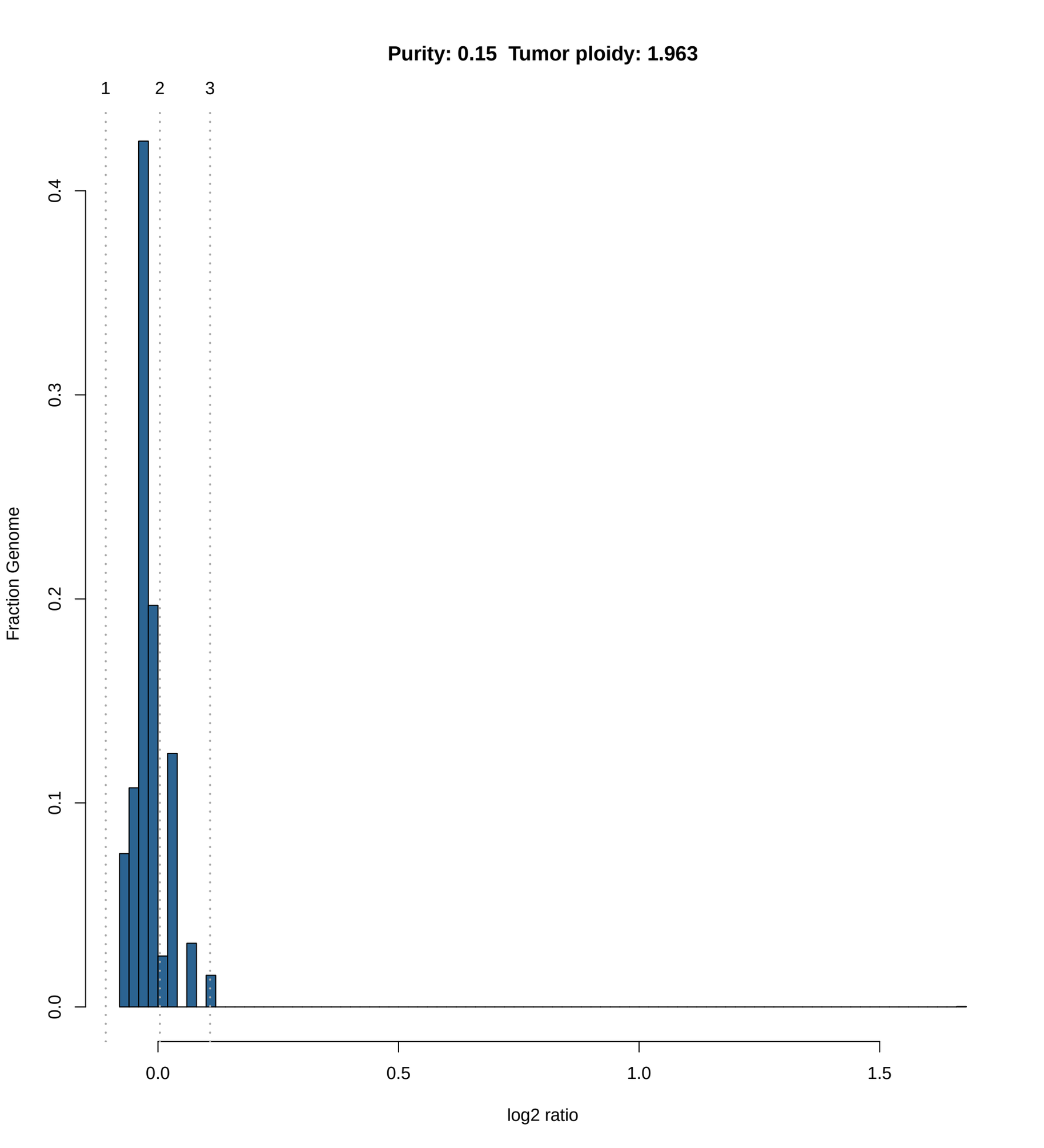
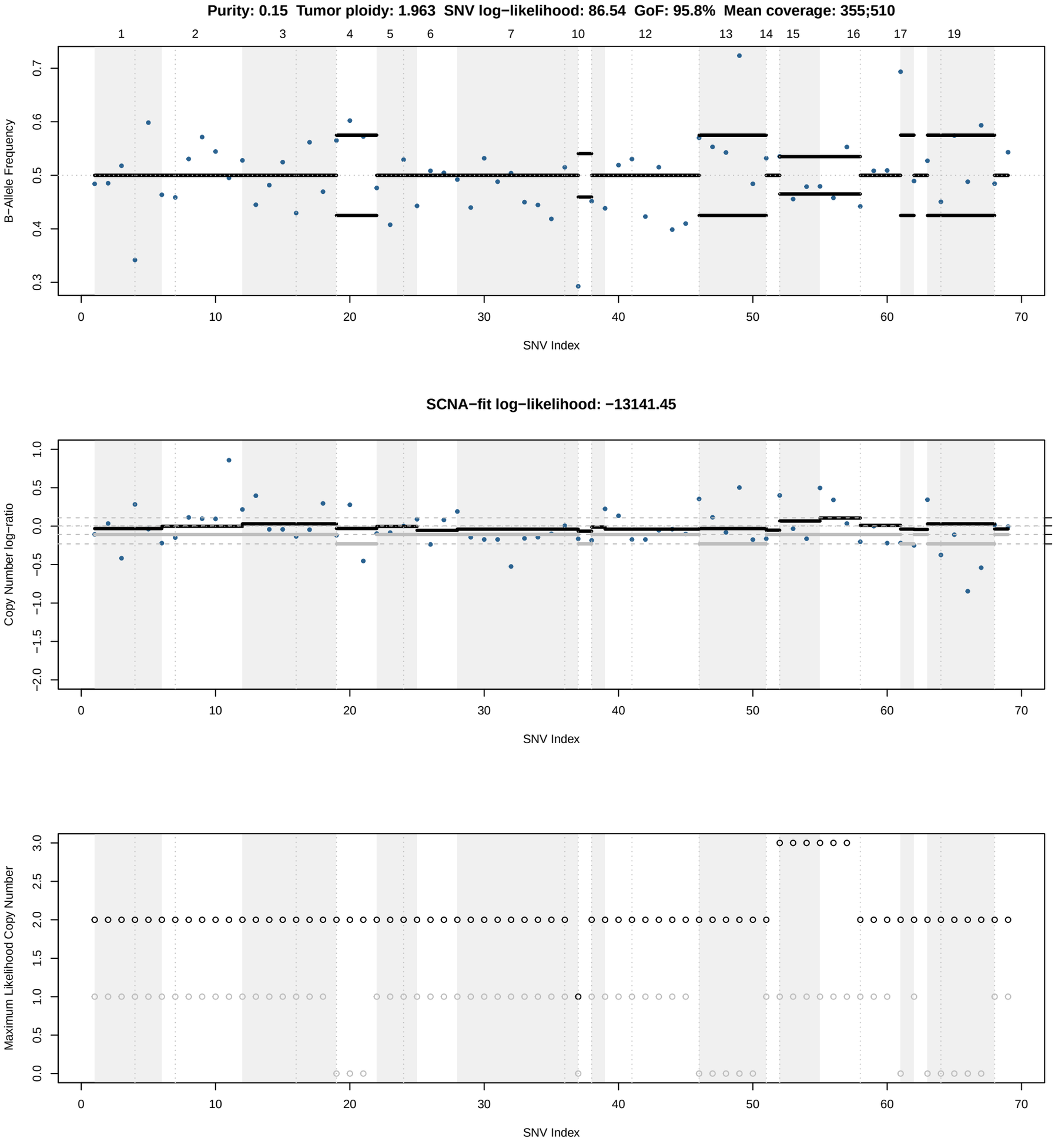
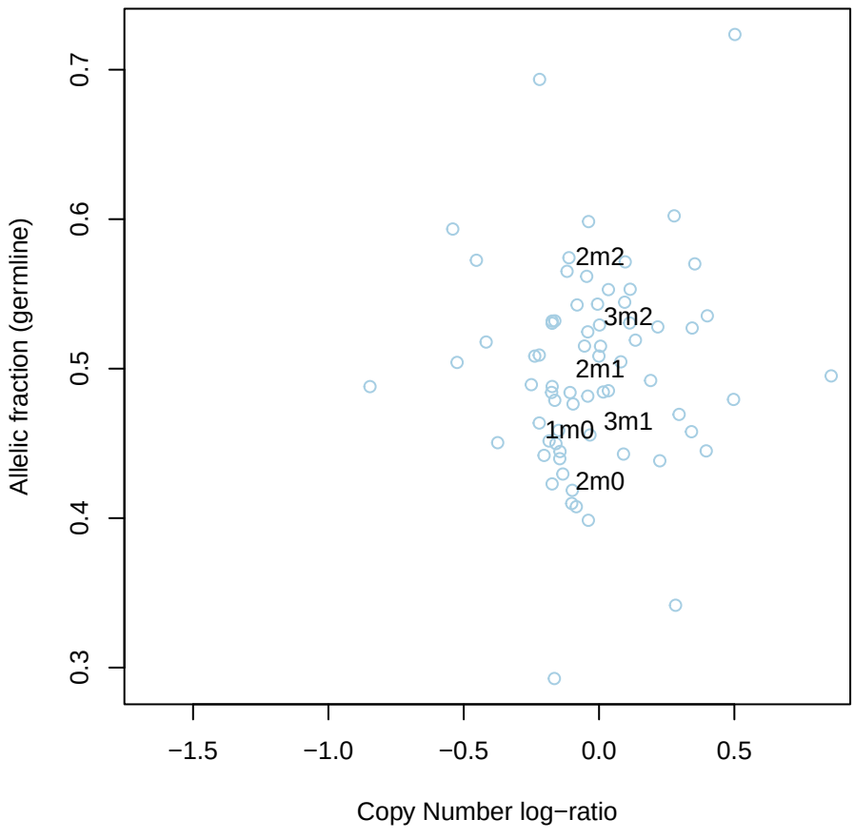
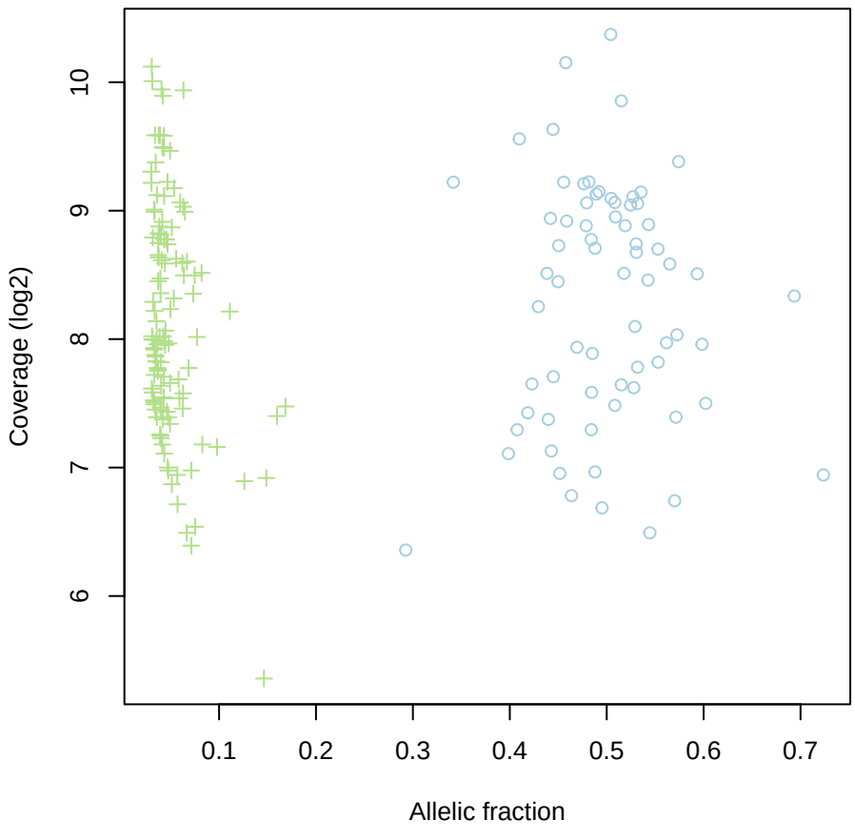
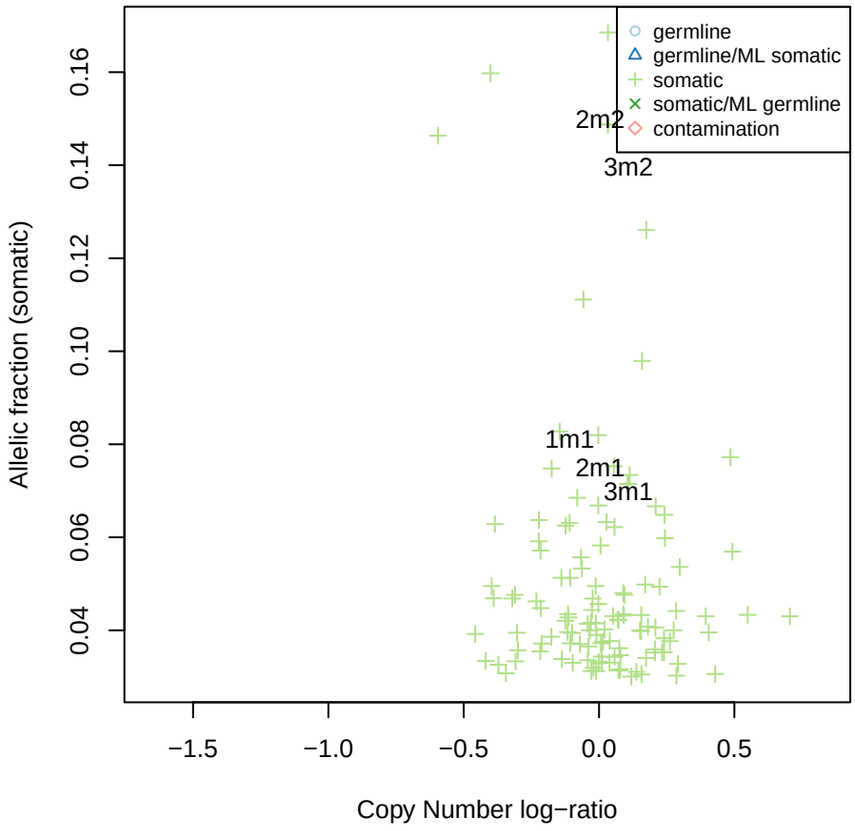
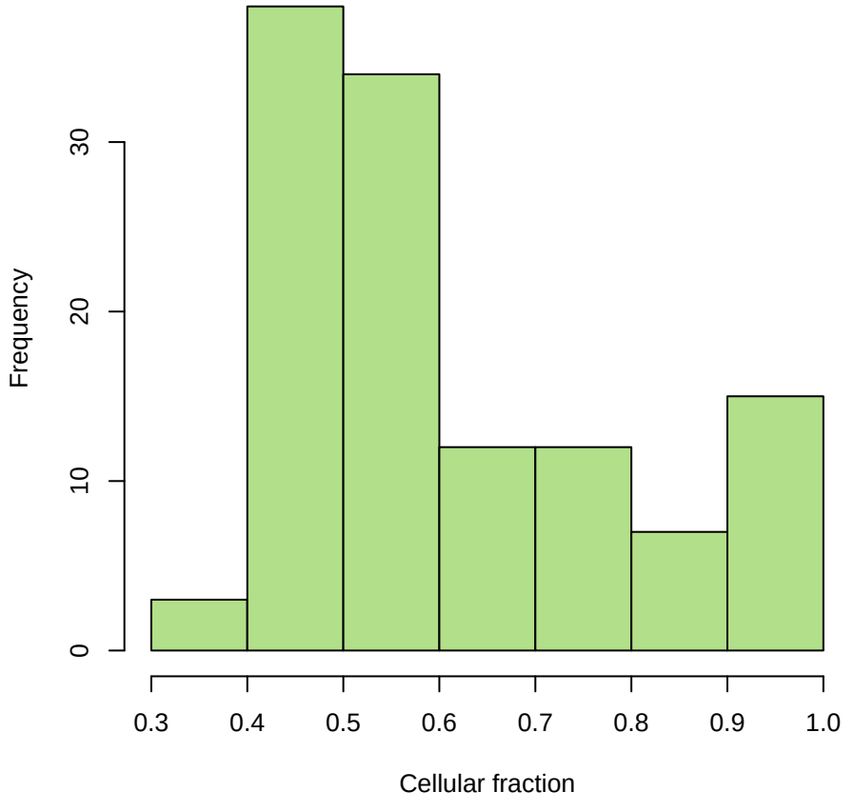

Purity: 0.15 Tumor ploidy: 1.963
1
2
3
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.0
0.5
1.0
1.5
log2 ratio

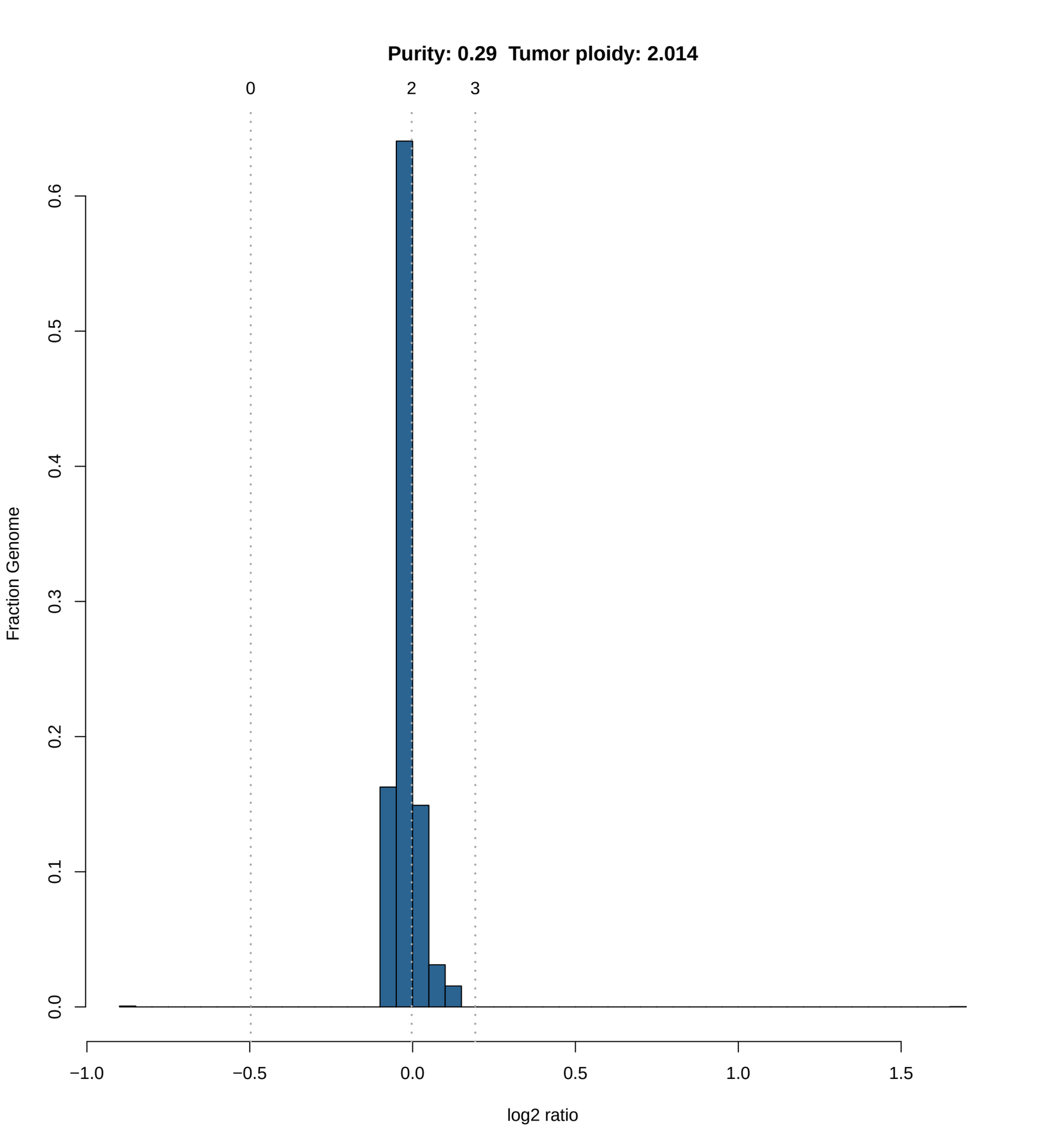

Purity: 0.15 Tumor ploidy: 1.963 SNV log−likelihood: 86.54 GoF: 95.8% Mean coverage: 355;510
1 2 3 4 5 6 7 10 12 13 14 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index
SCNA−fit log−likelihood: −13141.45
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 2
0 10 20 30 40 50 60 70
SNV Index
Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 10 20 30 40 50 60 70
SNV Index

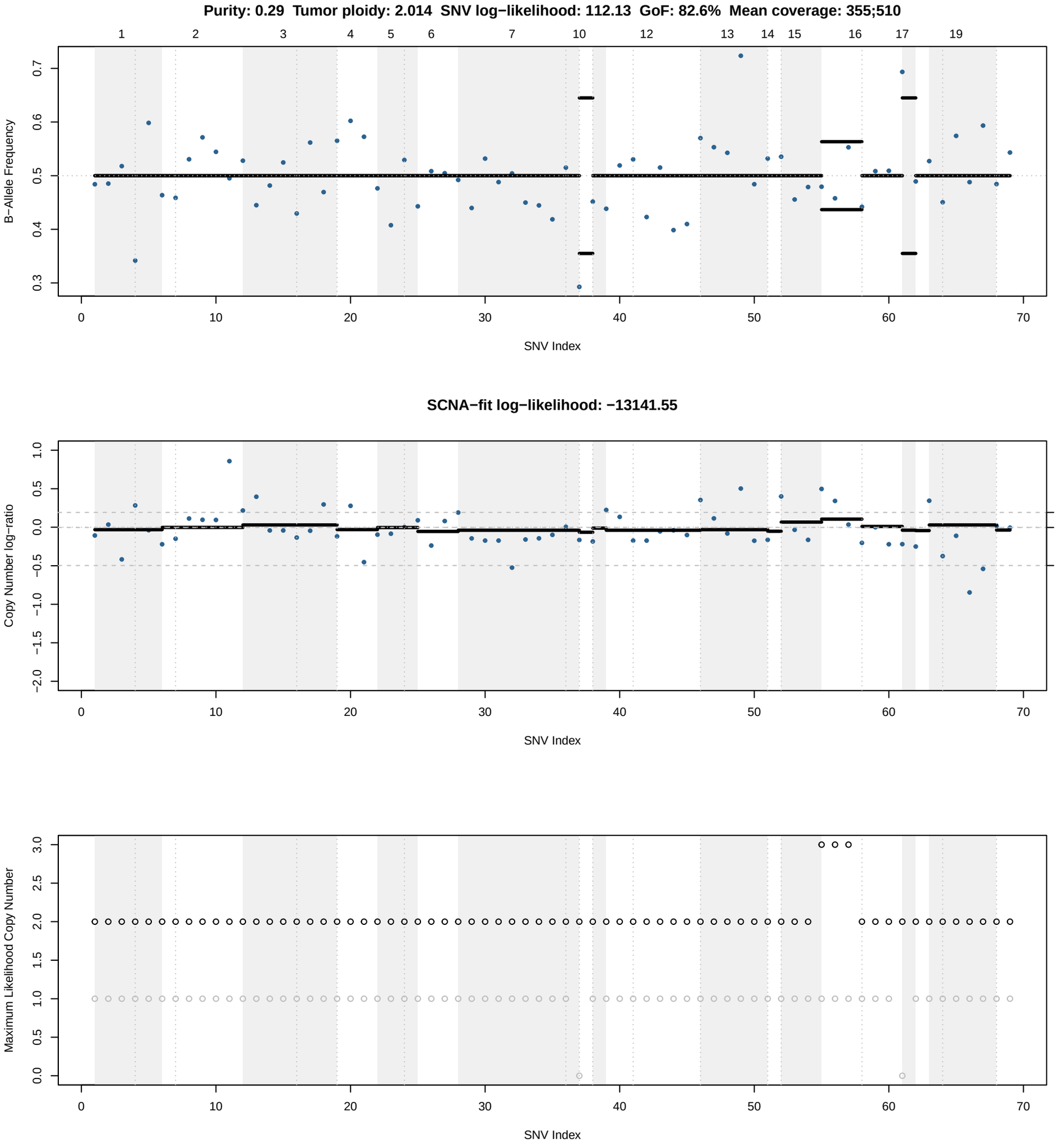

Allelic fraction (germline)
Copy Number log−ratio
2m2
3m2
2m1
3m1
1m0
2m0

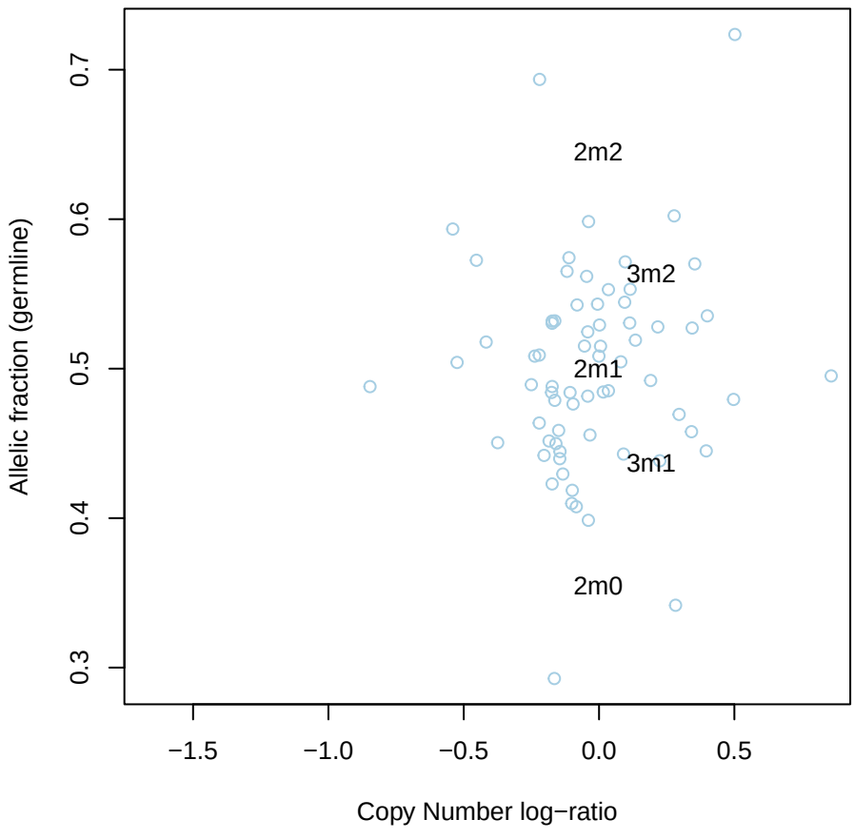

Coverage (log2)
Allelic fraction

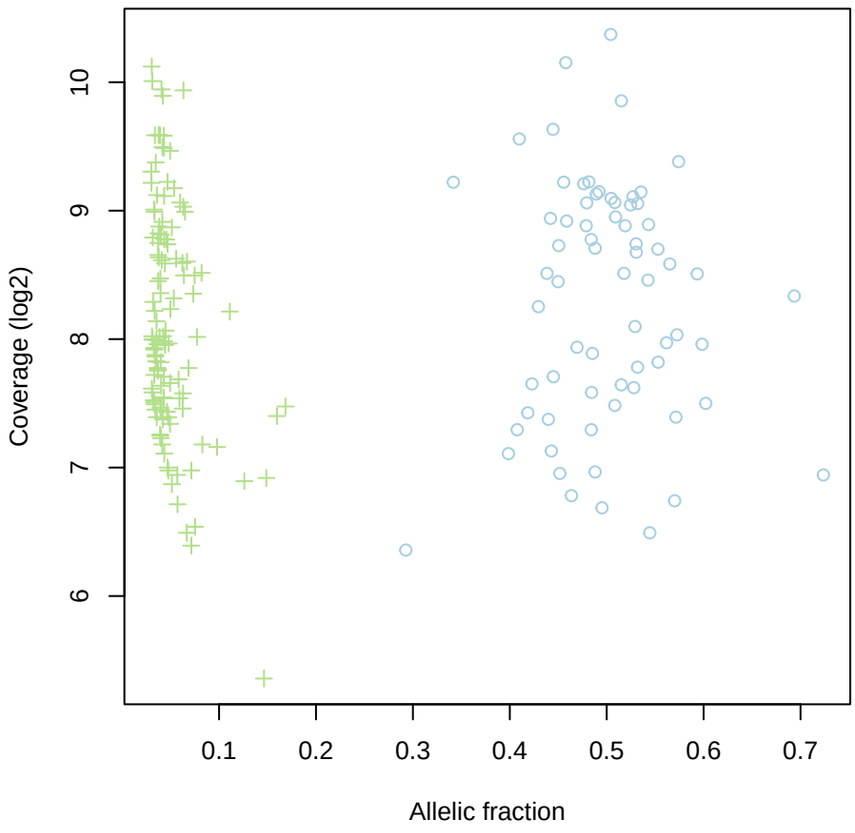

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
3m2
1m1
2m1
3m1

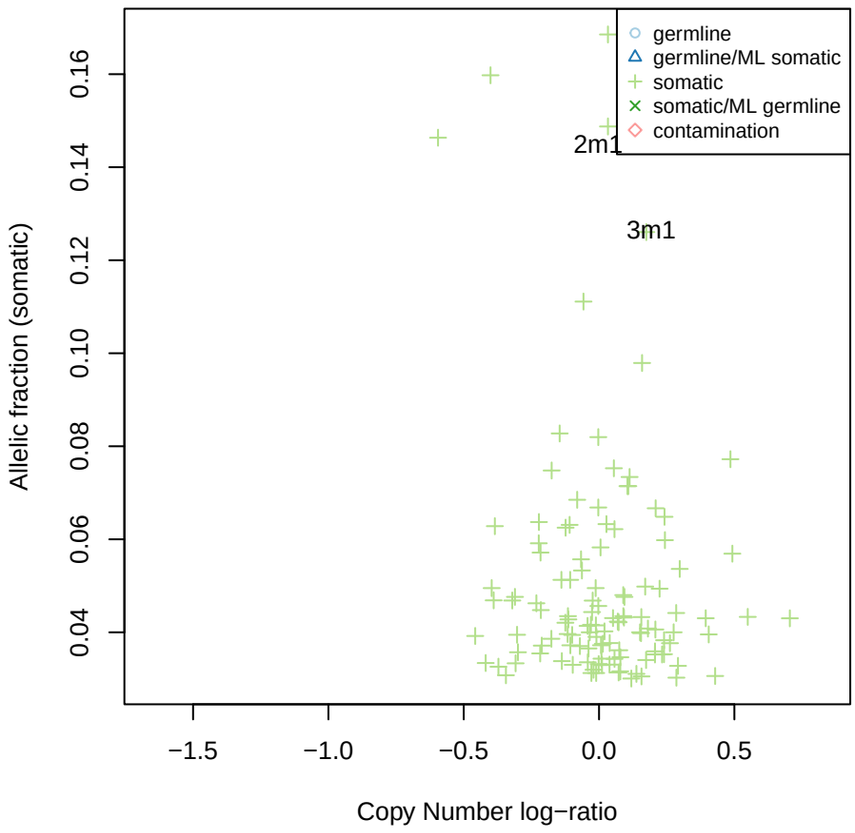

Frequency
Cellular fraction

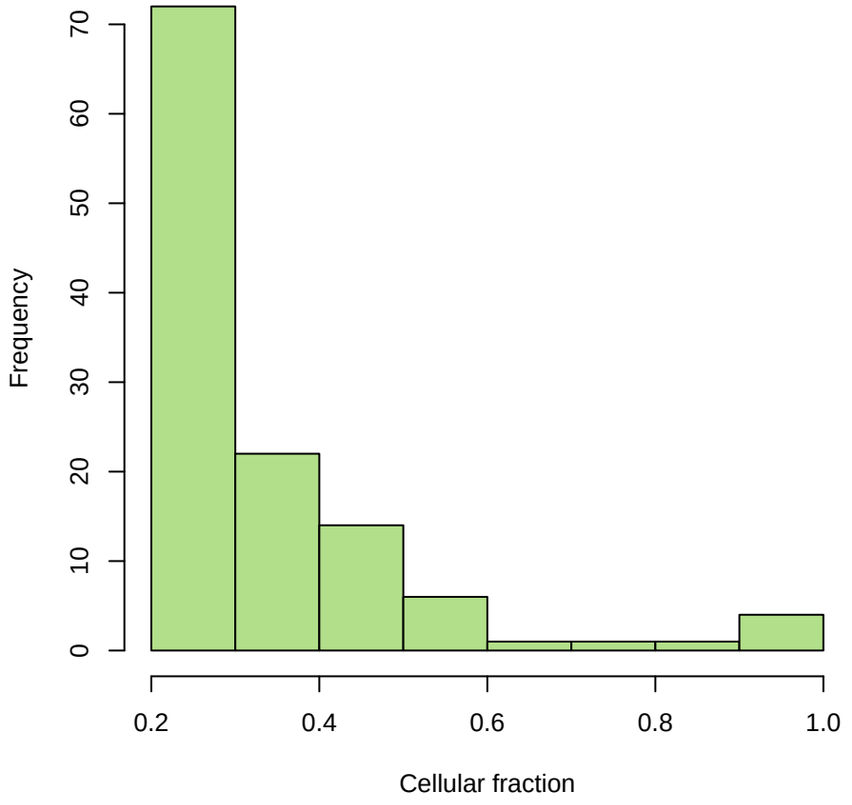

Purity: 0.29 Tumor ploidy: 2.014
0
2
3
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.6
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

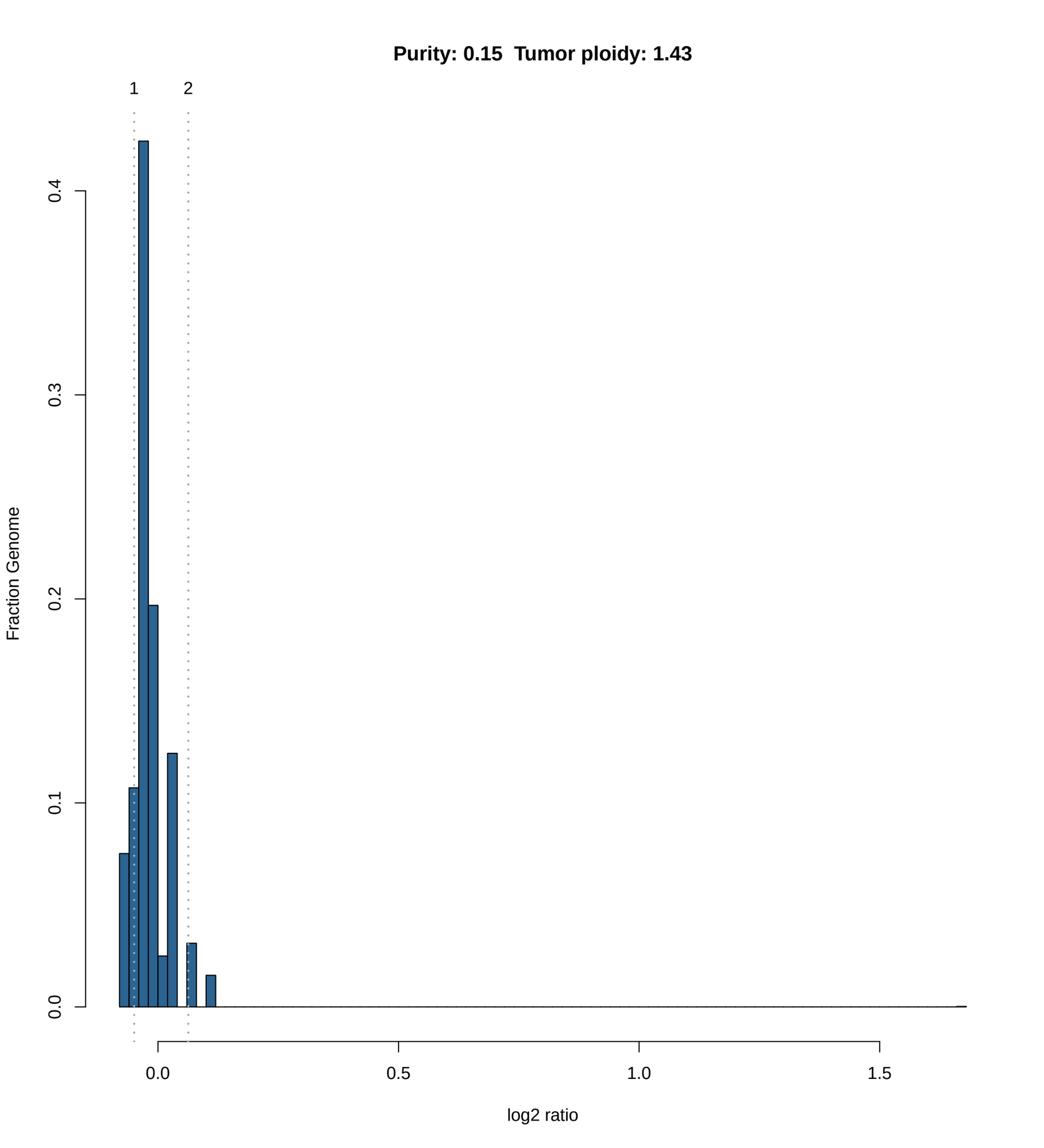

Purity: 0.29 Tumor ploidy: 2.014 SNV log−likelihood: 112.13 GoF: 82.6% Mean coverage: 355;510
1 2 3 4 5 6 7 10 12 13 14 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index
SCNA−fit log−likelihood: −13141.55
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 2
0 10 20 30 40 50 60 70
SNV Index
Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 10 20 30 40 50 60 70
SNV Index

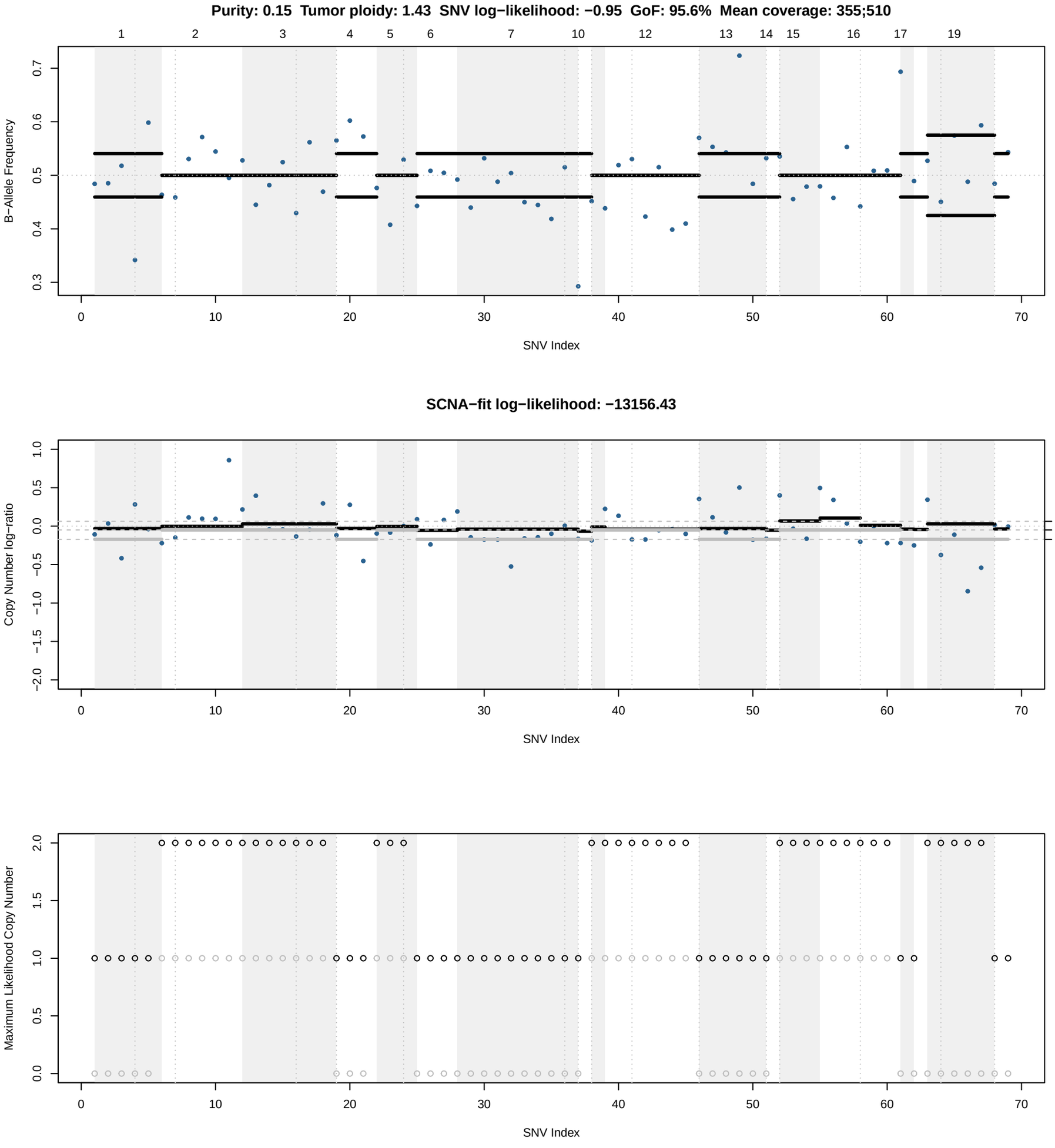

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
2m2
3m2
2m1
3m1
2m0
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

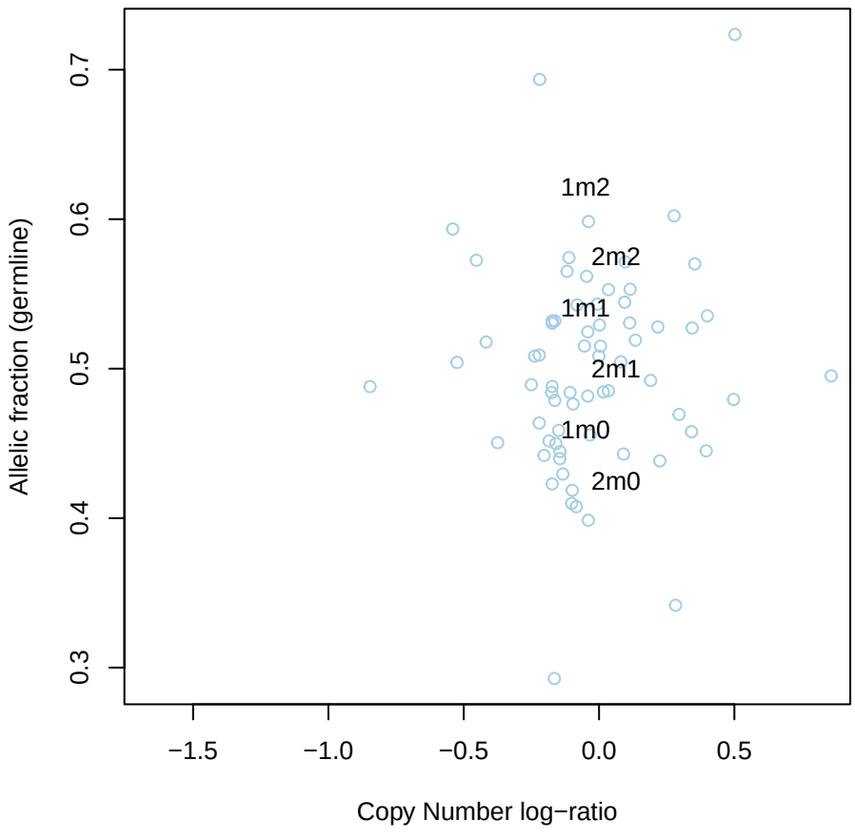

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

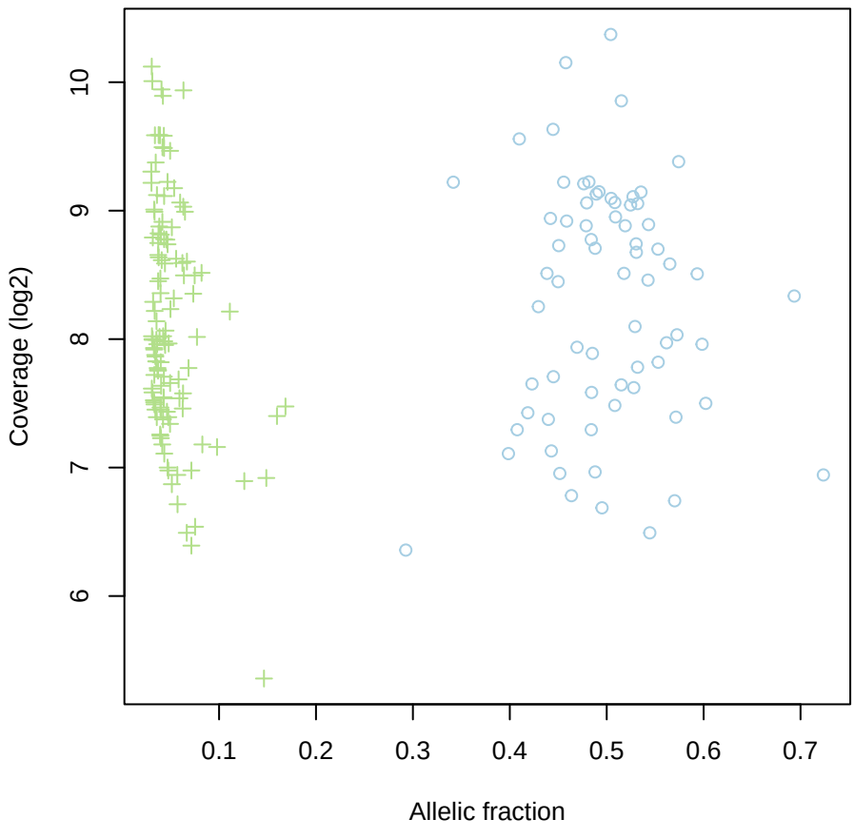

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

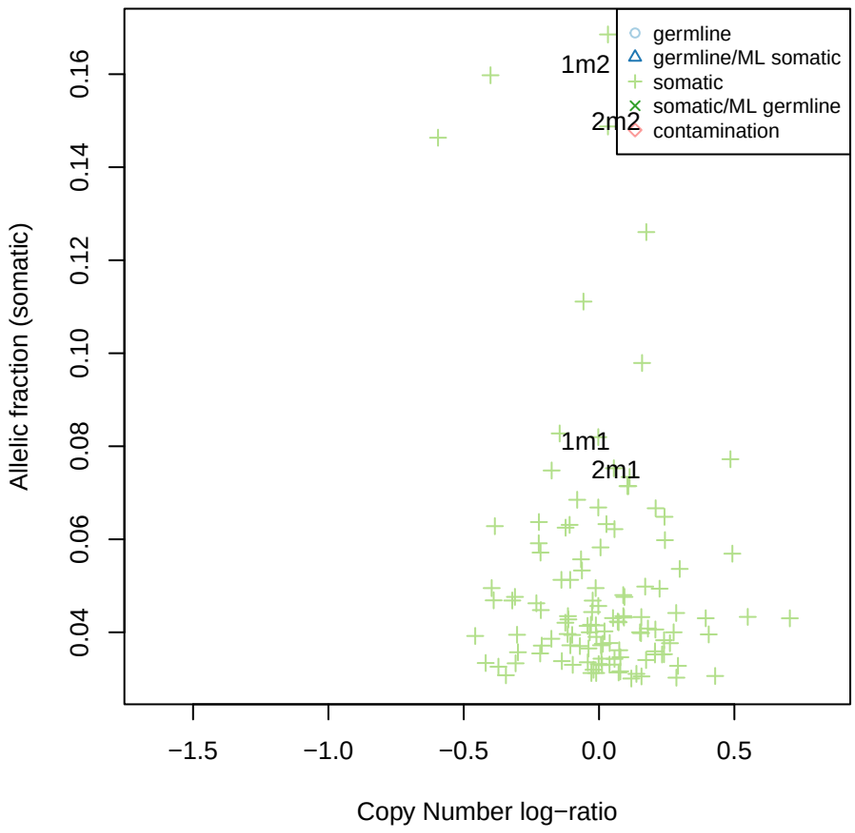

Frequency
0
10
20
30
40
50
60
70
0.2
0.4
0.6
0.8
1.0
Cellular fraction

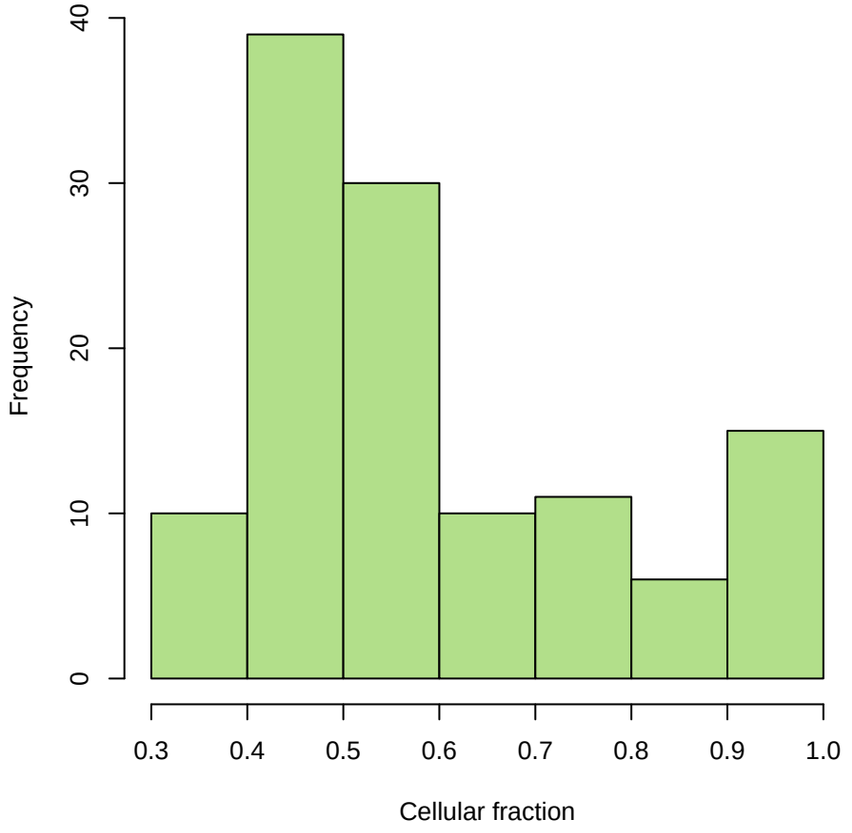

Purity: 0.15 Tumor ploidy: 1.43
1
2
0.4
0.3
0.2
0.1
0.0
Fraction Genome
0.0
0.5
1.0
1.5
log2 ratio

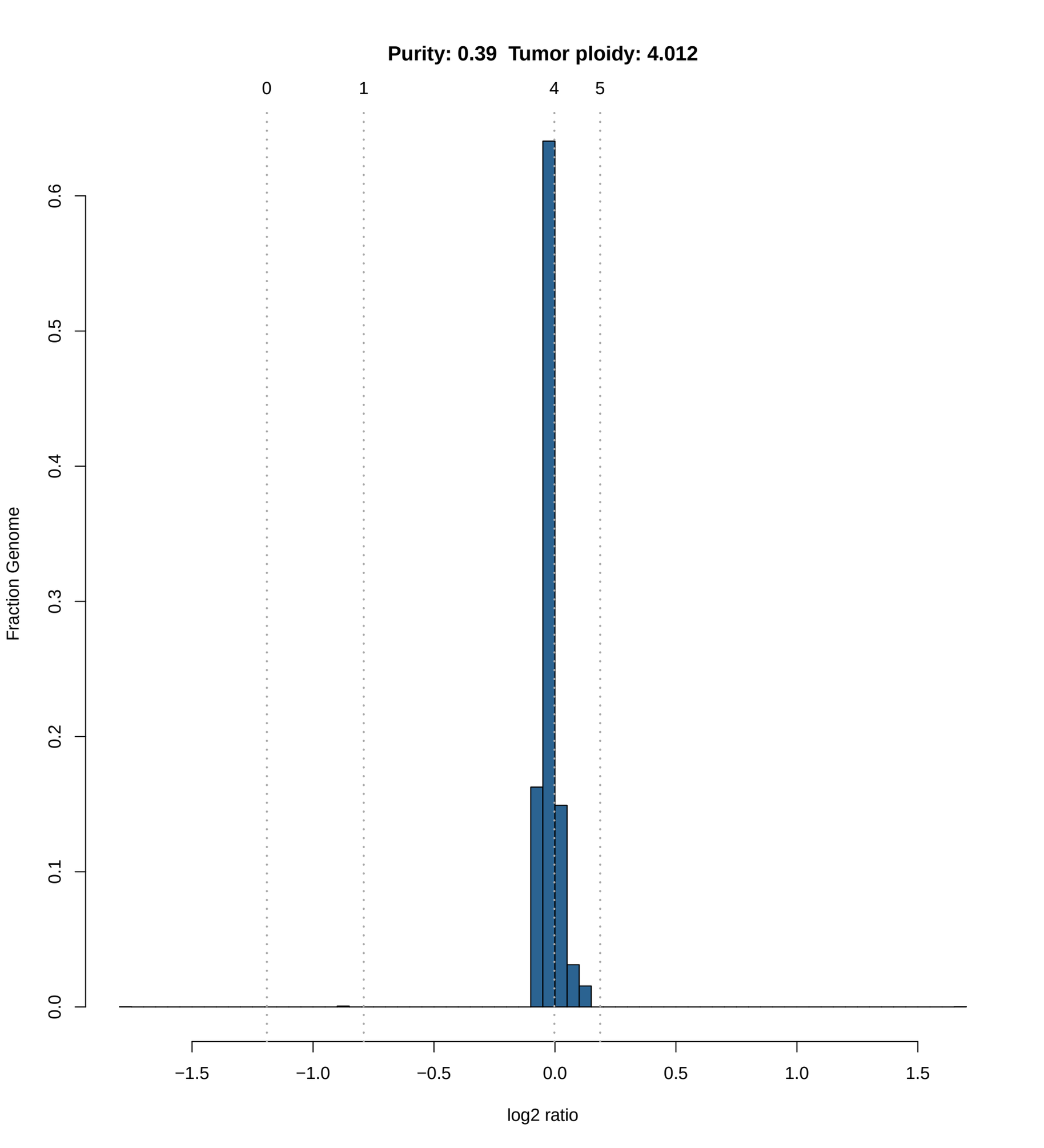

Purity: 0.15 Tumor ploidy: 1.43 SNV log−likelihood: −0.95 GoF: 95.6% Mean coverage: 355;510
1 2 3 4 5 6 7 10 12 13 14 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index
SCNA−fit log−likelihood: −13156.43
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2
0 10 20 30 40 50 60 70
SNV Index
Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 10 20 30 40 50 60 70
SNV Index

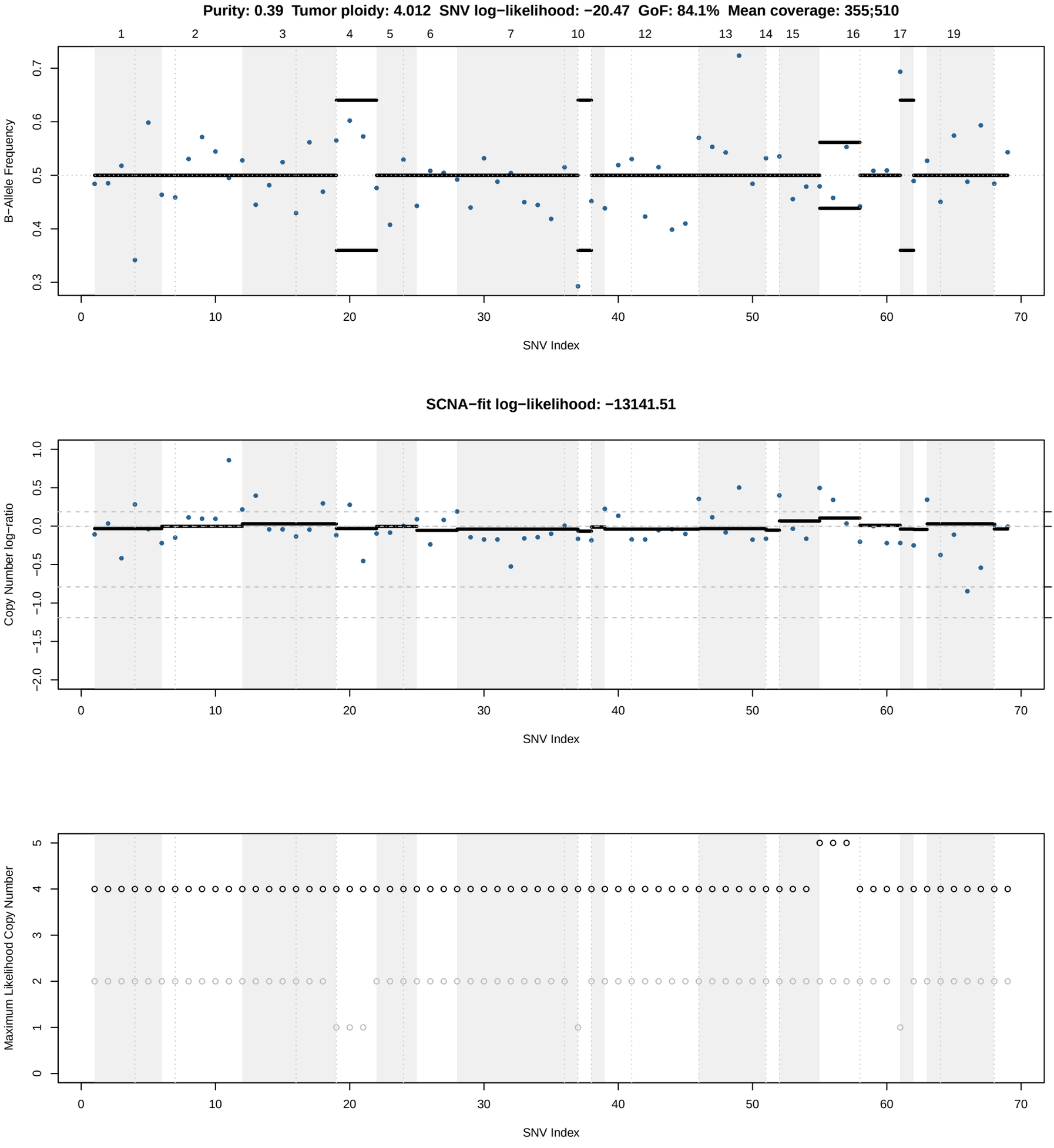

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
1m2
2m2
1m1
2m1
1m0
2m0
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

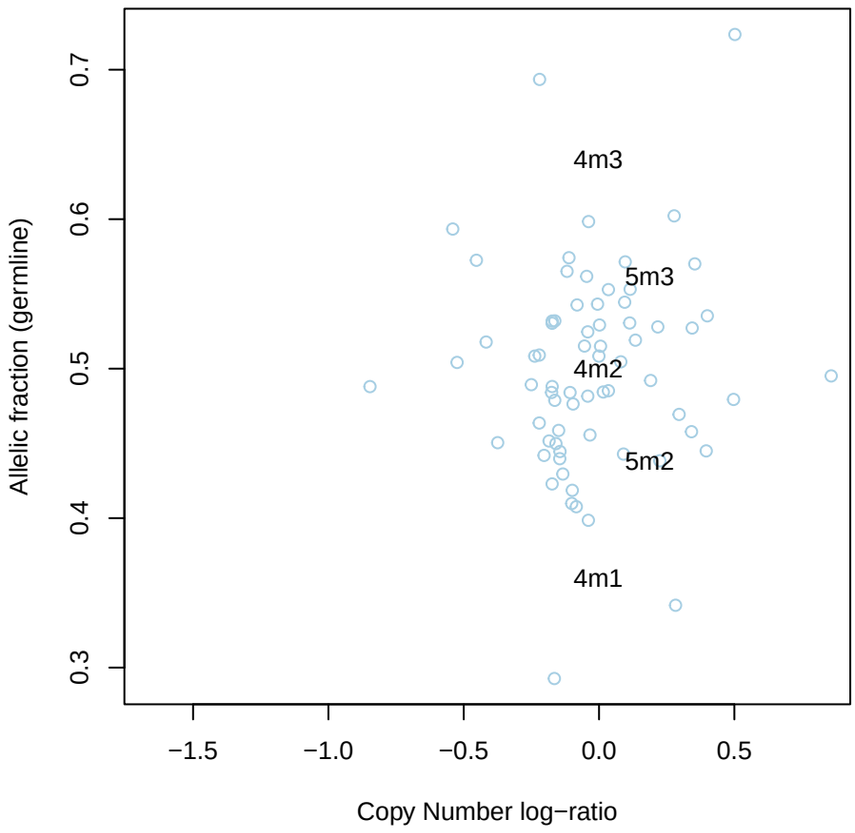

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

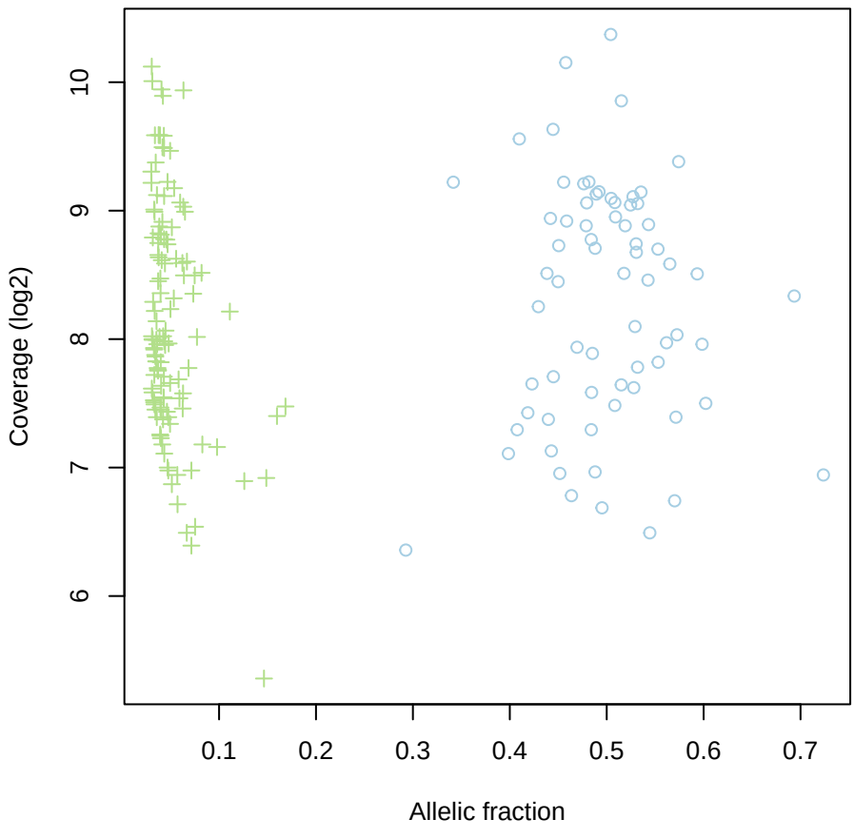

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m2
2m2
1m1
2m1
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

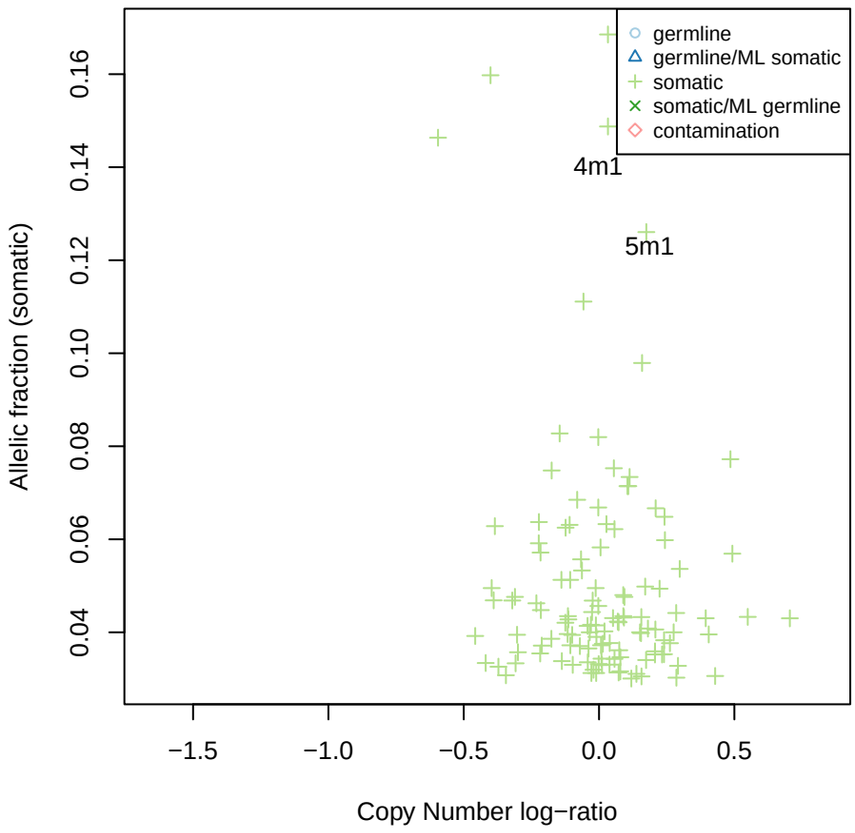

Frequency
0
10
20
30
40
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

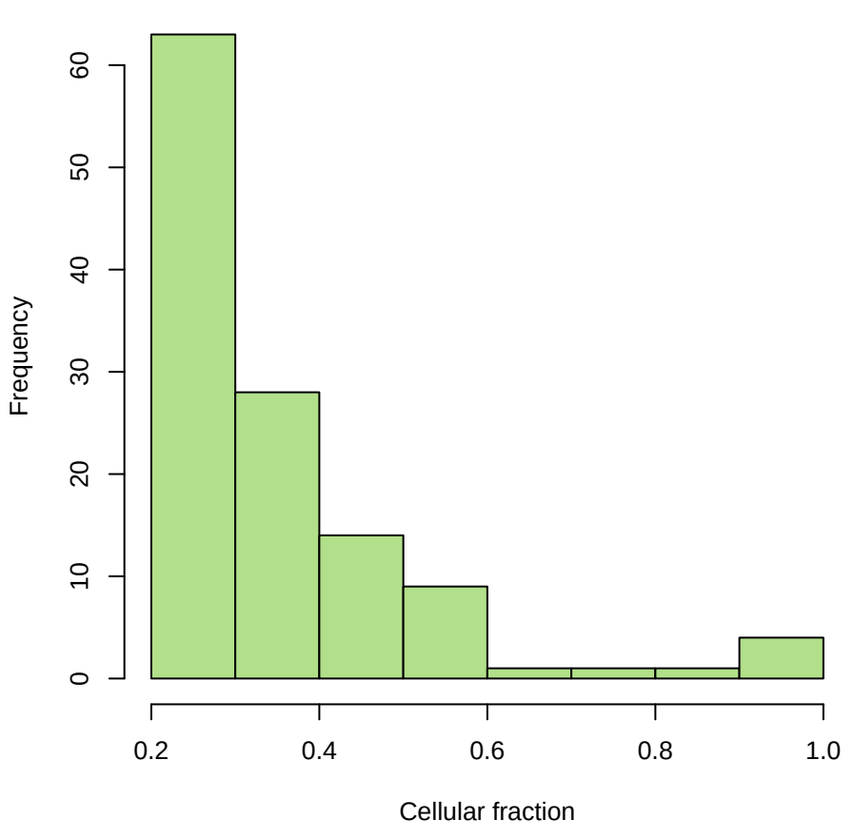

Purity: 0.39 Tumor ploidy: 4.012
0
1
4
5
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

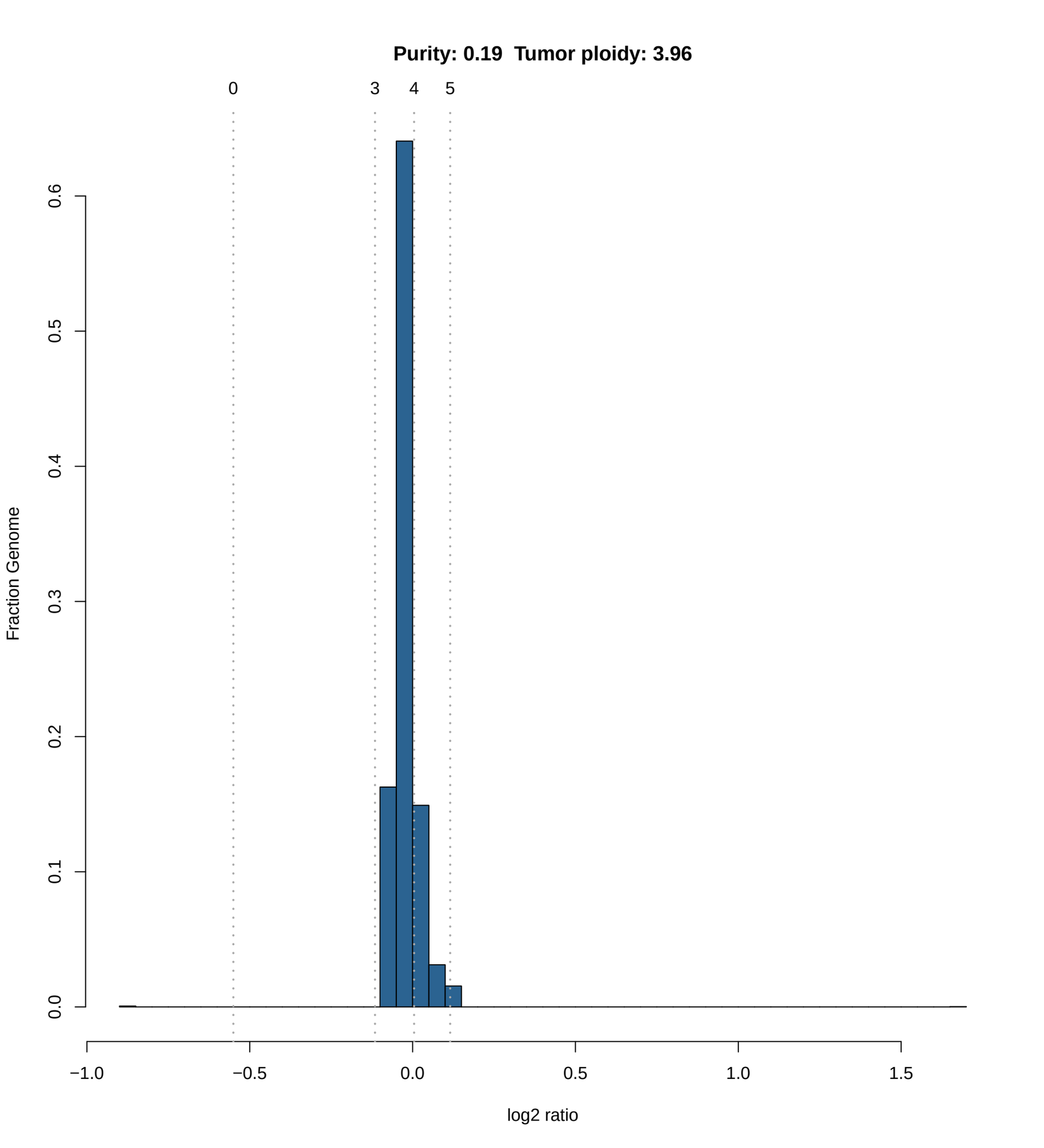

Purity: 0.39 Tumor ploidy: 4.012 SNV log−likelihood: −20.47 GoF: 84.1% Mean coverage: 355;510
1 2 3 4 5 6 7 10 12 13 14 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index
SCNA−fit log−likelihood: −13141.51
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 4
0 10 20 30 40 50 60 70
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5
0 10 20 30 40 50 60 70
SNV Index

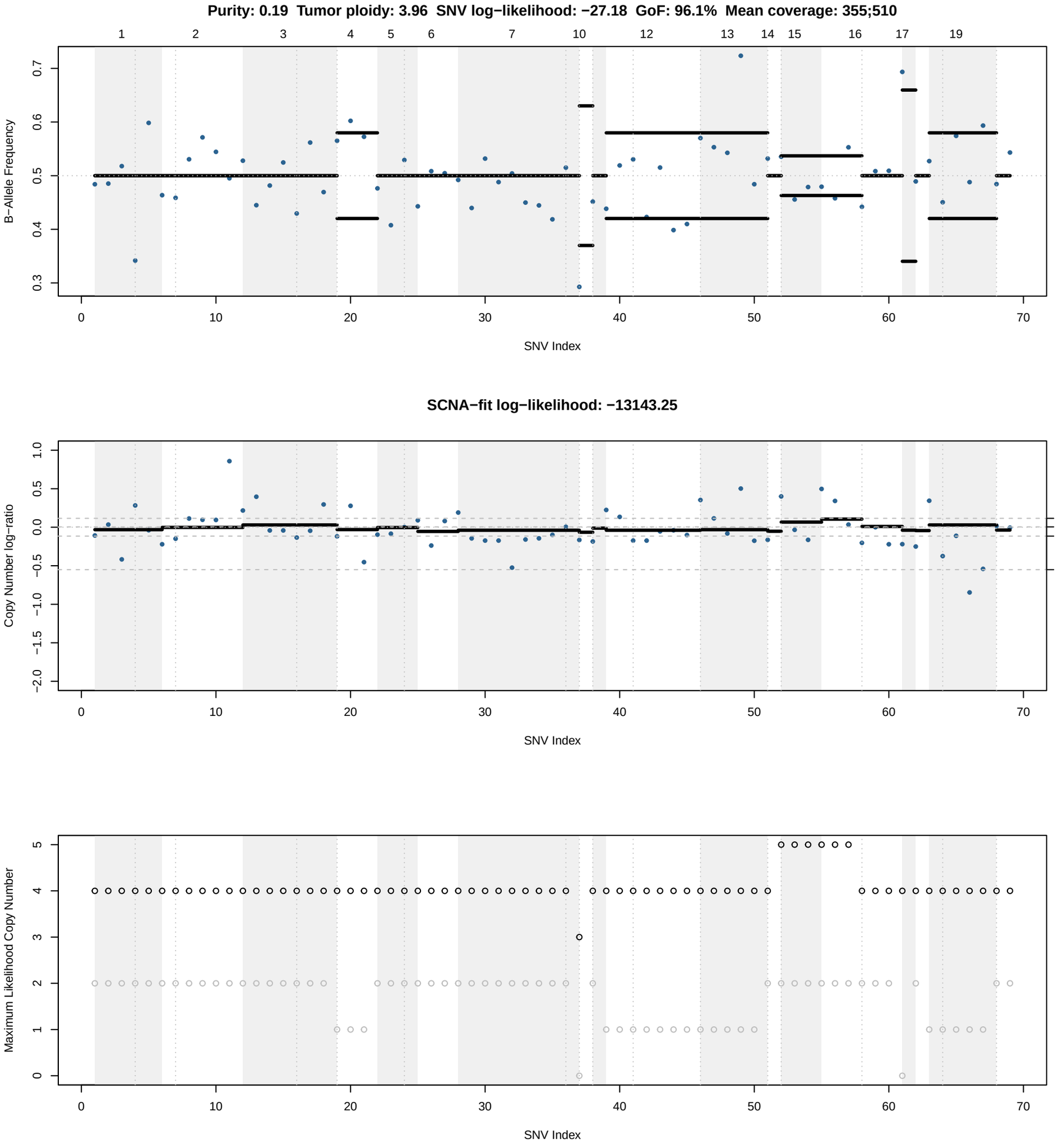

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
4m3
5m3
4m2
5m2
4m1
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

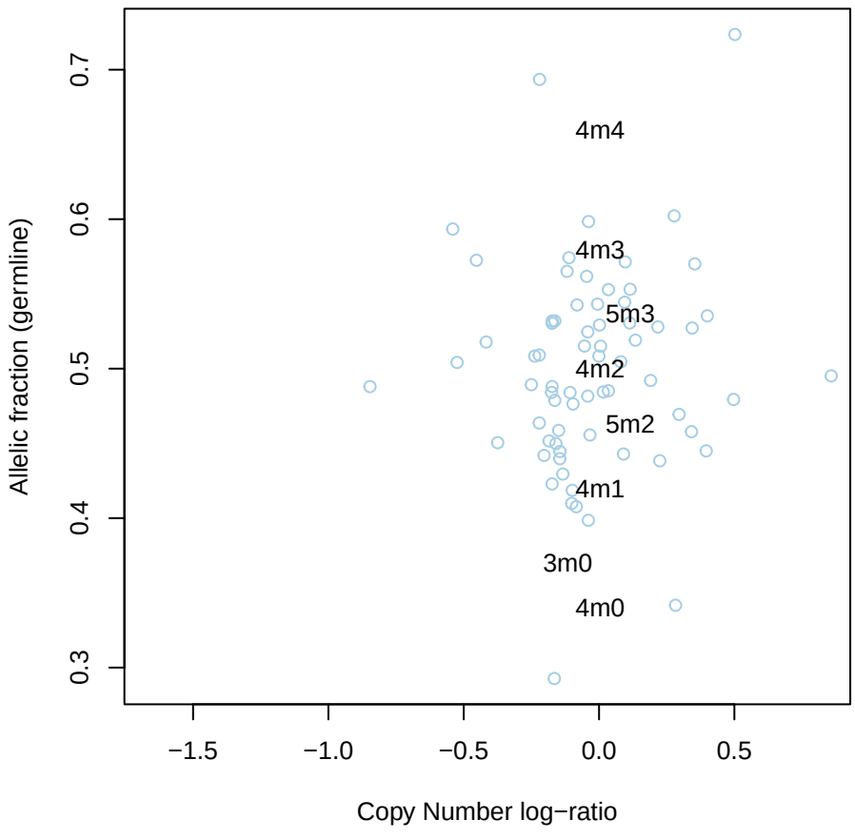

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

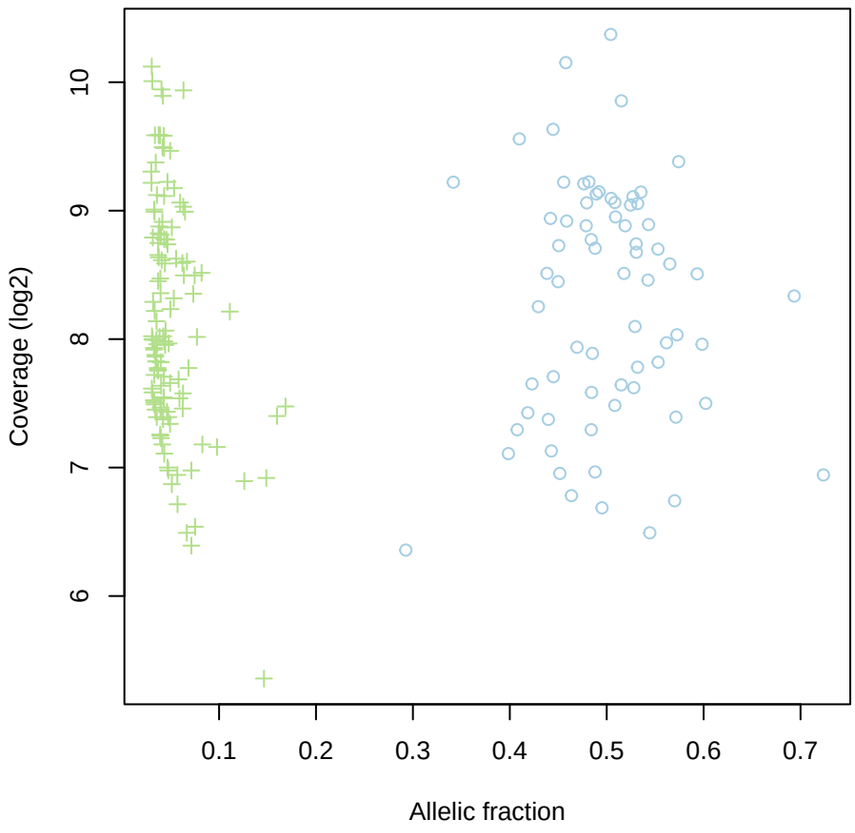

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
4m1
5m1
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

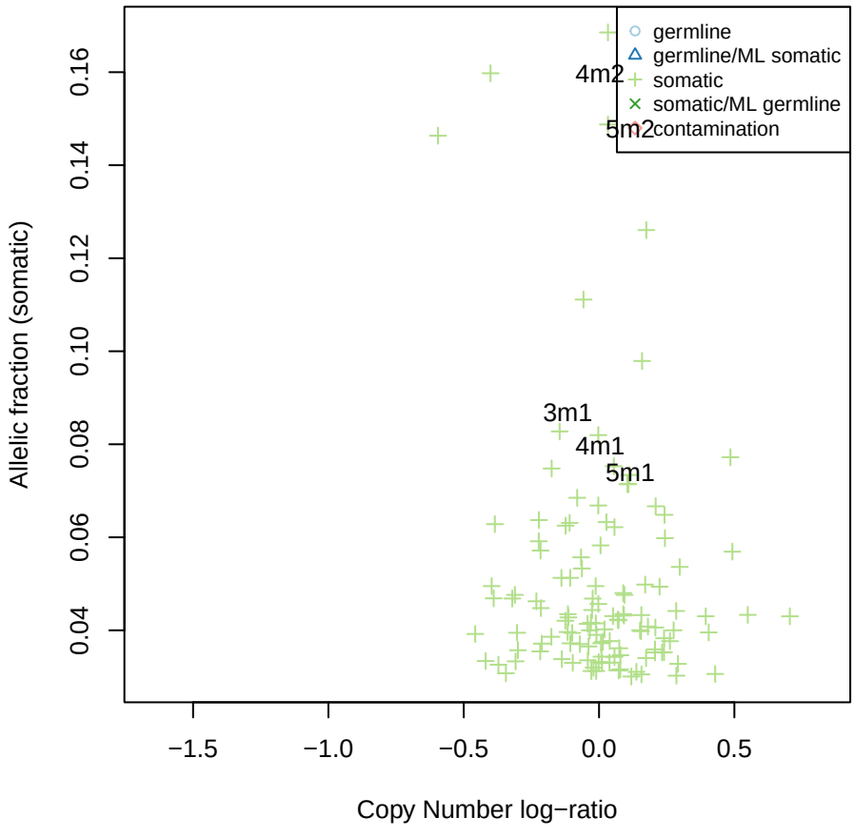

Frequency
0
10
20
30
40
50
60
0.2
0.4
0.6
0.8
1.0
Cellular fraction

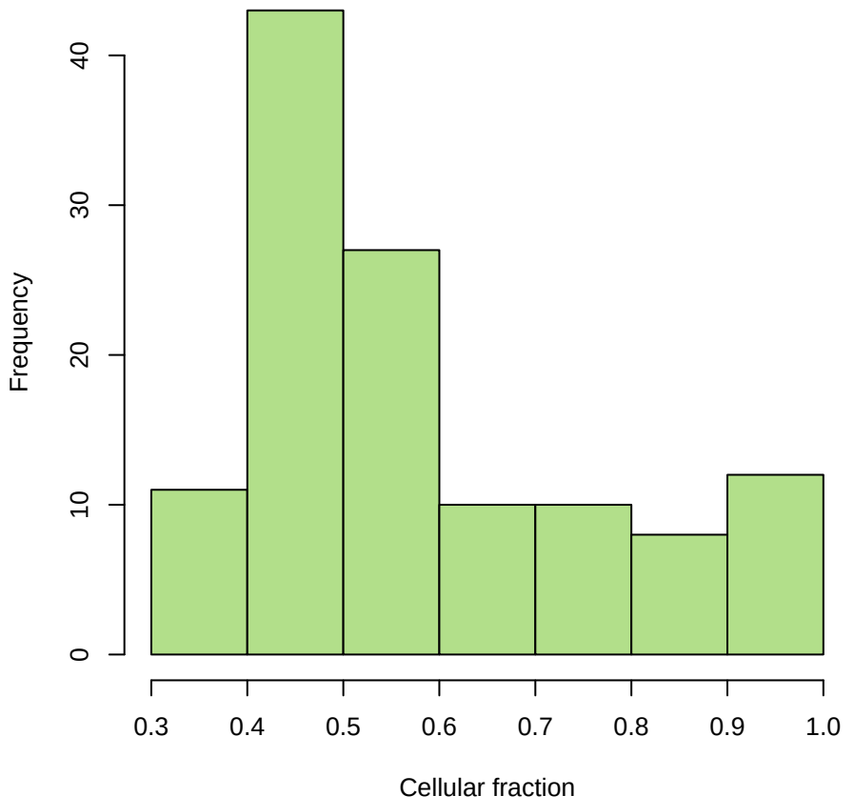

Purity: 0.19 Tumor ploidy: 3.96
0
3
4
5
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.6
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

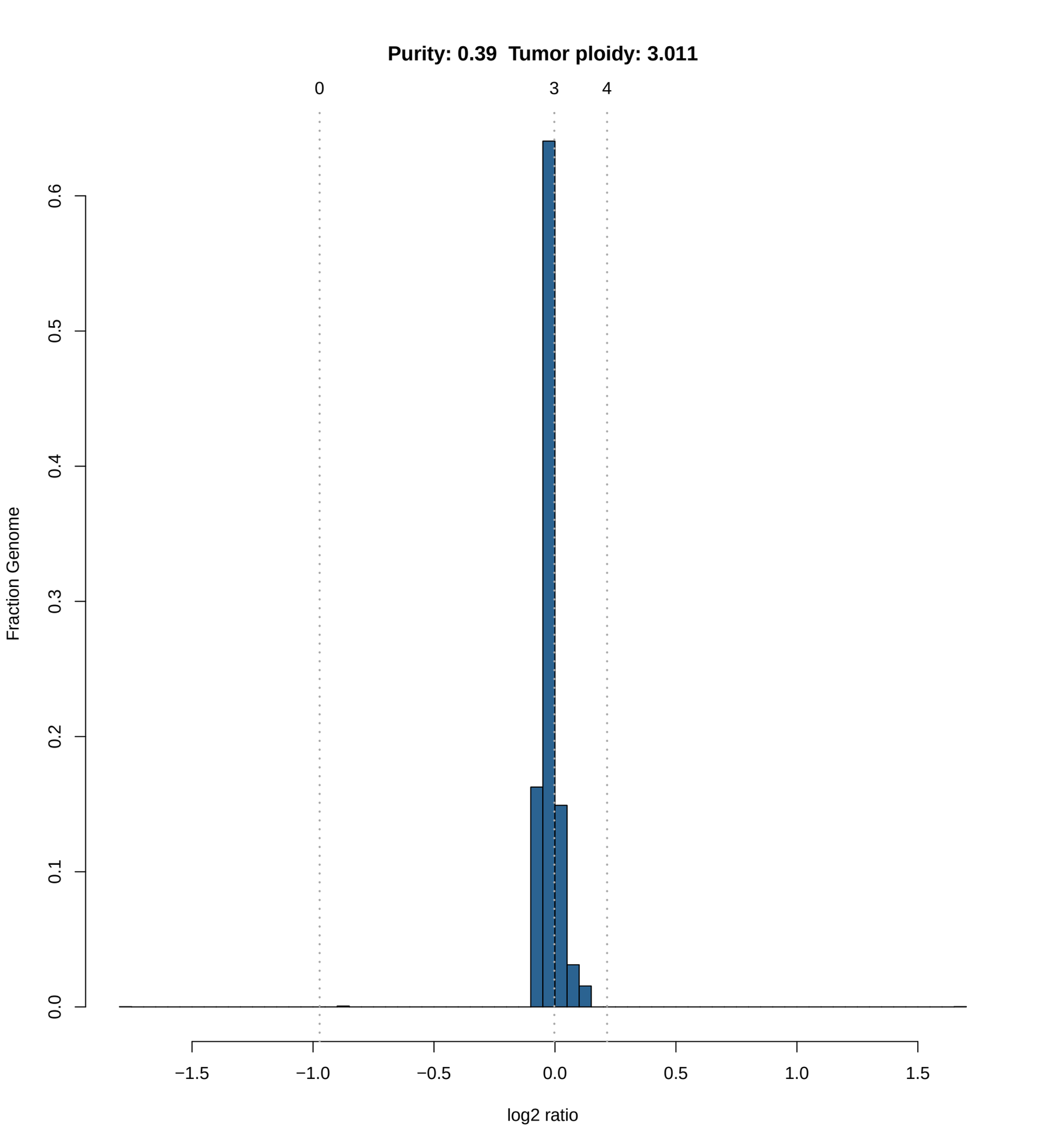

Purity: 0.19 Tumor ploidy: 3.96 SNV log−likelihood: −27.18 GoF: 96.1% Mean coverage: 355;510
1 2 3 4 5 6 7 10 12 13 14 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index
SCNA−fit log−likelihood: −13143.25
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 3 5
0 10 20 30 40 50 60 70
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5
0 10 20 30 40 50 60 70
SNV Index

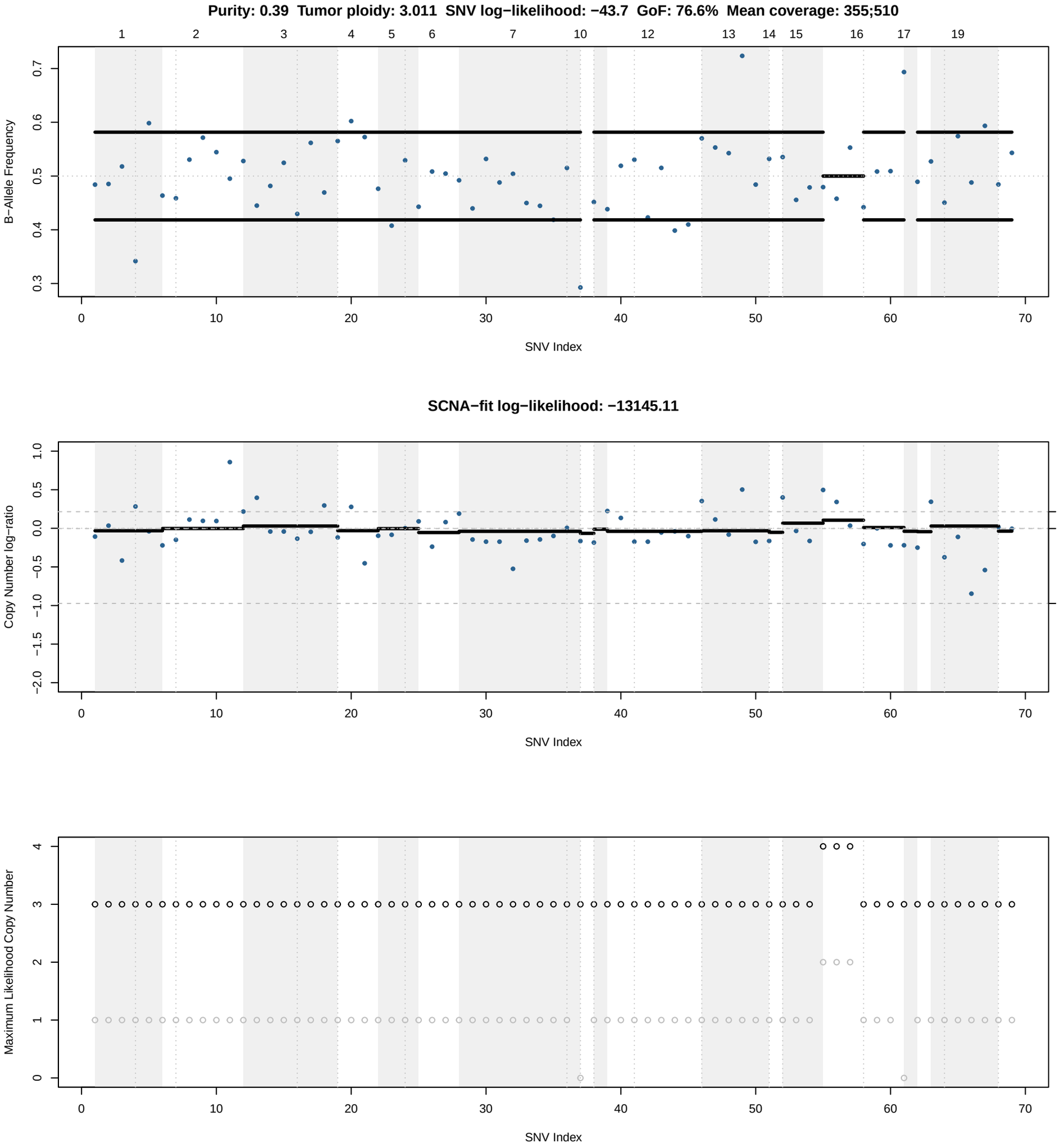

Allelic fraction (germline)
Copy Number log−ratio
4m4
4m3
5m3
4m2
5m2
4m1
3m0
4m0

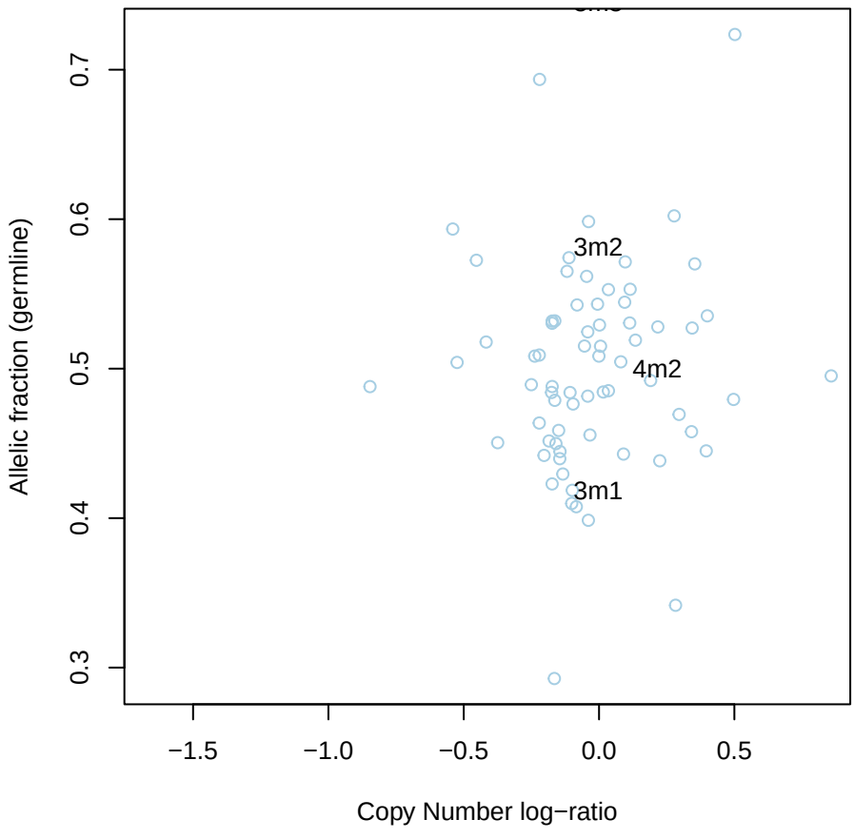

Coverage (log2)
Allelic fraction

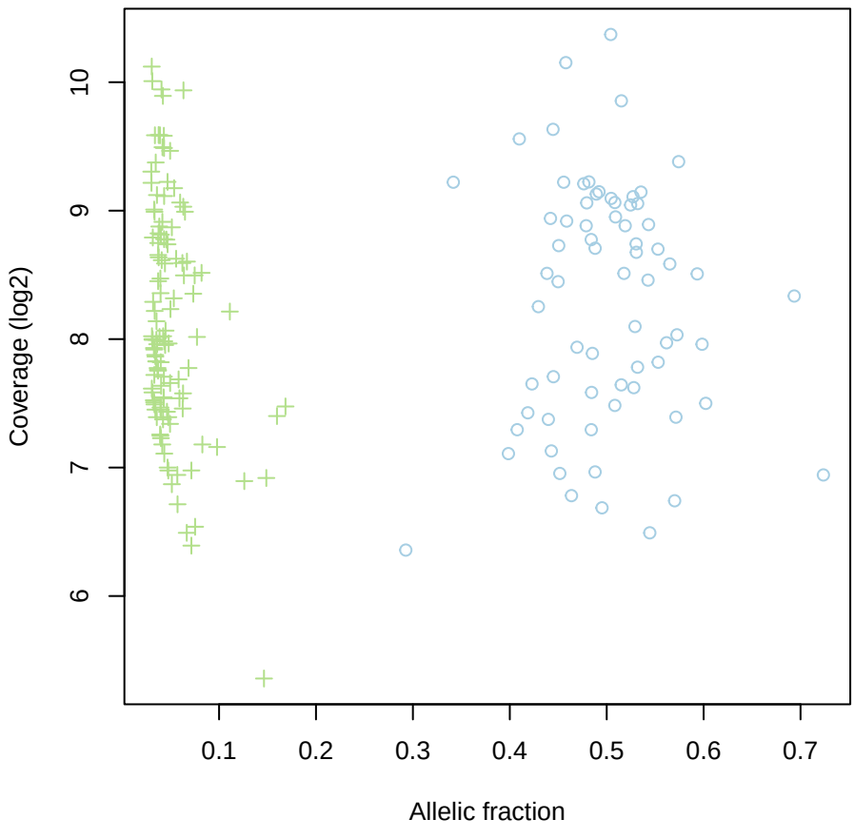

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m2
5m2
3m1
4m1
5m1

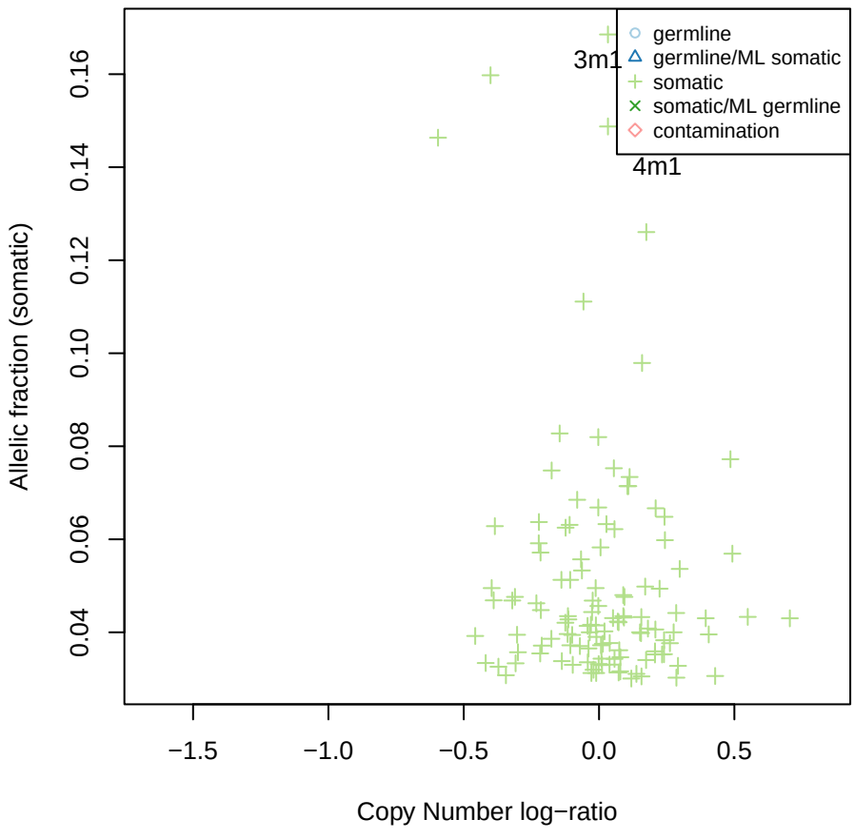

Frequency
Cellular fraction

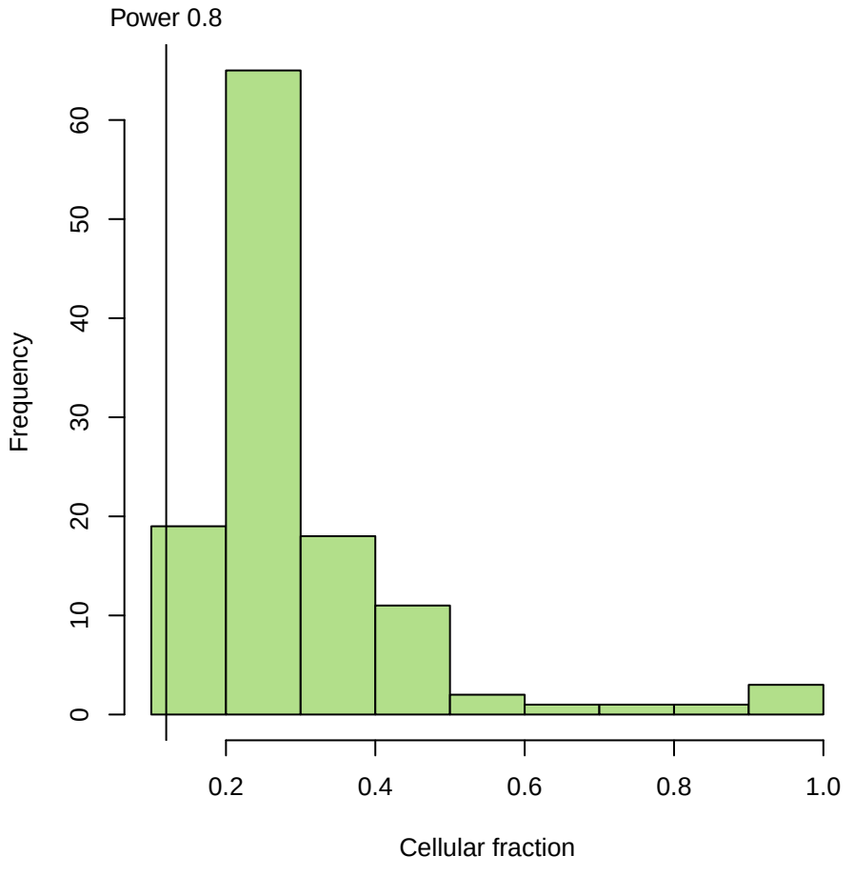

Purity: 0.39 Tumor ploidy: 3.011
0
3
4
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.6
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

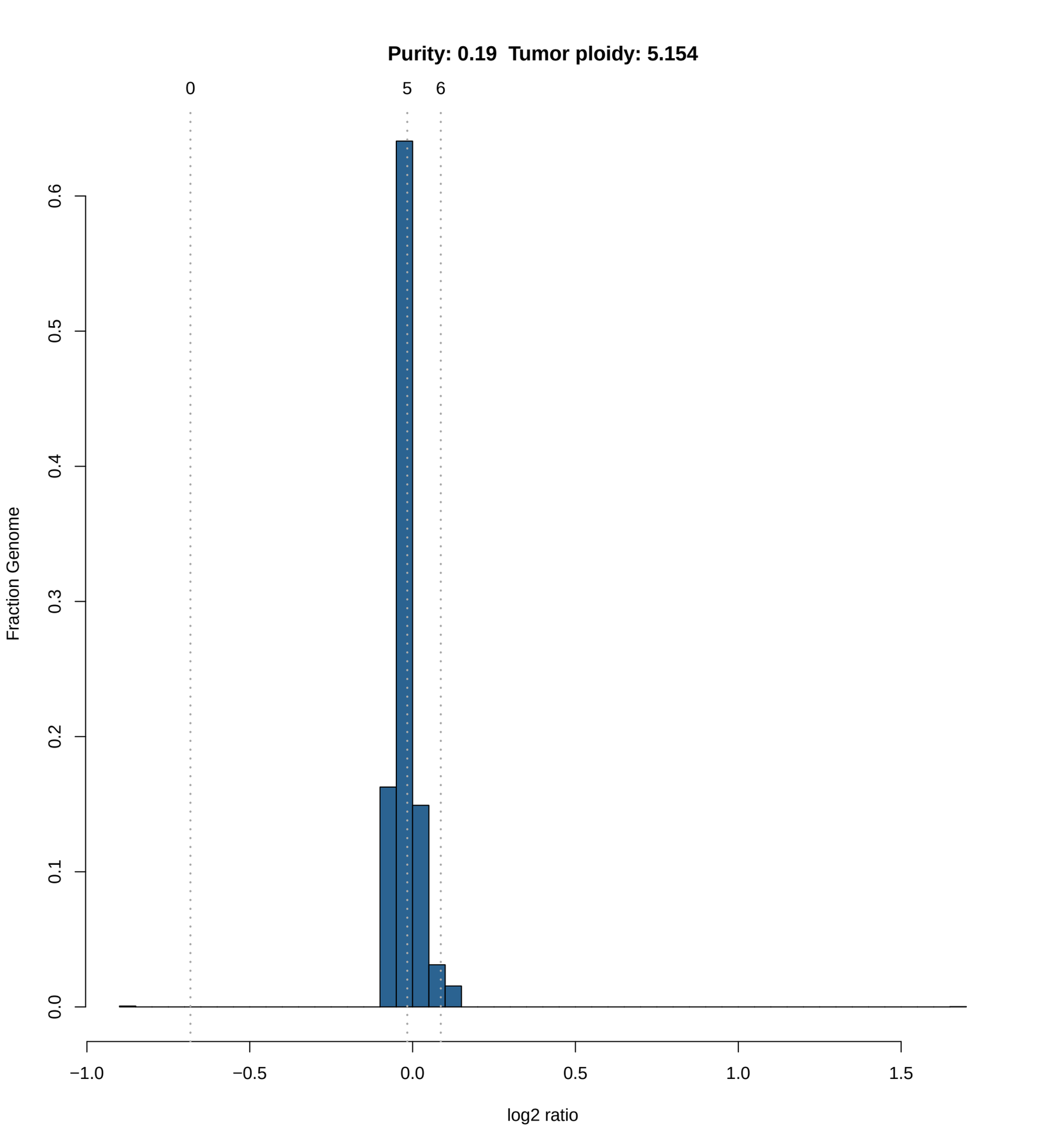

Purity: 0.39 Tumor ploidy: 3.011 SNV log−likelihood: −43.7 GoF: 76.6% Mean coverage: 355;510
1 2 3 4 5 6 7 10 12 13 14 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index
SCNA−fit log−likelihood: −13145.11
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 3 4
0 10 20 30 40 50 60 70
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4
0 10 20 30 40 50 60 70
SNV Index

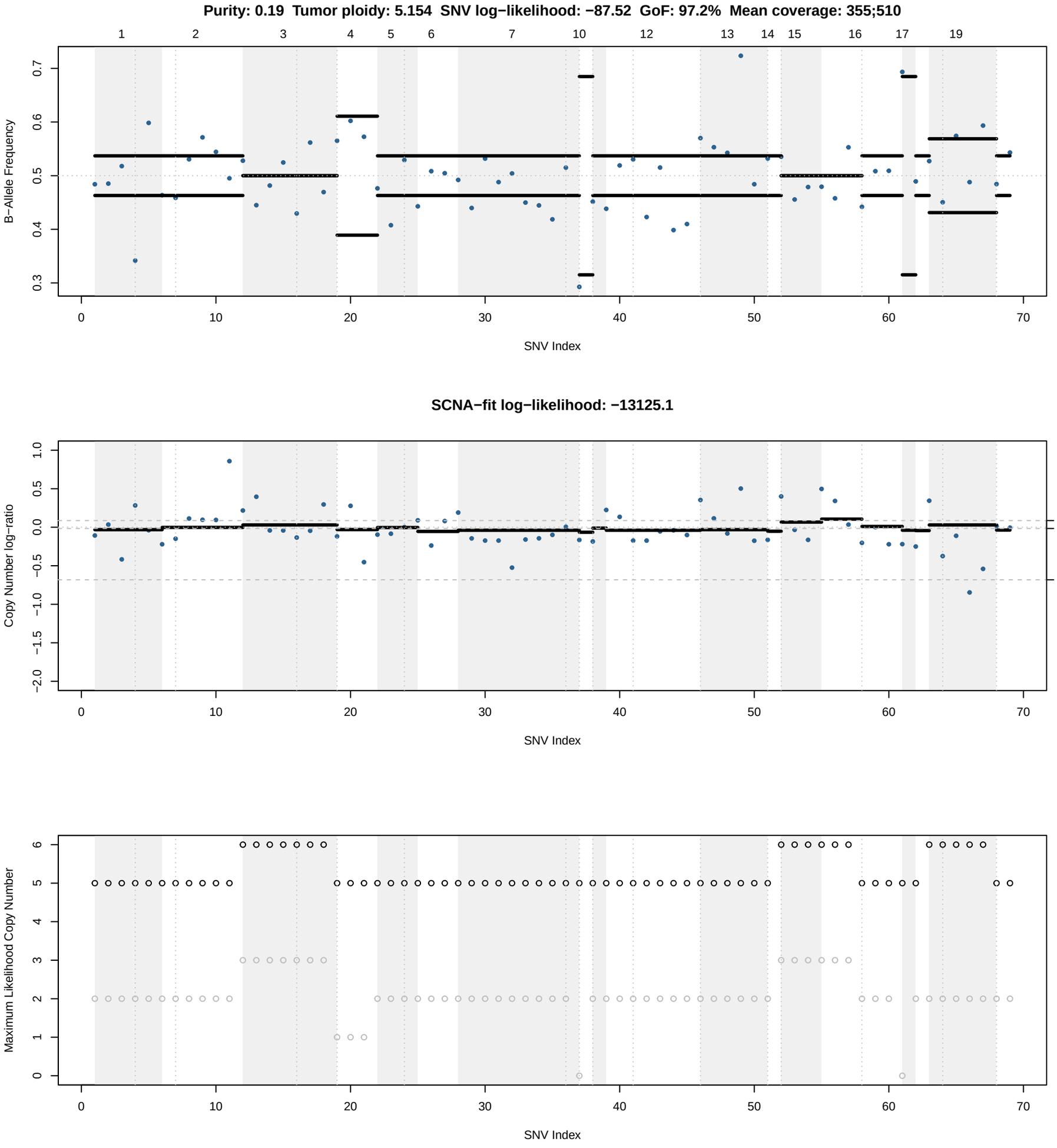

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
3m2
4m2
3m1
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

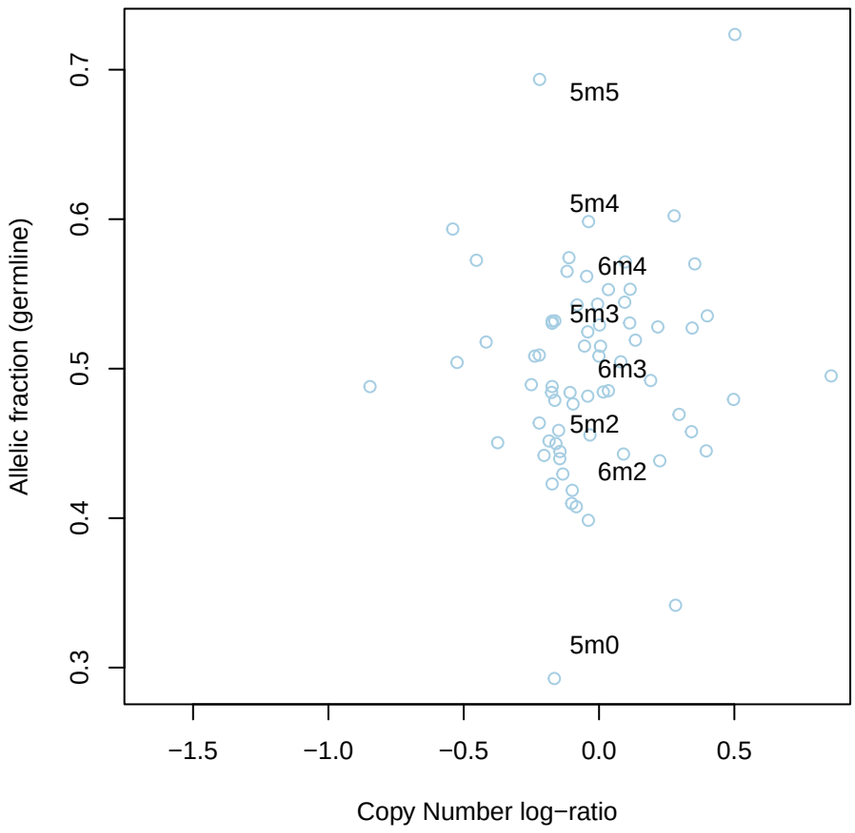

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

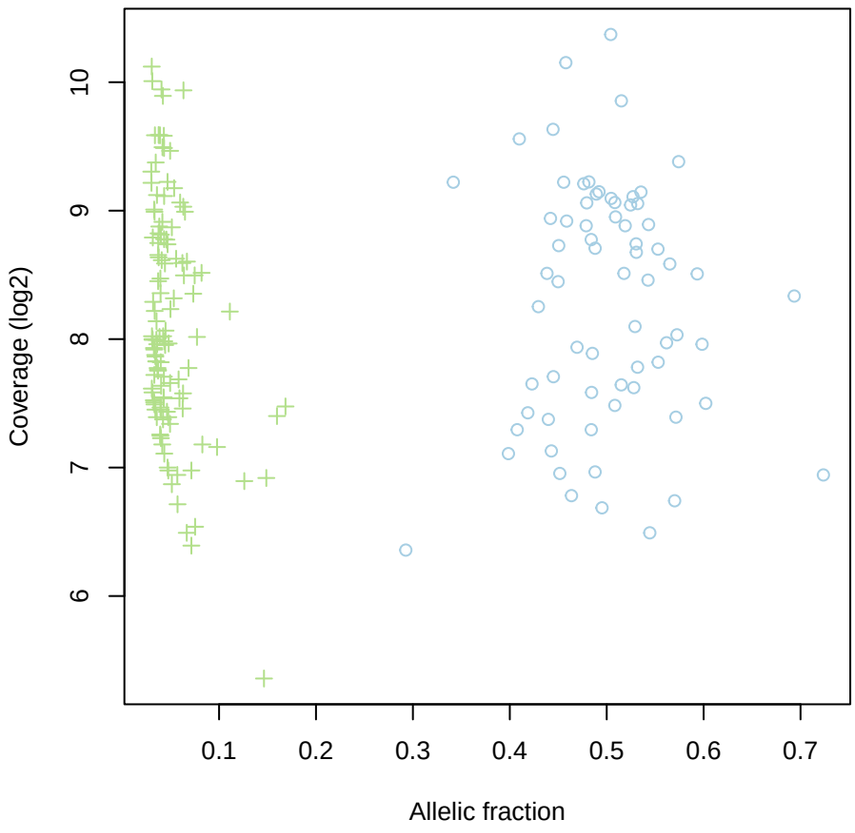

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

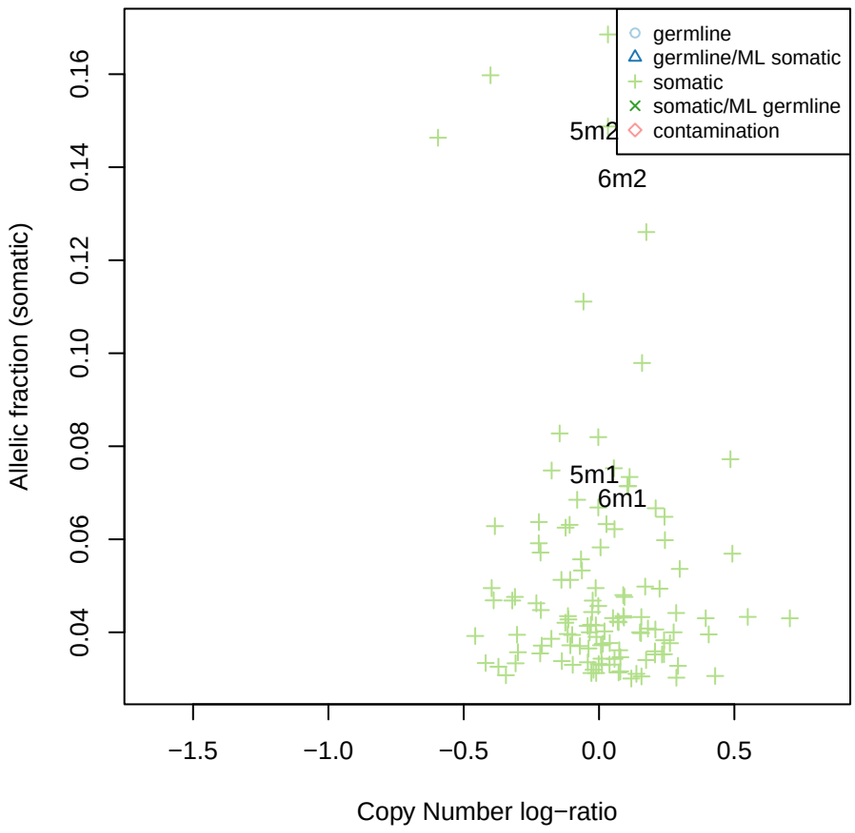

Power 0.8
Frequency
0
10
20
30
40
50
60
0.2
0.4
0.6
0.8
1.0
Cellular fraction

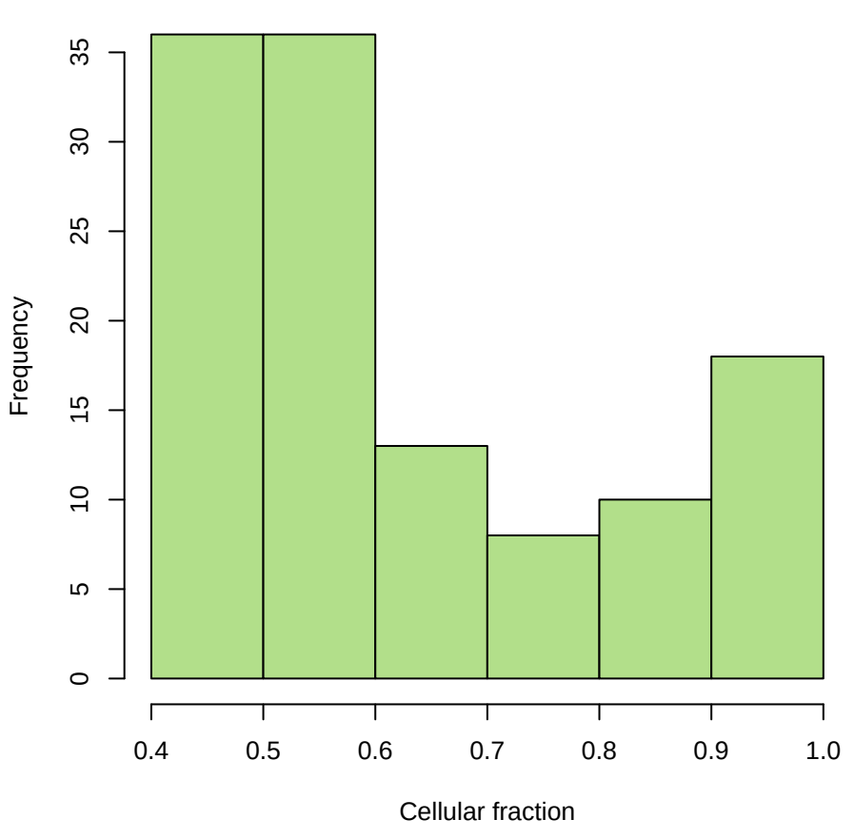

Purity: 0.19 Tumor ploidy: 5.154
0
5
6
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.6
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

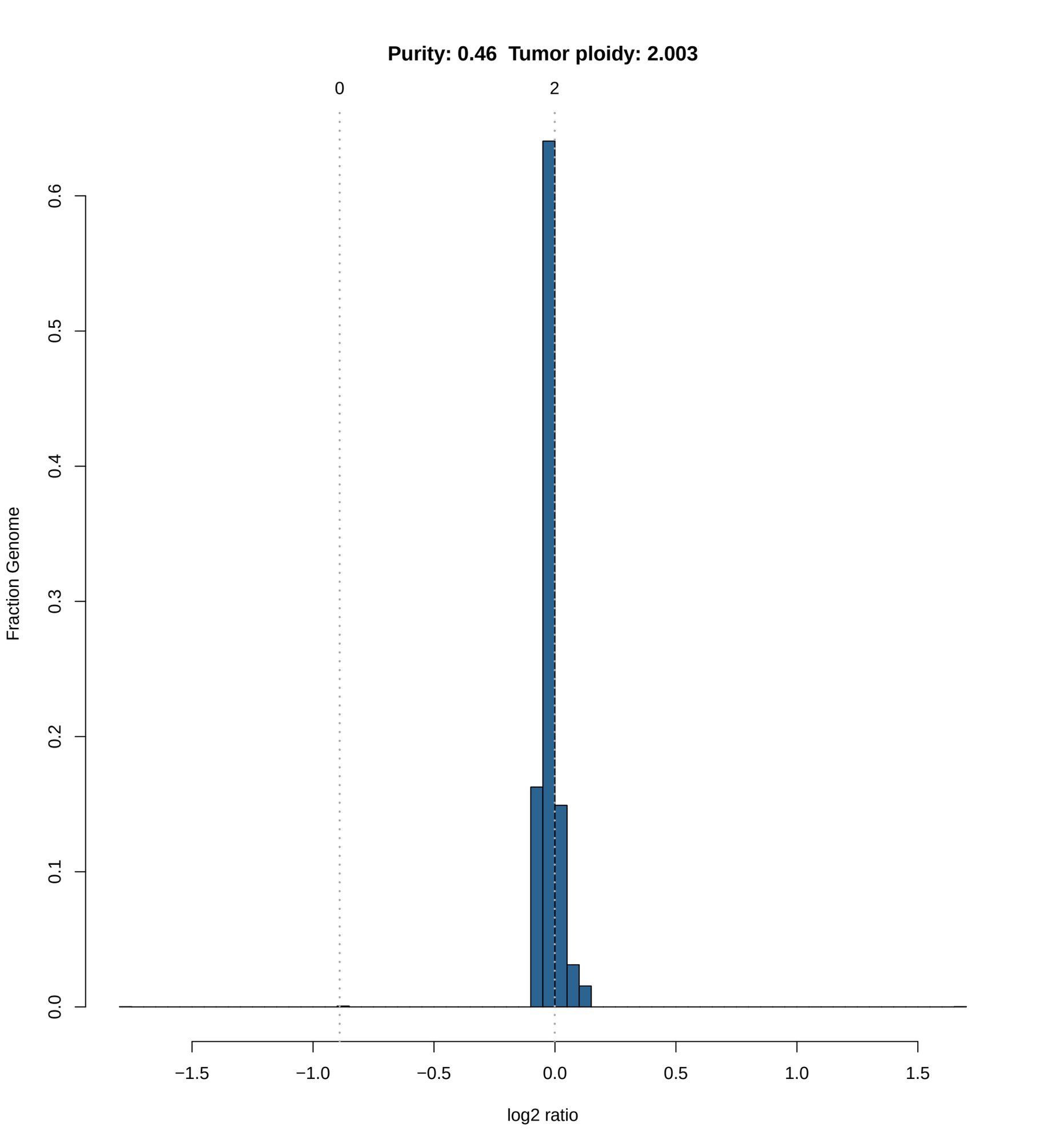

Purity: 0.19 Tumor ploidy: 5.154 SNV log−likelihood: −87.52 GoF: 97.2% Mean coverage: 355;510
1 2 3 4 5 6 7 10 12 13 14 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index
SCNA−fit log−likelihood: −13125.1
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
1
0
0 10 20 30 40 50 60 70
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 10 20 30 40 50 60 70
SNV Index

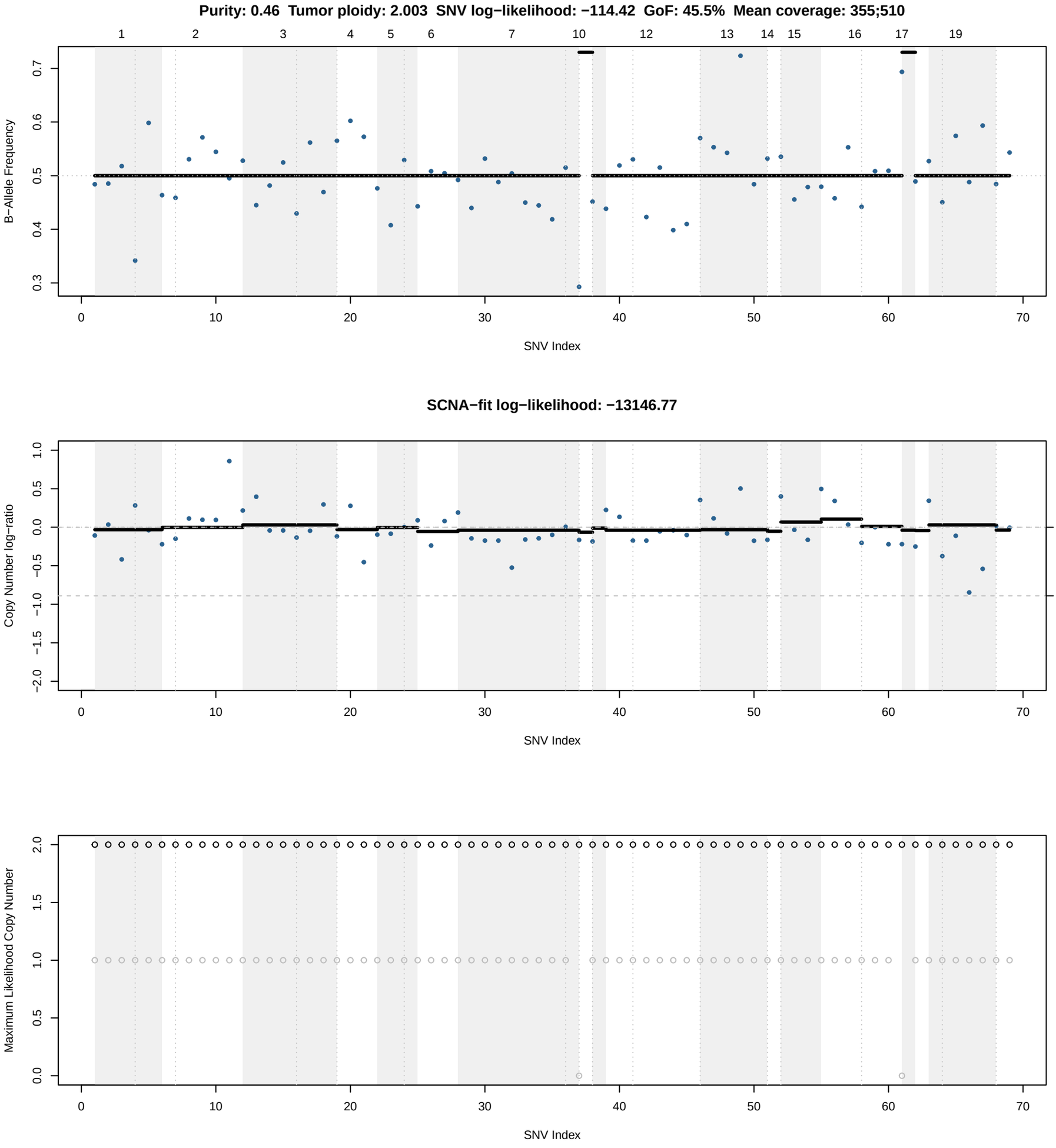

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
5m5
5m4
6m4
5m3
6m3
5m2
6m2
5m0
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

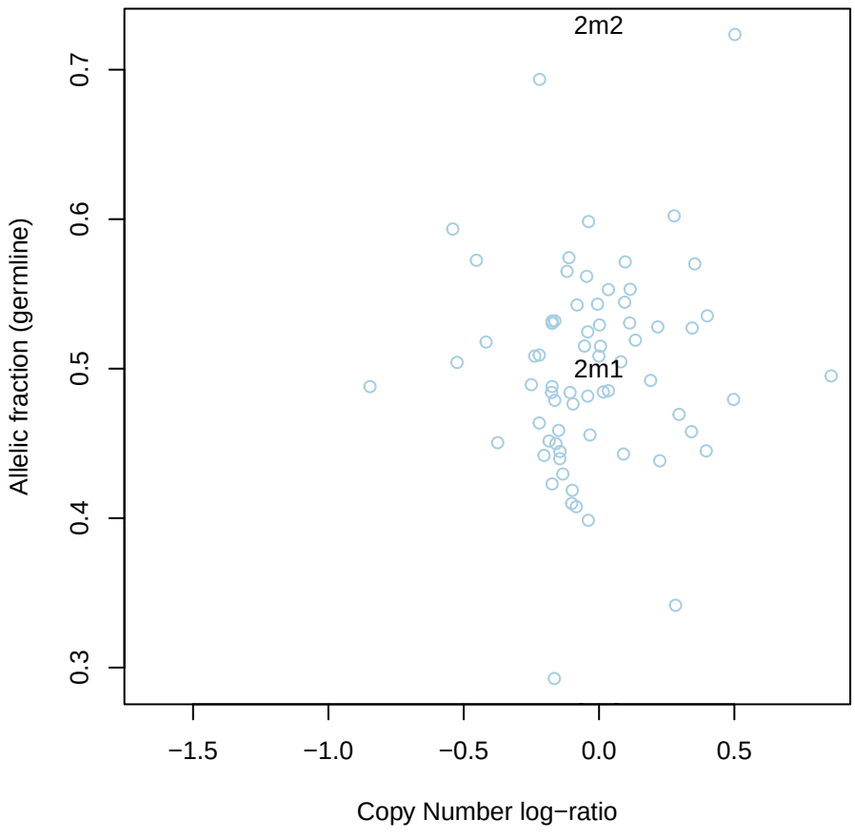

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

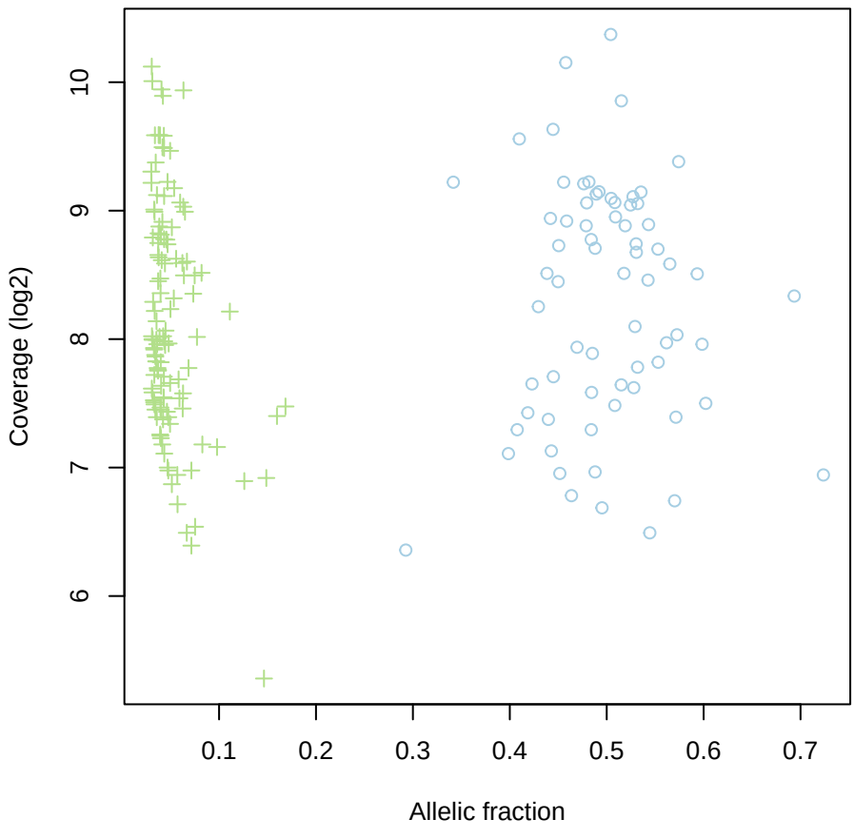

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
5m2
6m2
5m1
6m1
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

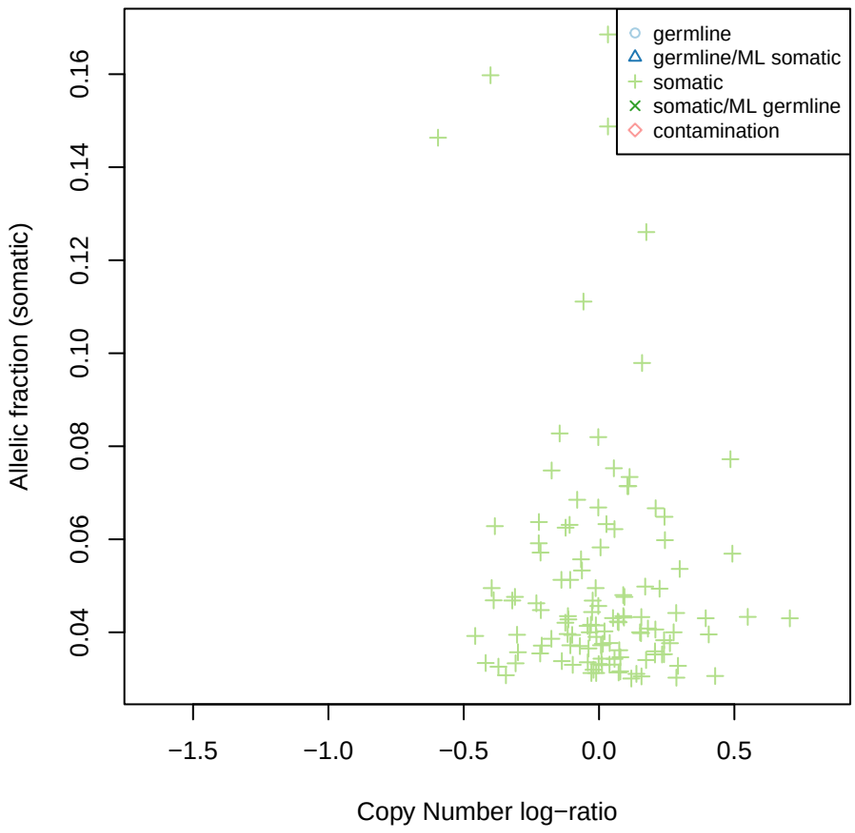

Frequency
0
5
10
15
20
25
30
35
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

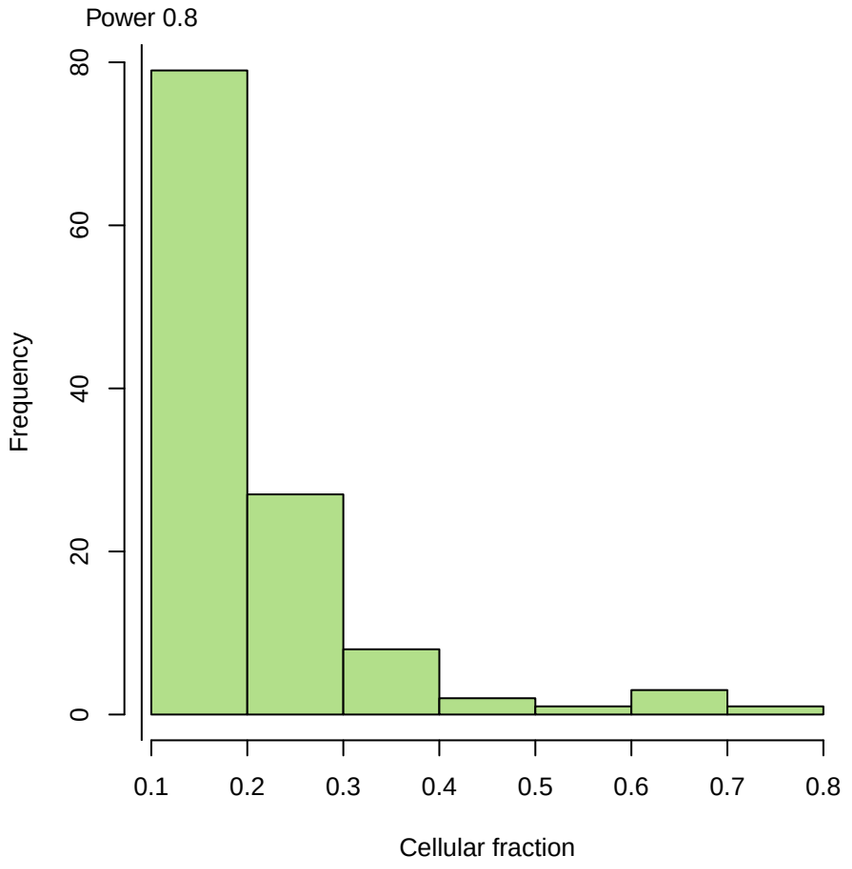

Purity: 0.46 Tumor ploidy: 2.003
0
2
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.6
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

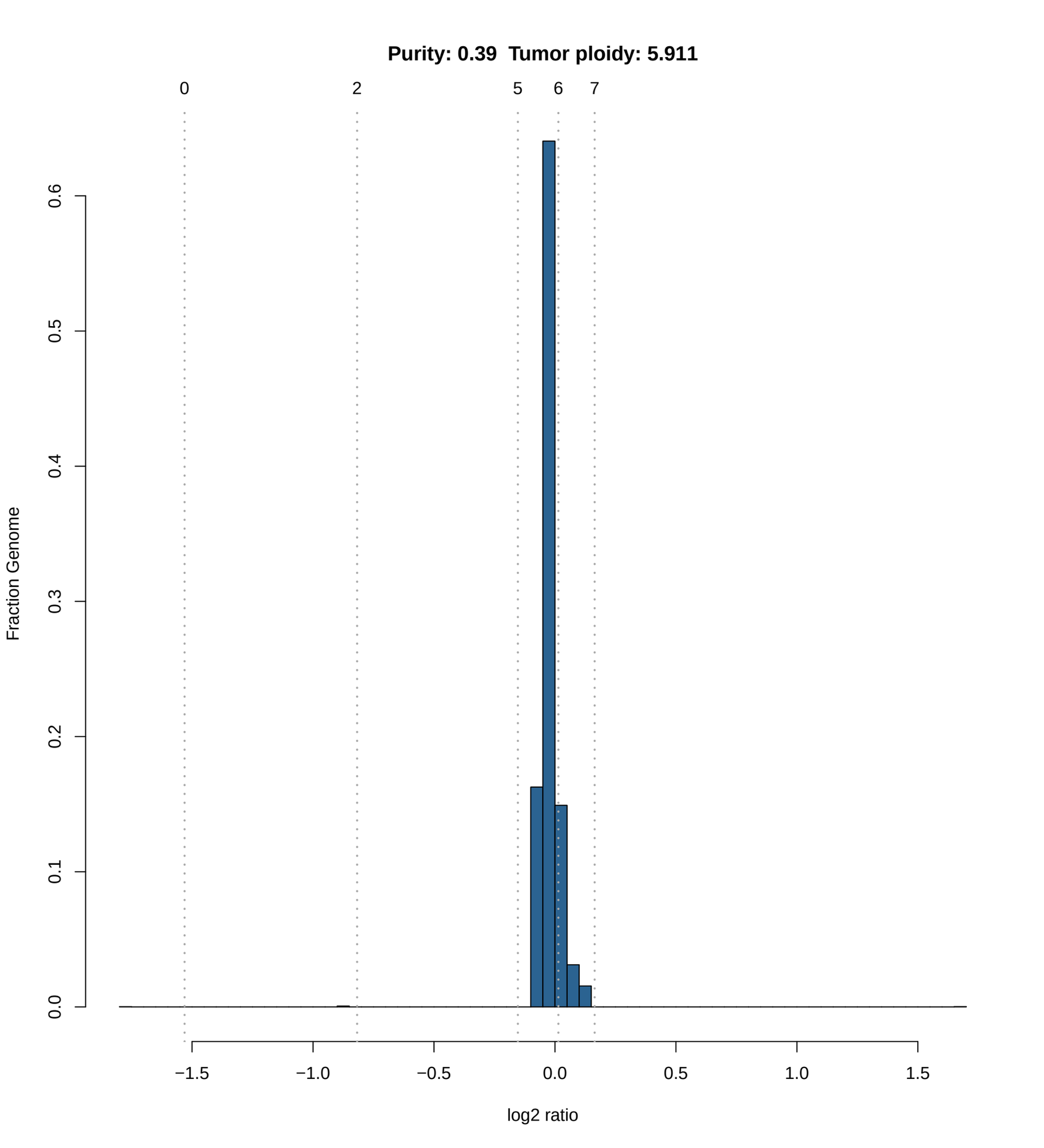

Purity: 0.46 Tumor ploidy: 2.003 SNV log−likelihood: −114.42 GoF: 45.5% Mean coverage: 355;510
1
2
3
4
5
6
7
10
12
13
14
15
16
17
19
B−Allele Frequency
0.3
0.4
0.5
0.6
0.7
0
10
20
30
40
50
60
70
SNV Index
SCNA−fit log−likelihood: −13146.77
Copy Number log−ratio
−2.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
2
0
SNV Index
Maximum Likelihood Copy Number
0.0
0.5
1.0
1.5
2.0
SNV Index

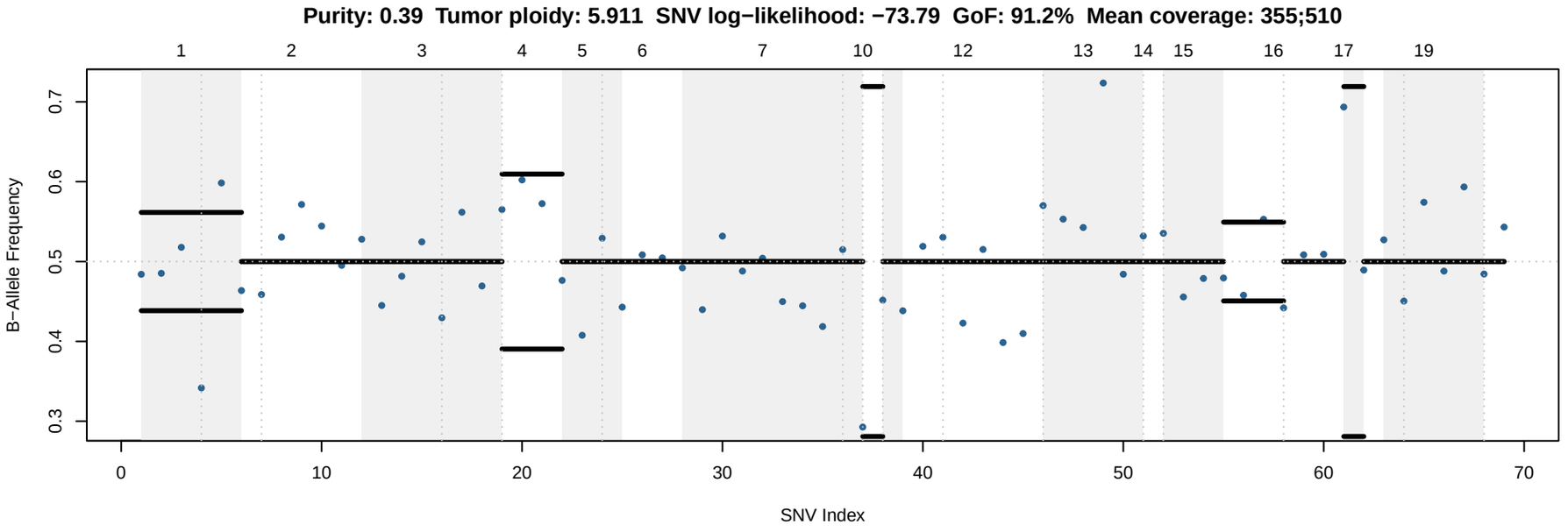

2m2
2m1
Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

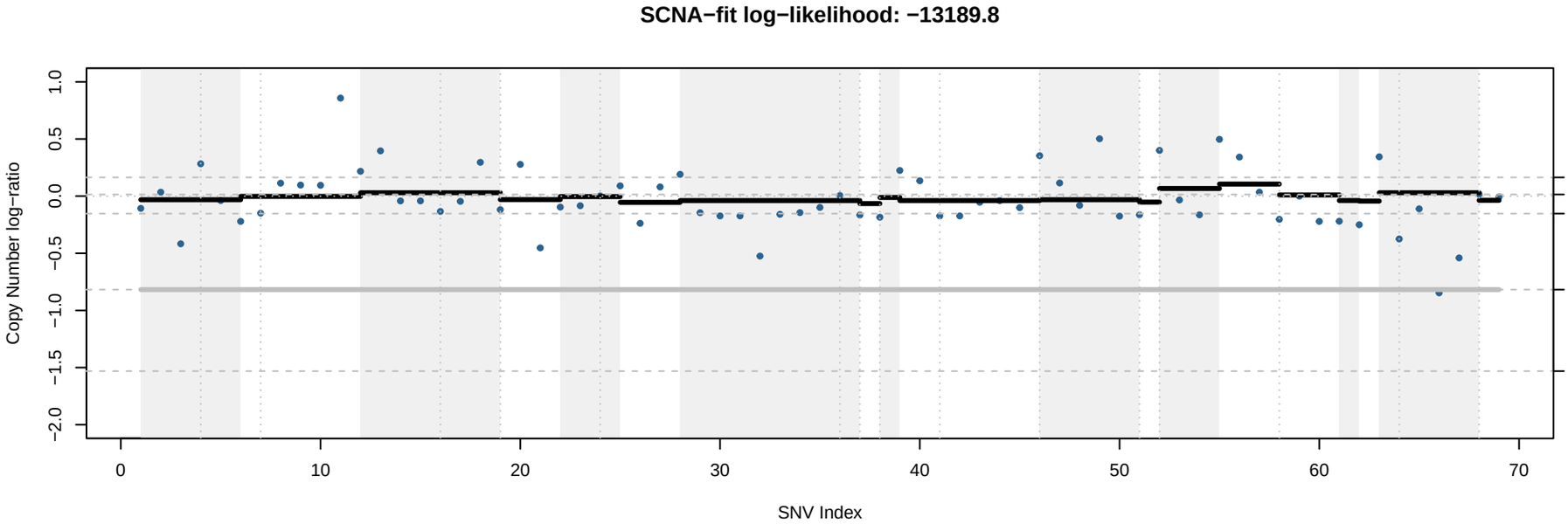

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

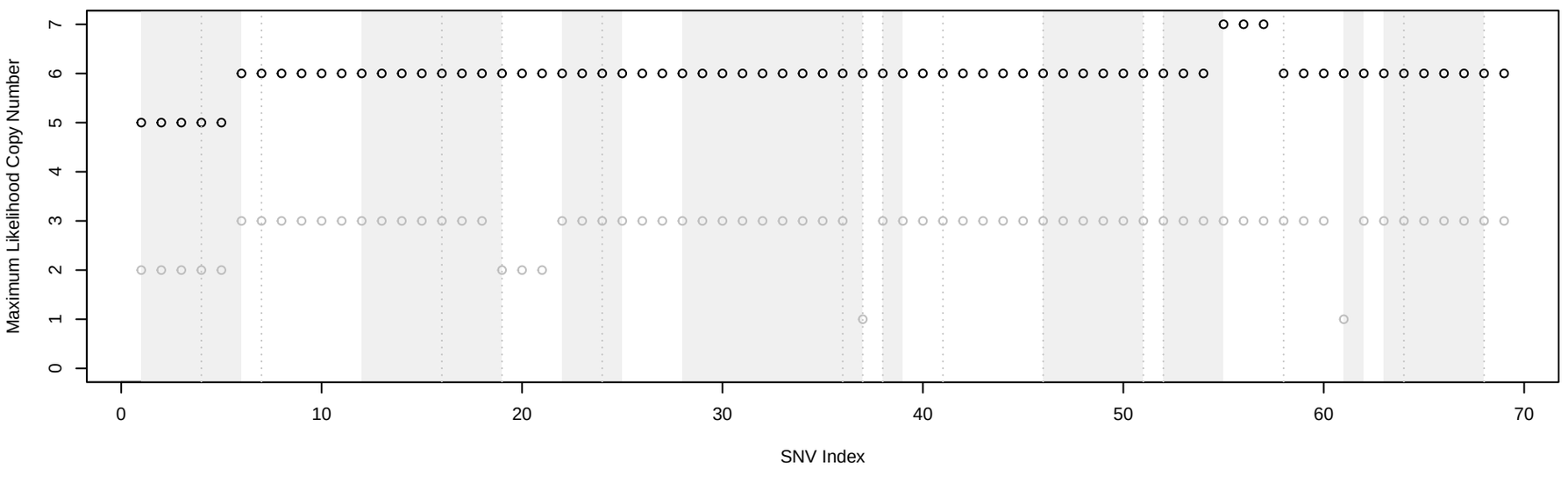

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

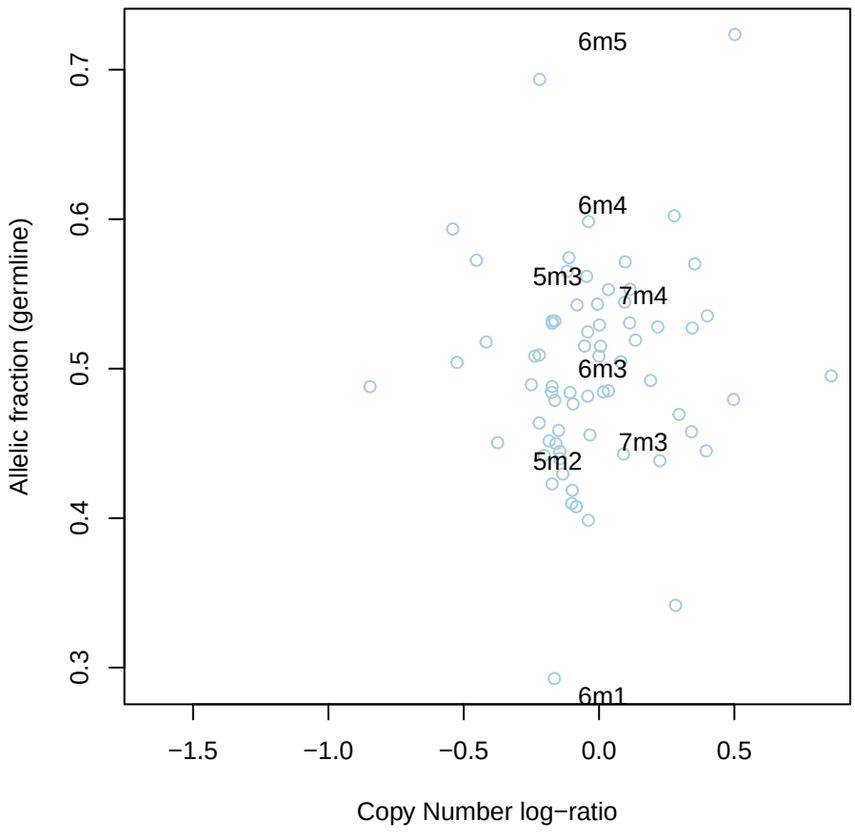

Power 0.8
Frequency
0
20
40
60
80
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
Cellular fraction

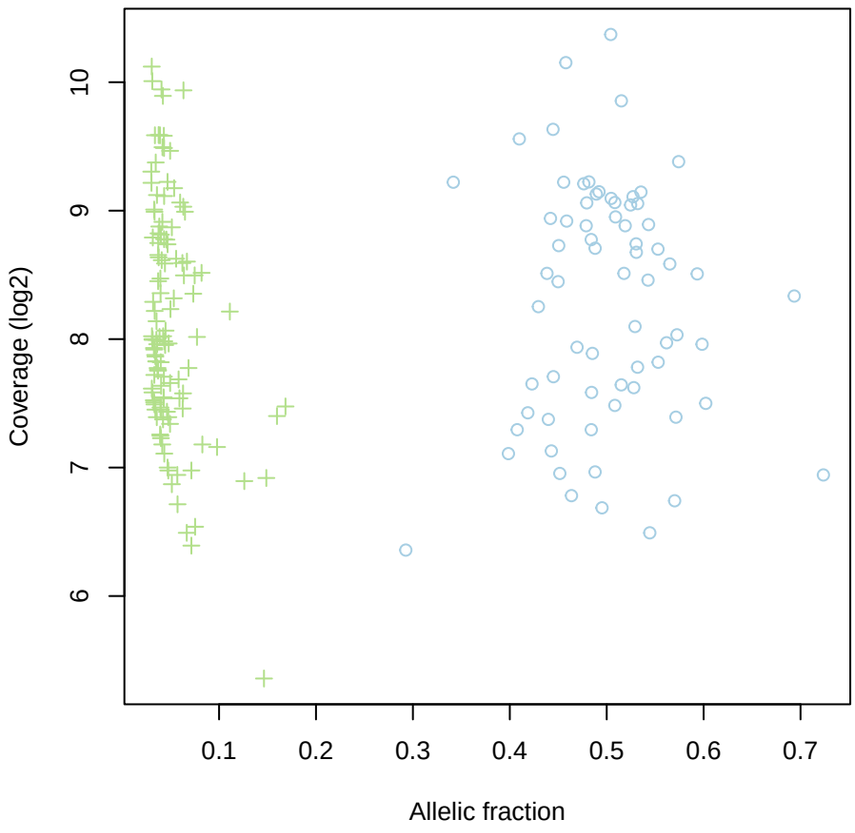

Purity: 0.39 Tumor ploidy: 5.911
0
2
5
6
7
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.6
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

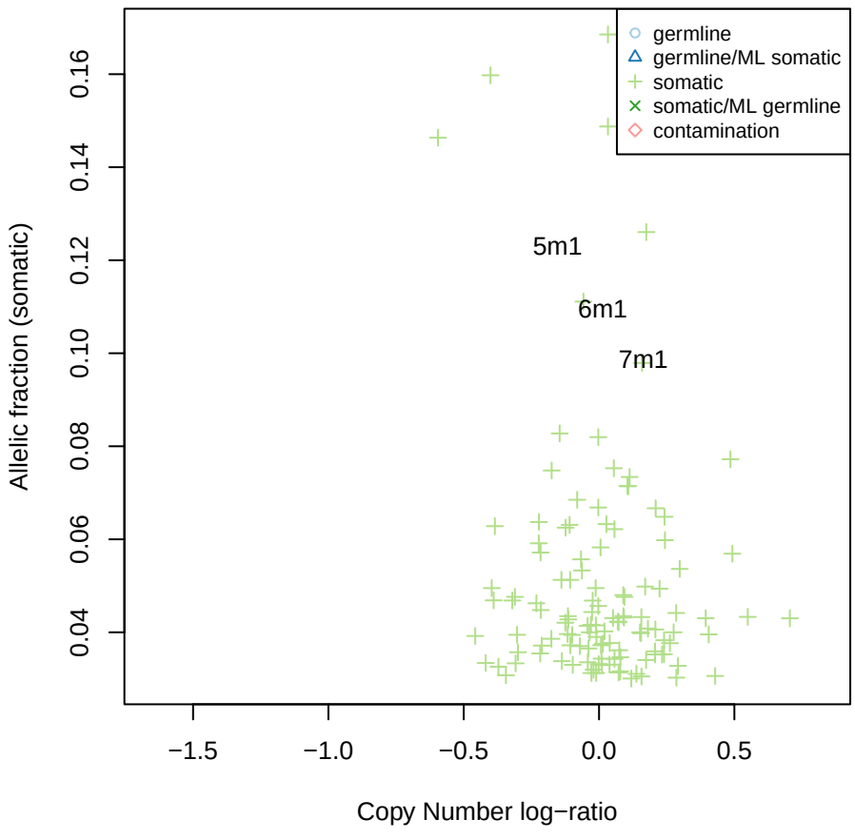

Purity: 0.39 Tumor ploidy: 5.911 SNV log−likelihood: −73.79 GoF: 91.2% Mean coverage: 355;510
1 2 3 4 5 6 7 10 12 13 14 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index

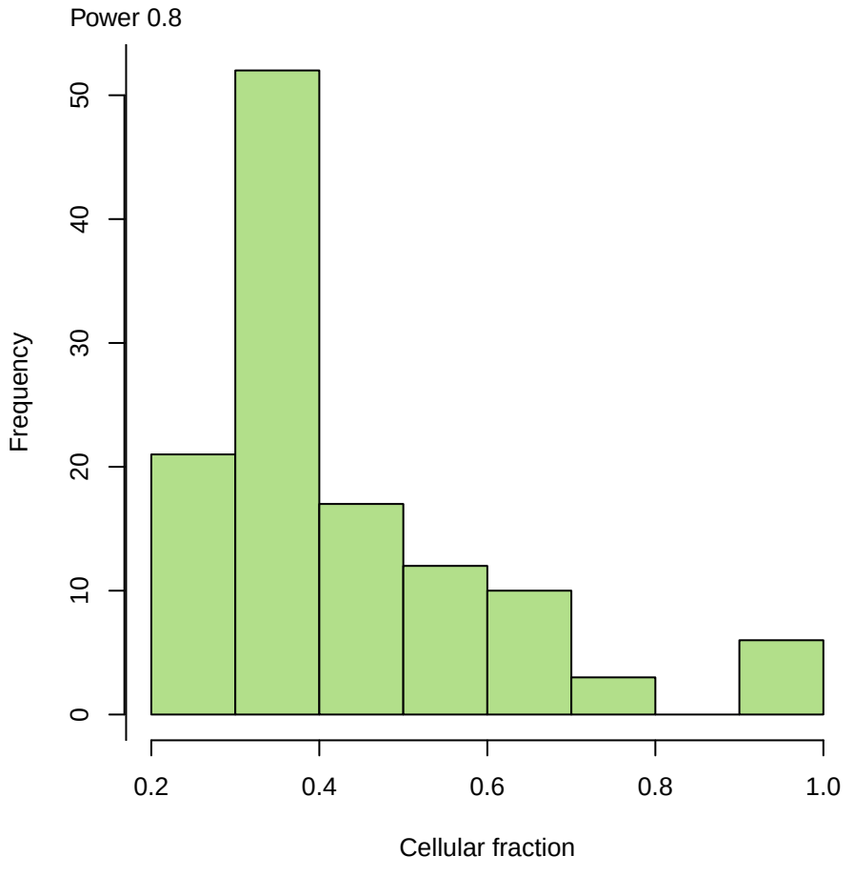

SCNA−fit log−likelihood: −13189.8
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 2 5 7
0 10 20 30 40 50 60 70
SNV Index

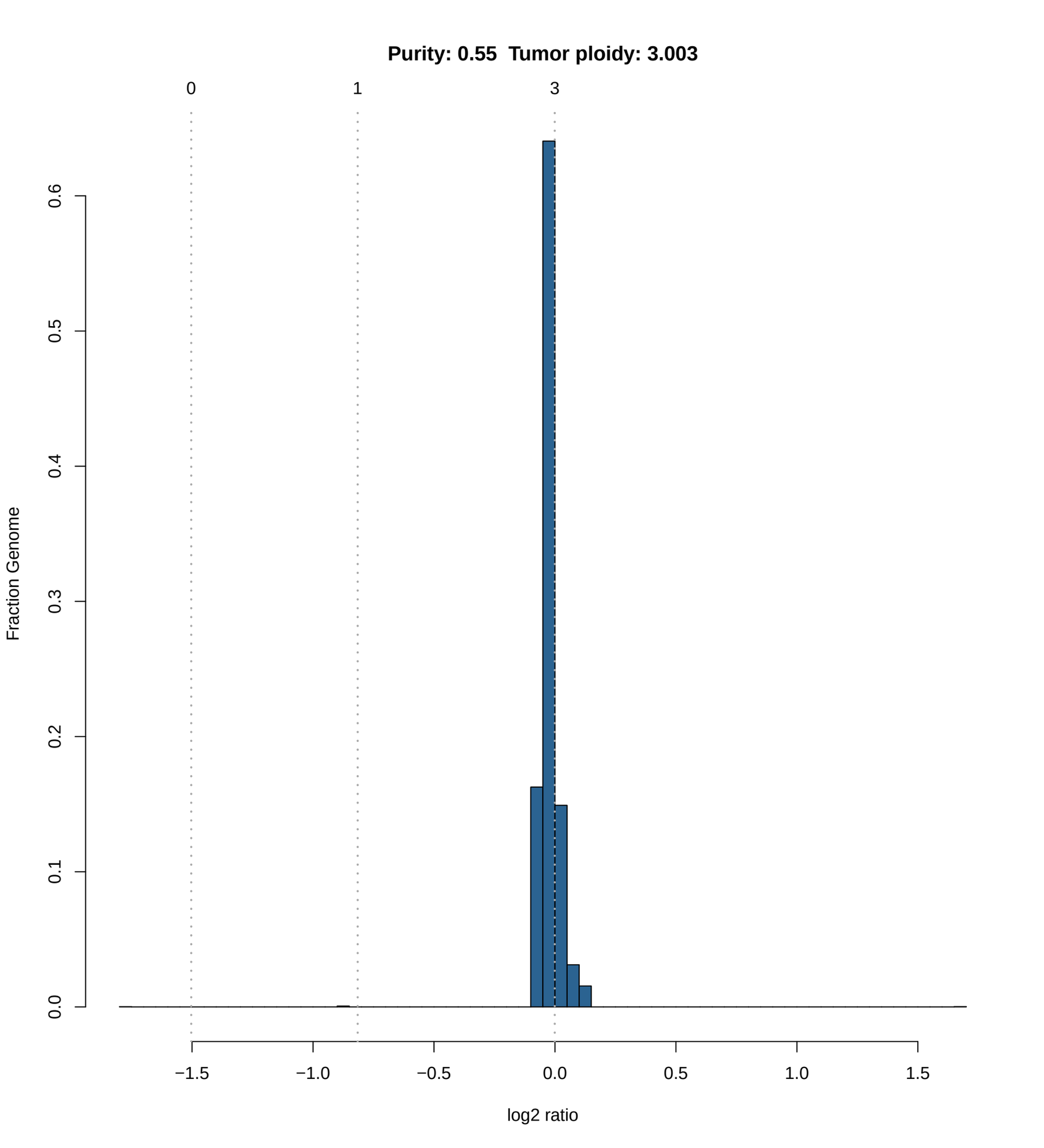

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 10 20 30 40 50 60 70
SNV Index

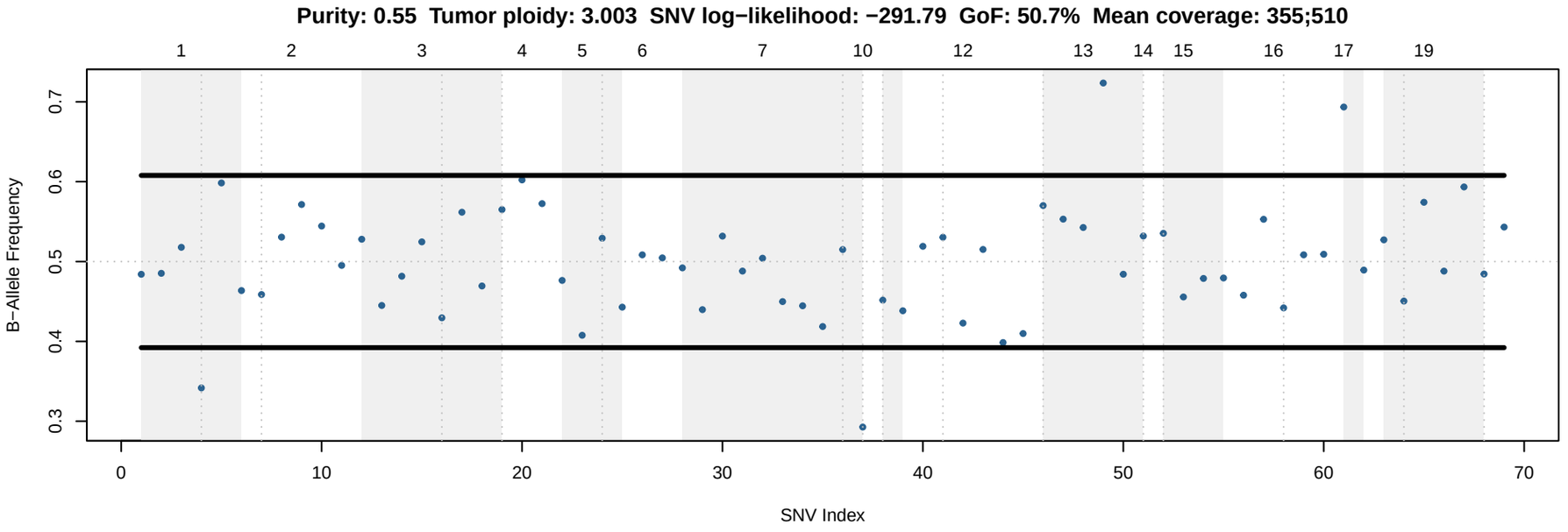

6m5
6m4
5m3
7m4
6m3
7m3
5m2
6m1
Allelic fraction (germline)
Copy Number log−ratio

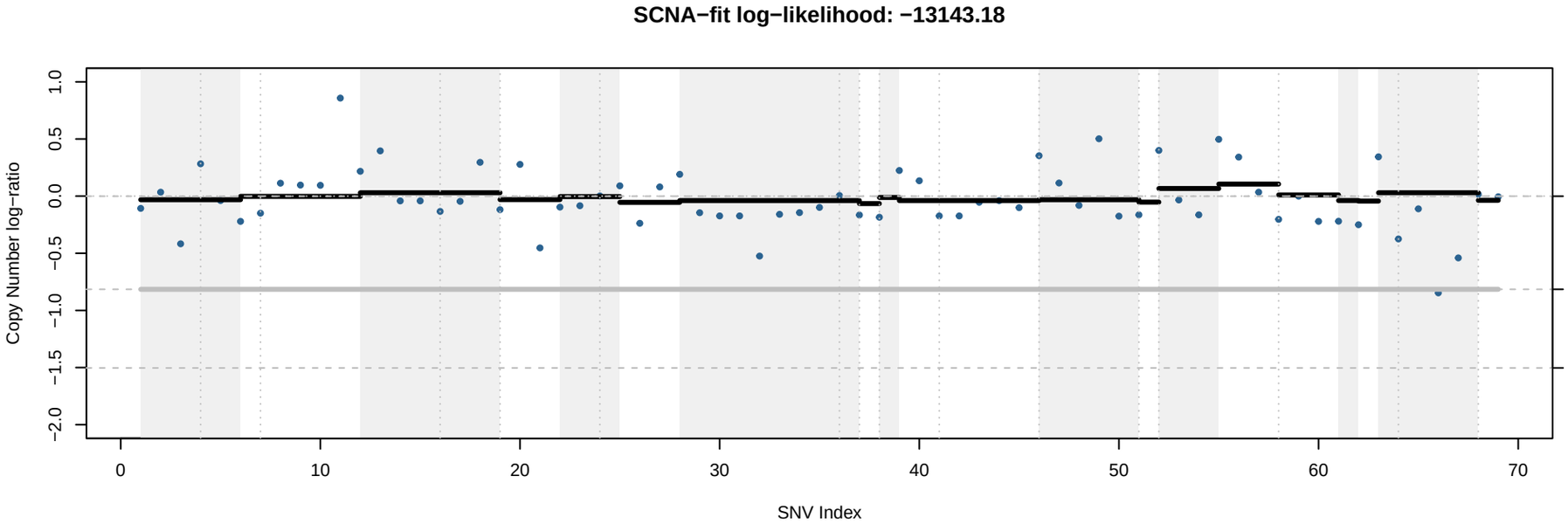

Coverage (log2)
Allelic fraction

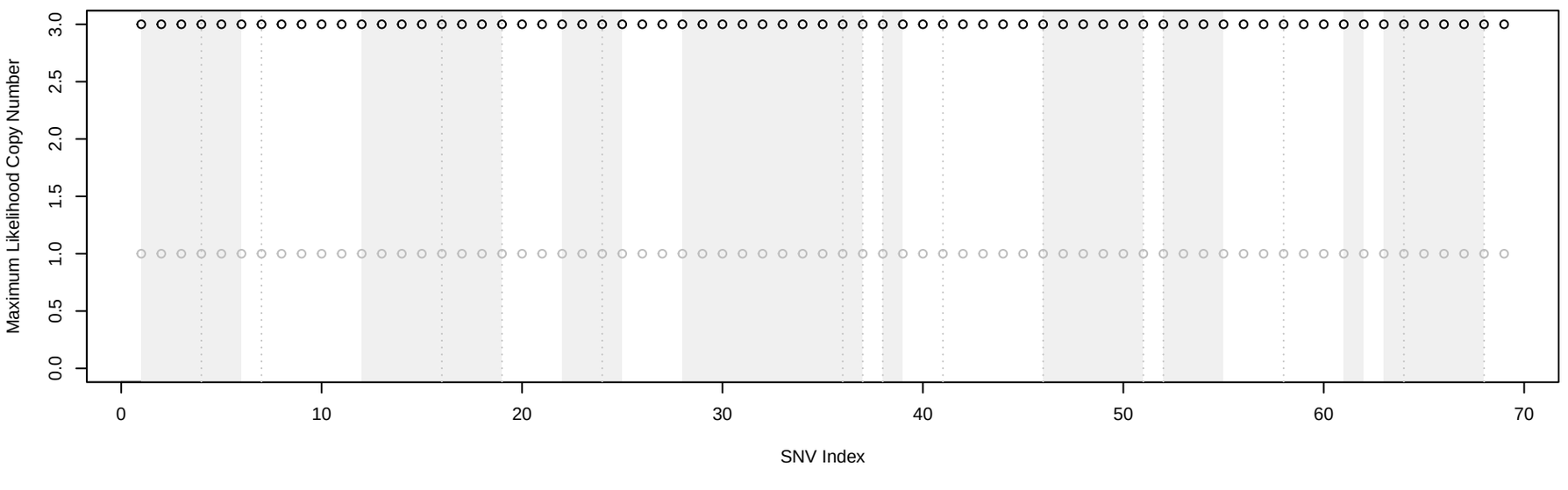

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

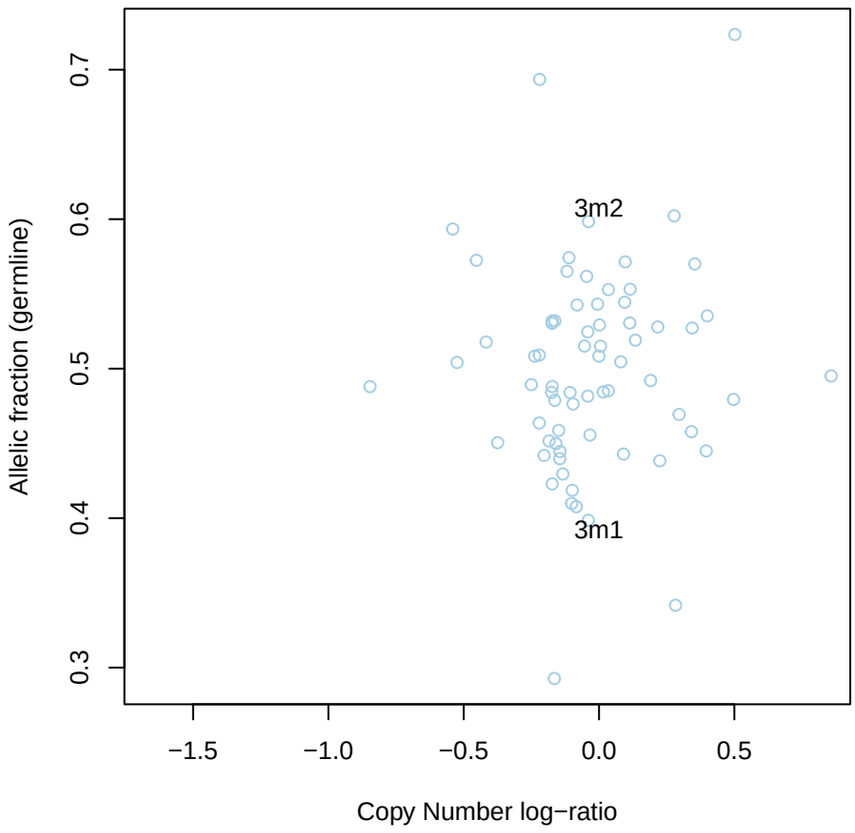

Power 0.8
Frequency
Cellular fraction

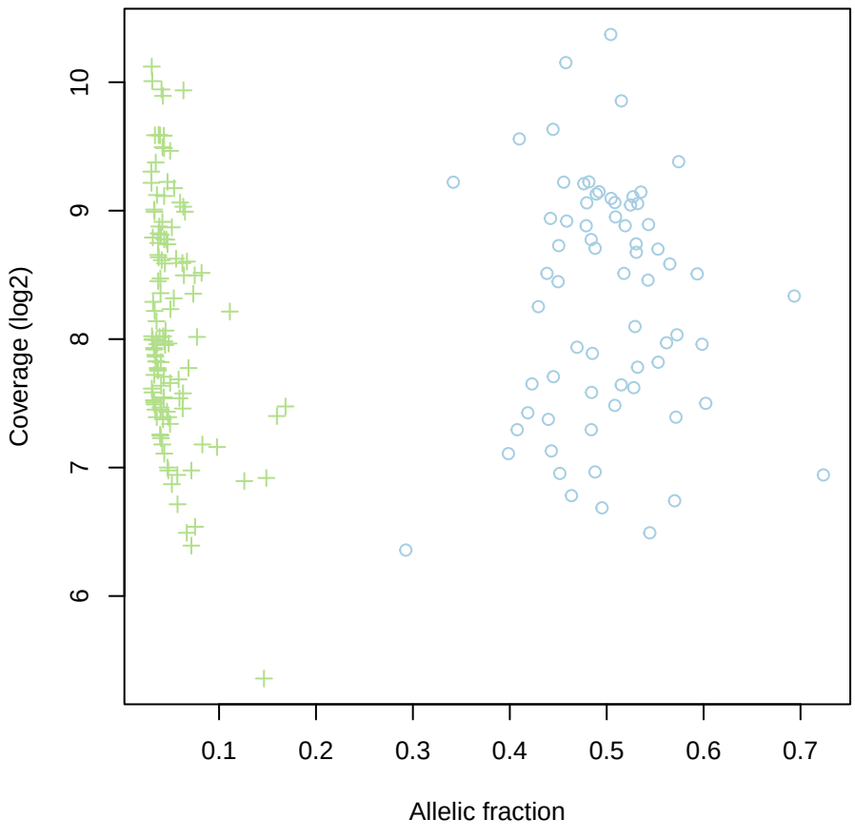

Purity: 0.55 Tumor ploidy: 3.003
0
1
3
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.6
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

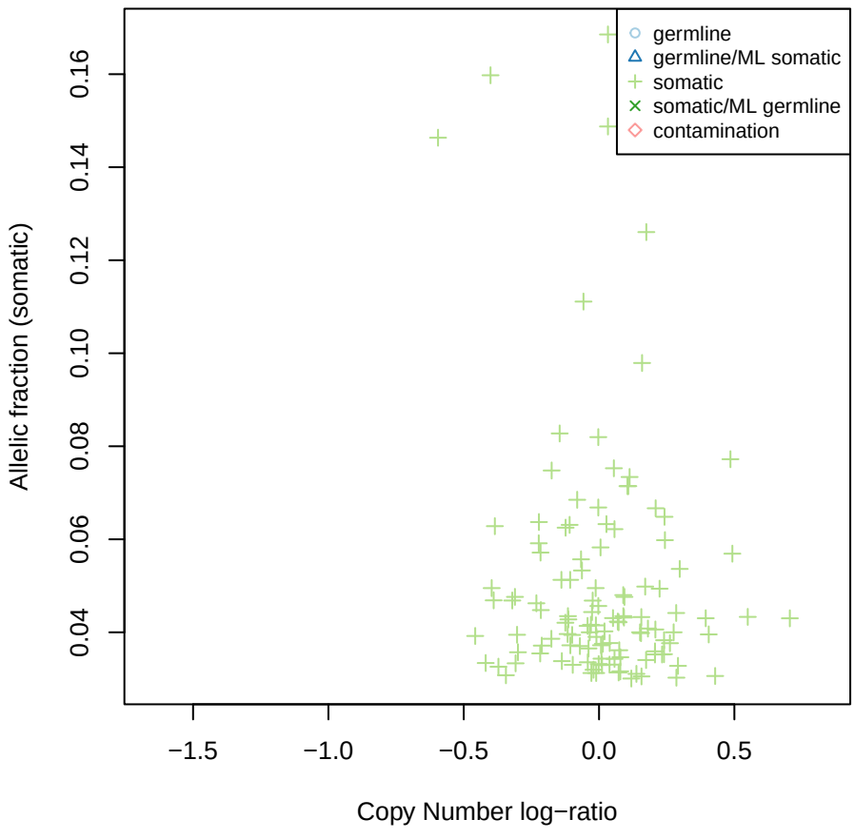

Purity: 0.55 Tumor ploidy: 3.003 SNV log−likelihood: −291.79 GoF: 50.7% Mean coverage: 355;510
1 2 3 4 5 6 7 10 12 13 14 15 16 17 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index

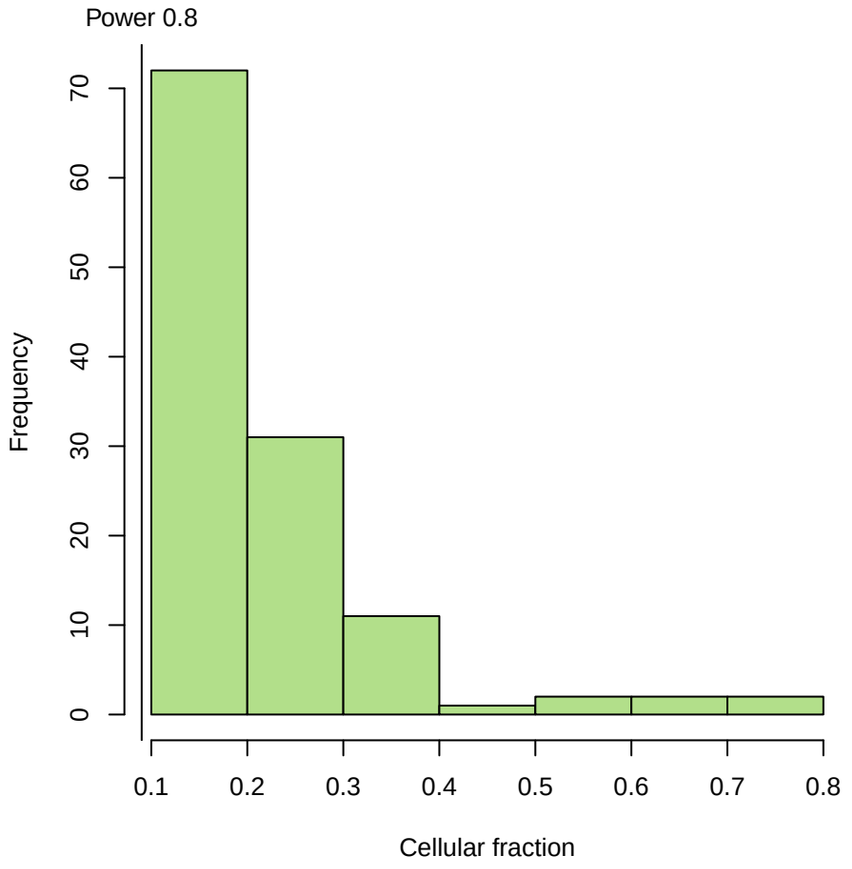

SCNA−fit log−likelihood: −13143.18
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 3
0 10 20 30 40 50 60 70
SNV Index

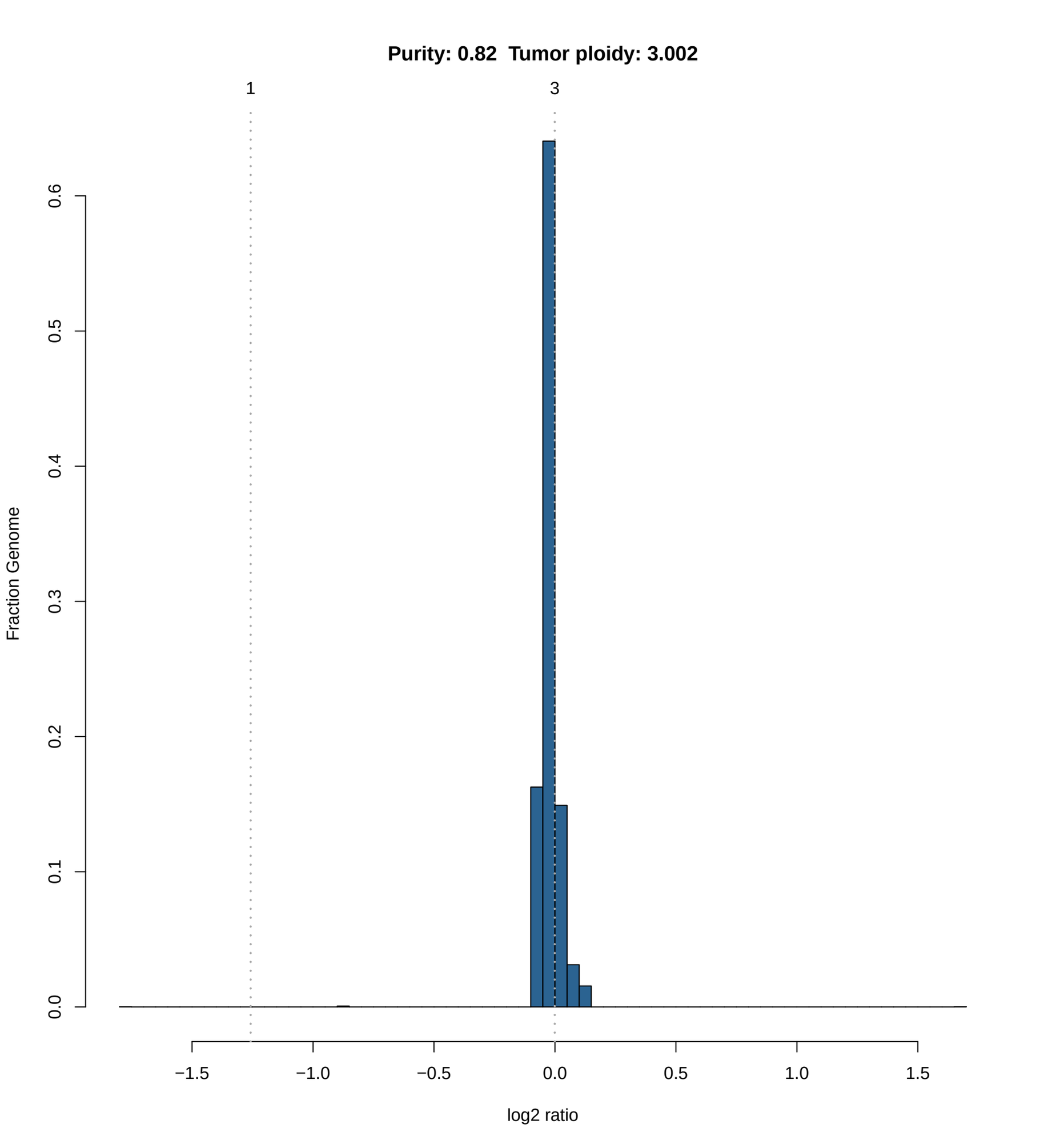

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 10 20 30 40 50 60 70
SNV Index

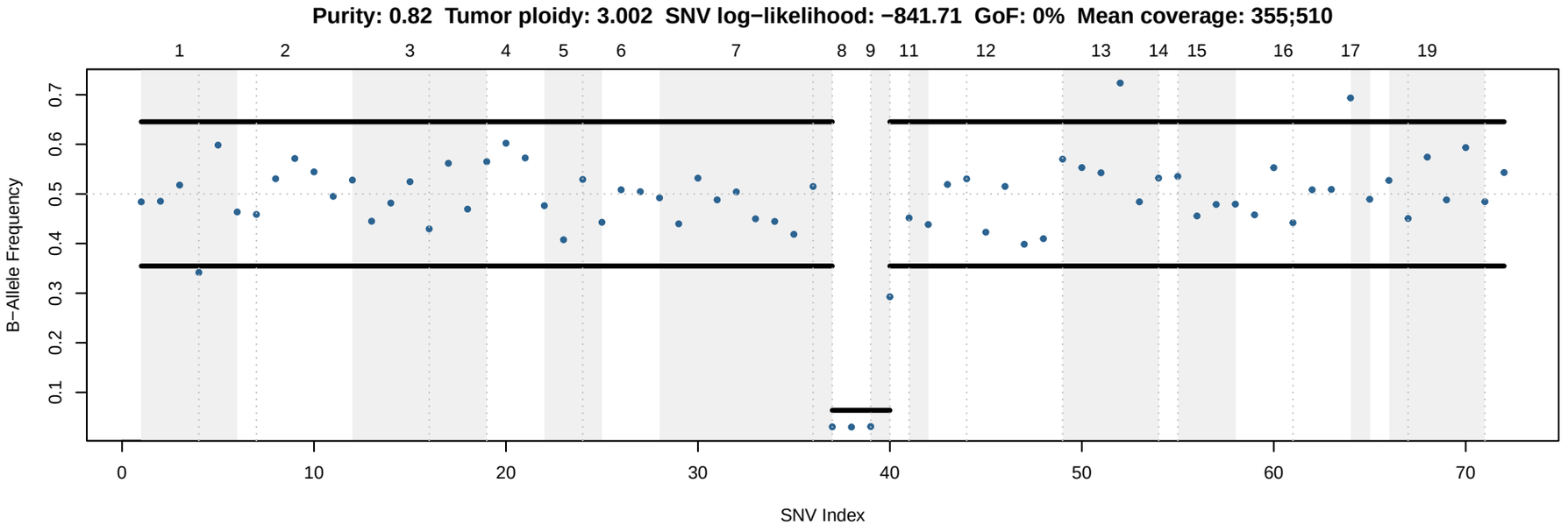

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
3m2
3m1
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

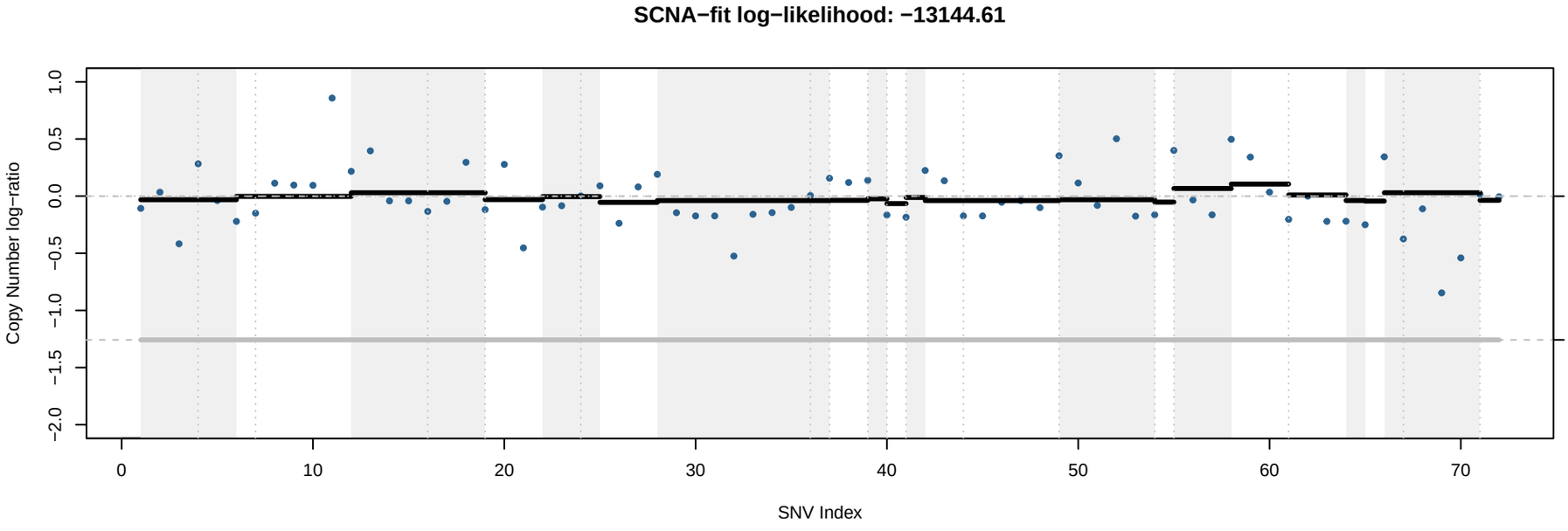

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

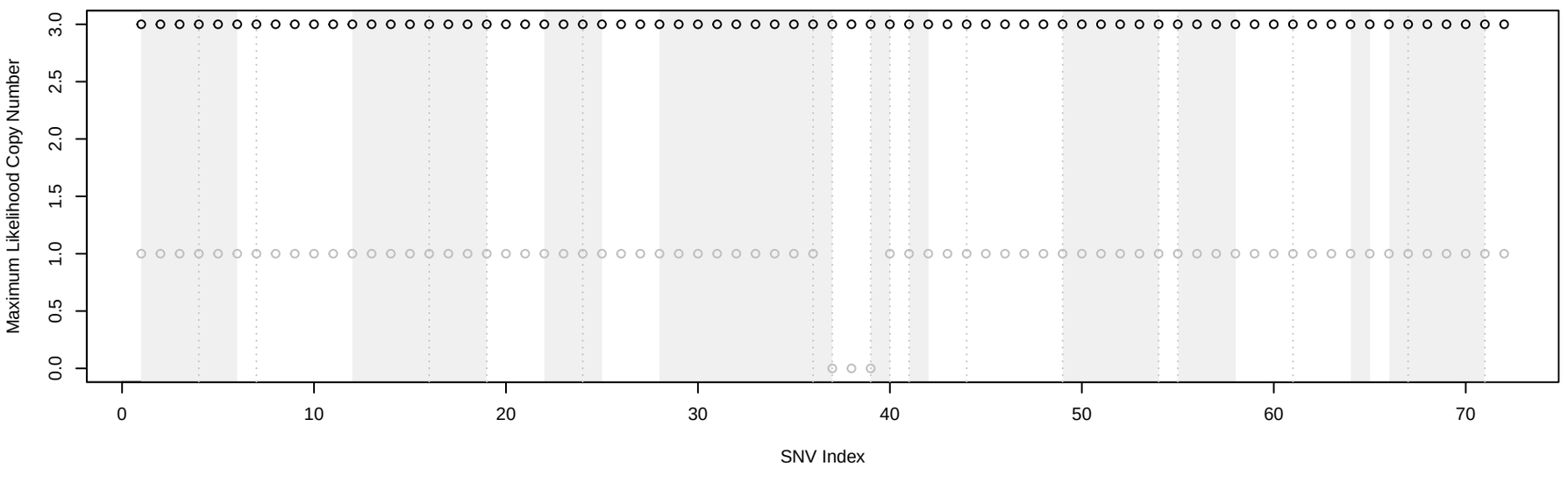

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−1.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

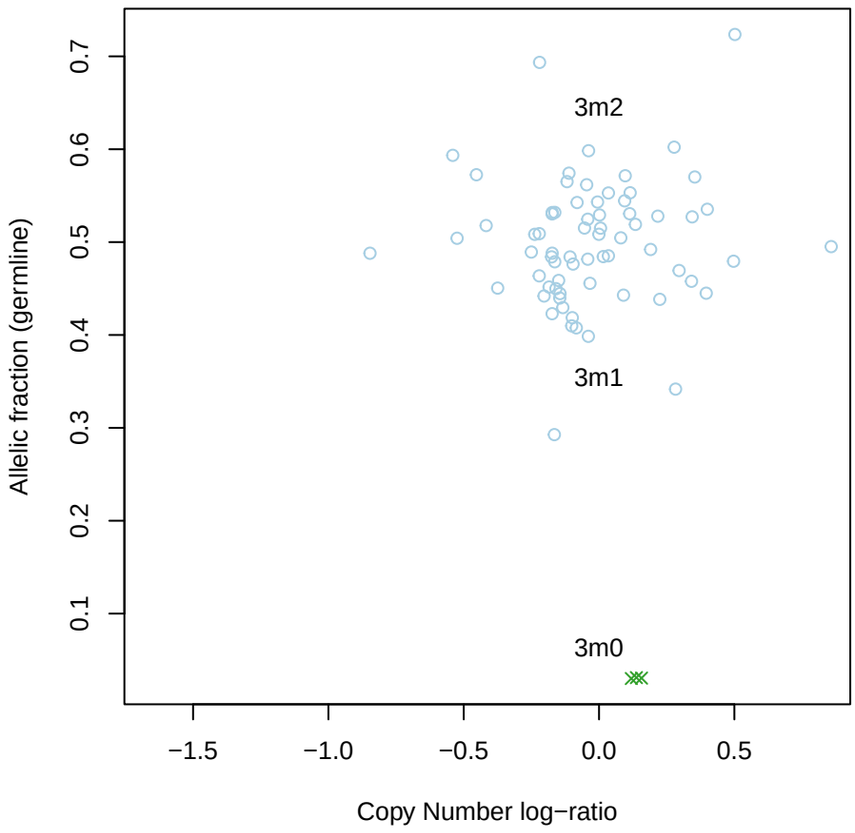

Power 0.8
Frequency
0
10
20
30
40
50
60
70
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
Cellular fraction

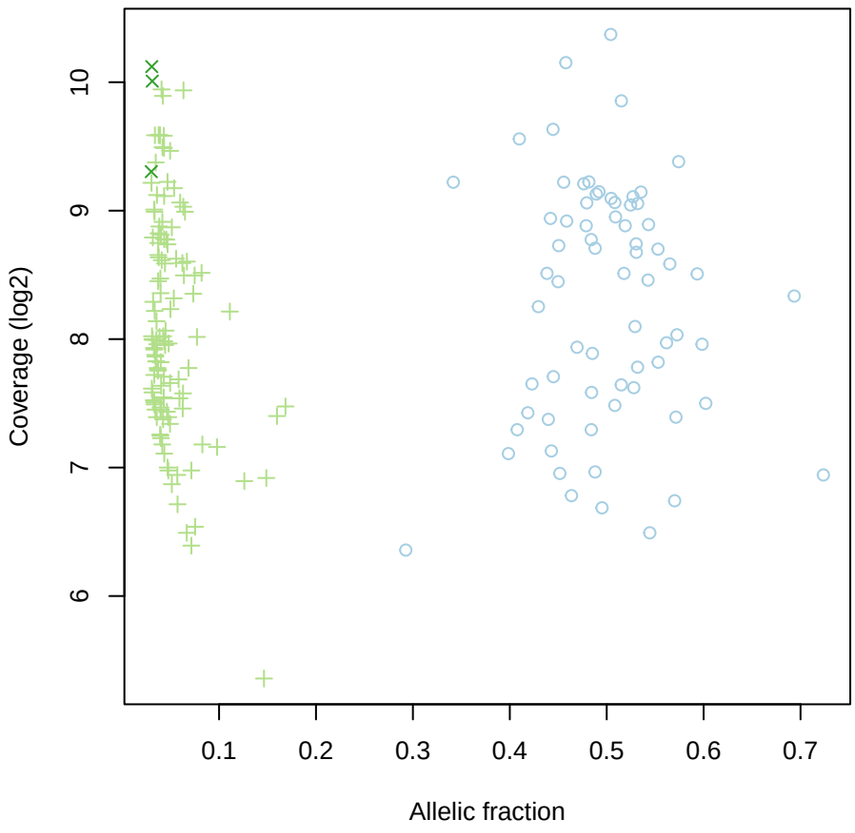

Purity: 0.82 Tumor ploidy: 3.002
1
3
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.6
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

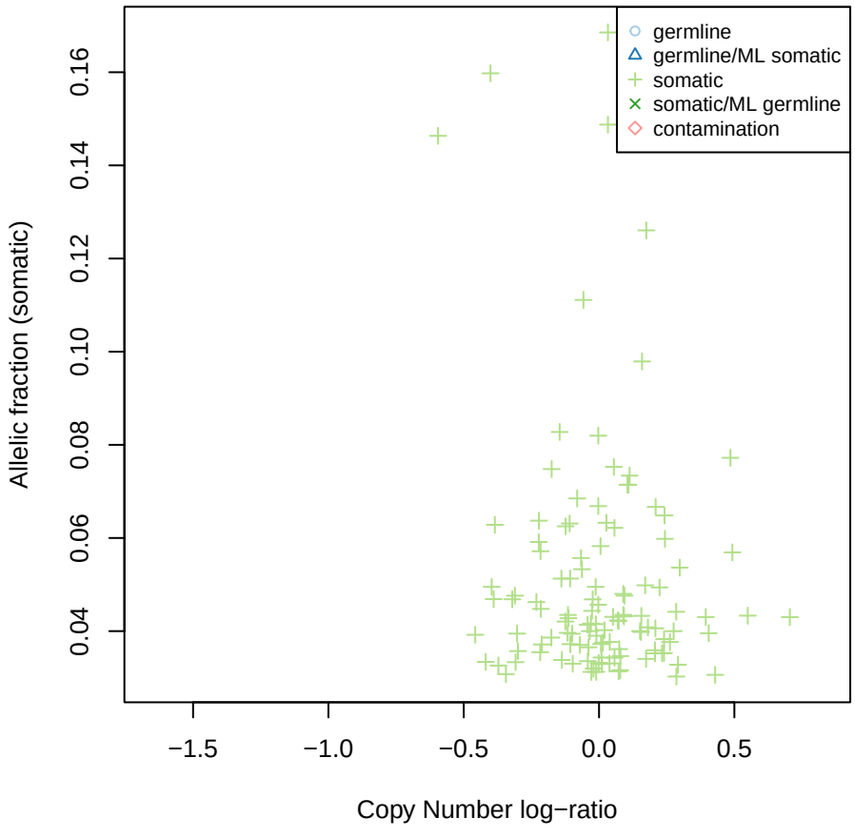

Purity: 0.82 Tumor ploidy: 3.002 SNV log−likelihood: −841.71 GoF: 0% Mean coverage: 355;510
1 2 3 4 5 6 7 8 9 11 12 13 14 15 16 17 19
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60 70
SNV Index

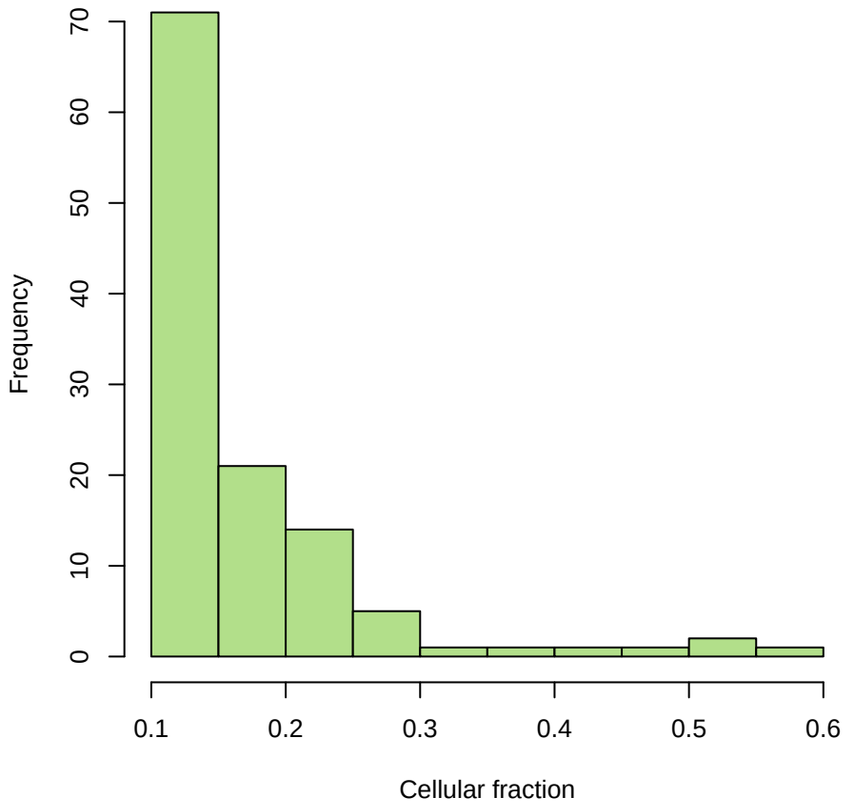

SCNA−fit log−likelihood: −13144.61
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
3
1
0 10 20 30 40 50 60 70
SNV Index

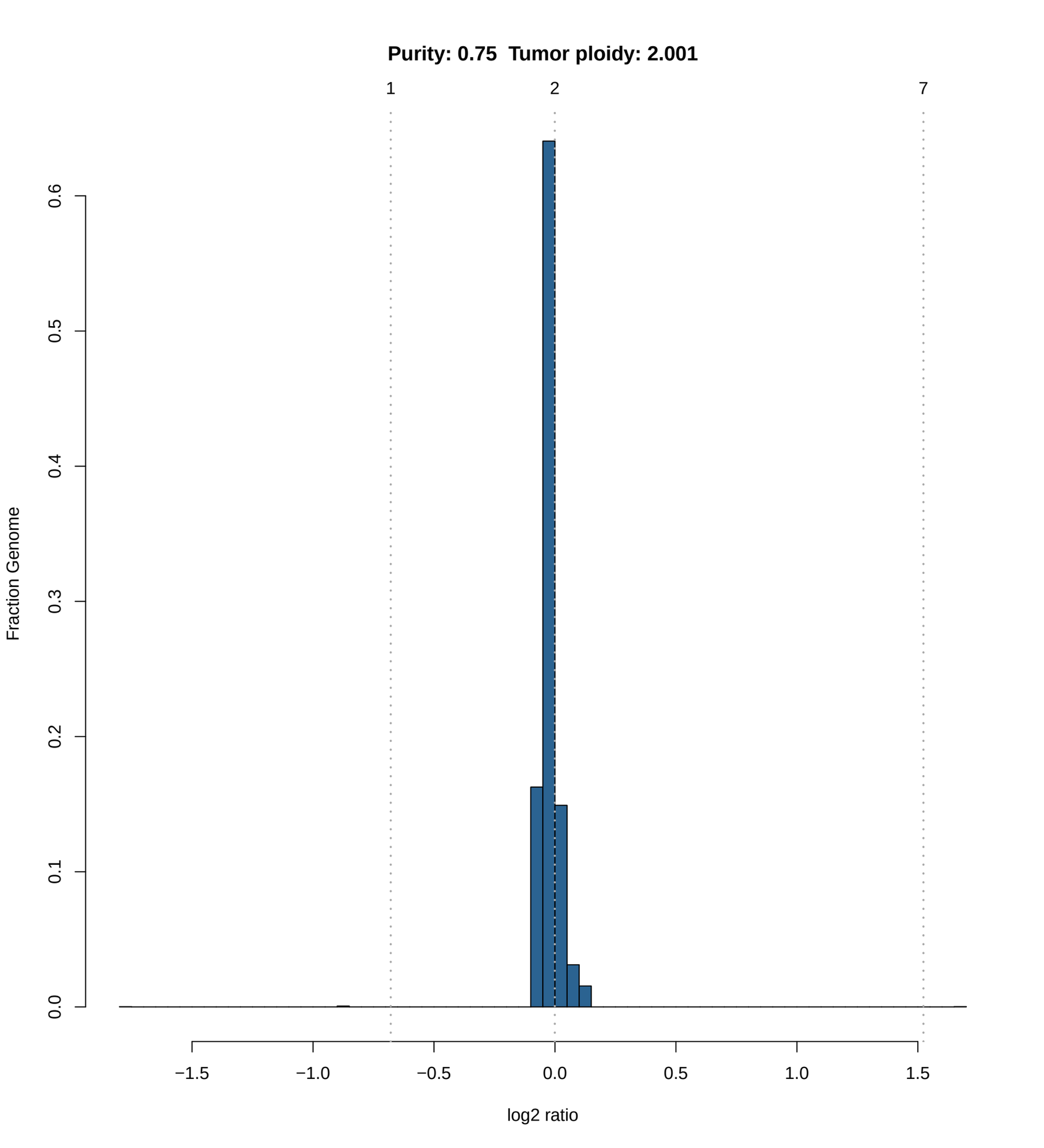

Maximum Likelihood Copy Number
3.0 2.5 2.0 1.5 1.0 0.5 0.0
0 10 20 30 40 50 60 70
SNV Index

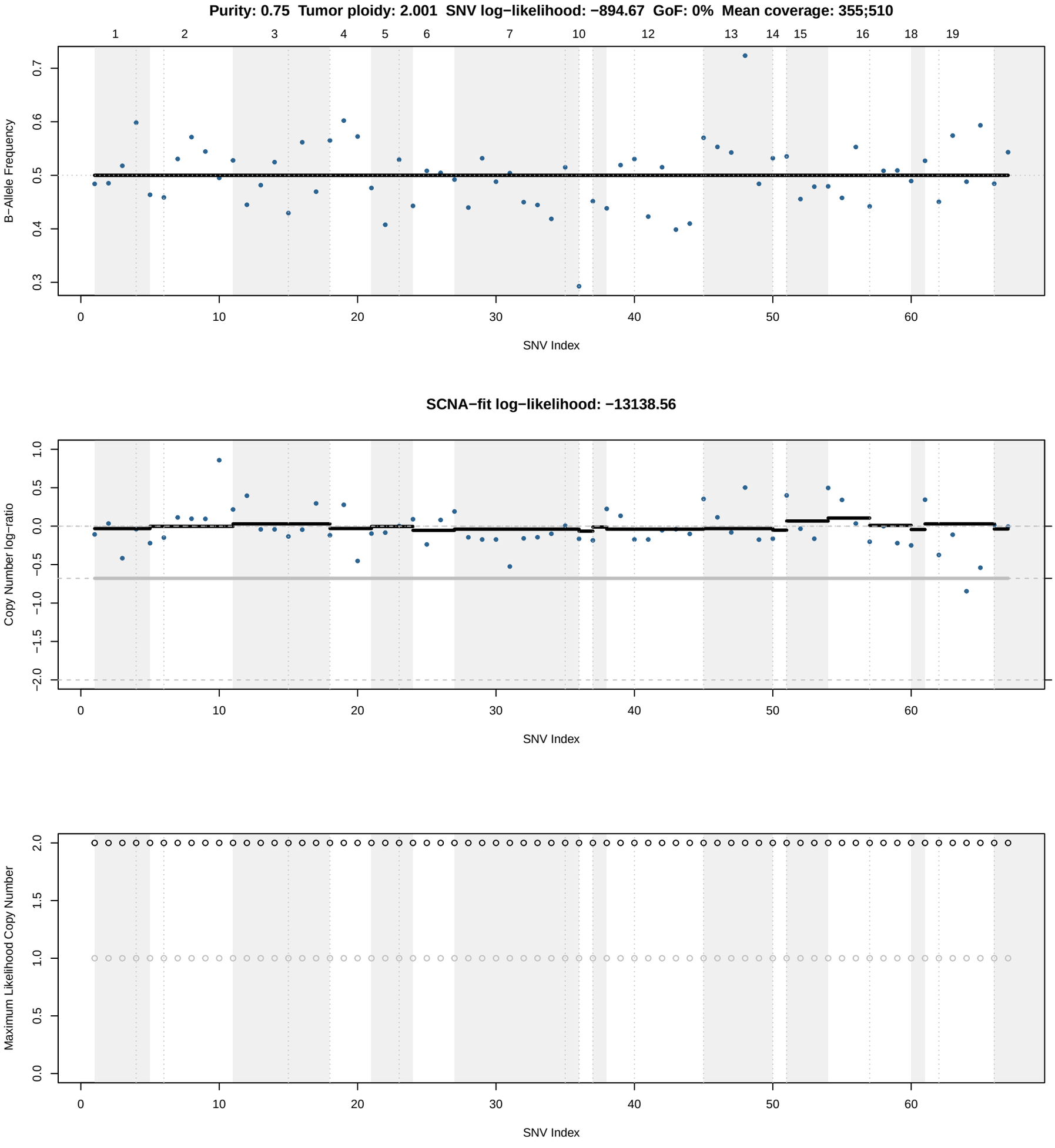

Allelic fraction (germline)
Copy Number log−ratio
3m2
3m1
3m0

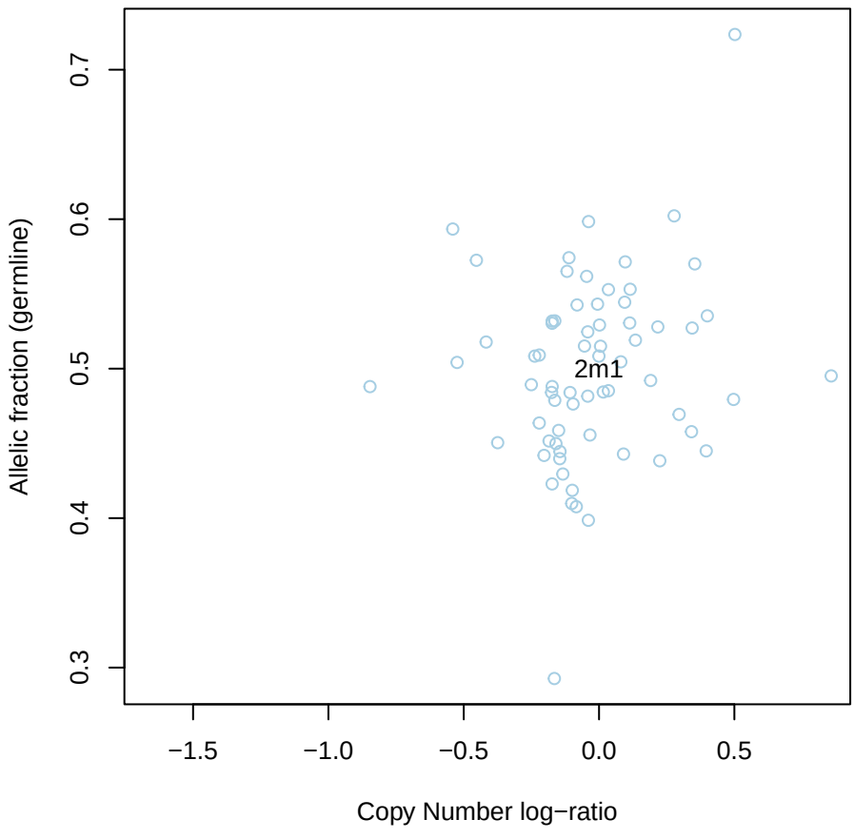

Coverage (log2)
Allelic fraction

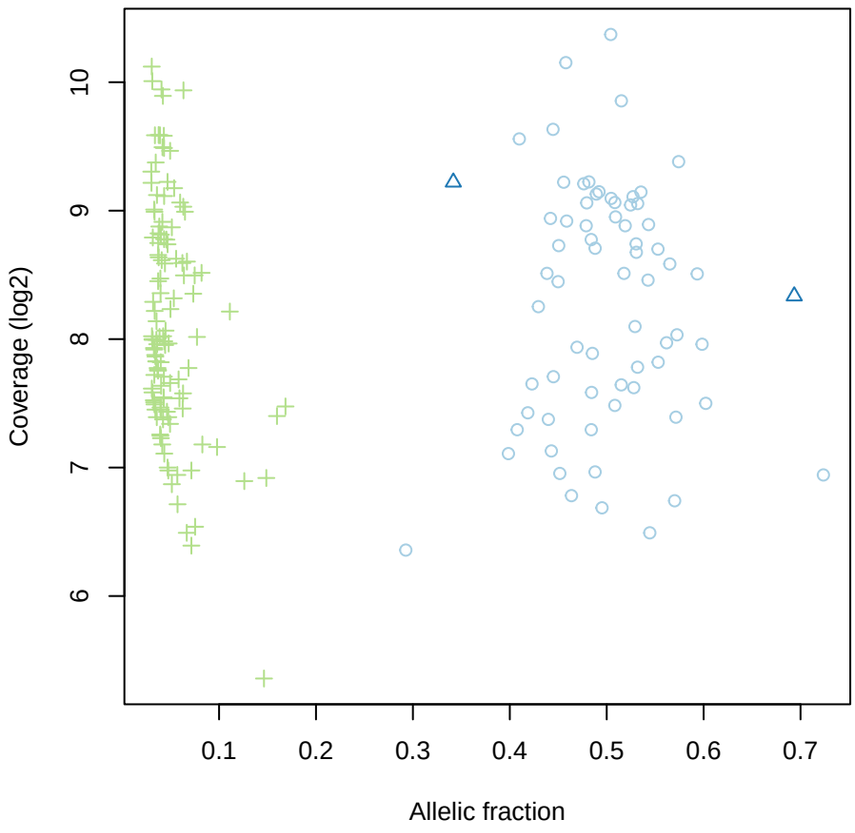

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

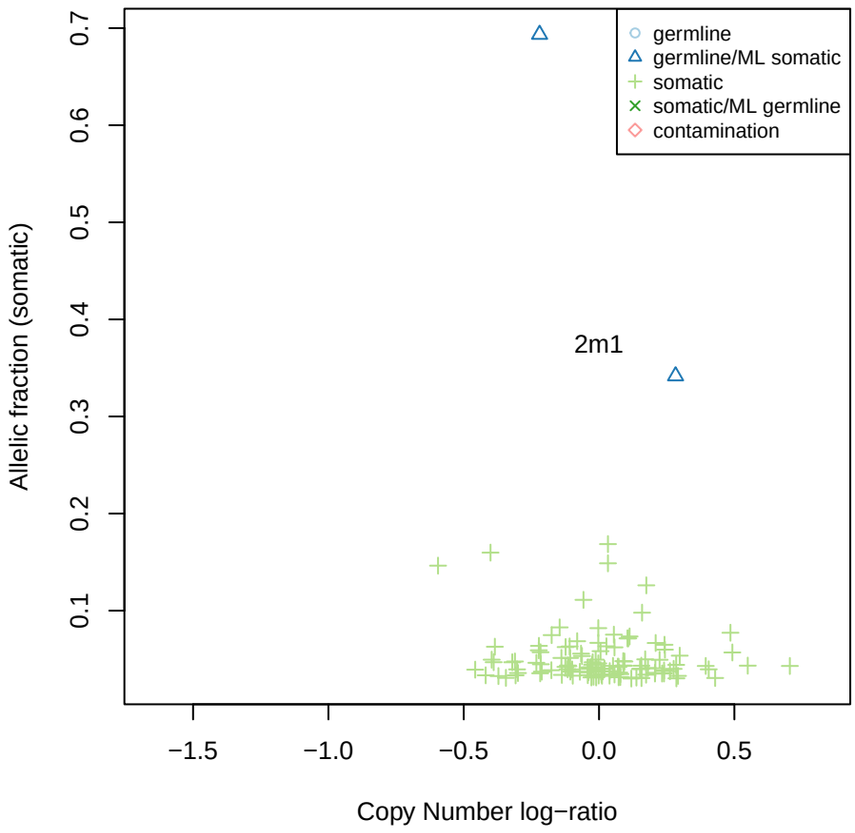

Frequency
Cellular fraction

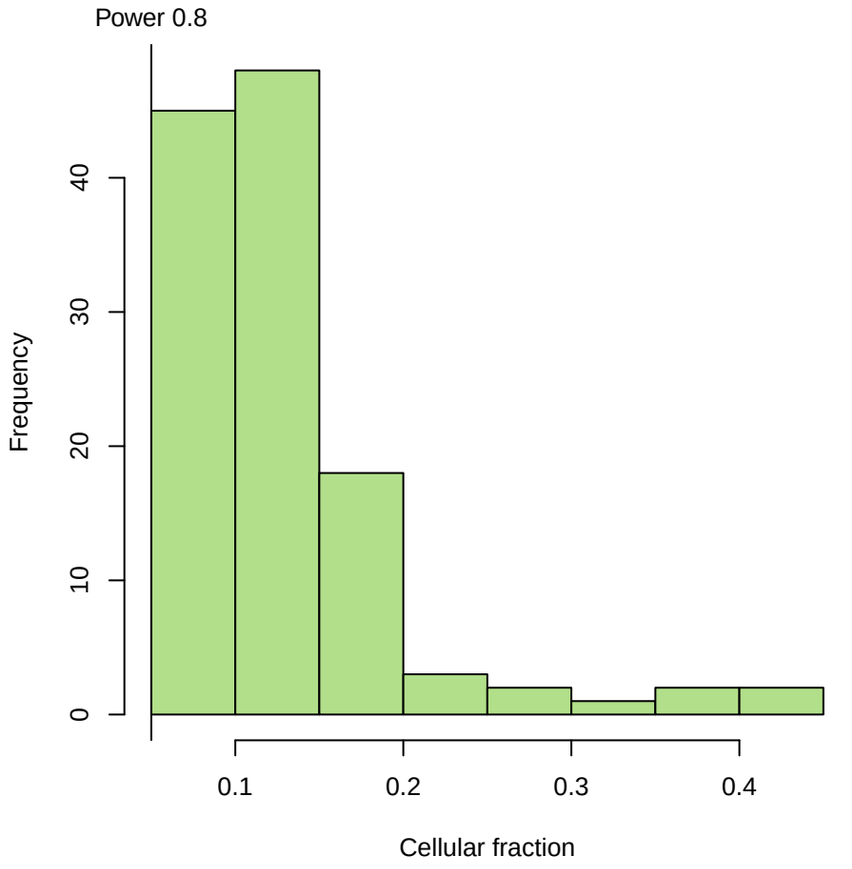

Purity: 0.75 Tumor ploidy: 2.001
1
2
7
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.6
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio


Purity: 0.75 Tumor ploidy: 2.001 SNV log−likelihood: −894.67 GoF: 0% Mean coverage: 355;510
1 2 3 4 5 6 7 10 12 13 14 15 16 18 19
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 10 20 30 40 50 60
SNV Index
SCNA−fit log−likelihood: −13138.56
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2
0 10 20 30 40 50 60
SNV Index
Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 10 20 30 40 50 60
SNV Index


Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
2m1
−1.5
−1.0
−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
0.7
Allelic fraction


Allelic fraction (somatic)
0.1
0.2
0.3
0.4
0.5
0.6
0.7
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
−1.5
−1.0
−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
Cellular fraction