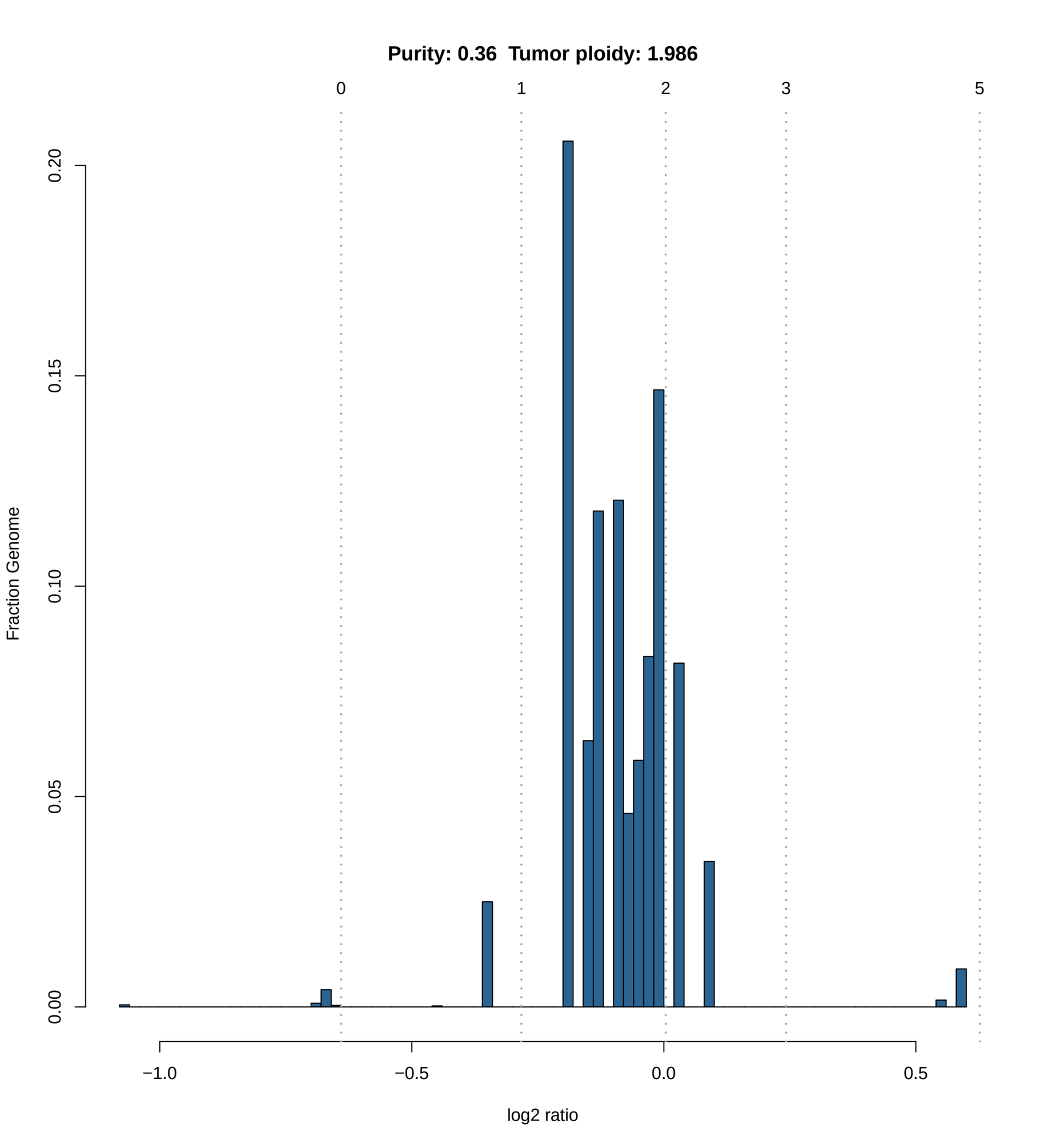
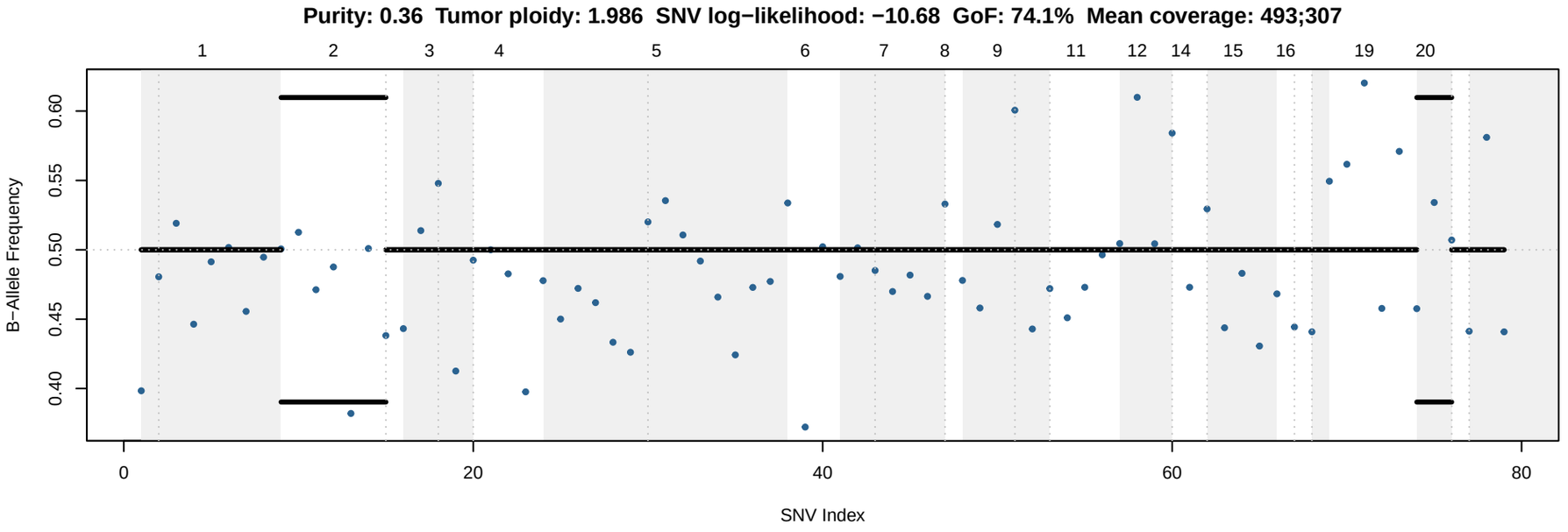
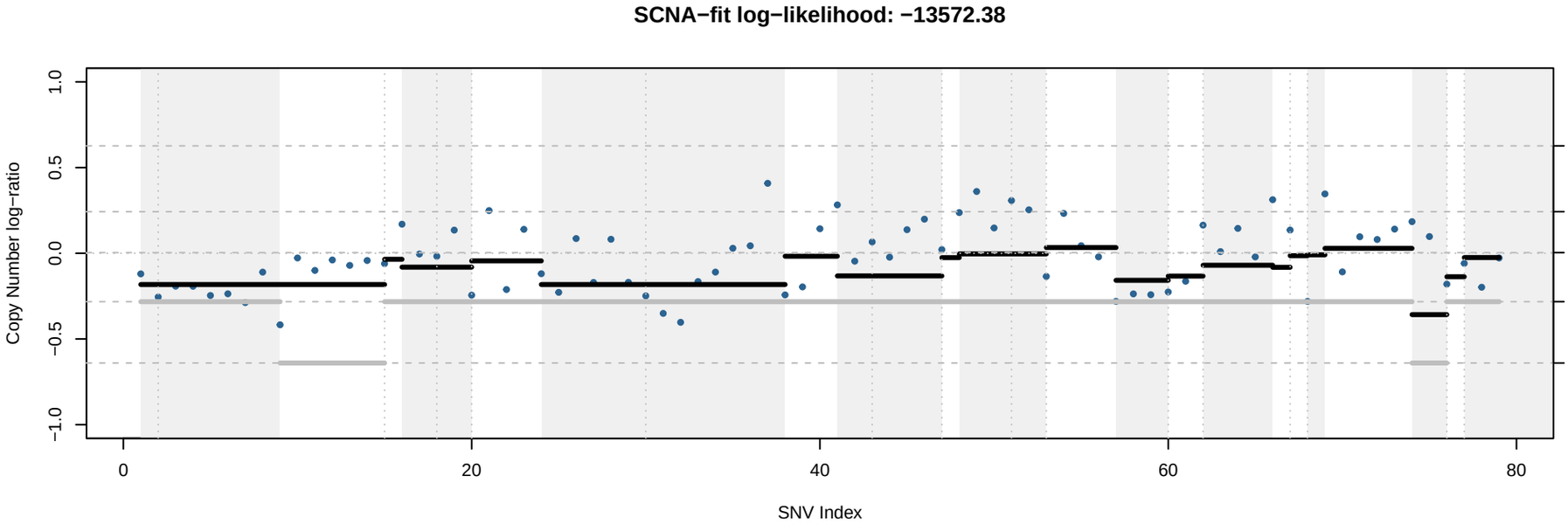
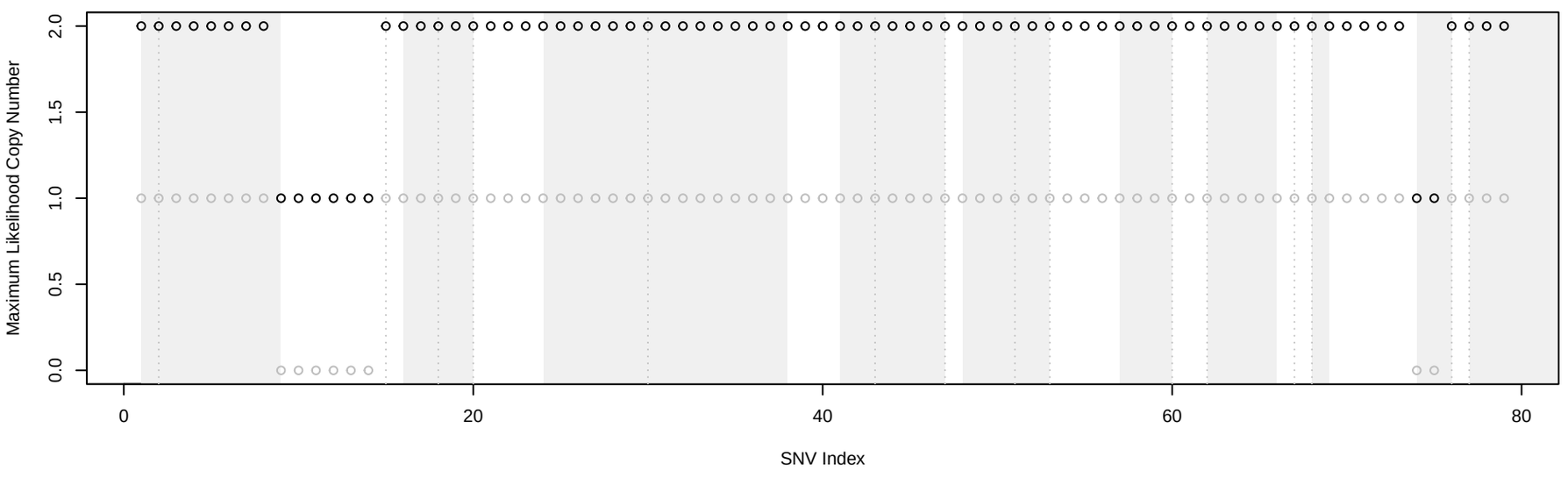
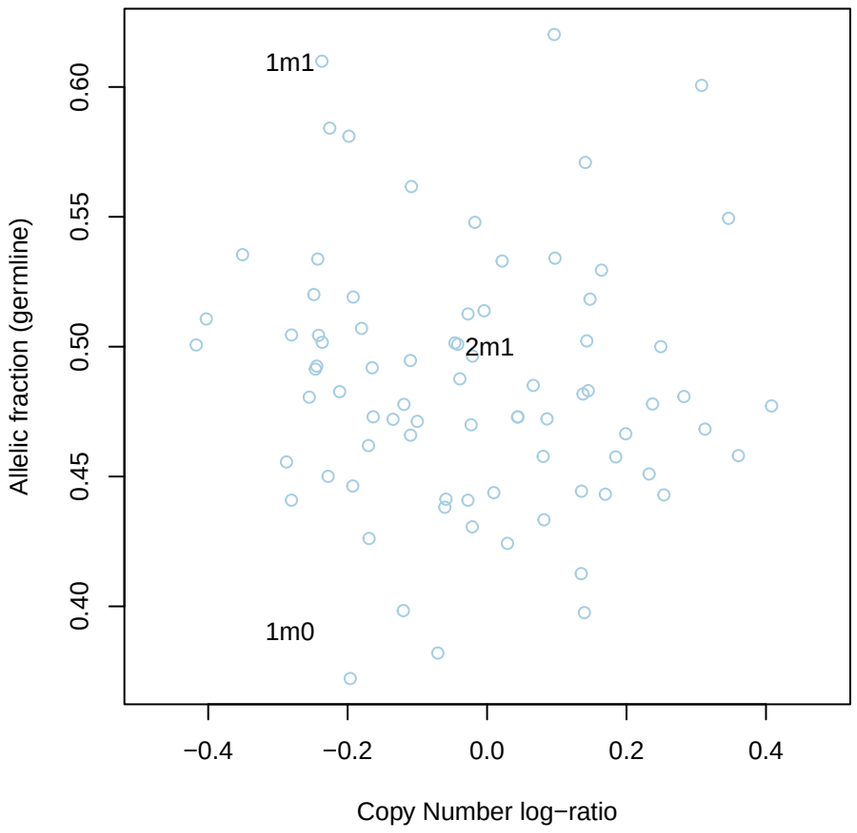
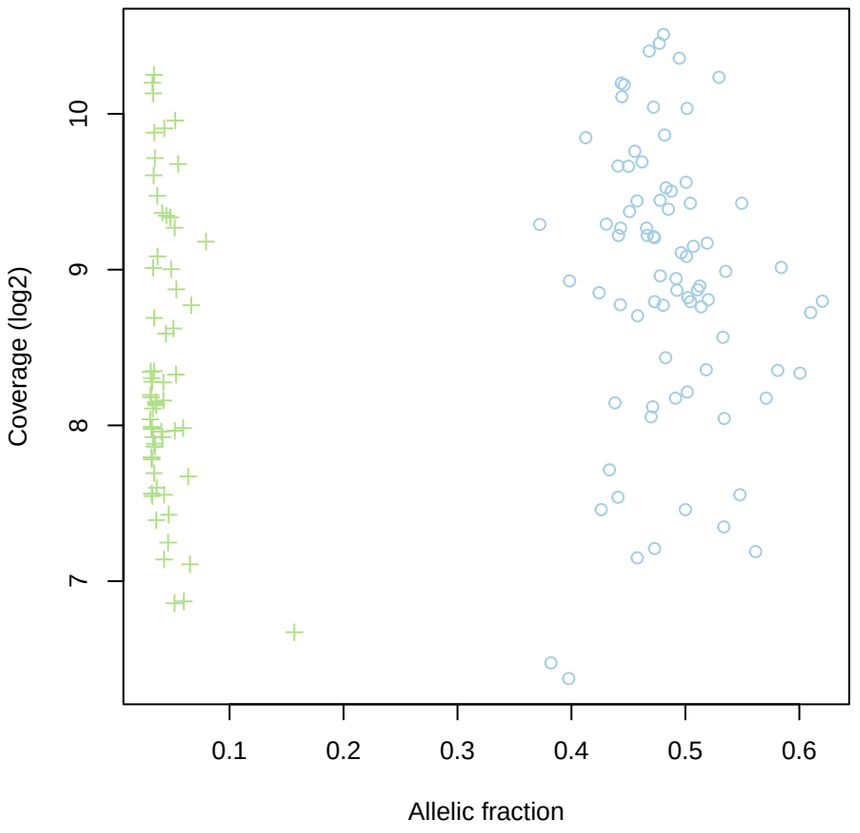

Purity: 0.36 Tumor ploidy: 1.986
0
1
2
3
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

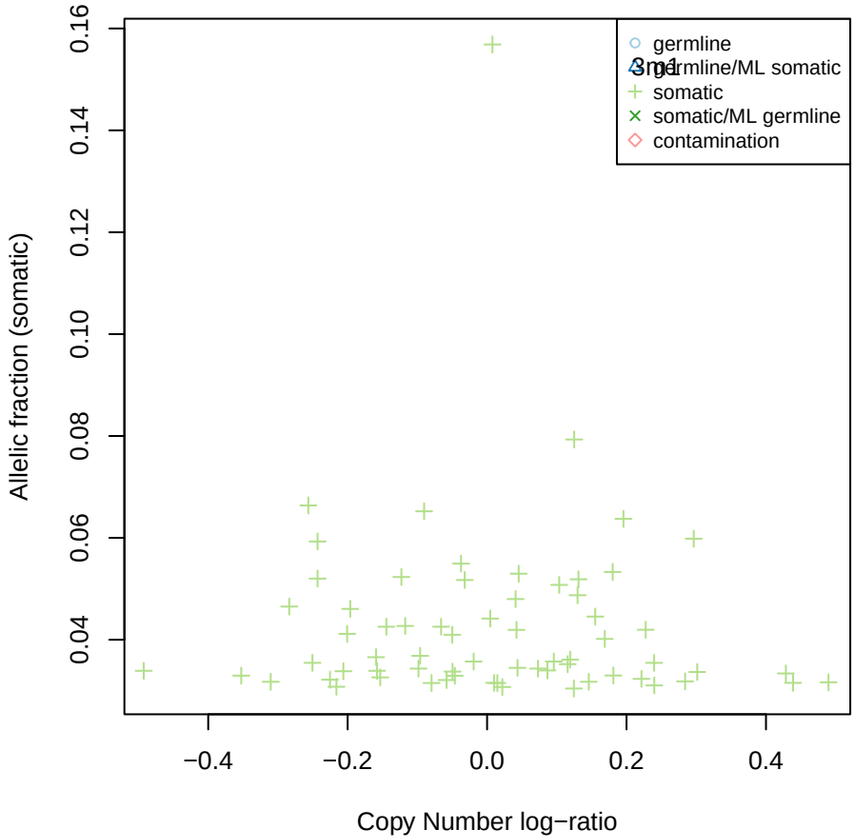

Purity: 0.36 Tumor ploidy: 1.986 SNV log−likelihood: −10.68 GoF: 74.1% Mean coverage: 493;307
1 2 3 4 5 6 7 8 9 11 12 14 15 16 19 20
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

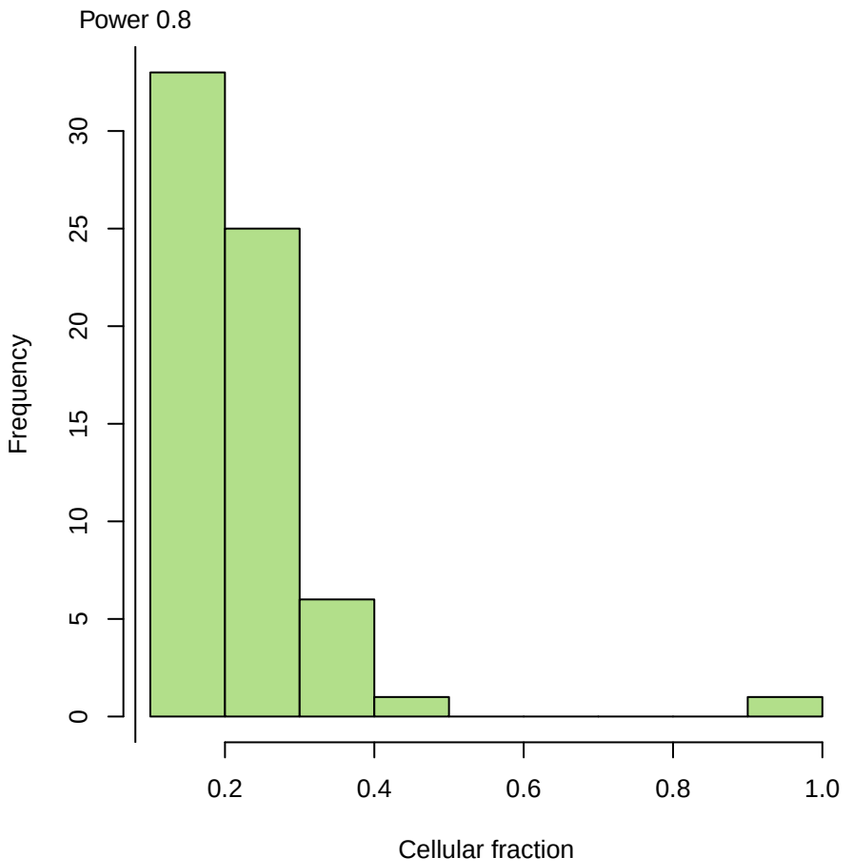

SCNA−fit log−likelihood: −13572.38
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 5
0 20 40 60 80
SNV Index

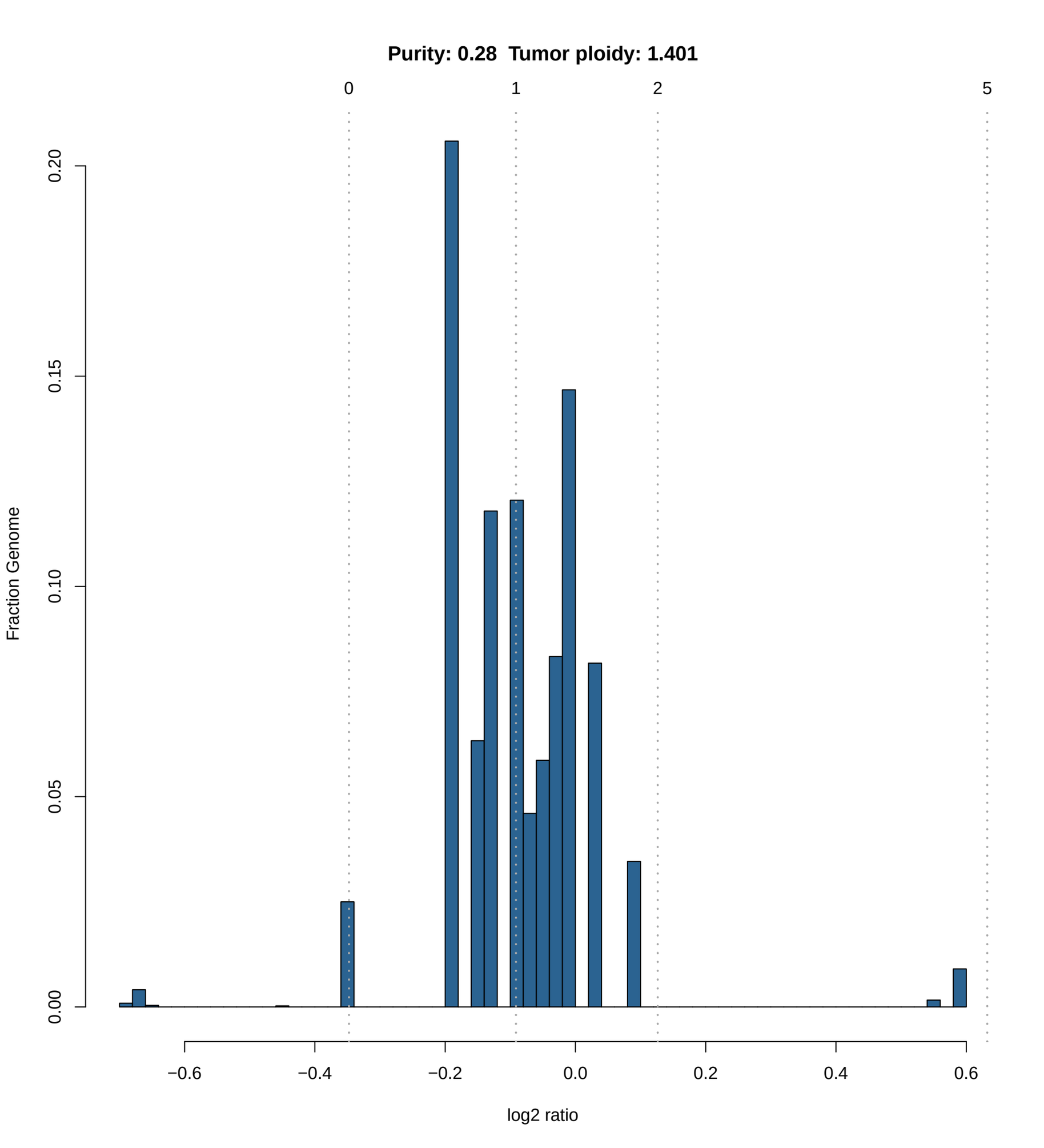

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 20 40 60 80
SNV Index

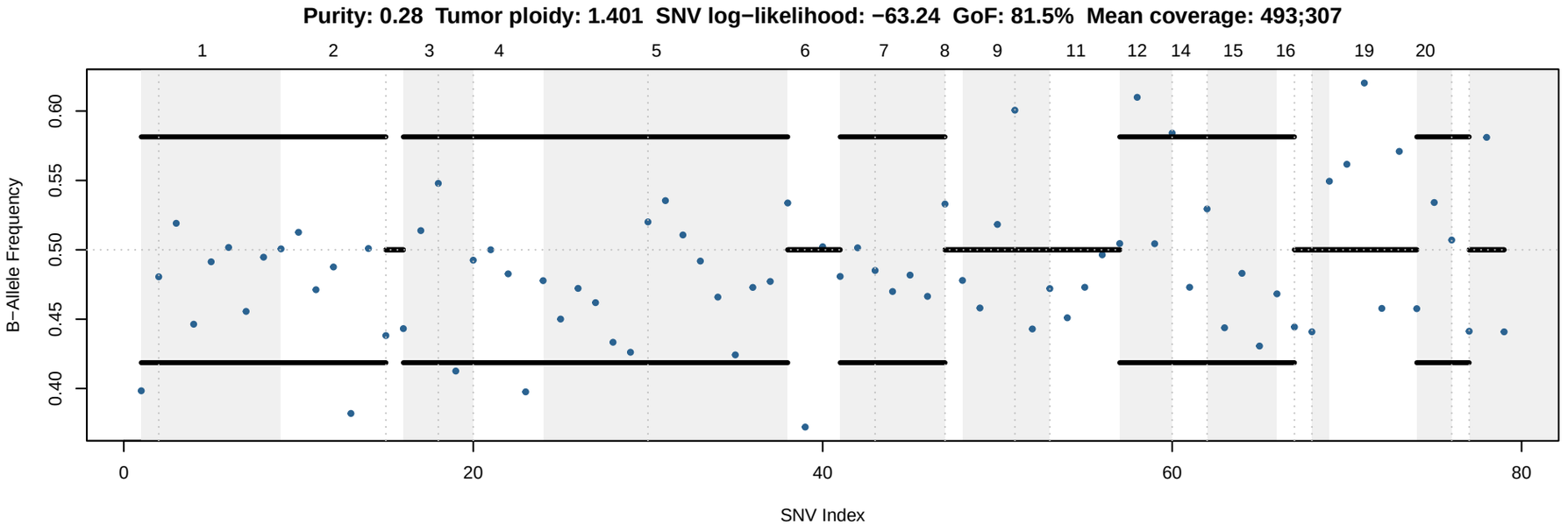

1m1
2m1
1m0
Allelic fraction (germline)
Copy Number log−ratio

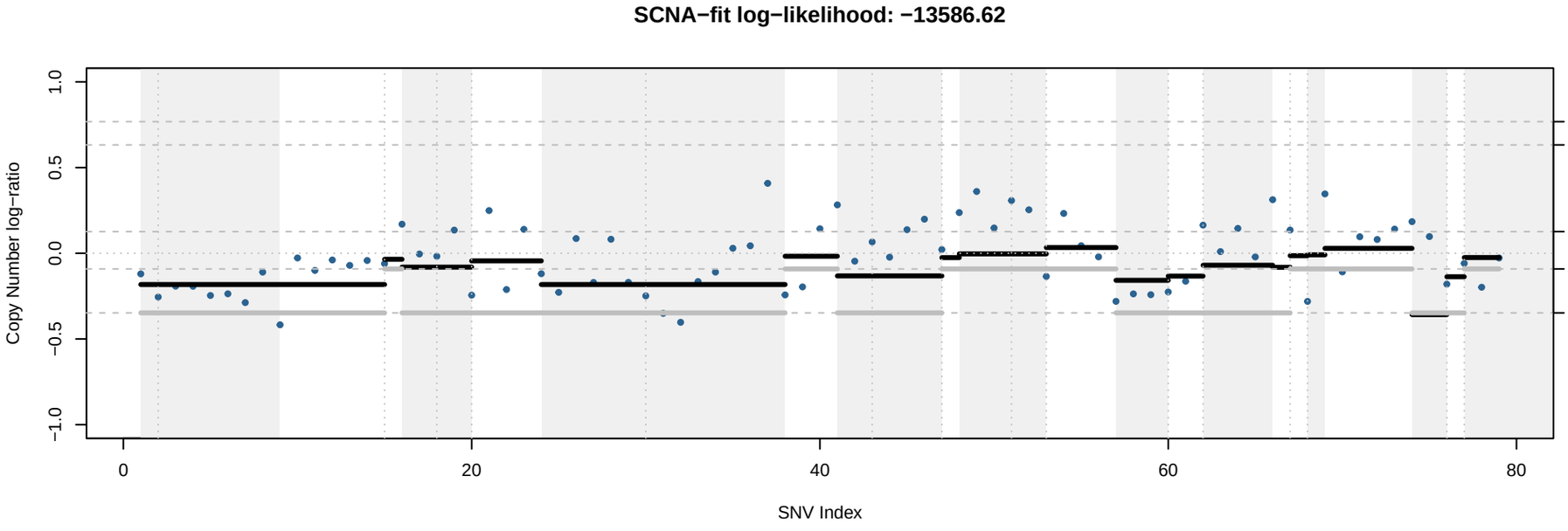

Coverage (log2)
Allelic fraction

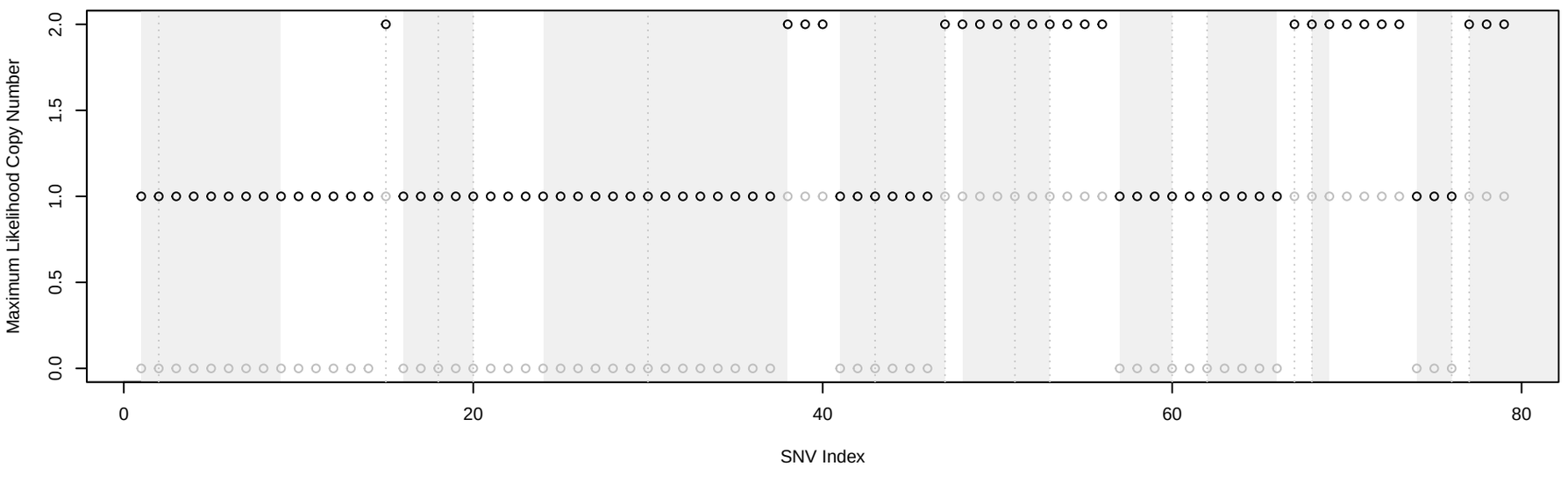

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
Allelic fraction (somatic)
Copy Number log−ratio

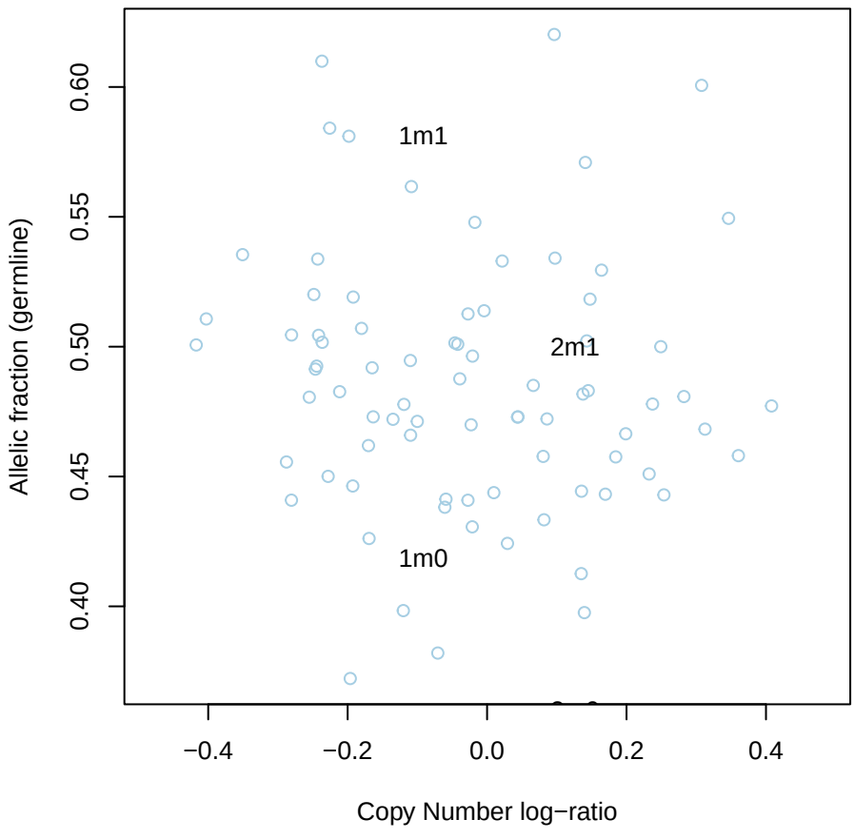

Power 0.8
Frequency
Cellular fraction

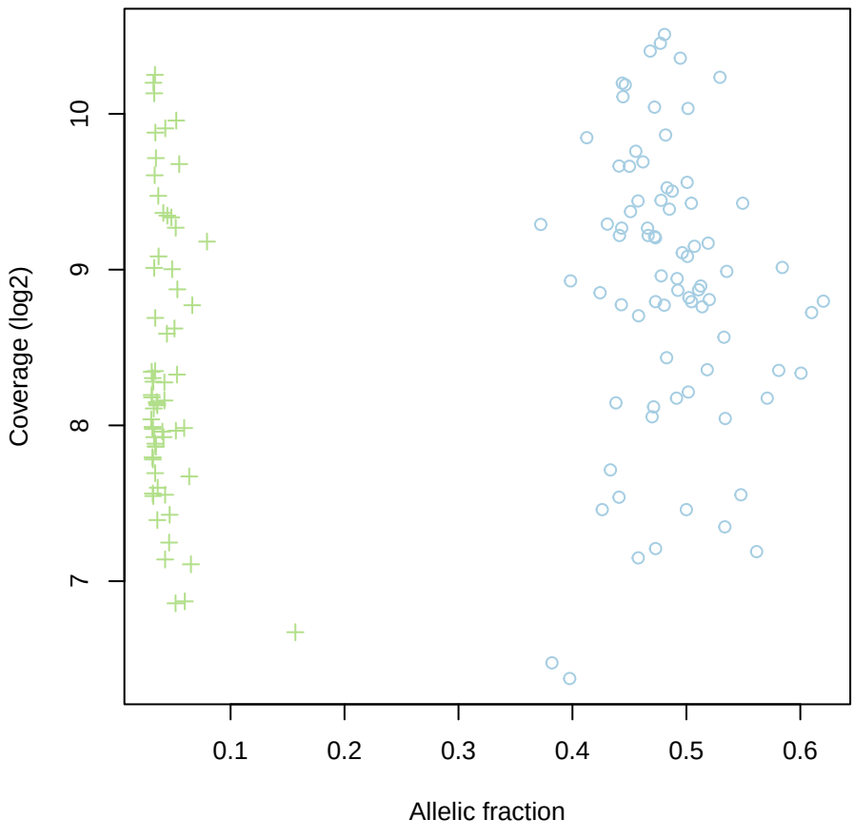

Purity: 0.28 Tumor ploidy: 1.401
0
1
2
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
log2 ratio

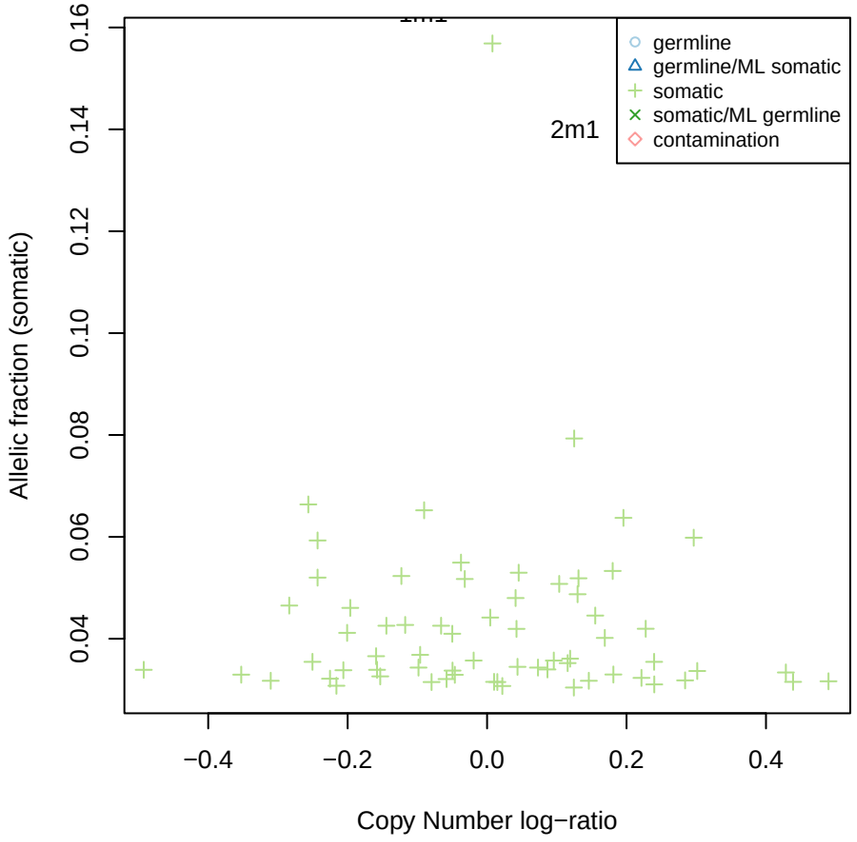

Purity: 0.28 Tumor ploidy: 1.401 SNV log−likelihood: −63.24 GoF: 81.5% Mean coverage: 493;307
1 2 3 4 5 6 7 8 9 11 12 14 15 16 19 20
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

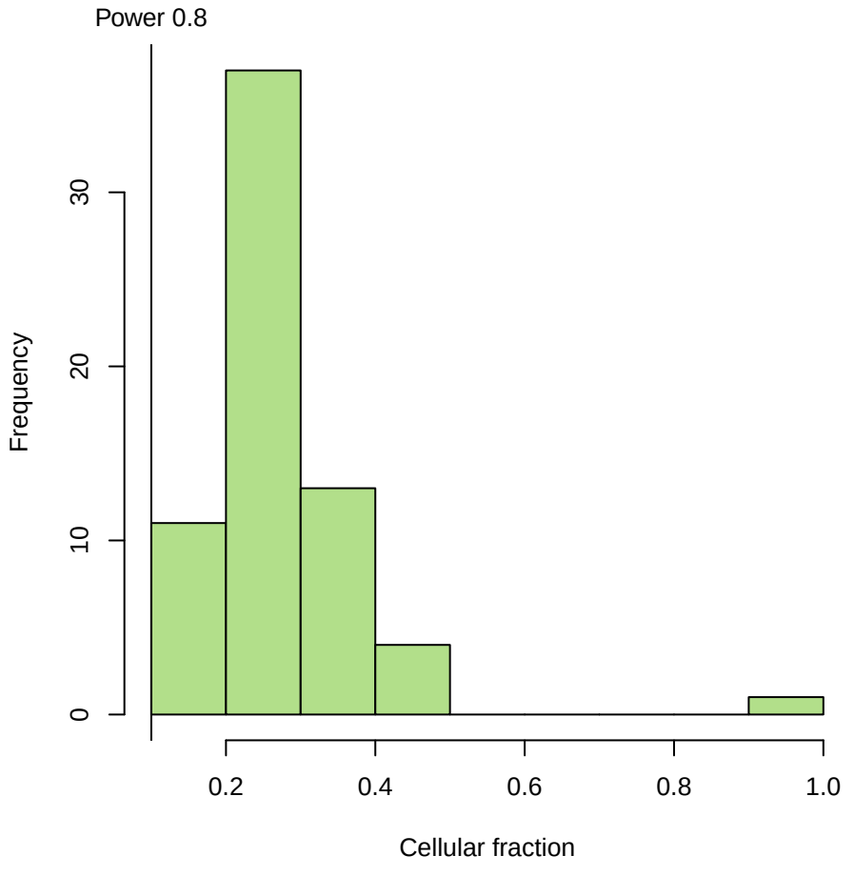

SCNA−fit log−likelihood: −13586.62
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 5
0 20 40 60 80
SNV Index

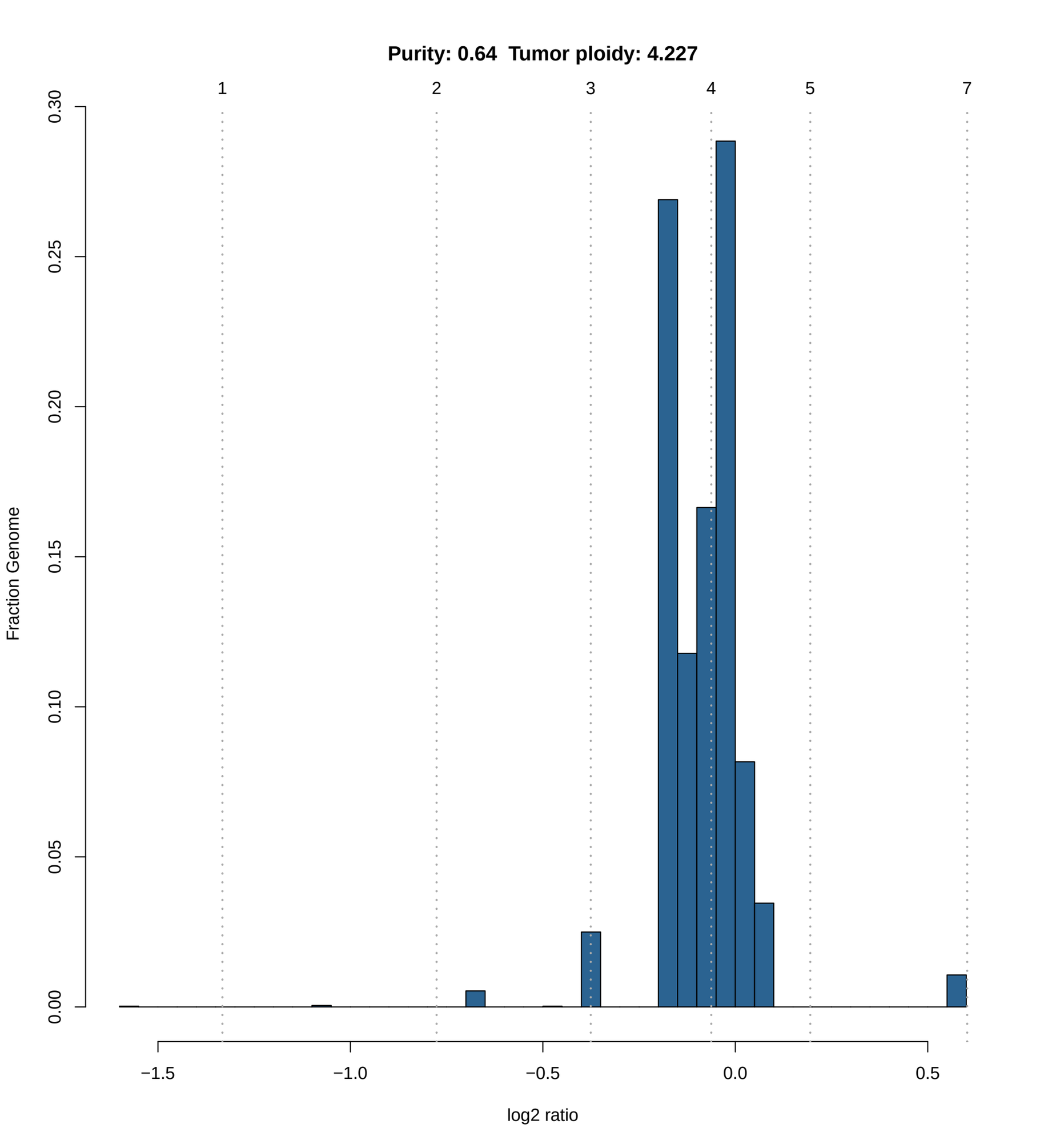

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 20 40 60 80
SNV Index

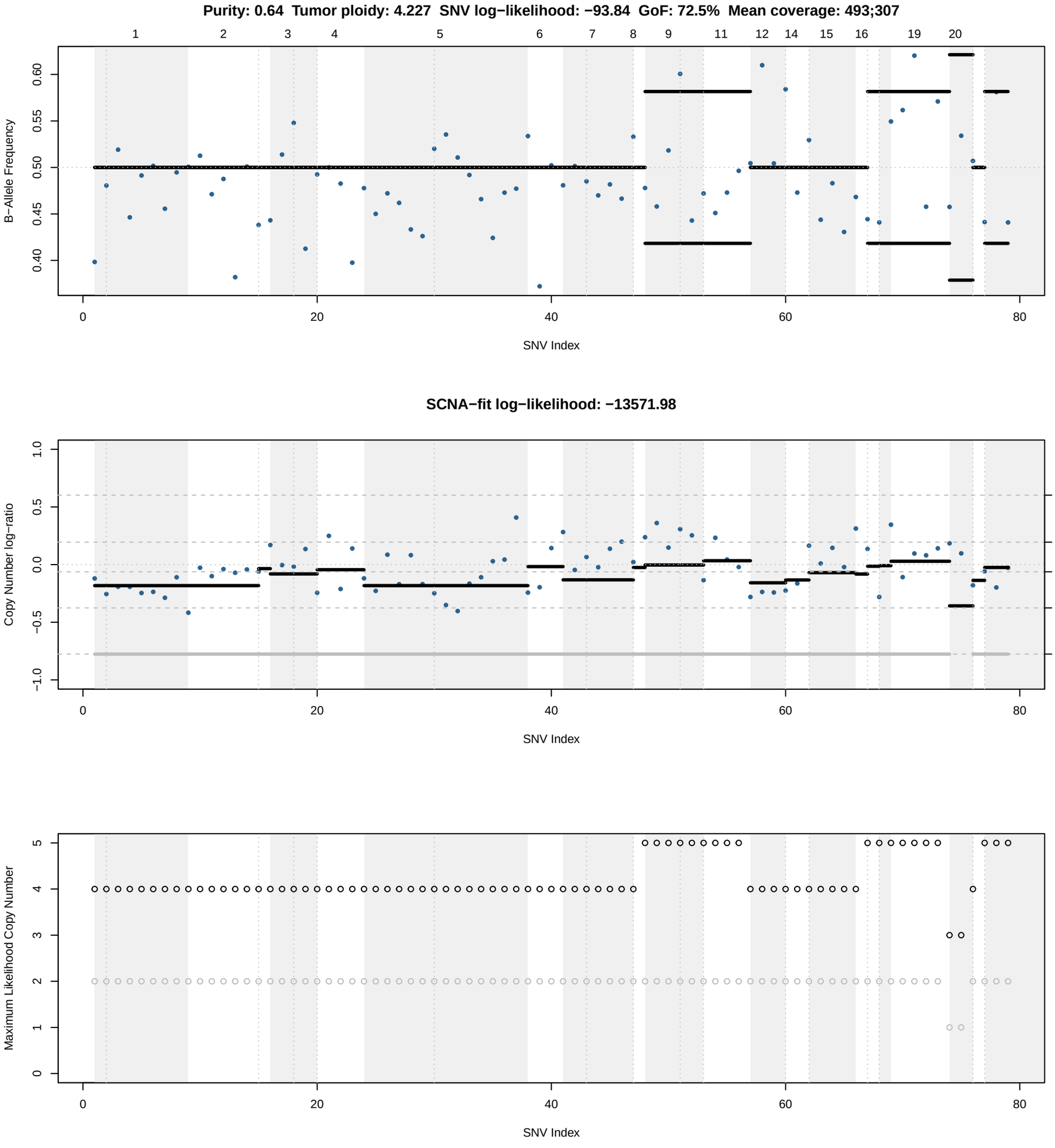

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
1m1
2m1
1m0
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

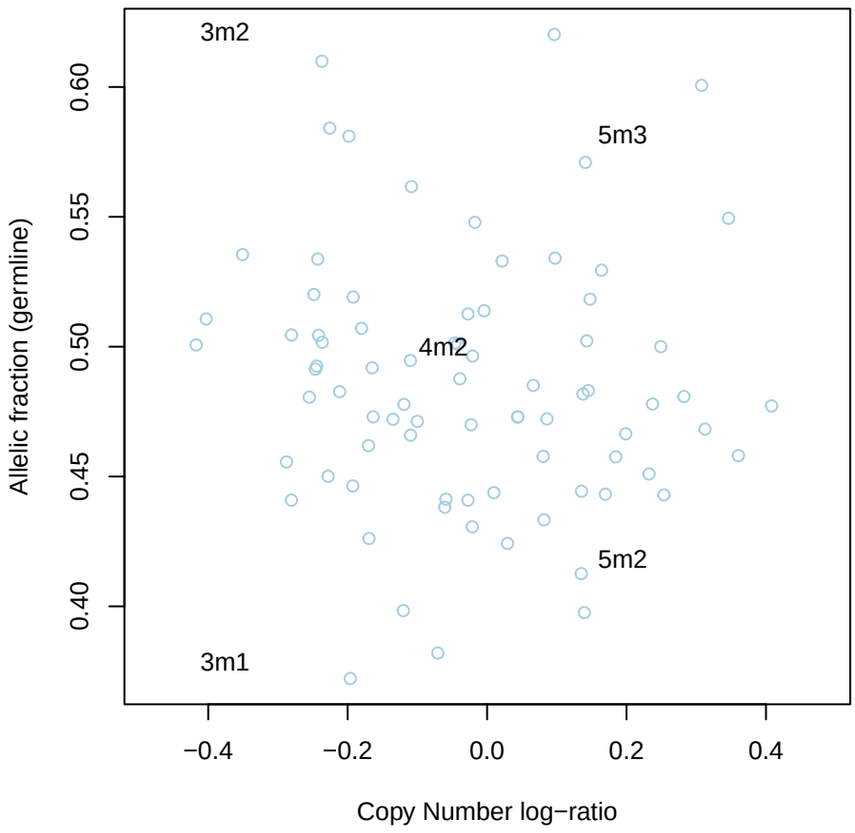

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

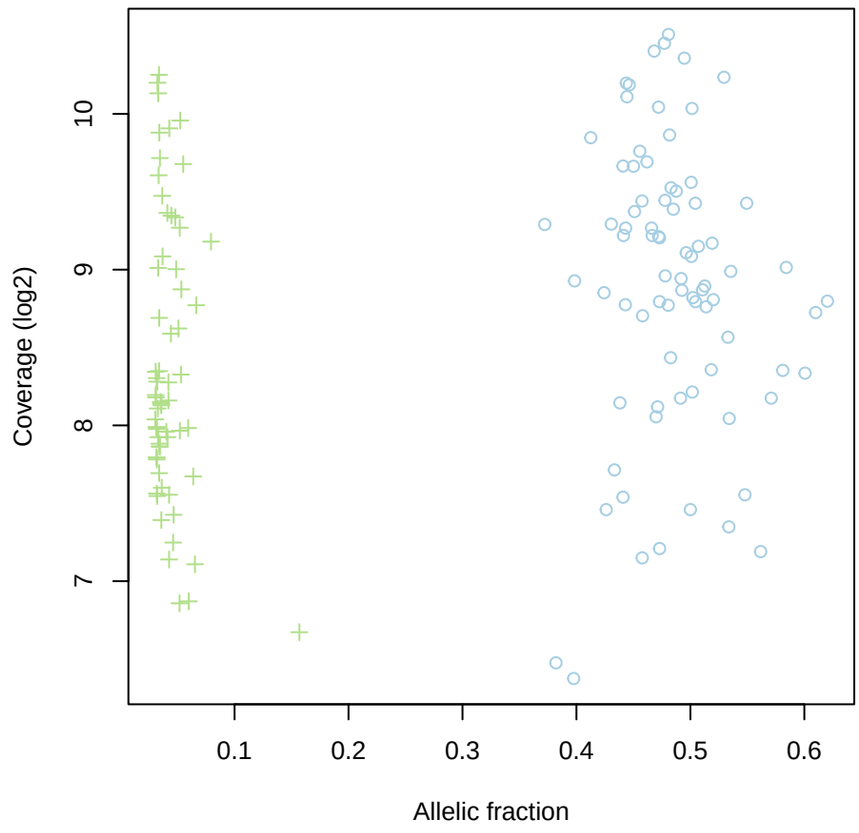

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

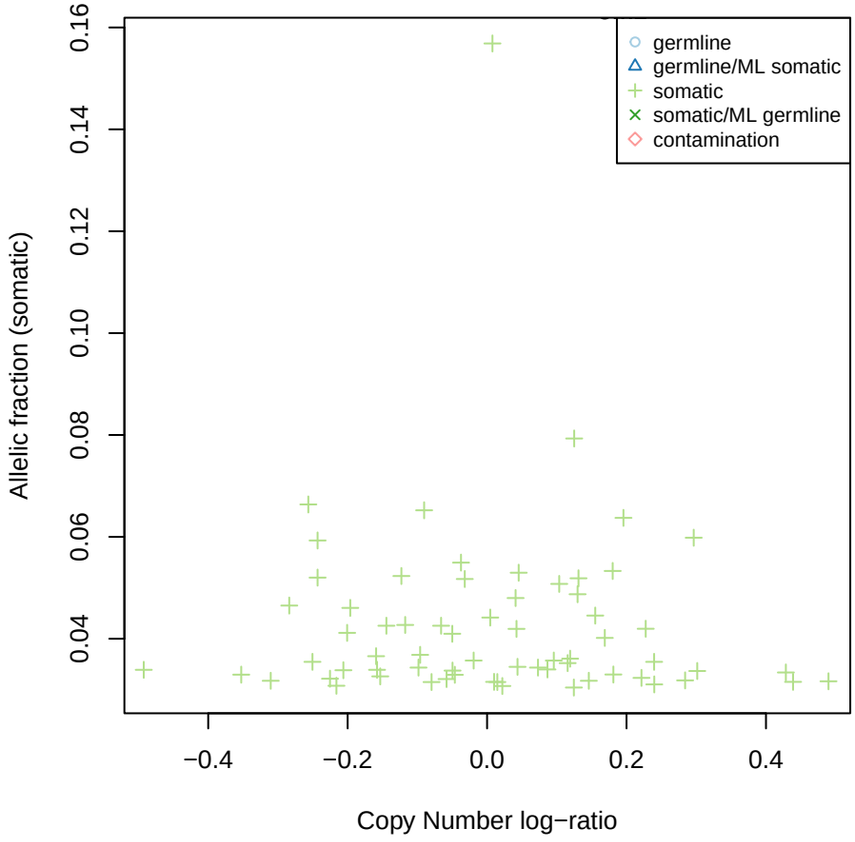

Power 0.8
Frequency
0
10
20
30
0.2
0.4
0.6
0.8
1.0
Cellular fraction

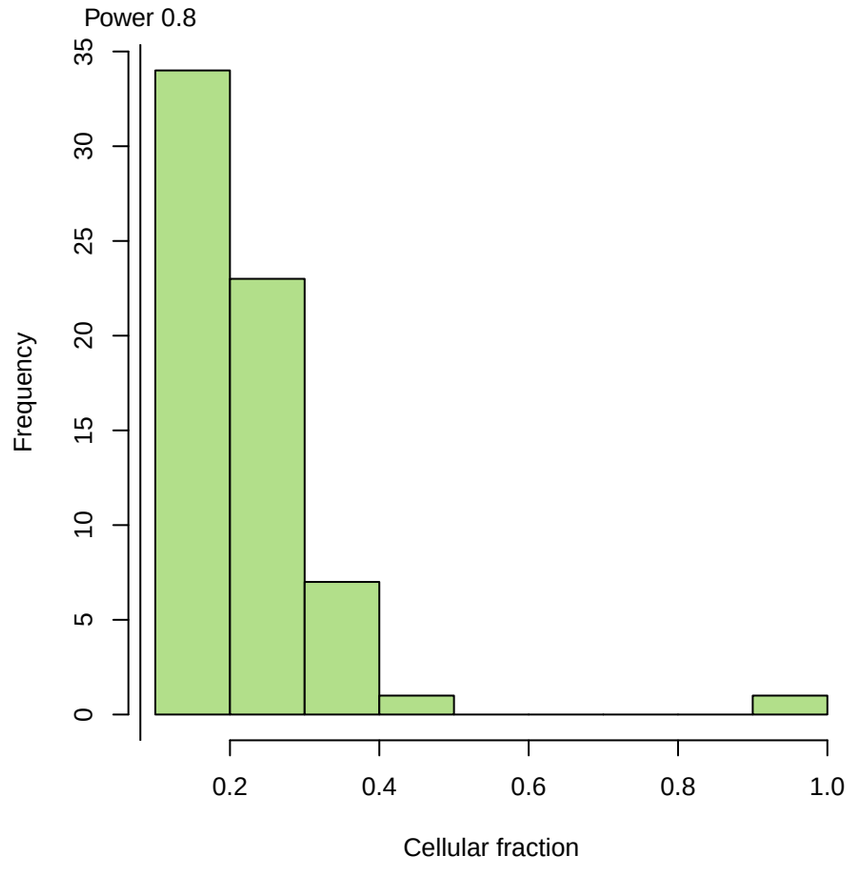

Purity: 0.64 Tumor ploidy: 4.227
1
2
3
4
5
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

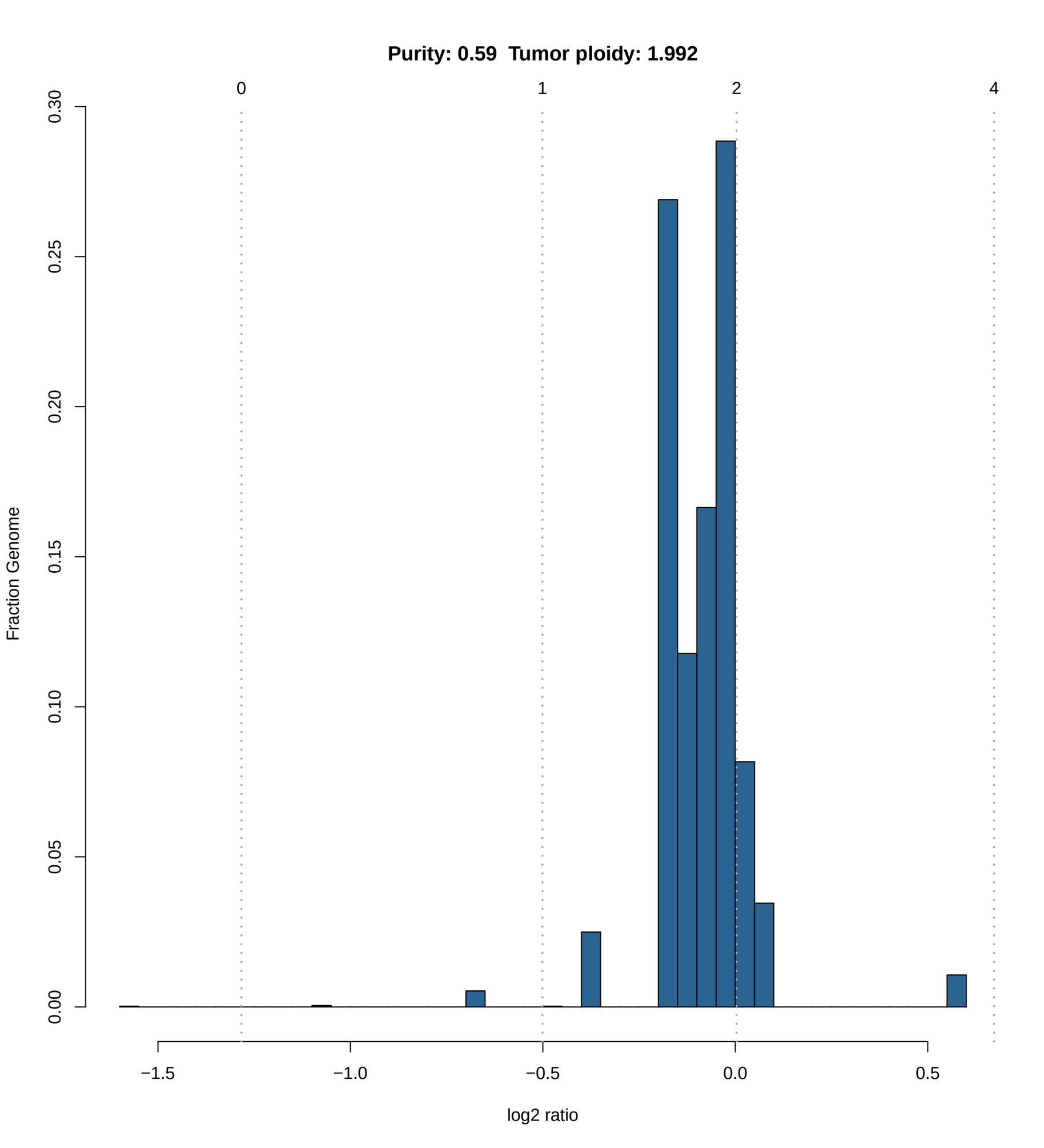

Purity: 0.64 Tumor ploidy: 4.227 SNV log−likelihood: −93.84 GoF: 72.5% Mean coverage: 493;307
1 2 3 4 5 6 7 8 9 11 12 14 15 16 19 20
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index
SCNA−fit log−likelihood: −13571.98
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 7
0 20 40 60 80
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80
SNV Index

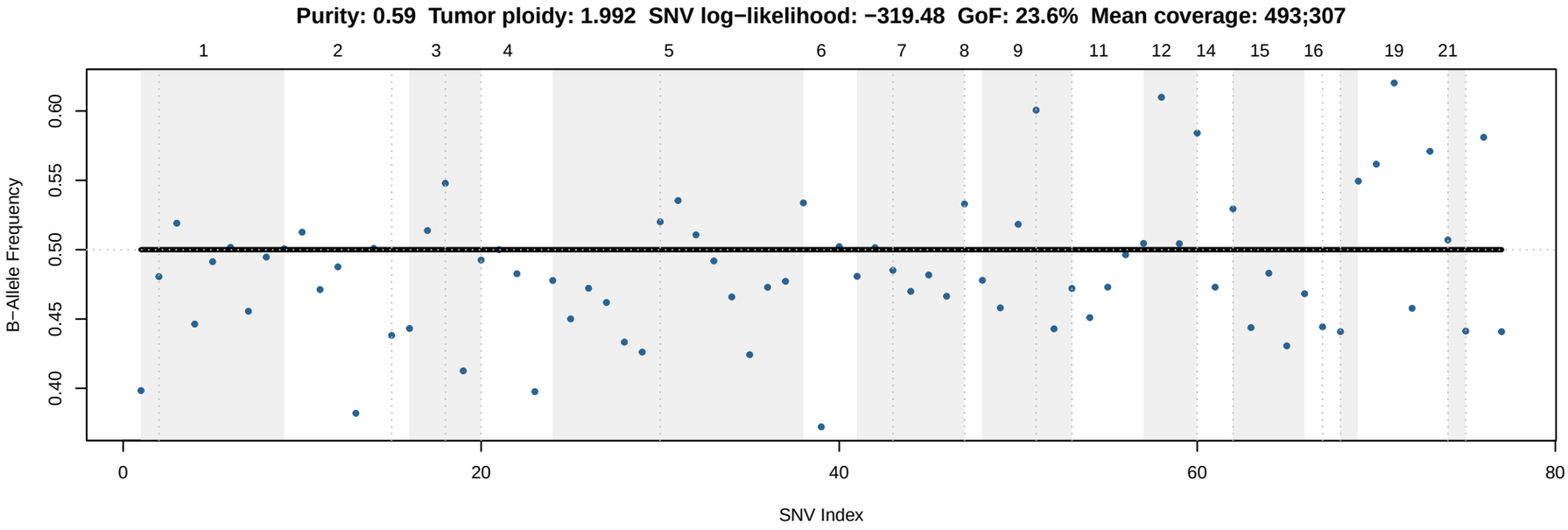

3m2
5m3
4m2
5m2
3m1
Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

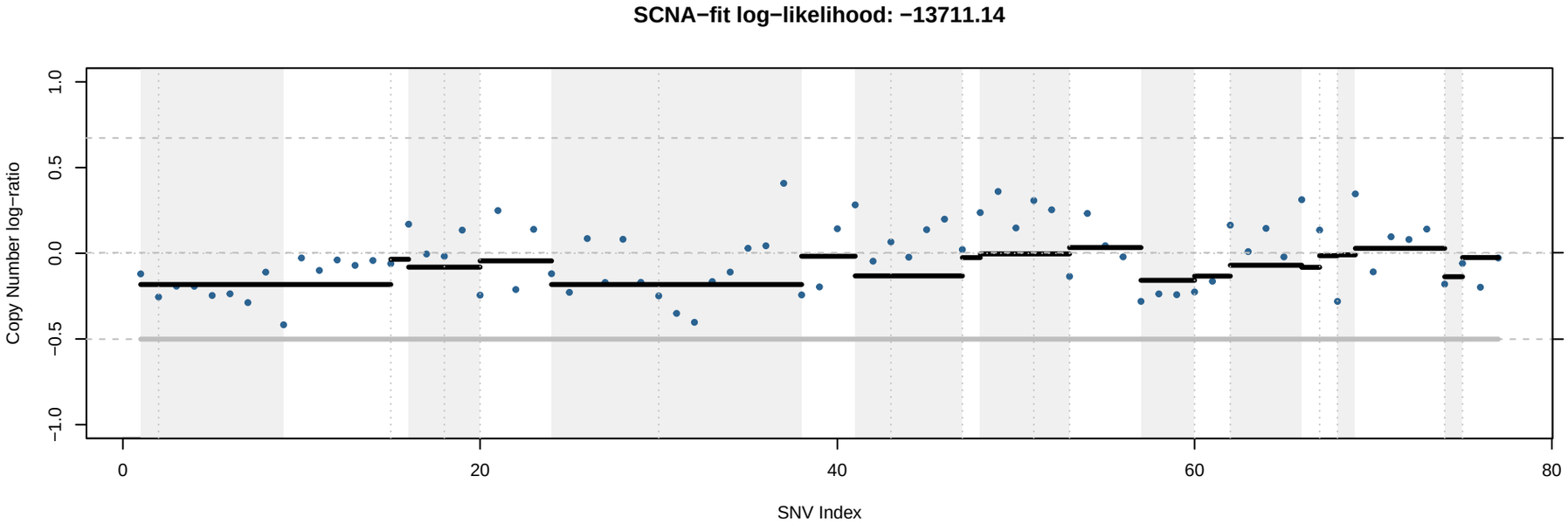

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

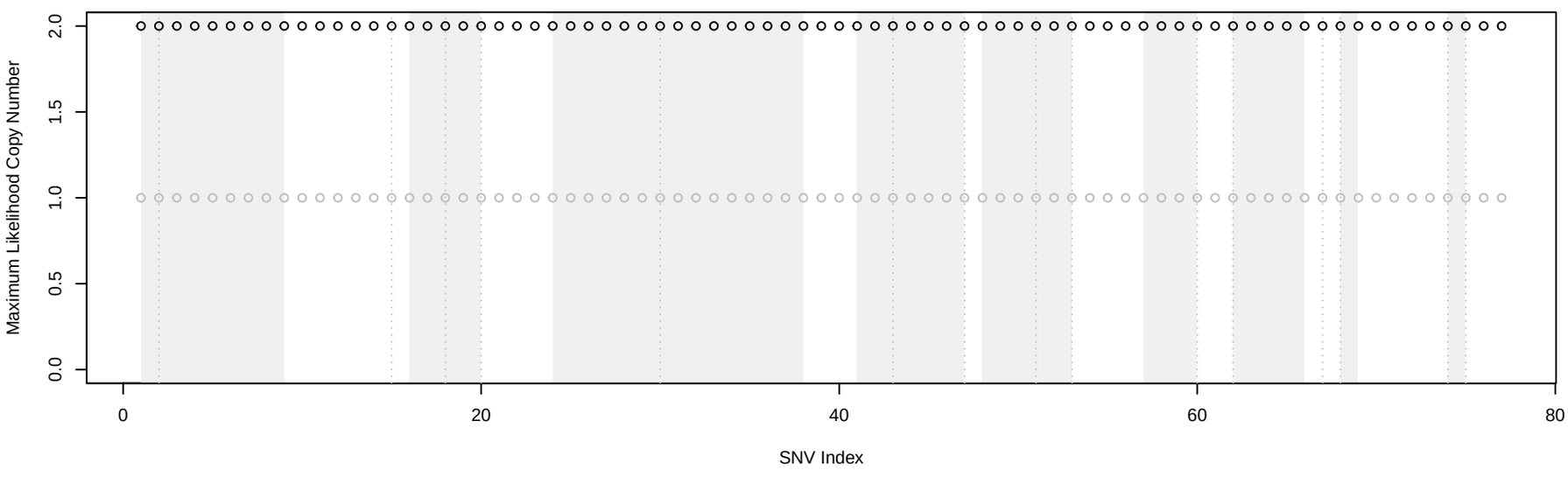

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

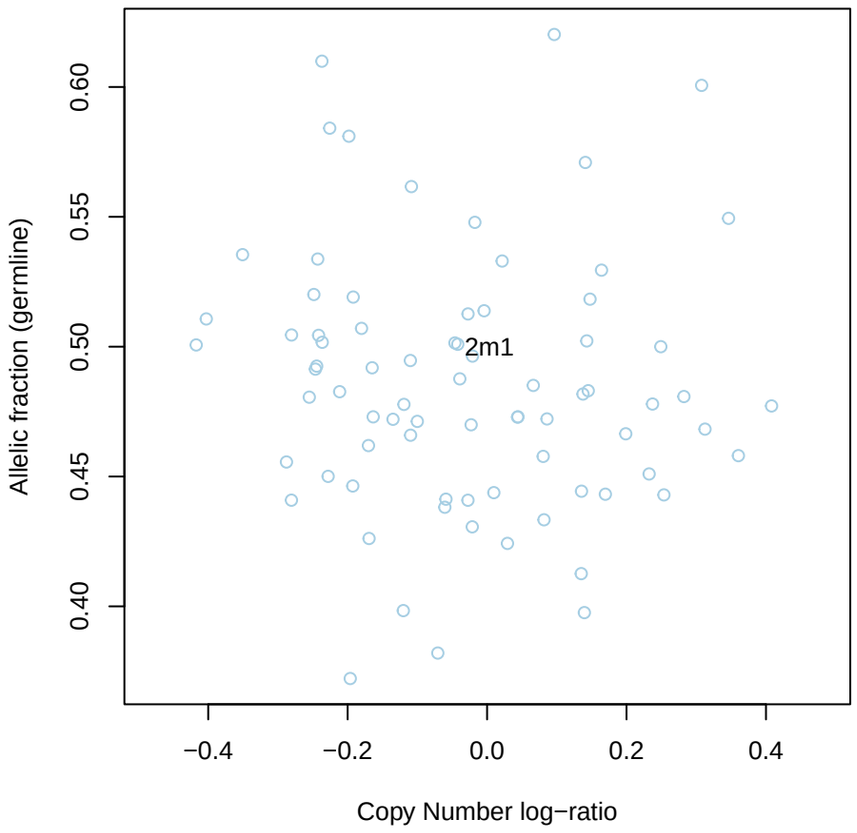

Power 0.8
Frequency
0
5
10
15
20
25
30
35
0.2
0.4
0.6
0.8
1.0
Cellular fraction

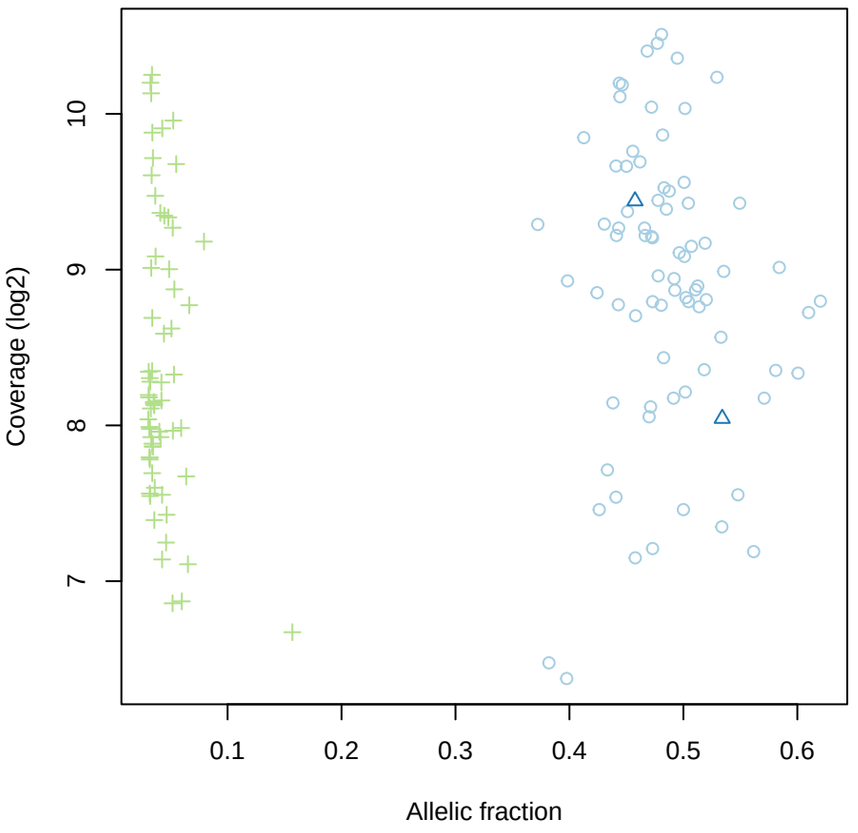

Purity: 0.59 Tumor ploidy: 1.992
0
1
2
4
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

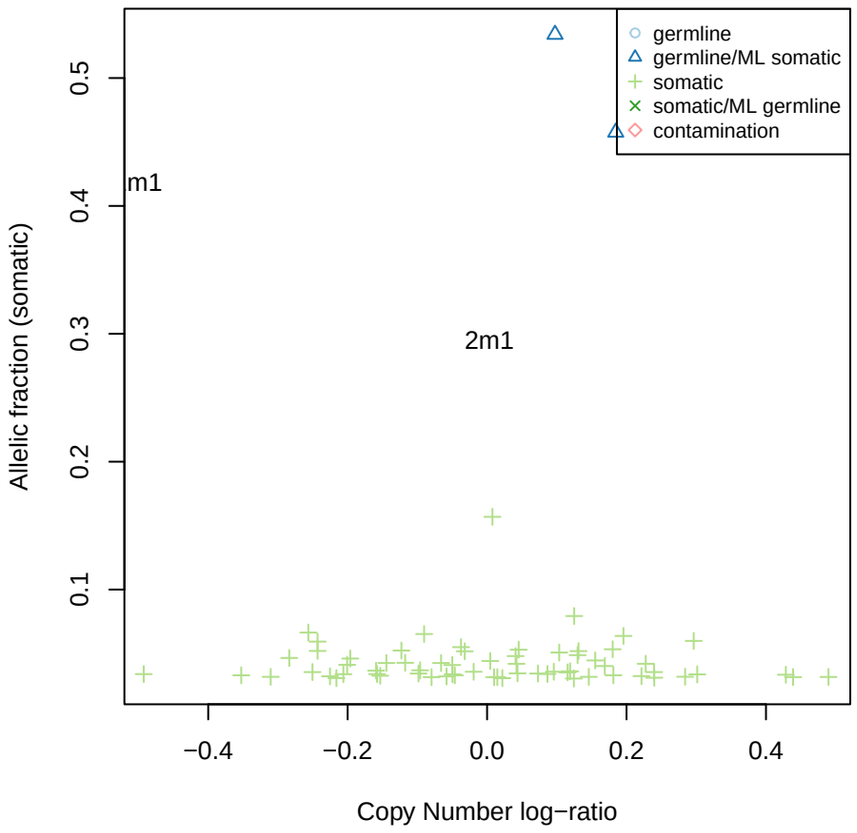

Purity: 0.59 Tumor ploidy: 1.992 SNV log−likelihood: −319.48 GoF: 23.6% Mean coverage: 493;307
1 2 3 4 5 6 7 8 9 11 12 14 15 16 19 21
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

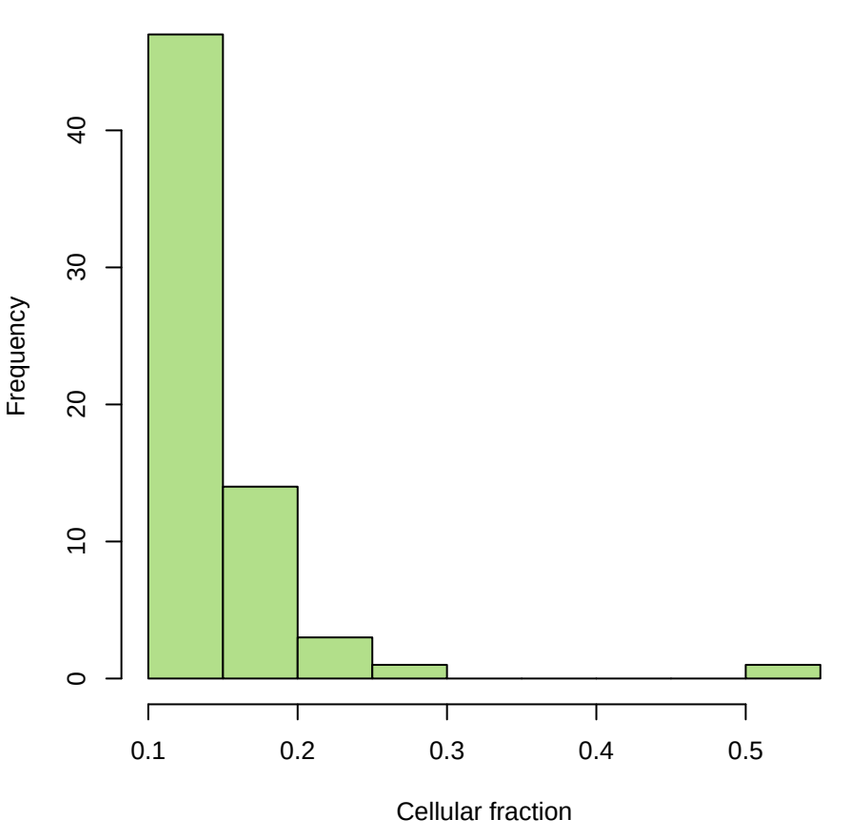

SCNA−fit log−likelihood: −13711.14
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 4
0 20 40 60 80
SNV Index

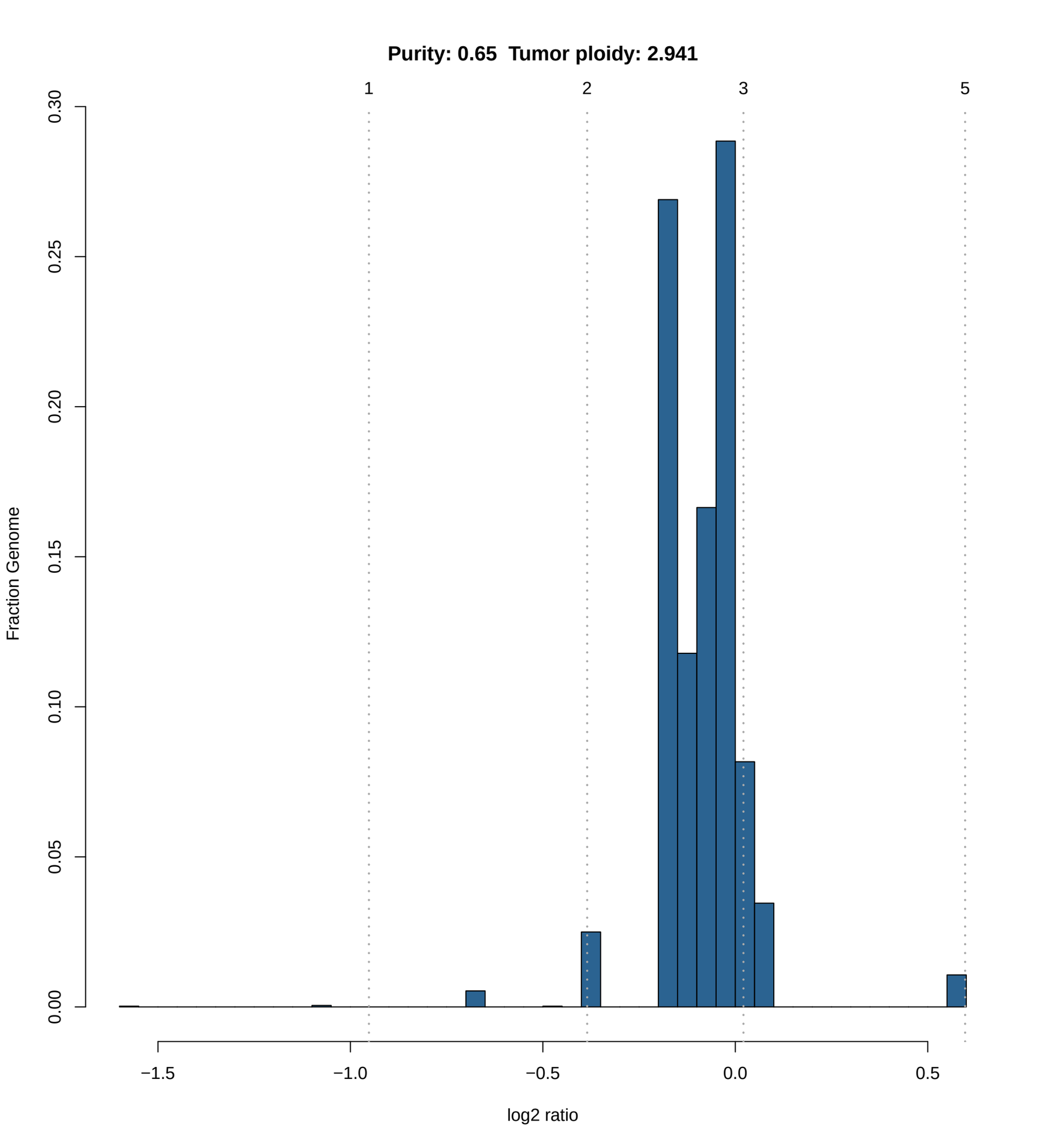

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 20 40 60 80
SNV Index

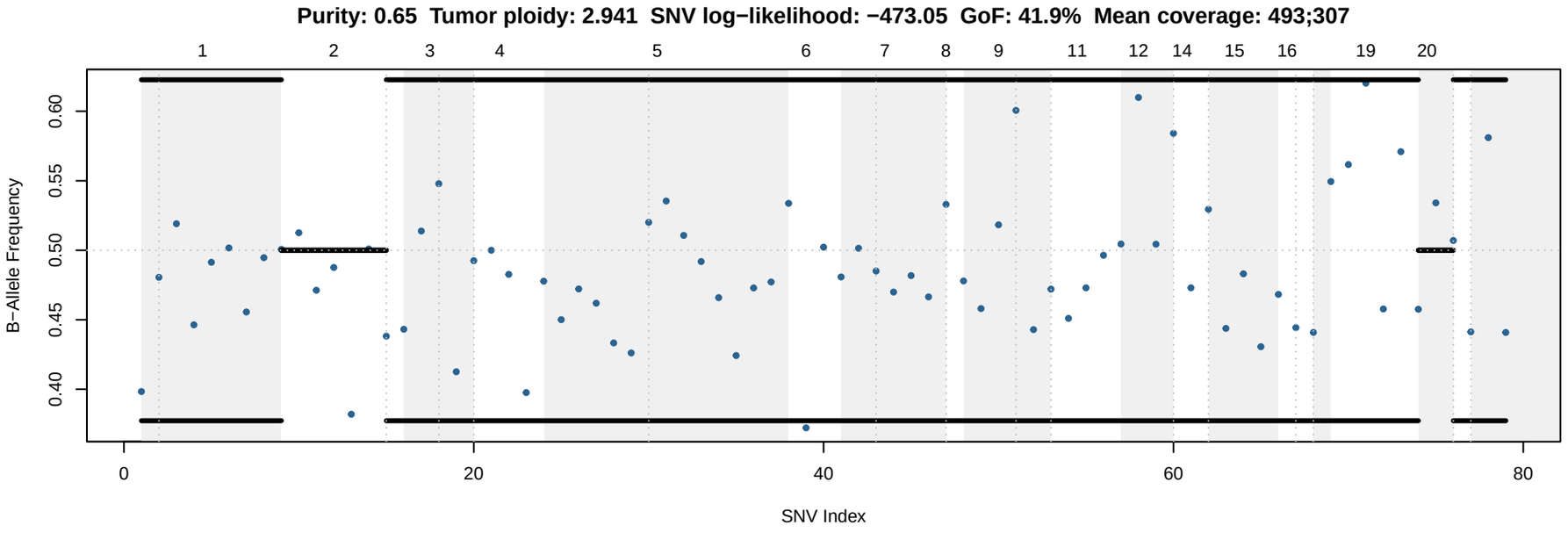

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
2m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

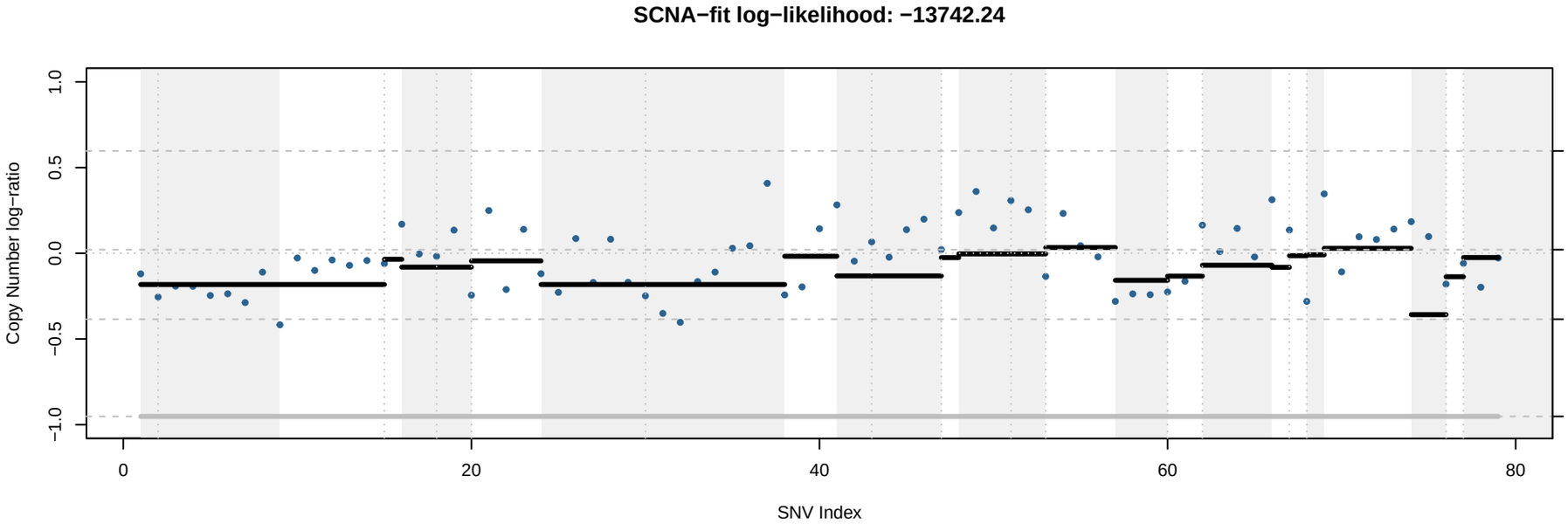

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

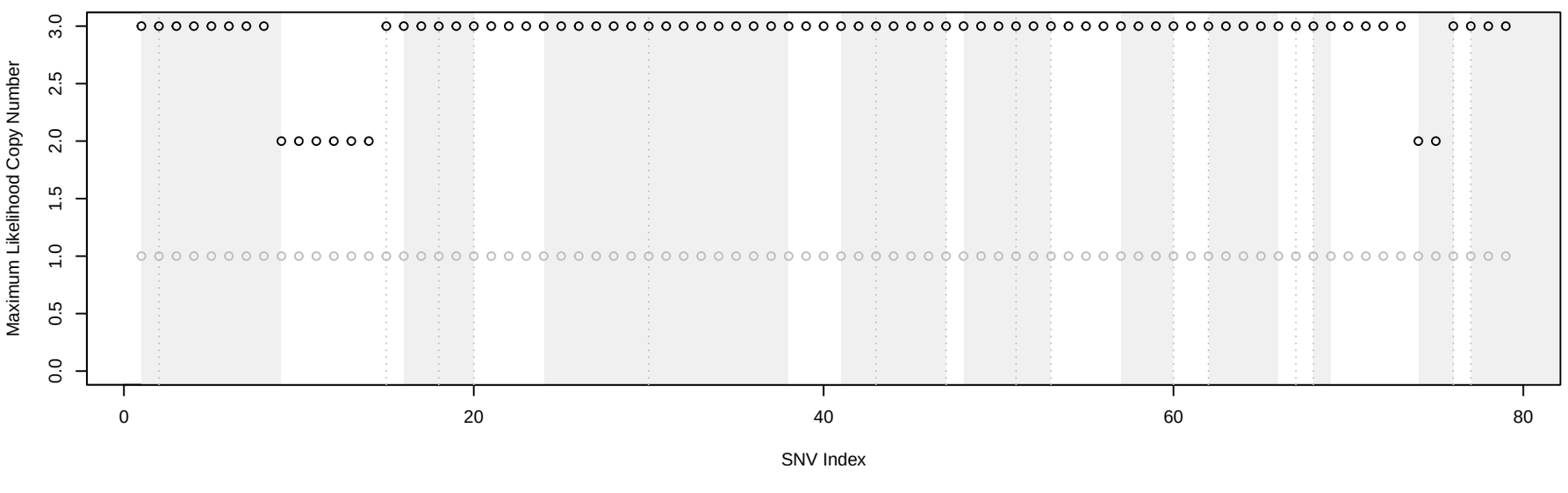

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.1
0.2
0.3
0.4
0.5
m1
2m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

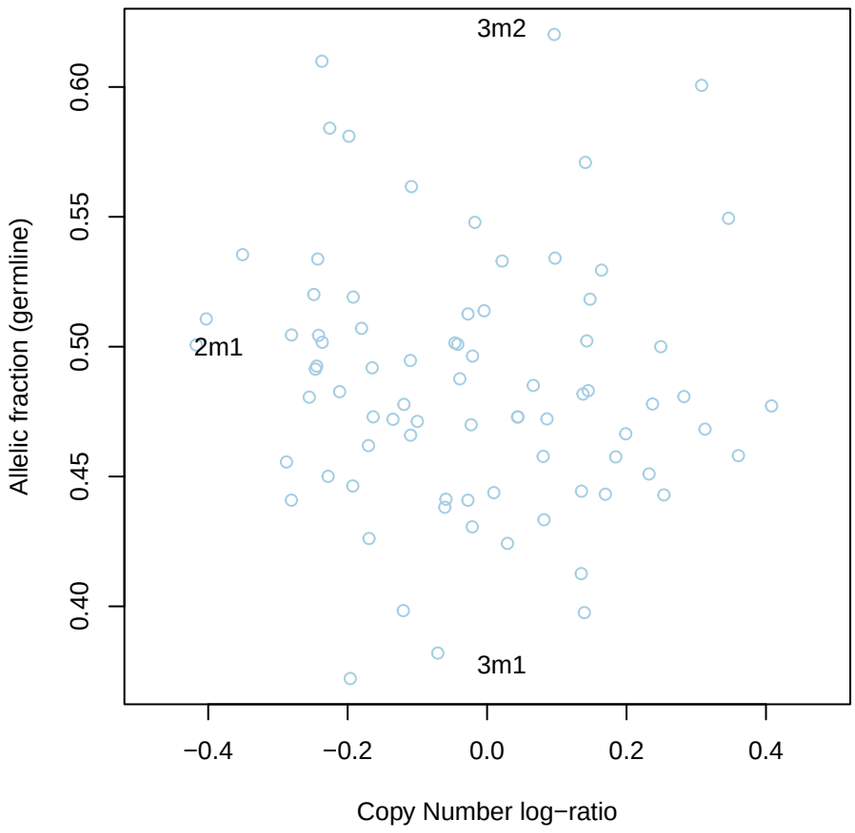

Frequency
0
10
20
30
40
0.1
0.2
0.3
0.4
0.5
Cellular fraction

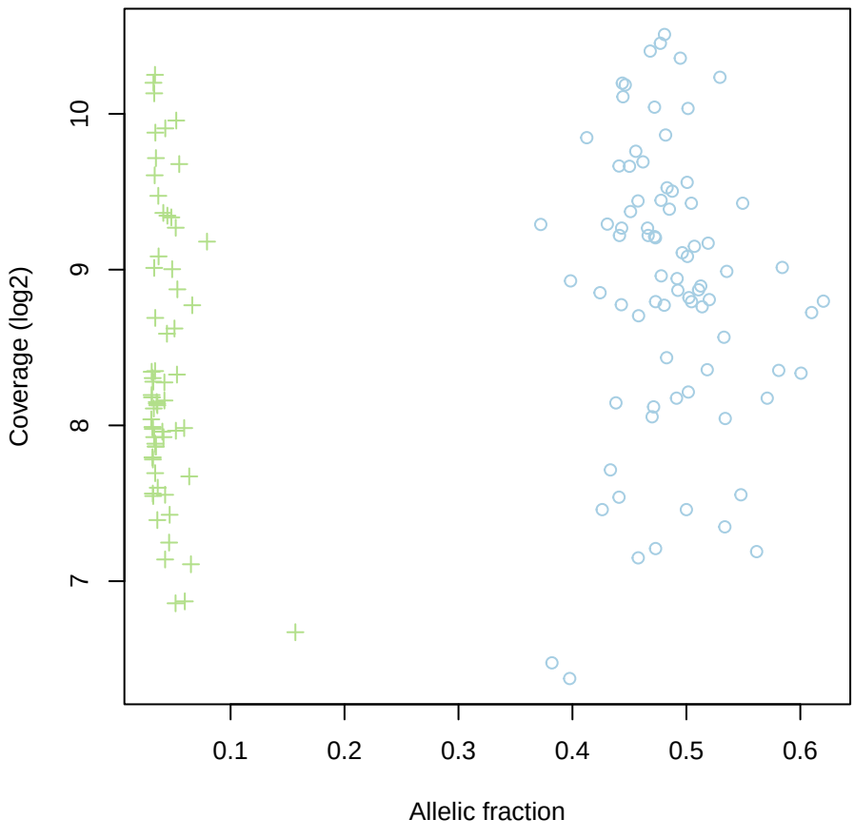

Purity: 0.65 Tumor ploidy: 2.941
1
2
3
5
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

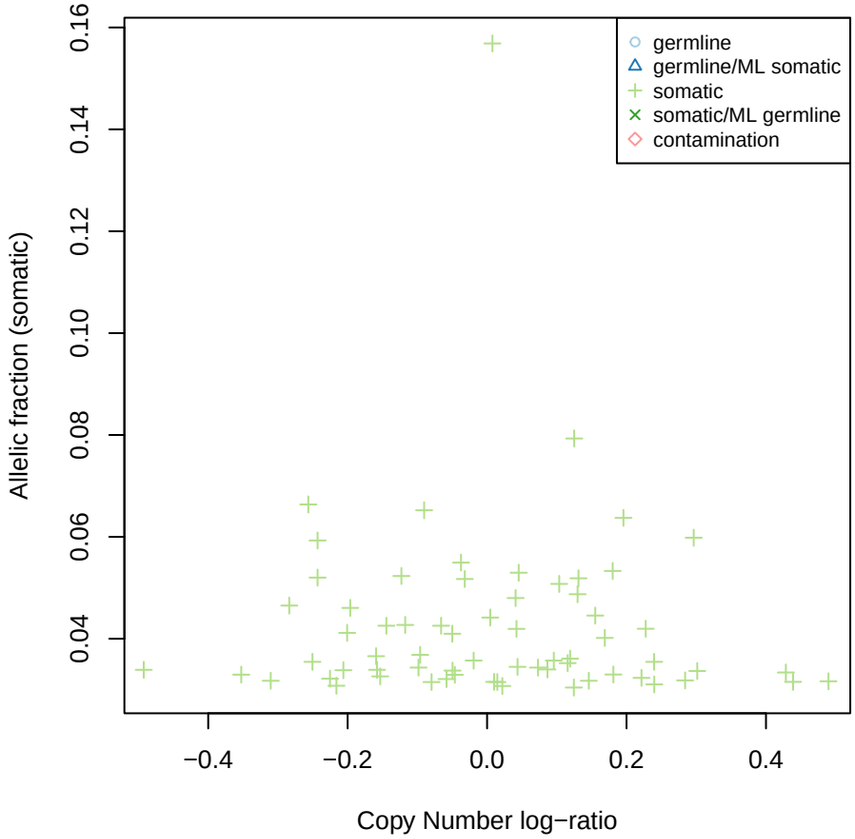

Purity: 0.65 Tumor ploidy: 2.941 SNV log−likelihood: −473.05 GoF: 41.9% Mean coverage: 493;307
1 2 3 4 5 6 7 8 9 11 12 14 15 16 19 20
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

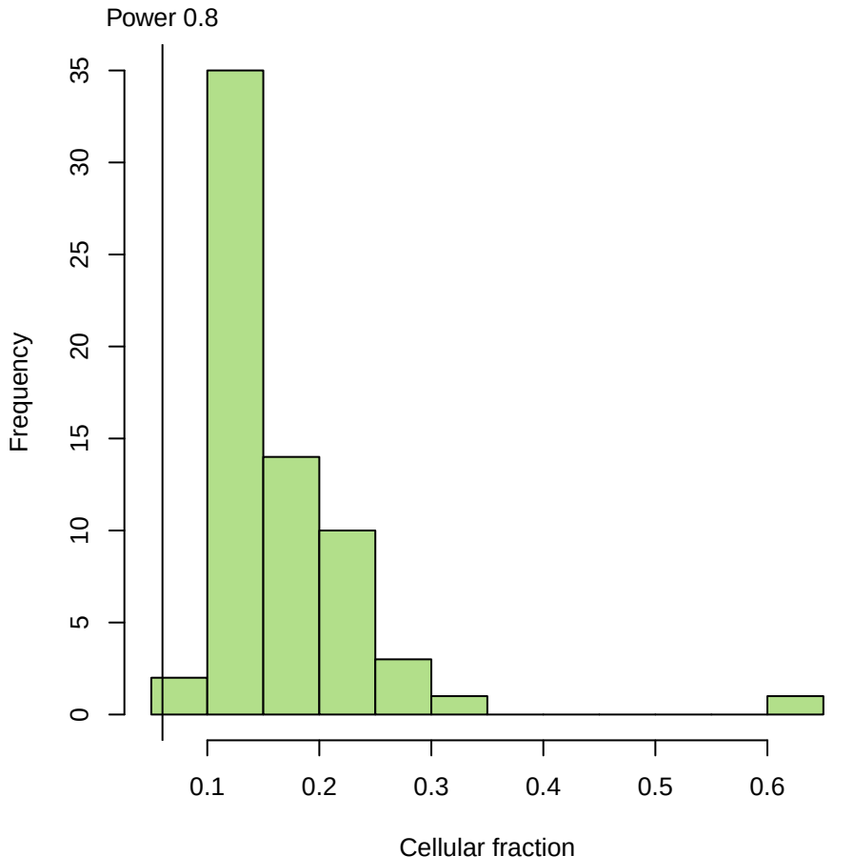

SCNA−fit log−likelihood: −13742.24
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 5
0 20 40 60 80
SNV Index


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


3m2
2m1
3m1
Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
−0.4
−0.2
0.0
0.2
0.4
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
0.14
0.16
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio


Power 0.8
Frequency
0
5
10
15
20
25
30
35
0.1
0.2
0.3
0.4
0.5
0.6
Cellular fraction