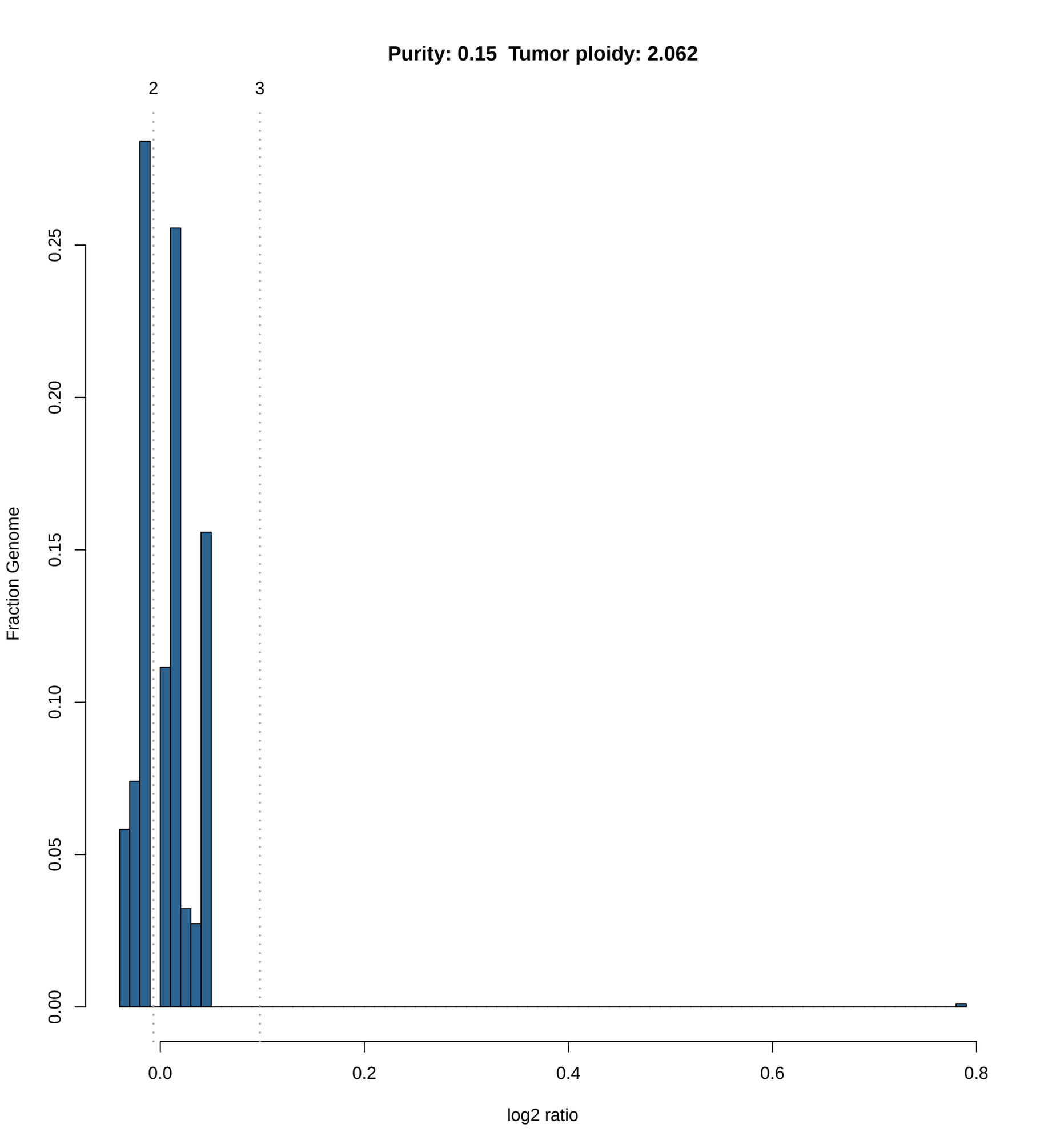
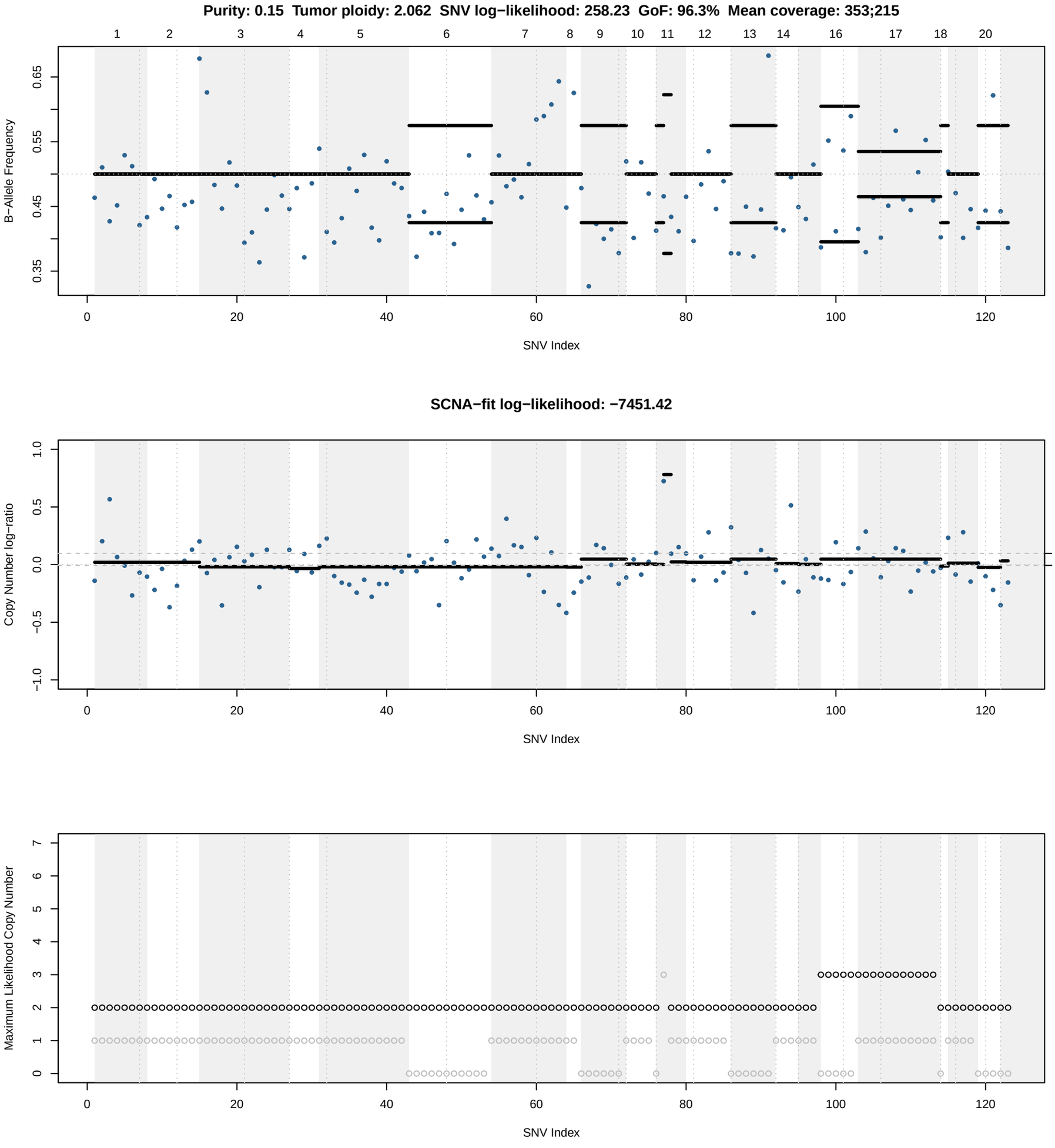
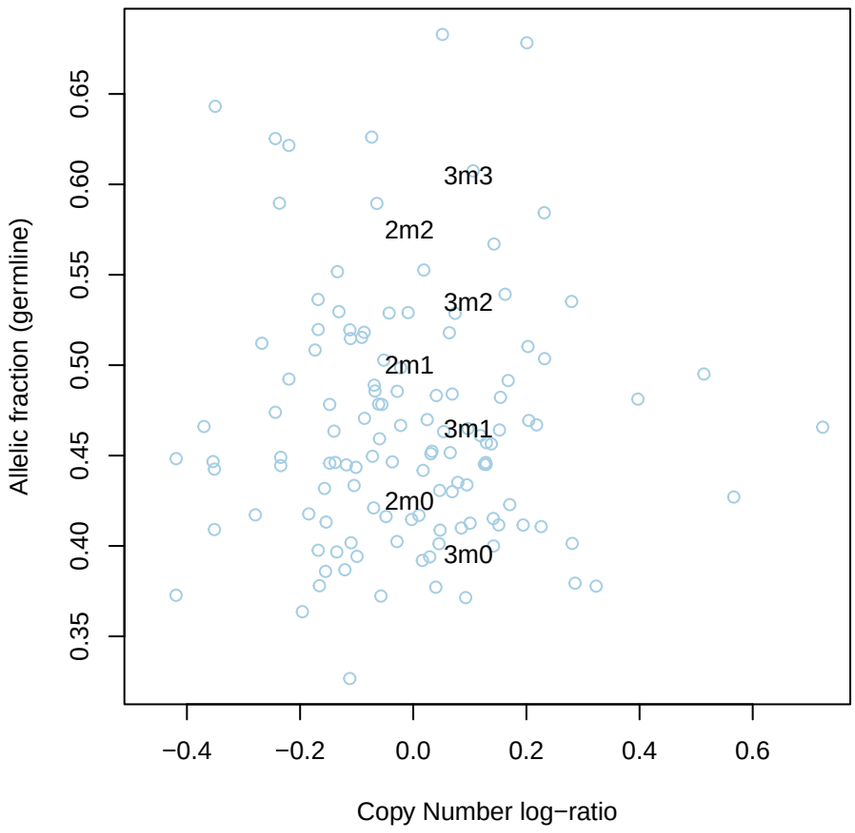
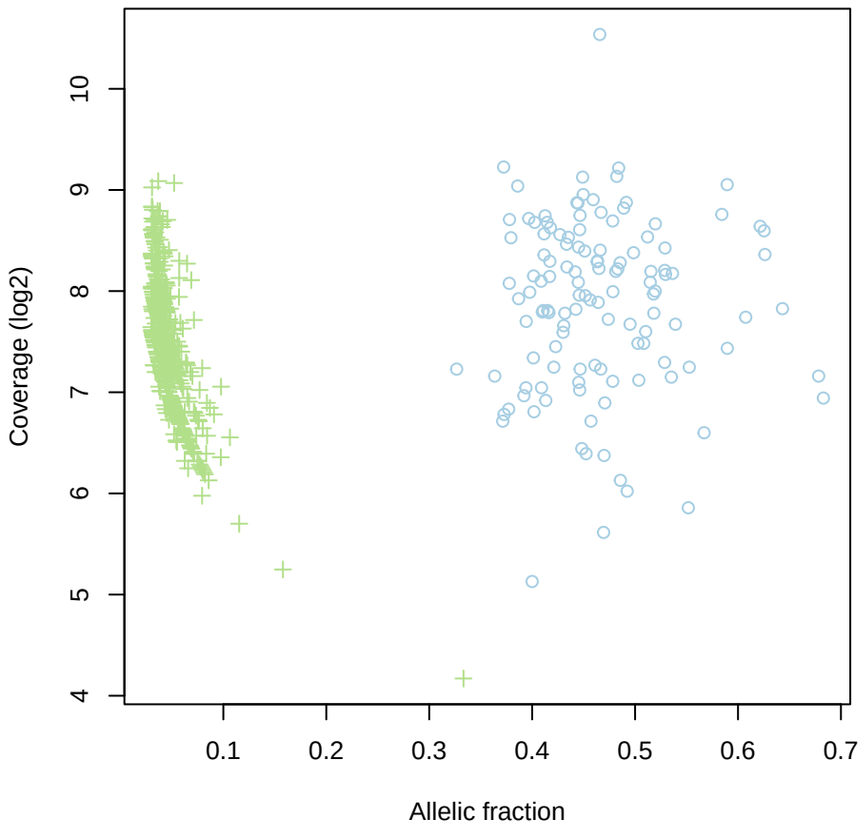
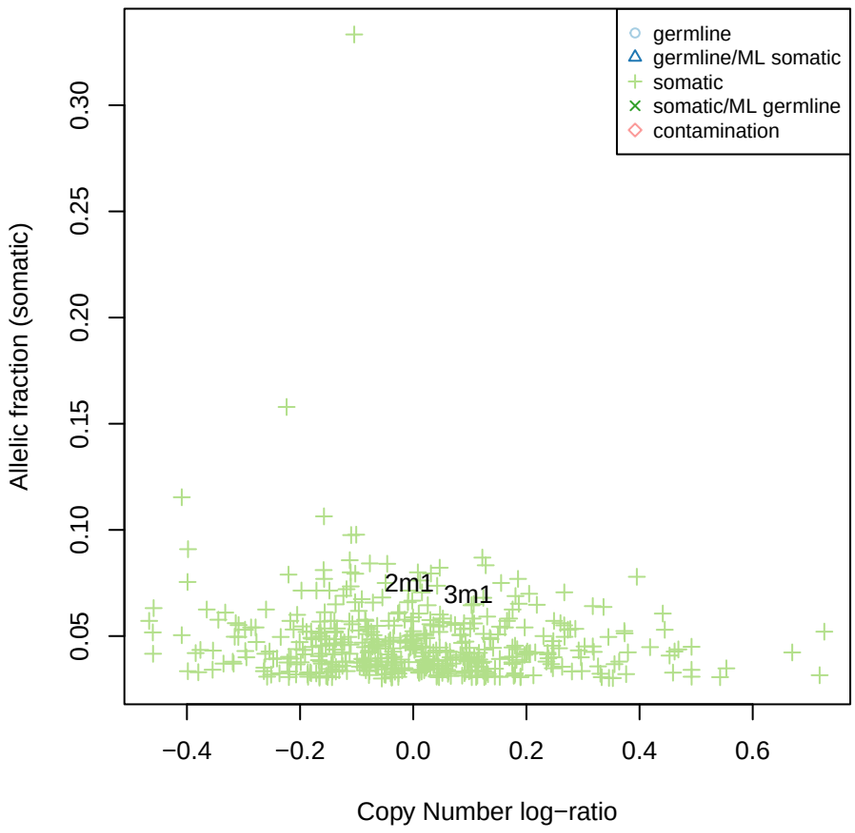
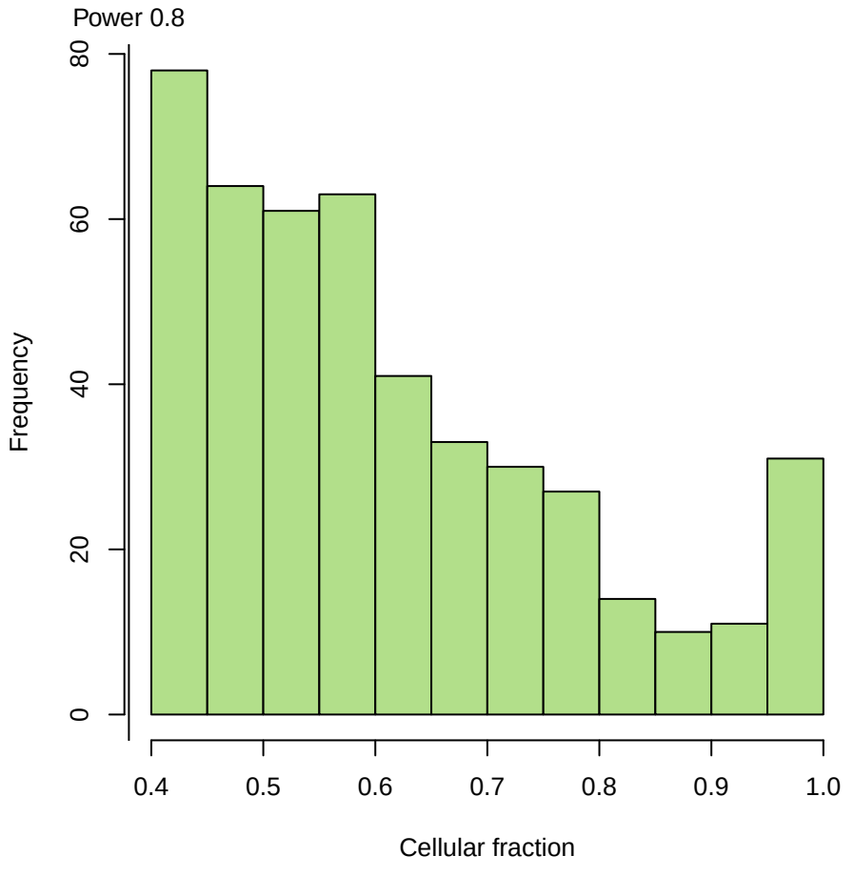

Purity: 0.15 Tumor ploidy: 2.062
2
3
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.2
0.4
0.6
0.8
log2 ratio

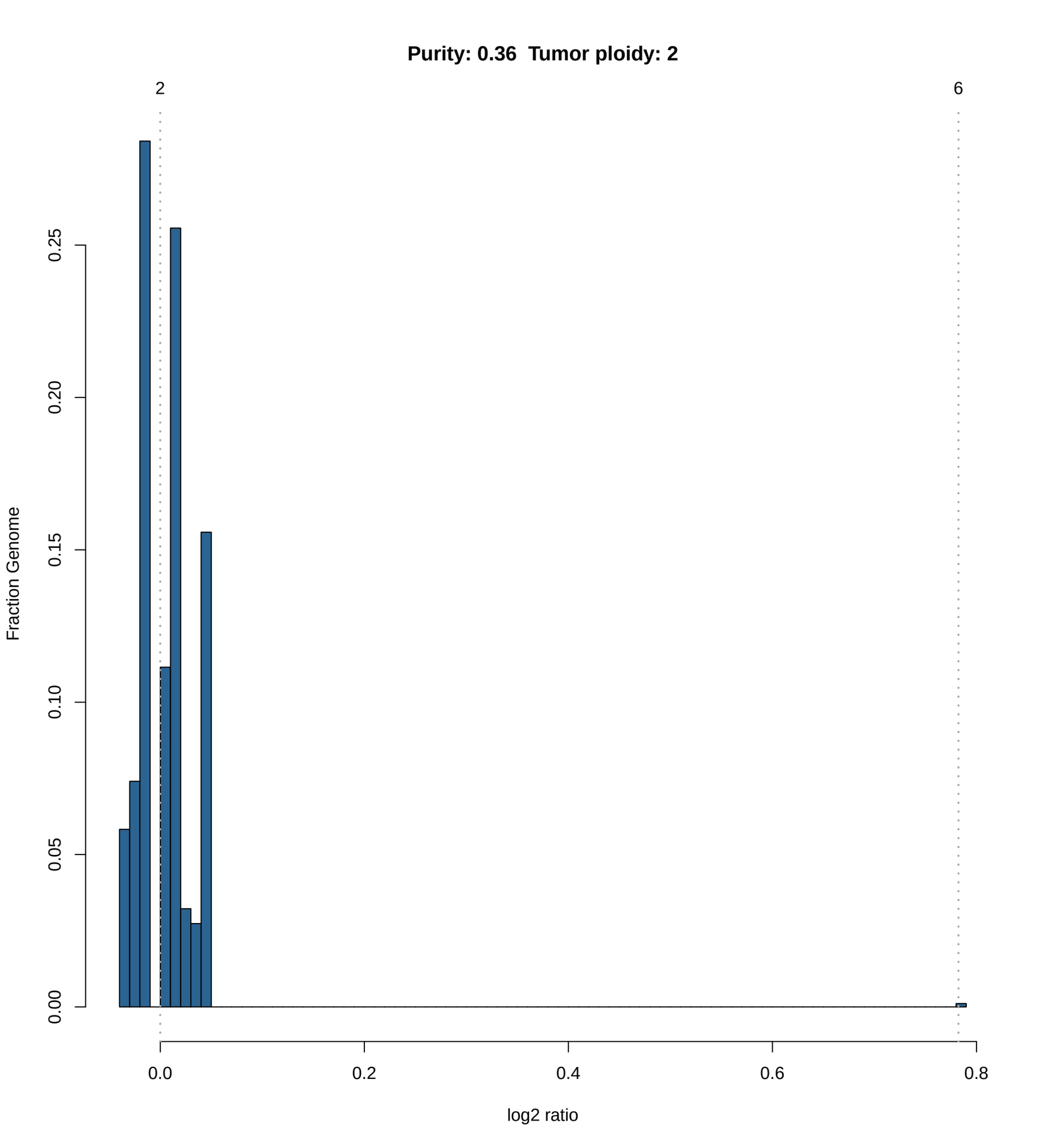

Purity: 0.15 Tumor ploidy: 2.062 SNV log−likelihood: 258.23 GoF: 96.3% Mean coverage: 353;215
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 20
B−Allele Frequency
0.35 0.45 0.55 0.65
0 20 40 60 80 100 120
SNV Index
SCNA−fit log−likelihood: −7451.42
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1
2
0 20 40 60 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

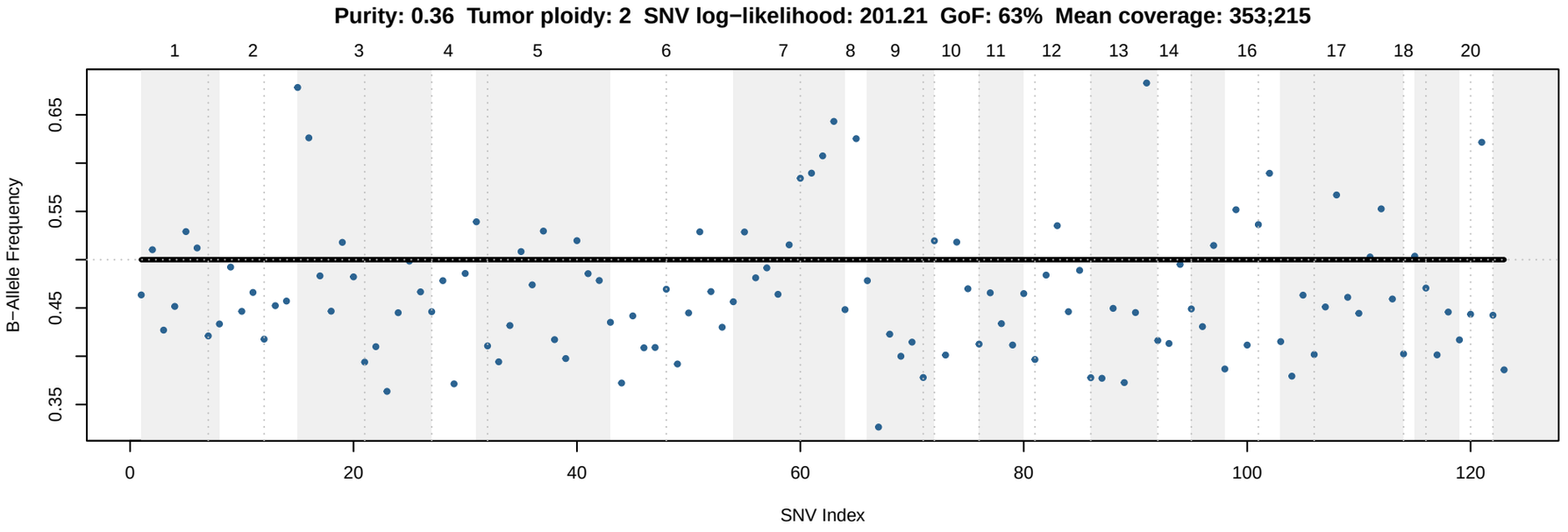

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
3m3
2m2
3m2
2m1
3m1
2m0
3m0
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

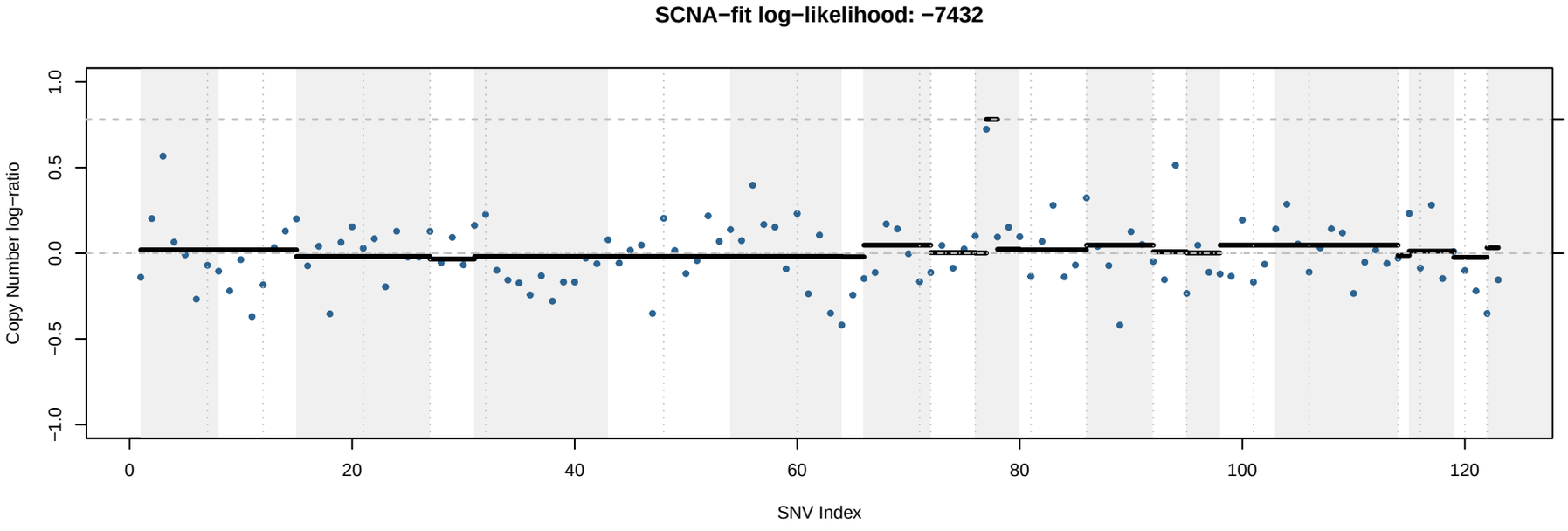

Coverage (log2)
4
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

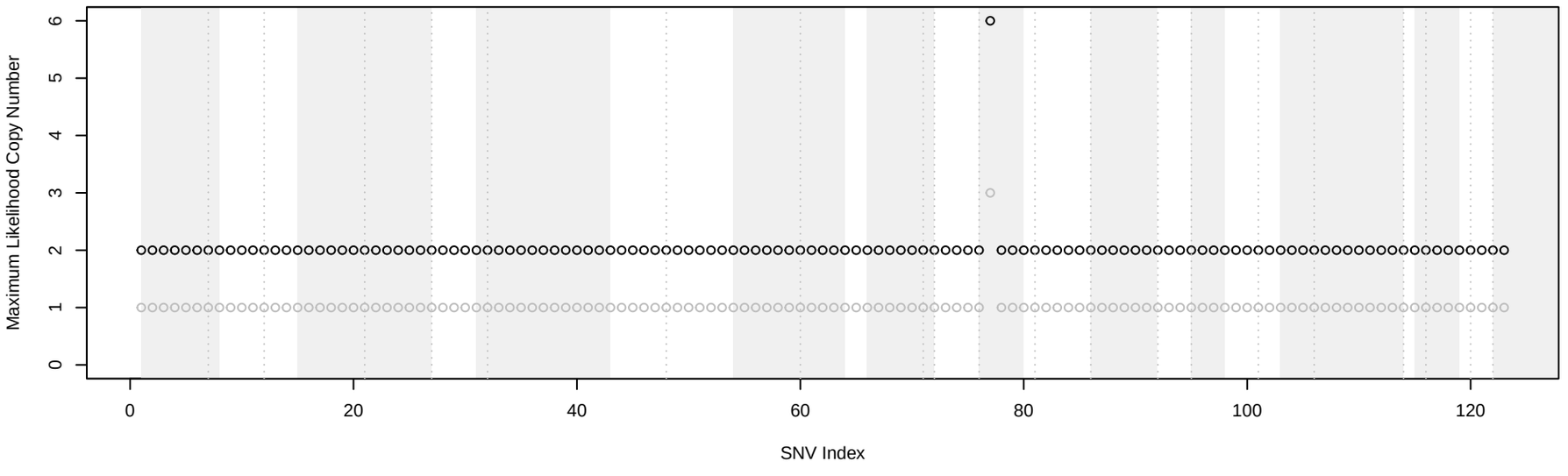

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0.30
2m1
3m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

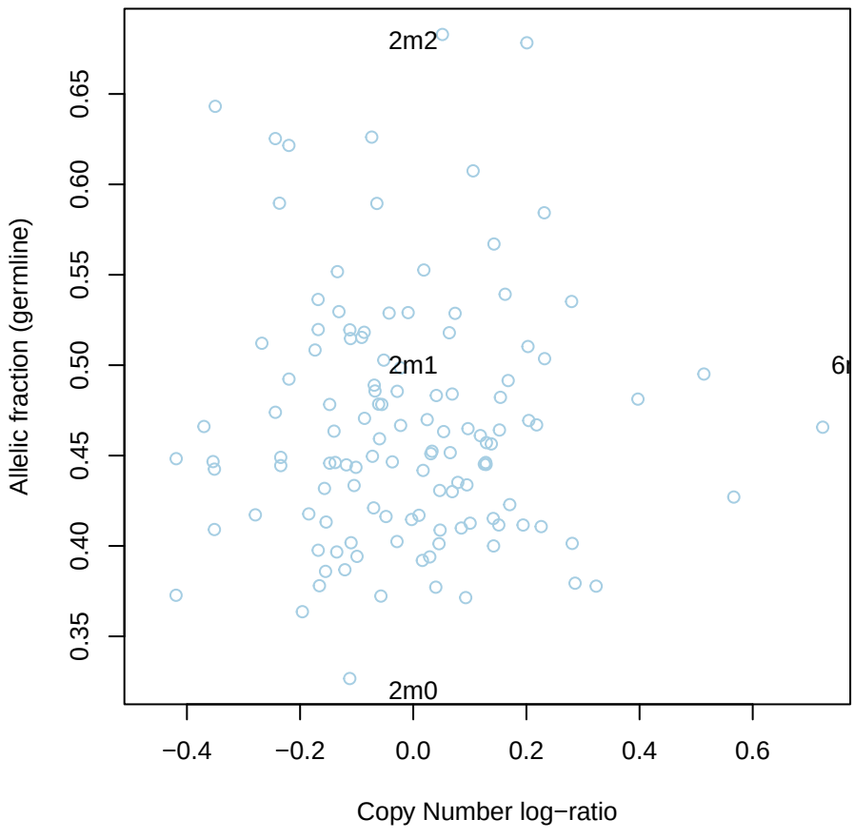

Power 0.8
Frequency
0
20
40
60
80
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

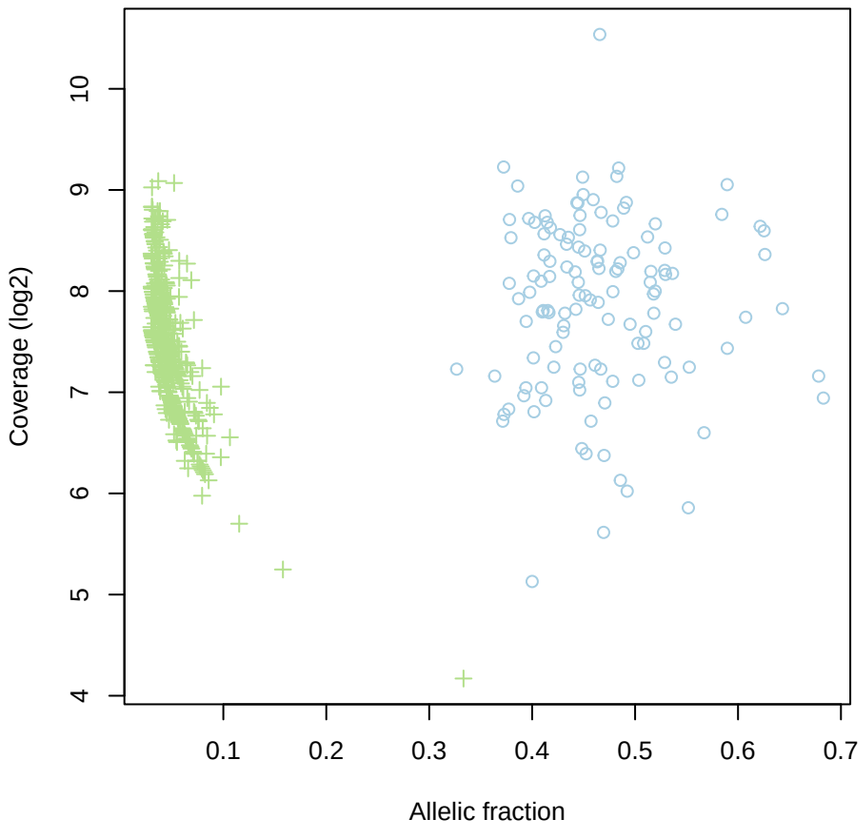

Purity: 0.36 Tumor ploidy: 2
2
6
Fraction Genome
0.00
0.05
0.10
0.15
0.20
0.25
0.0
0.2
0.4
0.6
0.8
log2 ratio

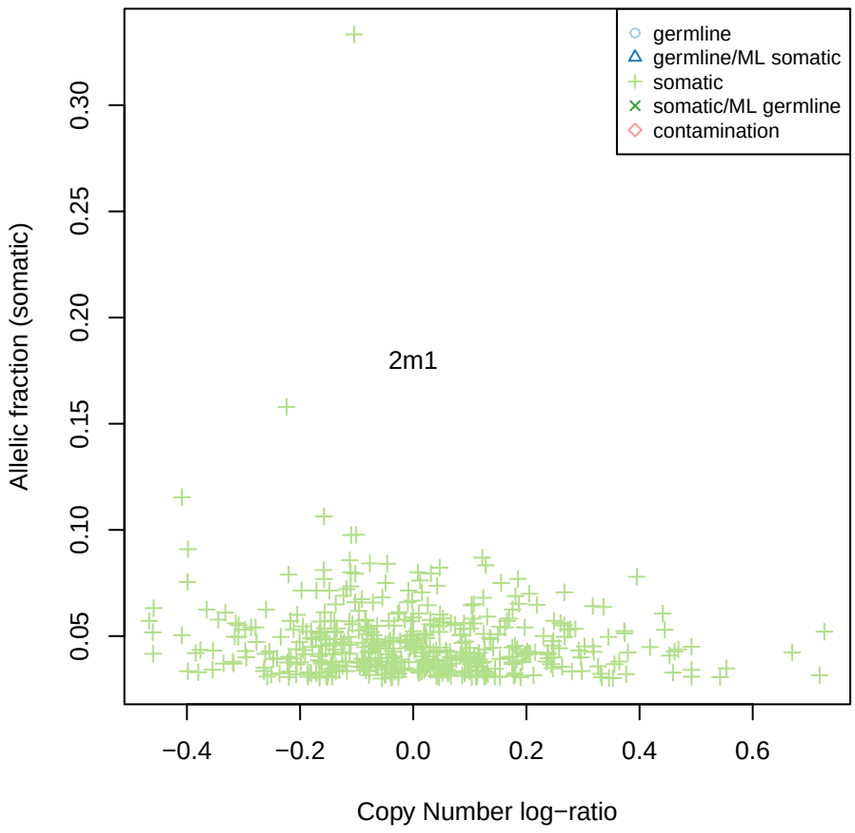

Purity: 0.36 Tumor ploidy: 2 SNV log−likelihood: 201.21 GoF: 63% Mean coverage: 353;215
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 20
B−Allele Frequency
0.35 0.45 0.55 0.65
0 20 40 60 80 100 120
SNV Index

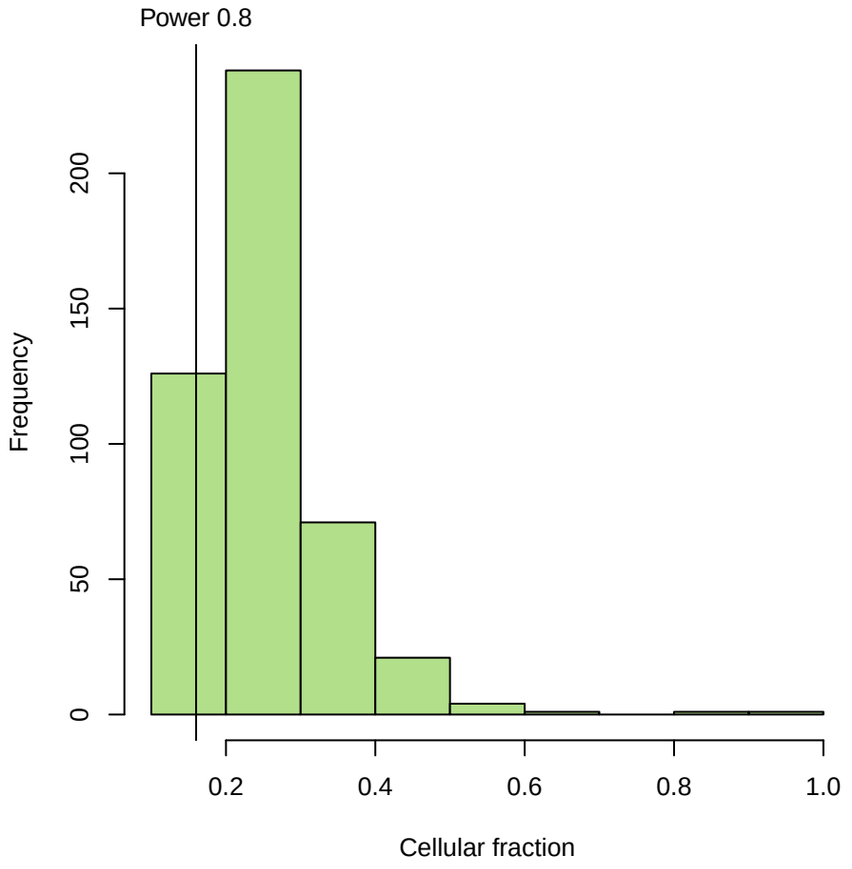

SCNA−fit log−likelihood: −7432
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 6
0 20 40 60 80 100 120
SNV Index

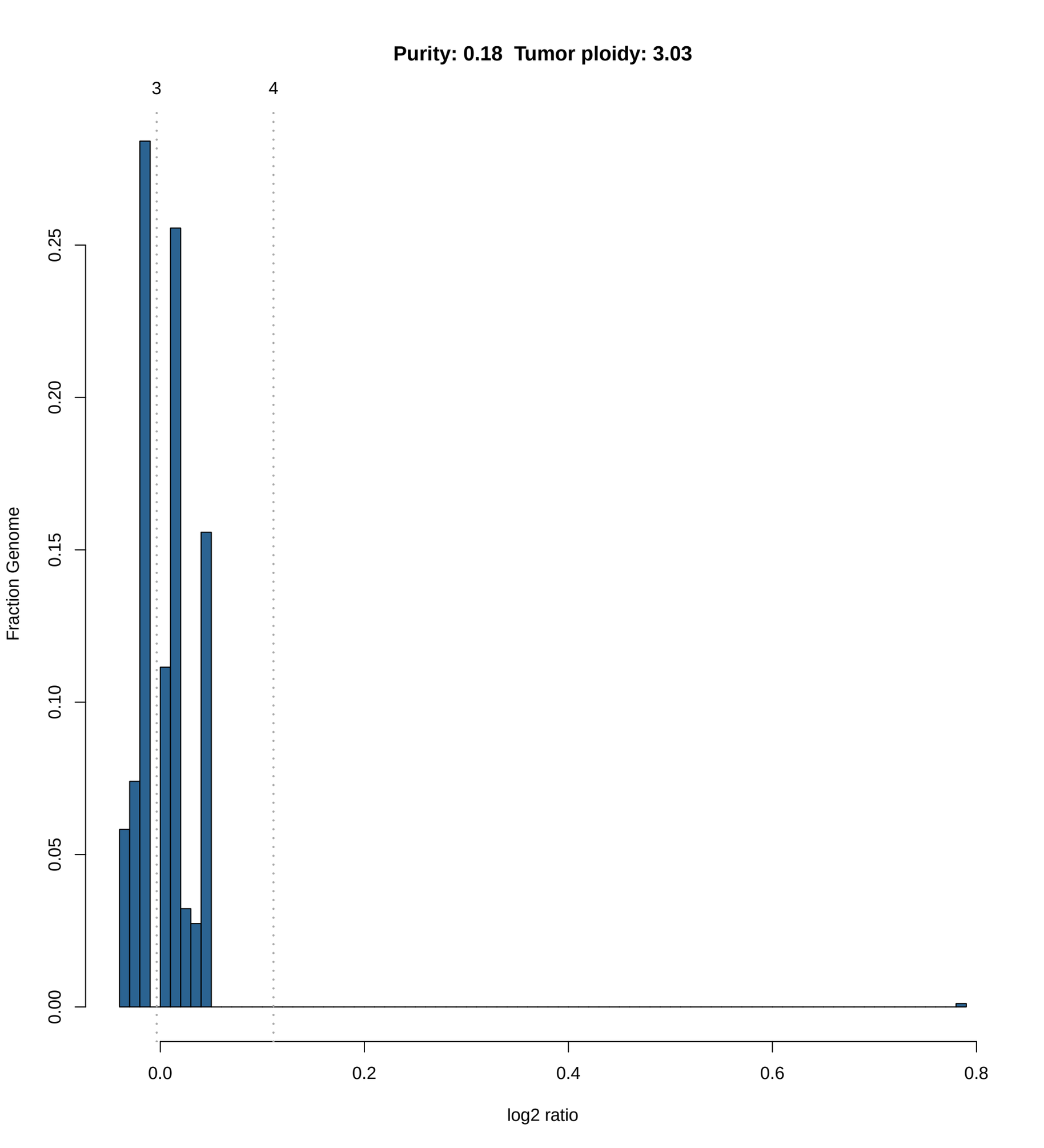

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120
SNV Index

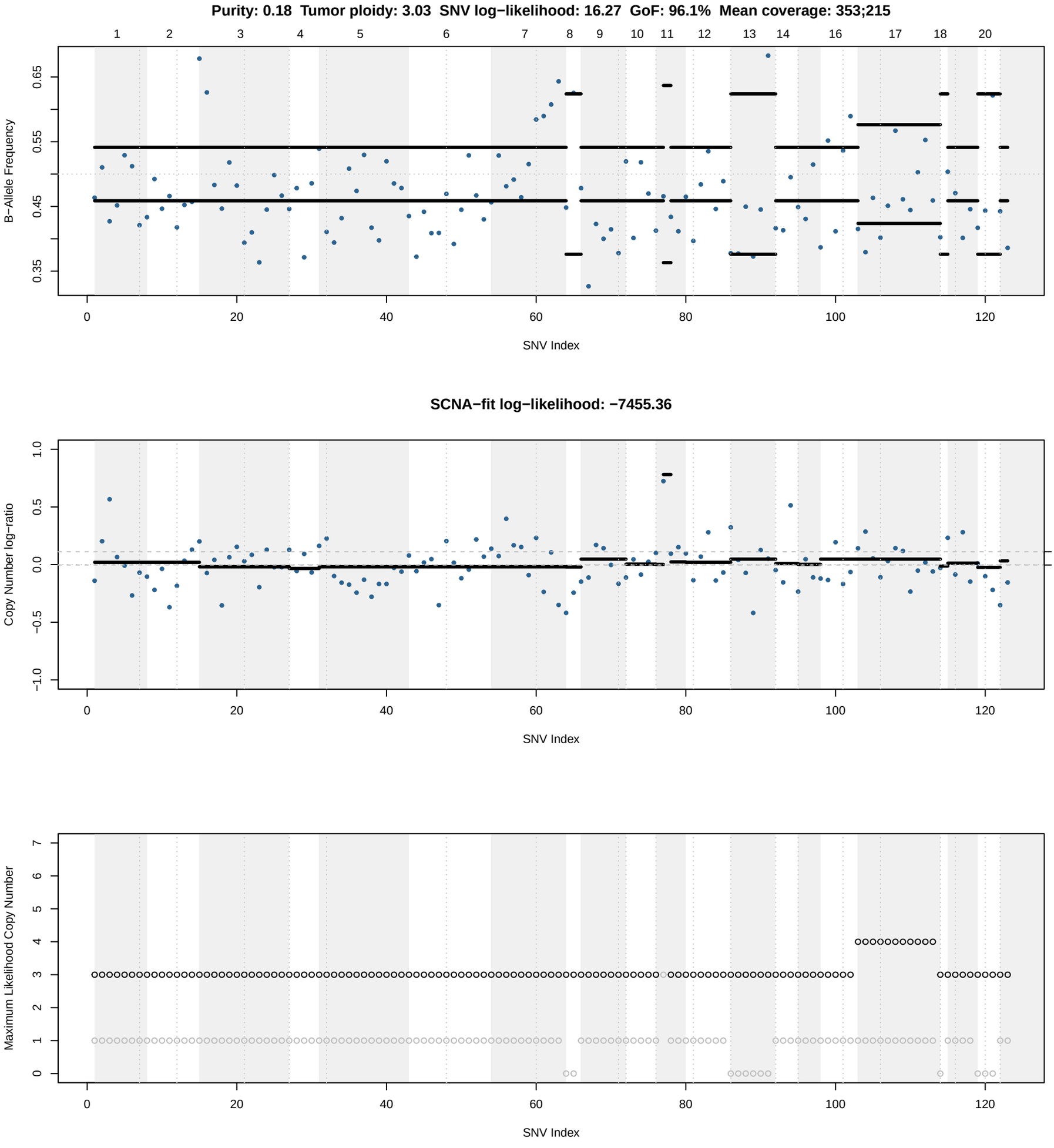

2m2
2m1
2m0
Allelic fraction (germline)
Copy Number log−ratio

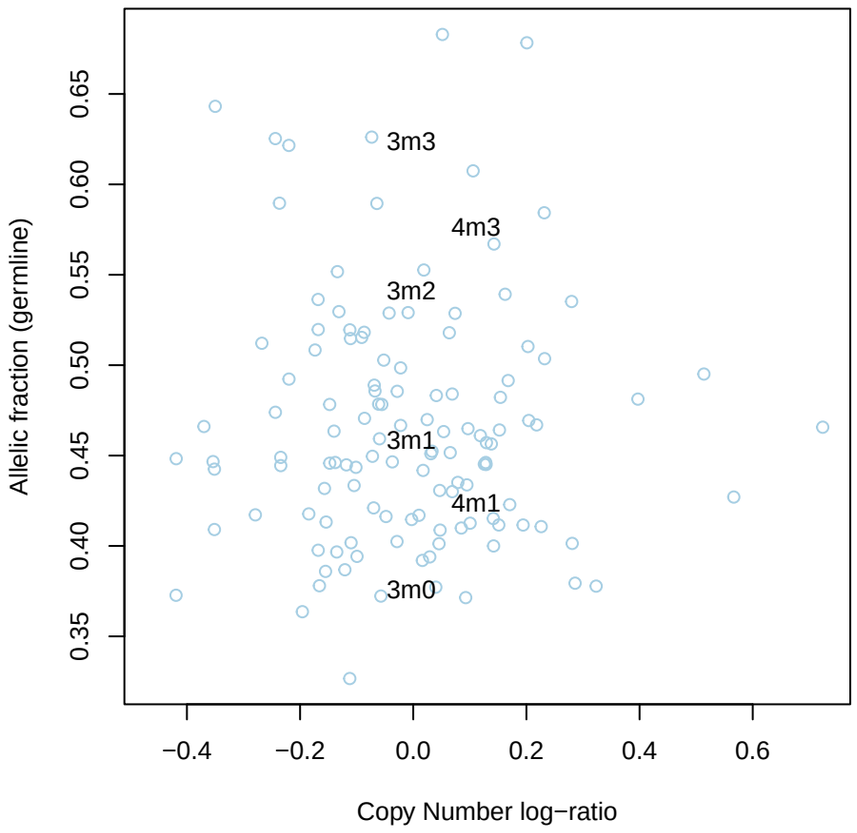

Coverage (log2)
Allelic fraction

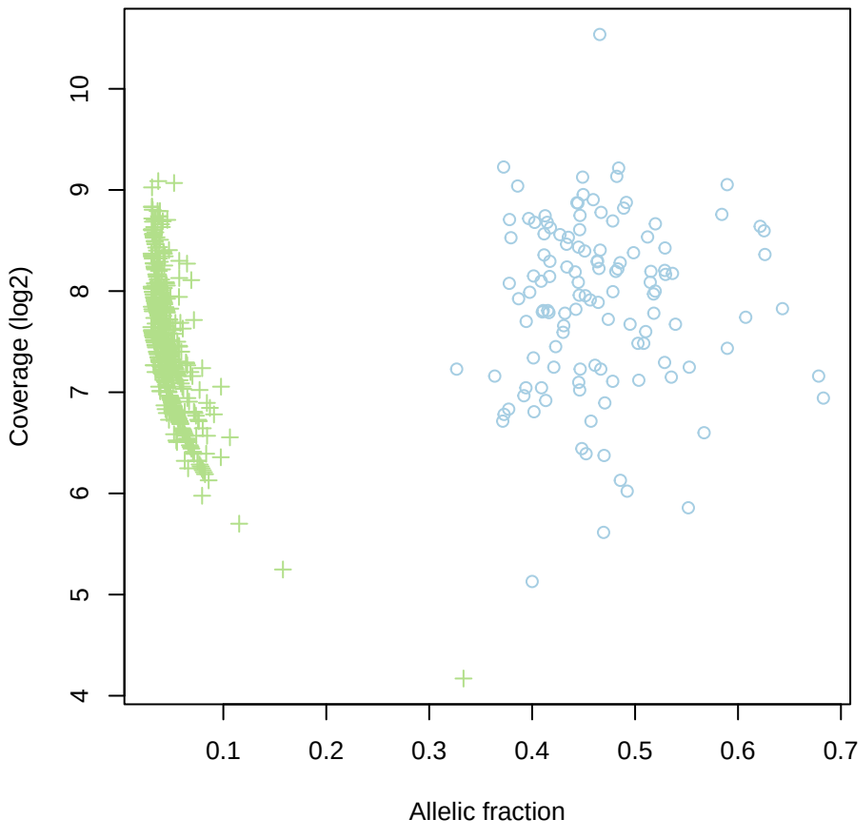

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
Allelic fraction (somatic)
Copy Number log−ratio

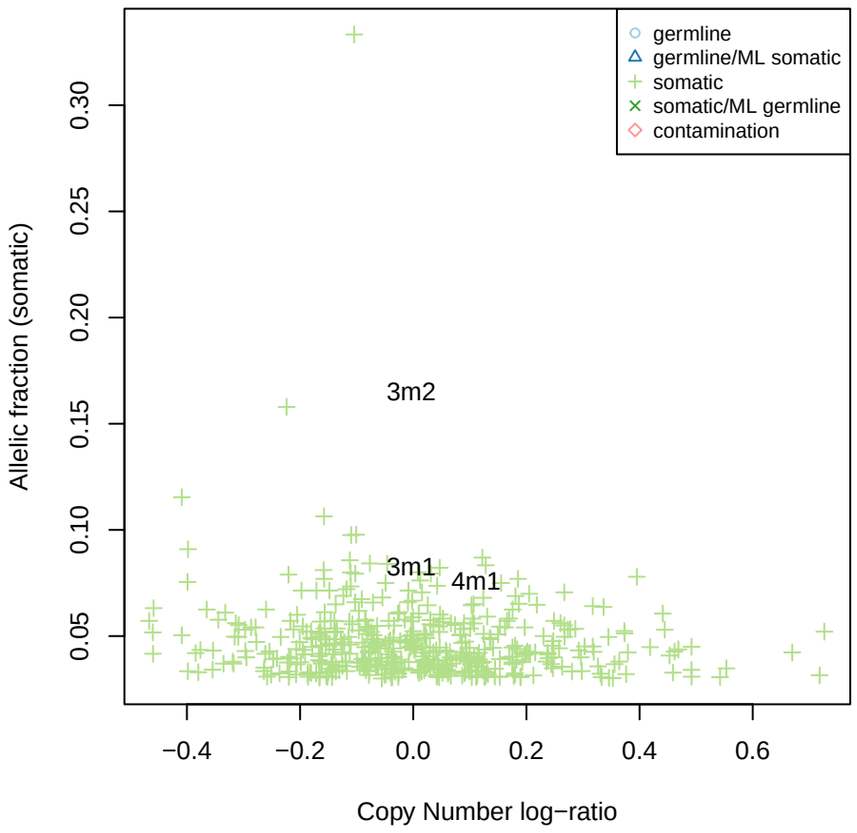

Power 0.8
Frequency
Cellular fraction

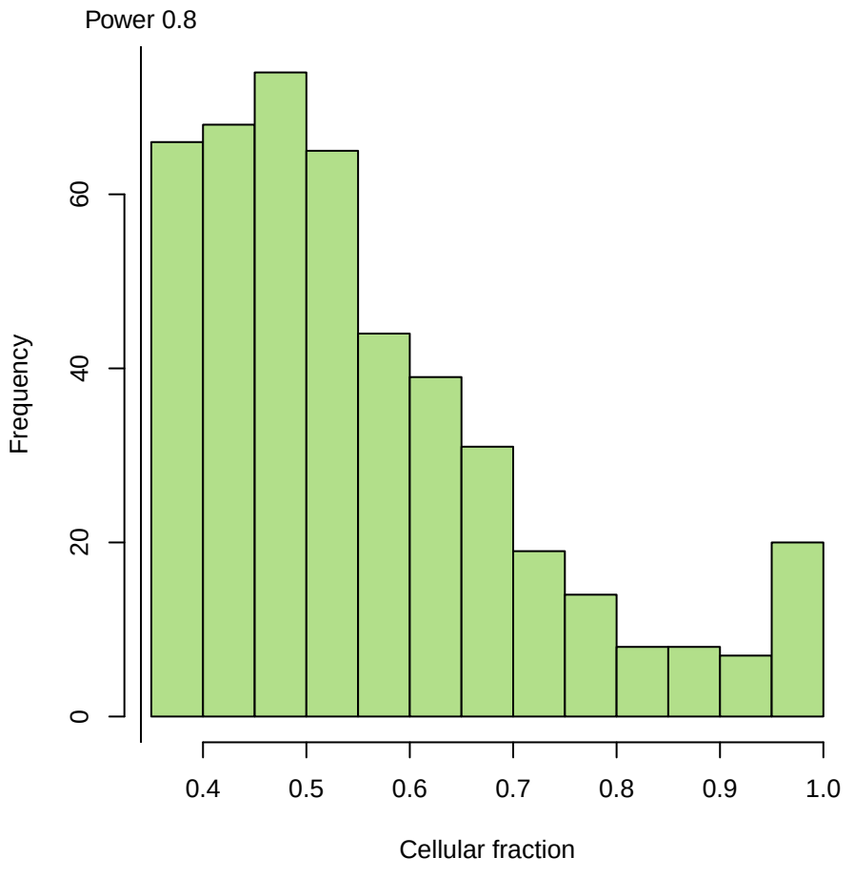

Purity: 0.18 Tumor ploidy: 3.03
3
4
Fraction Genome
0.00
0.05
0.10
0.15
0.20
0.25
0.0
0.2
0.4
0.6
0.8
log2 ratio

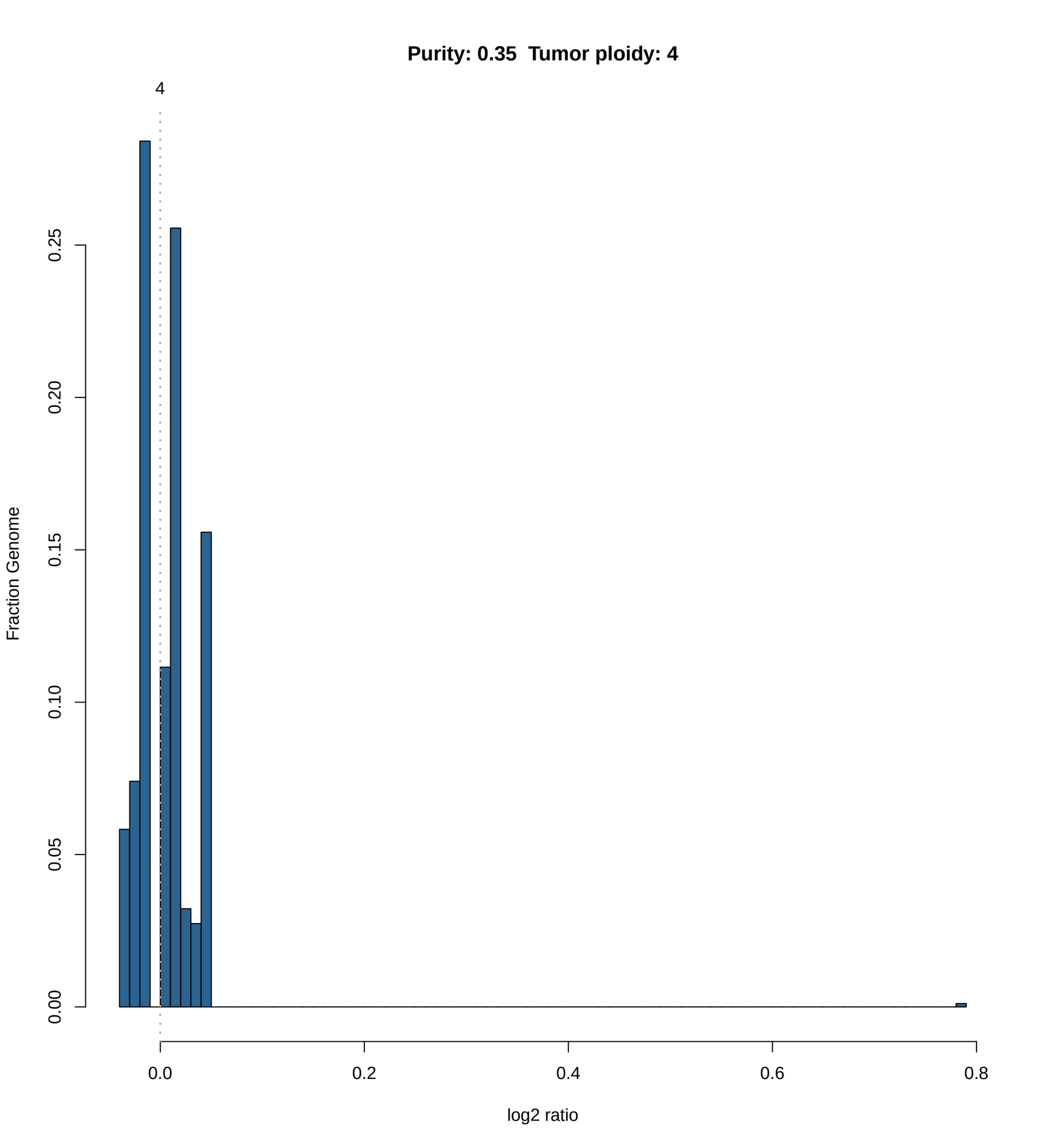

Purity: 0.18 Tumor ploidy: 3.03 SNV log−likelihood: 16.27 GoF: 96.1% Mean coverage: 353;215
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 20
B−Allele Frequency
0.35 0.45 0.55 0.65
0 20 40 60 80 100 120
SNV Index
SCNA−fit log−likelihood: −7455.36
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3
0 20 40 60 80 100 120
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

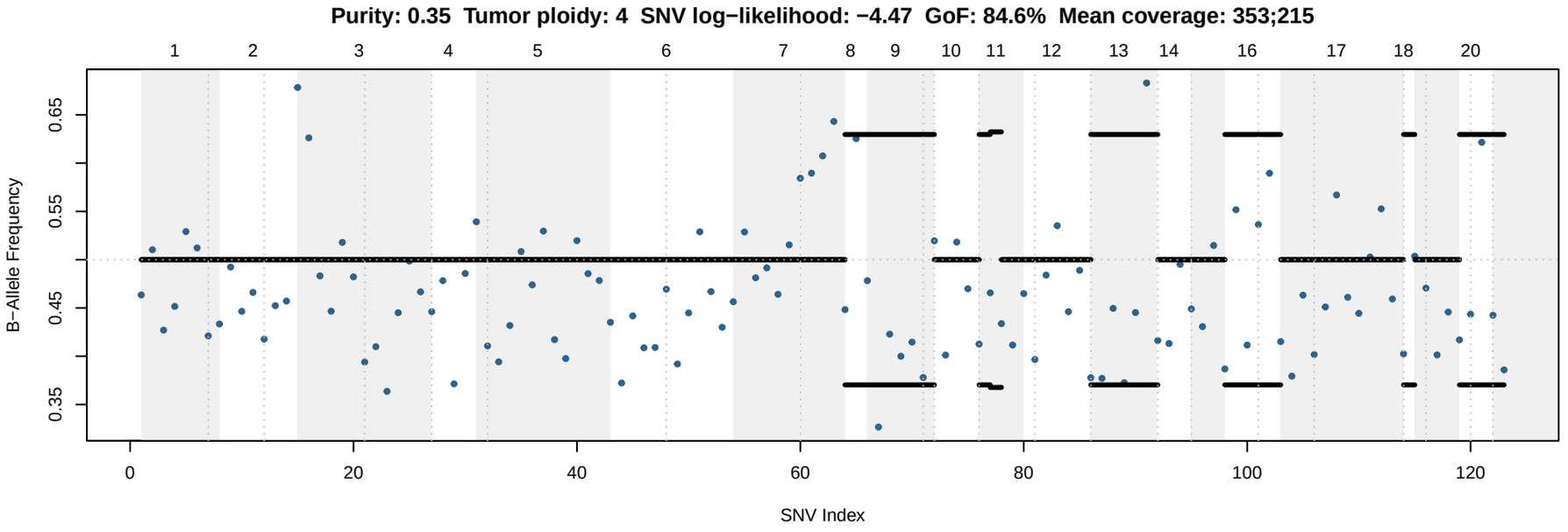

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
3m3
4m3
3m2
3m1
4m1
3m0
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

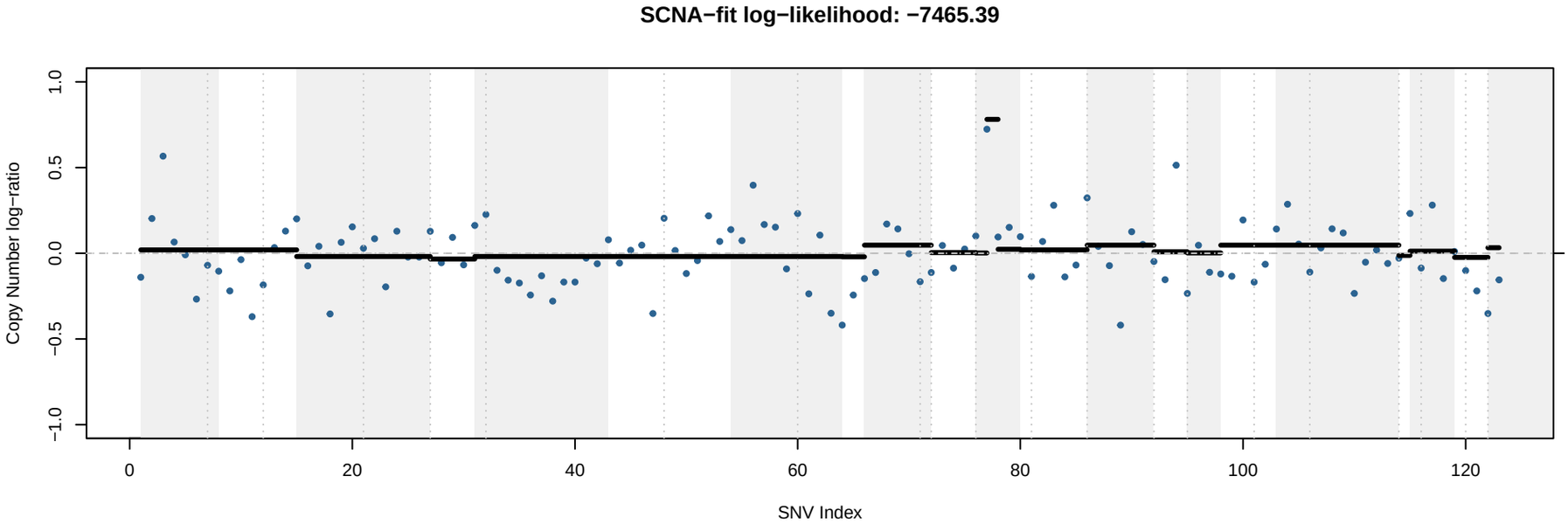

Coverage (log2)
4
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

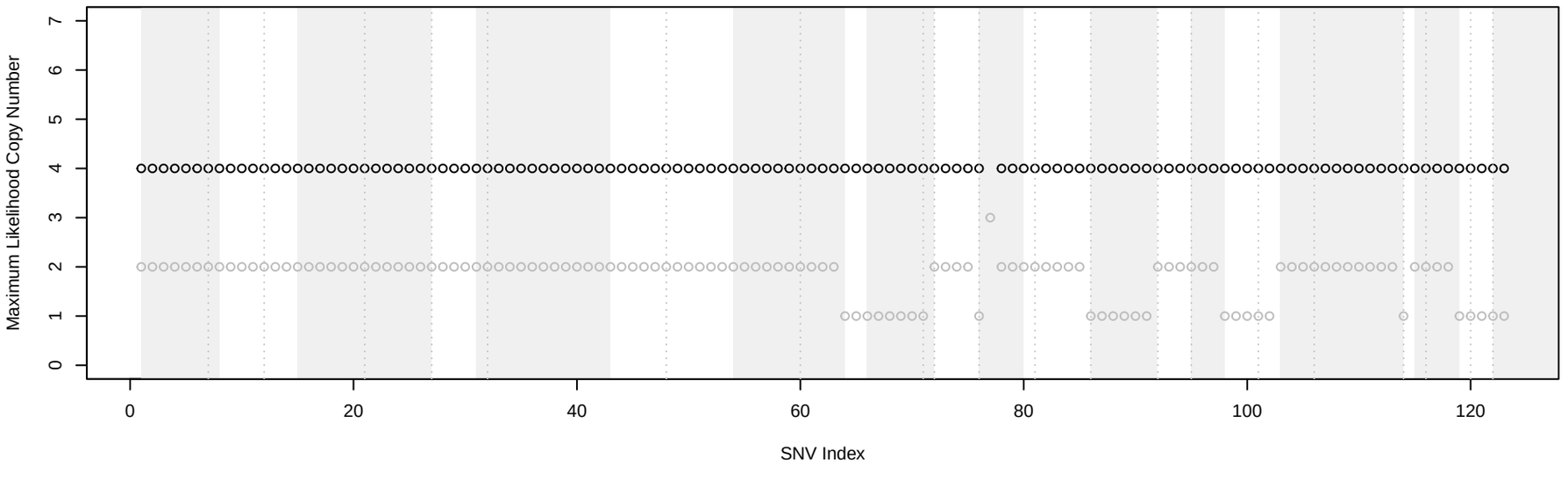

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0.30
3m2
3m1
4m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

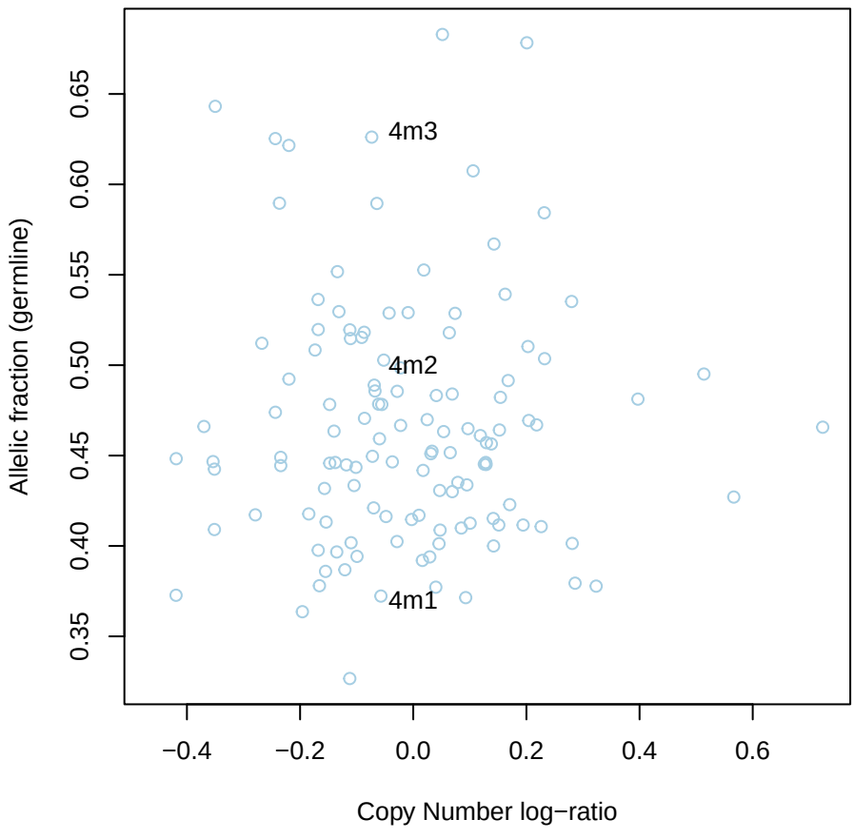

Power 0.8
Frequency
0
20
40
60
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

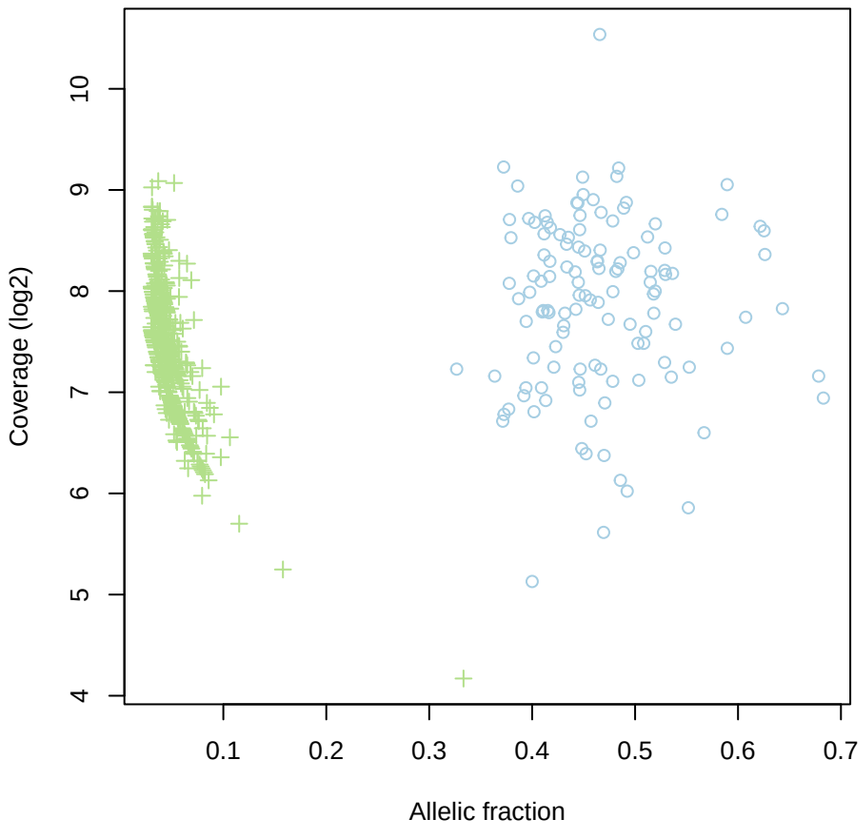

Purity: 0.35 Tumor ploidy: 4
4
Fraction Genome
0.00
0.05
0.10
0.15
0.20
0.25
0.0
0.2
0.4
0.6
0.8
log2 ratio

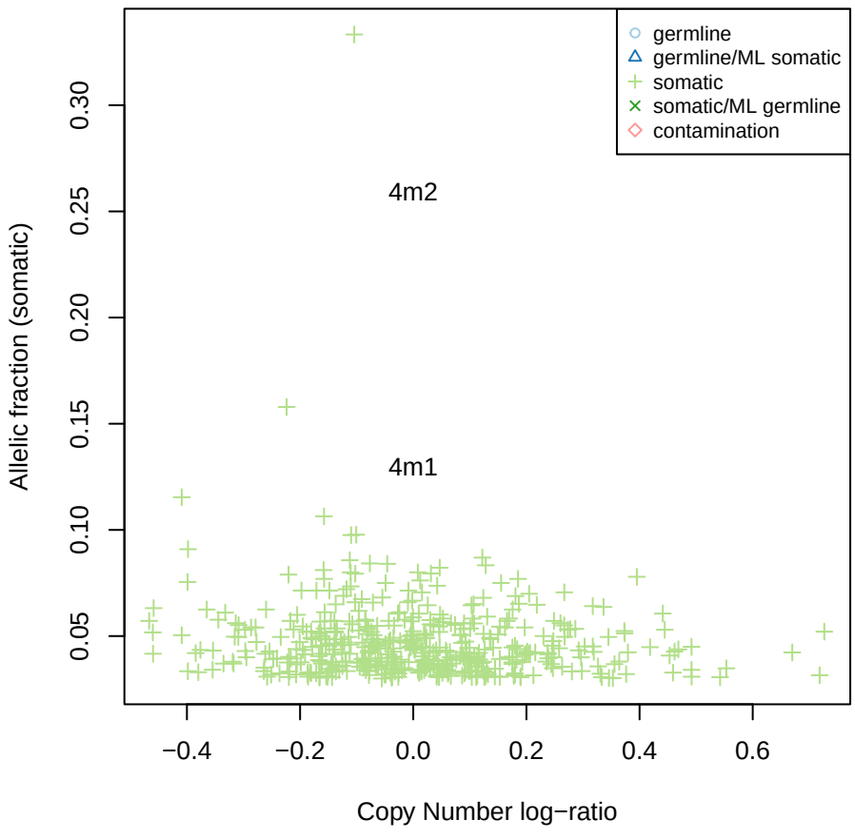

Purity: 0.35 Tumor ploidy: 4 SNV log−likelihood: −4.47 GoF: 84.6% Mean coverage: 353;215
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 20
B−Allele Frequency
0.35 0.45 0.55 0.65
0 20 40 60 80 100 120
SNV Index

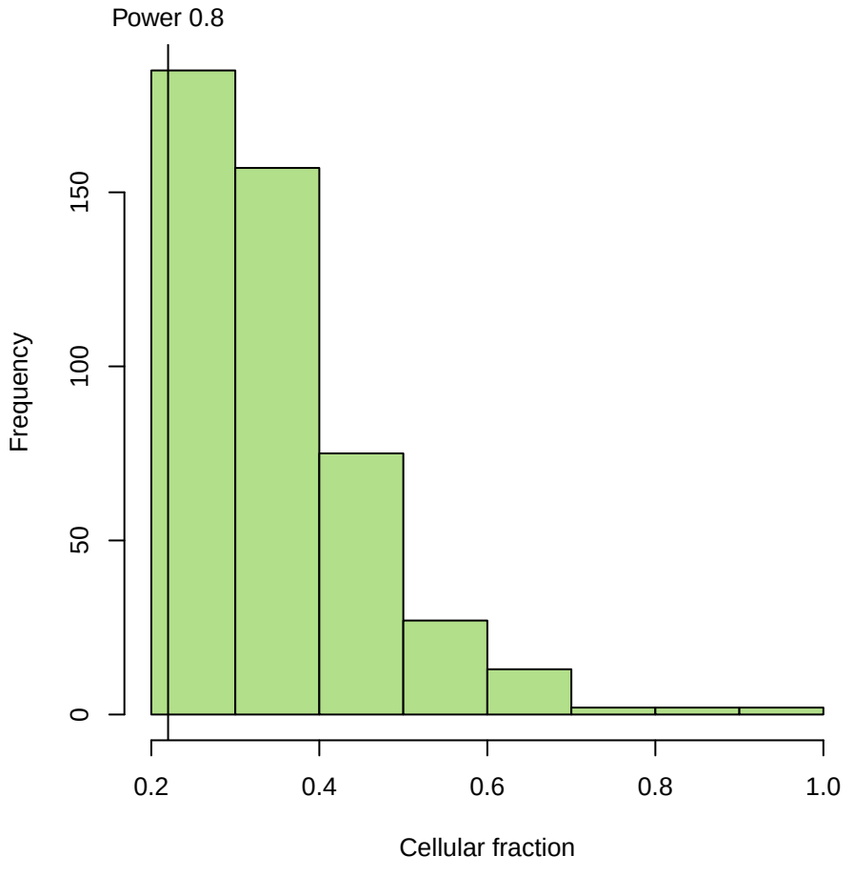

SCNA−fit log−likelihood: −7465.39
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4
0 20 40 60 80 100 120
SNV Index

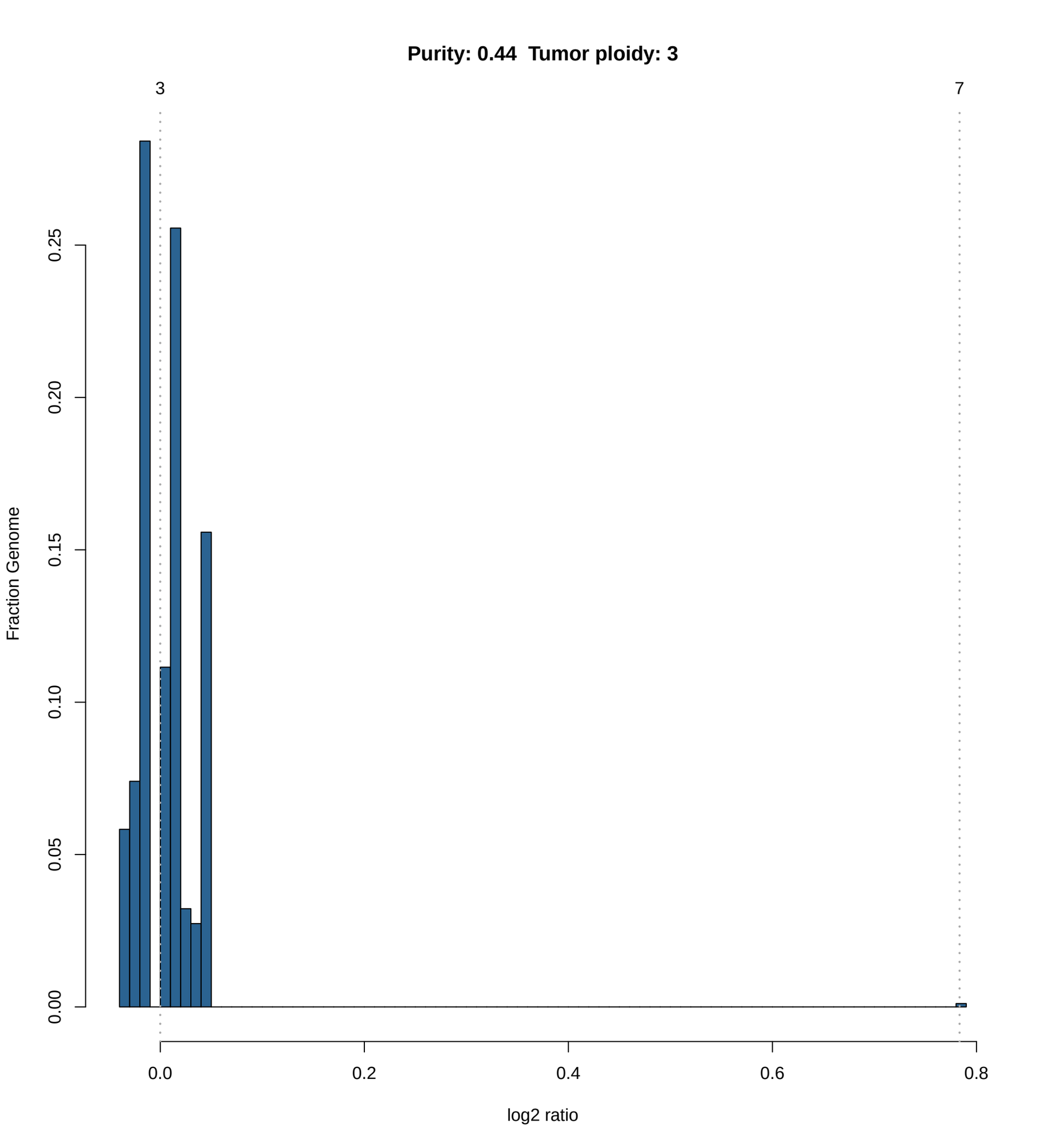

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

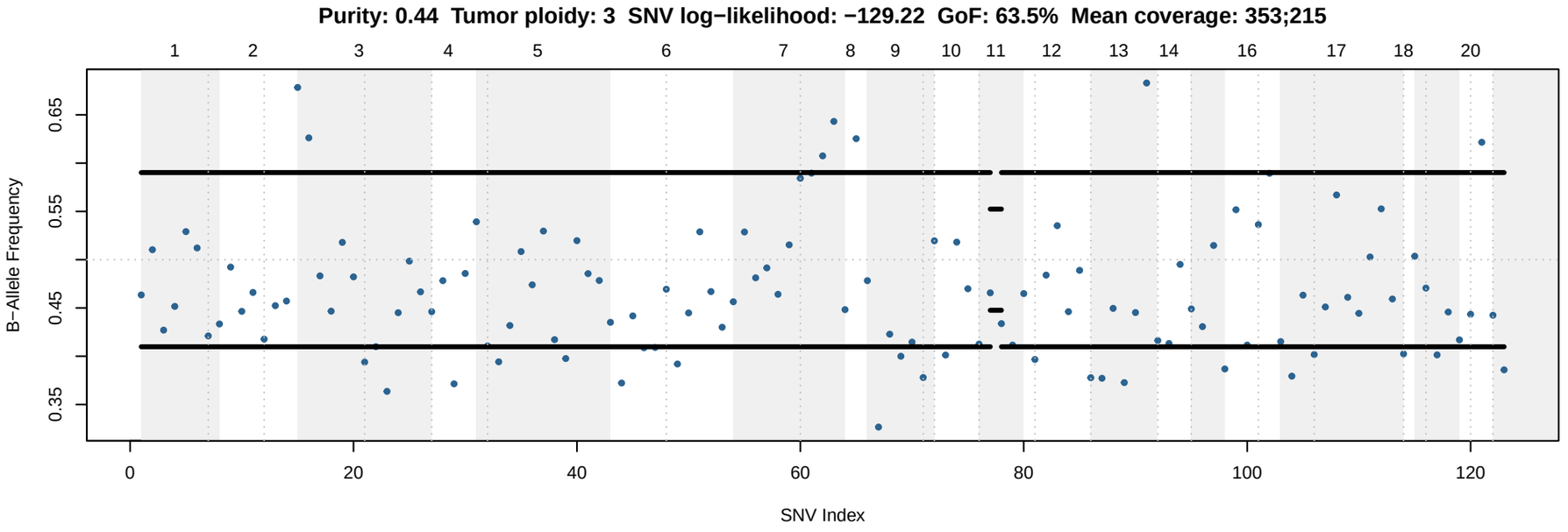

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
4m3
4m2
4m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

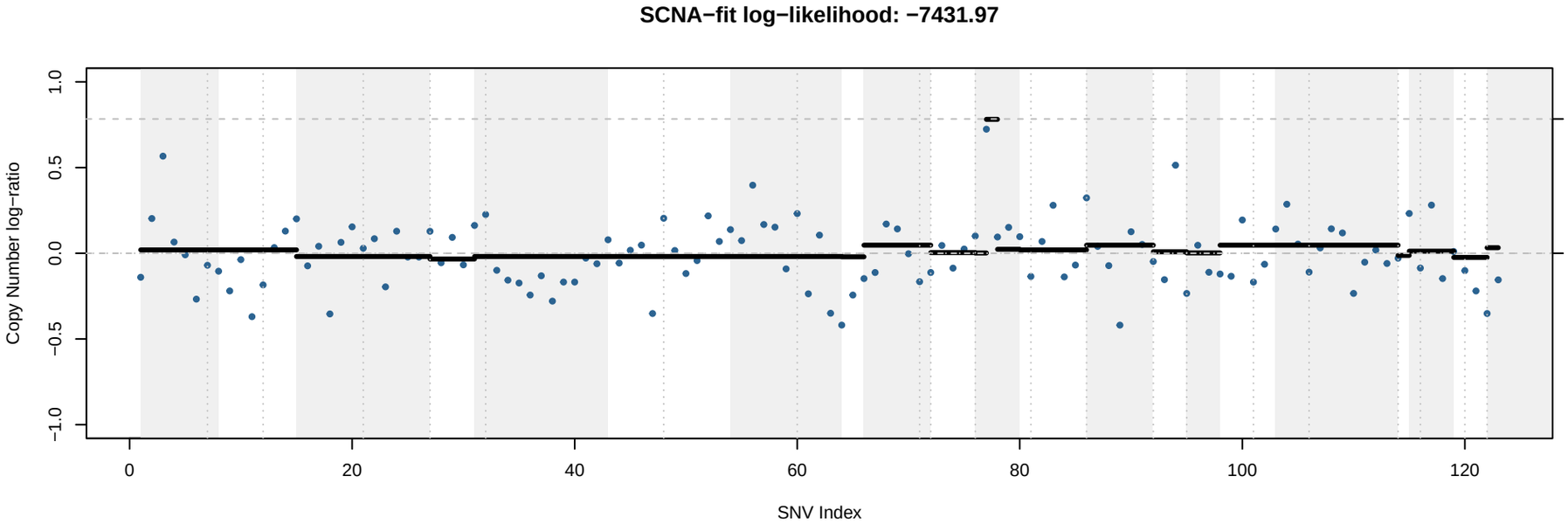

Coverage (log2)
4
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

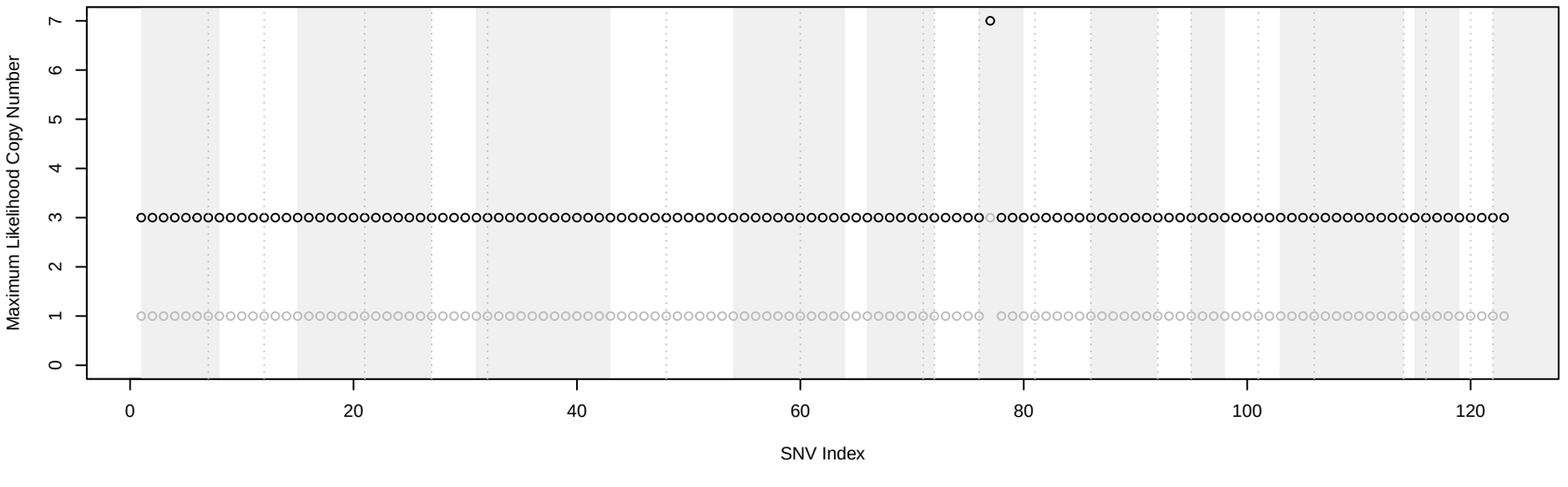

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0.30
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m2
4m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

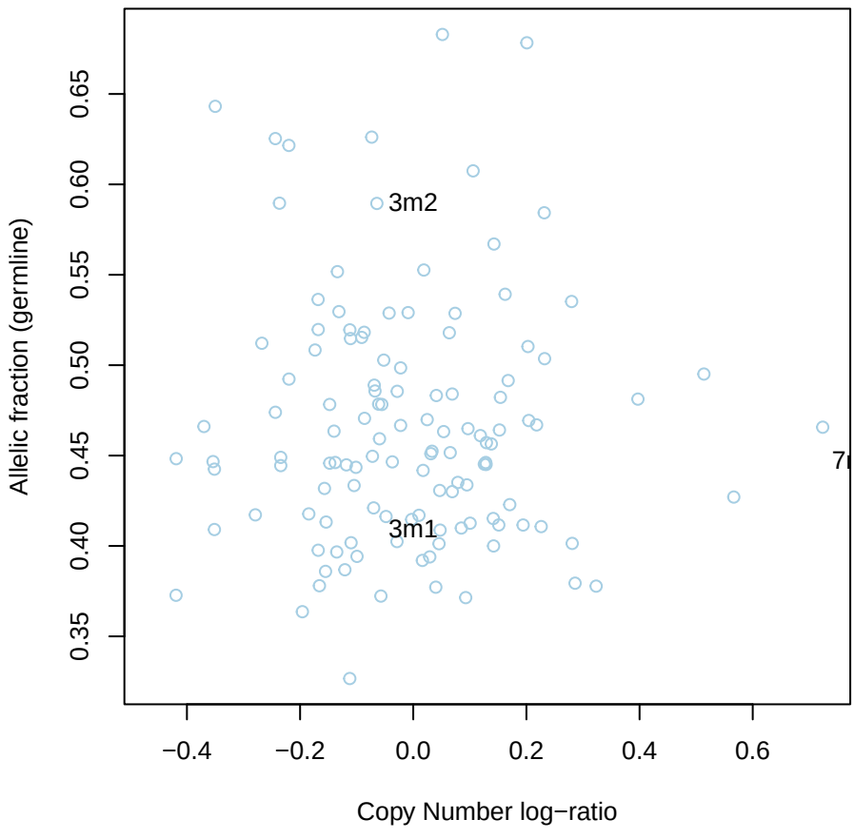

Power 0.8
Frequency
0
50
100
150
0.2
0.4
0.6
0.8
1.0
Cellular fraction

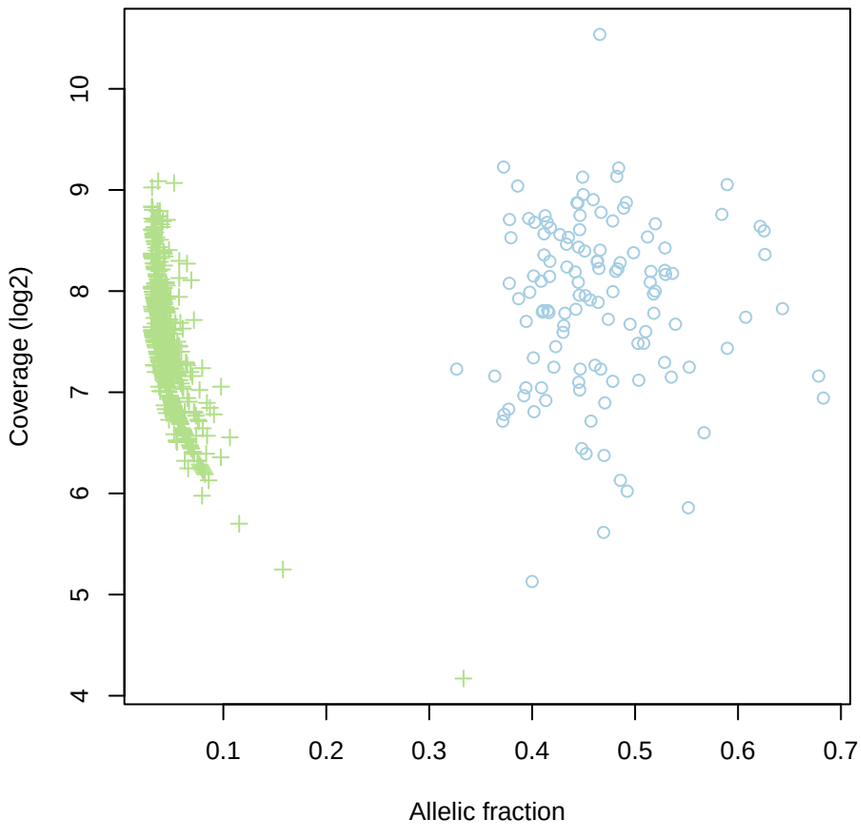

Purity: 0.44 Tumor ploidy: 3
3
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.2
0.4
0.6
0.8
log2 ratio

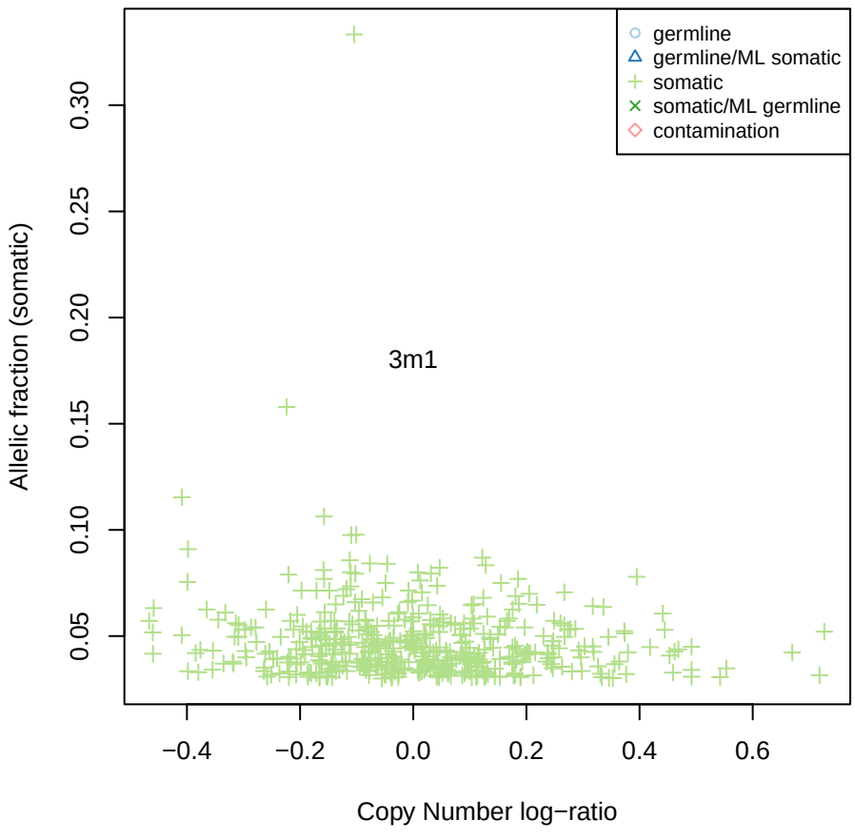

Purity: 0.44 Tumor ploidy: 3 SNV log−likelihood: −129.22 GoF: 63.5% Mean coverage: 353;215
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 20
B−Allele Frequency
0.35 0.45 0.55 0.65
0 20 40 60 80 100 120
SNV Index

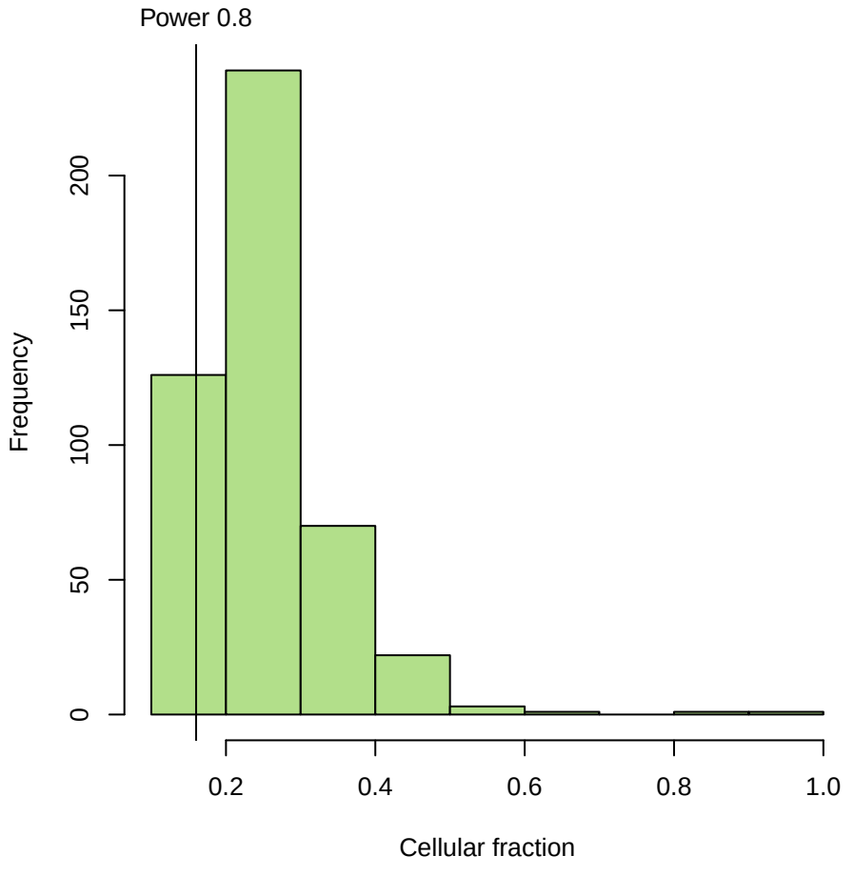

SCNA−fit log−likelihood: −7431.97
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
7
3
0 20 40 60 80 100 120
SNV Index

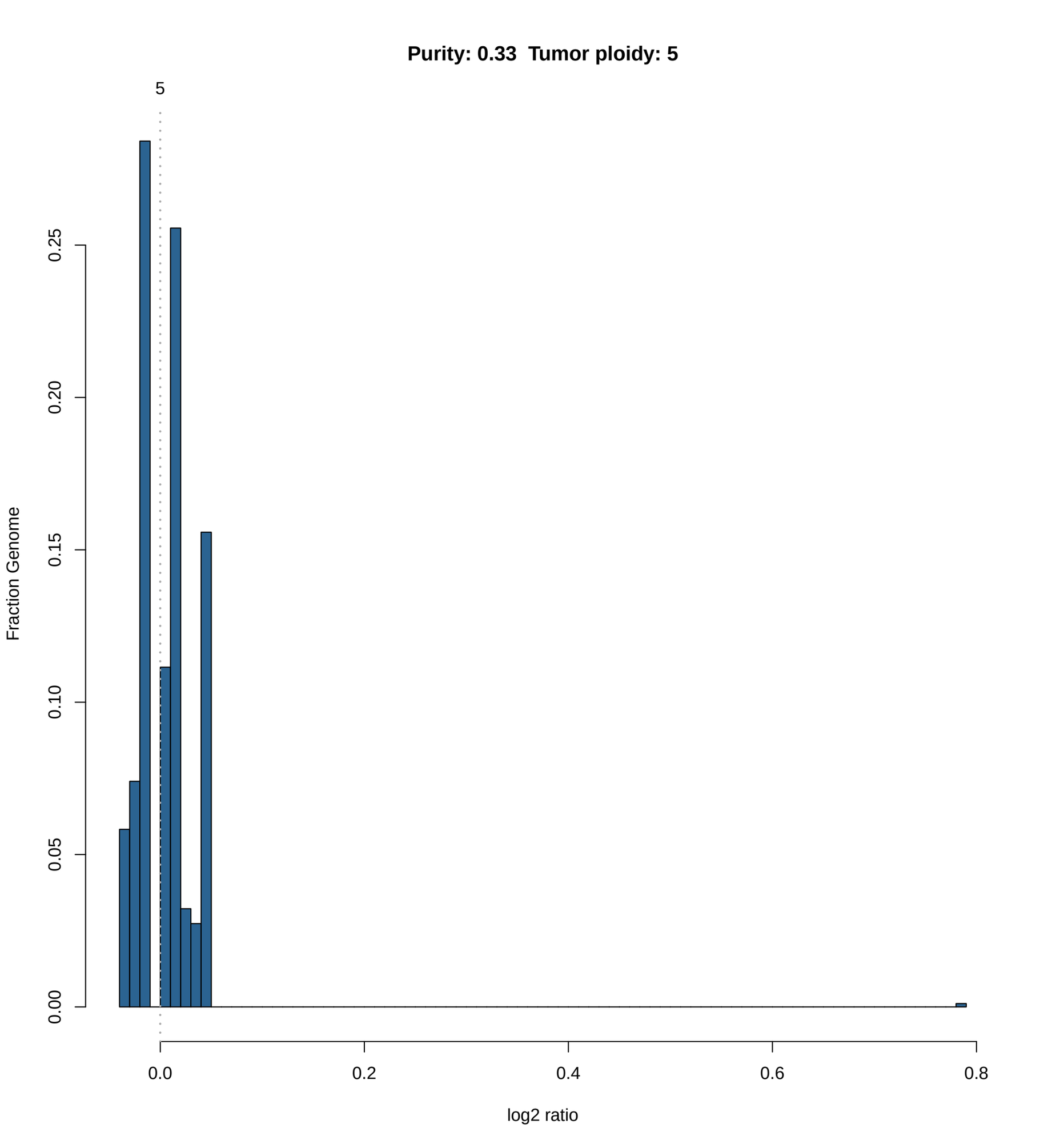

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

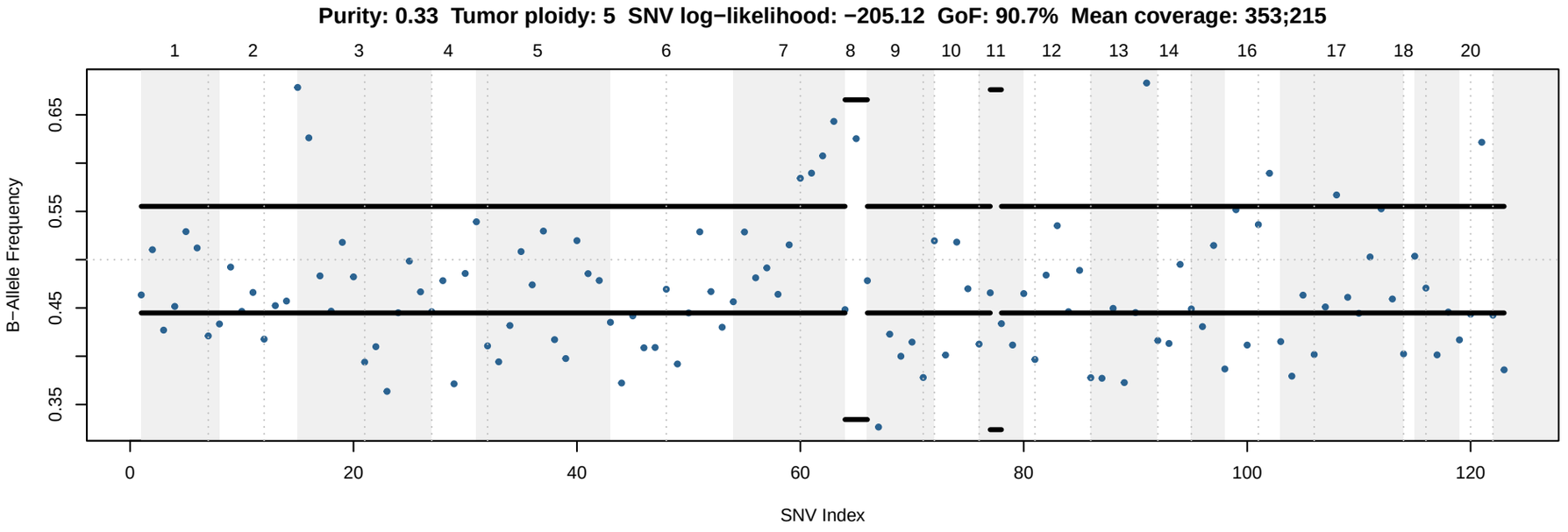

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
3m2
3m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

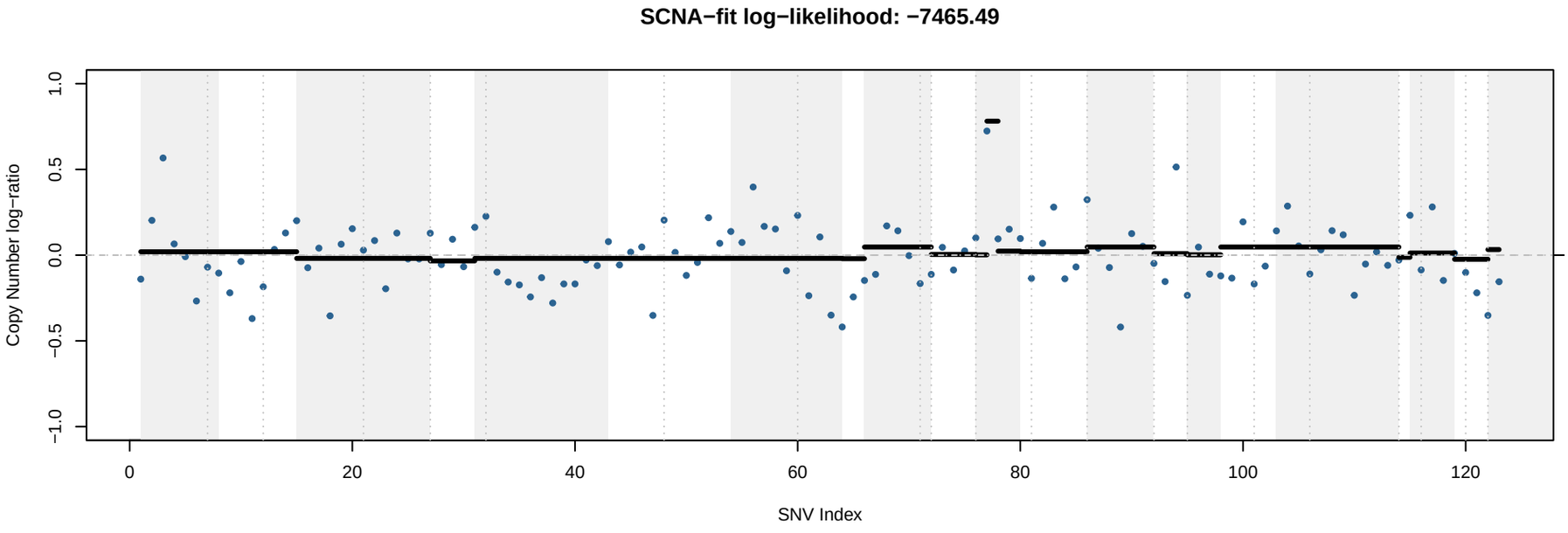

Coverage (log2)
4
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

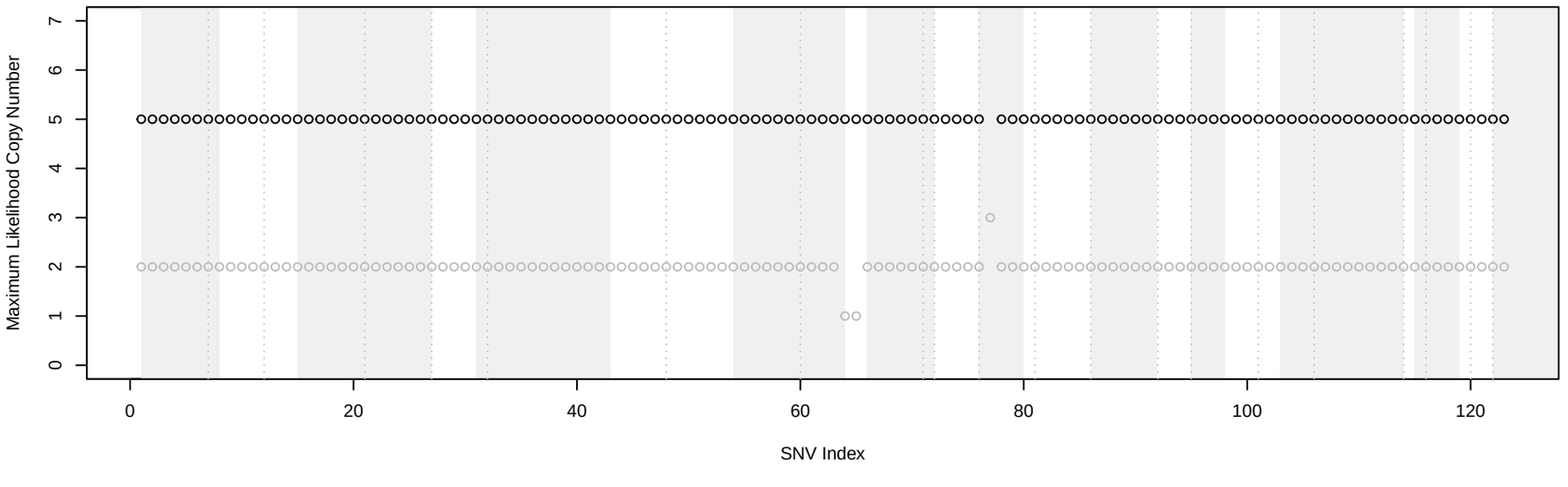

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0.30
3m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

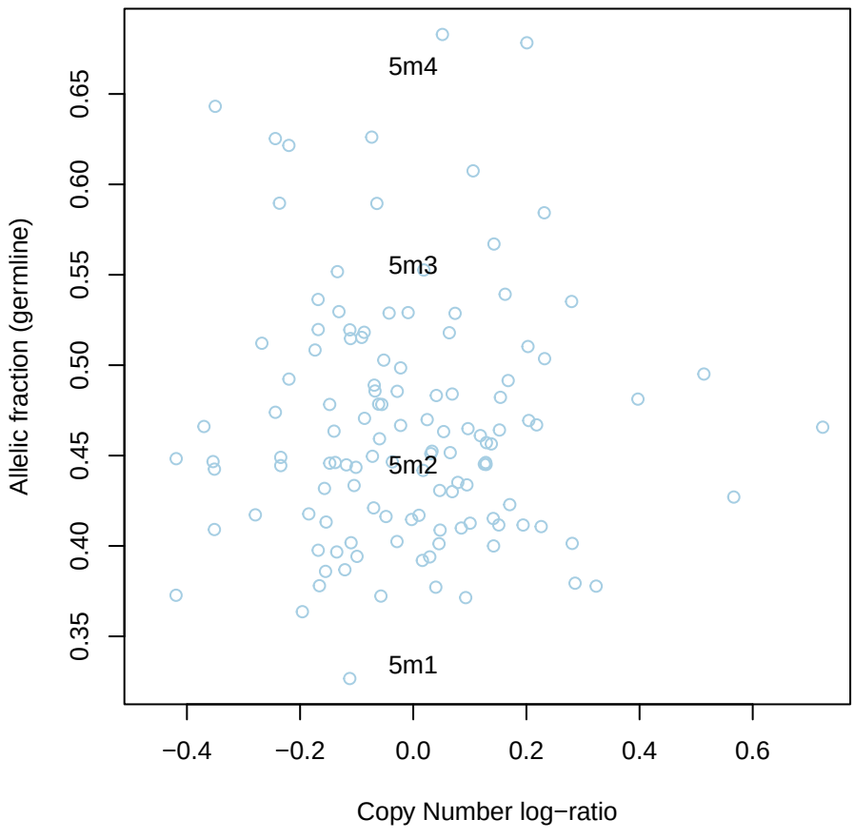

Power 0.8
Frequency
0
50
100
150
200
0.2
0.4
0.6
0.8
1.0
Cellular fraction

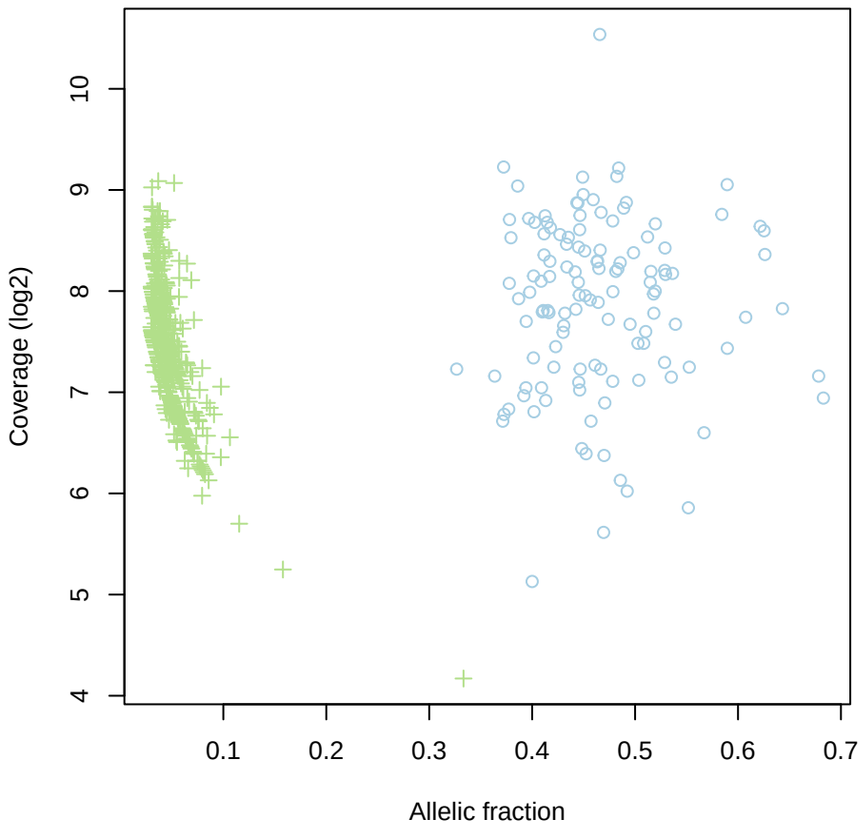

Purity: 0.33 Tumor ploidy: 5
5
Fraction Genome
0.00
0.05
0.10
0.15
0.20
0.25
0.0
0.2
0.4
0.6
0.8
log2 ratio

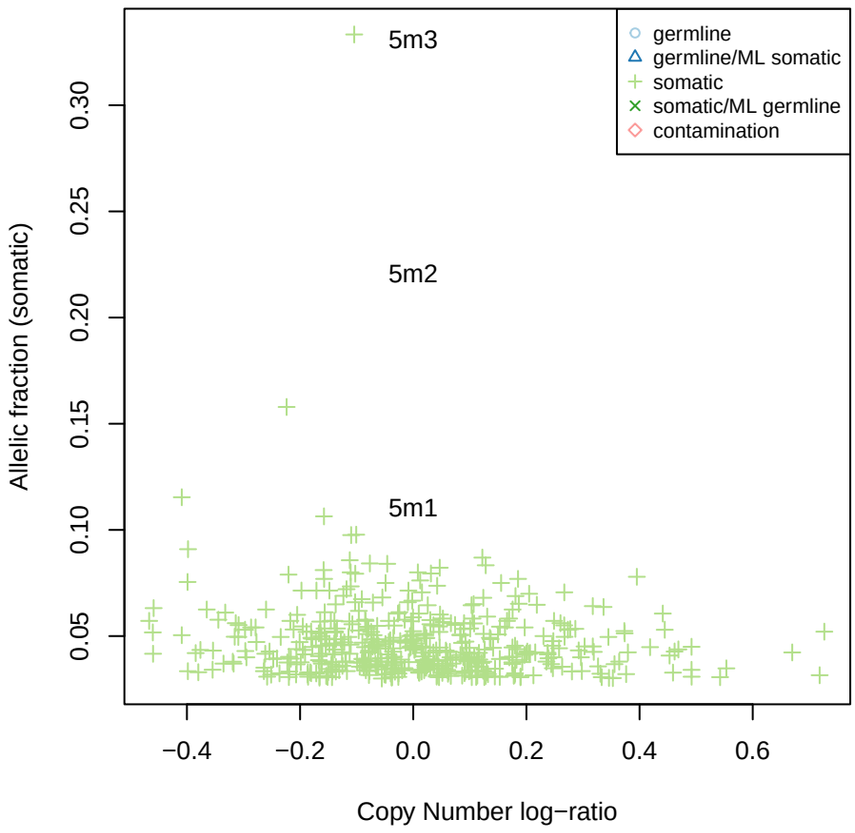

Purity: 0.33 Tumor ploidy: 5 SNV log−likelihood: −205.12 GoF: 90.7% Mean coverage: 353;215
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 20
B−Allele Frequency
0.35 0.45 0.55 0.65
0 20 40 60 80 100 120
SNV Index

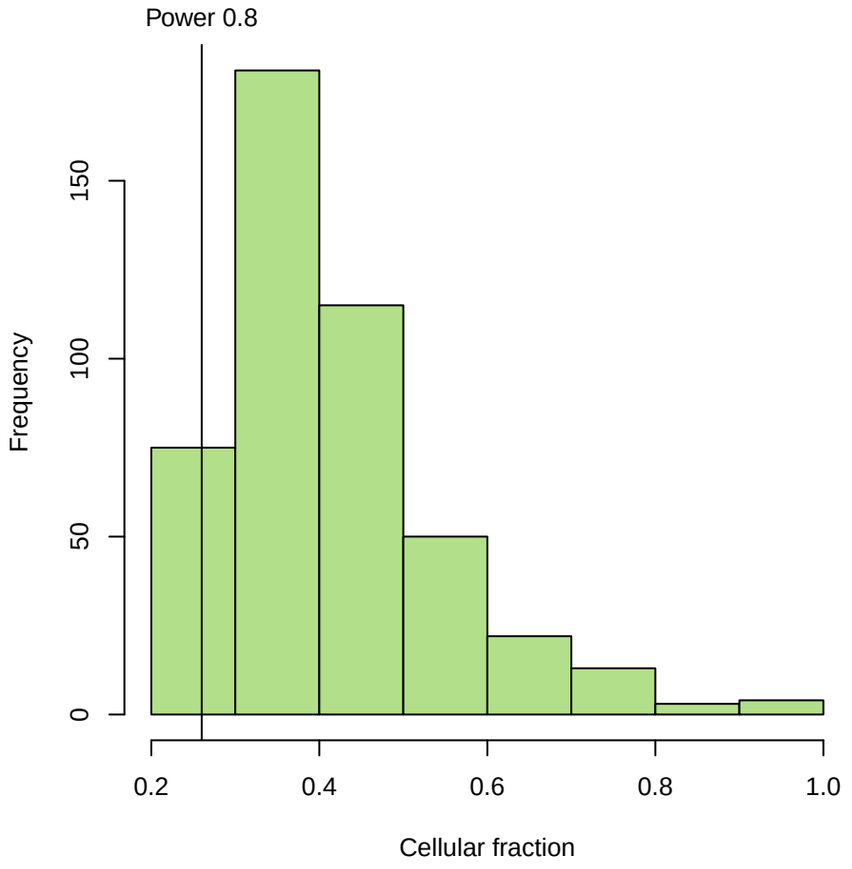

SCNA−fit log−likelihood: −7465.49
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
5
0 20 40 60 80 100 120
SNV Index

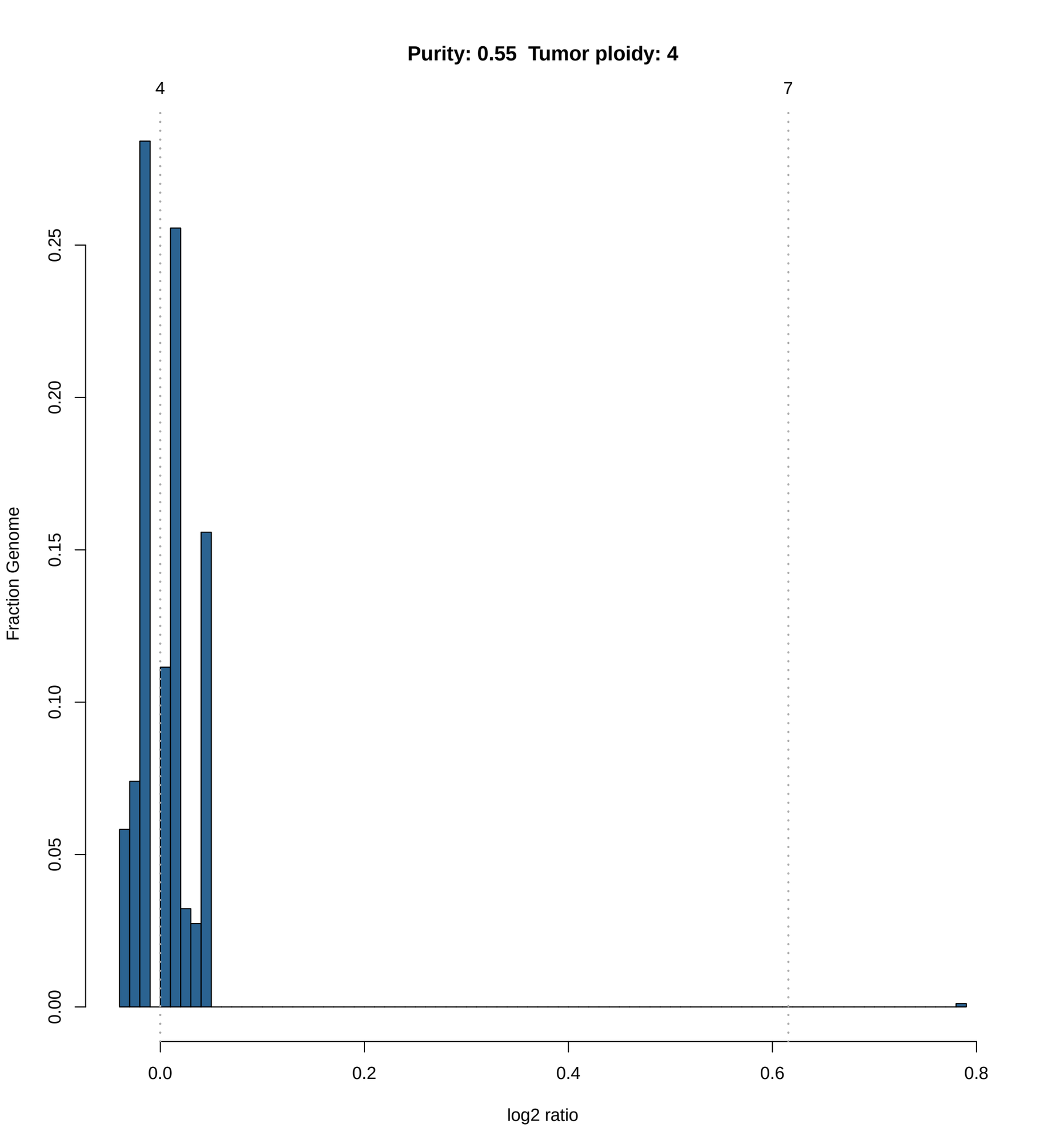

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

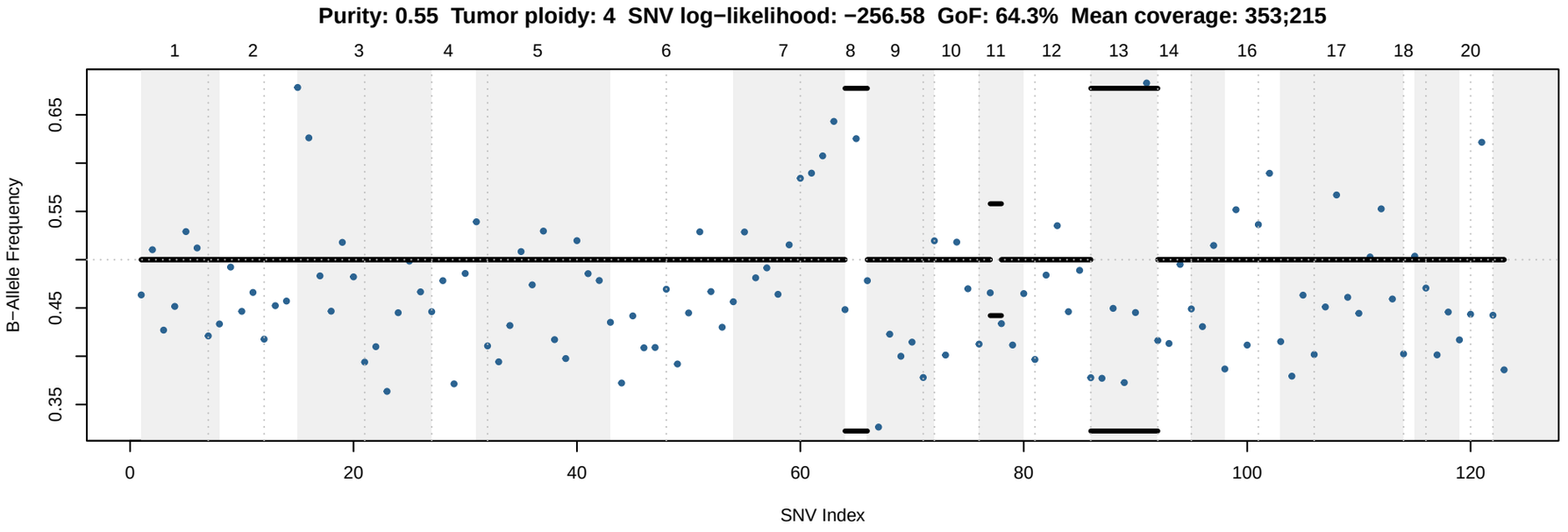

5m4
5m3
5m2
5m1
Allelic fraction (germline)
Copy Number log−ratio

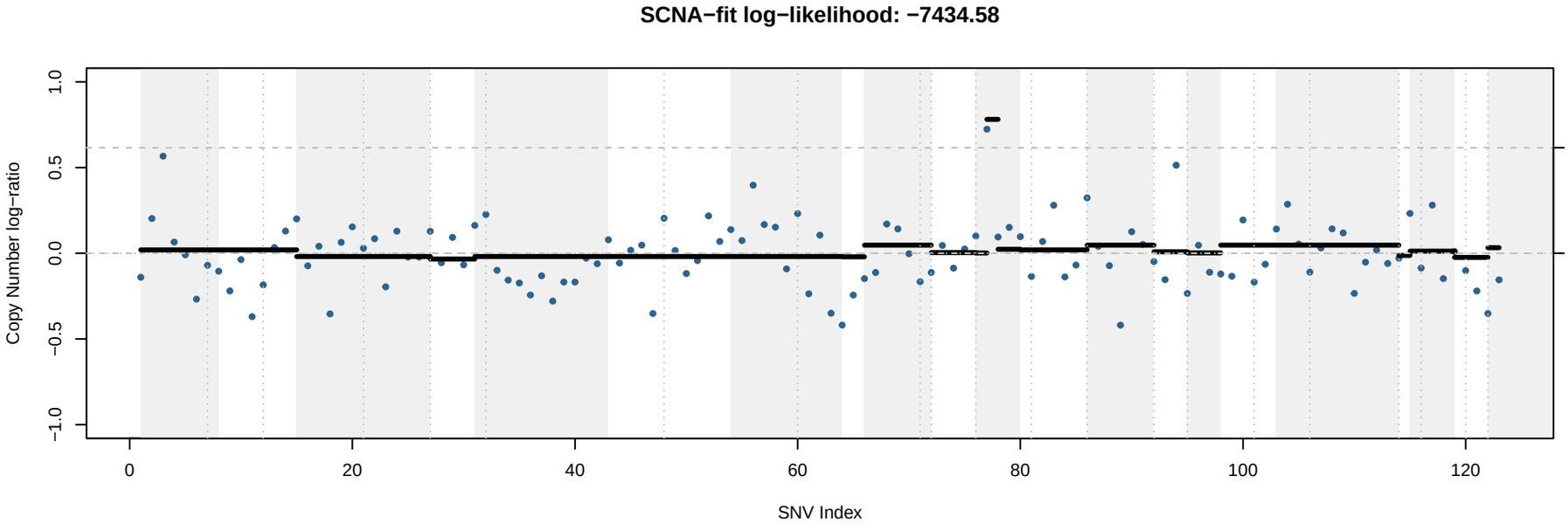

Coverage (log2)
Allelic fraction

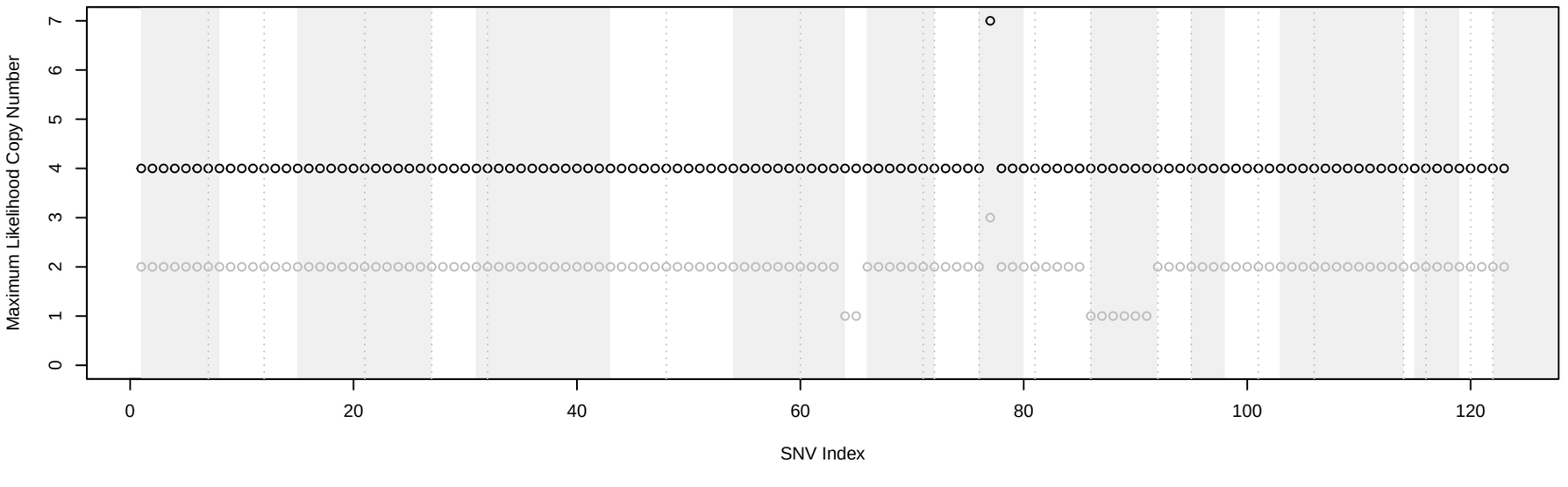

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m3
5m2
5m1
Allelic fraction (somatic)
Copy Number log−ratio

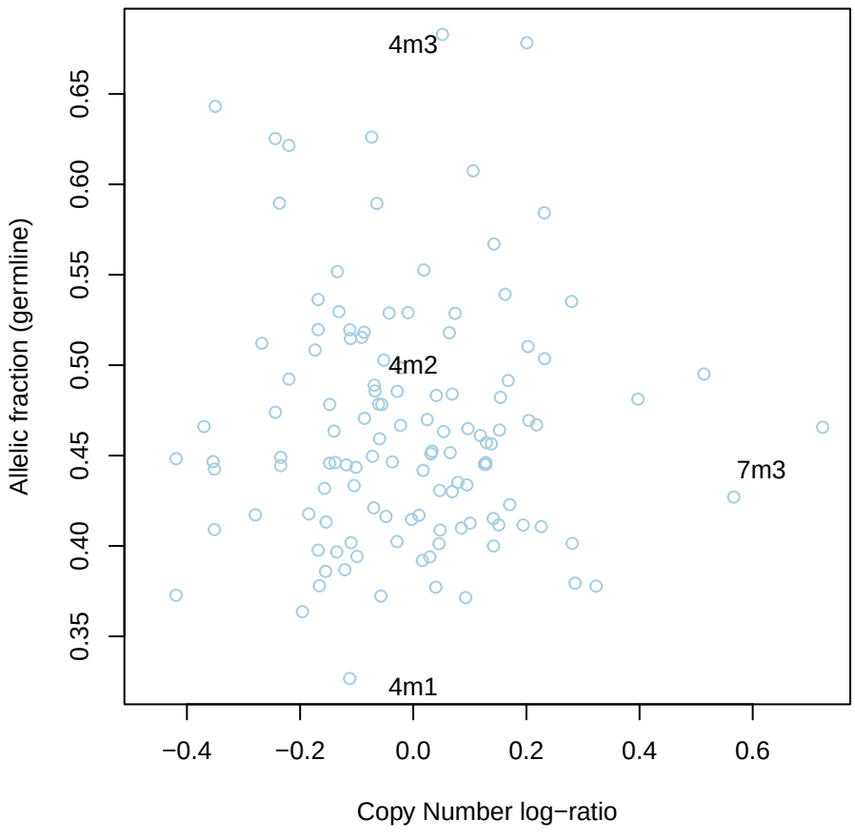

Power 0.8
Frequency
Cellular fraction

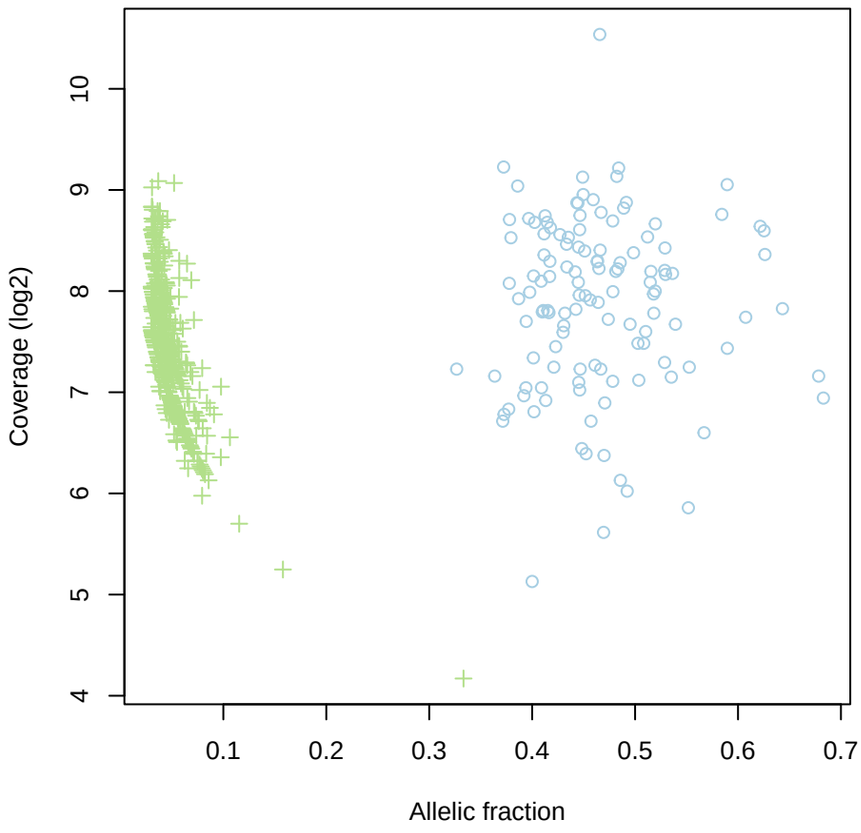

Purity: 0.55 Tumor ploidy: 4
4
7
Fraction Genome
0.00
0.05
0.10
0.15
0.20
0.25
0.0
0.2
0.4
0.6
0.8
log2 ratio

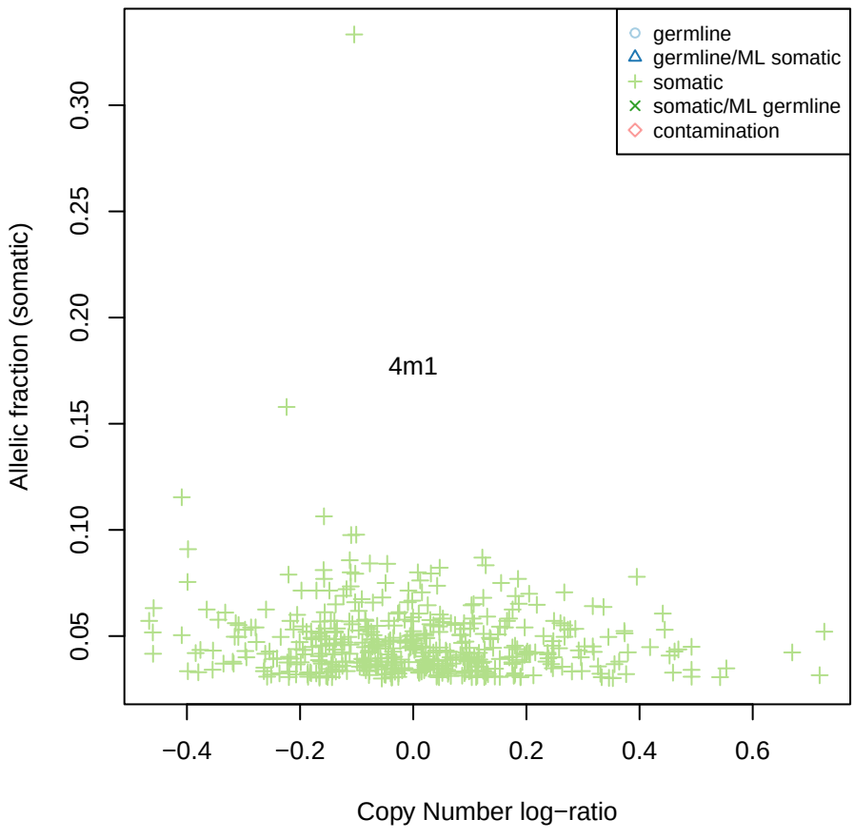

Purity: 0.55 Tumor ploidy: 4 SNV log−likelihood: −256.58 GoF: 64.3% Mean coverage: 353;215
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 20
B−Allele Frequency
0.35 0.45 0.55 0.65
0 20 40 60 80 100 120
SNV Index

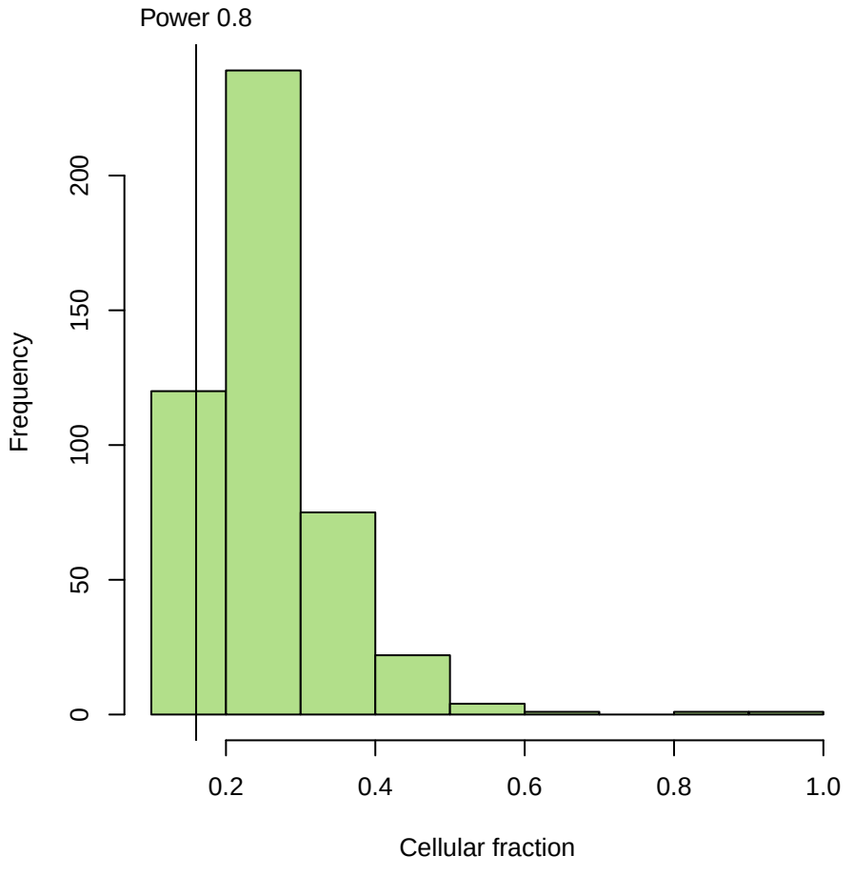

SCNA−fit log−likelihood: −7434.58
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
7
4
0 20 40 60 80 100 120
SNV Index

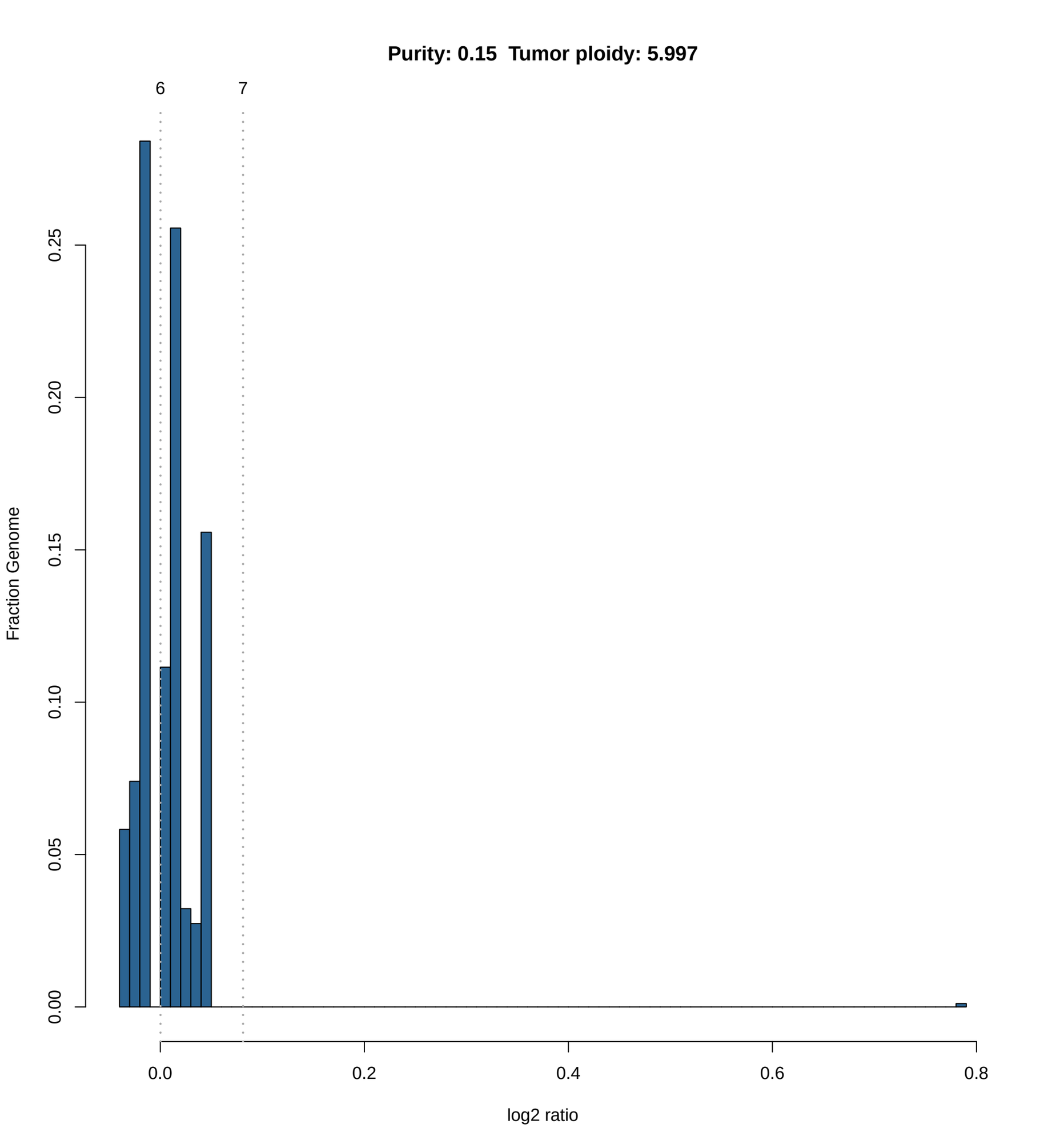

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

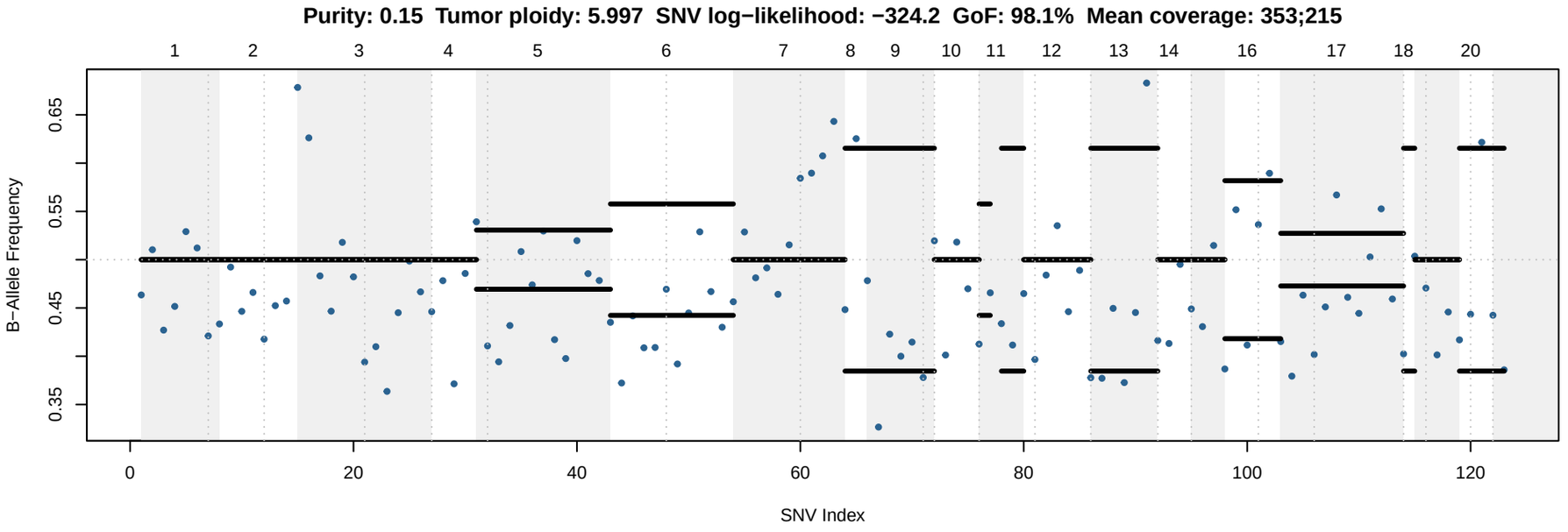

4m3
4m2
7m3
4m1
Allelic fraction (germline)
Copy Number log−ratio

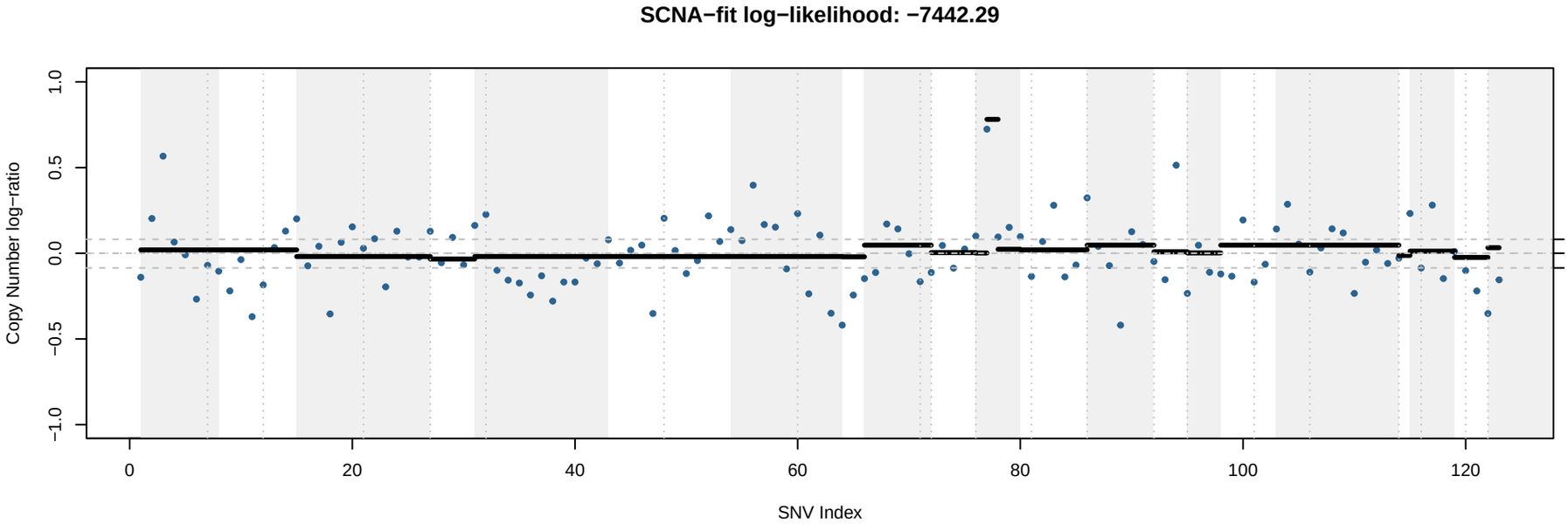

Coverage (log2)
Allelic fraction

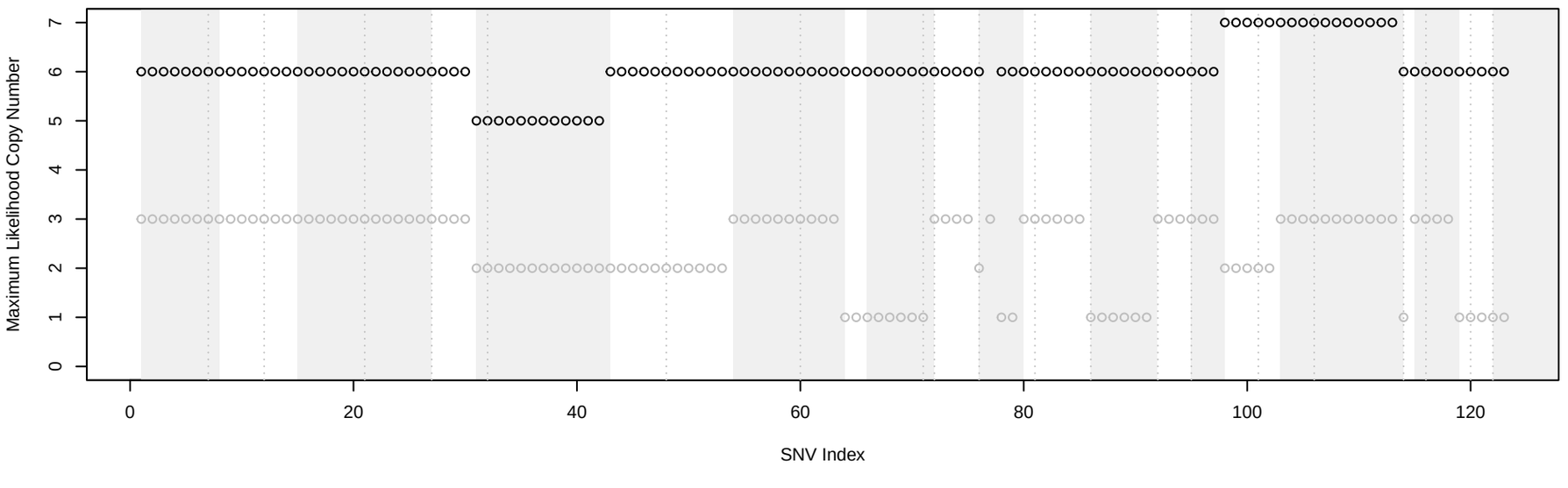

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
Allelic fraction (somatic)
Copy Number log−ratio

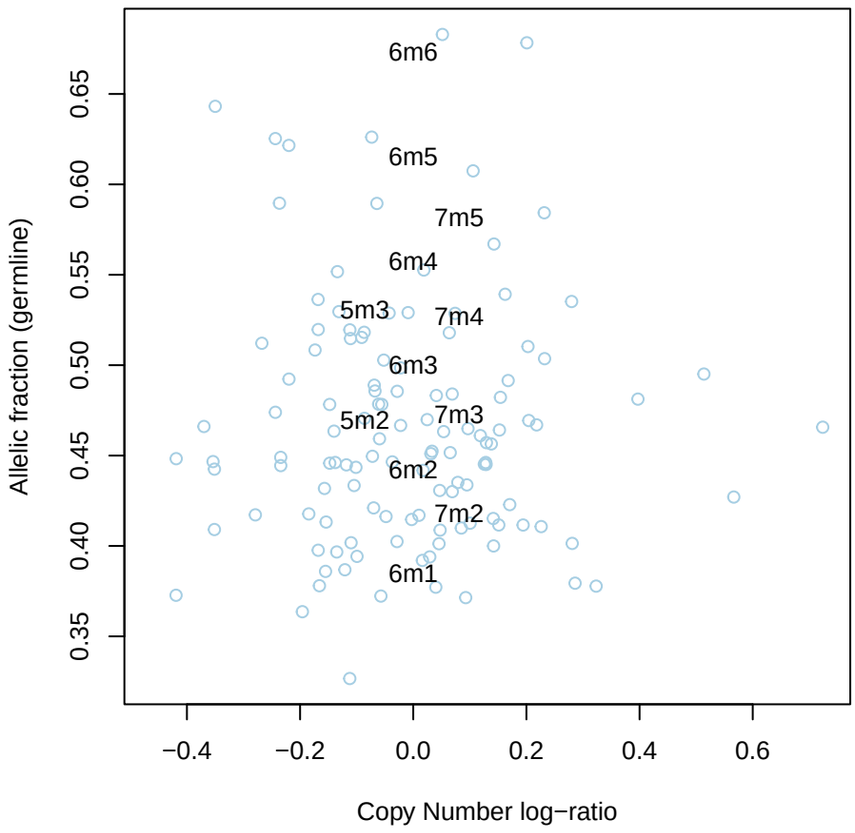

Power 0.8
Frequency
Cellular fraction

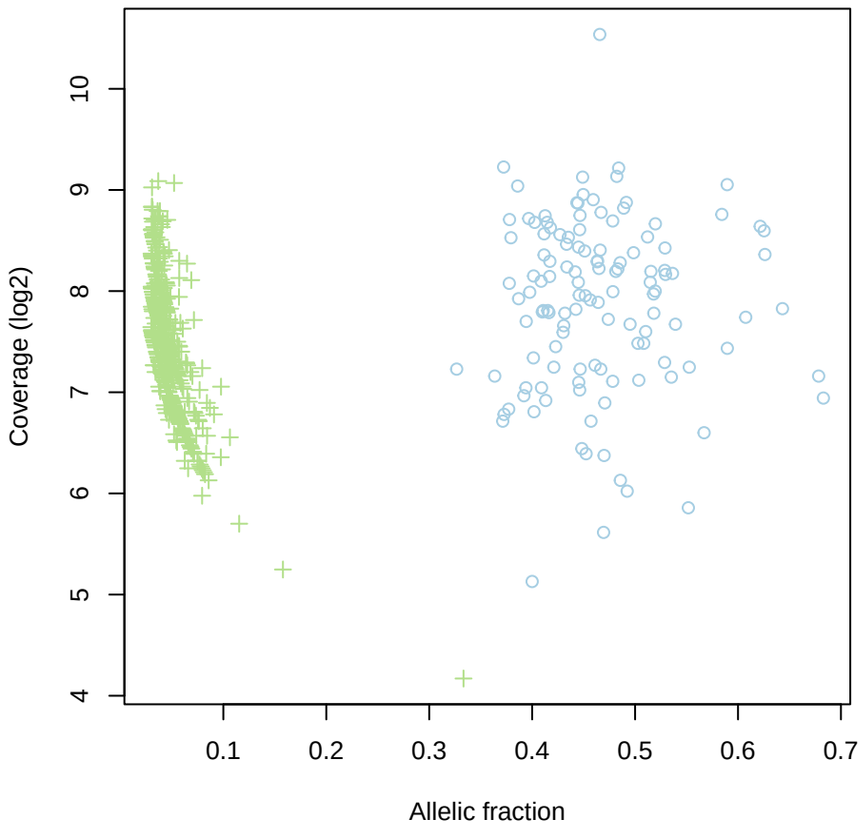

Purity: 0.15 Tumor ploidy: 5.997
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.2
0.4
0.6
0.8
log2 ratio

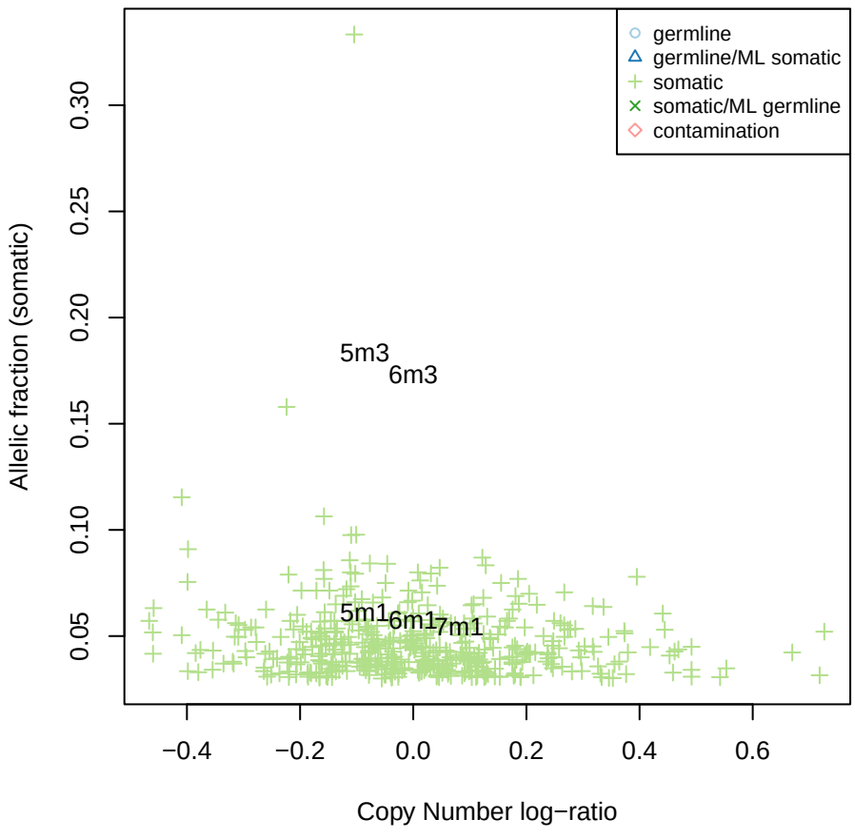

Purity: 0.15 Tumor ploidy: 5.997 SNV log−likelihood: −324.2 GoF: 98.1% Mean coverage: 353;215
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 20
B−Allele Frequency
0.35 0.45 0.55 0.65
0 20 40 60 80 100 120
SNV Index

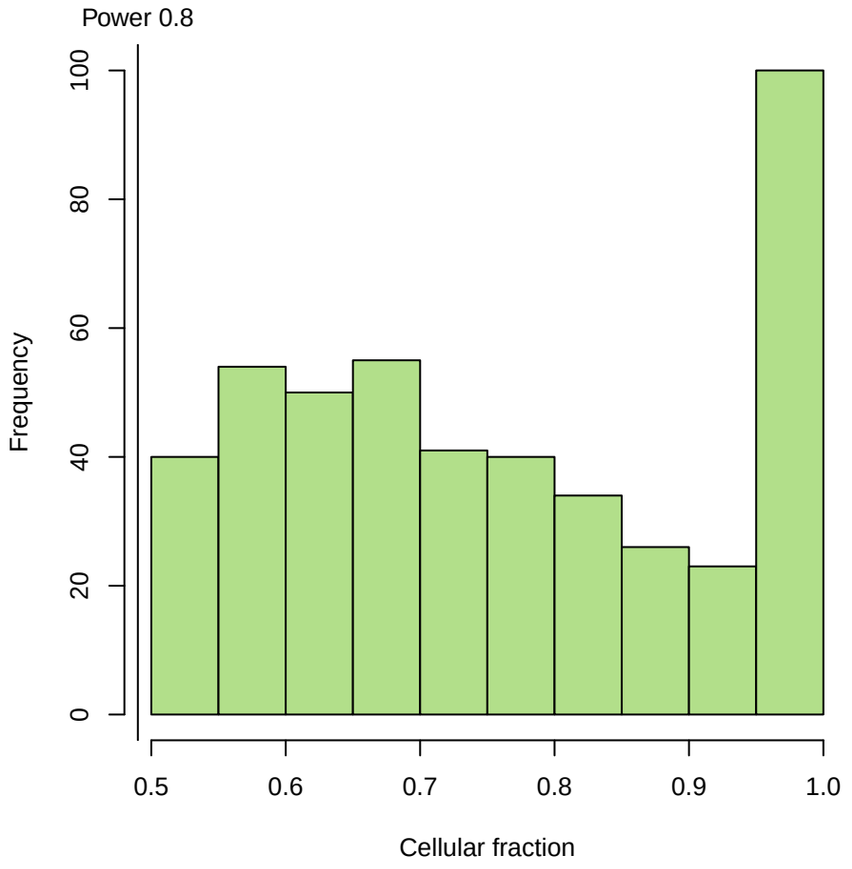

SCNA−fit log−likelihood: −7442.29
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
5 7
0 20 40 60 80 100 120
SNV Index

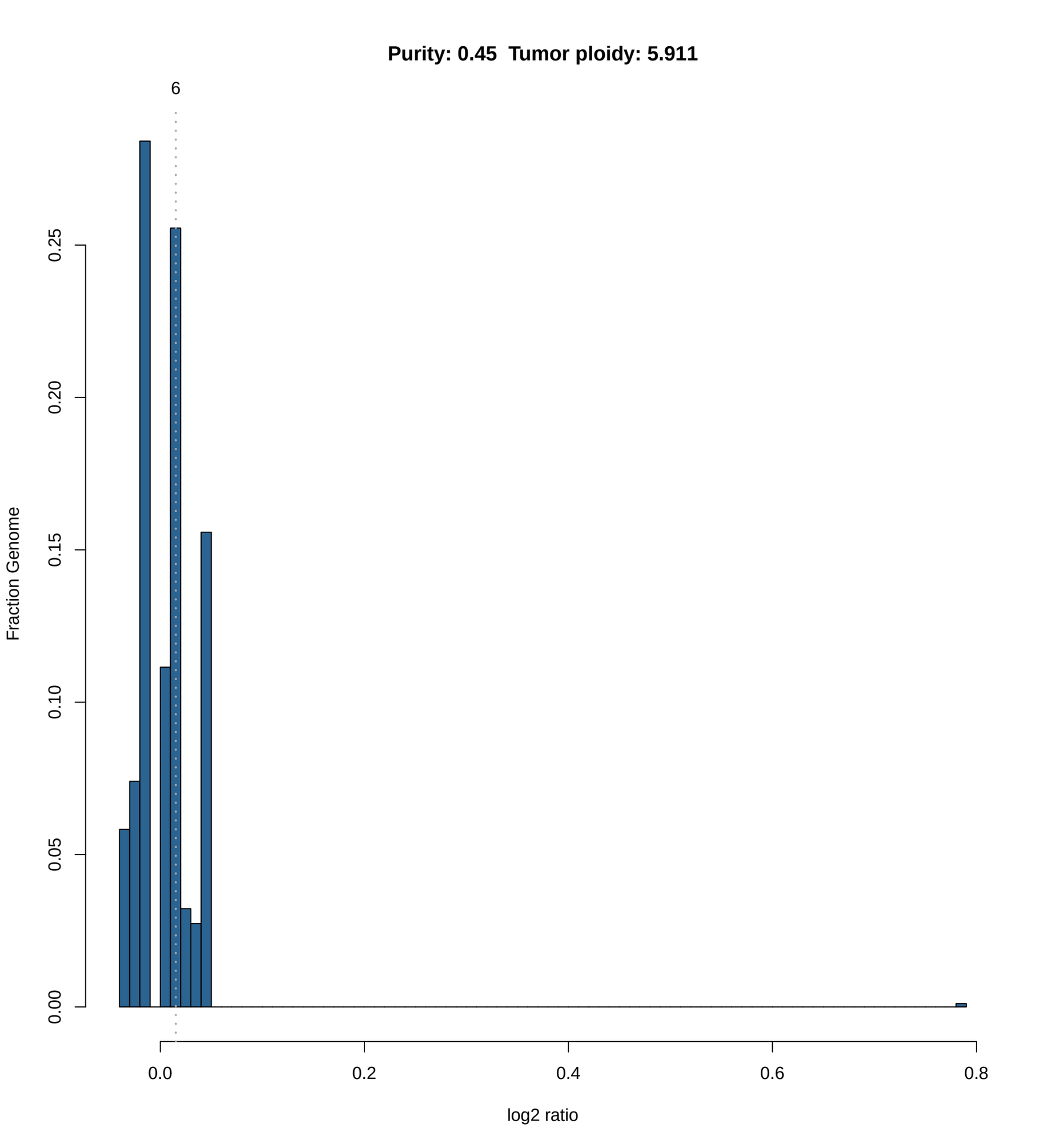

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

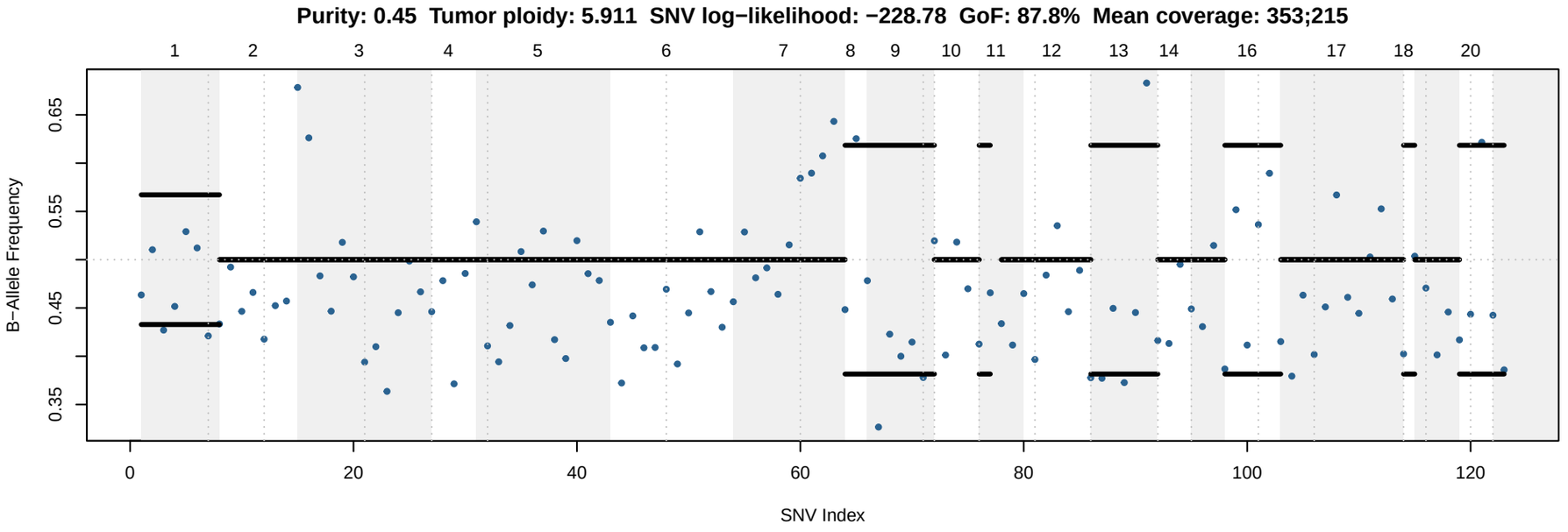

6m6
6m5
7m5
6m4
5m3
7m4
6m3
5m2
7m3
6m2
7m2
6m1
Allelic fraction (germline)
Copy Number log−ratio

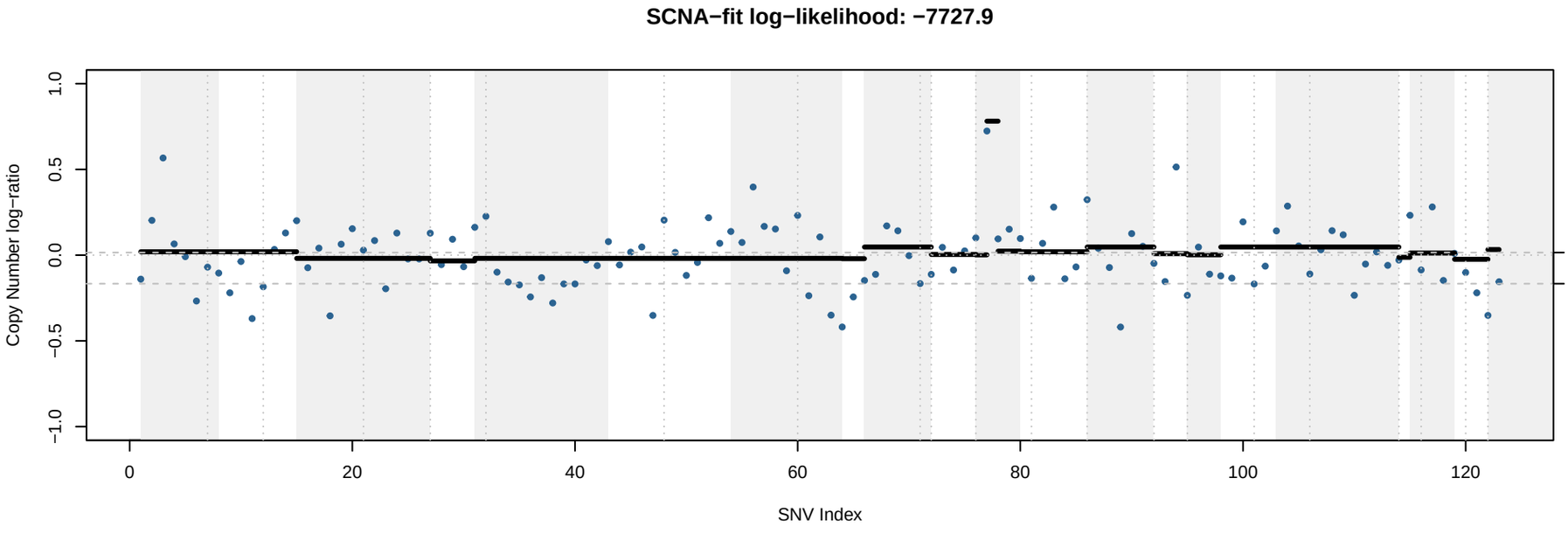

Coverage (log2)
Allelic fraction

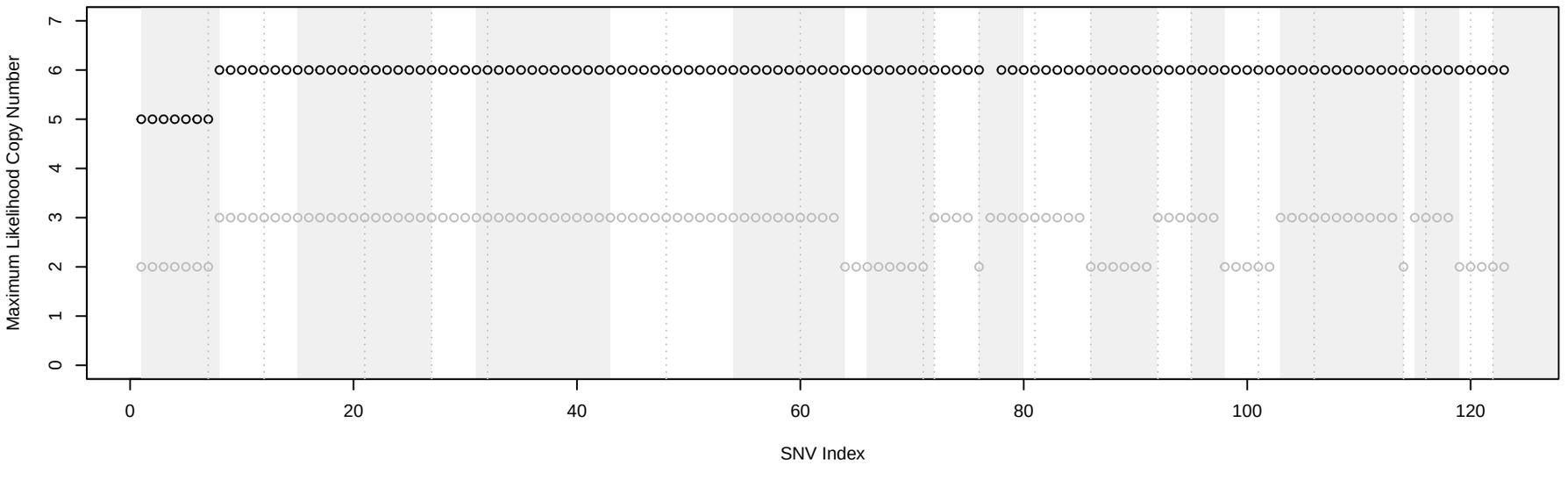

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m3
6m3
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

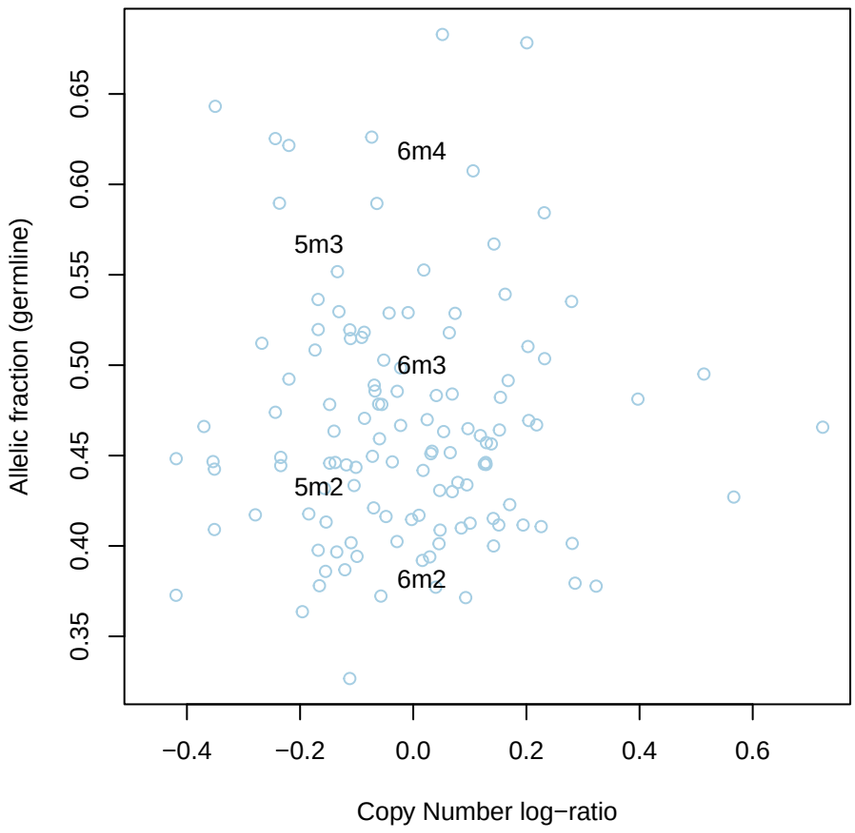

Power 0.8
Frequency
Cellular fraction

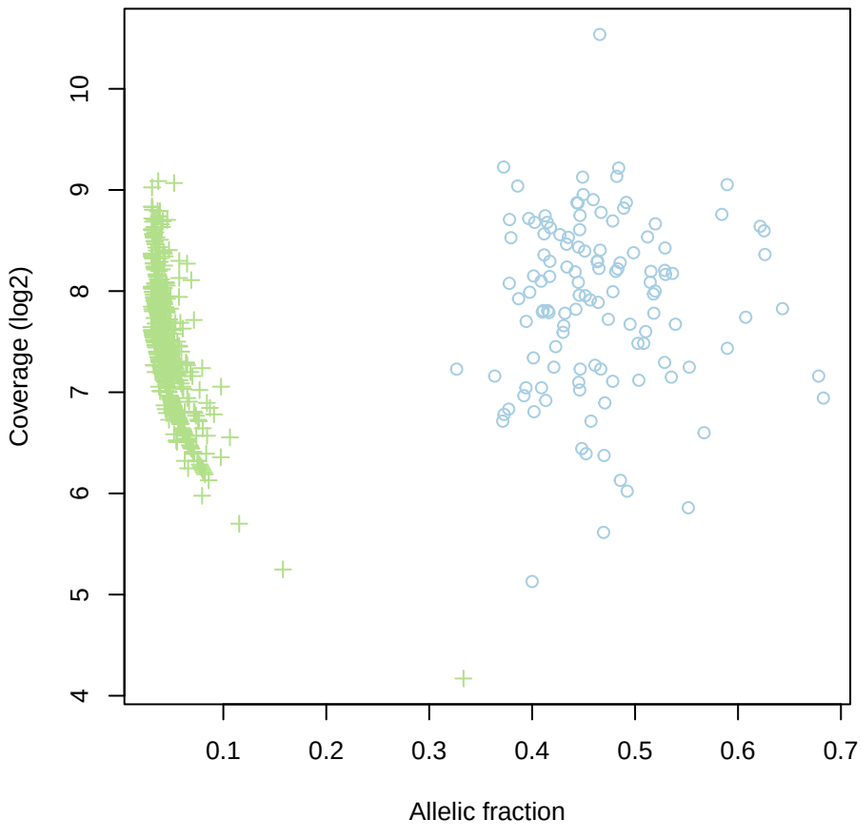

Purity: 0.45 Tumor ploidy: 5.911
6
Fraction Genome
0.00
0.05
0.10
0.15
0.20
0.25
0.0
0.2
0.4
0.6
0.8
log2 ratio

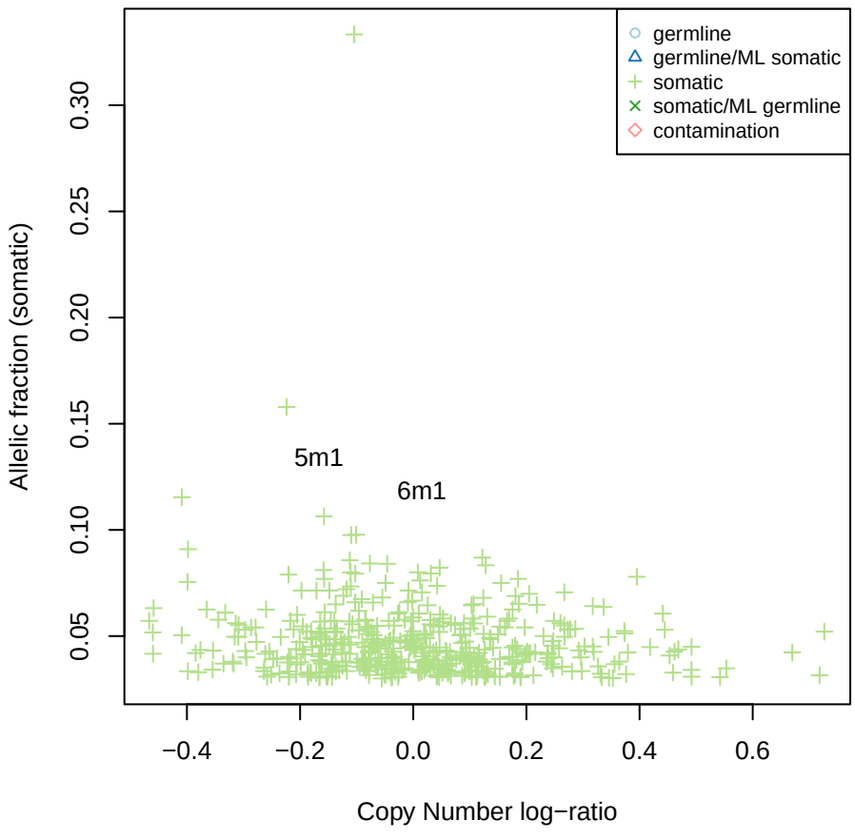

Purity: 0.45 Tumor ploidy: 5.911 SNV log−likelihood: −228.78 GoF: 87.8% Mean coverage: 353;215
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 20
B−Allele Frequency
0.35 0.45 0.55 0.65
0 20 40 60 80 100 120
SNV Index

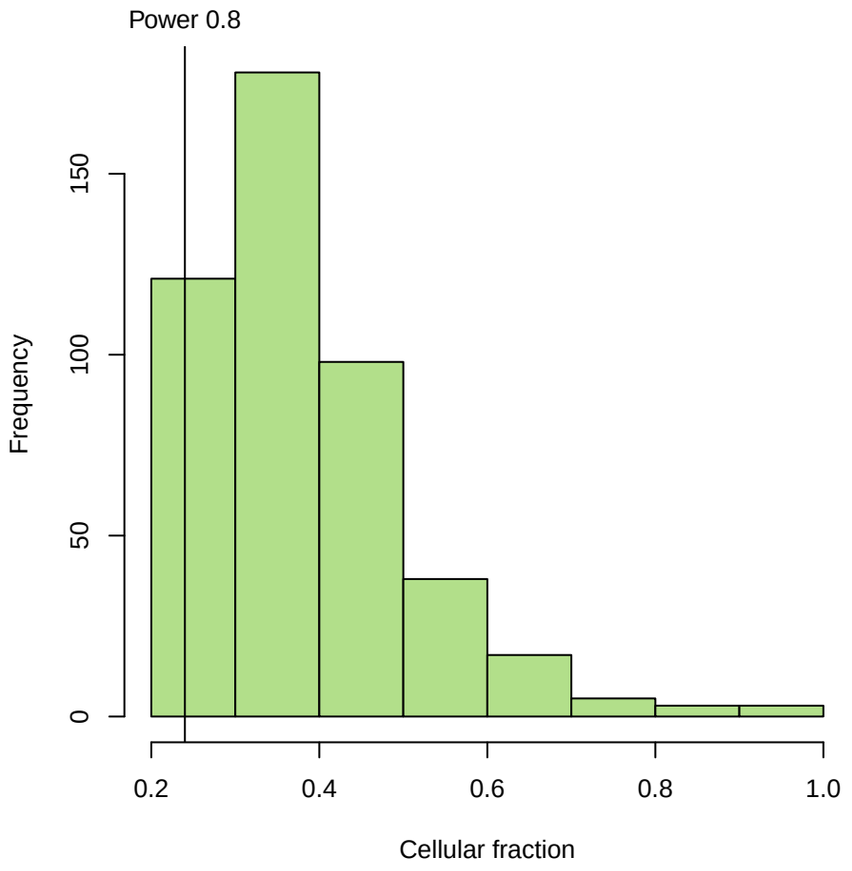

SCNA−fit log−likelihood: −7727.9
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
6
5
0 20 40 60 80 100 120
SNV Index

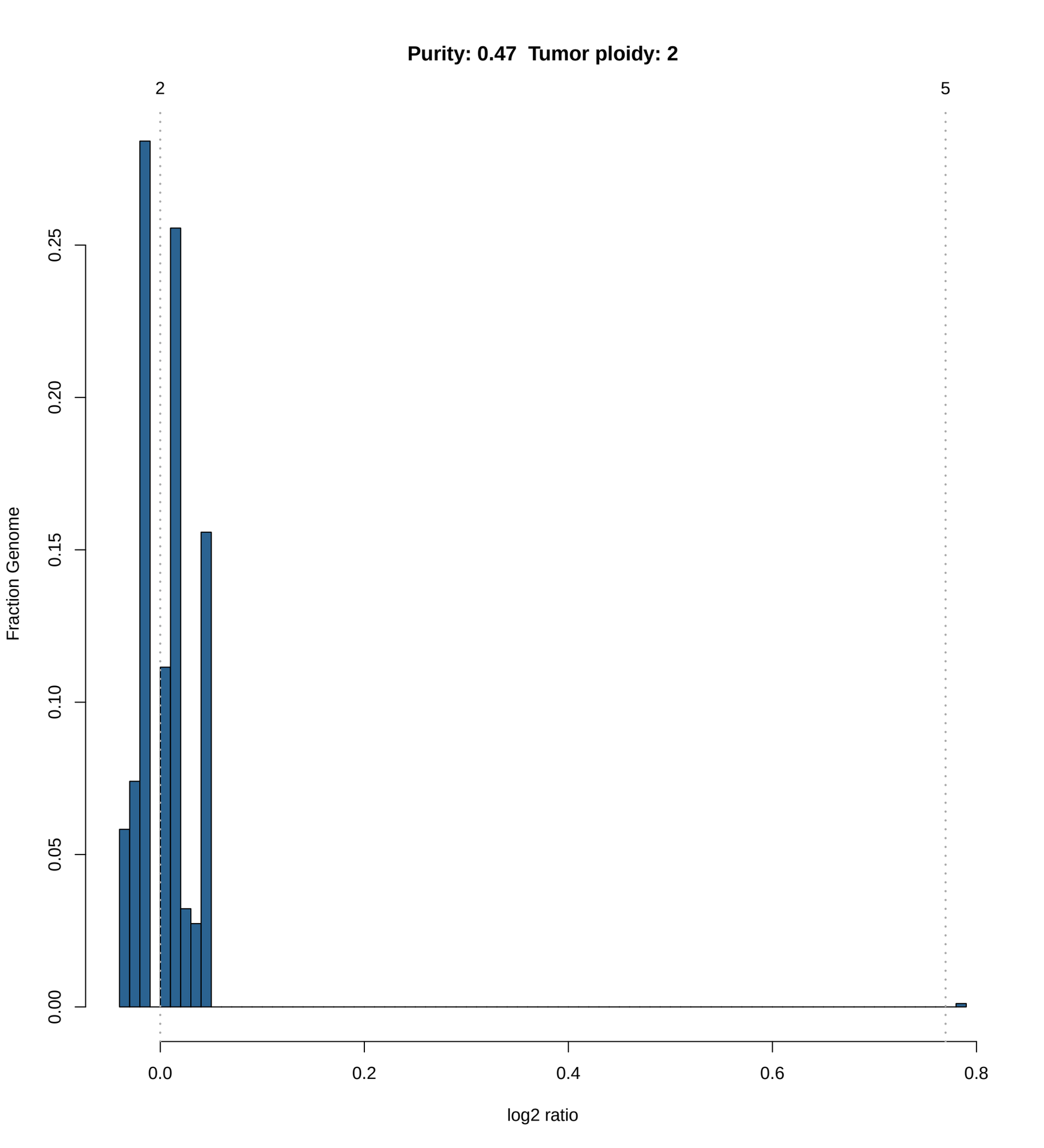

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

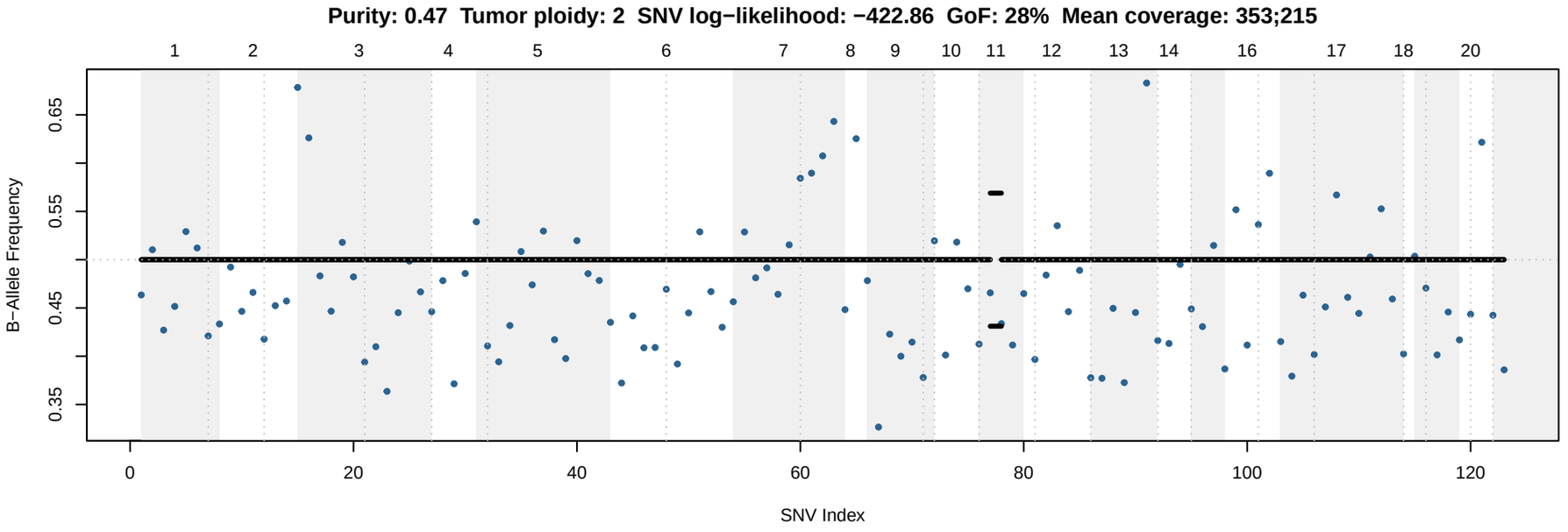

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
6m4
5m3
6m3
5m2
6m2
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

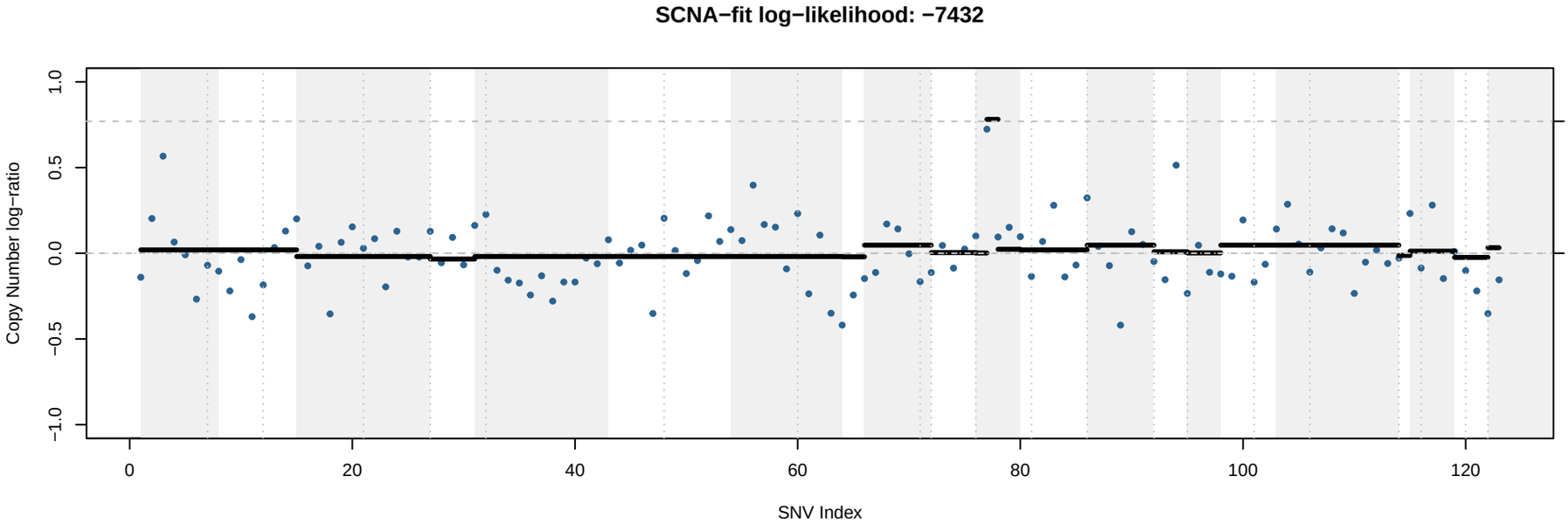

Coverage (log2)
4
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

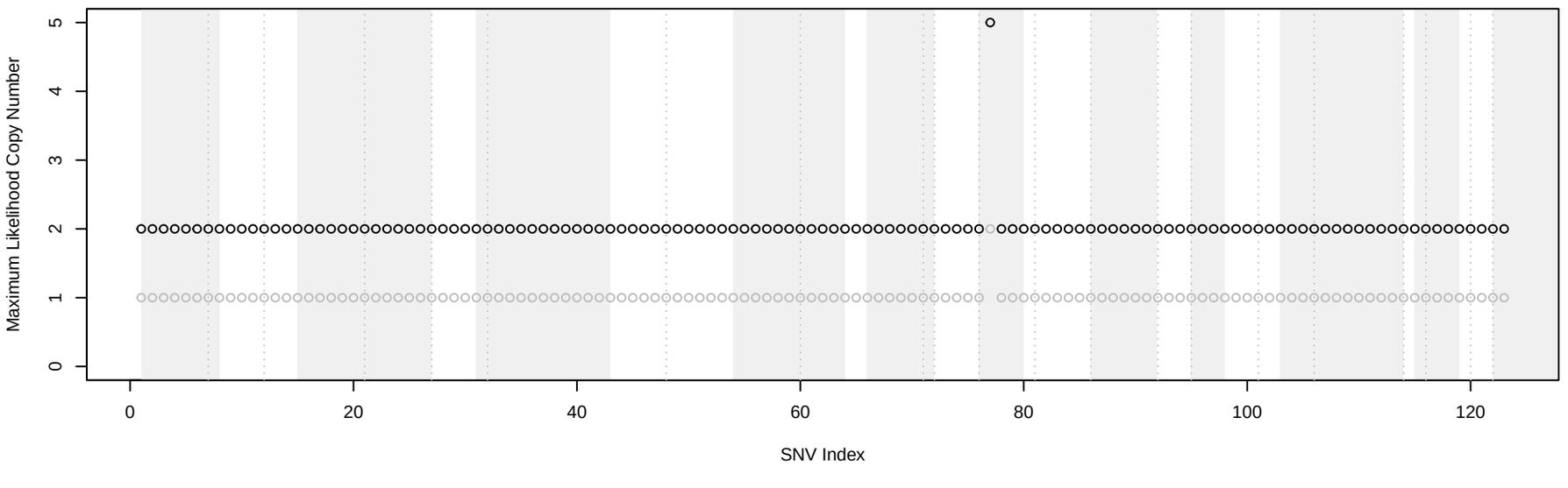

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0.30
5m1
6m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

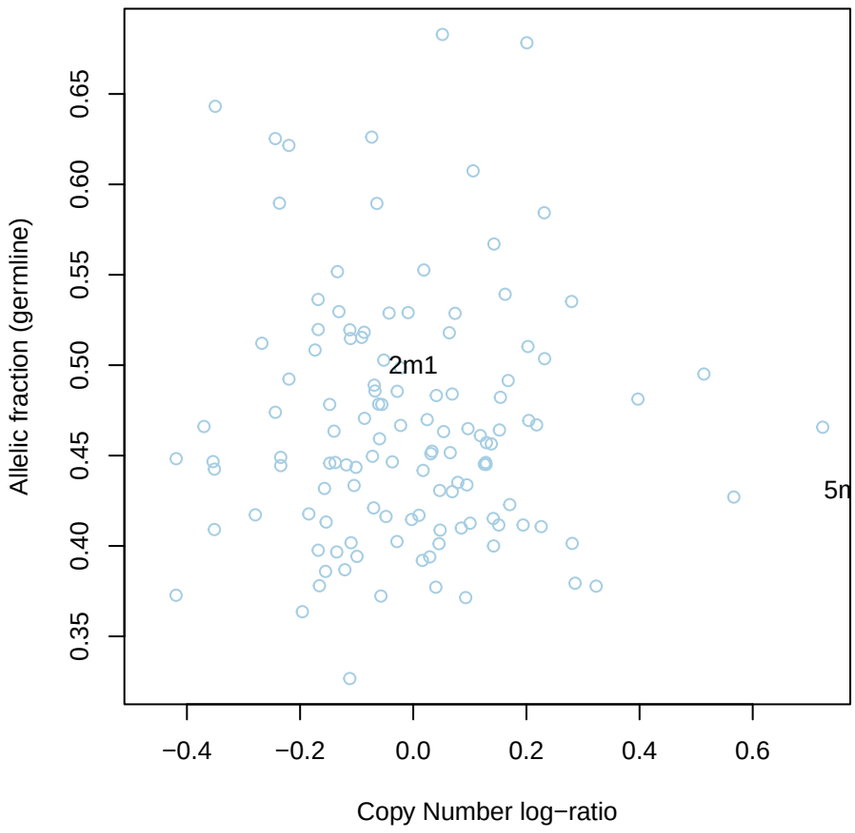

Power 0.8
Frequency
0
50
100
150
0.2
0.4
0.6
0.8
1.0
Cellular fraction

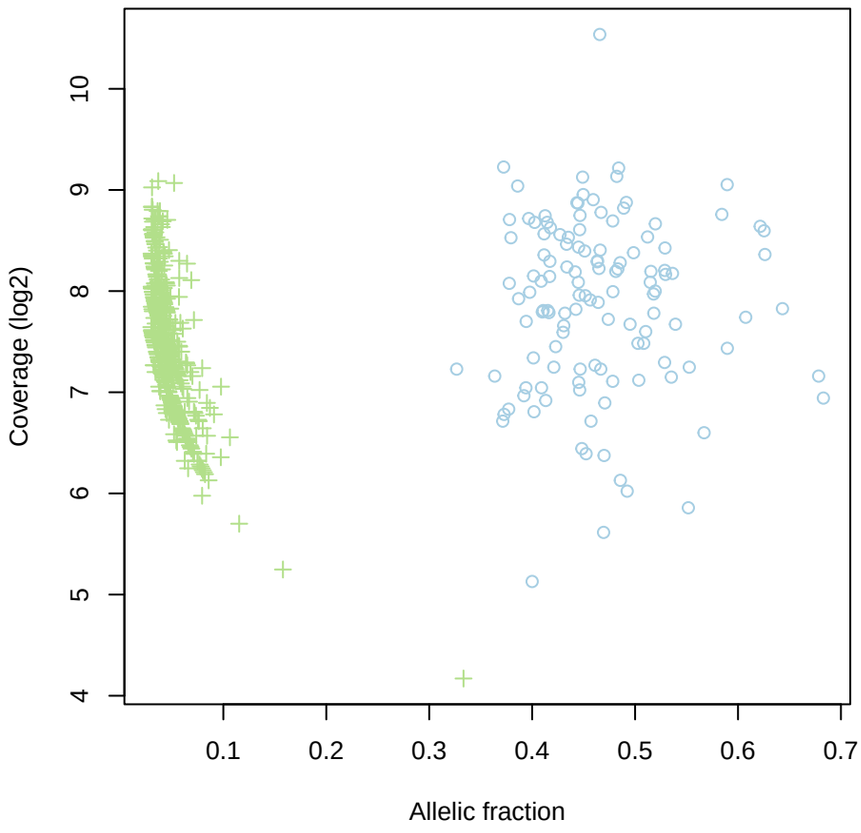

Purity: 0.47 Tumor ploidy: 2
2
5
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.2
0.4
0.6
0.8
log2 ratio

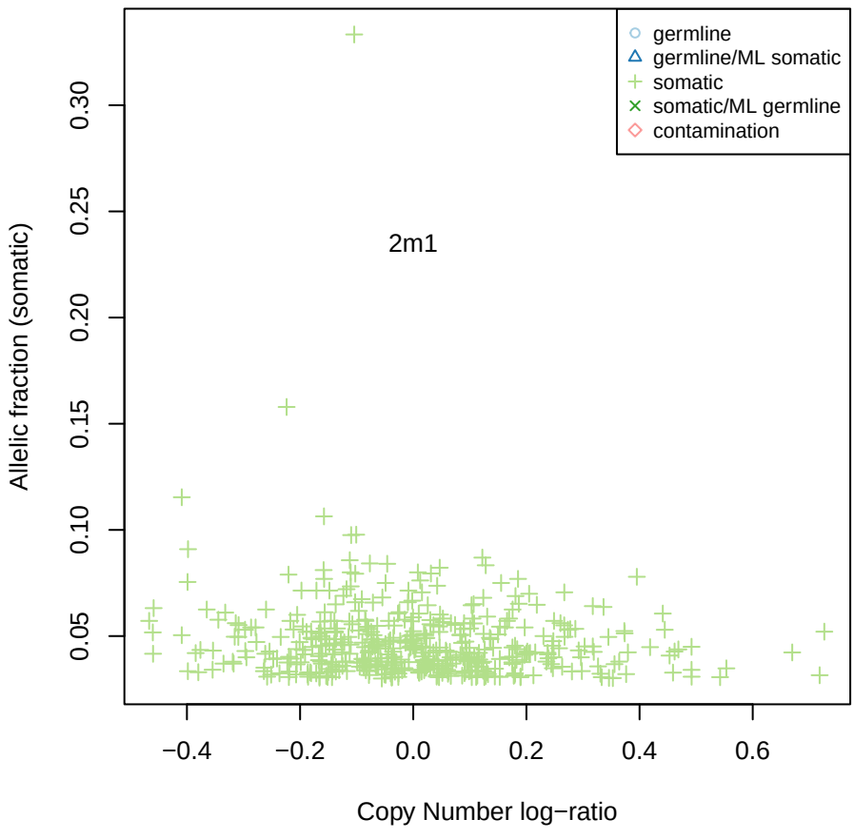

Purity: 0.47 Tumor ploidy: 2 SNV log−likelihood: −422.86 GoF: 28% Mean coverage: 353;215
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 20
B−Allele Frequency
0.35 0.45 0.55 0.65
0 20 40 60 80 100 120
SNV Index

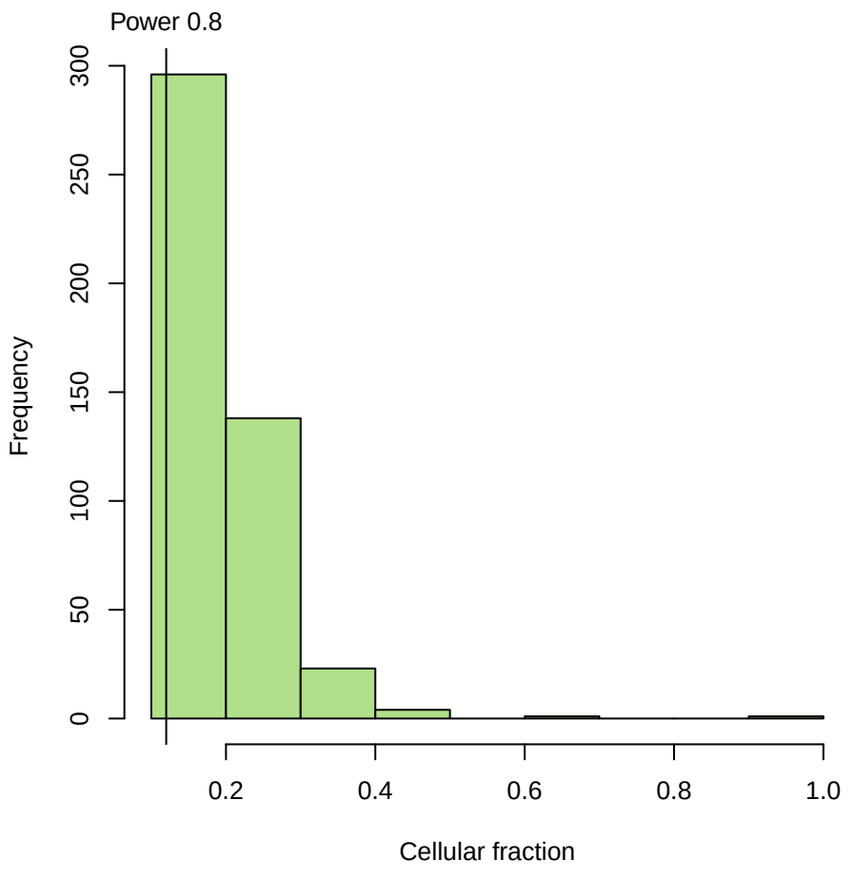

SCNA−fit log−likelihood: −7432
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 5
0 20 40 60 80 100 120
SNV Index

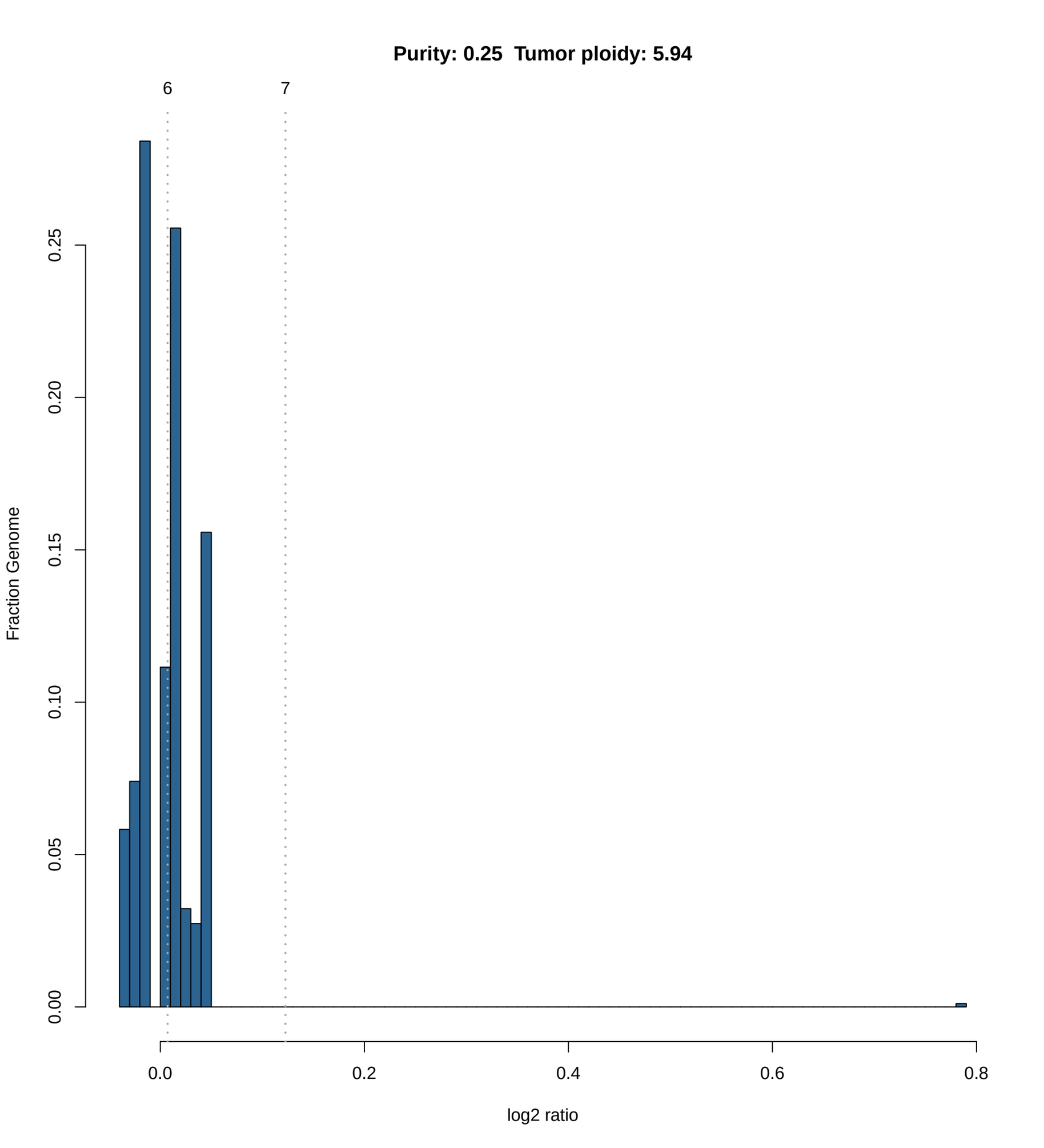

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120
SNV Index

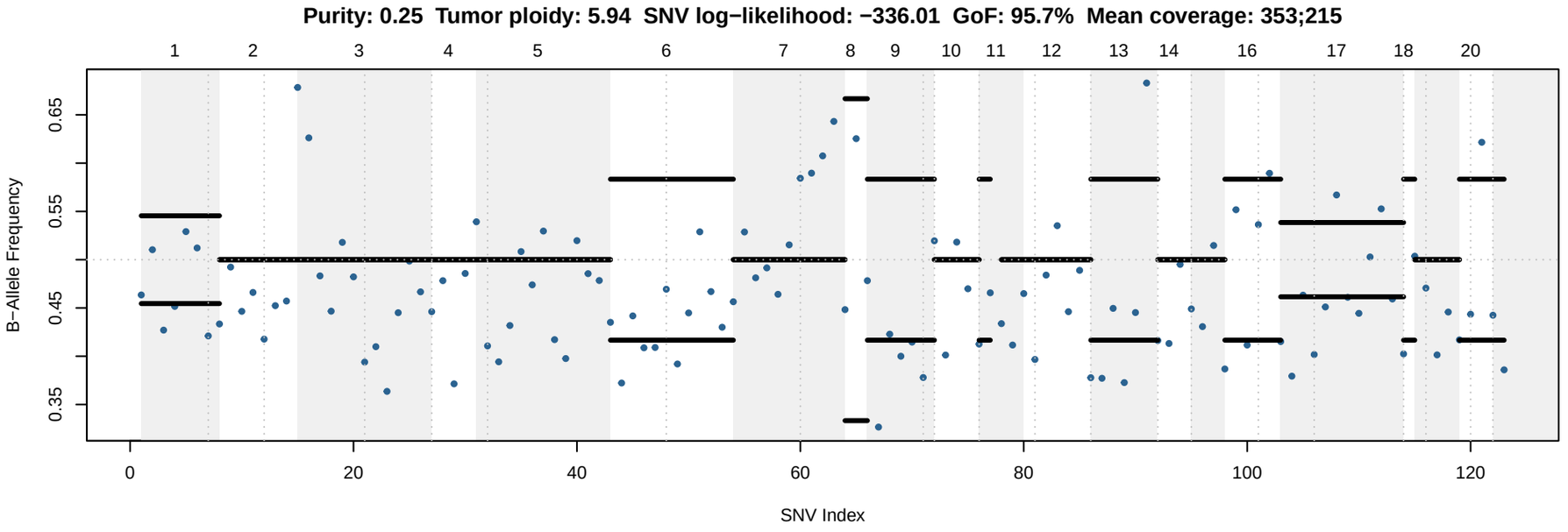

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
2m1
5m
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

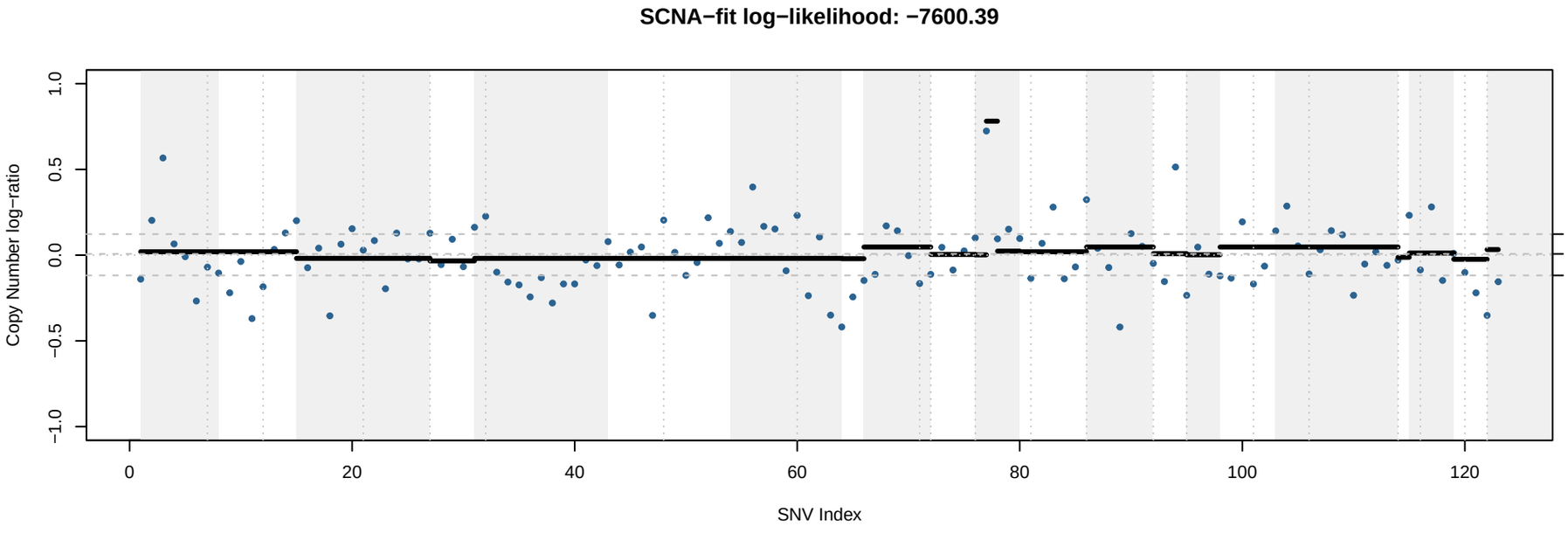

Coverage (log2)
4
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

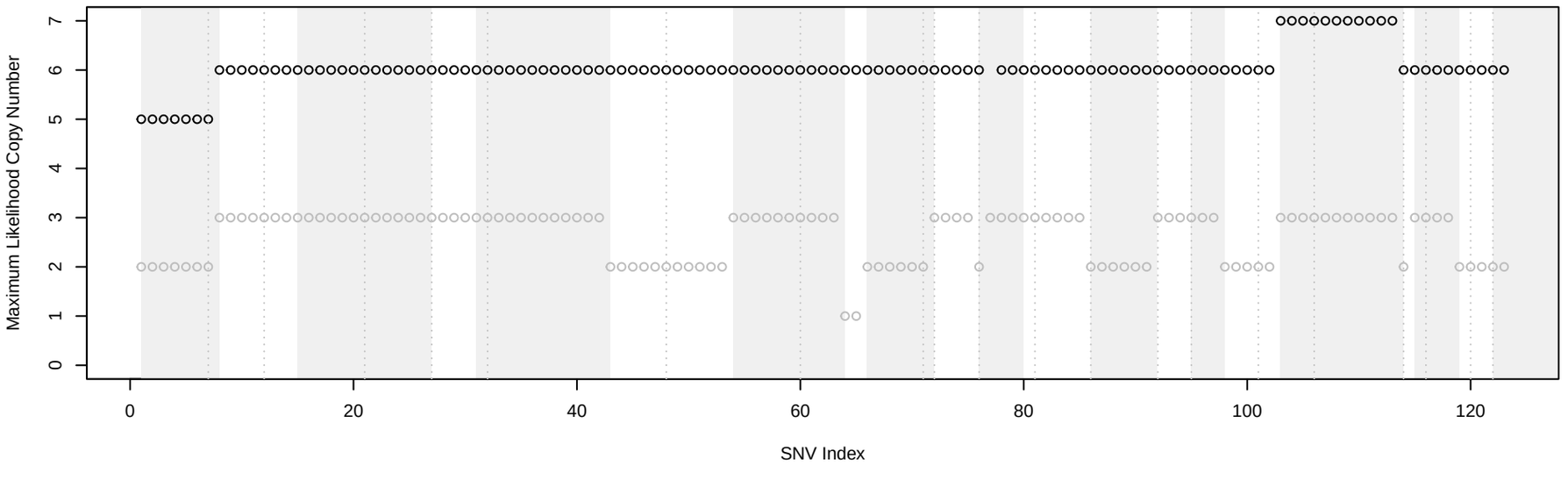

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0.30
2m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

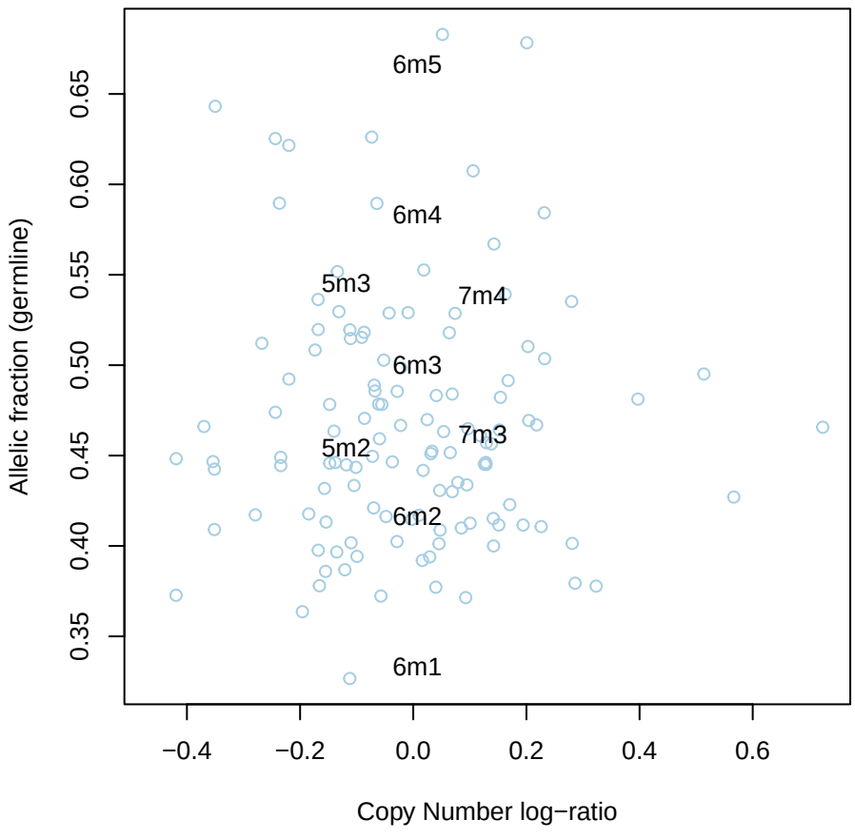

Power 0.8
Frequency
0
50
100
150
200
250
300
0.2
0.4
0.6
0.8
1.0
Cellular fraction

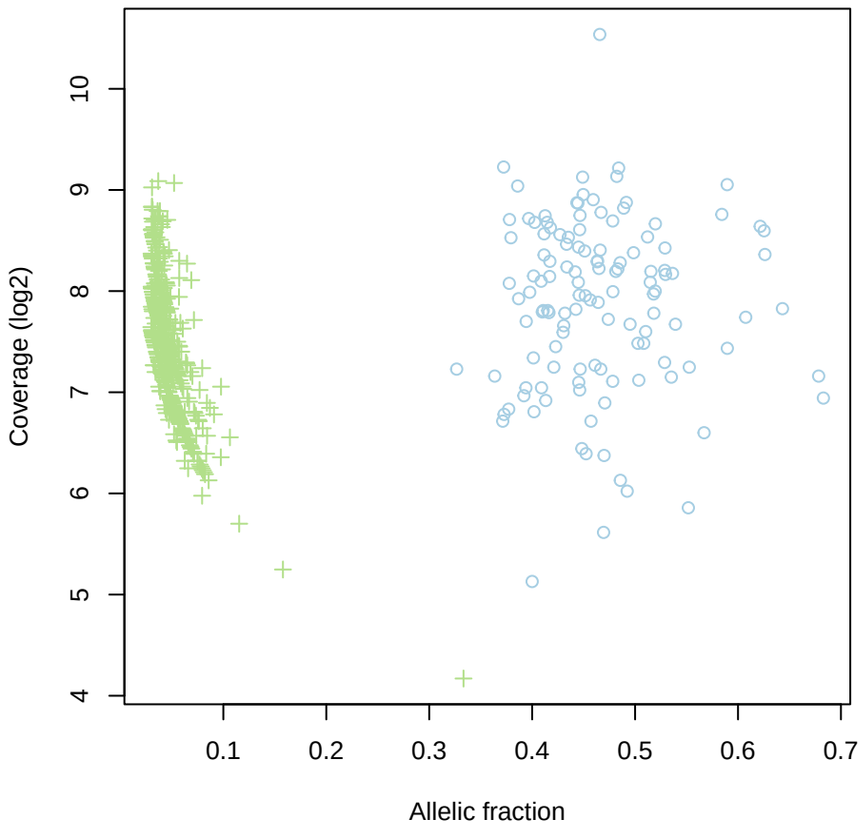

Purity: 0.25 Tumor ploidy: 5.94
6
7
Fraction Genome
0.00
0.05
0.10
0.15
0.20
0.25
0.0
0.2
0.4
0.6
0.8
log2 ratio

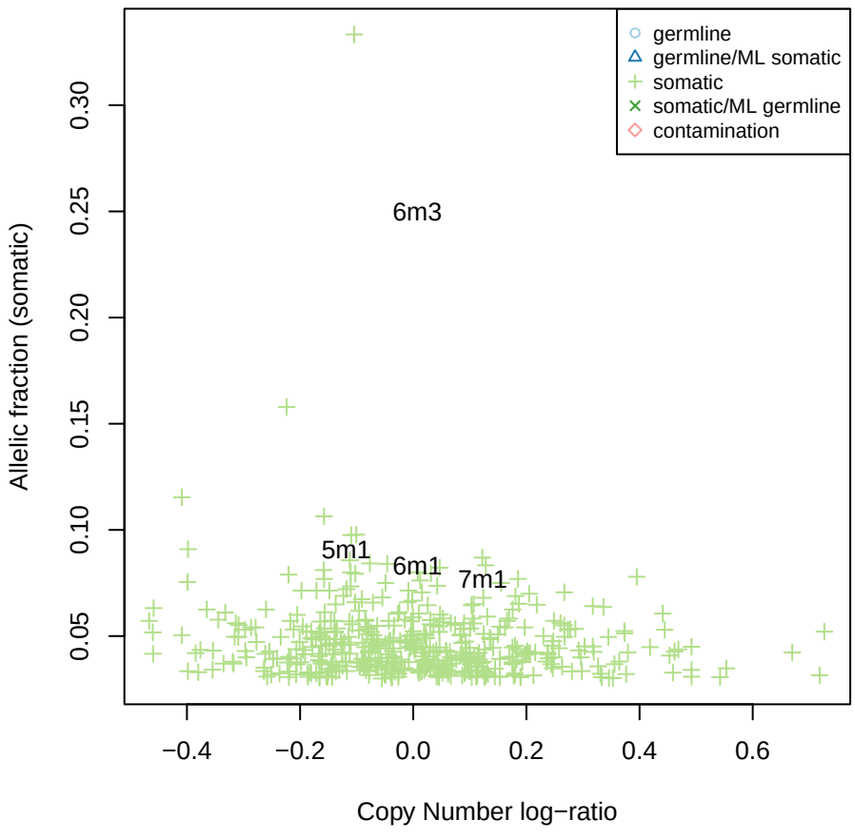

Purity: 0.25 Tumor ploidy: 5.94 SNV log−likelihood: −336.01 GoF: 95.7% Mean coverage: 353;215
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 20
B−Allele Frequency
0.35 0.45 0.55 0.65
0 20 40 60 80 100 120
SNV Index

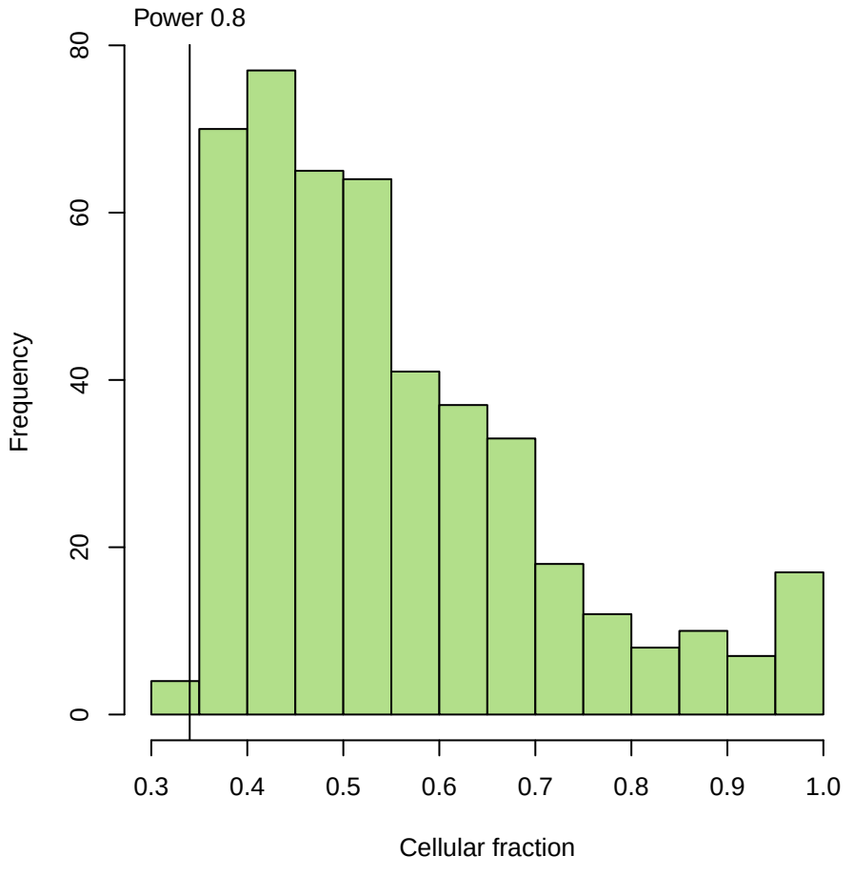

SCNA−fit log−likelihood: −7600.39
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
5 7
0 20 40 60 80 100 120
SNV Index

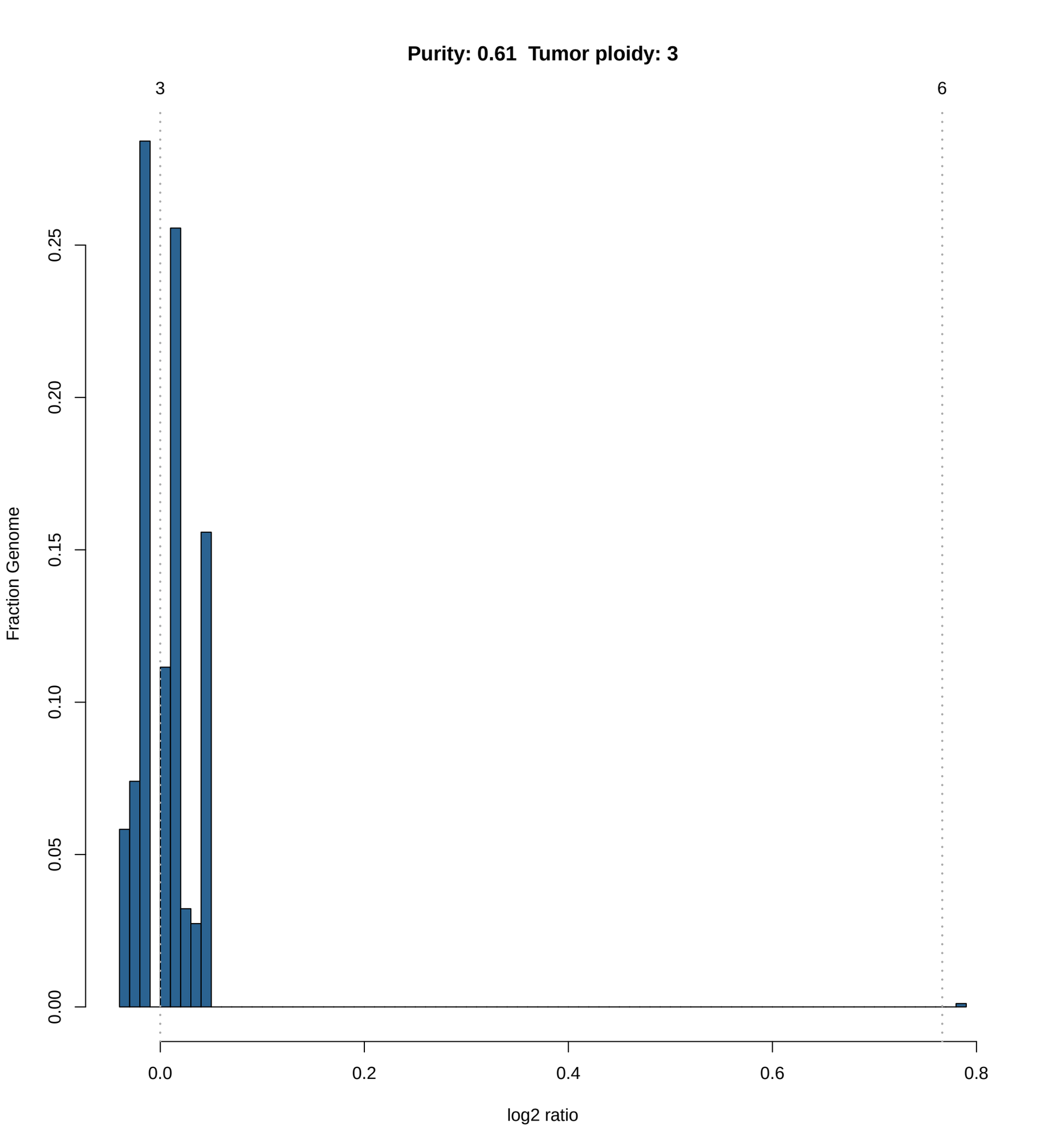

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

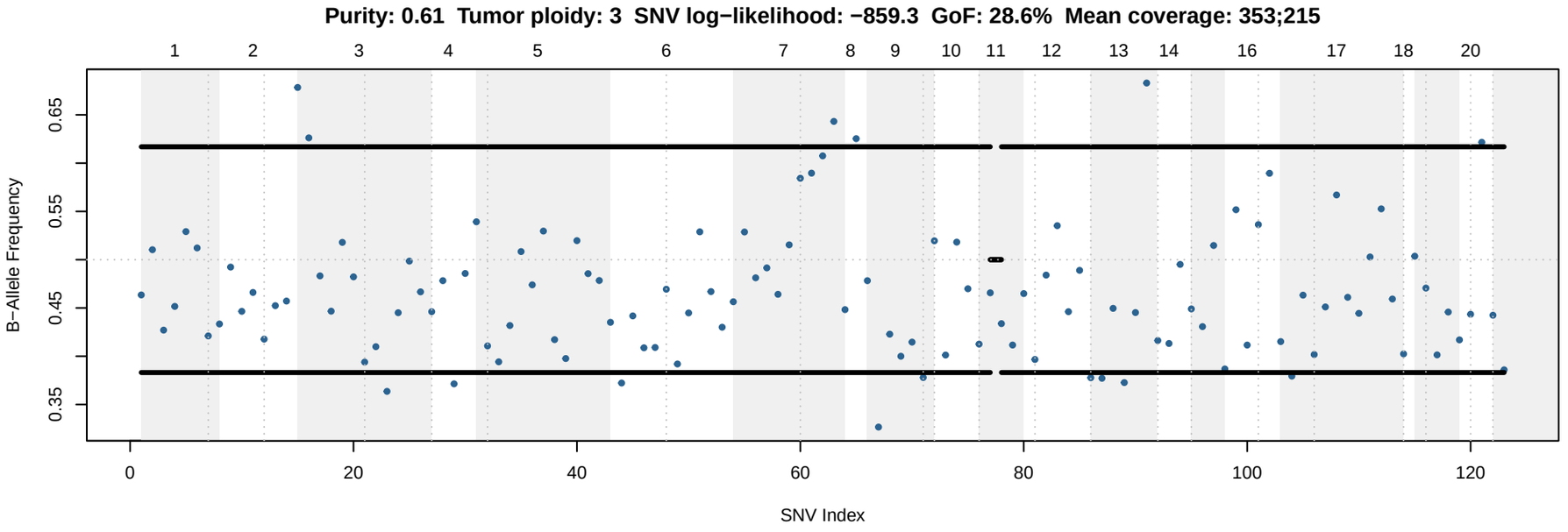

6m5
6m4
5m3
7m4
6m3
7m3
5m2
6m2
6m1
Allelic fraction (germline)
Copy Number log−ratio
0.35
0.40
0.45
0.50
0.55
0.60
0.65
−0.4
−0.2
0.0
0.2
0.4
0.6

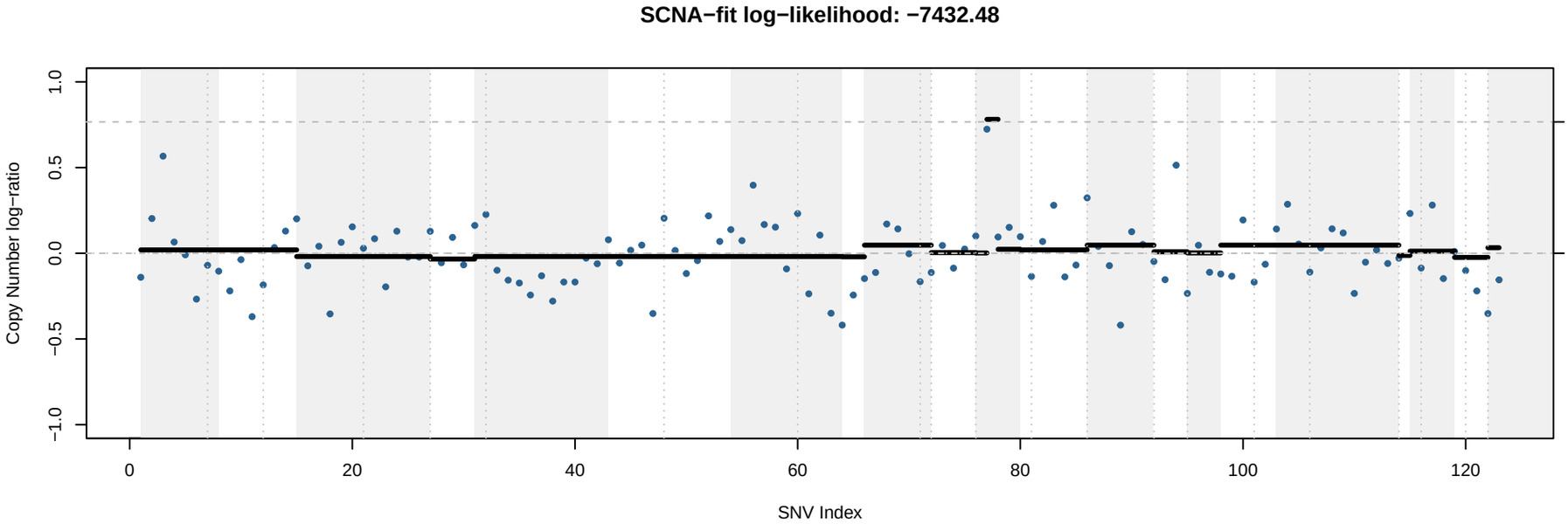

Coverage (log2)
Allelic fraction
4
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7

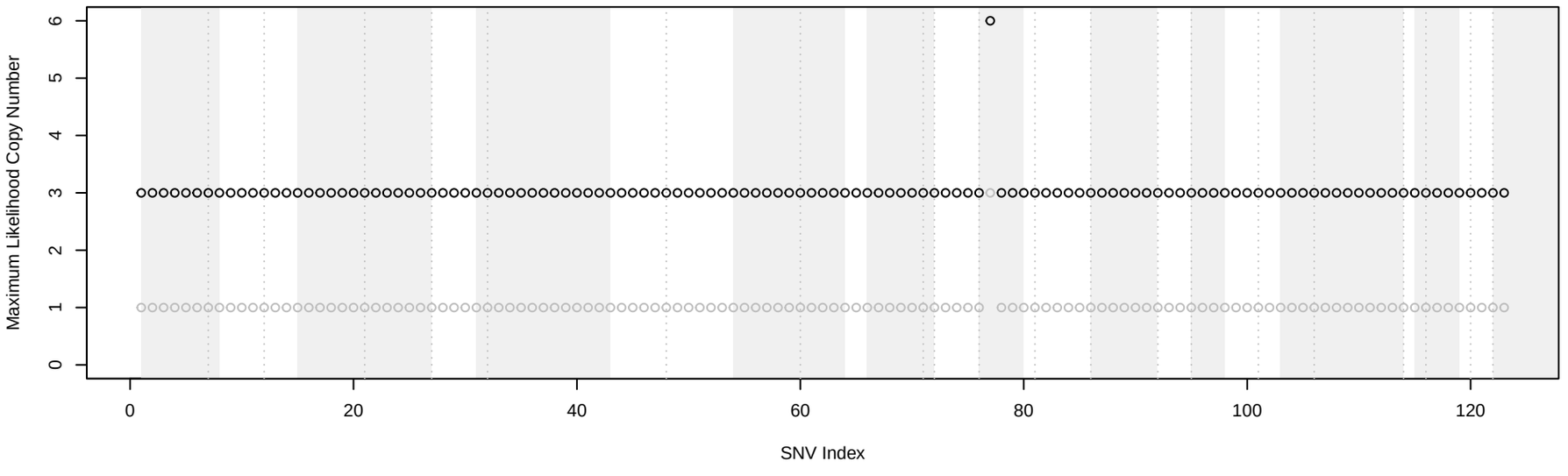

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m3
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
0.25
0.30
−0.4
−0.2
0.0
0.2
0.4
0.6

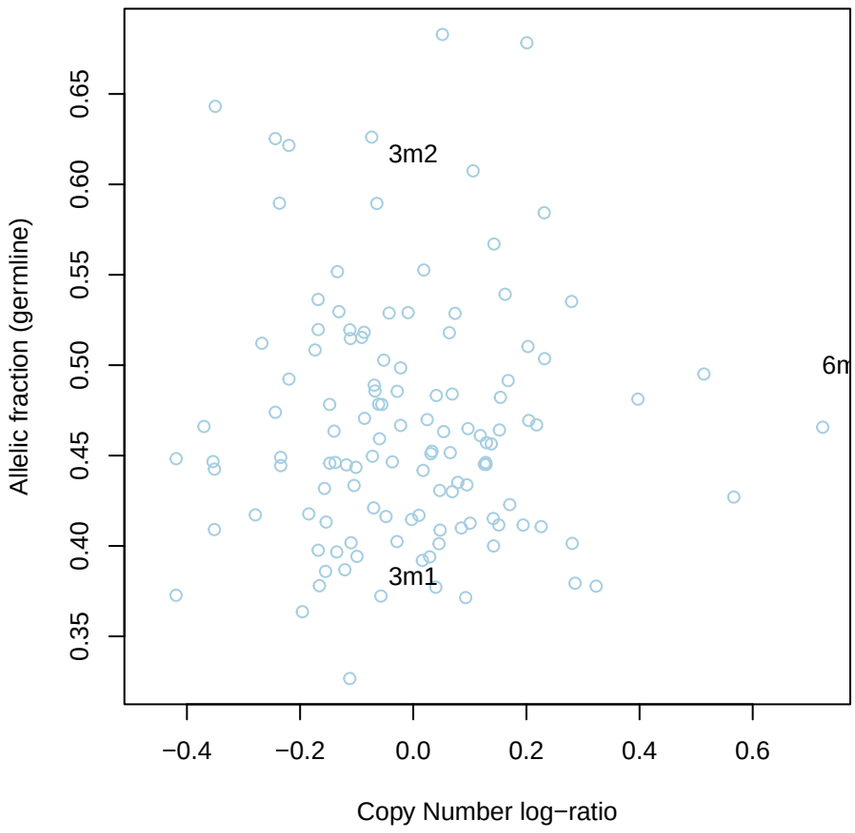

Power 0.8
Frequency
Cellular fraction
0
20
40
60
80
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0

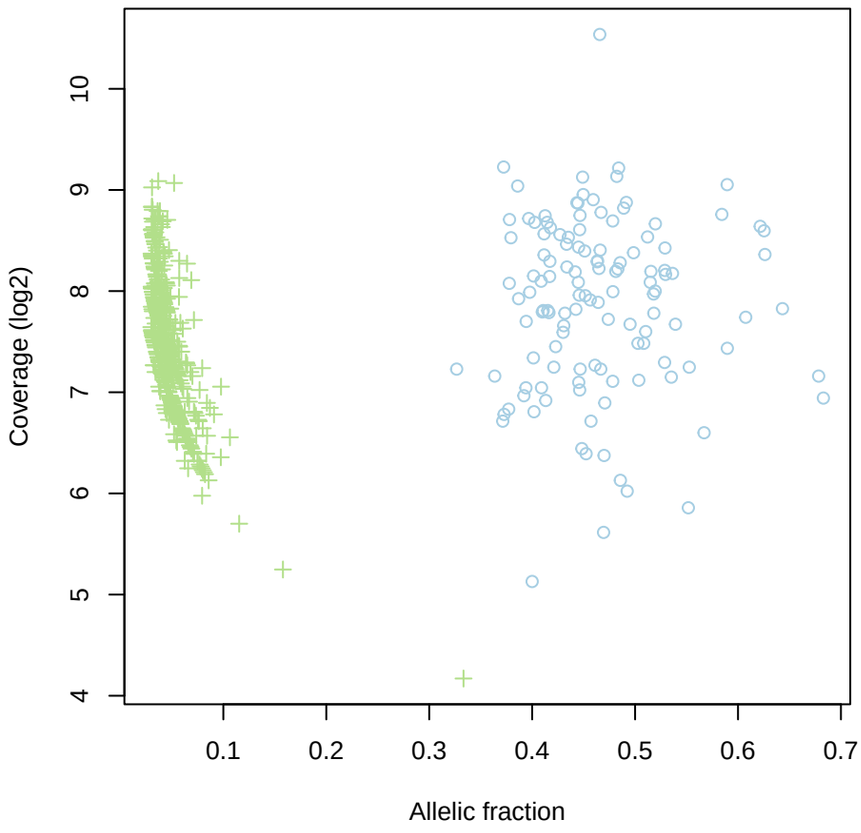

Purity: 0.61 Tumor ploidy: 3
3
6
Fraction Genome
0.00
0.05
0.10
0.15
0.20
0.25
0.0
0.2
0.4
0.6
0.8
log2 ratio

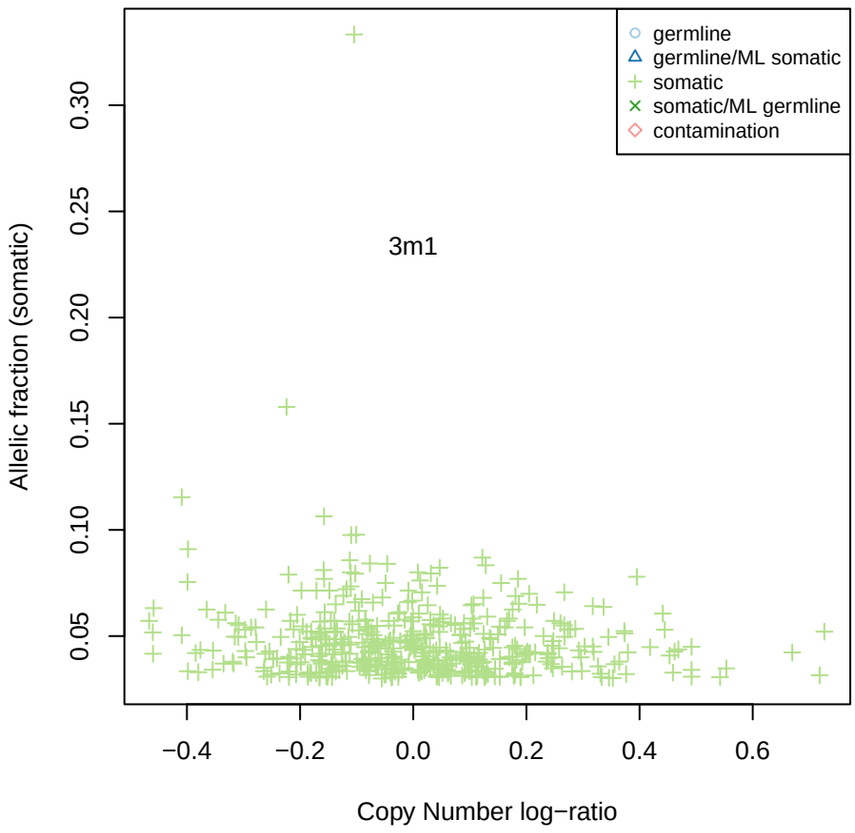

Purity: 0.61 Tumor ploidy: 3 SNV log−likelihood: −859.3 GoF: 28.6% Mean coverage: 353;215
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 20
B−Allele Frequency
0.35 0.45 0.55 0.65
0 20 40 60 80 100 120
SNV Index

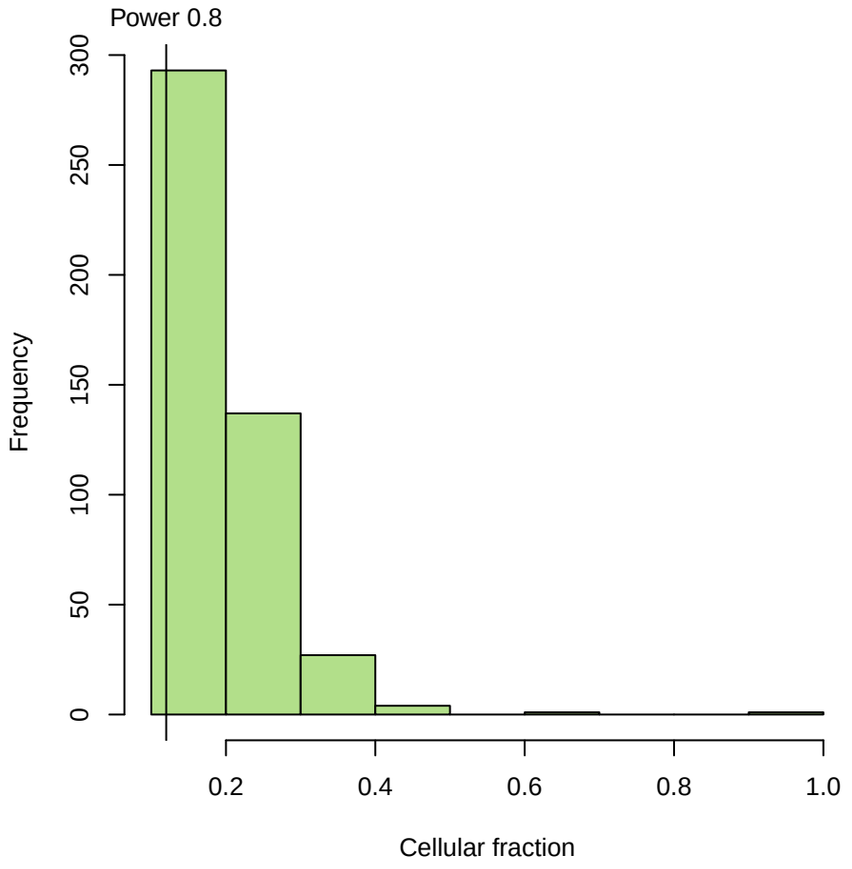

SCNA−fit log−likelihood: −7432.48
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 6
0 20 40 60 80 100 120
SNV Index

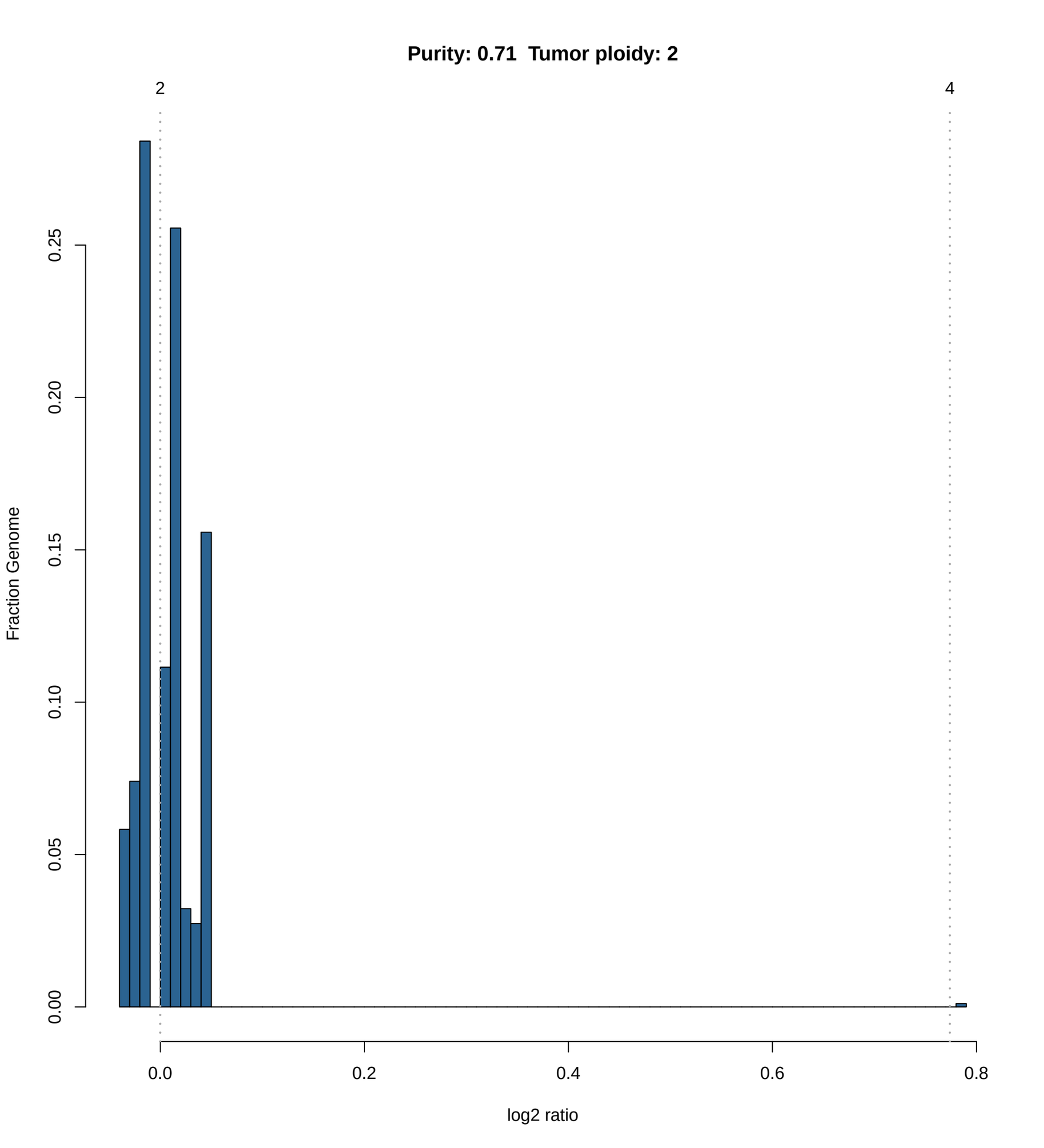

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120
SNV Index

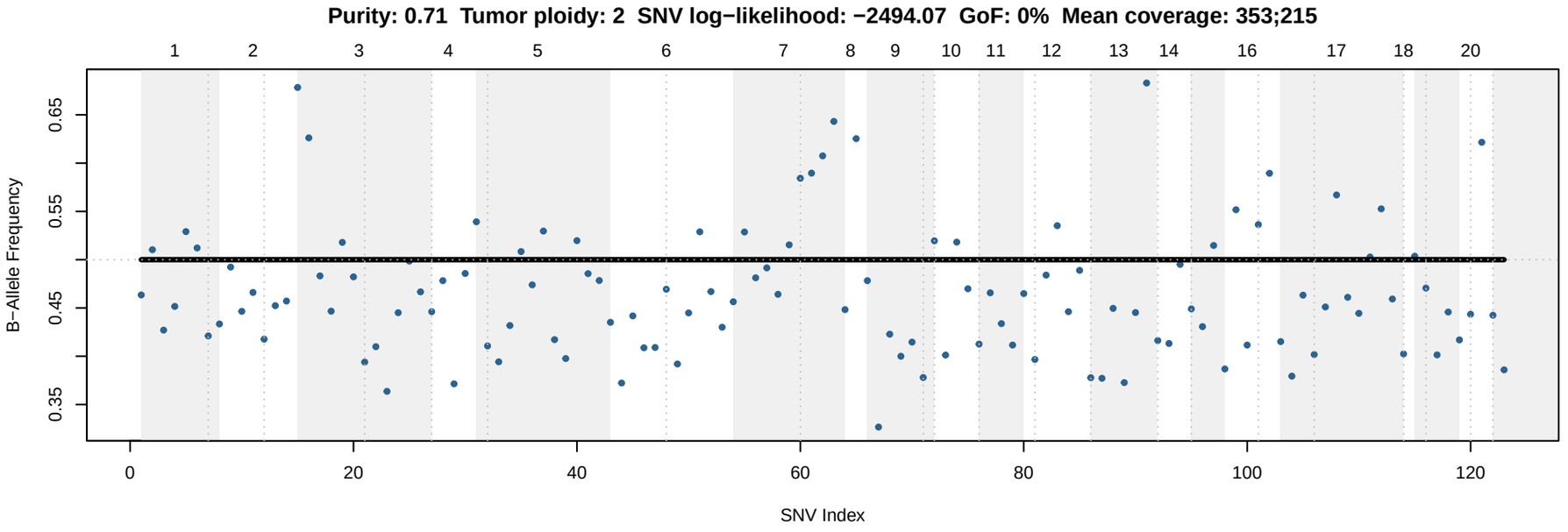

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
3m2
3m1
6m
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

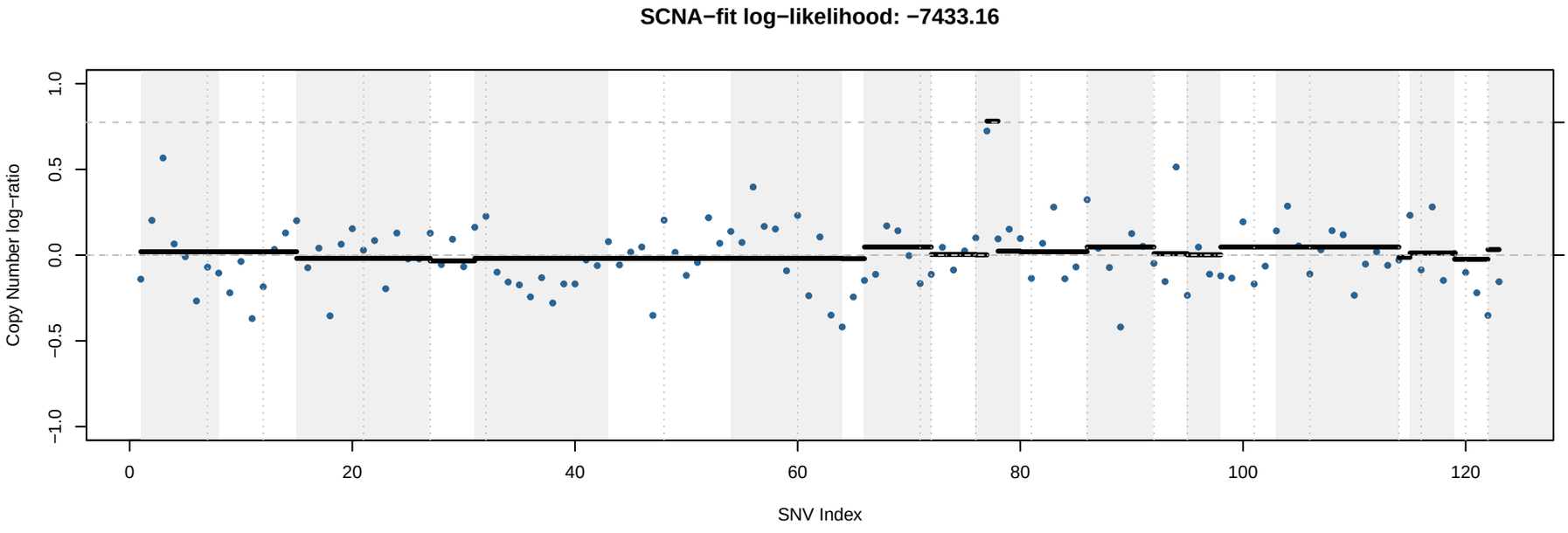

Coverage (log2)
4
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

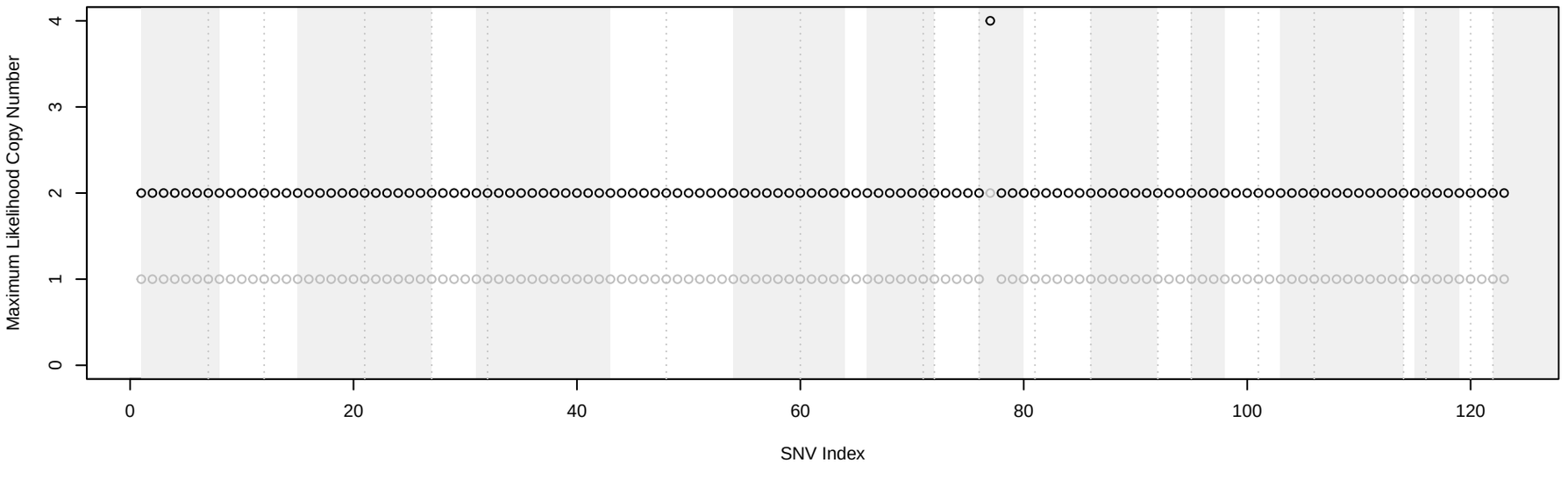

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0.30
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

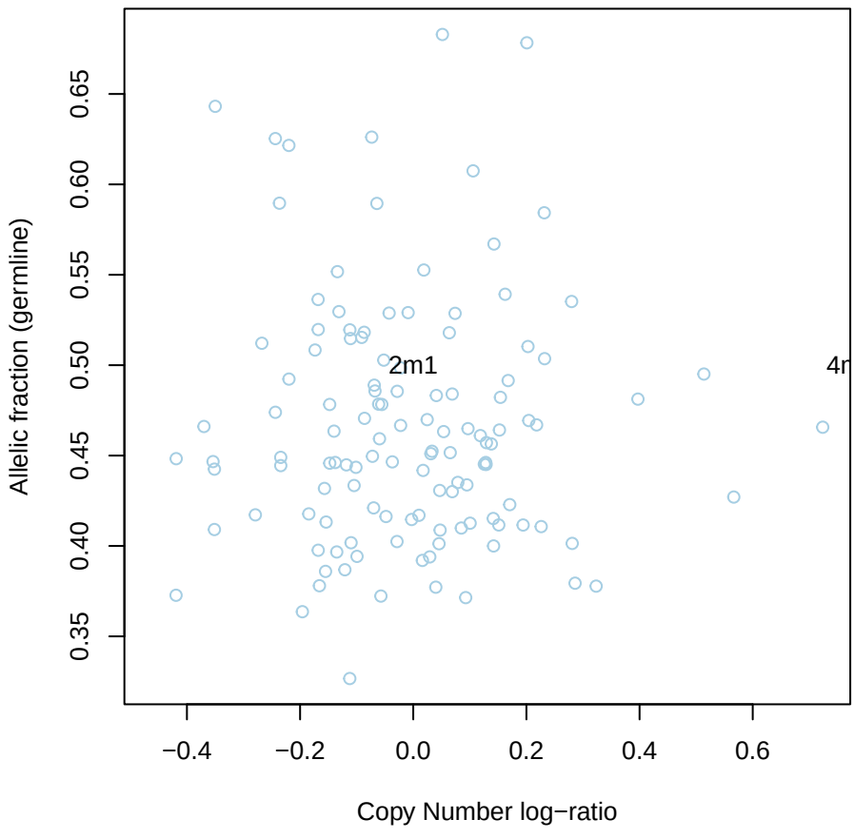

Power 0.8
Frequency
0
50
100
150
200
250
300
0.2
0.4
0.6
0.8
1.0
Cellular fraction

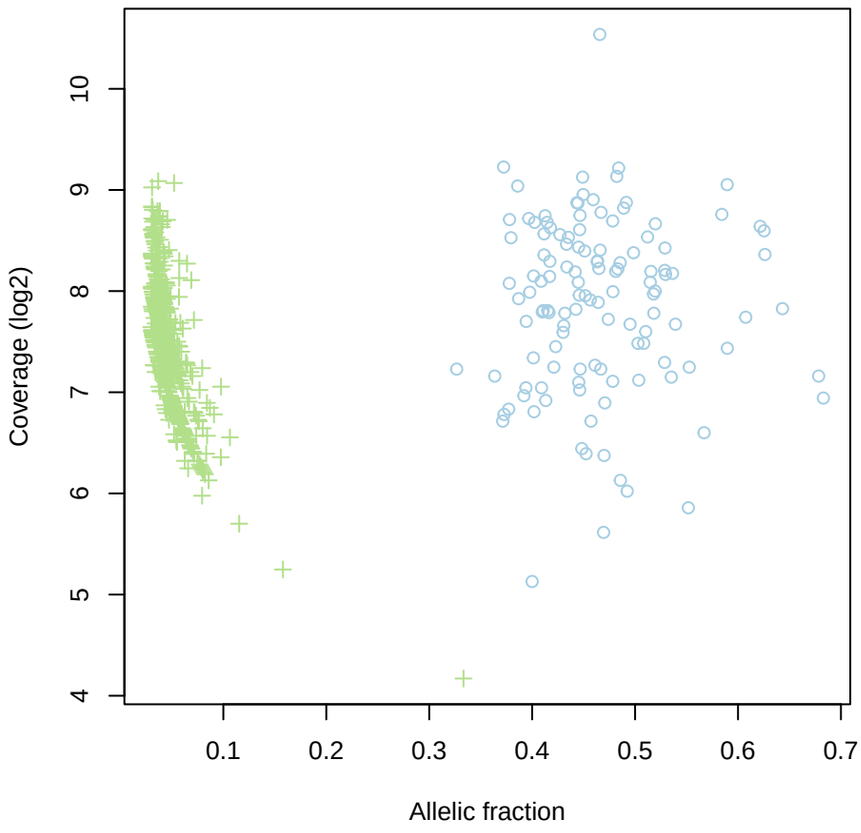

Purity: 0.71 Tumor ploidy: 2
2
4
Fraction Genome
0.00
0.05
0.10
0.15
0.20
0.25
0.0
0.2
0.4
0.6
0.8
log2 ratio

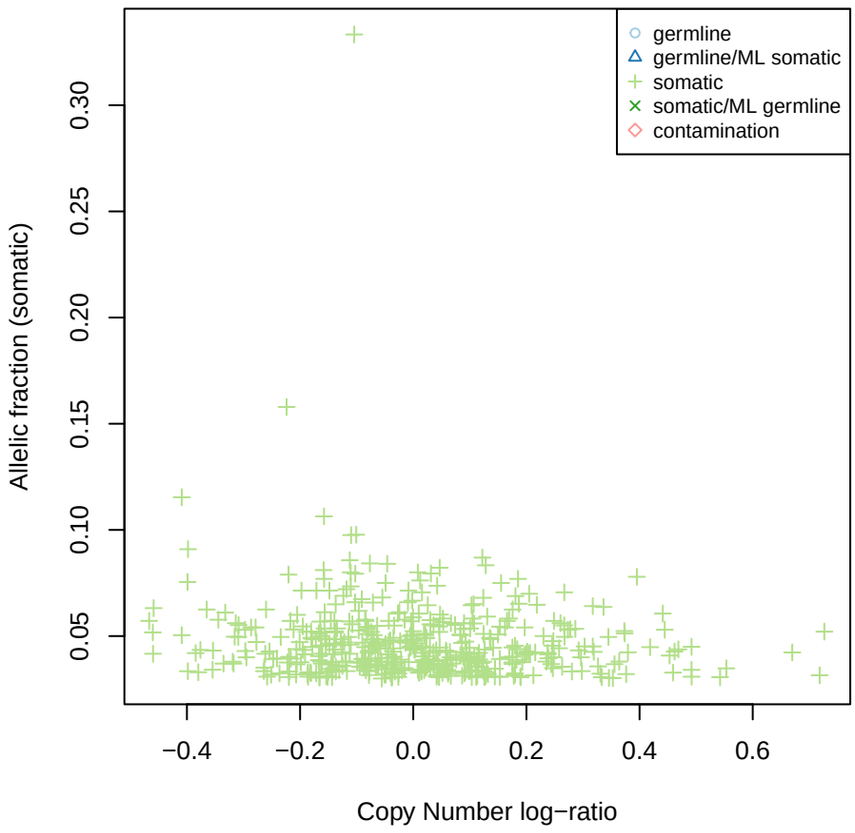

Purity: 0.71 Tumor ploidy: 2 SNV log−likelihood: −2494.07 GoF: 0% Mean coverage: 353;215
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 20
B−Allele Frequency
0.35 0.45 0.55 0.65
0 20 40 60 80 100 120
SNV Index

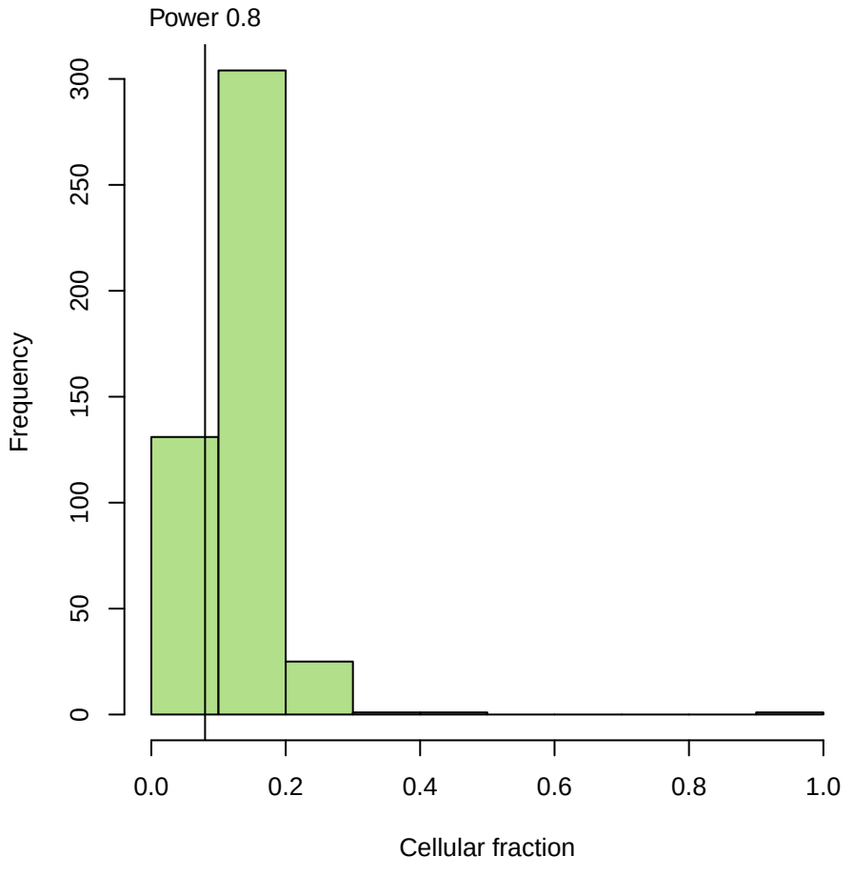

SCNA−fit log−likelihood: −7433.16
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 4
0 20 40 60 80 100 120
SNV Index

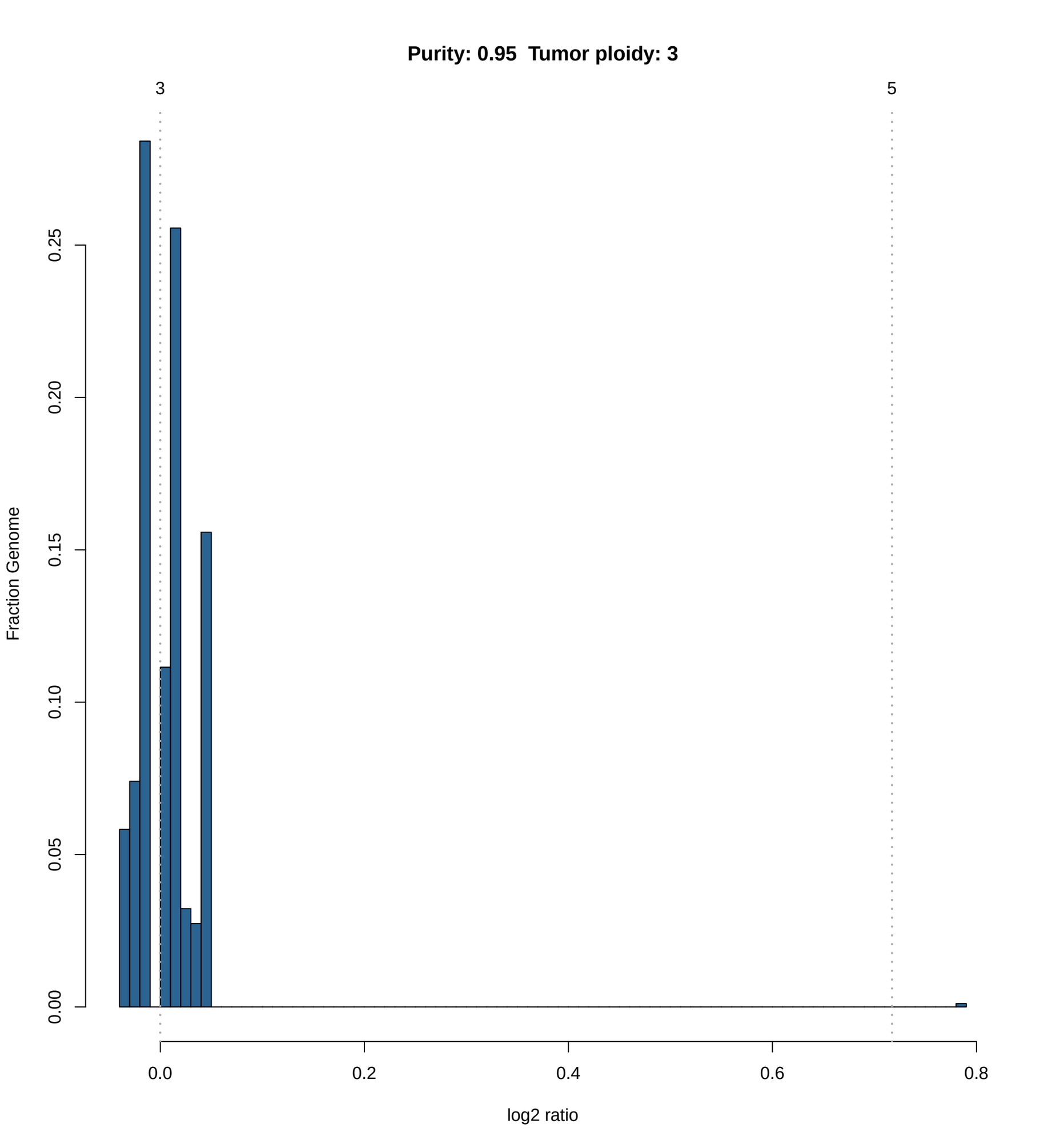

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120
SNV Index

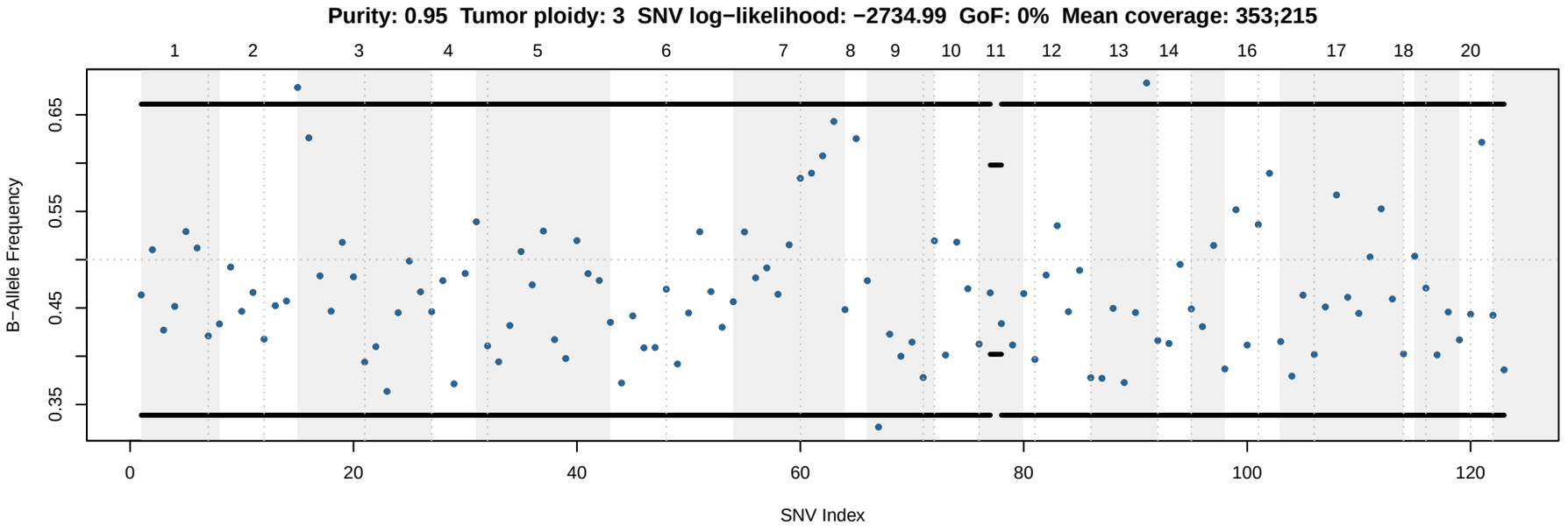

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
2m1
4r
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

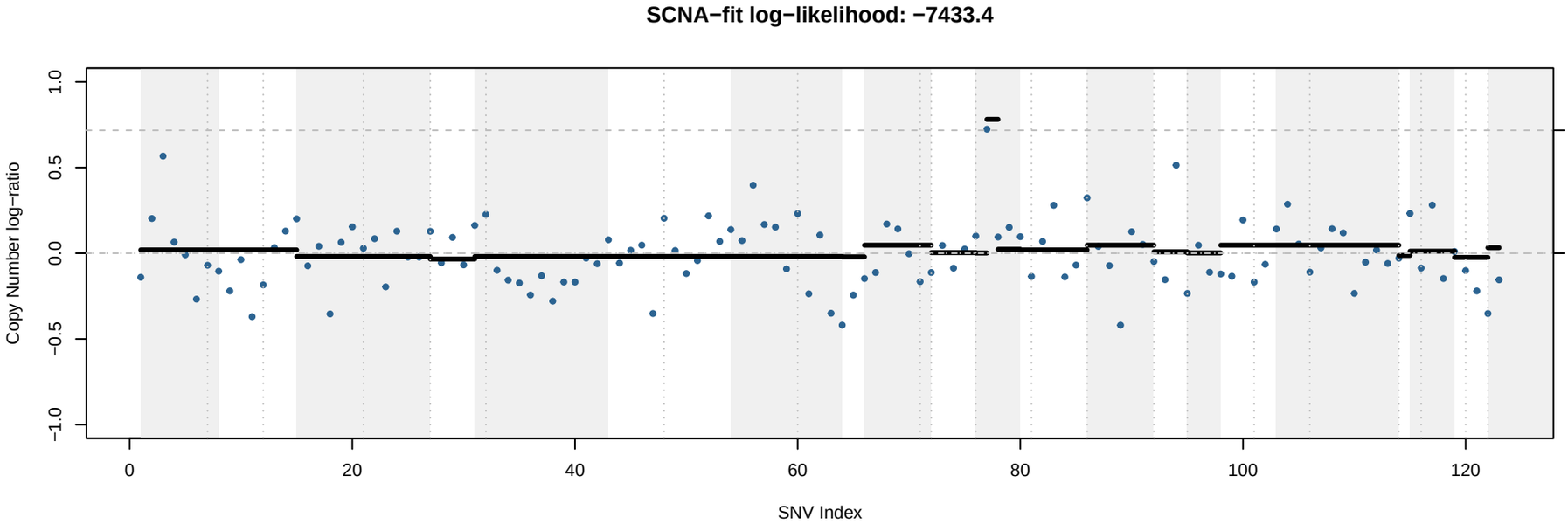

Coverage (log2)
4
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

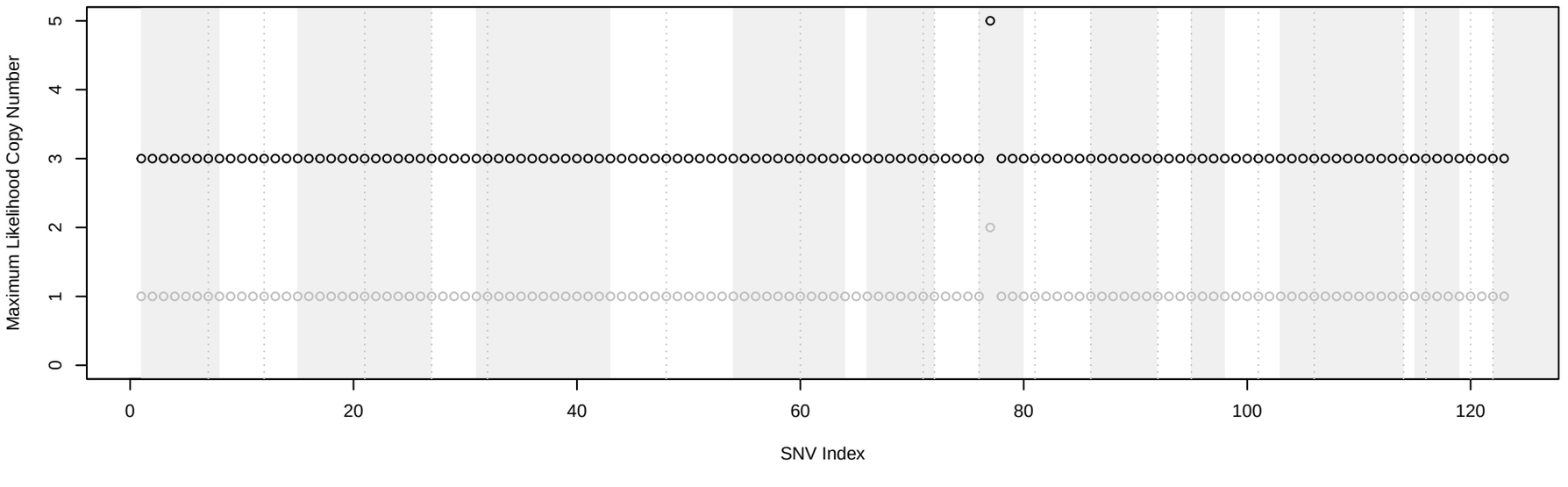

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0.30
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

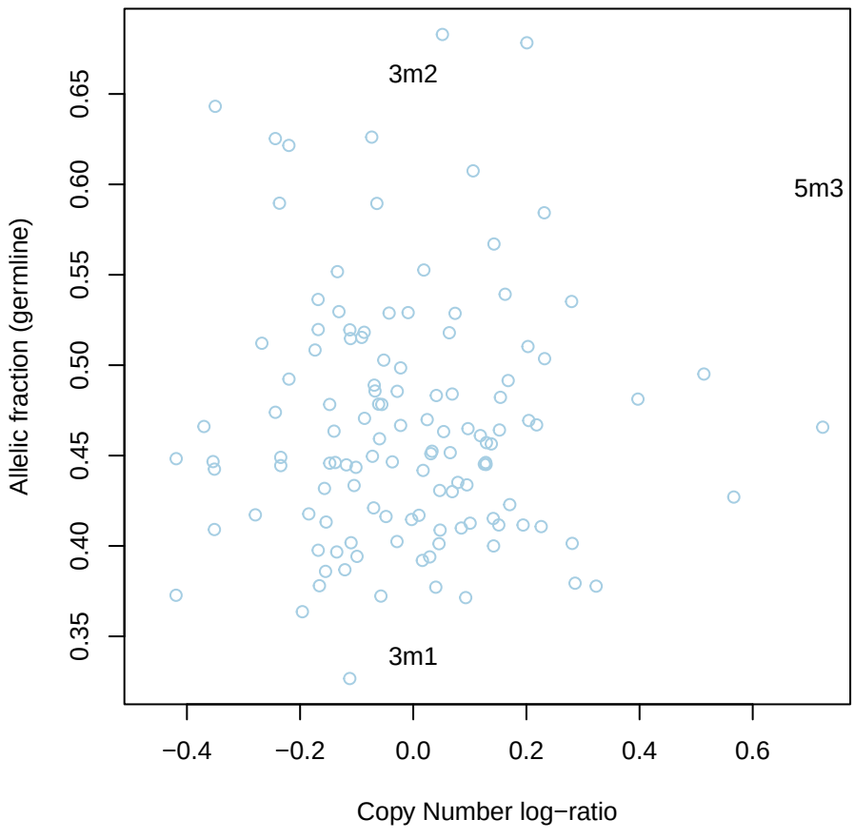

Power 0.8
Frequency
0
50
100
150
200
250
300
0.0
0.2
0.4
0.6
0.8
1.0
Cellular fraction

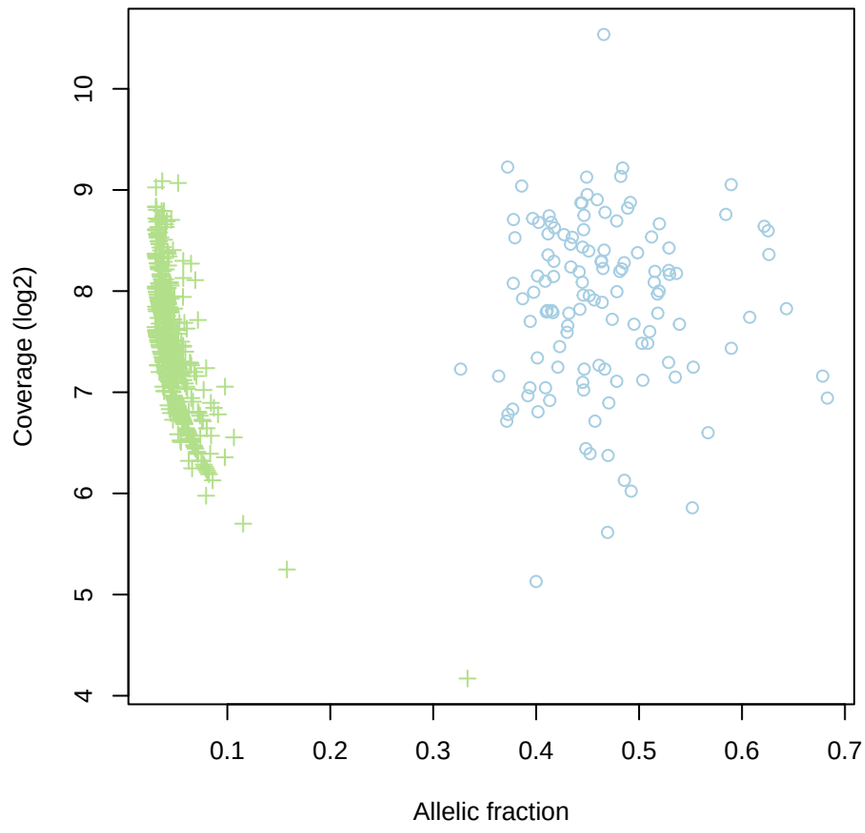

Purity: 0.95 Tumor ploidy: 3
3
5
Fraction Genome
0.00
0.05
0.10
0.15
0.20
0.25
0.0
0.2
0.4
0.6
0.8
log2 ratio

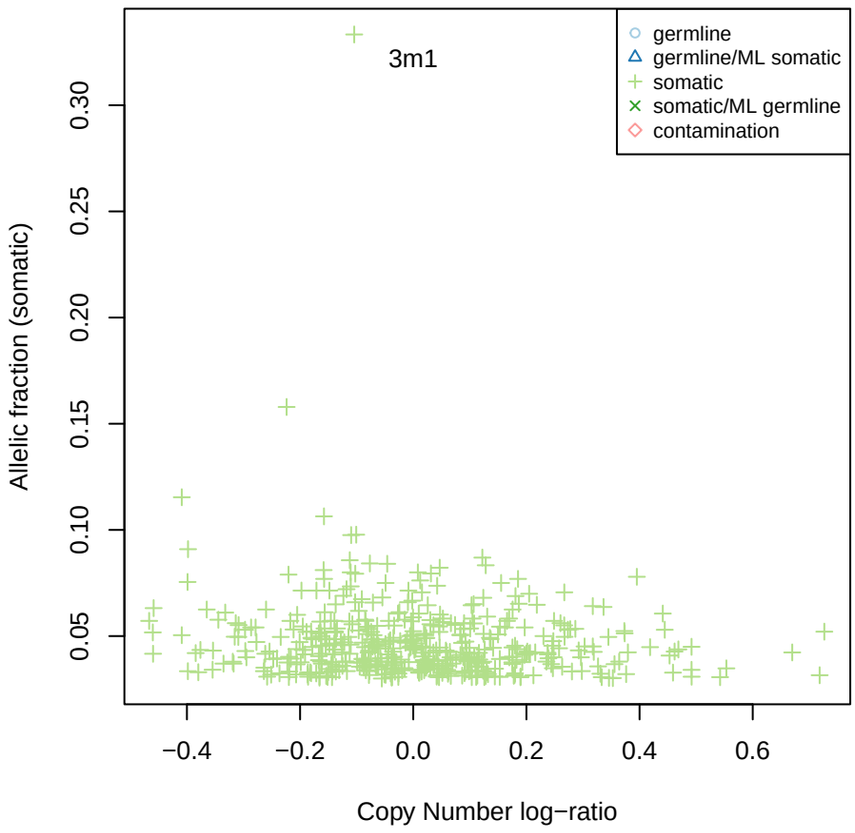

Purity: 0.95 Tumor ploidy: 3 SNV log−likelihood: −2734.99 GoF: 0% Mean coverage: 353;215
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 20
B−Allele Frequency
0.35 0.45 0.55 0.65
0 20 40 60 80 100 120
SNV Index

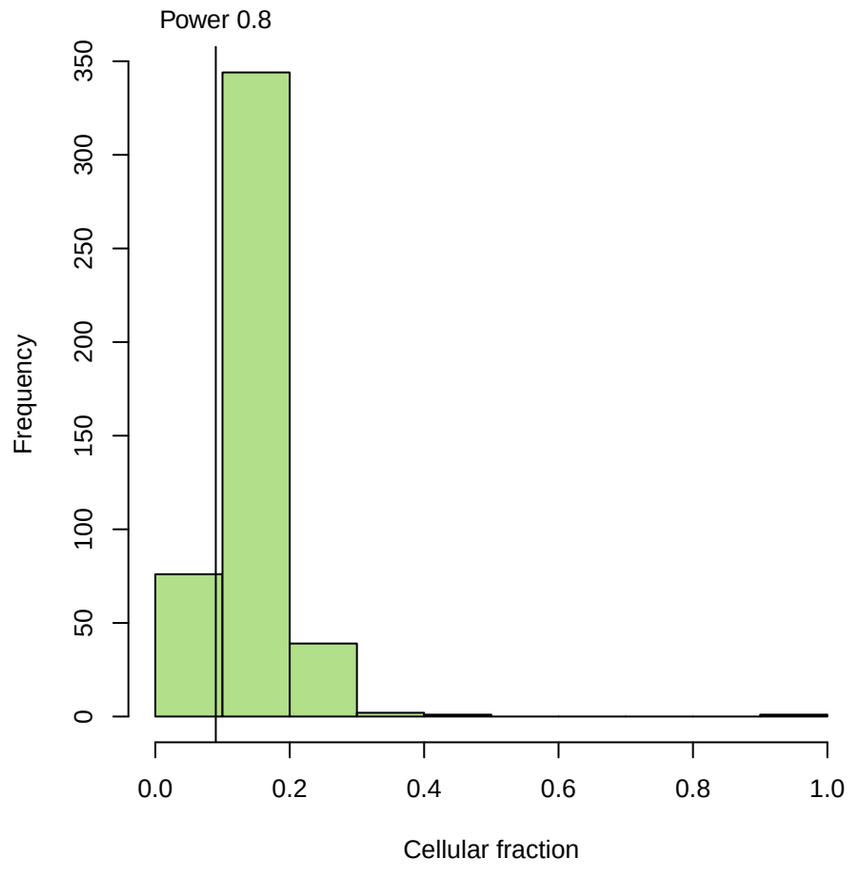

SCNA−fit log−likelihood: −7433.4
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
5
3
0 20 40 60 80 100 120
SNV Index


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


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


Coverage (log2)
Allelic fraction
4
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7


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


Power 0.8
Frequency
Cellular fraction
0
50
100
150
200
250
300
350
0.0
0.2
0.4
0.6
0.8
1.0