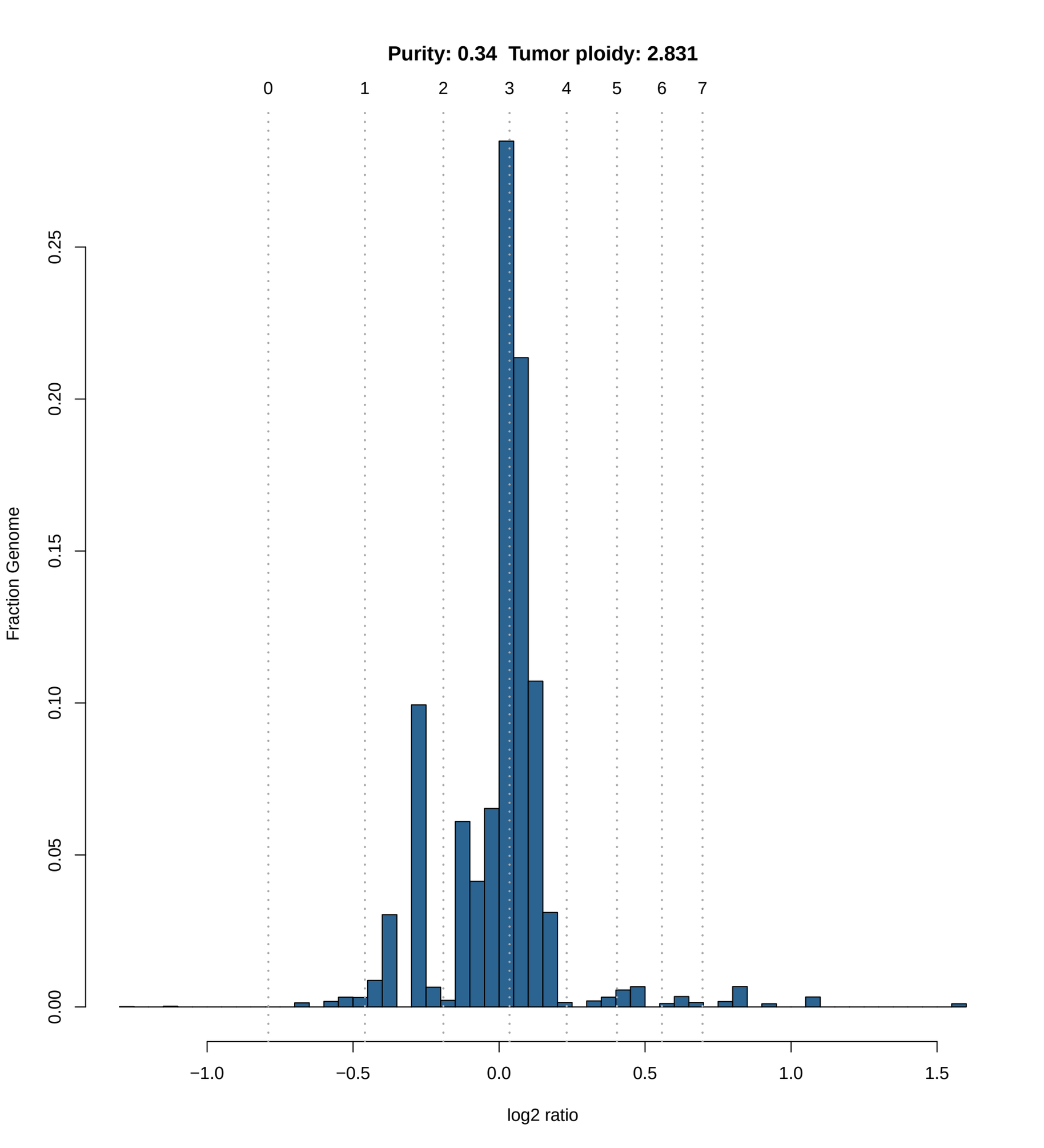
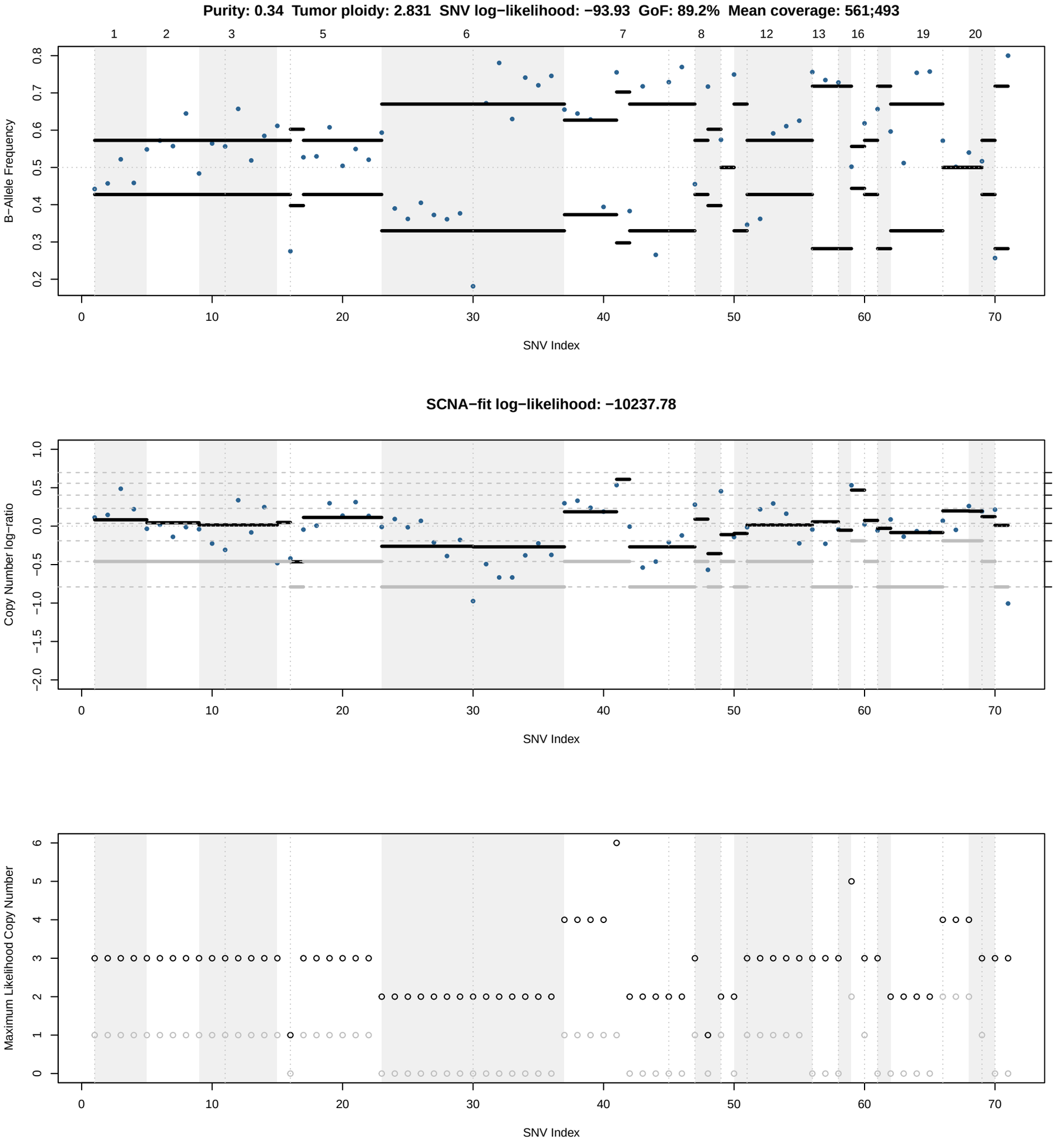
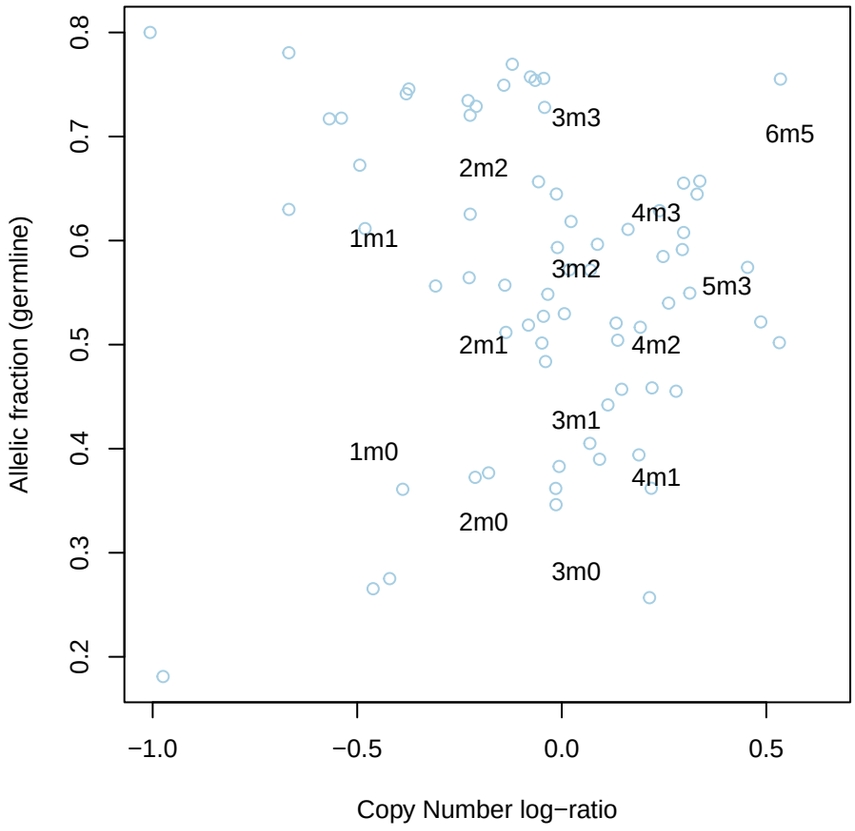
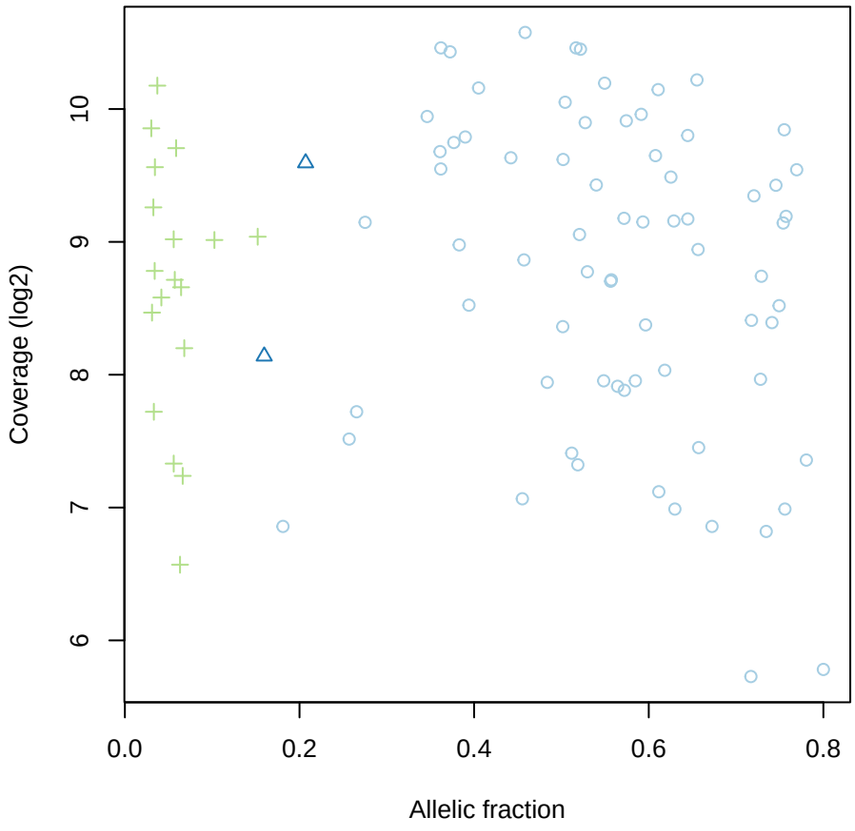
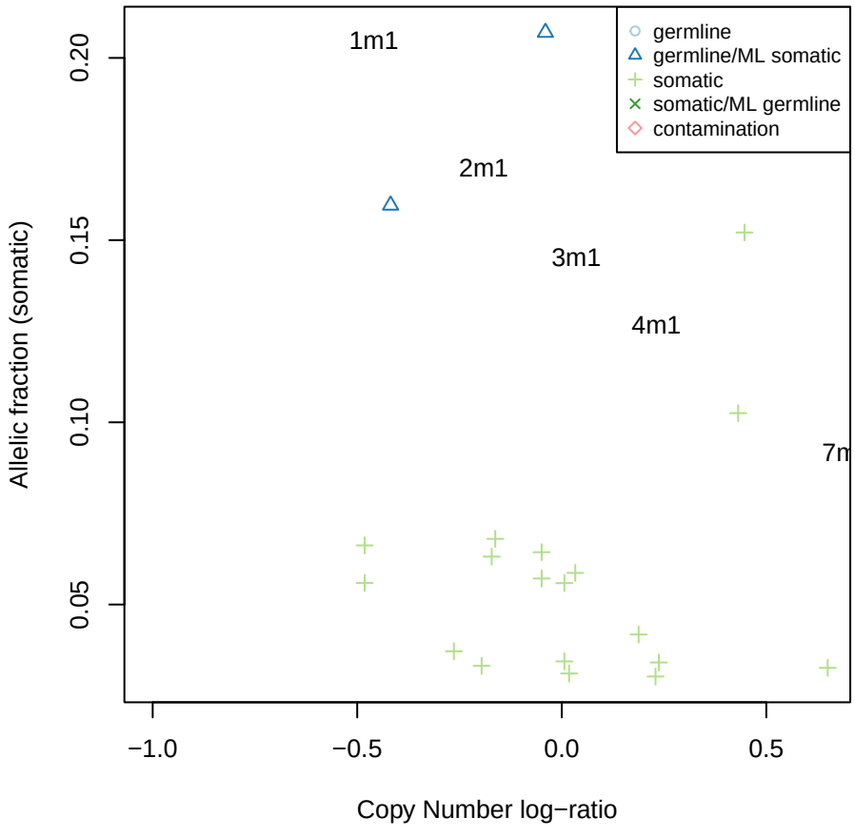
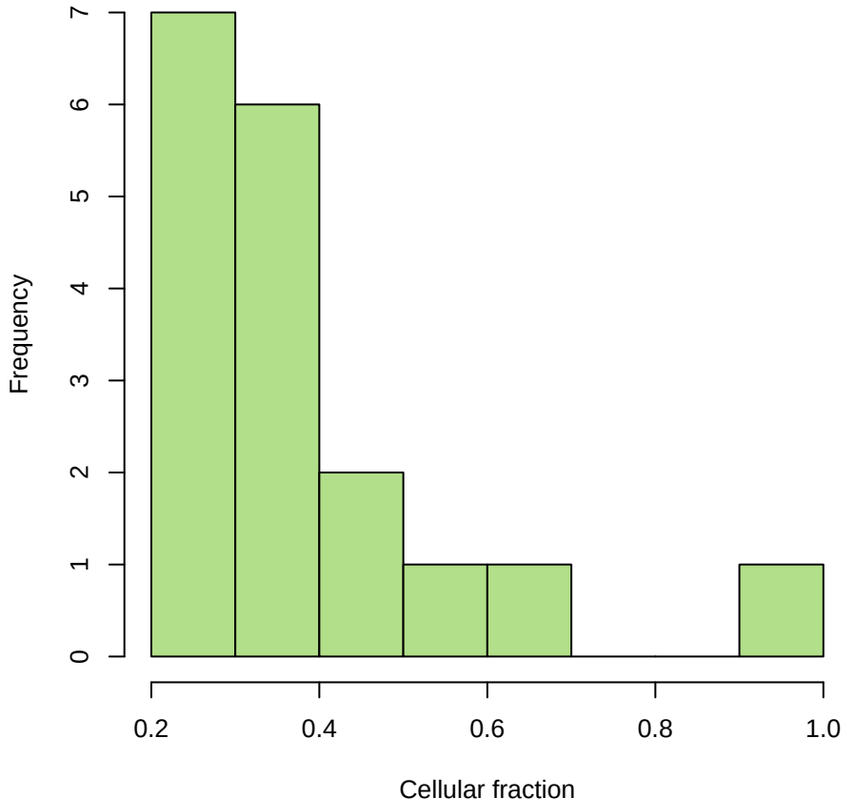

Purity: 0.34  Tumor ploidy: 2.831
0
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

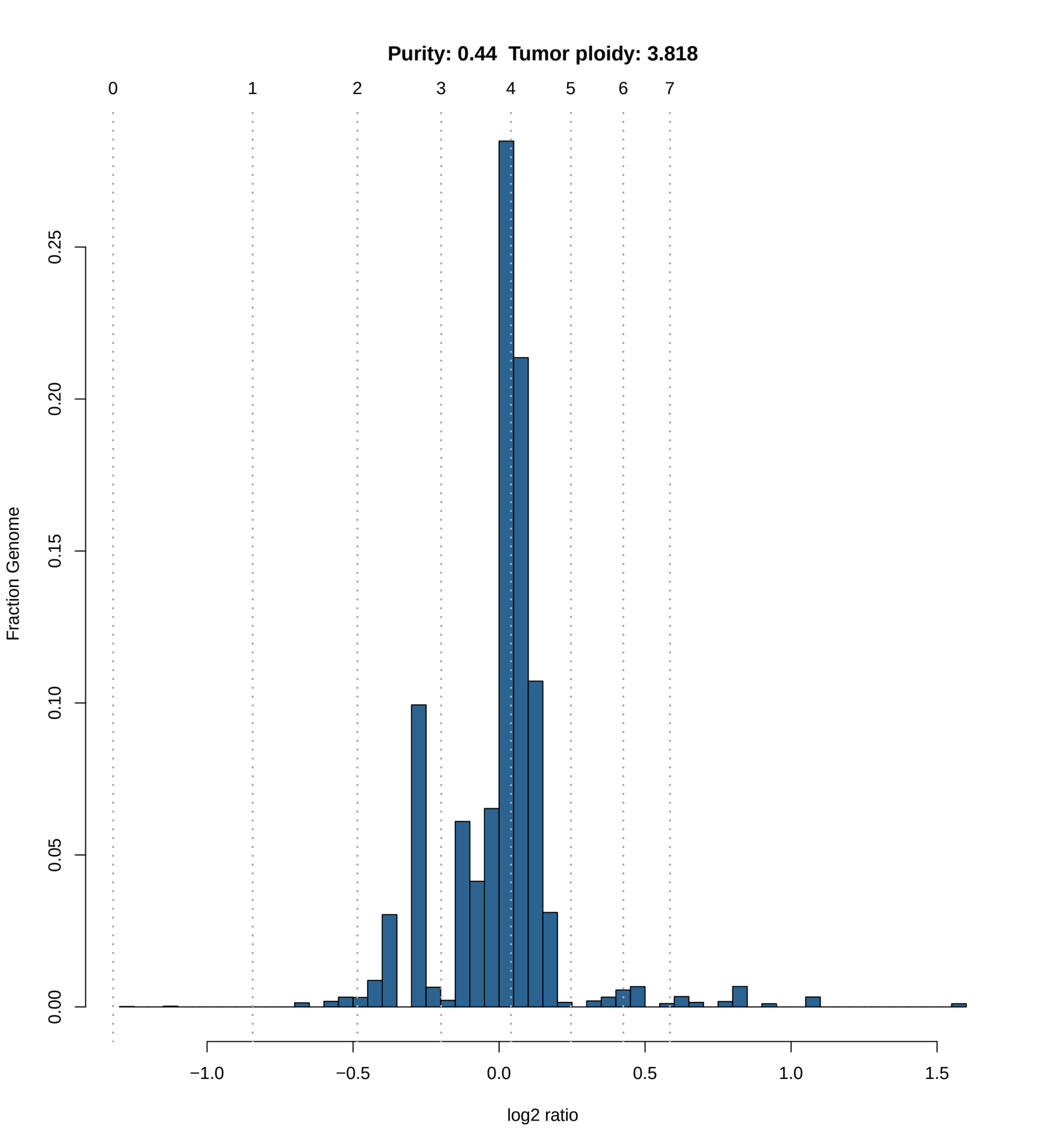

Purity: 0.34 Tumor ploidy: 2.831 SNV log−likelihood: −93.93 GoF: 89.2% Mean coverage: 561;493
1 2 3 5 6 7 8 12 13 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 10 20 30 40 50 60 70
SNV Index
SCNA−fit log−likelihood: −10237.78
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 5 7
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

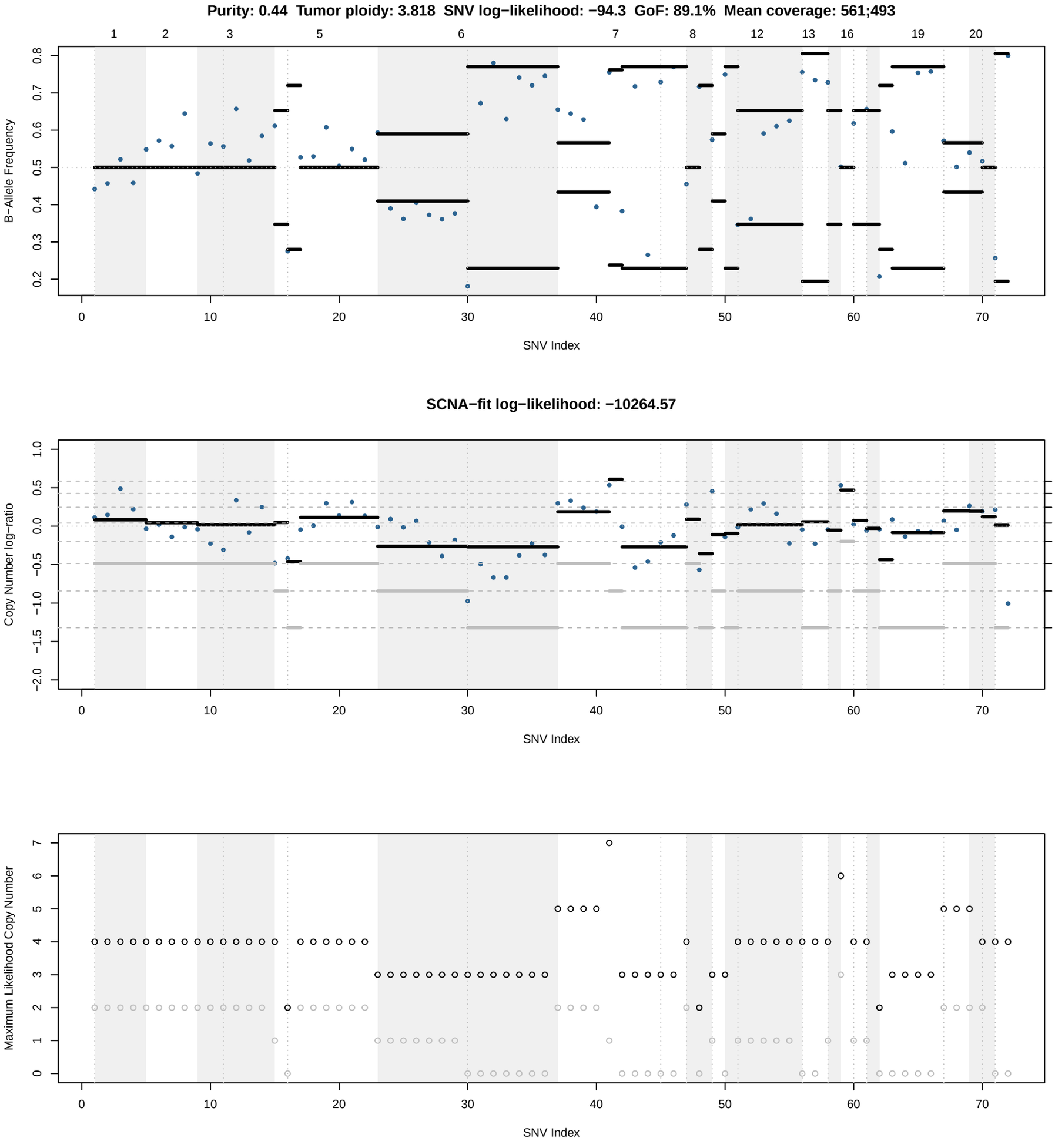

Allelic fraction (germline)
Copy Number log−ratio
1m1
2m2
3m3
6m5
4m3
3m2
5m3
2m1
4m2
3m1
1m0
4m1
2m0
3m0

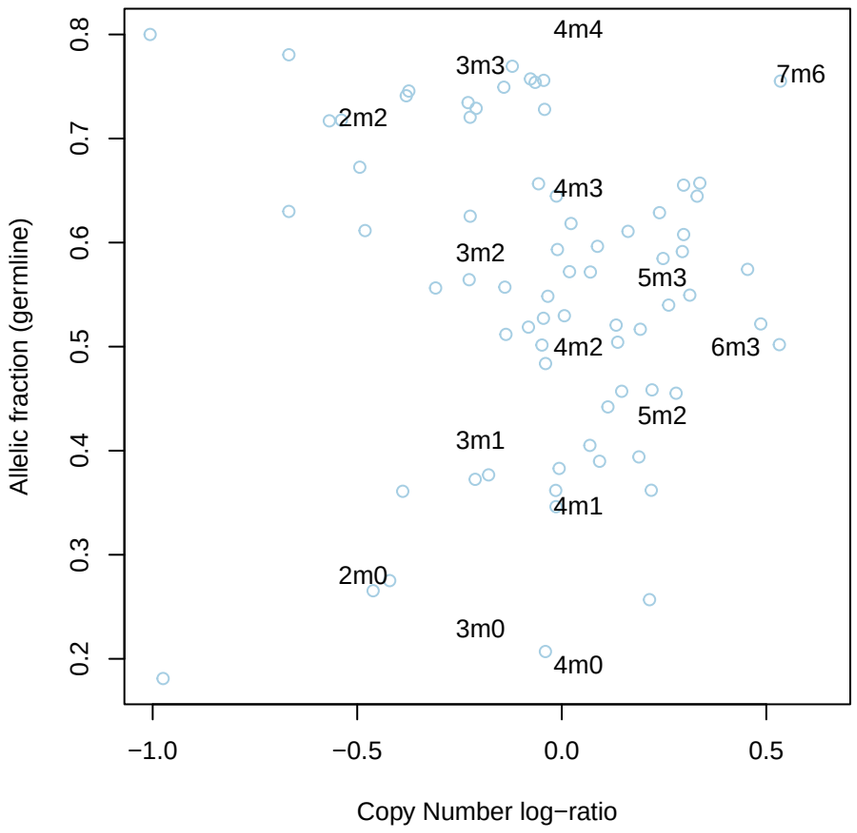

Coverage (log2)
Allelic fraction

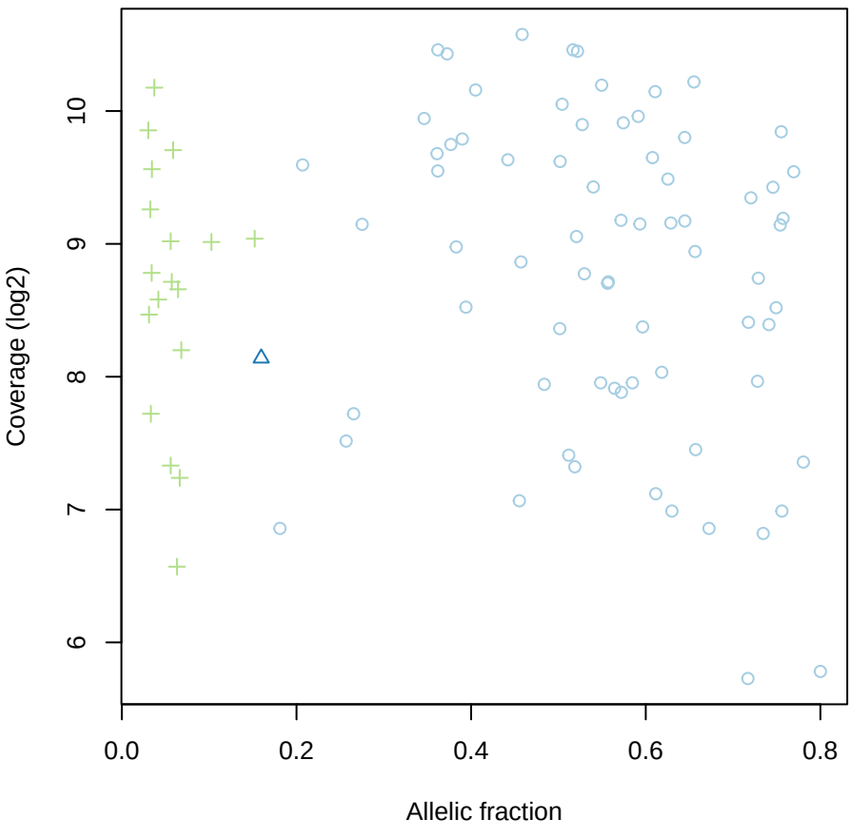

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
4m1

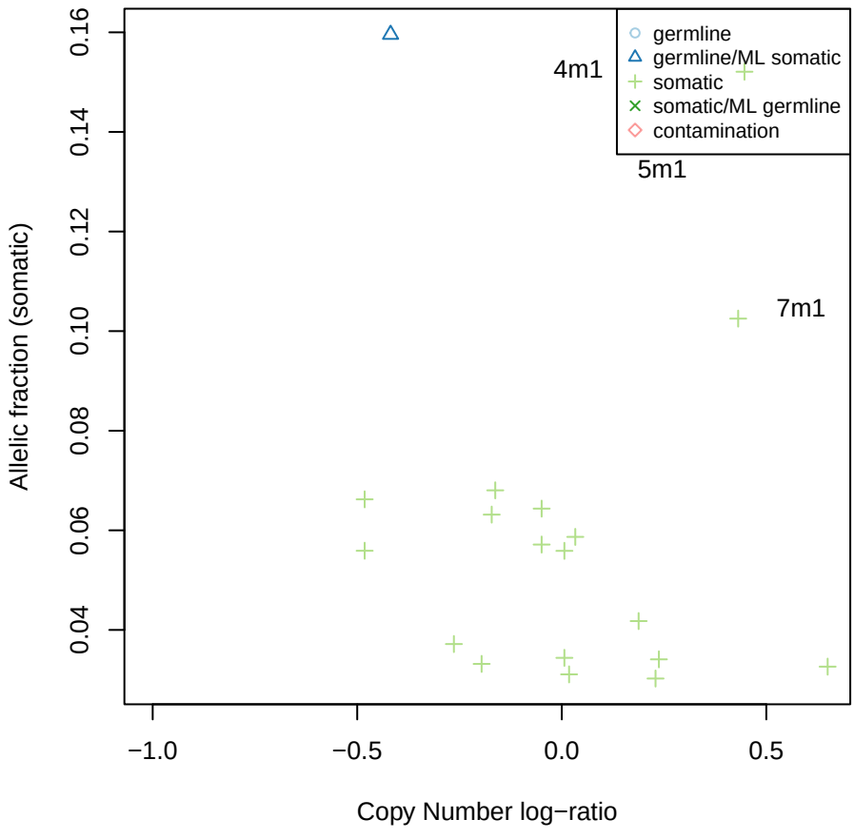

Frequency
Cellular fraction

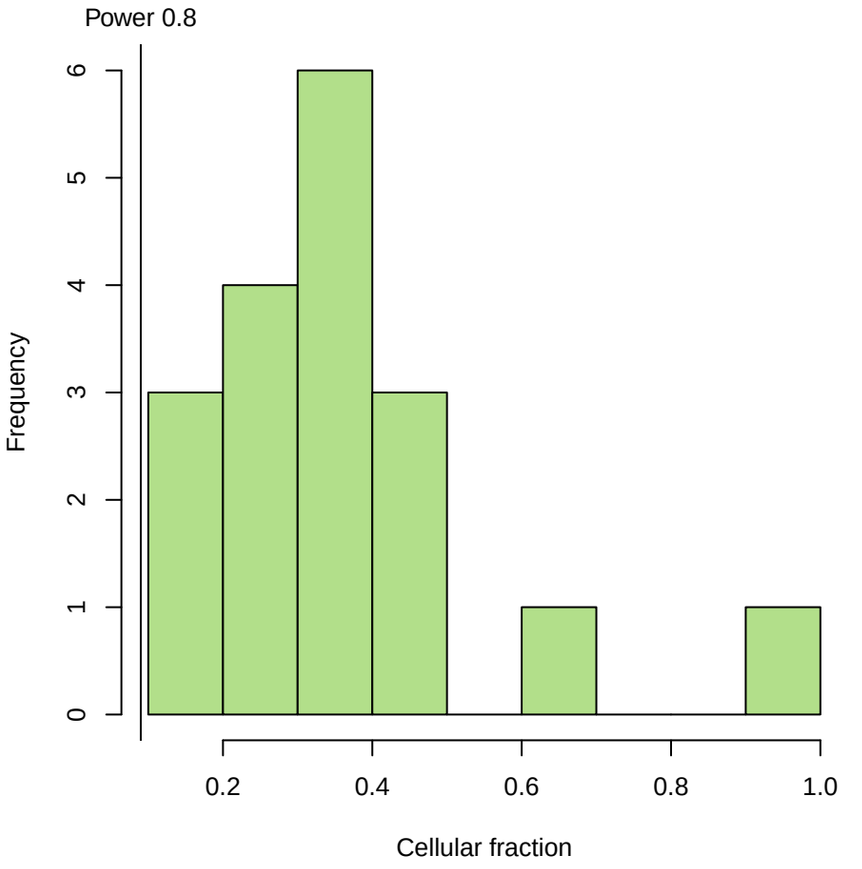

Purity: 0.44 Tumor ploidy: 3.818
0
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

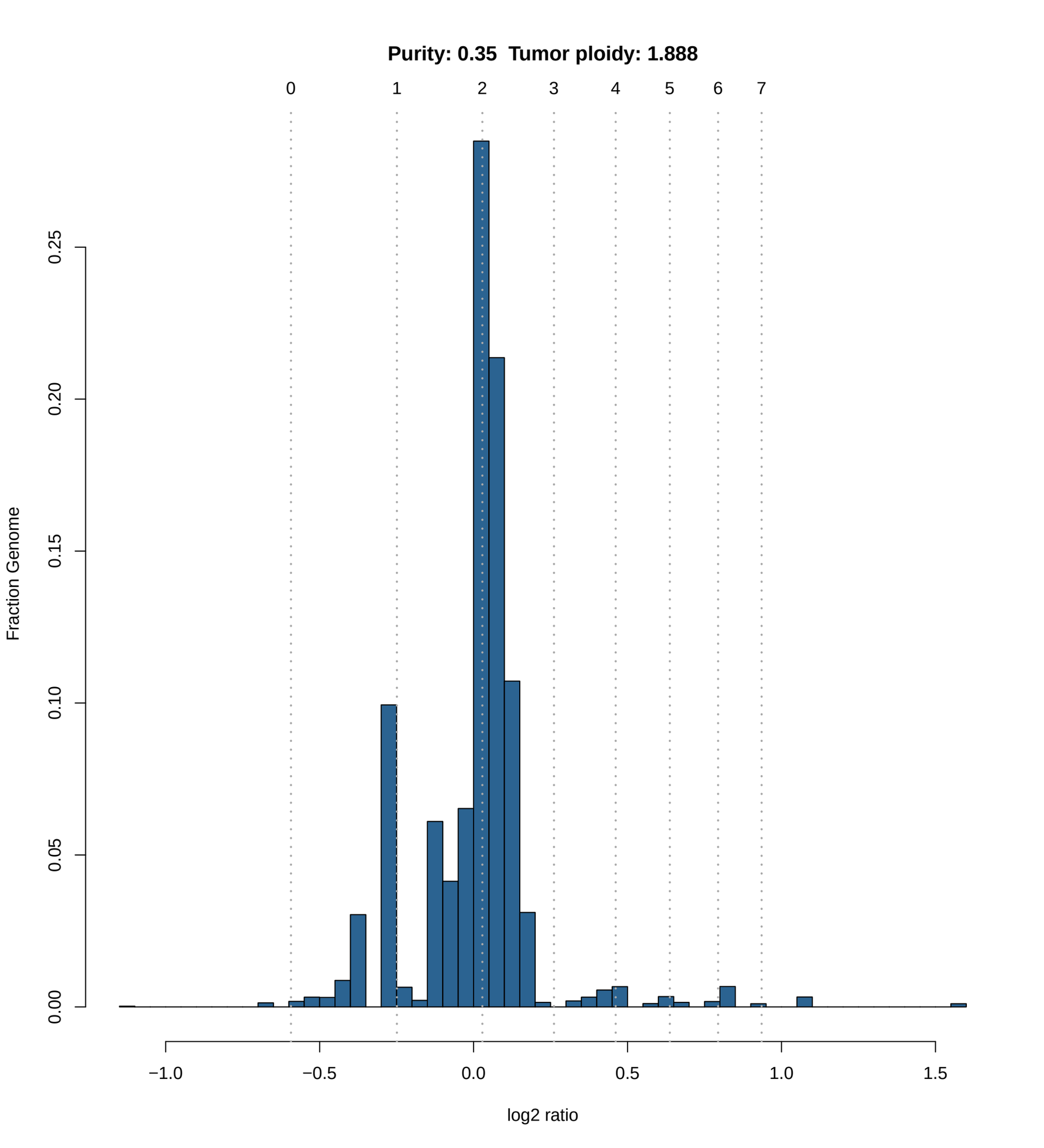

Purity: 0.44 Tumor ploidy: 3.818 SNV log−likelihood: −94.3 GoF: 89.1% Mean coverage: 561;493
1 2 3 5 6 7 8 12 13 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 10 20 30 40 50 60 70
SNV Index
SCNA−fit log−likelihood: −10264.57
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 6
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

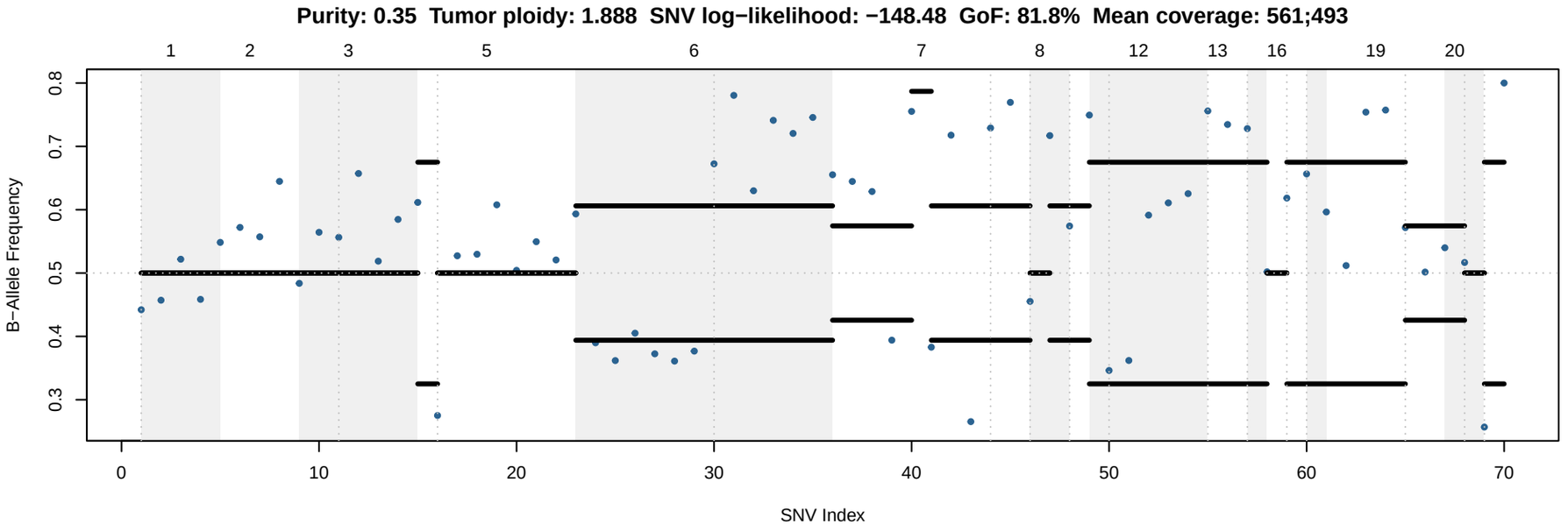

4m4
3m3
7m6
2m2
4m3
3m2
5m3
4m2
6m3
5m2
3m1
4m1
2m0
3m0
4m0
Allelic fraction (germline)
Copy Number log−ratio

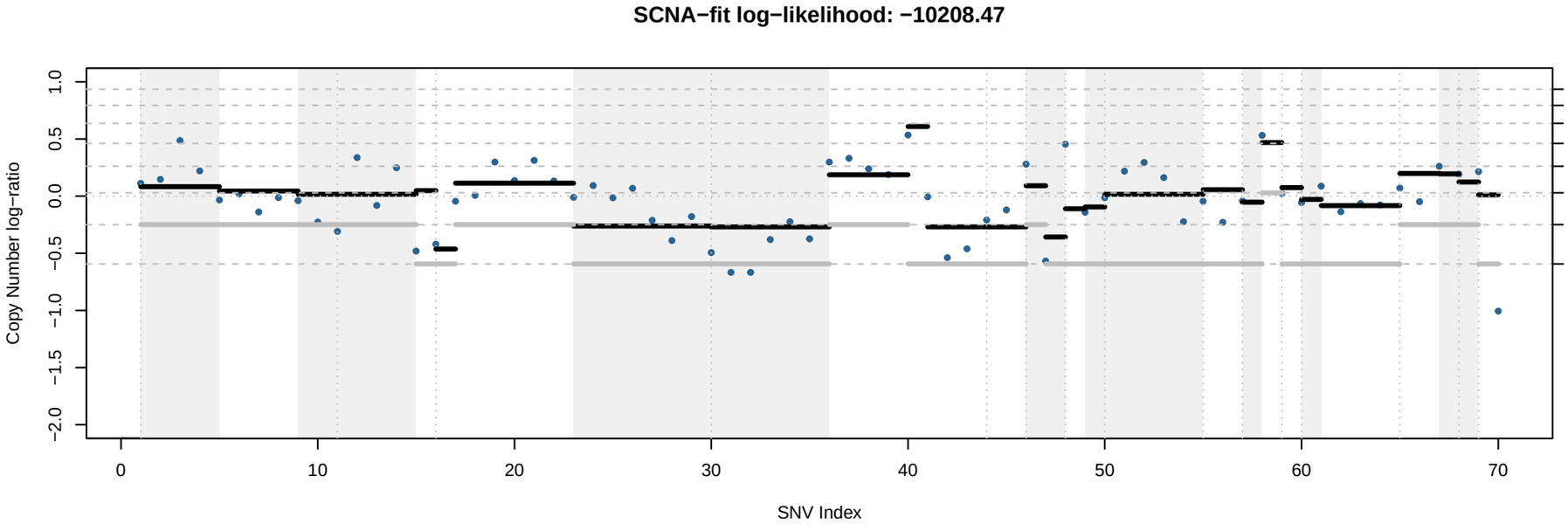

Coverage (log2)
Allelic fraction

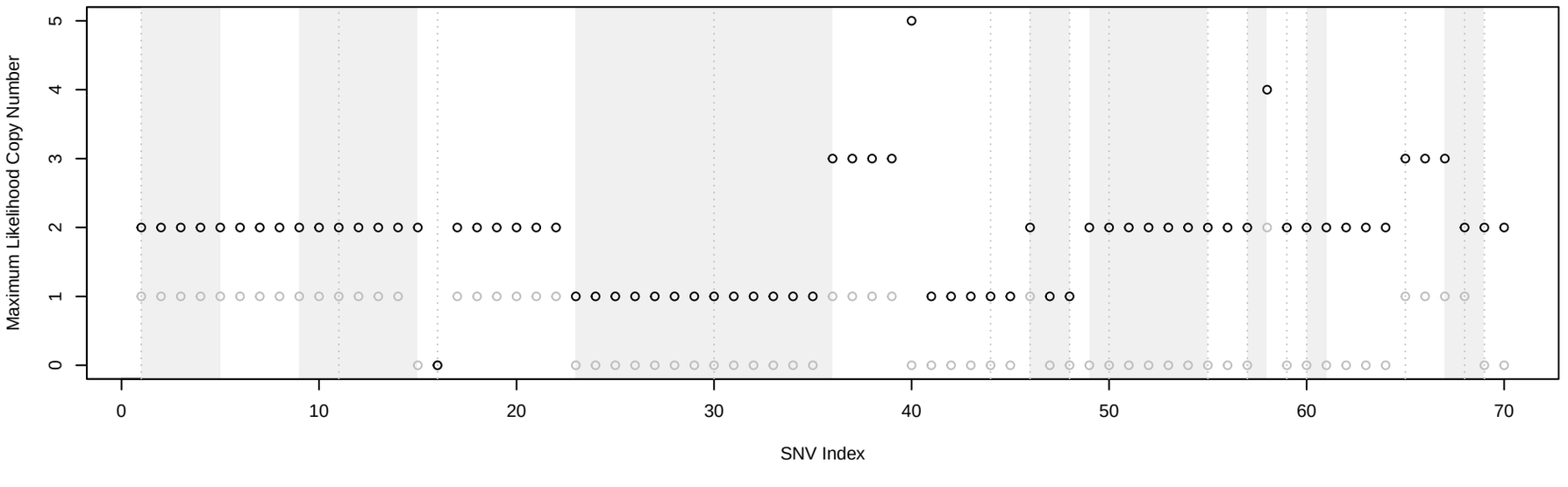

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

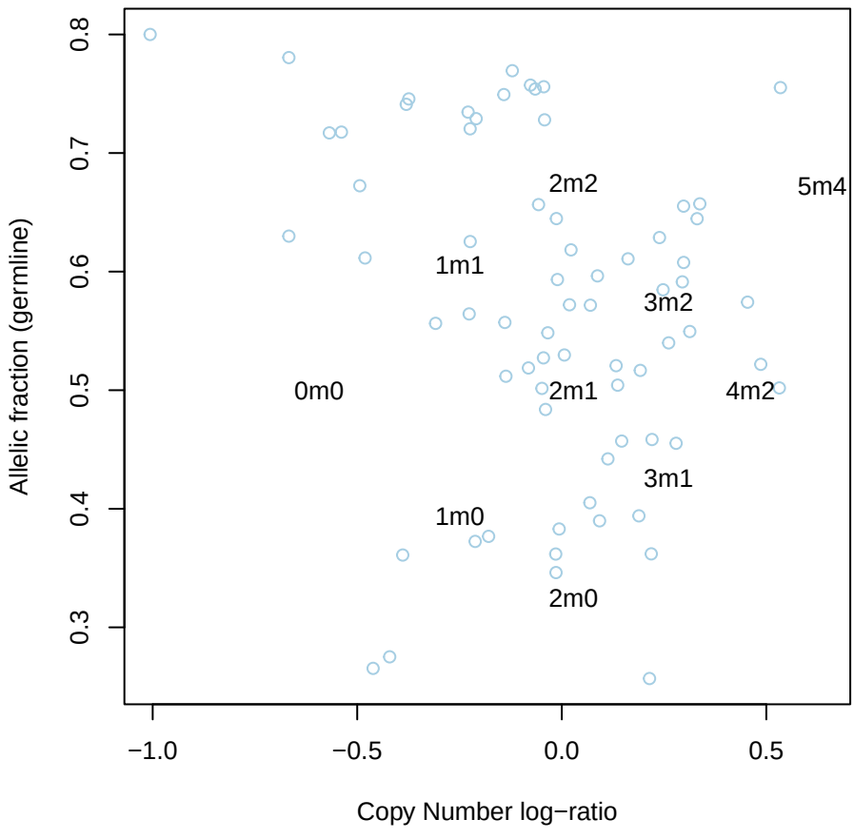

Power 0.8
Frequency
Cellular fraction

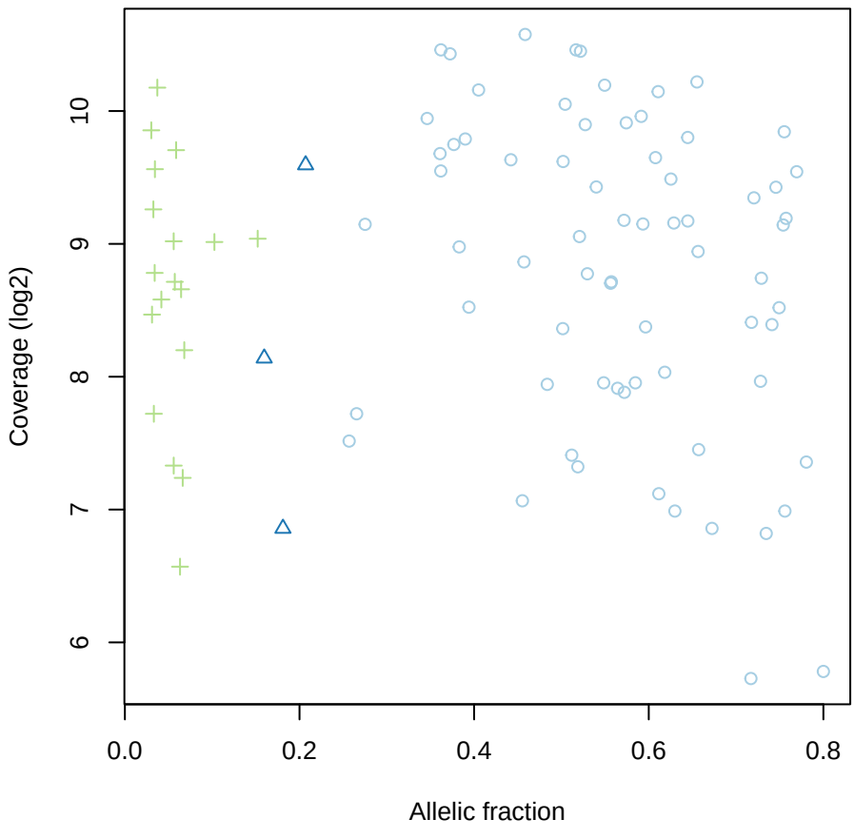

Purity: 0.35 Tumor ploidy: 1.888
0
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

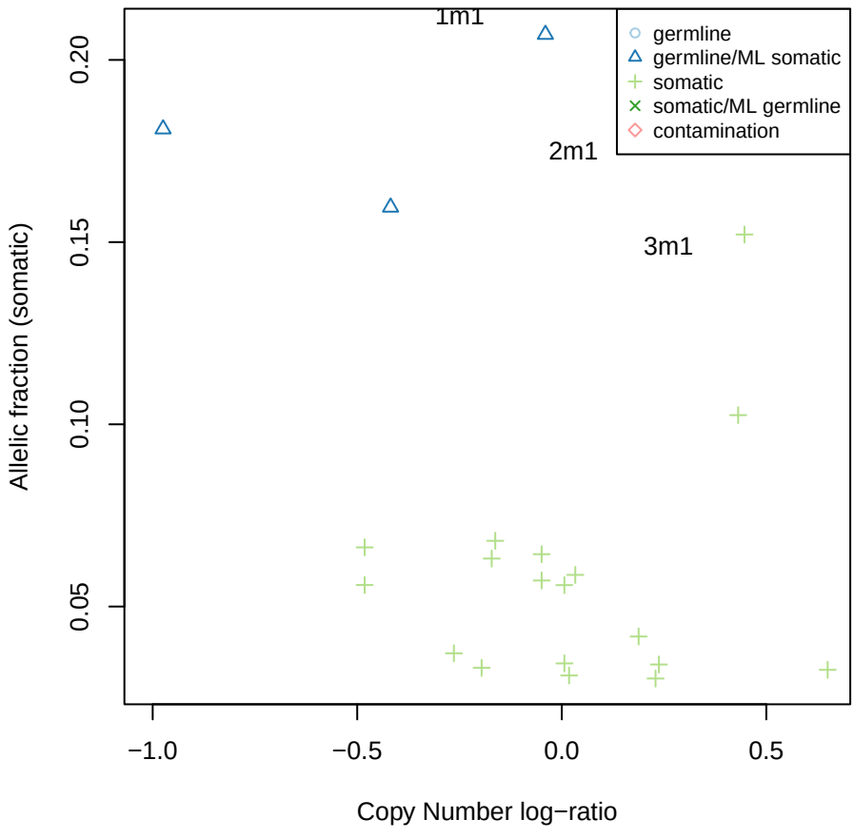

Purity: 0.35 Tumor ploidy: 1.888 SNV log−likelihood: −148.48 GoF: 81.8% Mean coverage: 561;493
1 2 3 5 6 7 8 12 13 16 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 10 20 30 40 50 60 70
SNV Index

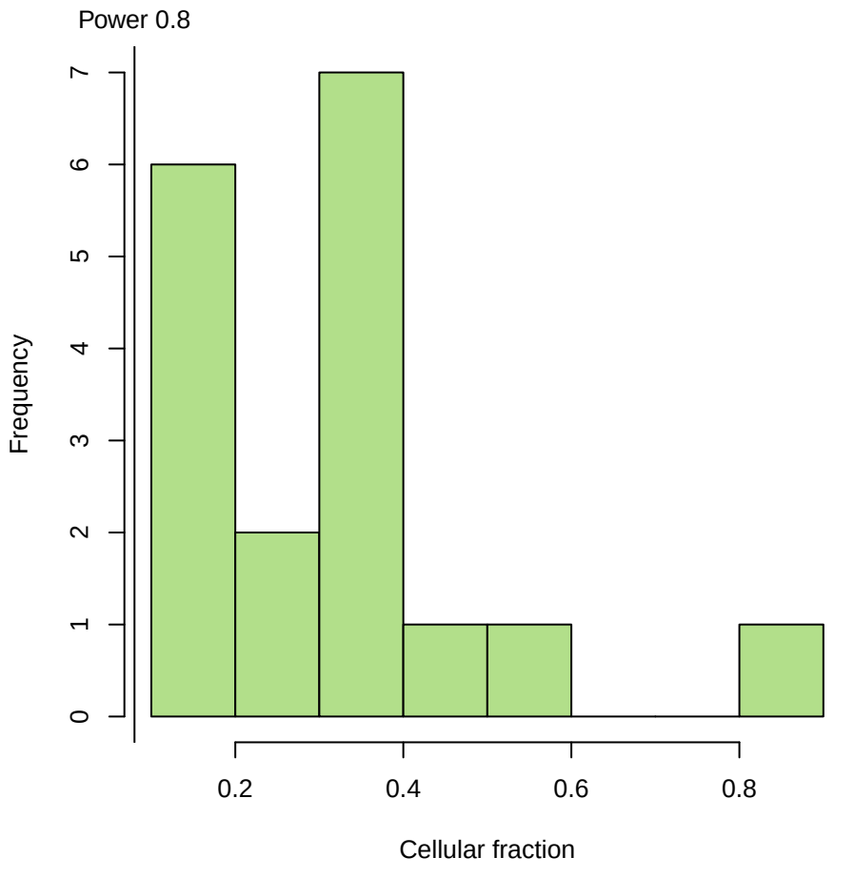

SCNA−fit log−likelihood: −10208.47
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 5 7
0 10 20 30 40 50 60 70
SNV Index

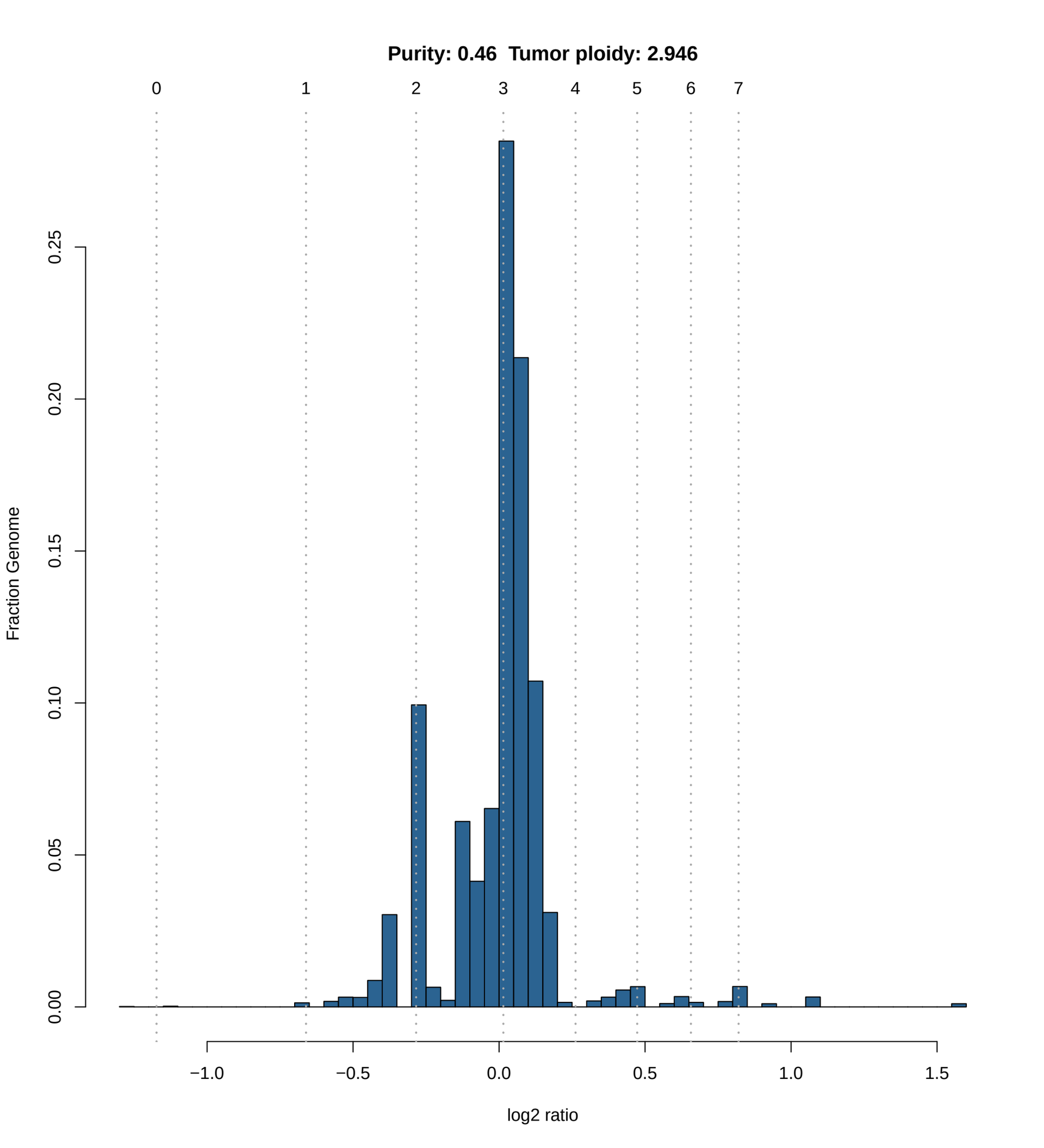

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 10 20 30 40 50 60 70
SNV Index

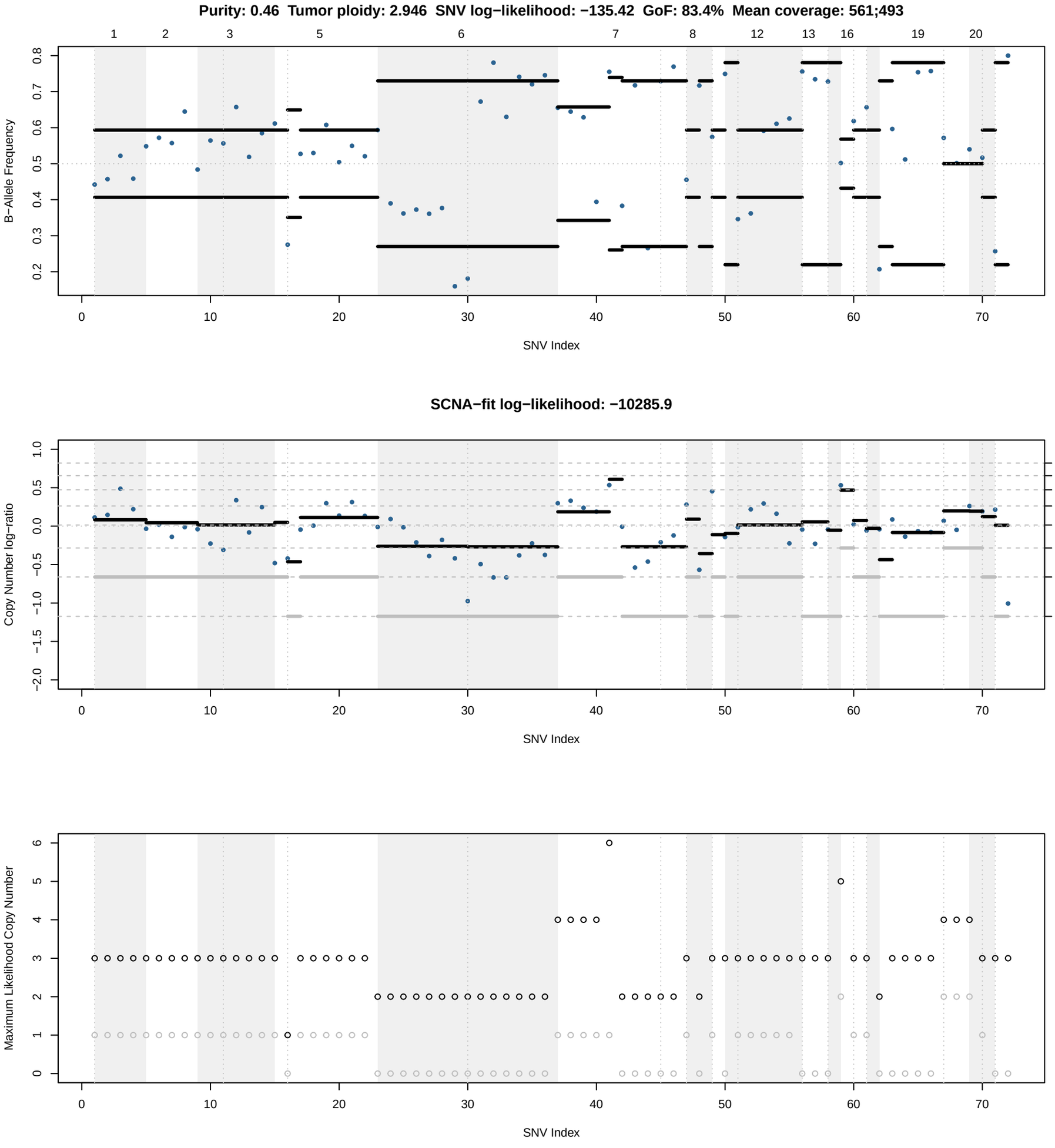

Allelic fraction (germline)
Copy Number log−ratio
0m0
1m0
1m1
2m0
2m1
2m2
3m1
3m2
4m2
5m4

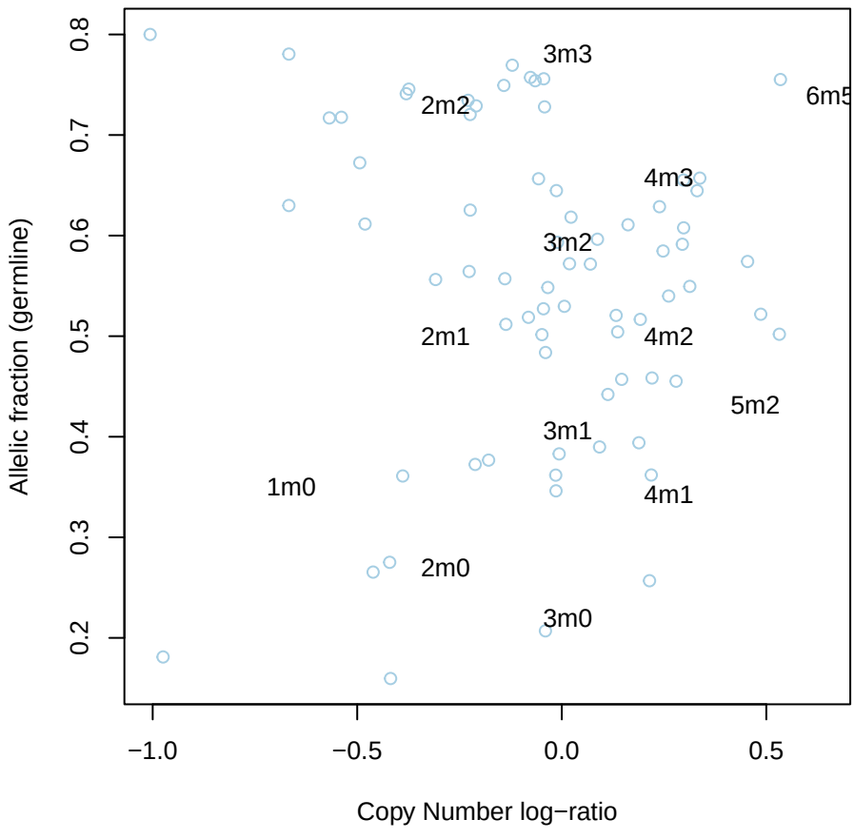

Coverage (log2)
Allelic fraction

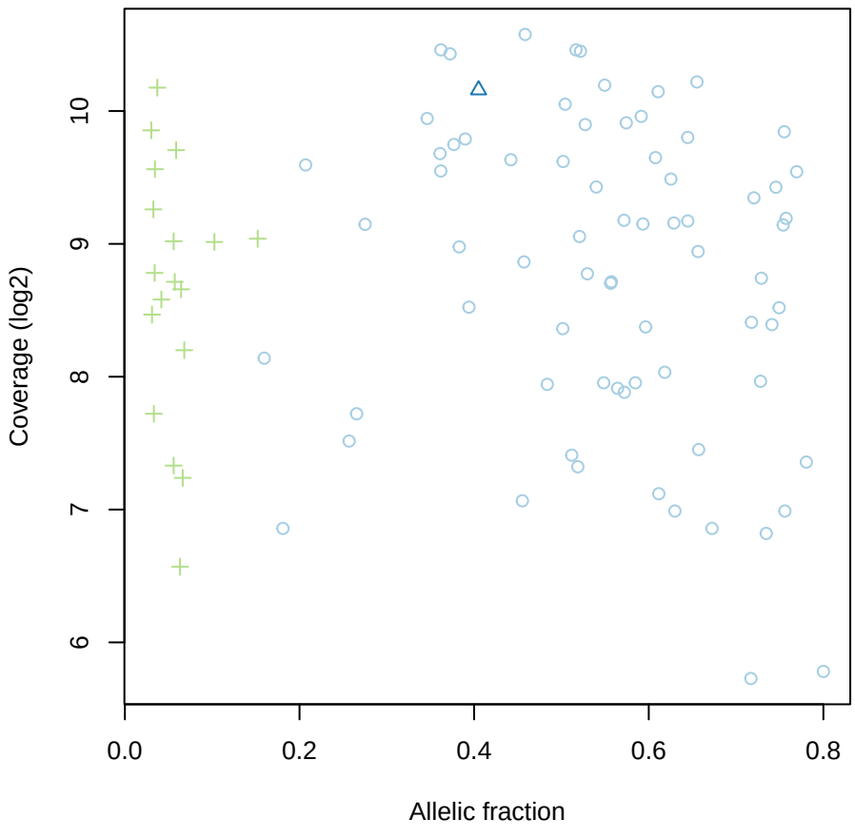

Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1
3m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

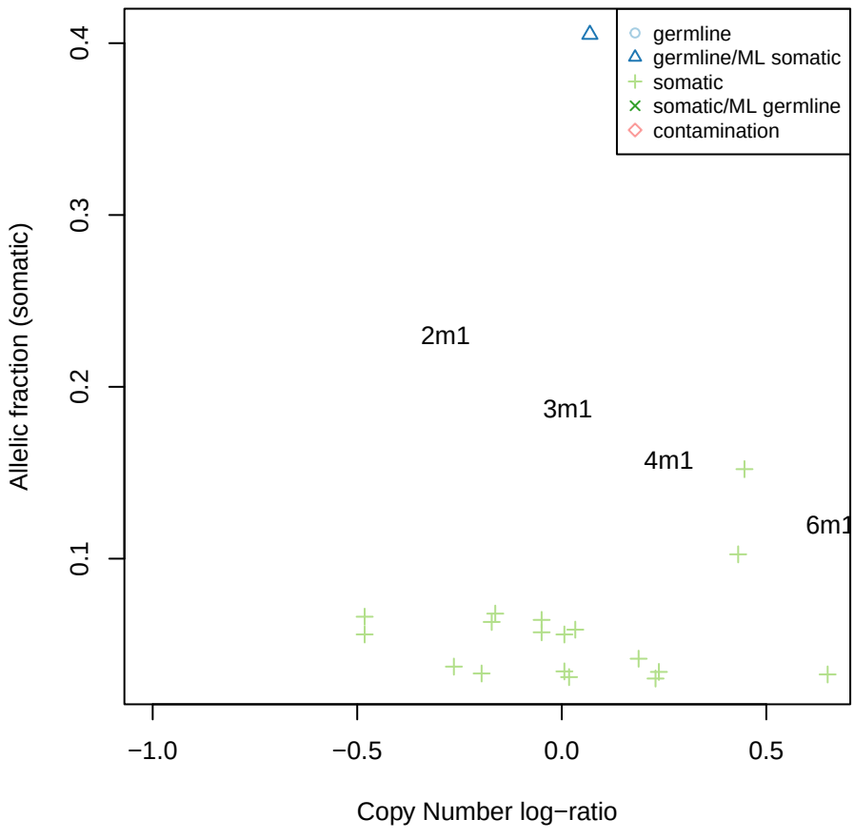

Power 0.8
Frequency
Cellular fraction

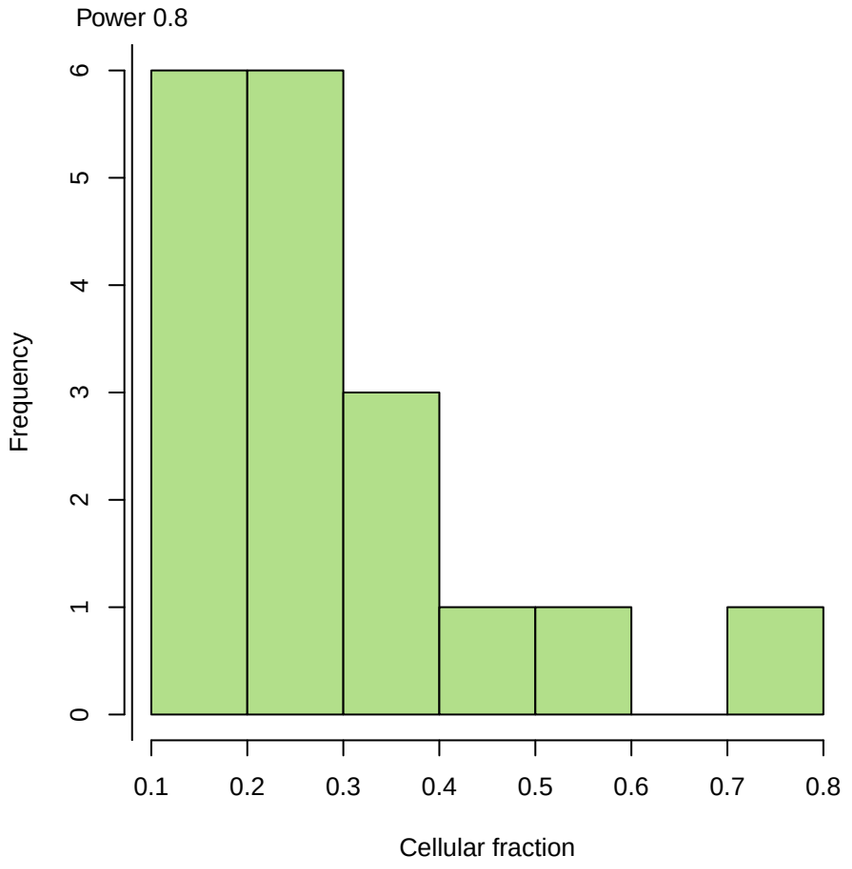

Purity: 0.46  Tumor ploidy: 2.946
0
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

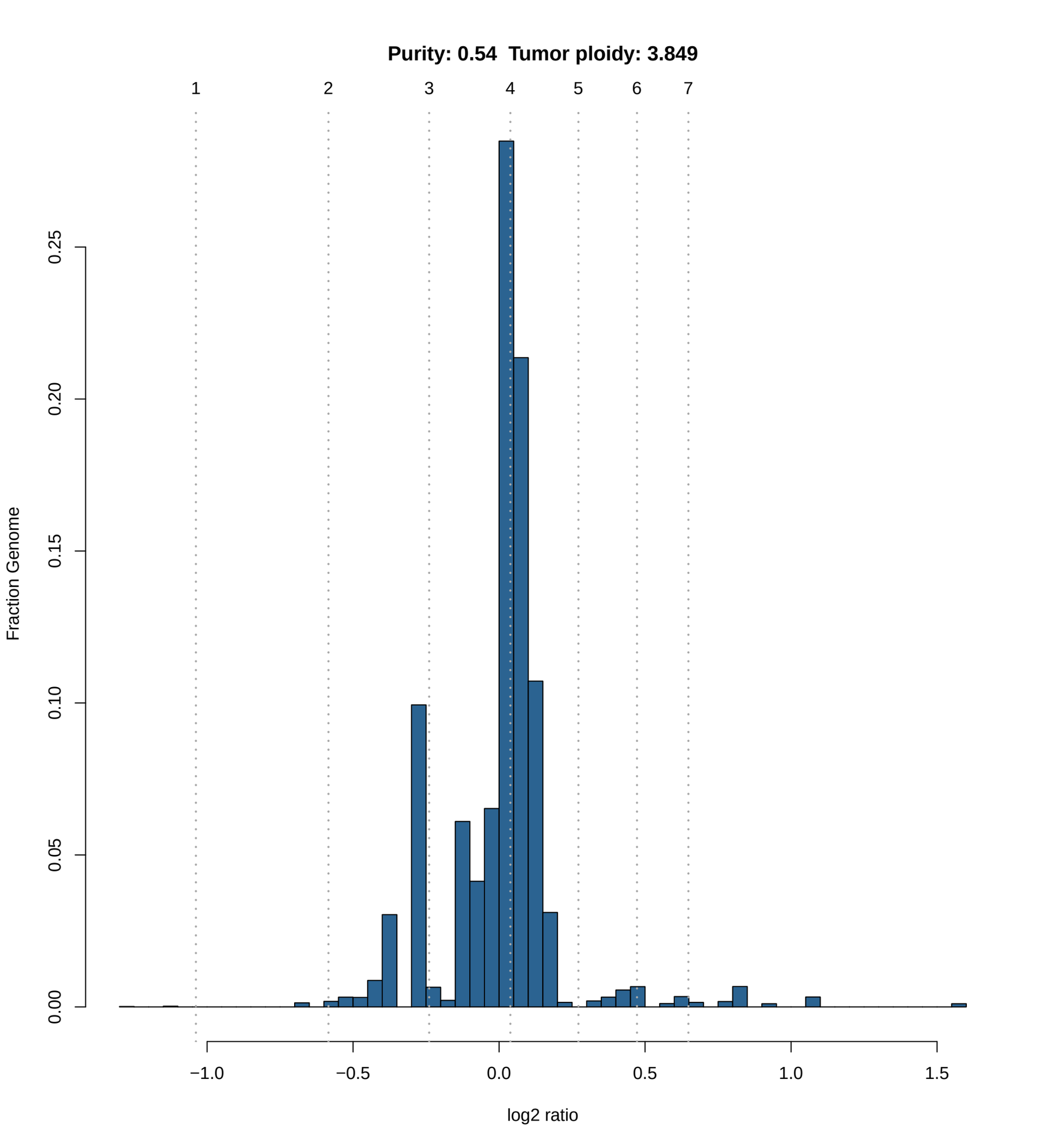

Purity: 0.46 Tumor ploidy: 2.946 SNV log−likelihood: −135.42 GoF: 83.4% Mean coverage: 561;493
1 2 3 5 6 7 8 12 13 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 10 20 30 40 50 60 70
SNV Index
SCNA−fit log−likelihood: −10285.9
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 6
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

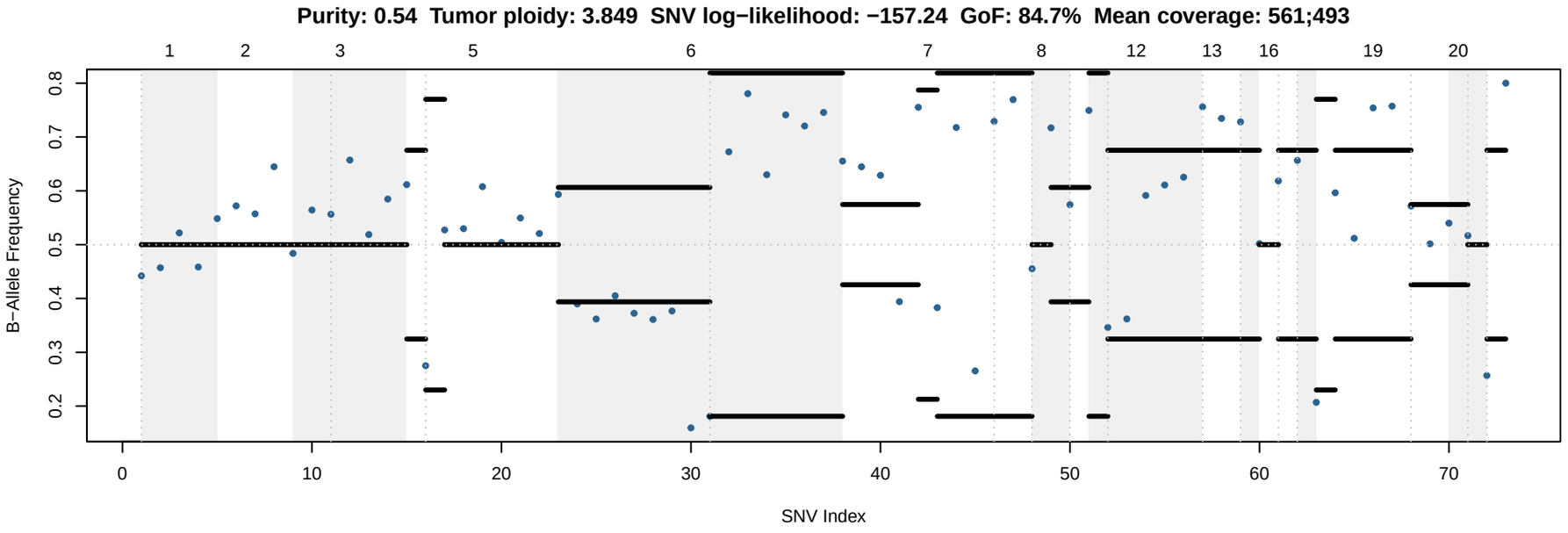

Allelic fraction (germline)
Copy Number log−ratio
3m3
2m2
6m5
4m3
3m2
2m1
4m2
5m2
3m1
1m0
4m1
2m0
3m0

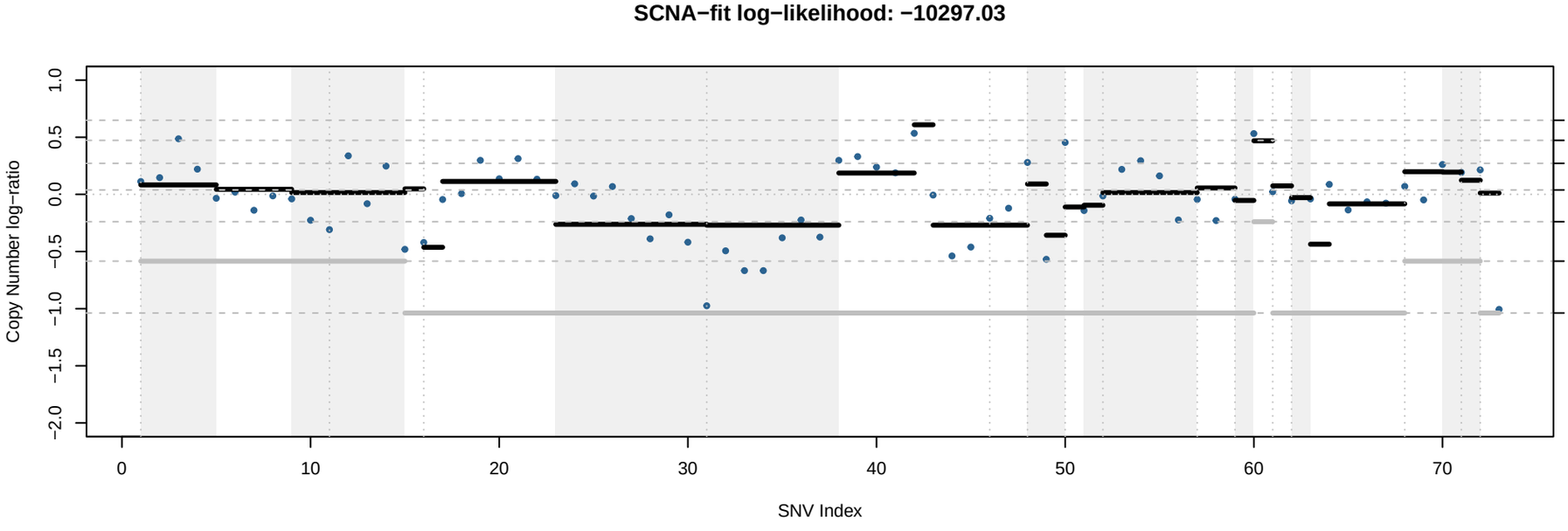

Coverage (log2)
Allelic fraction

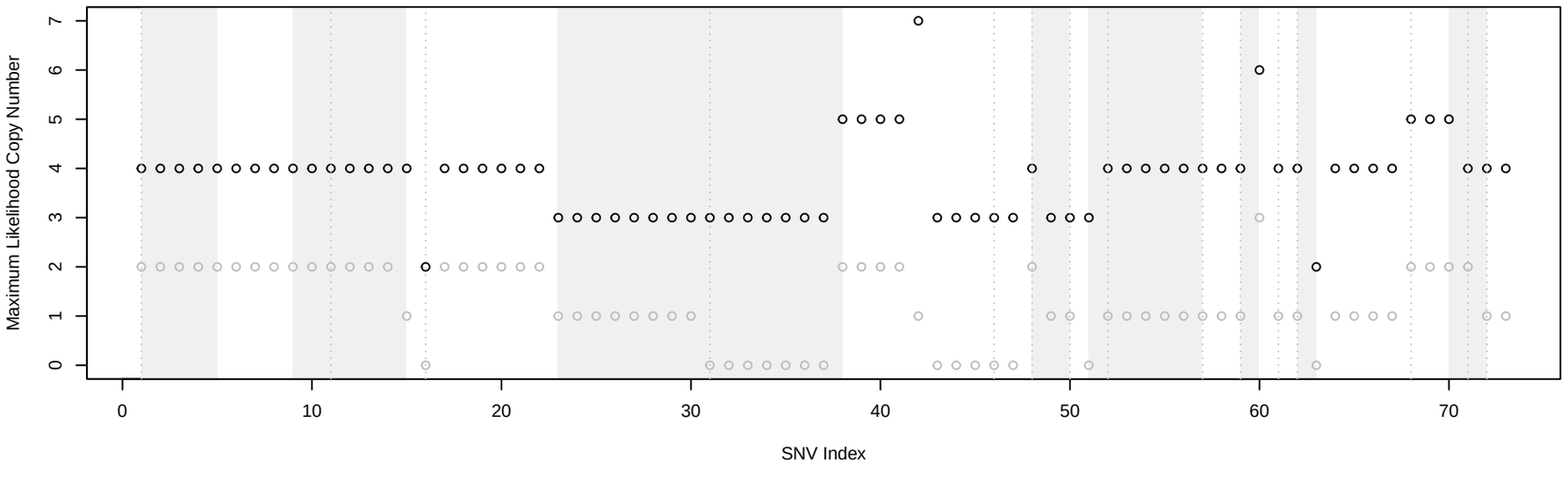

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m1
3m1
4m1
6m1

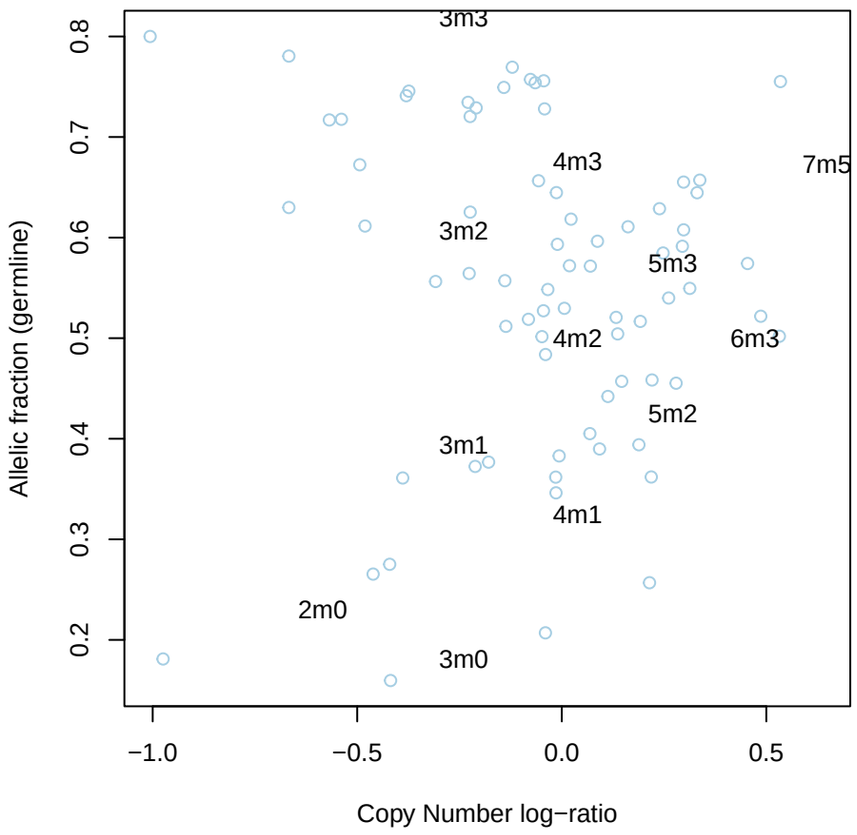

Power 0.8
Frequency
Cellular fraction

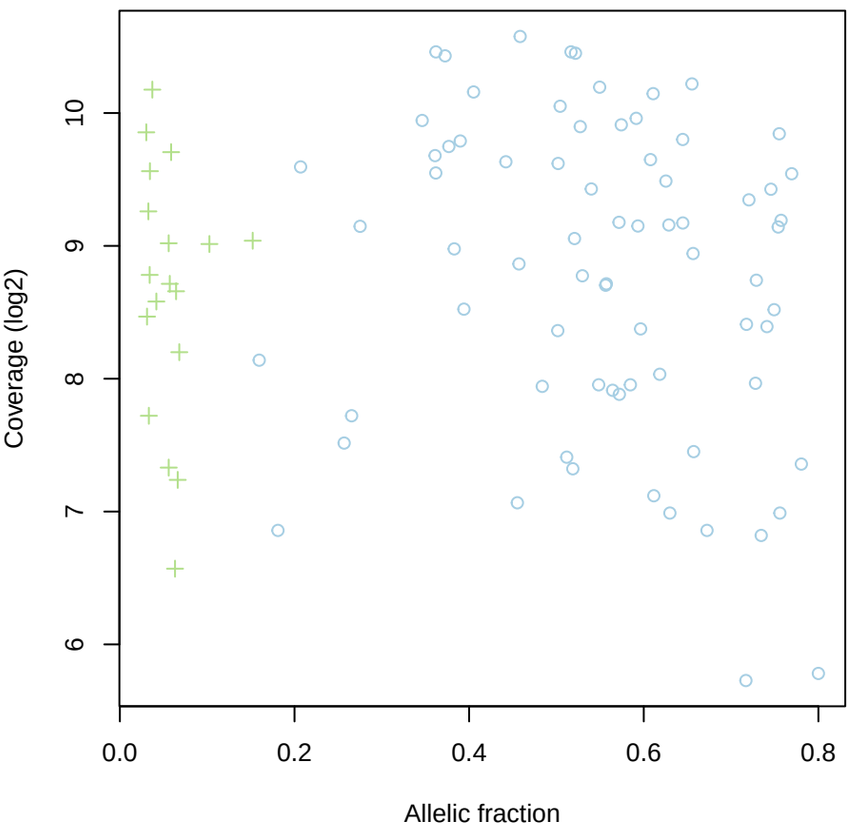

Purity: 0.54  Tumor ploidy: 3.849
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

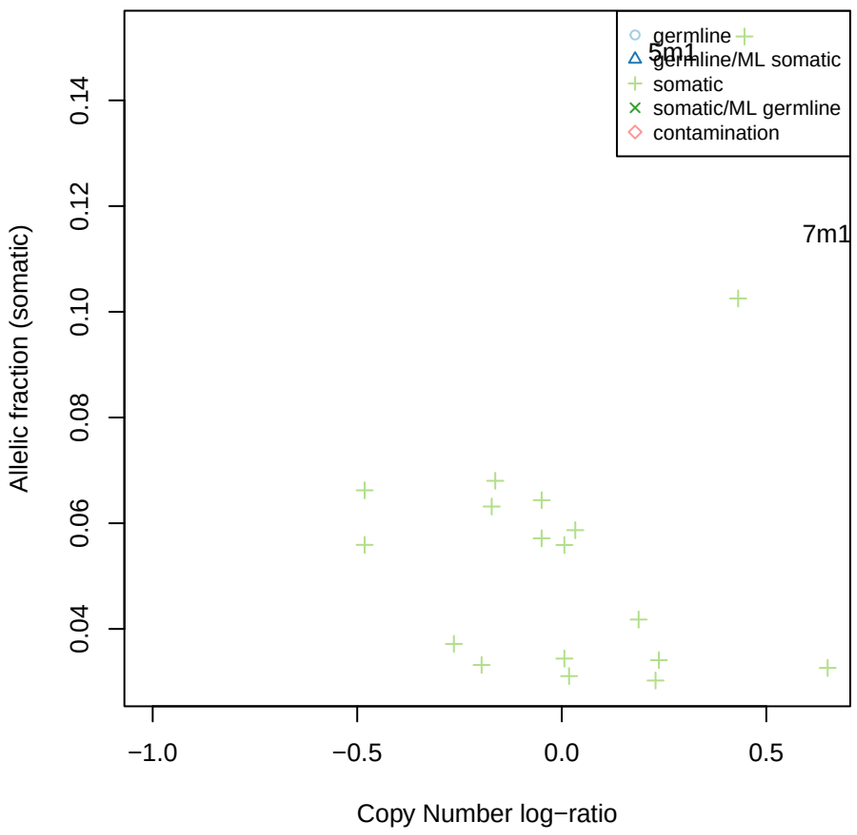

Purity: 0.54 Tumor ploidy: 3.849 SNV log−likelihood: −157.24 GoF: 84.7% Mean coverage: 561;493
1 2 3 5 6 7 8 12 13 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 10 20 30 40 50 60 70
SNV Index

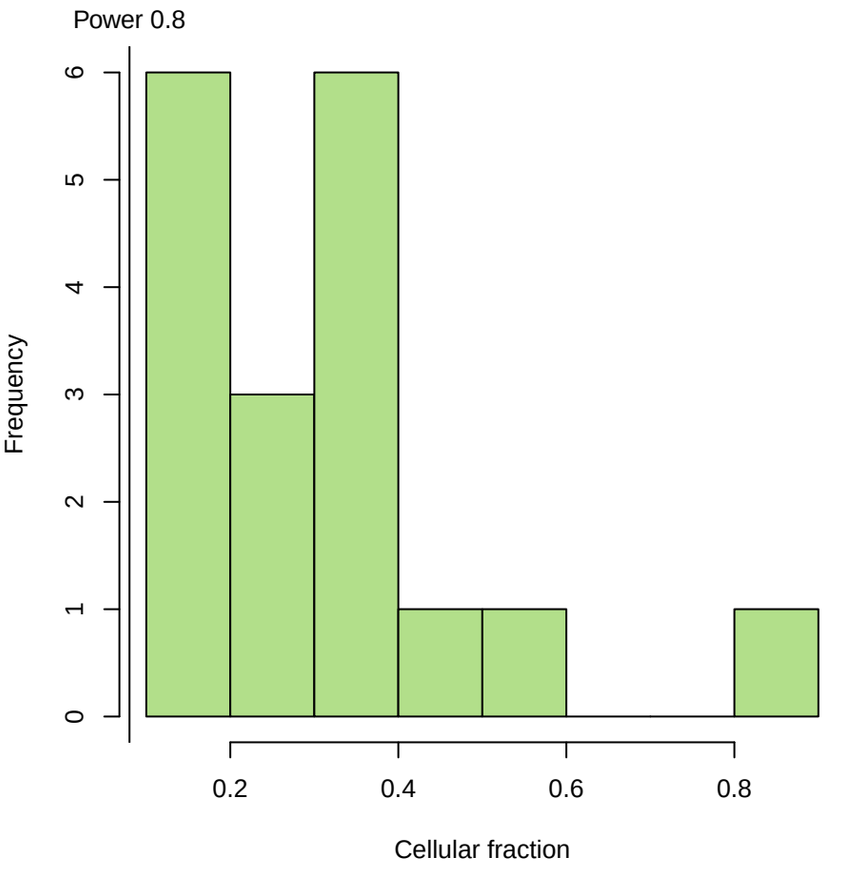

SCNA−fit log−likelihood: −10297.03
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 7
0 10 20 30 40 50 60 70
SNV Index

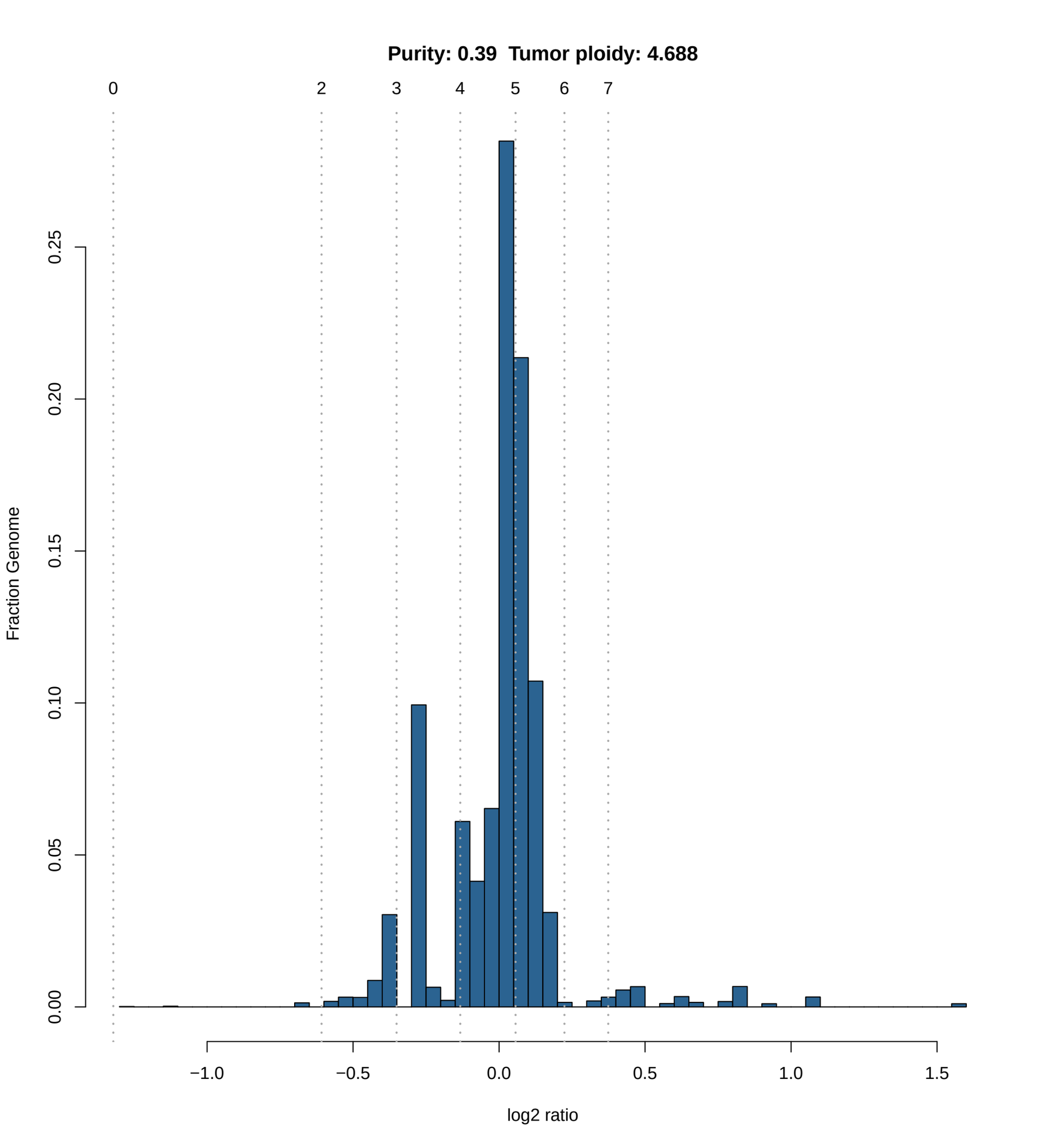

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 10 20 30 40 50 60 70
SNV Index

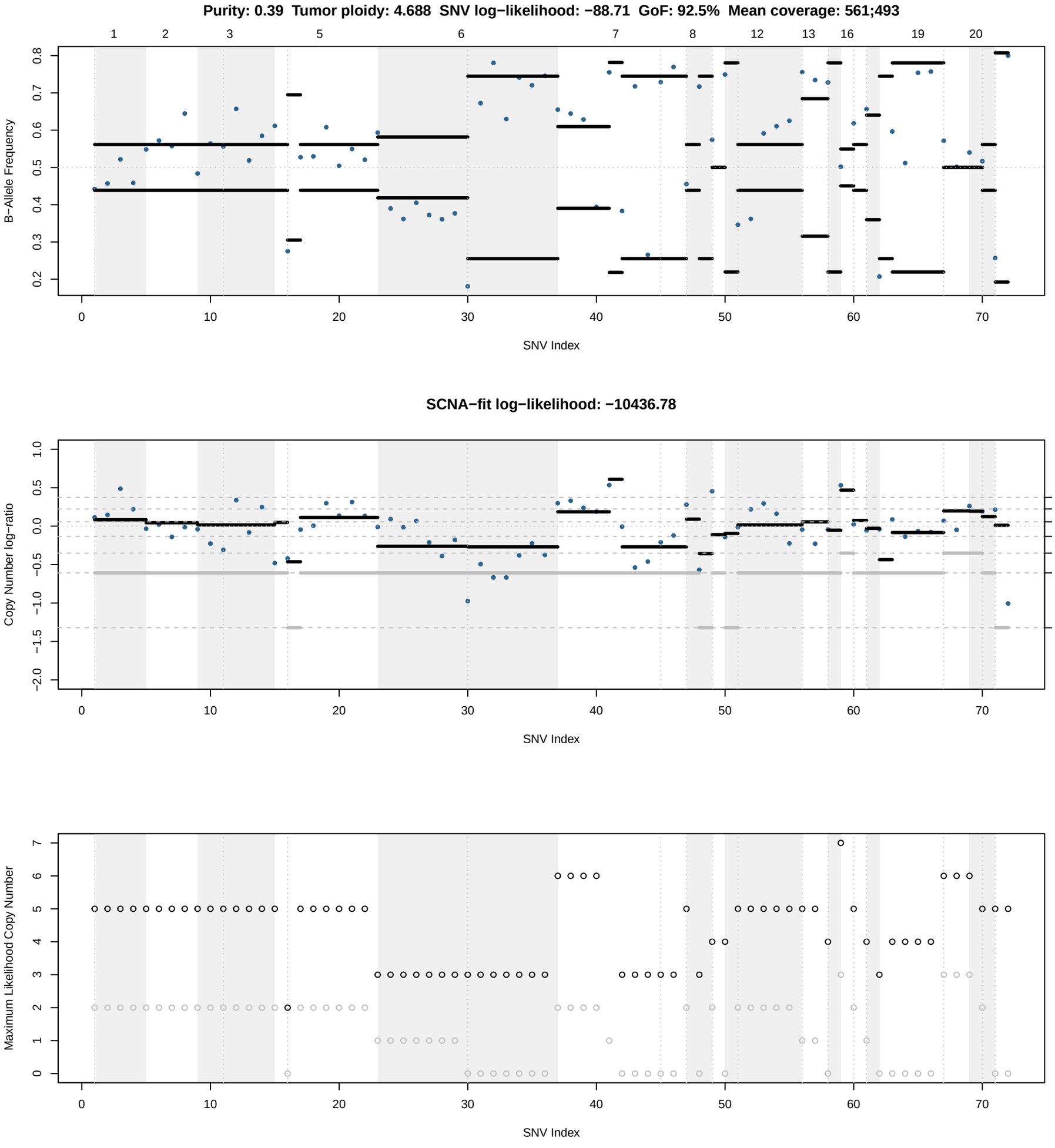

3m3
4m3
7m5
3m2
5m3
4m2
6m3
5m2
3m1
4m1
2m0
3m0
Allelic fraction (germline)
Copy Number log−ratio
0.2
0.3
0.4
0.5
0.6
0.7
0.8
−1.0
−0.5
0.0
0.5

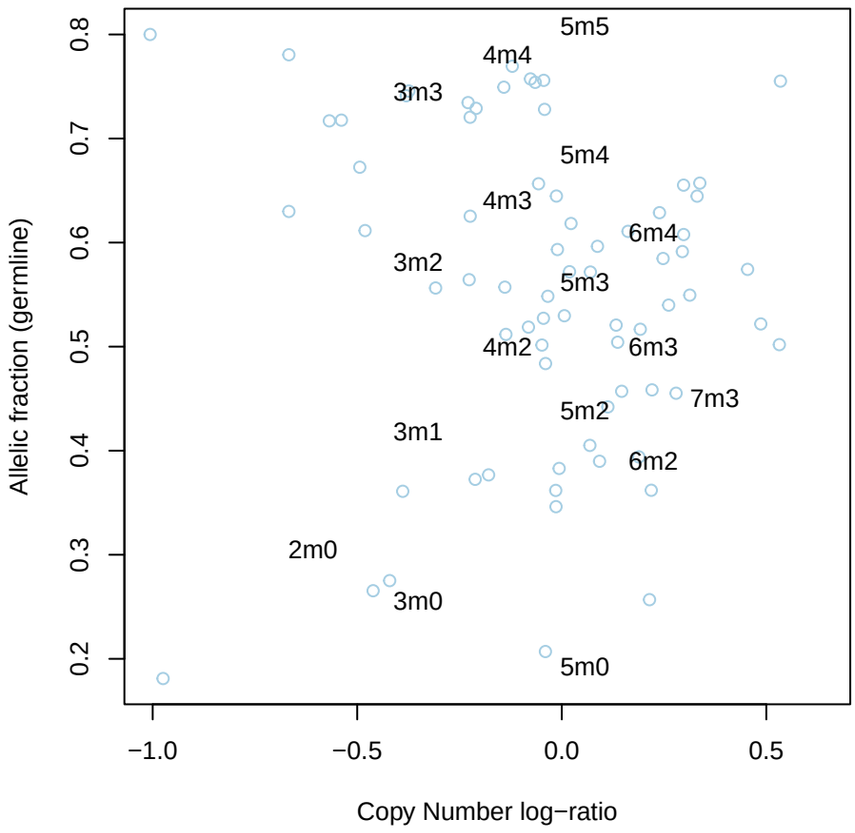

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.0
0.2
0.4
0.6
0.8

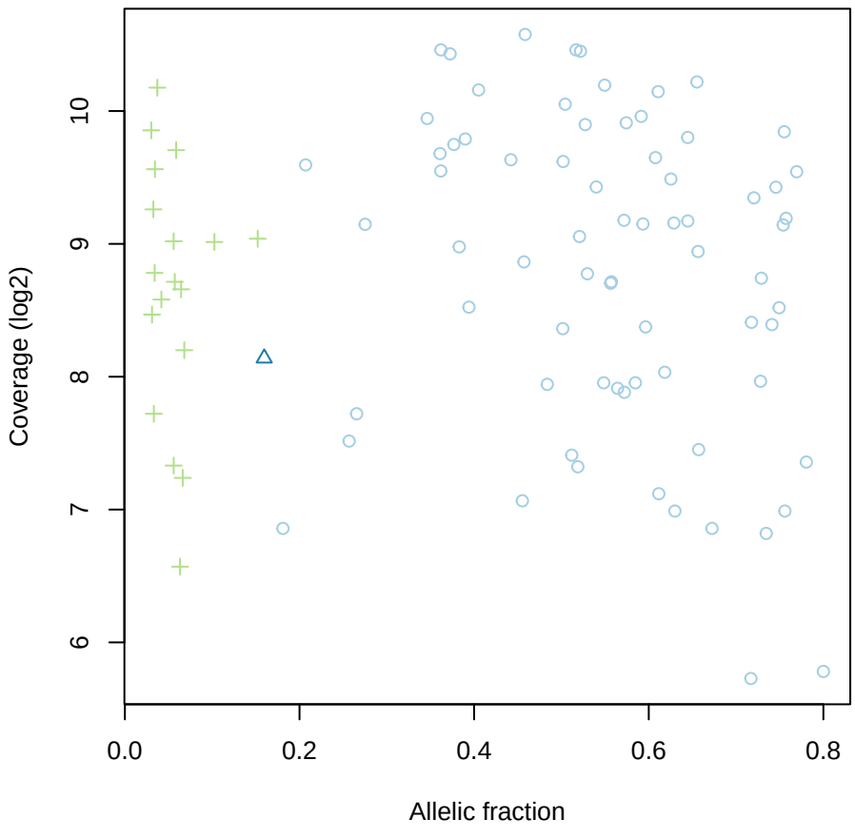

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
0.12
0.14
−1.0
−0.5
0.0
0.5

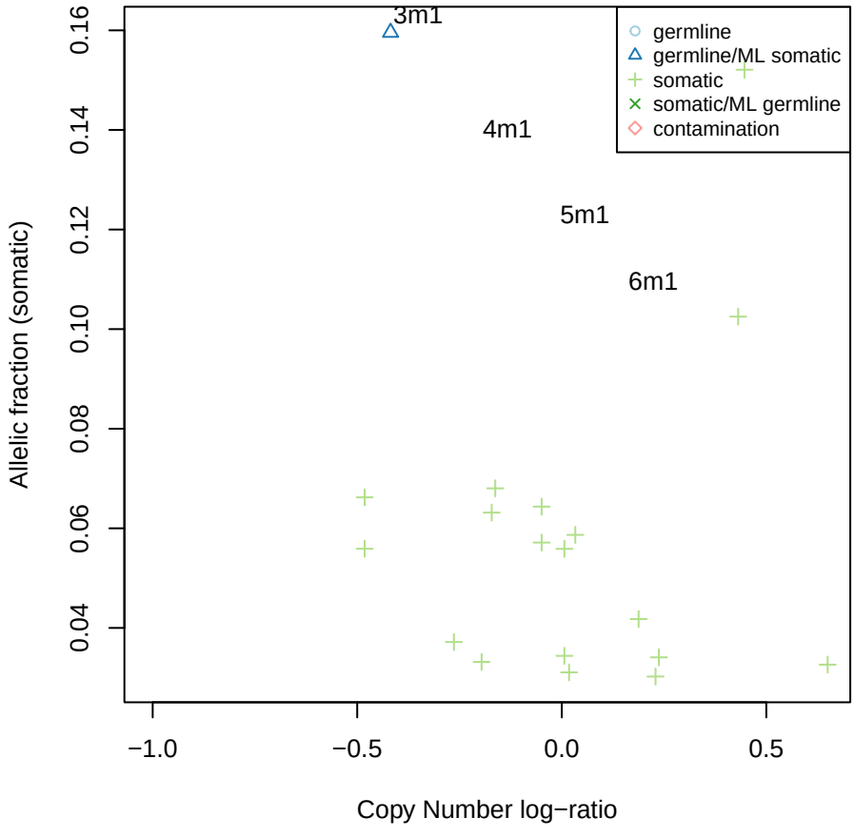

Power 0.8
Frequency
Cellular fraction
0
1
2
3
4
5
6
0.2
0.4
0.6
0.8

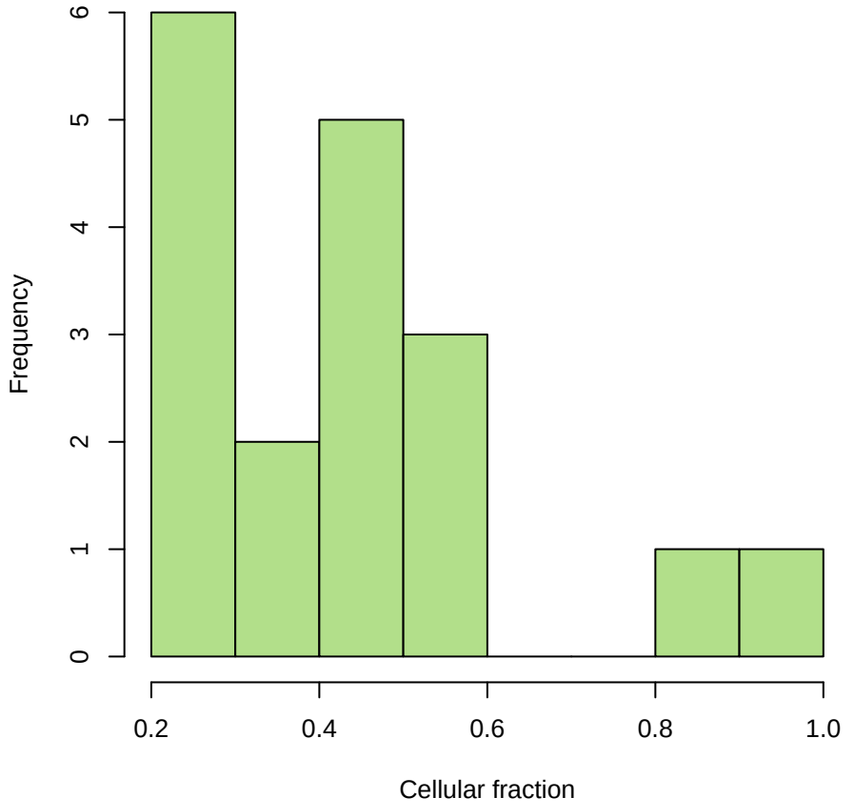

Purity: 0.39 Tumor ploidy: 4.688
0
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

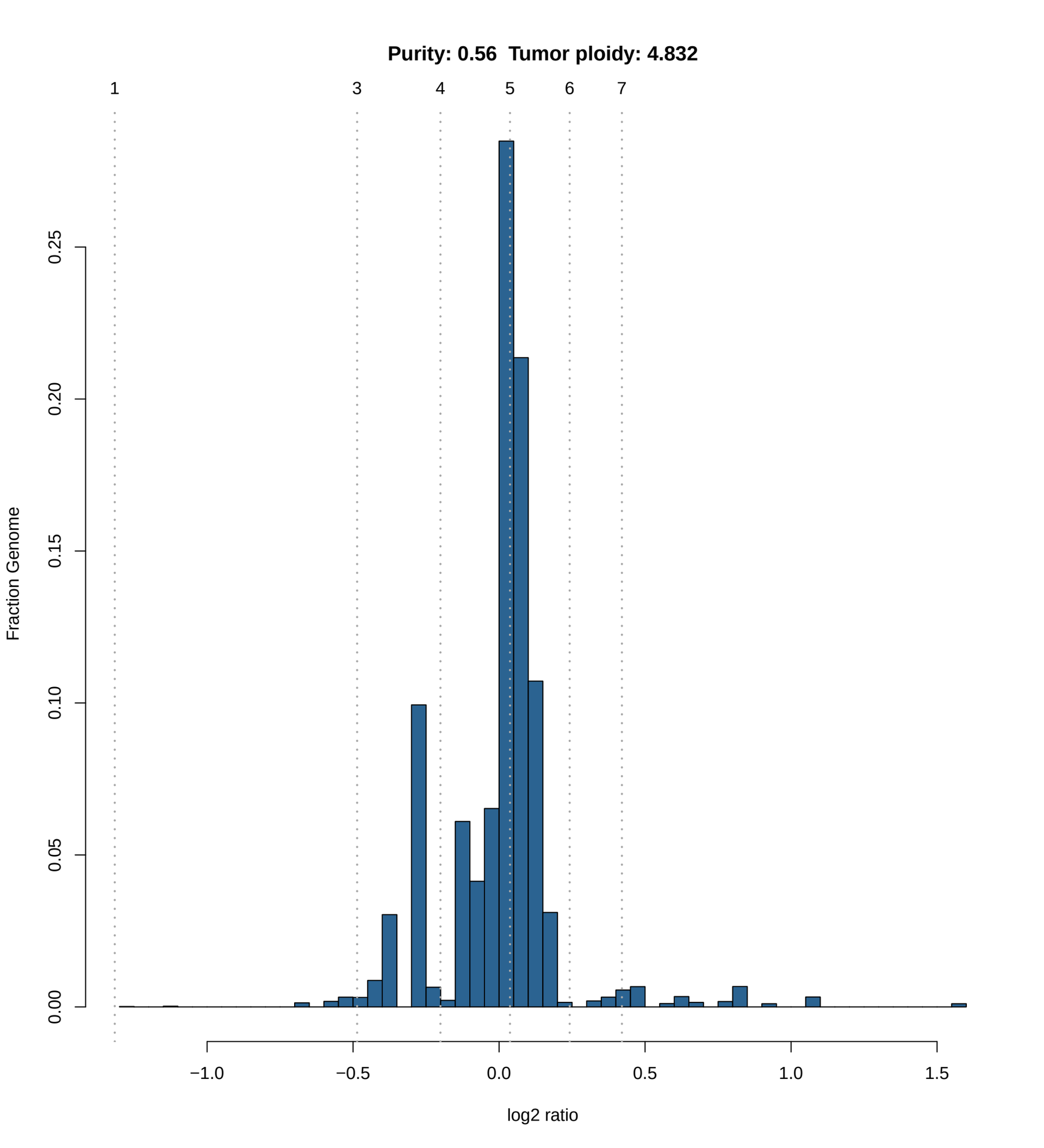

Purity: 0.39 Tumor ploidy: 4.688 SNV log−likelihood: −88.71 GoF: 92.5% Mean coverage: 561;493
1 2 3 5 6 7 8 12 13 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 10 20 30 40 50 60 70
SNV Index
SCNA−fit log−likelihood: −10436.78
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 2 3 4 6
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

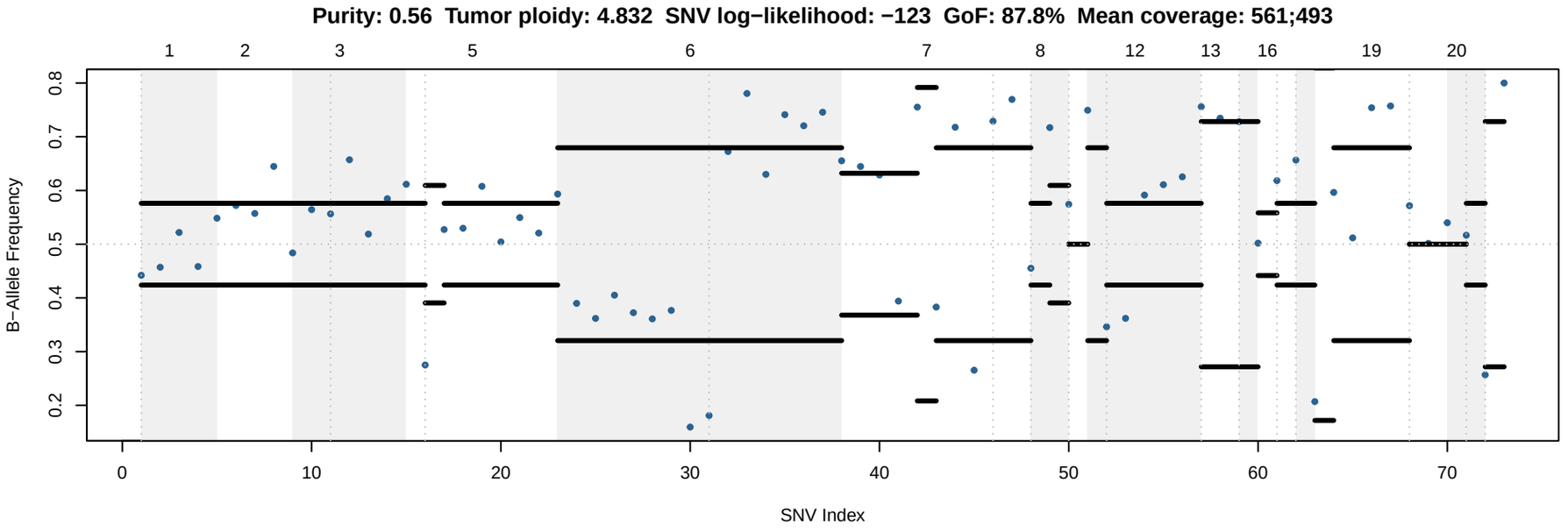

Allelic fraction (germline)
Copy Number log−ratio
5m5
4m4
3m3
5m4
4m3
6m4
3m2
5m3
4m2
6m3
7m3
5m2
3m1
6m2
2m0
3m0
5m0

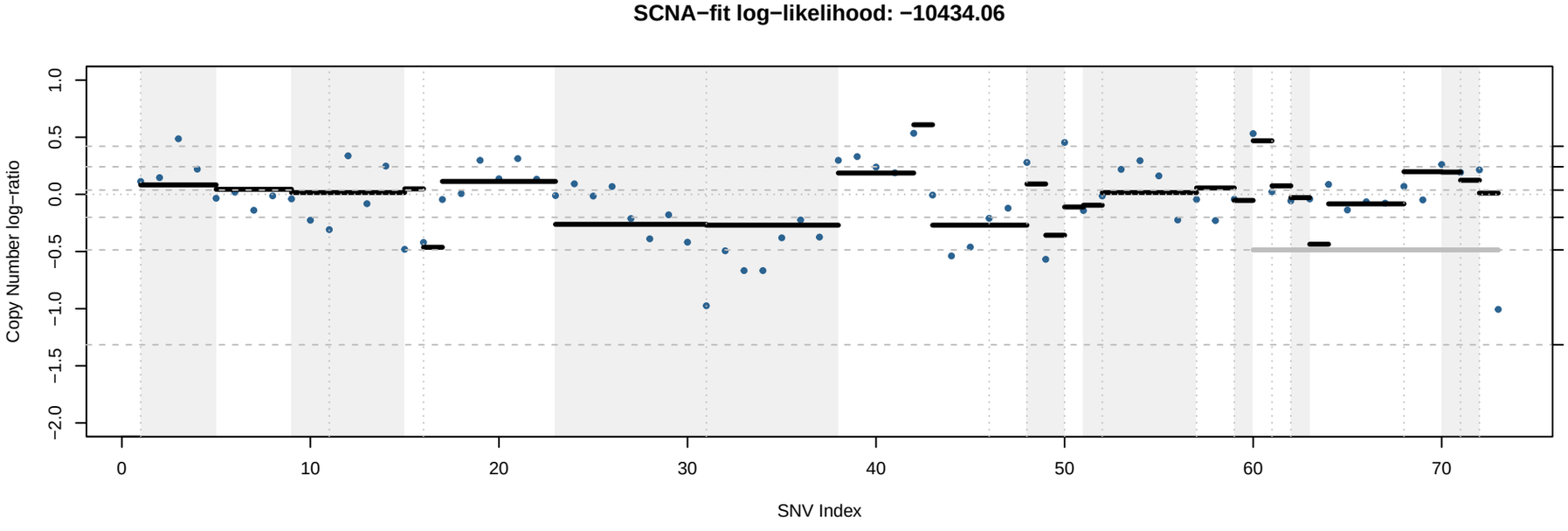

Coverage (log2)
Allelic fraction

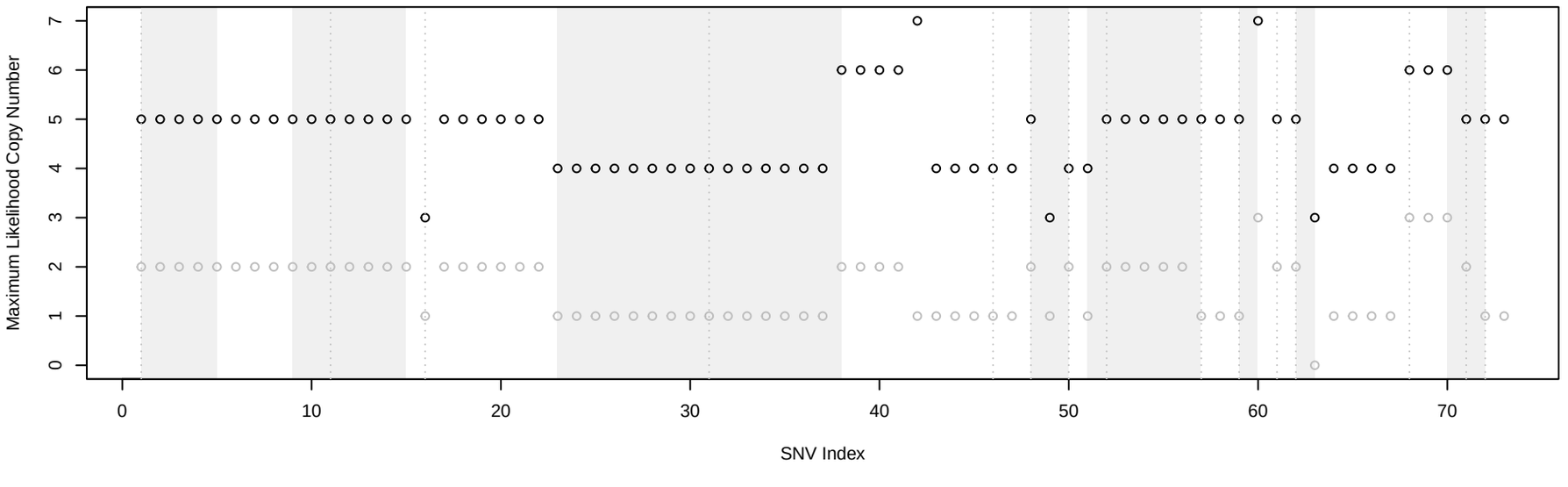

Allelic fraction (somatic)
Copy Number log−ratio
3m1
4m1
5m1
6m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

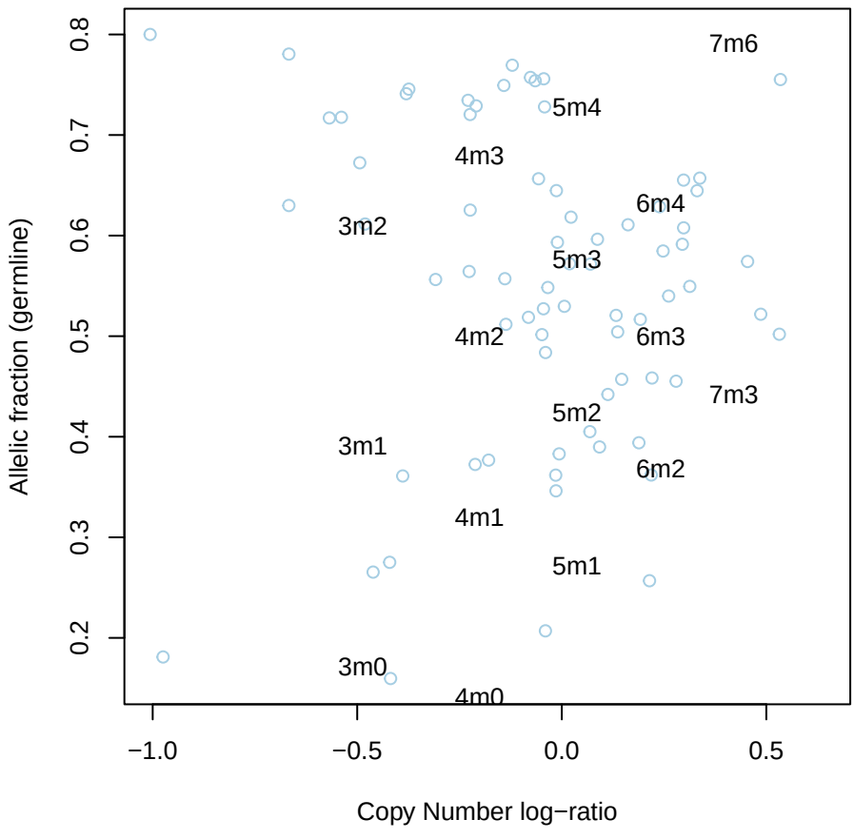

Frequency
Cellular fraction

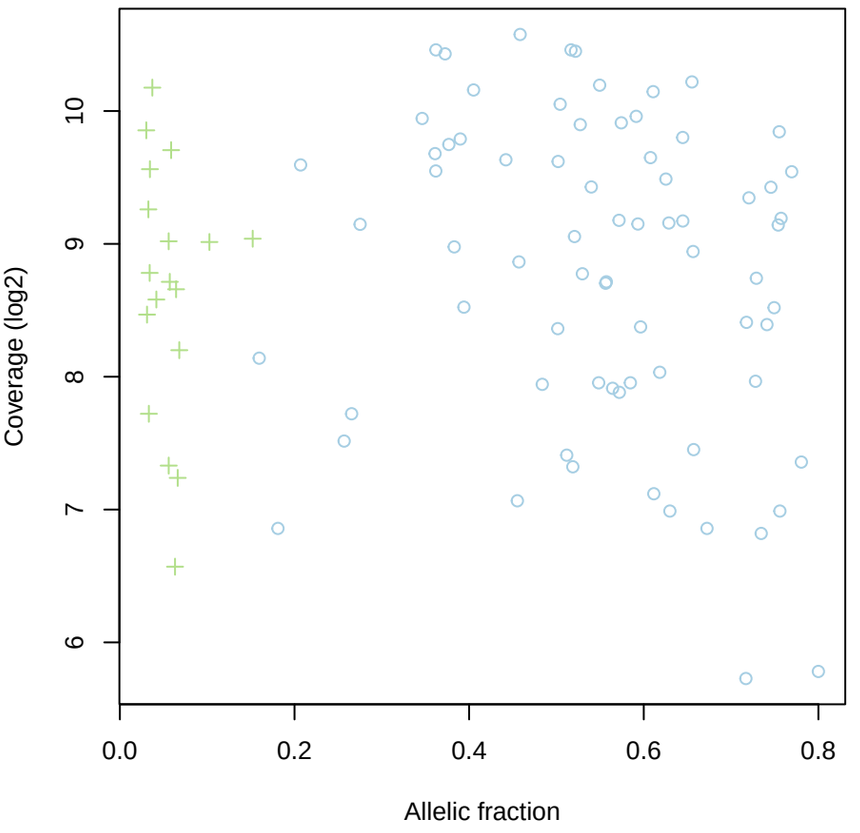

Purity: 0.56  Tumor ploidy: 4.832
1
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

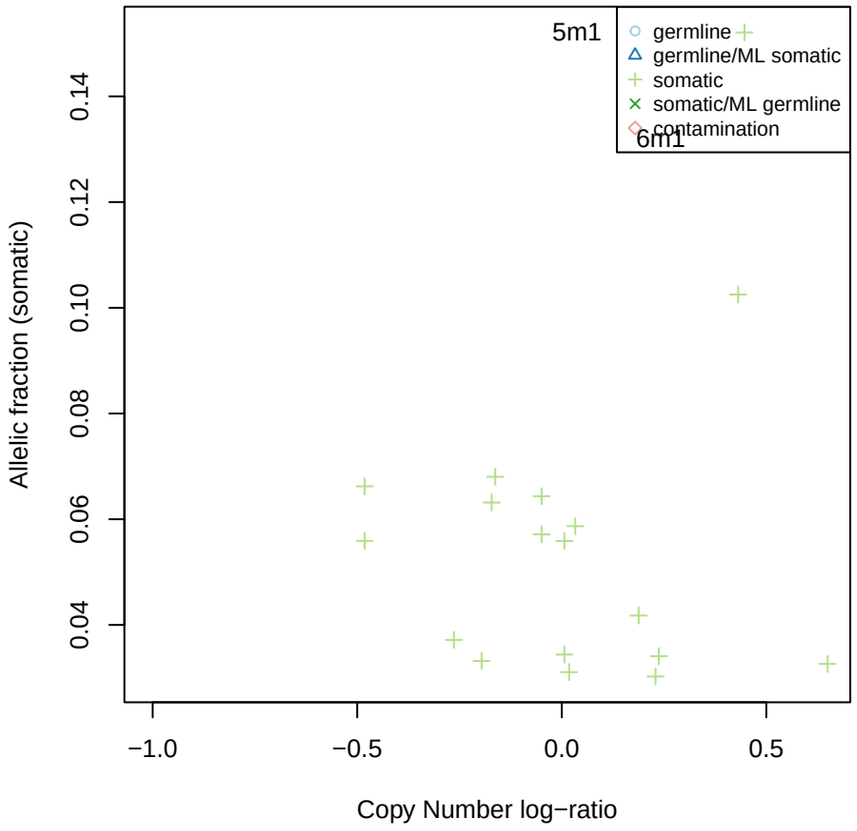

Purity: 0.56 Tumor ploidy: 4.832 SNV log−likelihood: −123 GoF: 87.8% Mean coverage: 561;493
1 2 3 5 6 7 8 12 13 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 10 20 30 40 50 60 70
SNV Index

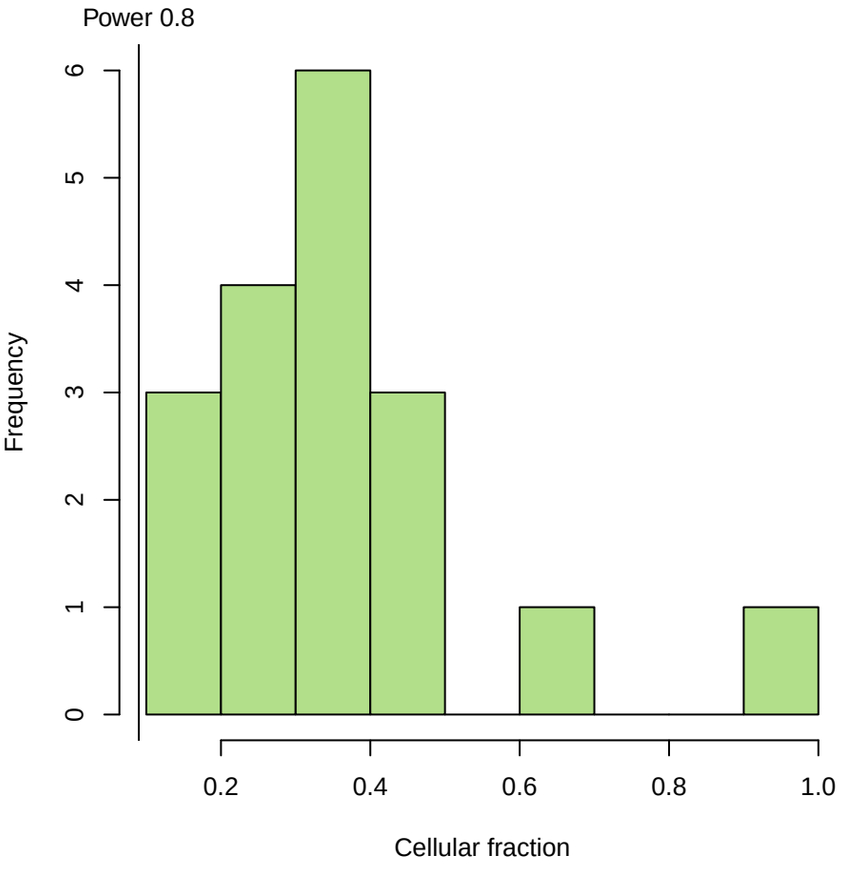

SCNA−fit log−likelihood: −10434.06
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
1 3 4 5 7
0 10 20 30 40 50 60 70
SNV Index

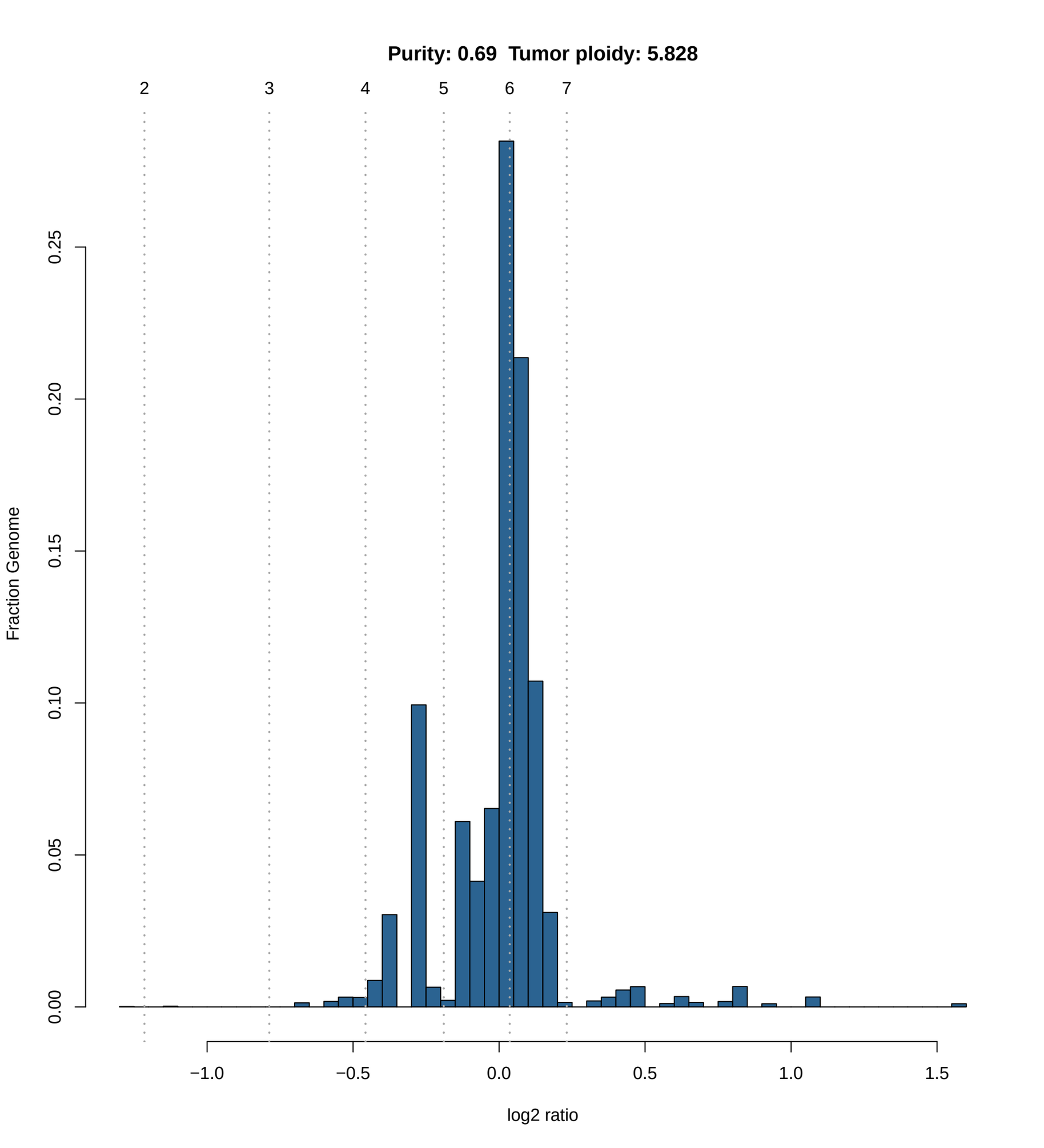

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 10 20 30 40 50 60 70
SNV Index

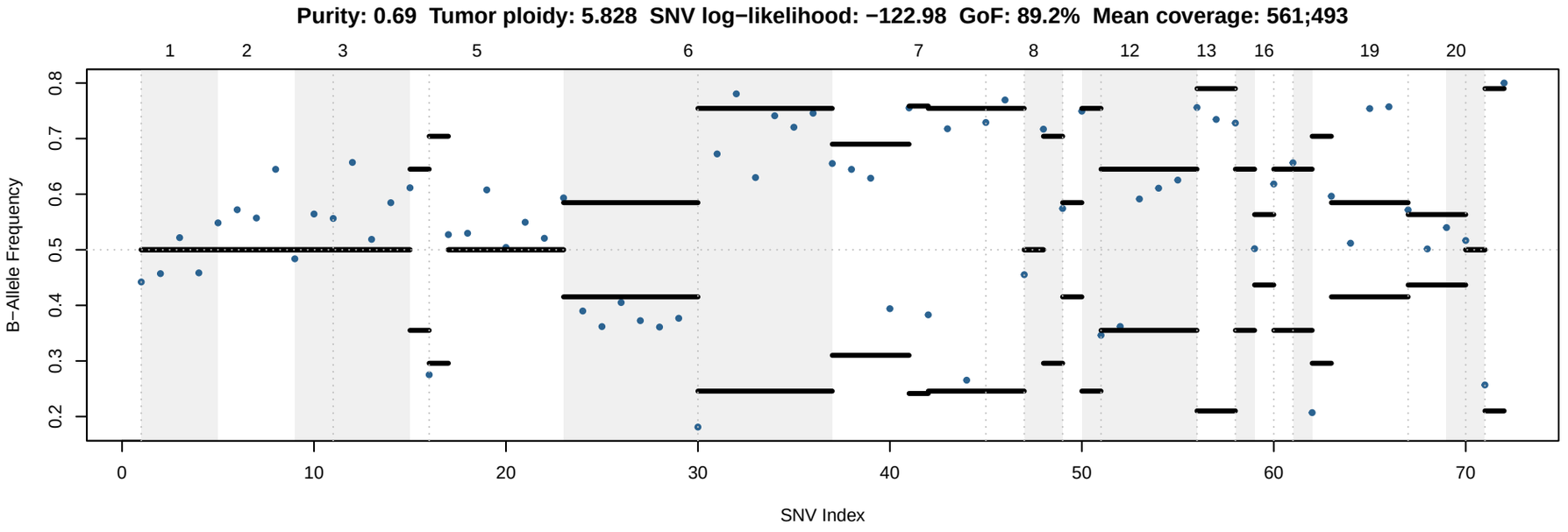

Allelic fraction (germline)
Copy Number log−ratio
7m6
5m4
4m3
6m4
3m2
5m3
4m2
6m3
7m3
5m2
3m1
6m2
4m1
5m1
3m0
4m0

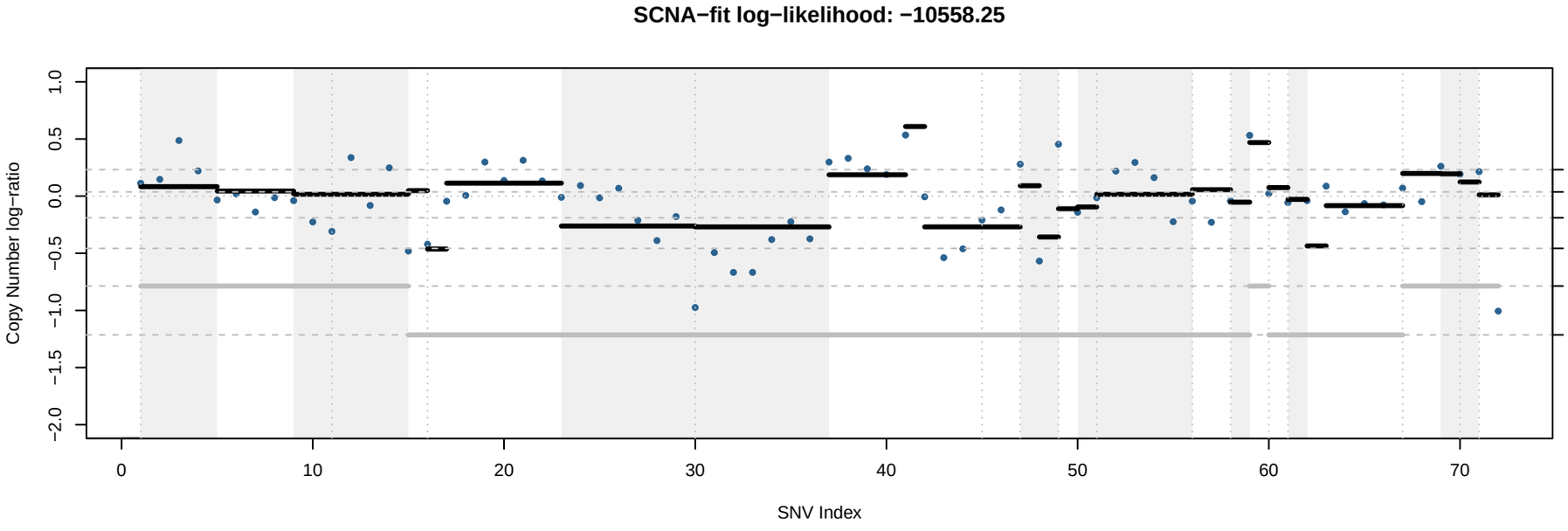

Coverage (log2)
Allelic fraction

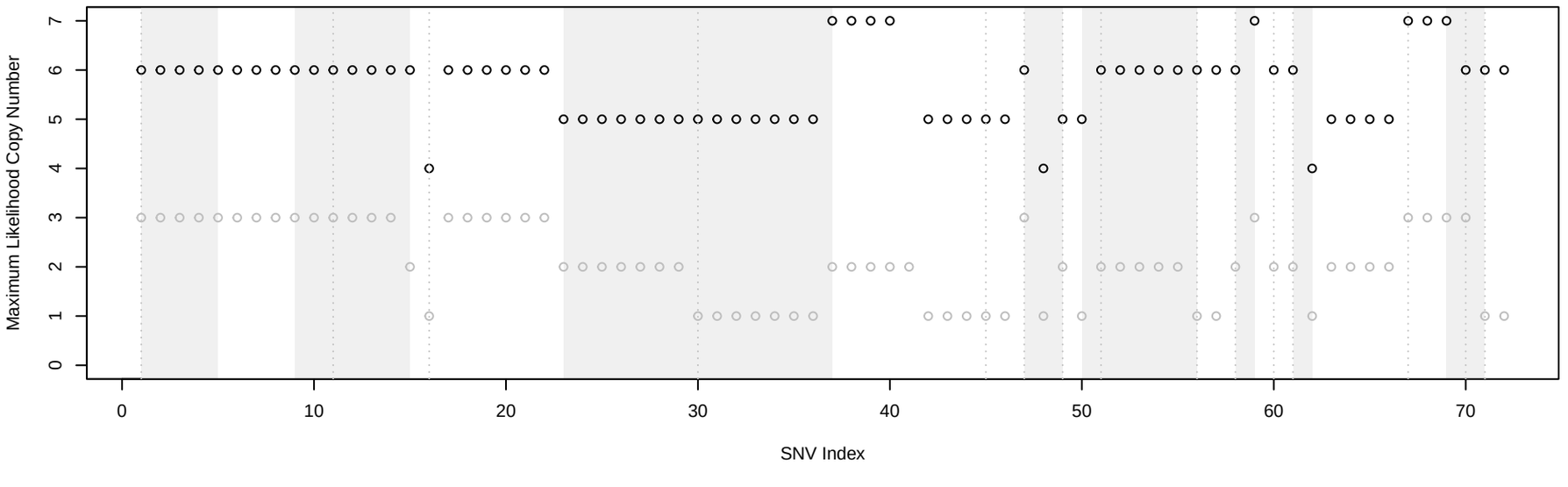

Allelic fraction (somatic)
Copy Number log−ratio
5m1
6m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

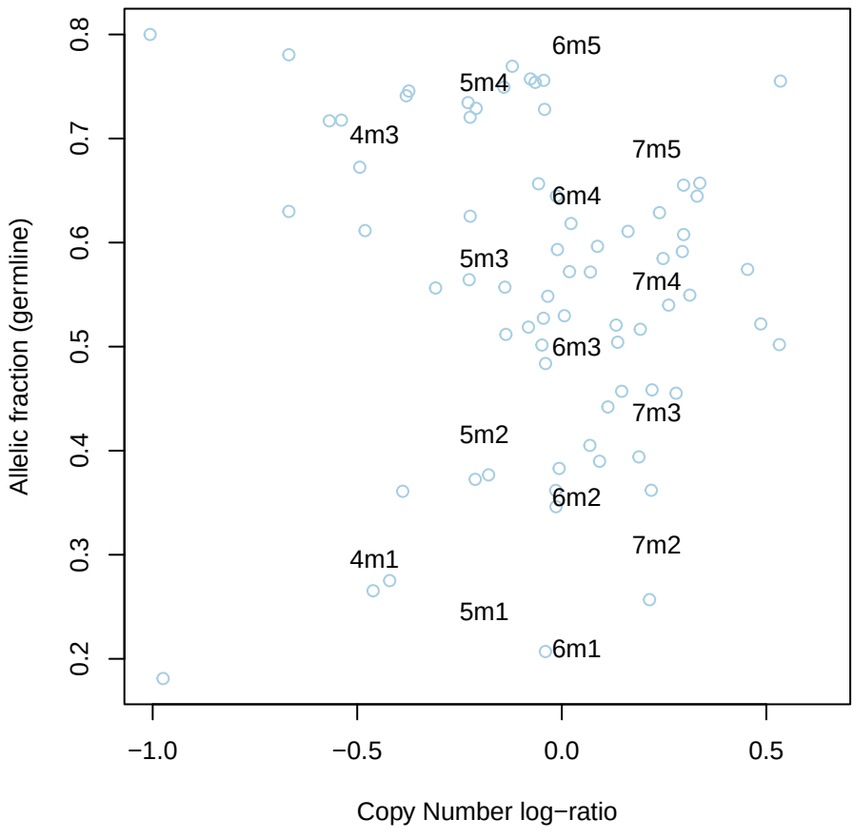

Power 0.8
Frequency
Cellular fraction

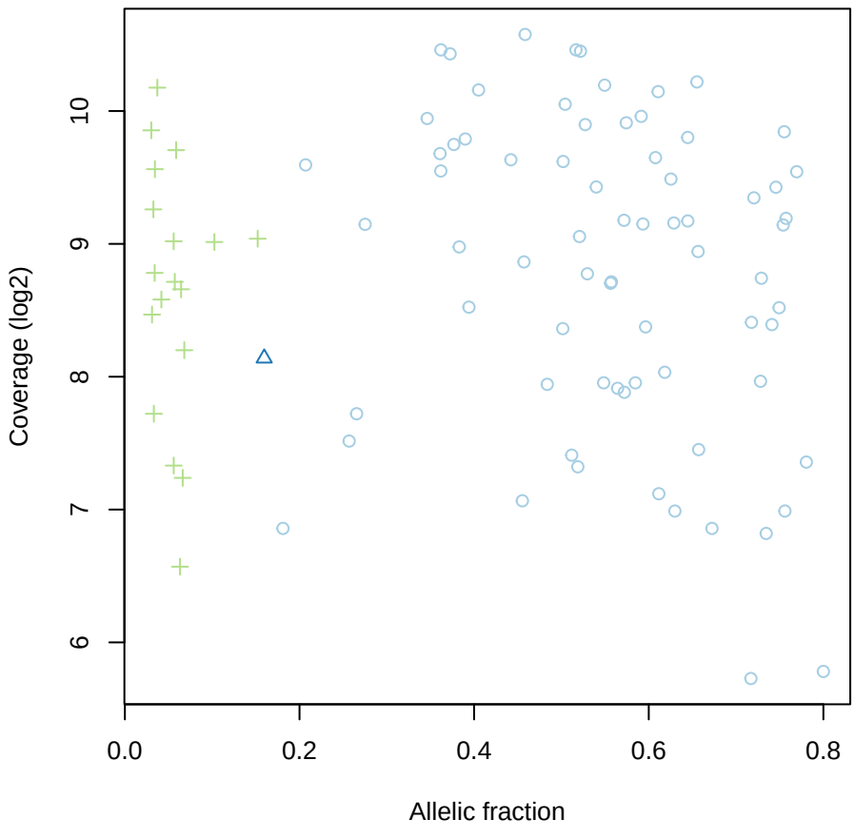

Purity: 0.69  Tumor ploidy: 5.828
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

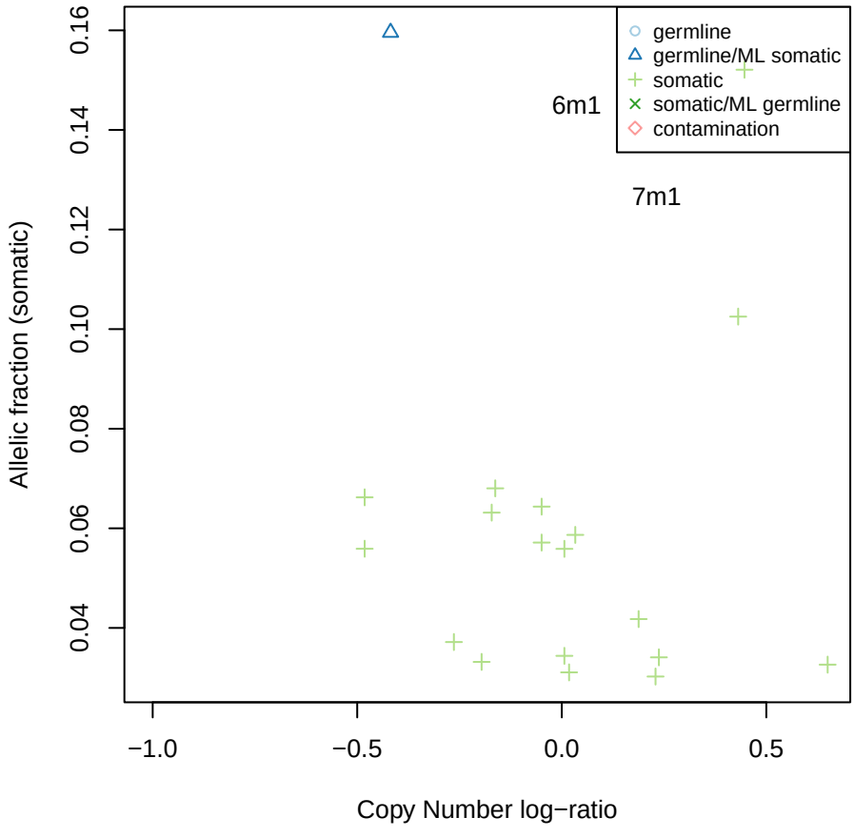

Purity: 0.69 Tumor ploidy: 5.828 SNV log−likelihood: −122.98 GoF: 89.2% Mean coverage: 561;493
1 2 3 5 6 7 8 12 13 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 10 20 30 40 50 60 70
SNV Index

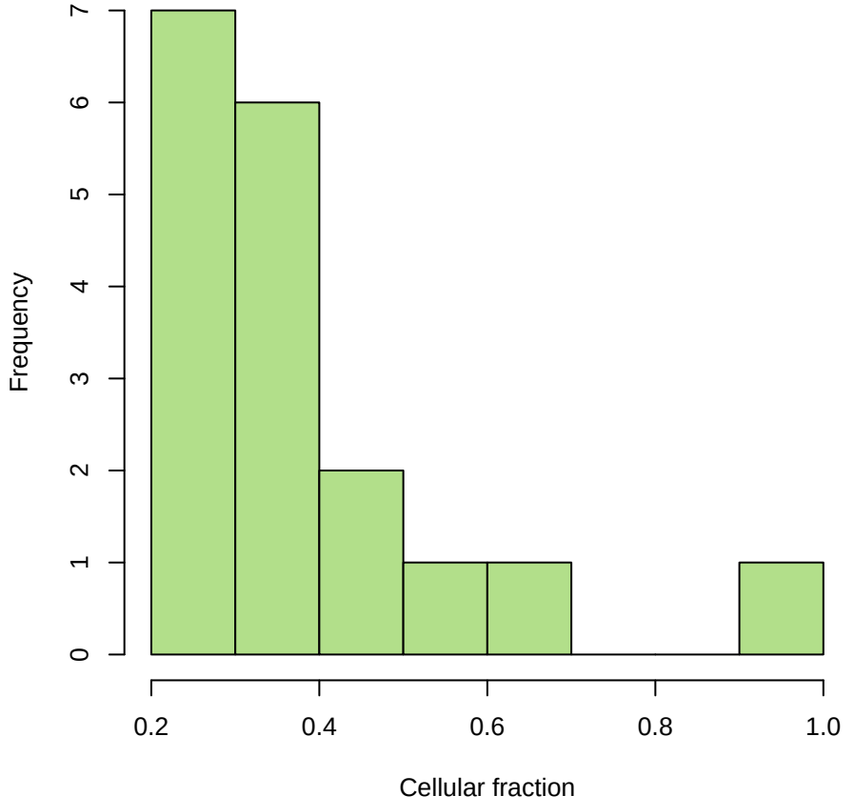

SCNA−fit log−likelihood: −10558.25
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0 −1.5 −2.0
2 3 4 5 6
0 10 20 30 40 50 60 70
SNV Index

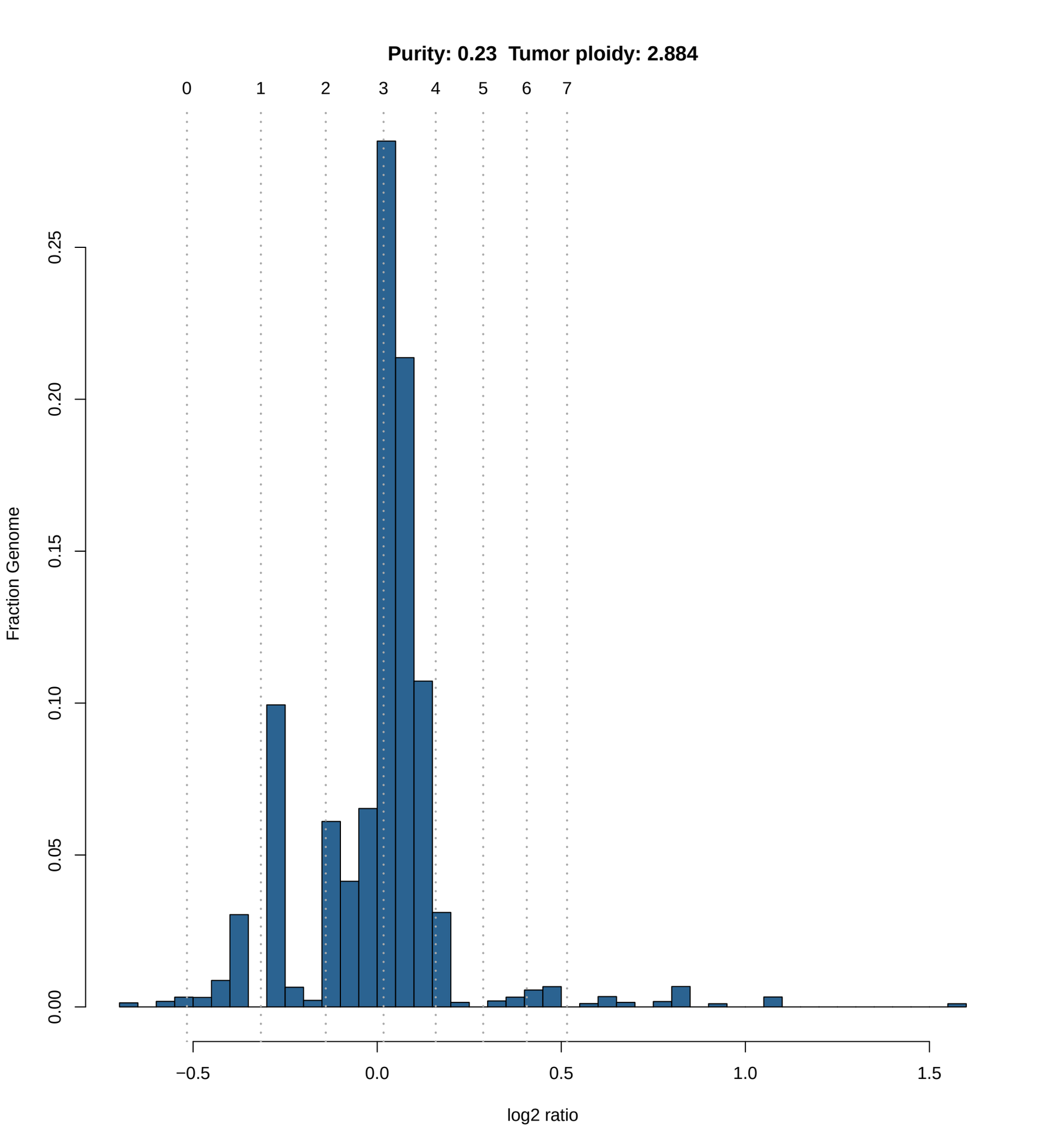

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 10 20 30 40 50 60 70
SNV Index

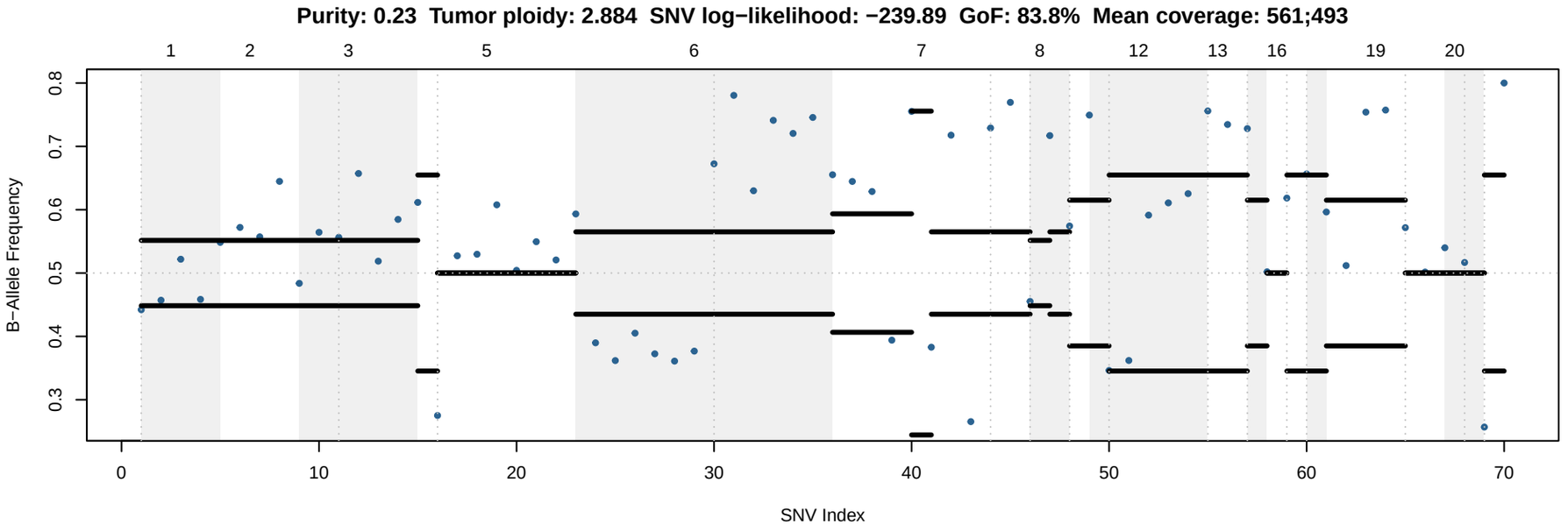

Allelic fraction (germline)
Copy Number log−ratio
6m5
5m4
4m3
7m5
6m4
5m3
7m4
6m3
7m3
5m2
6m2
7m2
4m1
5m1
6m1

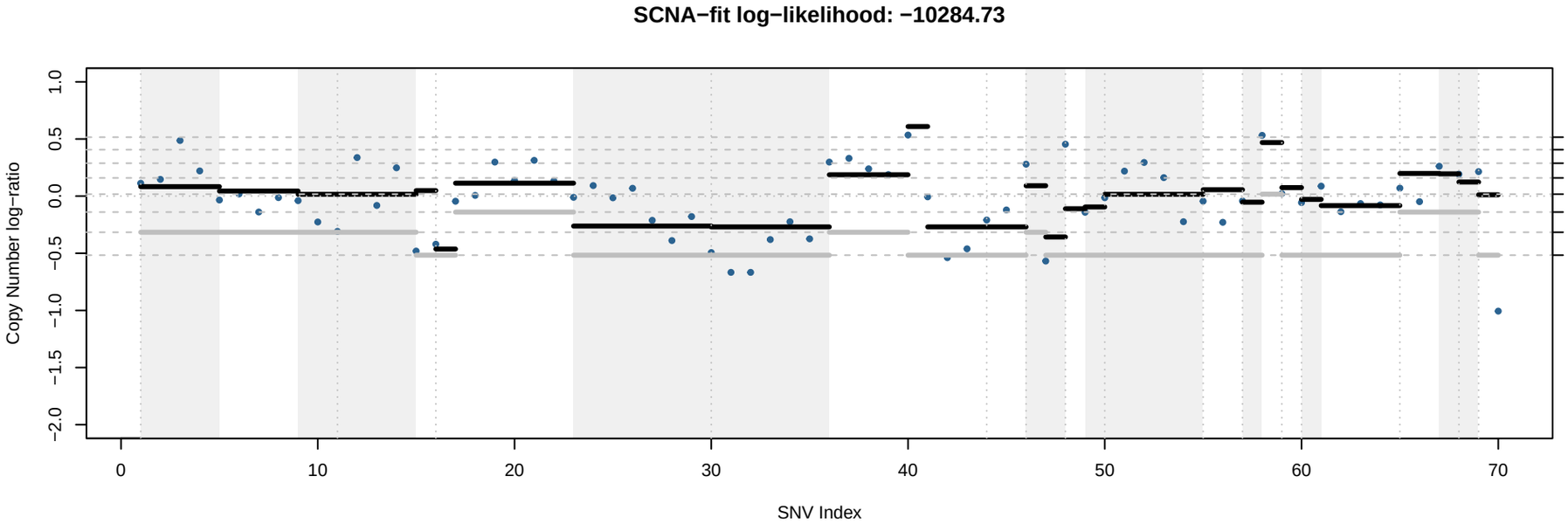

Coverage (log2)
Allelic fraction

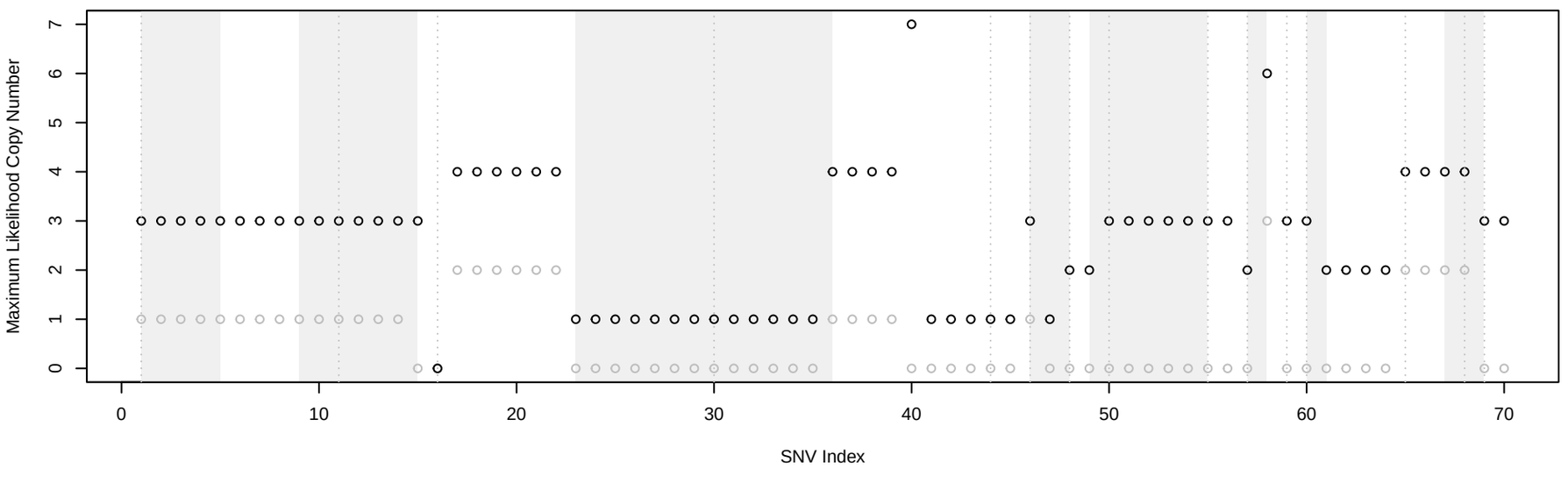

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m1
7m1

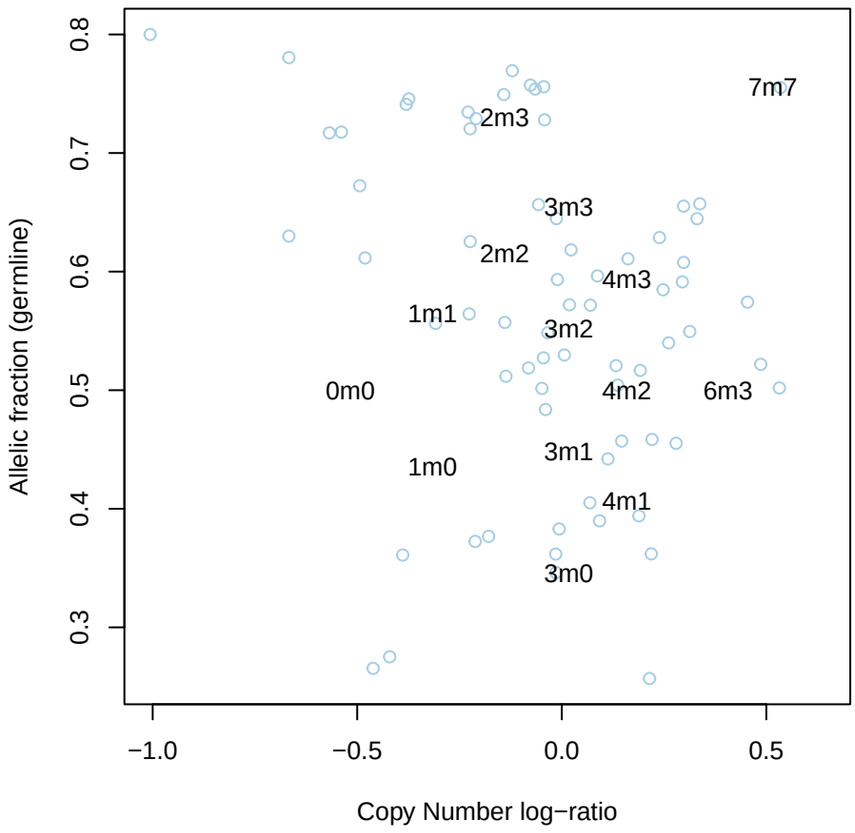

Frequency
Cellular fraction

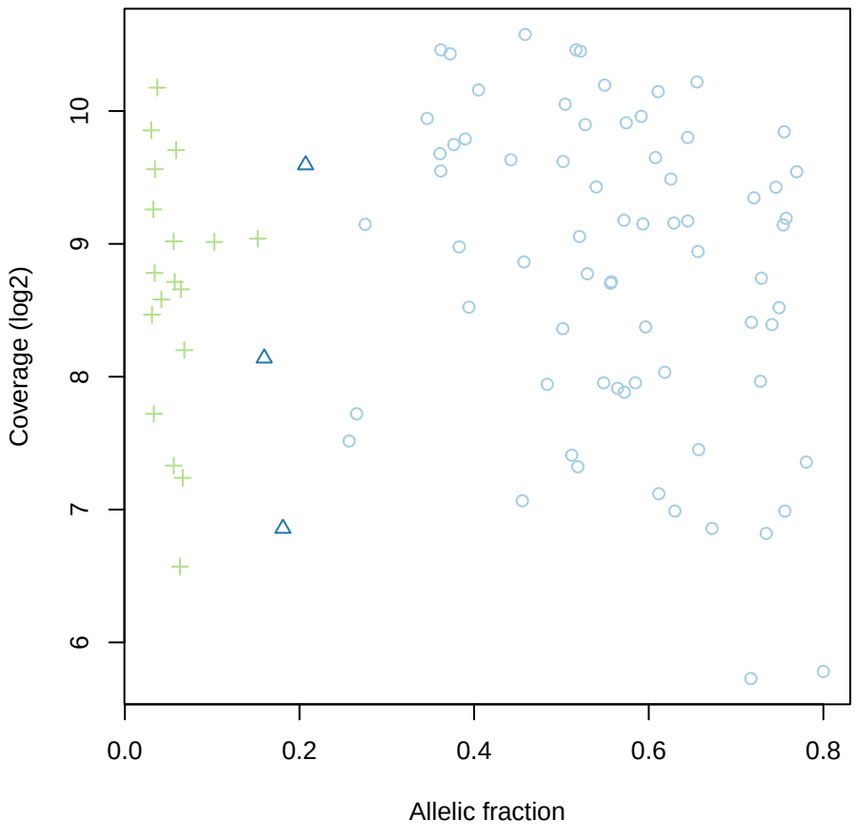

Purity: 0.23 Tumor ploidy: 2.884
0
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
log2 ratio

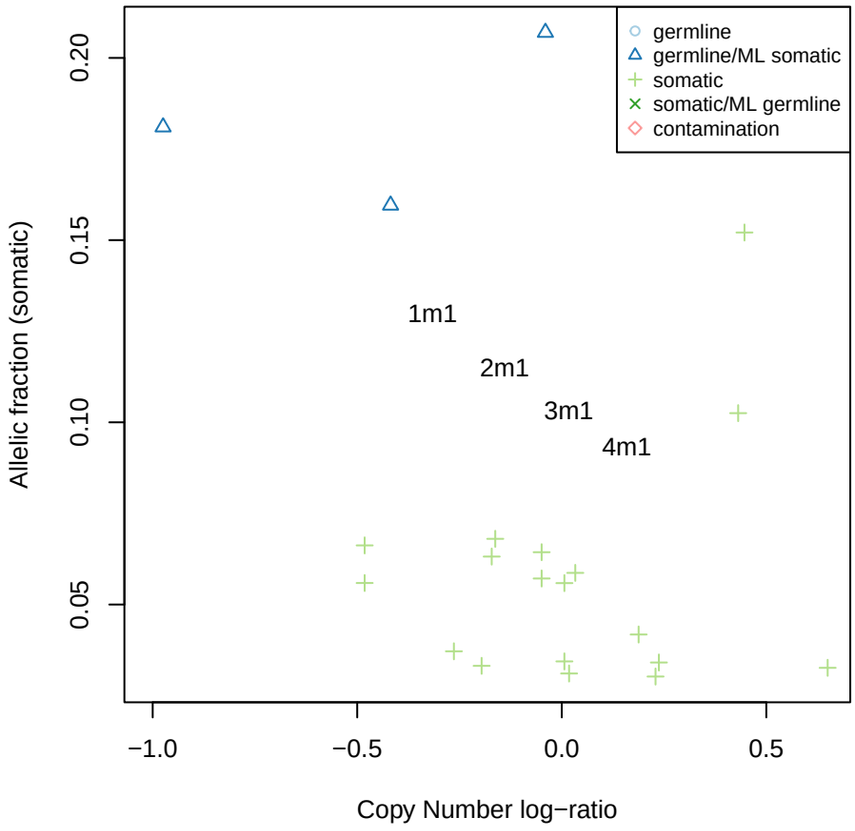

Purity: 0.23 Tumor ploidy: 2.884 SNV log−likelihood: −239.89 GoF: 83.8% Mean coverage: 561;493
1 2 3 5 6 7 8 12 13 16 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 10 20 30 40 50 60 70
SNV Index

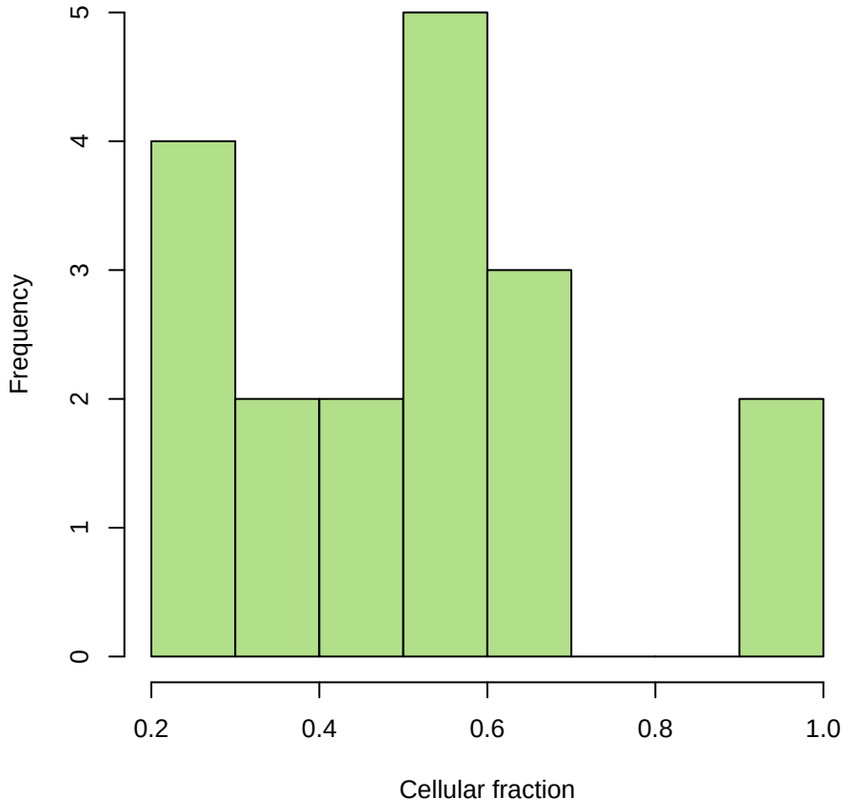

SCNA−fit log−likelihood: −10284.73
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 2 4 6
0 10 20 30 40 50 60 70
SNV Index

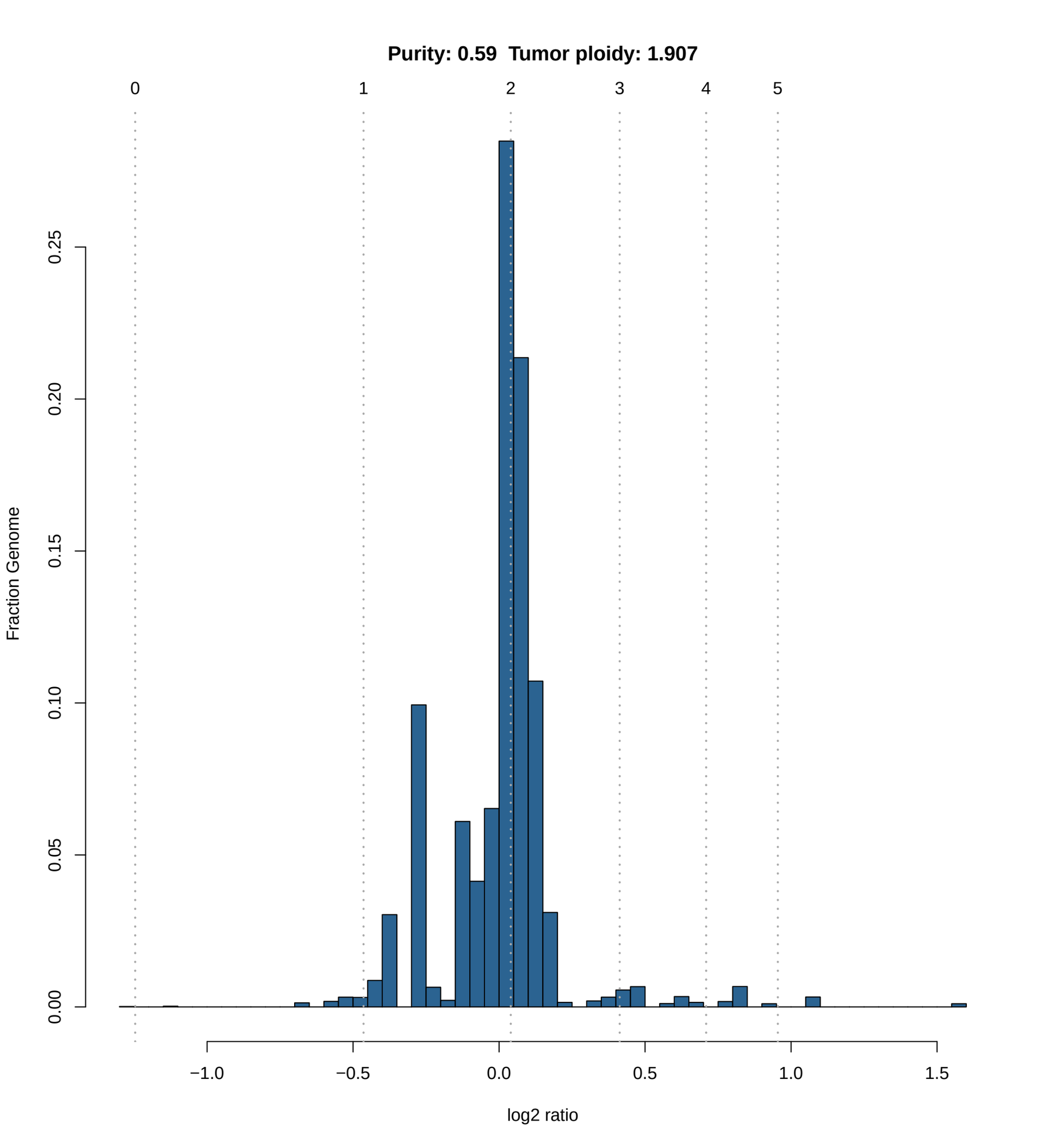

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 10 20 30 40 50 60 70
SNV Index

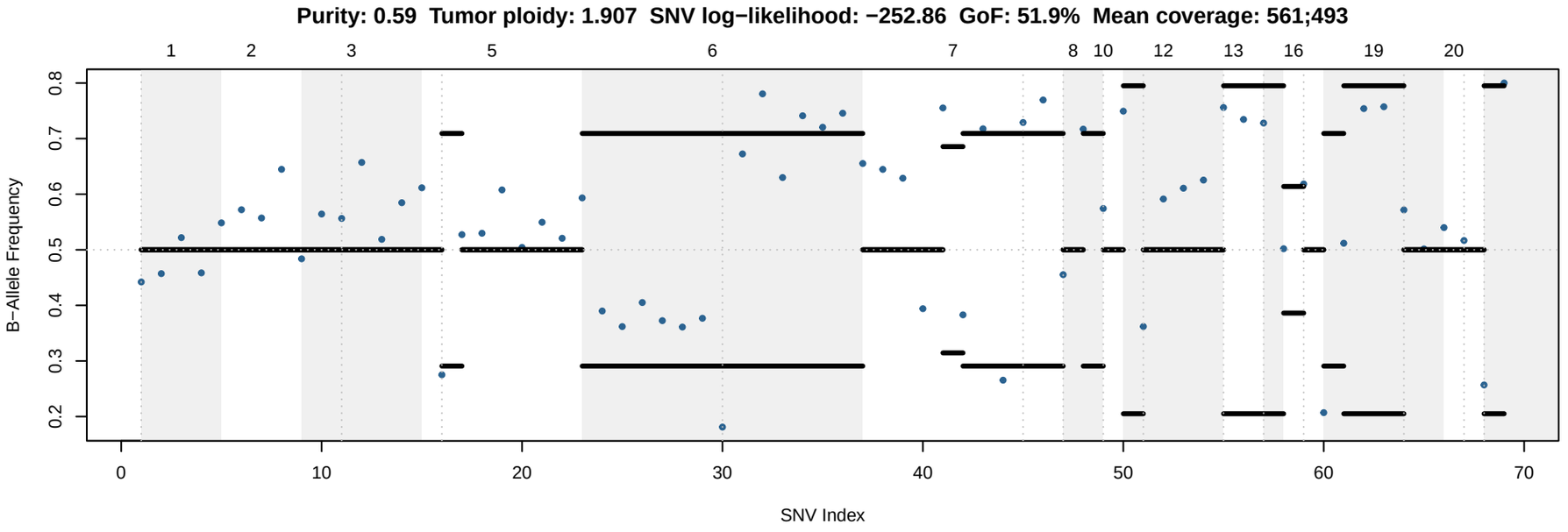

Allelic fraction (germline)
Copy Number log−ratio
7m7
2m3
3m3
2m2
4m3
1m1
3m2
0m0
4m2
6m3
3m1
1m0
4m1
3m0

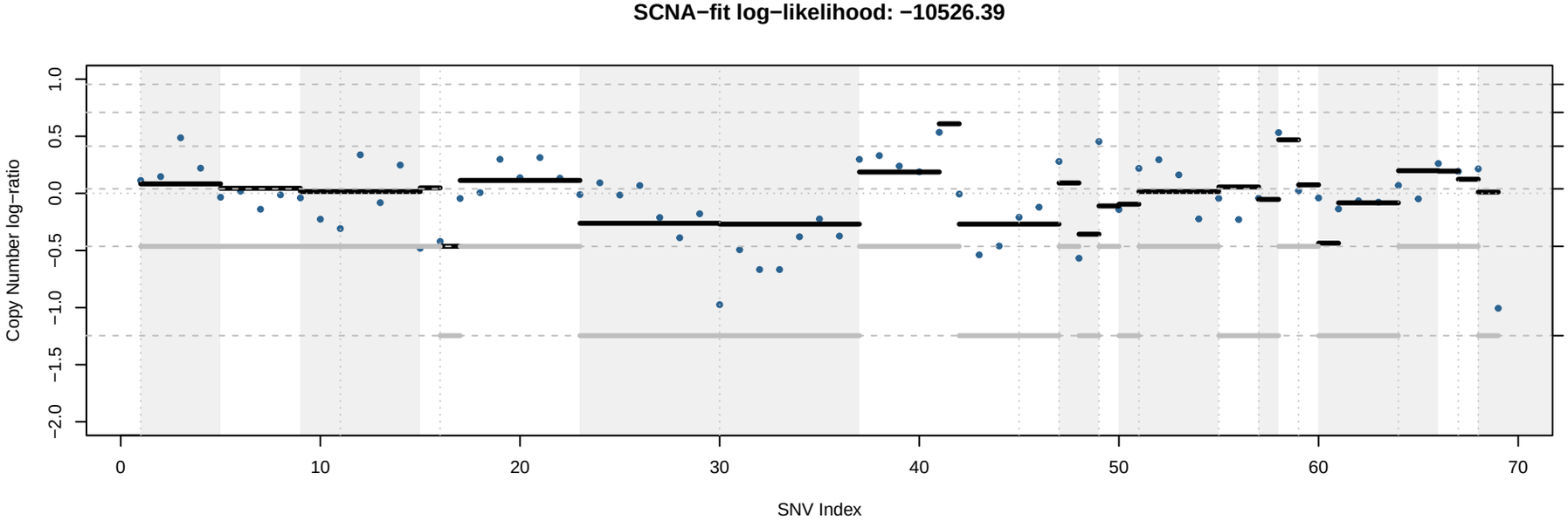

Coverage (log2)
Allelic fraction

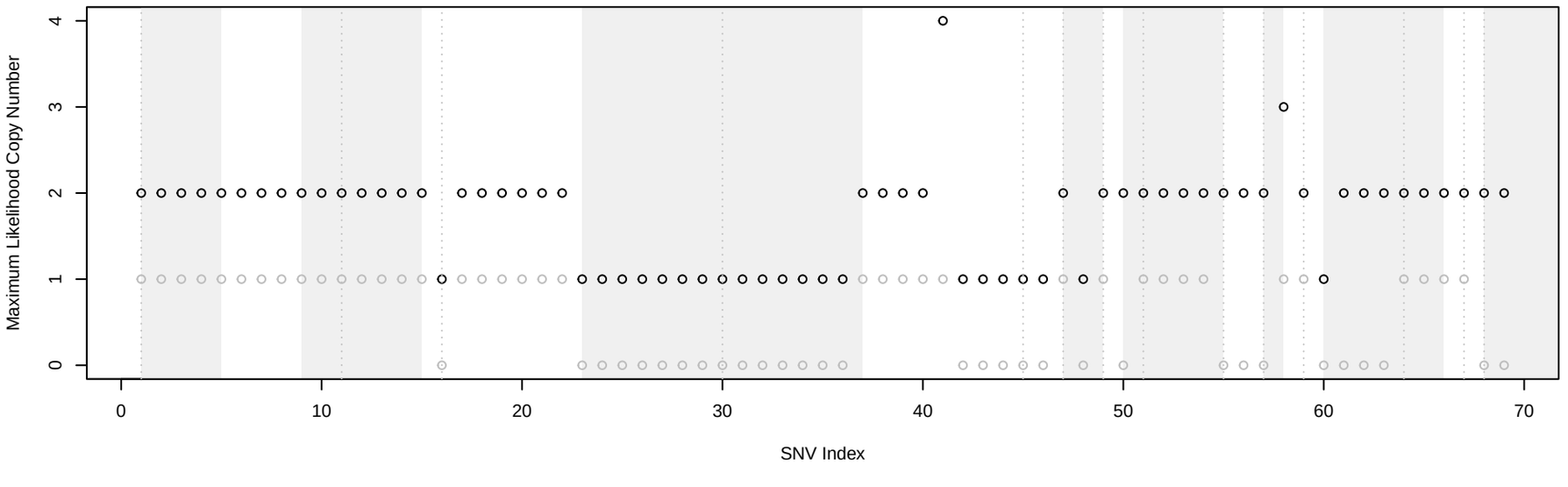

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
4m1

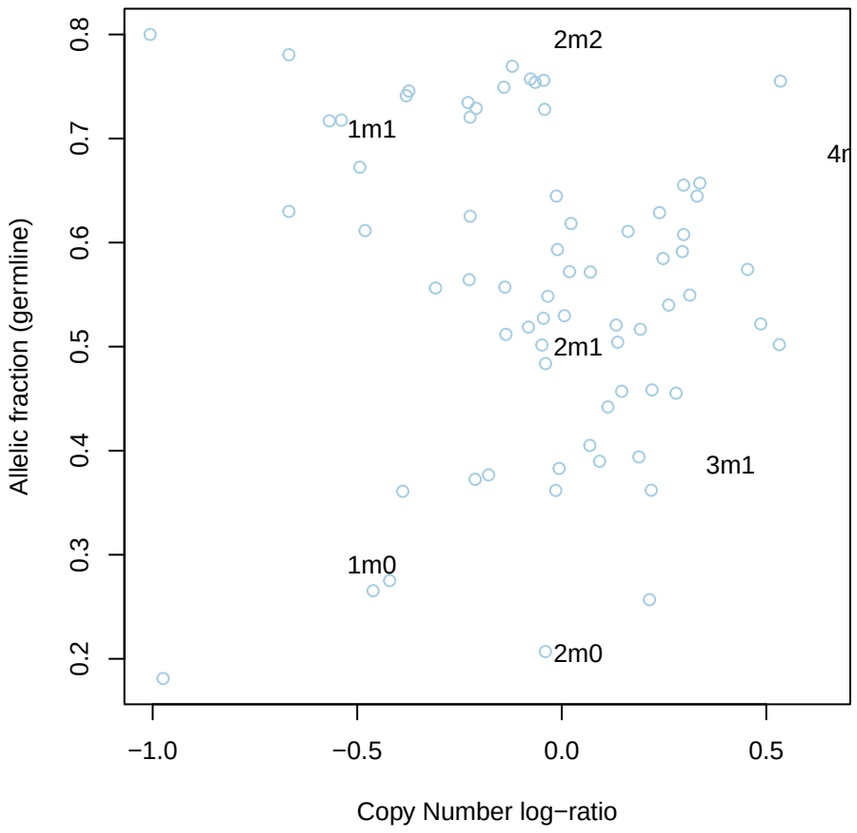

Frequency
Cellular fraction

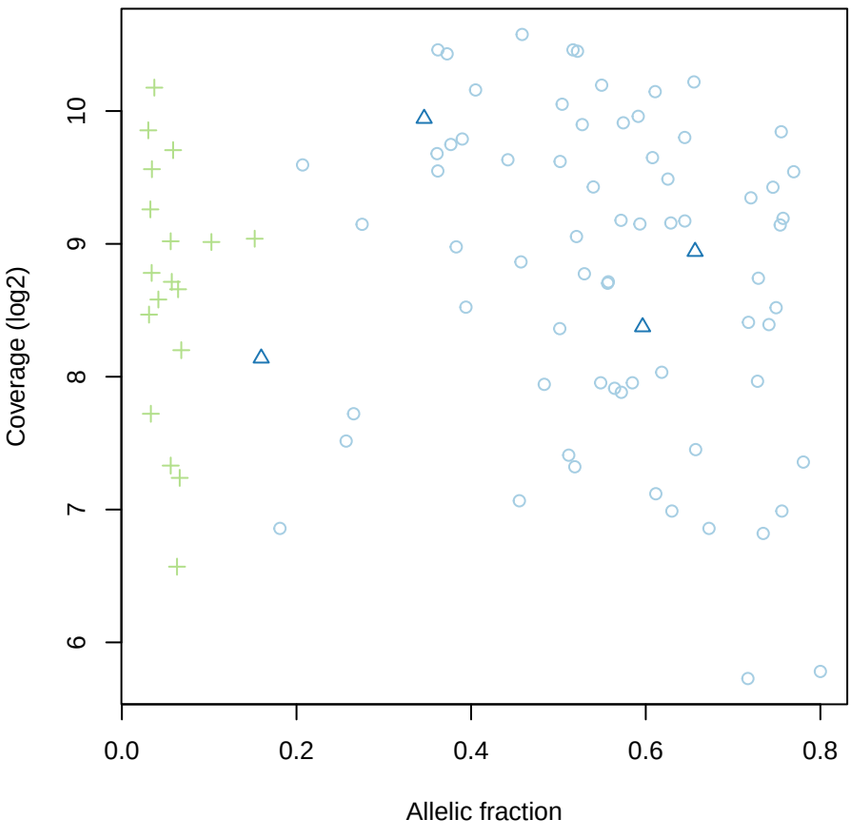

Purity: 0.59 Tumor ploidy: 1.907
0
1
2
3
4
5
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

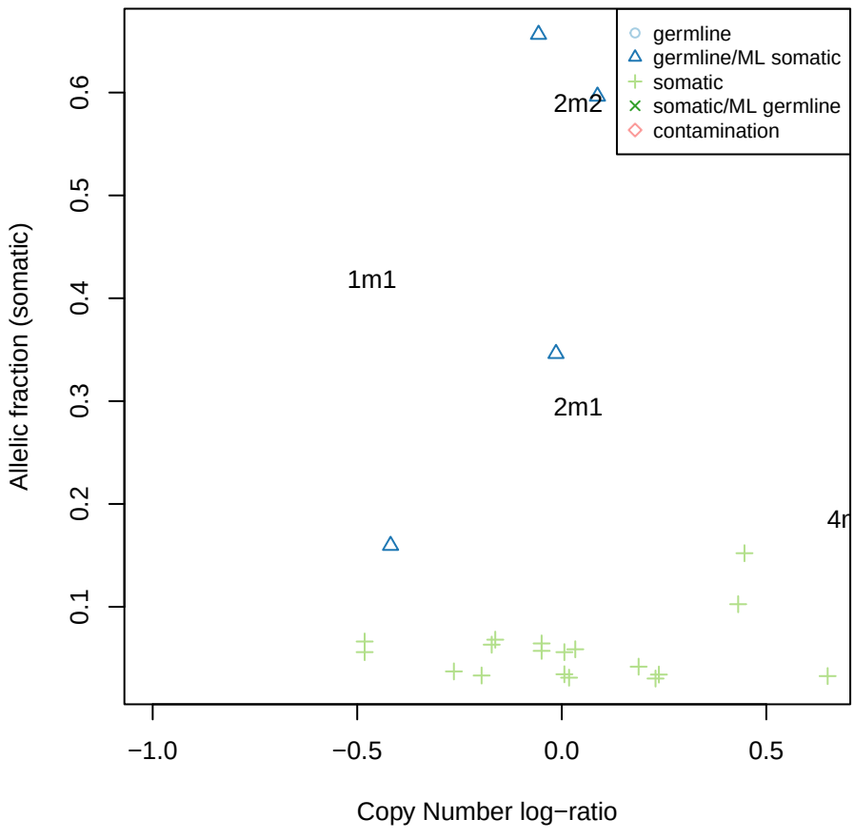

Purity: 0.59 Tumor ploidy: 1.907 SNV log−likelihood: −252.86 GoF: 51.9% Mean coverage: 561;493
1 2 3 5 6 7 8 10 12 13 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 10 20 30 40 50 60 70
SNV Index

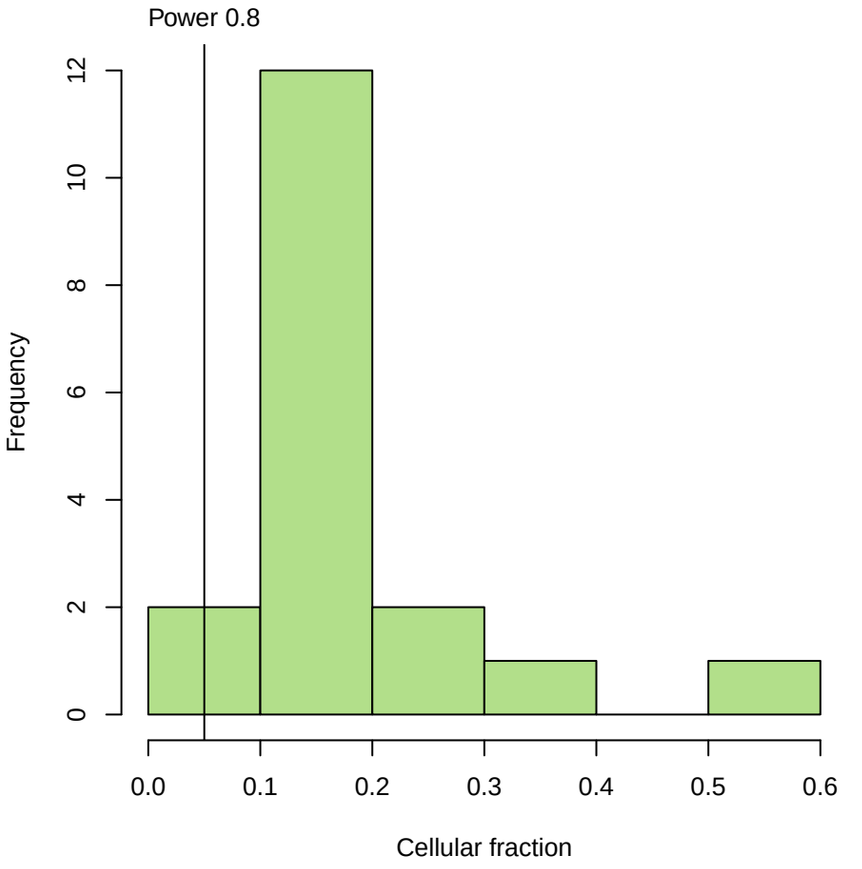

SCNA−fit log−likelihood: −10526.39
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5
0 10 20 30 40 50 60 70
SNV Index

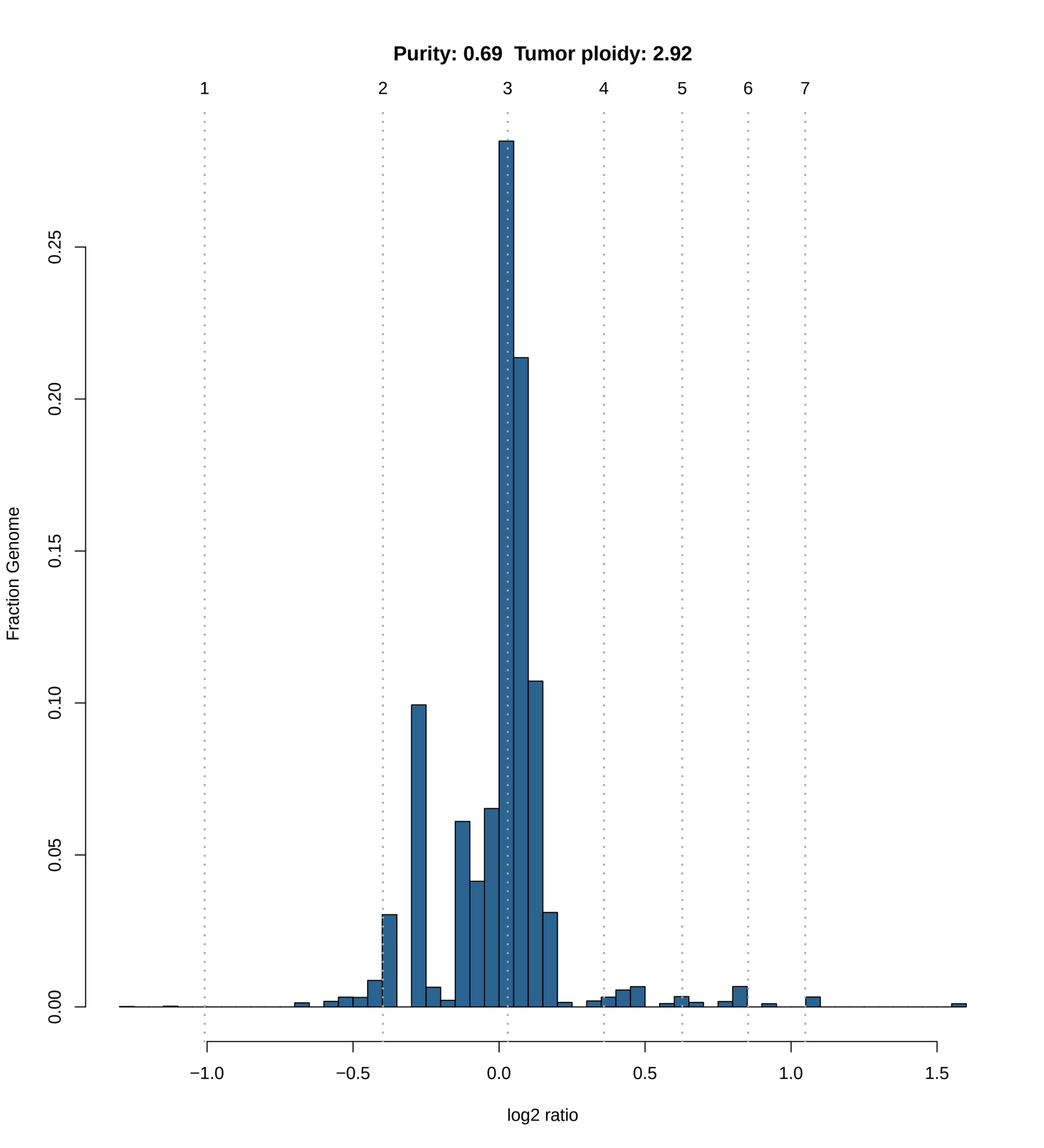

Maximum Likelihood Copy Number
0 1 2 3 4
0 10 20 30 40 50 60 70
SNV Index

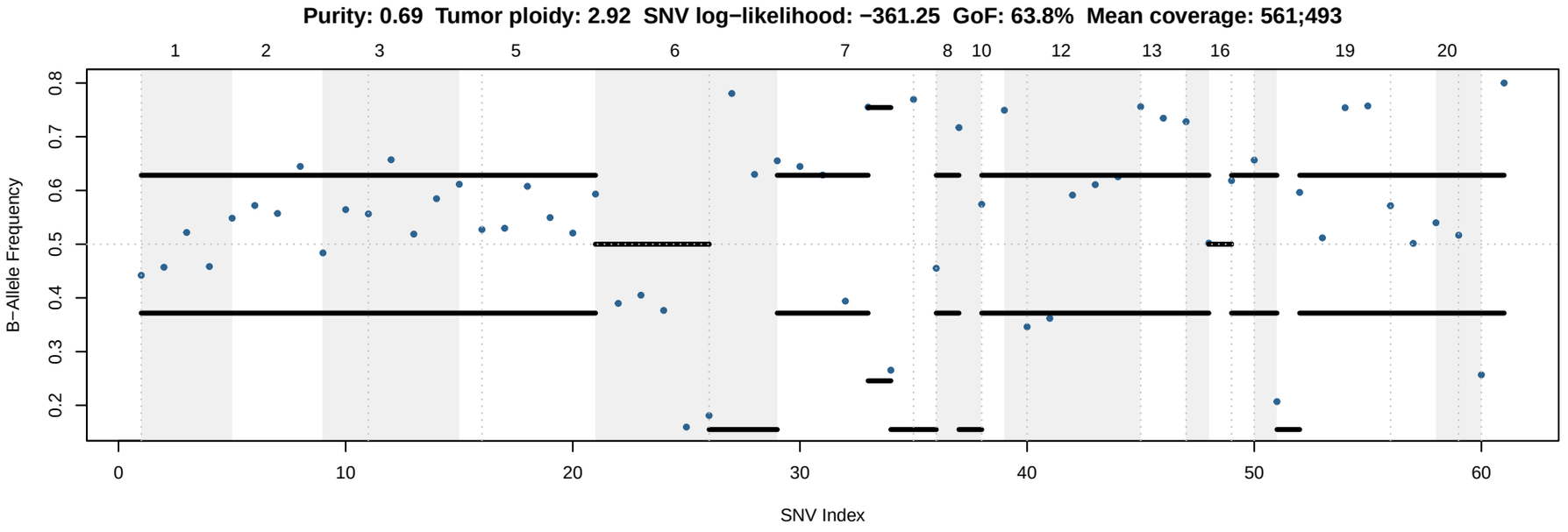

Allelic fraction (germline)
Copy Number log−ratio
2m2
1m1
2m1
3m1
1m0
2m0

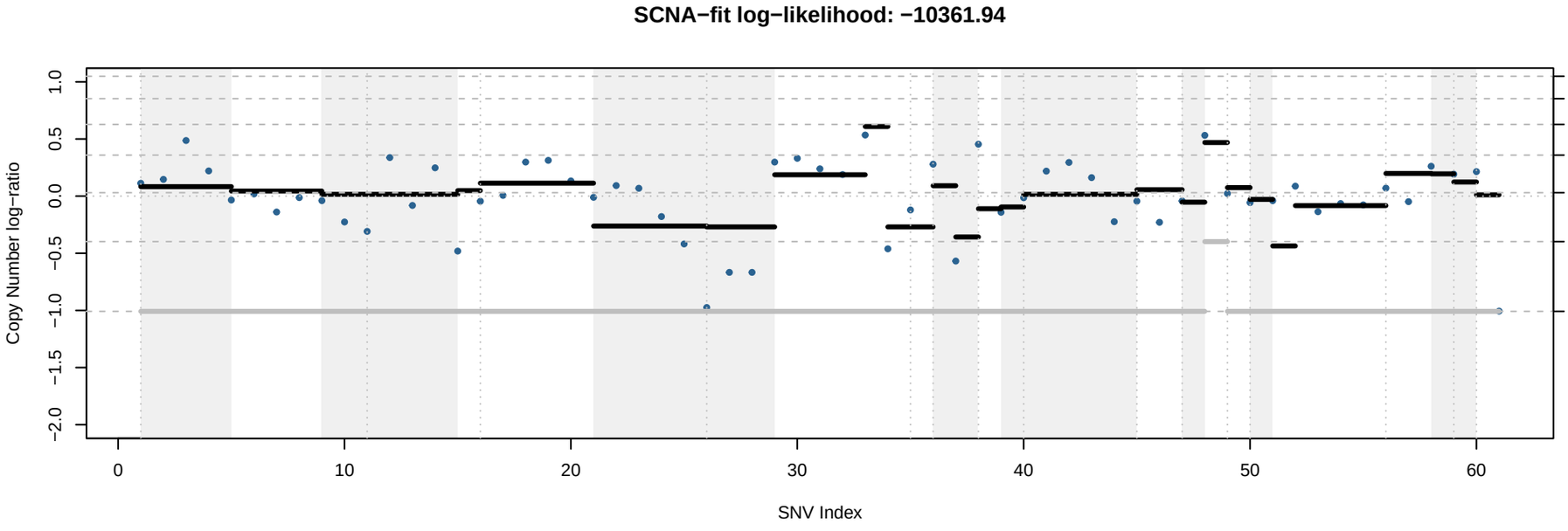

Coverage (log2)
Allelic fraction

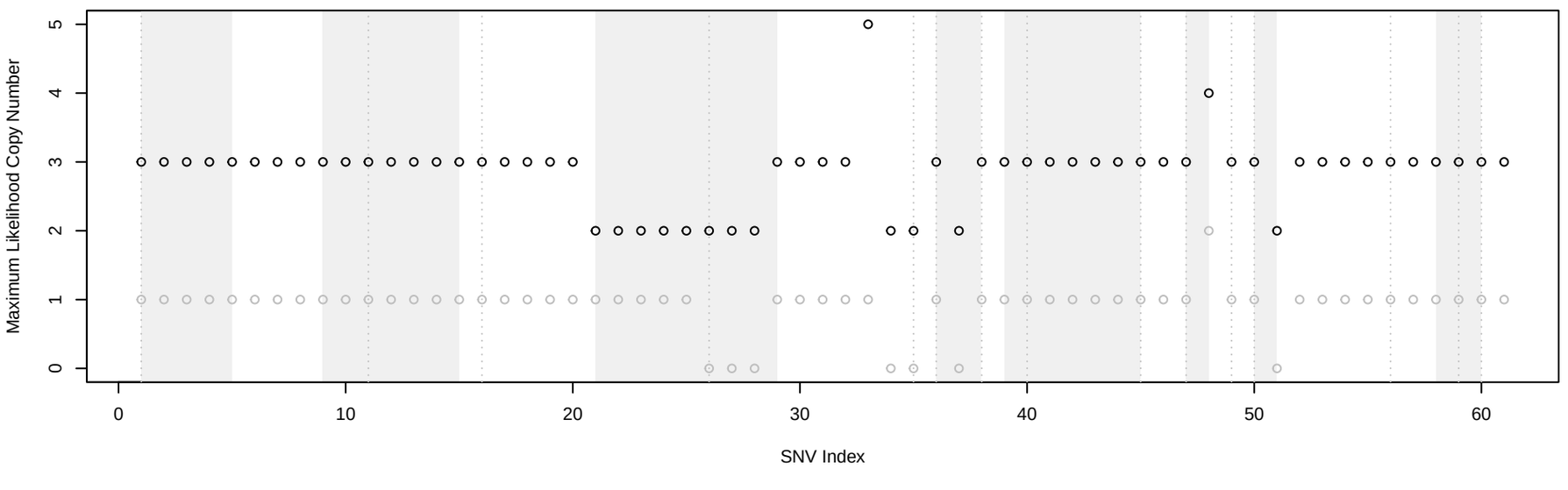

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m2
1m1
2m1

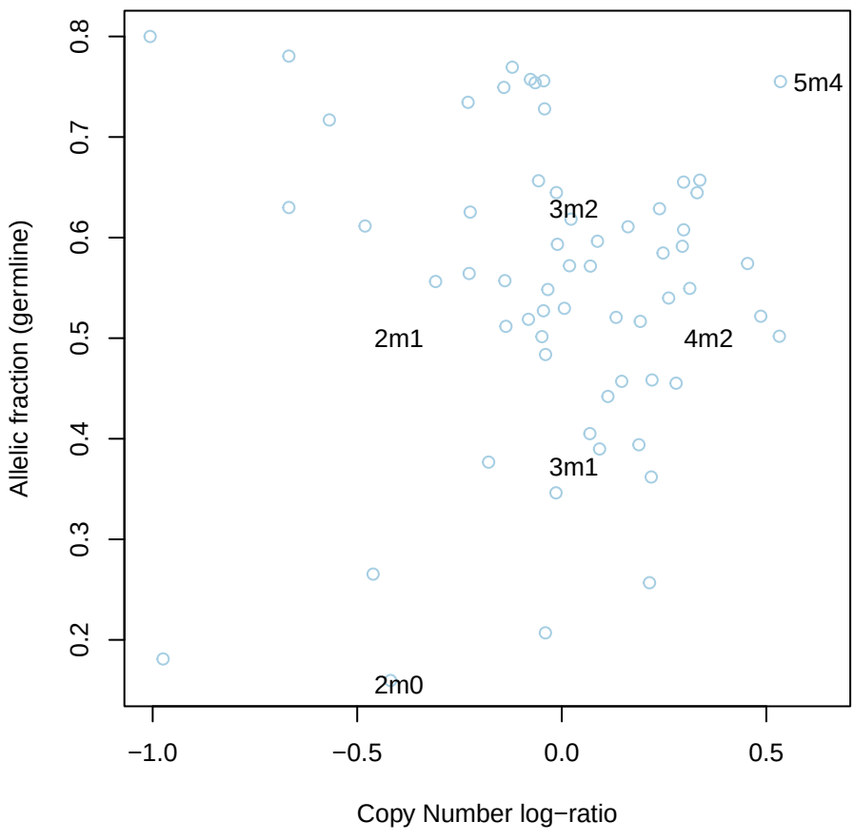

Power 0.8
Frequency
Cellular fraction

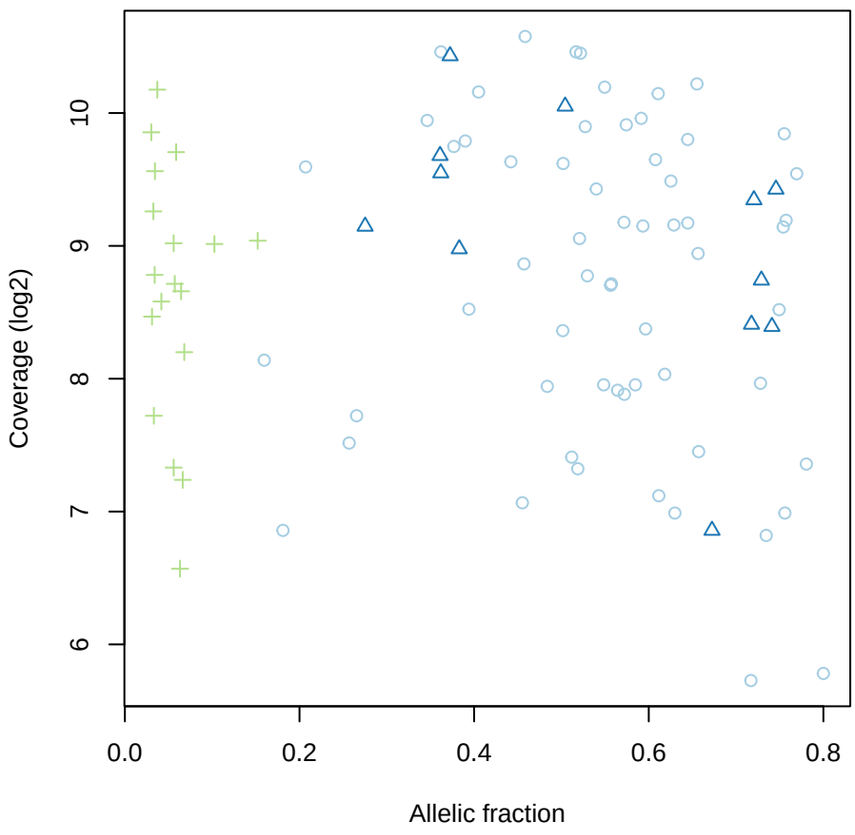

Purity: 0.69  Tumor ploidy: 2.92
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
1.5
log2 ratio

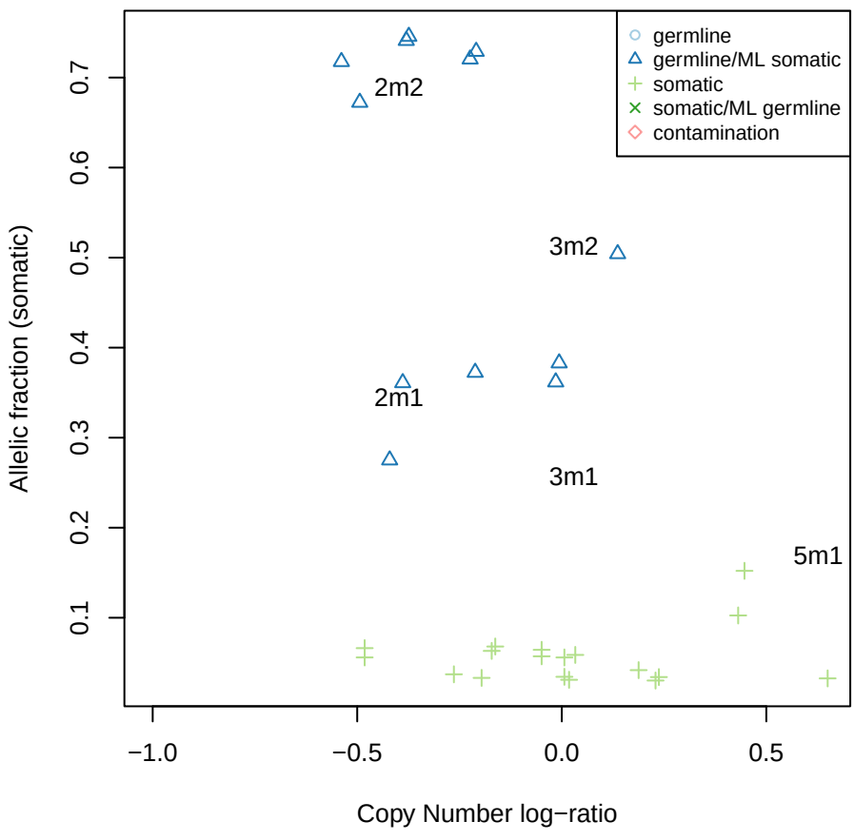

Purity: 0.69 Tumor ploidy: 2.92 SNV log−likelihood: −361.25 GoF: 63.8% Mean coverage: 561;493
1 2 3 5 6 7 8 10 12 13 16 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 10 20 30 40 50 60
SNV Index

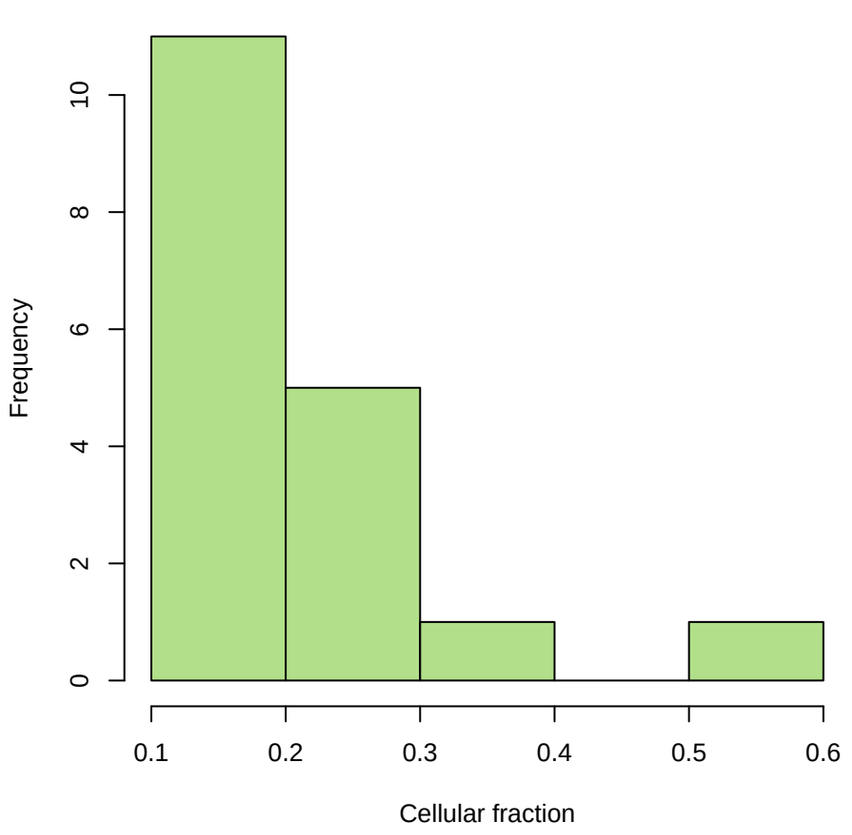

SCNA−fit log−likelihood: −10361.94
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6
0 10 20 30 40 50 60
SNV Index


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


Allelic fraction (germline)
Copy Number log−ratio
5m4
3m2
2m1
4m2
3m1
2m0


Coverage (log2)
Allelic fraction


germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m2
3m2
2m1
3m1
5m1


Frequency
Cellular fraction