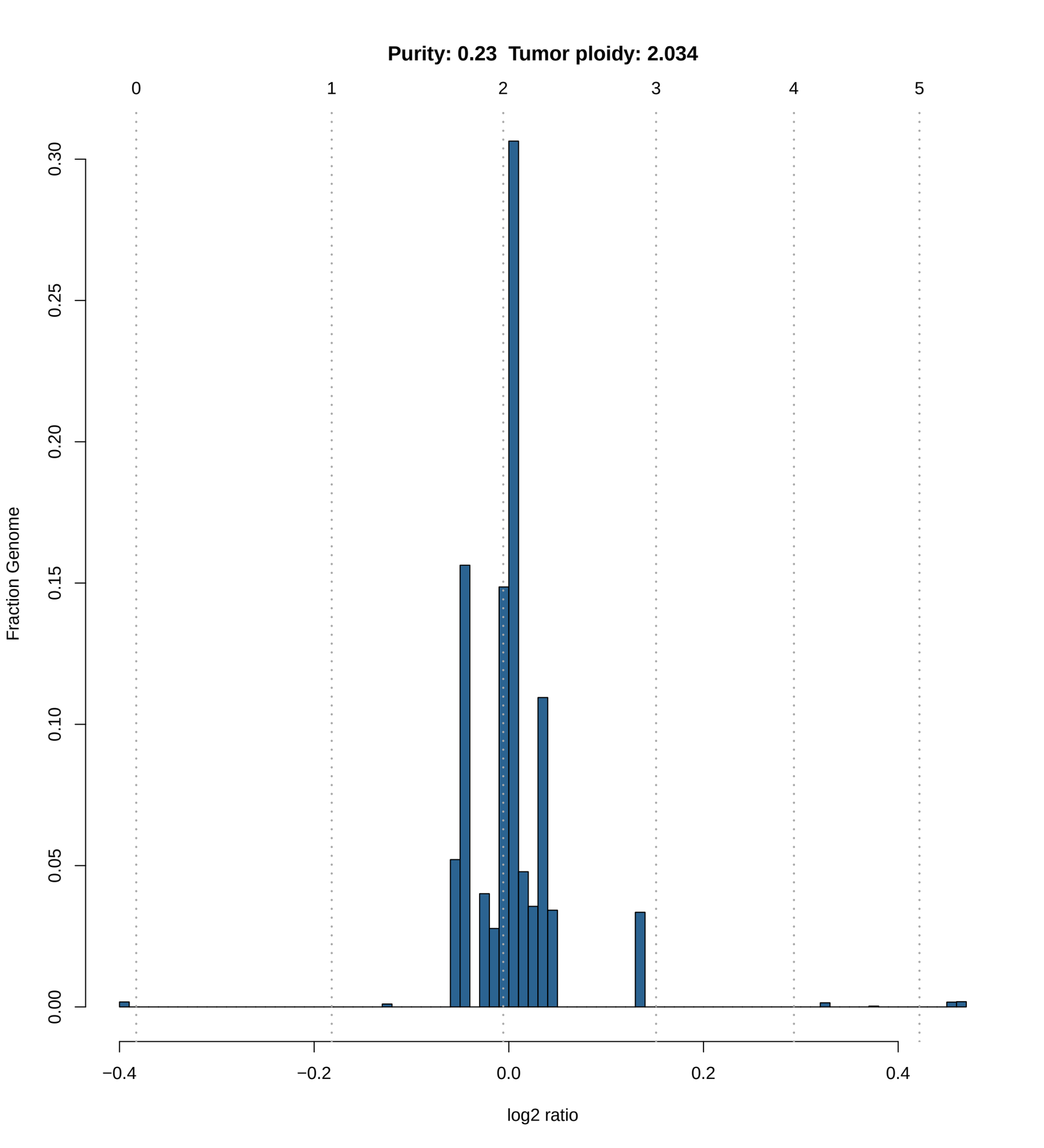
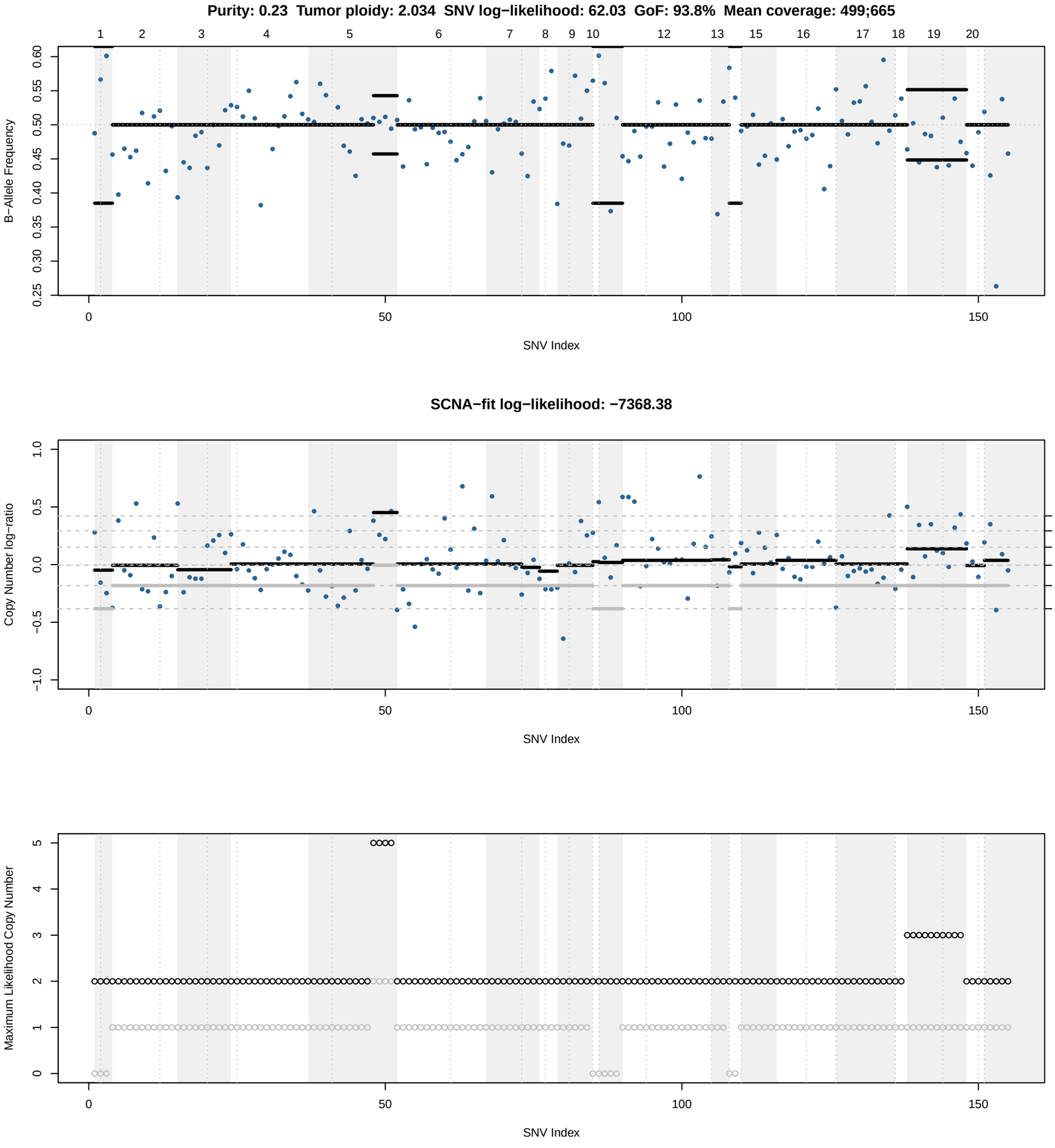
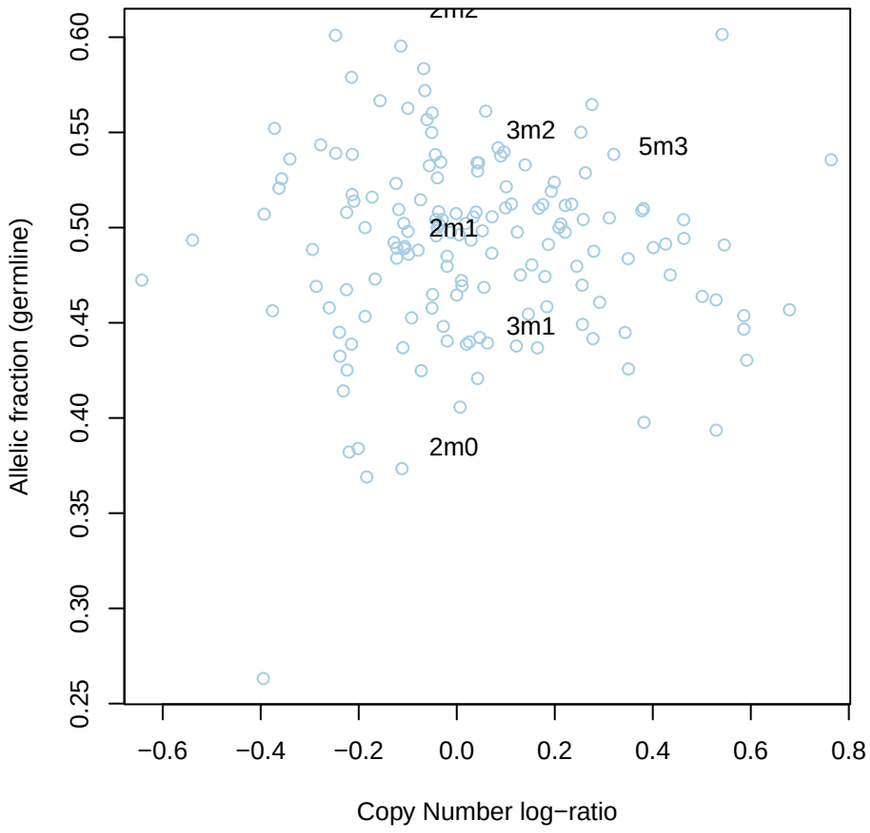
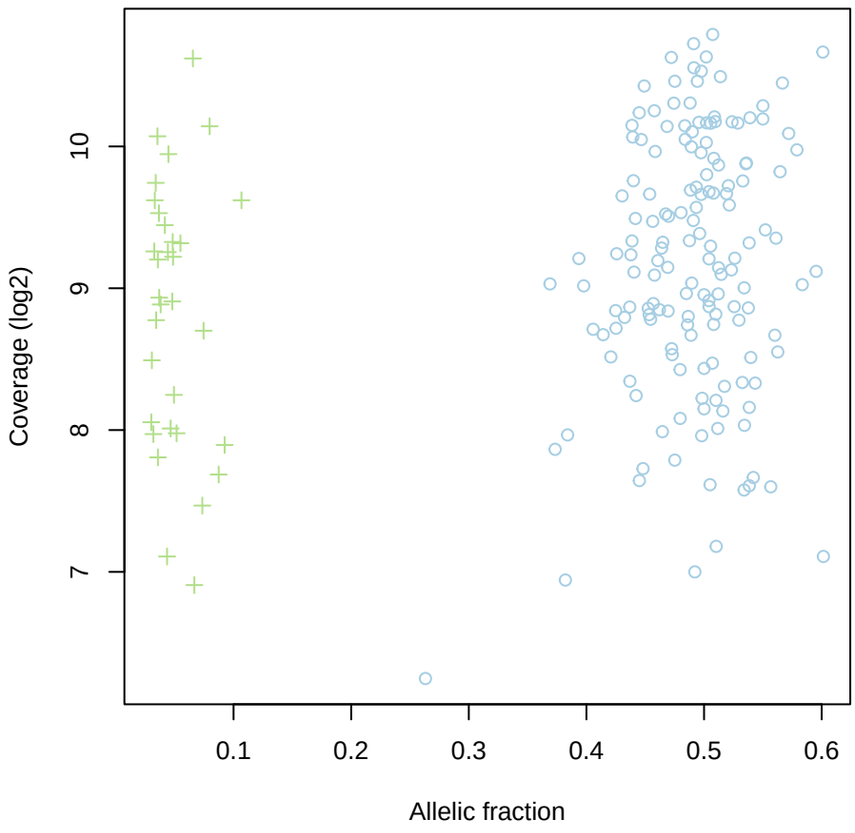
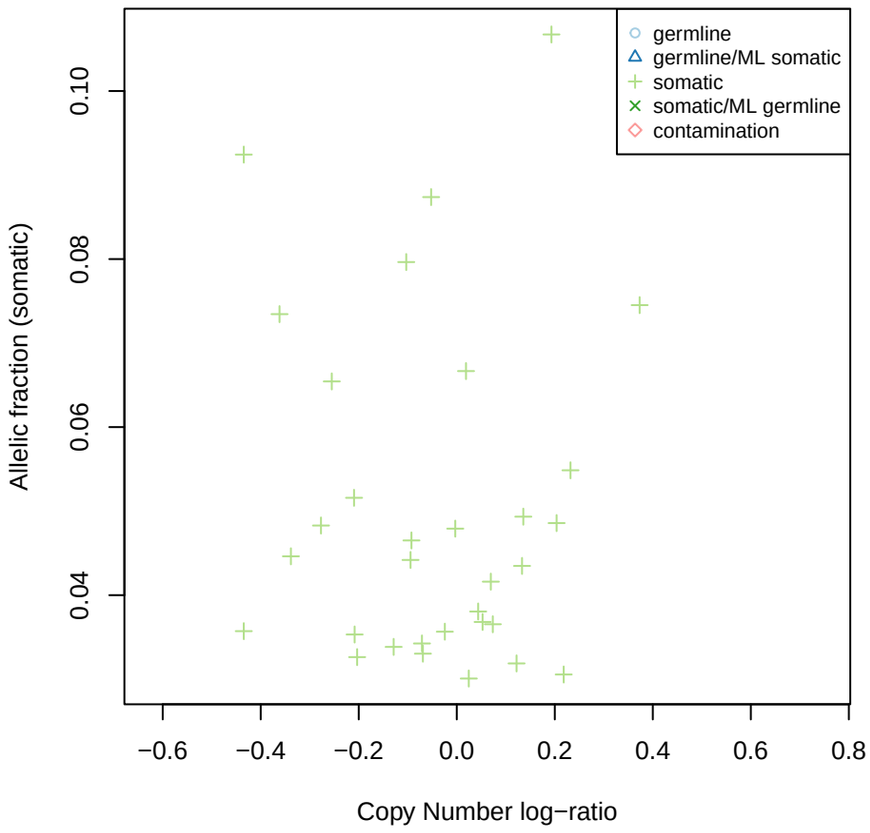
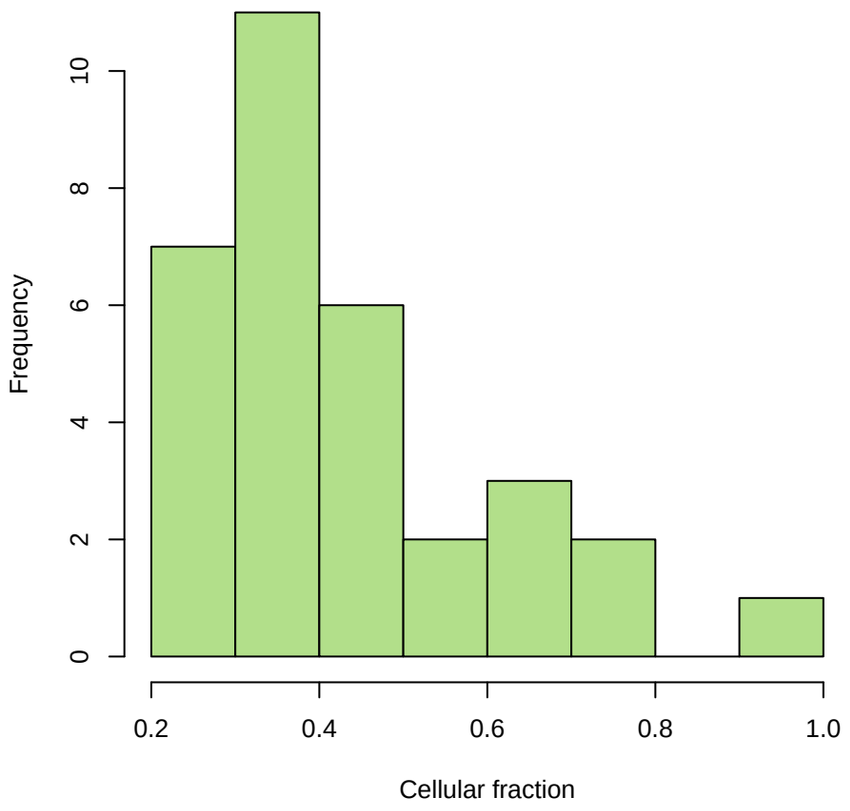

Purity: 0.23 Tumor ploidy: 2.034
0
1
2
3
4
5
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

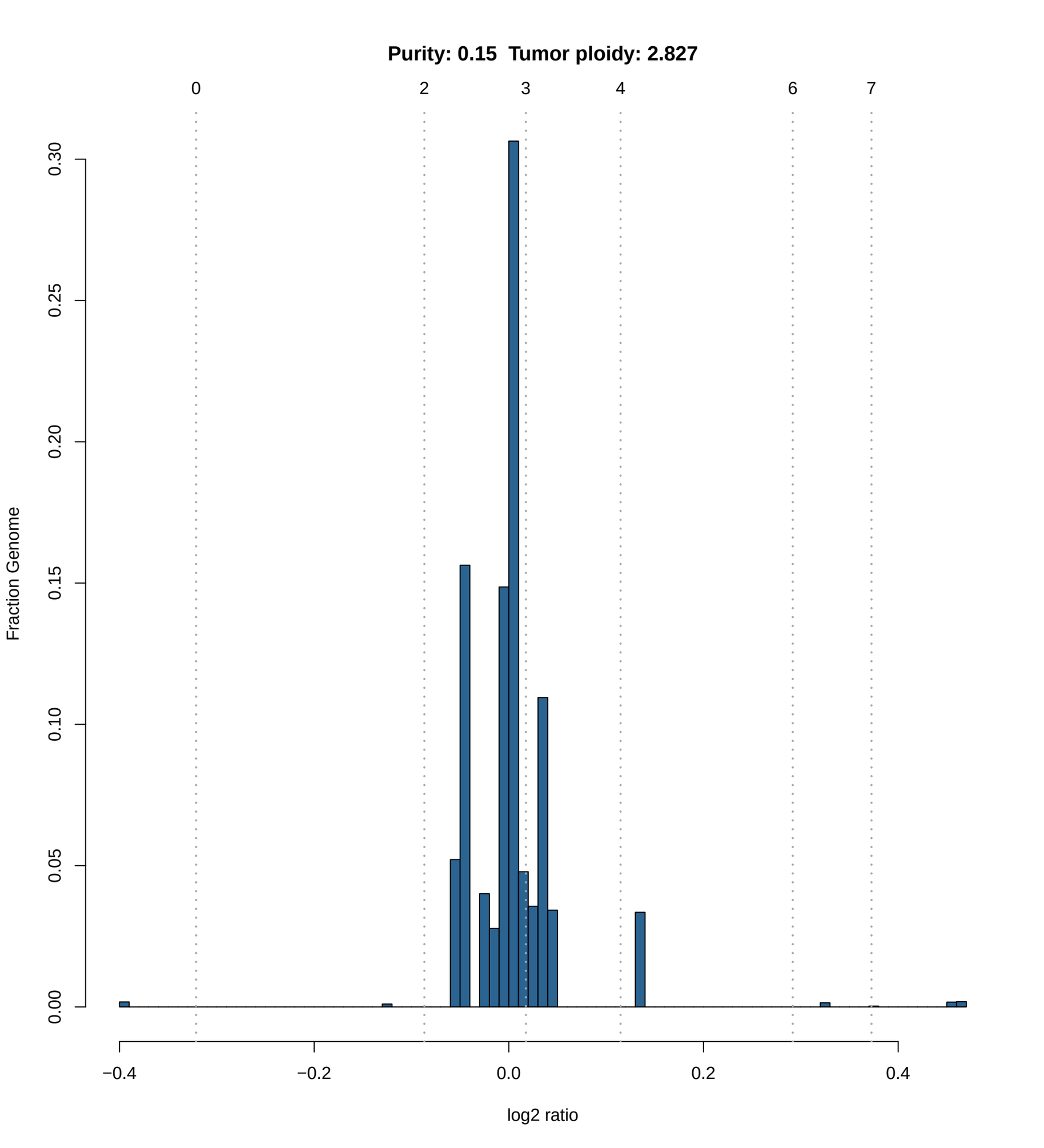

Purity: 0.23 Tumor ploidy: 2.034 SNV log−likelihood: 62.03 GoF: 93.8% Mean coverage: 499;665
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 18 19 20
B−Allele Frequency
0.25 0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index
SCNA−fit log−likelihood: −7368.38
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5
0 50 100 150
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

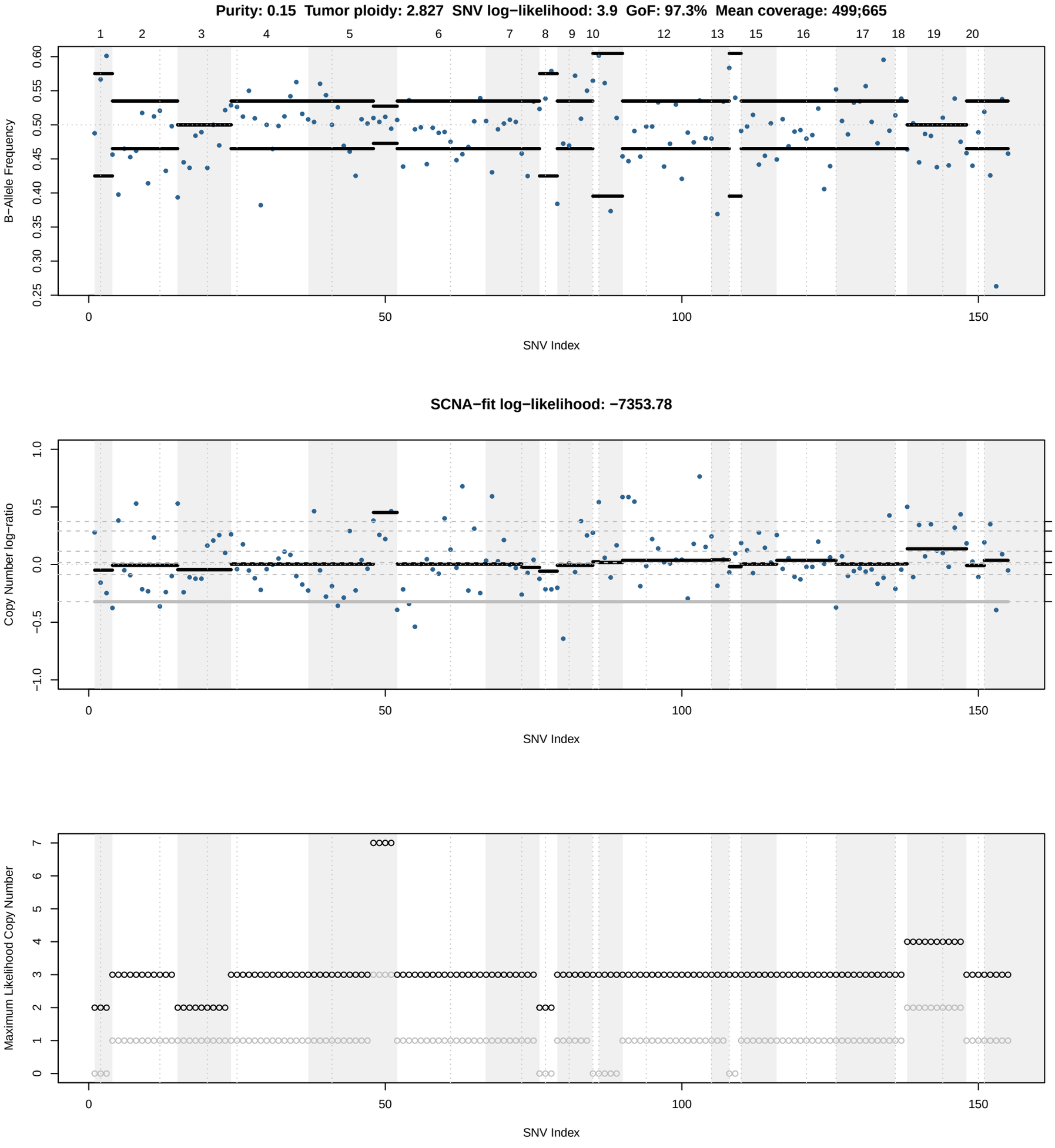

2m2
3m2
5m3
2m1
3m1
2m0
Allelic fraction (germline)
Copy Number log−ratio

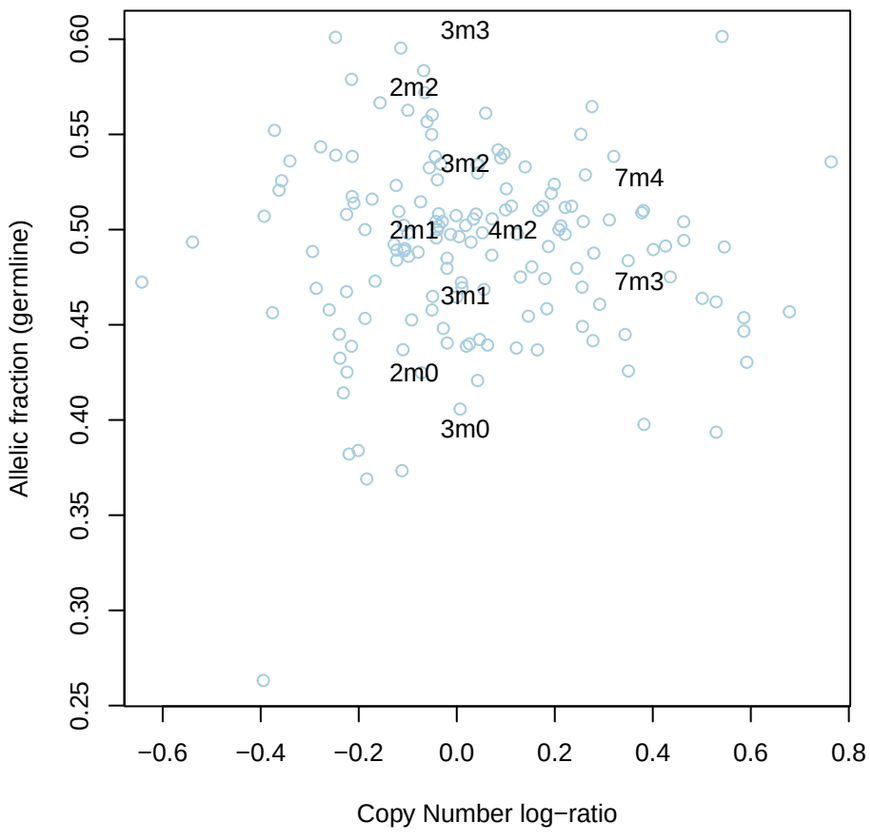

Coverage (log2)
Allelic fraction

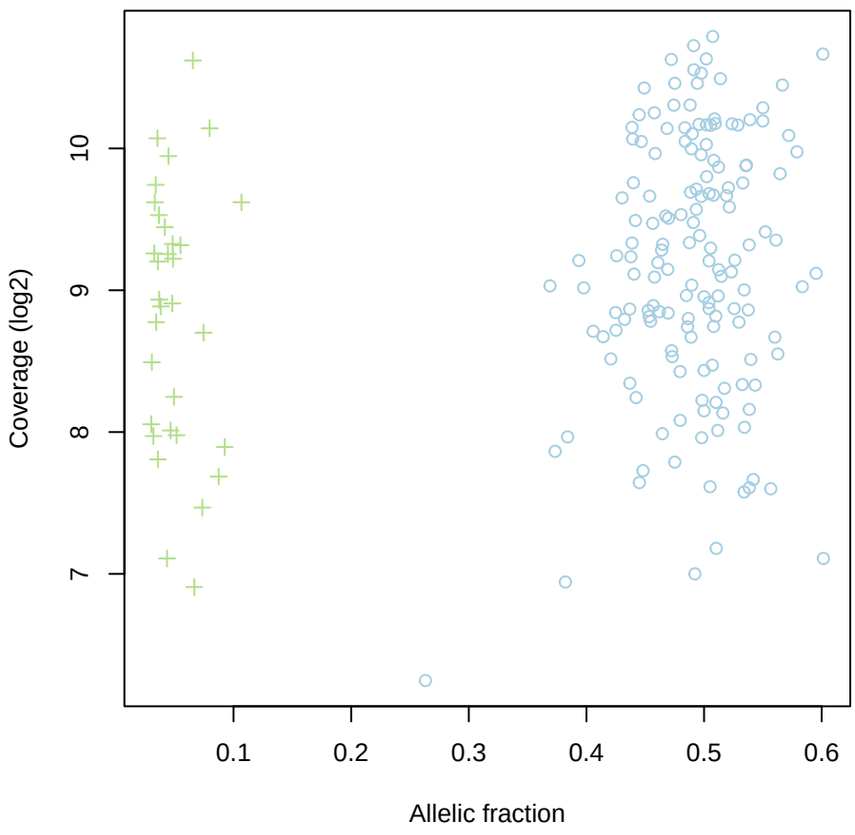

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

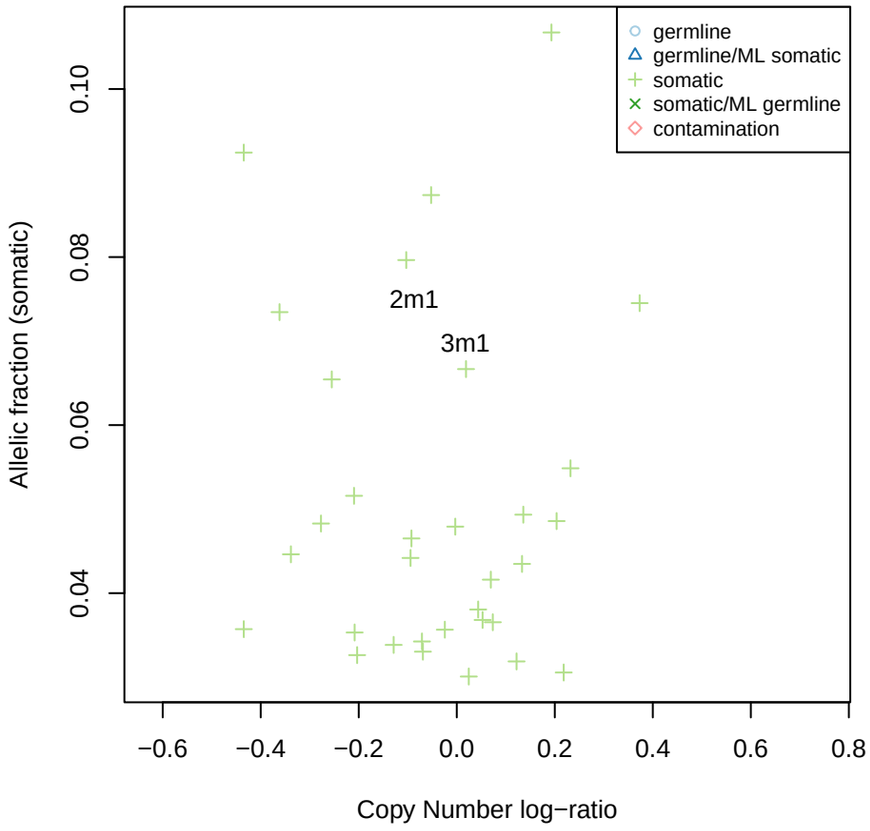

Frequency
Cellular fraction

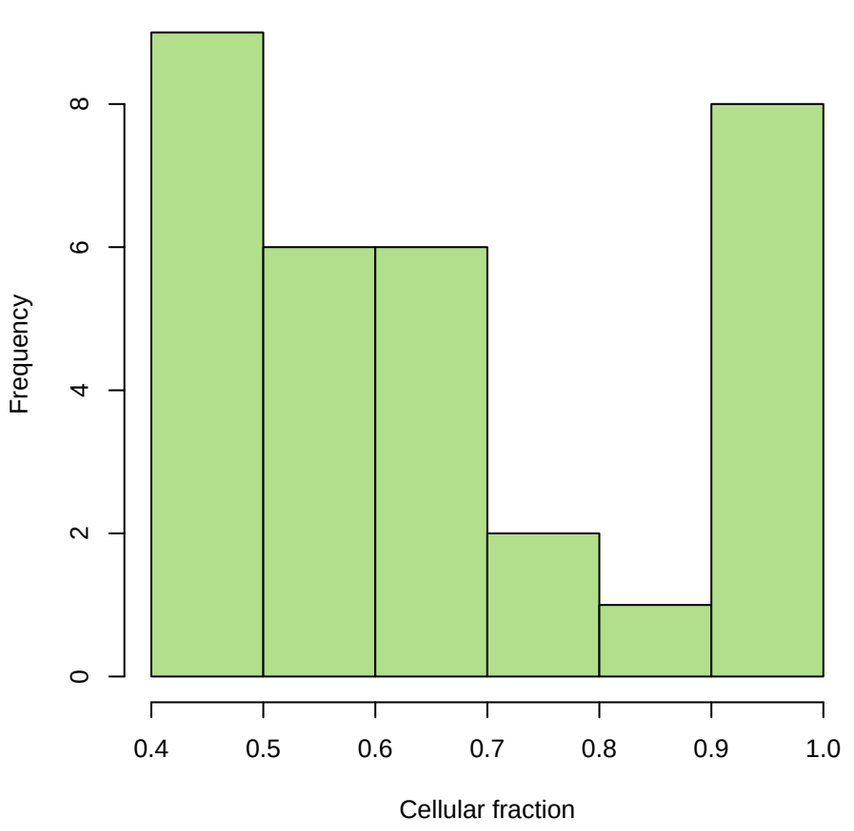

Purity: 0.15 Tumor ploidy: 2.827
0
2
3
4
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

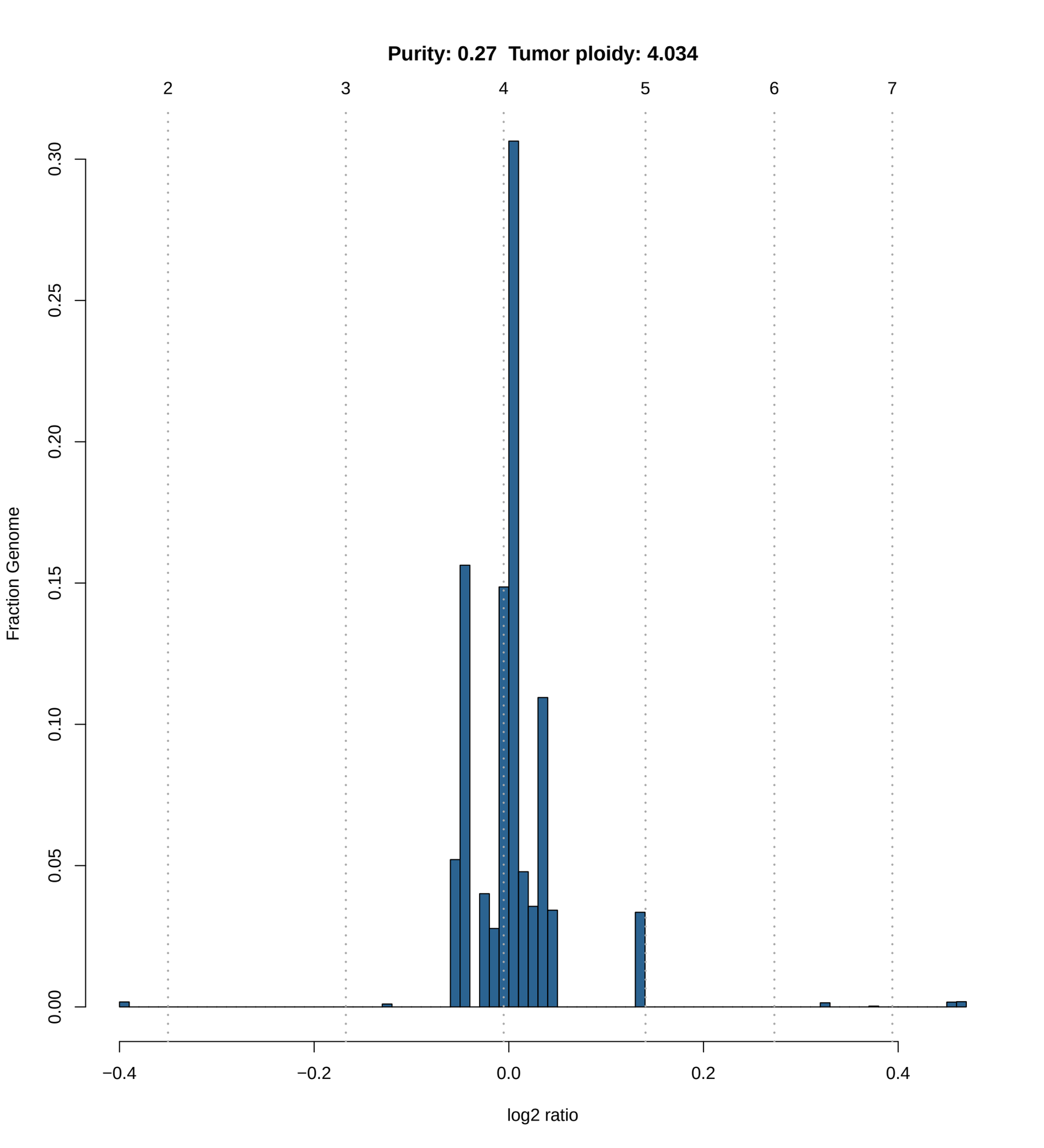

Purity: 0.15 Tumor ploidy: 2.827 SNV log−likelihood: 3.9 GoF: 97.3% Mean coverage: 499;665
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 18 19 20
B−Allele Frequency
0.25 0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index
SCNA−fit log−likelihood: −7353.78
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4 6
0 50 100 150
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

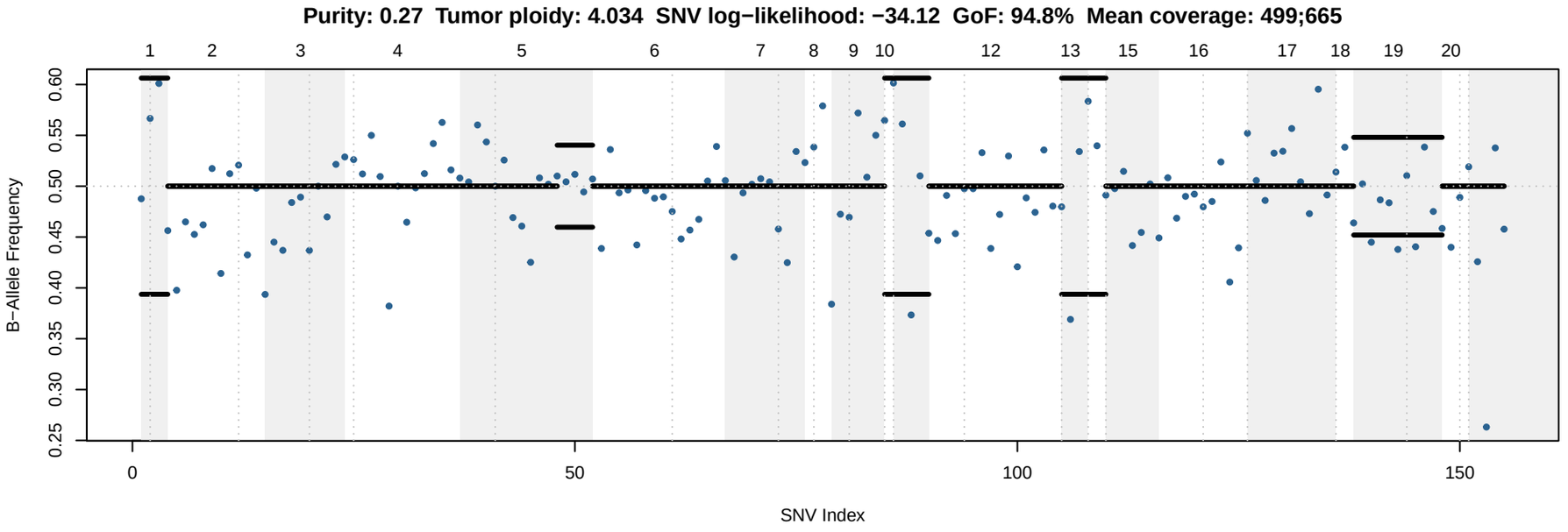

3m3
2m2
3m2
7m4
2m1
4m2
7m3
3m1
2m0
3m0
Allelic fraction (germline)
Copy Number log−ratio

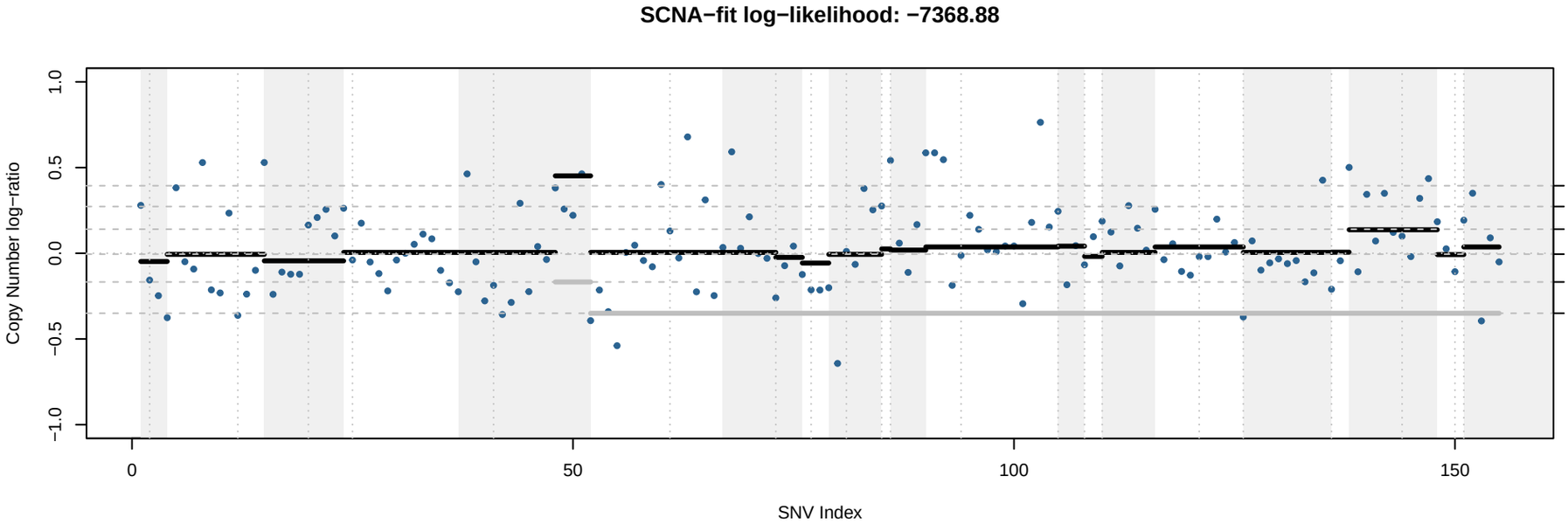

Coverage (log2)
Allelic fraction

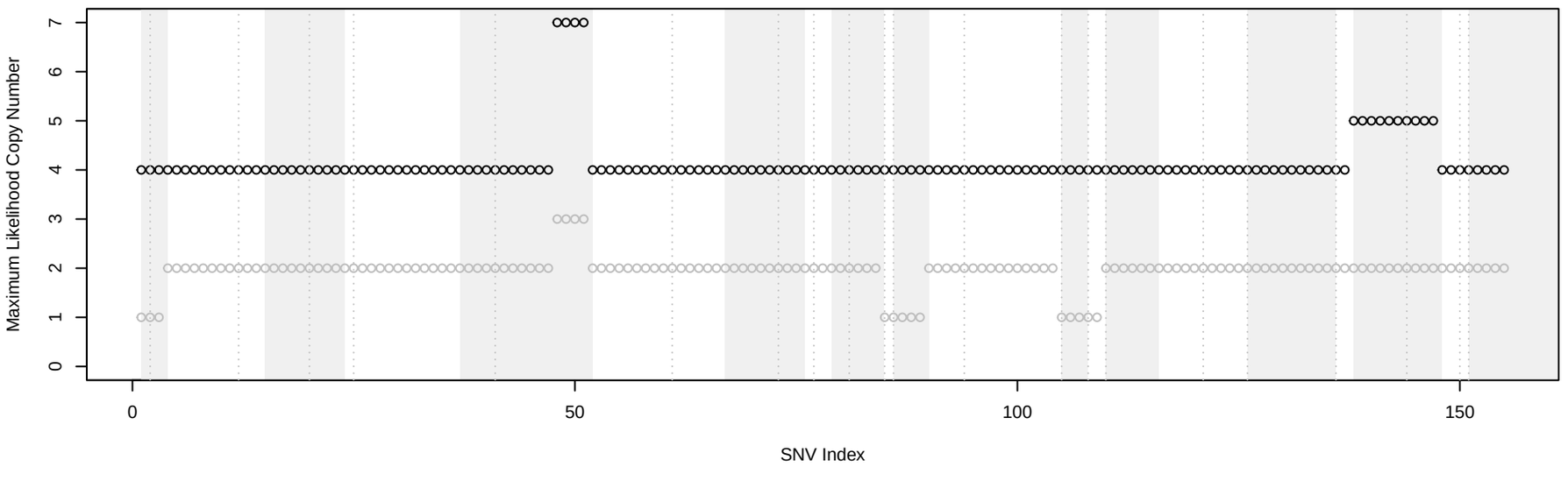

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
Allelic fraction (somatic)
Copy Number log−ratio

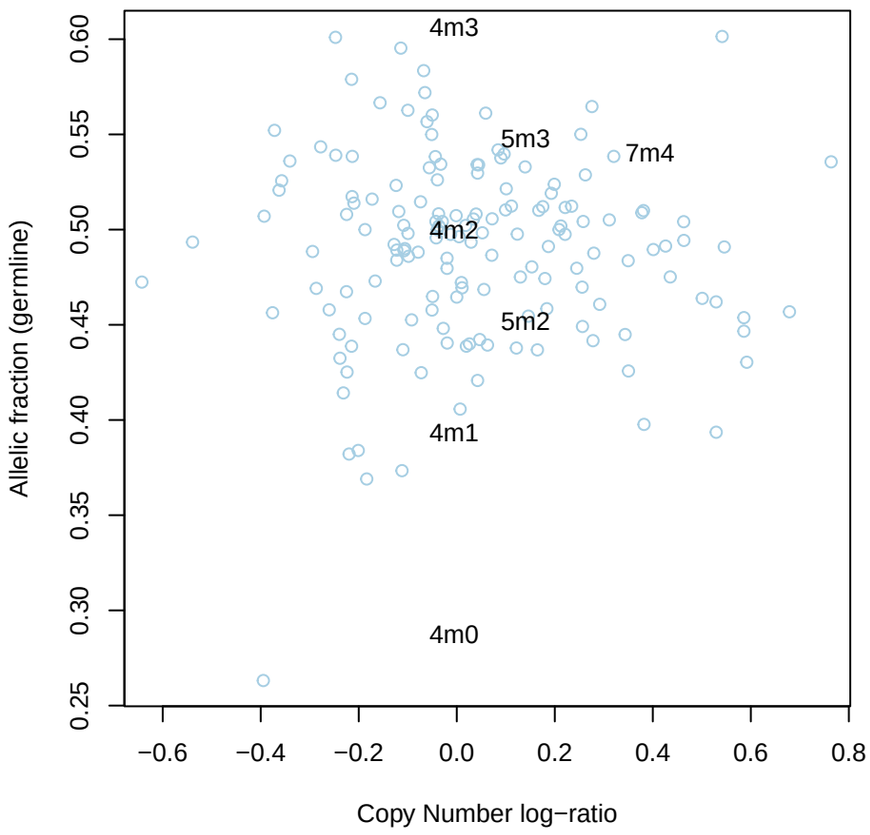

Frequency
Cellular fraction

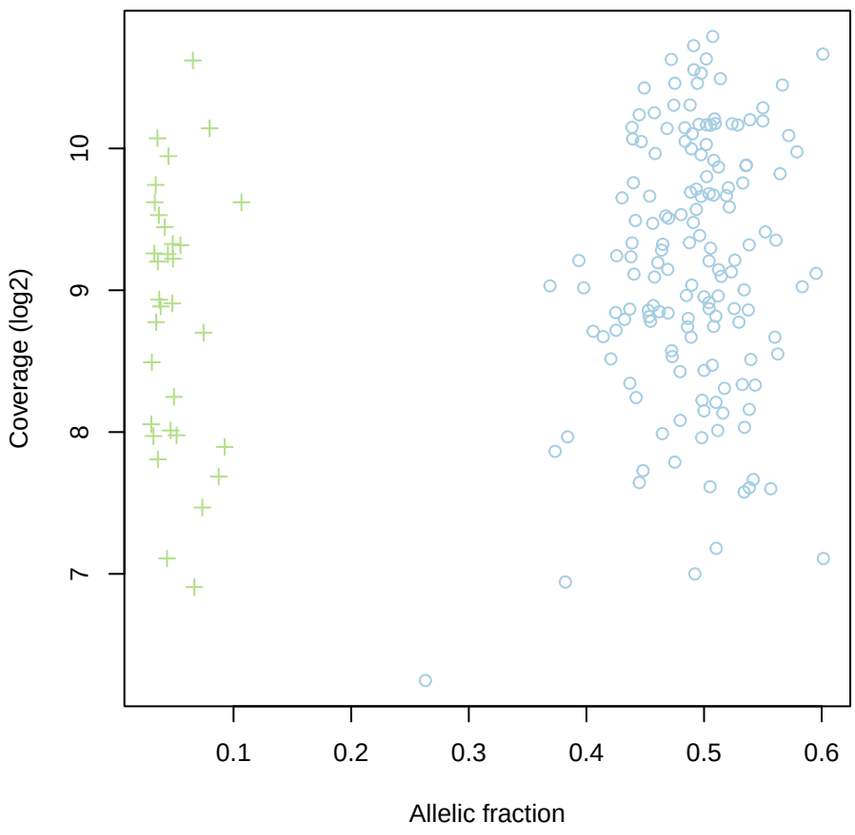

Purity: 0.27 Tumor ploidy: 4.034
2
3
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

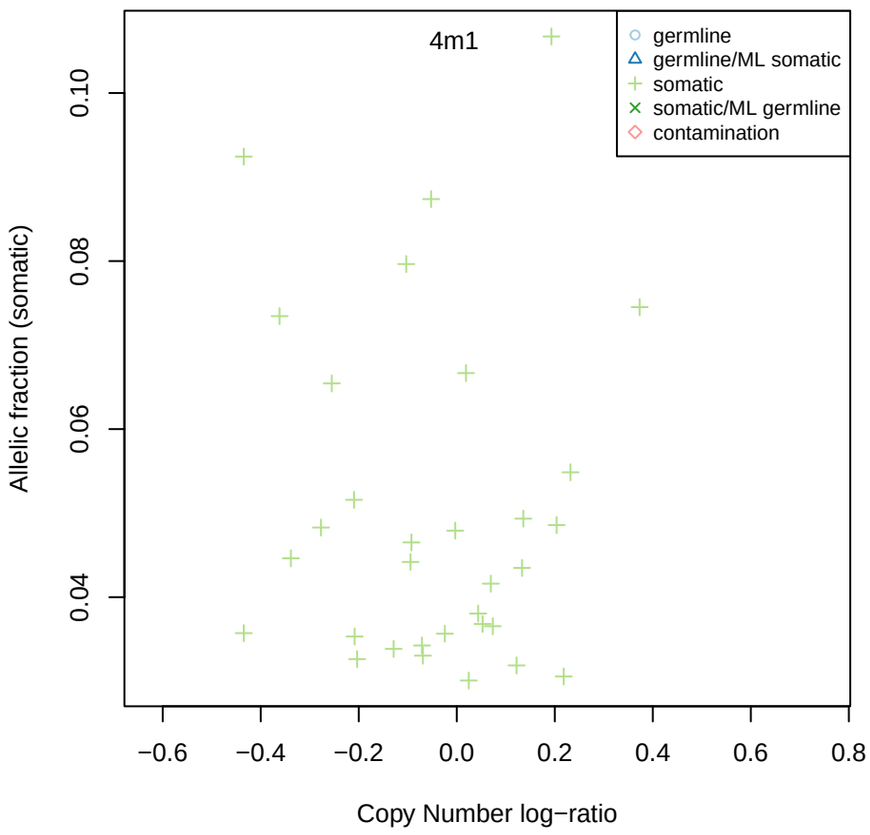

Purity: 0.27 Tumor ploidy: 4.034 SNV log−likelihood: −34.12 GoF: 94.8% Mean coverage: 499;665
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 18 19 20
B−Allele Frequency
0.25 0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

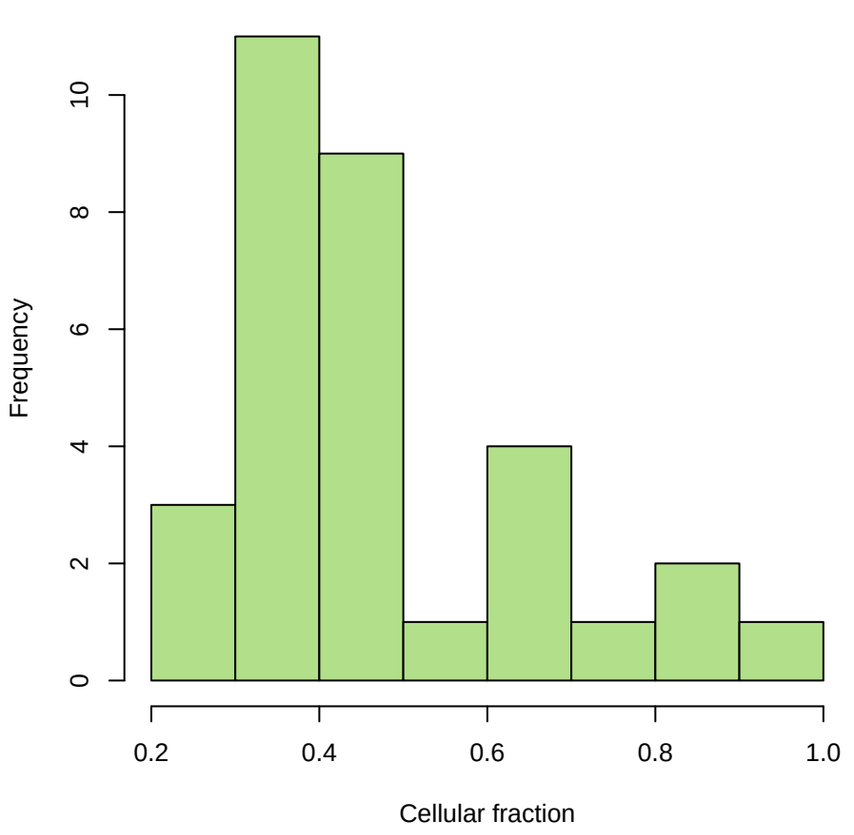

SCNA−fit log−likelihood: −7368.88
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
2 3 4 5 7
0 50 100 150
SNV Index

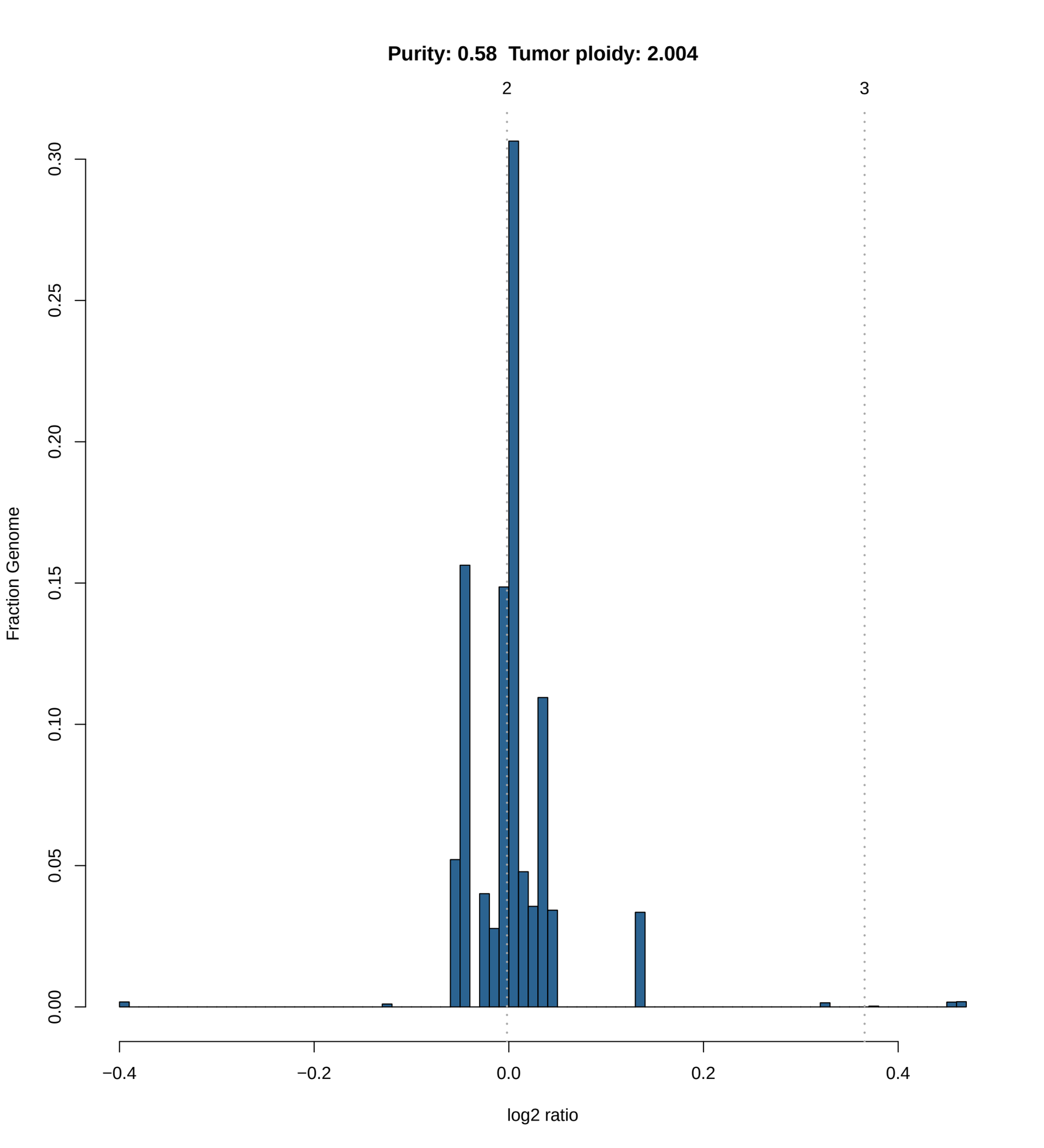

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

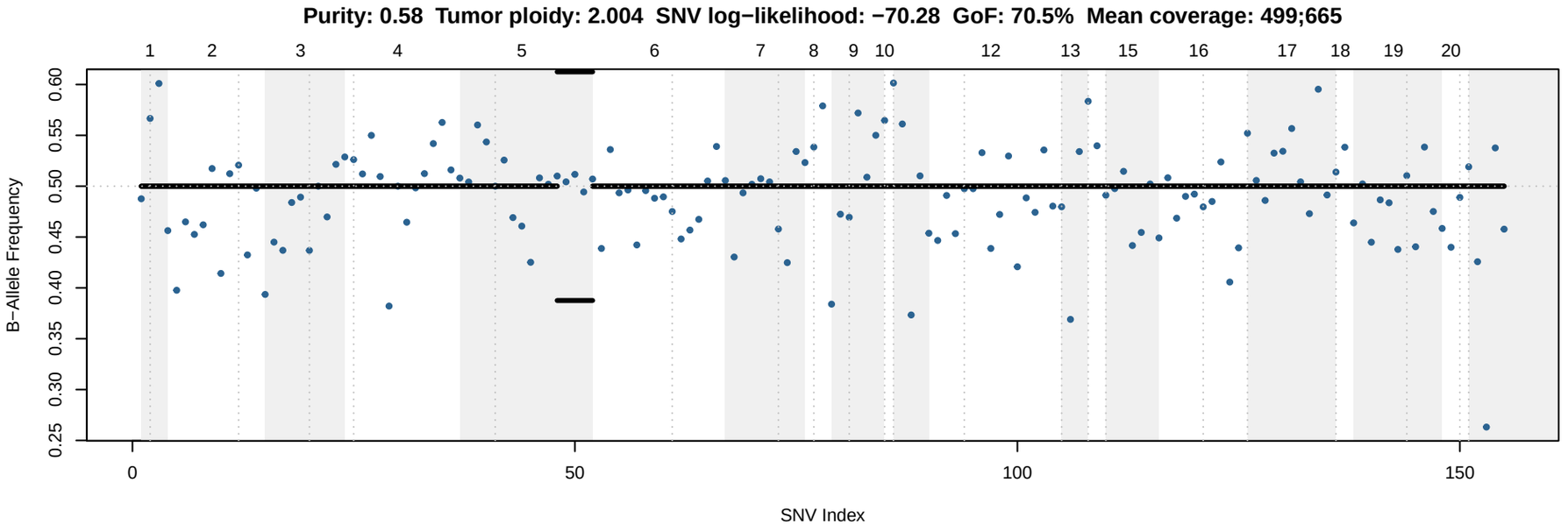

4m3
5m3
7m4
4m2
5m2
4m1
4m0
Allelic fraction (germline)
Copy Number log−ratio

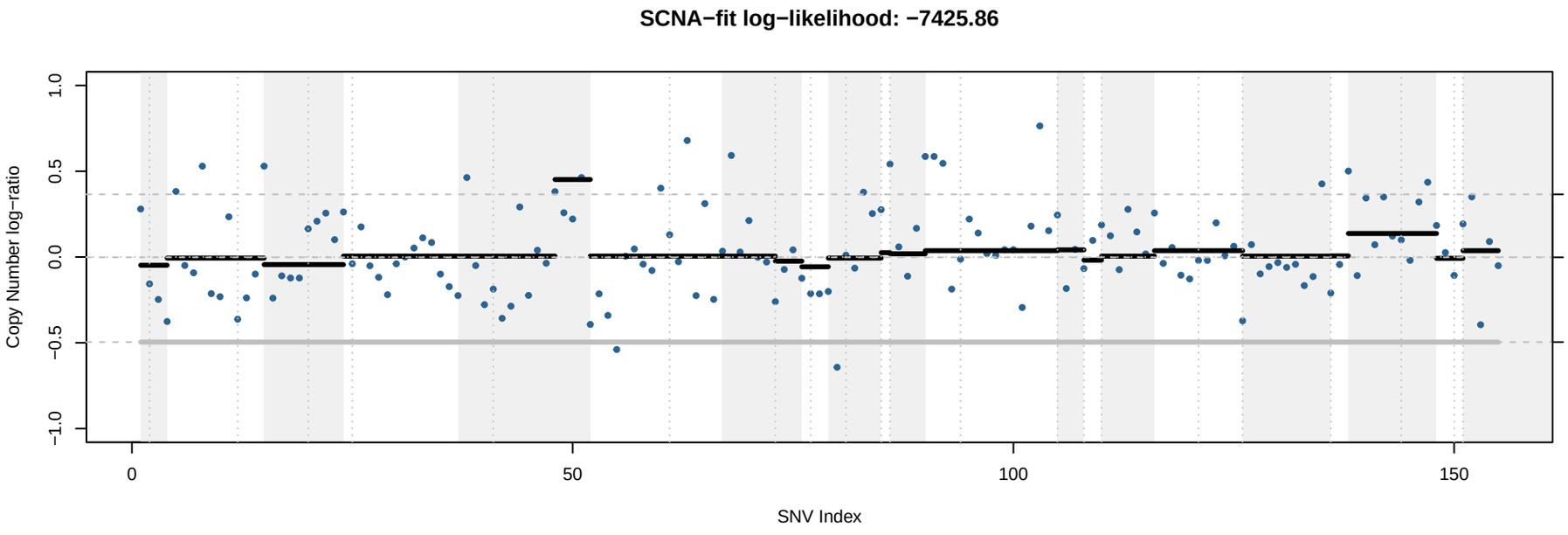

Coverage (log2)
Allelic fraction

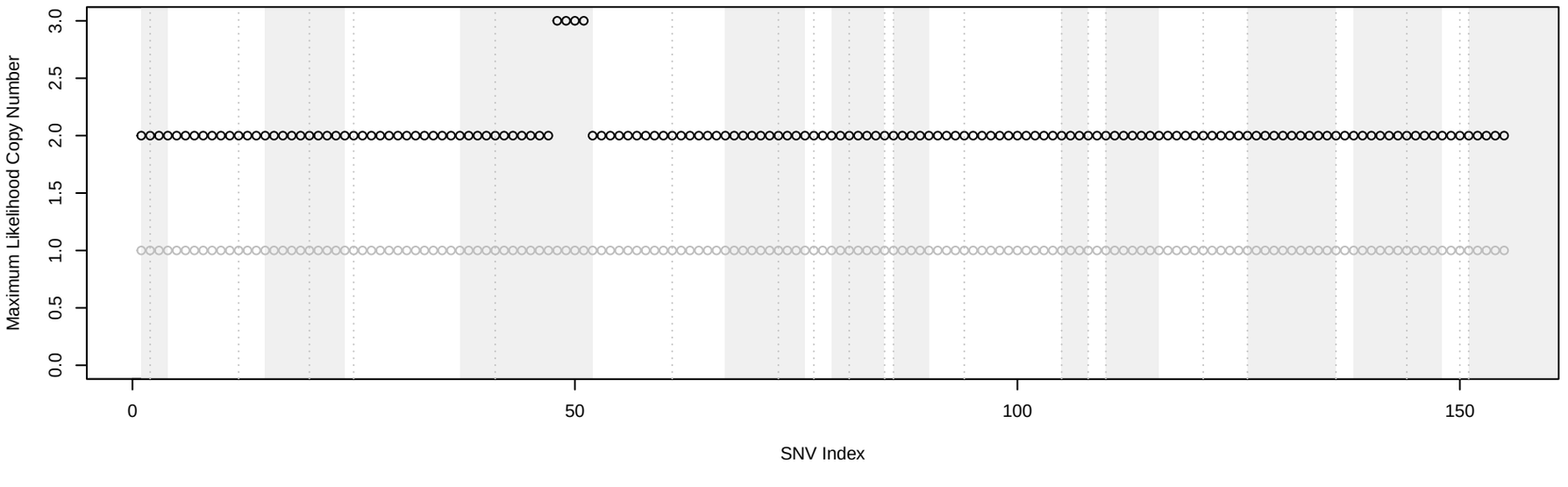

4m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

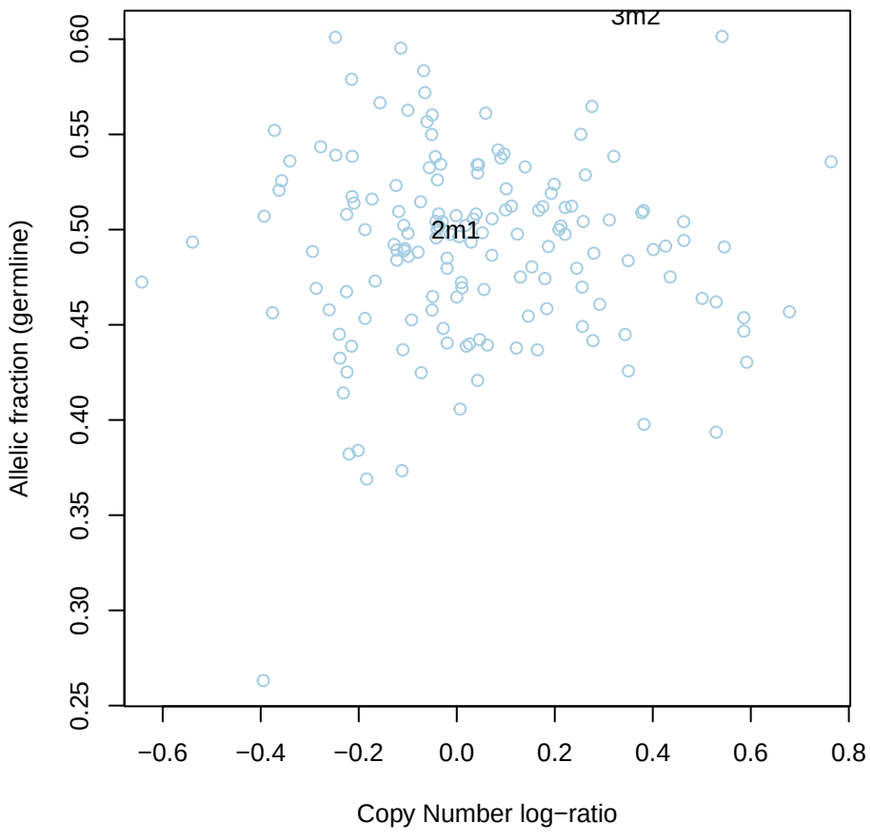

Frequency
Cellular fraction

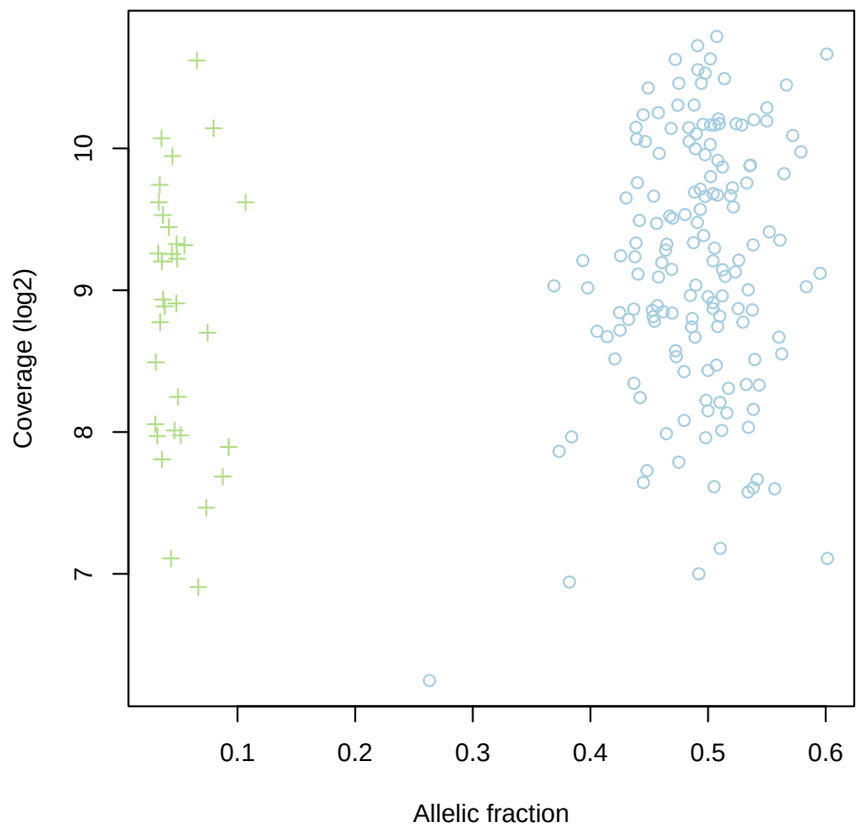

Purity: 0.58 Tumor ploidy: 2.004
2
3
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

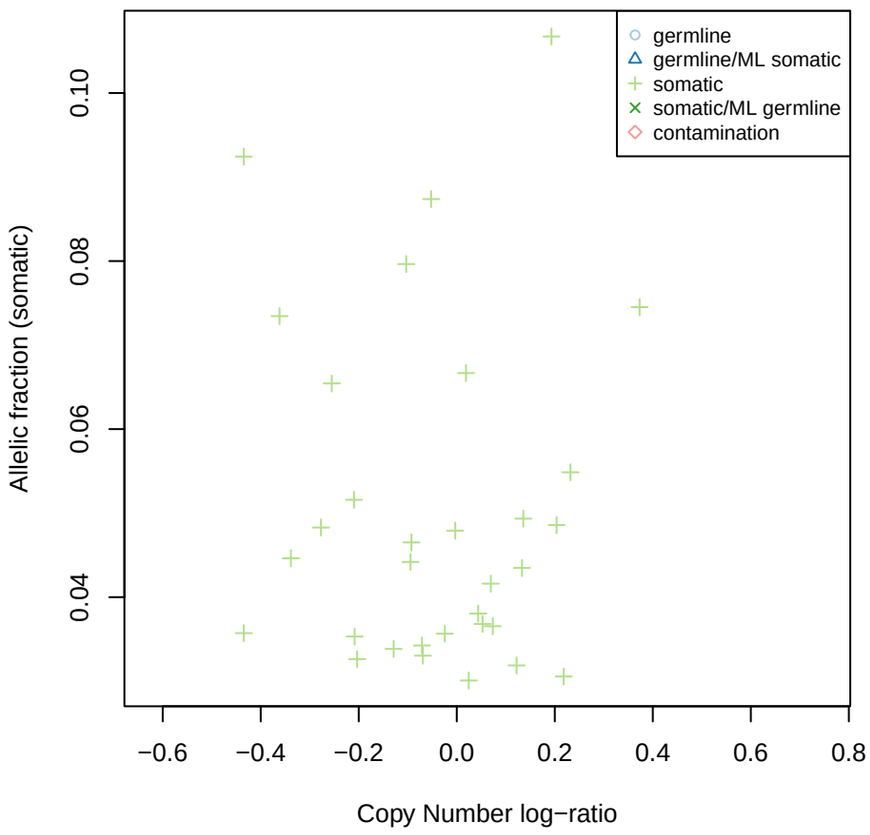

Purity: 0.58 Tumor ploidy: 2.004 SNV log−likelihood: −70.28 GoF: 70.5% Mean coverage: 499;665
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 18 19 20
B−Allele Frequency
0.25 0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

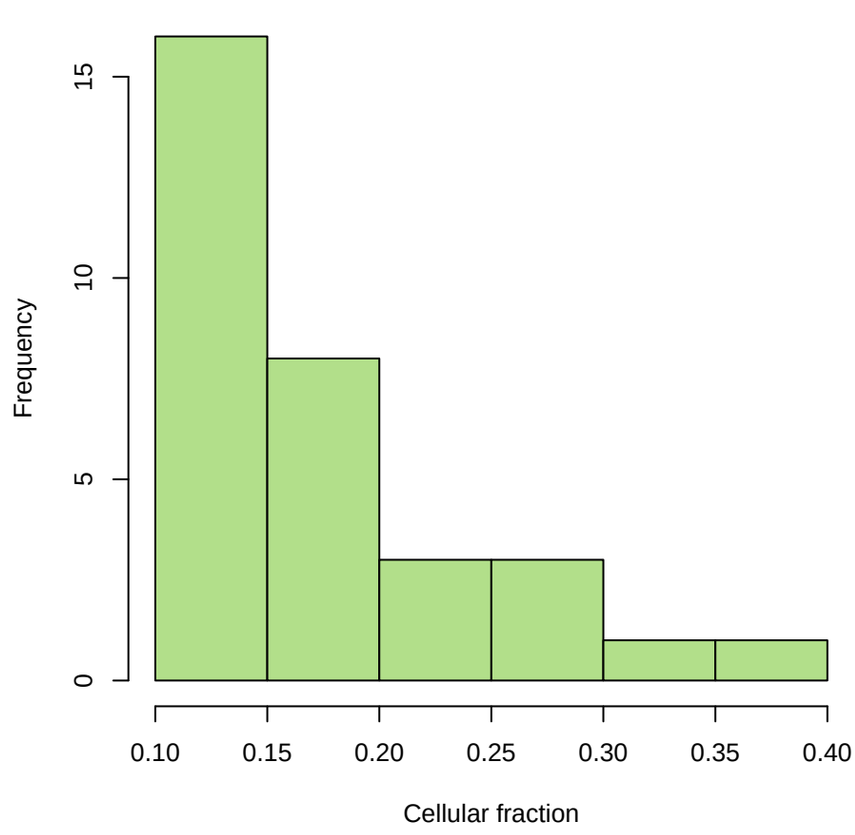

SCNA−fit log−likelihood: −7425.86
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3
0 50 100 150
SNV Index

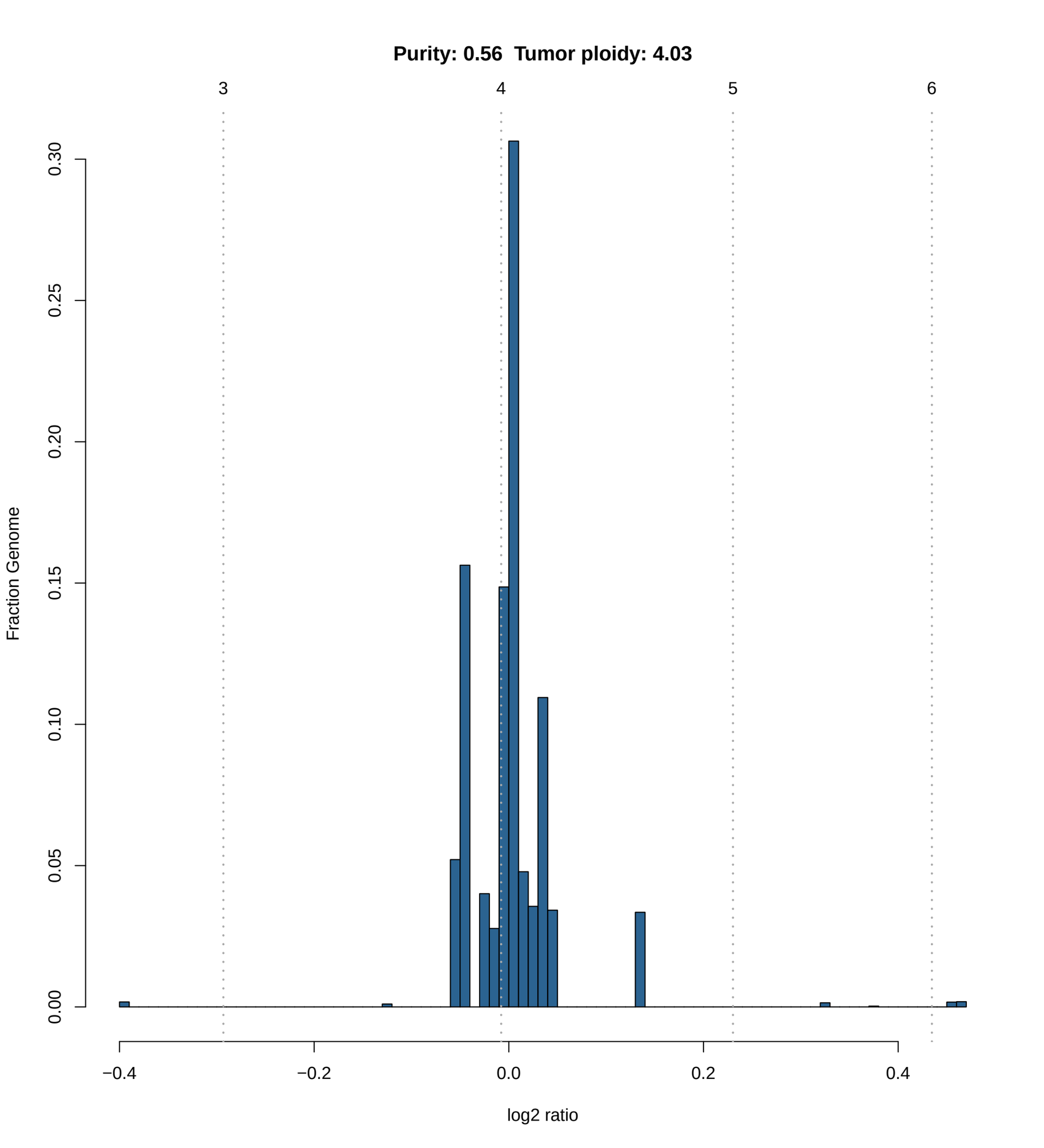

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

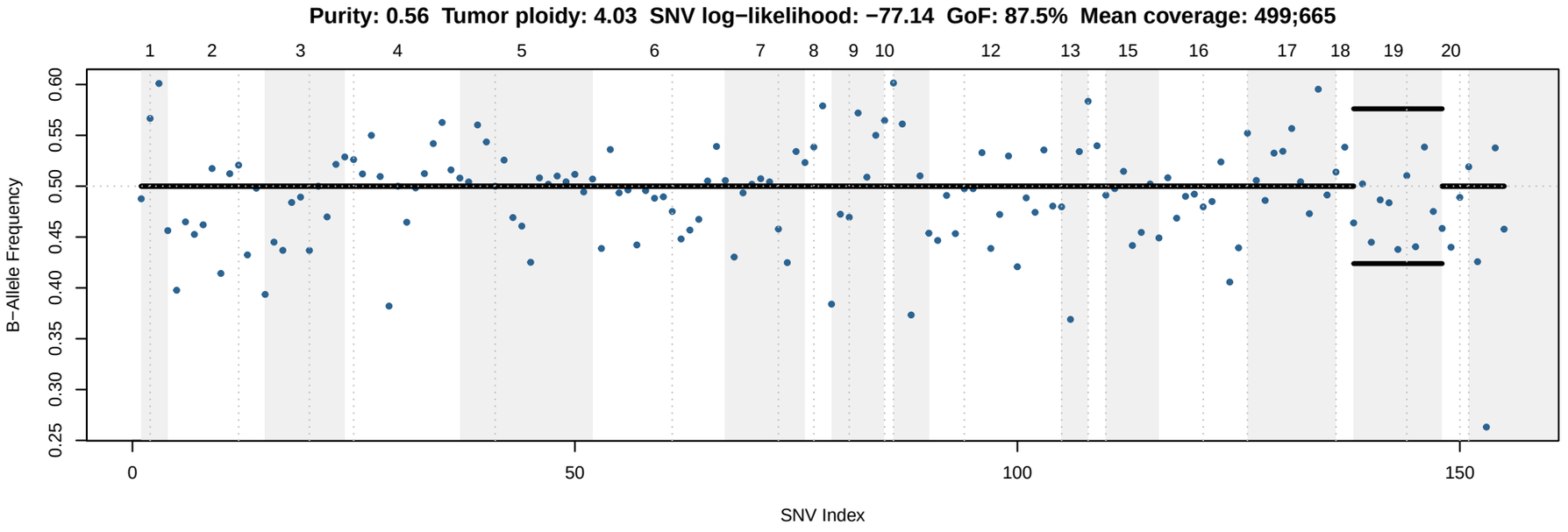

3m2
2m1
Allelic fraction (germline)
Copy Number log−ratio
0.25
0.30
0.35
0.40
0.45
0.50
0.55
0.60
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8

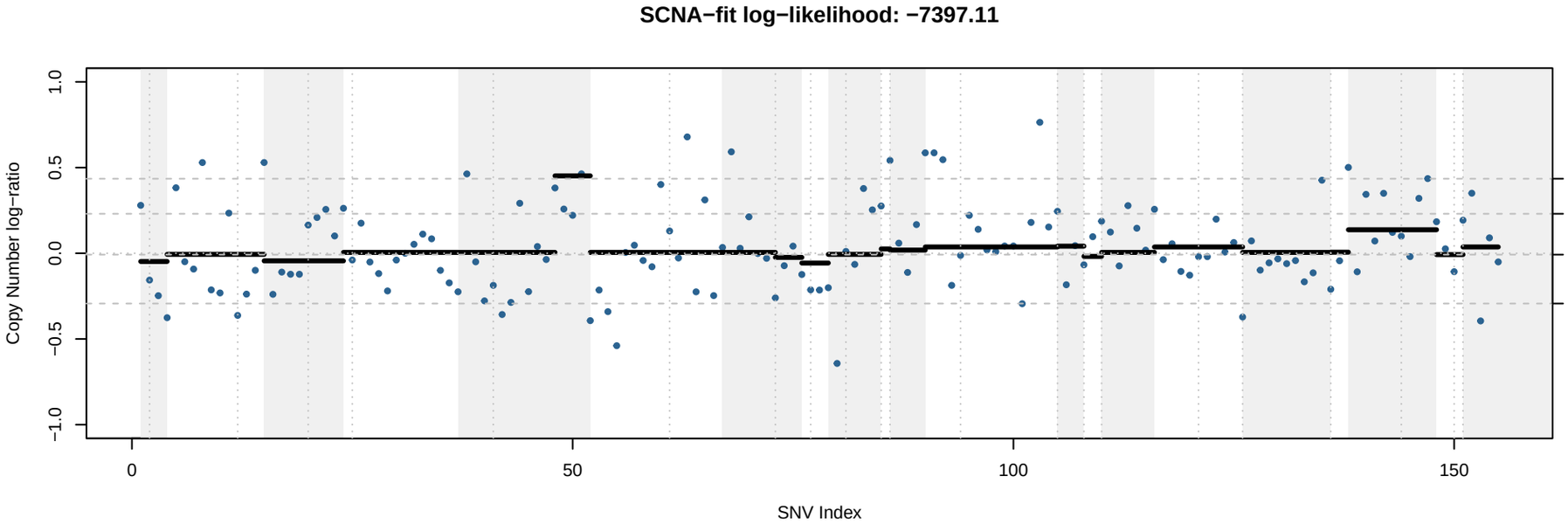

Coverage (log2)
Allelic fraction
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

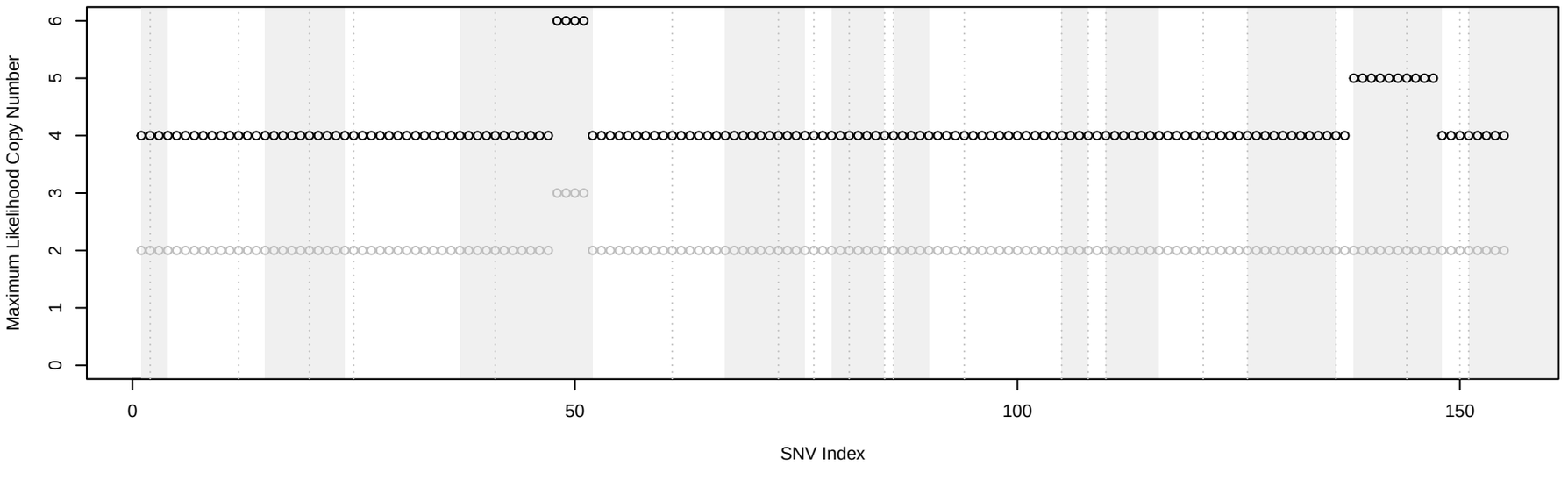

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8

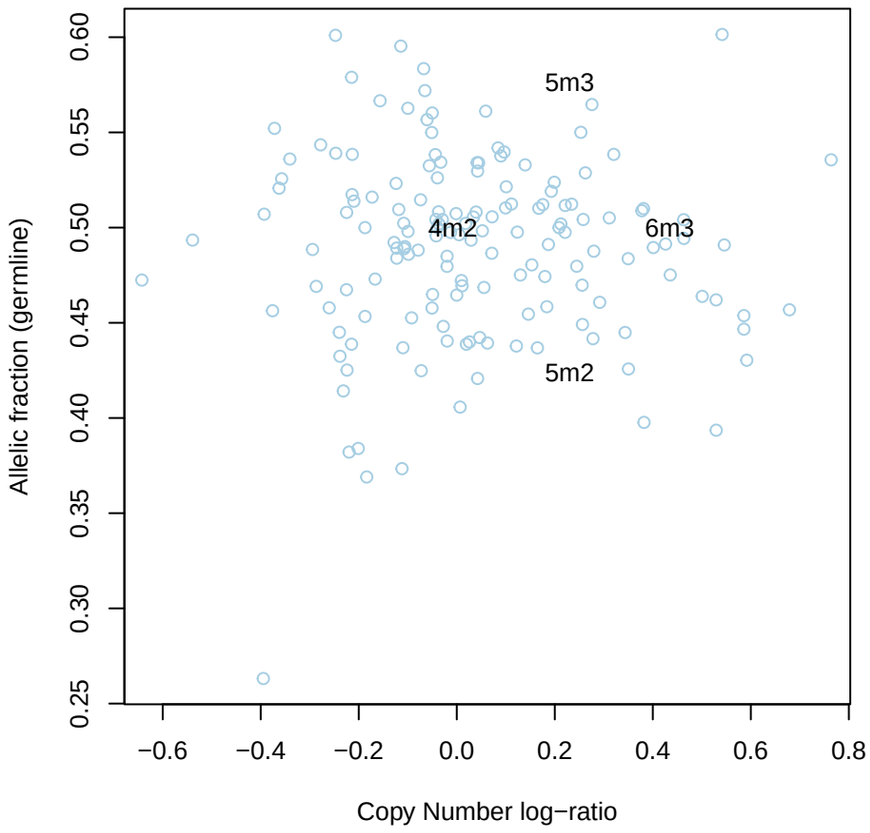

Frequency
Cellular fraction
0
5
10
15
0.10
0.15
0.20
0.25
0.30
0.35
0.40

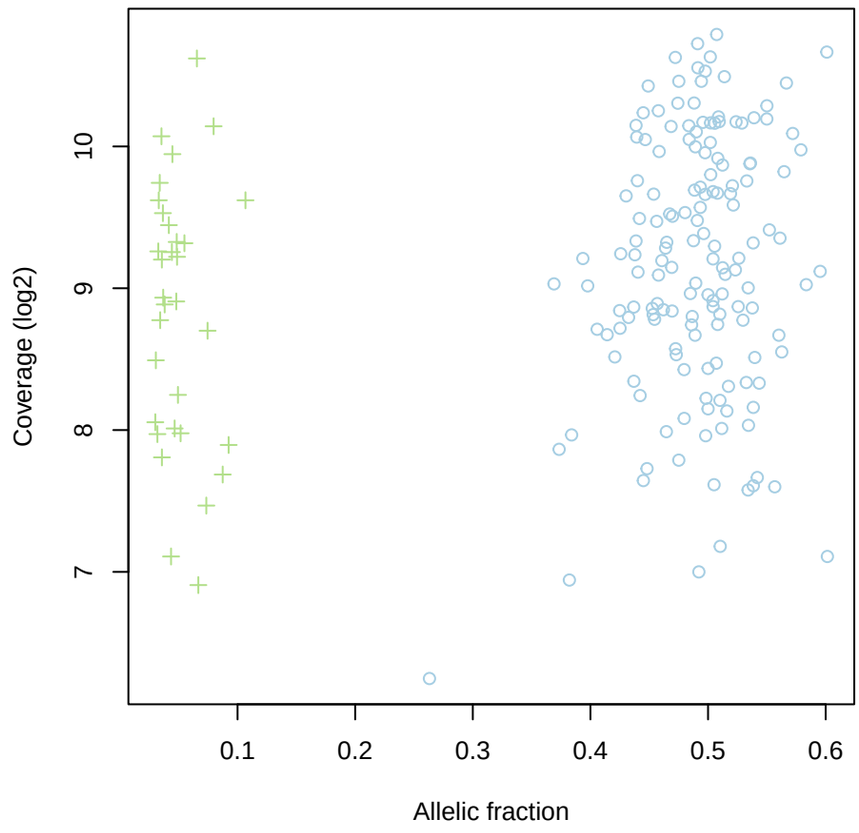

Purity: 0.56 Tumor ploidy: 4.03
3
4
5
6
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

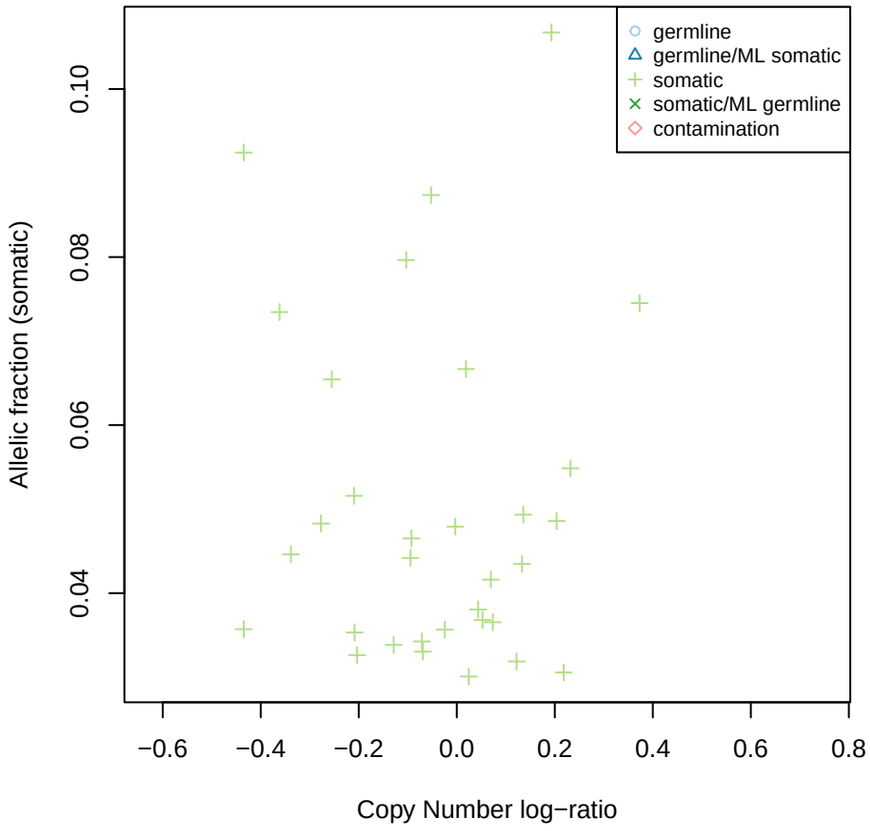

Purity: 0.56 Tumor ploidy: 4.03 SNV log−likelihood: −77.14 GoF: 87.5% Mean coverage: 499;665
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 18 19 20
B−Allele Frequency
0.25 0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

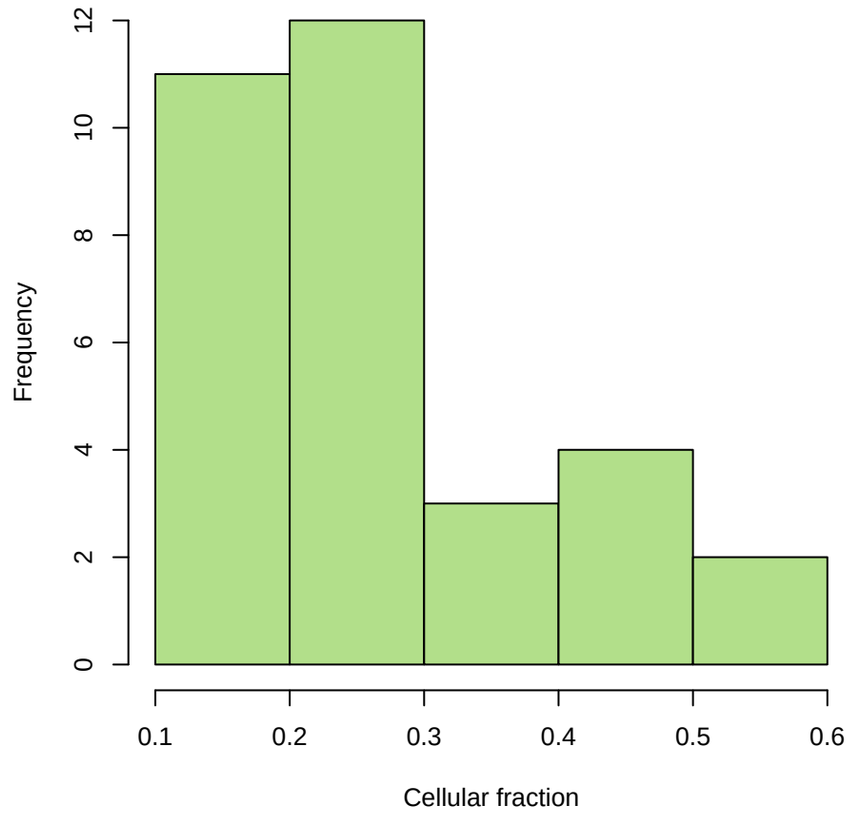

SCNA−fit log−likelihood: −7397.11
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
3 4 5 6
0 50 100 150
SNV Index

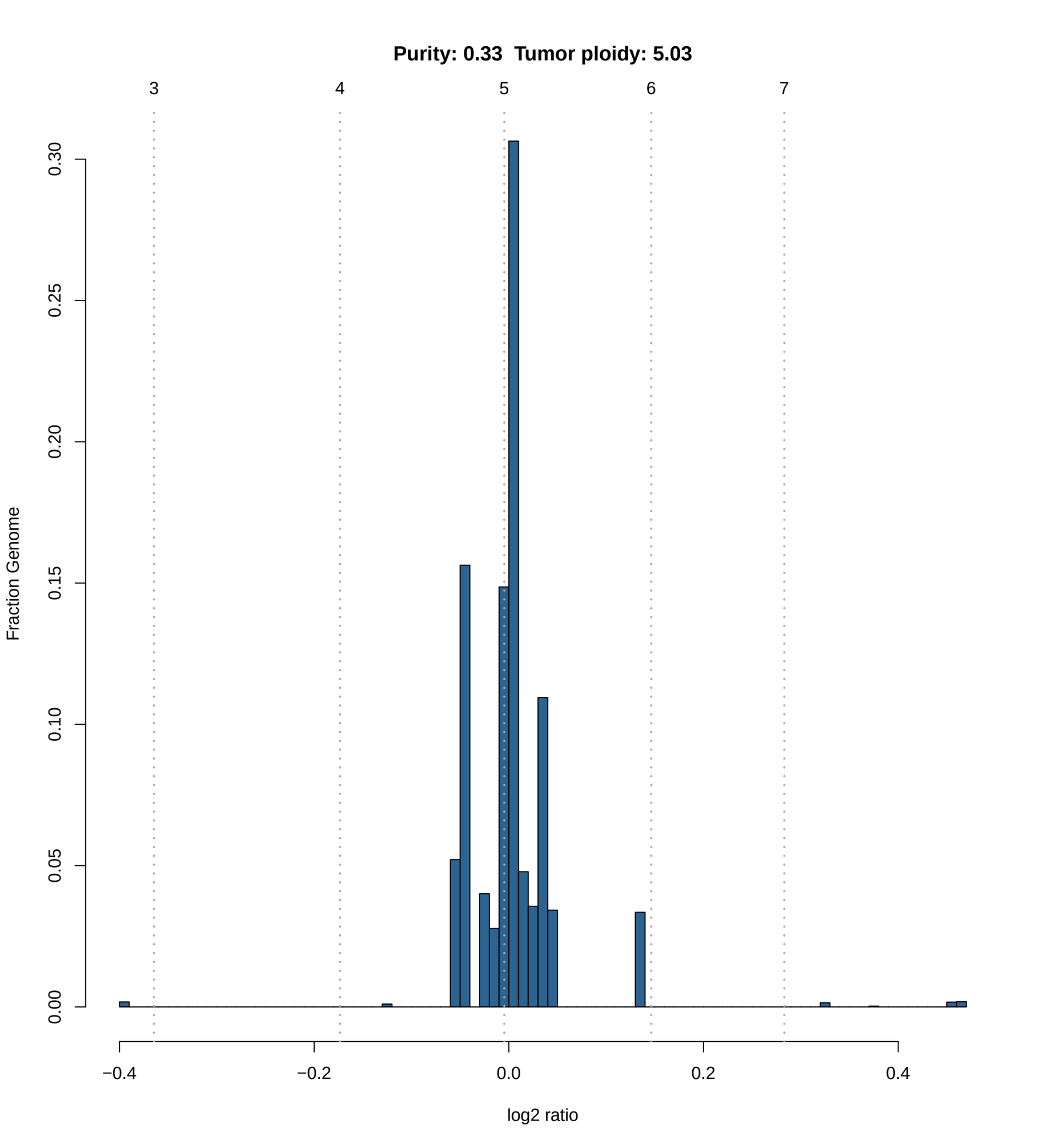

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

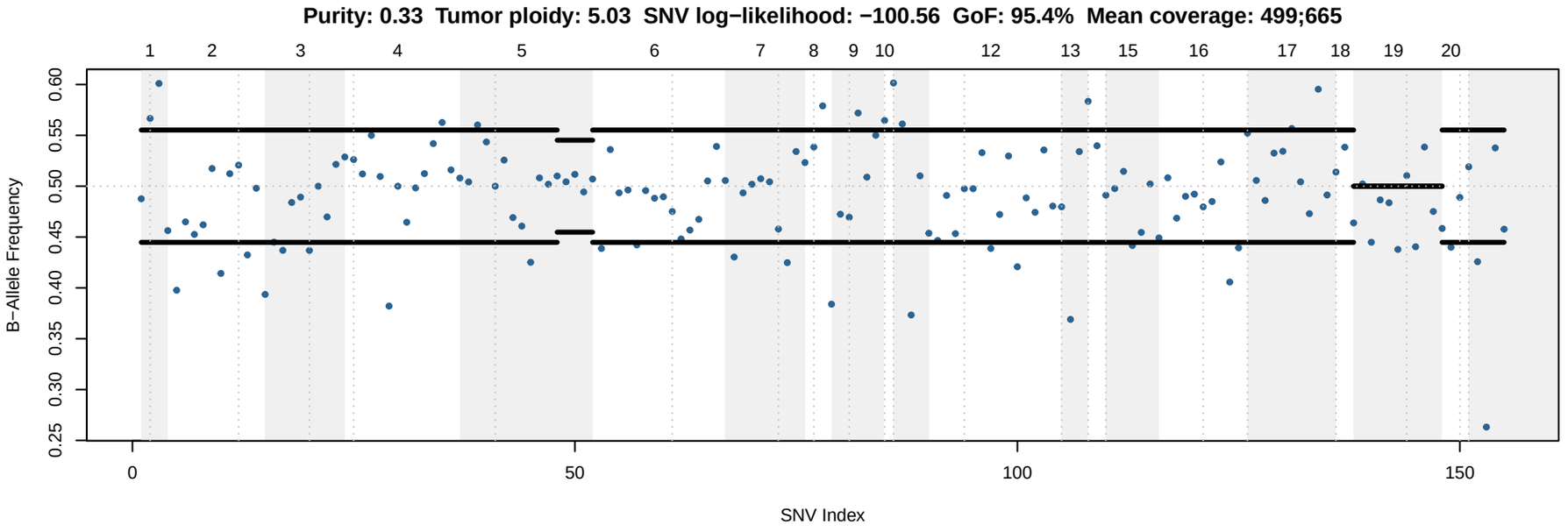

Allelic fraction (germline)
Copy Number log−ratio
5m3
4m2
6m3
5m2

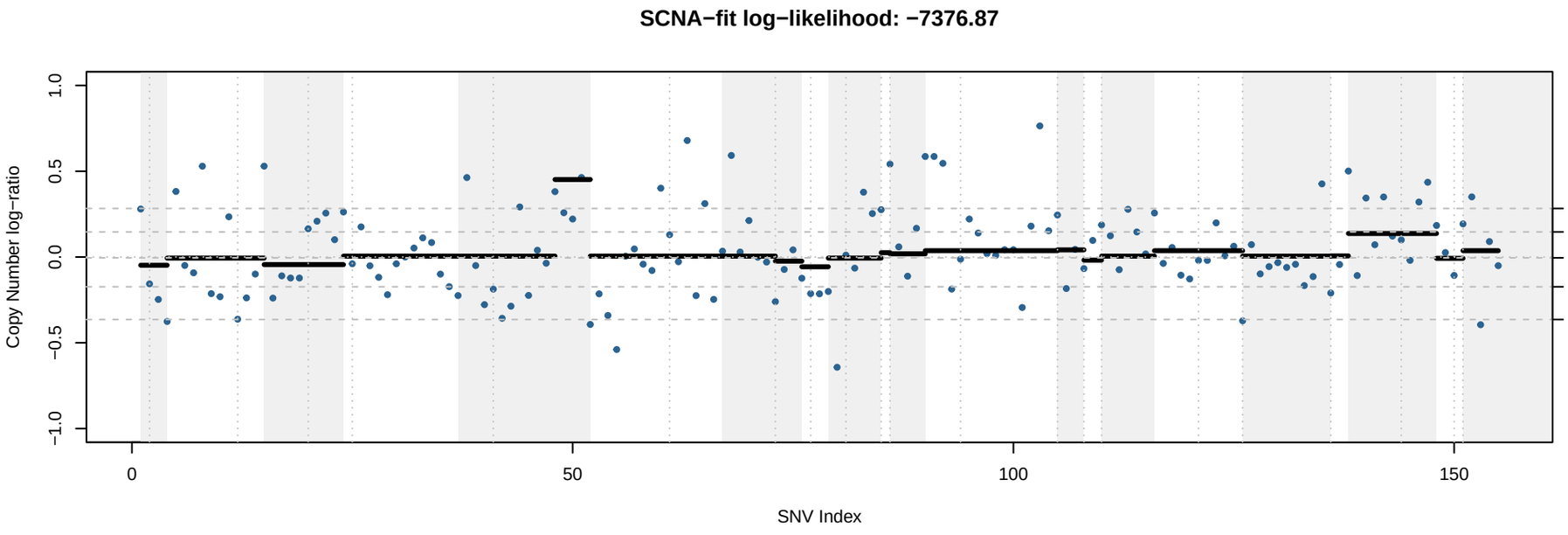

Coverage (log2)
Allelic fraction

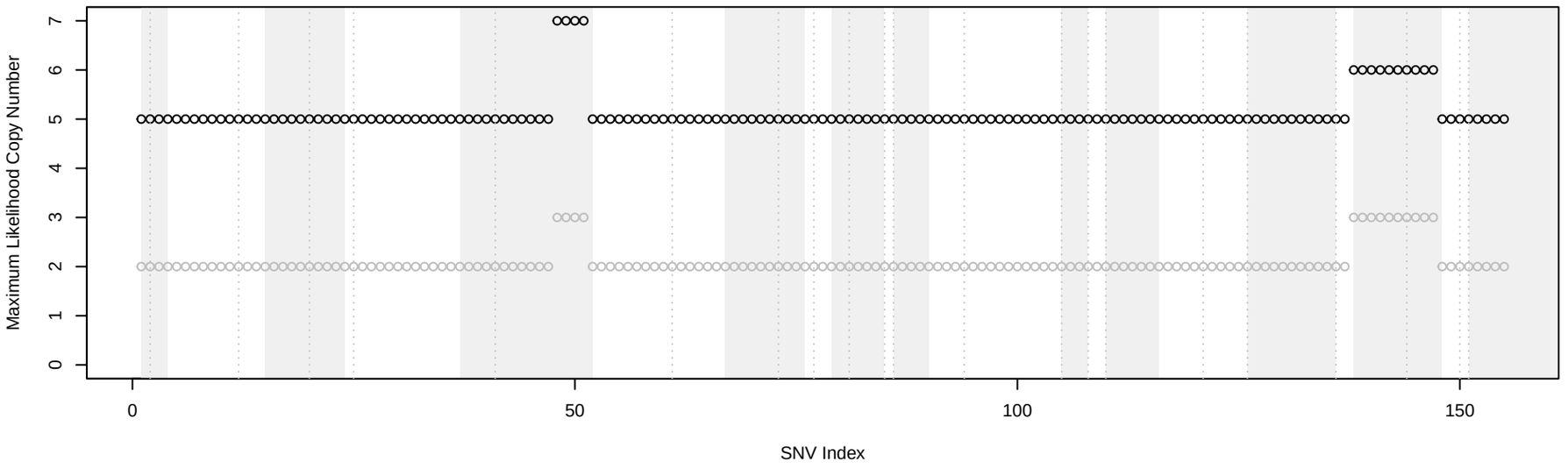

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

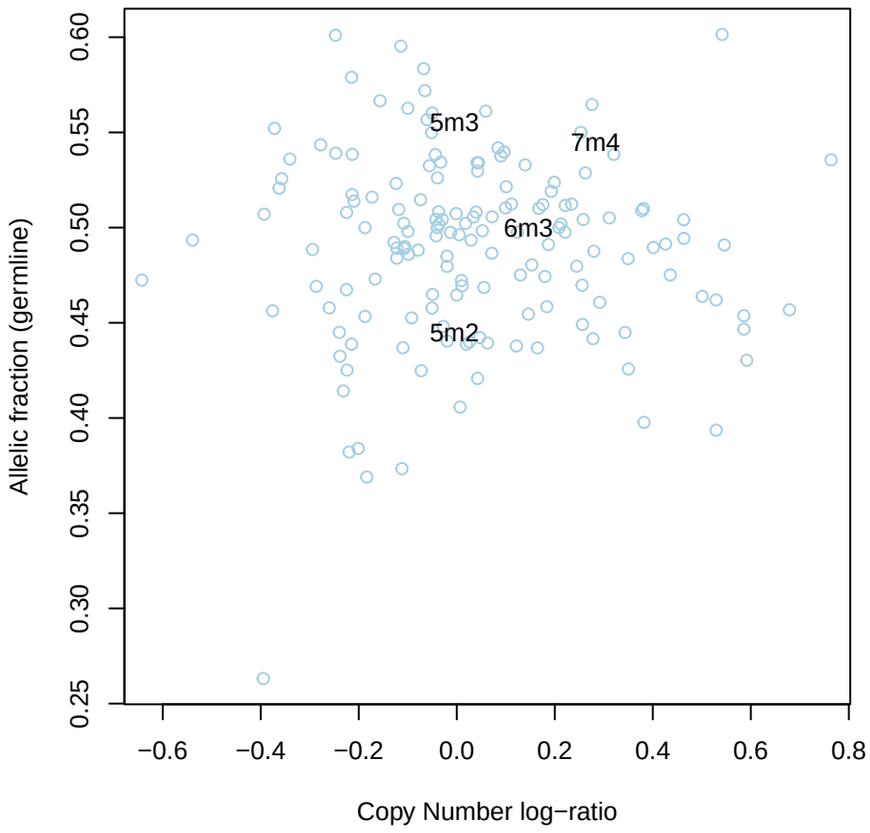

Frequency
Cellular fraction

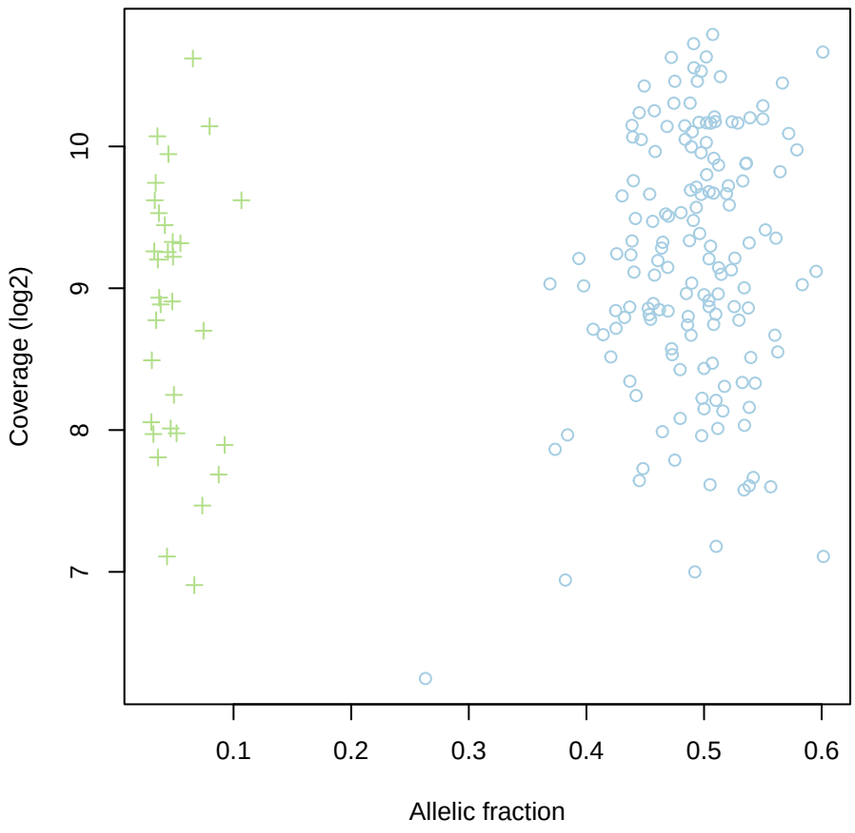

Purity: 0.33 Tumor ploidy: 5.03
3
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

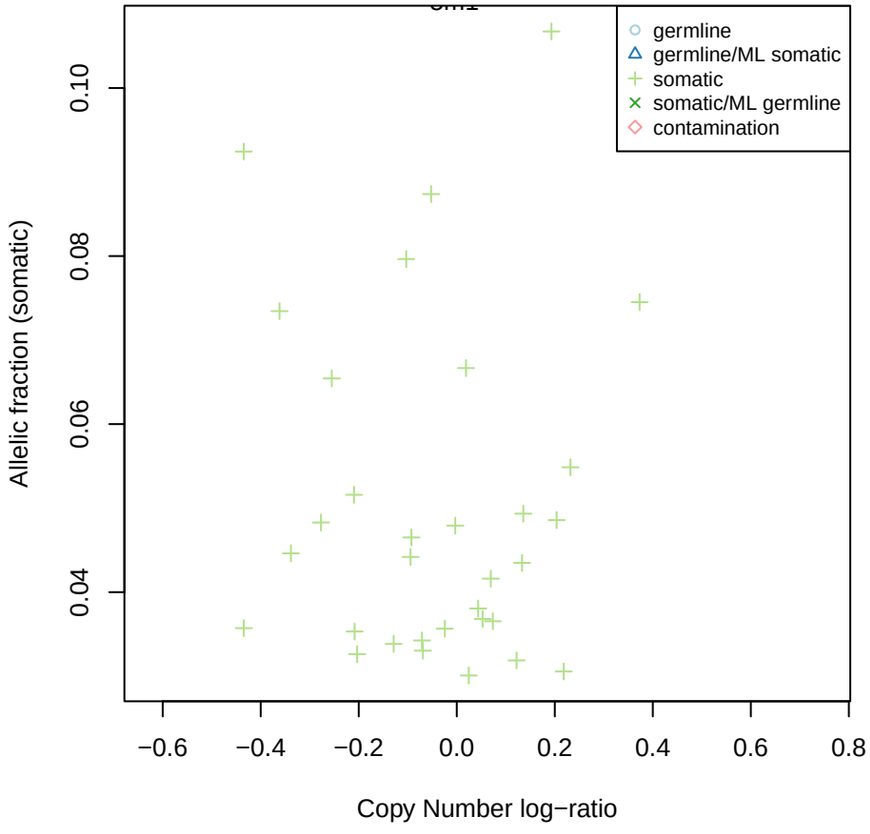

Purity: 0.33 Tumor ploidy: 5.03 SNV log−likelihood: −100.56 GoF: 95.4% Mean coverage: 499;665
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 18 19 20
B−Allele Frequency
0.25 0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

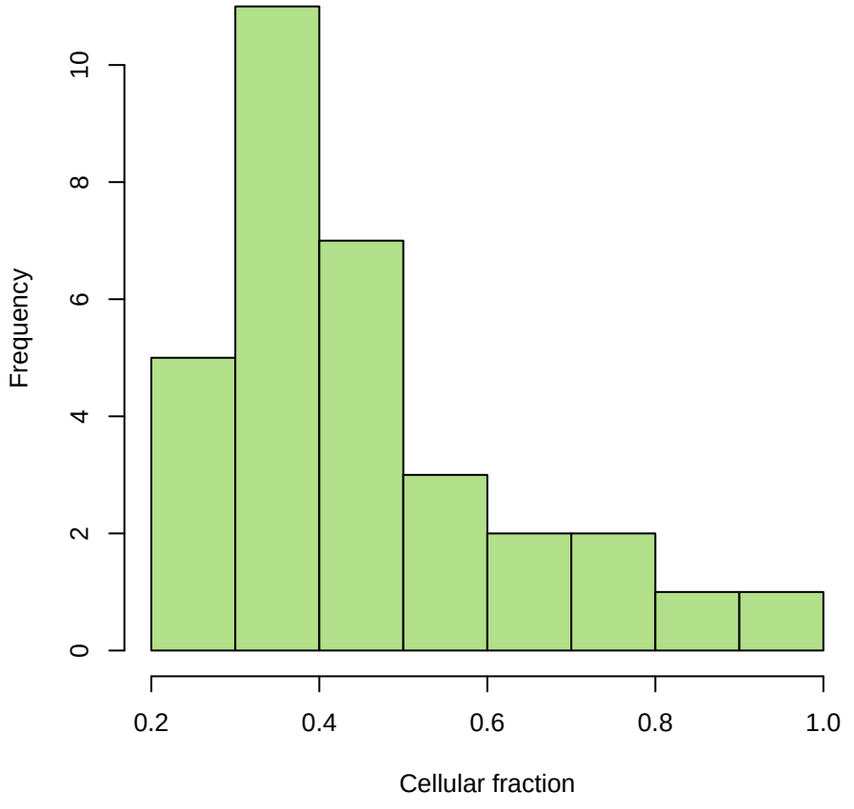

SCNA−fit log−likelihood: −7376.87
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
3 4 5 6
0 50 100 150
SNV Index

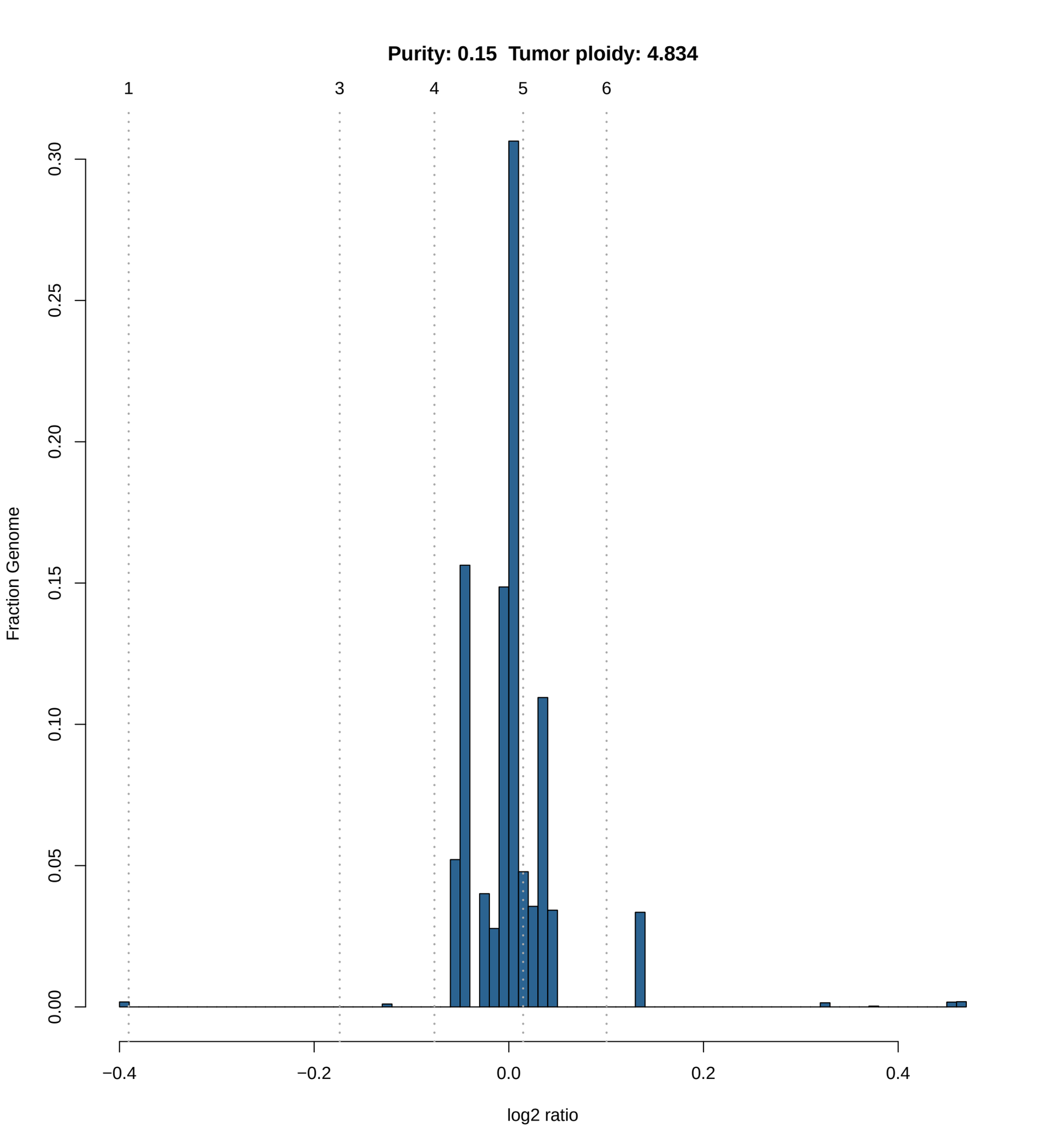

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

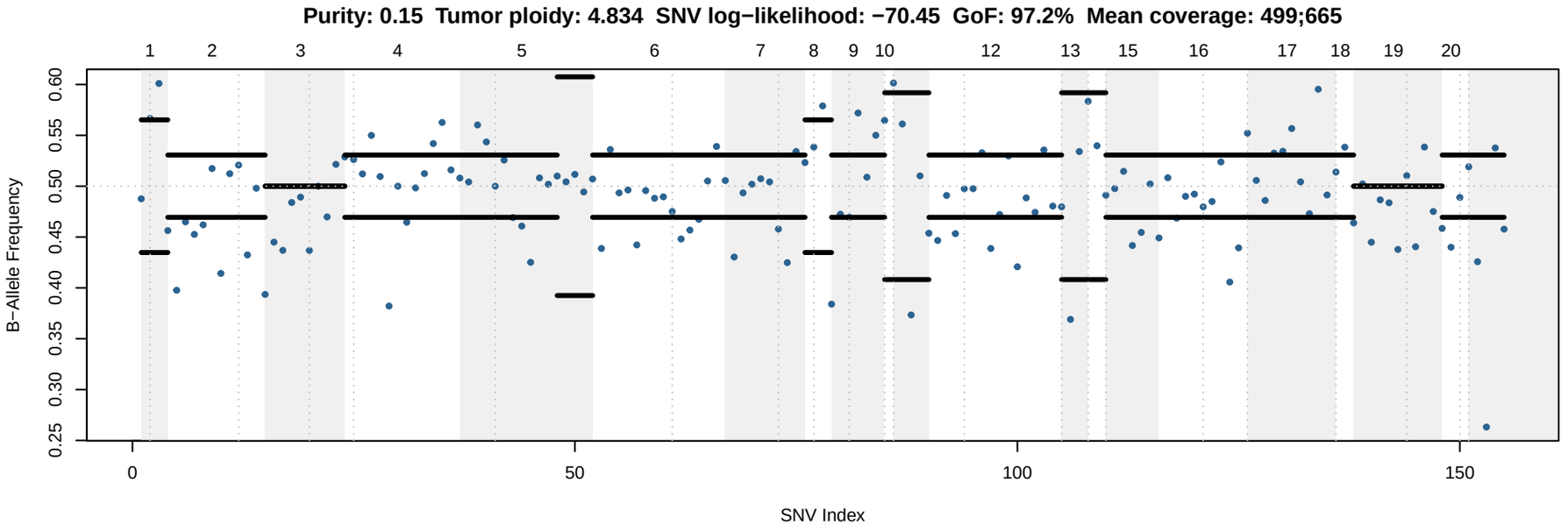

Allelic fraction (germline)
Copy Number log−ratio
5m3
7m4
6m3
5m2

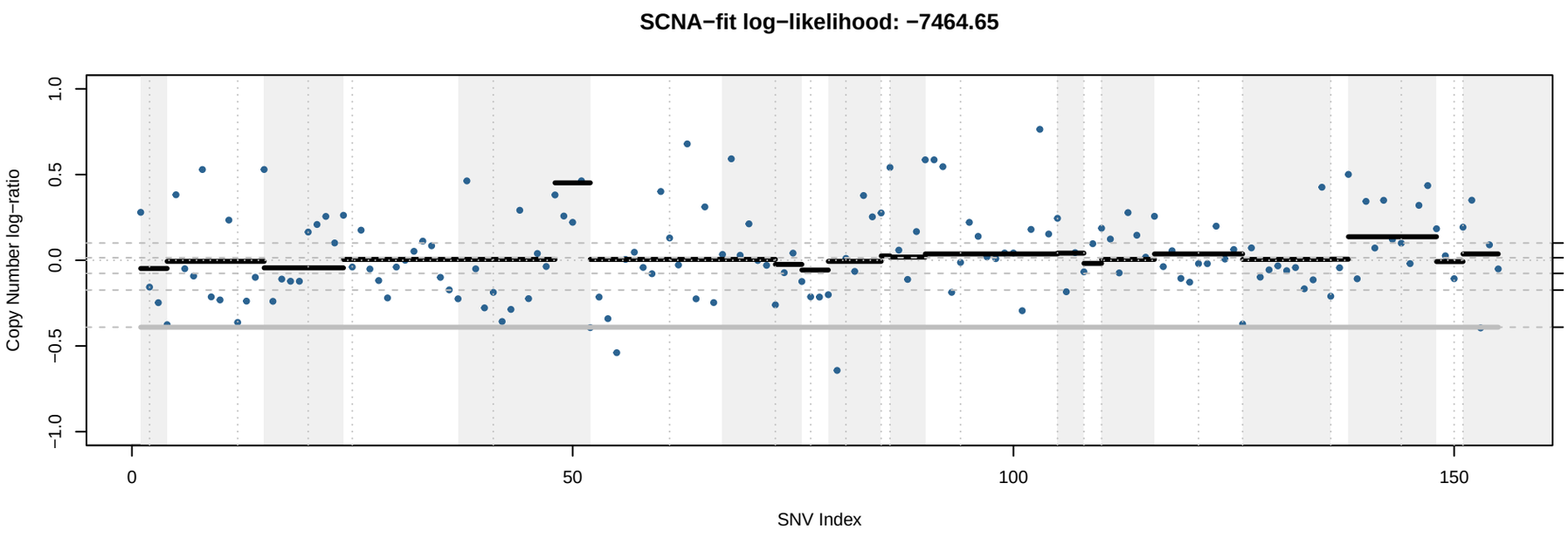

Coverage (log2)
Allelic fraction

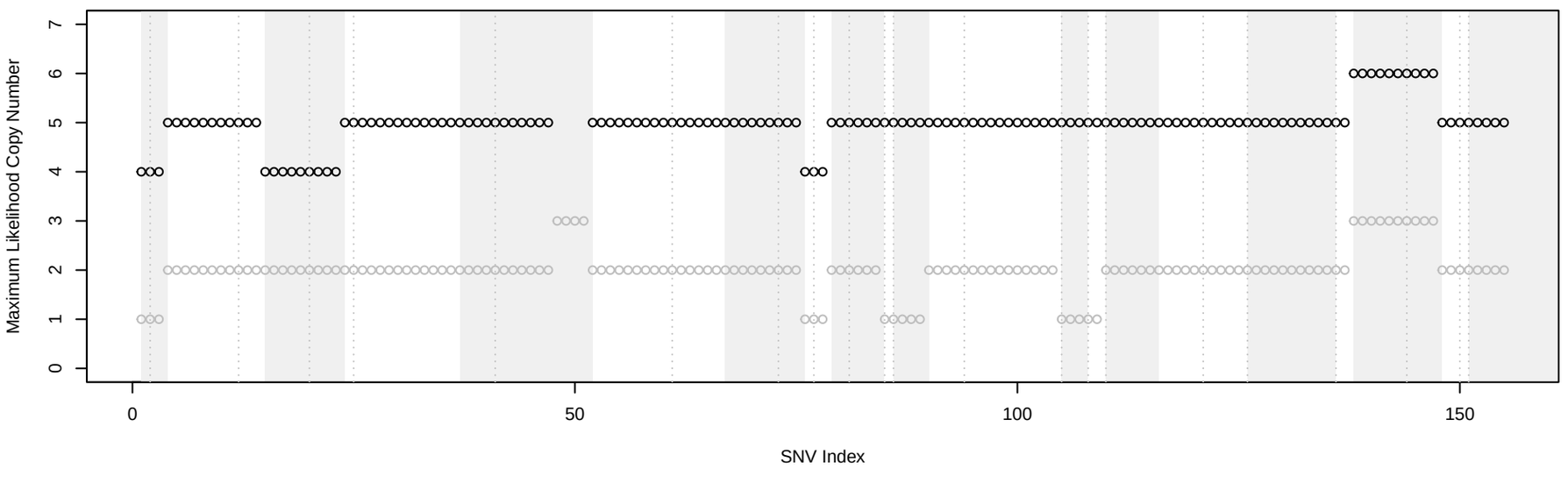

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

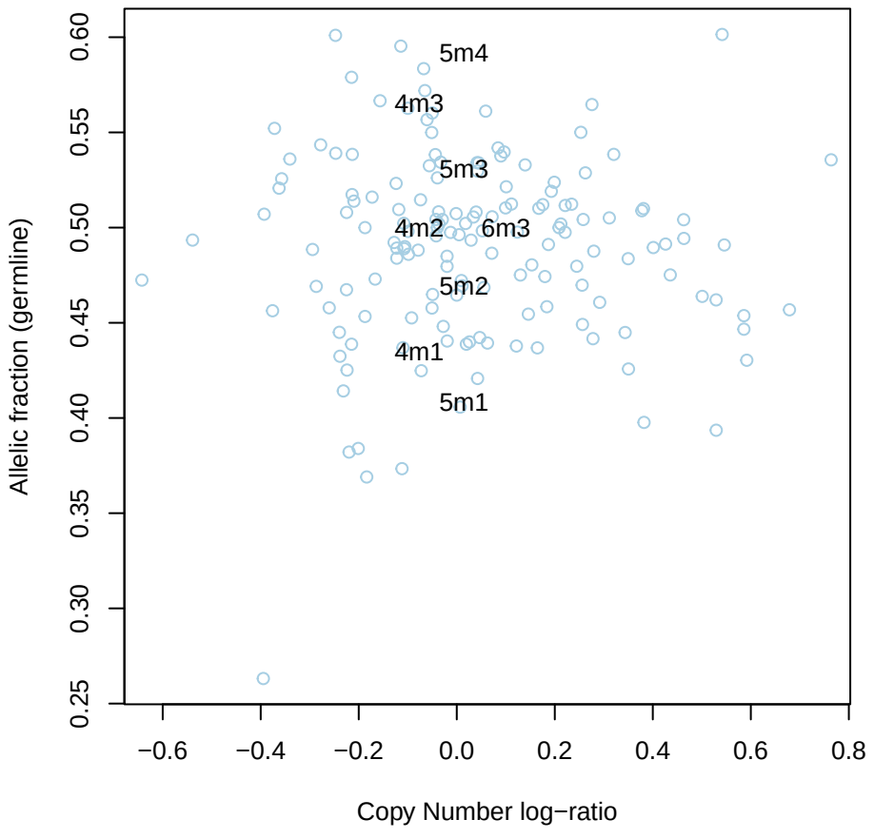

Frequency
Cellular fraction

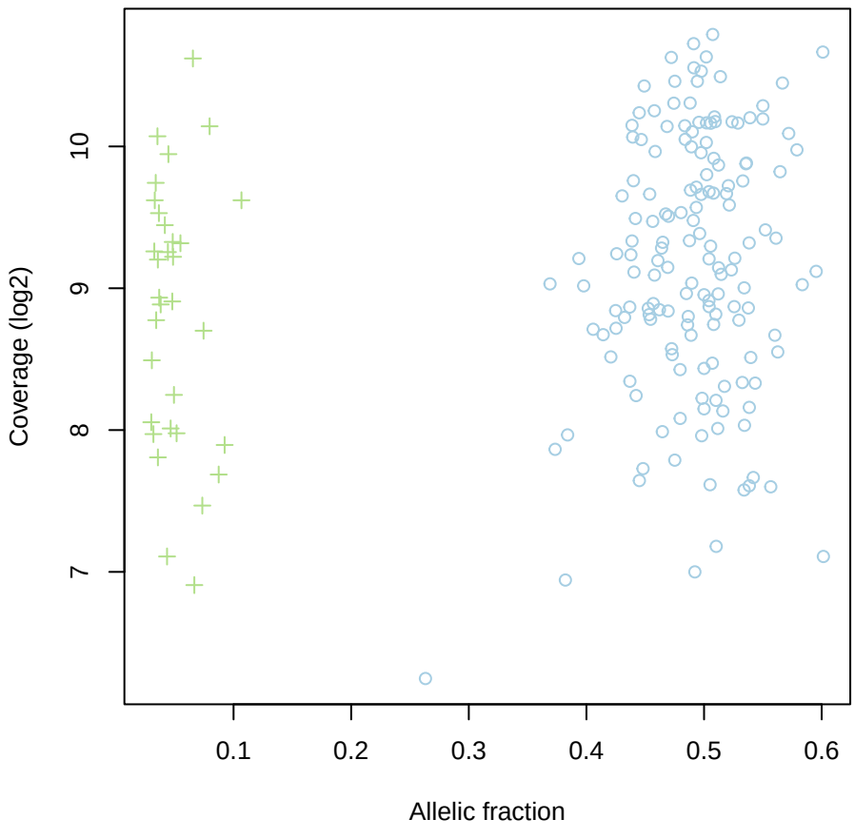

Purity: 0.15 Tumor ploidy: 4.834
1
3
4
5
6
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

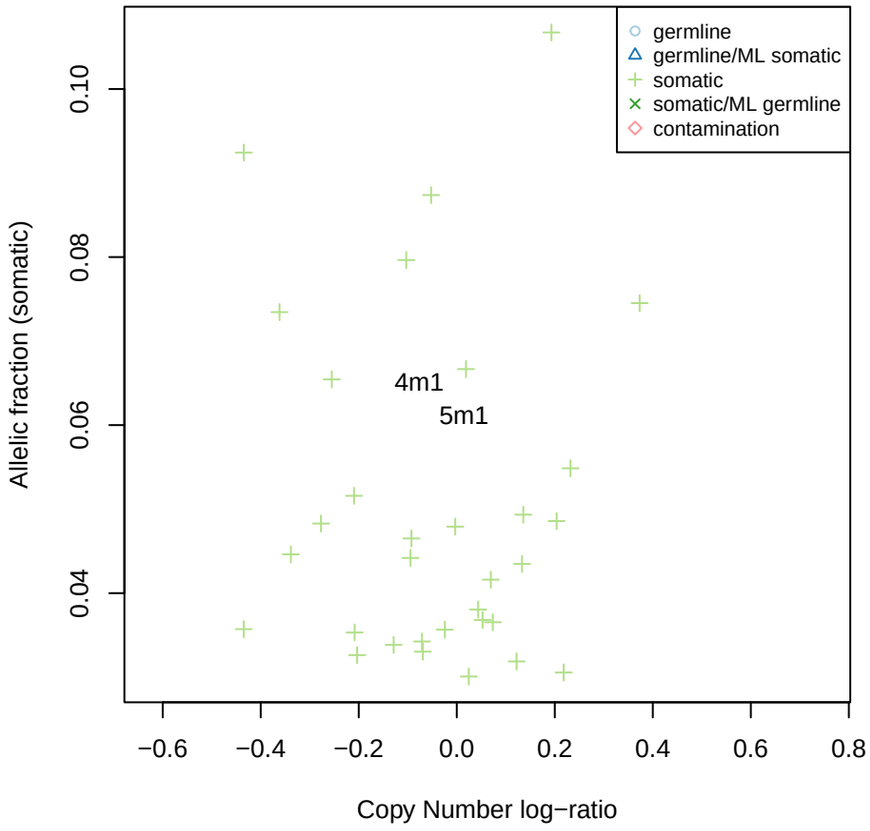

Purity: 0.15 Tumor ploidy: 4.834 SNV log−likelihood: −70.45 GoF: 97.2% Mean coverage: 499;665
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 18 19 20
B−Allele Frequency
0.25 0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

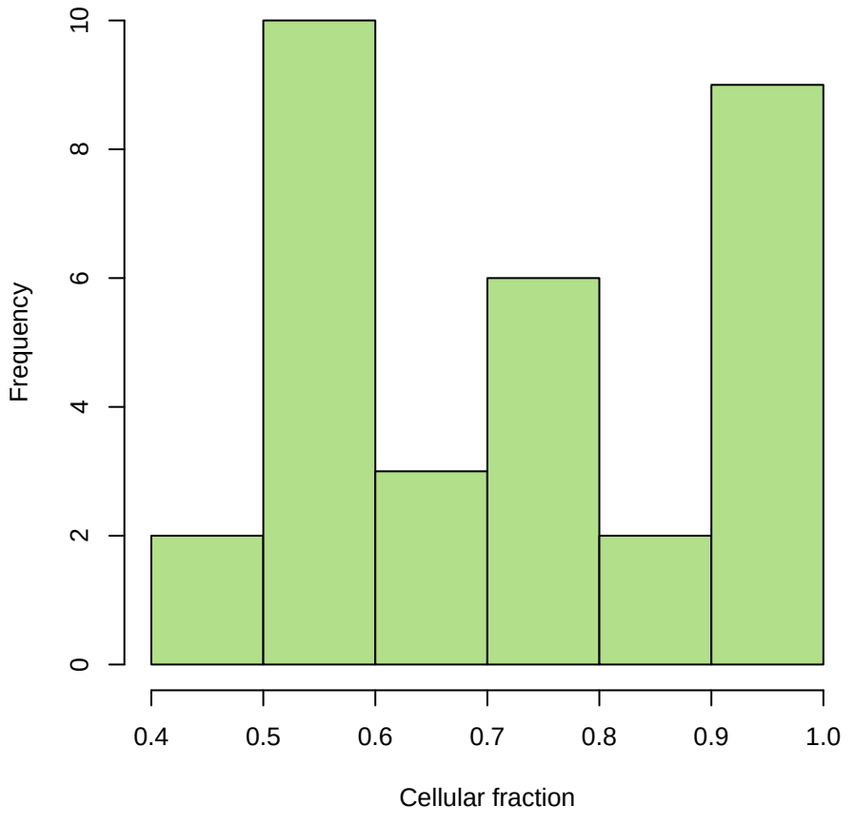

SCNA−fit log−likelihood: −7464.65
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
1 3 5
0 50 100 150
SNV Index

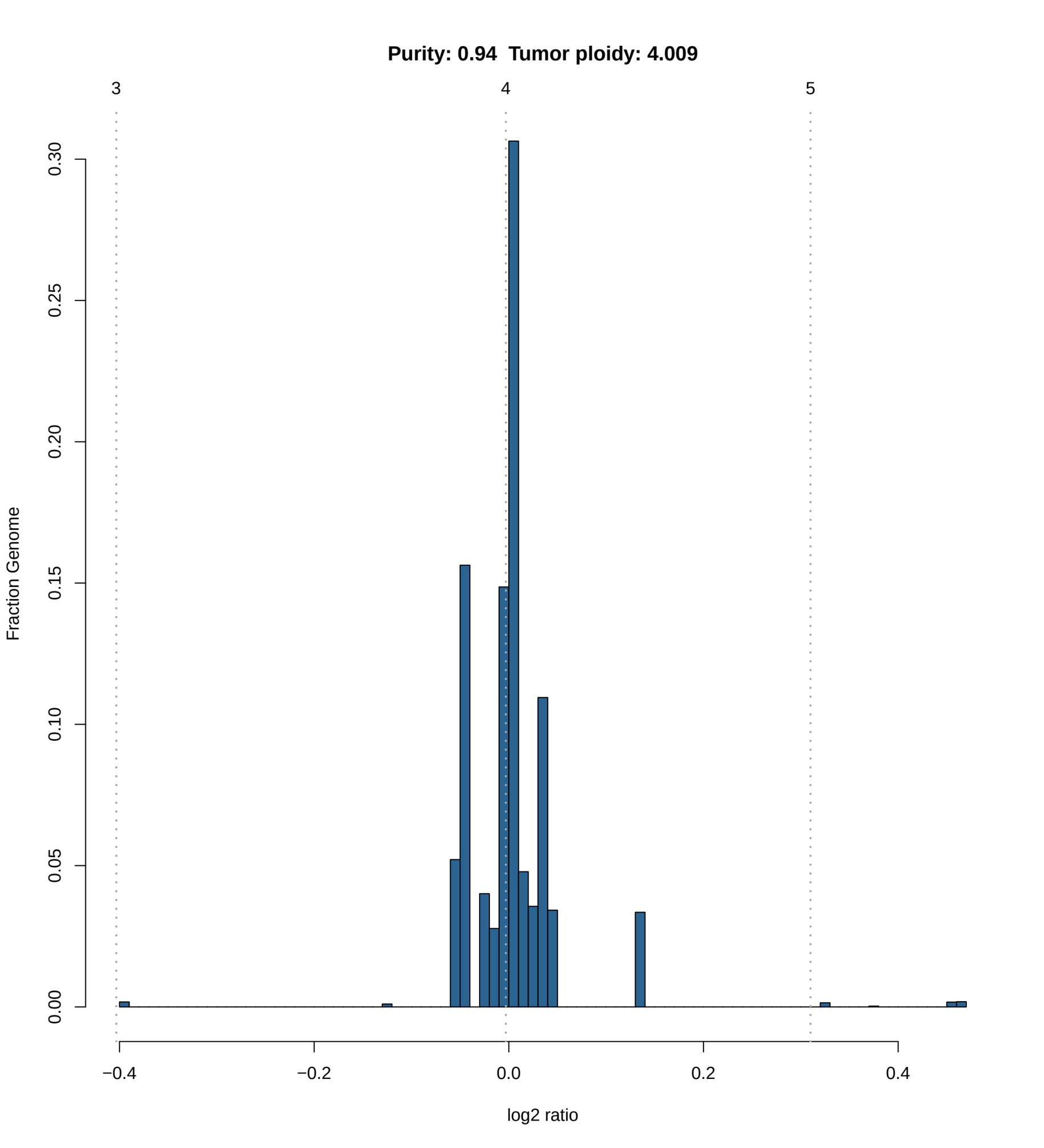

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

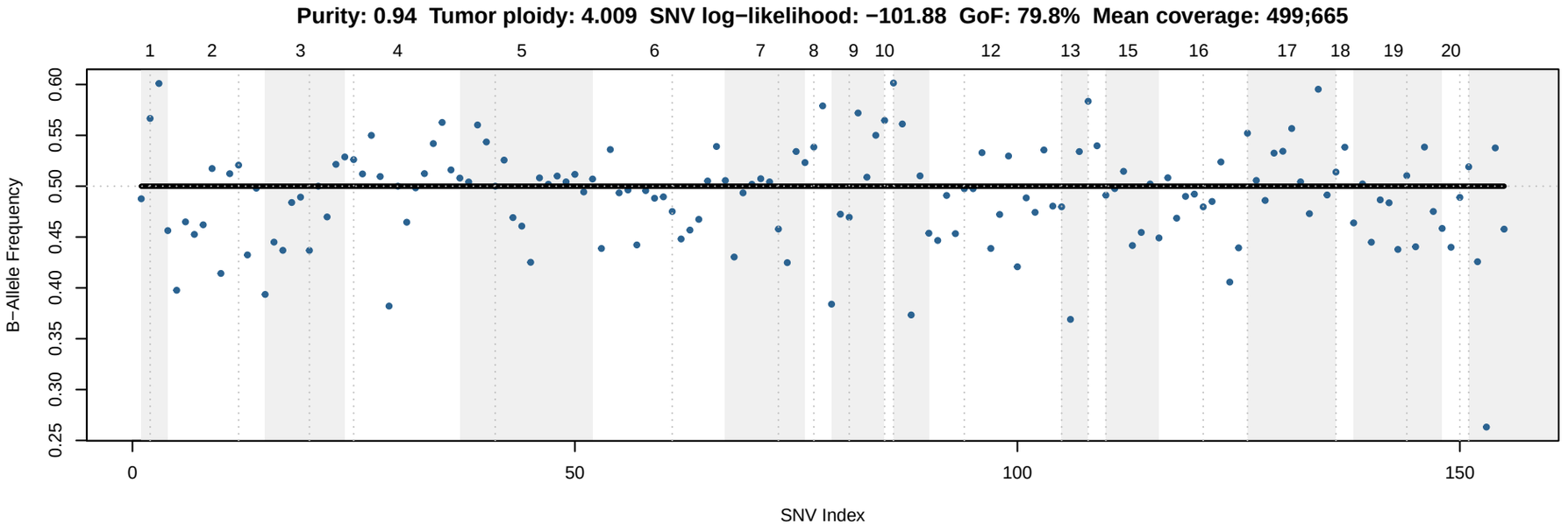

Allelic fraction (germline)
Copy Number log−ratio
5m4
4m3
5m3
4m2
6m3
5m2
4m1
5m1

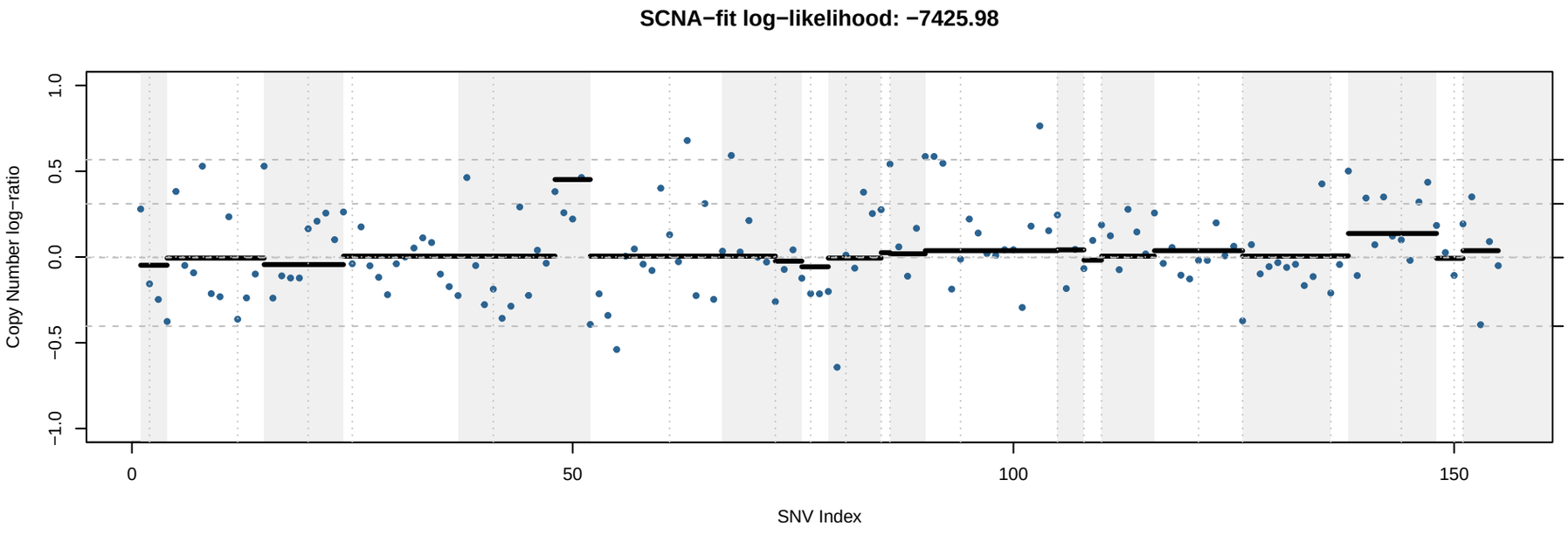

Coverage (log2)
Allelic fraction

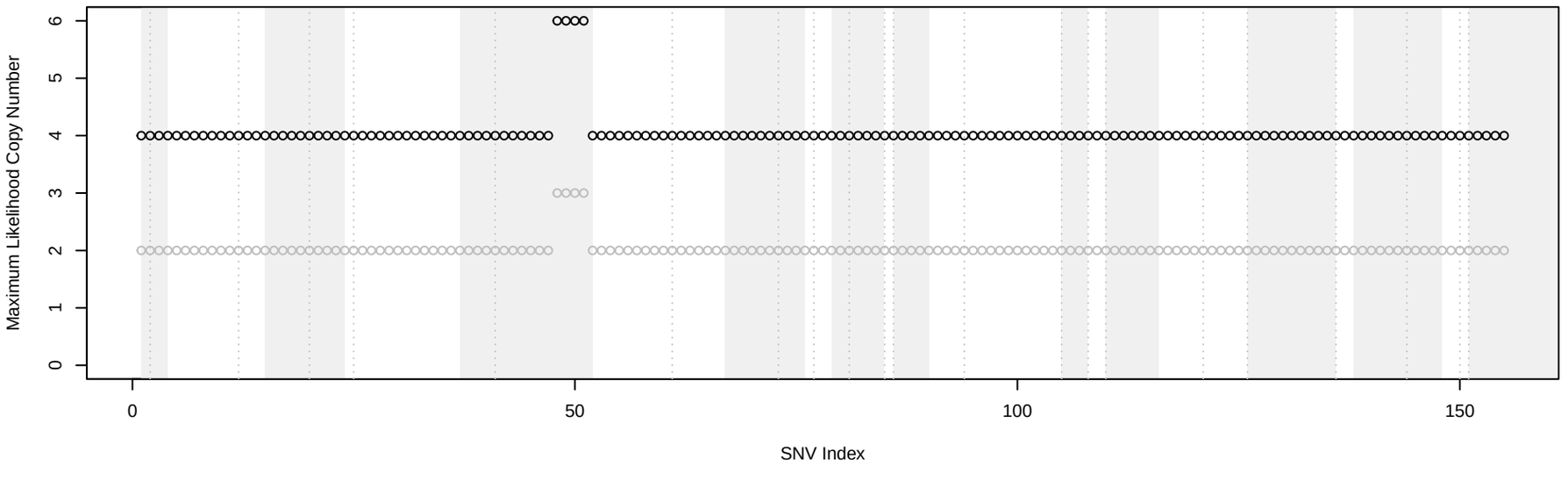

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
4m1
5m1

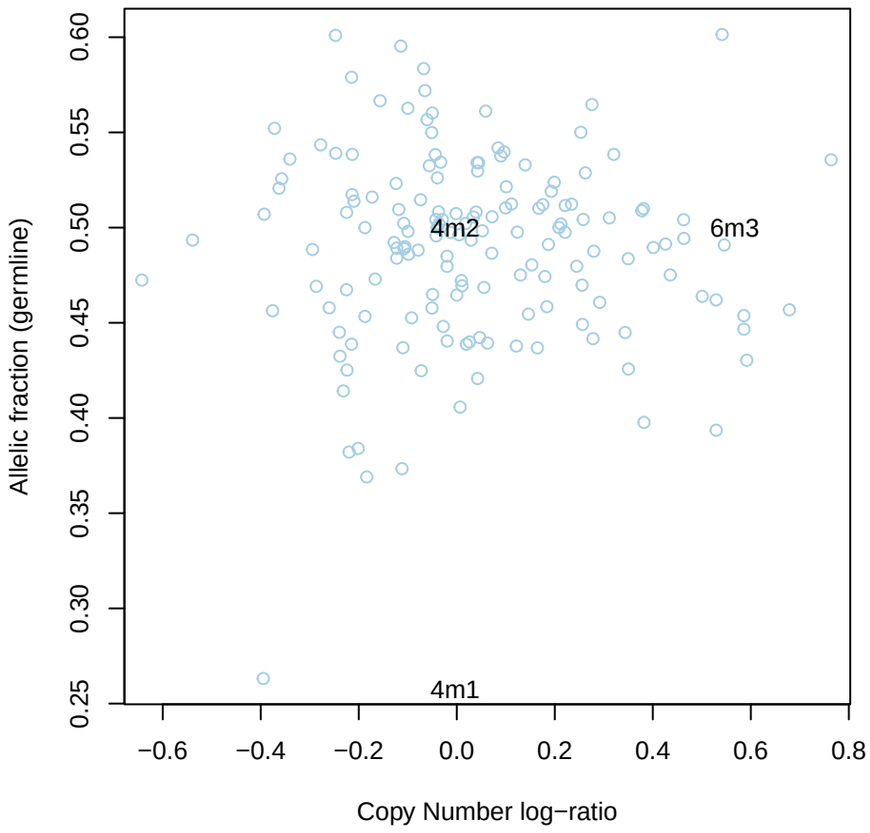

Frequency
Cellular fraction

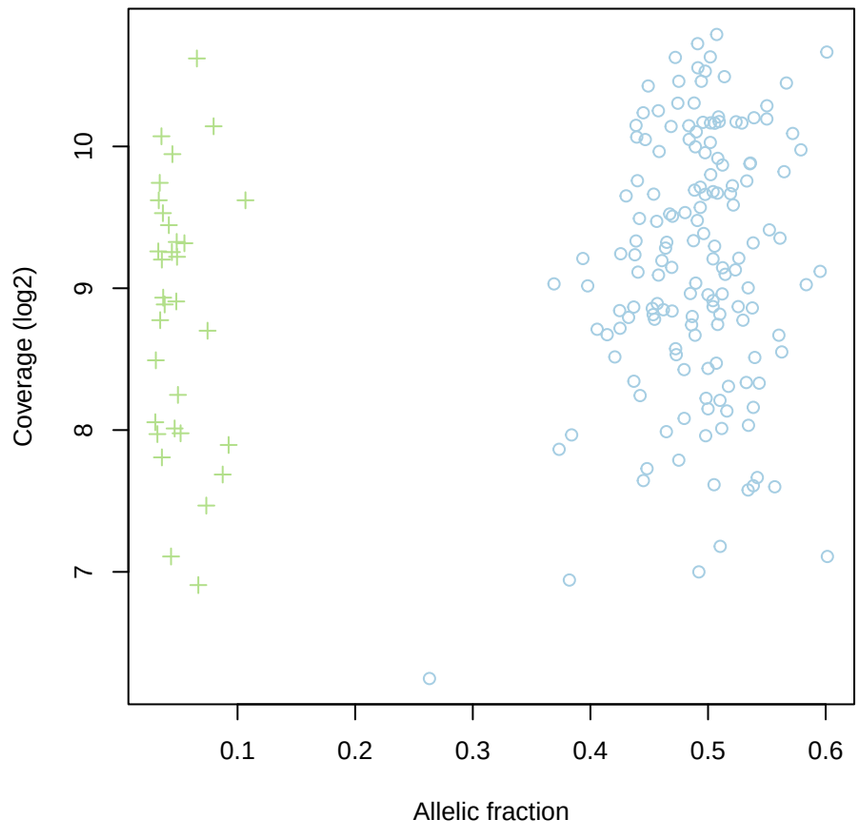

Purity: 0.94 Tumor ploidy: 4.009
3
4
5
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

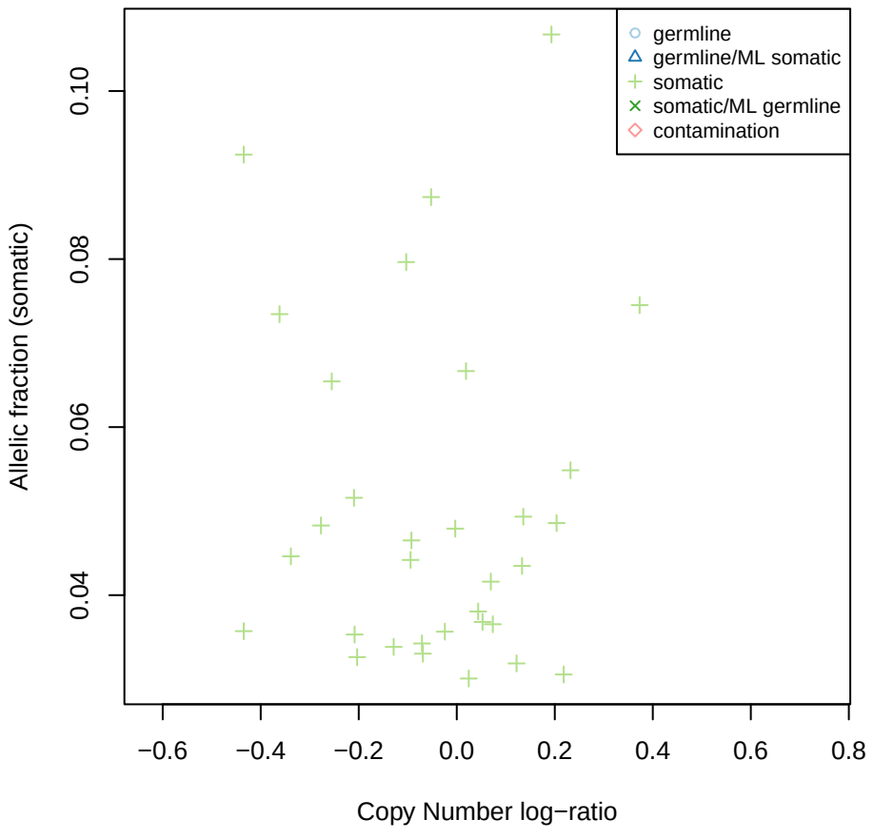

Purity: 0.94 Tumor ploidy: 4.009 SNV log−likelihood: −101.88 GoF: 79.8% Mean coverage: 499;665
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 18 19 20
B−Allele Frequency
0.25 0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

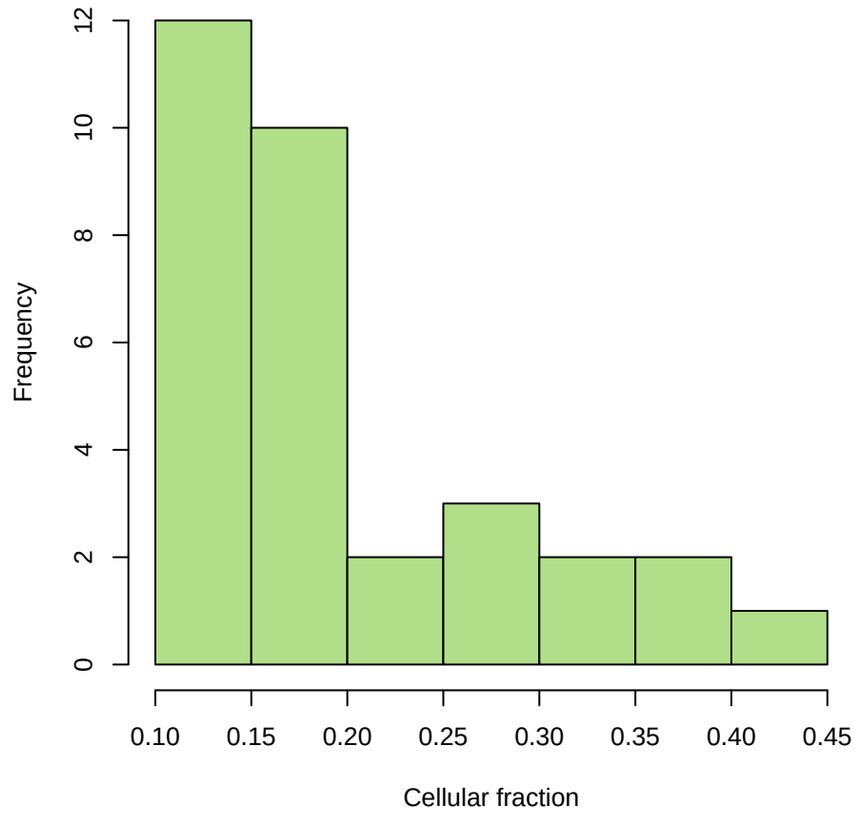

SCNA−fit log−likelihood: −7425.98
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6
0 50 100 150
SNV Index

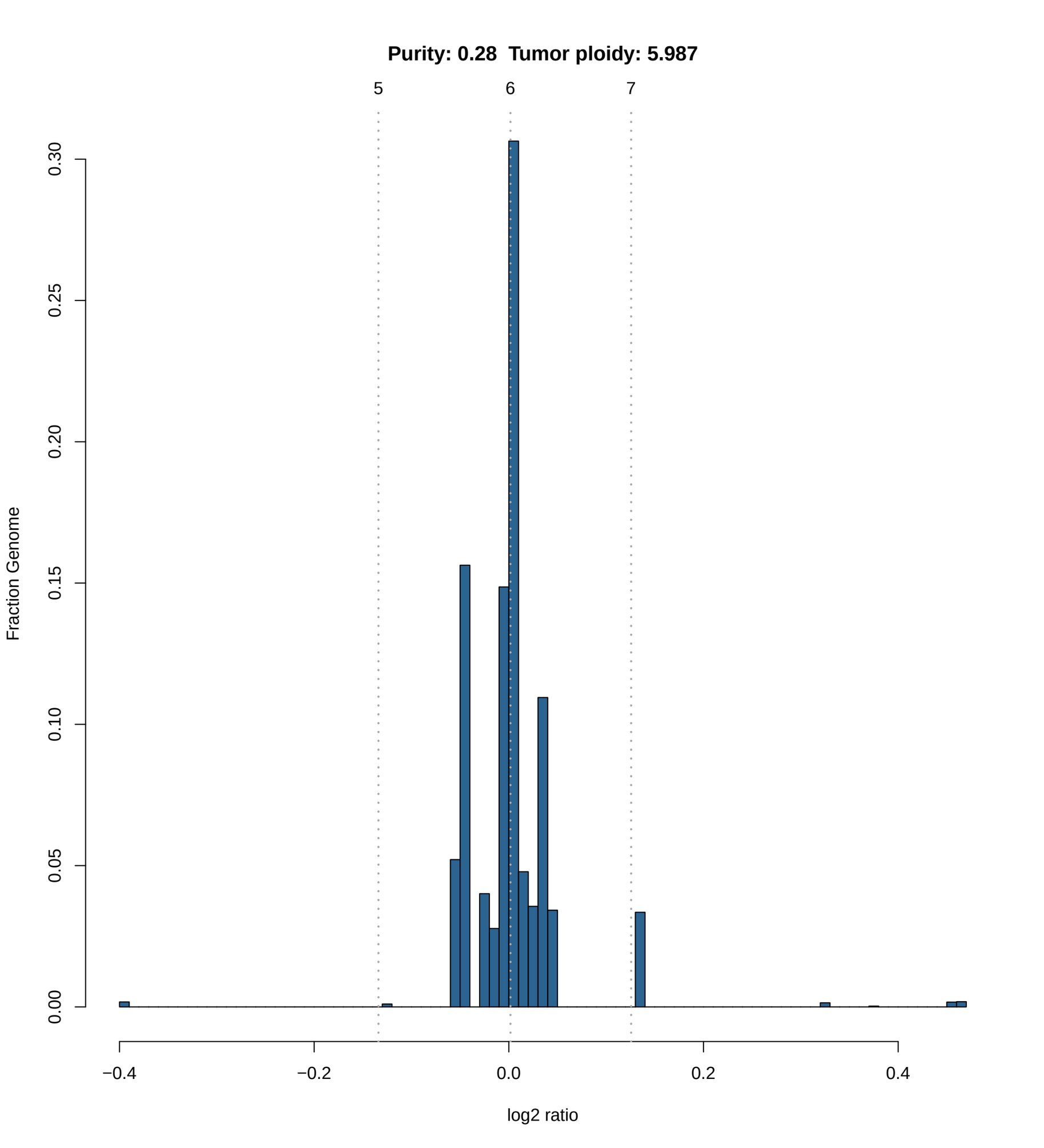

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

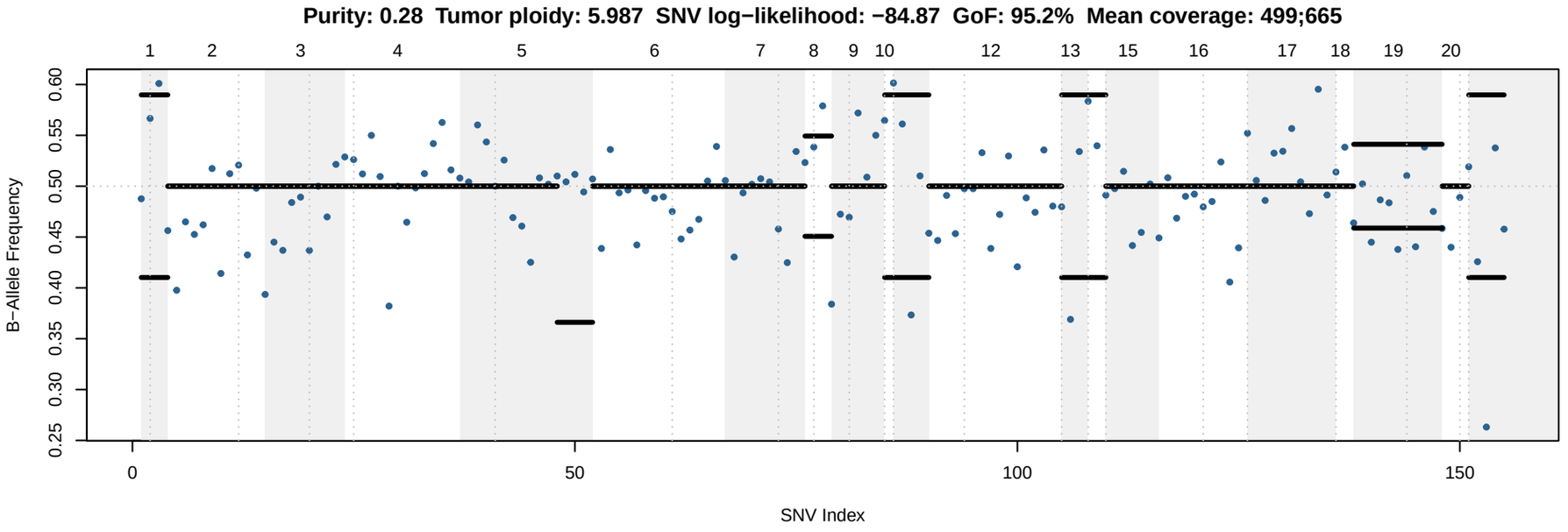

Allelic fraction (germline)
0.25
0.30
0.35
0.40
0.45
0.50
0.55
0.60
4m2
6m3
4m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

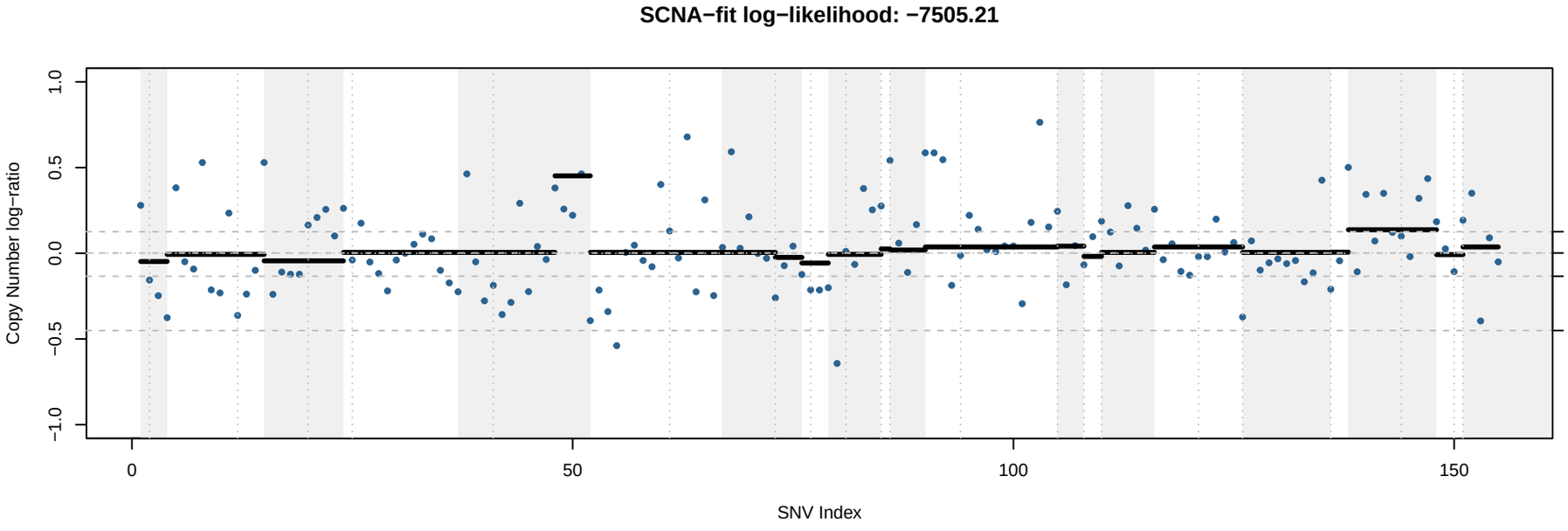

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

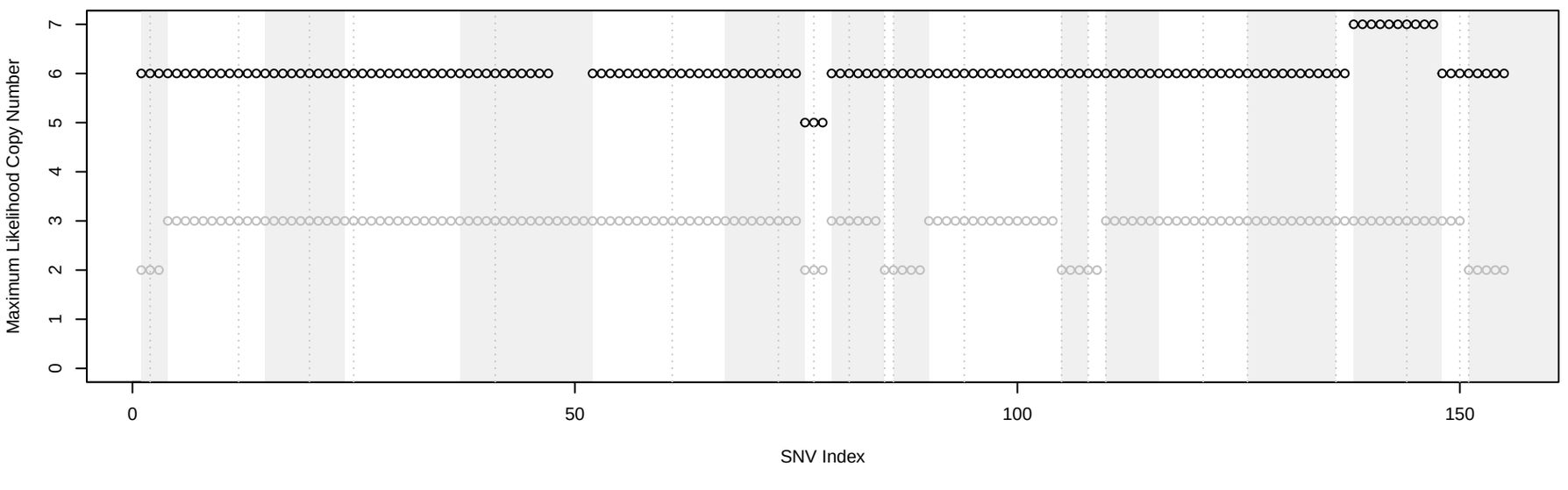

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio

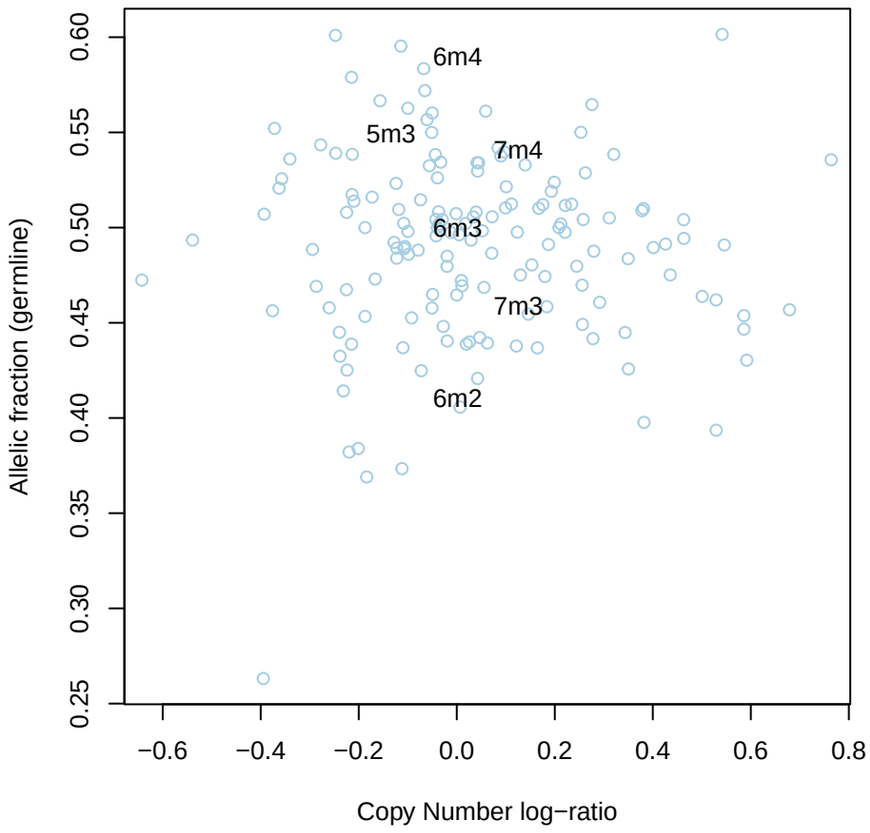

Frequency
0
2
4
6
8
10
12
0.10
0.15
0.20
0.25
0.30
0.35
0.40
0.45
Cellular fraction

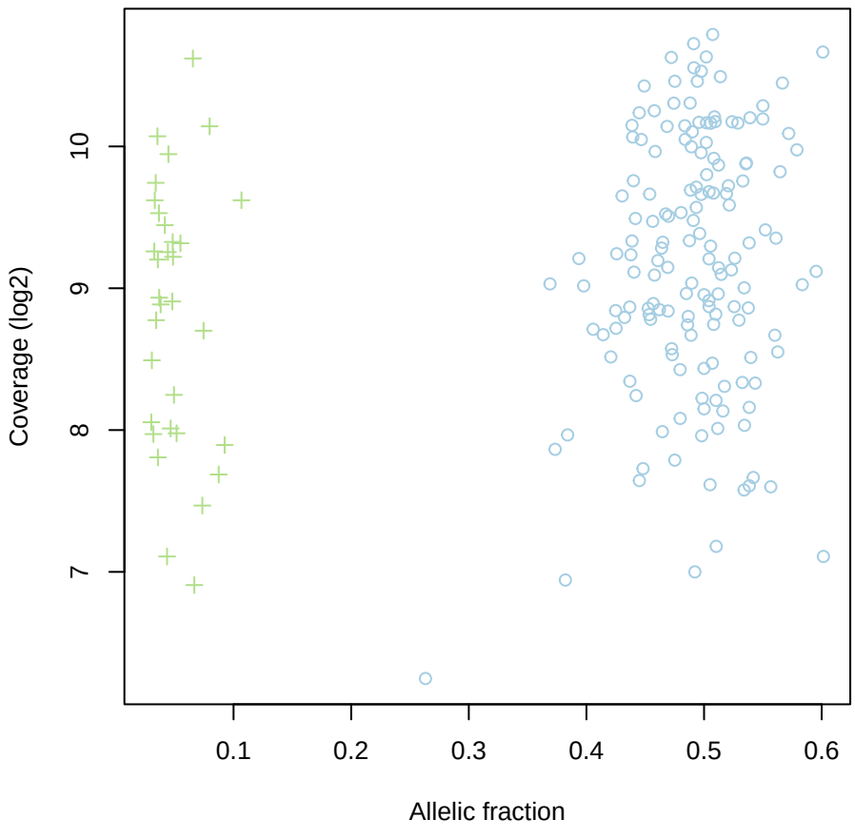

Purity: 0.28 Tumor ploidy: 5.987
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

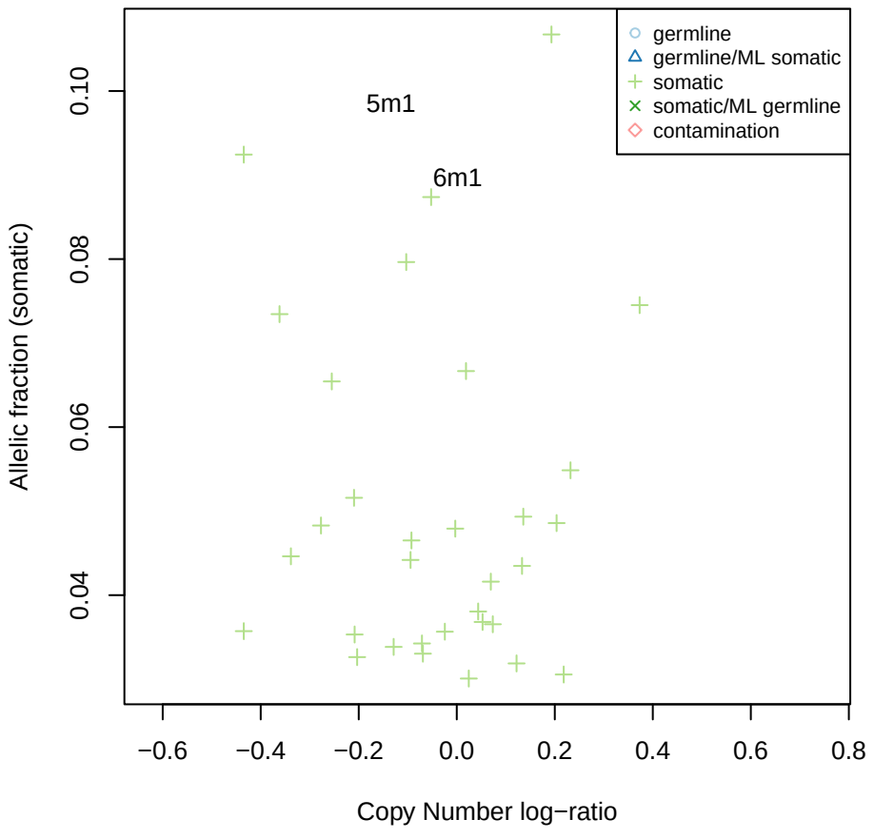

Purity: 0.28 Tumor ploidy: 5.987 SNV log−likelihood: −84.87 GoF: 95.2% Mean coverage: 499;665
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 18 19 20
B−Allele Frequency
0.25 0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

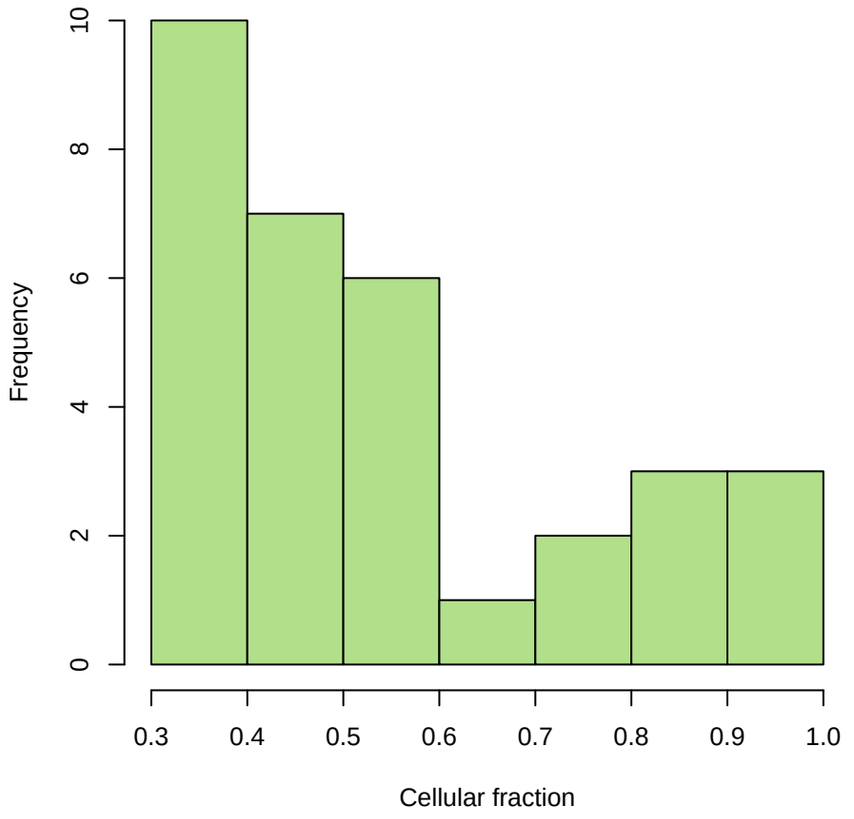

SCNA−fit log−likelihood: −7505.21
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
7 5 3
0 50 100 150
SNV Index

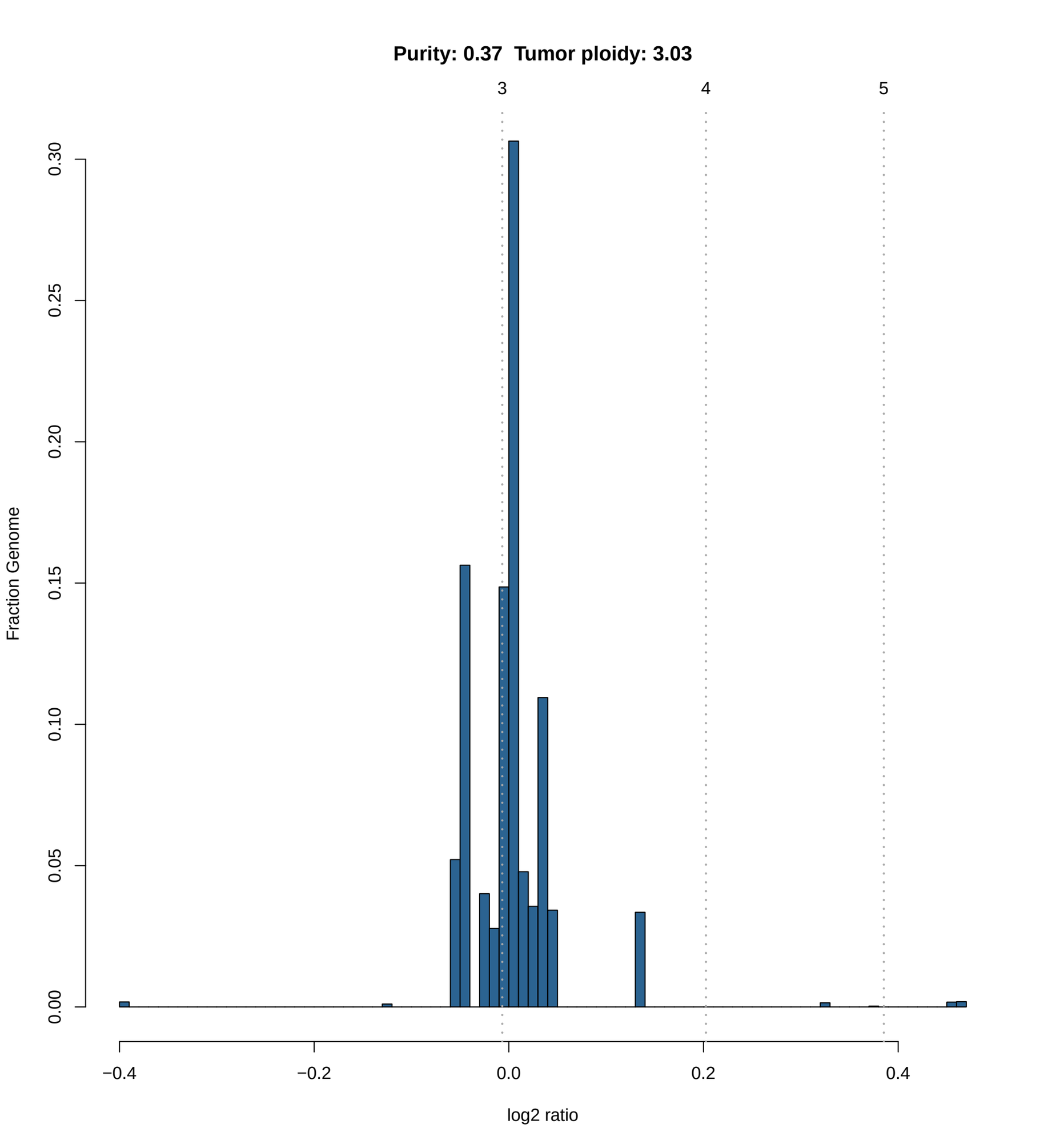

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

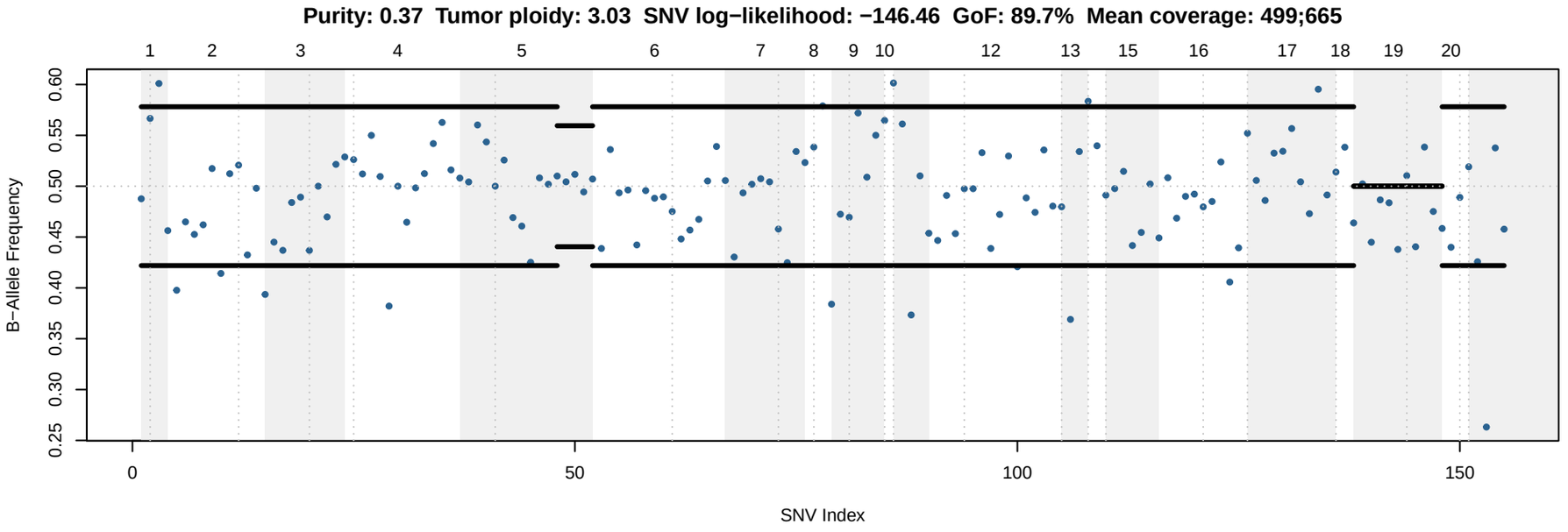

6m4
5m3
7m4
6m3
7m3
6m2
Allelic fraction (germline)
Copy Number log−ratio

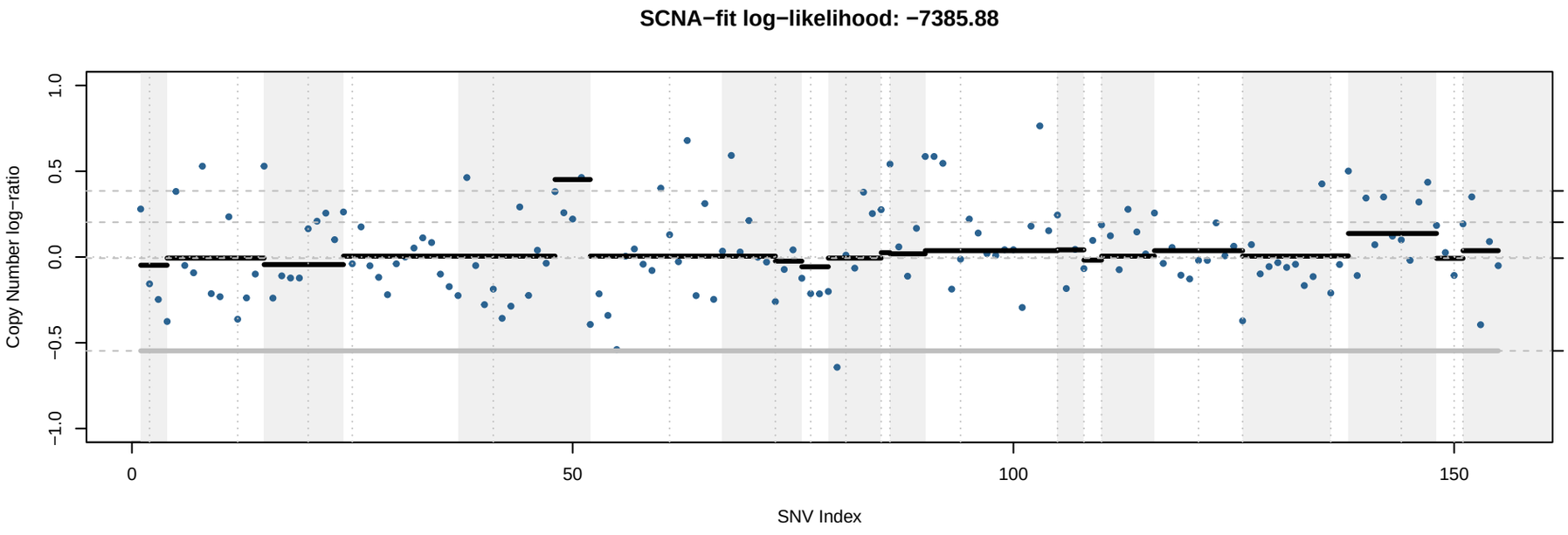

Coverage (log2)
Allelic fraction

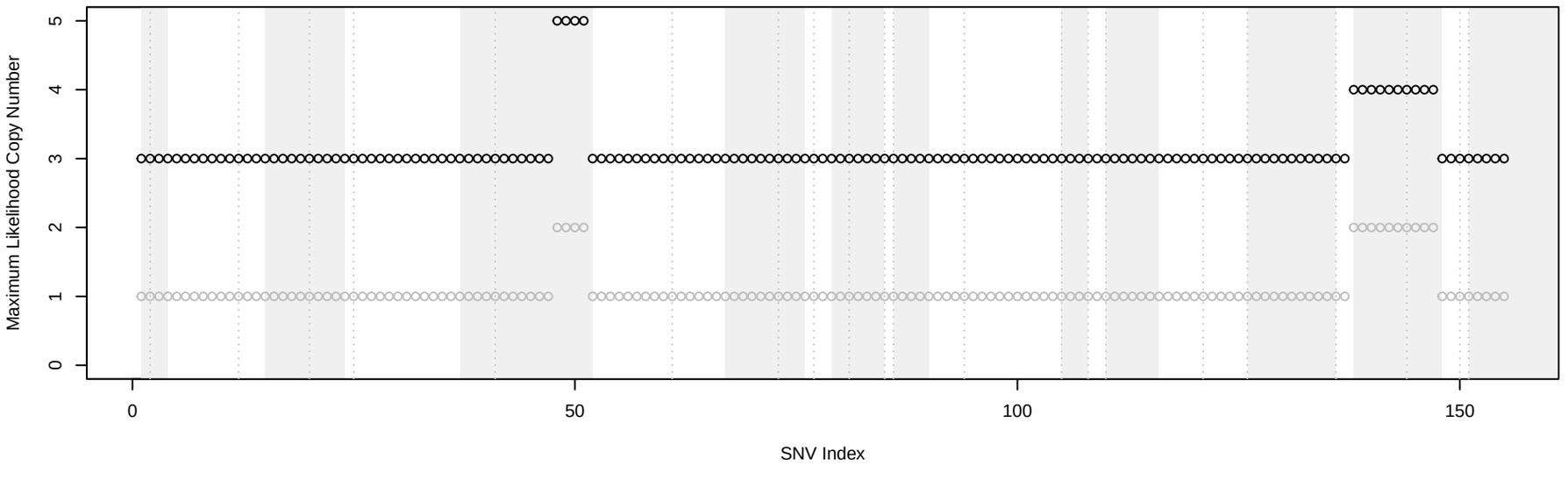

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio

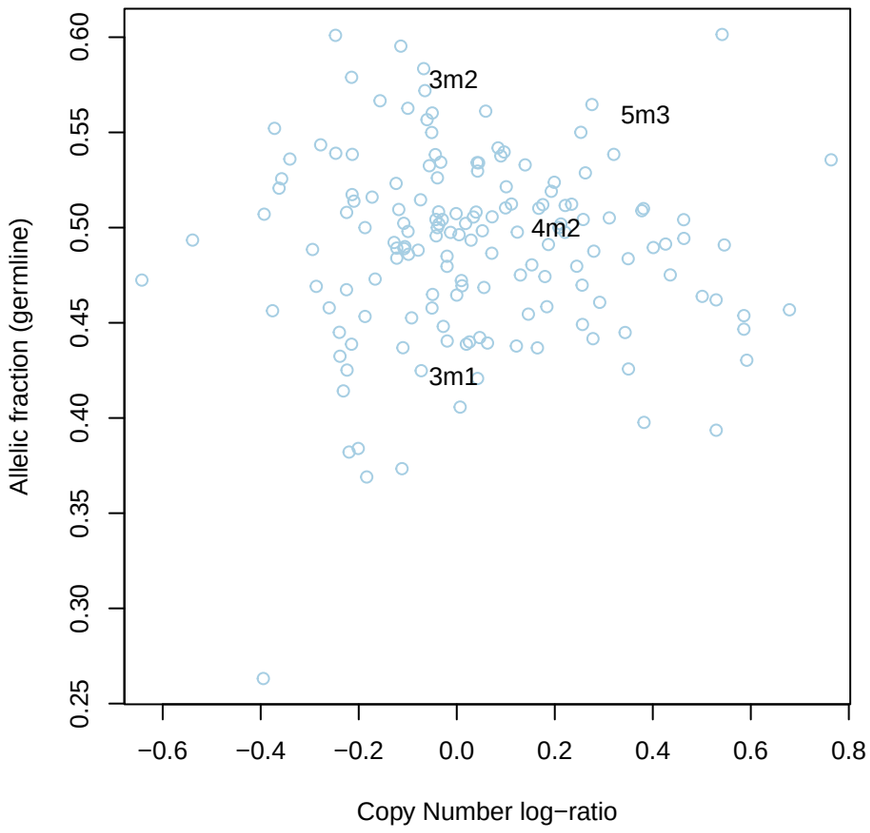

Frequency
Cellular fraction

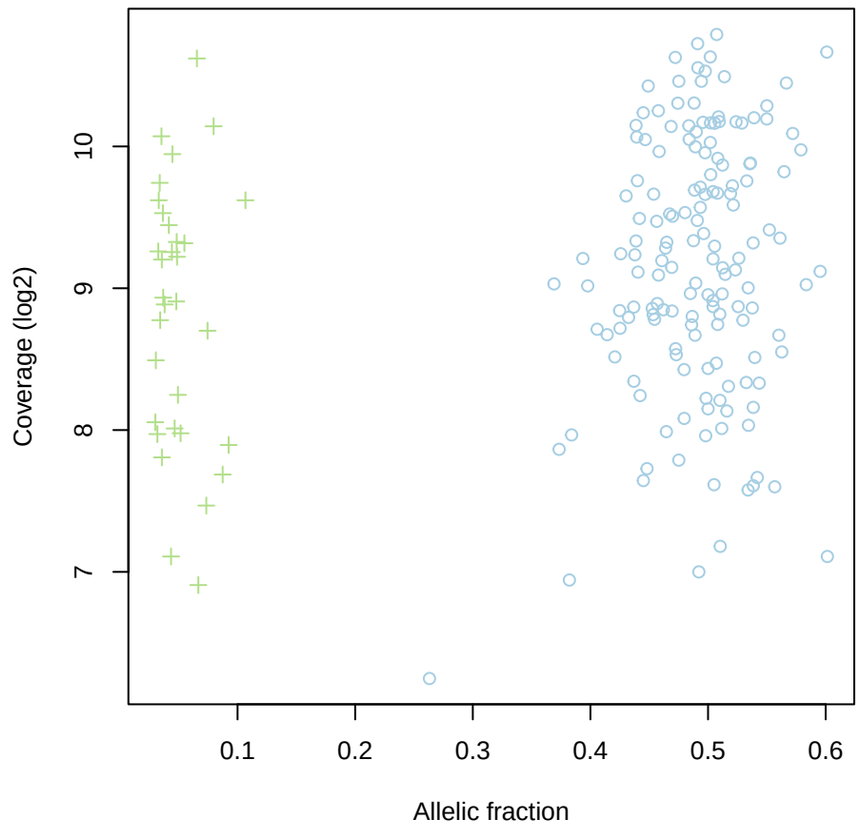

Purity: 0.37 Tumor ploidy: 3.03
3
4
5
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

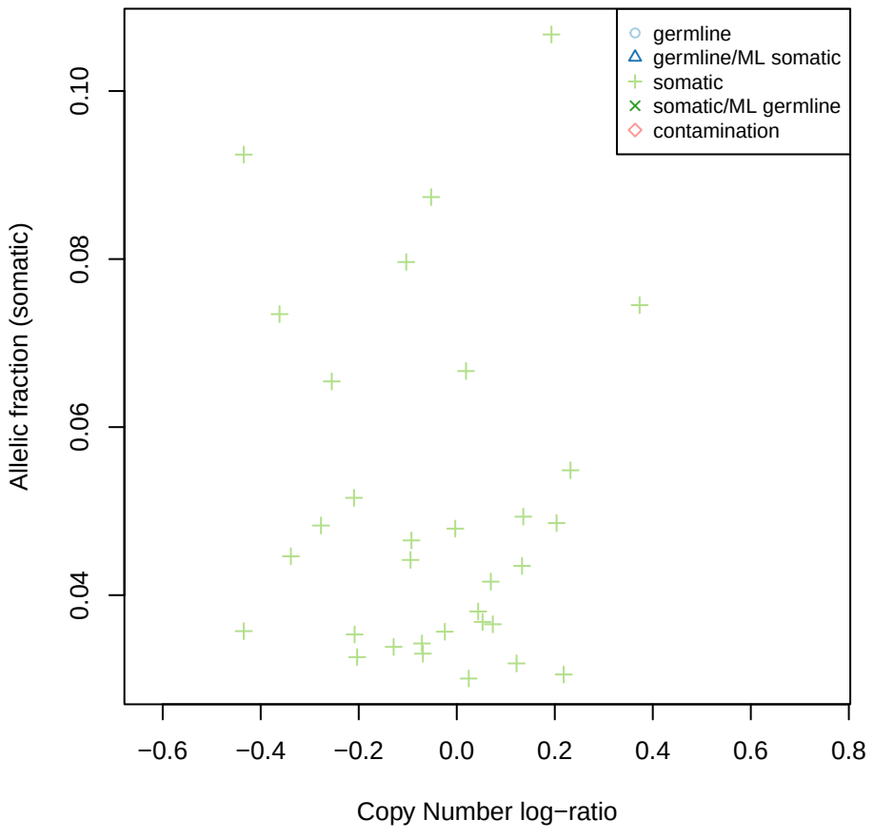

Purity: 0.37 Tumor ploidy: 3.03 SNV log−likelihood: −146.46 GoF: 89.7% Mean coverage: 499;665
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 18 19 20
B−Allele Frequency
0.25 0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

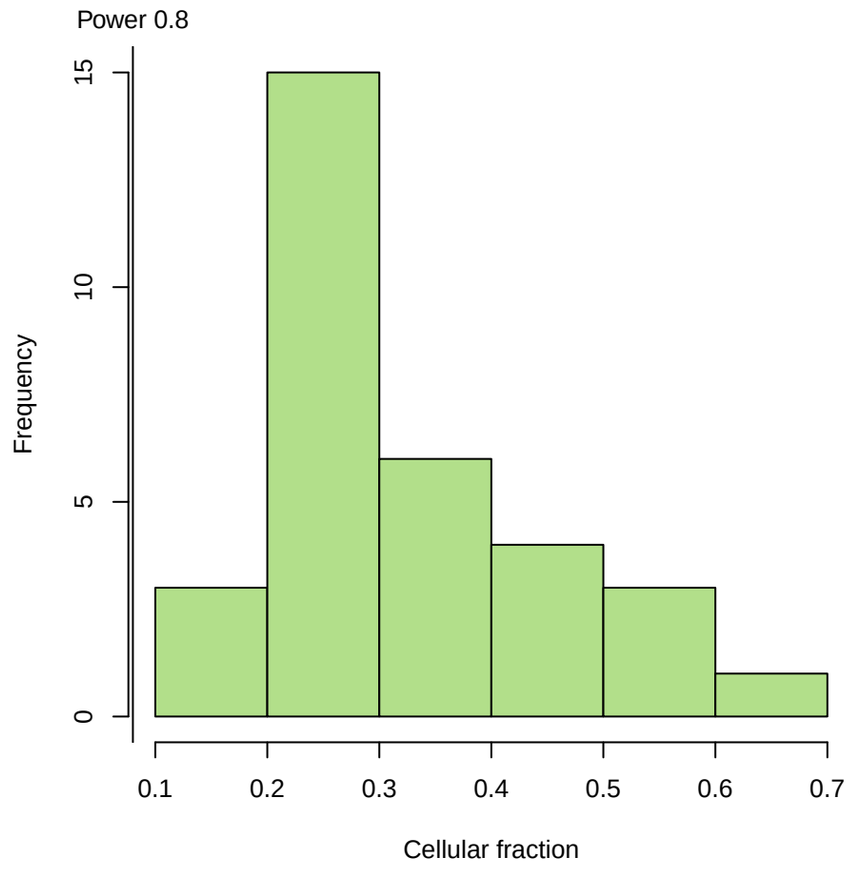

SCNA−fit log−likelihood: −7385.88
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
1 3 4 5
0 50 100 150
SNV Index

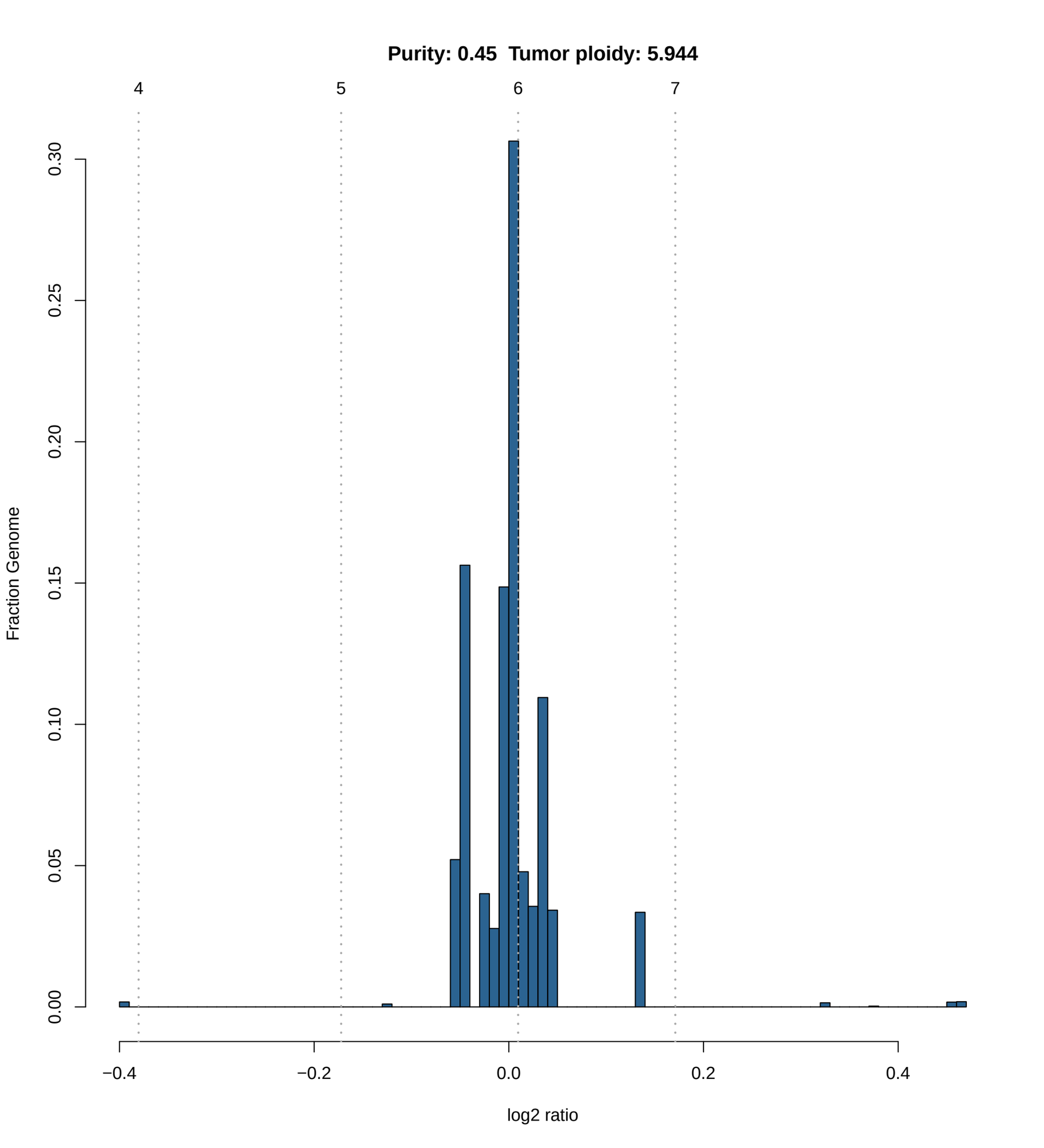

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

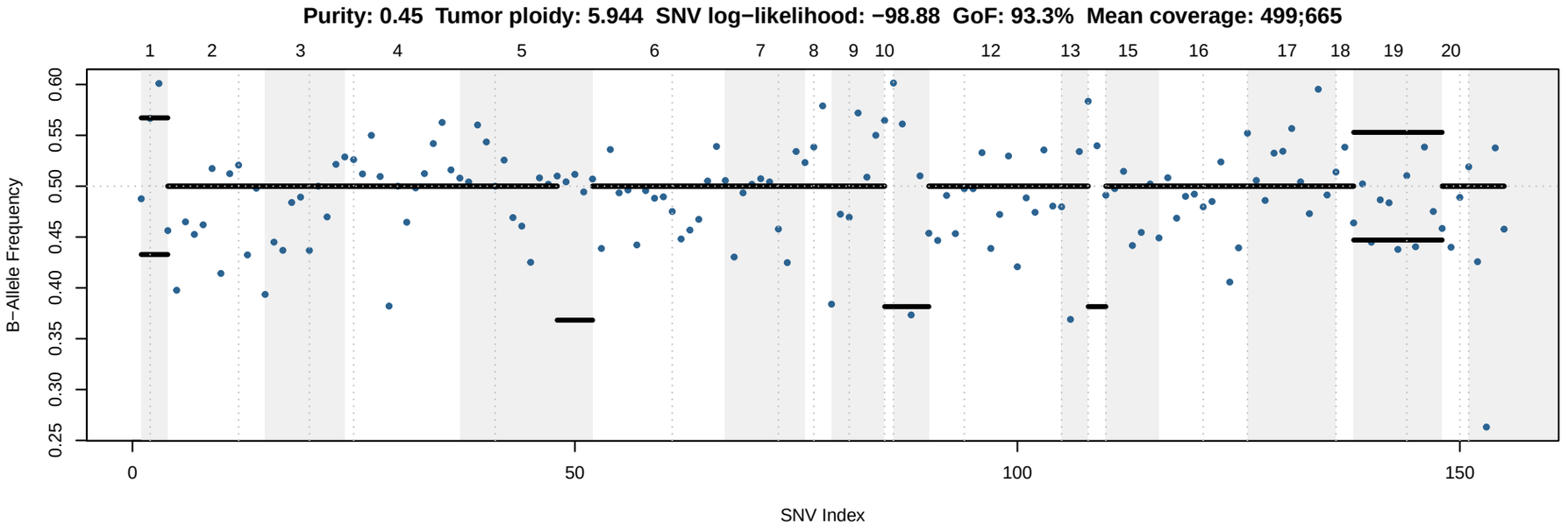

3m2
5m3
4m2
3m1
Allelic fraction (germline)
Copy Number log−ratio
0.25
0.30
0.35
0.40
0.45
0.50
0.55
0.60
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8

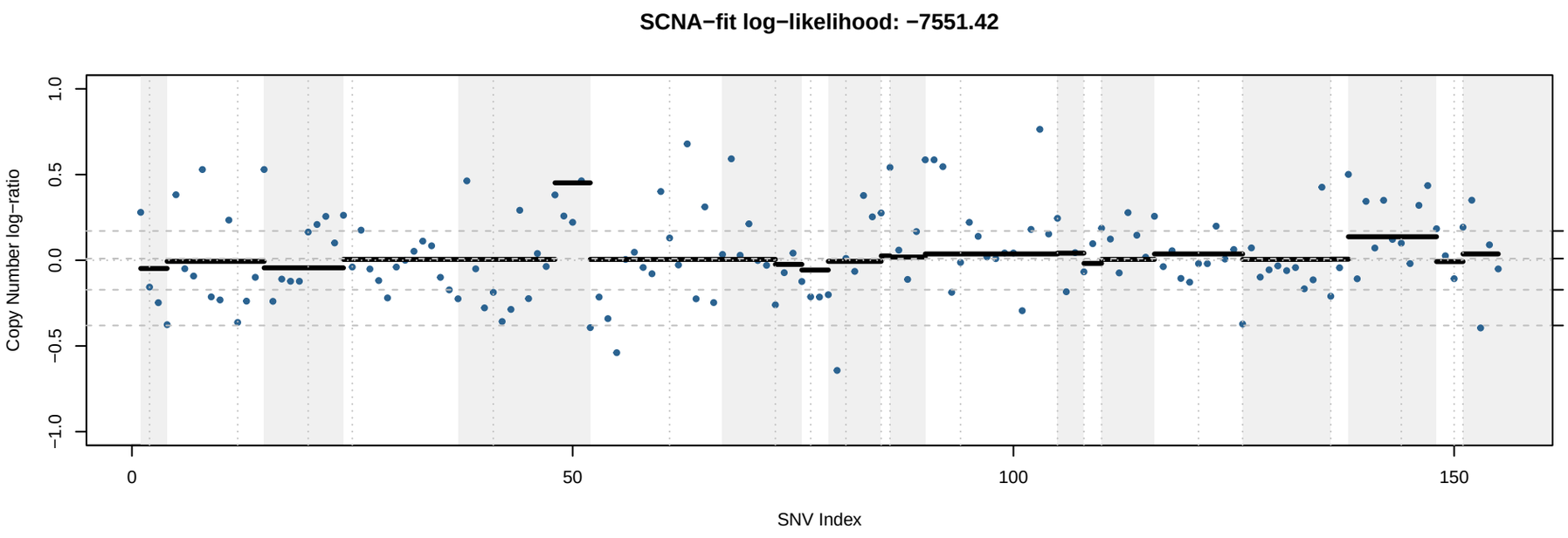

Coverage (log2)
Allelic fraction
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

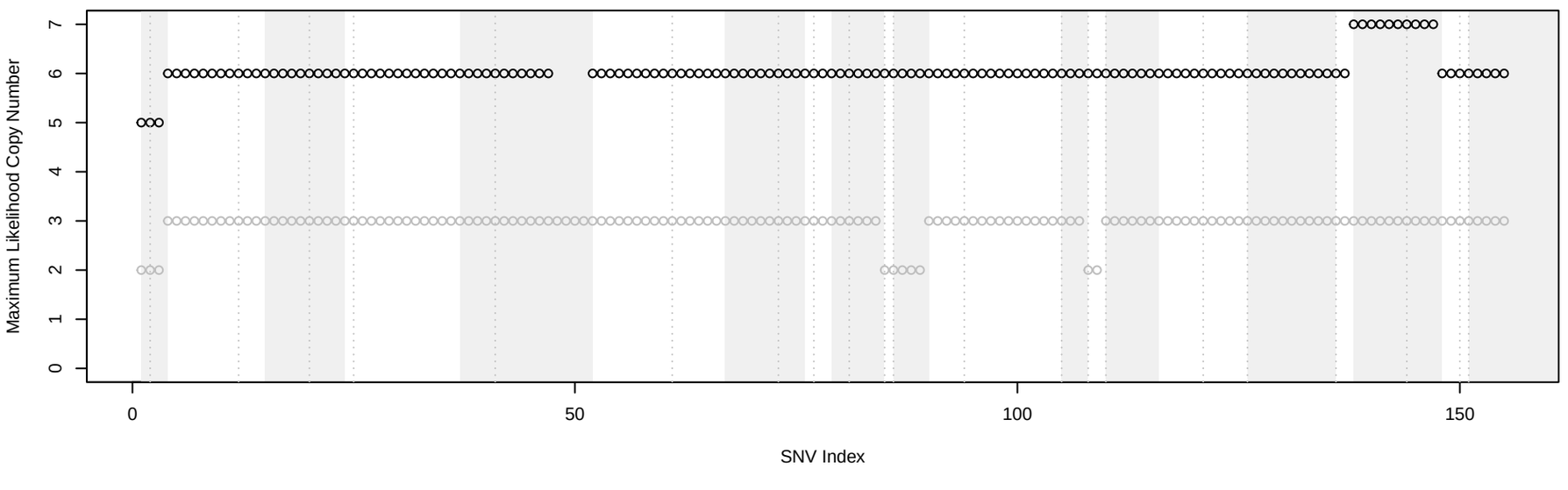

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8

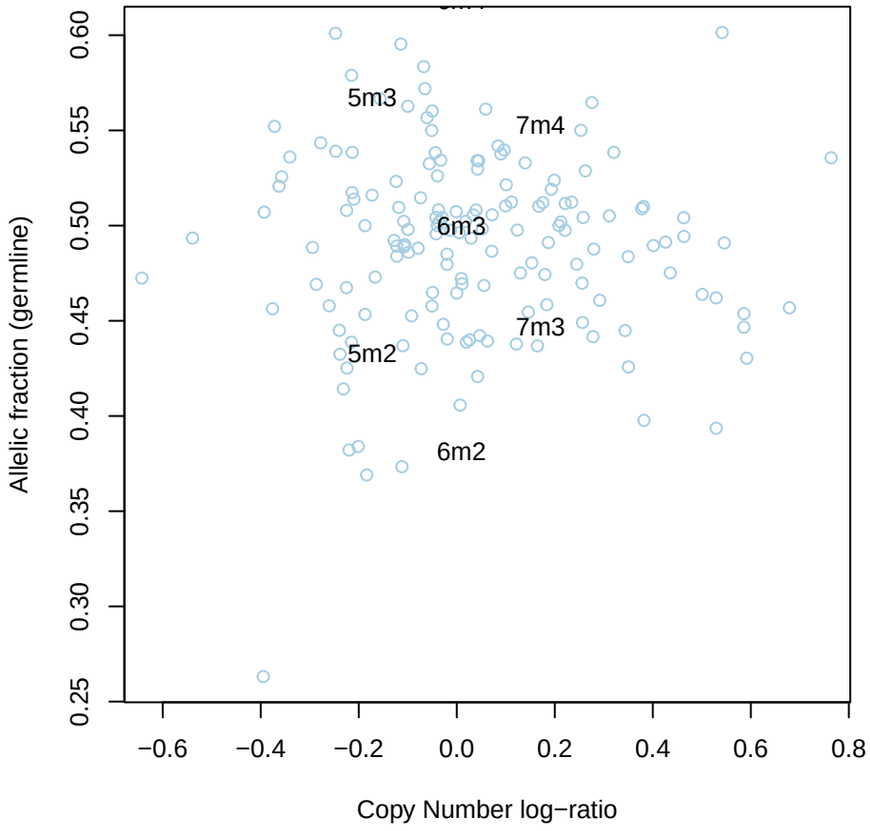

Power 0.8
Frequency
Cellular fraction
0
5
10
15
0.1
0.2
0.3
0.4
0.5
0.6
0.7

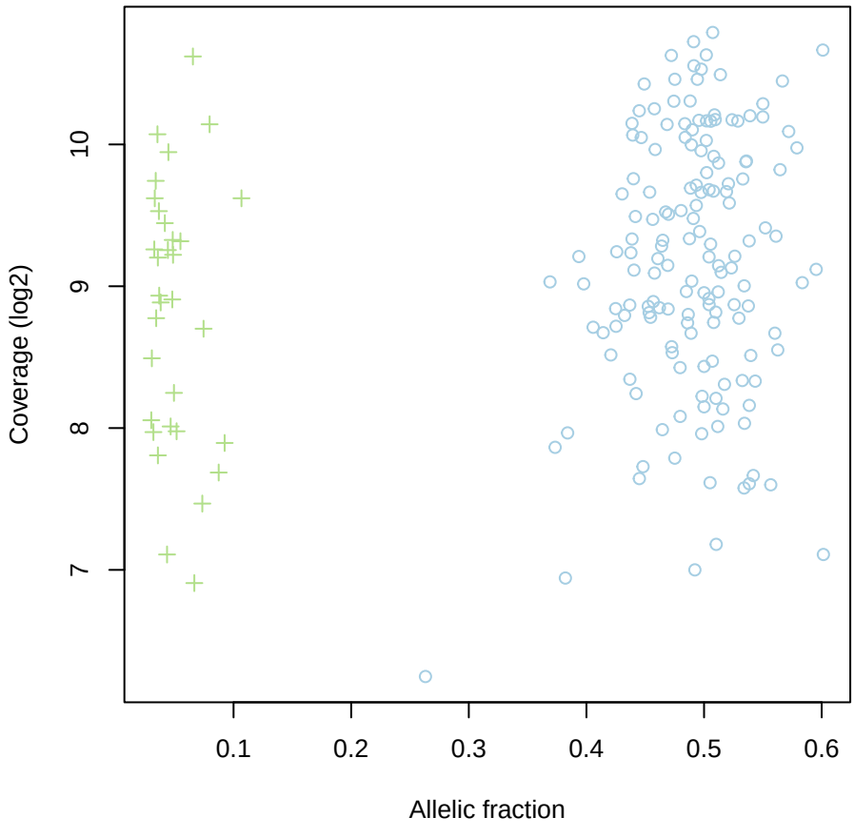

Purity: 0.45 Tumor ploidy: 5.944
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

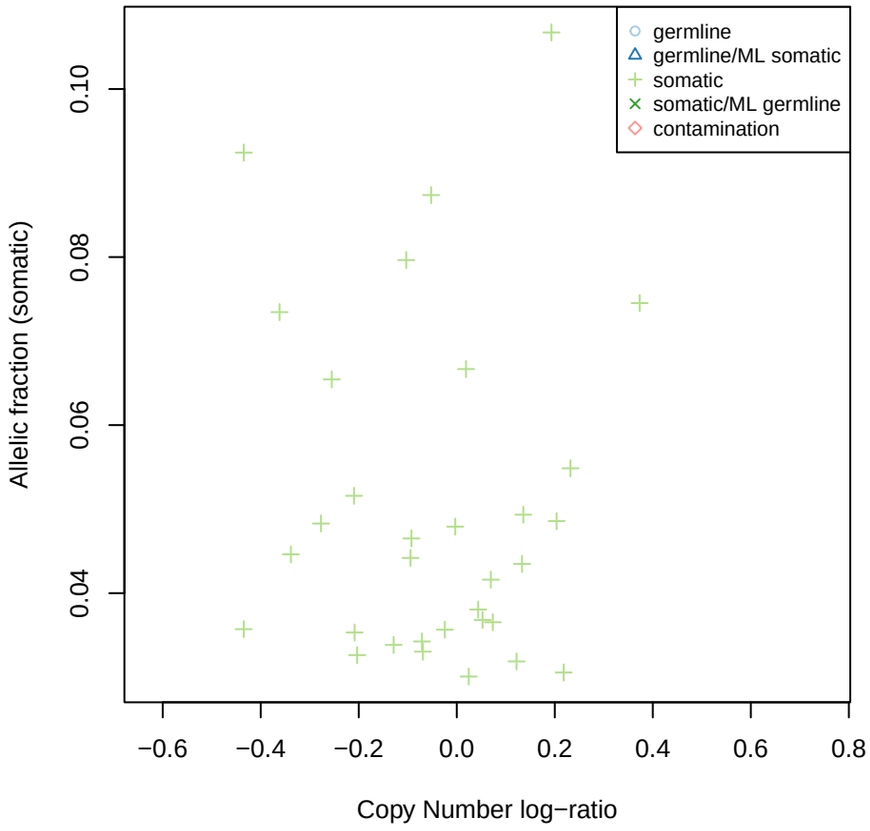

Purity: 0.45 Tumor ploidy: 5.944 SNV log−likelihood: −98.88 GoF: 93.3% Mean coverage: 499;665
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 18 19 20
B−Allele Frequency
0.25 0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

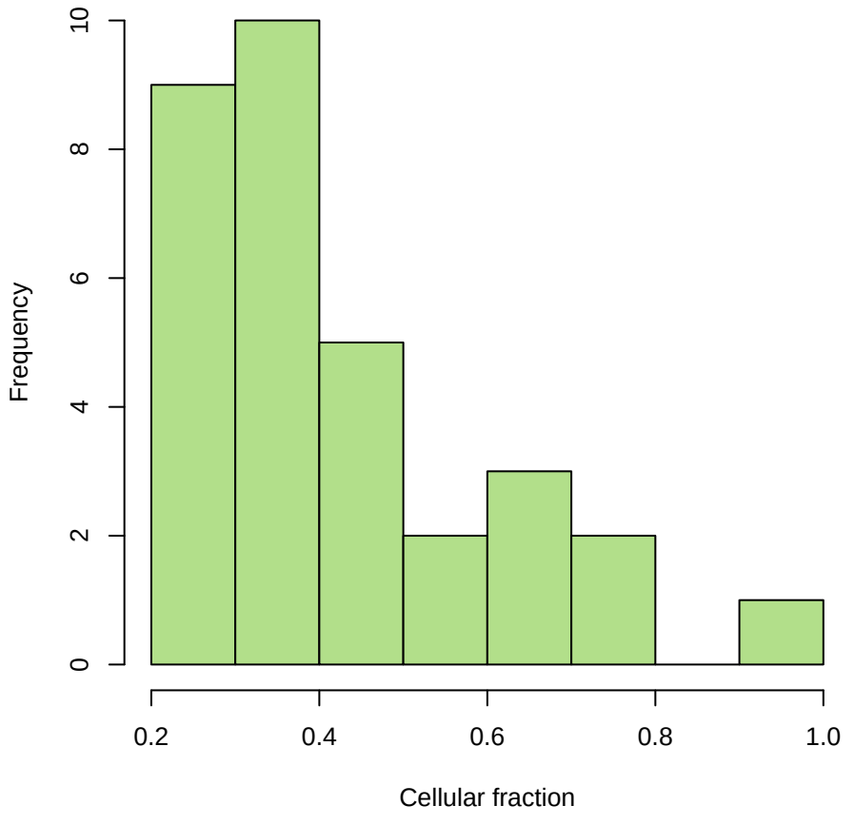

SCNA−fit log−likelihood: −7551.42
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
4 5 6 7
0 50 100 150
SNV Index

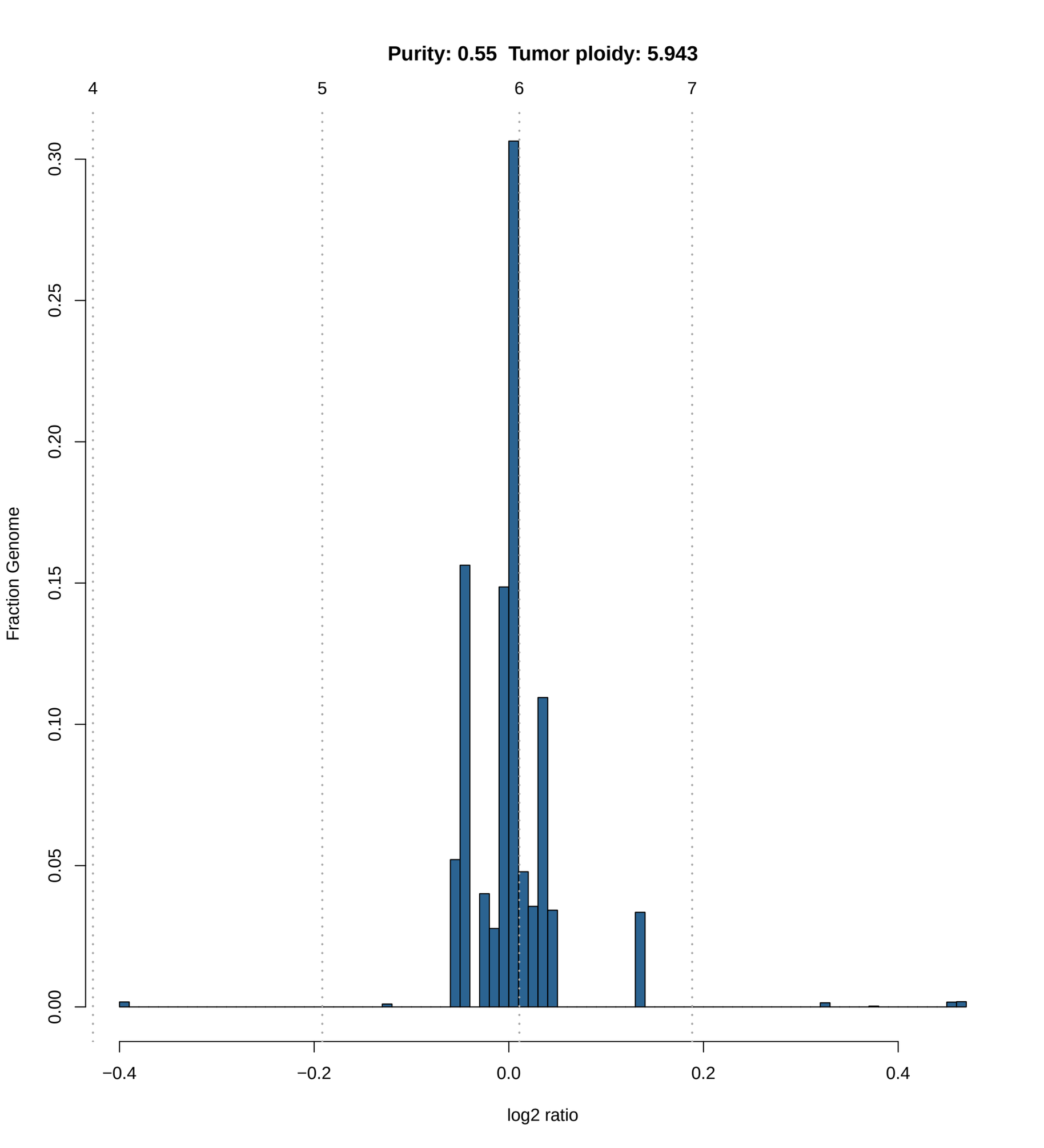

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

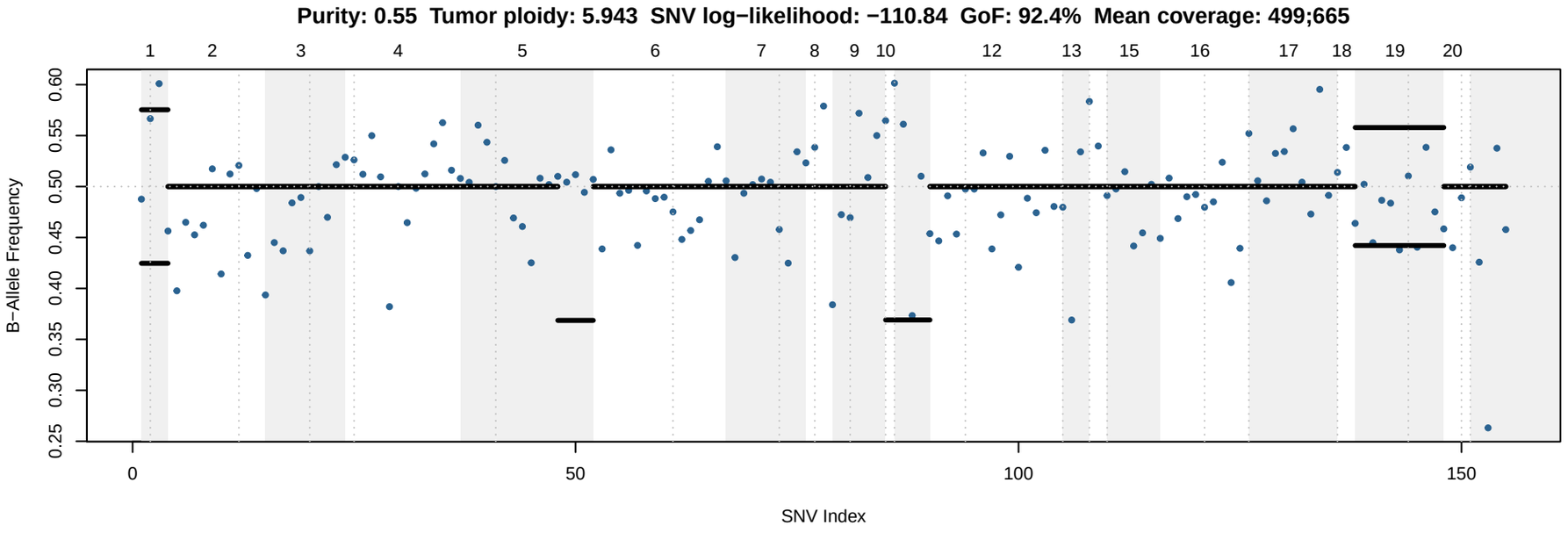

Allelic fraction (germline)
Copy Number log−ratio
5m3
7m4
6m3
7m3
5m2
6m2

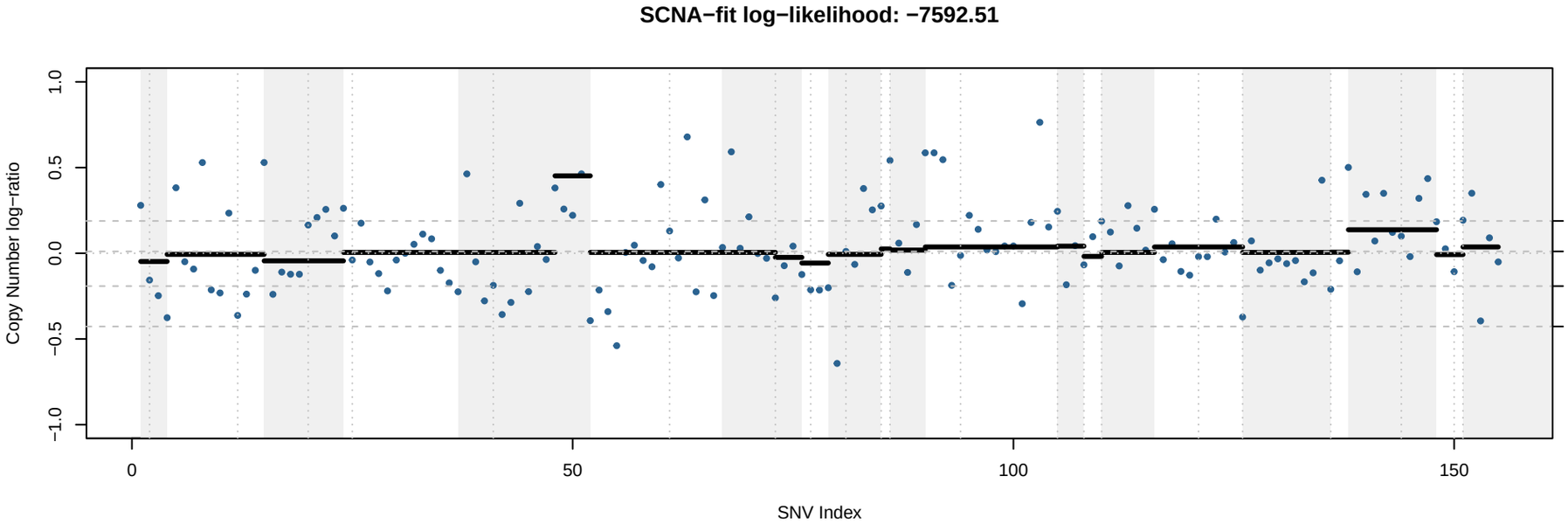

Coverage (log2)
Allelic fraction

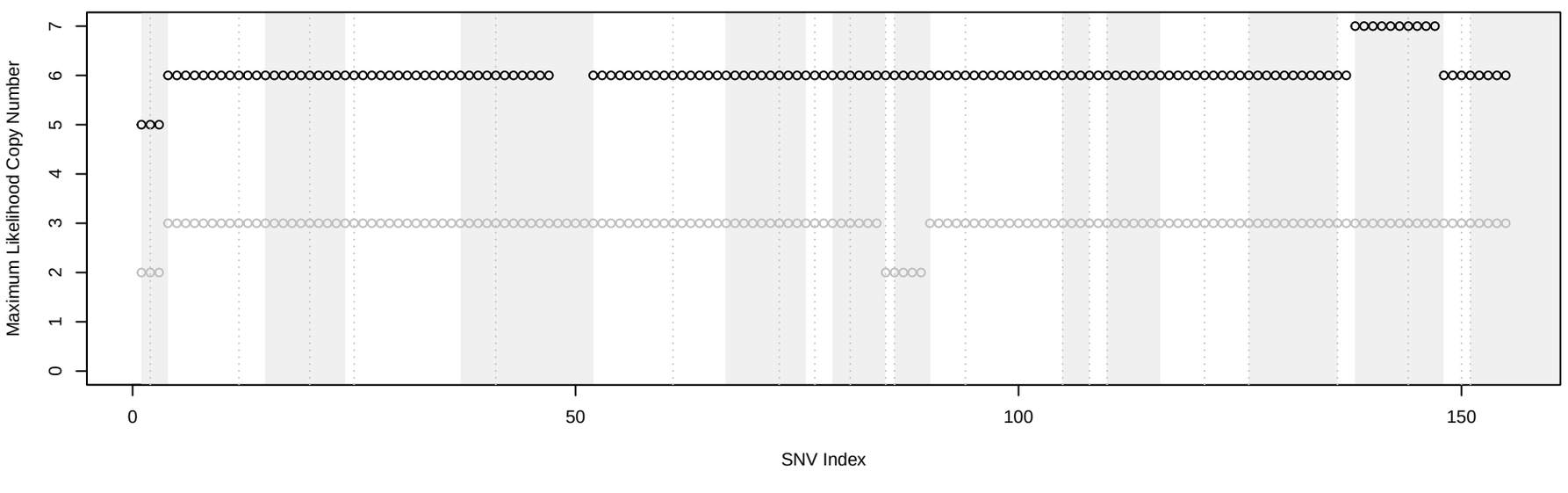

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

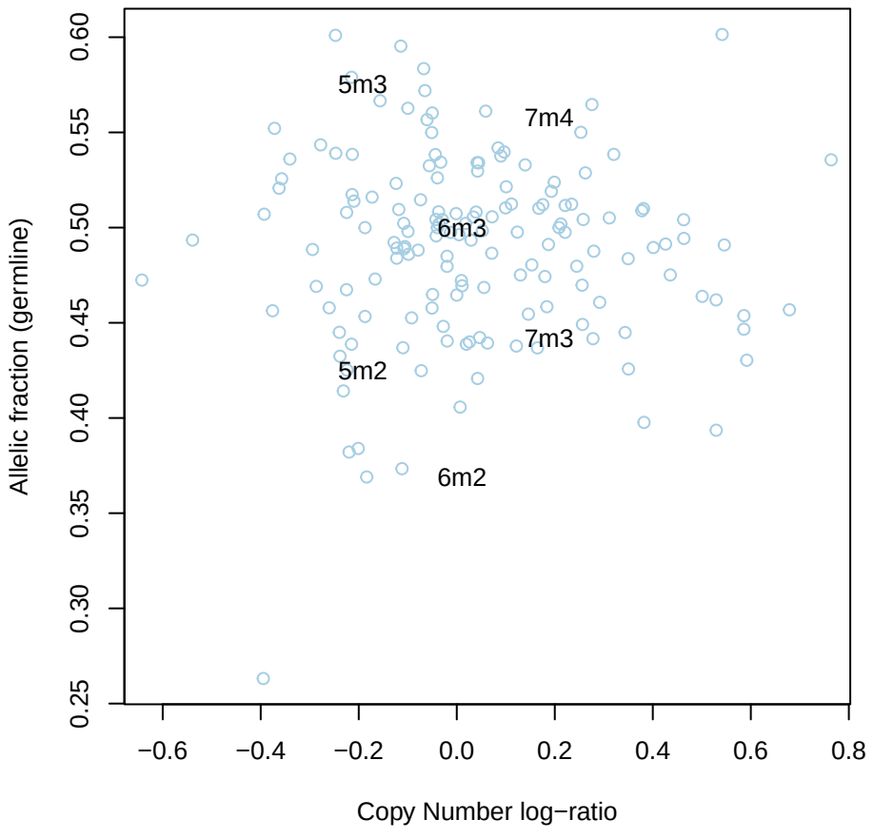

Frequency
Cellular fraction

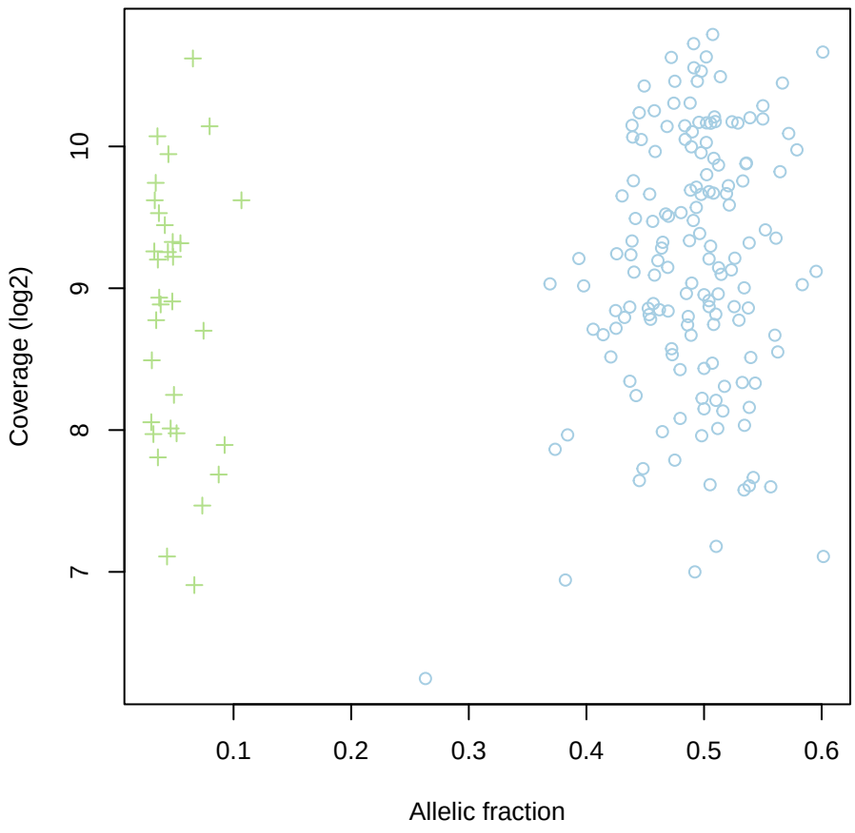

Purity: 0.55 Tumor ploidy: 5.943
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

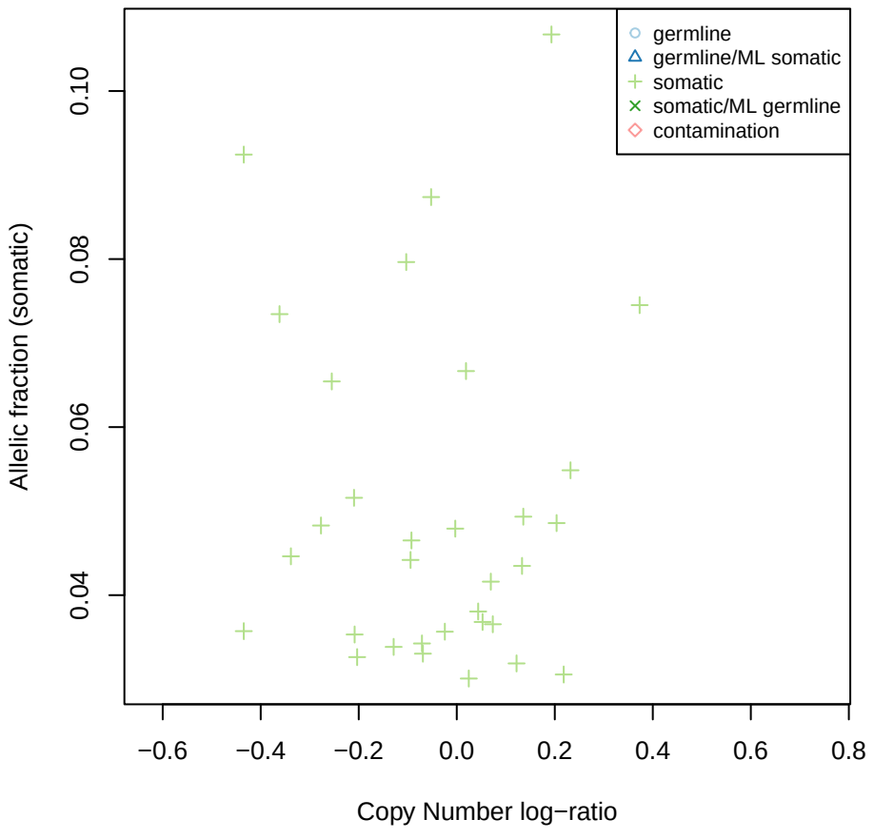

Purity: 0.55 Tumor ploidy: 5.943 SNV log−likelihood: −110.84 GoF: 92.4% Mean coverage: 499;665
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 18 19 20
B−Allele Frequency
0.25 0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

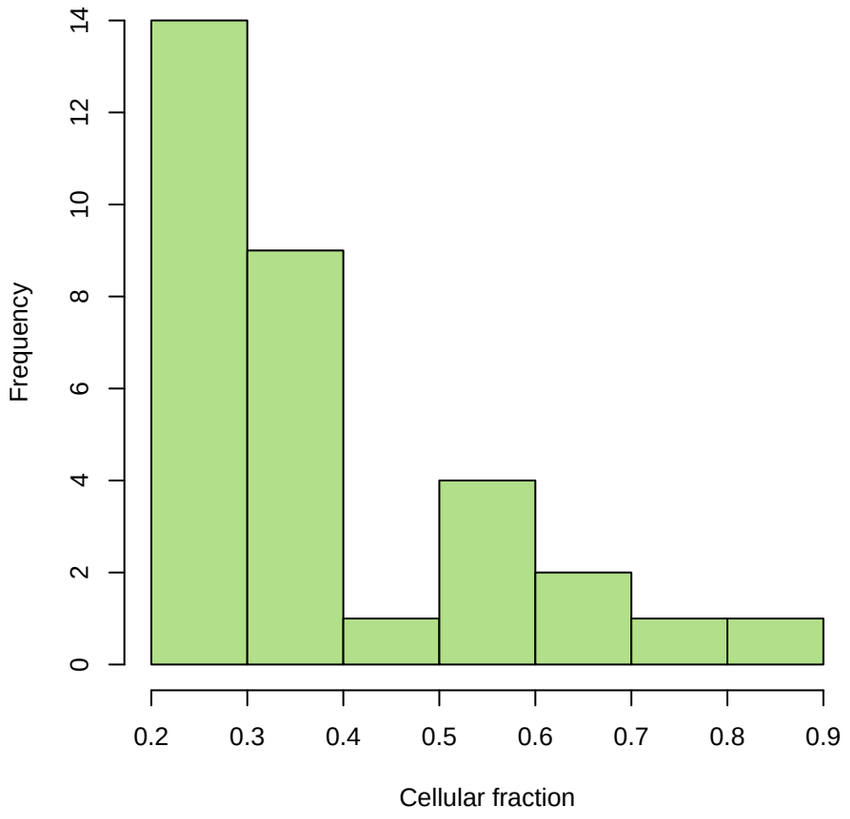

SCNA−fit log−likelihood: −7592.51
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
4 5 6 7
0 50 100 150
SNV Index

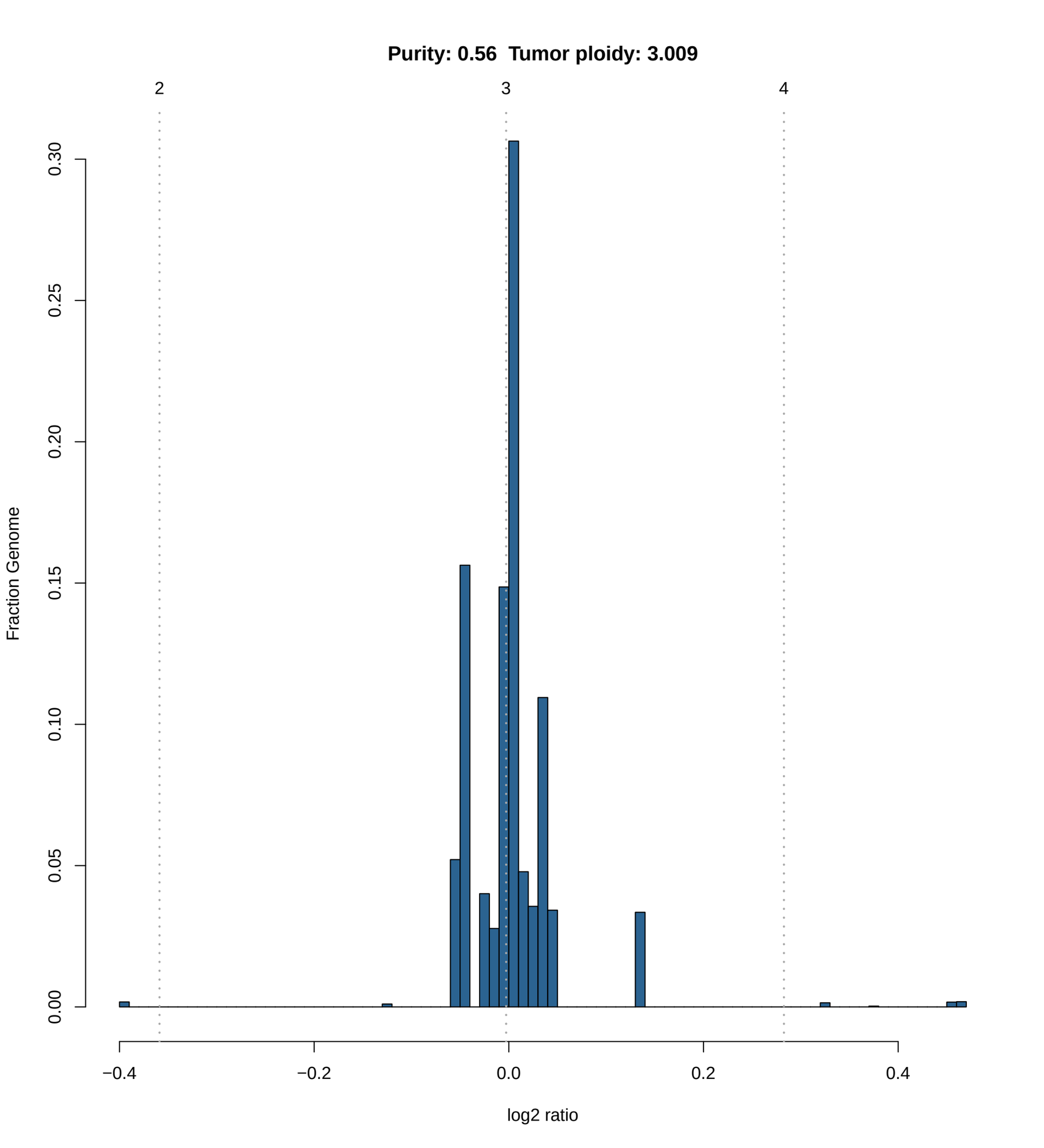

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

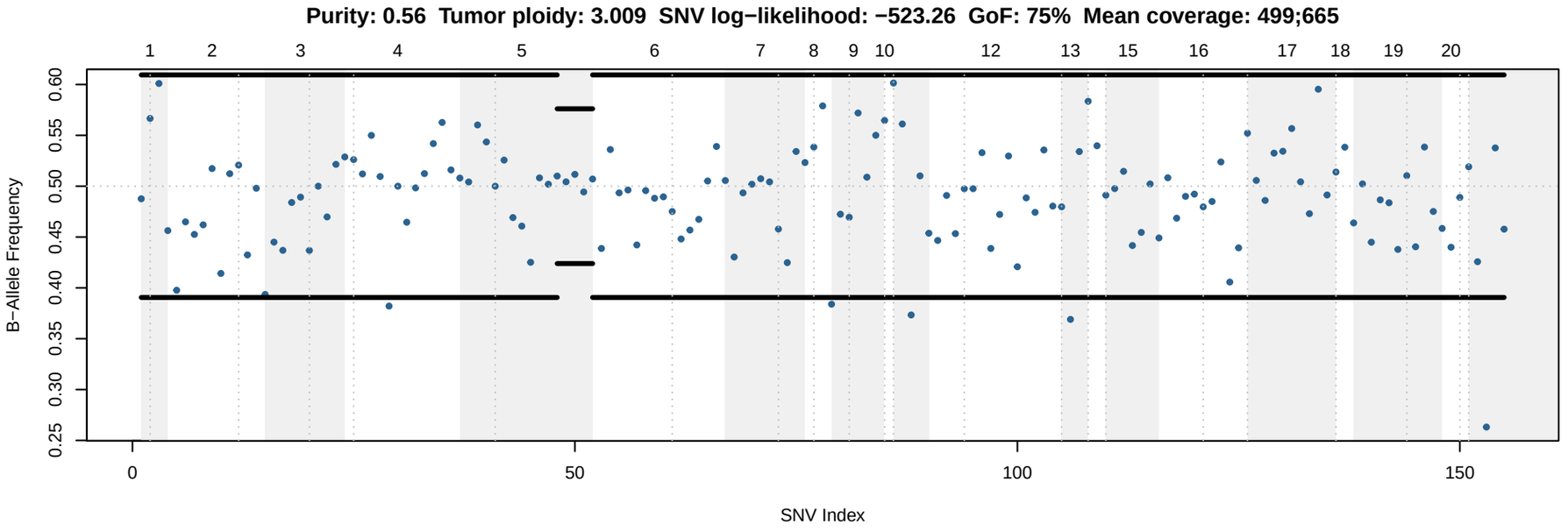

Allelic fraction (germline)
Copy Number log−ratio
5m3
7m4
6m3
7m3
5m2
6m2

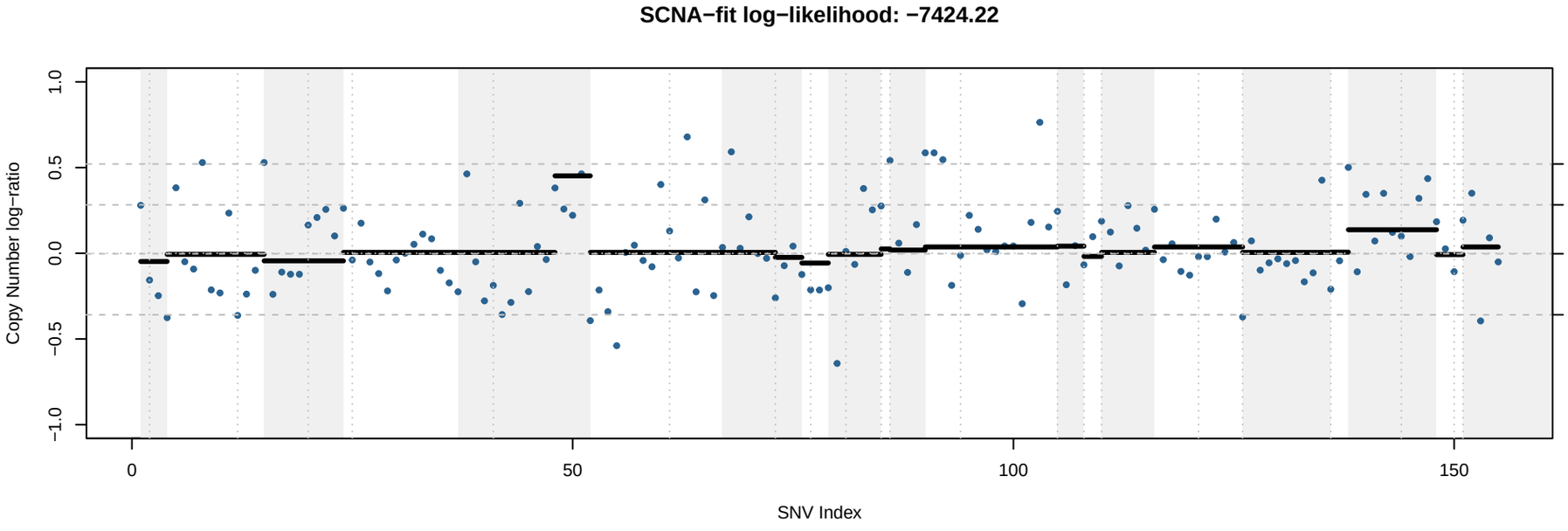

Coverage (log2)
Allelic fraction

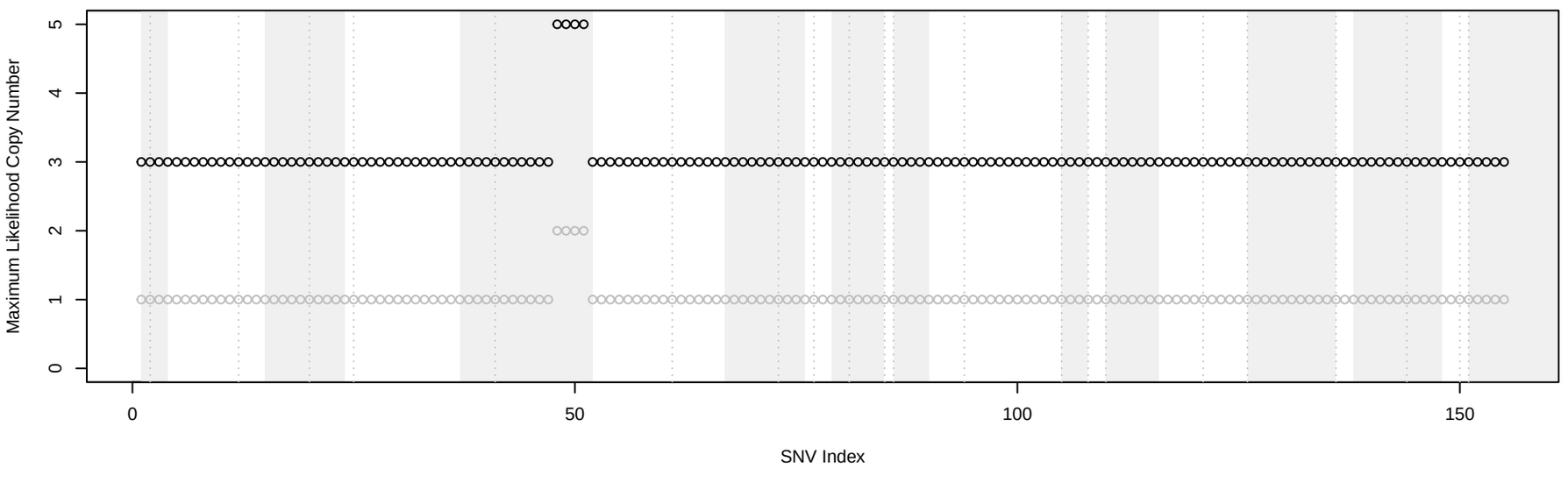

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

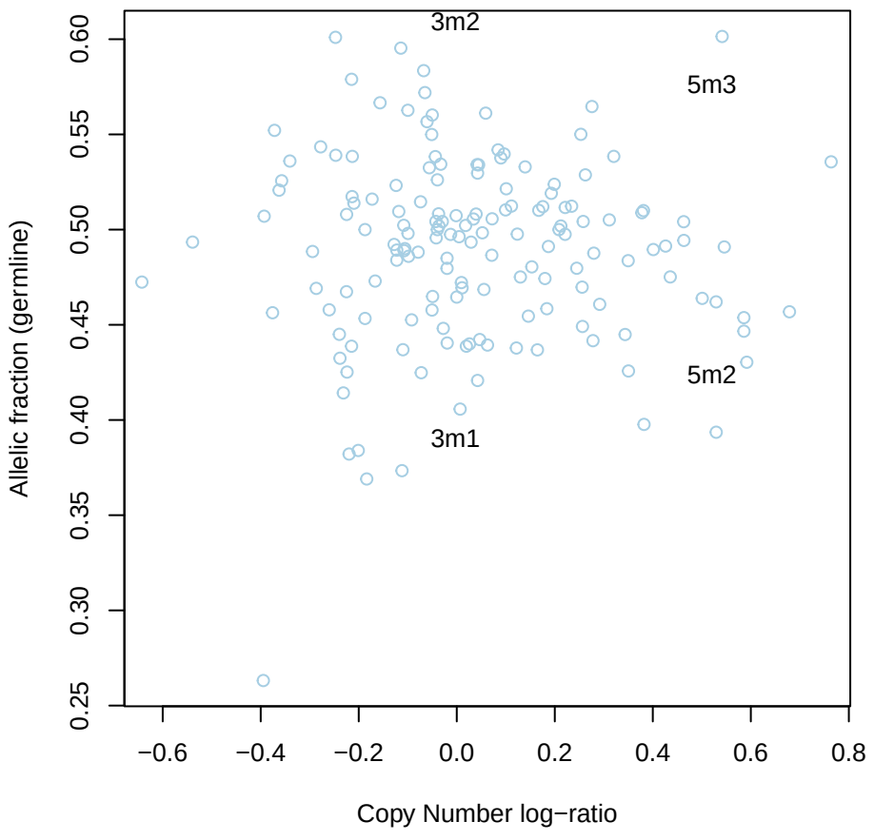

Frequency
Cellular fraction

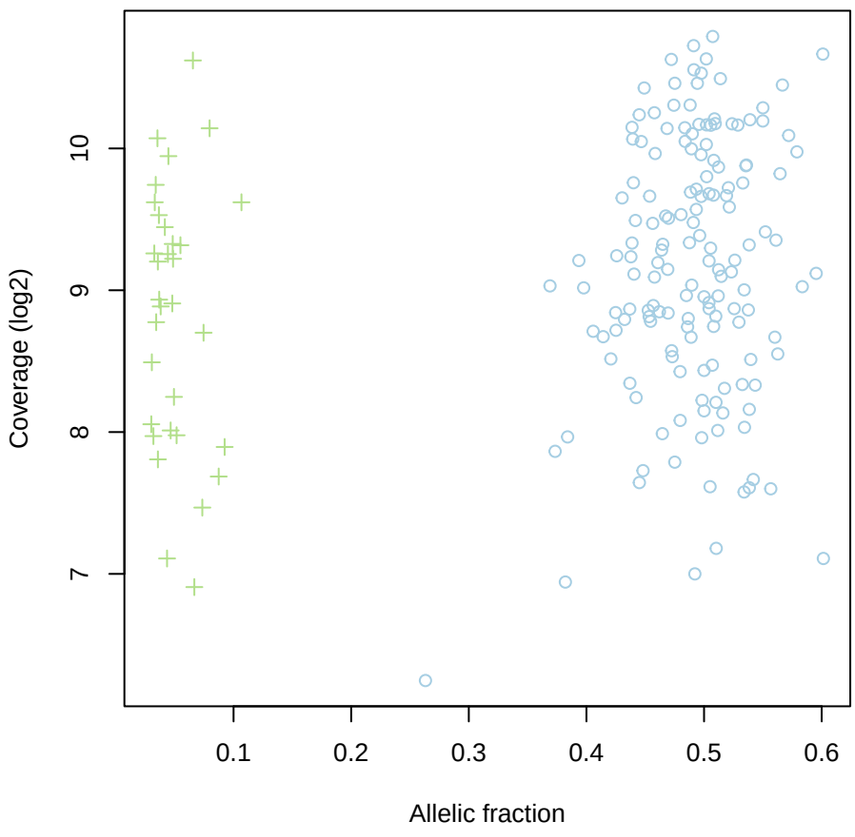

Purity: 0.56 Tumor ploidy: 3.009
2
3
4
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

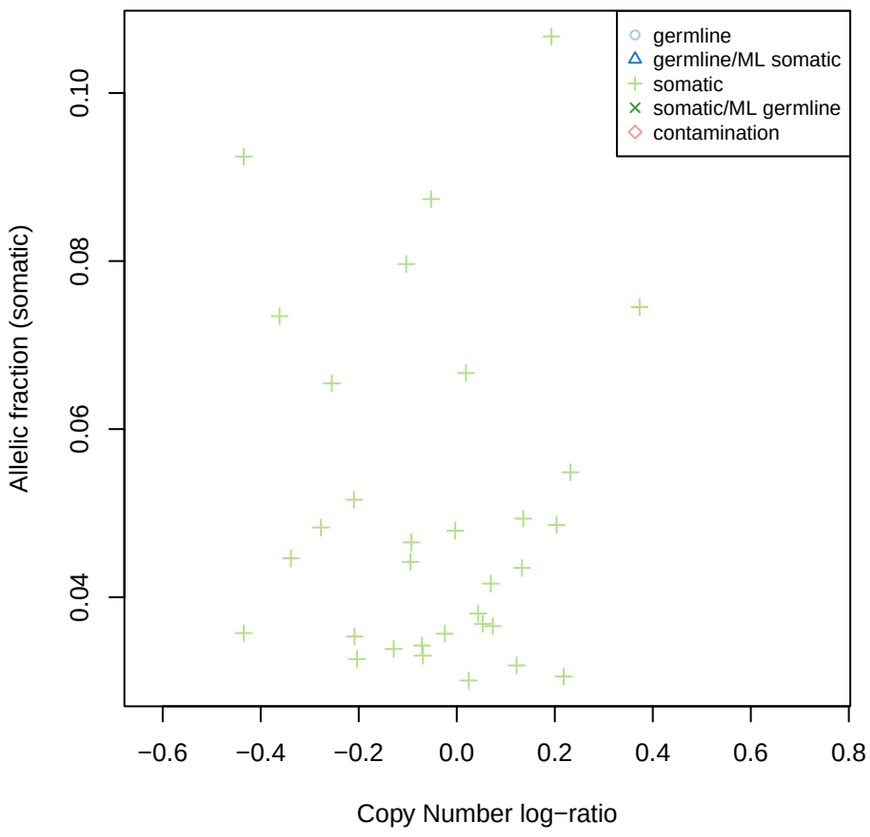

Purity: 0.56 Tumor ploidy: 3.009 SNV log−likelihood: −523.26 GoF: 75% Mean coverage: 499;665
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 18 19 20
B−Allele Frequency
0.25 0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

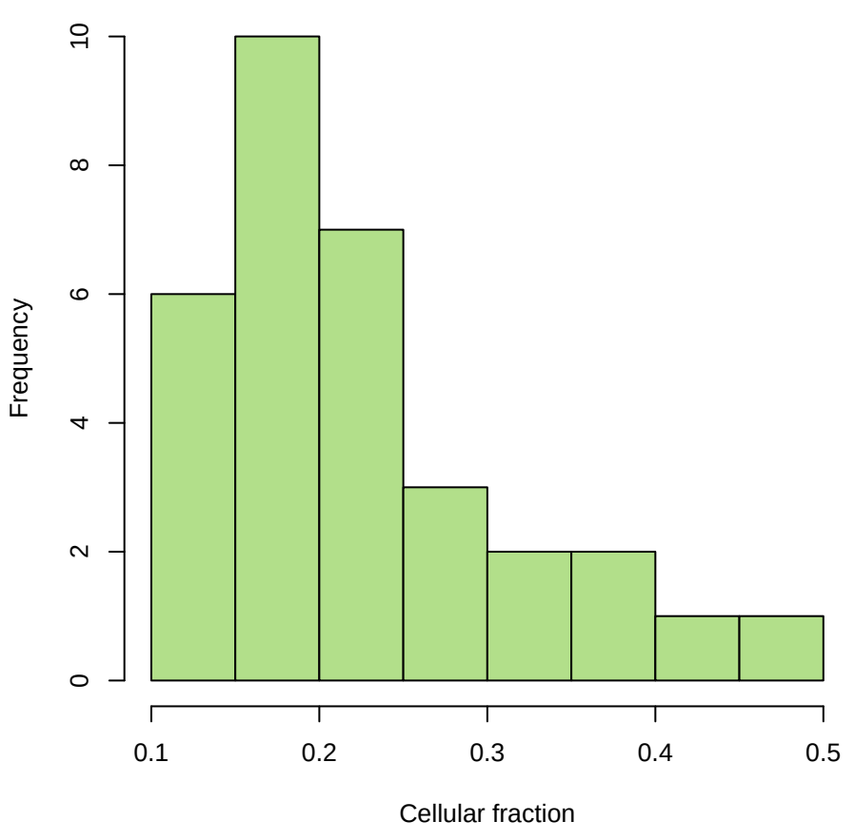

SCNA−fit log−likelihood: −7424.22
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5
0 50 100 150
SNV Index

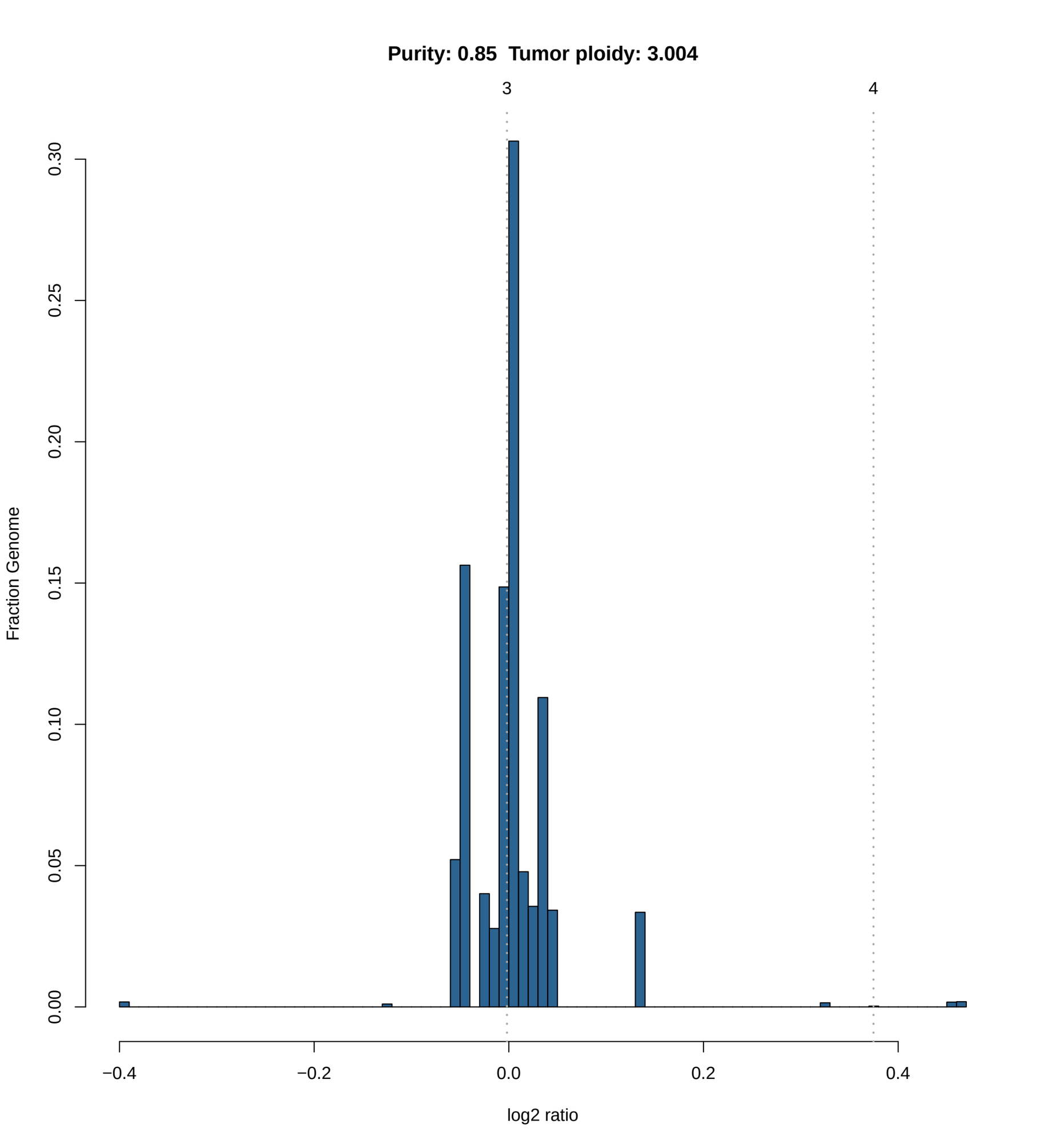

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

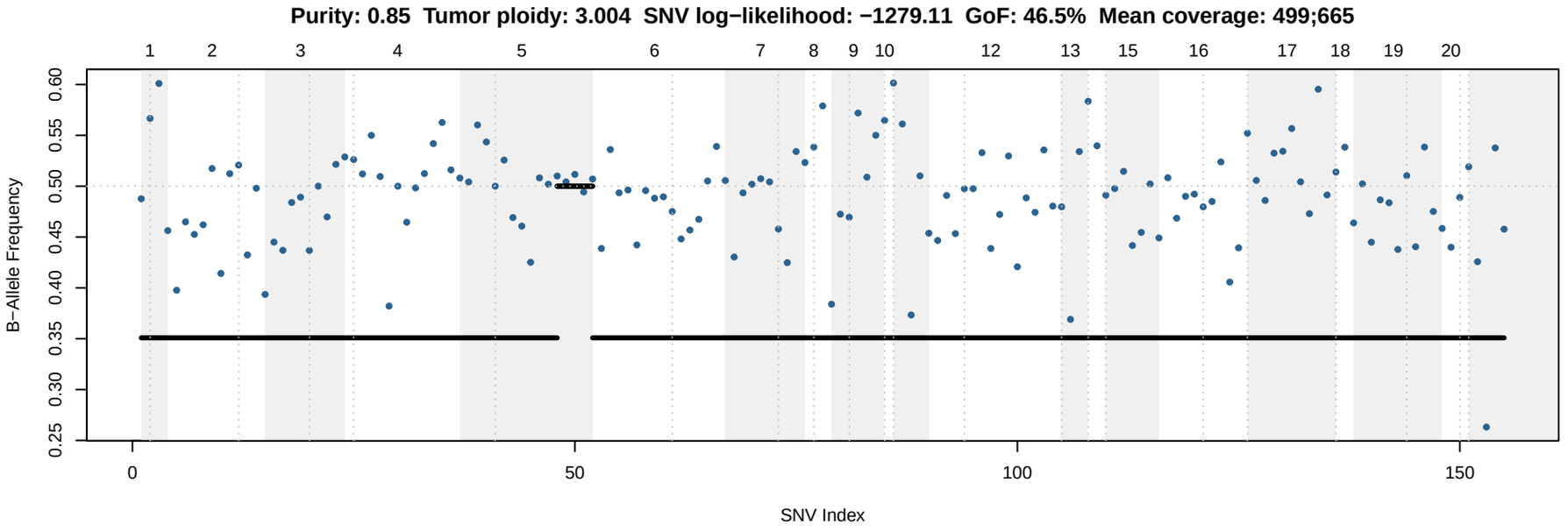

3m2
5m3
5m2
3m1
Allelic fraction (germline)
Copy Number log−ratio

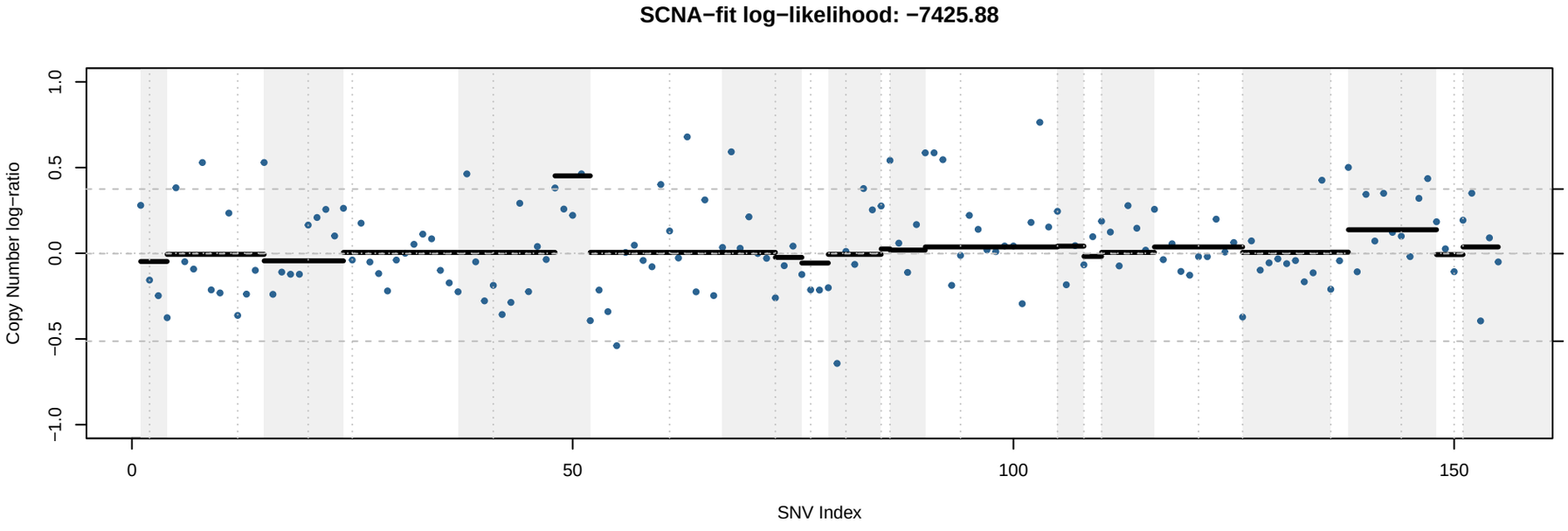

Coverage (log2)
Allelic fraction

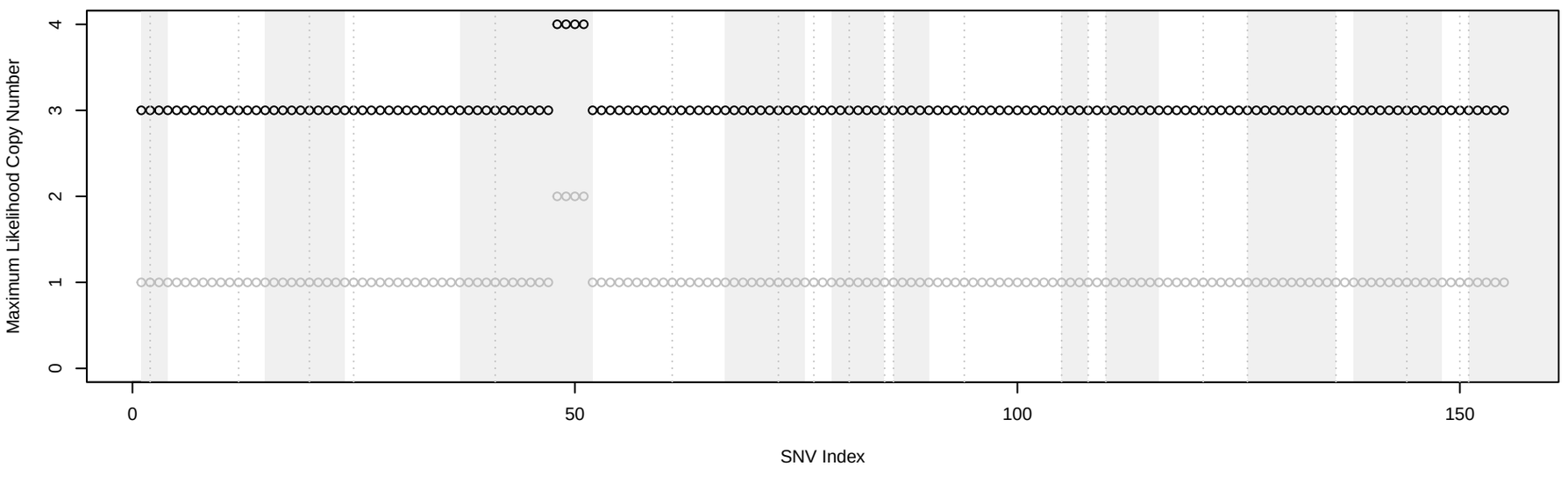

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

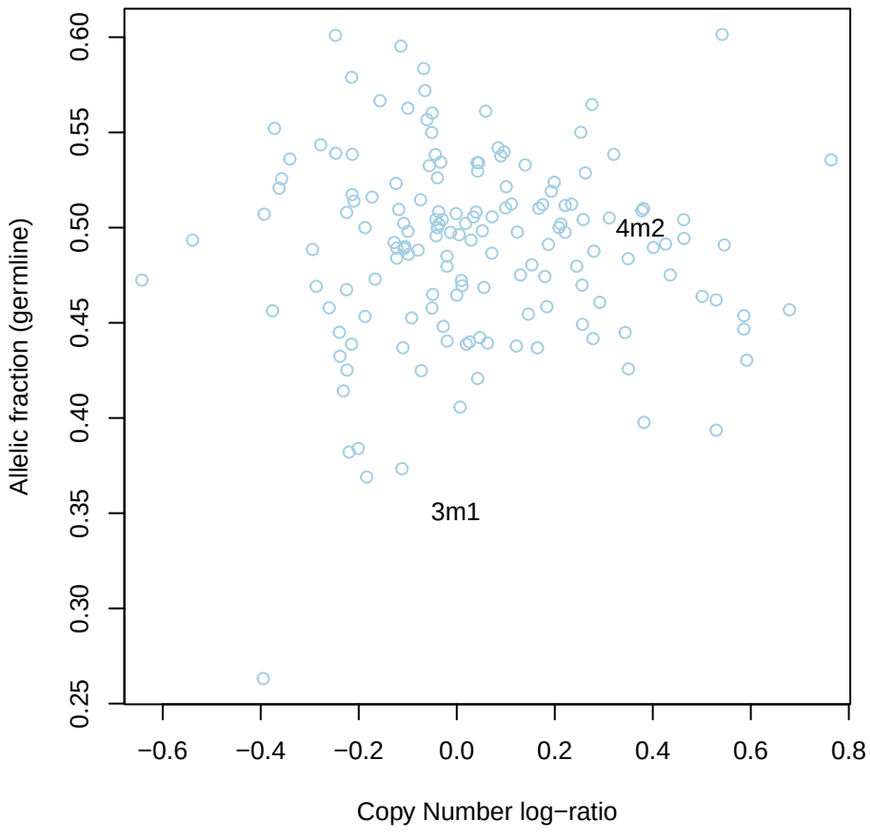

Frequency
Cellular fraction

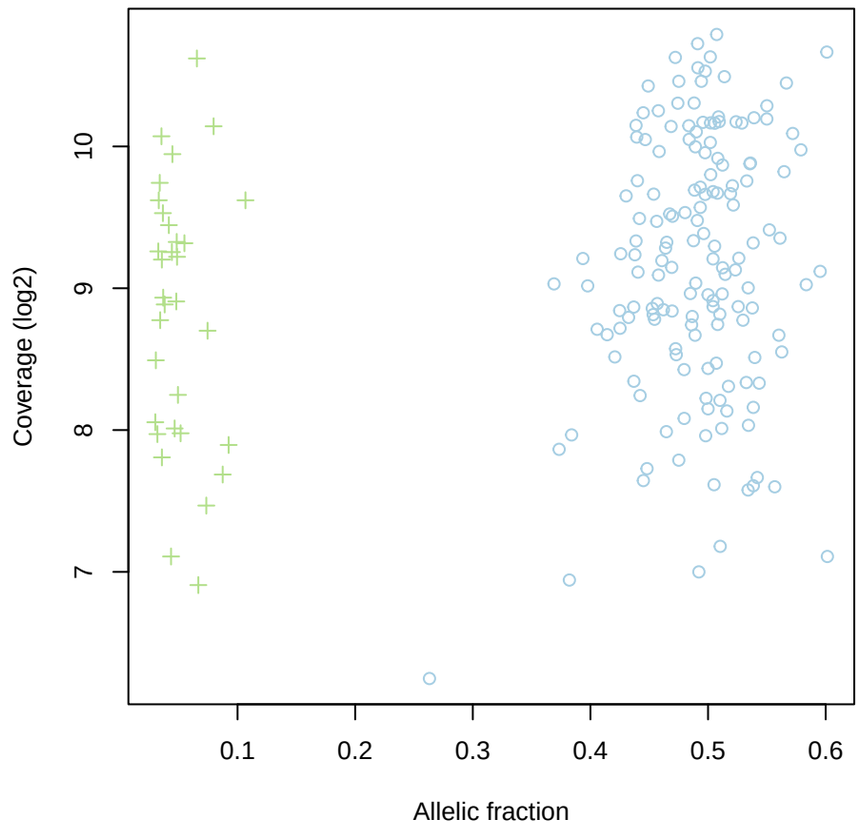

Purity: 0.85 Tumor ploidy: 3.004
3
4
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

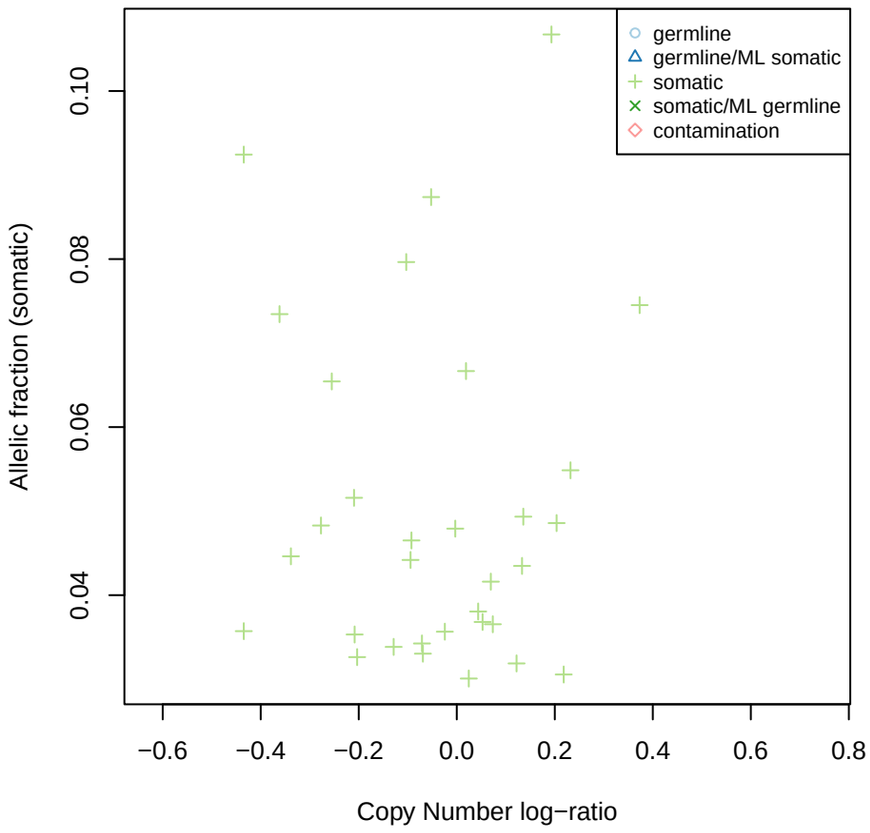

Purity: 0.85 Tumor ploidy: 3.004 SNV log−likelihood: −1279.11 GoF: 46.5% Mean coverage: 499;665
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 18 19 20
B−Allele Frequency
0.25 0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

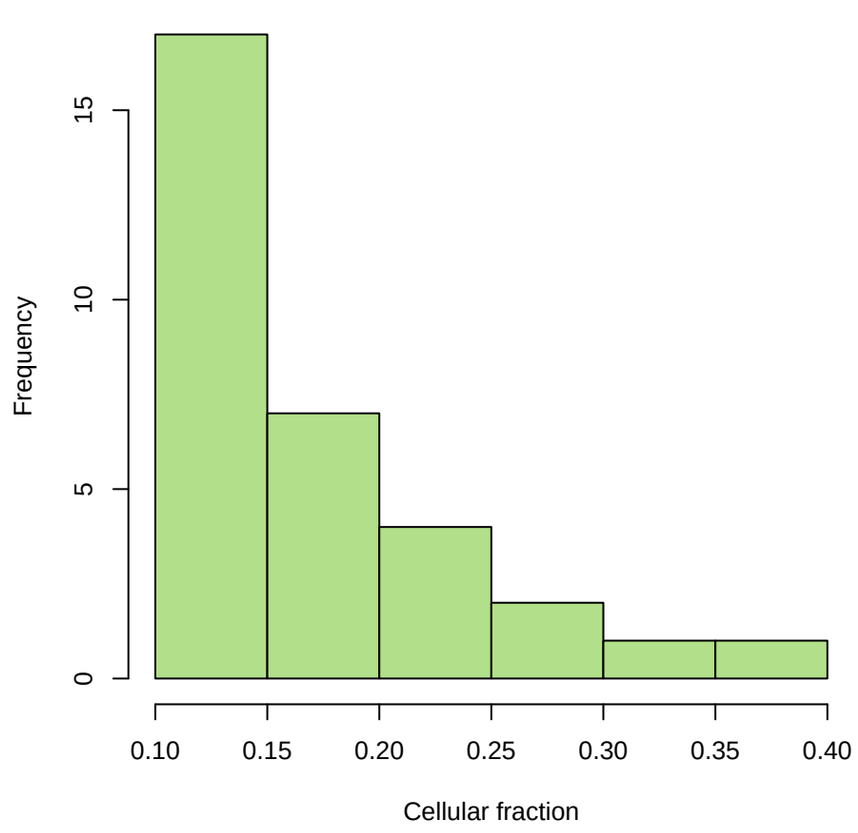

SCNA−fit log−likelihood: −7425.88
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
2 3 4
0 50 100 150
SNV Index


Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index


Allelic fraction (germline)
0.25
0.30
0.35
0.40
0.45
0.50
0.55
0.60
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio
4m2
3m1


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
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination


Frequency
0
5
10
15
0.10
0.15
0.20
0.25
0.30
0.35
0.40
Cellular fraction