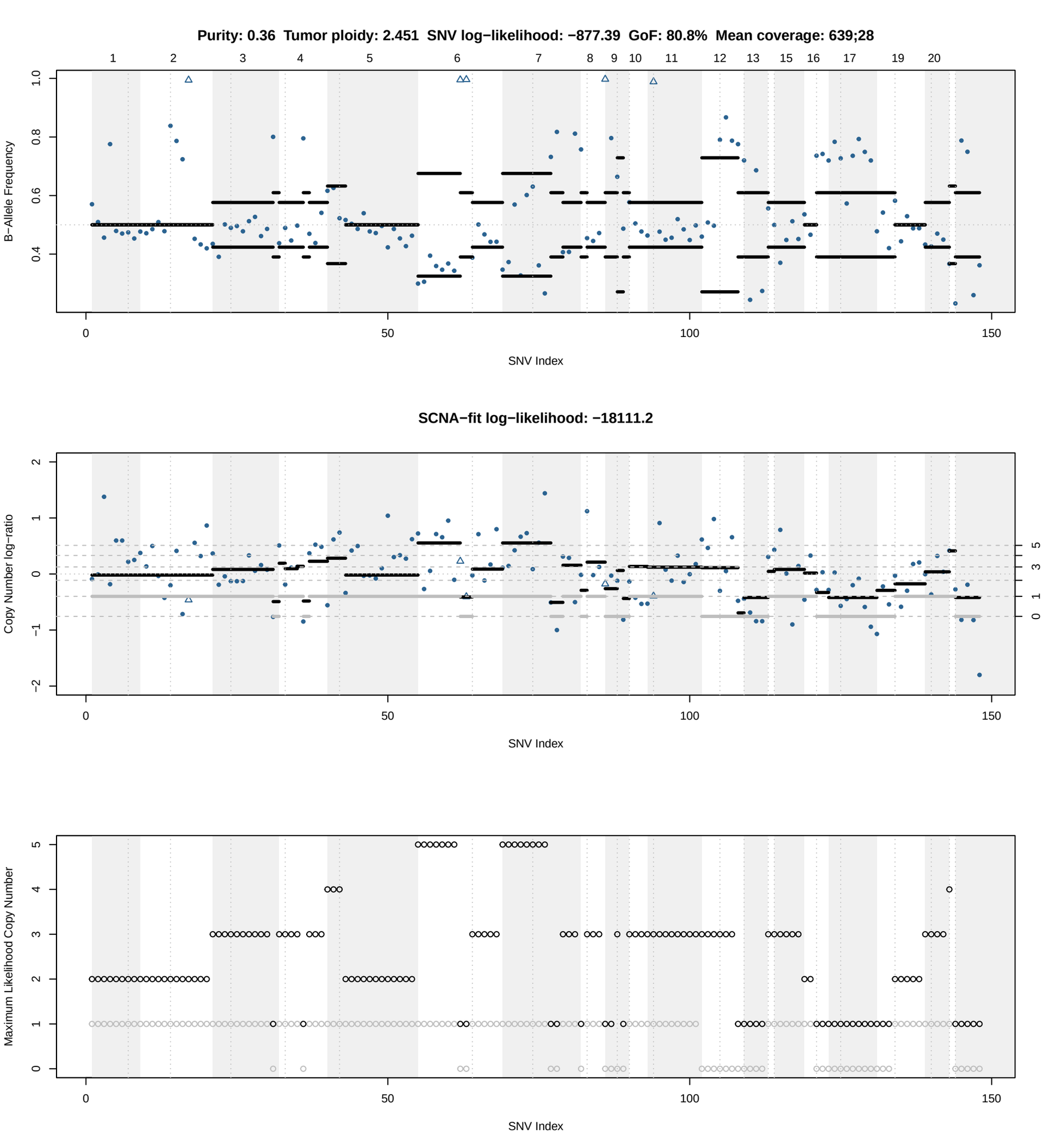

Allelic fraction (germline)
Copy Number log−ratio
1m1
2m2
4m3
3m2
2m1
3m1
1m0
4m1

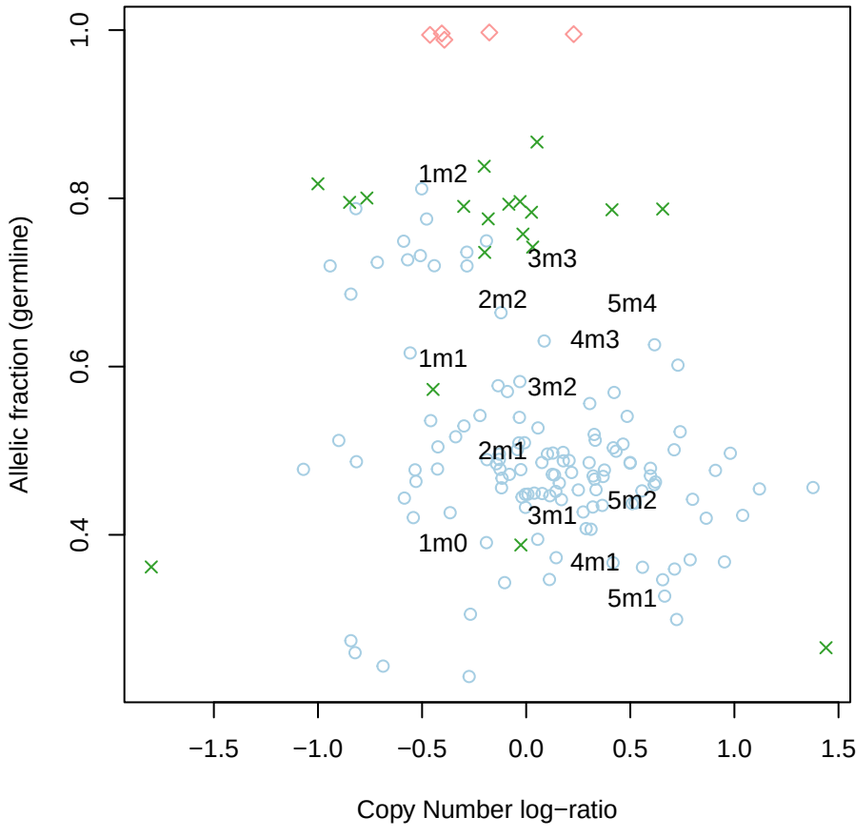

Coverage (log2)
Allelic fraction

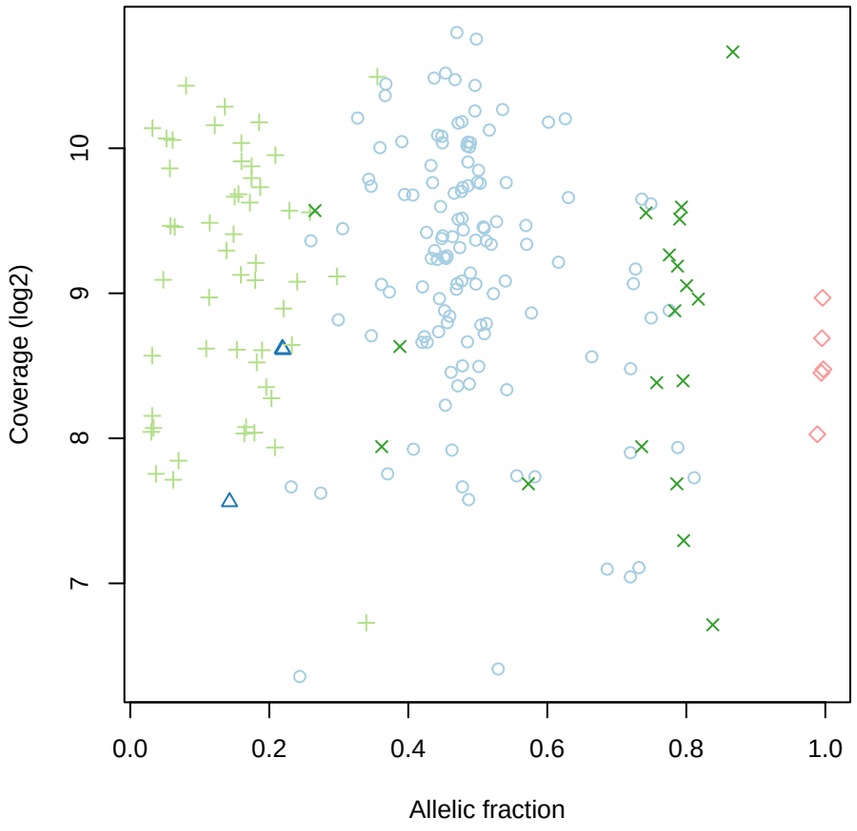

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
4m2
2m1
3m1
4m1

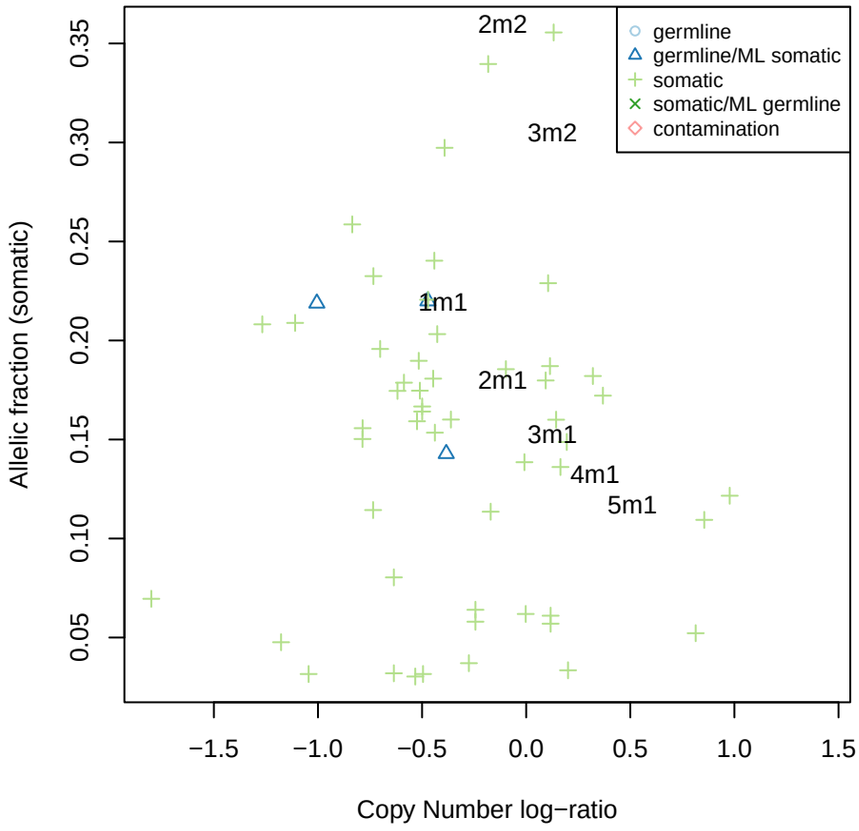

Frequency
Cellular fraction

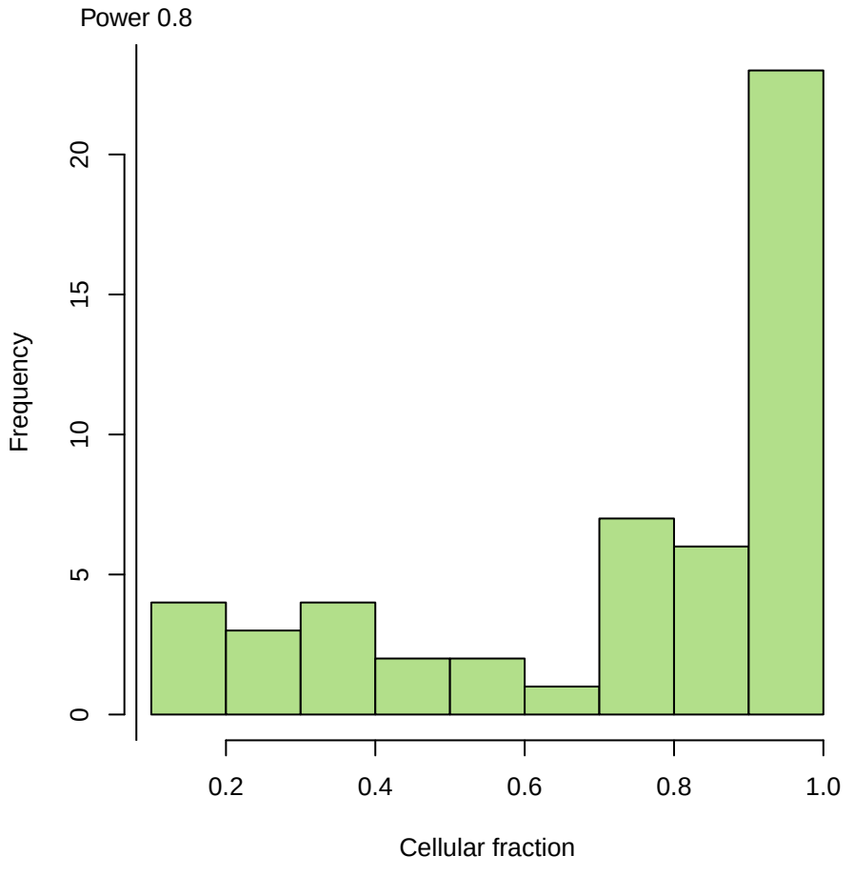

Purity: 0.36 Tumor ploidy: 2.451
0
1
2
3
4
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1
0
1
2
log2 ratio

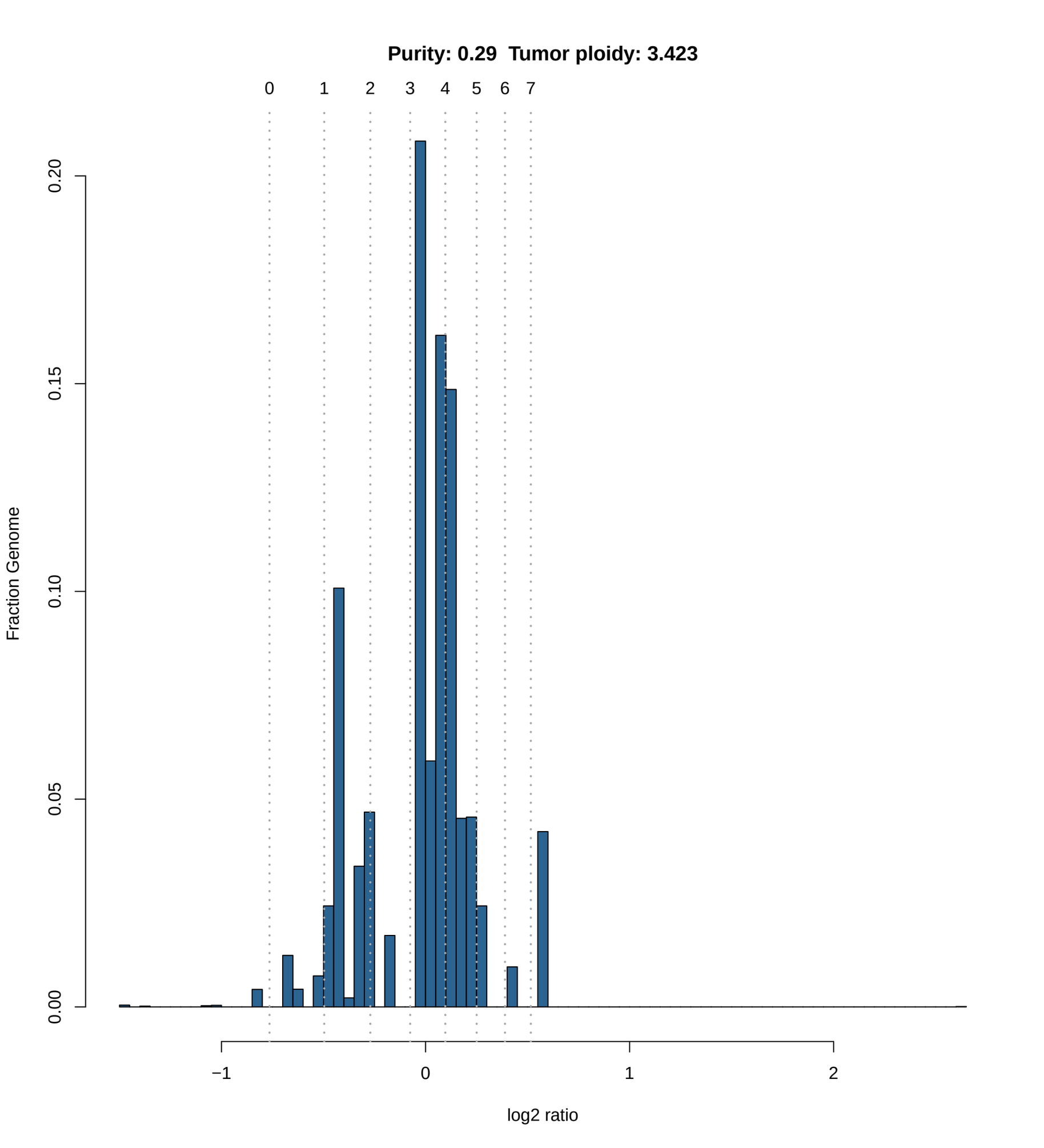

Purity: 0.36 Tumor ploidy: 2.451 SNV log−likelihood: −877.39 GoF: 80.8% Mean coverage: 639;28
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 19 20
B−Allele Frequency
1.0 0.8 0.6 0.4
0 50 100 150
SNV Index
SCNA−fit log−likelihood: −18111.2
Copy Number log−ratio
2 1 0 −1 −2
0 1 3 5
0 50 100 150
SNV Index
Maximum Likelihood Copy Number
5 4 3 2 1 0
0 50 100 150
SNV Index

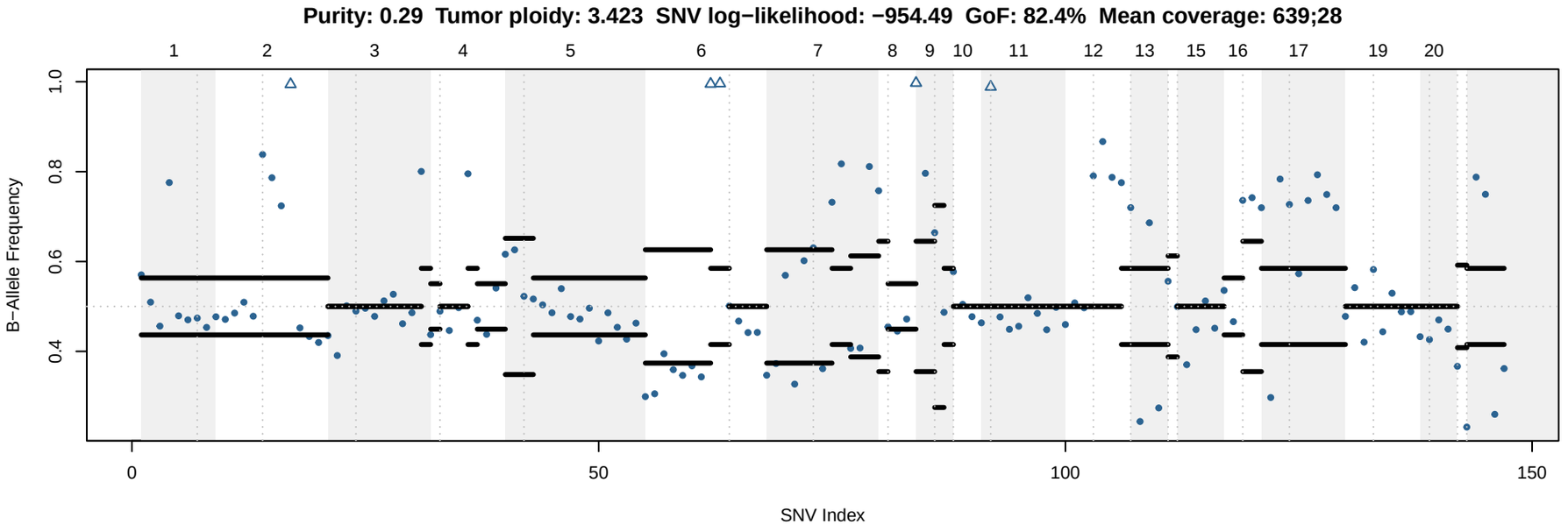

Allelic fraction (germline)
Copy Number log−ratio
1m2
3m3
2m2
5m4
4m3
1m1
3m2
2m1
5m2
3m1
1m0
4m1
5m1

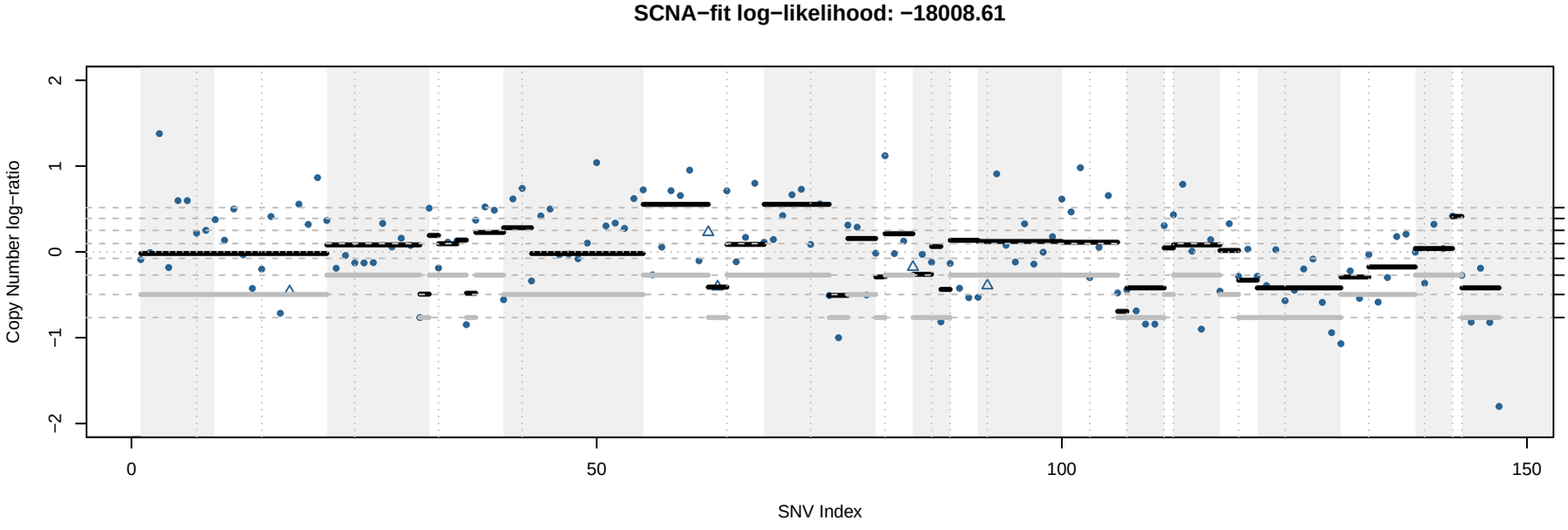

Coverage (log2)
Allelic fraction

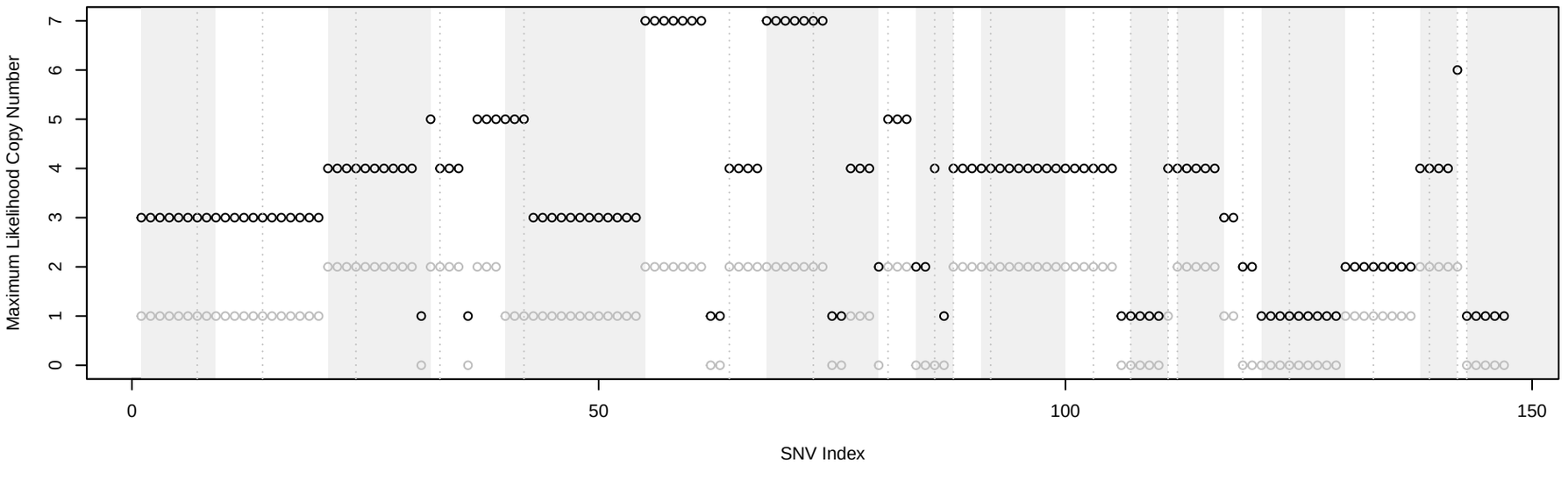

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
3m2
1m1
2m1
3m1
4m1
5m1

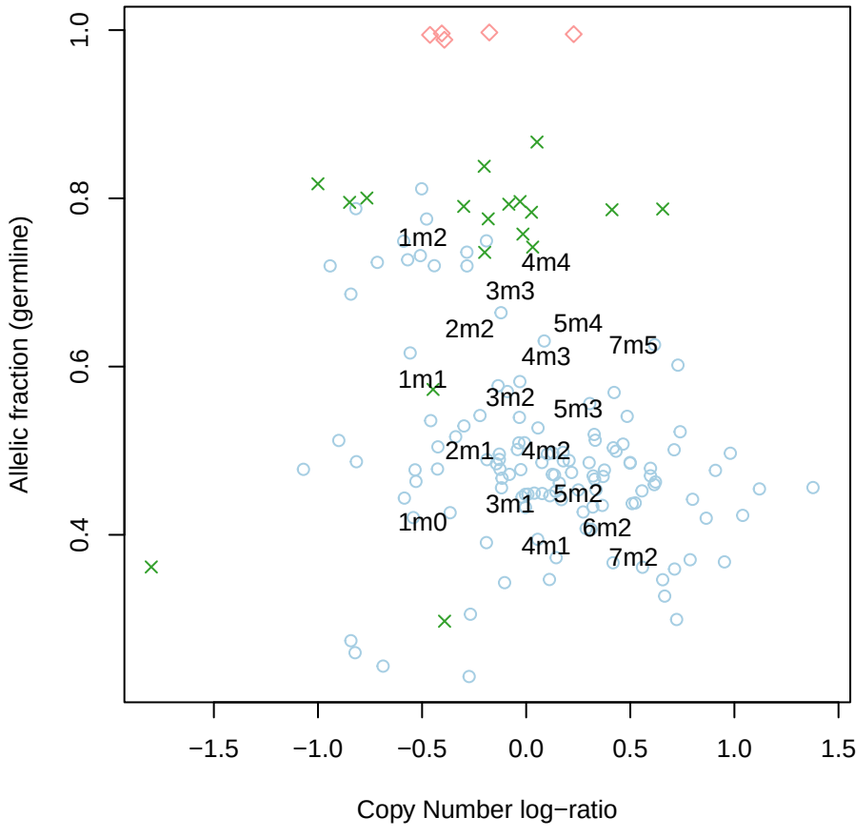

Power 0.8
Frequency
Cellular fraction

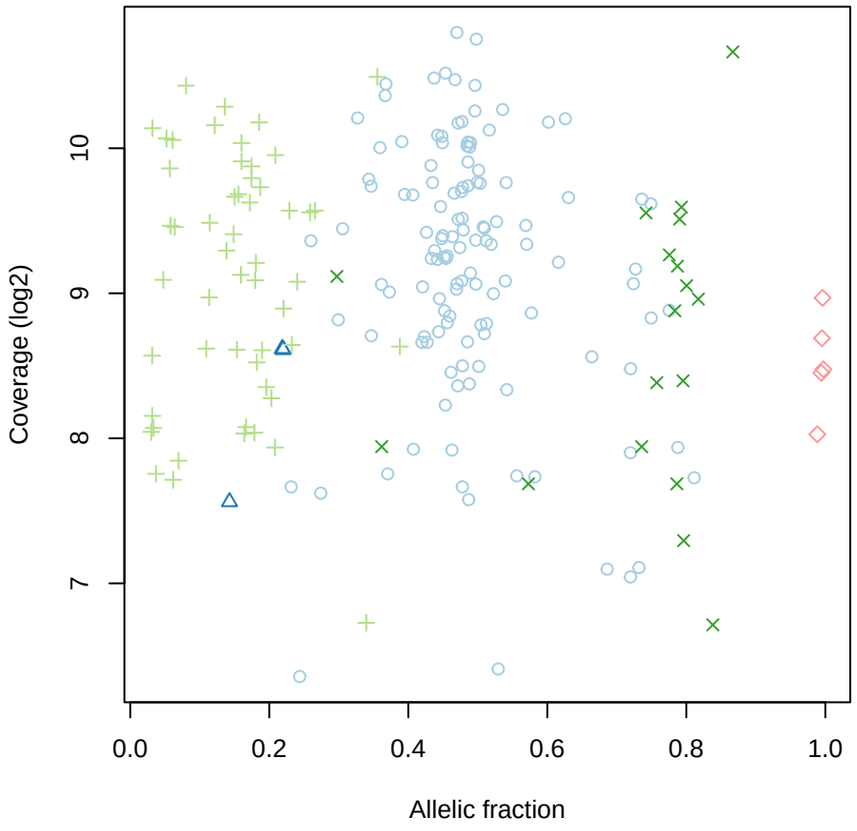

Purity: 0.29 Tumor ploidy: 3.423
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1
0
1
2
log2 ratio

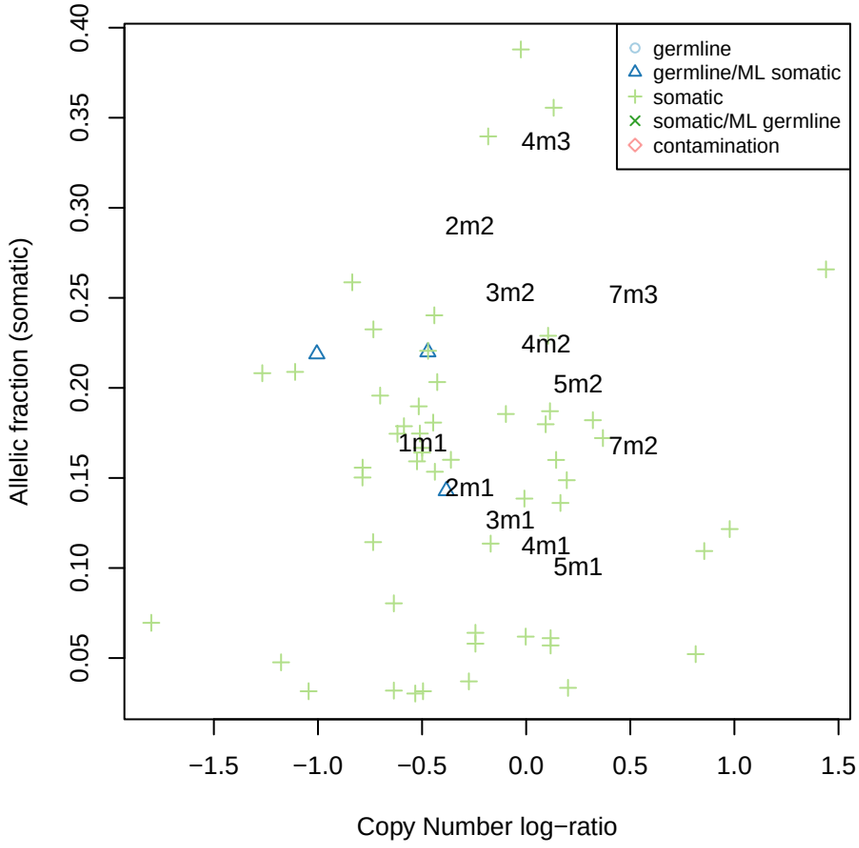

Purity: 0.29 Tumor ploidy: 3.423 SNV log−likelihood: −954.49 GoF: 82.4% Mean coverage: 639;28
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.4 0.6 0.8 1.0
0 50 100 150
SNV Index

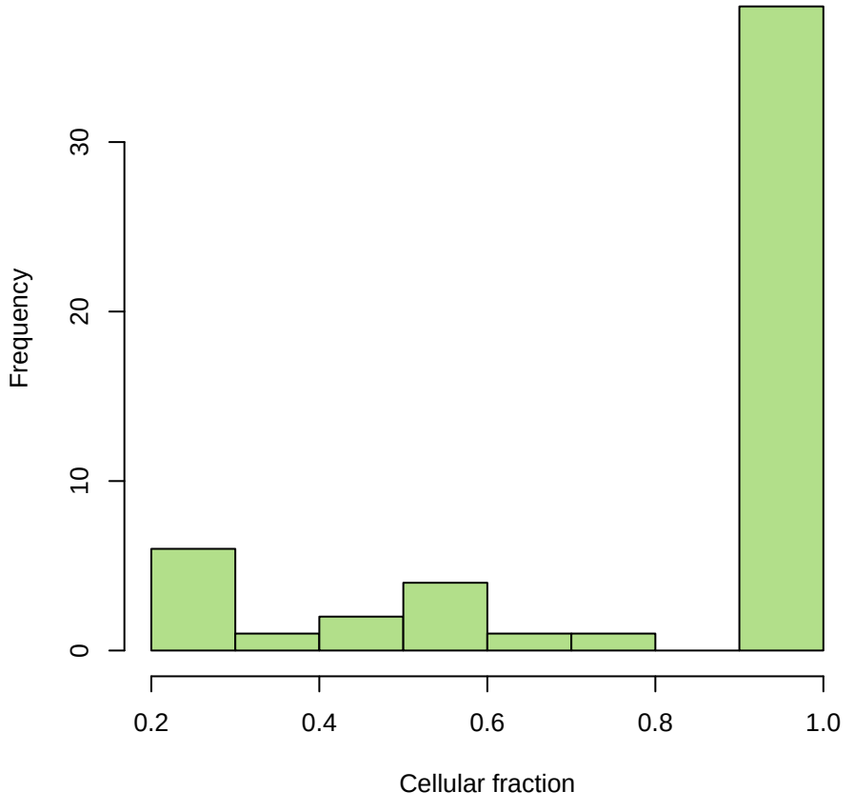

SCNA−fit log−likelihood: −18008.61
Copy Number log−ratio
−2 −1 0 1 2
0 2 4 6
0 50 100 150
SNV Index

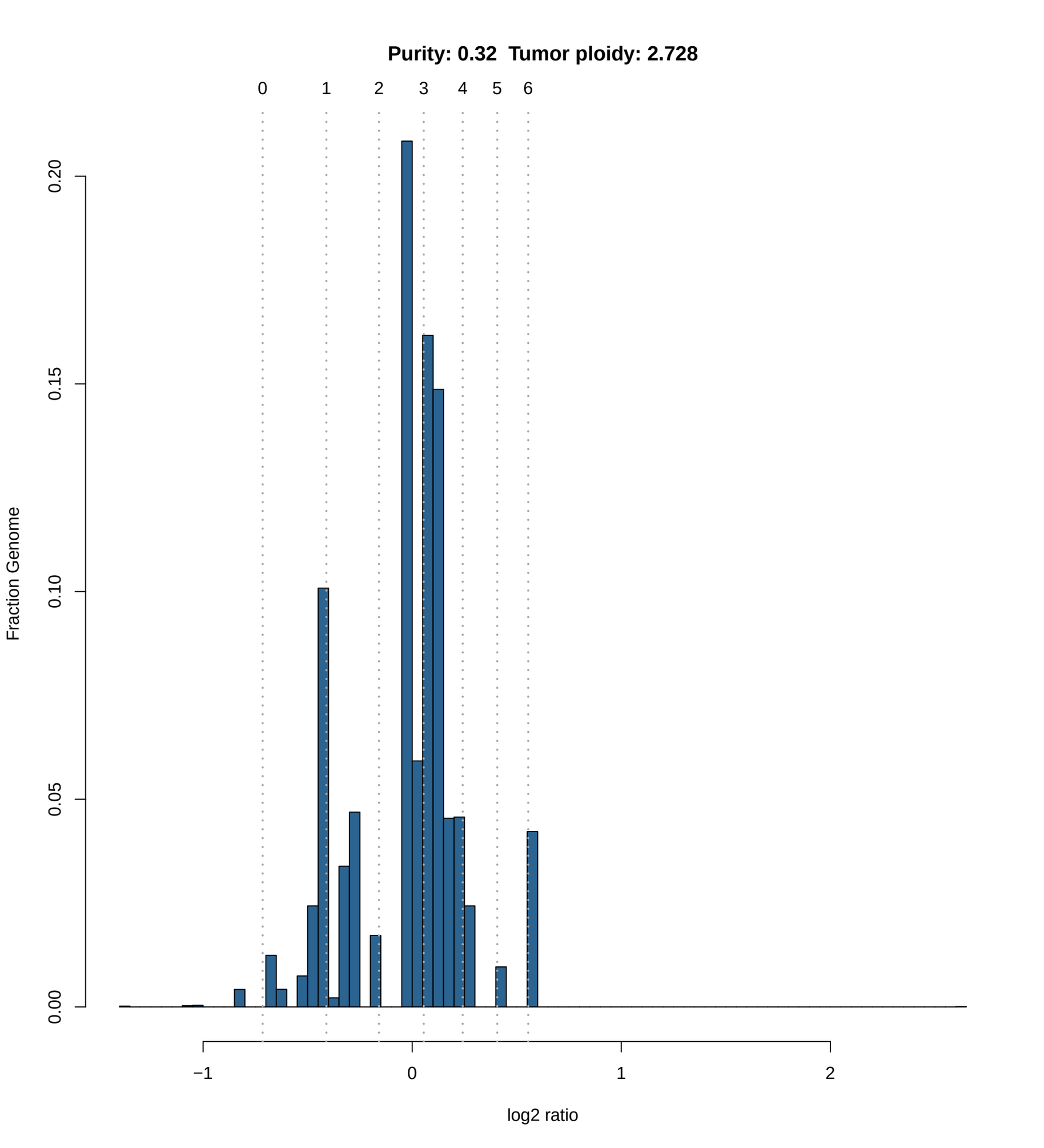

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

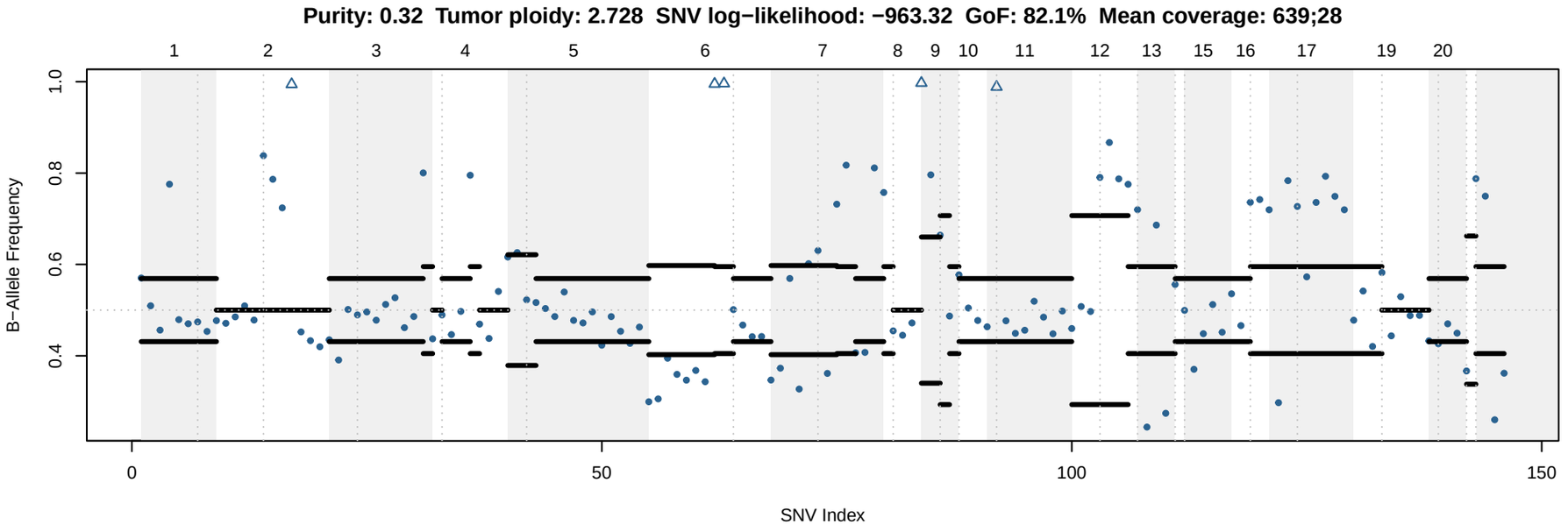

Allelic fraction (germline)
Copy Number log−ratio
1m2
4m4
3m3
2m2
5m4
7m5
4m3
1m1
3m2
5m3
2m1
4m2
5m2
3m1
6m2
1m0
4m1
7m2

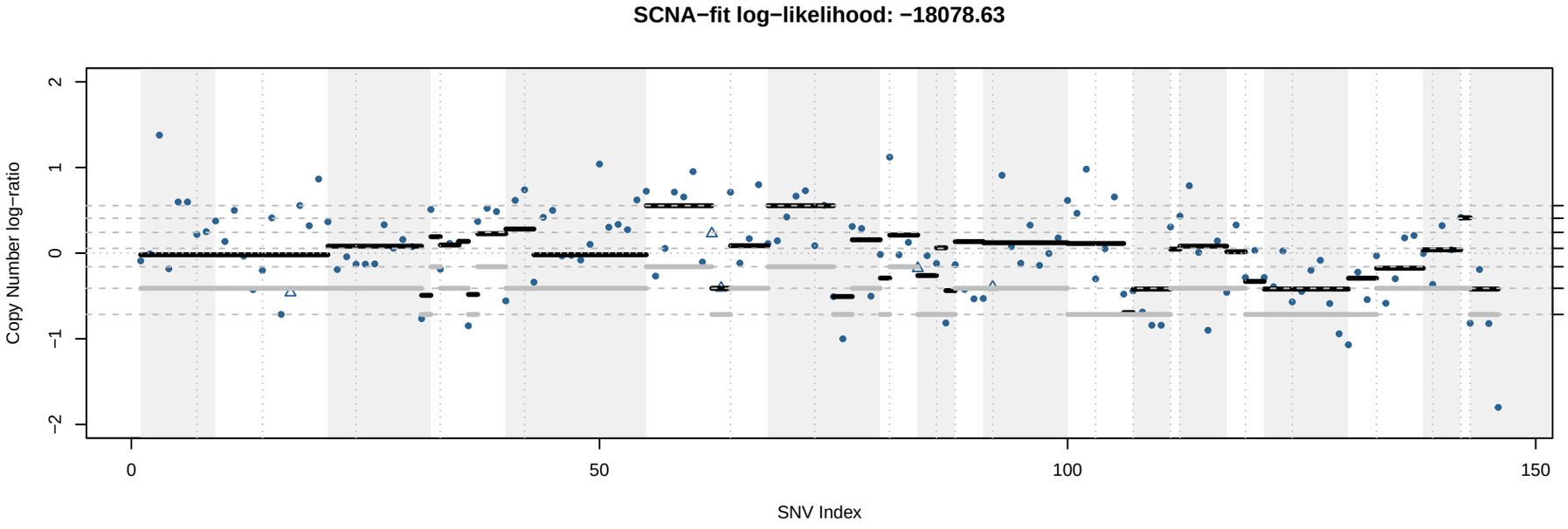

Coverage (log2)
Allelic fraction

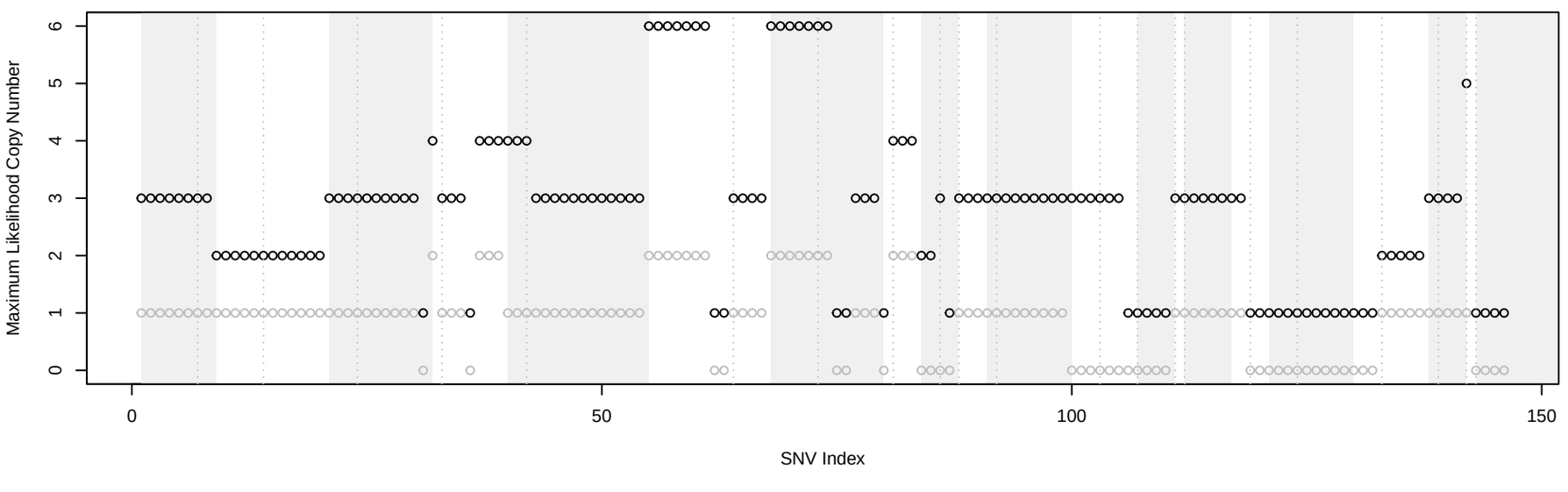

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
4m3
2m2
3m2
7m3
4m2
5m2
1m1
7m2
2m1
3m1
4m1
5m1

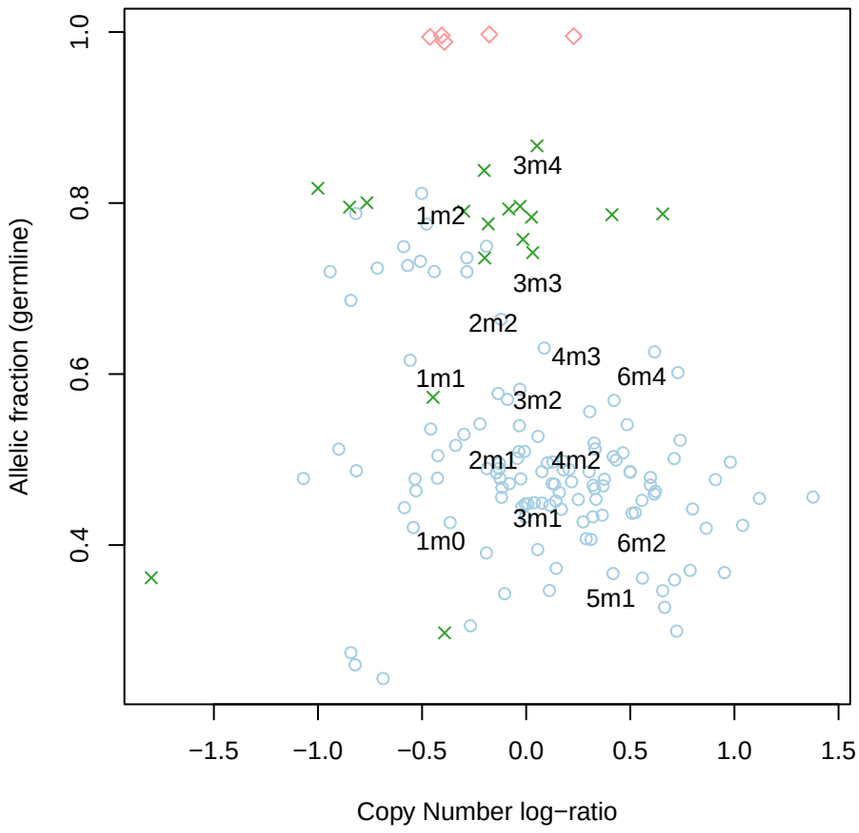

Frequency
Cellular fraction

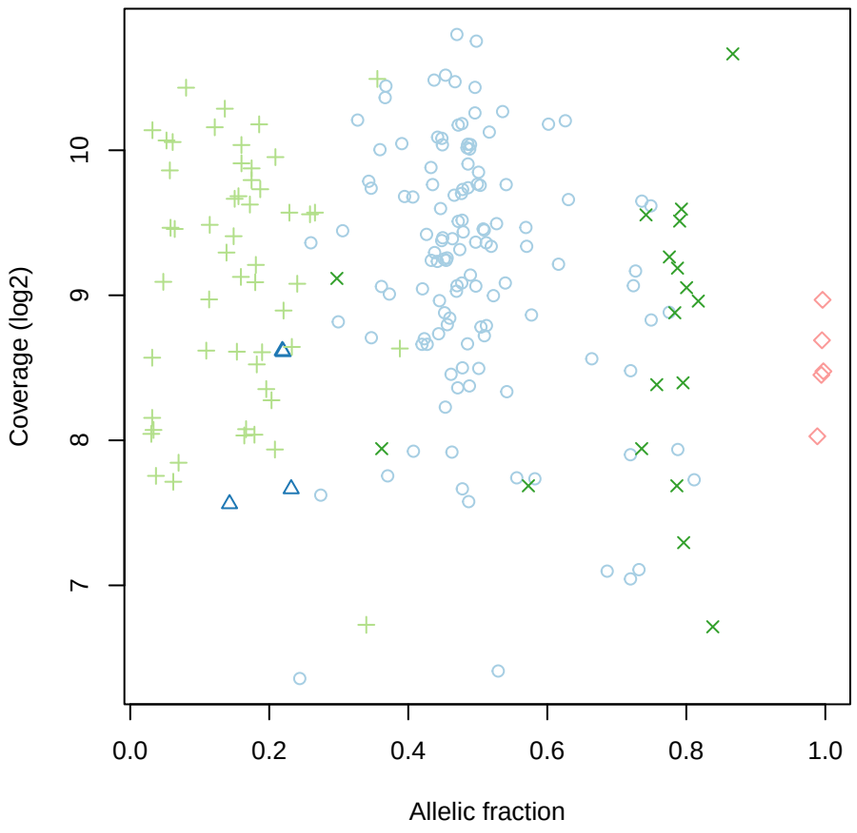

Purity: 0.32 Tumor ploidy: 2.728
0
1
2
3
4
5
6
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1
0
1
2
log2 ratio

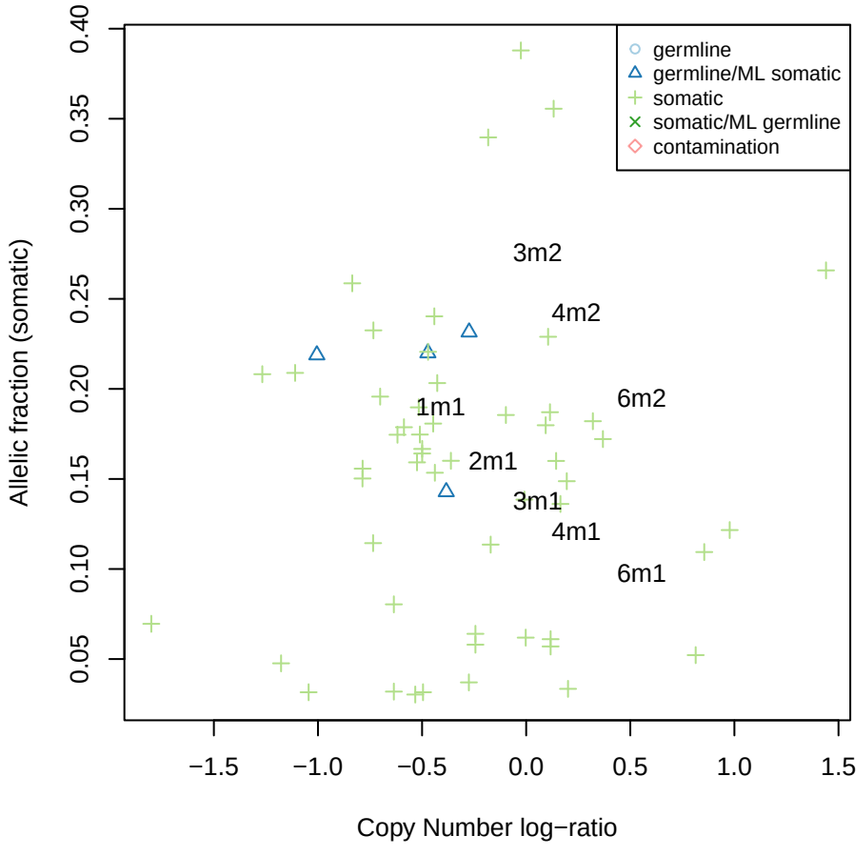

Purity: 0.32 Tumor ploidy: 2.728 SNV log−likelihood: −963.32 GoF: 82.1% Mean coverage: 639;28
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.4 0.6 0.8 1.0
0 50 100 150
SNV Index

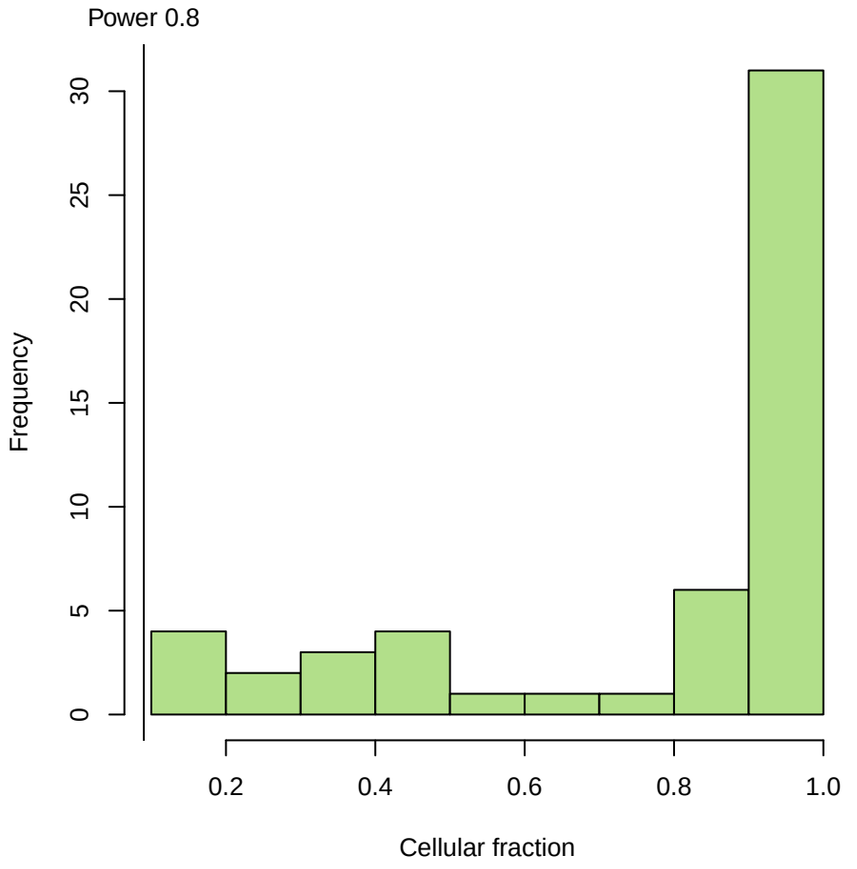

SCNA−fit log−likelihood: −18078.63
Copy Number log−ratio
−2 −1 0 1 2
0 1 3 5
0 50 100 150
SNV Index

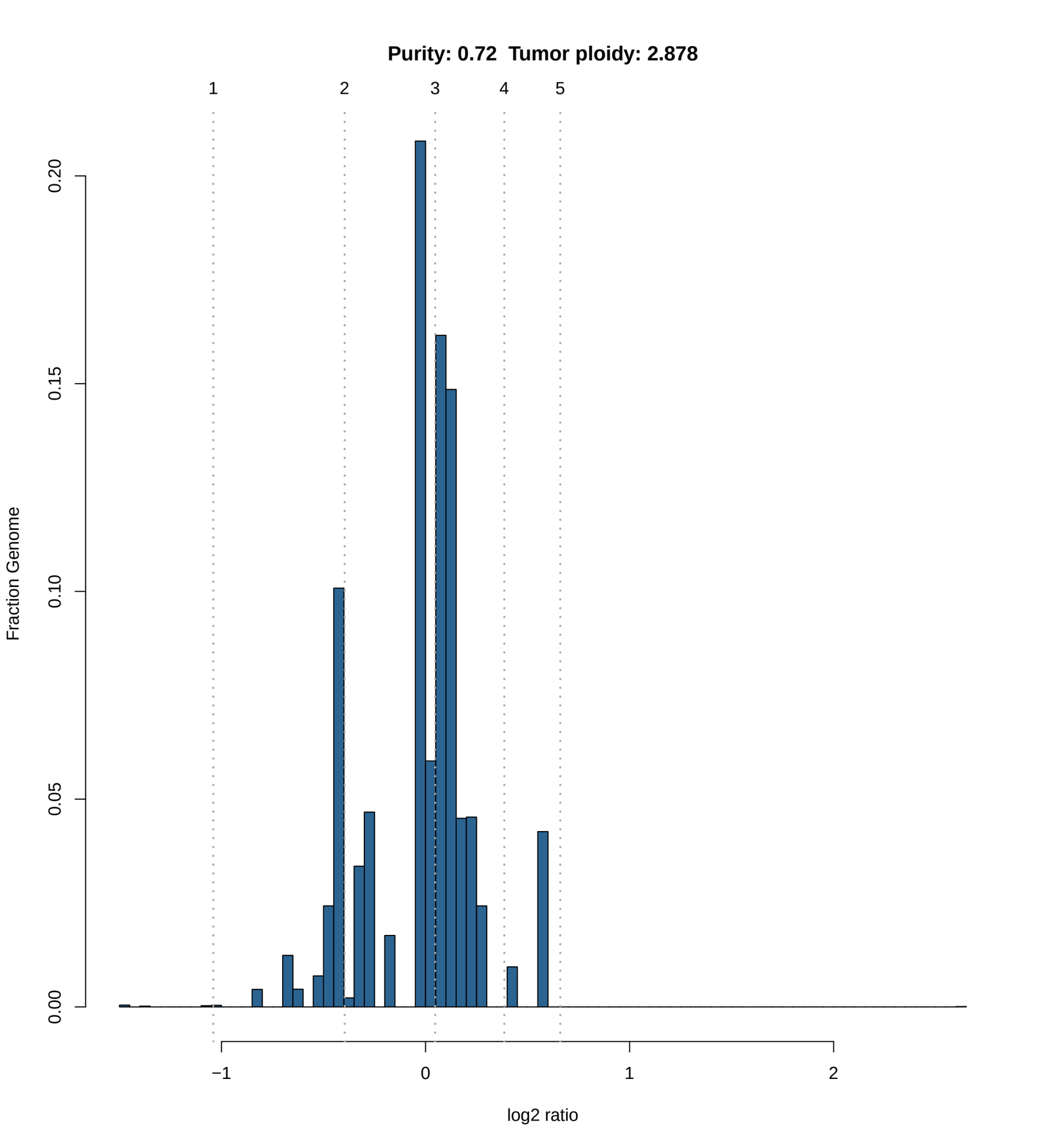

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

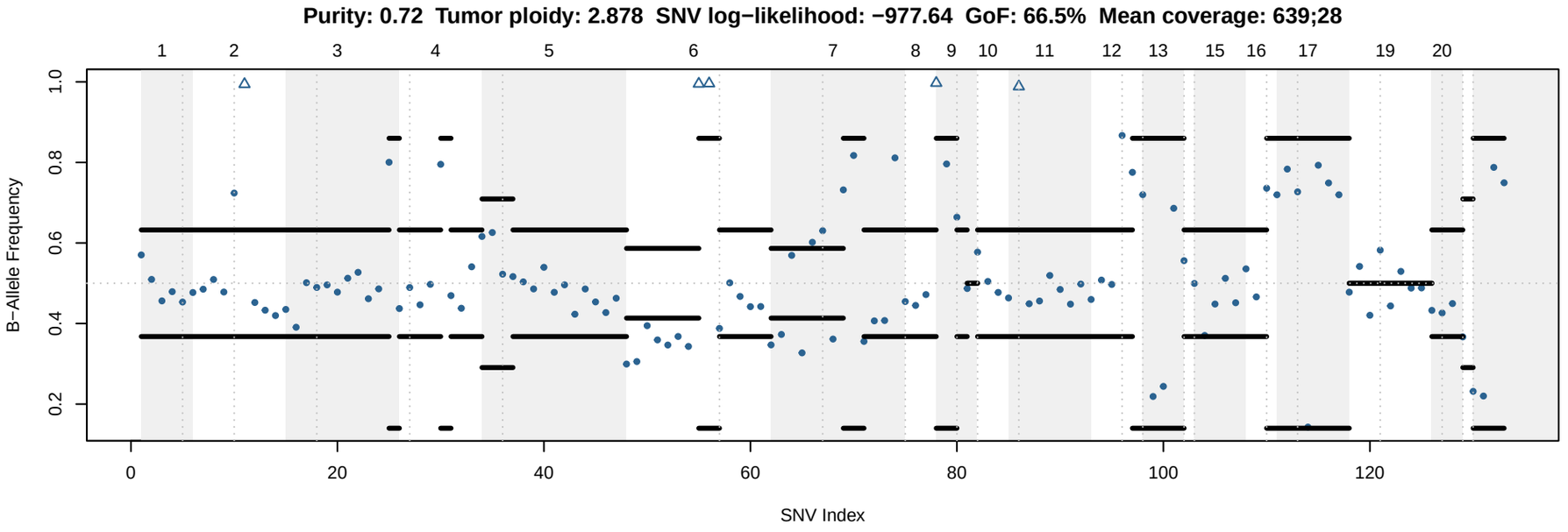

Allelic fraction (germline)
Copy Number log−ratio
3m4
1m2
3m3
2m2
4m3
1m1
6m4
3m2
2m1
4m2
3m1
1m0
6m2
5m1

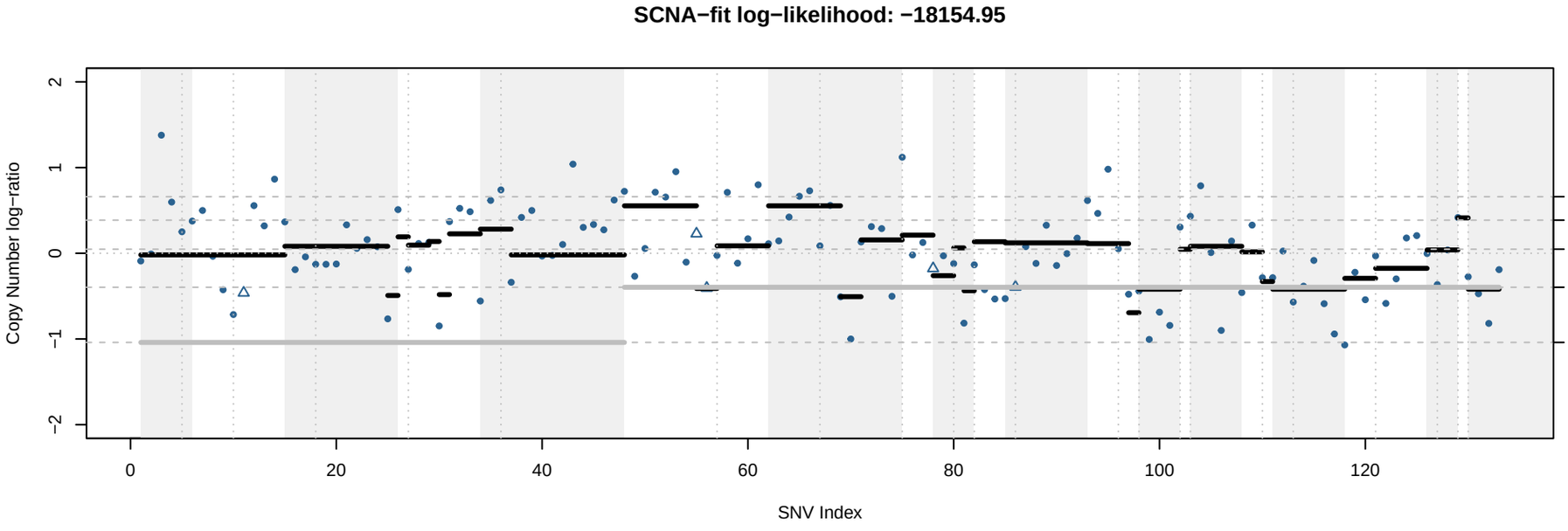

Coverage (log2)
Allelic fraction

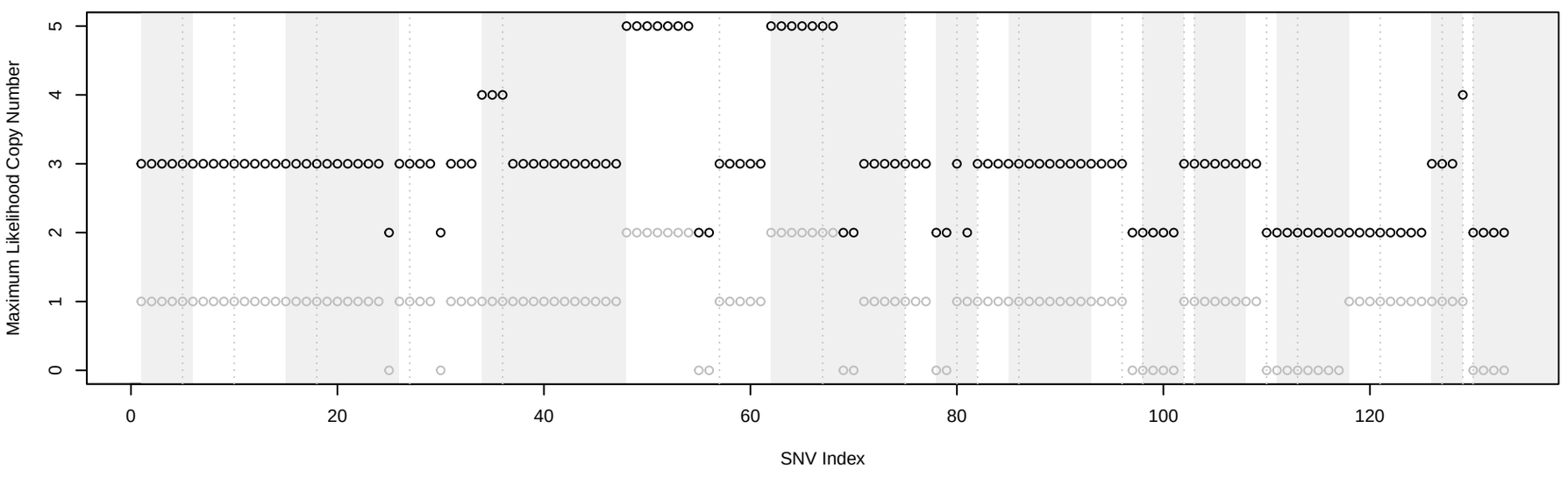

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m2
4m2
1m1
6m2
2m1
3m1
4m1
6m1

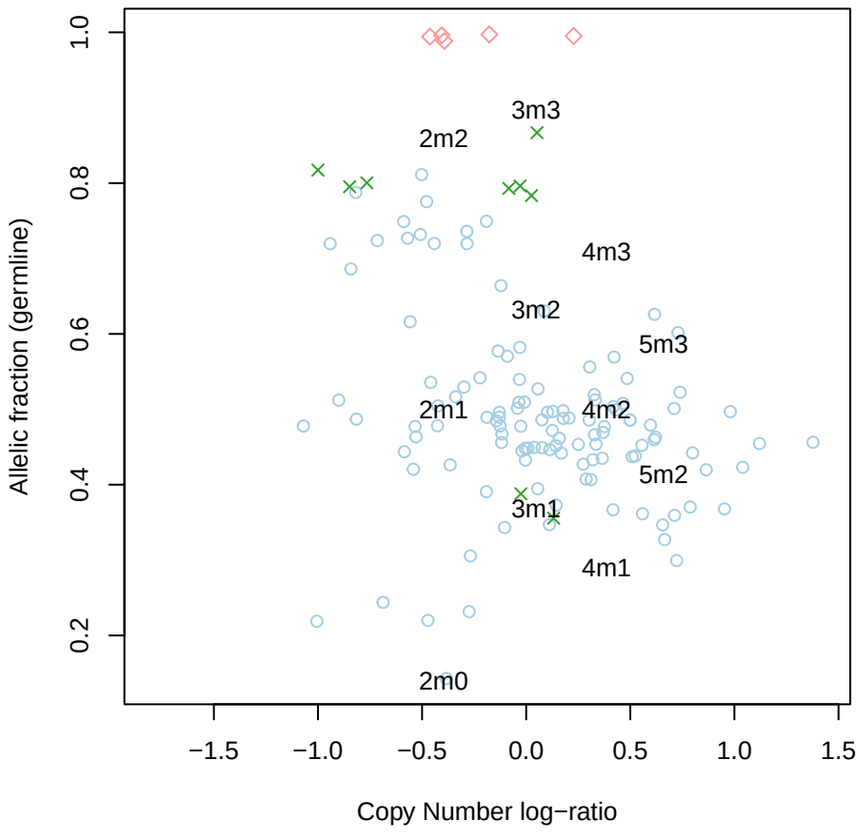

Power 0.8
Frequency
Cellular fraction

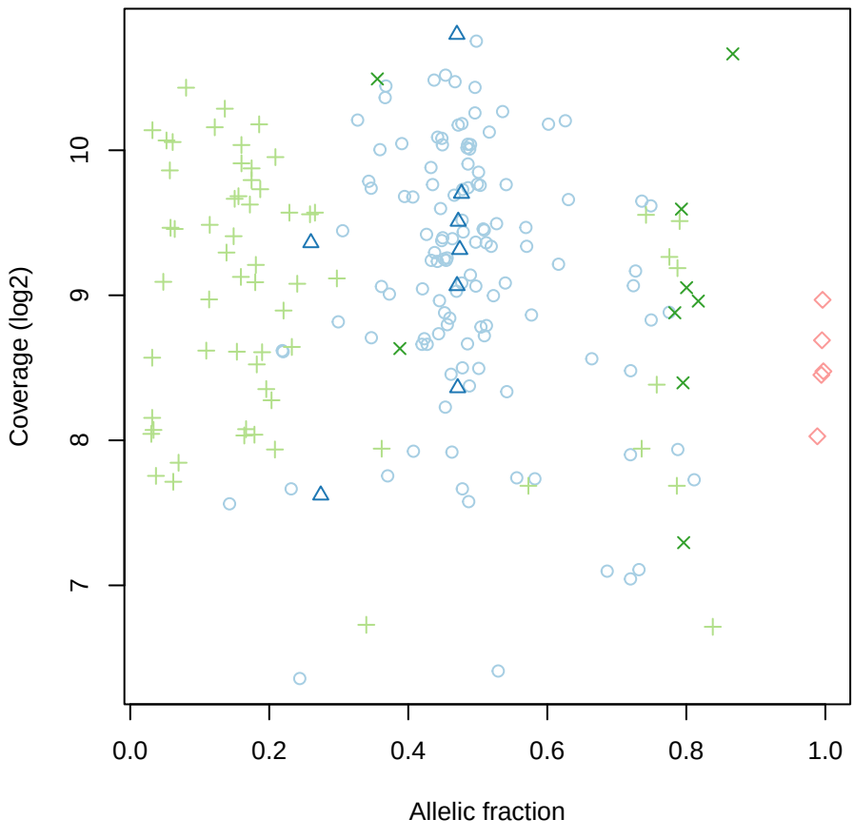

Purity: 0.72 Tumor ploidy: 2.878
1
2
3
4
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1
0
1
2
log2 ratio

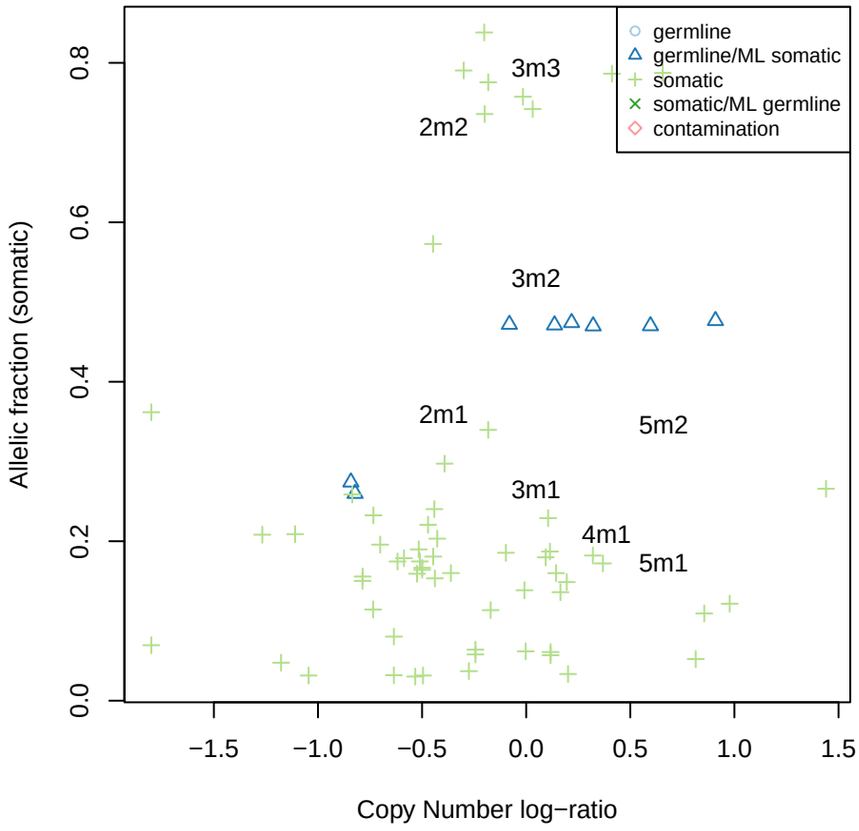

Purity: 0.72 Tumor ploidy: 2.878 SNV log−likelihood: −977.64 GoF: 66.5% Mean coverage: 639;28
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.2 0.4 0.6 0.8 1.0
0 20 40 60 80 100 120
SNV Index

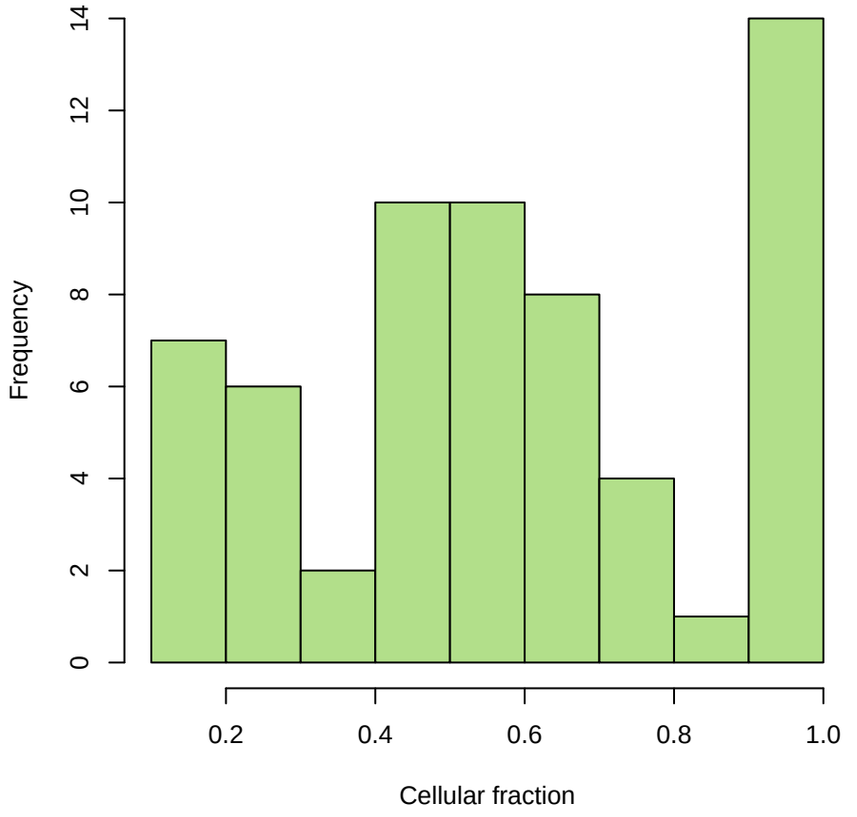

SCNA−fit log−likelihood: −18154.95
Copy Number log−ratio
−2 −1 0 1 2
1 2 3 4
0 20 40 60 80 100 120
SNV Index


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
3m3
2m2
4m3
3m2
5m3
2m1
4m2
5m2
3m1
4m1
2m0


Coverage (log2)
Allelic fraction


germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m3
2m2
3m2
2m1
5m2
3m1
4m1
5m1


Frequency
Cellular fraction