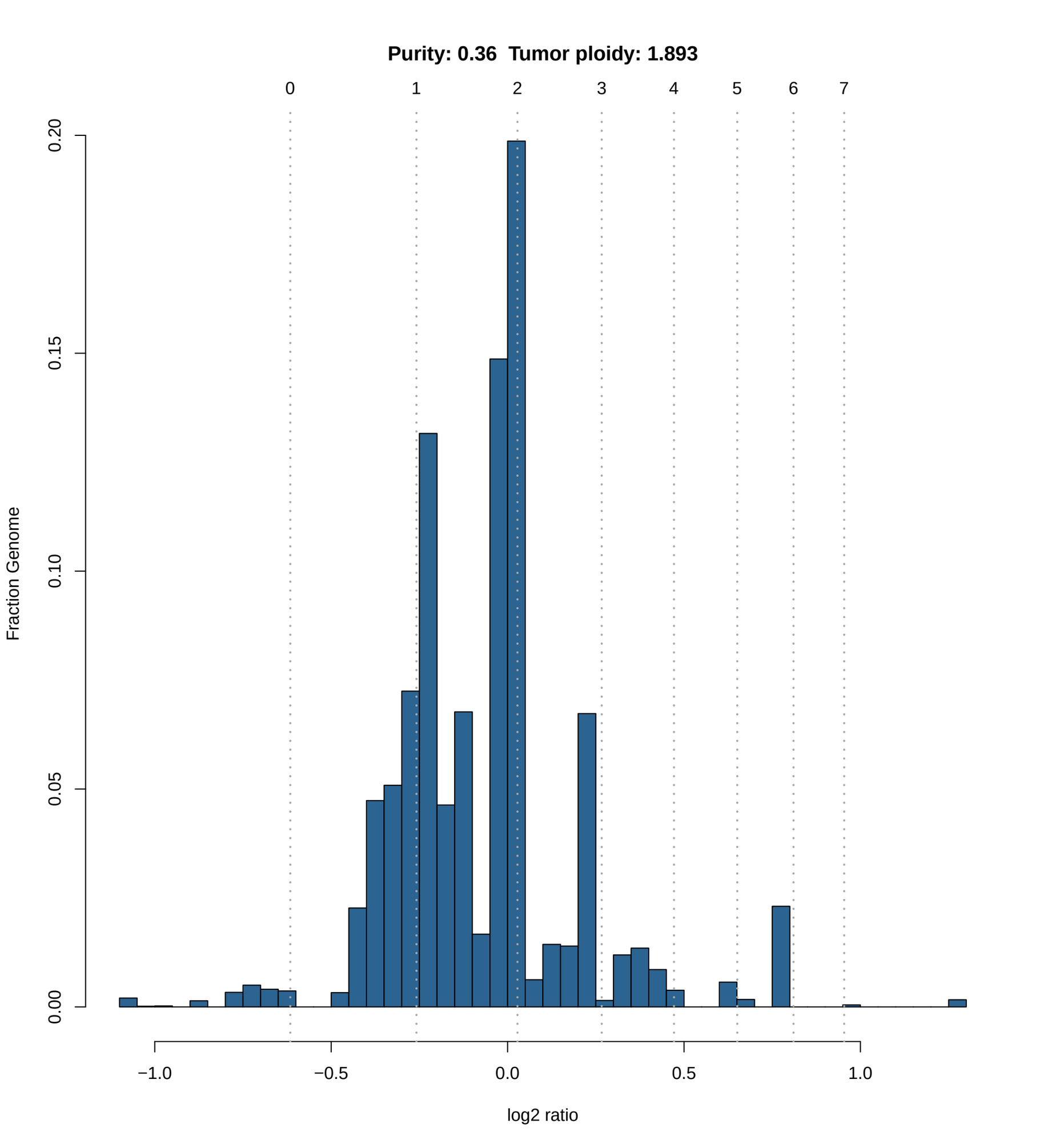
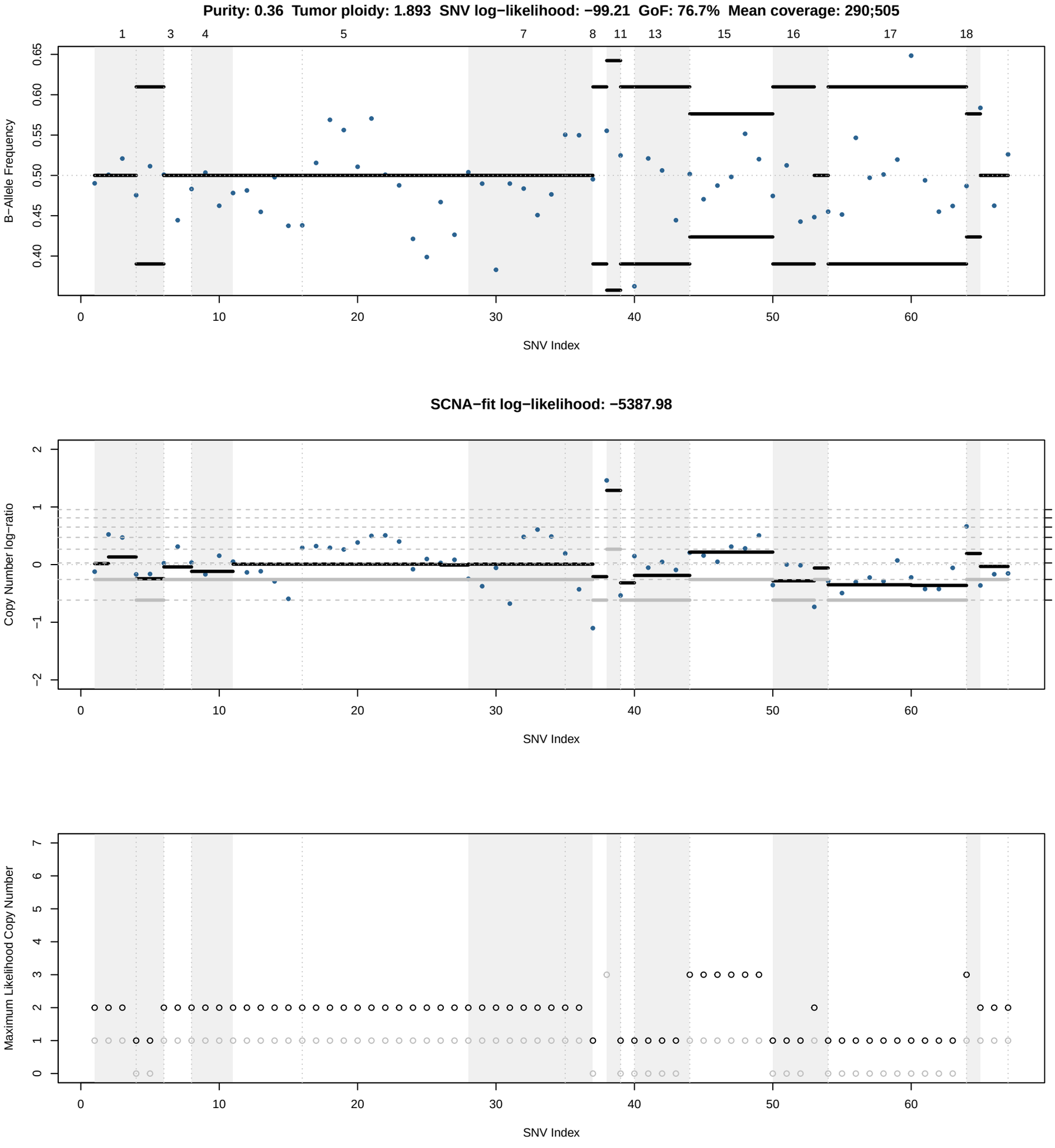
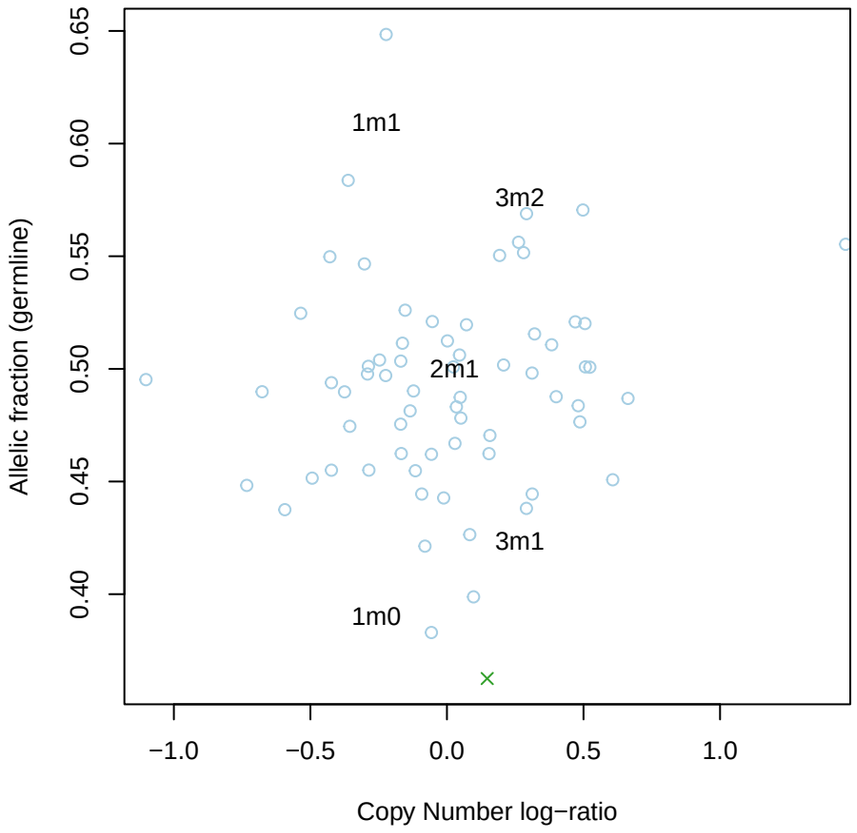
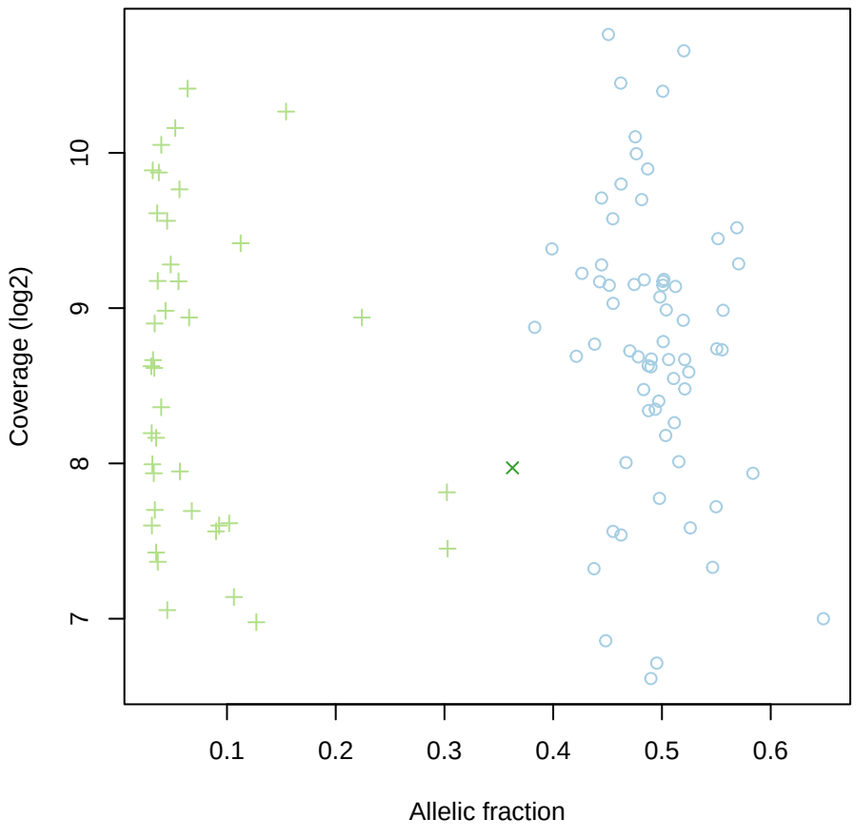
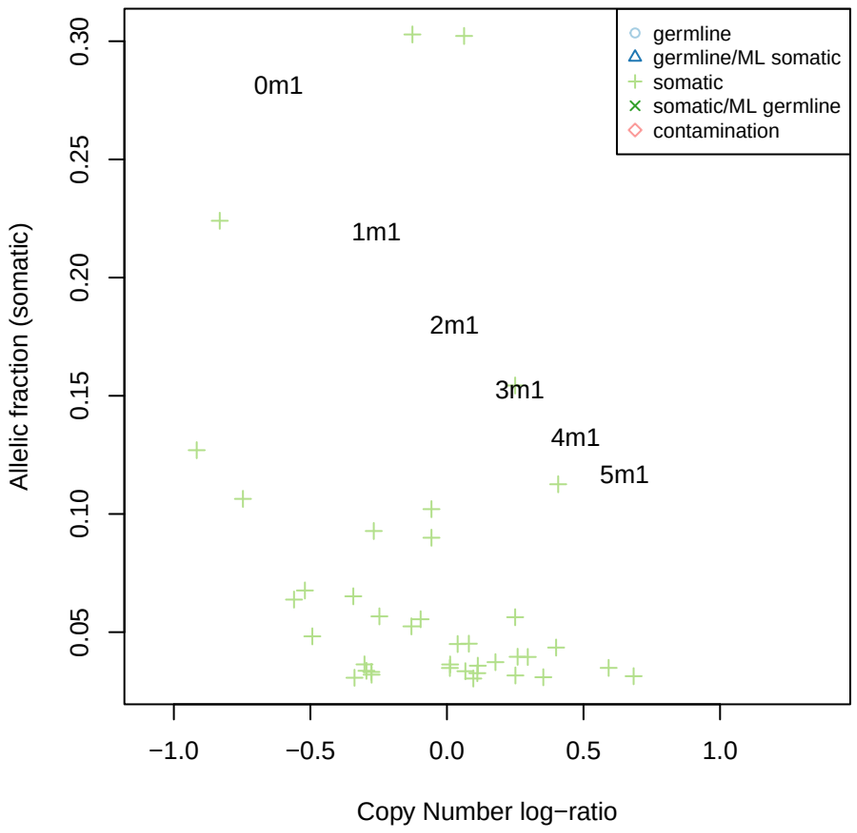
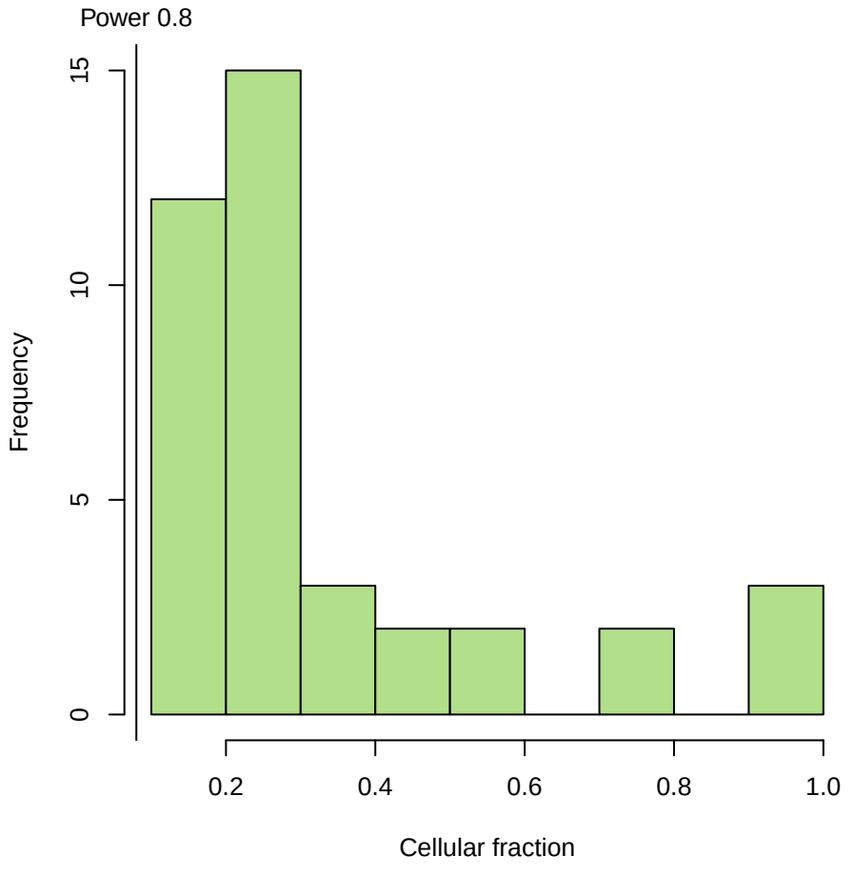

Purity: 0.36 Tumor ploidy: 1.893
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

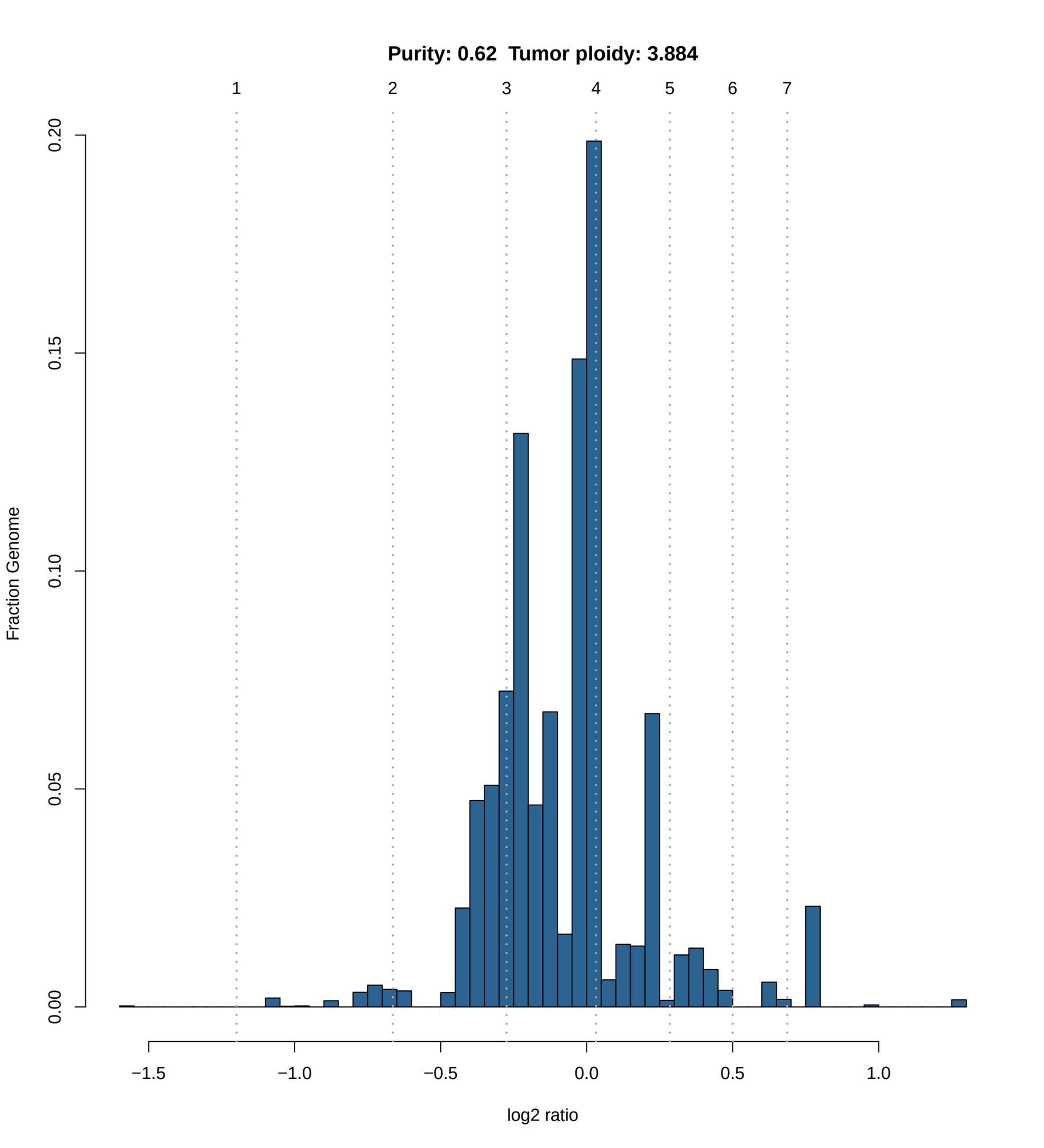

Purity: 0.36 Tumor ploidy: 1.893 SNV log−likelihood: −99.21 GoF: 76.7% Mean coverage: 290;505
1 3 4 5 7 8 11 13 15 16 17 18
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60 0.65
0 10 20 30 40 50 60
SNV Index
SCNA−fit log−likelihood: −5387.98
Copy Number log−ratio
−2 −1 0 1 2
0 1 3 5 7
0 10 20 30 40 50 60
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 10 20 30 40 50 60
SNV Index

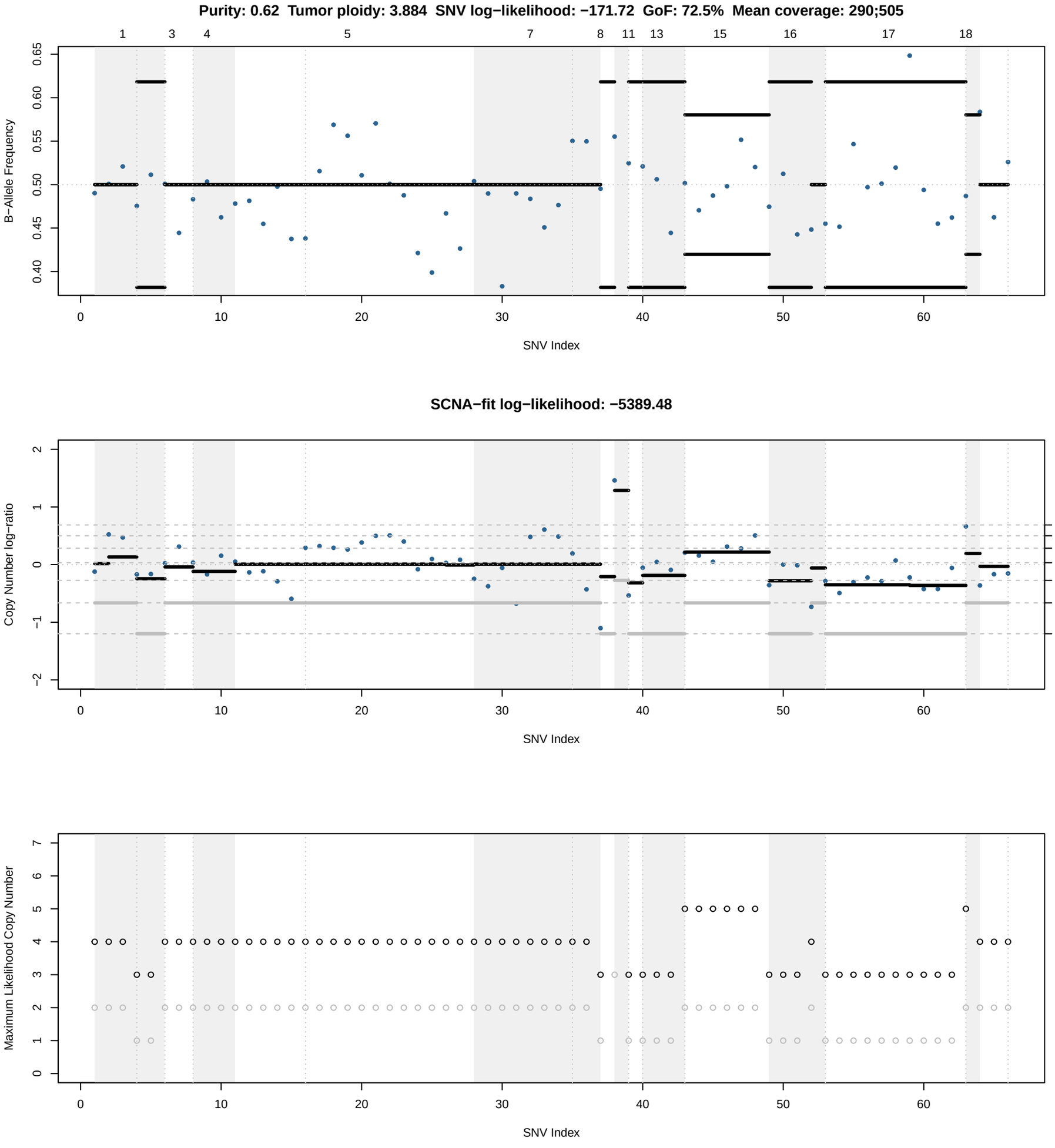

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
1m1
3m2
2m1
3m1
1m0
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

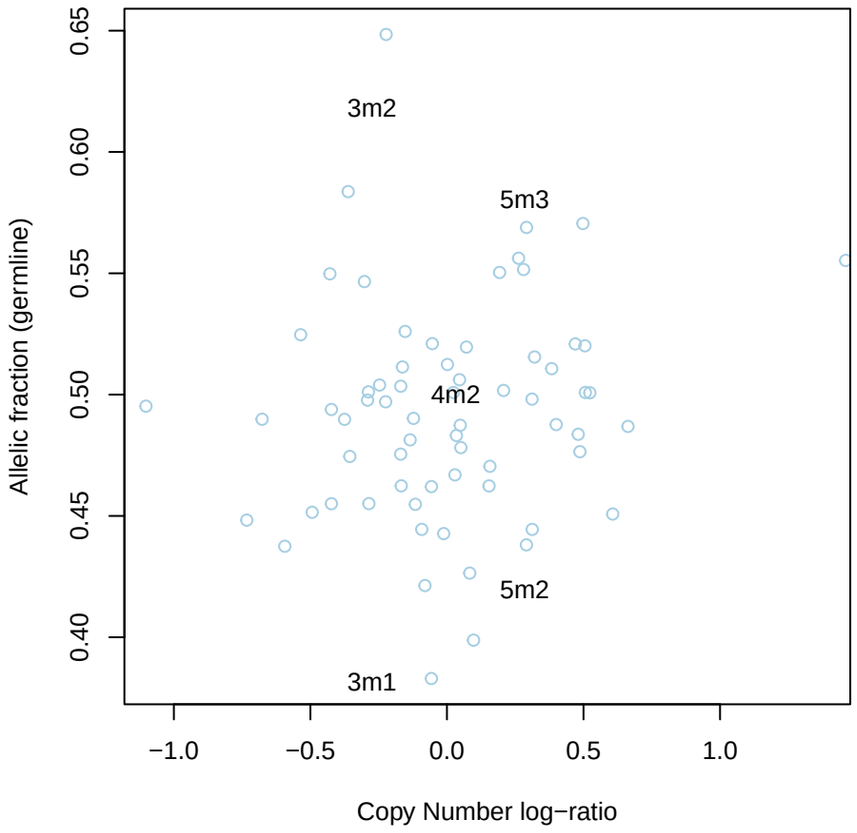

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

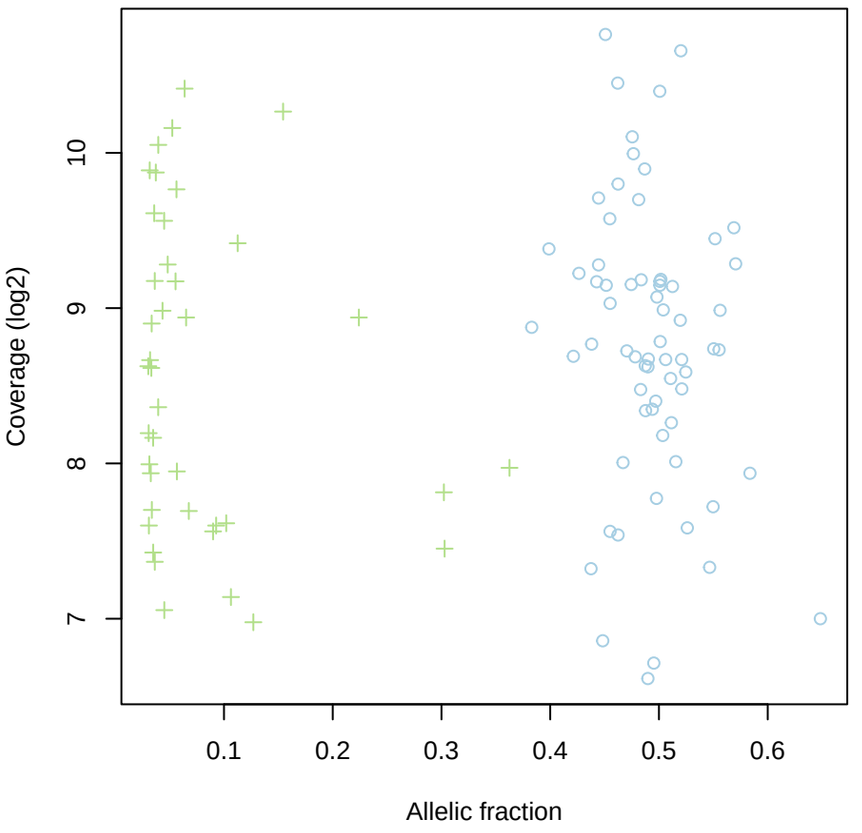

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0.30
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
0m1
1m1
2m1
3m1
4m1
5m1
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

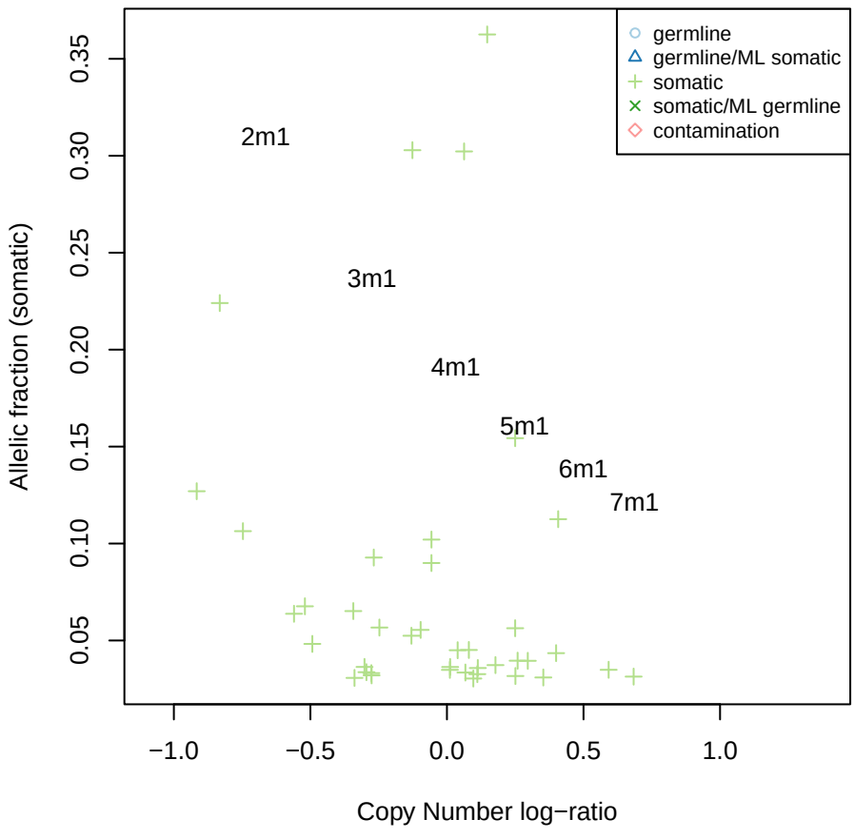

Power 0.8
Frequency
0
5
10
15
0.2
0.4
0.6
0.8
1.0
Cellular fraction

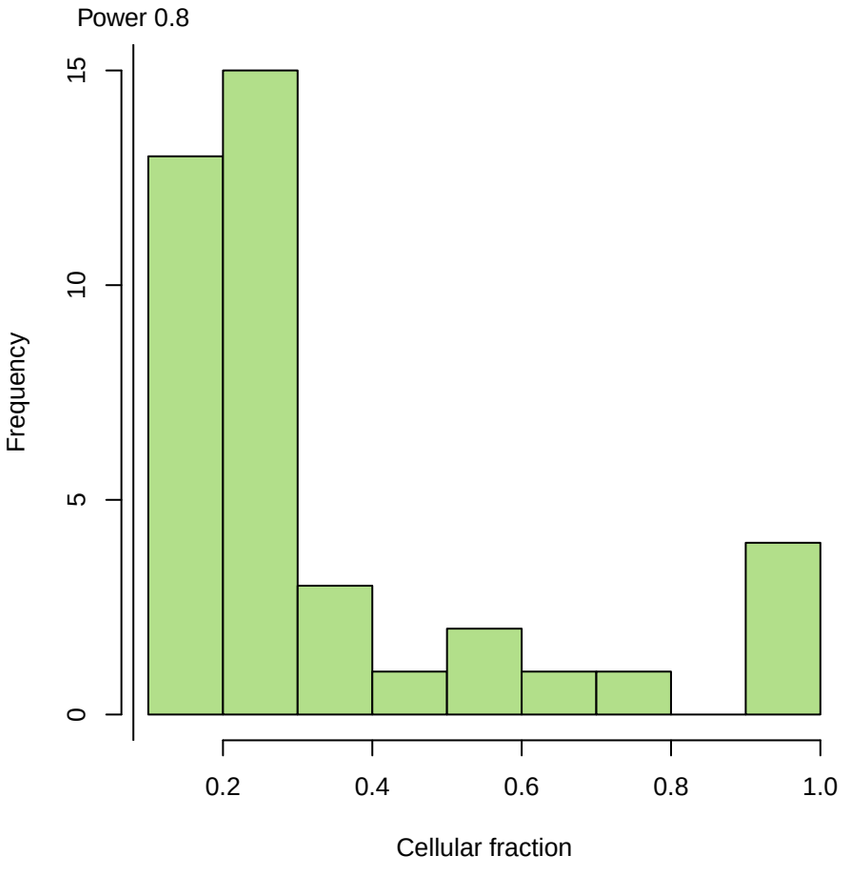

Purity: 0.62 Tumor ploidy: 3.884
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

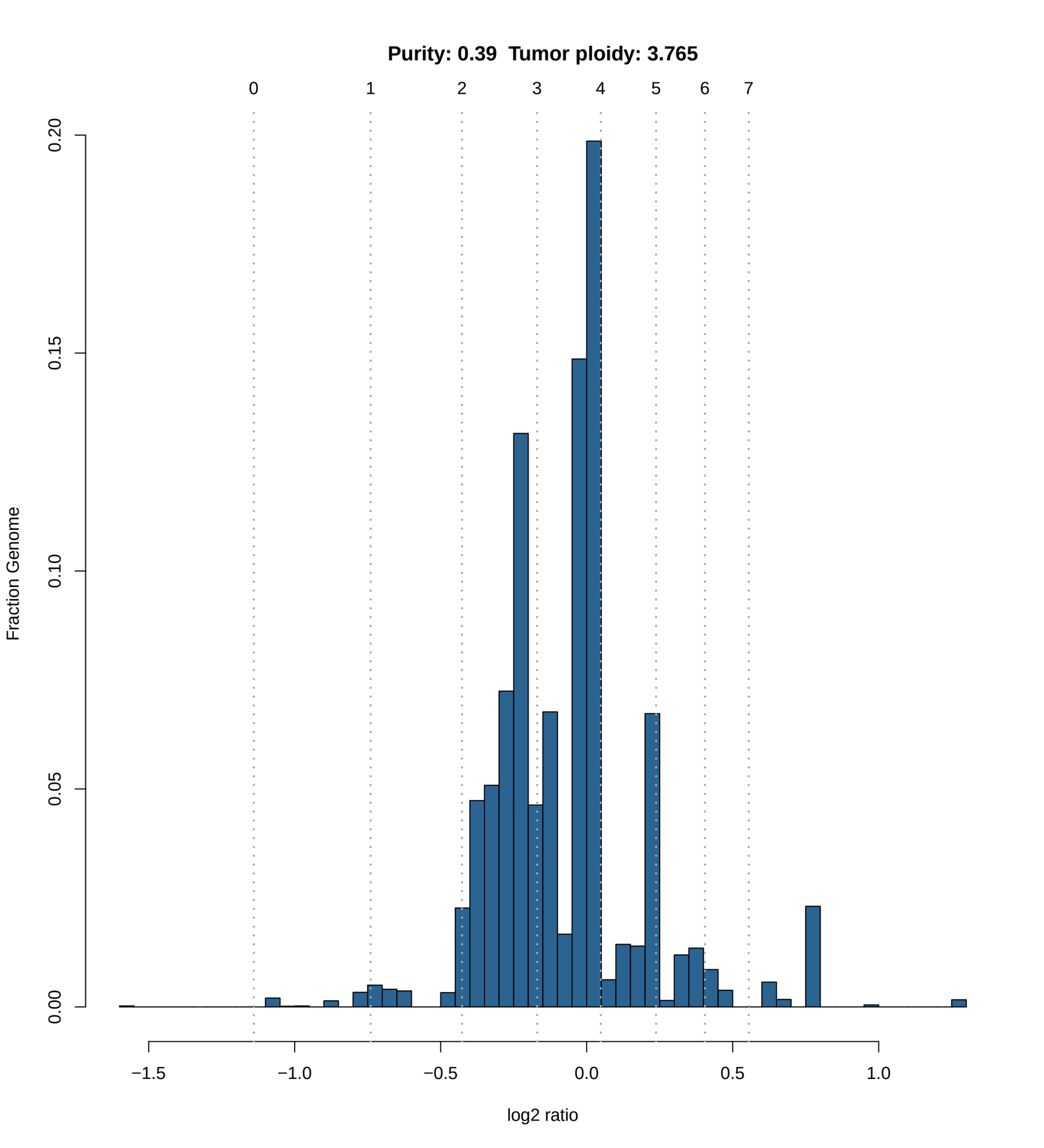

Purity: 0.62 Tumor ploidy: 3.884 SNV log−likelihood: −171.72 GoF: 72.5% Mean coverage: 290;505
1 3 4 5 7 8 11 13 15 16 17 18
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60 0.65
0 10 20 30 40 50 60
SNV Index
SCNA−fit log−likelihood: −5389.48
Copy Number log−ratio
−2 −1 0 1 2
1 2 3 4 6
0 10 20 30 40 50 60
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 10 20 30 40 50 60
SNV Index

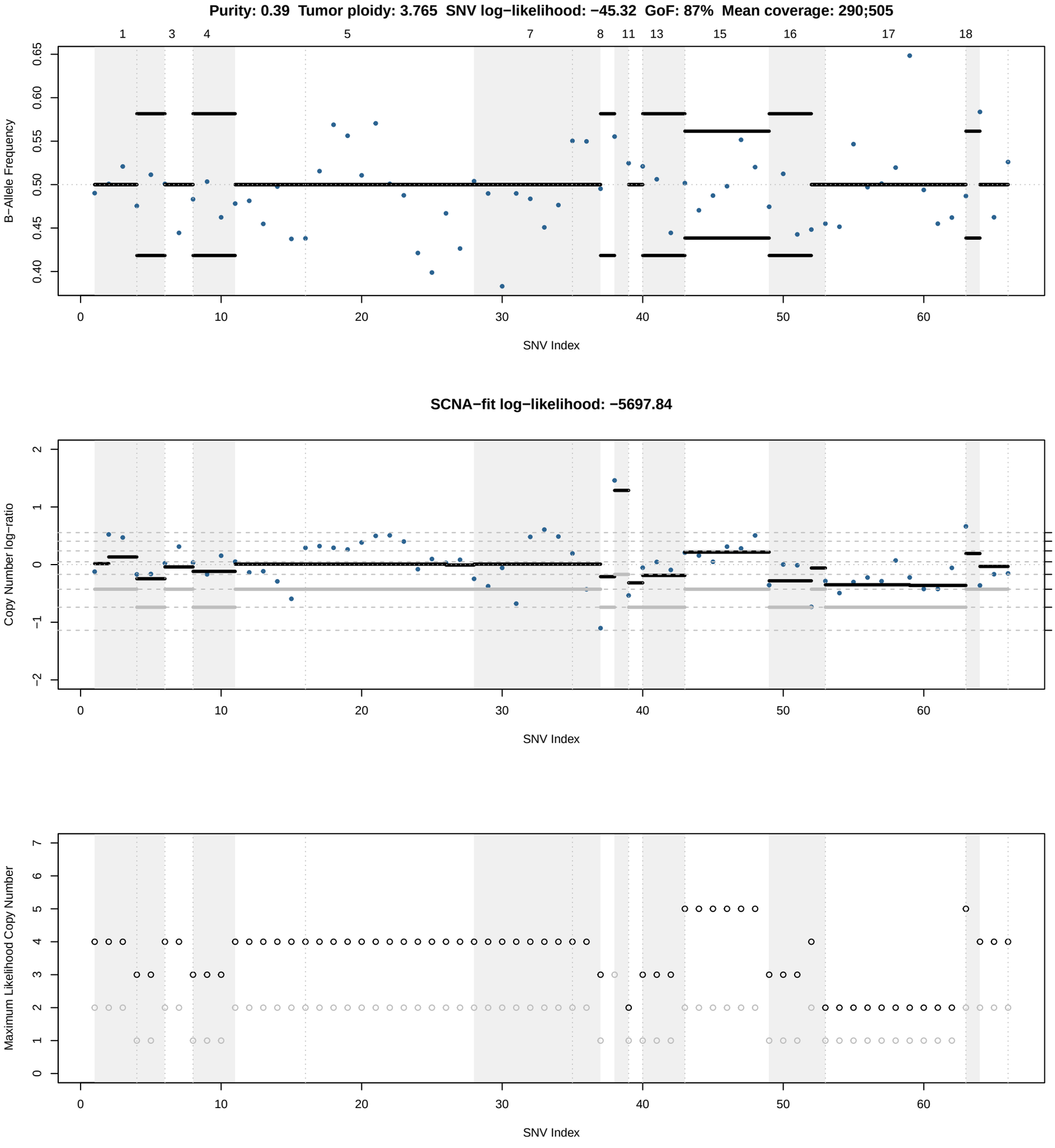

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
3m2
5m3
4m2
5m2
3m1
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

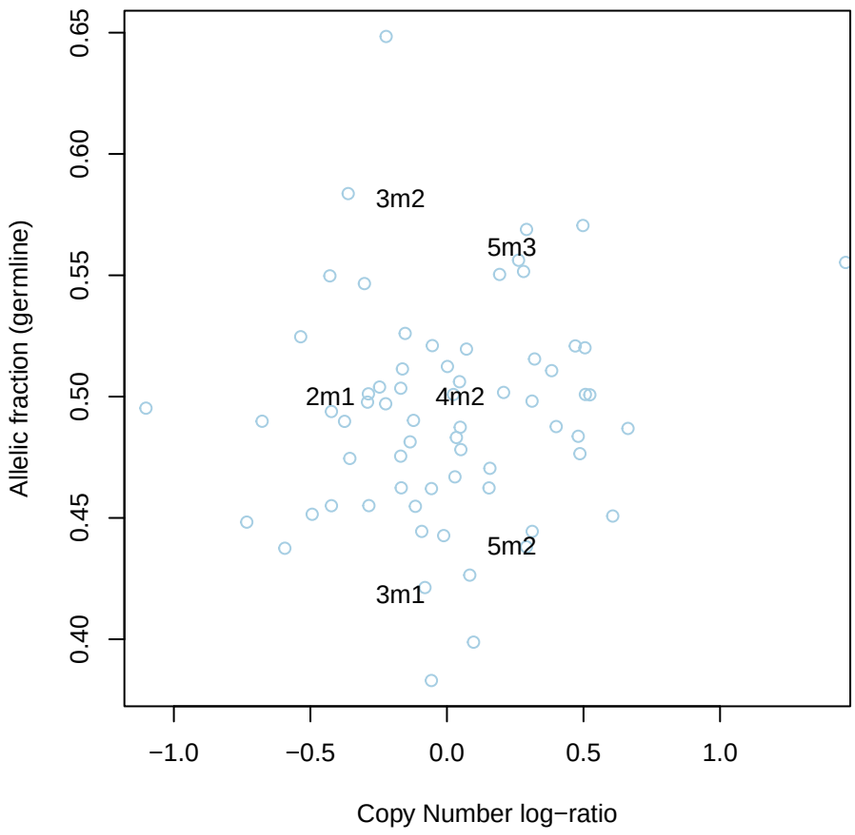

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

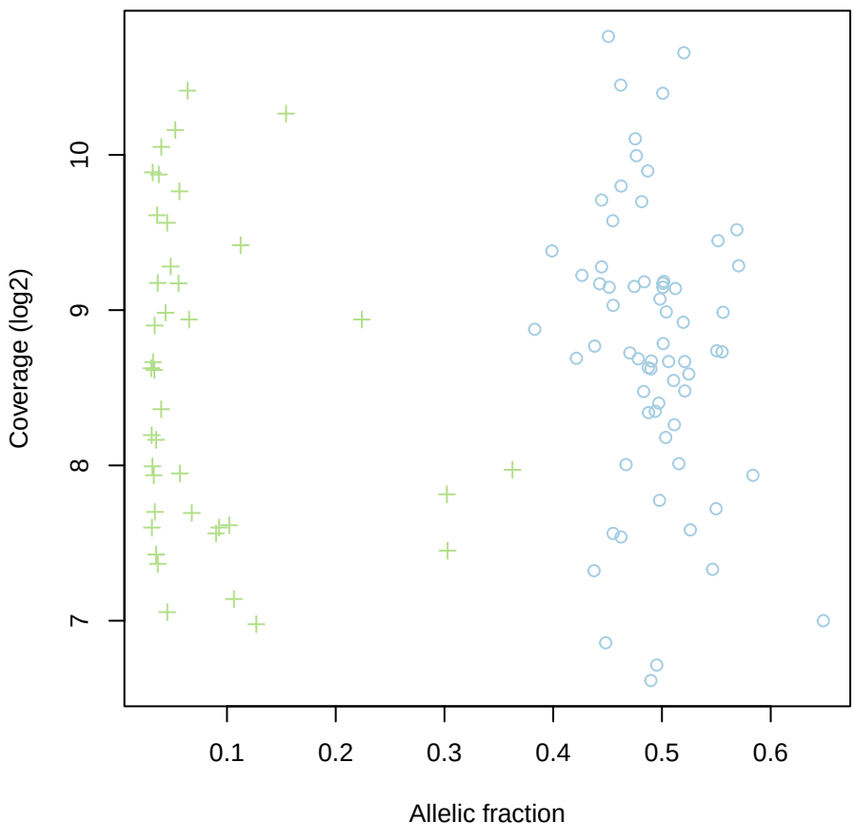

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0.30
0.35
2m1
3m1
4m1
5m1
6m1
7m1
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

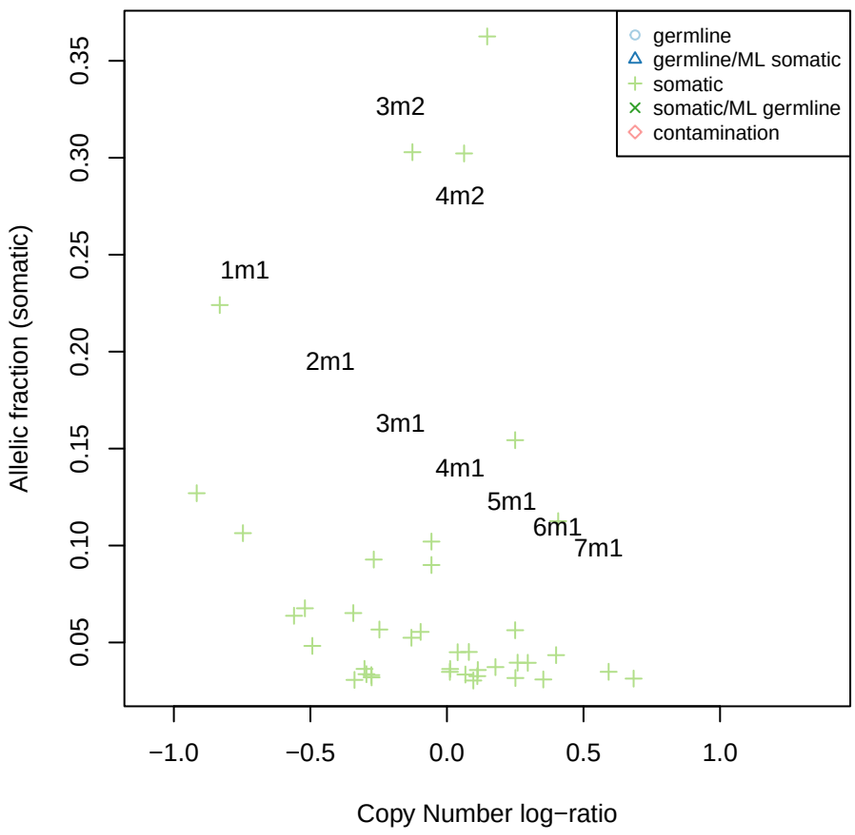

Power 0.8
Frequency
0
5
10
15
0.2
0.4
0.6
0.8
1.0
Cellular fraction

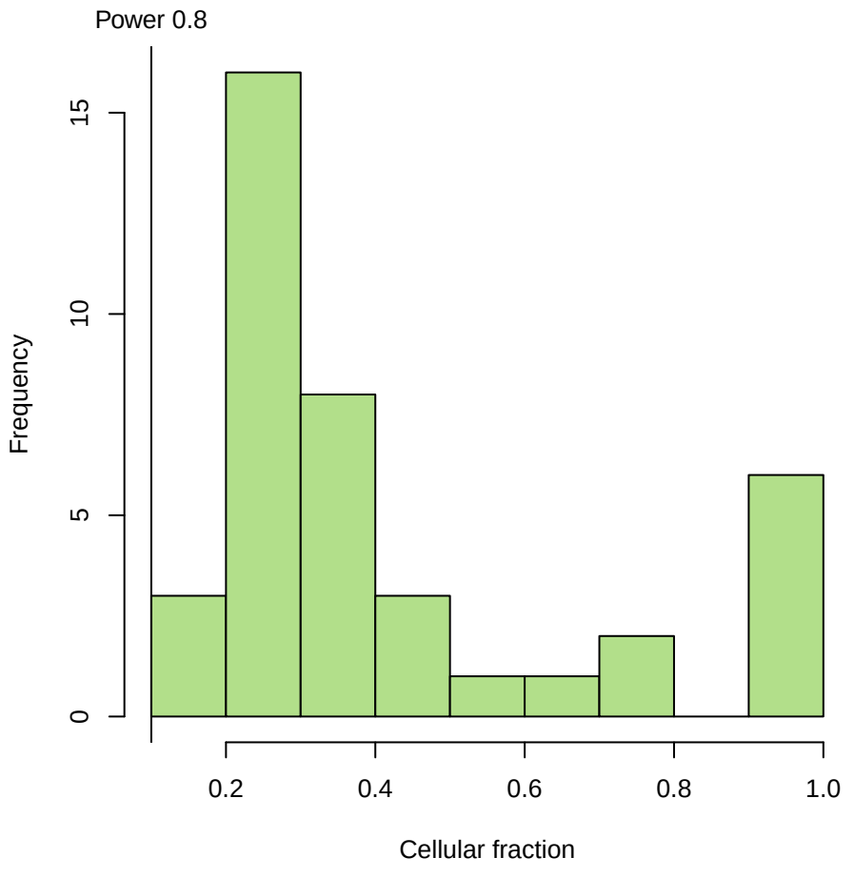

Purity: 0.39 Tumor ploidy: 3.765
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

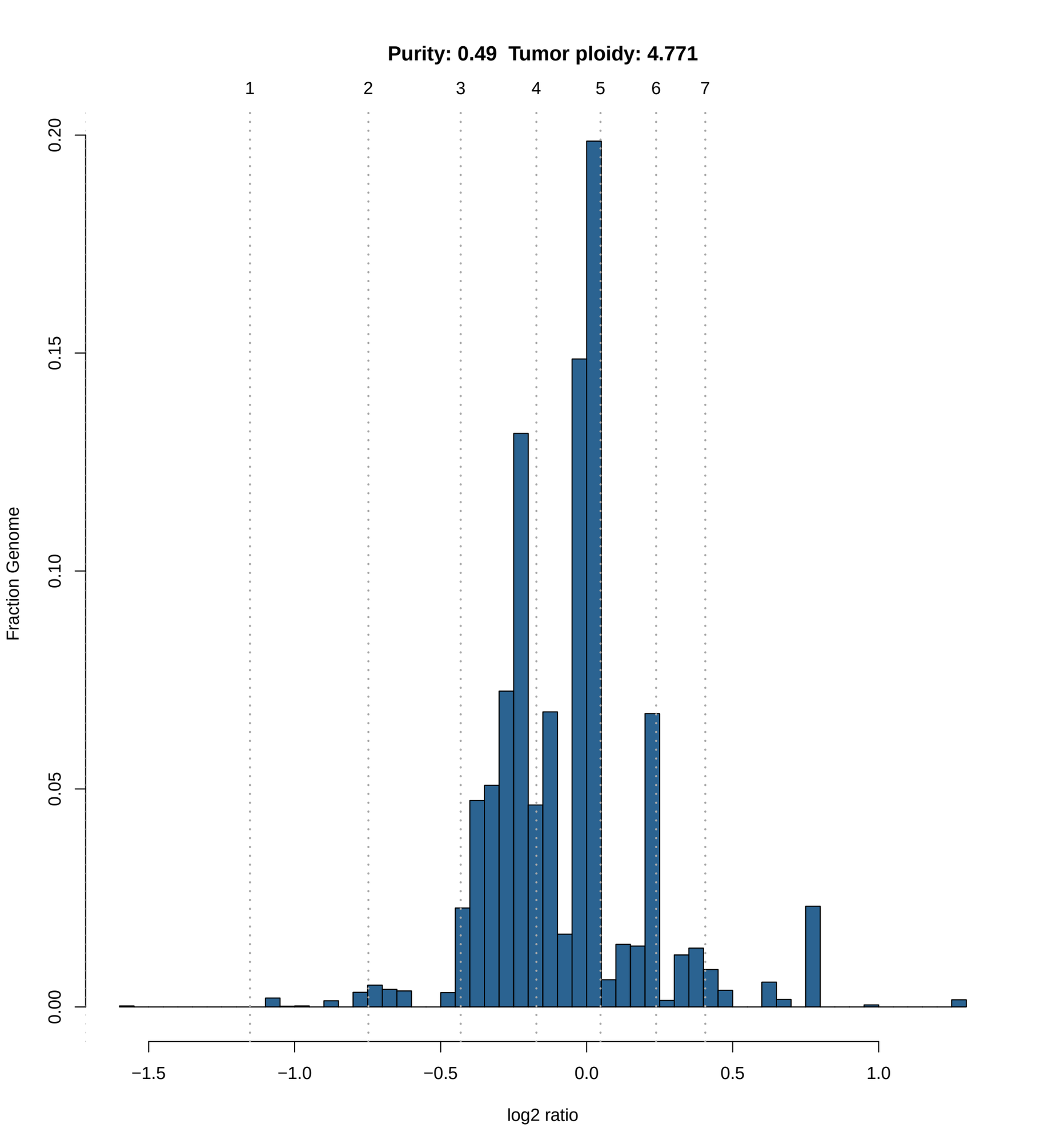

Purity: 0.39 Tumor ploidy: 3.765 SNV log−likelihood: −45.32 GoF: 87% Mean coverage: 290;505
1 3 4 5 7 8 11 13 15 16 17 18
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60 0.65
0 10 20 30 40 50 60
SNV Index
SCNA−fit log−likelihood: −5697.84
Copy Number log−ratio
−2 −1 0 1 2
0 1 2 4 6
0 10 20 30 40 50 60
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 10 20 30 40 50 60
SNV Index

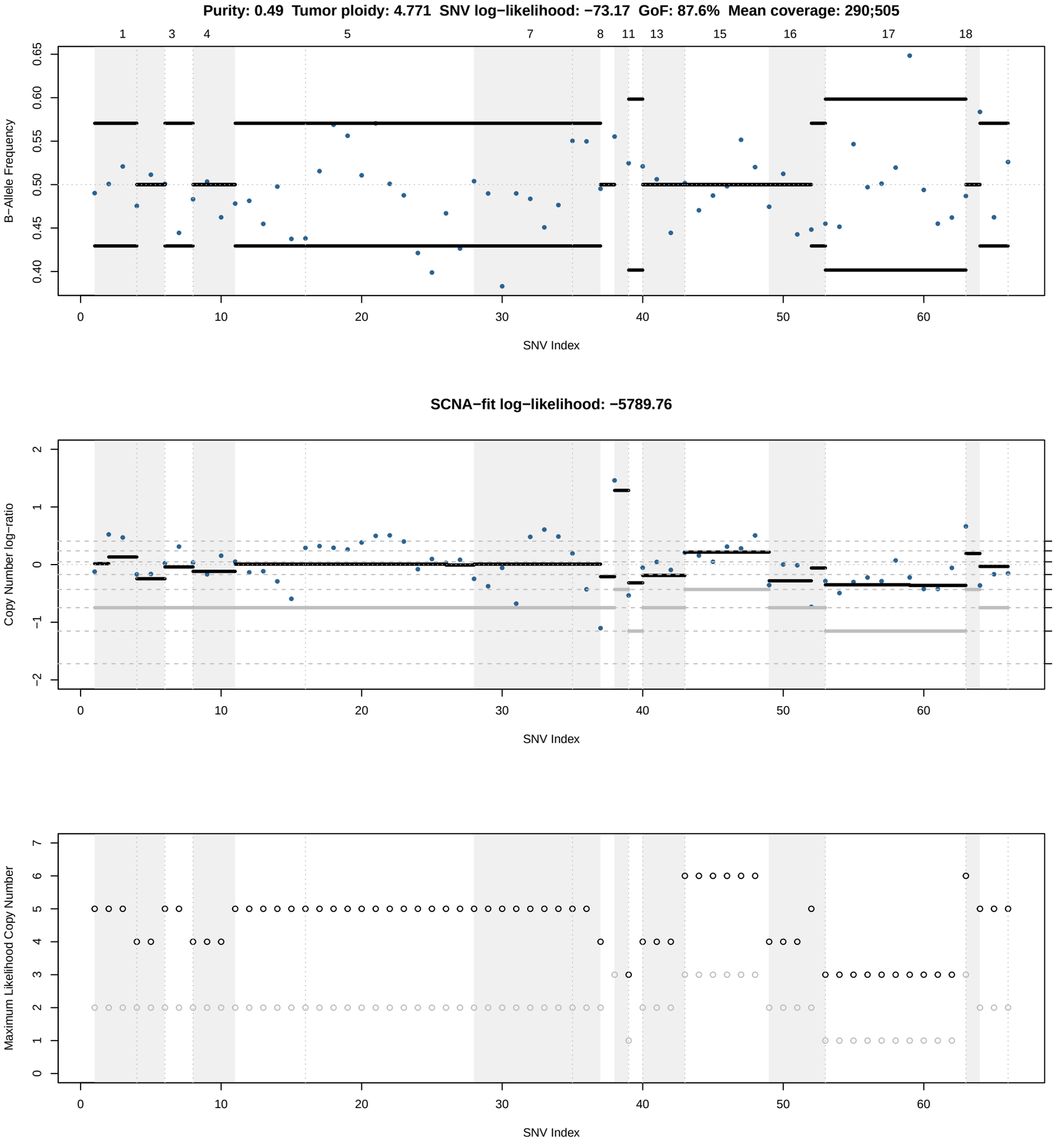

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
3m2
5m3
2m1
4m2
5m2
3m1
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

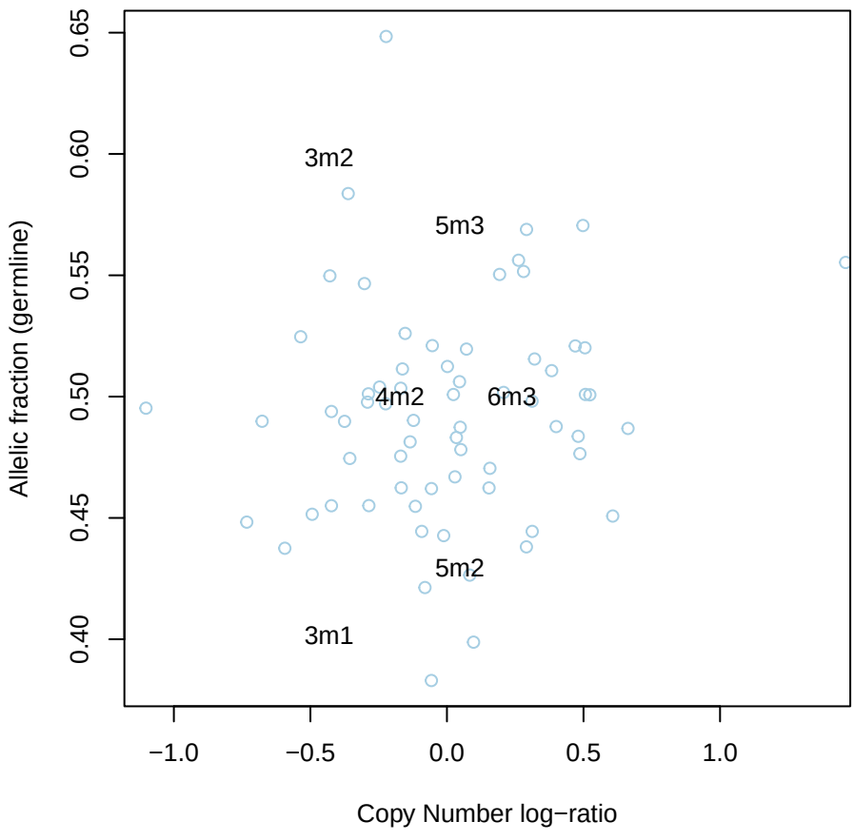

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

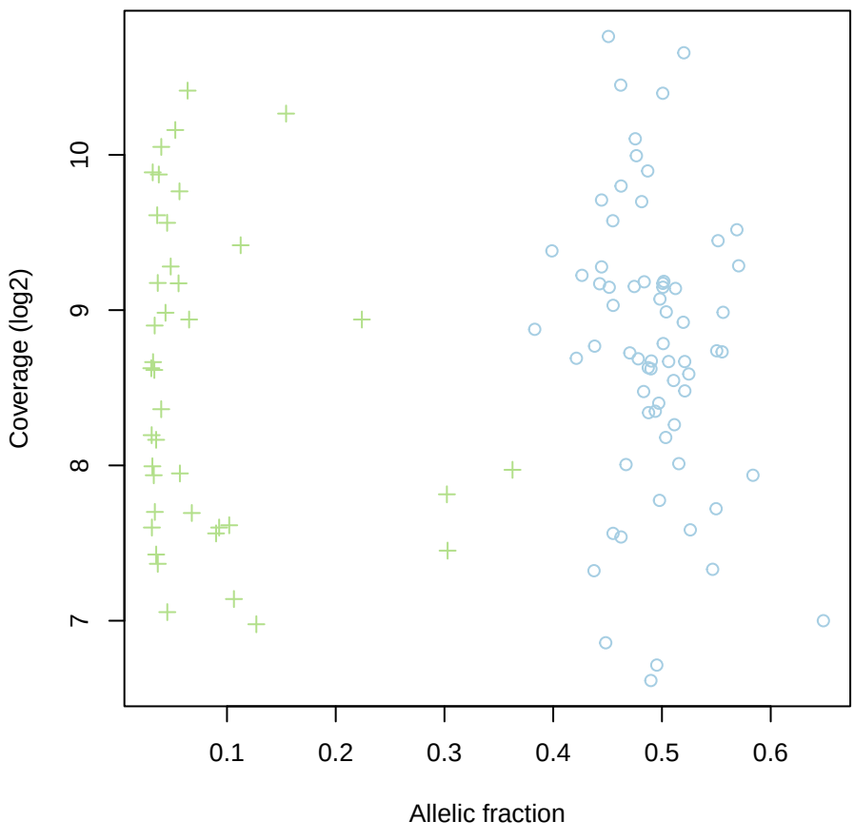

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0.30
0.35
3m2
4m2
1m1
2m1
3m1
4m1
5m1
6m1
7m1
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

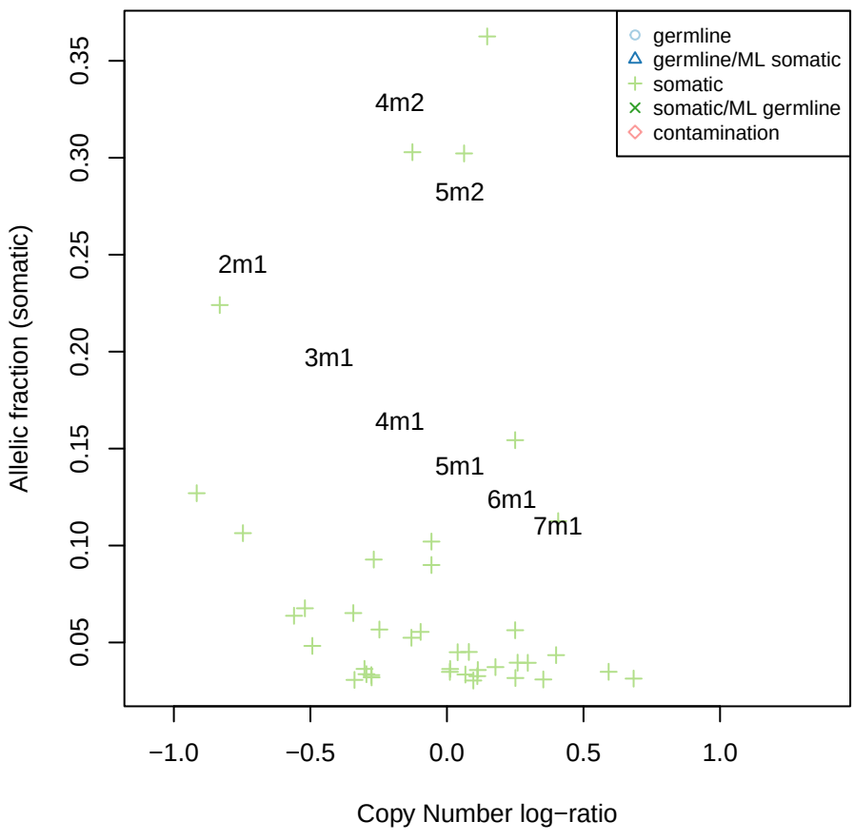

Power 0.8
Frequency
0
5
10
15
0.2
0.4
0.6
0.8
1.0
Cellular fraction

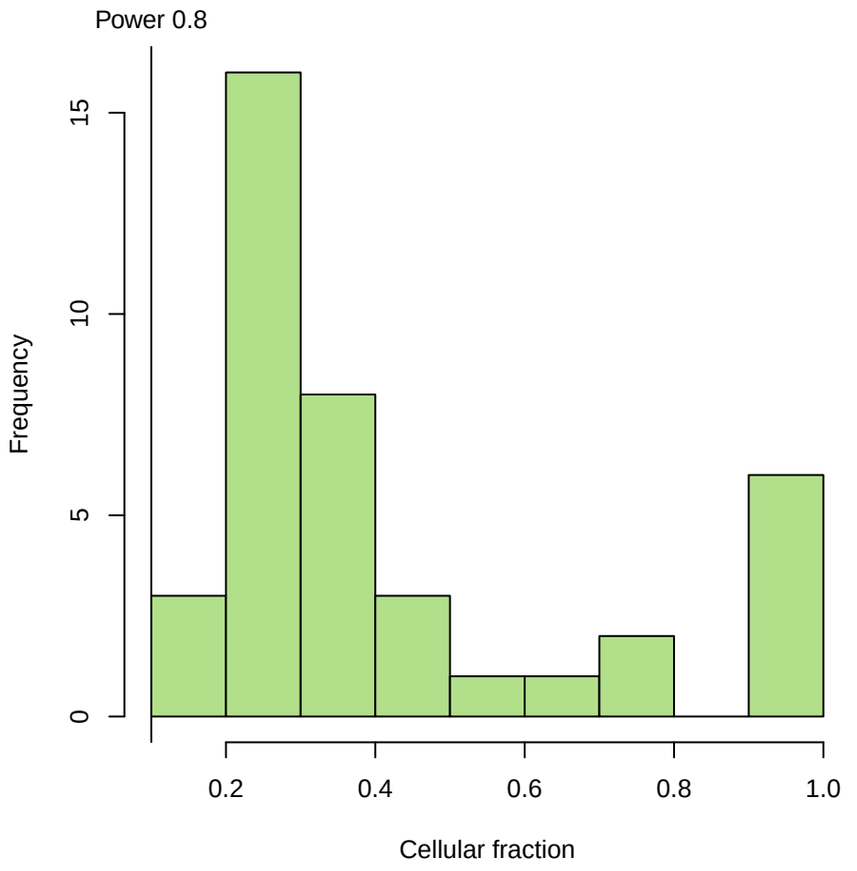

Purity: 0.49 Tumor ploidy: 4.771
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

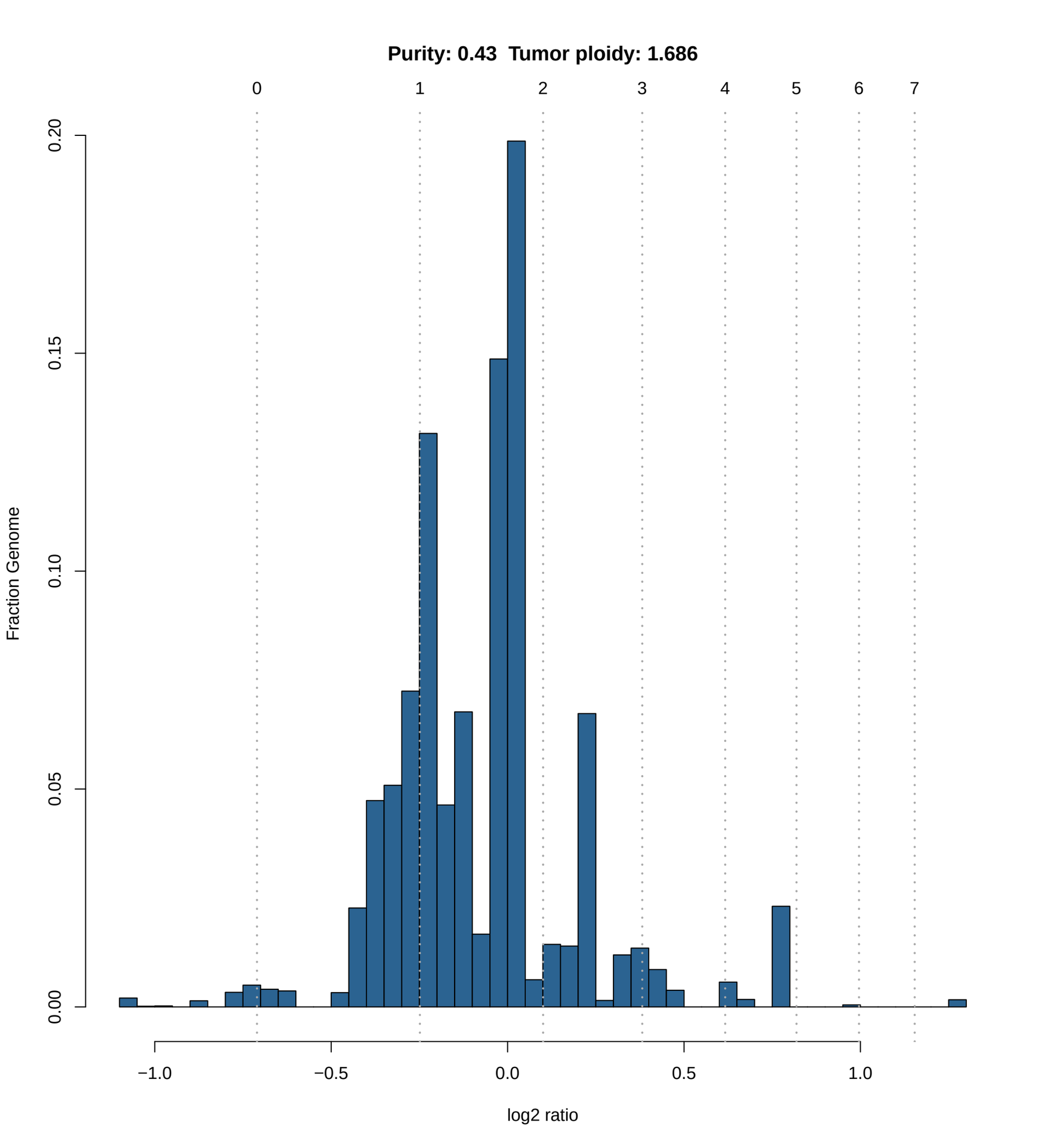

Purity: 0.49 Tumor ploidy: 4.771 SNV log−likelihood: −73.17 GoF: 87.6% Mean coverage: 290;505
1 3 4 5 7 8 11 13 15 16 17 18
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60 0.65
0 10 20 30 40 50 60
SNV Index
SCNA−fit log−likelihood: −5789.76
Copy Number log−ratio
−2 −1 0 1 2
0 1 2 3 5 7
0 10 20 30 40 50 60
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 10 20 30 40 50 60
SNV Index

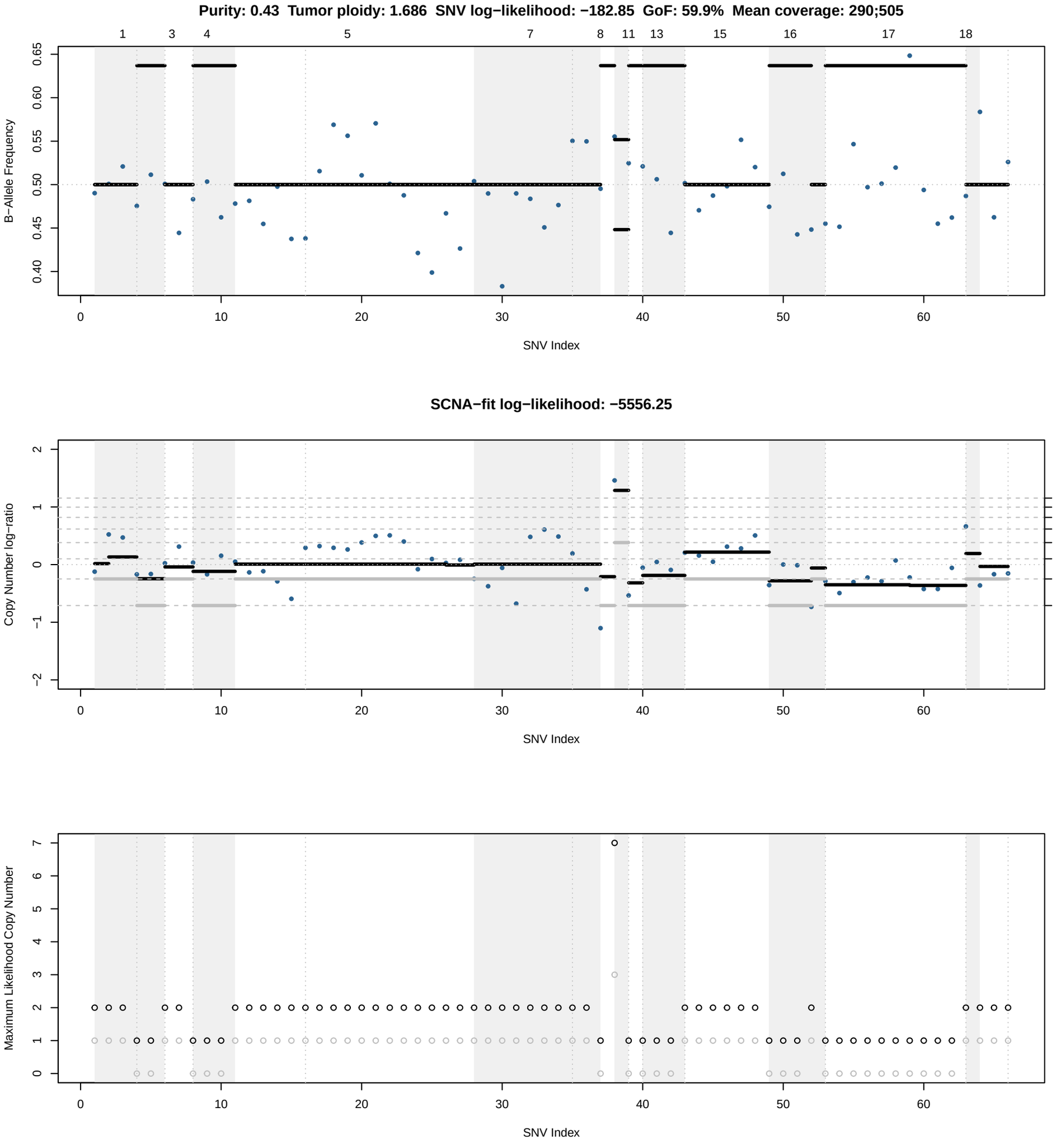

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
3m2
5m3
4m2
6m3
5m2
3m1
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

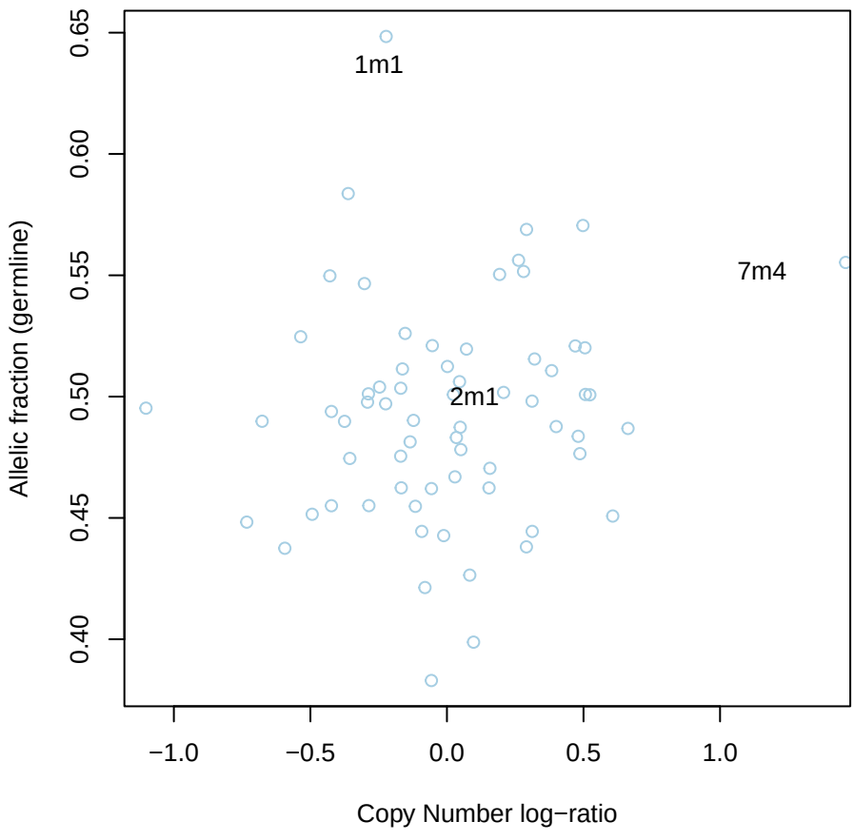

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

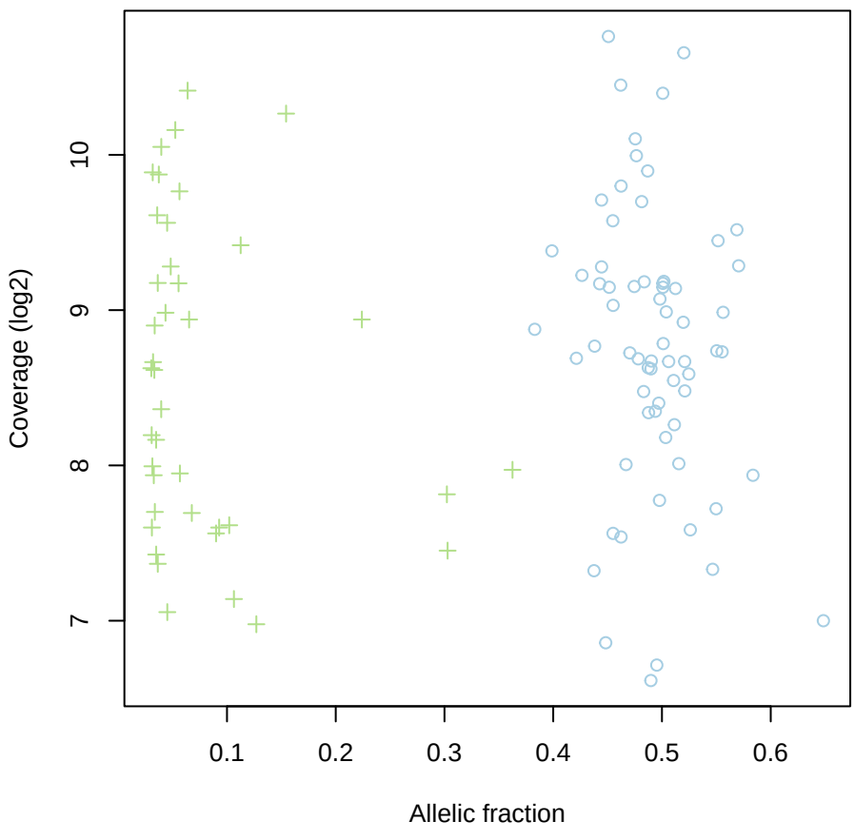

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0.30
0.35
4m2
5m2
2m1
3m1
4m1
5m1
6m1
7m1
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

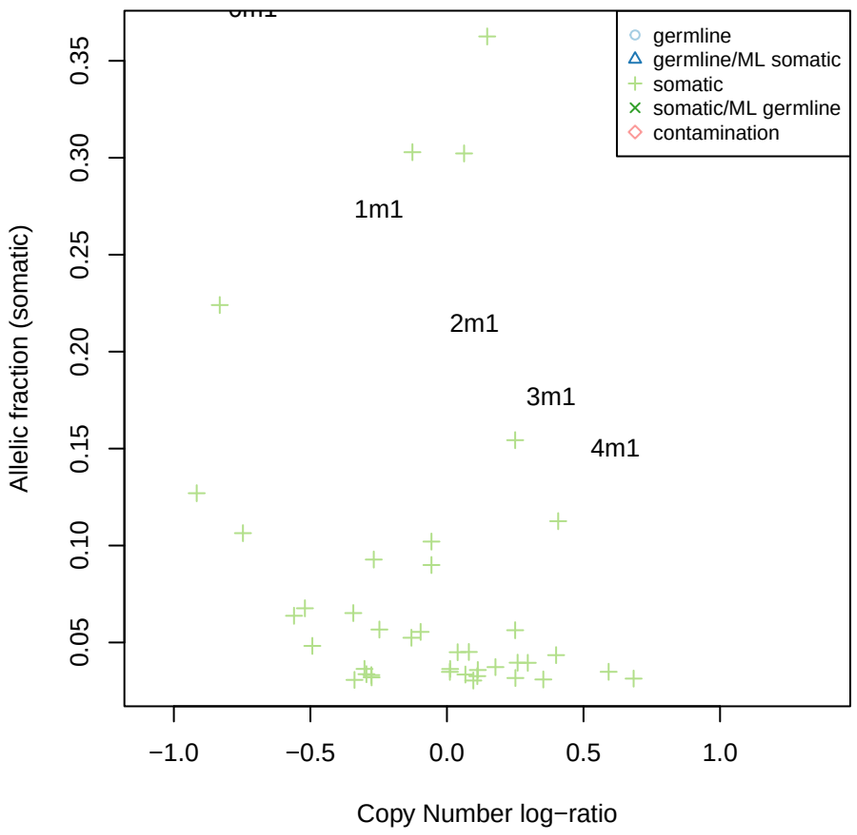

Power 0.8
Frequency
0
5
10
15
0.2
0.4
0.6
0.8
1.0
Cellular fraction

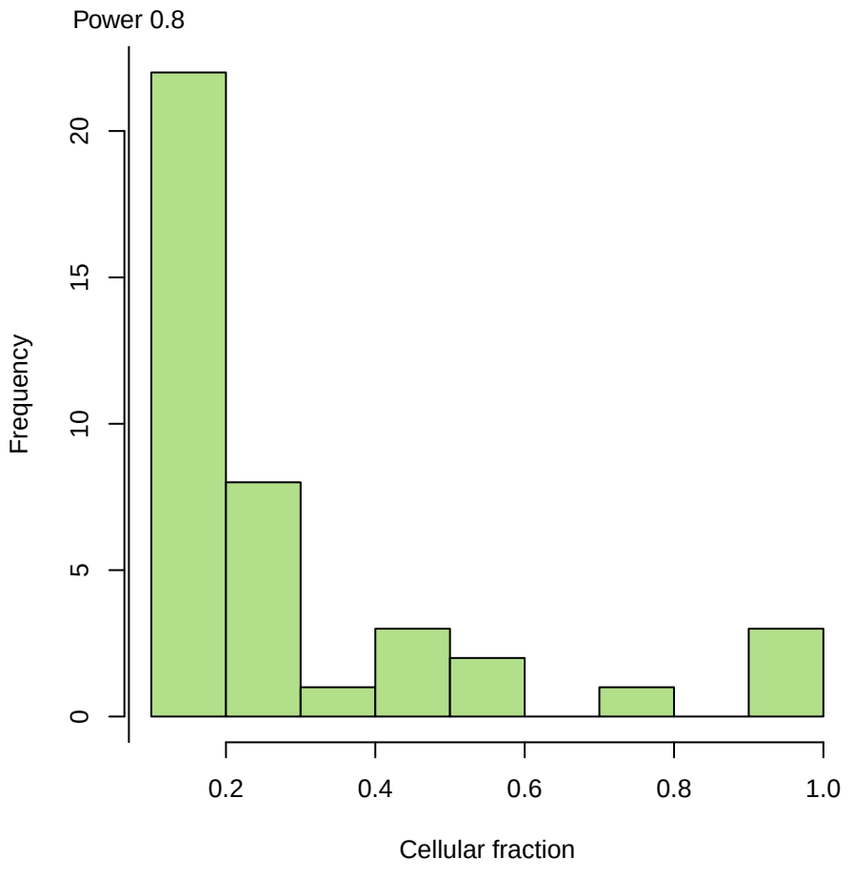

Purity: 0.43 Tumor ploidy: 1.686
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

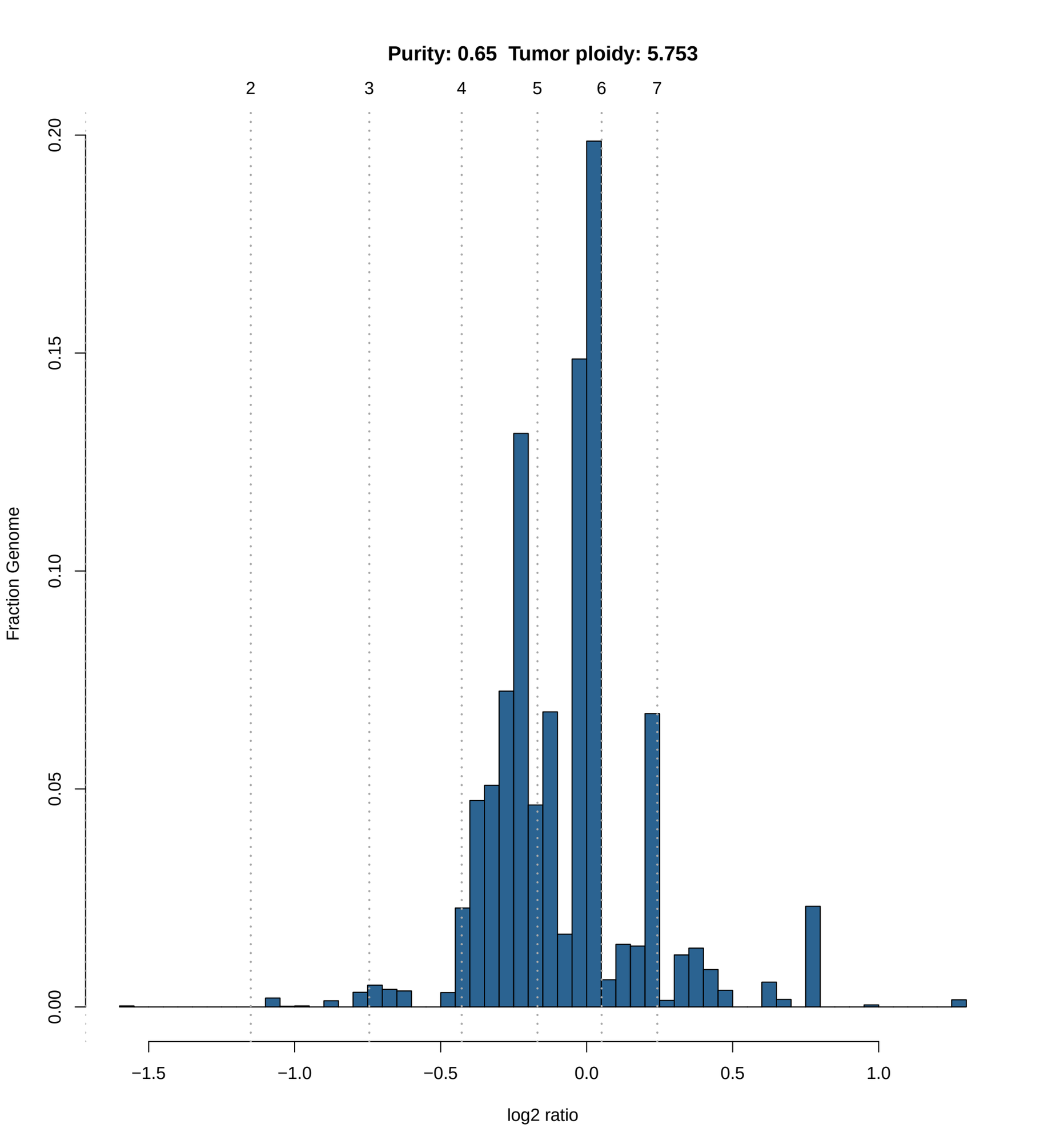

Purity: 0.43 Tumor ploidy: 1.686 SNV log−likelihood: −182.85 GoF: 59.9% Mean coverage: 290;505
1 3 4 5 7 8 11 13 15 16 17 18
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60 0.65
0 10 20 30 40 50 60
SNV Index
SCNA−fit log−likelihood: −5556.25
Copy Number log−ratio
−2 −1 0 1 2
0 1 2 4 6
0 10 20 30 40 50 60
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 10 20 30 40 50 60
SNV Index

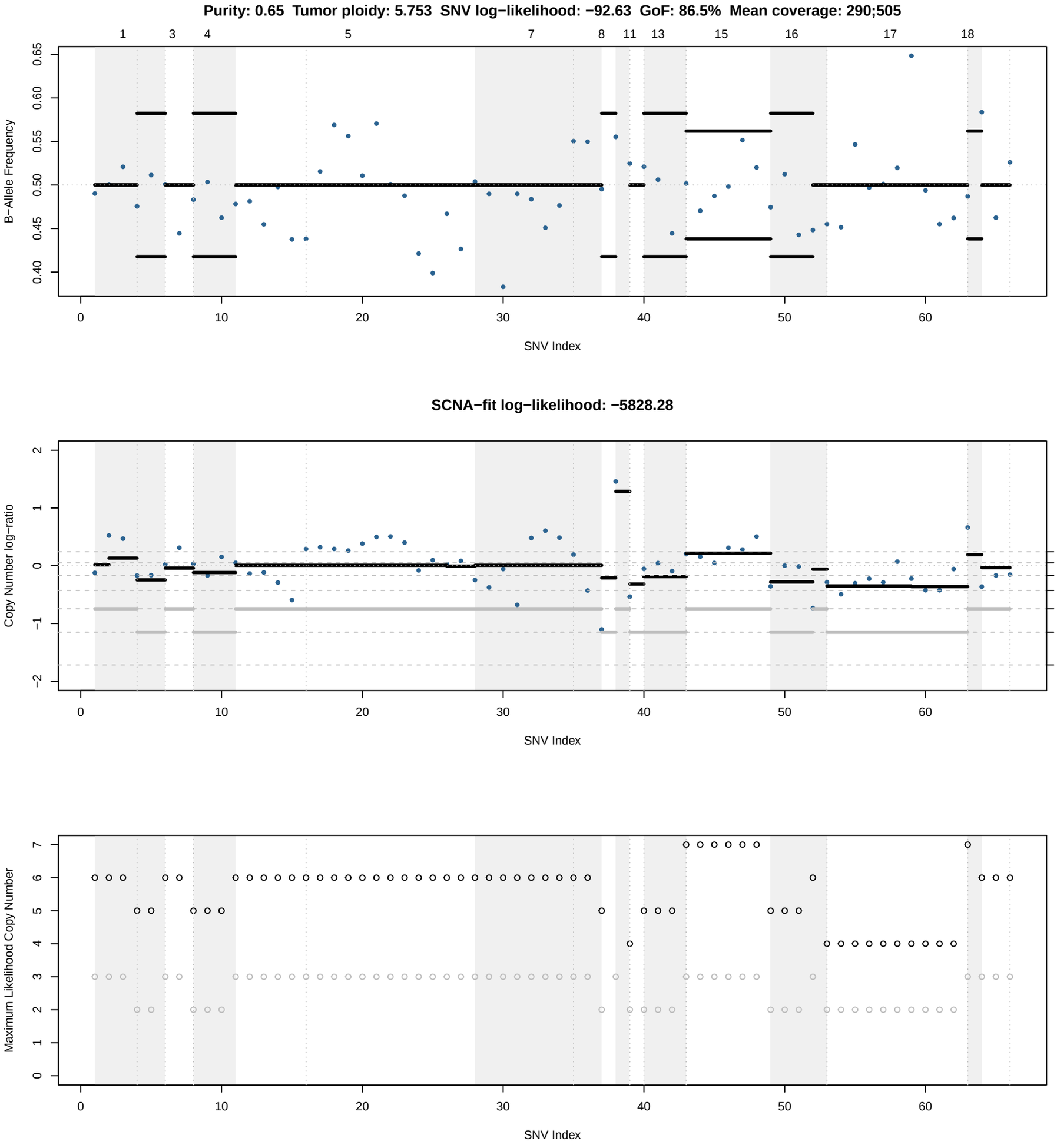

1m1
7m4
2m1
Allelic fraction (germline)
Copy Number log−ratio
0.40
0.45
0.50
0.55
0.60
0.65
−1.0
−0.5
0.0
0.5
1.0

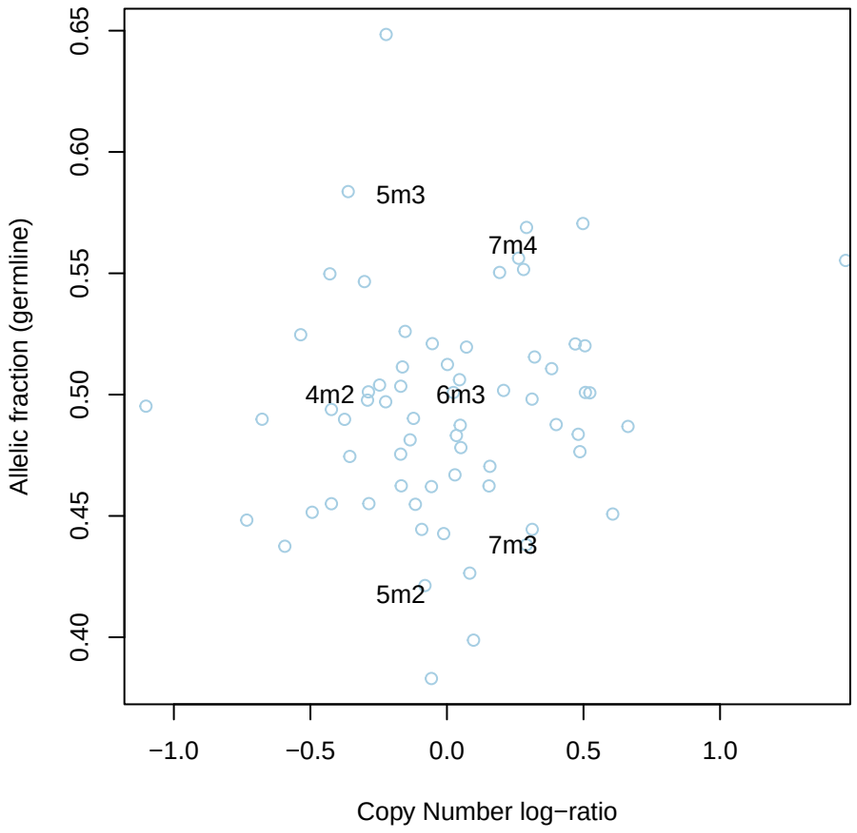

Coverage (log2)
Allelic fraction
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

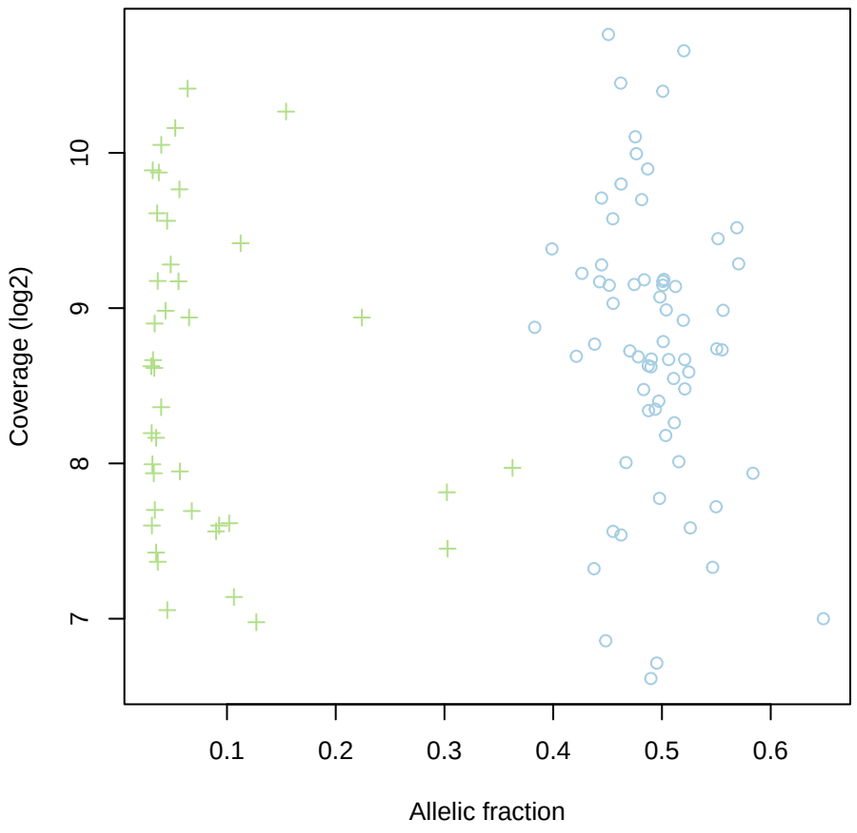

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
4m1
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
0.25
0.30
0.35
−1.0
−0.5
0.0
0.5
1.0

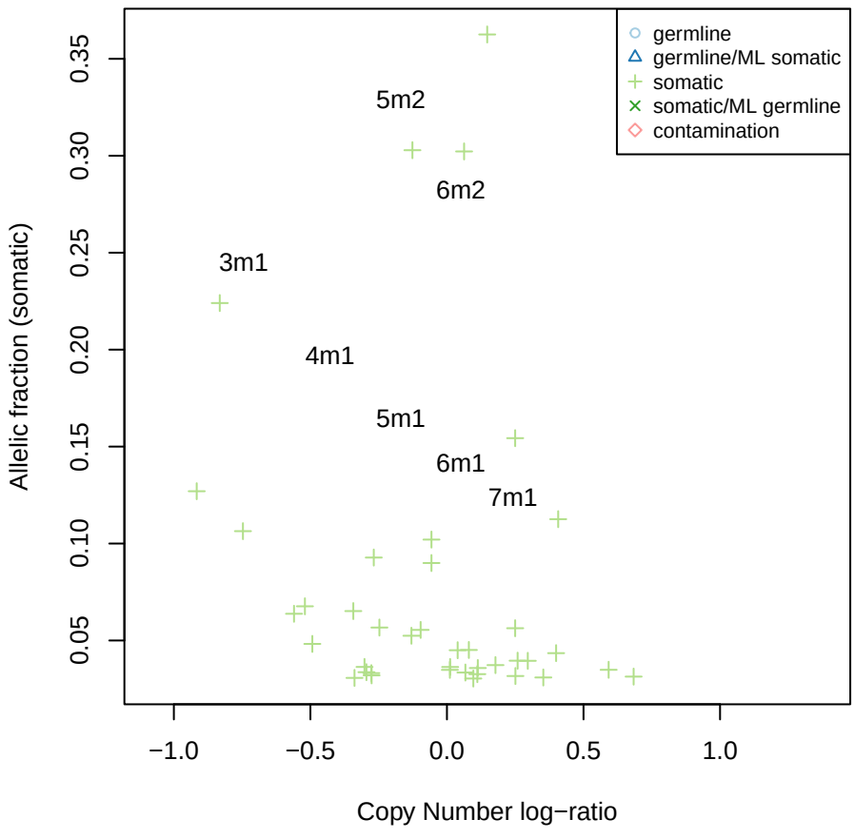

Power 0.8
Frequency
Cellular fraction
0
5
10
15
20
0.2
0.4
0.6
0.8
1.0

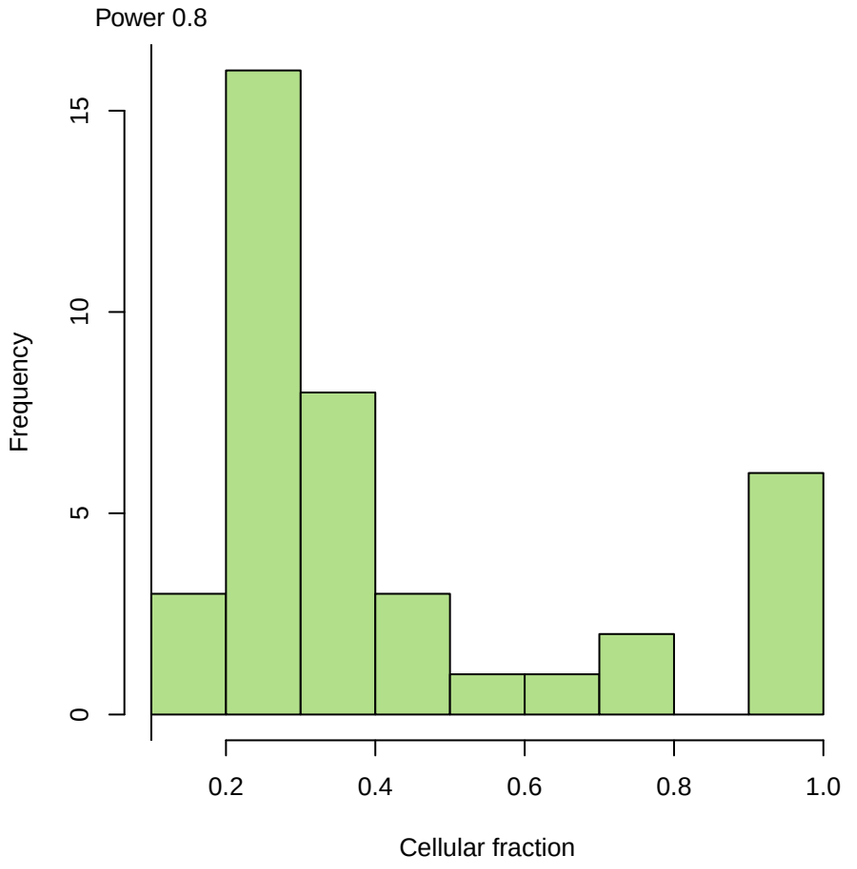

Purity: 0.65 Tumor ploidy: 5.753
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

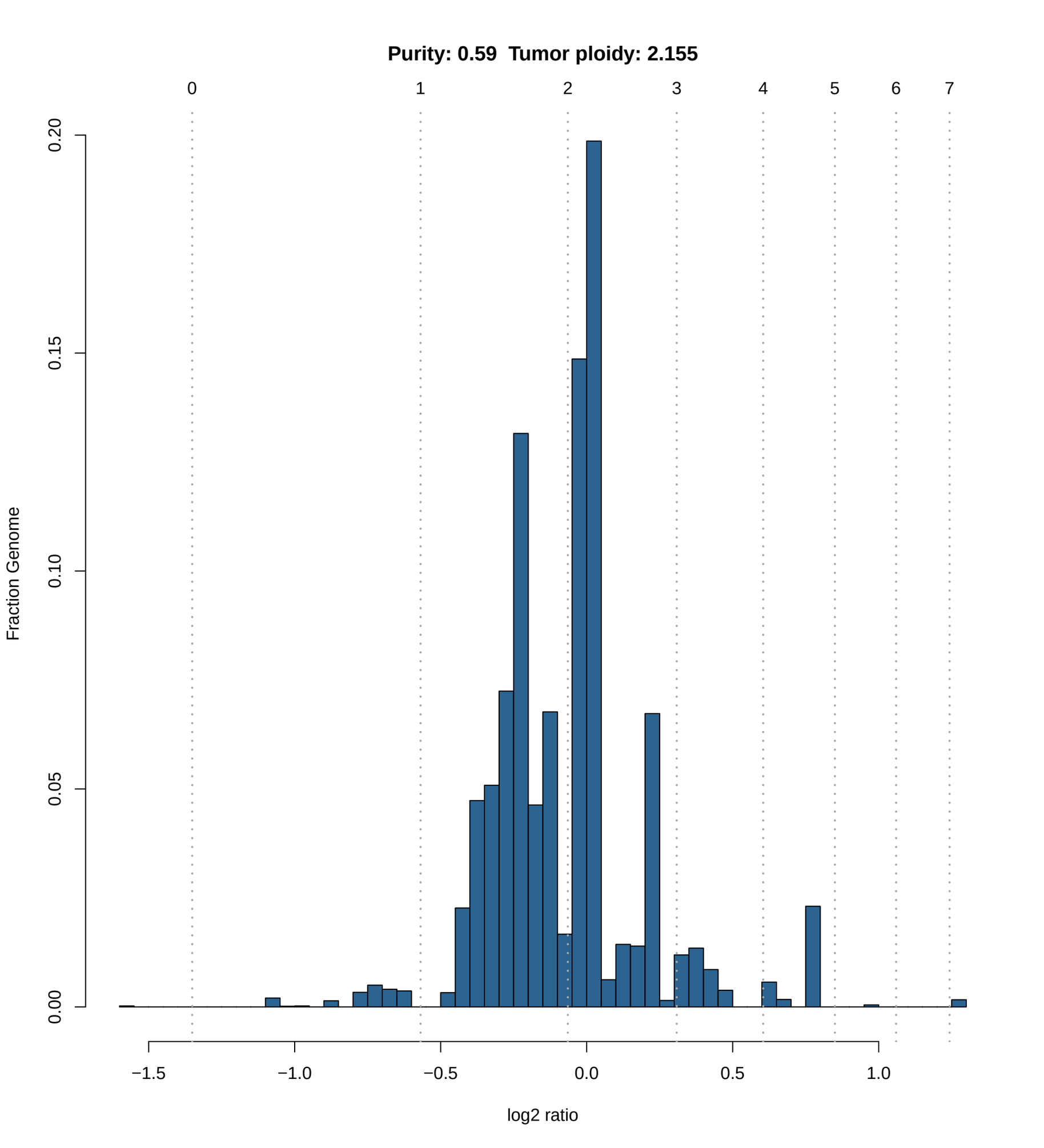

Purity: 0.65 Tumor ploidy: 5.753 SNV log−likelihood: −92.63 GoF: 86.5% Mean coverage: 290;505
1 3 4 5 7 8 11 13 15 16 17 18
B−Allele Frequency
0.40 0.45 0.50 0.55 0.60 0.65
0 10 20 30 40 50 60
SNV Index
SCNA−fit log−likelihood: −5828.28
Copy Number log−ratio
−2 −1 0 1 2
1 2 3 4 6
0 10 20 30 40 50 60
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 10 20 30 40 50 60
SNV Index

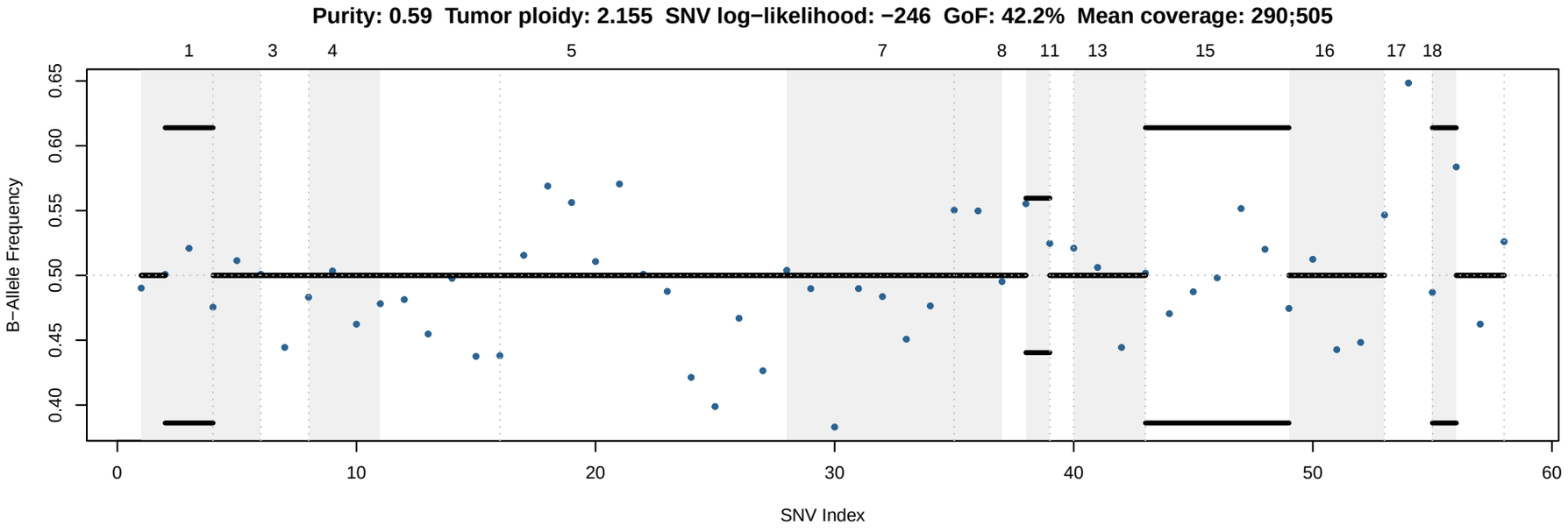

Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
5m3
7m4
4m2
6m3
7m3
5m2
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

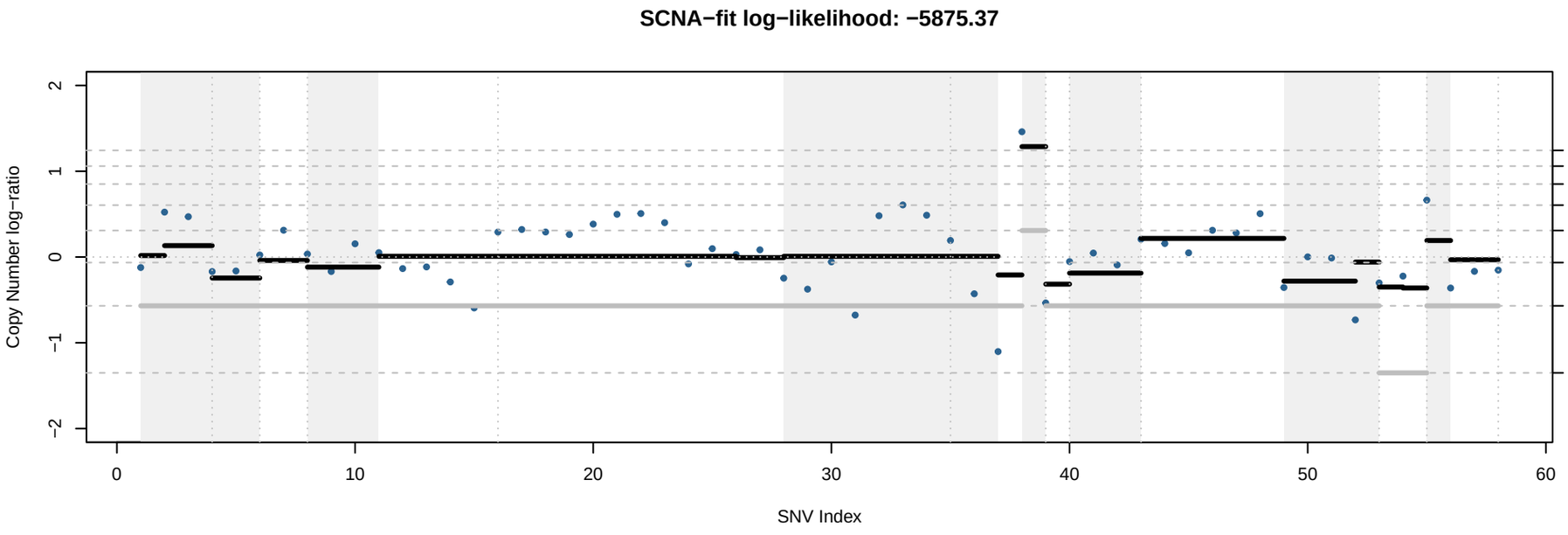

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

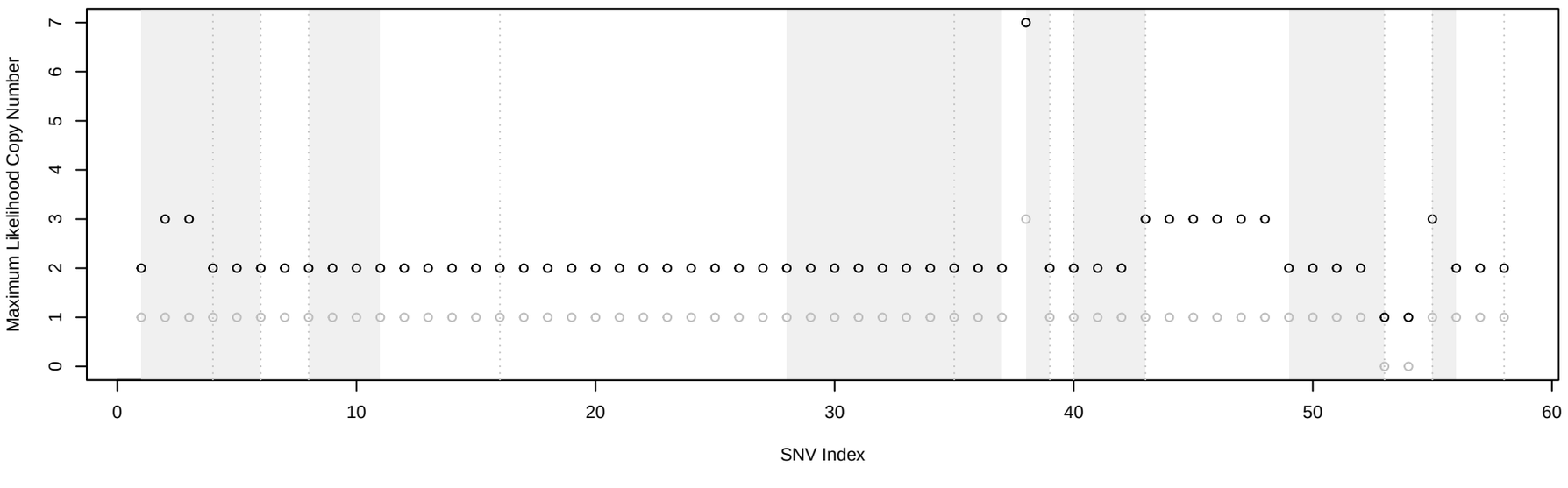

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0.30
0.35
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m2
6m2
3m1
4m1
5m1
6m1
7m1
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

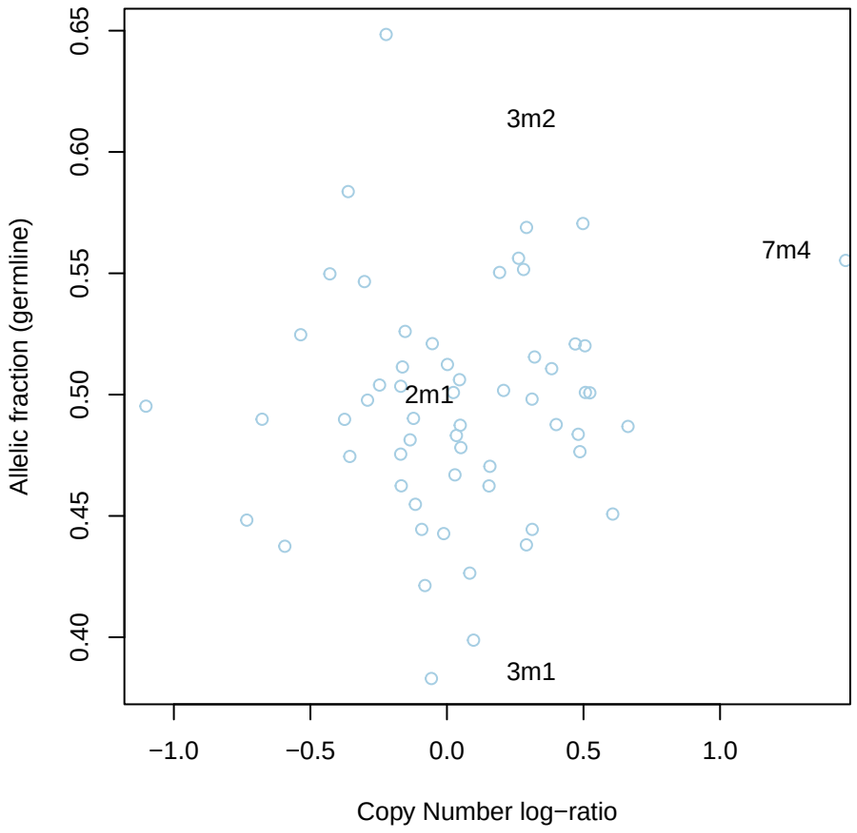

Power 0.8
Frequency
0
5
10
15
0.2
0.4
0.6
0.8
1.0
Cellular fraction

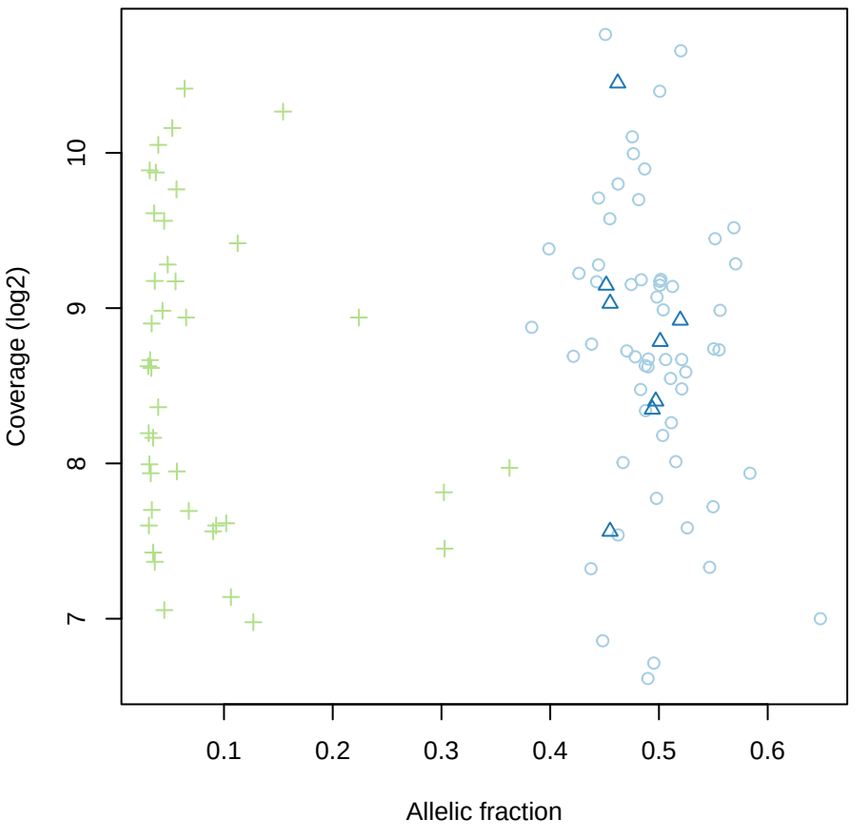

Purity: 0.59 Tumor ploidy: 2.155
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

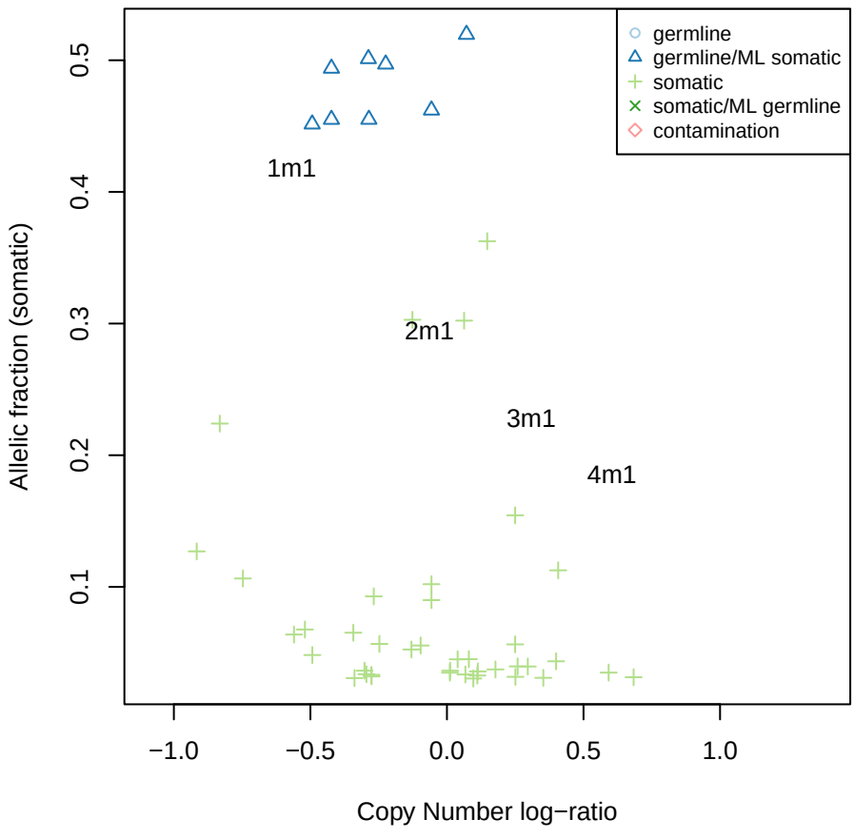

Purity: 0.59 Tumor ploidy: 2.155 SNV log−likelihood: −246 GoF: 42.2% Mean coverage: 290;505
1
3
4
5
7
8
11
13
15
16
17
18
B−Allele Frequency
0.40
0.45
0.50
0.55
0.60
0.65
0
10
20
30
40
50
60
SNV Index

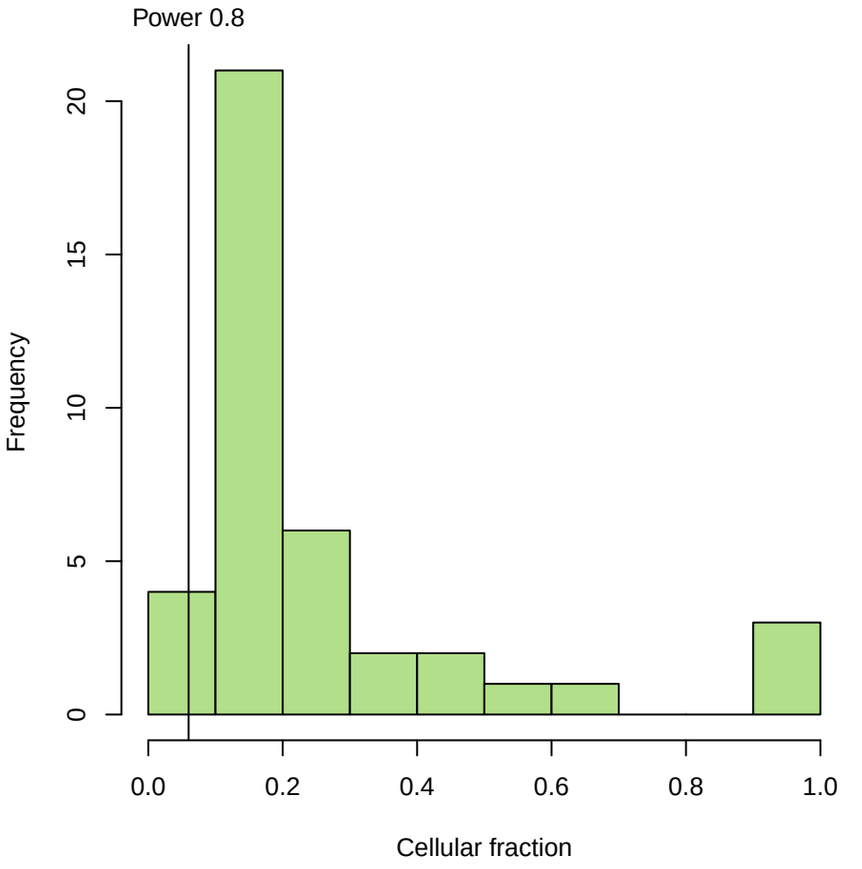

SCNA−fit log−likelihood: −5875.37
Copy Number log−ratio
−2
−1
0
1
2
0
1
2
3
4
6
0
10
20
30
40
50
60
SNV Index


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


Allelic fraction (germline)
0.40
0.45
0.50
0.55
0.60
0.65
3m2
7m4
2m1
3m1
−1.0
−0.5
0.0
0.5
1.0
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
1m1
2m1
3m1
4m1
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio


Power 0.8
Frequency
0
5
10
15
20
0.0
0.2
0.4
0.6
0.8
1.0
Cellular fraction