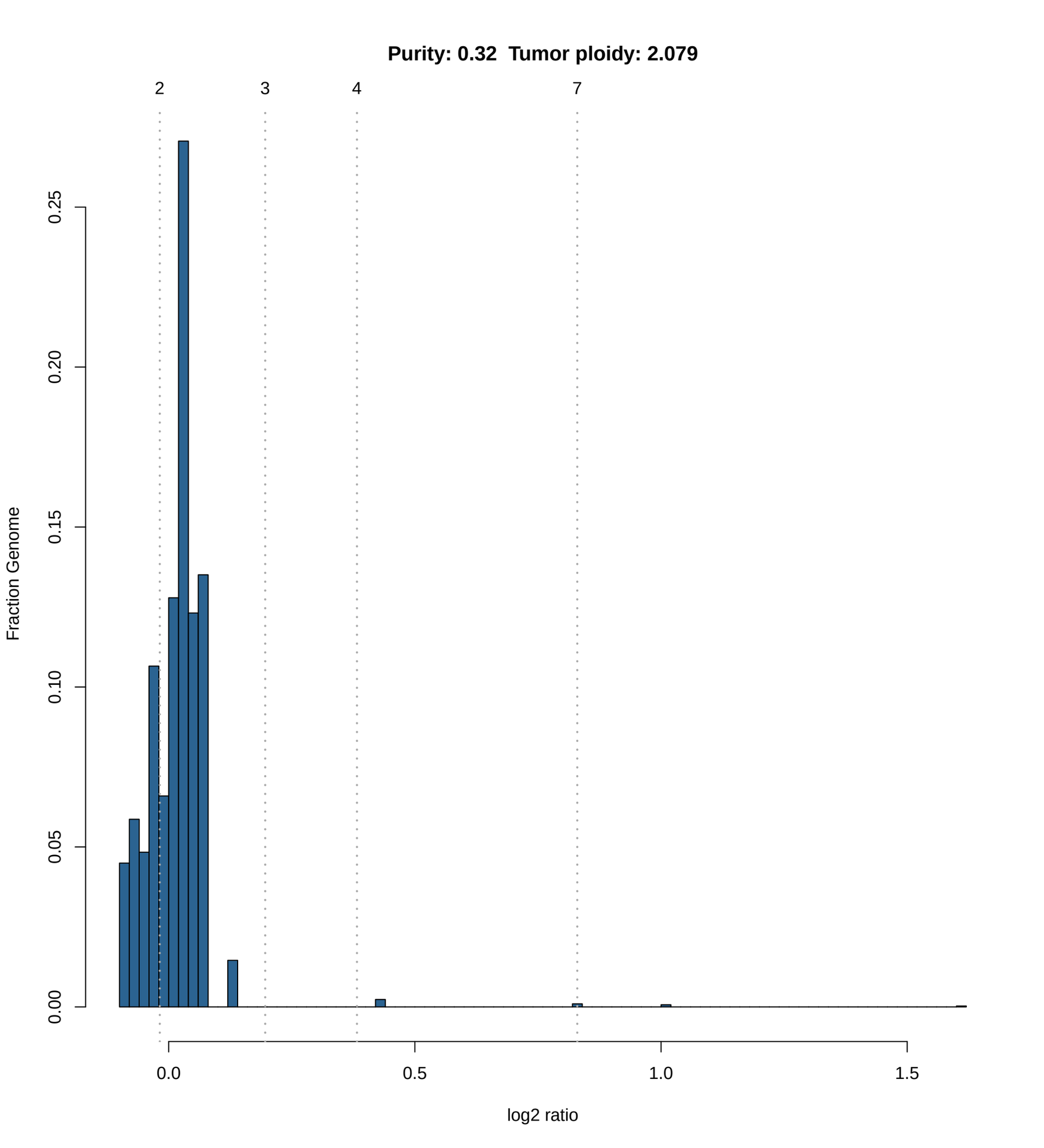
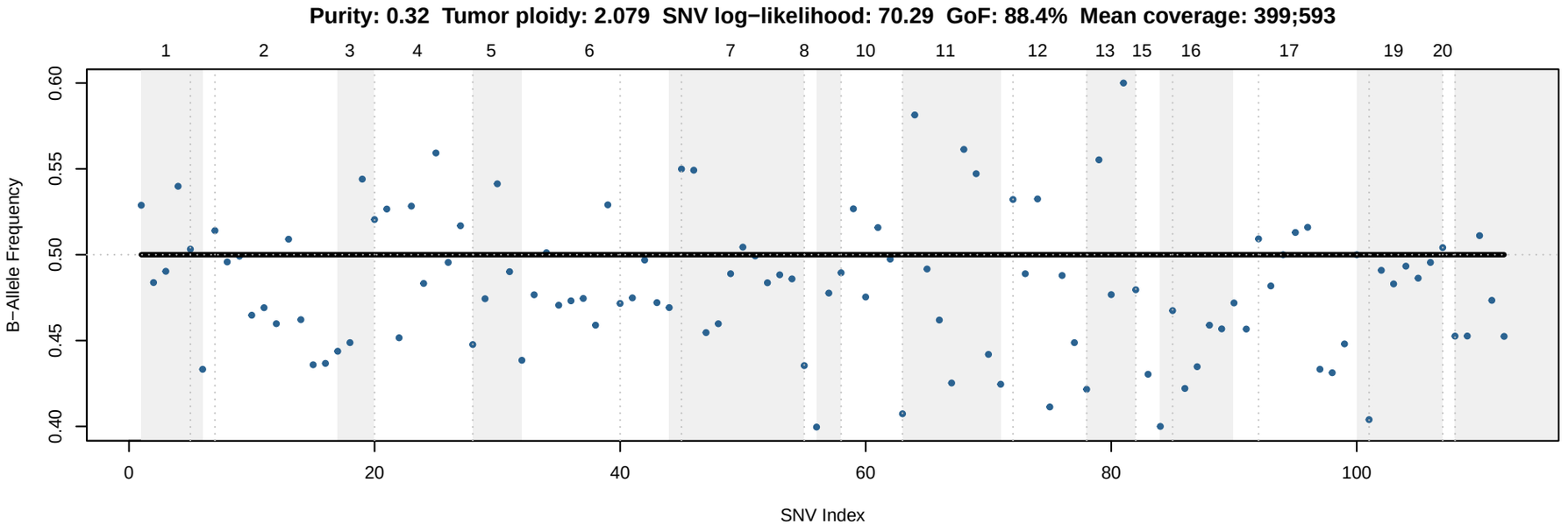
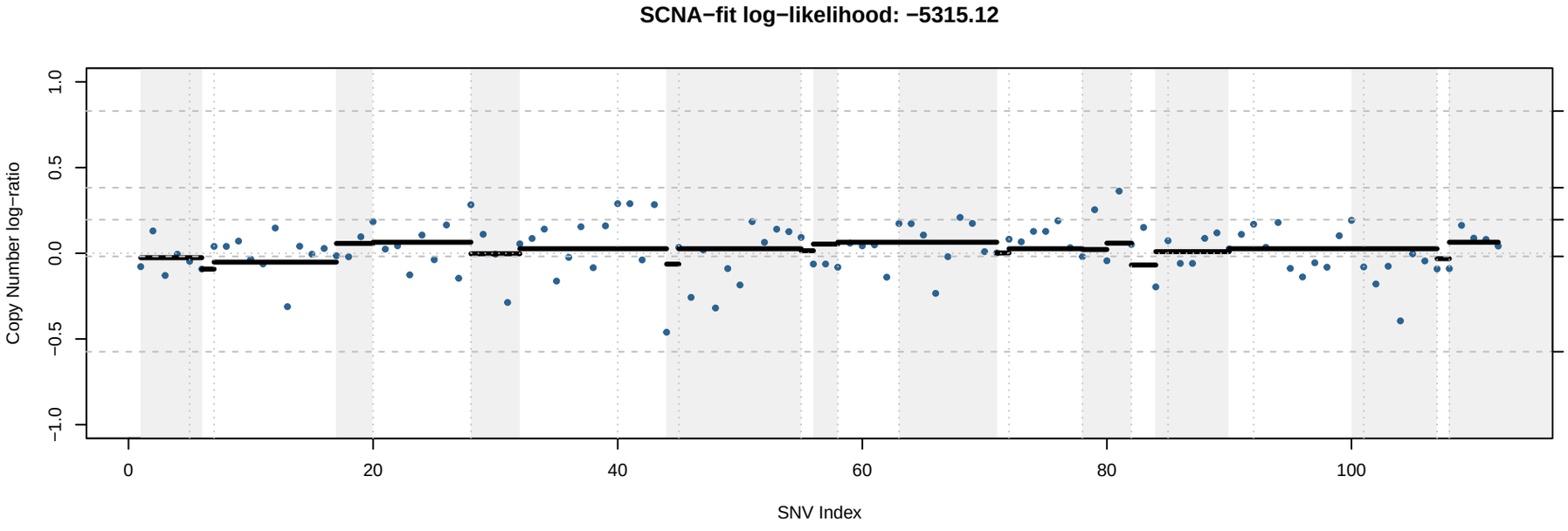
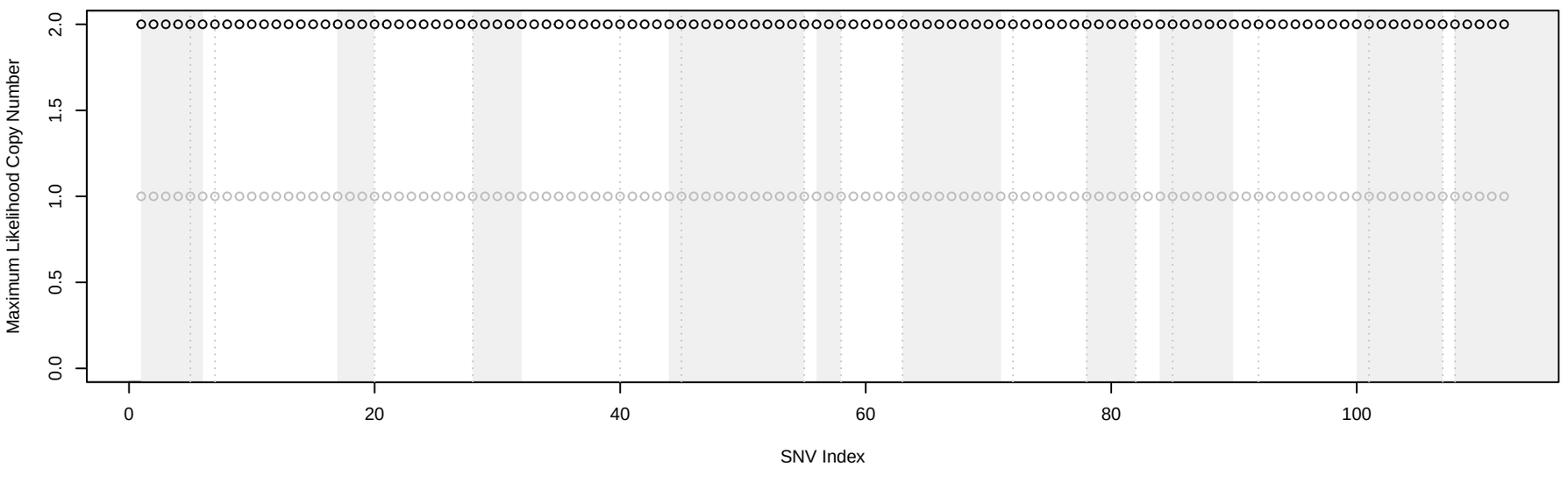
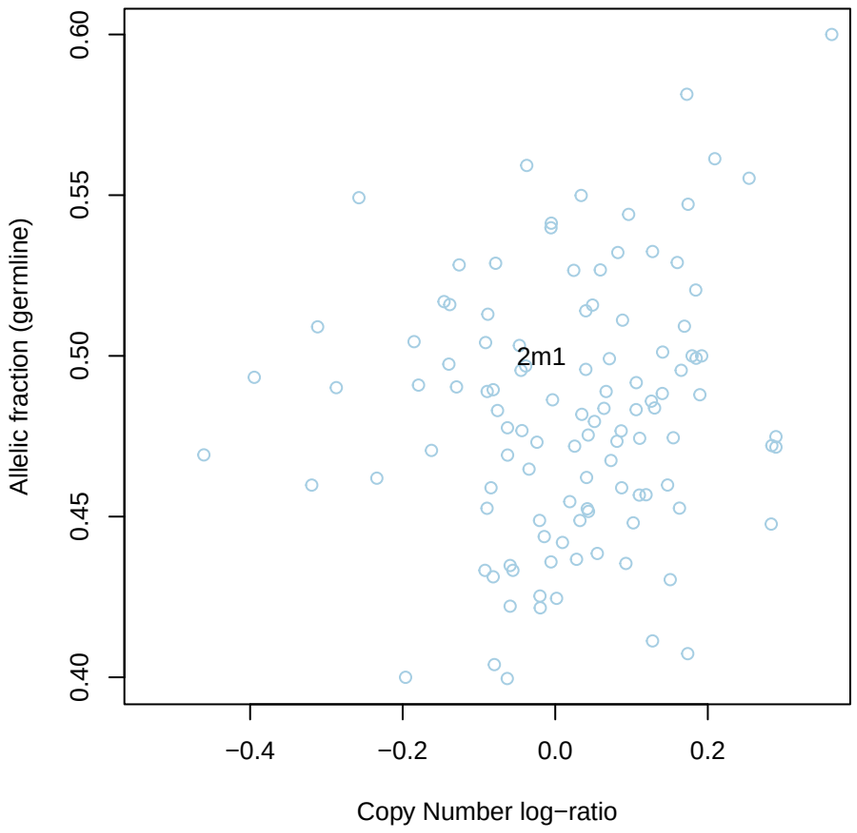
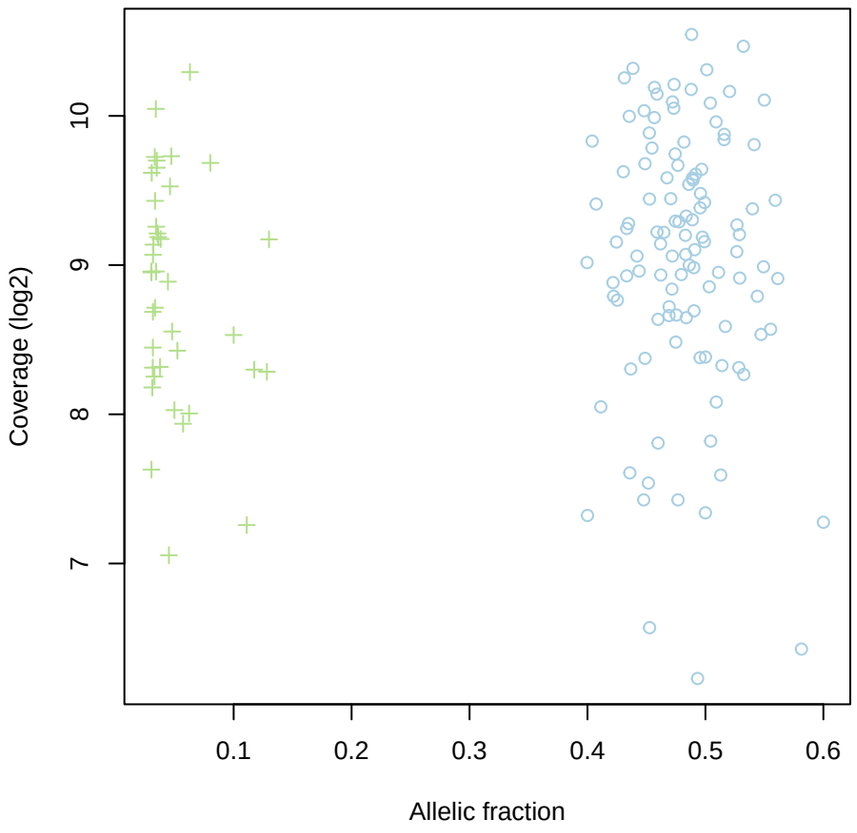

Purity: 0.32 Tumor ploidy: 2.079
2
3
4
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
1.5
log2 ratio

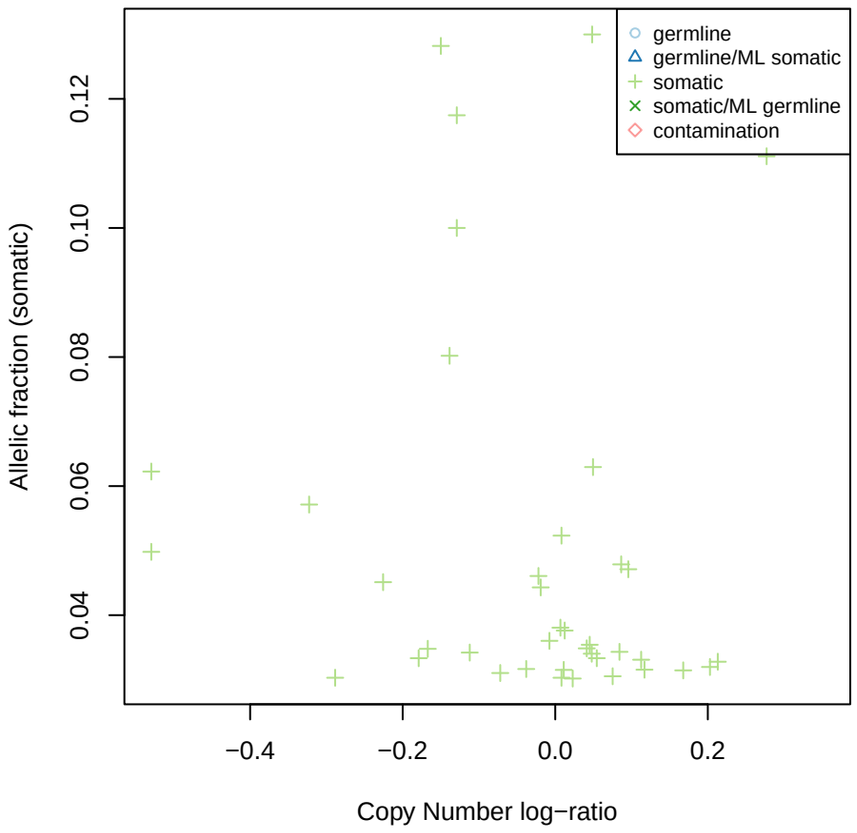

Purity: 0.32 Tumor ploidy: 2.079 SNV log−likelihood: 70.29 GoF: 88.4% Mean coverage: 399;593
1 2 3 4 5 6 7 8 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

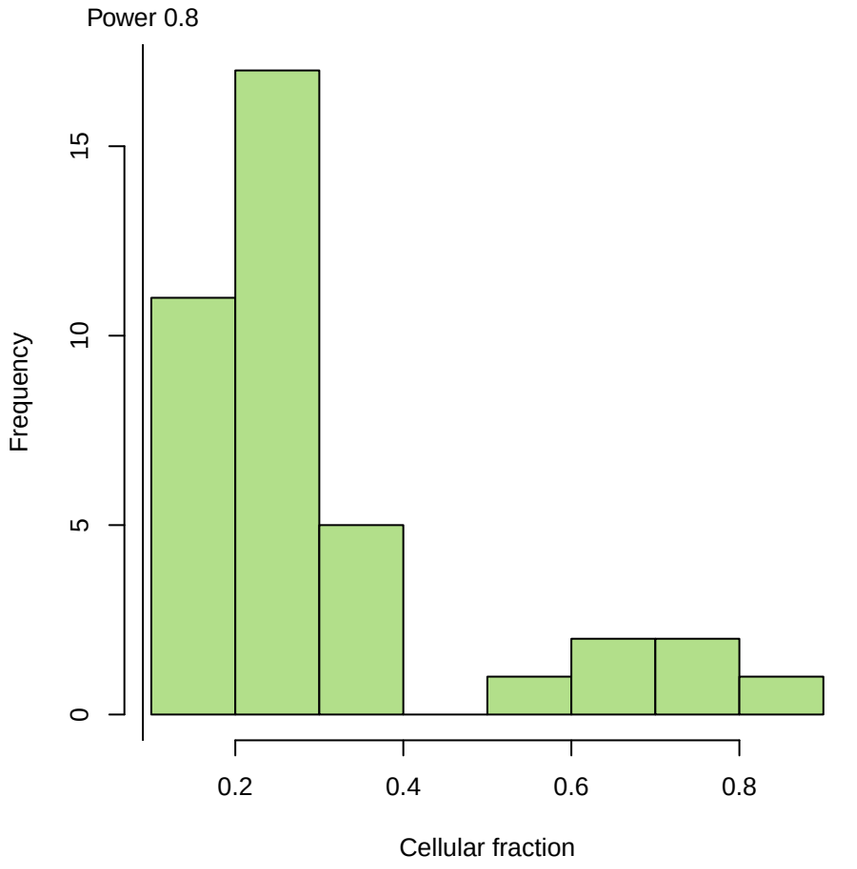

SCNA−fit log−likelihood: −5315.12
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 3 4 7
0 20 40 60 80 100
SNV Index

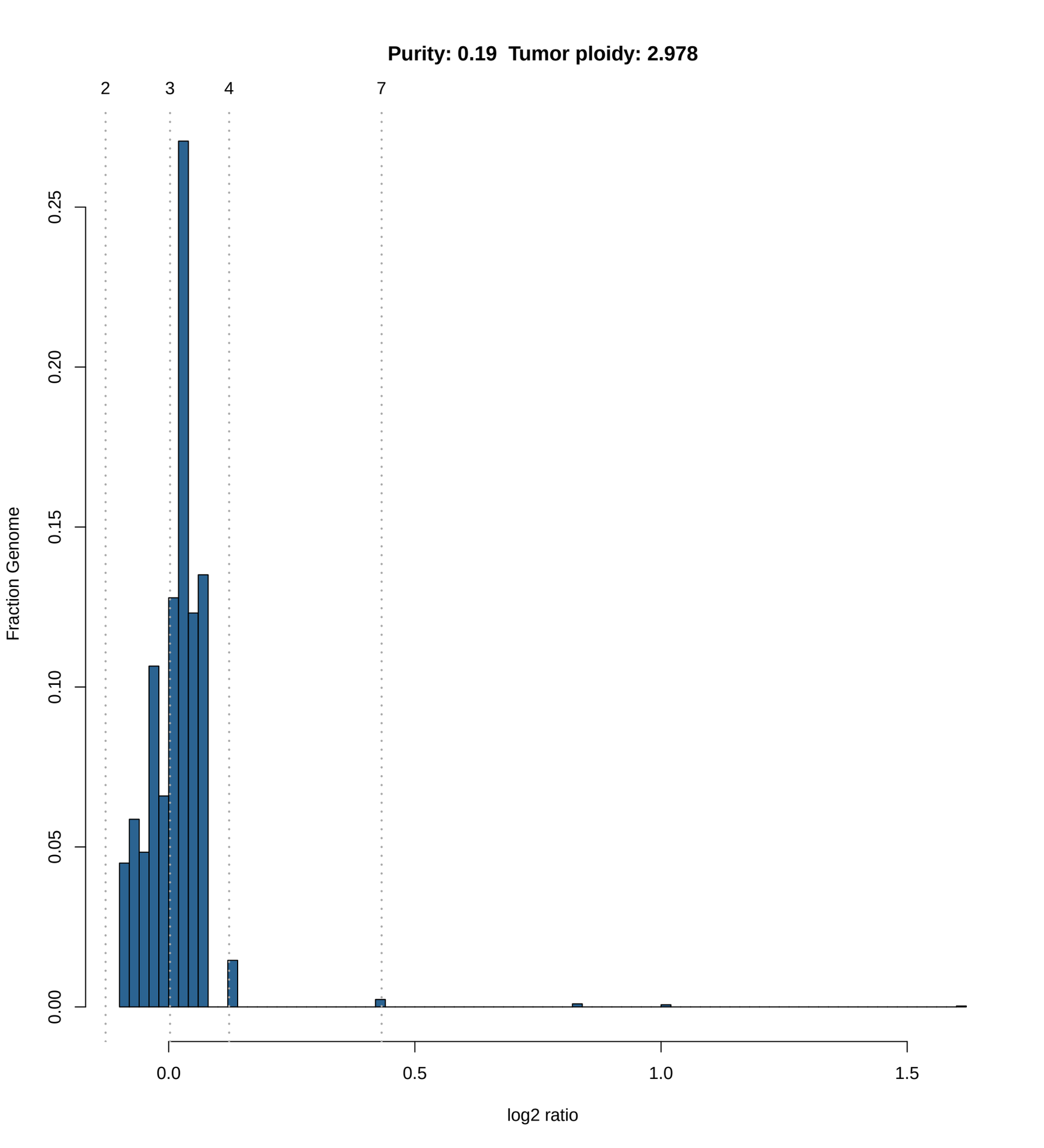

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 20 40 60 80 100
SNV Index

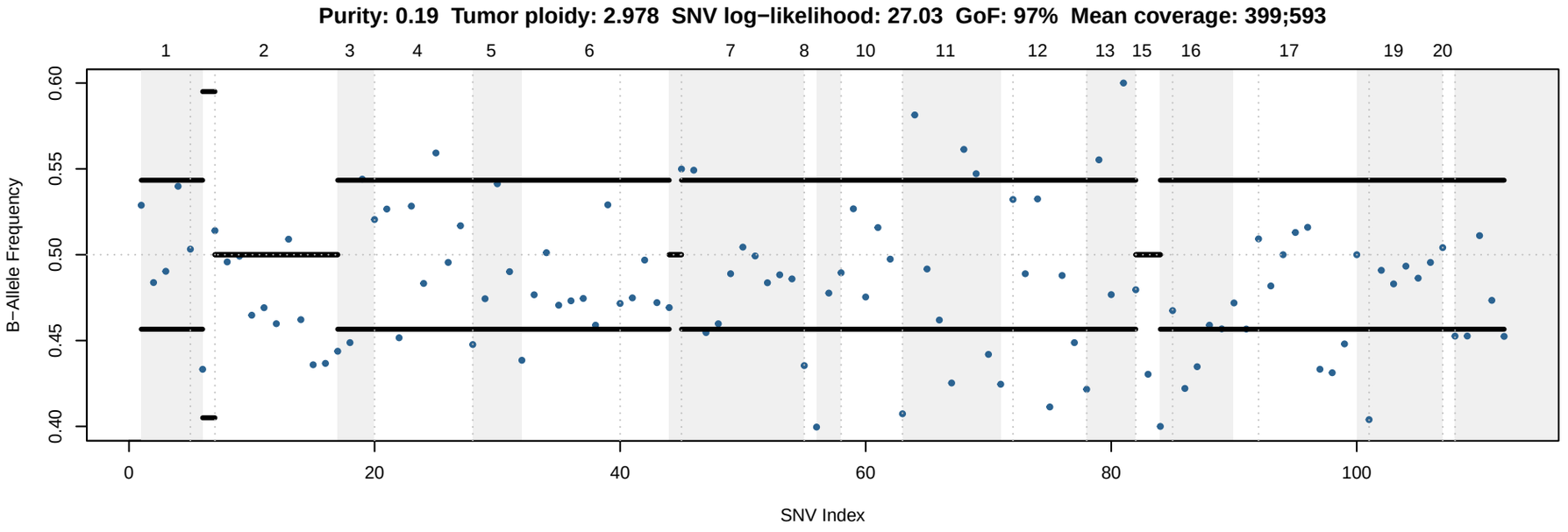

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
2m1
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

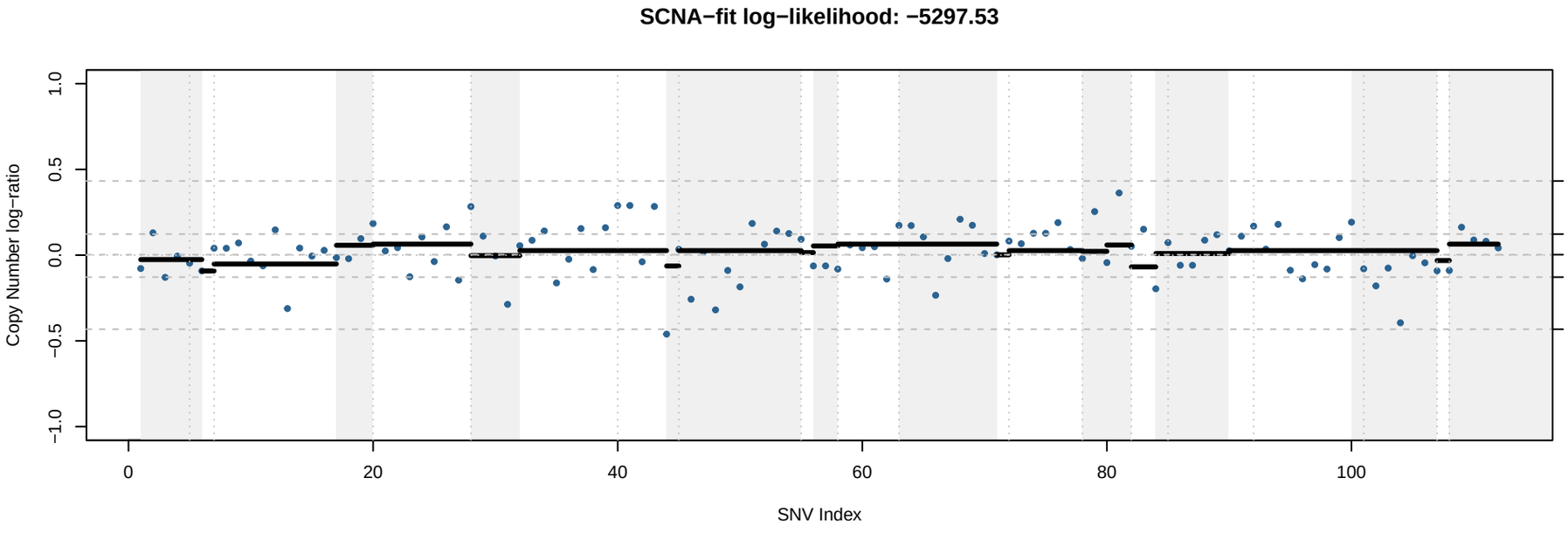

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

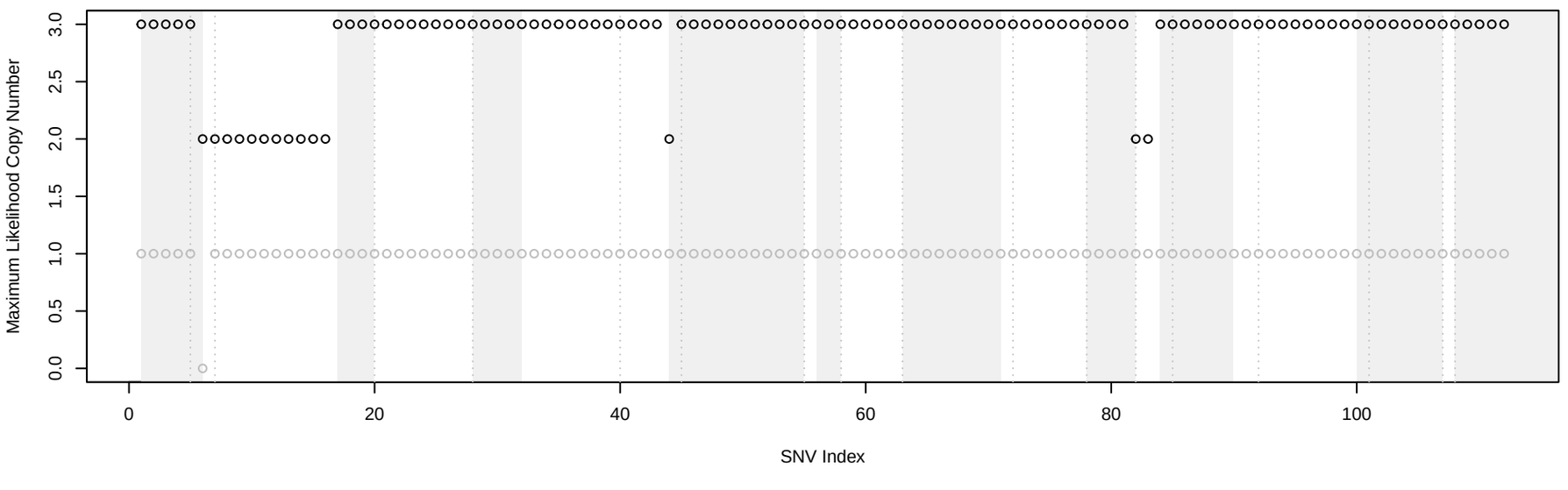

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

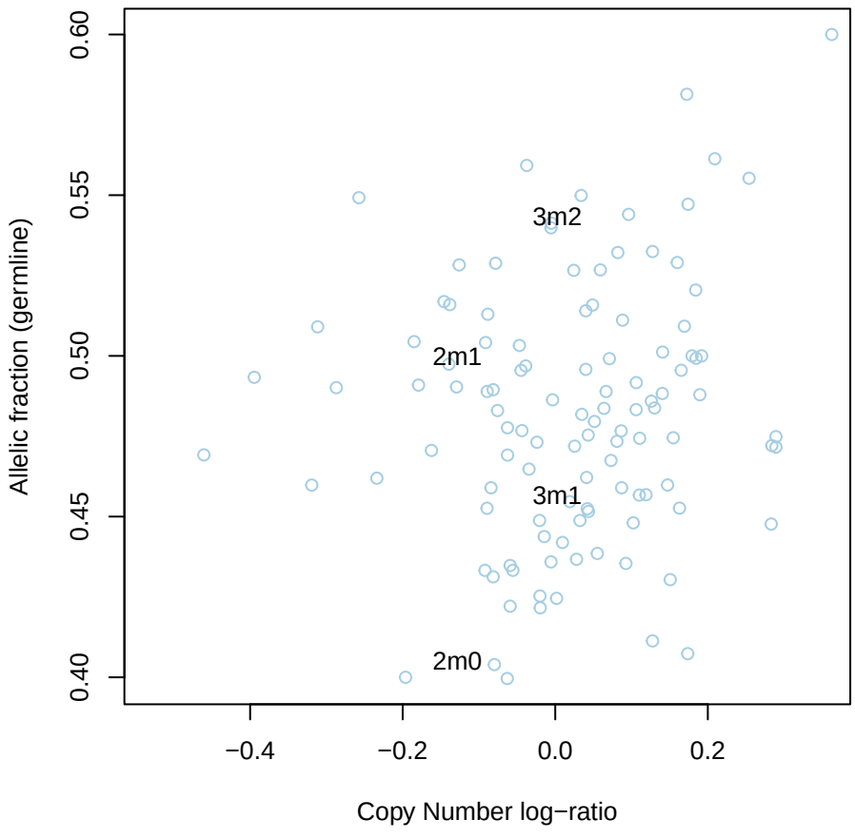

Power 0.8
Frequency
0
5
10
15
0.2
0.4
0.6
0.8
Cellular fraction

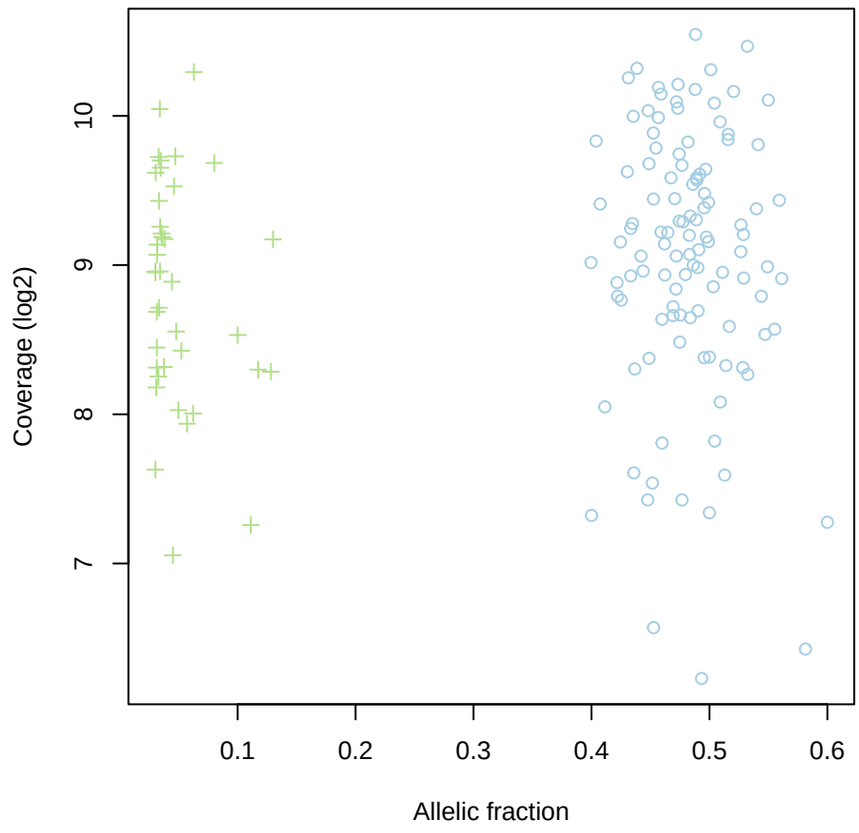

Purity: 0.19 Tumor ploidy: 2.978
2
3
4
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
1.5
log2 ratio

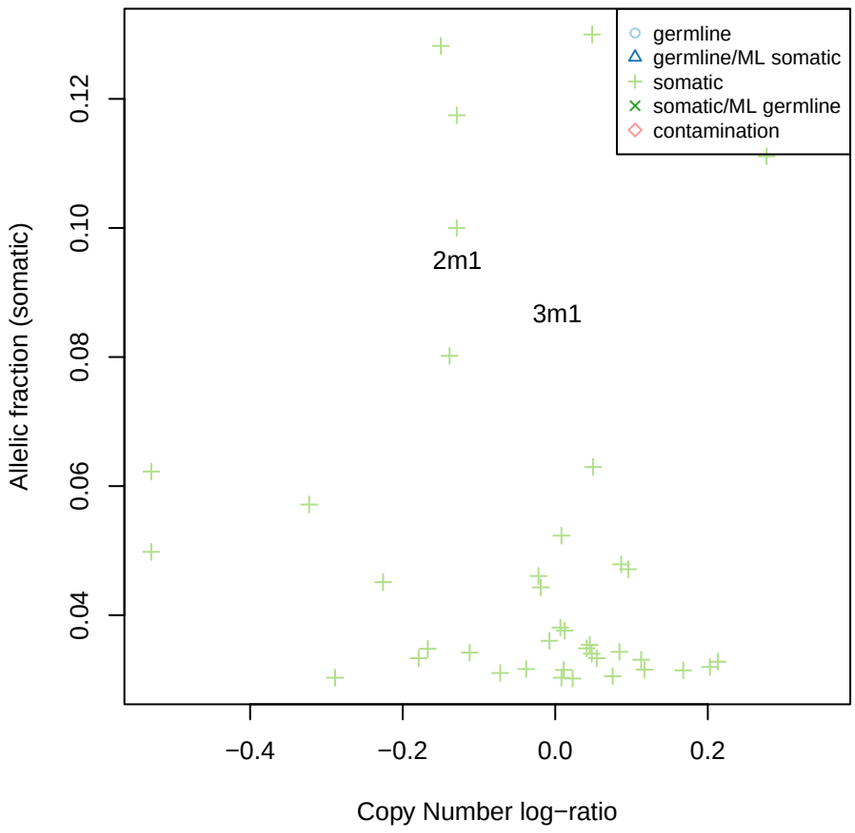

Purity: 0.19 Tumor ploidy: 2.978 SNV log−likelihood: 27.03 GoF: 97% Mean coverage: 399;593
1 2 3 4 5 6 7 8 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

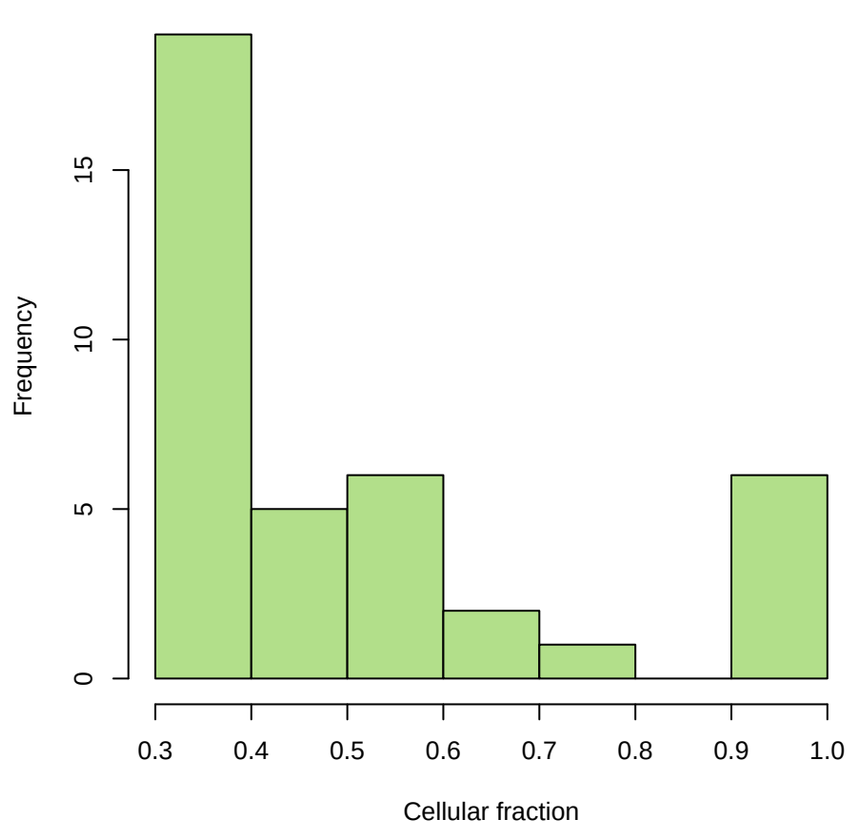

SCNA−fit log−likelihood: −5297.53
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4 7
0 20 40 60 80 100
SNV Index

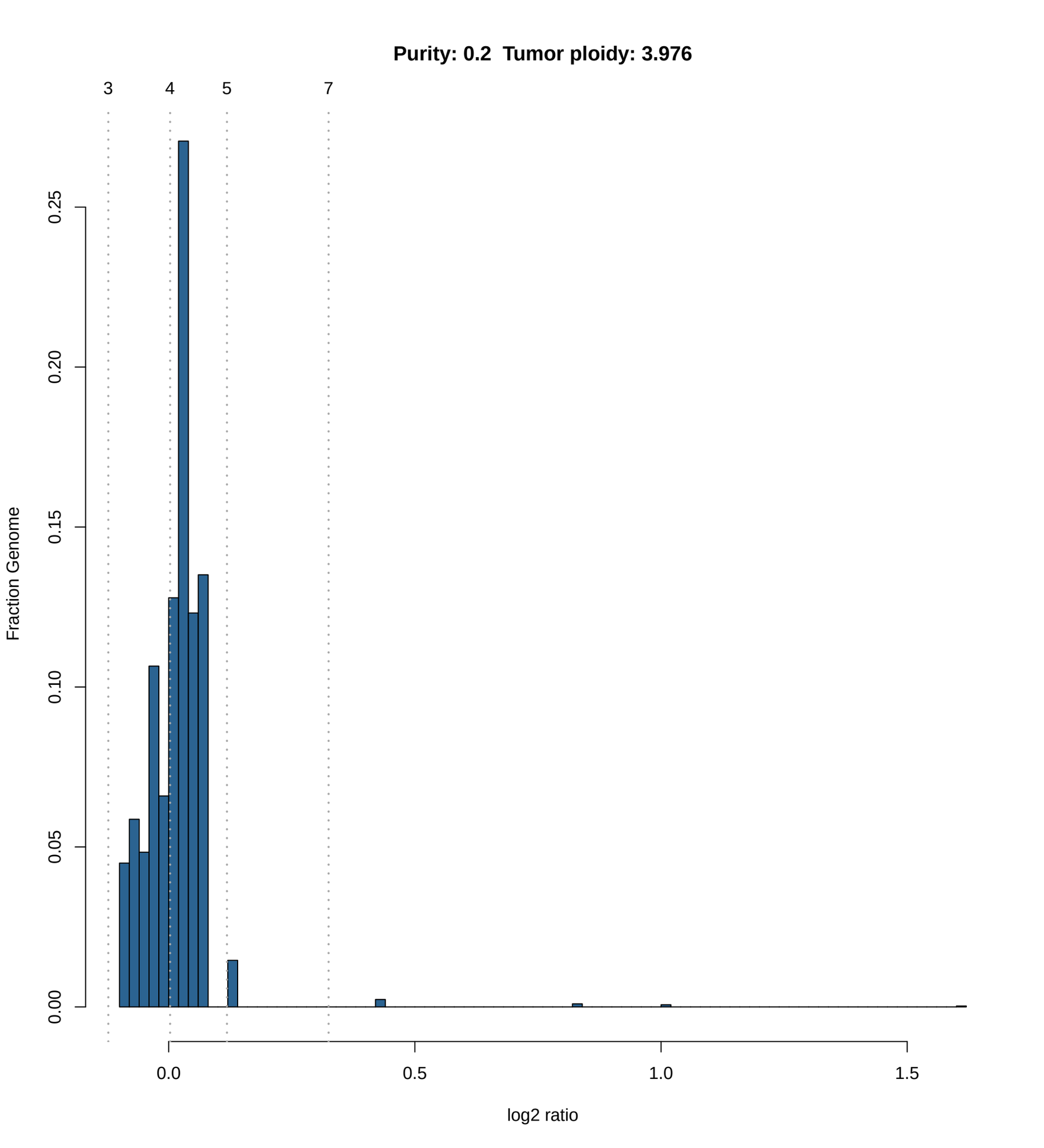

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100
SNV Index

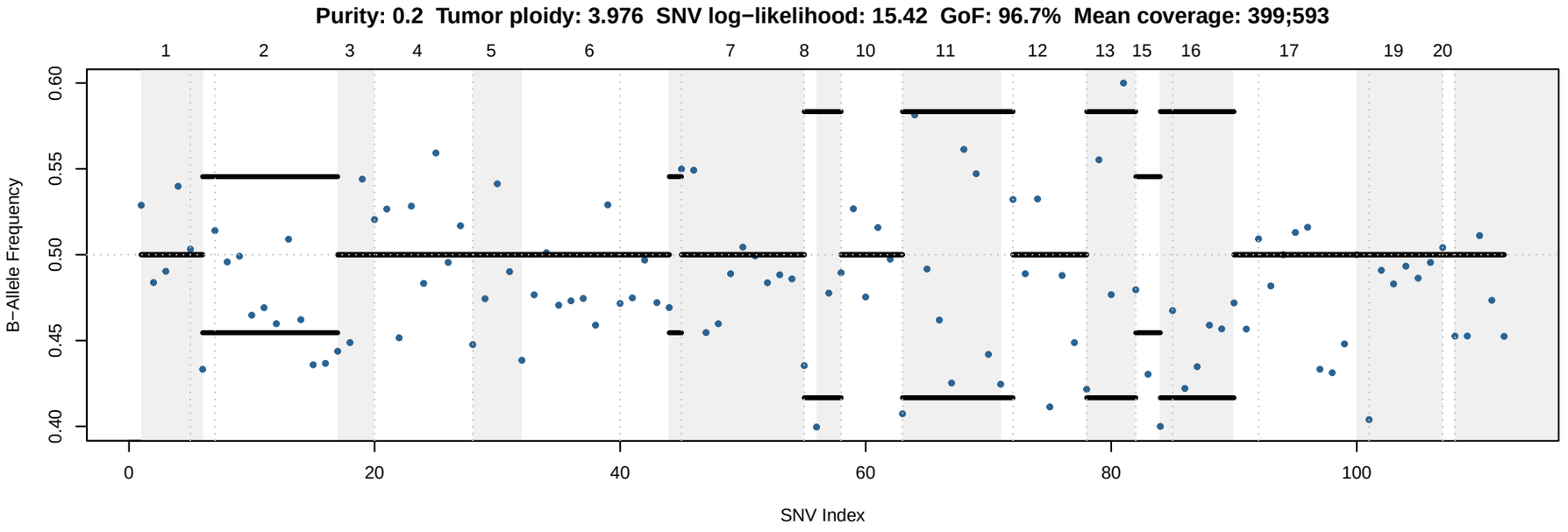

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
3m2
2m1
3m1
2m0
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

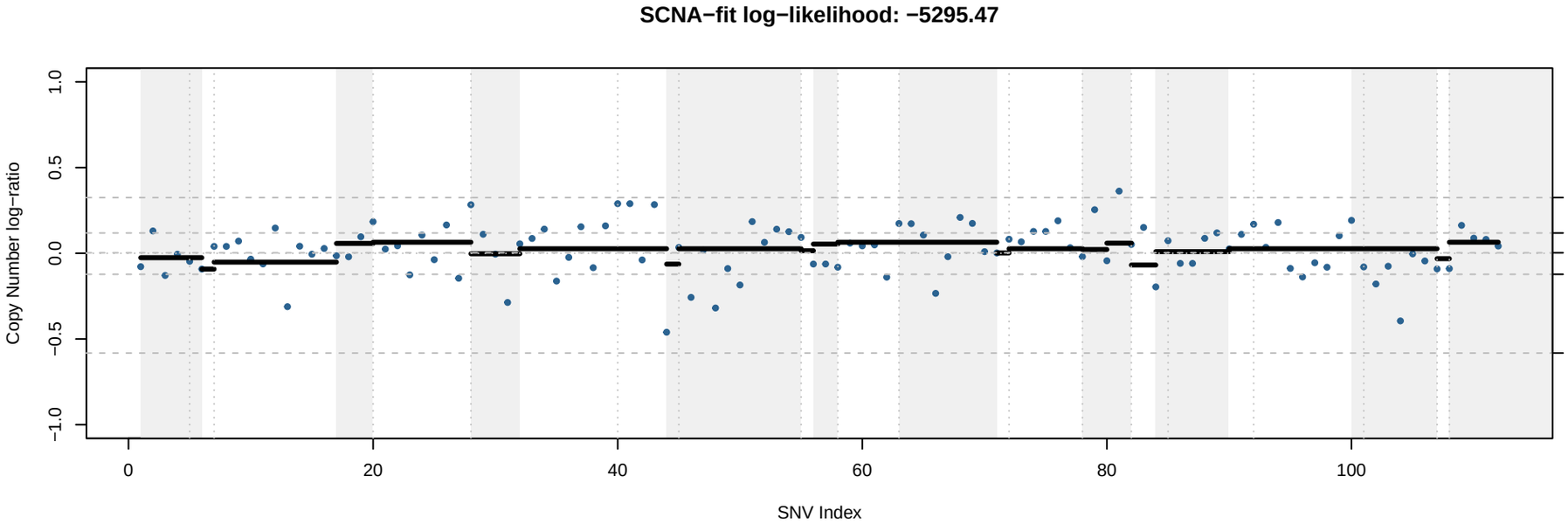

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

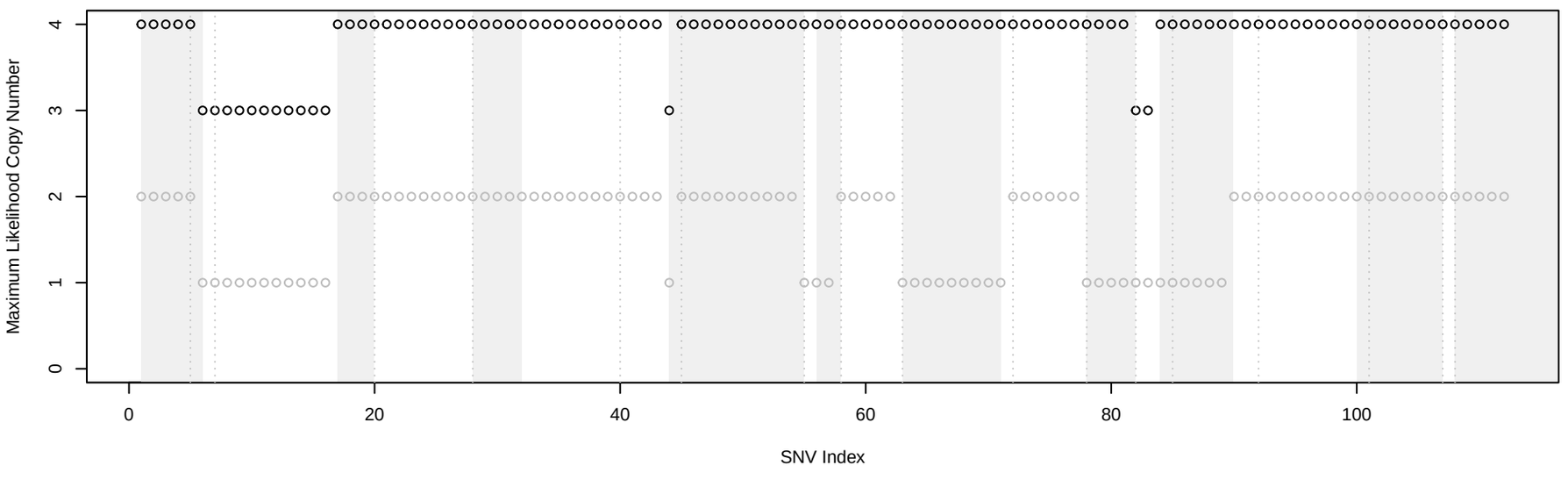

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

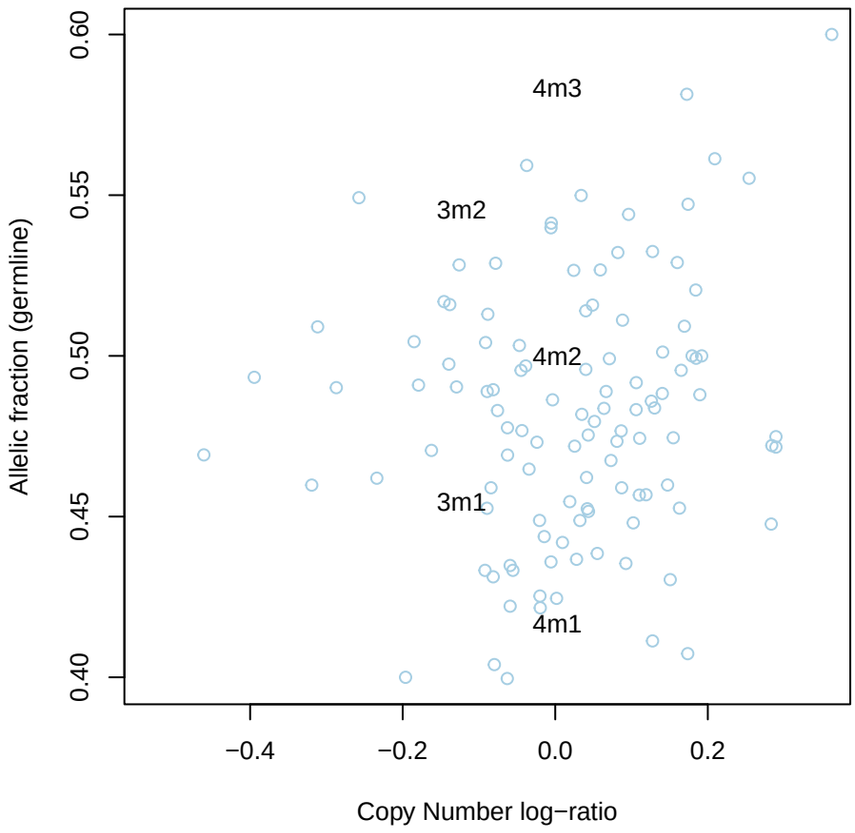

Frequency
0
5
10
15
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

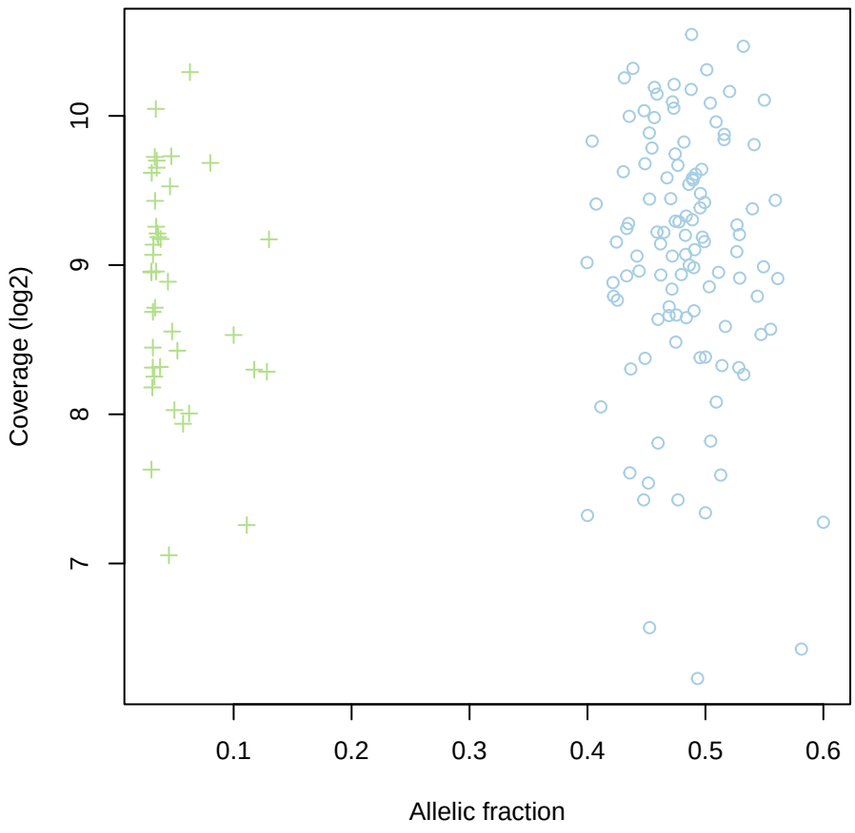

Purity: 0.2 Tumor ploidy: 3.976
3
4
5
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
1.5
log2 ratio

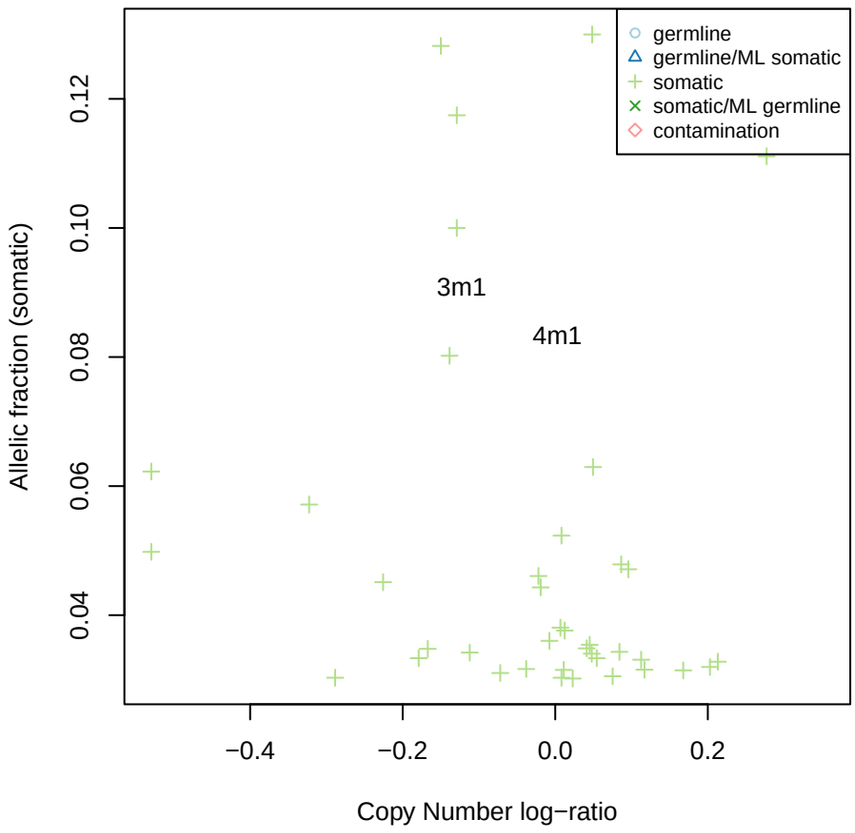

Purity: 0.2 Tumor ploidy: 3.976 SNV log−likelihood: 15.42 GoF: 96.7% Mean coverage: 399;593
1 2 3 4 5 6 7 8 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

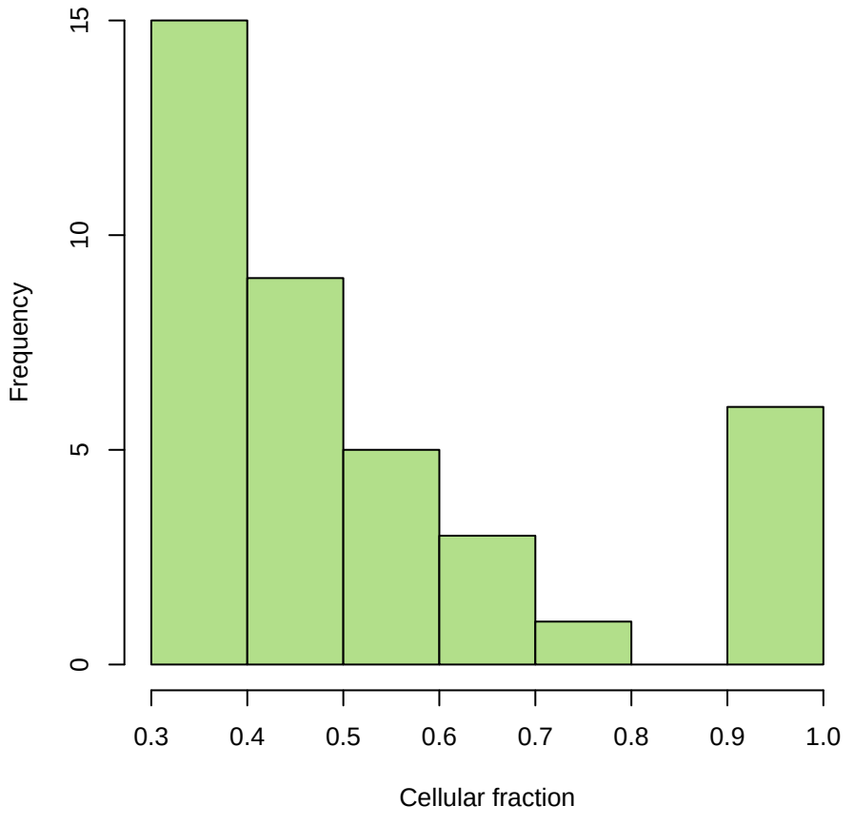

SCNA−fit log−likelihood: −5295.47
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 3 5 7
0 20 40 60 80 100
SNV Index

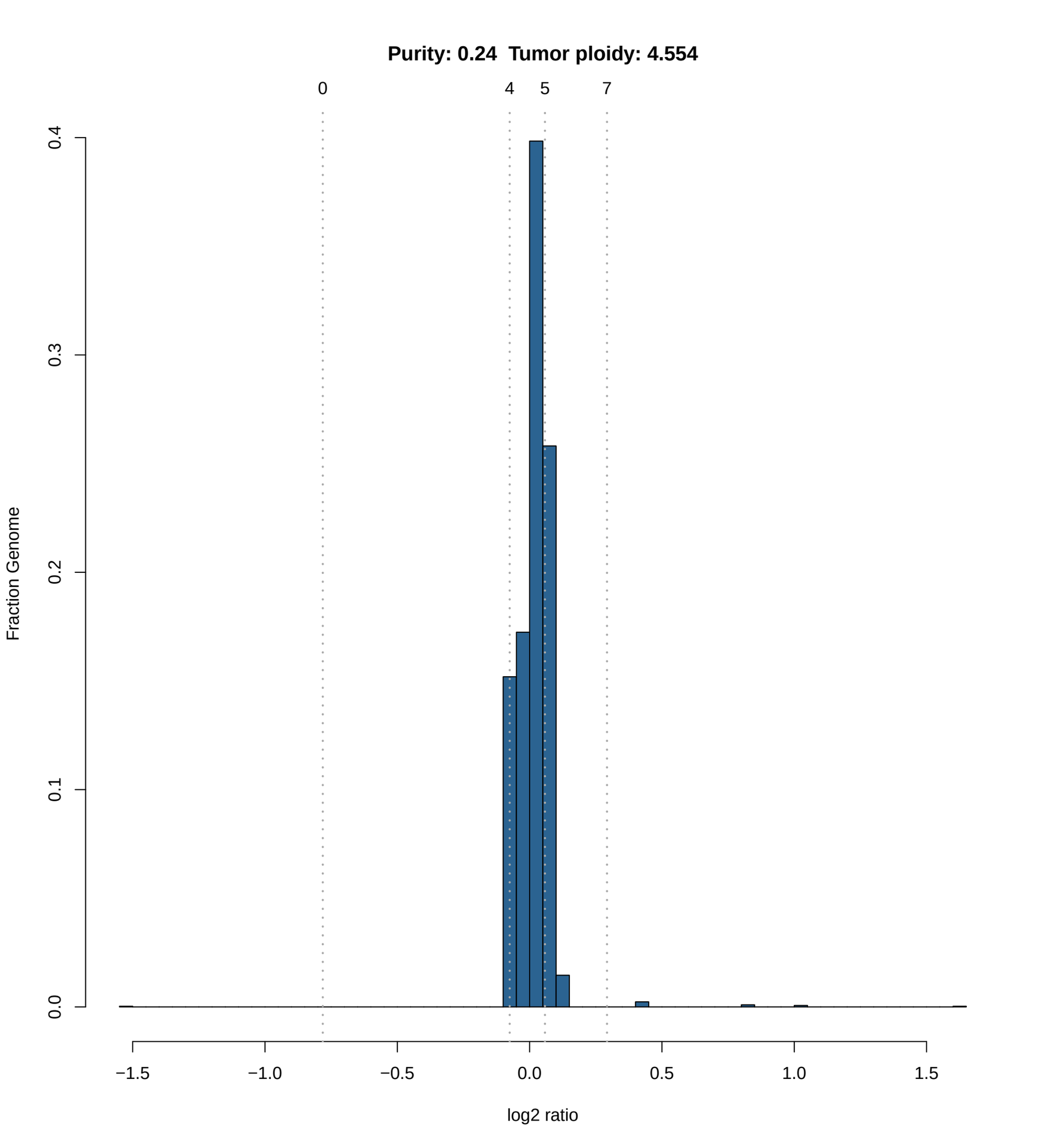

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100
SNV Index

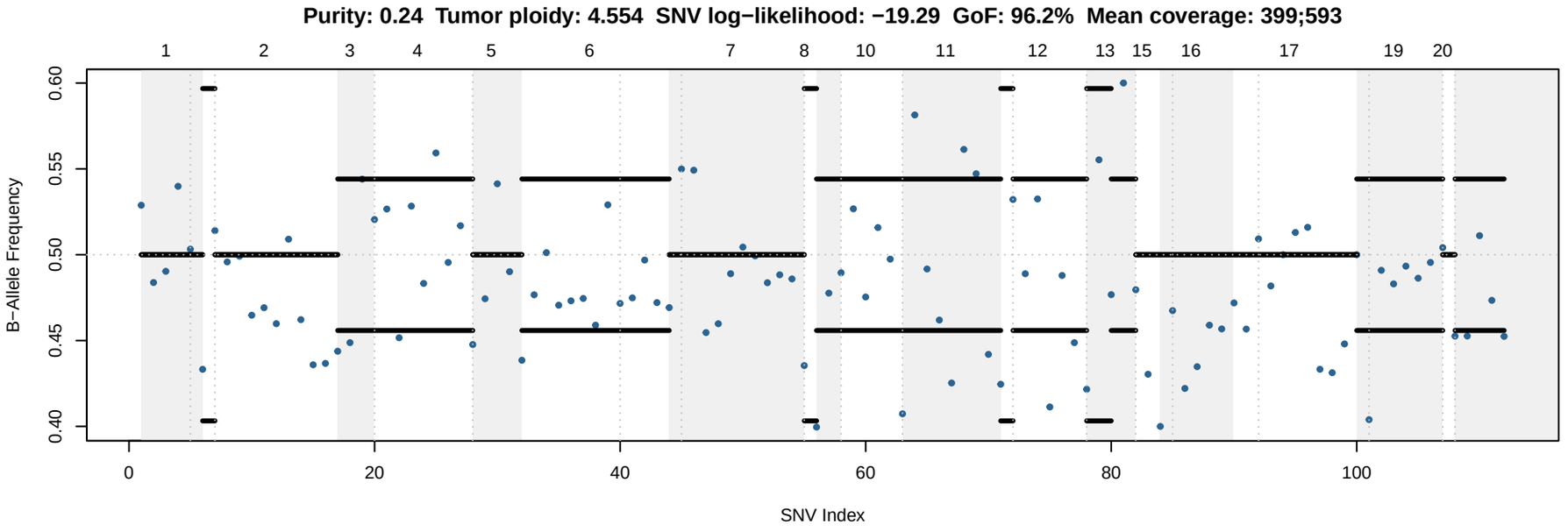

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
4m3
3m2
4m2
3m1
4m1
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

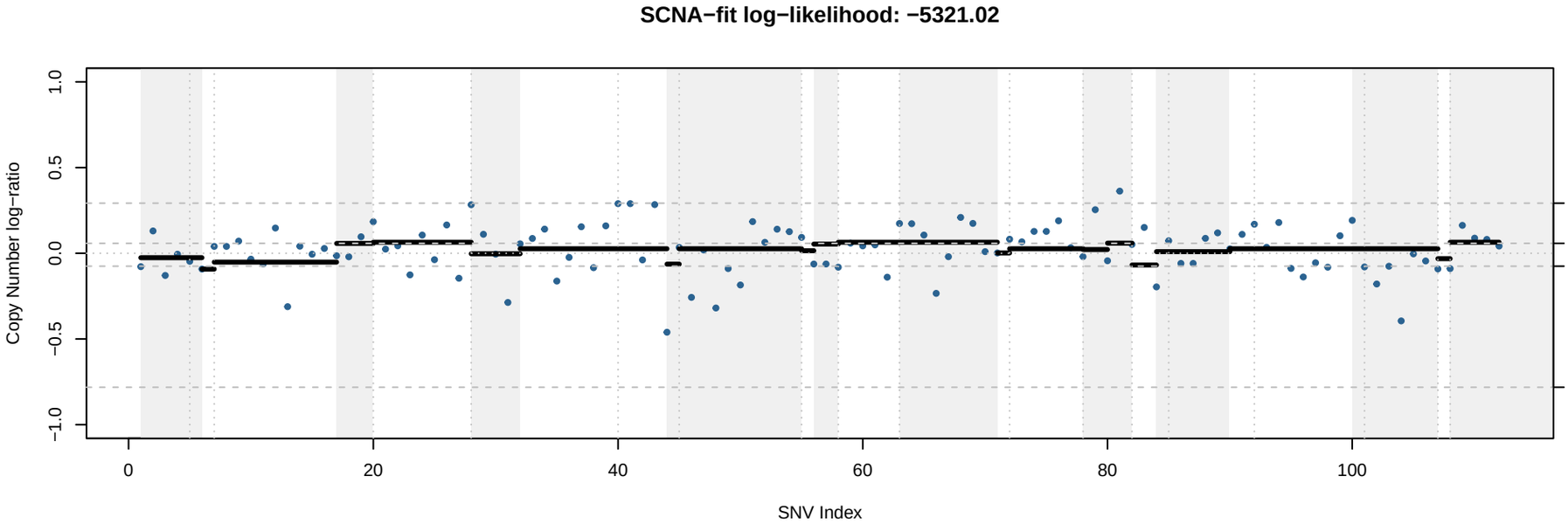

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

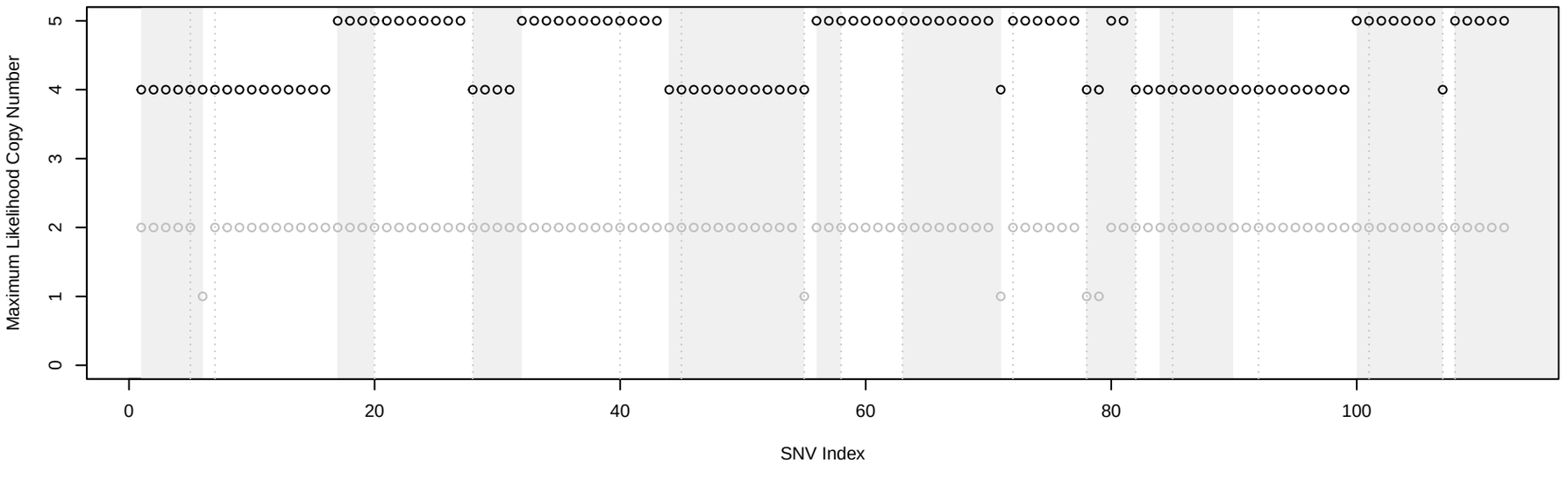

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

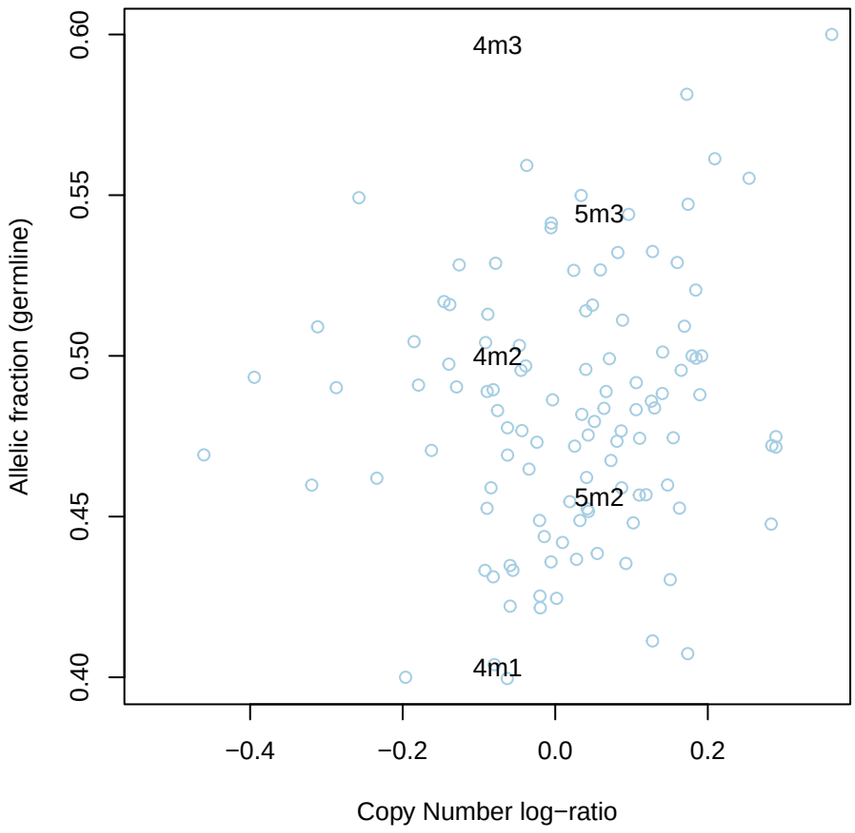

Frequency
0
5
10
15
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

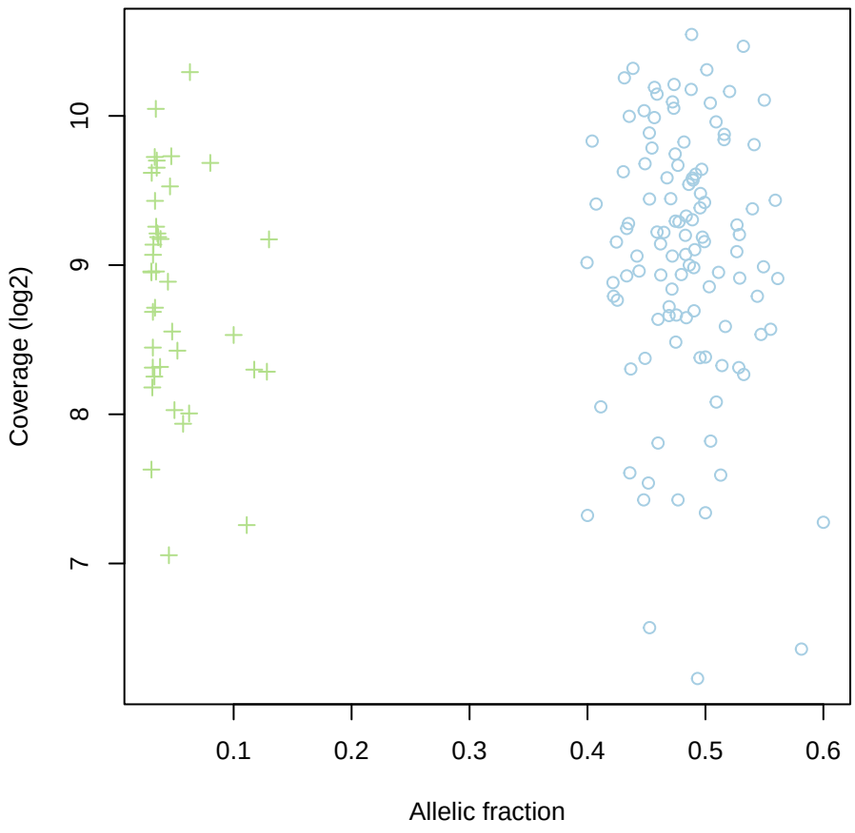

Purity: 0.24 Tumor ploidy: 4.554
0
4
5
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

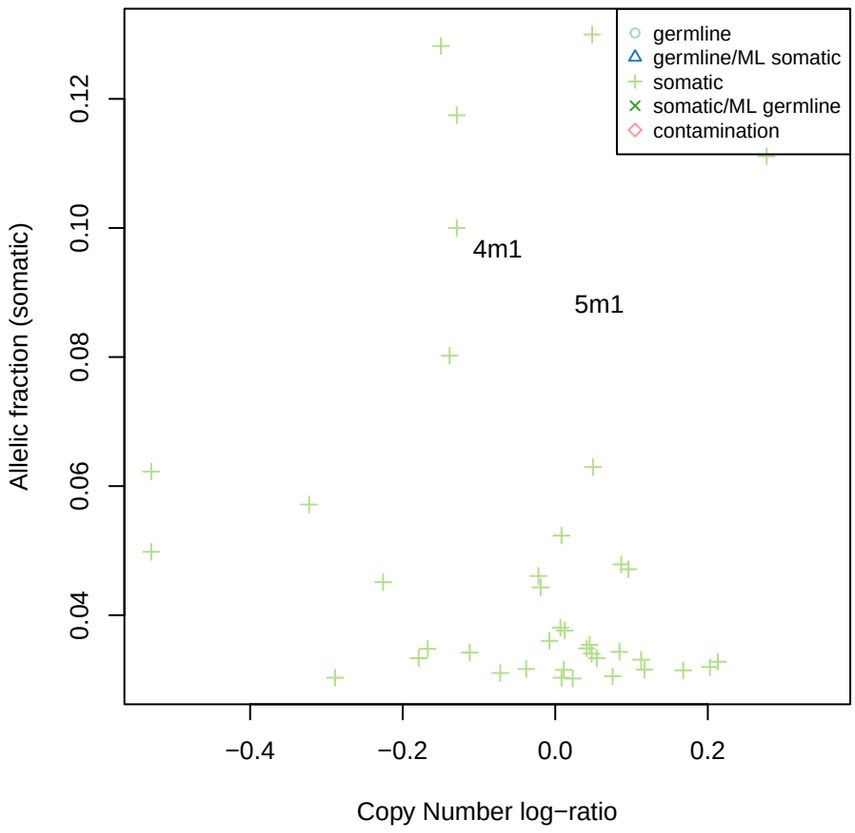

Purity: 0.24 Tumor ploidy: 4.554 SNV log−likelihood: −19.29 GoF: 96.2% Mean coverage: 399;593
1 2 3 4 5 6 7 8 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

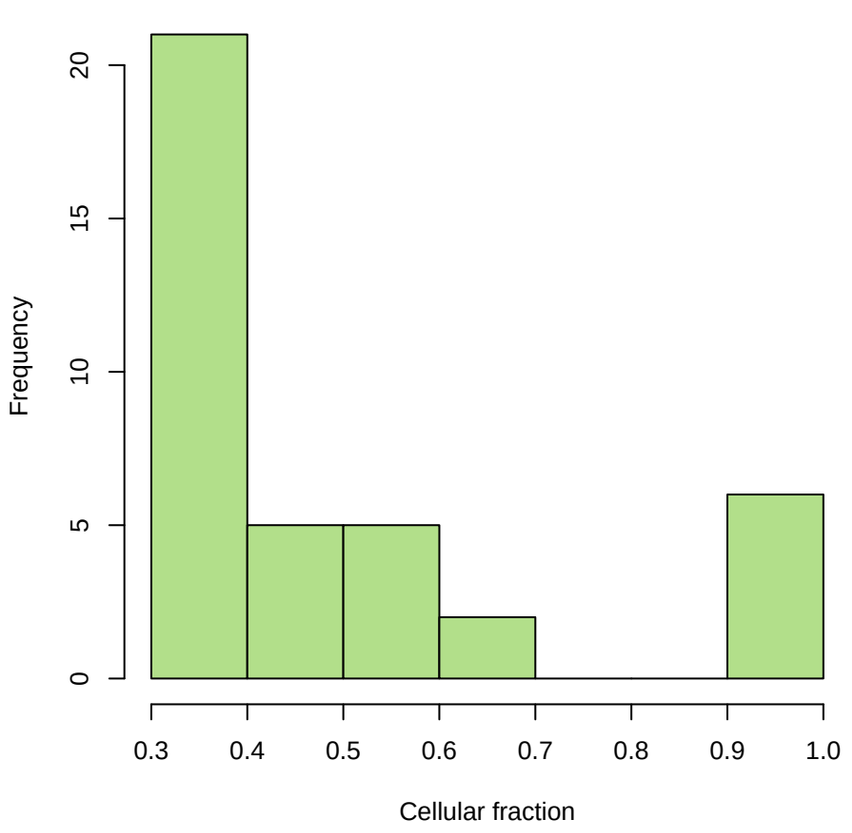

SCNA−fit log−likelihood: −5321.02
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 4 7
0 20 40 60 80 100
SNV Index

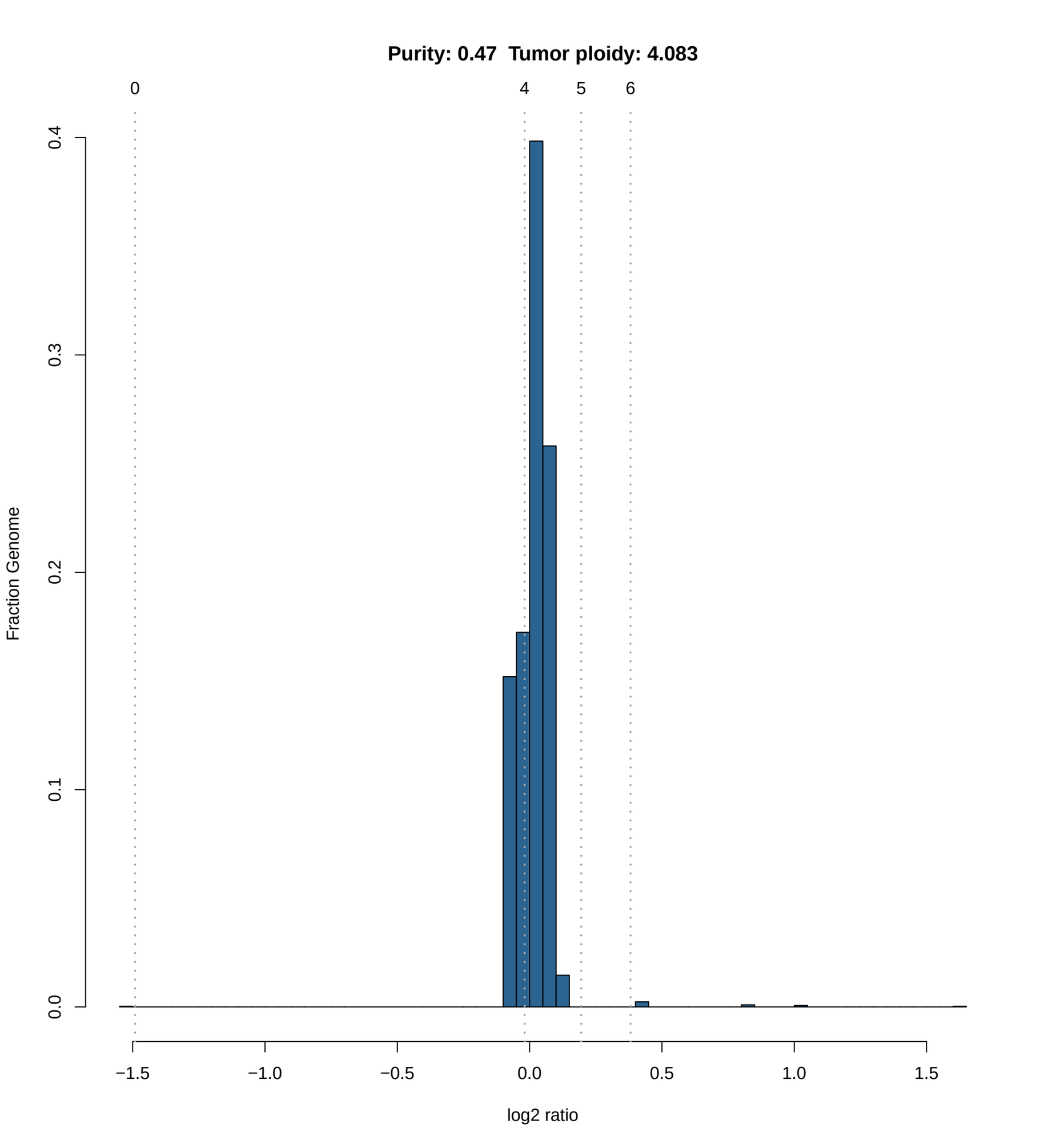

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100
SNV Index

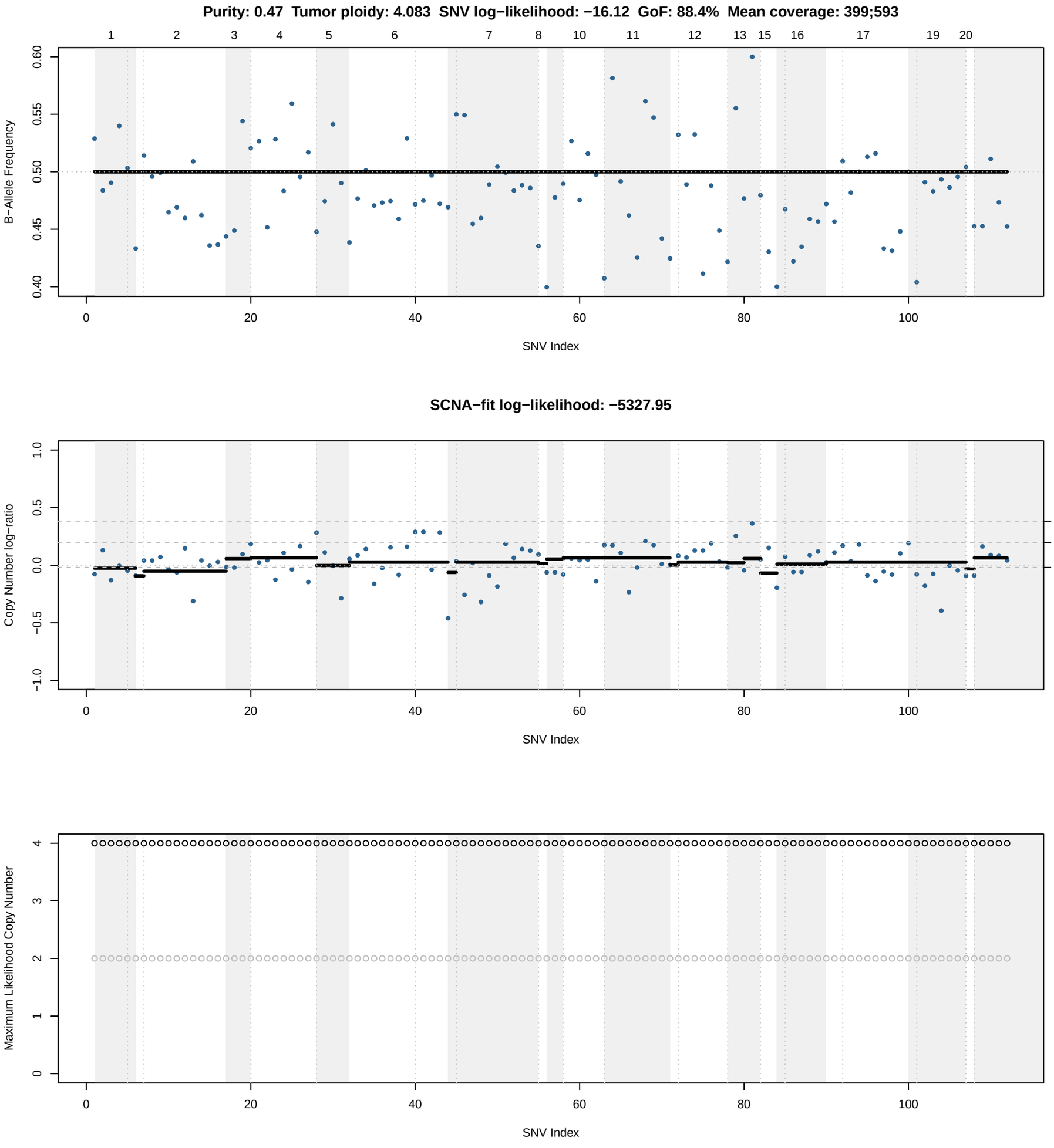

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
4m3
5m3
4m2
5m2
4m1
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

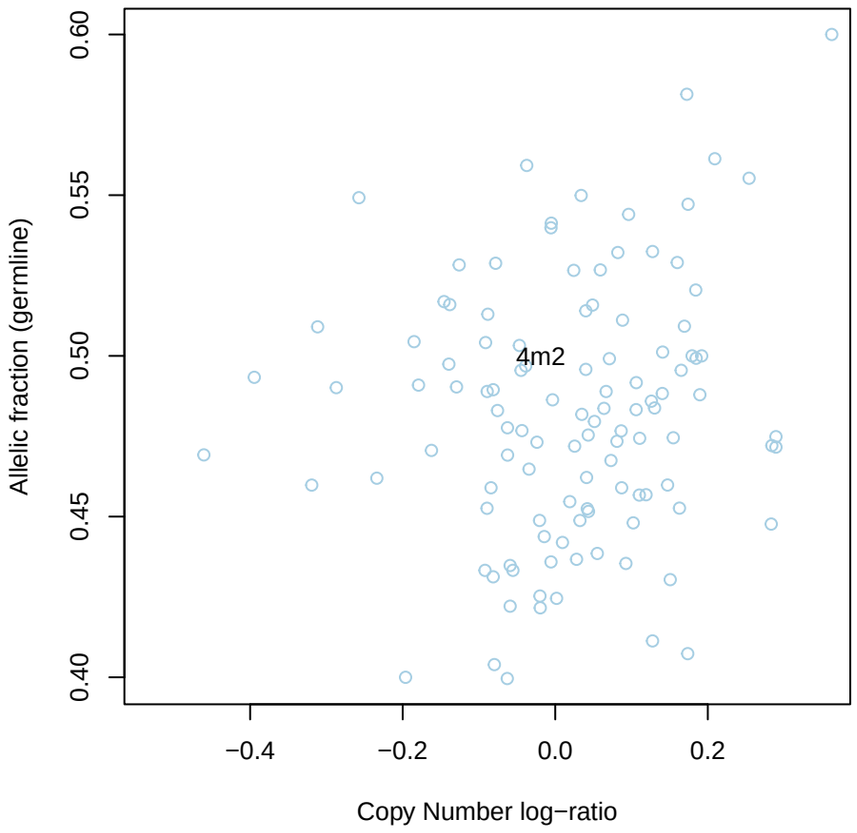

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

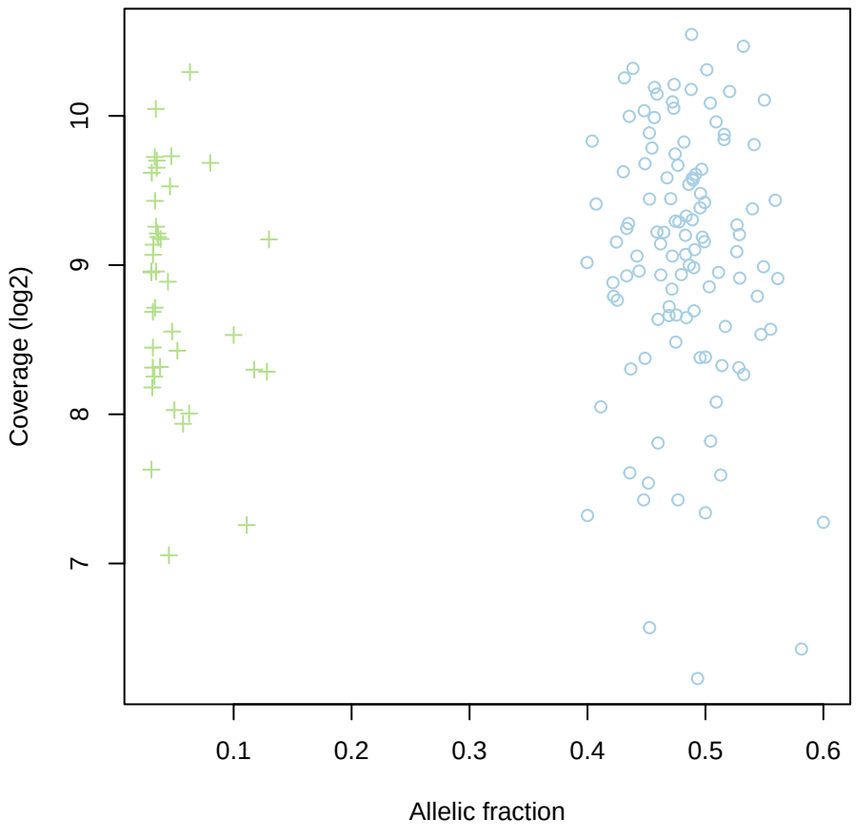

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
4m1
5m1
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

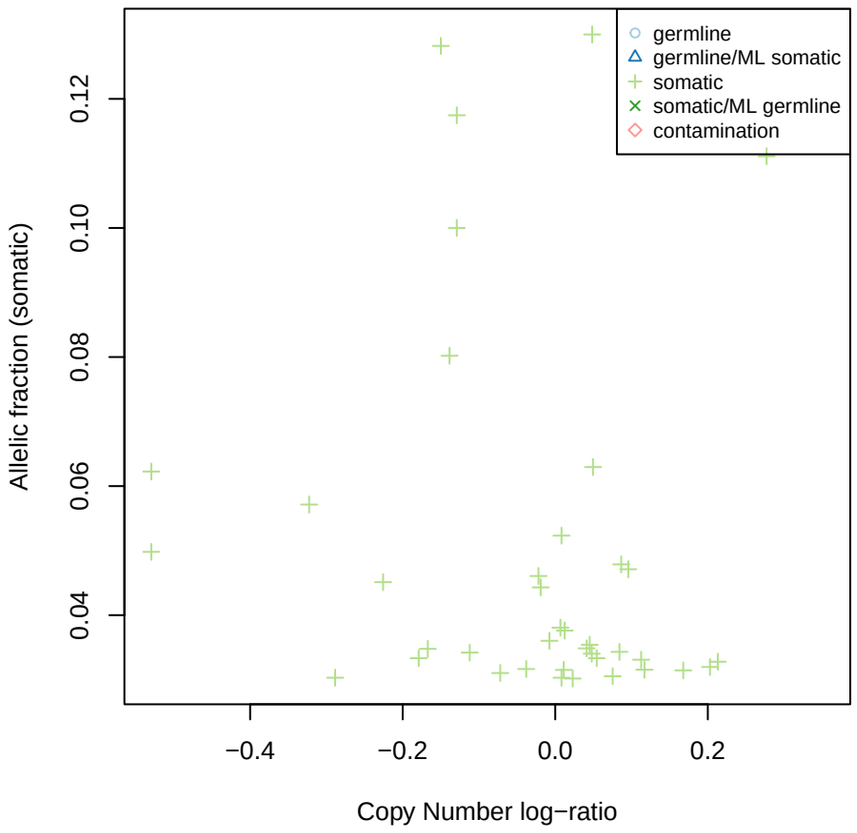

Frequency
0
5
10
15
20
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

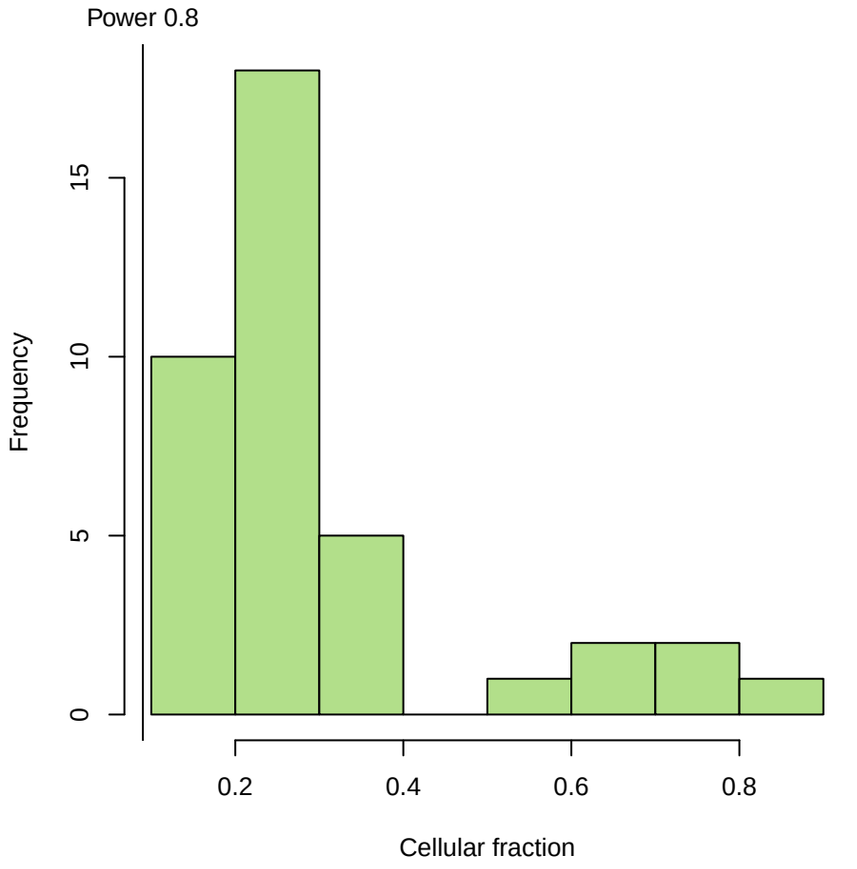

Purity: 0.47 Tumor ploidy: 4.083
0
4
5
6
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

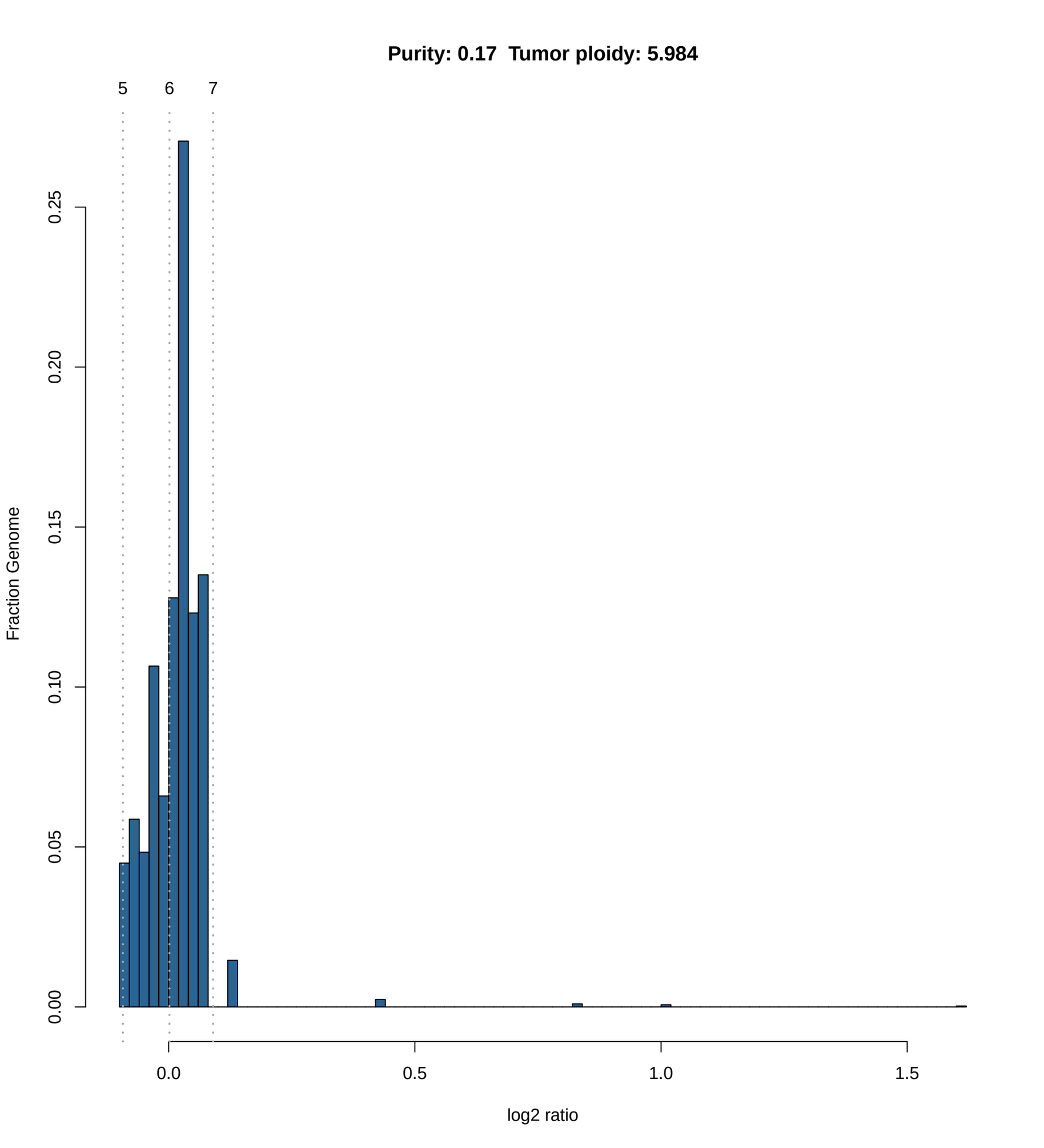

Purity: 0.47 Tumor ploidy: 4.083 SNV log−likelihood: −16.12 GoF: 88.4% Mean coverage: 399;593
1 2 3 4 5 6 7 8 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index
SCNA−fit log−likelihood: −5327.95
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5 6
0 20 40 60 80 100
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100
SNV Index

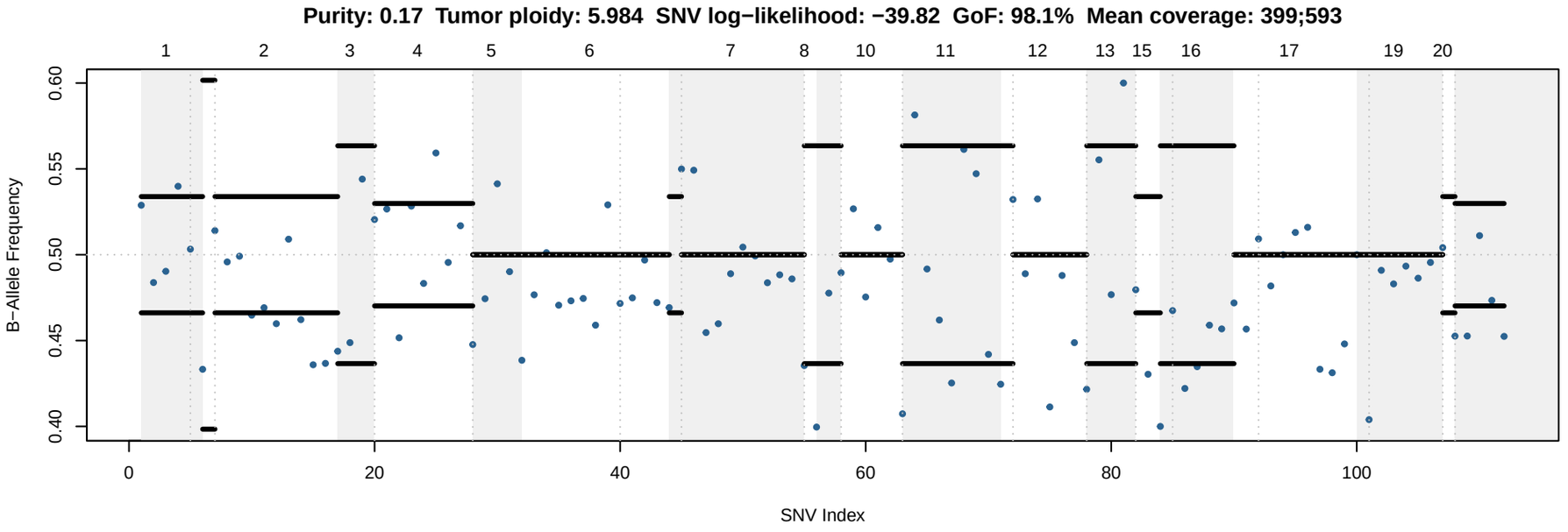

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
4m2
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

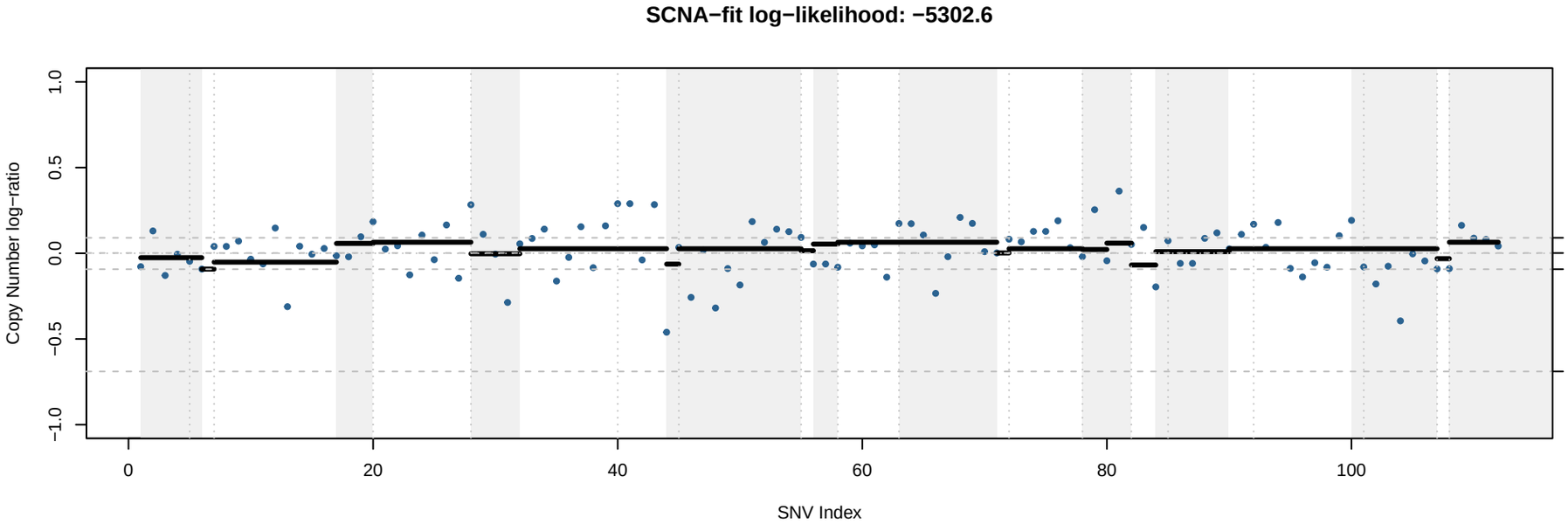

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

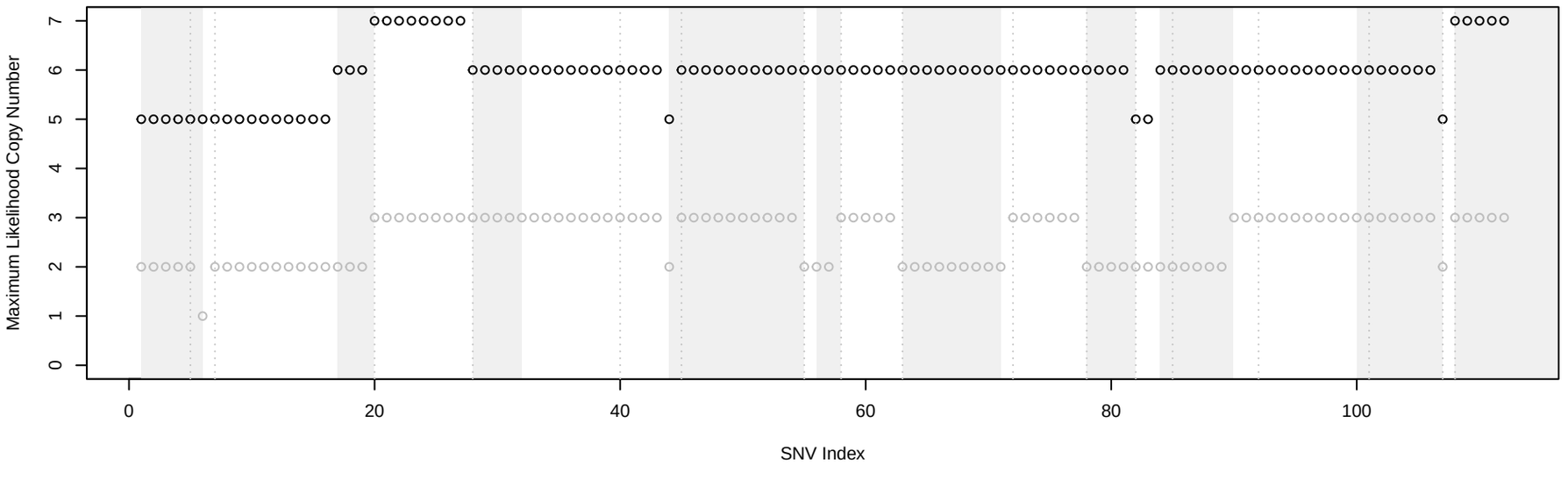

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

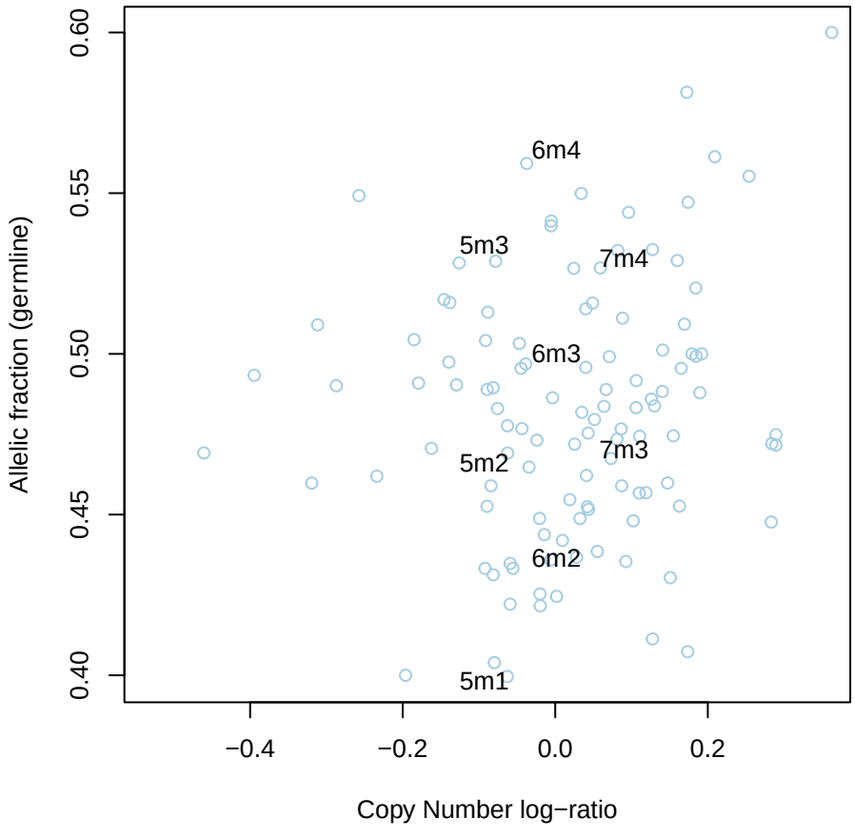

Power 0.8
Frequency
0
5
10
15
0.2
0.4
0.6
0.8
Cellular fraction

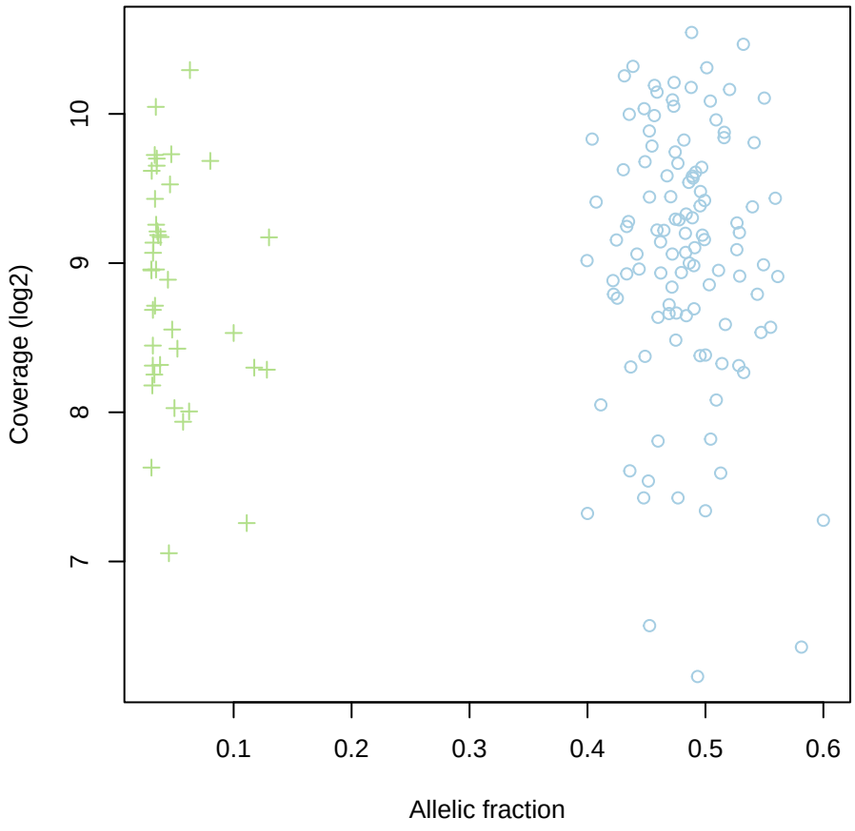

Purity: 0.17 Tumor ploidy: 5.984
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
1.5
log2 ratio

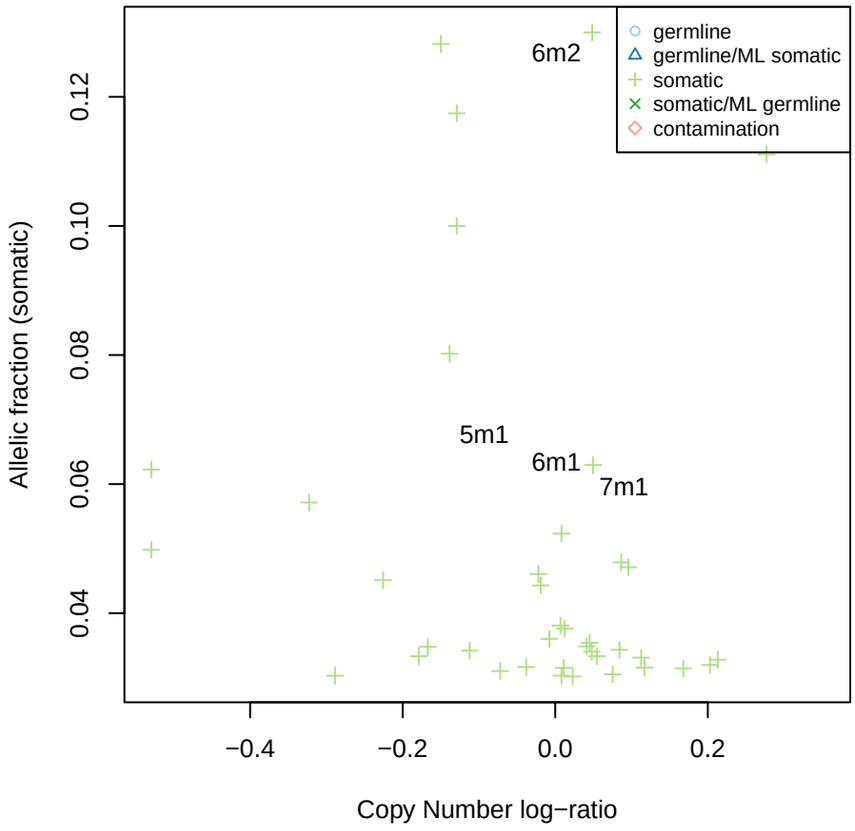

Purity: 0.17 Tumor ploidy: 5.984 SNV log−likelihood: −39.82 GoF: 98.1% Mean coverage: 399;593
1 2 3 4 5 6 7 8 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

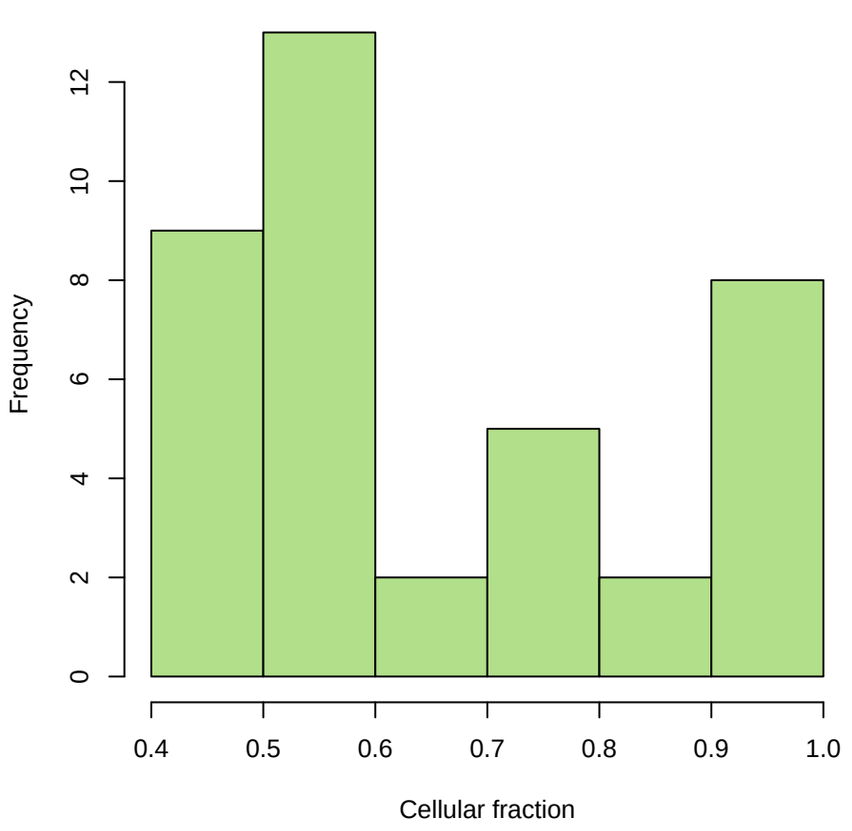

SCNA−fit log−likelihood: −5302.6
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 5 7
0 20 40 60 80 100
SNV Index

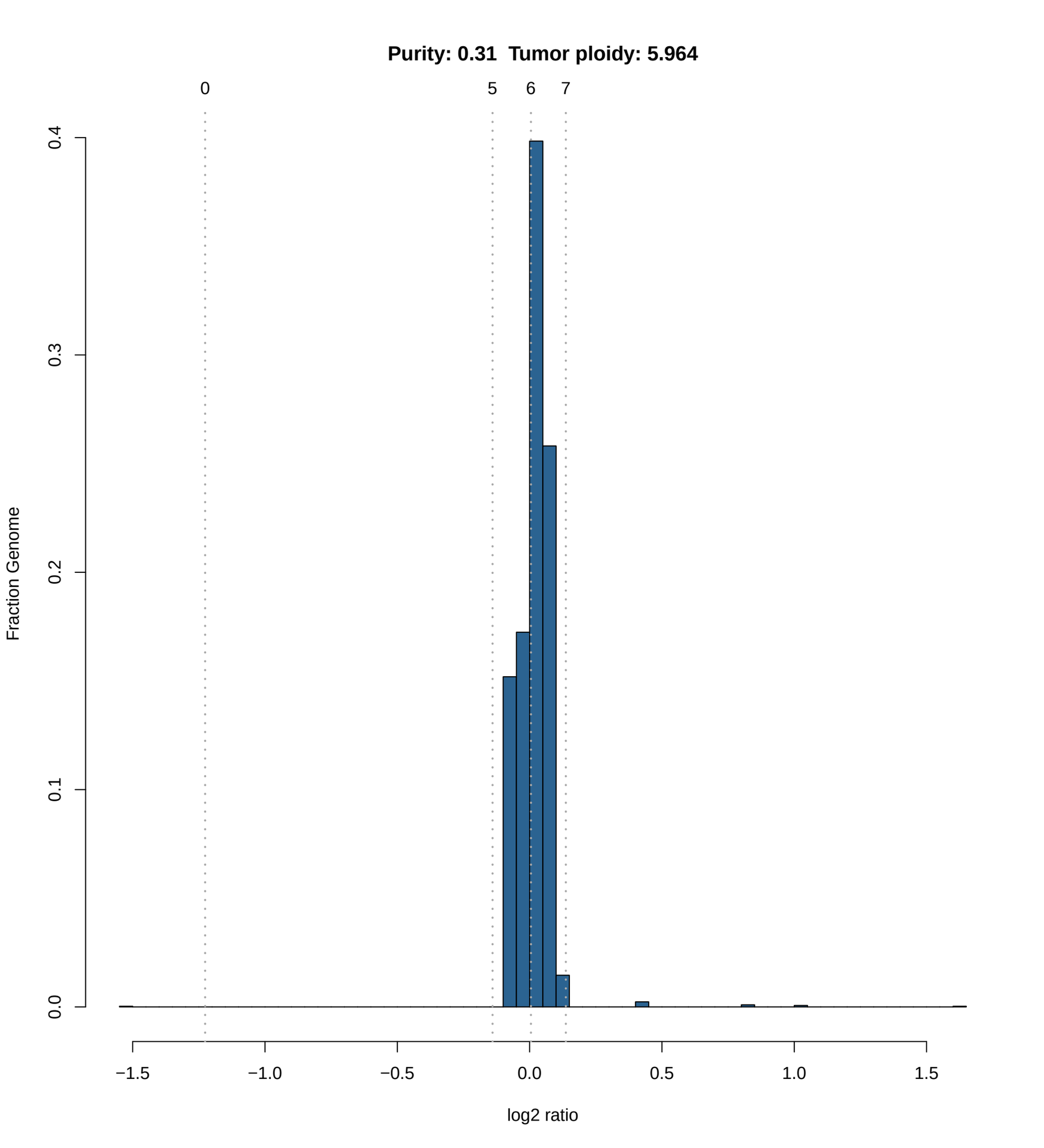

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

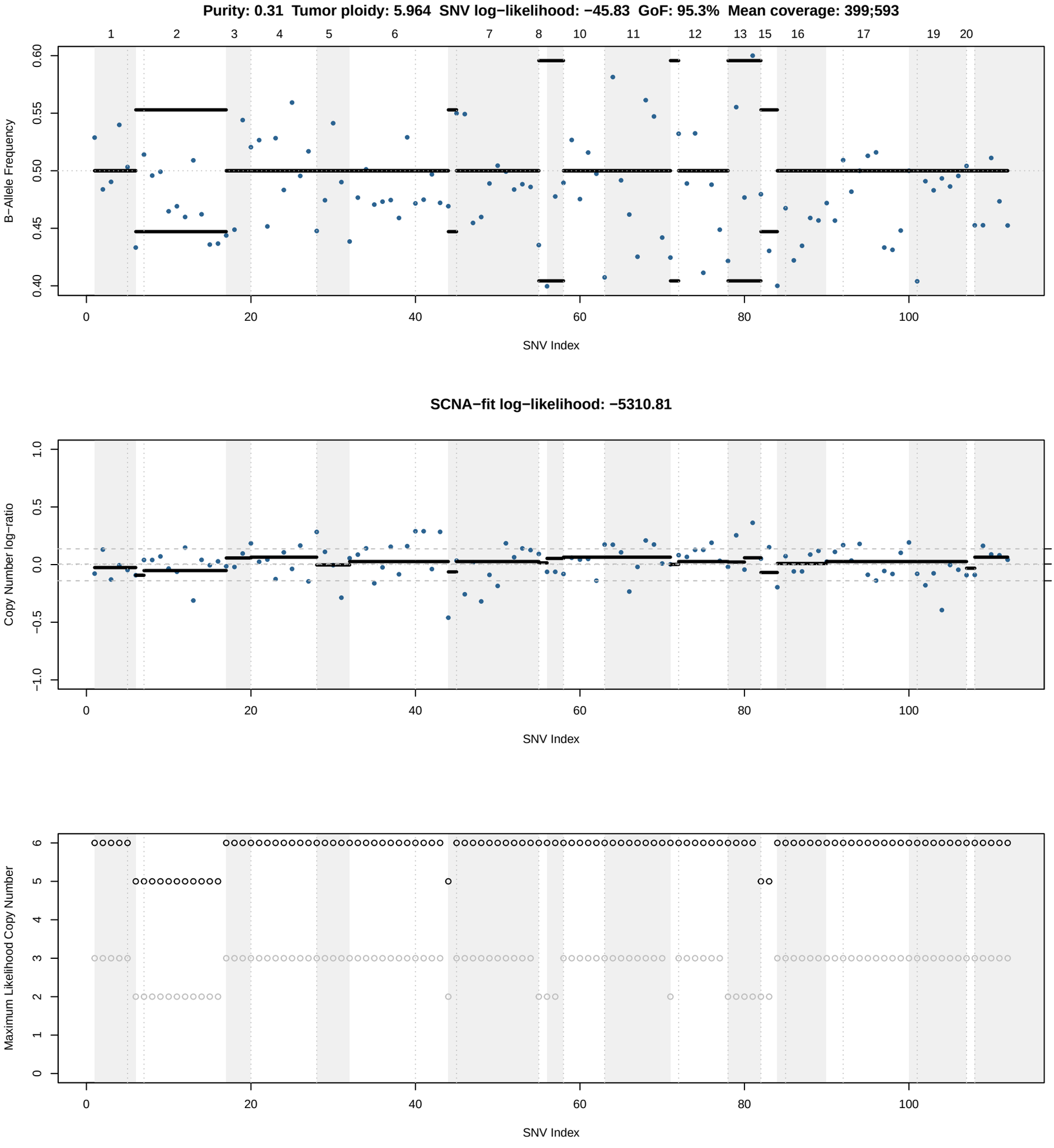

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
6m4
5m3
7m4
6m3
5m2
7m3
6m2
5m1
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

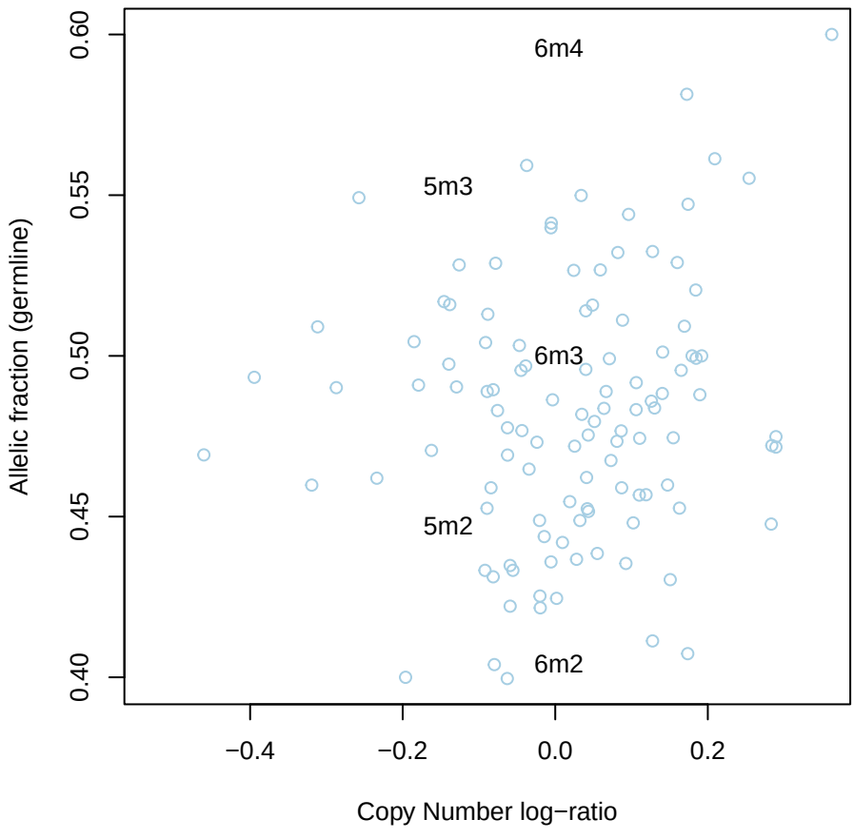

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

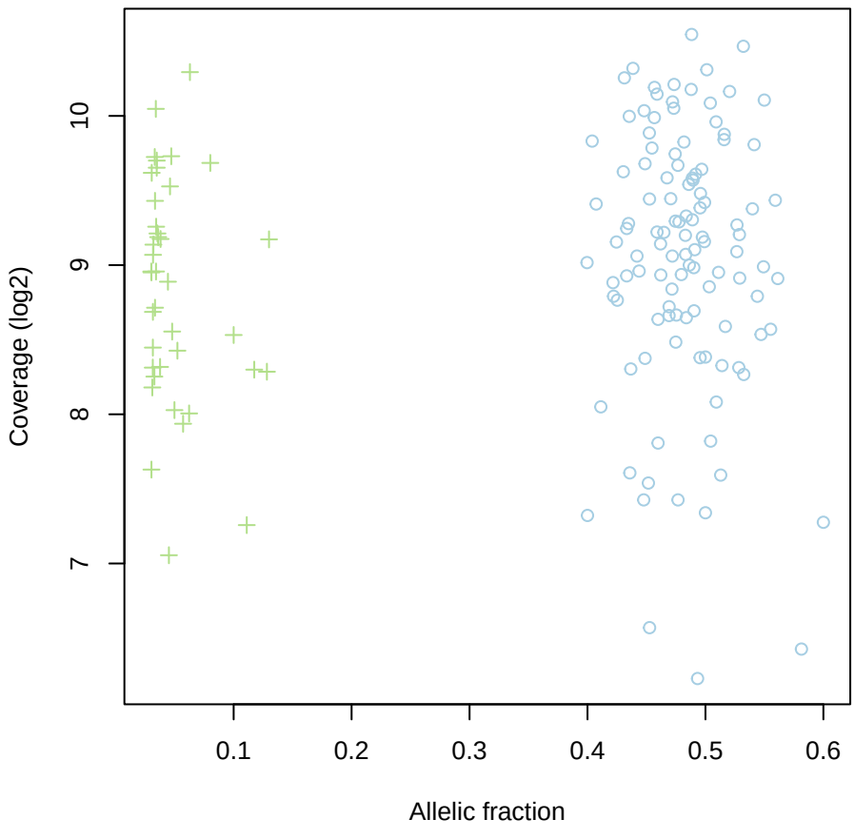

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
6m2
5m1
6m1
7m1
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

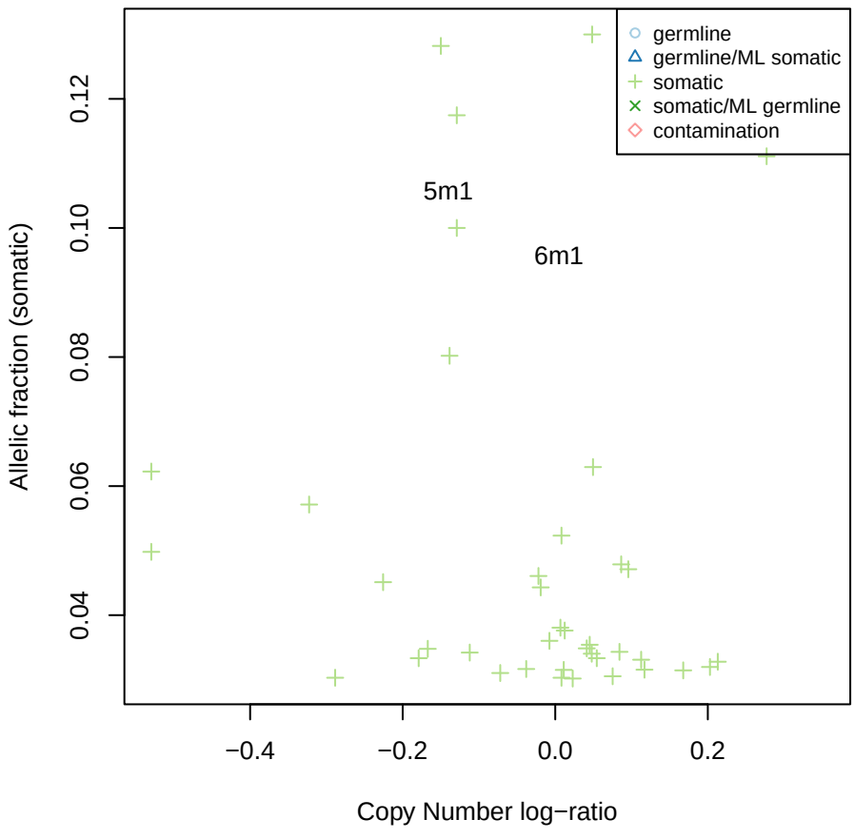

Frequency
0
2
4
6
8
10
12
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

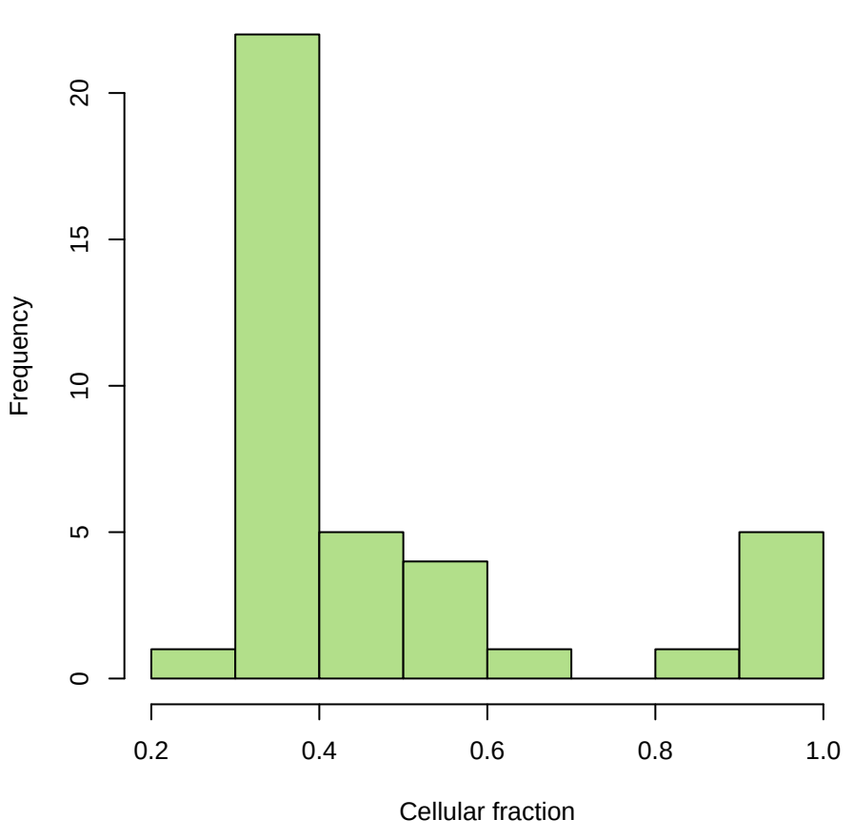

Purity: 0.31 Tumor ploidy: 5.964
0
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

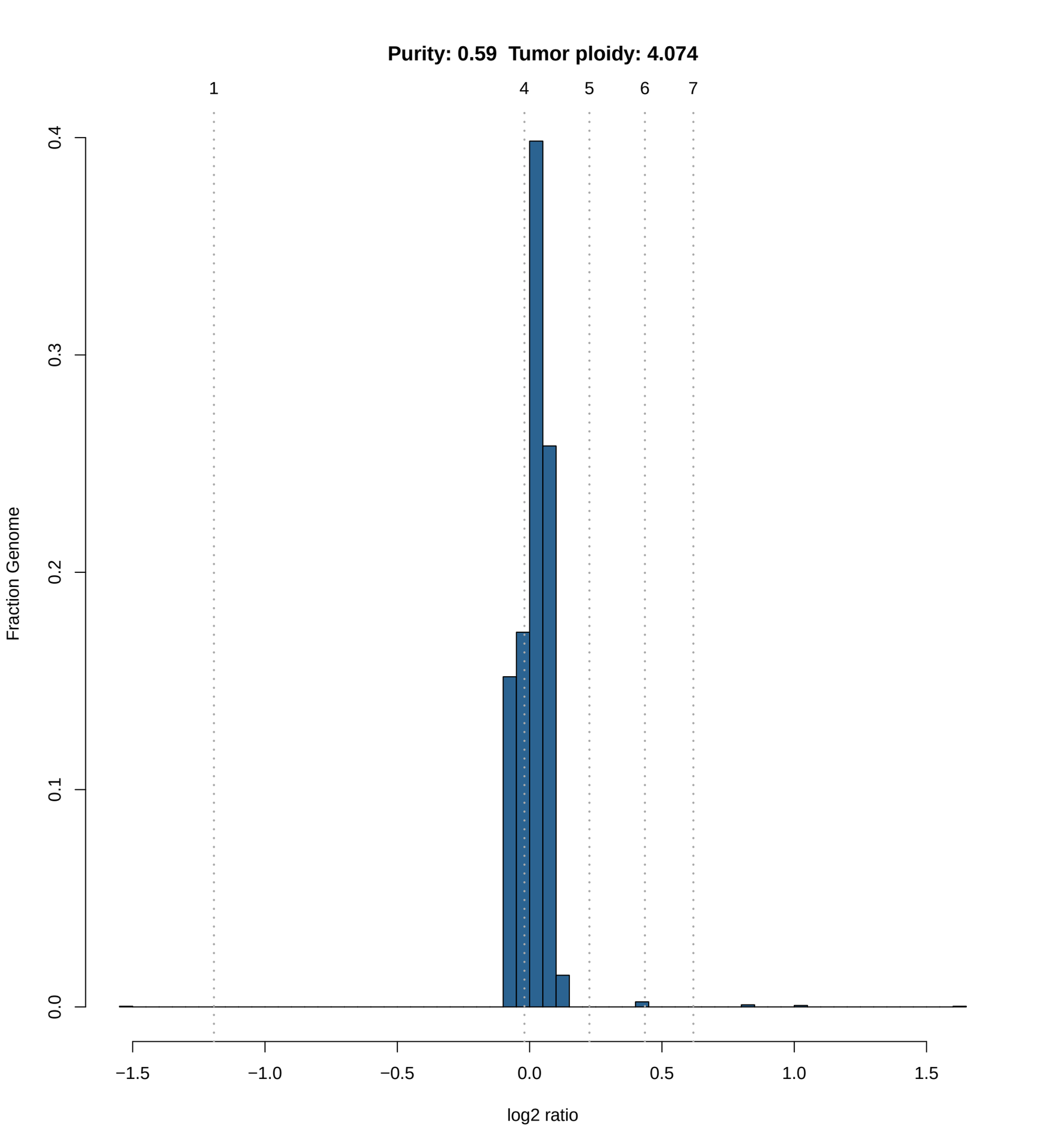

Purity: 0.31 Tumor ploidy: 5.964 SNV log−likelihood: −45.83 GoF: 95.3% Mean coverage: 399;593
1 2 3 4 5 6 7 8 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index
SCNA−fit log−likelihood: −5310.81
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
5 6
0 20 40 60 80 100
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100
SNV Index

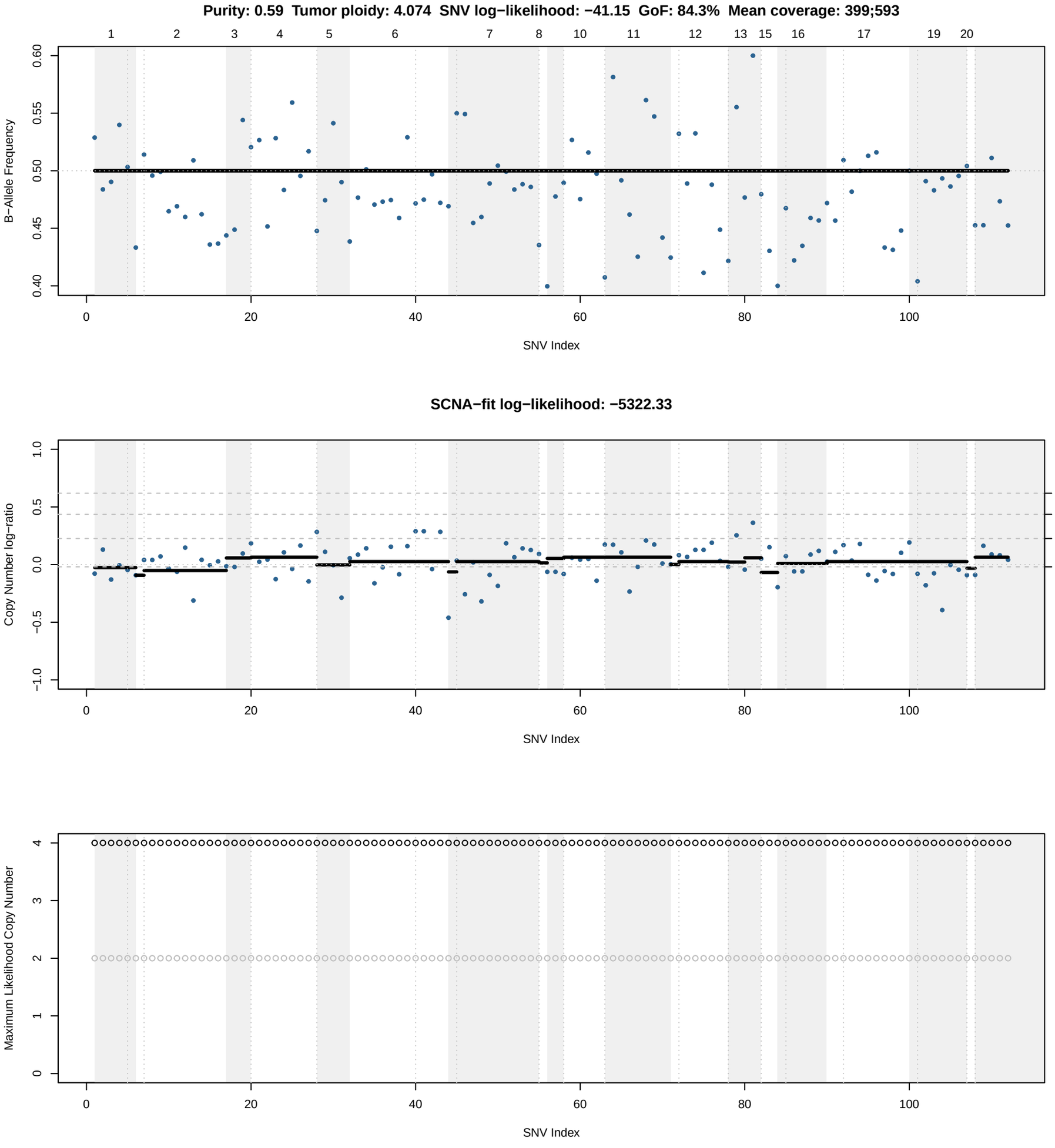

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
6m4
5m3
6m3
5m2
6m2
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

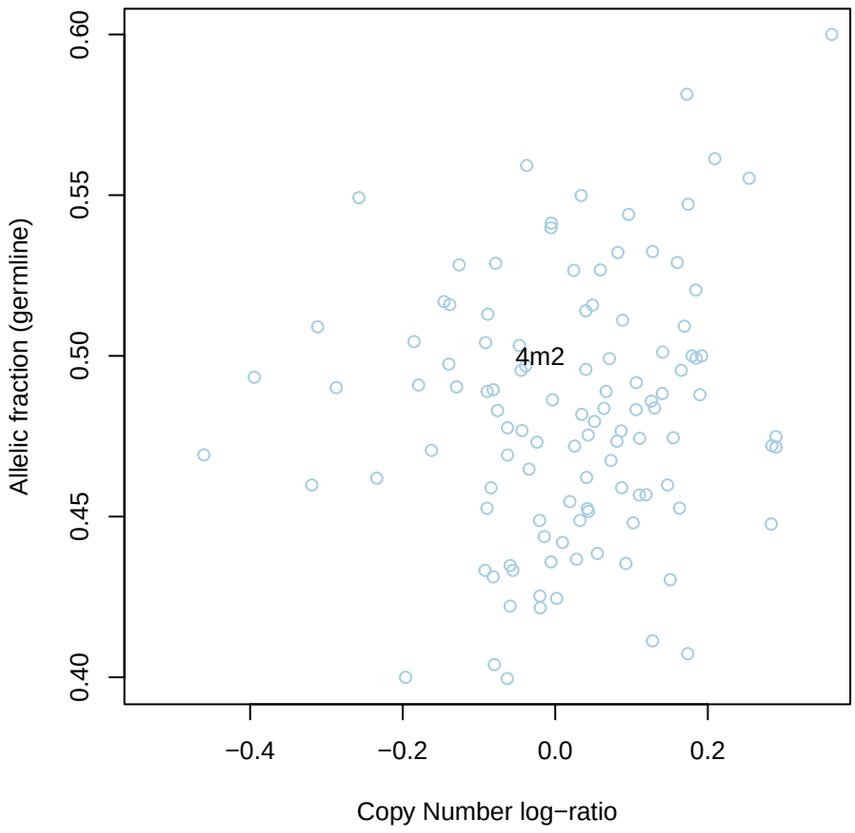

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

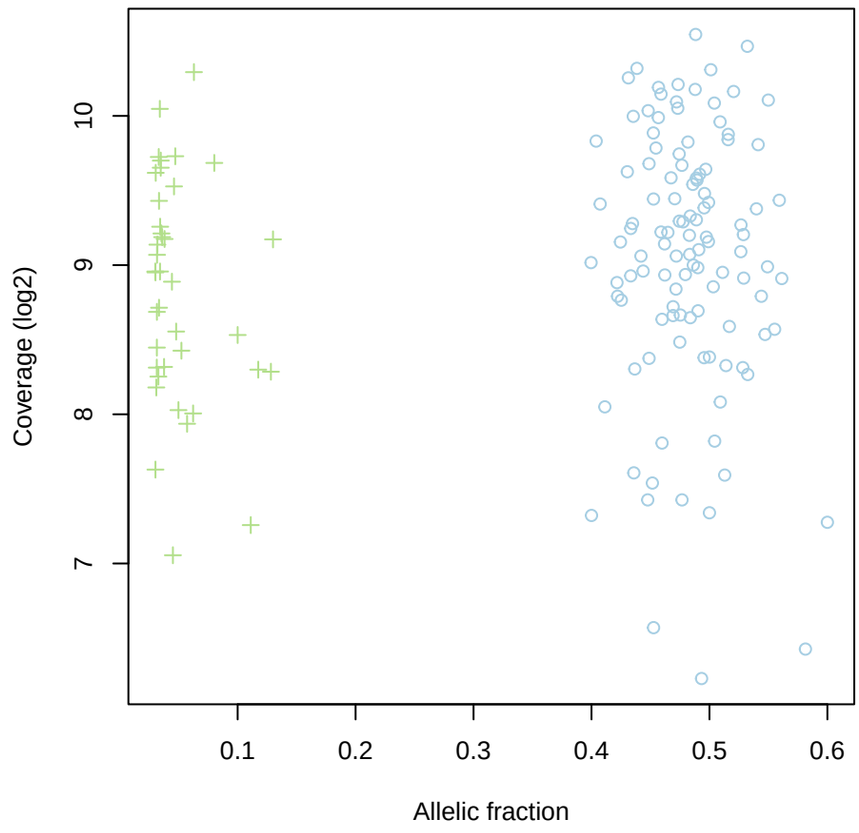

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
5m1
6m1
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

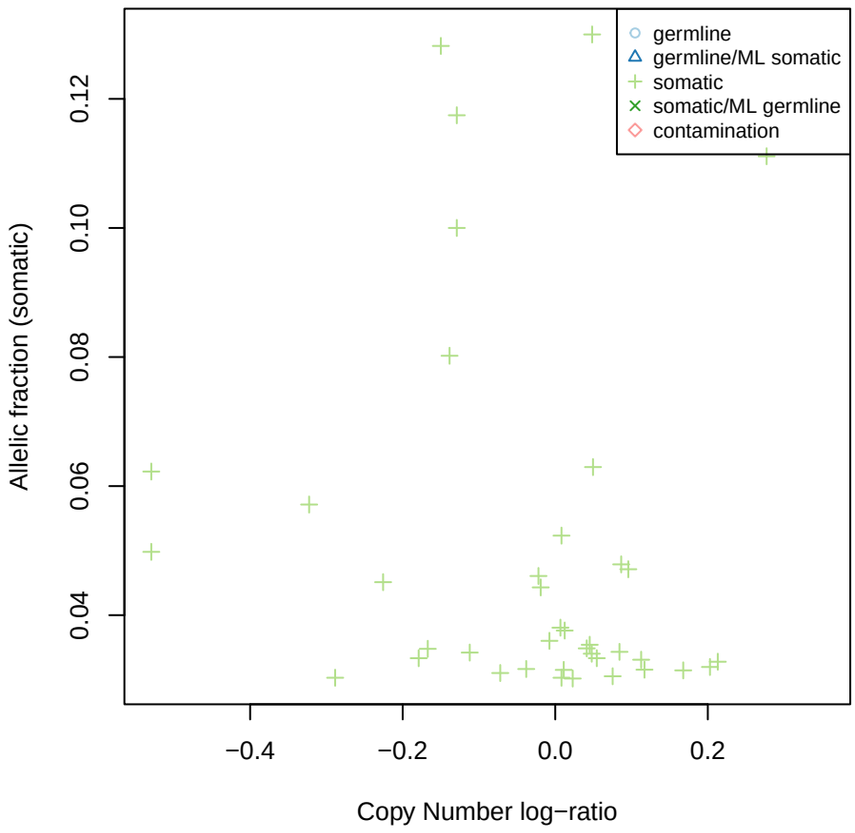

Frequency
0
5
10
15
20
0.2
0.4
0.6
0.8
1.0
Cellular fraction

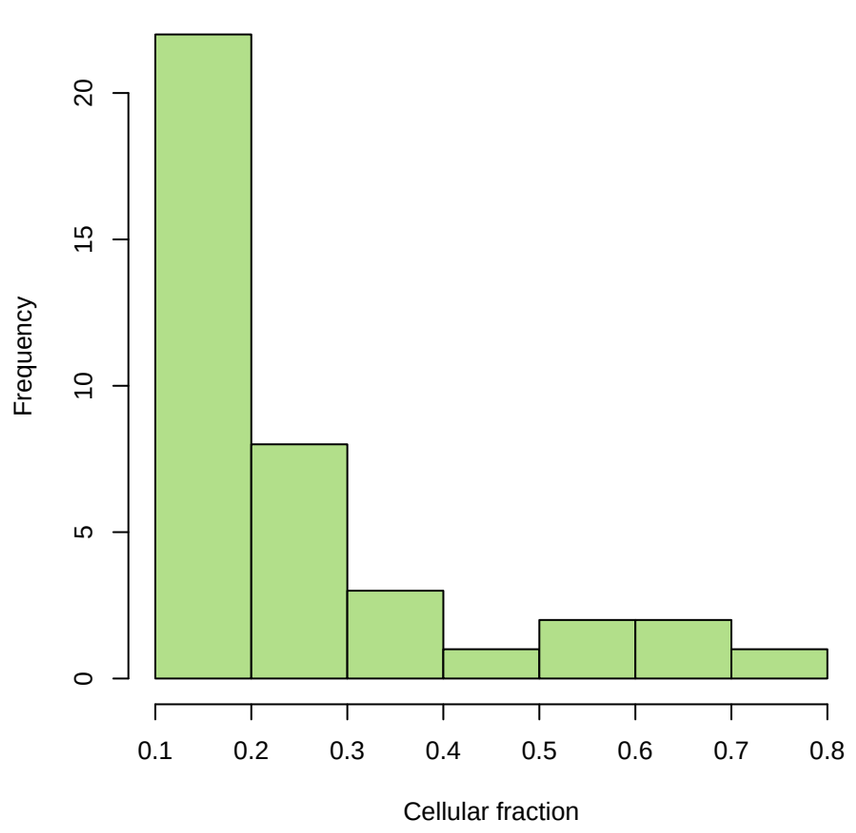

Purity: 0.59 Tumor ploidy: 4.074
1
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

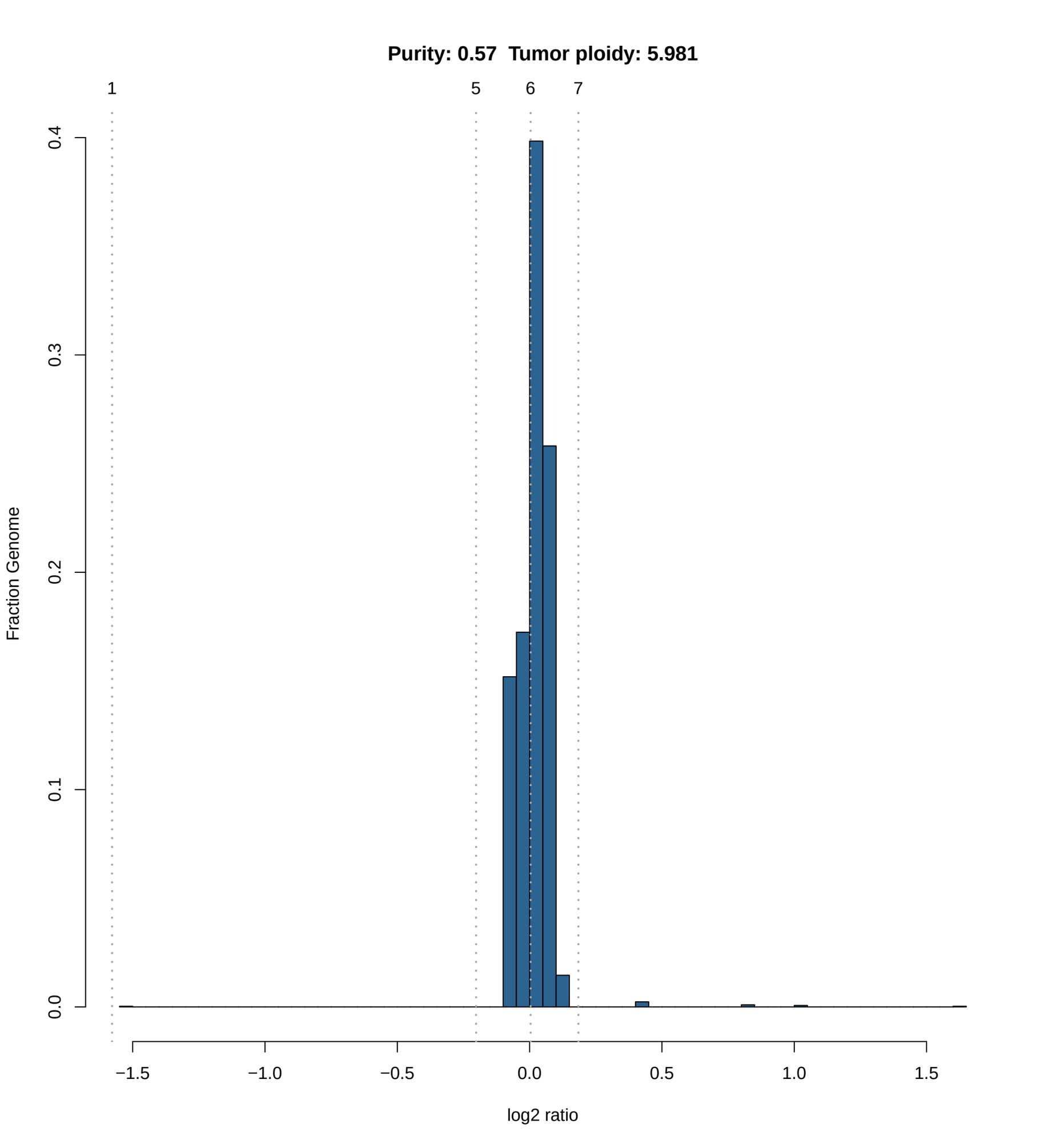

Purity: 0.59 Tumor ploidy: 4.074 SNV log−likelihood: −41.15 GoF: 84.3% Mean coverage: 399;593
1 2 3 4 5 6 7 8 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index
SCNA−fit log−likelihood: −5322.33
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5 6 7
0 20 40 60 80 100
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100
SNV Index

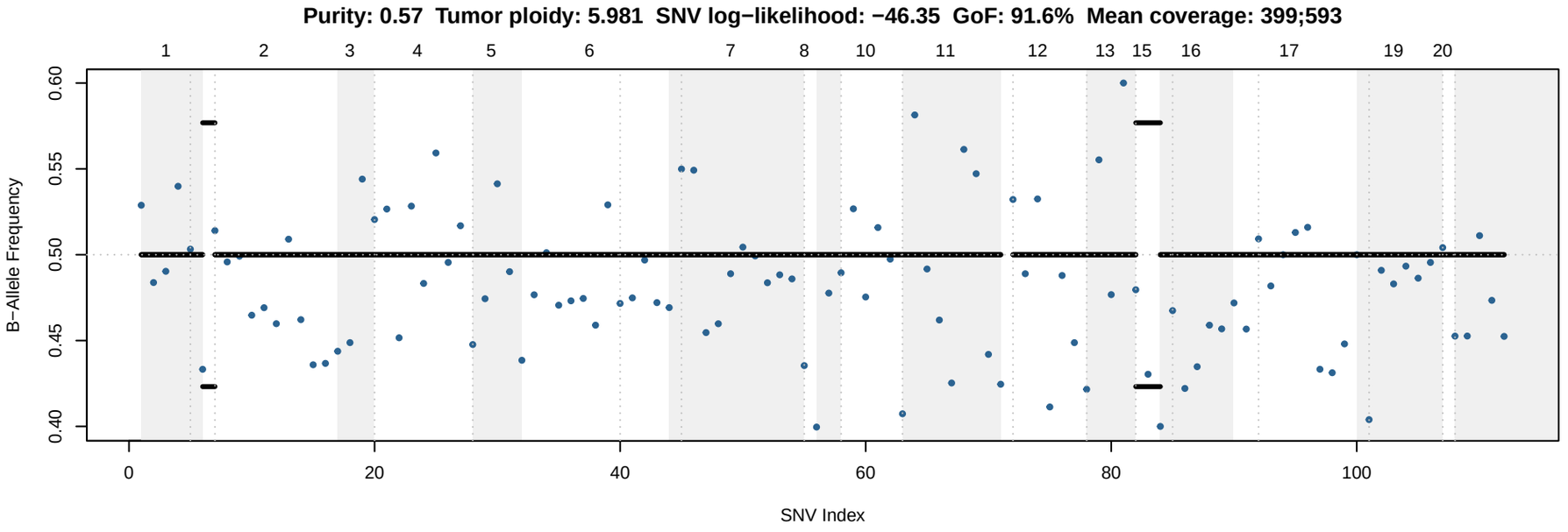

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
4m2
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

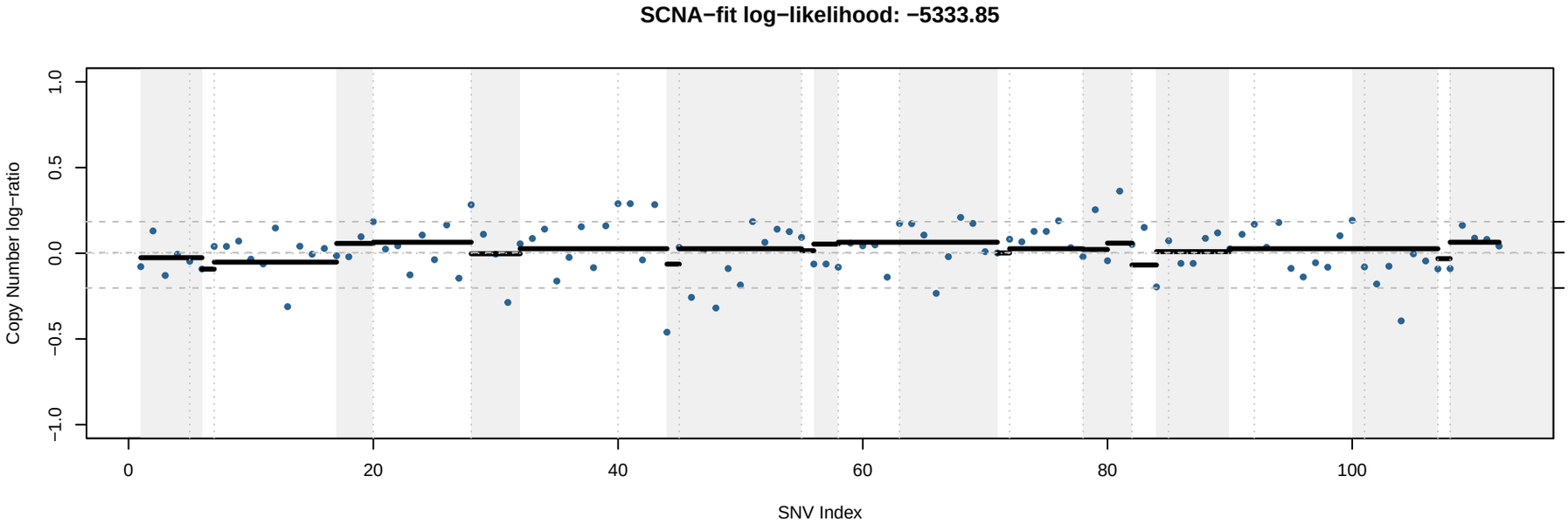

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

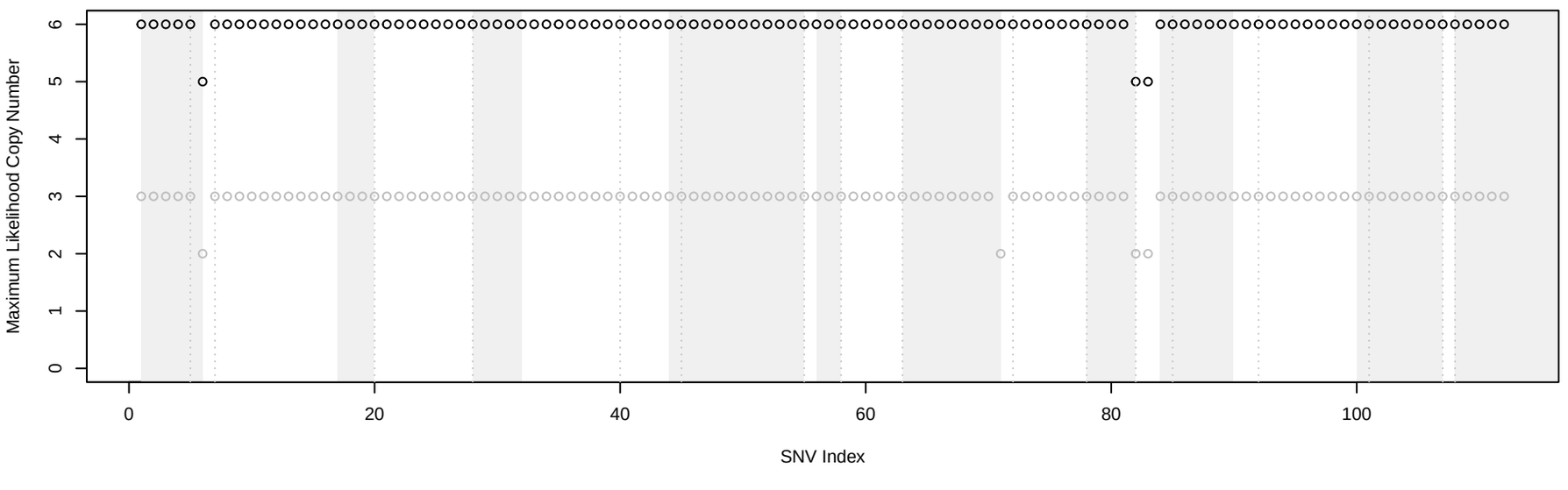

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

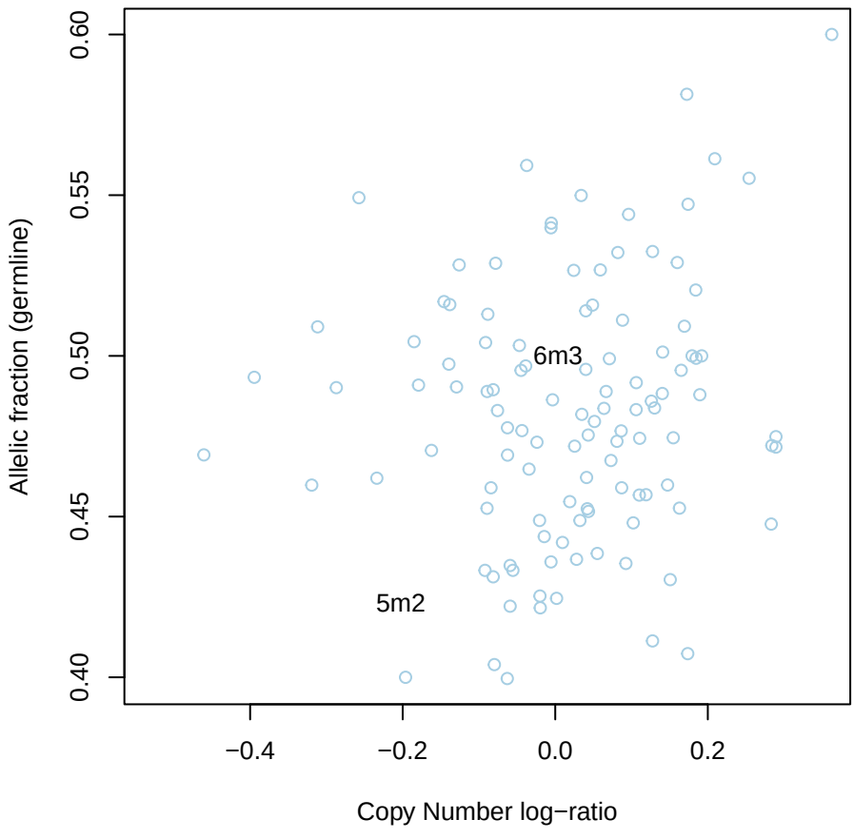

Frequency
0
5
10
15
20
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
Cellular fraction

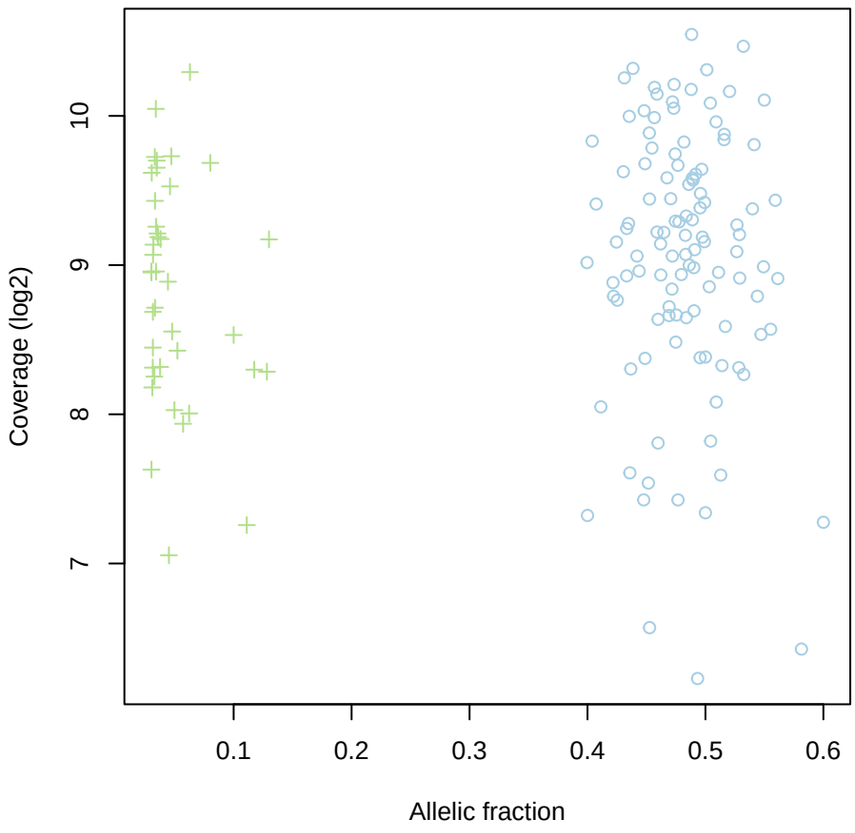

Purity: 0.57 Tumor ploidy: 5.981
1
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

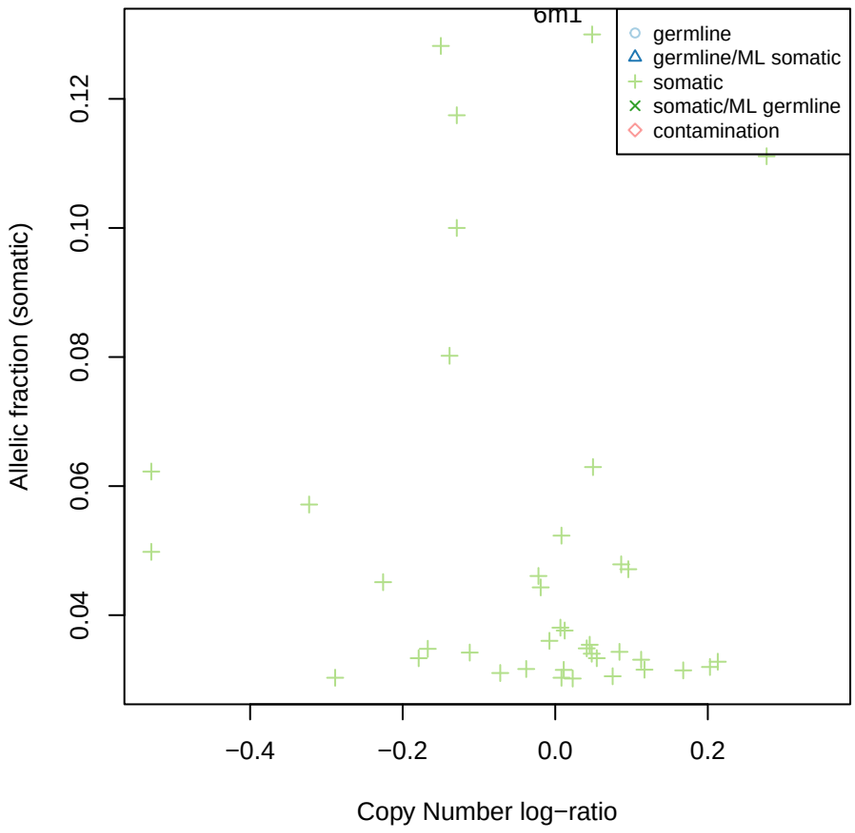

Purity: 0.57 Tumor ploidy: 5.981 SNV log−likelihood: −46.35 GoF: 91.6% Mean coverage: 399;593
1 2 3 4 5 6 7 8 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

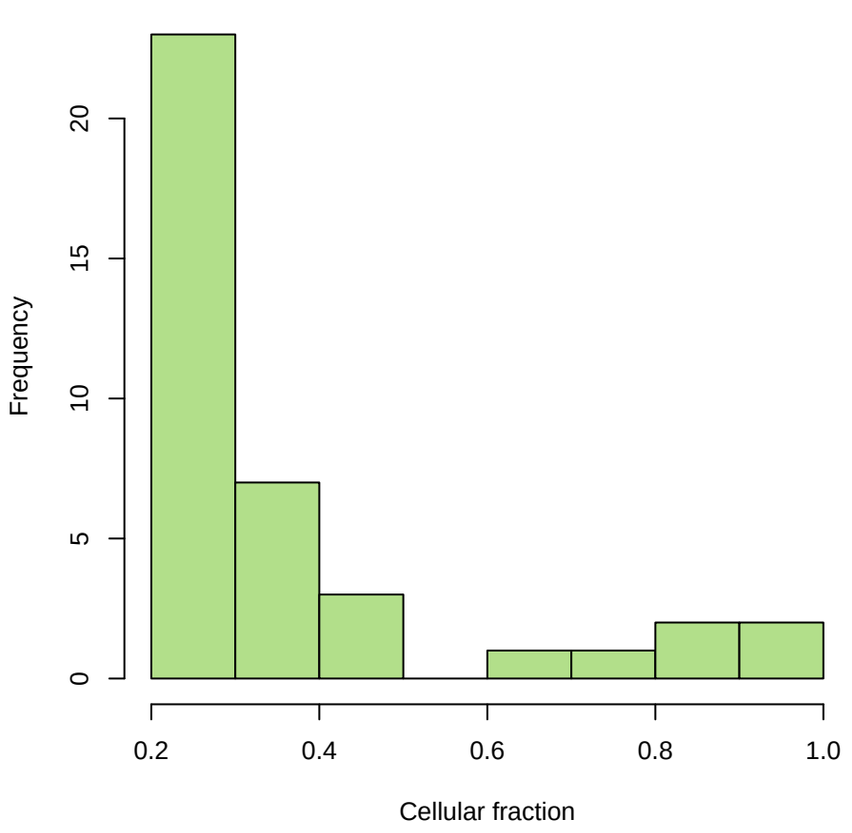

SCNA−fit log−likelihood: −5333.85
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
5 6 7
0 20 40 60 80 100
SNV Index

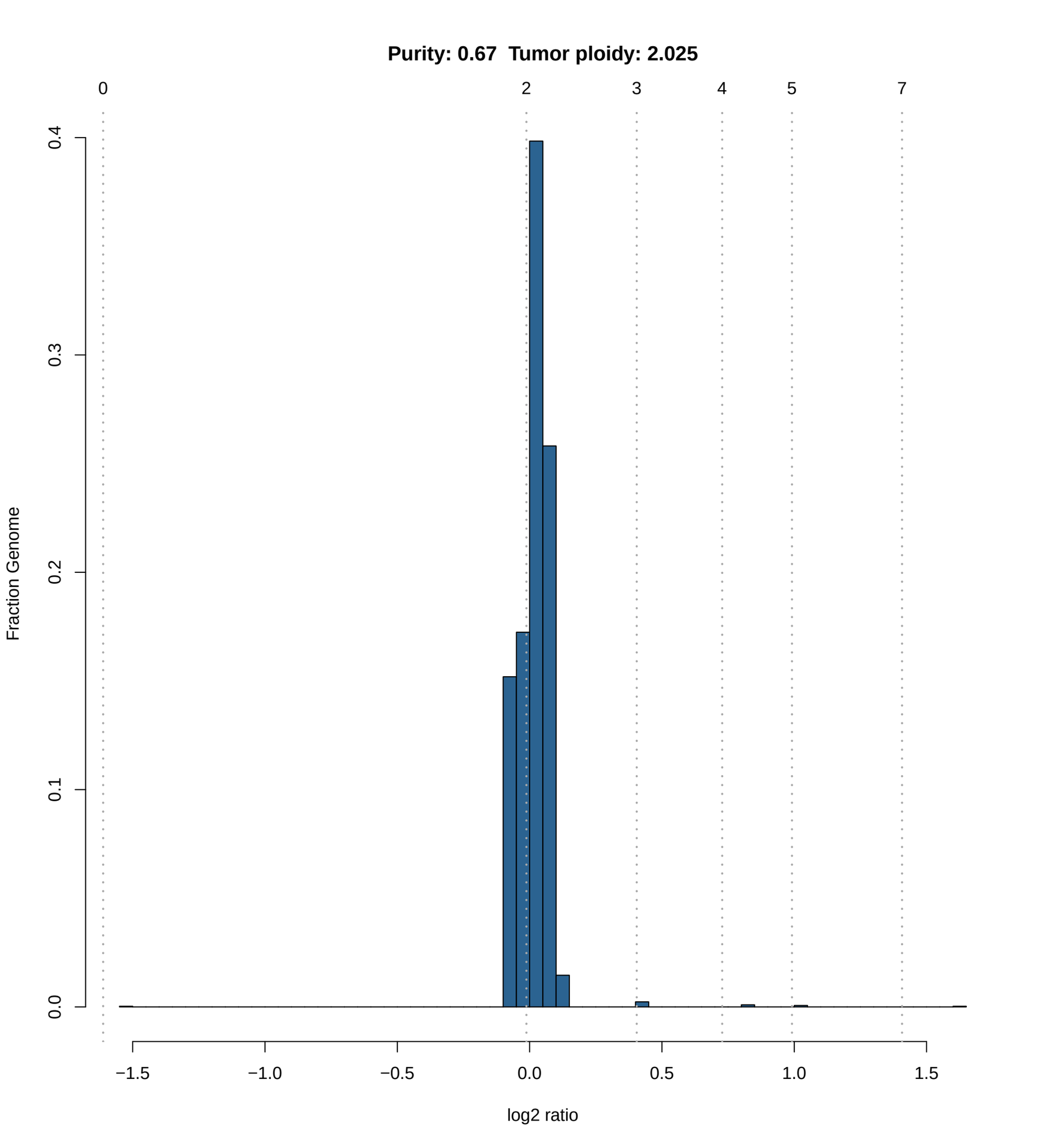

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100
SNV Index

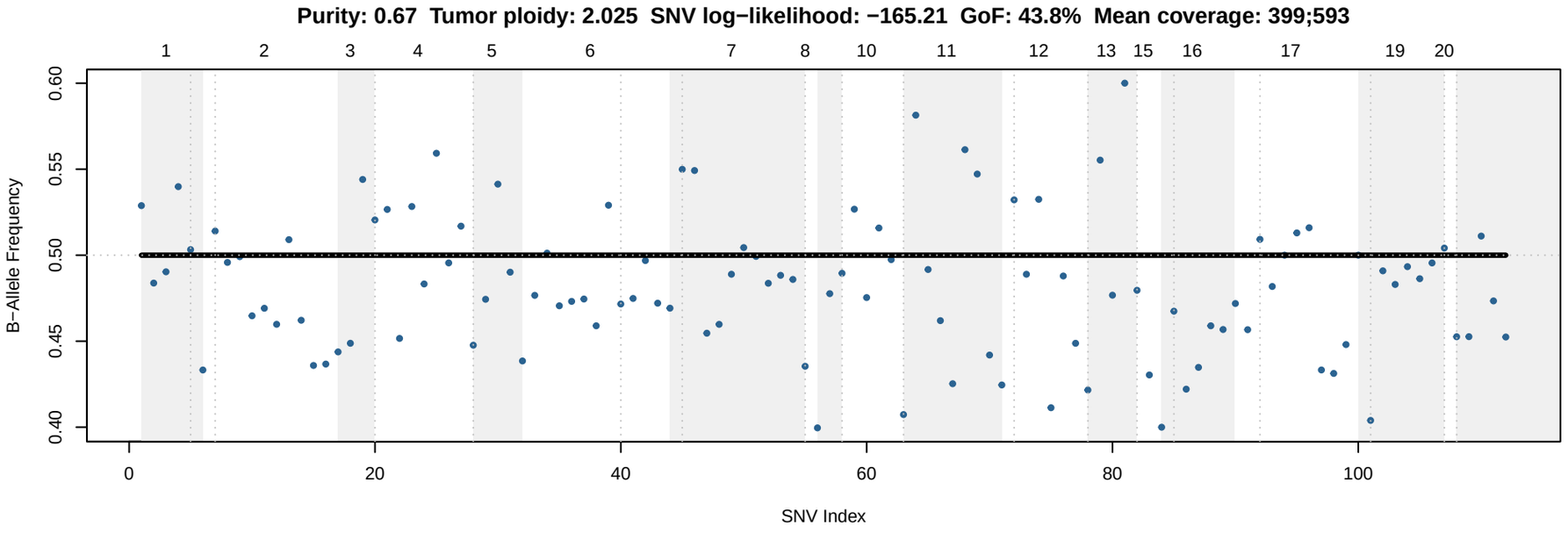

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
6m3
5m2
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

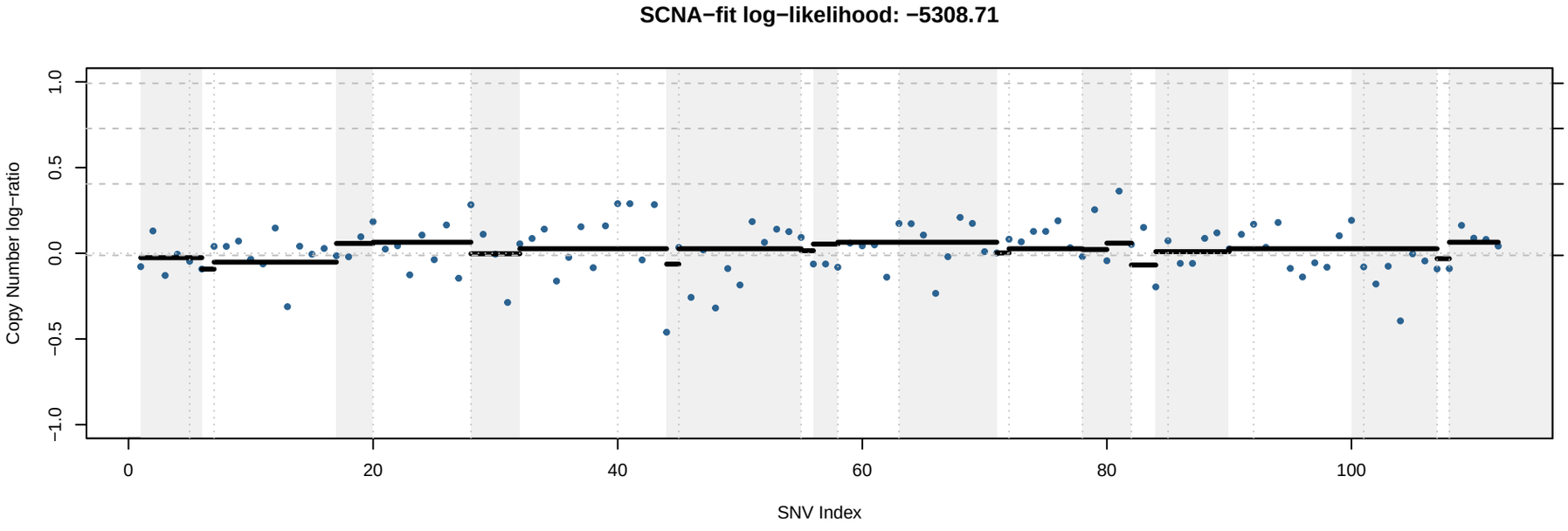

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

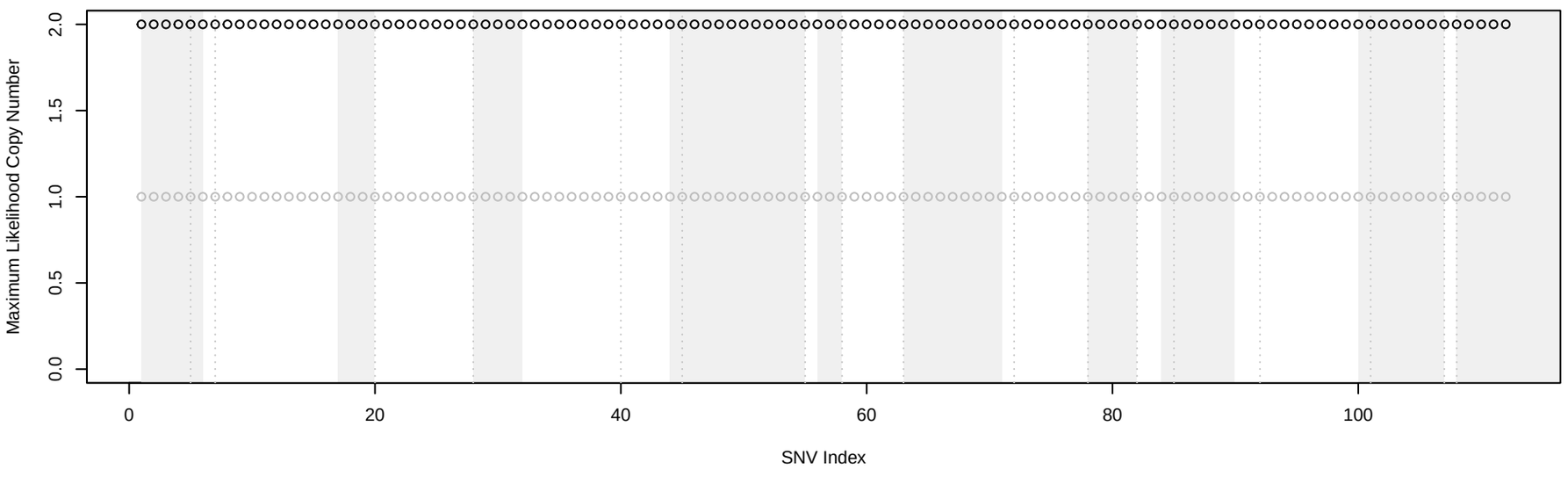

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
6m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

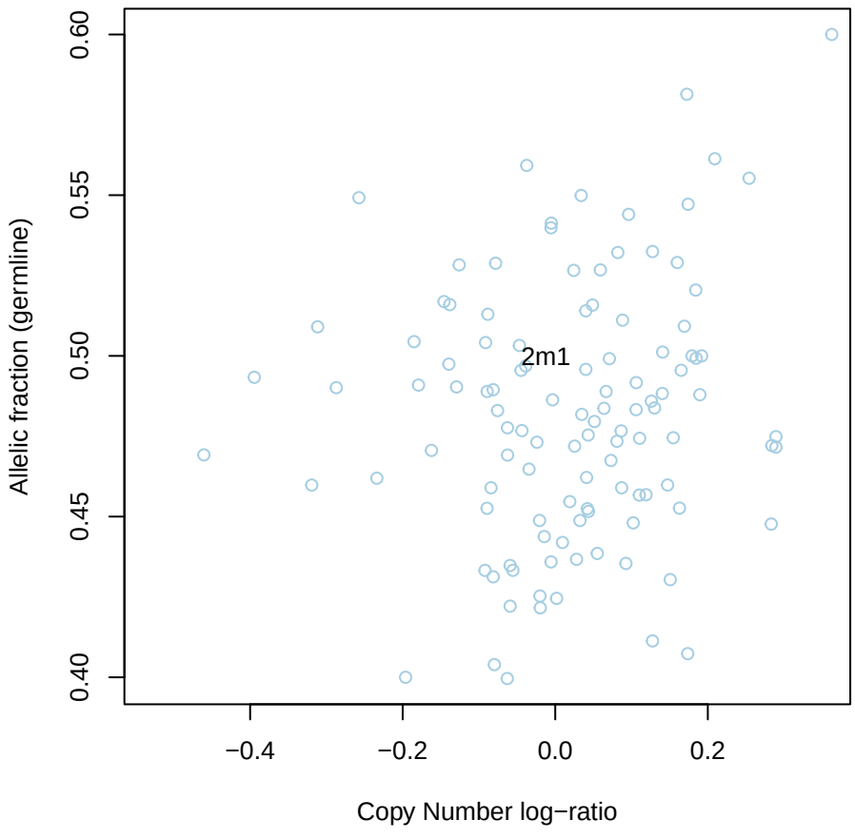

Frequency
0
5
10
15
20
0.2
0.4
0.6
0.8
1.0
Cellular fraction

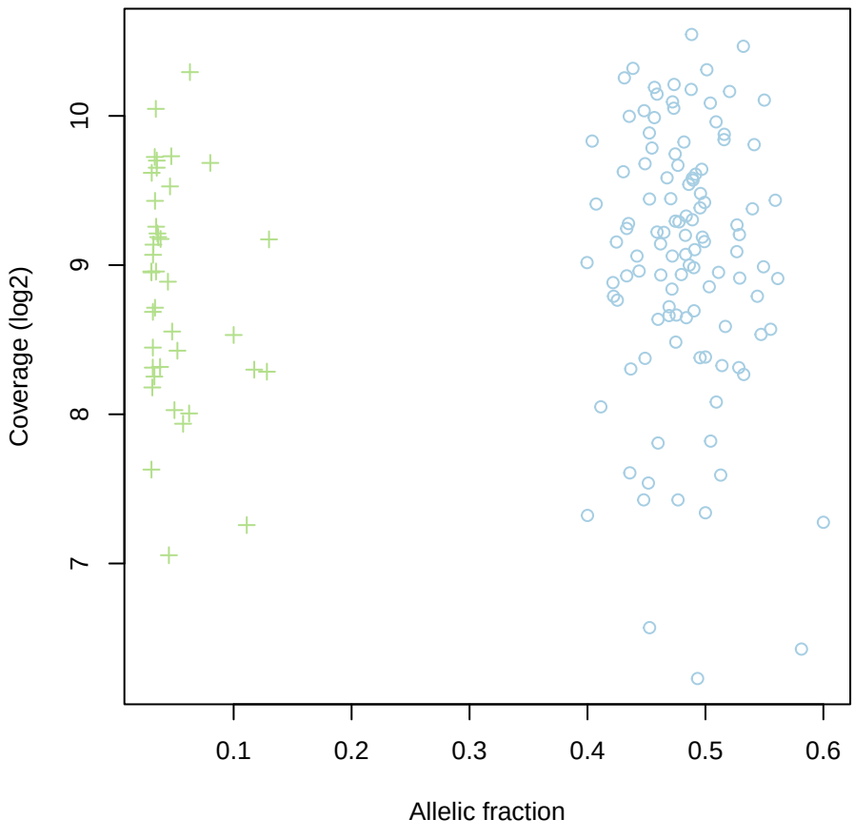

Purity: 0.67 Tumor ploidy: 2.025
0
2
3
4
5
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

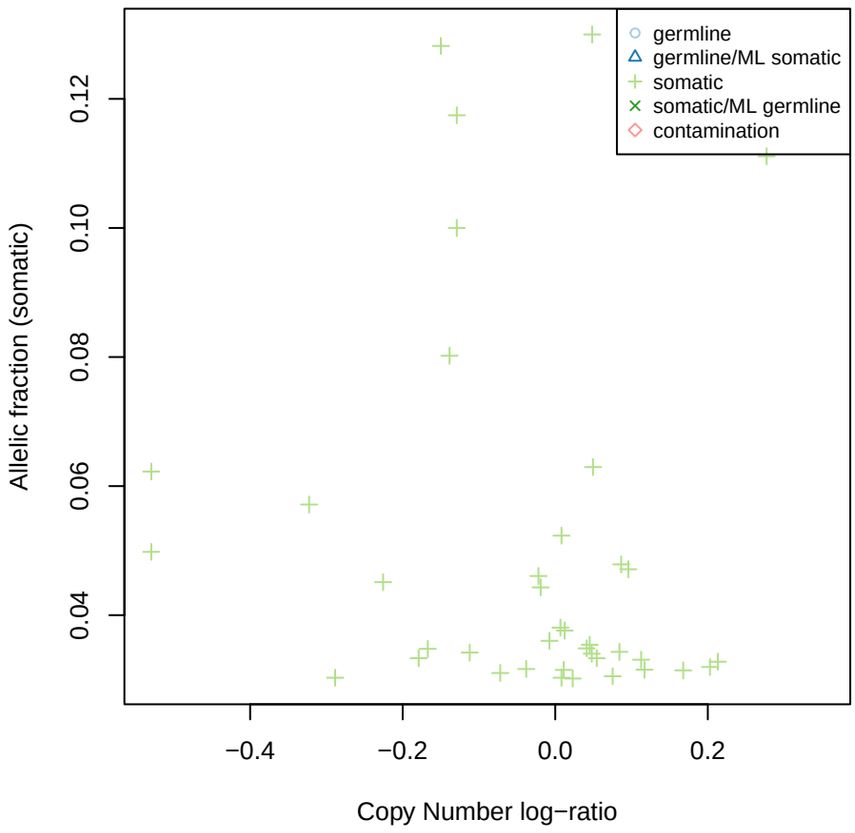

Purity: 0.67 Tumor ploidy: 2.025 SNV log−likelihood: −165.21 GoF: 43.8% Mean coverage: 399;593
1
2
3
4
5
6
7
8
10
11
12
13
15
16
17
19
20
B−Allele Frequency
0.40
0.45
0.50
0.55
0.60
0
20
40
60
80
100
SNV Index

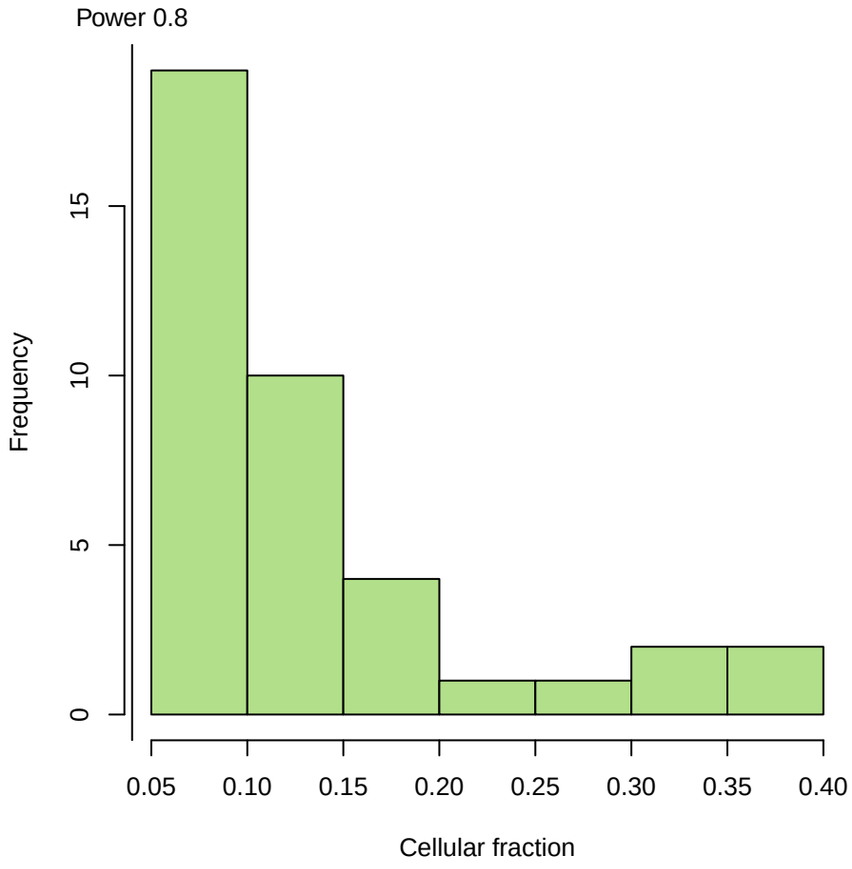

SCNA−fit log−likelihood: −5308.71
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
2
3
4
5
0
20
40
60
80
100
SNV Index

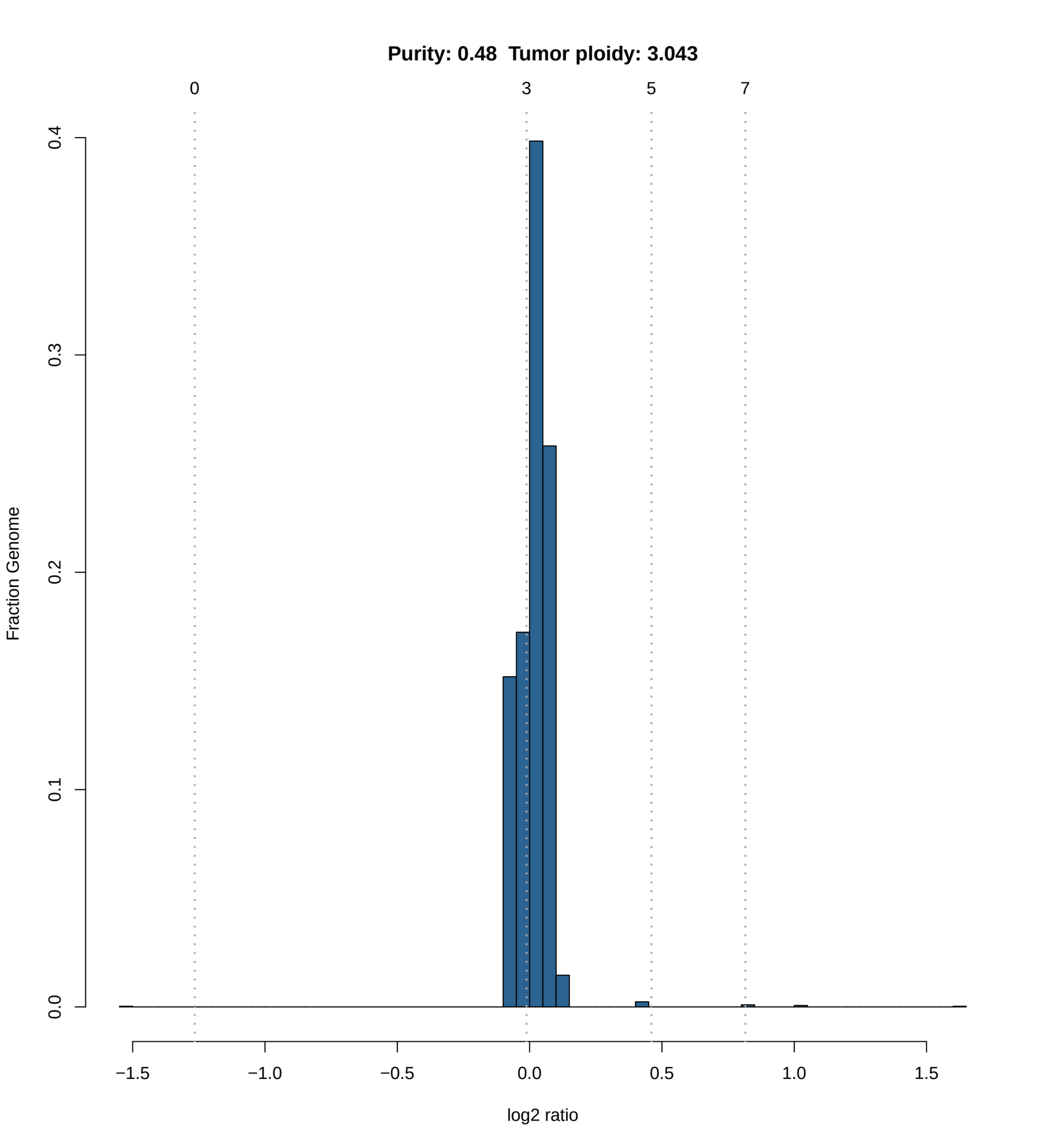

Maximum Likelihood Copy Number
0.0
0.5
1.0
1.5
2.0
0
20
40
60
80
100
SNV Index

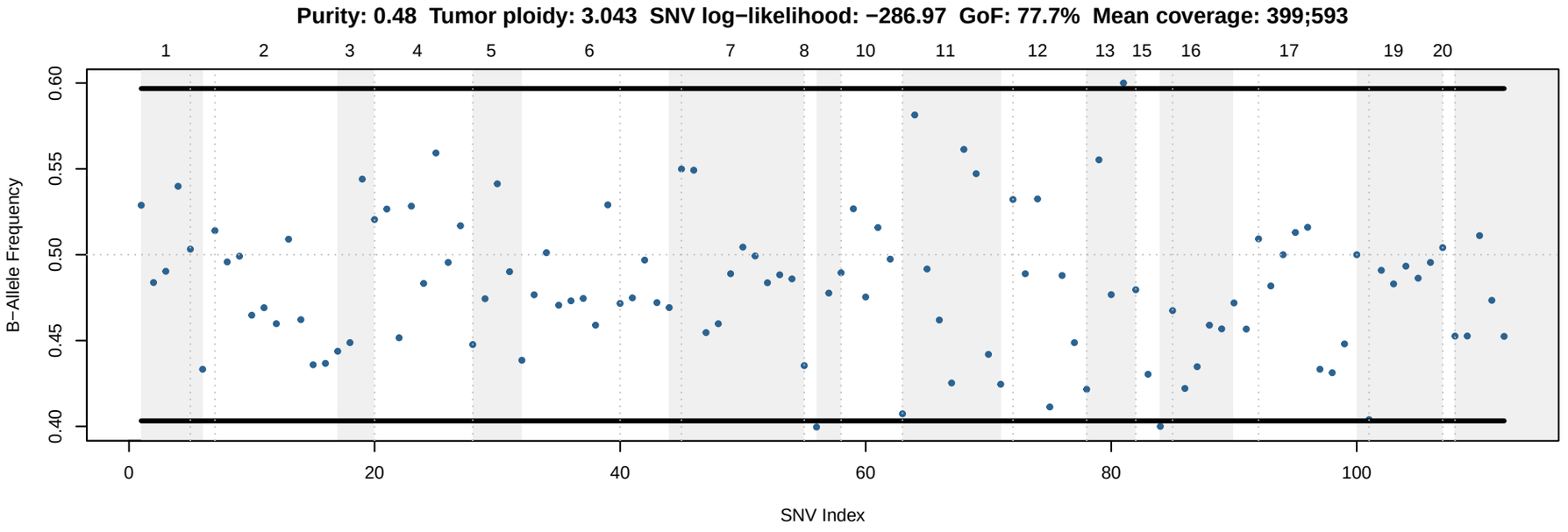

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
2m1
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

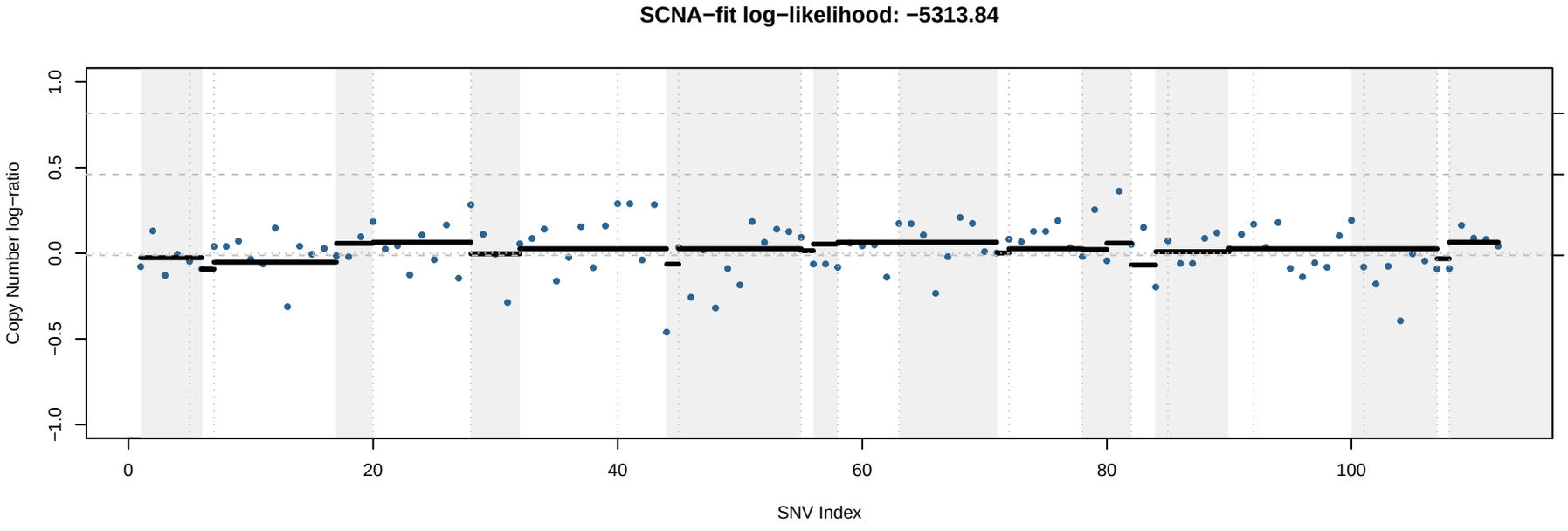

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

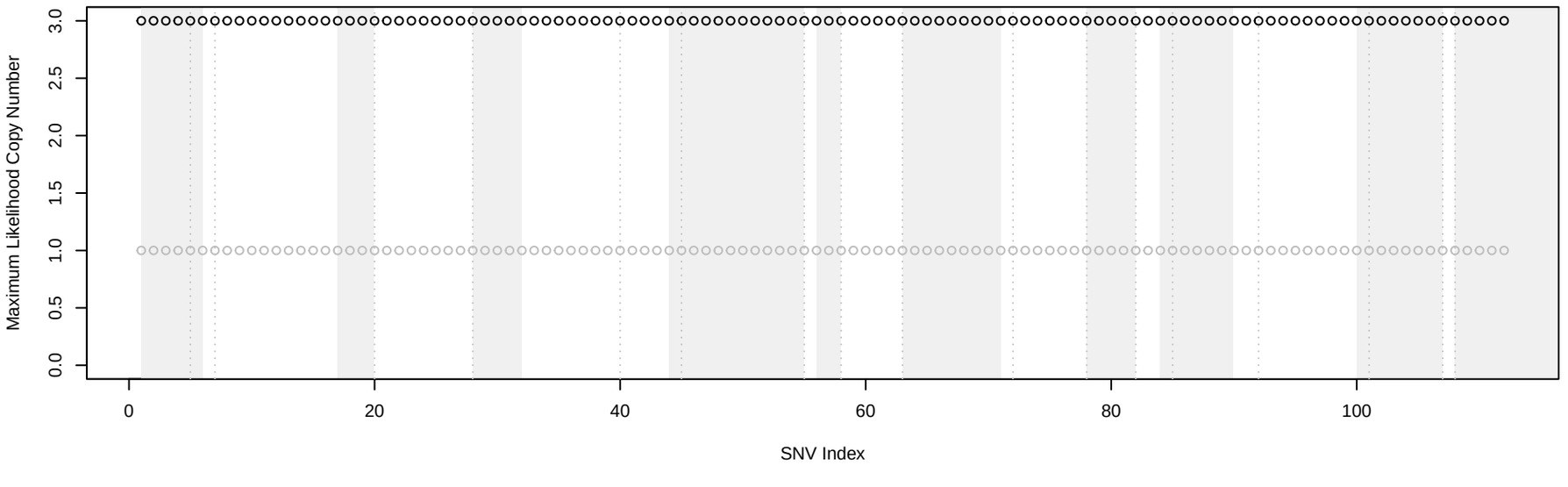

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

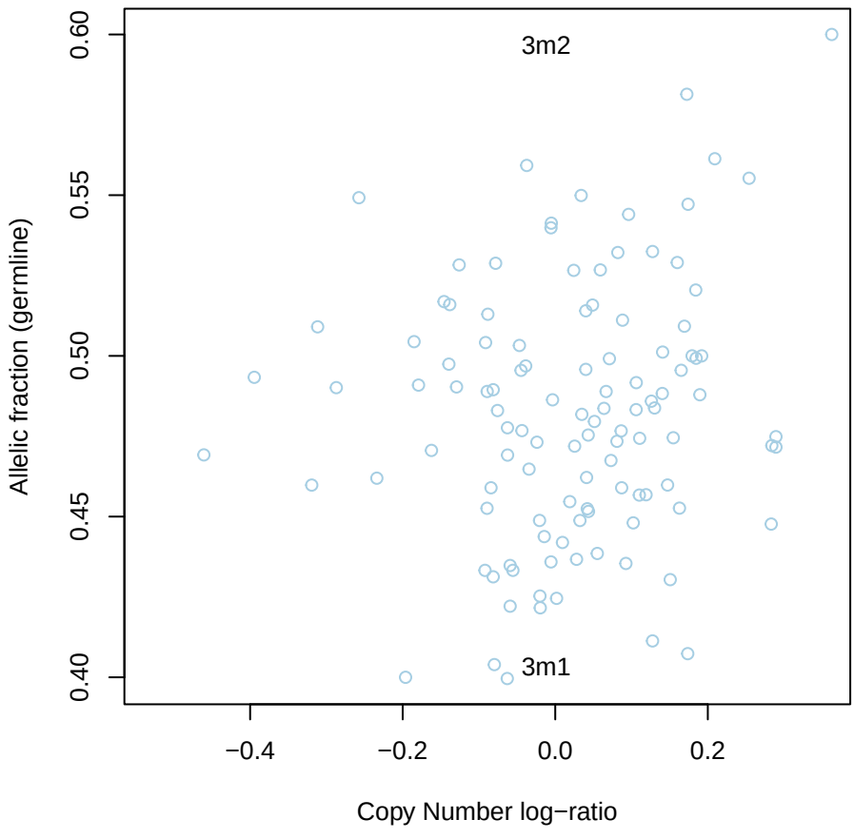

Power 0.8
Frequency
0
5
10
15
0.05
0.10
0.15
0.20
0.25
0.30
0.35
0.40
Cellular fraction

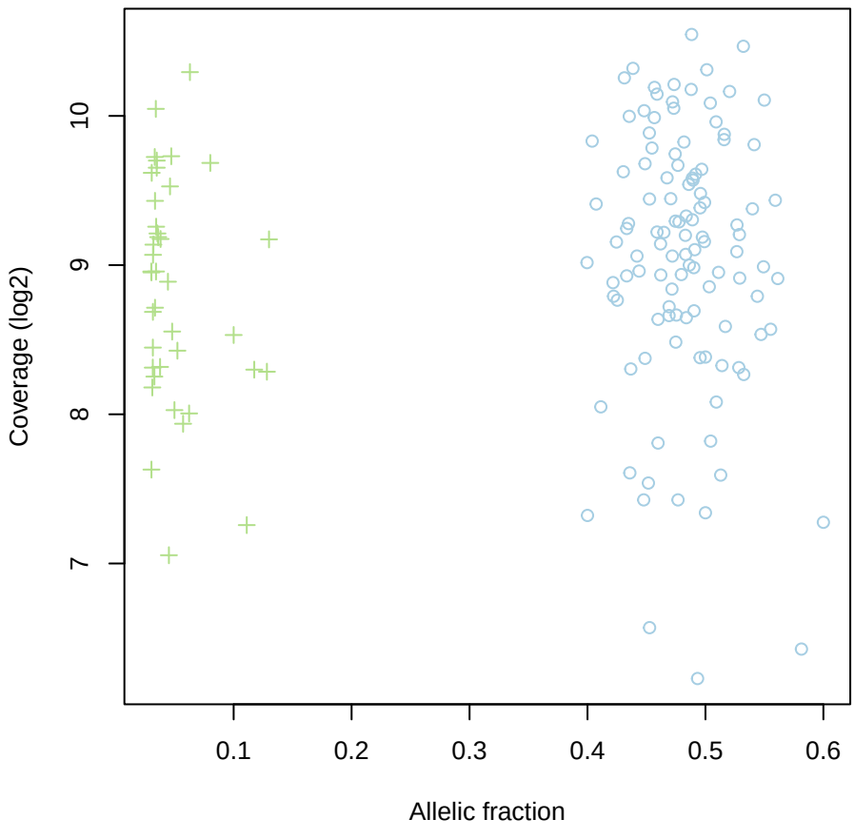

Purity: 0.48 Tumor ploidy: 3.043
0
3
5
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

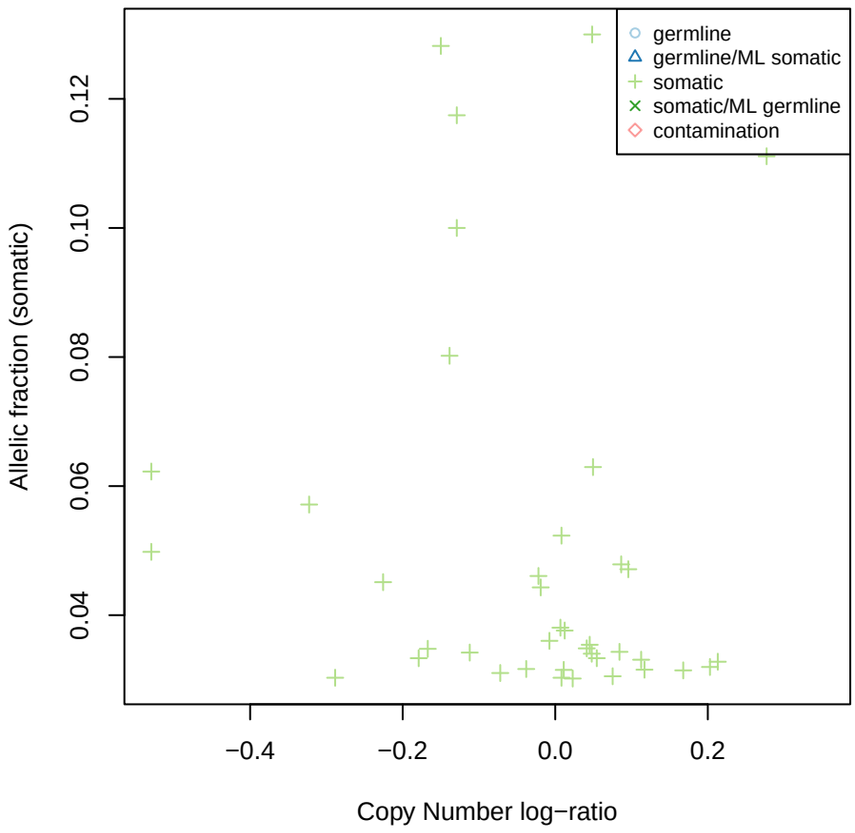

Purity: 0.48 Tumor ploidy: 3.043 SNV log−likelihood: −286.97 GoF: 77.7% Mean coverage: 399;593
1 2 3 4 5 6 7 8 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

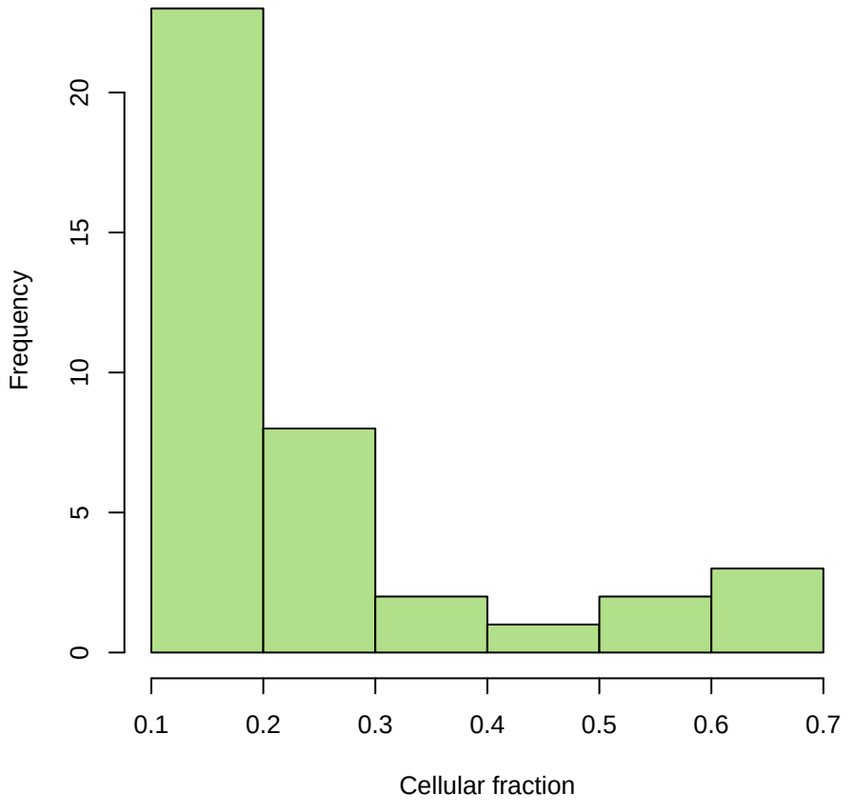

SCNA−fit log−likelihood: −5313.84
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 5 7
0 20 40 60 80 100
SNV Index

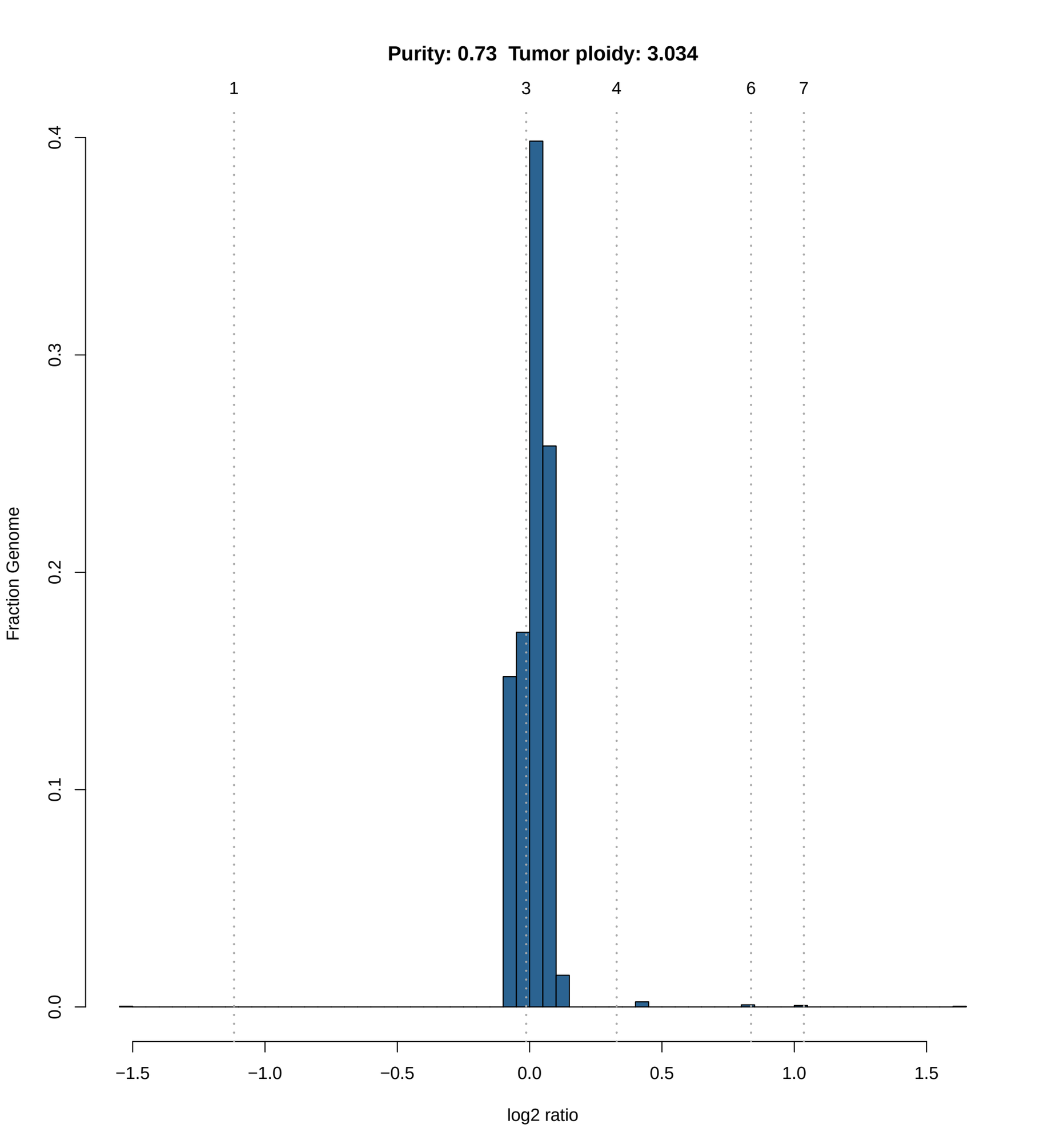

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100
SNV Index

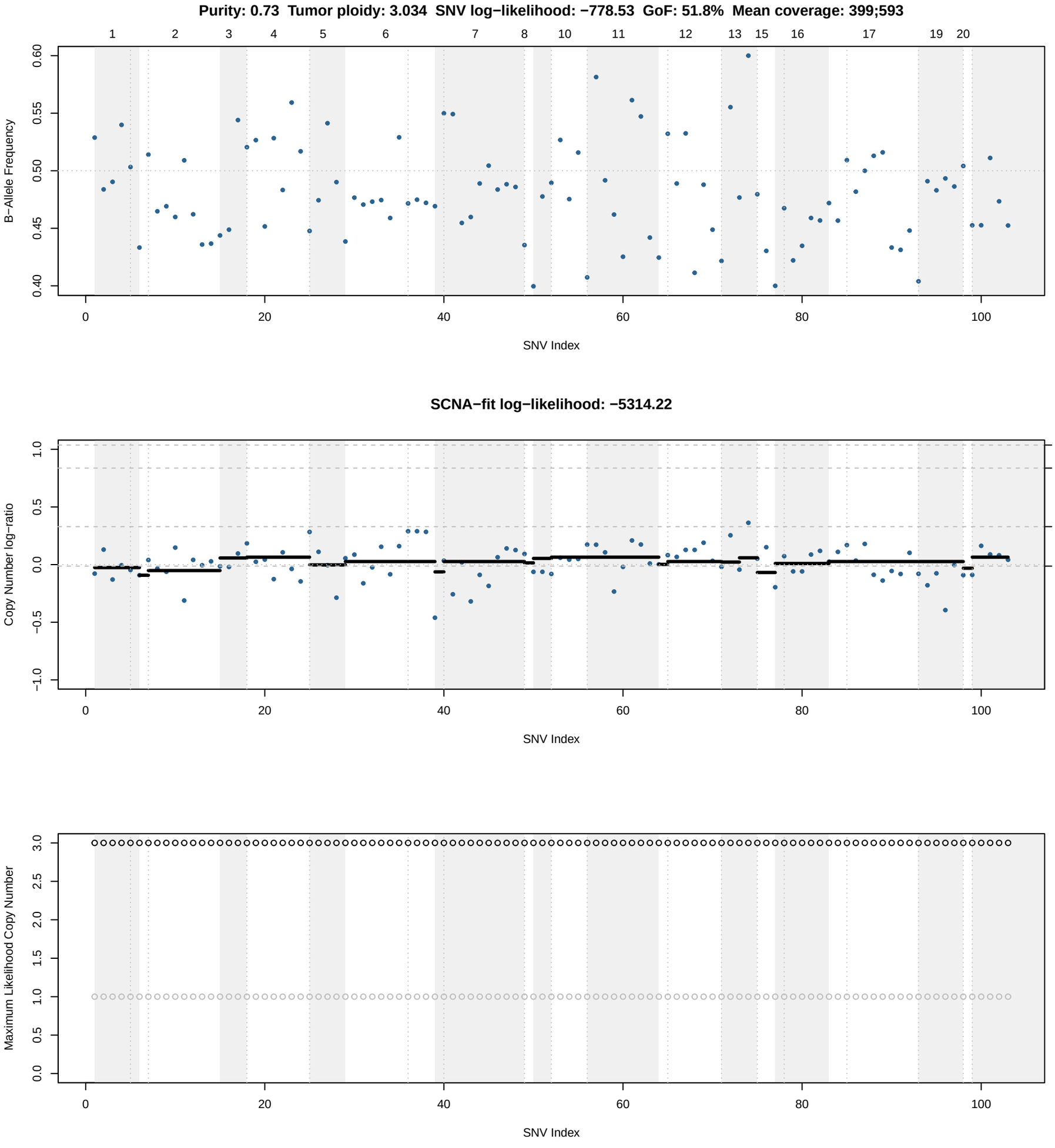

3m2
3m1
Allelic fraction (germline)
Copy Number log−ratio
0.40
0.45
0.50
0.55
0.60
−0.4
−0.2
0.0
0.2

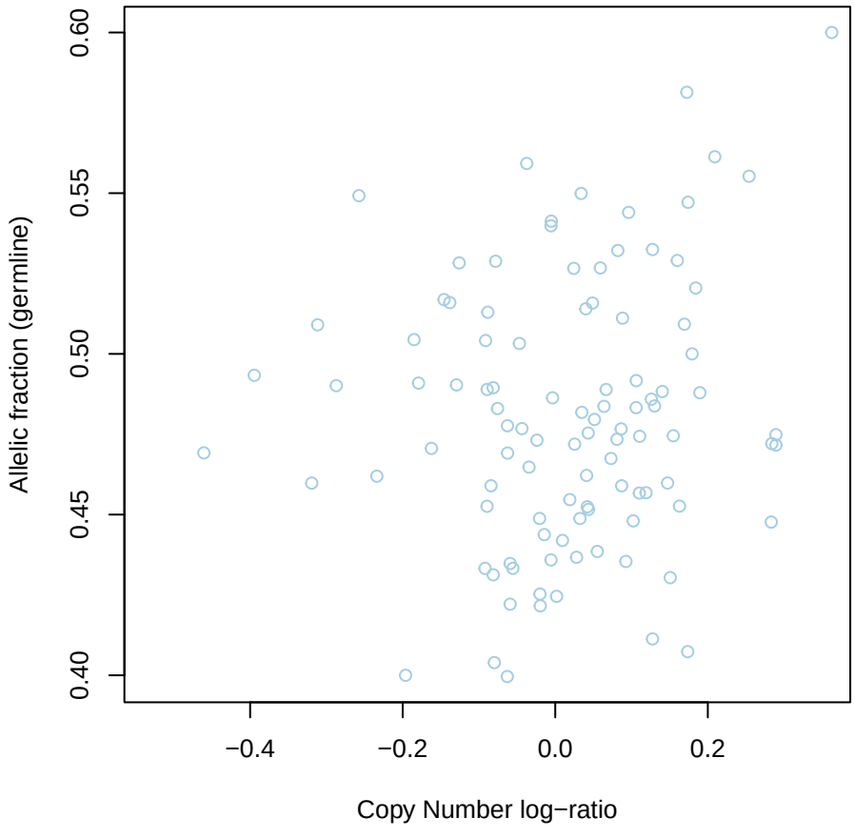

Coverage (log2)
Allelic fraction
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

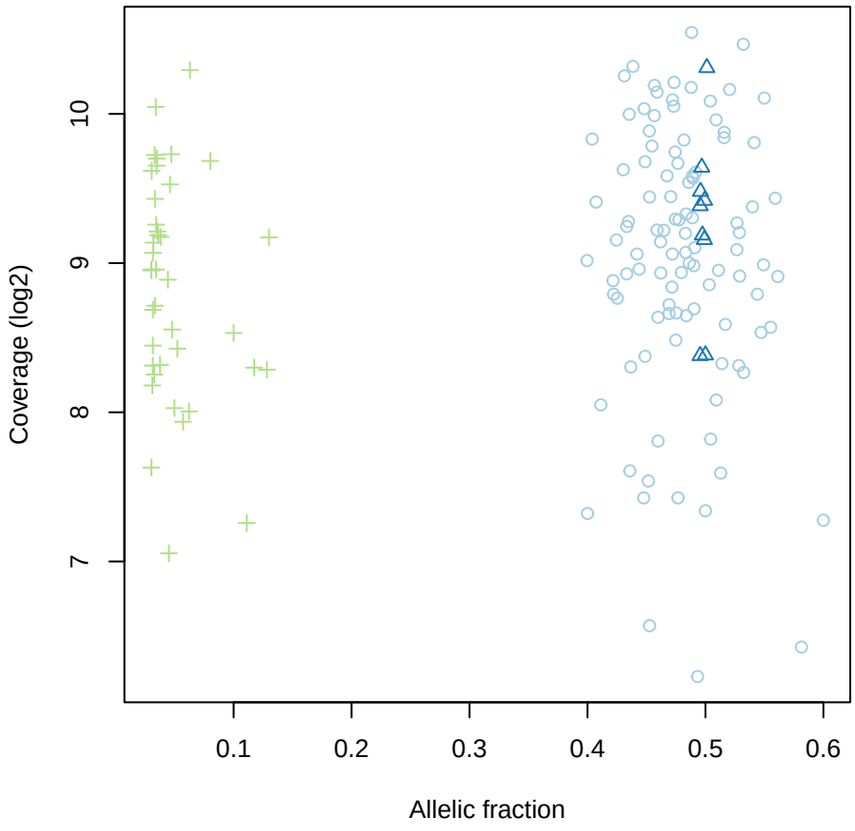

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
0.12
−0.4
−0.2
0.0
0.2

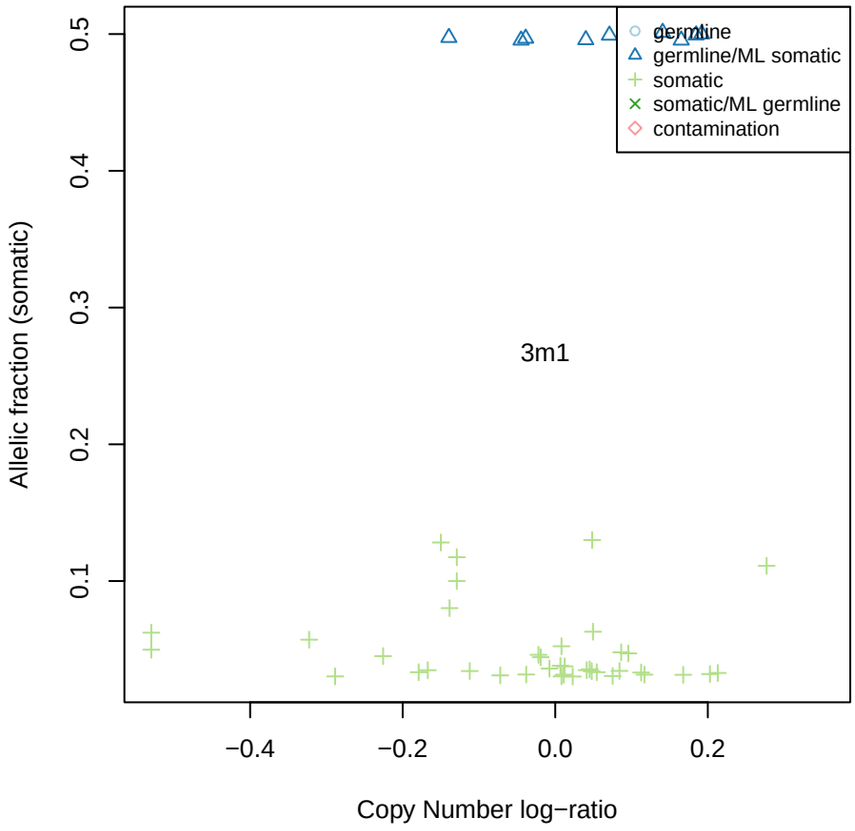

Frequency
Cellular fraction
0
5
10
15
20
0.1
0.2
0.3
0.4
0.5
0.6
0.7

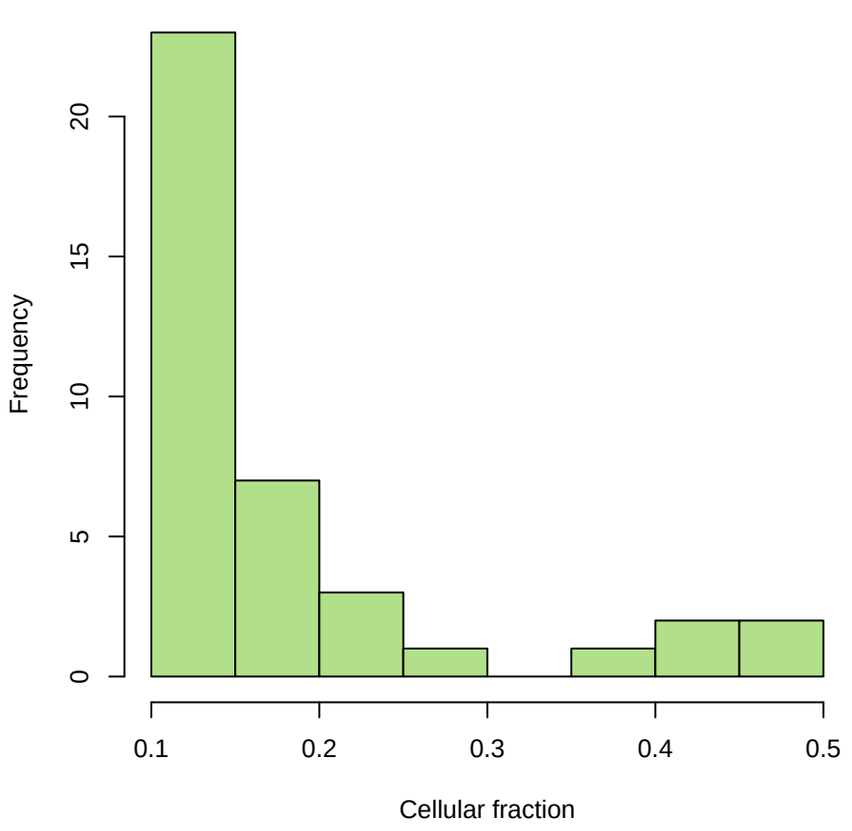

Purity: 0.73 Tumor ploidy: 3.034
1
3
4
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

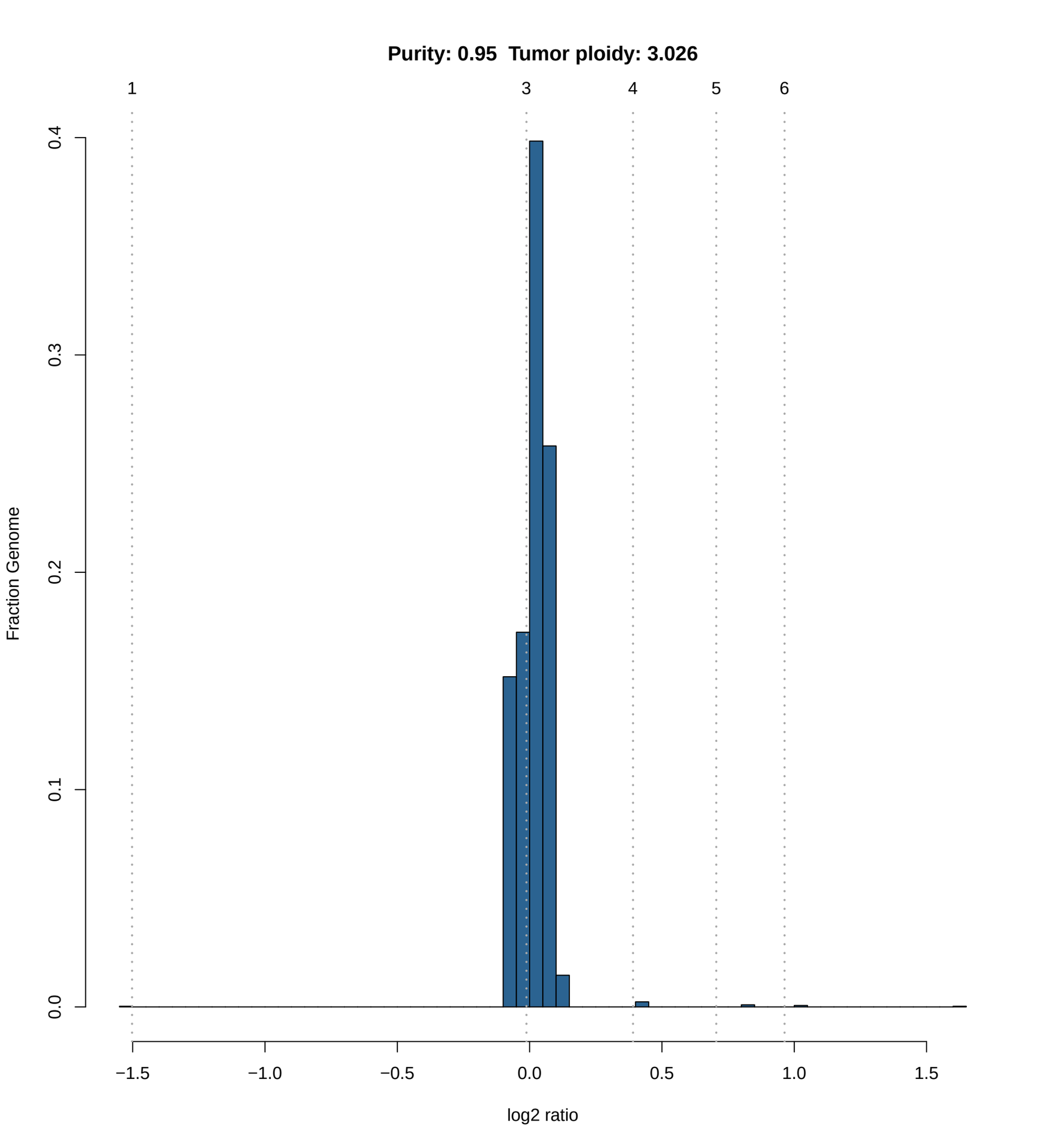

Purity: 0.73 Tumor ploidy: 3.034 SNV log−likelihood: −778.53 GoF: 51.8% Mean coverage: 399;593
1 2 3 4 5 6 7 8 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index
SCNA−fit log−likelihood: −5314.22
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 6 7
0 20 40 60 80 100
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
SNV Index

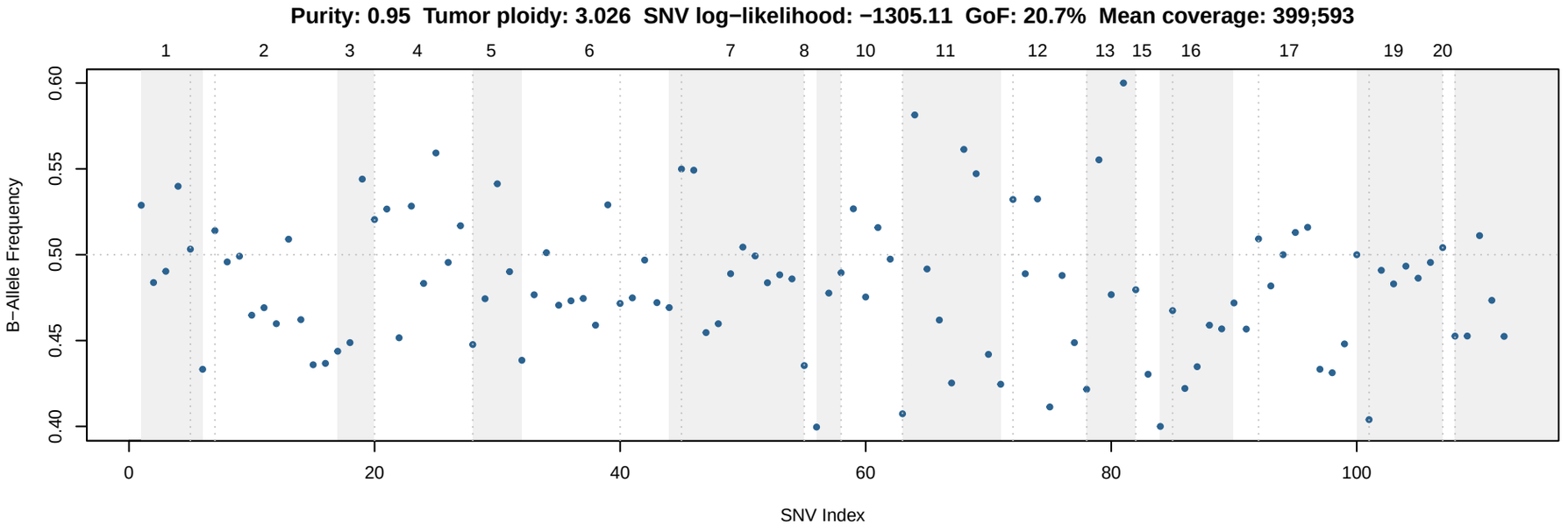

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

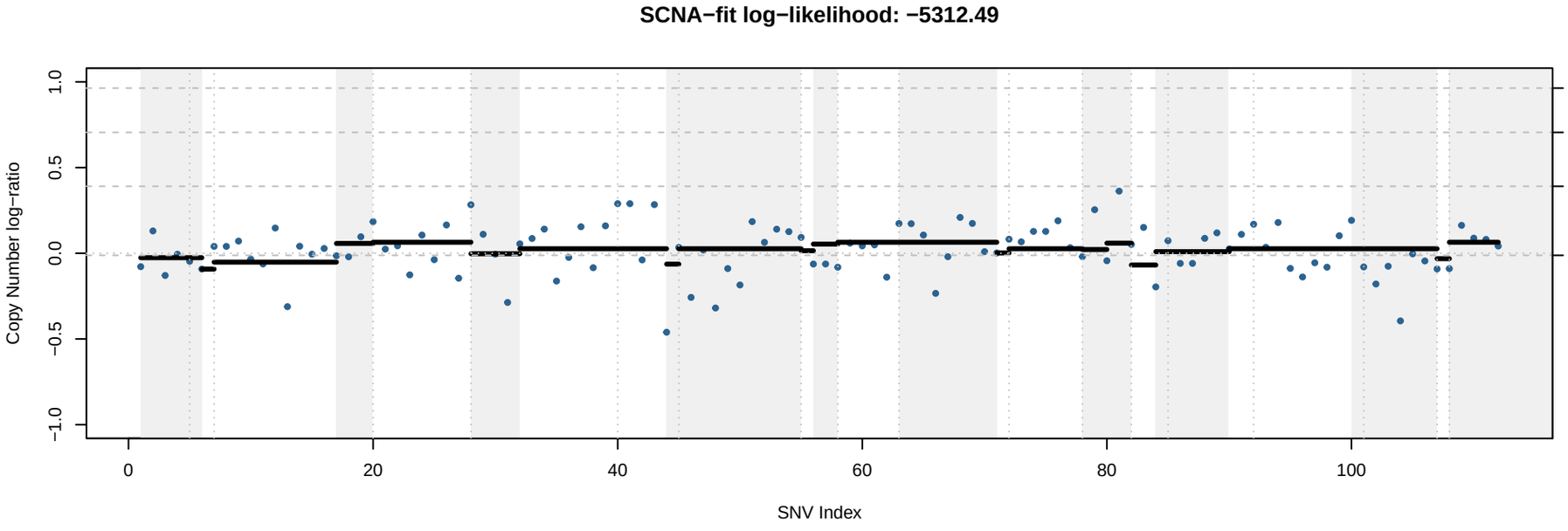

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

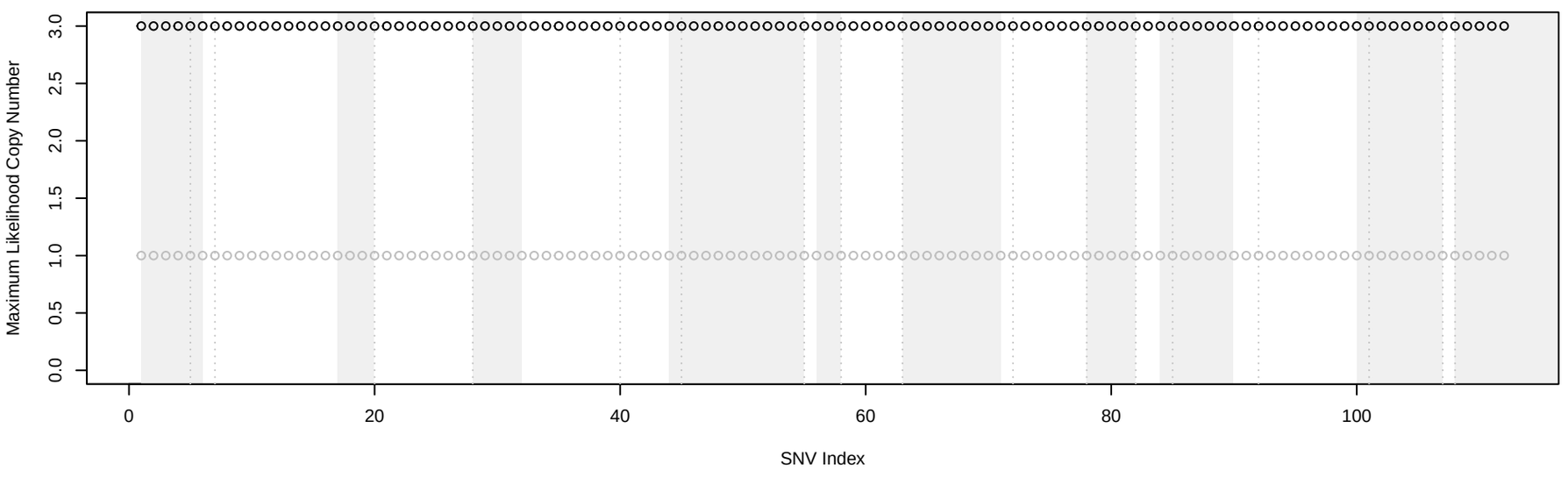

Allelic fraction (somatic)
0.1
0.2
0.3
0.4
0.5
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
−0.4
−0.2
0.0
0.2
Copy Number log−ratio

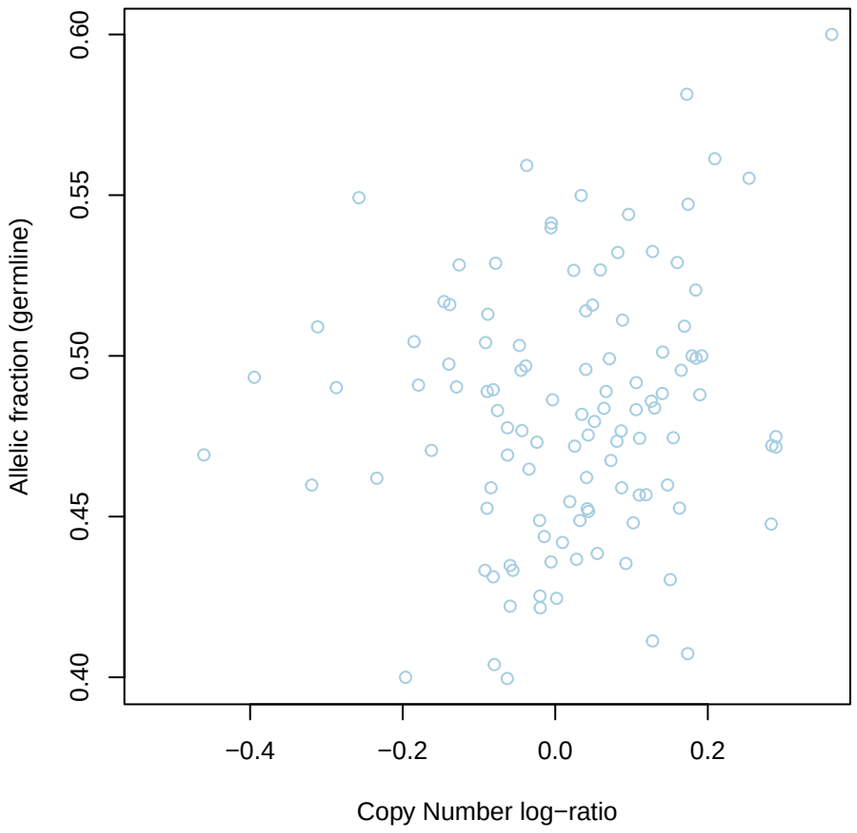

Frequency
0
5
10
15
20
0.1
0.2
0.3
0.4
0.5
Cellular fraction

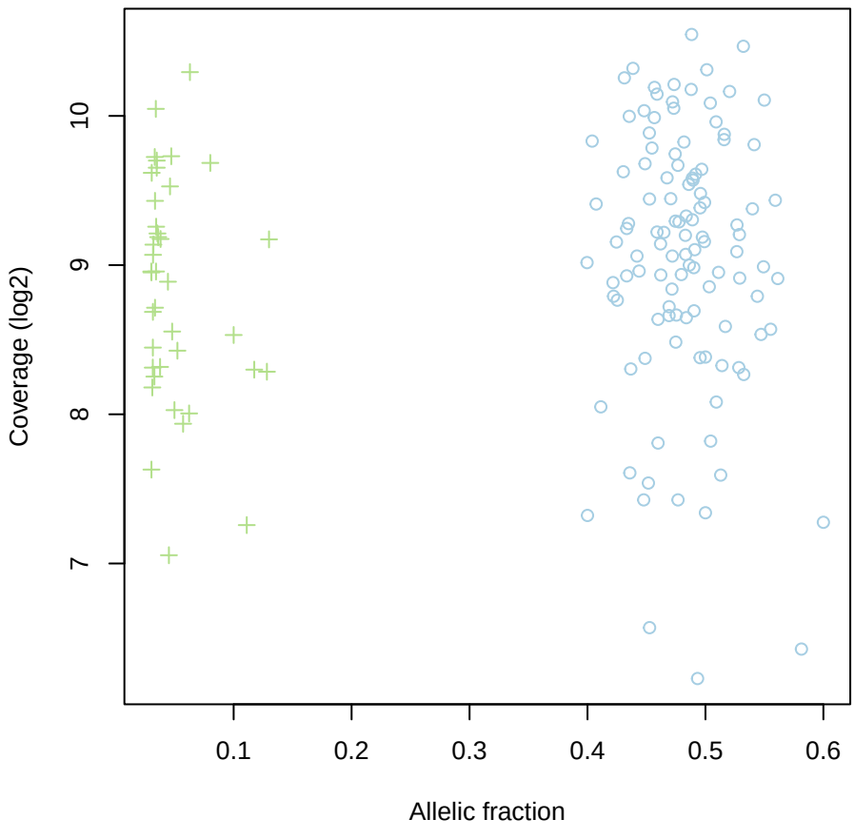

Purity: 0.95 Tumor ploidy: 3.026
1
3
4
5
6
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

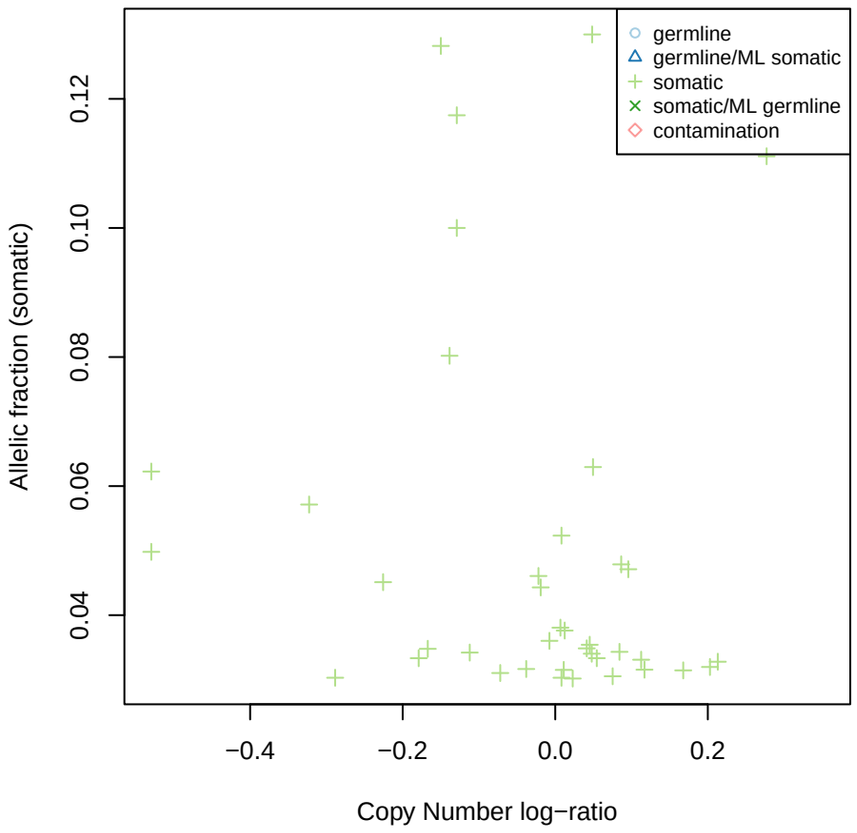

Purity: 0.95 Tumor ploidy: 3.026 SNV log−likelihood: −1305.11 GoF: 20.7% Mean coverage: 399;593
1 2 3 4 5 6 7 8 10 11 12 13 15 16 17 19 20
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

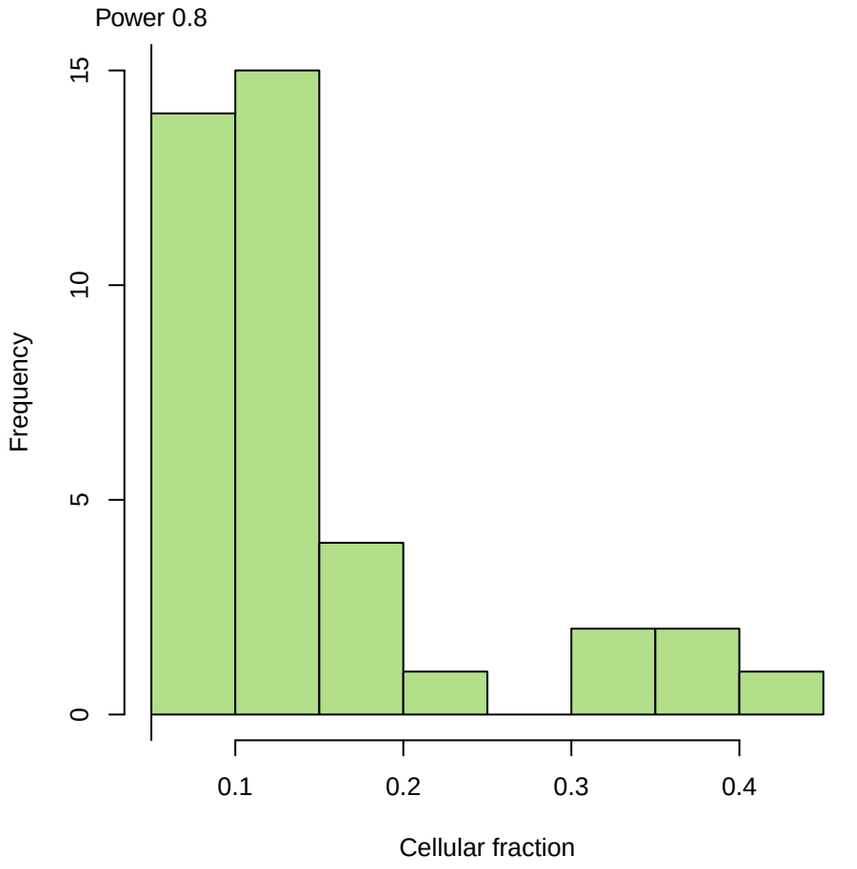

SCNA−fit log−likelihood: −5312.49
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6
0 20 40 60 80 100
SNV Index


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


Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
−0.4
−0.2
0.0
0.2
Copy Number log−ratio


Coverage (log2)
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
−0.4
−0.2
0.0
0.2
Copy Number log−ratio


Power 0.8
Frequency
0
5
10
15
0.1
0.2
0.3
0.4
Cellular fraction