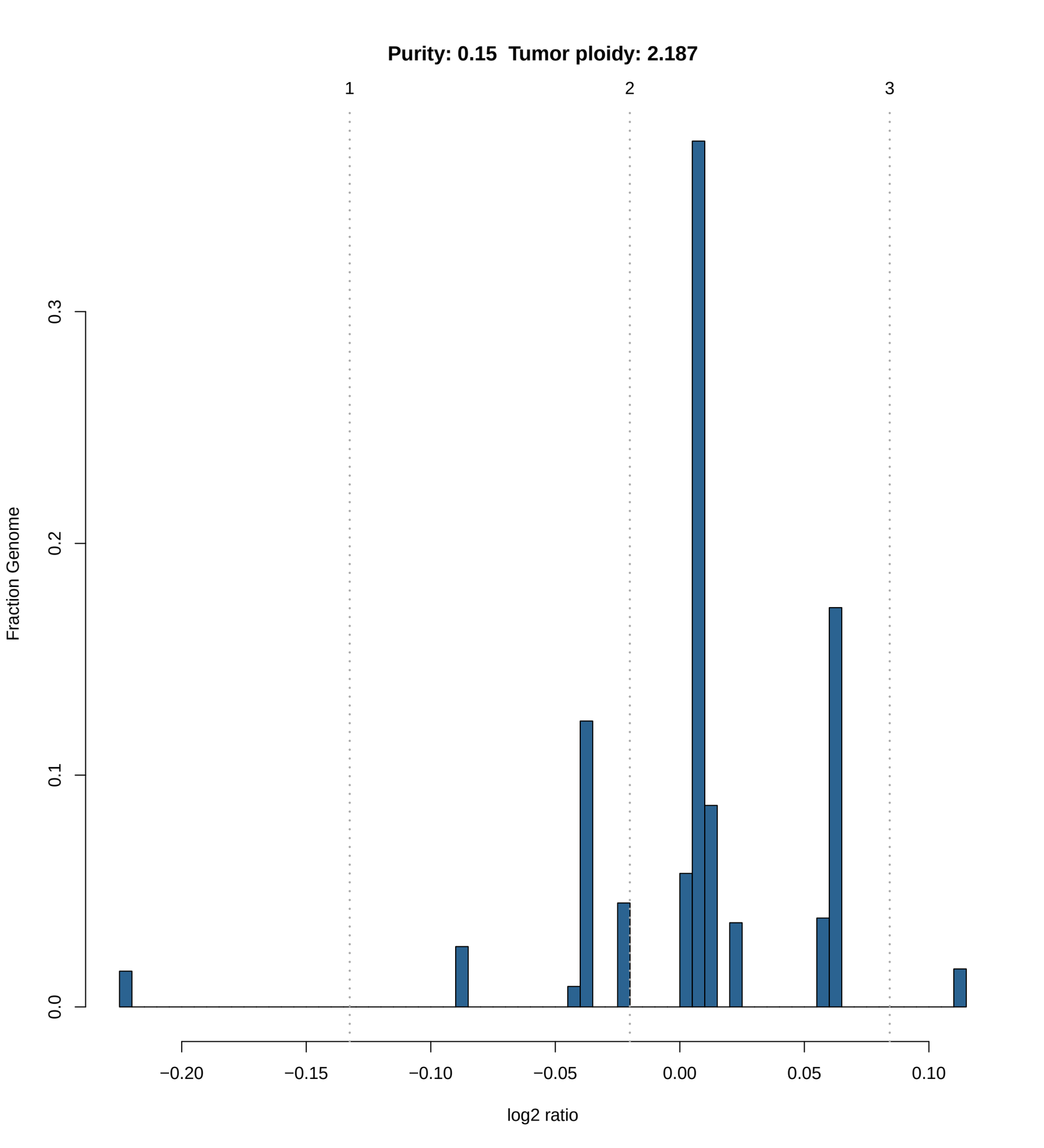
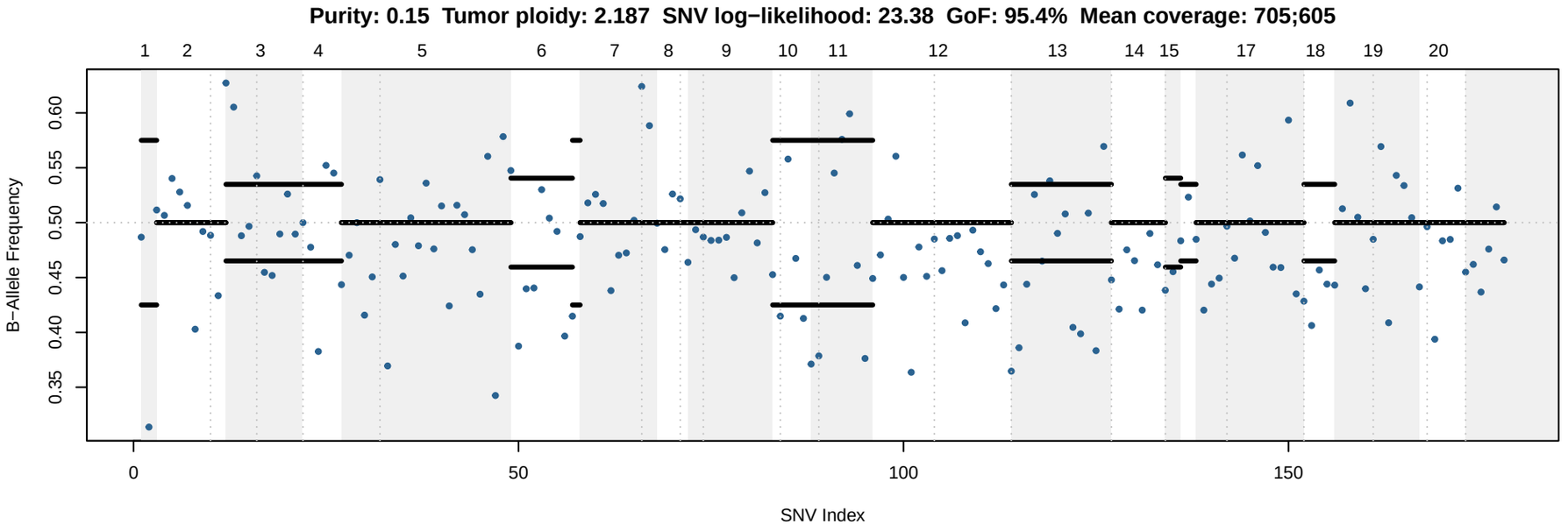
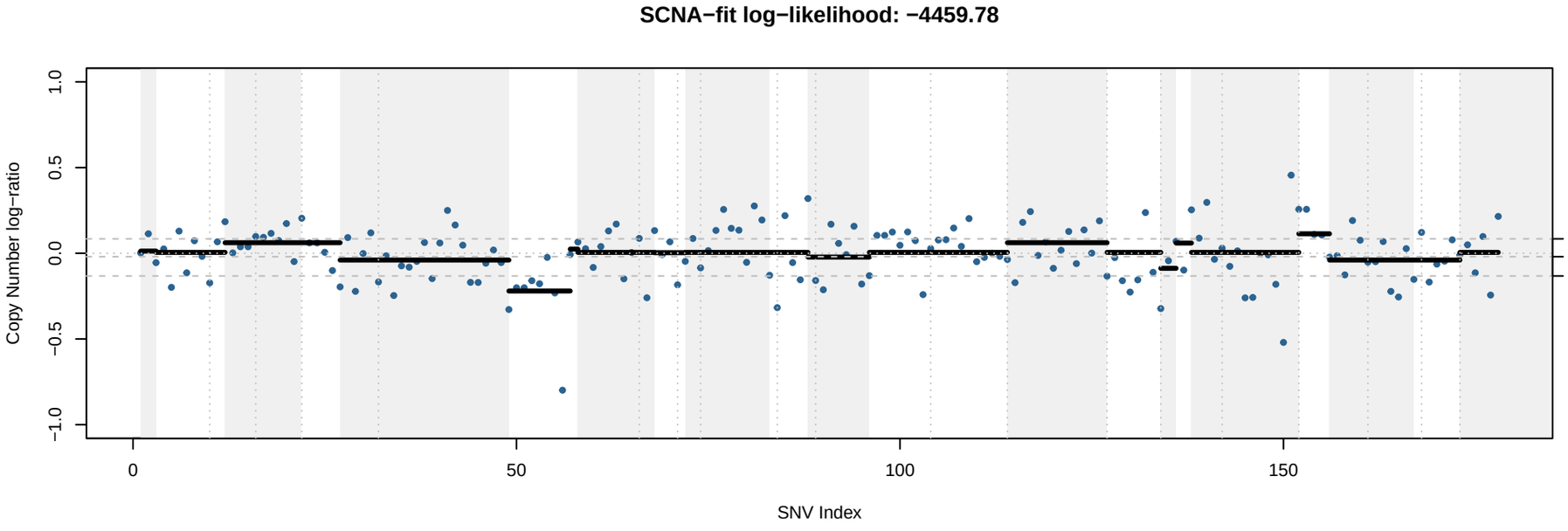
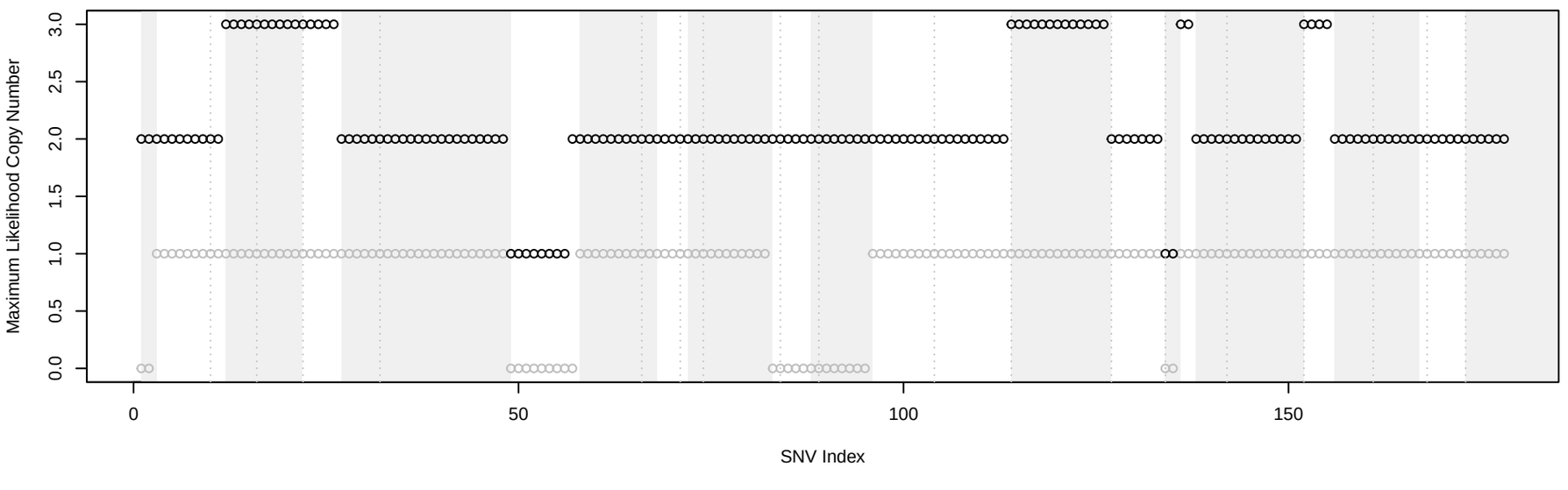
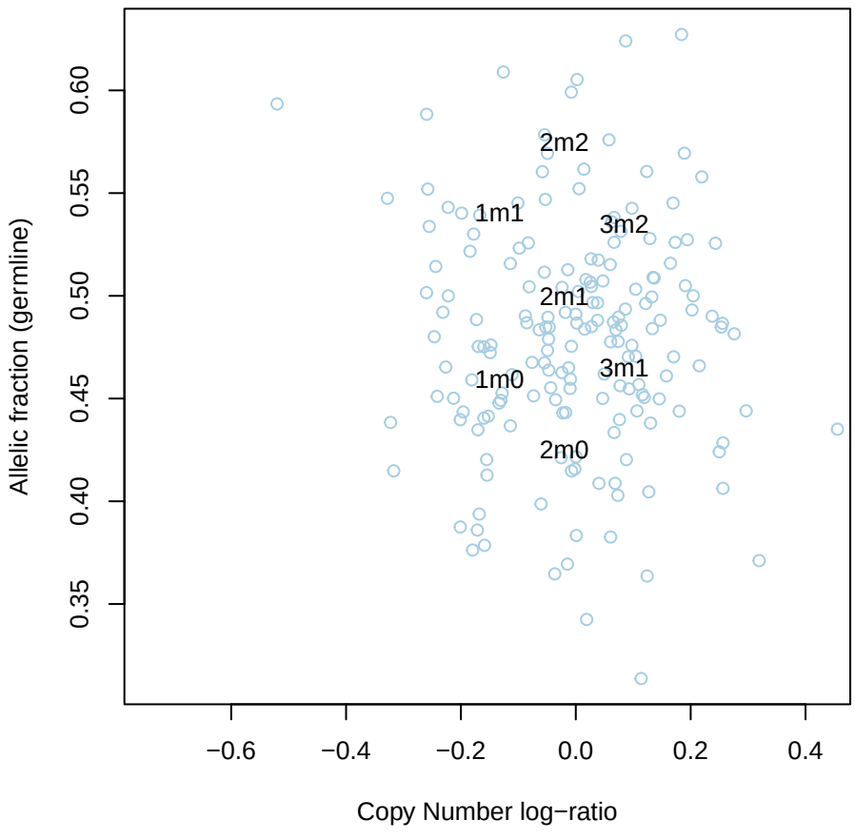
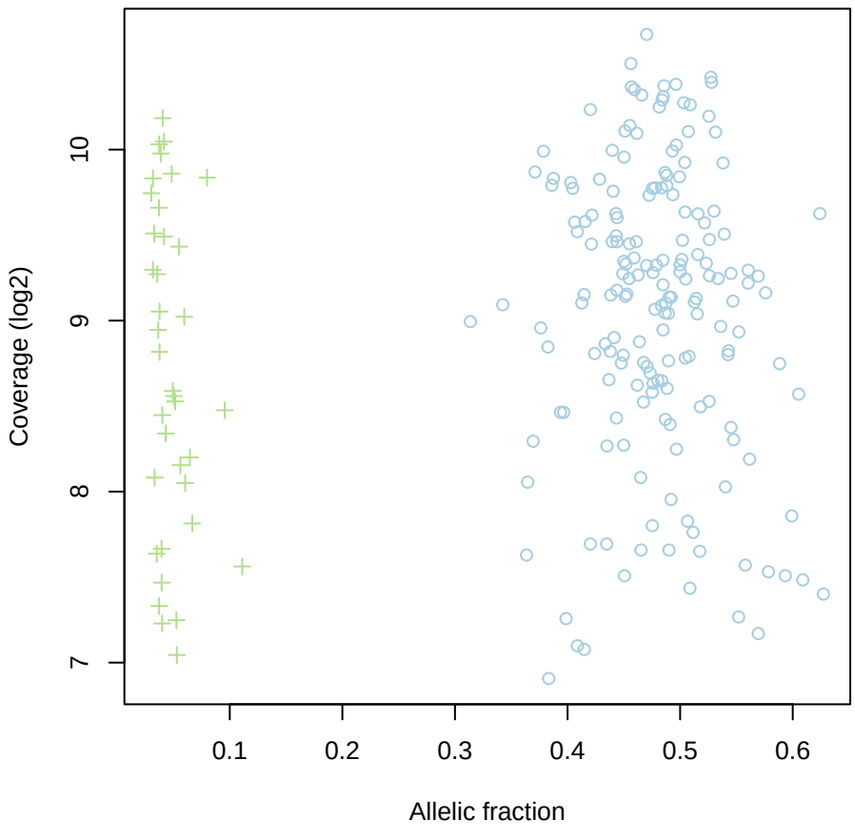

Purity: 0.15 Tumor ploidy: 2.187
1
2
3
0.3
0.2
0.1
0.0
Fraction Genome
−0.20
−0.15
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

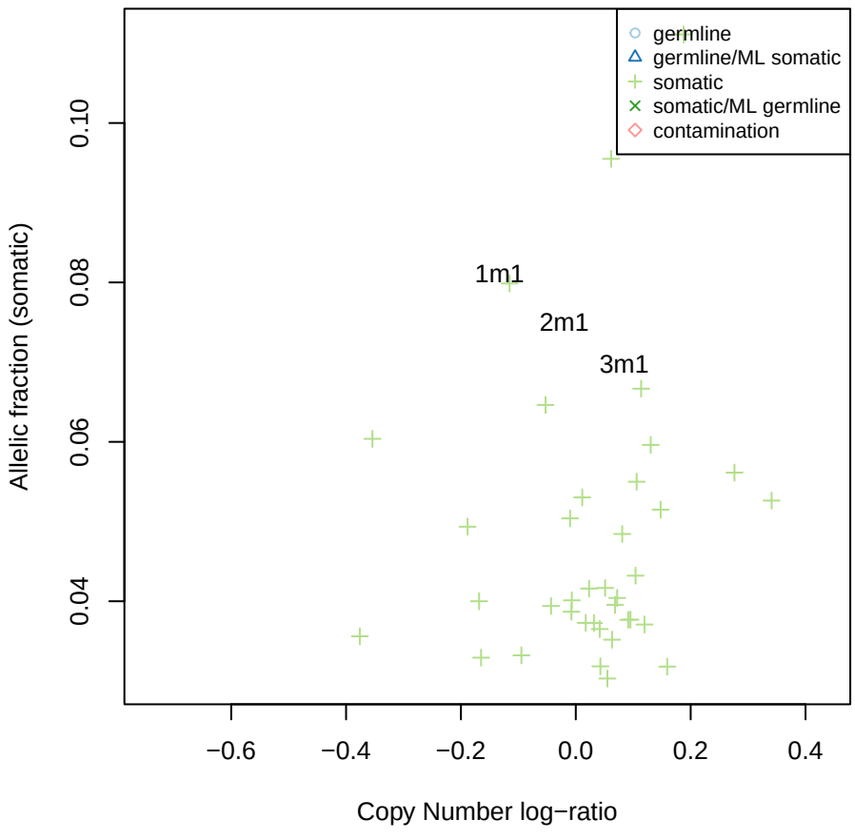

Purity: 0.15 Tumor ploidy: 2.187 SNV log−likelihood: 23.38 GoF: 95.4% Mean coverage: 705;605
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

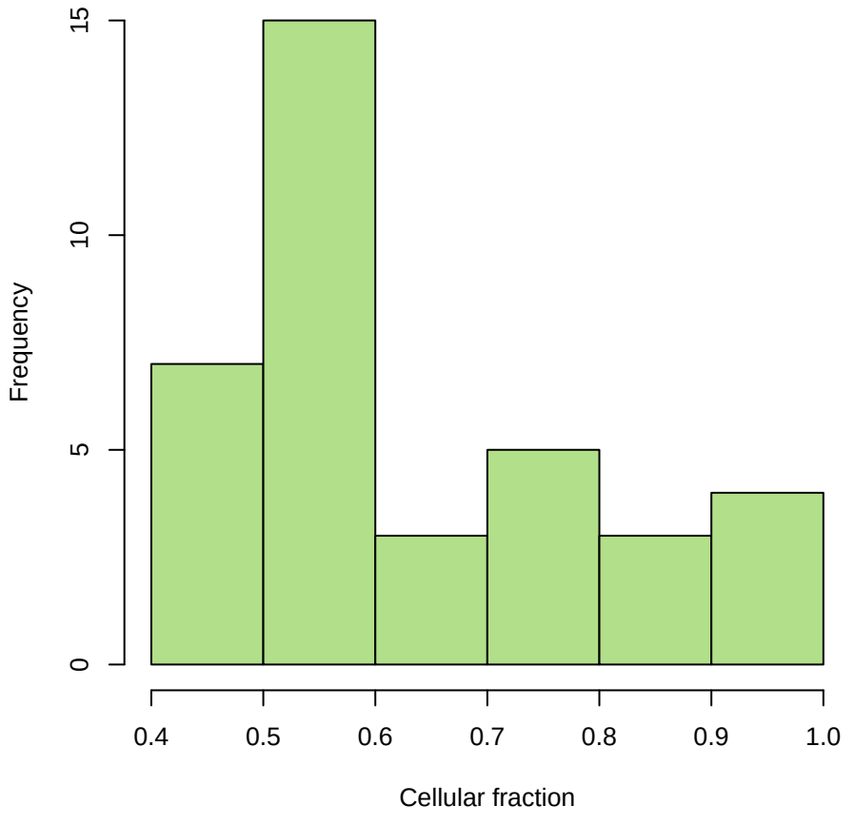

SCNA−fit log−likelihood: −4459.78
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
1 3
0 50 100 150
SNV Index

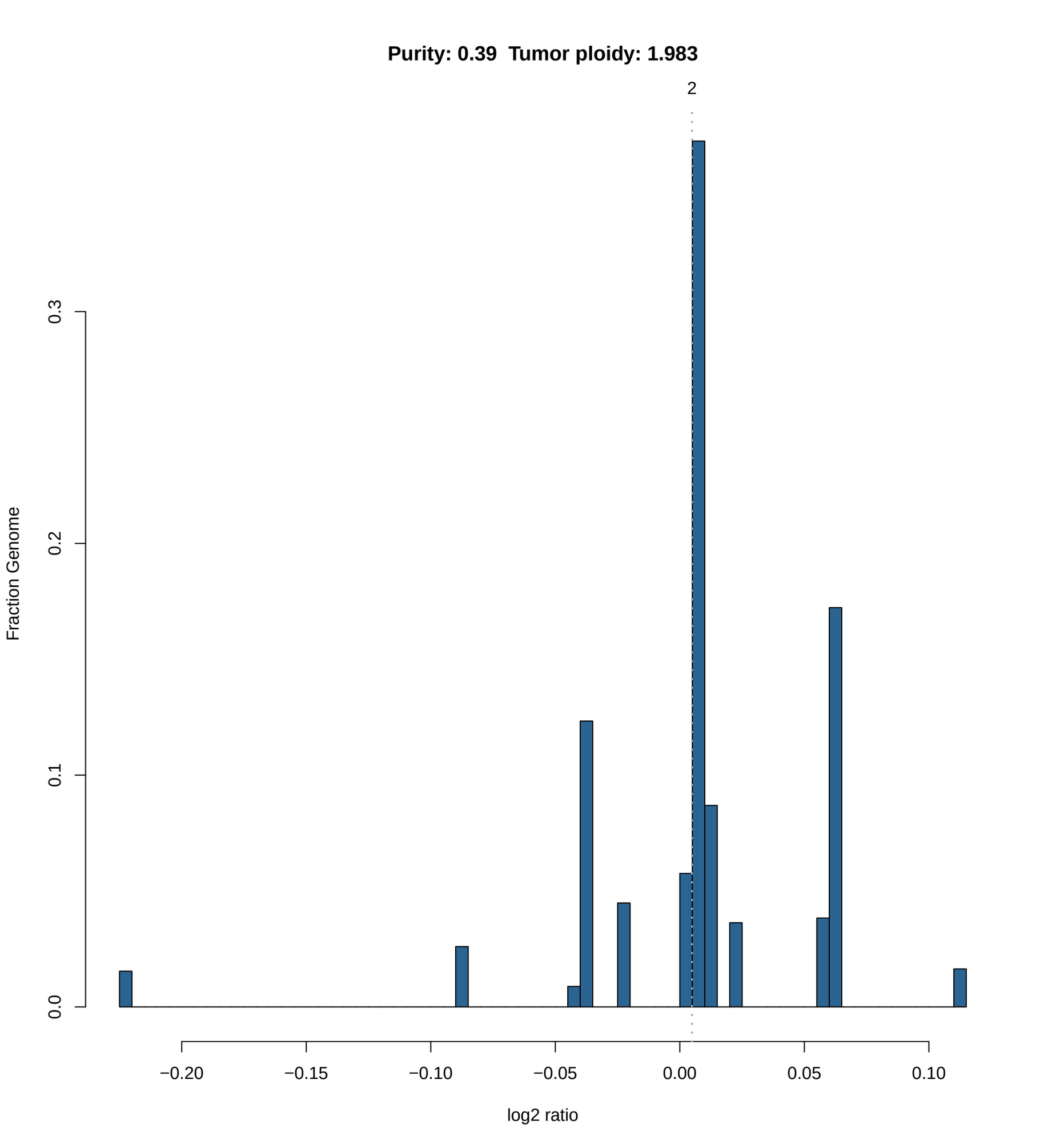

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

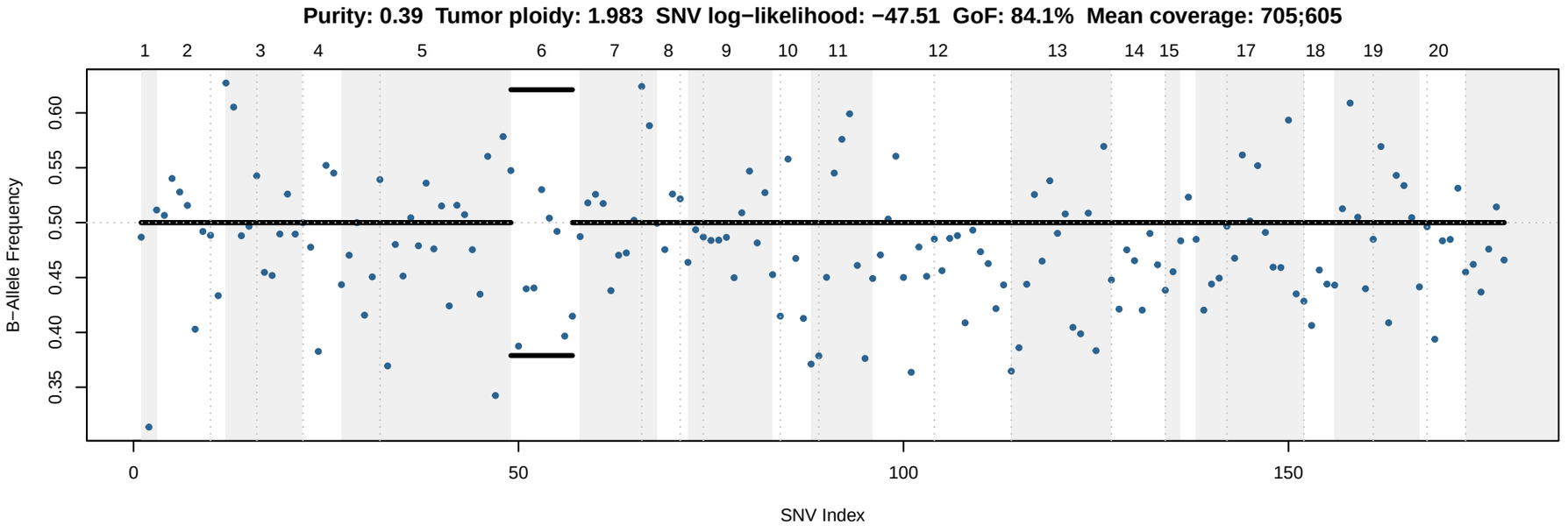

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
2m2
1m1
3m2
2m1
1m0
3m1
2m0
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

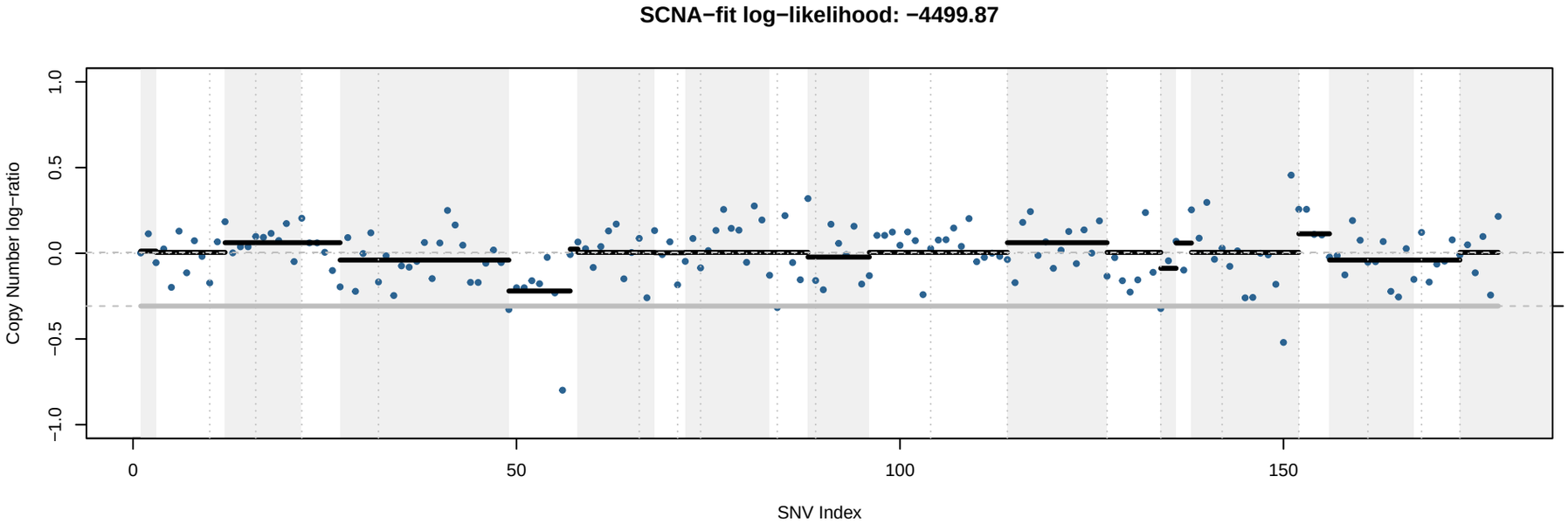

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

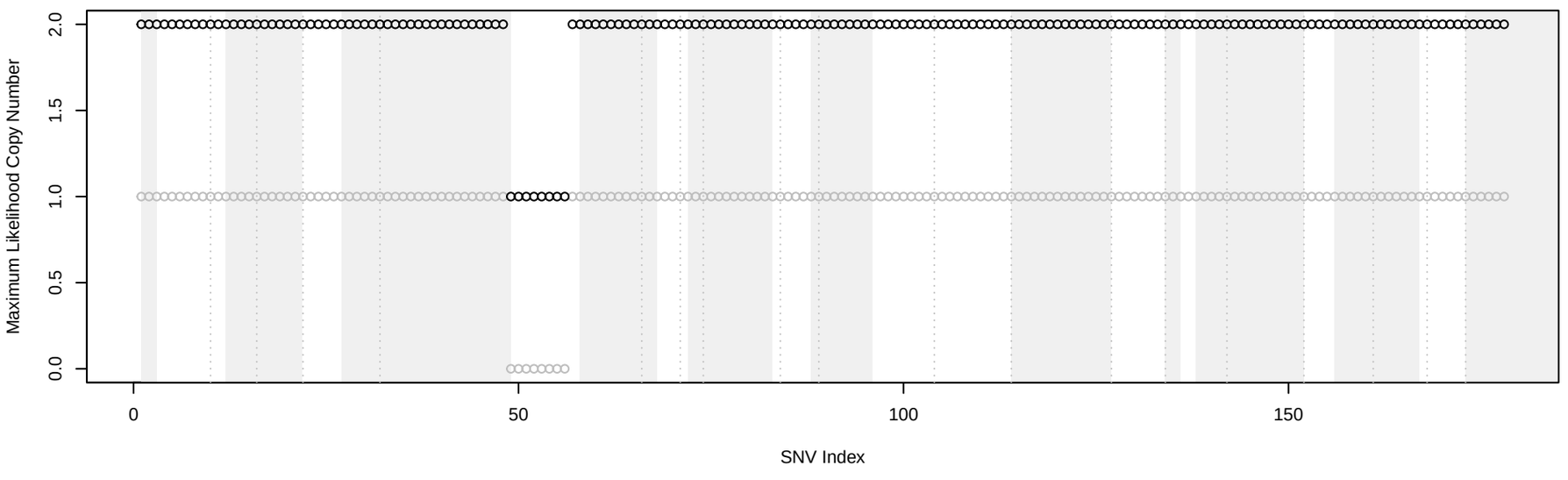

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
1m1
2m1
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

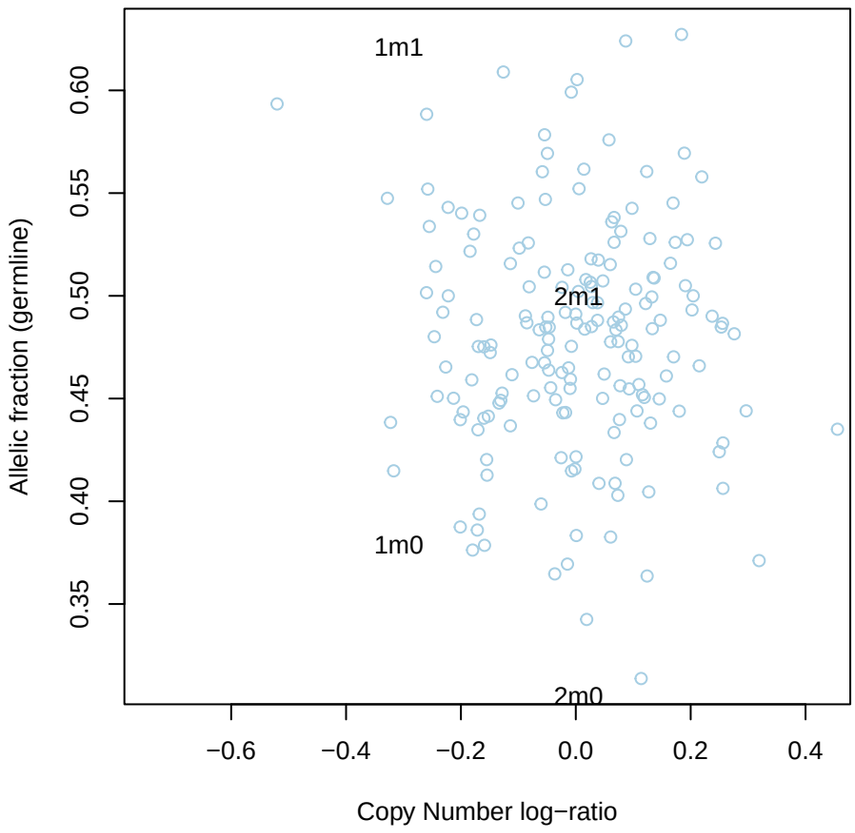

Frequency
0
5
10
15
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

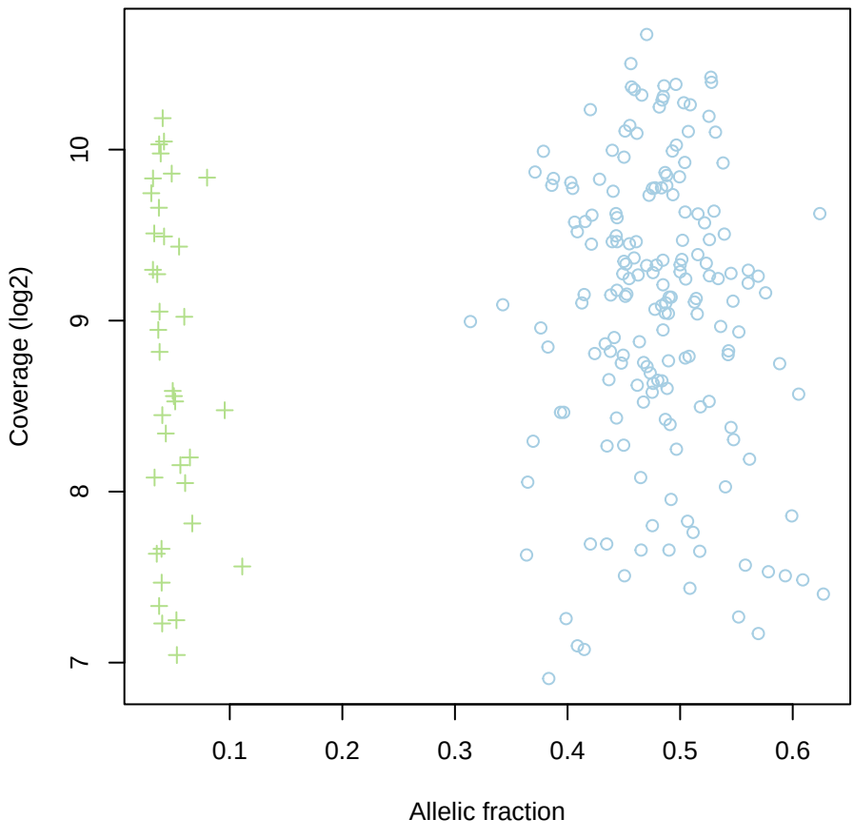

Purity: 0.39 Tumor ploidy: 1.983
2
Fraction Genome
0.0
0.1
0.2
0.3
−0.20
−0.15
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

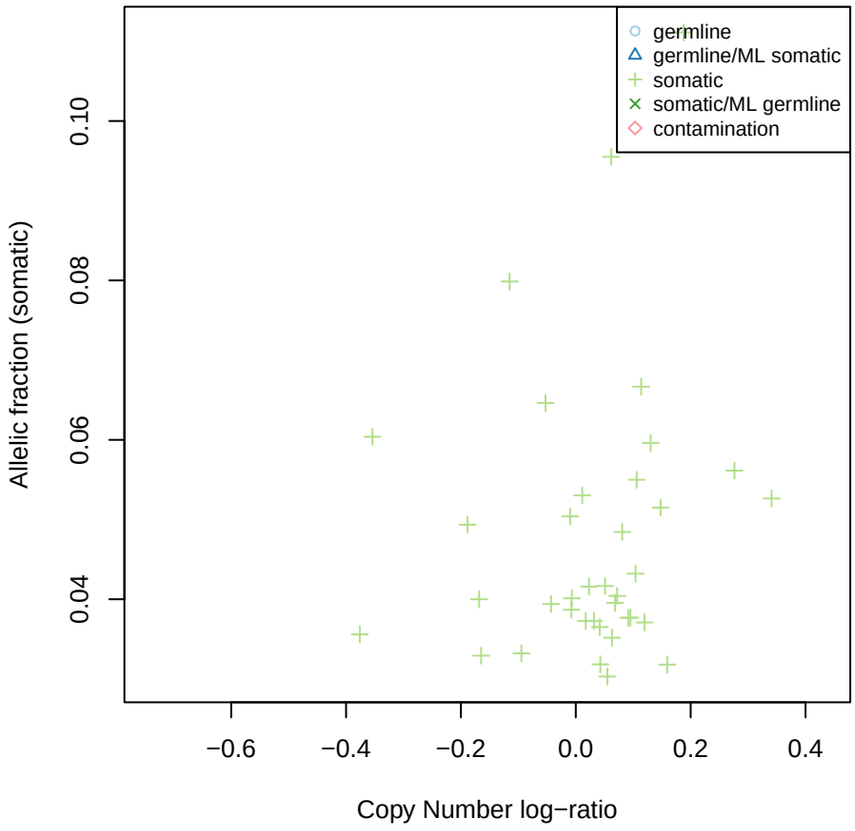

Purity: 0.39 Tumor ploidy: 1.983 SNV log−likelihood: −47.51 GoF: 84.1% Mean coverage: 705;605
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

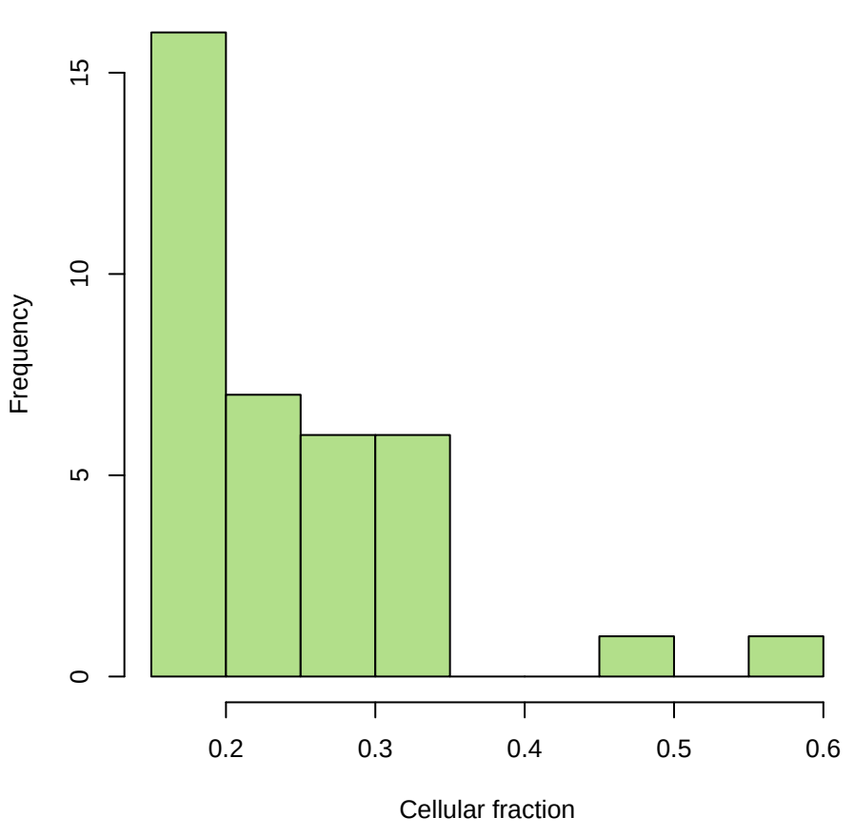

SCNA−fit log−likelihood: −4499.87
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2
0 50 100 150
SNV Index

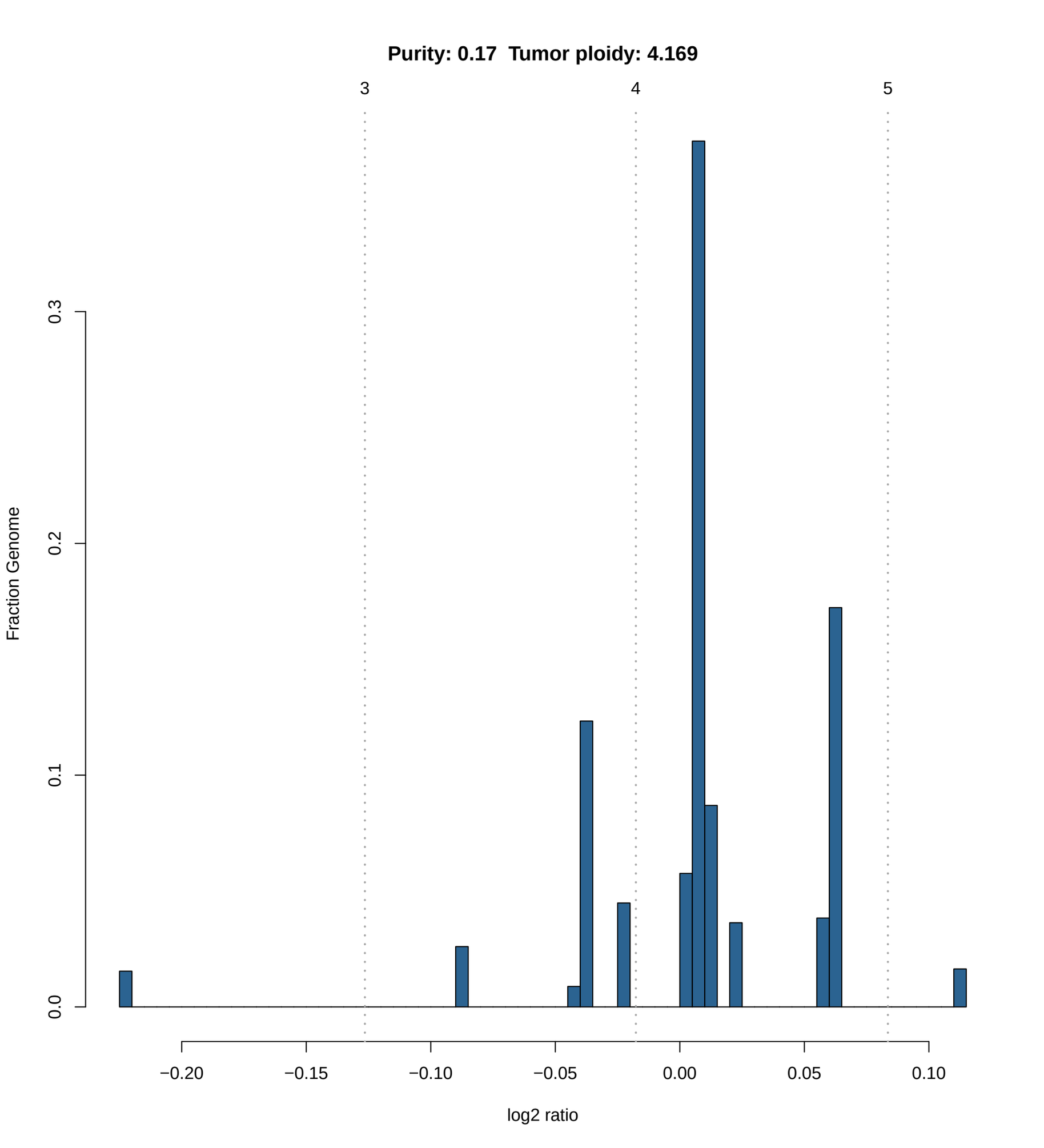

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 50 100 150
SNV Index

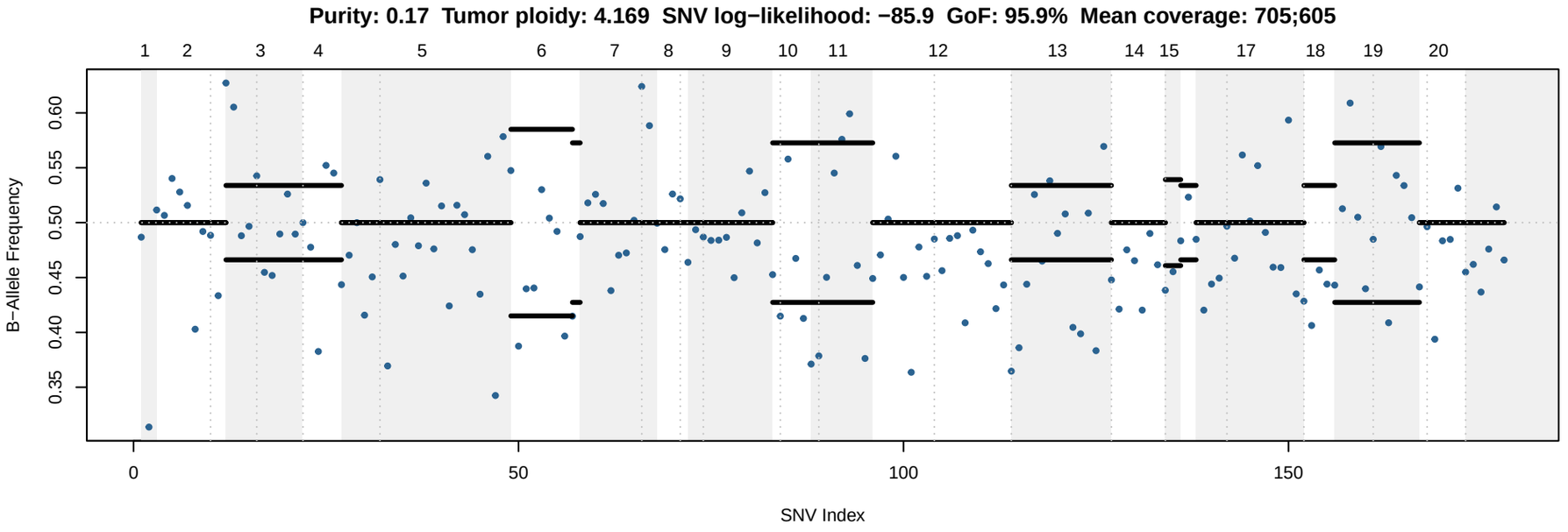

1m1
2m1
1m0
2m0
Allelic fraction (germline)
Copy Number log−ratio

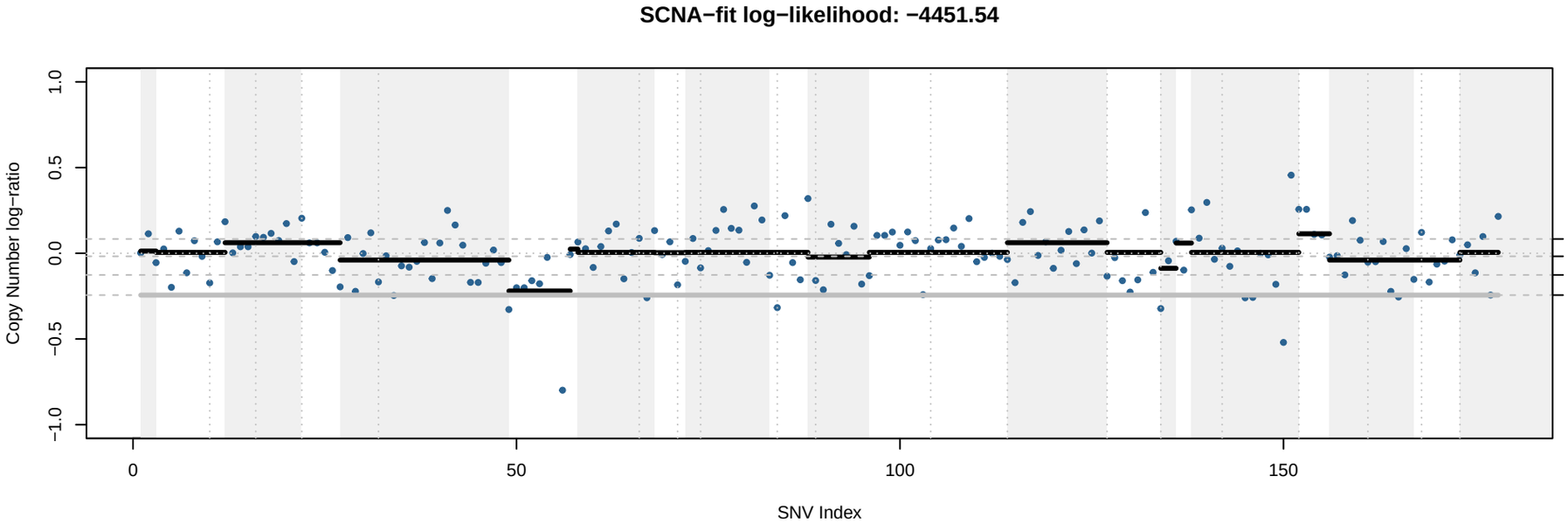

Coverage (log2)
Allelic fraction

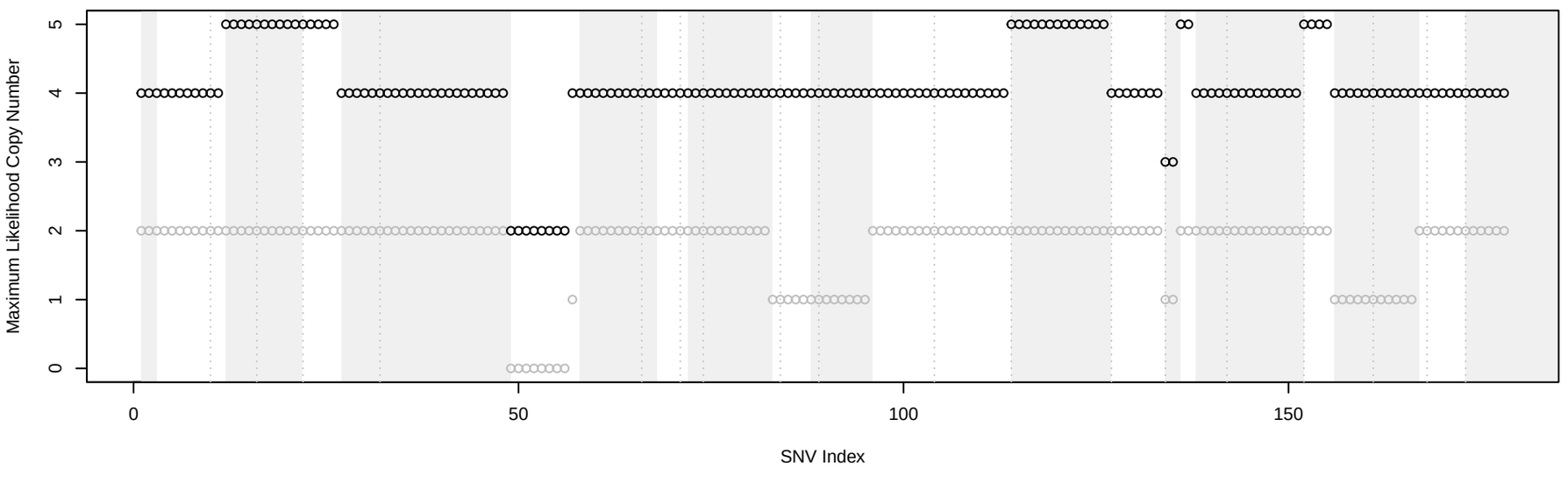

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

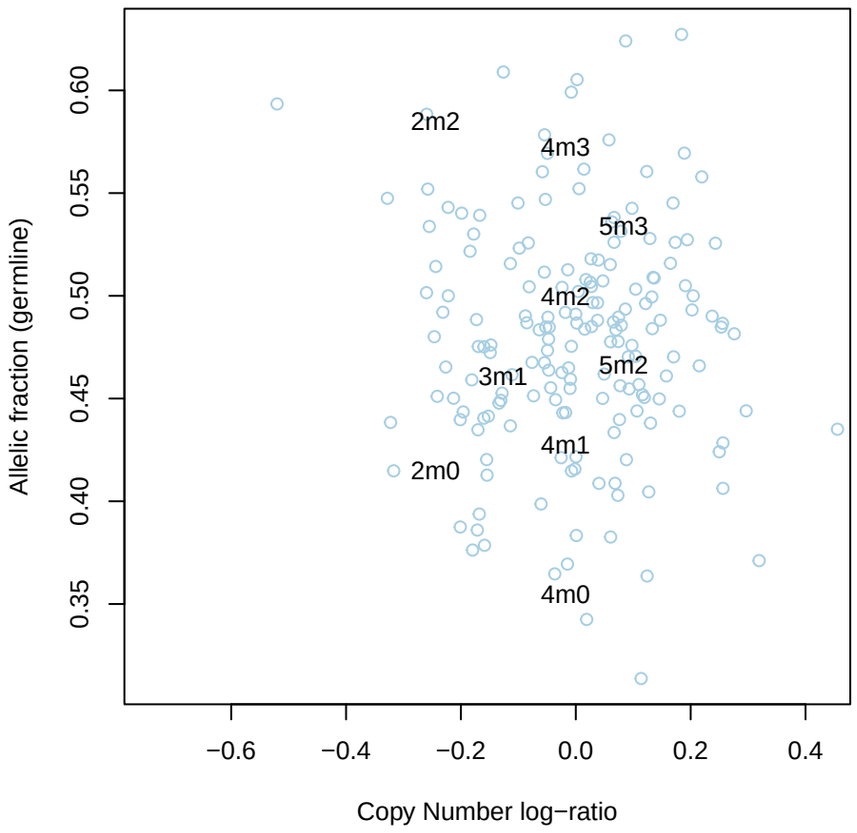

Frequency
Cellular fraction

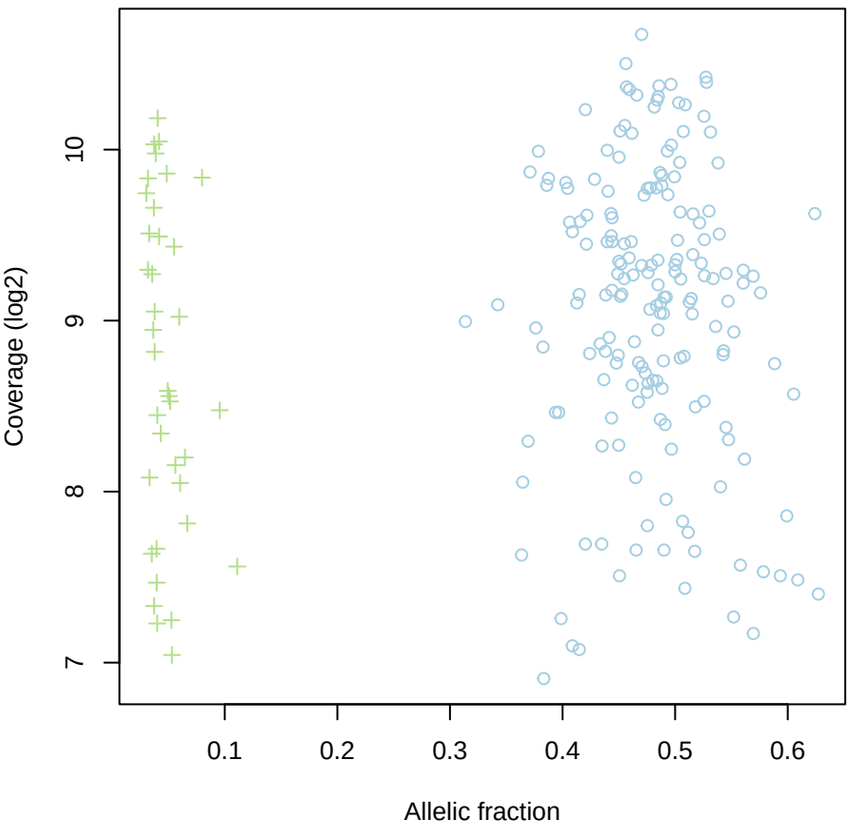

Purity: 0.17 Tumor ploidy: 4.169
3
4
5
0.0
0.1
0.2
0.3
Fraction Genome
−0.20
−0.15
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

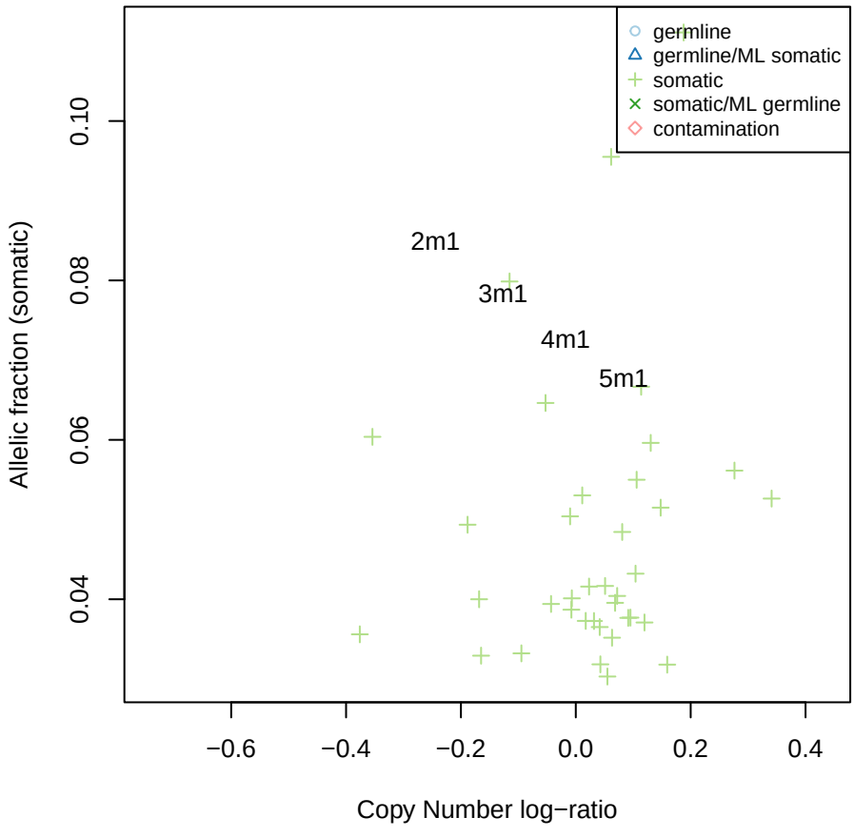

Purity: 0.17 Tumor ploidy: 4.169 SNV log−likelihood: −85.9 GoF: 95.9% Mean coverage: 705;605
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

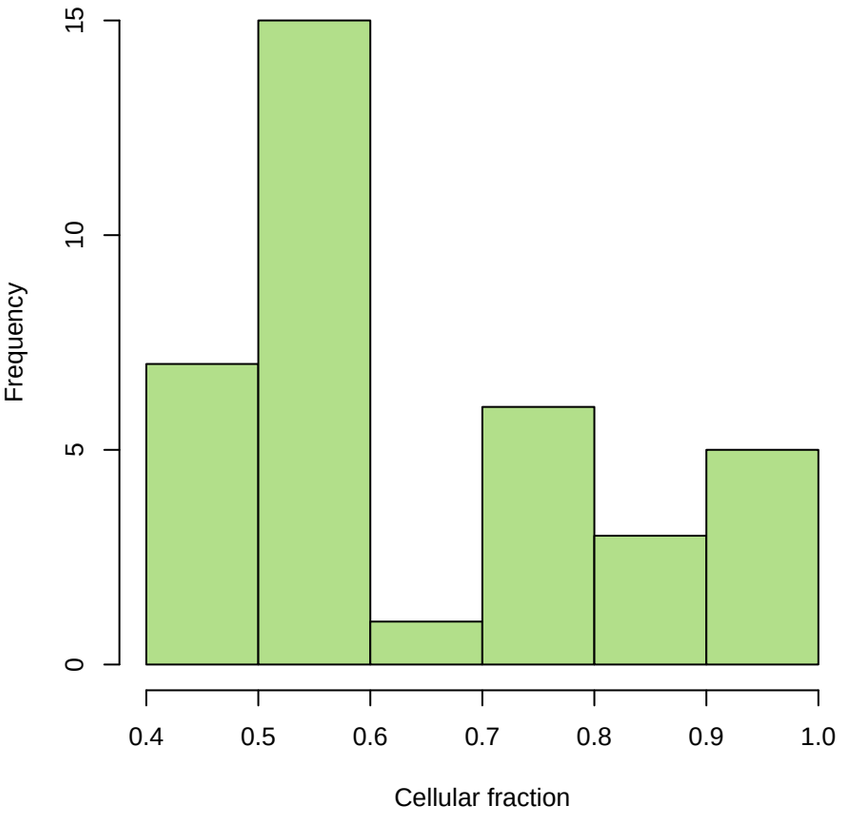

SCNA−fit log−likelihood: −4451.54
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
4
2
0 50 100 150
SNV Index

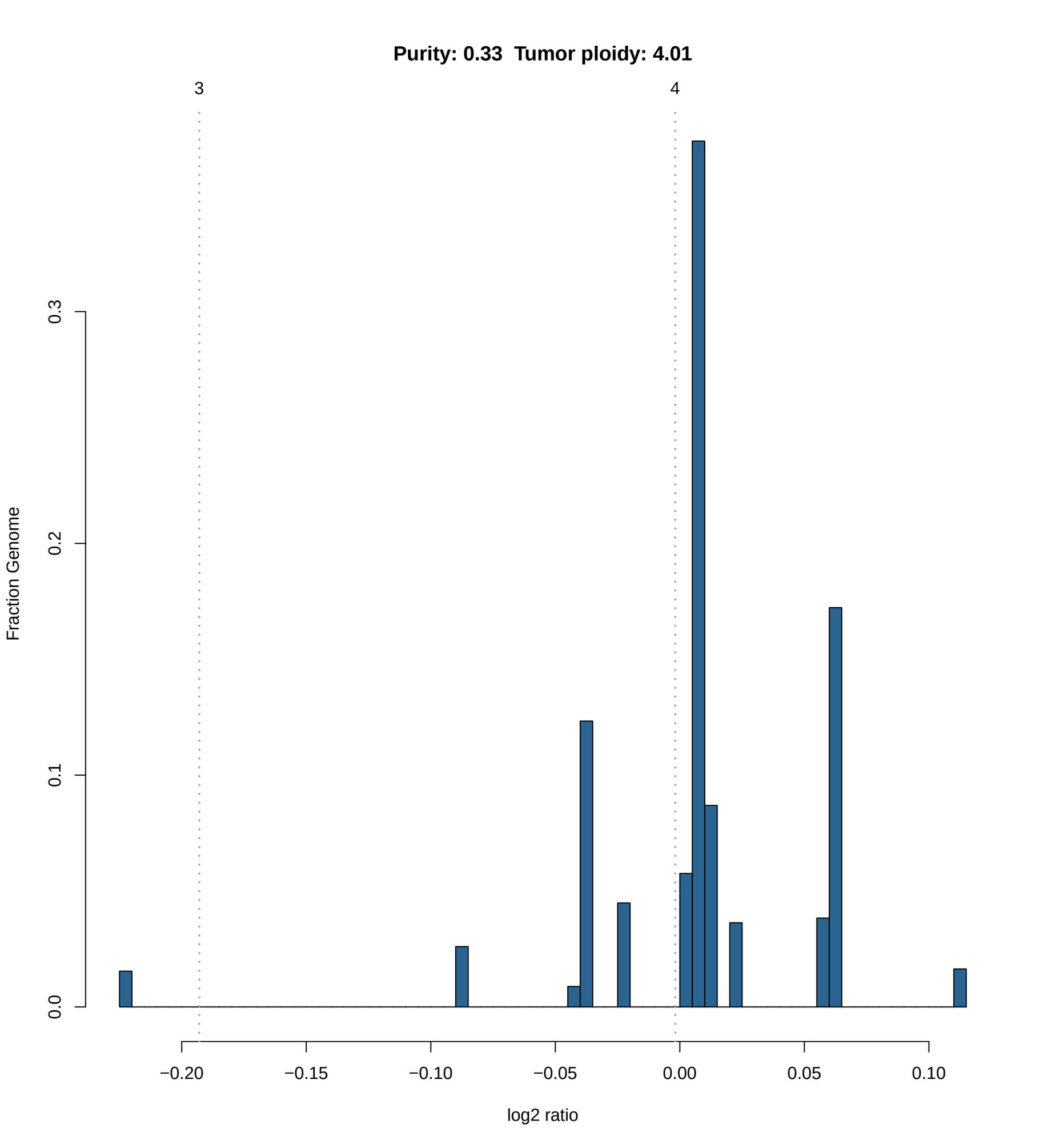

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

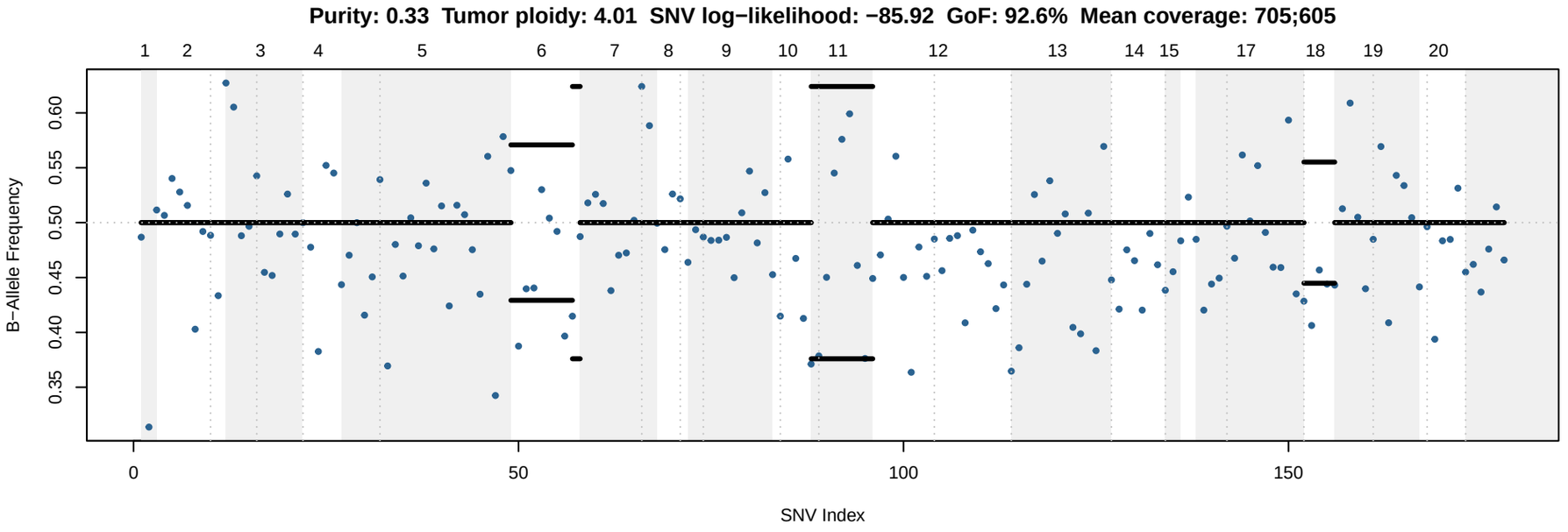

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
2m2
4m3
5m3
4m2
5m2
3m1
4m1
2m0
4m0
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

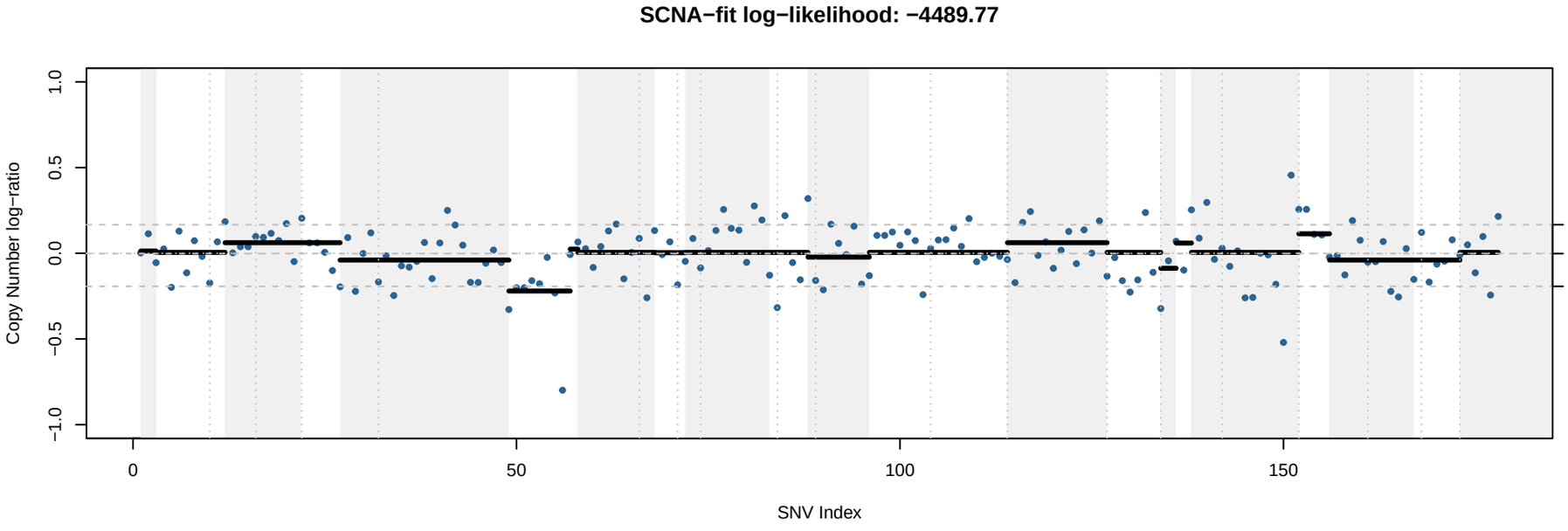

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

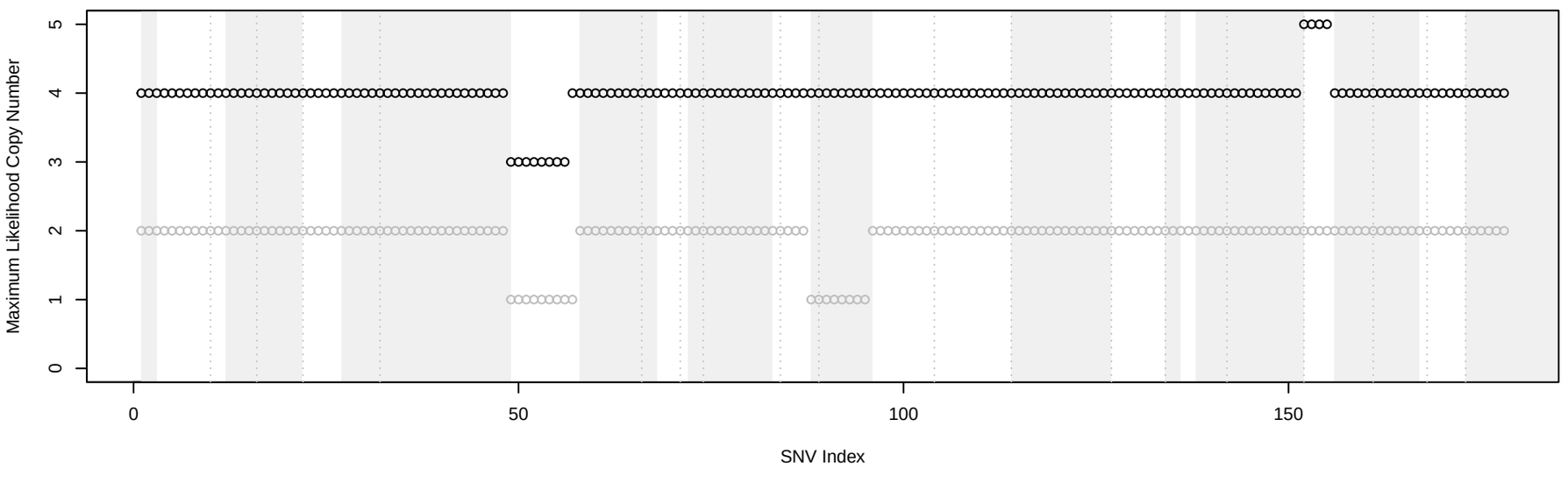

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
2m1
3m1
4m1
5m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

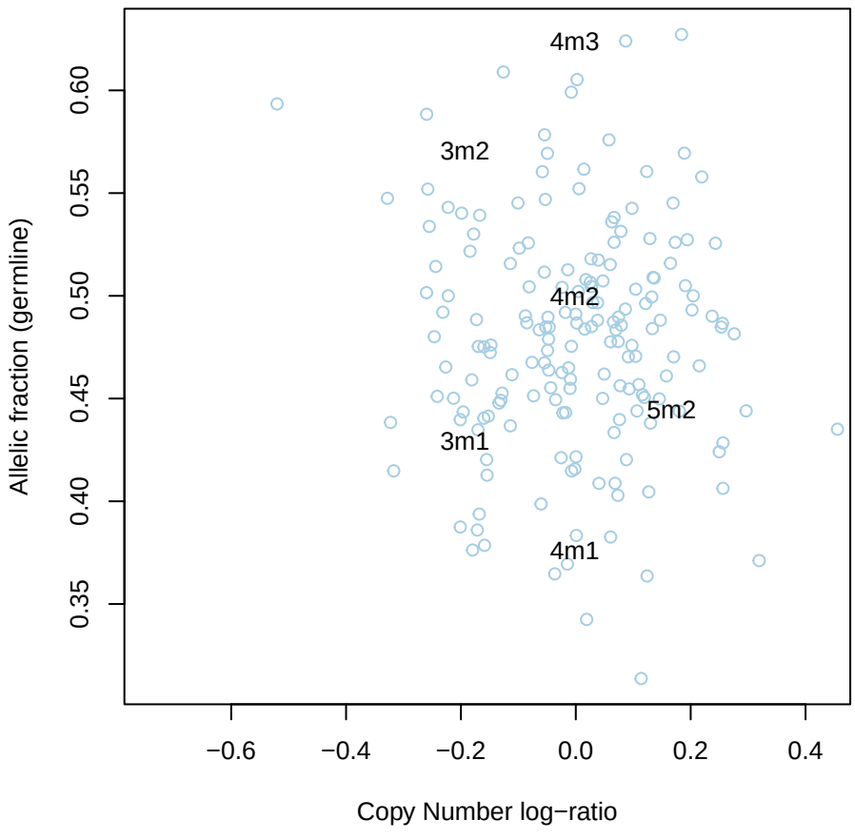

Frequency
0
5
10
15
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

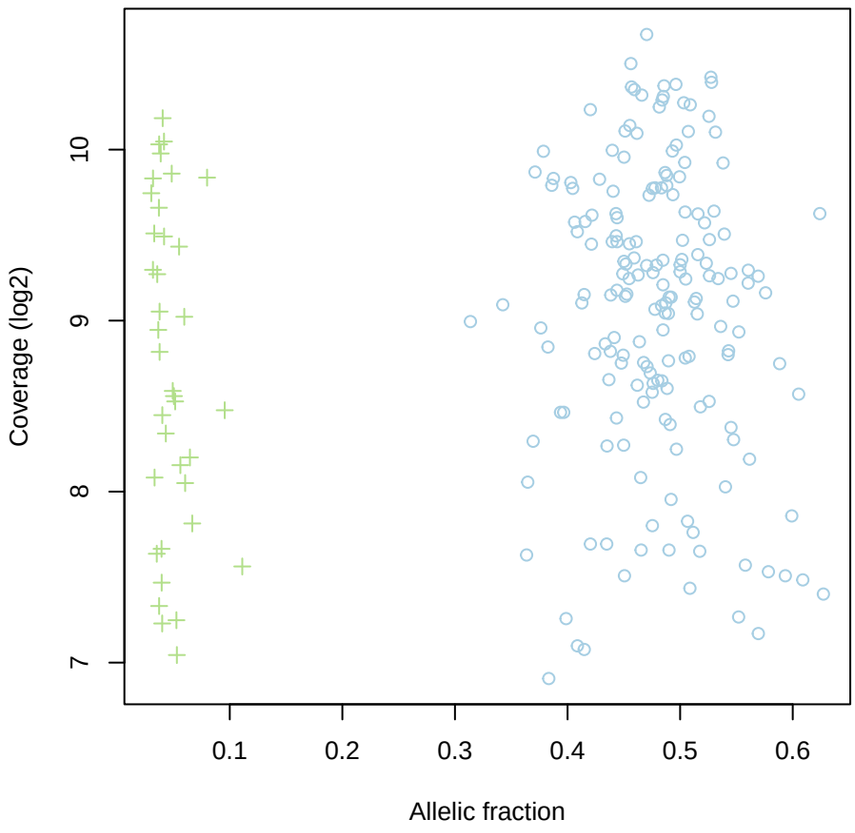

Purity: 0.33 Tumor ploidy: 4.01
3
4
0.0
0.1
0.2
0.3
Fraction Genome
−0.20
−0.15
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

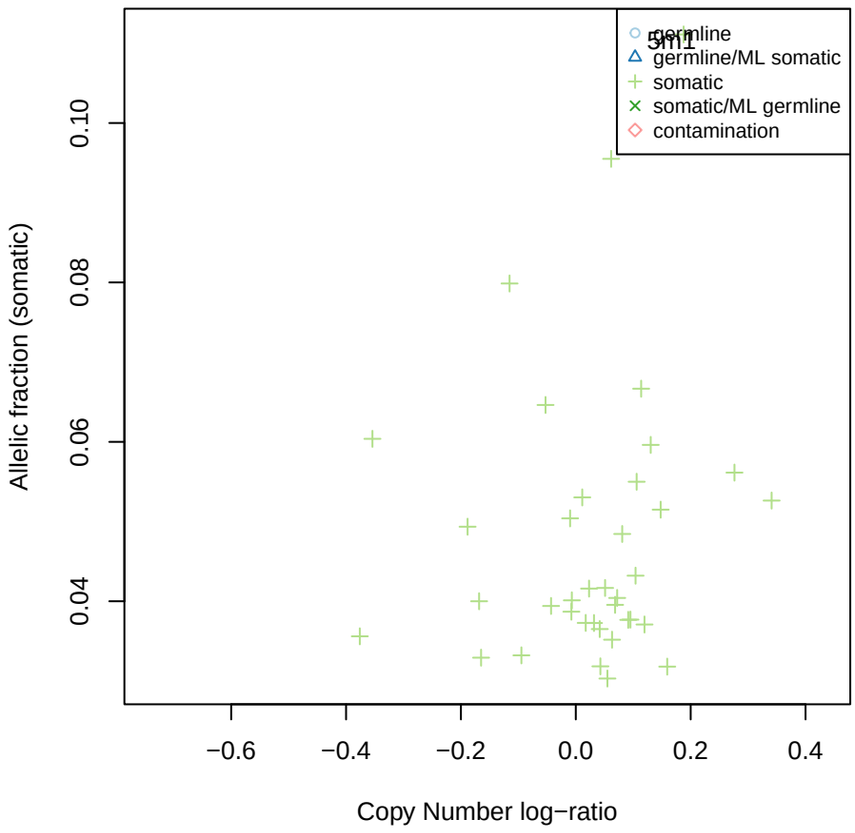

Purity: 0.33 Tumor ploidy: 4.01 SNV log−likelihood: −85.92 GoF: 92.6% Mean coverage: 705;605
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

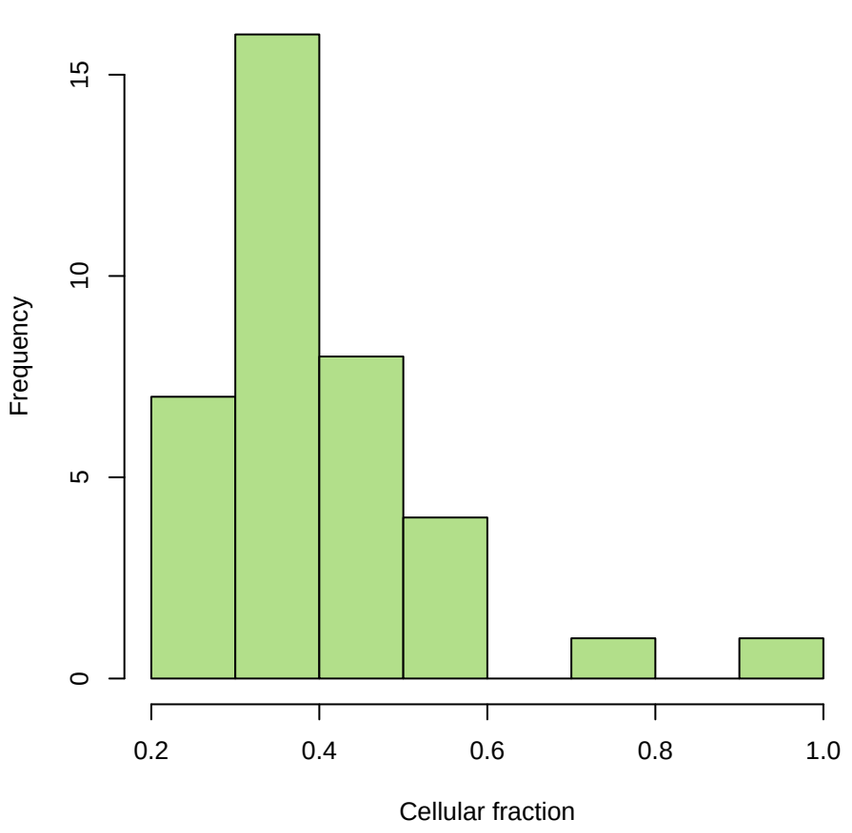

SCNA−fit log−likelihood: −4489.77
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5
0 50 100 150
SNV Index

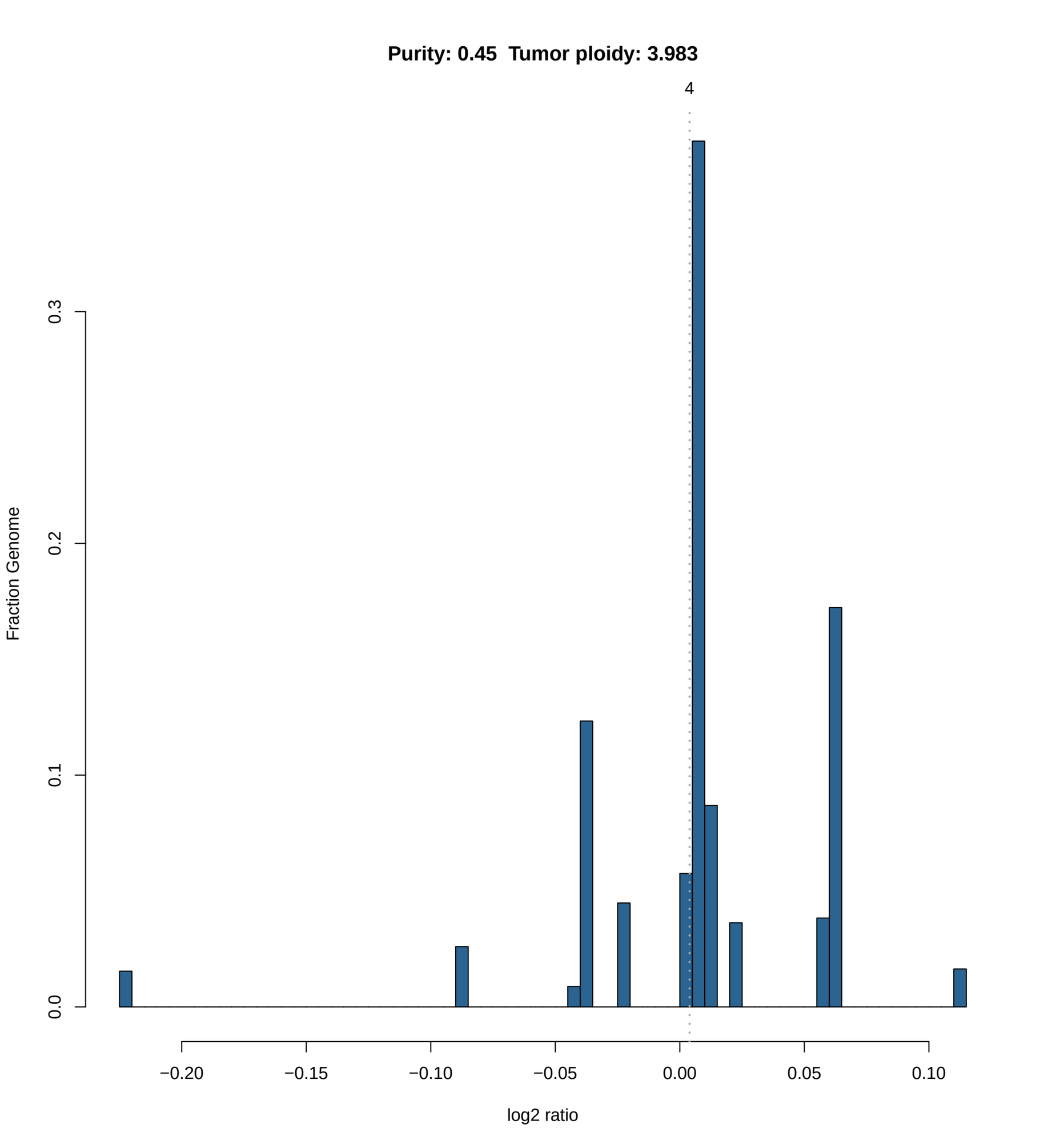

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

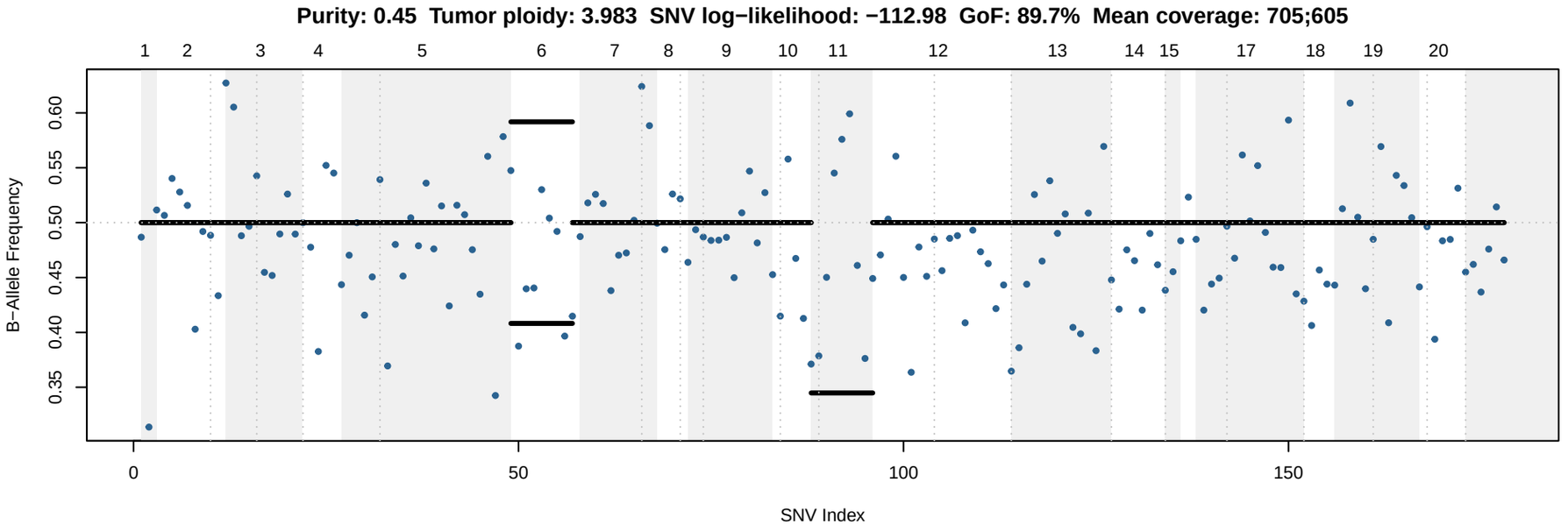

4m3
3m2
4m2
5m2
3m1
4m1
Allelic fraction (germline)
Copy Number log−ratio

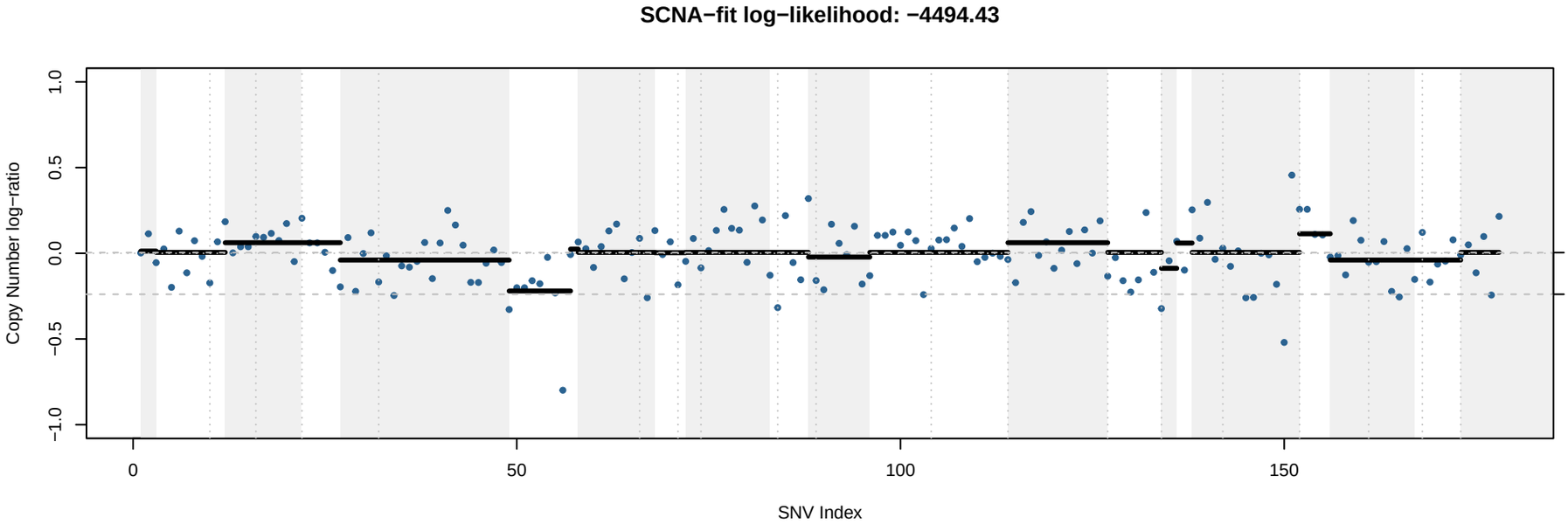

Coverage (log2)
Allelic fraction

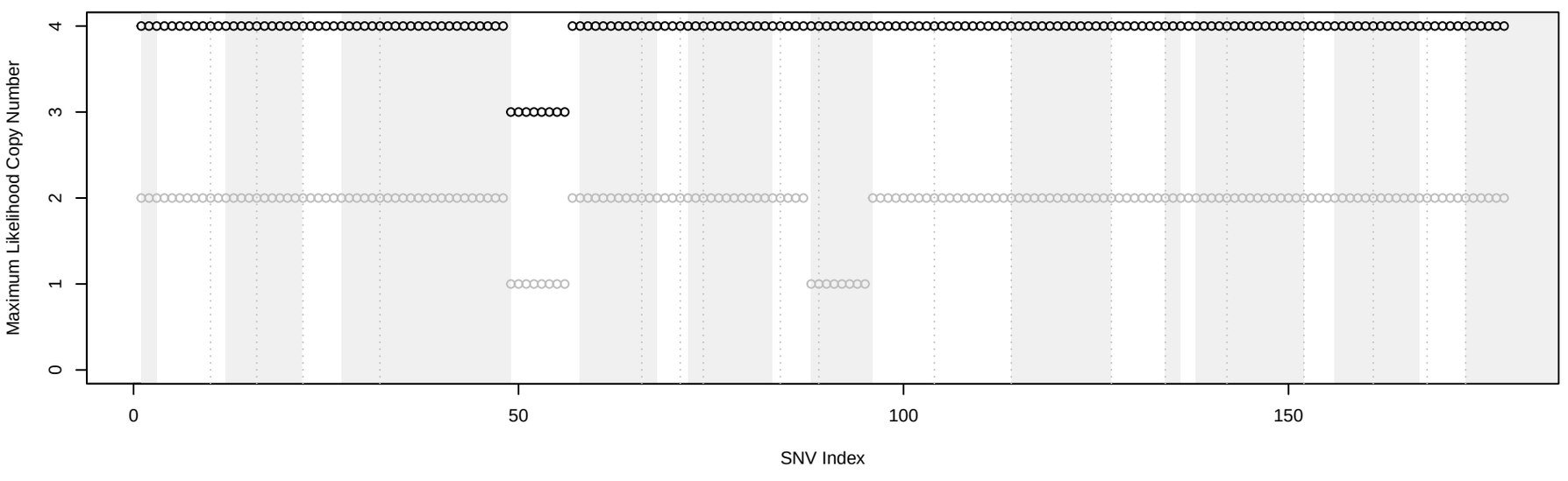

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

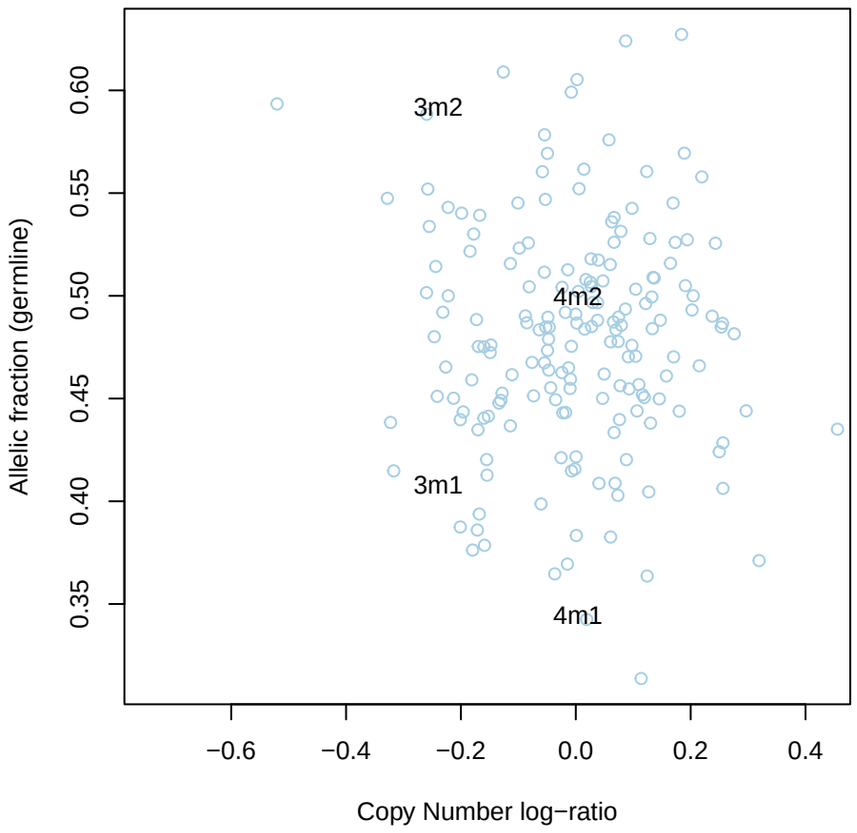

Frequency
Cellular fraction

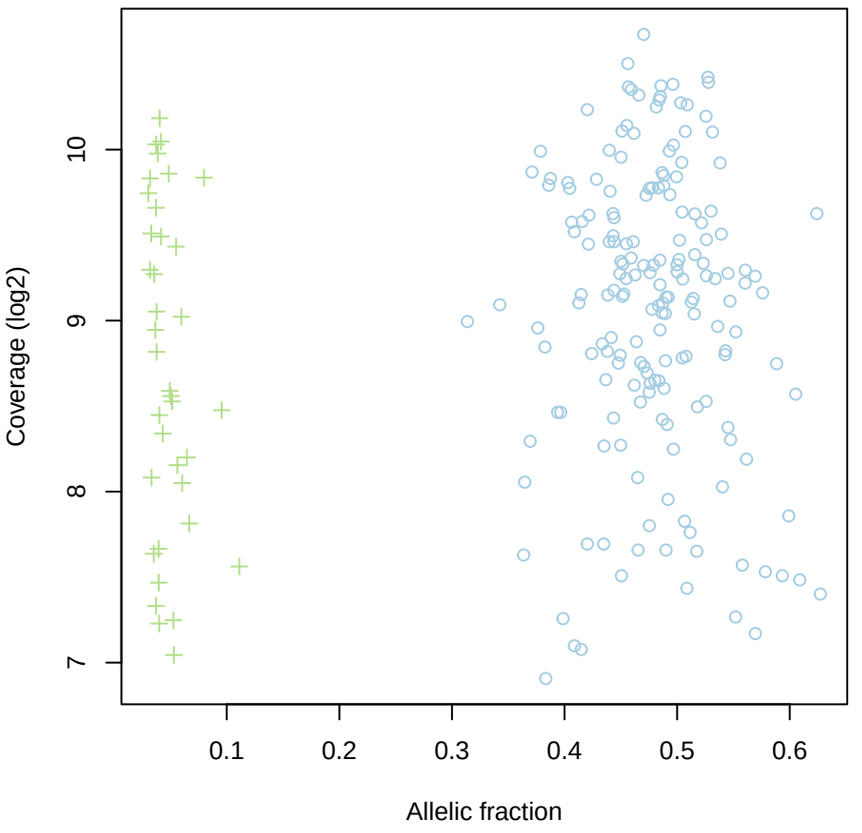

Purity: 0.45 Tumor ploidy: 3.983
4
Fraction Genome
0.0
0.1
0.2
0.3
−0.20
−0.15
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

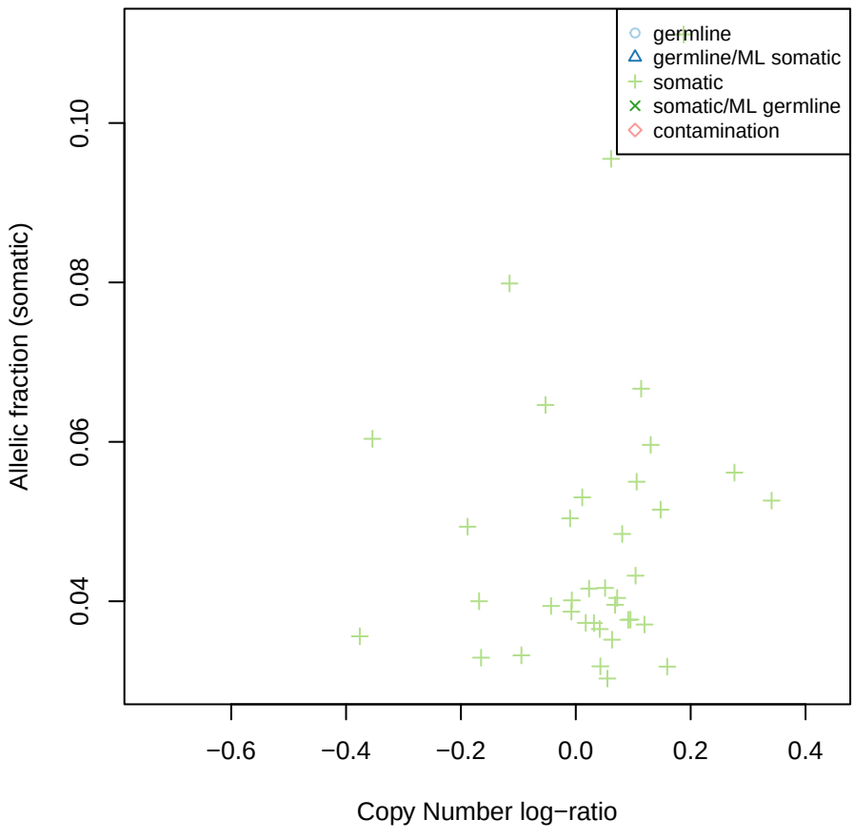

Purity: 0.45 Tumor ploidy: 3.983 SNV log−likelihood: −112.98 GoF: 89.7% Mean coverage: 705;605
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

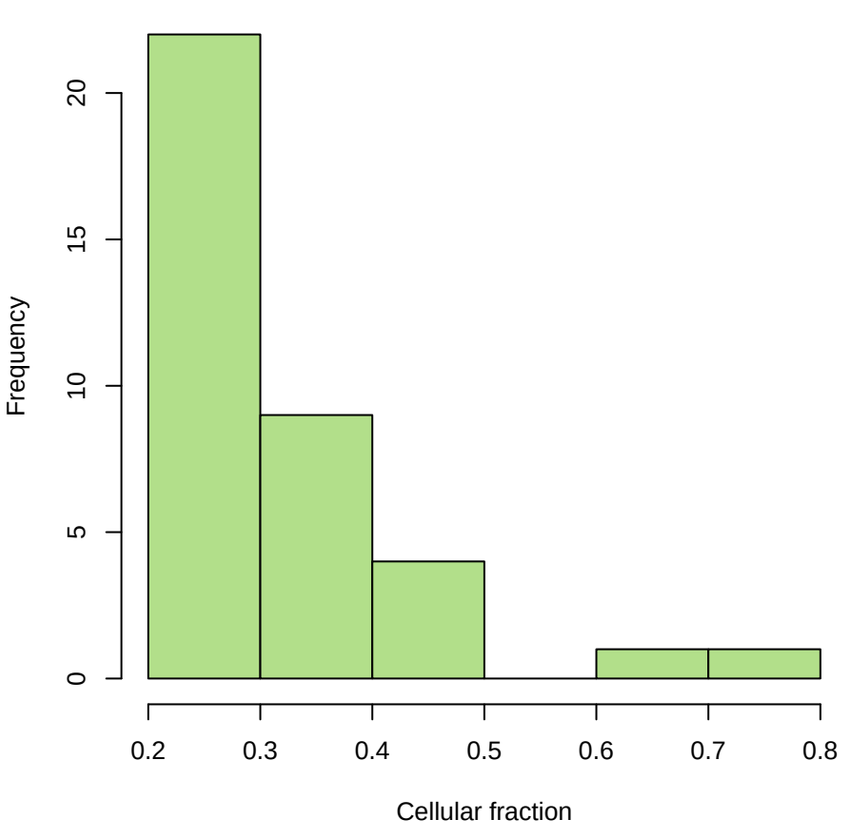

SCNA−fit log−likelihood: −4494.43
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4
3
0 50 100 150
SNV Index

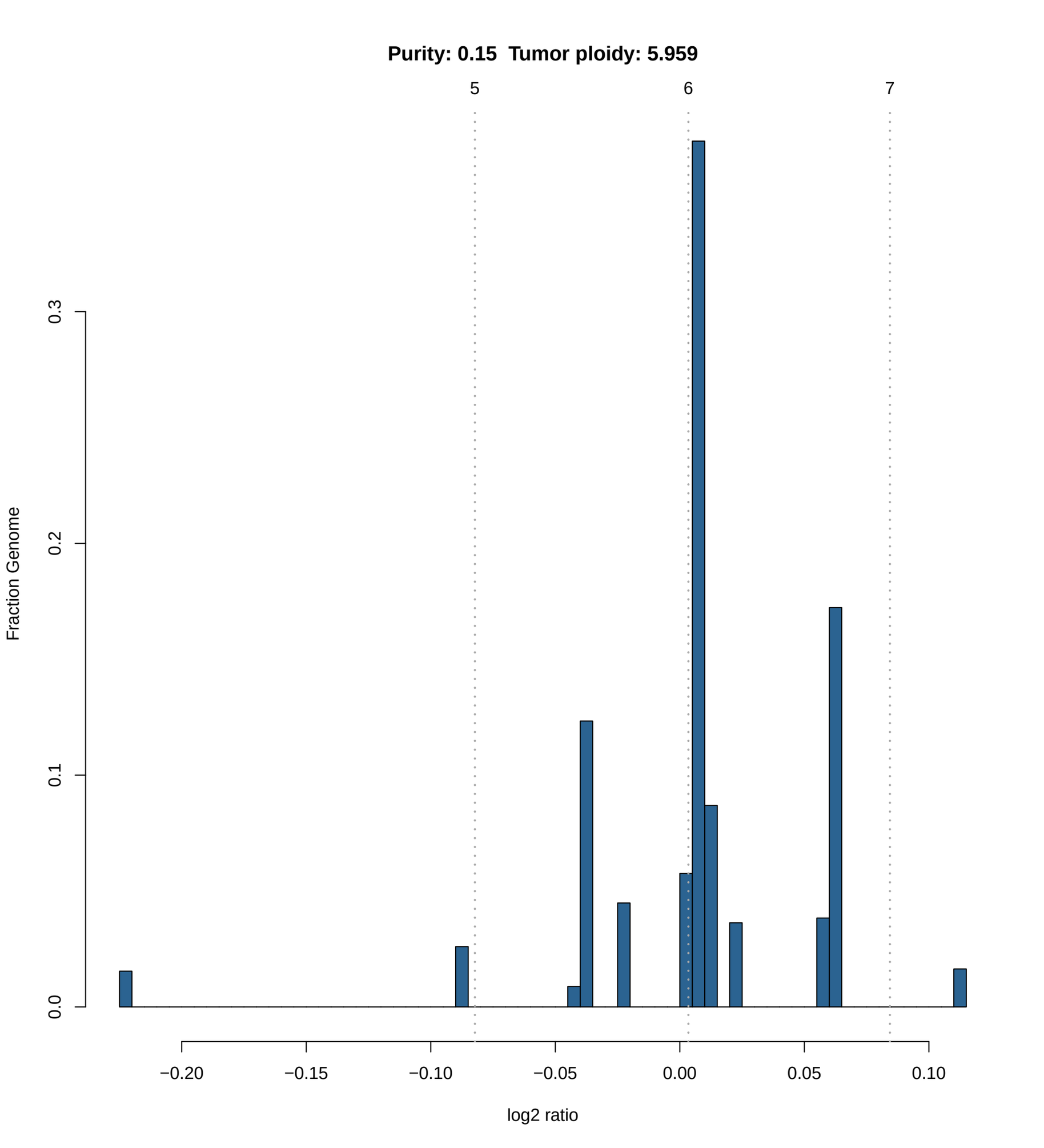

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

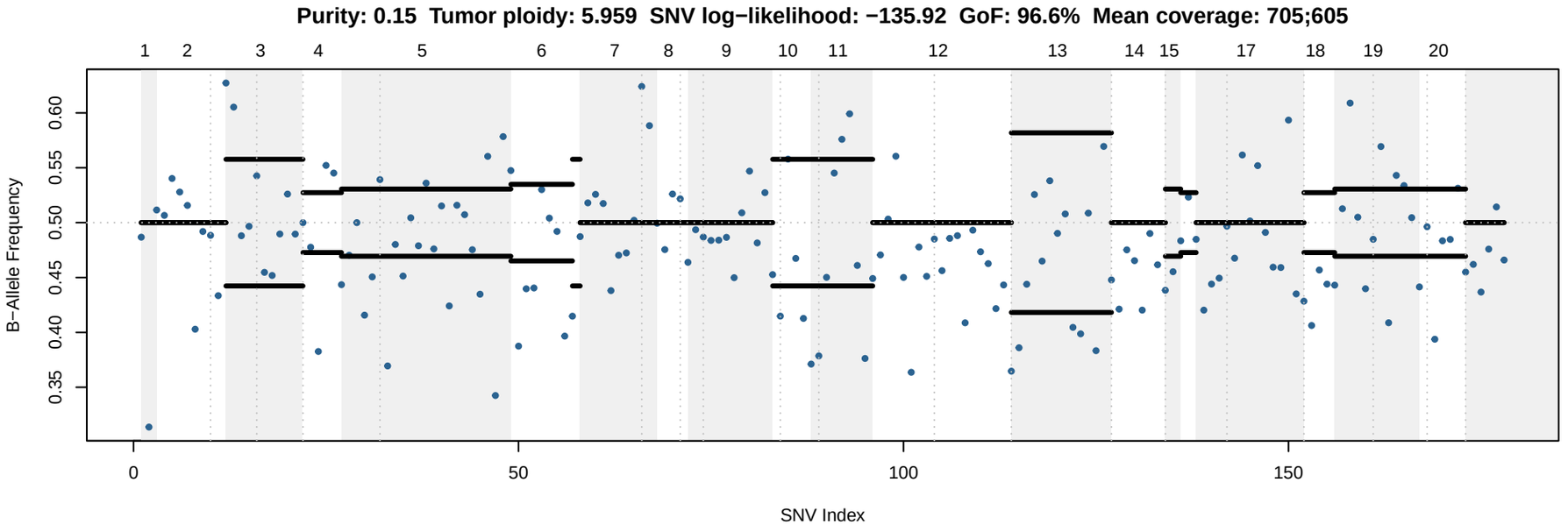

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
3m2
4m2
3m1
4m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

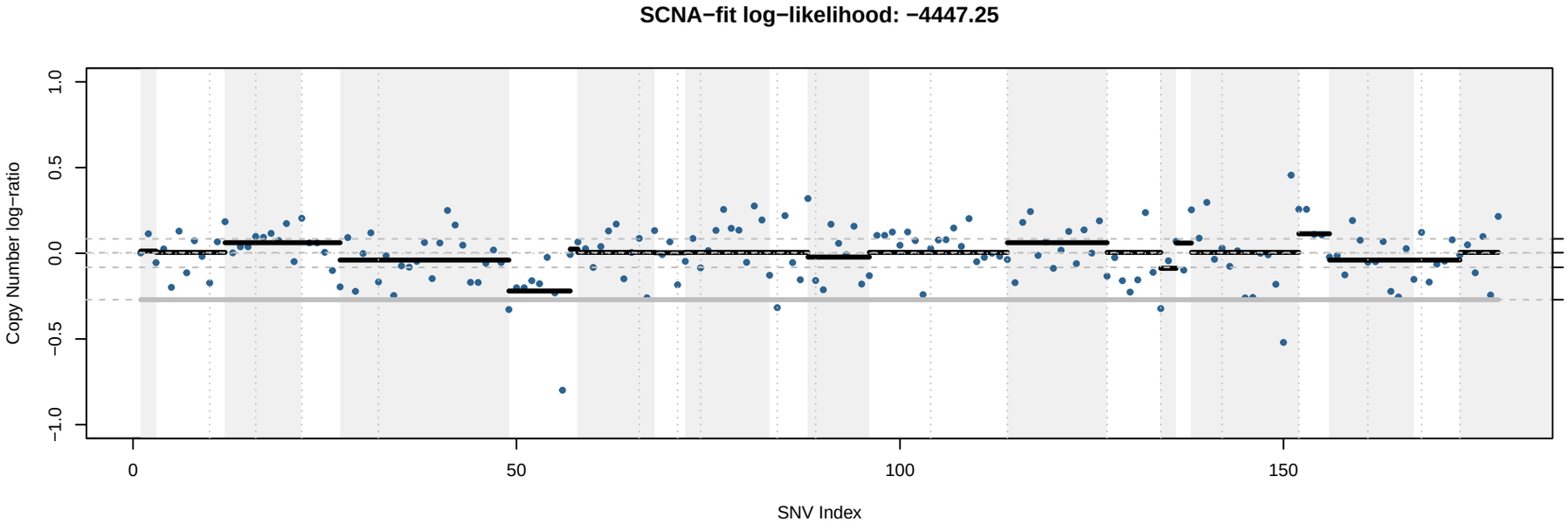

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

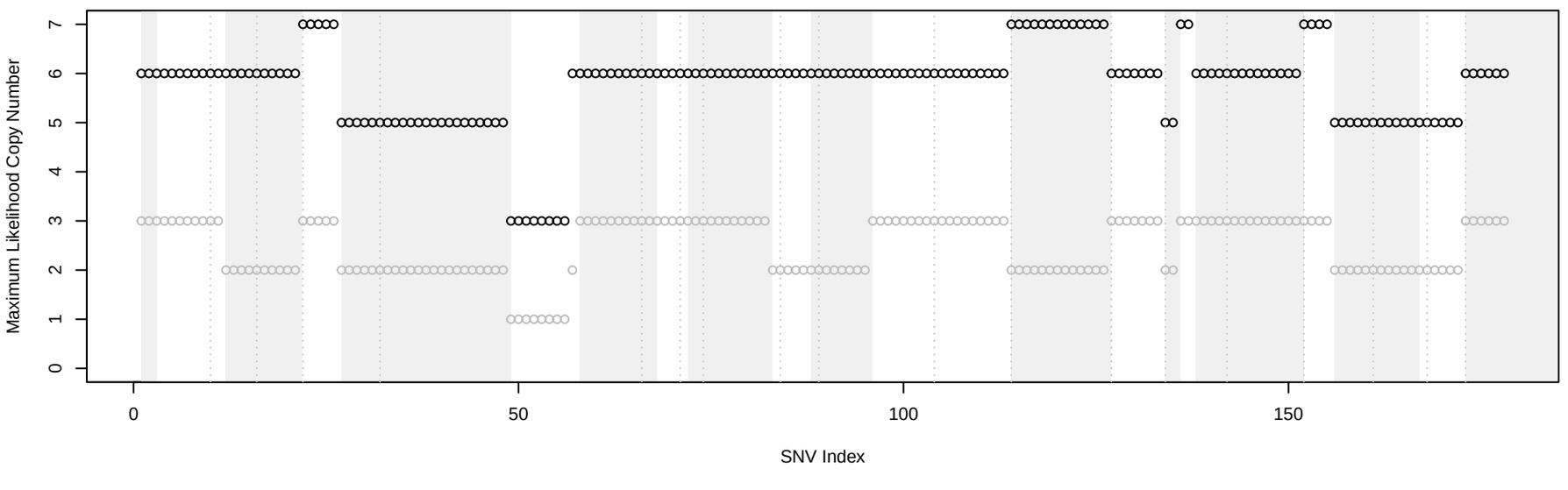

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

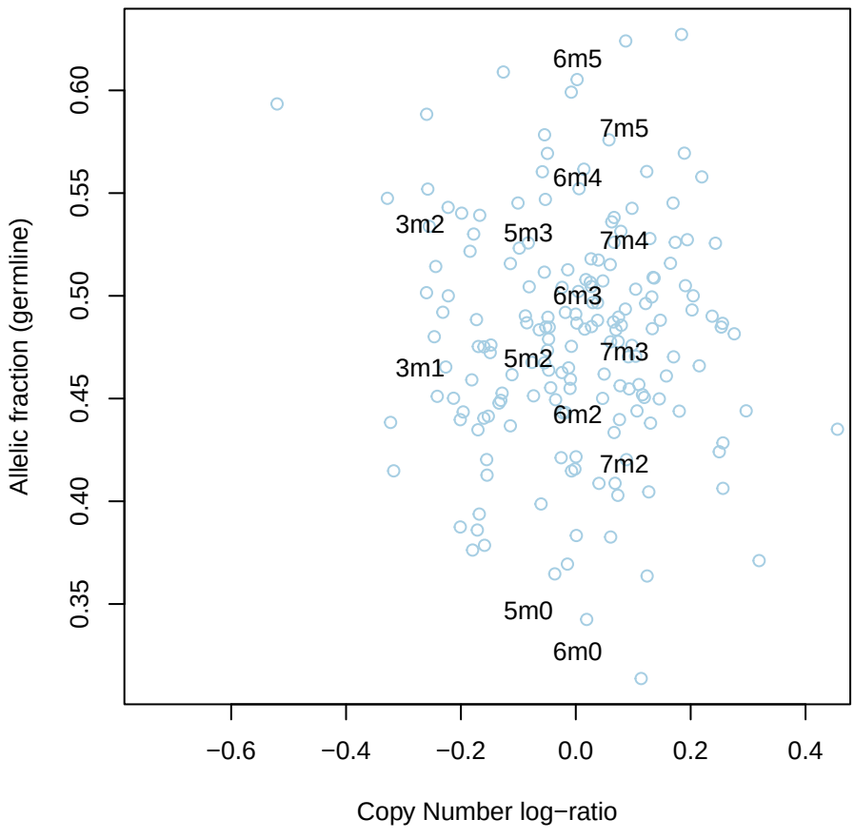

Frequency
0
5
10
15
20
0.2
0.3
0.4
0.5
0.6
0.7
0.8
Cellular fraction

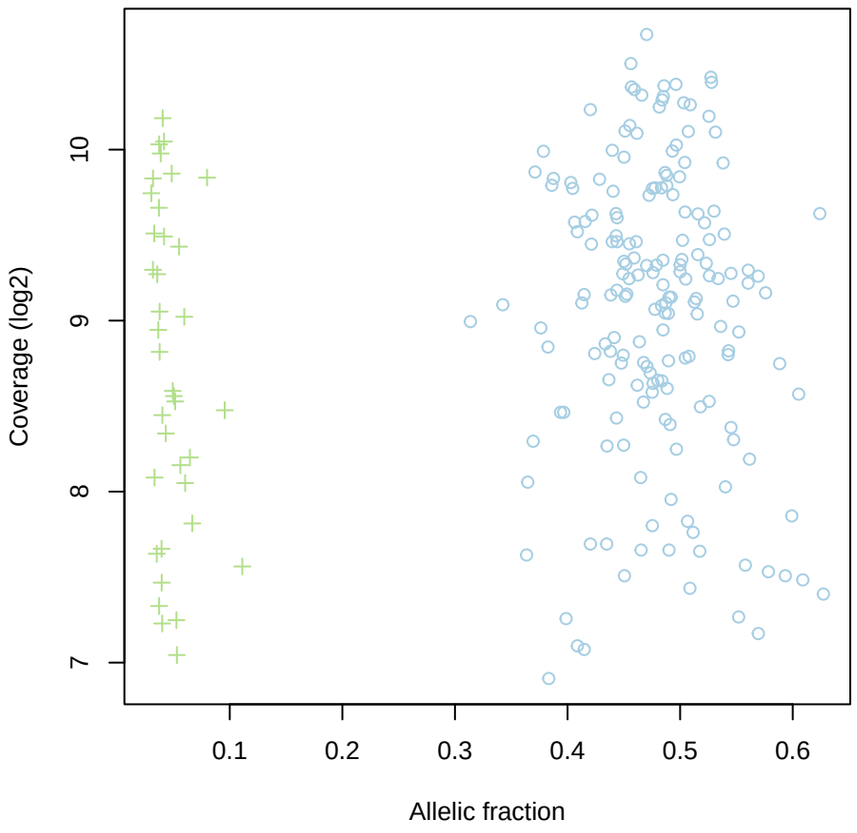

Purity: 0.15 Tumor ploidy: 5.959
5
6
7
Fraction Genome
0.0
0.1
0.2
0.3
−0.20
−0.15
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

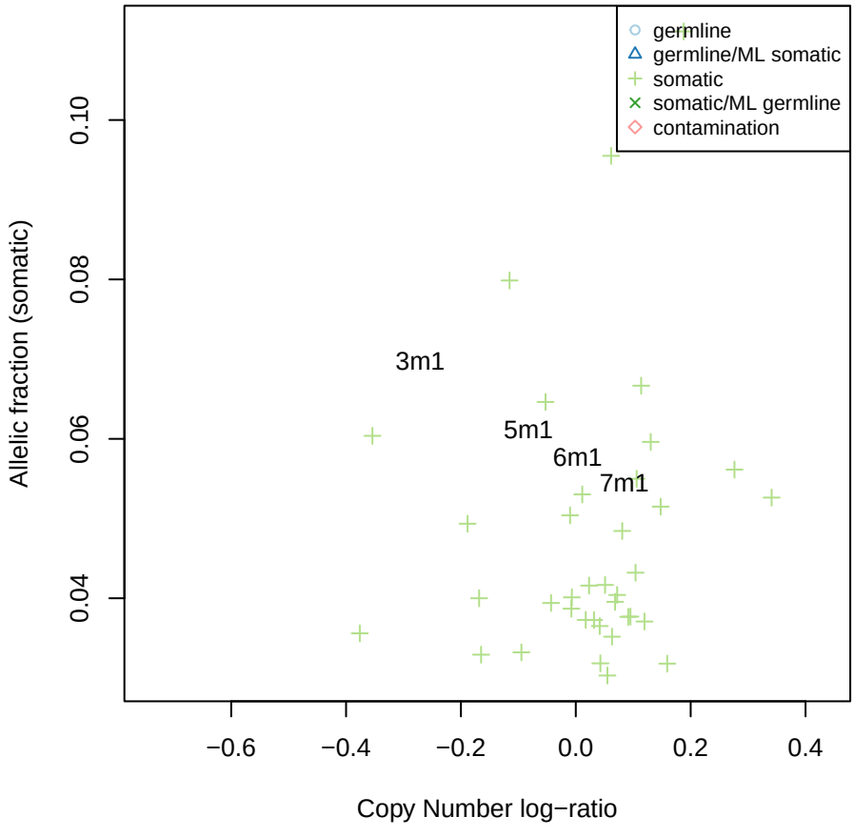

Purity: 0.15 Tumor ploidy: 5.959 SNV log−likelihood: −135.92 GoF: 96.6% Mean coverage: 705;605
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

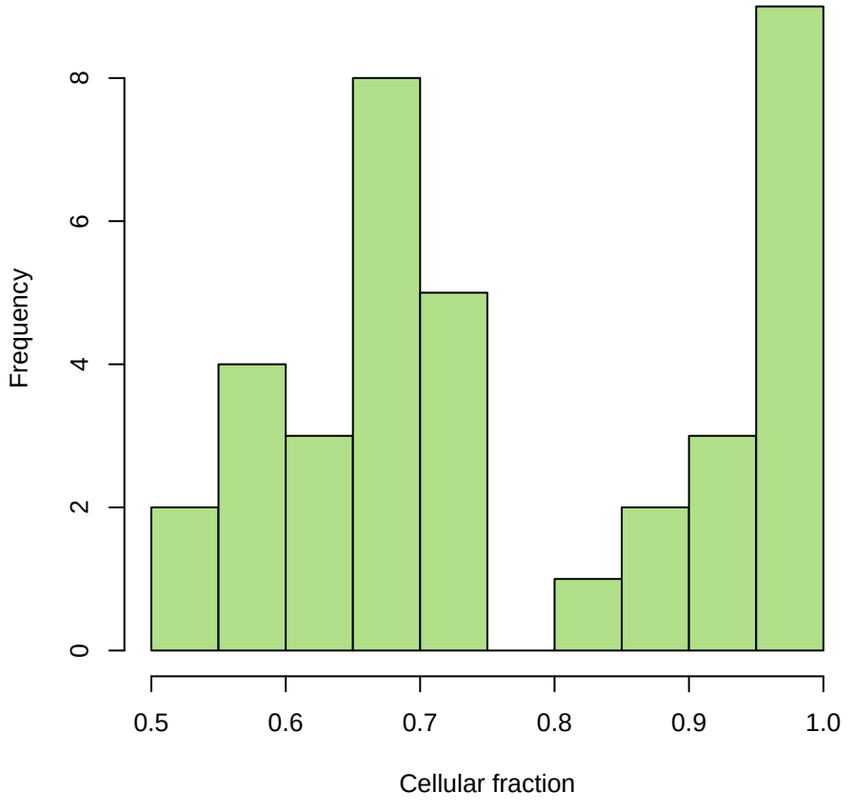

SCNA−fit log−likelihood: −4447.25
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
3 5 7
0 50 100 150
SNV Index

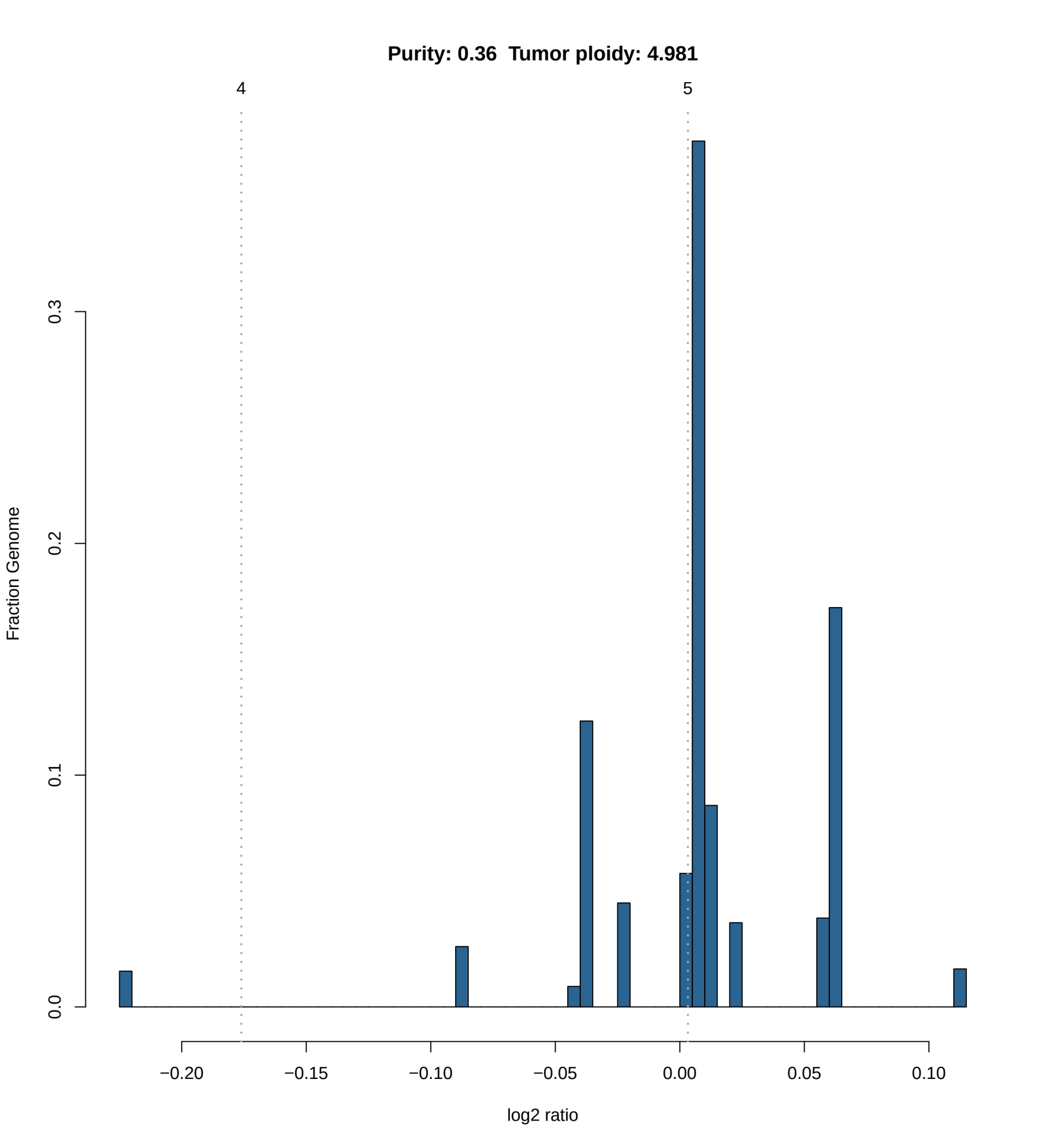

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

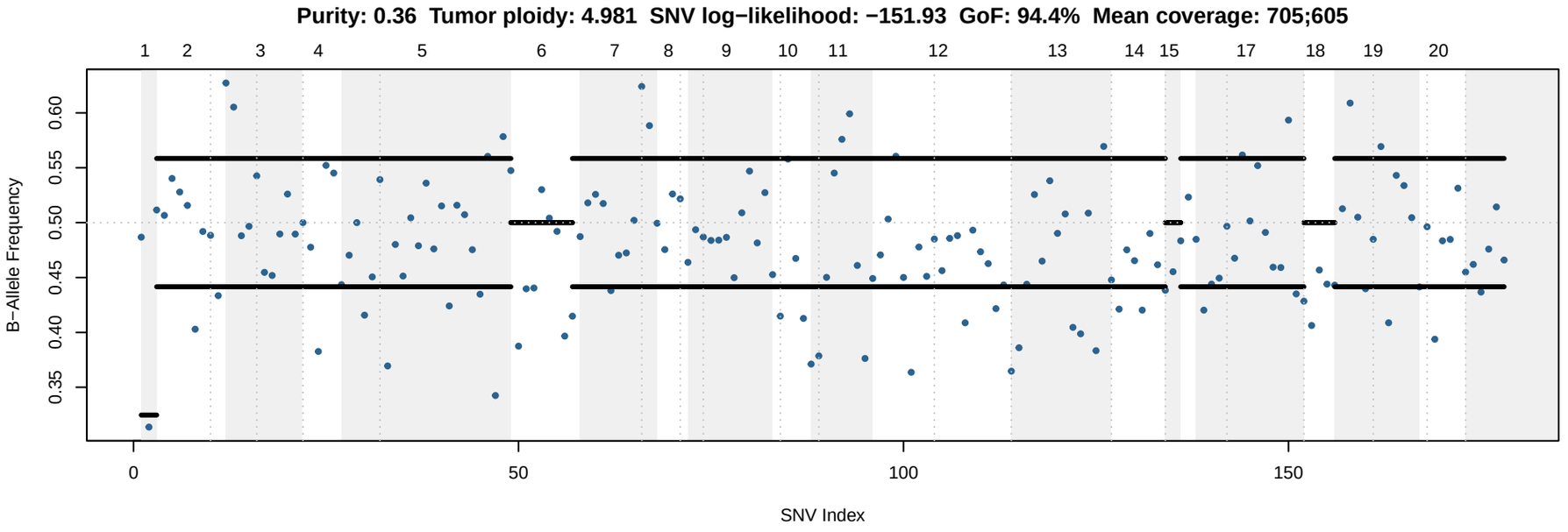

Allelic fraction (germline)
Copy Number log−ratio
6m5
7m5
6m4
3m2
5m3
7m4
6m3
3m1
5m2
7m3
6m2
7m2
5m0
6m0

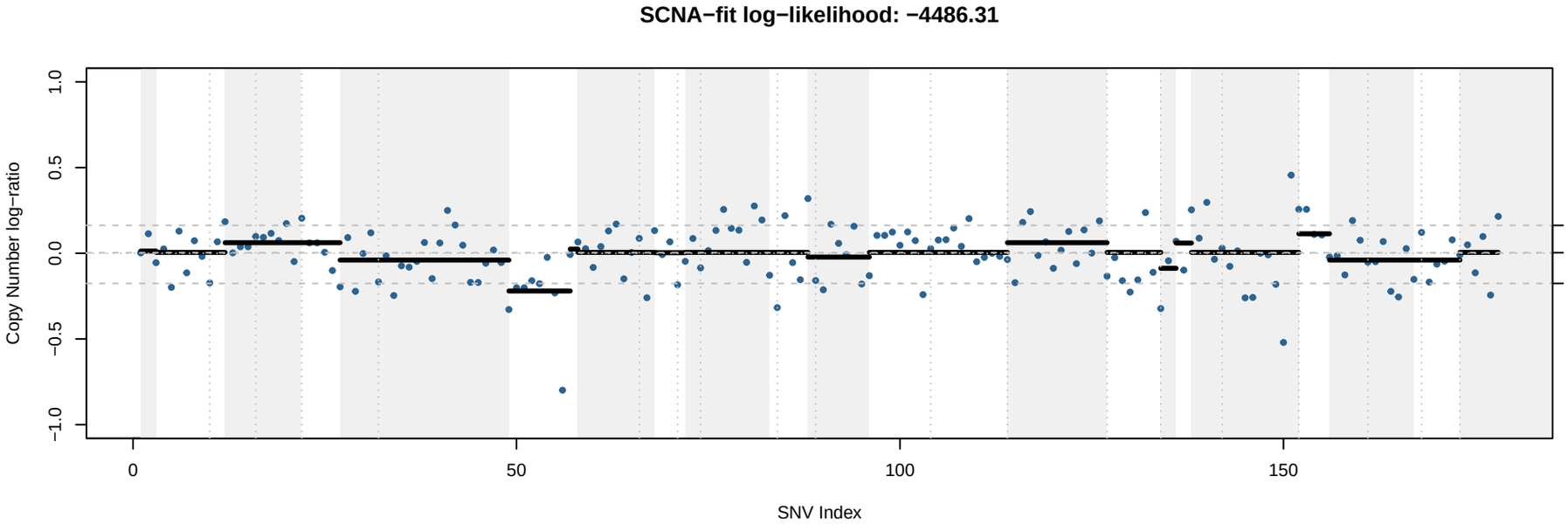

Coverage (log2)
Allelic fraction

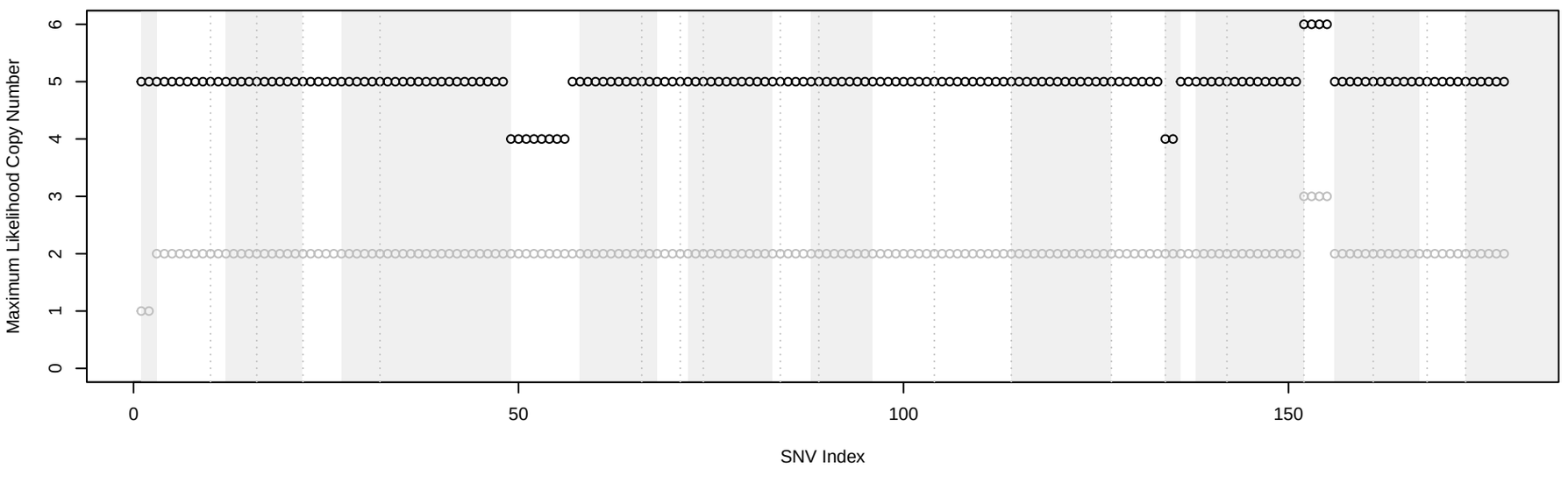

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m1
5m1
6m1
7m1

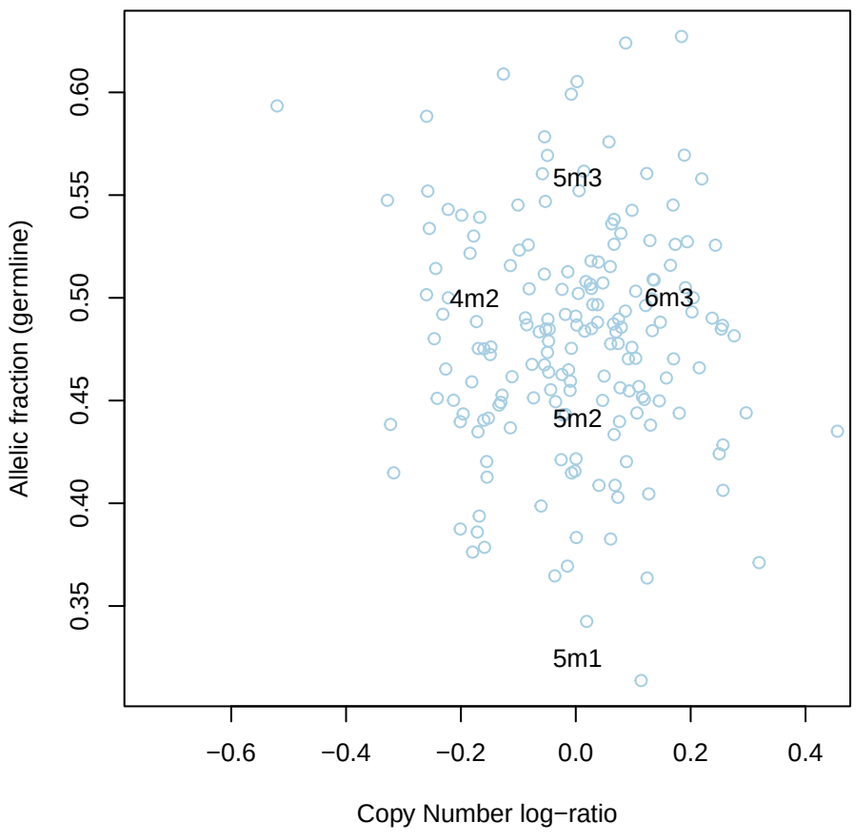

Frequency
Cellular fraction

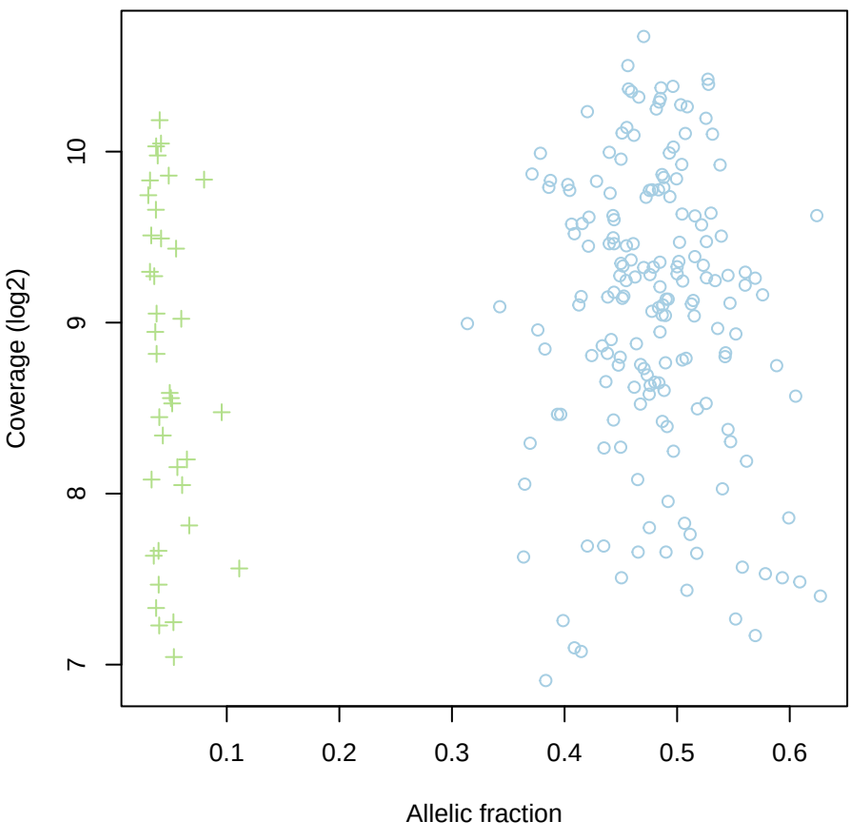

Purity: 0.36 Tumor ploidy: 4.981
4
5
0.0
0.1
0.2
0.3
Fraction Genome
−0.20
−0.15
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

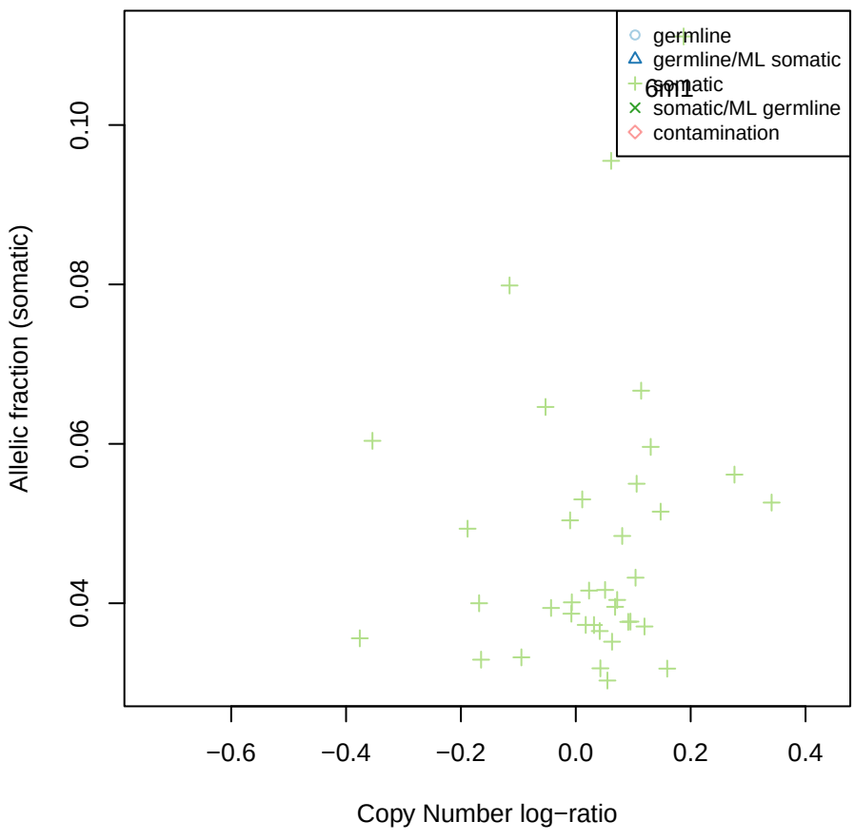

Purity: 0.36 Tumor ploidy: 4.981 SNV log−likelihood: −151.93 GoF: 94.4% Mean coverage: 705;605
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

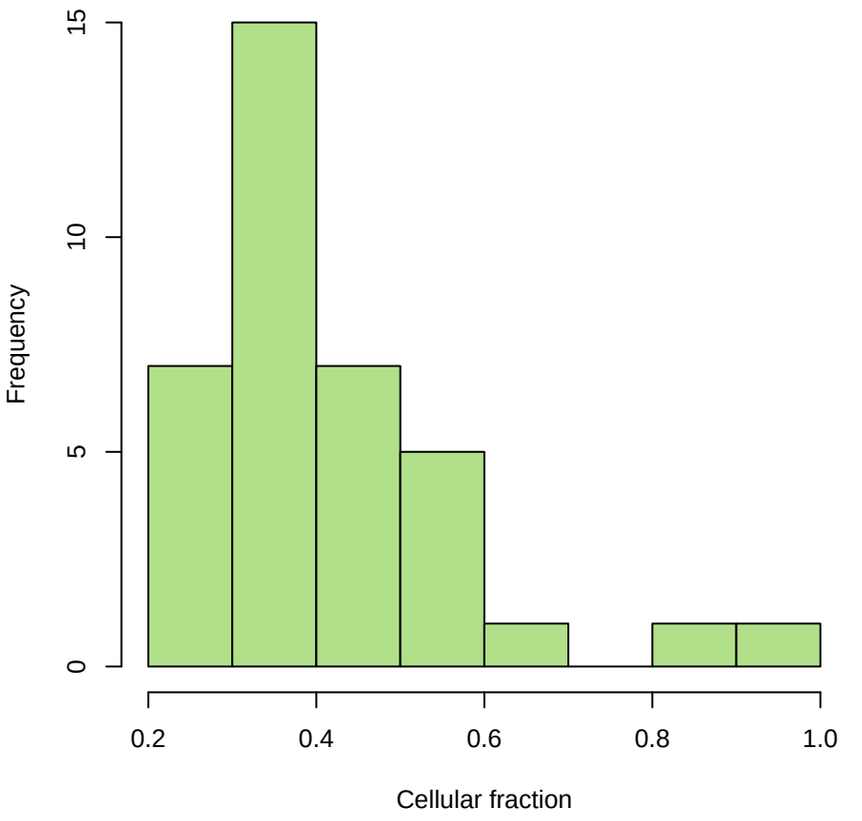

SCNA−fit log−likelihood: −4486.31
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
4 5 6
0 50 100 150
SNV Index

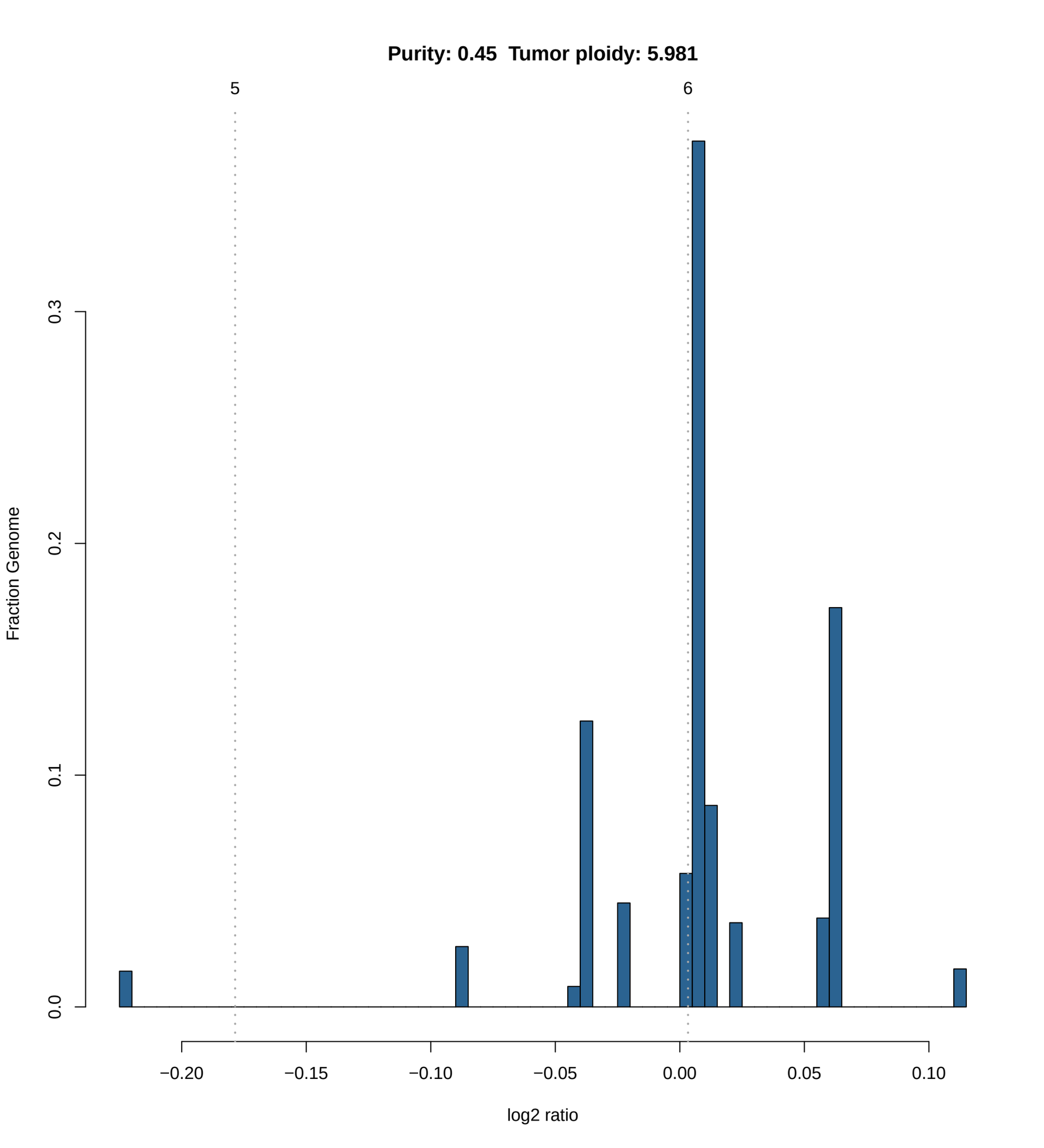

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

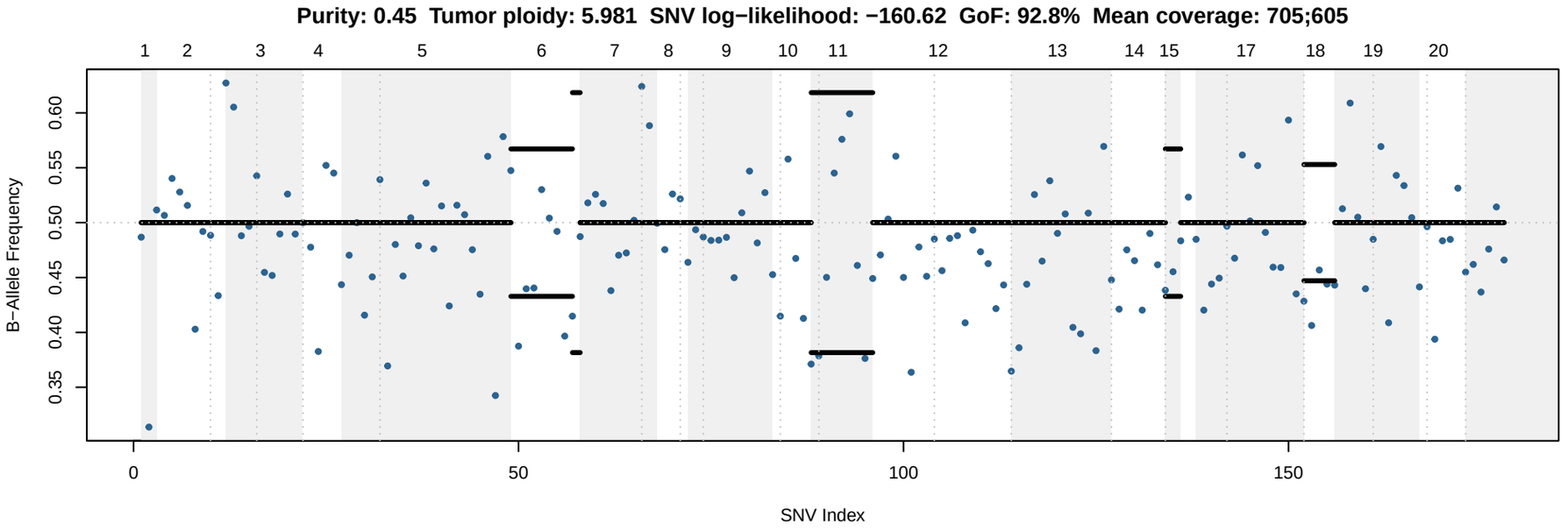

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
5m3
4m2
6m3
5m2
5m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

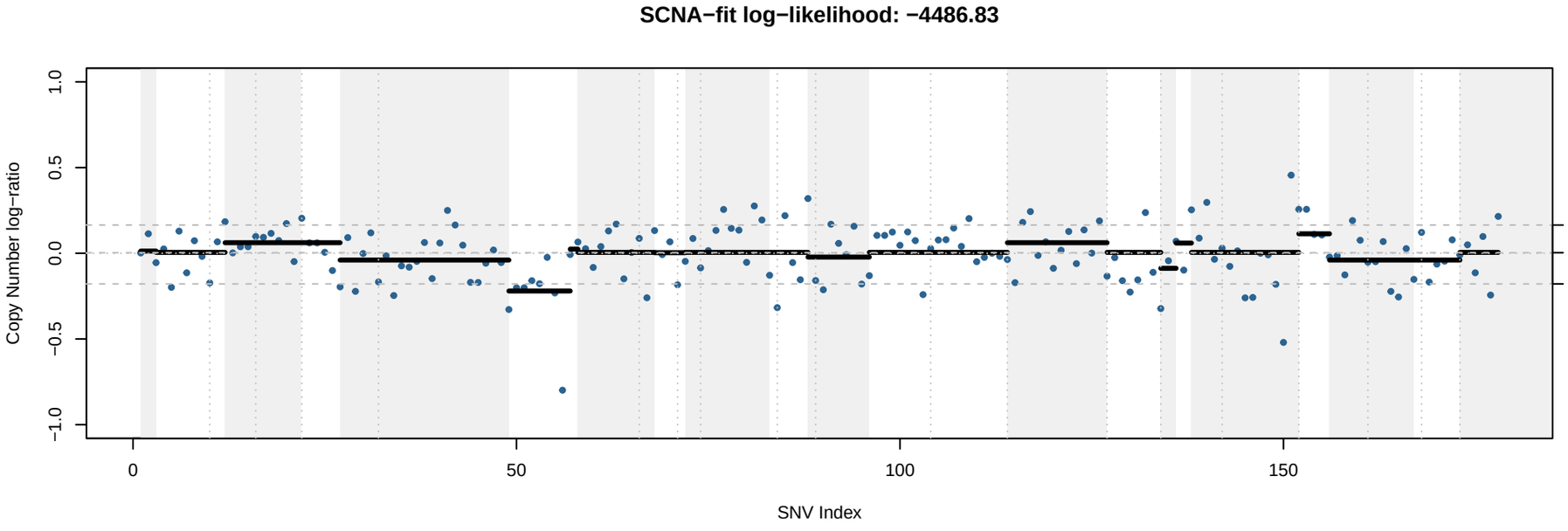

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

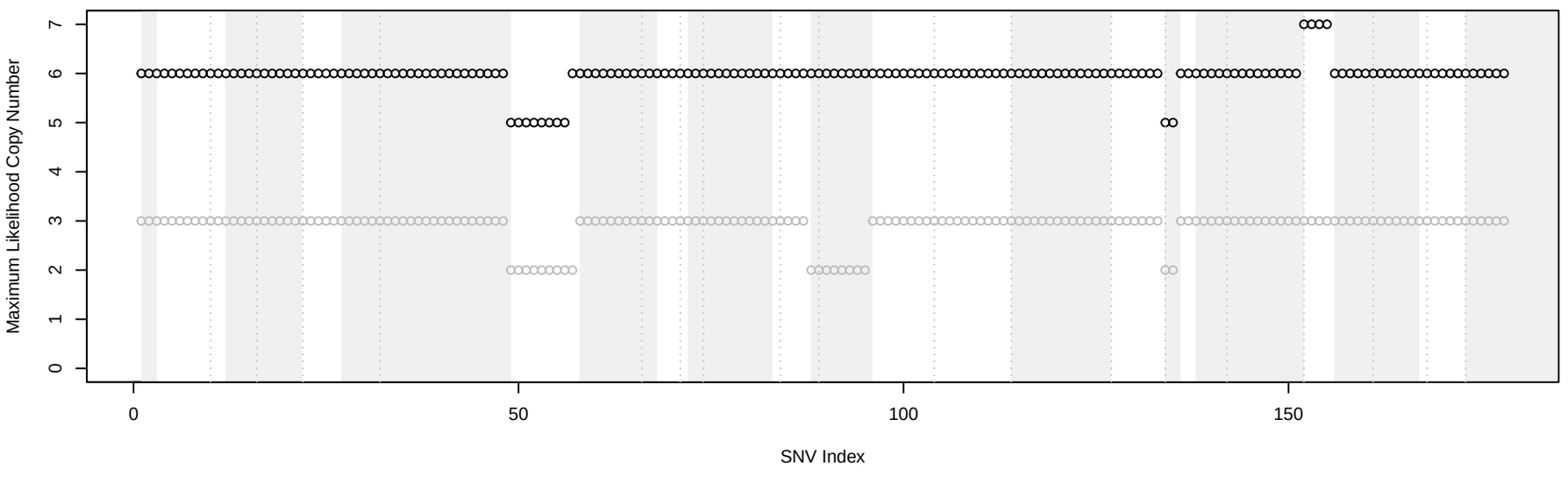

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m1
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

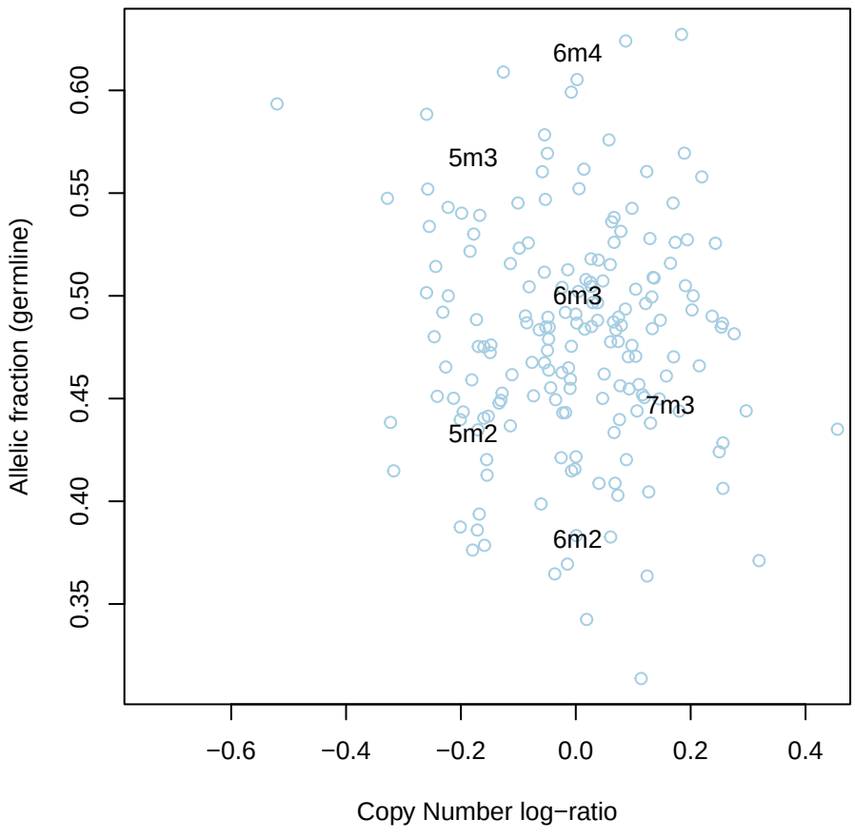

Frequency
0
5
10
15
0.2
0.4
0.6
0.8
1.0
Cellular fraction

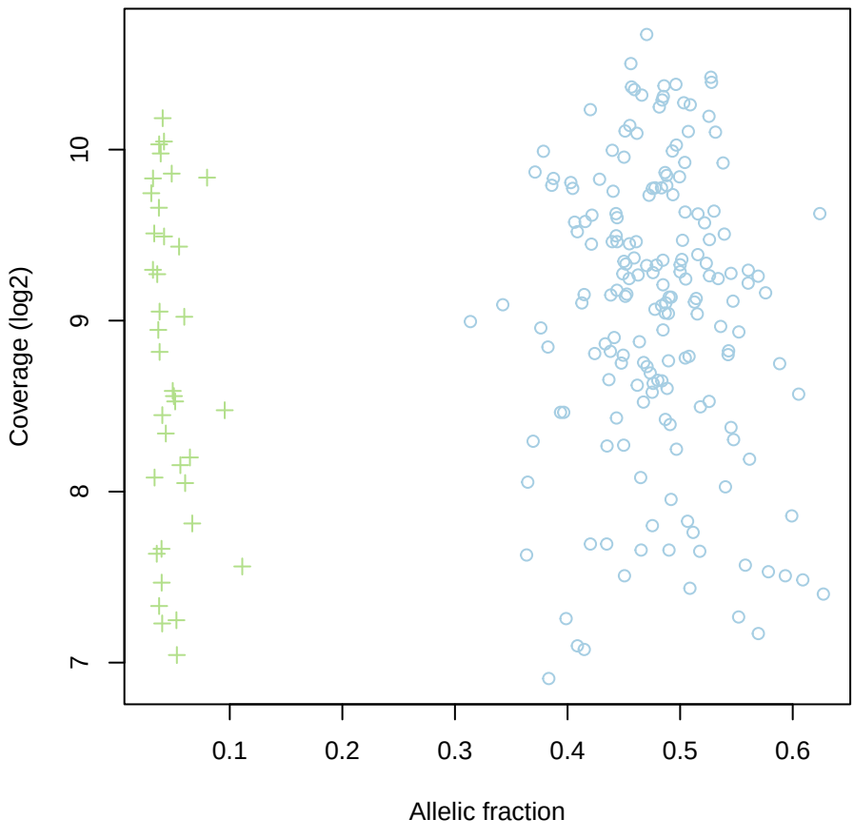

Purity: 0.45 Tumor ploidy: 5.981
5
6
0.0
0.1
0.2
0.3
Fraction Genome
−0.20
−0.15
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

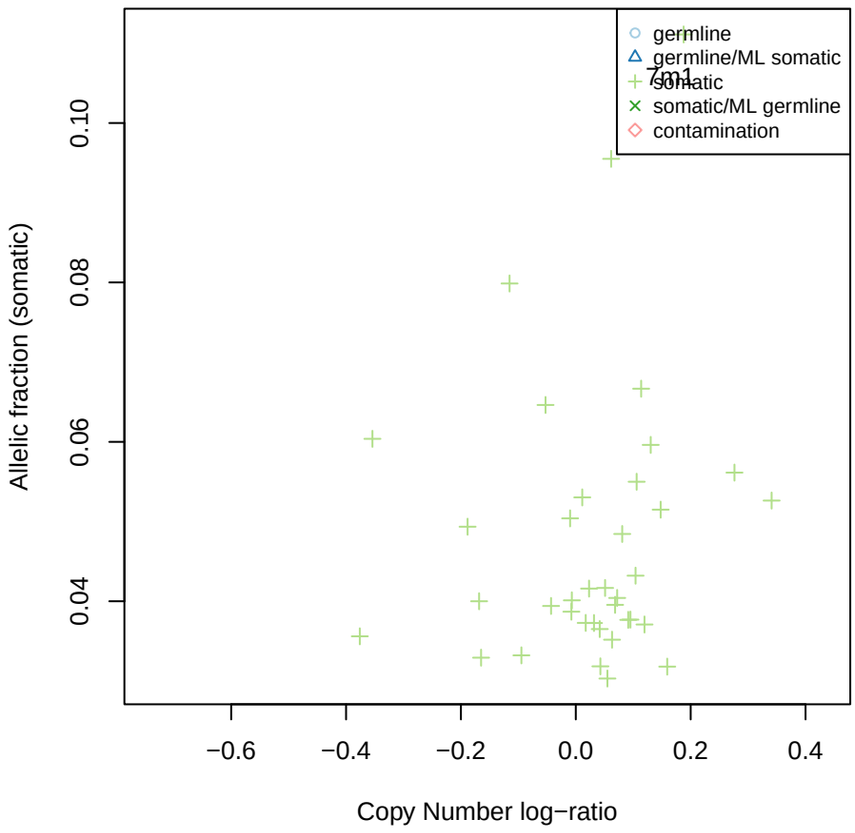

Purity: 0.45 Tumor ploidy: 5.981 SNV log−likelihood: −160.62 GoF: 92.8% Mean coverage: 705;605
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

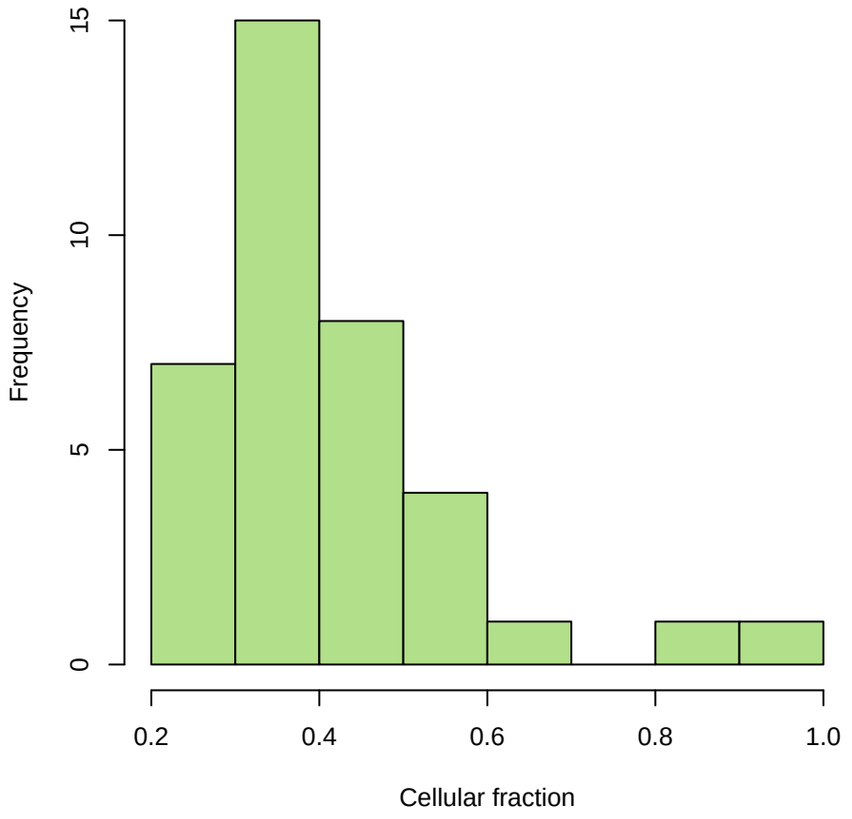

SCNA−fit log−likelihood: −4486.83
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
5 6 7
0 50 100 150
SNV Index

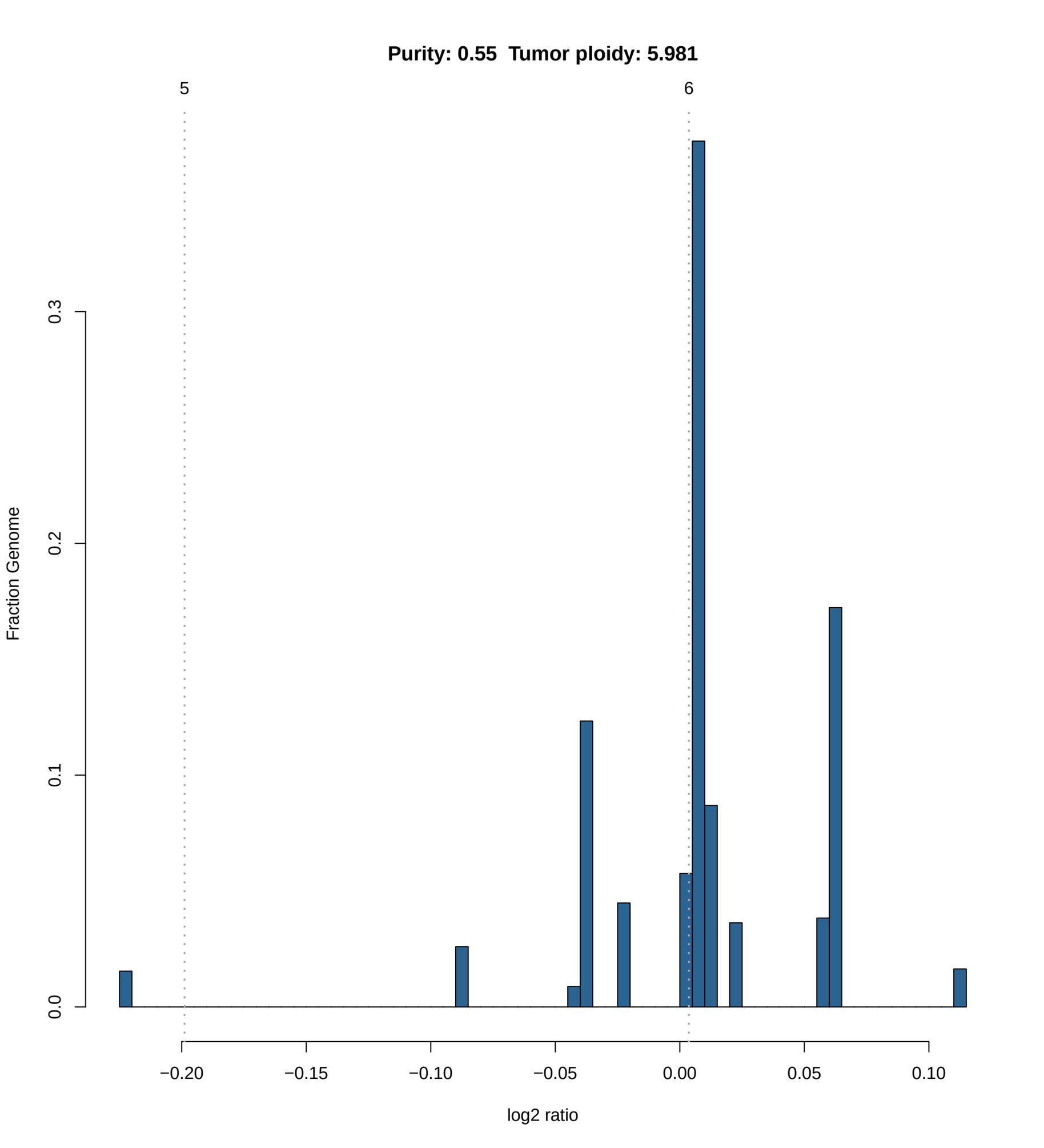

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

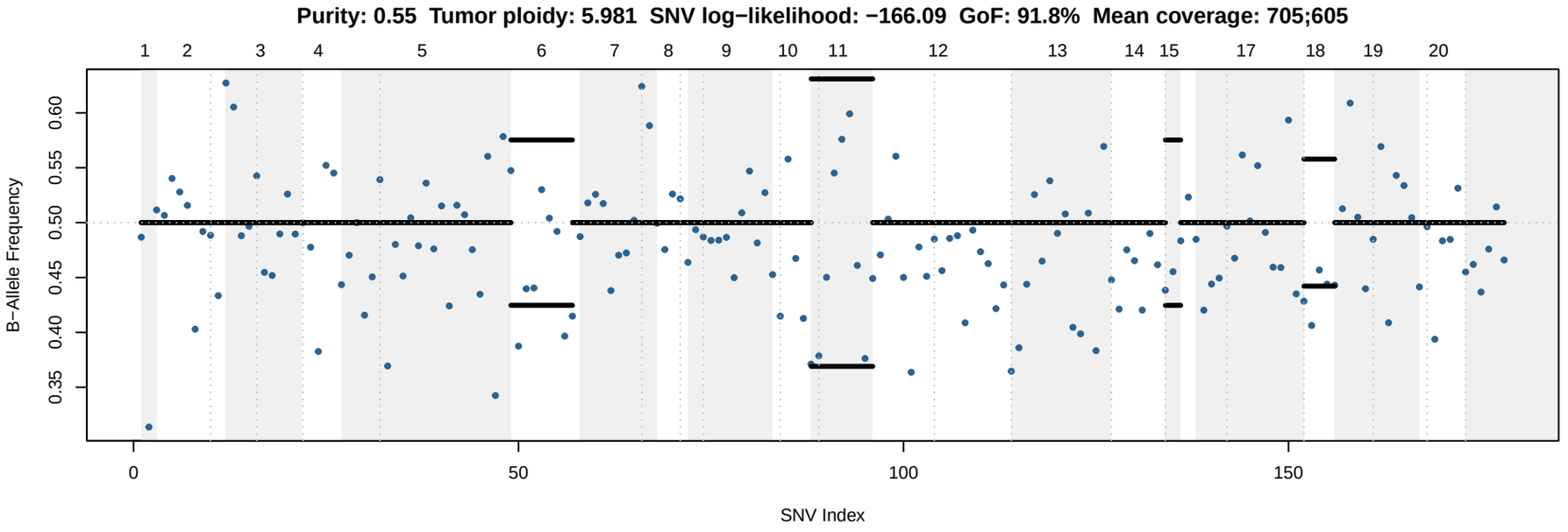

6m4
5m3
6m3
7m3
5m2
6m2
Allelic fraction (germline)
Copy Number log−ratio

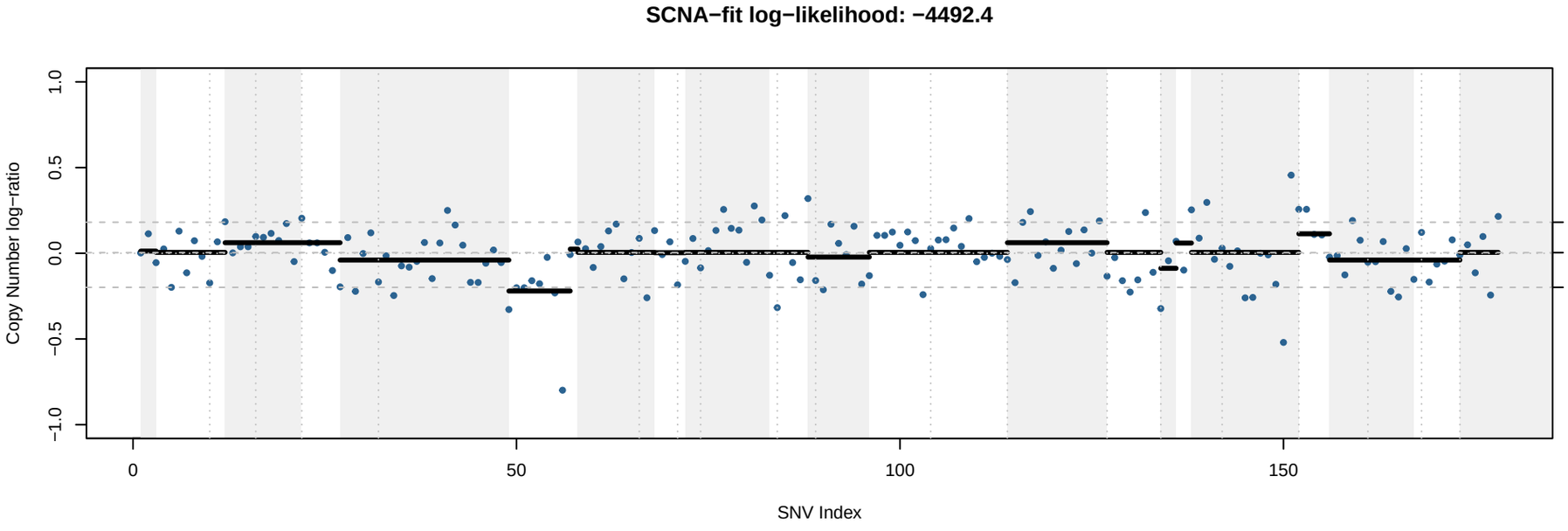

Coverage (log2)
Allelic fraction

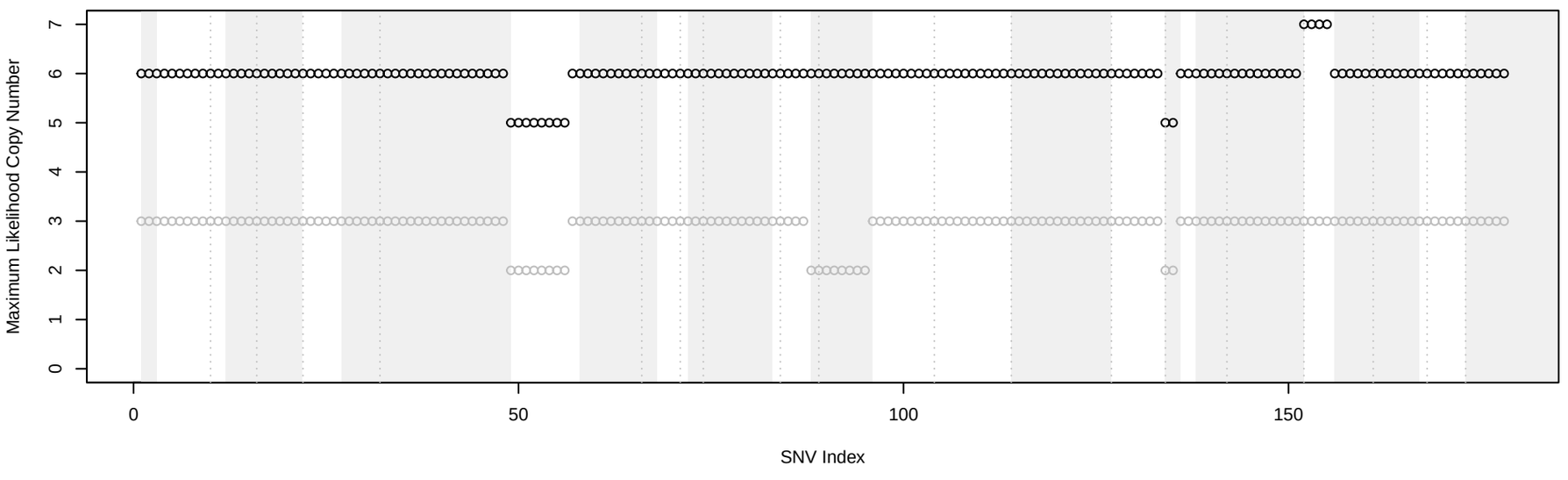

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
7m1
Allelic fraction (somatic)
Copy Number log−ratio

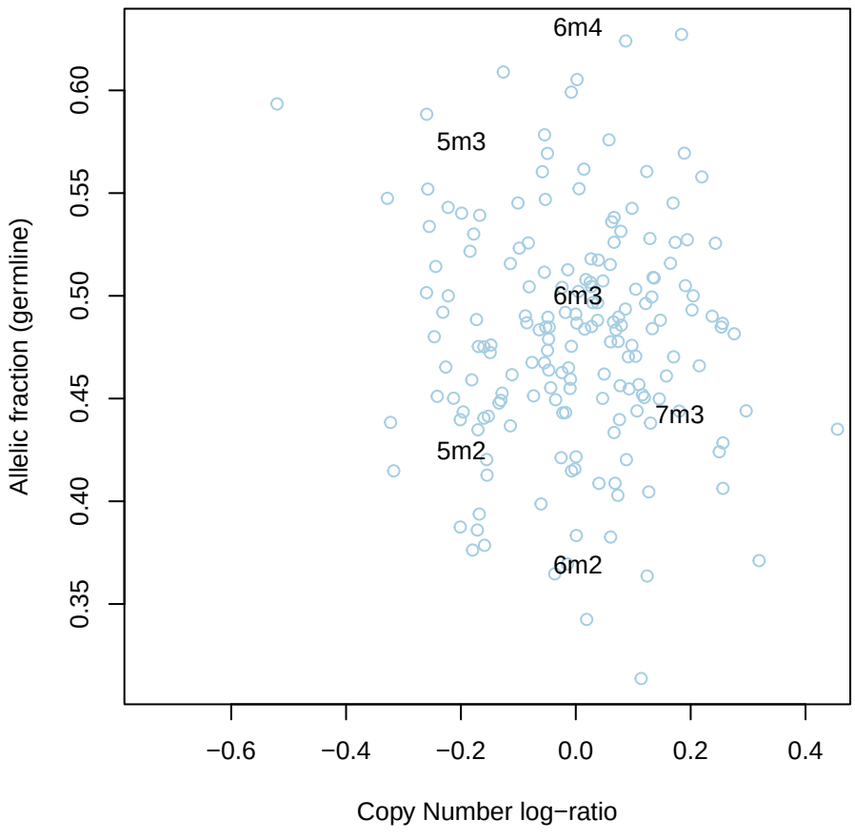

Frequency
Cellular fraction

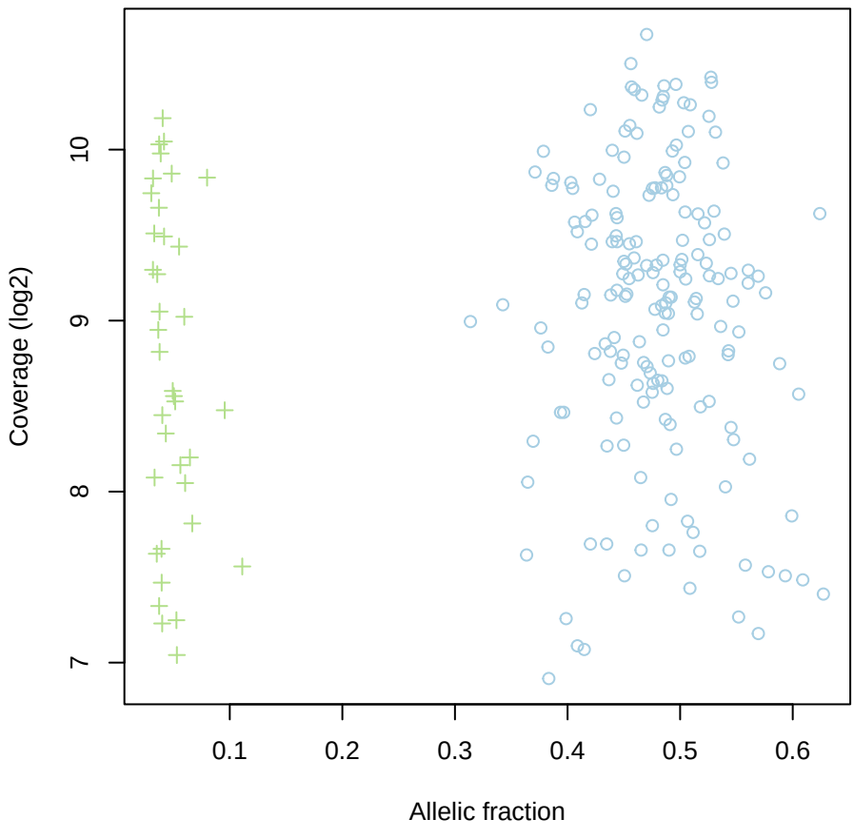

Purity: 0.55 Tumor ploidy: 5.981
5
6
Fraction Genome
0.0
0.1
0.2
0.3
−0.20
−0.15
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

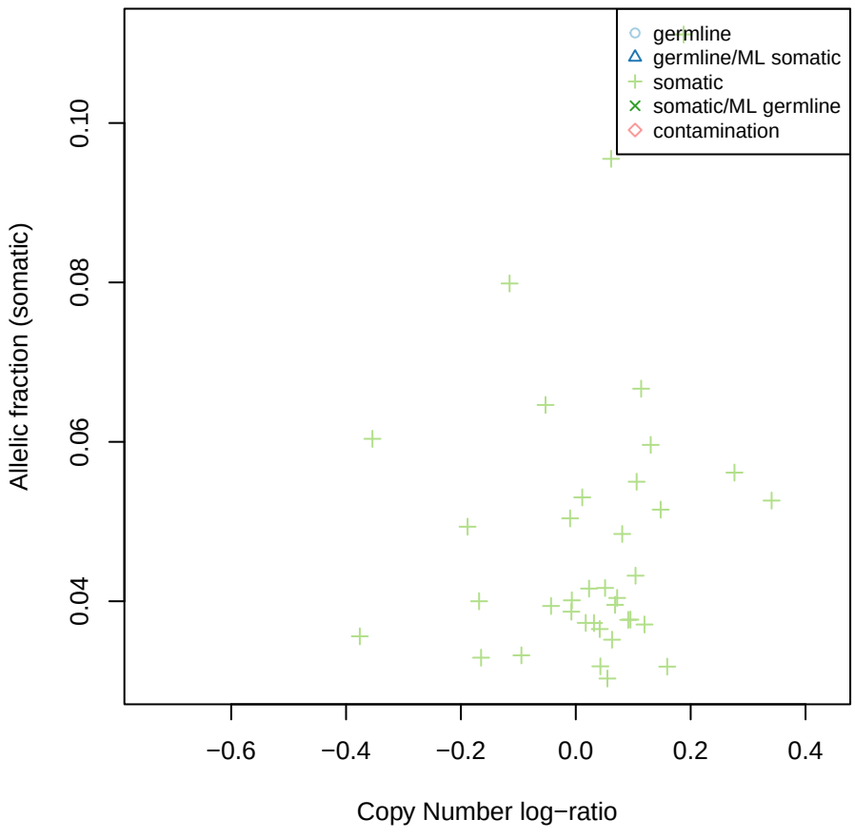

Purity: 0.55 Tumor ploidy: 5.981 SNV log−likelihood: −166.09 GoF: 91.8% Mean coverage: 705;605
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

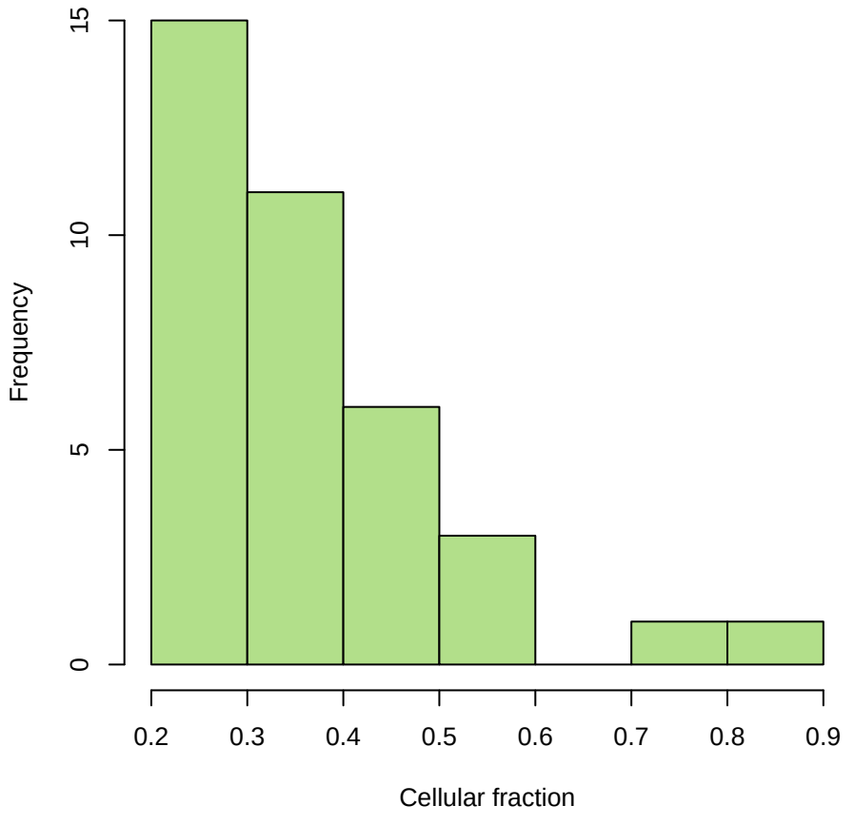

SCNA−fit log−likelihood: −4492.4
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
5 6 7
0 50 100 150
SNV Index

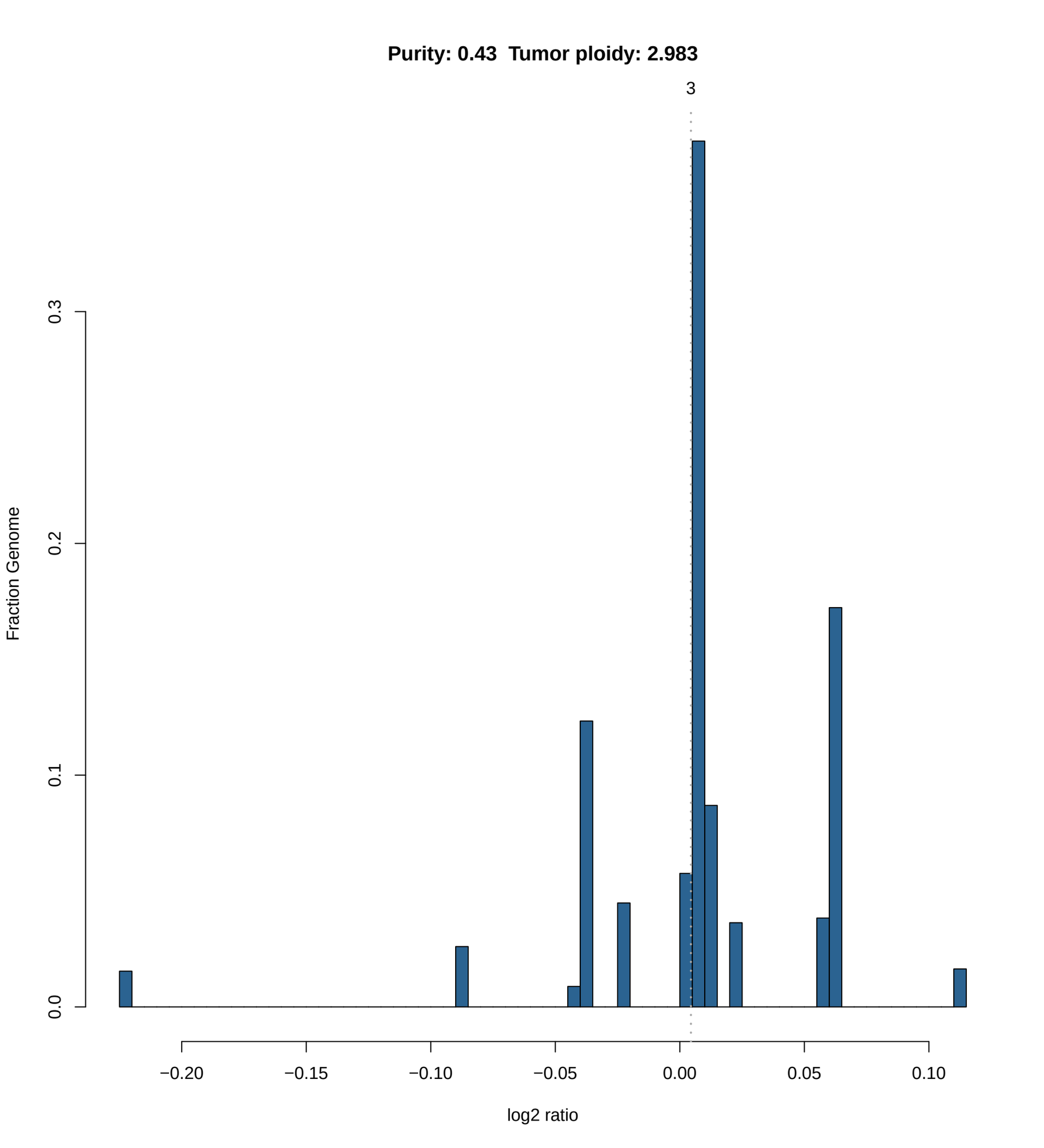

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

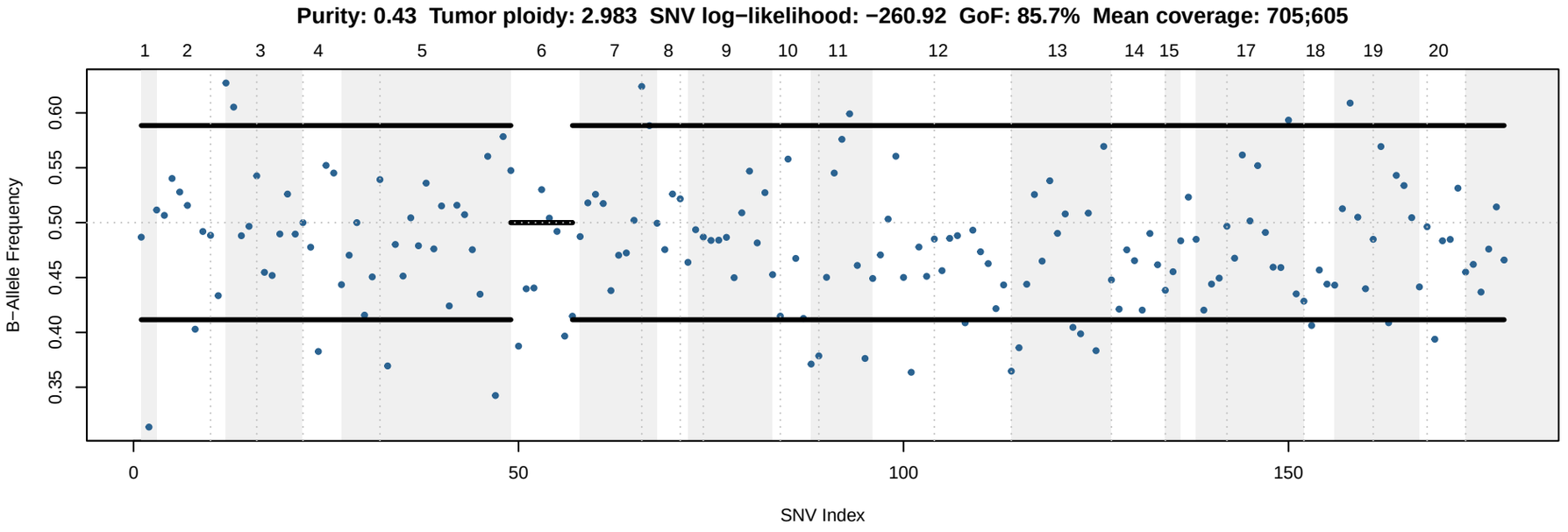

6m4
5m3
6m3
7m3
5m2
6m2
Allelic fraction (germline)
Copy Number log−ratio

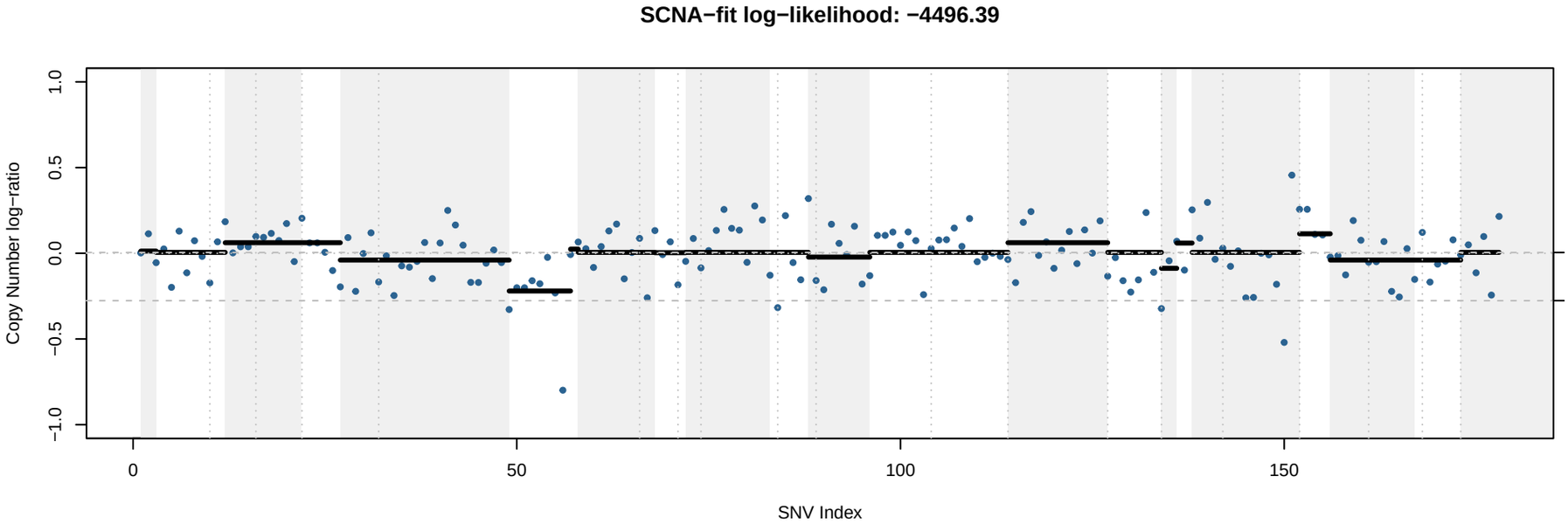

Coverage (log2)
Allelic fraction

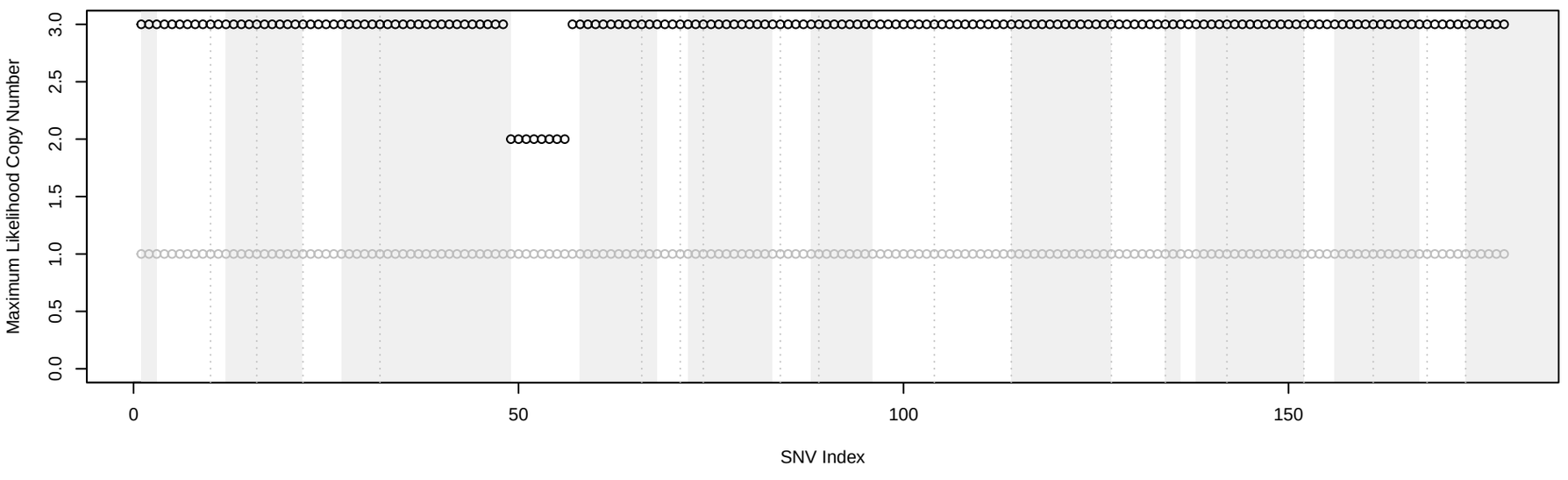

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

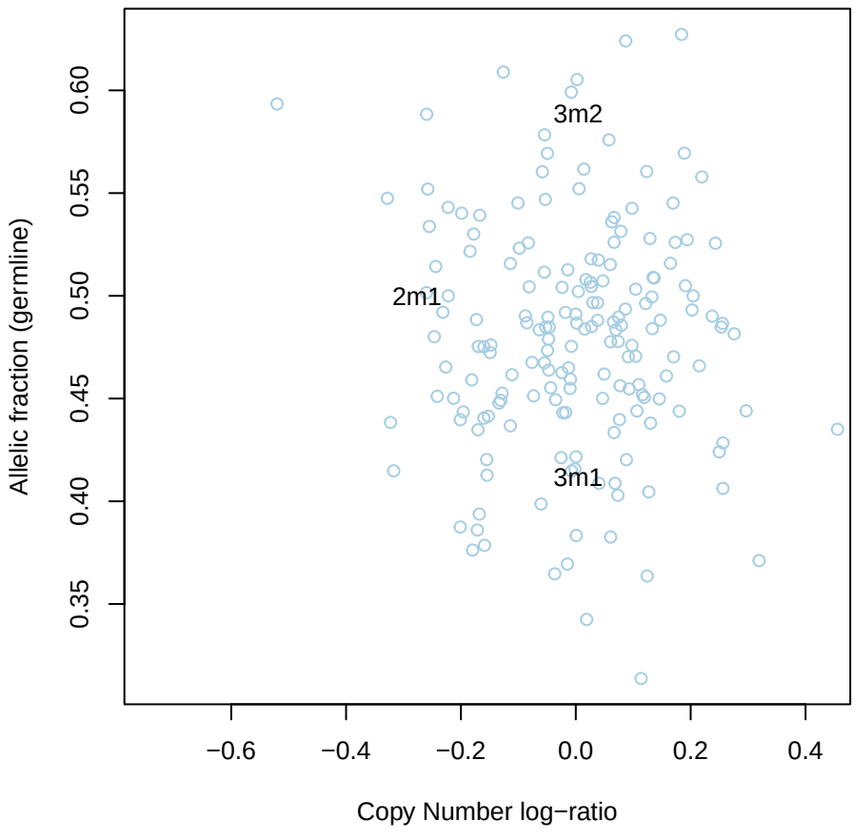

Frequency
Cellular fraction

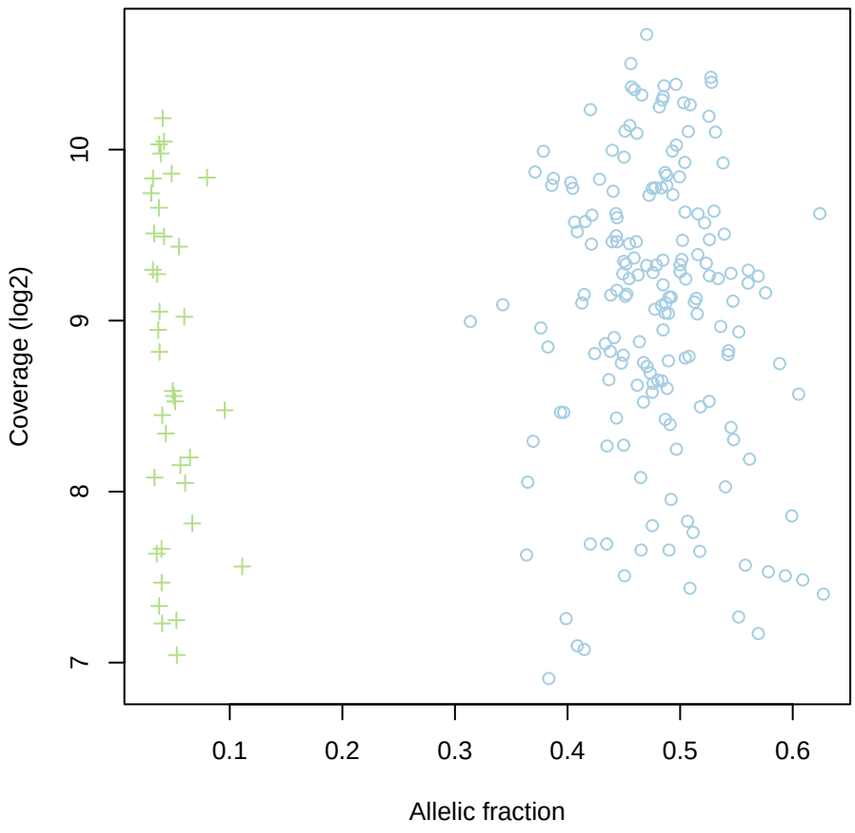

Purity: 0.43 Tumor ploidy: 2.983
3
Fraction Genome
0.0
0.1
0.2
0.3
−0.20
−0.15
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

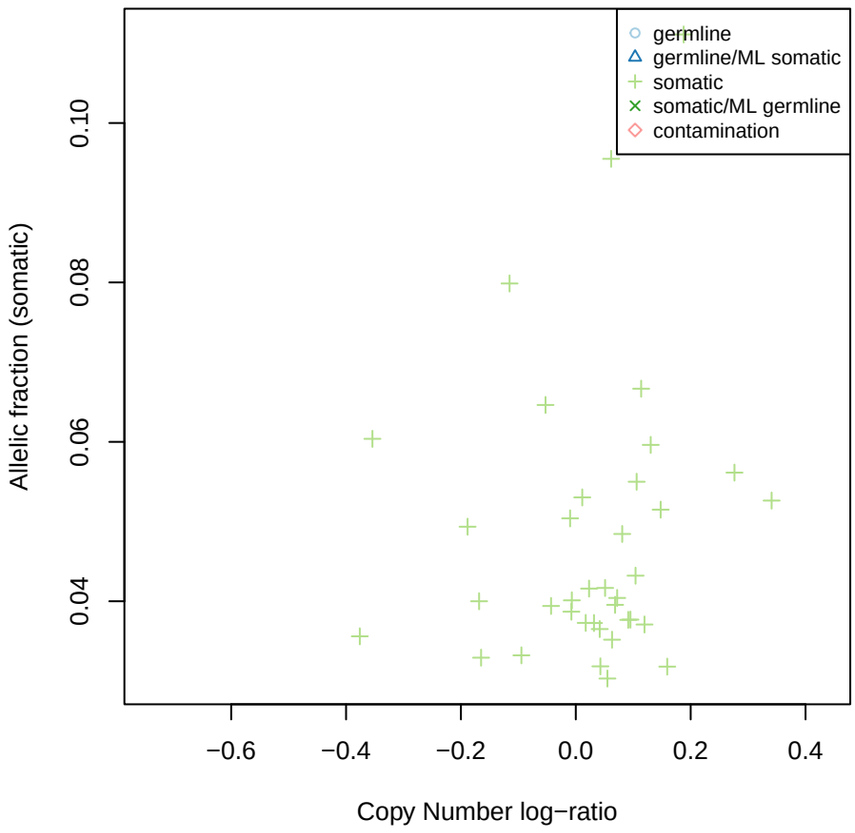

Purity: 0.43 Tumor ploidy: 2.983 SNV log−likelihood: −260.92 GoF: 85.7% Mean coverage: 705;605
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

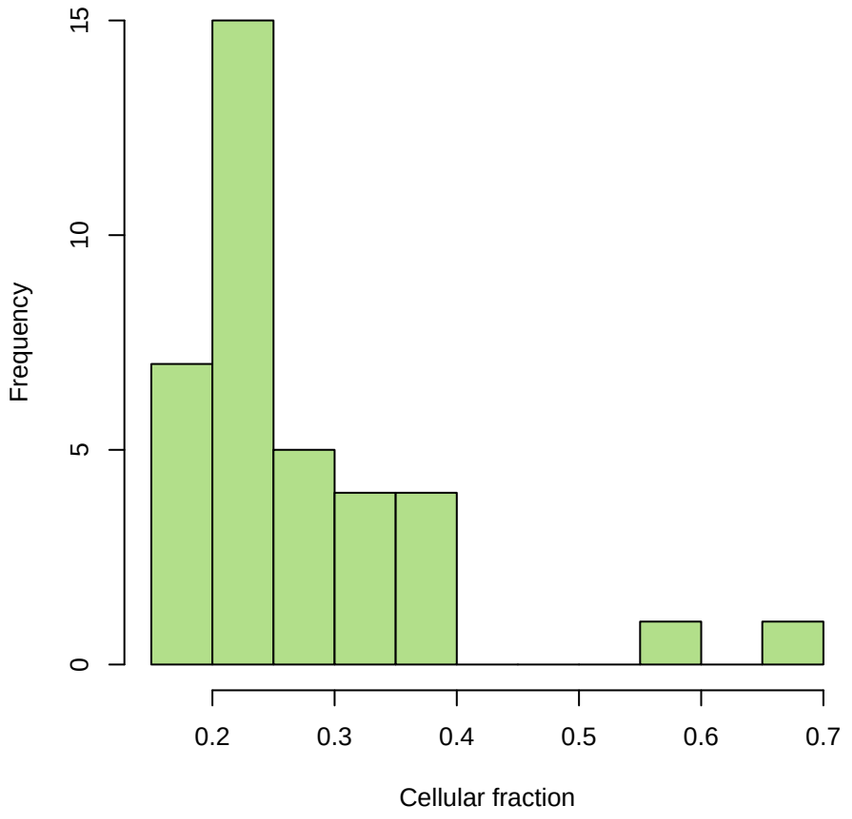

SCNA−fit log−likelihood: −4496.39
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
3
2
0 50 100 150
SNV Index

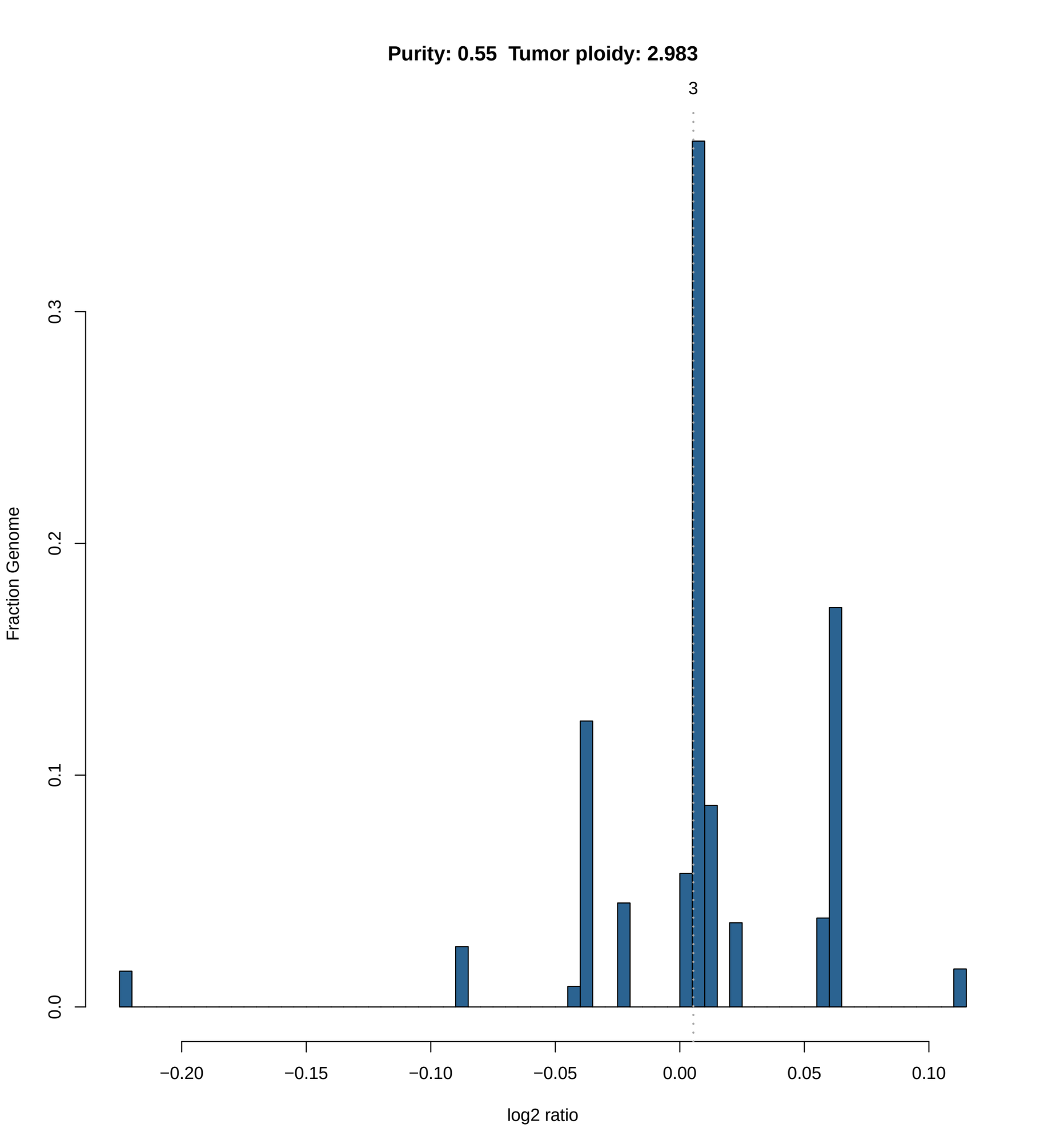

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

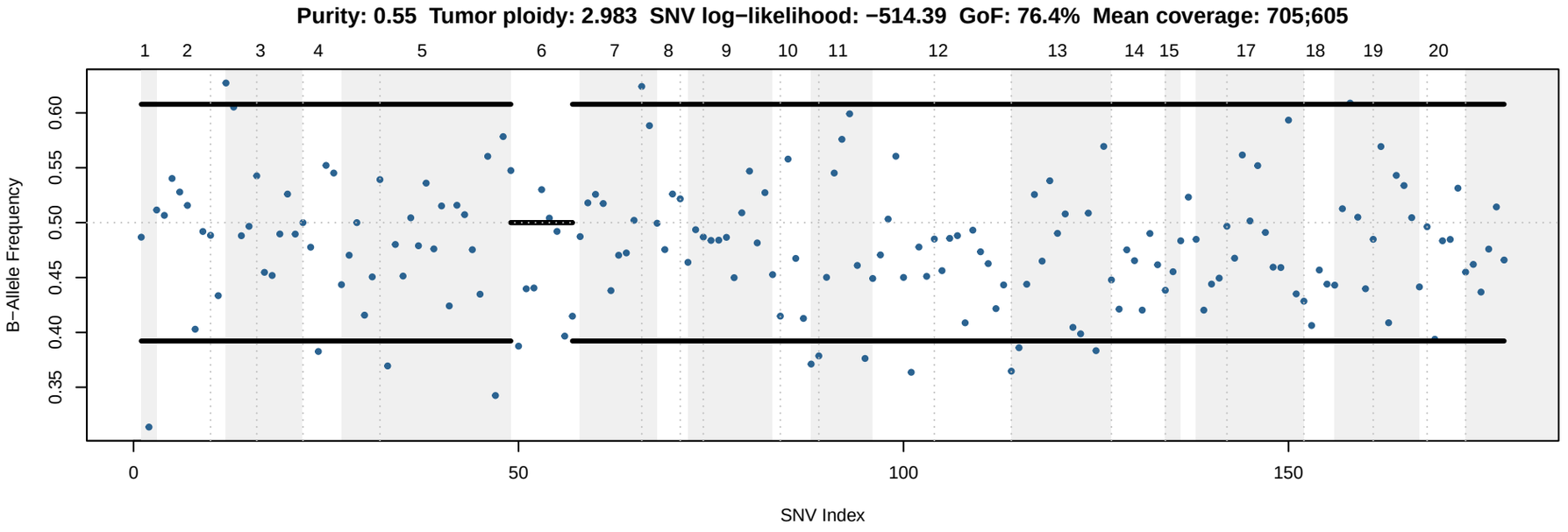

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
3m2
2m1
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

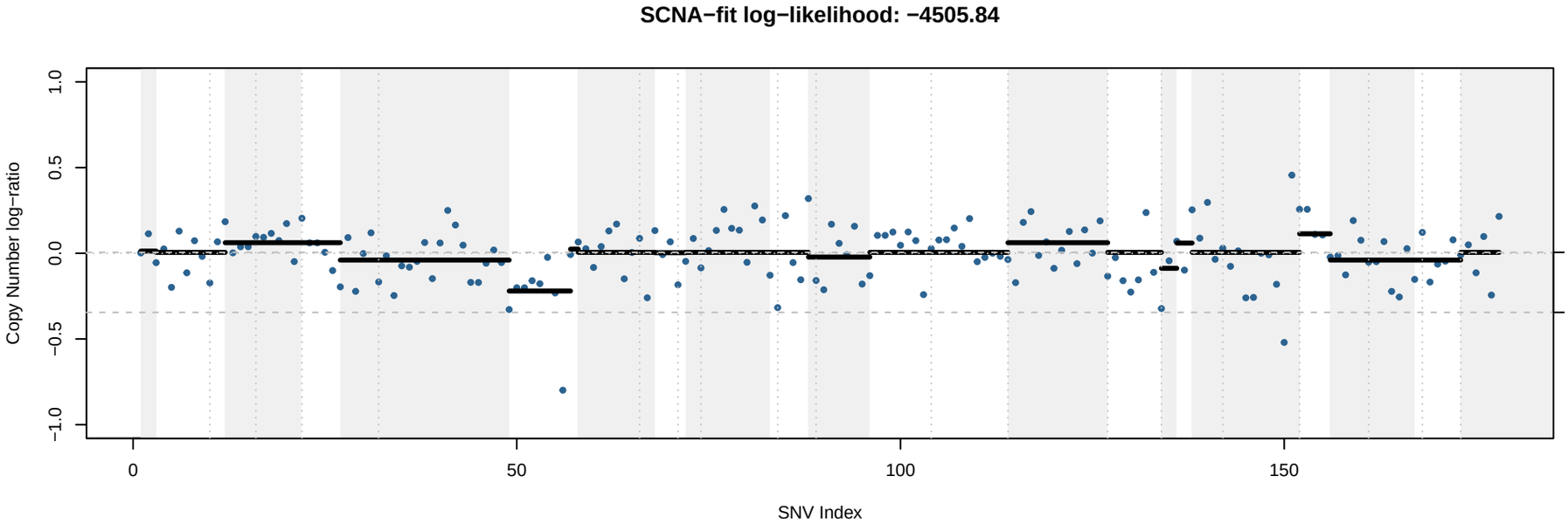

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

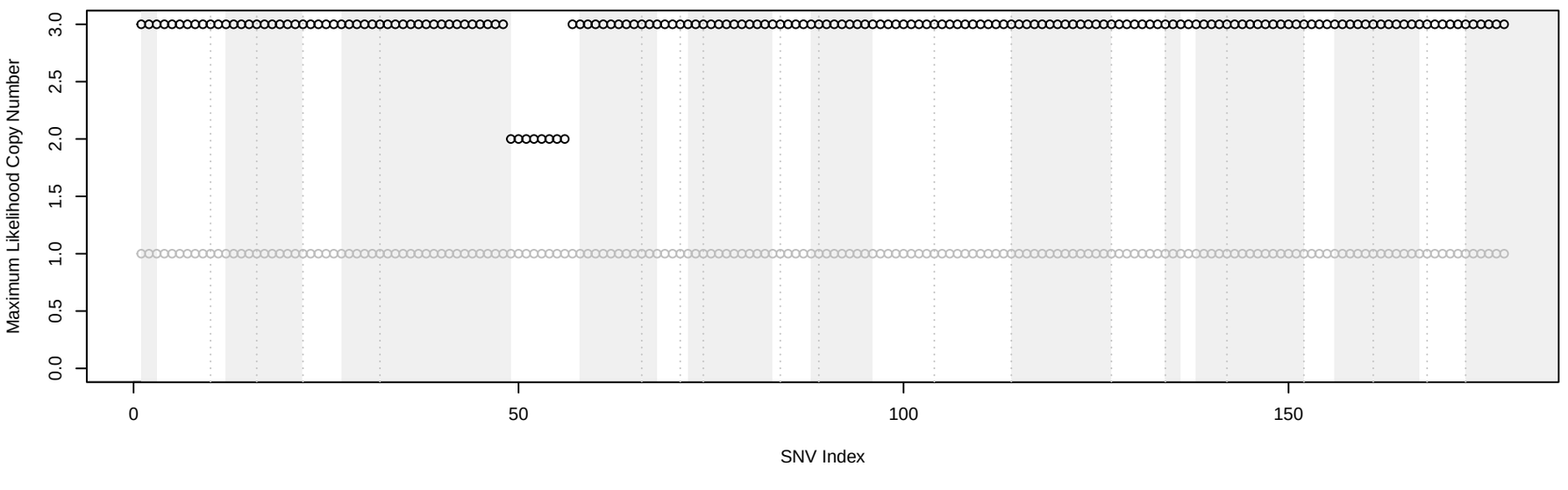

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

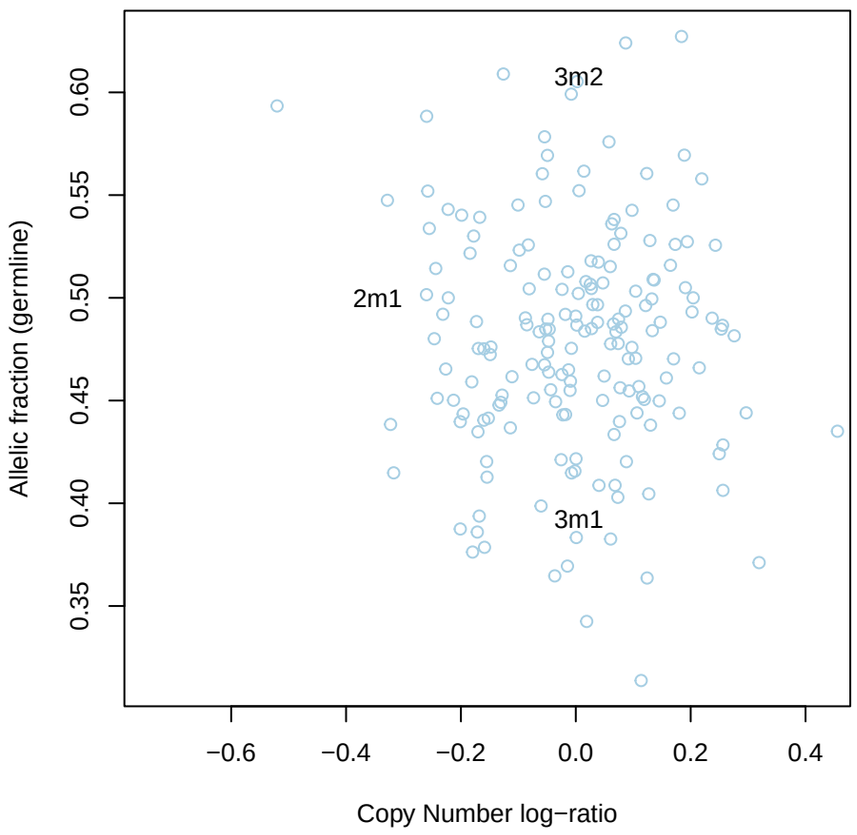

Frequency
0
5
10
15
0.2
0.3
0.4
0.5
0.6
0.7
Cellular fraction

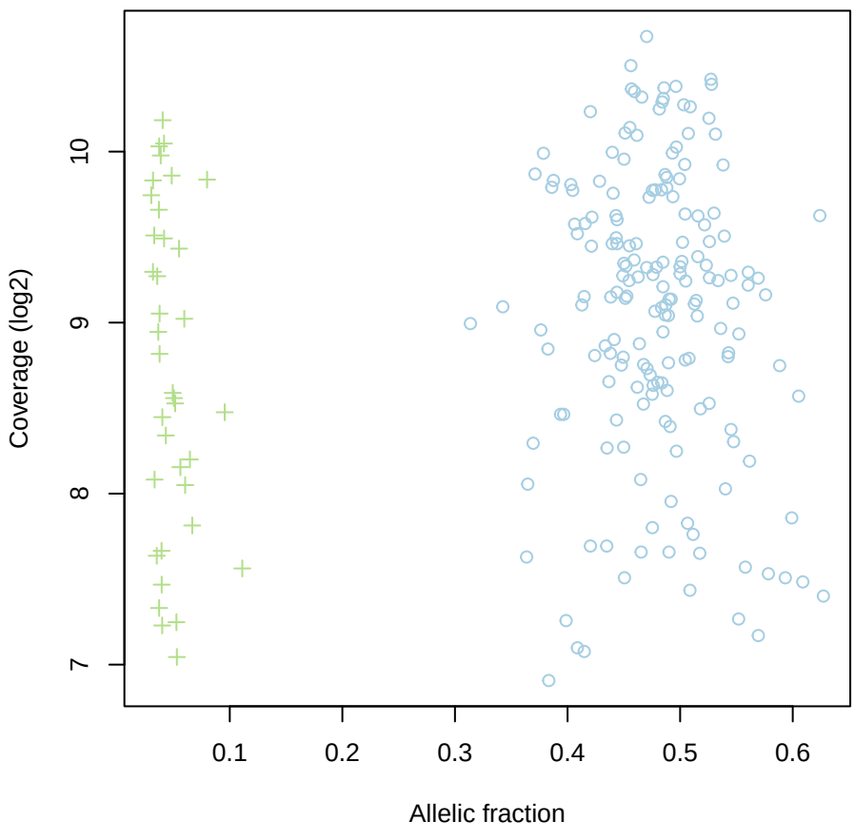

Purity: 0.55 Tumor ploidy: 2.983
3
Fraction Genome
0.0
0.1
0.2
0.3
−0.20
−0.15
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

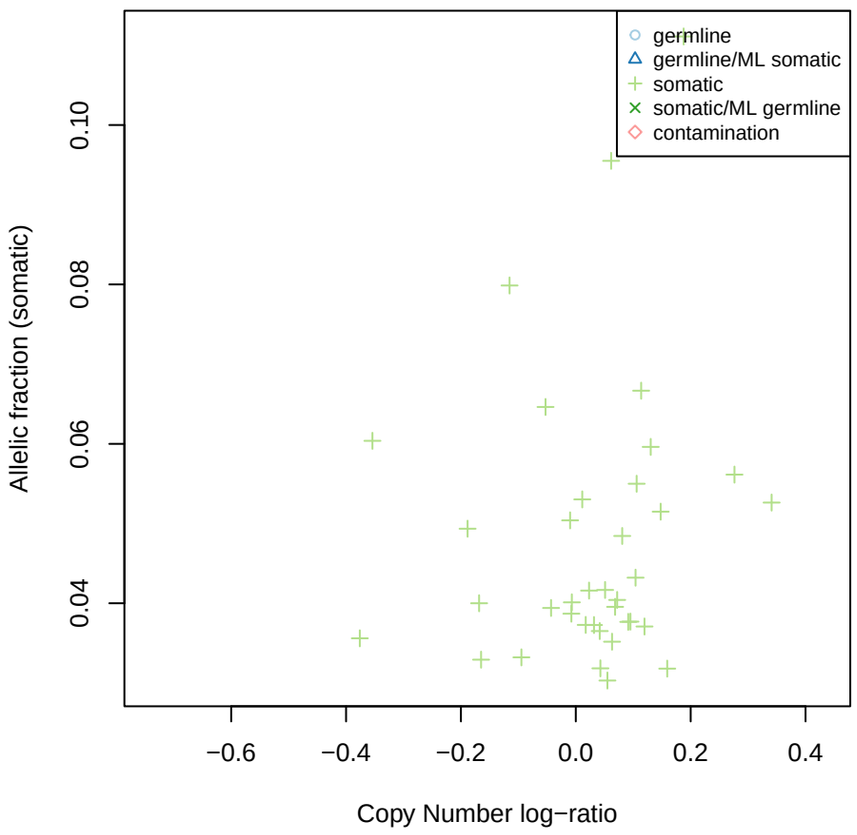

Purity: 0.55 Tumor ploidy: 2.983 SNV log−likelihood: −514.39 GoF: 76.4% Mean coverage: 705;605
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

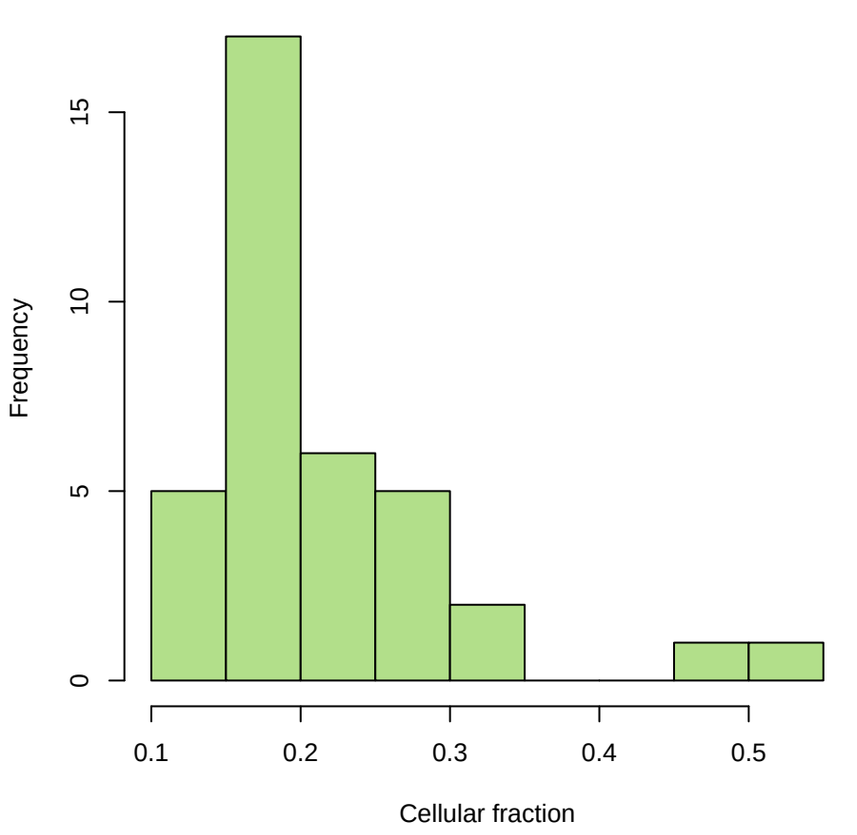

SCNA−fit log−likelihood: −4505.84
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3
0 50 100 150
SNV Index


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


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


Frequency
0
5
10
15
0.1
0.2
0.3
0.4
0.5
Cellular fraction