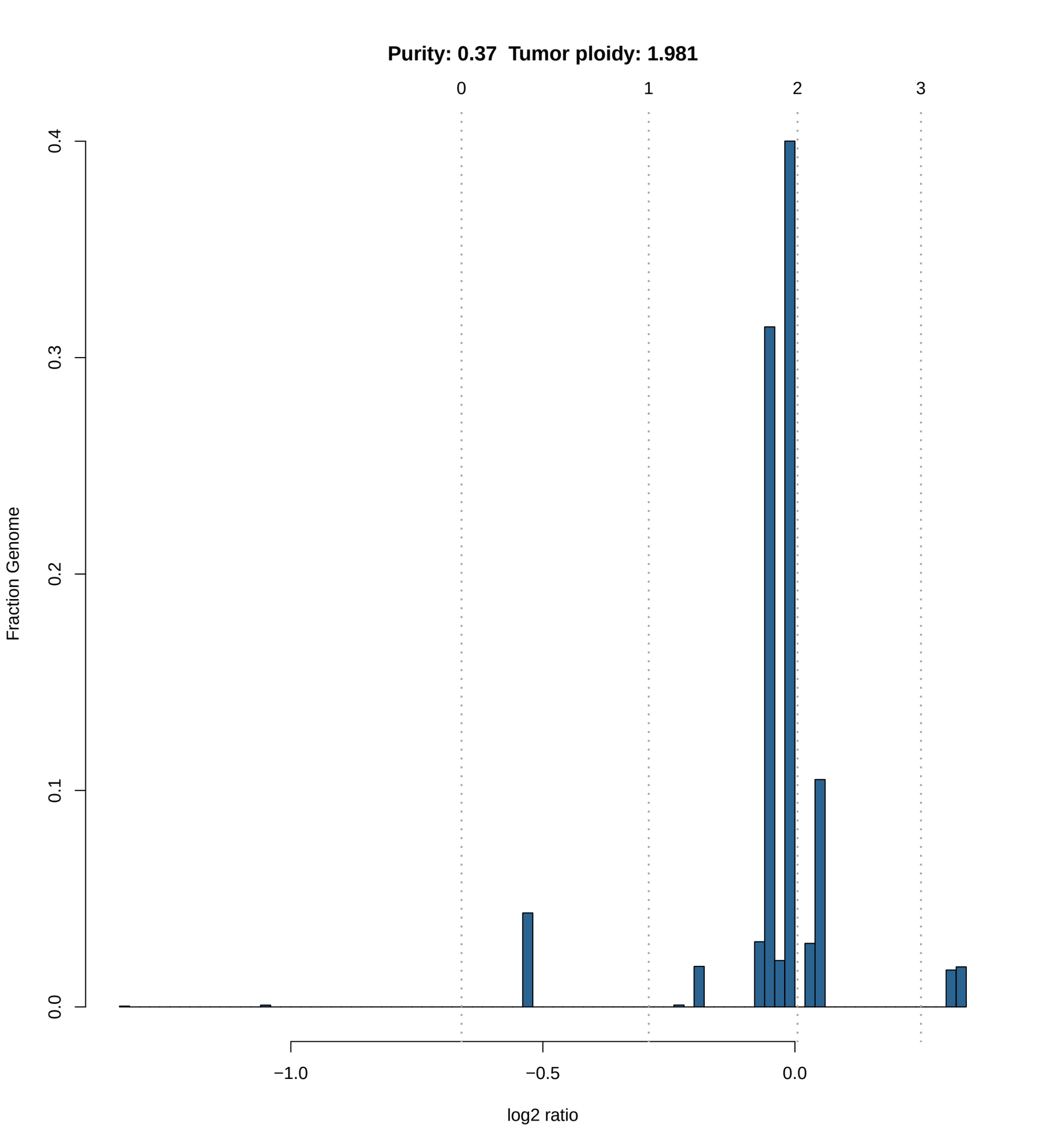
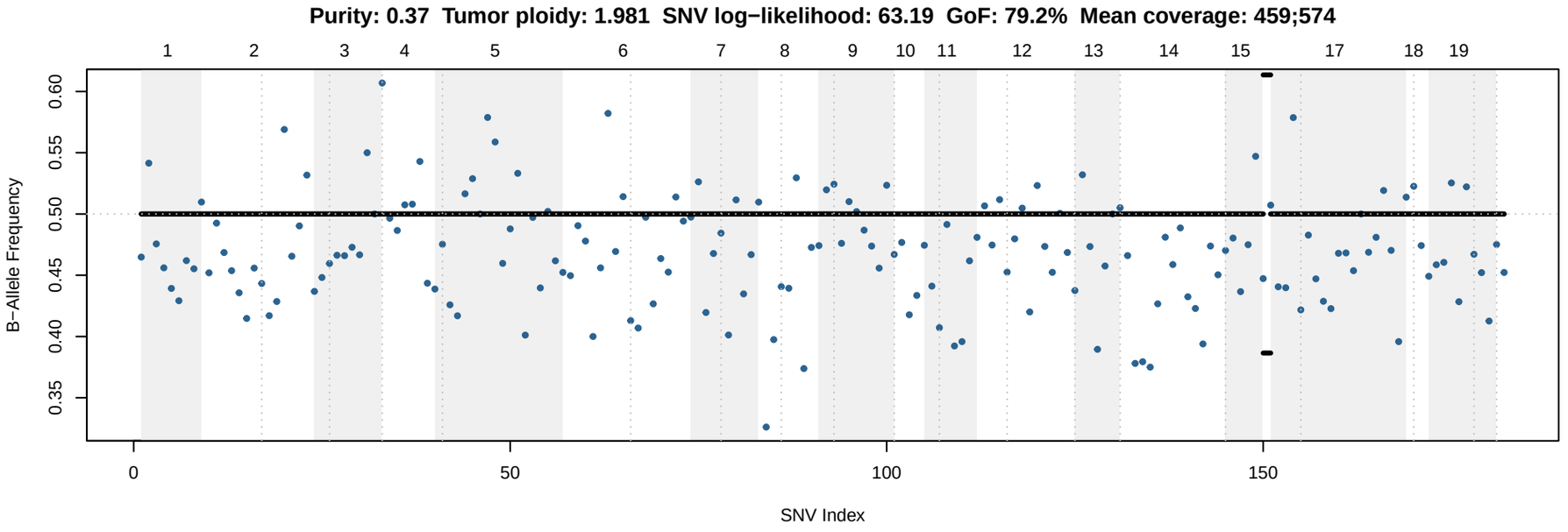
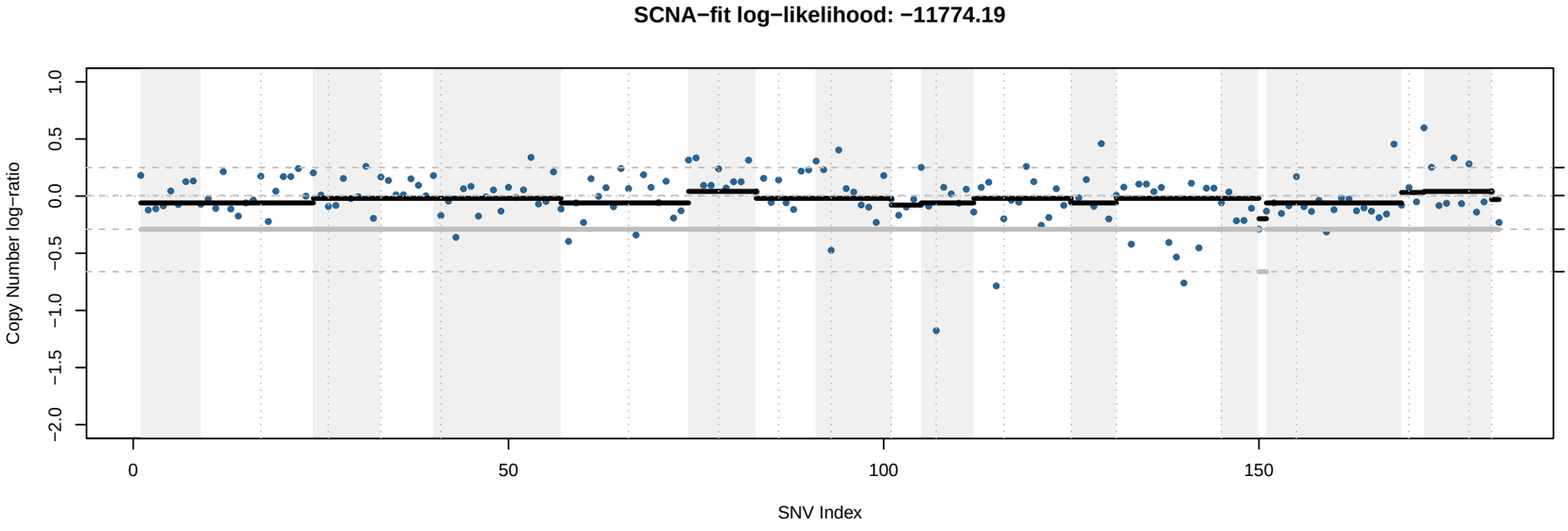
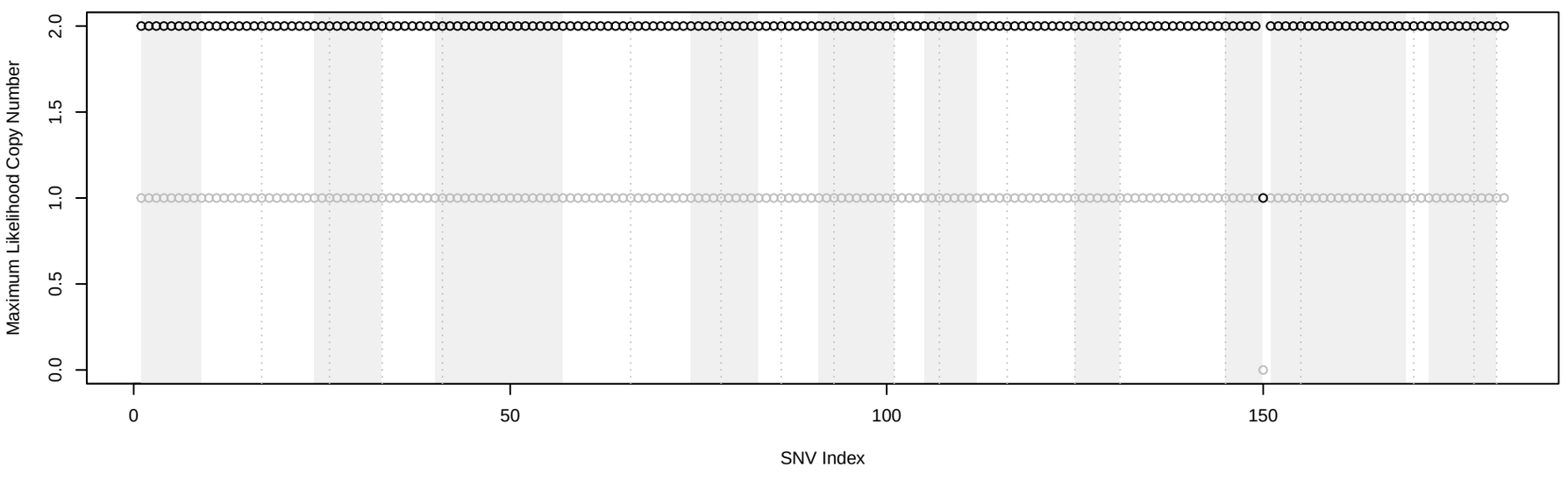
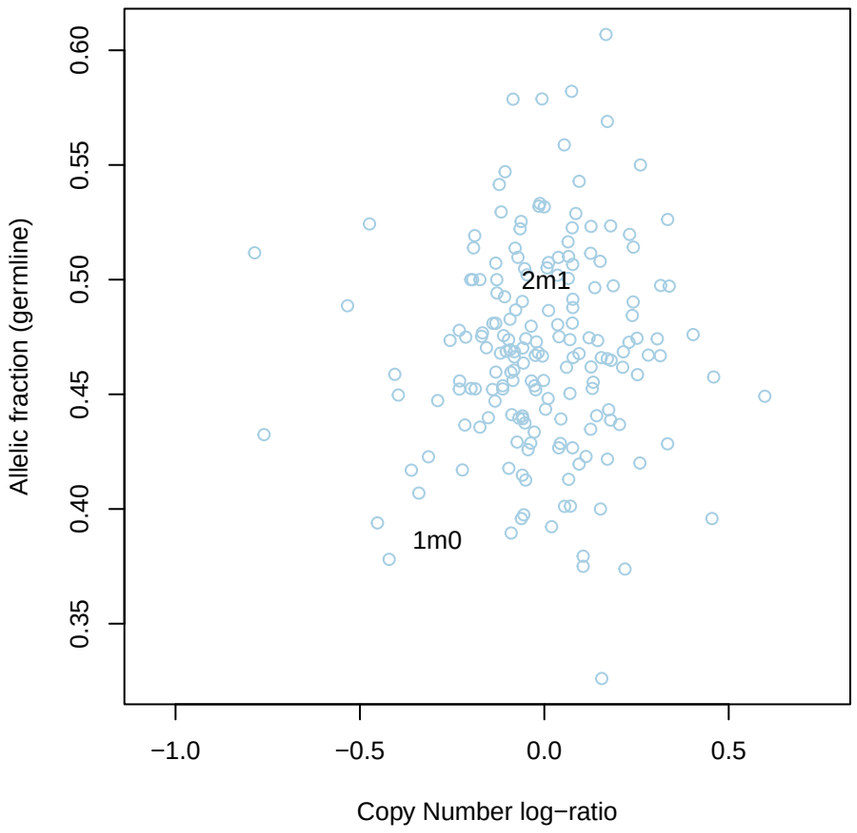
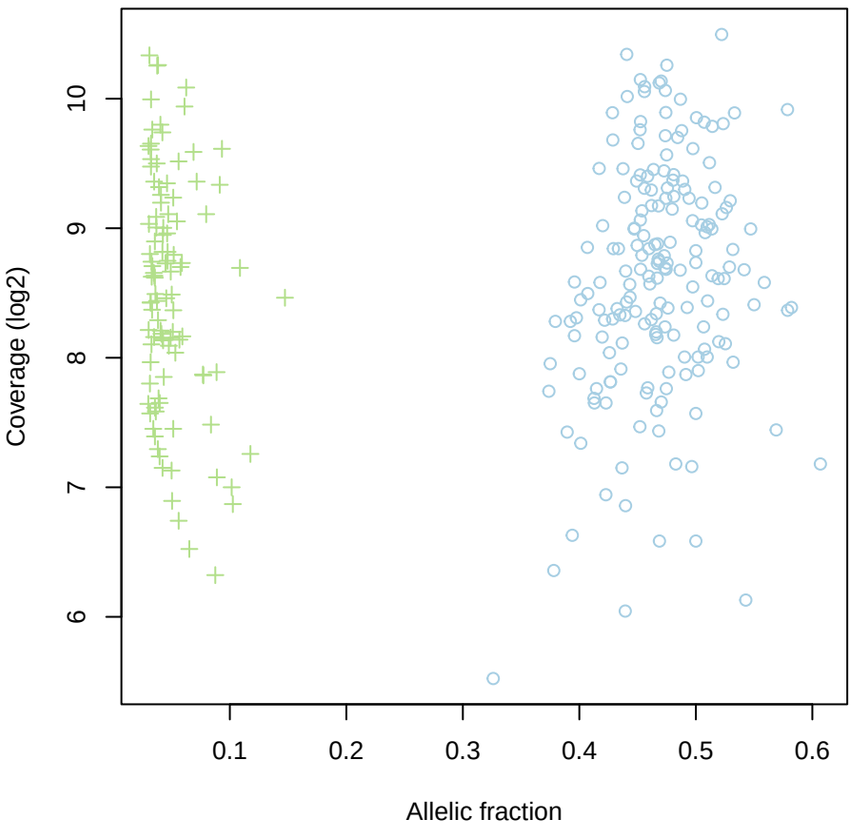

Purity: 0.37 Tumor ploidy: 1.981
0
1
2
3
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
log2 ratio

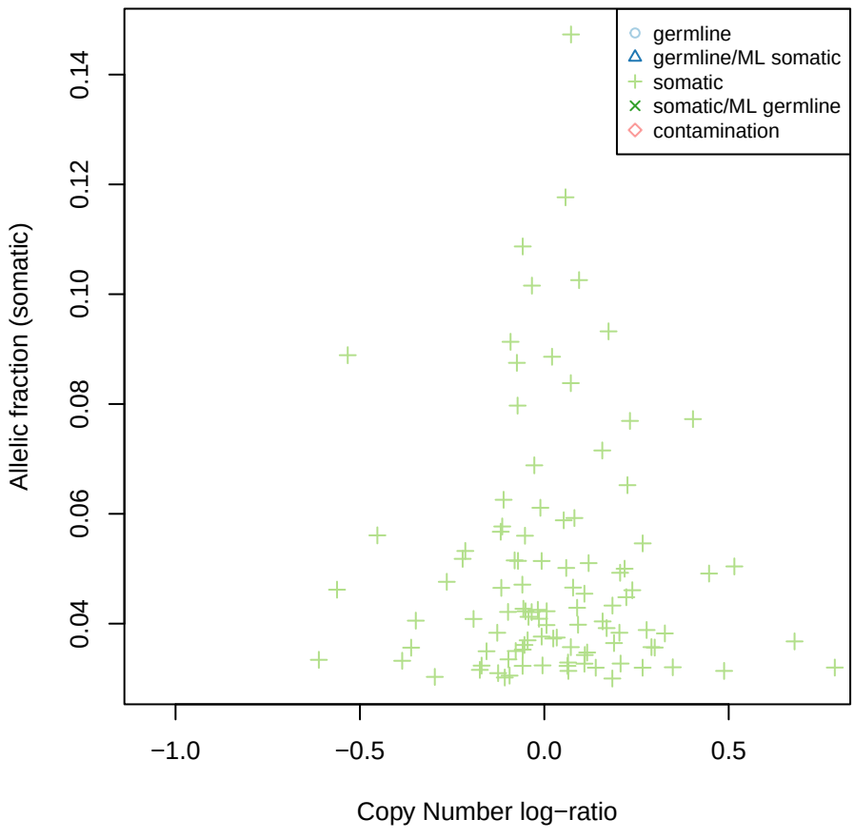

Purity: 0.37 Tumor ploidy: 1.981 SNV log−likelihood: 63.19 GoF: 79.2% Mean coverage: 459;574
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
17
18
19
B−Allele Frequency
0.35
0.40
0.45
0.50
0.55
0.60
0
50
100
150
SNV Index

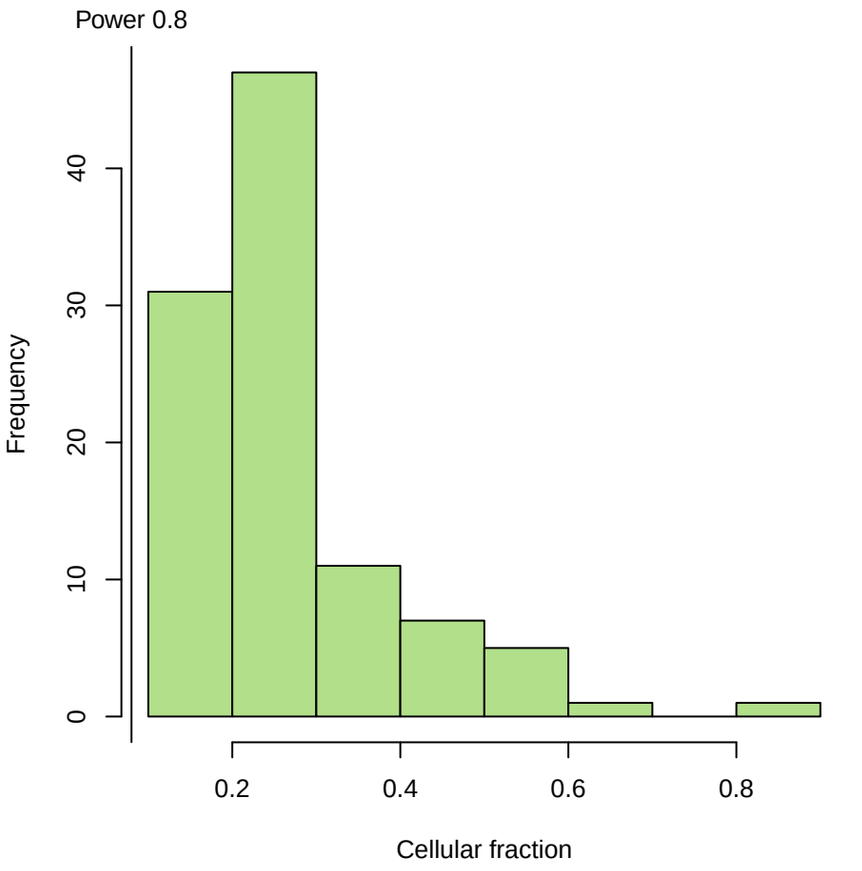

SCNA−fit log−likelihood: −11774.19
Copy Number log−ratio
−2.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
0
1
2
3
0
50
100
150
SNV Index

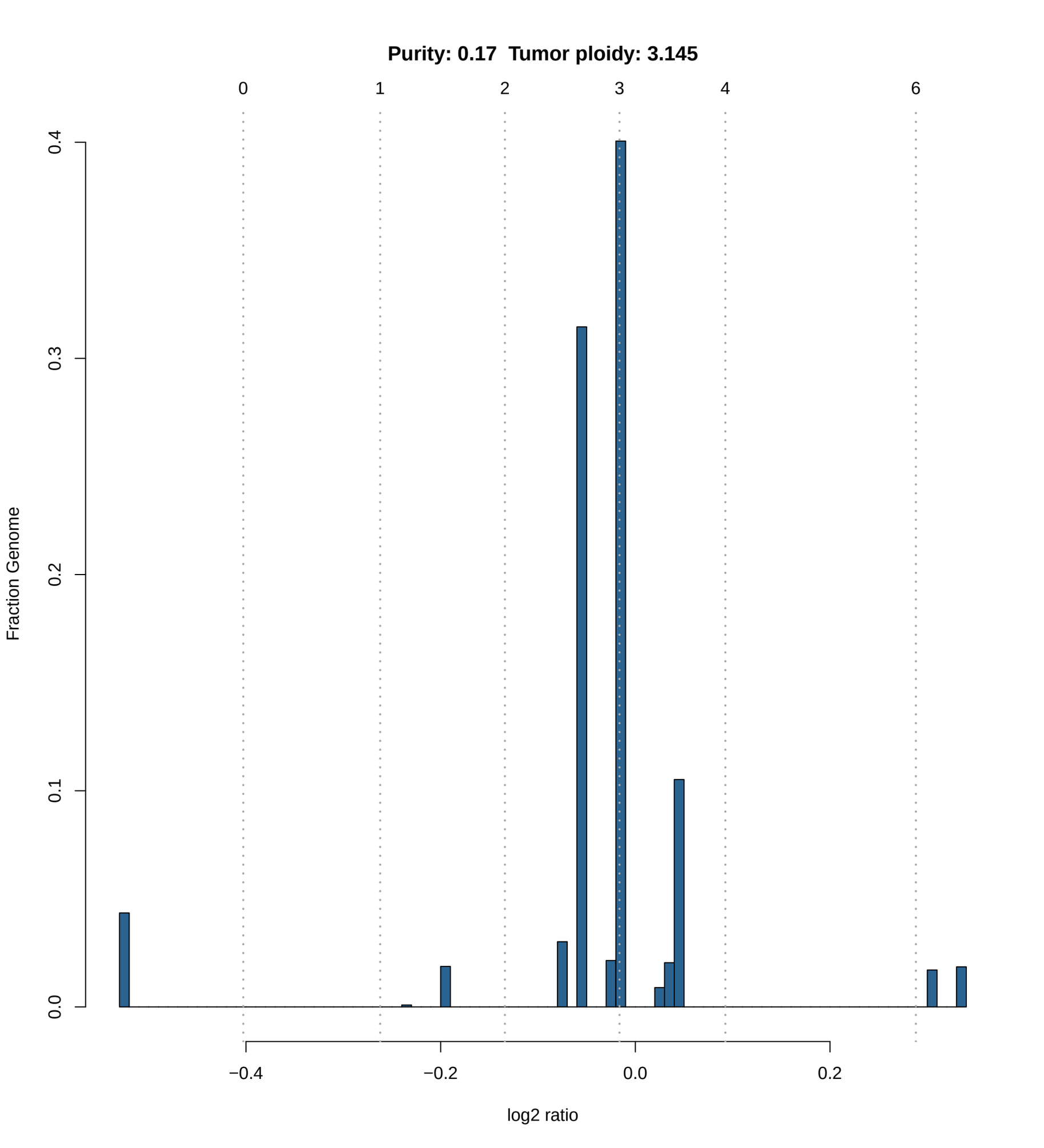

Maximum Likelihood Copy Number
0.0
0.5
1.0
1.5
2.0
0
50
100
150
SNV Index

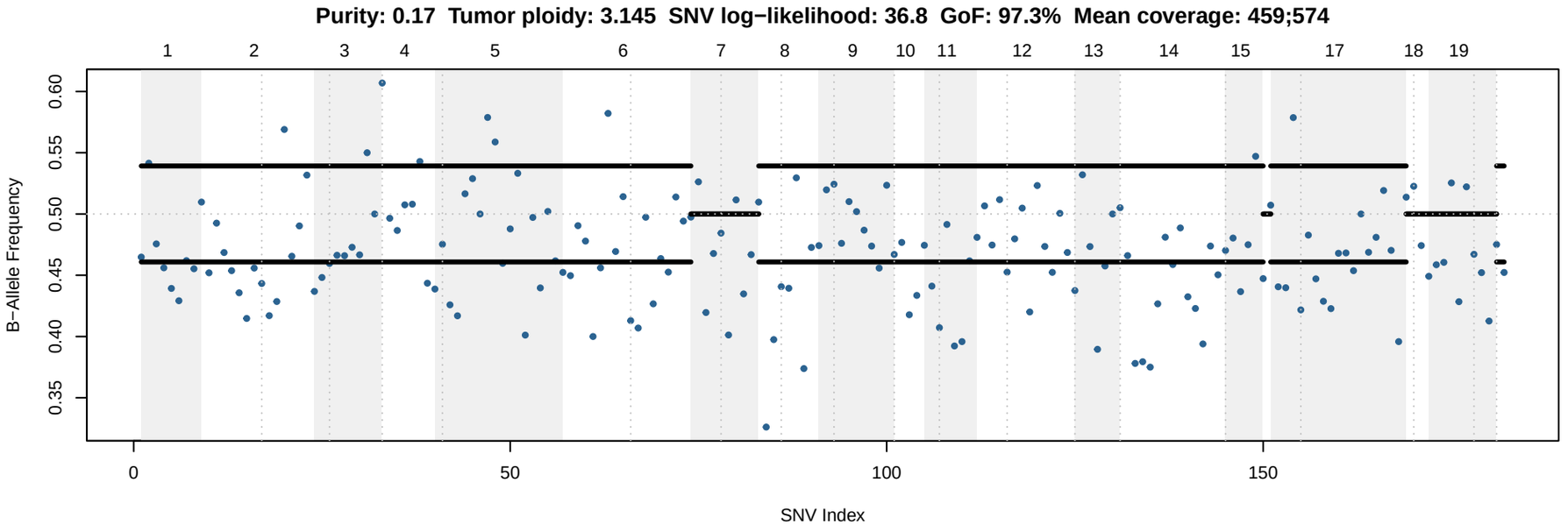

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
2m1
1m0
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

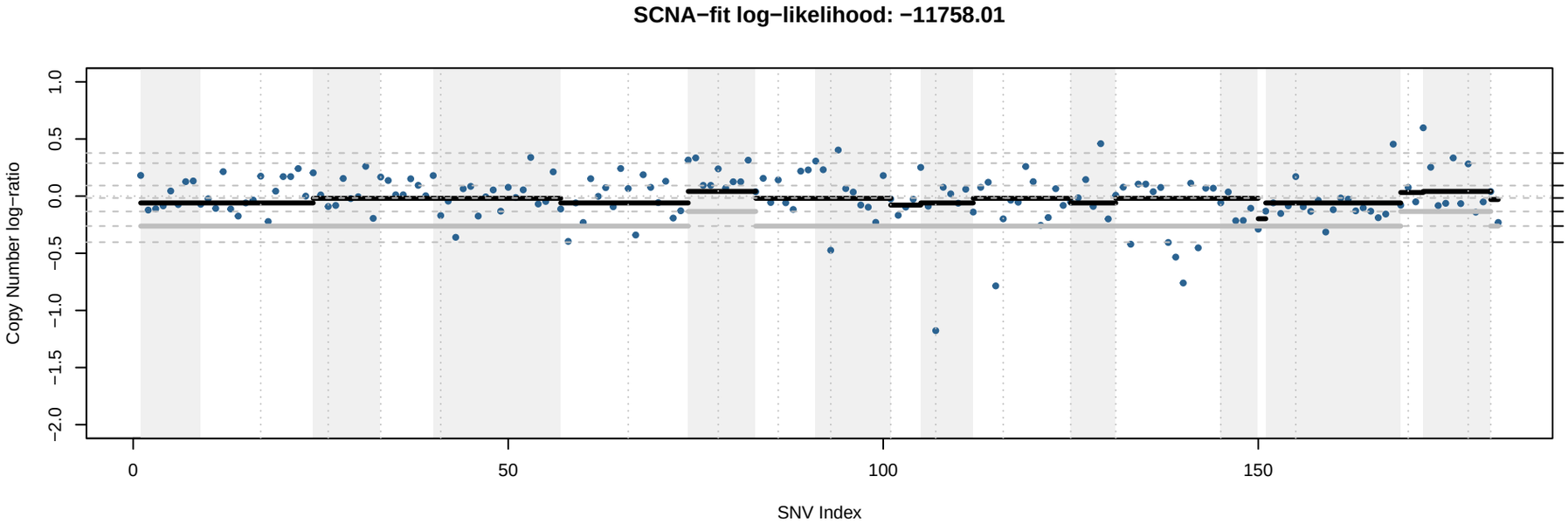

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

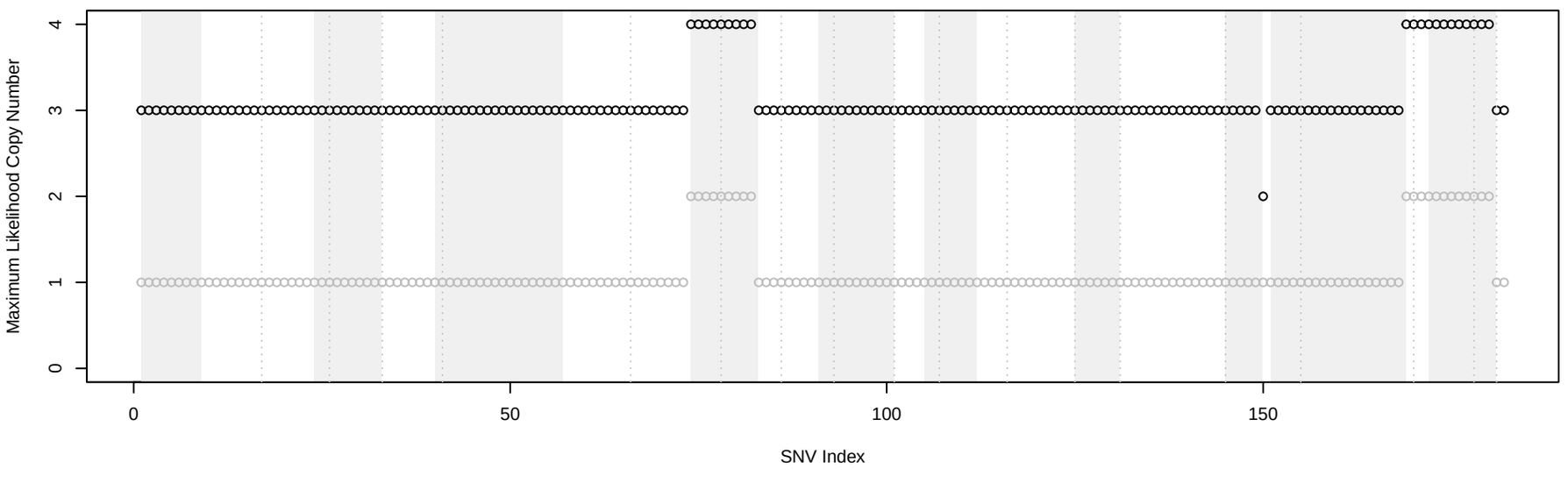

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

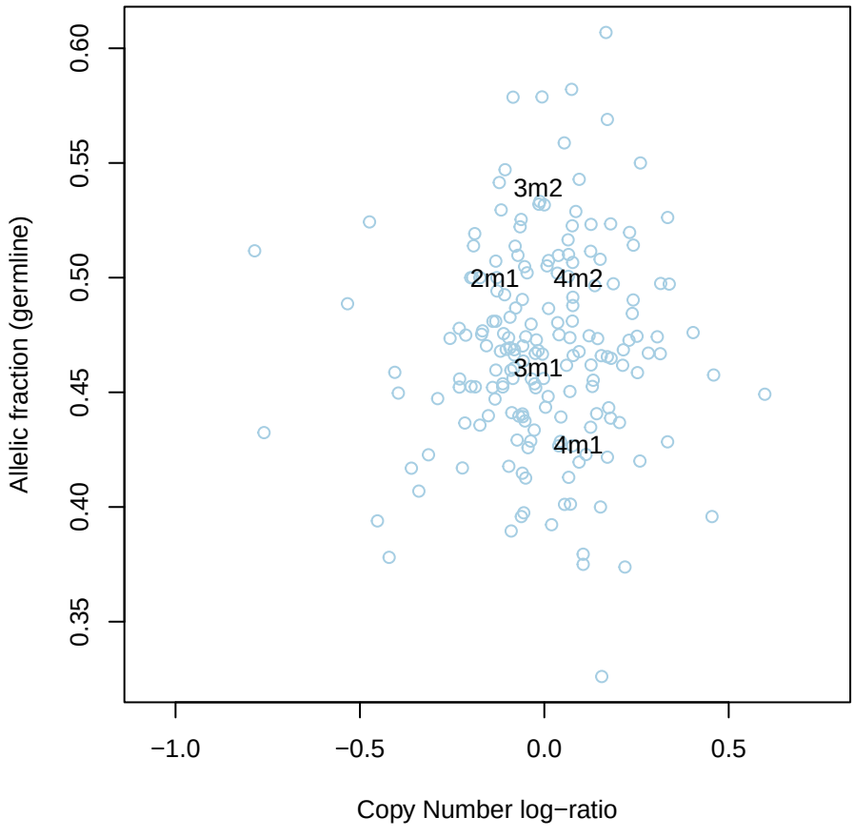

Power 0.8
Frequency
0
10
20
30
40
0.2
0.4
0.6
0.8
Cellular fraction

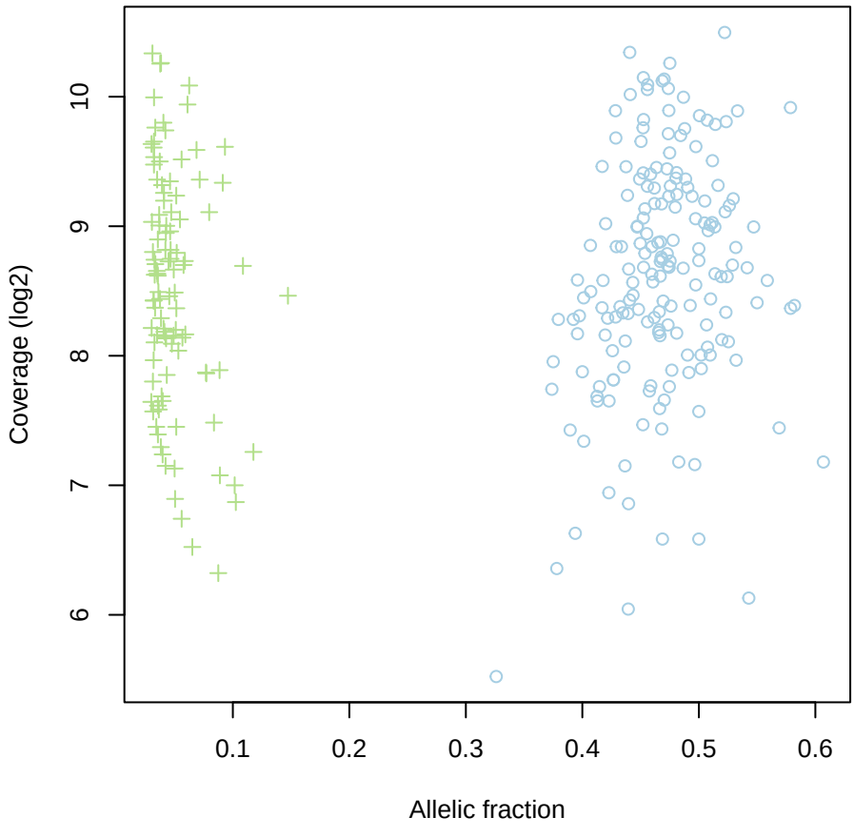

Purity: 0.17 Tumor ploidy: 3.145
0
1
2
3
4
6
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.4
−0.2
0.0
0.2
log2 ratio

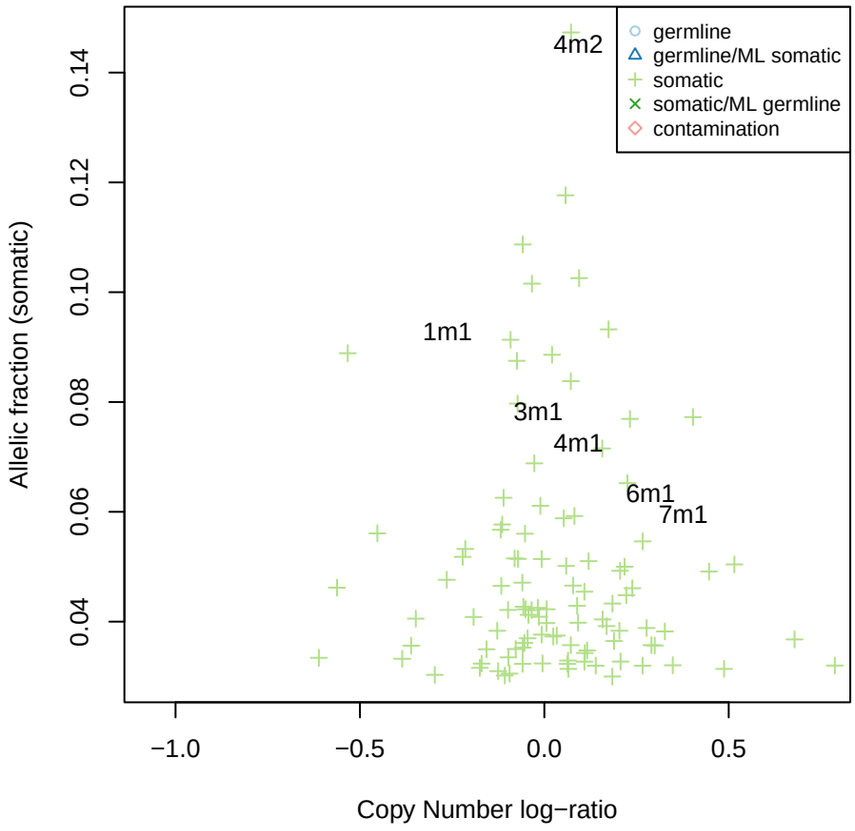

Purity: 0.17 Tumor ploidy: 3.145 SNV log−likelihood: 36.8 GoF: 97.3% Mean coverage: 459;574
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

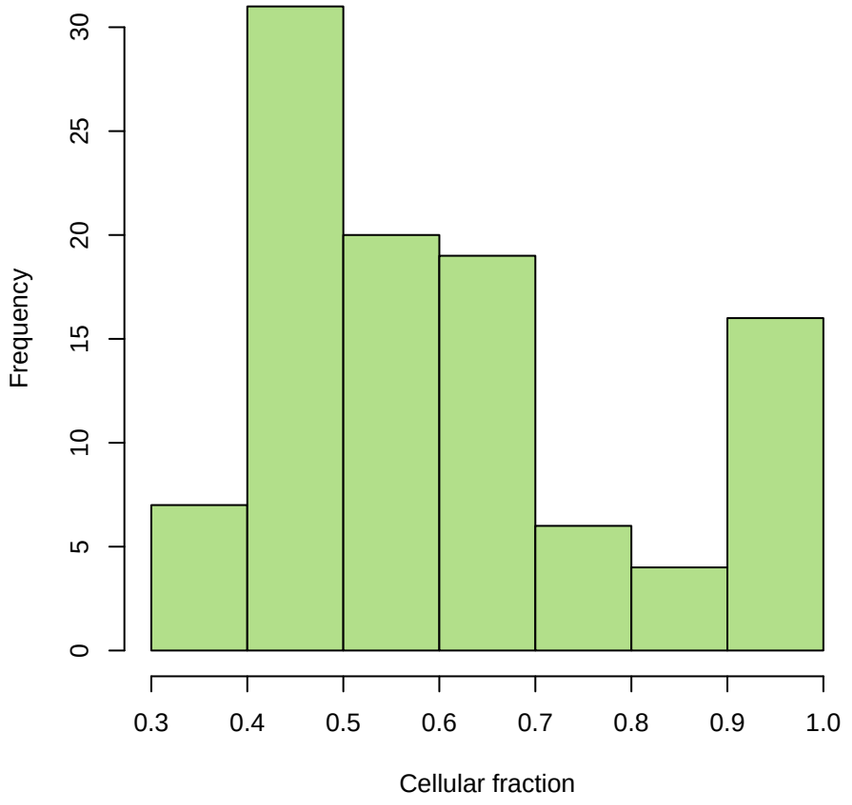

SCNA−fit log−likelihood: −11758.01
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 2 4 7
0 50 100 150
SNV Index

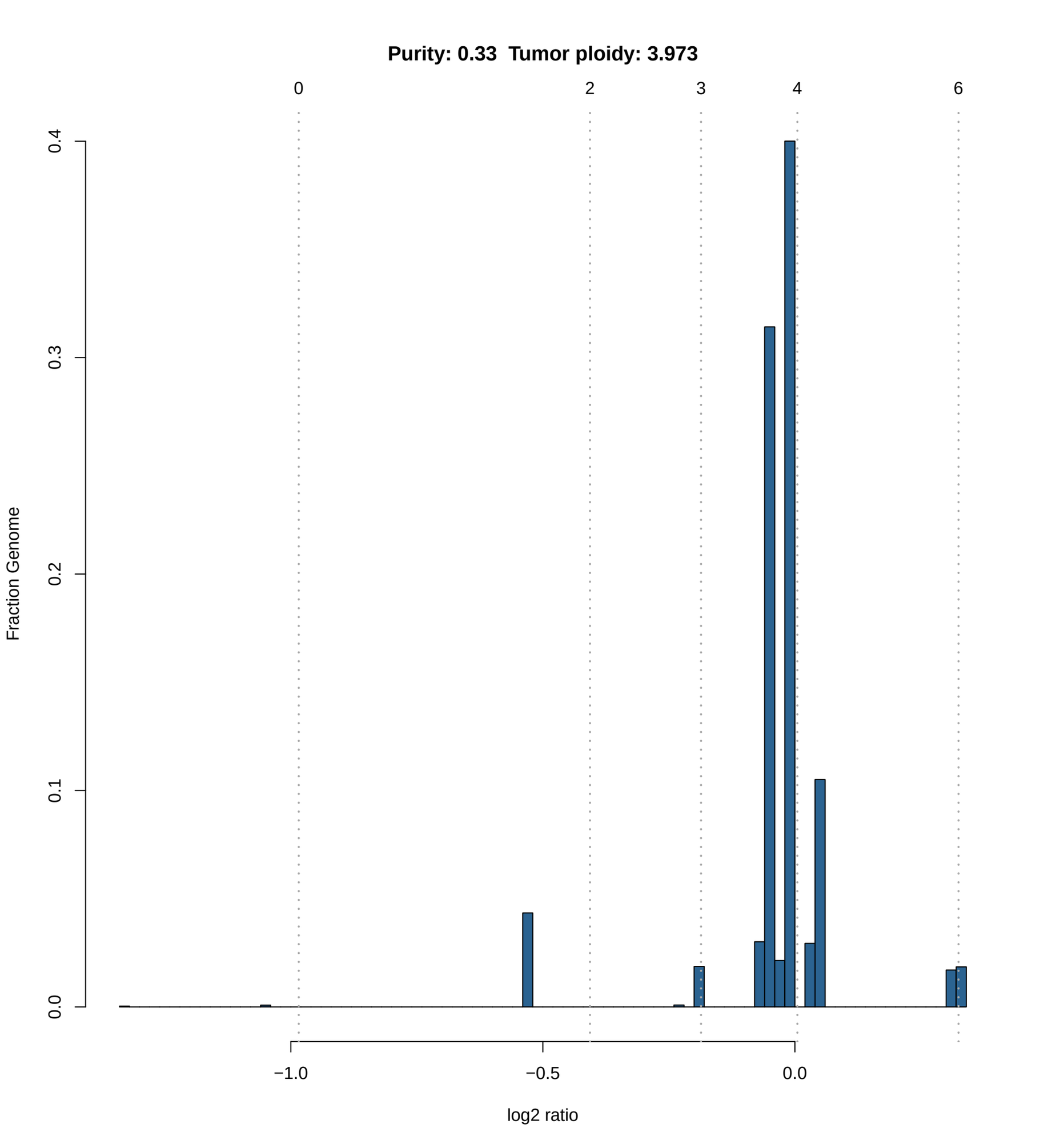

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

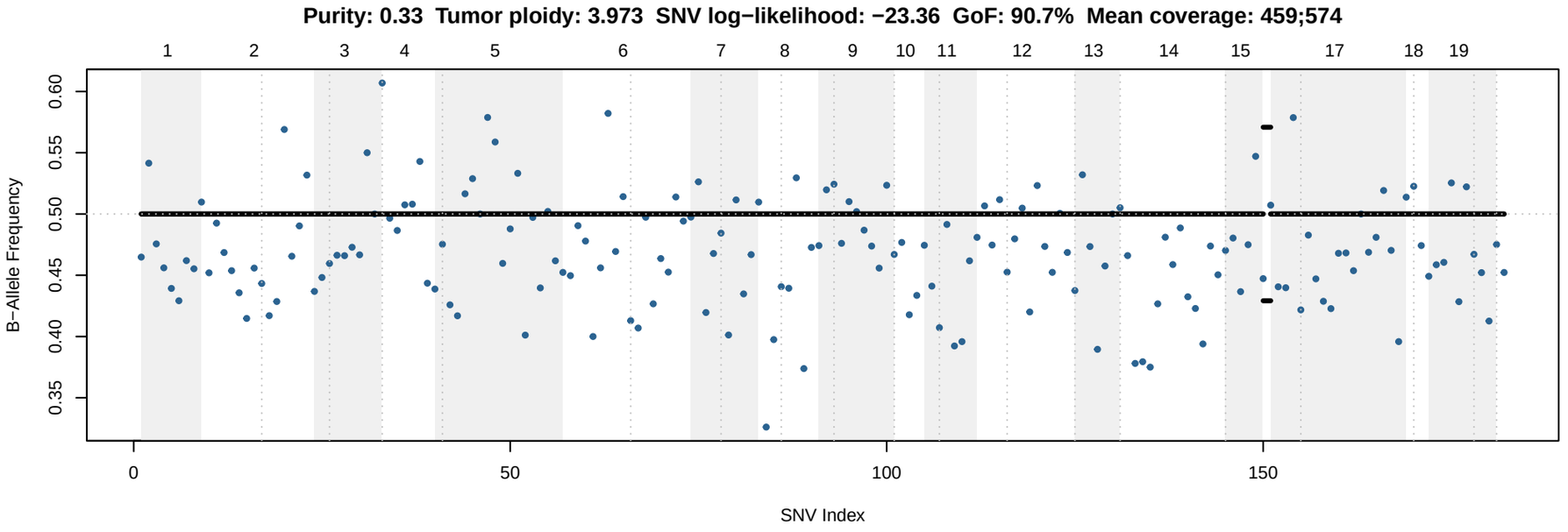

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
3m2
2m1
4m2
3m1
4m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

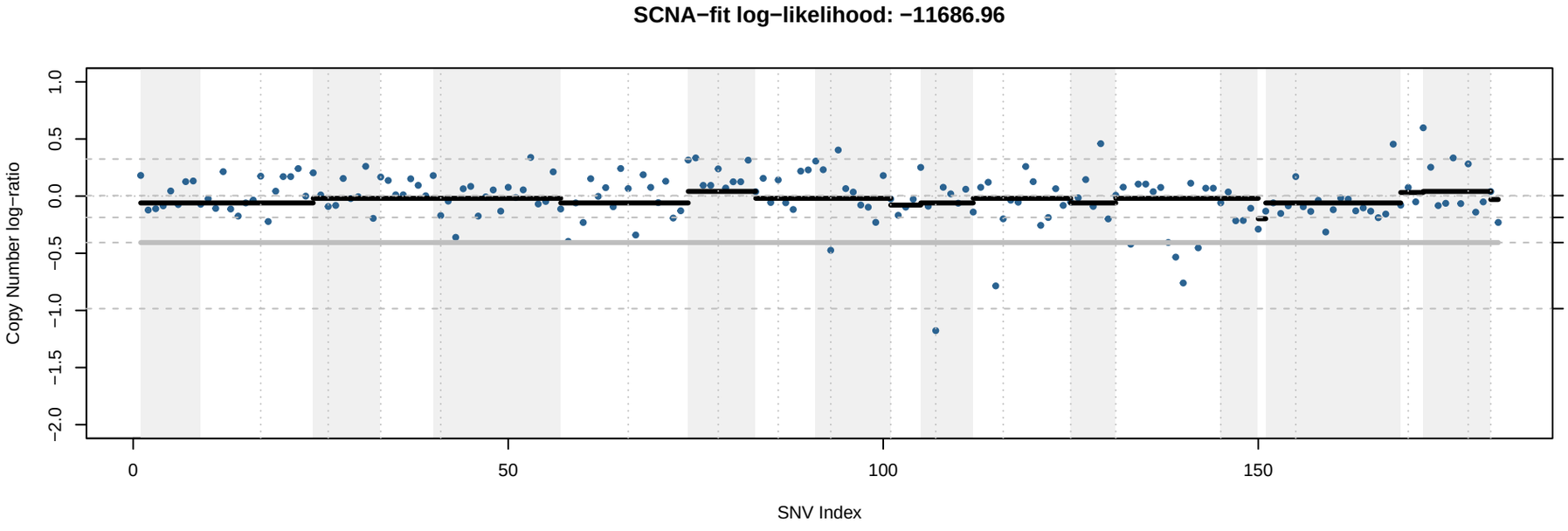

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

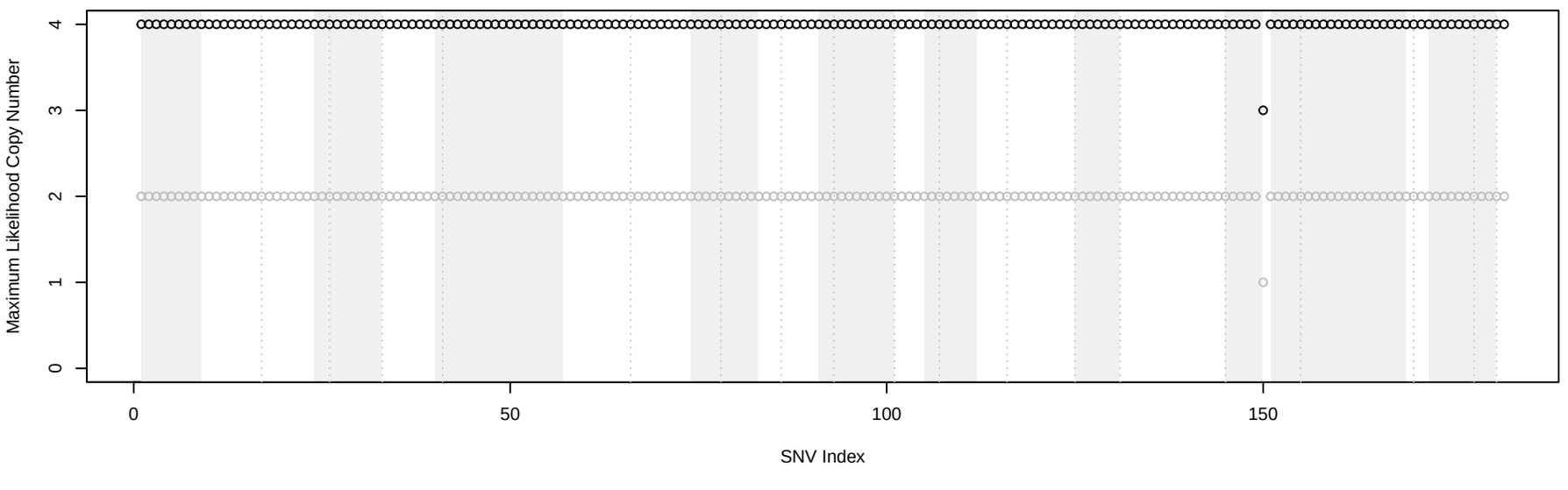

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m2
1m1
3m1
4m1
6m1
7m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

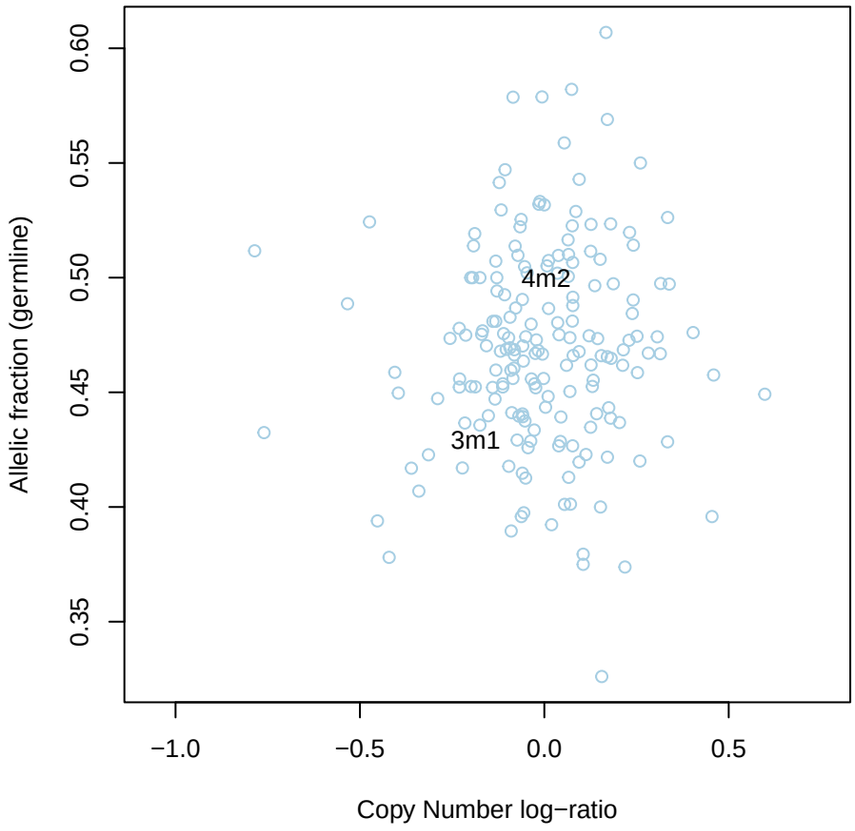

Frequency
0
5
10
15
20
25
30
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

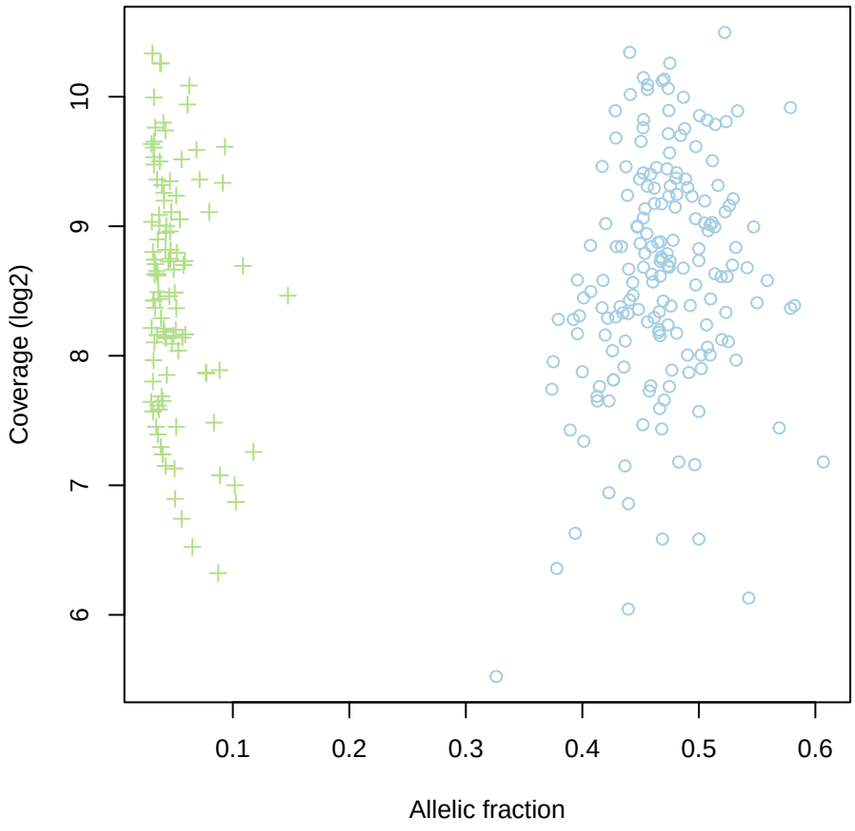

Purity: 0.33 Tumor ploidy: 3.973
0
2
3
4
6
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
log2 ratio

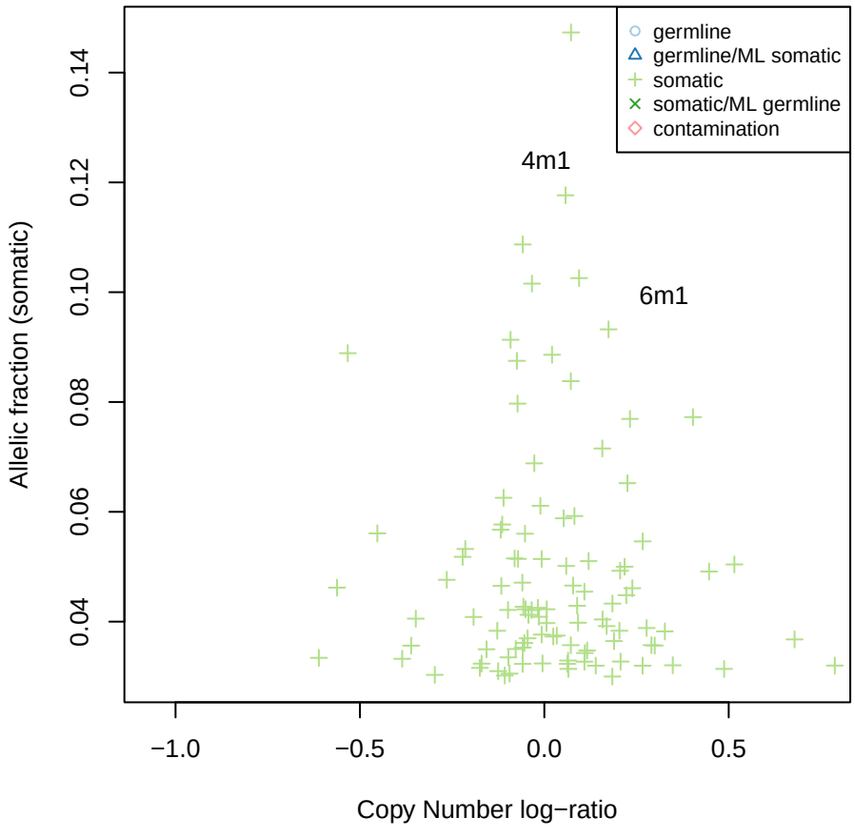

Purity: 0.33 Tumor ploidy: 3.973 SNV log−likelihood: −23.36 GoF: 90.7% Mean coverage: 459;574
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

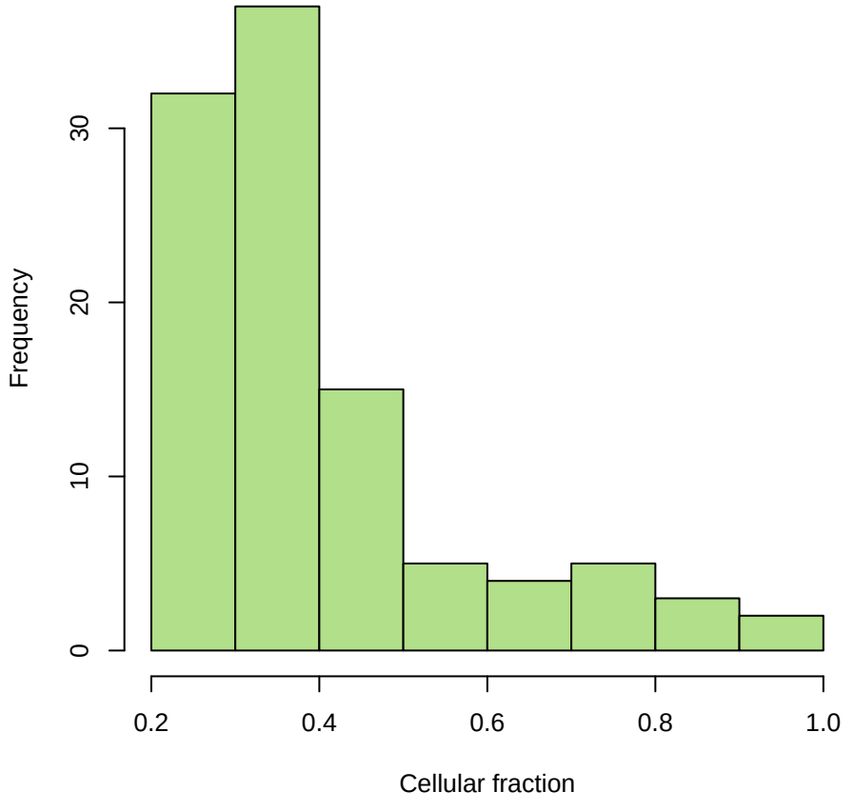

SCNA−fit log−likelihood: −11686.96
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 2 3 6
0 50 100 150
SNV Index

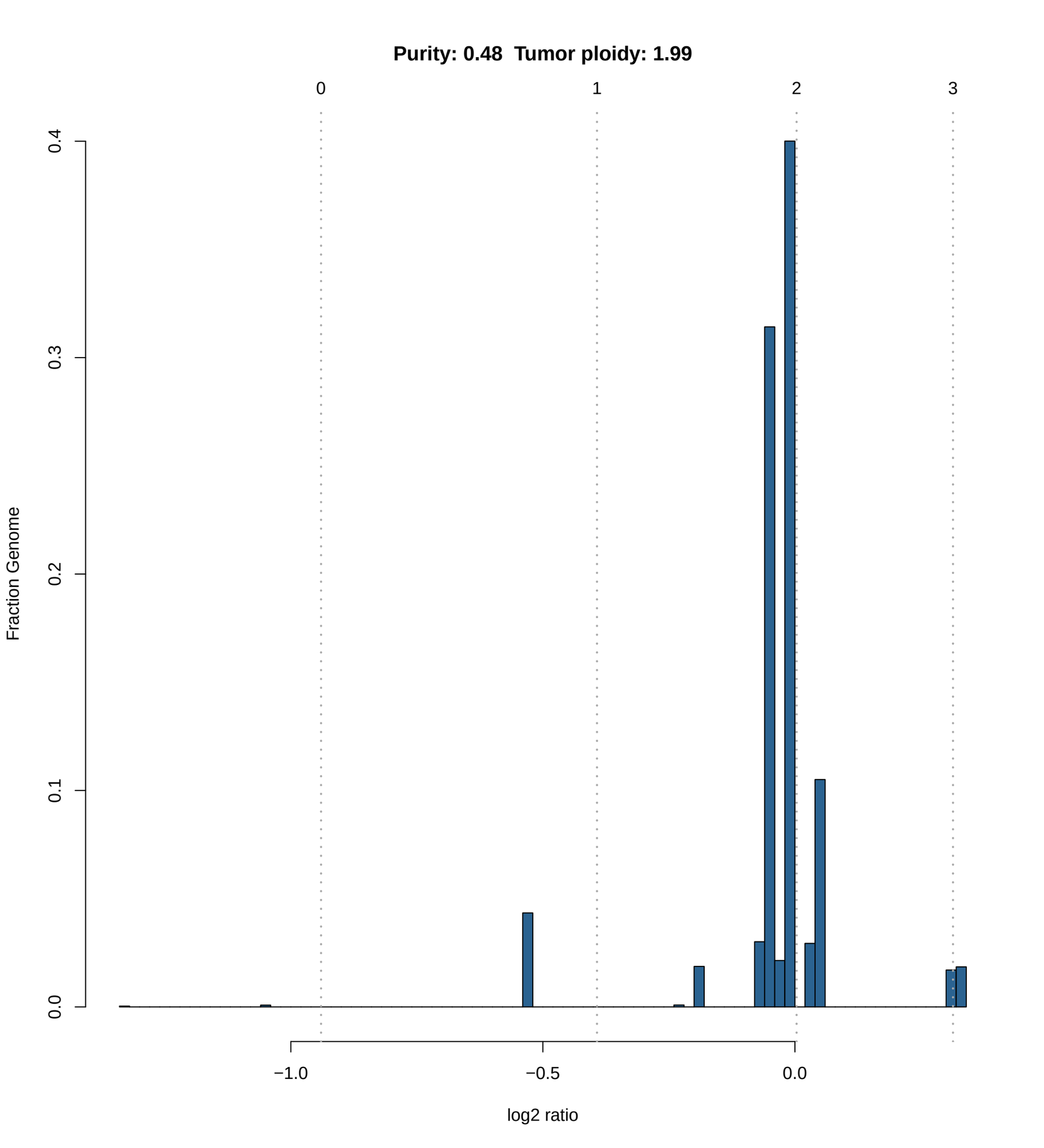

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

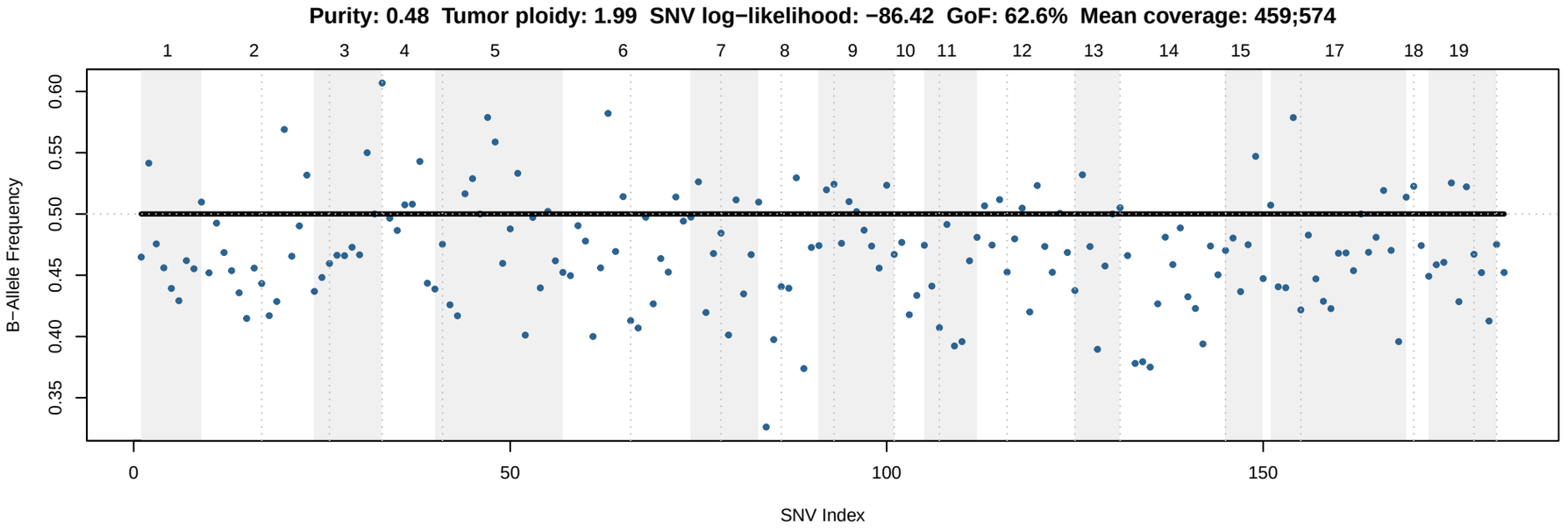

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
4m2
3m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

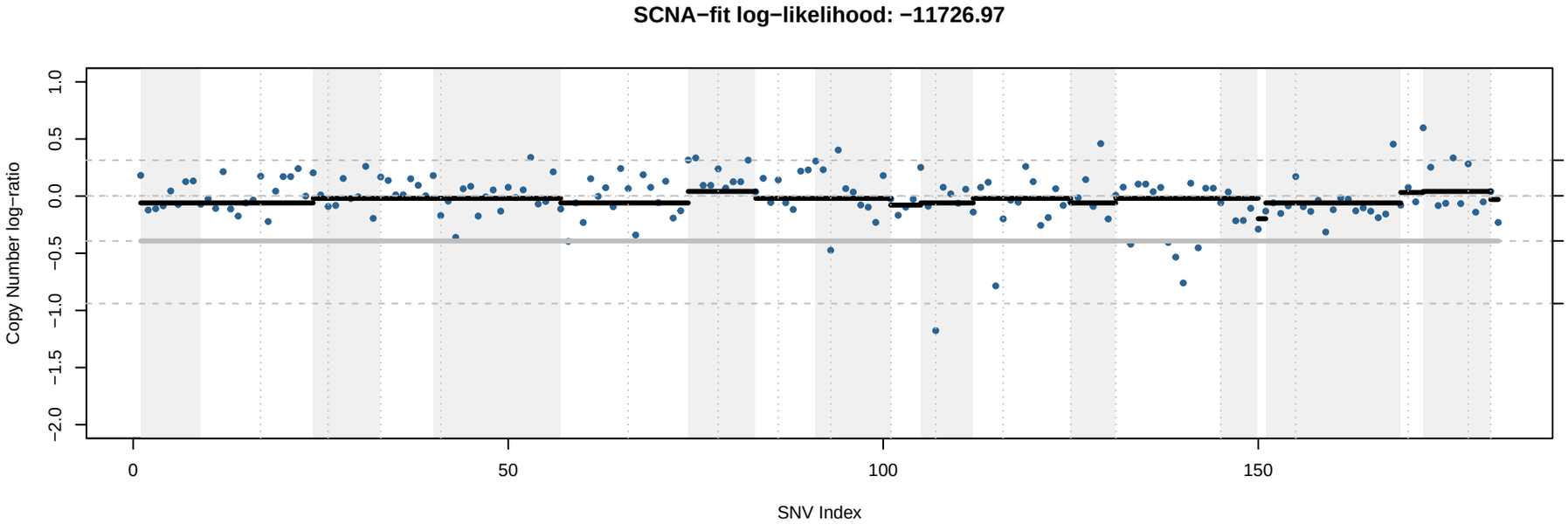

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

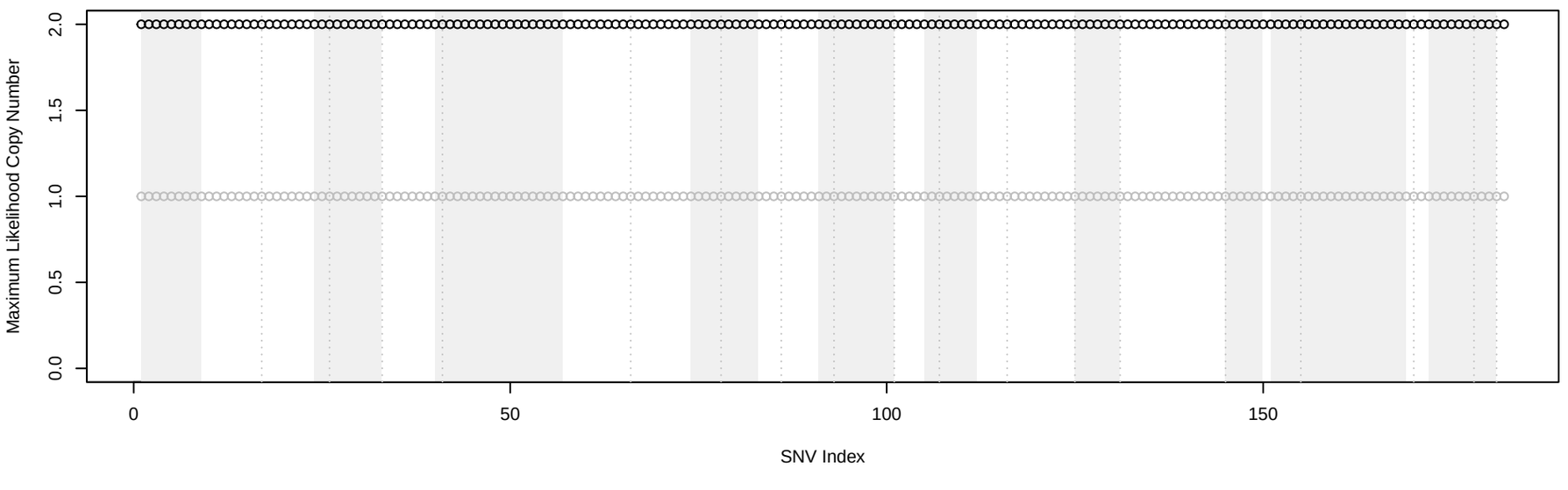

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
4m1
6m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

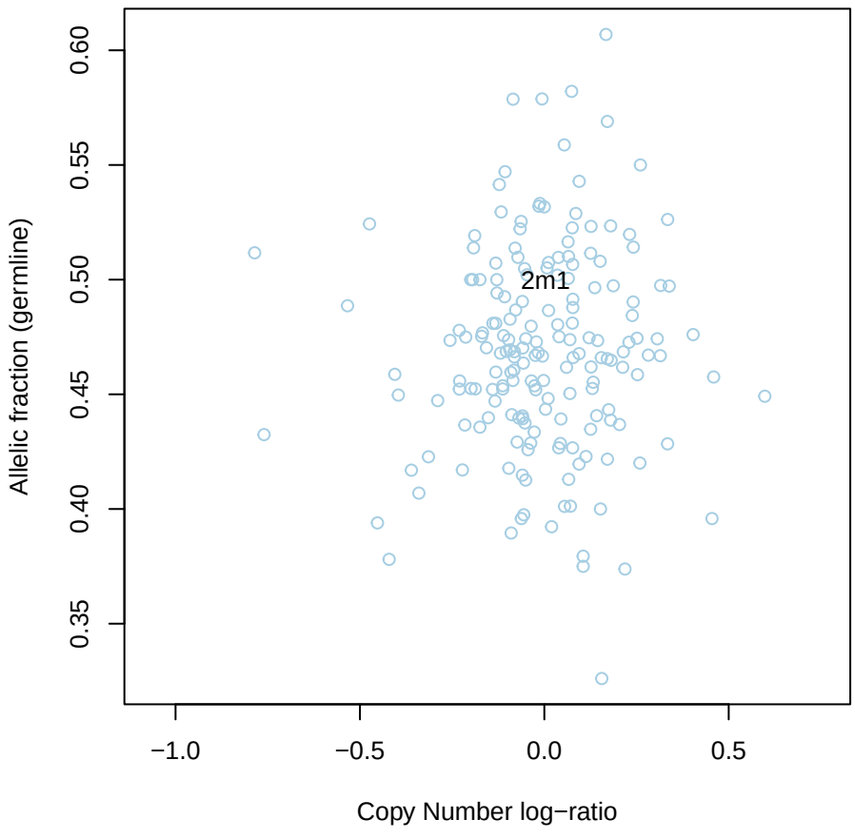

Frequency
0
10
20
30
0.2
0.4
0.6
0.8
1.0
Cellular fraction

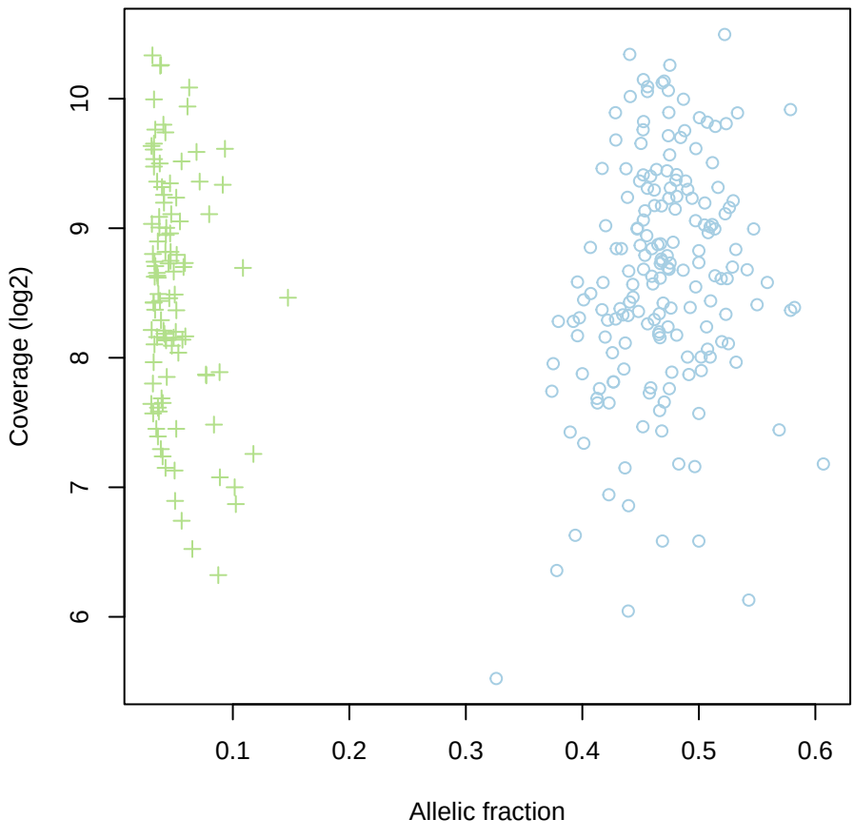

Purity: 0.48 Tumor ploidy: 1.99
0
1
2
3
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
log2 ratio

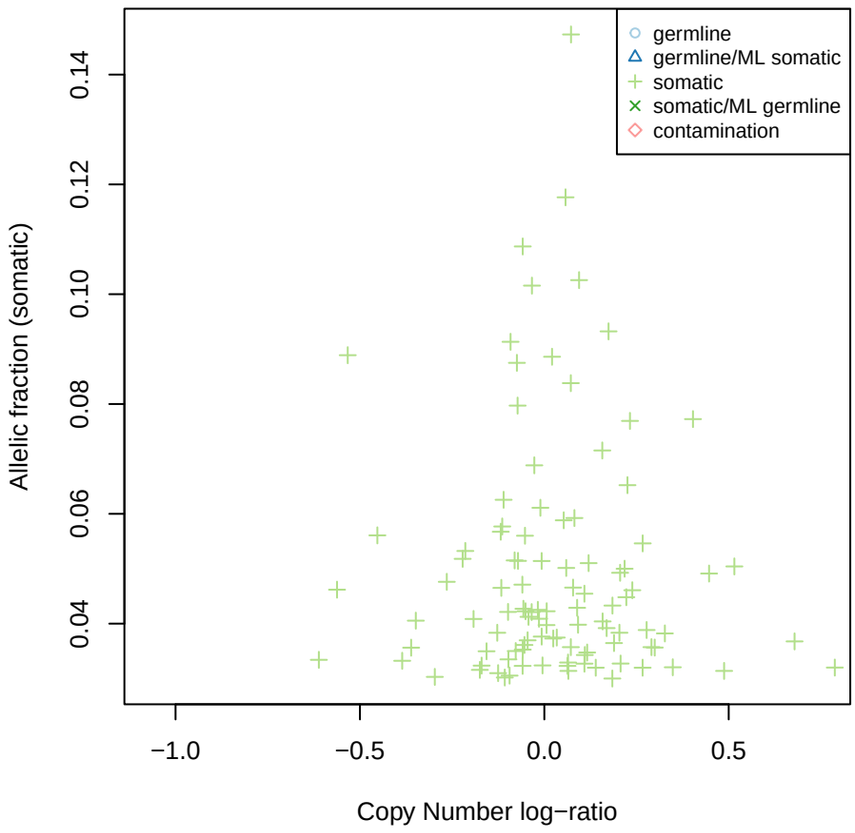

Purity: 0.48 Tumor ploidy: 1.99 SNV log−likelihood: −86.42 GoF: 62.6% Mean coverage: 459;574
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
17
18
19
B−Allele Frequency
0.35
0.40
0.45
0.50
0.55
0.60
0
50
100
150
SNV Index

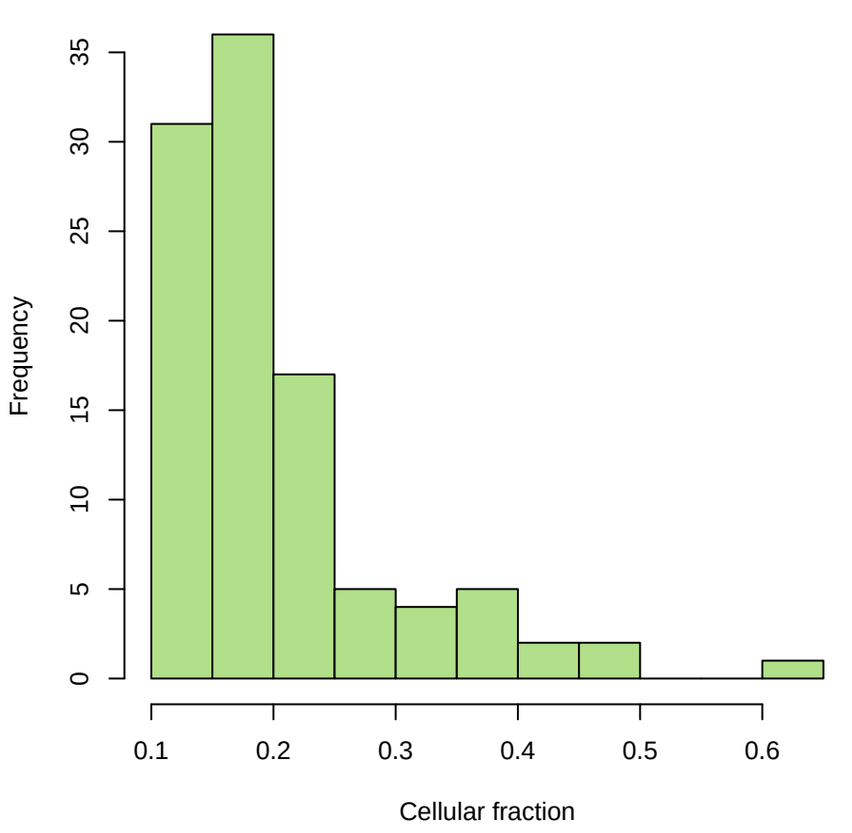

SCNA−fit log−likelihood: −11726.97
Copy Number log−ratio
−2.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
0
1
2
3
0
50
100
150
SNV Index

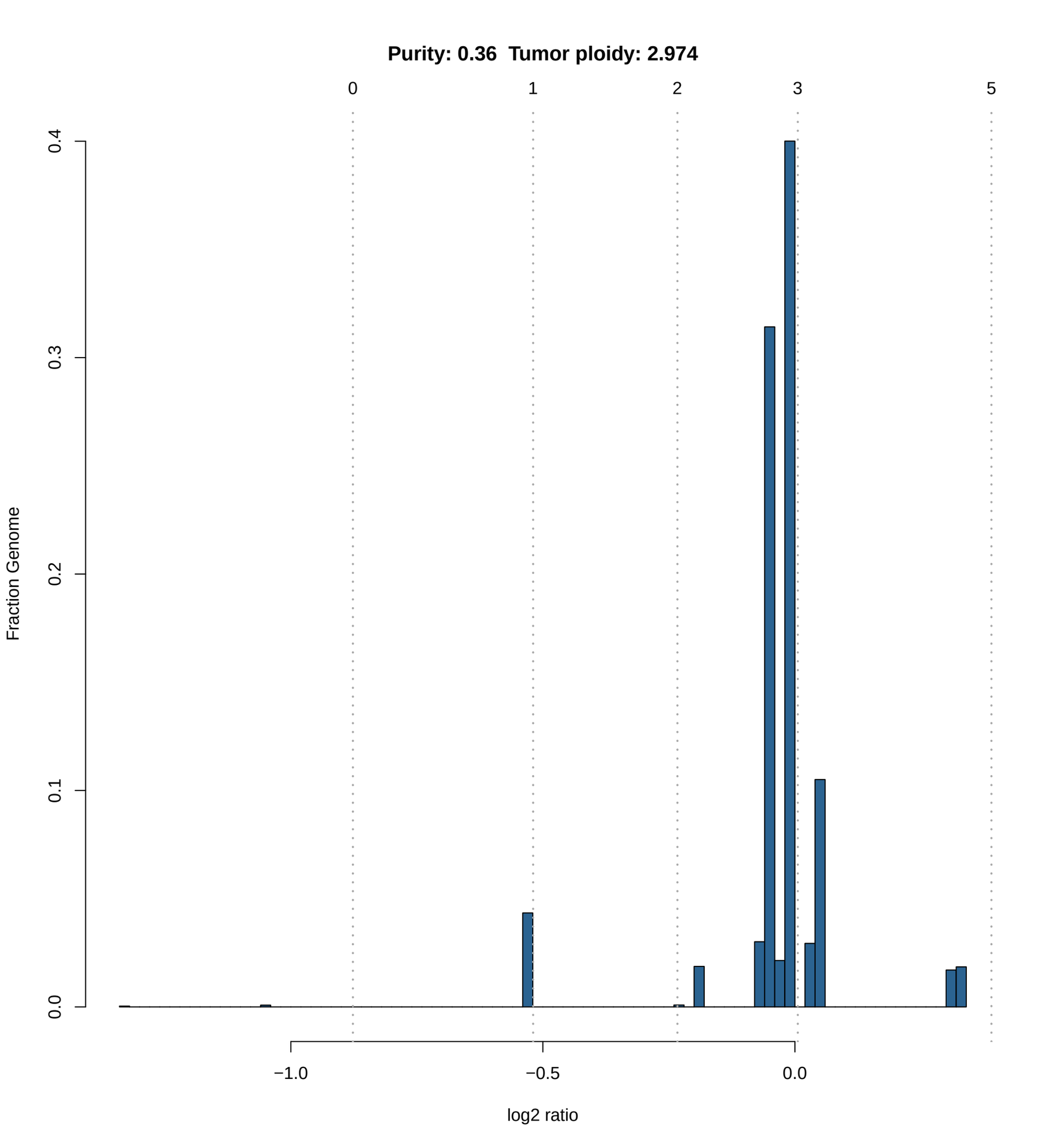

Maximum Likelihood Copy Number
0.0
0.5
1.0
1.5
2.0
0
50
100
150
SNV Index

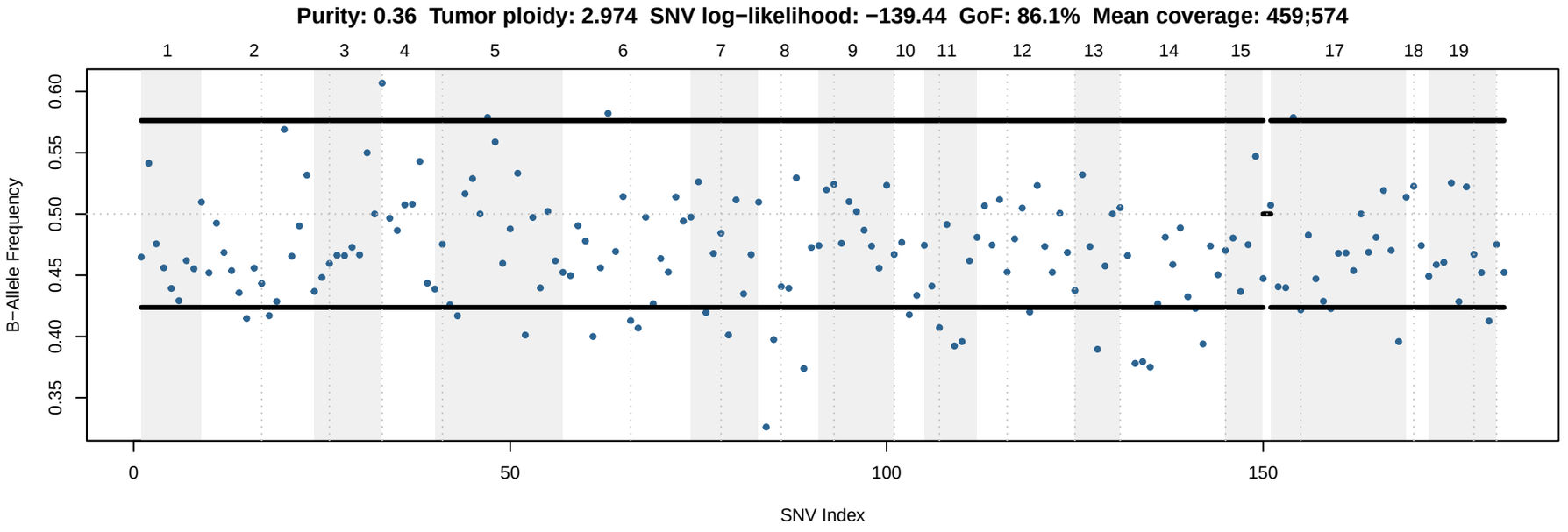

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
2m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

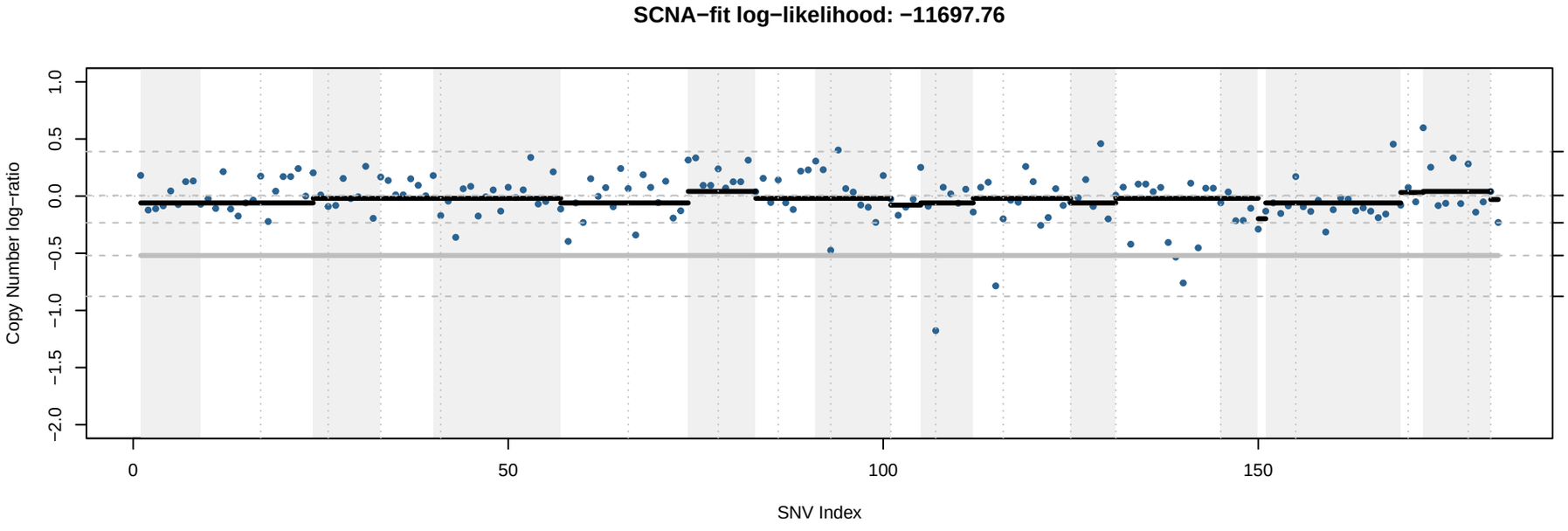

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

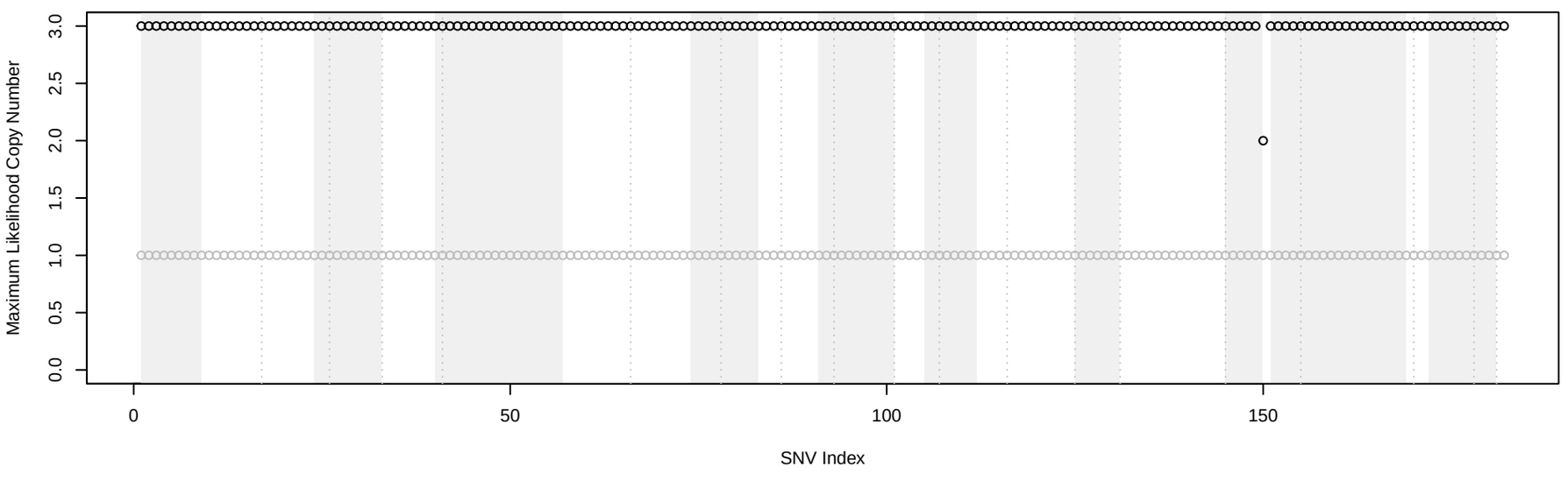

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

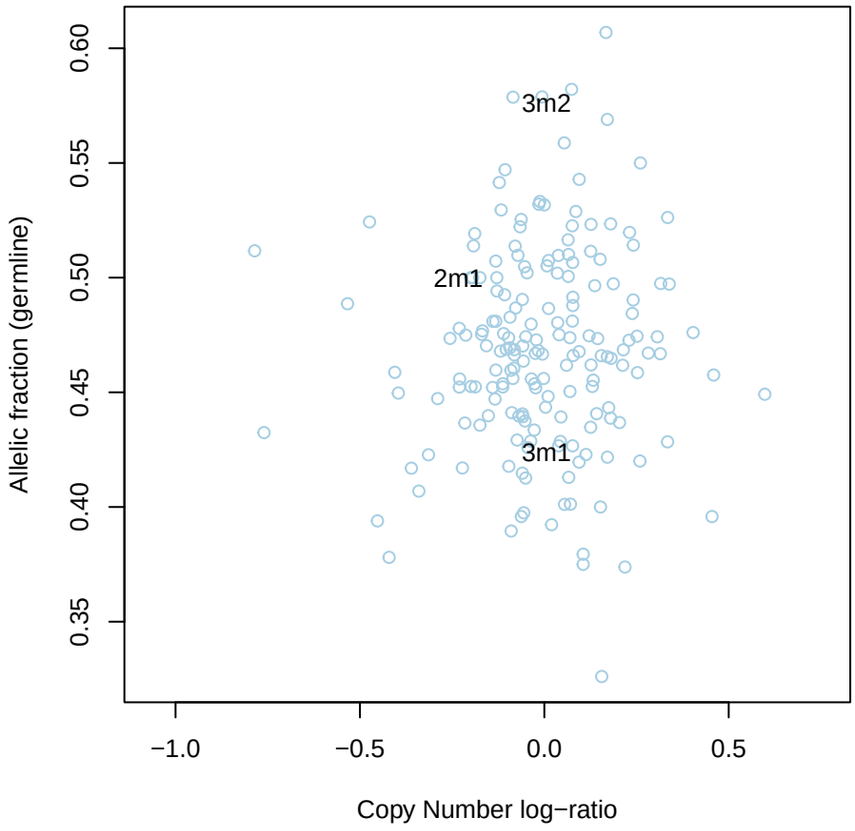

Frequency
0
5
10
15
20
25
30
35
0.1
0.2
0.3
0.4
0.5
0.6
Cellular fraction

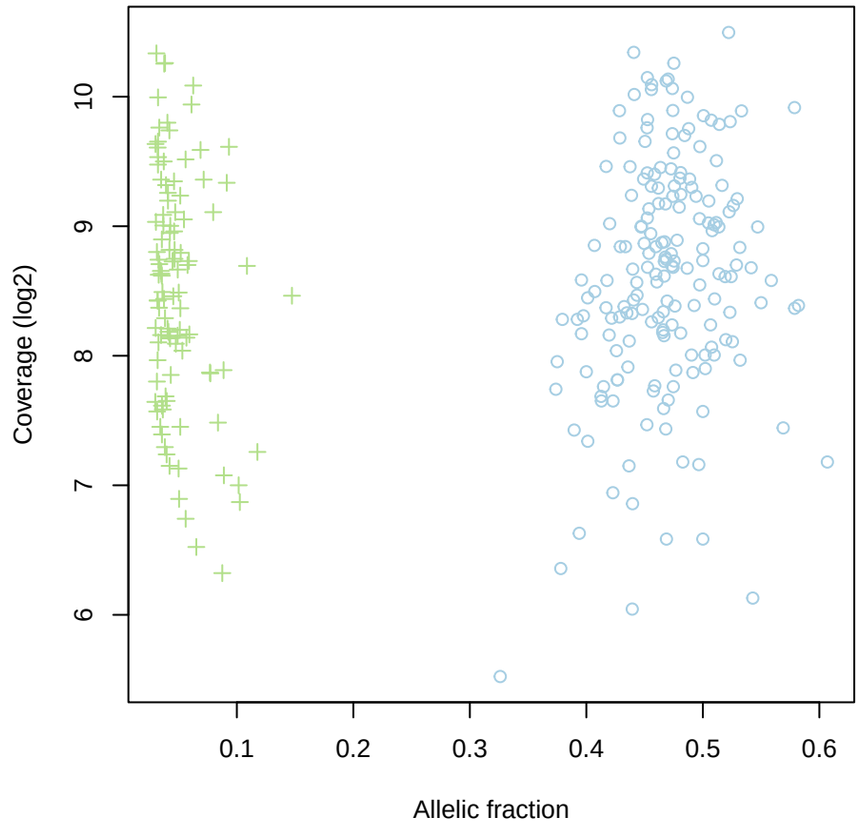

Purity: 0.36 Tumor ploidy: 2.974
0
1
2
3
5
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
log2 ratio

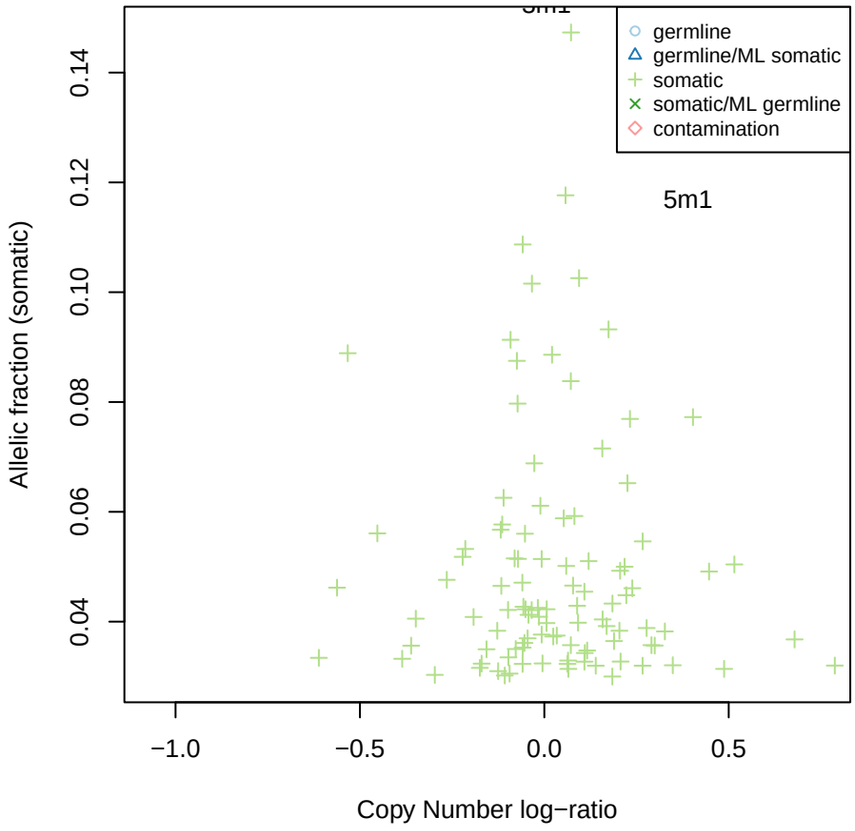

Purity: 0.36 Tumor ploidy: 2.974 SNV log−likelihood: −139.44 GoF: 86.1% Mean coverage: 459;574
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

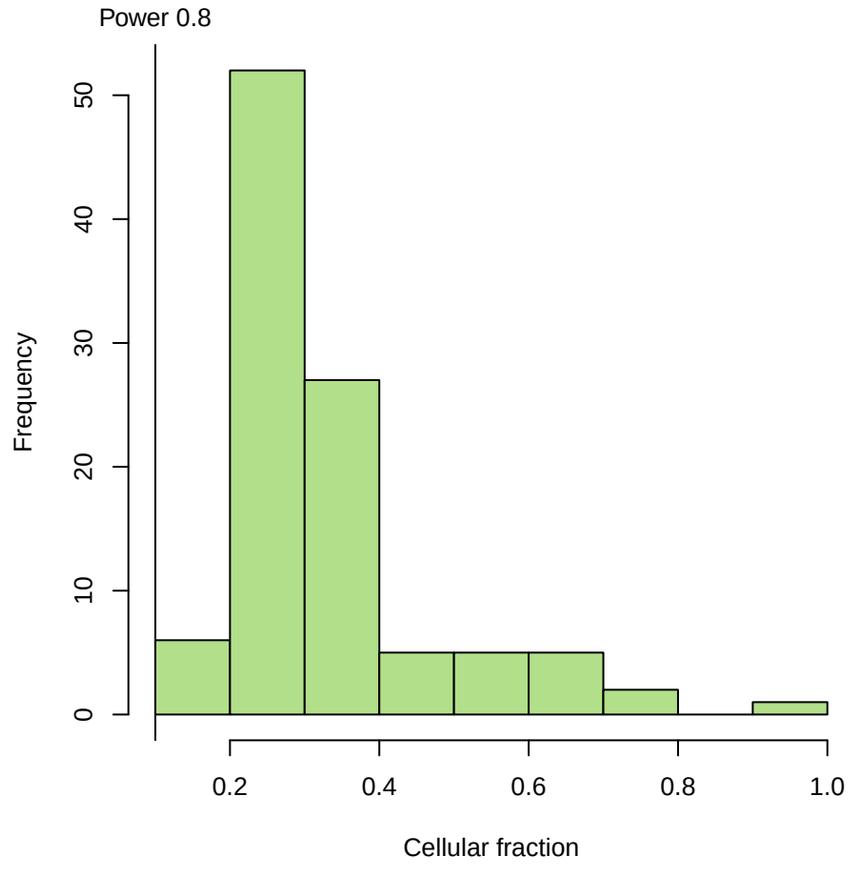

SCNA−fit log−likelihood: −11697.76
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 5
0 50 100 150
SNV Index

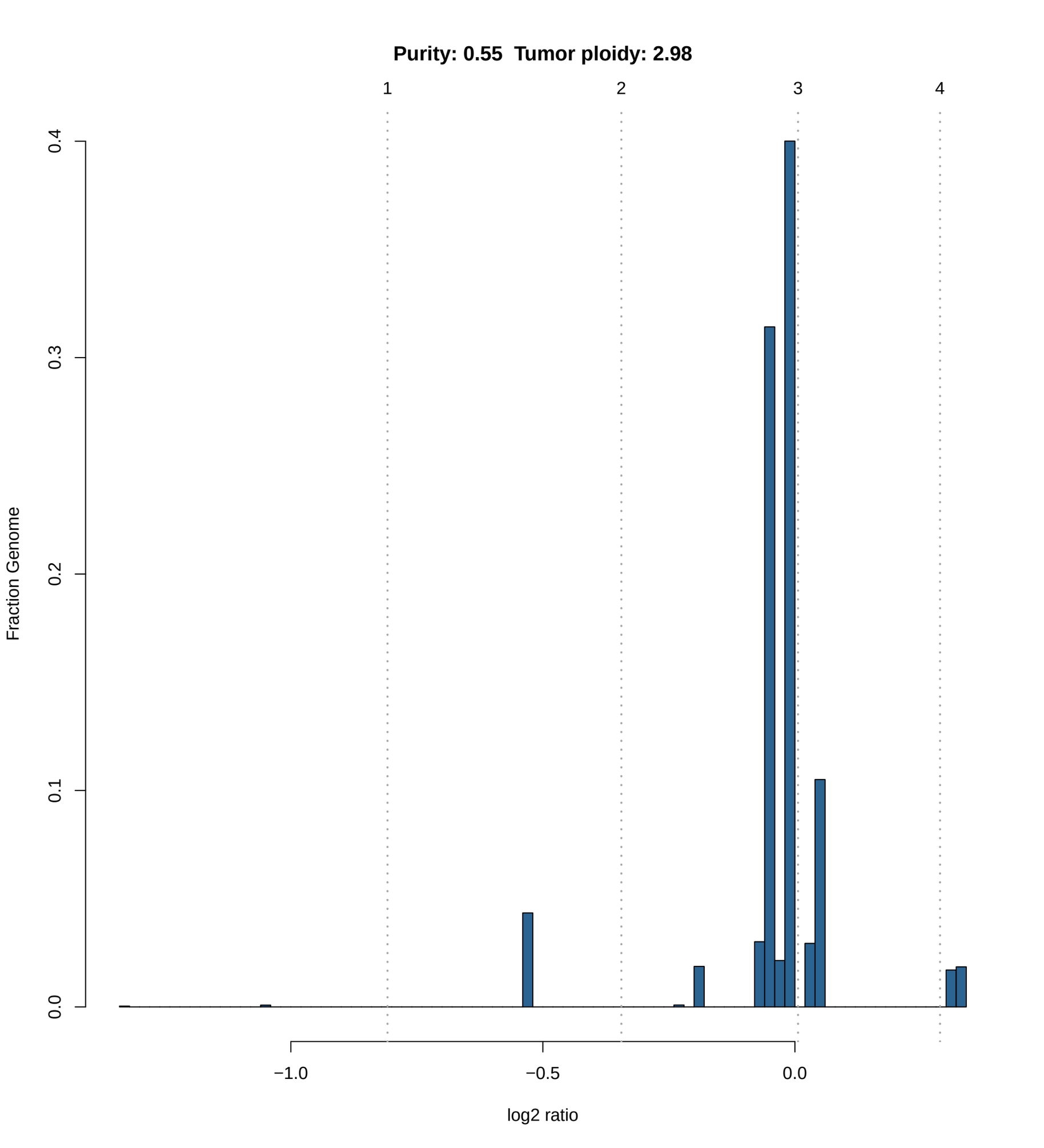

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

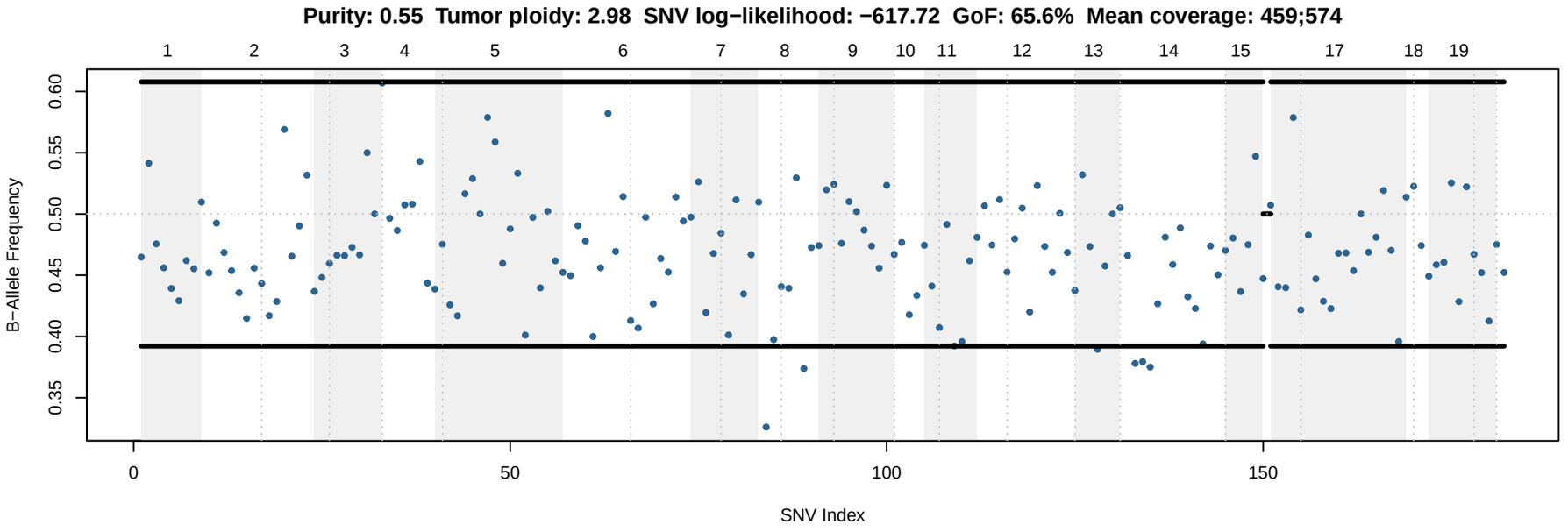

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
3m2
2m1
3m1
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

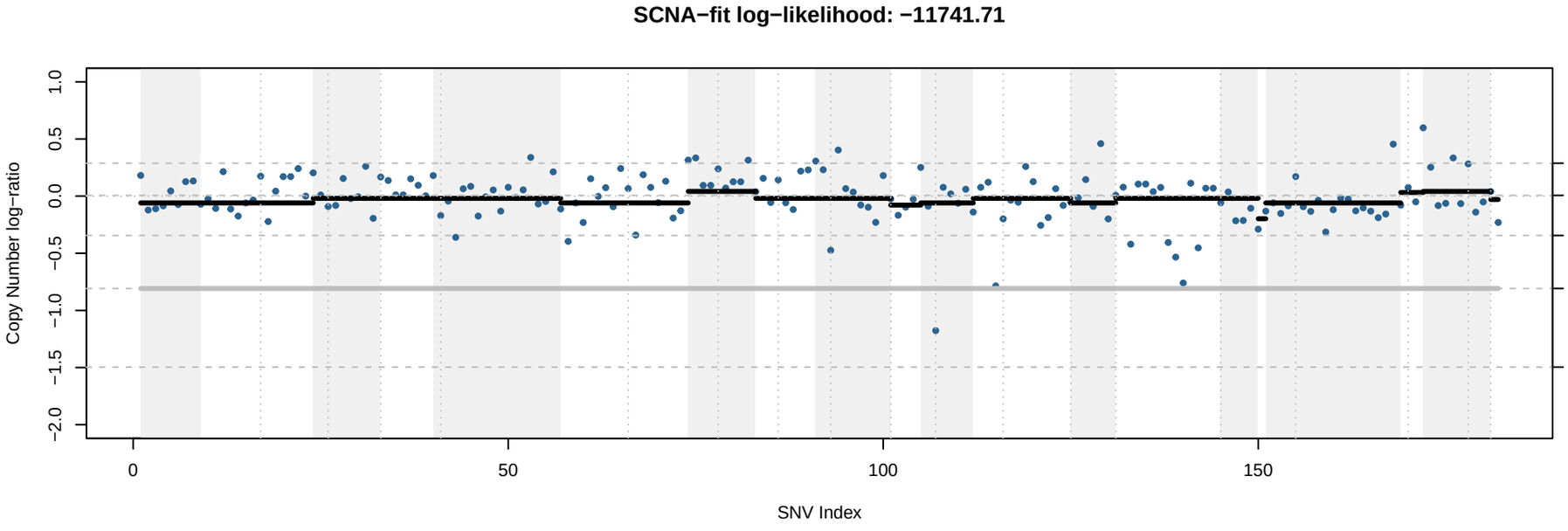

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

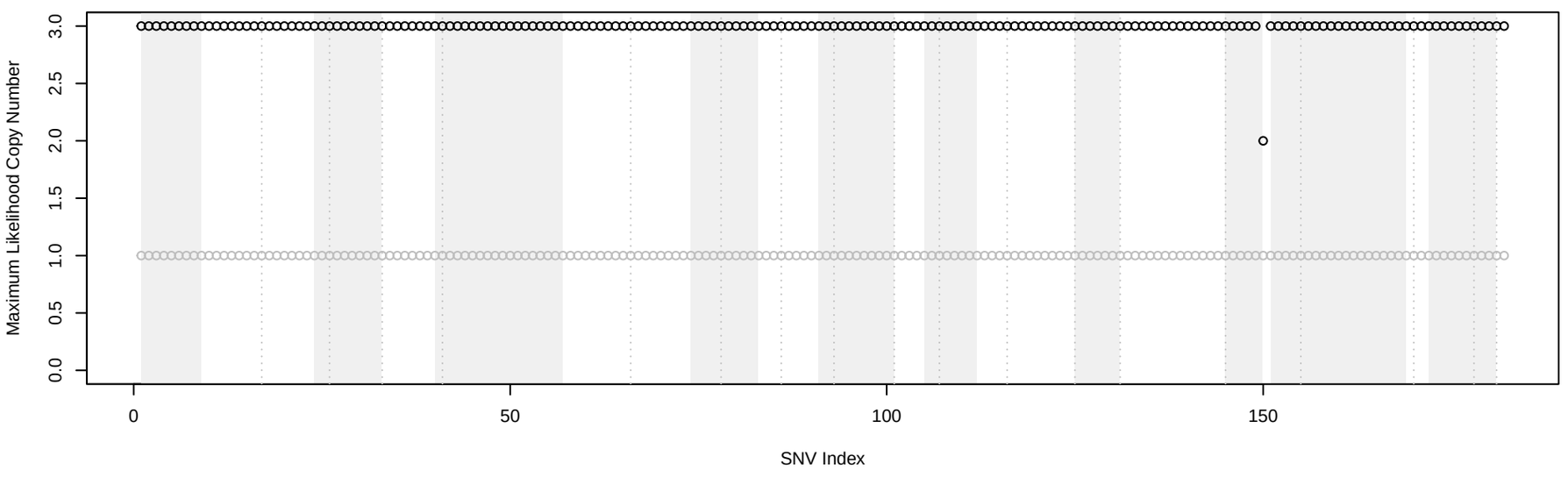

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

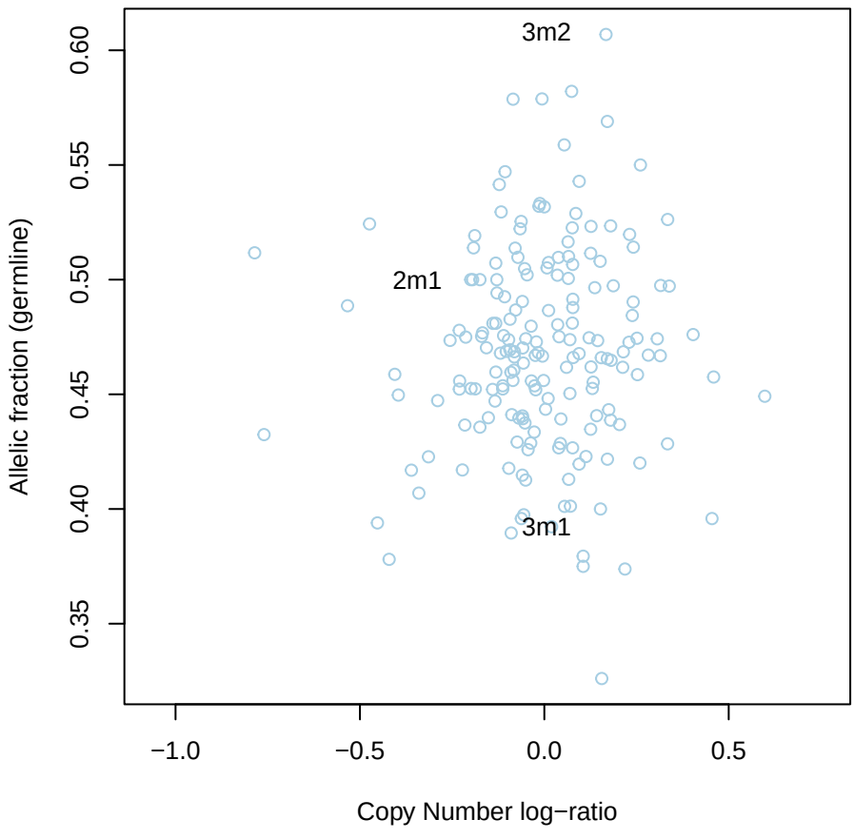

Power 0.8
Frequency
0
10
20
30
40
50
0.2
0.4
0.6
0.8
1.0
Cellular fraction

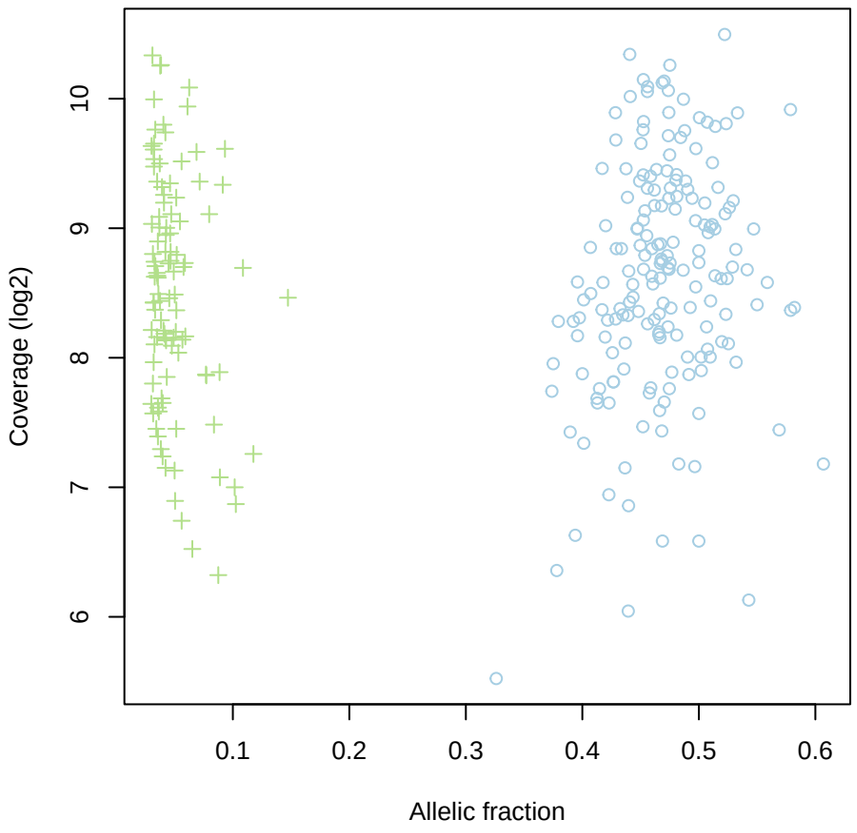

Purity: 0.55 Tumor ploidy: 2.98
1
2
3
4
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
log2 ratio

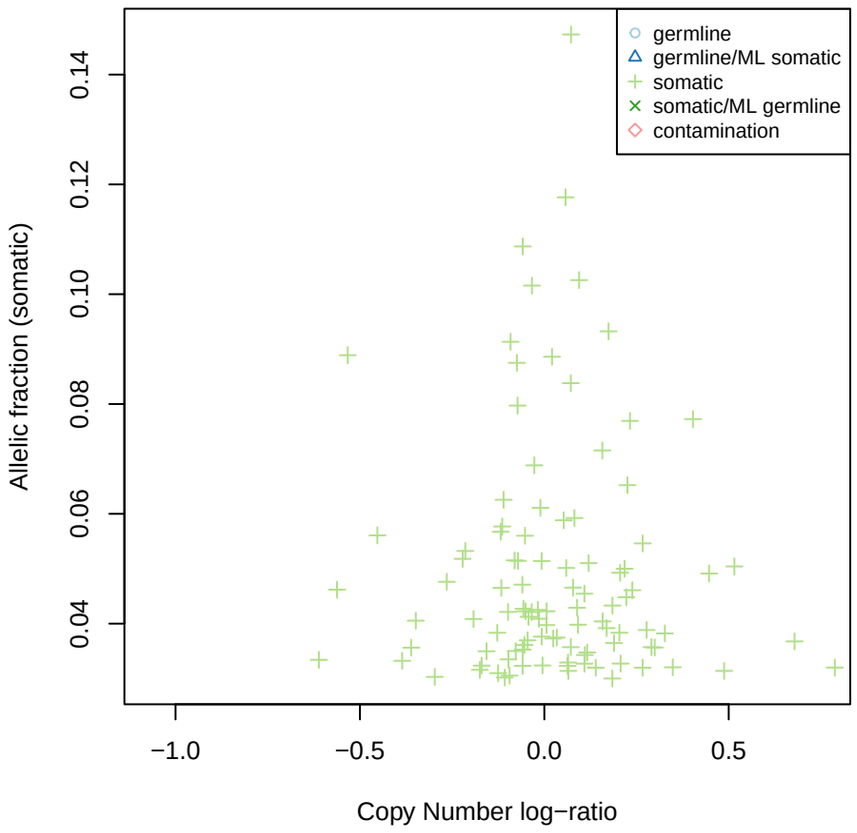

Purity: 0.55 Tumor ploidy: 2.98 SNV log−likelihood: −617.72 GoF: 65.6% Mean coverage: 459;574
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 50 100 150
SNV Index

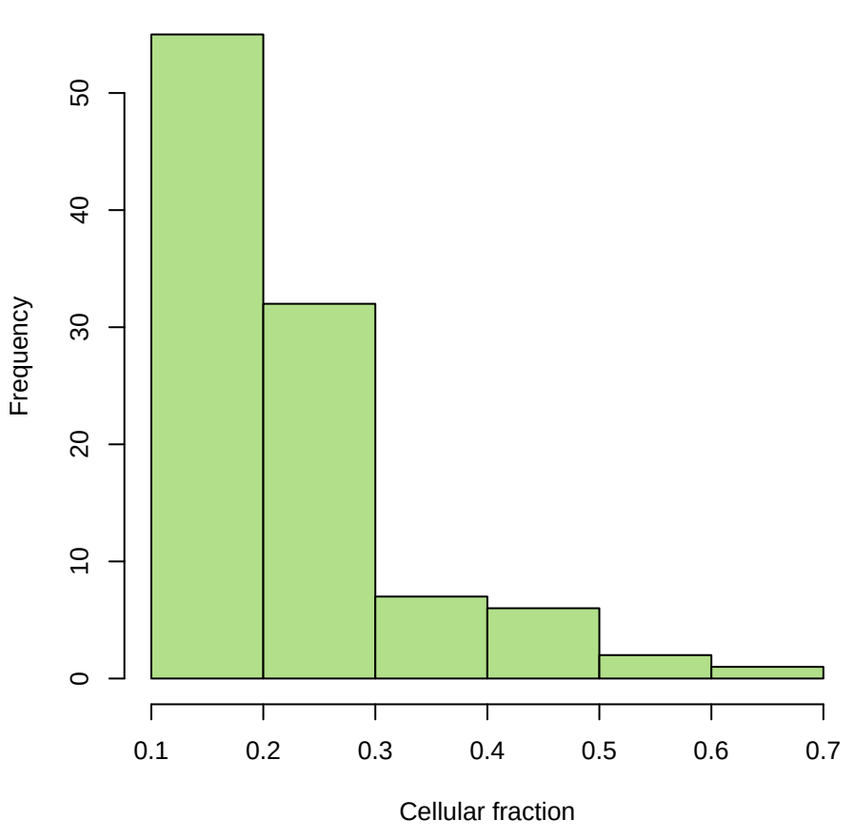

SCNA−fit log−likelihood: −11741.71
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4
0 50 100 150
SNV Index

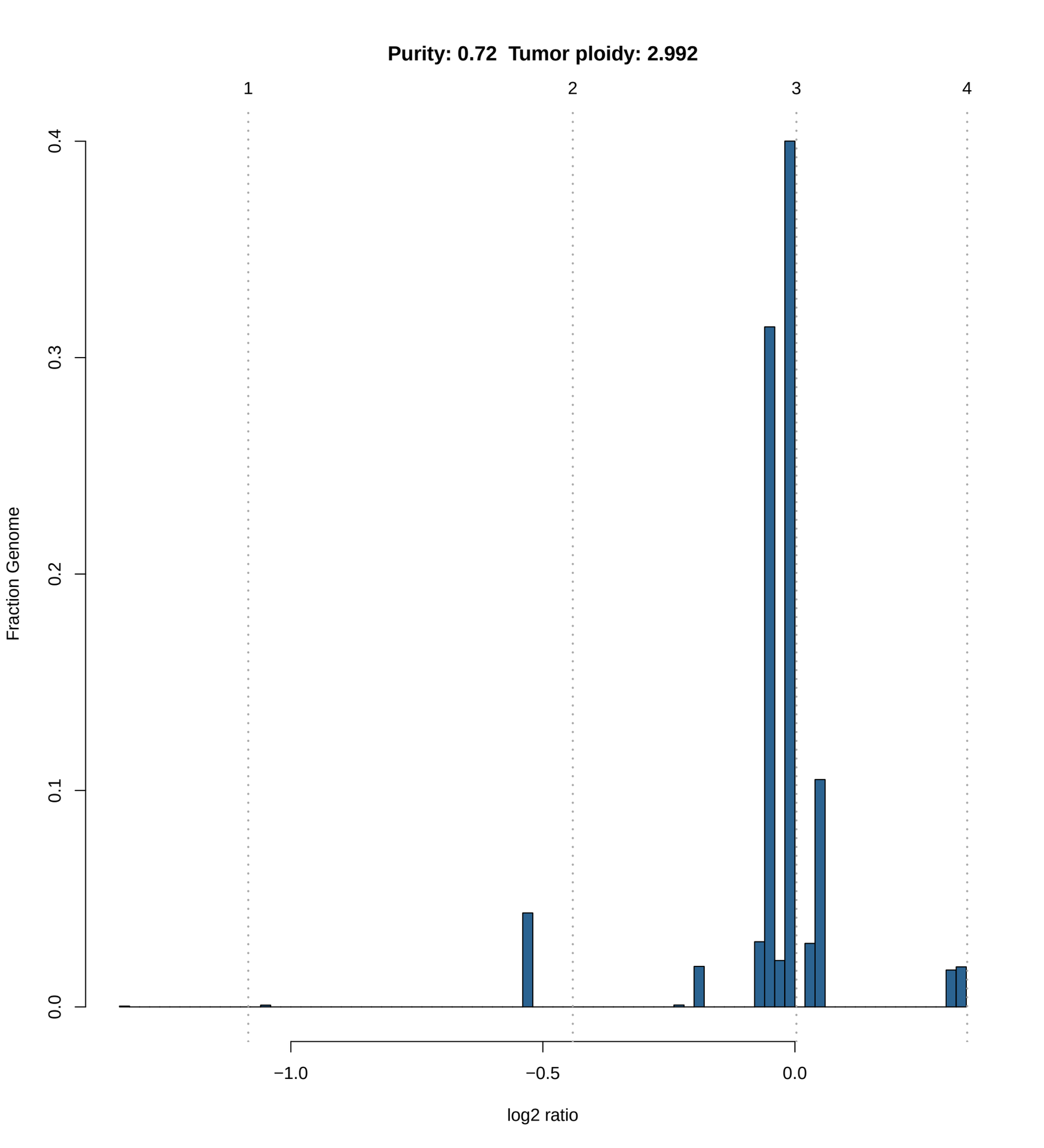

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

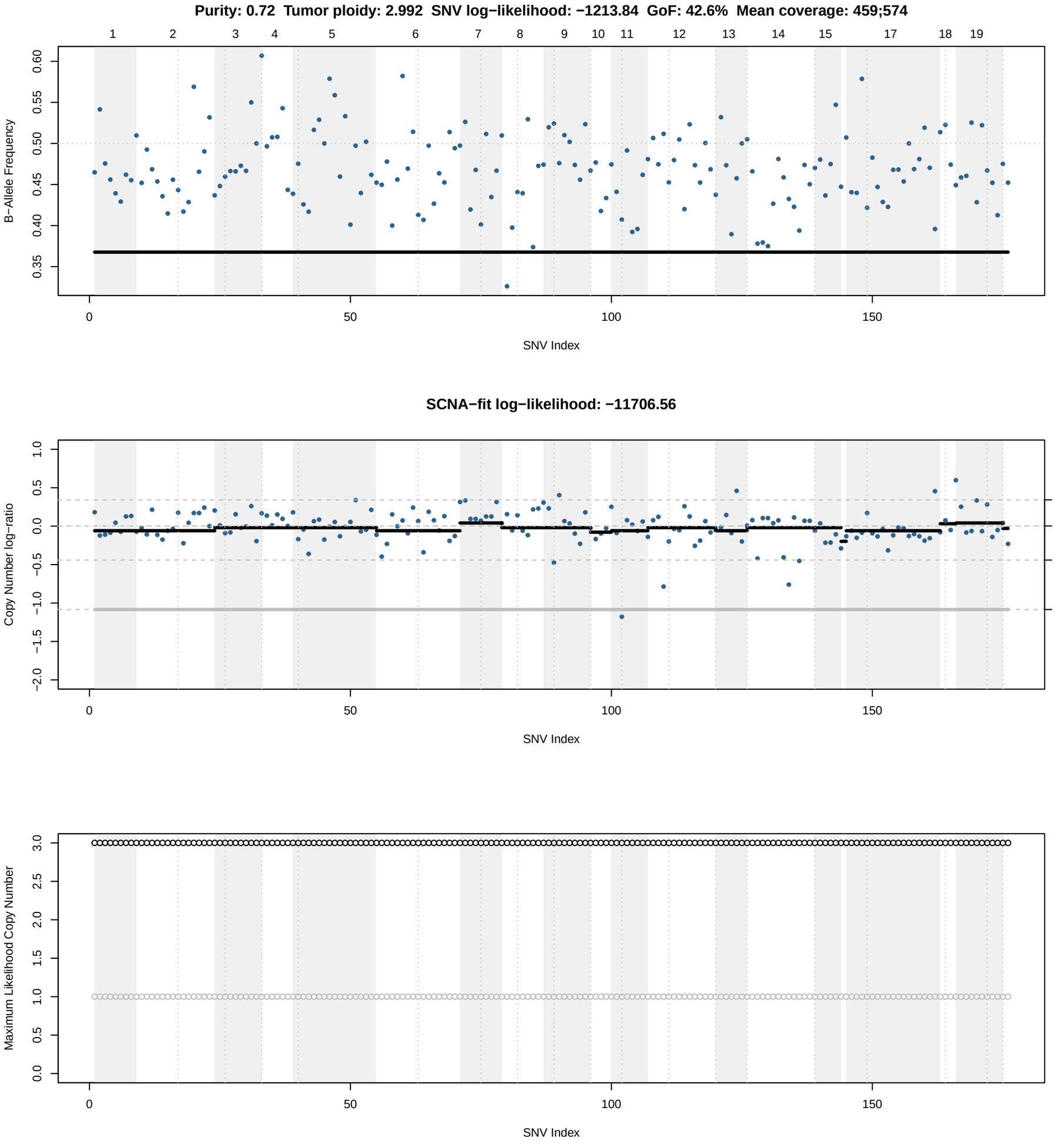

3m2
2m1
3m1
Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

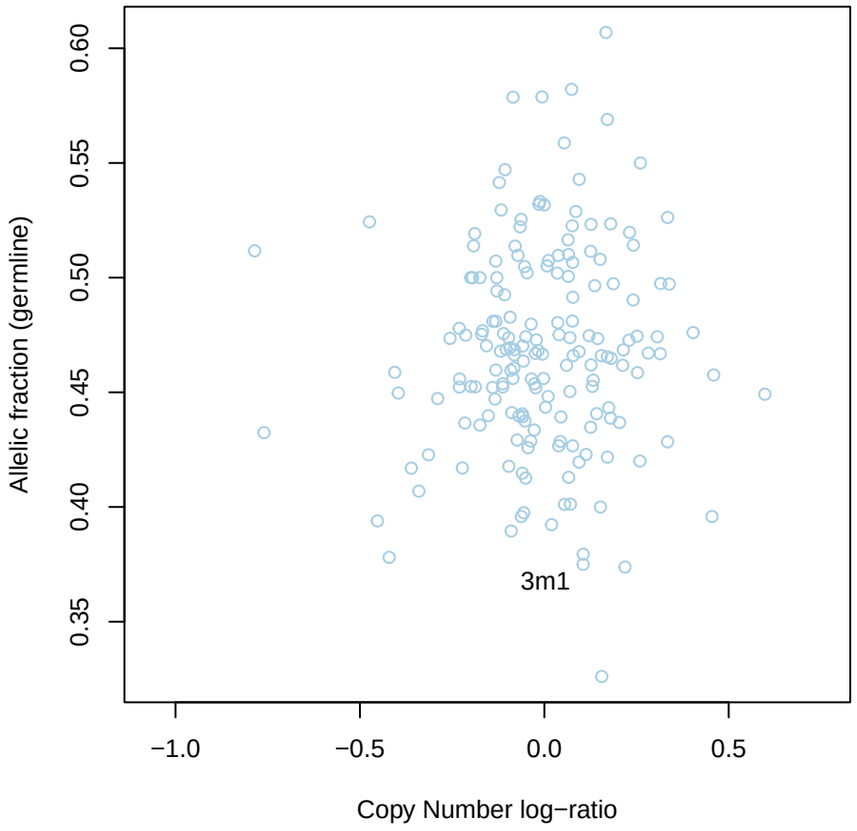

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

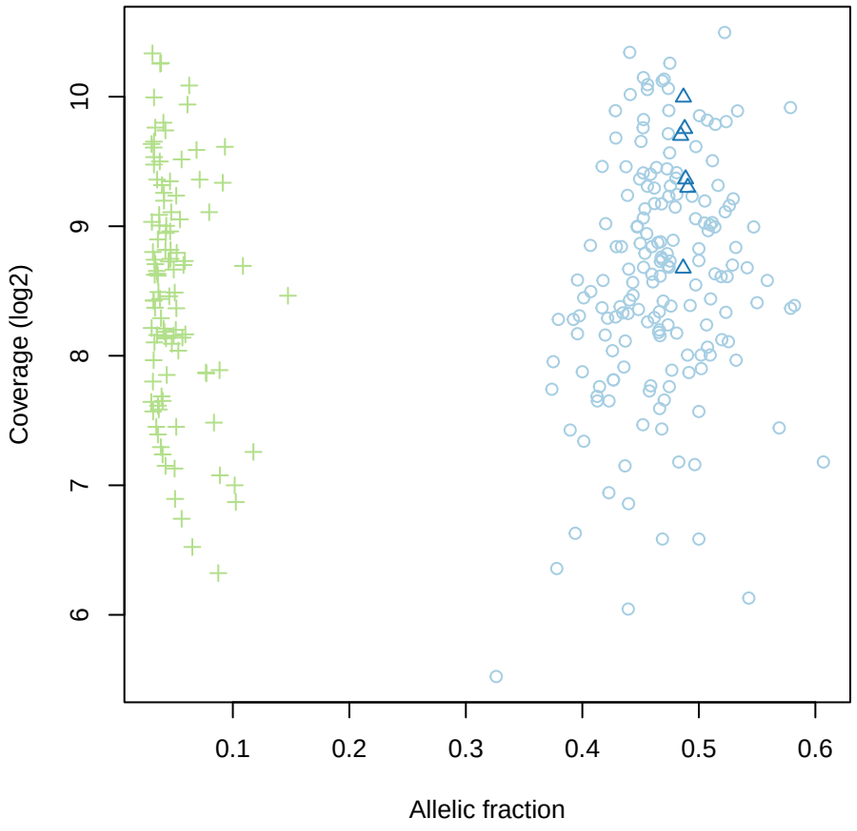

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
−1.0
−0.5
0.0
0.5
Copy Number log−ratio

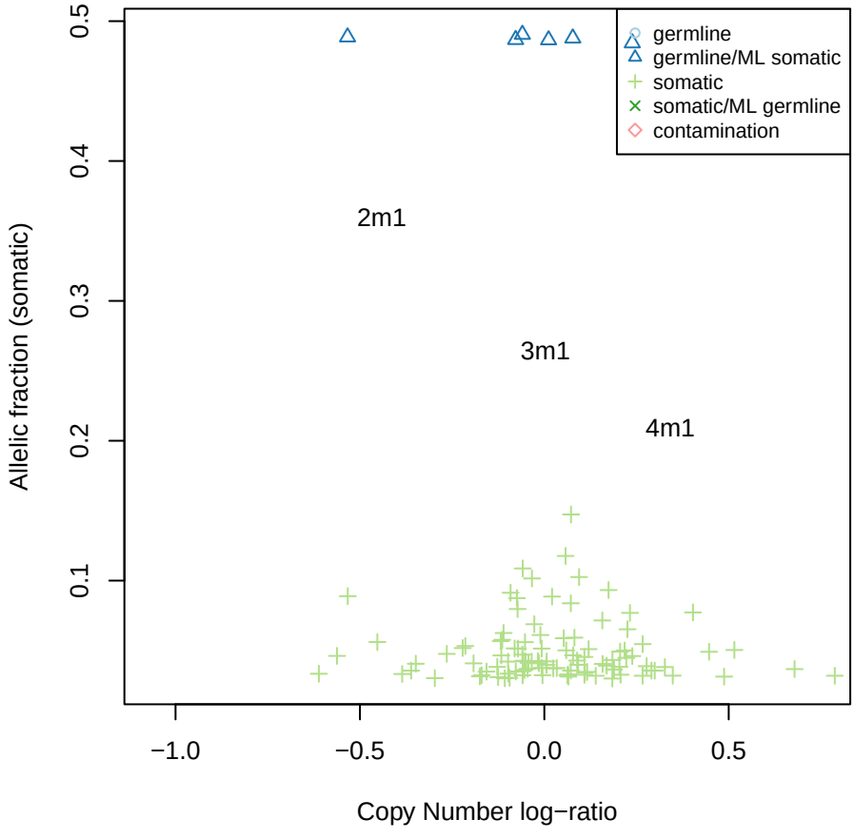

Frequency
0
10
20
30
40
50
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Cellular fraction

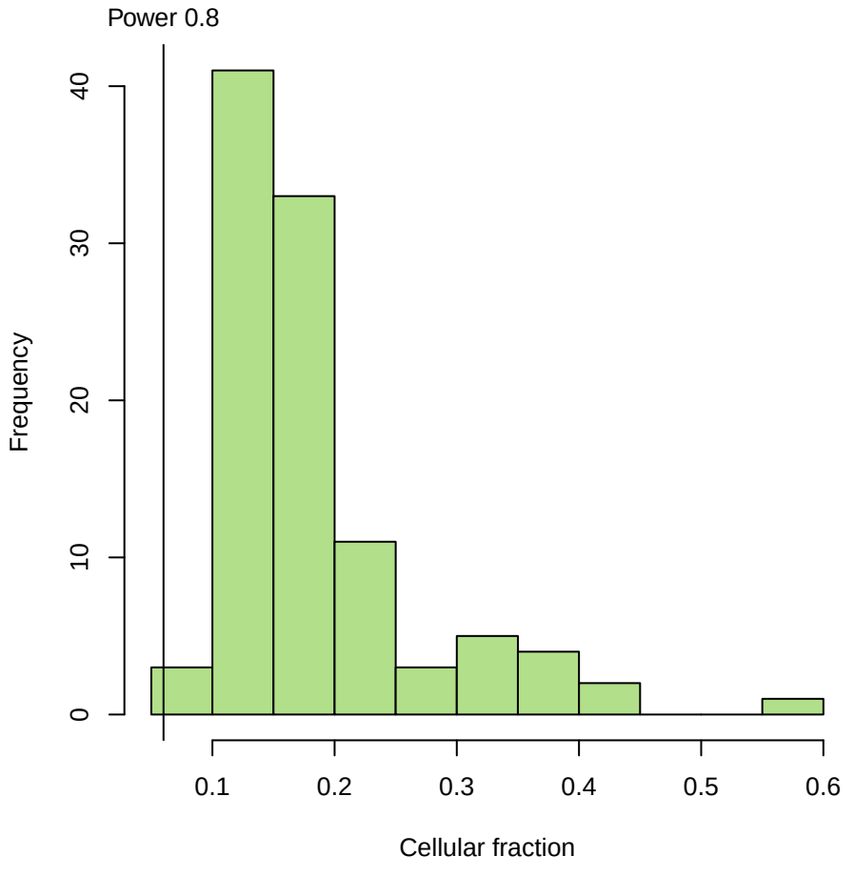

Purity: 0.72 Tumor ploidy: 2.992
1
2
3
4
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−1.0
−0.5
0.0
log2 ratio


Purity: 0.72 Tumor ploidy: 2.992 SNV log−likelihood: −1213.84 GoF: 42.6% Mean coverage: 459;574
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 18 19
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: −11706.56
Copy Number log−ratio
−2.0 −1.5 −1.0 −0.5 0.0 0.5 1.0
1 2 3 4
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
−1.0
−0.5
0.0
0.5
Copy Number log−ratio
3m1


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


Allelic fraction (somatic)
0.1
0.2
0.3
0.4
0.5
−1.0
−0.5
0.0
0.5
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1


Power 0.8
Frequency
0
10
20
30
40
0.1
0.2
0.3
0.4
0.5
0.6
Cellular fraction