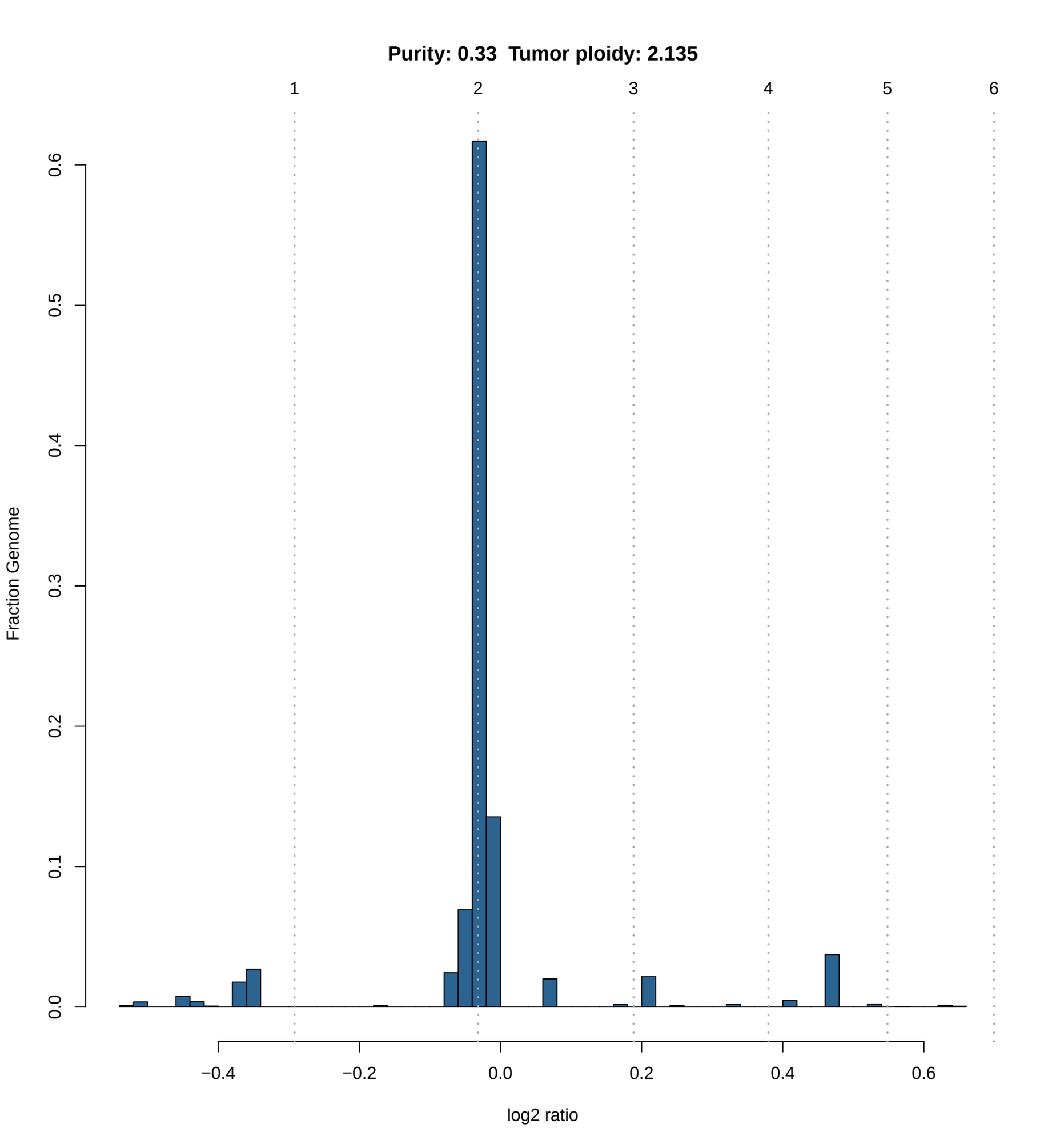
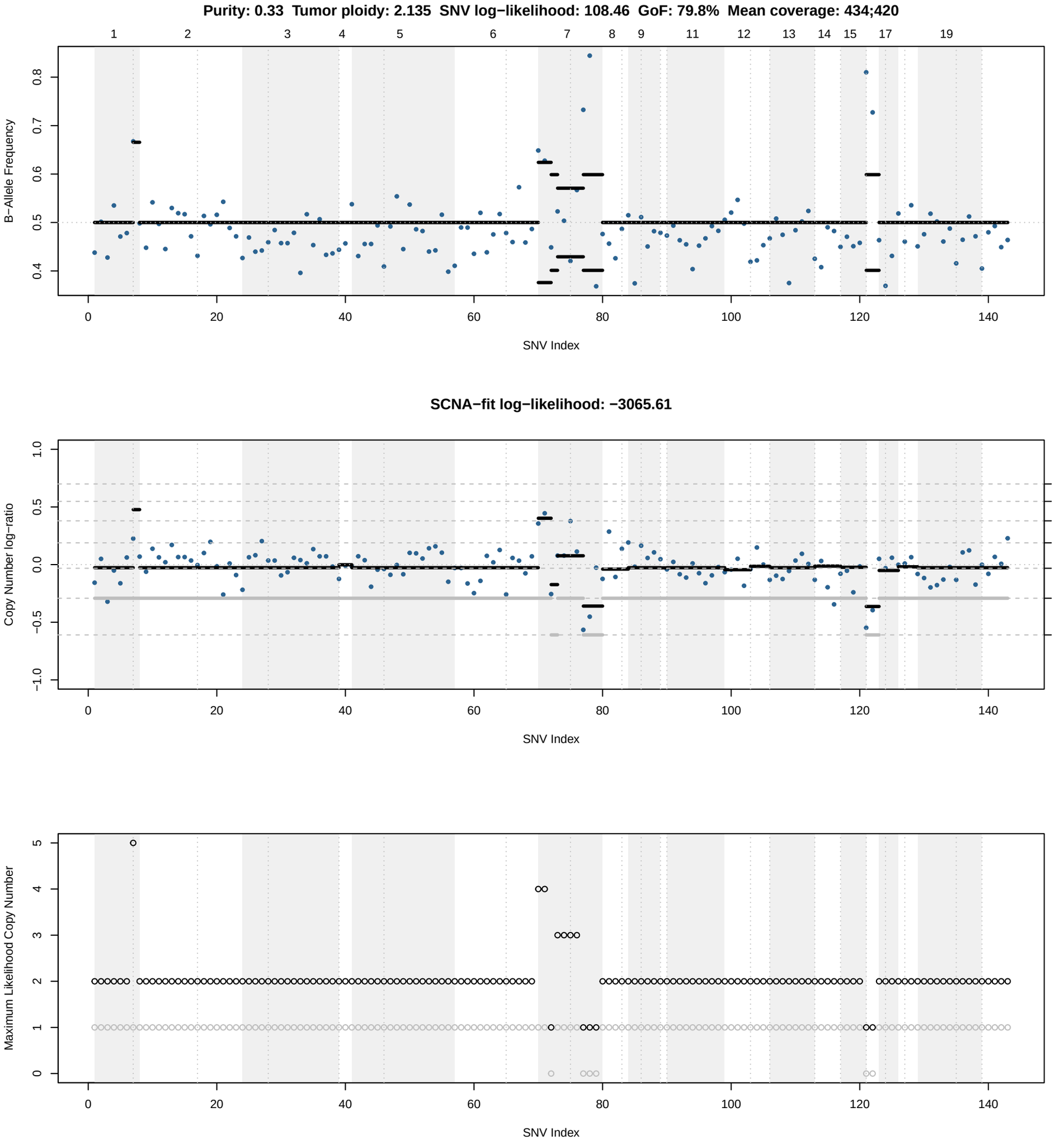
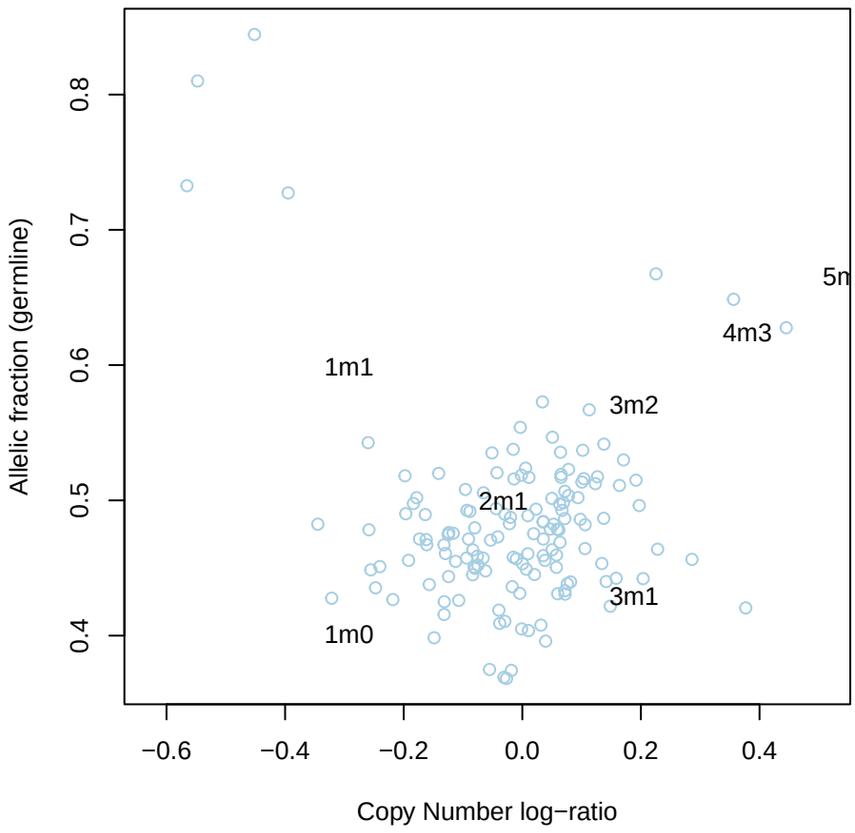
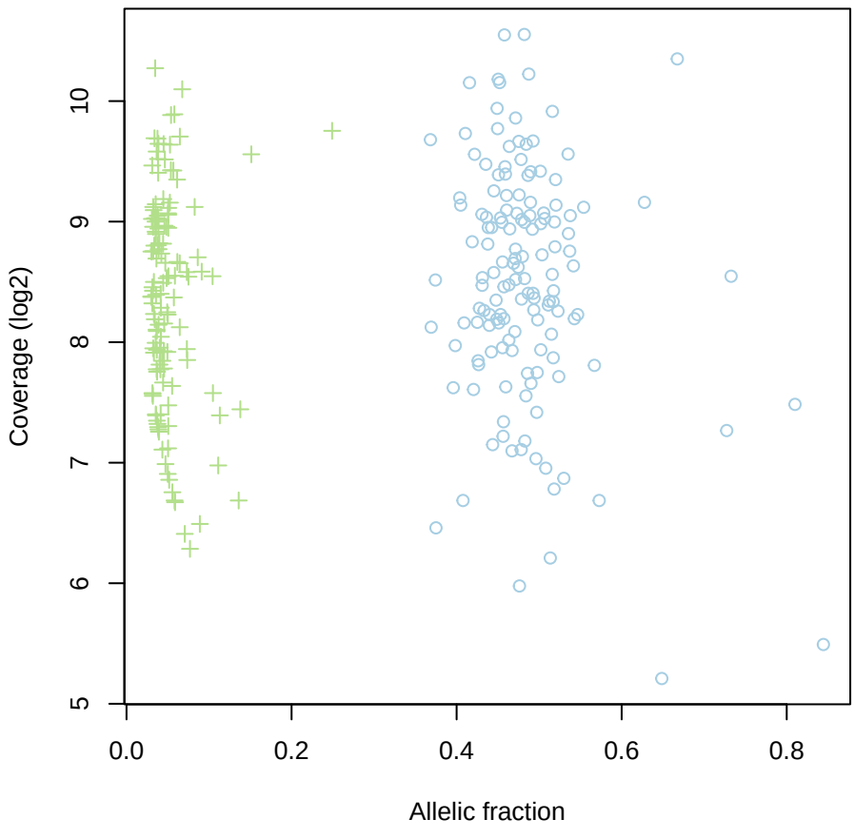
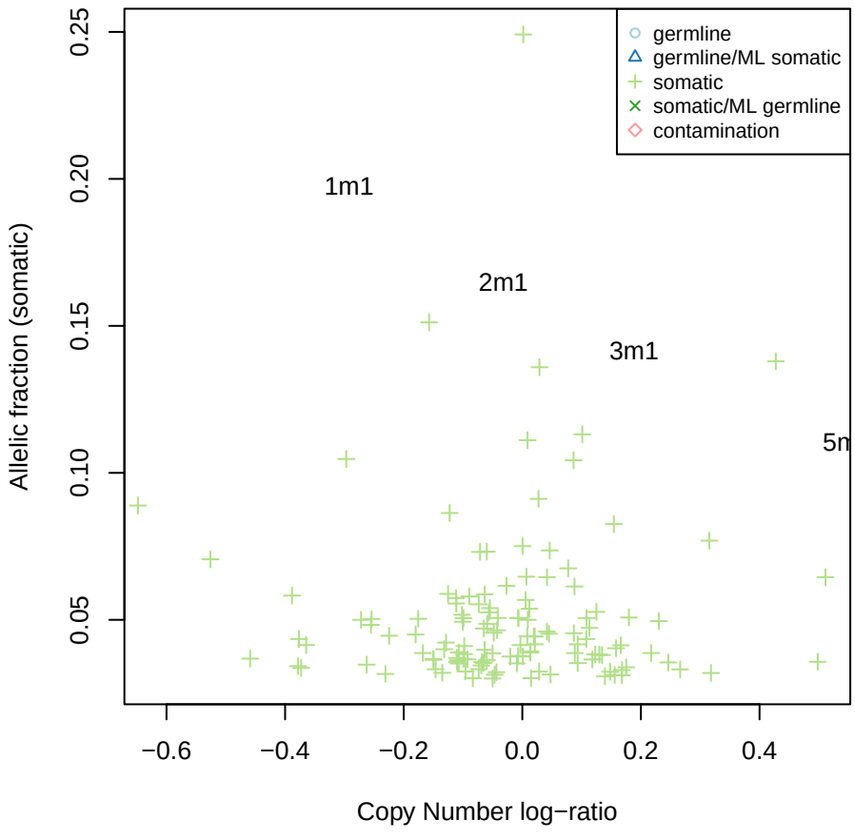
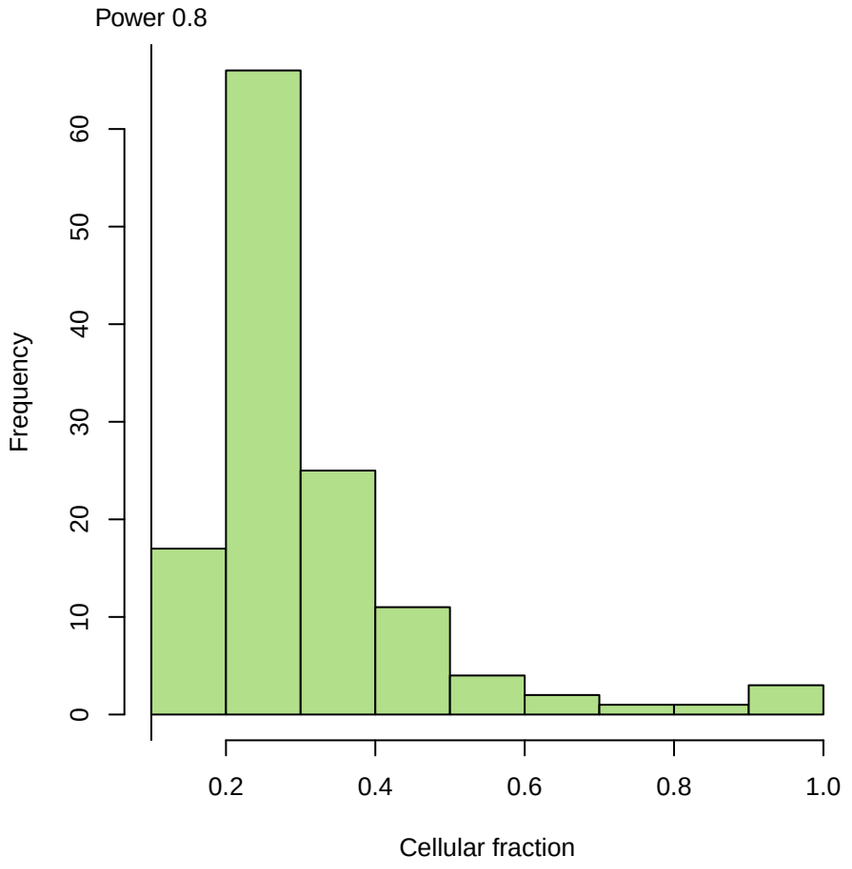

Purity: 0.33 Tumor ploidy: 2.135
1
2
3
4
5
6
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
0.6
log2 ratio

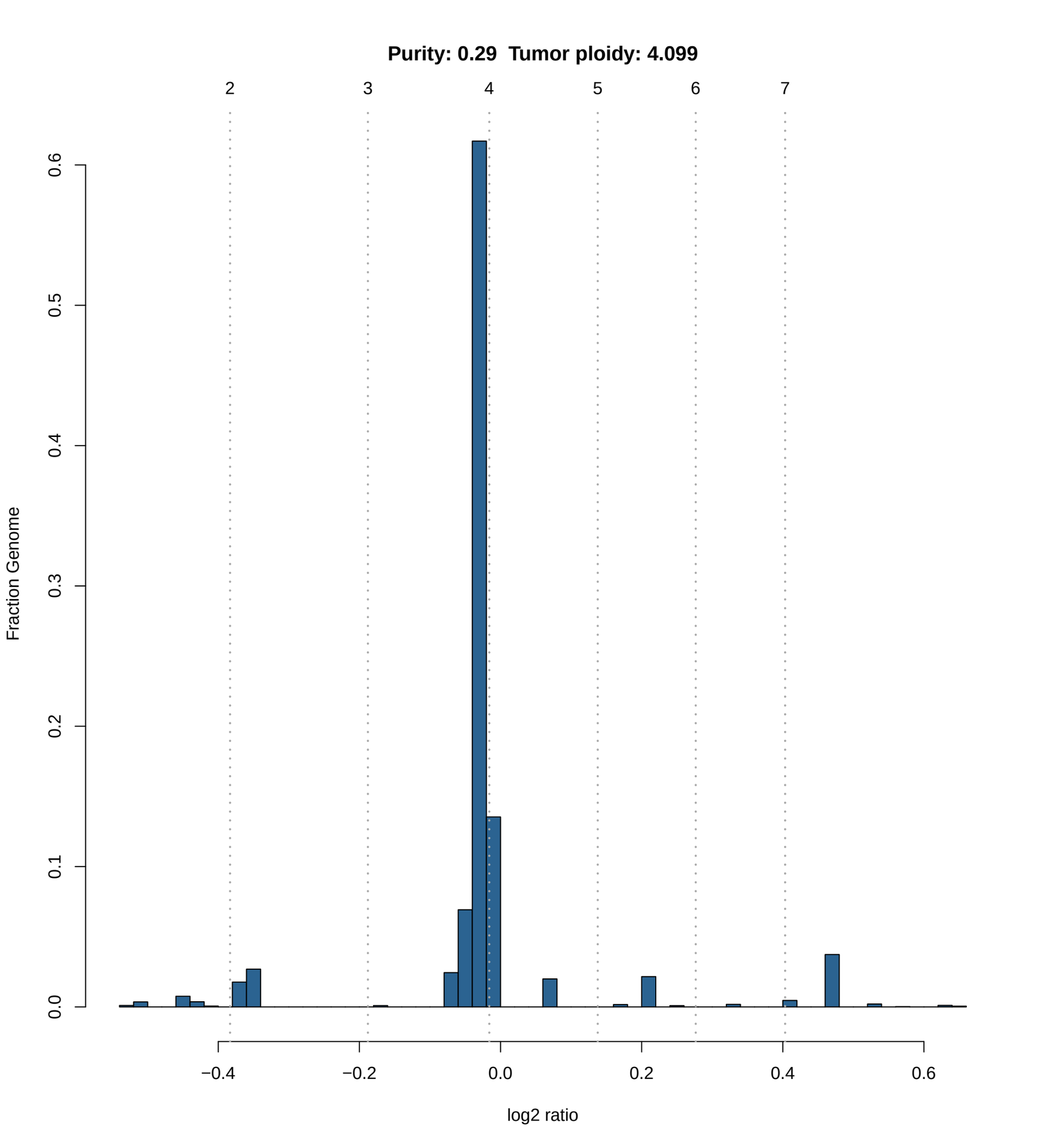

Purity: 0.33 Tumor ploidy: 2.135 SNV log−likelihood: 108.46 GoF: 79.8% Mean coverage: 434;420
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 19
B−Allele Frequency
0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index
SCNA−fit log−likelihood: −3065.61
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

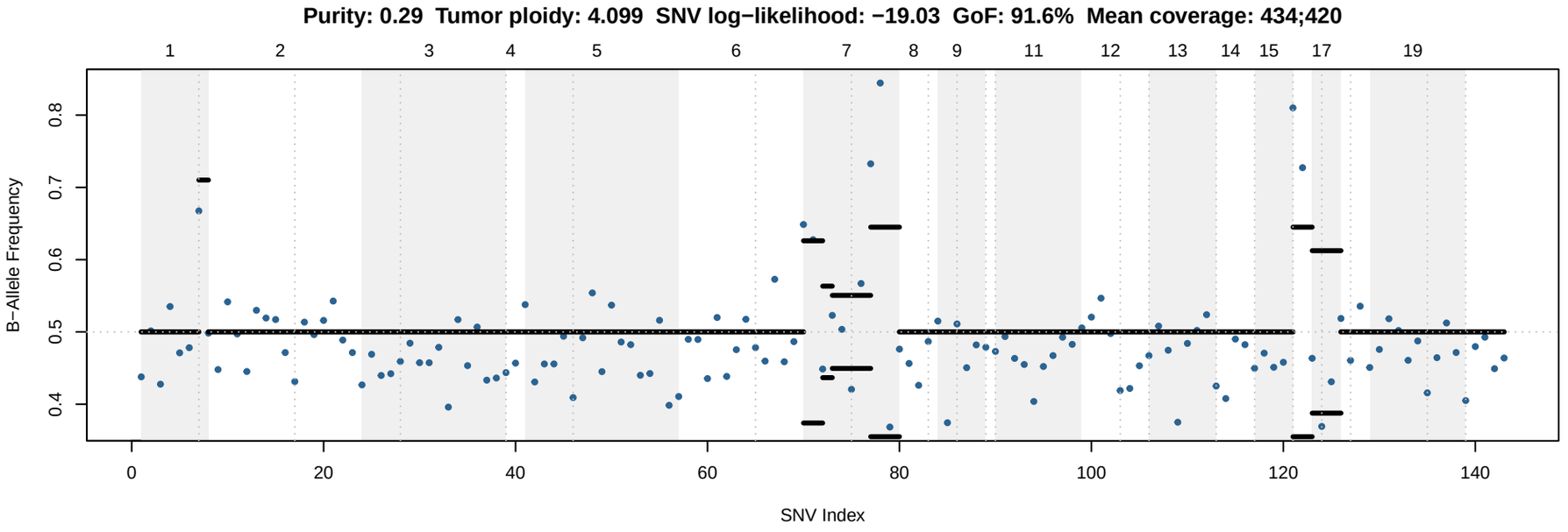

Allelic fraction (germline)
0.4
0.5
0.6
0.7
0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio
1m1
3m2
2m1
3m1
1m0
4m3
5m

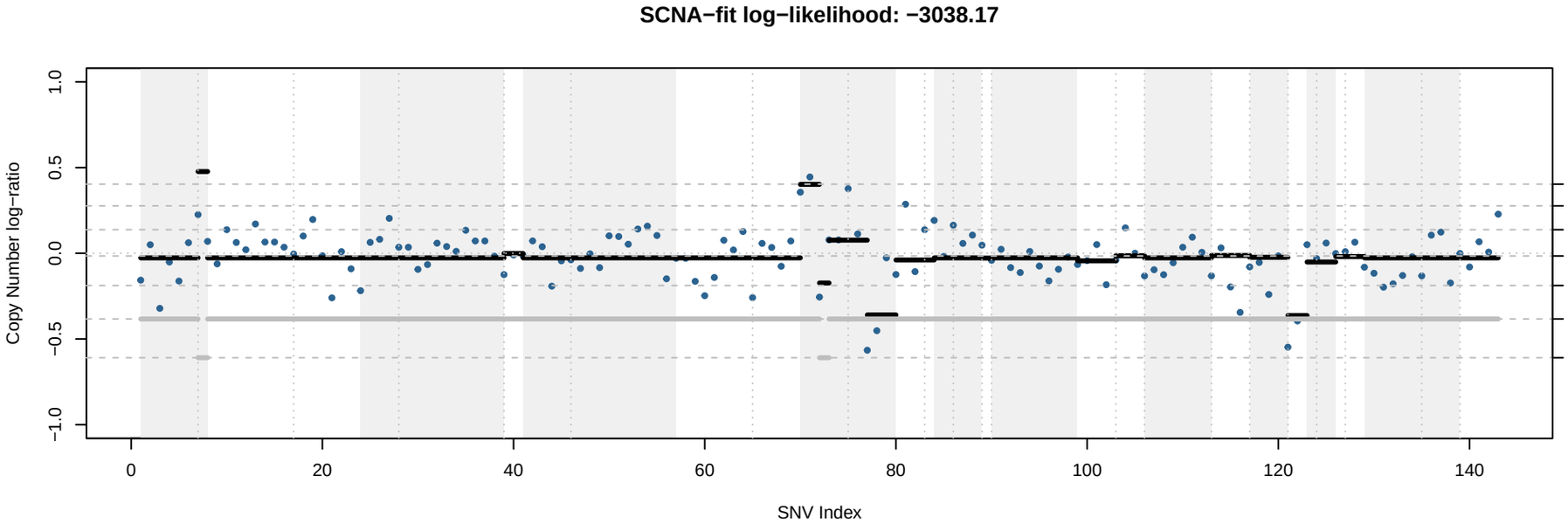

Coverage (log2)
5
6
7
8
9
10
0.0
0.2
0.4
0.6
0.8
Allelic fraction

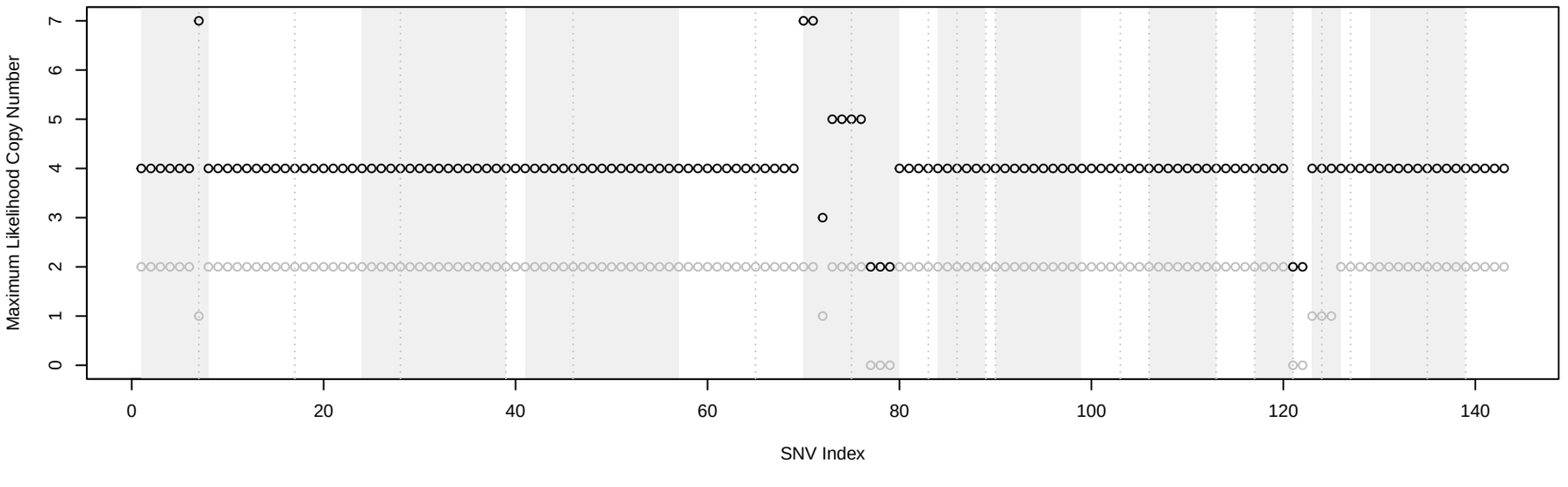

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
5m

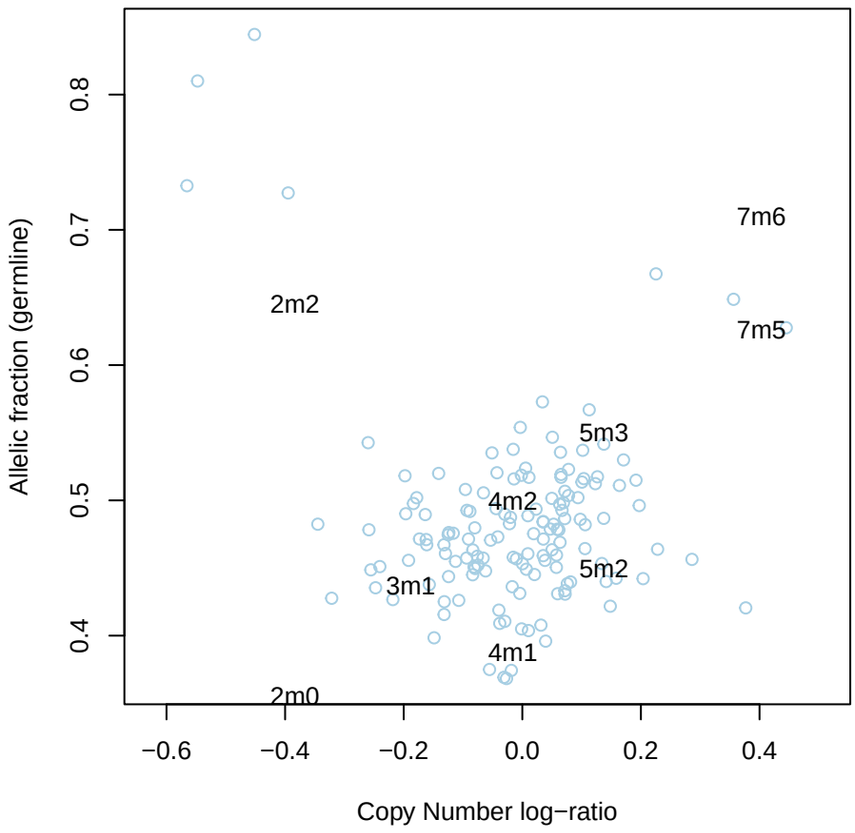

Power 0.8
Frequency
0
10
20
30
40
50
60
0.2
0.4
0.6
0.8
1.0
Cellular fraction

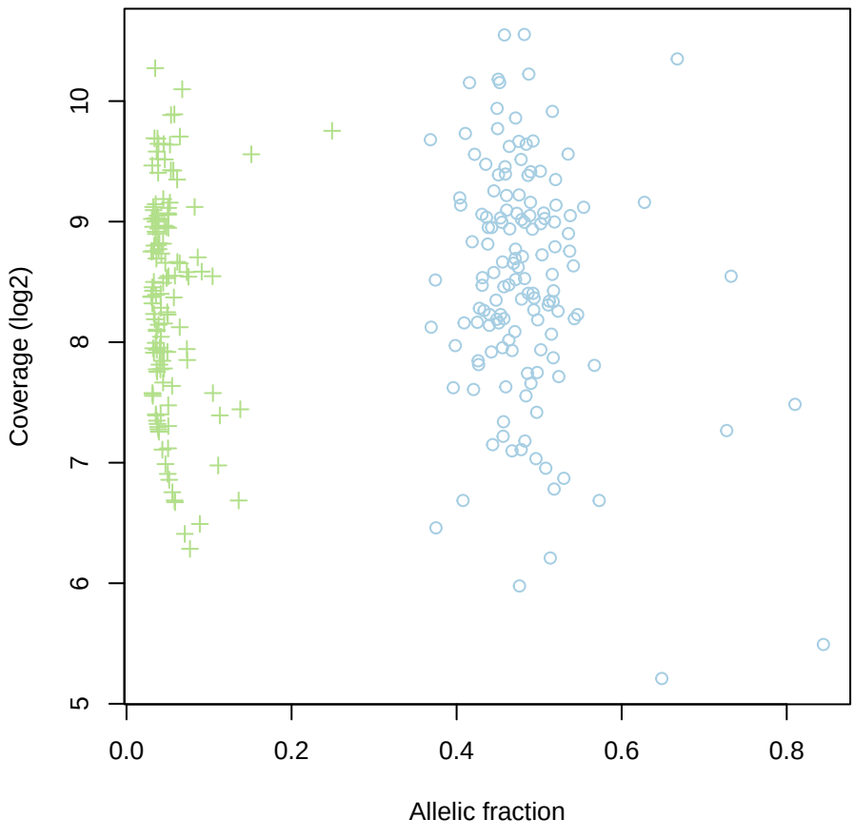

Purity: 0.29 Tumor ploidy: 4.099
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
0.6
log2 ratio

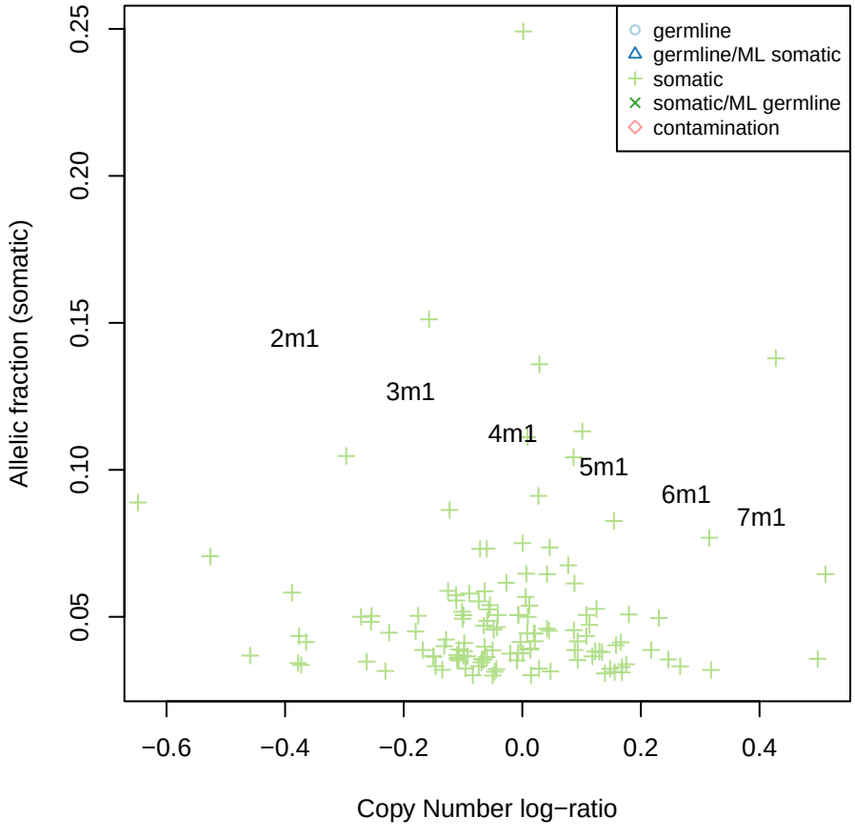

Purity: 0.29 Tumor ploidy: 4.099 SNV log−likelihood: −19.03 GoF: 91.6% Mean coverage: 434;420
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 19
B−Allele Frequency
0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index

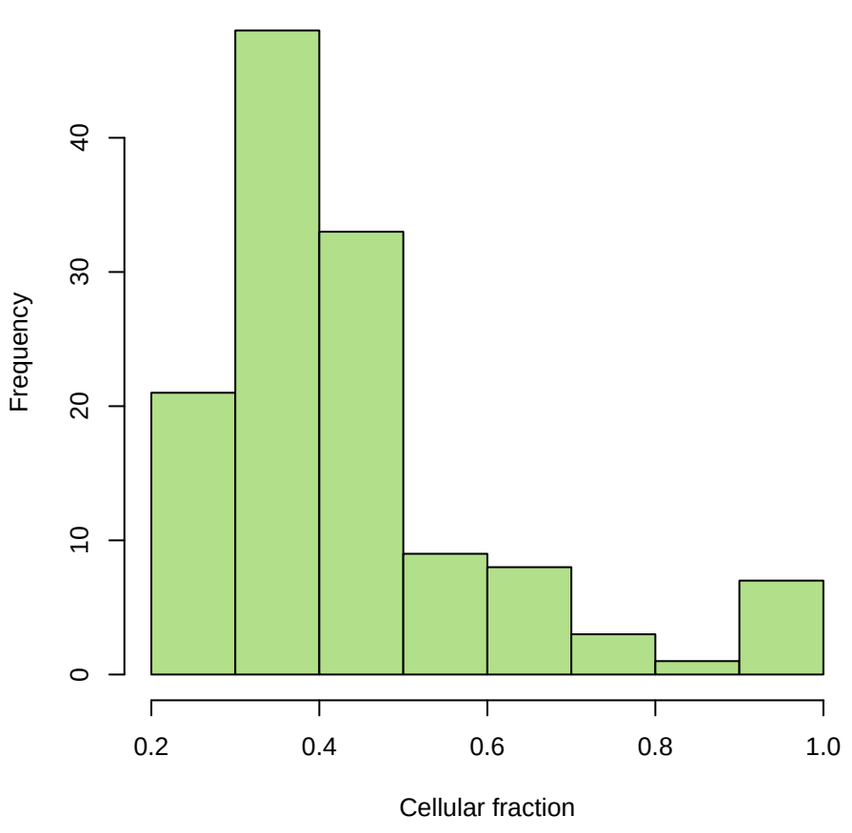

SCNA−fit log−likelihood: −3038.17
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 7
0 20 40 60 80 100 120 140
SNV Index

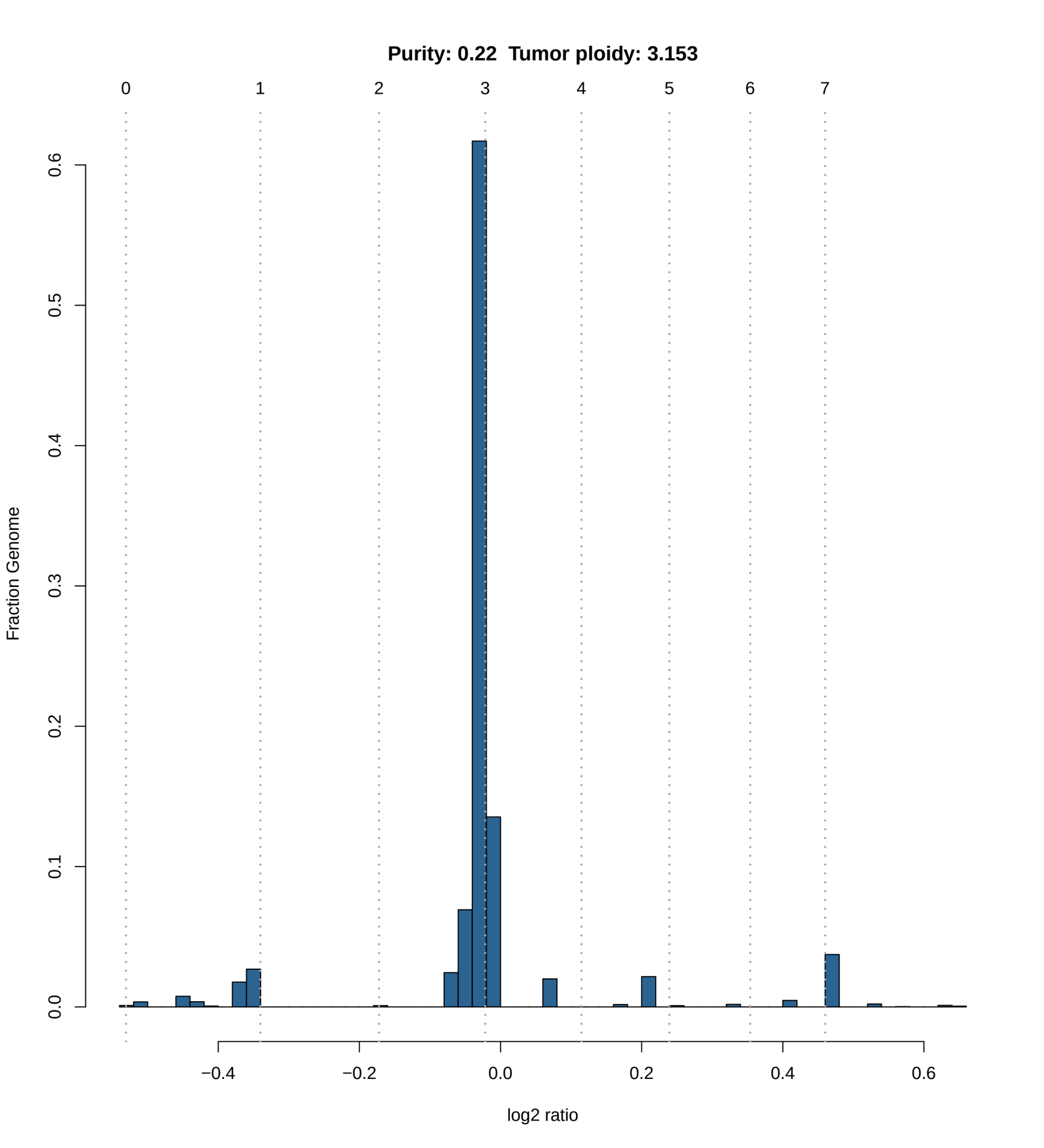

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

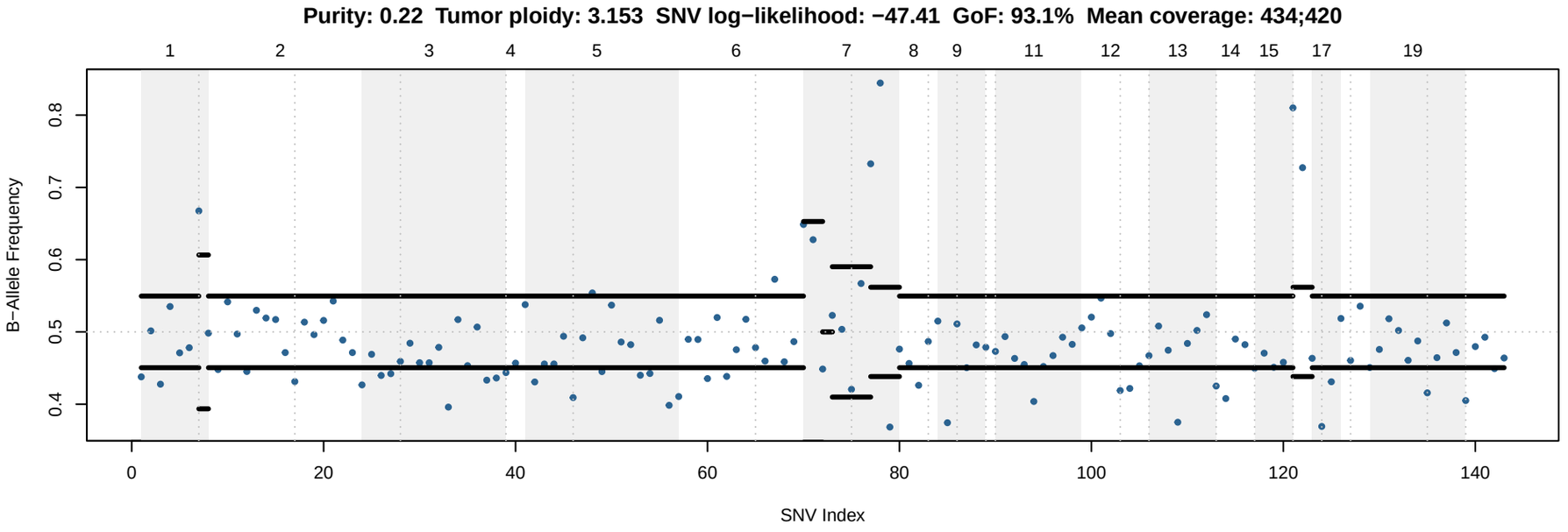

Allelic fraction (germline)
Copy Number log−ratio
2m2
7m6
7m5
5m3
4m2
5m2
3m1
4m1
2m0

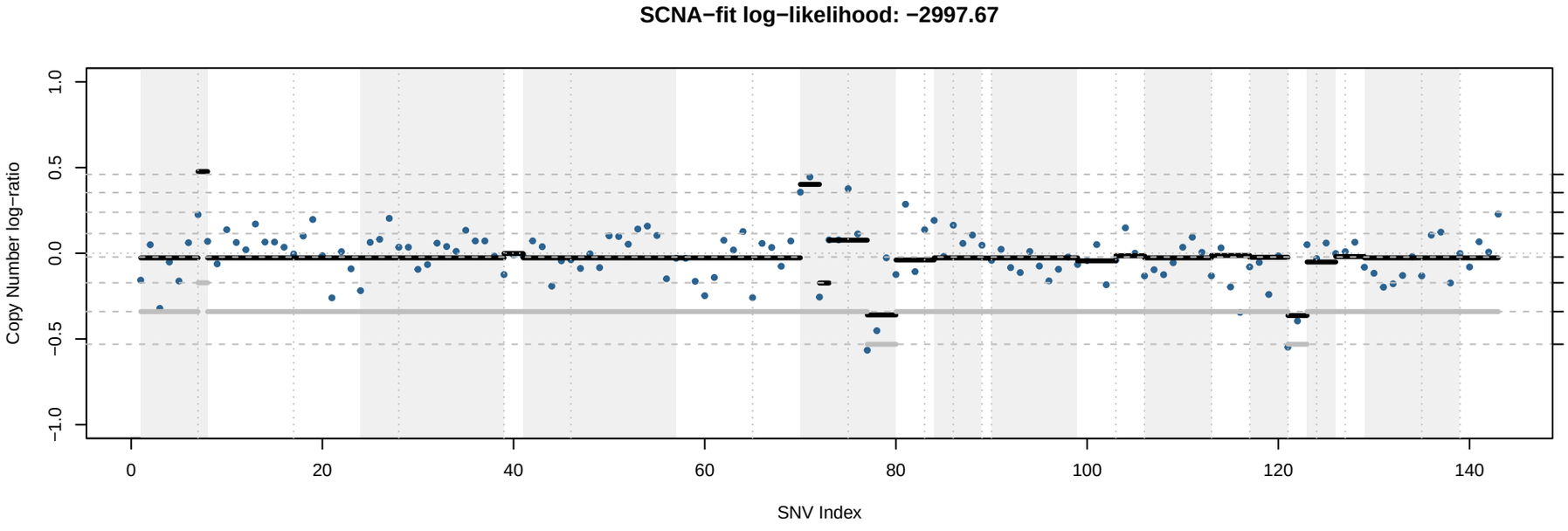

Coverage (log2)
Allelic fraction

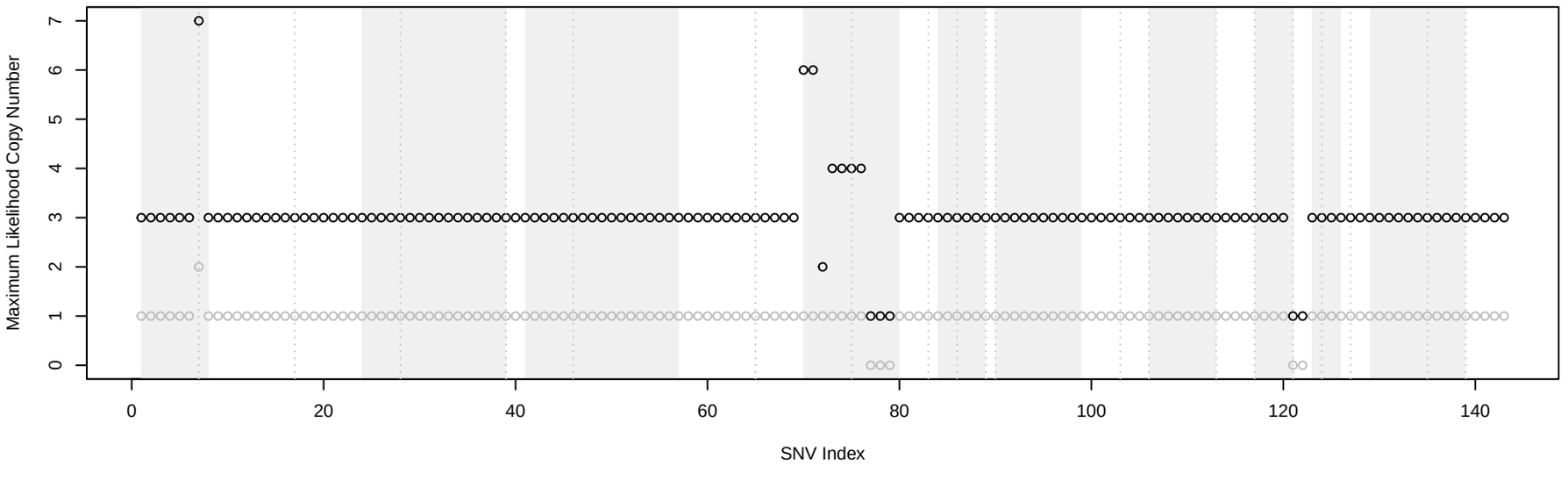

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m1
3m1
4m1
5m1
6m1
7m1

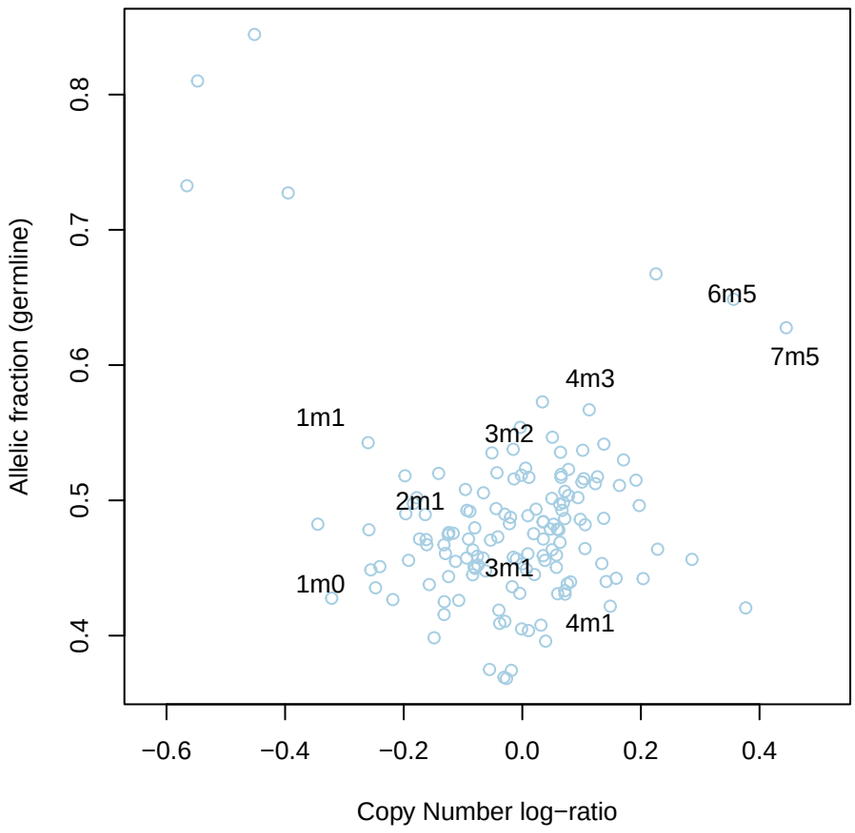

Frequency
Cellular fraction

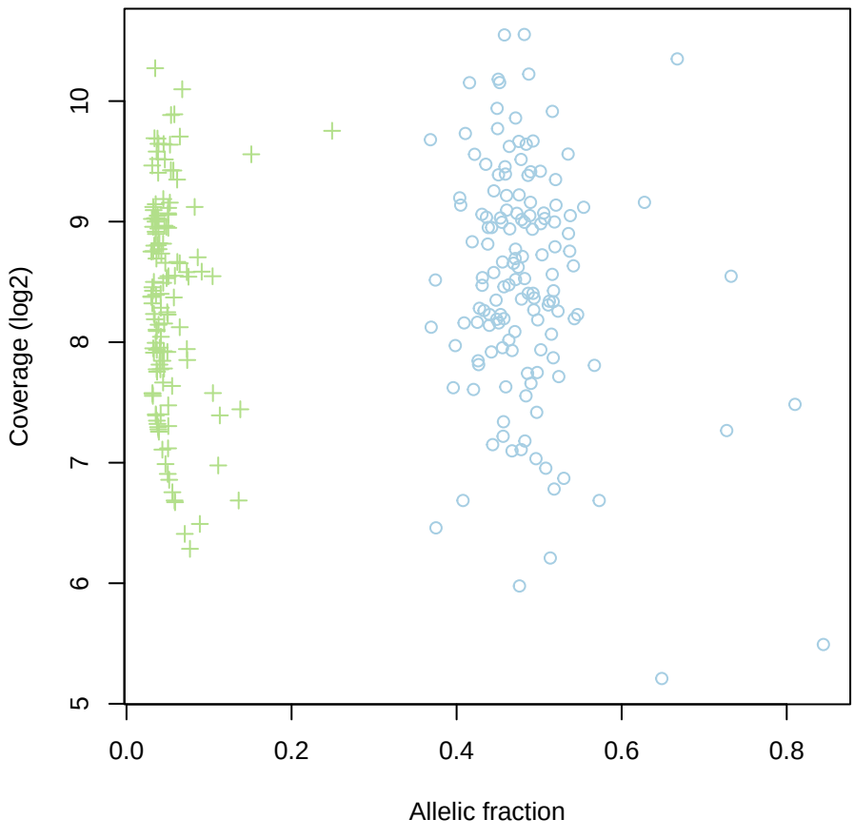

Purity: 0.22 Tumor ploidy: 3.153
0
1
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
0.6
log2 ratio

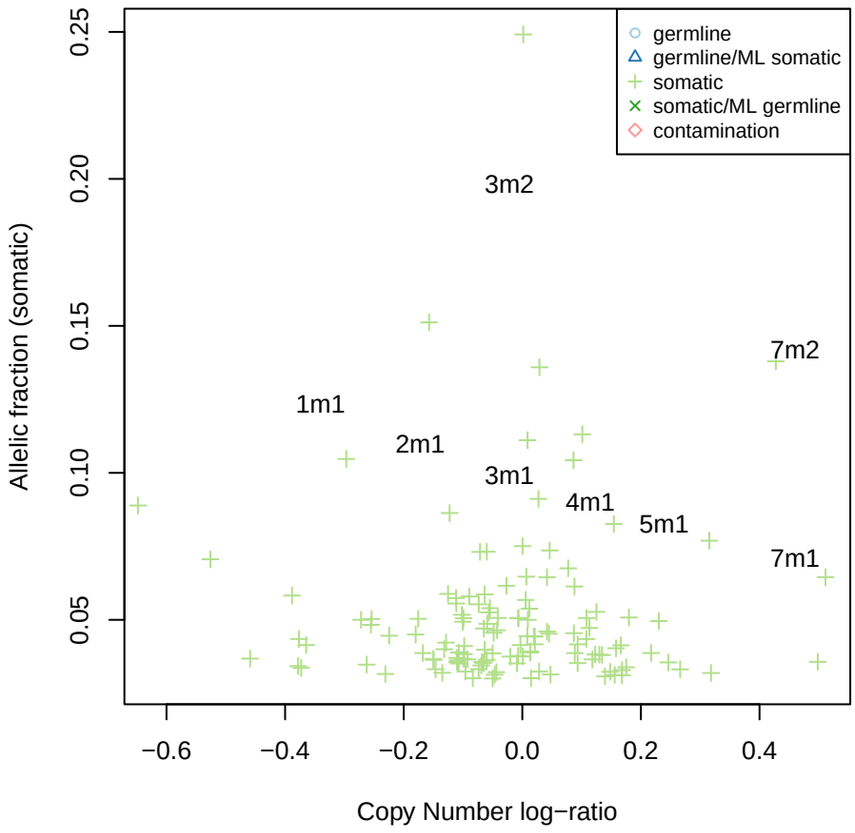

Purity: 0.22 Tumor ploidy: 3.153 SNV log−likelihood: −47.41 GoF: 93.1% Mean coverage: 434;420
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 19
B−Allele Frequency
0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index

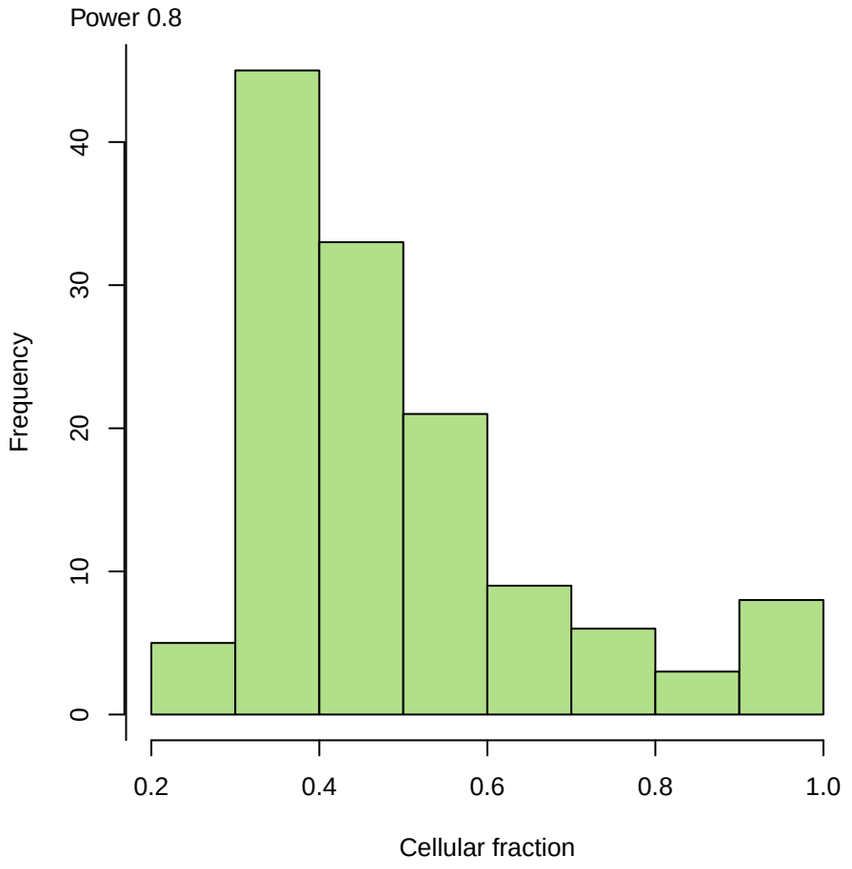

SCNA−fit log−likelihood: −2997.67
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 5 7
0 20 40 60 80 100 120 140
SNV Index

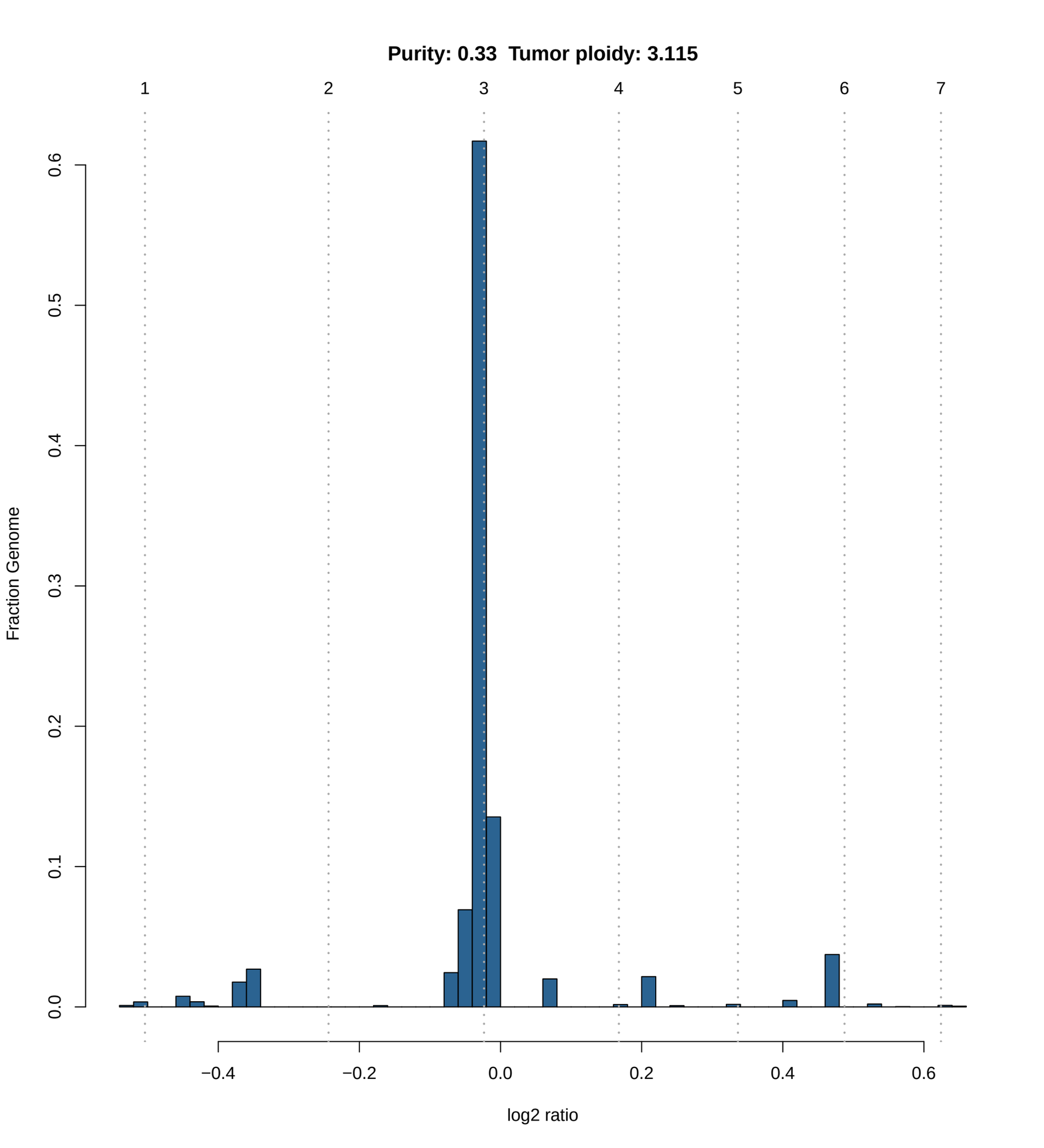

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

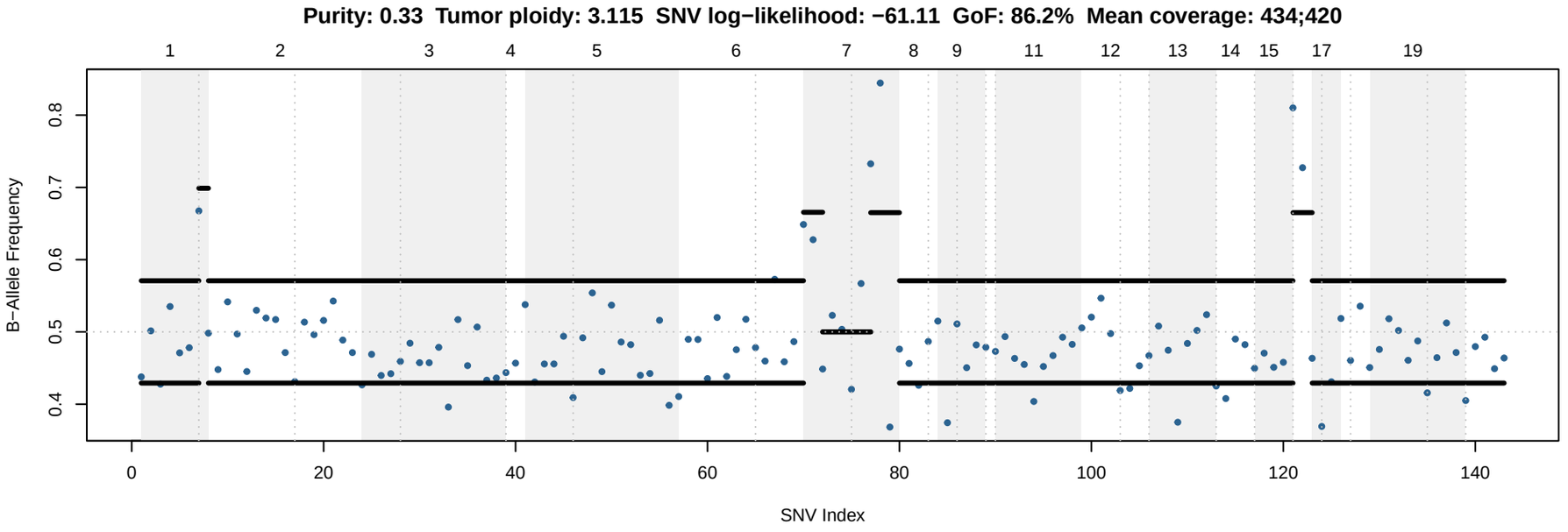

Allelic fraction (germline)
Copy Number log−ratio
1m1
2m1
1m0
3m2
3m1
4m3
4m1
6m5
7m5

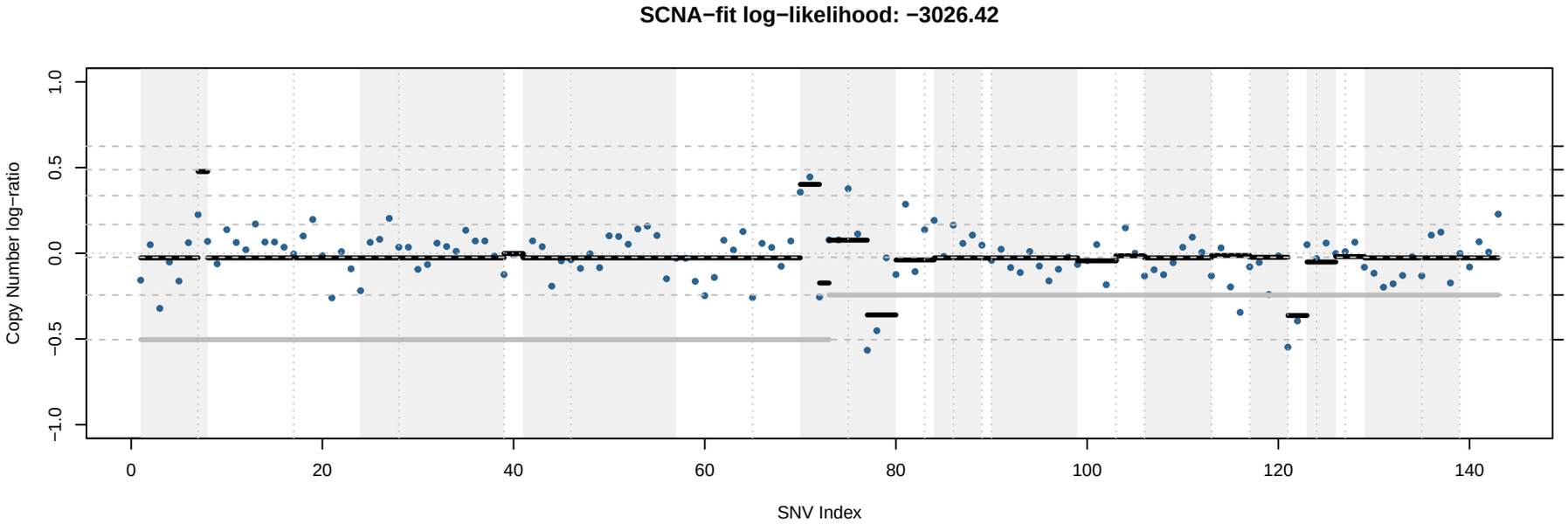

Coverage (log2)
Allelic fraction

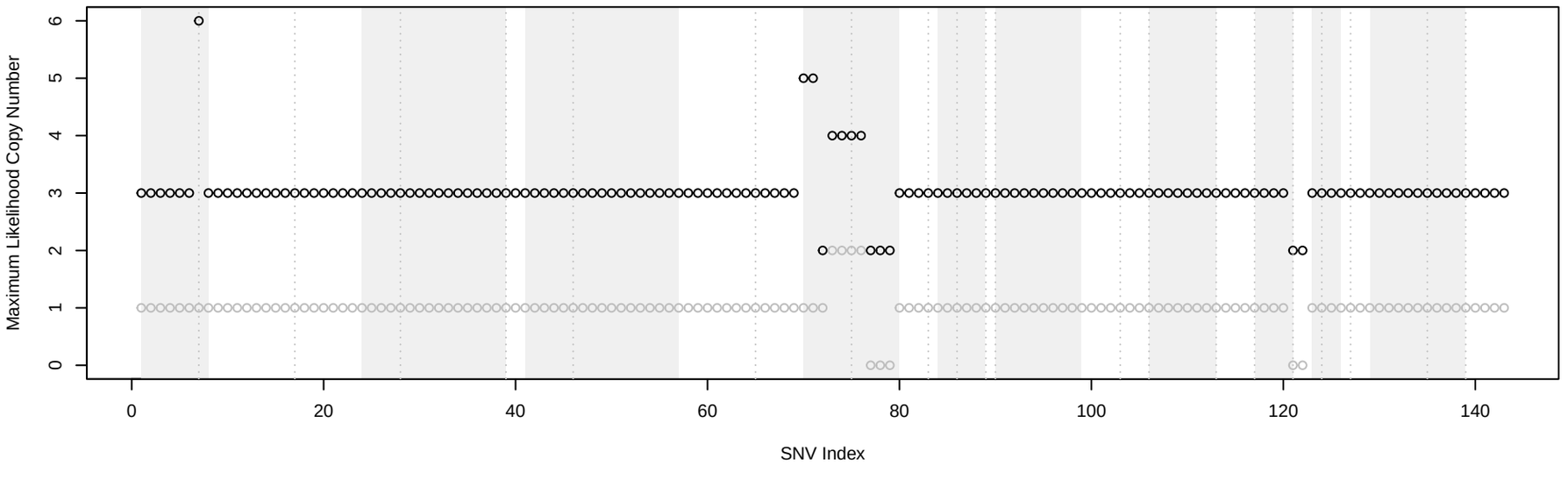

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1
3m1
3m2
4m1
5m1
7m1
7m2

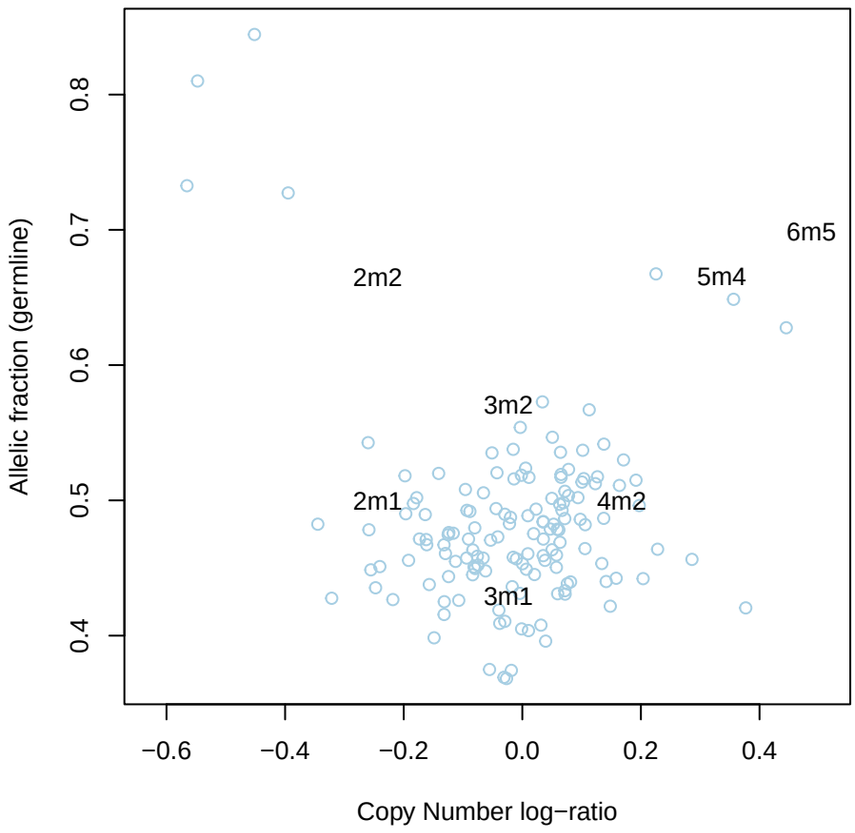

Power 0.8
Frequency
Cellular fraction

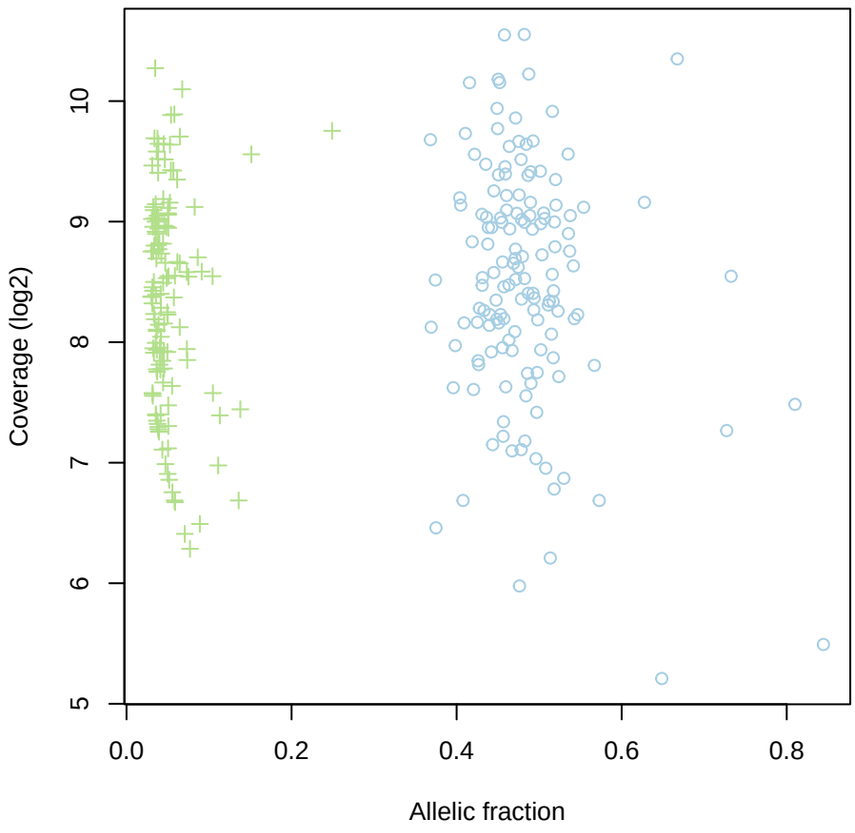

Purity: 0.33 Tumor ploidy: 3.115
1
2
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
0.6
log2 ratio

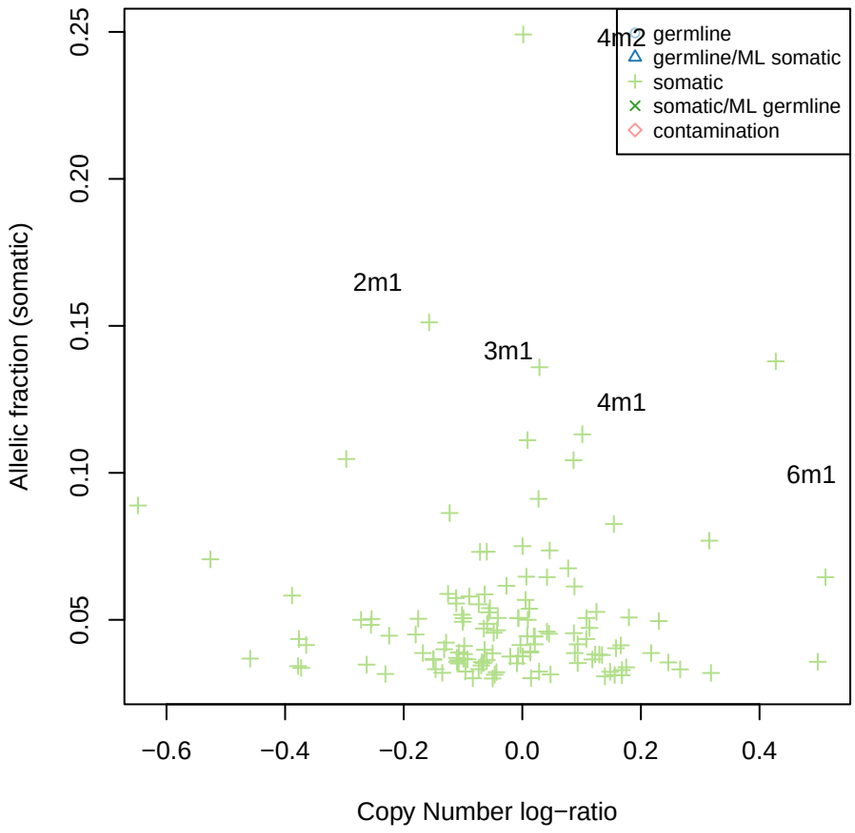

Purity: 0.33 Tumor ploidy: 3.115 SNV log−likelihood: −61.11 GoF: 86.2% Mean coverage: 434;420
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 19
B−Allele Frequency
0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index

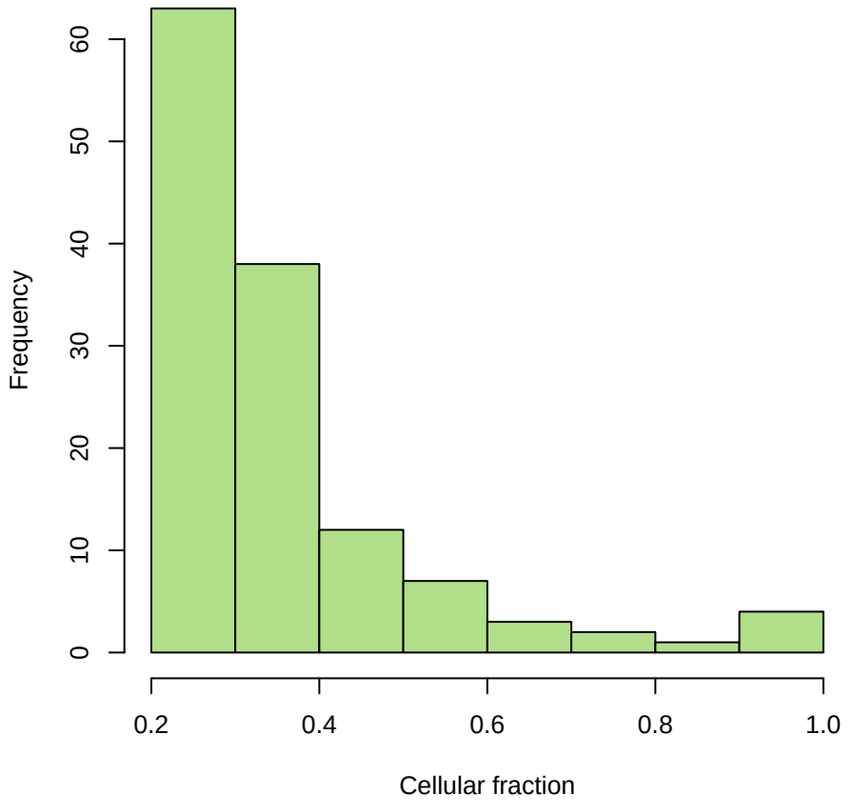

SCNA−fit log−likelihood: −3026.42
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

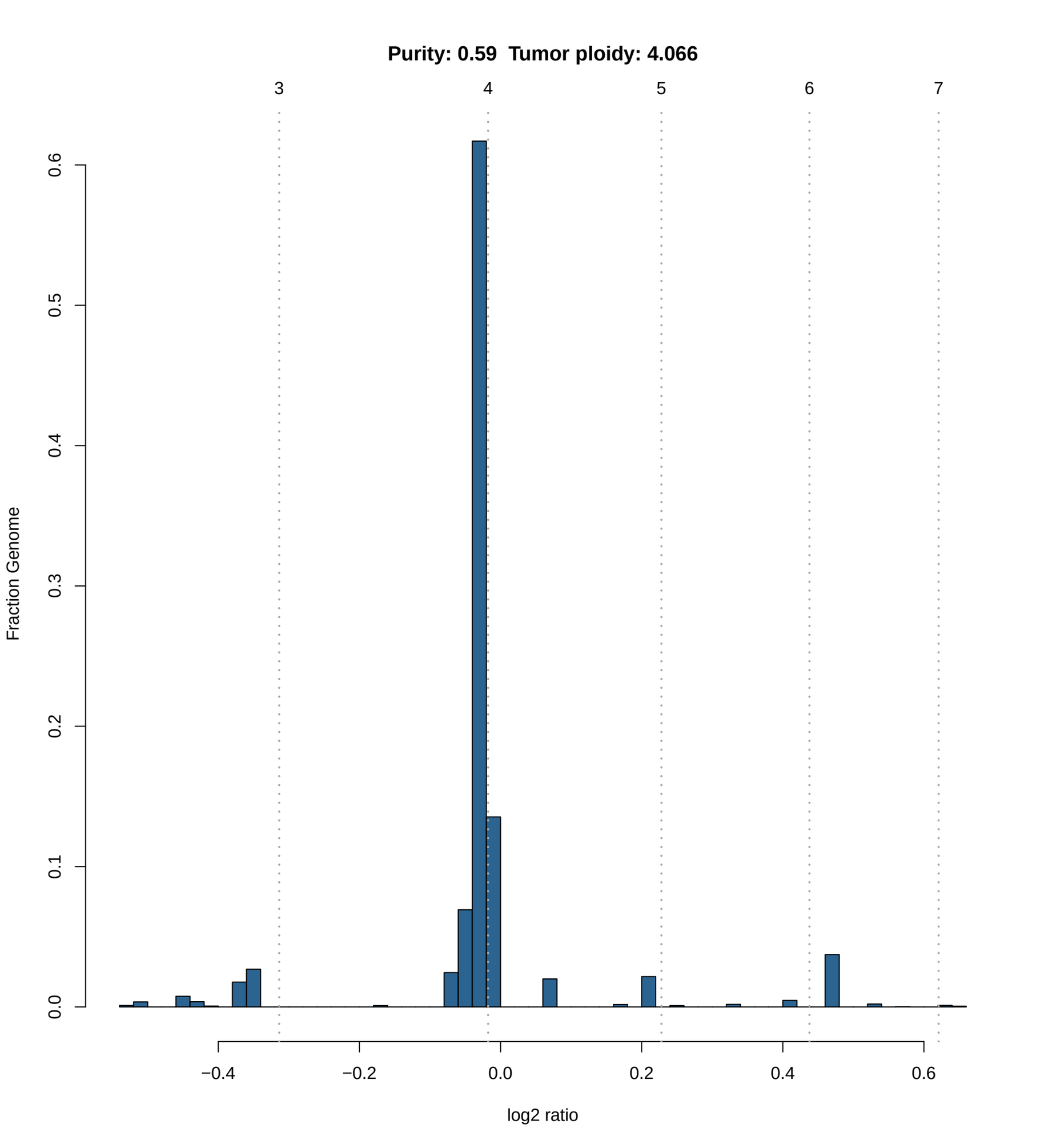

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

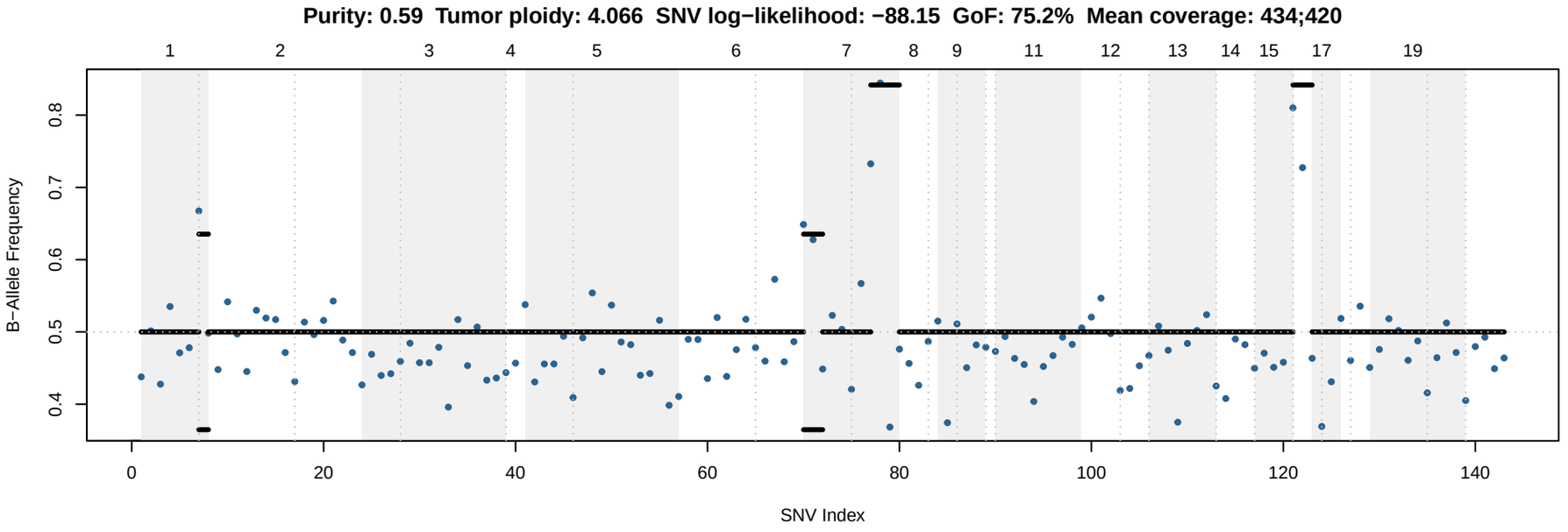

Allelic fraction (germline)
0.4
0.5
0.6
0.7
0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio
2m2
6m5
5m4
3m2
2m1
4m2
3m1

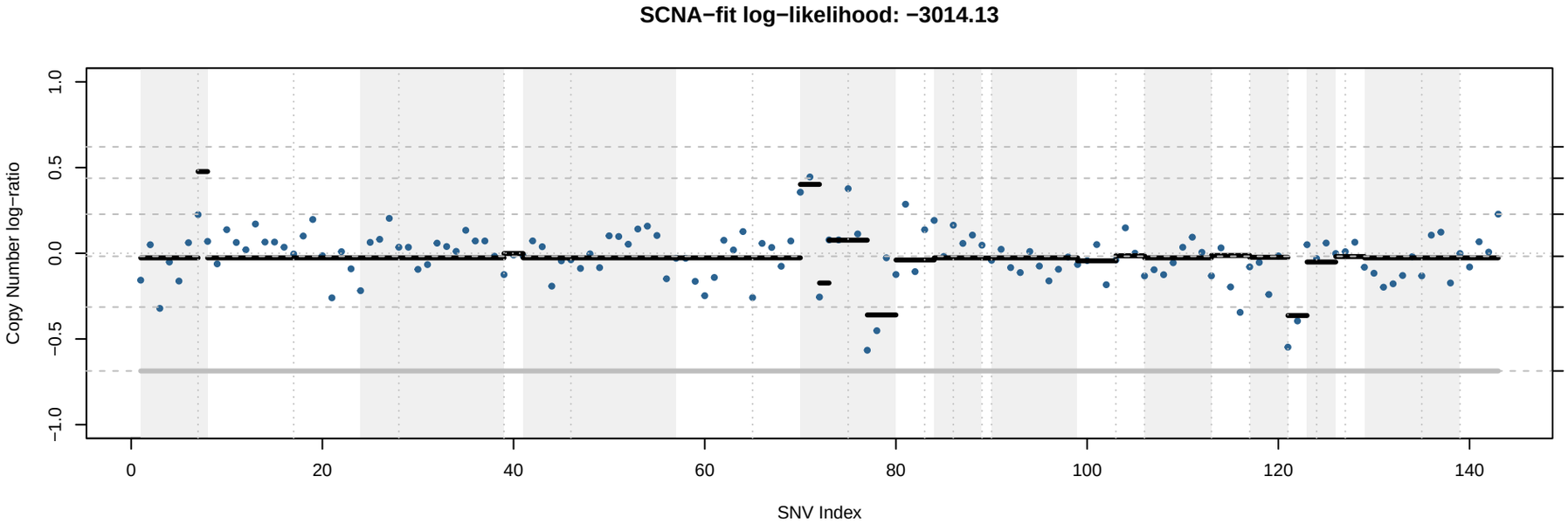

Coverage (log2)
5
6
7
8
9
10
0.0
0.2
0.4
0.6
0.8
Allelic fraction

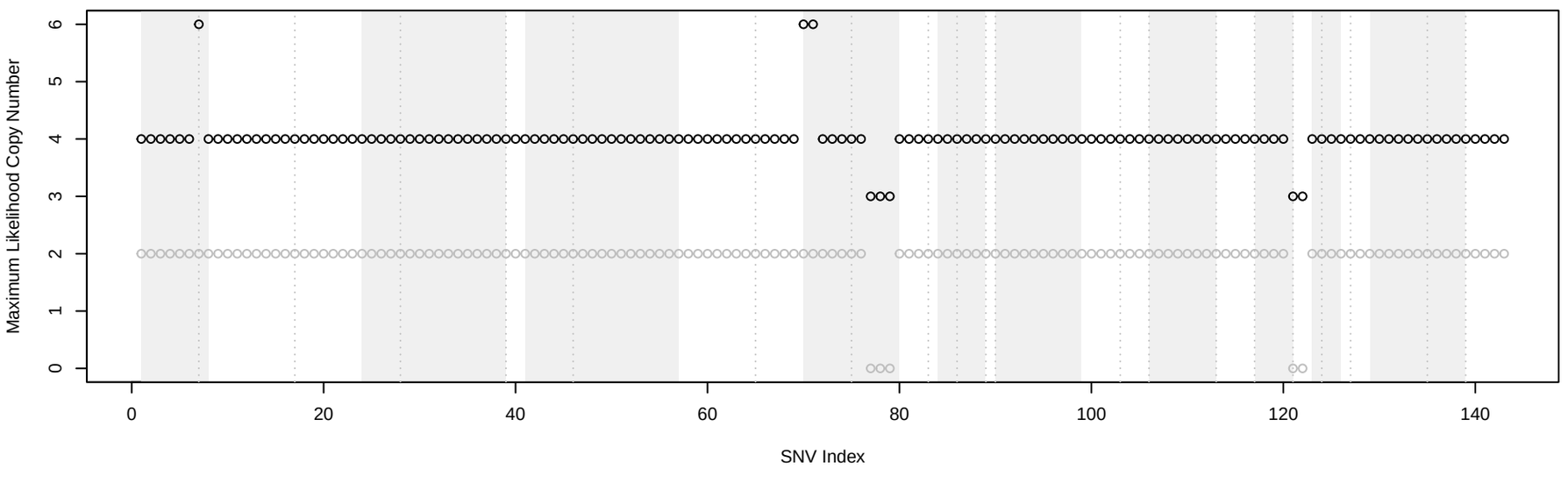

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m2
2m1
3m1
4m1
6m1

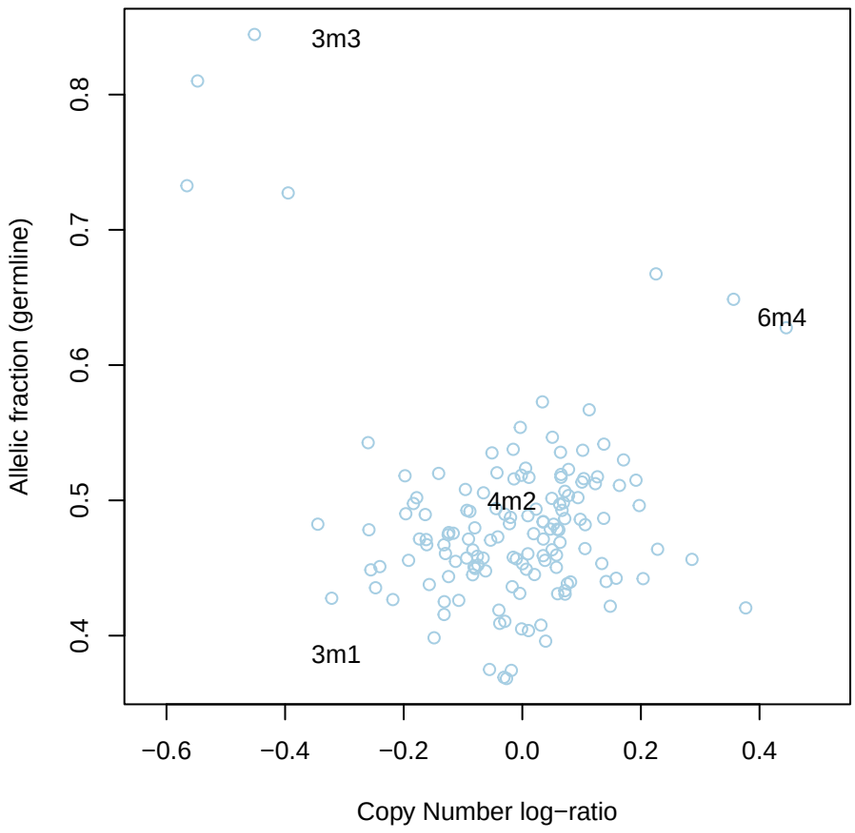

Frequency
0
10
20
30
40
50
60
0.2
0.4
0.6
0.8
1.0
Cellular fraction

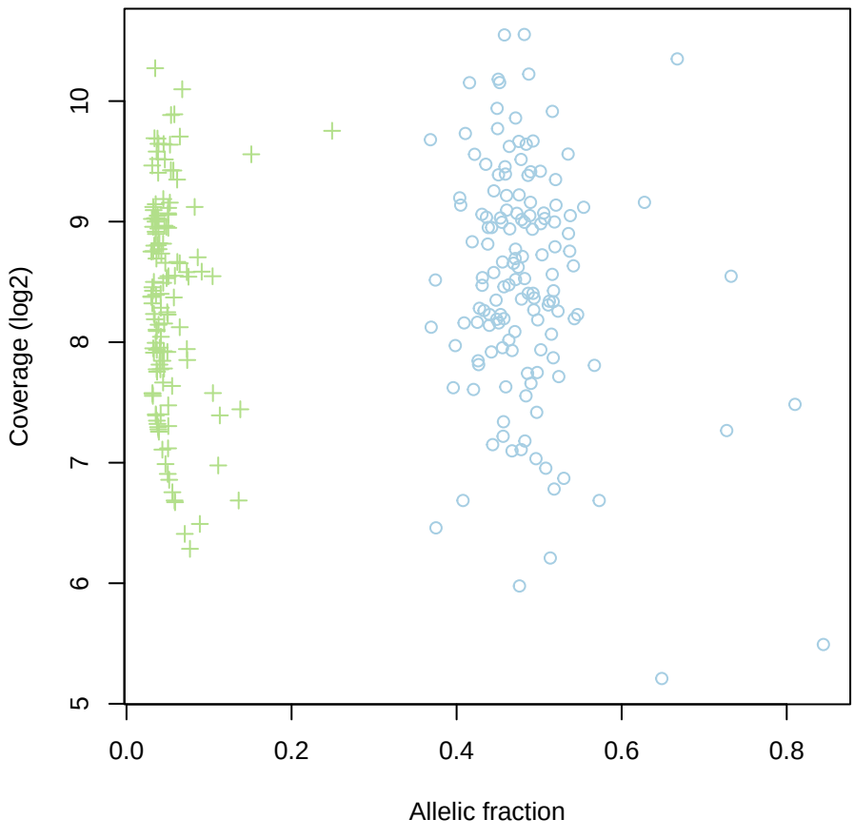

Purity: 0.59 Tumor ploidy: 4.066
3
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
0.6
log2 ratio

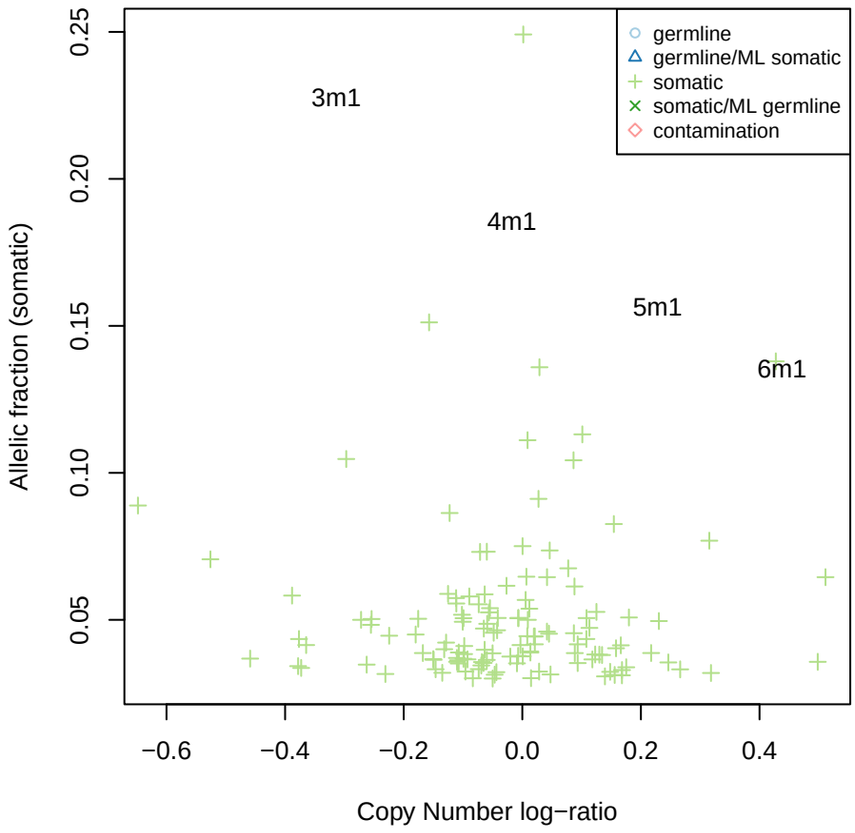

Purity: 0.59 Tumor ploidy: 4.066 SNV log−likelihood: −88.15 GoF: 75.2% Mean coverage: 434;420
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 19
B−Allele Frequency
0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index

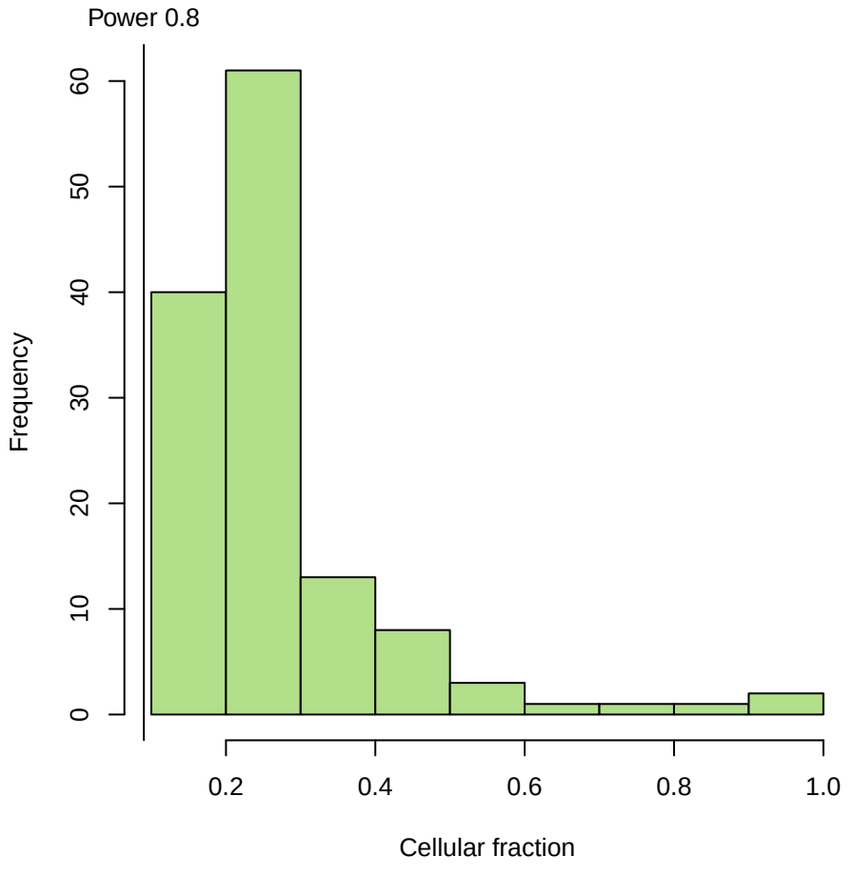

SCNA−fit log−likelihood: −3014.13
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

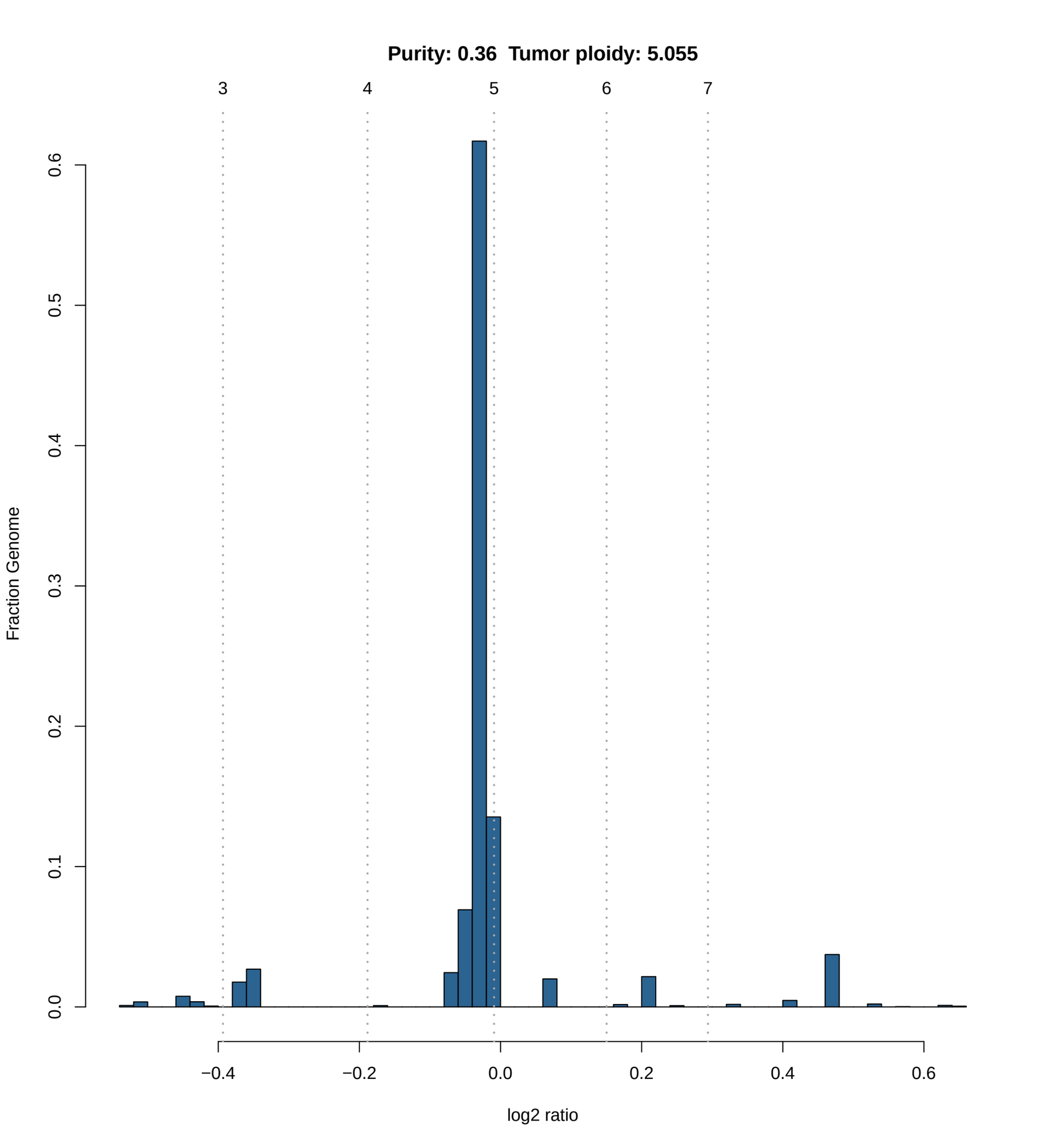

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

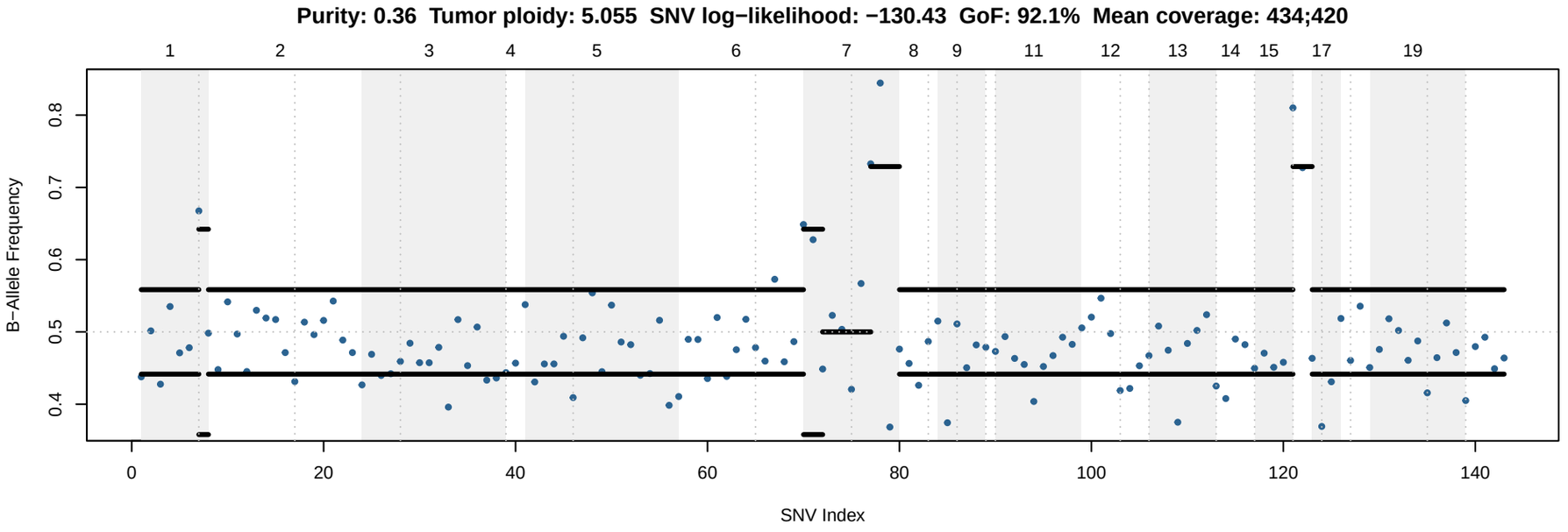

3m3
6m4
4m2
3m1
Allelic fraction (germline)
Copy Number log−ratio
0.4
0.5
0.6
0.7
0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4

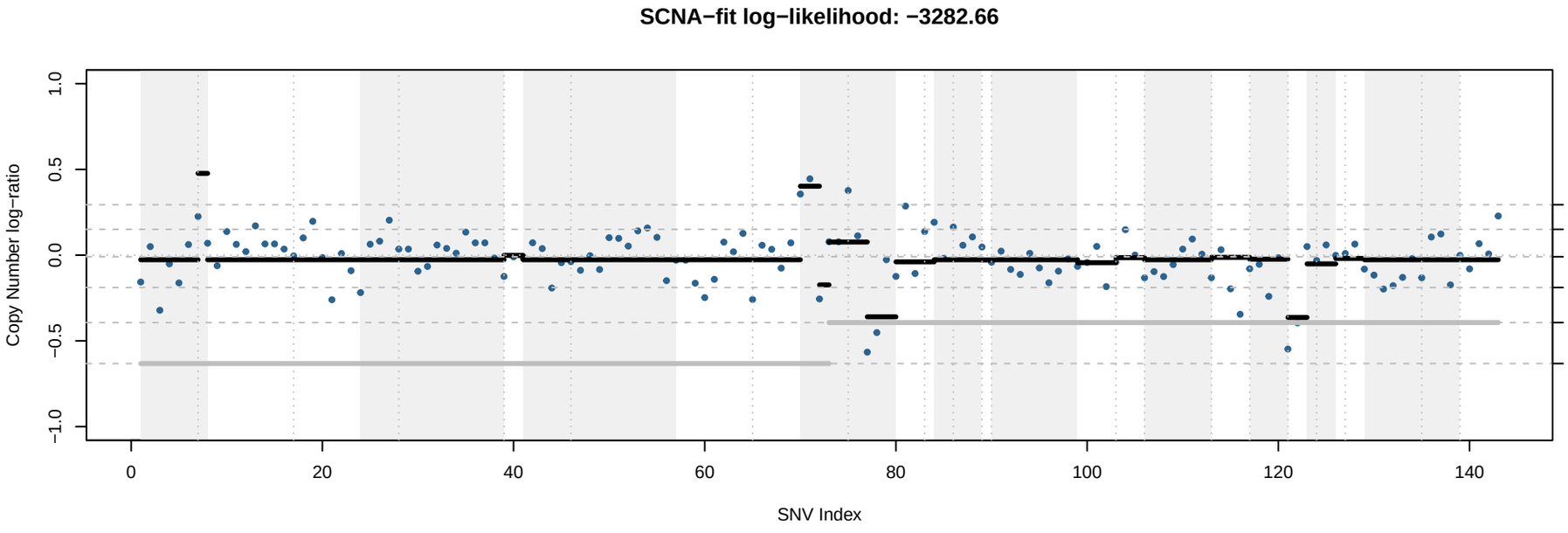

Coverage (log2)
Allelic fraction
5
6
7
8
9
10
0.0
0.2
0.4
0.6
0.8

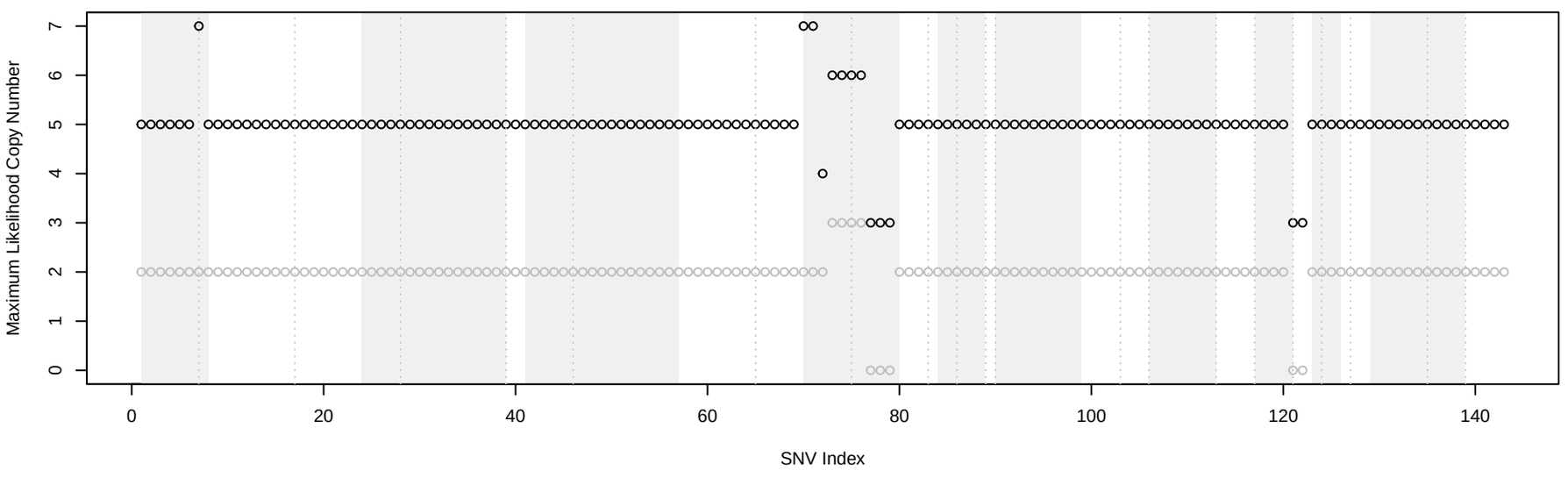

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
0.25
−0.6
−0.4
−0.2
0.0
0.2
0.4

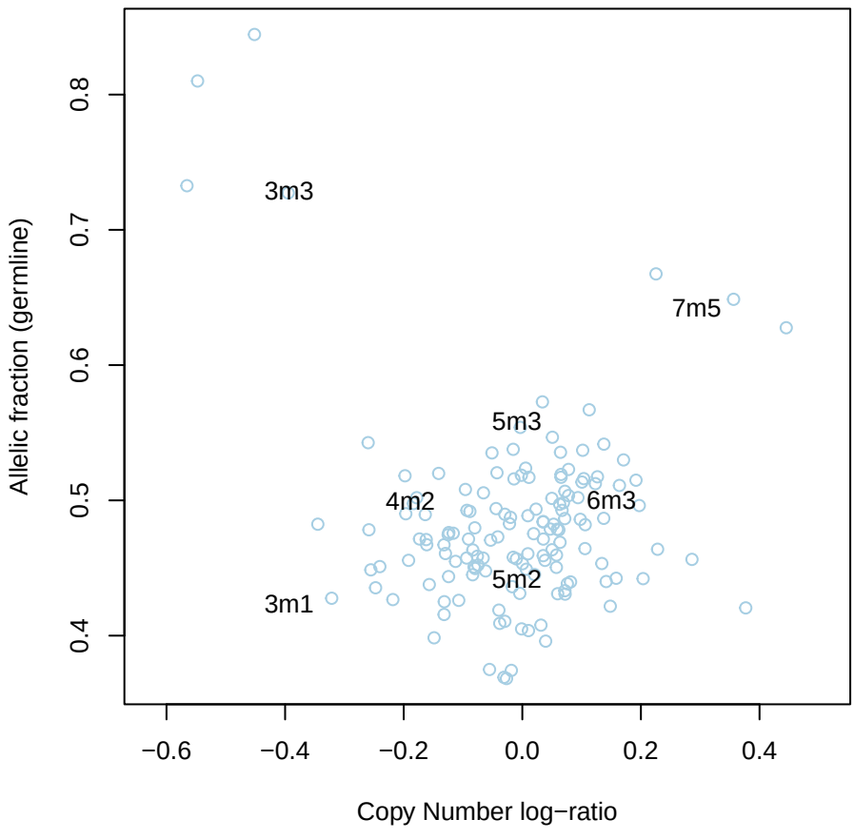

Power 0.8
Frequency
Cellular fraction
0
10
20
30
40
50
60
0.2
0.4
0.6
0.8
1.0

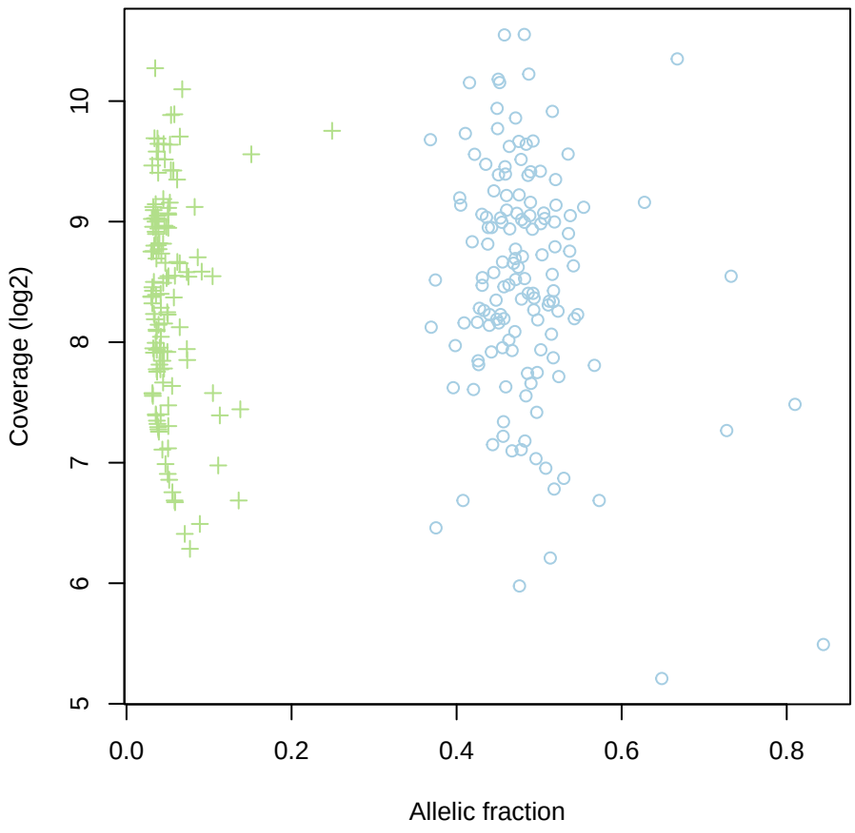

Purity: 0.36 Tumor ploidy: 5.055
3
4
5
6
7
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
log2 ratio

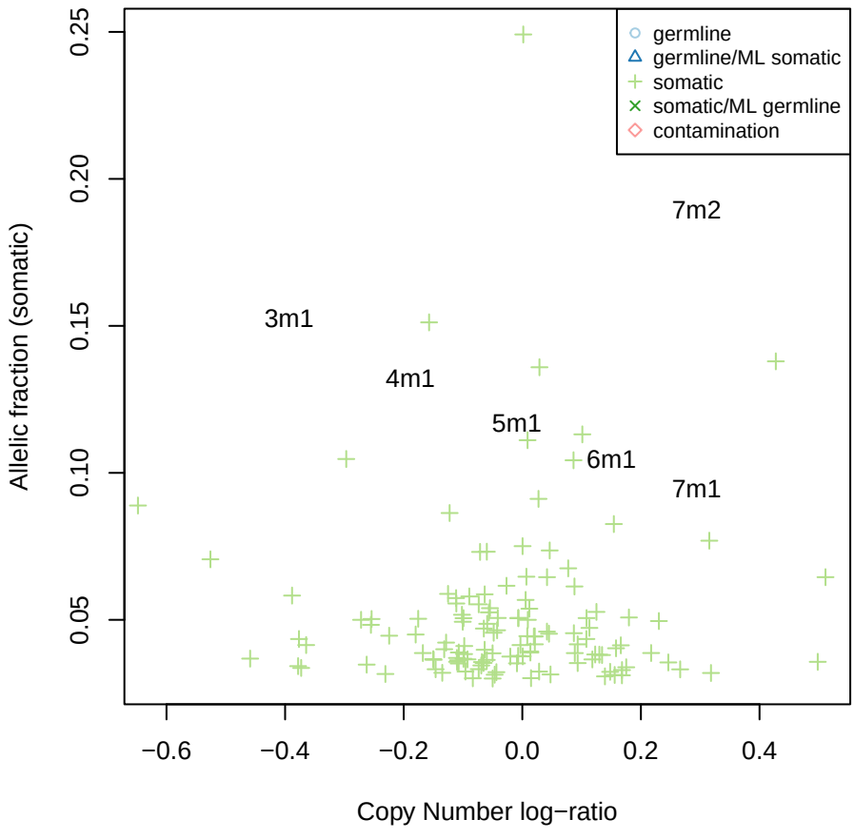

Purity: 0.36 Tumor ploidy: 5.055 SNV log−likelihood: −130.43 GoF: 92.1% Mean coverage: 434;420
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 19
B−Allele Frequency
0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index

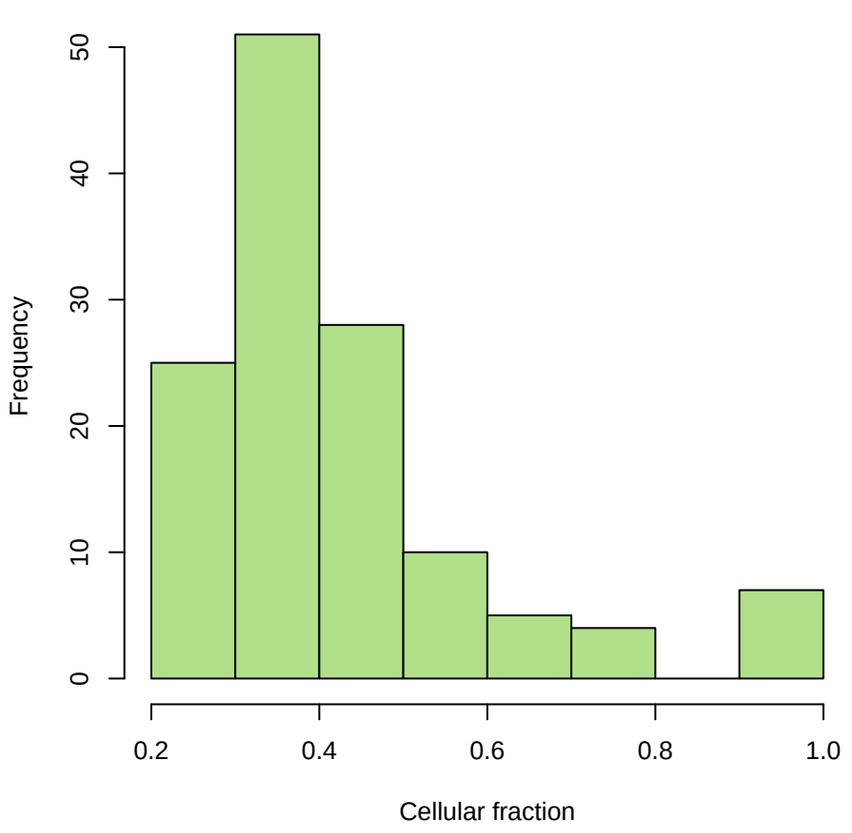

SCNA−fit log−likelihood: −3282.66
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

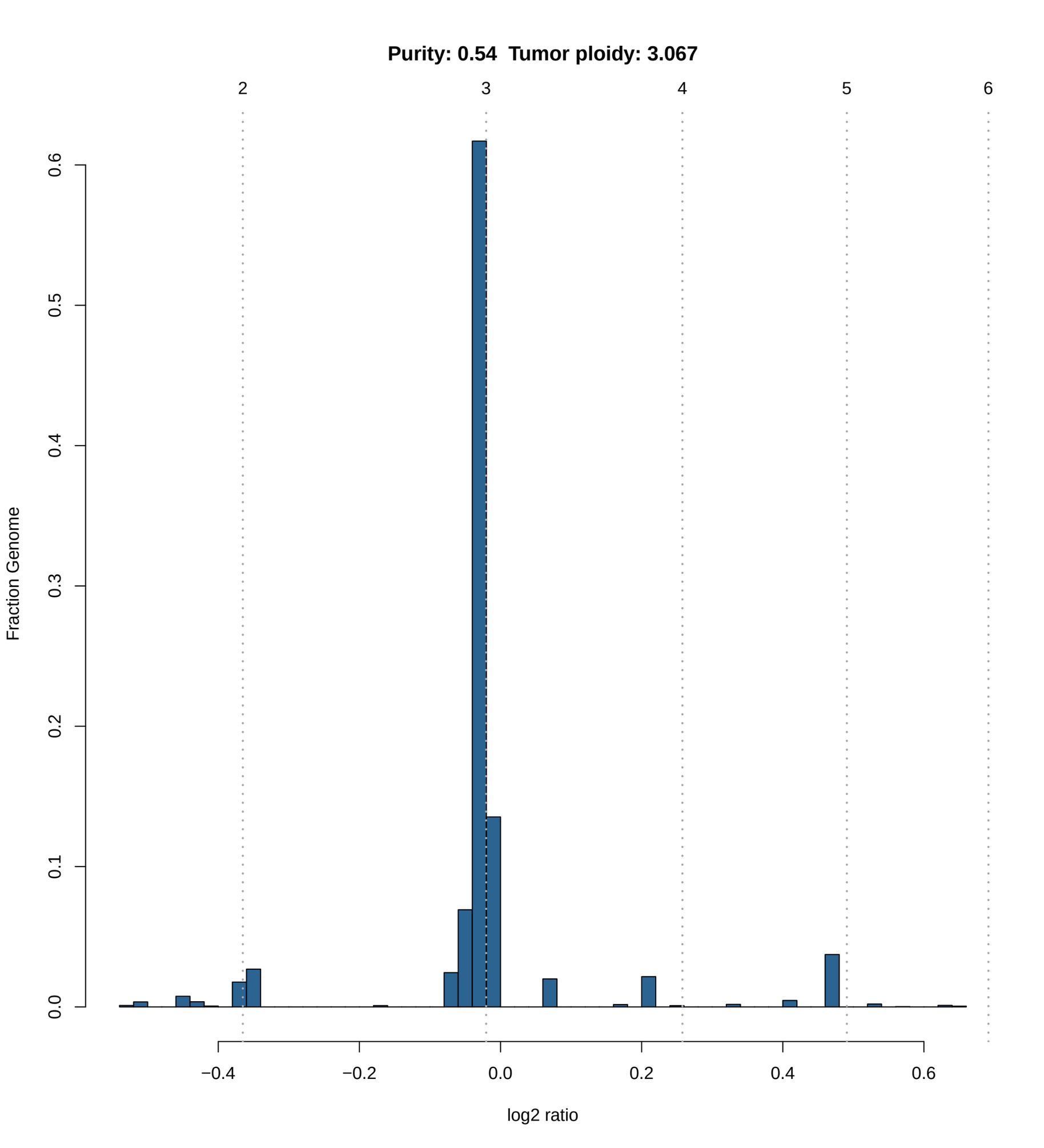

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

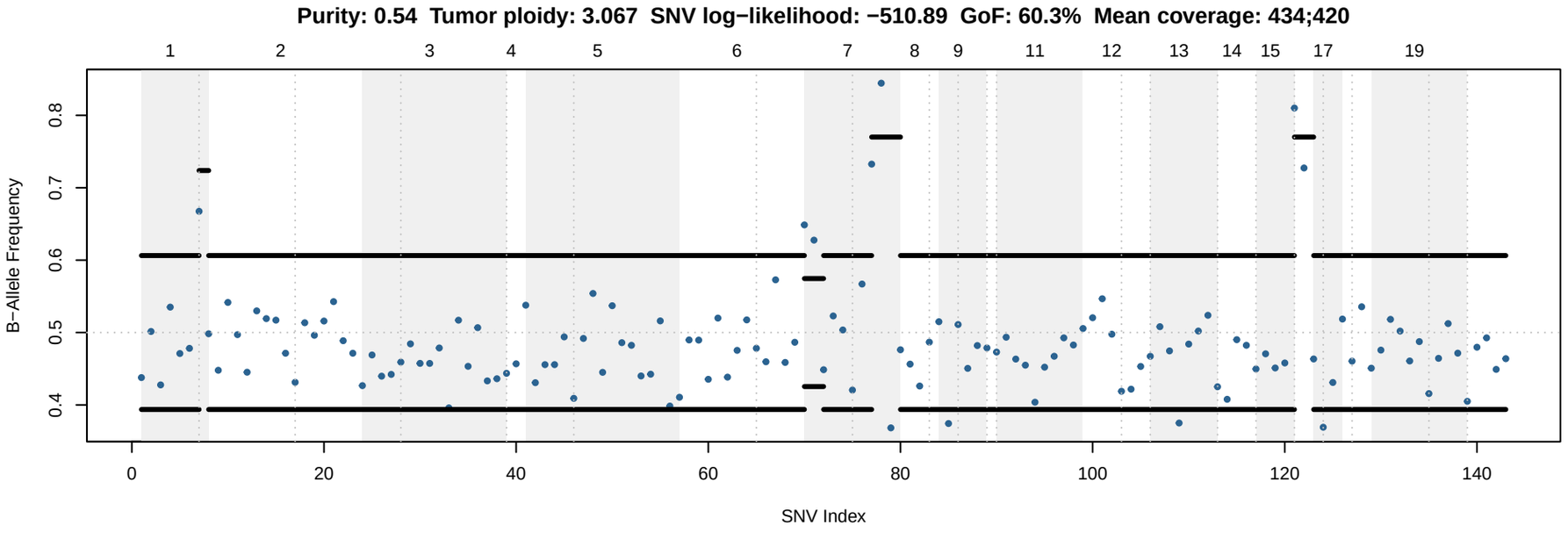

Allelic fraction (germline)
0.4
0.5
0.6
0.7
0.8
3m3
7m5
5m3
4m2
6m3
5m2
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

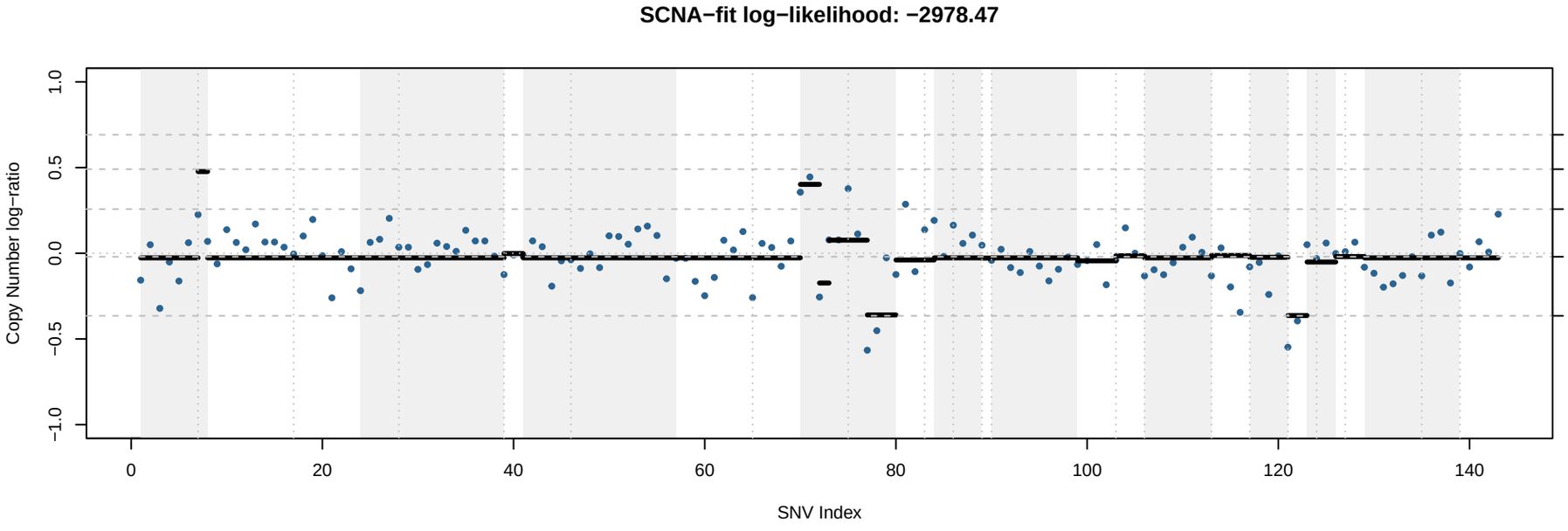

Coverage (log2)
5
6
7
8
9
10
0.0
0.2
0.4
0.6
0.8
Allelic fraction

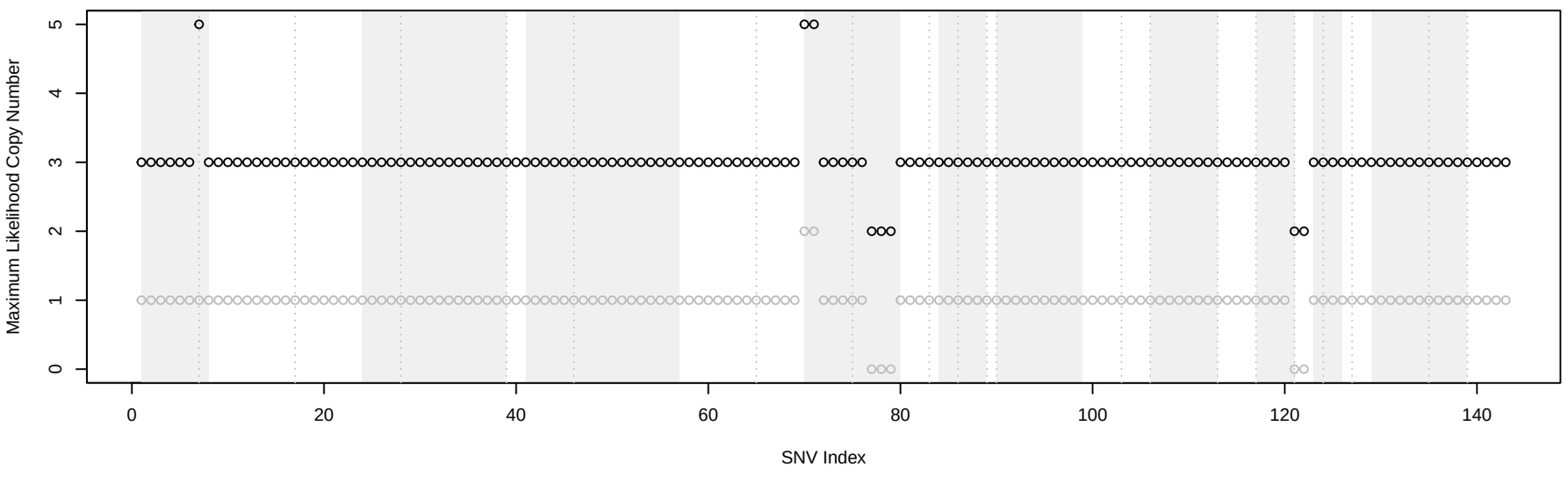

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
7m2
3m1
4m1
5m1
6m1
7m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

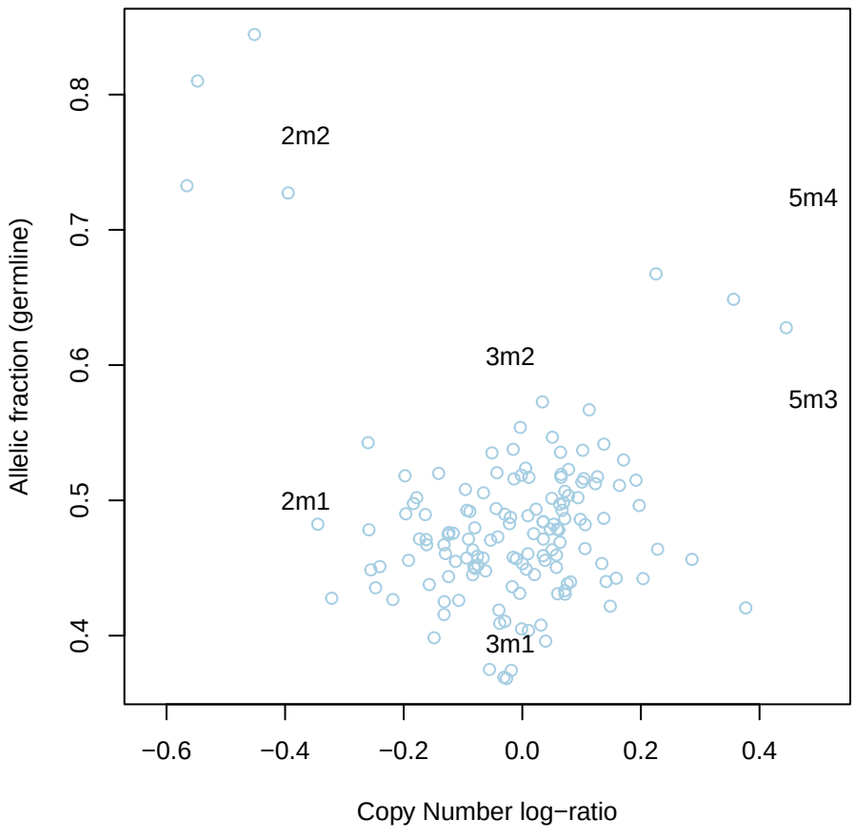

Frequency
0
10
20
30
40
50
0.2
0.4
0.6
0.8
1.0
Cellular fraction

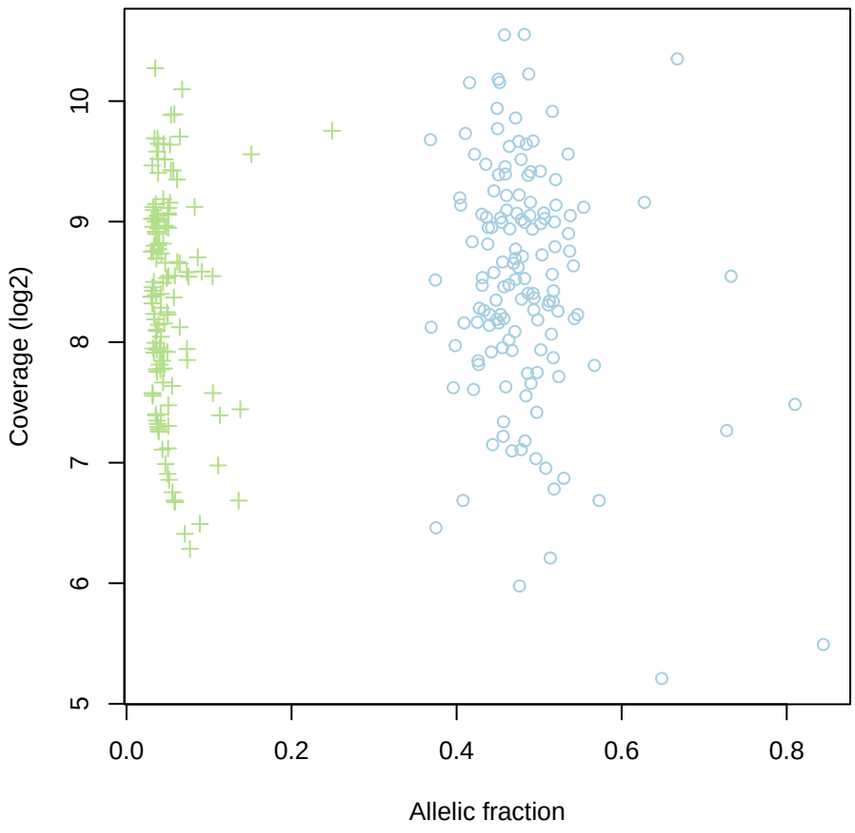

Purity: 0.54 Tumor ploidy: 3.067
2
3
4
5
6
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
0.6
log2 ratio

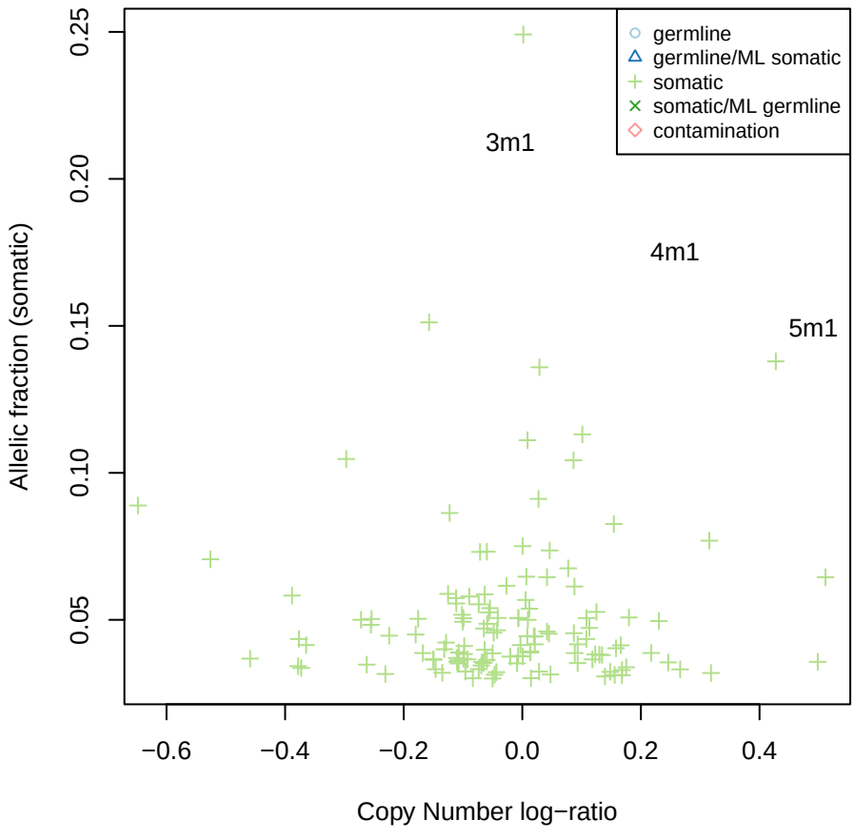

Purity: 0.54 Tumor ploidy: 3.067 SNV log−likelihood: −510.89 GoF: 60.3% Mean coverage: 434;420
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 19
B−Allele Frequency
0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index

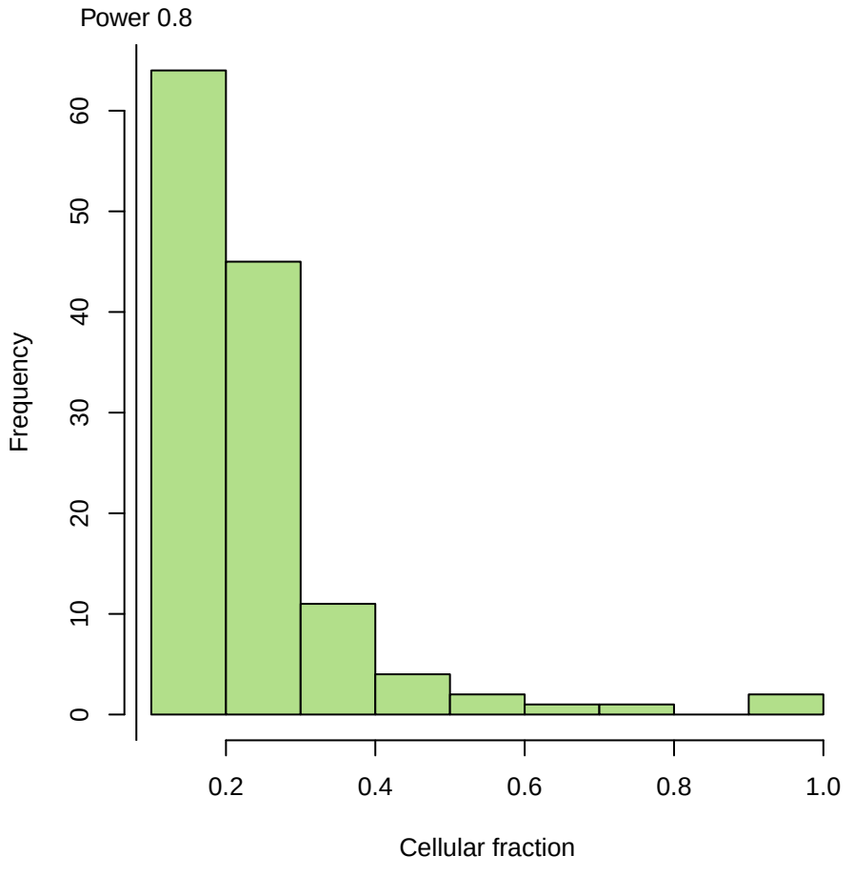

SCNA−fit log−likelihood: −2978.47
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6
0 20 40 60 80 100 120 140
SNV Index

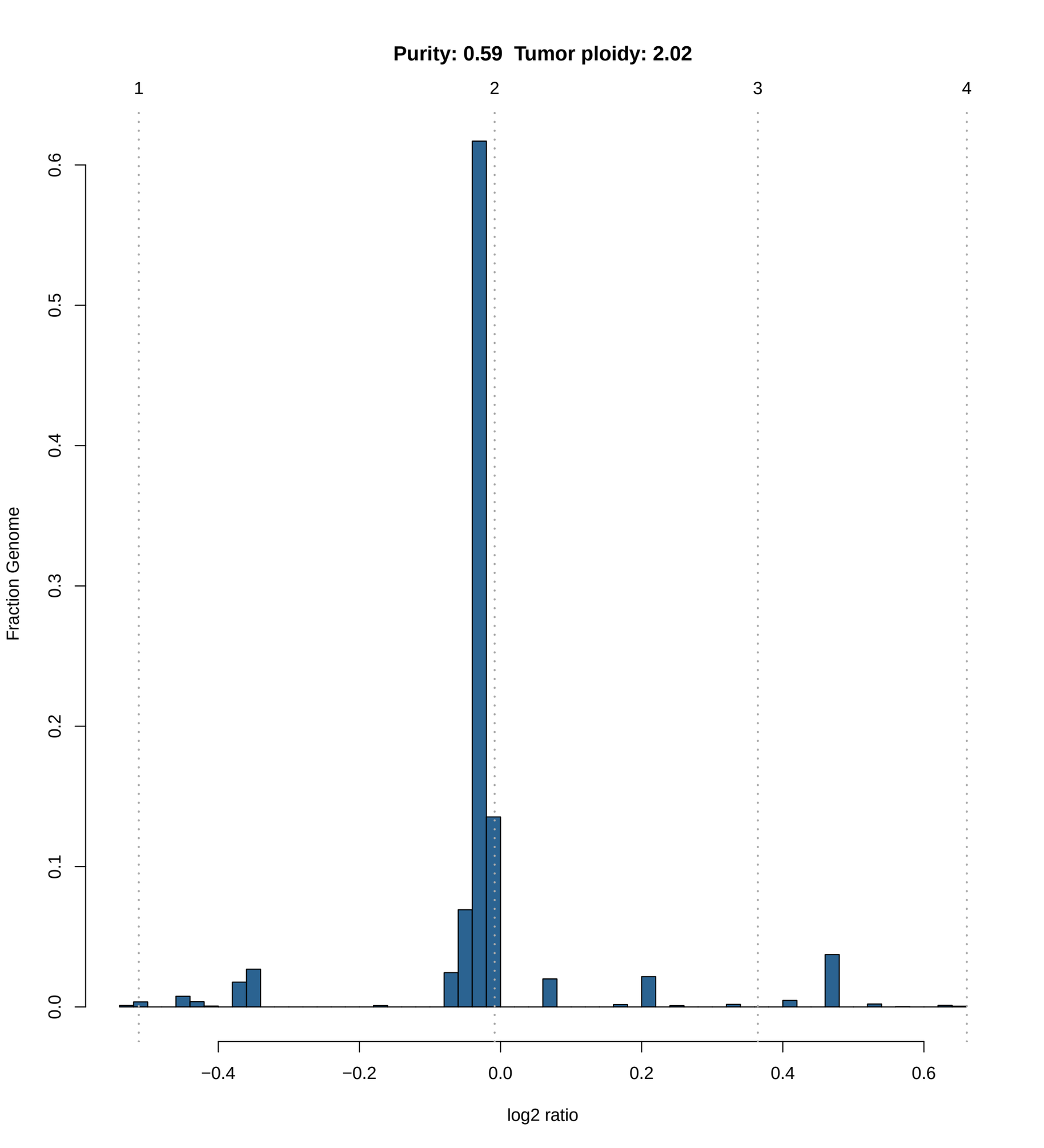

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120 140
SNV Index

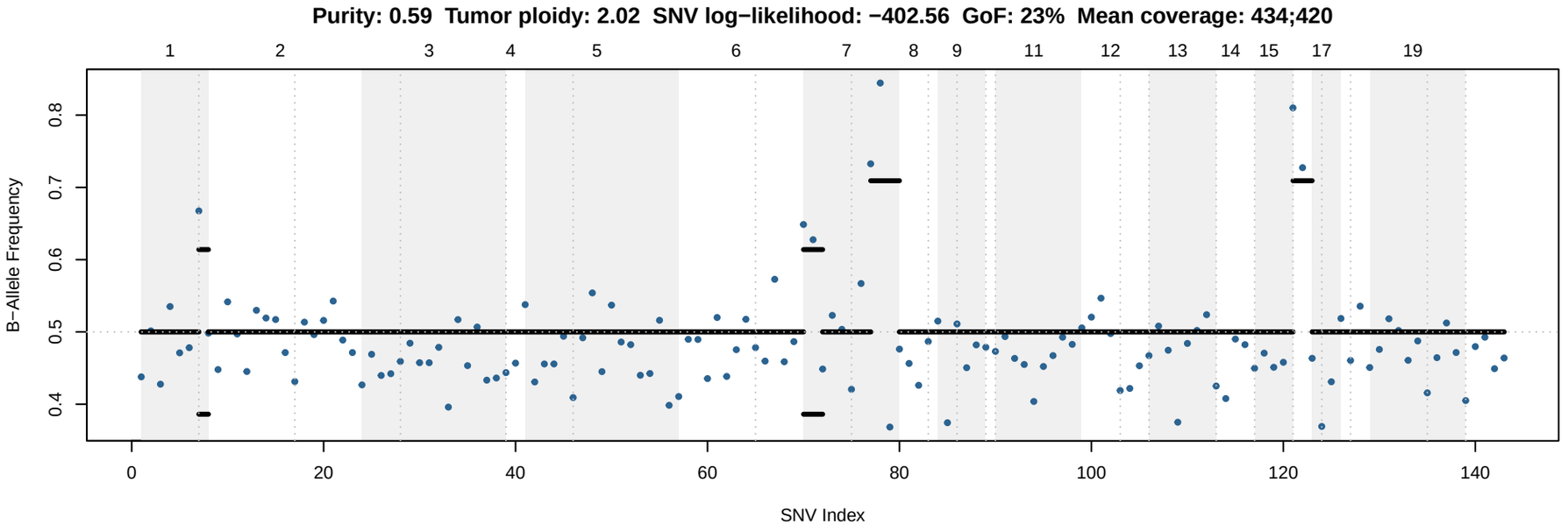

Allelic fraction (germline)
0.4
0.5
0.6
0.7
0.8
2m2
5m4
3m2
5m3
2m1
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

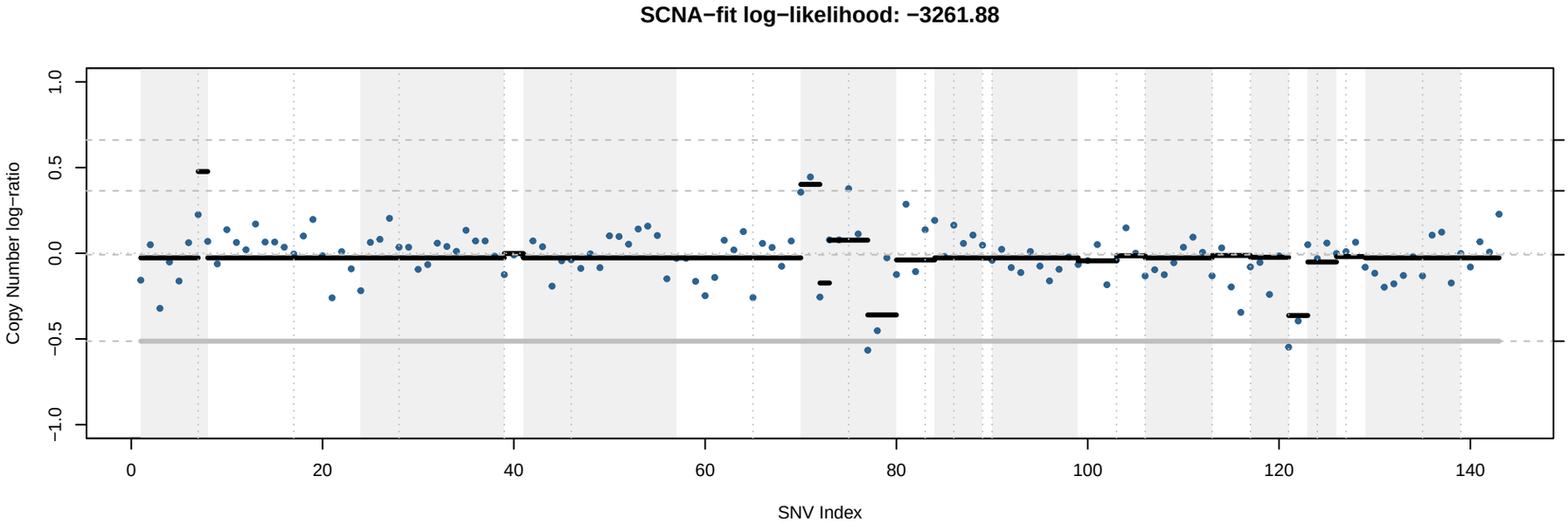

Coverage (log2)
5
6
7
8
9
10
0.0
0.2
0.4
0.6
0.8
Allelic fraction

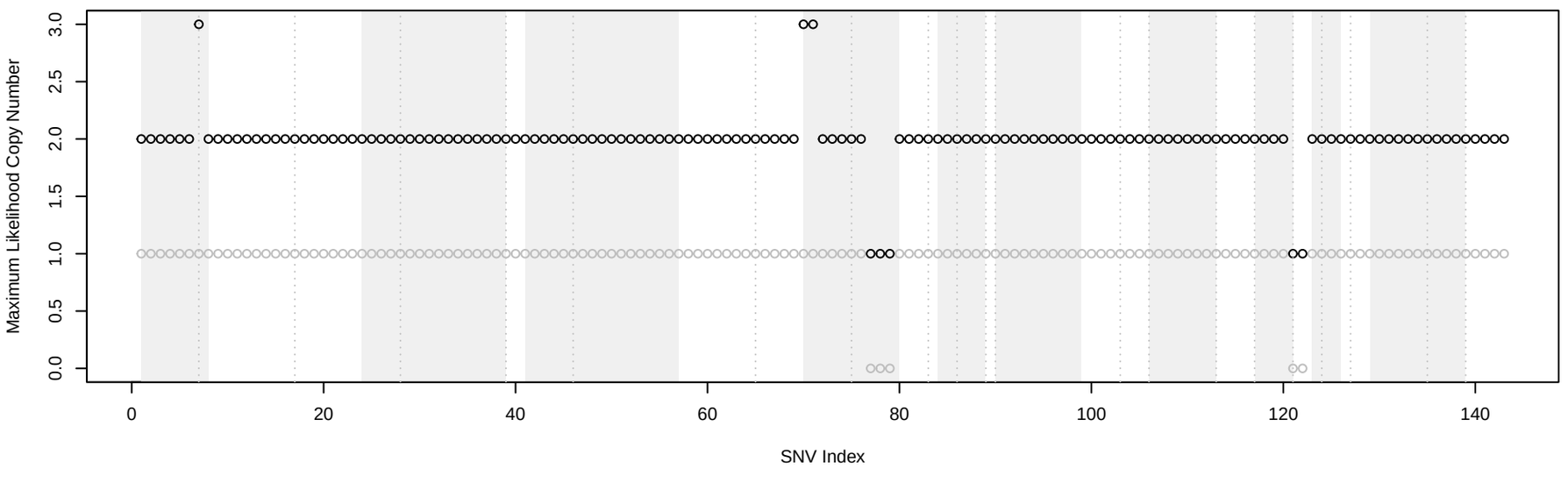

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

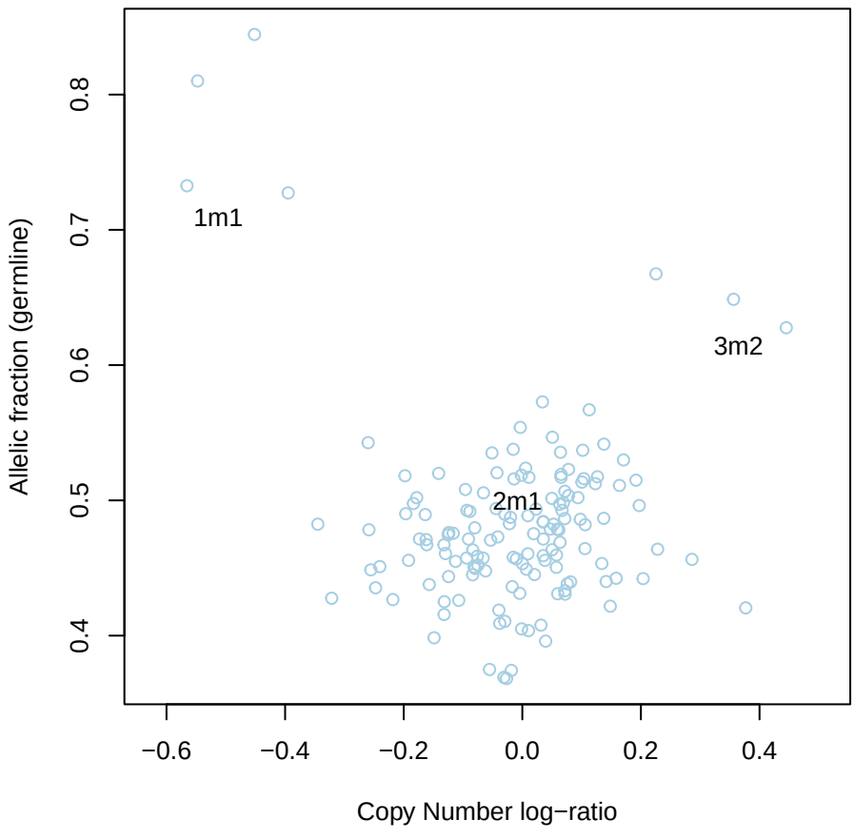

Power 0.8
Frequency
0
10
20
30
40
50
60
0.2
0.4
0.6
0.8
1.0
Cellular fraction

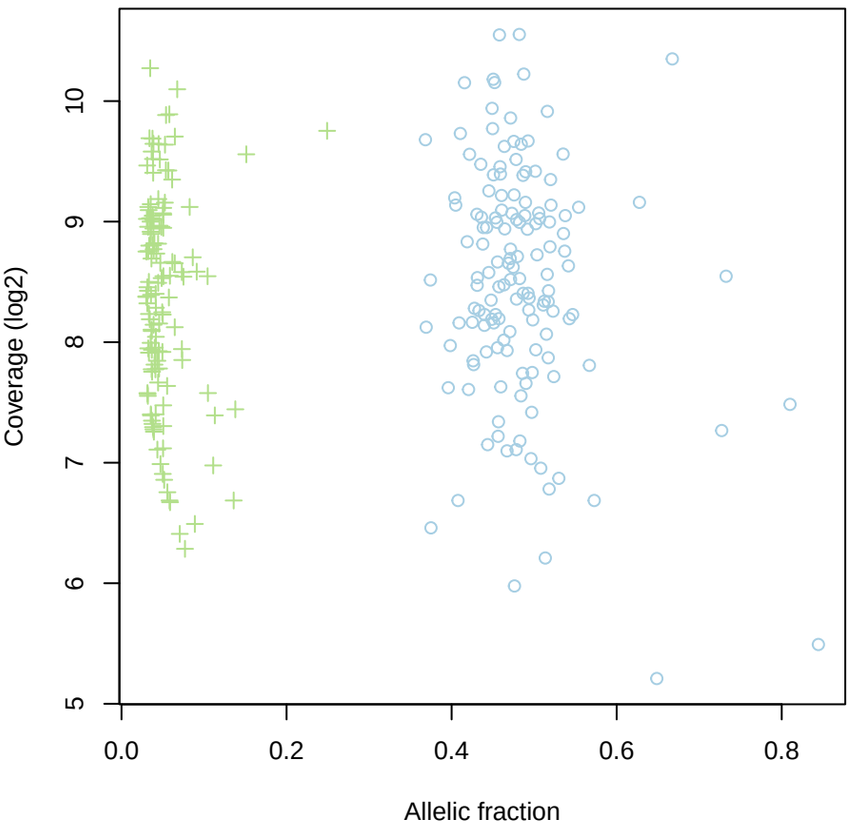

Purity: 0.59 Tumor ploidy: 2.02
1
2
3
4
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
log2 ratio

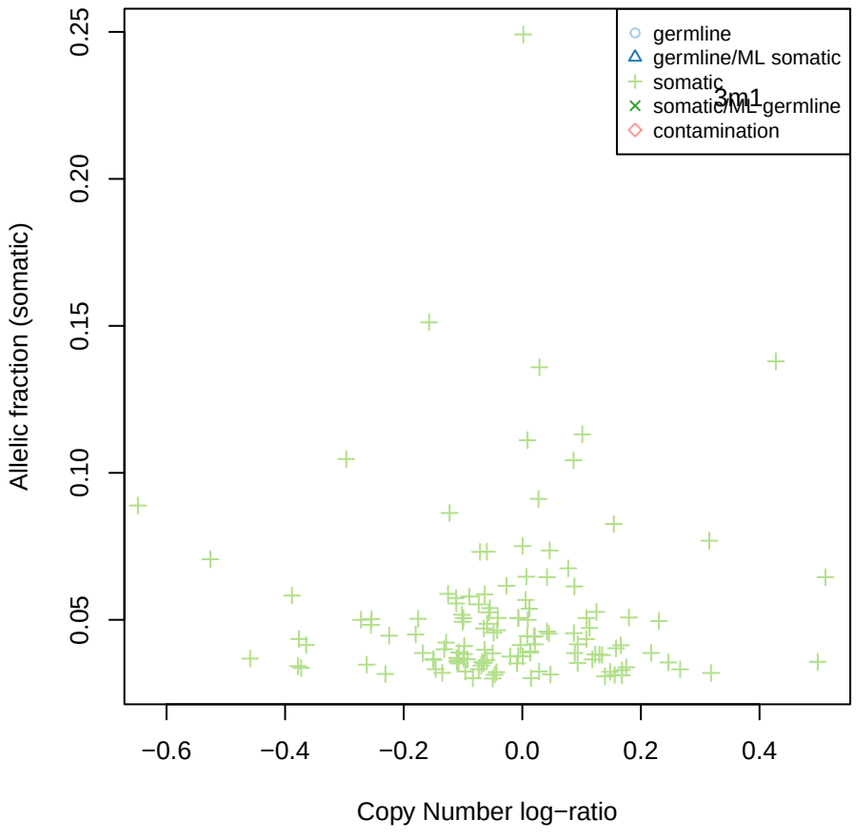

Purity: 0.59 Tumor ploidy: 2.02 SNV log−likelihood: −402.56 GoF: 23% Mean coverage: 434;420
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 19
B−Allele Frequency
0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index

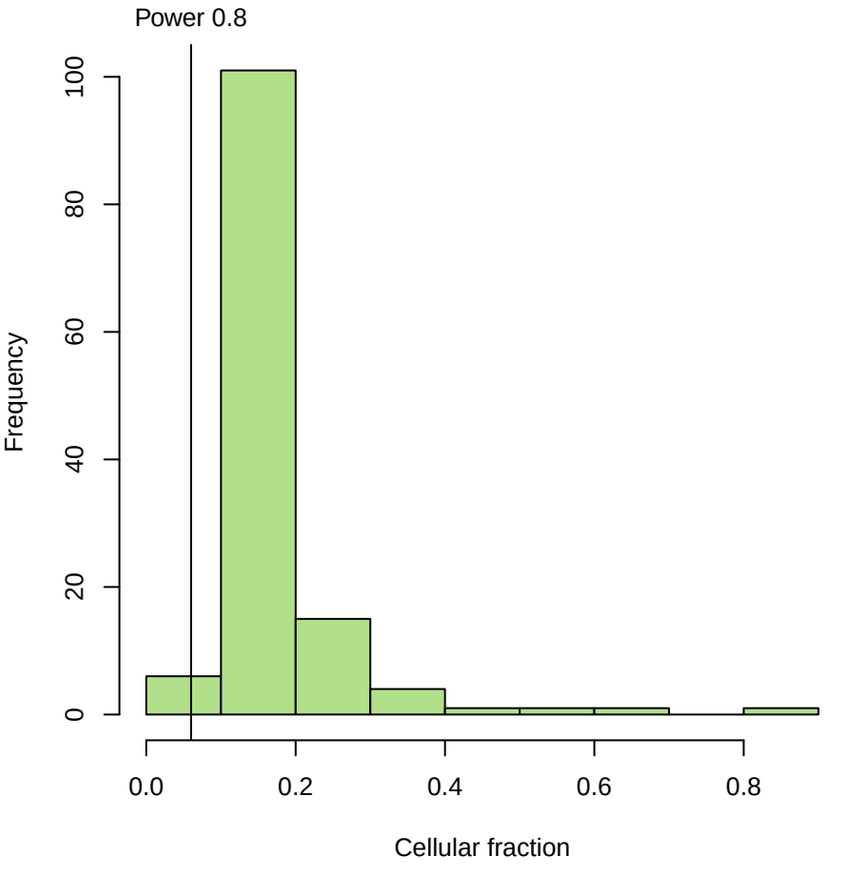

SCNA−fit log−likelihood: −3261.88
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4
0 20 40 60 80 100 120 140
SNV Index

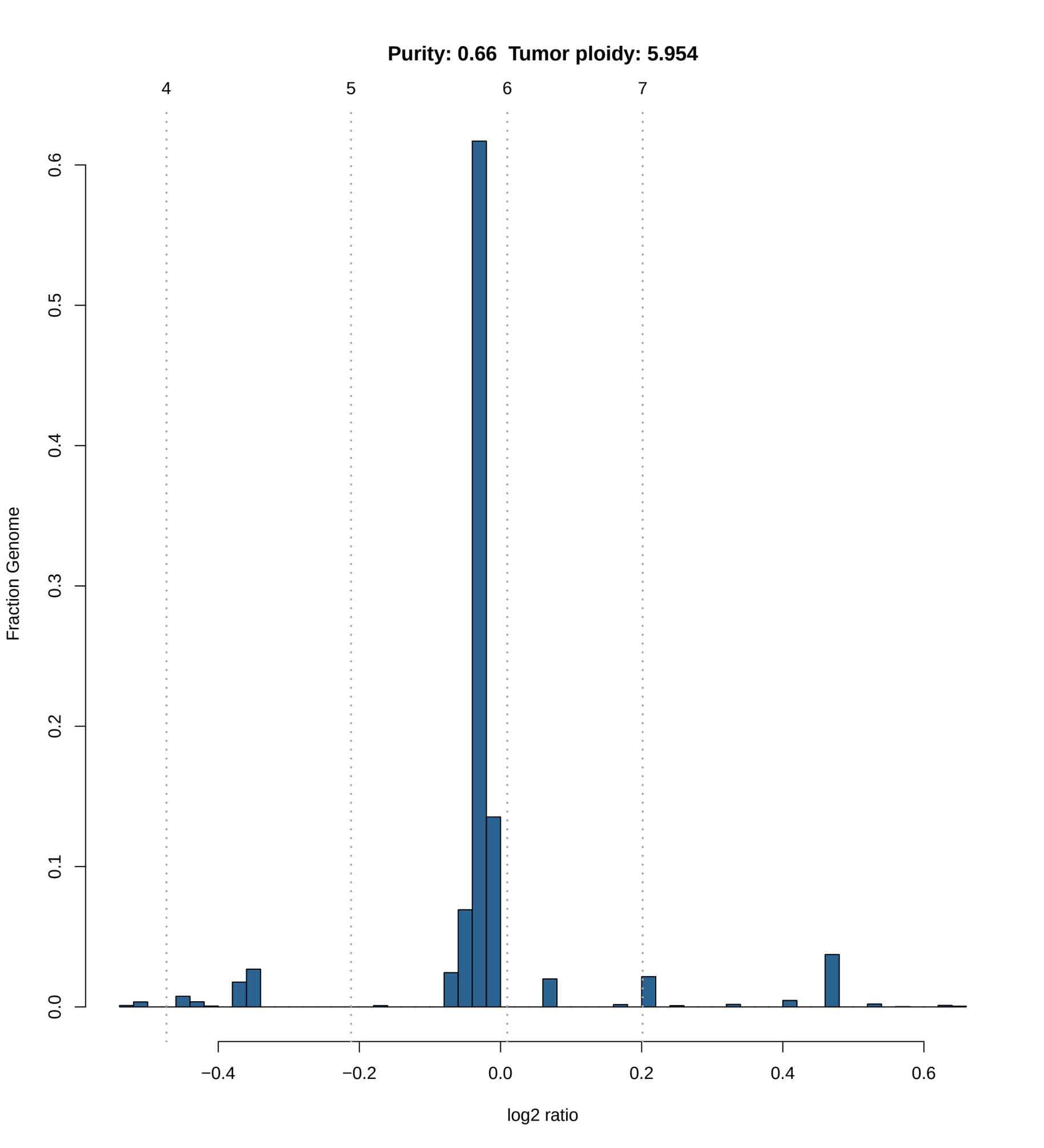

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120 140
SNV Index

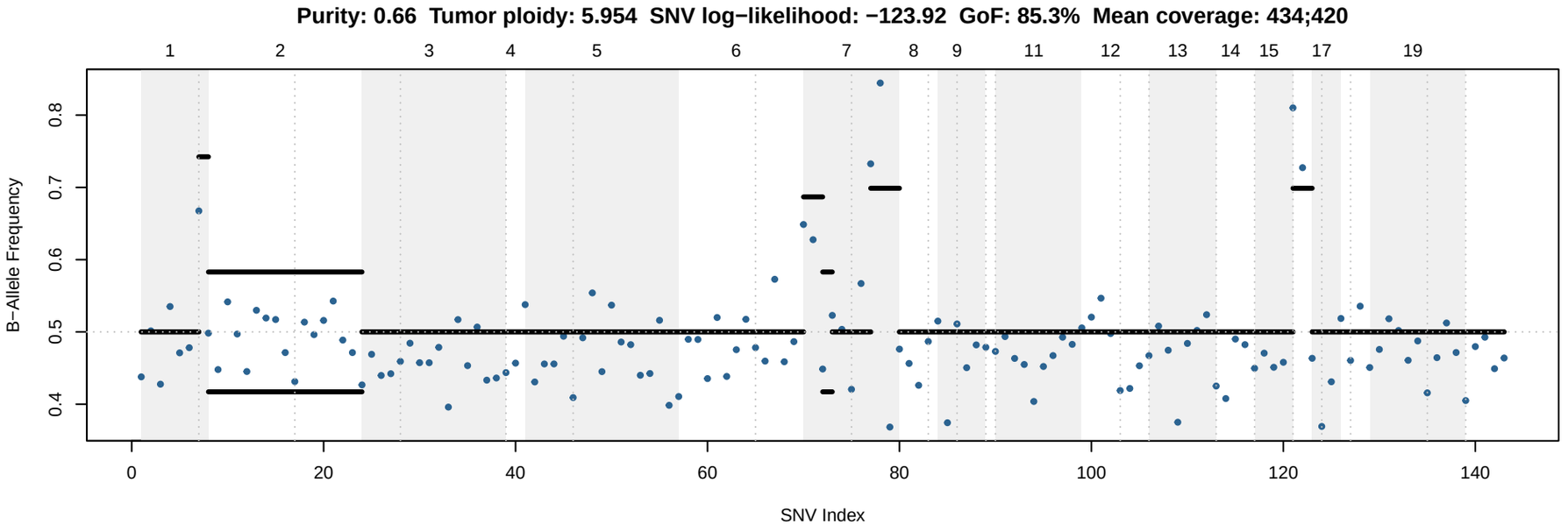

Allelic fraction (germline)
0.4
0.5
0.6
0.7
0.8
1m1
2m1
3m2
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

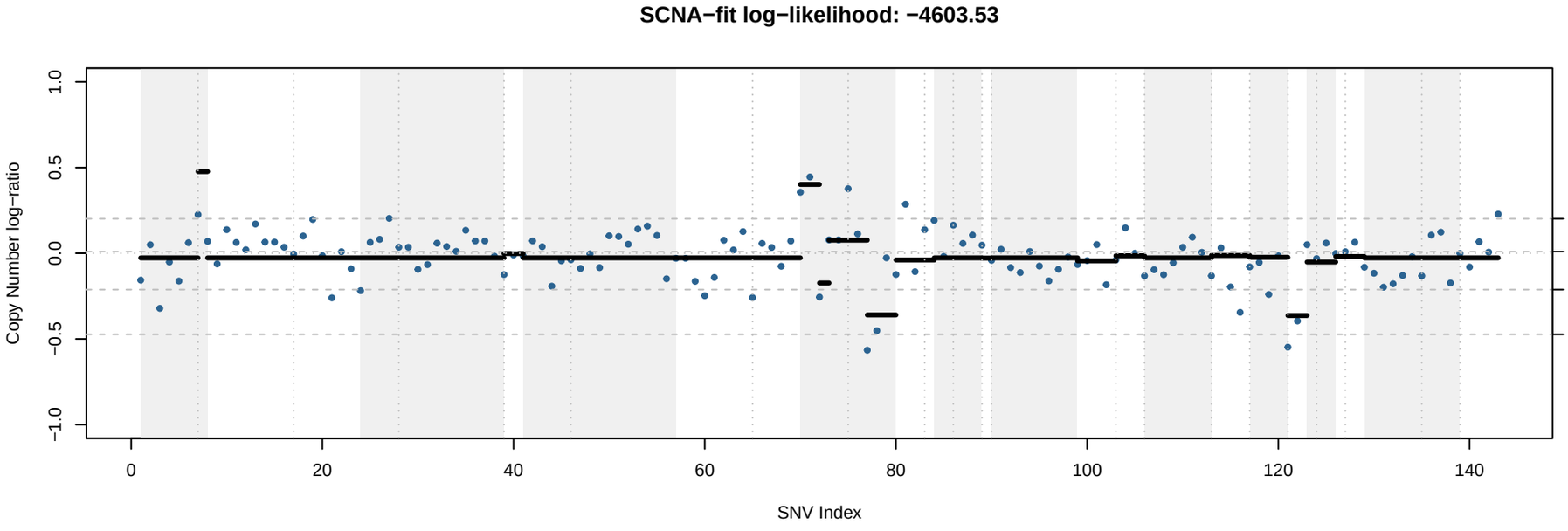

Coverage (log2)
5
6
7
8
9
10
0.0
0.2
0.4
0.6
0.8
Allelic fraction

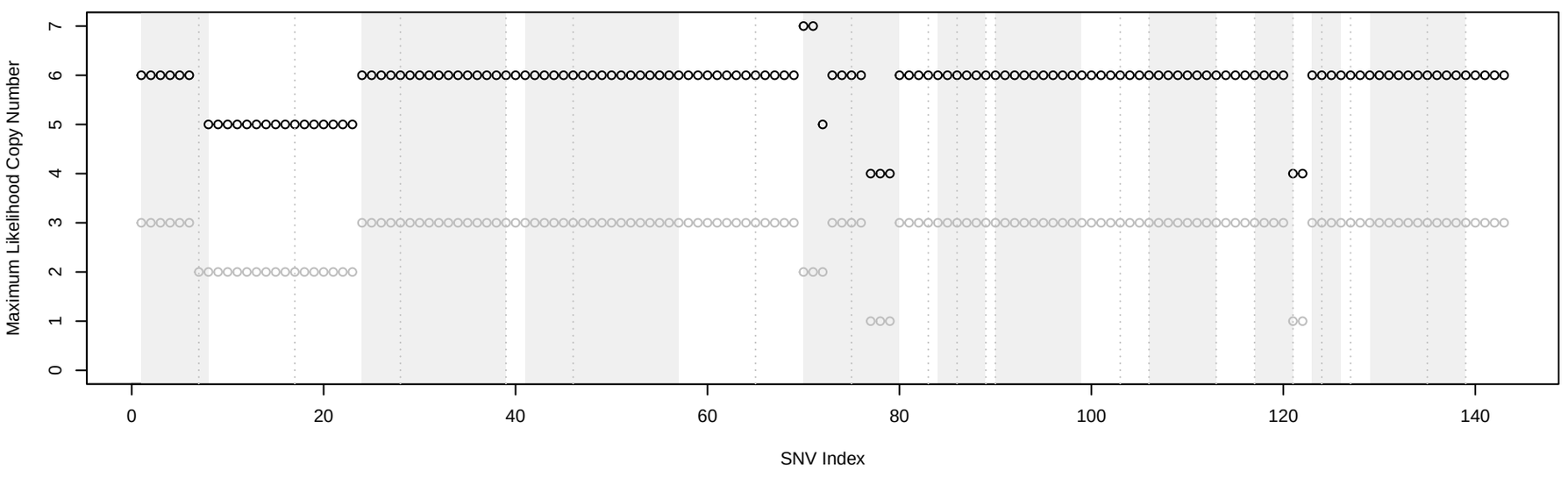

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

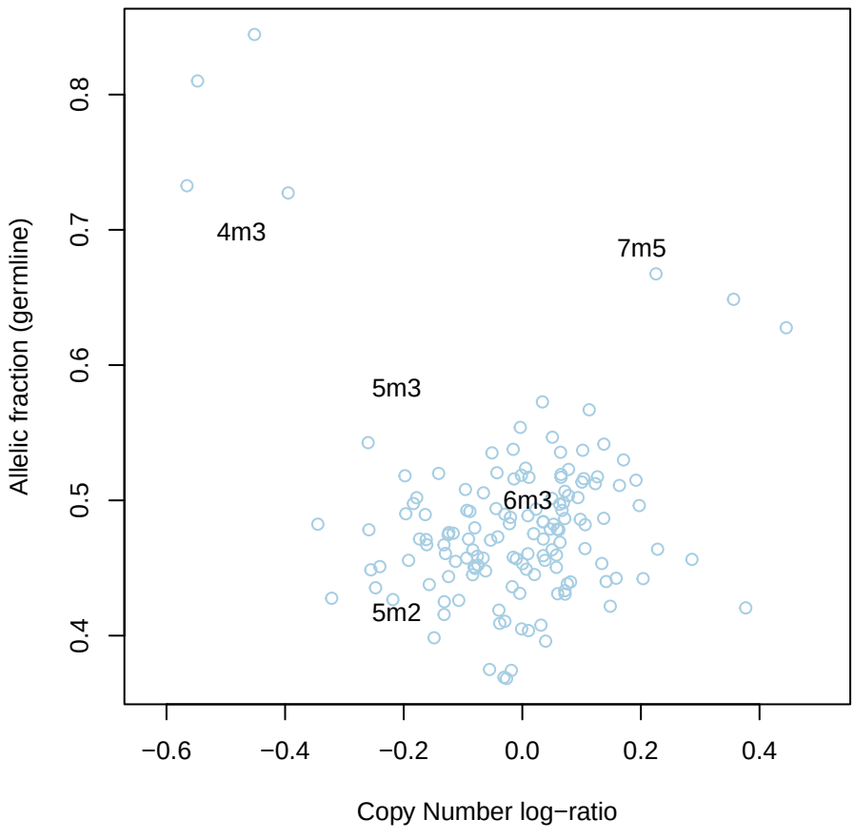

Power 0.8
Frequency
0
20
40
60
80
100
0.0
0.2
0.4
0.6
0.8
Cellular fraction

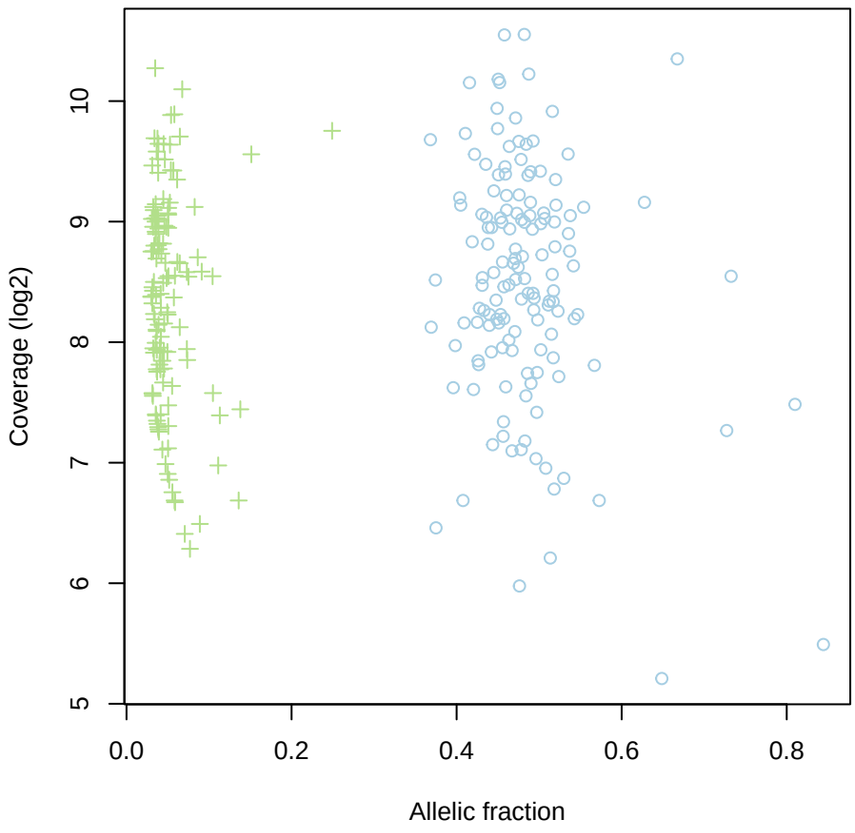

Purity: 0.66 Tumor ploidy: 5.954
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
0.6
log2 ratio

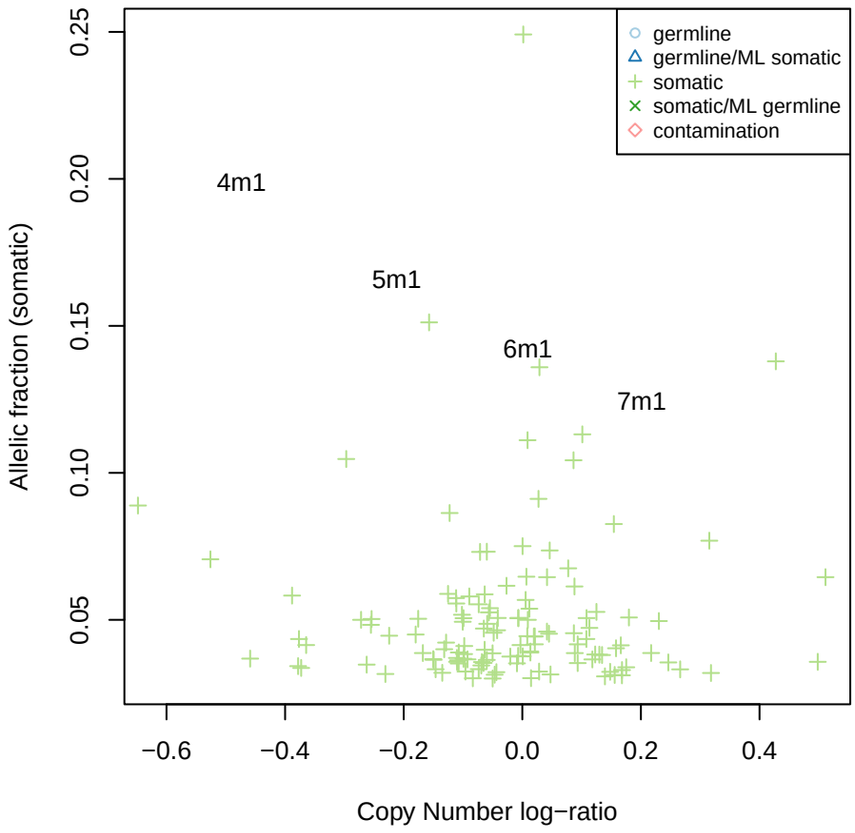

Purity: 0.66 Tumor ploidy: 5.954 SNV log−likelihood: −123.92 GoF: 85.3% Mean coverage: 434;420
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 19
B−Allele Frequency
0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index

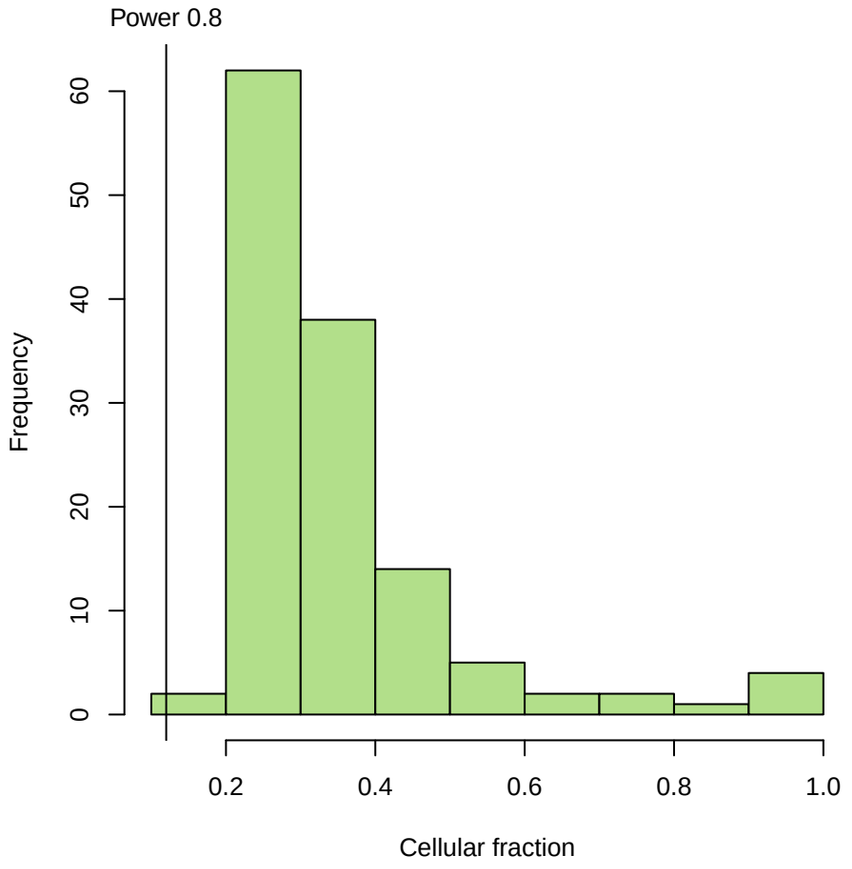

SCNA−fit log−likelihood: −4603.53
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

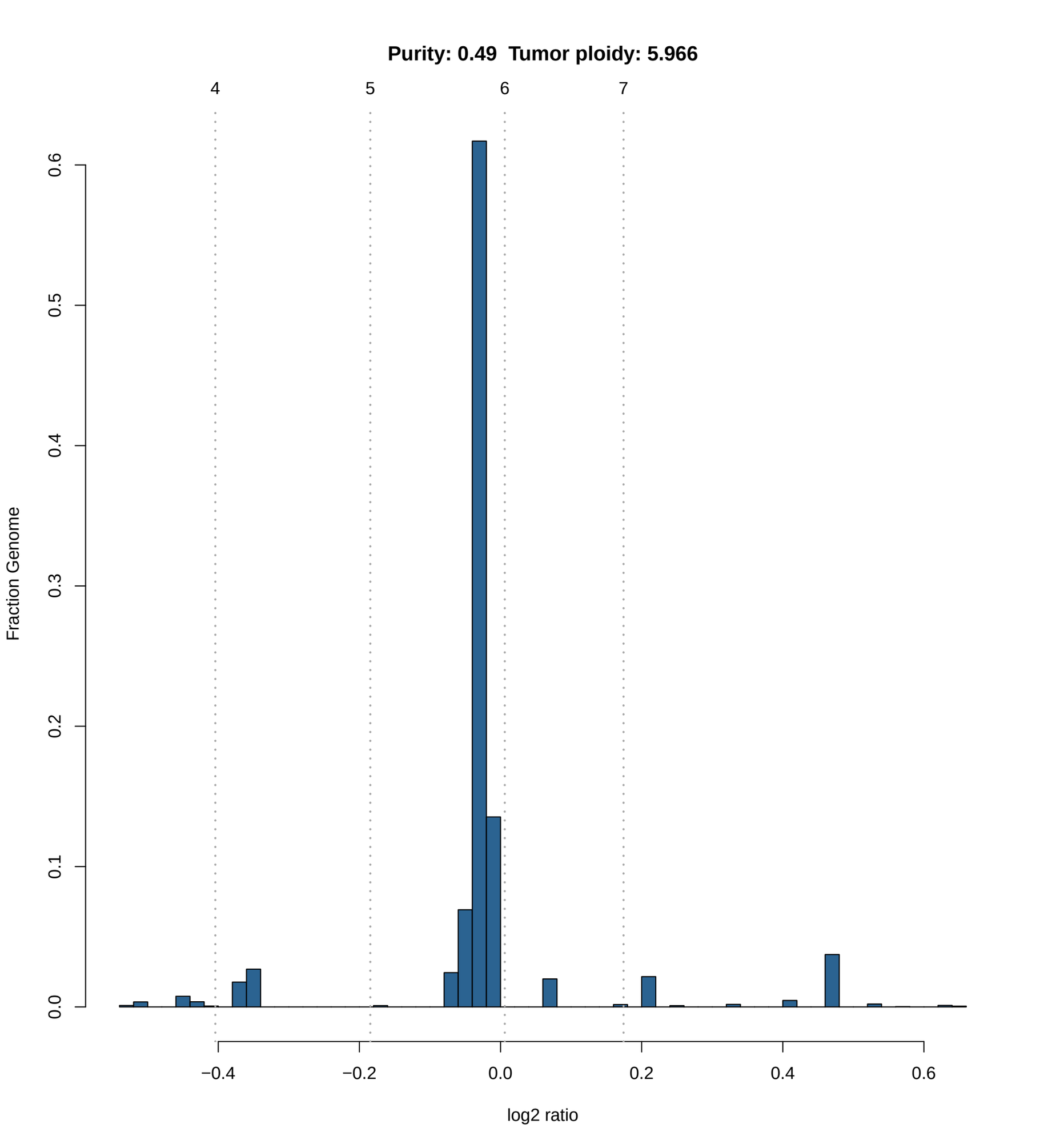

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

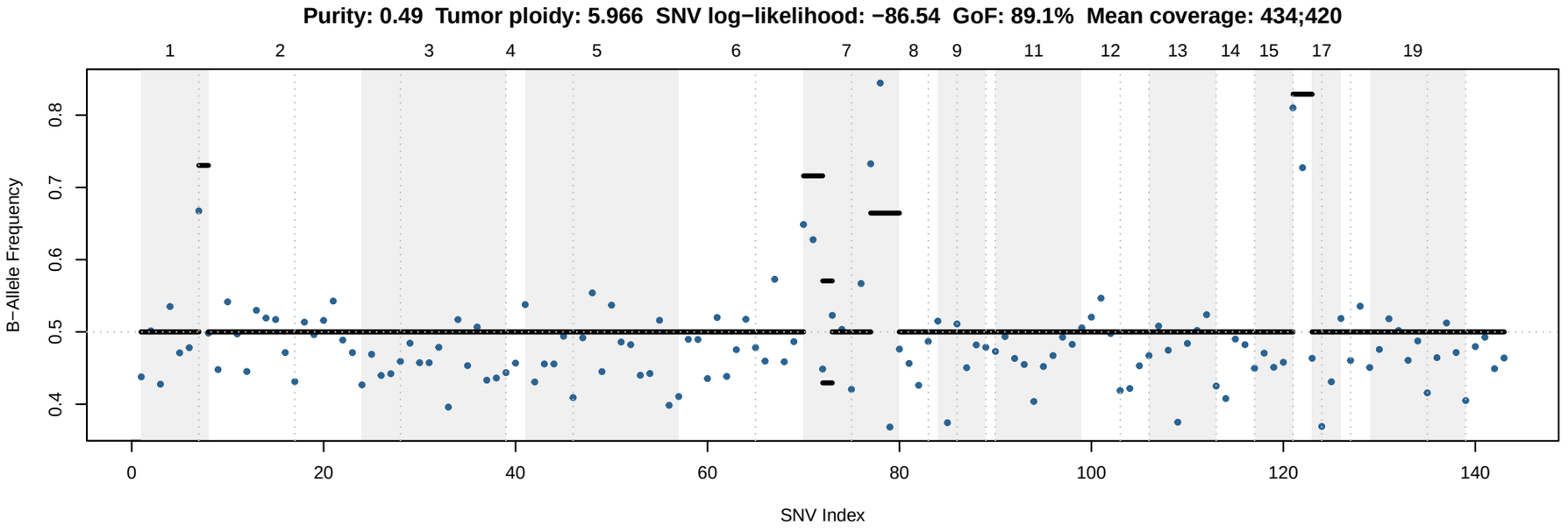

Allelic fraction (germline)
0.4
0.5
0.6
0.7
0.8
4m3
7m5
5m3
6m3
5m2
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

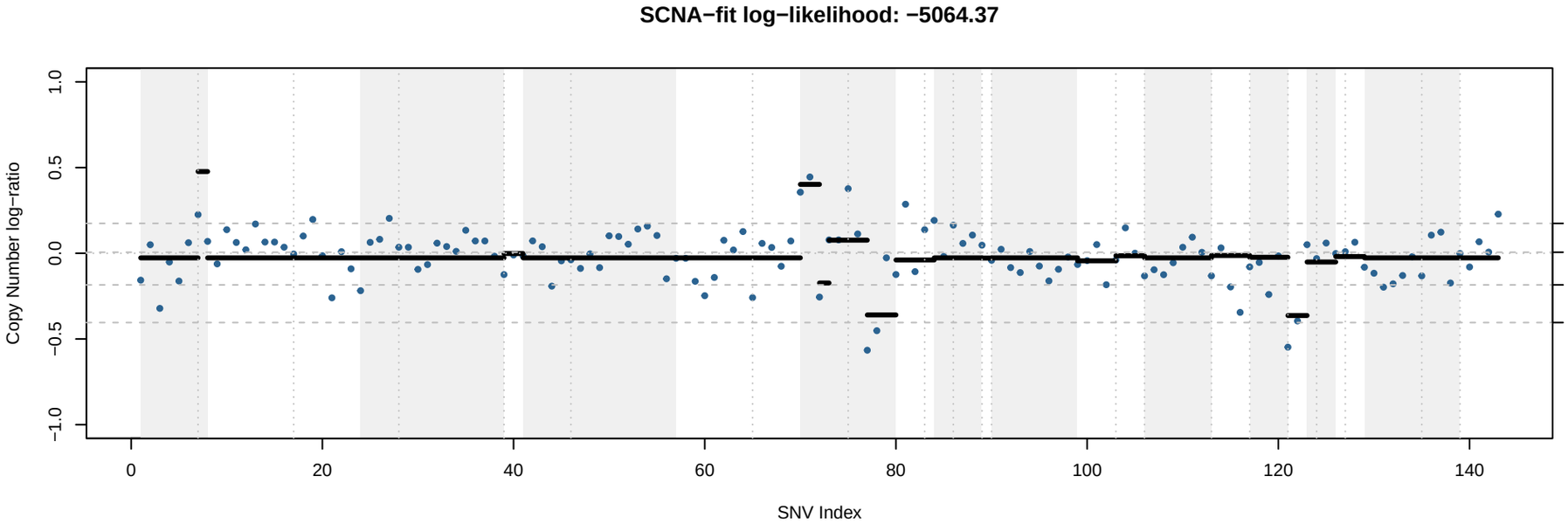

Coverage (log2)
5
6
7
8
9
10
0.0
0.2
0.4
0.6
0.8
Allelic fraction

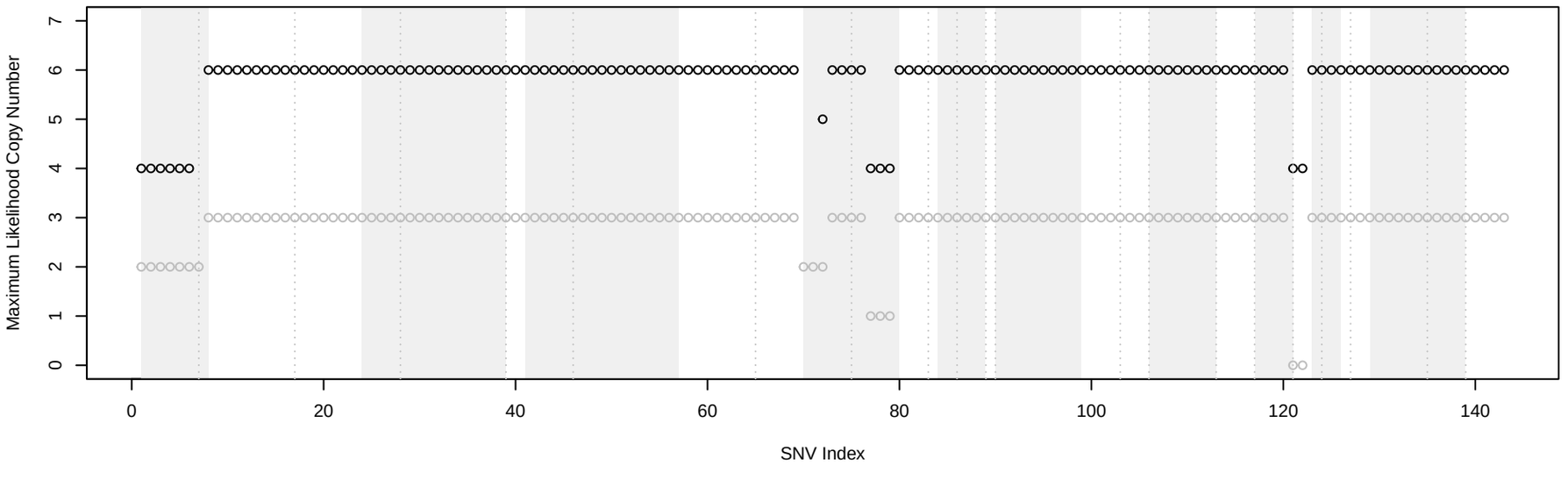

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
4m1
5m1
6m1
7m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

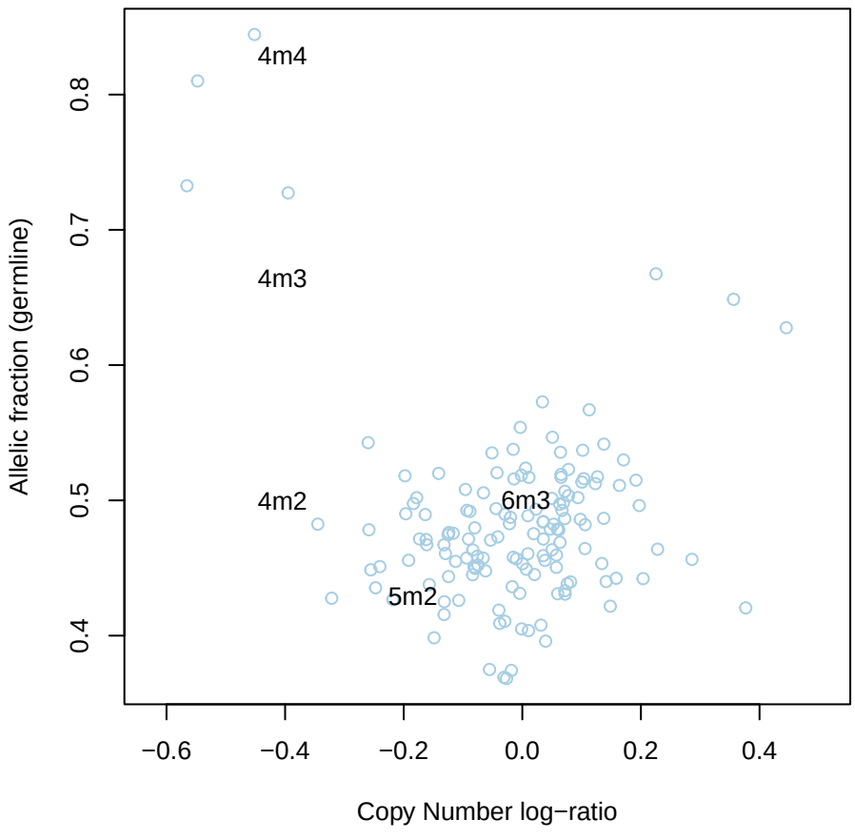

Power 0.8
Frequency
0
10
20
30
40
50
60
0.2
0.4
0.6
0.8
1.0
Cellular fraction

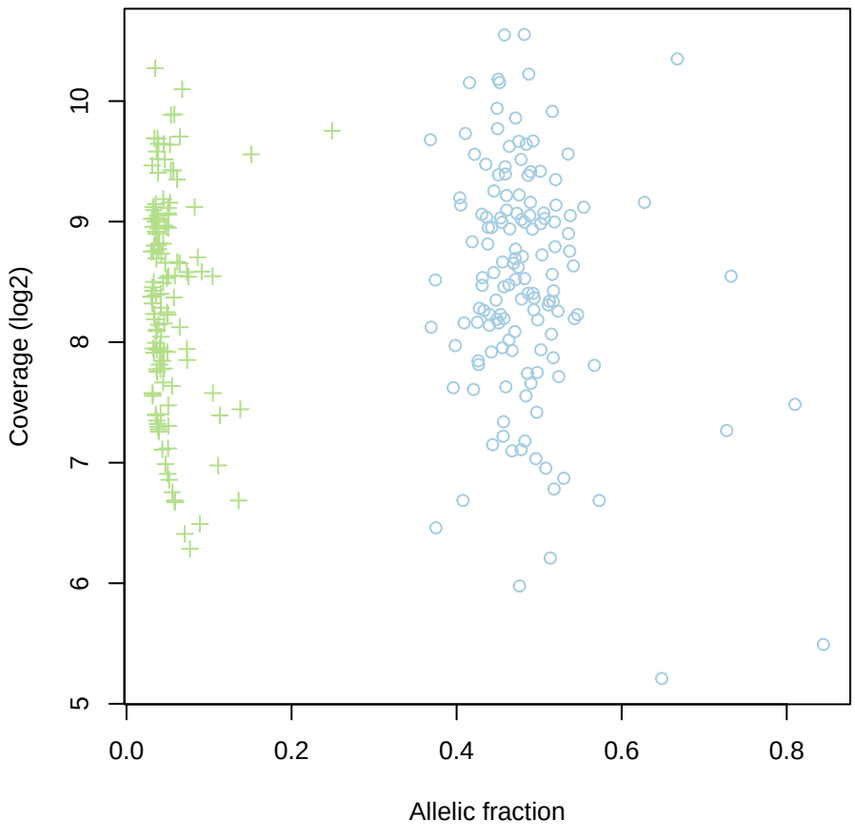

Purity: 0.49 Tumor ploidy: 5.966
4
5
6
7
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
0.6
log2 ratio

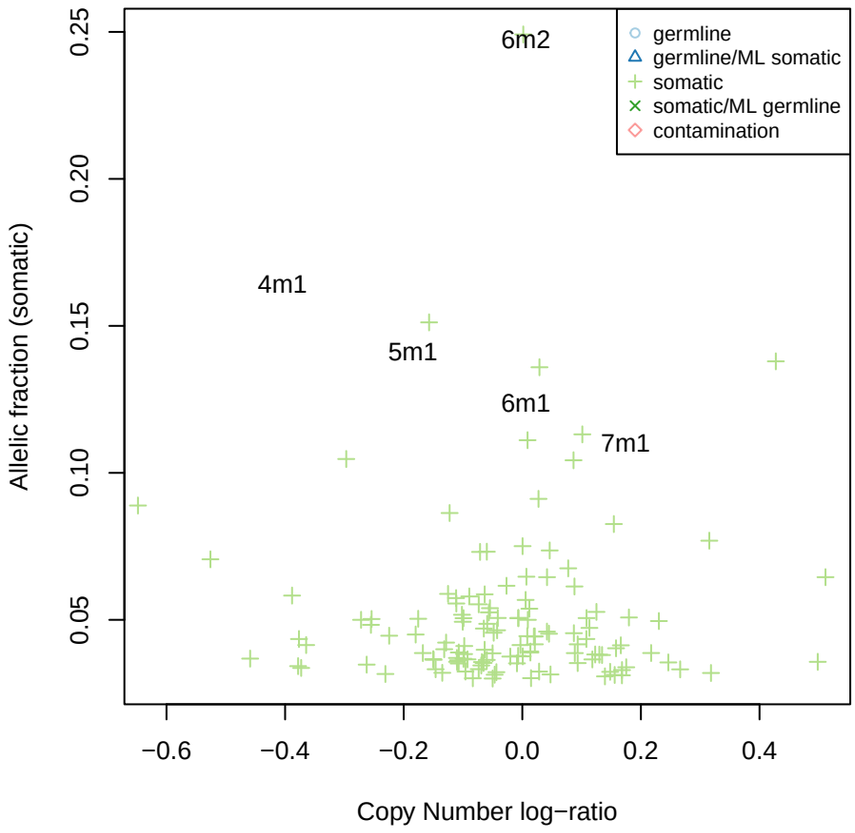

Purity: 0.49 Tumor ploidy: 5.966 SNV log−likelihood: −86.54 GoF: 89.1% Mean coverage: 434;420
1 2 3 4 5 6 7 8 9 11 12 13 14 15 17 19
B−Allele Frequency
0.4 0.5 0.6 0.7 0.8
0 20 40 60 80 100 120 140
SNV Index

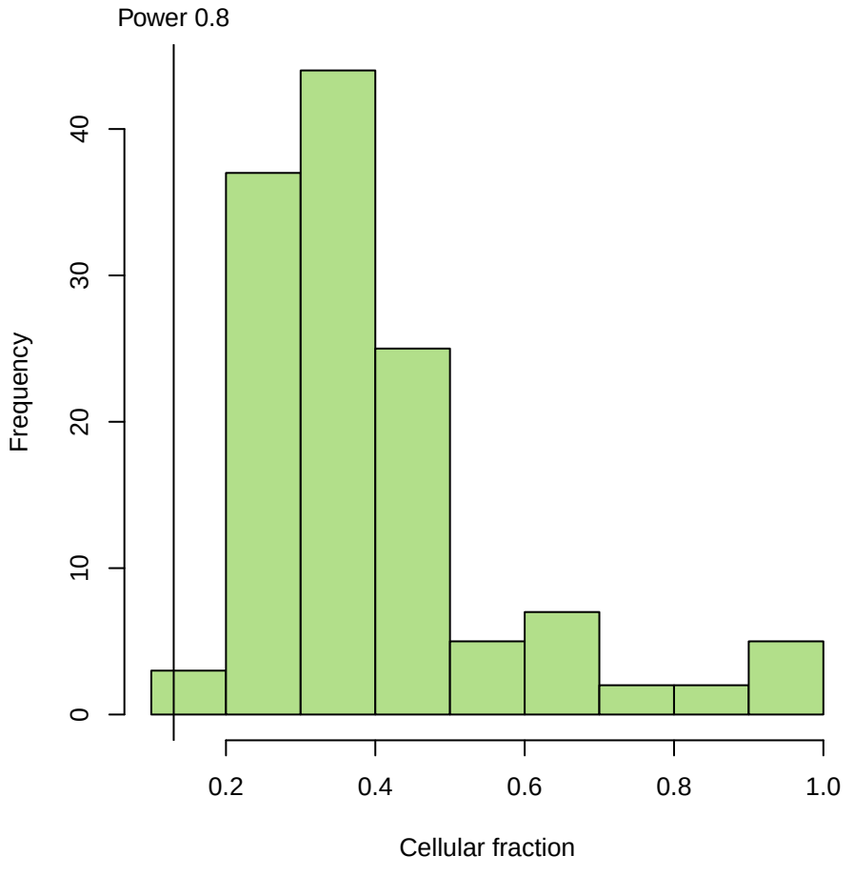

SCNA−fit log−likelihood: −5064.37
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

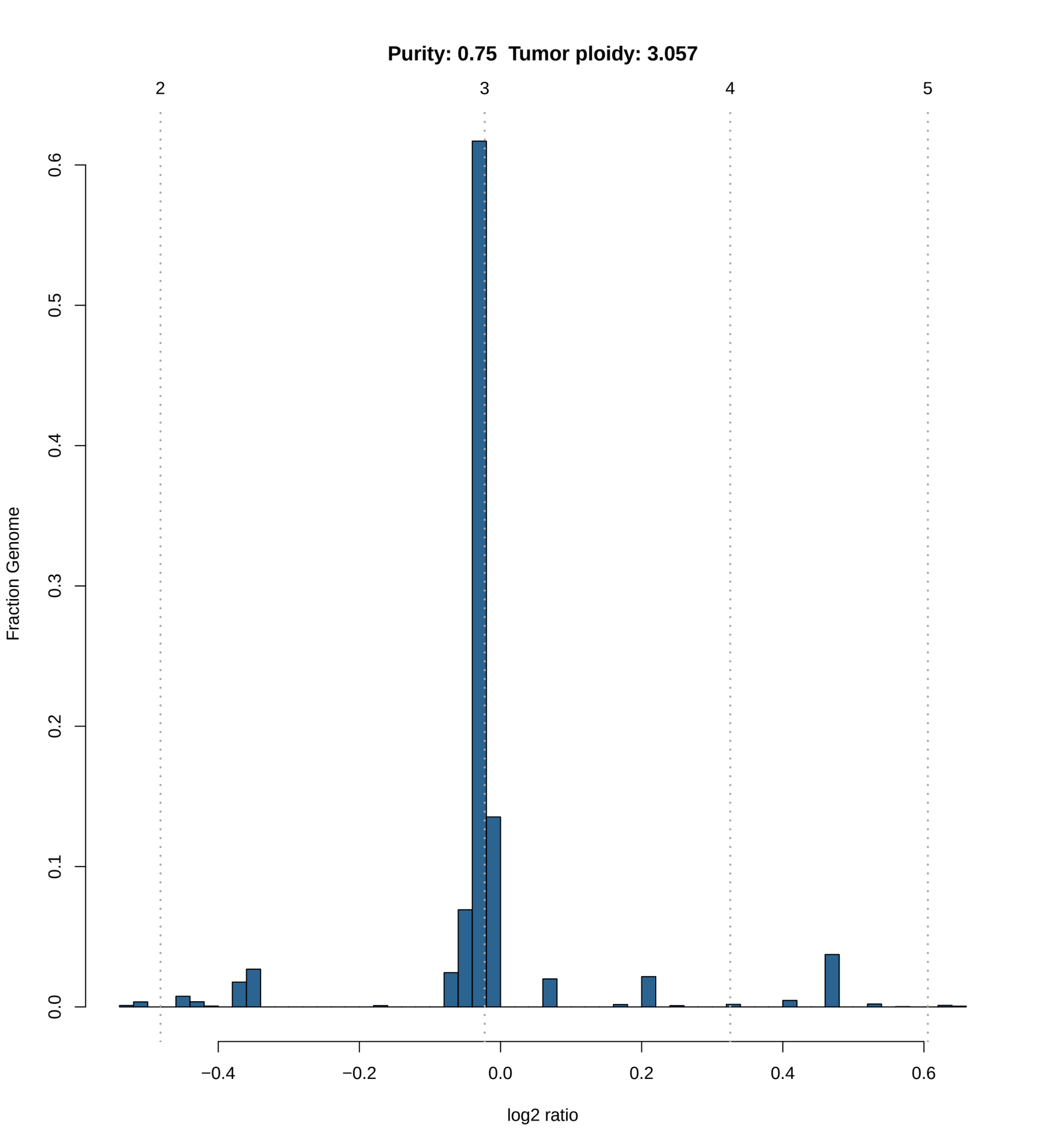

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120 140
SNV Index

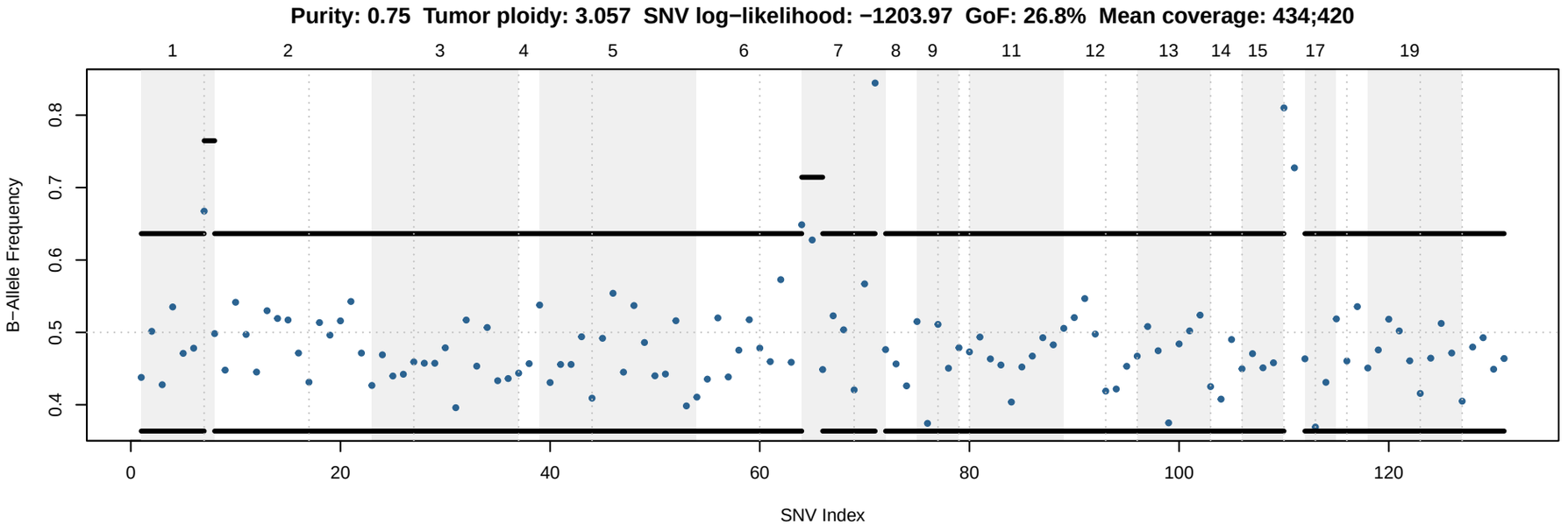

4m4
4m3
4m2
6m3
5m2
Allelic fraction (germline)
Copy Number log−ratio

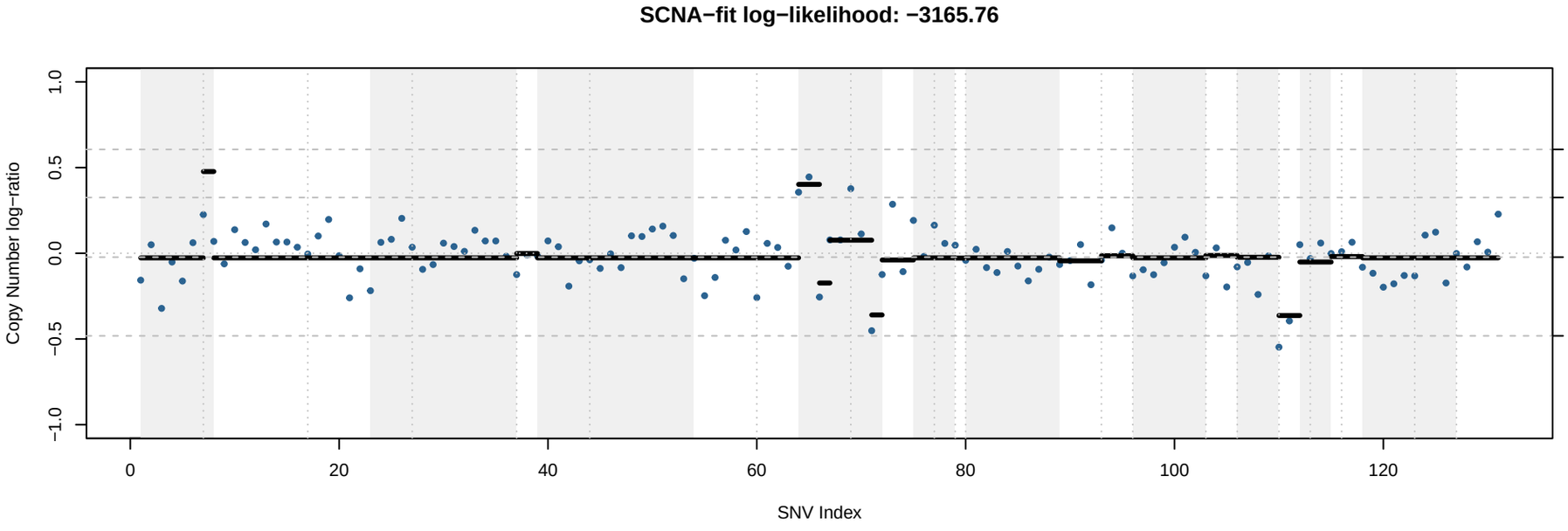

Coverage (log2)
Allelic fraction

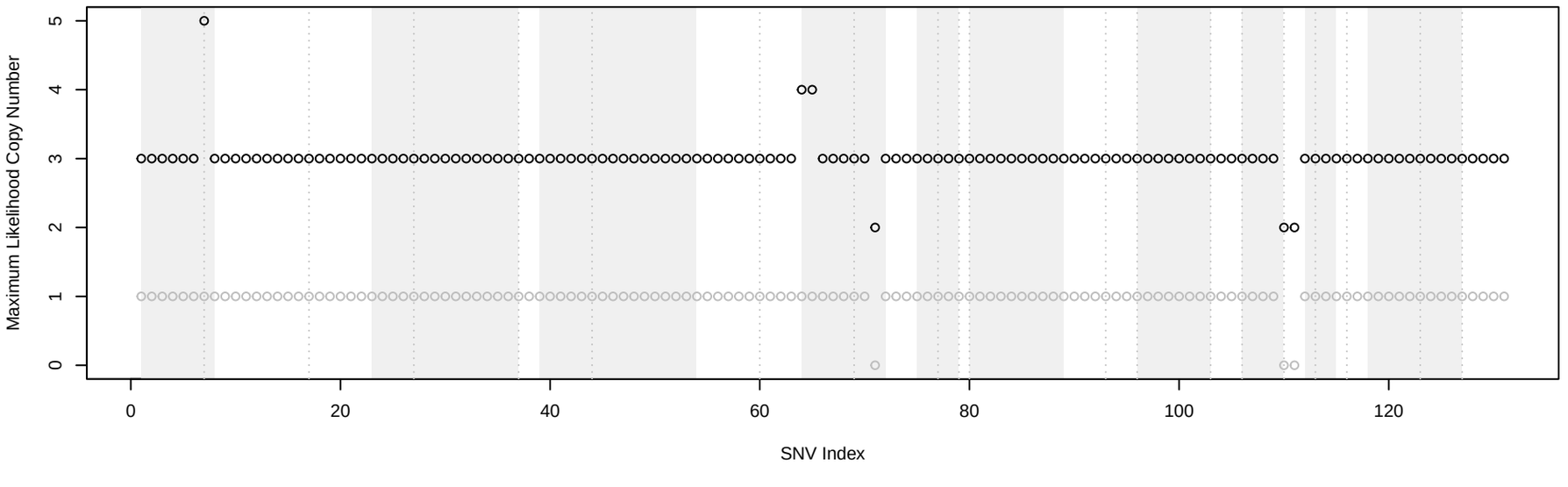

6m2
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

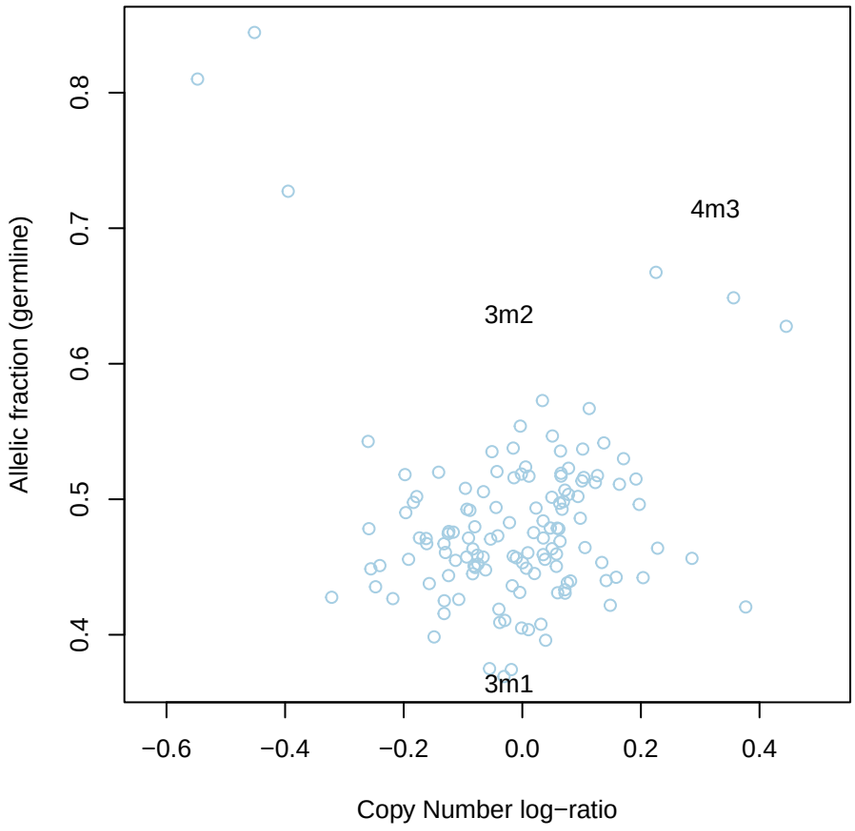

Power 0.8
Frequency
Cellular fraction

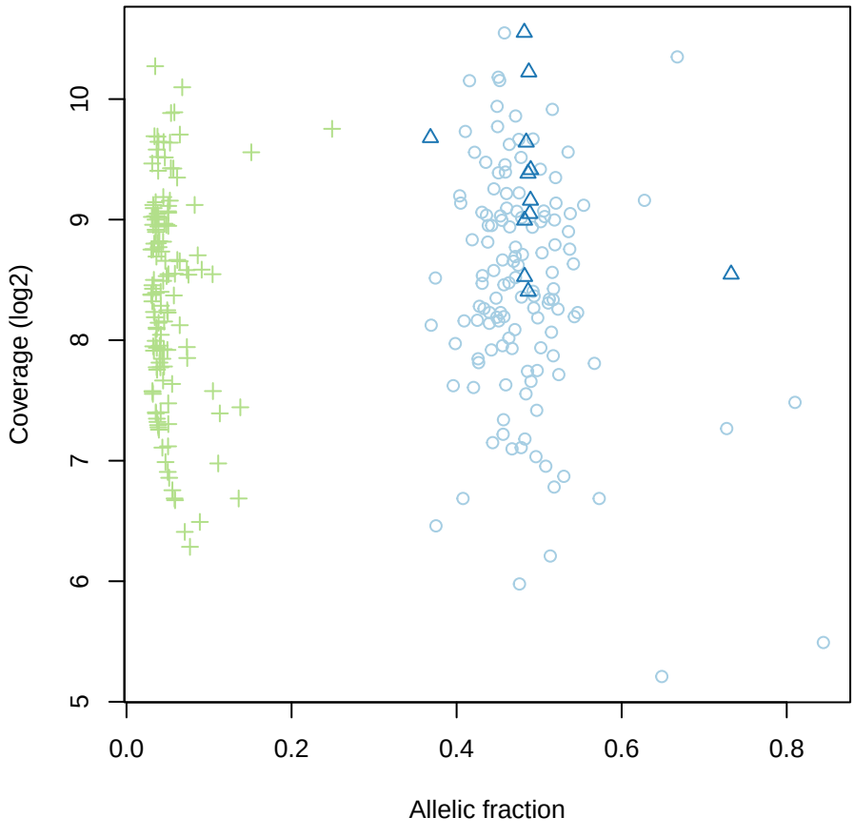

Purity: 0.75 Tumor ploidy: 3.057
2
3
4
5
Fraction Genome
0.0
0.1
0.2
0.3
0.4
0.5
0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
log2 ratio

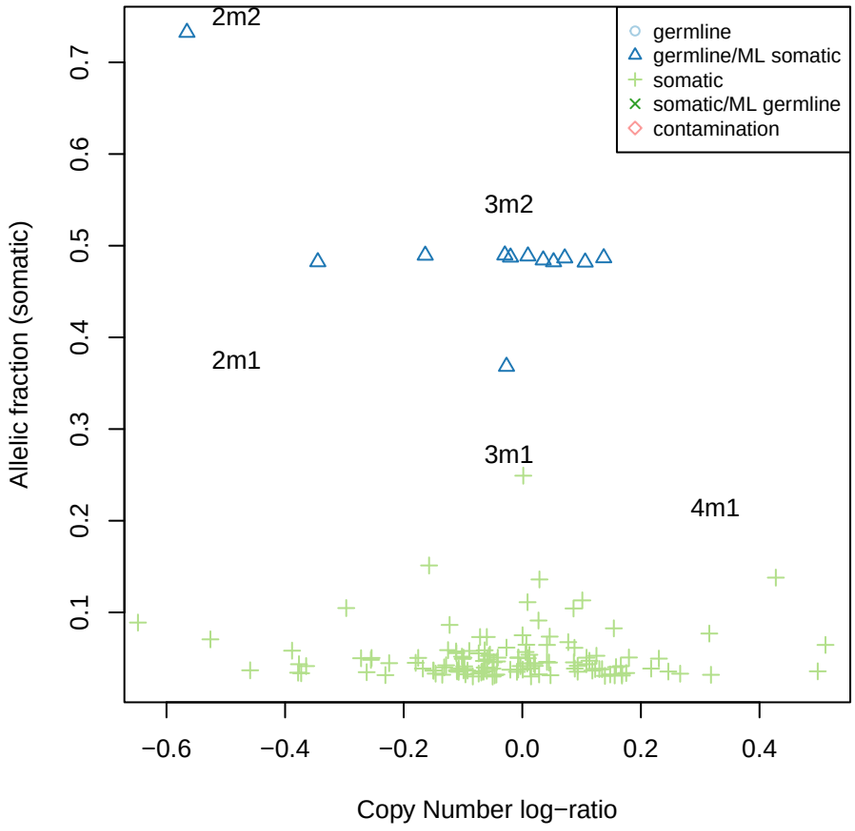

Purity: 0.75 Tumor ploidy: 3.057 SNV log−likelihood: −1203.97 GoF: 26.8% Mean coverage: 434;420
1
2
3
4
5
6
7
8
9
11
12
13
14
15
17
19
B−Allele Frequency
0.4
0.5
0.6
0.7
0.8
0
20
40
60
80
100
120
SNV Index

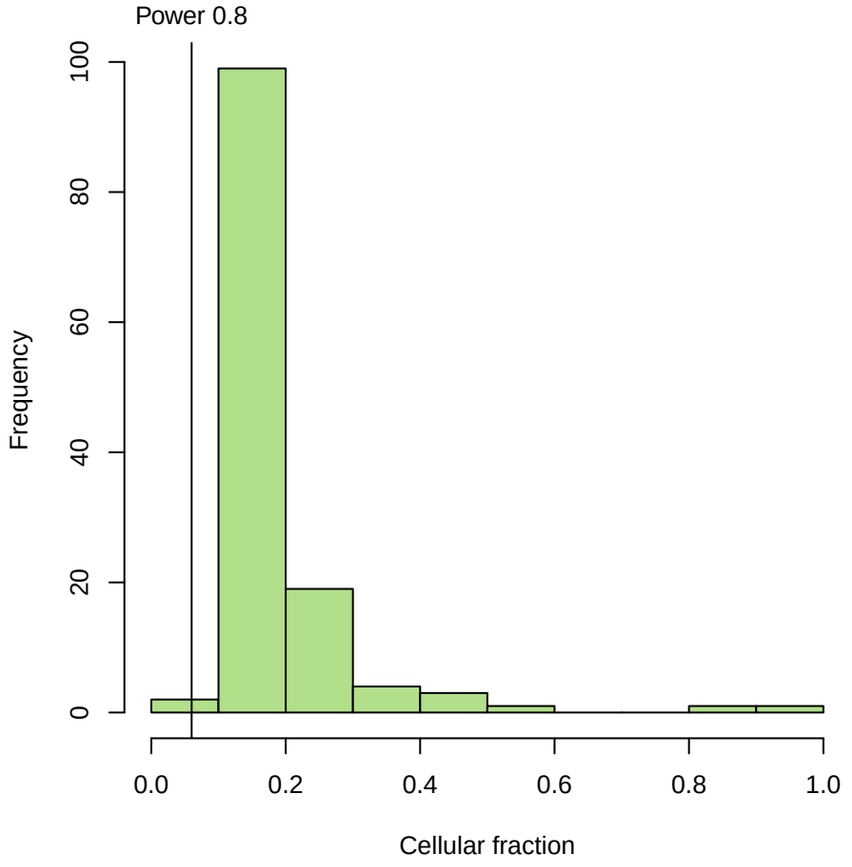

SCNA−fit log−likelihood: −3165.76
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
2
3
4
5
0
20
40
60
80
100
120
SNV Index


Maximum Likelihood Copy Number
0
1
2
3
4
5
0
20
40
60
80
100
120
SNV Index


Allelic fraction (germline)
0.4
0.5
0.6
0.7
0.8
4m3
3m2
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio


Coverage (log2)
5
6
7
8
9
10
0.0
0.2
0.4
0.6
0.8
Allelic fraction


Allelic fraction (somatic)
0.1
0.2
0.3
0.4
0.5
0.6
0.7
2m2
3m2
2m1
3m1
4m1
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


Power 0.8
Frequency
0
20
40
60
80
100
0.0
0.2
0.4
0.6
0.8
1.0
Cellular fraction