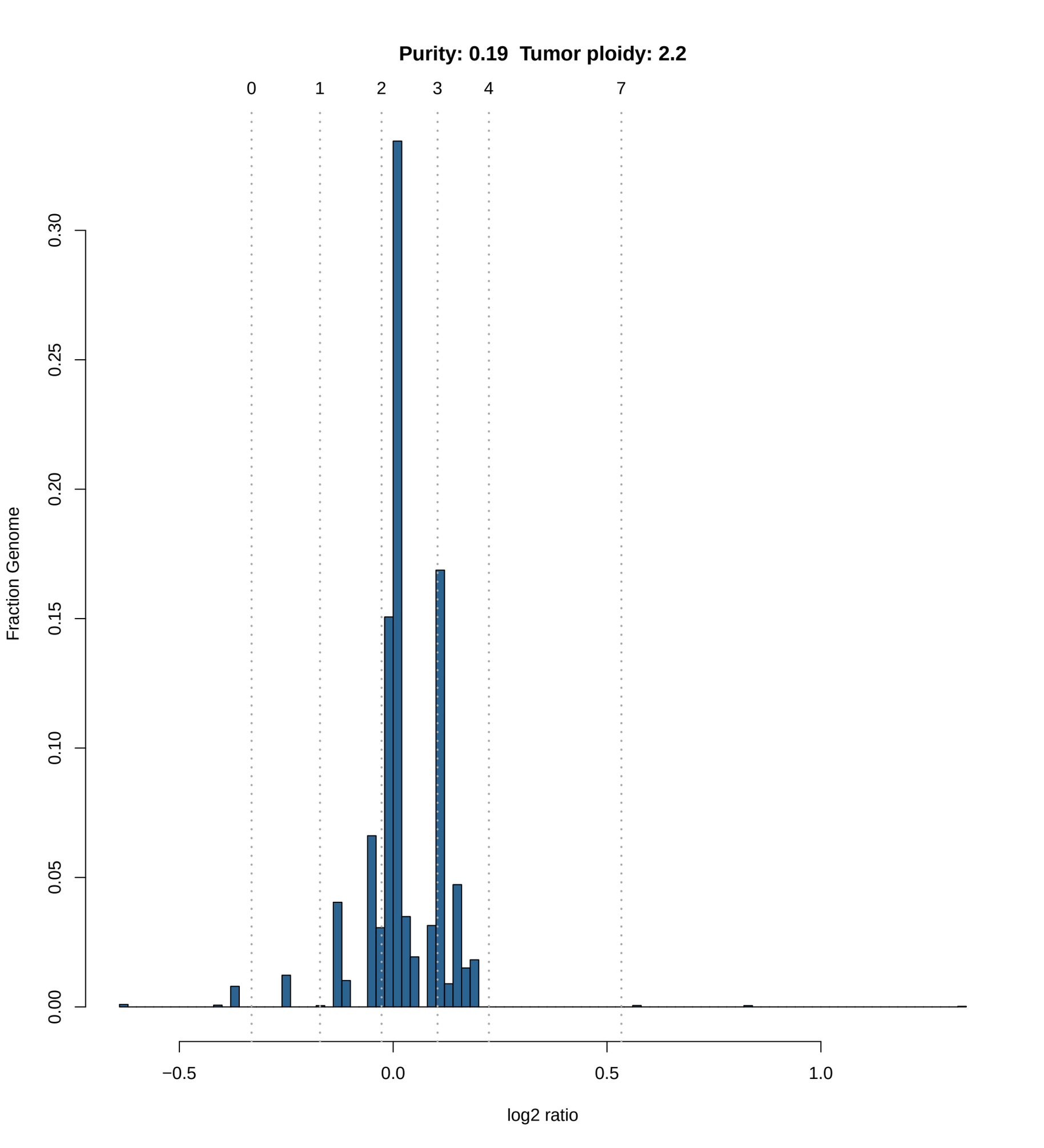
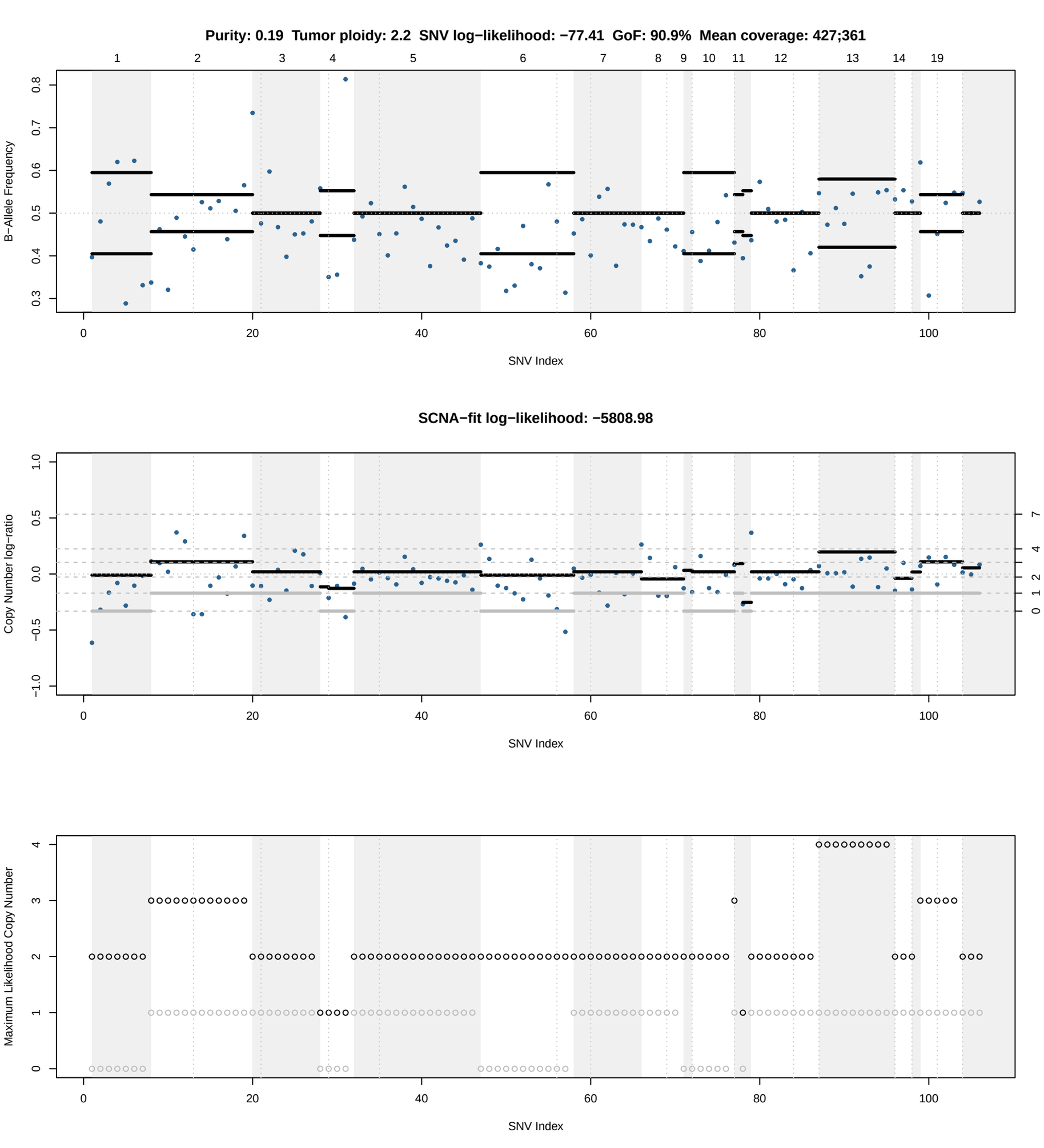
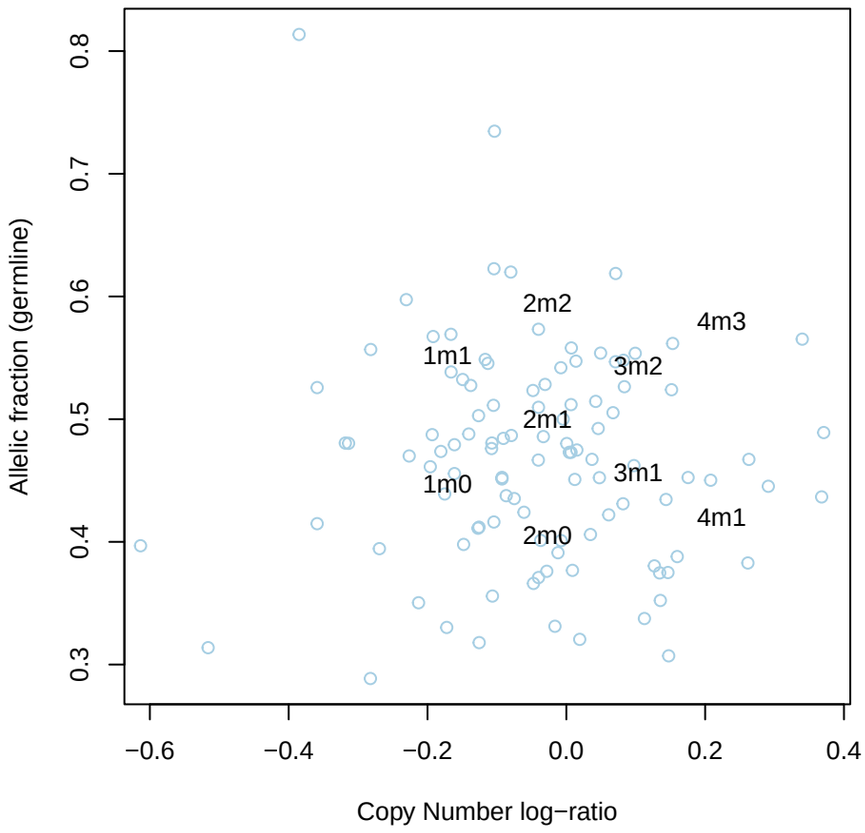
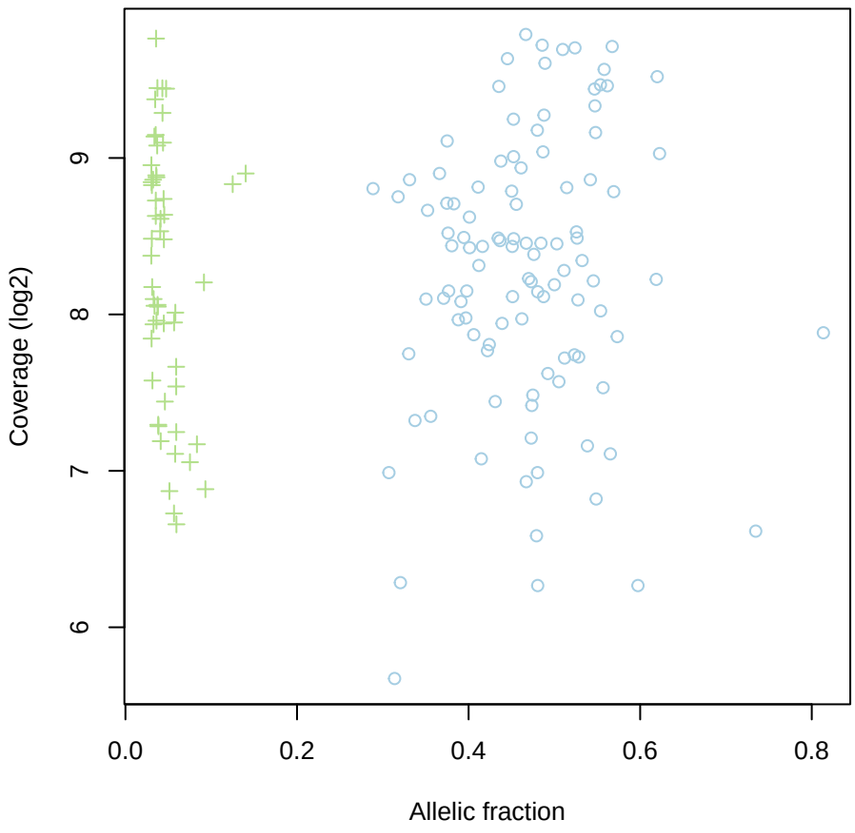
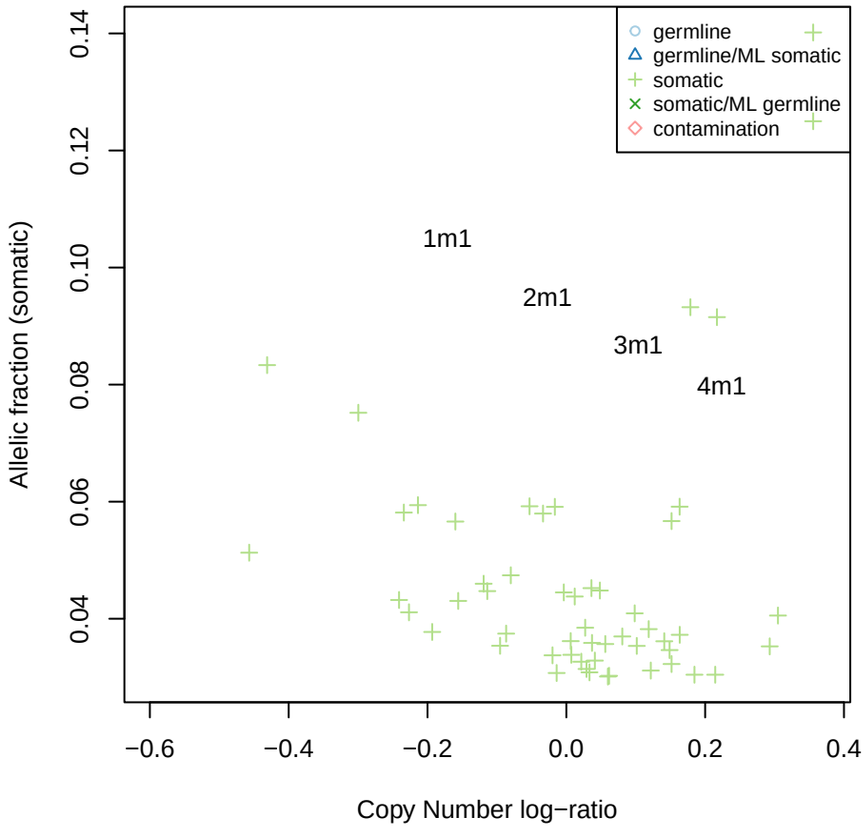
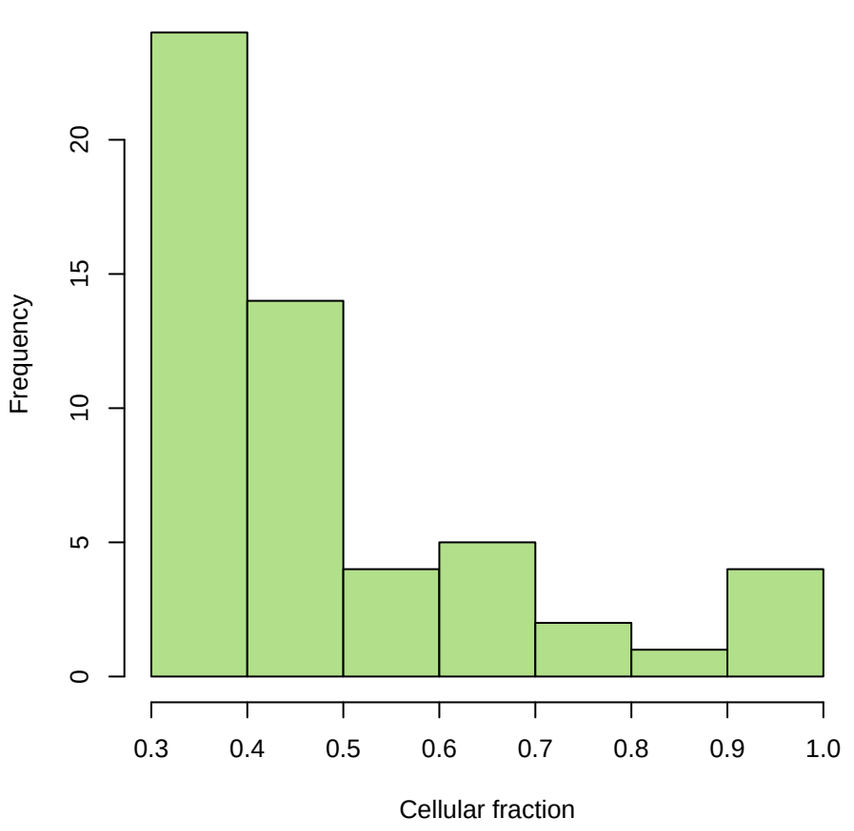

Purity: 0.19  Tumor ploidy: 2.2
0
1
2
3
4
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

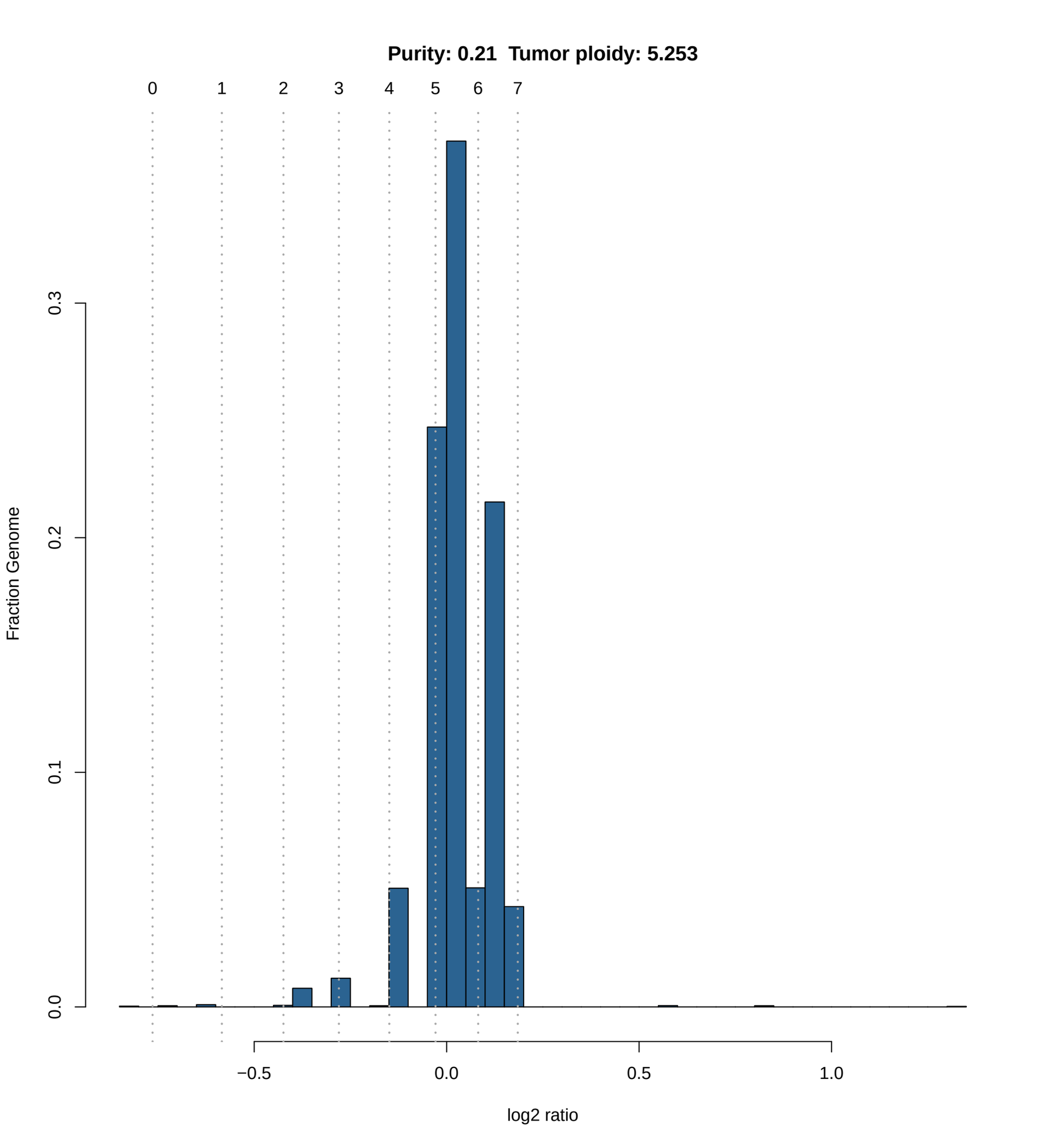

Purity: 0.19 Tumor ploidy: 2.2 SNV log−likelihood: −77.41 GoF: 90.9% Mean coverage: 427;361
1 2 3 4 5 6 7 8 9 10 11 12 13 14 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100
SNV Index
SCNA−fit log−likelihood: −5808.98
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 4 7
0 20 40 60 80 100
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100
SNV Index

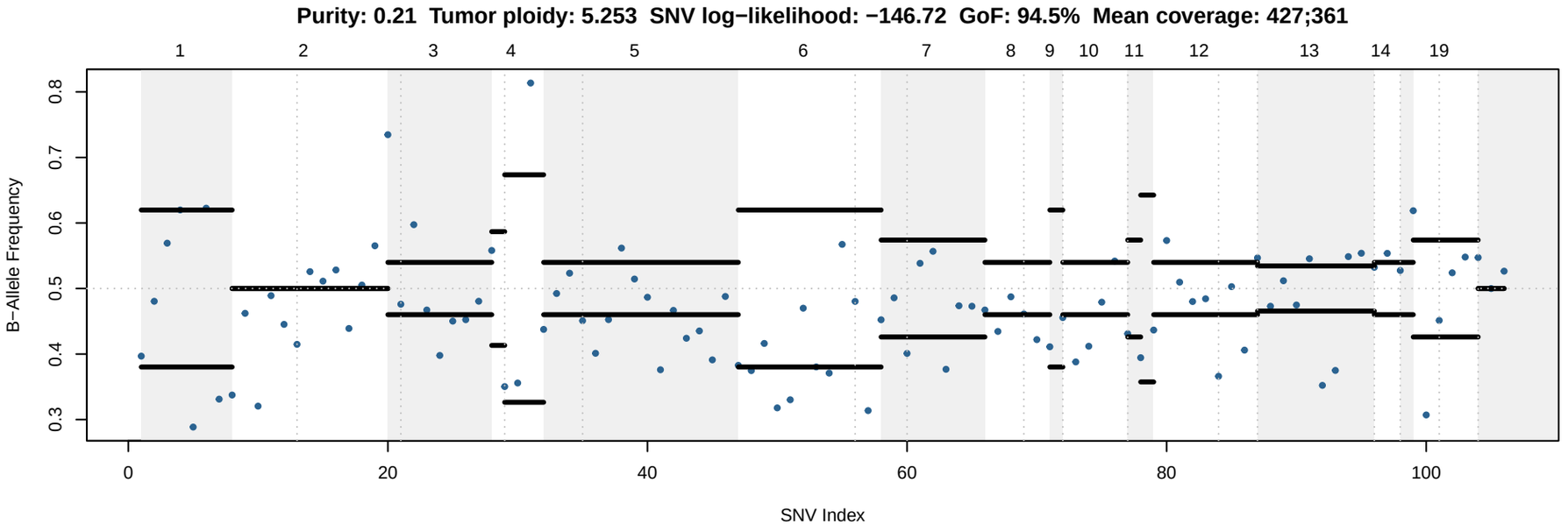

Allelic fraction (germline)
Copy Number log−ratio
2m2
4m3
1m1
3m2
2m1
3m1
1m0
4m1
2m0

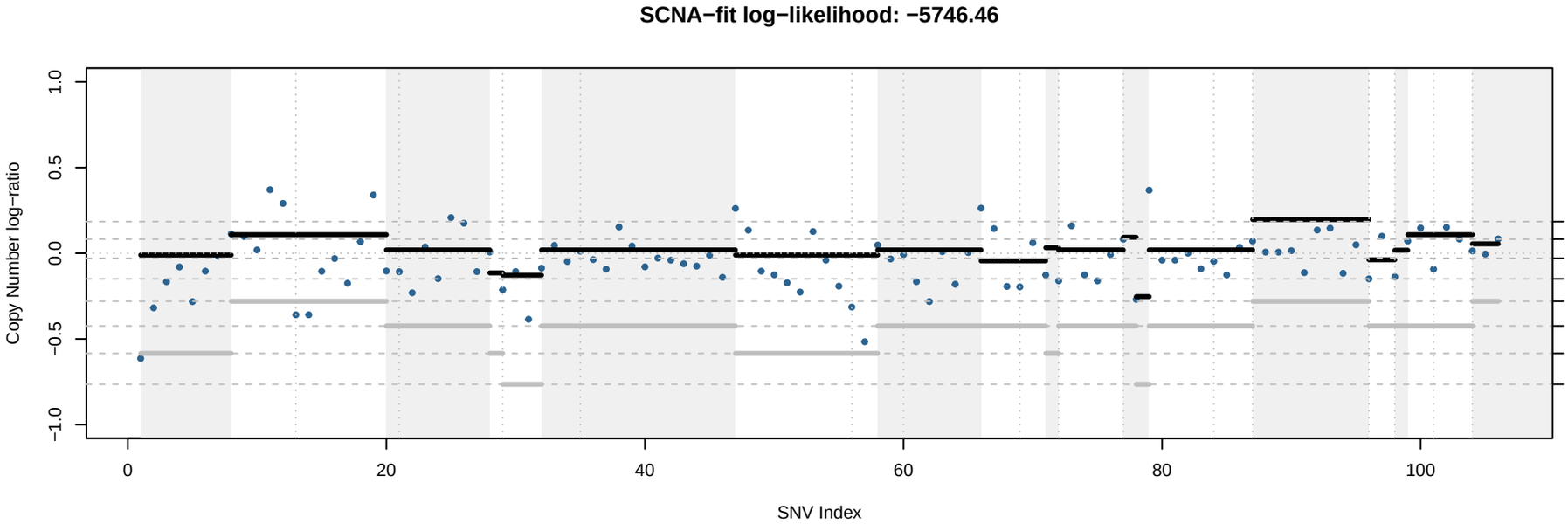

Coverage (log2)
Allelic fraction

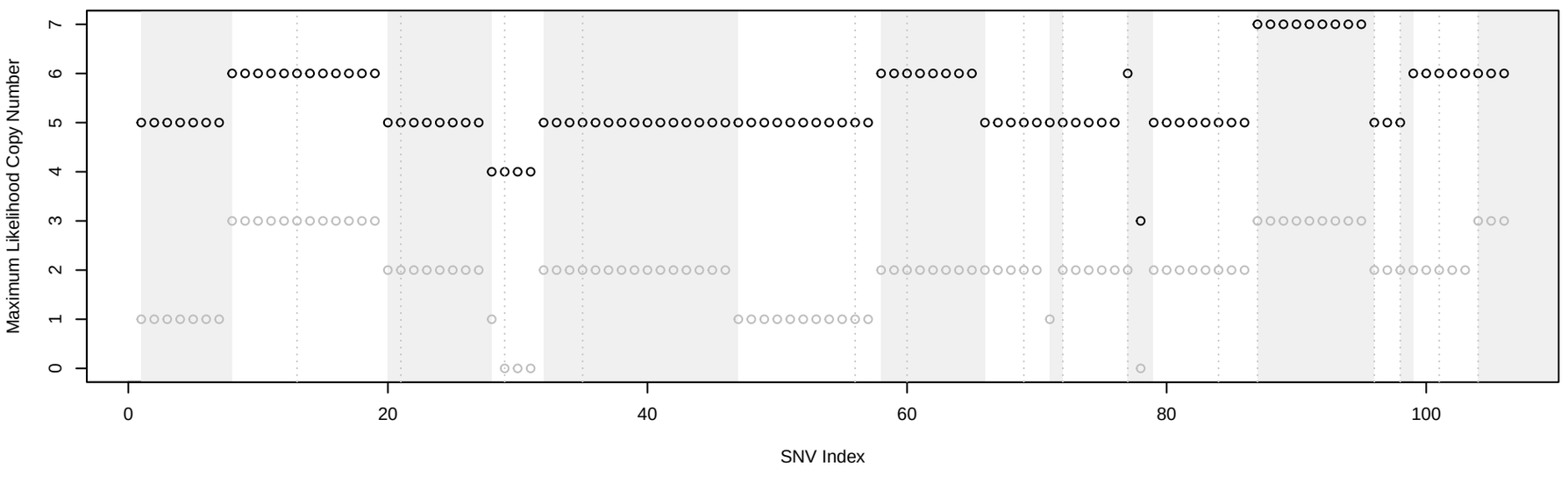

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1
3m1
4m1

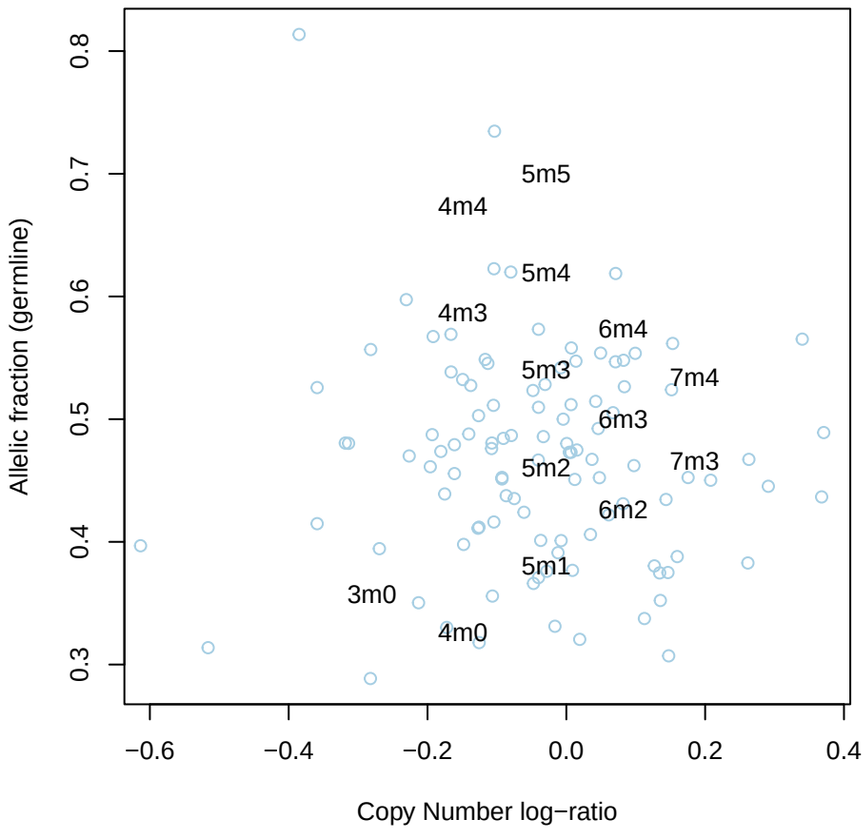

Frequency
Cellular fraction

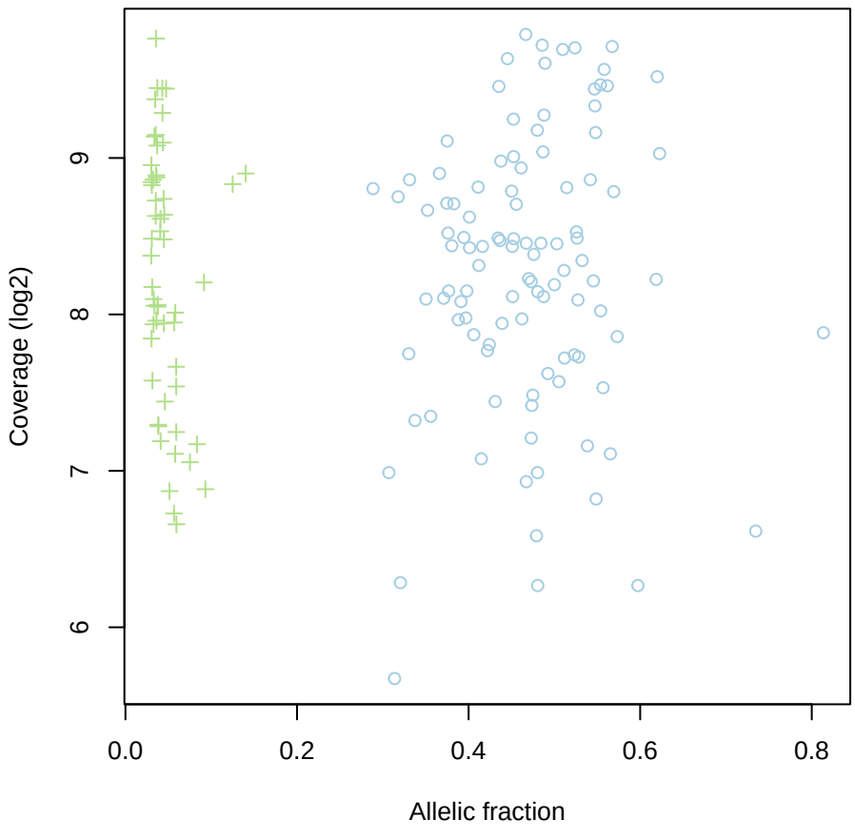

Purity: 0.21  Tumor ploidy: 5.253
0
1
2
3
4
5
6
7
0.0
0.1
0.2
0.3
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

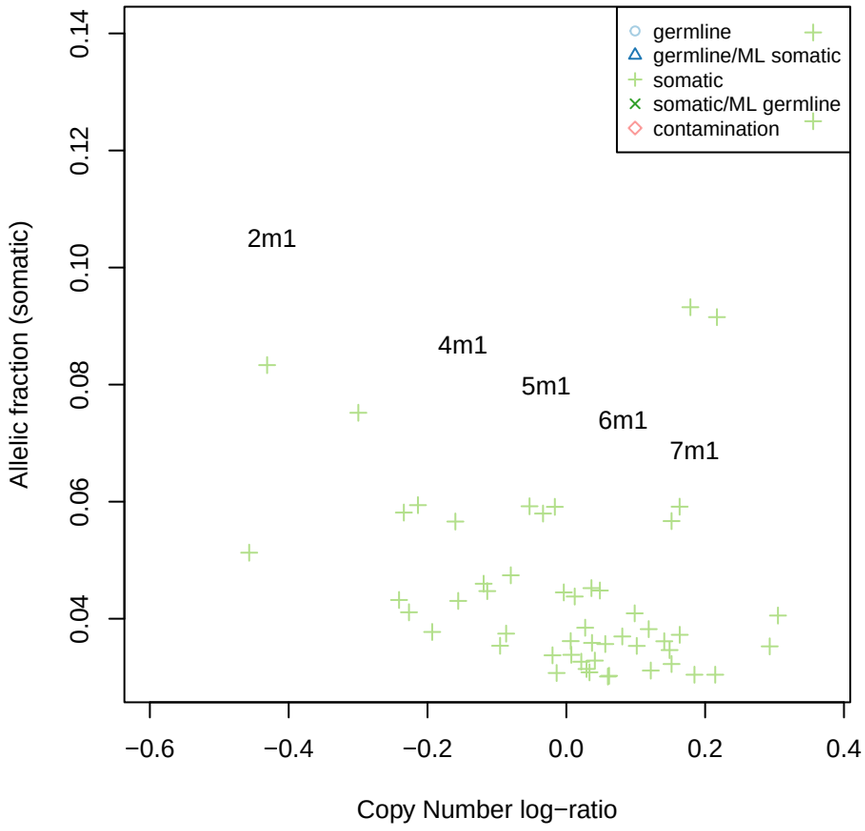

Purity: 0.21 Tumor ploidy: 5.253 SNV log−likelihood: −146.72 GoF: 94.5% Mean coverage: 427;361
1 2 3 4 5 6 7 8 9 10 11 12 13 14 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100
SNV Index

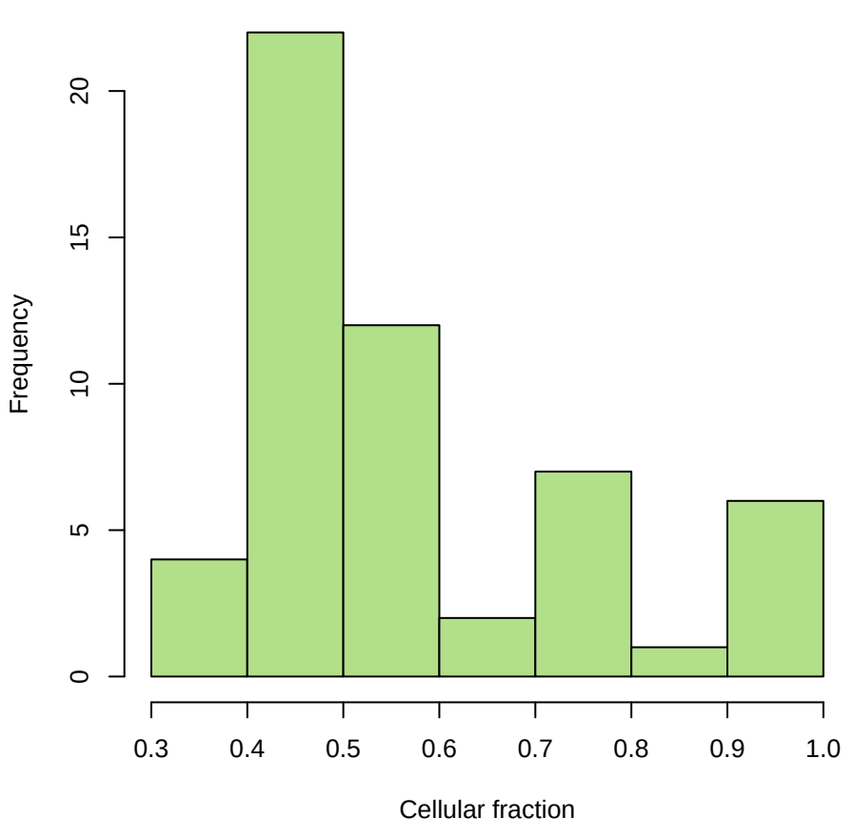

SCNA−fit log−likelihood: −5746.46
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 5 7
0 20 40 60 80 100
SNV Index

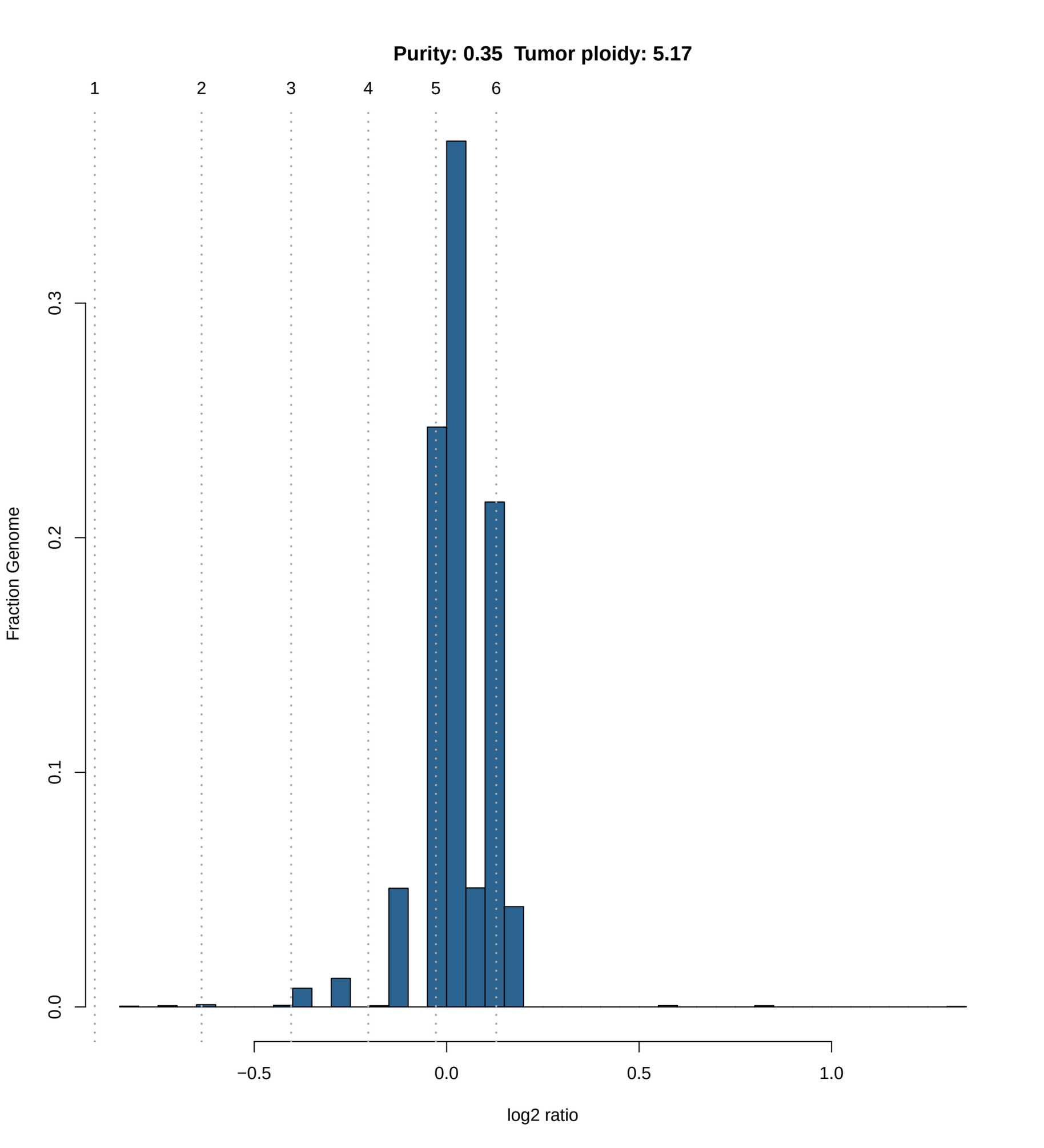

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

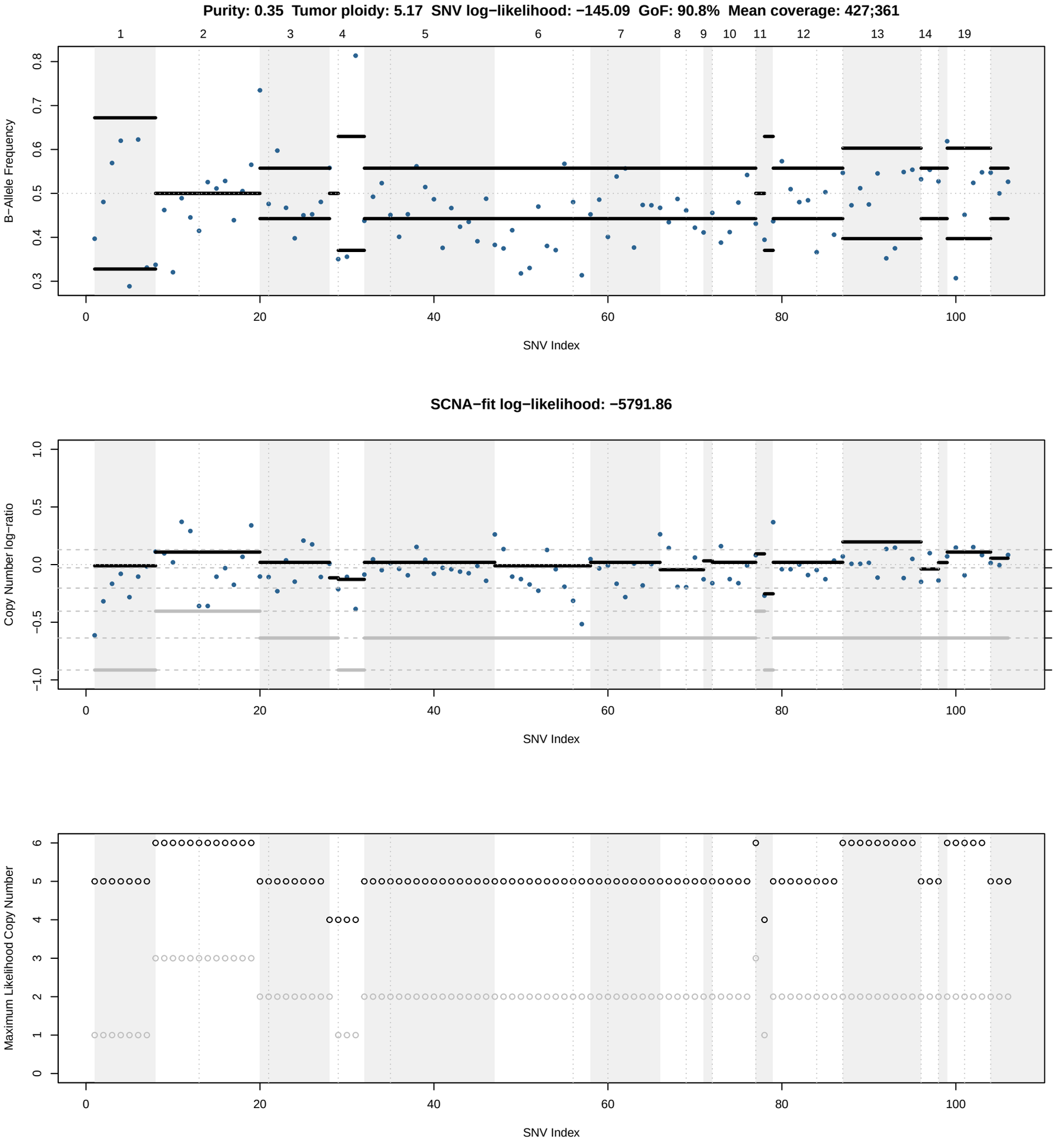

Allelic fraction (germline)
Copy Number log−ratio
5m5
4m4
5m4
4m3
6m4
5m3
7m4
6m3
5m2
7m3
6m2
5m1
3m0
4m0

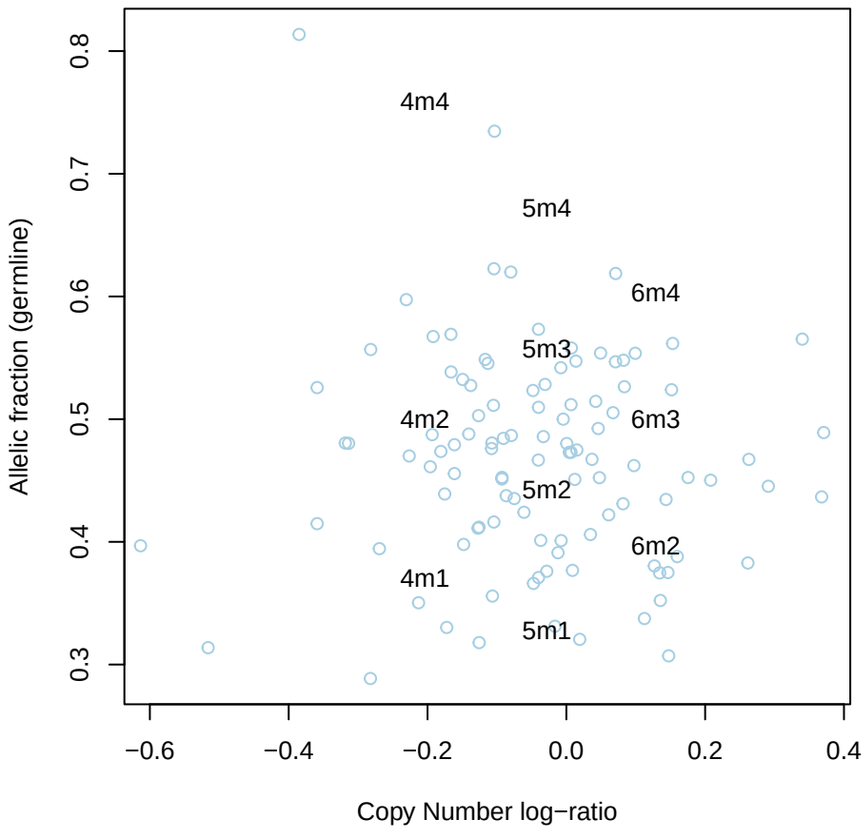

Coverage (log2)
Allelic fraction

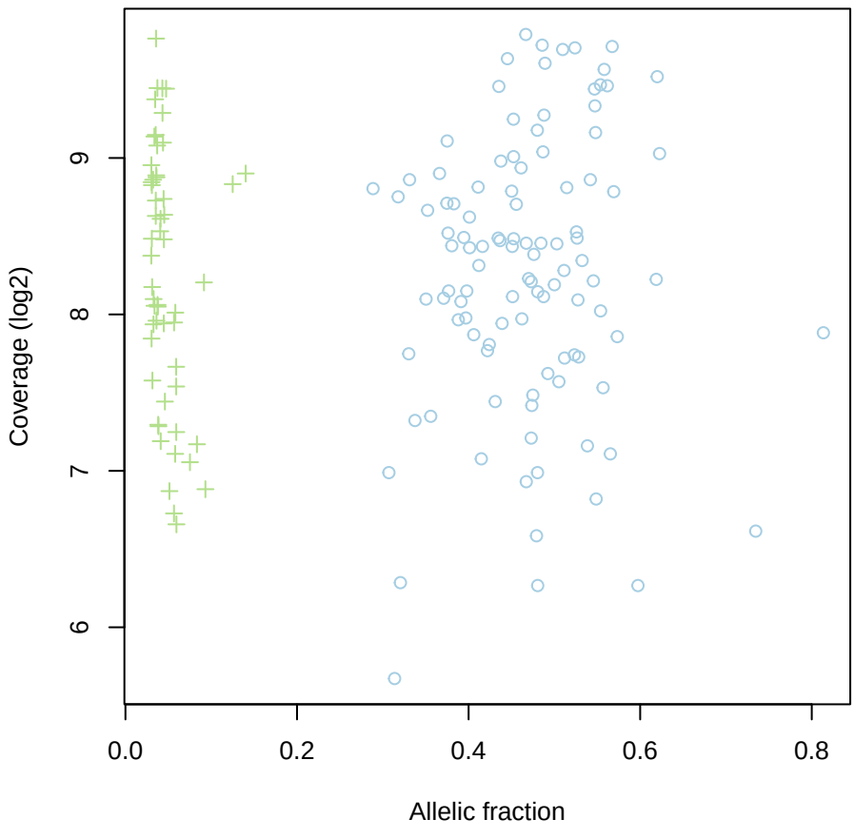

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m1
4m1
5m1
6m1
7m1

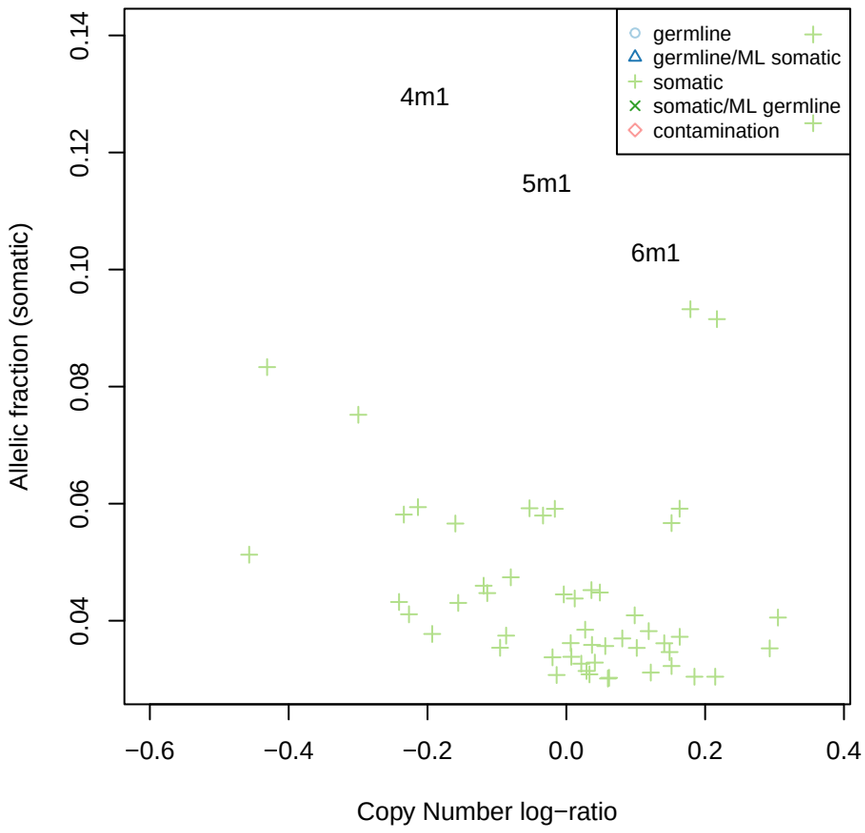

Frequency
Cellular fraction

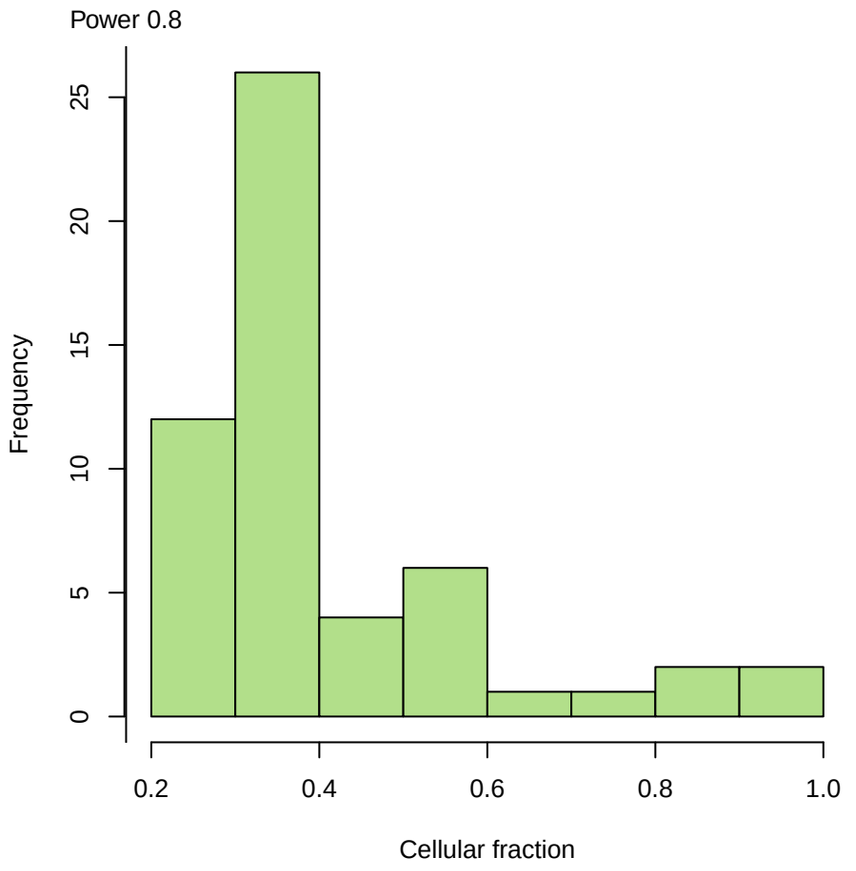

Purity: 0.35  Tumor ploidy: 5.17
1
2
3
4
5
6
0.0
0.1
0.2
0.3
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

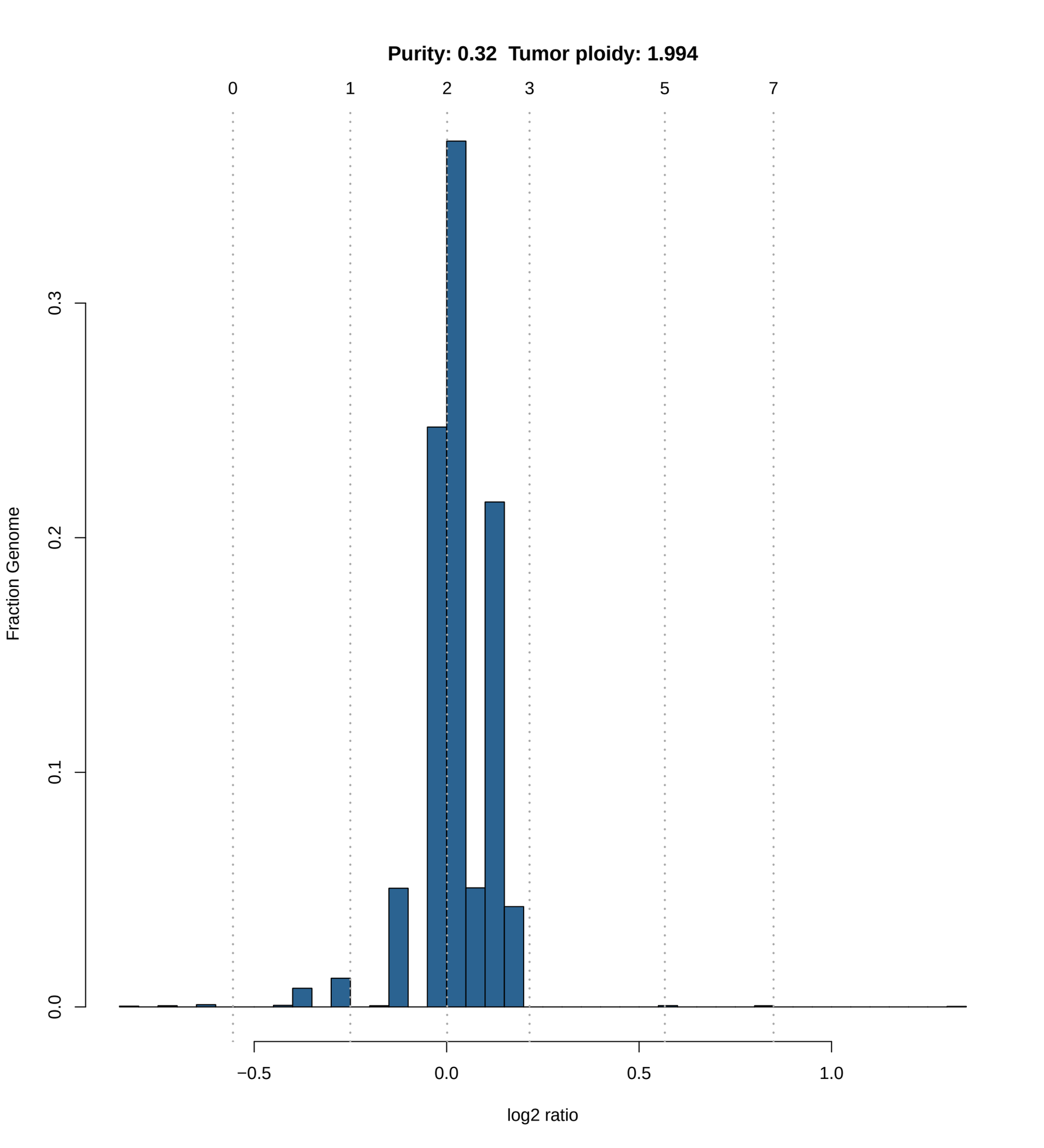

Purity: 0.35 Tumor ploidy: 5.17 SNV log−likelihood: −145.09 GoF: 90.8% Mean coverage: 427;361
1 2 3 4 5 6 7 8 9 10 11 12 13 14 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100
SNV Index
SCNA−fit log−likelihood: −5791.86
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6
0 20 40 60 80 100
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100
SNV Index

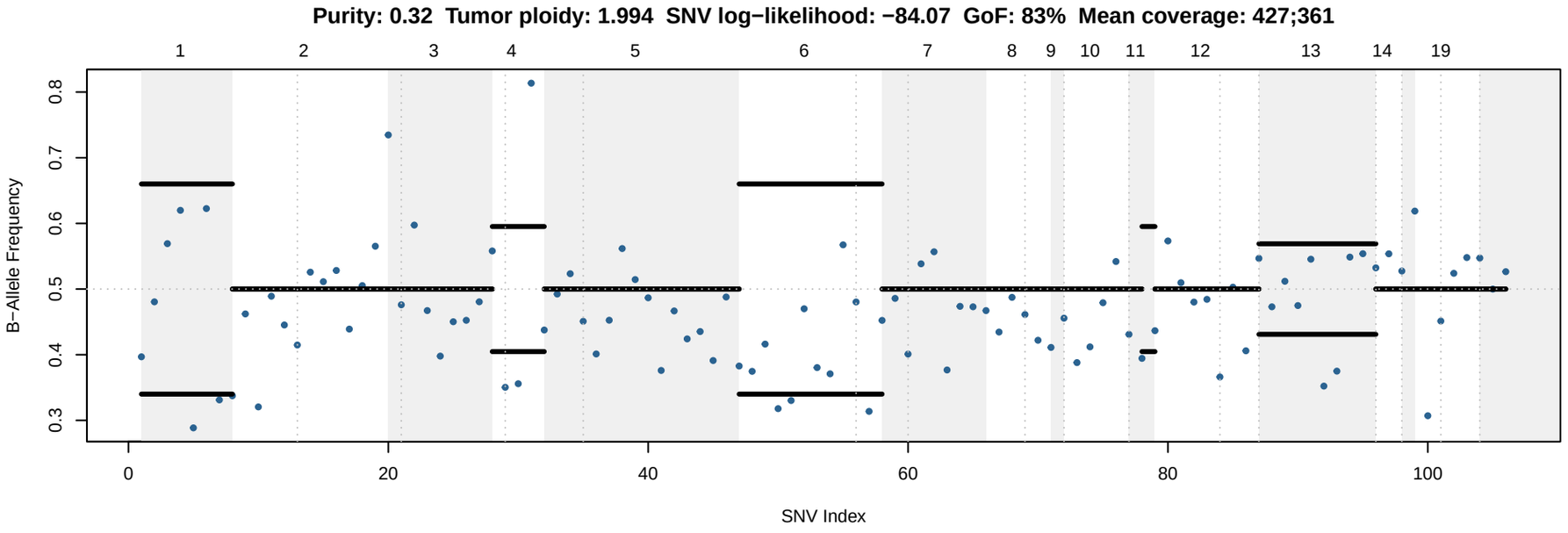

Allelic fraction (germline)
Copy Number log−ratio
4m4
5m4
6m4
5m3
4m2
6m3
5m2
6m2
4m1
5m1

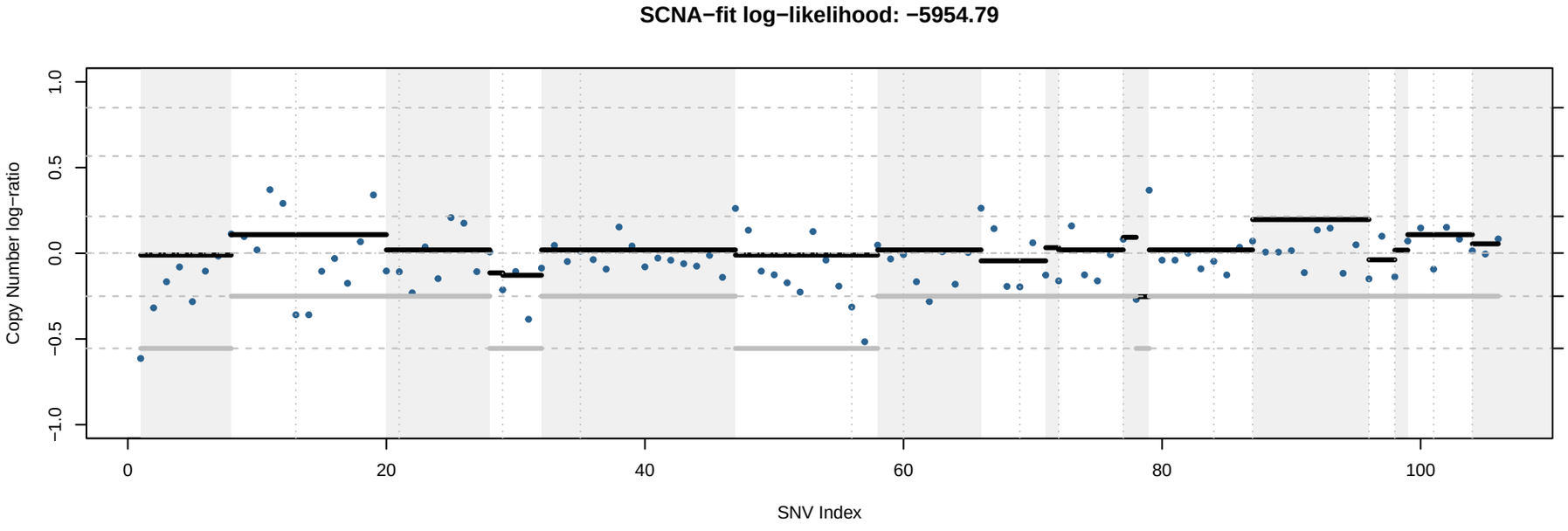

Coverage (log2)
Allelic fraction

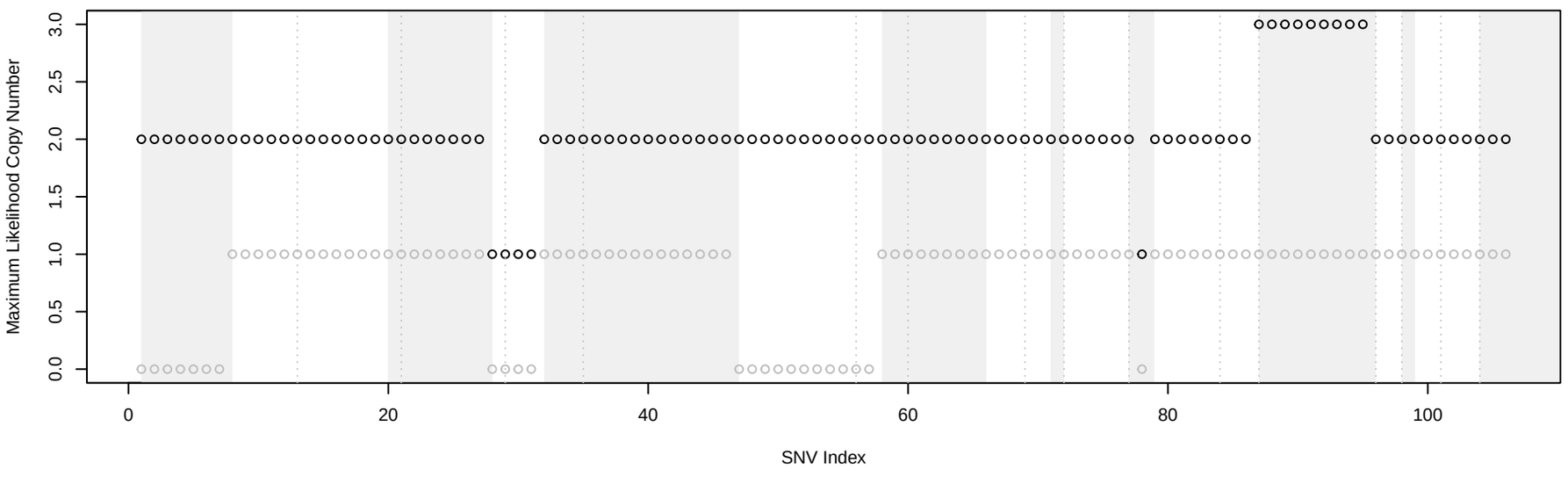

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
4m1
5m1
6m1

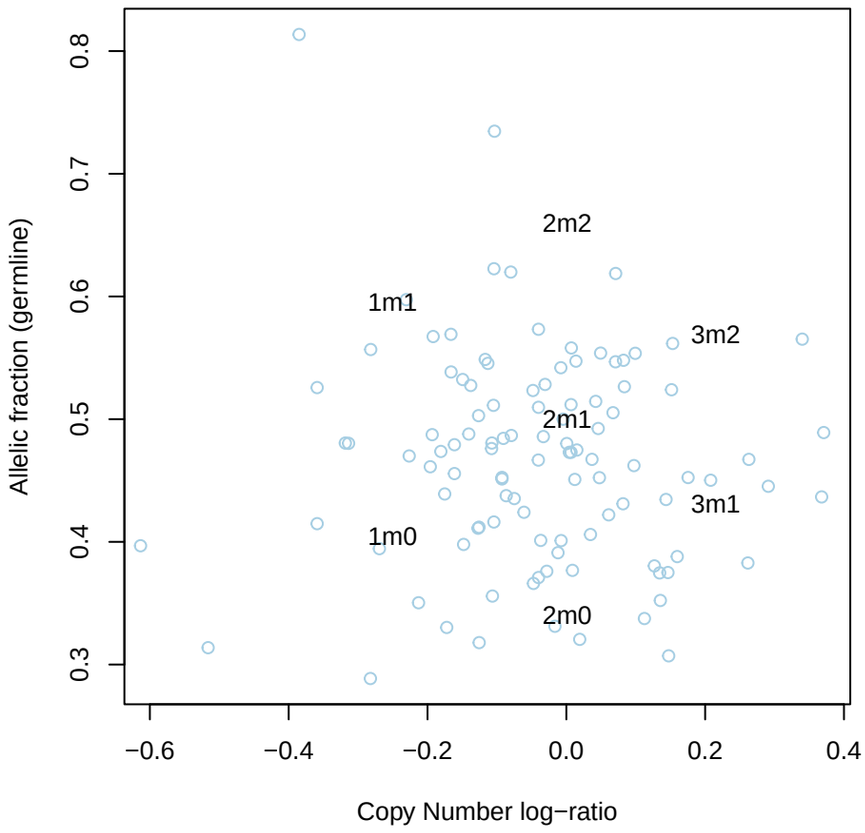

Power 0.8
Frequency
Cellular fraction

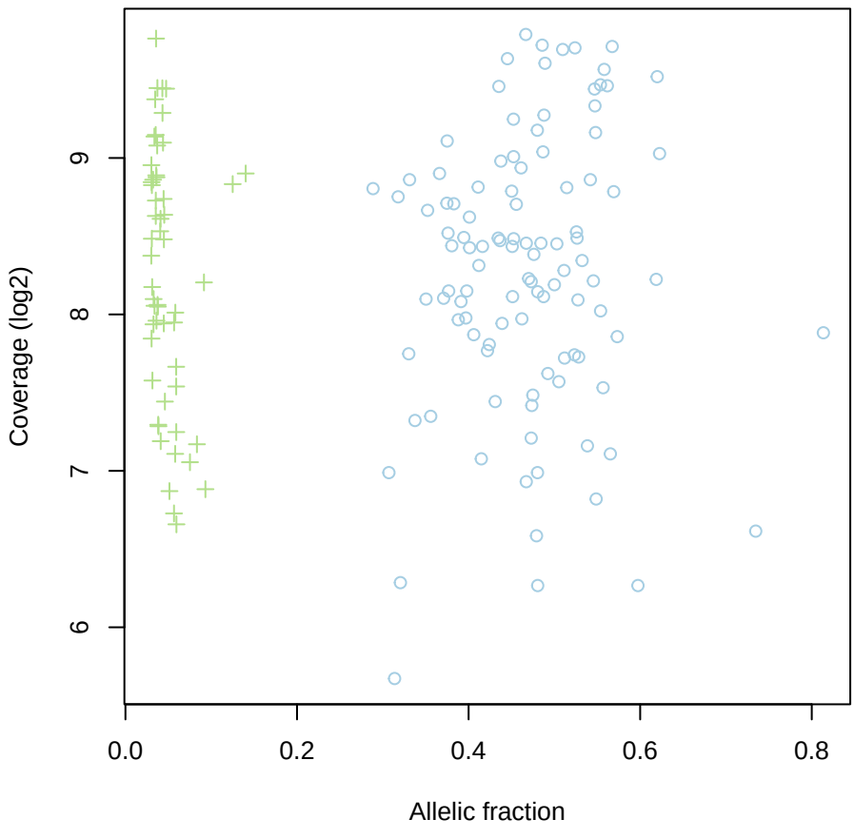

Purity: 0.32  Tumor ploidy: 1.994
0
1
2
3
5
7
0.0
0.1
0.2
0.3
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

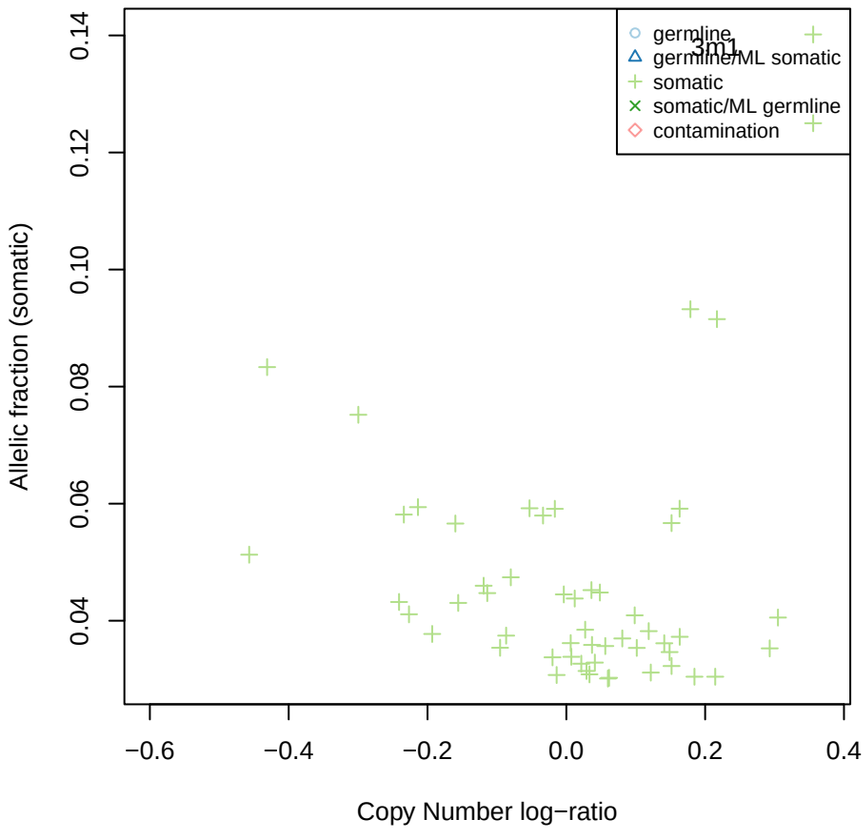

Purity: 0.32 Tumor ploidy: 1.994 SNV log−likelihood: −84.07 GoF: 83% Mean coverage: 427;361
1 2 3 4 5 6 7 8 9 10 11 12 13 14 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100
SNV Index

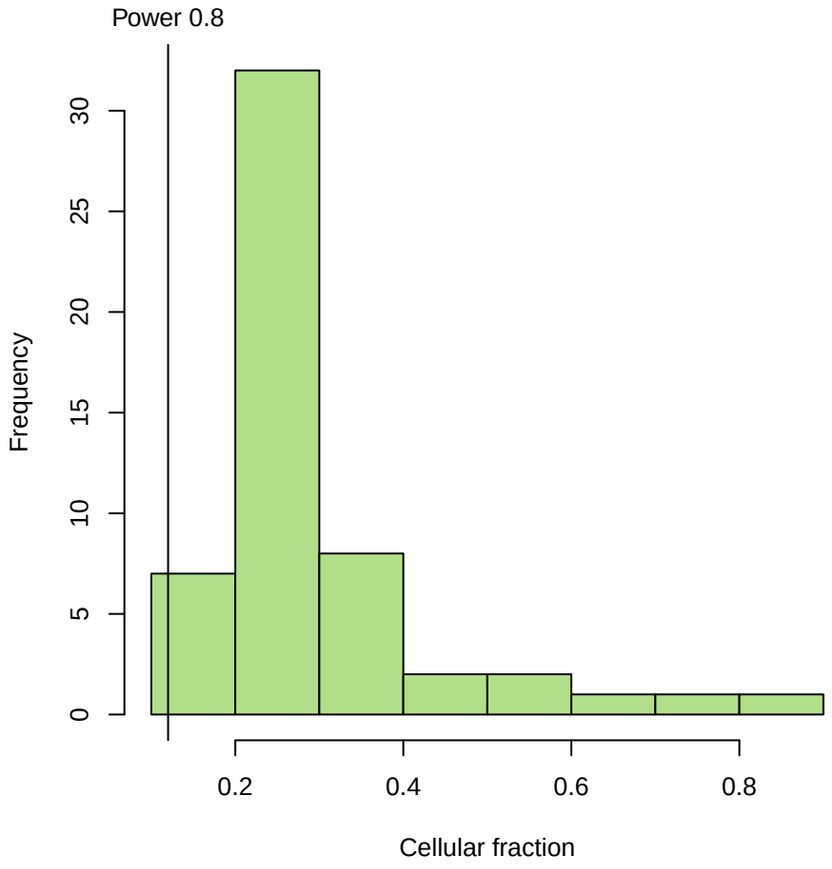

SCNA−fit log−likelihood: −5954.79
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 5 7
0 20 40 60 80 100
SNV Index

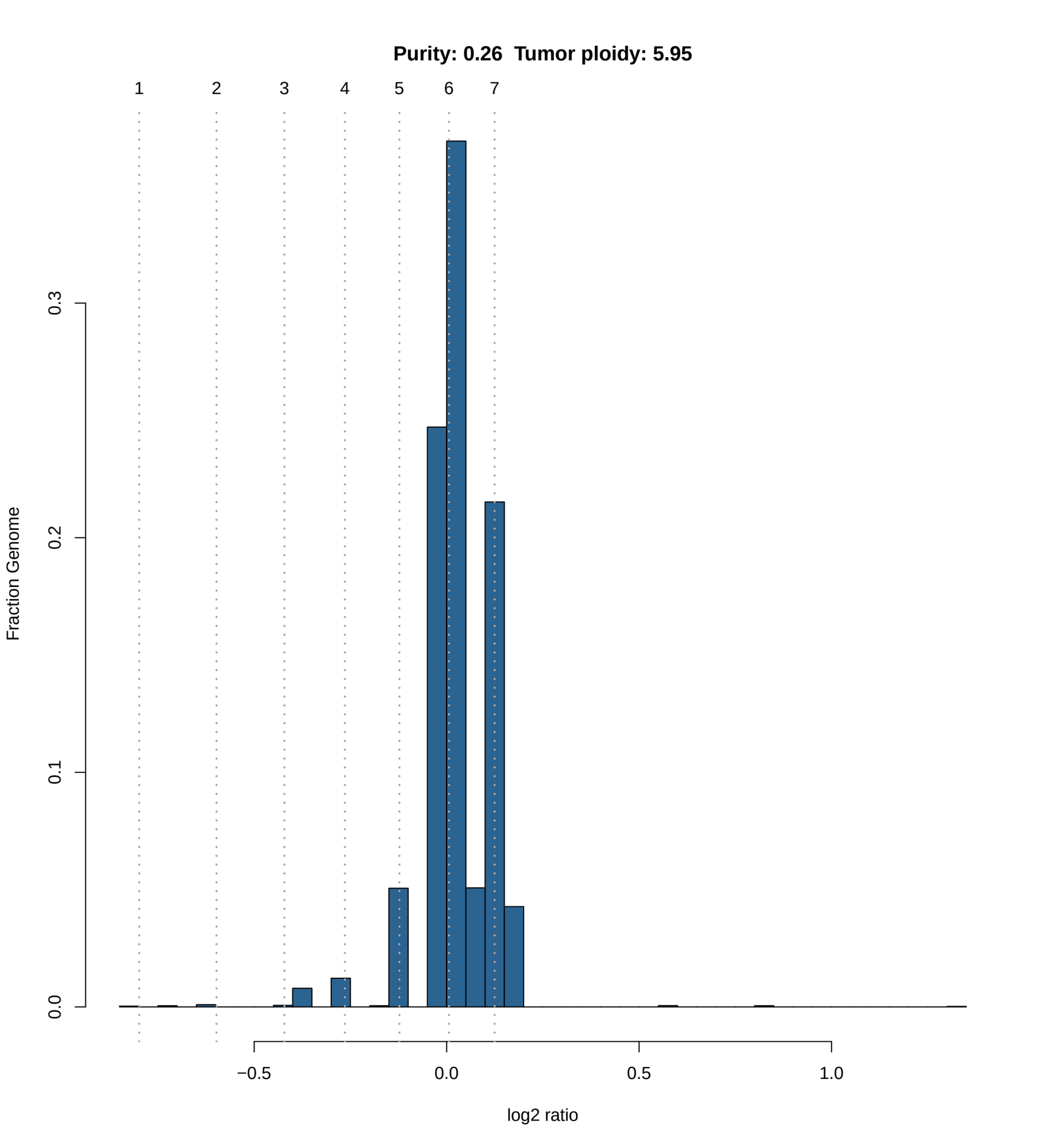

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100
SNV Index

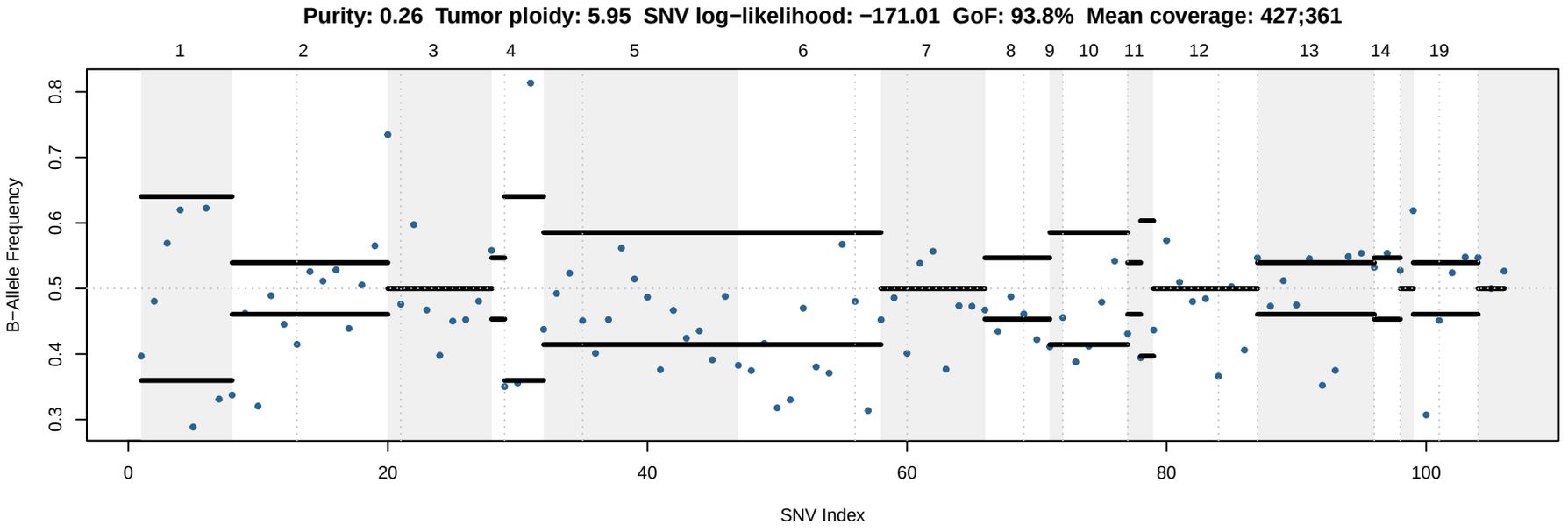

Allelic fraction (germline)
Copy Number log−ratio
2m2
1m1
3m2
2m1
3m1
1m0
2m0

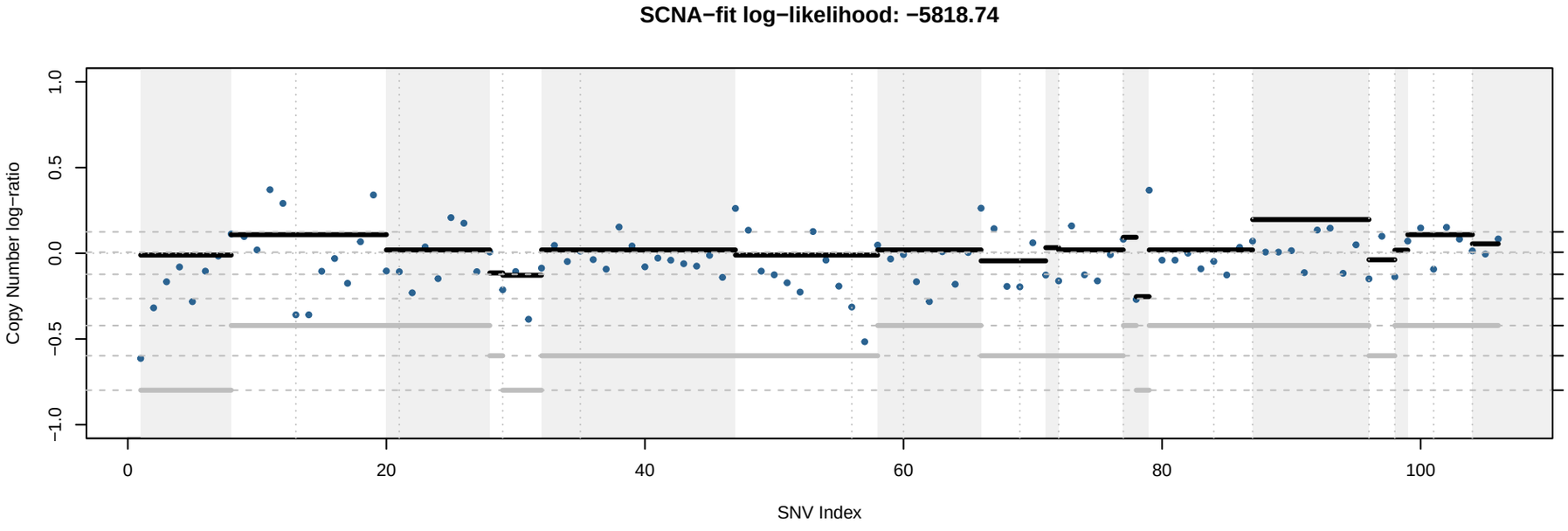

Coverage (log2)
Allelic fraction

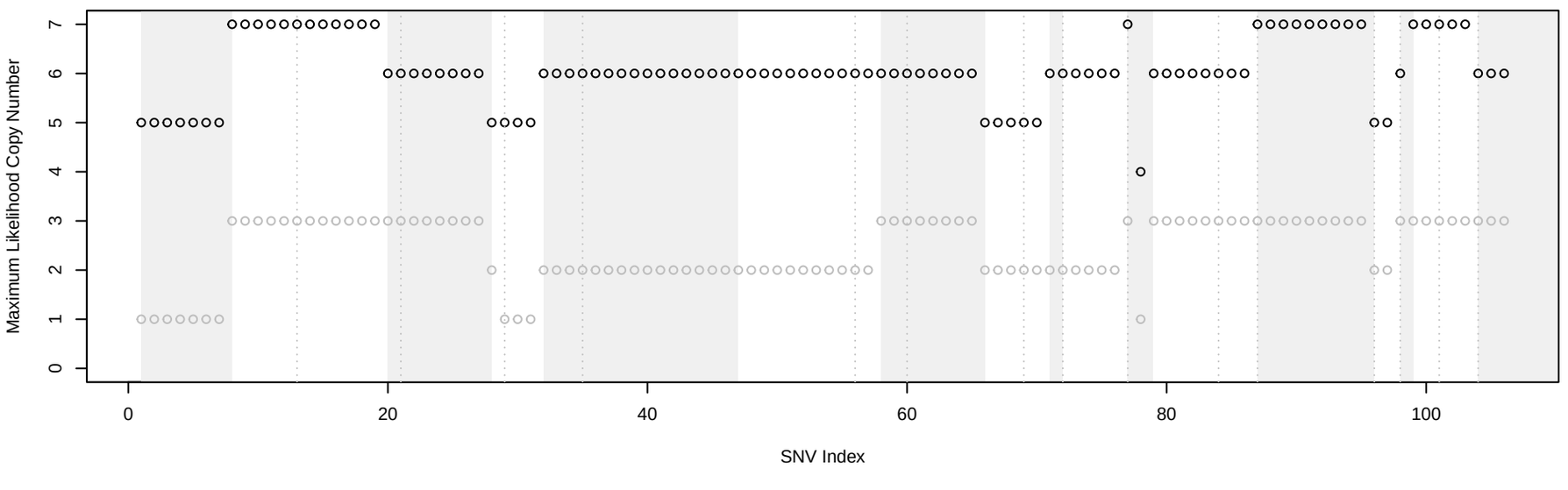

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1

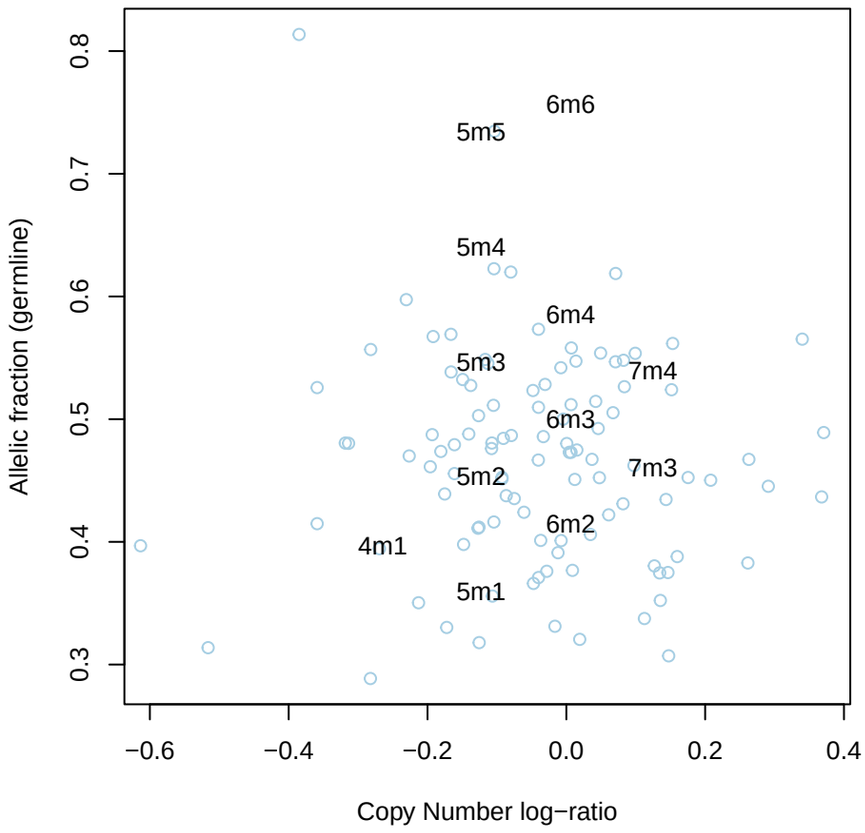

Power 0.8
Frequency
Cellular fraction

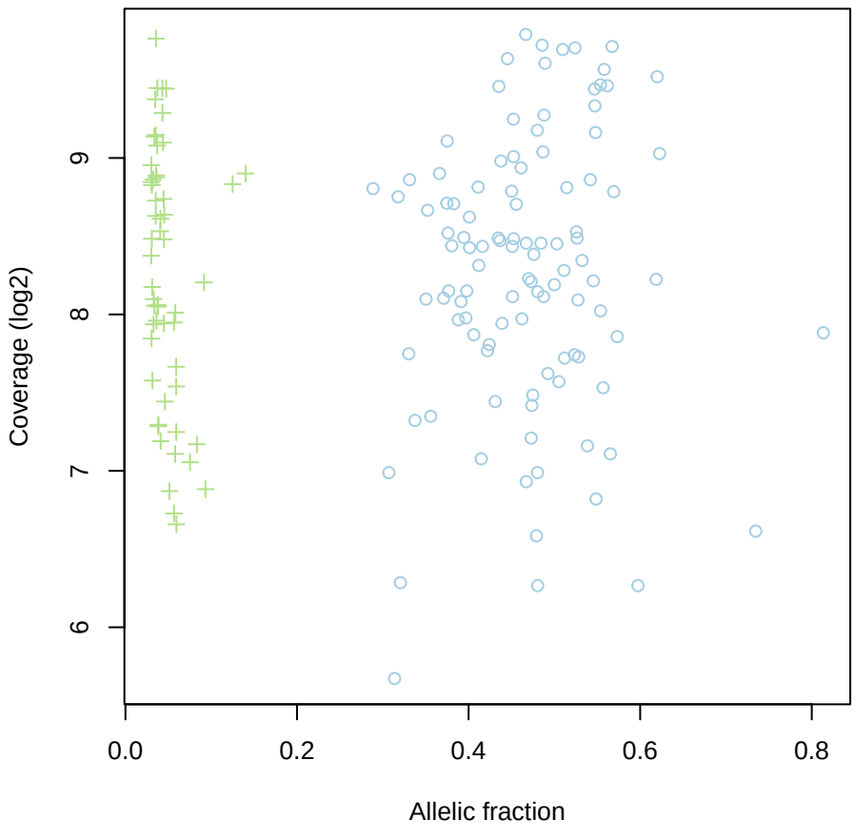

Purity: 0.26  Tumor ploidy: 5.95
1
2
3
4
5
6
7
0.0
0.1
0.2
0.3
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

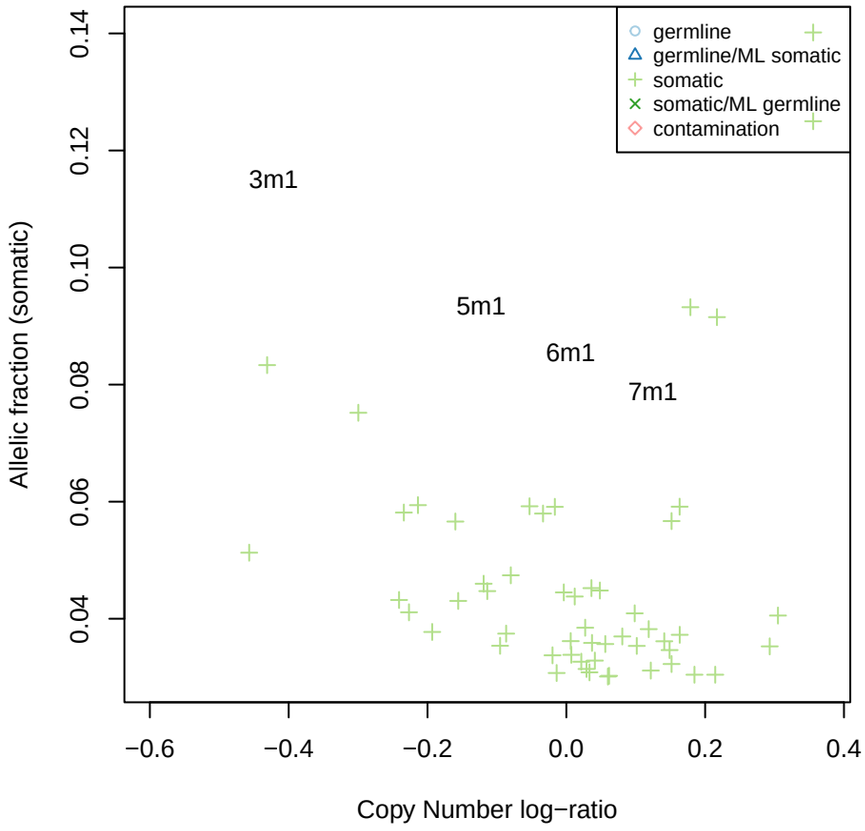

Purity: 0.26 Tumor ploidy: 5.95 SNV log−likelihood: −171.01 GoF: 93.8% Mean coverage: 427;361
1 2 3 4 5 6 7 8 9 10 11 12 13 14 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100
SNV Index

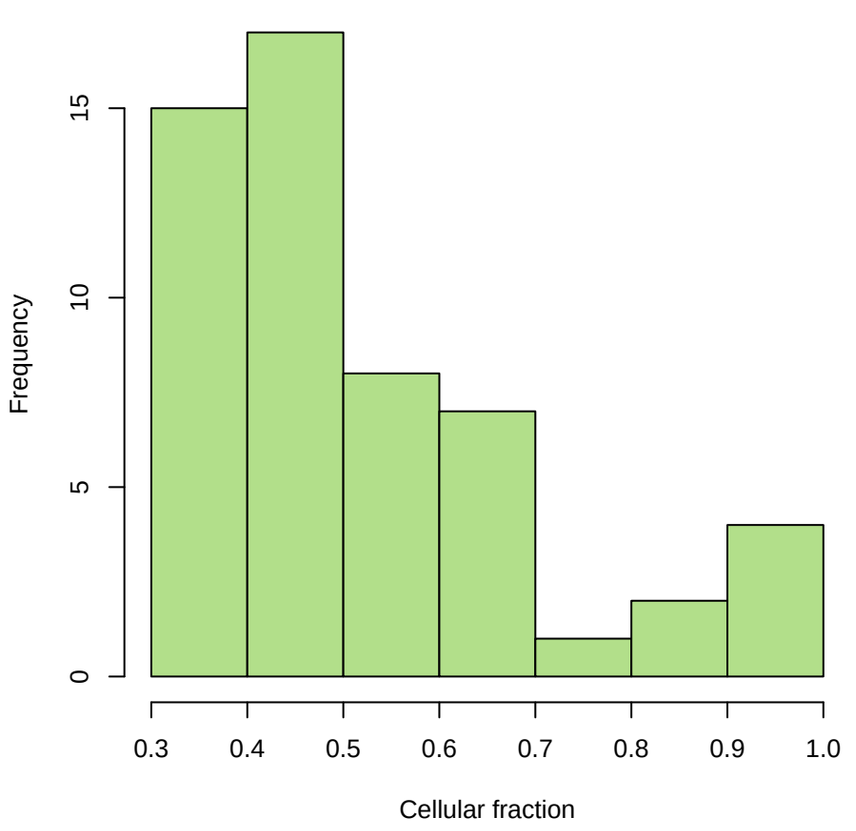

SCNA−fit log−likelihood: −5818.74
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 6
0 20 40 60 80 100
SNV Index

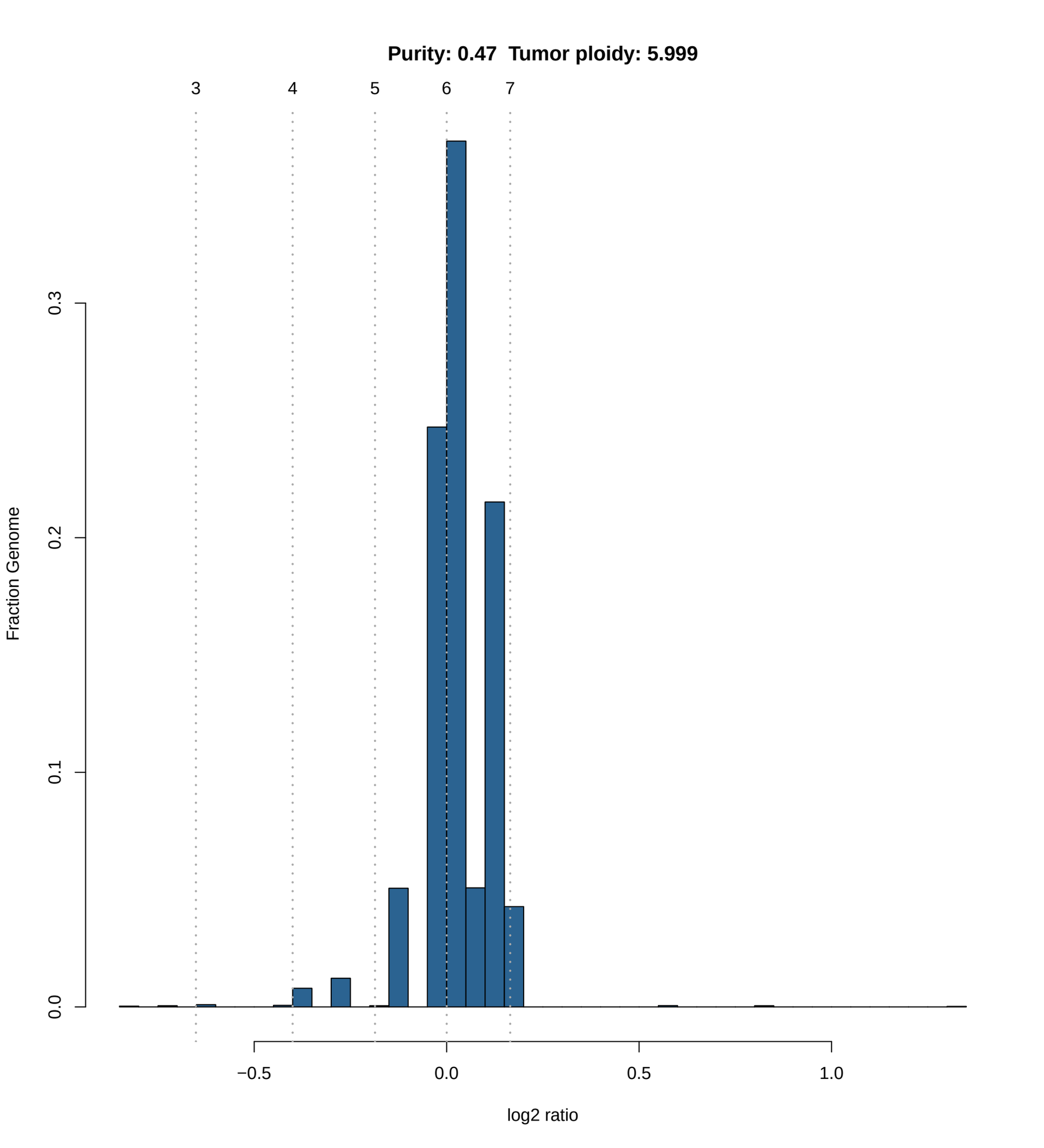

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

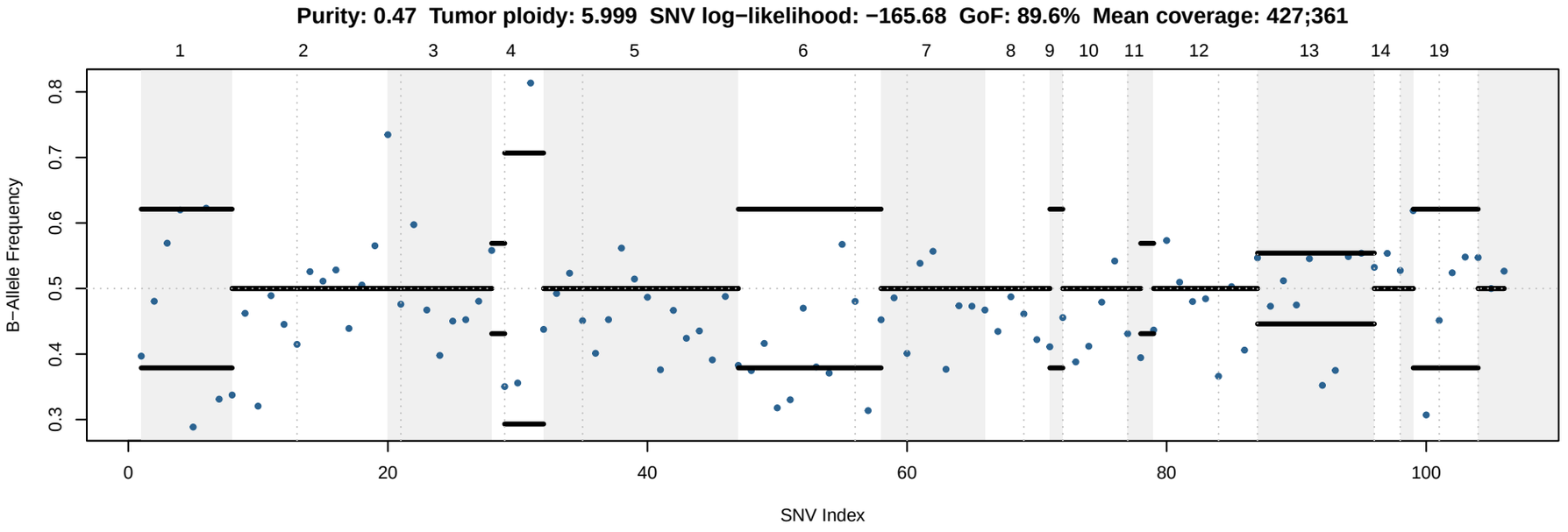

Allelic fraction (germline)
Copy Number log−ratio
6m6
5m5
5m4
6m4
5m3
7m4
6m3
7m3
5m2
6m2
4m1
5m1

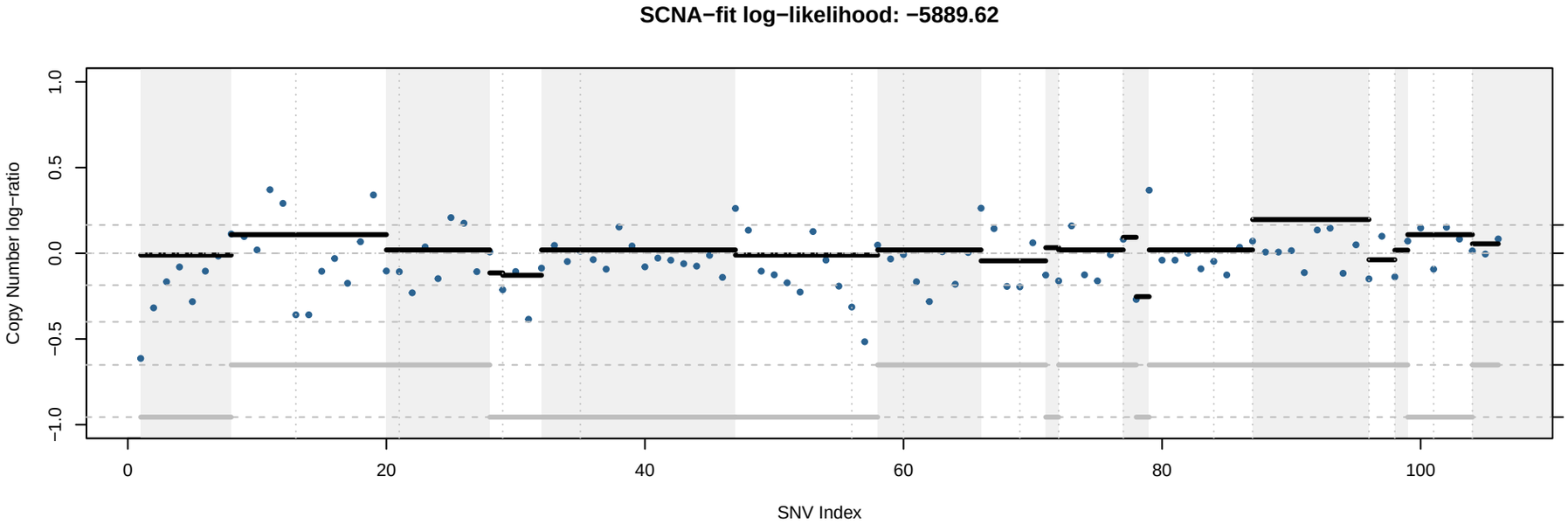

Coverage (log2)
Allelic fraction

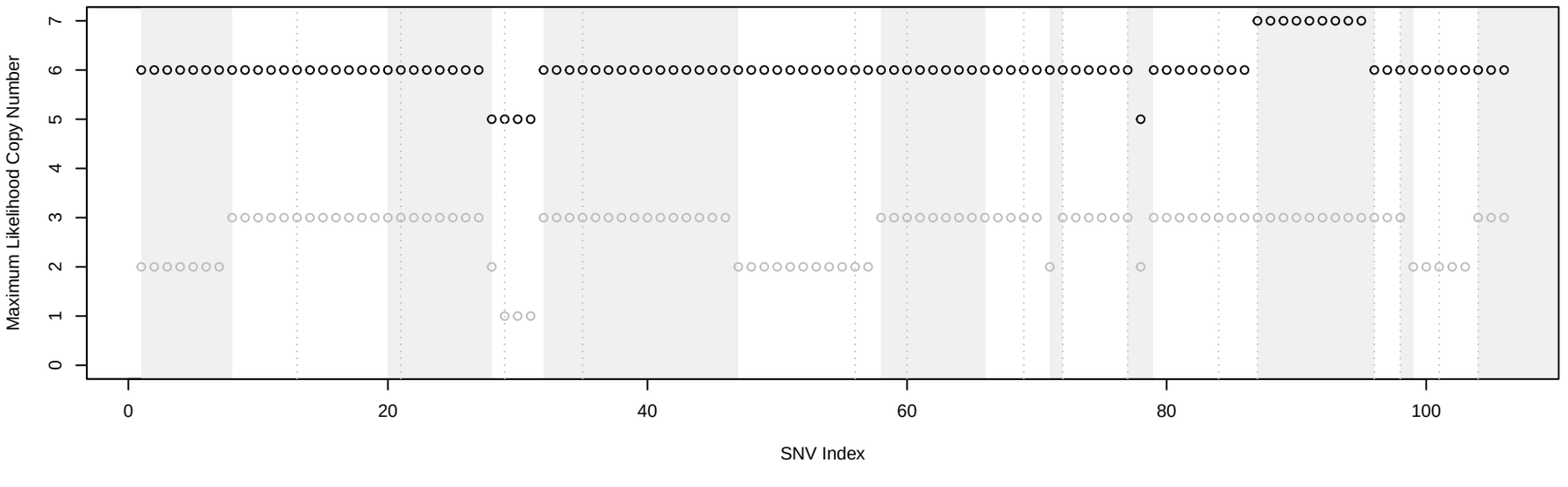

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m1
5m1
6m1
7m1

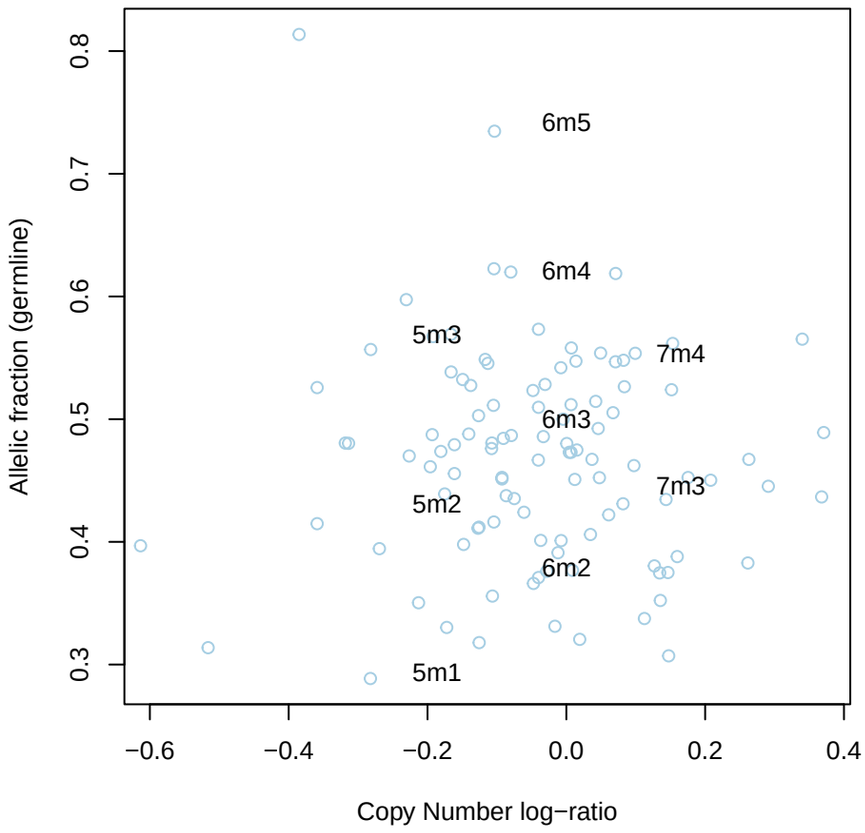

Frequency
Cellular fraction

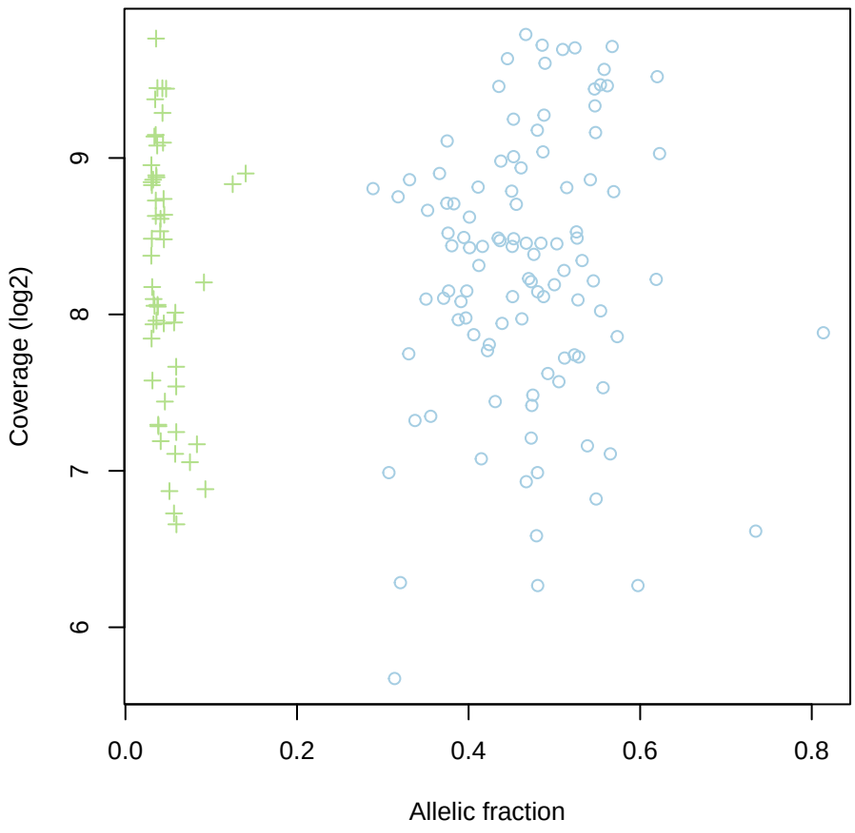

Purity: 0.47  Tumor ploidy: 5.999
3
4
5
6
7
0.0
0.1
0.2
0.3
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

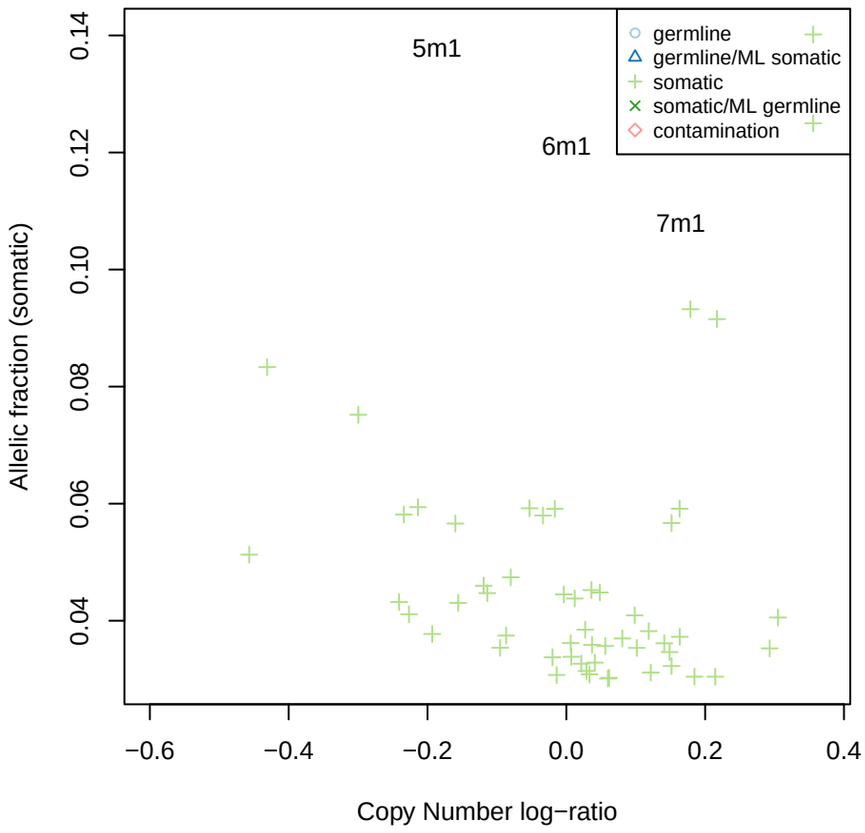

Purity: 0.47 Tumor ploidy: 5.999 SNV log−likelihood: −165.68 GoF: 89.6% Mean coverage: 427;361
1 2 3 4 5 6 7 8 9 10 11 12 13 14 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100
SNV Index

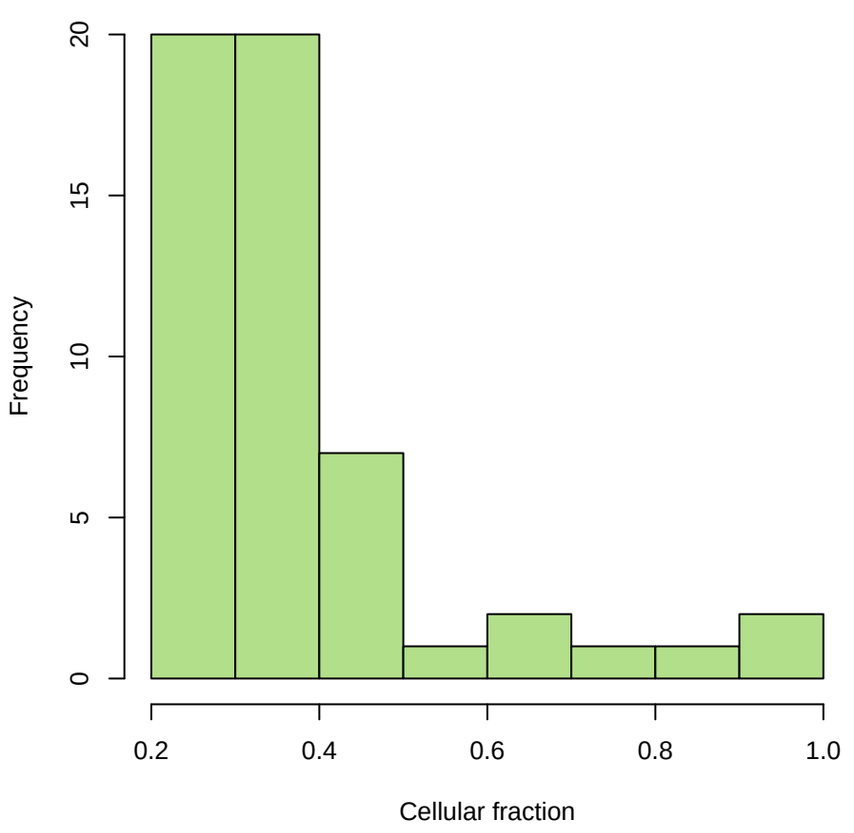

SCNA−fit log−likelihood: −5889.62
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

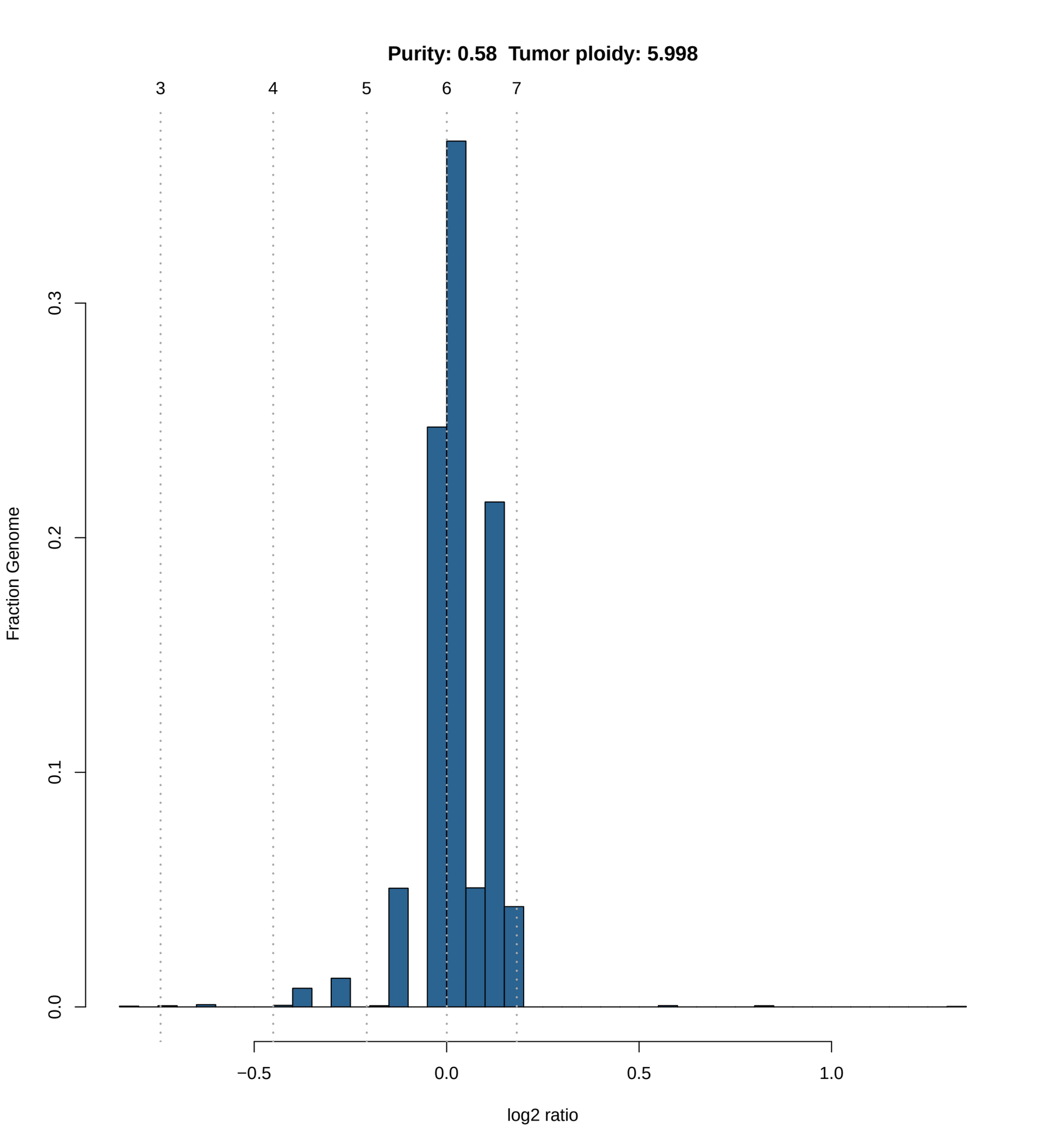

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

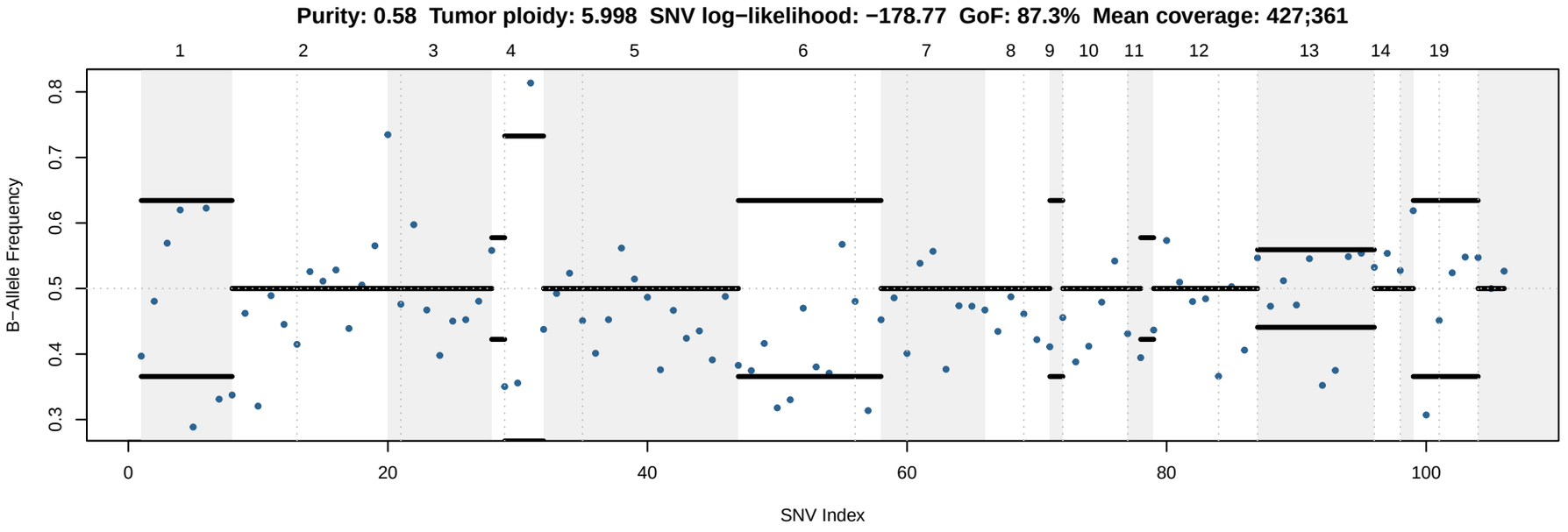

Allelic fraction (germline)
Copy Number log−ratio
6m5
6m4
5m3
7m4
6m3
7m3
5m2
6m2
5m1

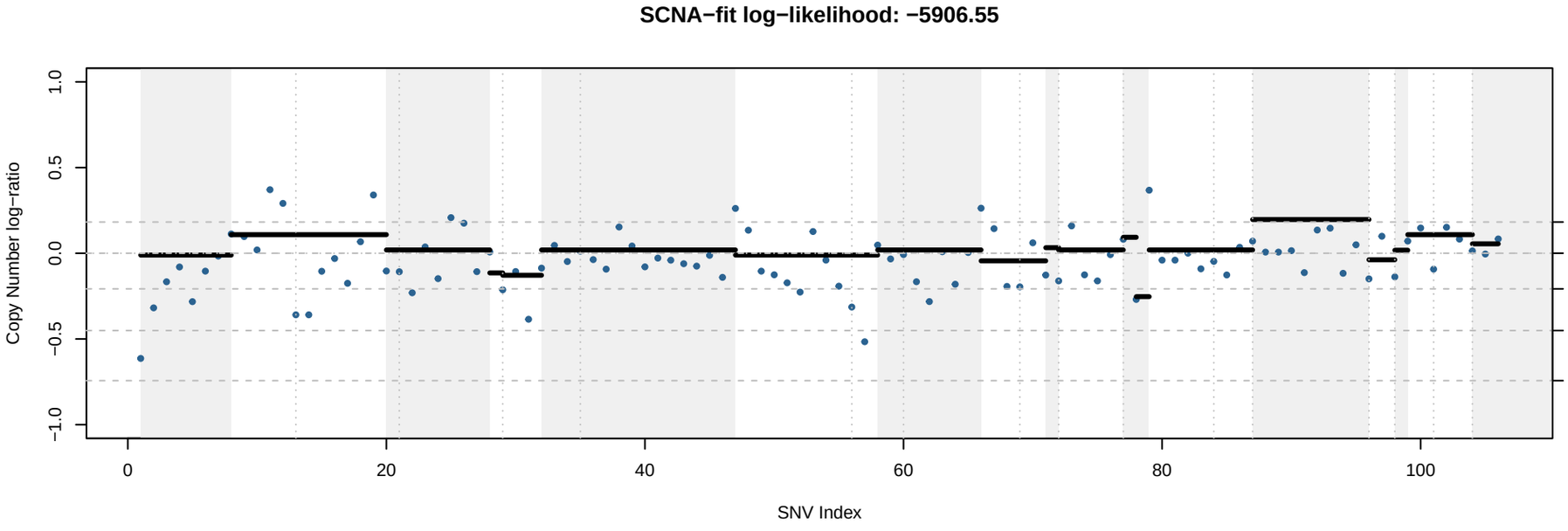

Coverage (log2)
Allelic fraction

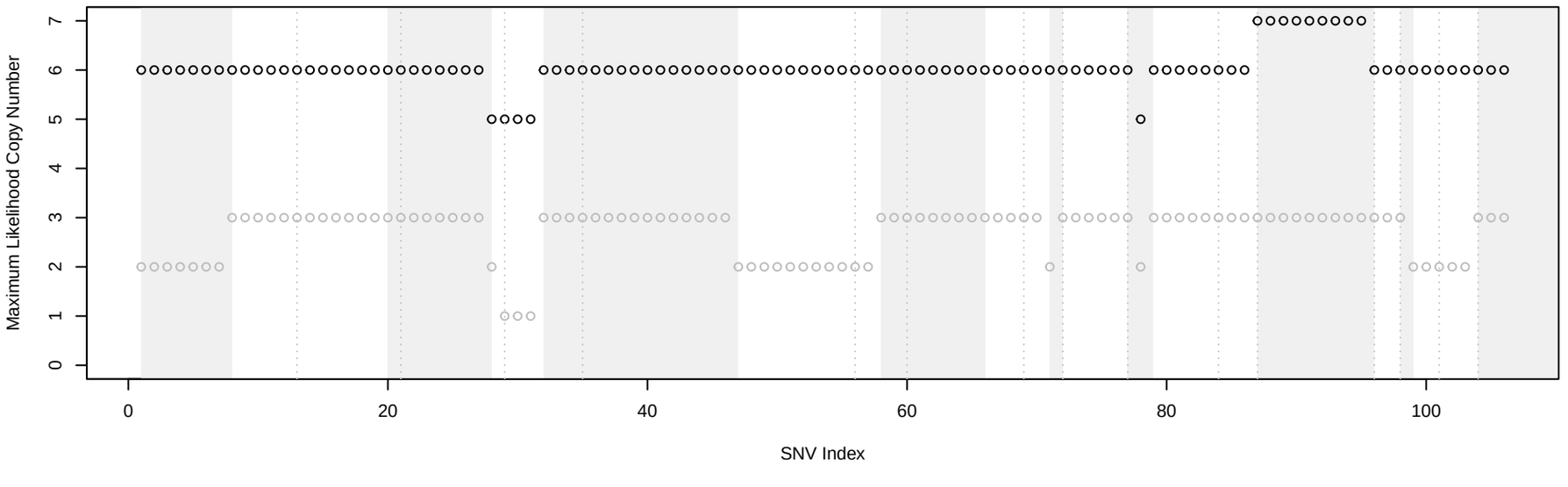

Allelic fraction (somatic)
Copy Number log−ratio
5m1
6m1
7m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

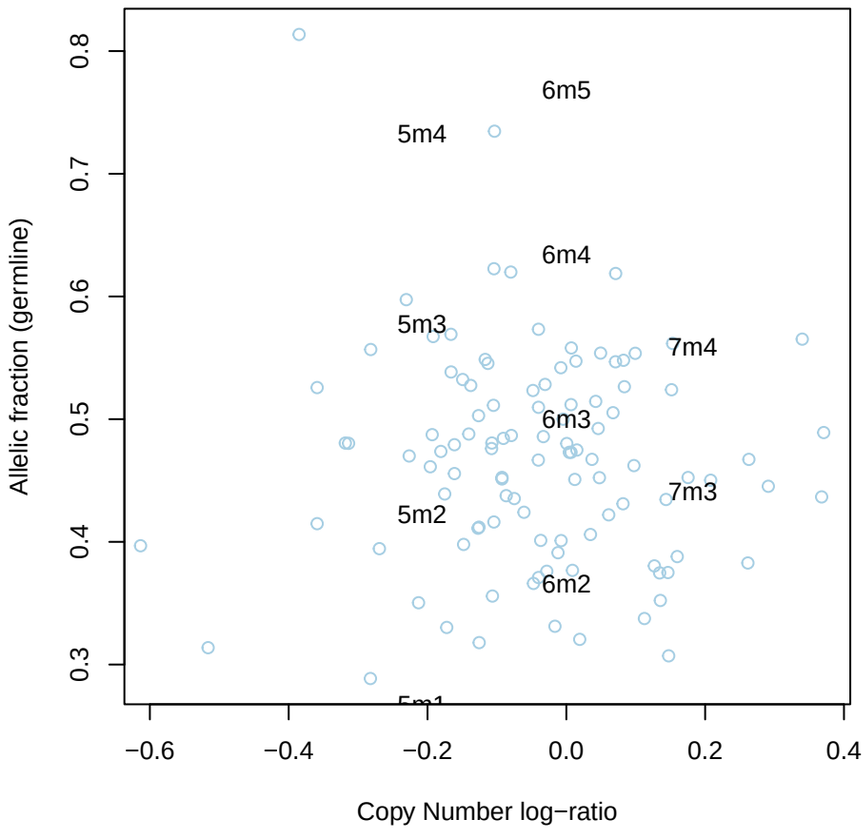

Frequency
Cellular fraction

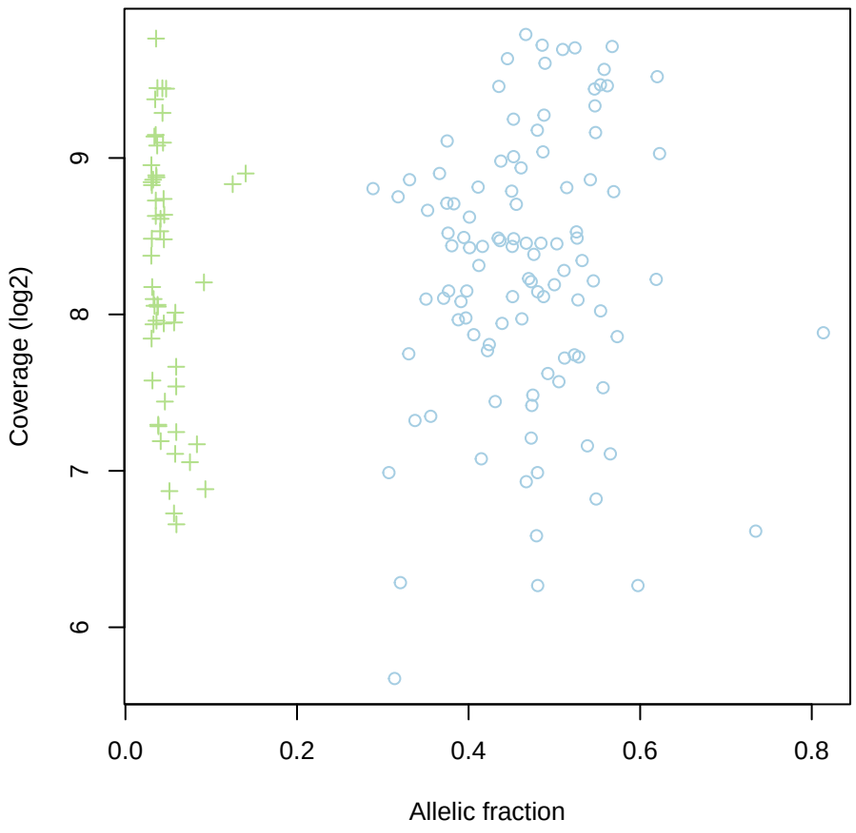

Purity: 0.58  Tumor ploidy: 5.998
3
4
5
6
7
0.0
0.1
0.2
0.3
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

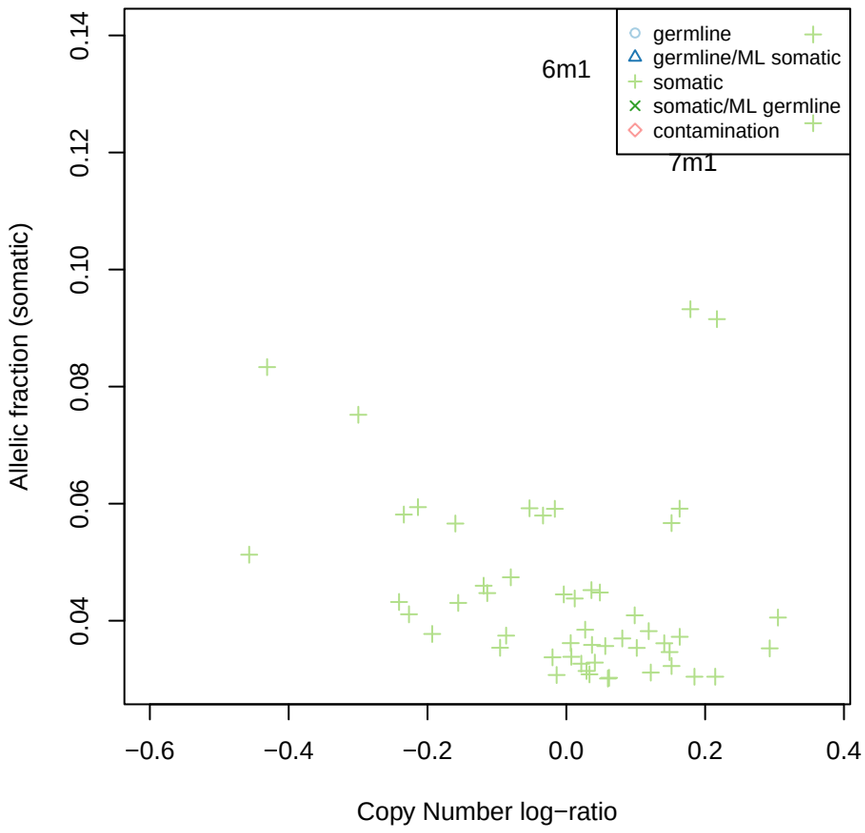

Purity: 0.58 Tumor ploidy: 5.998 SNV log−likelihood: −178.77 GoF: 87.3% Mean coverage: 427;361
1 2 3 4 5 6 7 8 9 10 11 12 13 14 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100
SNV Index

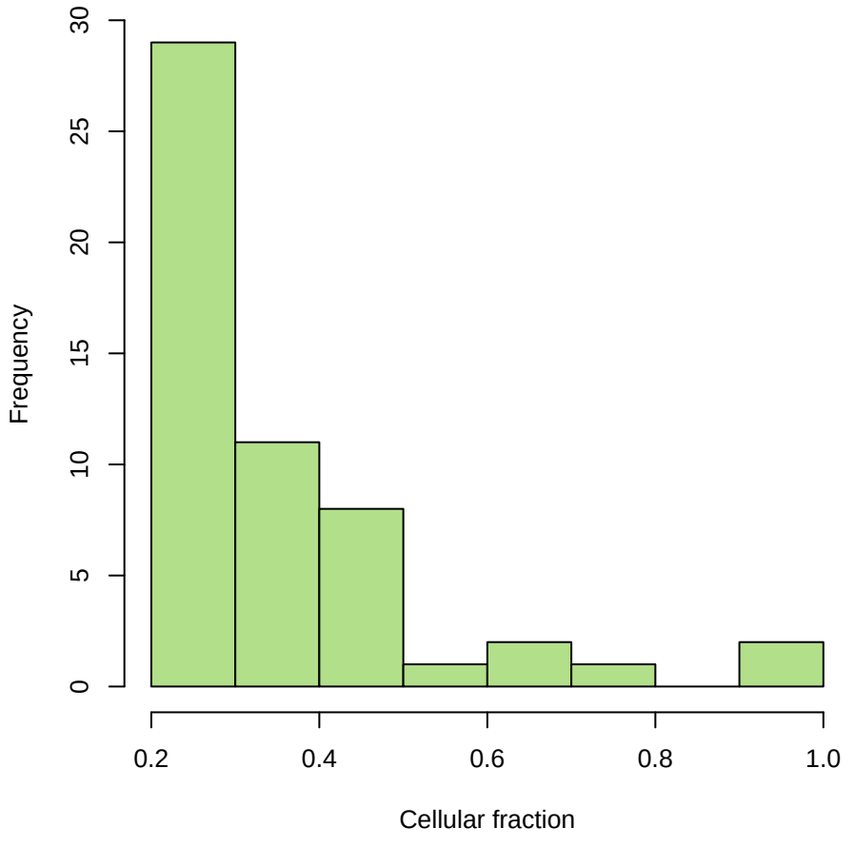

SCNA−fit log−likelihood: −5906.55
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 20 40 60 80 100
SNV Index

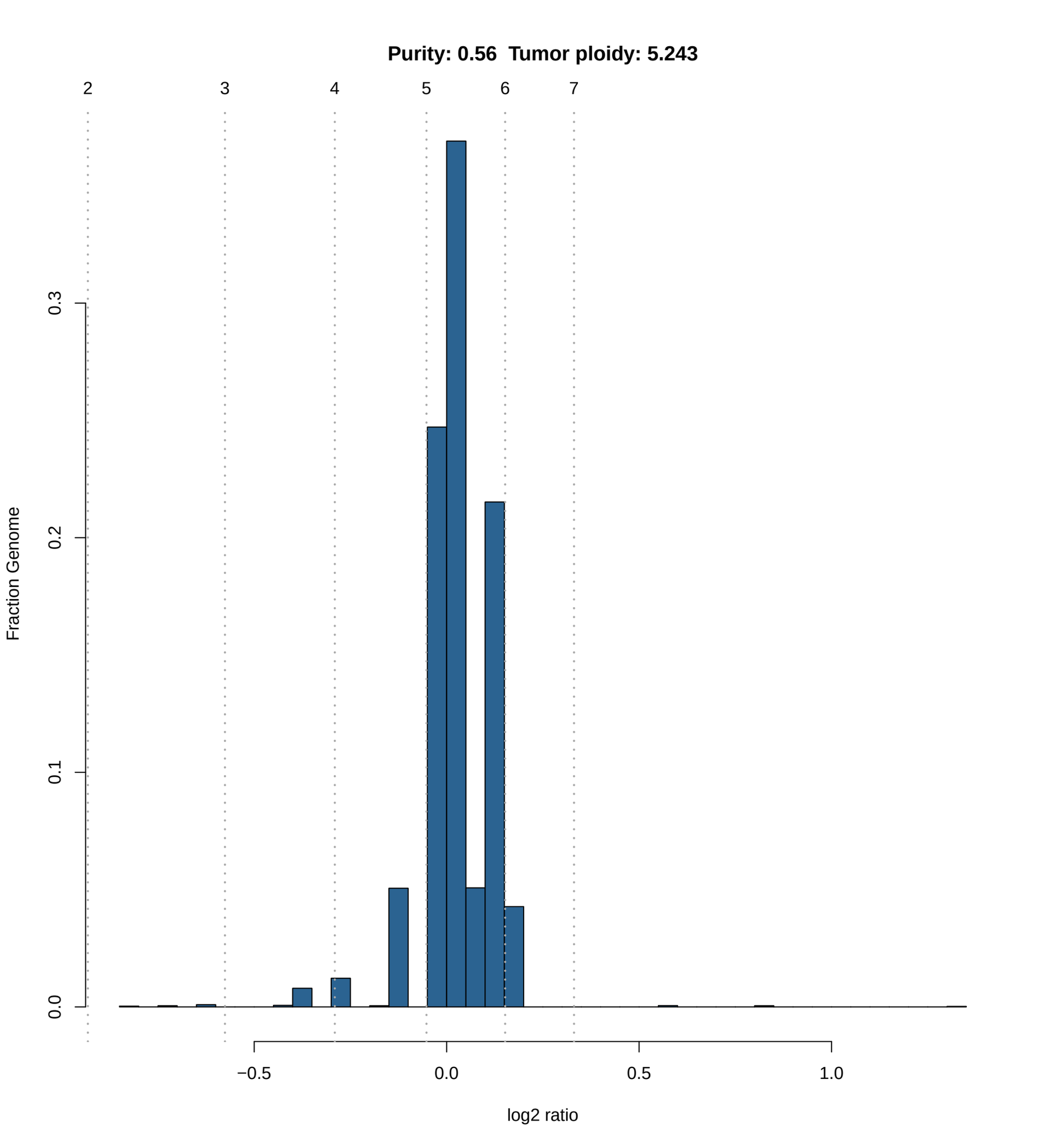

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

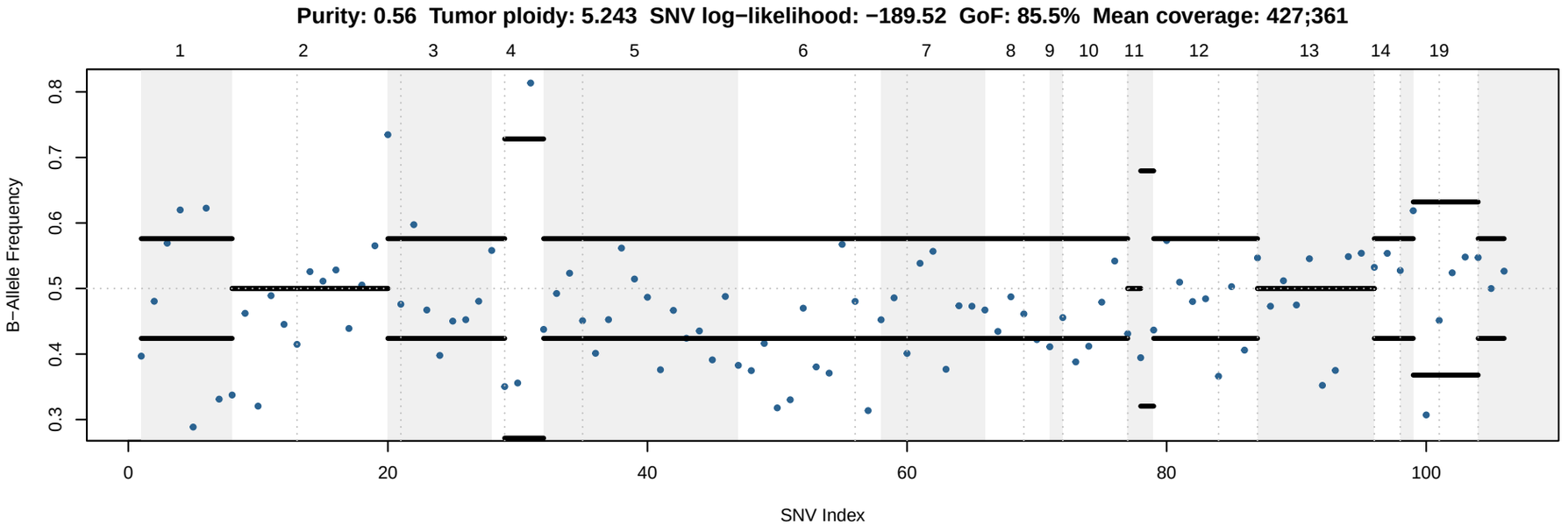

Allelic fraction (germline)
Copy Number log−ratio
6m5
5m4
6m4
5m3
7m4
6m3
7m3
5m2
6m2
5m1

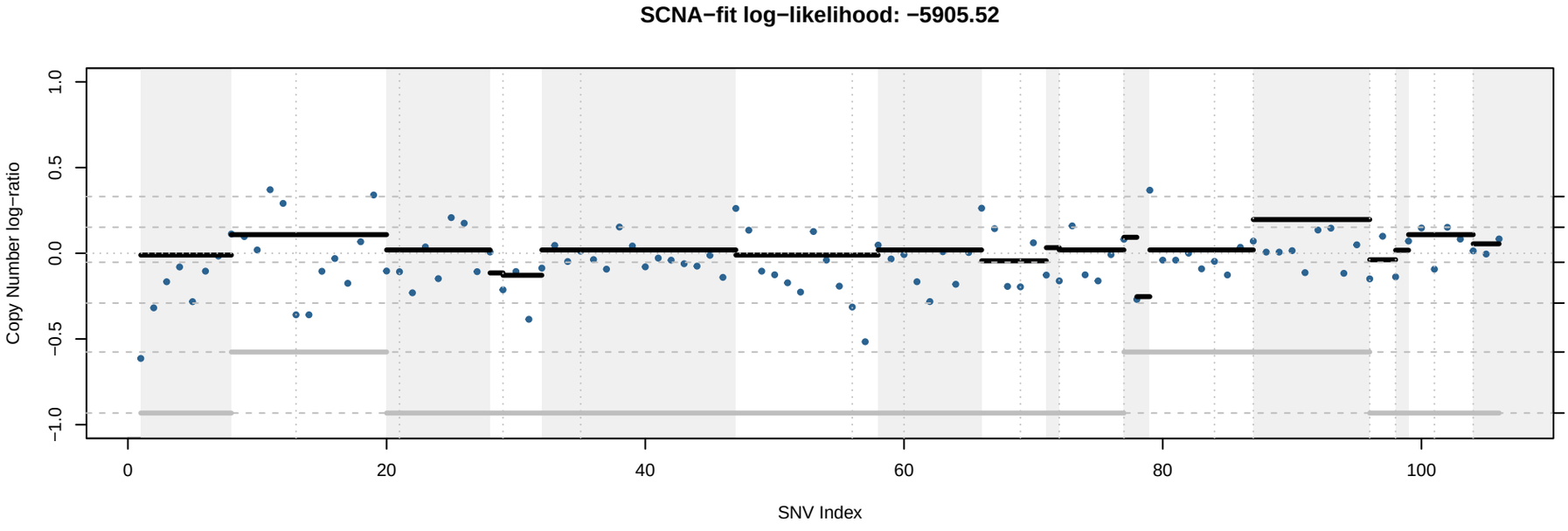

Coverage (log2)
Allelic fraction

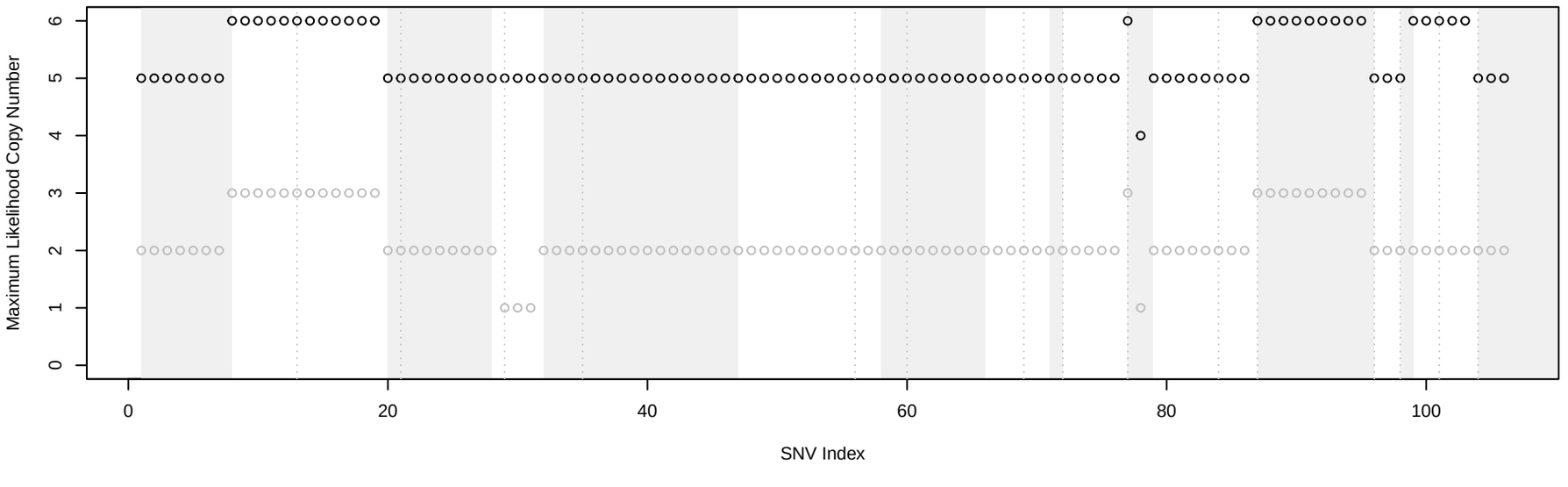

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

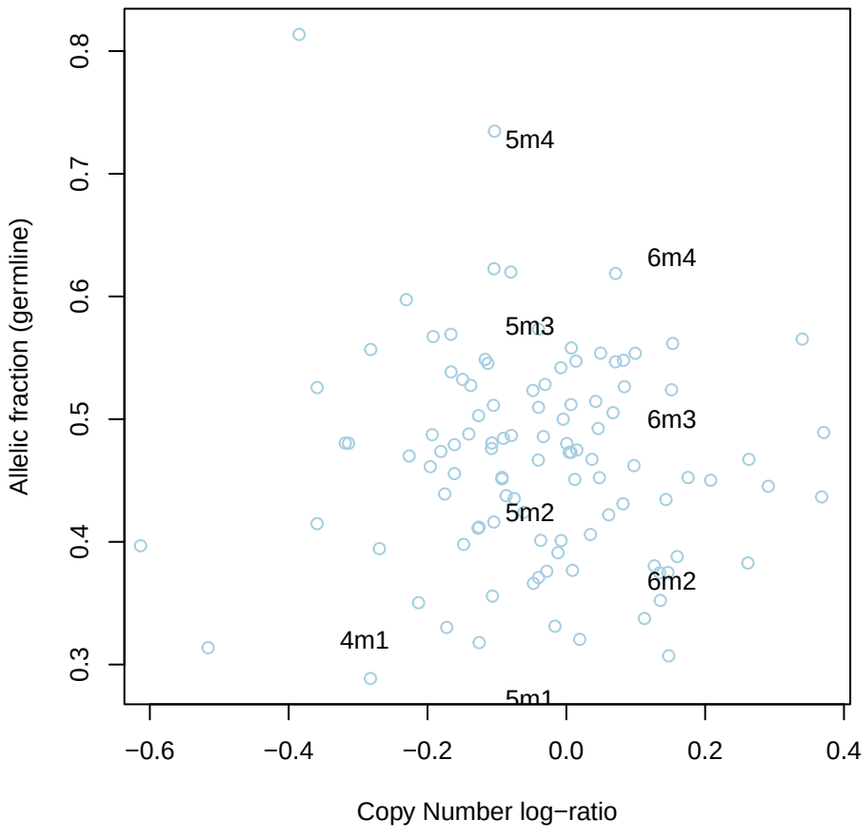

Frequency
Cellular fraction

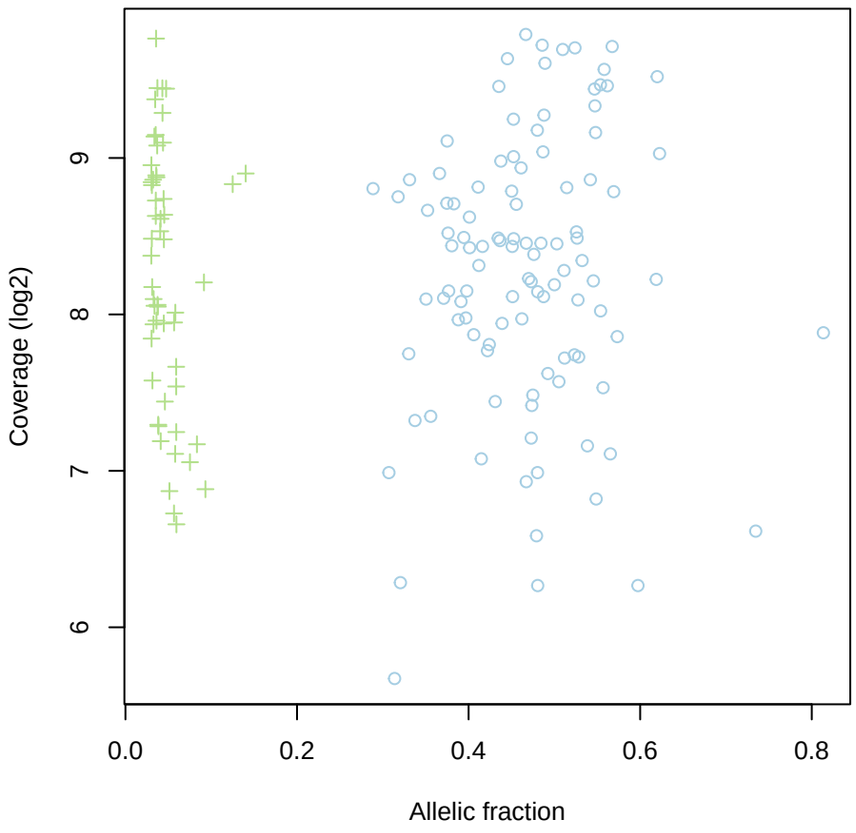

Purity: 0.56  Tumor ploidy: 5.243
2
3
4
5
6
7
0.0
0.1
0.2
0.3
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

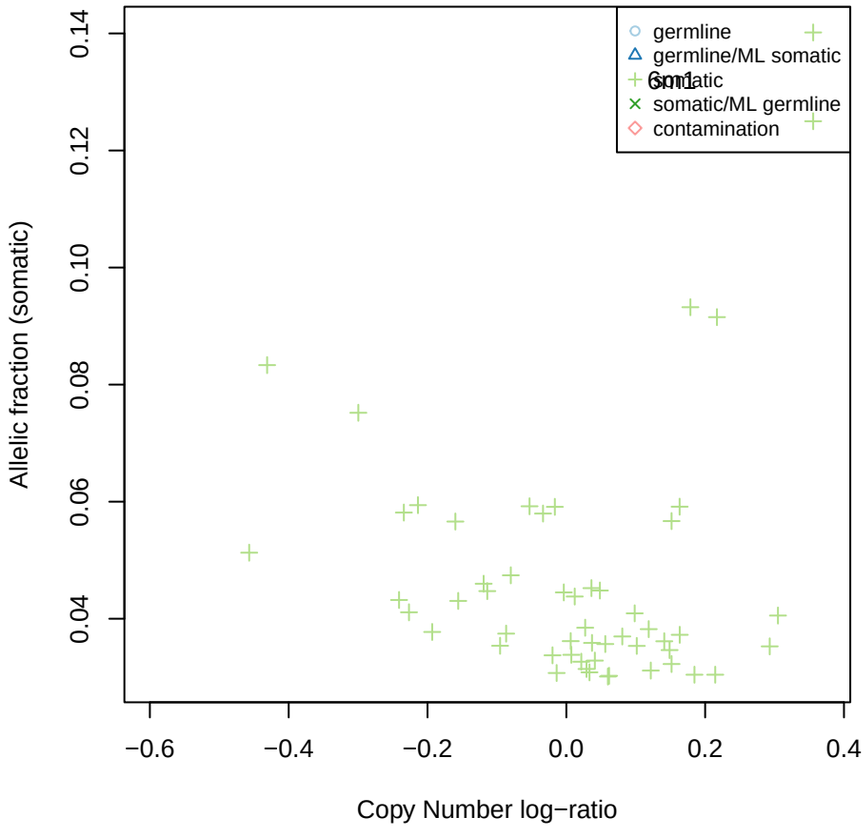

Purity: 0.56 Tumor ploidy: 5.243 SNV log−likelihood: −189.52 GoF: 85.5% Mean coverage: 427;361
1 2 3 4 5 6 7 8 9 10 11 12 13 14 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100
SNV Index

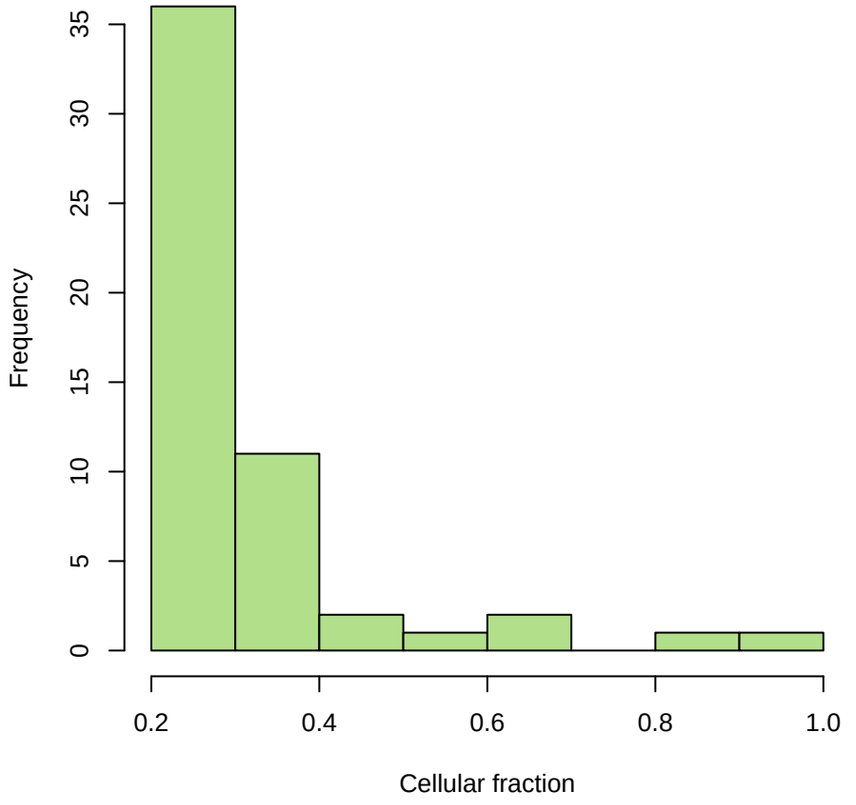

SCNA−fit log−likelihood: −5905.52
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

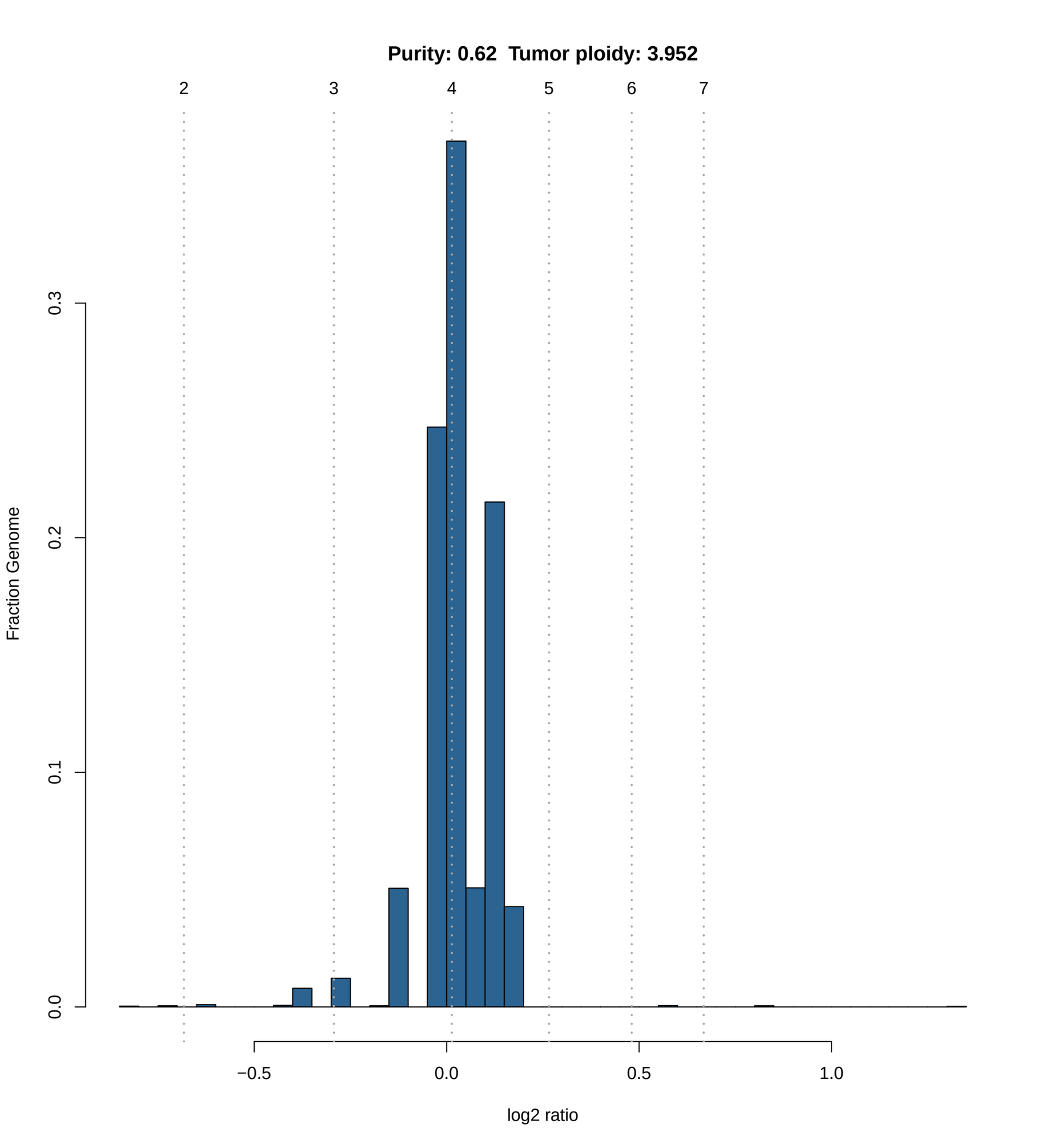

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100
SNV Index

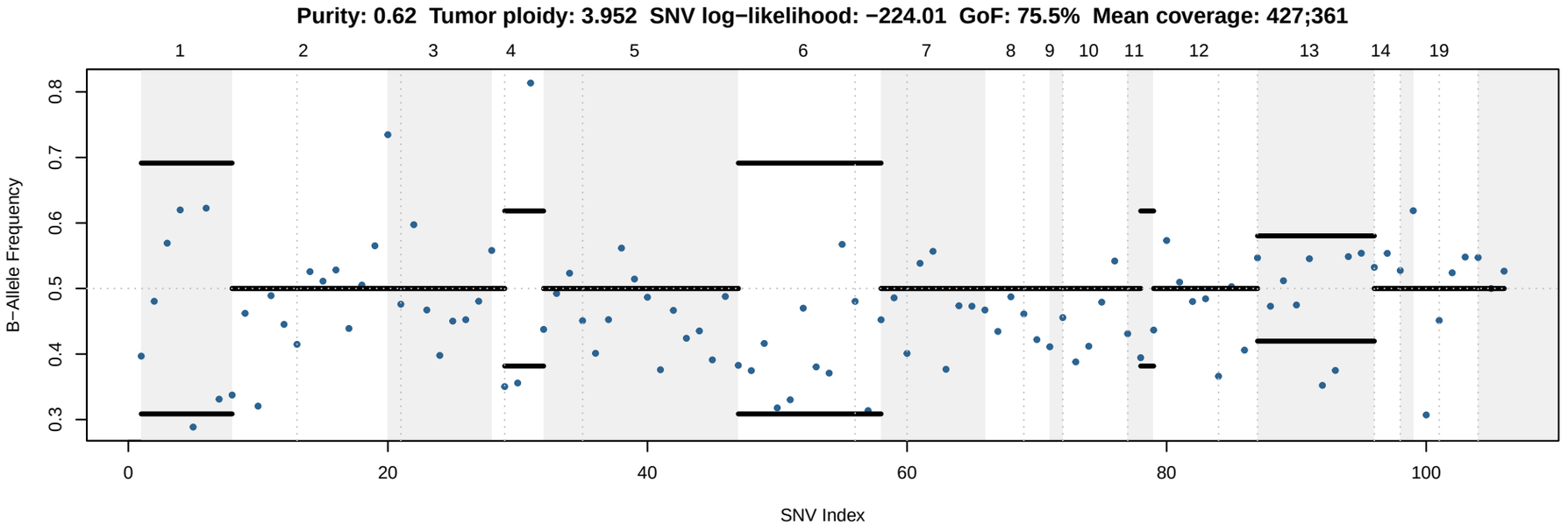

Allelic fraction (germline)
Copy Number log−ratio
5m4
6m4
5m3
6m3
5m2
6m2
4m1
5m1

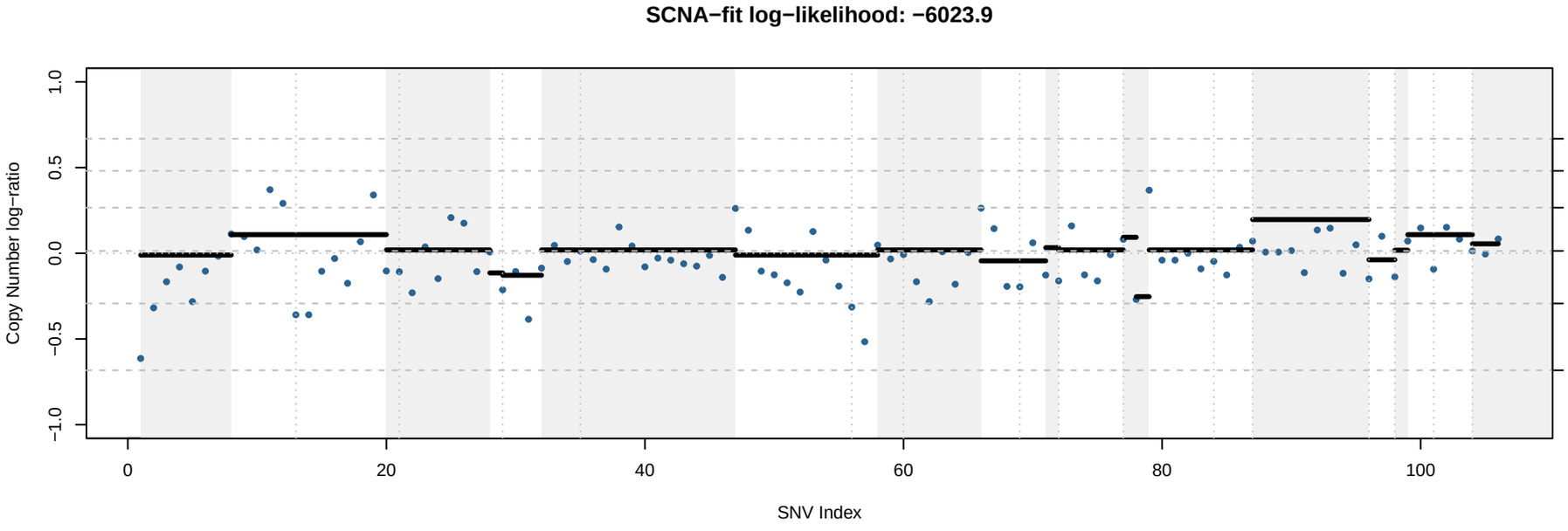

Coverage (log2)
Allelic fraction

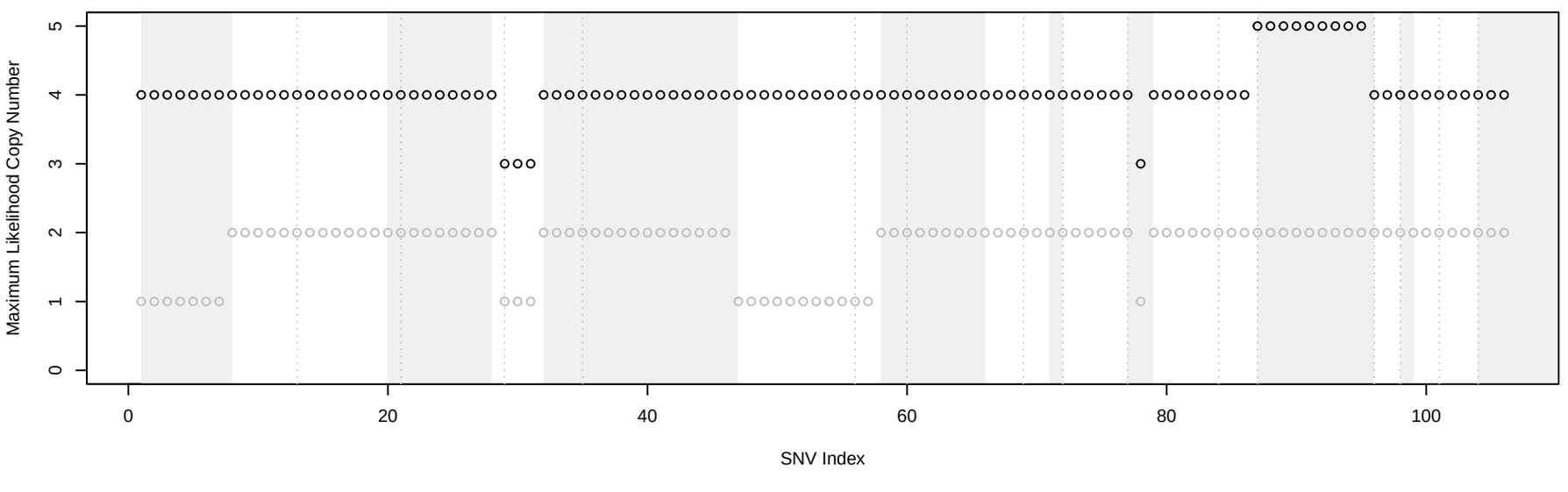

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

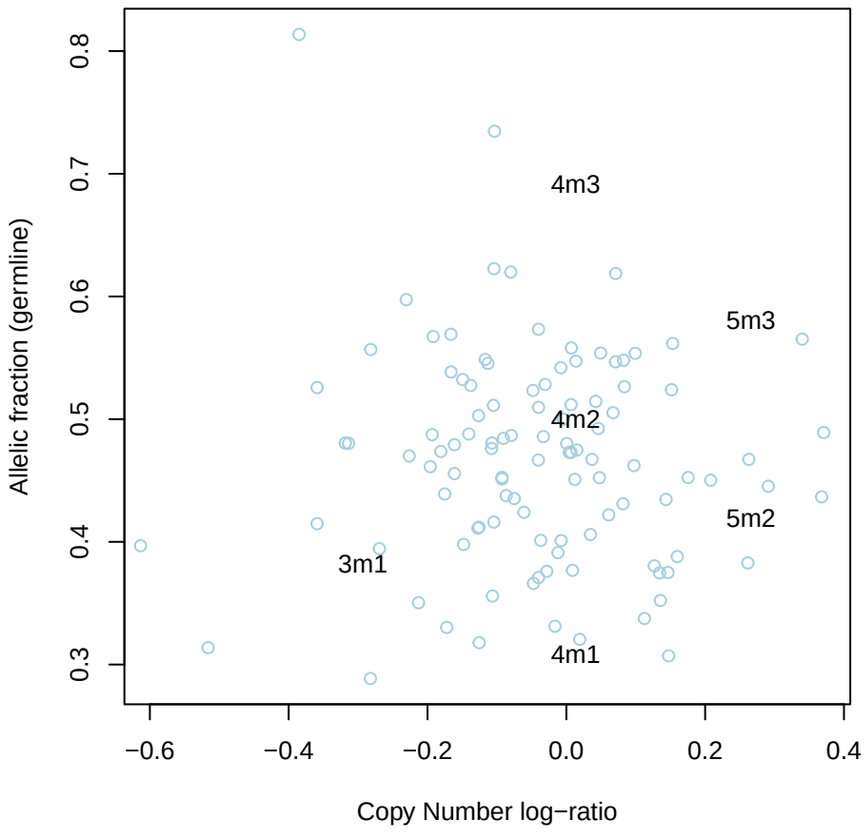

Frequency
Cellular fraction

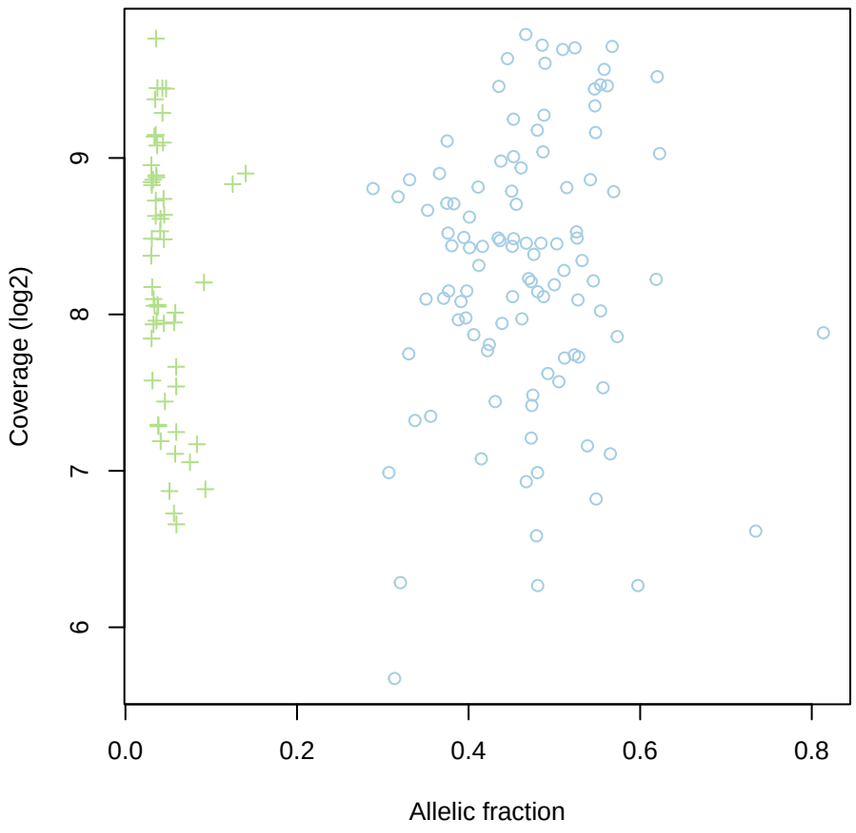

Purity: 0.62  Tumor ploidy: 3.952
2
3
4
5
6
7
0.0
0.1
0.2
0.3
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

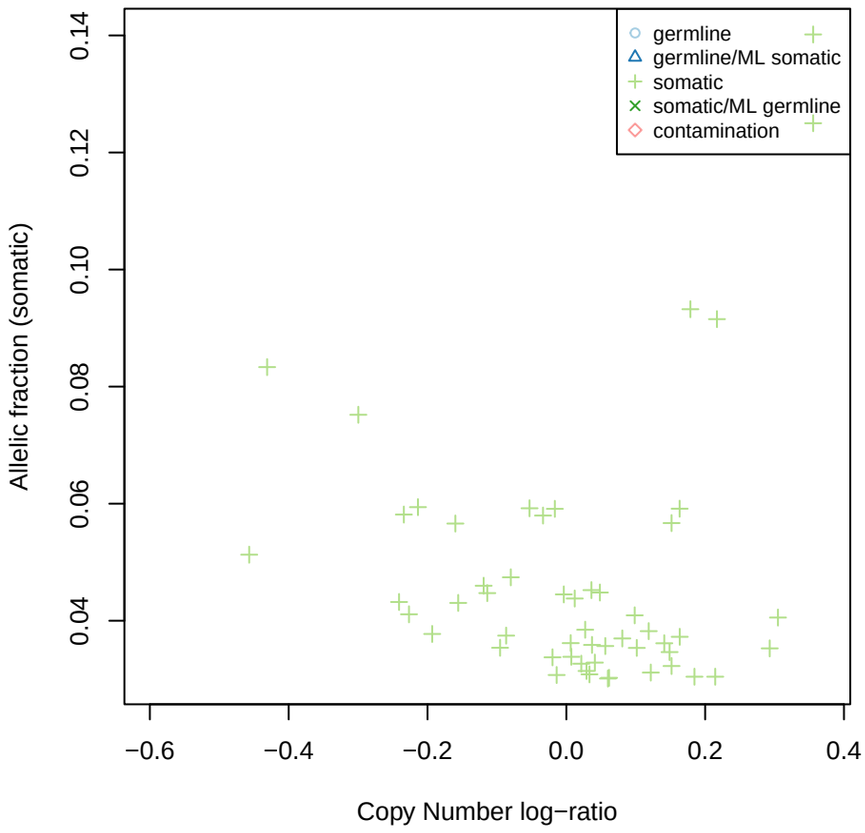

Purity: 0.62 Tumor ploidy: 3.952 SNV log−likelihood: −224.01 GoF: 75.5% Mean coverage: 427;361
1 2 3 4 5 6 7 8 9 10 11 12 13 14 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100
SNV Index

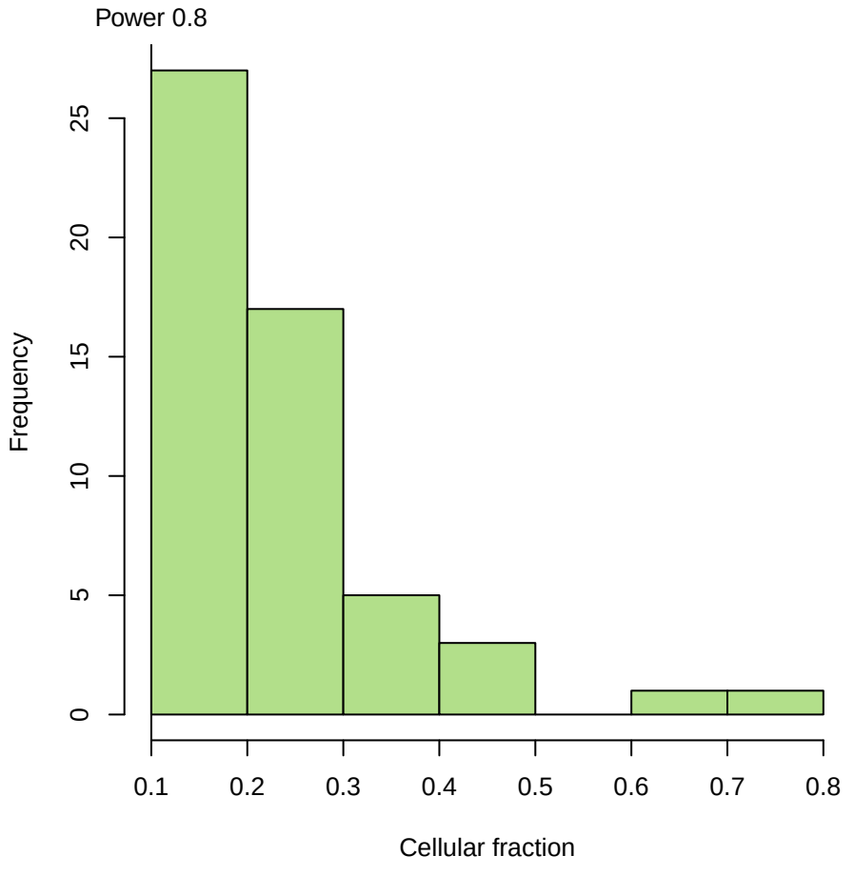

SCNA−fit log−likelihood: −6023.9
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

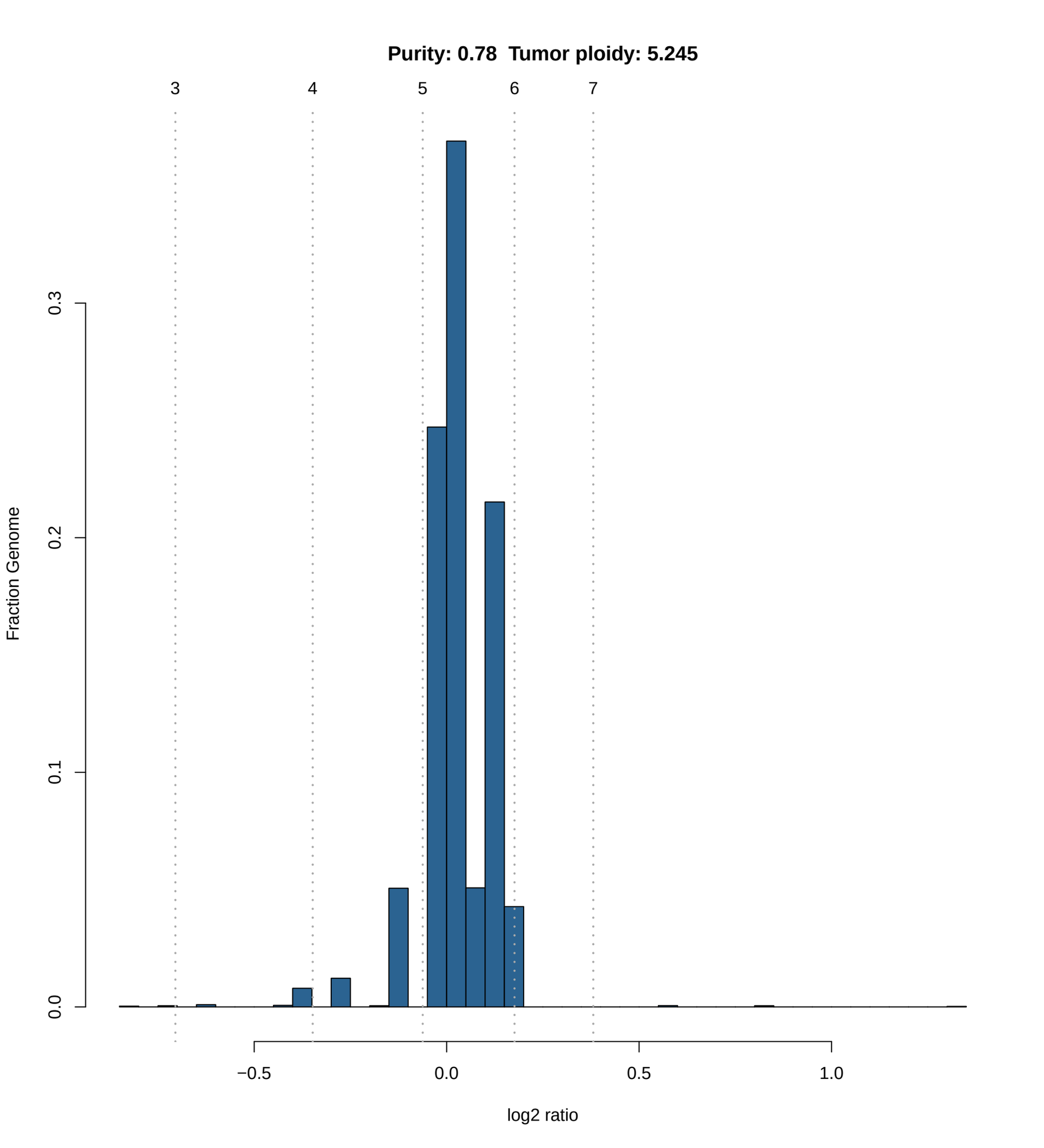

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100
SNV Index

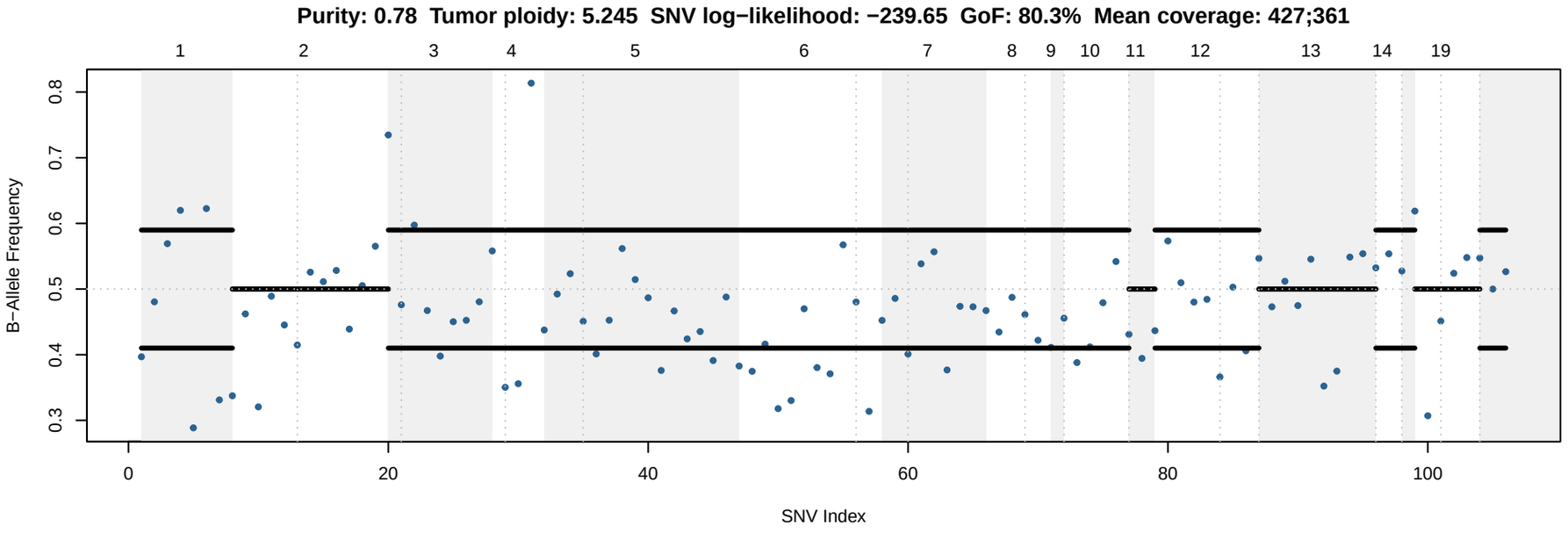

Allelic fraction (germline)
Copy Number log−ratio
4m3
5m3
4m2
5m2
3m1
4m1

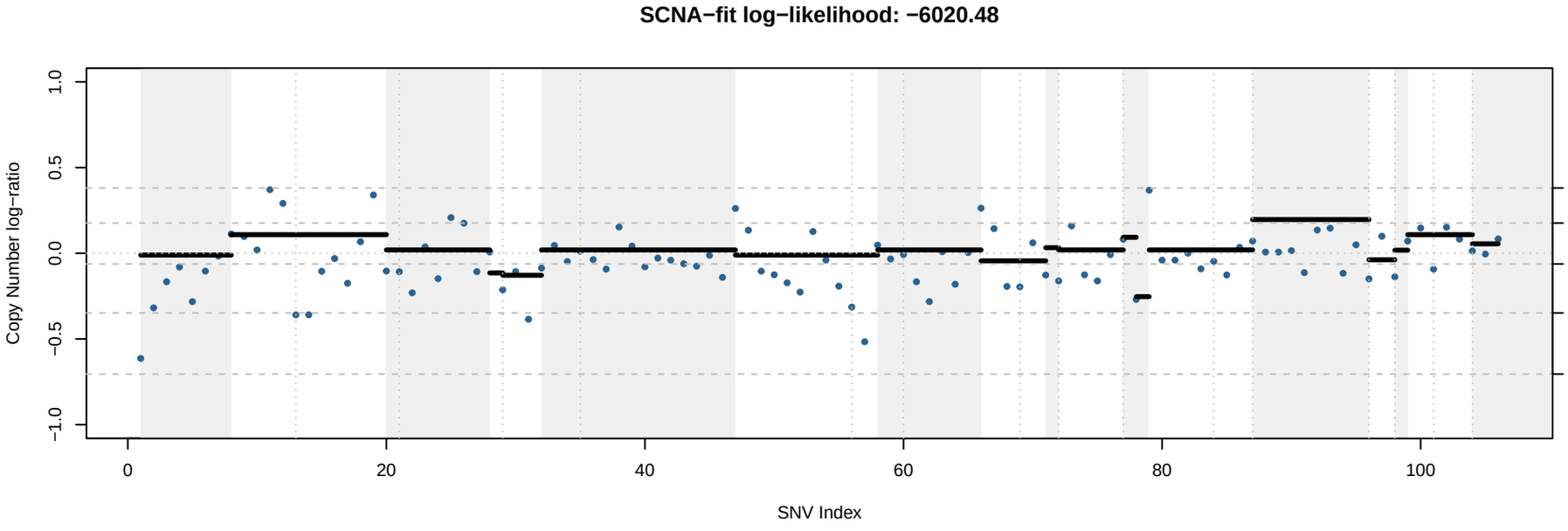

Coverage (log2)
Allelic fraction

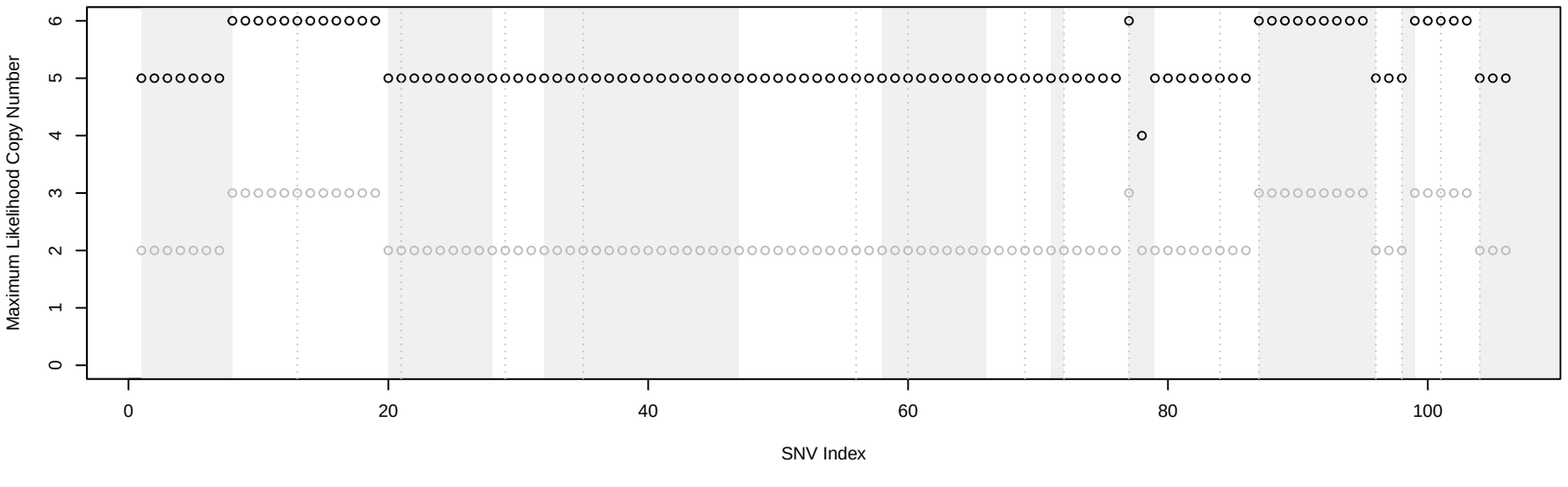

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

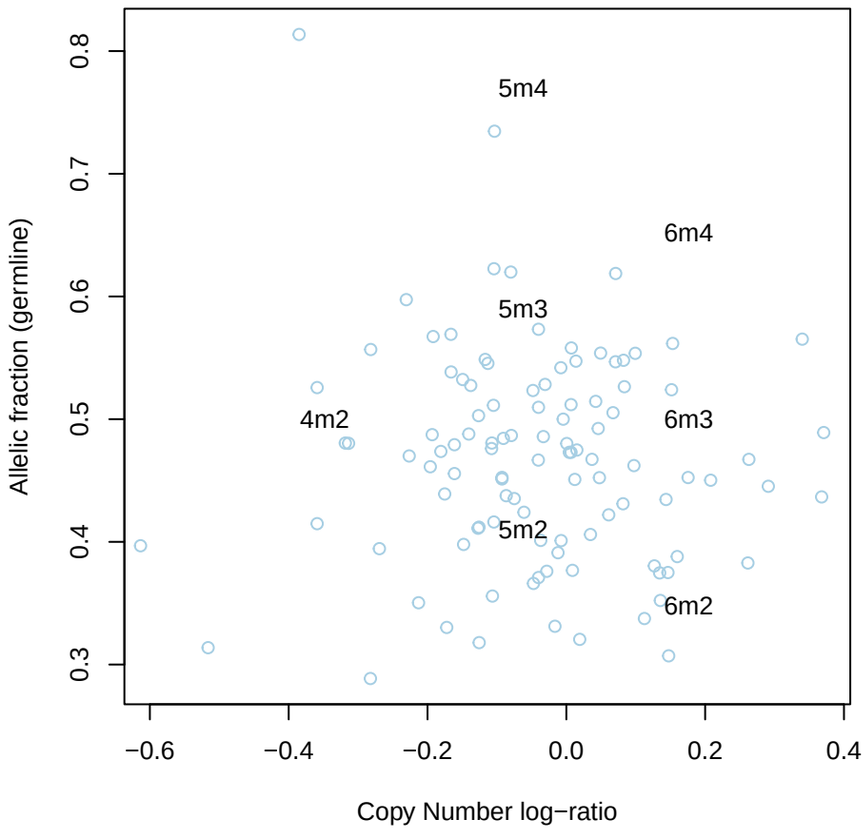

Power 0.8
Frequency
Cellular fraction

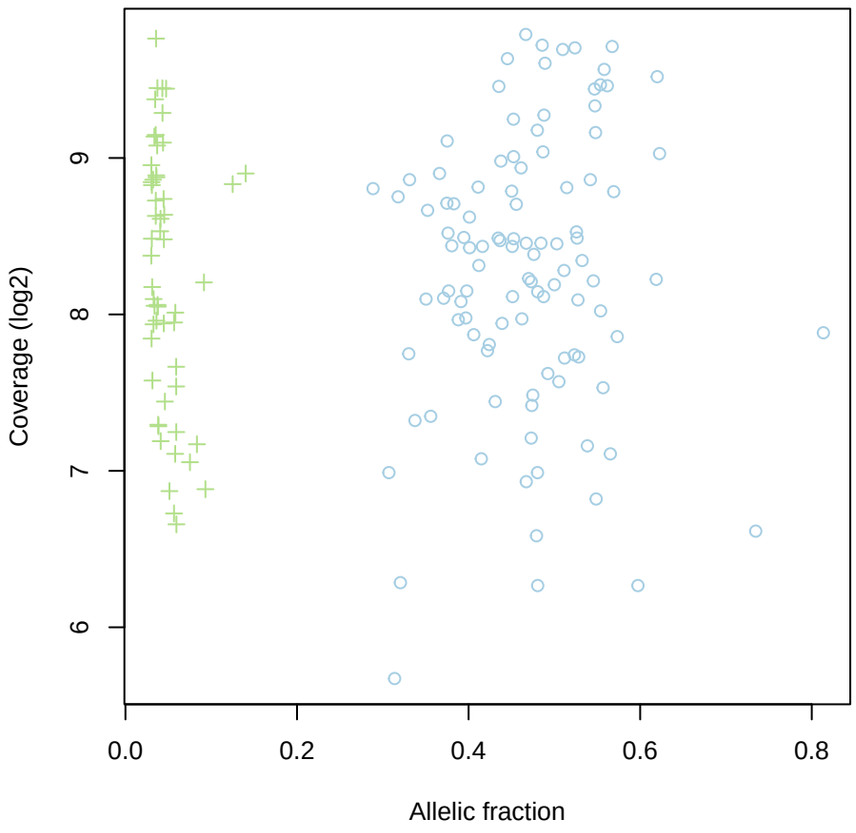

Purity: 0.78  Tumor ploidy: 5.245
3
4
5
6
7
0.0
0.1
0.2
0.3
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

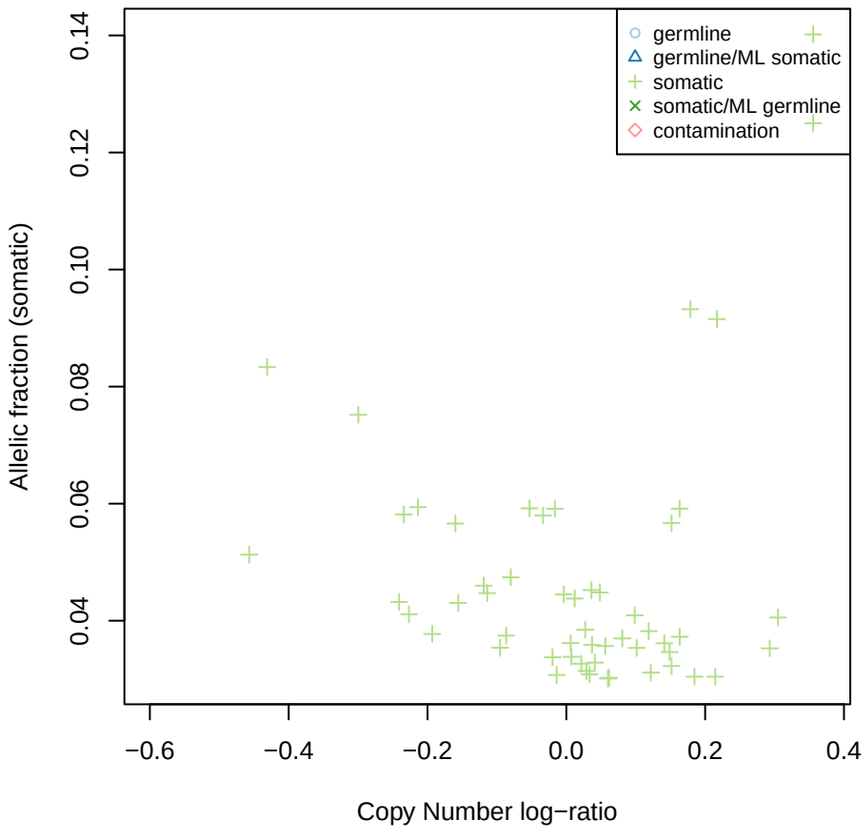

Purity: 0.78 Tumor ploidy: 5.245 SNV log−likelihood: −239.65 GoF: 80.3% Mean coverage: 427;361
1
2
3
4
5
6
7
8
9
10
11
12
13
14
19
B−Allele Frequency
0.3
0.4
0.5
0.6
0.7
0.8
0
20
40
60
80
100
SNV Index

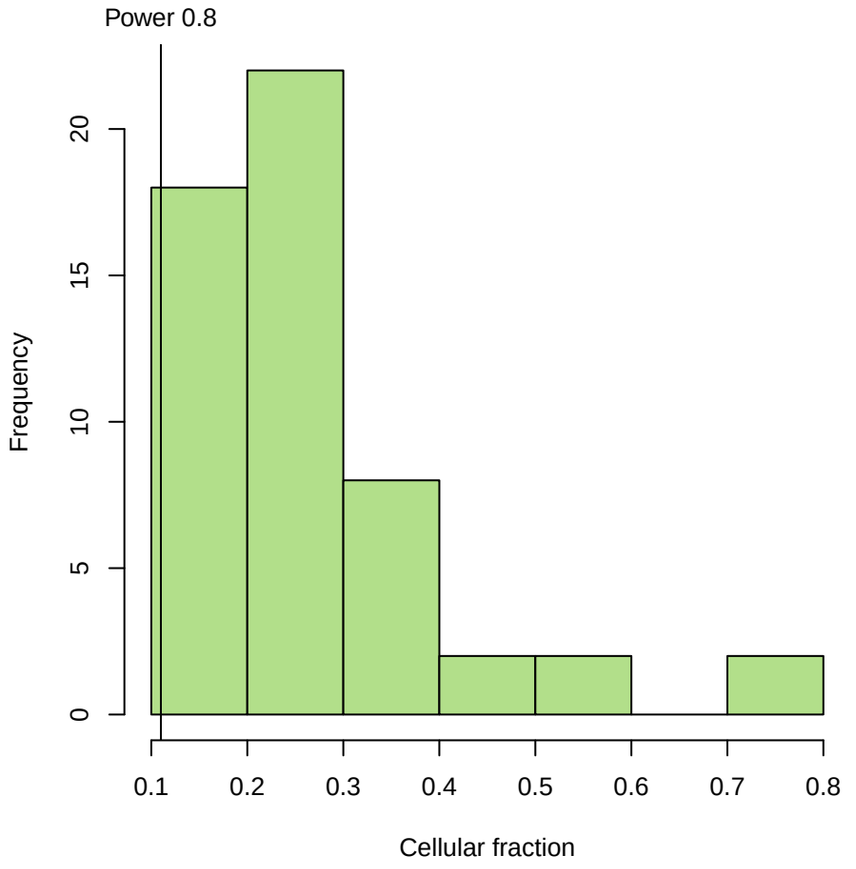

SCNA−fit log−likelihood: −6020.48
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
3
4
5
6
7
0
20
40
60
80
100
SNV Index

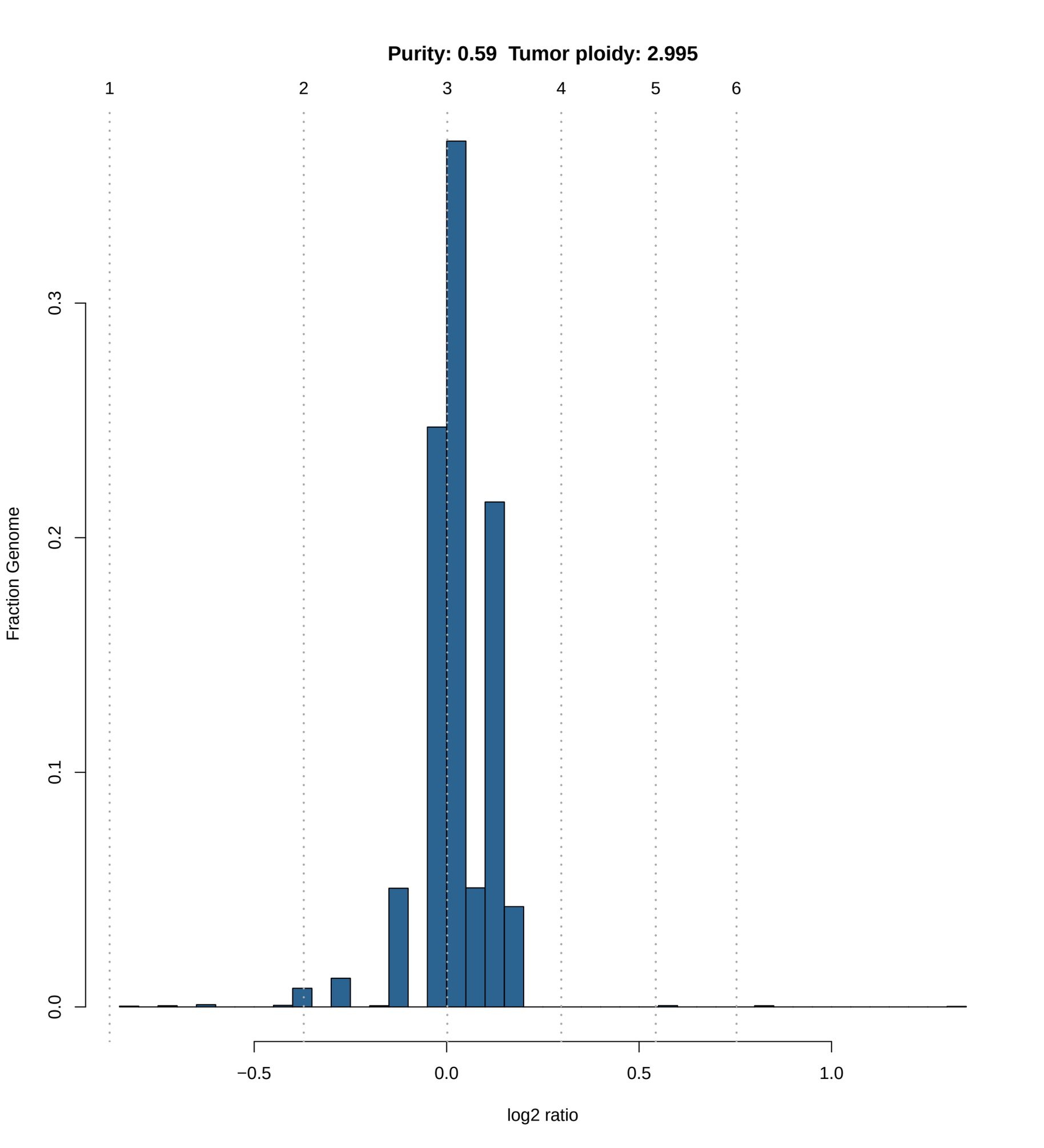

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
0
20
40
60
80
100
SNV Index

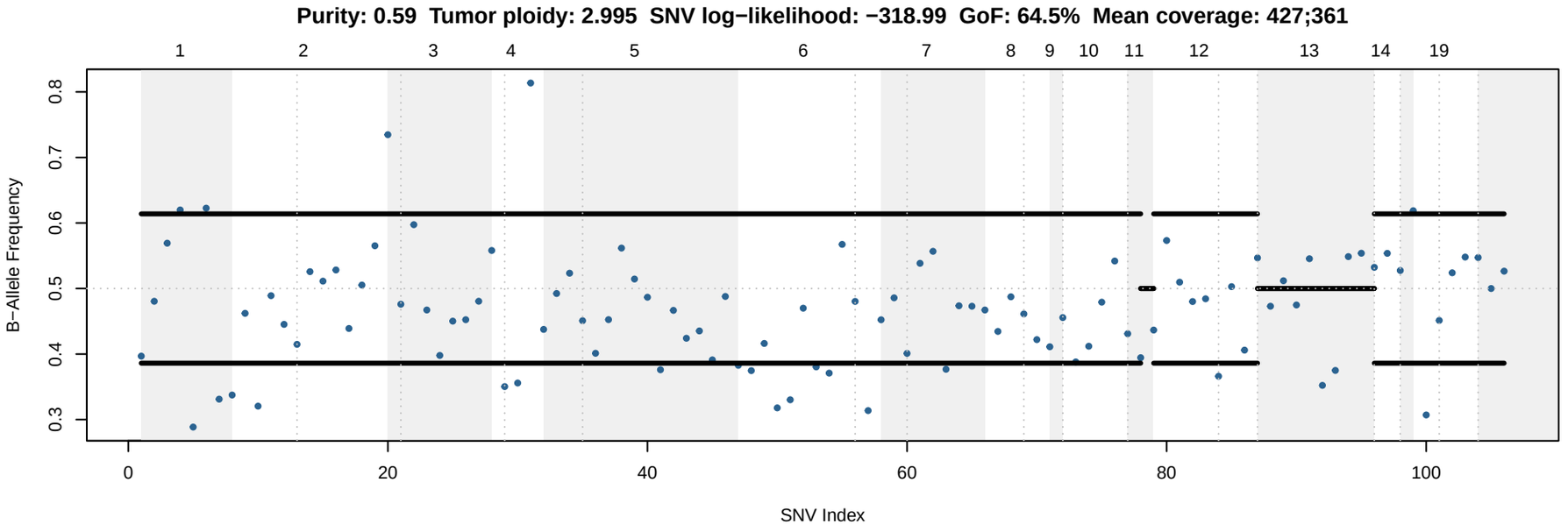

Allelic fraction (germline)
Copy Number log−ratio
5m4
6m4
5m3
4m2
6m3
5m2
6m2

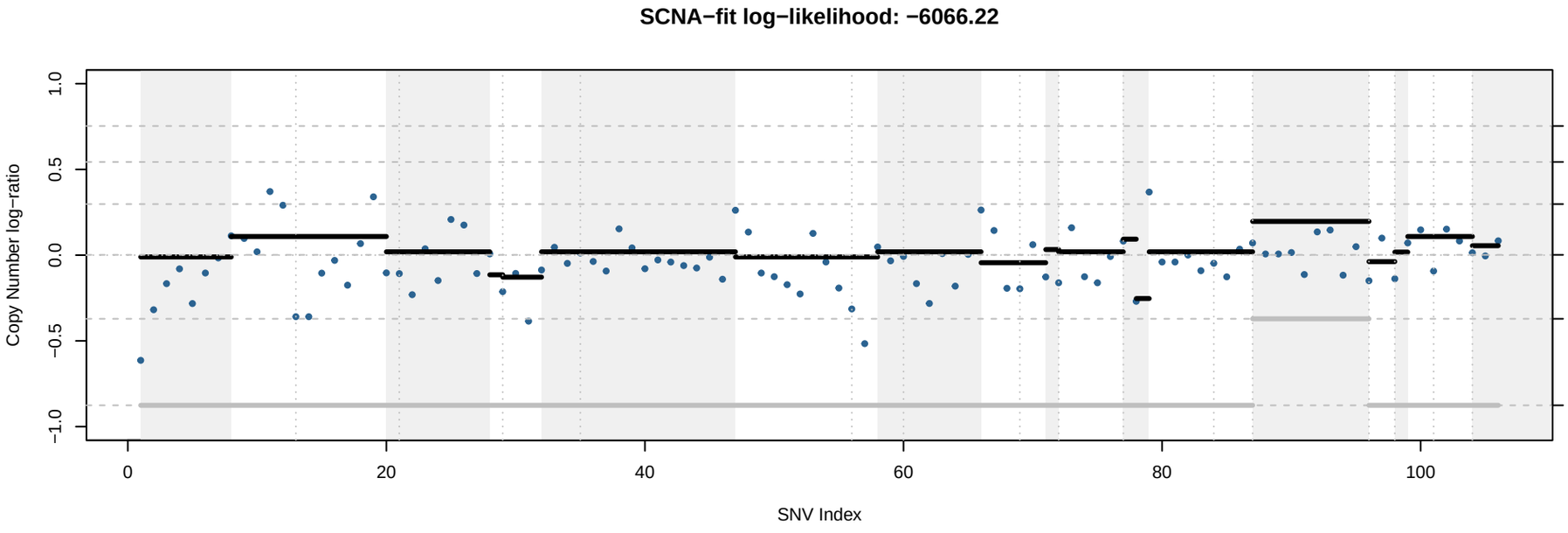

Coverage (log2)
Allelic fraction

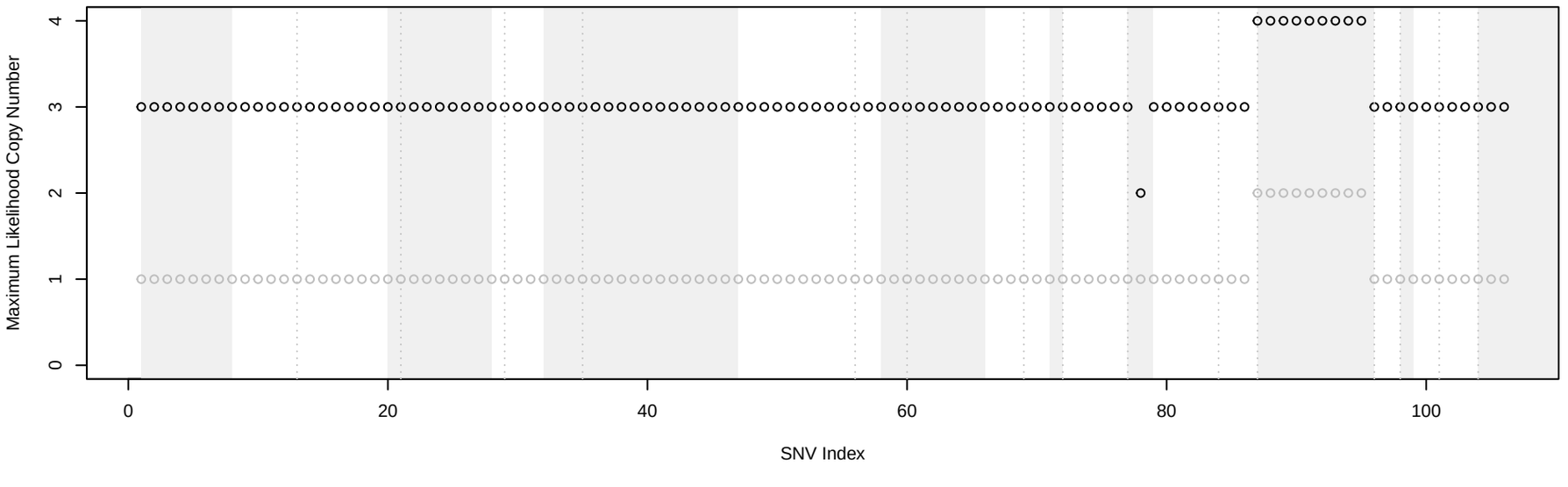

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

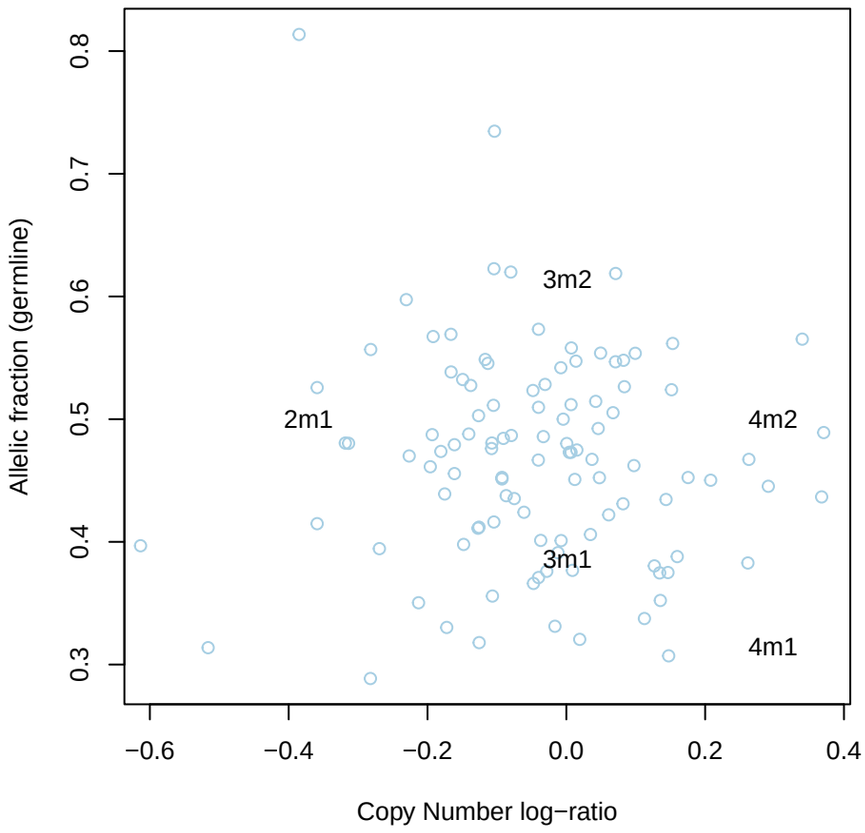

Power 0.8
Frequency
Cellular fraction

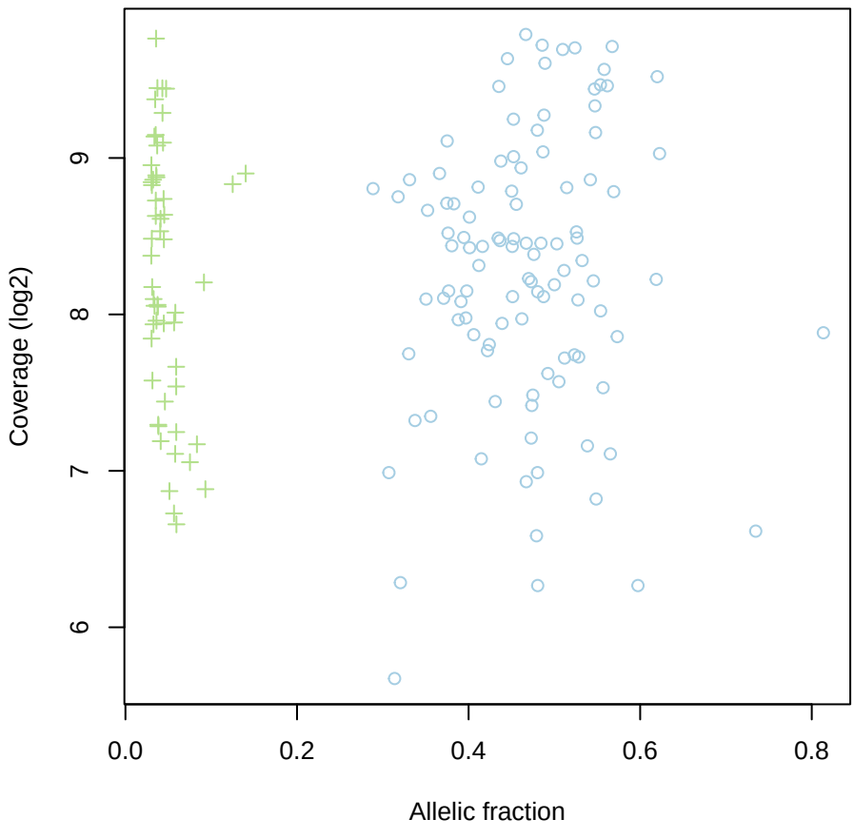

Purity: 0.59  Tumor ploidy: 2.995
1
2
3
4
5
6
0.0
0.1
0.2
0.3
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

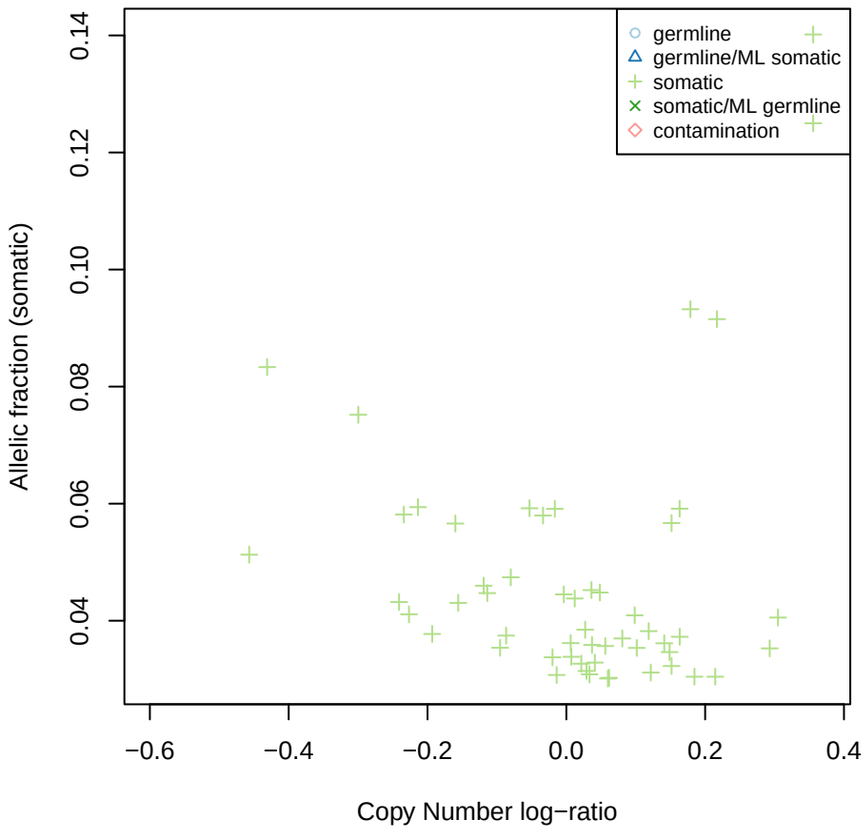

Purity: 0.59 Tumor ploidy: 2.995 SNV log−likelihood: −318.99 GoF: 64.5% Mean coverage: 427;361
1
2
3
4
5
6
7
8
9
10
11
12
13
14
19
B−Allele Frequency
0.3
0.4
0.5
0.6
0.7
0.8
0
20
40
60
80
100
SNV Index

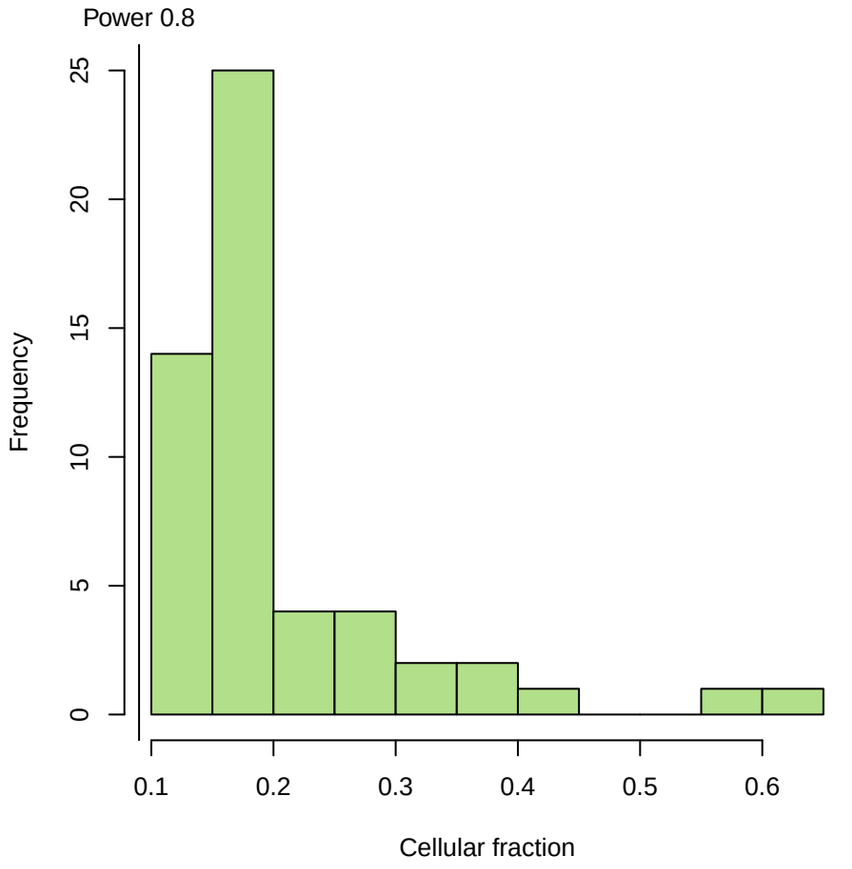

SCNA−fit log−likelihood: −6066.22
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1
2
3
4
5
6
0
20
40
60
80
100
SNV Index

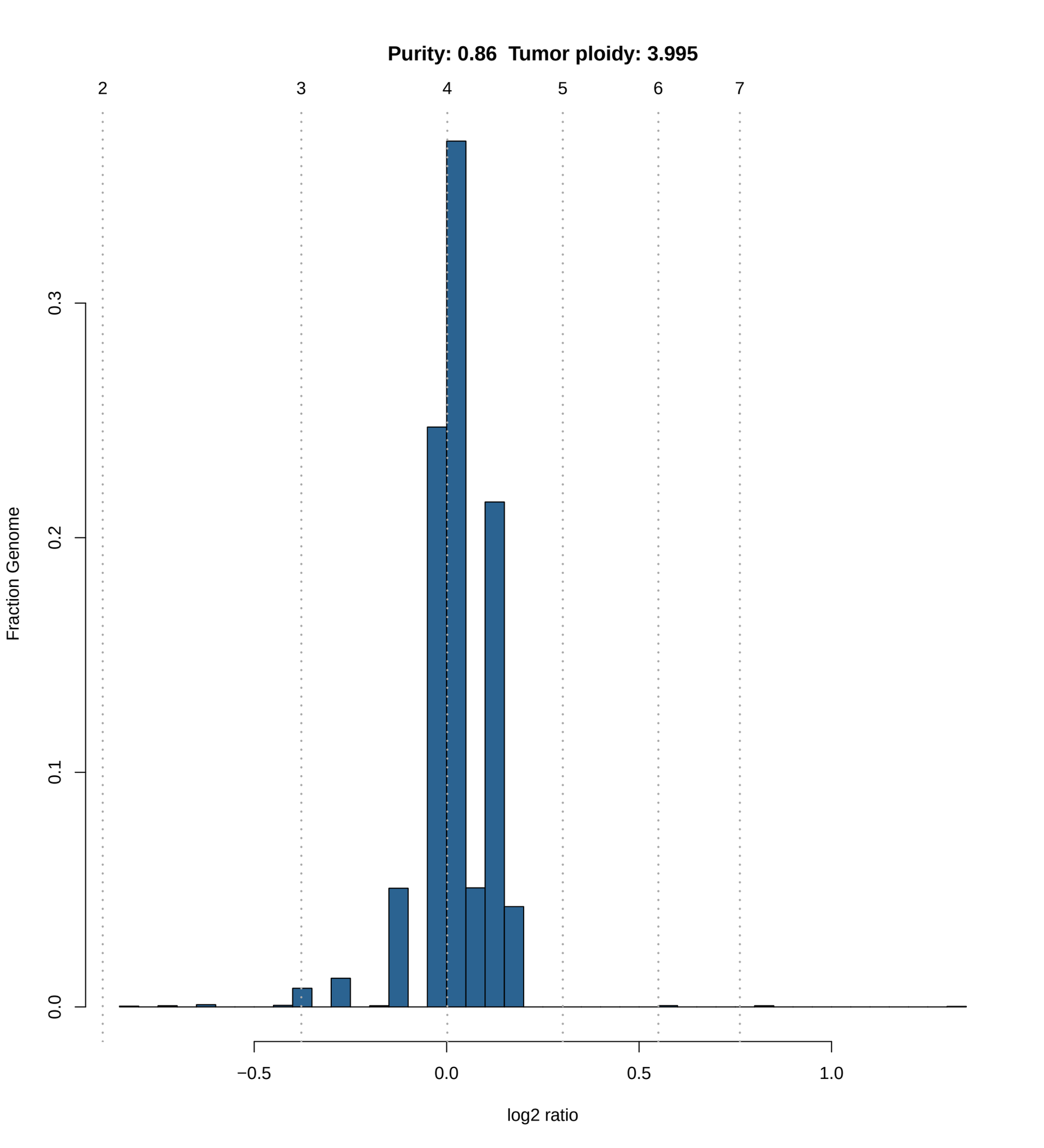

Maximum Likelihood Copy Number
0
1
2
3
4
0
20
40
60
80
100
SNV Index

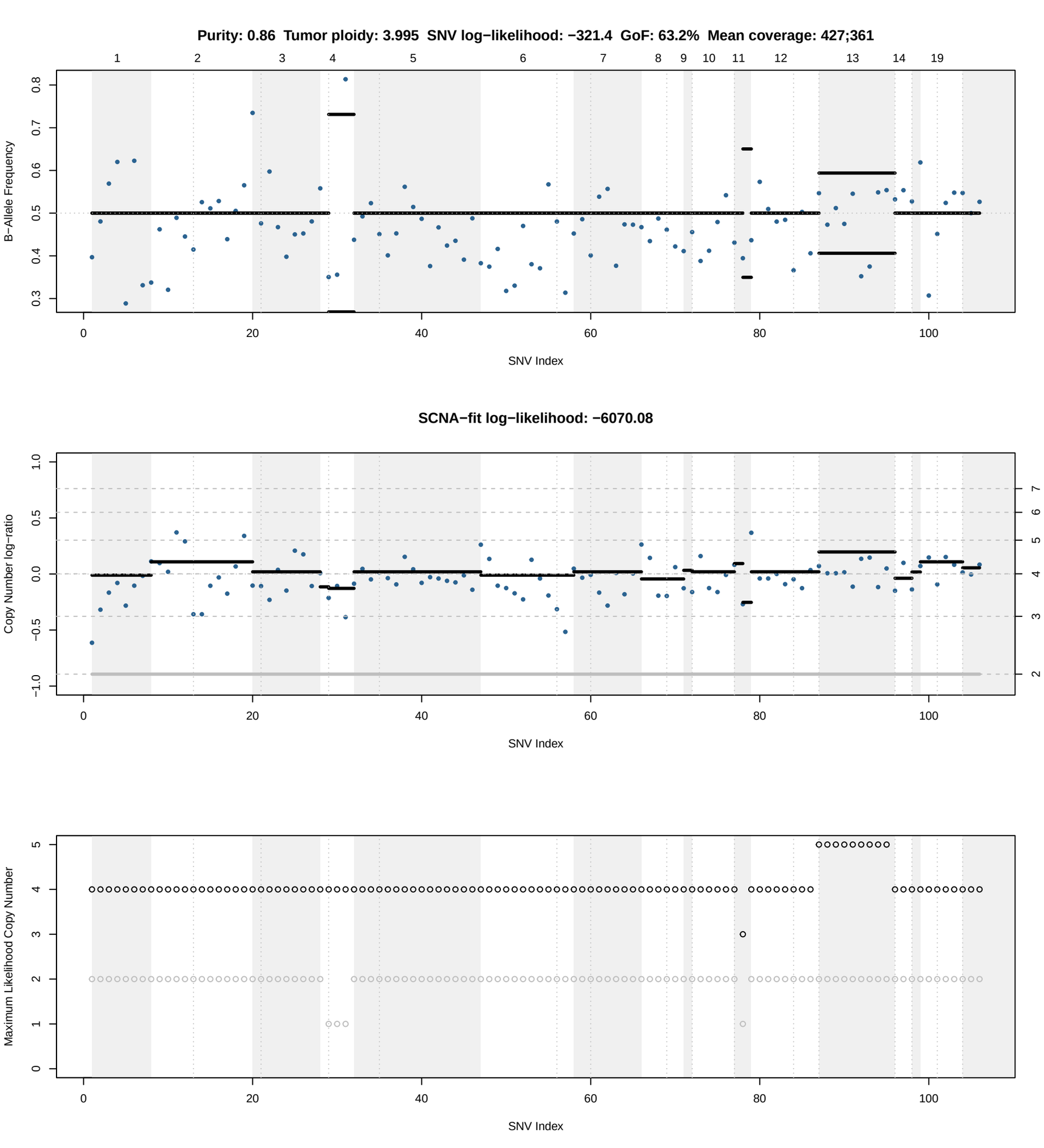

Allelic fraction (germline)
Copy Number log−ratio
2m1
3m2
3m1
4m2
4m1

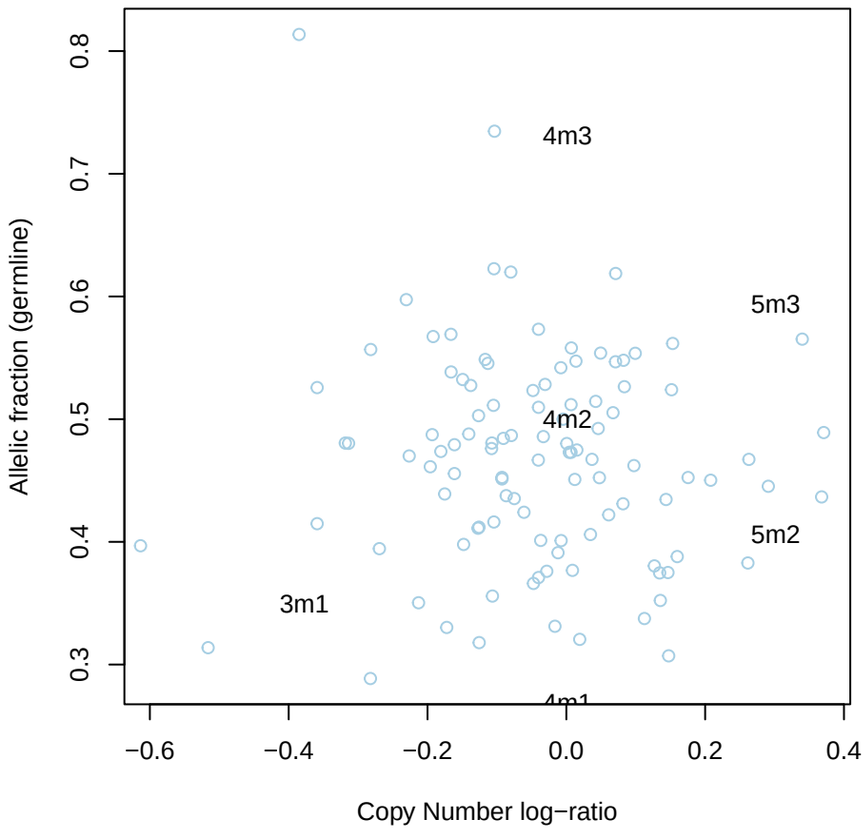

Coverage (log2)
Allelic fraction

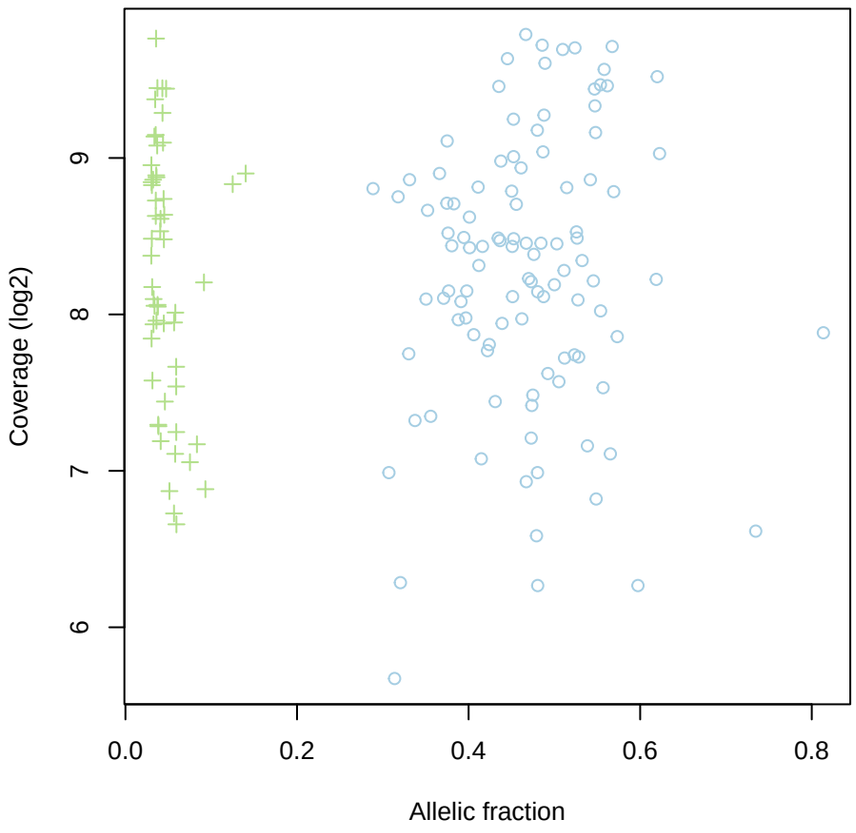

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

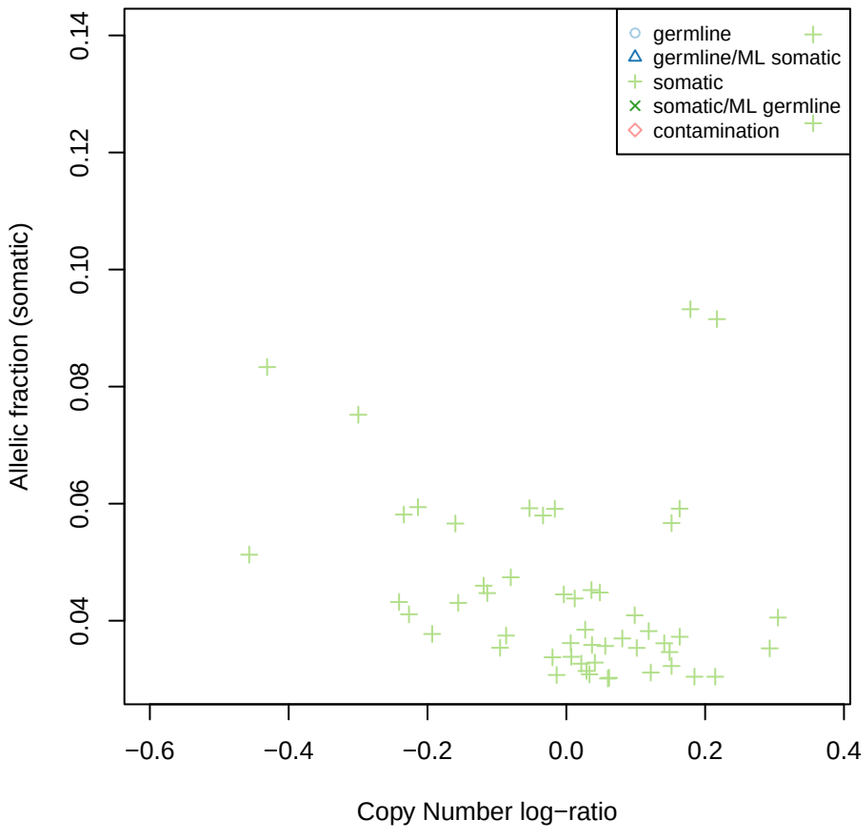

Power 0.8
Frequency
Cellular fraction

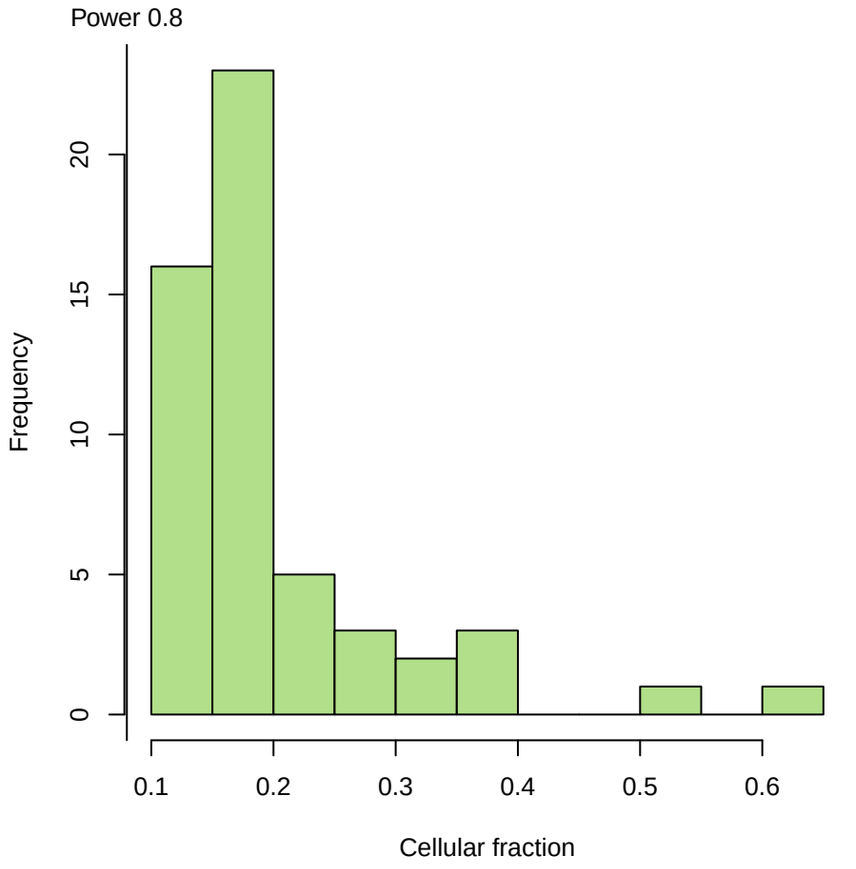

Purity: 0.86  Tumor ploidy: 3.995
2
3
4
5
6
7
0.0
0.1
0.2
0.3
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

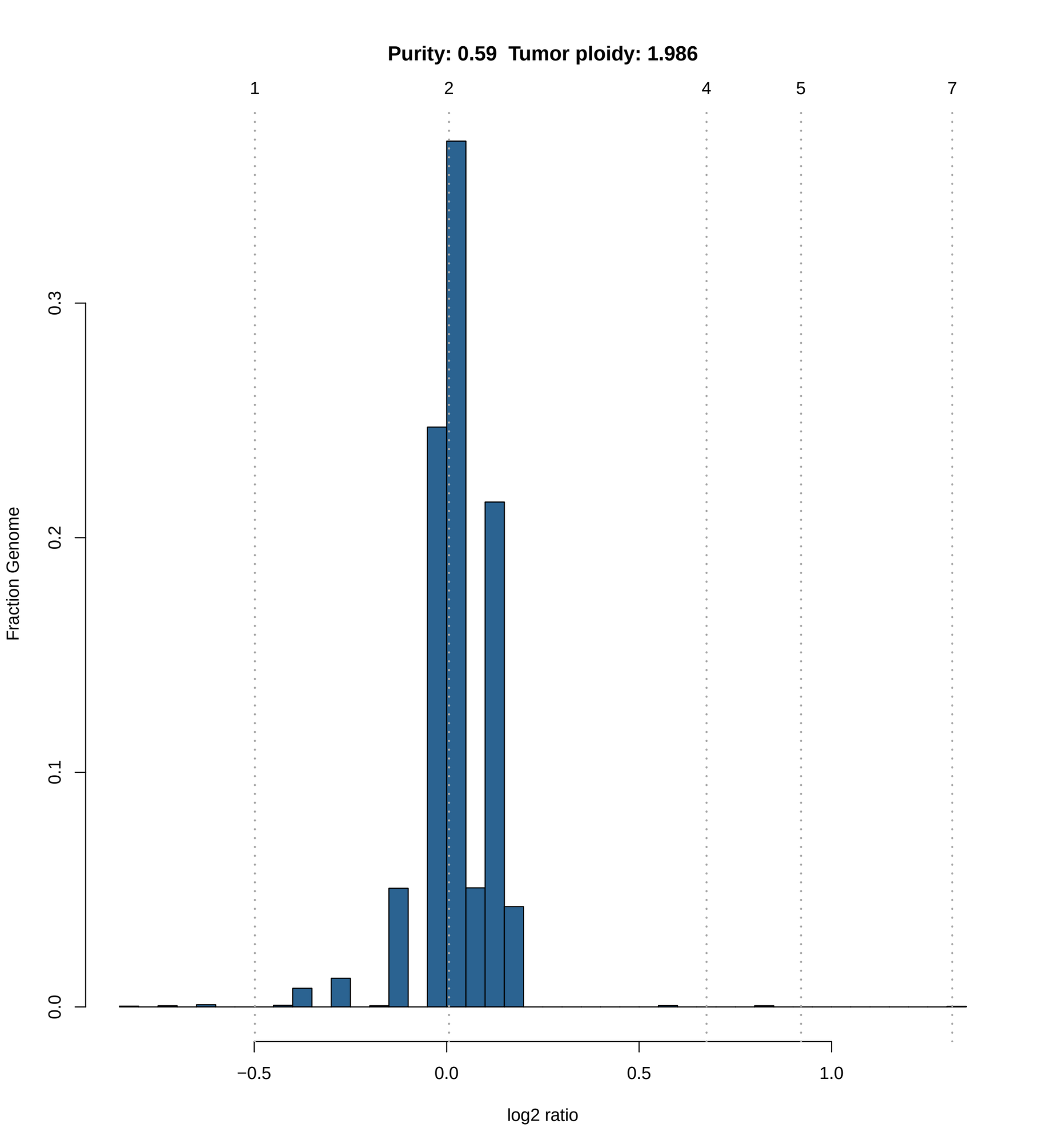

Purity: 0.86 Tumor ploidy: 3.995 SNV log−likelihood: −321.4 GoF: 63.2% Mean coverage: 427;361
1 2 3 4 5 6 7 8 9 10 11 12 13 14 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100
SNV Index
SCNA−fit log−likelihood: −6070.08
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 20 40 60 80 100
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100
SNV Index

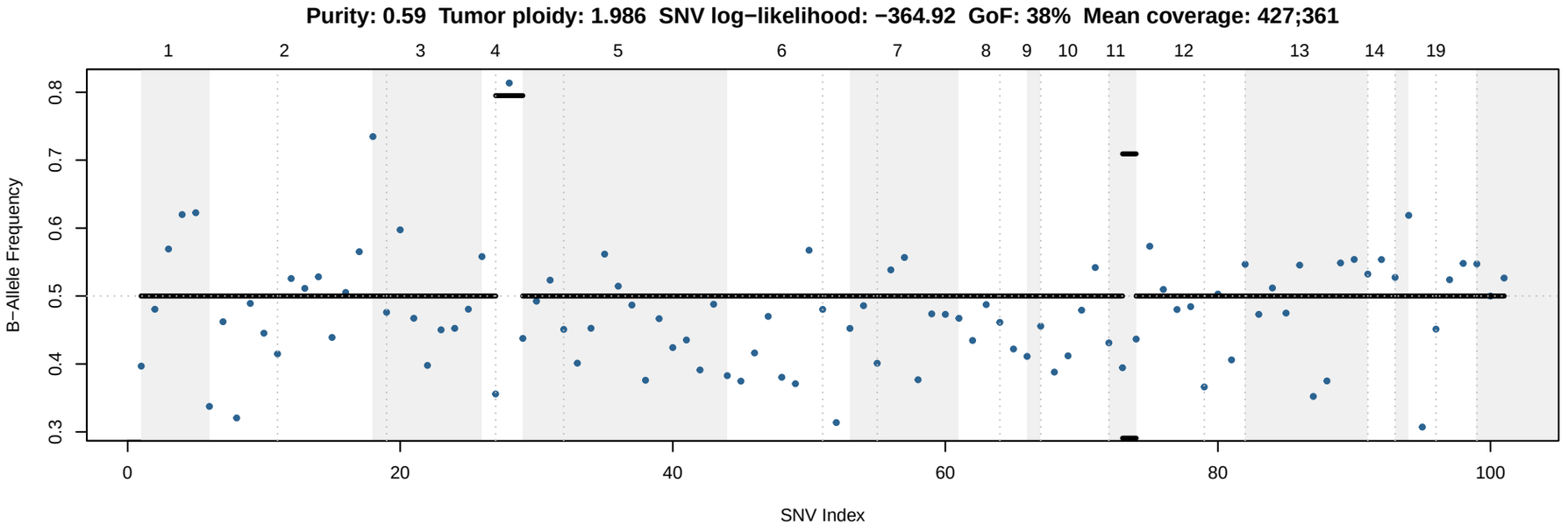

Allelic fraction (germline)
Copy Number log−ratio
4m3
5m3
4m2
5m2
3m1
4m1

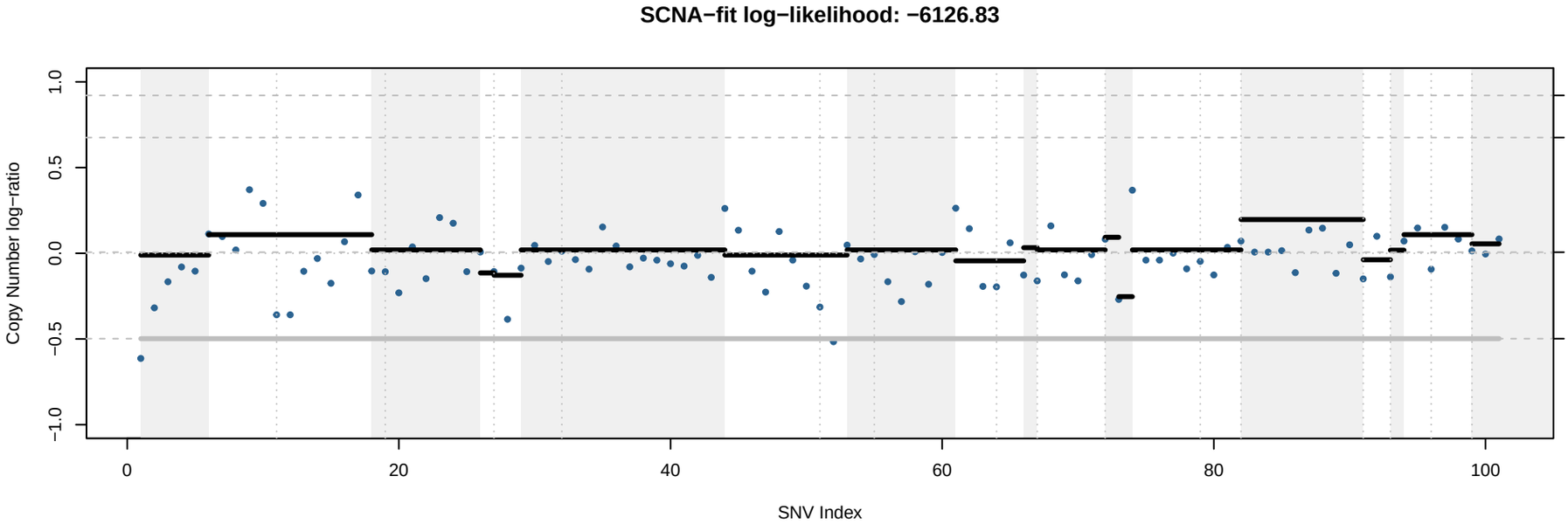

Coverage (log2)
Allelic fraction

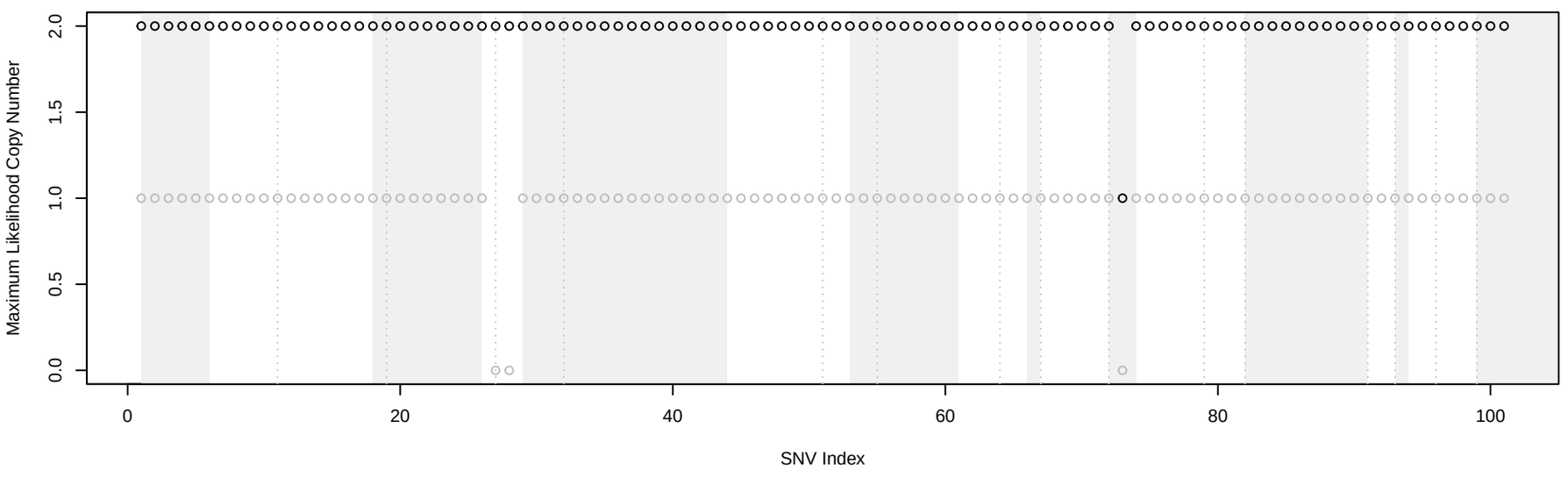

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

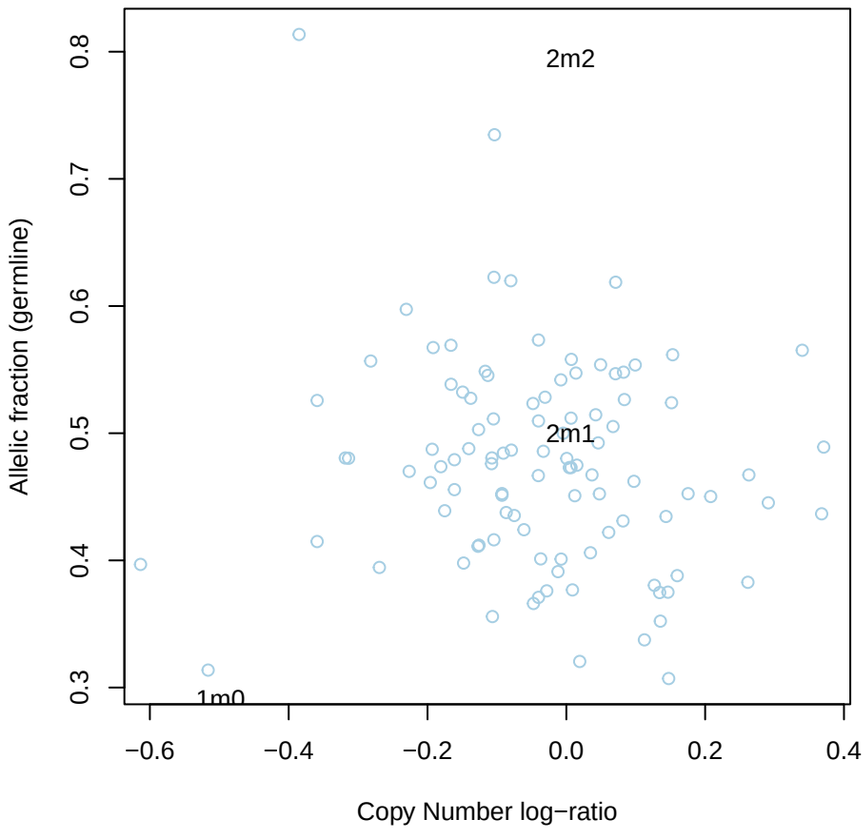

Power 0.8
Frequency
Cellular fraction

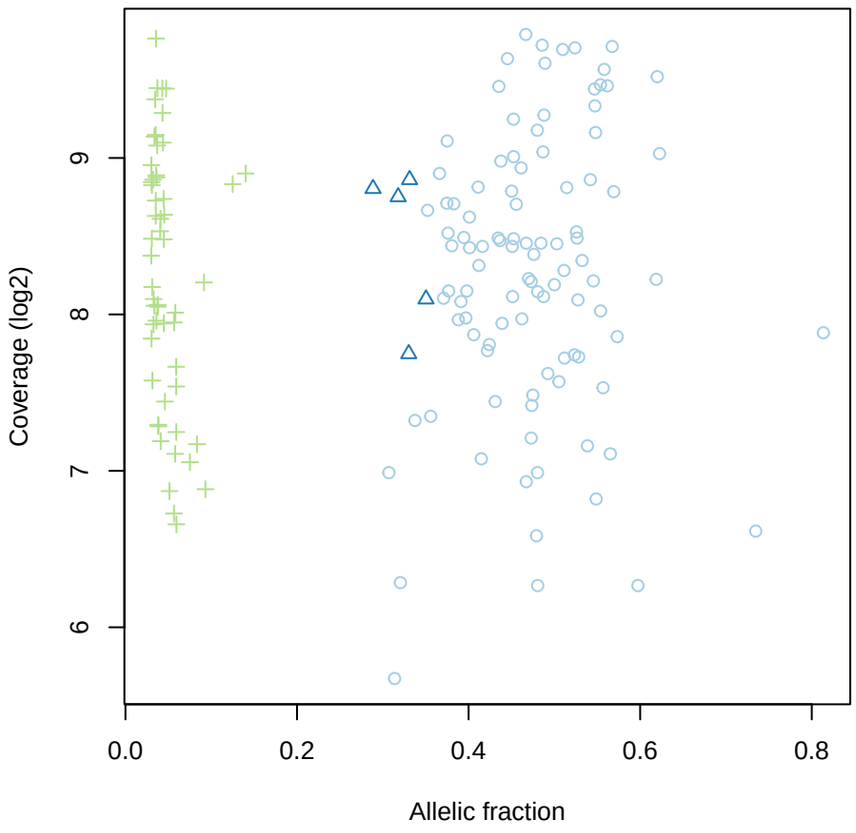

Purity: 0.59  Tumor ploidy: 1.986
1
2
4
5
7
0.0
0.1
0.2
0.3
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

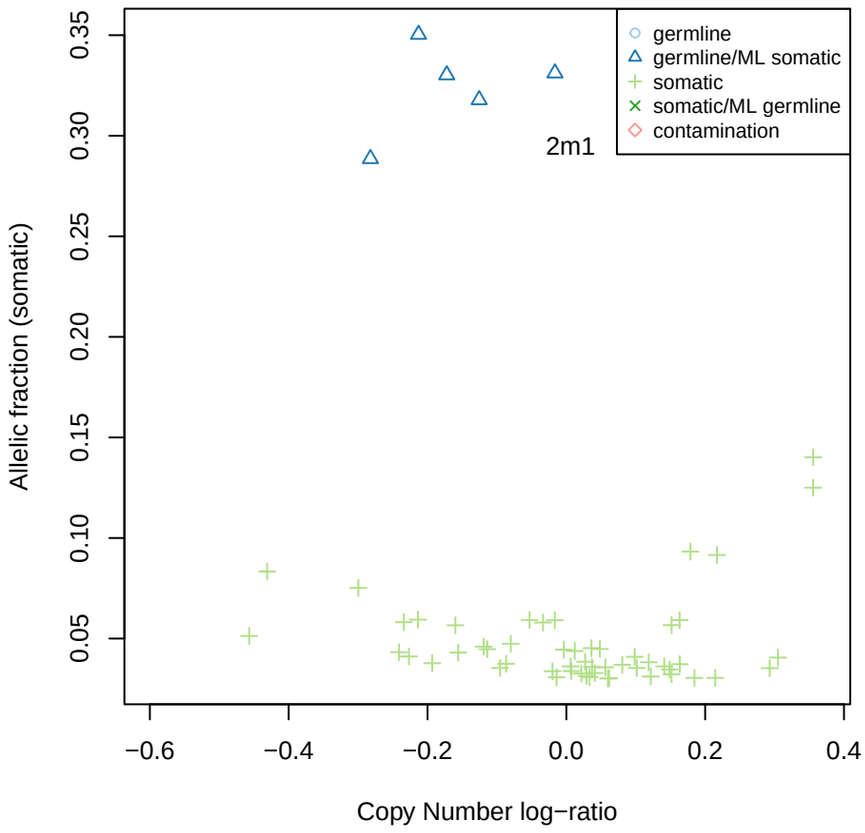

Purity: 0.59 Tumor ploidy: 1.986 SNV log−likelihood: −364.92 GoF: 38% Mean coverage: 427;361
1
2
3
4
5
6
7
8
9
10
11
12
13
14
19
B−Allele Frequency
0.3
0.4
0.5
0.6
0.7
0.8
0
20
40
60
80
100
SNV Index

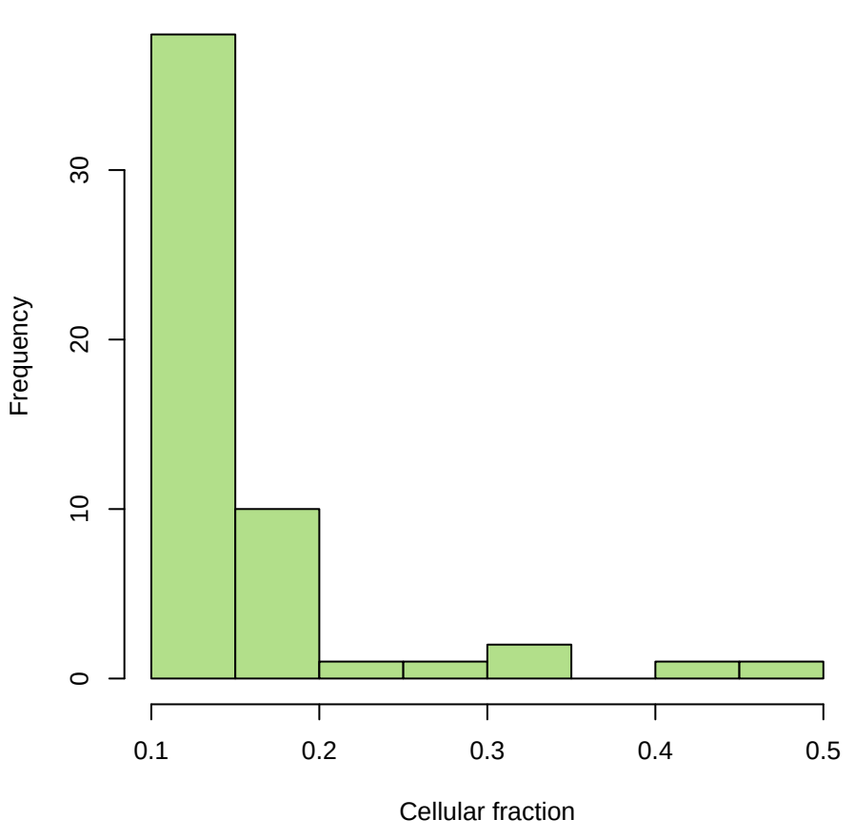

SCNA−fit log−likelihood: −6126.83
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1
2
4
5
0
20
40
60
80
100
SNV Index

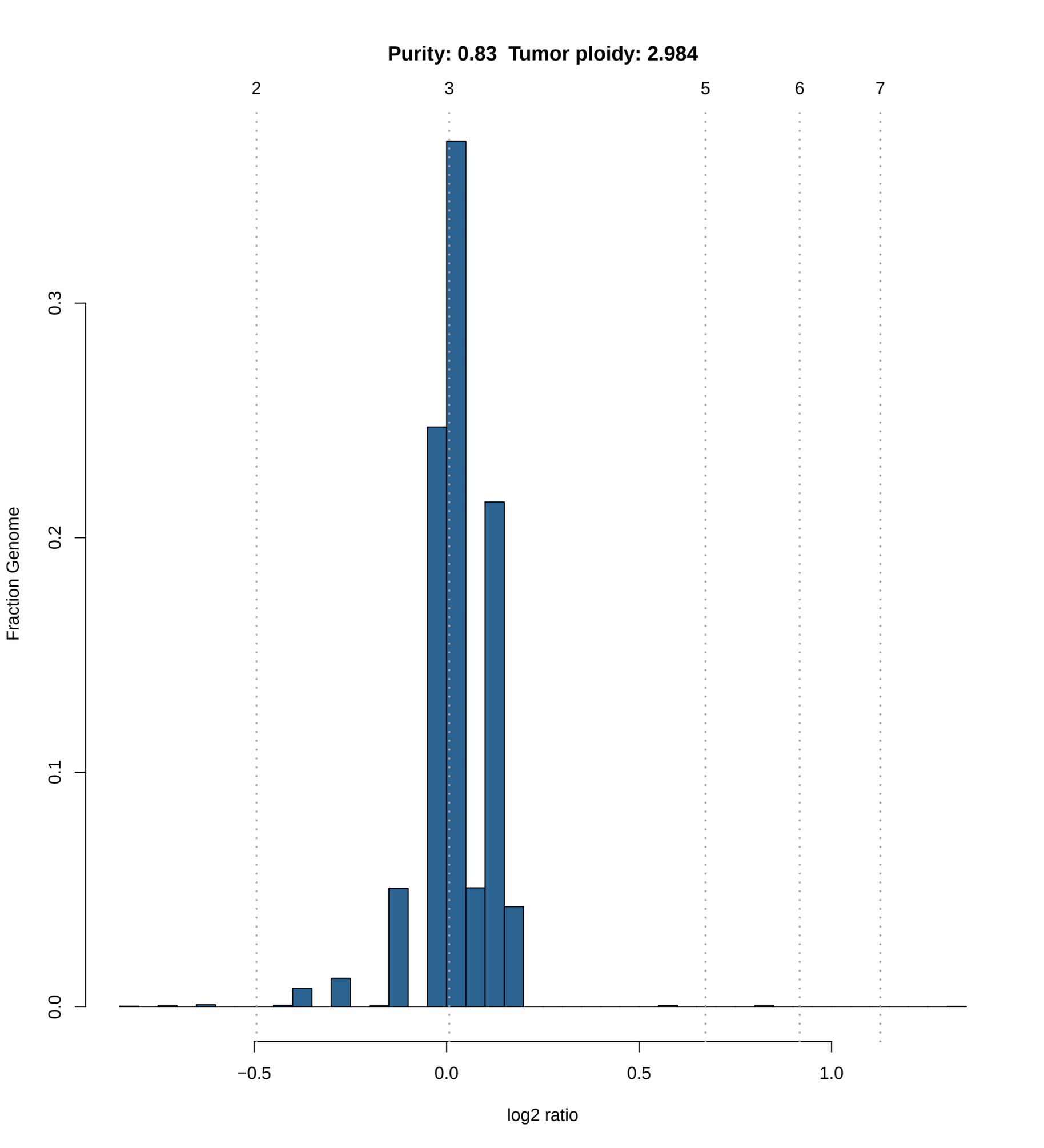

Maximum Likelihood Copy Number
0.0
0.5
1.0
1.5
2.0
0
20
40
60
80
100
SNV Index

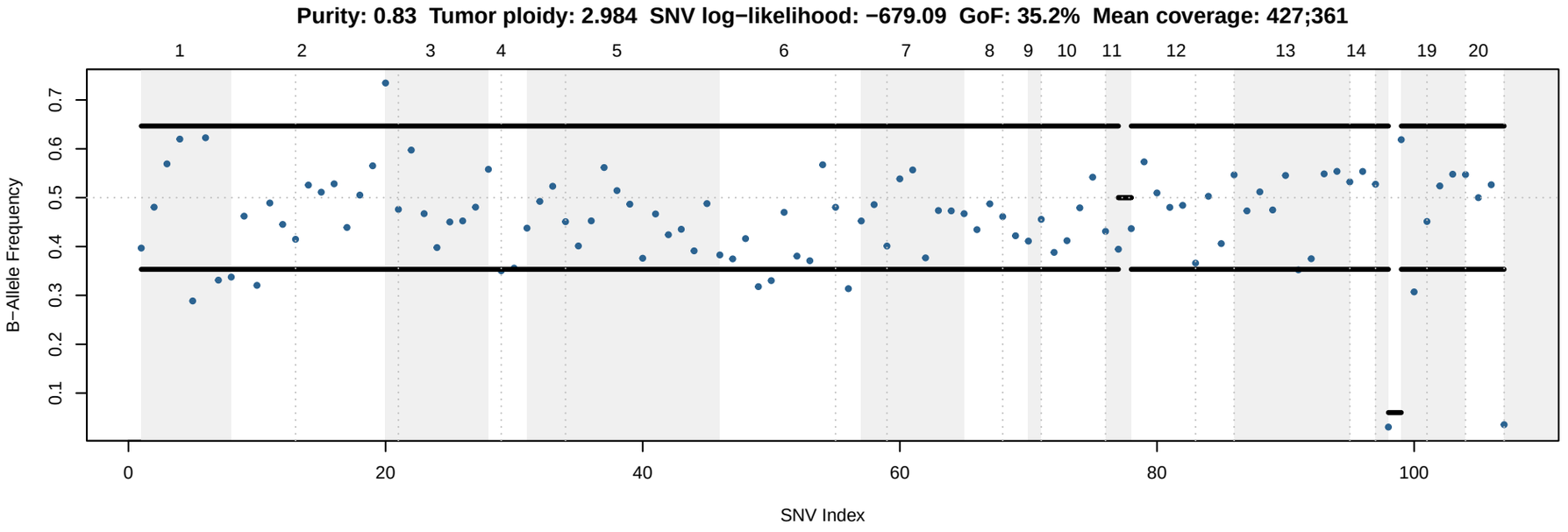

2m2
2m1
1m0
Allelic fraction (germline)
Copy Number log−ratio

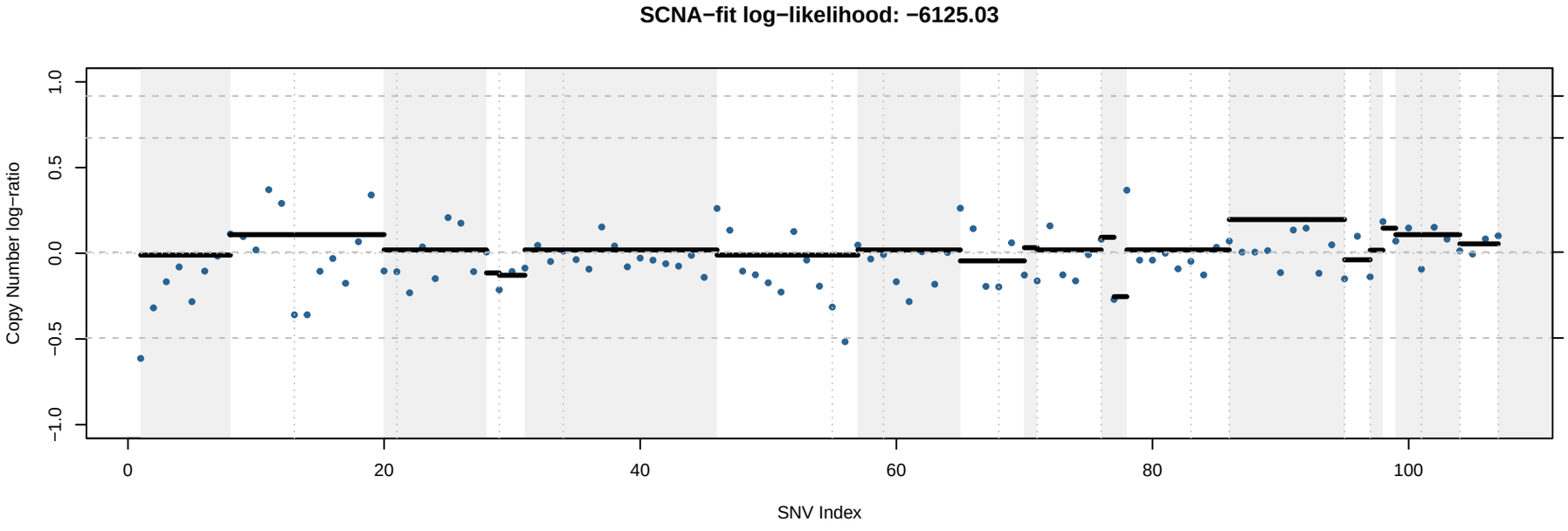

Coverage (log2)
Allelic fraction

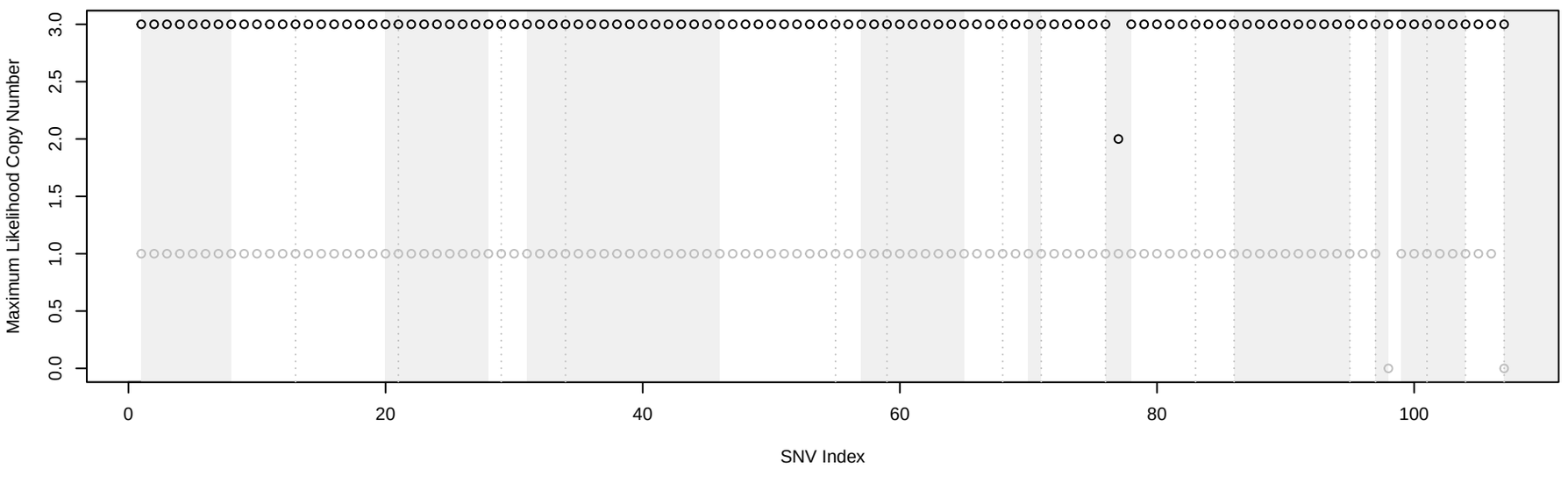

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
Allelic fraction (somatic)
Copy Number log−ratio

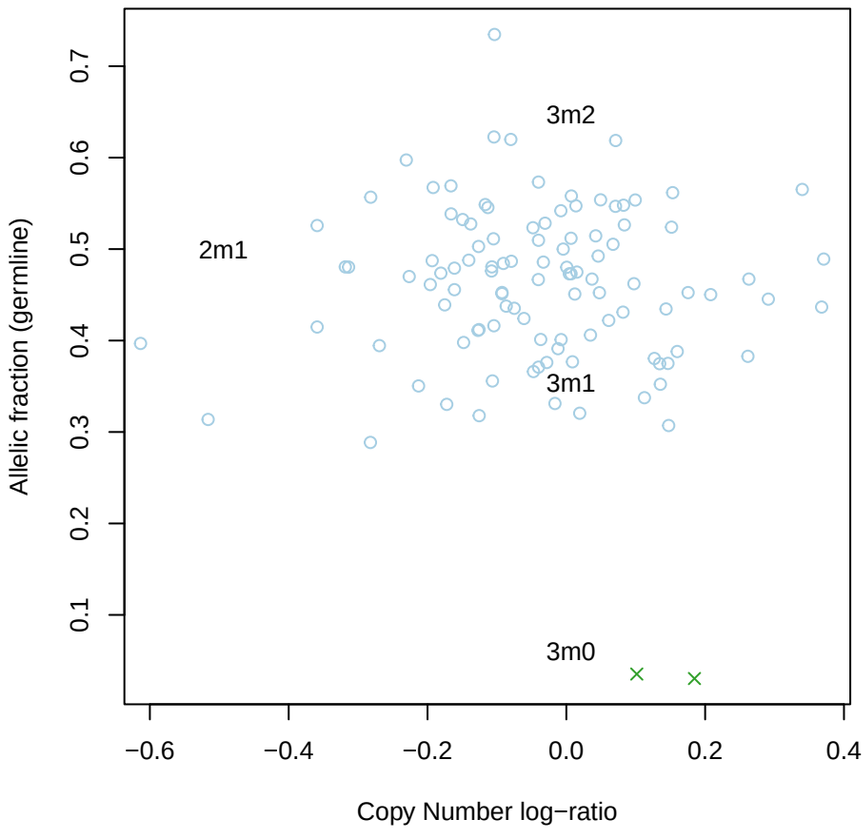

Frequency
Cellular fraction

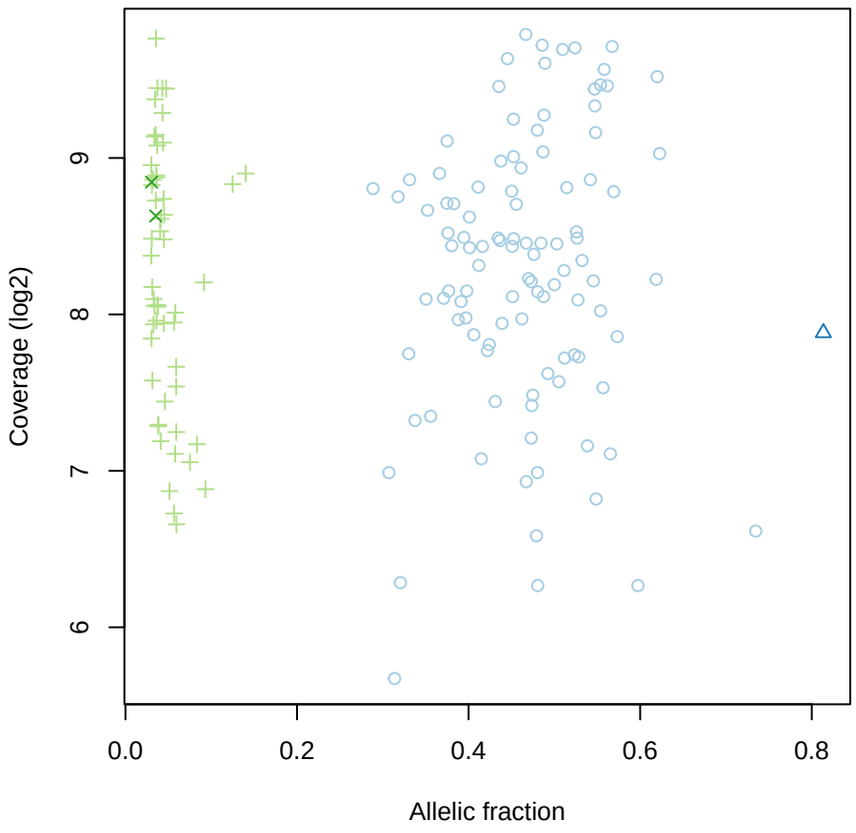

Purity: 0.83  Tumor ploidy: 2.984
2
3
5
6
7
0.0
0.1
0.2
0.3
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

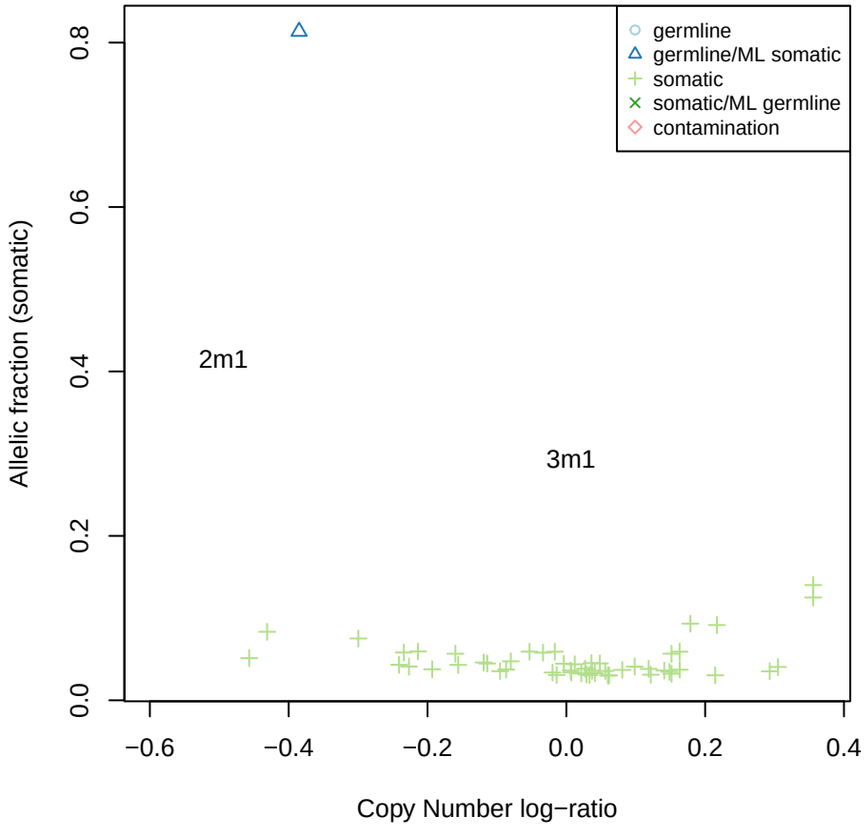

Purity: 0.83 Tumor ploidy: 2.984 SNV log−likelihood: −679.09 GoF: 35.2% Mean coverage: 427;361
1
2
3
4
5
6
7
8
9
10
11
12
13
14
19
20
B−Allele Frequency
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0
20
40
60
80
100
SNV Index

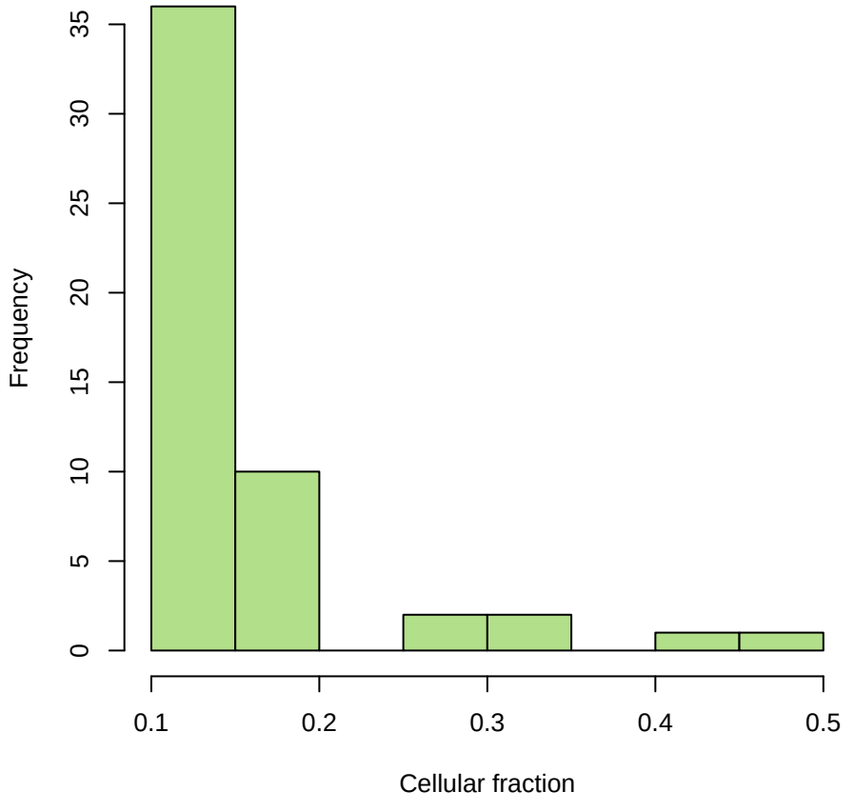

SCNA−fit log−likelihood: −6125.03
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
2
3
5
6
0
20
40
60
80
100
SNV Index


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)
Copy Number log−ratio
2m1
3m2
3m1
3m0


Coverage (log2)
Allelic fraction


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


Frequency
Cellular fraction