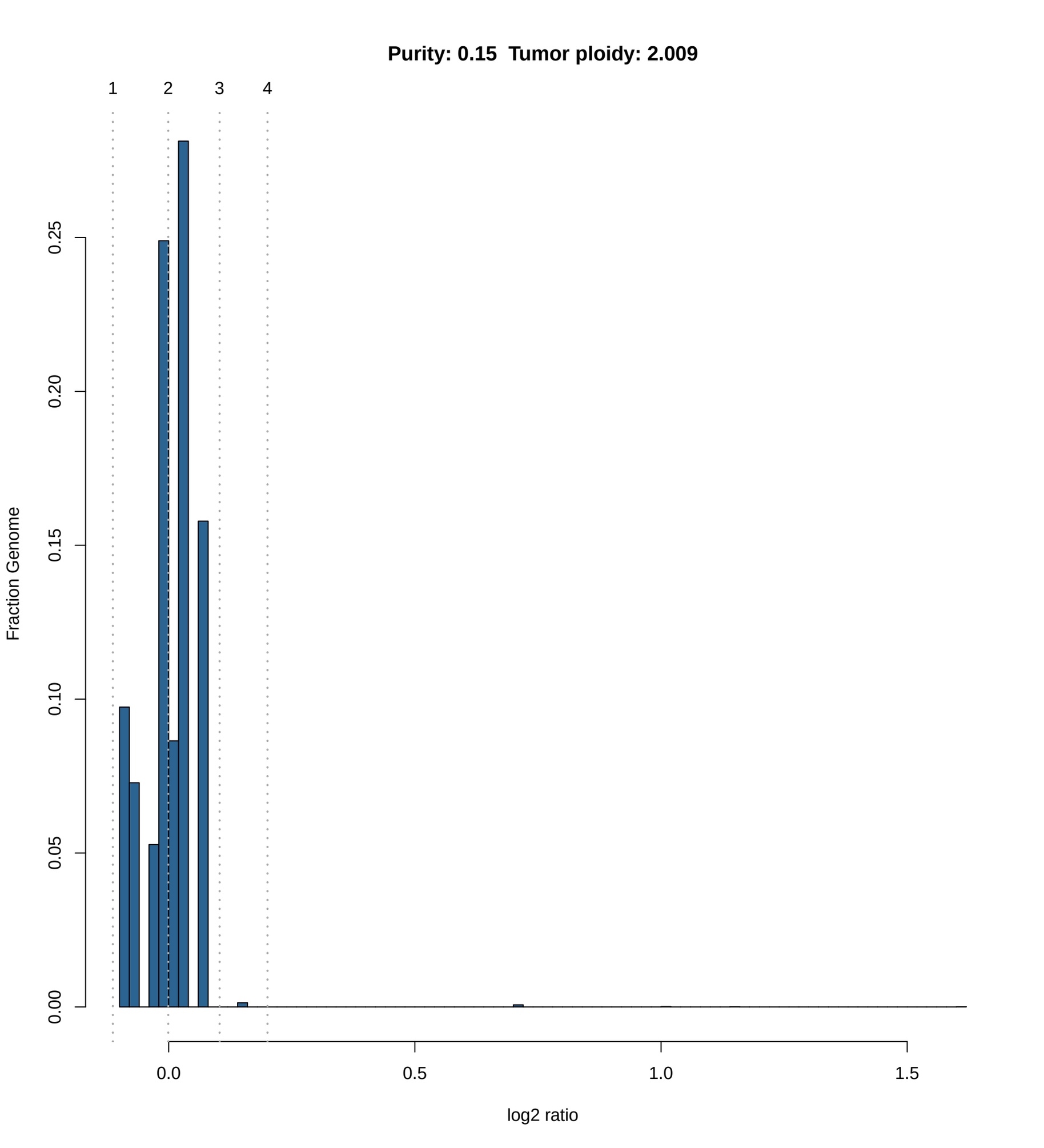
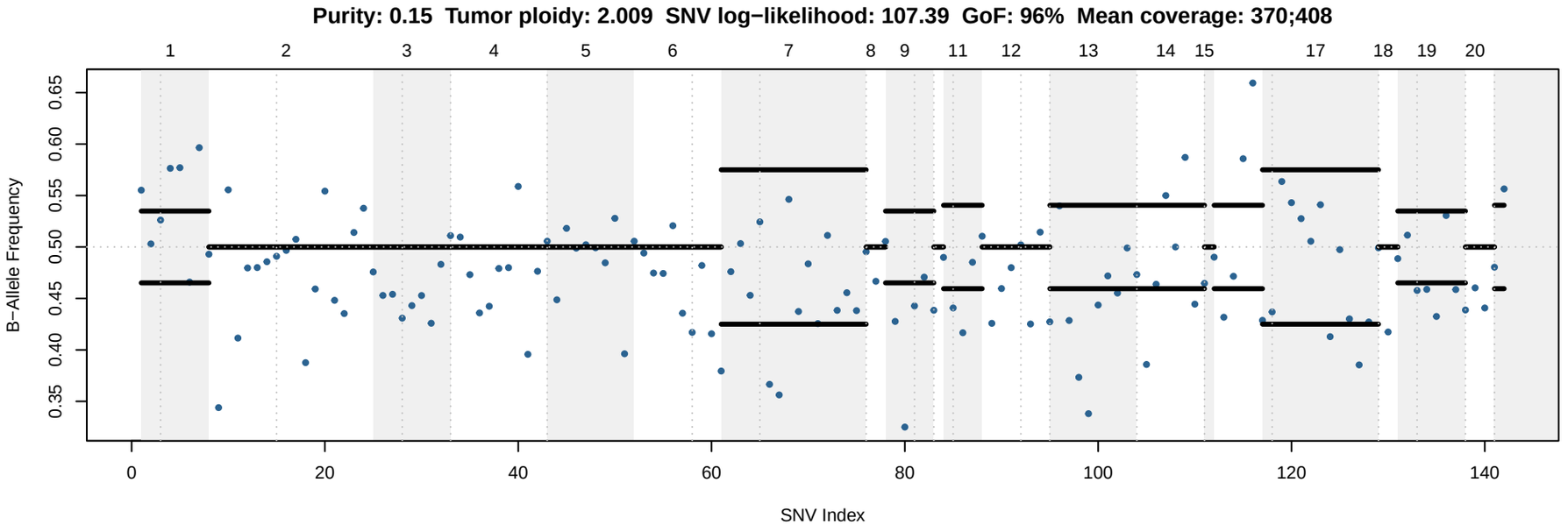
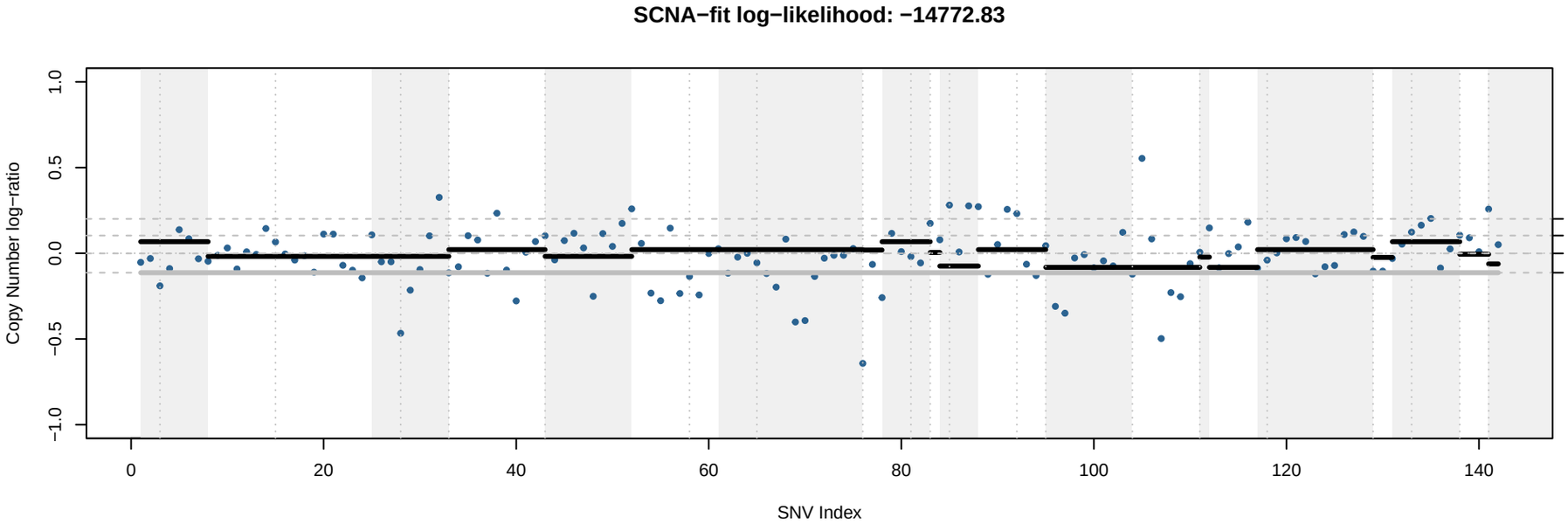
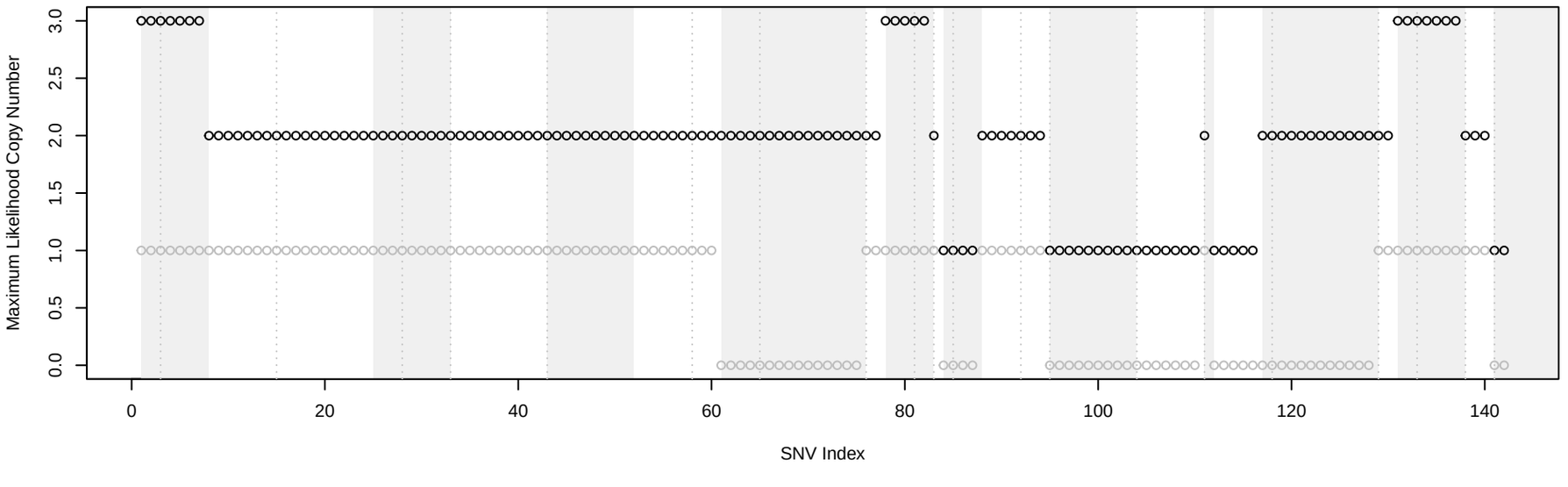
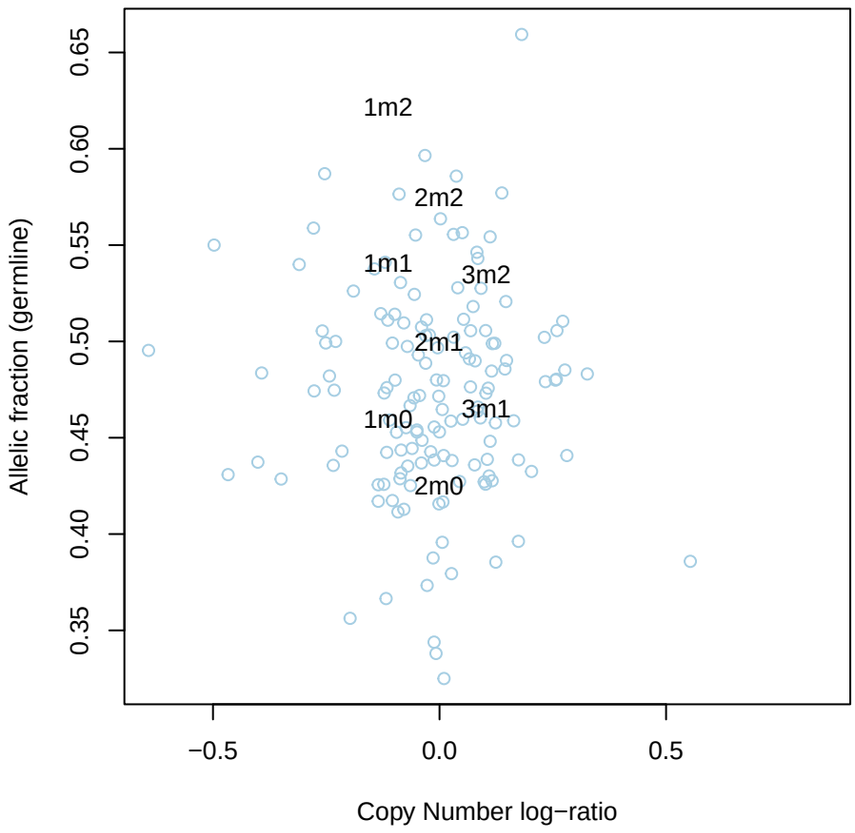
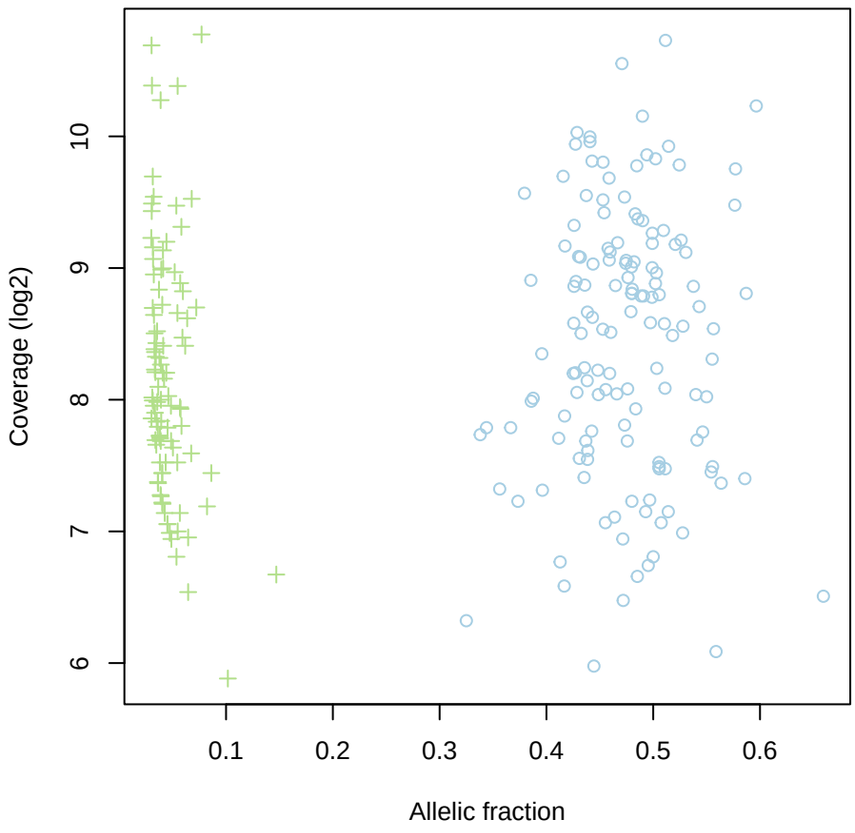

Purity: 0.15 Tumor ploidy: 2.009
1
2
3
4
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
1.5
log2 ratio

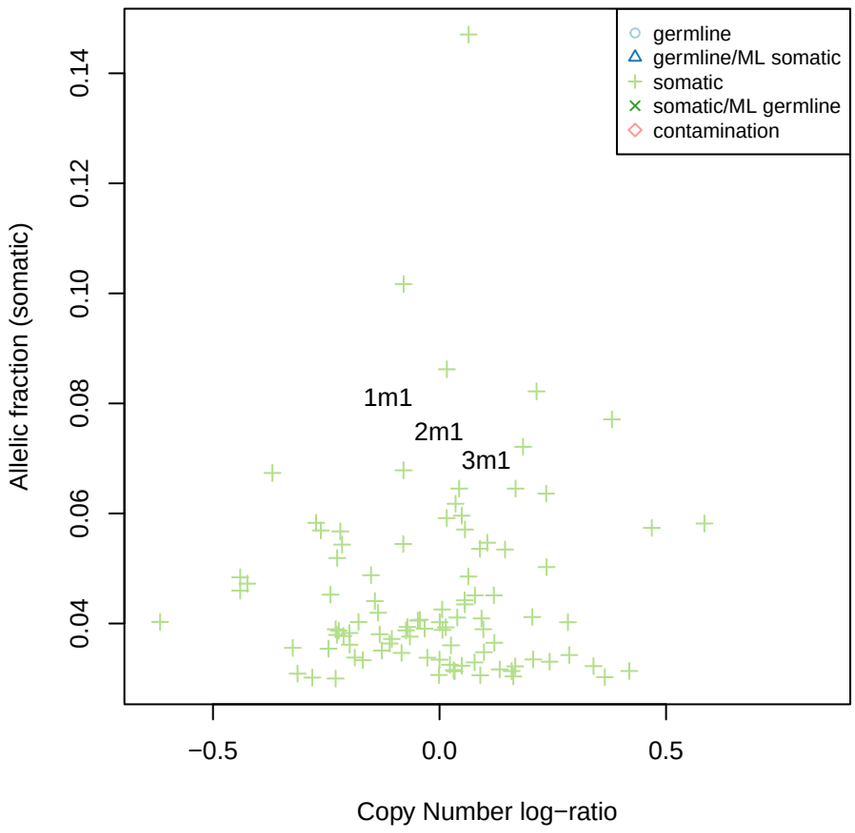

Purity: 0.15 Tumor ploidy: 2.009 SNV log−likelihood: 107.39 GoF: 96% Mean coverage: 370;408
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

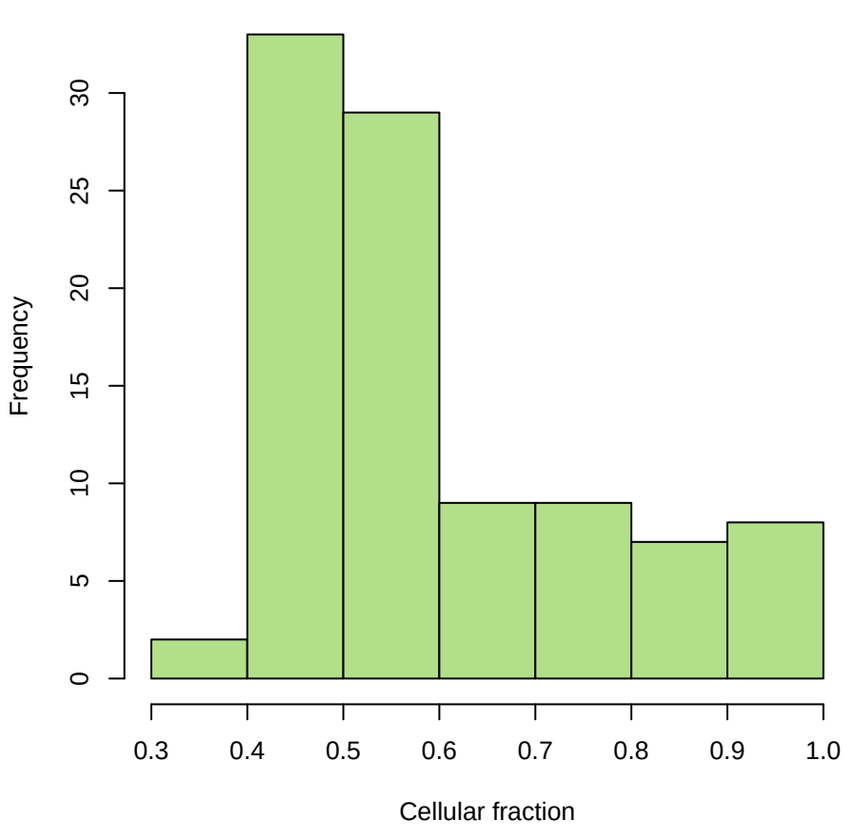

SCNA−fit log−likelihood: −14772.83
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
1 3
0 20 40 60 80 100 120 140
SNV Index

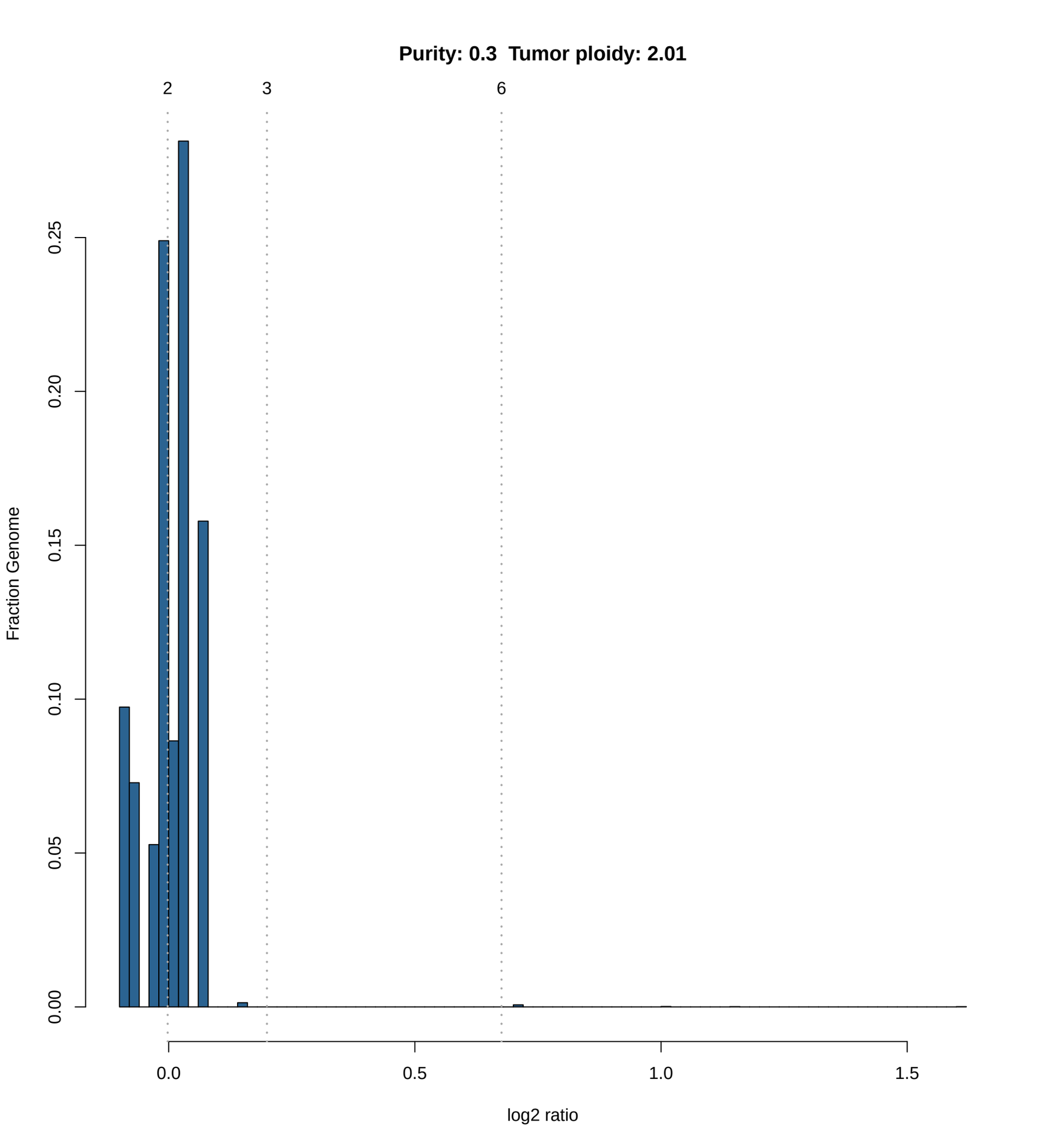

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120 140
SNV Index

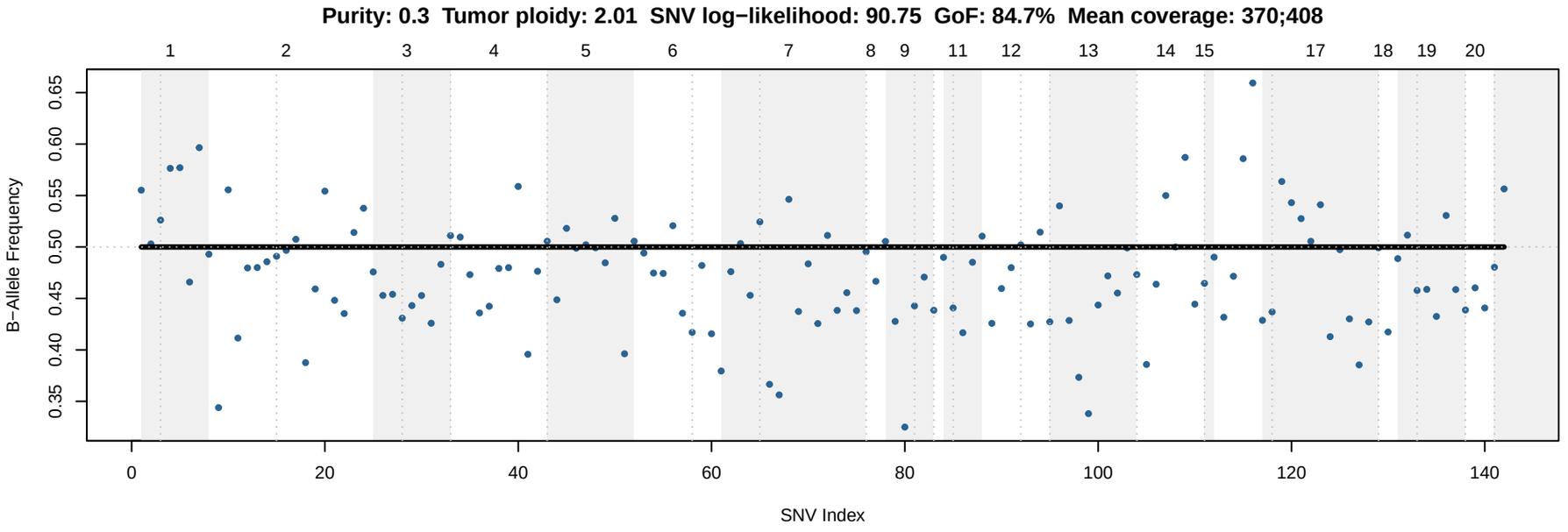

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
1m2
2m2
1m1
3m2
2m1
1m0
3m1
2m0
−0.5
0.0
0.5
Copy Number log−ratio

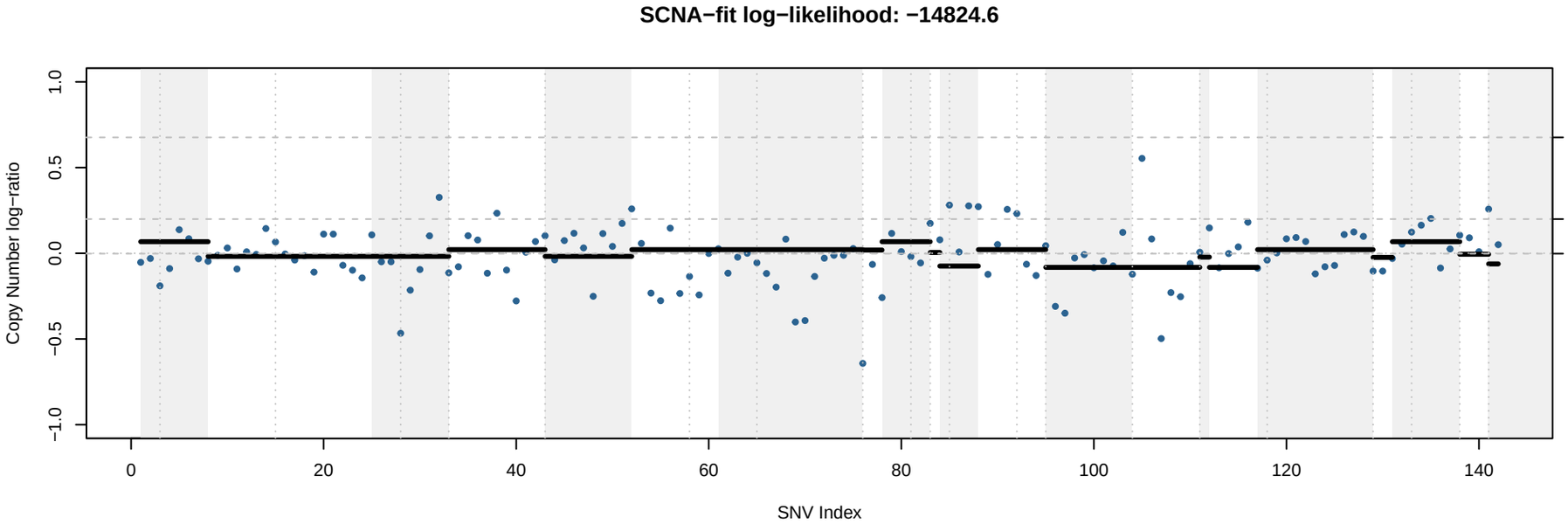

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

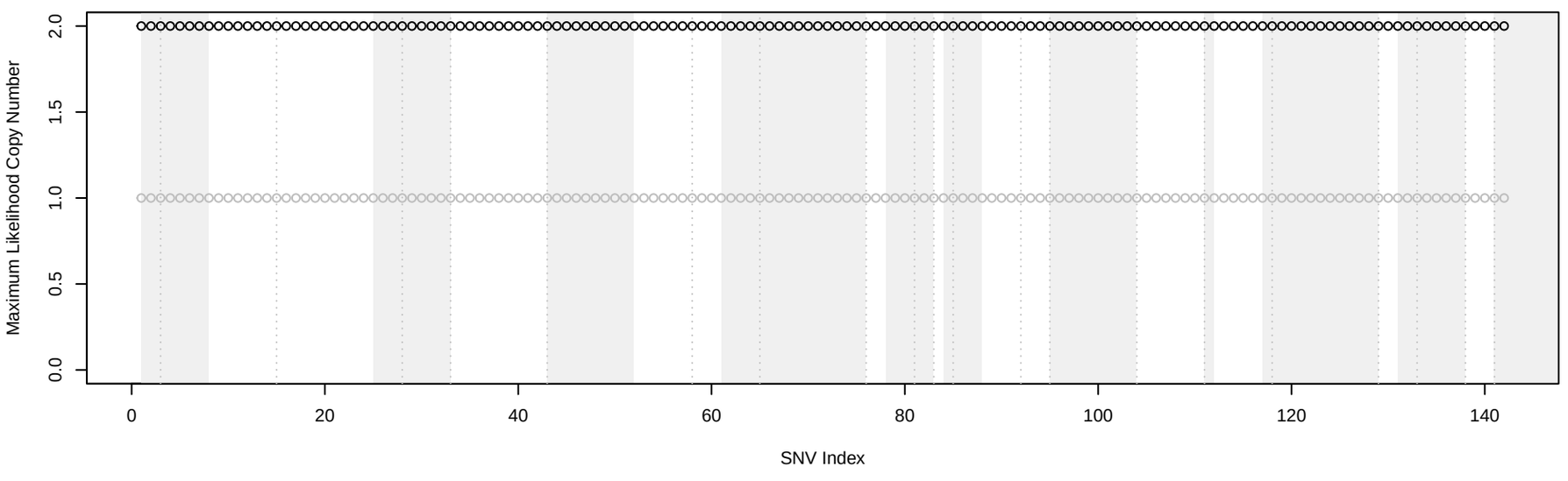

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
−0.5
0.0
0.5
Copy Number log−ratio

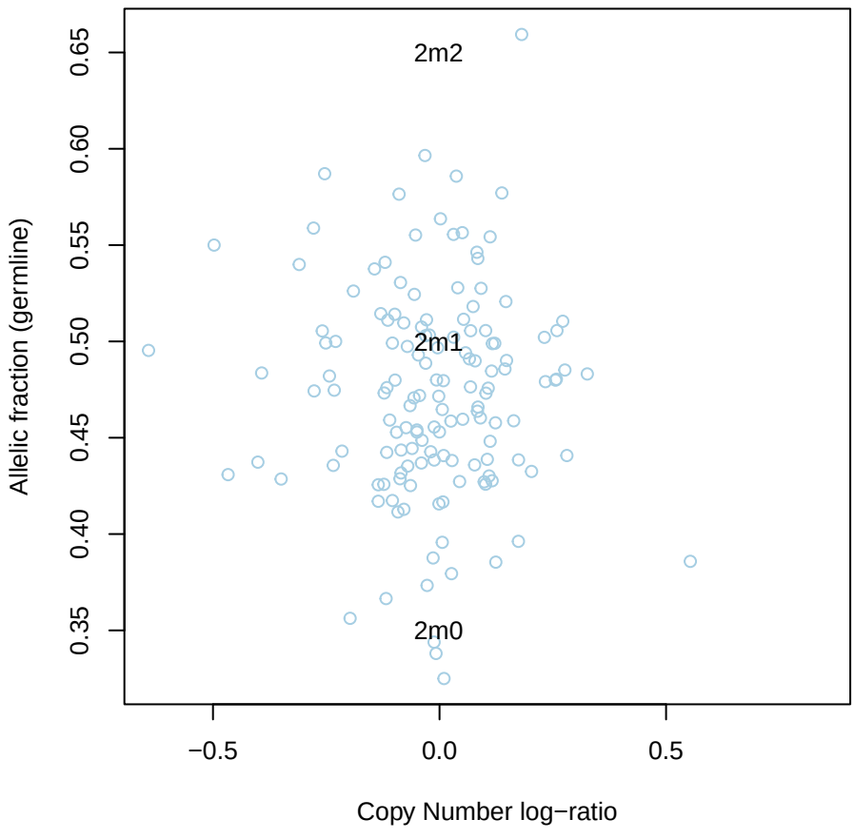

Frequency
0
5
10
15
20
25
30
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

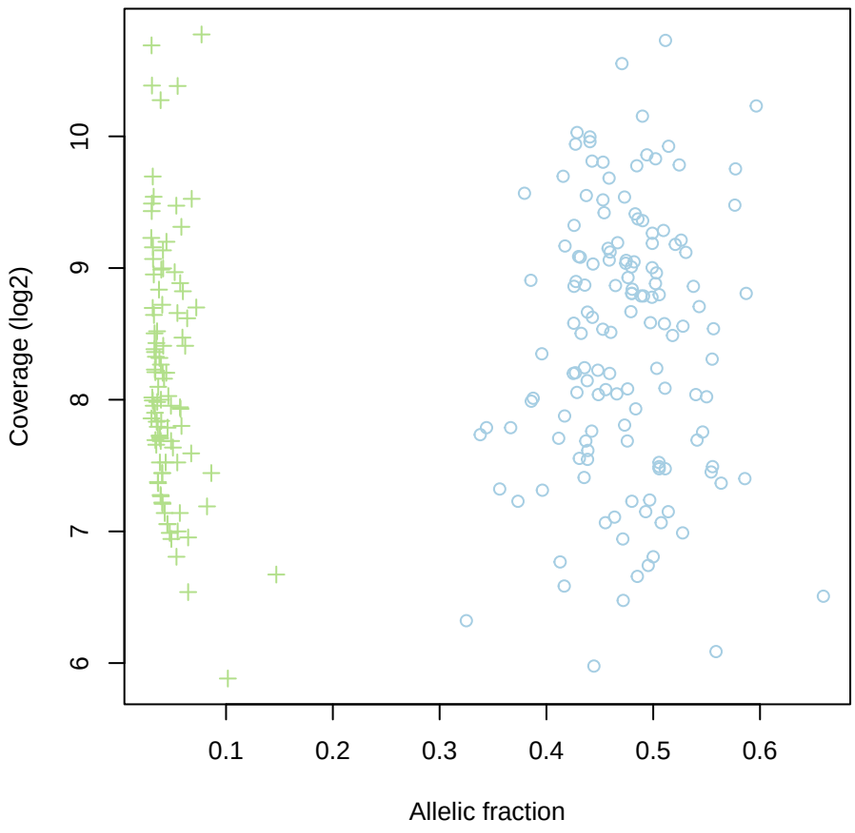

Purity: 0.3 Tumor ploidy: 2.01
2
3
6
Fraction Genome
0.00
0.05
0.10
0.15
0.20
0.25
0.0
0.5
1.0
1.5
log2 ratio

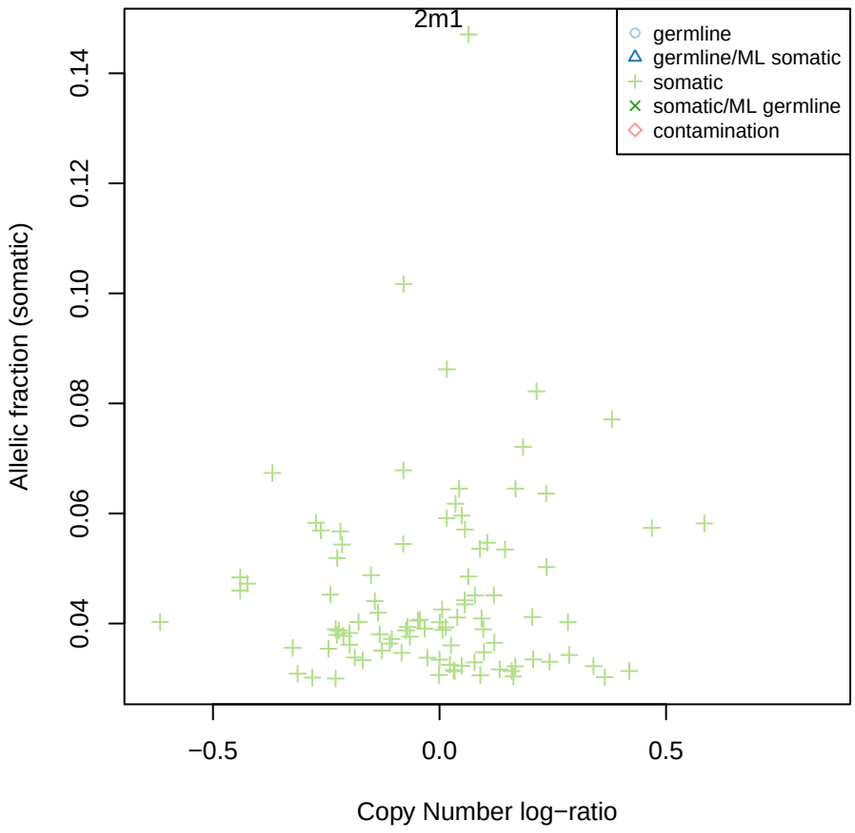

Purity: 0.3 Tumor ploidy: 2.01 SNV log−likelihood: 90.75 GoF: 84.7% Mean coverage: 370;408
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

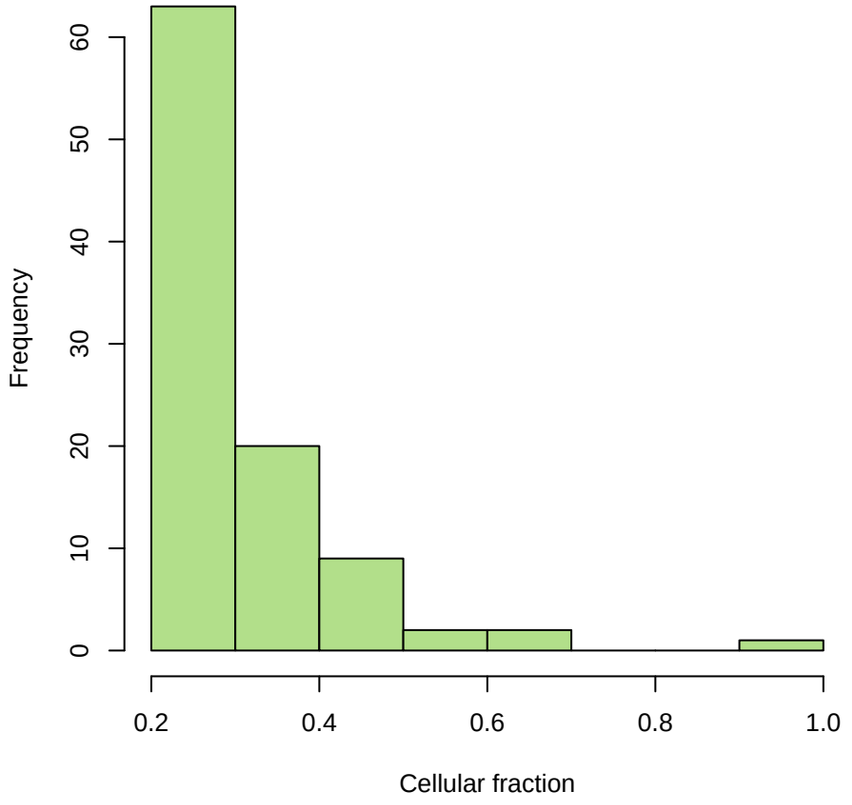

SCNA−fit log−likelihood: −14824.6
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
6 3 2
0 20 40 60 80 100 120 140
SNV Index

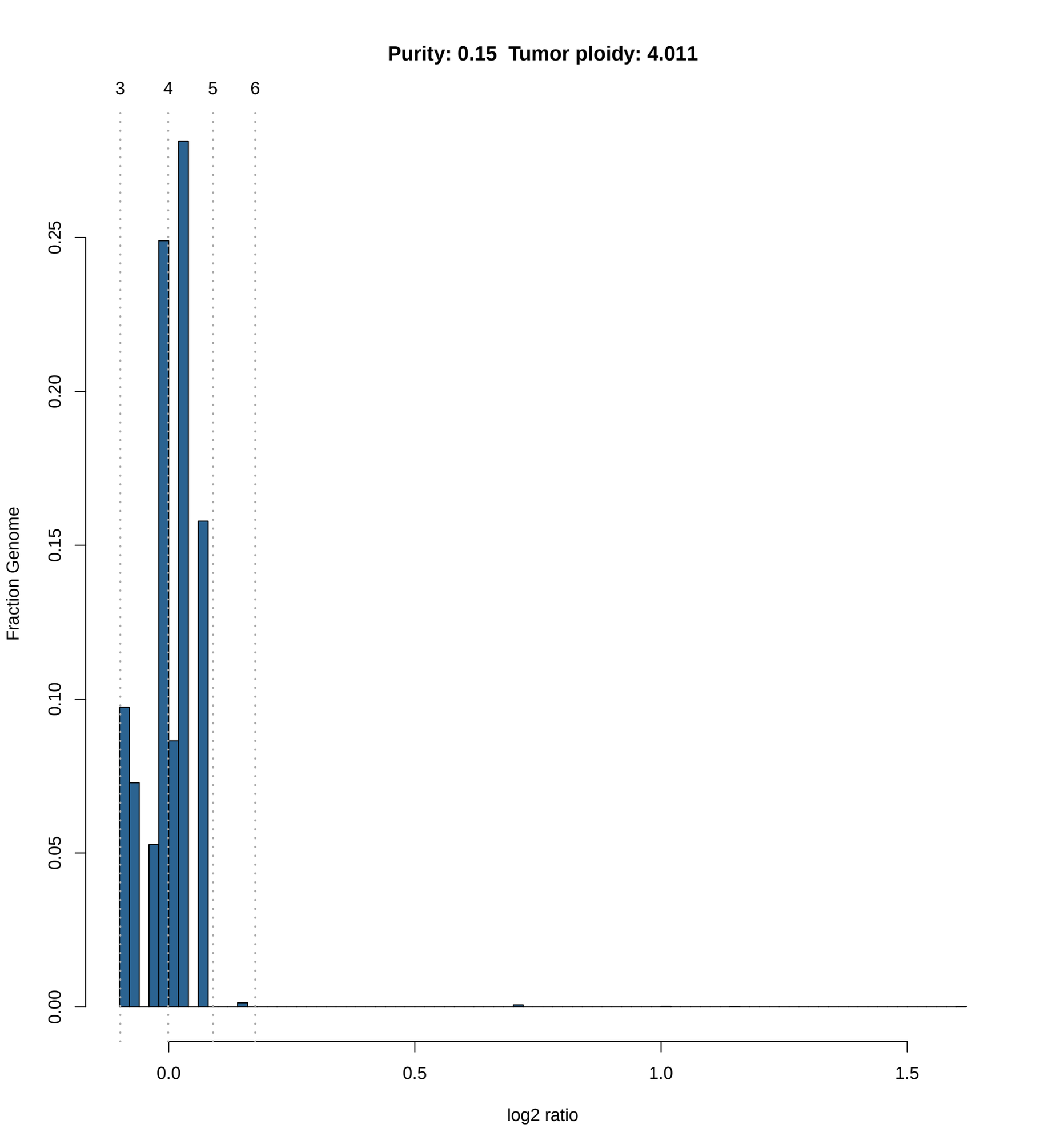

Maximum Likelihood Copy Number
2.0 1.5 1.0 0.5 0.0
0 20 40 60 80 100 120 140
SNV Index

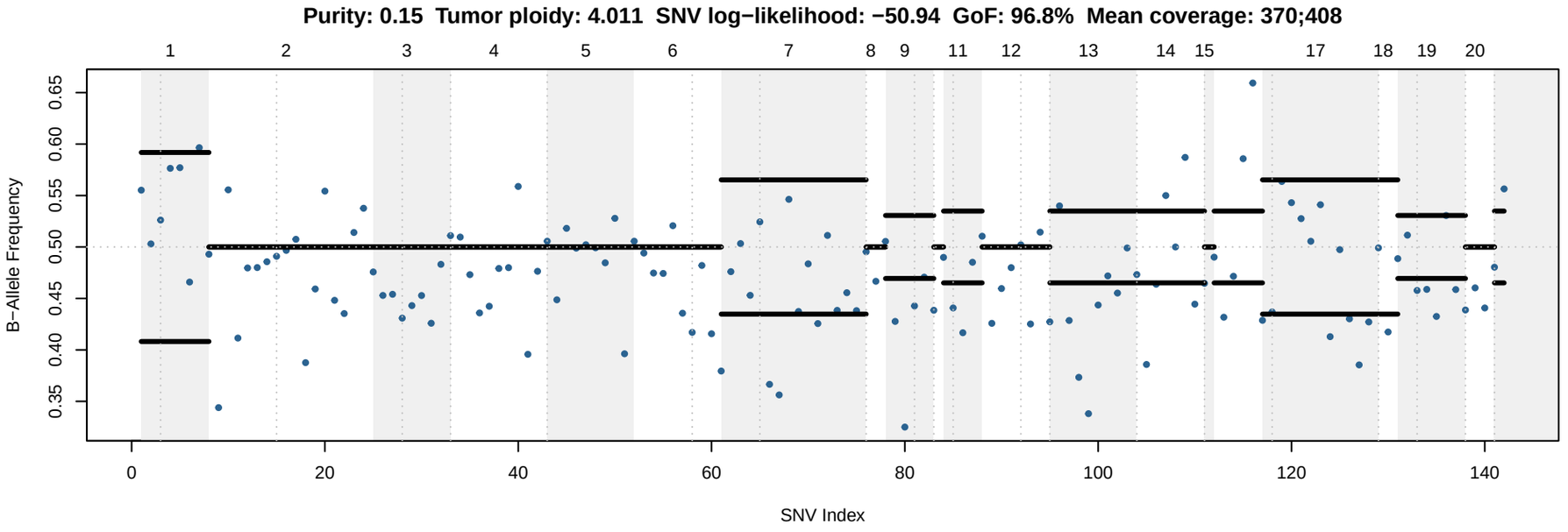

2m2
2m1
2m0
Allelic fraction (germline)
Copy Number log−ratio
0.35
0.40
0.45
0.50
0.55
0.60
0.65
−0.5
0.0
0.5

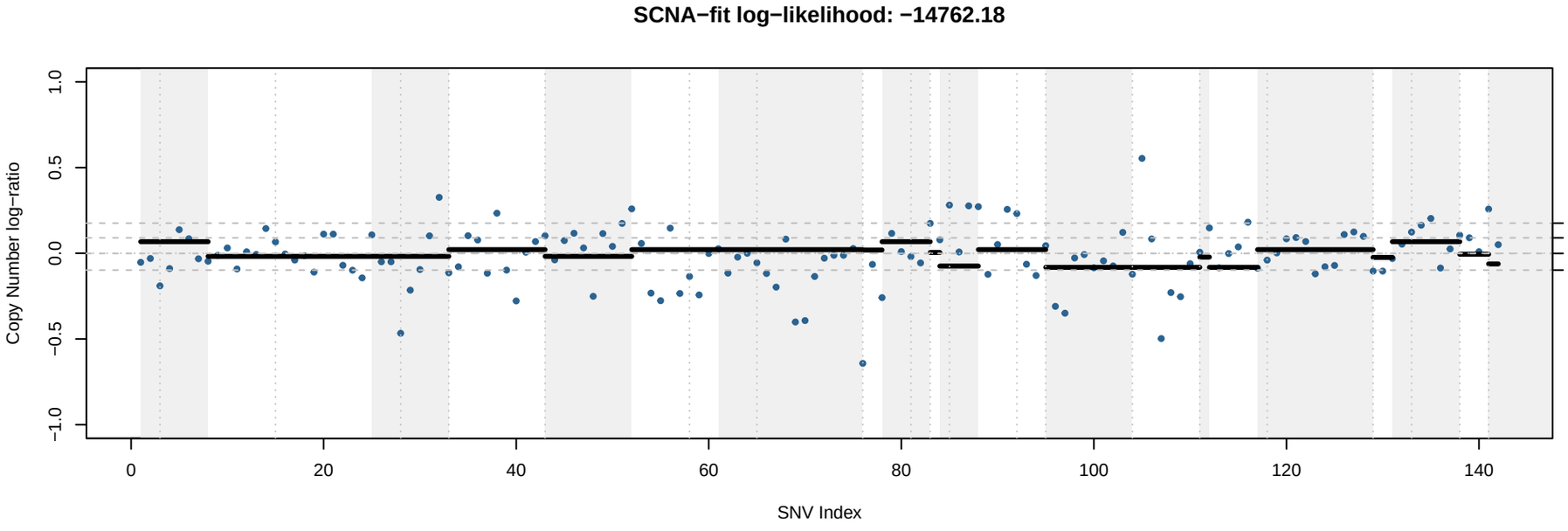

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

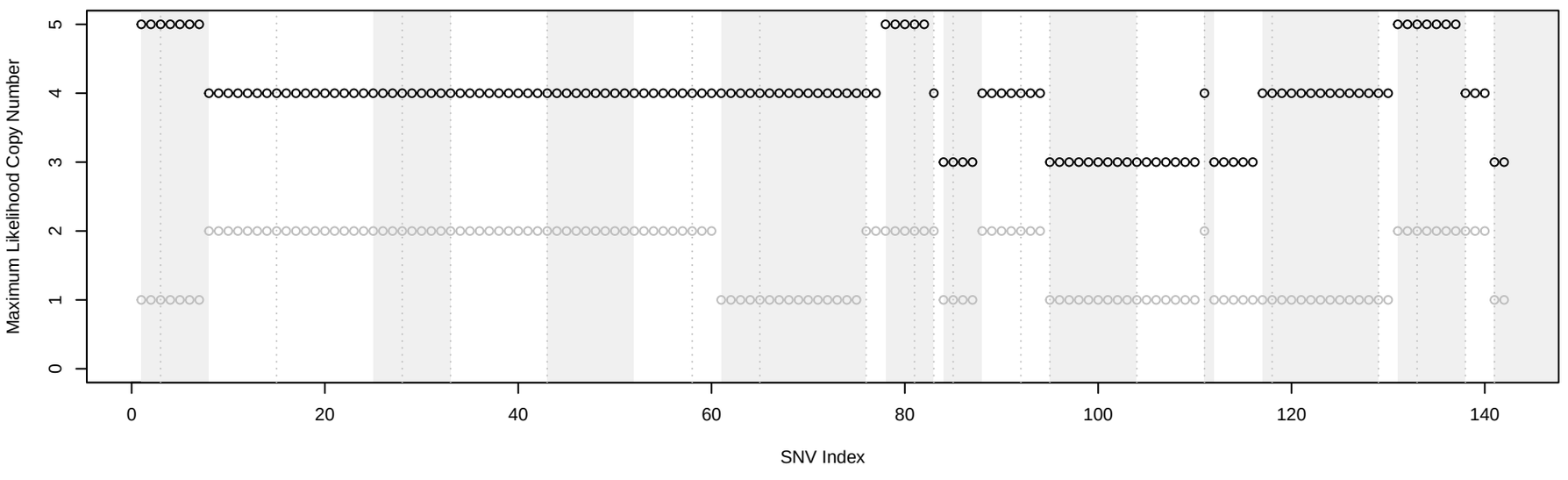

2m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
0.12
0.14
−0.5
0.0
0.5

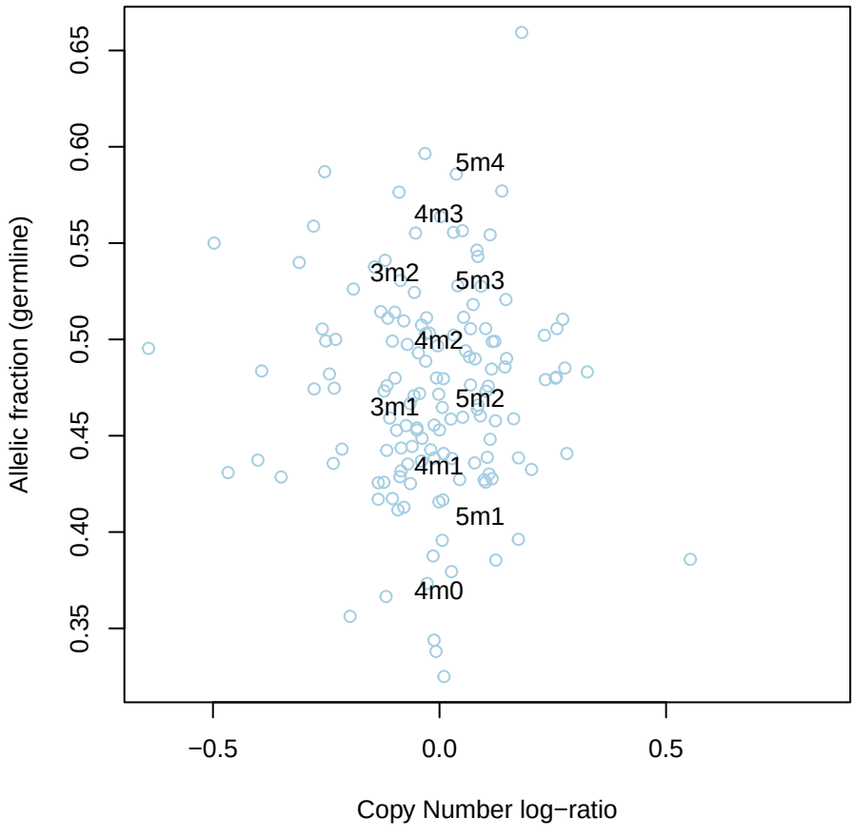

Frequency
Cellular fraction
0
10
20
30
40
50
60
0.2
0.4
0.6
0.8
1.0

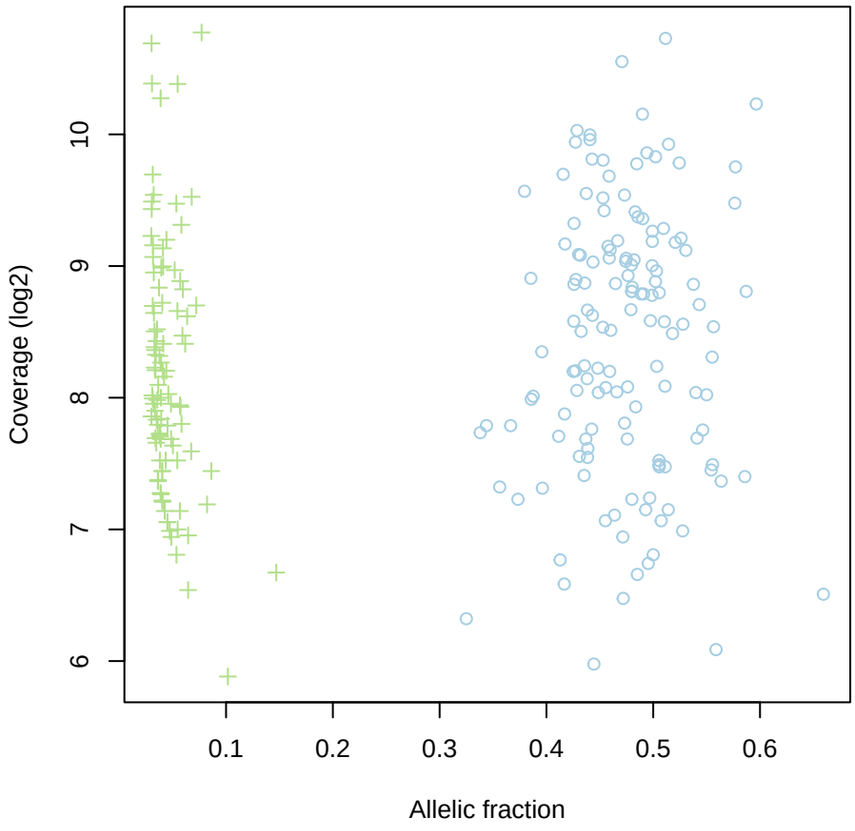

Purity: 0.15 Tumor ploidy: 4.011
3
4
5
6
Fraction Genome
0.00
0.05
0.10
0.15
0.20
0.25
0.0
0.5
1.0
1.5
log2 ratio

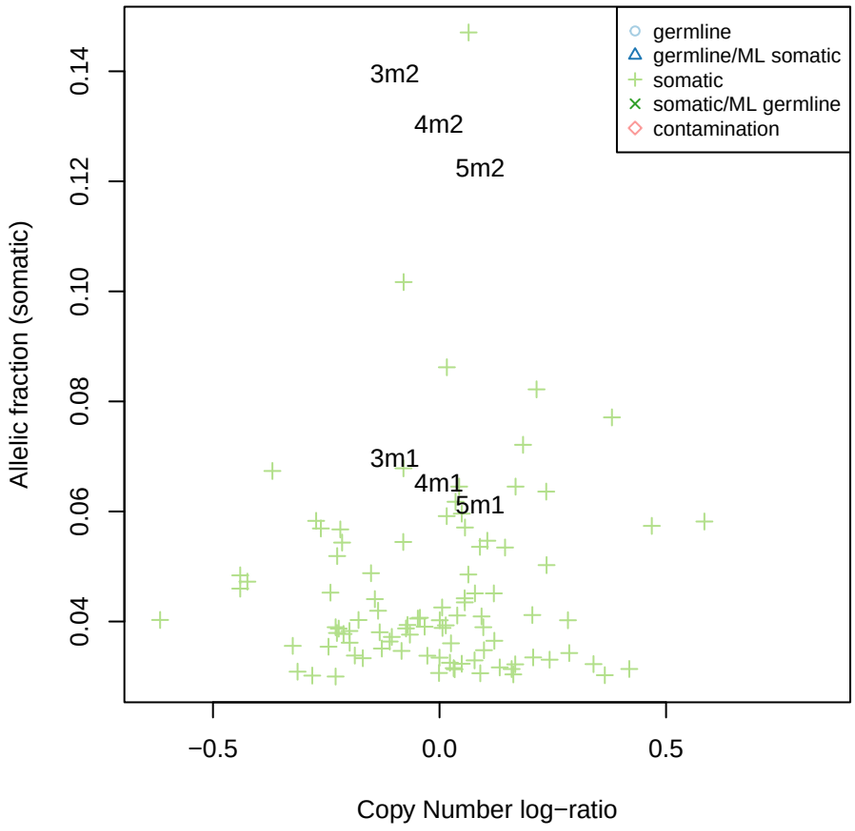

Purity: 0.15 Tumor ploidy: 4.011 SNV log−likelihood: −50.94 GoF: 96.8% Mean coverage: 370;408
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

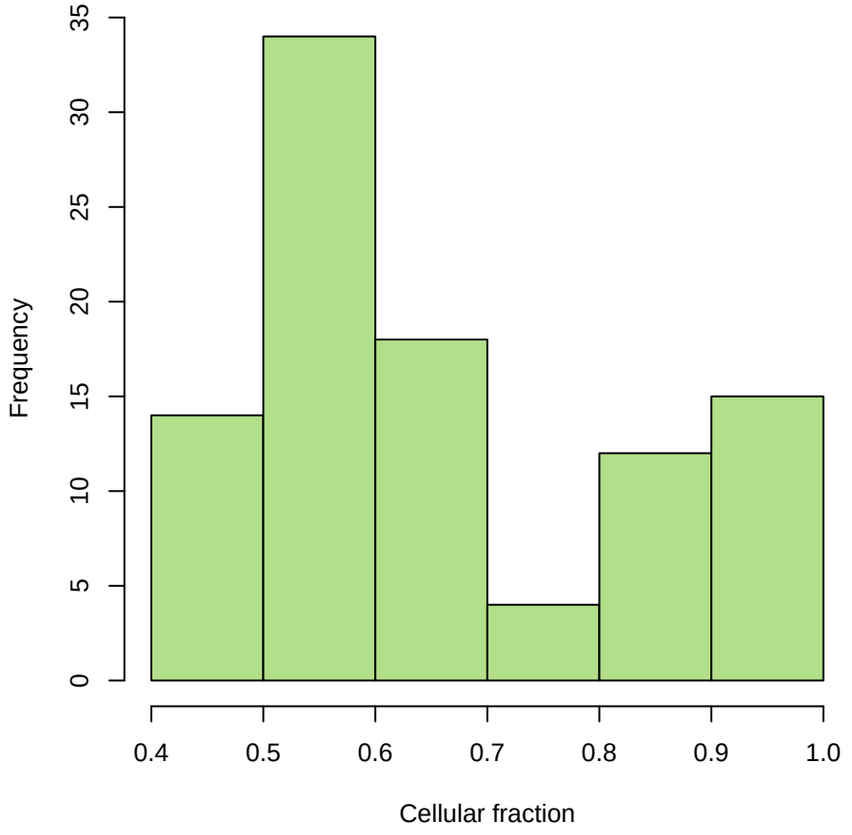

SCNA−fit log−likelihood: −14762.18
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 5
0 20 40 60 80 100 120 140
SNV Index

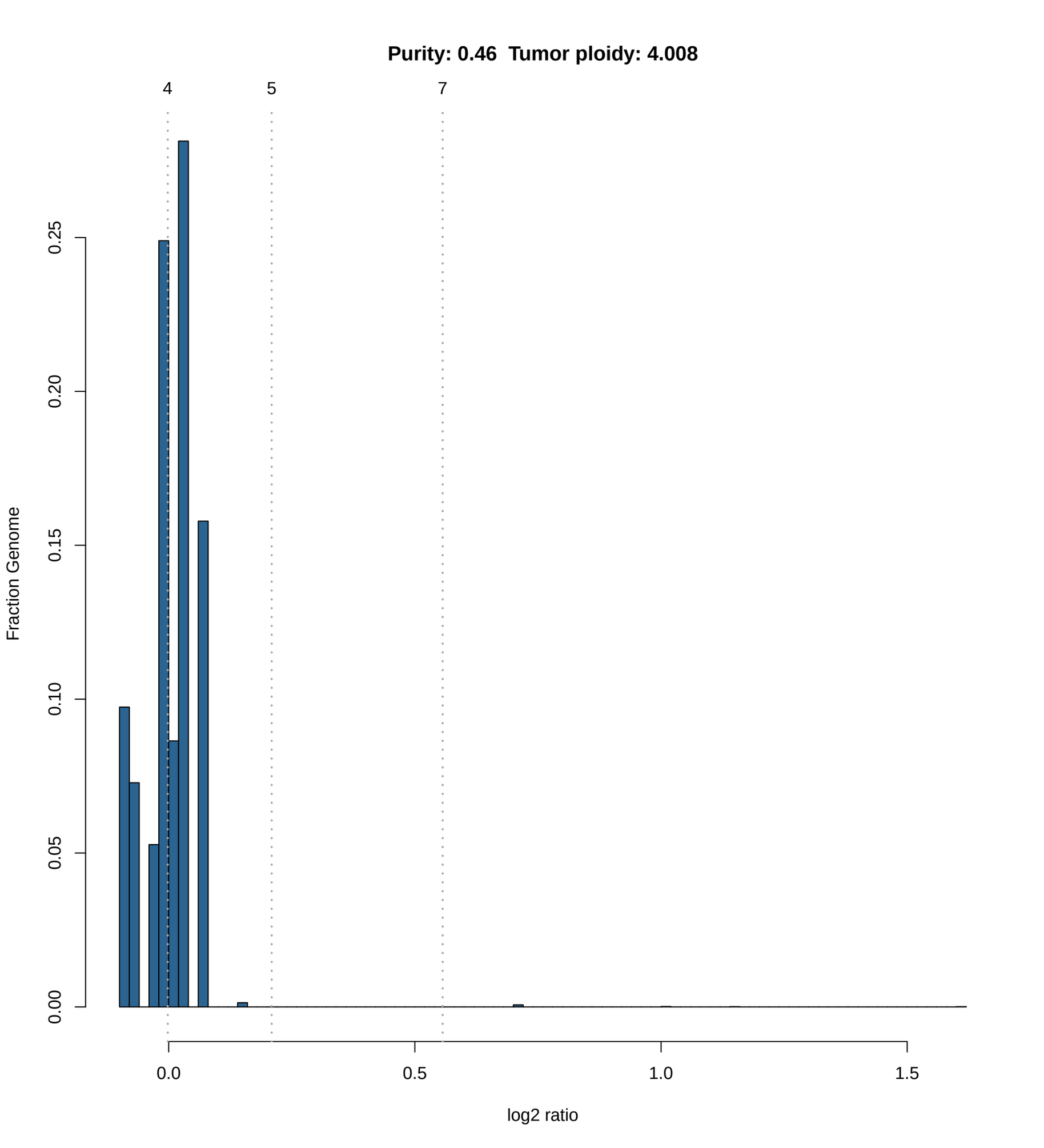

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

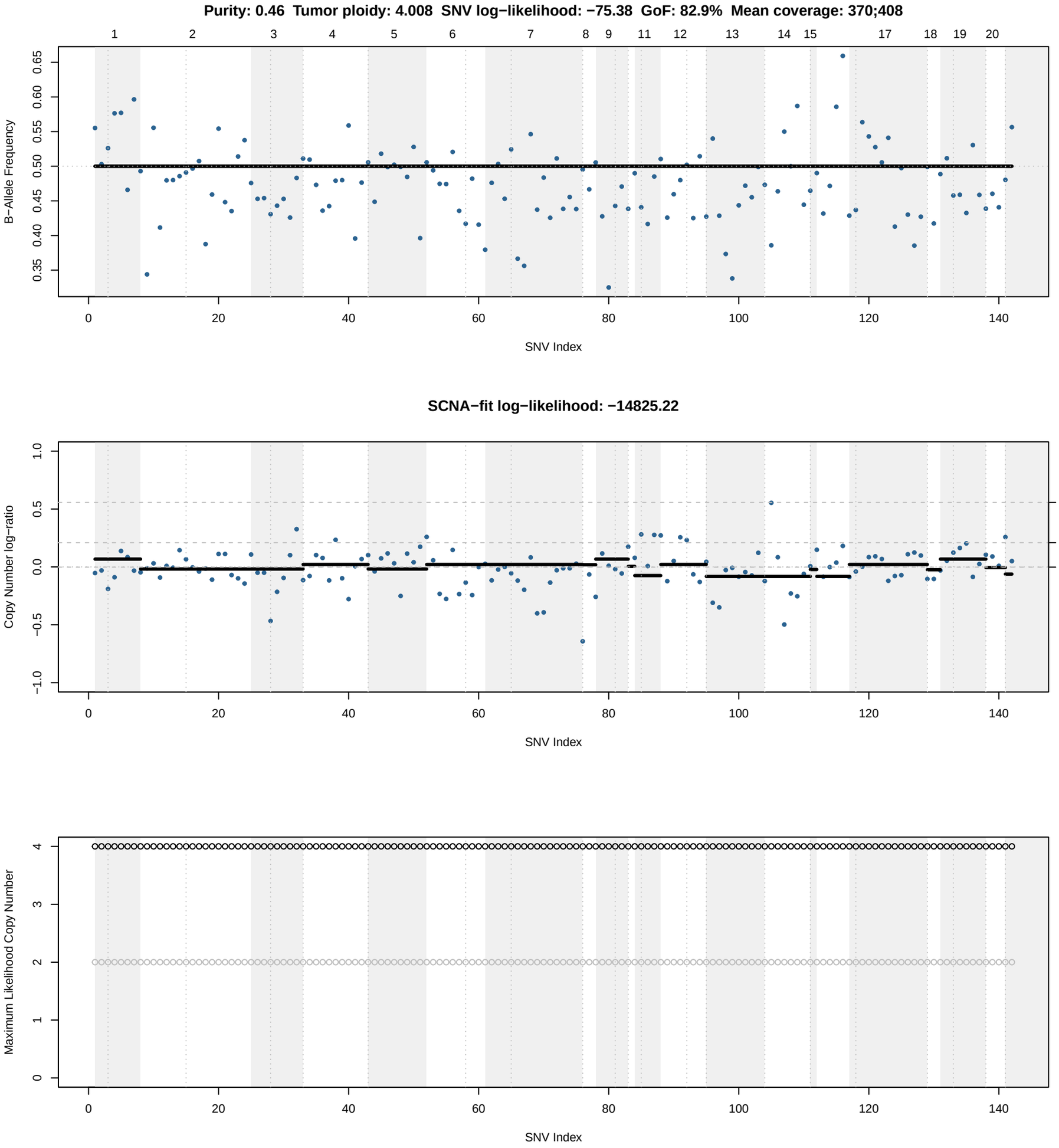

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
5m4
4m3
3m2
5m3
4m2
3m1
5m2
4m1
5m1
4m0
−0.5
0.0
0.5
Copy Number log−ratio

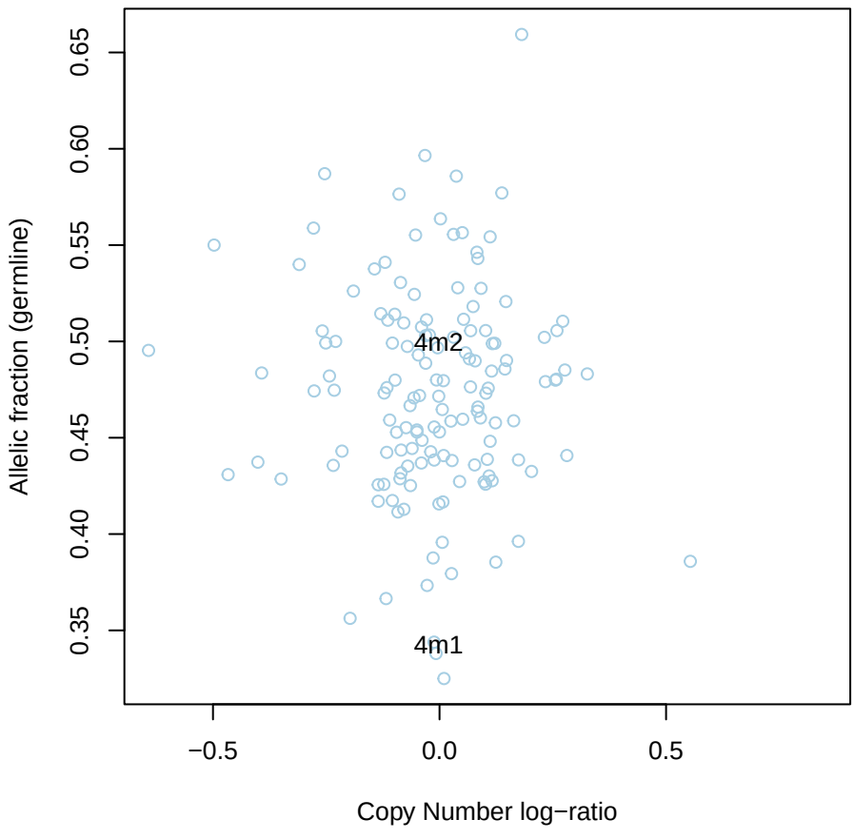

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

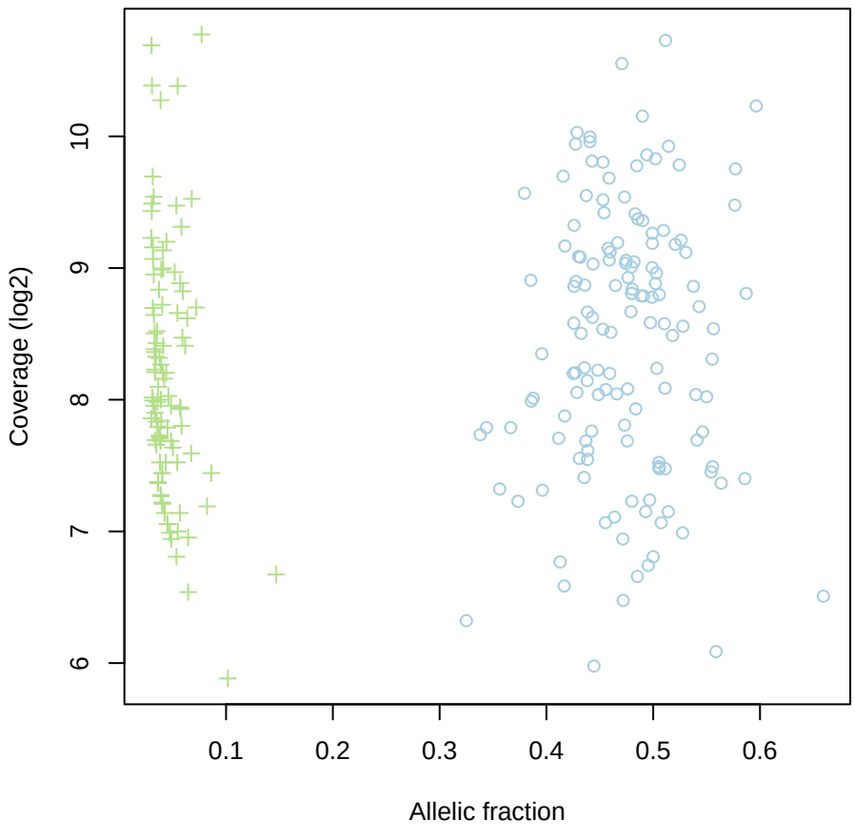

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
3m2
4m2
5m2
3m1
4m1
5m1
−0.5
0.0
0.5
Copy Number log−ratio

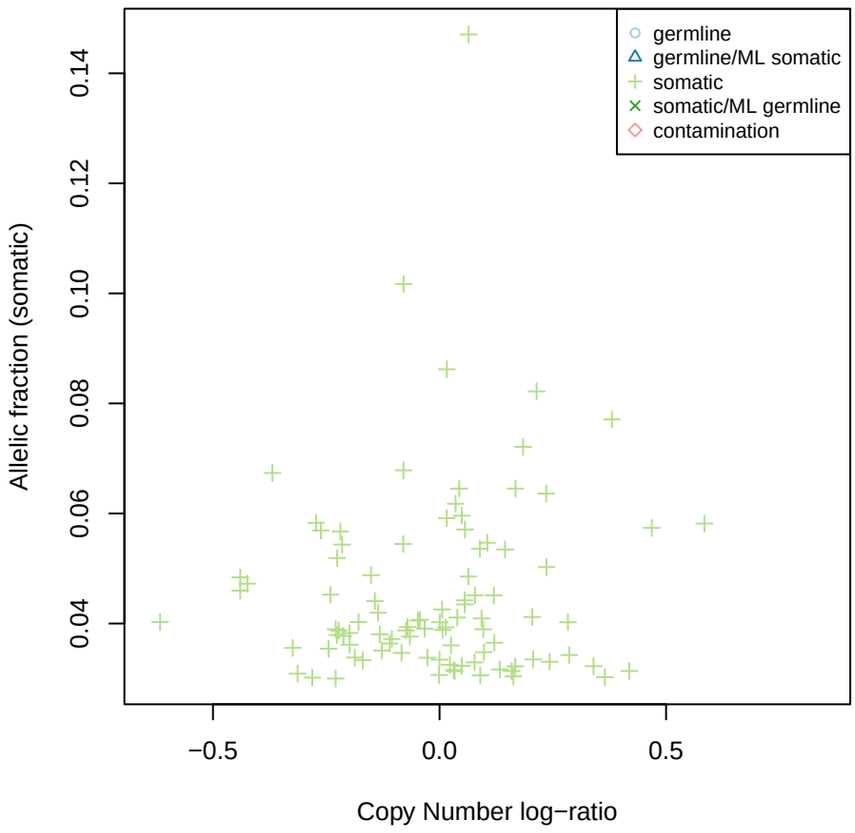

Frequency
0
5
10
15
20
25
30
35
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

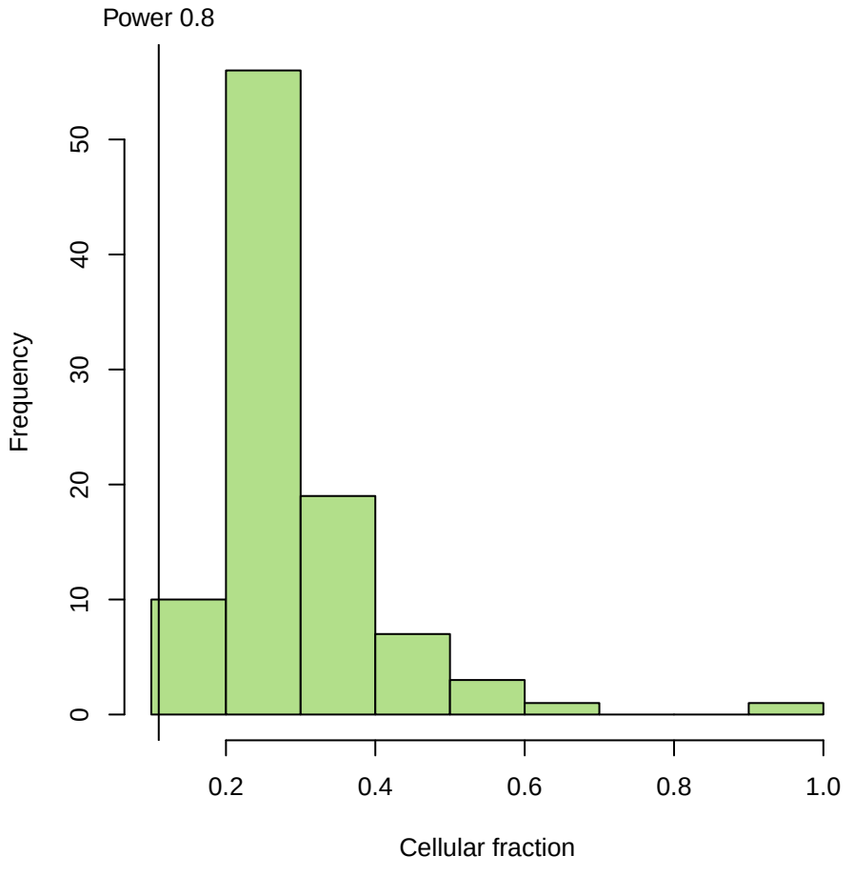

Purity: 0.46 Tumor ploidy: 4.008
4
5
7
Fraction Genome
0.00
0.05
0.10
0.15
0.20
0.25
0.0
0.5
1.0
1.5
log2 ratio

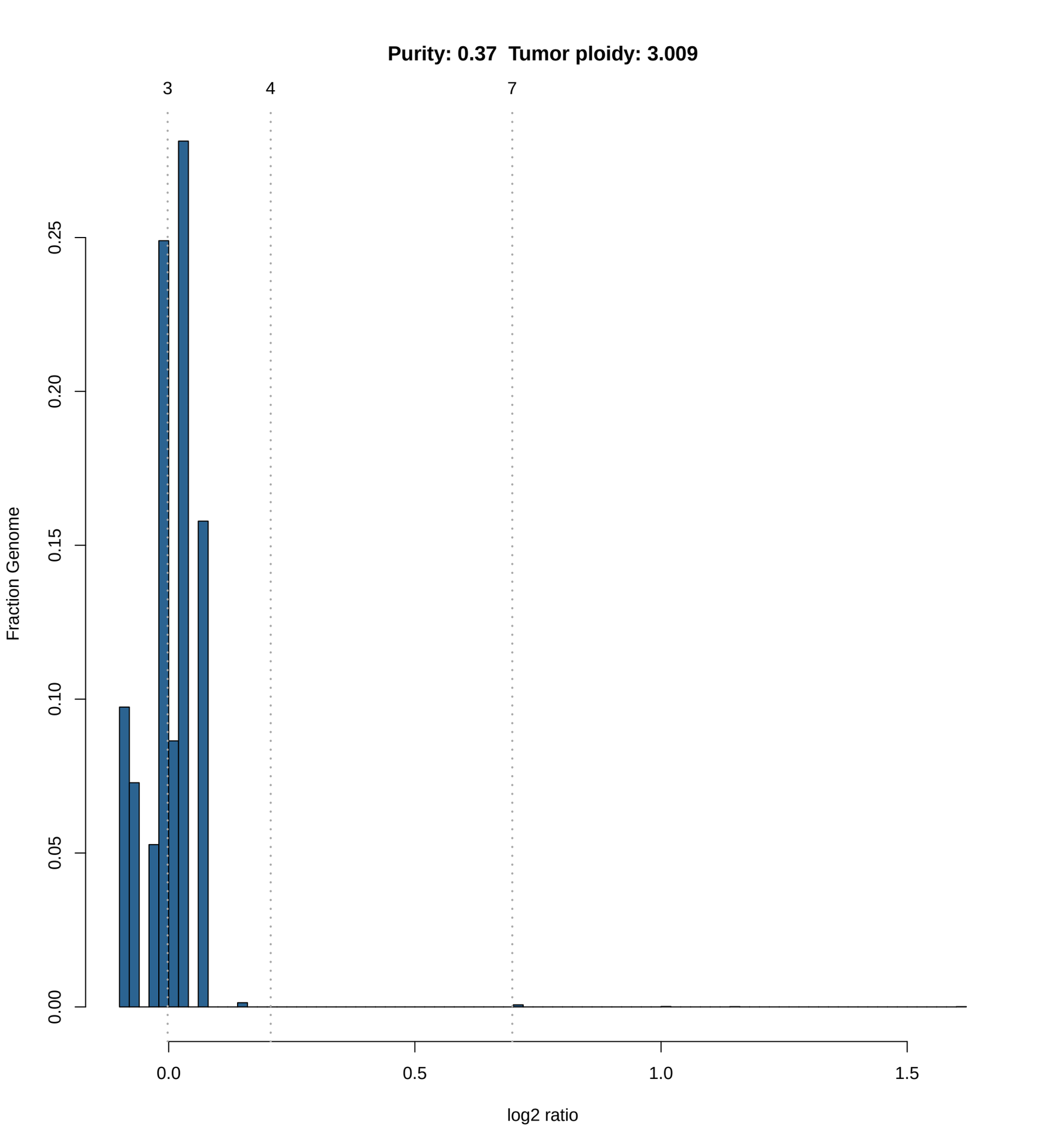

Purity: 0.46 Tumor ploidy: 4.008 SNV log−likelihood: −75.38 GoF: 82.9% Mean coverage: 370;408
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index
SCNA−fit log−likelihood: −14825.22
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5 7
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

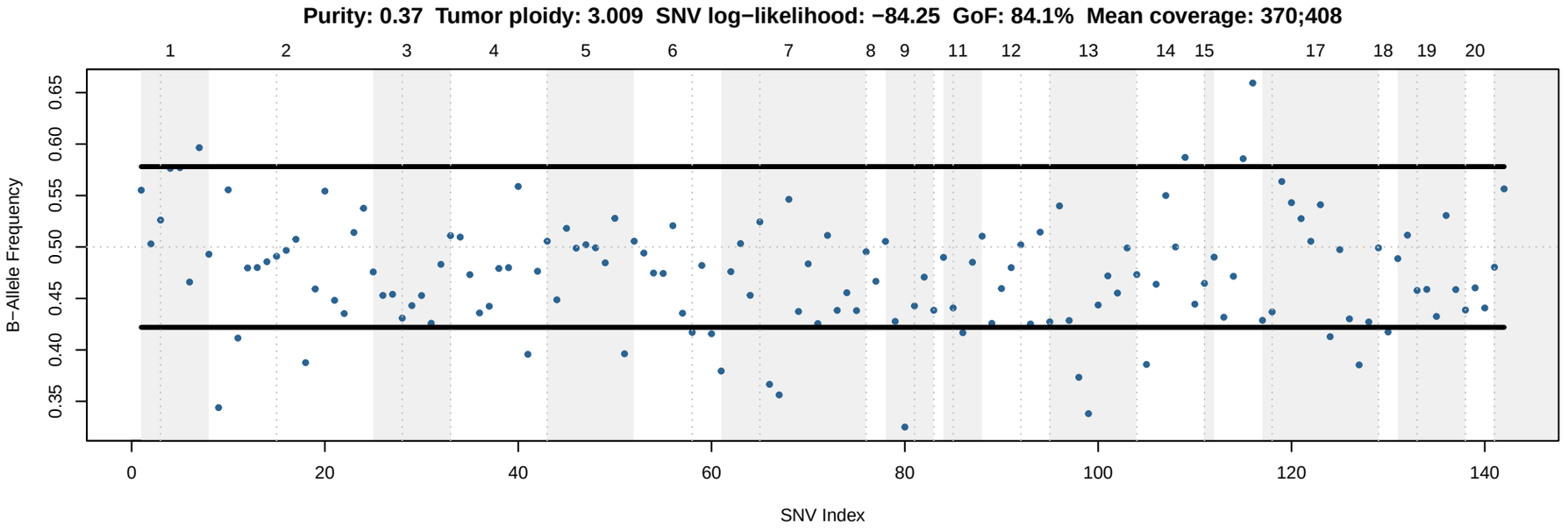

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
4m2
4m1
−0.5
0.0
0.5
Copy Number log−ratio

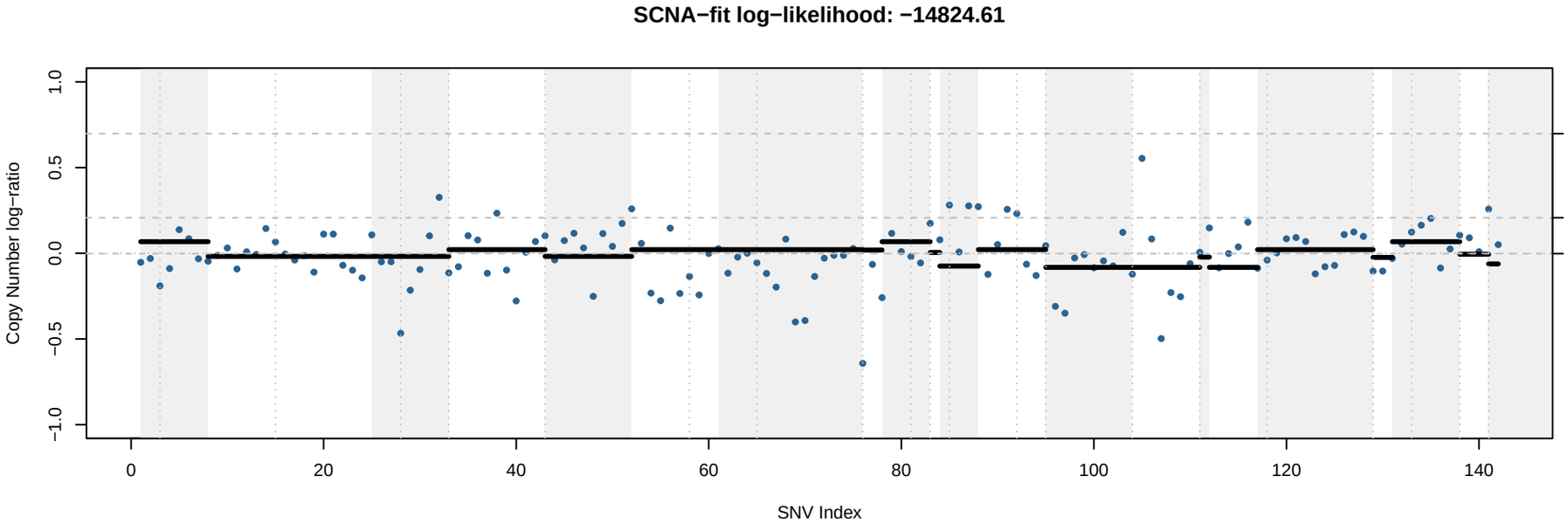

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

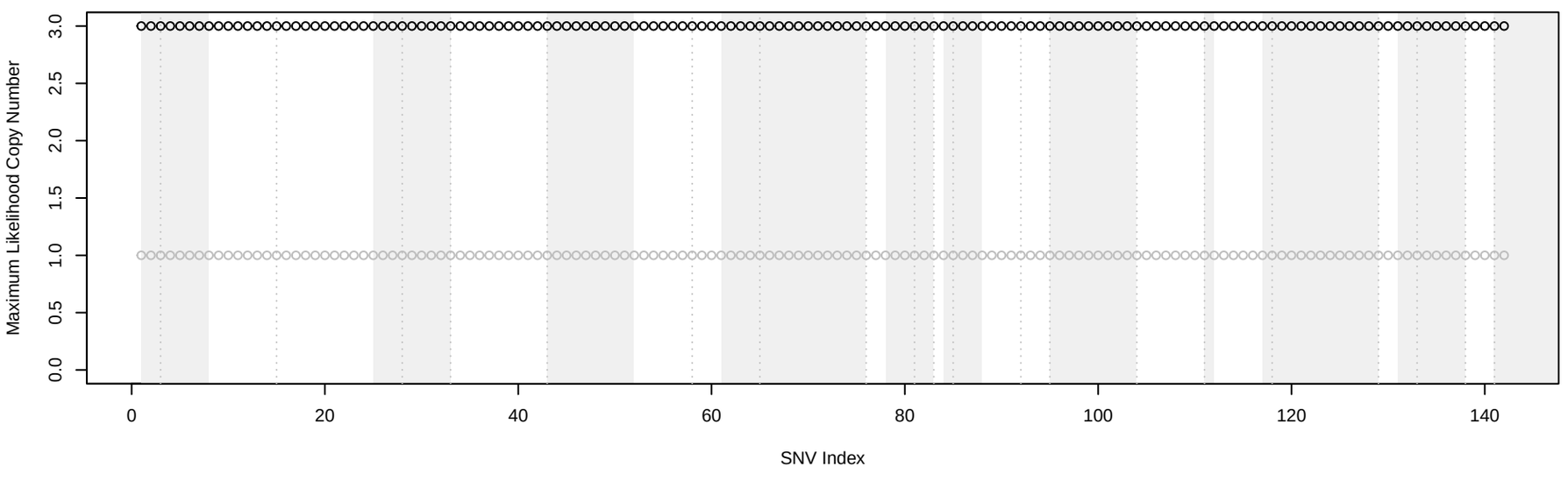

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.5
0.0
0.5
Copy Number log−ratio

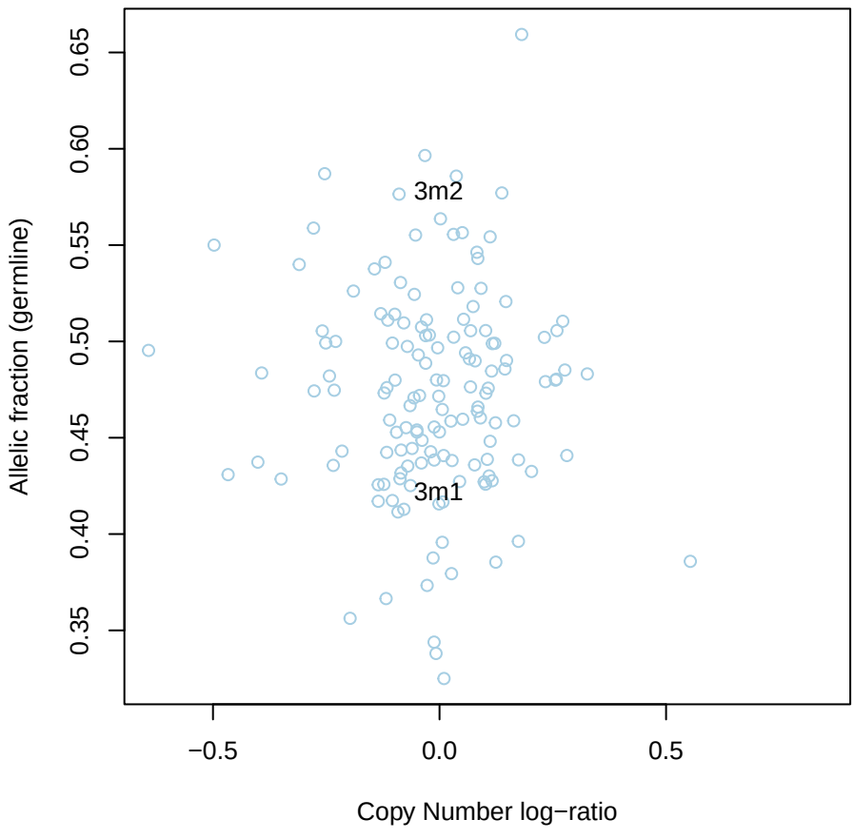

Power 0.8
Frequency
0
10
20
30
40
50
0.2
0.4
0.6
0.8
1.0
Cellular fraction

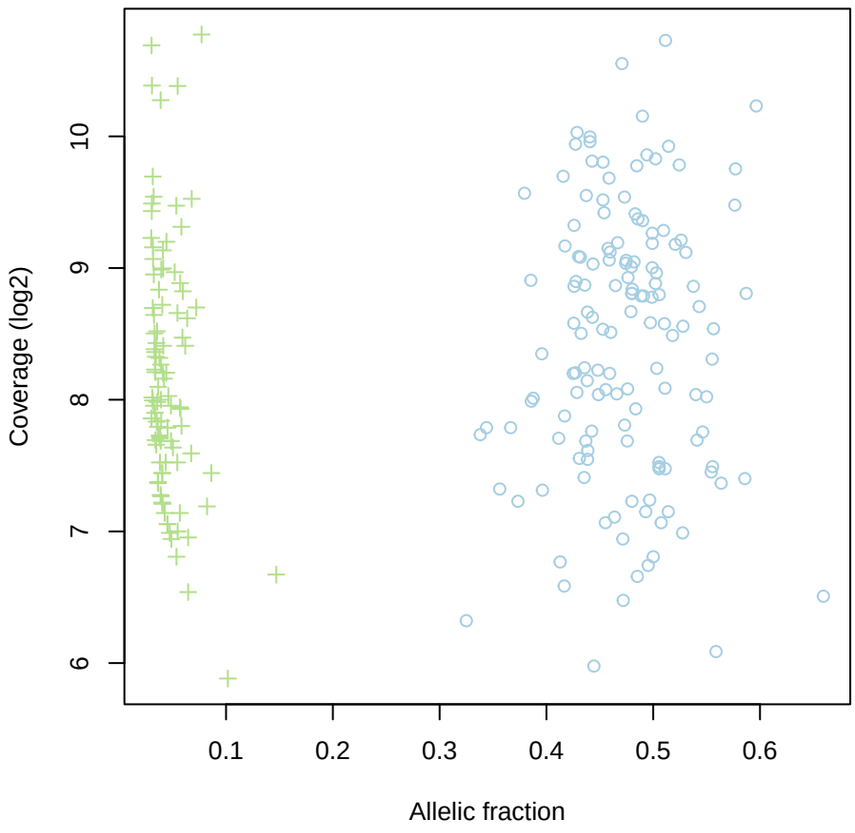

Purity: 0.37 Tumor ploidy: 3.009
3
4
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
1.5
log2 ratio

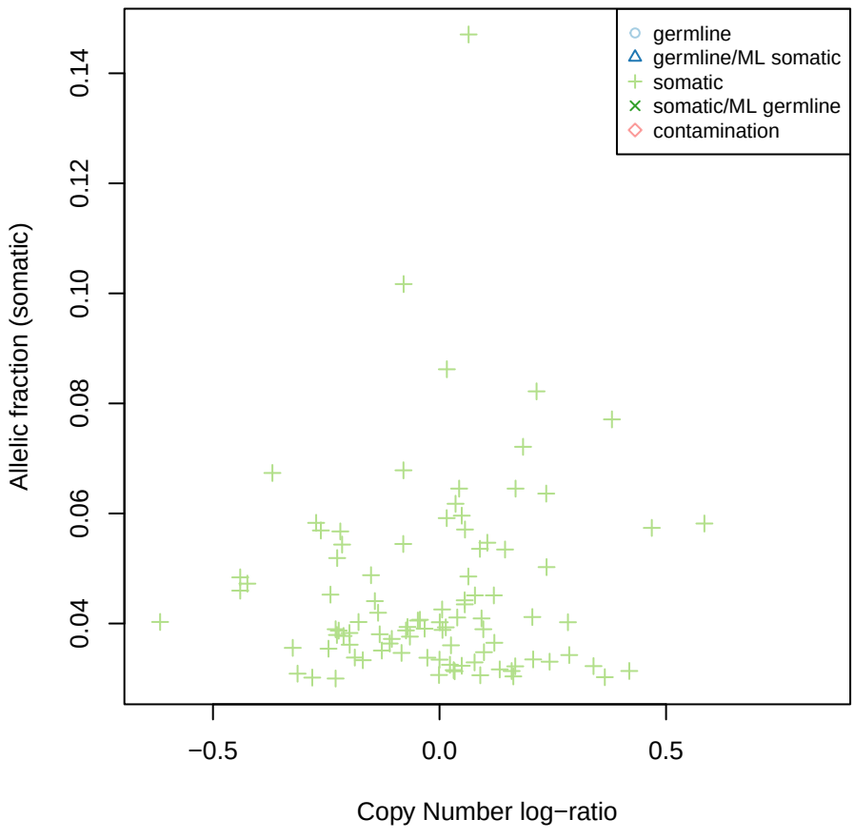

Purity: 0.37 Tumor ploidy: 3.009 SNV log−likelihood: −84.25 GoF: 84.1% Mean coverage: 370;408
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

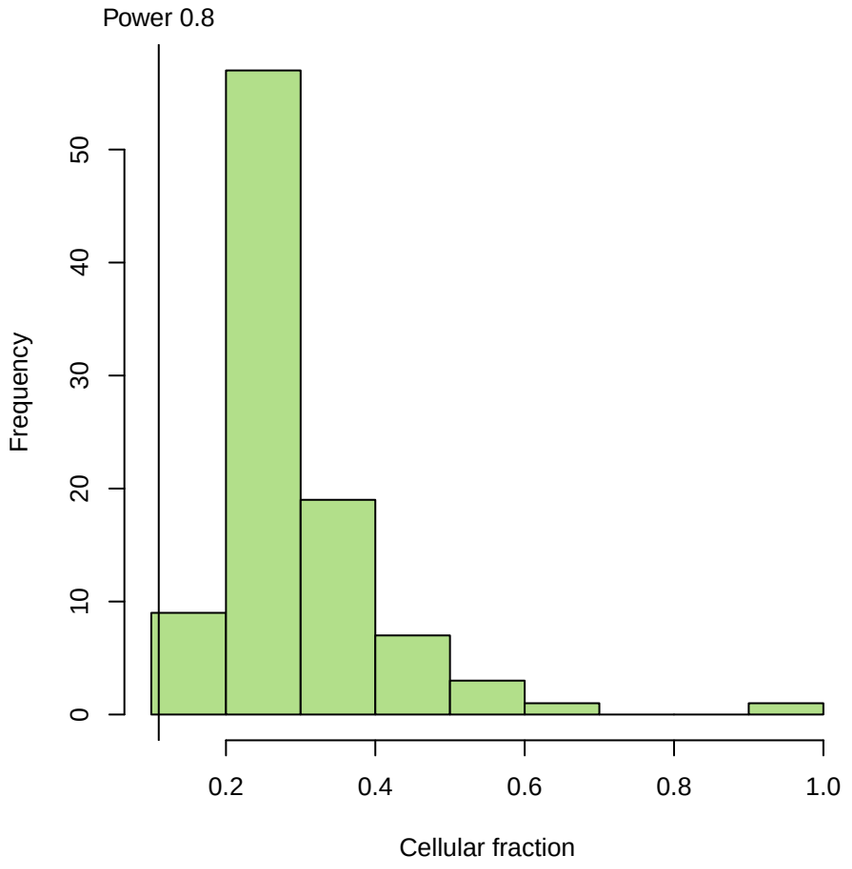

SCNA−fit log−likelihood: −14824.61
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
7 4 3
0 20 40 60 80 100 120 140
SNV Index

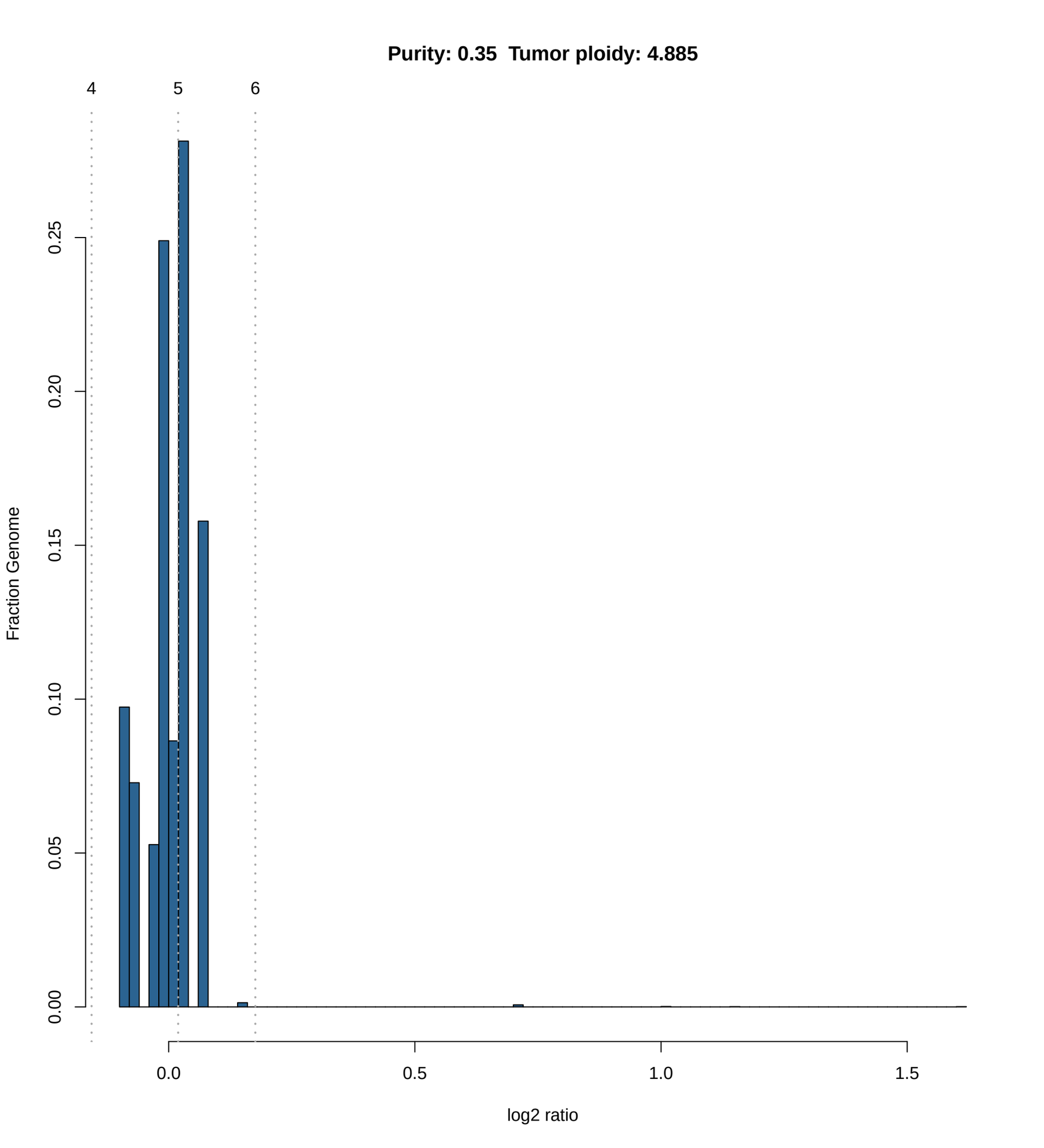

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120 140
SNV Index

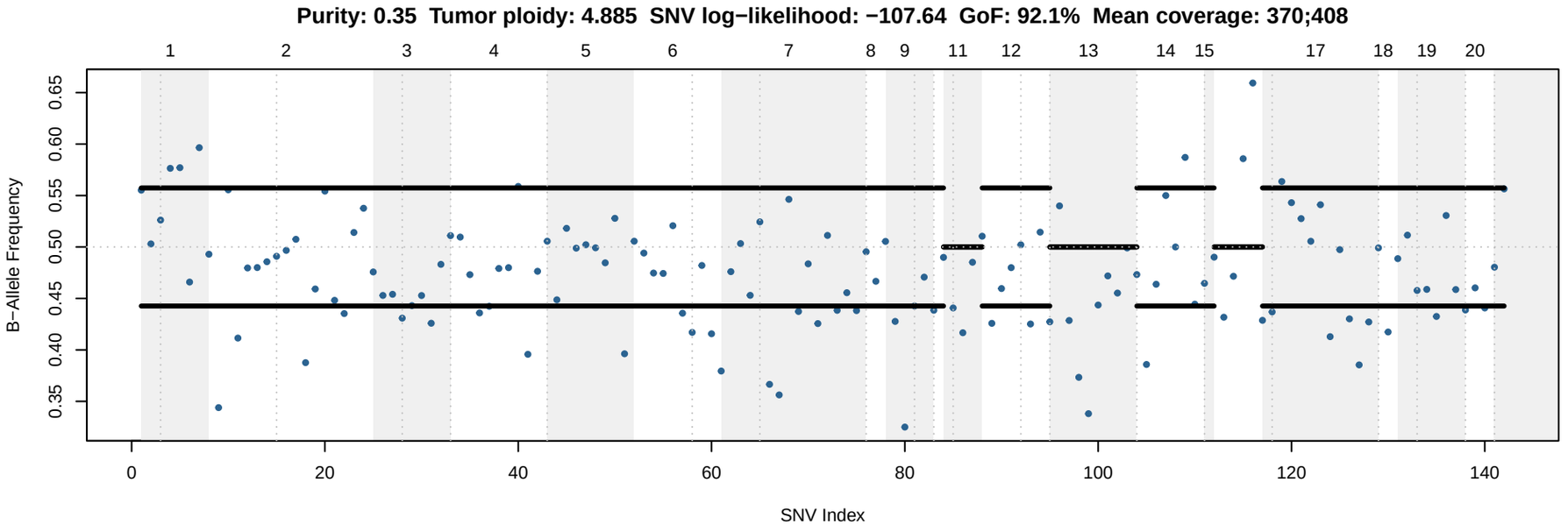

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
3m2
3m1
−0.5
0.0
0.5
Copy Number log−ratio

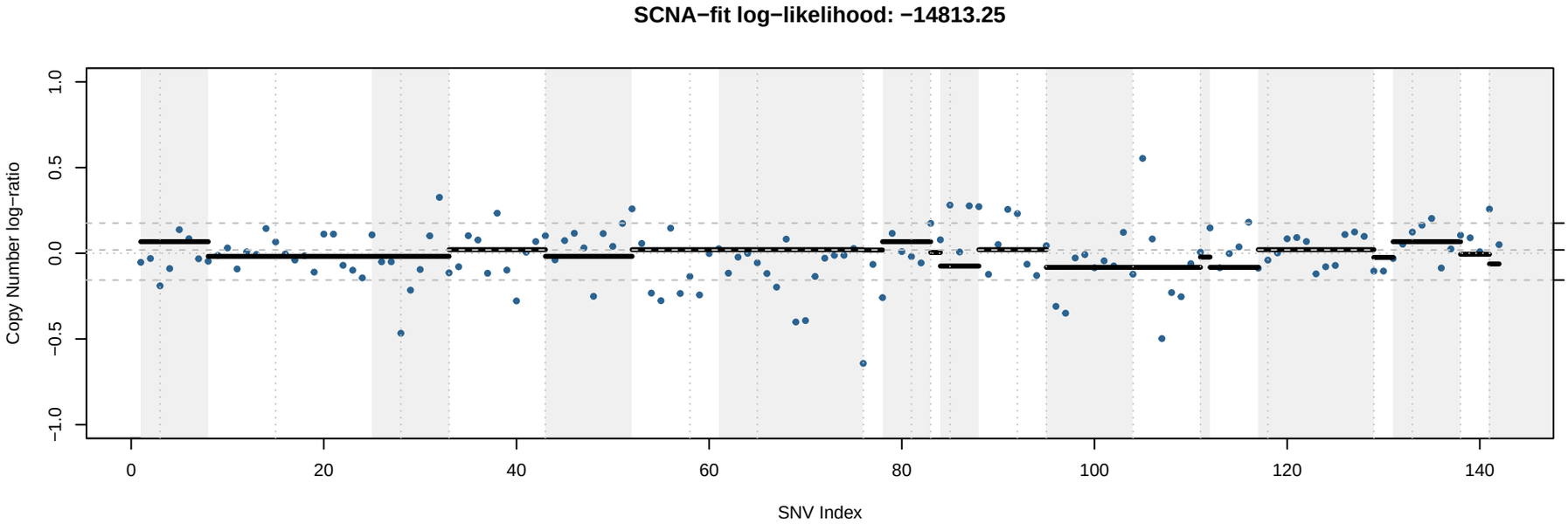

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

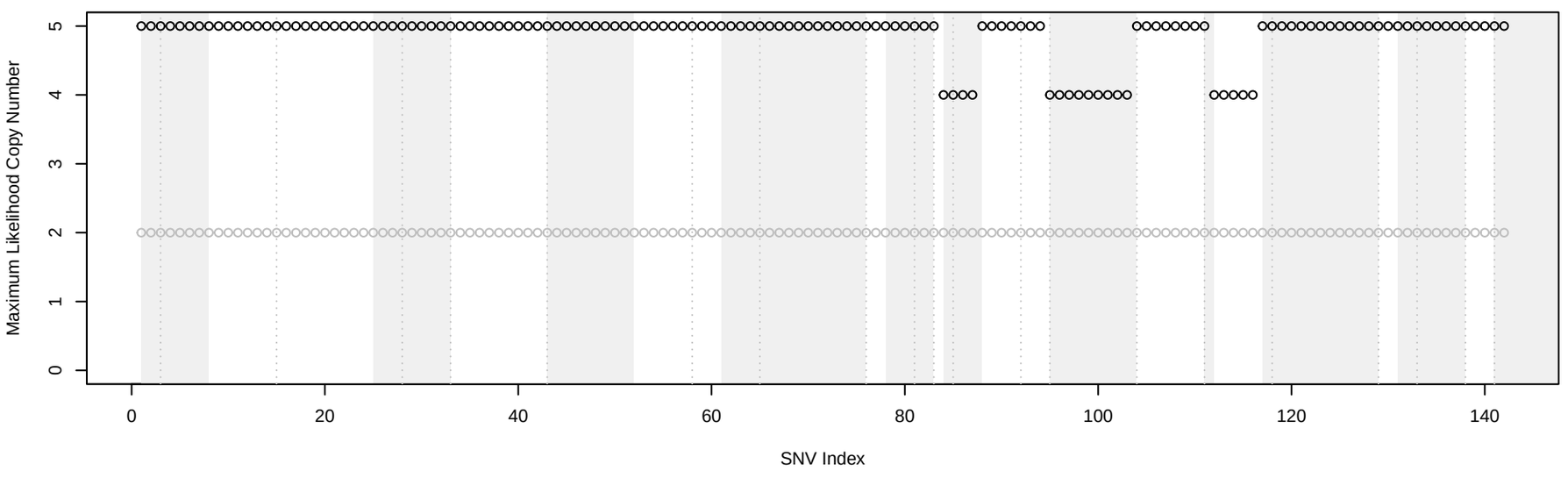

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.5
0.0
0.5
Copy Number log−ratio

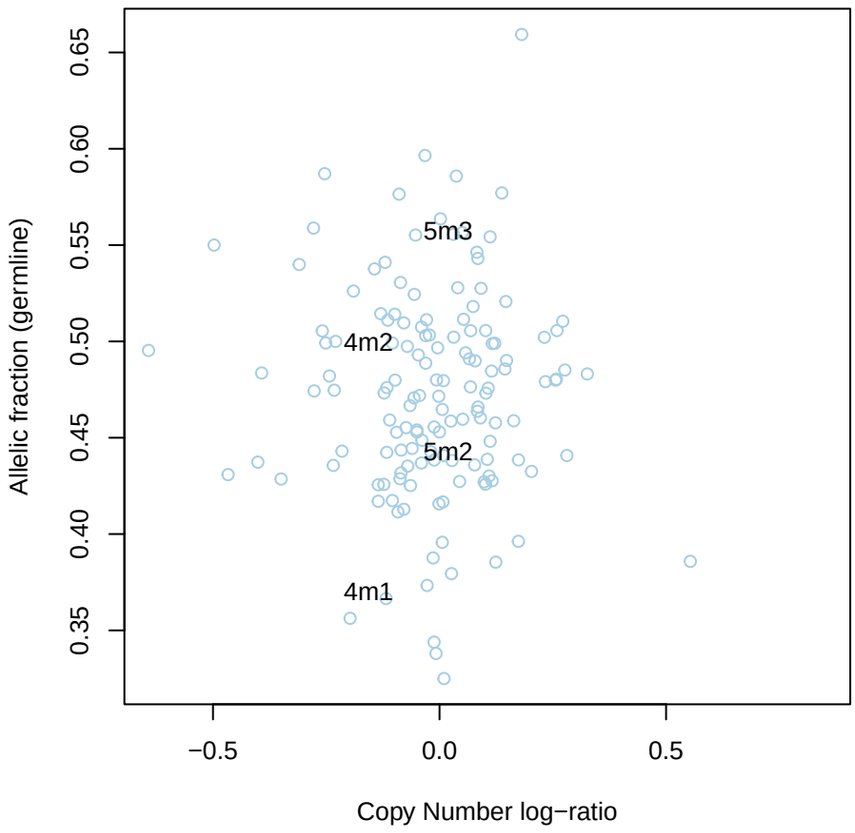

Power 0.8
Frequency
0
10
20
30
40
50
0.2
0.4
0.6
0.8
1.0
Cellular fraction

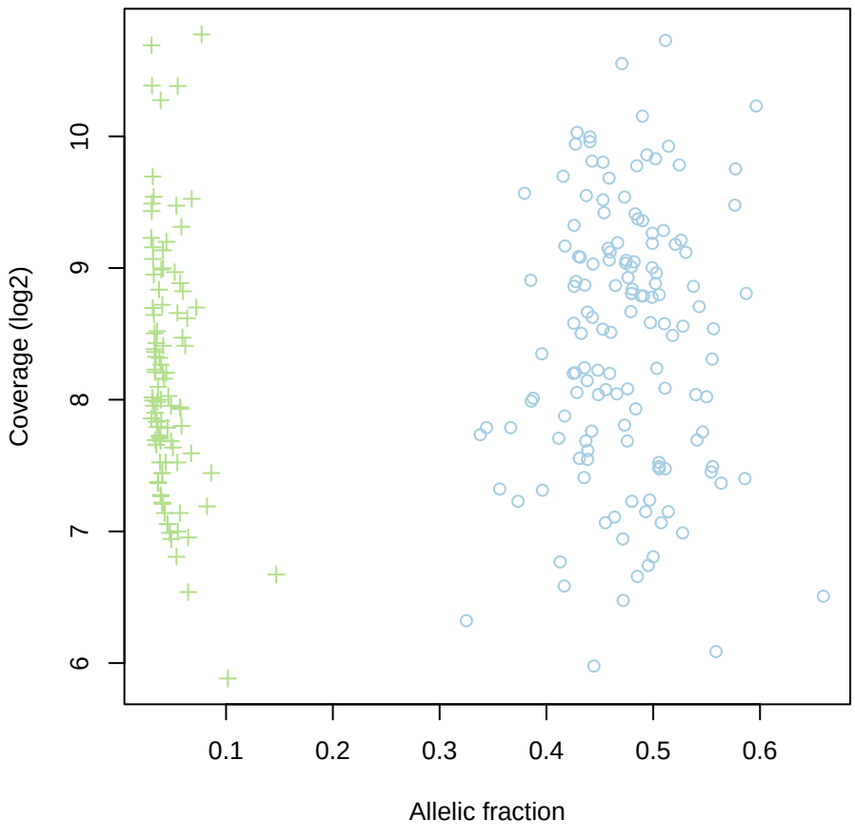

Purity: 0.35 Tumor ploidy: 4.885
4
5
6
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
1.5
log2 ratio

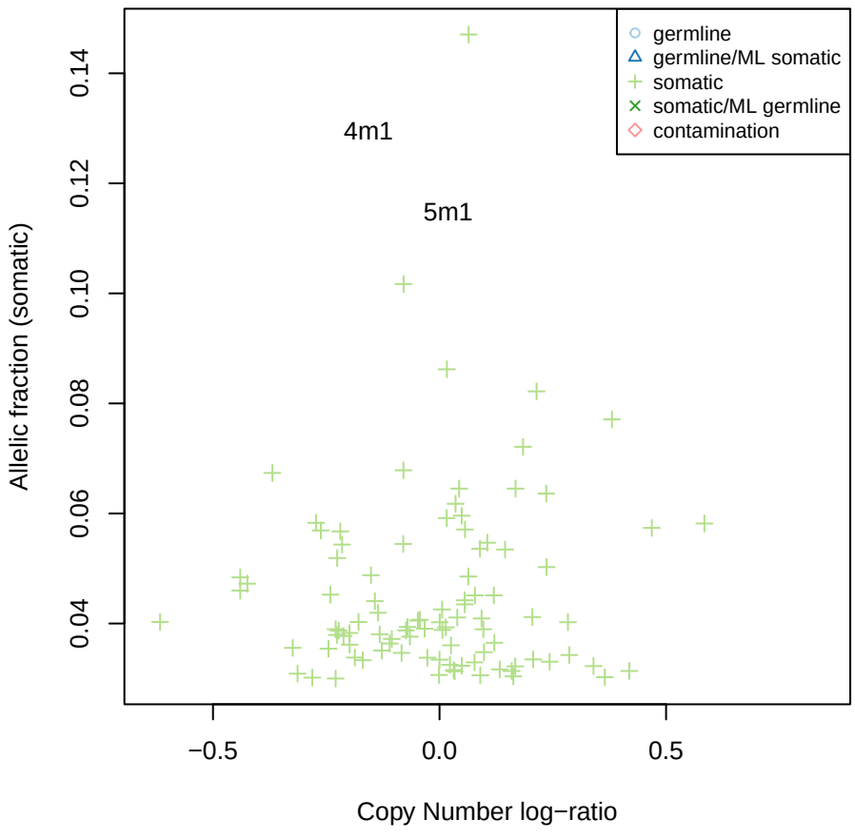

Purity: 0.35 Tumor ploidy: 4.885 SNV log−likelihood: −107.64 GoF: 92.1% Mean coverage: 370;408
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

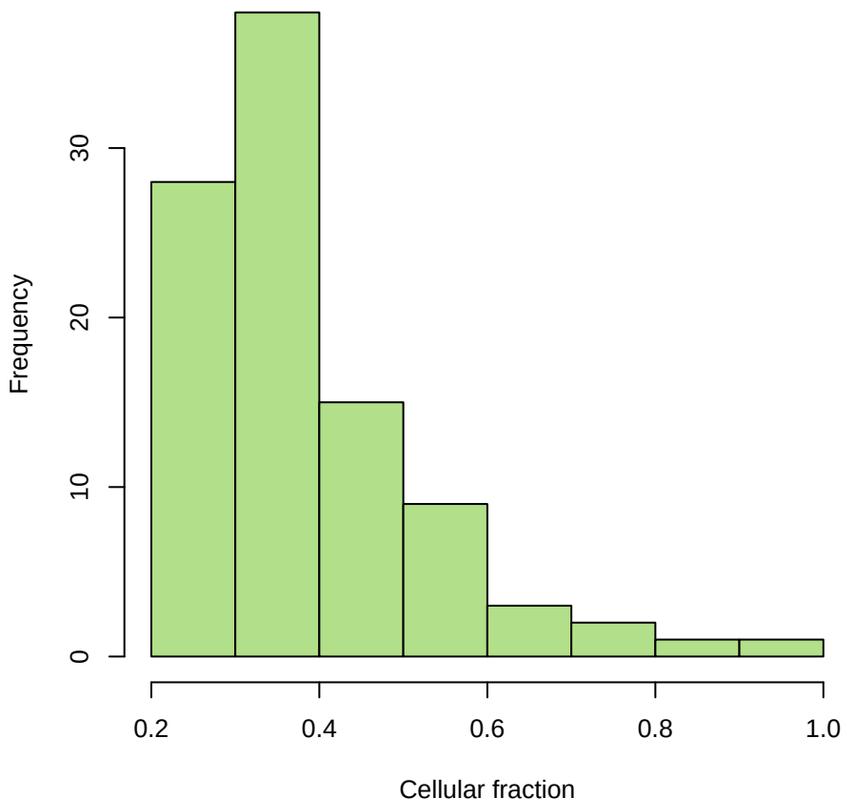

SCNA−fit log−likelihood: −14813.25
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
4 5 6
0 20 40 60 80 100 120 140
SNV Index

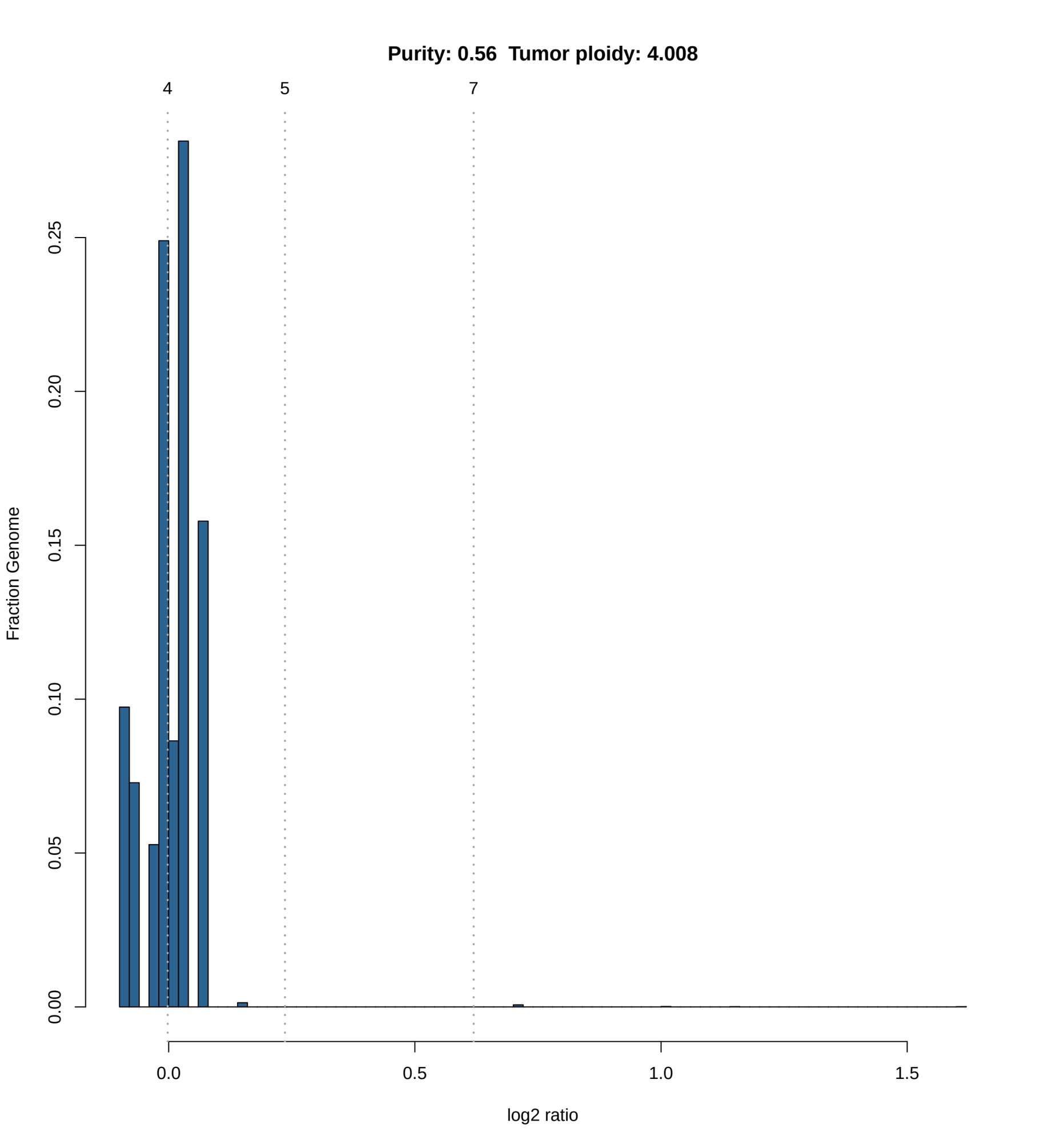

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

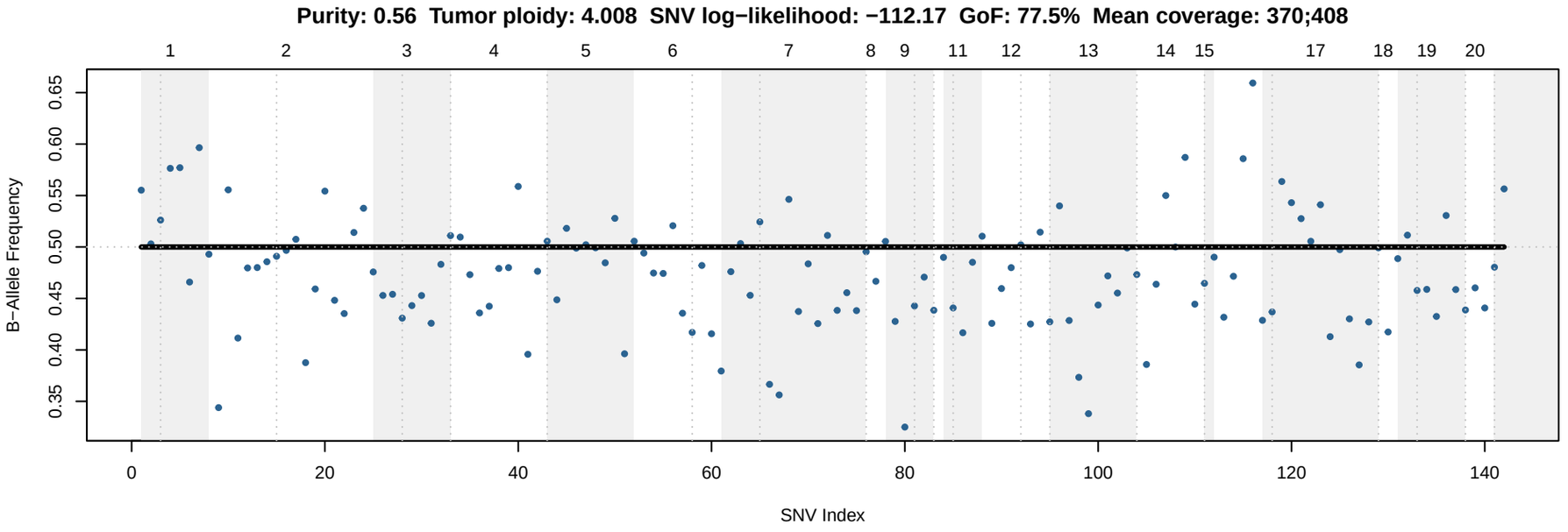

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
5m3
4m2
5m2
4m1
−0.5
0.0
0.5
Copy Number log−ratio

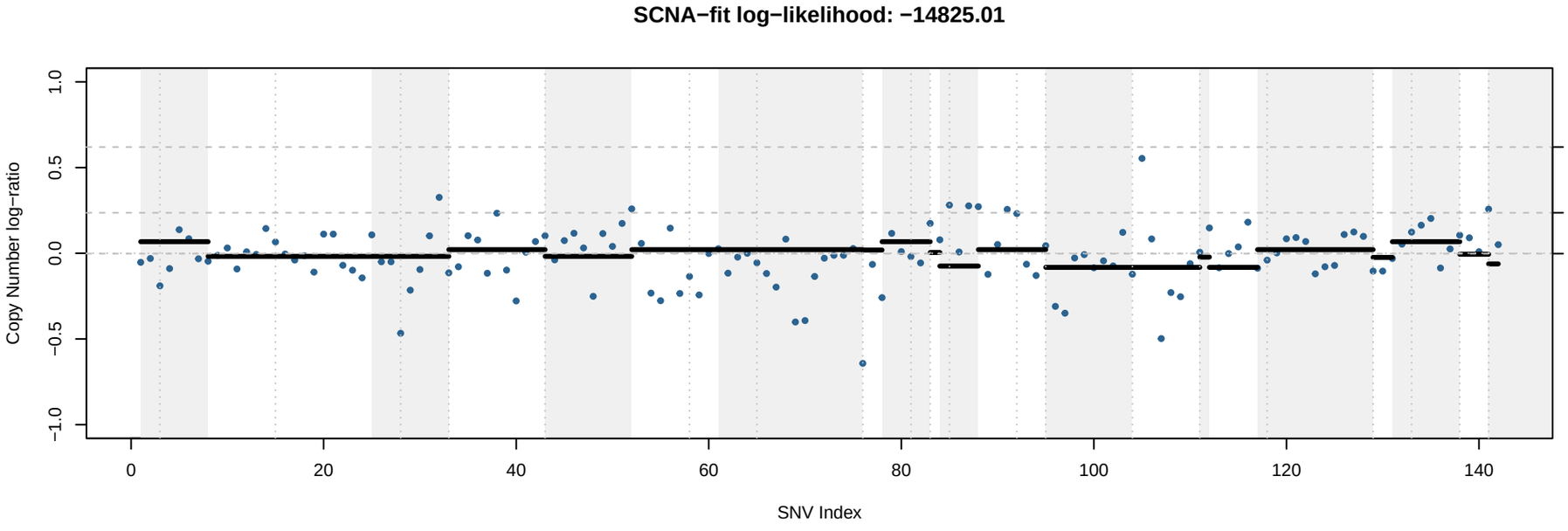

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

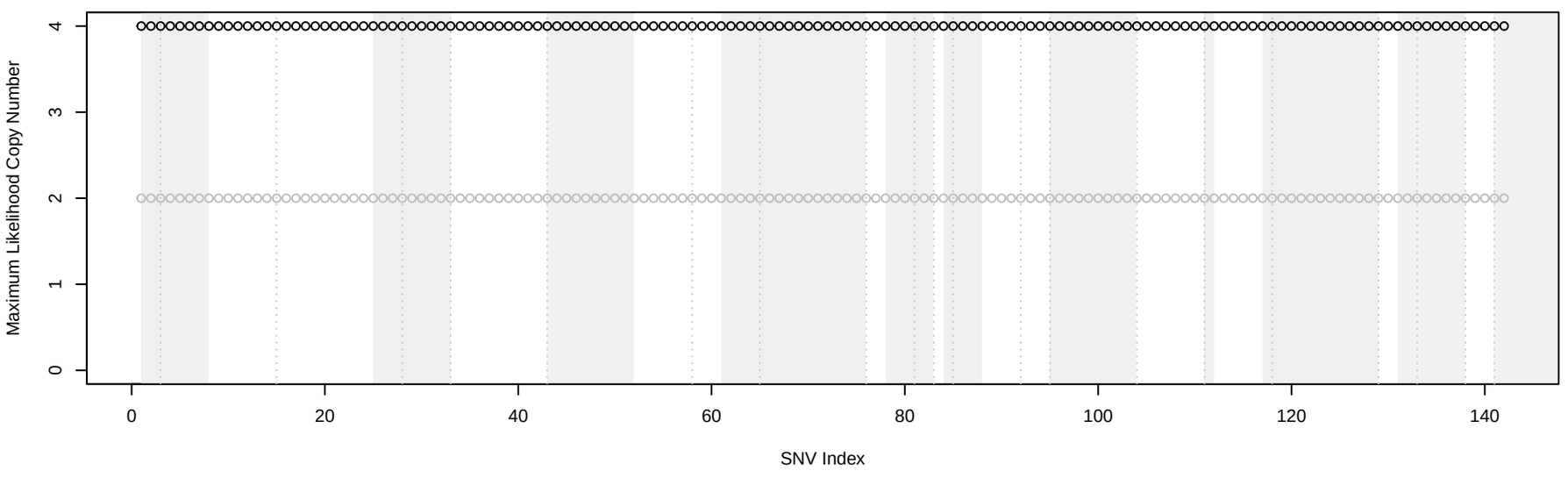

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
−0.5
0.0
0.5
Copy Number log−ratio

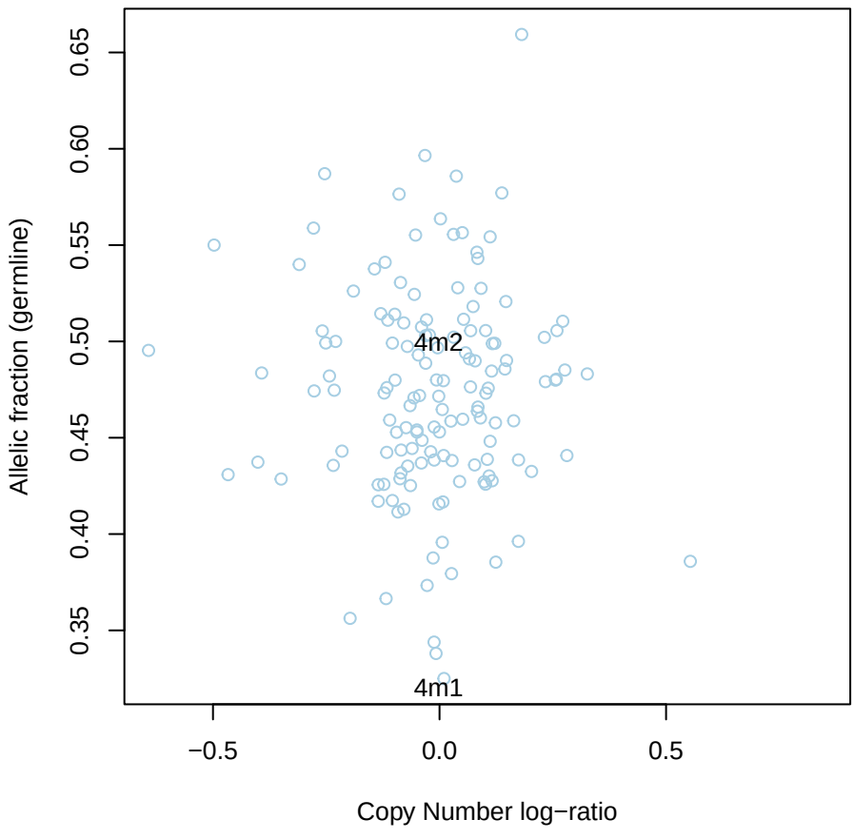

Frequency
0
10
20
30
0.2
0.4
0.6
0.8
1.0
Cellular fraction

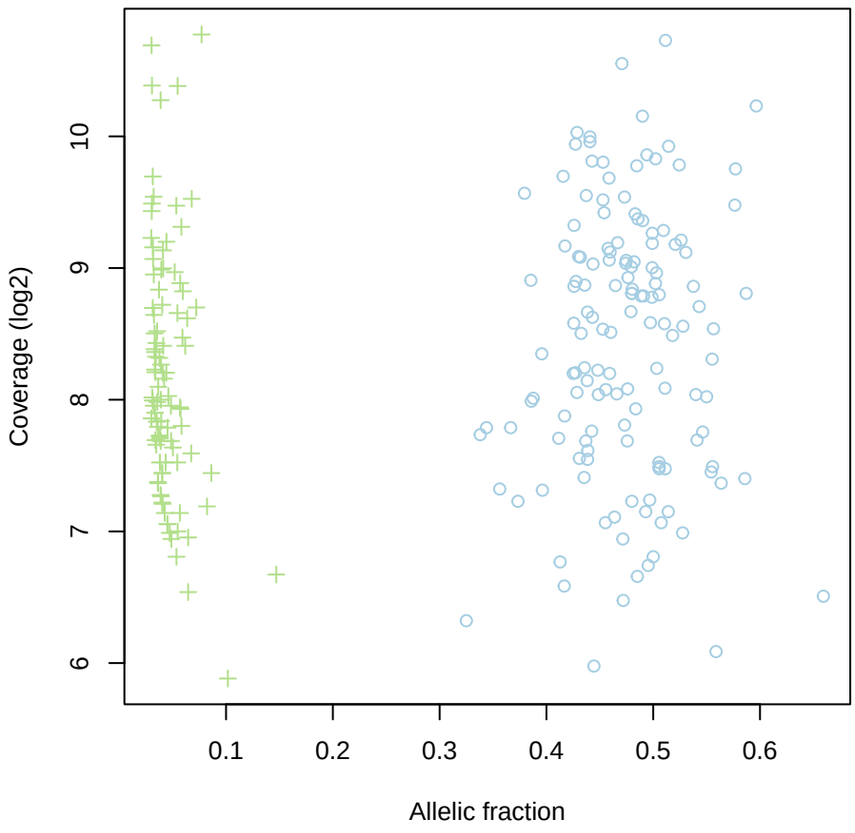

Purity: 0.56 Tumor ploidy: 4.008
4
5
7
Fraction Genome
0.00
0.05
0.10
0.15
0.20
0.25
0.0
0.5
1.0
1.5
log2 ratio

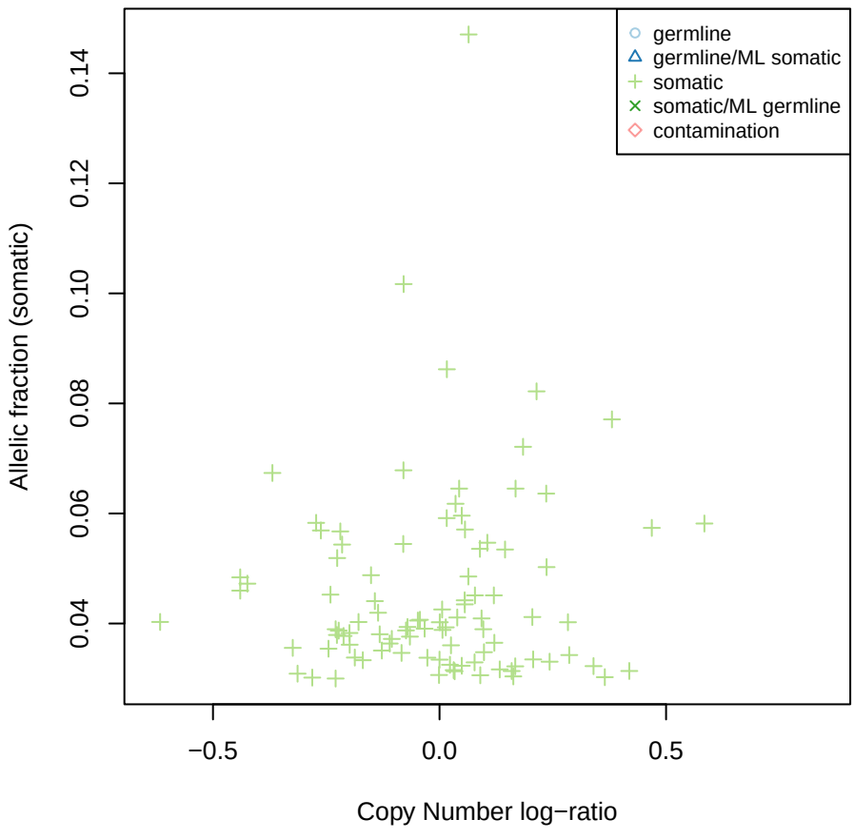

Purity: 0.56 Tumor ploidy: 4.008 SNV log−likelihood: −112.17 GoF: 77.5% Mean coverage: 370;408
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

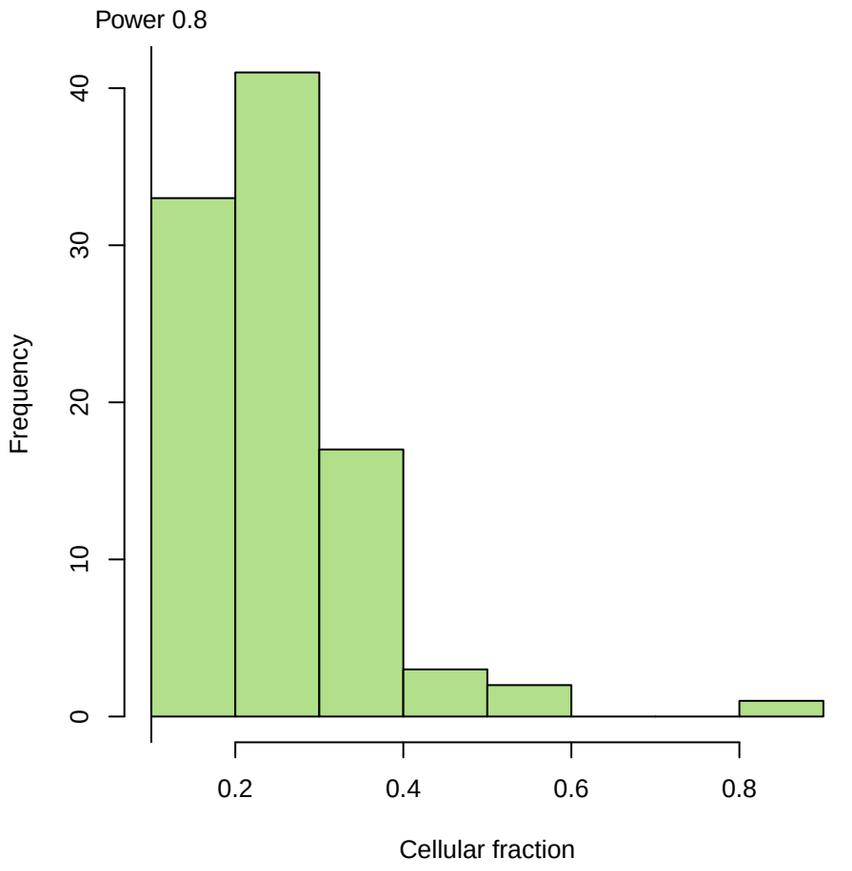

SCNA−fit log−likelihood: −14825.01
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5 7
0 20 40 60 80 100 120 140
SNV Index

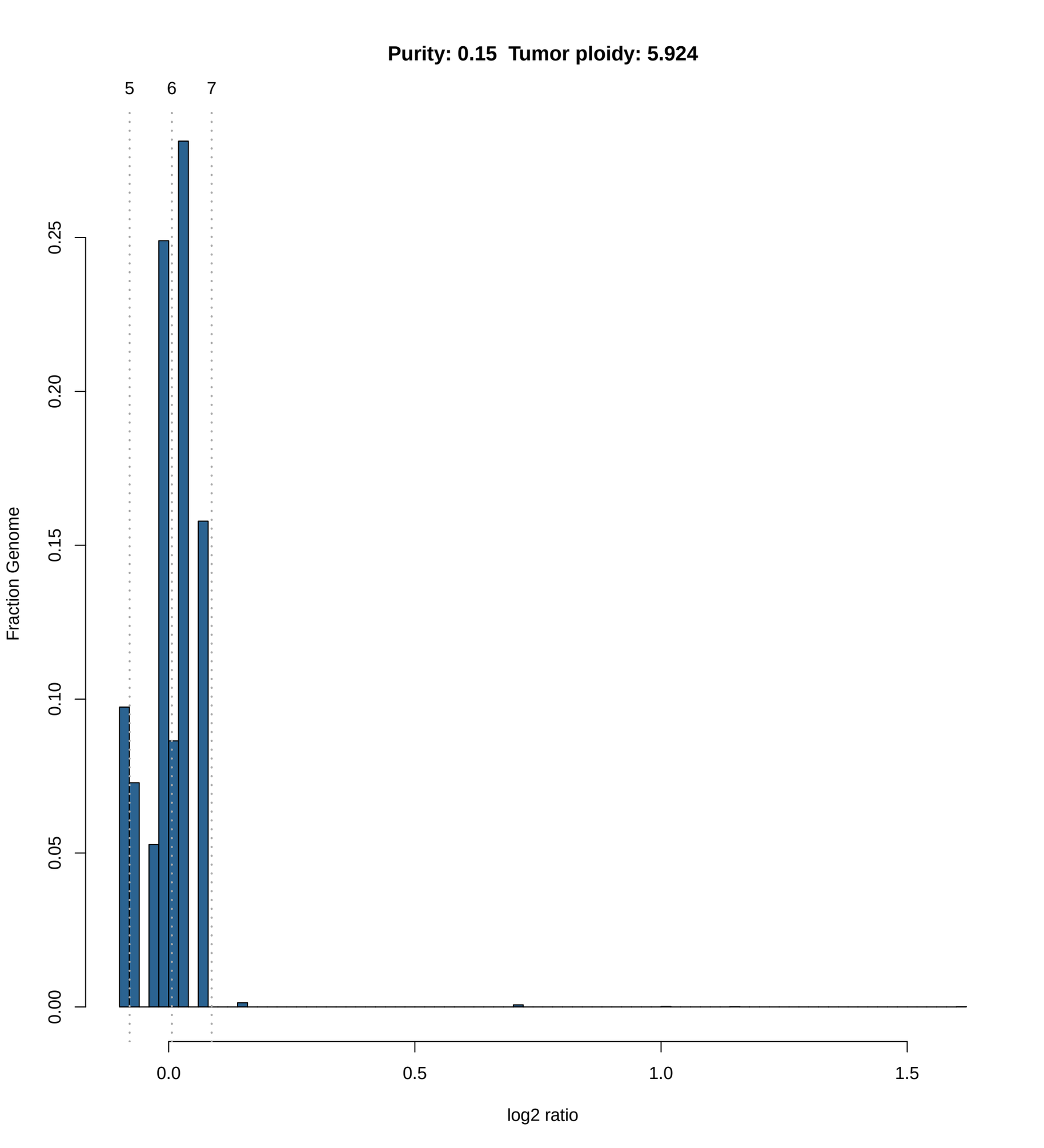

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120 140
SNV Index

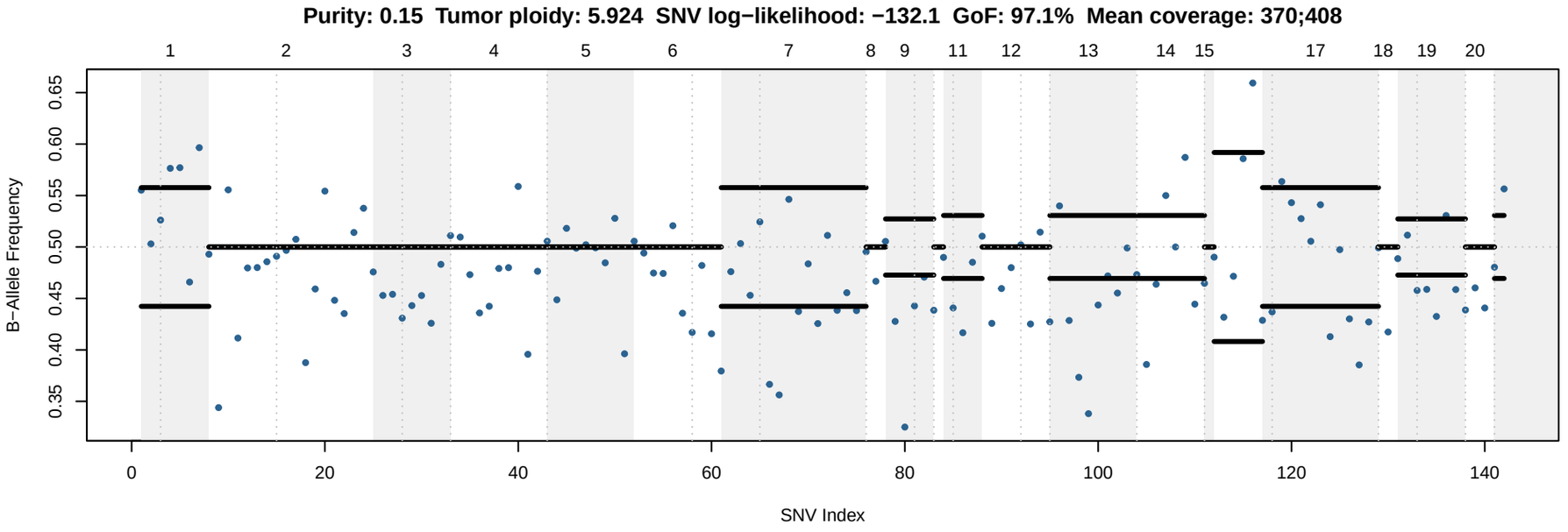

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
4m2
4m1
−0.5
0.0
0.5
Copy Number log−ratio

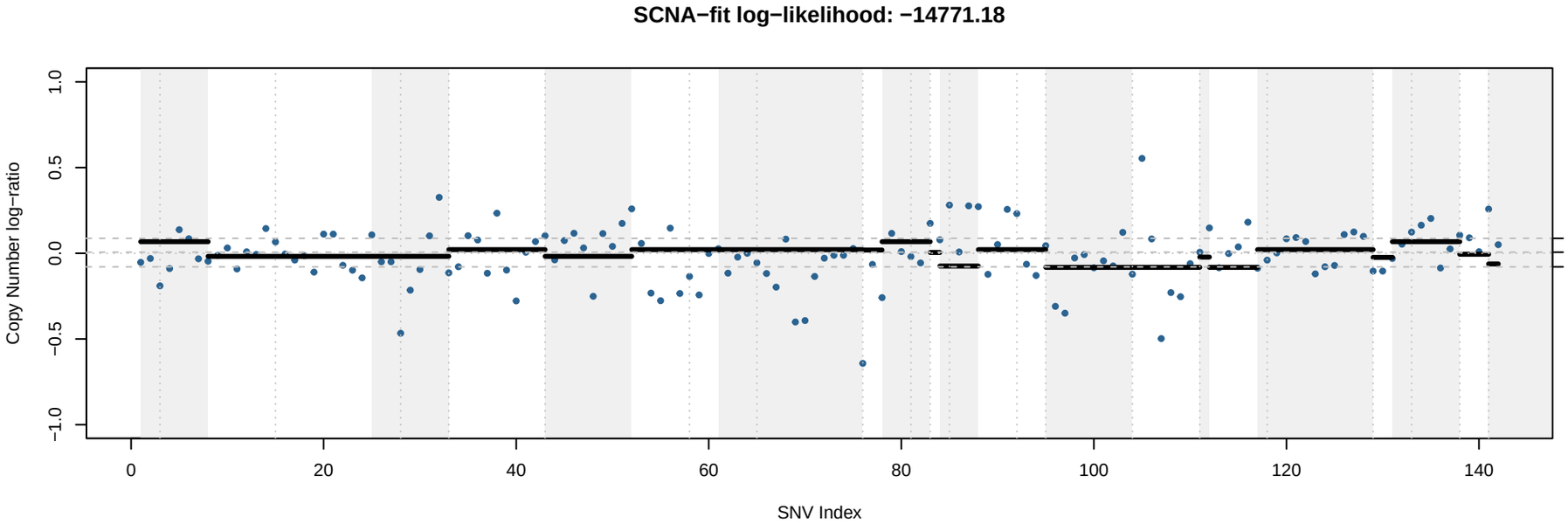

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

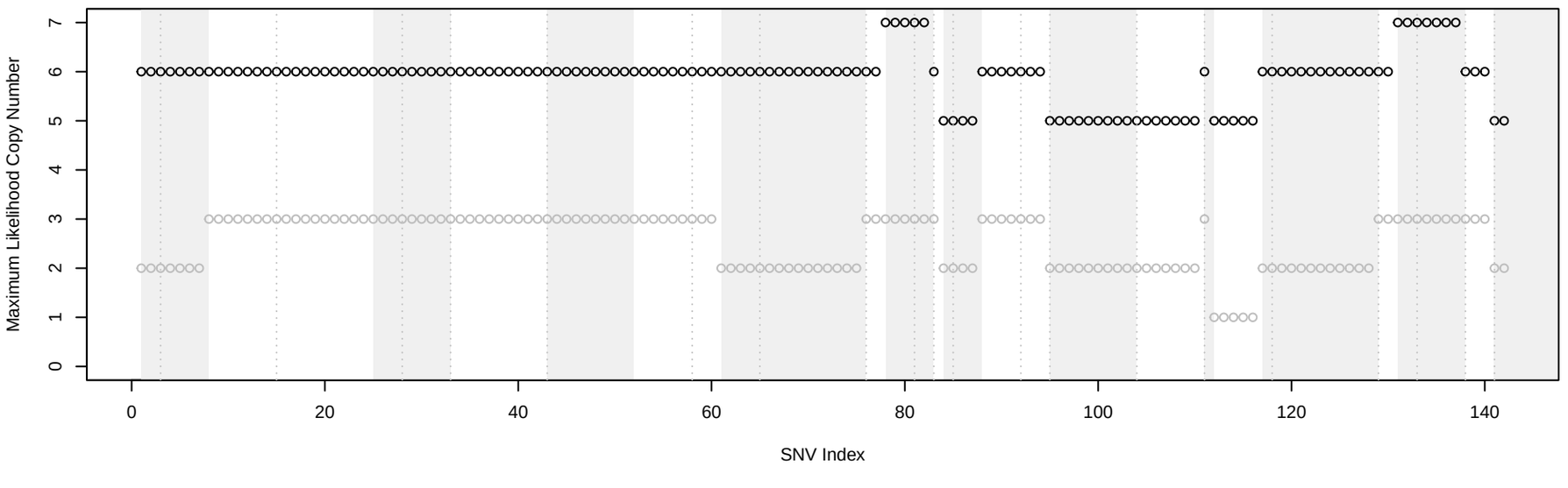

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.5
0.0
0.5
Copy Number log−ratio

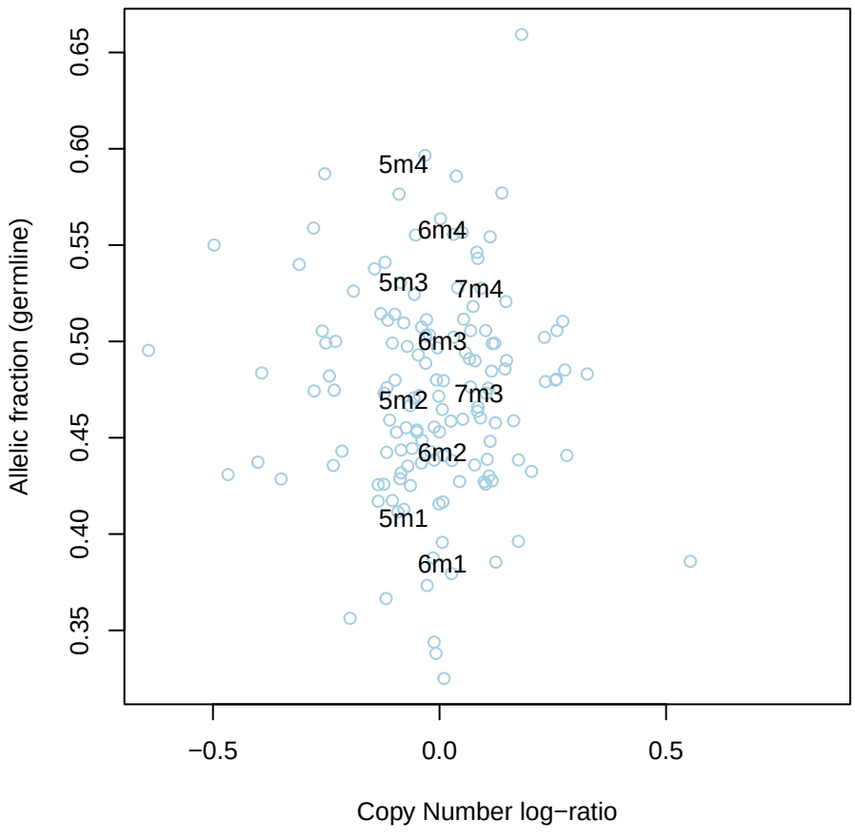

Power 0.8
Frequency
0
10
20
30
40
0.2
0.4
0.6
0.8
Cellular fraction

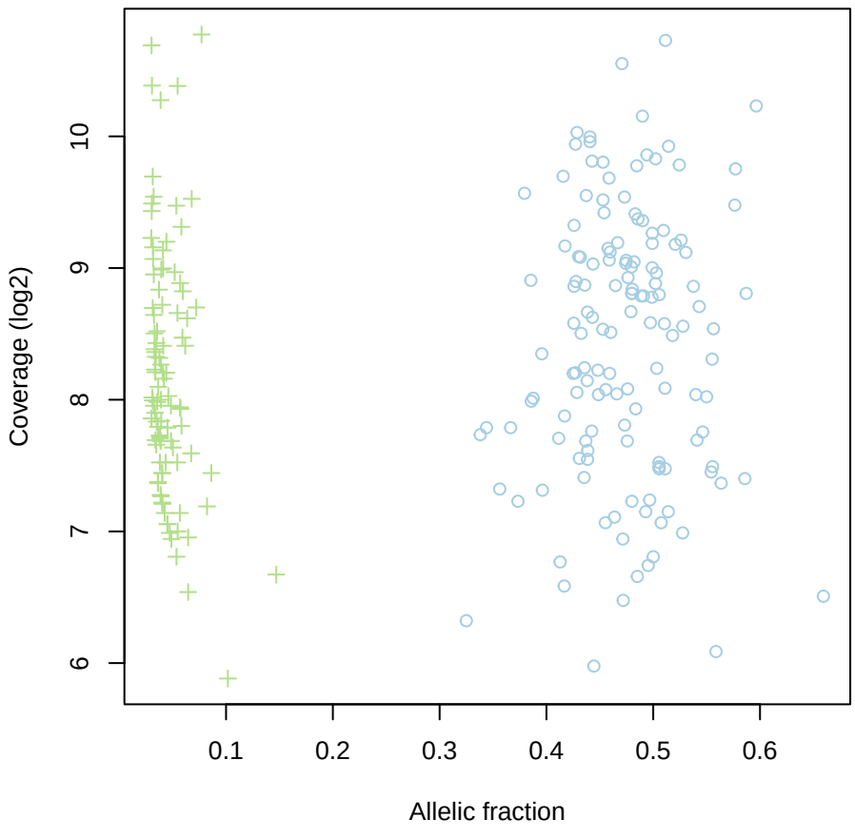

Purity: 0.15 Tumor ploidy: 5.924
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
1.5
log2 ratio

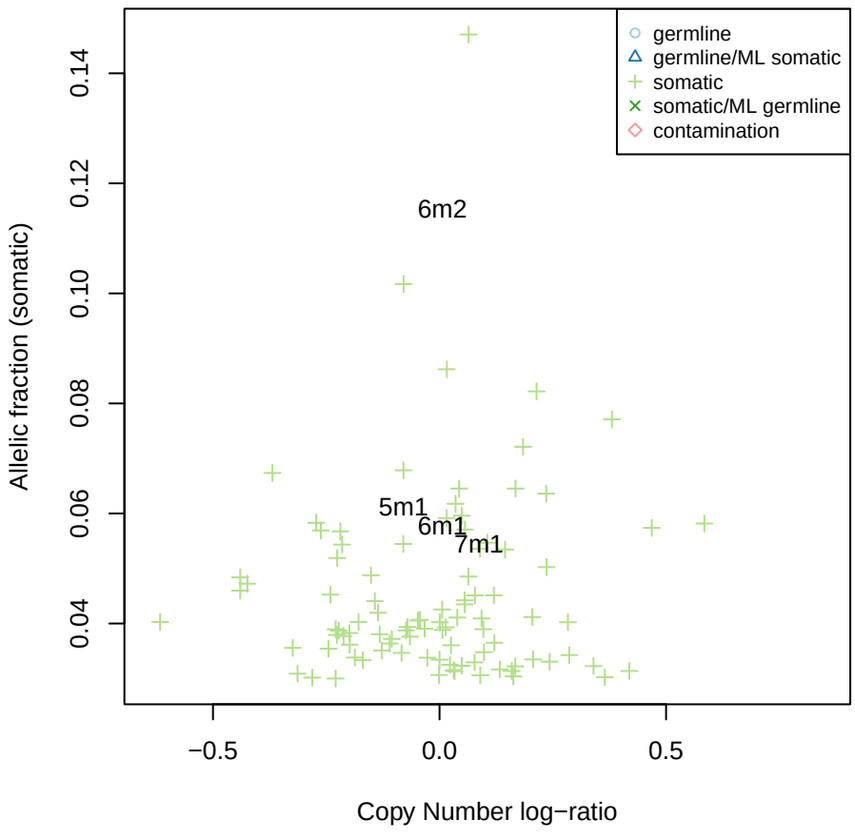

Purity: 0.15 Tumor ploidy: 5.924 SNV log−likelihood: −132.1 GoF: 97.1% Mean coverage: 370;408
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

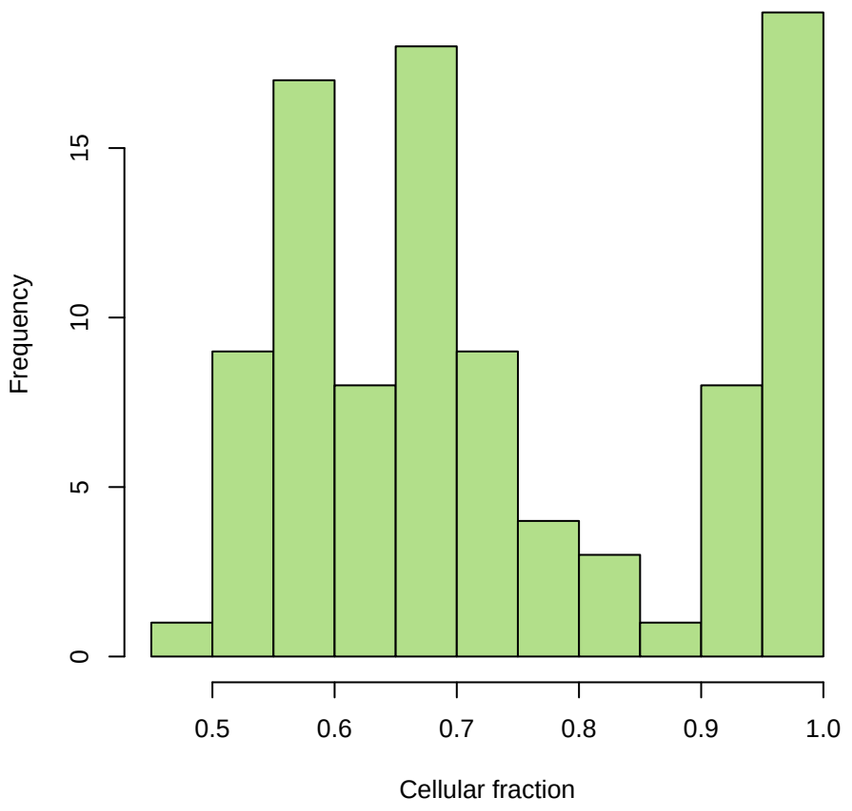

SCNA−fit log−likelihood: −14771.18
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
5 7
0 20 40 60 80 100 120 140
SNV Index

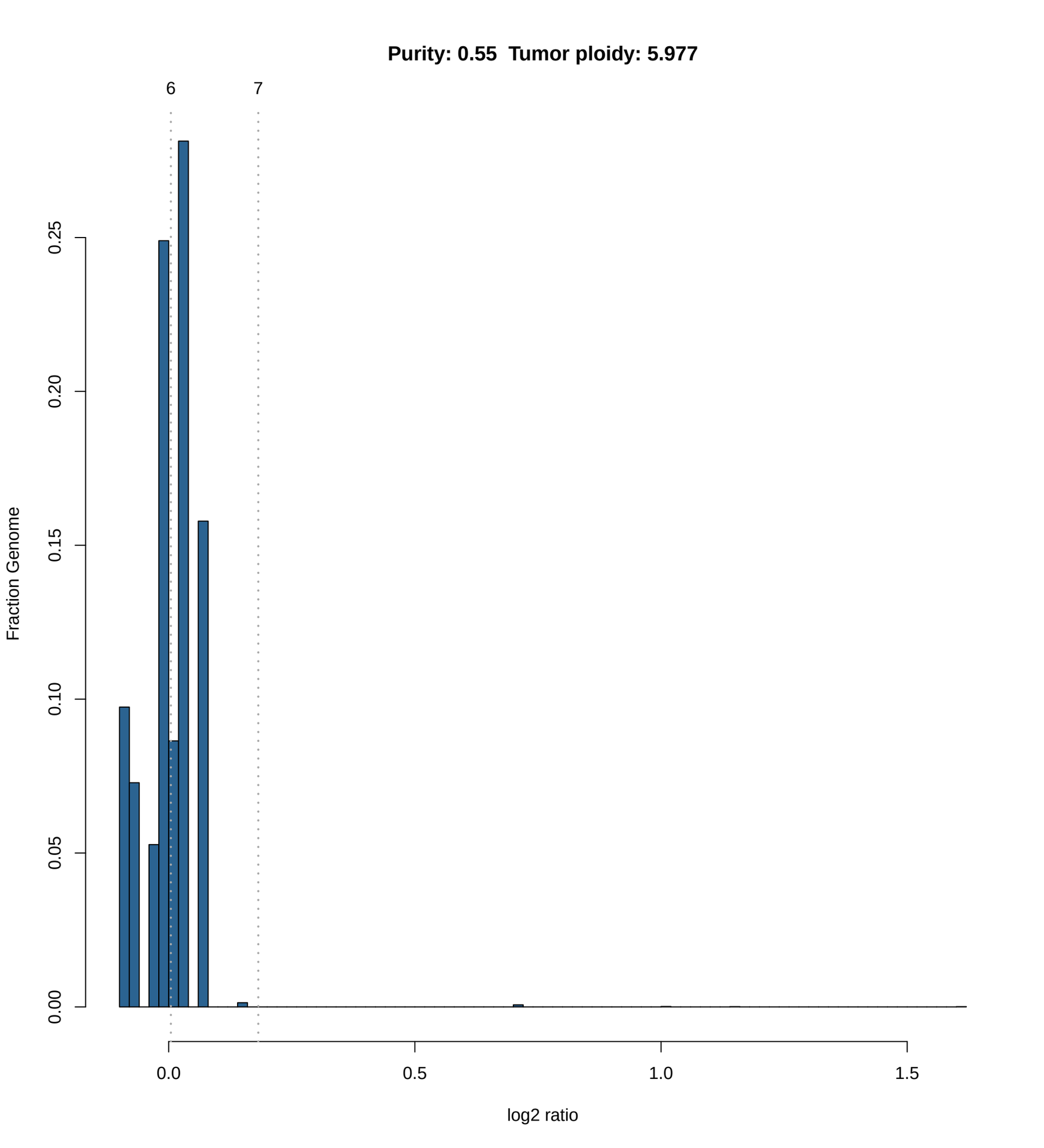

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

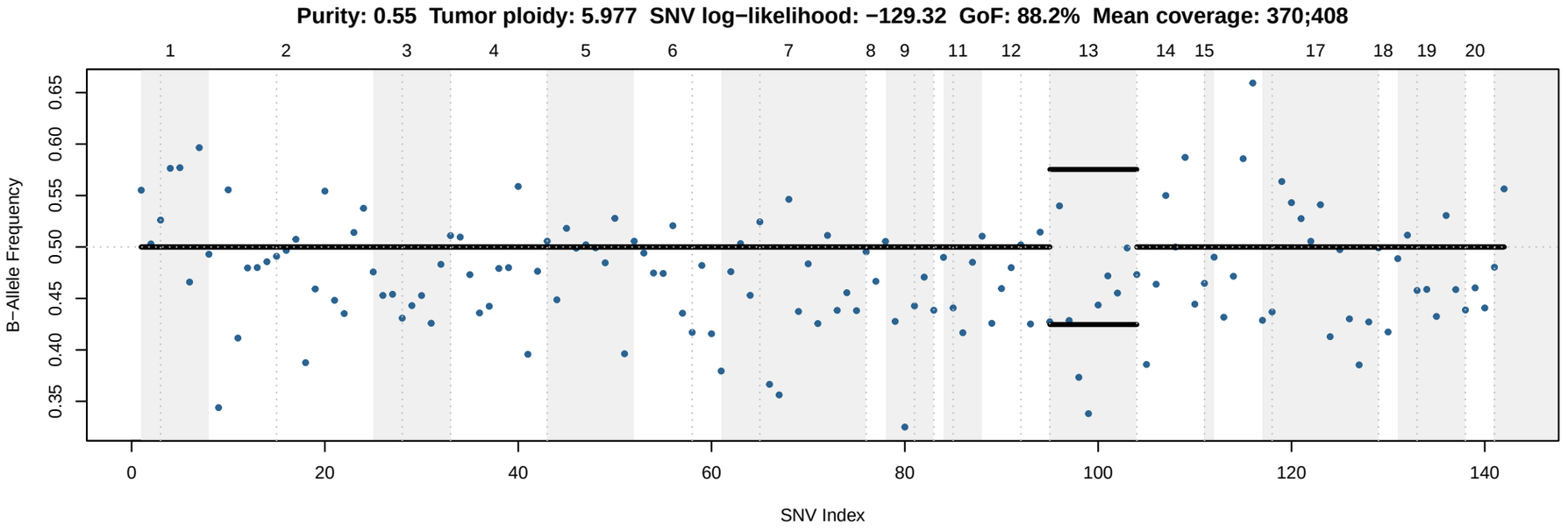

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
5m4
6m4
5m3
7m4
6m3
5m2
7m3
6m2
5m1
6m1
−0.5
0.0
0.5
Copy Number log−ratio

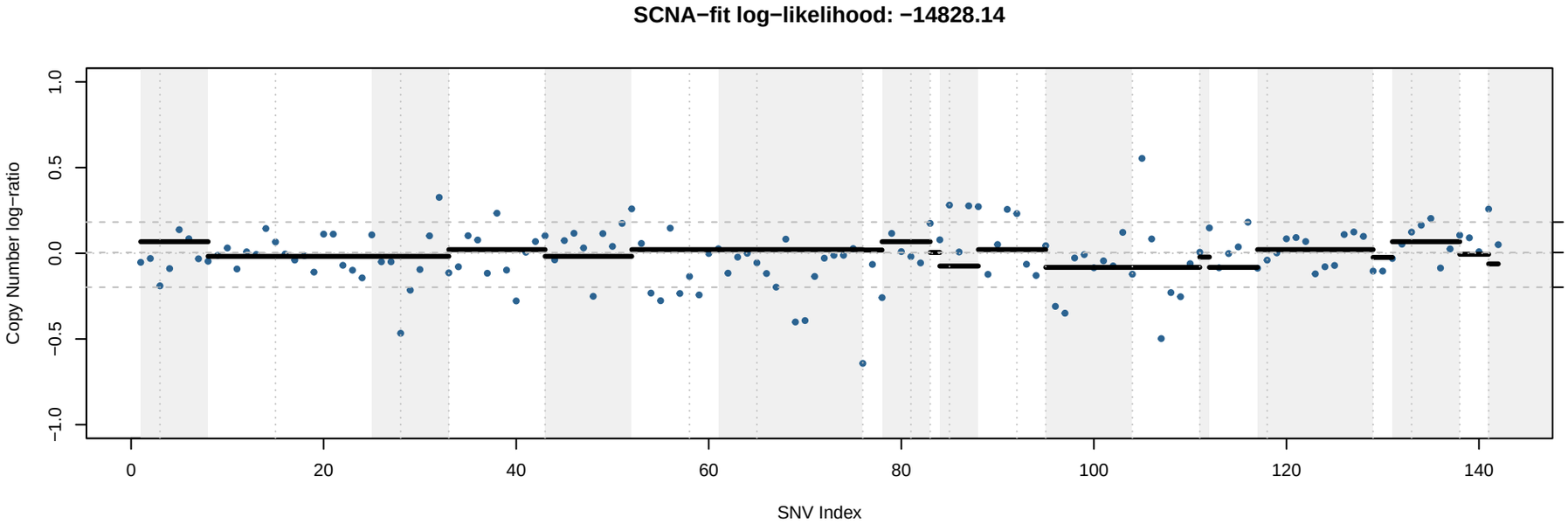

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

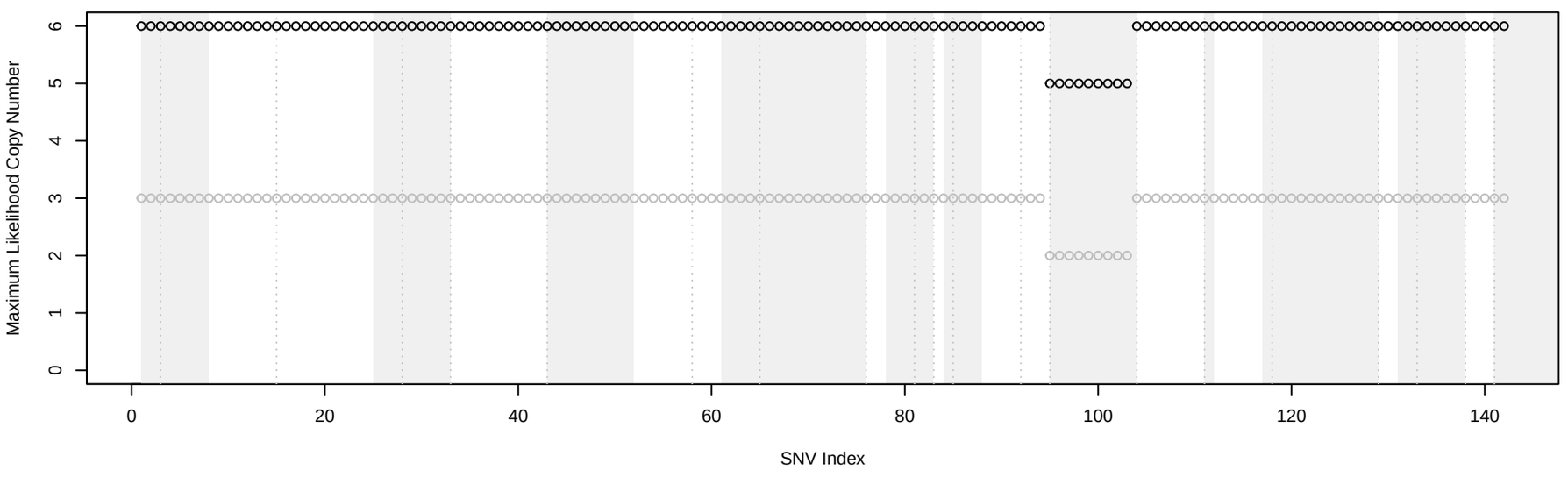

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
6m2
5m1
6m1
7m1
−0.5
0.0
0.5
Copy Number log−ratio

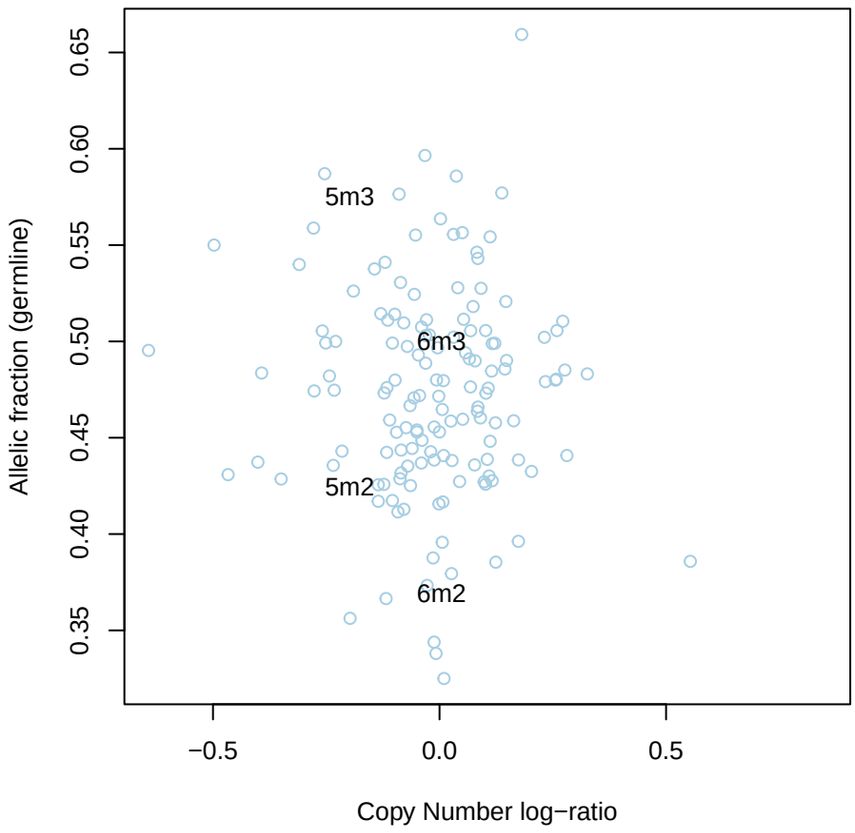

Frequency
0
5
10
15
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

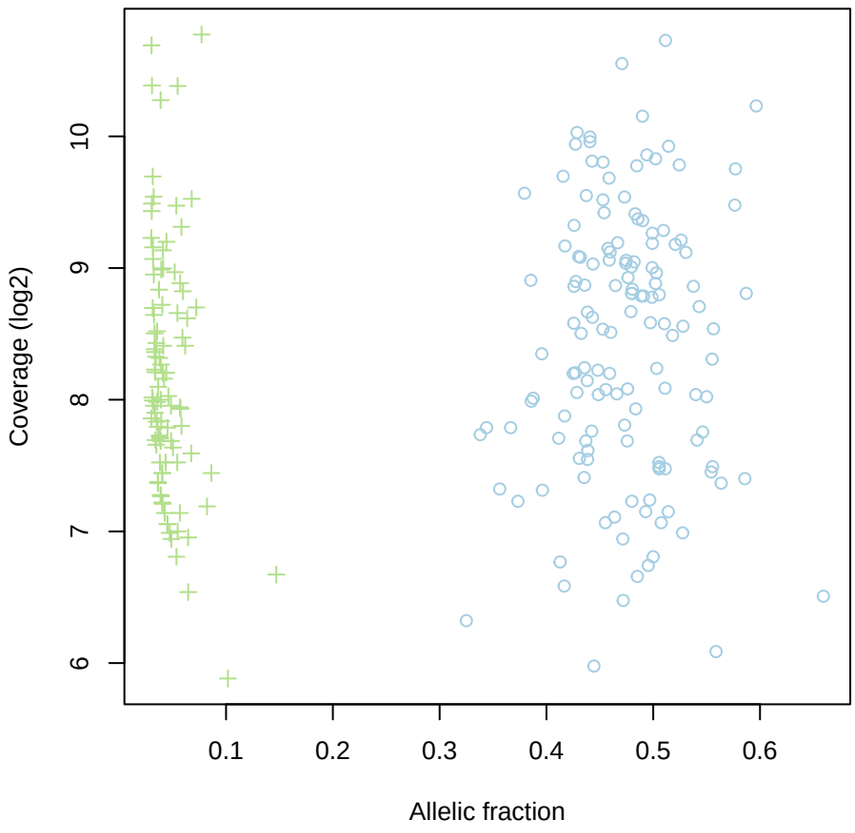

Purity: 0.55 Tumor ploidy: 5.977
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
1.5
log2 ratio

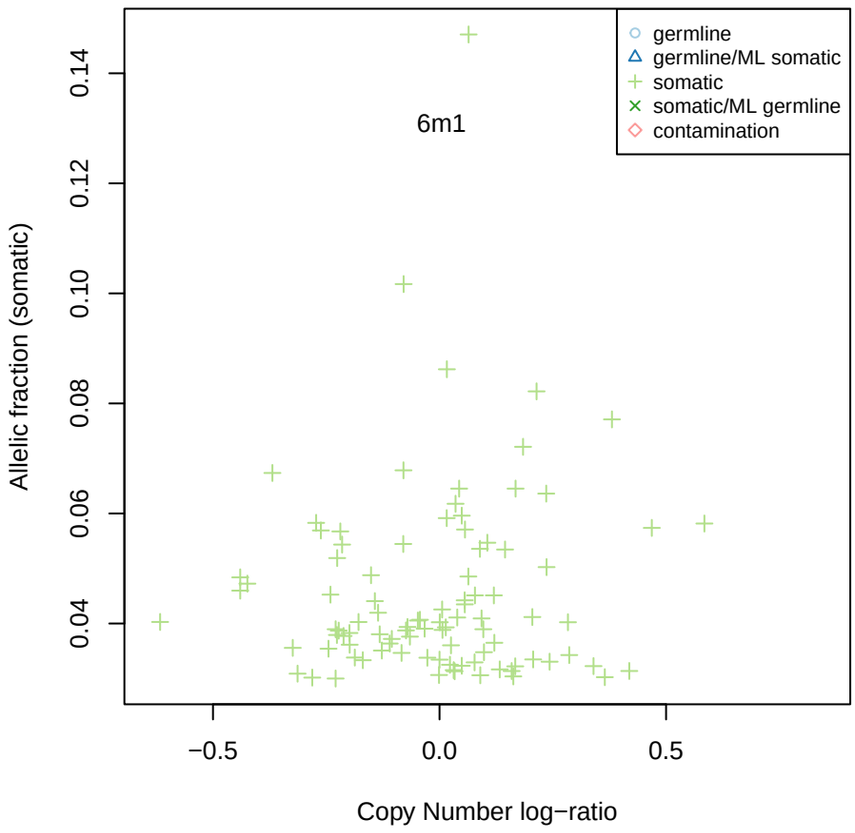

Purity: 0.55 Tumor ploidy: 5.977 SNV log−likelihood: −129.32 GoF: 88.2% Mean coverage: 370;408
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

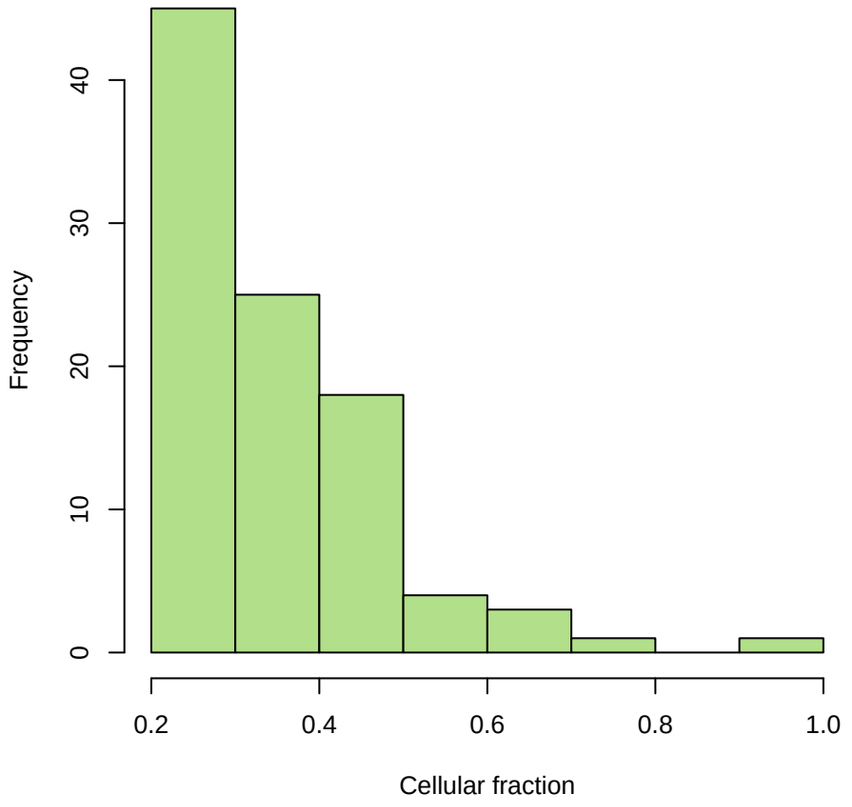

SCNA−fit log−likelihood: −14828.14
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
5 6 7
0 20 40 60 80 100 120 140
SNV Index

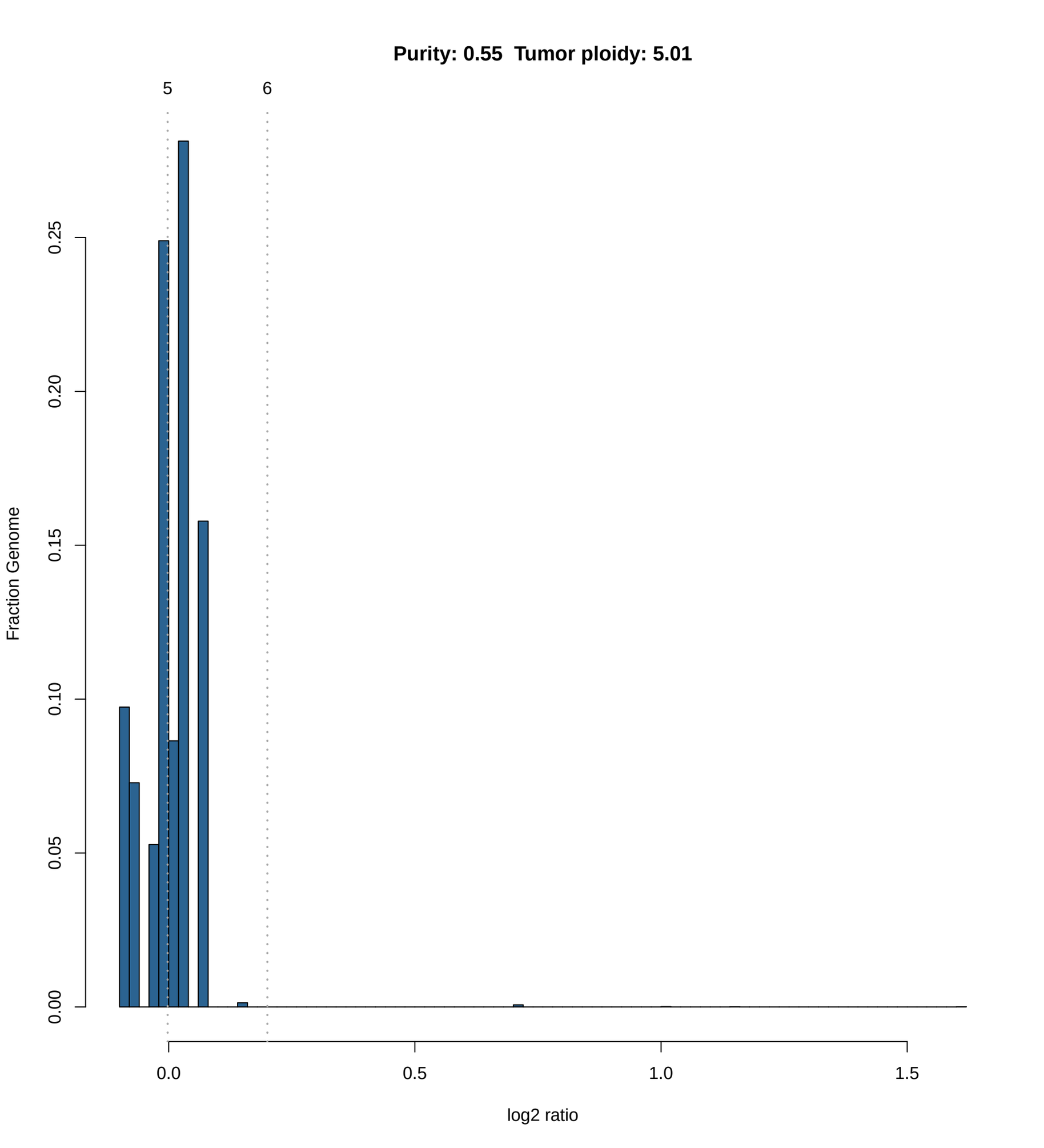

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

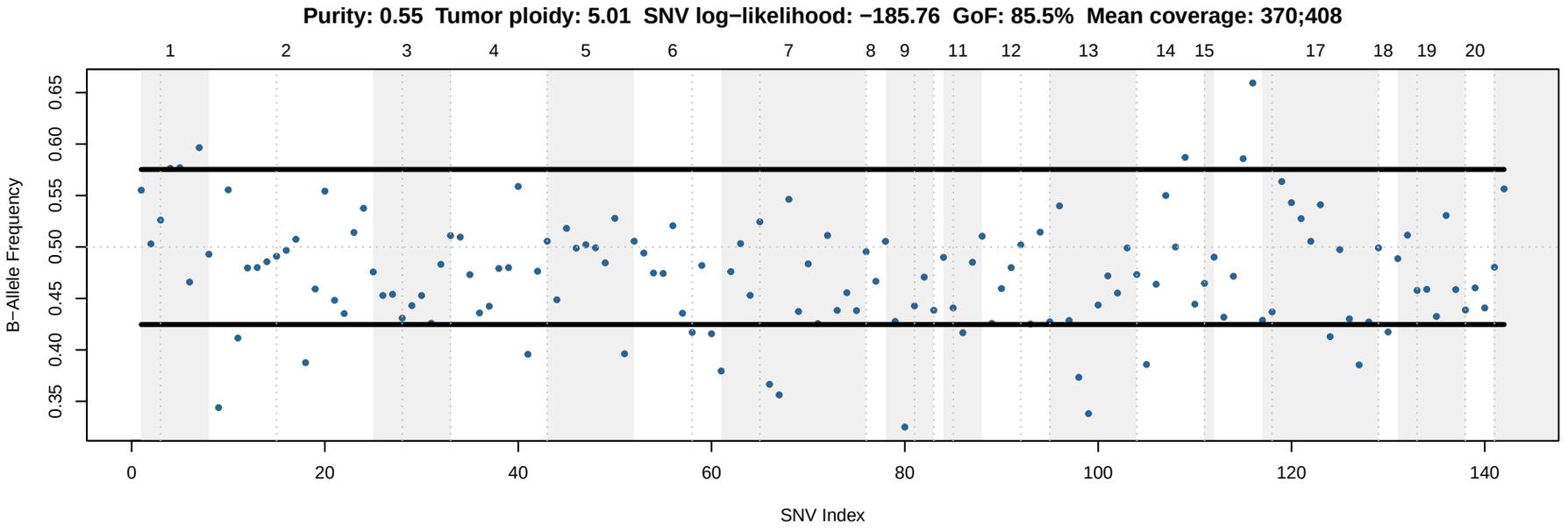

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
5m3
6m3
5m2
6m2
−0.5
0.0
0.5
Copy Number log−ratio

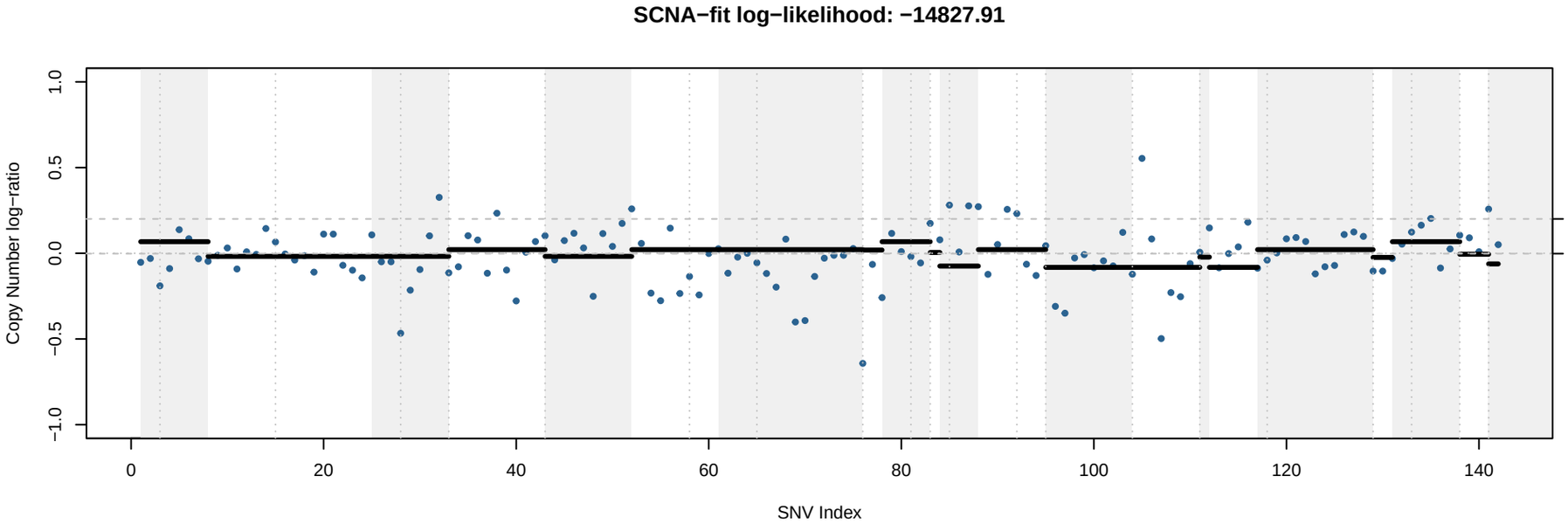

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

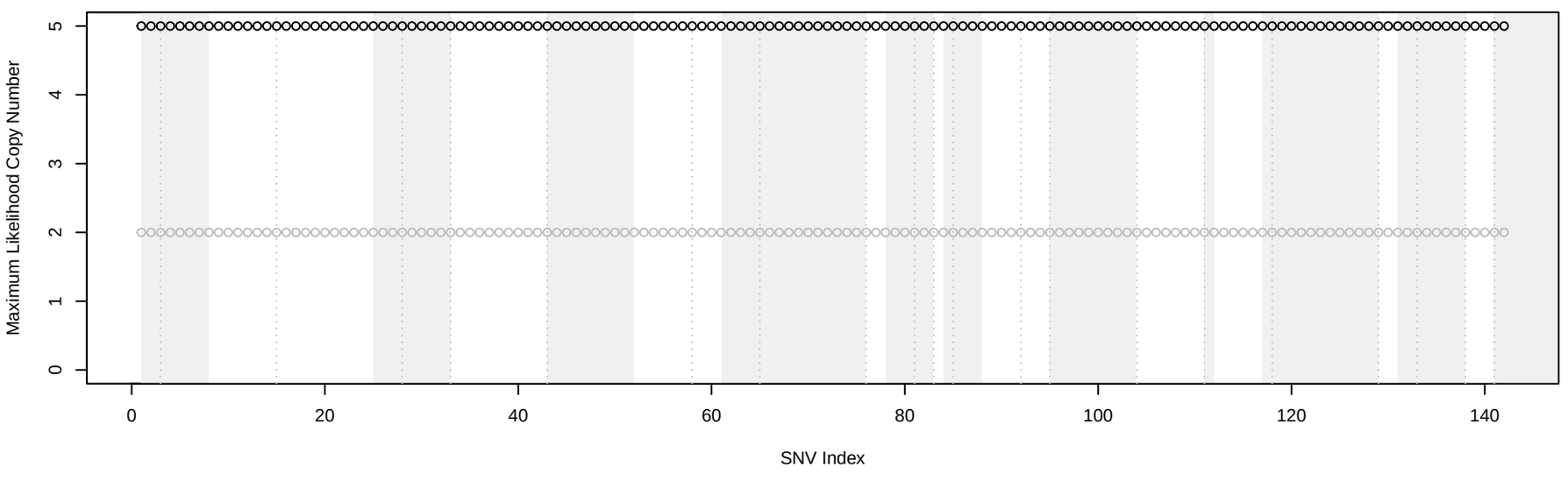

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m1
−0.5
0.0
0.5
Copy Number log−ratio

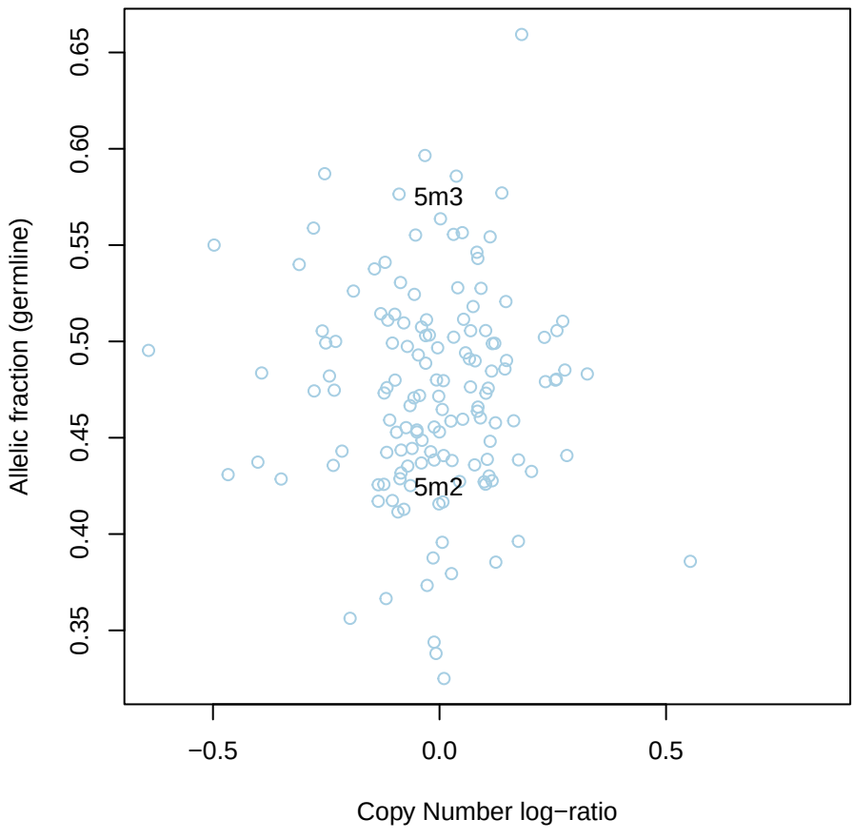

Frequency
0
10
20
30
40
0.2
0.4
0.6
0.8
1.0
Cellular fraction

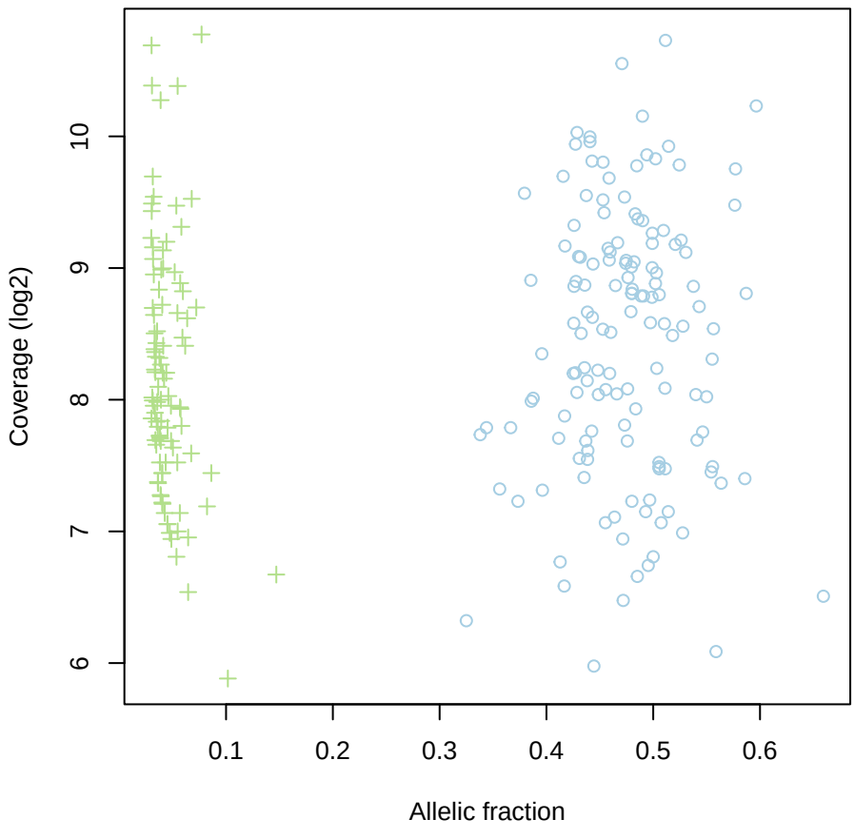

Purity: 0.55 Tumor ploidy: 5.01
5
6
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
1.5
log2 ratio

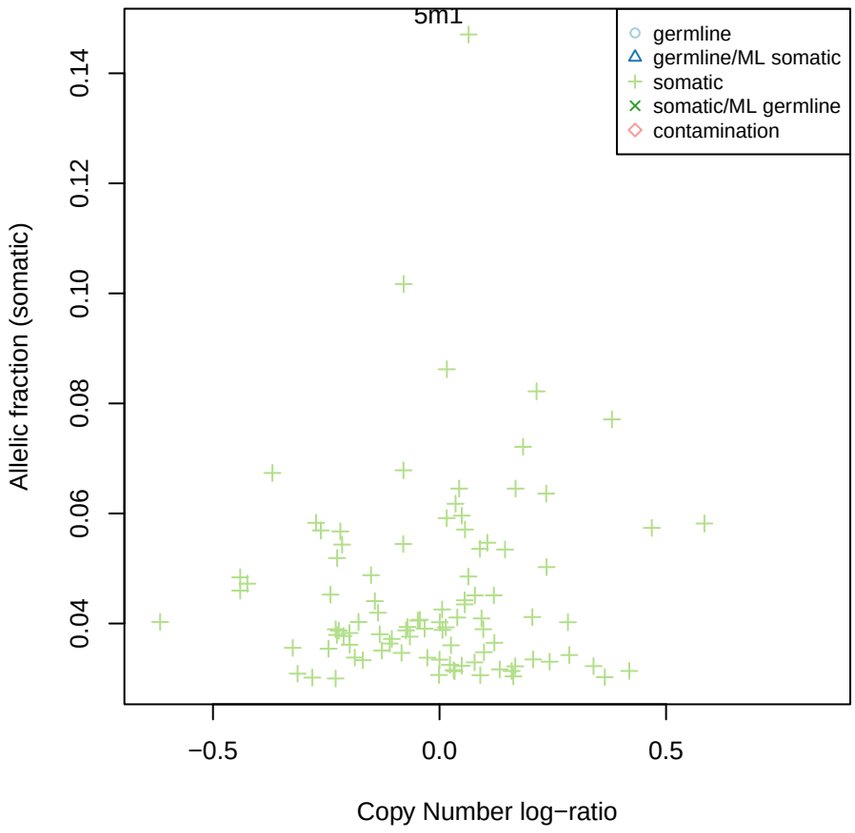

Purity: 0.55 Tumor ploidy: 5.01 SNV log−likelihood: −185.76 GoF: 85.5% Mean coverage: 370;408
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

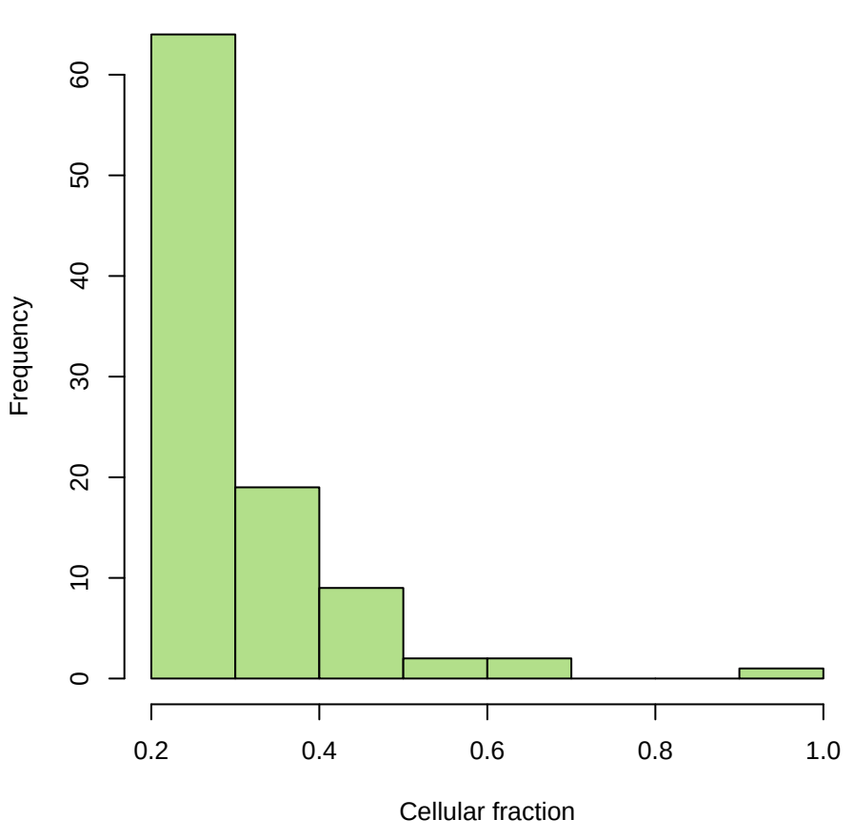

SCNA−fit log−likelihood: −14827.91
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
5 6
0 20 40 60 80 100 120 140
SNV Index

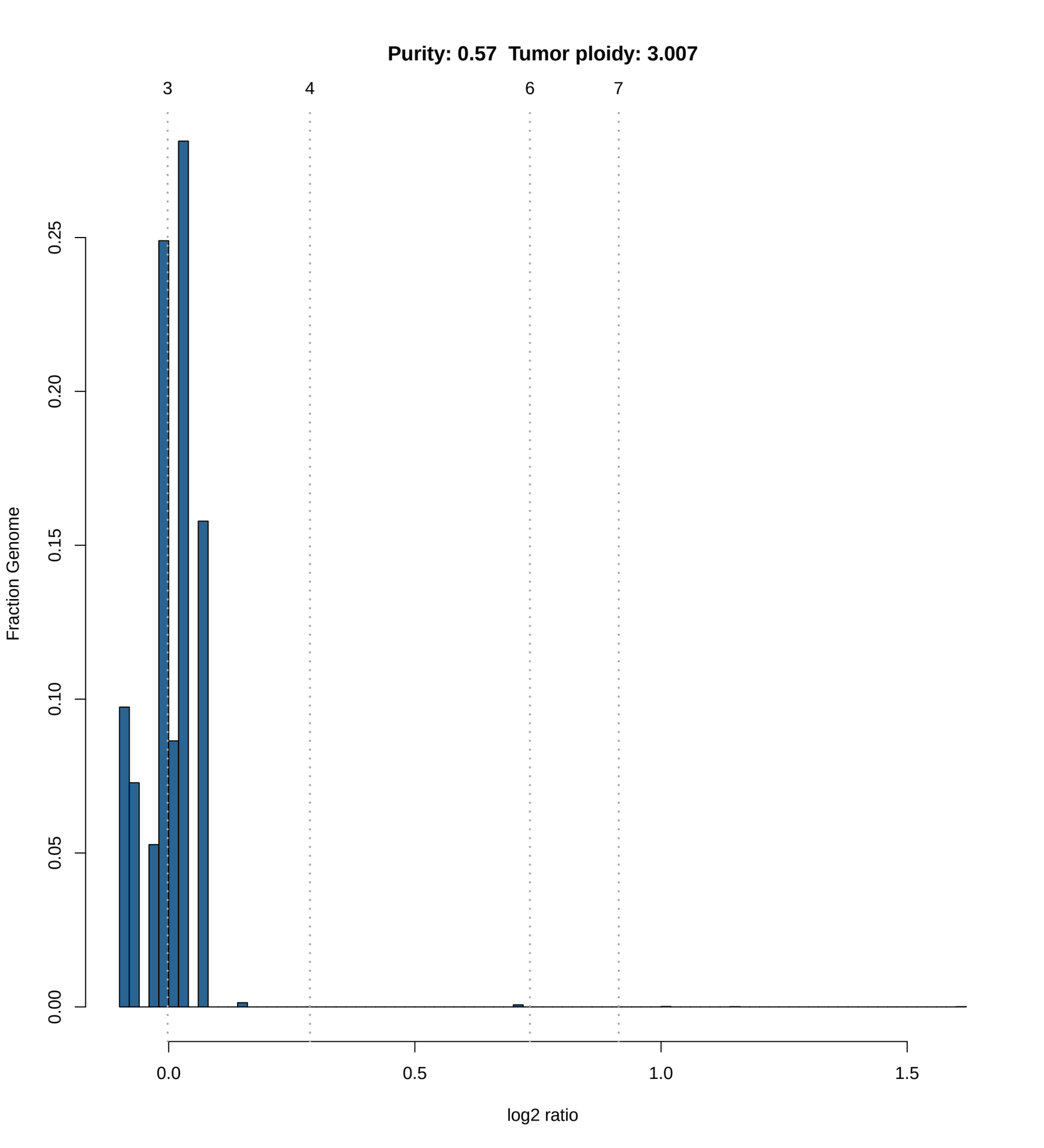

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

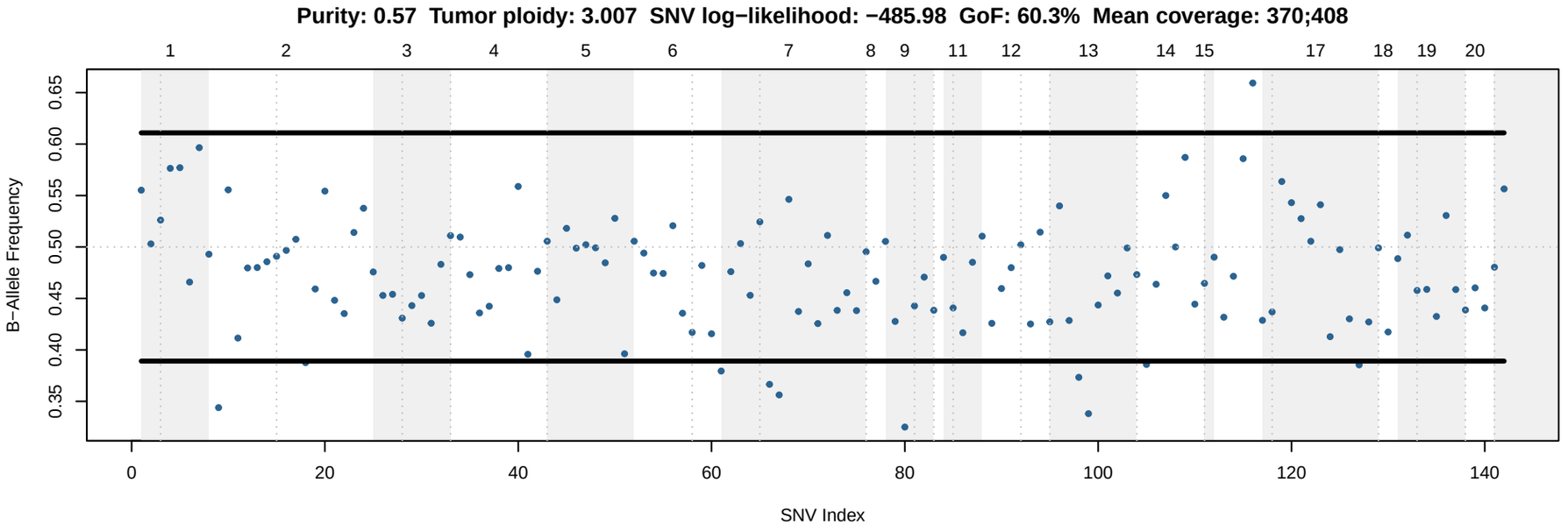

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
5m3
5m2
−0.5
0.0
0.5
Copy Number log−ratio

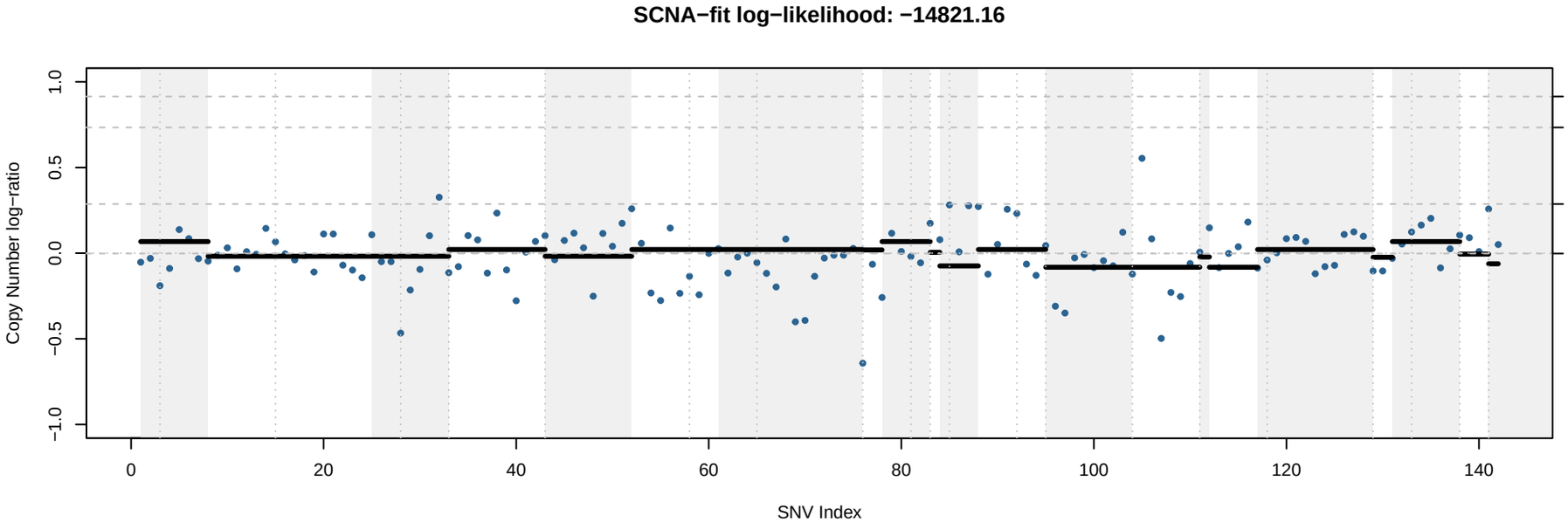

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

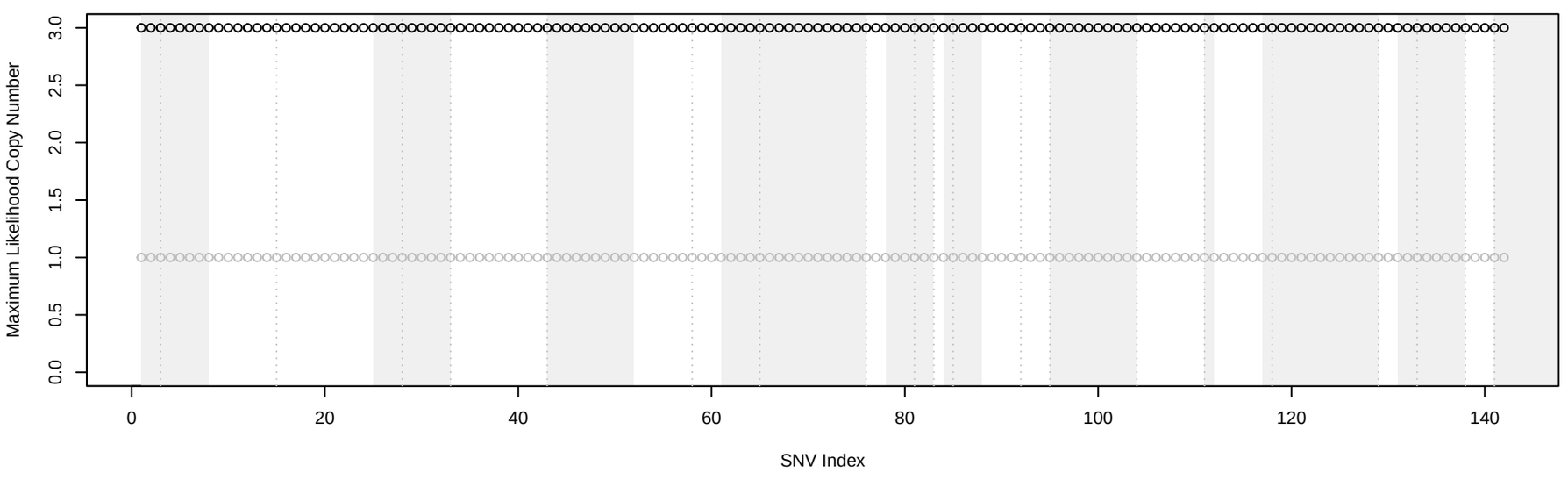

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
5m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.5
0.0
0.5
Copy Number log−ratio

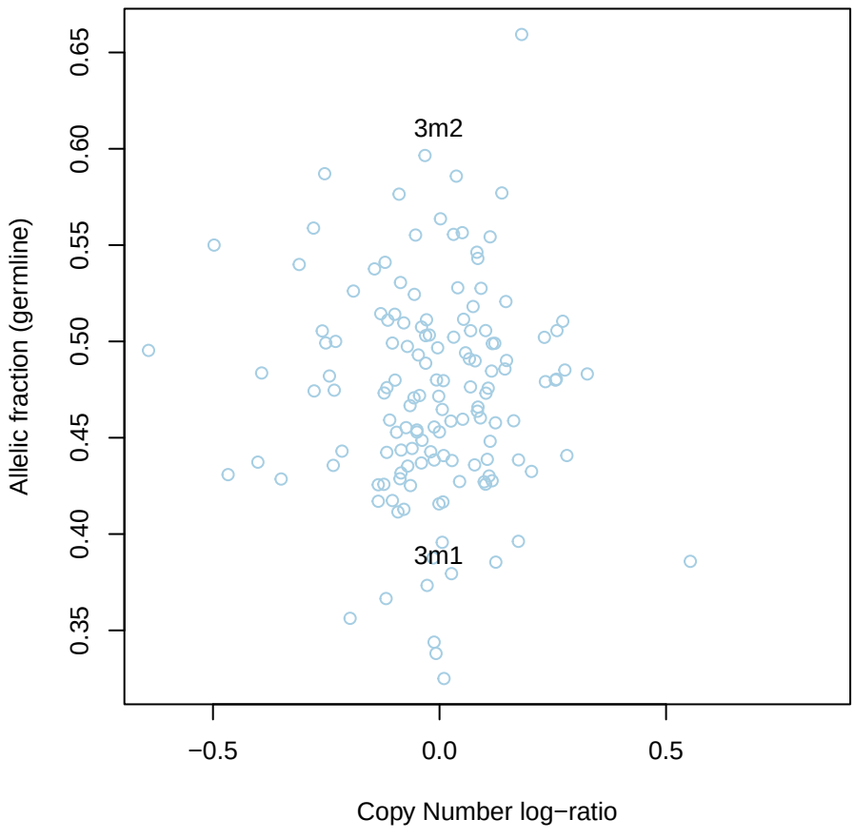

Frequency
0
10
20
30
40
50
60
0.2
0.4
0.6
0.8
1.0
Cellular fraction

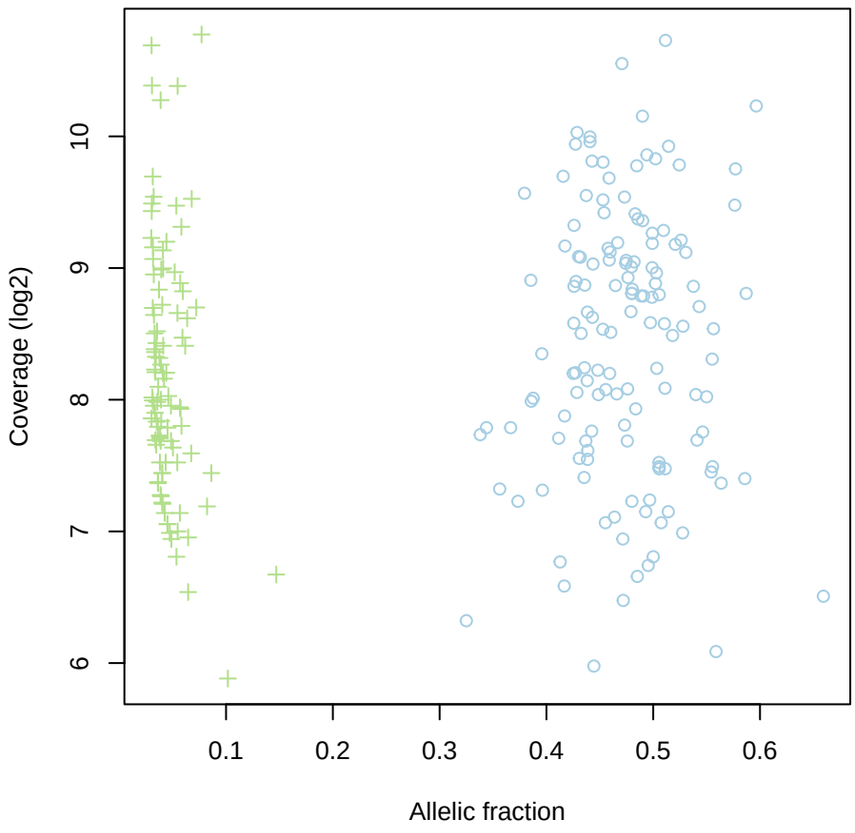

Purity: 0.57 Tumor ploidy: 3.007
3
4
6
7
Fraction Genome
0.00
0.05
0.10
0.15
0.20
0.25
0.0
0.5
1.0
1.5
log2 ratio

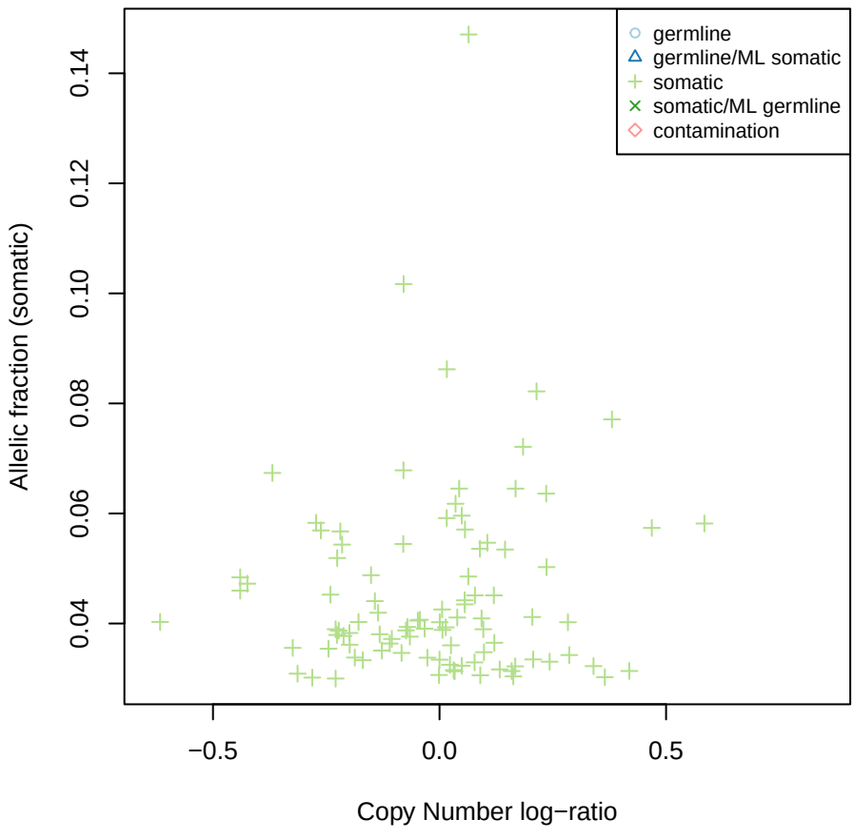

Purity: 0.57 Tumor ploidy: 3.007 SNV log−likelihood: −485.98 GoF: 60.3% Mean coverage: 370;408
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

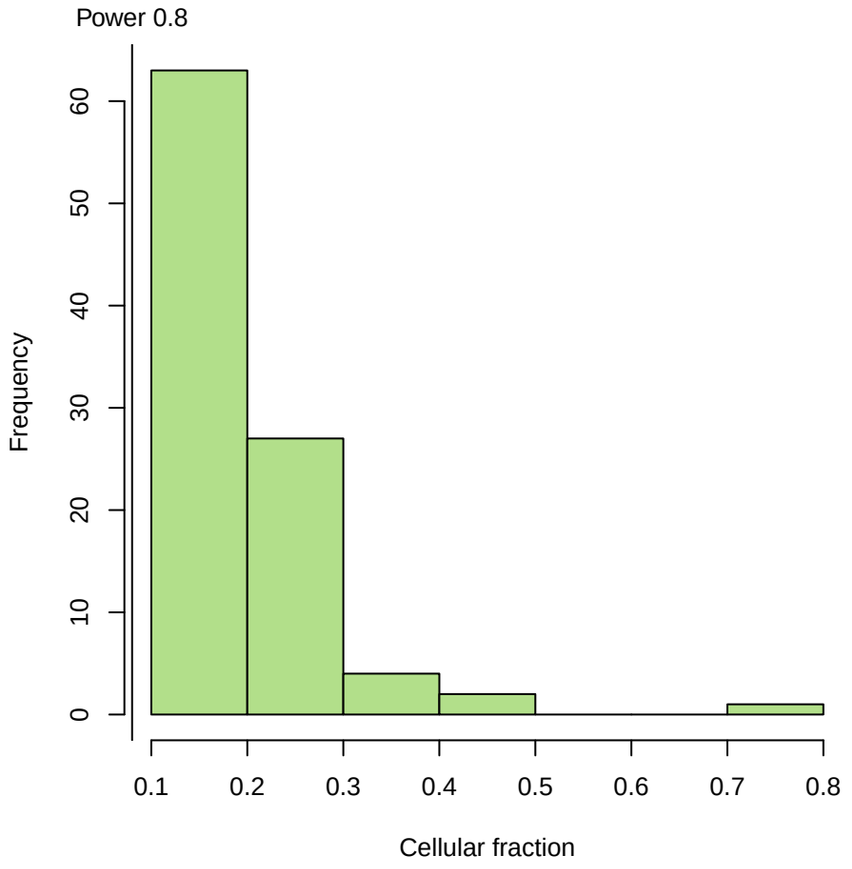

SCNA−fit log−likelihood: −14821.16
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 6 7
0 20 40 60 80 100 120 140
SNV Index

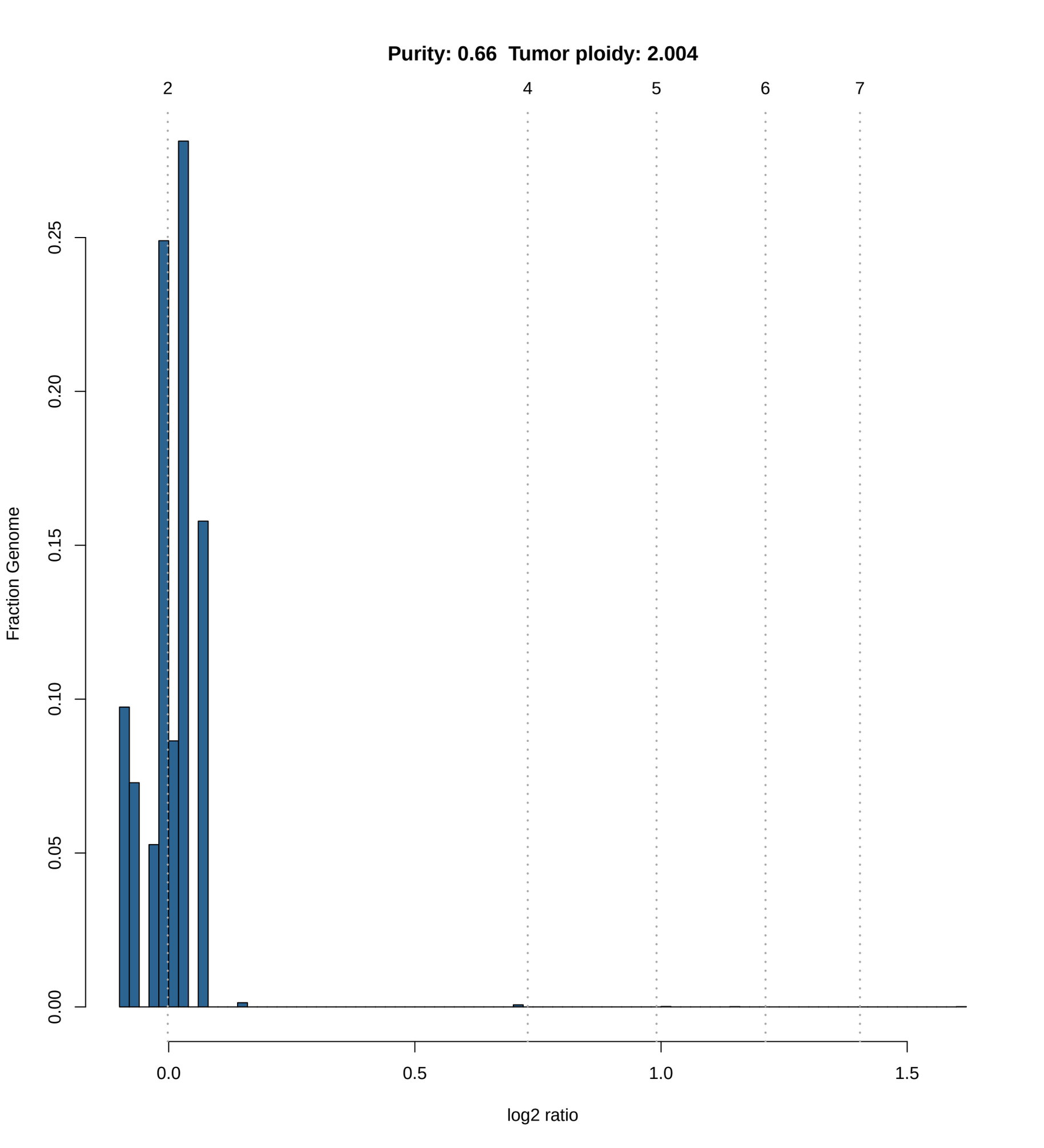

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120 140
SNV Index

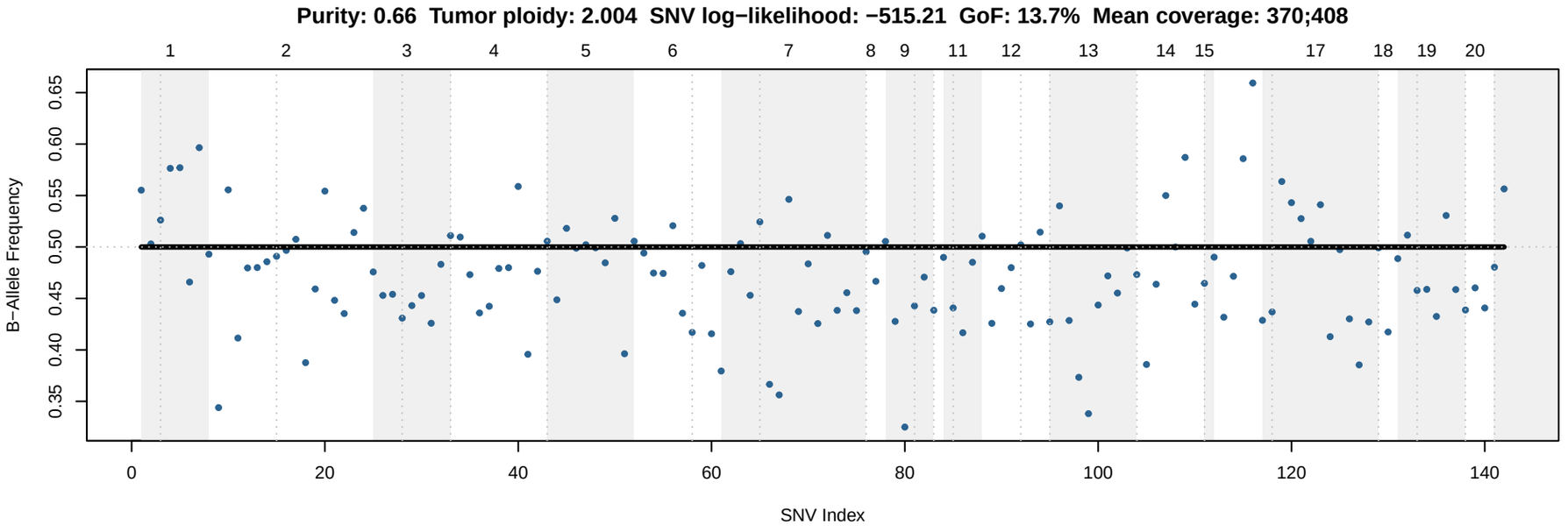

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
3m2
3m1
−0.5
0.0
0.5
Copy Number log−ratio

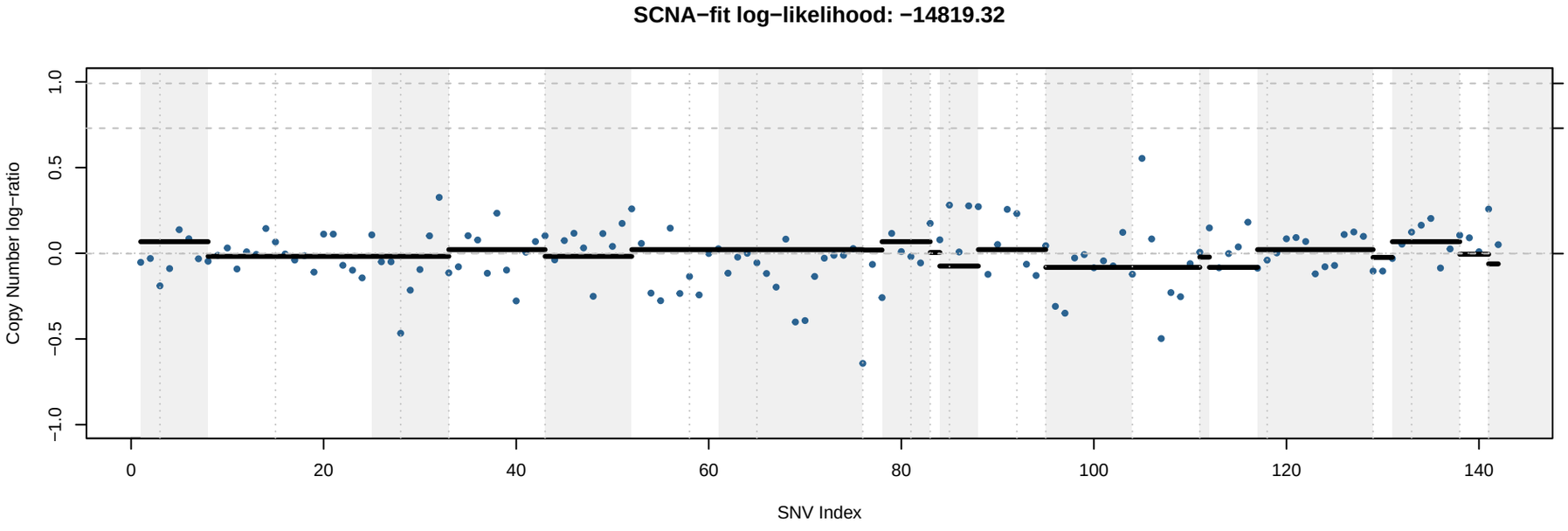

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

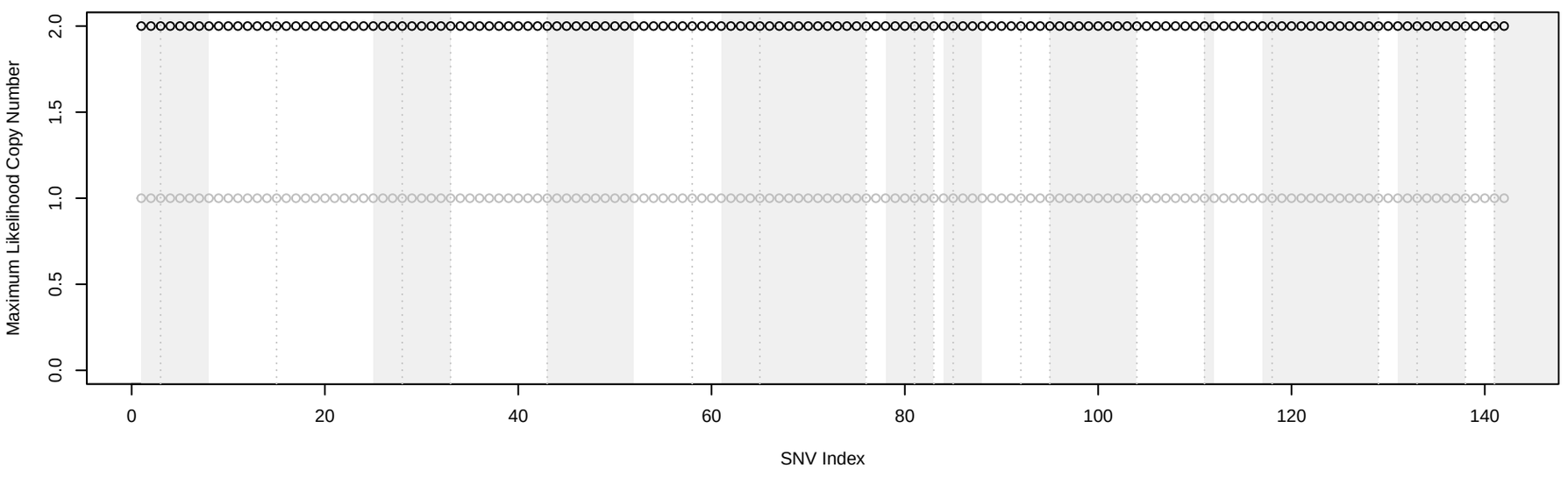

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.5
0.0
0.5
Copy Number log−ratio

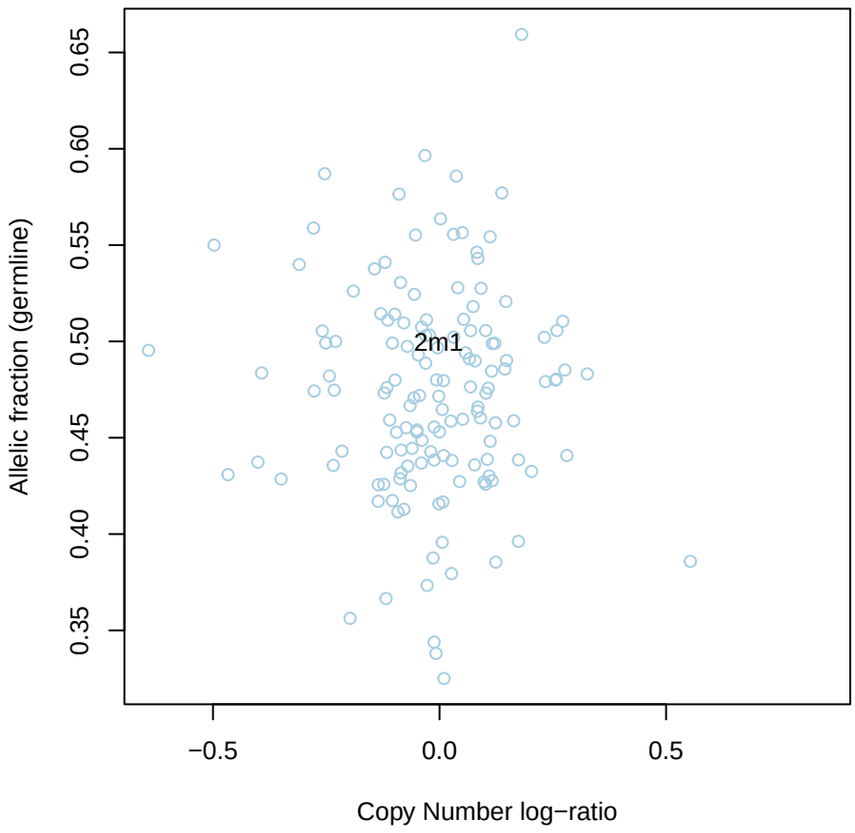

Power 0.8
Frequency
0
10
20
30
40
50
60
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
Cellular fraction

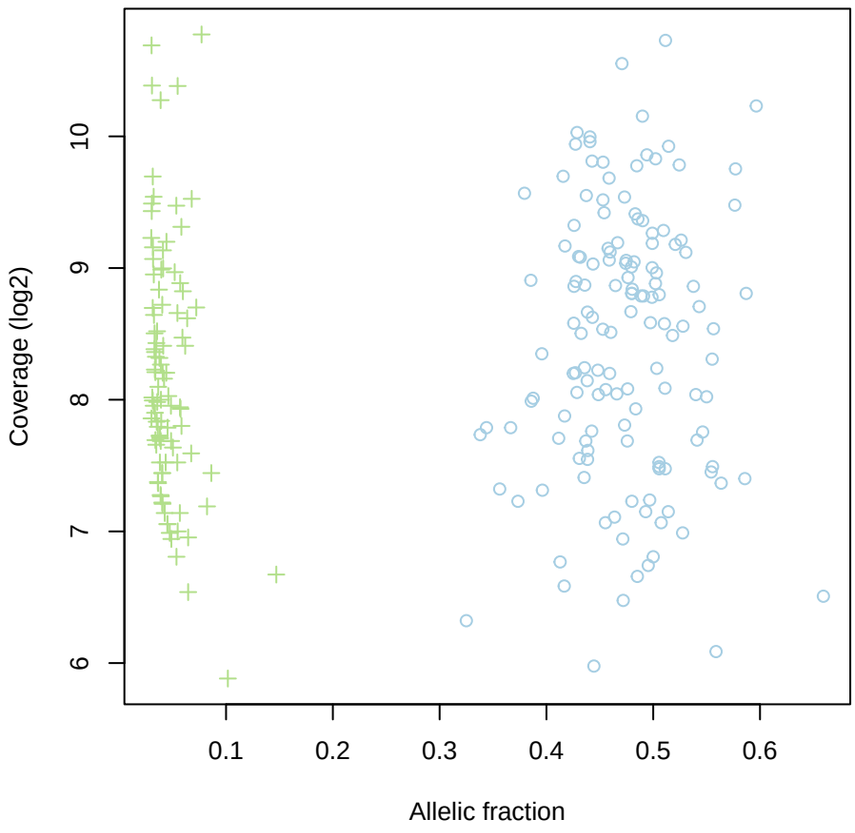

Purity: 0.66 Tumor ploidy: 2.004
2
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
1.5
log2 ratio

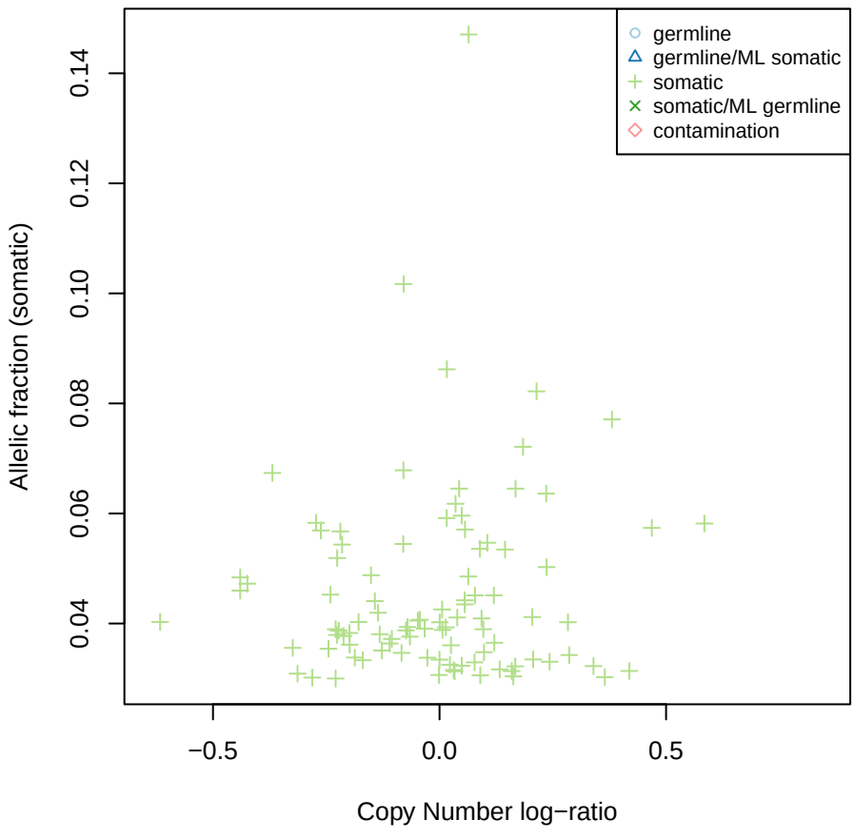

Purity: 0.66 Tumor ploidy: 2.004 SNV log−likelihood: −515.21 GoF: 13.7% Mean coverage: 370;408
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

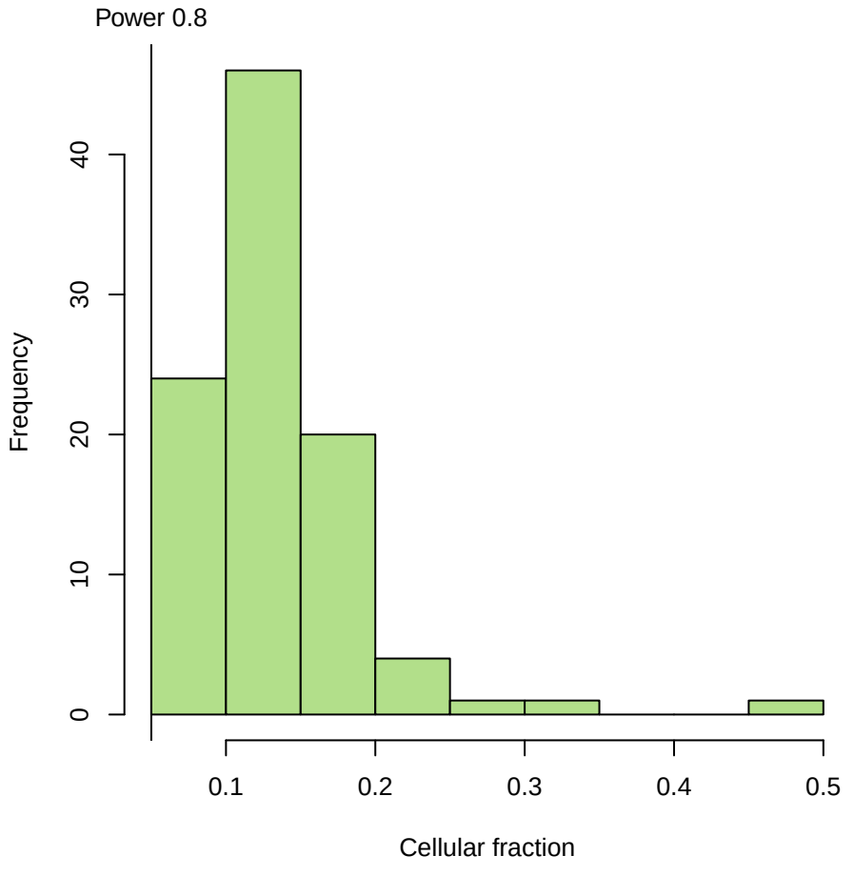

SCNA−fit log−likelihood: −14819.32
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 4 5
0 20 40 60 80 100 120 140
SNV Index

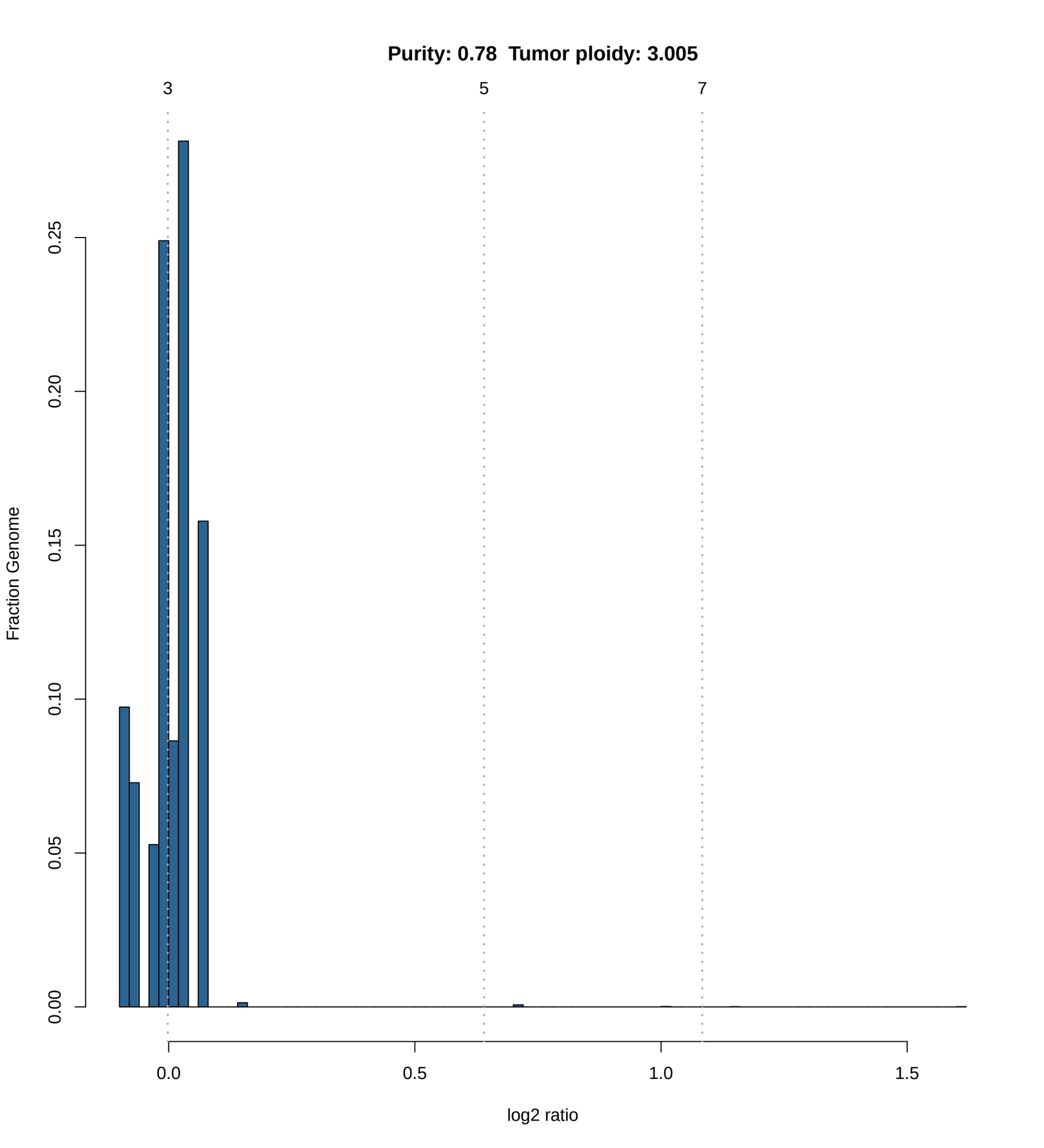

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 20 40 60 80 100 120 140
SNV Index

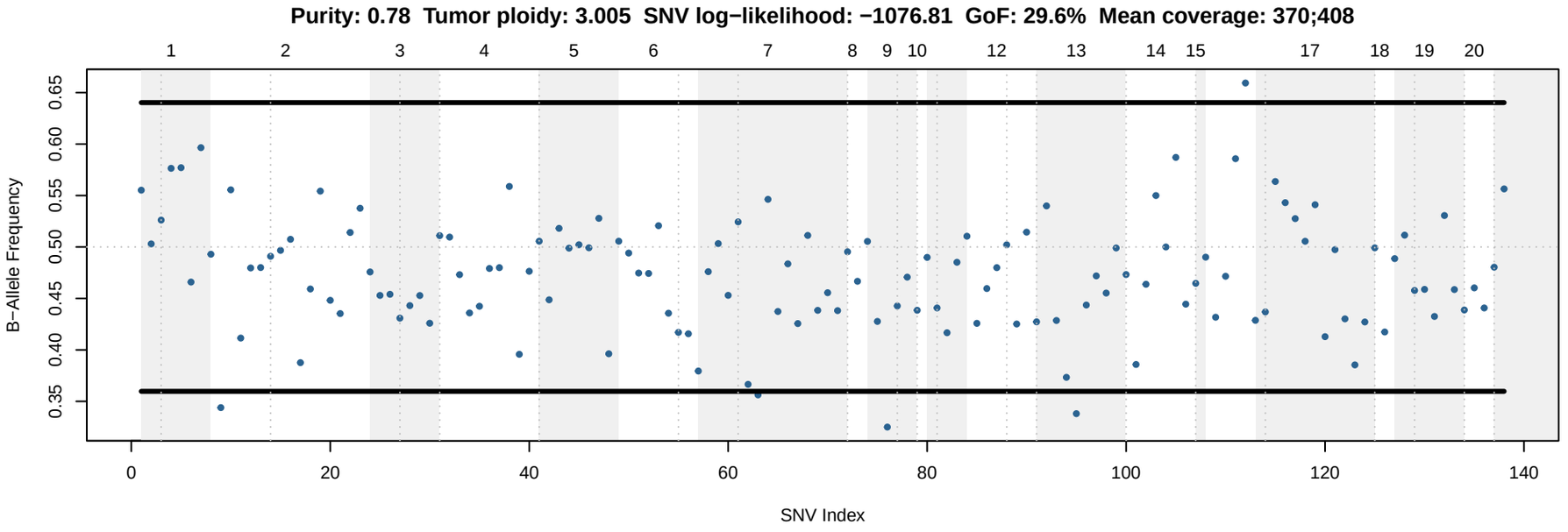

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
2m1
−0.5
0.0
0.5
Copy Number log−ratio

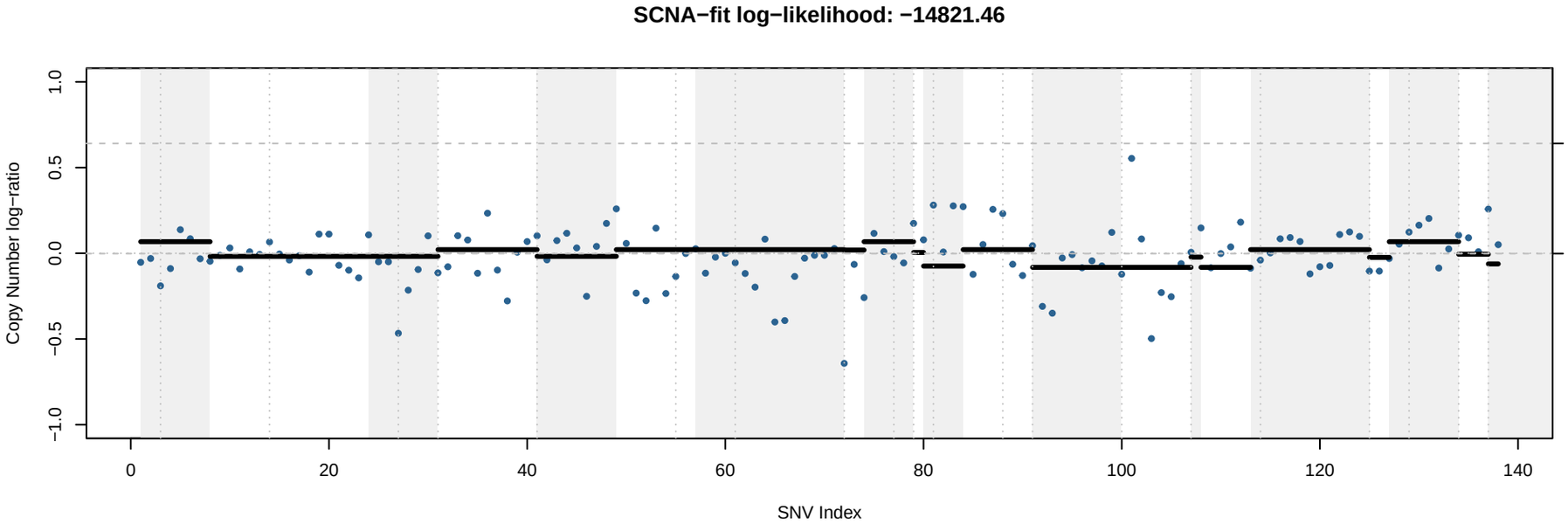

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

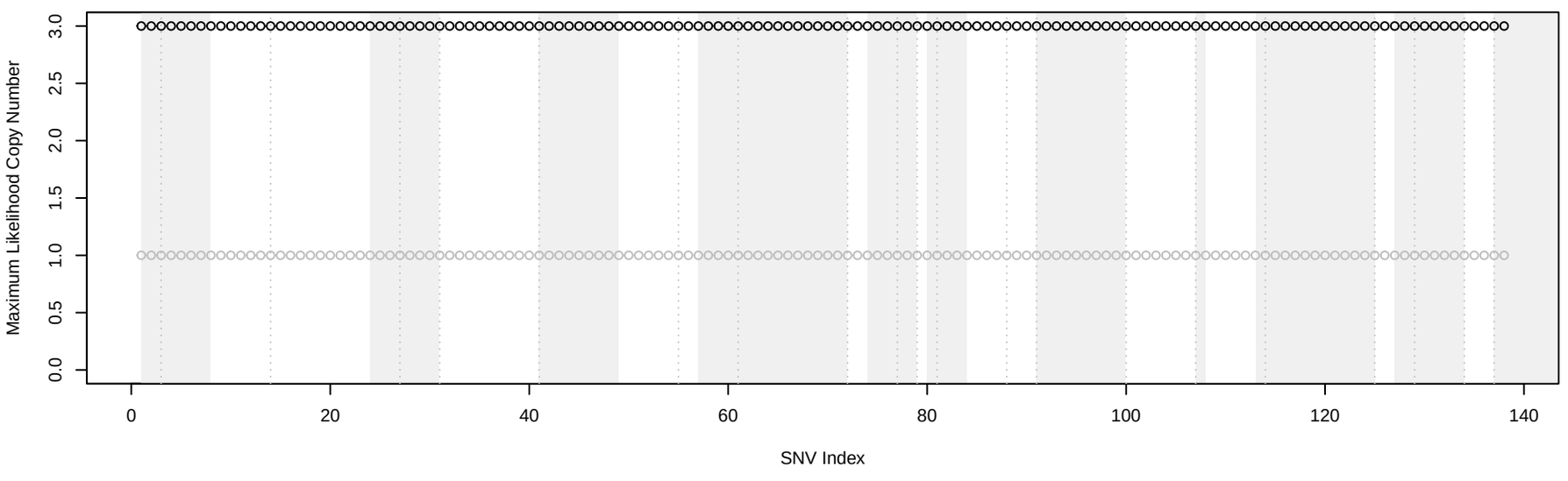

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
−0.5
0.0
0.5
Copy Number log−ratio

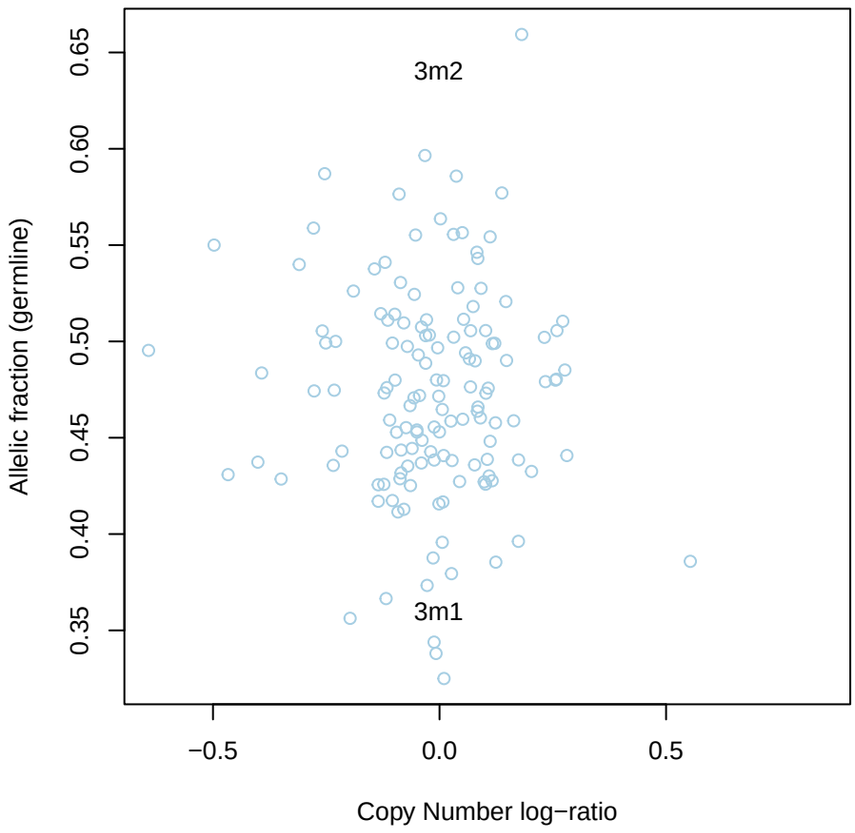

Power 0.8
Frequency
0
10
20
30
40
0.1
0.2
0.3
0.4
0.5
Cellular fraction

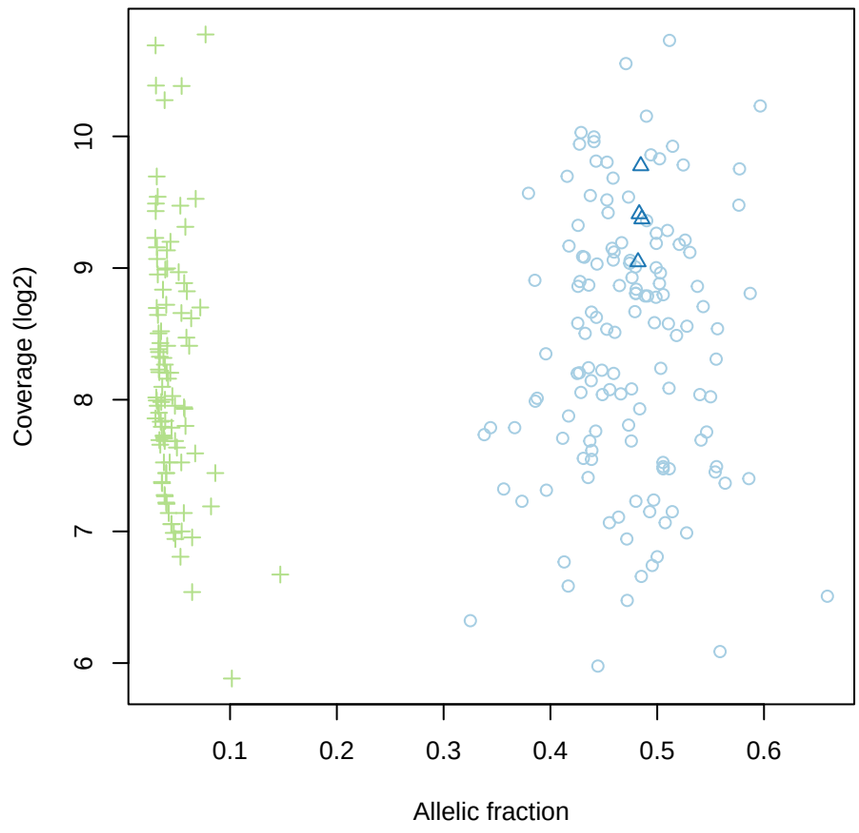

Purity: 0.78 Tumor ploidy: 3.005
3
5
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
1.5
log2 ratio

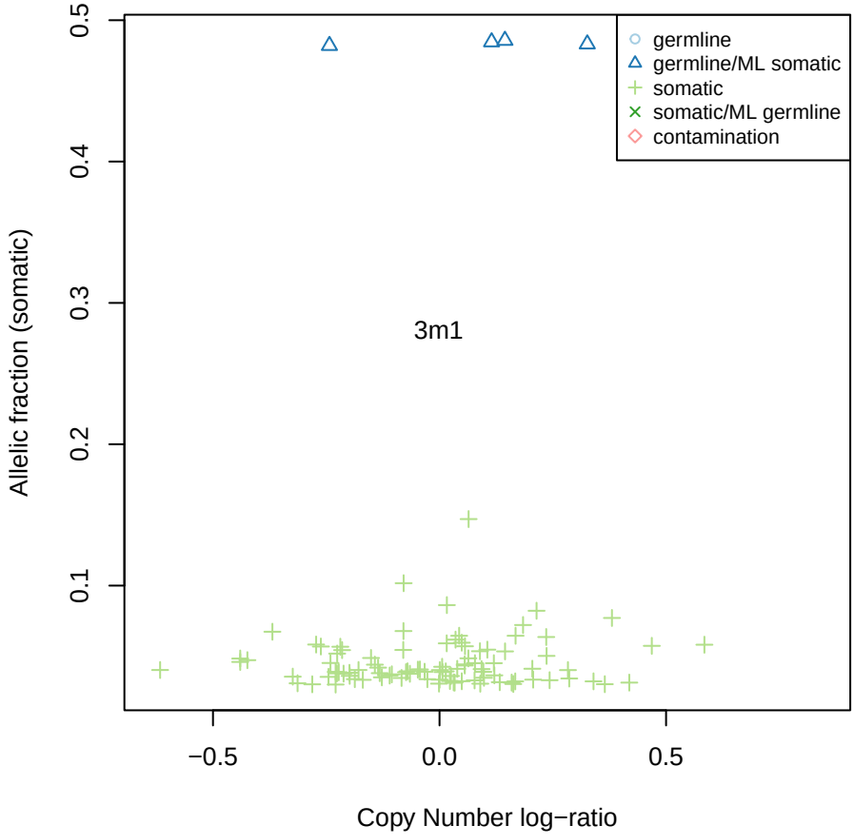

Purity: 0.78 Tumor ploidy: 3.005 SNV log−likelihood: −1076.81 GoF: 29.6% Mean coverage: 370;408
1 2 3 4 5 6 7 8 9 10 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 20 40 60 80 100 120 140
SNV Index

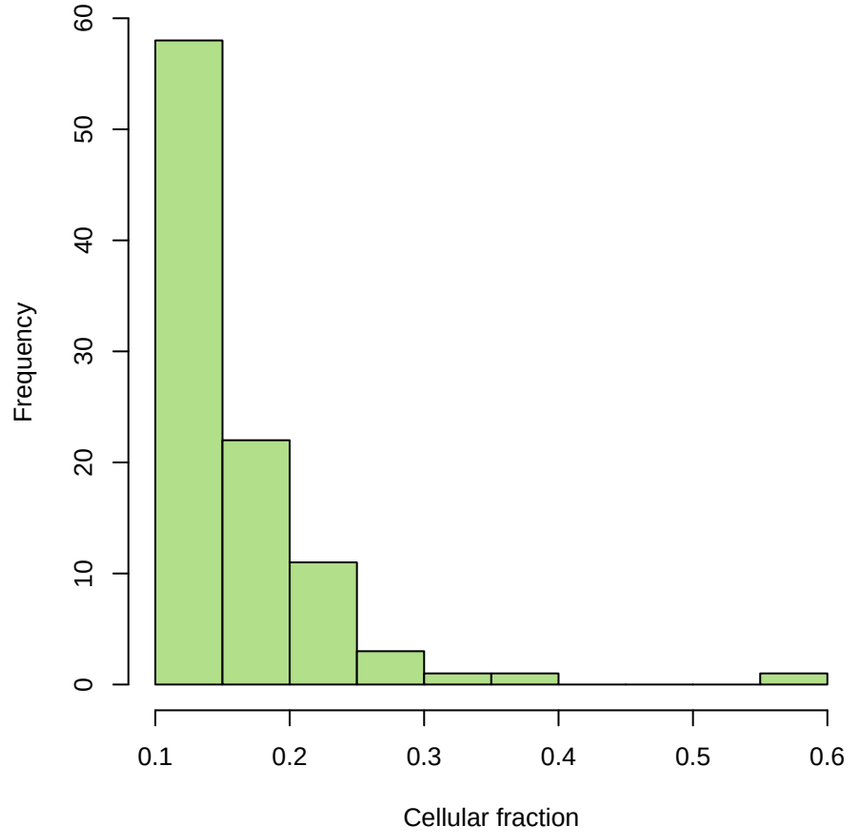

SCNA−fit log−likelihood: −14821.46
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
5
3
0 20 40 60 80 100 120 140
SNV Index


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
3m1
Allelic fraction (germline)
Copy Number log−ratio
0.35
0.40
0.45
0.50
0.55
0.60
0.65
−0.5
0.0
0.5


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


germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
Allelic fraction (somatic)
Copy Number log−ratio
0.1
0.2
0.3
0.4
0.5
−0.5
0.0
0.5


Frequency
Cellular fraction
0
10
20
30
40
50
60
0.1
0.2
0.3
0.4
0.5
0.6