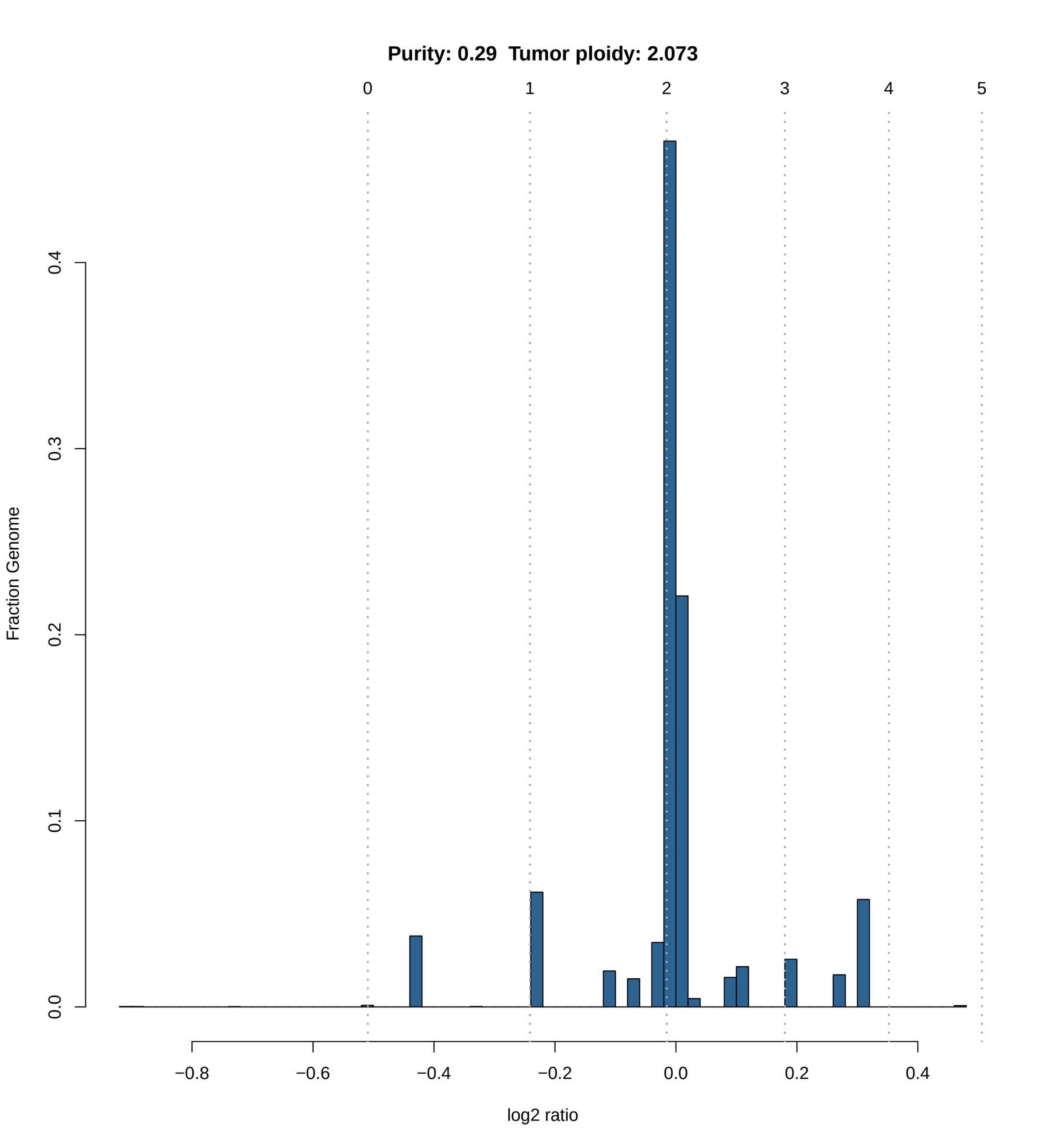
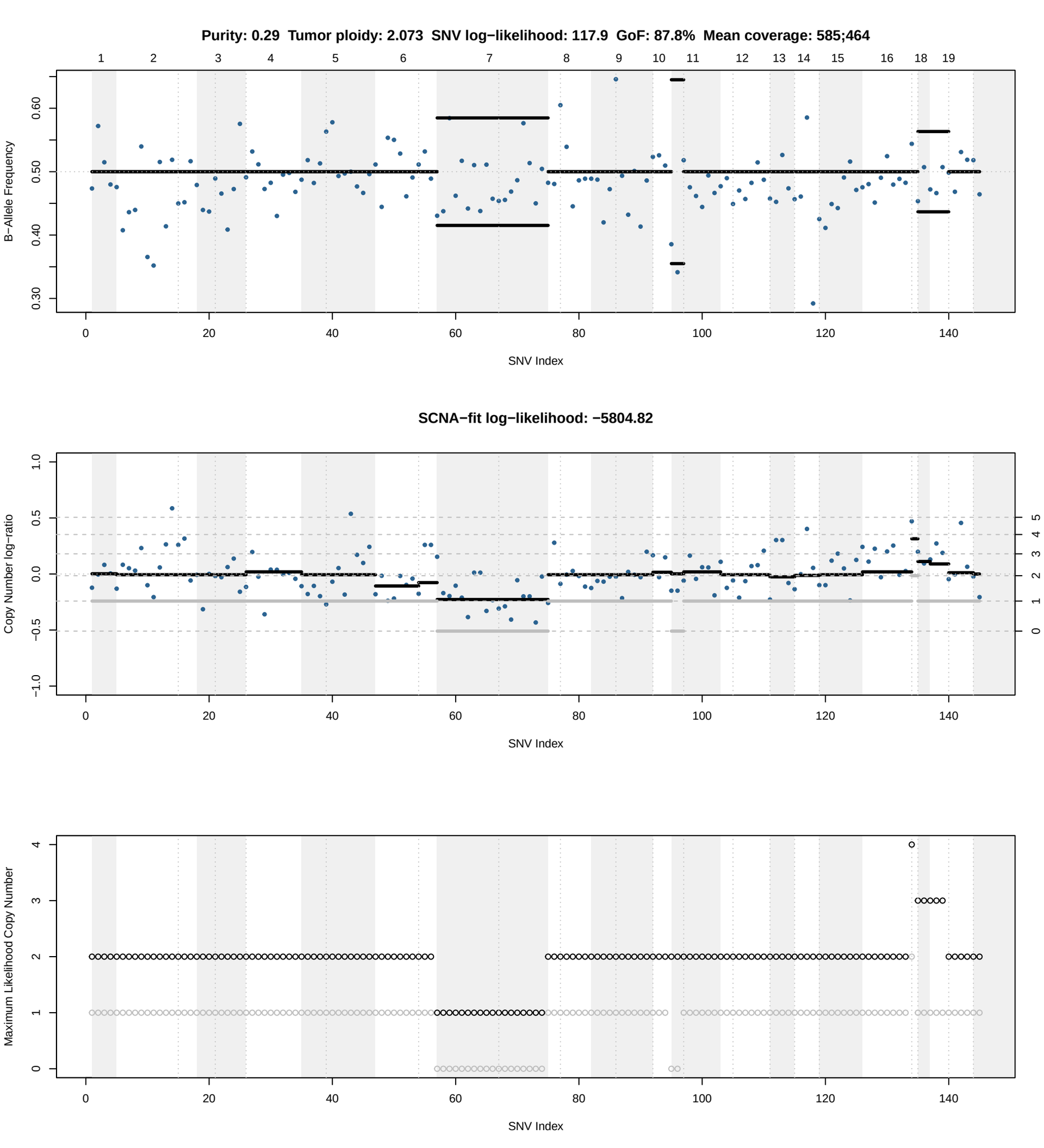
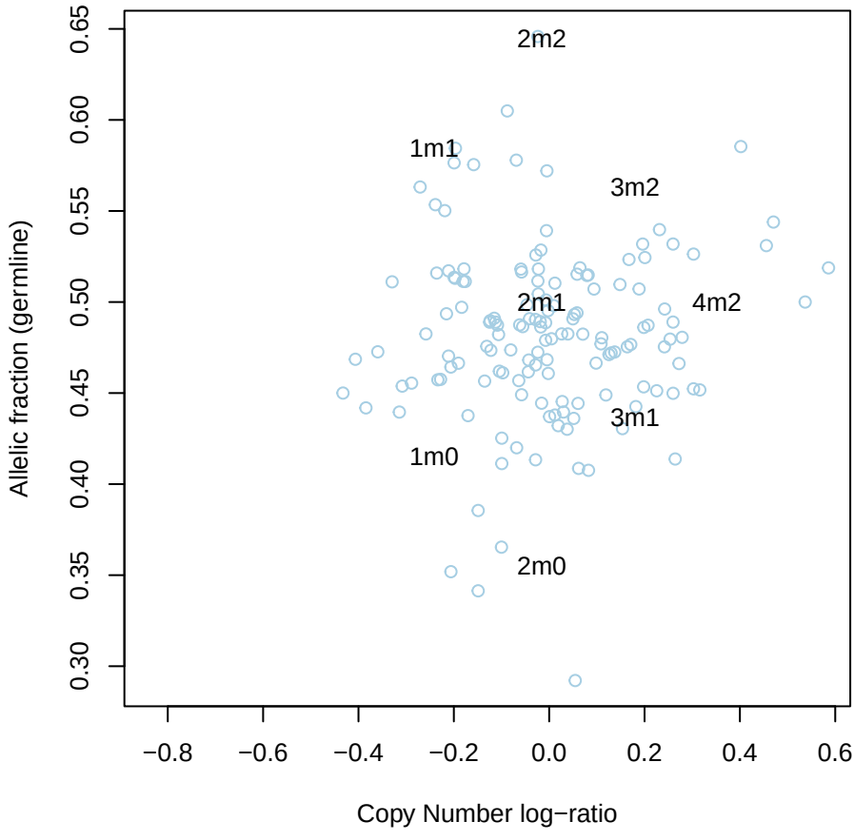
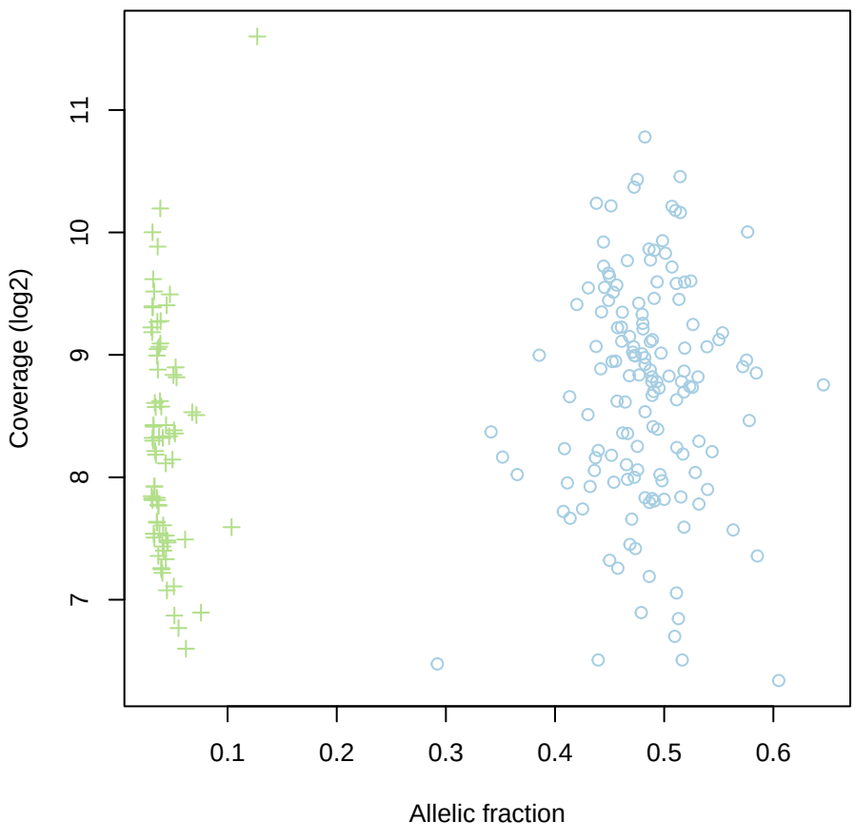
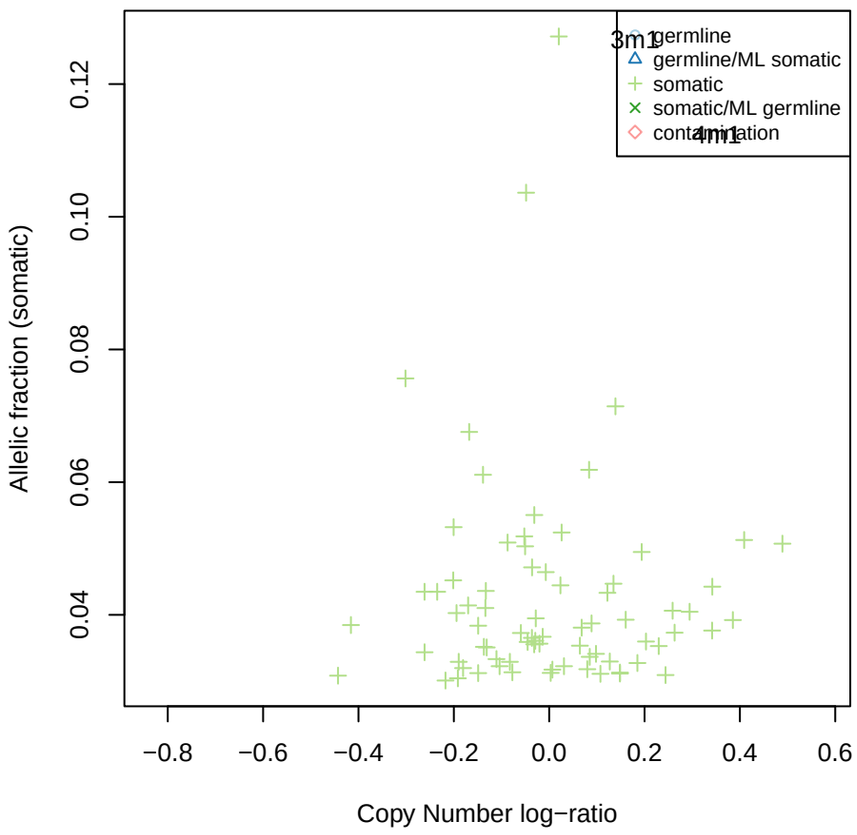
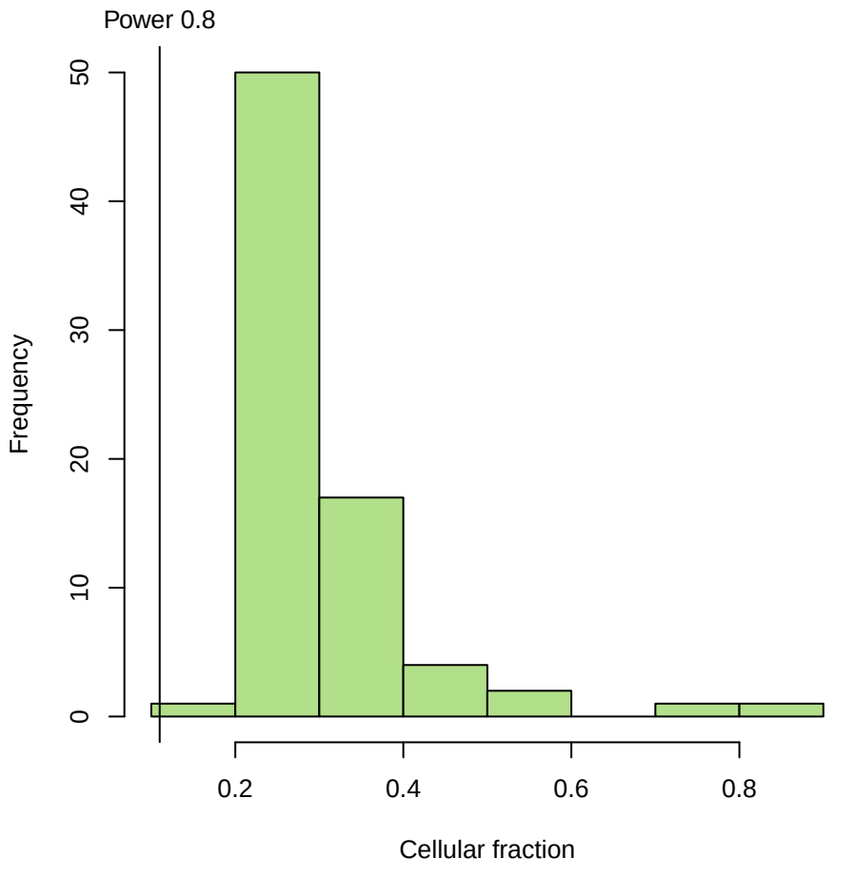

Purity: 0.29 Tumor ploidy: 2.073
0
1
2
3
4
5
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

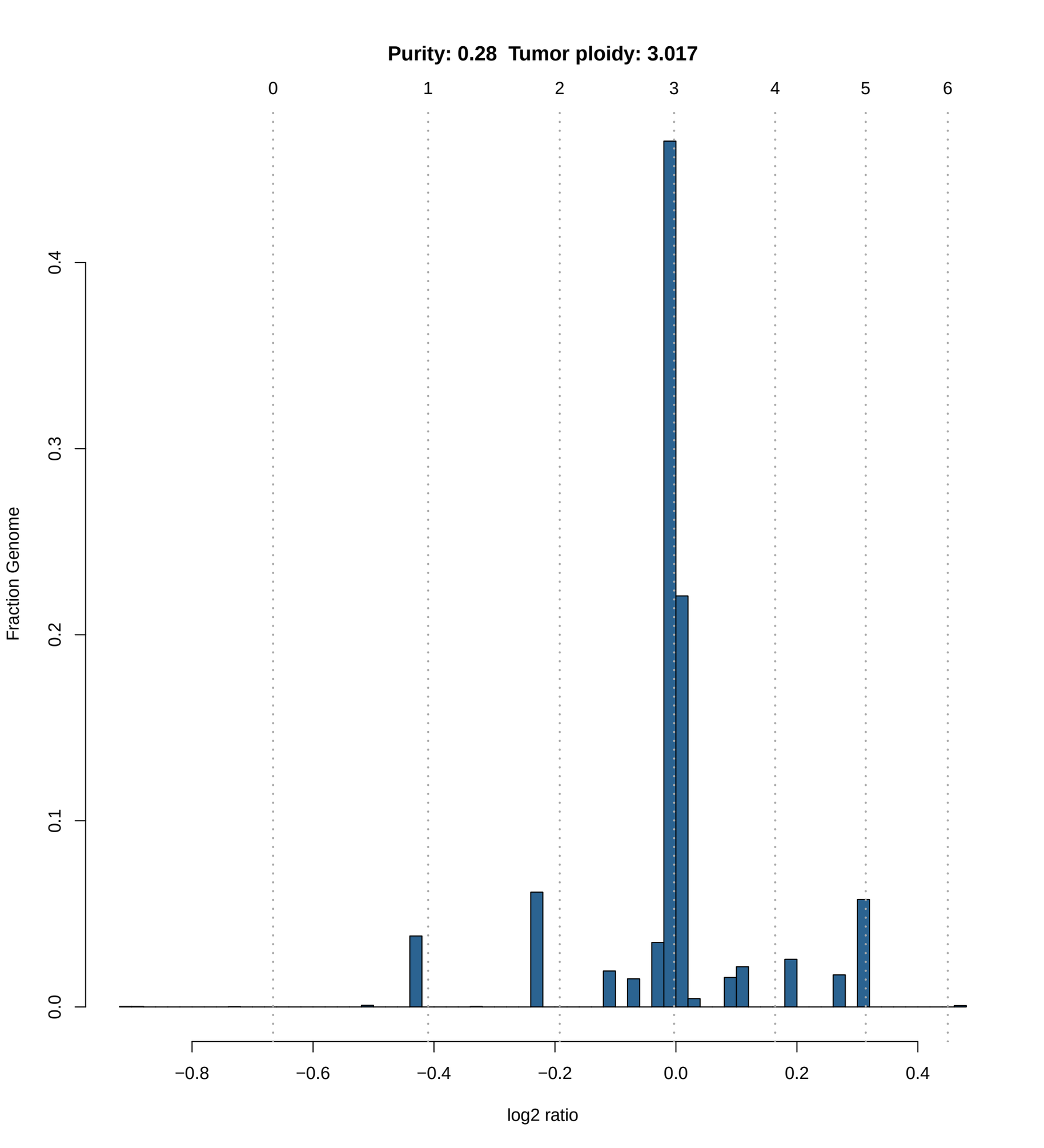

Purity: 0.29 Tumor ploidy: 2.073 SNV log−likelihood: 117.9 GoF: 87.8% Mean coverage: 585;464
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 18 19
B−Allele Frequency
0.30 0.40 0.50 0.60
0 20 40 60 80 100 120 140
SNV Index
SCNA−fit log−likelihood: −5804.82
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120 140
SNV Index

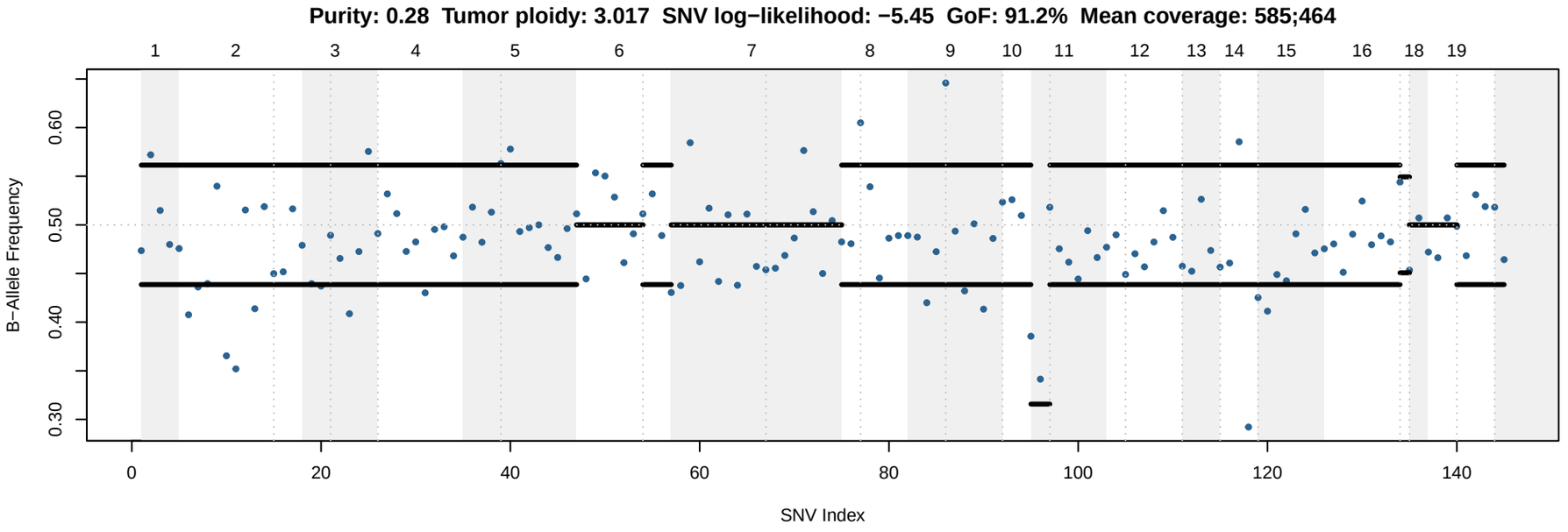

2m2
1m1
3m2
2m1
4m2
3m1
1m0
2m0
Allelic fraction (germline)
Copy Number log−ratio

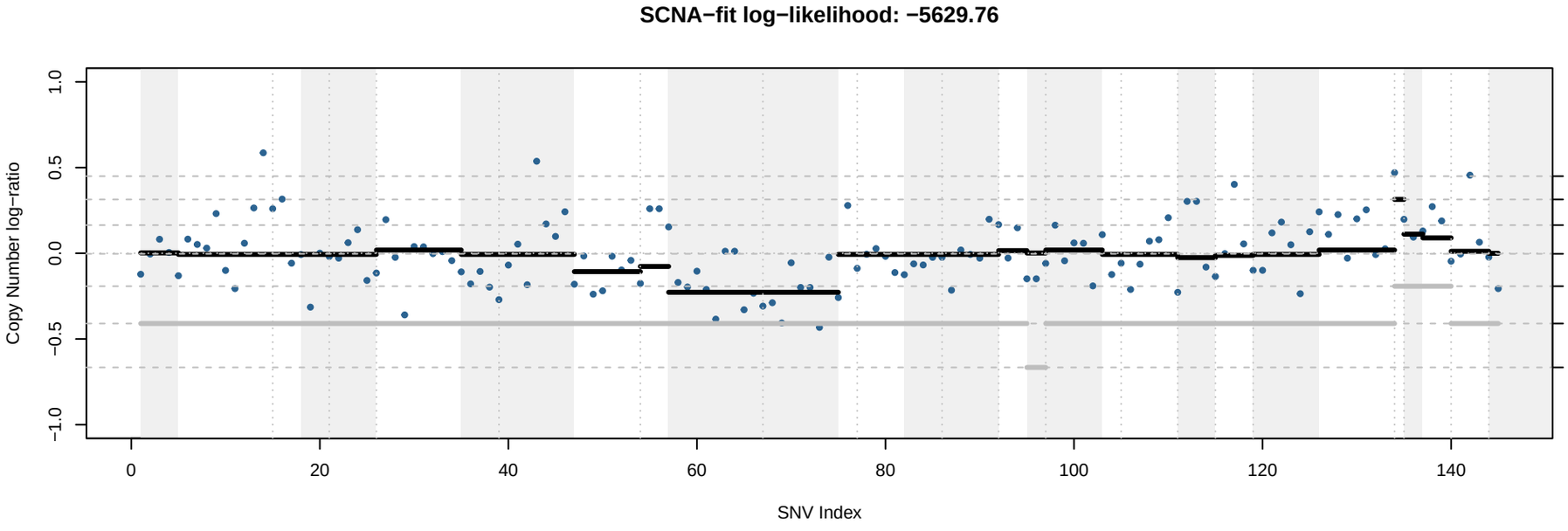

Coverage (log2)
Allelic fraction

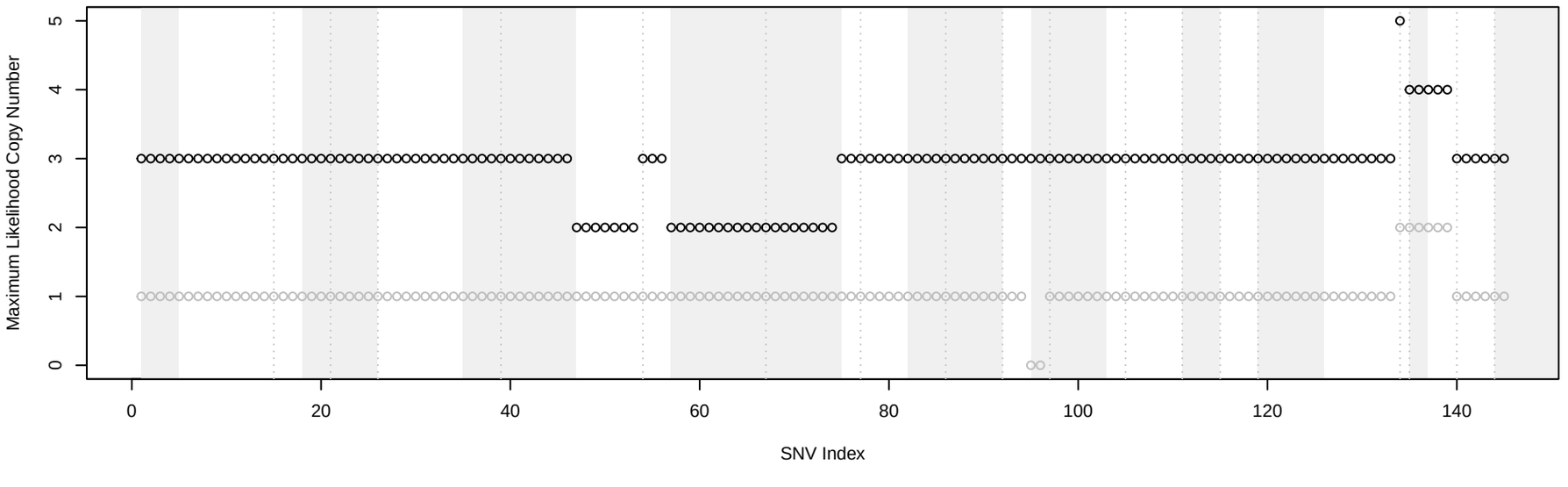

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
Allelic fraction (somatic)
Copy Number log−ratio

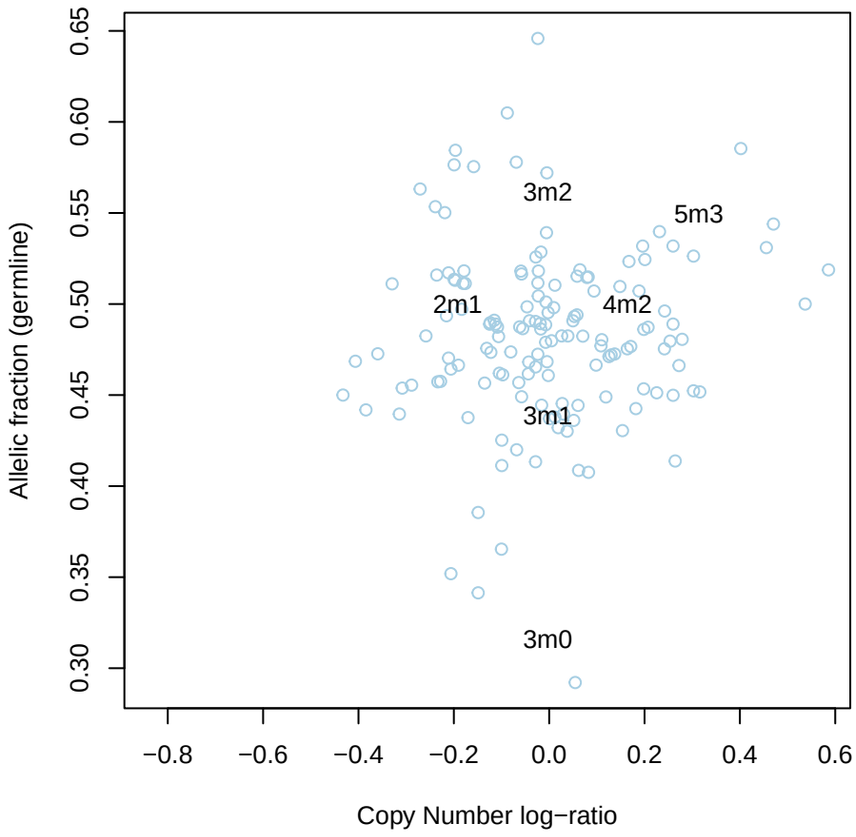

Power 0.8
Frequency
Cellular fraction

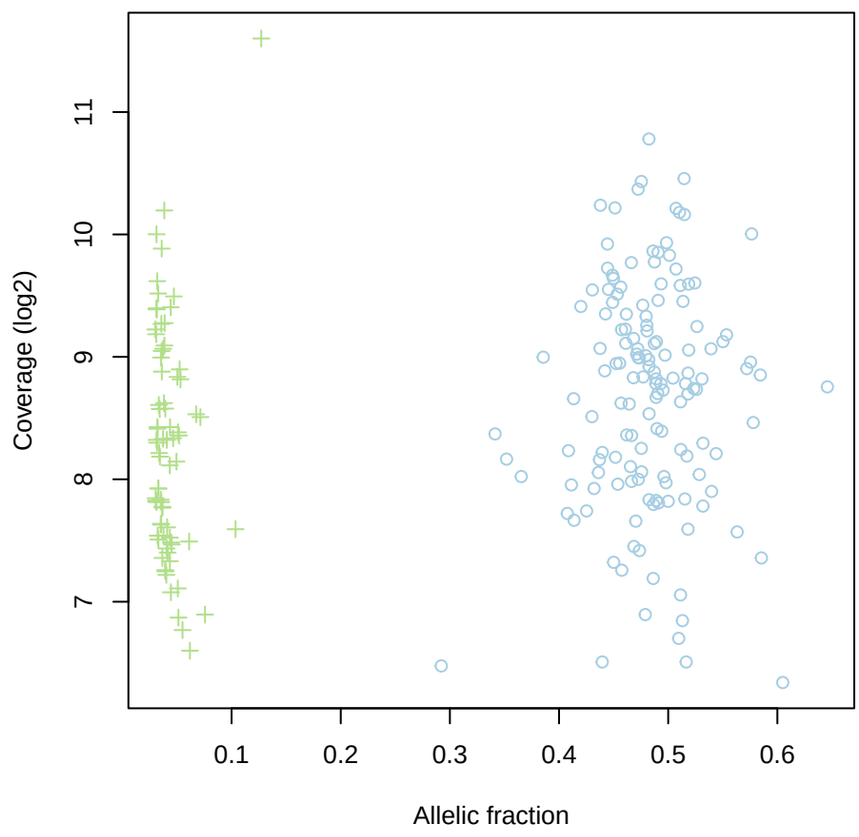

Purity: 0.28 Tumor ploidy: 3.017
0
1
2
3
4
5
6
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

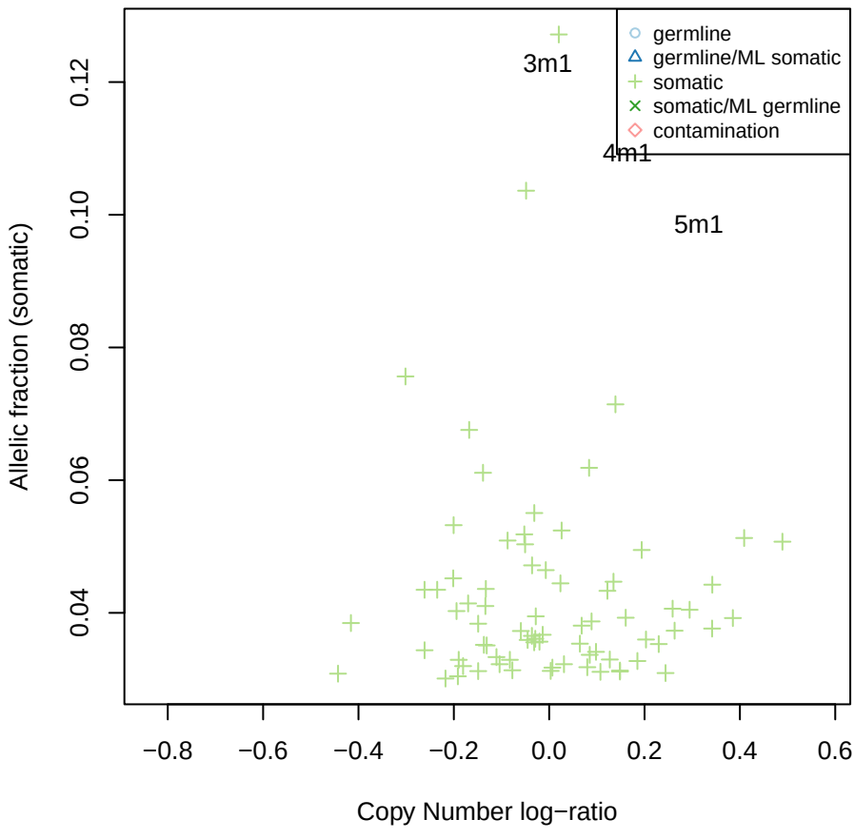

Purity: 0.28 Tumor ploidy: 3.017 SNV log−likelihood: −5.45 GoF: 91.2% Mean coverage: 585;464
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 18 19
B−Allele Frequency
0.30 0.40 0.50 0.60
0 20 40 60 80 100 120 140
SNV Index

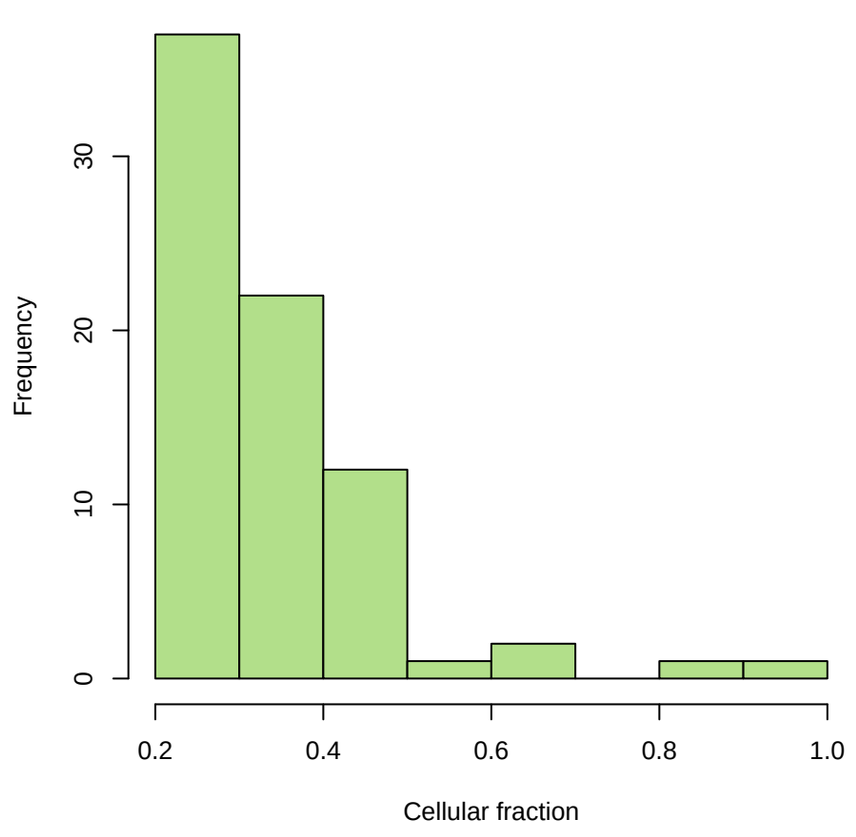

SCNA−fit log−likelihood: −5629.76
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

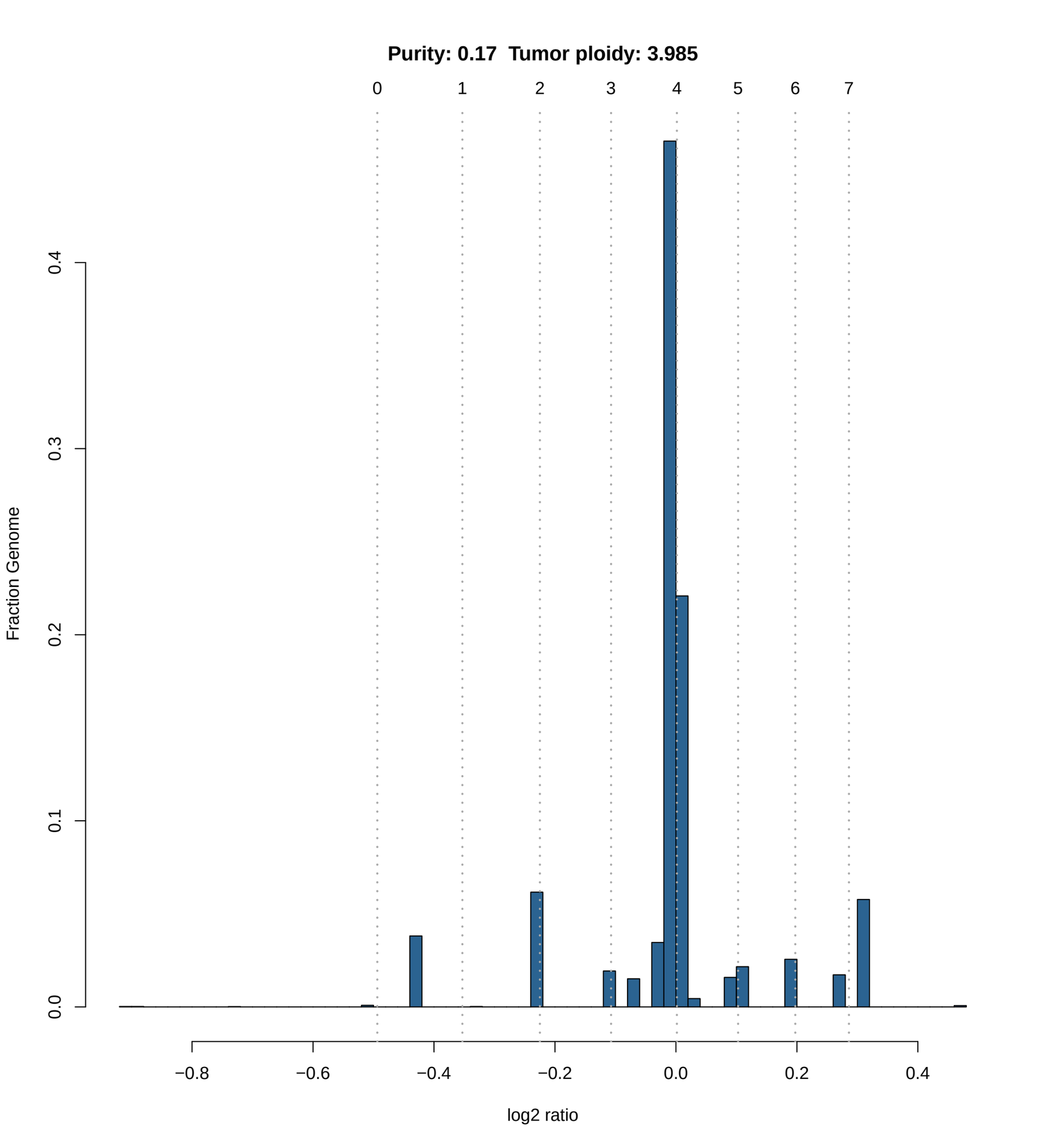

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

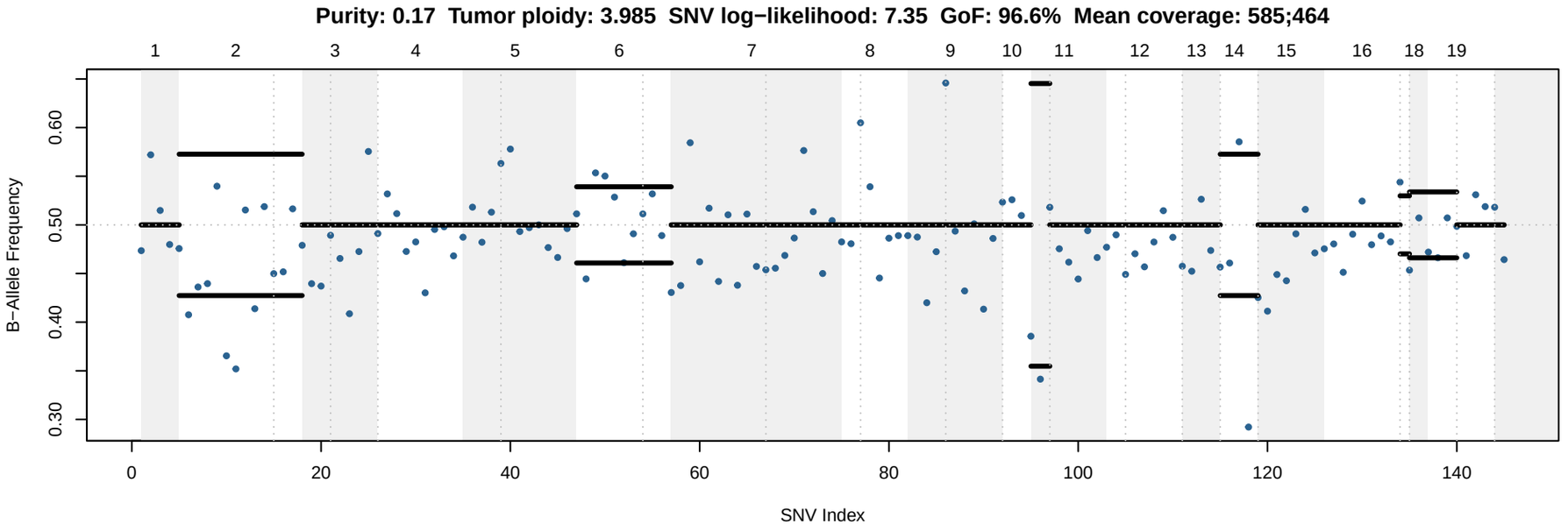

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
0.65
3m2
5m3
2m1
4m2
3m1
3m0
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

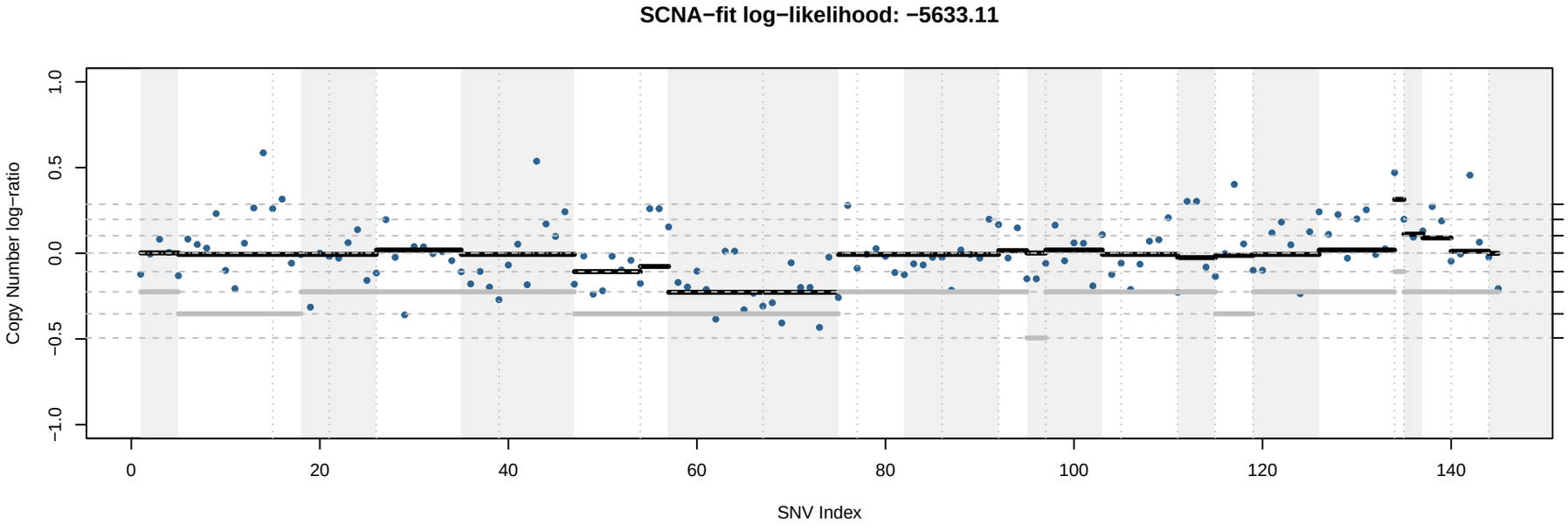

Coverage (log2)
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

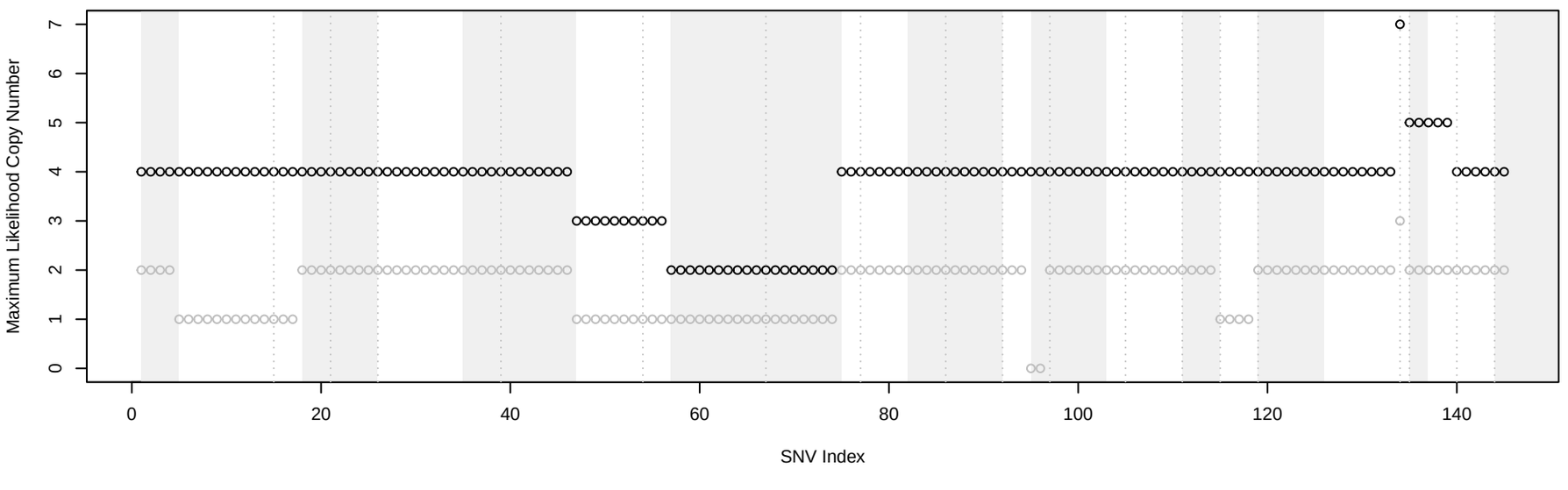

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

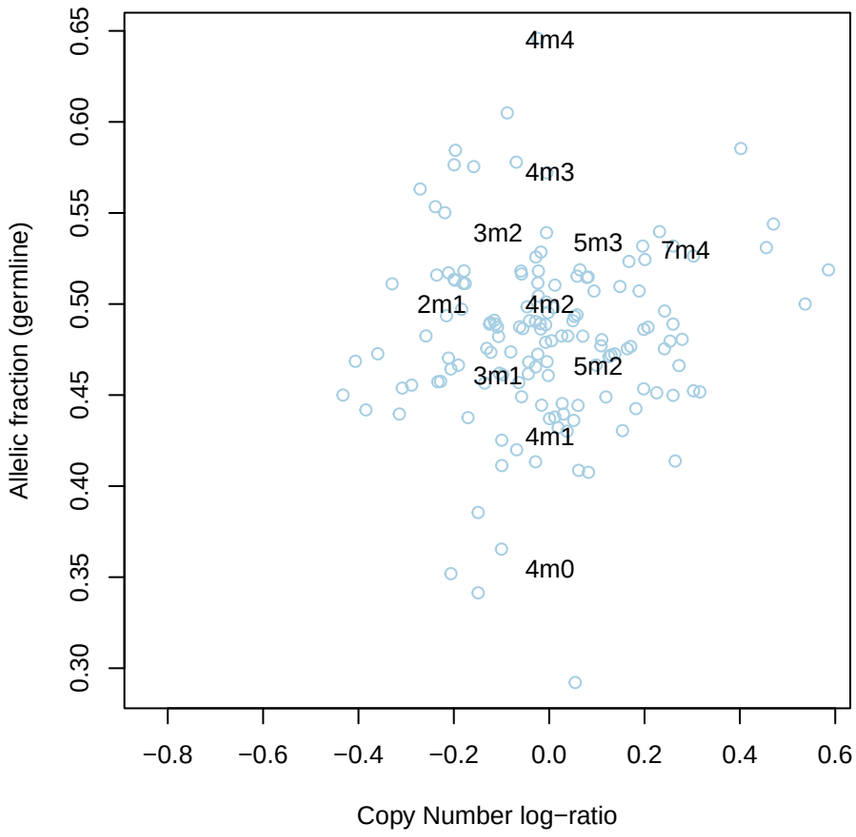

Frequency
0
10
20
30
0.2
0.4
0.6
0.8
1.0
Cellular fraction

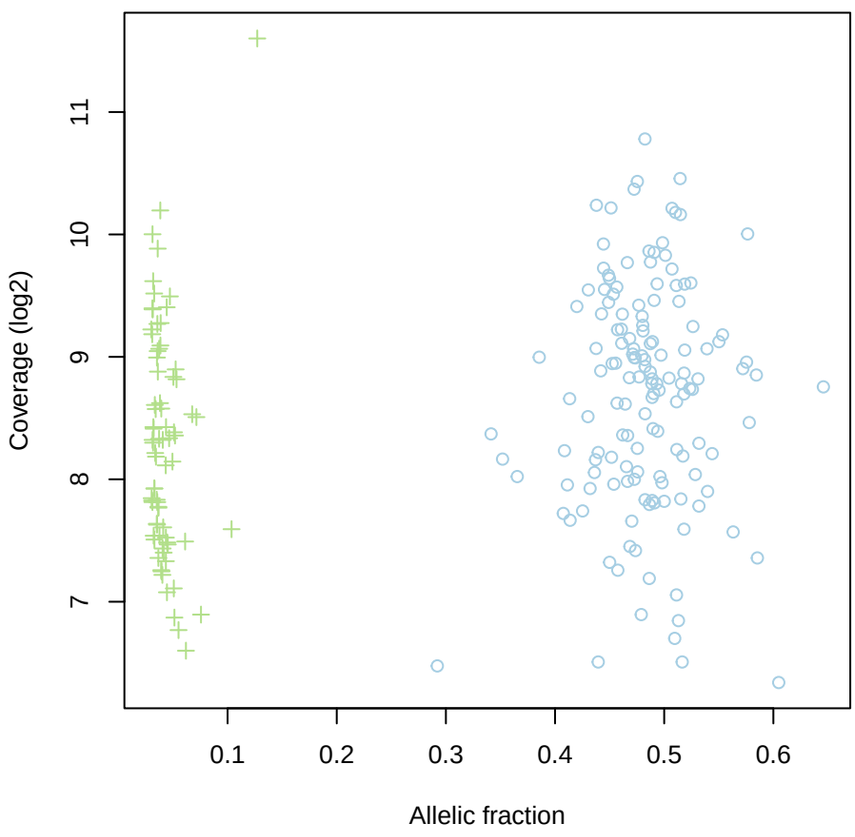

Purity: 0.17 Tumor ploidy: 3.985
0
1
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

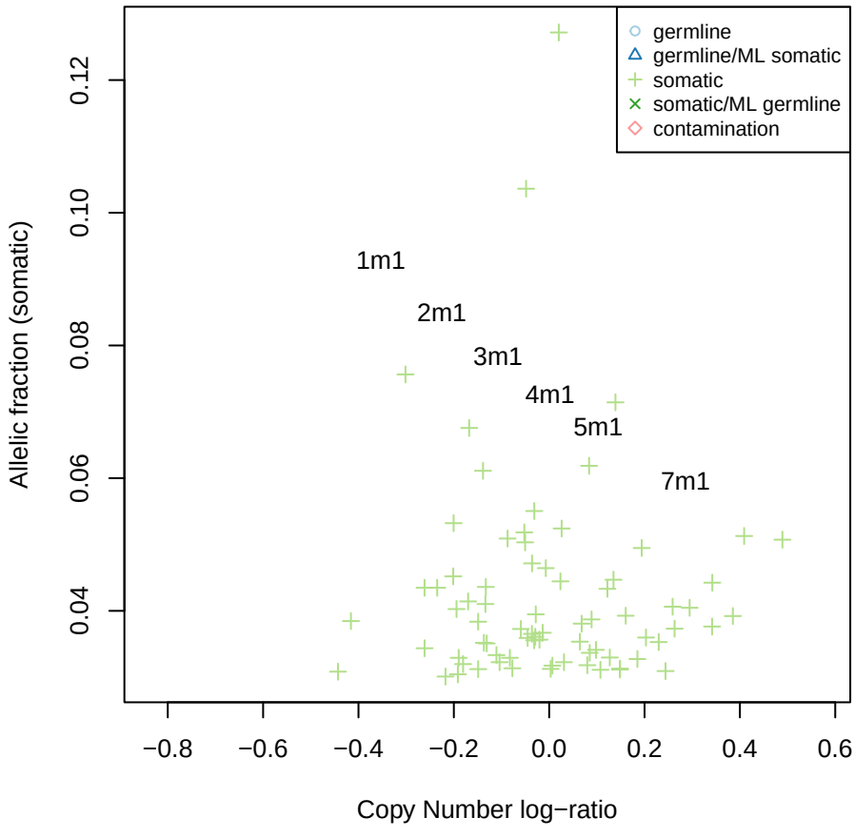

Purity: 0.17 Tumor ploidy: 3.985 SNV log−likelihood: 7.35 GoF: 96.6% Mean coverage: 585;464
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 18 19
B−Allele Frequency
0.30 0.40 0.50 0.60
0 20 40 60 80 100 120 140
SNV Index

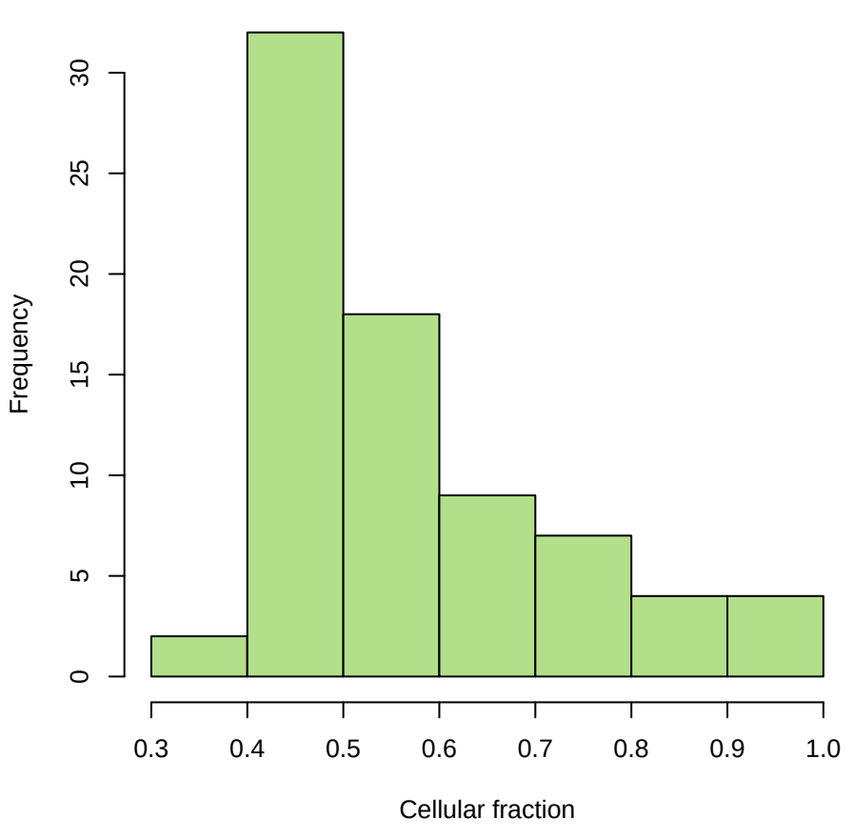

SCNA−fit log−likelihood: −5633.11
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4 6
0 20 40 60 80 100 120 140
SNV Index

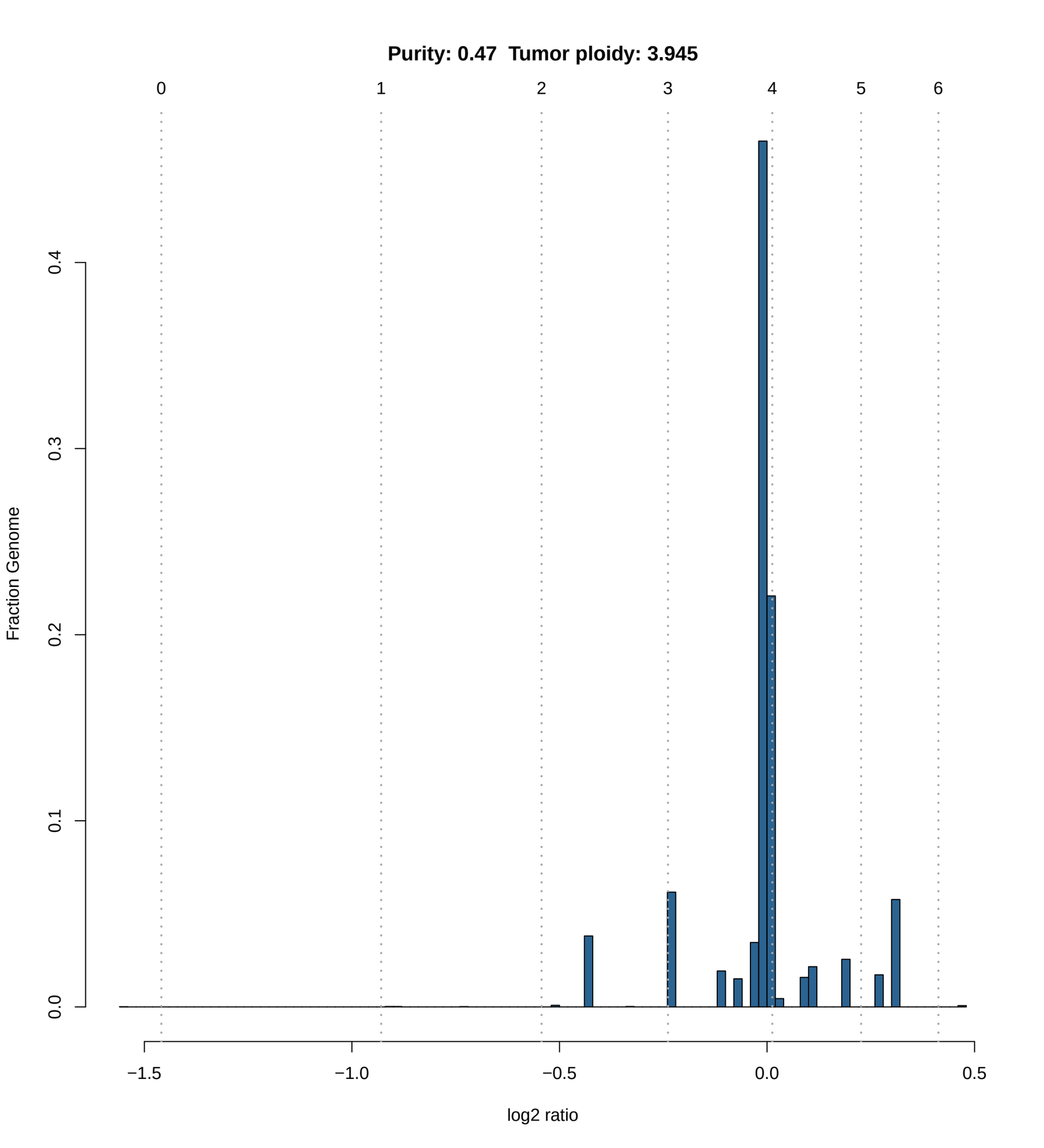

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

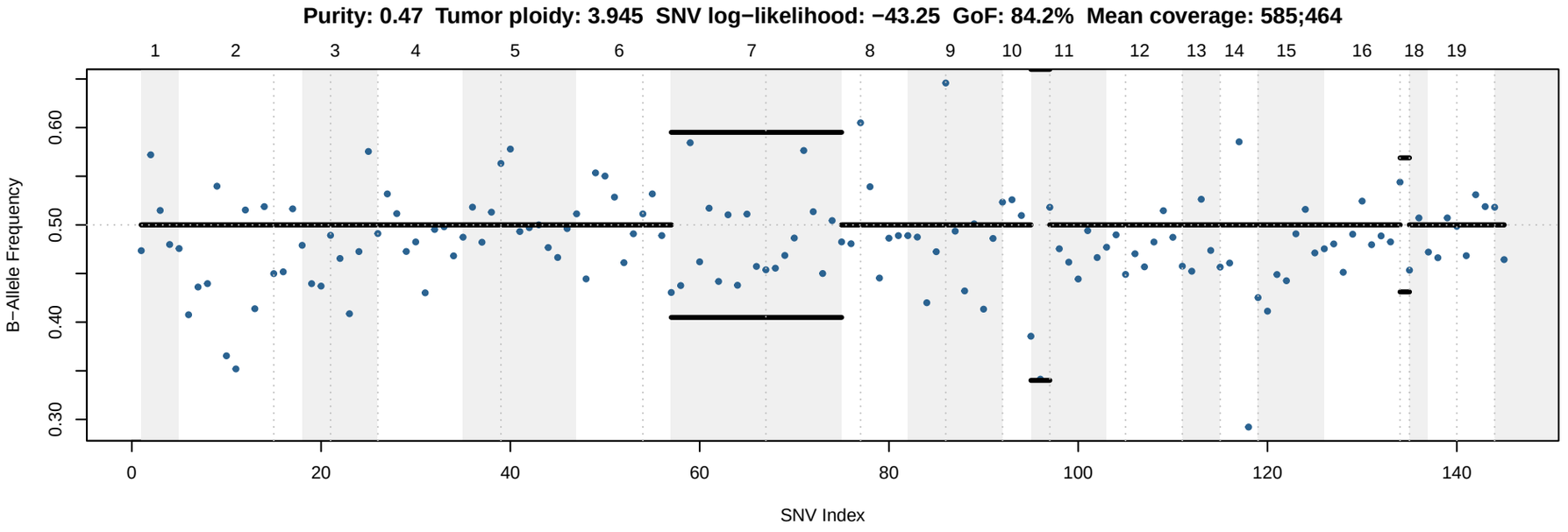

Allelic fraction (germline)
Copy Number log−ratio
4m4
4m3
3m2
5m3
7m4
2m1
4m2
5m2
3m1
4m1
4m0

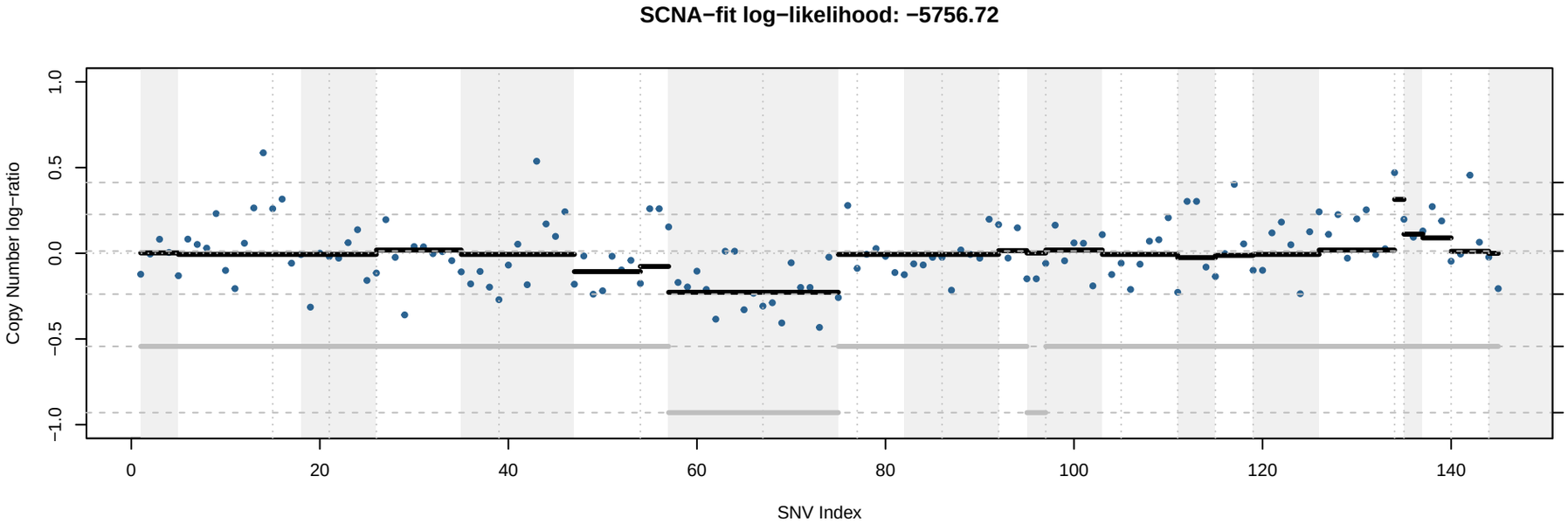

Coverage (log2)
Allelic fraction

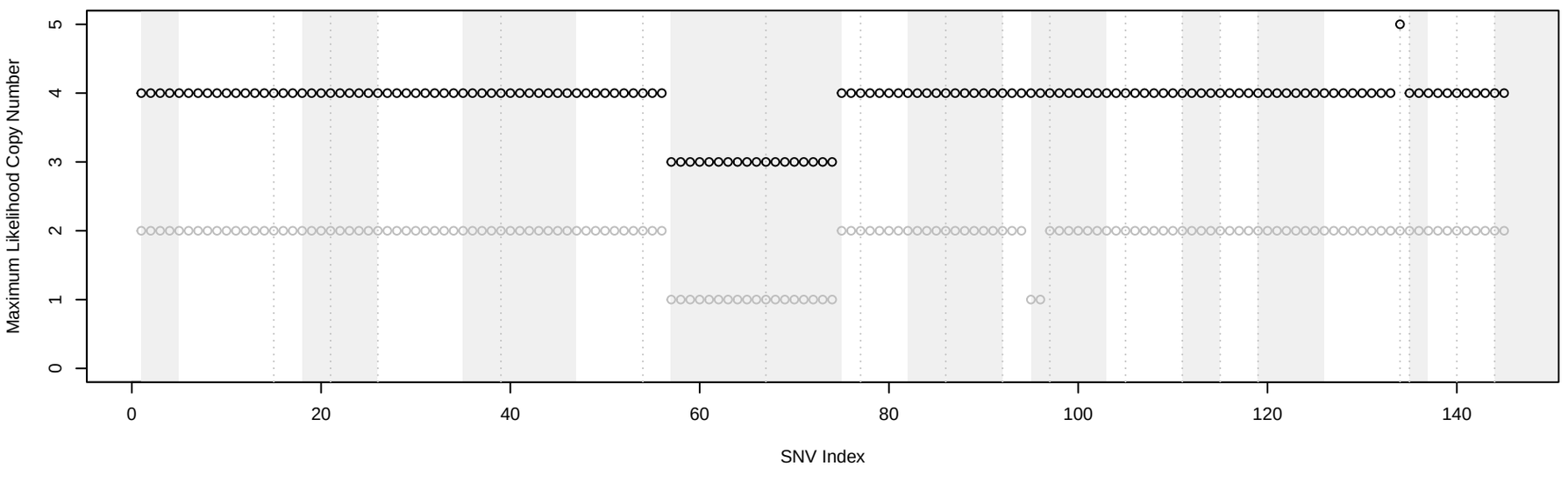

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1
3m1
4m1
5m1
7m1

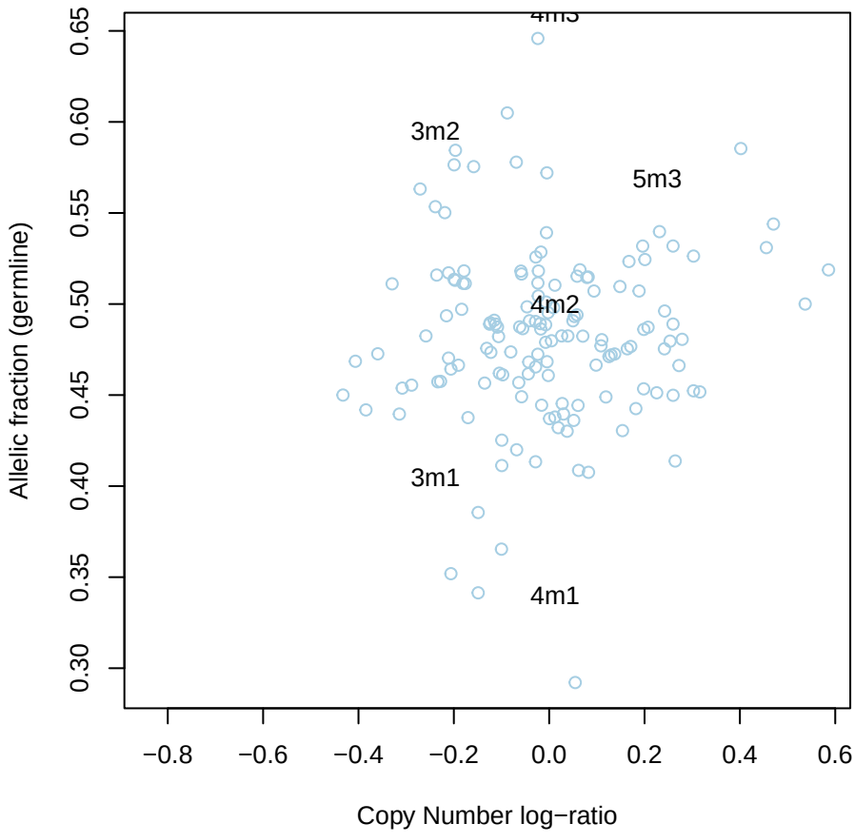

Frequency
Cellular fraction

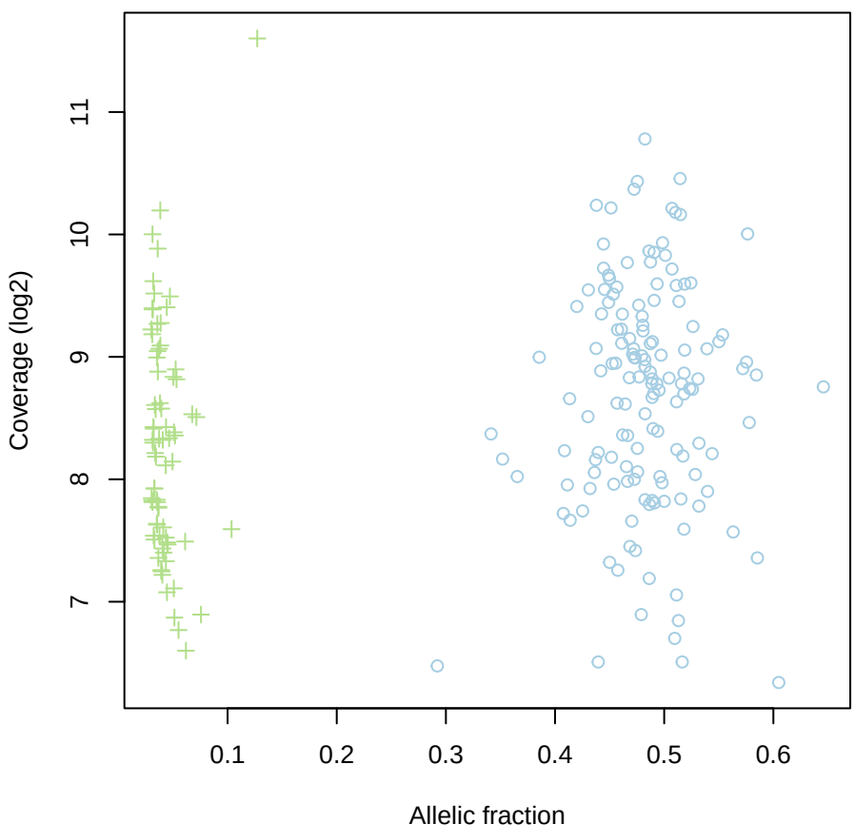

Purity: 0.47 Tumor ploidy: 3.945
0
1
2
3
4
5
6
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

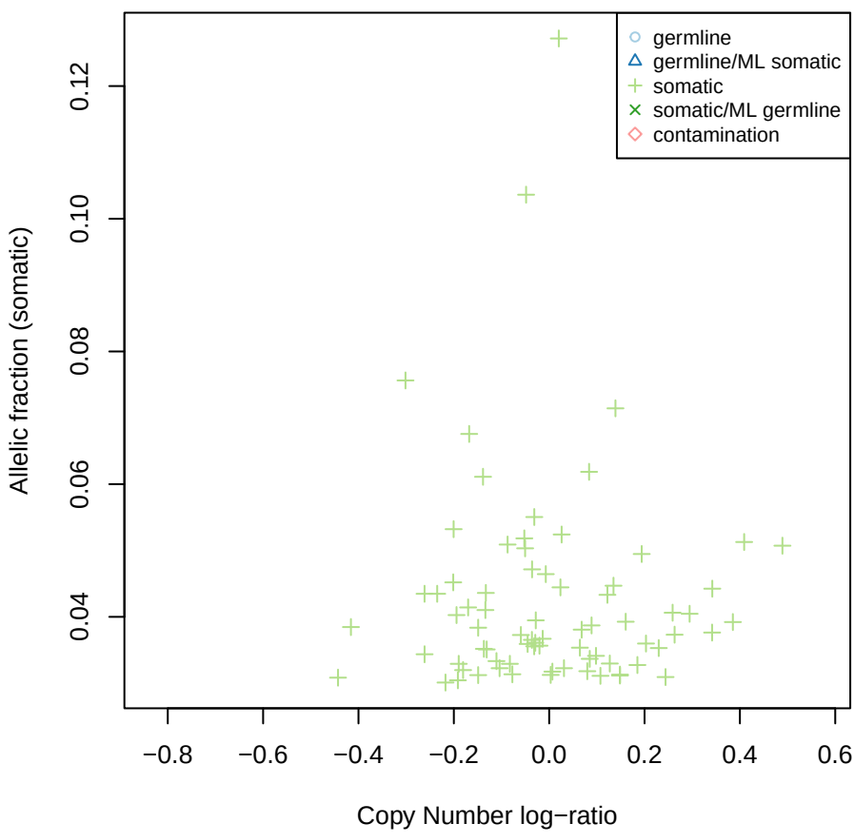

Purity: 0.47 Tumor ploidy: 3.945 SNV log−likelihood: −43.25 GoF: 84.2% Mean coverage: 585;464
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 18 19
B−Allele Frequency
0.30 0.40 0.50 0.60
0 20 40 60 80 100 120 140
SNV Index

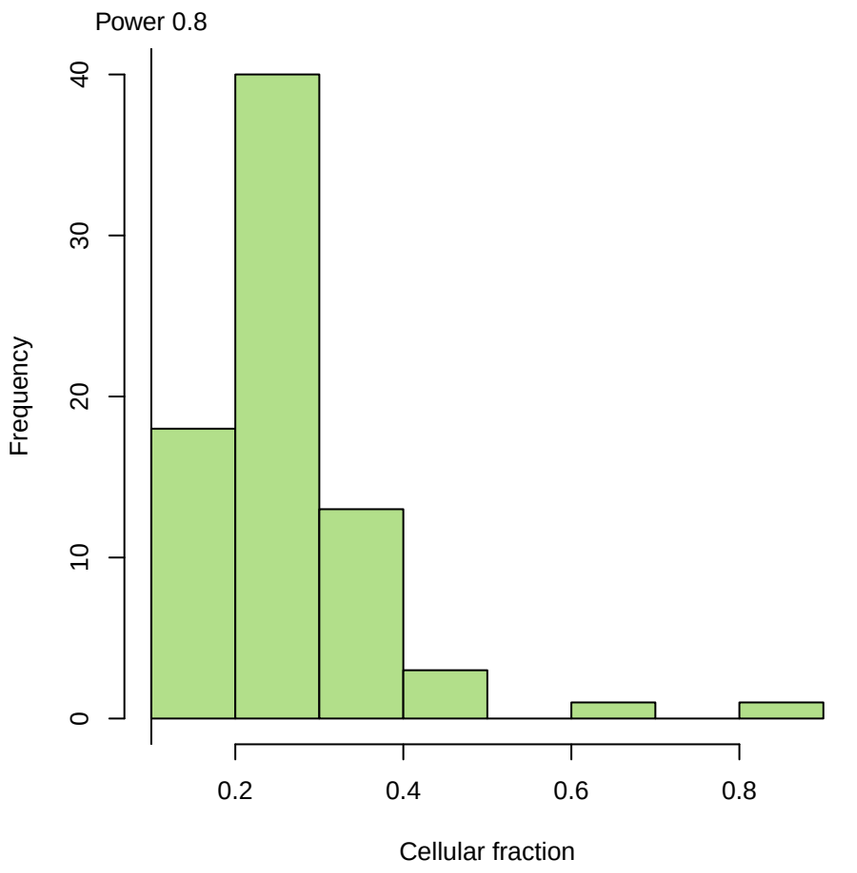

SCNA−fit log−likelihood: −5756.72
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

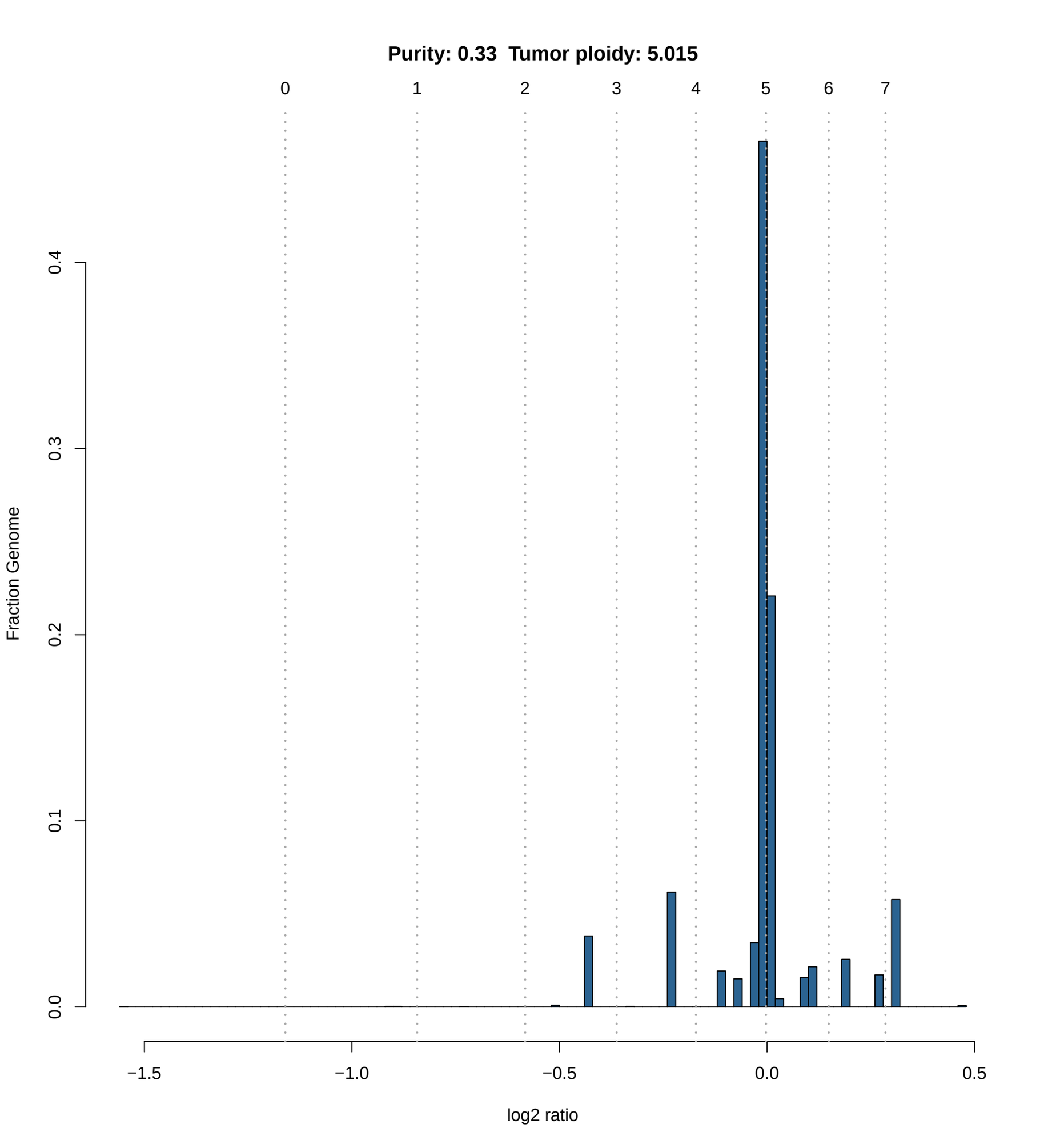

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

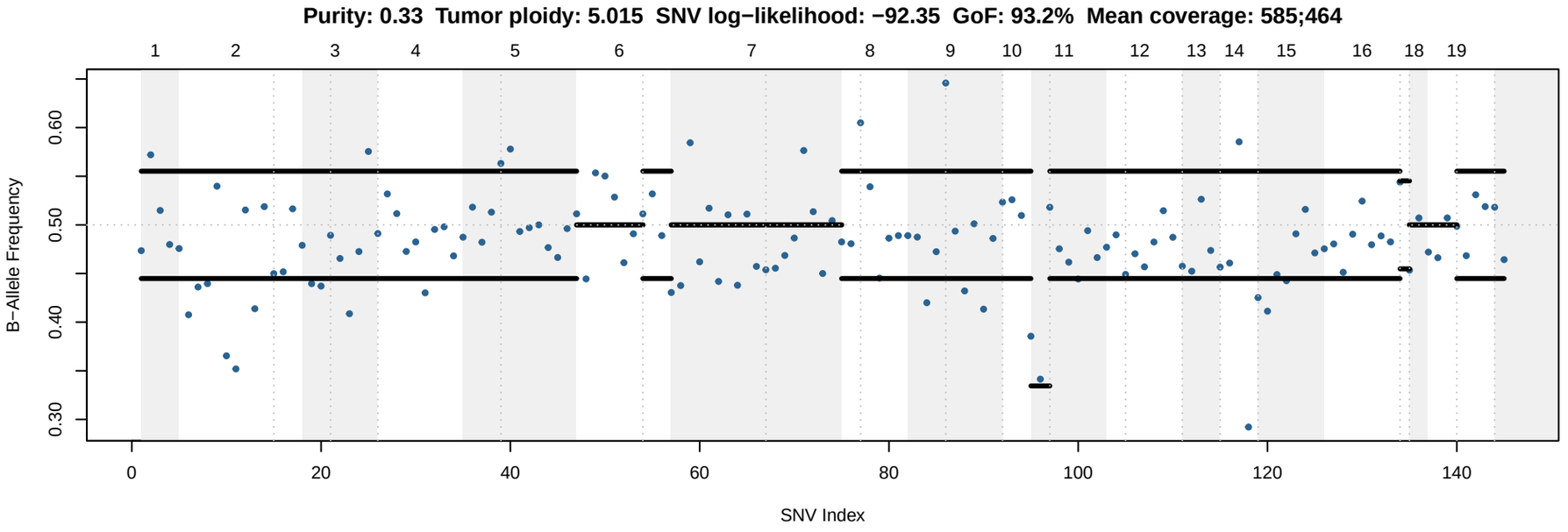

4m3
3m2
5m3
4m2
3m1
4m1
Allelic fraction (germline)
Copy Number log−ratio

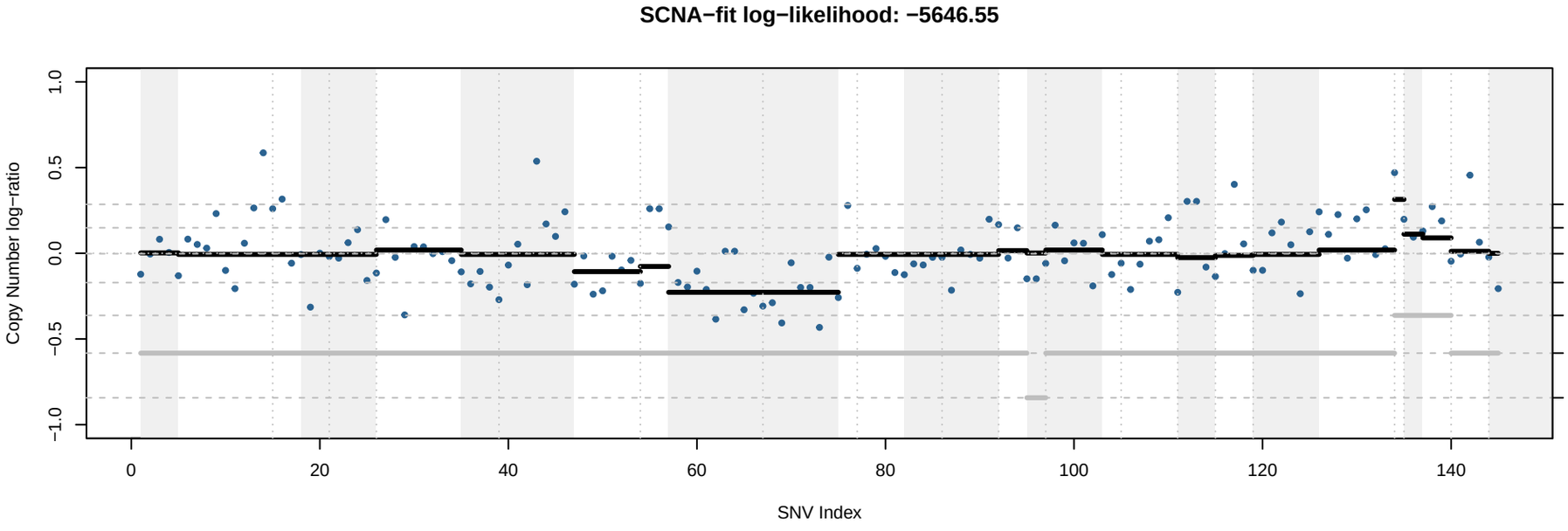

Coverage (log2)
Allelic fraction

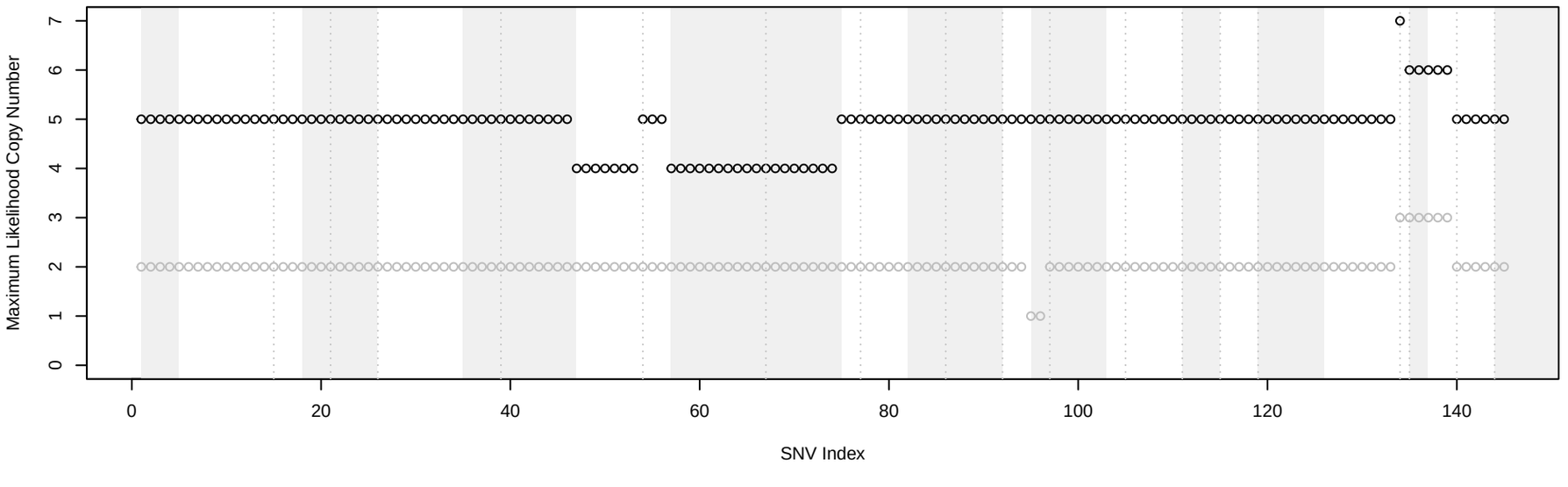

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

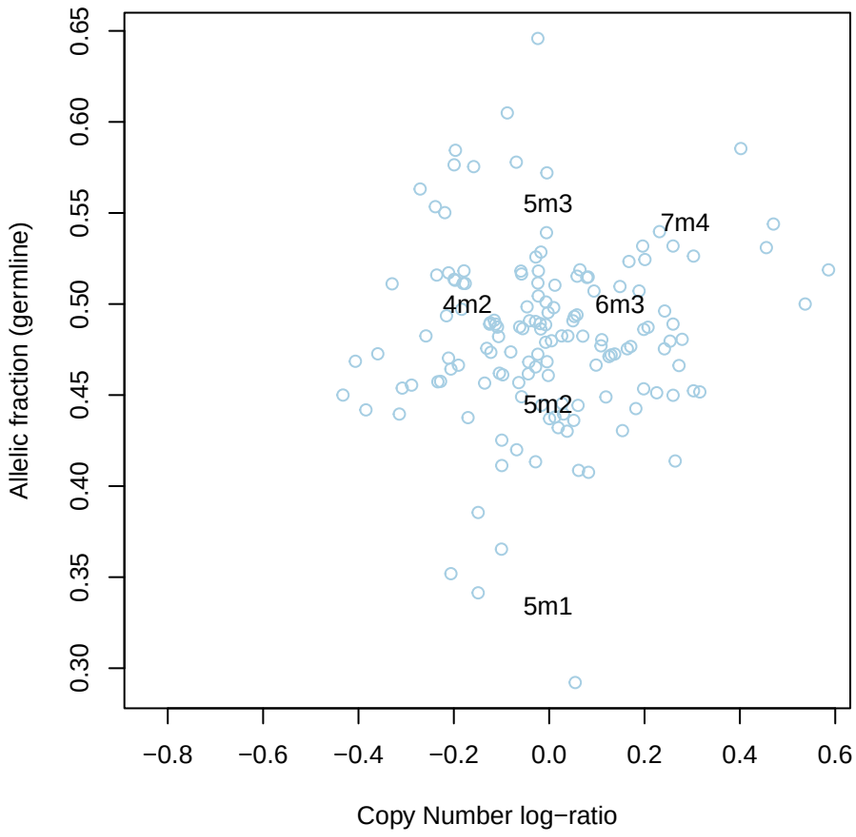

Power 0.8
Frequency
Cellular fraction

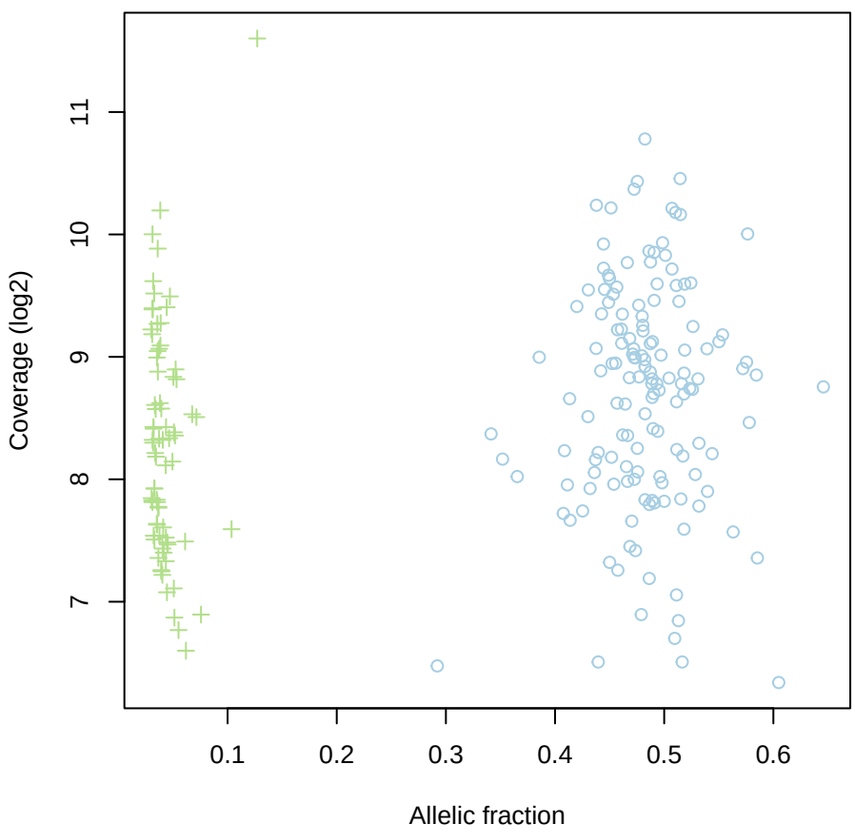

Purity: 0.33 Tumor ploidy: 5.015
0
1
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

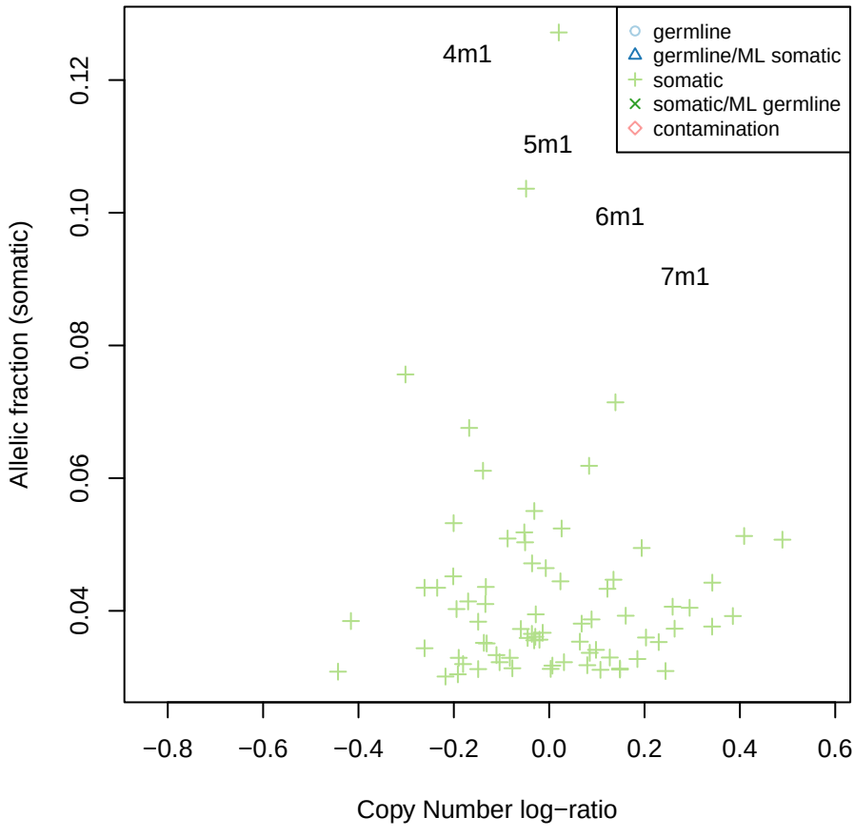

Purity: 0.33 Tumor ploidy: 5.015 SNV log−likelihood: −92.35 GoF: 93.2% Mean coverage: 585;464
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 18 19
B−Allele Frequency
0.30 0.40 0.50 0.60
0 20 40 60 80 100 120 140
SNV Index

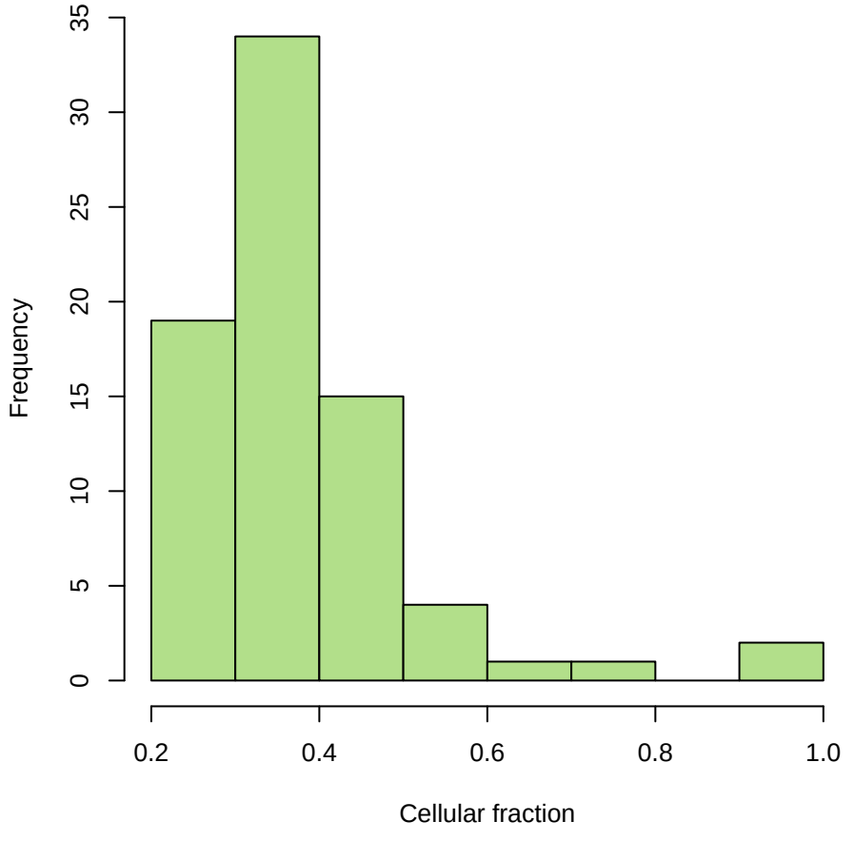

SCNA−fit log−likelihood: −5646.55
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

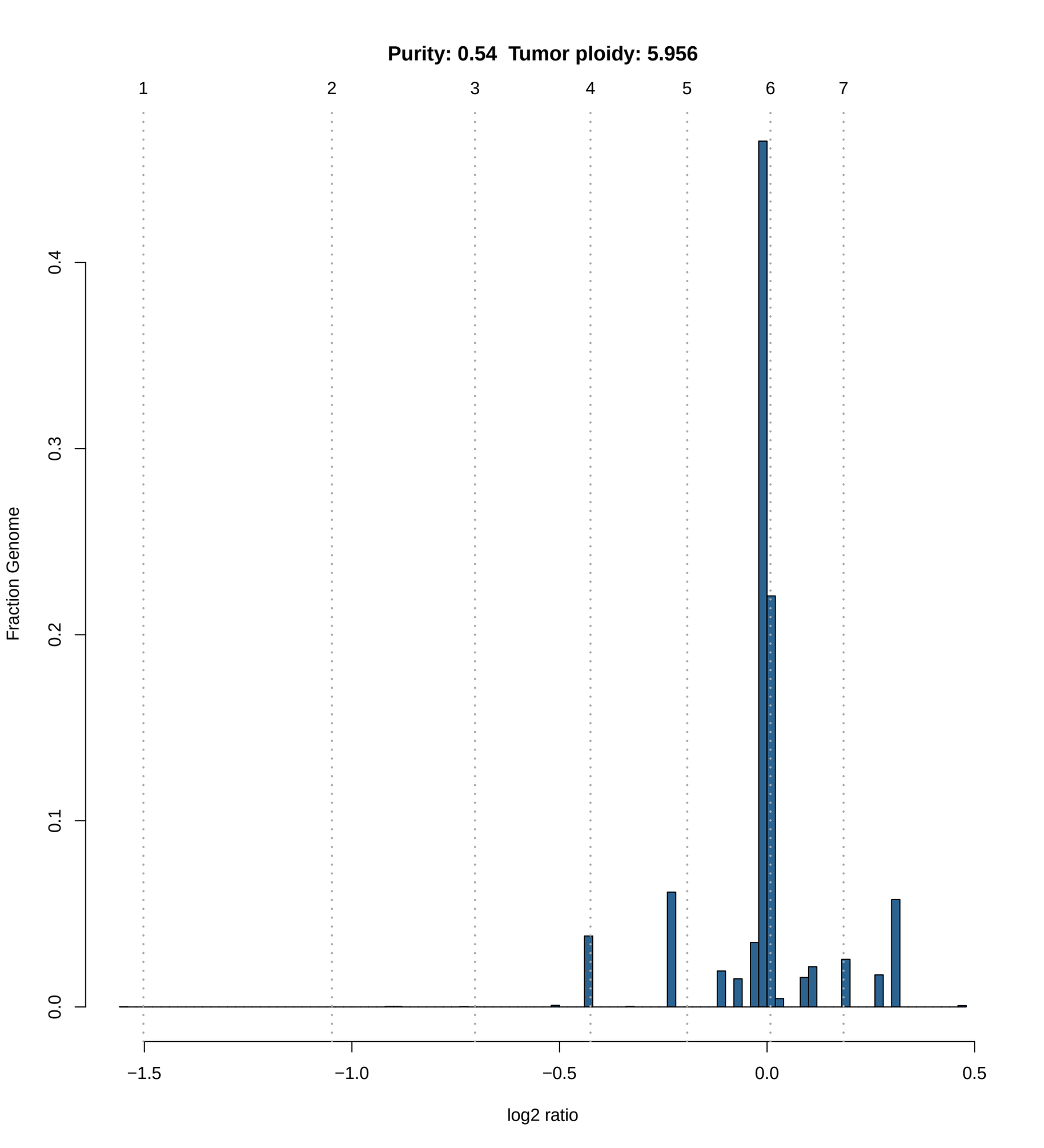

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

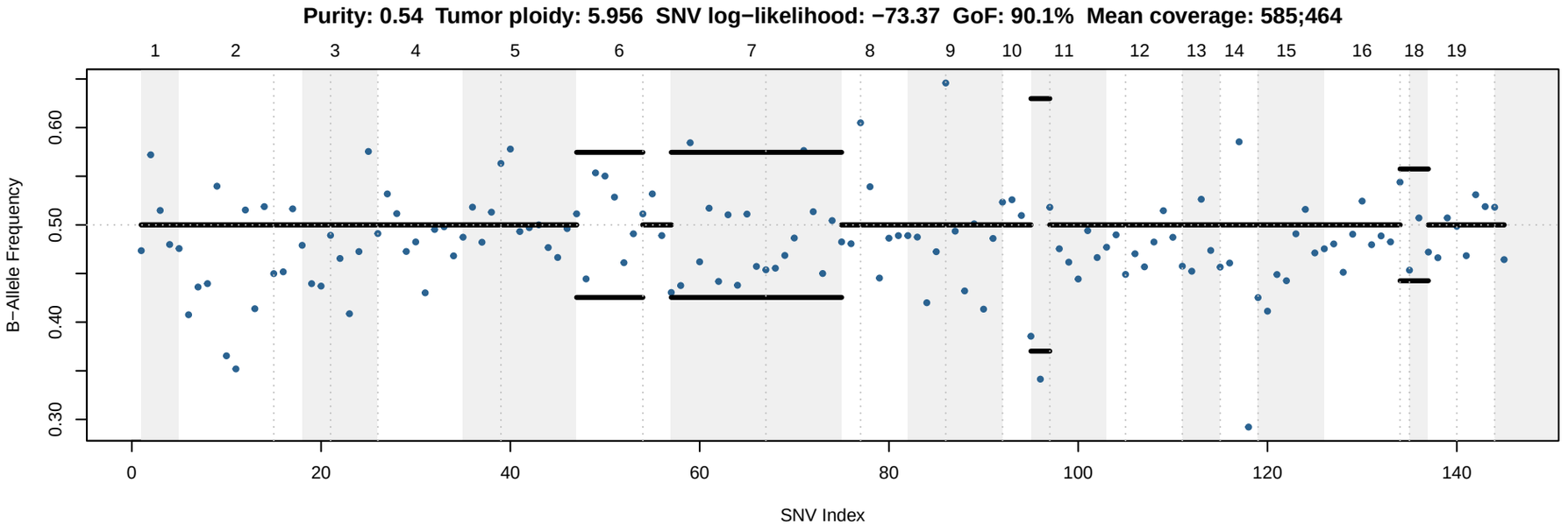

Allelic fraction (germline)
Copy Number log−ratio
5m3
7m4
4m2
6m3
5m2
5m1

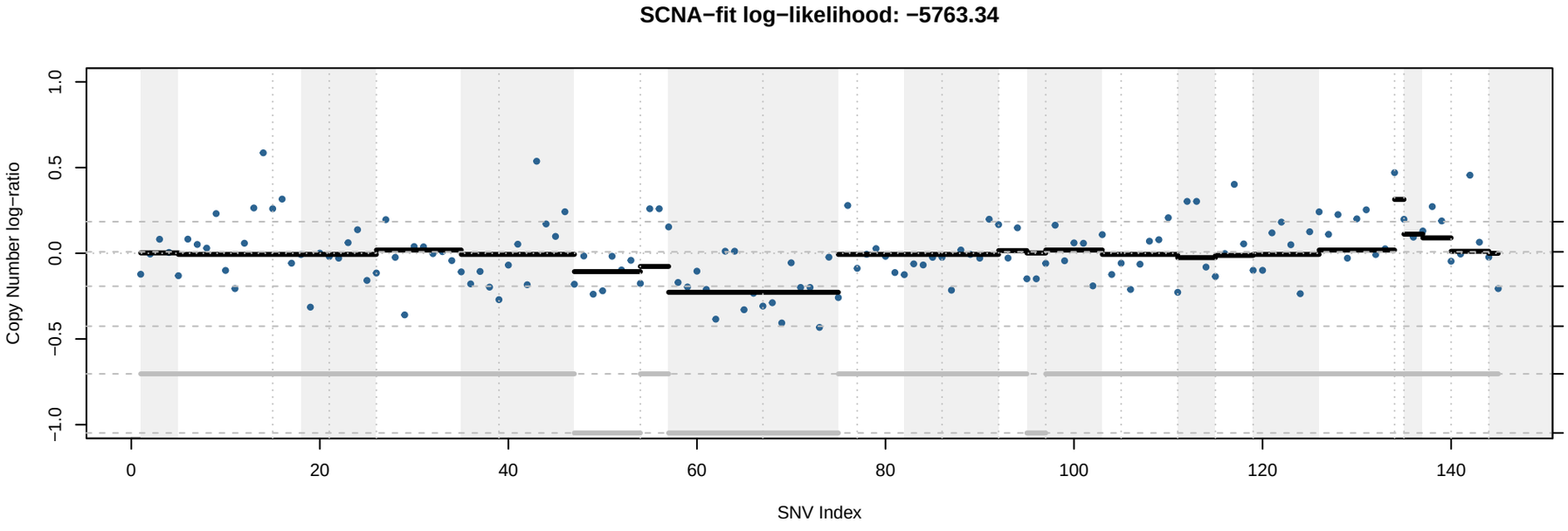

Coverage (log2)
Allelic fraction

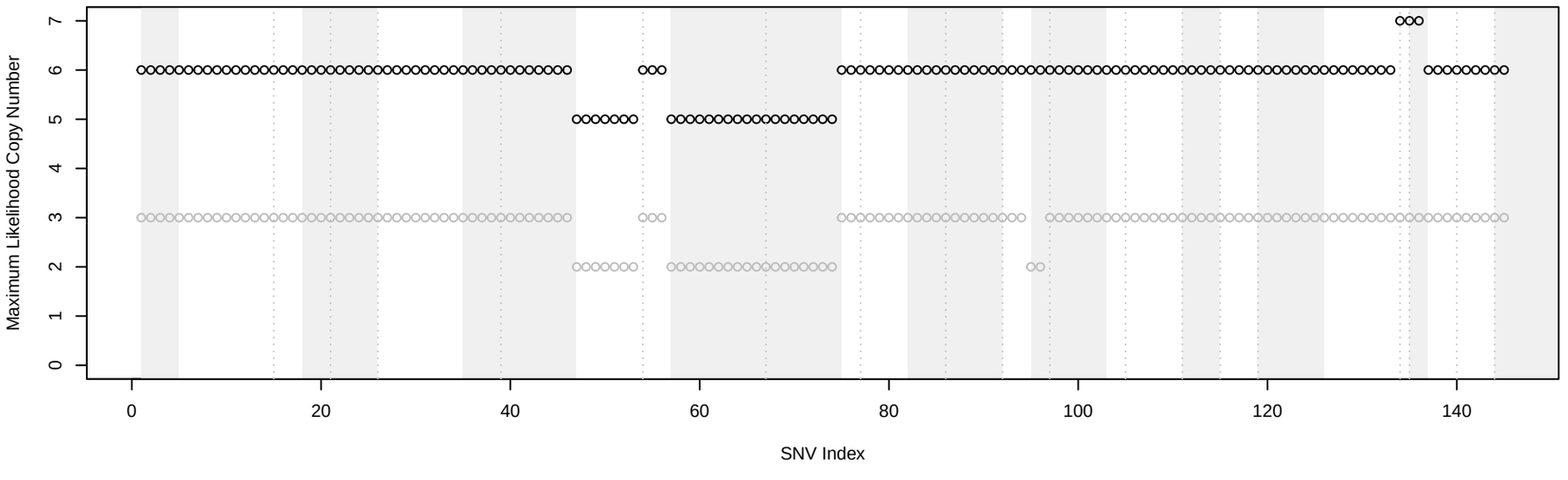

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
7m1

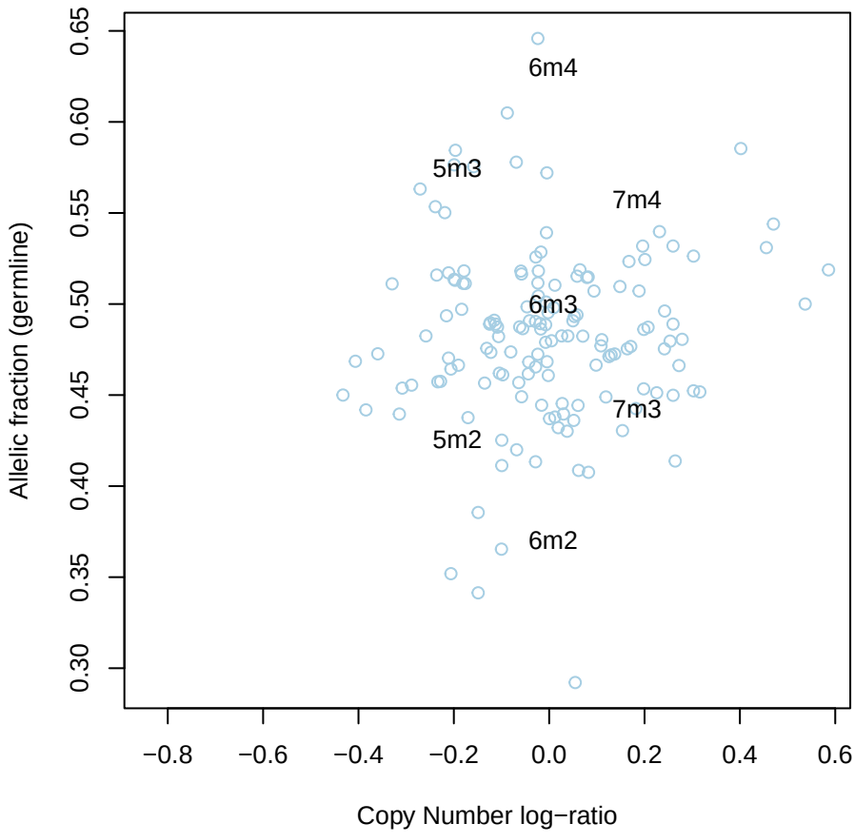

Frequency
Cellular fraction

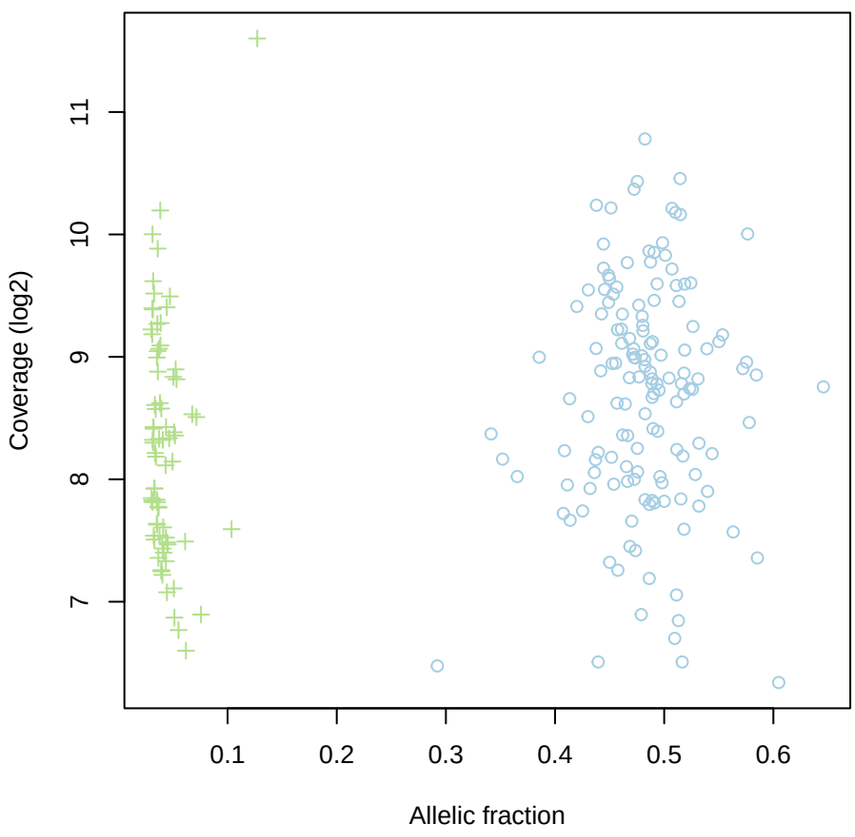

Purity: 0.54 Tumor ploidy: 5.956
1
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

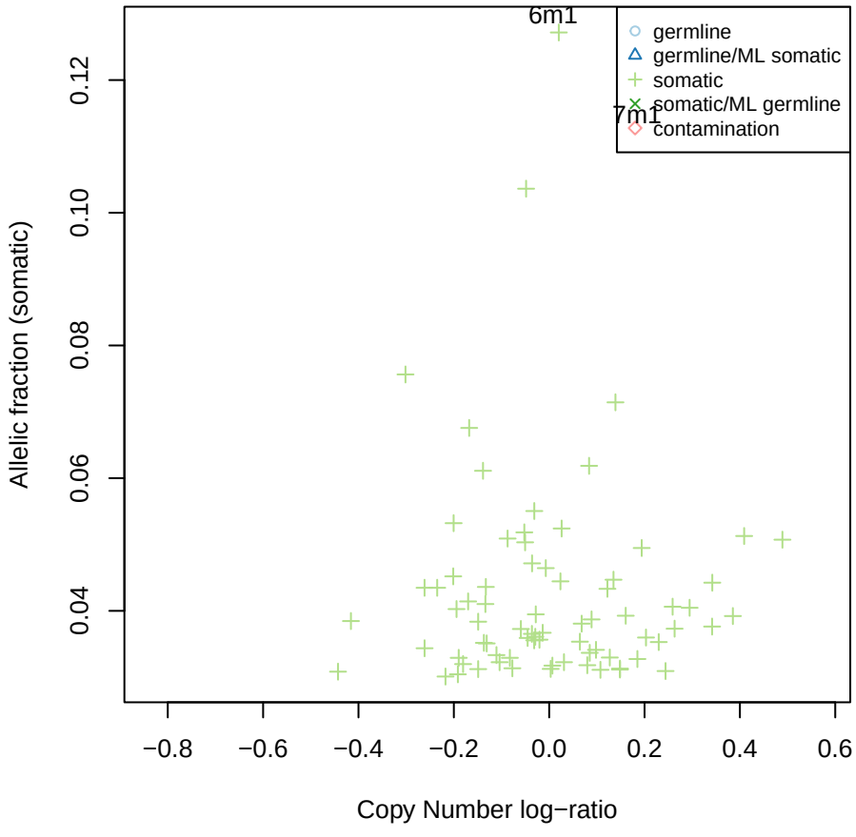

Purity: 0.54 Tumor ploidy: 5.956 SNV log−likelihood: −73.37 GoF: 90.1% Mean coverage: 585;464
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 18 19
B−Allele Frequency
0.30 0.40 0.50 0.60
0 20 40 60 80 100 120 140
SNV Index

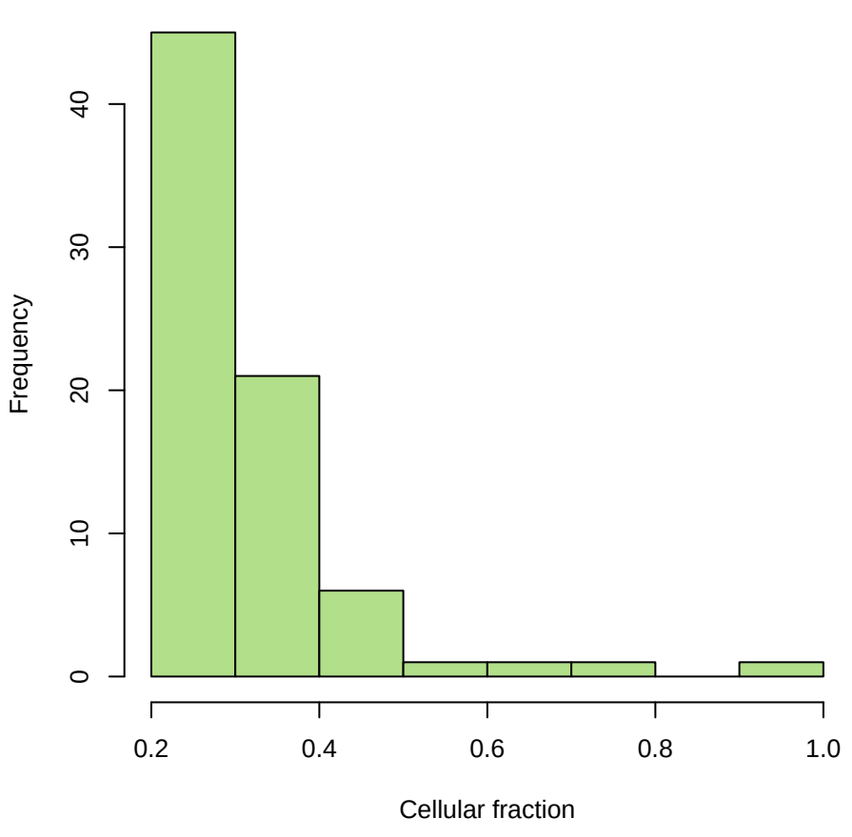

SCNA−fit log−likelihood: −5763.34
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

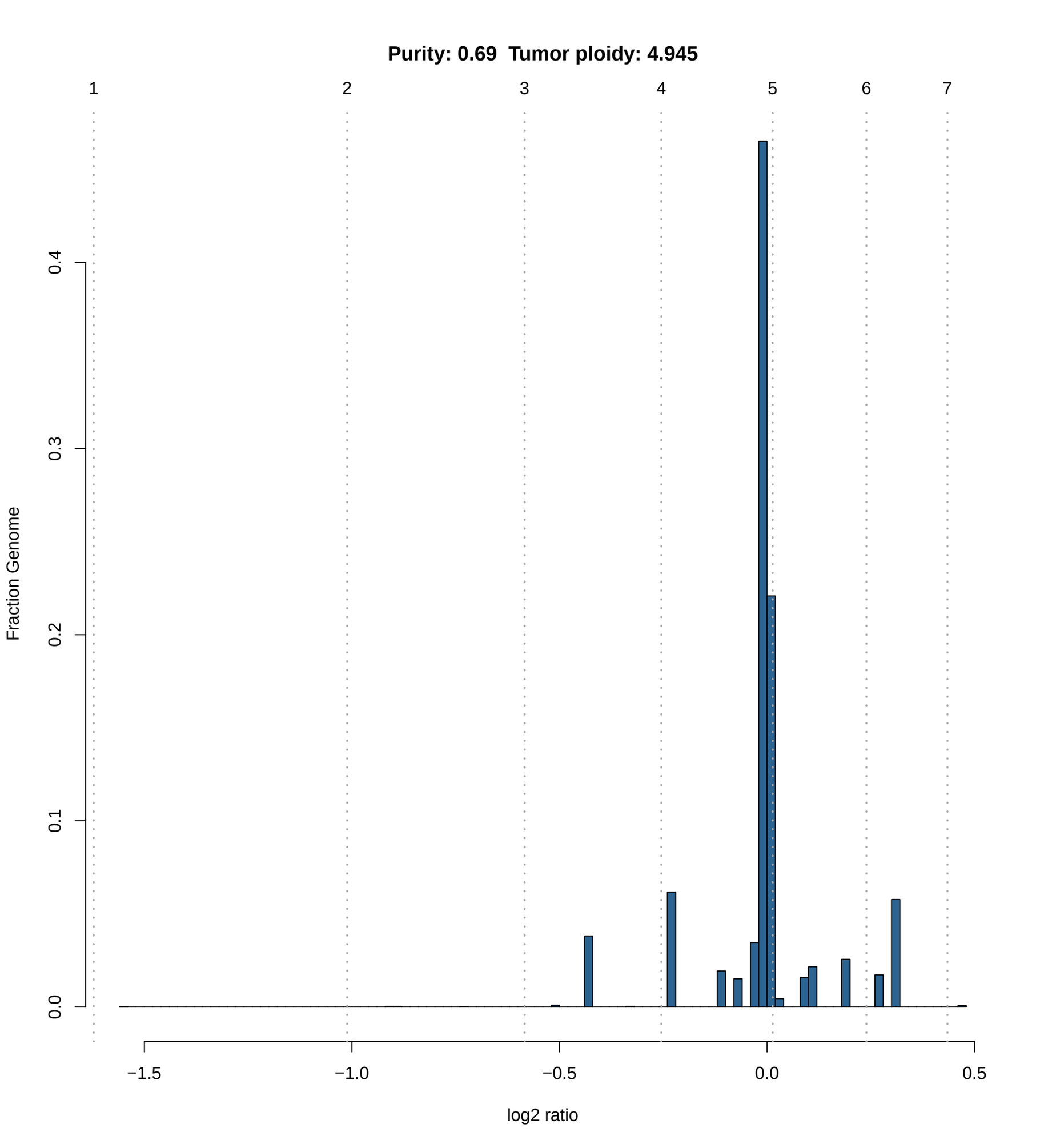

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

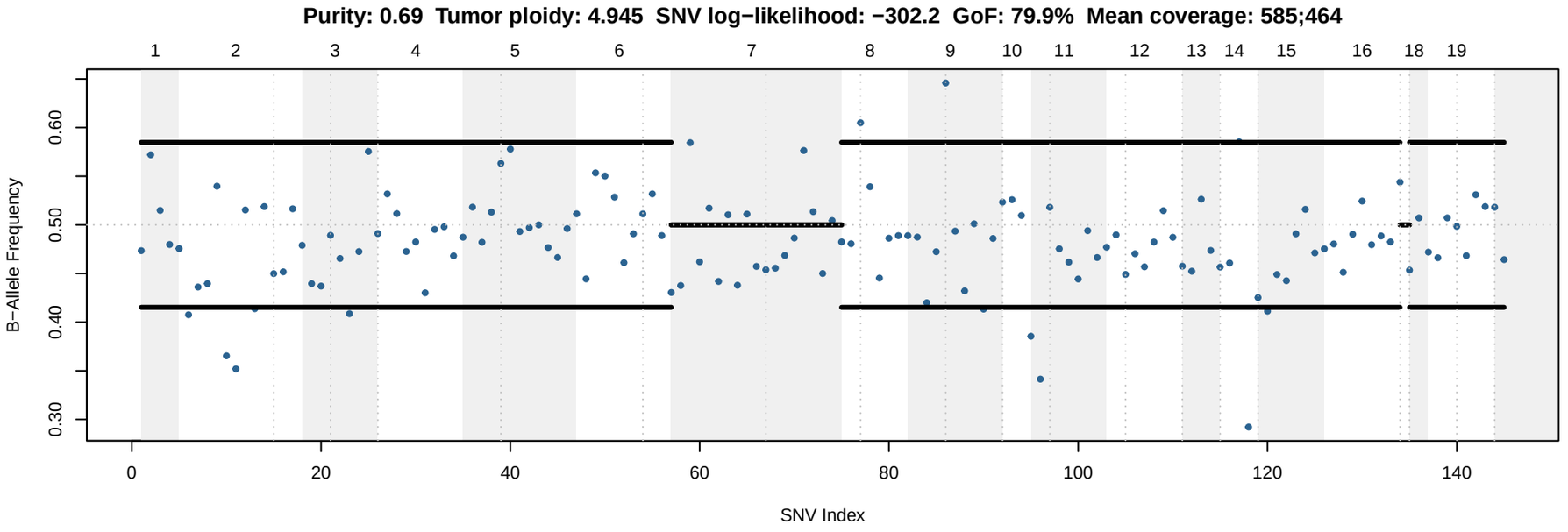

Allelic fraction (germline)
Copy Number log−ratio
6m4
5m3
7m4
6m3
7m3
5m2
6m2

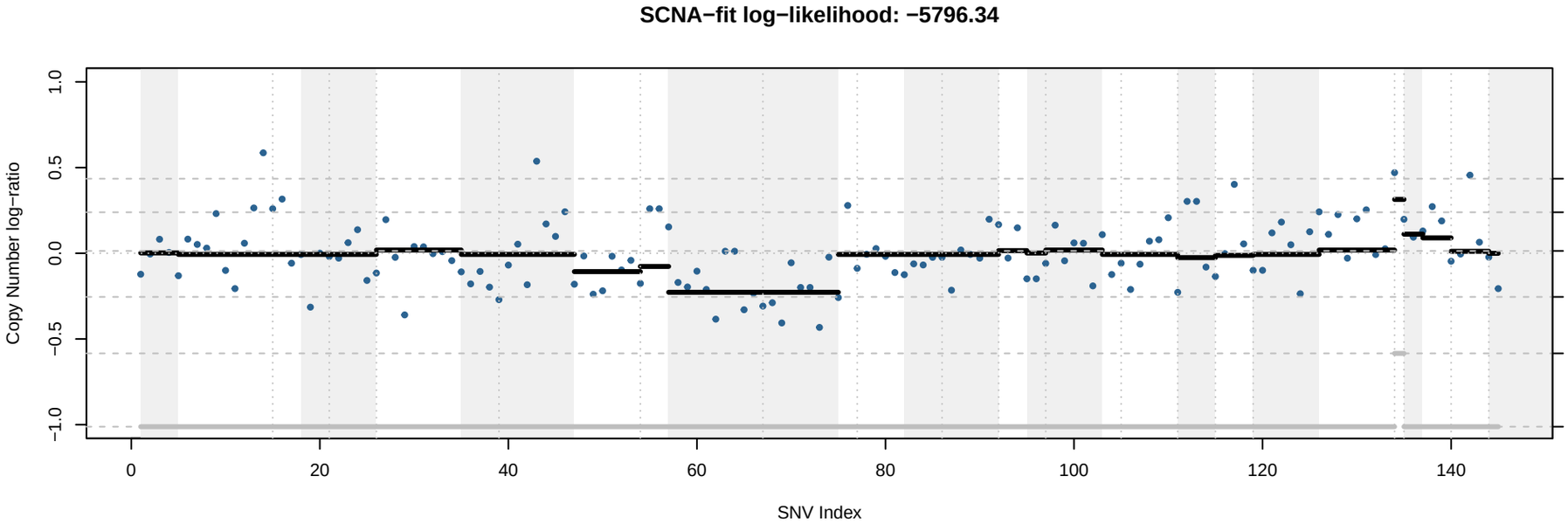

Coverage (log2)
Allelic fraction

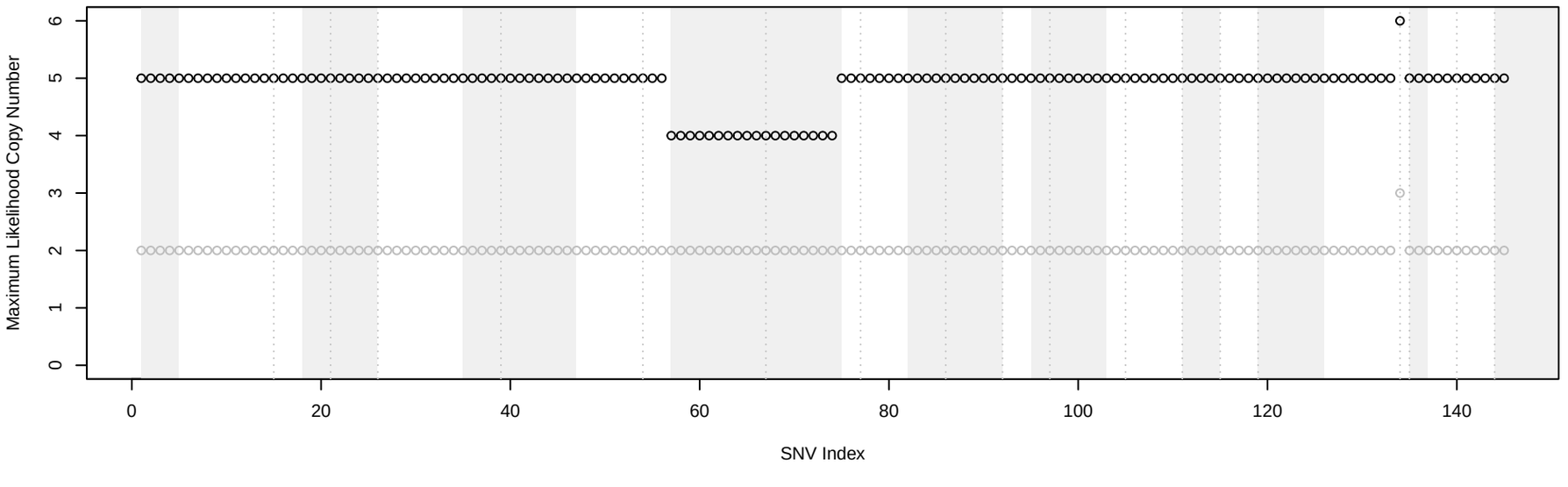

Allelic fraction (somatic)
Copy Number log−ratio
6m1
7m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

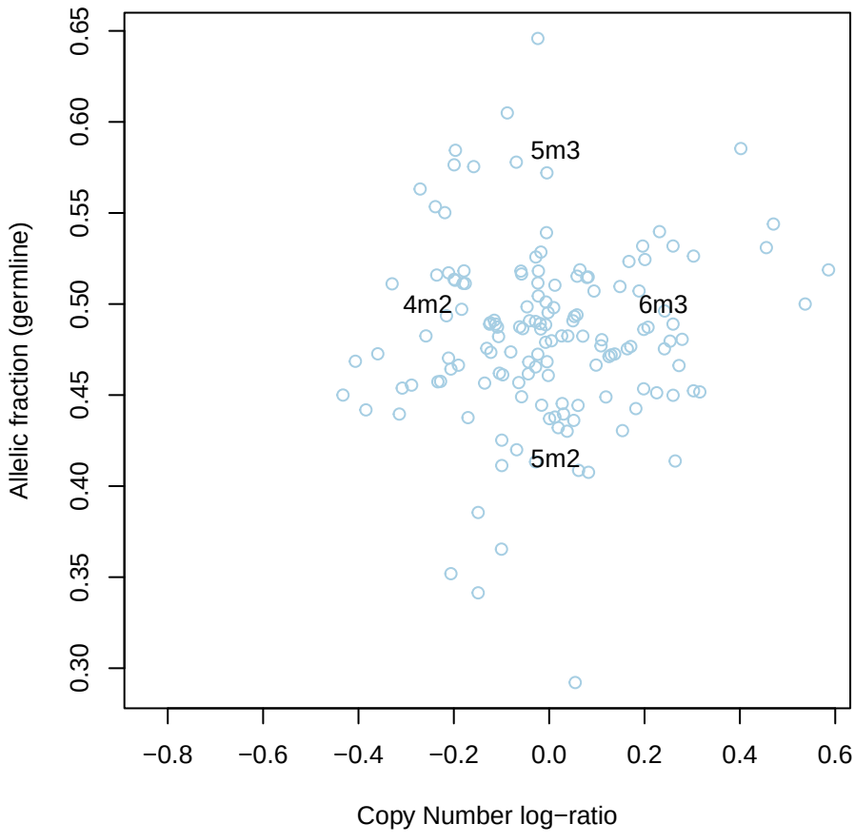

Frequency
Cellular fraction

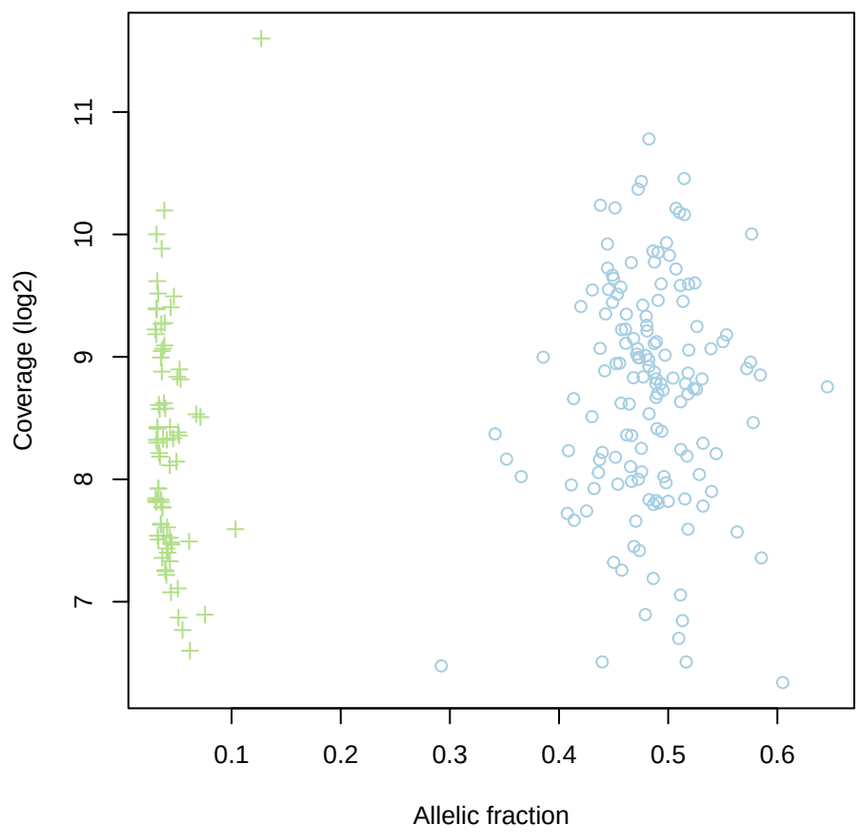

Purity: 0.69 Tumor ploidy: 4.945
1
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

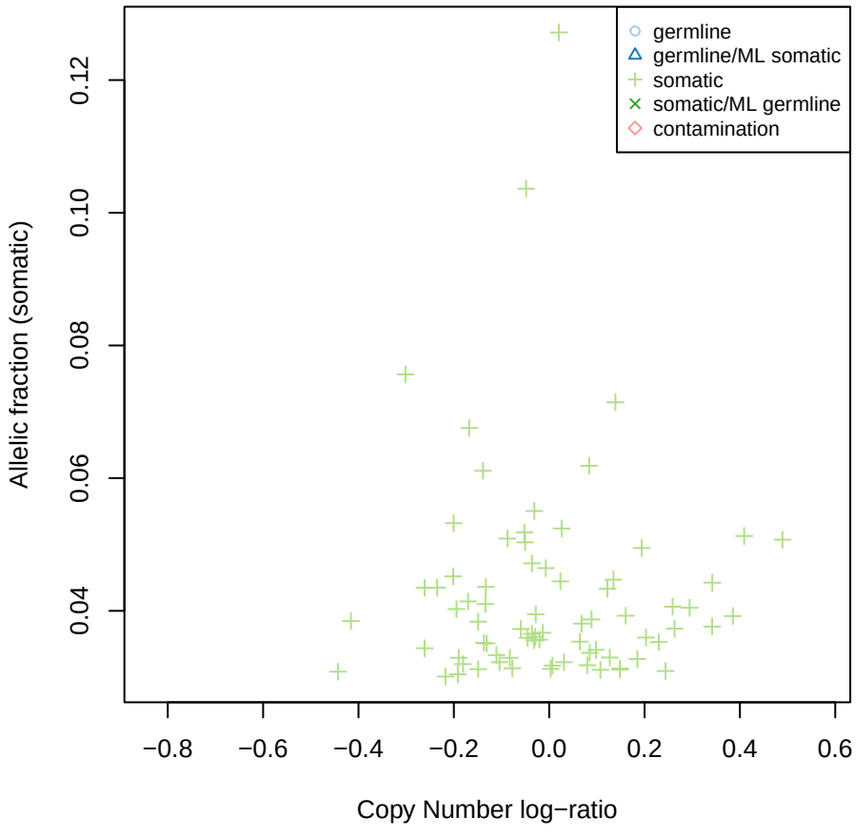

Purity: 0.69 Tumor ploidy: 4.945 SNV log−likelihood: −302.2 GoF: 79.9% Mean coverage: 585;464
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 18 19
B−Allele Frequency
0.30 0.40 0.50 0.60
0 20 40 60 80 100 120 140
SNV Index

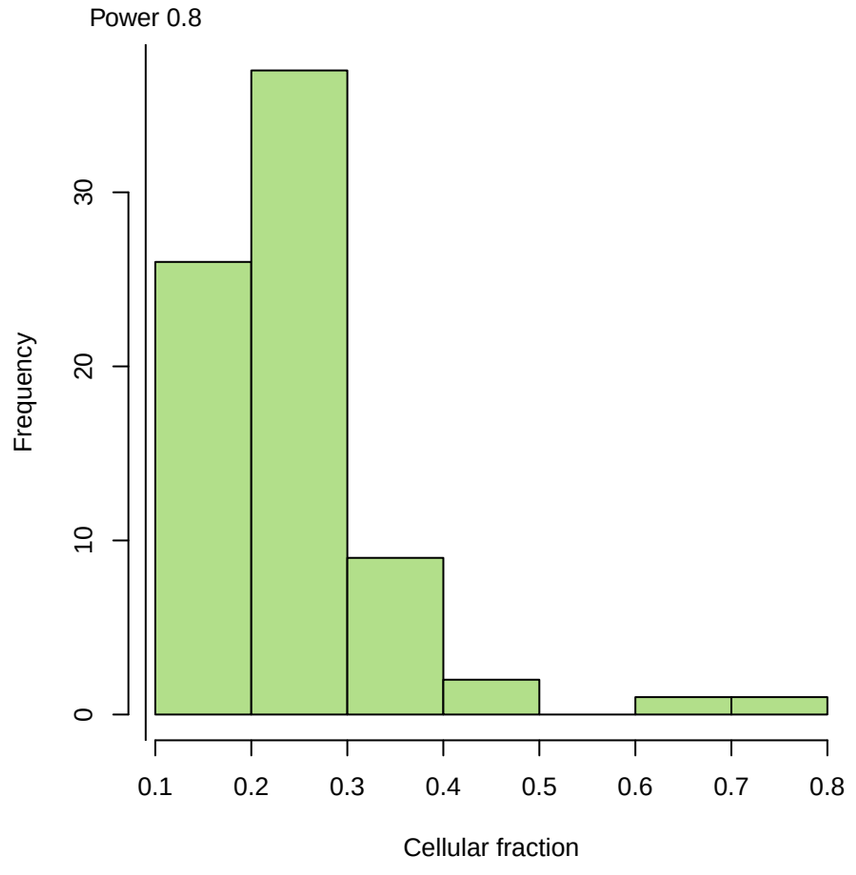

SCNA−fit log−likelihood: −5796.34
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

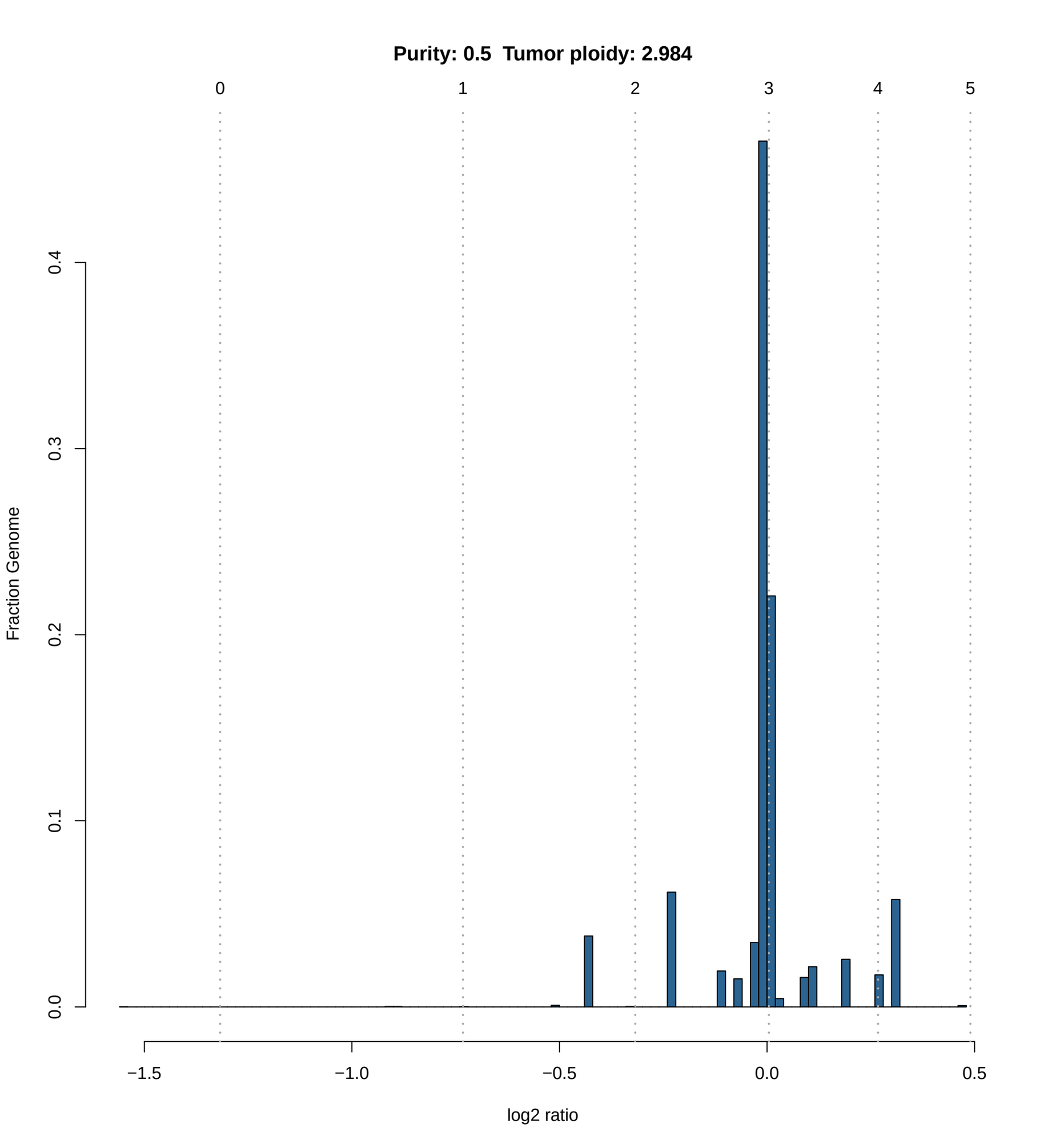

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

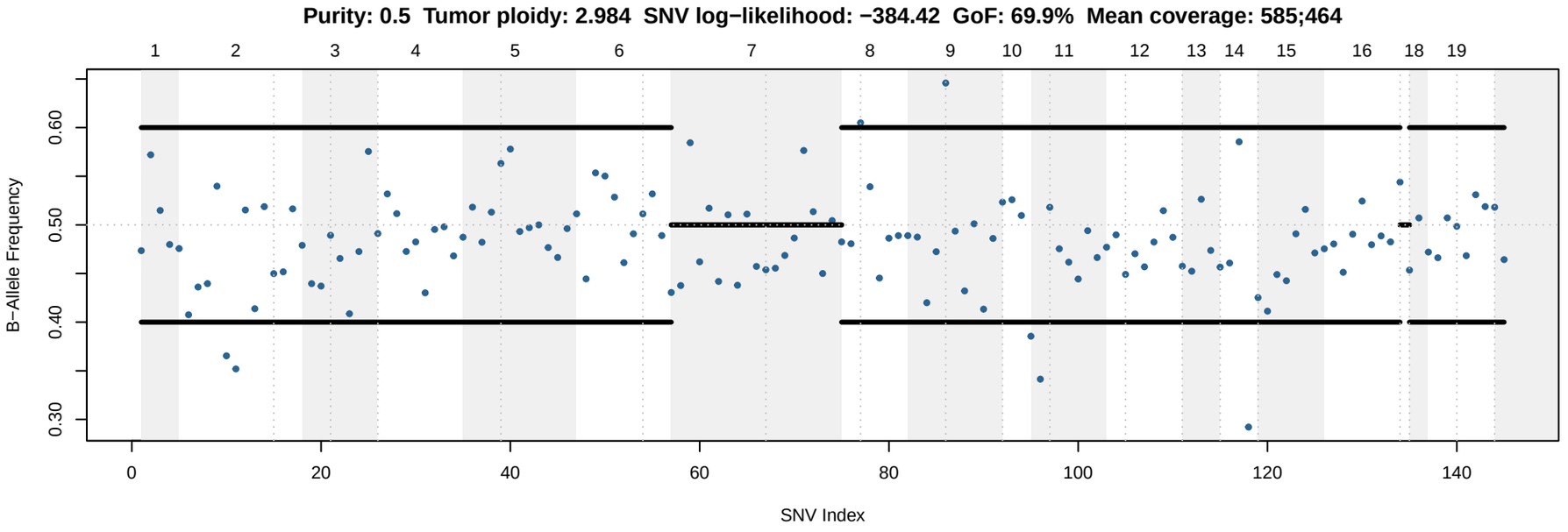

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
0.65
5m3
4m2
6m3
5m2
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

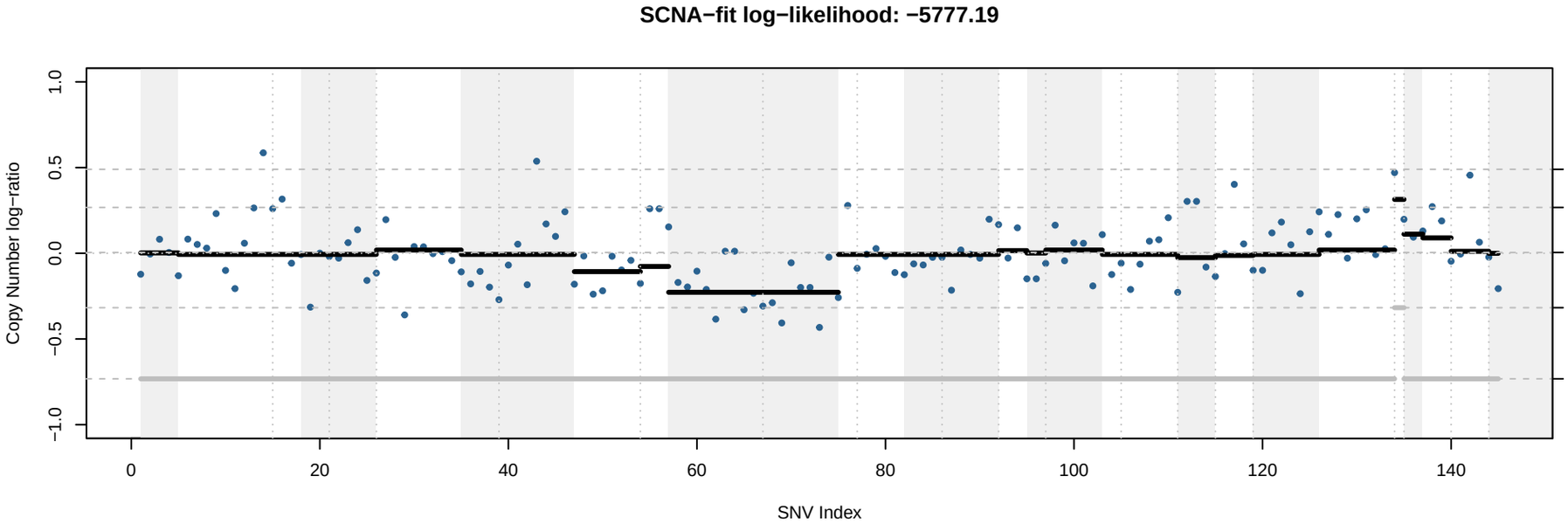

Coverage (log2)
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

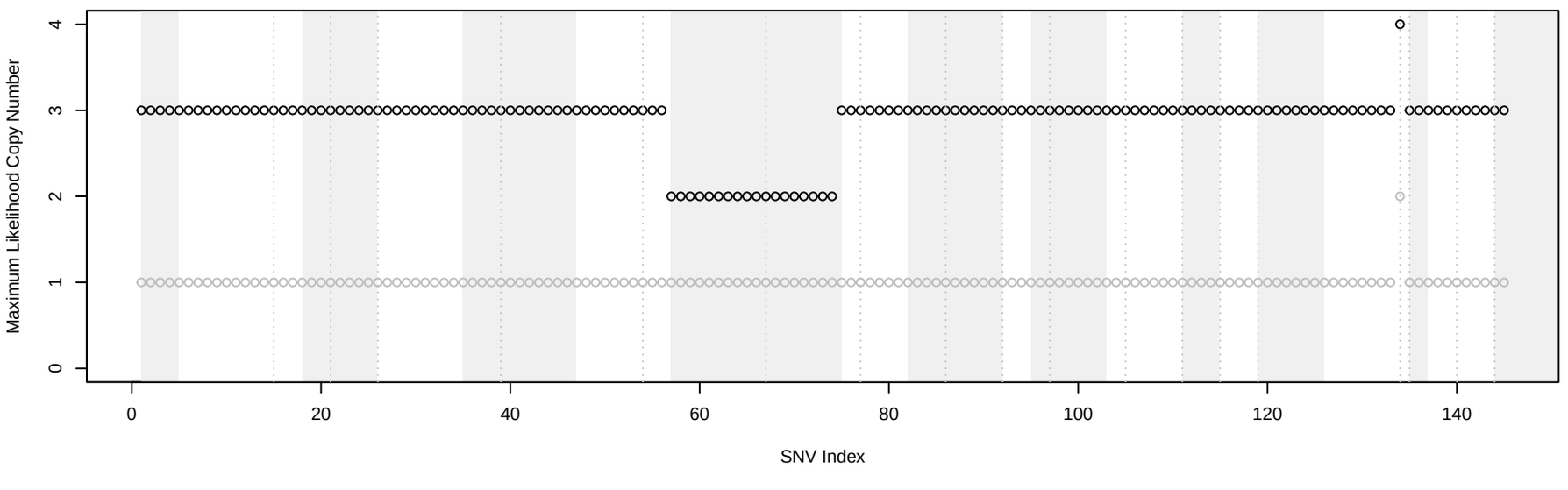

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

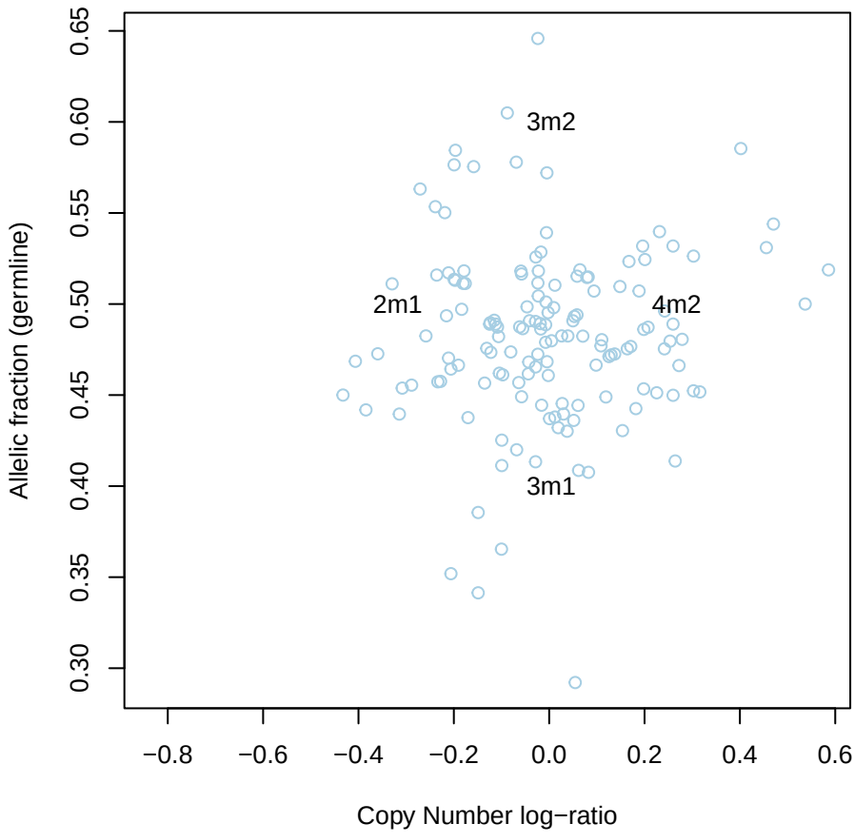

Power 0.8
Frequency
0
10
20
30
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
Cellular fraction

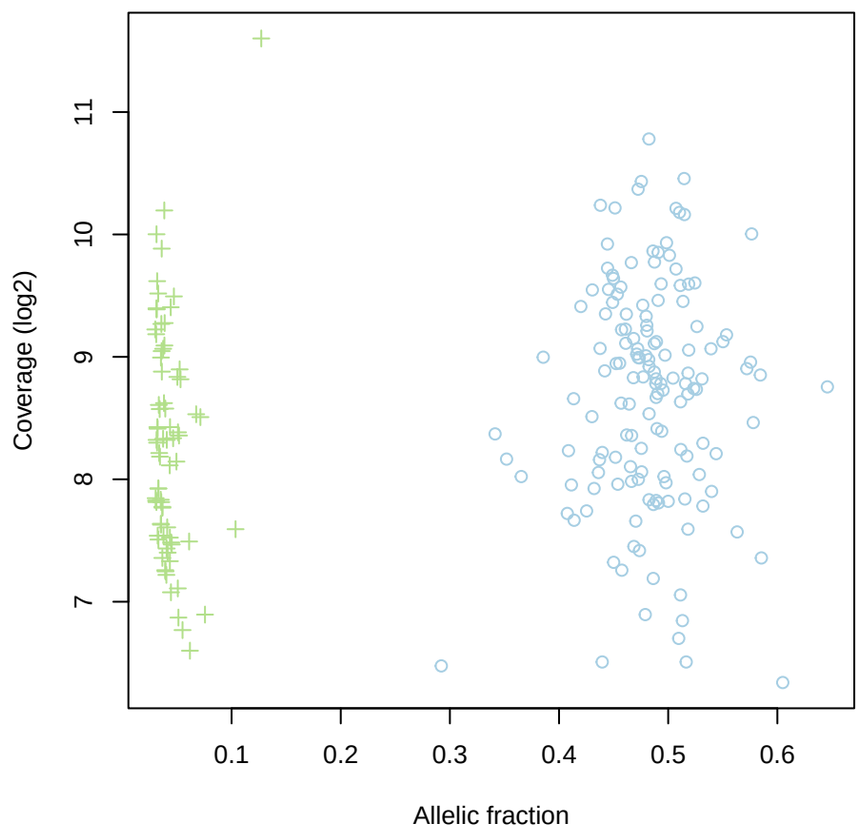

Purity: 0.5 Tumor ploidy: 2.984
0
1
2
3
4
5
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

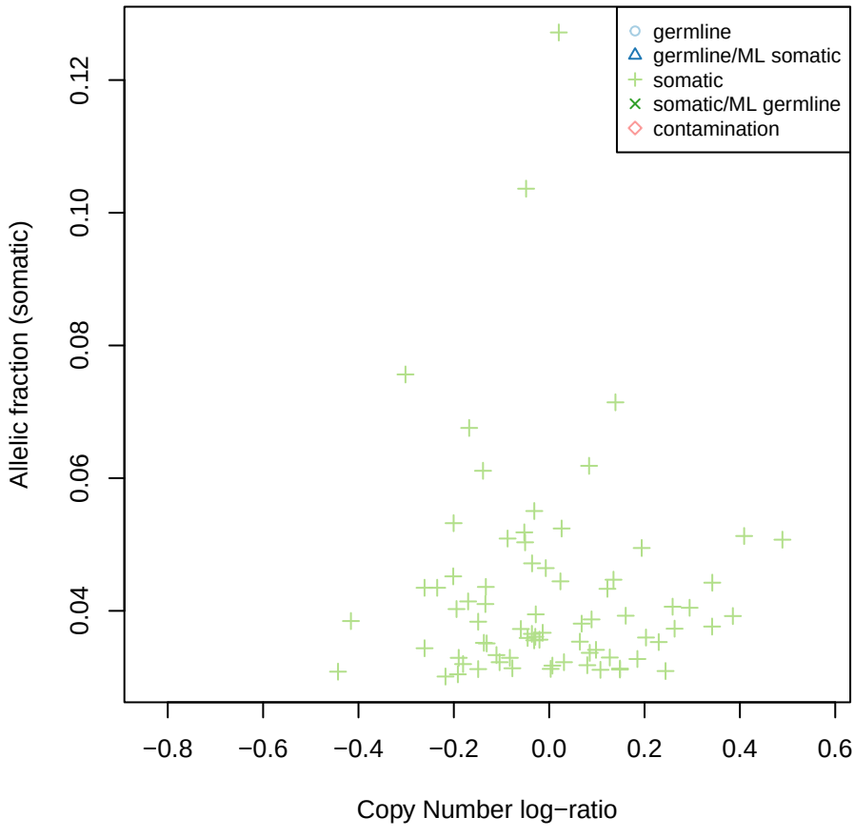

Purity: 0.5 Tumor ploidy: 2.984 SNV log−likelihood: −384.42 GoF: 69.9% Mean coverage: 585;464
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 18 19
B−Allele Frequency
0.30 0.40 0.50 0.60
0 20 40 60 80 100 120 140
SNV Index

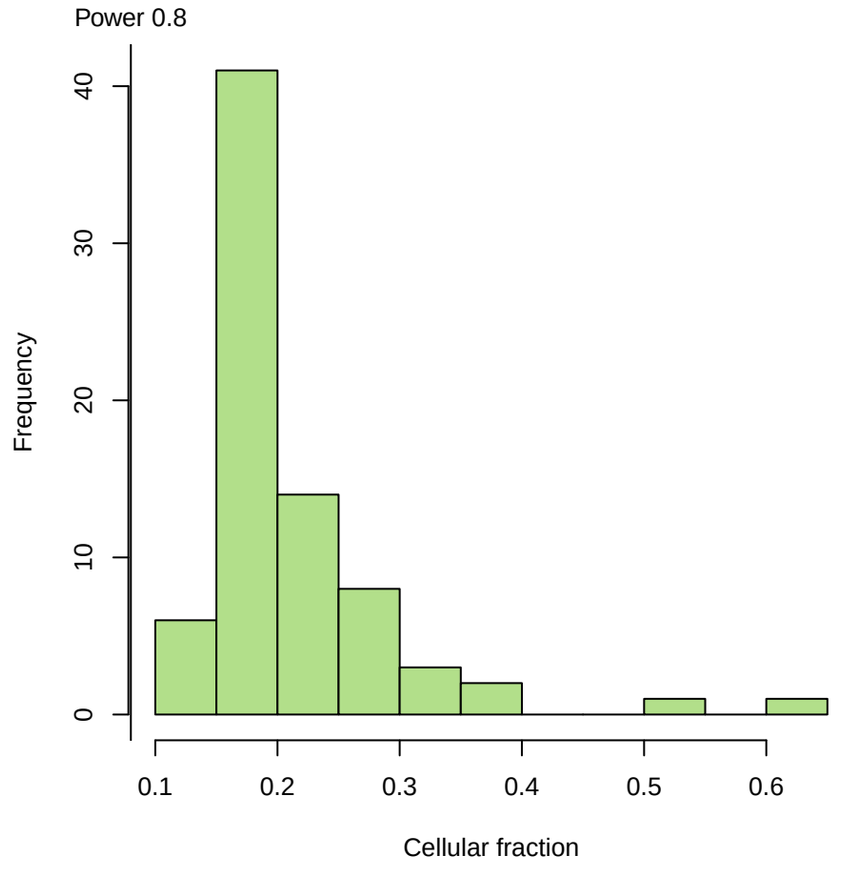

SCNA−fit log−likelihood: −5777.19
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

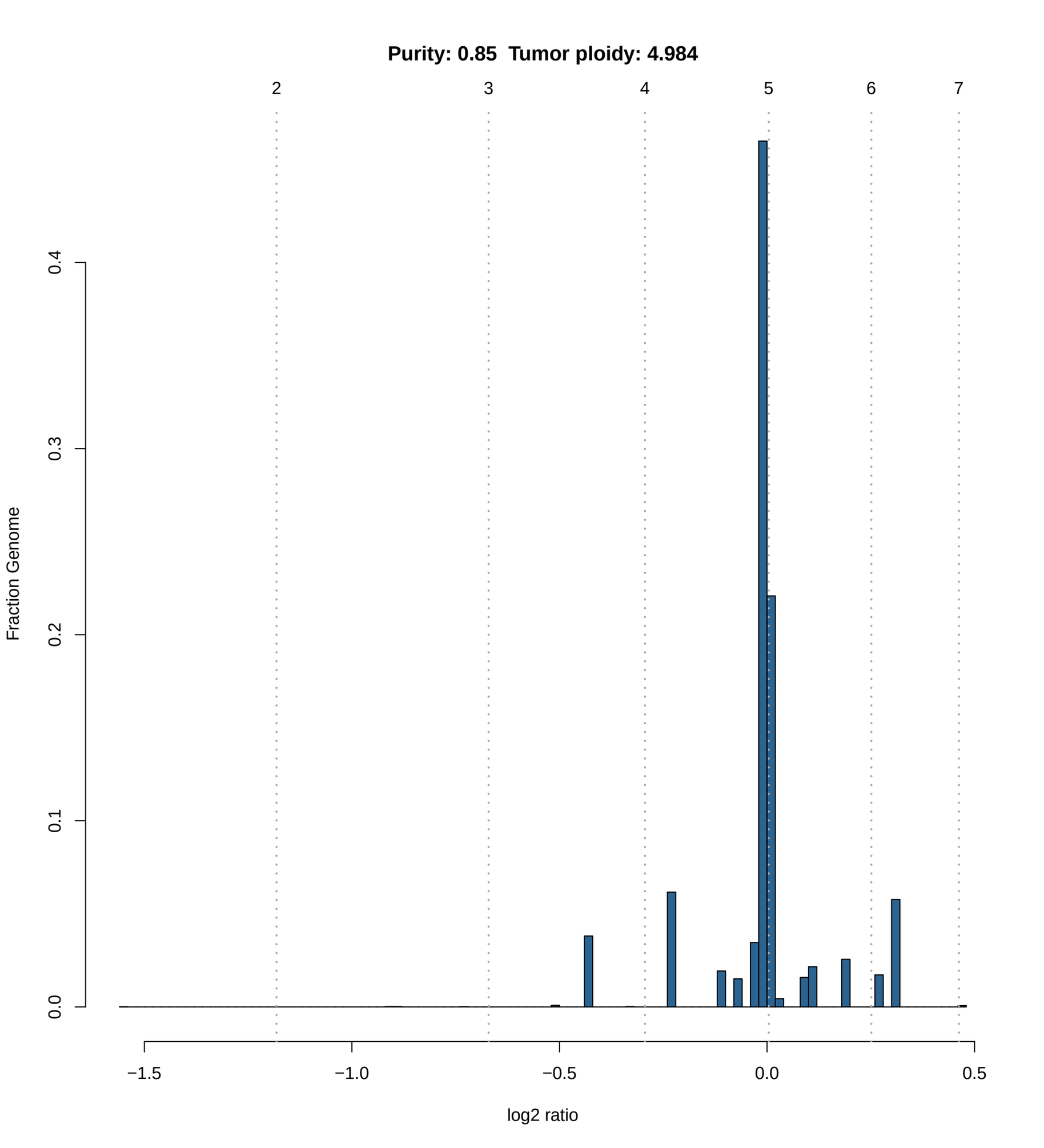

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120 140
SNV Index

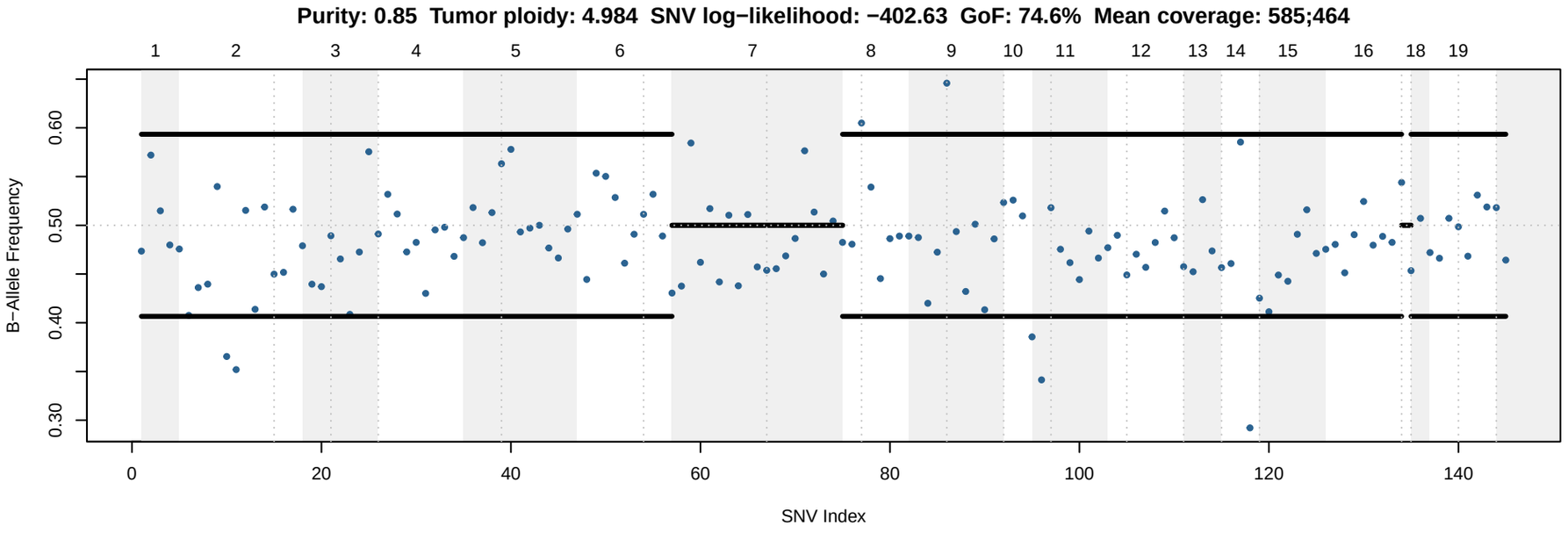

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
0.65
3m2
2m1
4m2
3m1
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

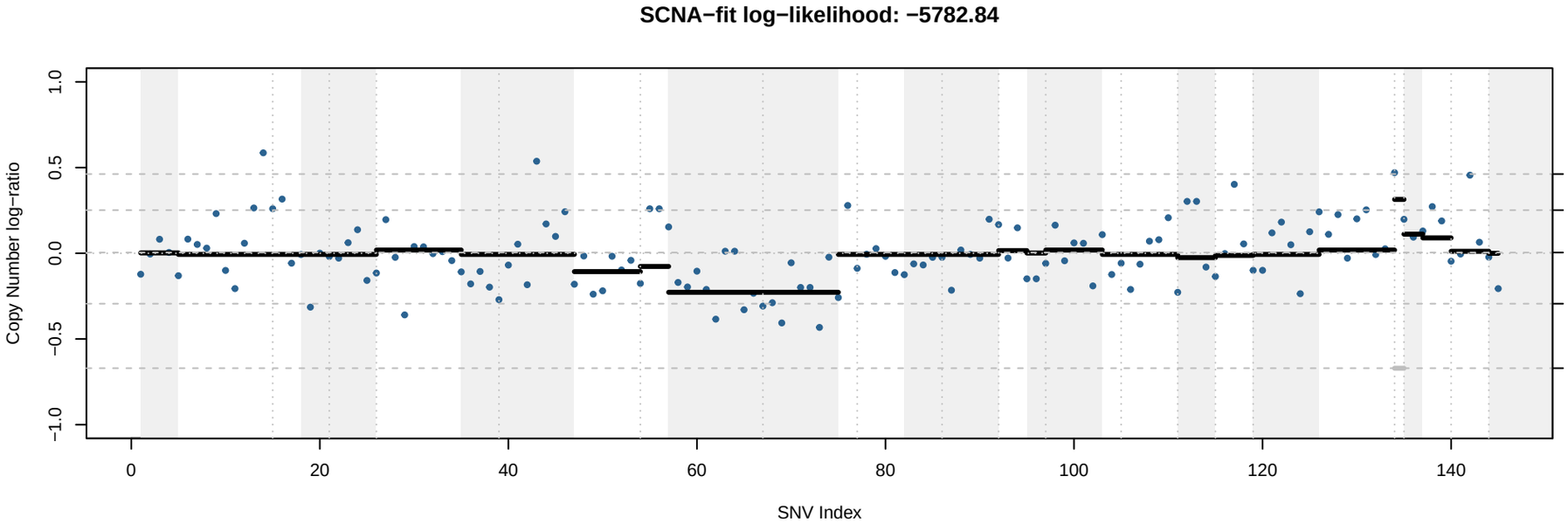

Coverage (log2)
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

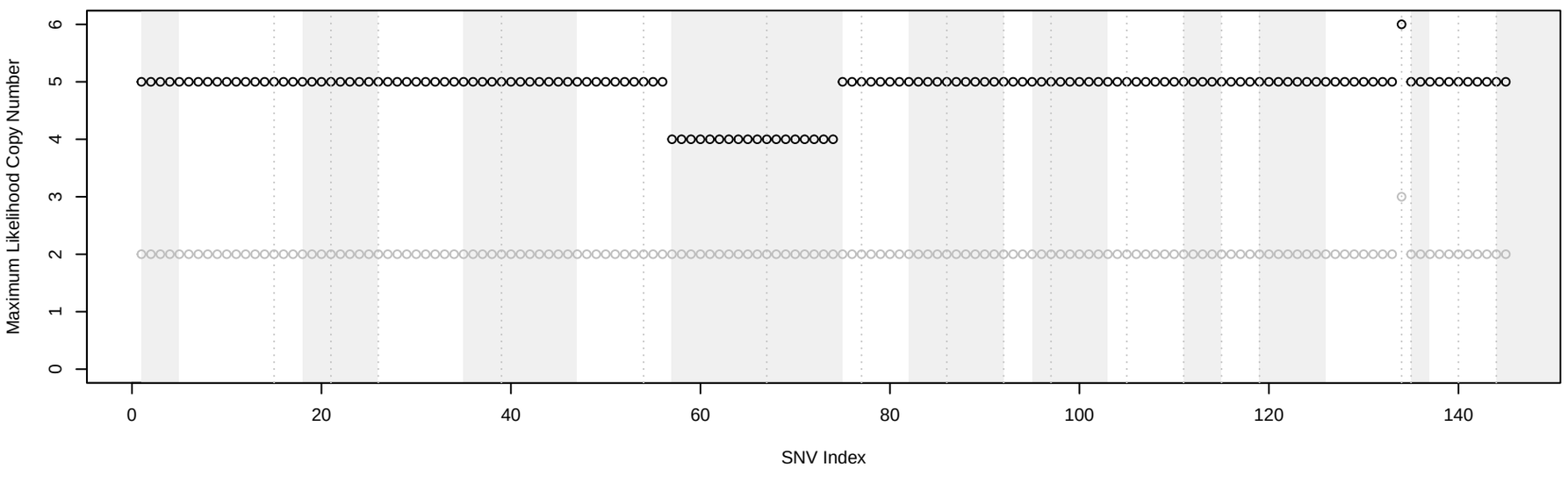

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

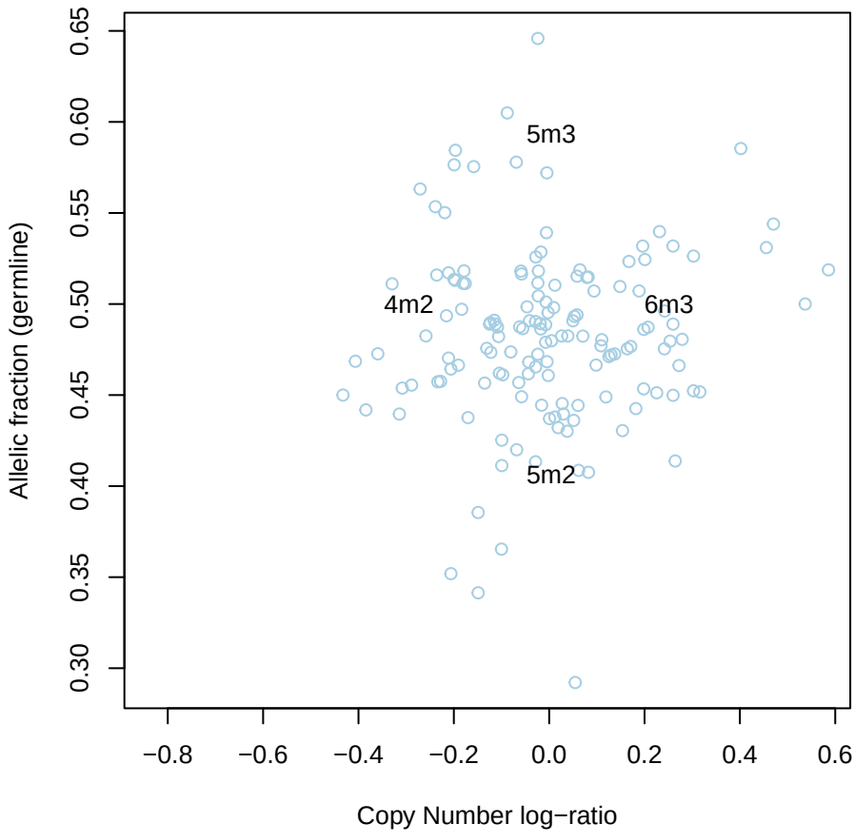

Power 0.8
Frequency
0
10
20
30
40
0.1
0.2
0.3
0.4
0.5
0.6
Cellular fraction

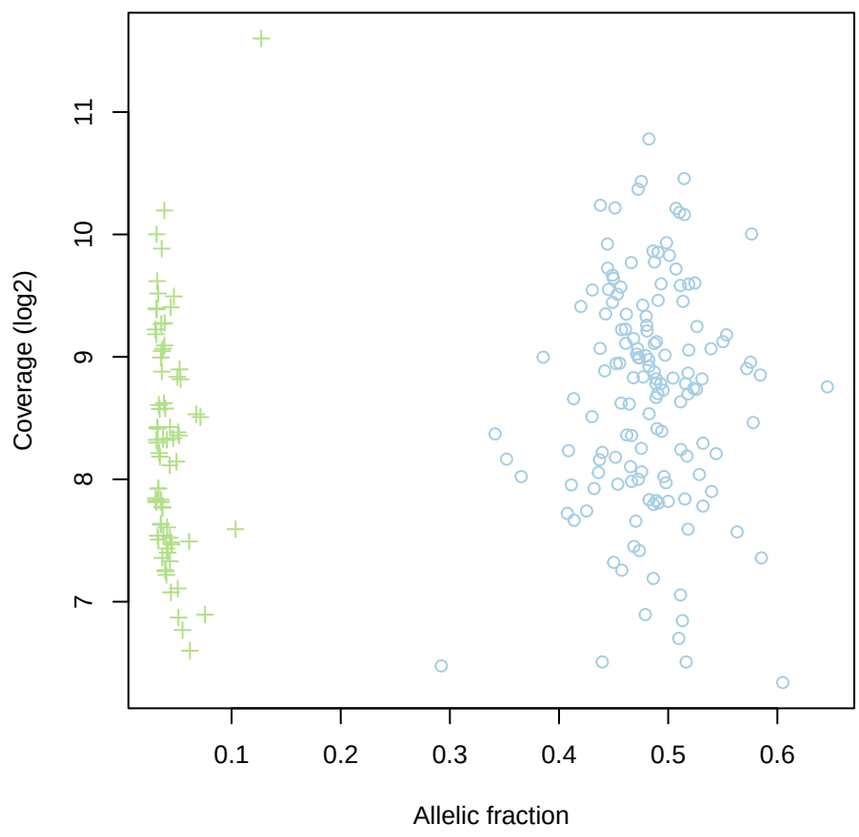

Purity: 0.85 Tumor ploidy: 4.984
2
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

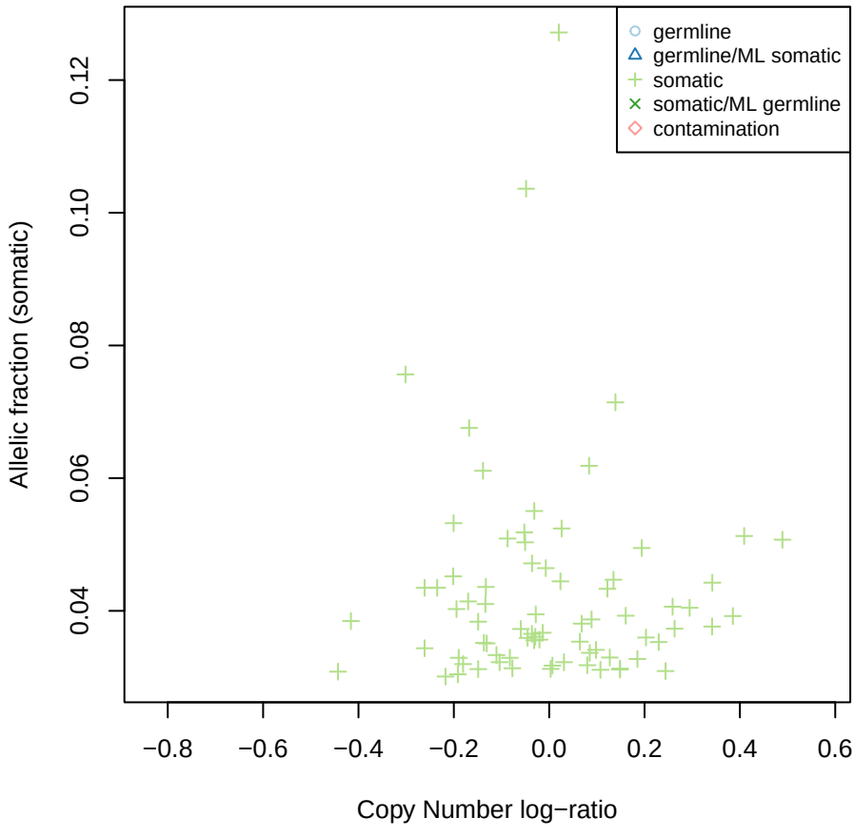

Purity: 0.85 Tumor ploidy: 4.984 SNV log−likelihood: −402.63 GoF: 74.6% Mean coverage: 585;464
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 18 19
B−Allele Frequency
0.30 0.40 0.50 0.60
0 20 40 60 80 100 120 140
SNV Index

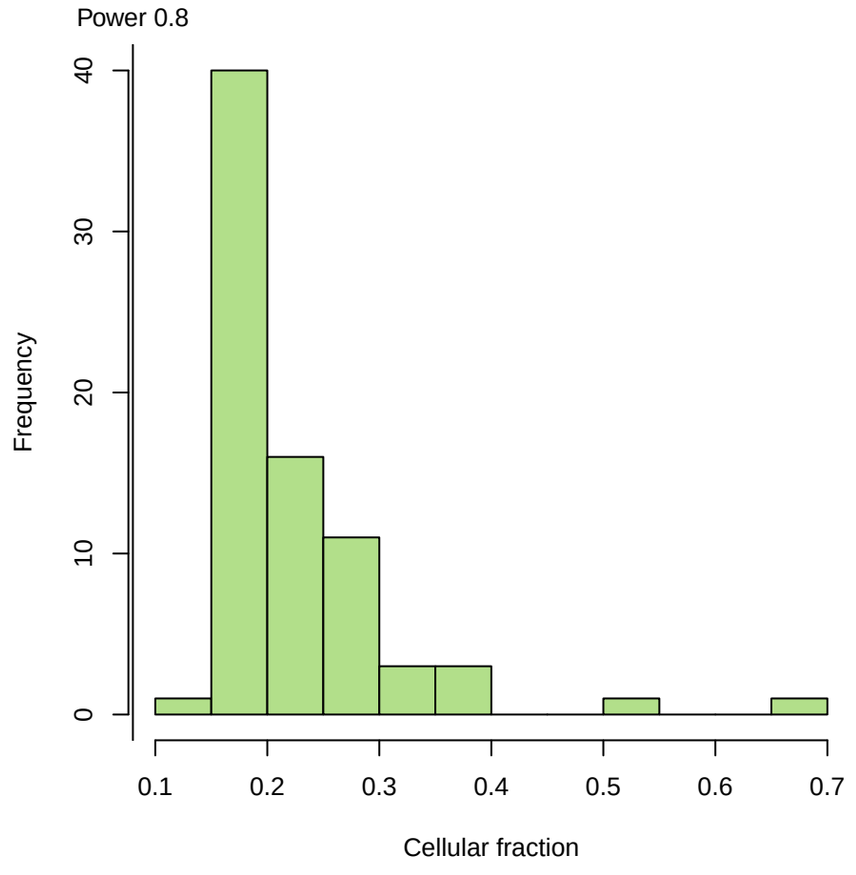

SCNA−fit log−likelihood: −5782.84
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

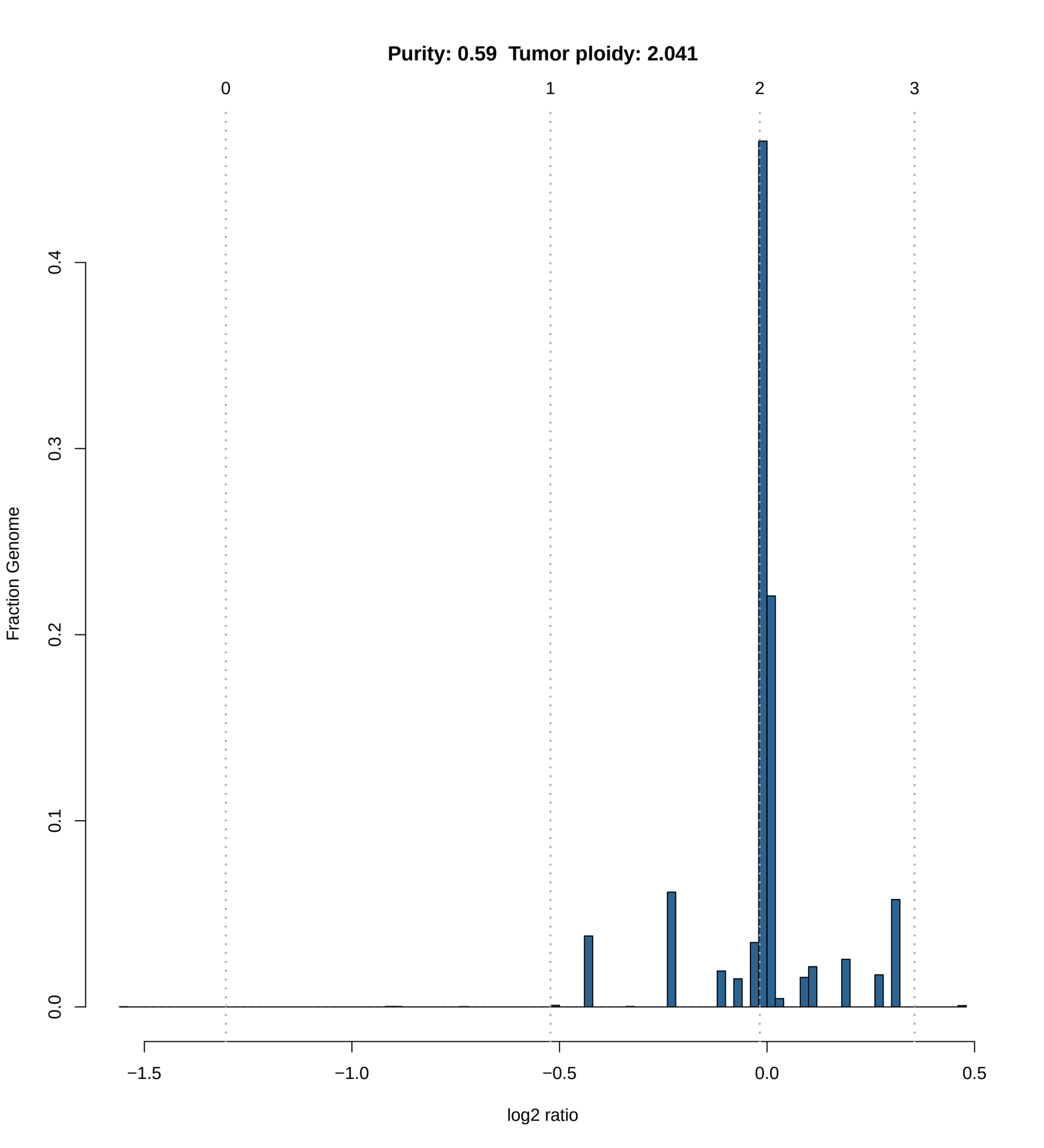

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

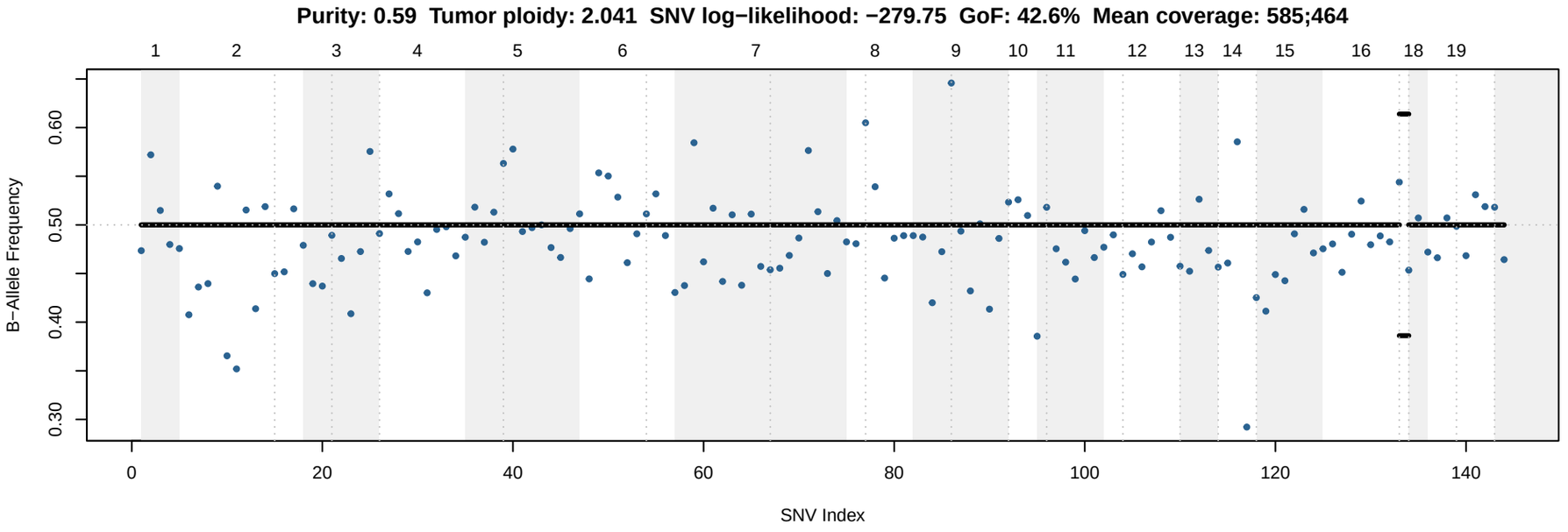

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
0.65
5m3
4m2
6m3
5m2
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

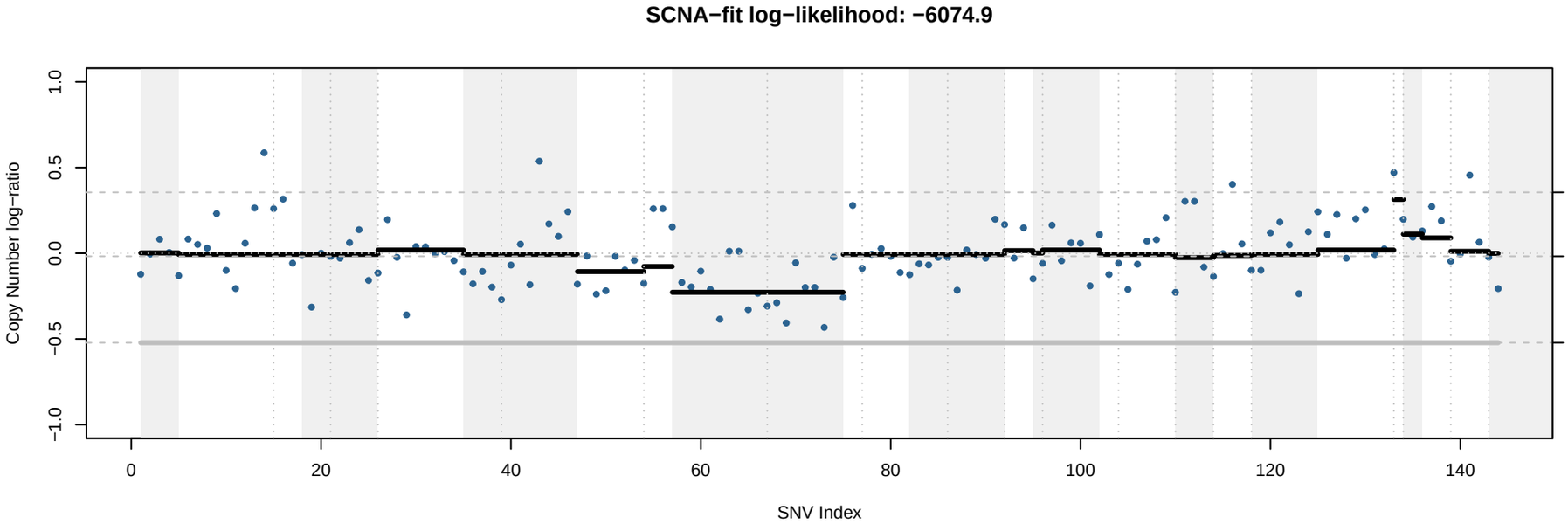

Coverage (log2)
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

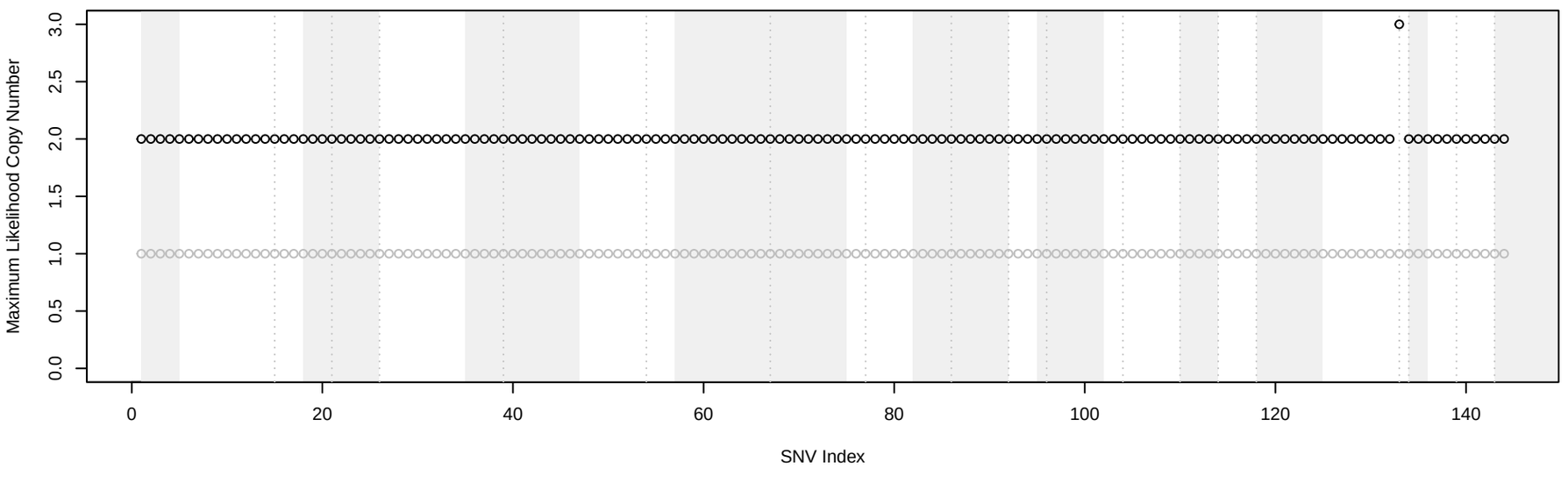

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

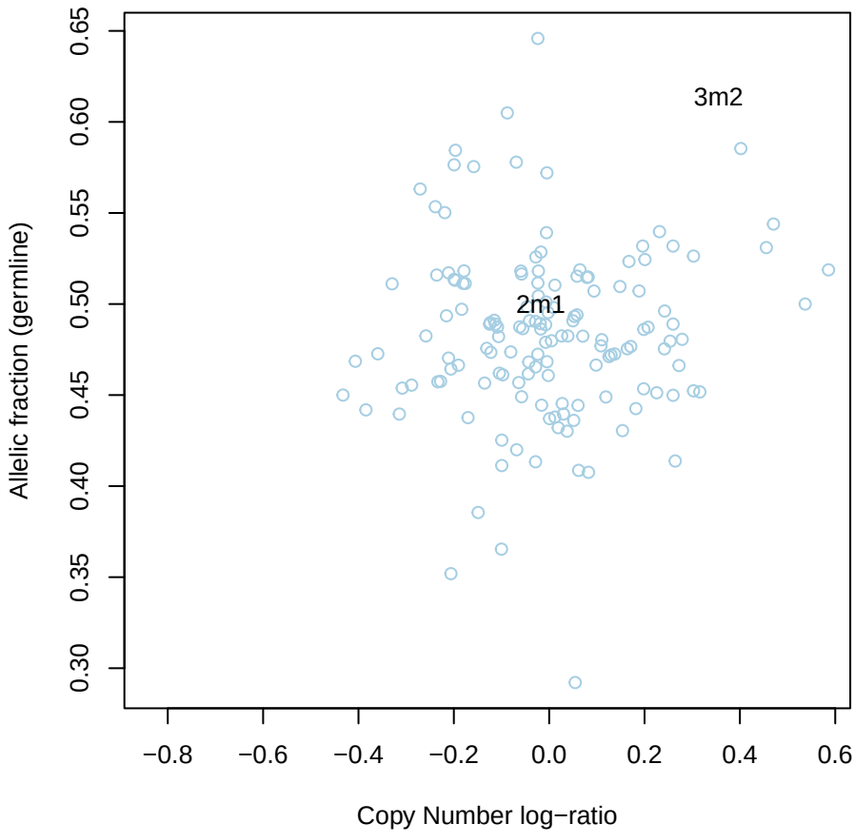

Power 0.8
Frequency
0
10
20
30
40
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Cellular fraction

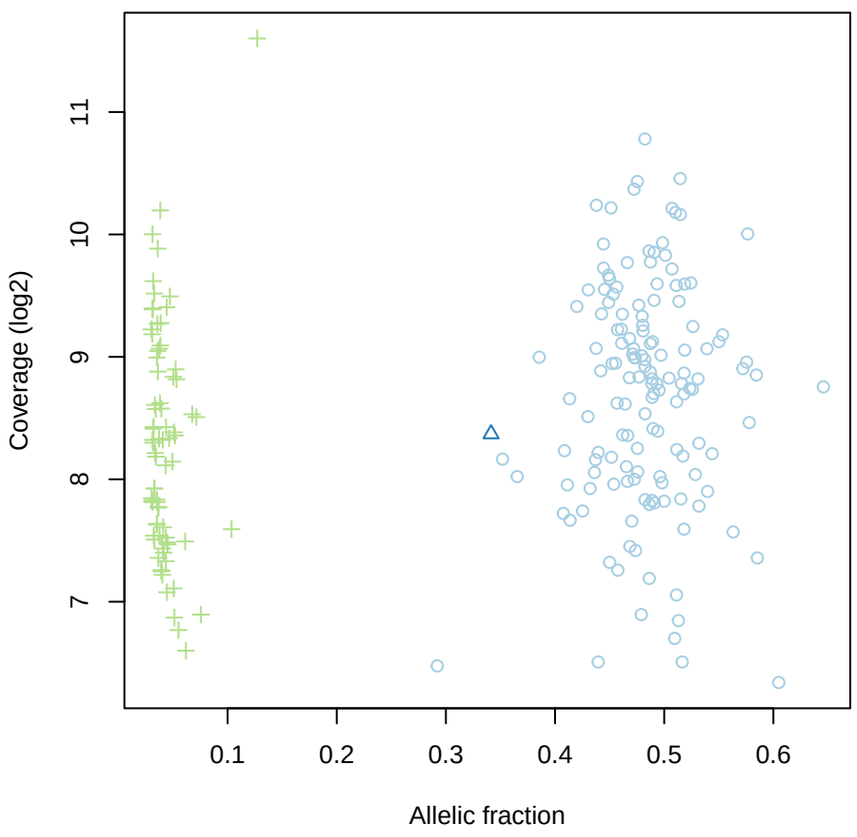

Purity: 0.59 Tumor ploidy: 2.041
0
1
2
3
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

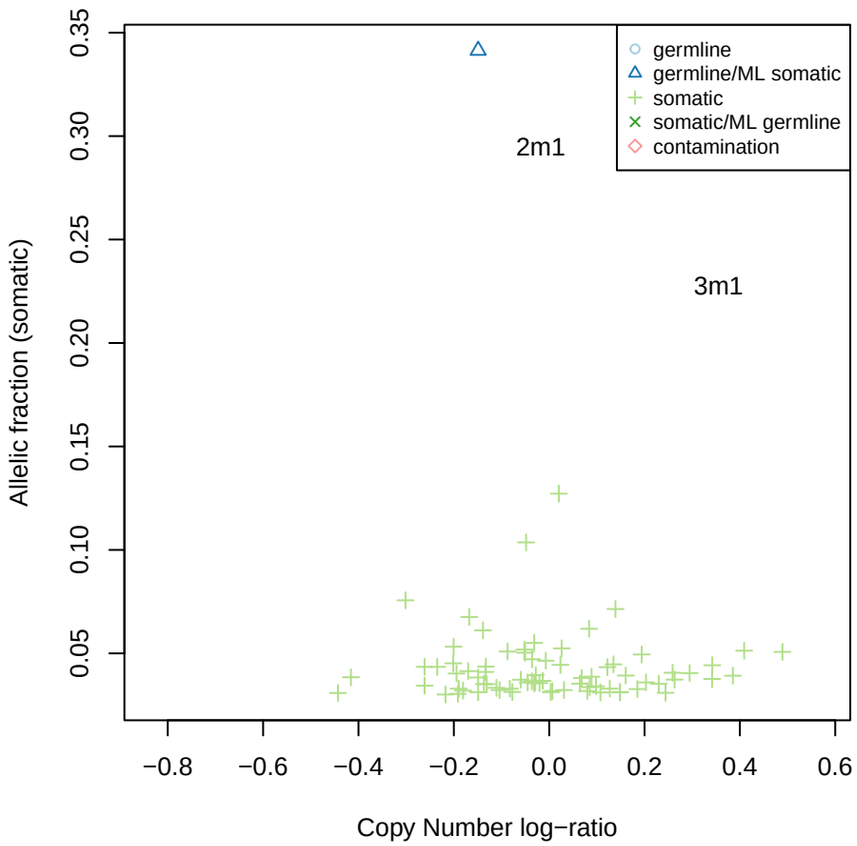

Purity: 0.59 Tumor ploidy: 2.041 SNV log−likelihood: −279.75 GoF: 42.6% Mean coverage: 585;464
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 18 19
B−Allele Frequency
0.30 0.40 0.50 0.60
0 20 40 60 80 100 120 140
SNV Index

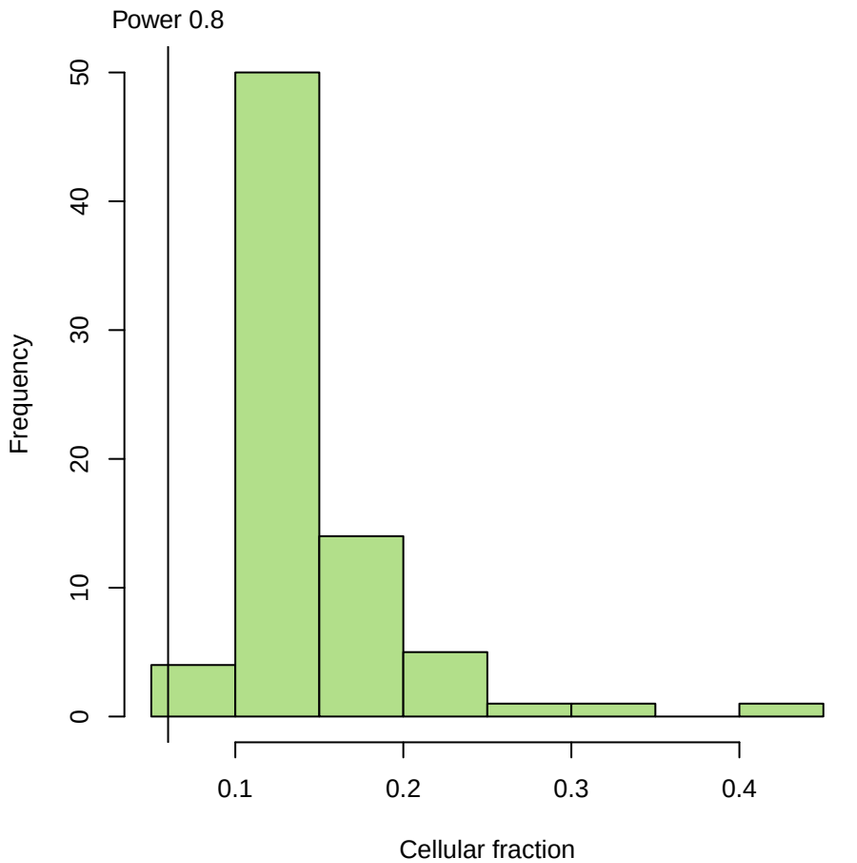

SCNA−fit log−likelihood: −6074.9
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3
0 20 40 60 80 100 120 140
SNV Index

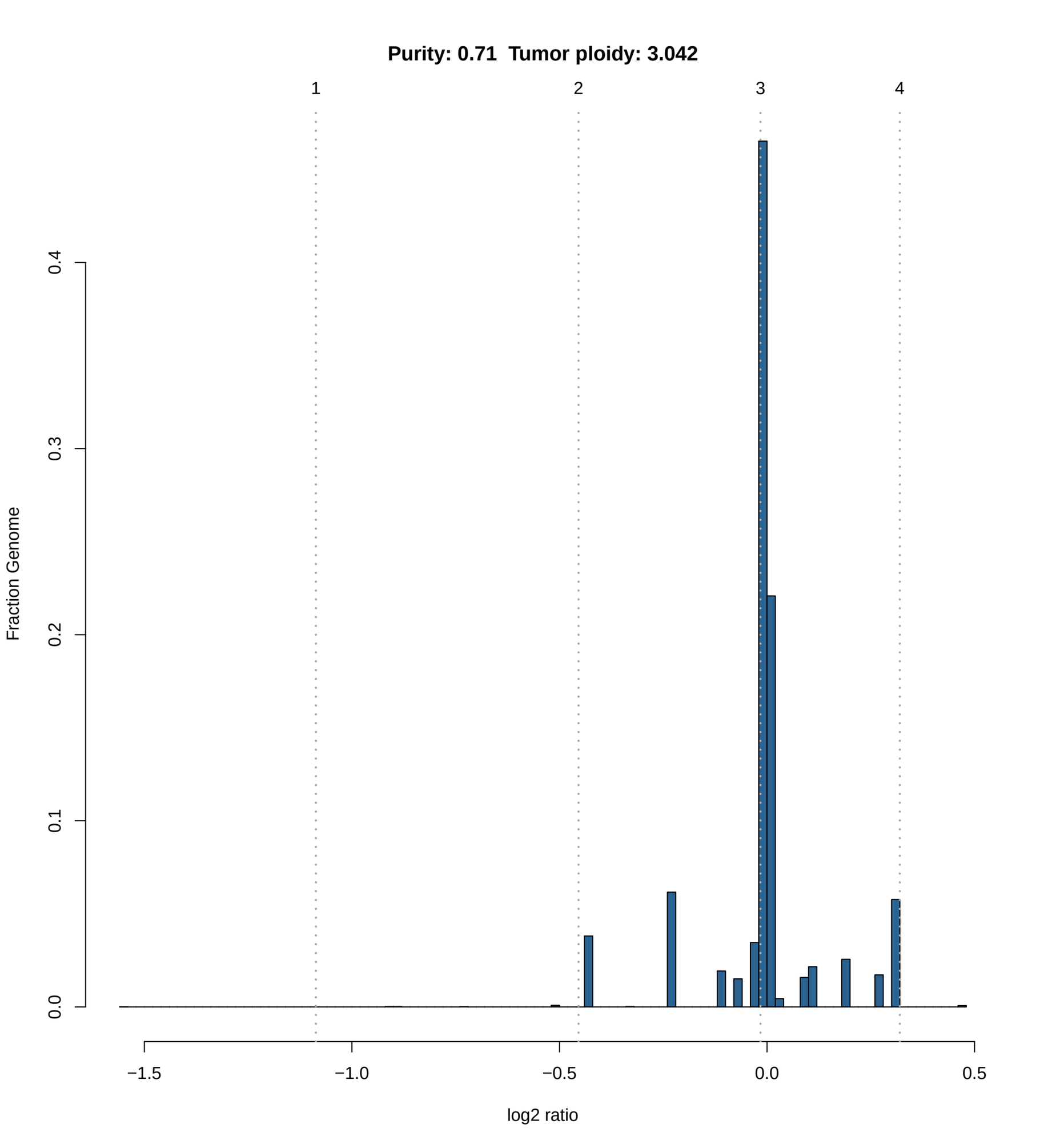

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120 140
SNV Index

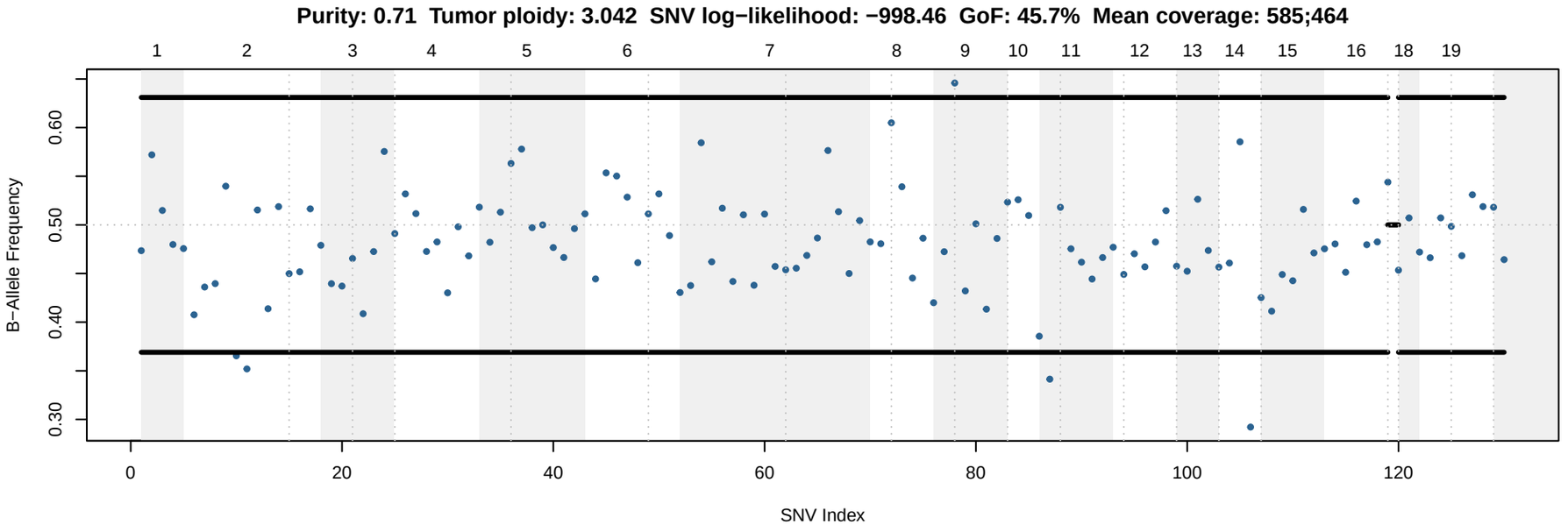

3m2
2m1
Allelic fraction (germline)
Copy Number log−ratio
0.30
0.35
0.40
0.45
0.50
0.55
0.60
0.65
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6

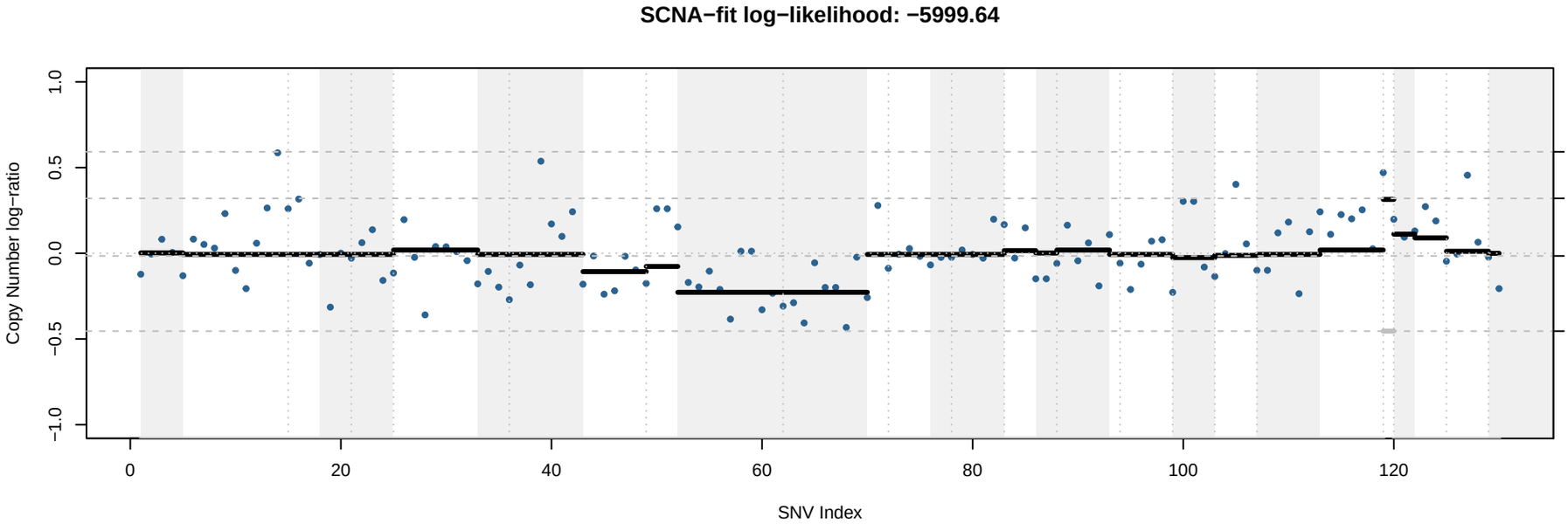

Coverage (log2)
Allelic fraction
7
8
9
10
11
0.1
0.2
0.3
0.4
0.5
0.6

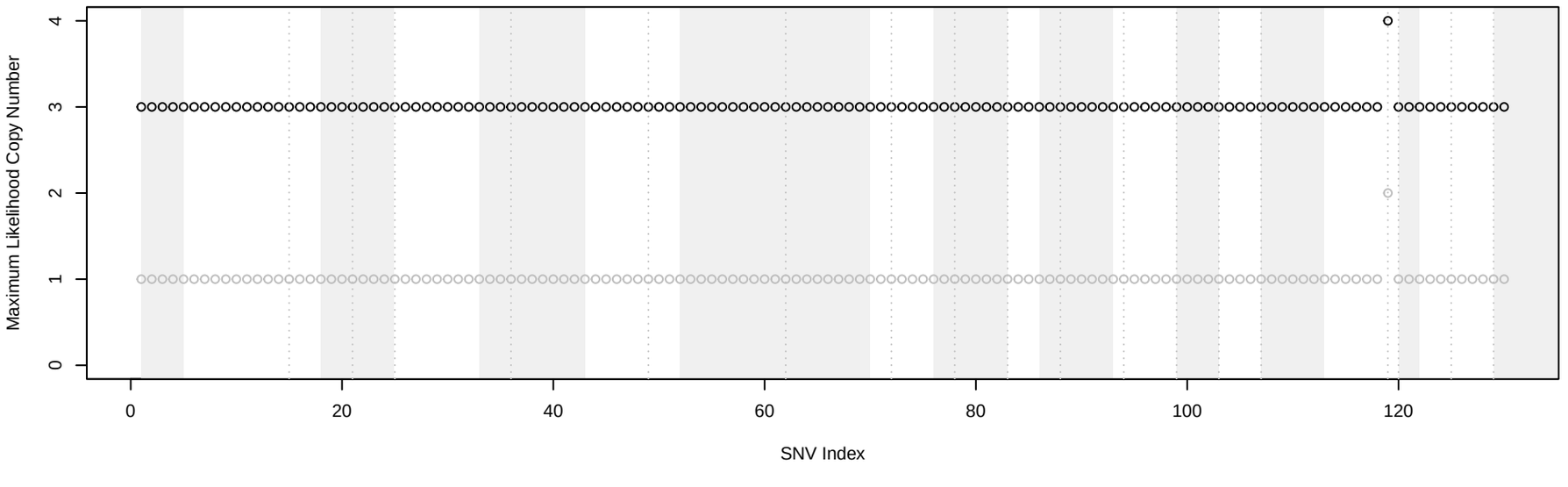

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
0.25
0.30
0.35
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6

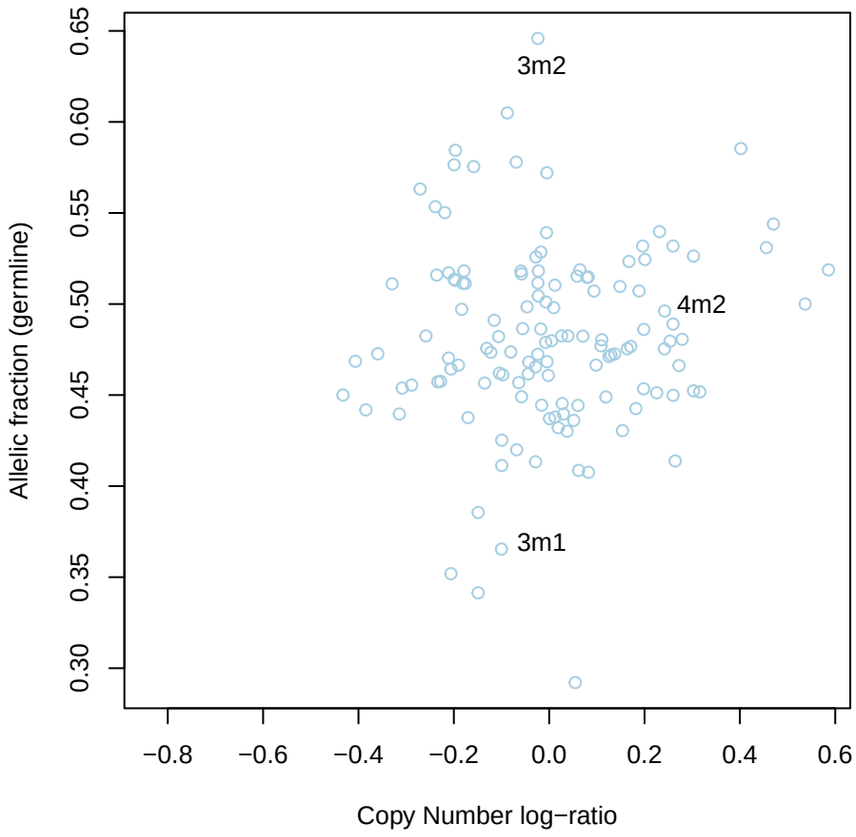

Power 0.8
Frequency
Cellular fraction
0
10
20
30
40
50
0.1
0.2
0.3
0.4

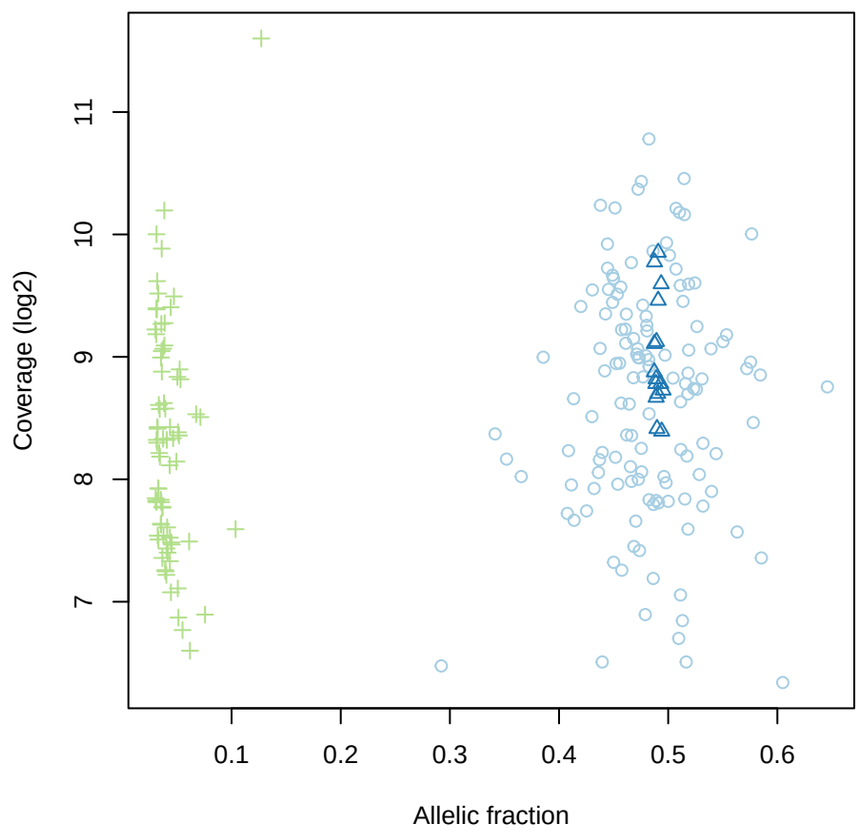

Purity: 0.71 Tumor ploidy: 3.042
1
2
3
4
0.0
0.1
0.2
0.3
0.4
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

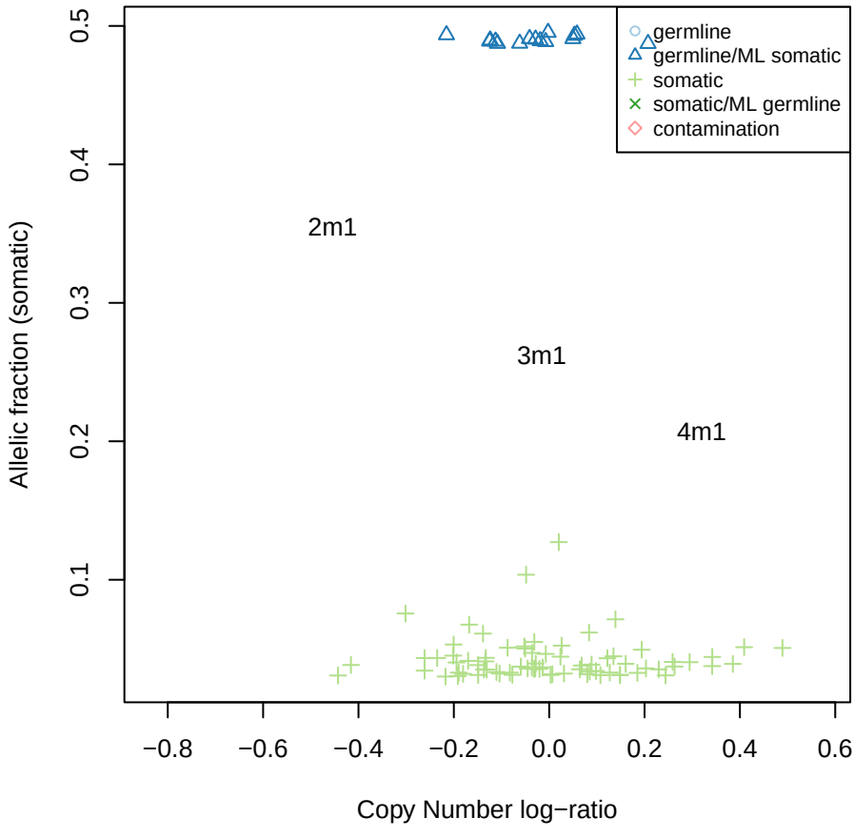

Purity: 0.71 Tumor ploidy: 3.042 SNV log−likelihood: −998.46 GoF: 45.7% Mean coverage: 585;464
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 18 19
B−Allele Frequency
0.30 0.40 0.50 0.60
0 20 40 60 80 100 120
SNV Index

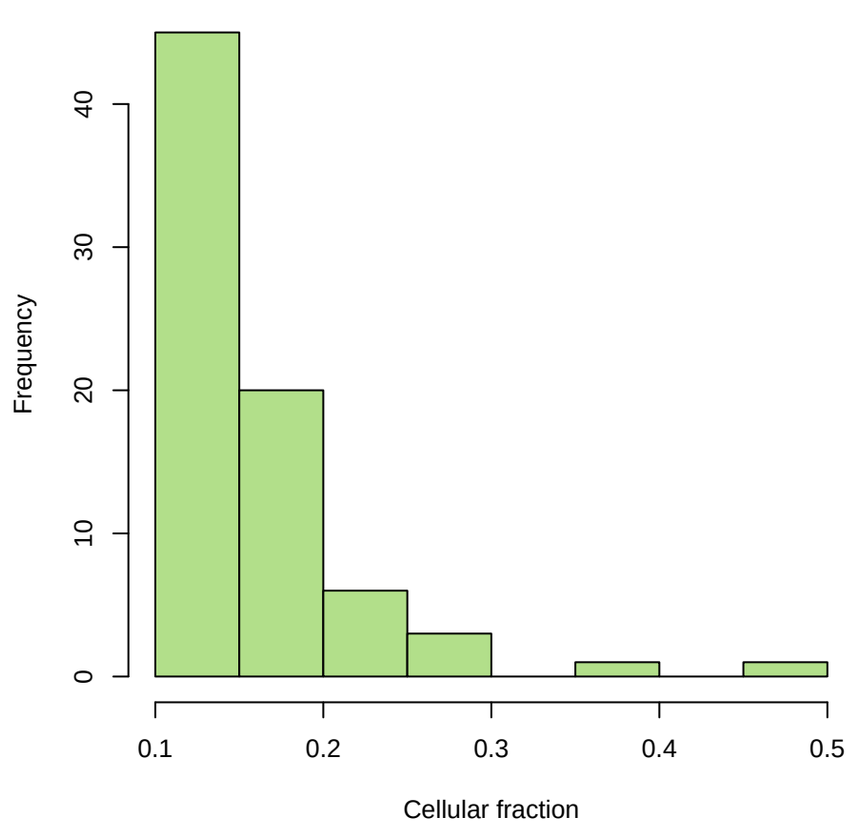

SCNA−fit log−likelihood: −5999.64
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5
0 20 40 60 80 100 120
SNV Index


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


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


Coverage (log2)
Allelic fraction


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


Frequency
Cellular fraction