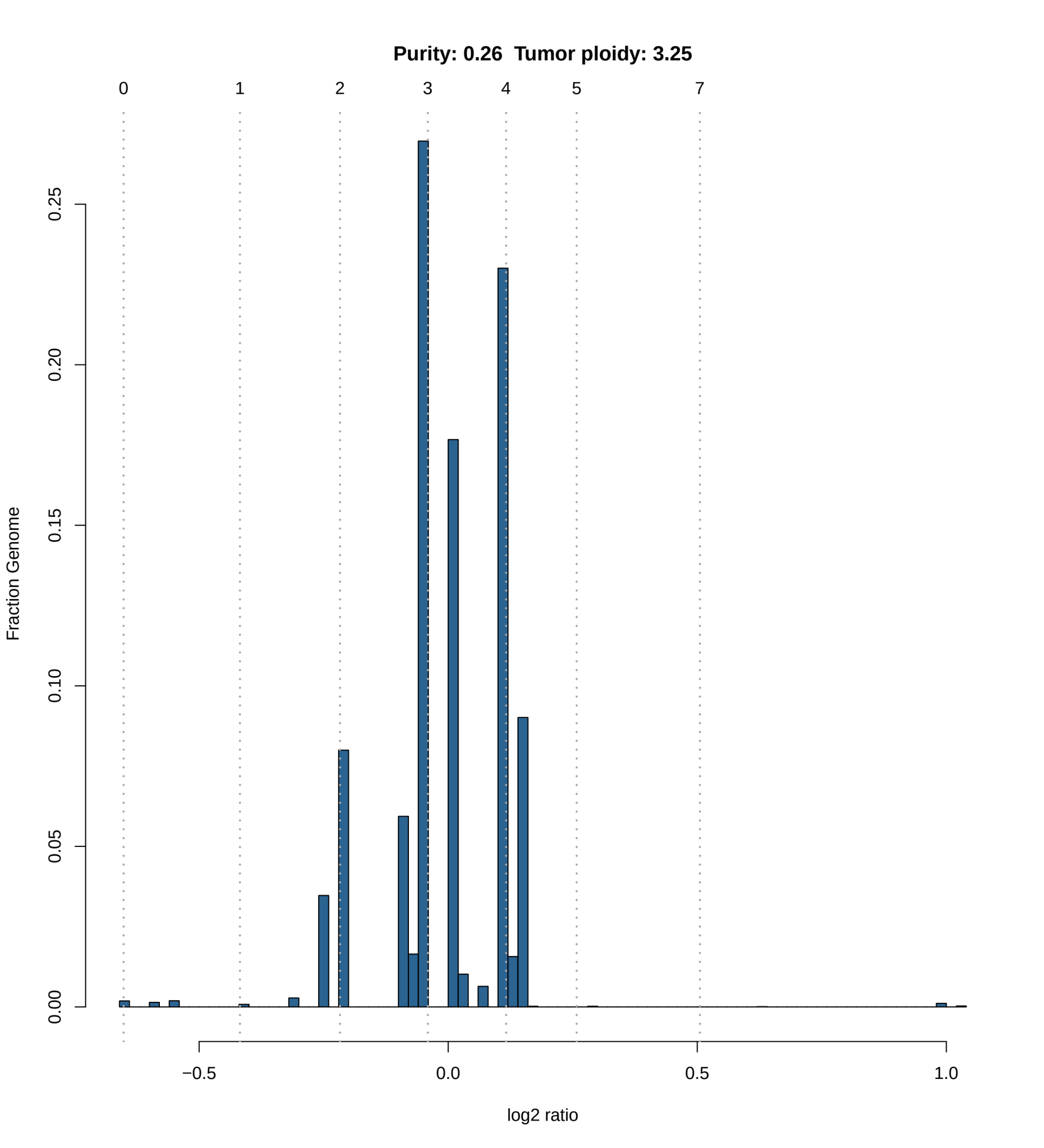
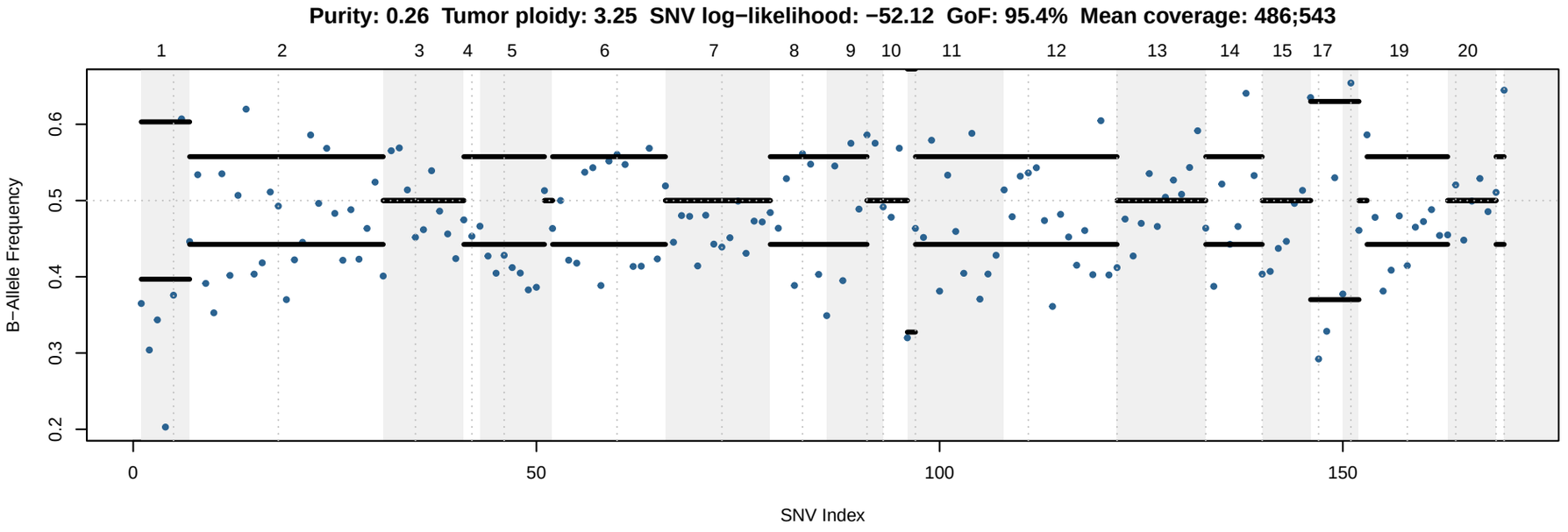
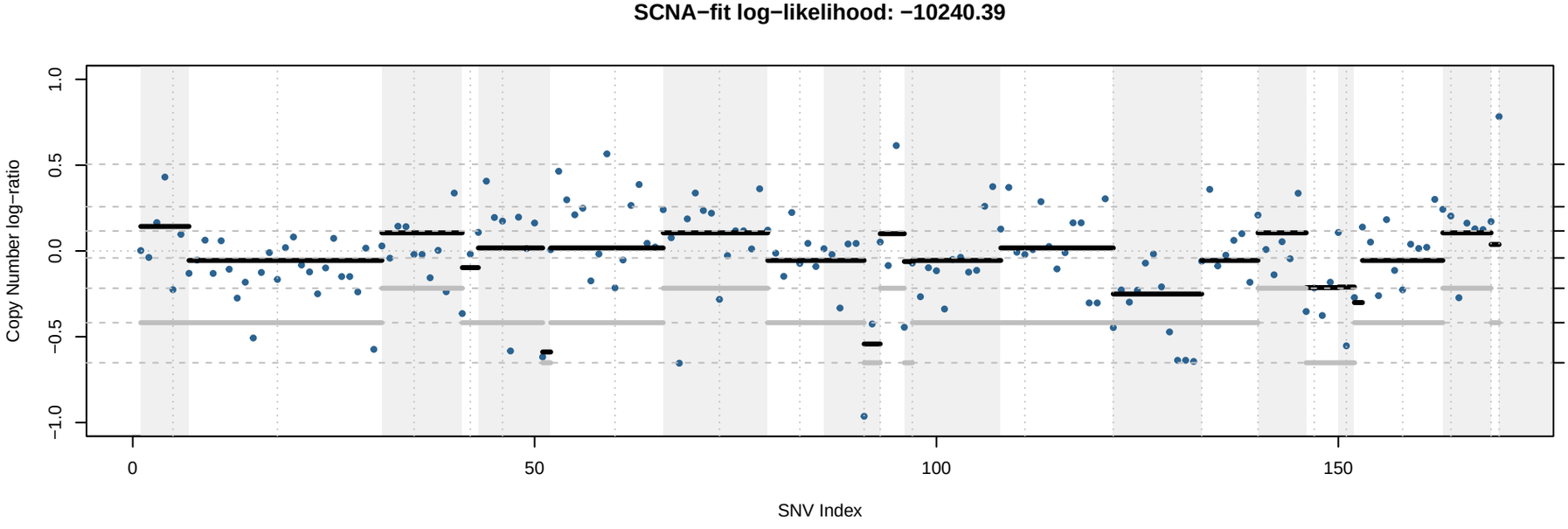
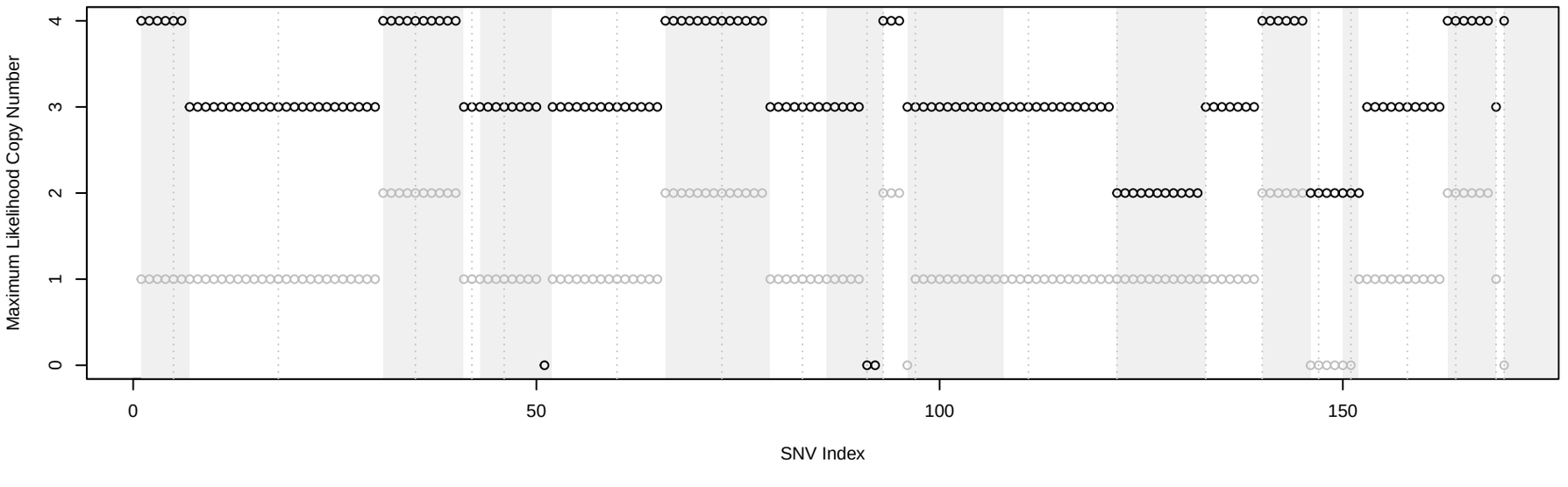
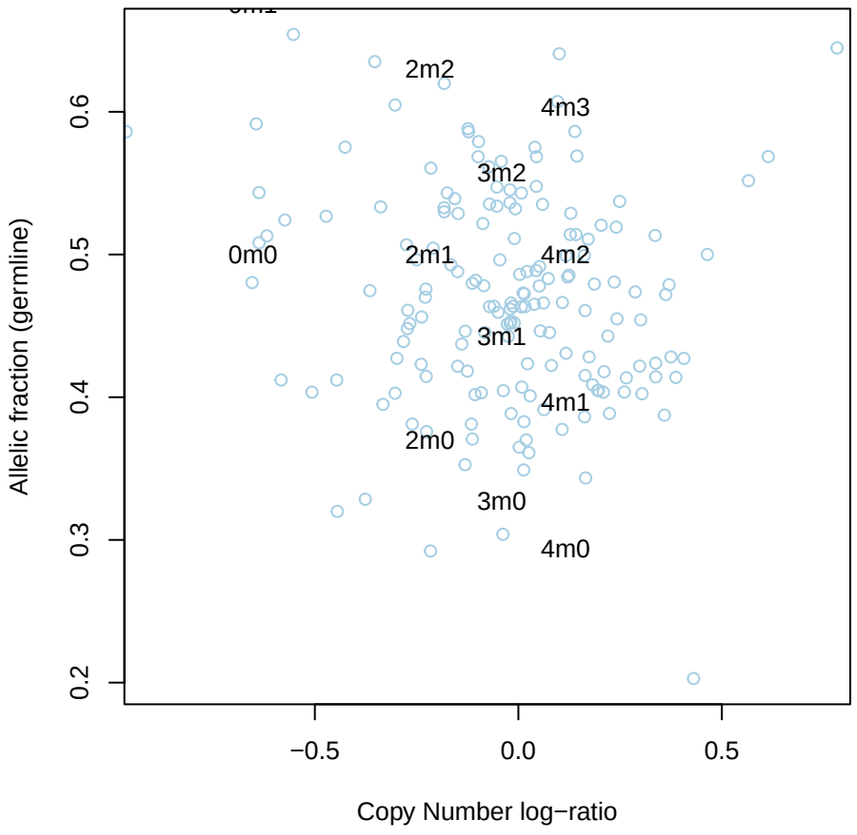
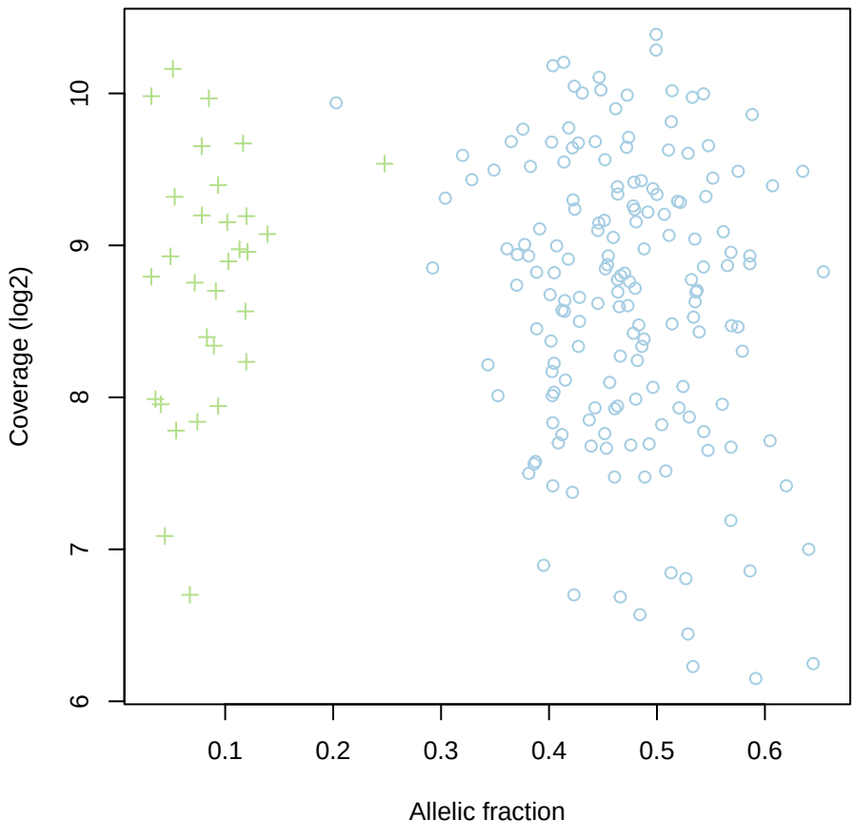

Purity: 0.26 Tumor ploidy: 3.25
0
1
2
3
4
5
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

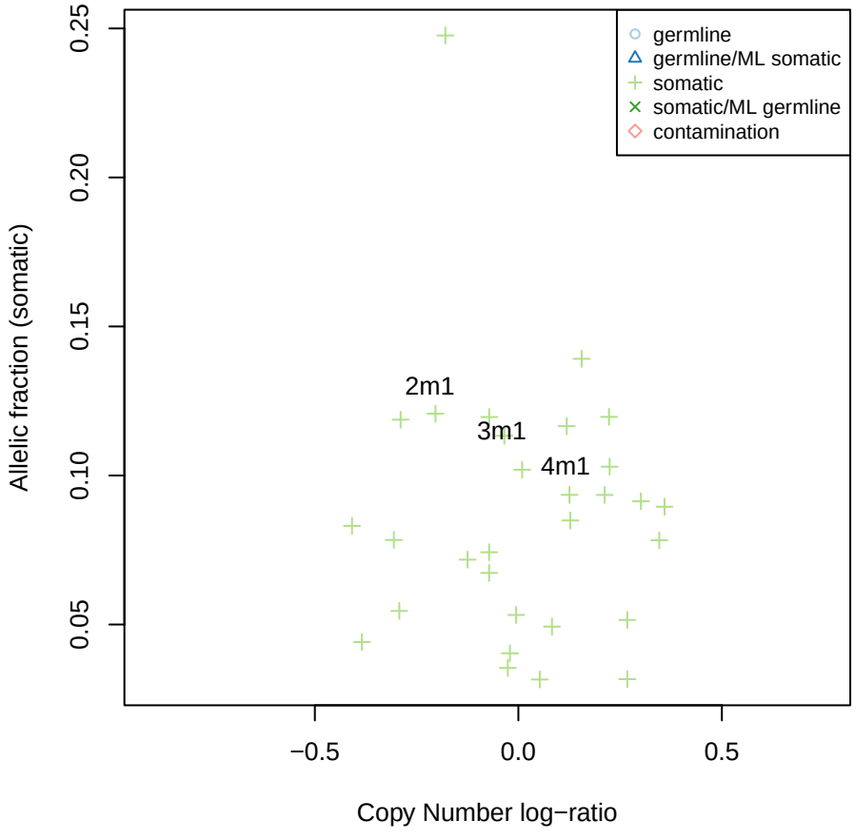

Purity: 0.26 Tumor ploidy: 3.25 SNV log−likelihood: −52.12 GoF: 95.4% Mean coverage: 486;543
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
17
19
20
B−Allele Frequency
0.2
0.3
0.4
0.5
0.6
0
50
100
150
SNV Index

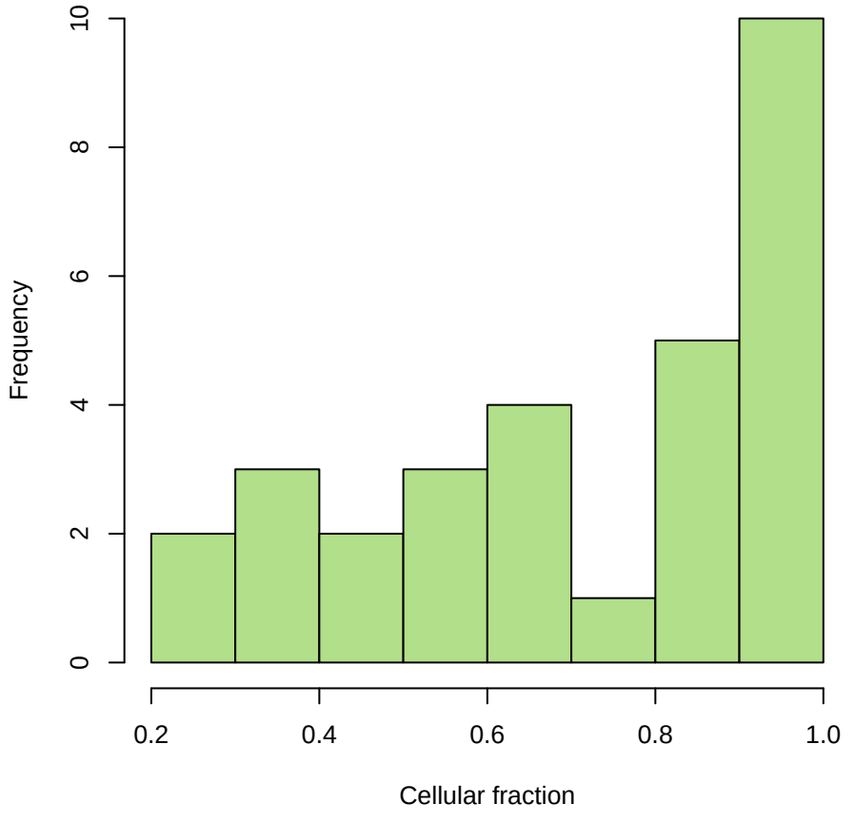

SCNA−fit log−likelihood: −10240.39
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
0
1
2
3
4
7
0
50
100
150
SNV Index

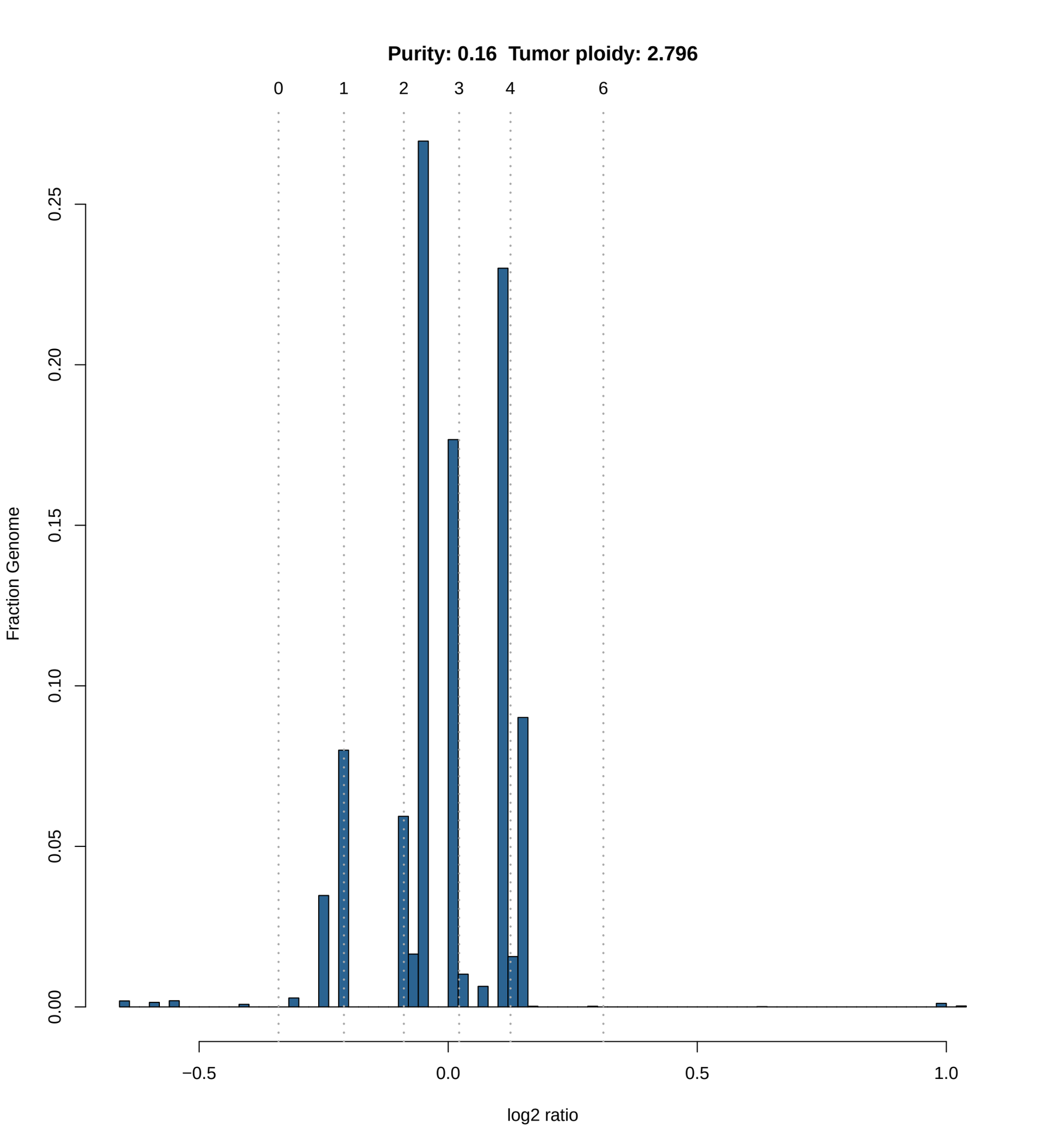

Maximum Likelihood Copy Number
0
1
2
3
4
0
50
100
150
SNV Index

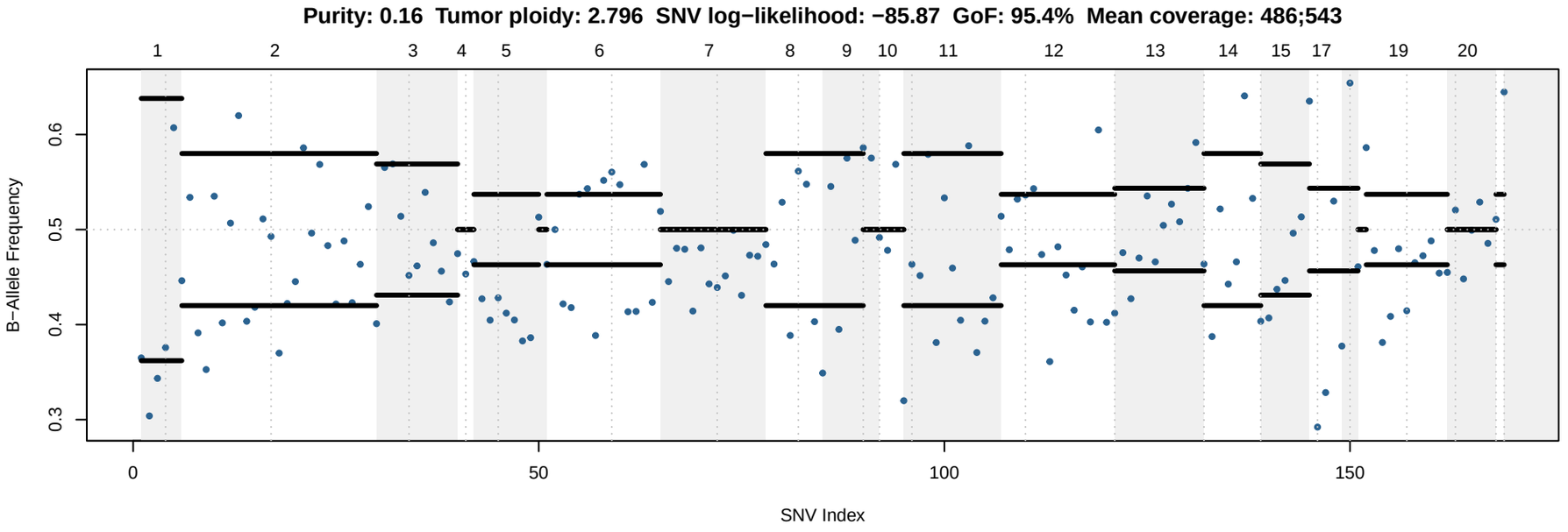

2m2
4m3
3m2
0m0
2m1
4m2
3m1
4m1
2m0
3m0
4m0
Allelic fraction (germline)
Copy Number log−ratio

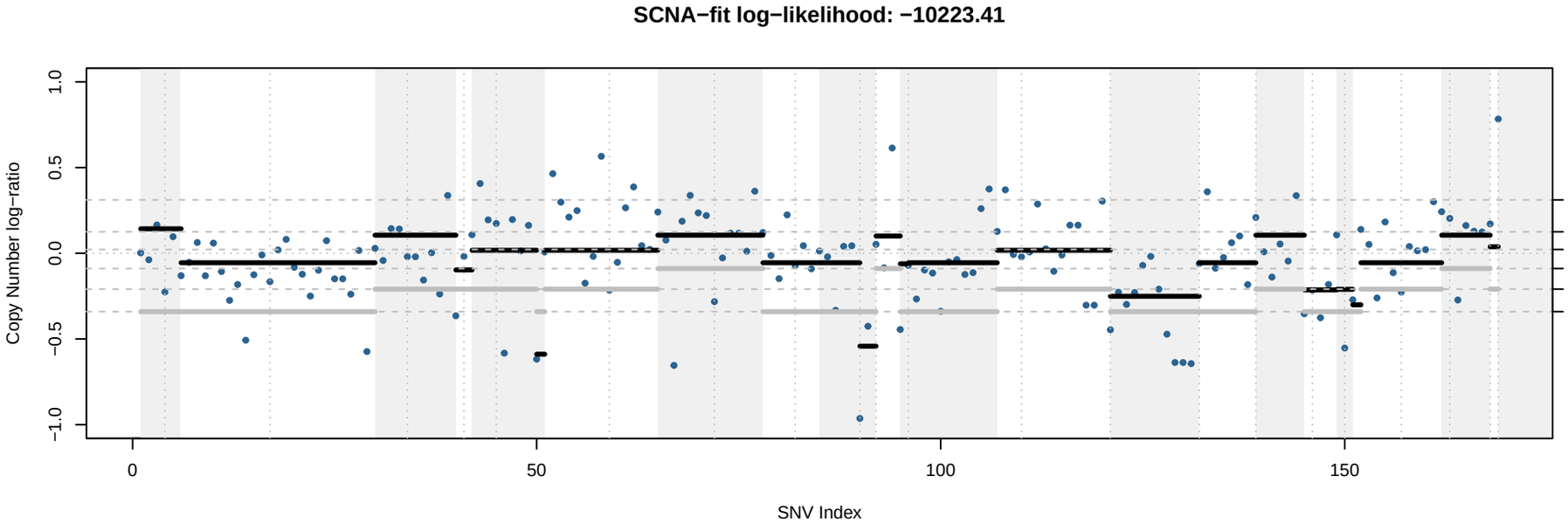

Coverage (log2)
Allelic fraction

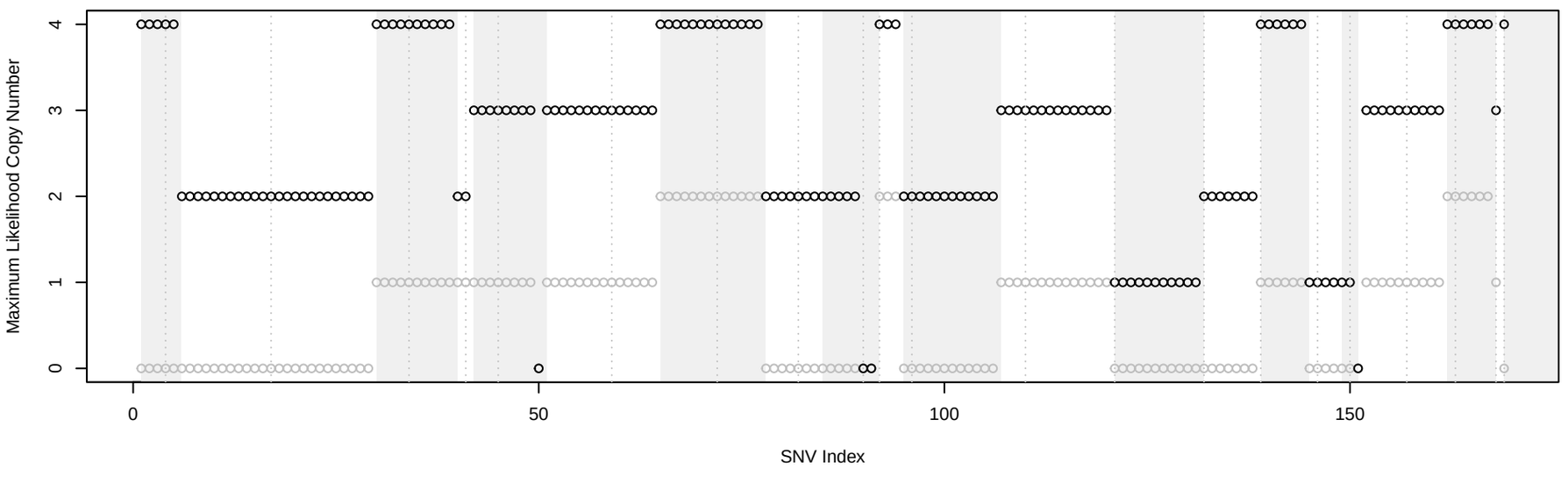

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1
Allelic fraction (somatic)
Copy Number log−ratio

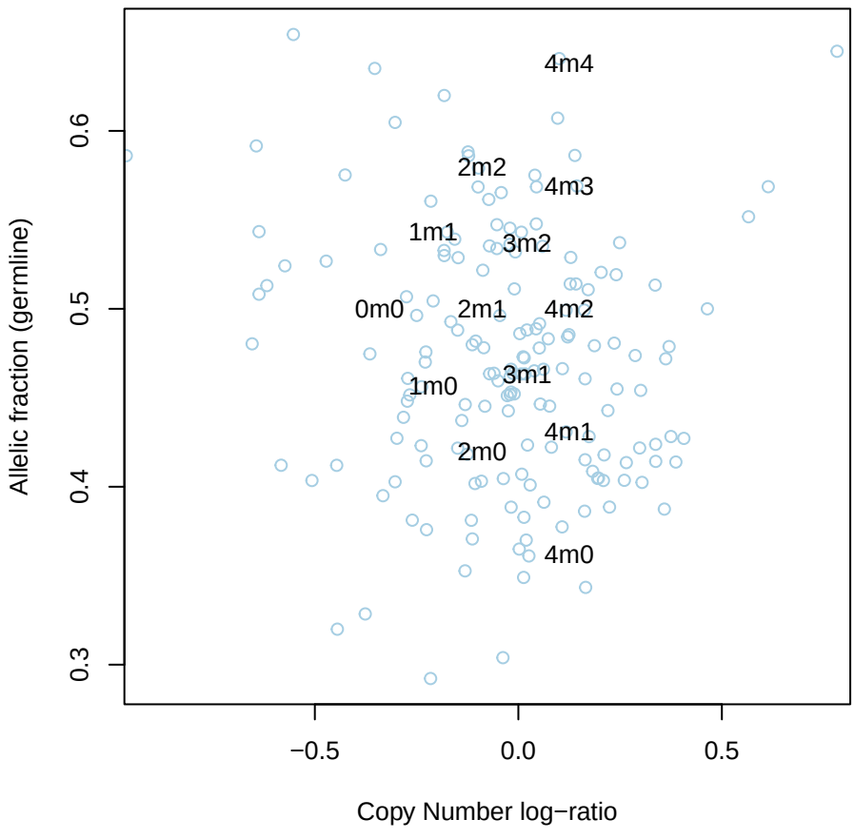

Frequency
Cellular fraction

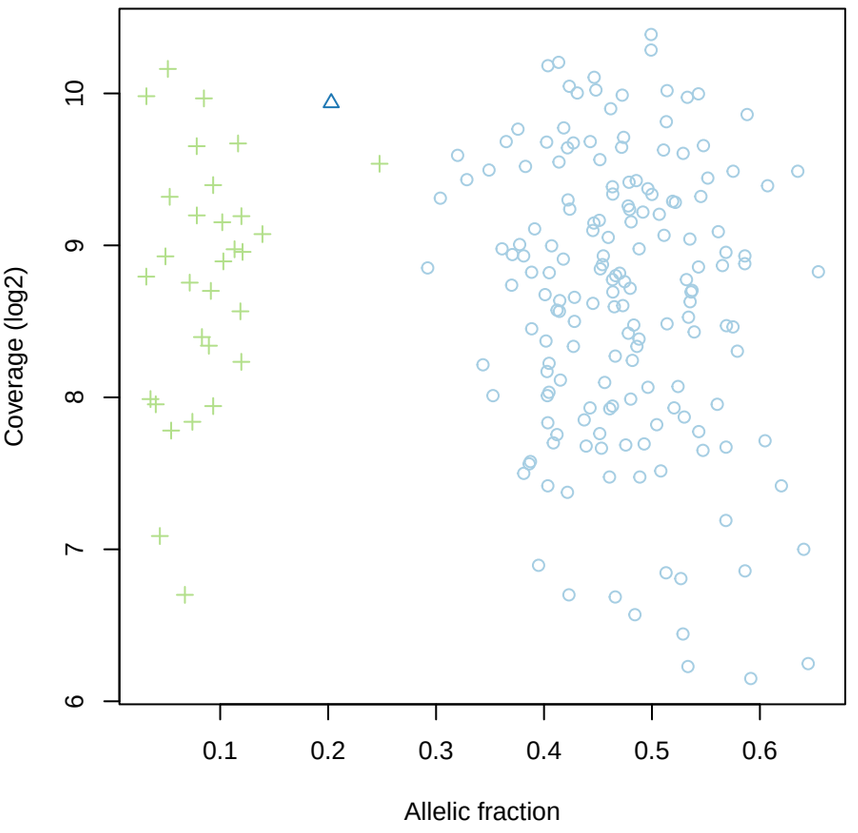

Purity: 0.16 Tumor ploidy: 2.796
0
1
2
3
4
6
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

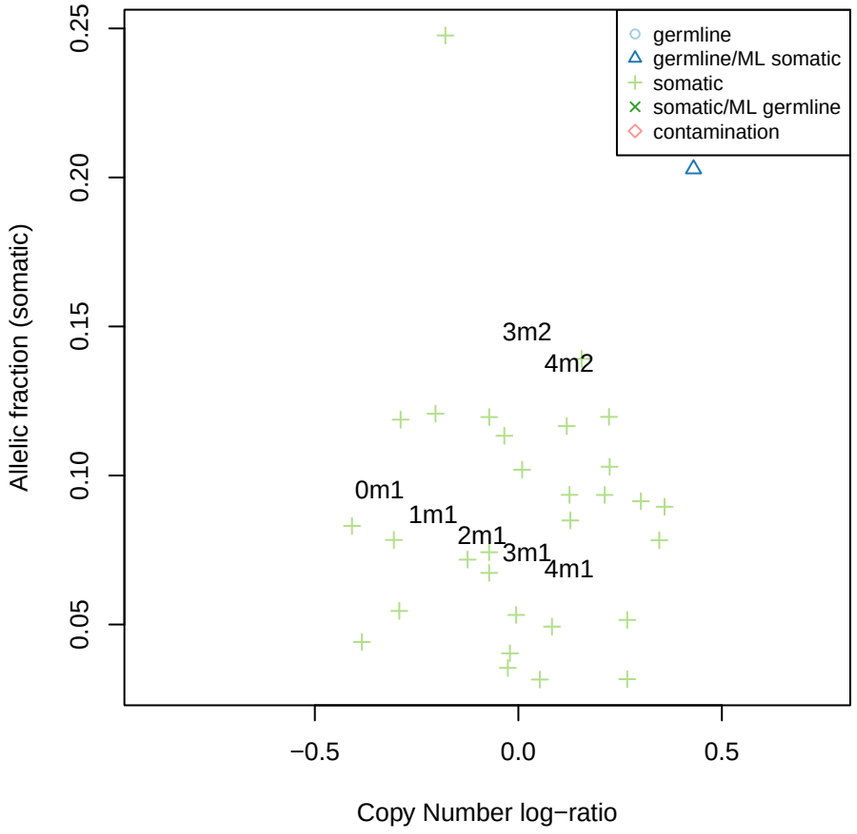

Purity: 0.16 Tumor ploidy: 2.796 SNV log−likelihood: −85.87 GoF: 95.4% Mean coverage: 486;543
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
17
19
20
B−Allele Frequency
0.3
0.4
0.5
0.6
0
50
100
150
SNV Index

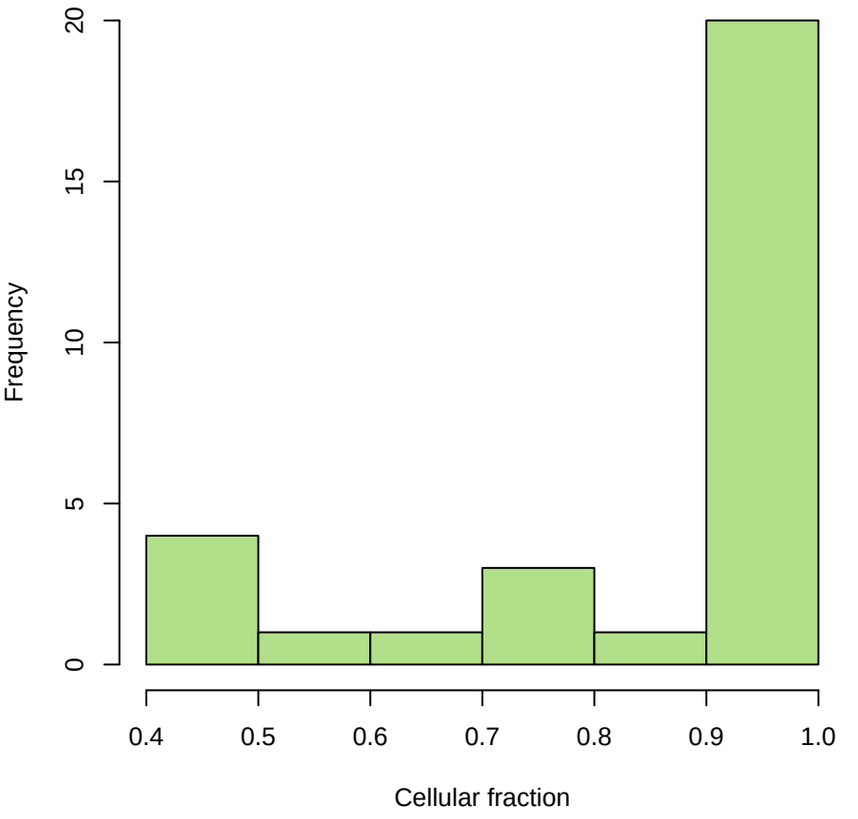

SCNA−fit log−likelihood: −10223.41
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
0
2
4
6
0
50
100
150
SNV Index

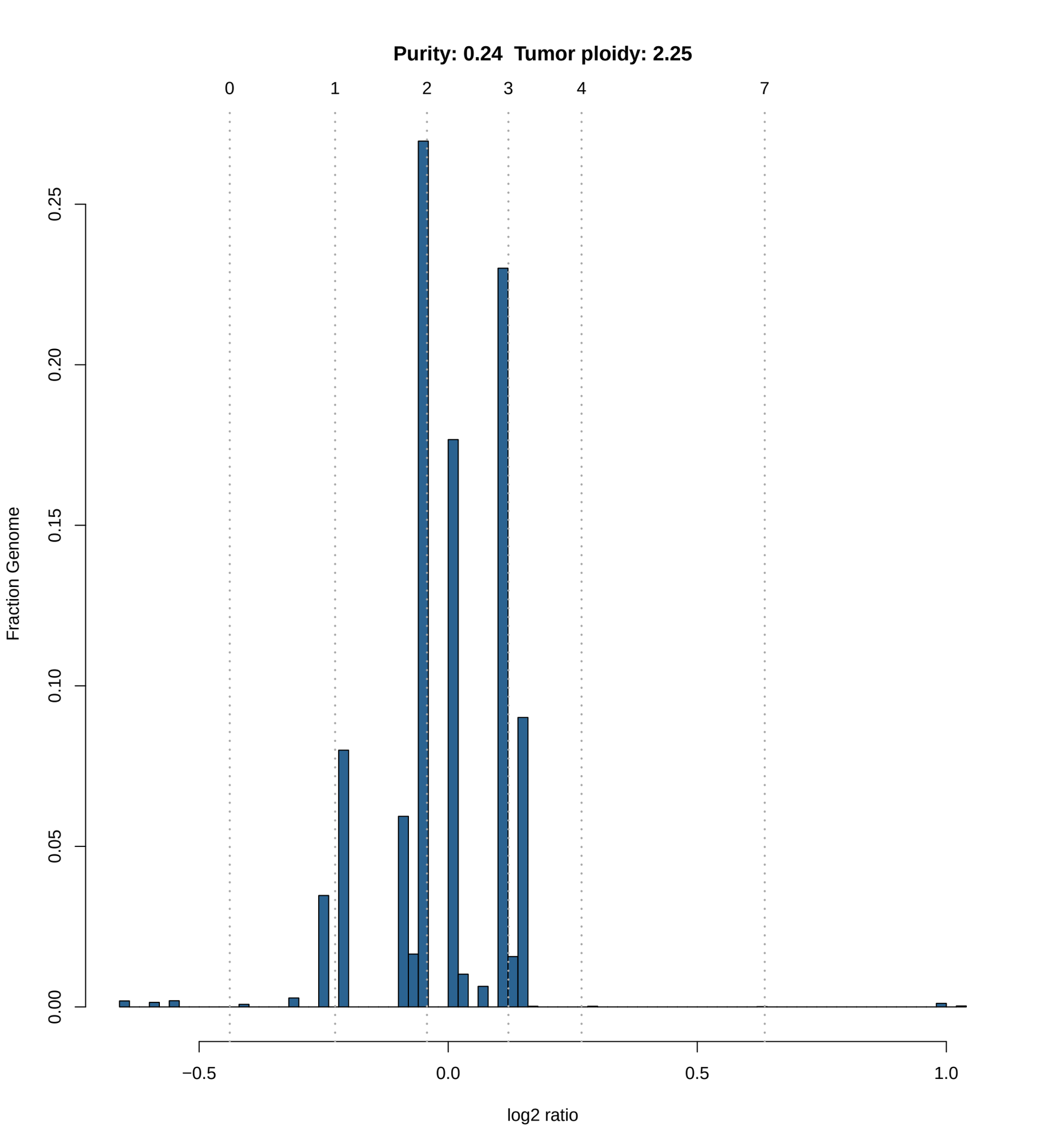

Maximum Likelihood Copy Number
0
1
2
3
4
0
50
100
150
SNV Index

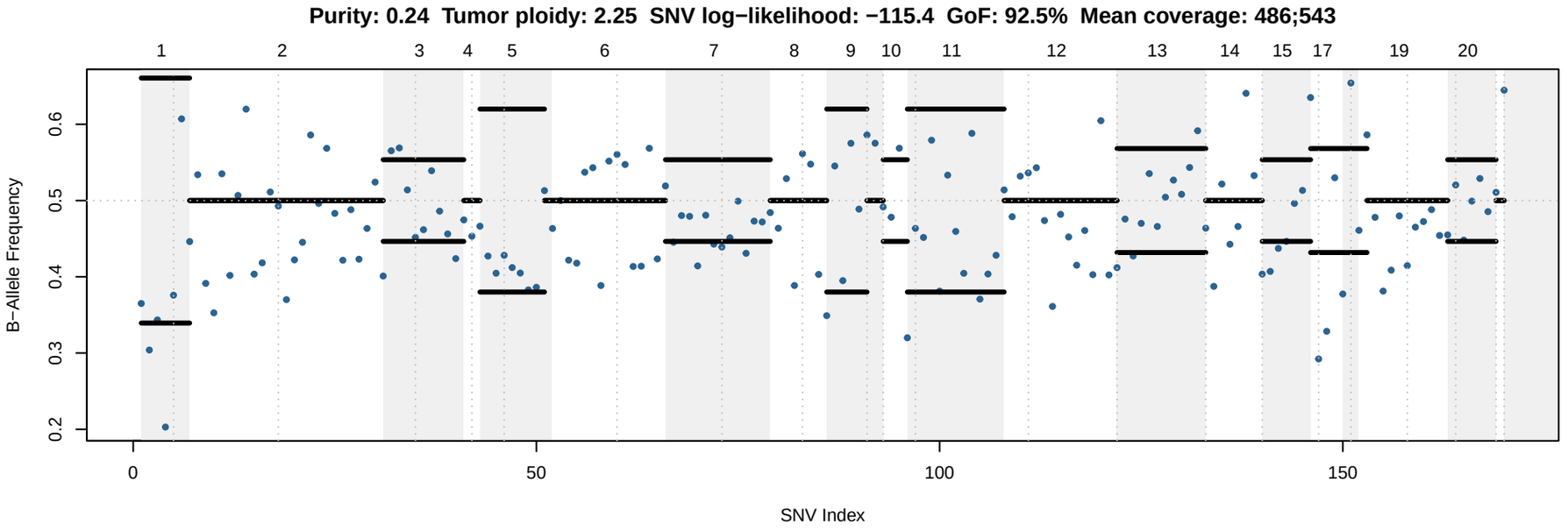

Allelic fraction (germline)
Copy Number log−ratio
4m4
2m2
4m3
1m1
3m2
0m0
2m1
4m2
3m1
1m0
4m1
2m0
4m0

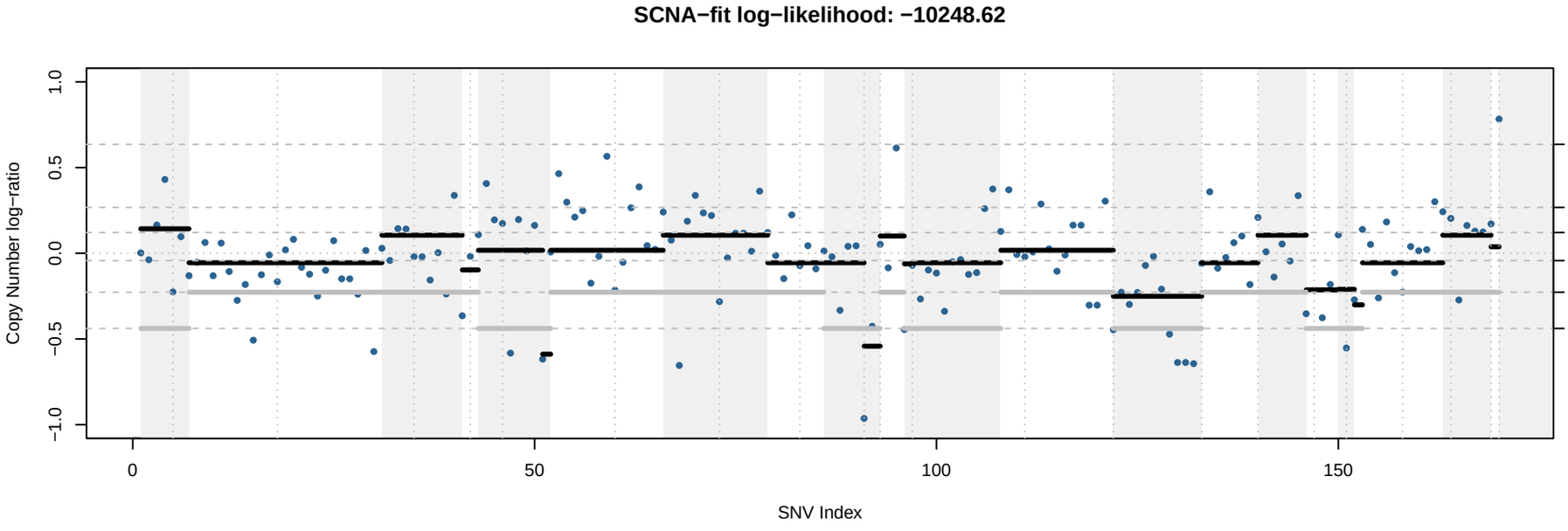

Coverage (log2)
Allelic fraction

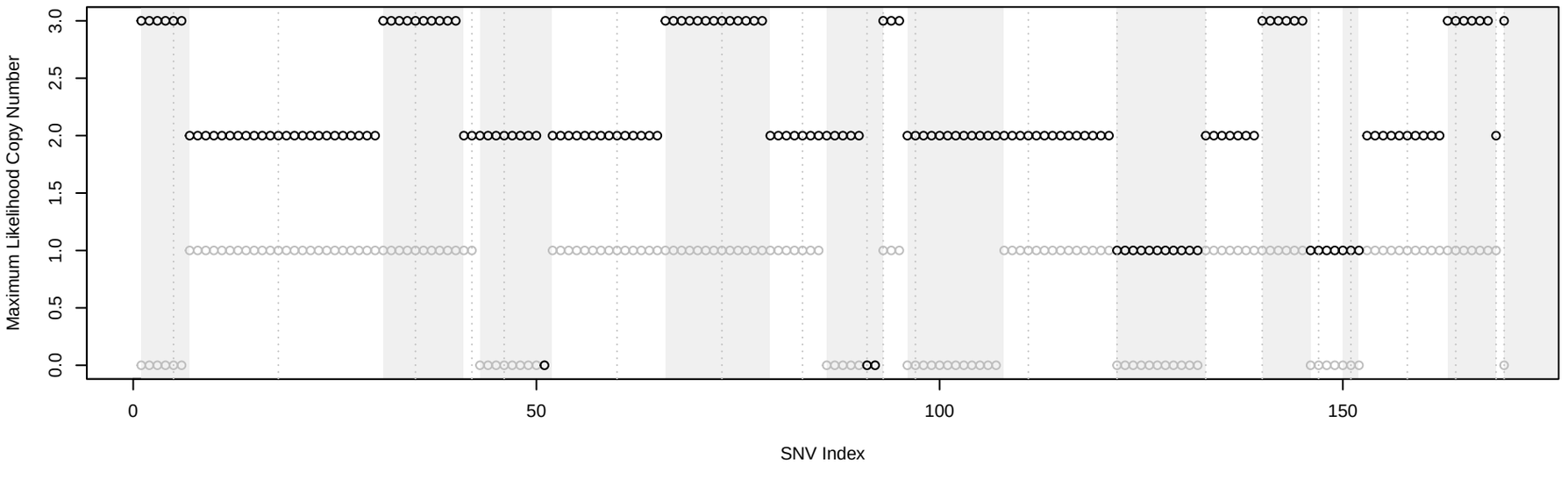

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m2
4m2
0m1
1m1
2m1
3m1
4m1

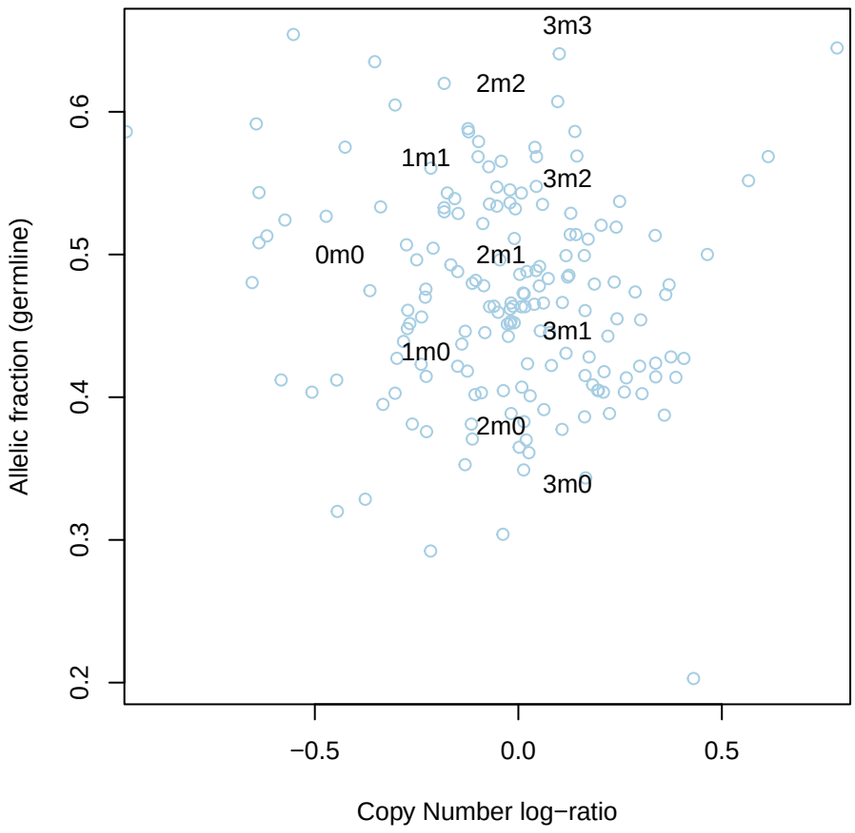

Frequency
Cellular fraction

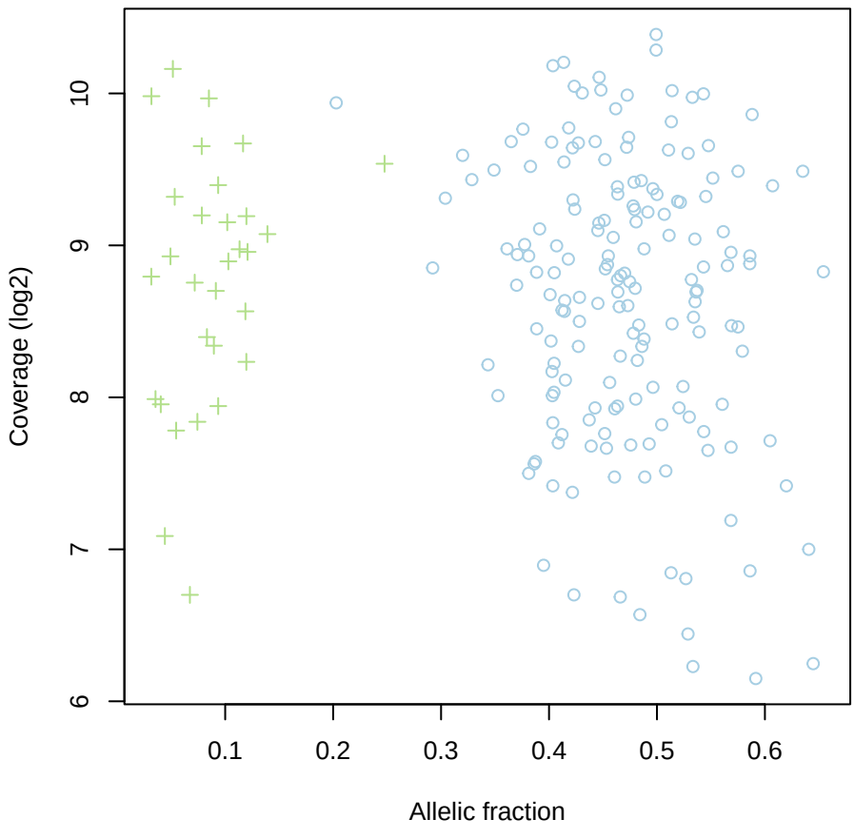

Purity: 0.24 Tumor ploidy: 2.25
0
1
2
3
4
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

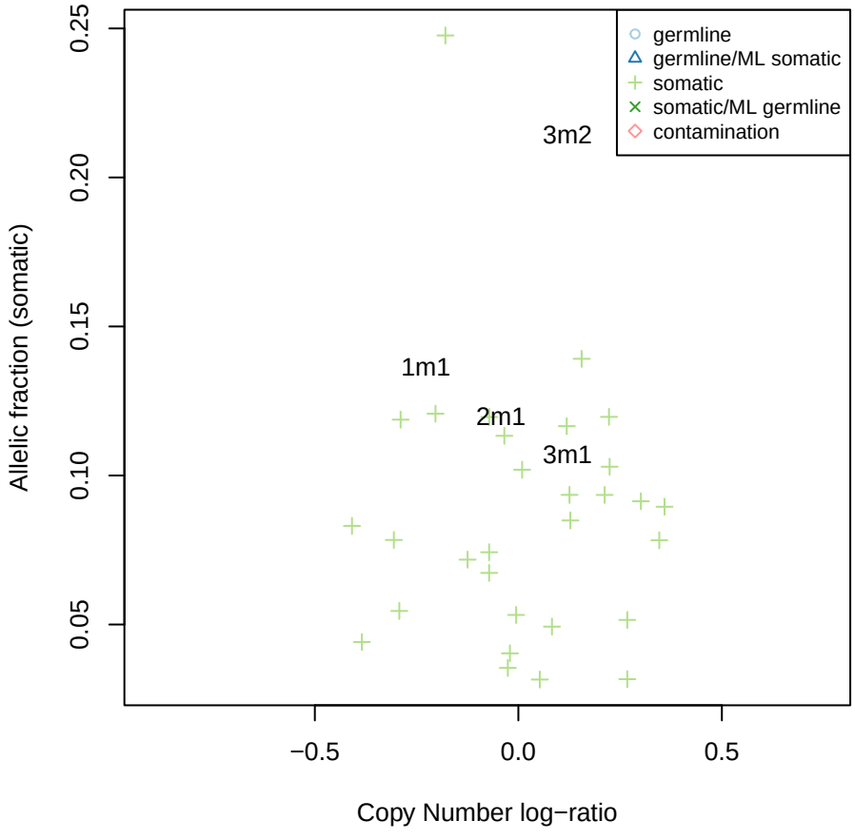

Purity: 0.24 Tumor ploidy: 2.25 SNV log−likelihood: −115.4 GoF: 92.5% Mean coverage: 486;543
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
17
19
20
B−Allele Frequency
0.2
0.3
0.4
0.5
0.6
0
50
100
150
SNV Index

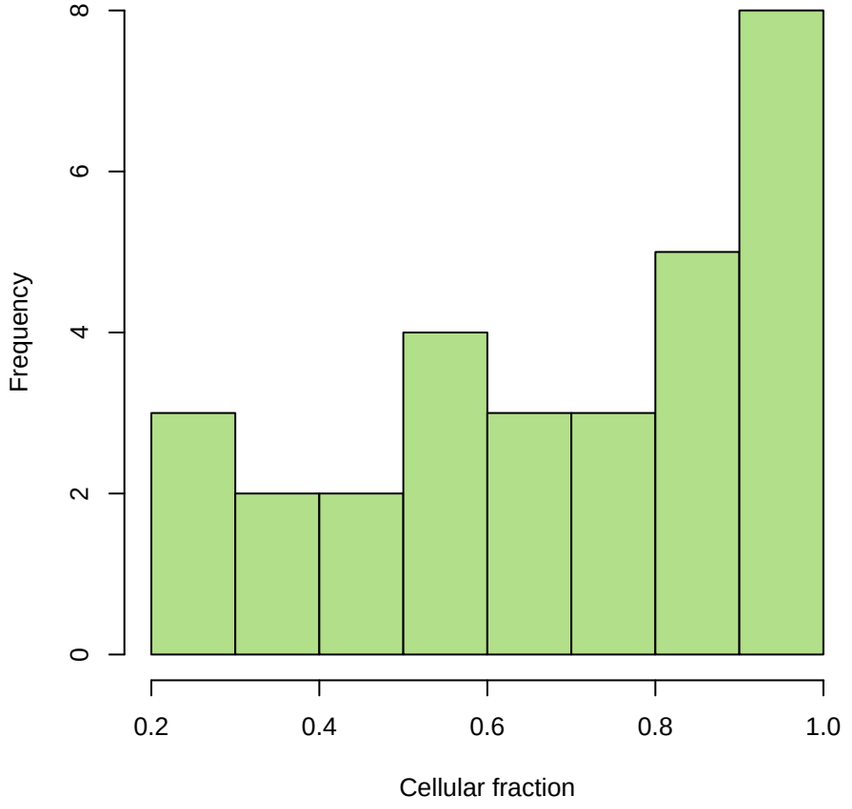

SCNA−fit log−likelihood: −10248.62
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
0
1
2
3
4
7
0
50
100
150
SNV Index

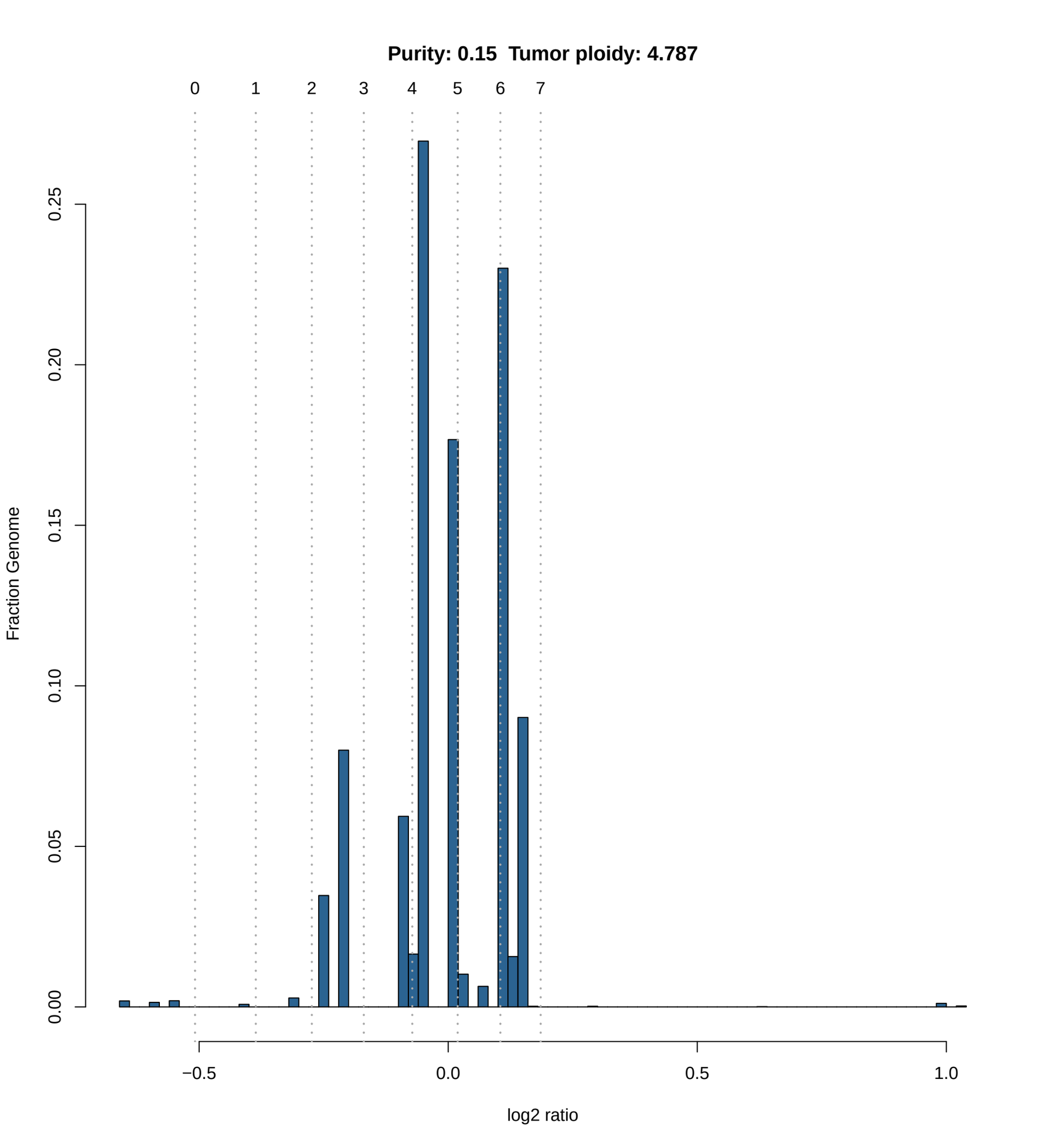

Maximum Likelihood Copy Number
0.0
0.5
1.0
1.5
2.0
2.5
3.0
0
50
100
150
SNV Index

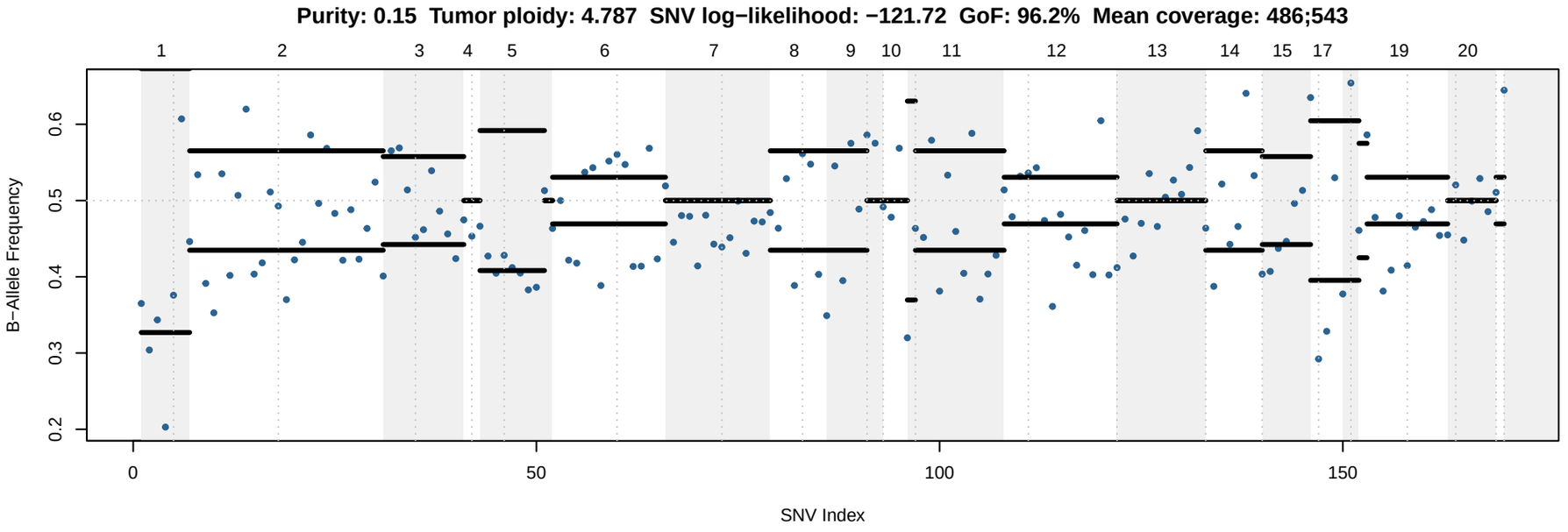

3m3
2m2
1m1
3m2
0m0
2m1
3m1
1m0
2m0
3m0
Allelic fraction (germline)
Copy Number log−ratio

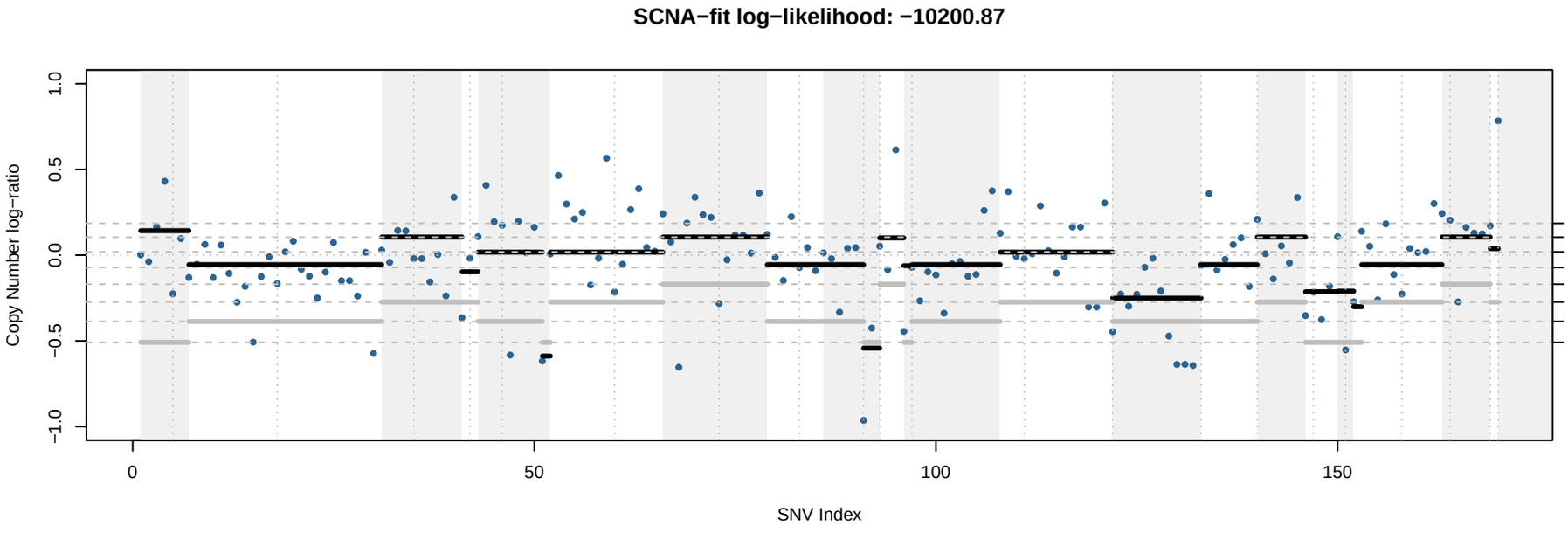

Coverage (log2)
Allelic fraction

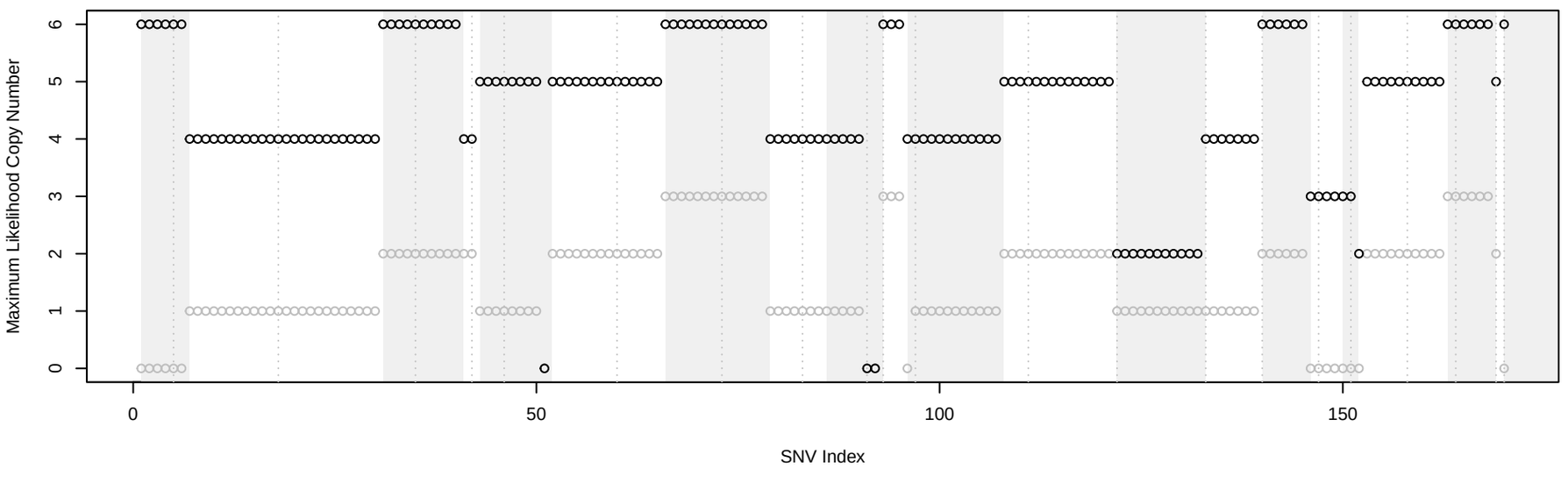

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m2
1m1
2m1
3m1
Allelic fraction (somatic)
Copy Number log−ratio

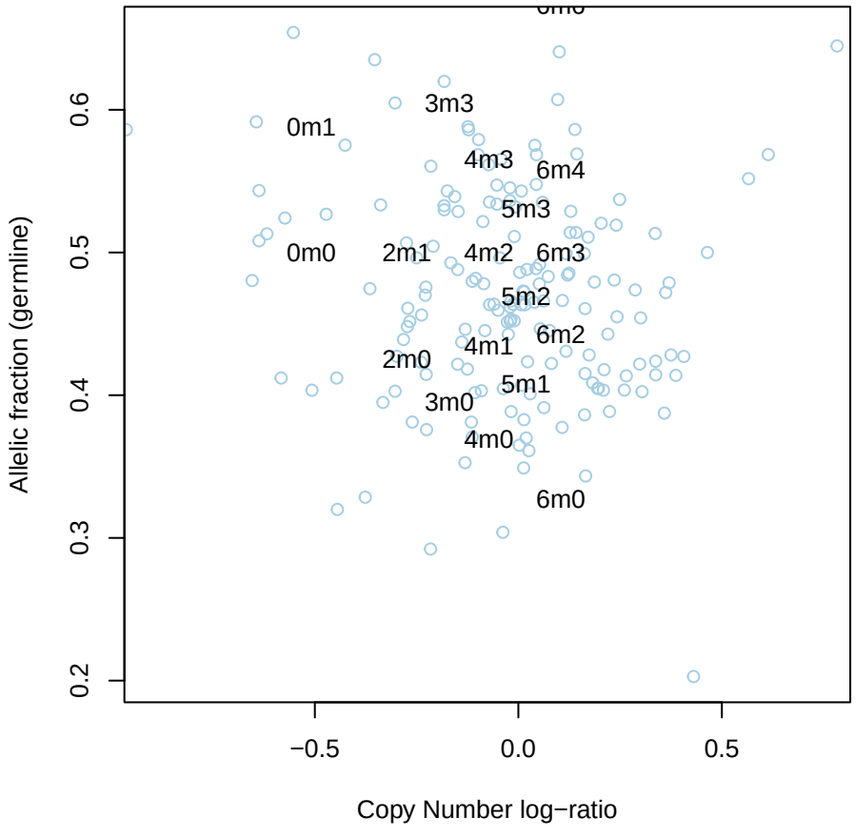

Frequency
Cellular fraction

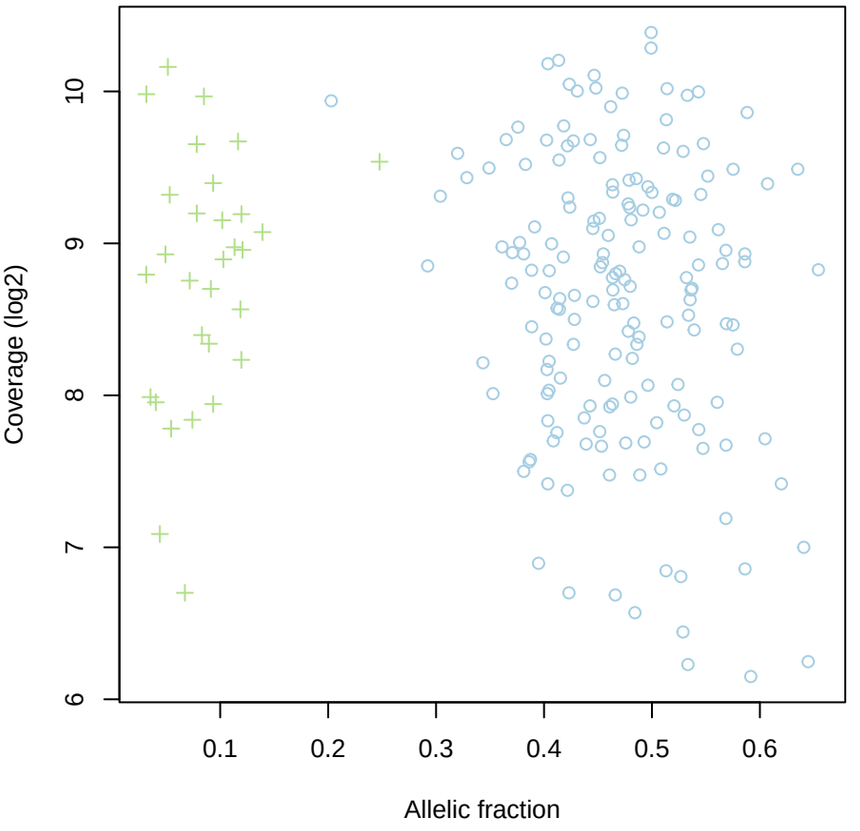

Purity: 0.15 Tumor ploidy: 4.787
0
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

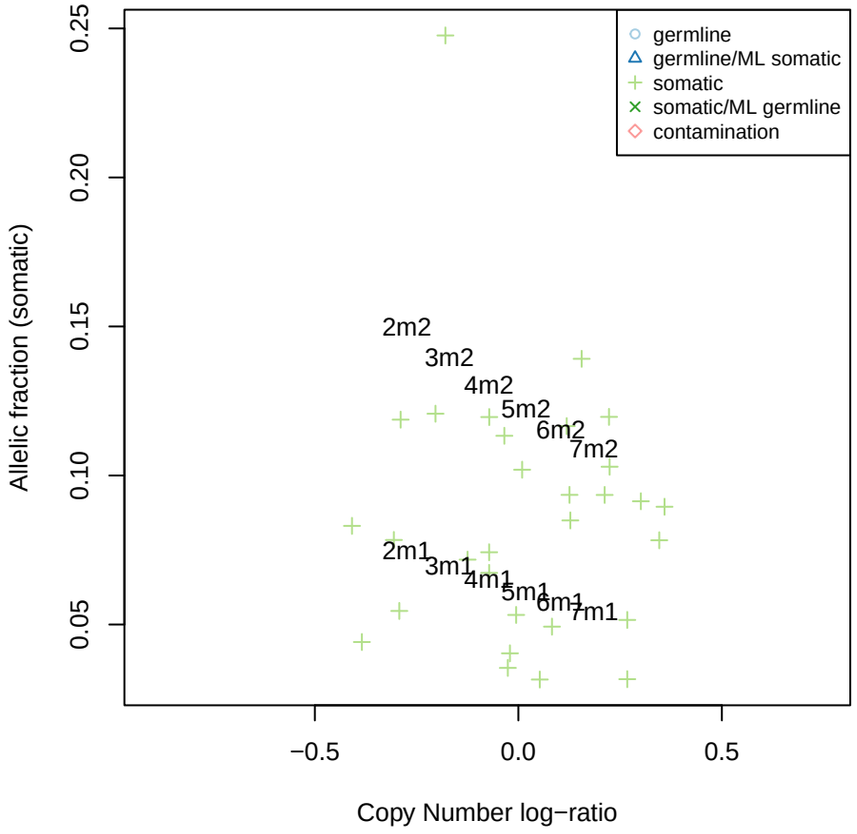

Purity: 0.15 Tumor ploidy: 4.787 SNV log−likelihood: −121.72 GoF: 96.2% Mean coverage: 486;543
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
17
19
20
B−Allele Frequency
0.2
0.3
0.4
0.5
0.6
0
50
100
150
SNV Index

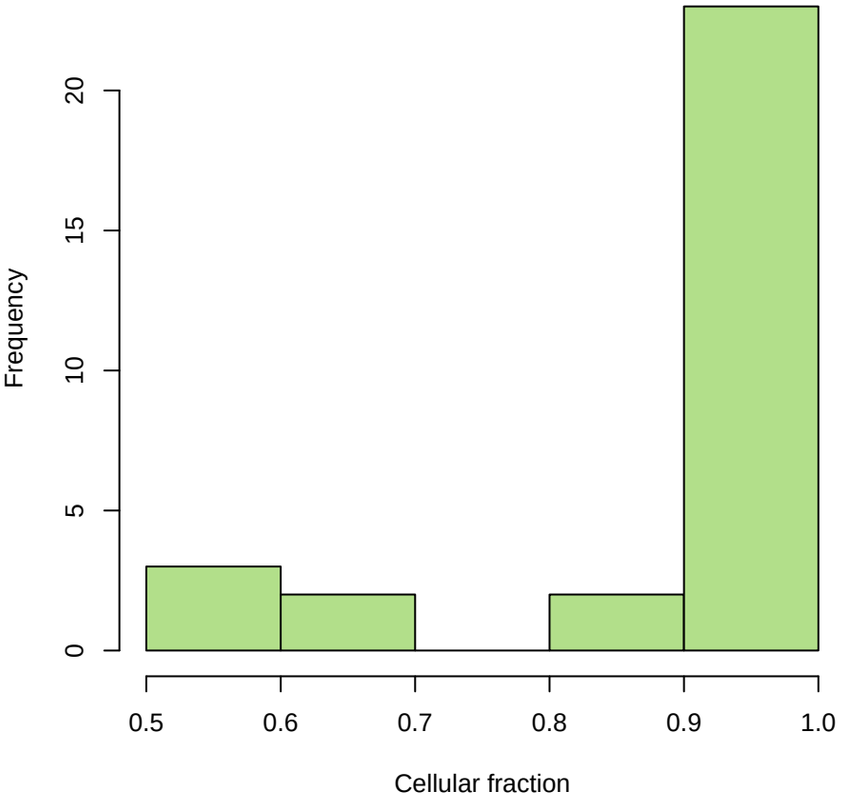

SCNA−fit log−likelihood: −10200.87
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
0
2
4
6
0
50
100
150
SNV Index

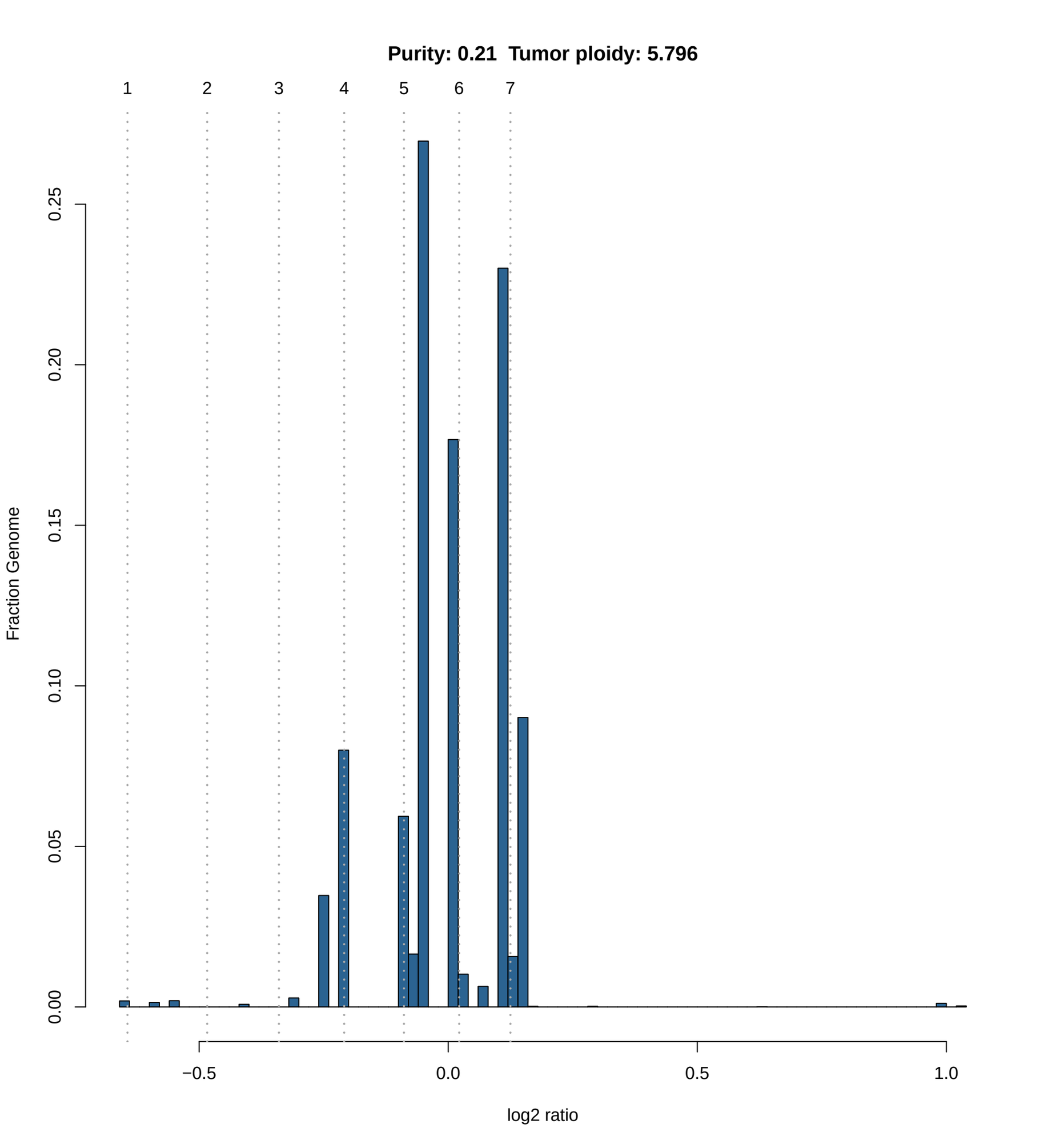

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
0
50
100
150
SNV Index

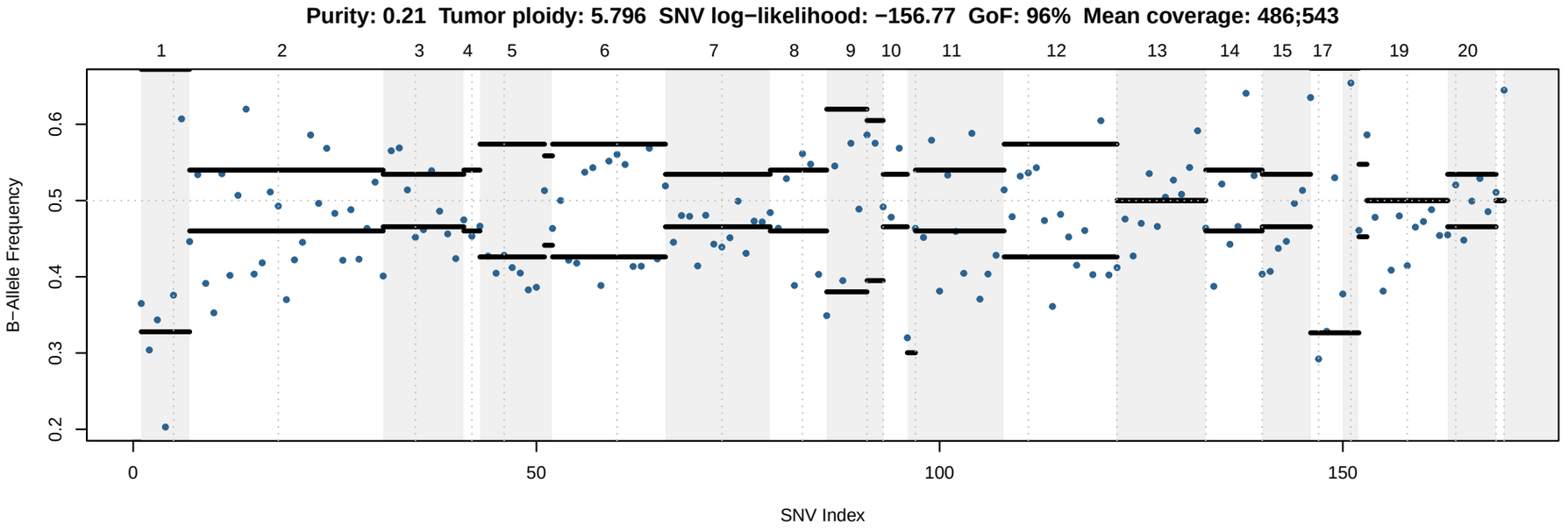

Allelic fraction (germline)
Copy Number log−ratio
0m1
3m3
4m3
6m4
5m3
0m0
2m1
4m2
6m3
5m2
6m2
4m1
2m0
5m1
3m0
4m0
6m0

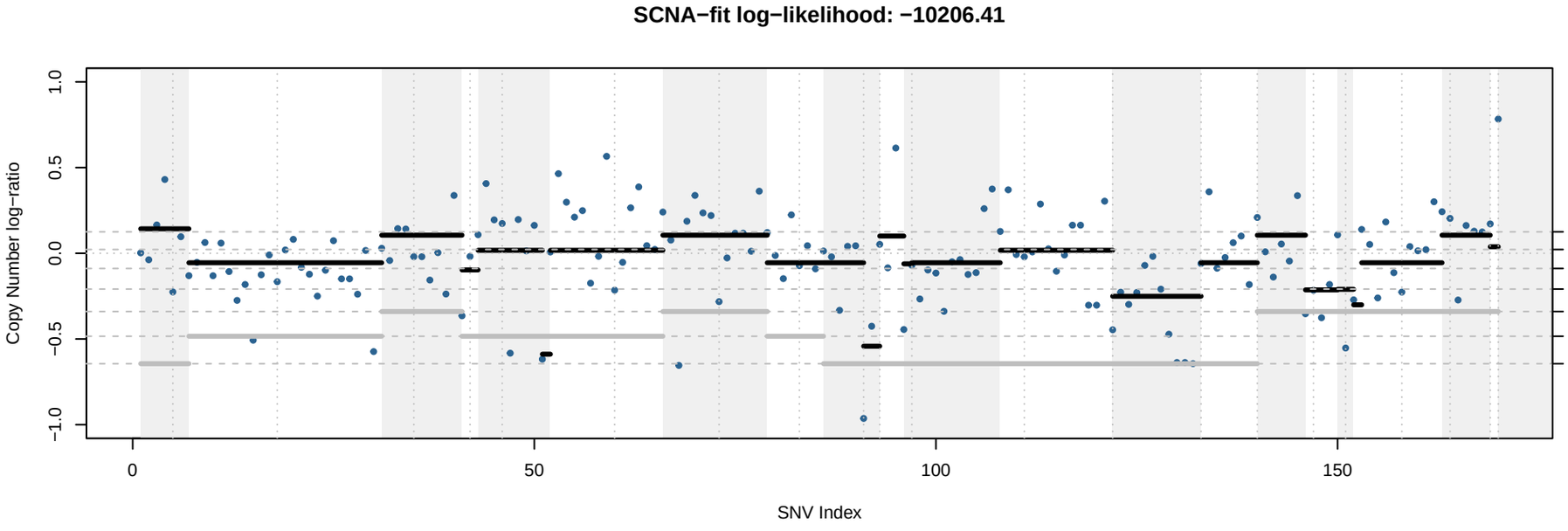

Coverage (log2)
Allelic fraction

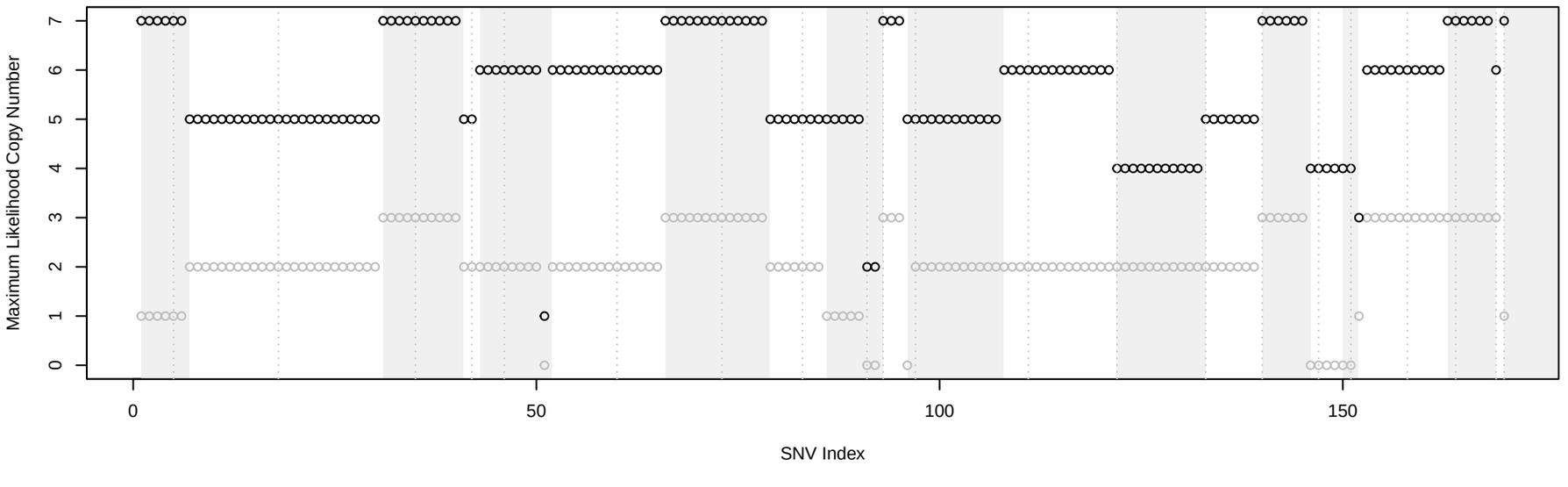

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m2
3m2
4m2
5m2
6m2
7m2
2m1
3m1
4m1
5m1
6m1
7m1

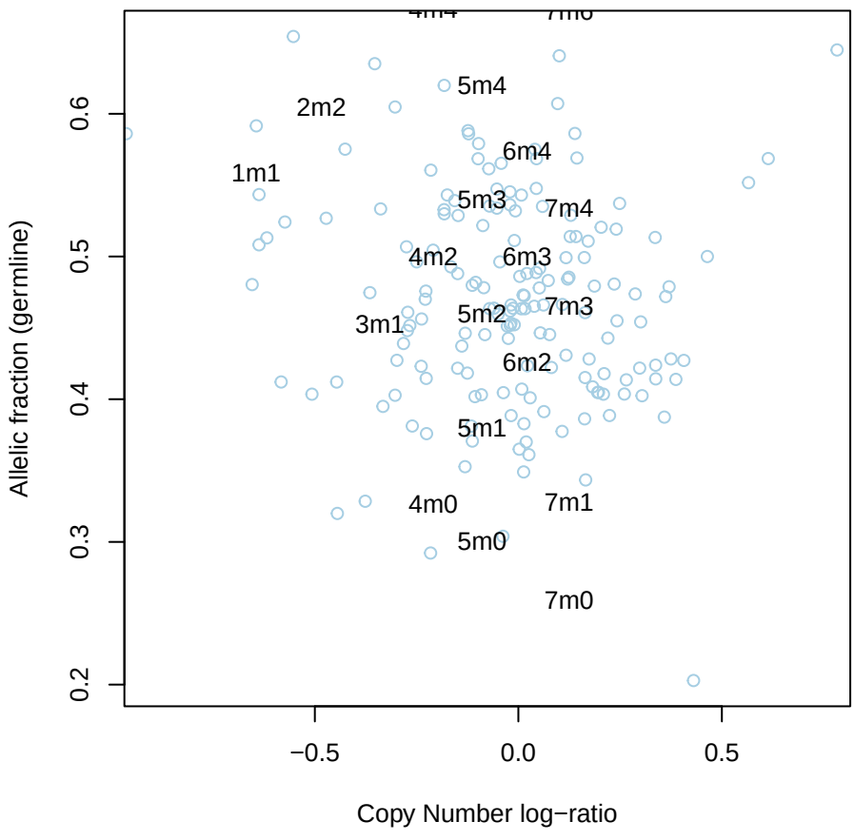

Frequency
Cellular fraction

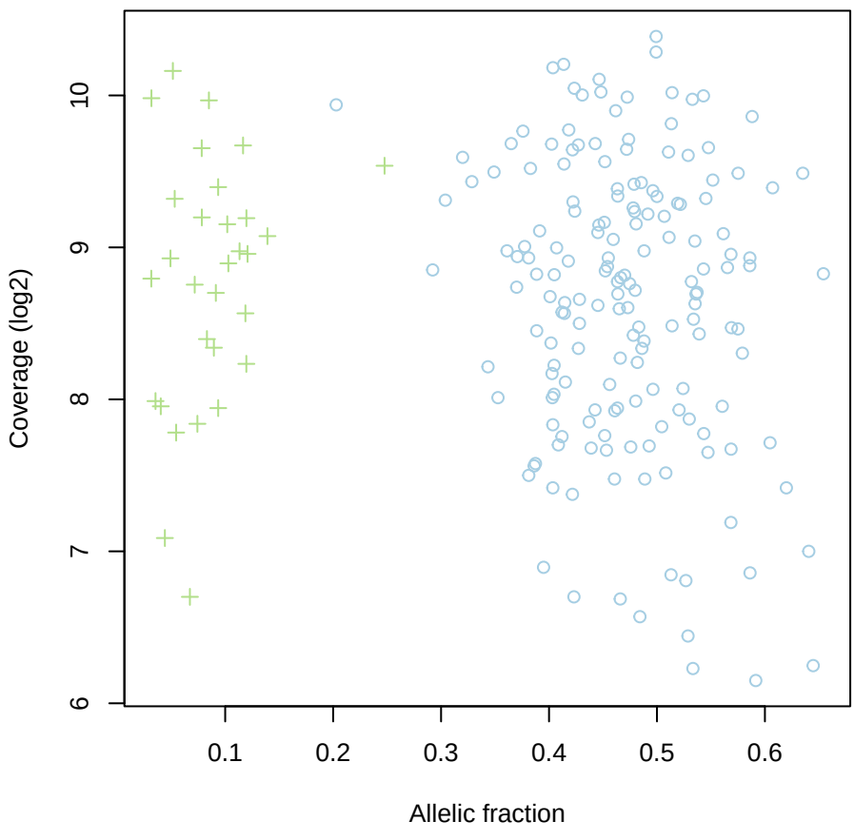

Purity: 0.21 Tumor ploidy: 5.796
1
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

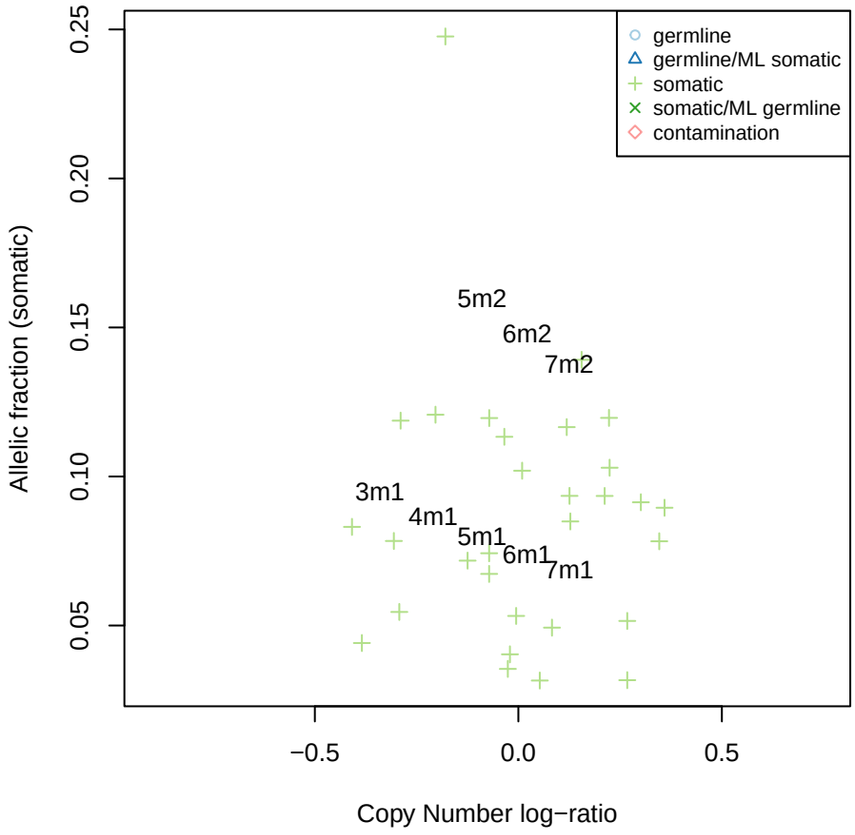

Purity: 0.21 Tumor ploidy: 5.796 SNV log−likelihood: −156.77 GoF: 96% Mean coverage: 486;543
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

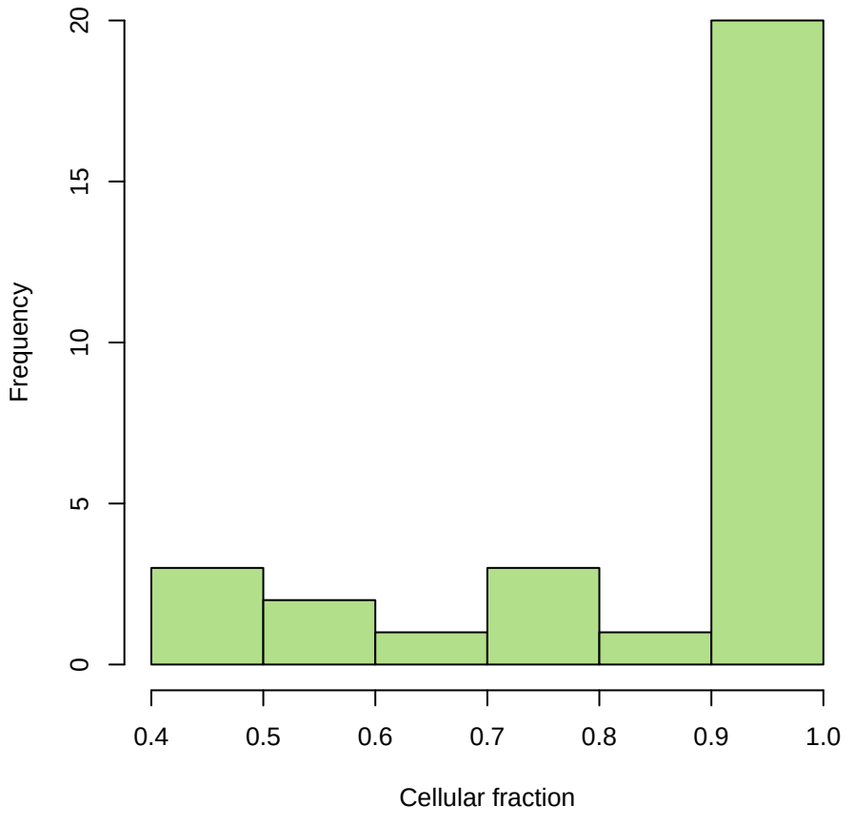

SCNA−fit log−likelihood: −10206.41
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 5 7
0 50 100 150
SNV Index

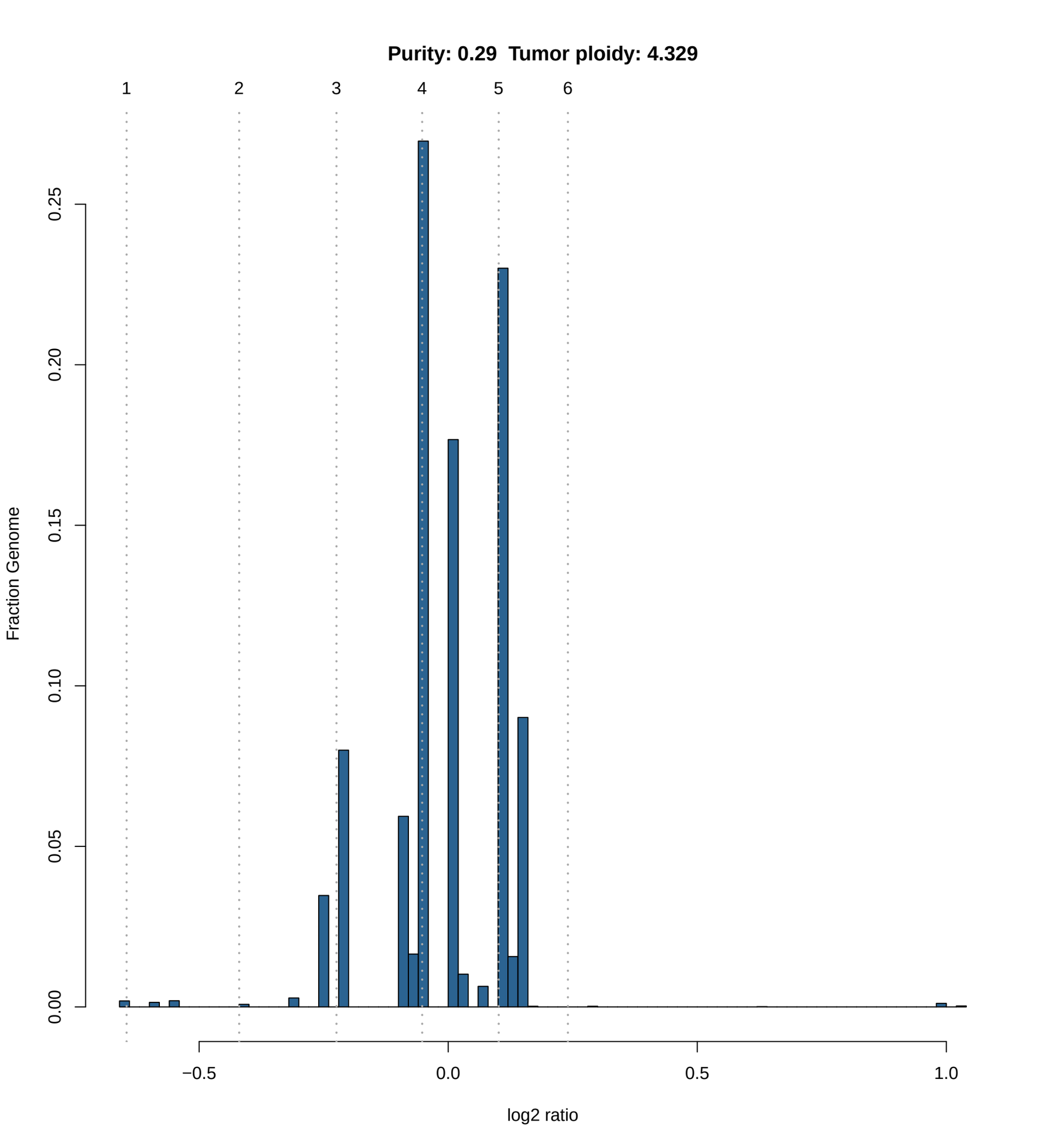

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

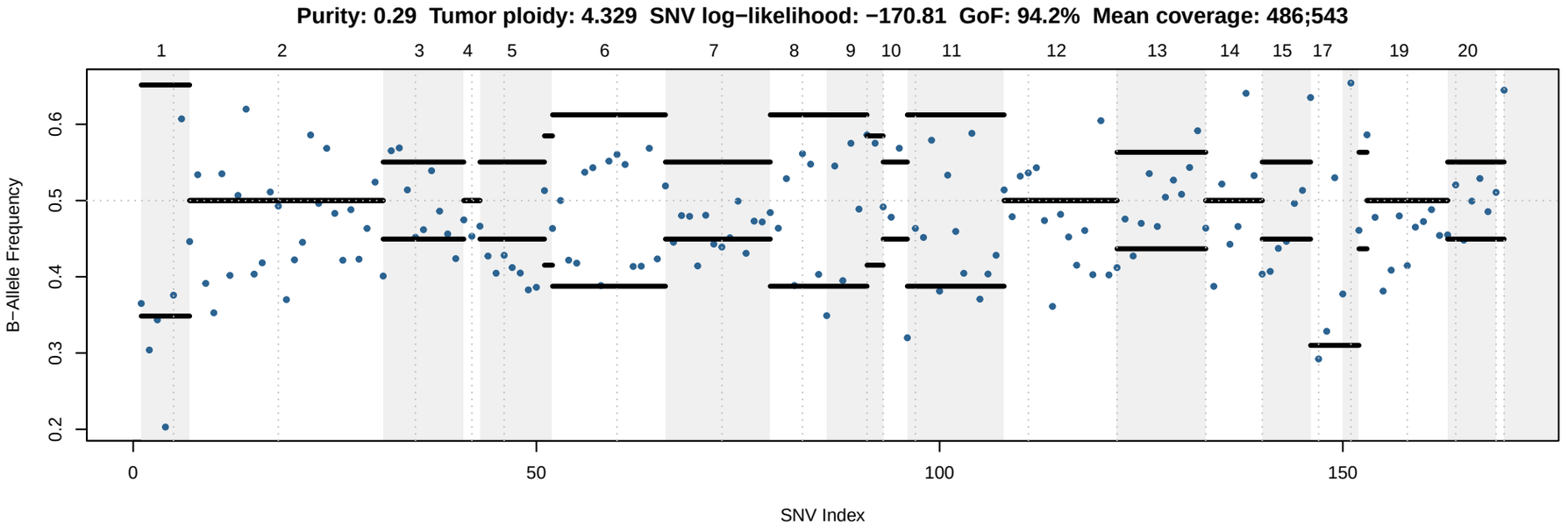

Allelic fraction (germline)
Copy Number log−ratio
0.2
0.3
0.4
0.5
0.6
−0.5
0.0
0.5
1m1
2m2
3m1
4m0
4m2
5m0
5m1
5m2
5m3
5m4
6m2
6m3
6m4
7m0
7m1
7m3
7m4

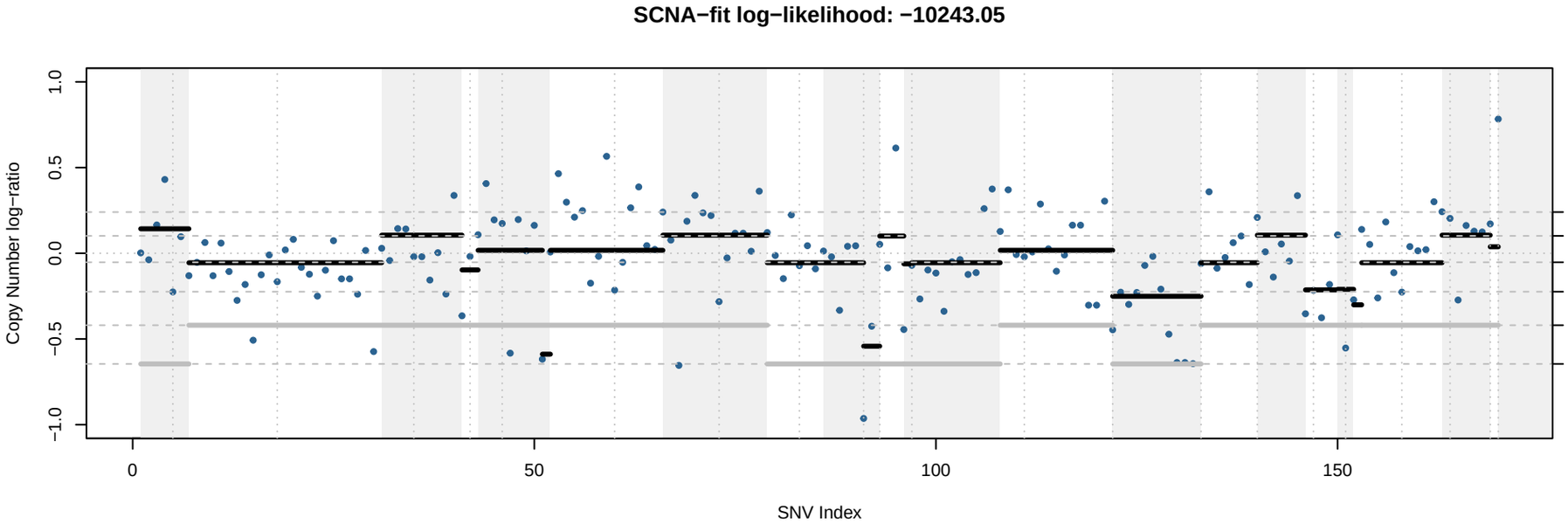

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

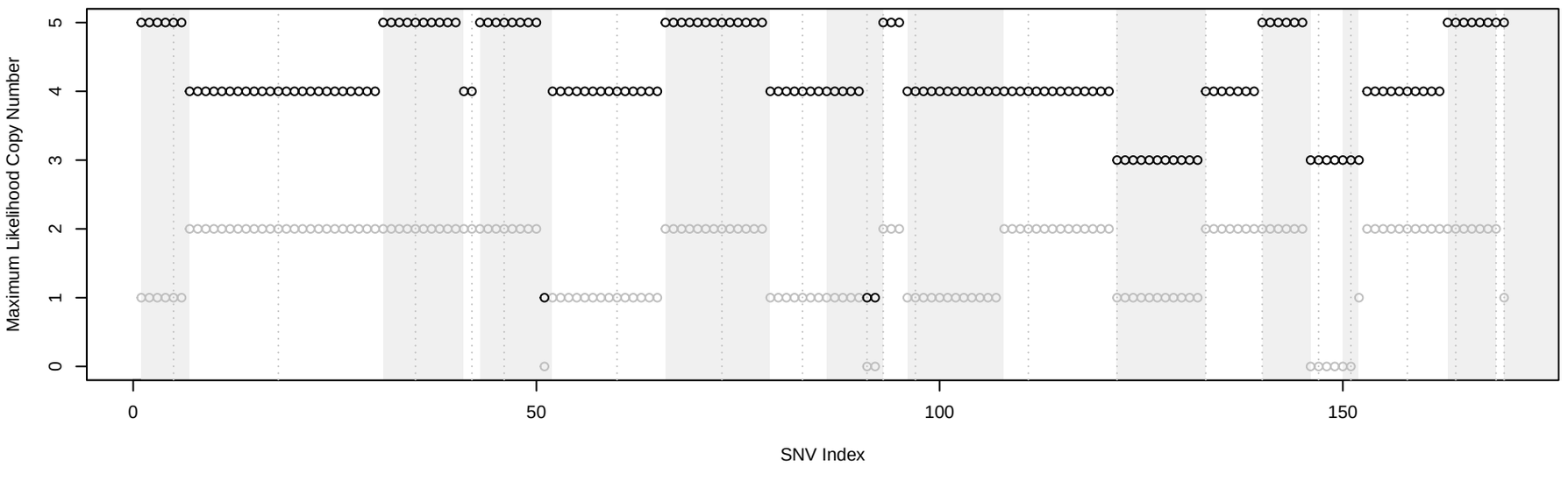

Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
0.25
−0.5
0.0
0.5
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
5m2
6m1
6m2
7m1
7m2

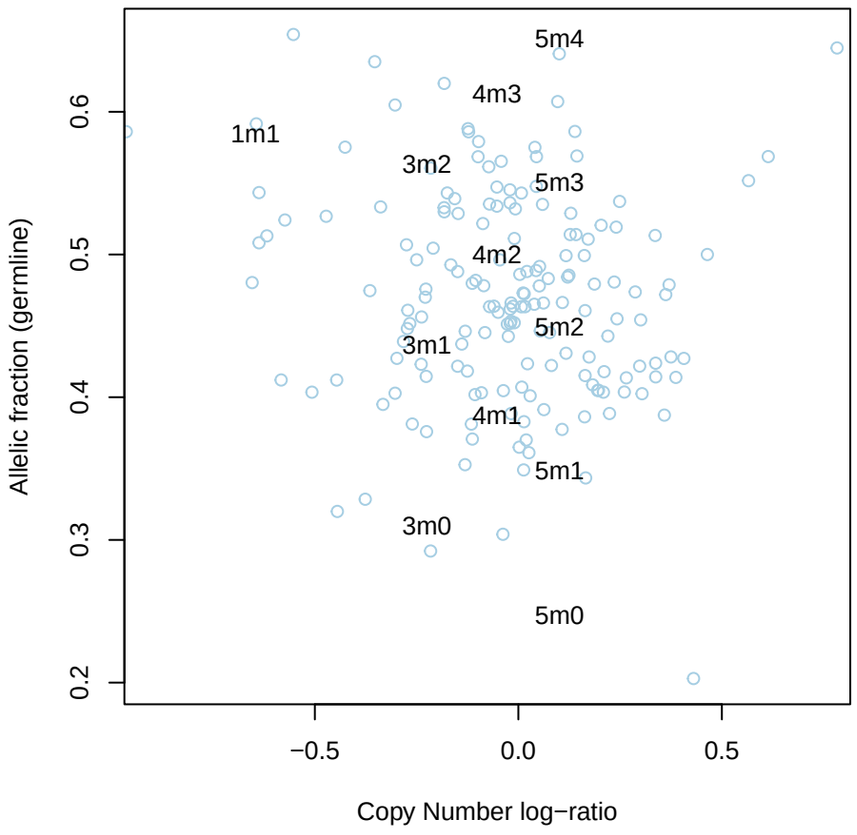

Frequency
Cellular fraction
0
5
10
15
20
0.4
0.5
0.6
0.7
0.8
0.9
1.0

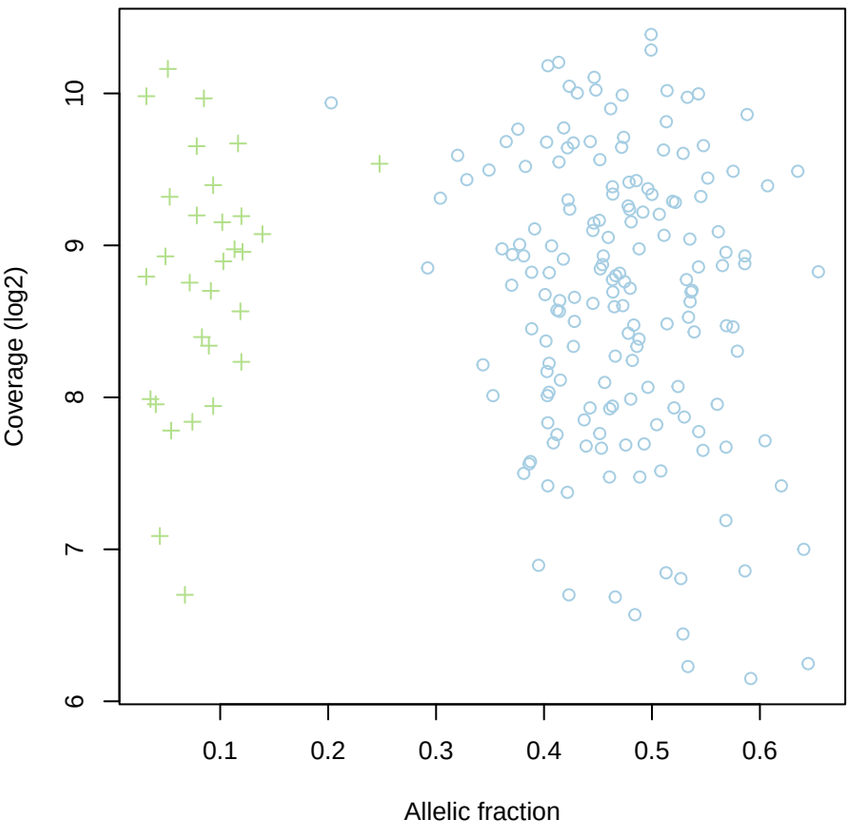

Purity: 0.29 Tumor ploidy: 4.329
1
2
3
4
5
6
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

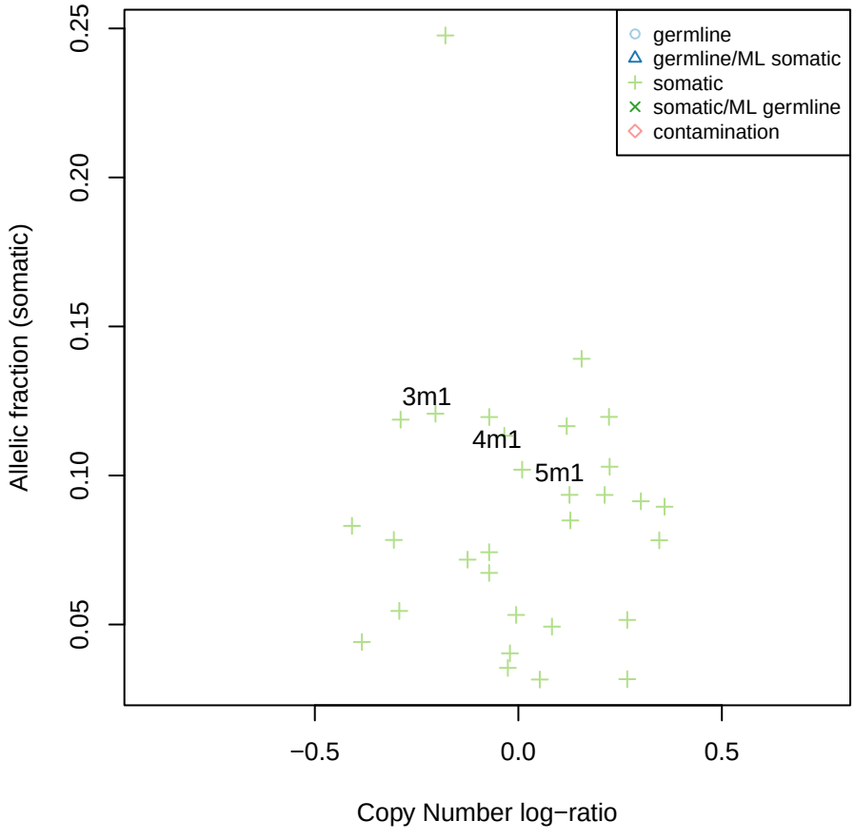

Purity: 0.29 Tumor ploidy: 4.329 SNV log−likelihood: −170.81 GoF: 94.2% Mean coverage: 486;543
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

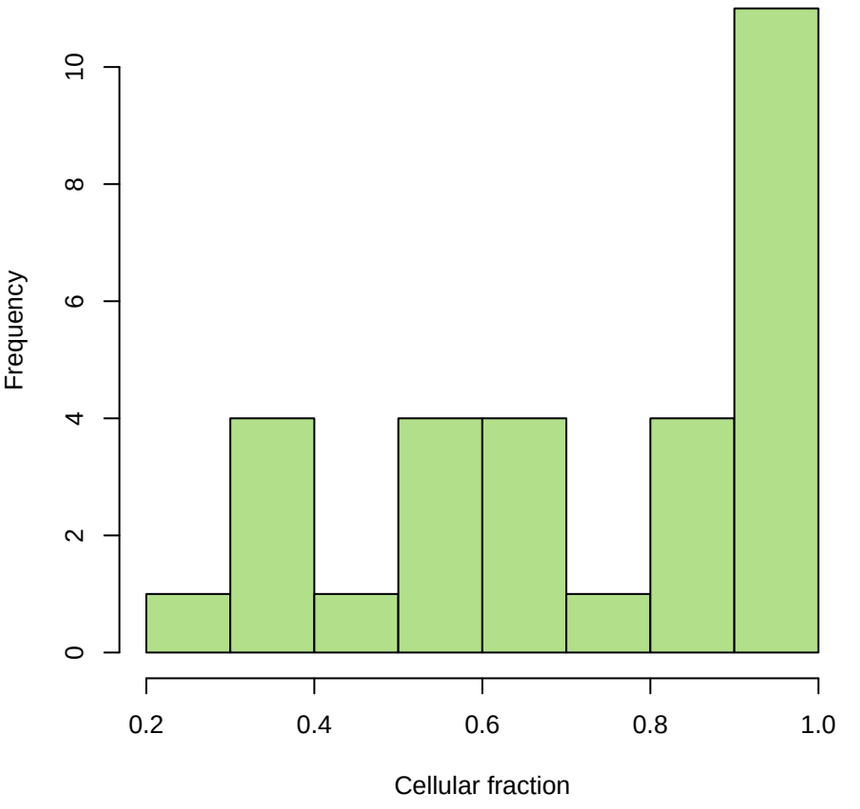

SCNA−fit log−likelihood: −10243.05
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5
0 50 100 150
SNV Index

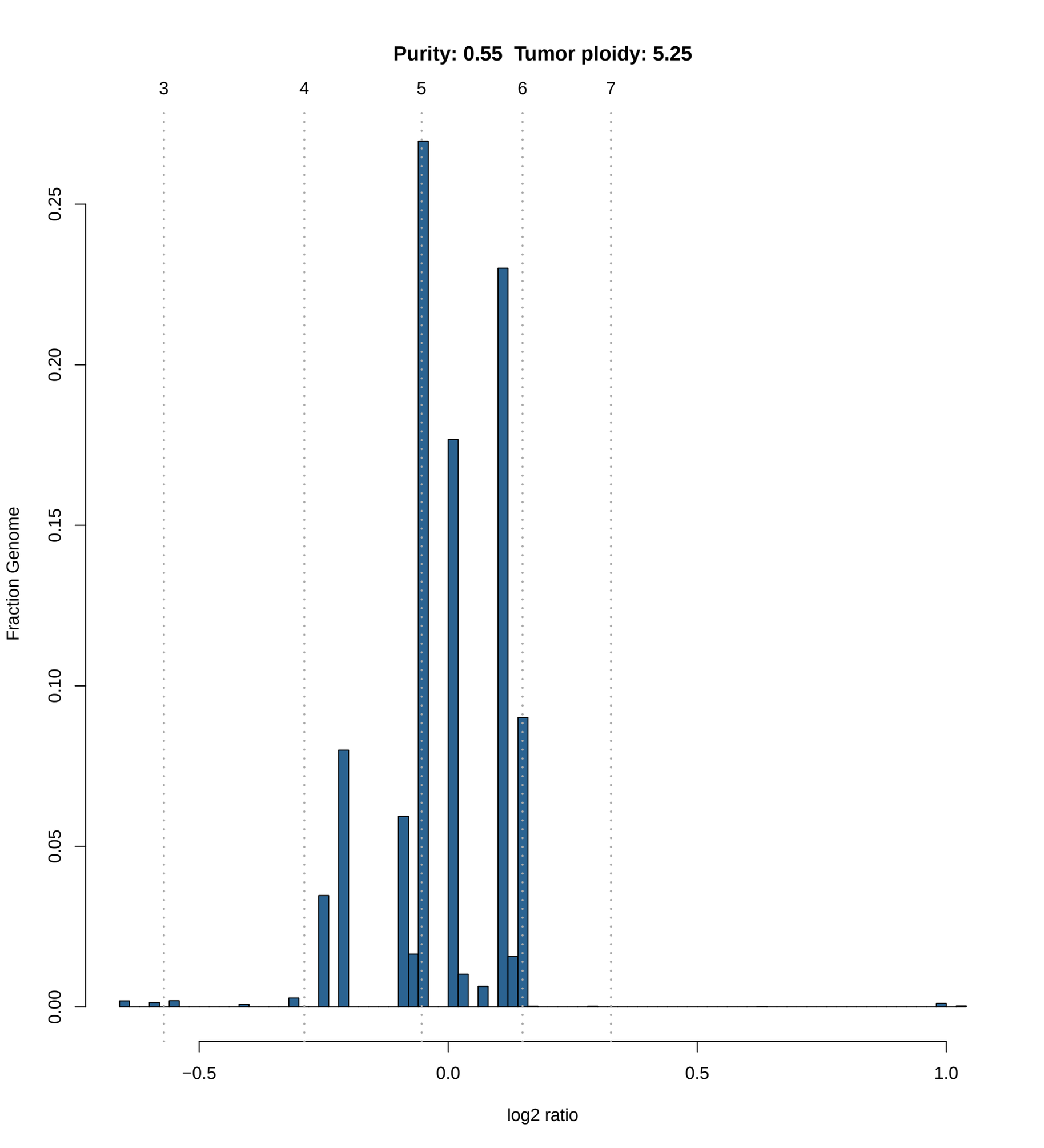

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

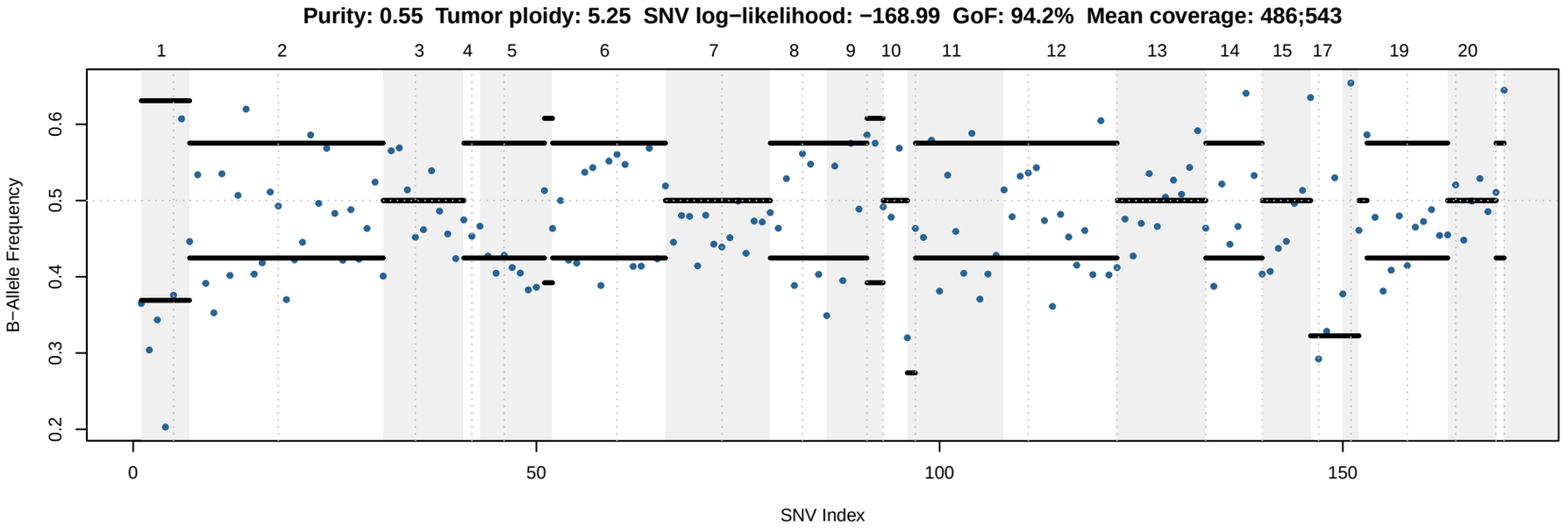

5m4
4m3
1m1
3m2
5m3
4m2
5m2
3m1
4m1
5m1
3m0
5m0
Allelic fraction (germline)
Copy Number log−ratio

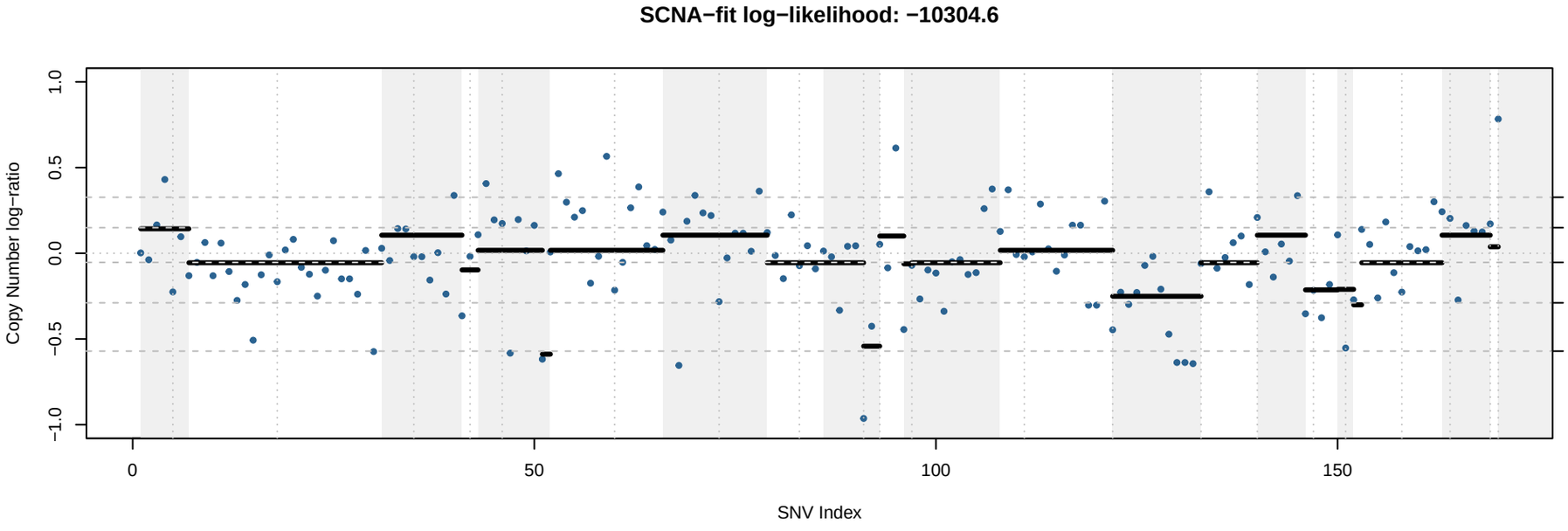

Coverage (log2)
Allelic fraction

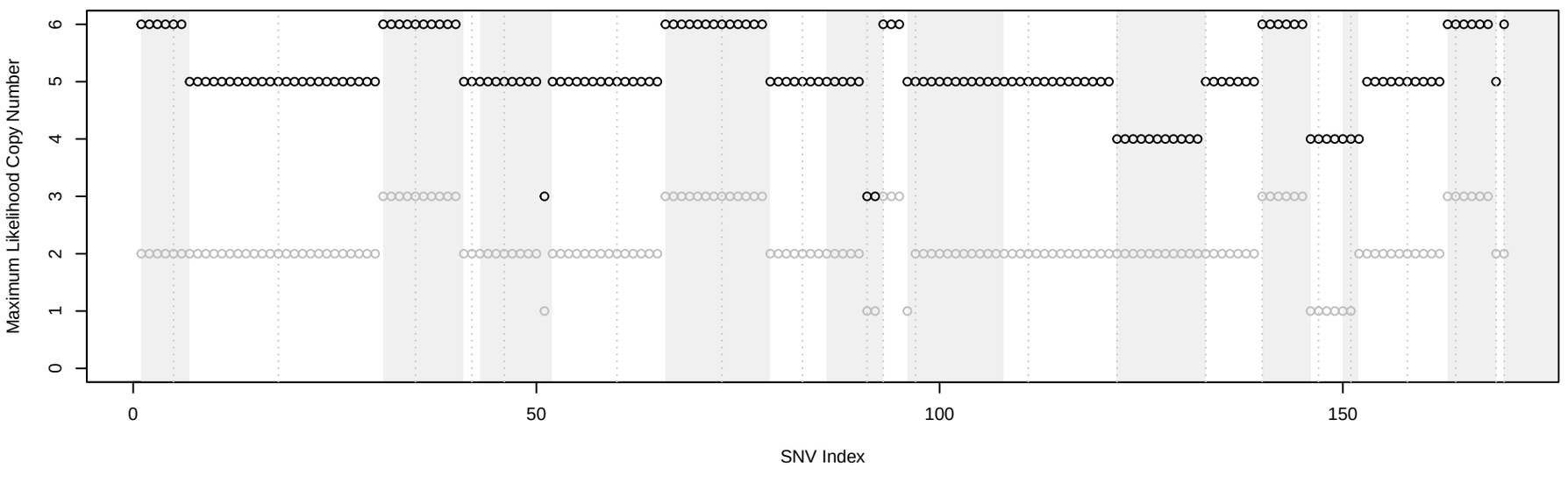

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
Allelic fraction (somatic)
Copy Number log−ratio

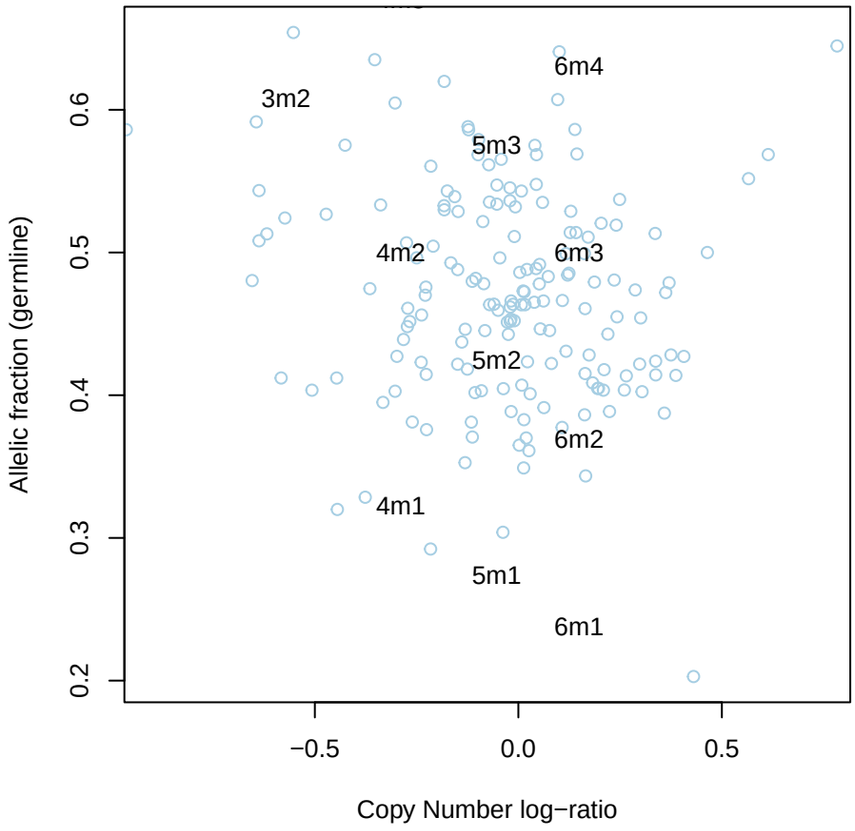

Frequency
Cellular fraction

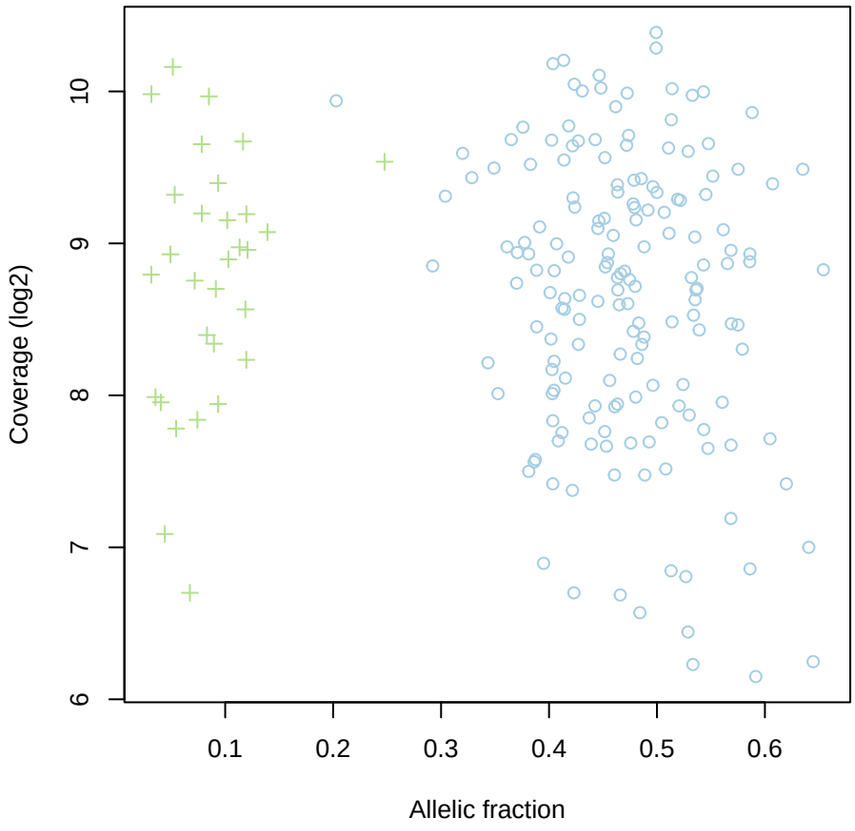

Purity: 0.55 Tumor ploidy: 5.25
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

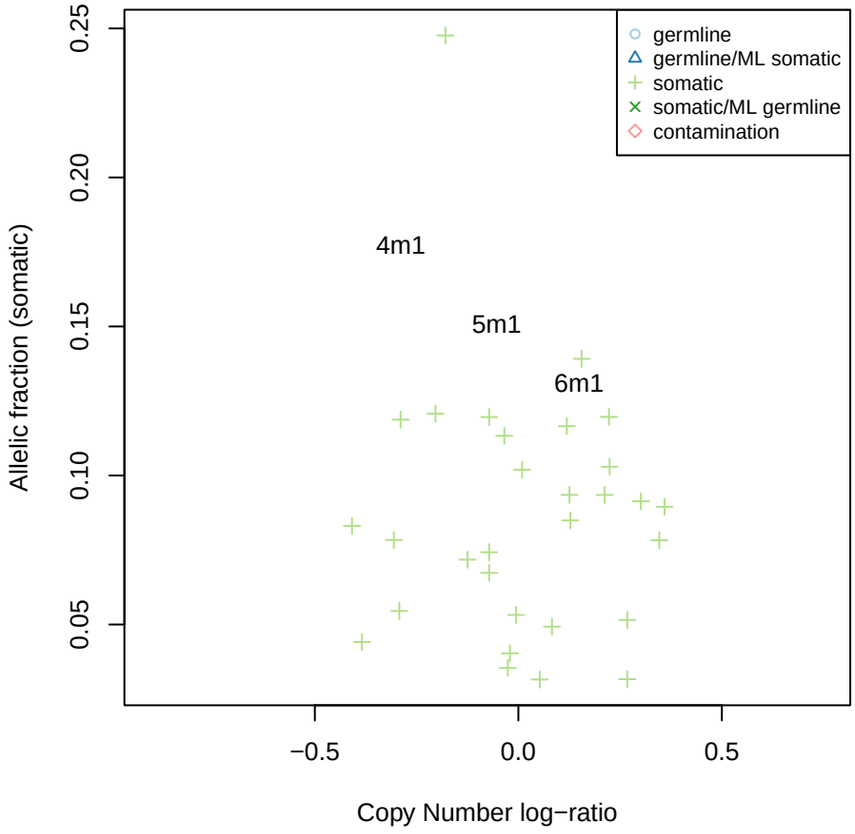

Purity: 0.55 Tumor ploidy: 5.25 SNV log−likelihood: −168.99 GoF: 94.2% Mean coverage: 486;543
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
17
19
20
B−Allele Frequency
0.2
0.3
0.4
0.5
0.6
0
50
100
150
SNV Index

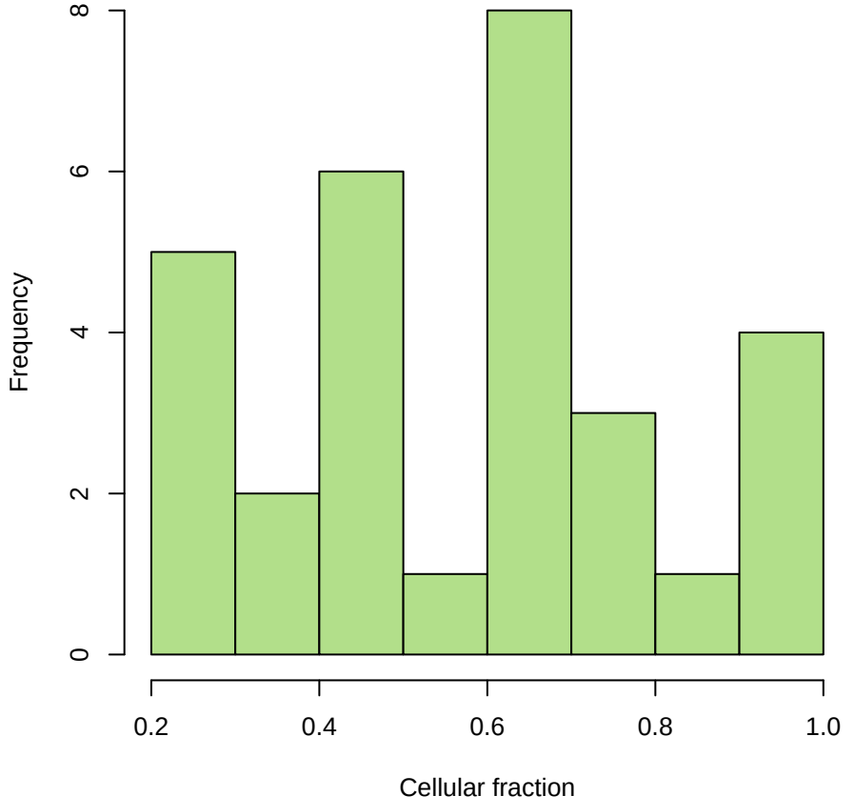

SCNA−fit log−likelihood: −10304.6
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
3
4
5
6
7
0
50
100
150
SNV Index

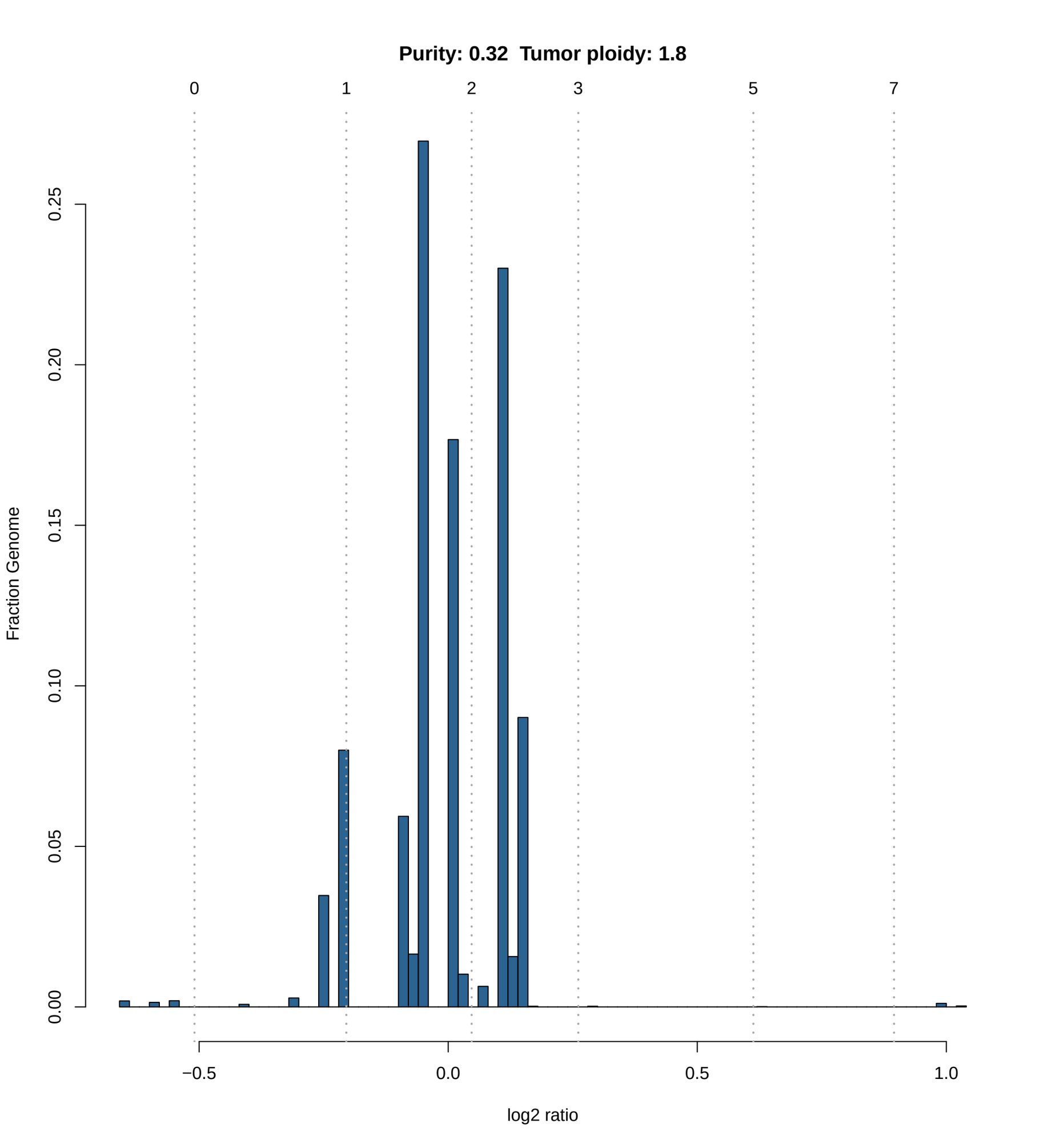

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
0
50
100
150
SNV Index

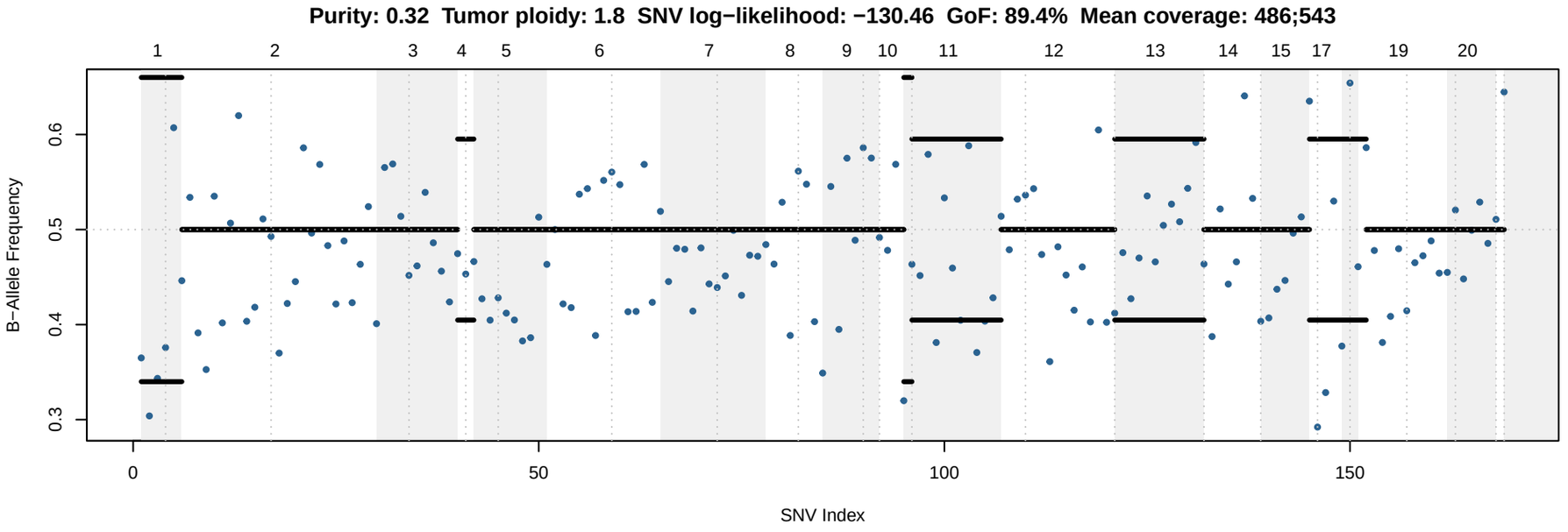

Allelic fraction (germline)
Copy Number log−ratio
3m2
6m4
5m3
4m2
6m3
5m2
6m2
4m1
5m1
6m1

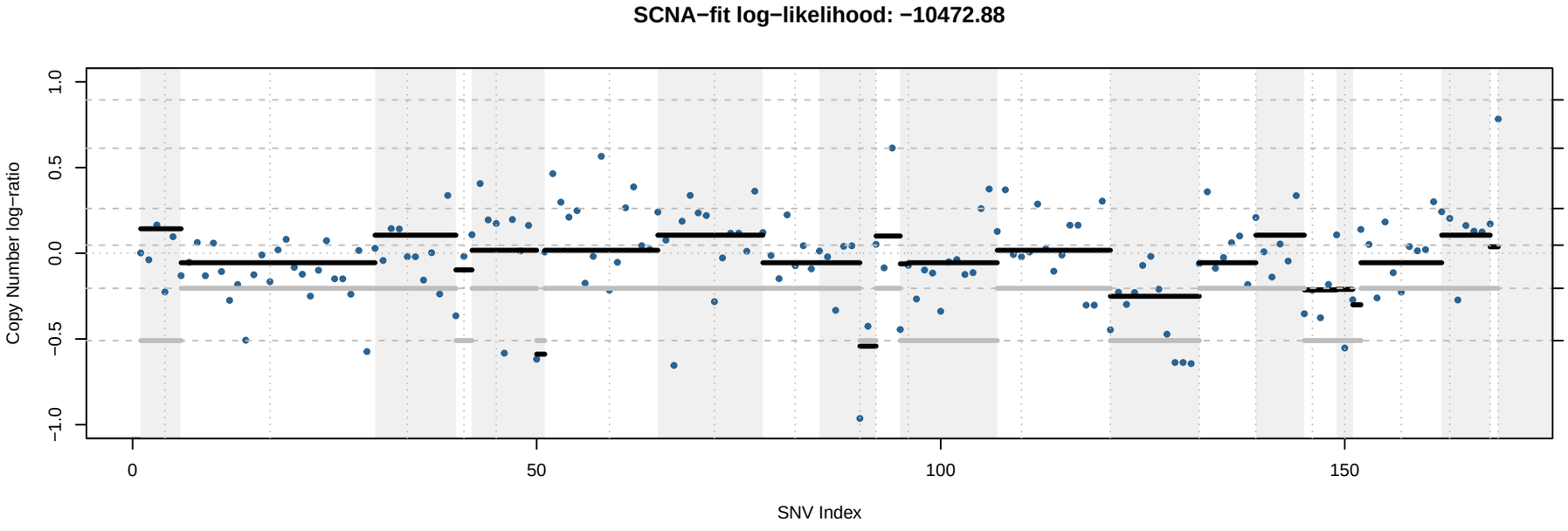

Coverage (log2)
Allelic fraction

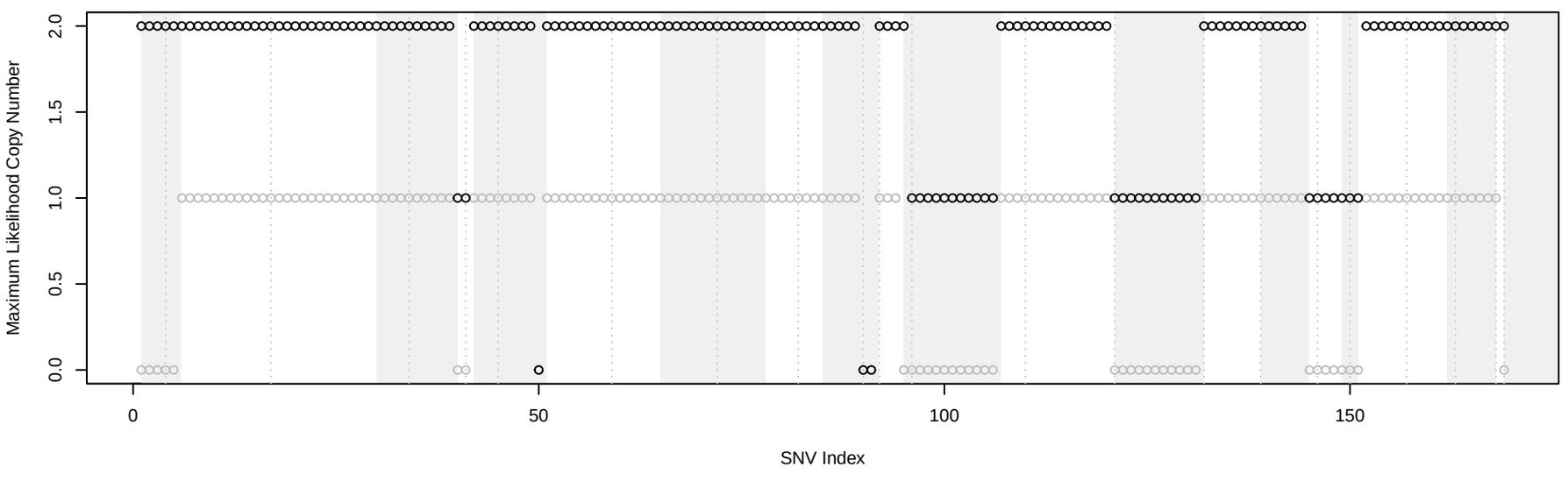

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1

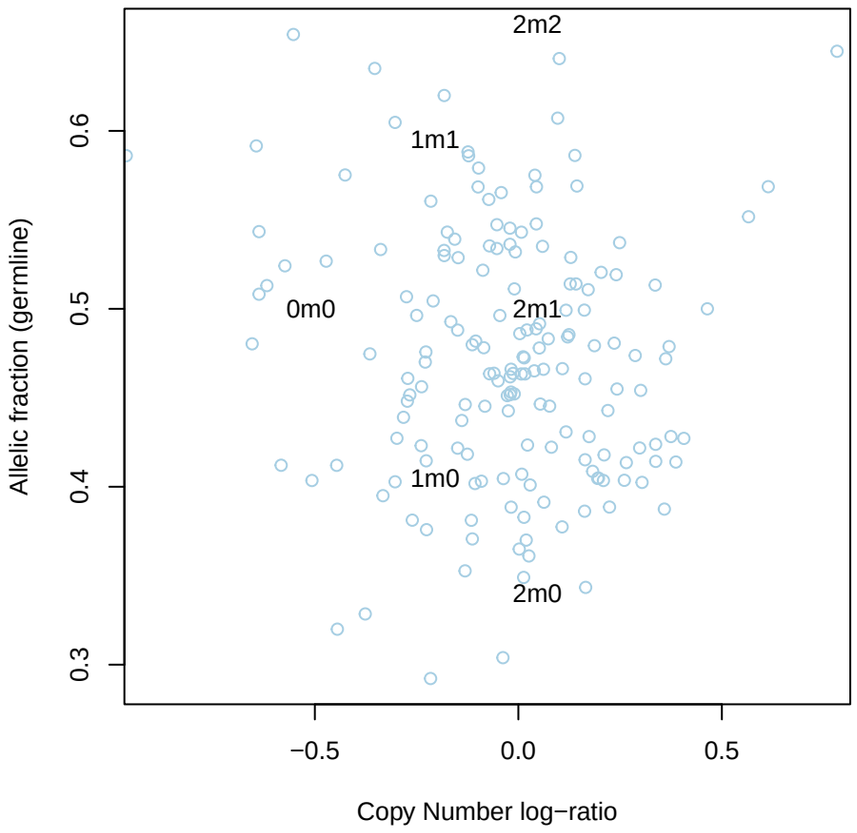

Frequency
Cellular fraction

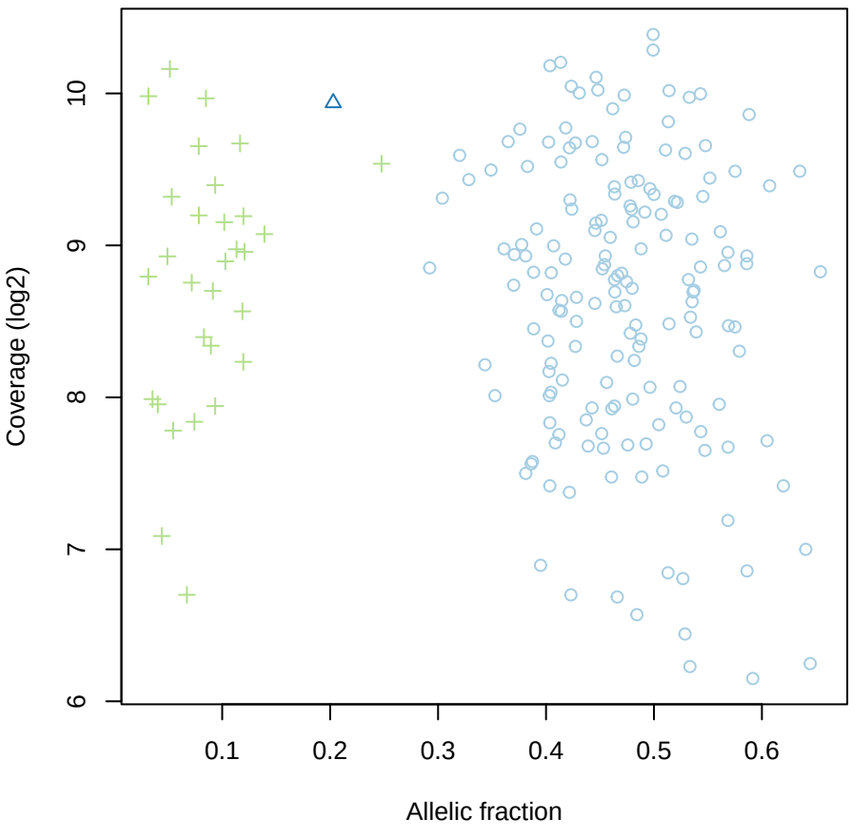

Purity: 0.32 Tumor ploidy: 1.8
0
1
2
3
5
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

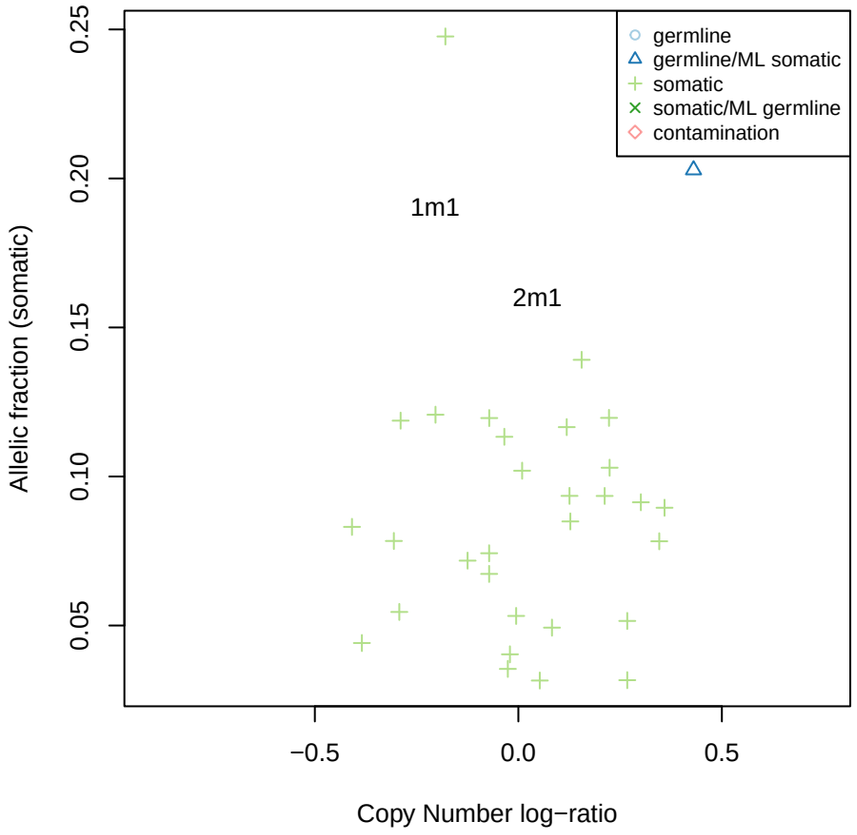

Purity: 0.32 Tumor ploidy: 1.8 SNV log−likelihood: −130.46 GoF: 89.4% Mean coverage: 486;543
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
17
19
20
B−Allele Frequency
0.3
0.4
0.5
0.6
0
50
100
150
SNV Index

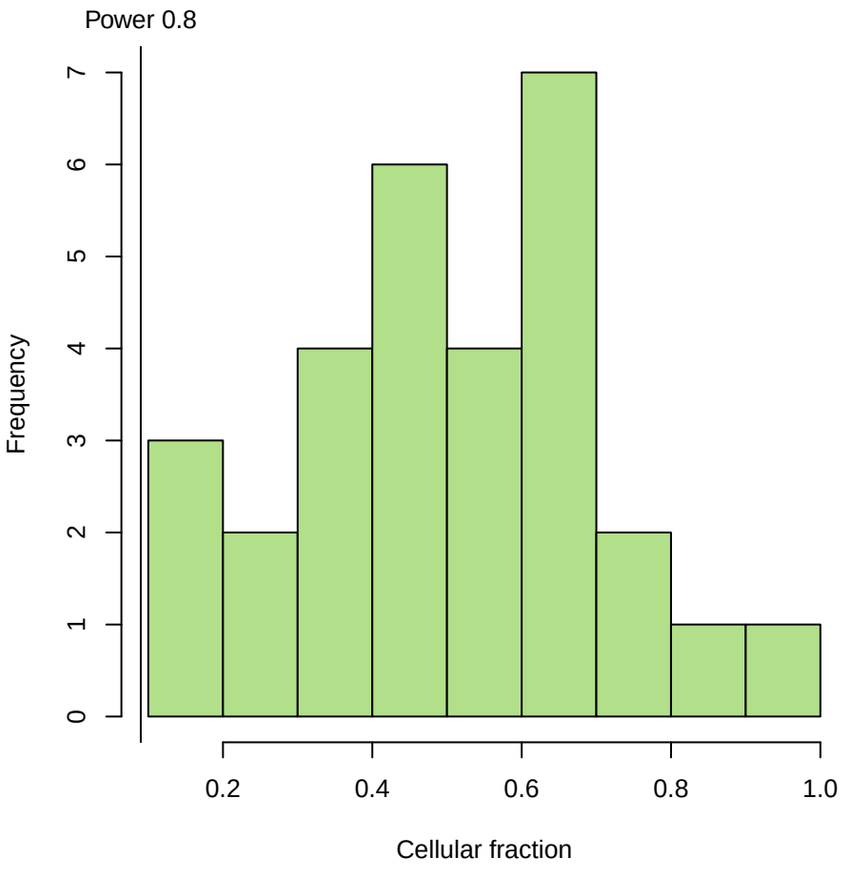

SCNA−fit log−likelihood: −10472.88
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
0
1
2
3
5
7
0
50
100
150
SNV Index

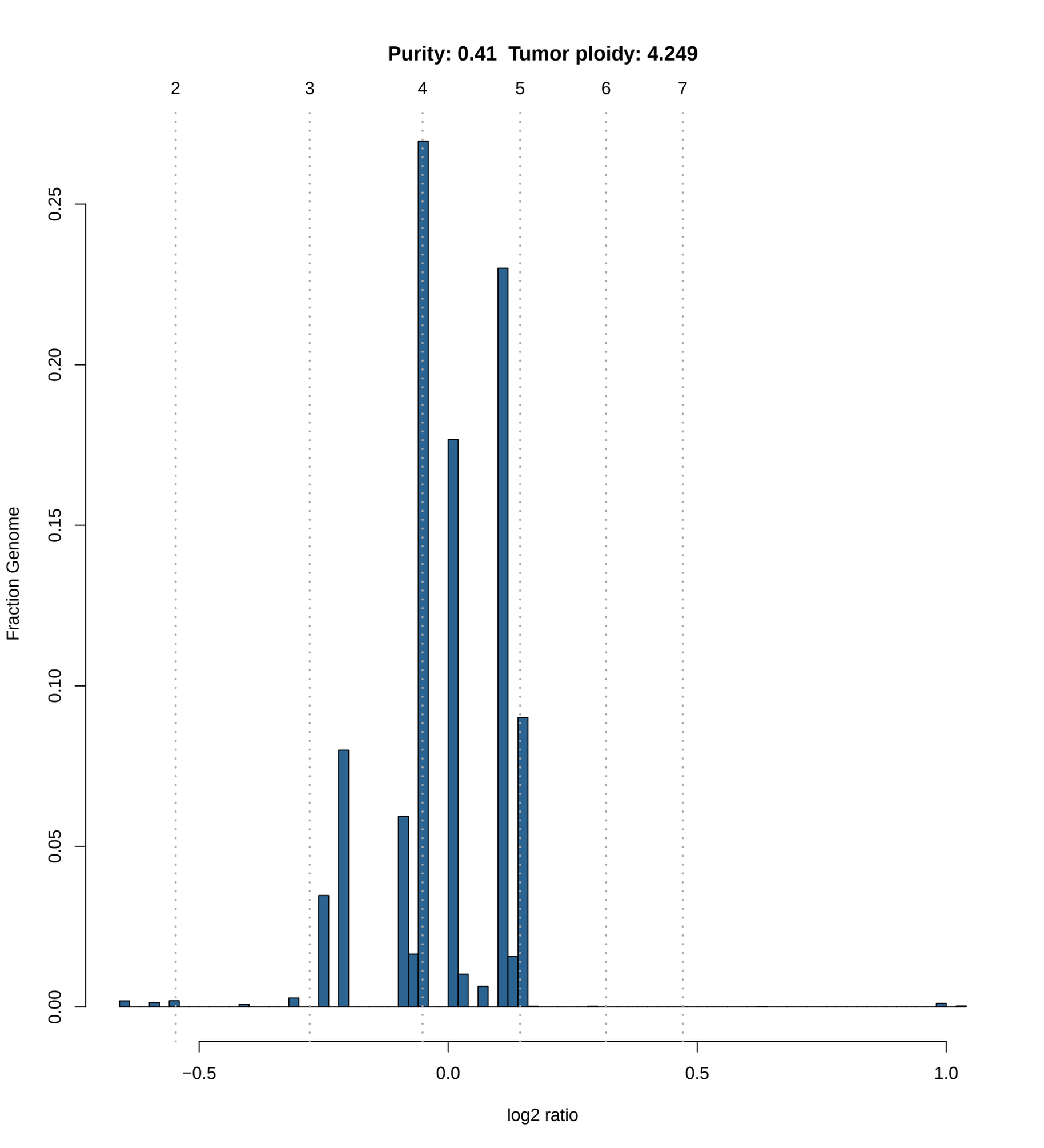

Maximum Likelihood Copy Number
0.0
0.5
1.0
1.5
2.0
0
50
100
150
SNV Index

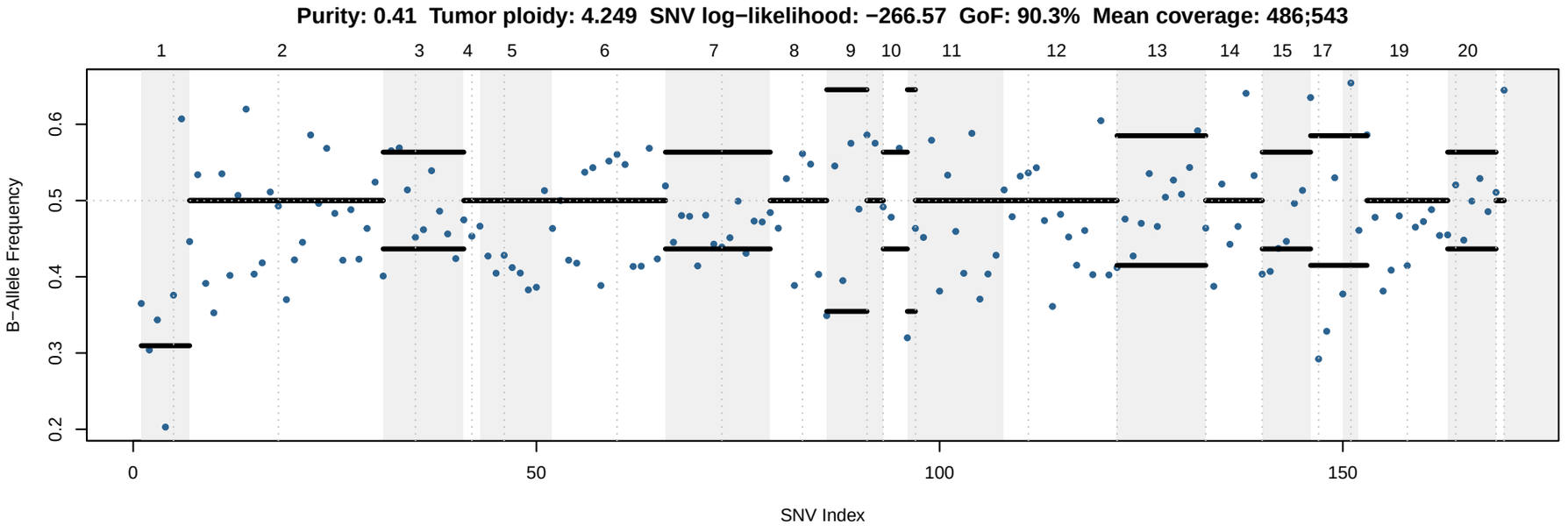

2m2
1m1
0m0
2m1
1m0
2m0
Allelic fraction (germline)
Copy Number log−ratio

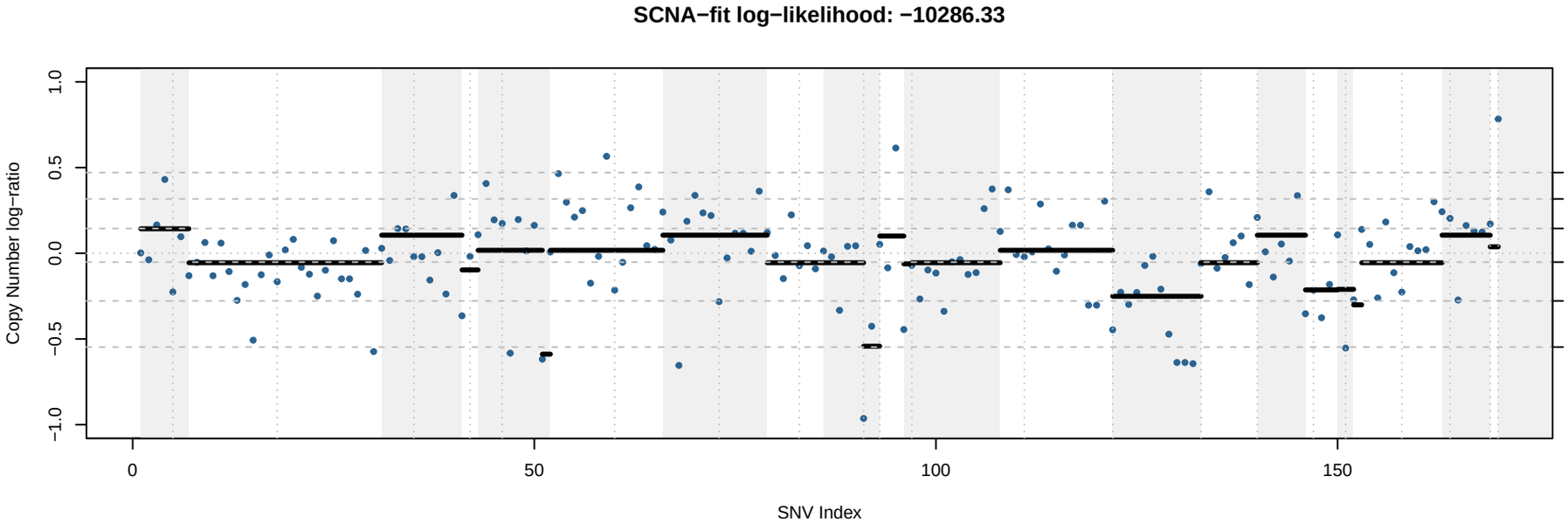

Coverage (log2)
Allelic fraction

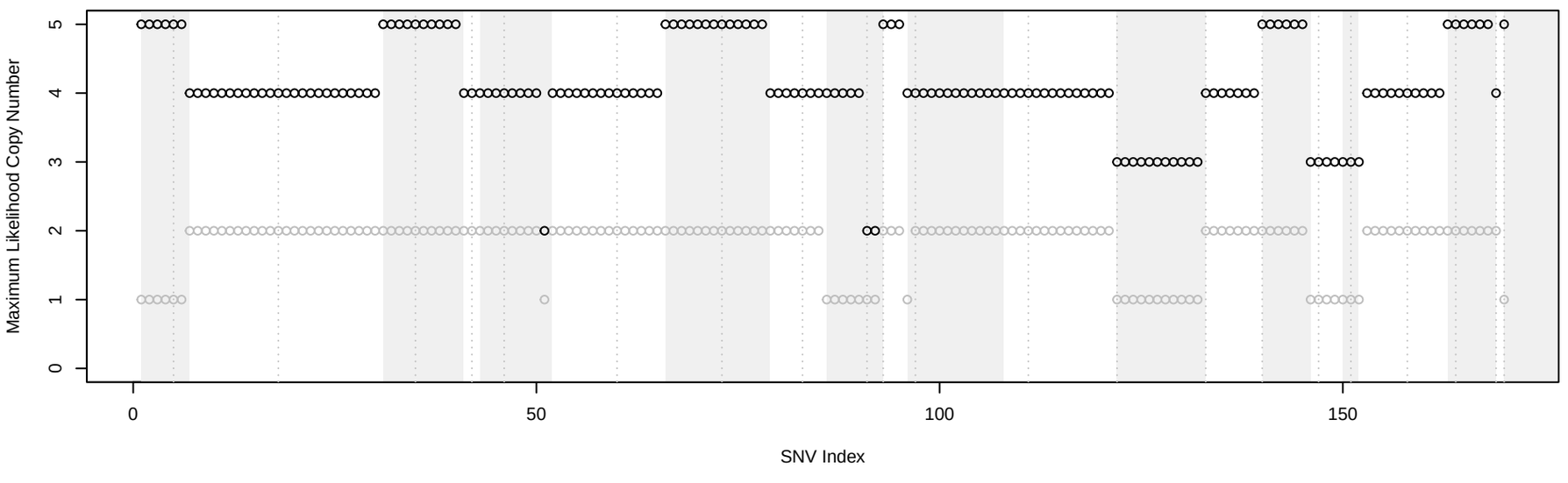

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
Allelic fraction (somatic)
Copy Number log−ratio

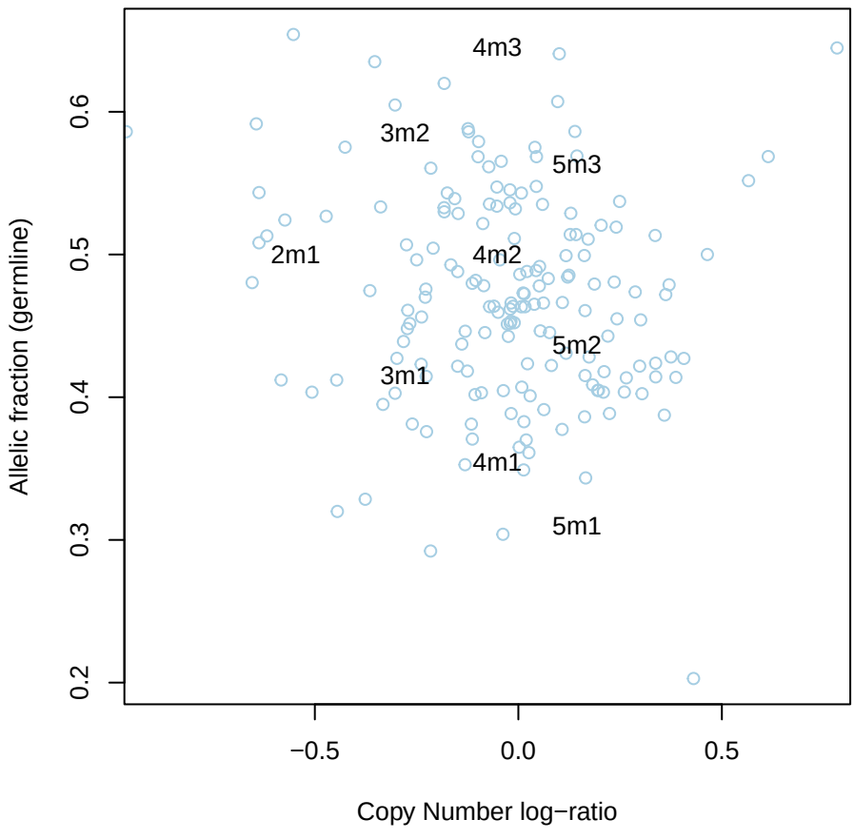

Power 0.8
Frequency
Cellular fraction

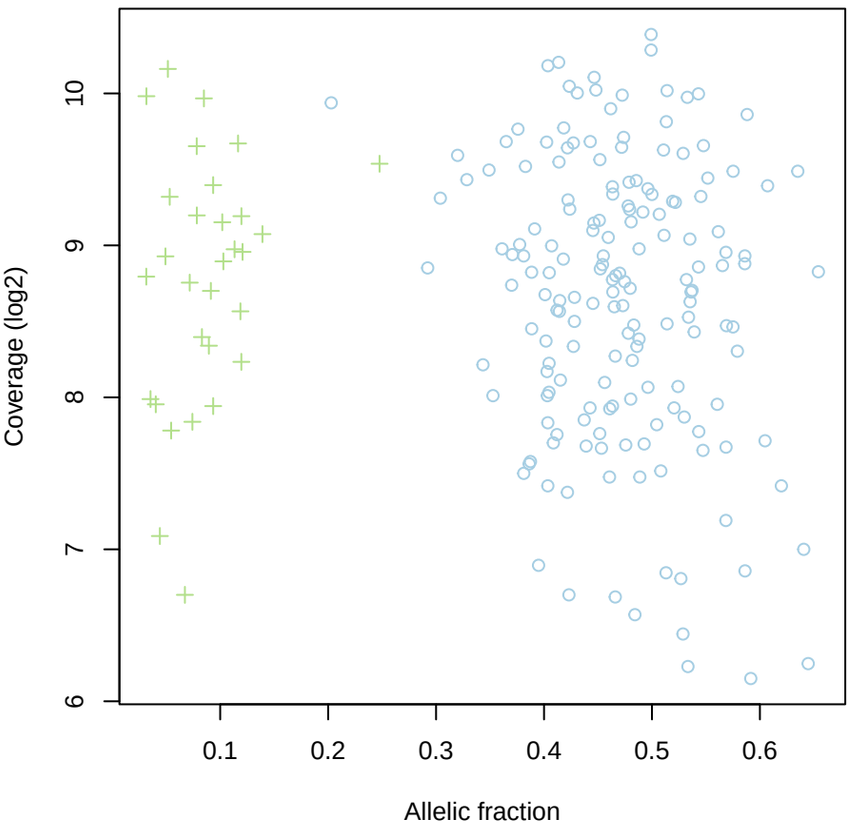

Purity: 0.41 Tumor ploidy: 4.249
2
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

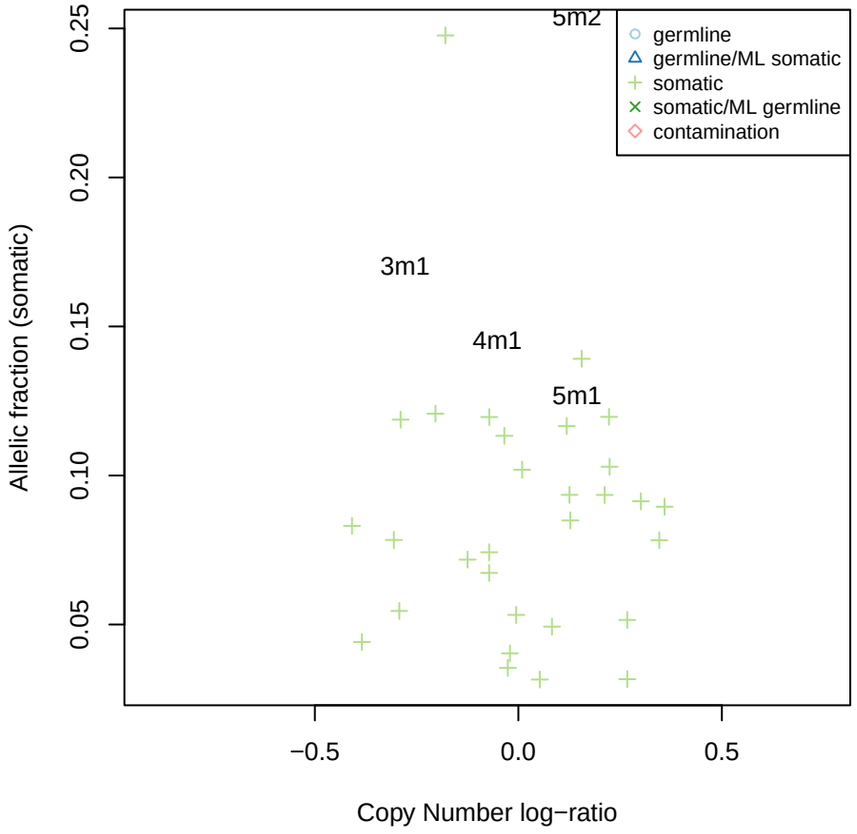

Purity: 0.41 Tumor ploidy: 4.249 SNV log−likelihood: −266.57 GoF: 90.3% Mean coverage: 486;543
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6
0 50 100 150
SNV Index

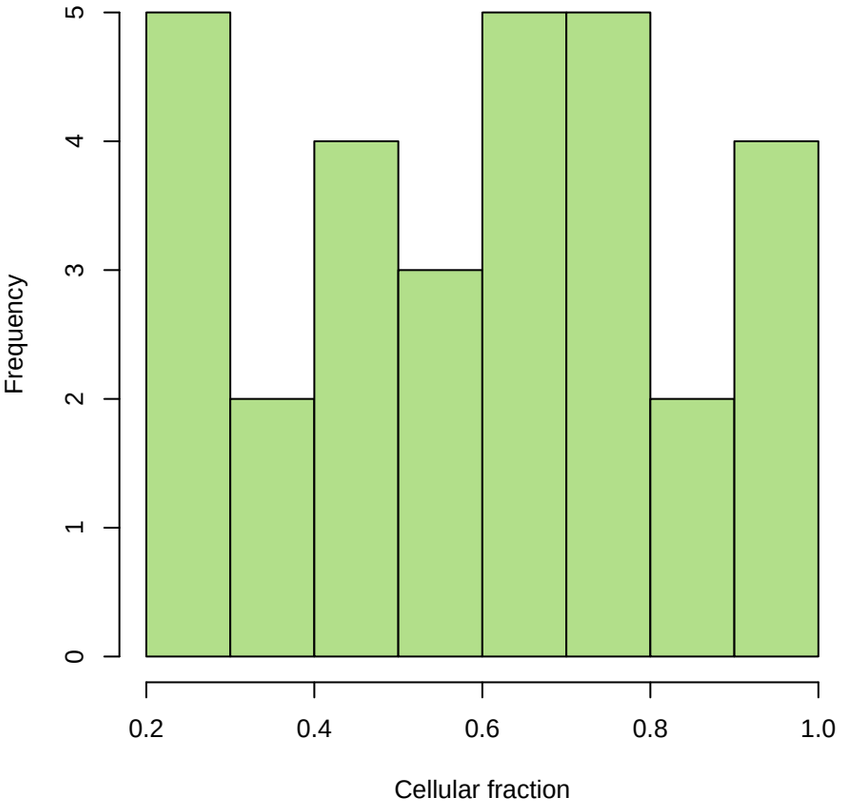

SCNA−fit log−likelihood: −10286.33
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 50 100 150
SNV Index

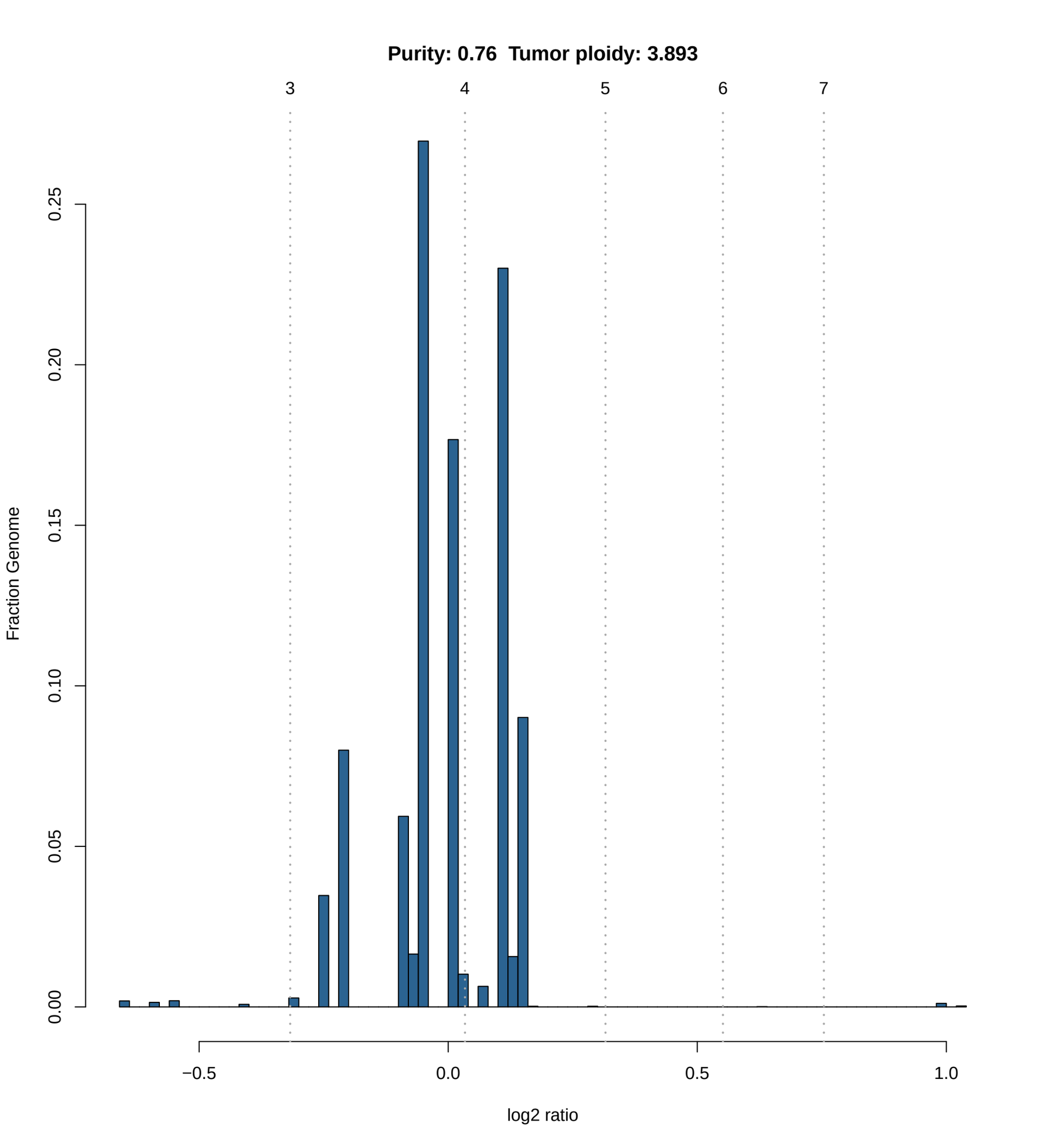

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

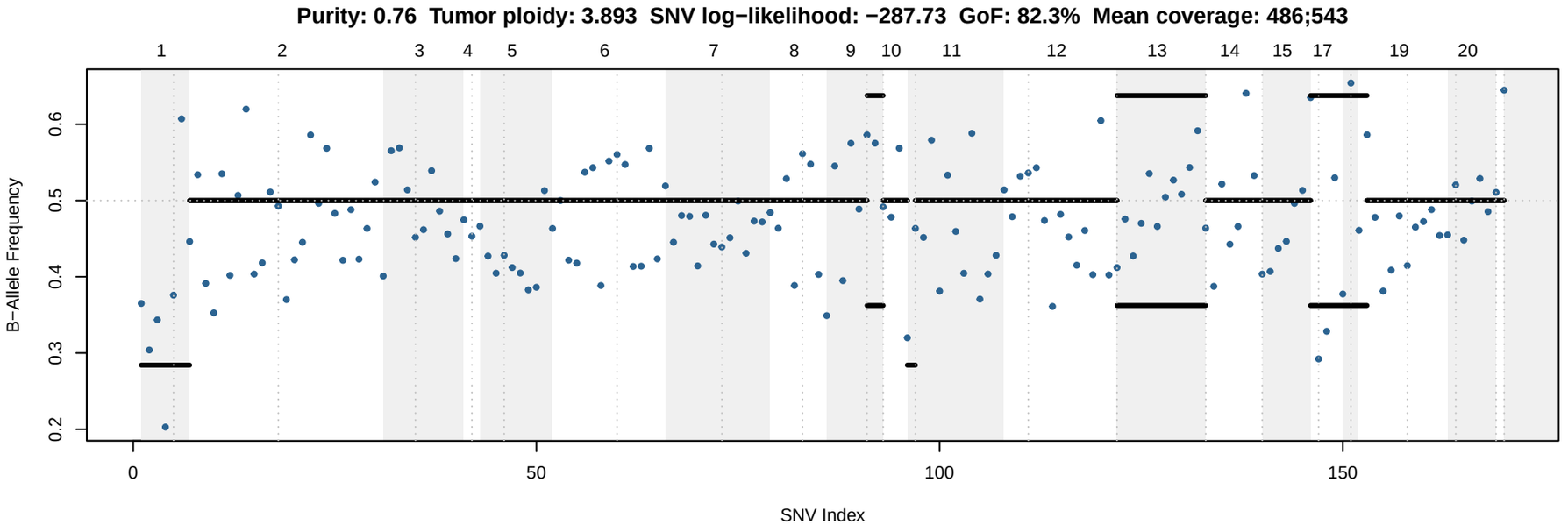

4m3
3m2
5m3
2m1
4m2
5m2
3m1
4m1
5m1
Allelic fraction (germline)
Copy Number log−ratio
0.2
0.3
0.4
0.5
0.6
−0.5
0.0
0.5

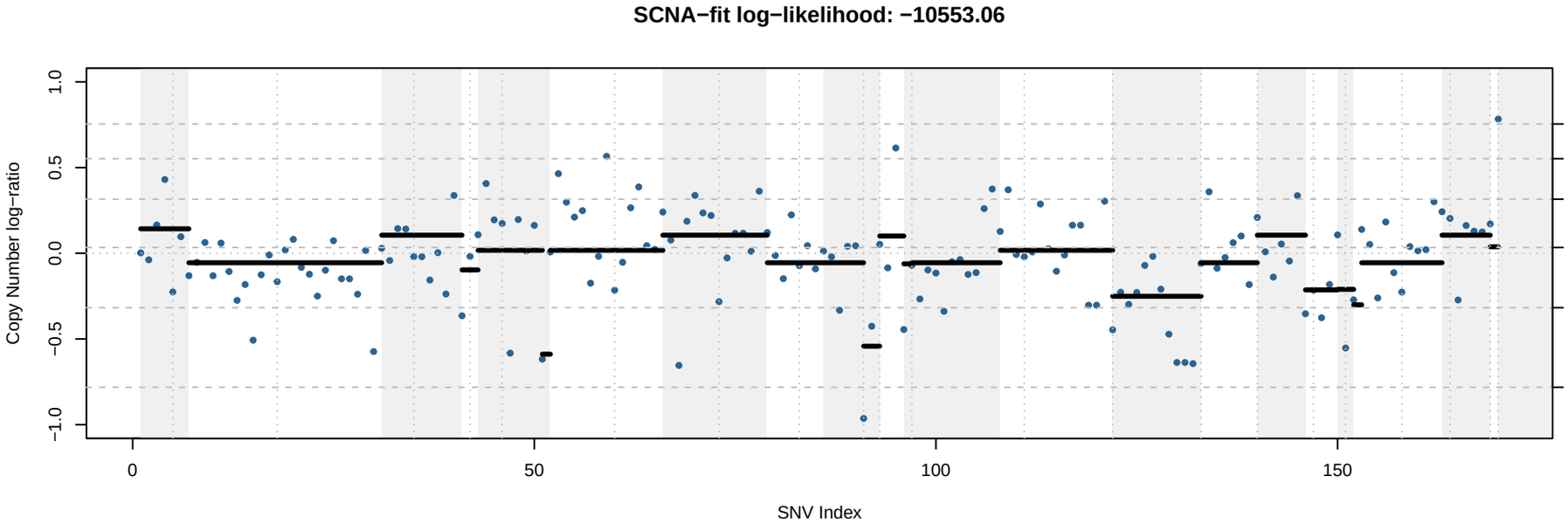

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

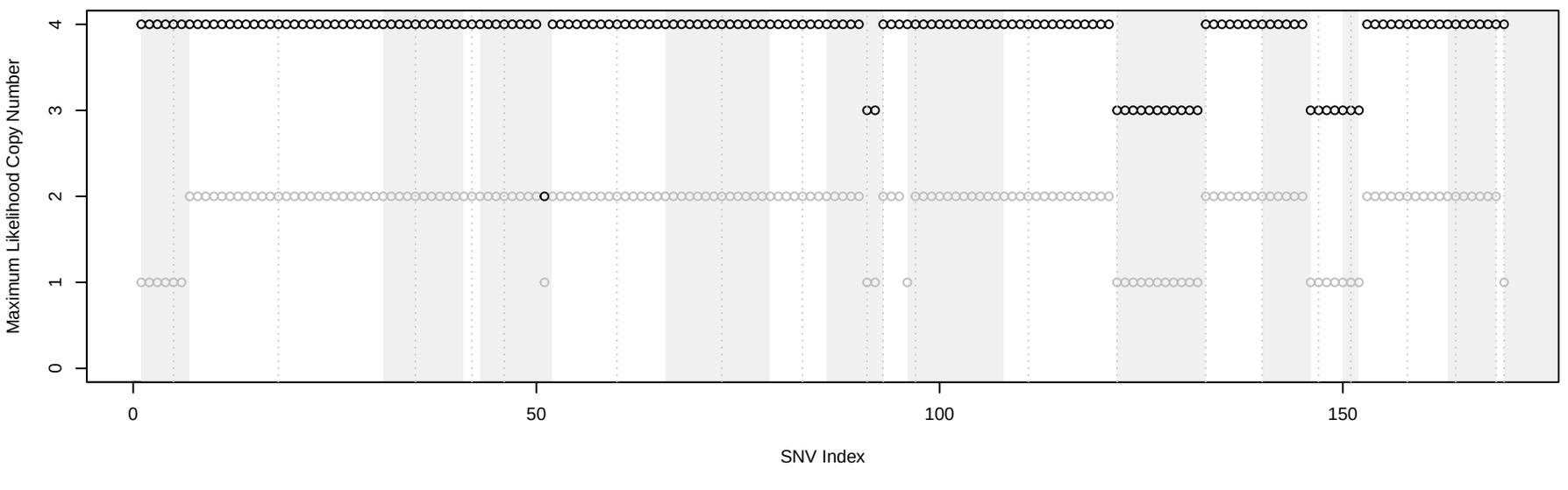

5m2
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
0.25
−0.5
0.0
0.5

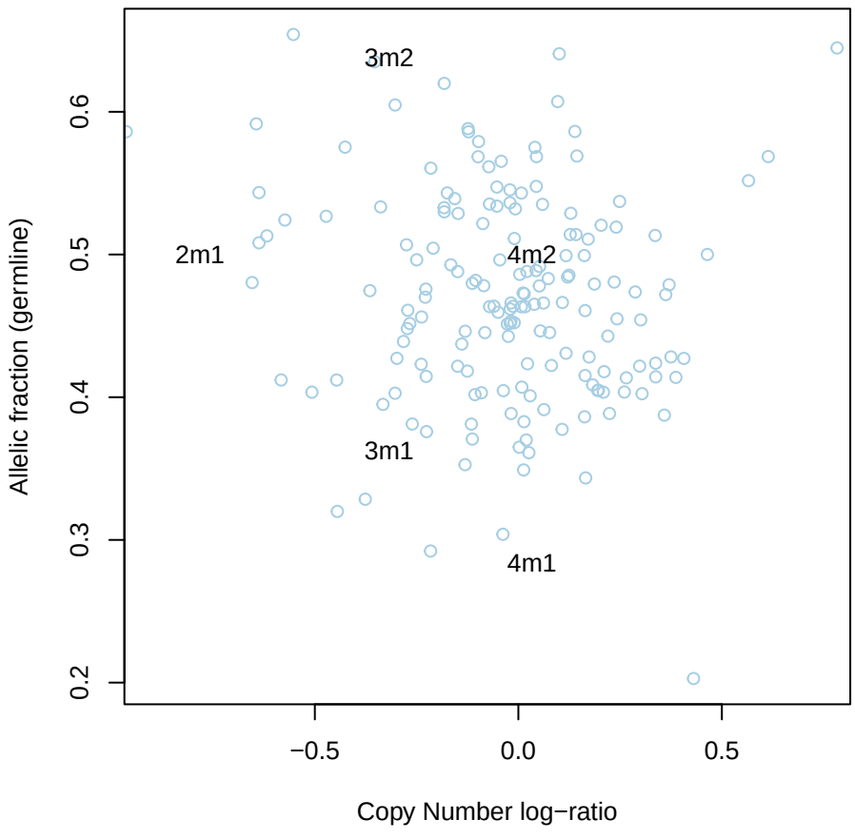

Frequency
Cellular fraction
0
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0

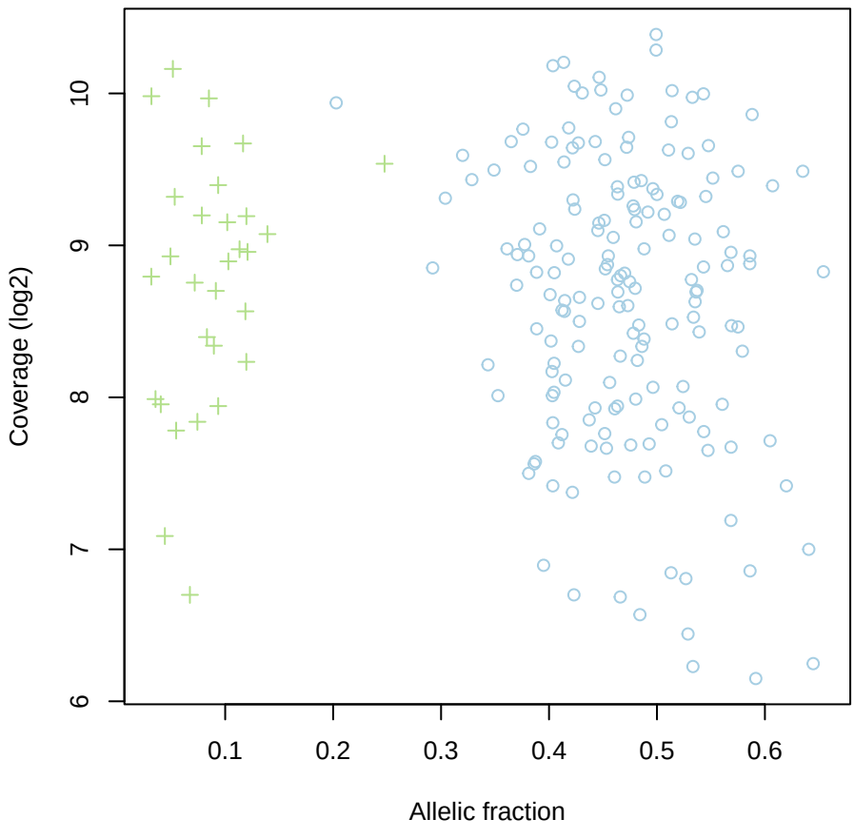

Purity: 0.76 Tumor ploidy: 3.893
3
4
5
6
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

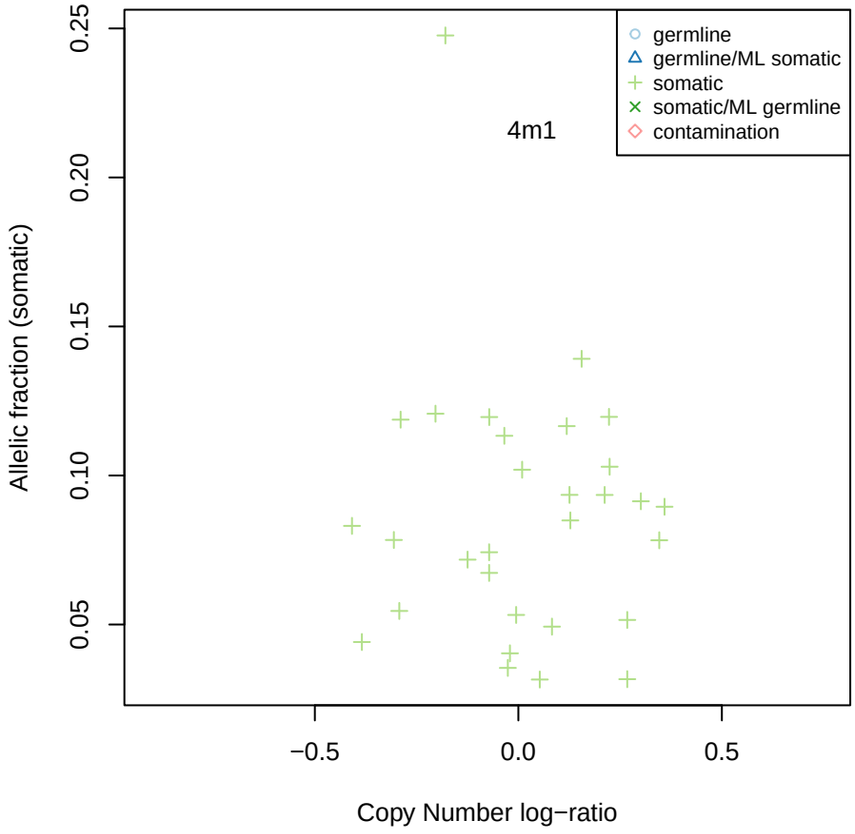

Purity: 0.76 Tumor ploidy: 3.893 SNV log−likelihood: −287.73 GoF: 82.3% Mean coverage: 486;543
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
17
19
20
B−Allele Frequency
0.2
0.3
0.4
0.5
0.6
0
50
100
150
SNV Index

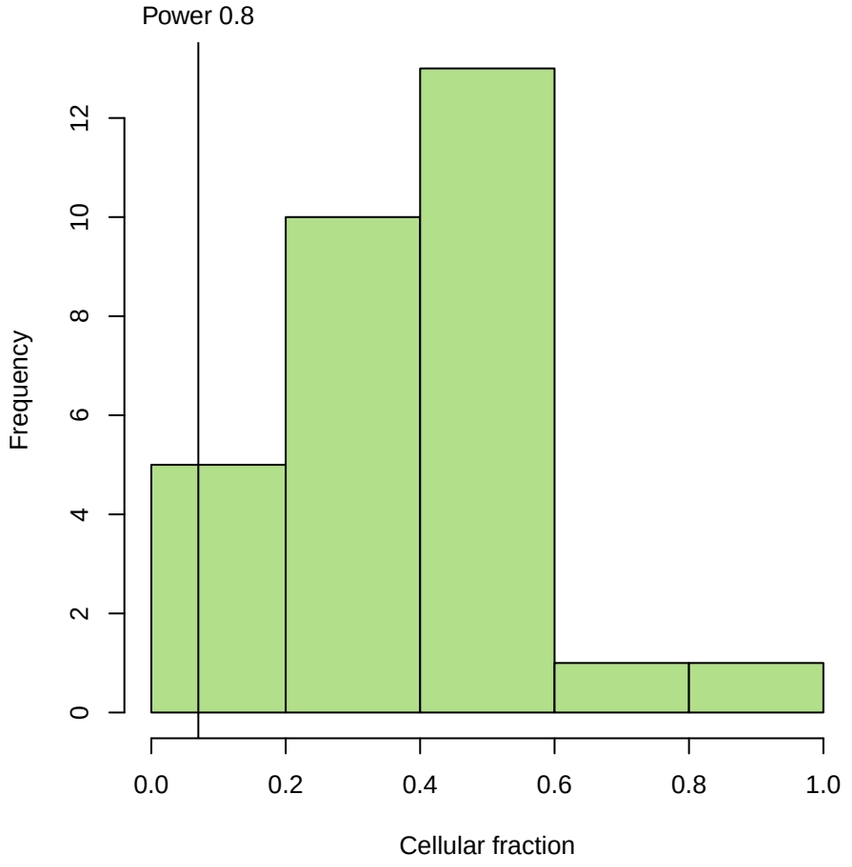

SCNA−fit log−likelihood: −10553.06
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
2
3
4
5
6
7
0
50
100
150
SNV Index

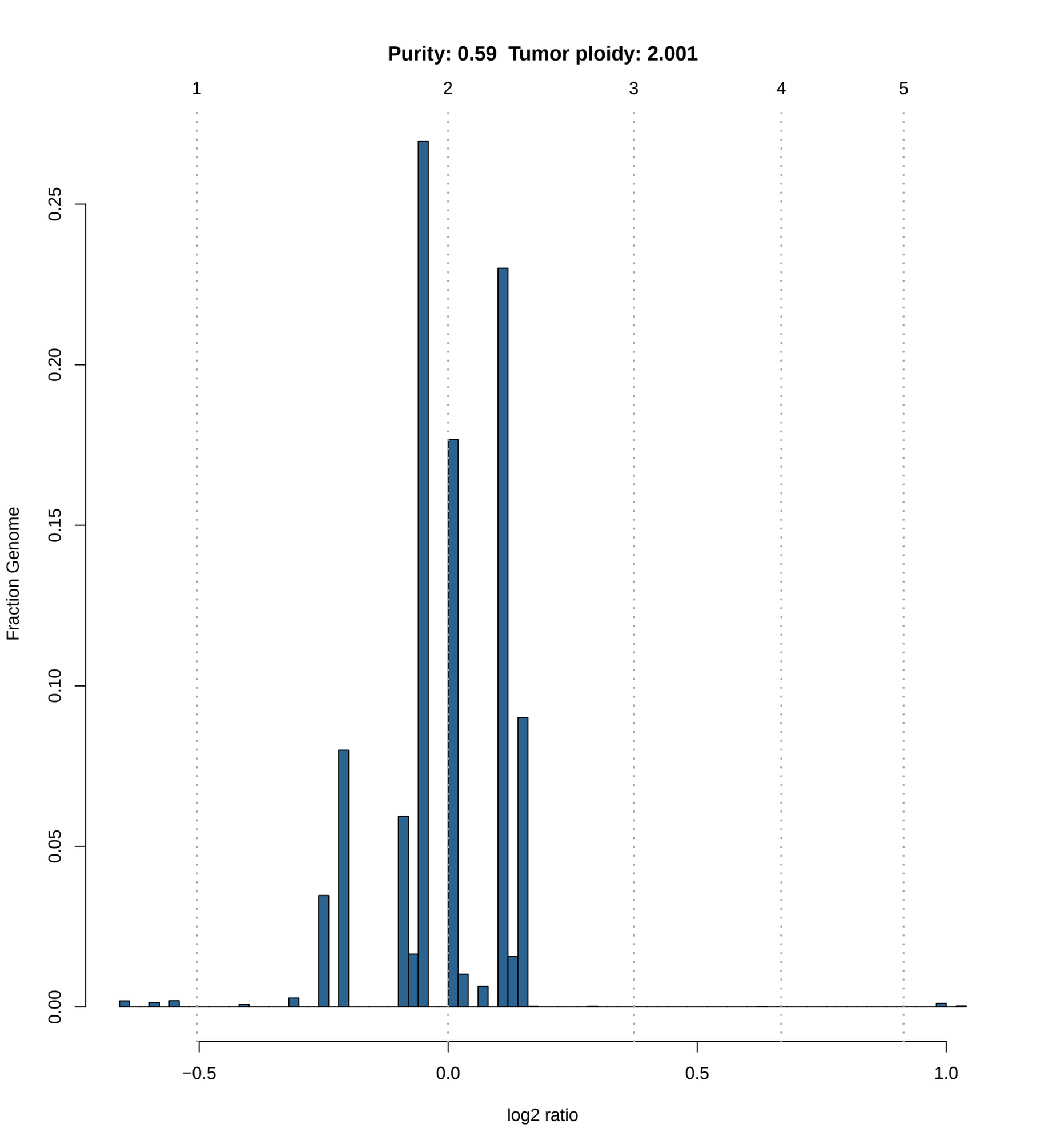

Maximum Likelihood Copy Number
0
1
2
3
4
0
50
100
150
SNV Index

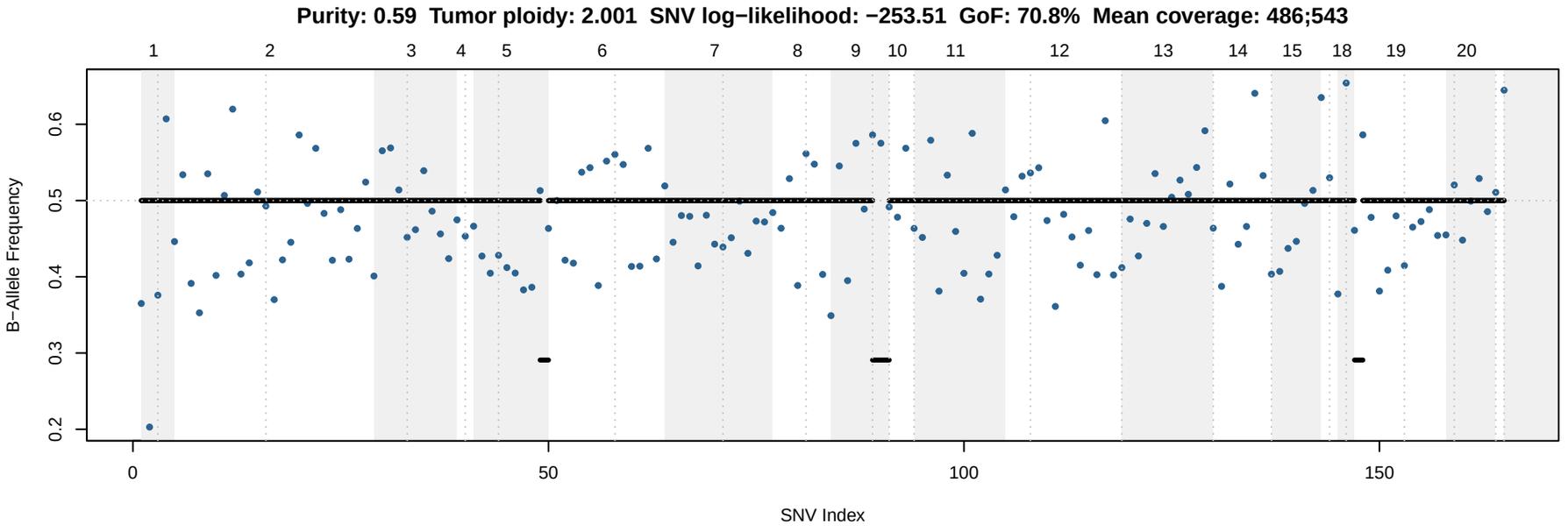

3m2
2m1
4m2
3m1
4m1
Allelic fraction (germline)
Copy Number log−ratio

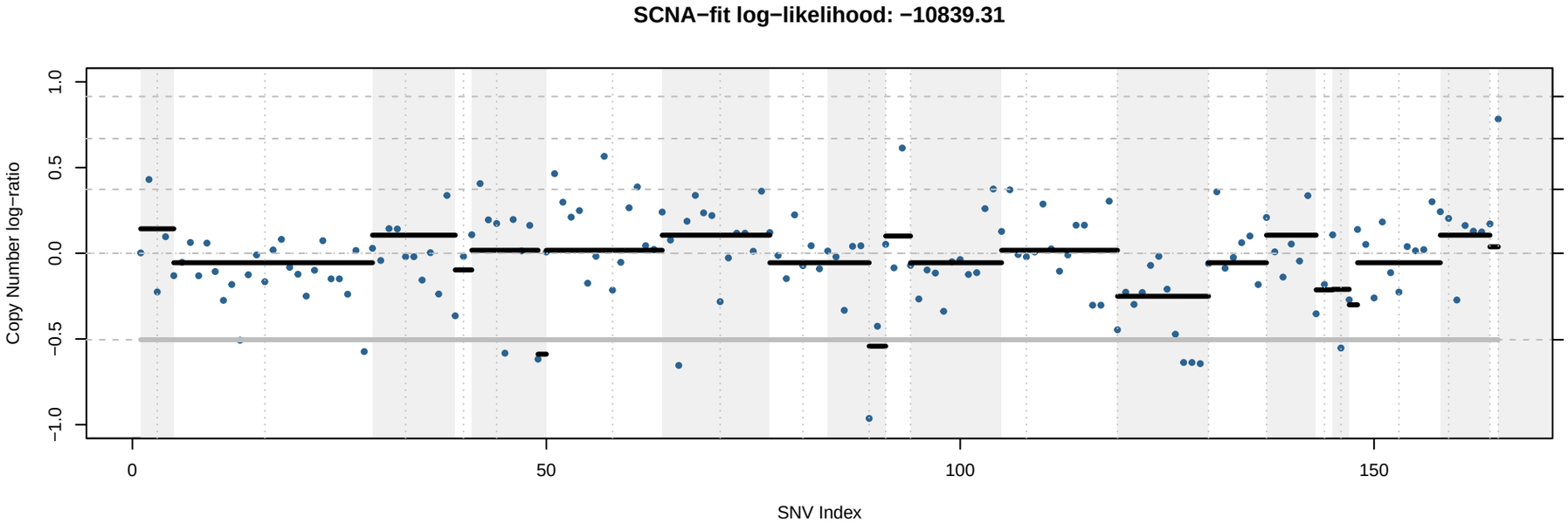

Coverage (log2)
Allelic fraction

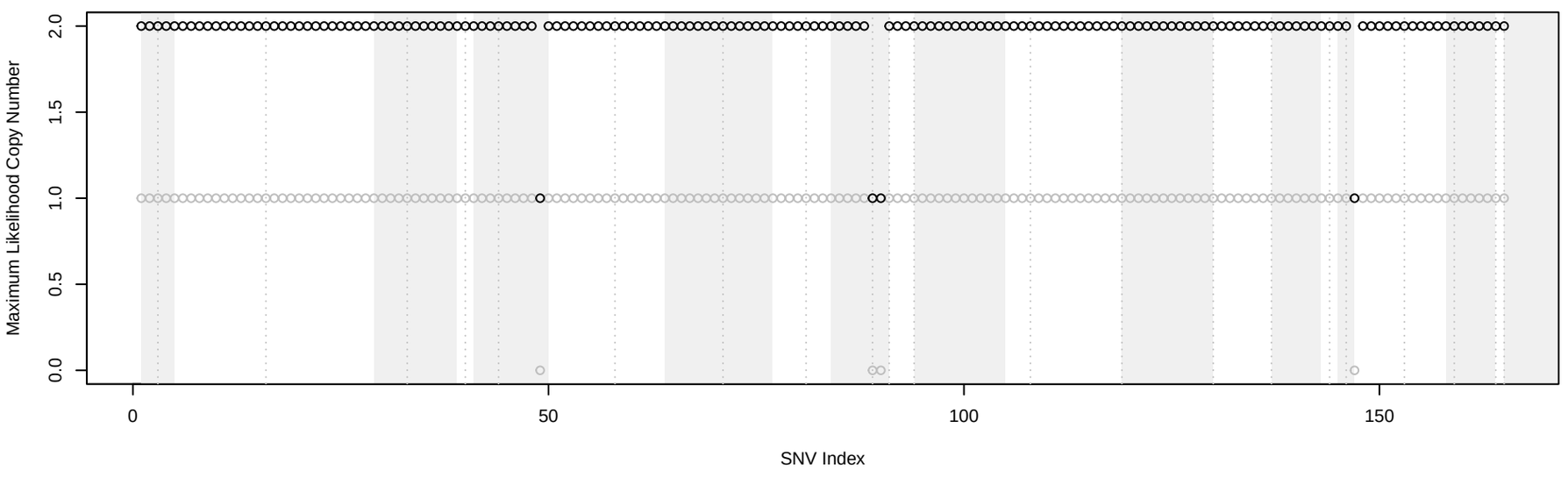

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
Allelic fraction (somatic)
Copy Number log−ratio

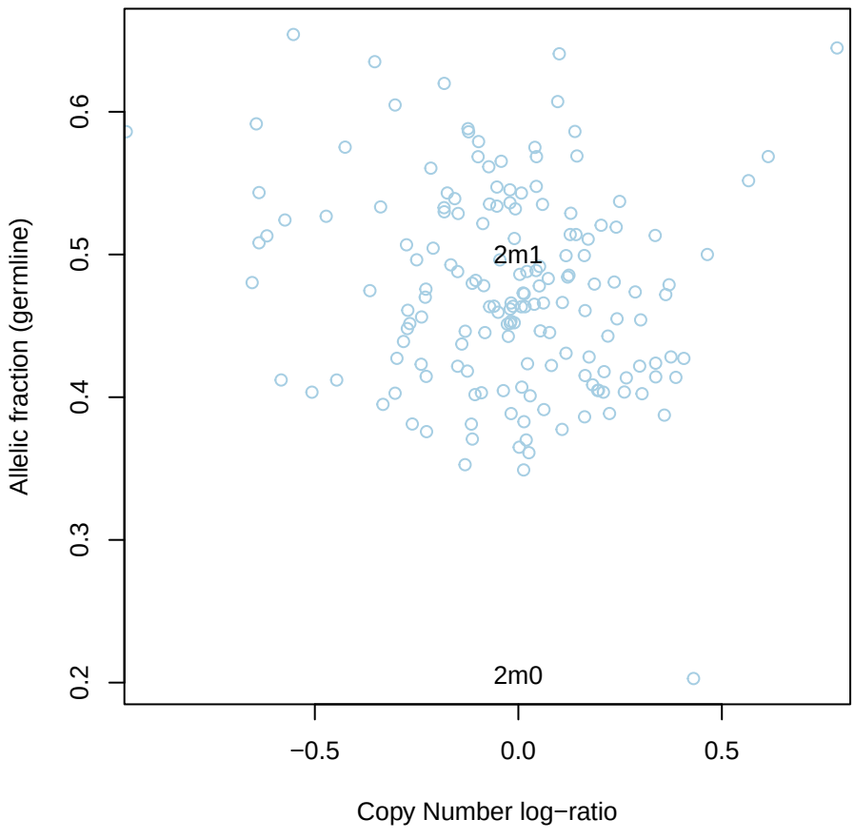

Power 0.8
Frequency
Cellular fraction

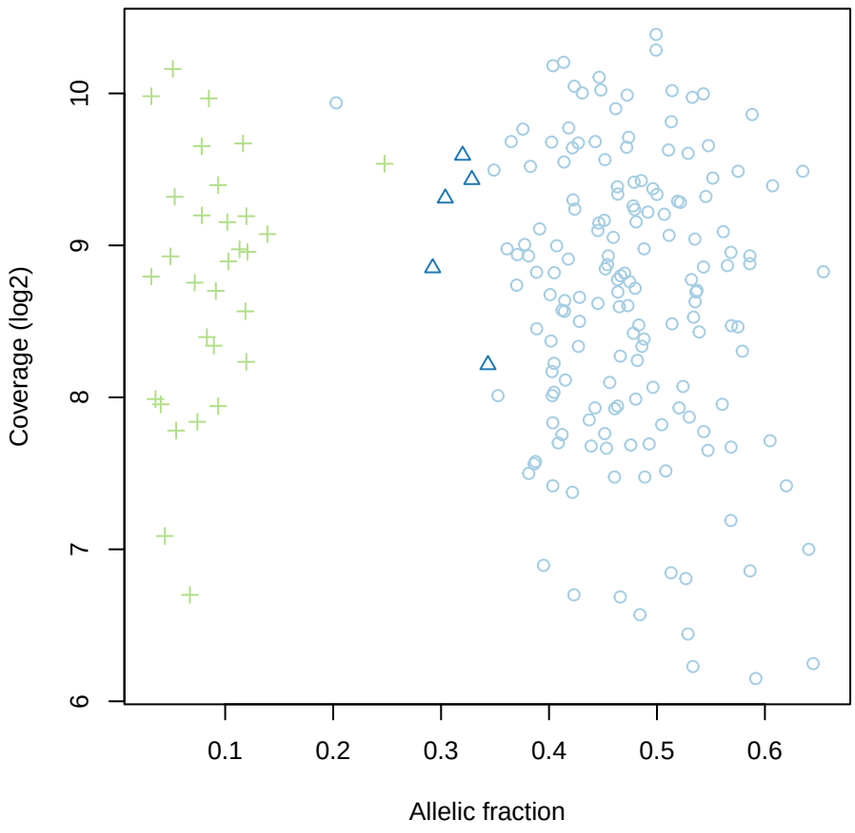

Purity: 0.59 Tumor ploidy: 2.001
1
2
3
4
5
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

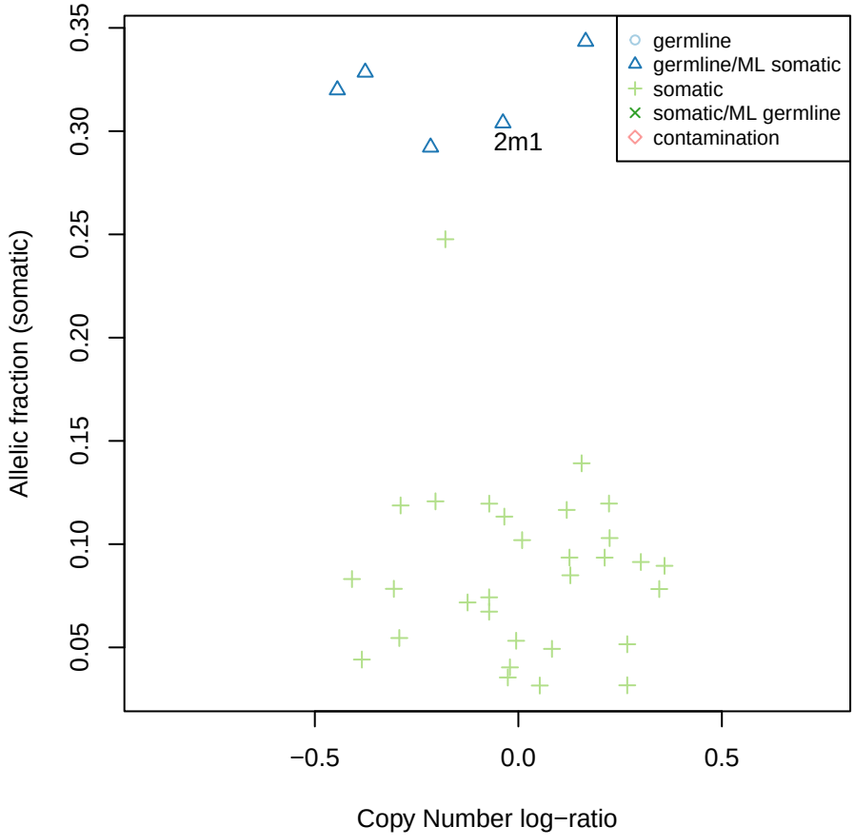

Purity: 0.59 Tumor ploidy: 2.001 SNV log−likelihood: −253.51 GoF: 70.8% Mean coverage: 486;543
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
18
19
20
B−Allele Frequency
0.2
0.3
0.4
0.5
0.6
0
50
100
150
SNV Index

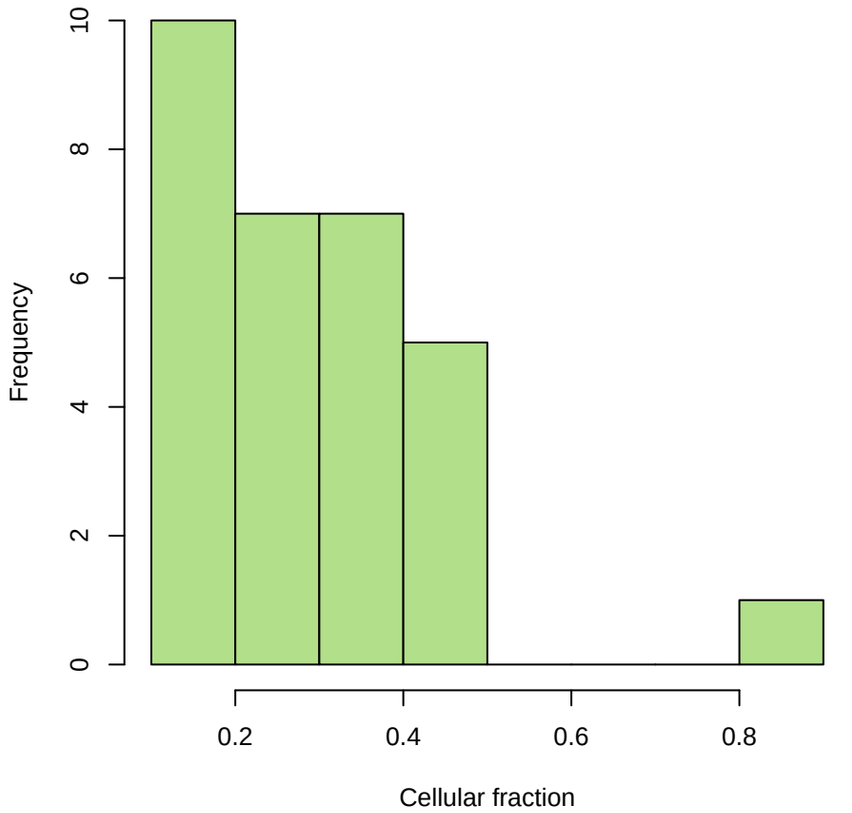

SCNA−fit log−likelihood: −10839.31
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1
2
3
4
5
0
50
100
150
SNV Index

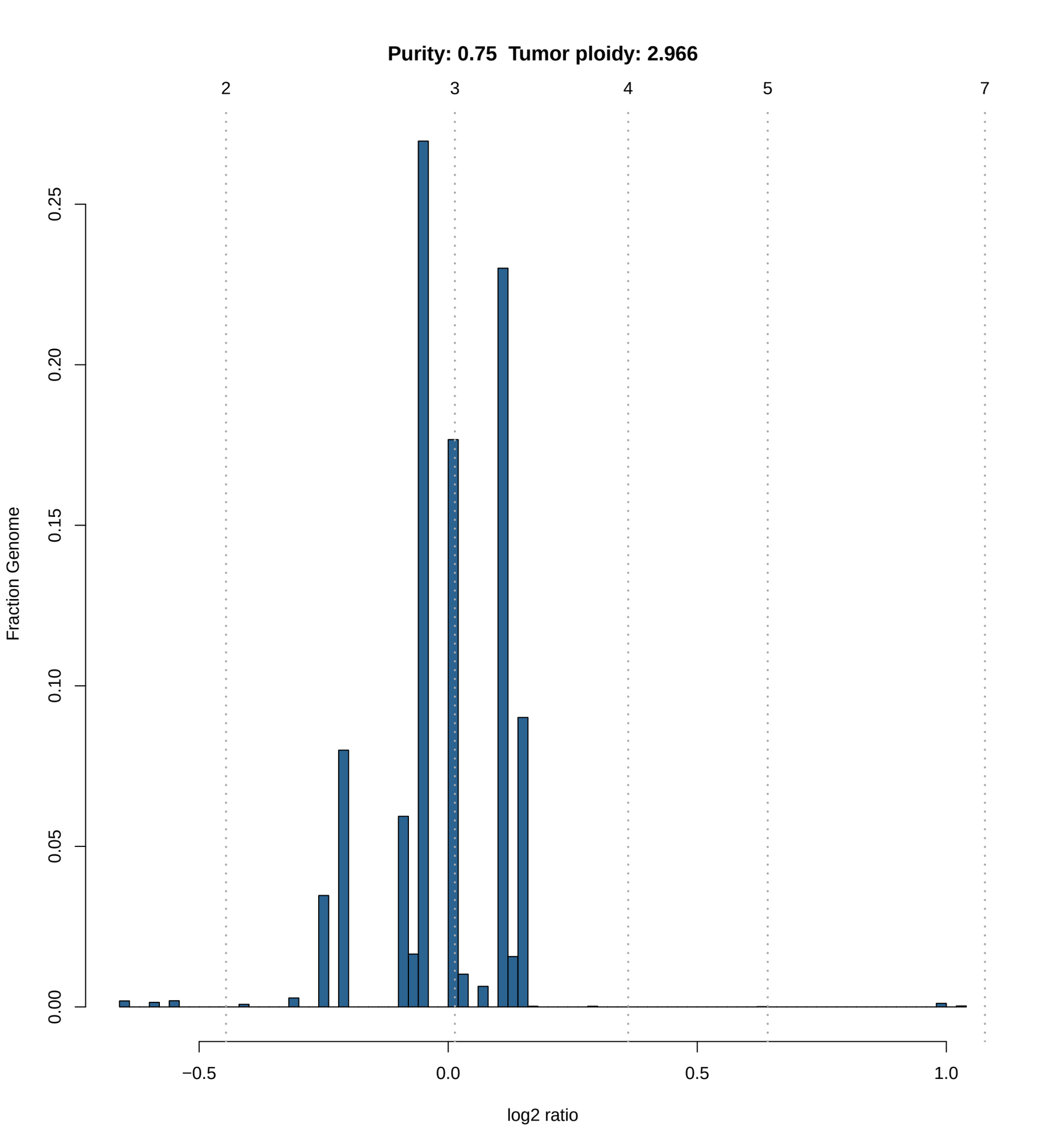

Maximum Likelihood Copy Number
0.0
0.5
1.0
1.5
2.0
0
50
100
150
SNV Index

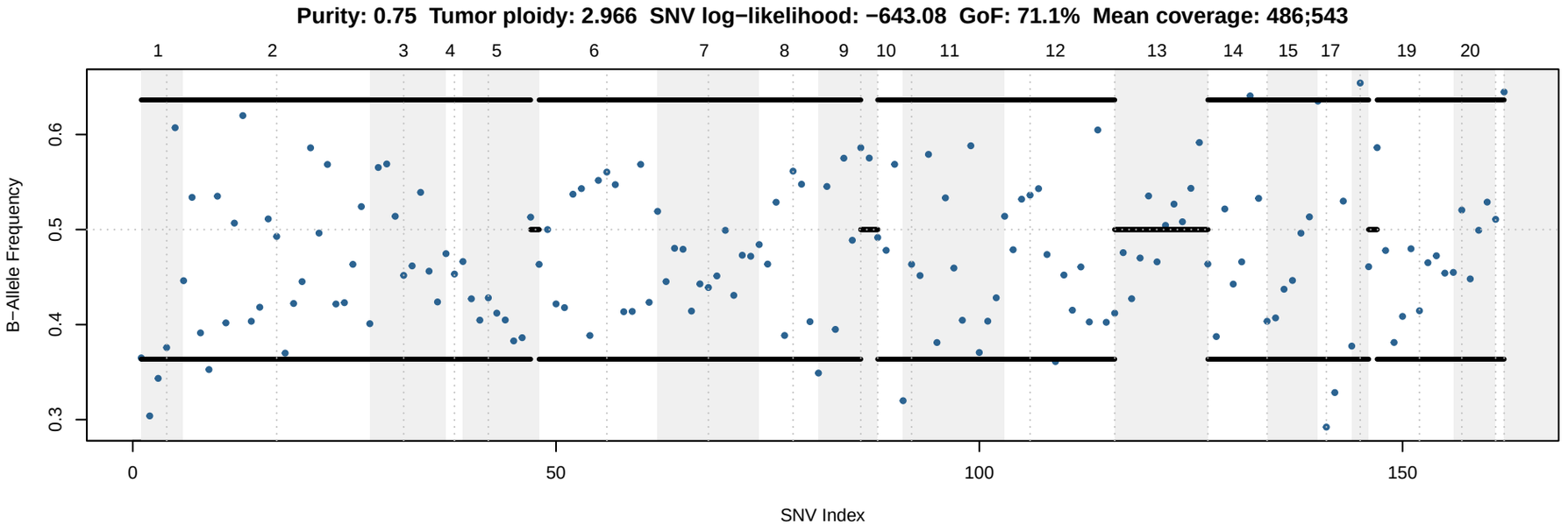

Allelic fraction (germline)
0.2
0.3
0.4
0.5
0.6
2m1
2m0
−0.5
0.0
0.5
Copy Number log−ratio

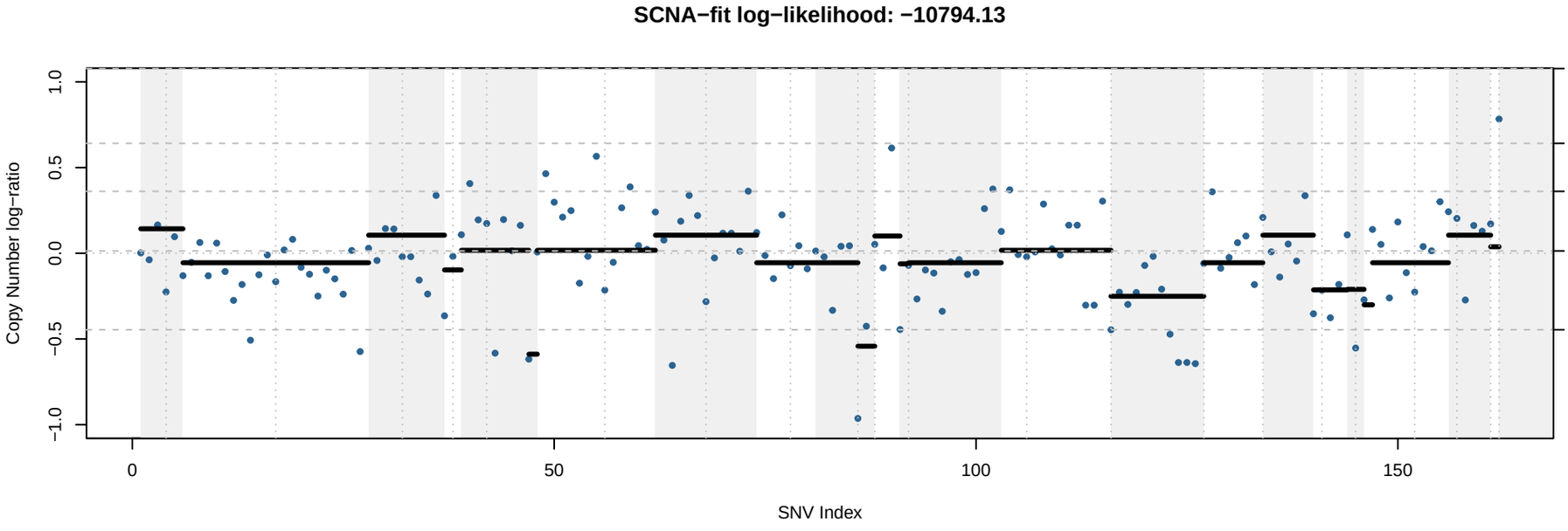

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

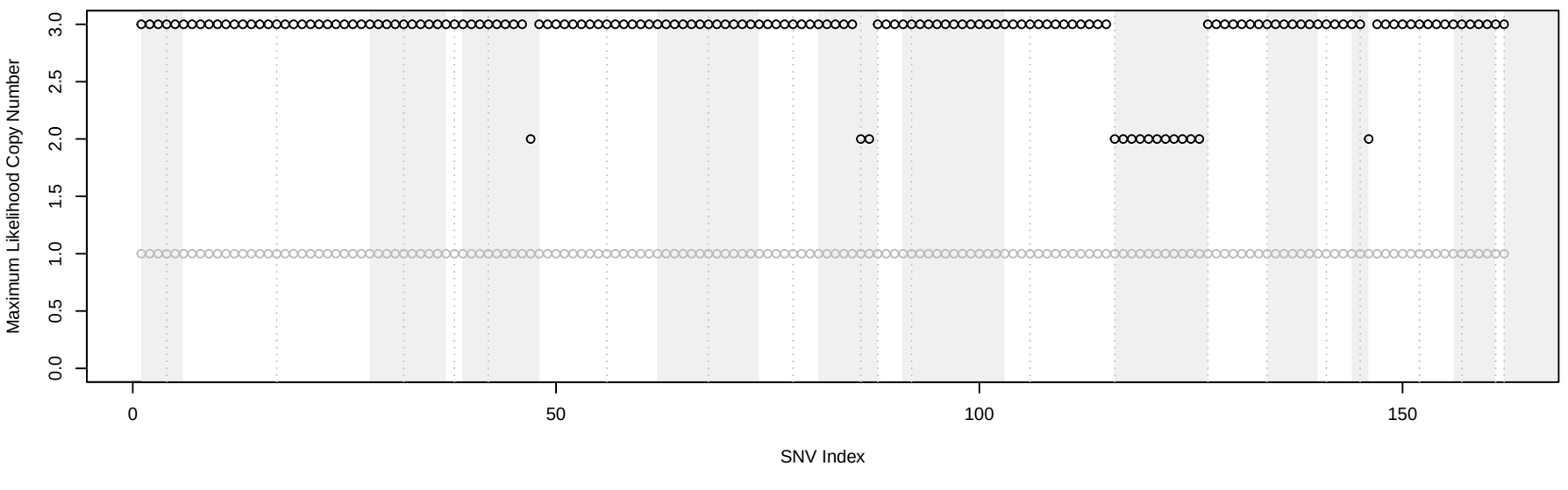

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0.30
0.35
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
−0.5
0.0
0.5
Copy Number log−ratio

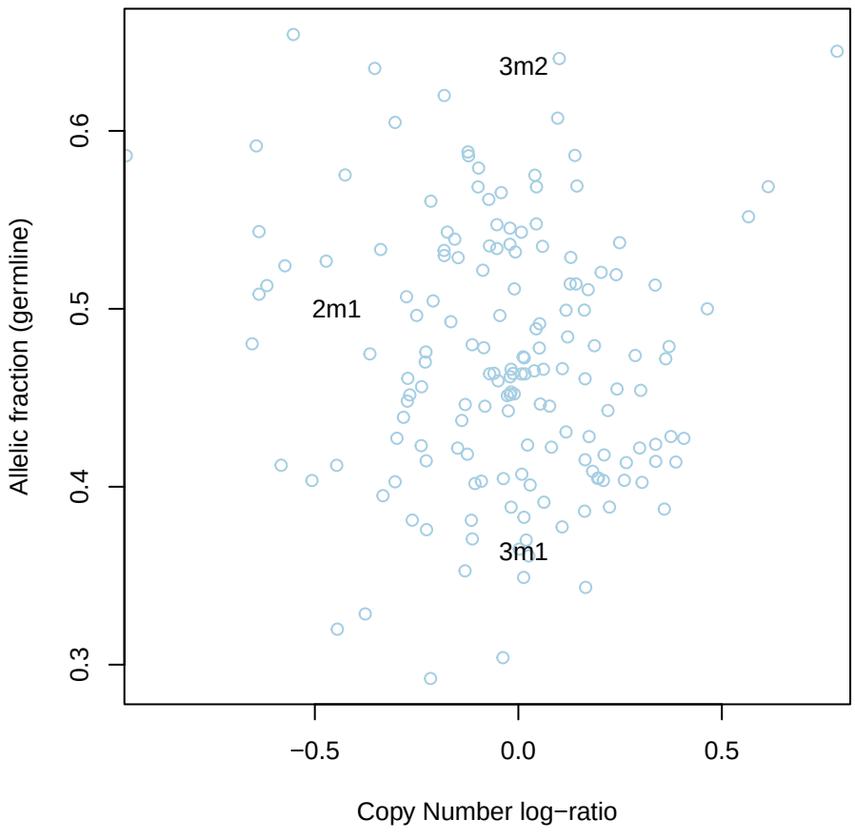

Frequency
0
2
4
6
8
10
0.2
0.4
0.6
0.8
Cellular fraction

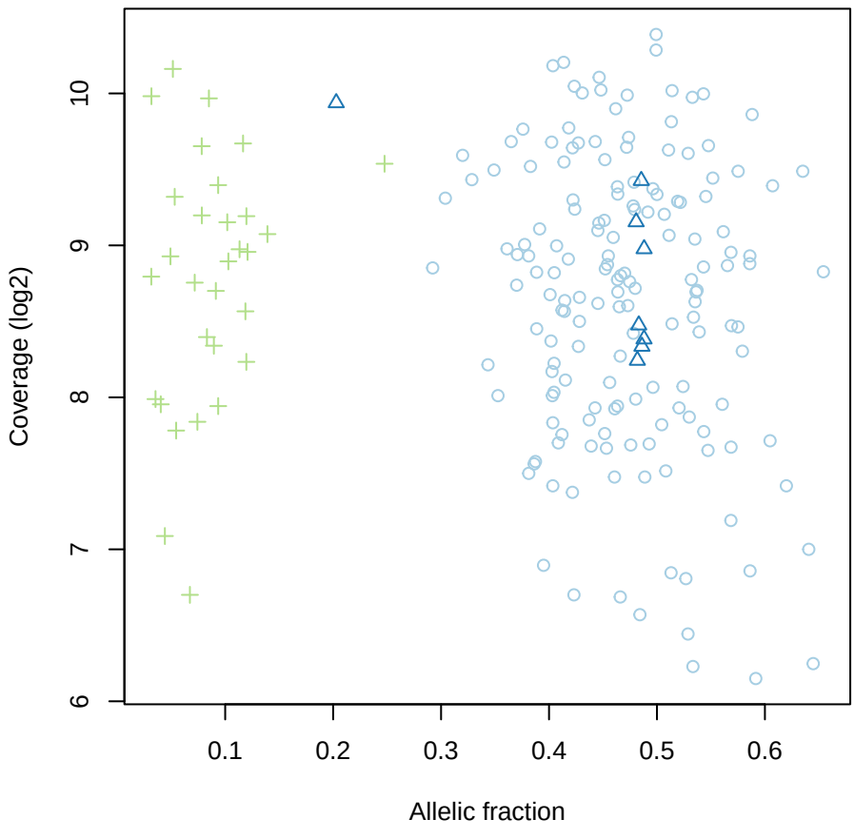

Purity: 0.75 Tumor ploidy: 2.966
2
3
4
5
7
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

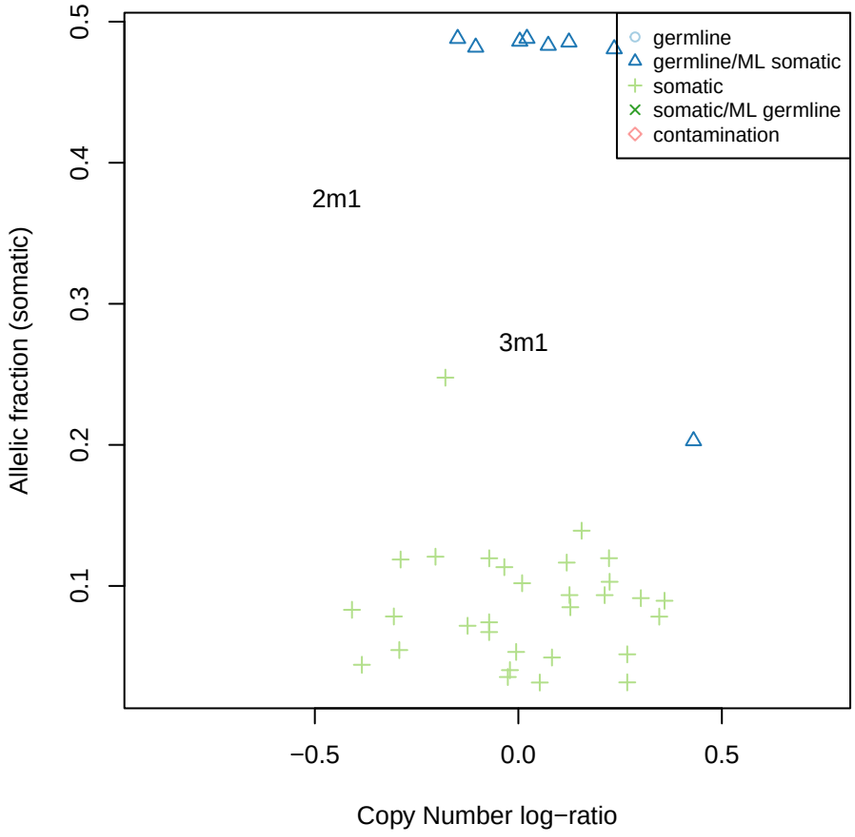

Purity: 0.75 Tumor ploidy: 2.966 SNV log−likelihood: −643.08 GoF: 71.1% Mean coverage: 486;543
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
17
19
20
B−Allele Frequency
0.3
0.4
0.5
0.6
0
50
100
150
SNV Index

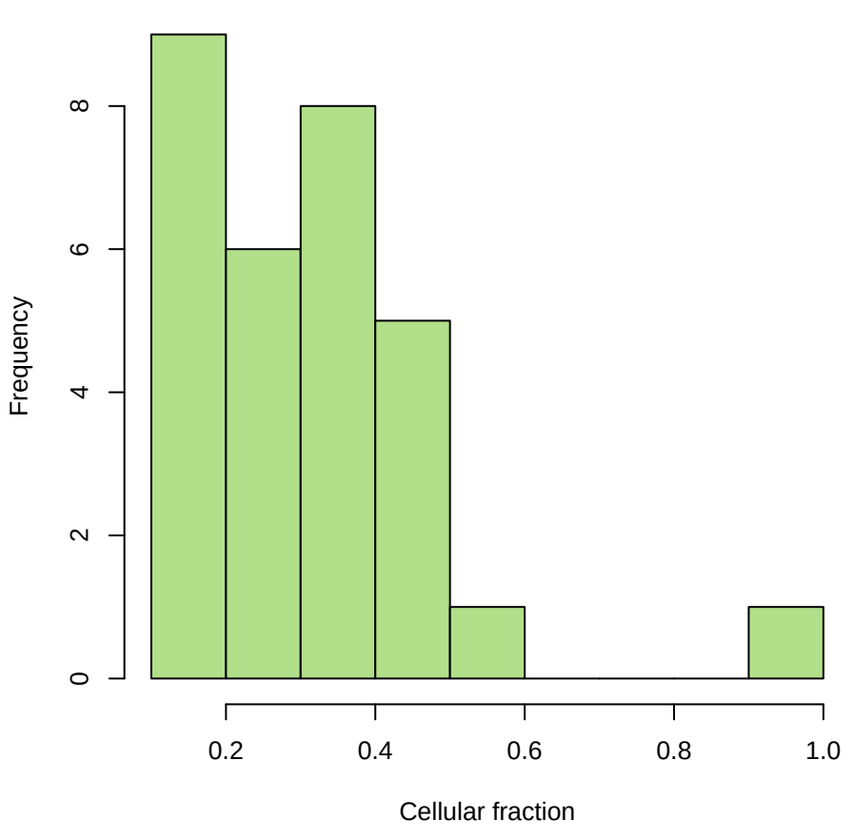

SCNA−fit log−likelihood: −10794.13
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
2
3
4
5
7
0
50
100
150
SNV Index


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


3m2
2m1
3m1
Allelic fraction (germline)
Copy Number log−ratio
0.3
0.4
0.5
0.6
−0.5
0.0
0.5


Coverage (log2)
Allelic fraction
6
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
2m1
3m1
Allelic fraction (somatic)
Copy Number log−ratio
0.1
0.2
0.3
0.4
0.5
−0.5
0.0
0.5


Frequency
Cellular fraction
0
2
4
6
8
0.2
0.4
0.6
0.8
1.0