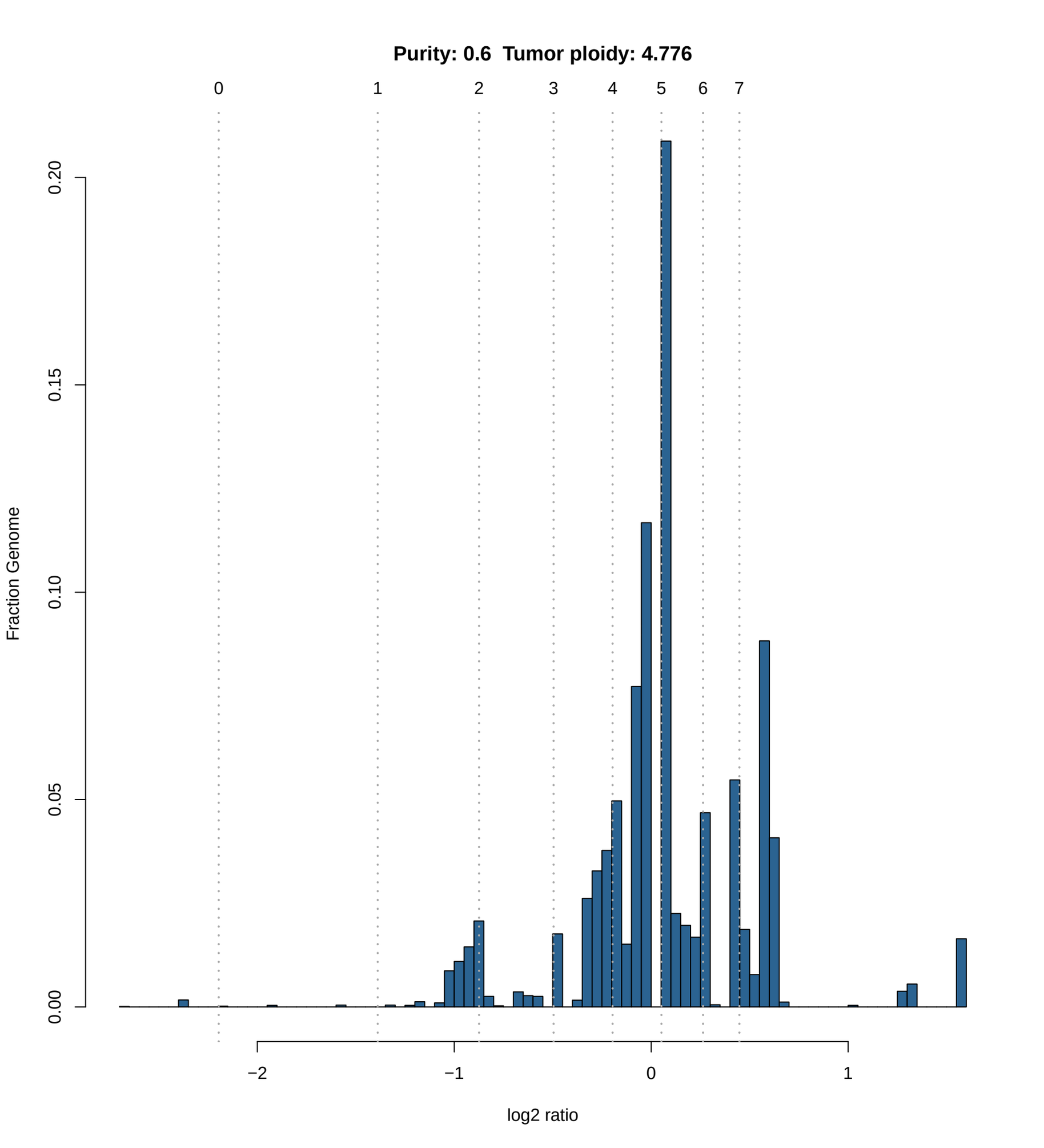
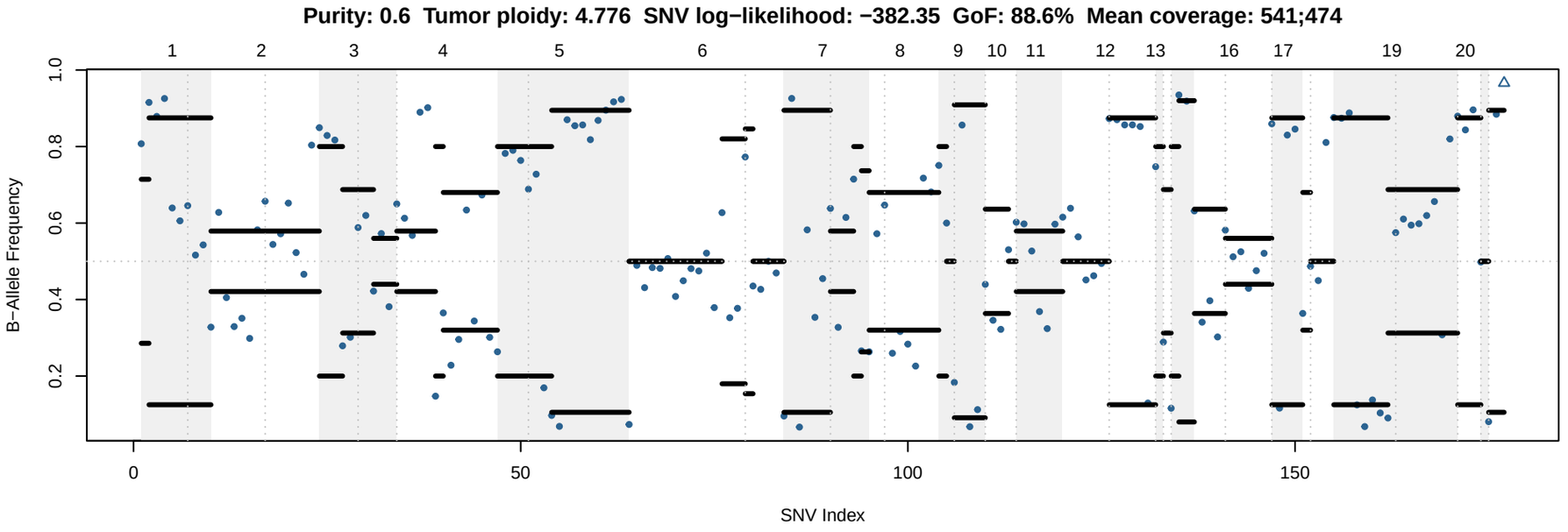
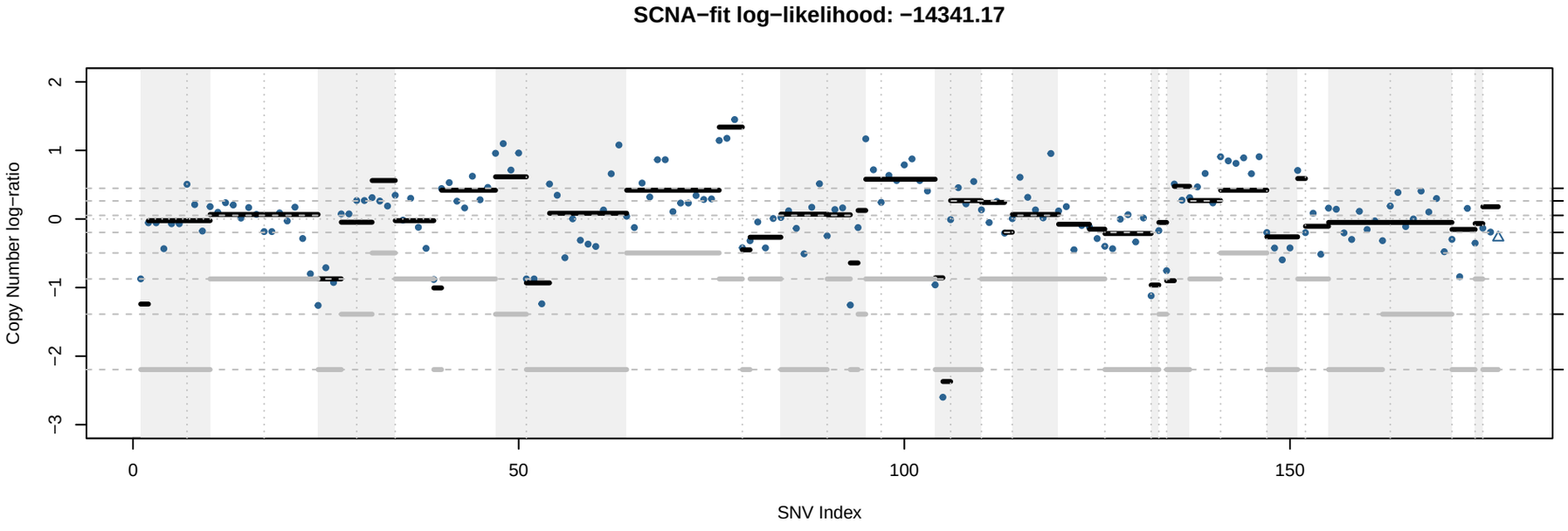
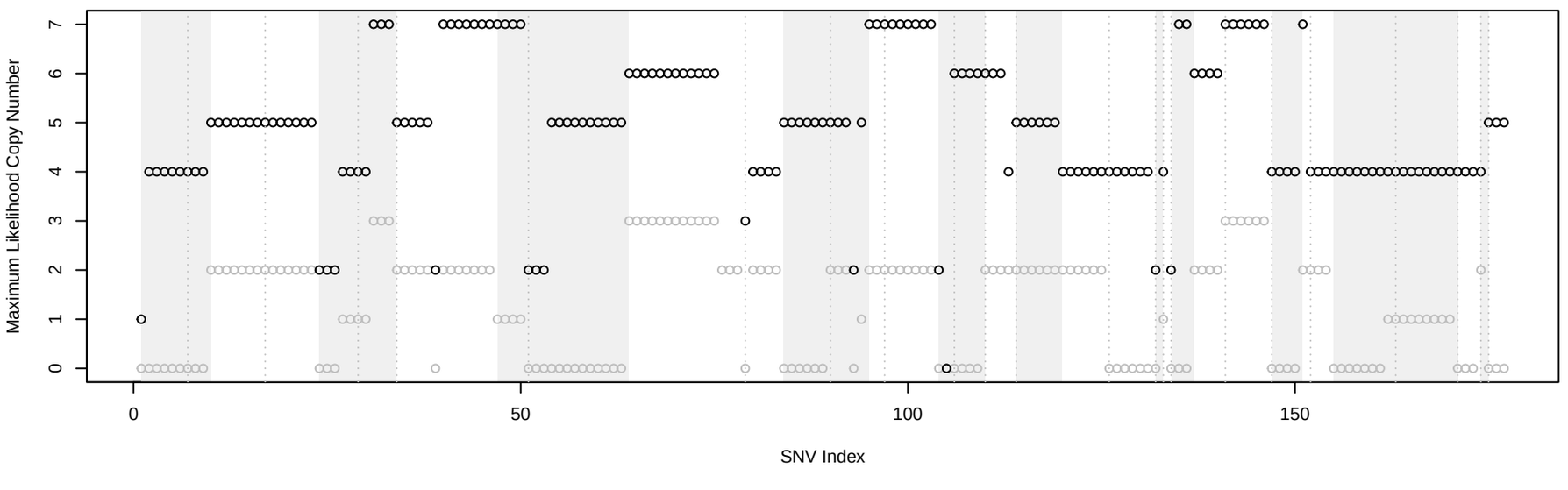
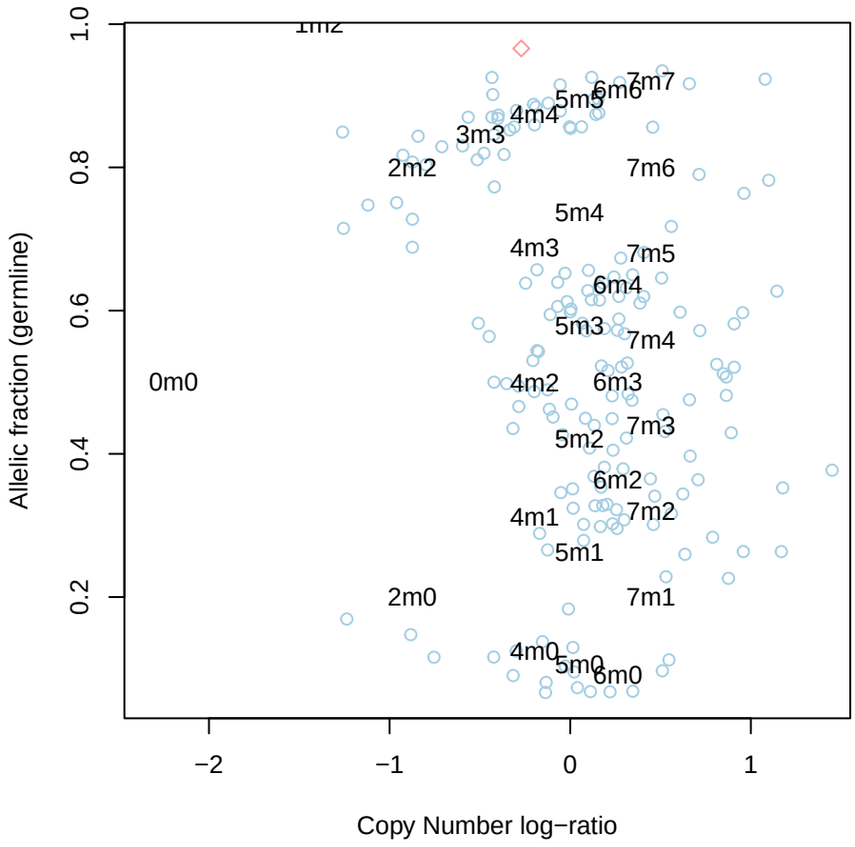
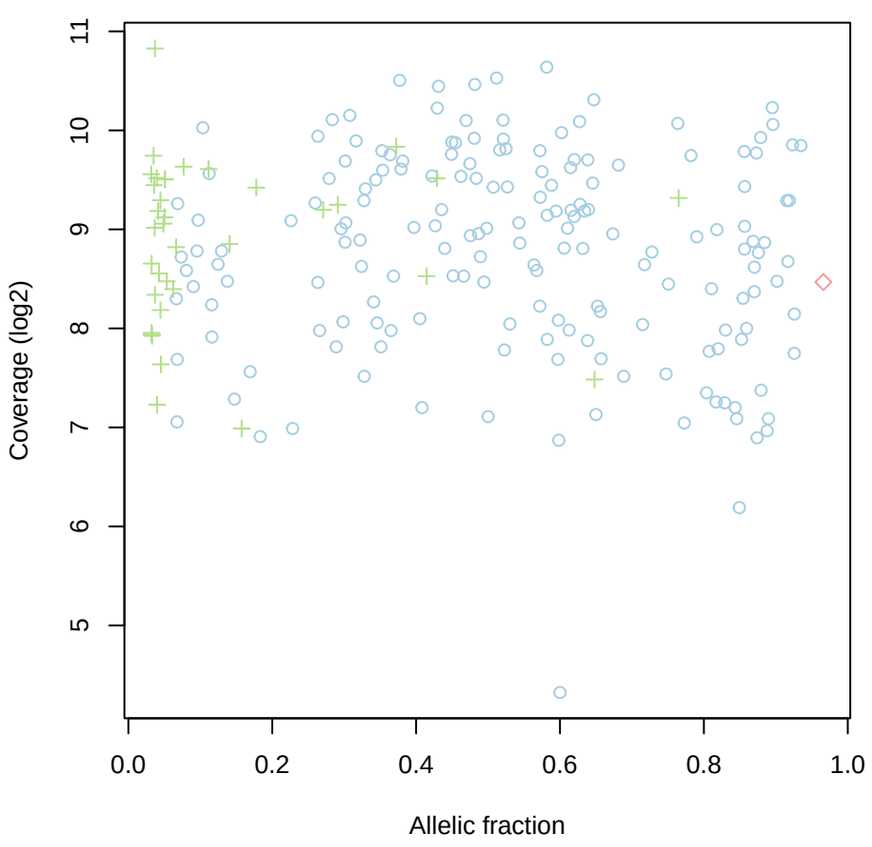

Purity: 0.6 Tumor ploidy: 4.776
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−2
−1
0
1
log2 ratio

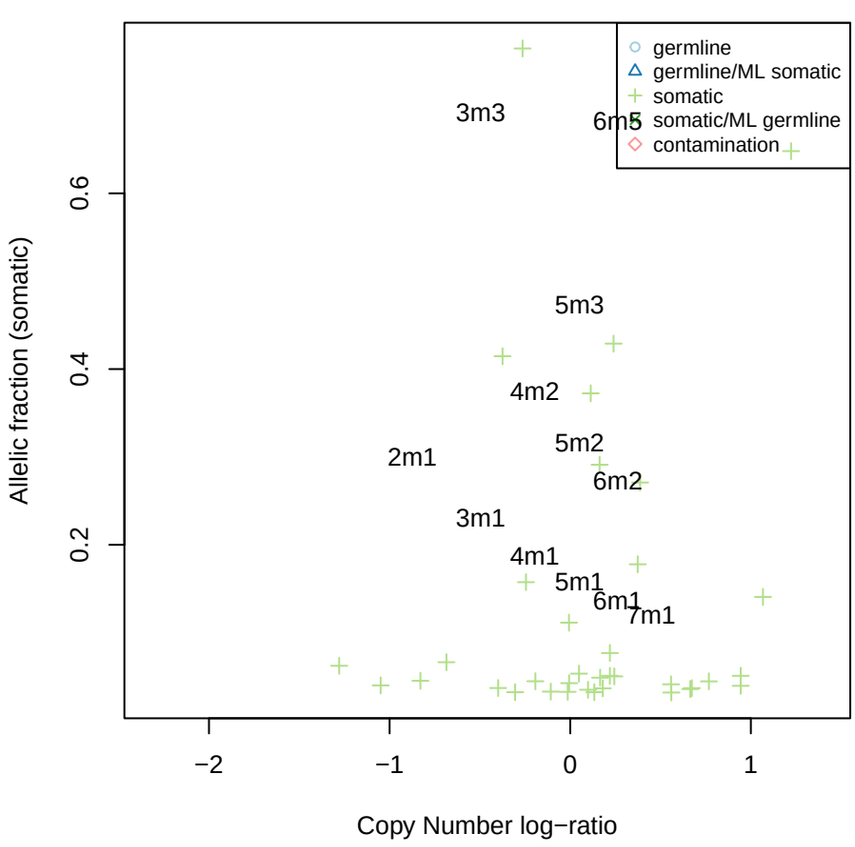

Purity: 0.6 Tumor ploidy: 4.776 SNV log−likelihood: −382.35 GoF: 88.6% Mean coverage: 541;474
1 2 3 4 5 6 7 8 9 10 11 12 13 16 17 19 20
B−Allele Frequency
0.2 0.4 0.6 0.8 1.0
0 50 100 150
SNV Index

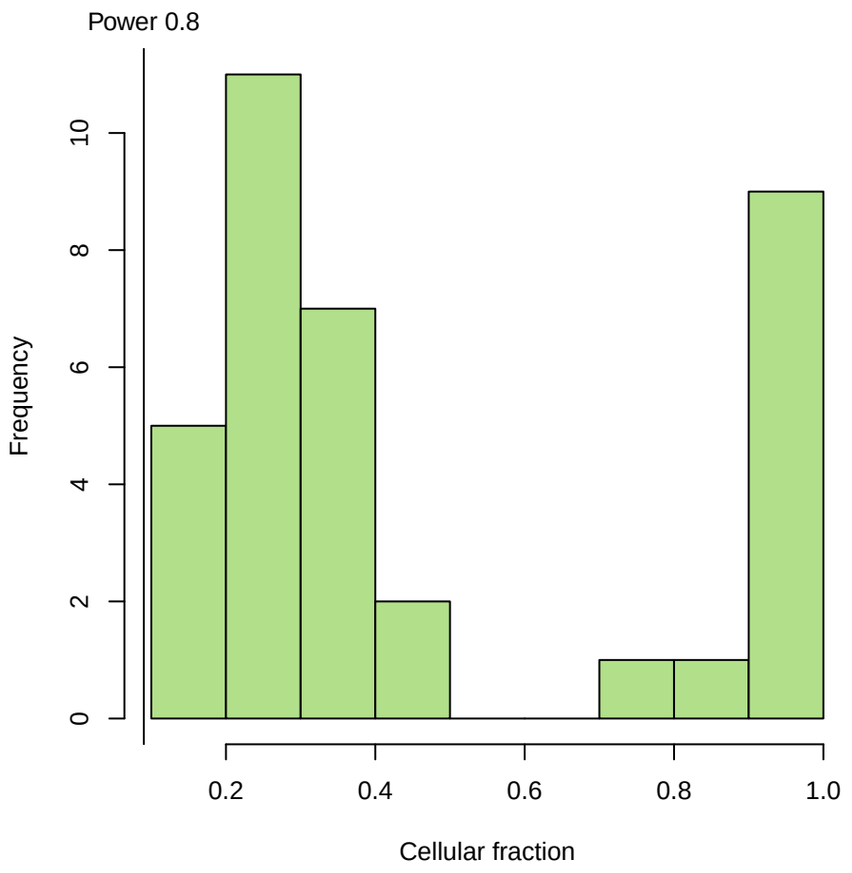

SCNA−fit log−likelihood: −14341.17
Copy Number log−ratio
−3 −2 −1 0 1 2
0 1 2 3 5 7
0 50 100 150
SNV Index

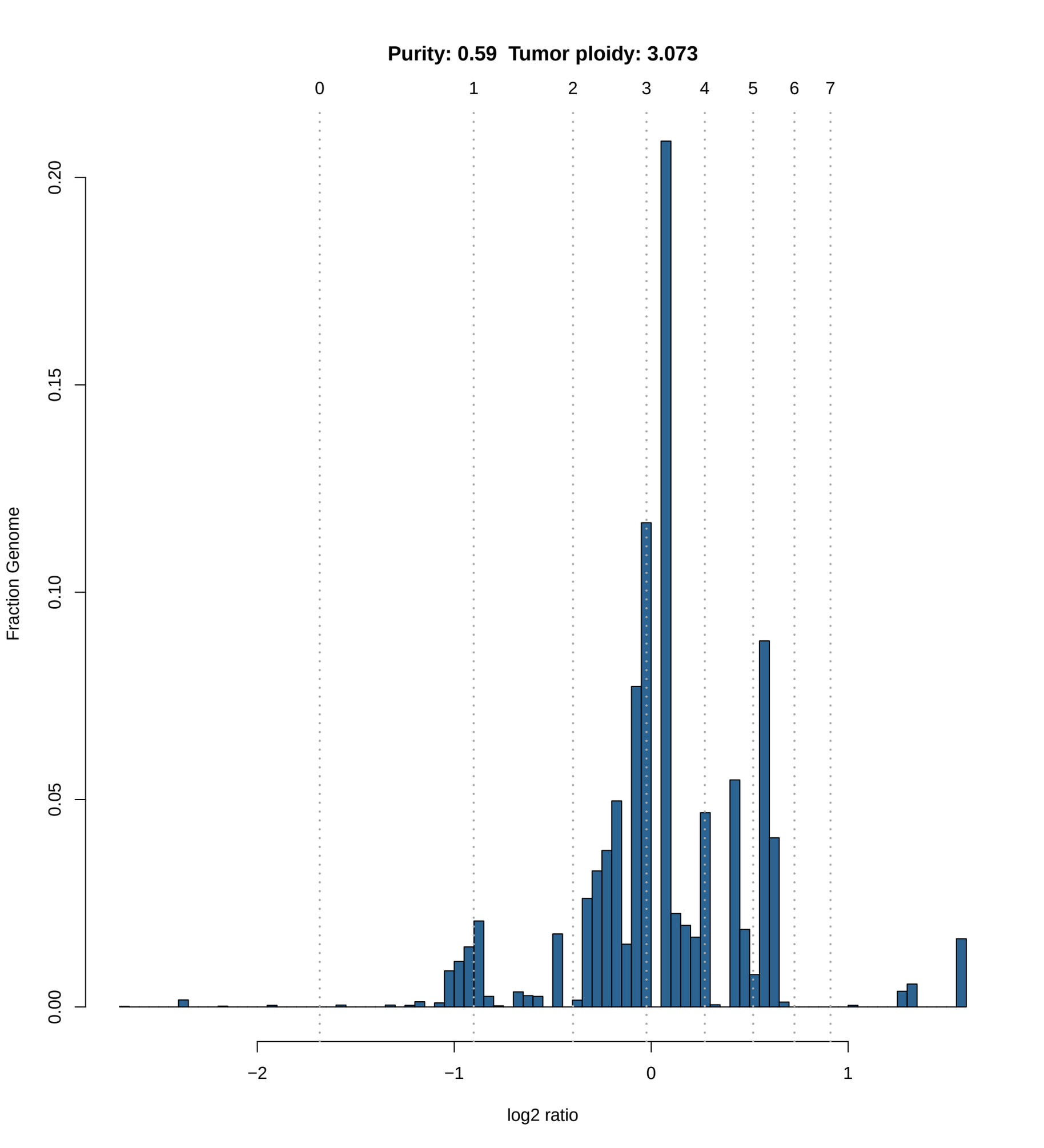

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

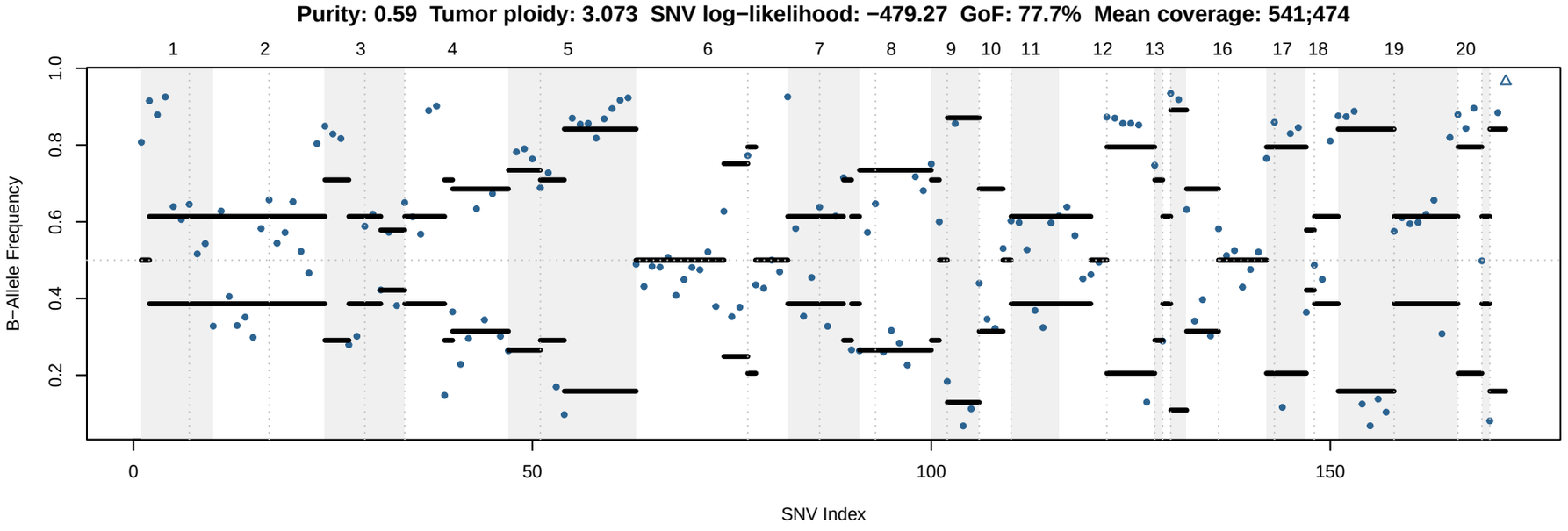

Allelic fraction (germline)
Copy Number log−ratio
1m2
7m7
6m6
5m5
4m4
3m3
2m2
7m6
5m4
4m3
7m5
6m4
5m3
7m4
0m0
4m2
6m3
7m3
5m2
6m2
4m1
7m2
5m1
2m0
7m1
4m0
5m0
6m0

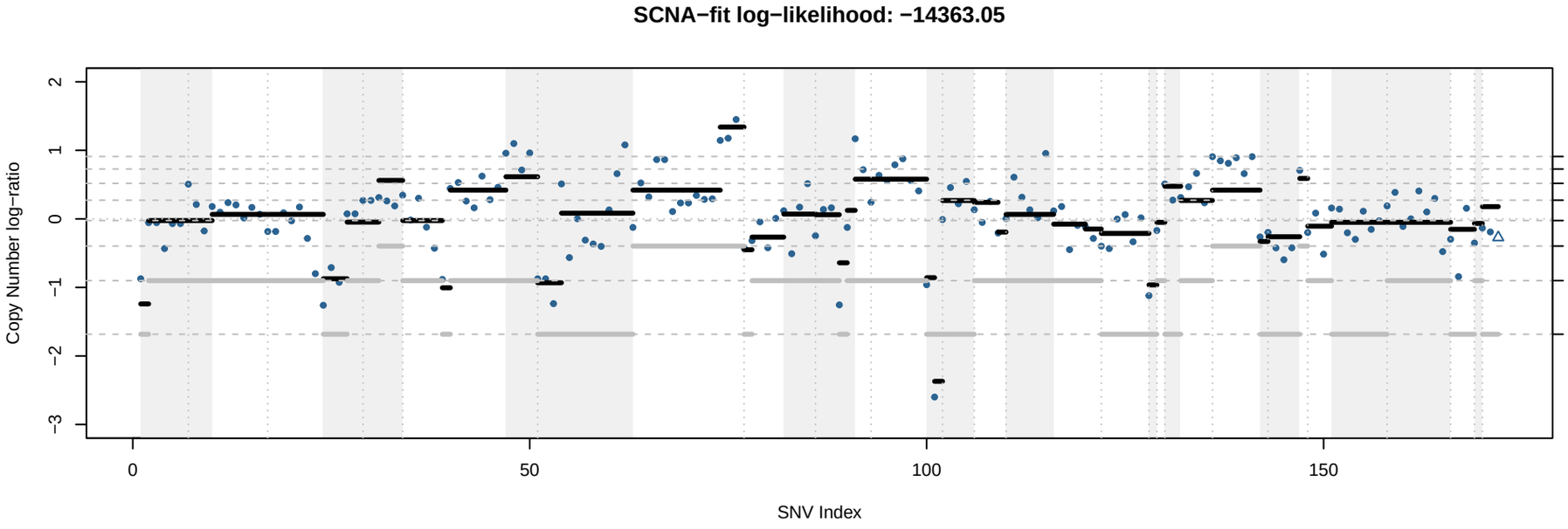

Coverage (log2)
Allelic fraction

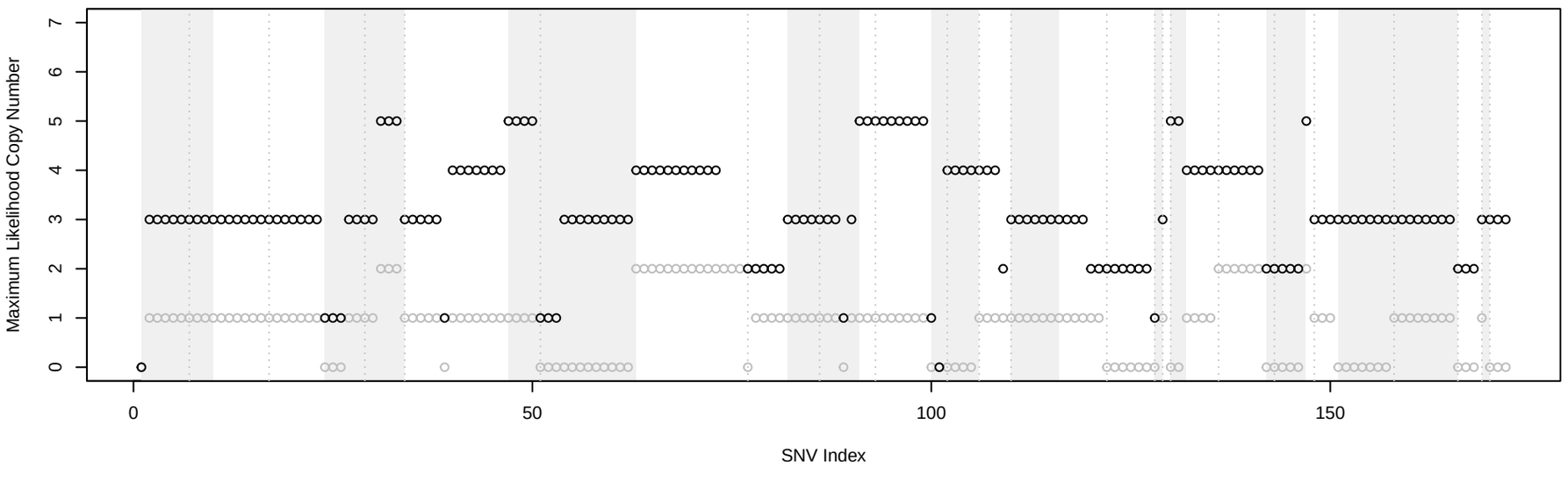

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m3
6m5
5m3
4m2
2m1
5m2
6m2
3m1
4m1
5m1
6m1
7m1

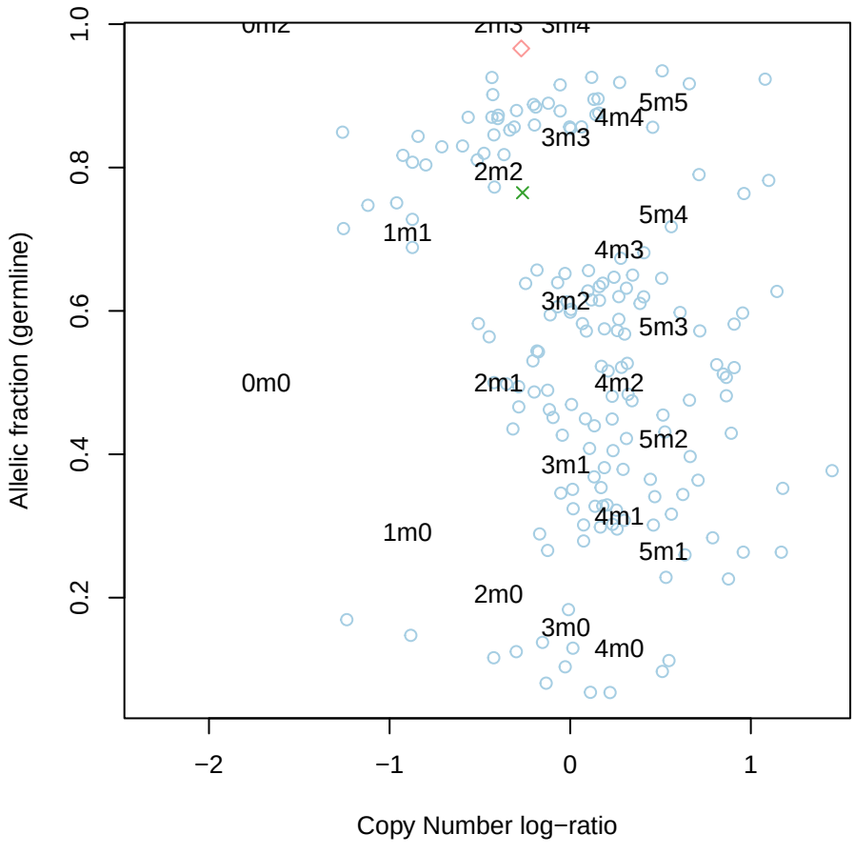

Power 0.8
Frequency
Cellular fraction

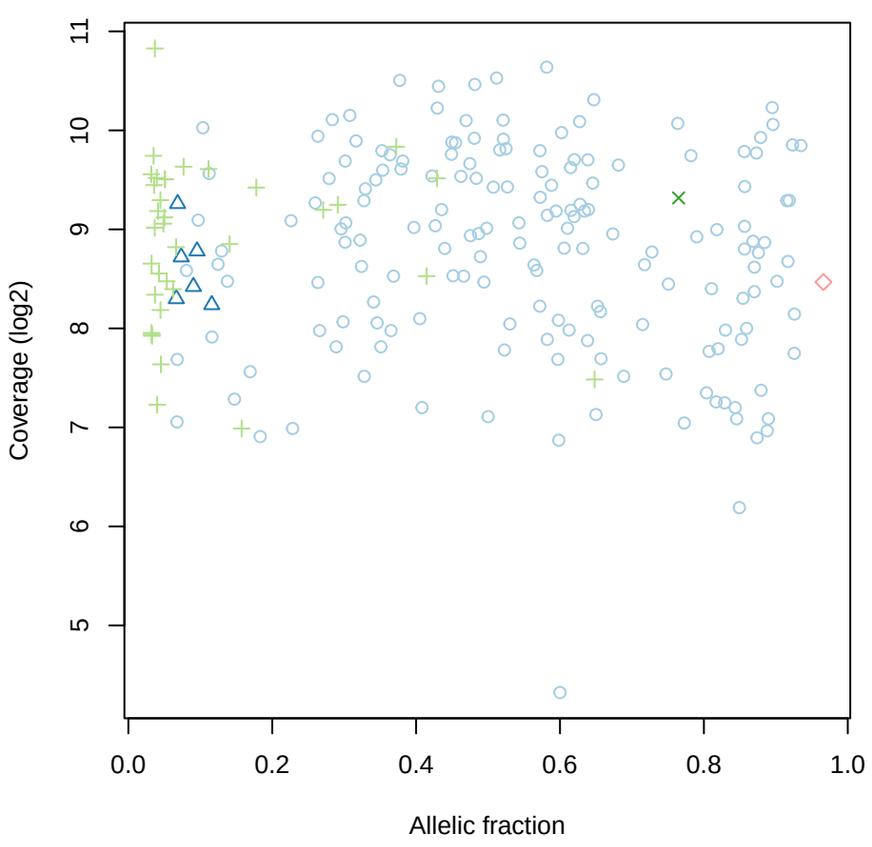

Purity: 0.59 Tumor ploidy: 3.073
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−2
−1
0
1
log2 ratio

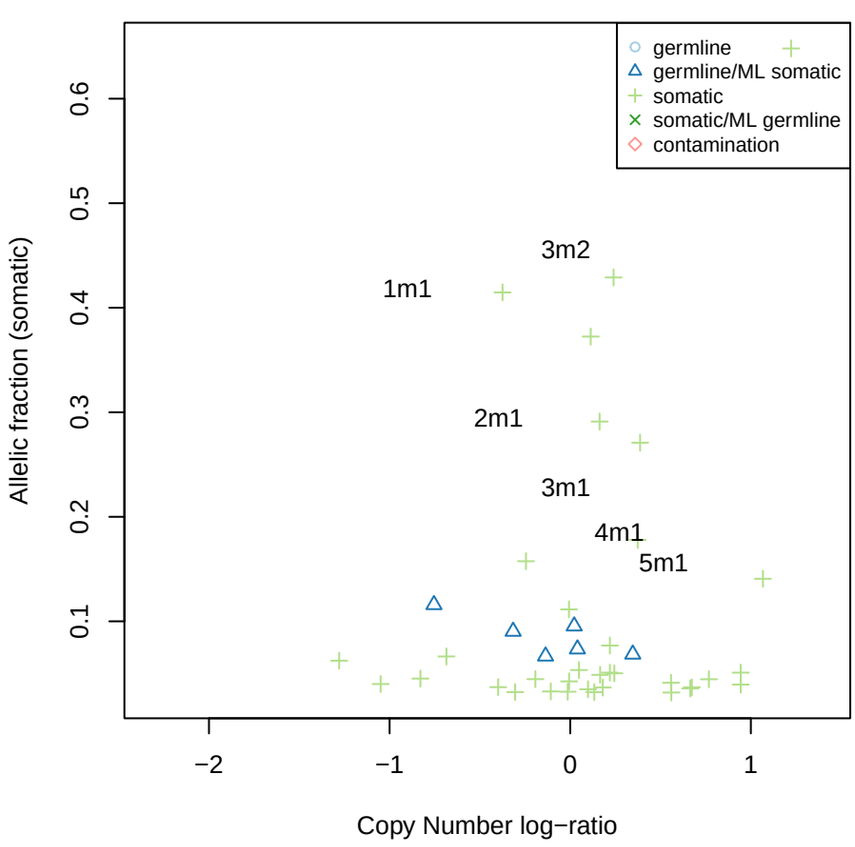

Purity: 0.59 Tumor ploidy: 3.073 SNV log−likelihood: −479.27 GoF: 77.7% Mean coverage: 541;474
1
2
3
4
5
6
7
8
9
10
11
12
13
16
17
18
19
20
B−Allele Frequency
0.2
0.4
0.6
0.8
1.0
0
50
100
150
SNV Index

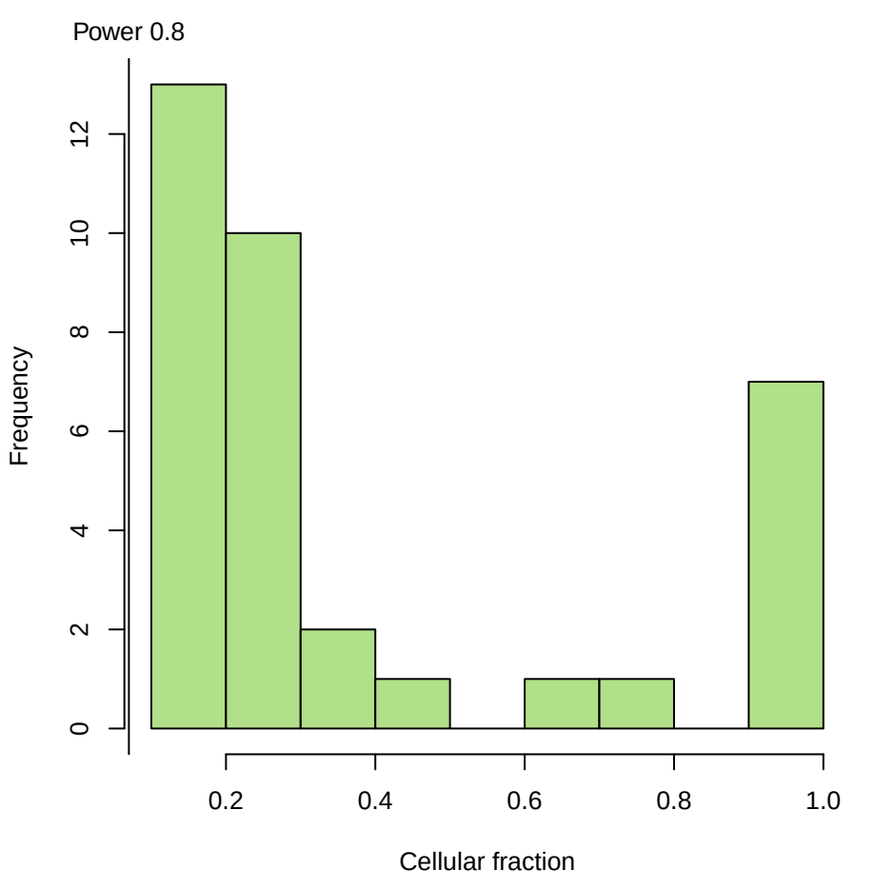

SCNA−fit log−likelihood: −14363.05
Copy Number log−ratio
−3
−2
−1
0
1
2
0
1
2
3
5
7
0
50
100
150
SNV Index

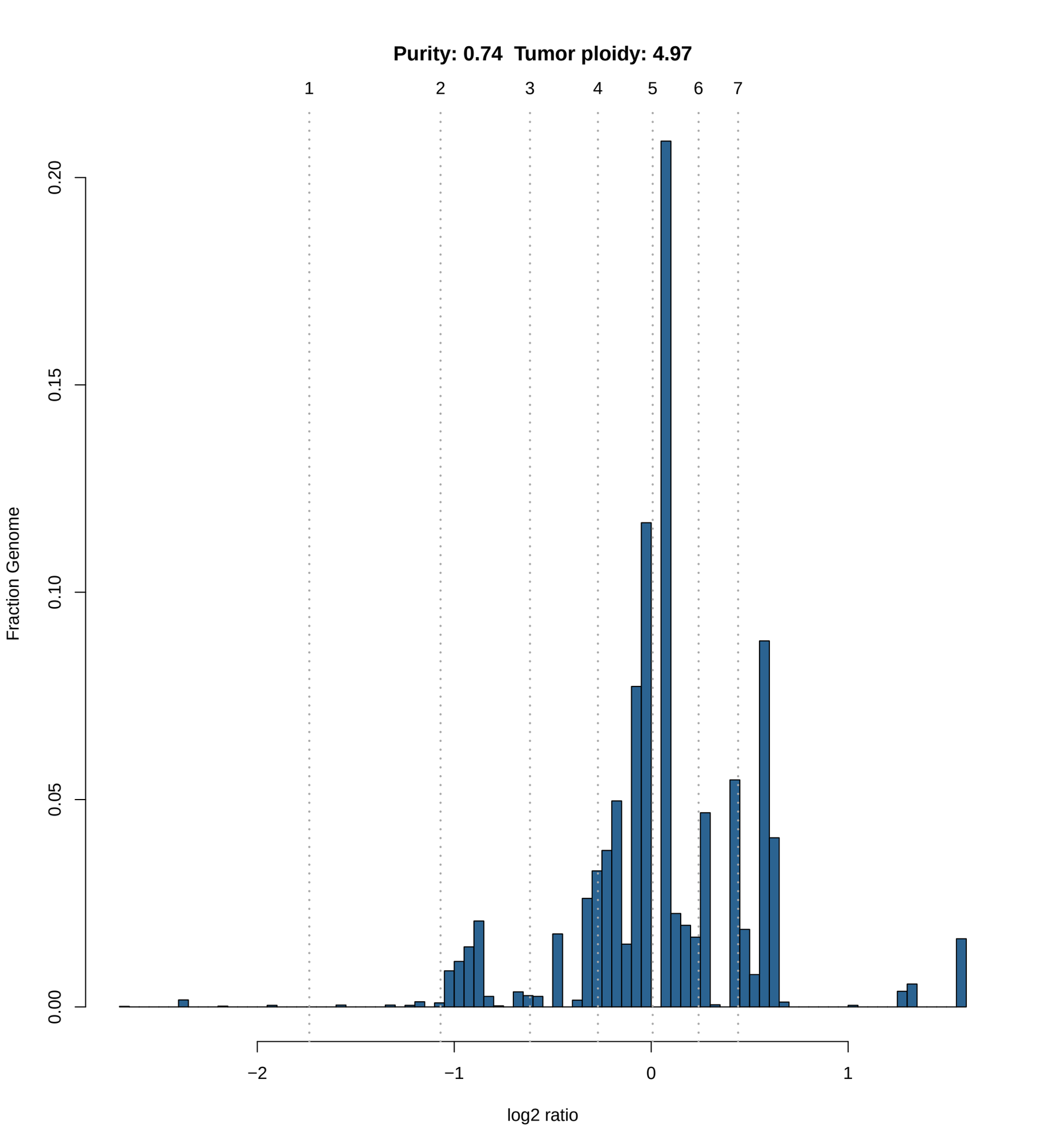

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
7
0
50
100
150
SNV Index

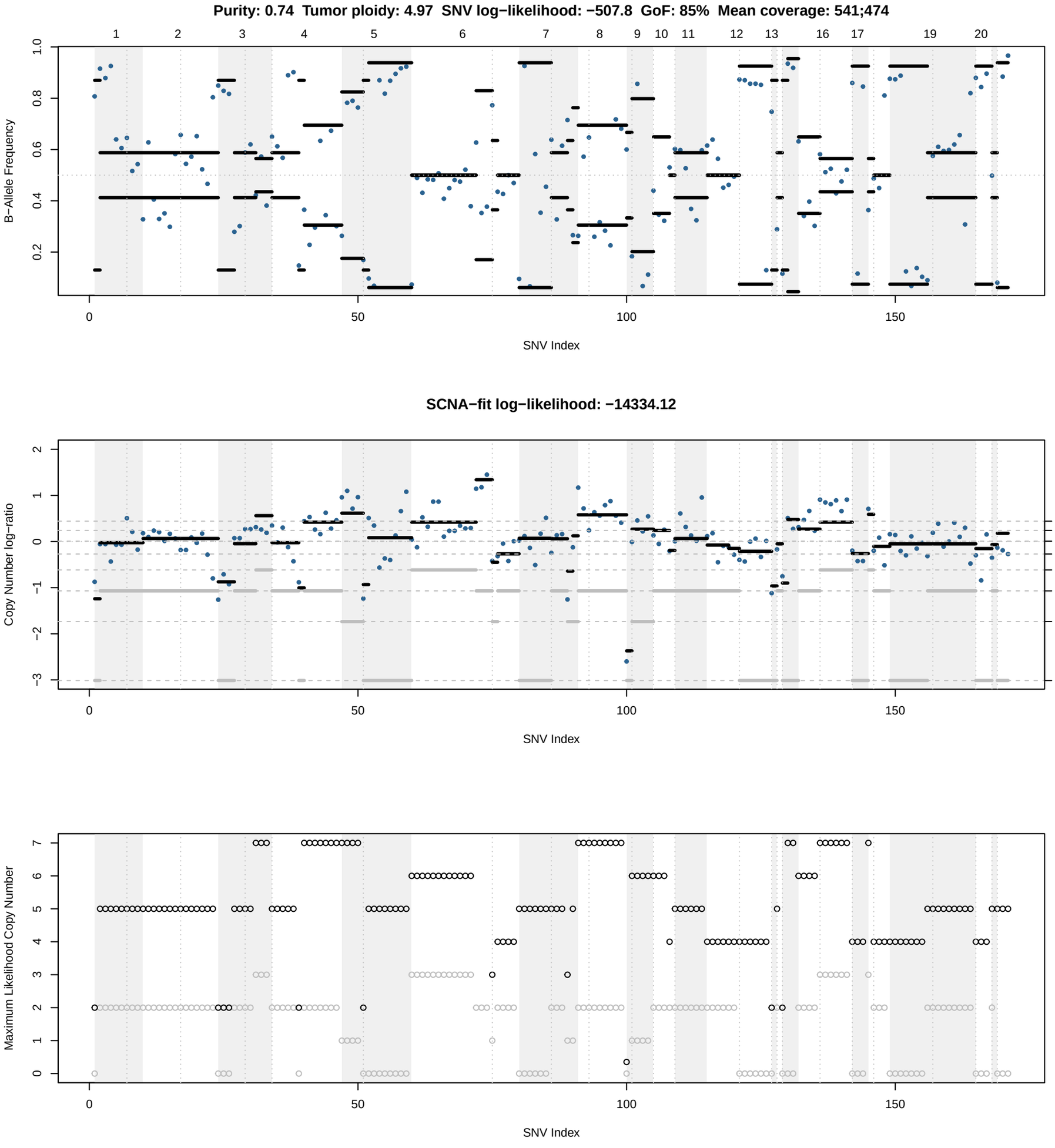

Allelic fraction (germline)
Copy Number log−ratio
0m2
2m3
3m4
5m5
4m4
3m3
2m2
5m4
1m1
4m3
3m2
5m3
0m0
2m1
4m2
5m2
3m1
4m1
1m0
5m1
2m0
3m0
4m0

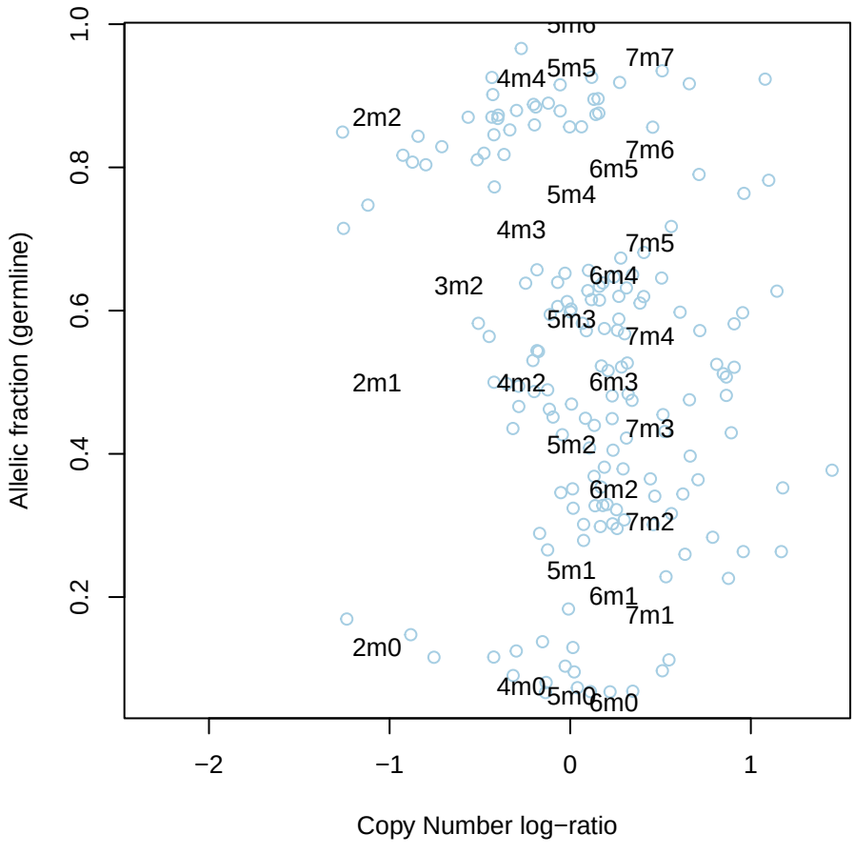

Coverage (log2)
Allelic fraction

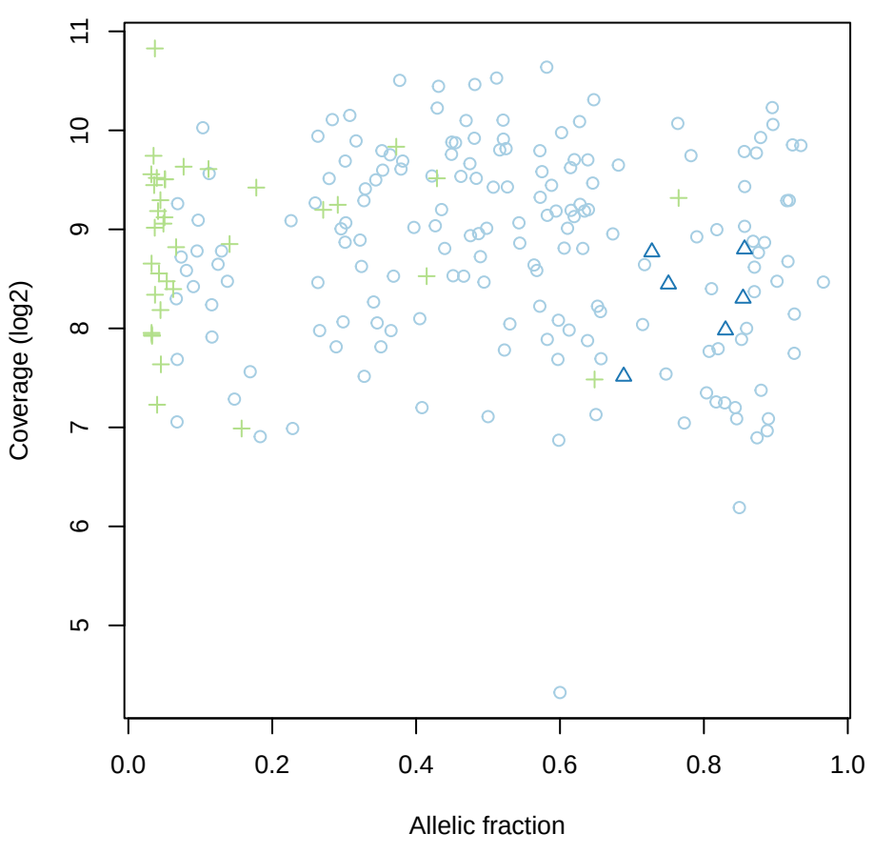

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m2
1m1
2m1
3m1
4m1
5m1

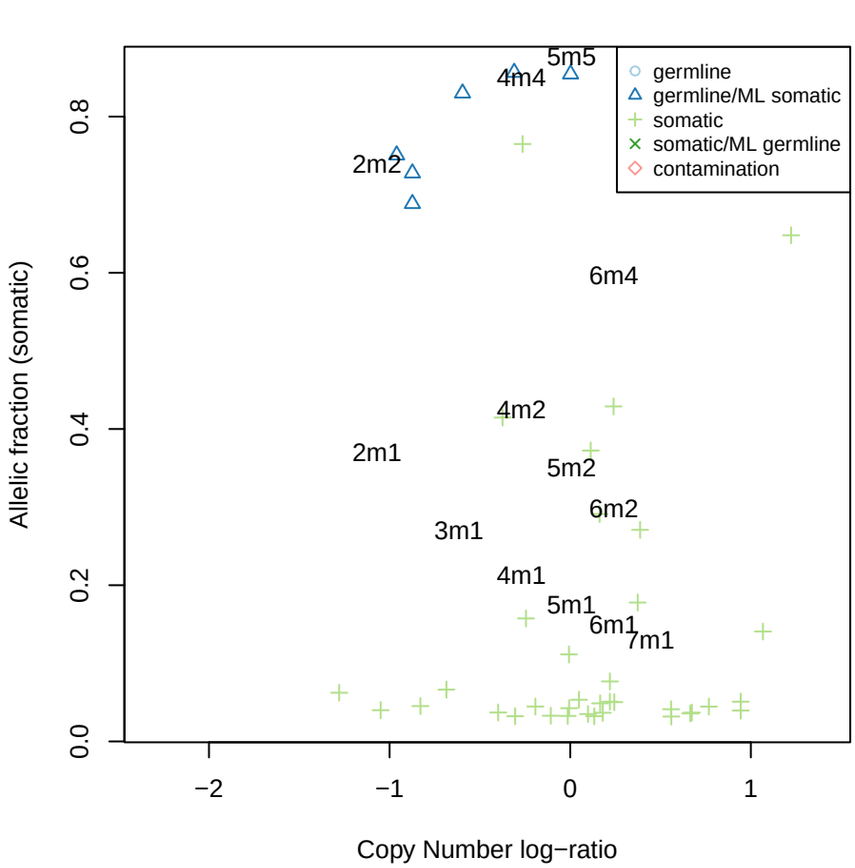

Power 0.8
Frequency
Cellular fraction

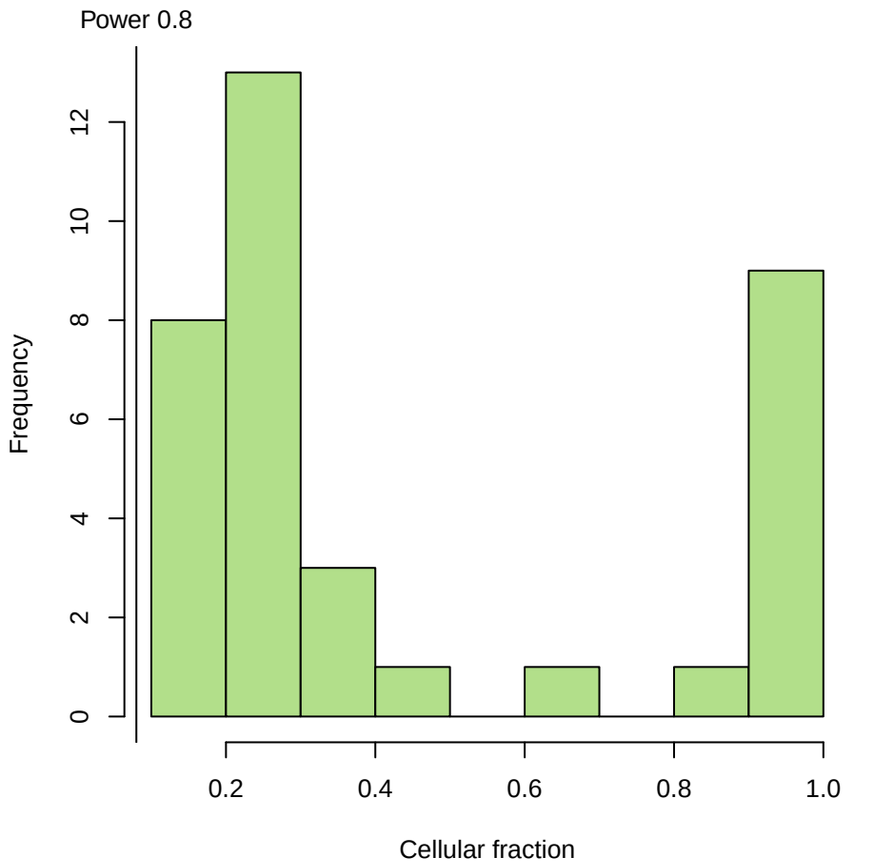

Purity: 0.74 Tumor ploidy: 4.97
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−2
−1
0
1
log2 ratio

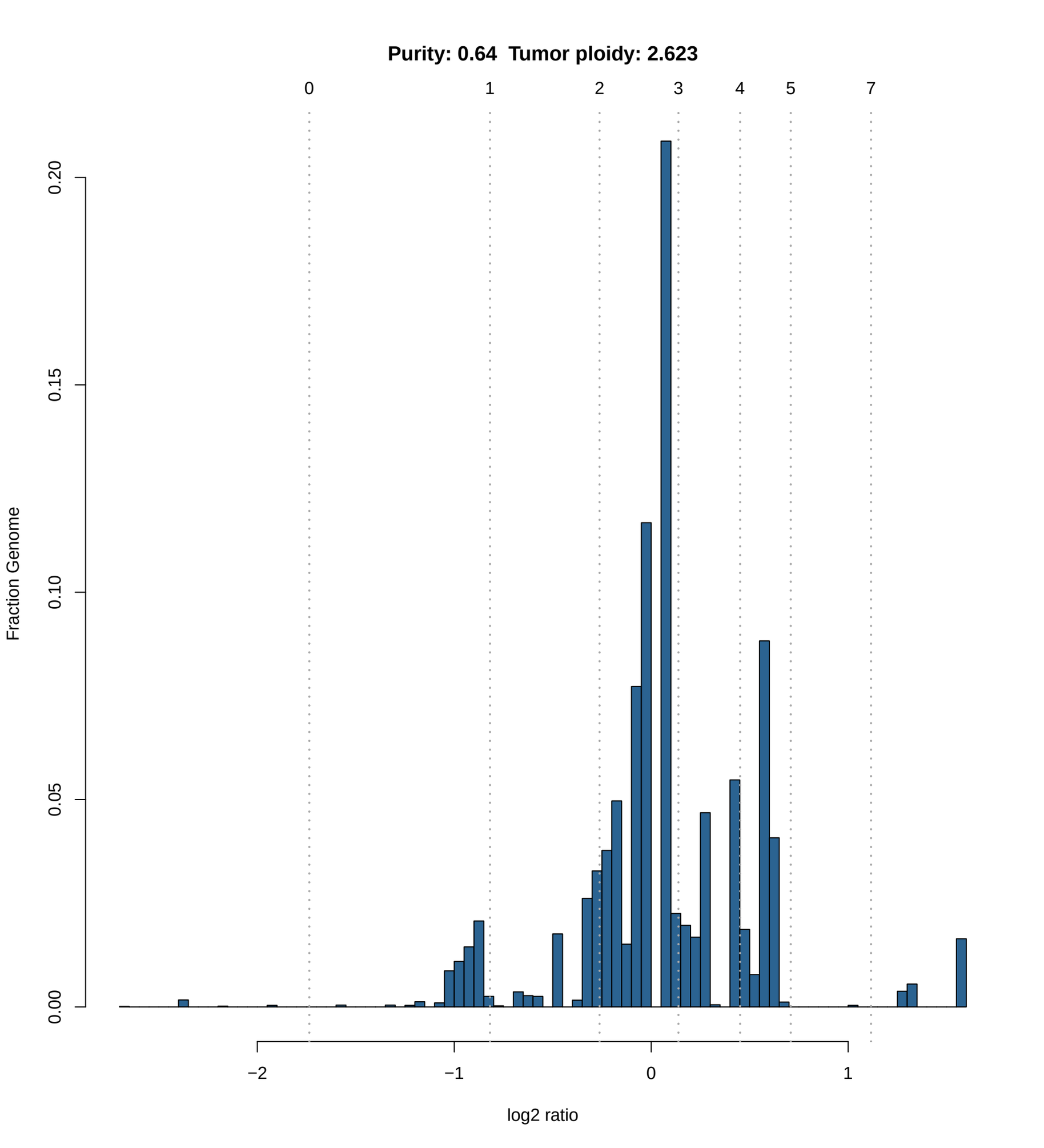

Purity: 0.74 Tumor ploidy: 4.97 SNV log−likelihood: −507.8 GoF: 85% Mean coverage: 541;474
1 2 3 4 5 6 7 8 9 10 11 12 13 16 17 19 20
B−Allele Frequency
0.2 0.4 0.6 0.8 1.0
0 50 100 150
SNV Index
SCNA−fit log−likelihood: −14334.12
Copy Number log−ratio
−3 −2 −1 0 1 2
0 1 2 3 5 7
0 50 100 150
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

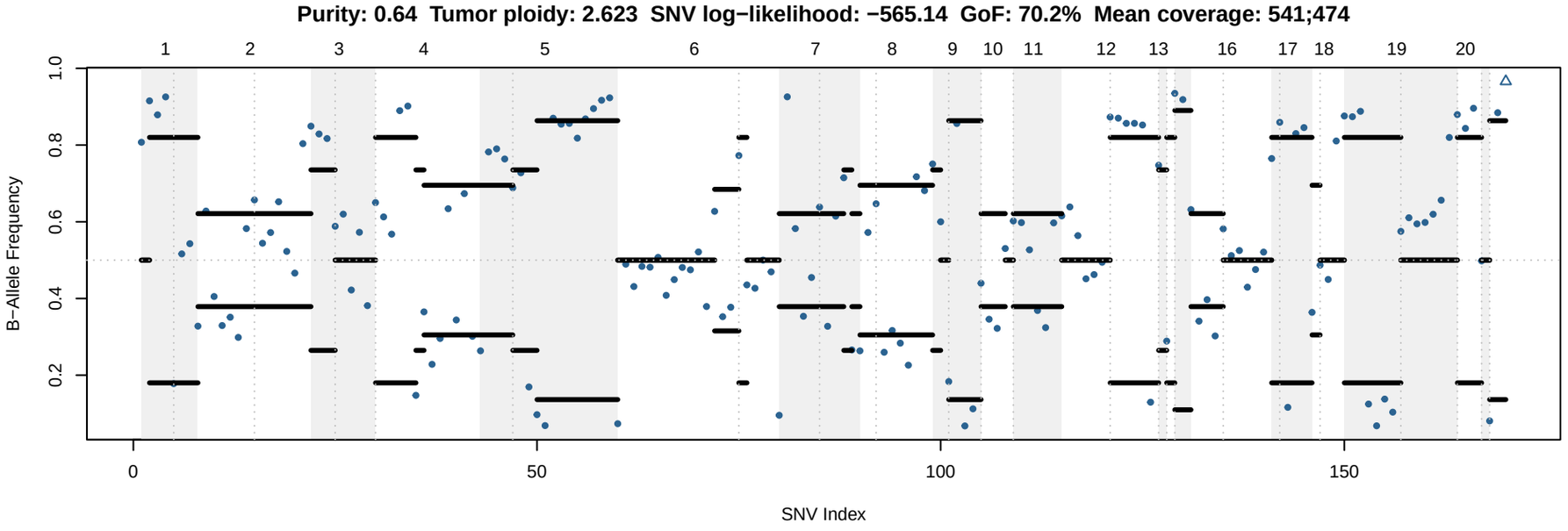

Allelic fraction (germline)
Copy Number log−ratio
5m6
7m7
5m5
4m4
2m2
7m6
6m5
5m4
4m3
7m5
3m2
6m4
5m3
7m4
2m1
4m2
6m3
7m3
5m2
6m2
7m2
5m1
6m1
7m1
2m0
4m0
5m0
6m0

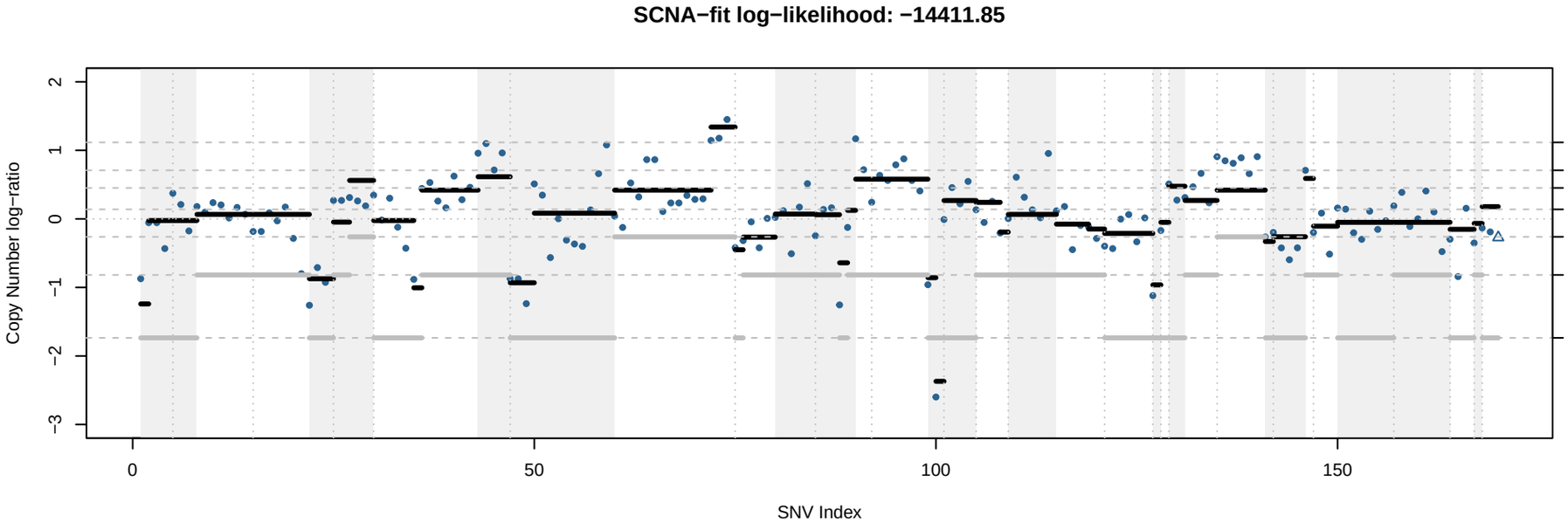

Coverage (log2)
Allelic fraction

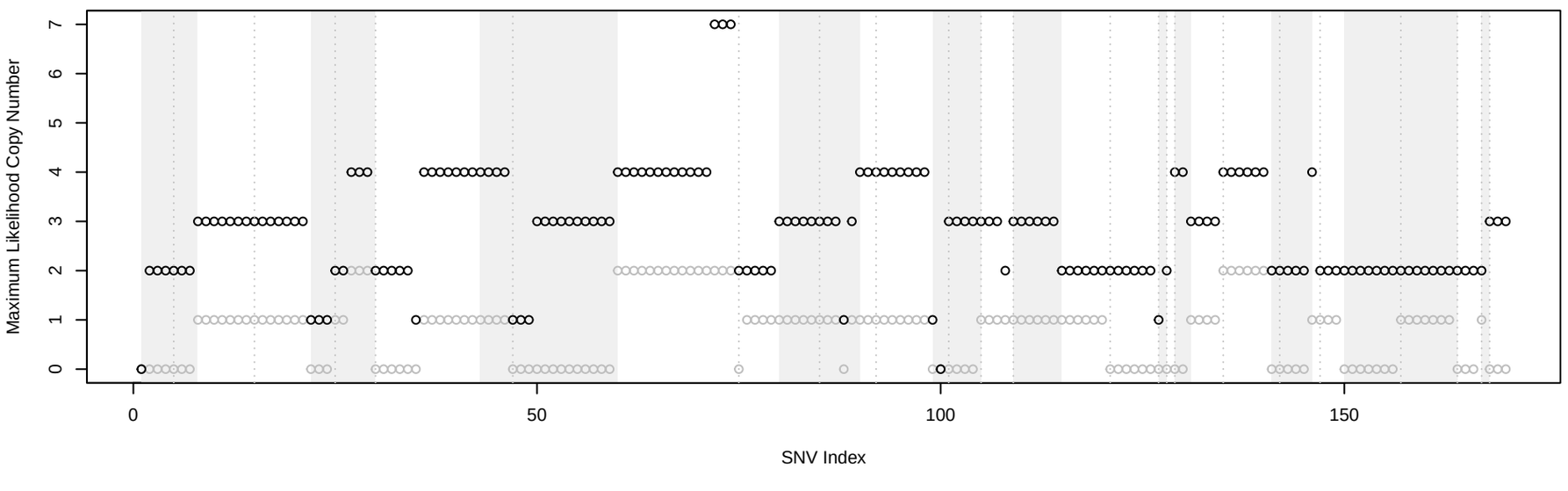

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m5
4m4
2m2
6m4
4m2
2m1
5m2
6m2
3m1
4m1
5m1
6m1
7m1

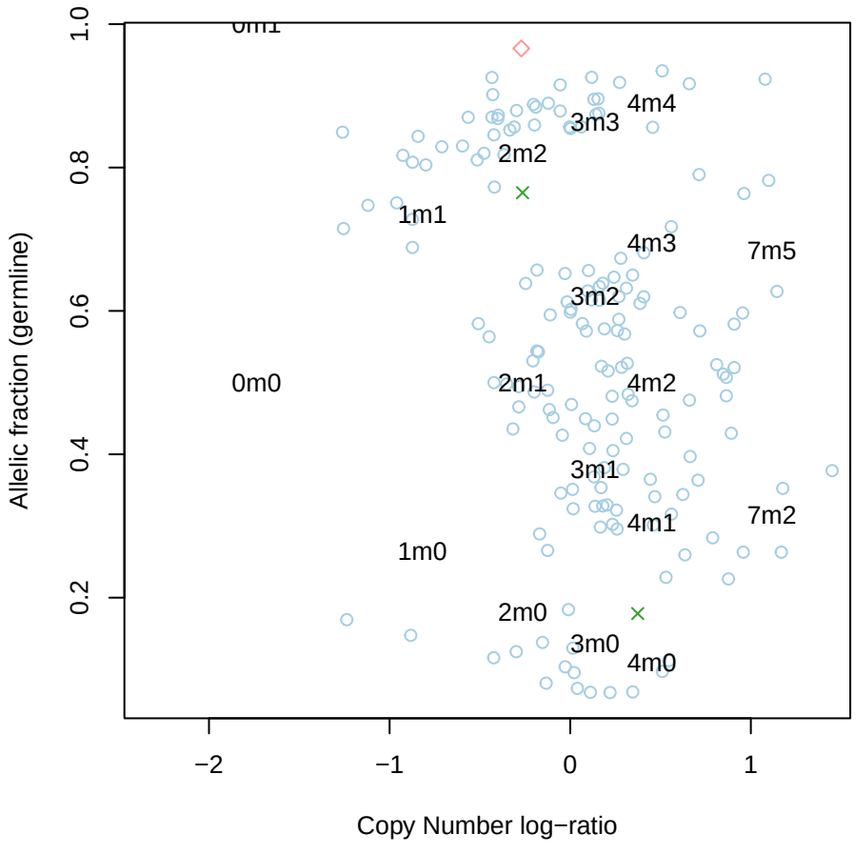

Power 0.8
Frequency
Cellular fraction

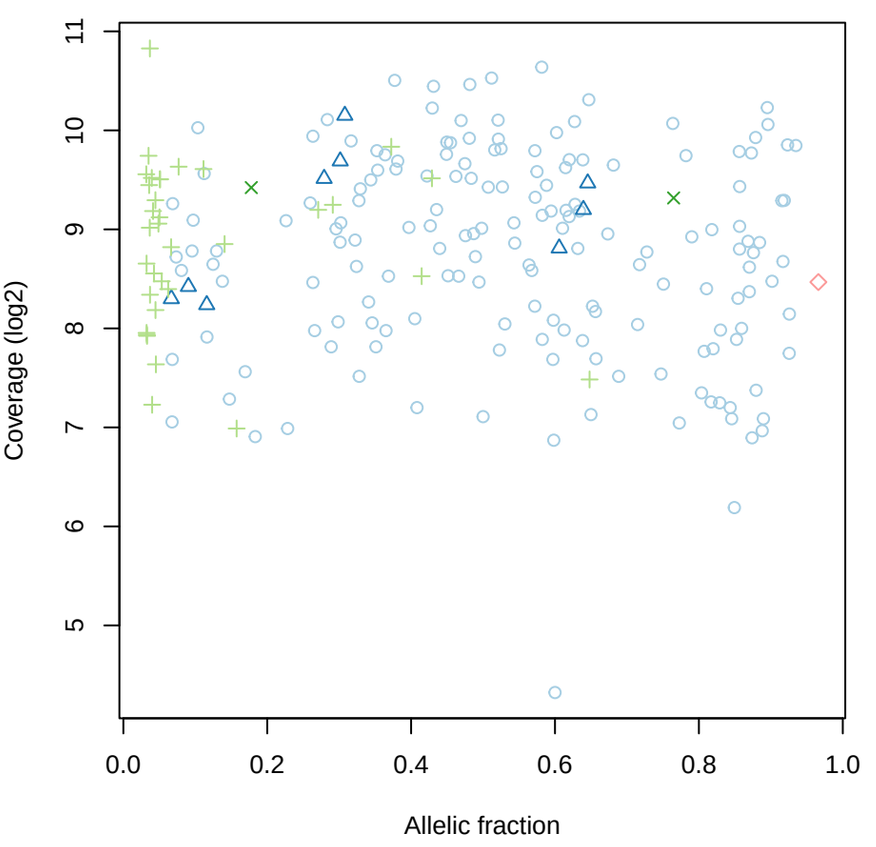

Purity: 0.64 Tumor ploidy: 2.623
0
1
2
3
4
5
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−2
−1
0
1
log2 ratio

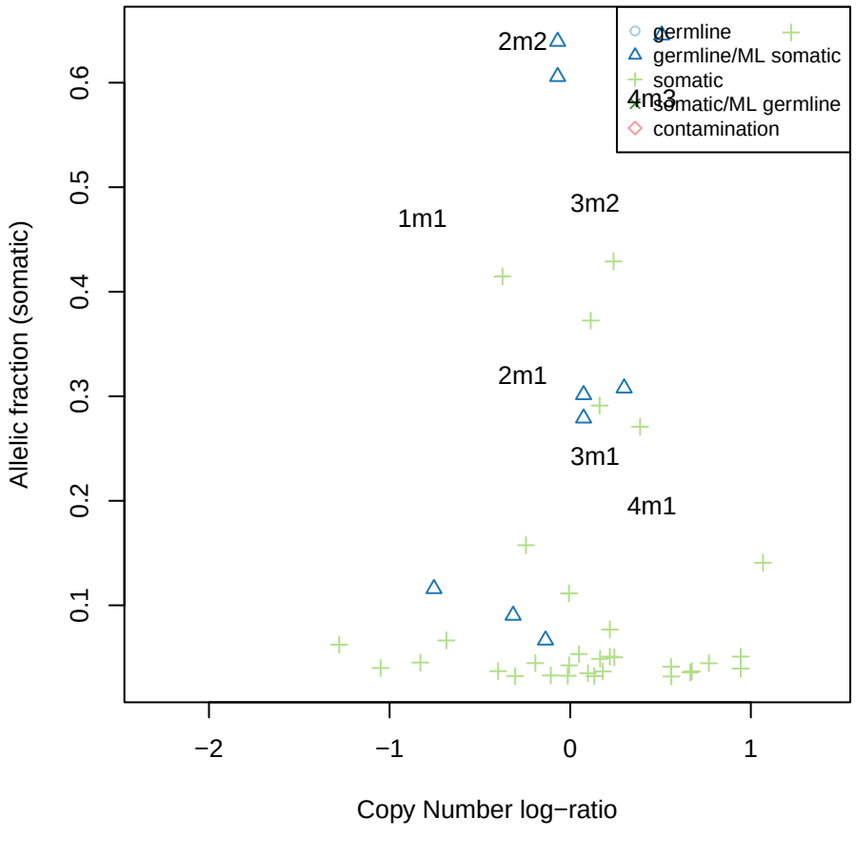

Purity: 0.64 Tumor ploidy: 2.623 SNV log−likelihood: −565.14 GoF: 70.2% Mean coverage: 541;474
1 2 3 4 5 6 7 8 9 10 11 12 13 16 17 18 19 20
B−Allele Frequency
0.2 0.4 0.6 0.8 1.0
0 50 100 150
SNV Index

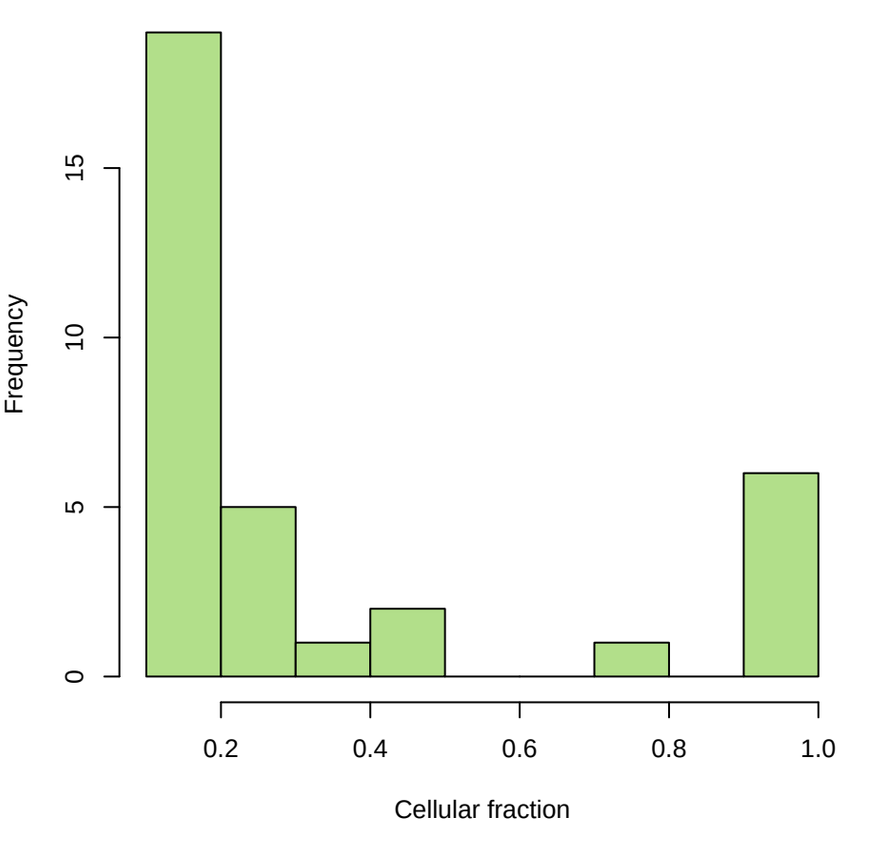

SCNA−fit log−likelihood: −14411.85
Copy Number log−ratio
−3 −2 −1 0 1 2
0 1 2 3 5 7
0 50 100 150
SNV Index

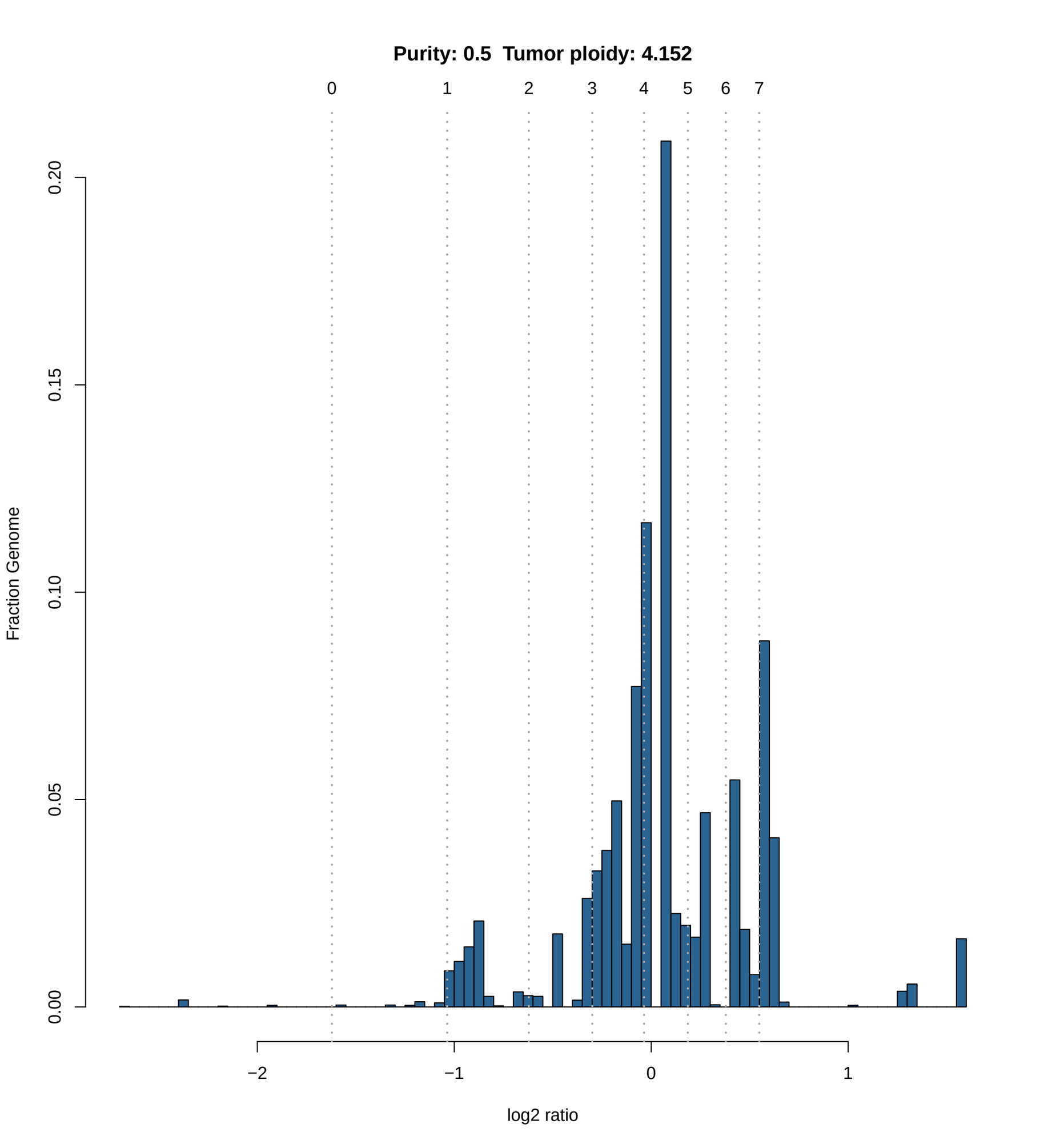

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

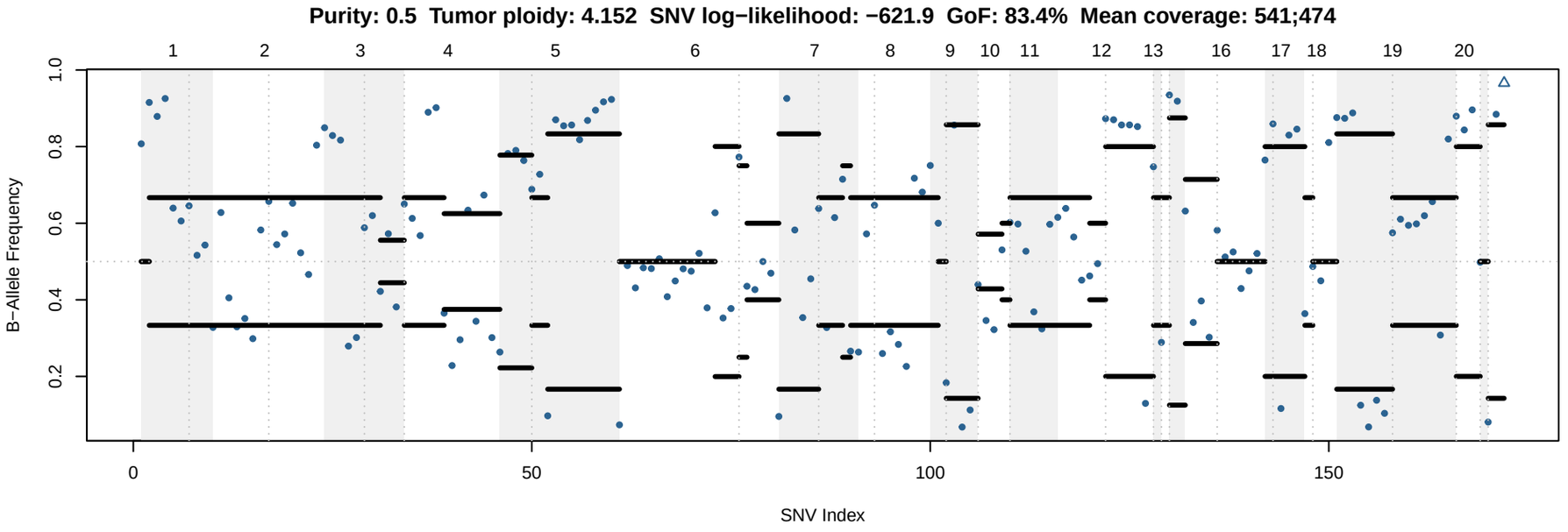

Allelic fraction (germline)
Copy Number log−ratio
0m1
4m4
3m3
2m2
1m1
4m3
7m5
3m2
0m0
2m1
4m2
3m1
4m1
7m2
1m0
2m0
3m0
4m0

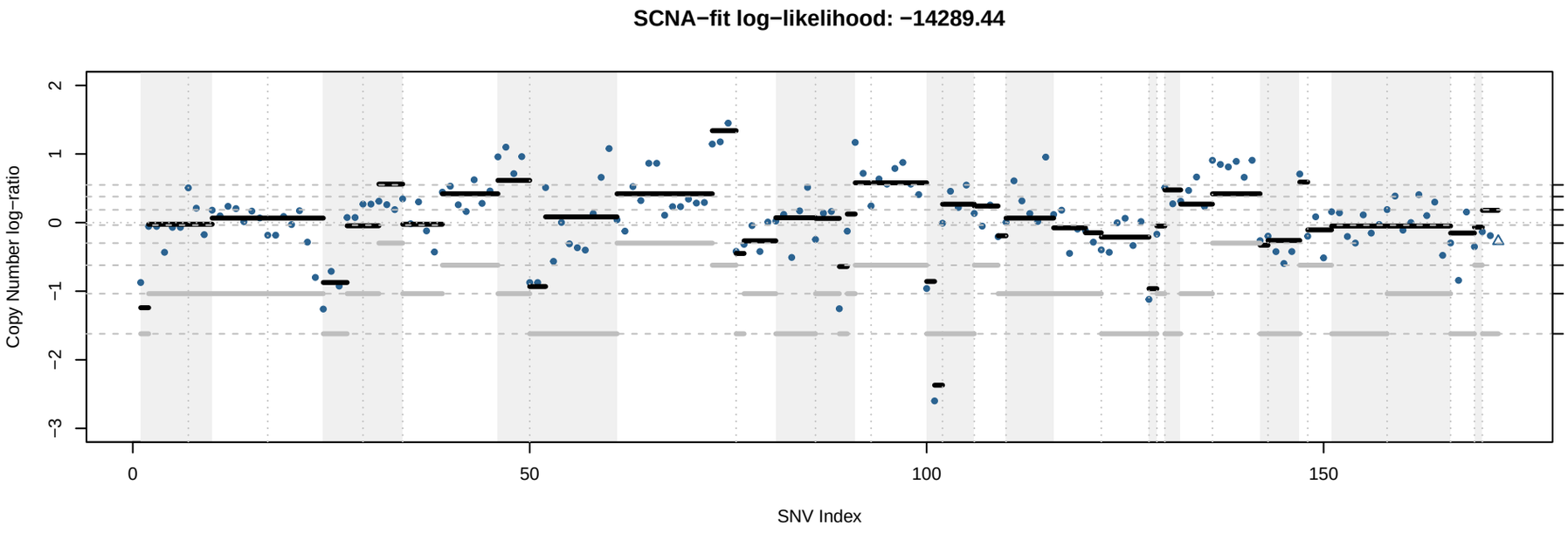

Coverage (log2)
Allelic fraction

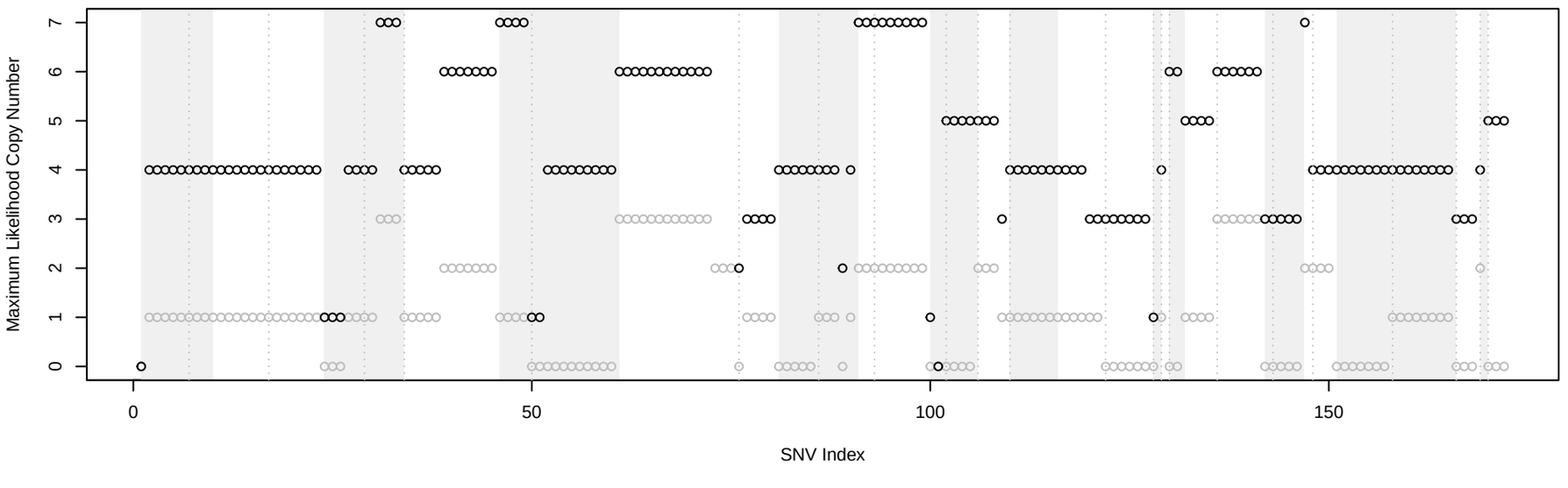

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
4m3
1m1
3m2
2m1
3m1
4m1

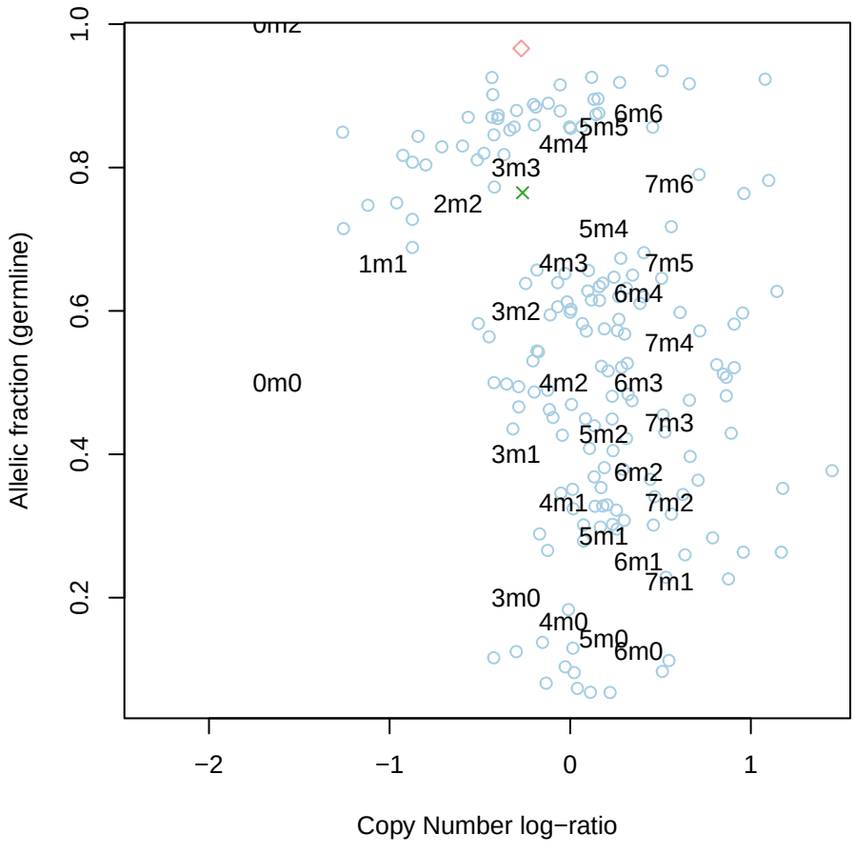

Frequency
Cellular fraction

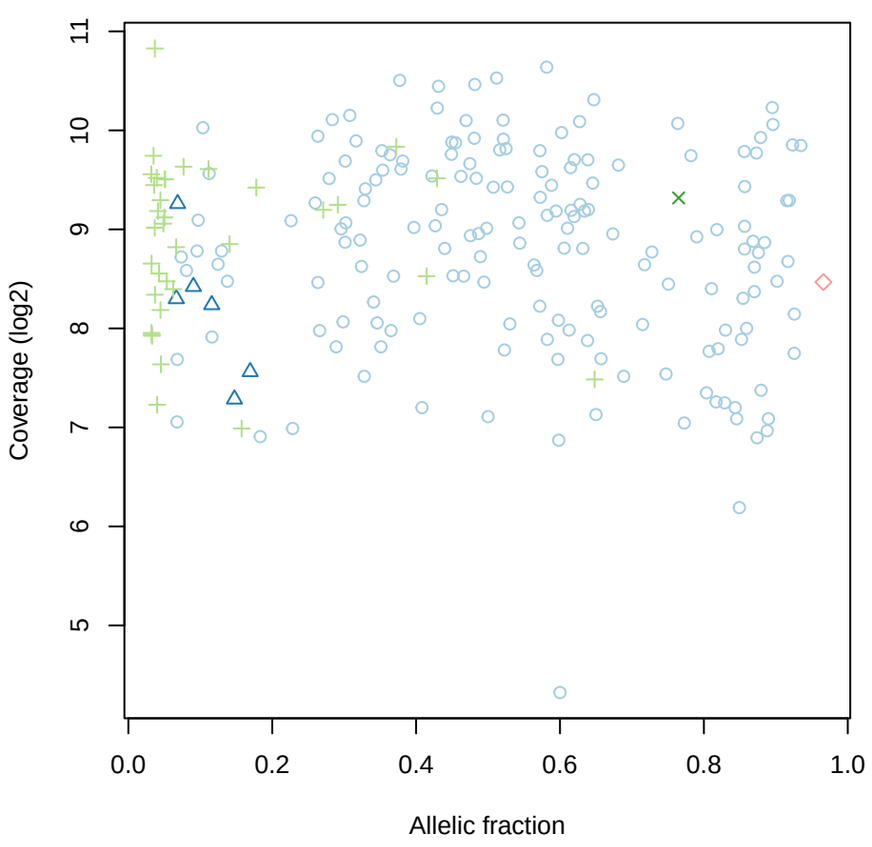

Purity: 0.5 Tumor ploidy: 4.152
0
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−2
−1
0
1
log2 ratio

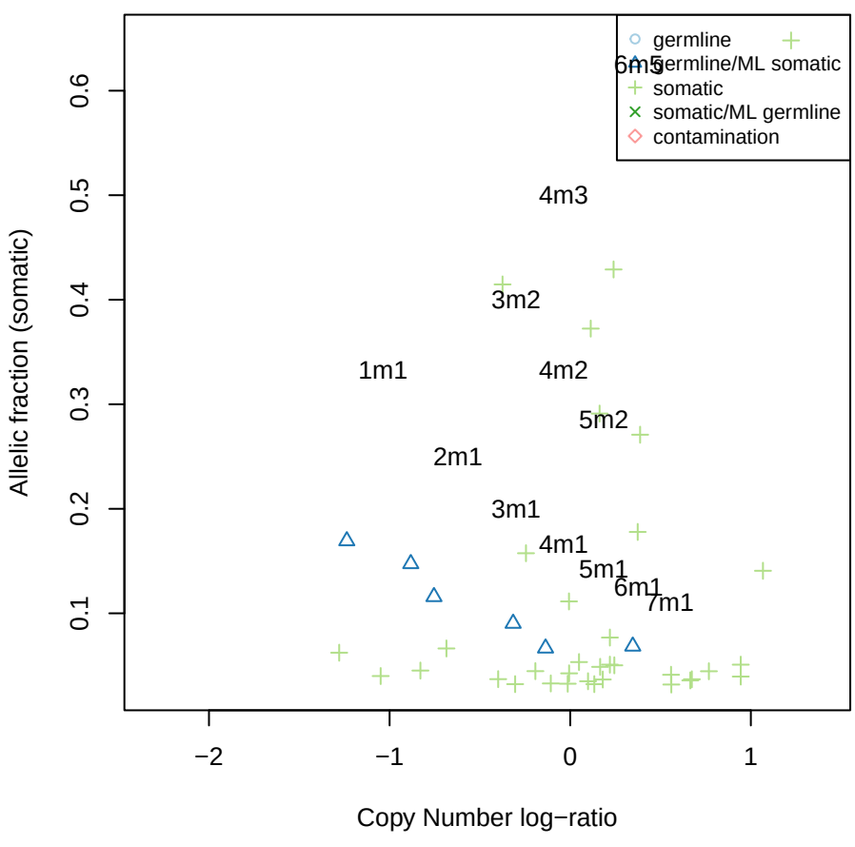

Purity: 0.5 Tumor ploidy: 4.152 SNV log−likelihood: −621.9 GoF: 83.4% Mean coverage: 541;474
1
2
3
4
5
6
7
8
9
10
11
12
13
16
17
18
19
20
B−Allele Frequency
0.2
0.4
0.6
0.8
1.0
0
50
100
150
SNV Index

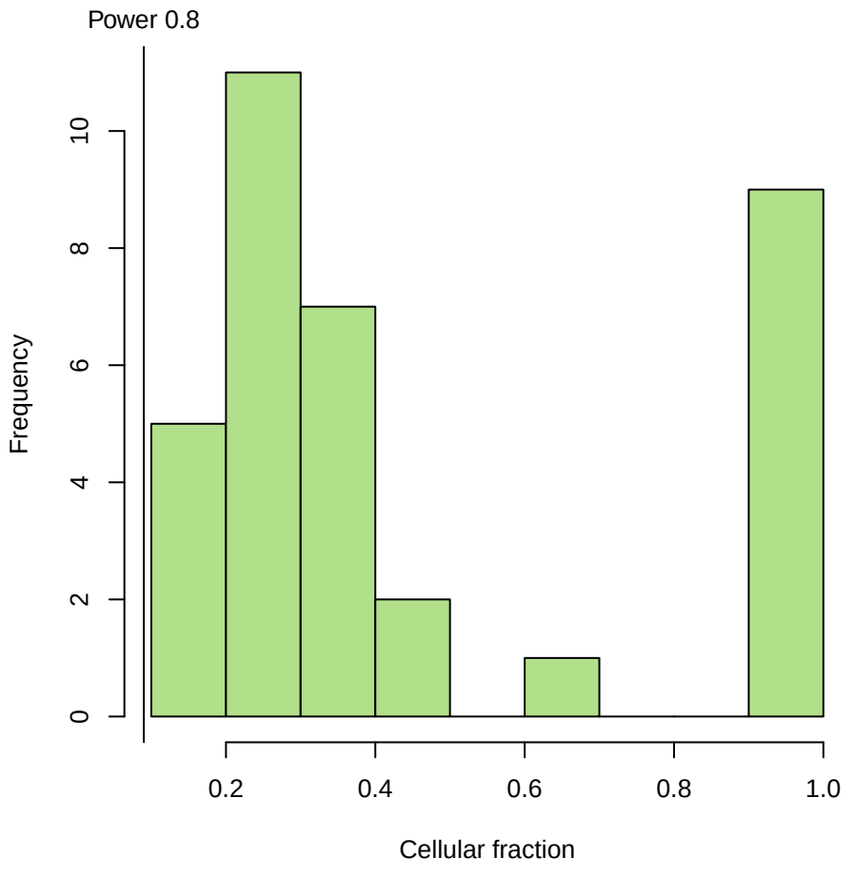

SCNA−fit log−likelihood: −14289.44
Copy Number log−ratio
−3
−2
−1
0
1
2
0
1
2
4
6
0
50
100
150
SNV Index

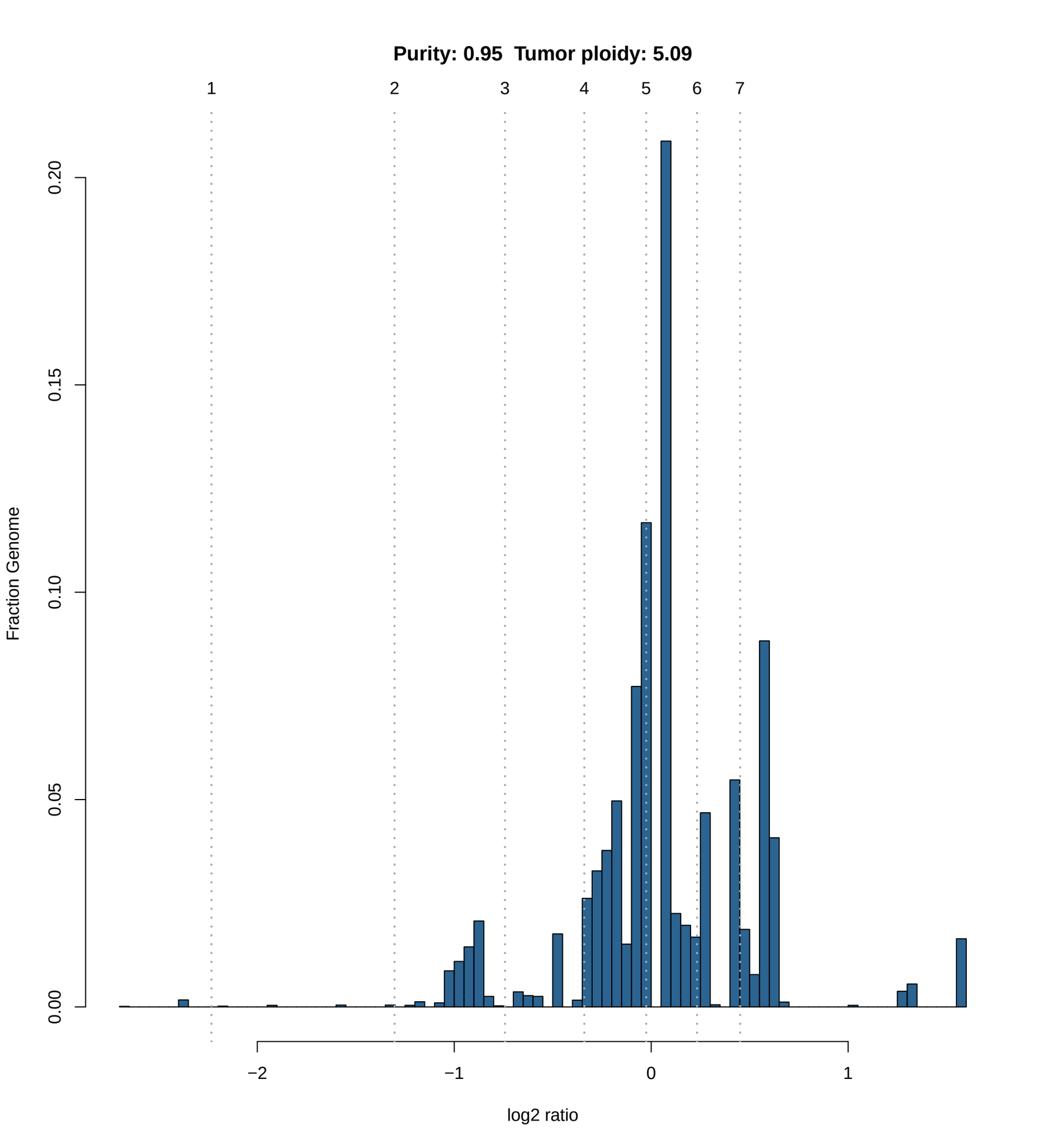

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
7
0
50
100
150
SNV Index

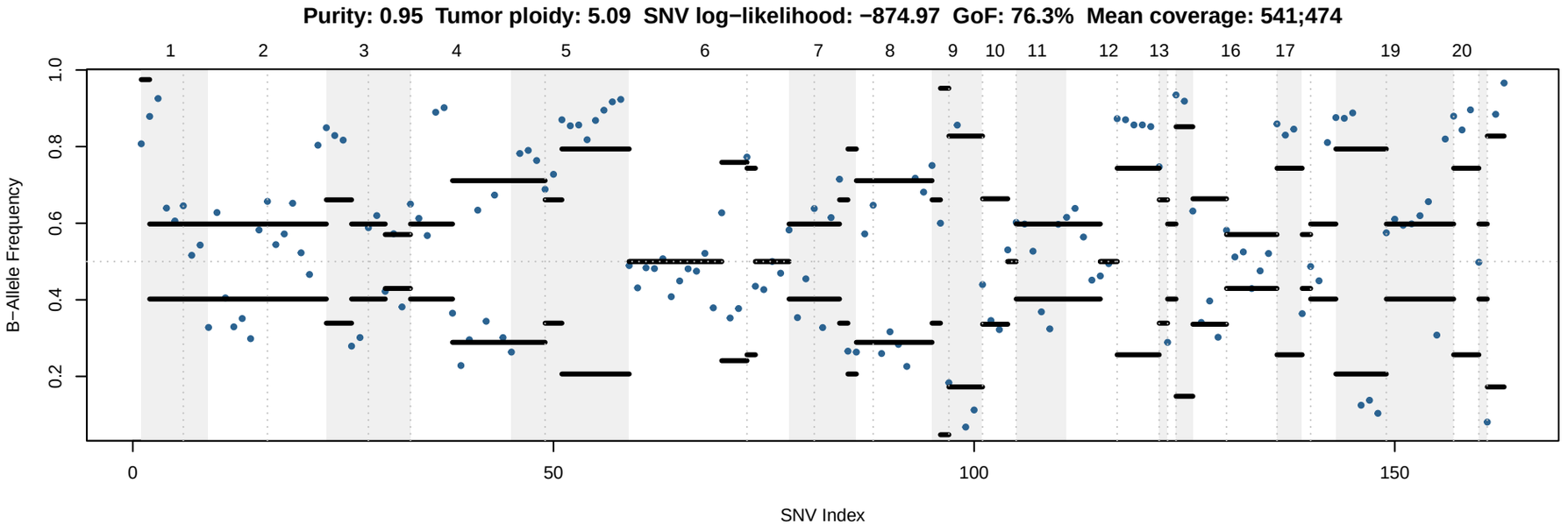

Allelic fraction (germline)
Copy Number log−ratio
0m2
6m6
5m5
4m4
3m3
7m6
2m2
5m4
1m1
4m3
7m5
6m4
3m2
7m4
0m0
4m2
6m3
7m3
5m2
3m1
6m2
4m1
7m2
5m1
6m1
7m1
3m0
4m0
5m0
6m0

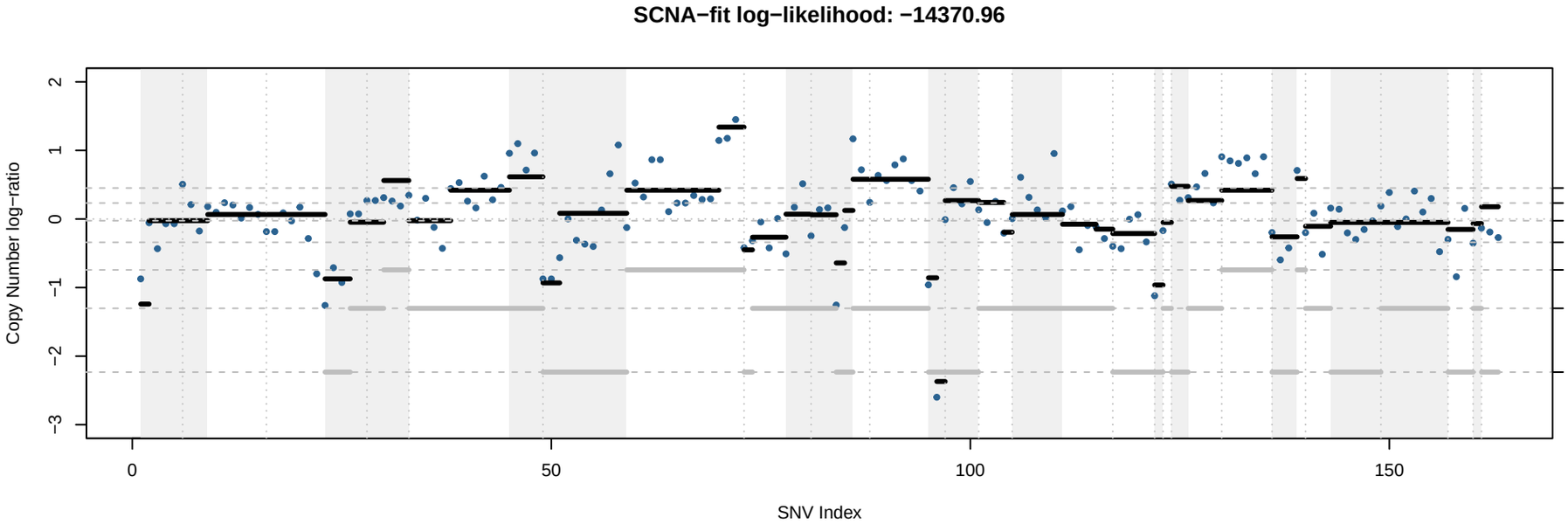

Coverage (log2)
Allelic fraction

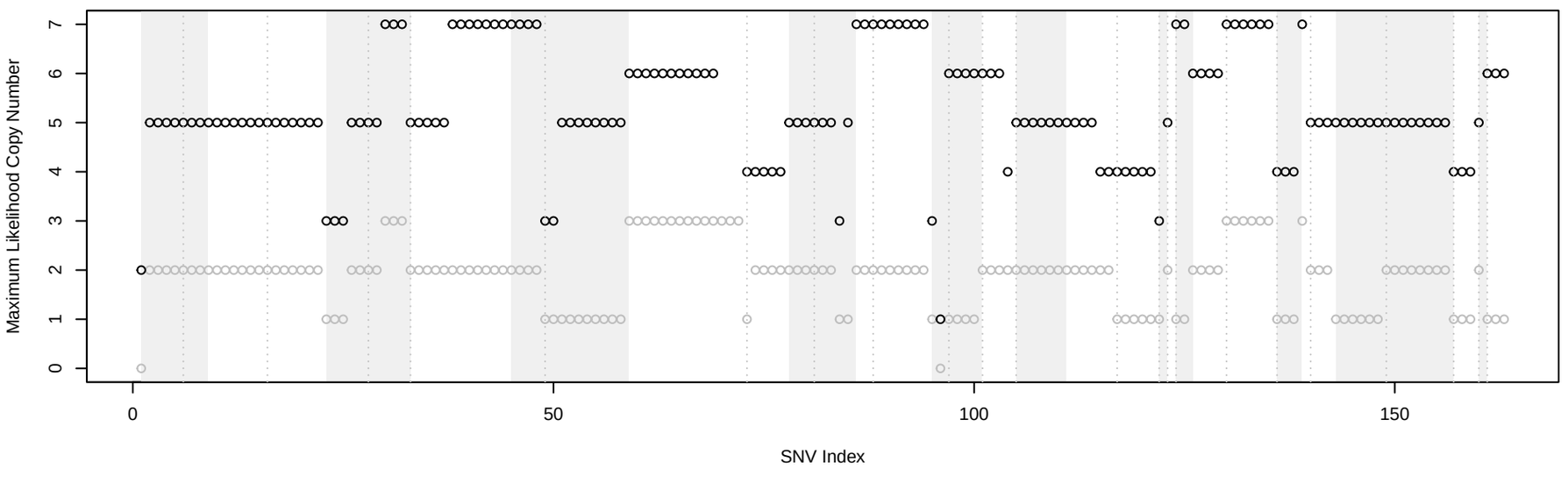

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
6m5
4m3
3m2
1m1
4m2
5m2
2m1
3m1
4m1
5m1
6m1
7m1

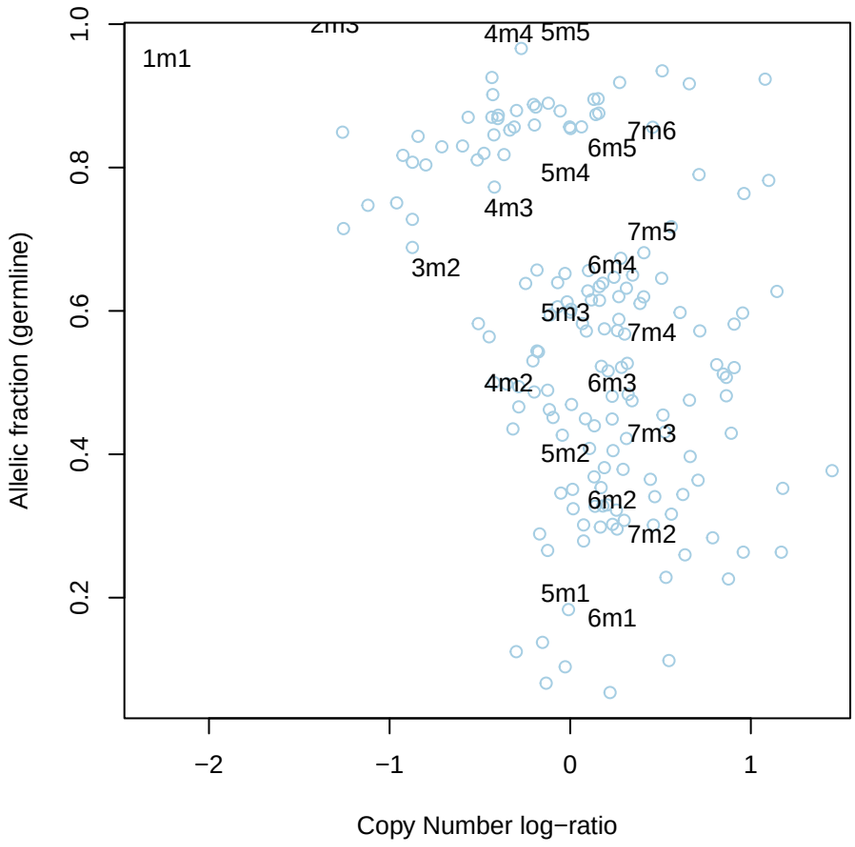

Power 0.8
Frequency
Cellular fraction

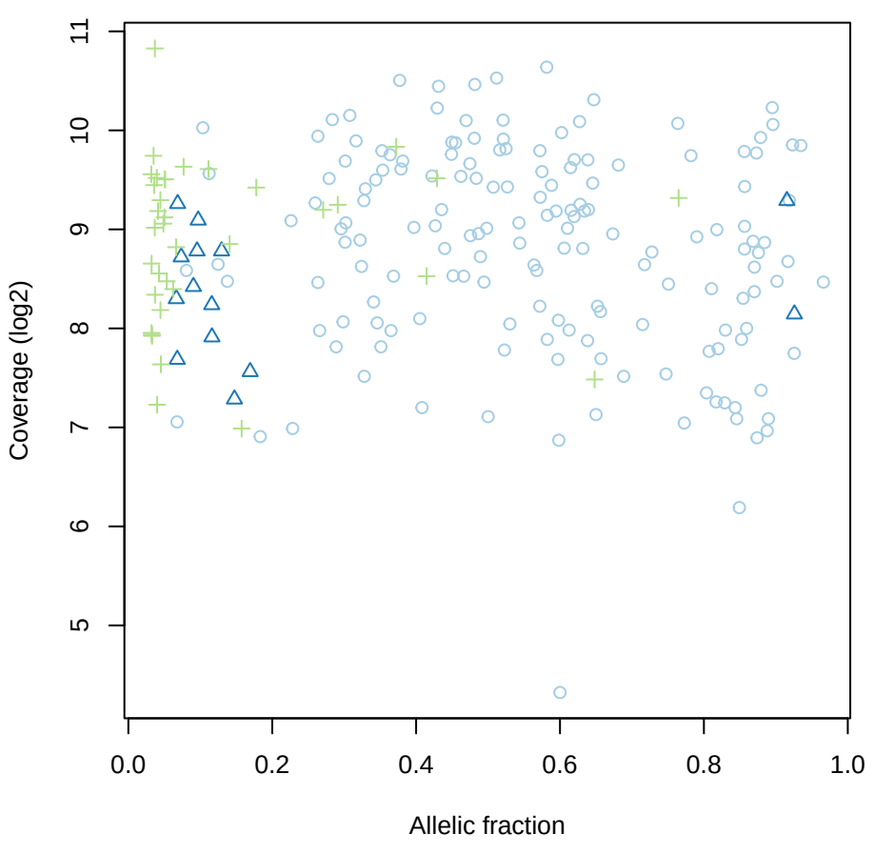

Purity: 0.95 Tumor ploidy: 5.09
1
2
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−2
−1
0
1
log2 ratio

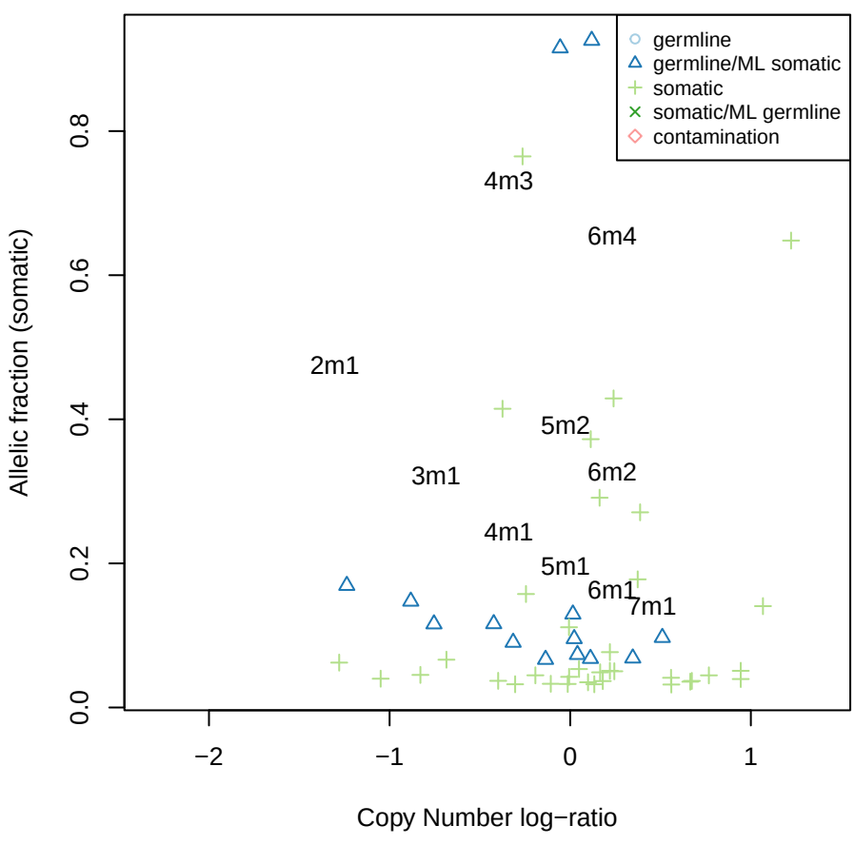

Purity: 0.95 Tumor ploidy: 5.09 SNV log−likelihood: −874.97 GoF: 76.3% Mean coverage: 541;474
1
2
3
4
5
6
7
8
9
10
11
12
13
16
17
19
20
B−Allele Frequency
0.2
0.4
0.6
0.8
1.0
0
50
100
150
SNV Index

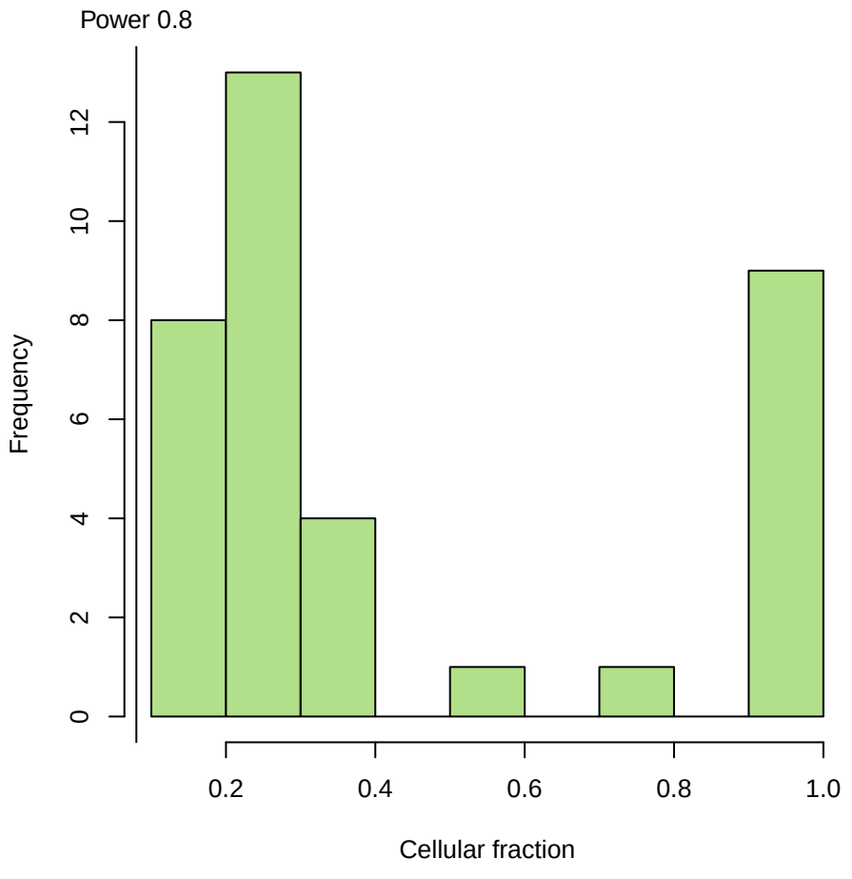

SCNA−fit log−likelihood: −14370.96
Copy Number log−ratio
−3
−2
−1
0
1
2
1
2
3
4
6
0
50
100
150
SNV Index


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


Allelic fraction (germline)
Copy Number log−ratio
1m1
2m3
4m4
5m5
7m6
6m5
5m4
4m3
7m5
3m2
6m4
5m3
7m4
4m2
6m3
7m3
5m2
6m2
7m2
5m1
6m1


Coverage (log2)
Allelic fraction


germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
4m3
6m4
2m1
5m2
3m1
6m2
4m1
5m1
6m1
7m1


Power 0.8
Frequency
Cellular fraction