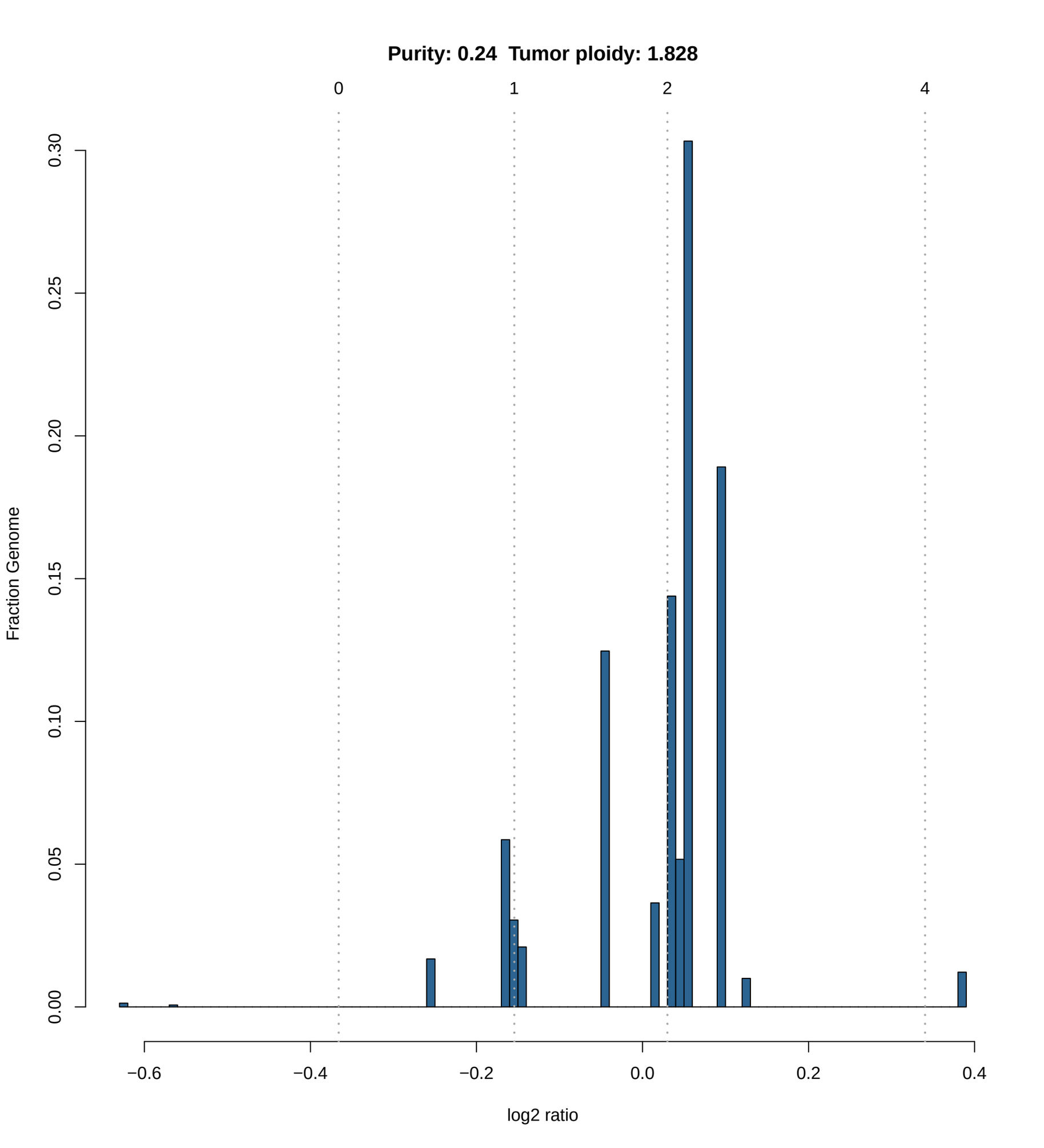
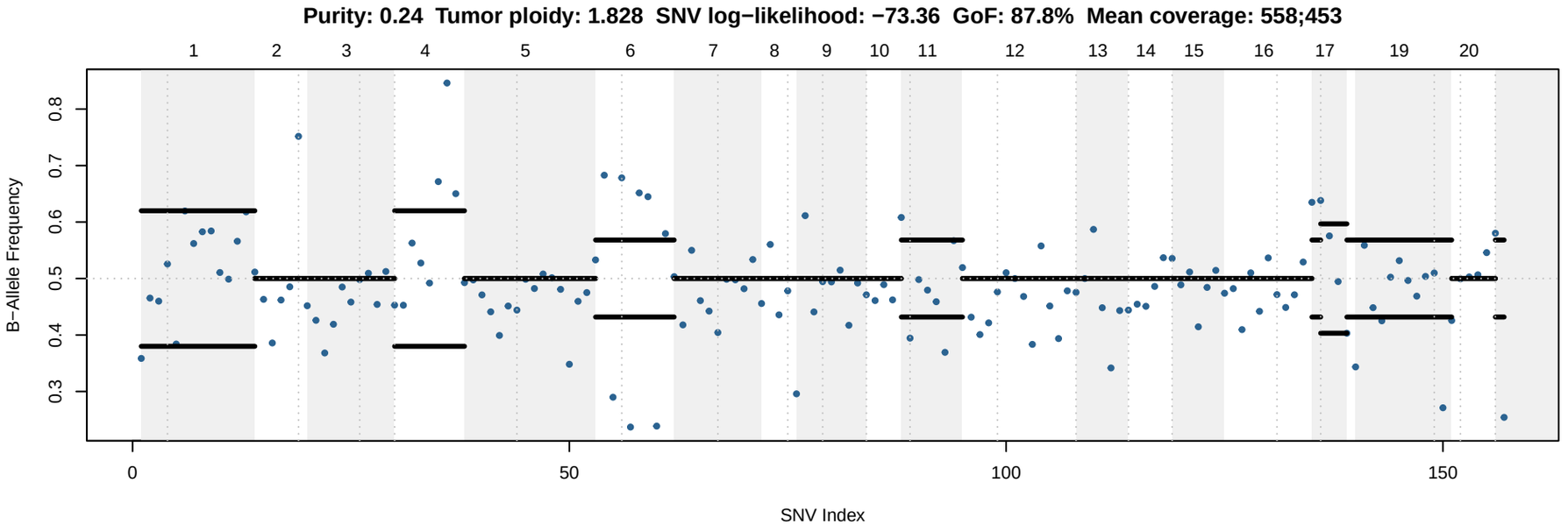
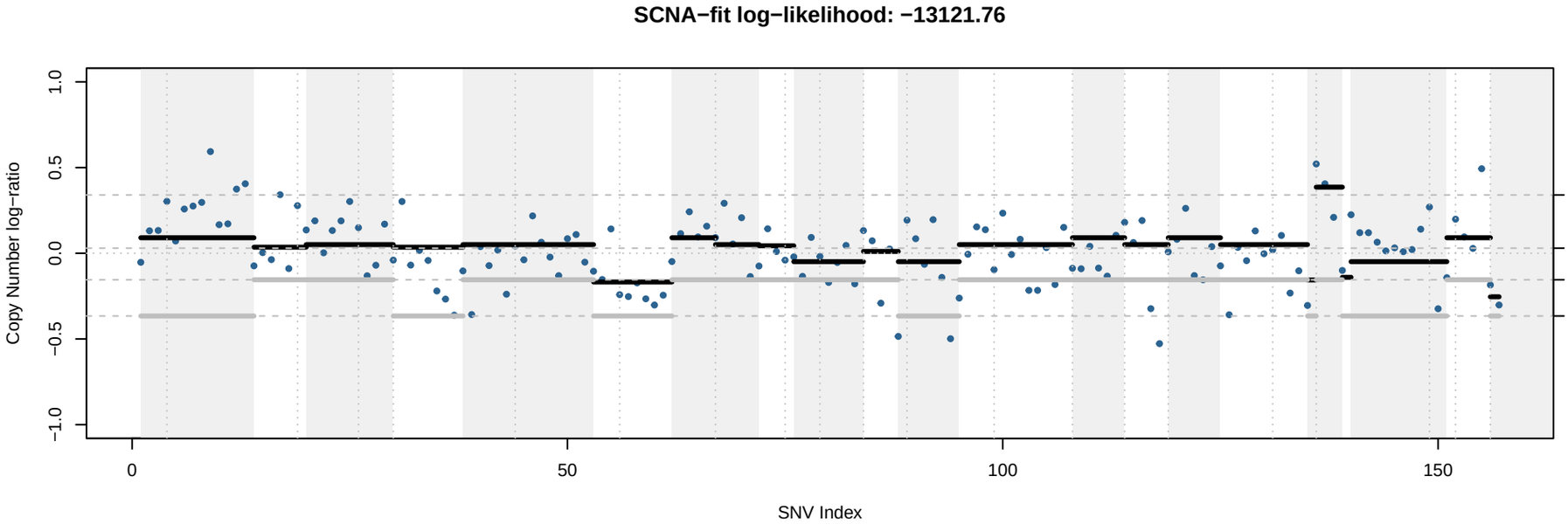
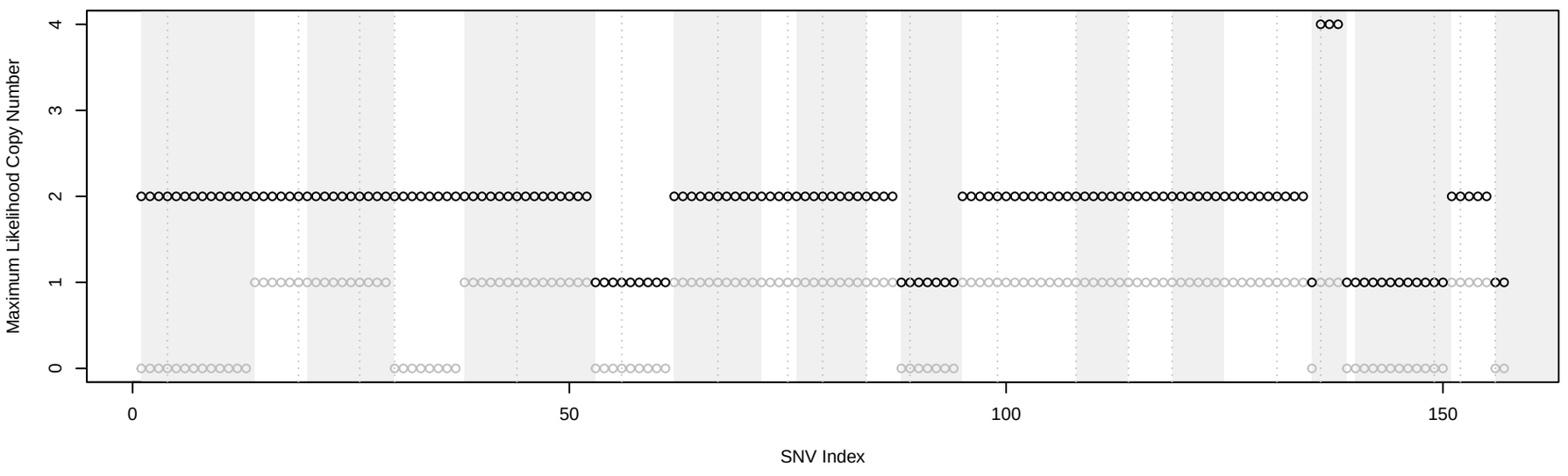
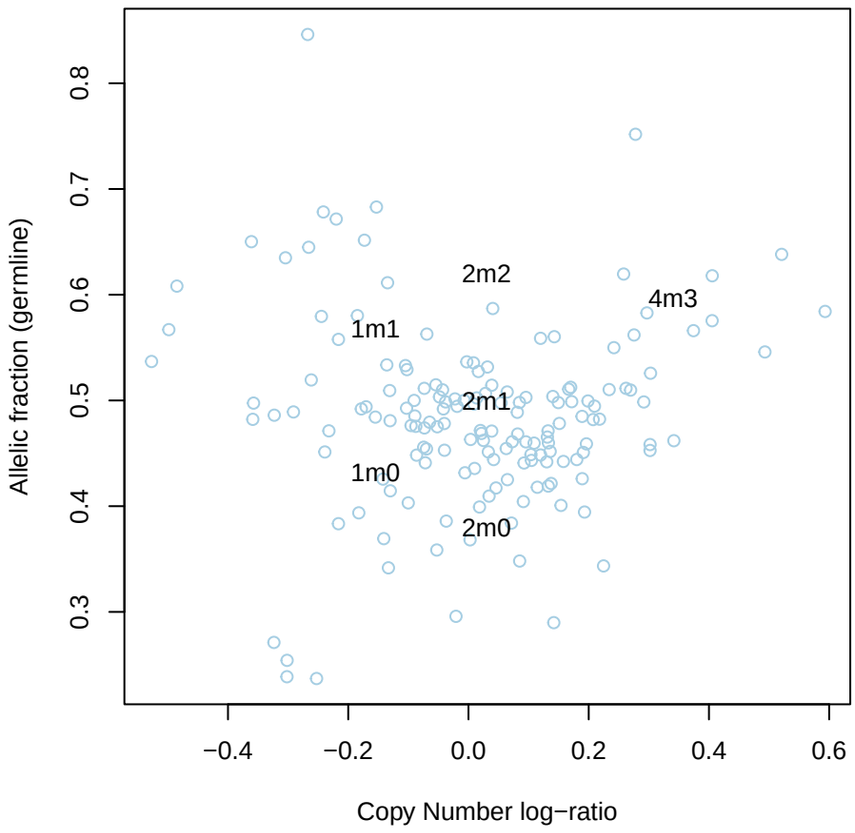
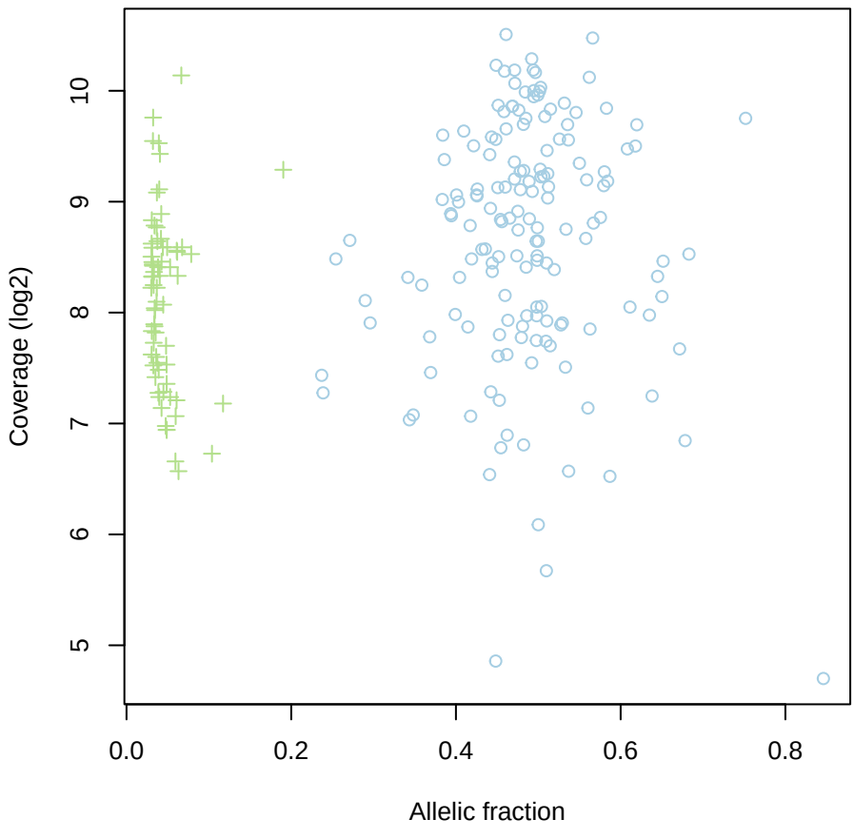

Purity: 0.24 Tumor ploidy: 1.828
0
1
2
4
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

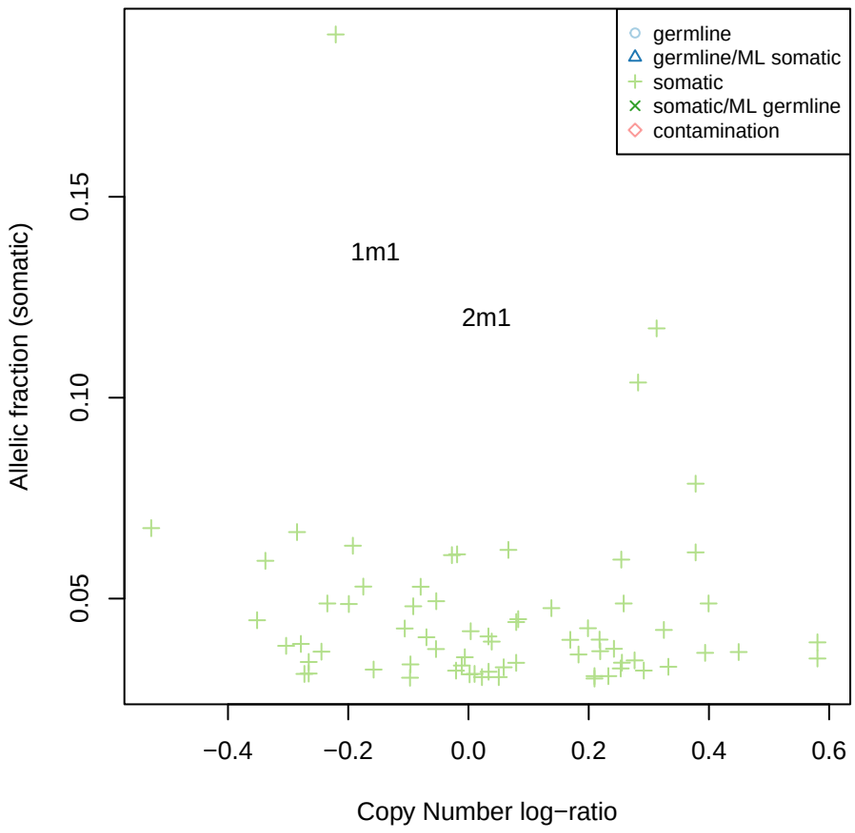

Purity: 0.24 Tumor ploidy: 1.828 SNV log−likelihood: −73.36 GoF: 87.8% Mean coverage: 558;453
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

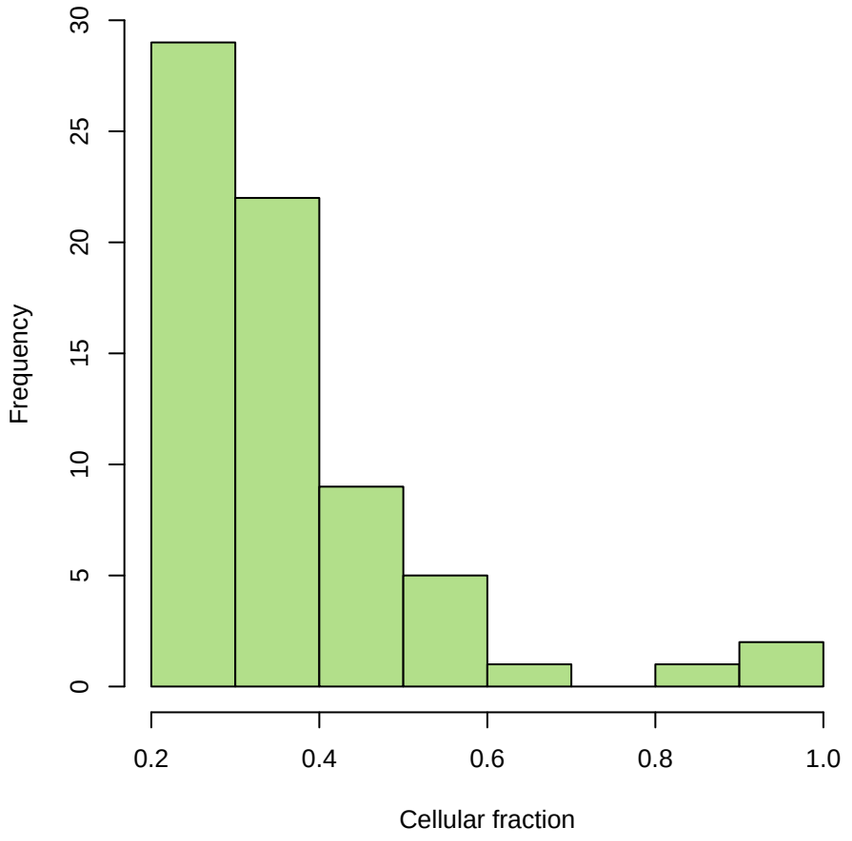

SCNA−fit log−likelihood: −13121.76
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 4
0 50 100 150
SNV Index

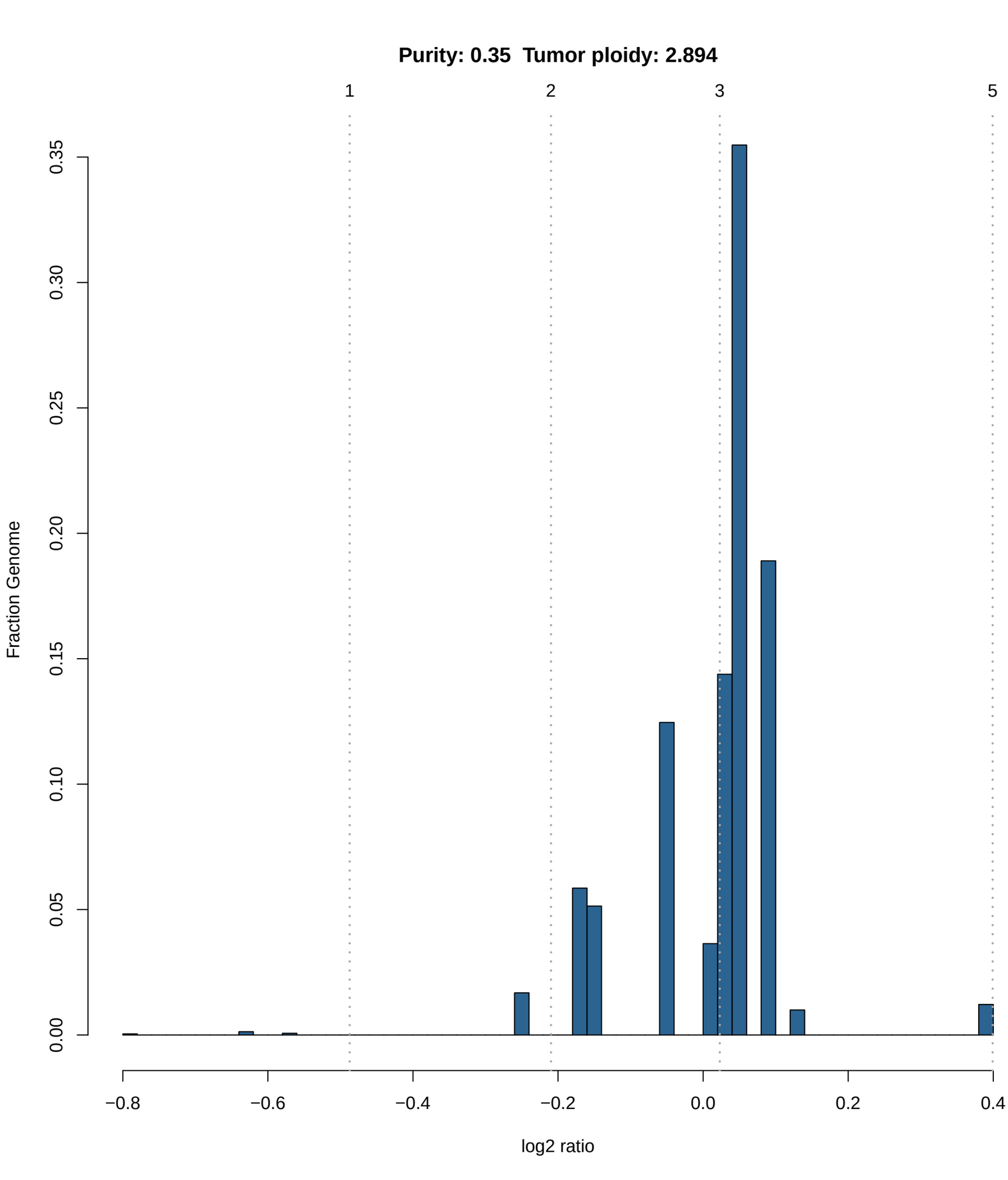

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

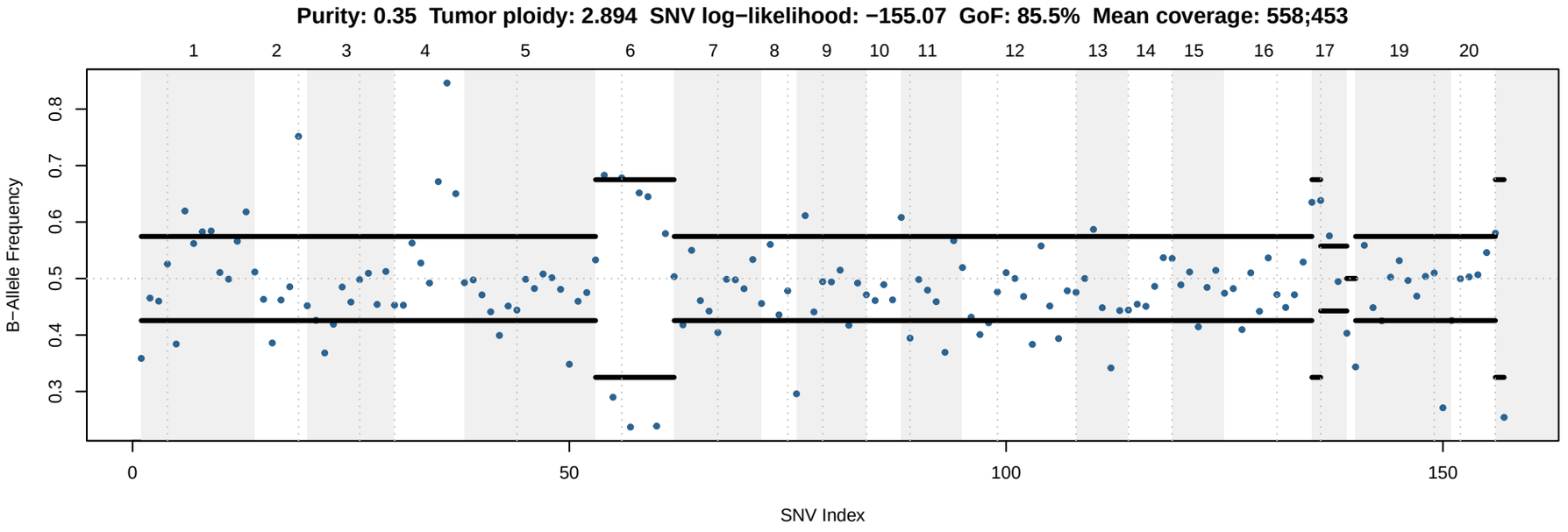

Allelic fraction (germline)
Copy Number log−ratio
2m2
4m3
1m1
2m1
1m0
2m0

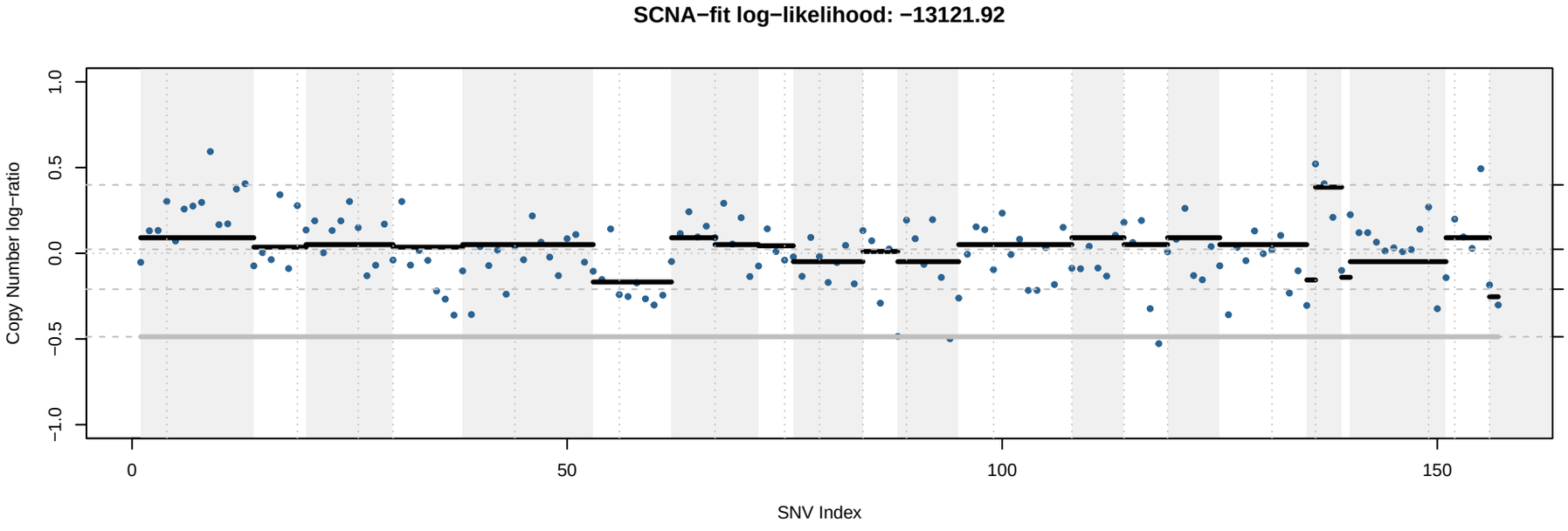

Coverage (log2)
Allelic fraction

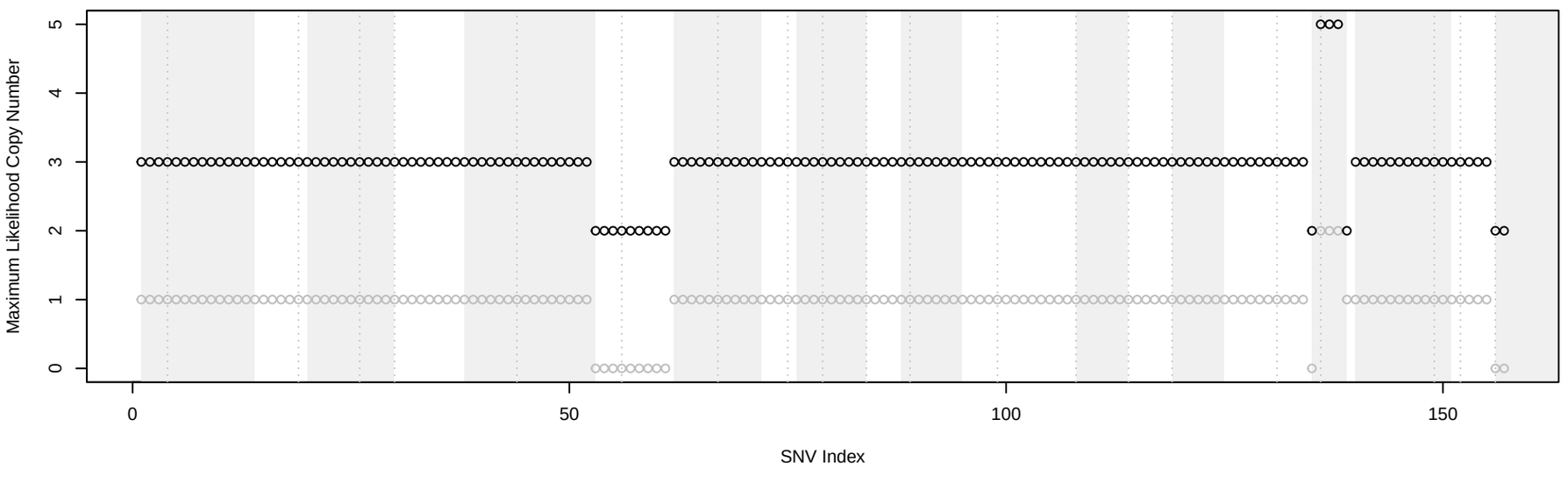

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1

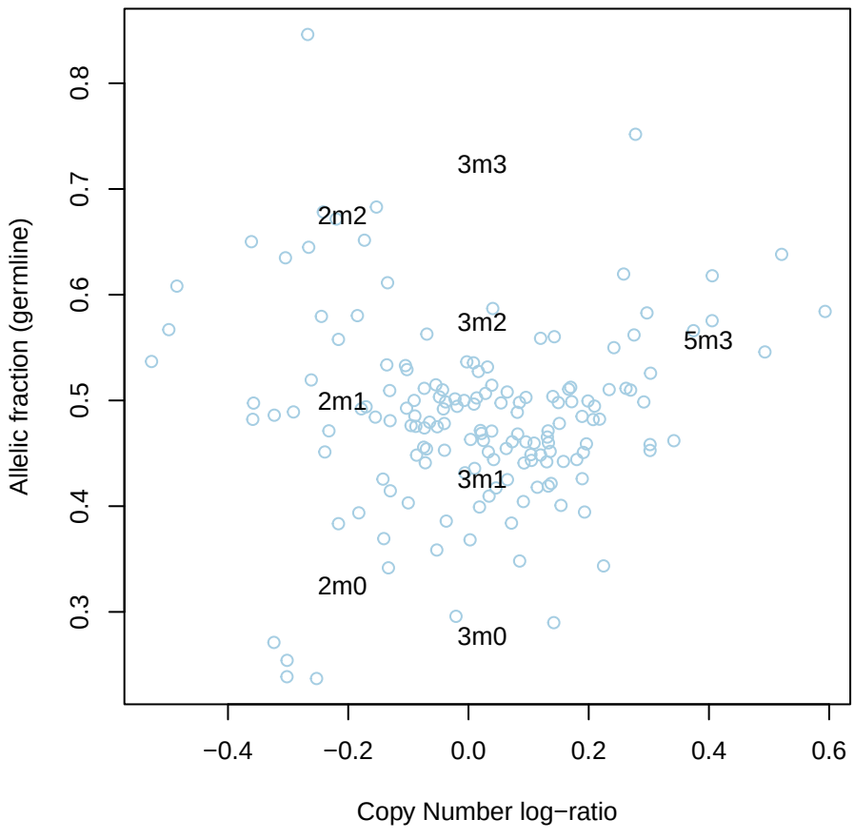

Frequency
Cellular fraction

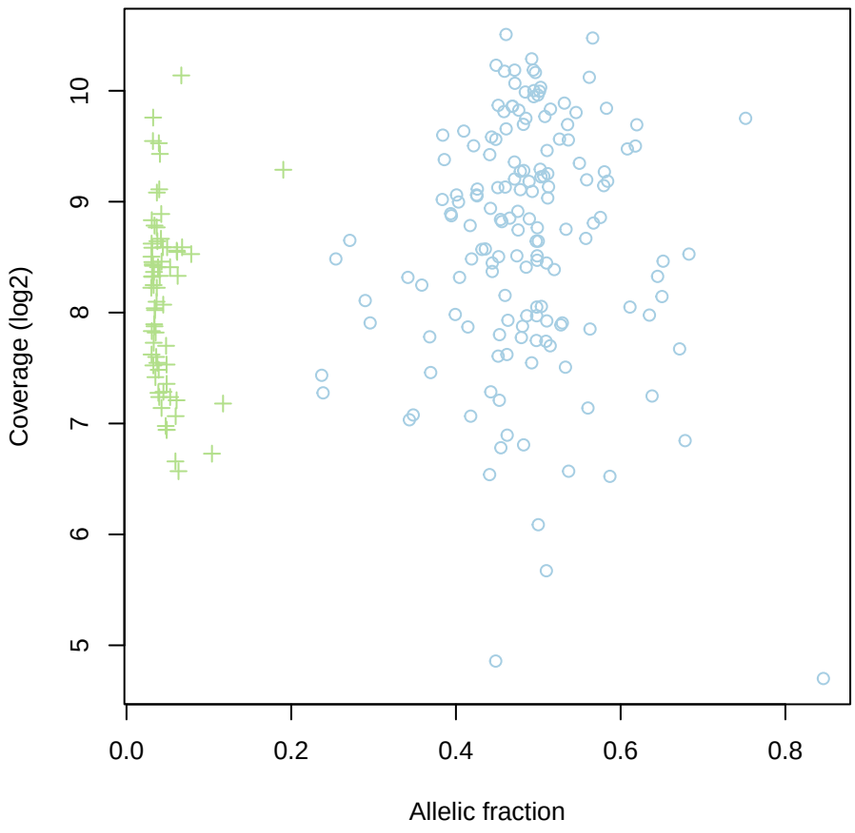

Purity: 0.35 Tumor ploidy: 2.894
1
2
3
5
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

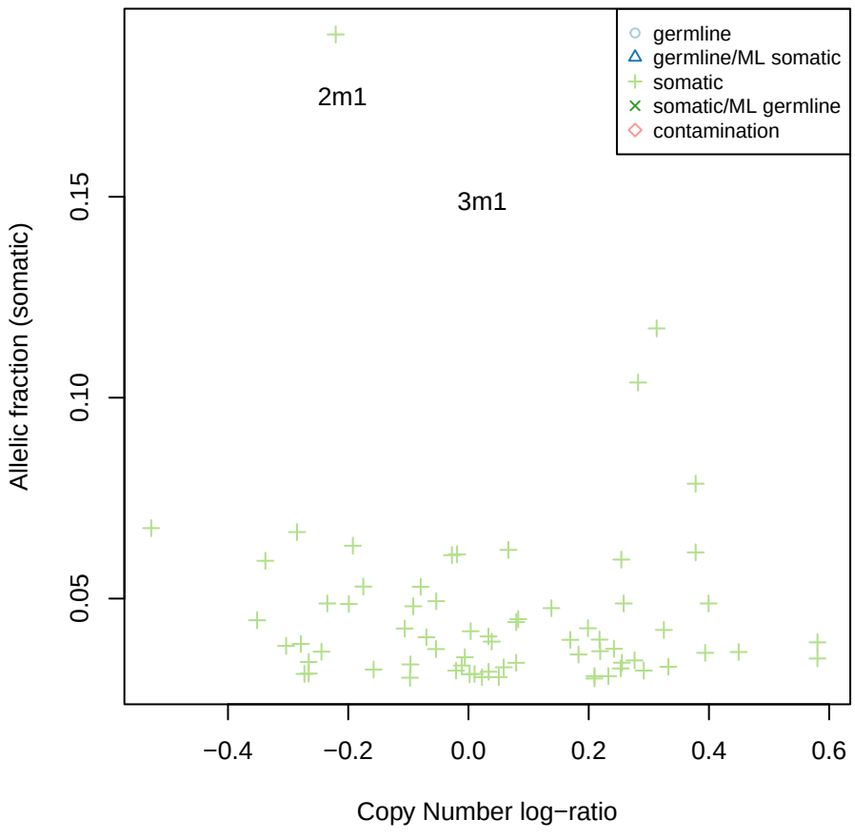

Purity: 0.35 Tumor ploidy: 2.894 SNV log−likelihood: −155.07 GoF: 85.5% Mean coverage: 558;453
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

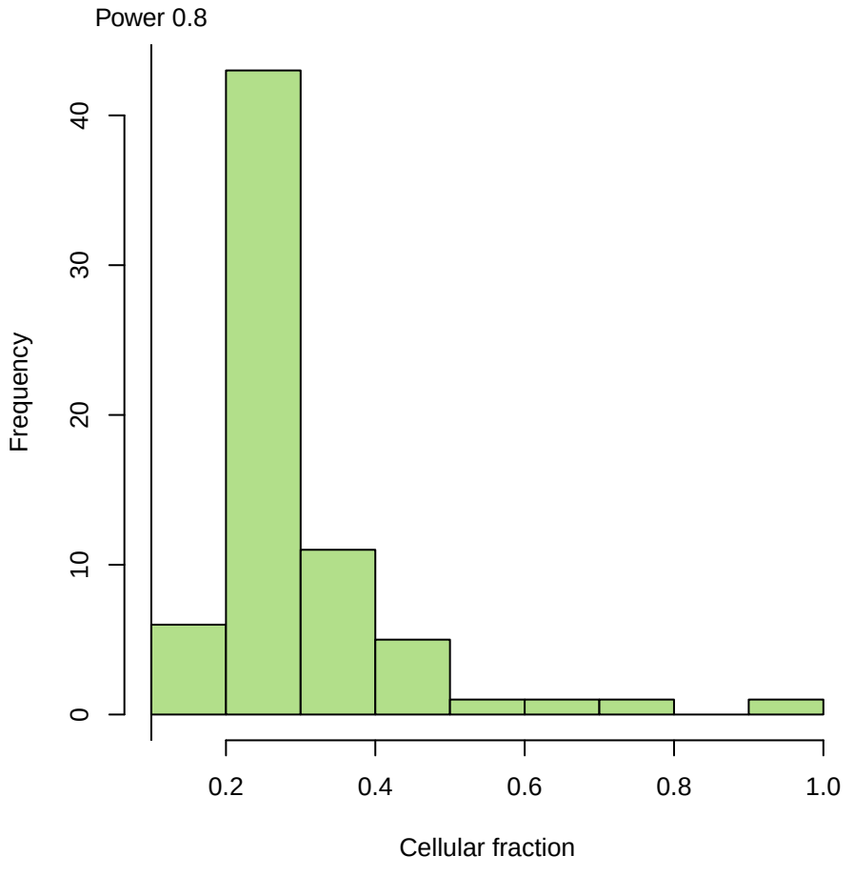

SCNA−fit log−likelihood: −13121.92
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 5
0 50 100 150
SNV Index

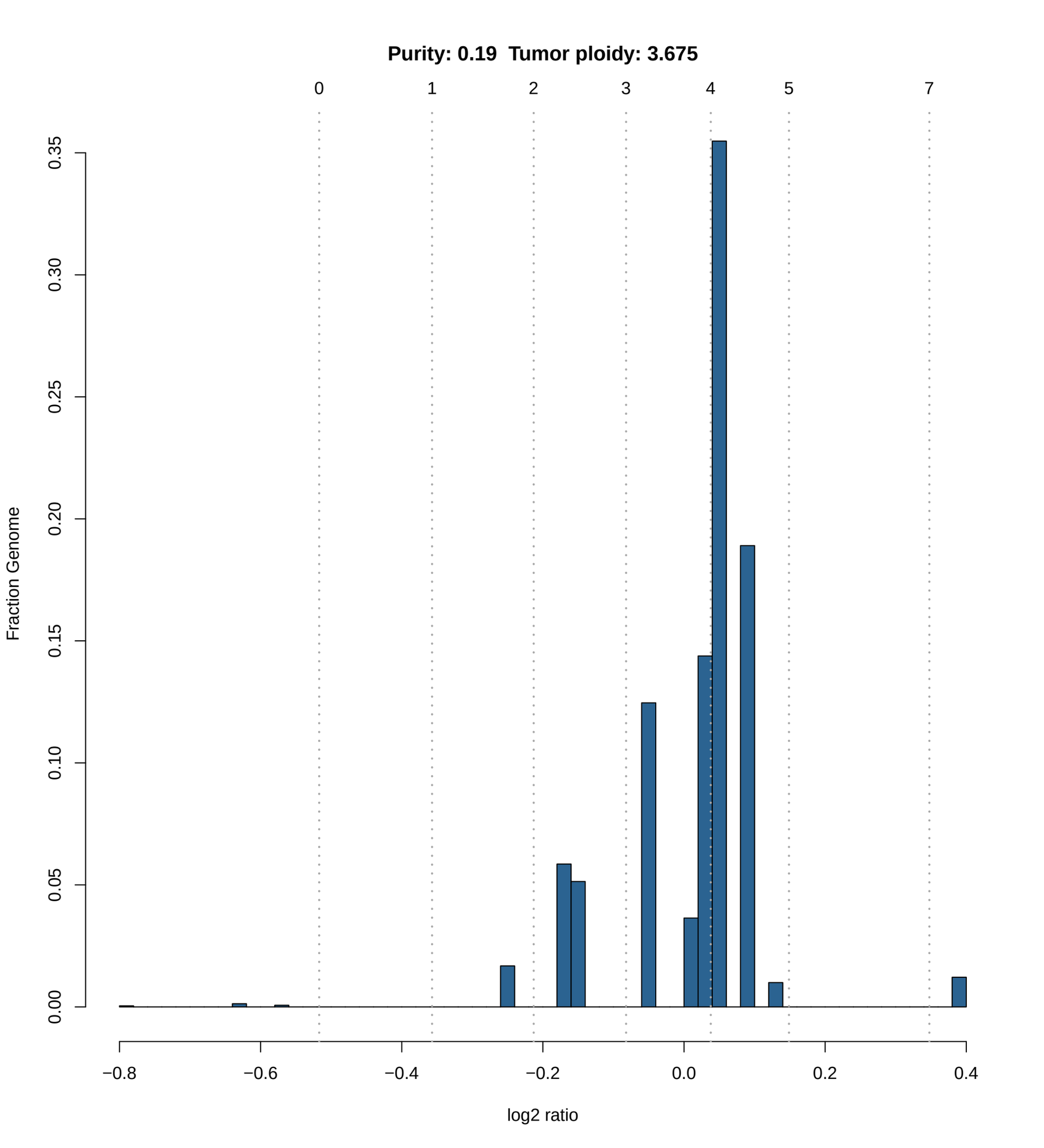

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

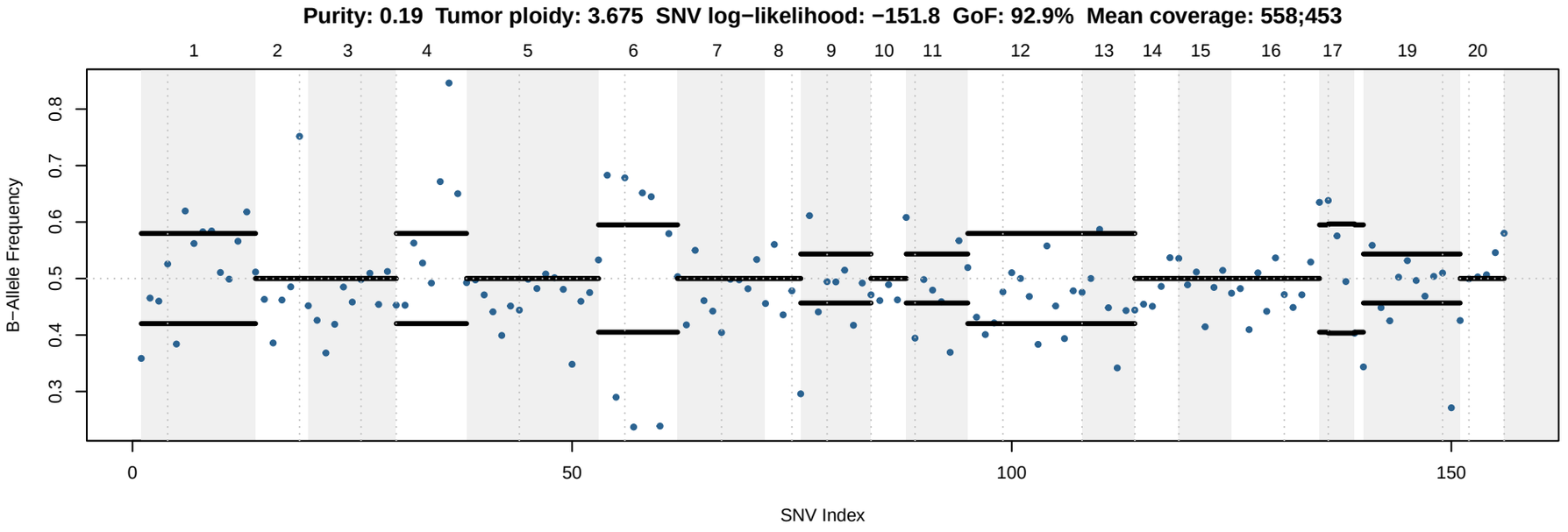

Allelic fraction (germline)
Copy Number log−ratio
3m3
2m2
3m2
5m3
2m1
3m1
2m0
3m0

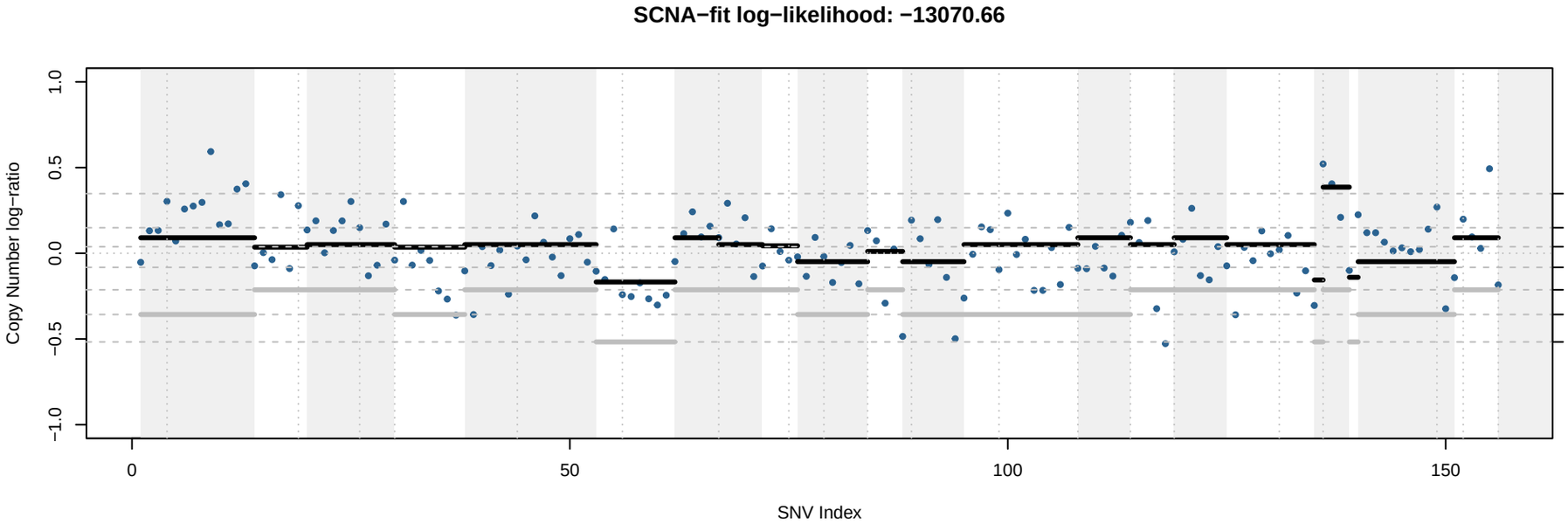

Coverage (log2)
Allelic fraction

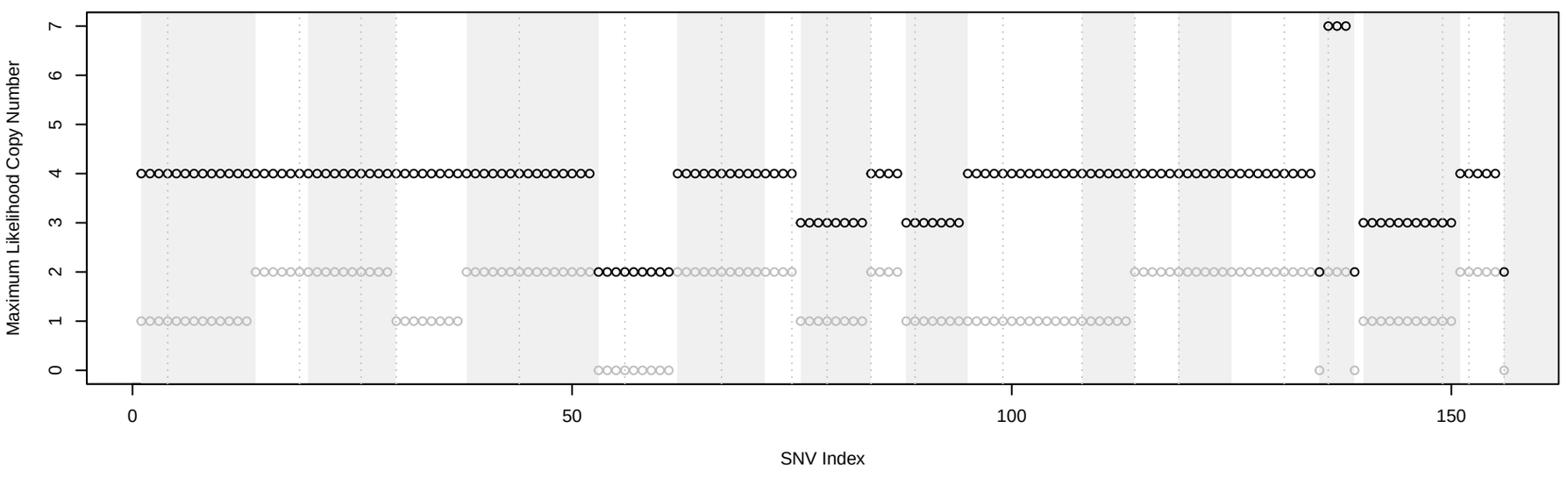

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1

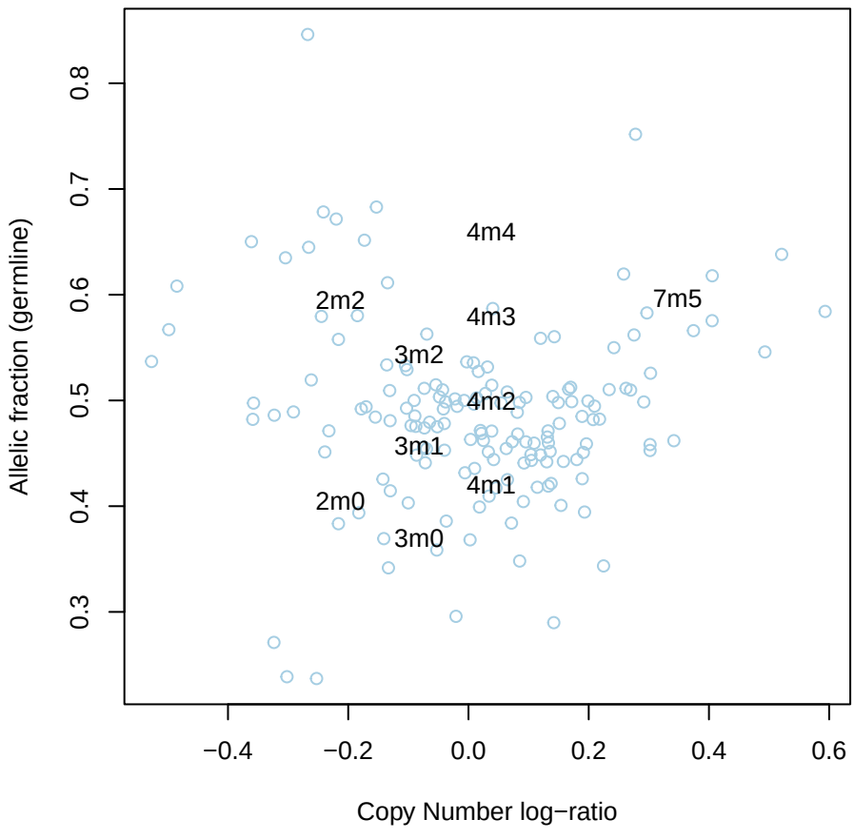

Power 0.8
Frequency
Cellular fraction

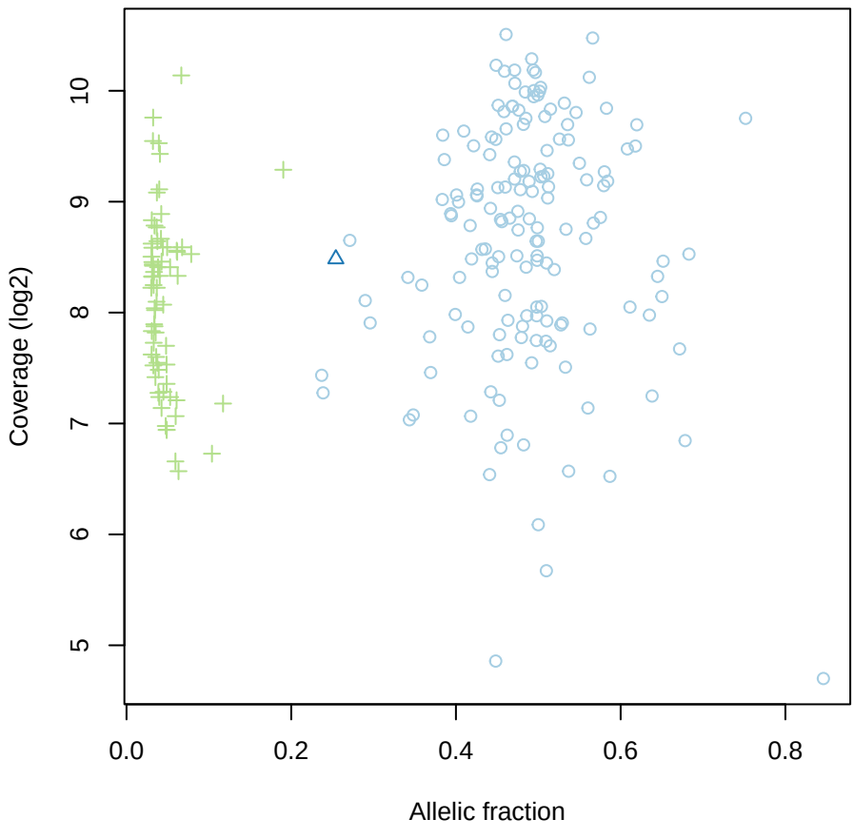

Purity: 0.19 Tumor ploidy: 3.675
0
1
2
3
4
5
7
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

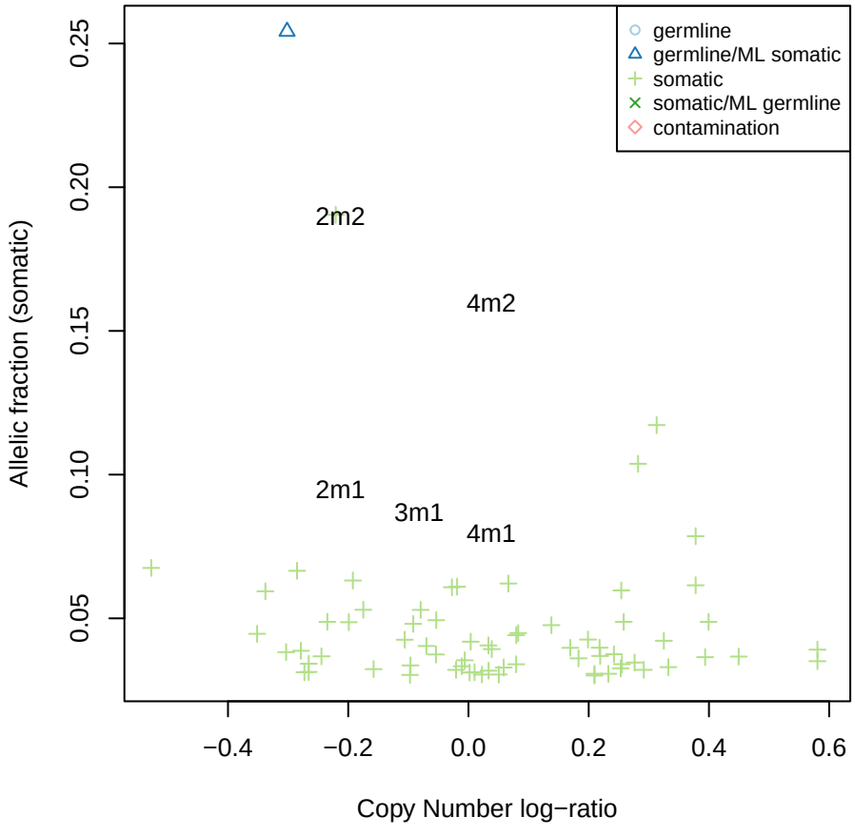

Purity: 0.19 Tumor ploidy: 3.675 SNV log−likelihood: −151.8 GoF: 92.9% Mean coverage: 558;453
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

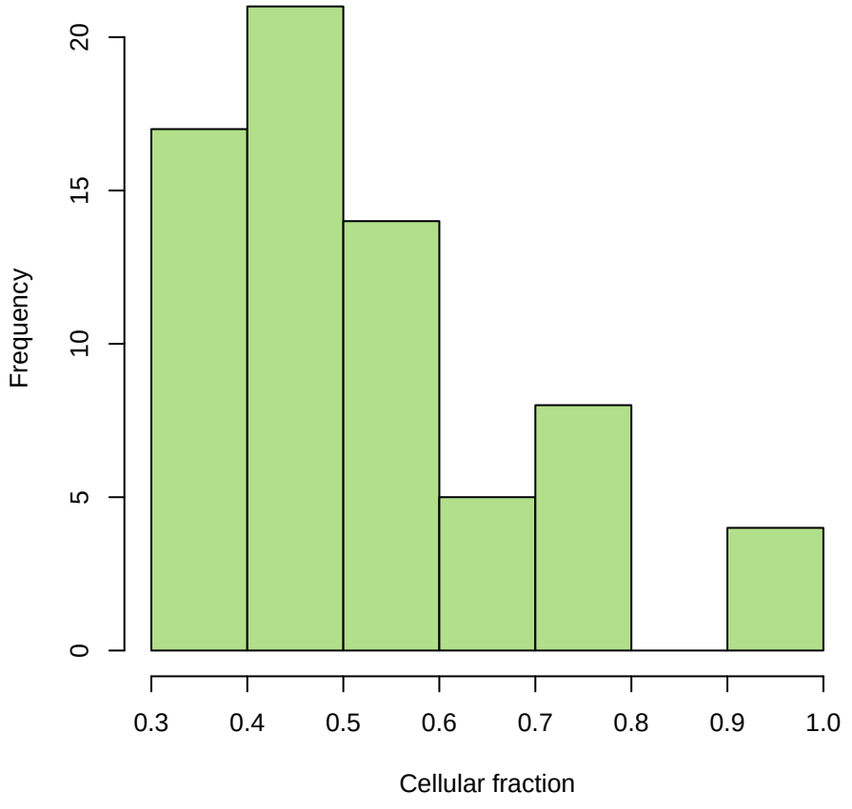

SCNA−fit log−likelihood: −13070.66
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 4 7
0 50 100 150
SNV Index

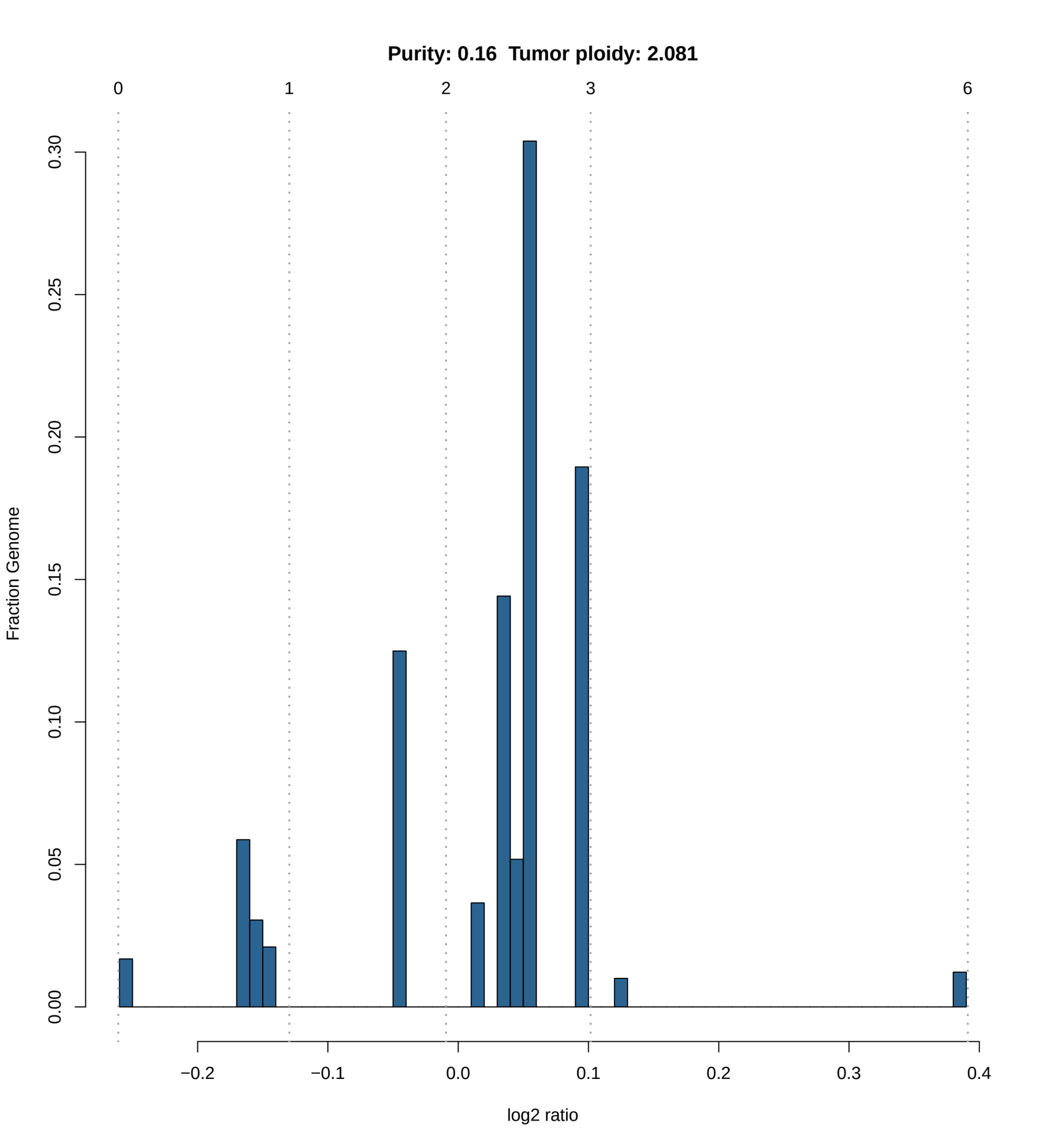

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

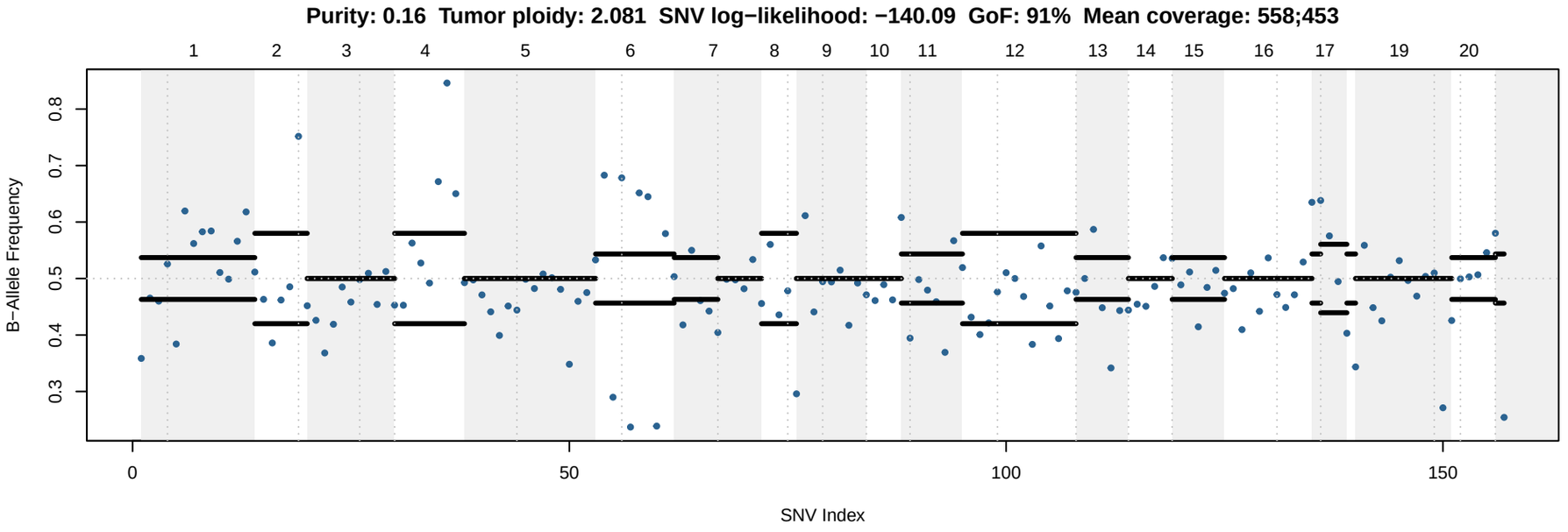

Allelic fraction (germline)
Copy Number log−ratio
4m4
2m2
7m5
4m3
3m2
4m2
3m1
4m1
2m0
3m0

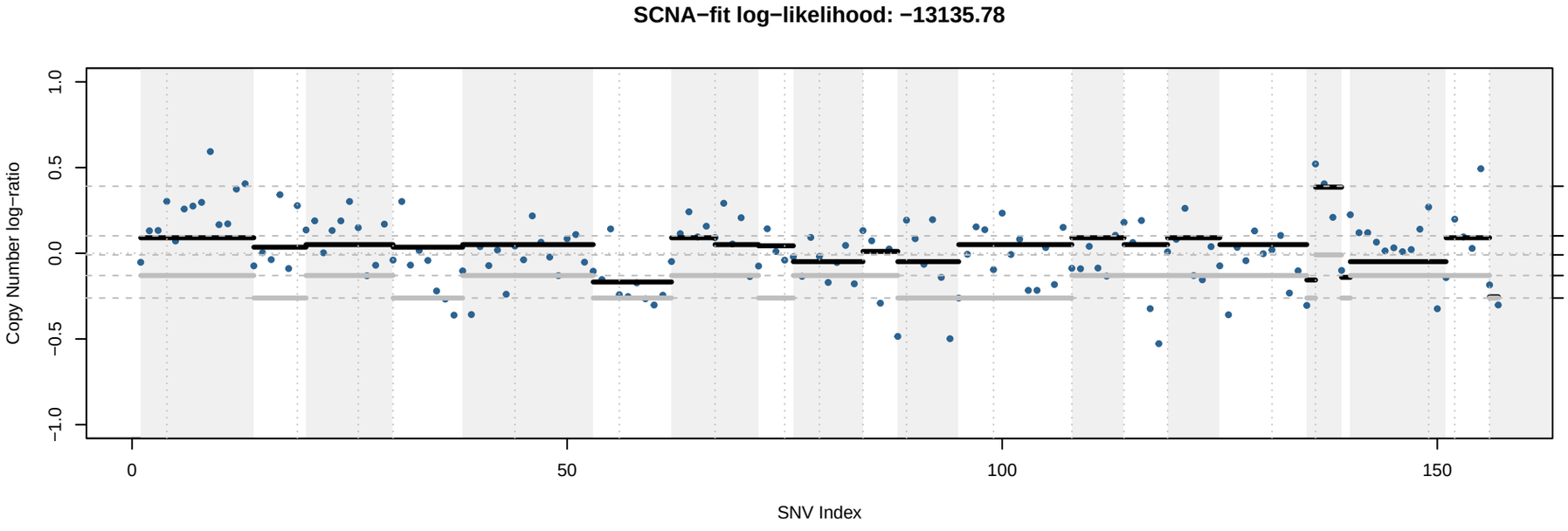

Coverage (log2)
Allelic fraction

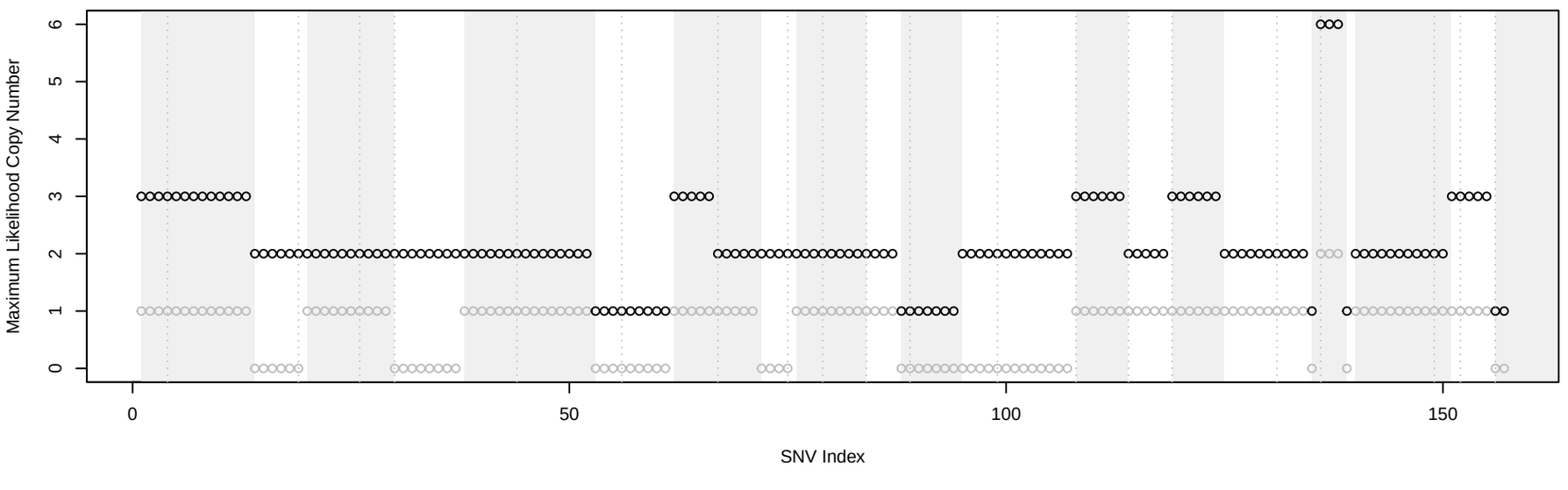

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m2
4m2
2m1
3m1
4m1

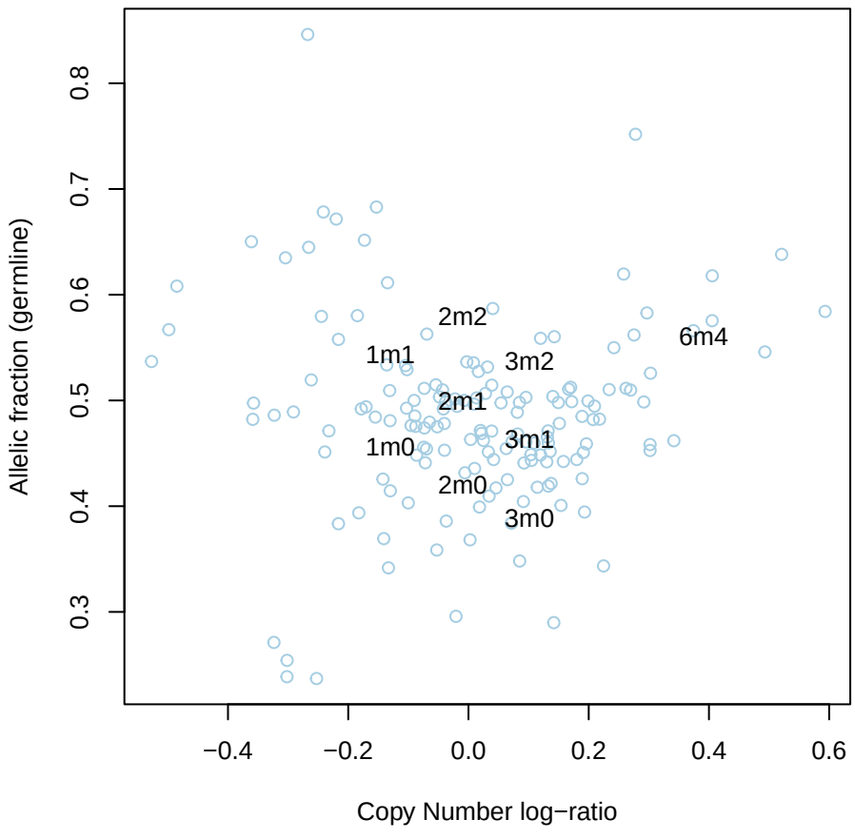

Frequency
Cellular fraction

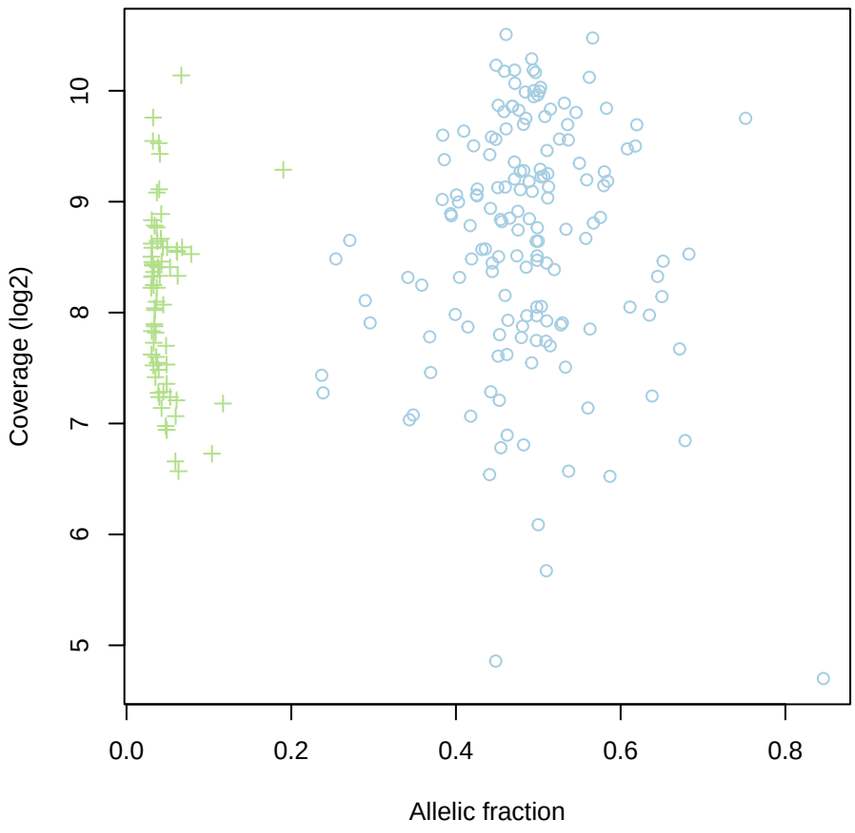

Purity: 0.16 Tumor ploidy: 2.081
0
1
2
3
6
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.2
−0.1
0.0
0.1
0.2
0.3
0.4
log2 ratio

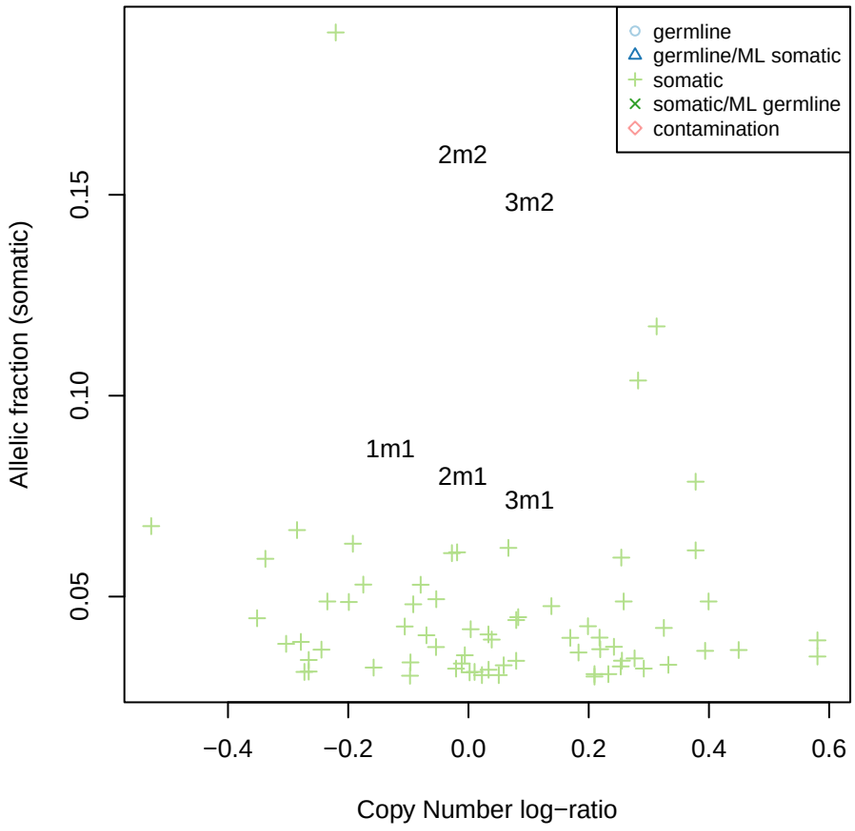

Purity: 0.16 Tumor ploidy: 2.081 SNV log−likelihood: −140.09 GoF: 91% Mean coverage: 558;453
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

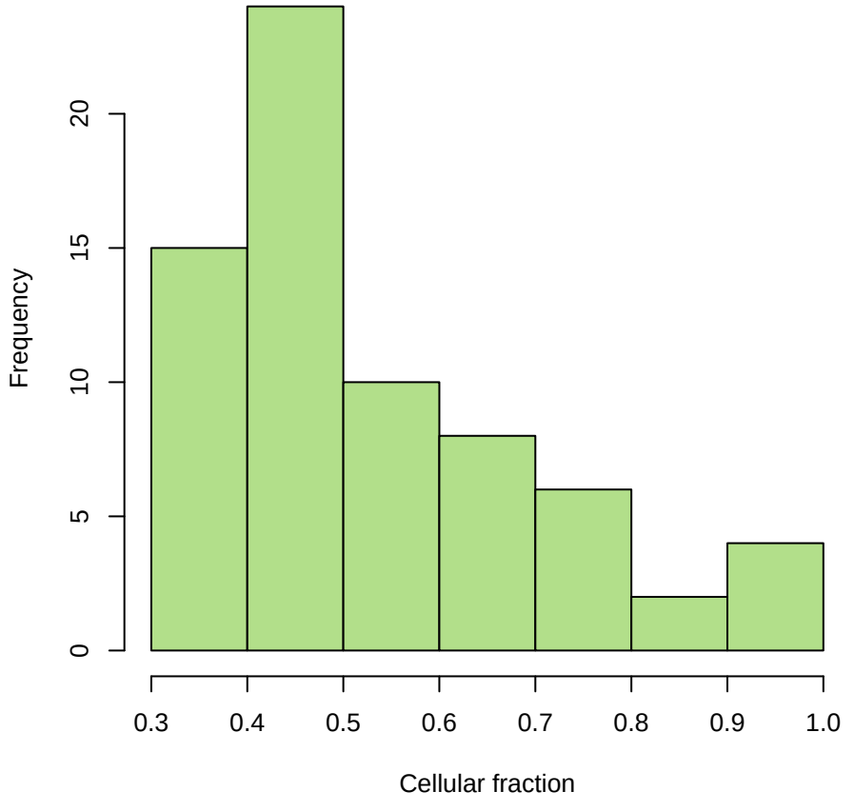

SCNA−fit log−likelihood: −13135.78
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 6
0 50 100 150
SNV Index

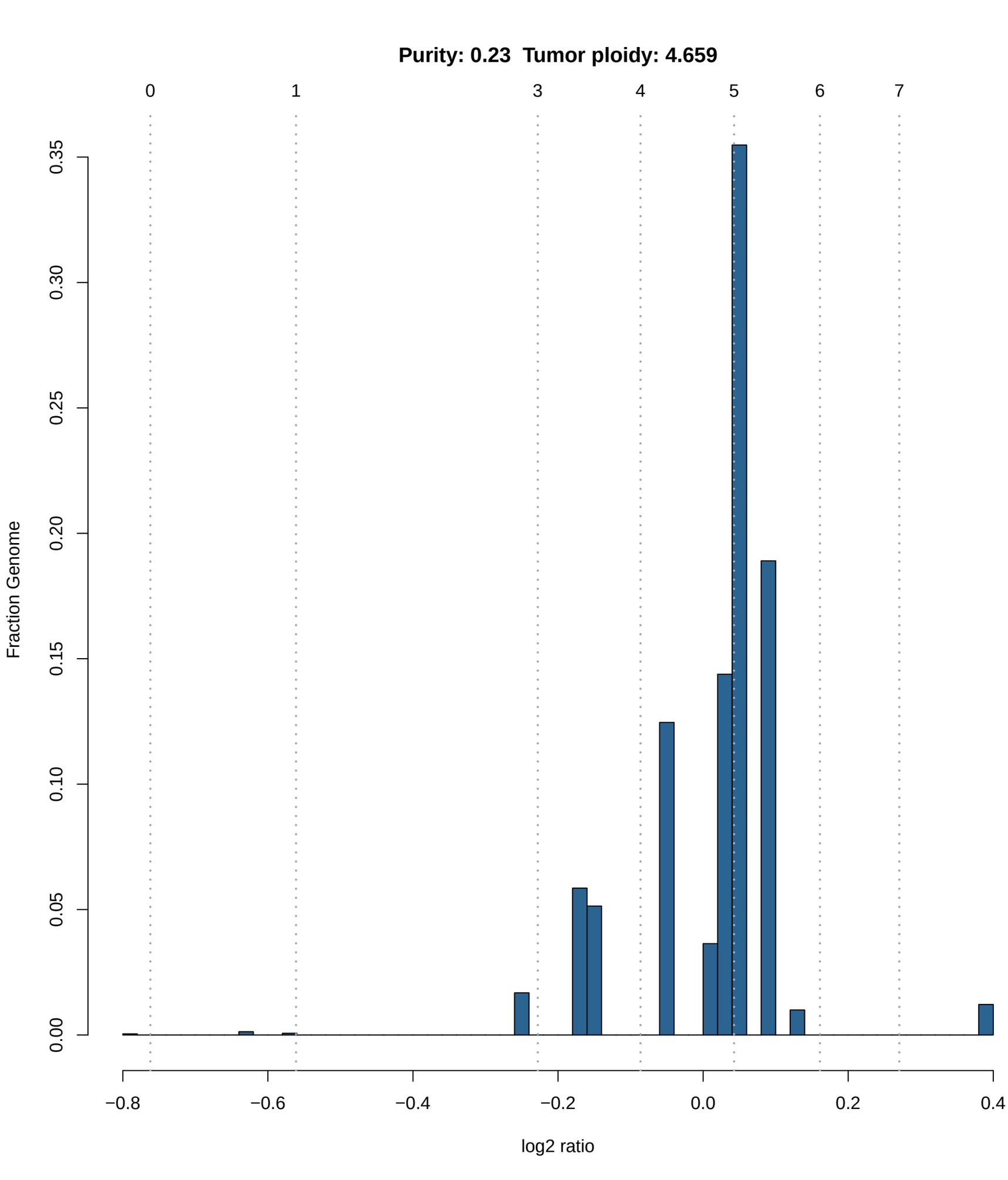

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

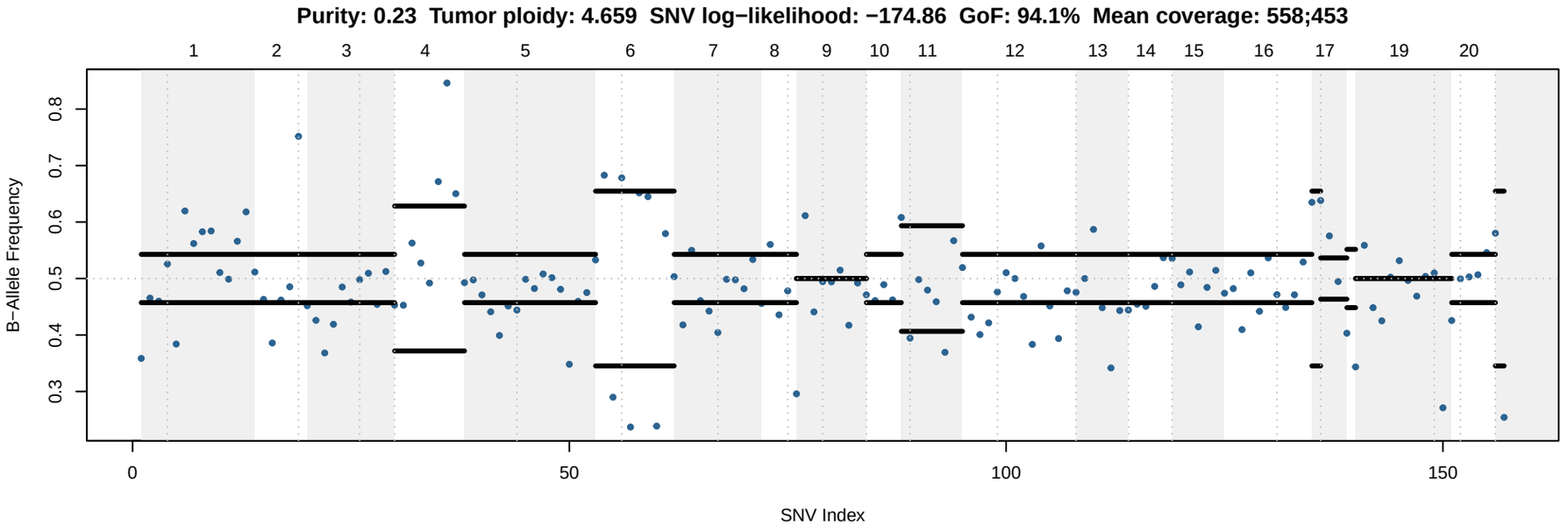

Allelic fraction (germline)
Copy Number log−ratio
2m2
6m4
1m1
3m2
2m1
3m1
1m0
2m0
3m0

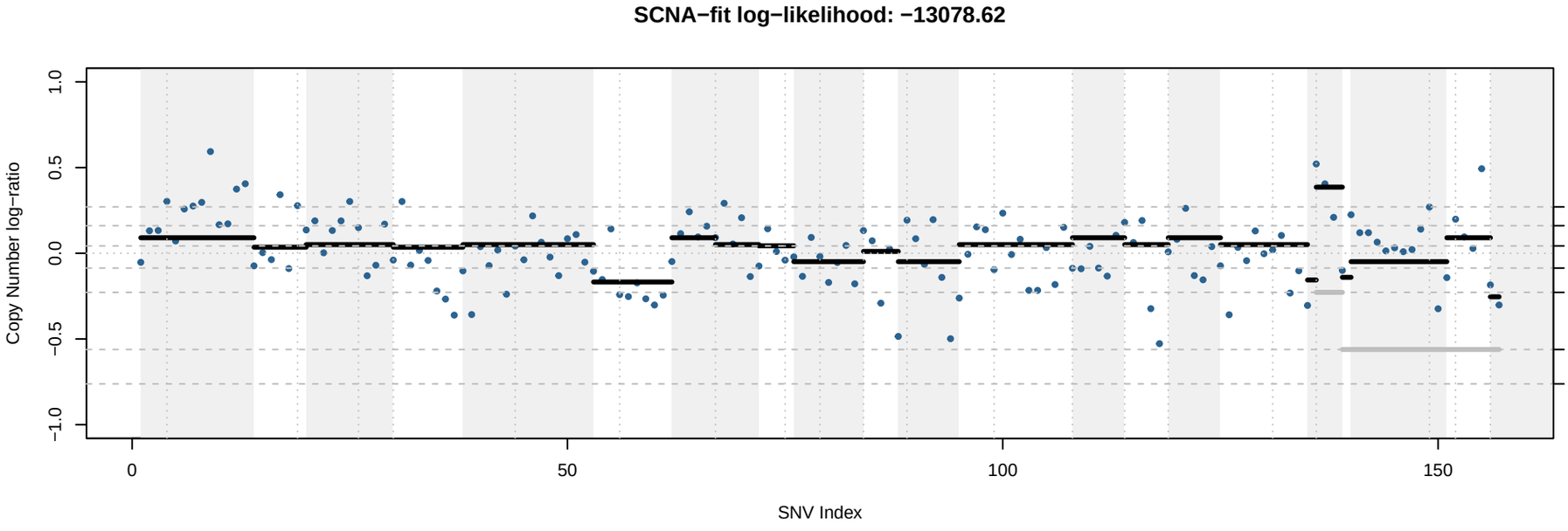

Coverage (log2)
Allelic fraction

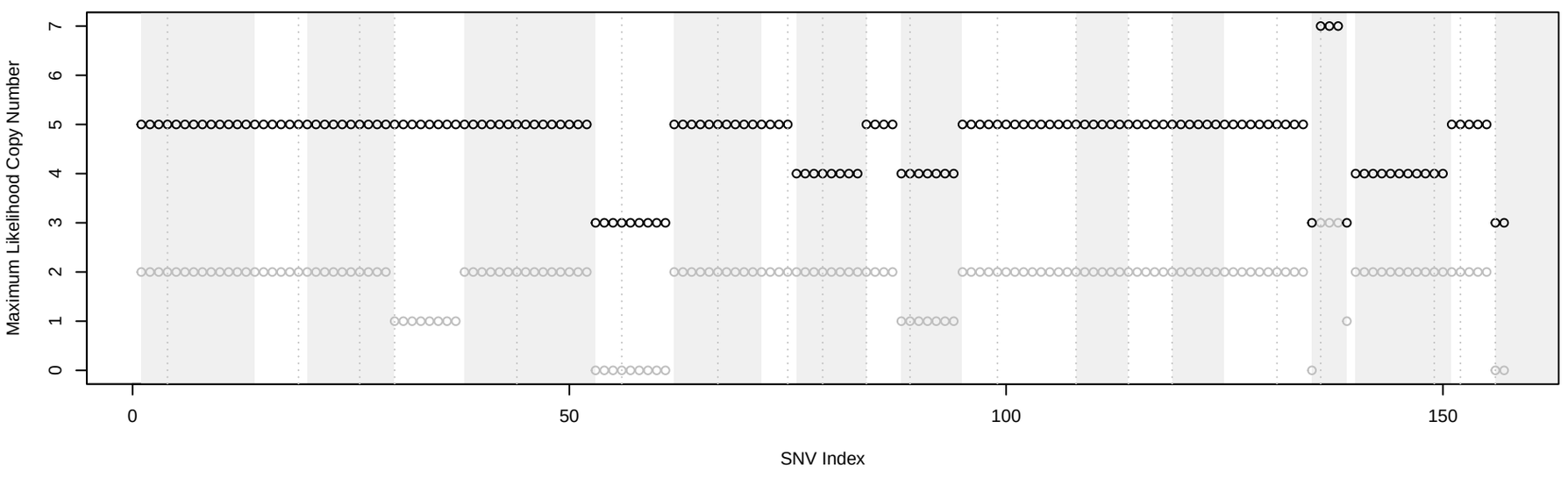

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m2
3m2
1m1
2m1
3m1

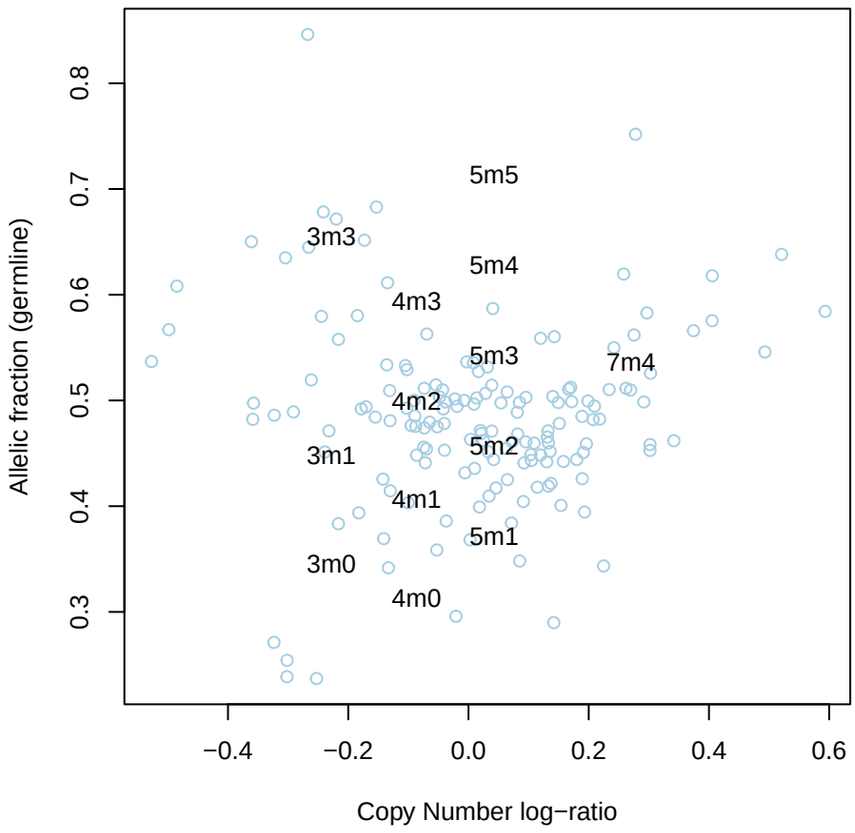

Frequency
Cellular fraction

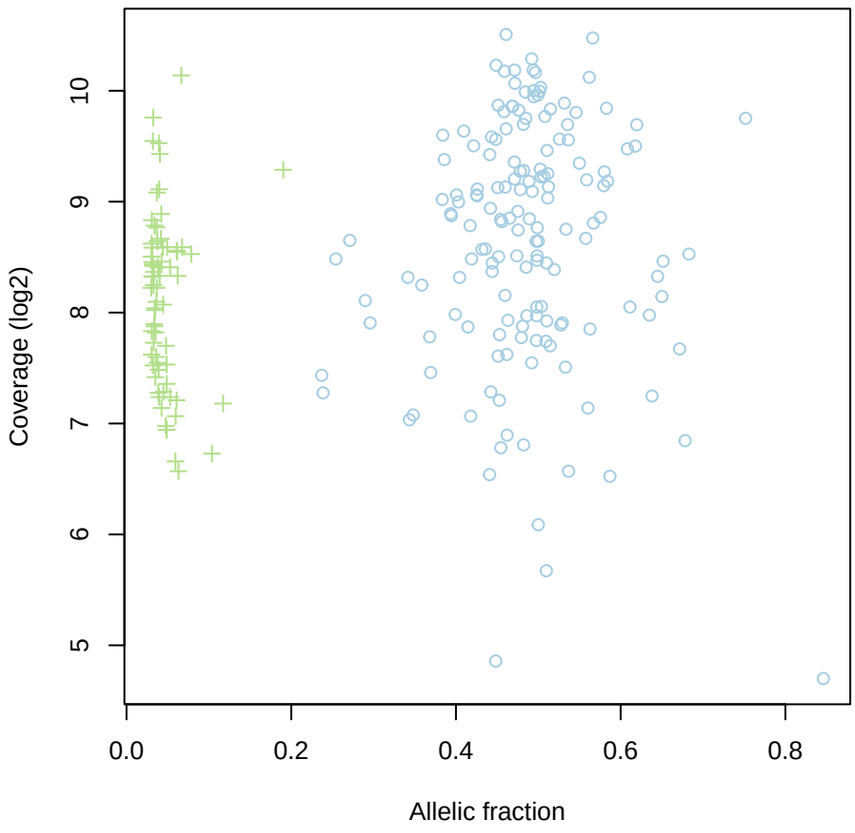

Purity: 0.23 Tumor ploidy: 4.659
0
1
3
4
5
6
7
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

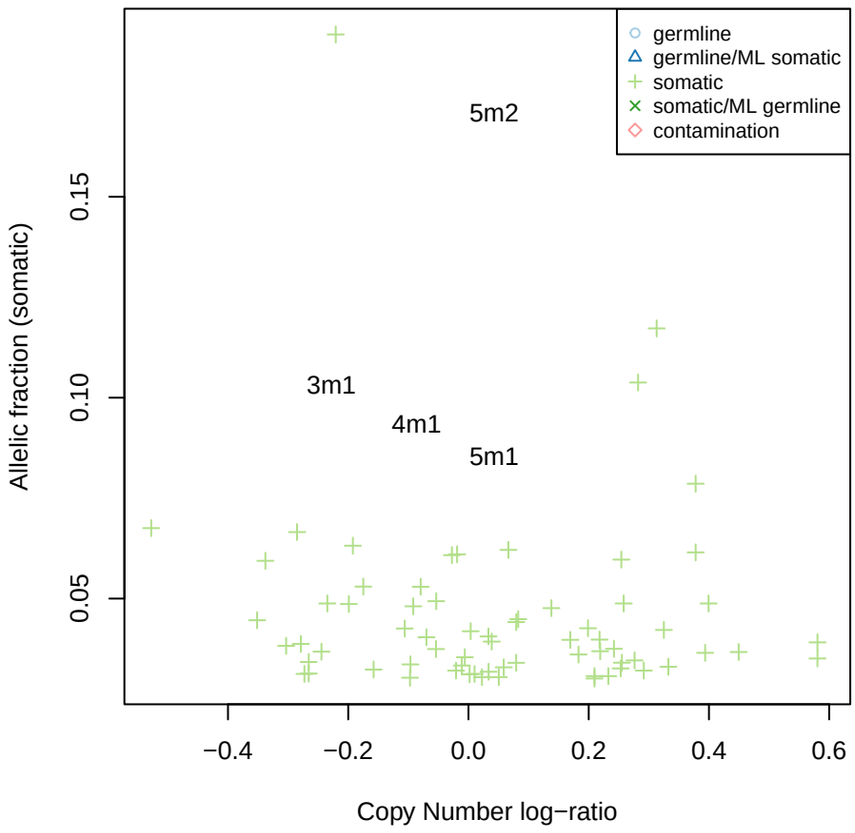

Purity: 0.23 Tumor ploidy: 4.659 SNV log−likelihood: −174.86 GoF: 94.1% Mean coverage: 558;453
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

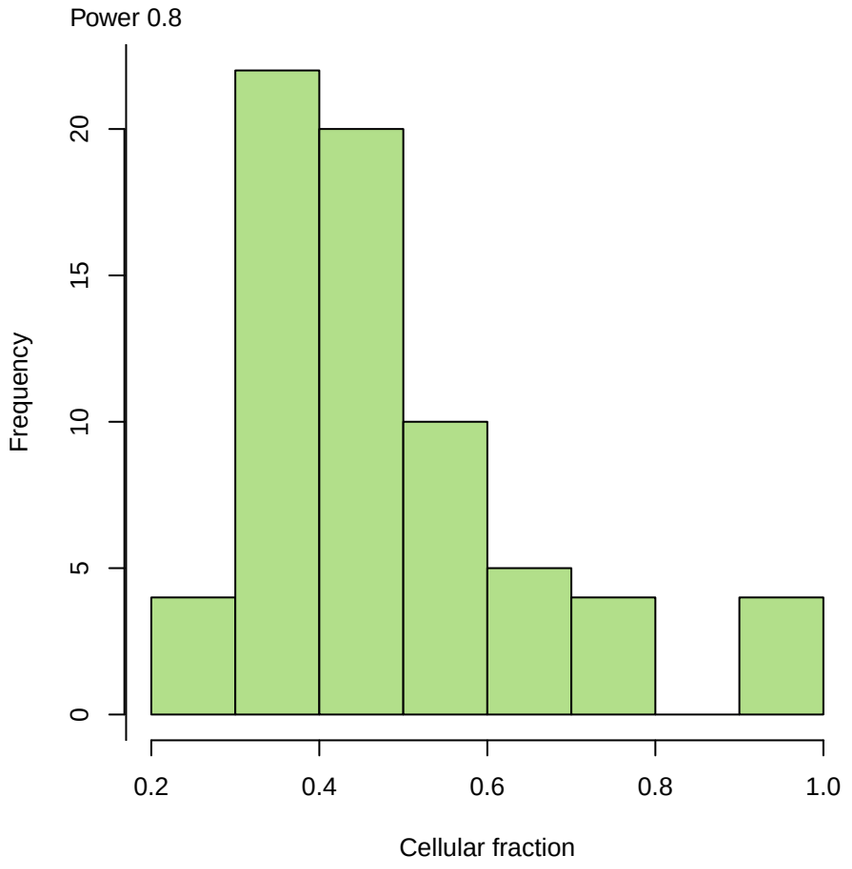

SCNA−fit log−likelihood: −13078.62
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 3 5 7
0 50 100 150
SNV Index

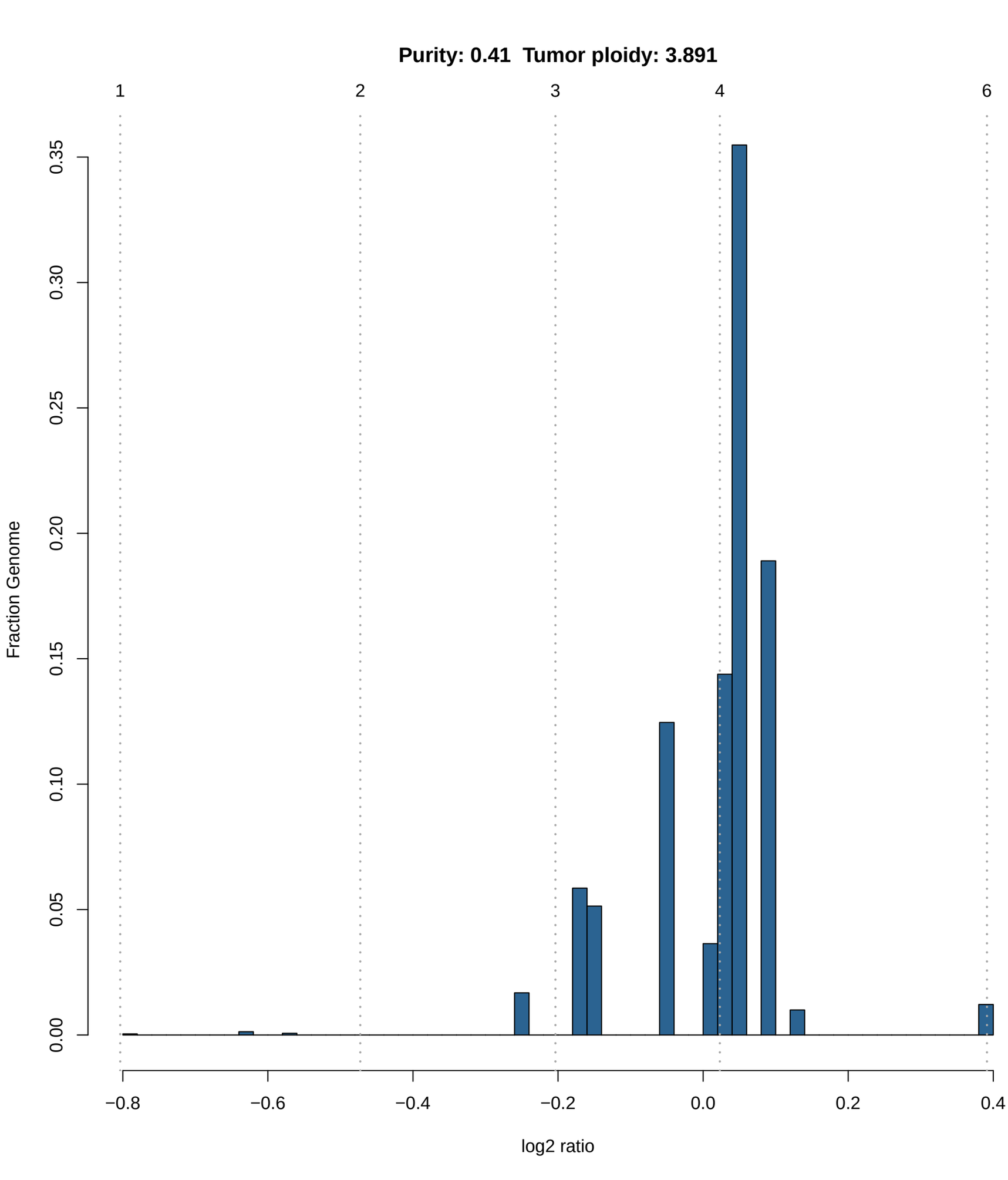

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

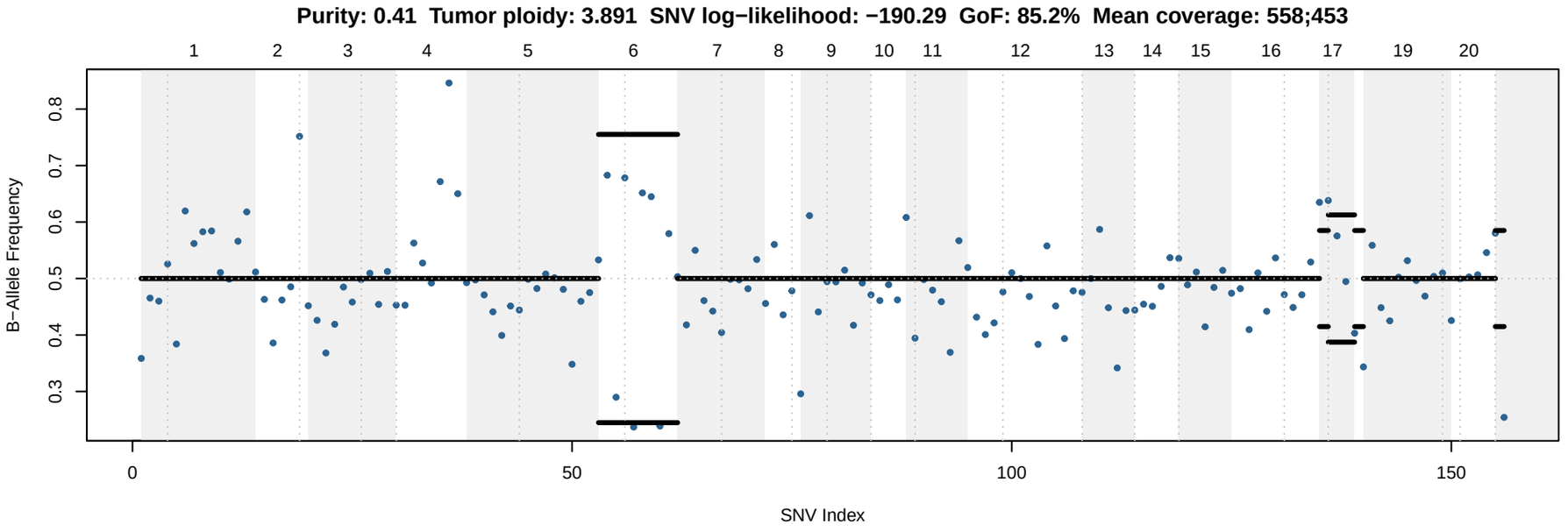

Allelic fraction (germline)
Copy Number log−ratio
5m5
3m3
5m4
4m3
5m3
7m4
4m2
5m2
3m1
4m1
5m1
3m0
4m0

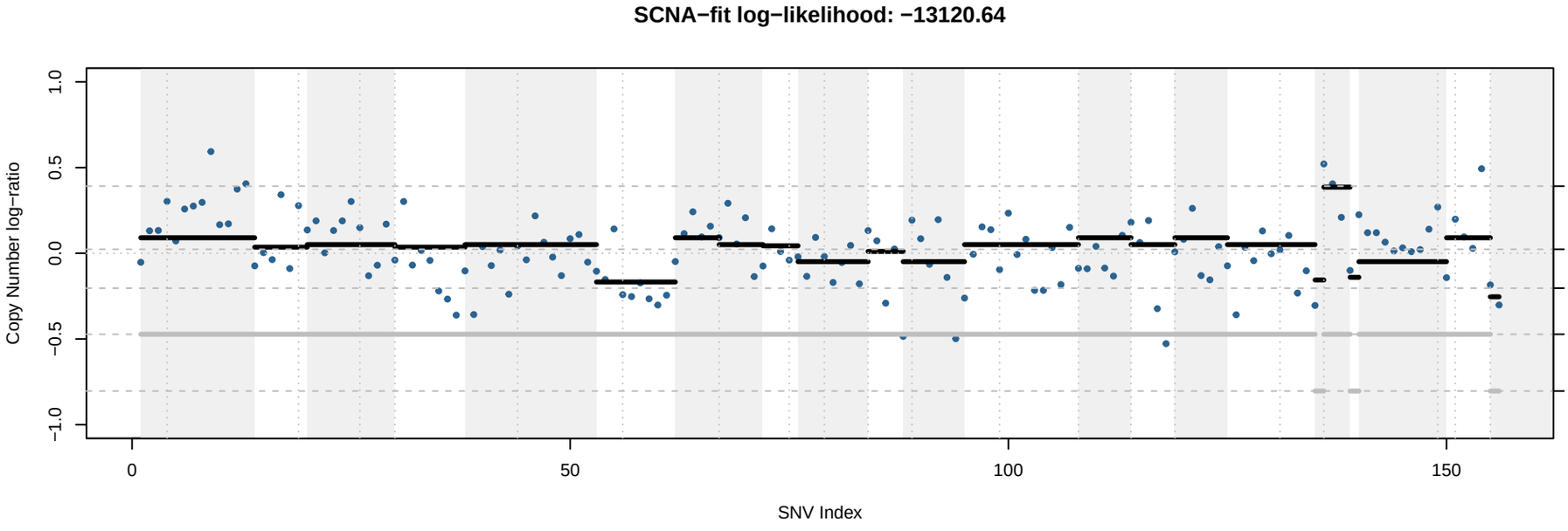

Coverage (log2)
Allelic fraction

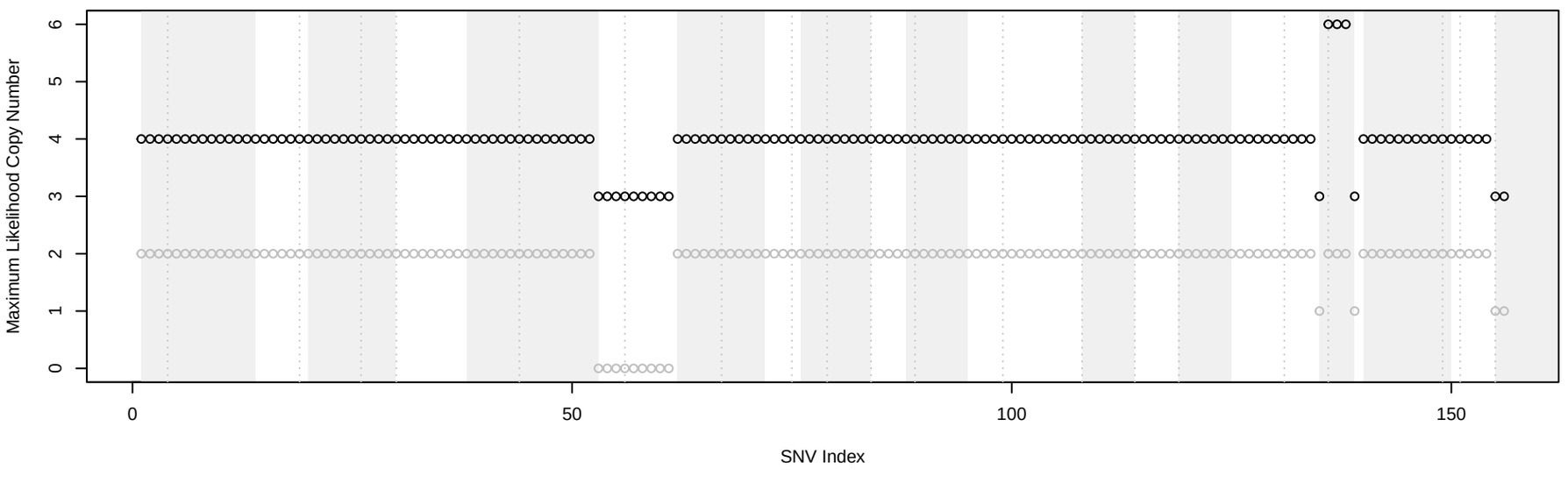

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
5m2
3m1
4m1
5m1

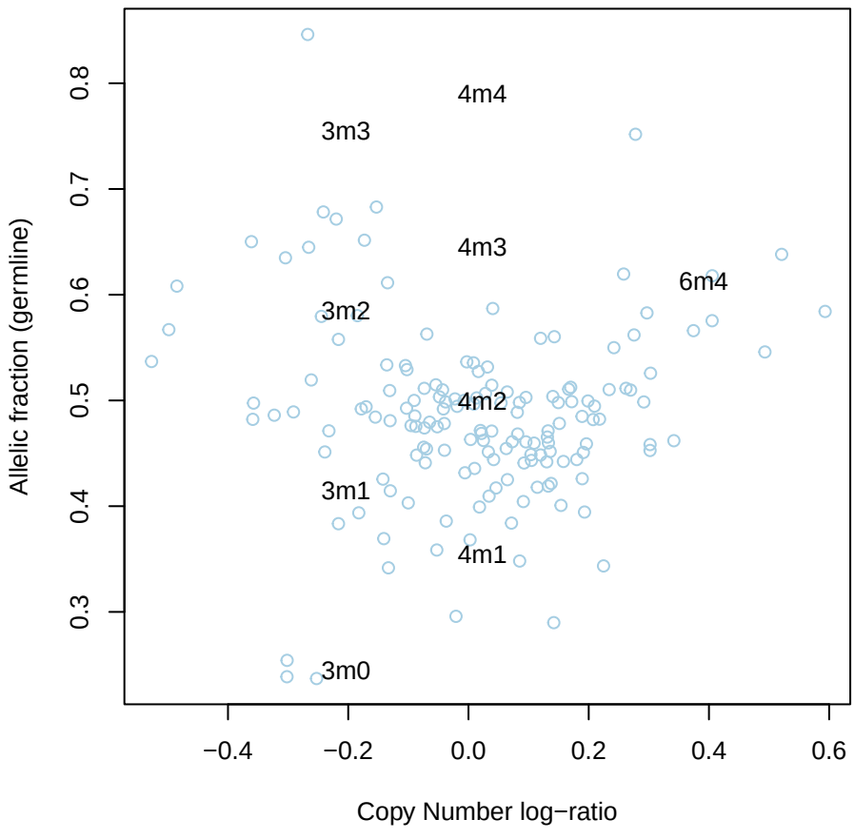

Power 0.8
Frequency
Cellular fraction

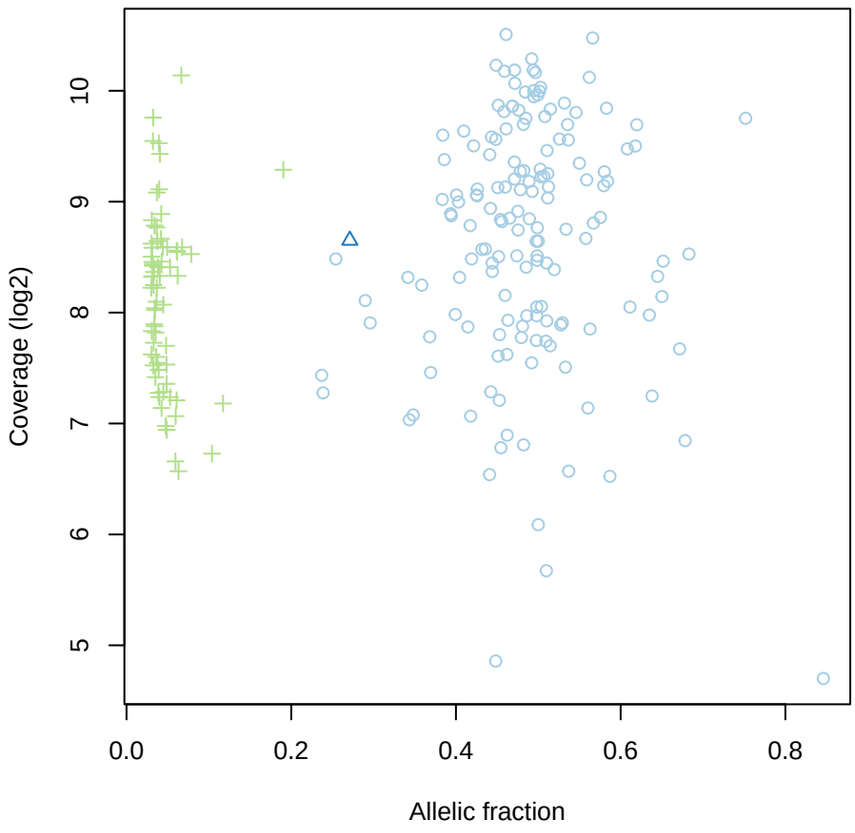

Purity: 0.41 Tumor ploidy: 3.891
1
2
3
4
6
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

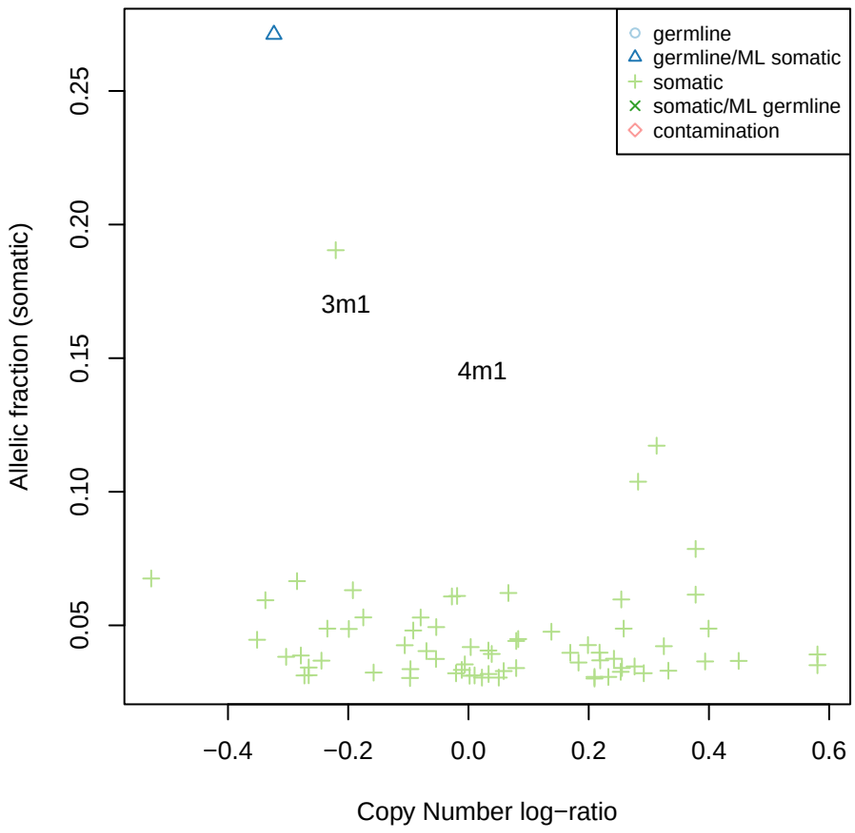

Purity: 0.41 Tumor ploidy: 3.891 SNV log−likelihood: −190.29 GoF: 85.2% Mean coverage: 558;453
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

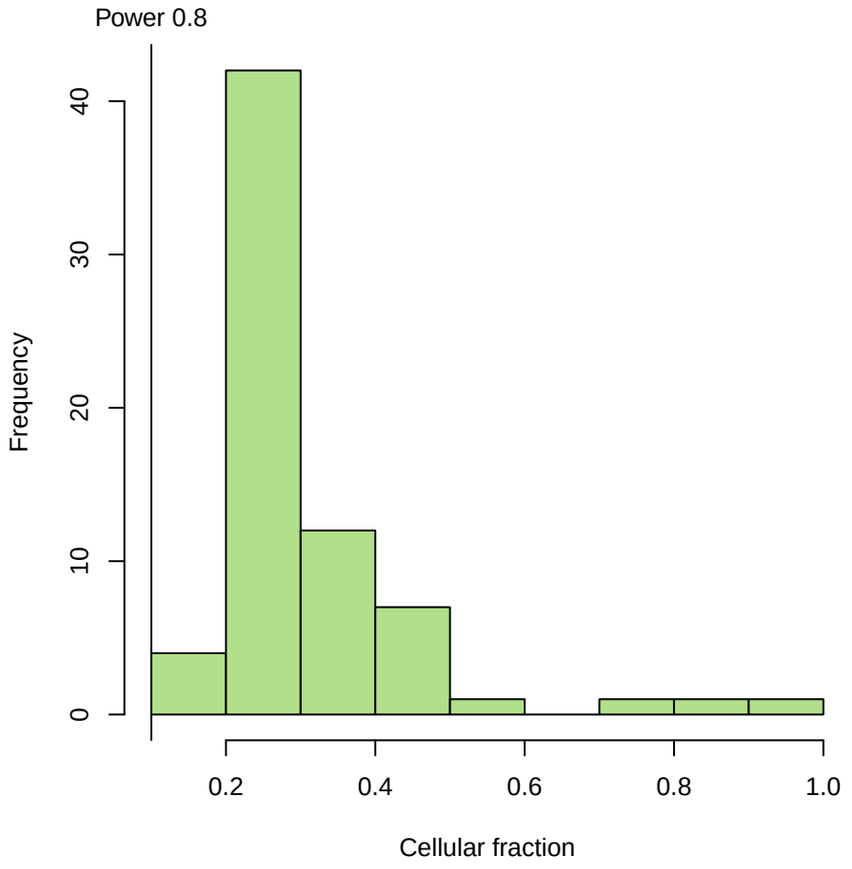

SCNA−fit log−likelihood: −13120.64
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 6
0 50 100 150
SNV Index

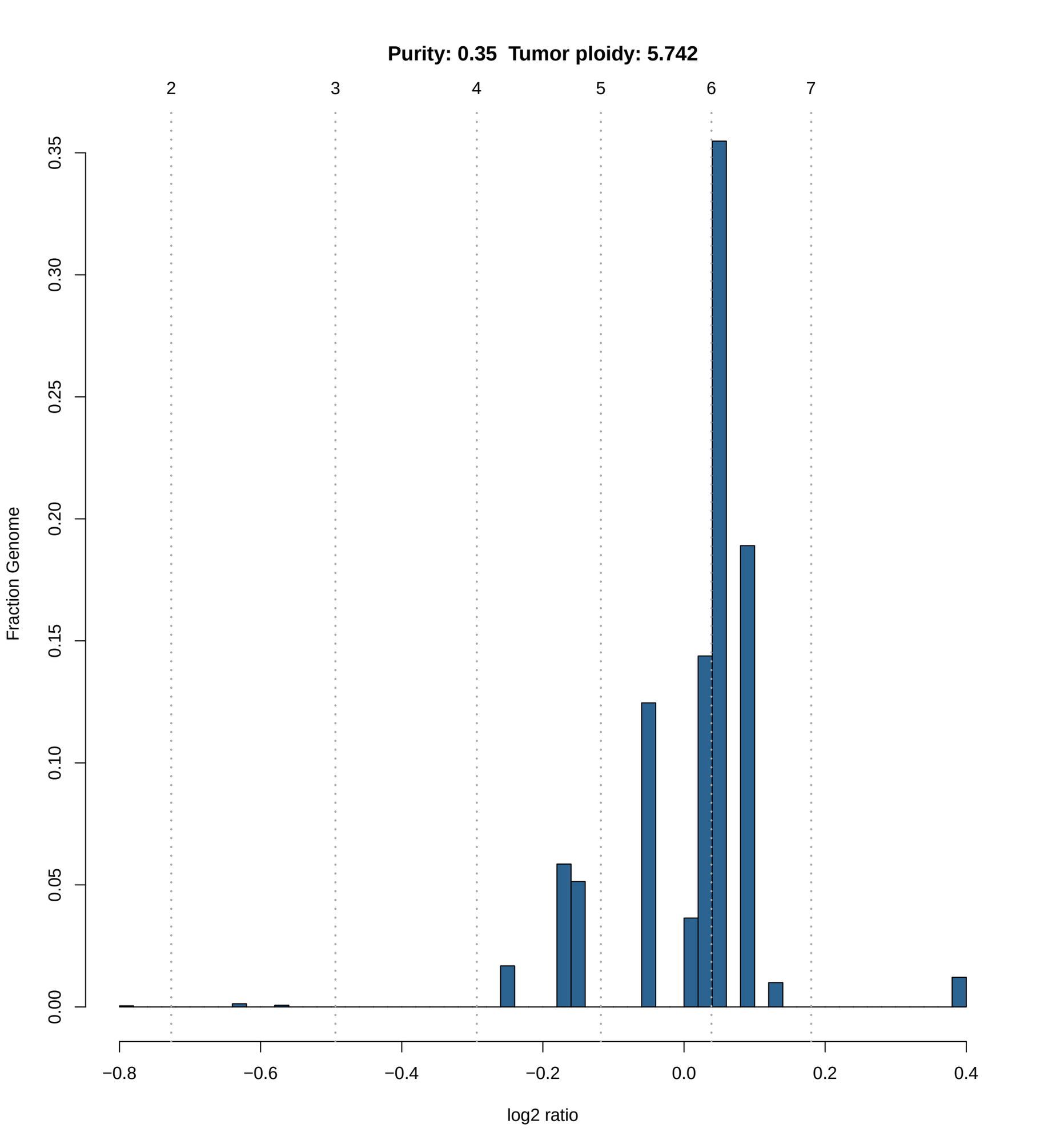

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

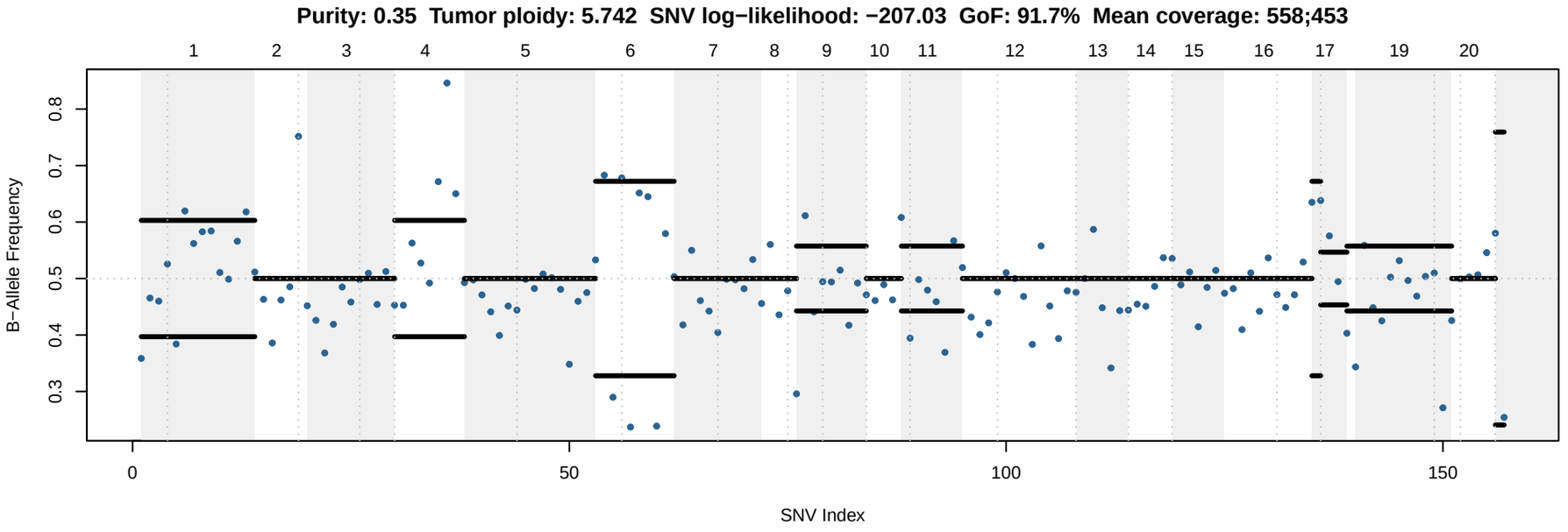

Allelic fraction (germline)
Copy Number log−ratio
4m4
3m3
4m3
6m4
3m2
4m2
3m1
4m1
3m0

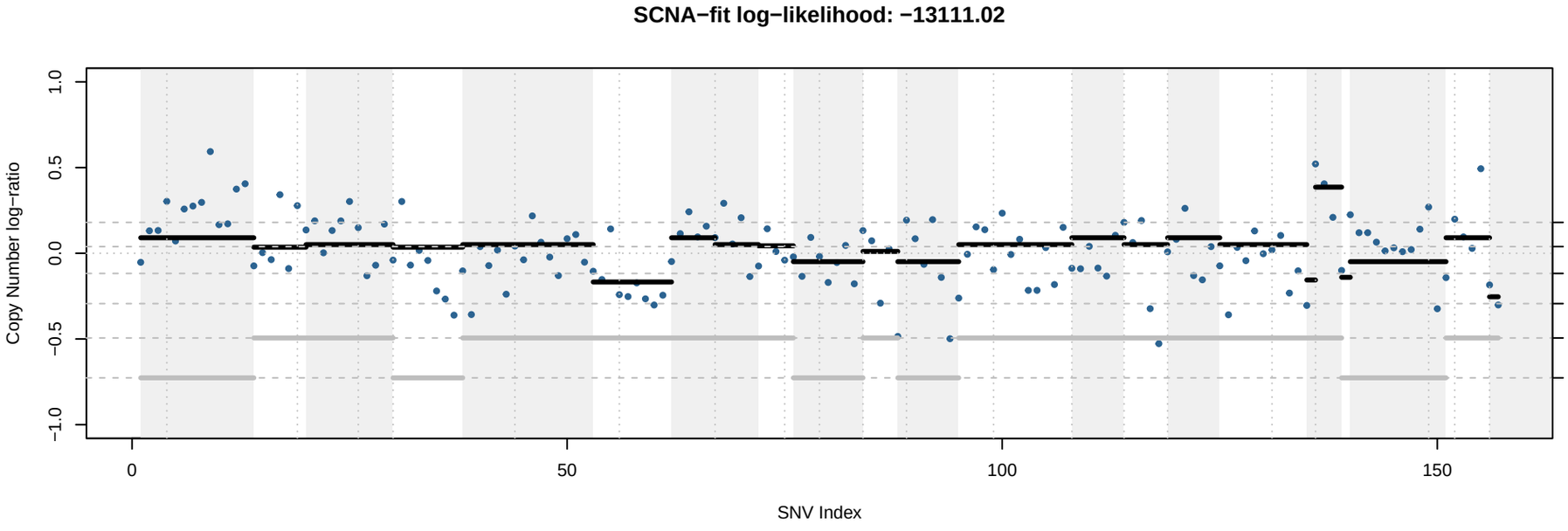

Coverage (log2)
Allelic fraction

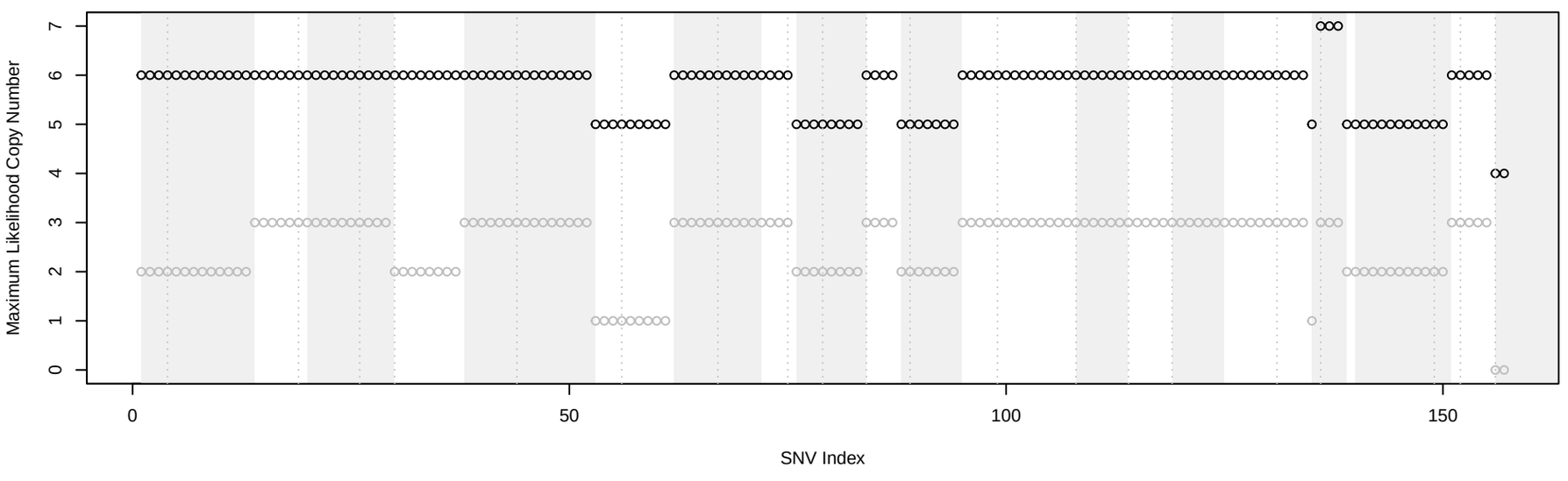

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m1
4m1

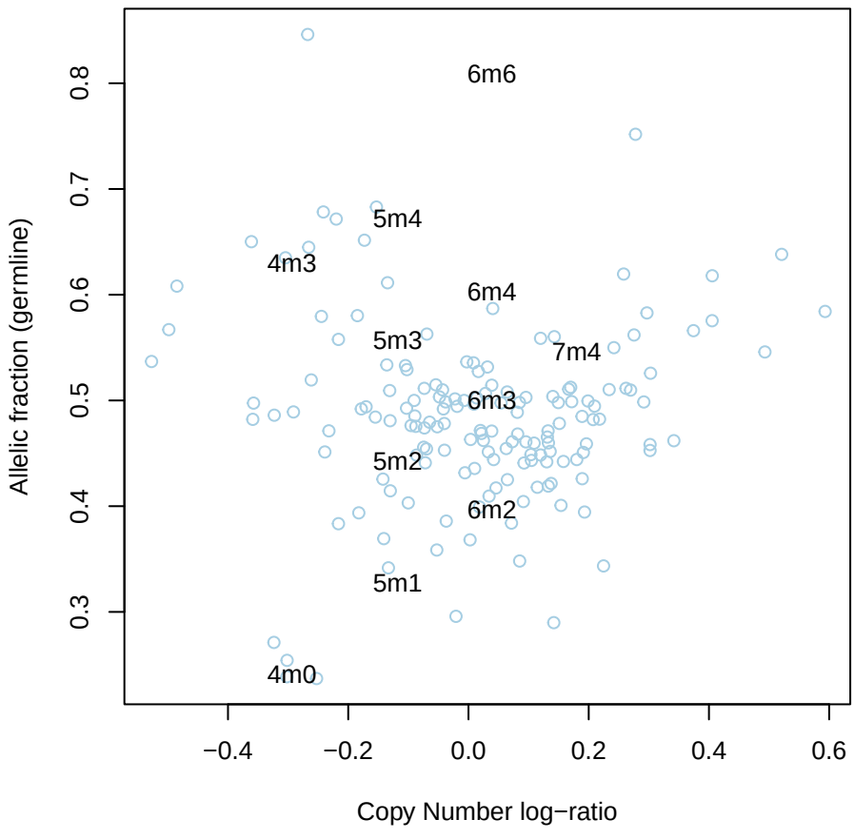

Power 0.8
Frequency
Cellular fraction

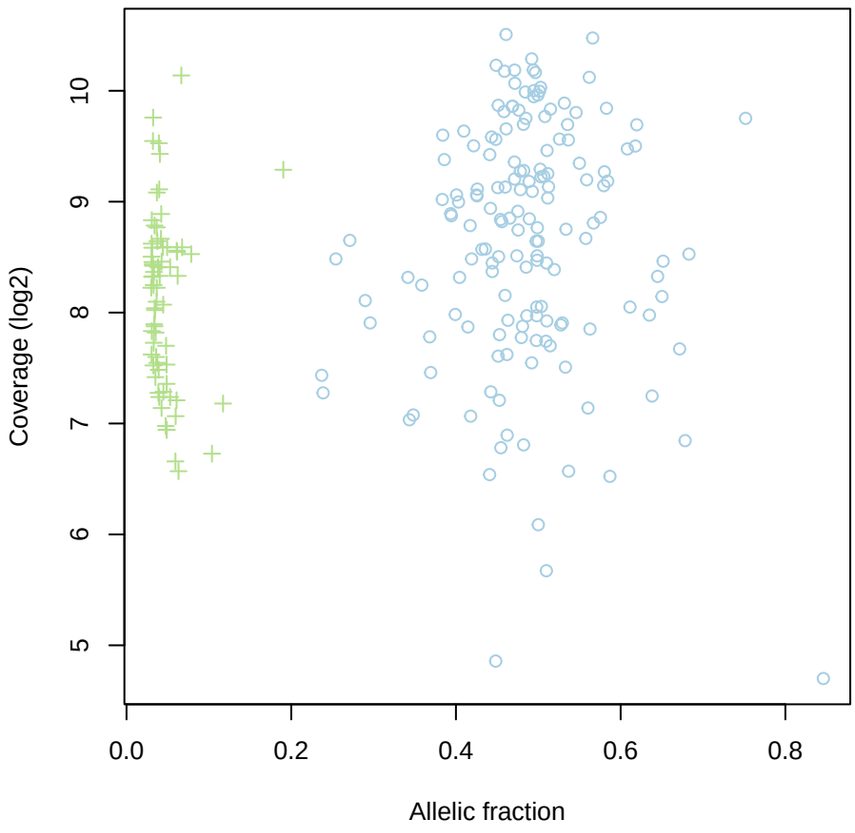

Purity: 0.35 Tumor ploidy: 5.742
2
3
4
5
6
7
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

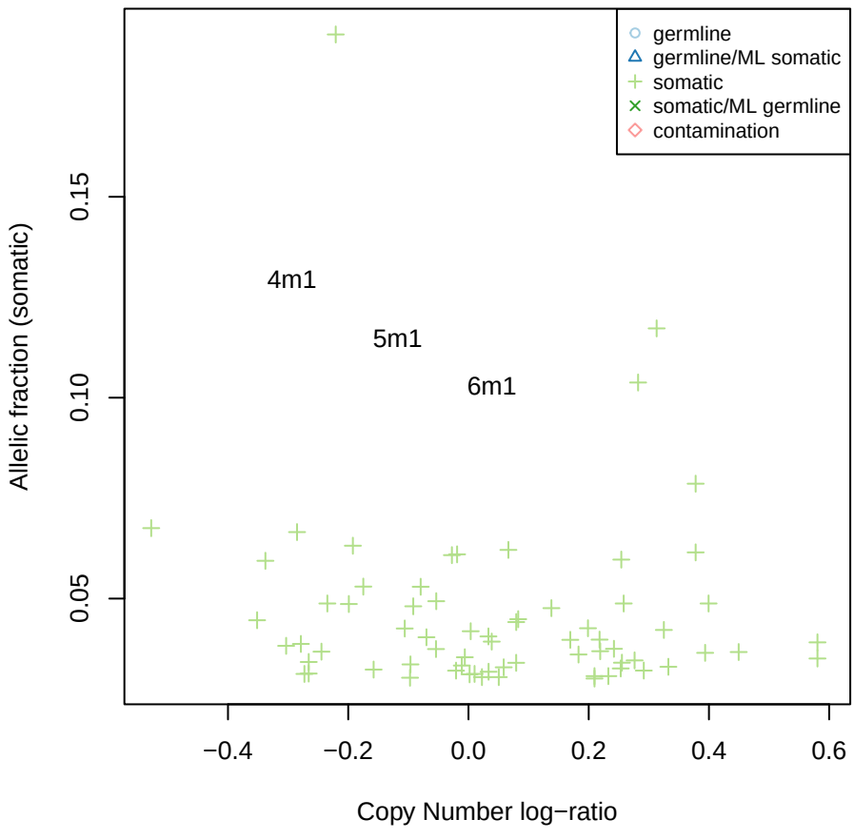

Purity: 0.35 Tumor ploidy: 5.742 SNV log−likelihood: −207.03 GoF: 91.7% Mean coverage: 558;453
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

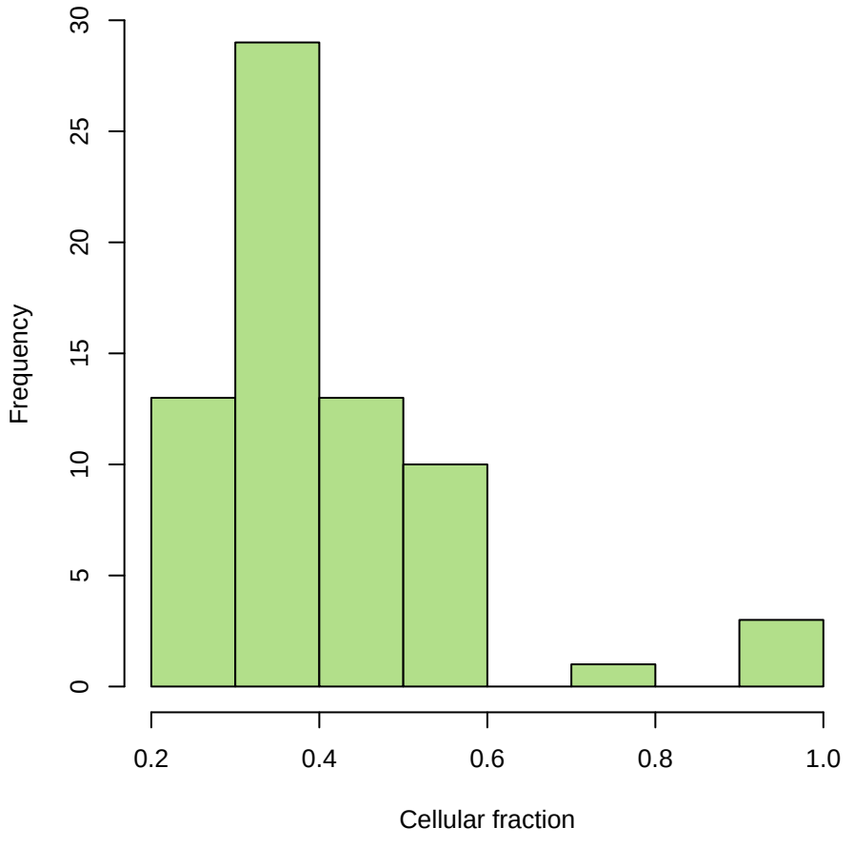

SCNA−fit log−likelihood: −13111.02
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6
0 50 100 150
SNV Index

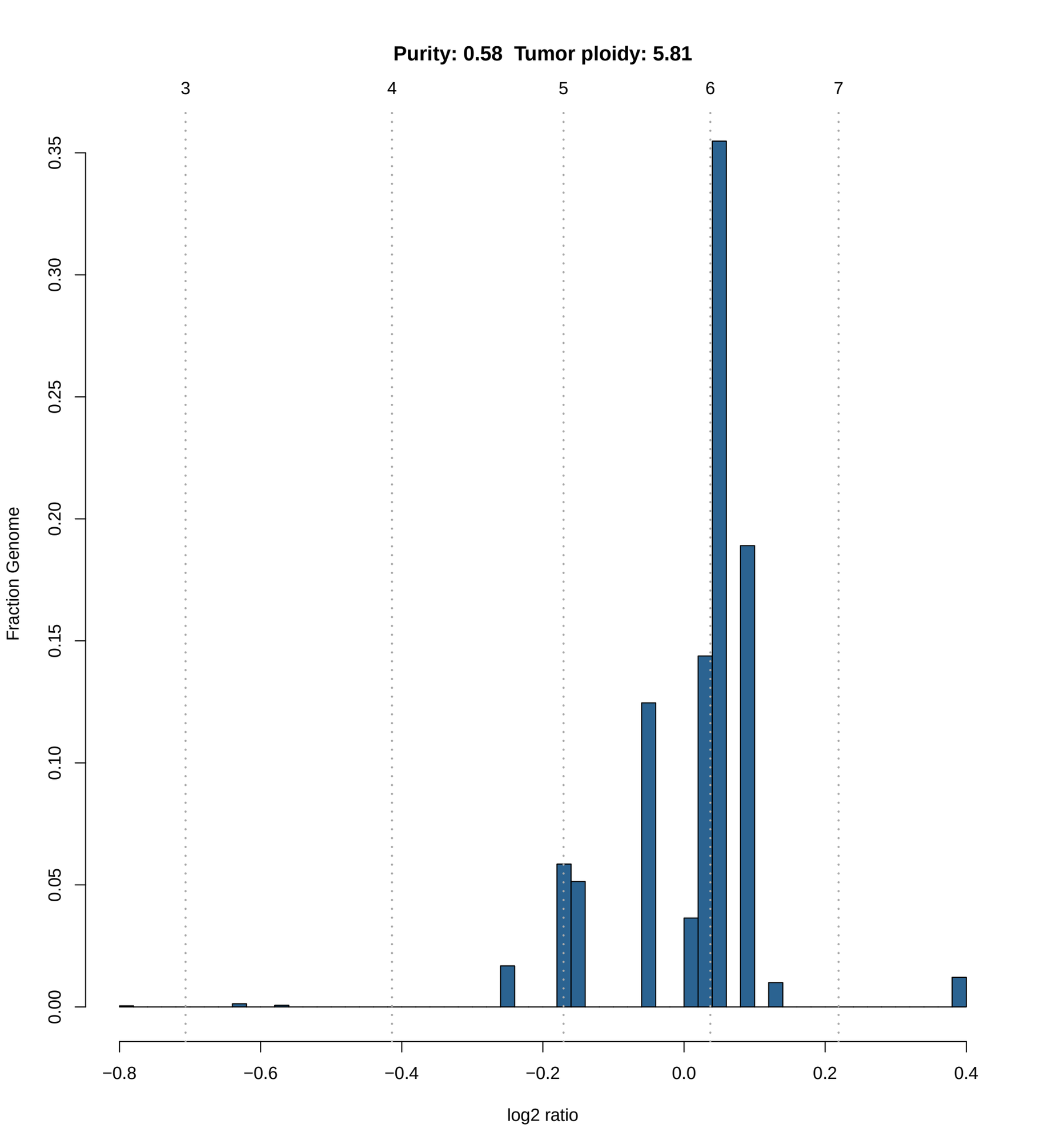

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

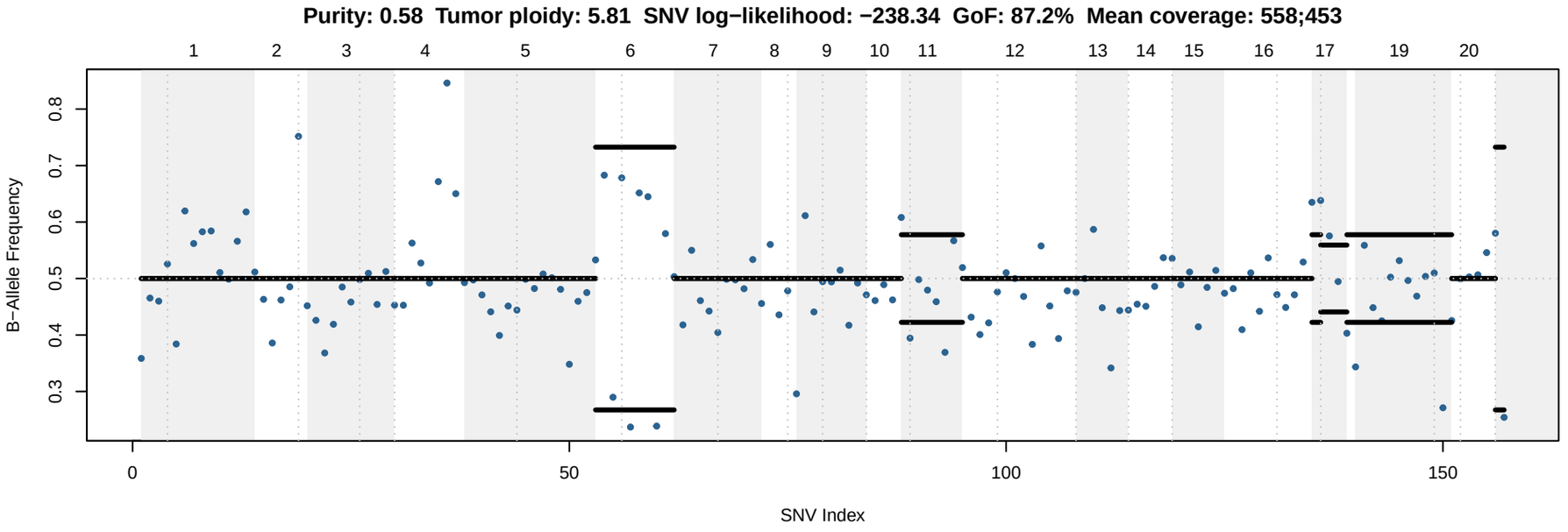

Allelic fraction (germline)
Copy Number log−ratio
6m6
5m4
4m3
6m4
5m3
7m4
6m3
5m2
6m2
5m1
4m0

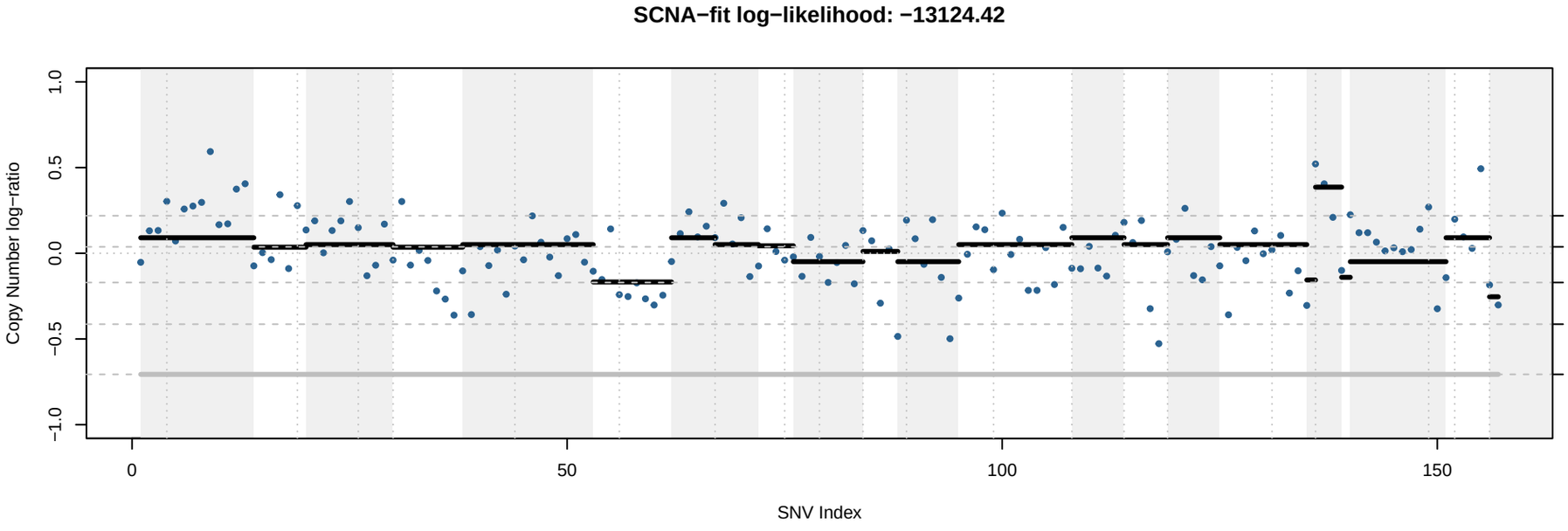

Coverage (log2)
Allelic fraction

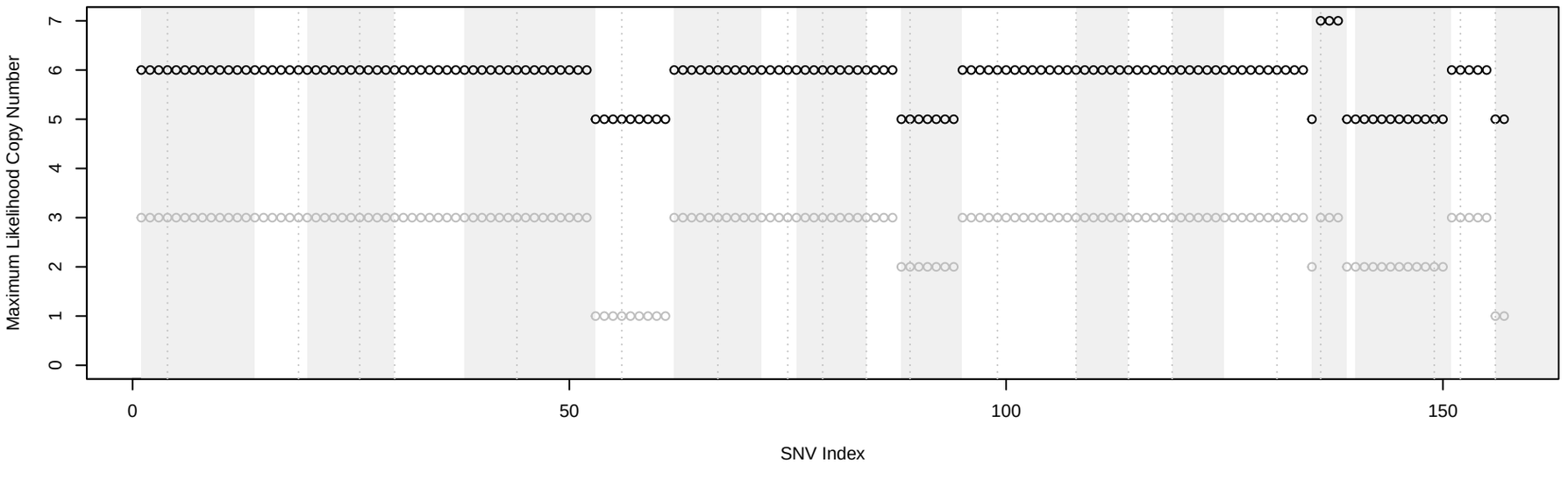

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
4m1
5m1
6m1

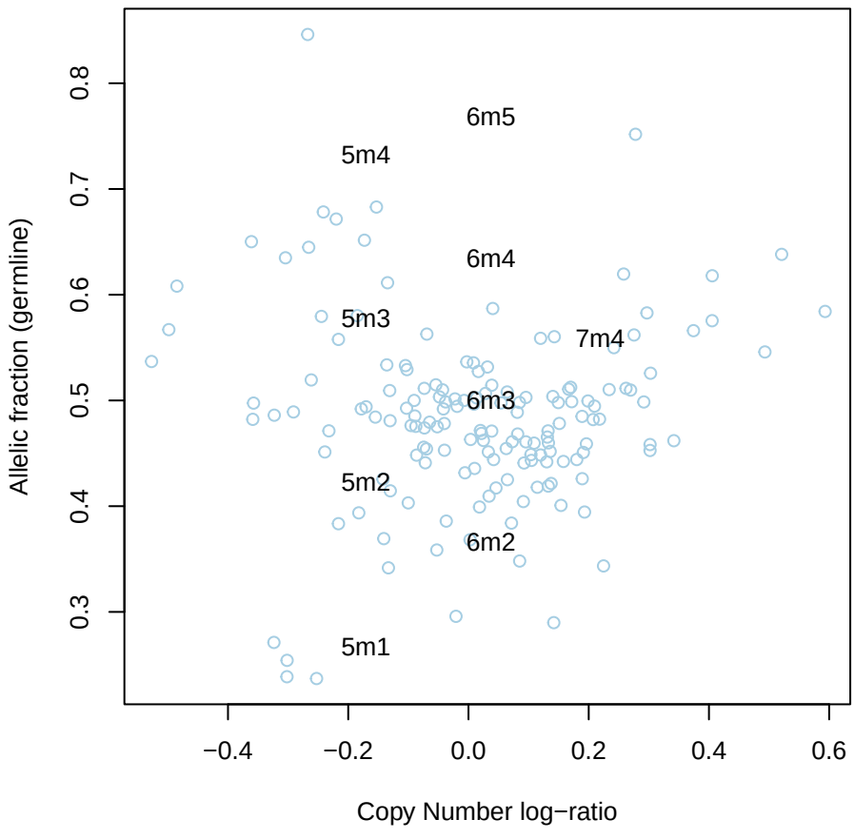

Frequency
Cellular fraction

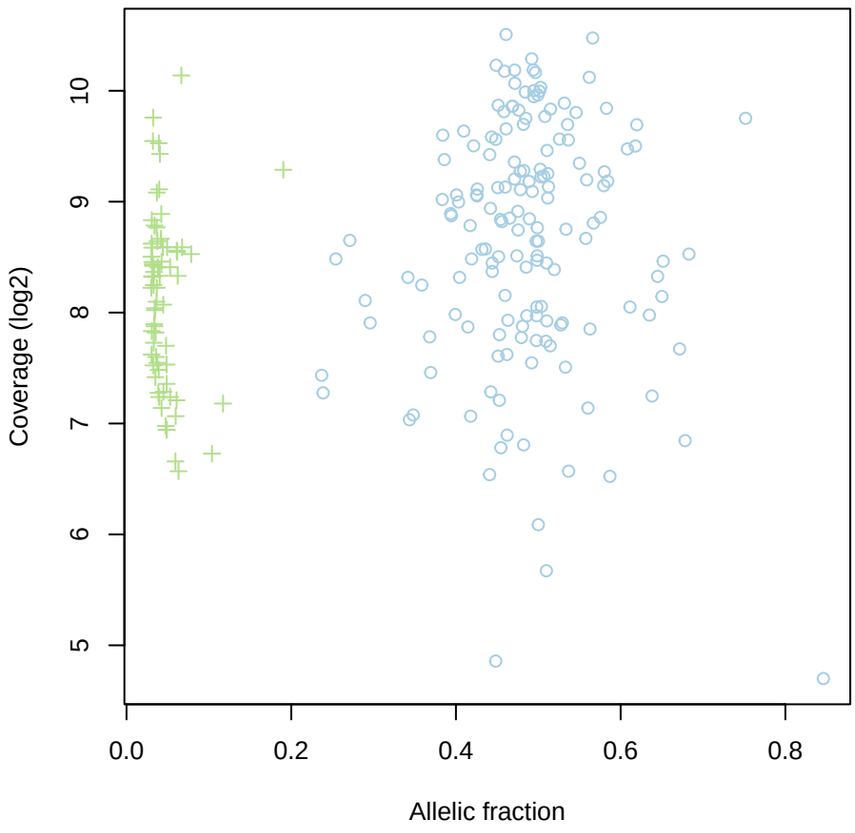

Purity: 0.58 Tumor ploidy: 5.81
3
4
5
6
7
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

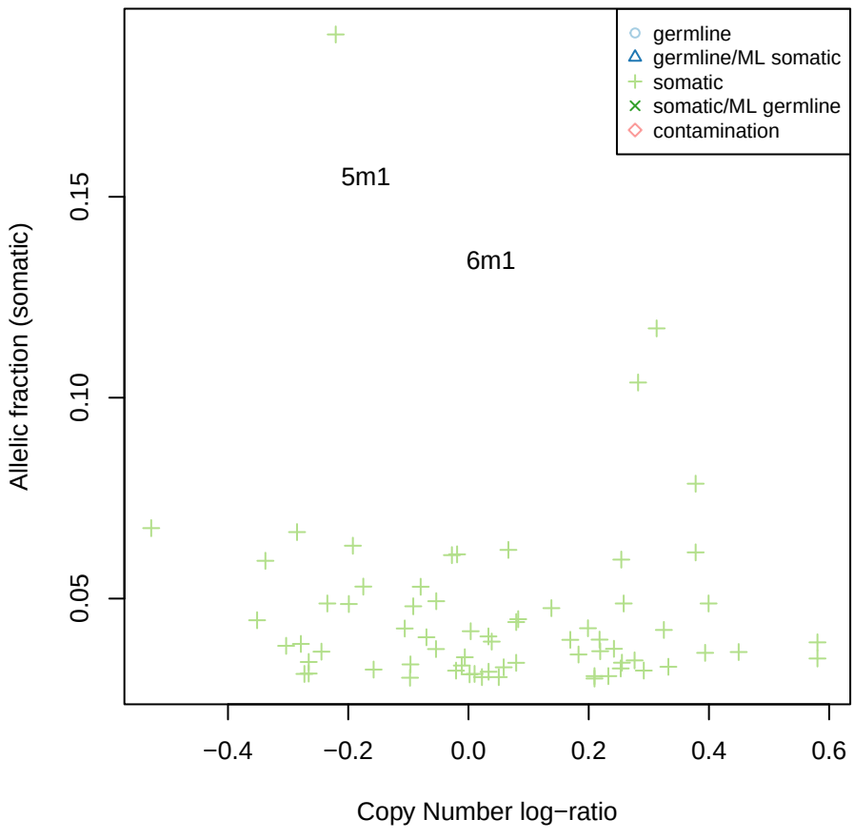

Purity: 0.58 Tumor ploidy: 5.81 SNV log−likelihood: −238.34 GoF: 87.2% Mean coverage: 558;453
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

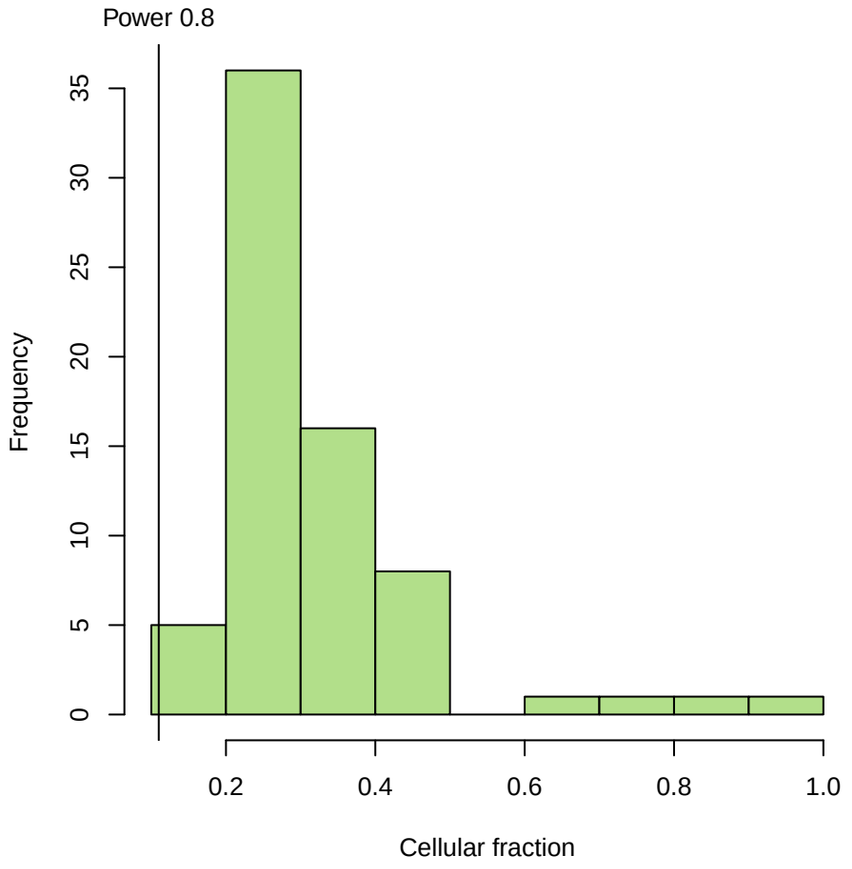

SCNA−fit log−likelihood: −13124.42
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 50 100 150
SNV Index

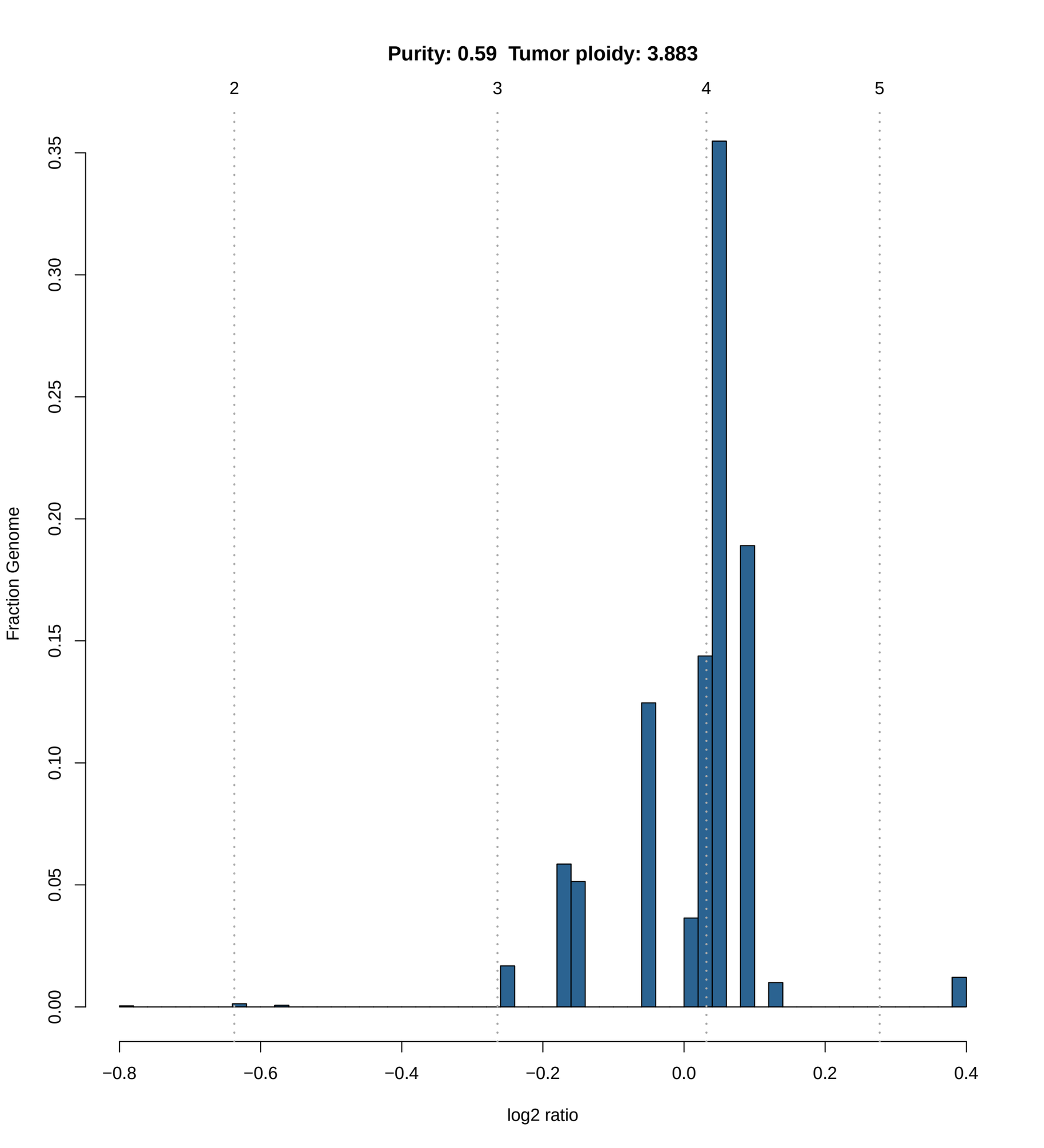

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

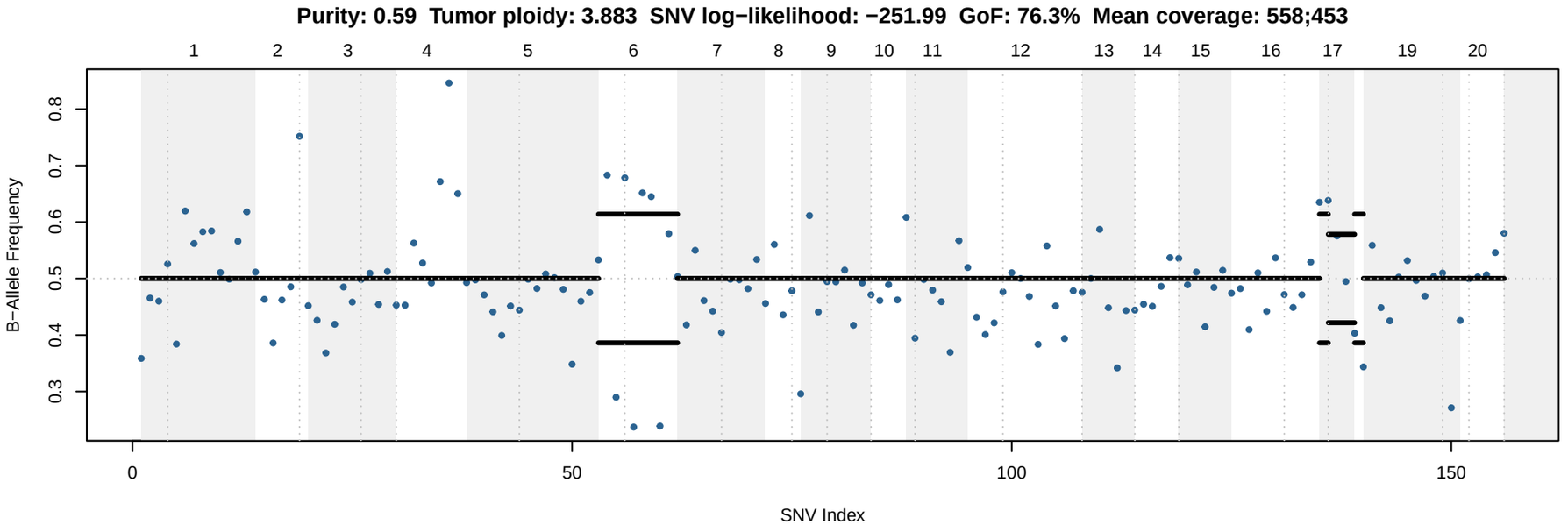

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
0.8
6m5
5m4
6m4
5m3
7m4
6m3
5m2
6m2
5m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

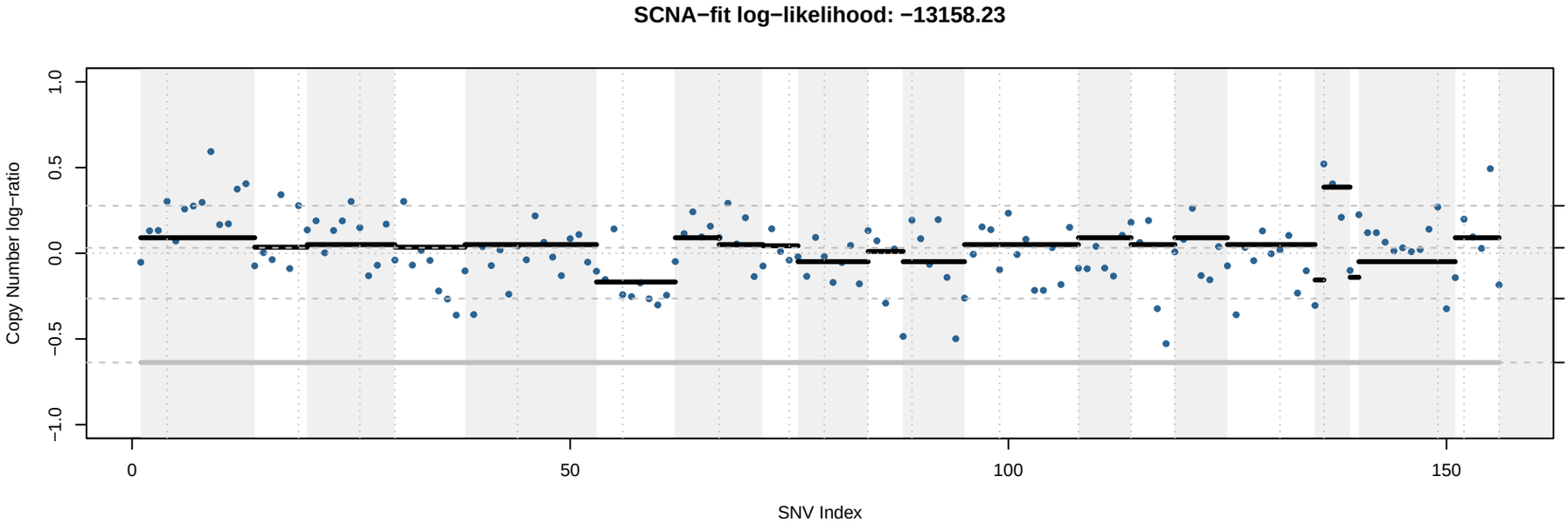

Coverage (log2)
5
6
7
8
9
10
0.0
0.2
0.4
0.6
0.8
Allelic fraction

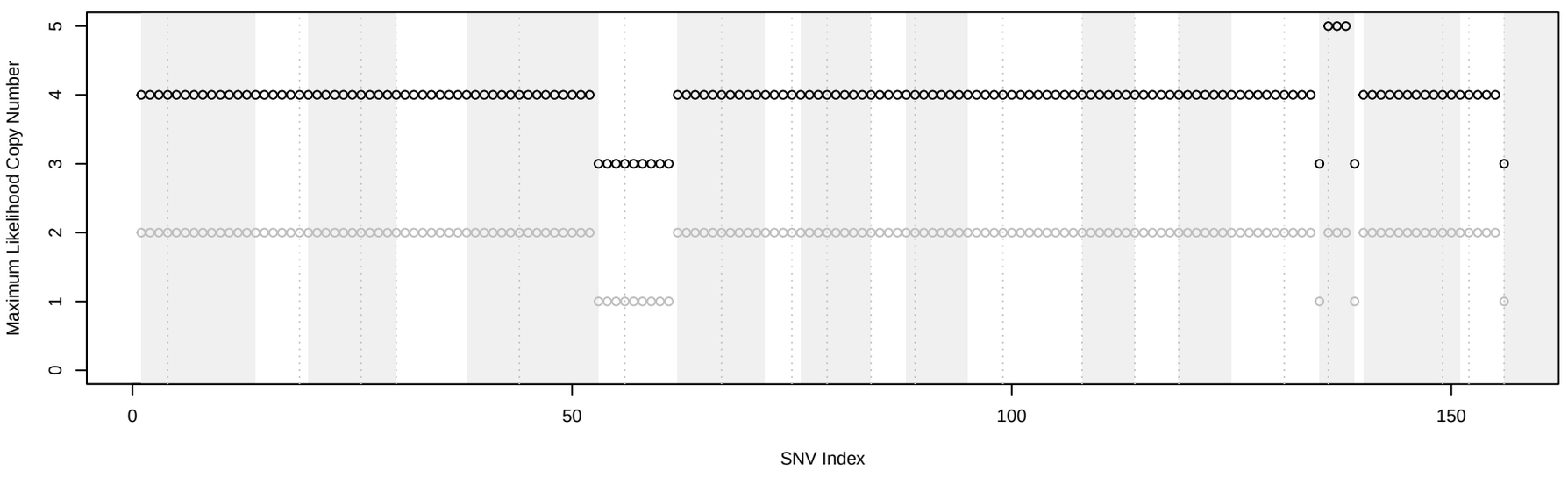

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
5m1
6m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

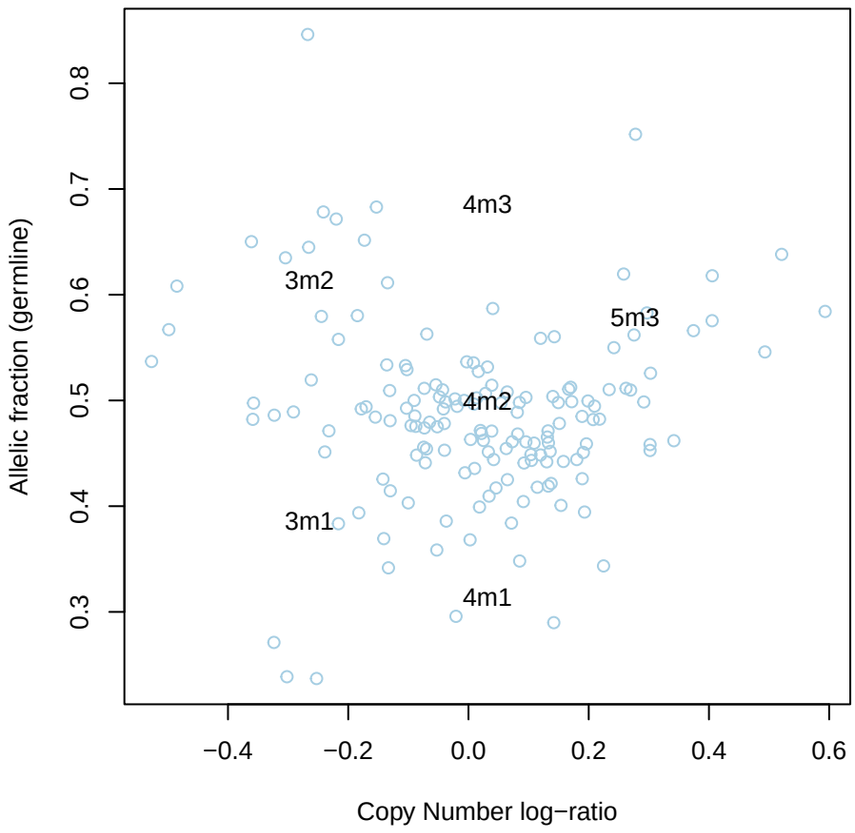

Power 0.8
Frequency
0
5
10
15
20
25
30
35
0.2
0.4
0.6
0.8
1.0
Cellular fraction

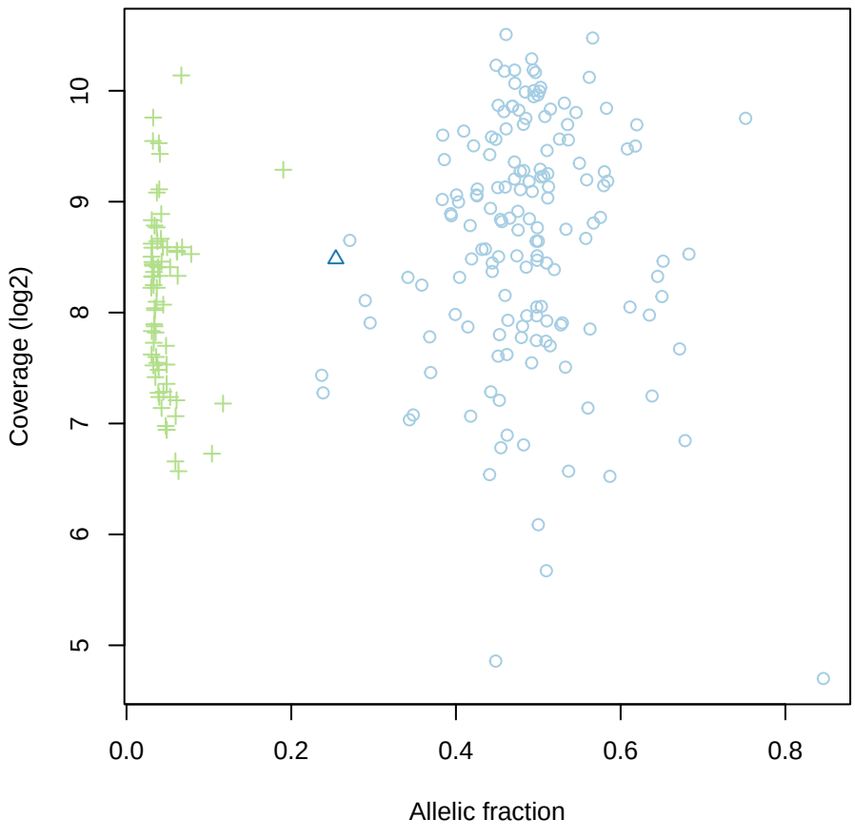

Purity: 0.59 Tumor ploidy: 3.883
2
3
4
5
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

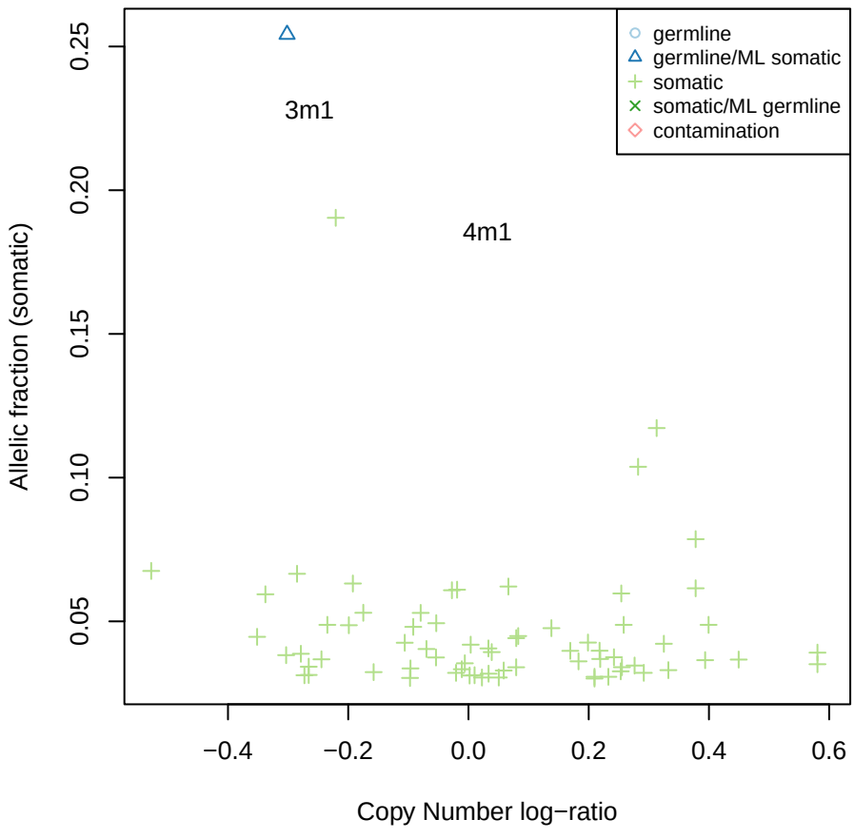

Purity: 0.59 Tumor ploidy: 3.883 SNV log−likelihood: −251.99 GoF: 76.3% Mean coverage: 558;453
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

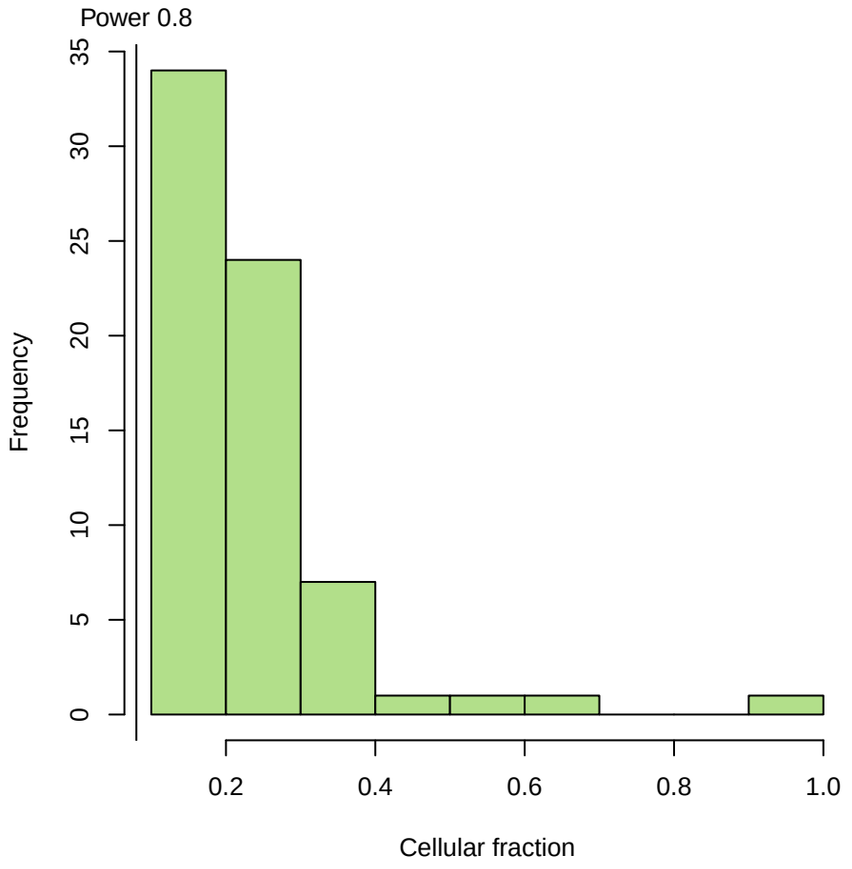

SCNA−fit log−likelihood: −13158.23
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5
0 50 100 150
SNV Index

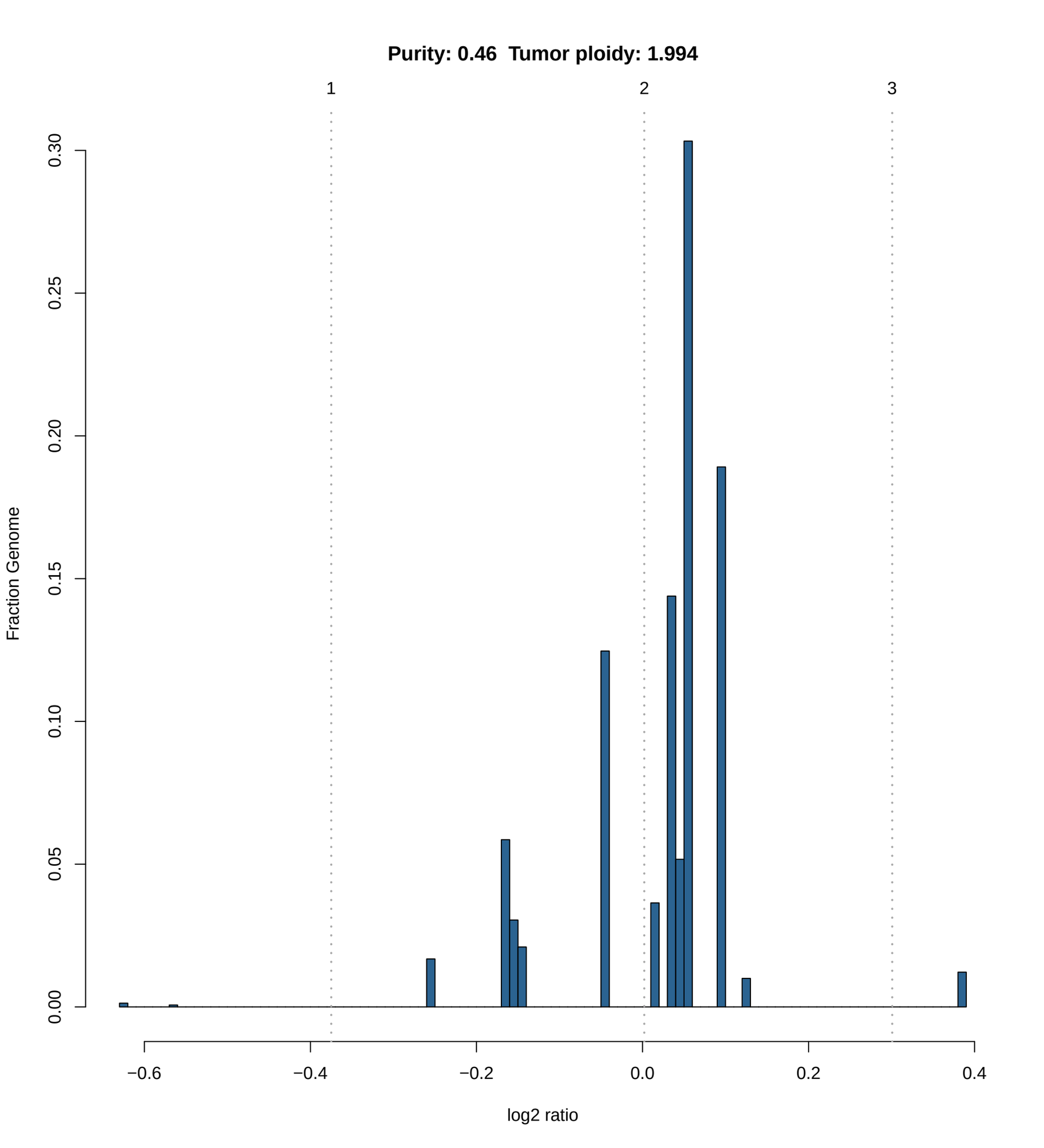

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

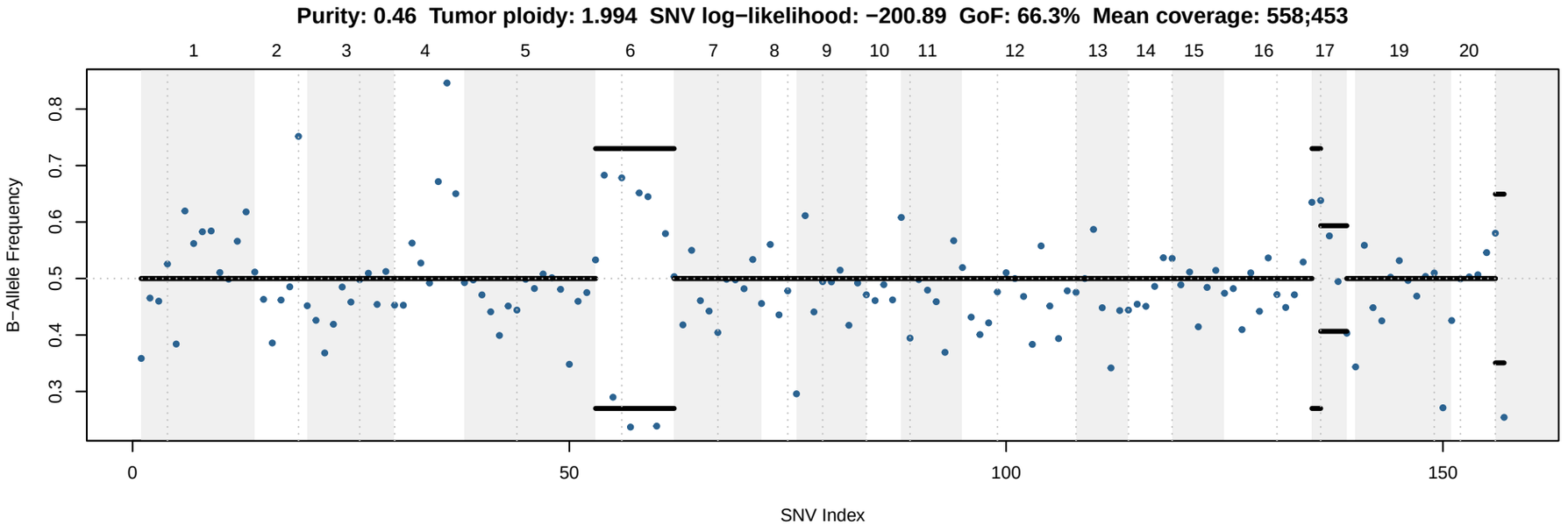

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
5m3
4m2
3m1
4m1

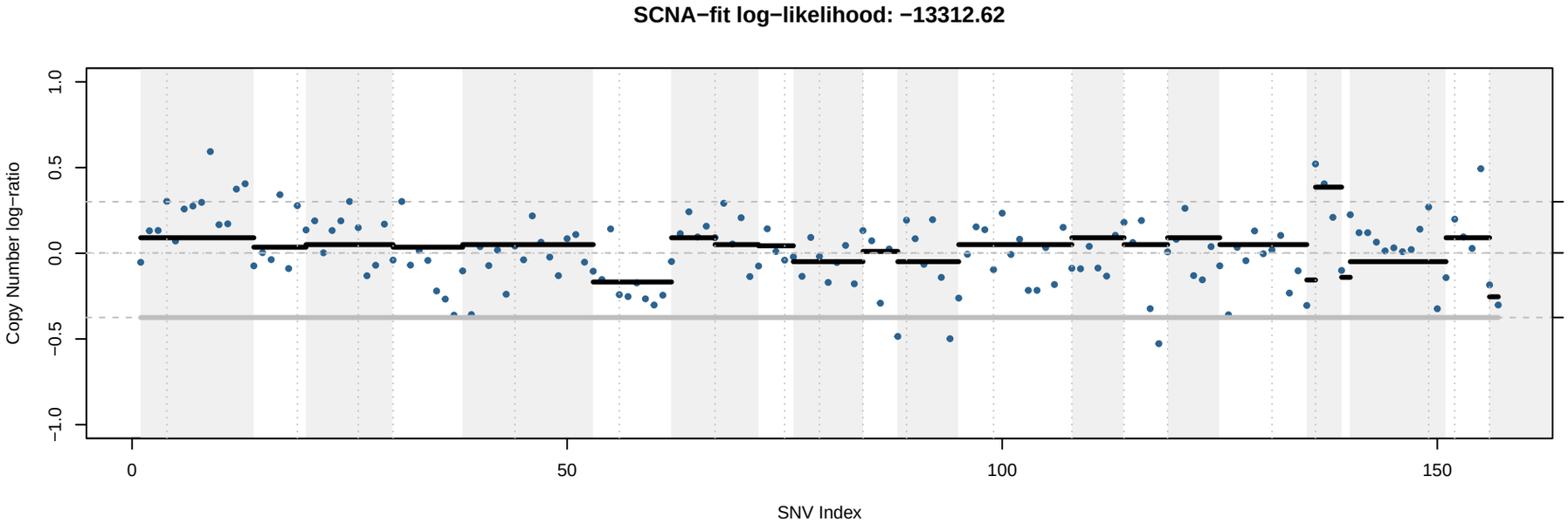

Coverage (log2)
Allelic fraction

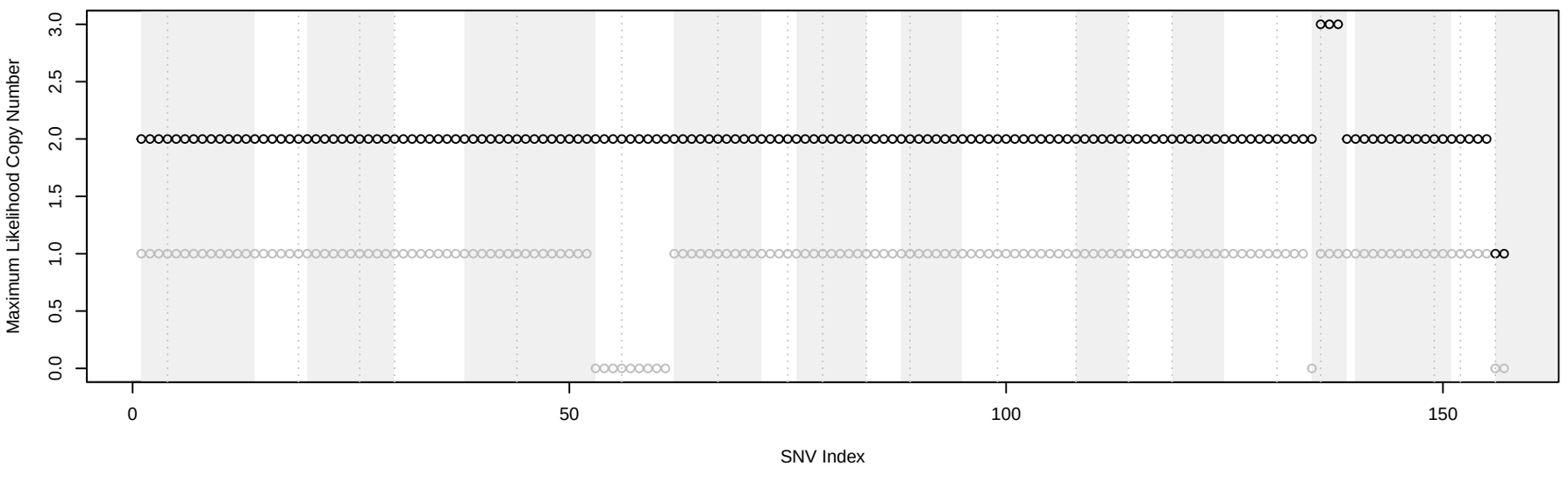

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1

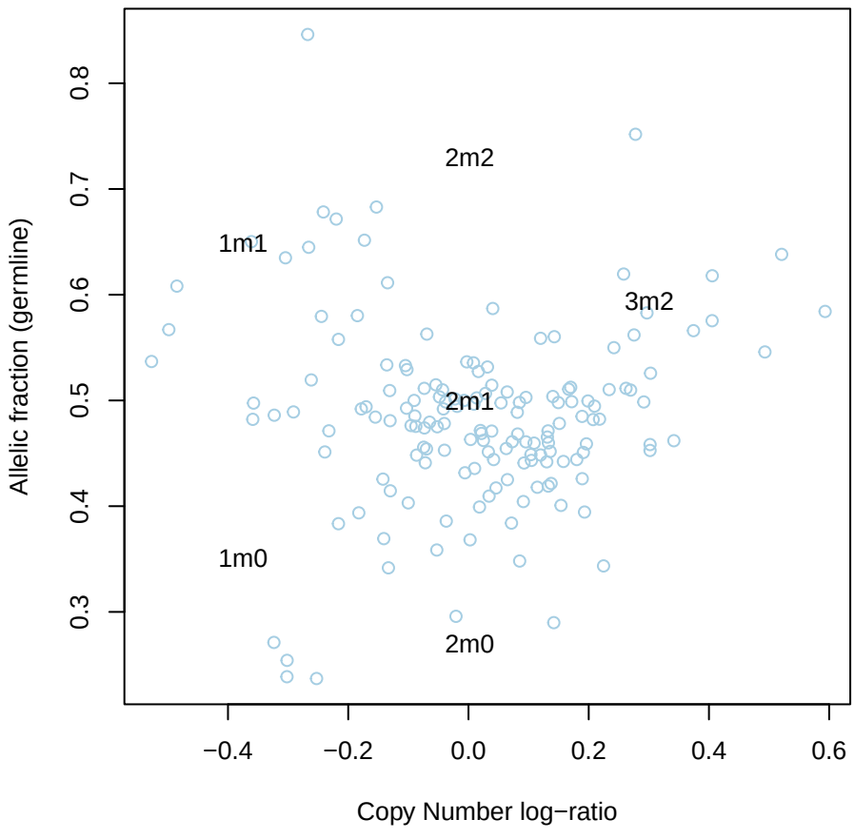

Power 0.8
Frequency
Cellular fraction

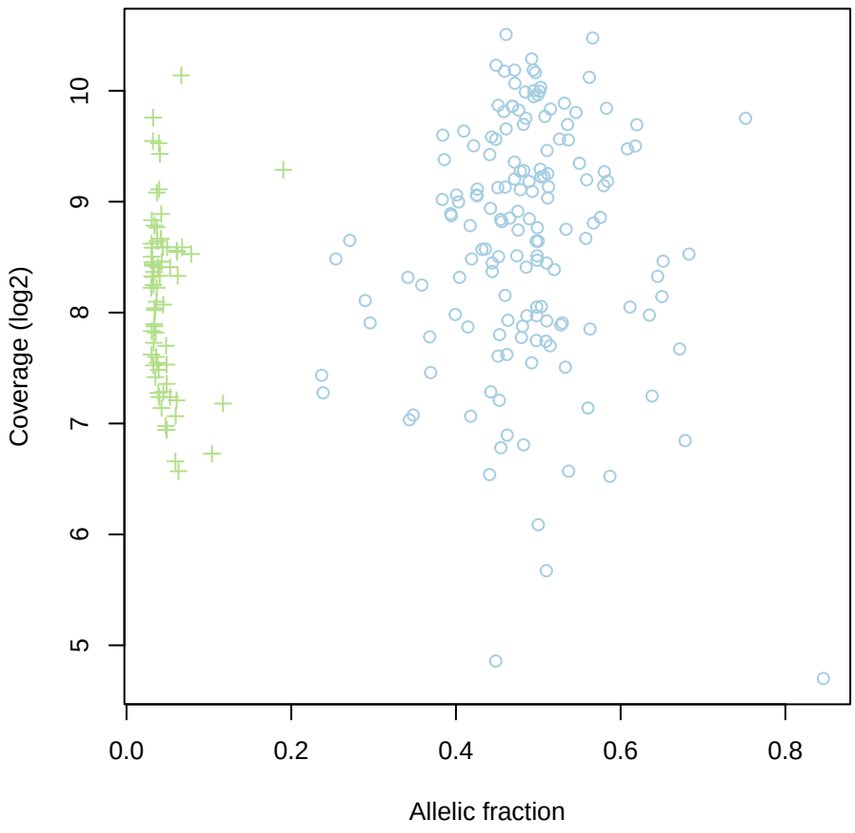

Purity: 0.46 Tumor ploidy: 1.994
1
2
3
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

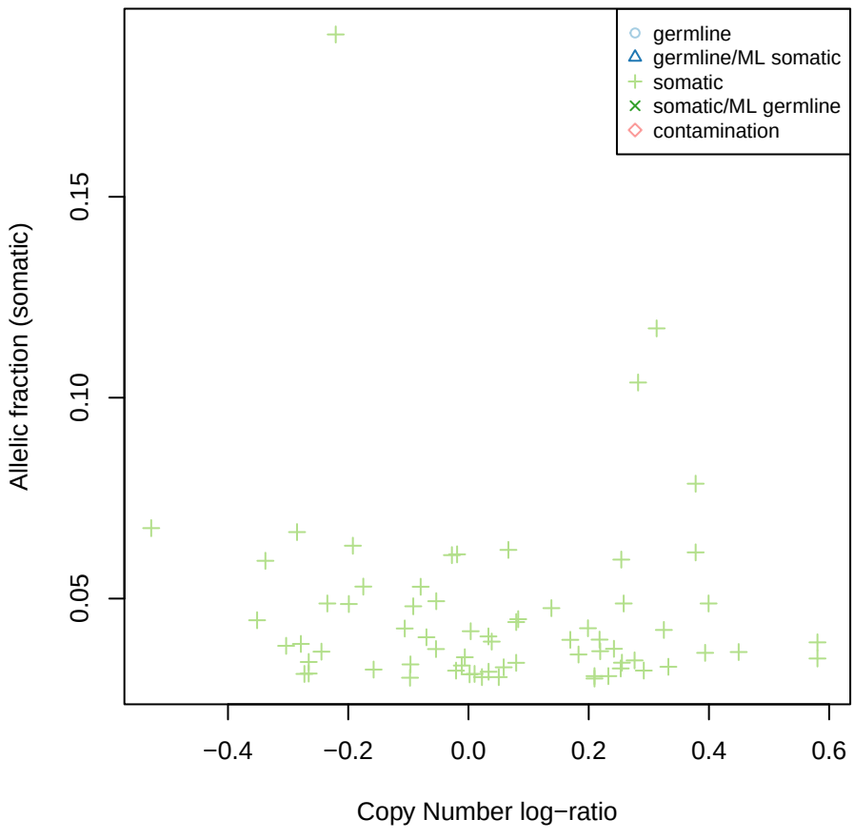

Purity: 0.46 Tumor ploidy: 1.994 SNV log−likelihood: −200.89 GoF: 66.3% Mean coverage: 558;453
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

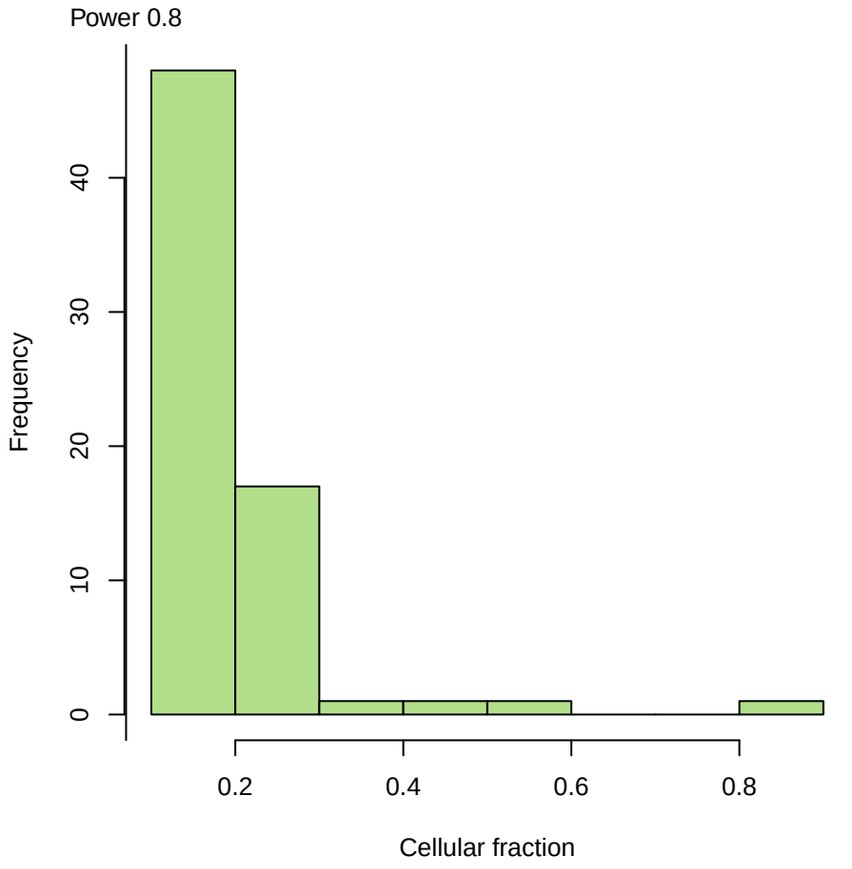

SCNA−fit log−likelihood: −13312.62
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3
0 50 100 150
SNV Index

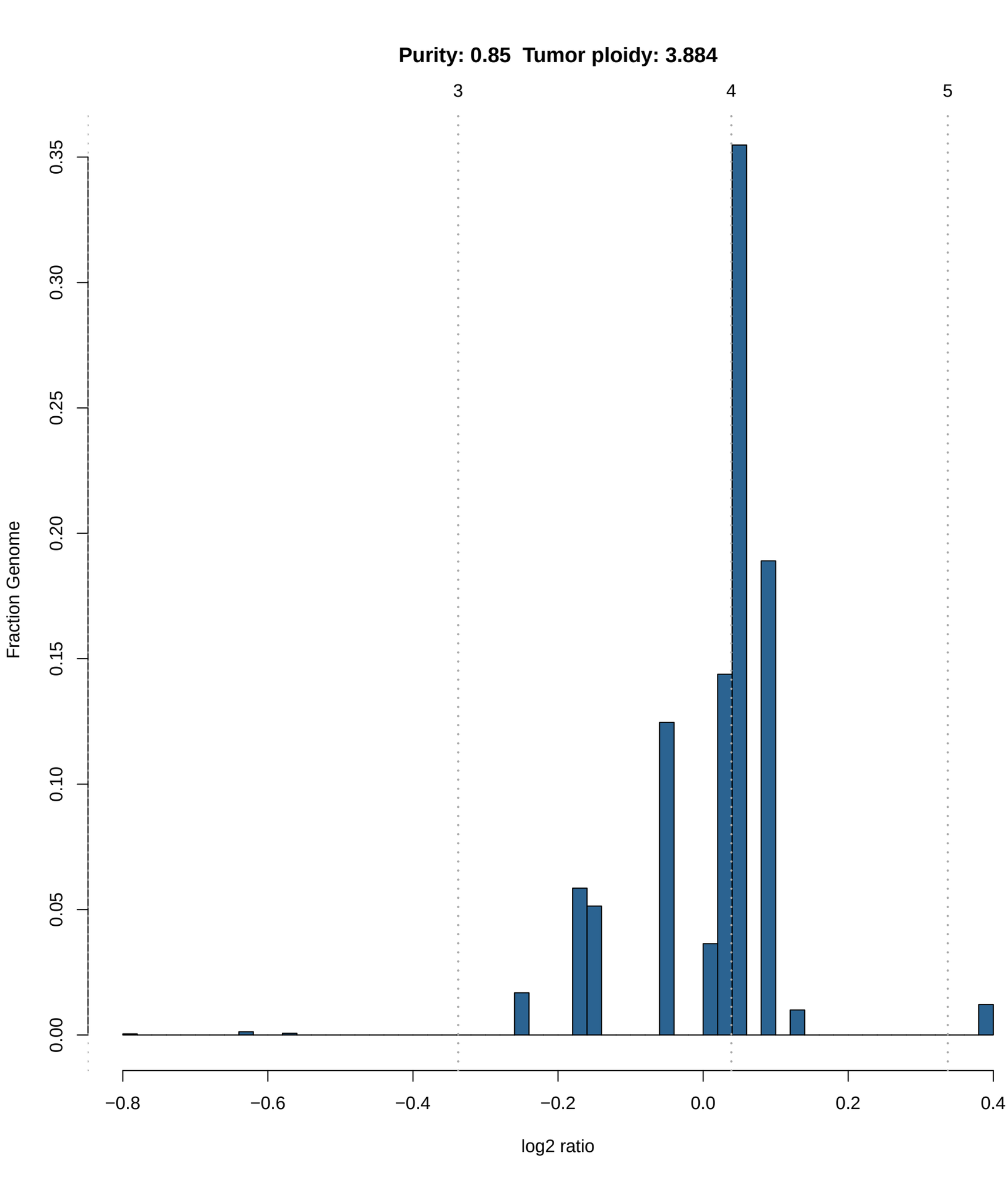

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

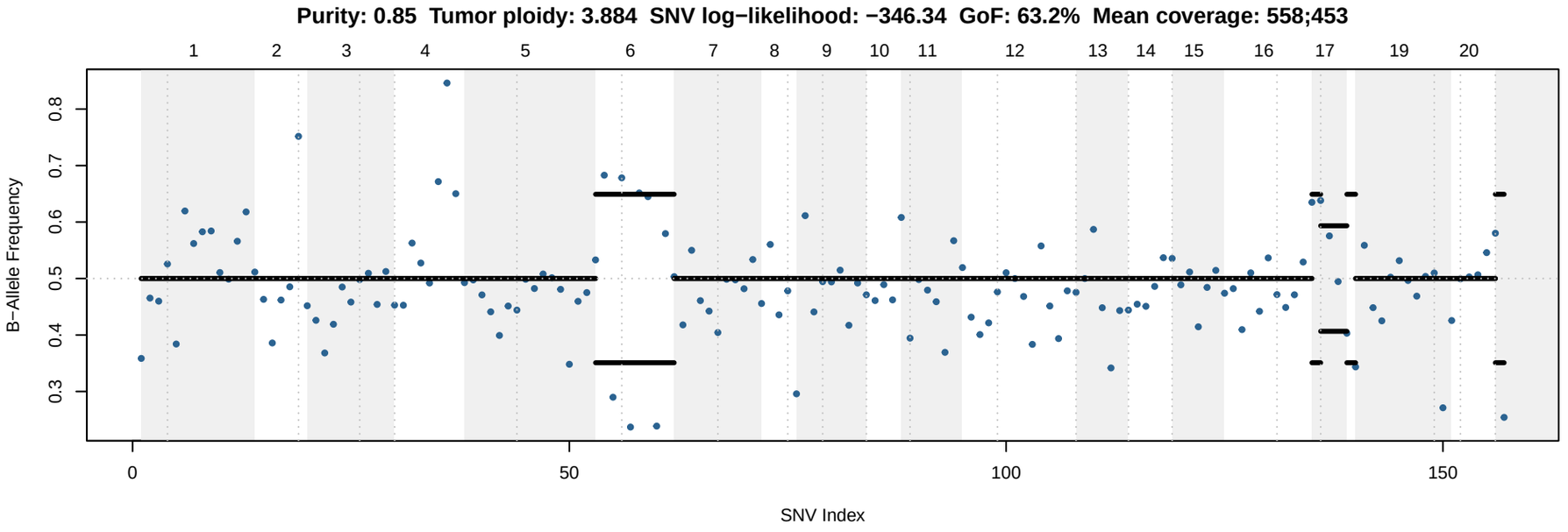

Allelic fraction (germline)
Copy Number log−ratio
1m1
2m2
3m2
2m1
1m0
2m0

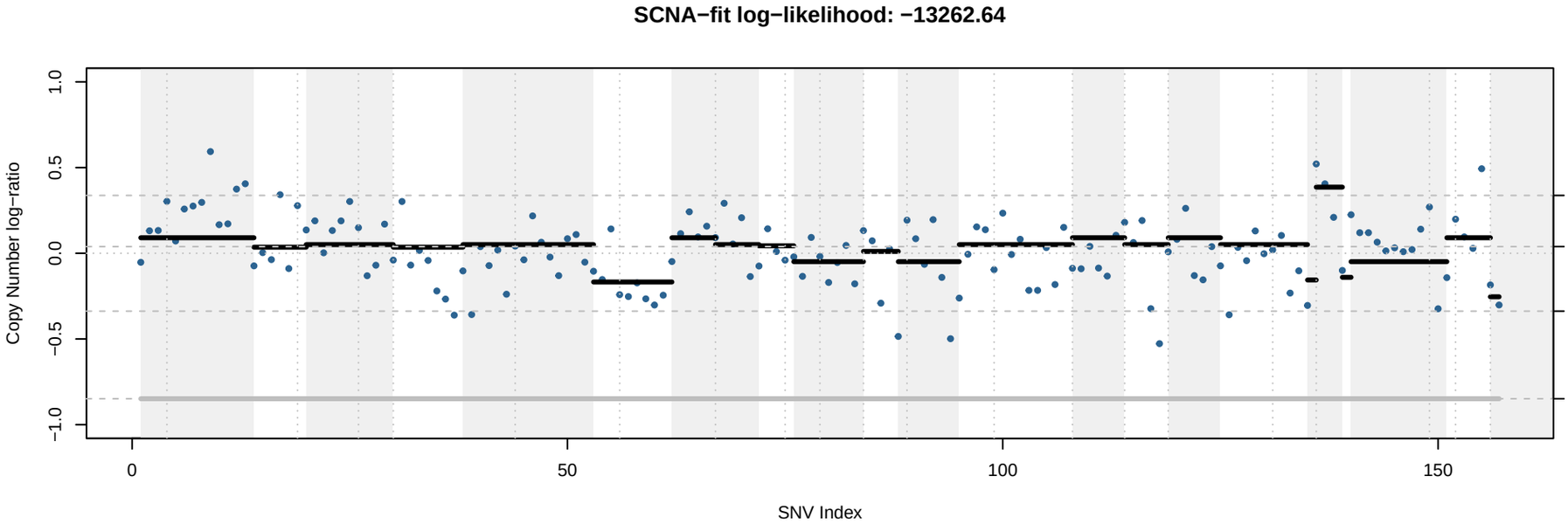

Coverage (log2)
Allelic fraction

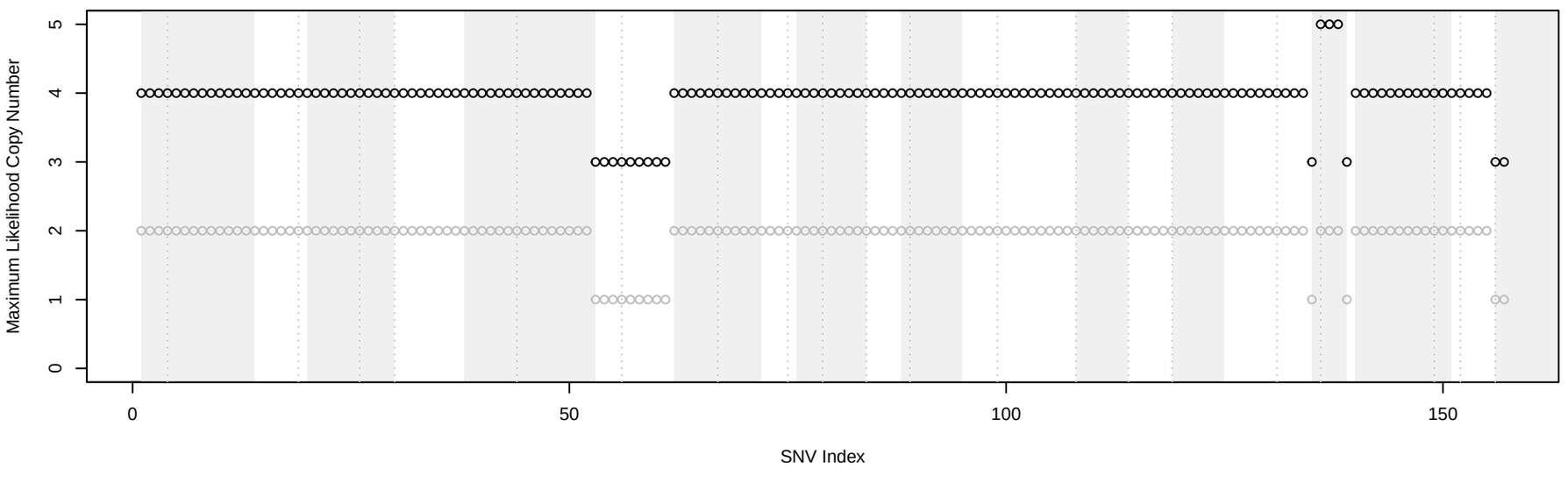

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

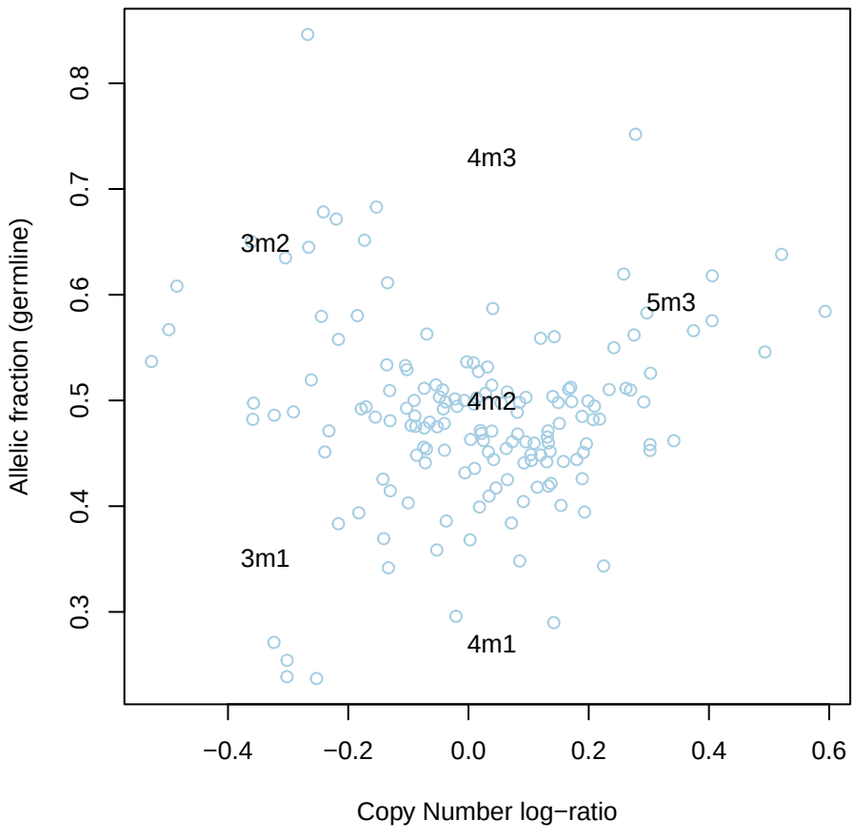

Power 0.8
Frequency
Cellular fraction

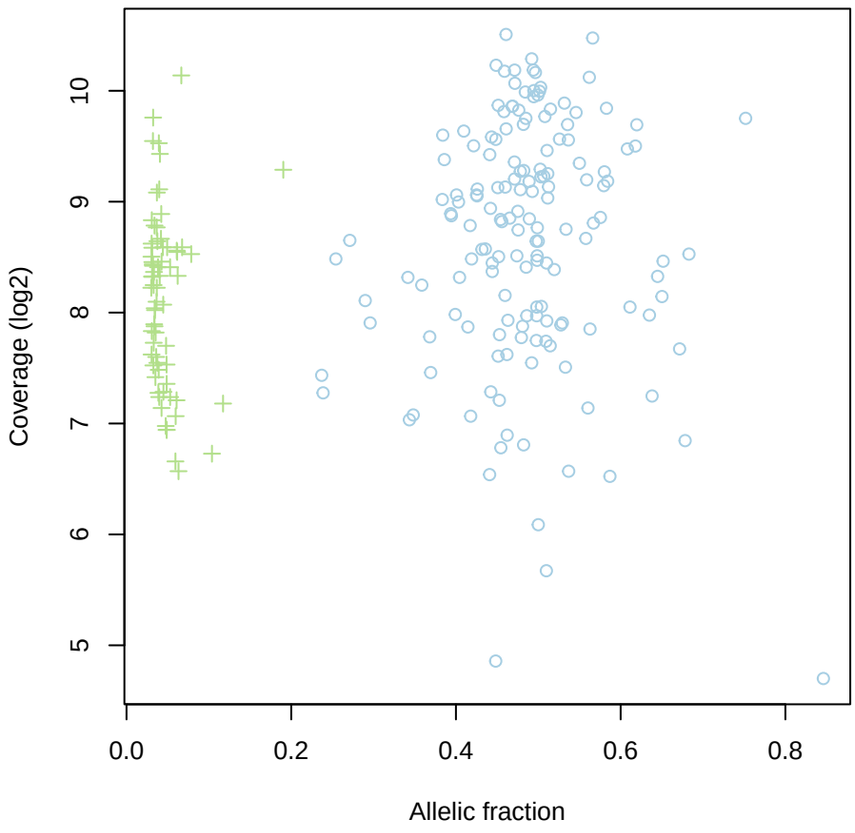

Purity: 0.85 Tumor ploidy: 3.884
3
4
5
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

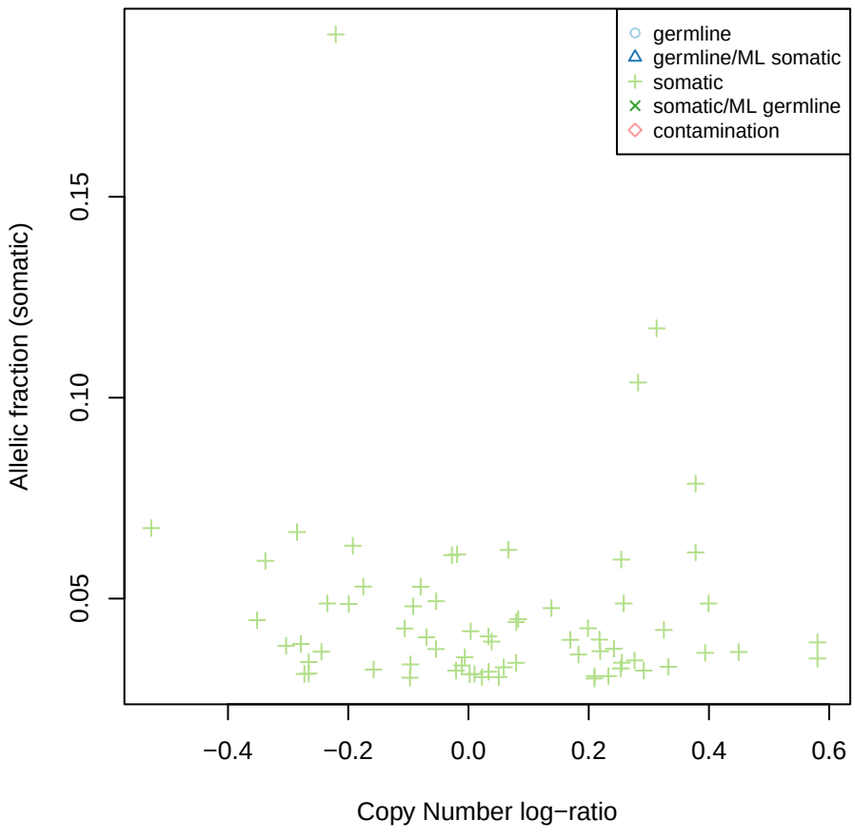

Purity: 0.85 Tumor ploidy: 3.884 SNV log−likelihood: −346.34 GoF: 63.2% Mean coverage: 558;453
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

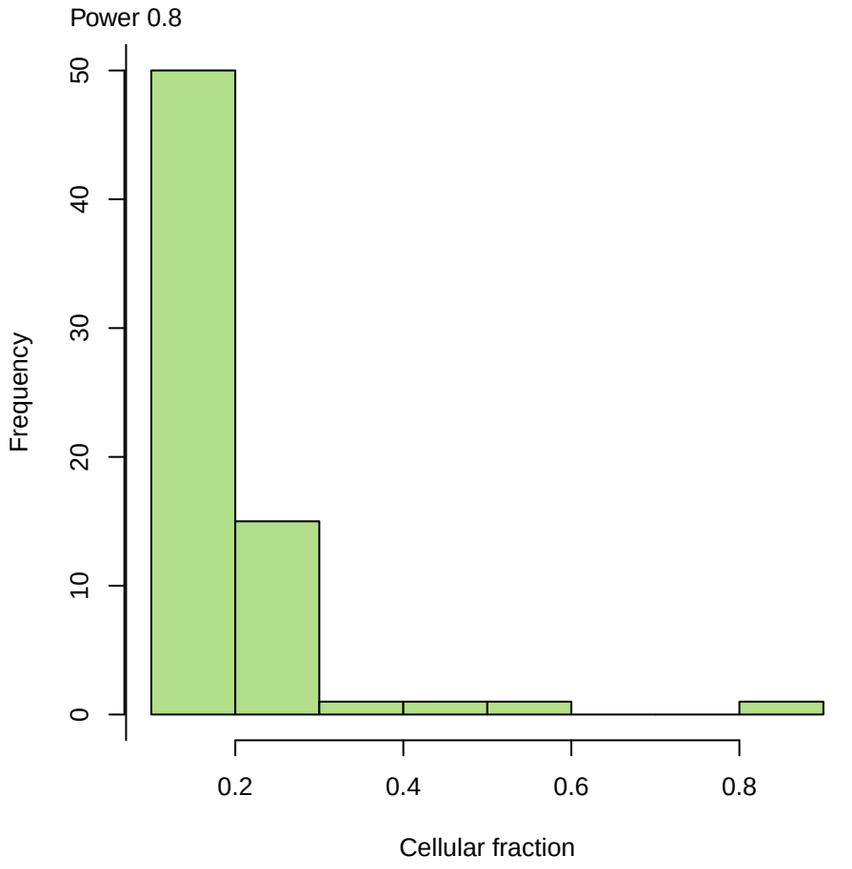

SCNA−fit log−likelihood: −13262.64
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5
0 50 100 150
SNV Index

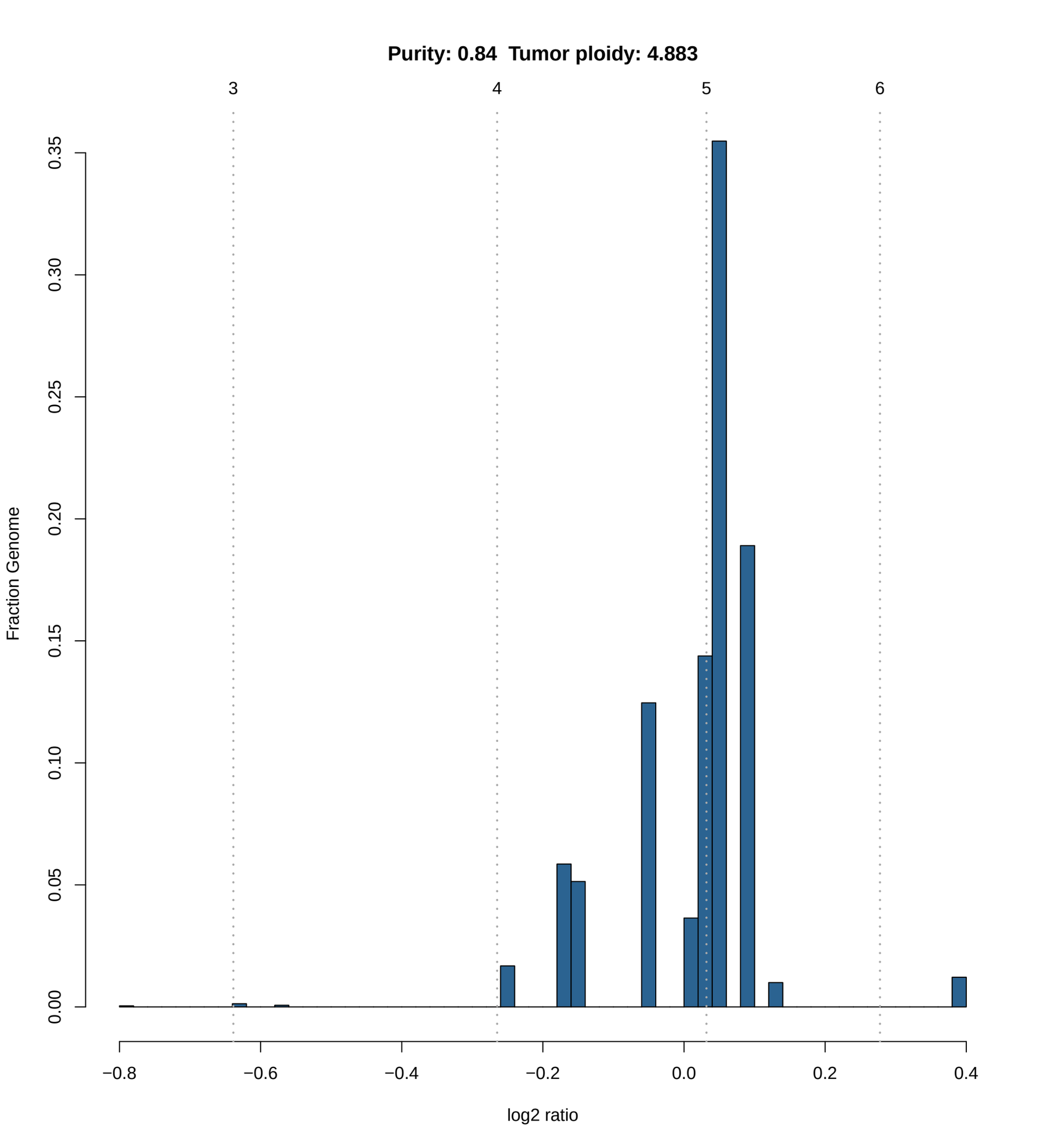

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

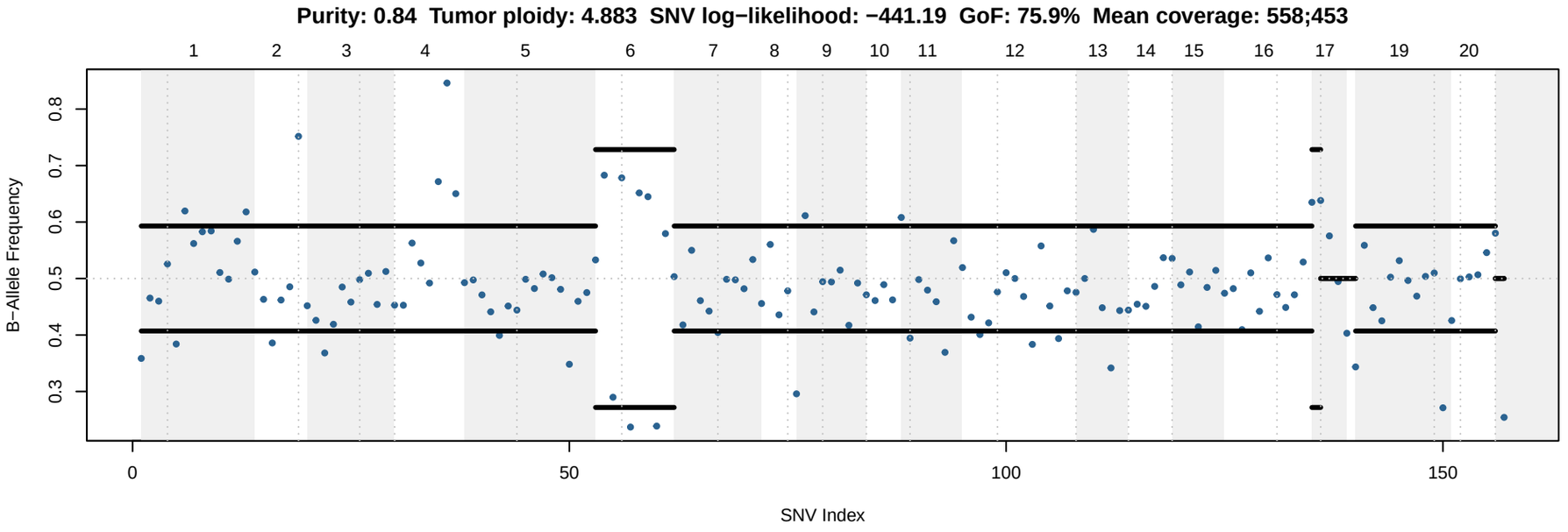

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
5m3
4m2
3m1
4m1

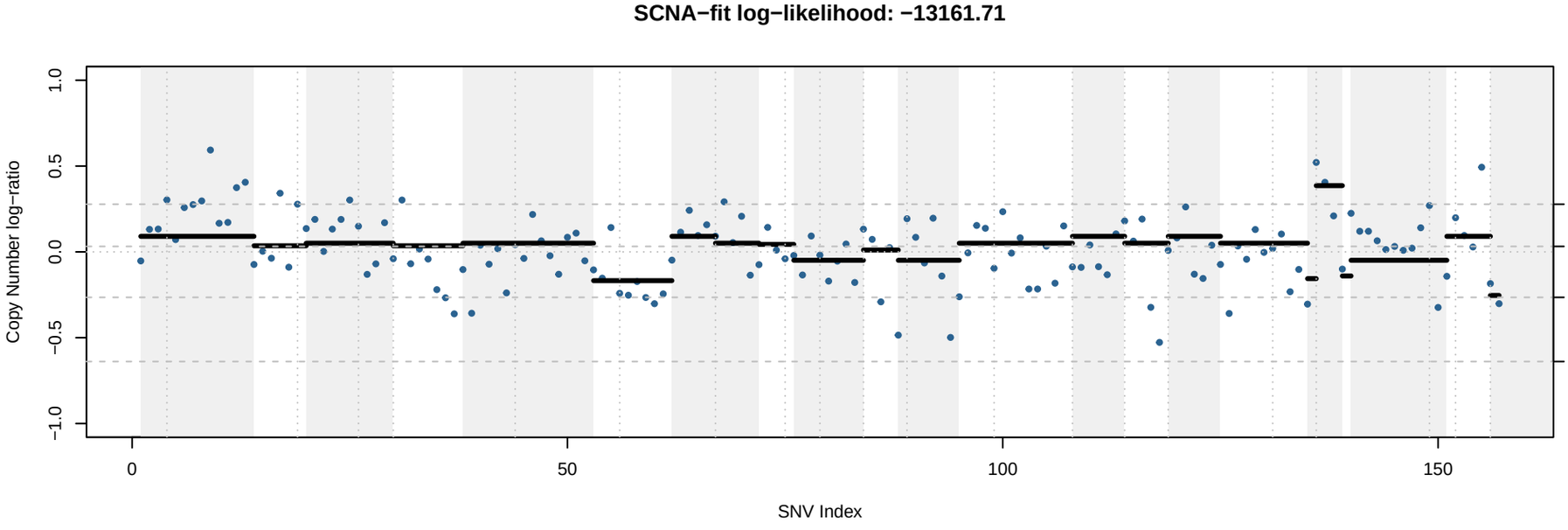

Coverage (log2)
Allelic fraction

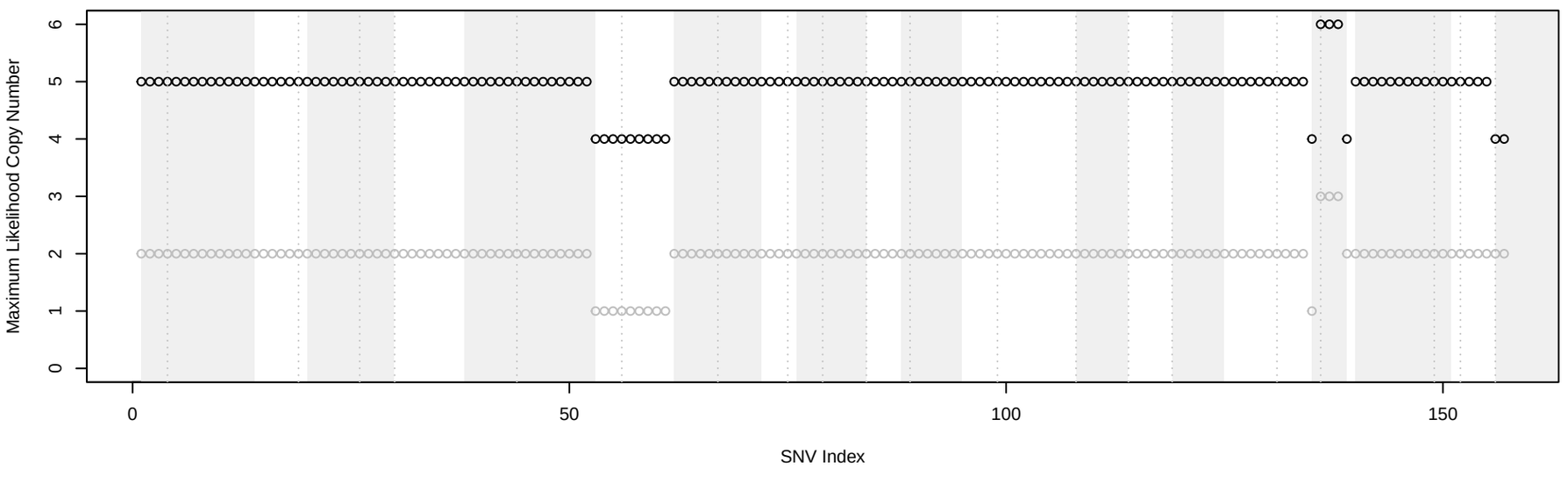

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

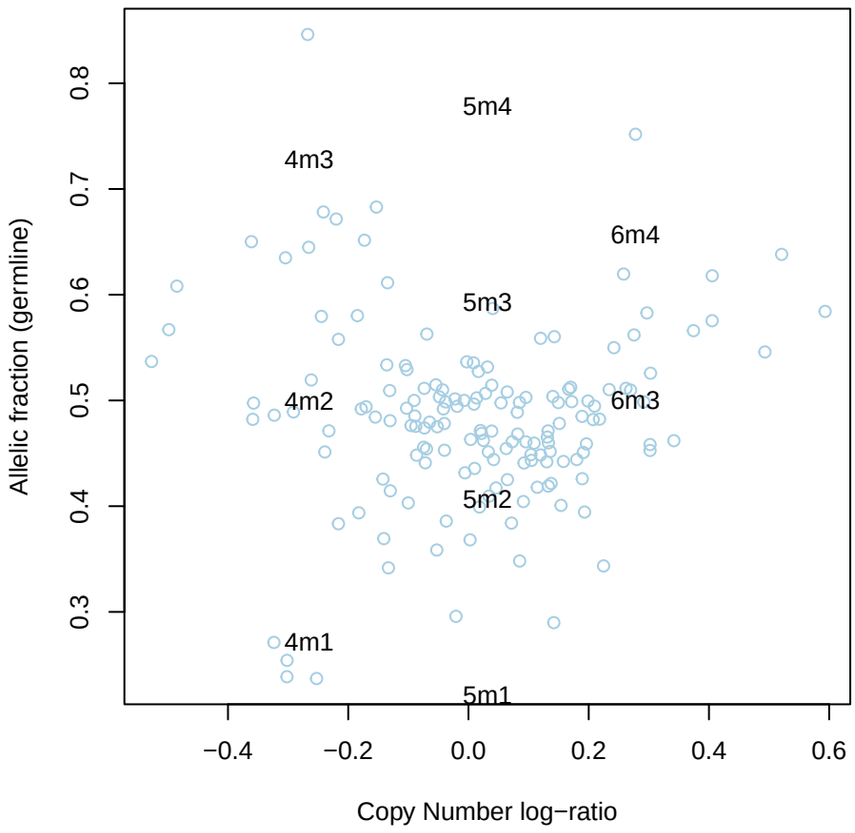

Power 0.8
Frequency
Cellular fraction

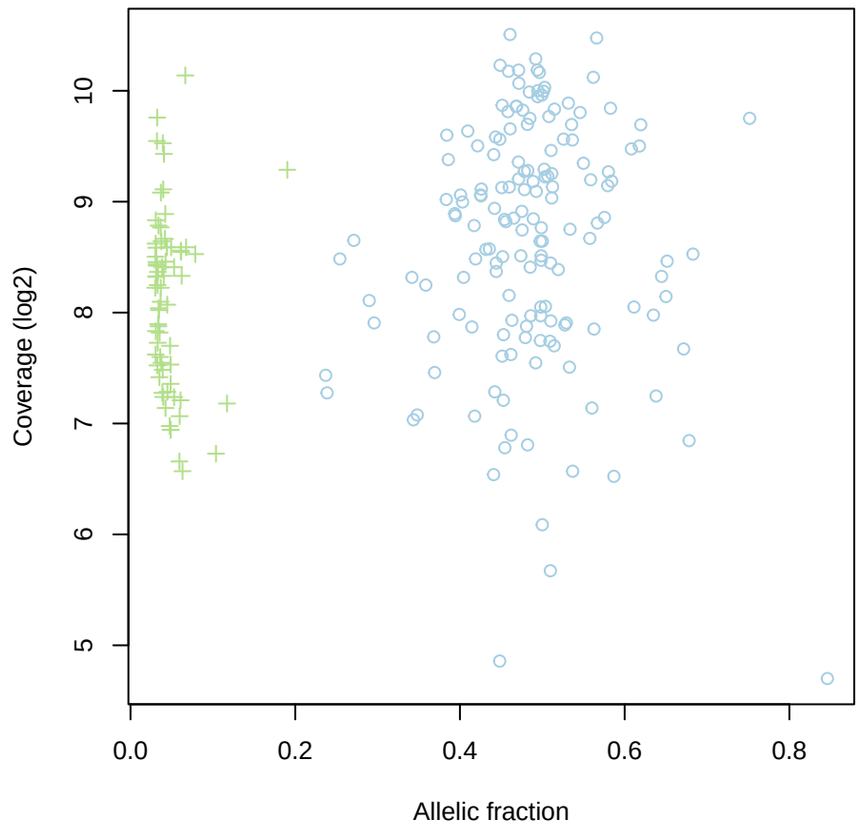

Purity: 0.84 Tumor ploidy: 4.883
3
4
5
6
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

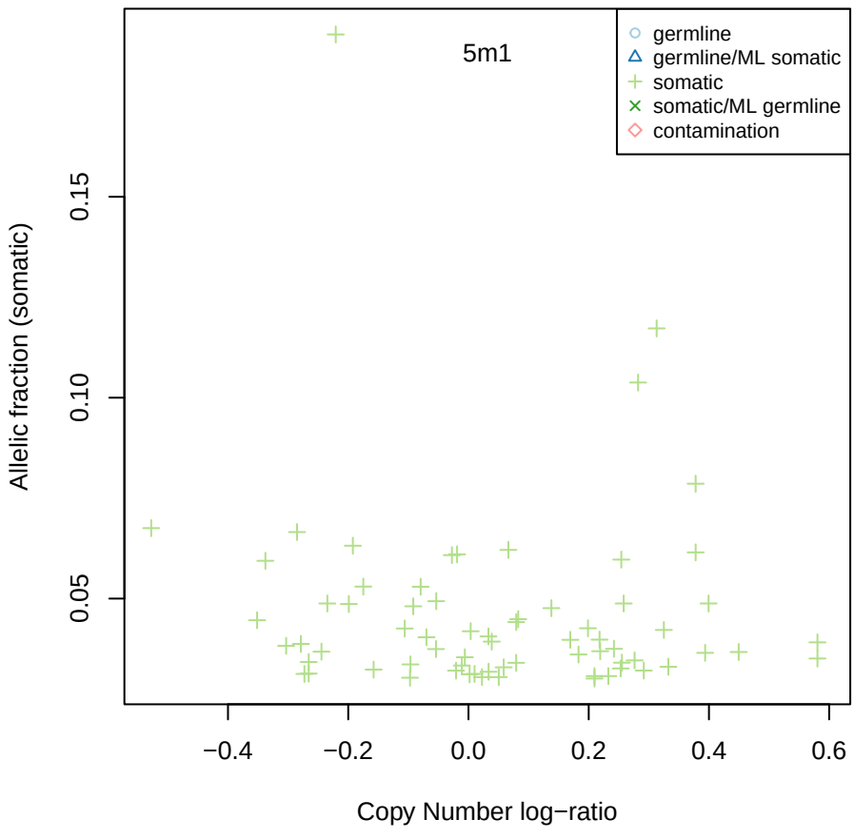

Purity: 0.84 Tumor ploidy: 4.883 SNV log−likelihood: −441.19 GoF: 75.9% Mean coverage: 558;453
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

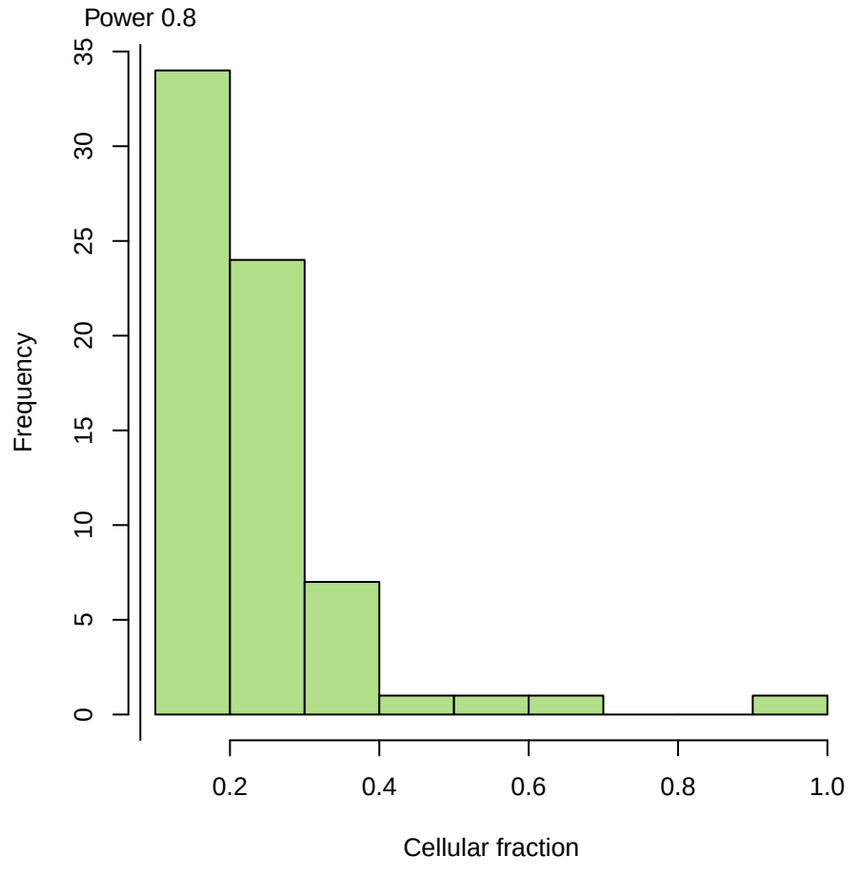

SCNA−fit log−likelihood: −13161.71
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6
0 50 100 150
SNV Index

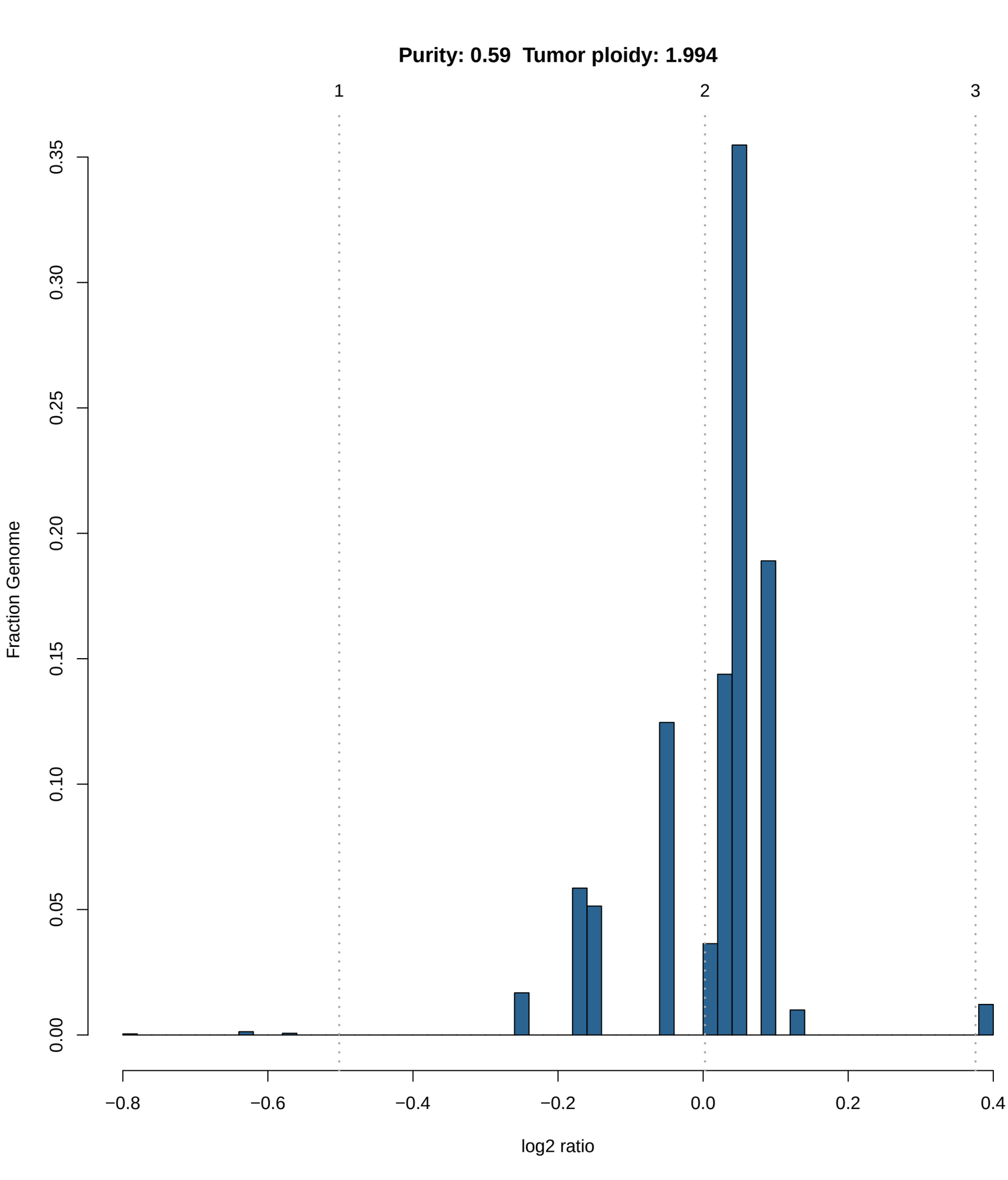

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

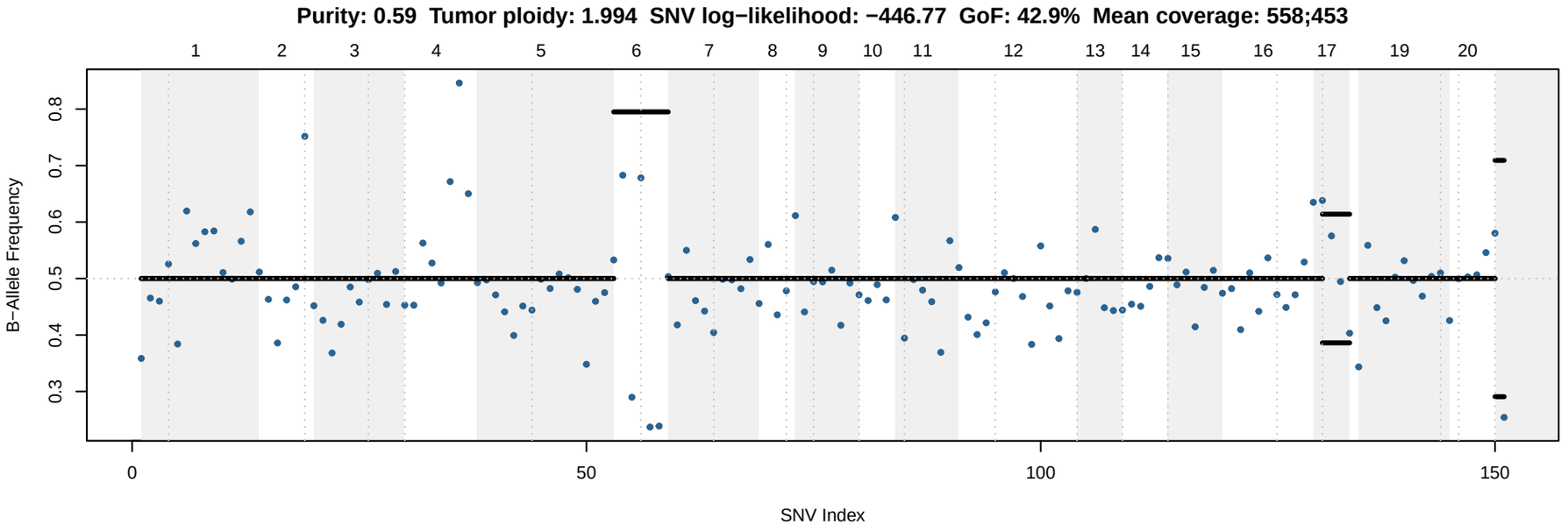

Allelic fraction (germline)
Copy Number log−ratio
5m4
4m3
6m4
5m3
4m2
6m3
5m2
4m1
5m1

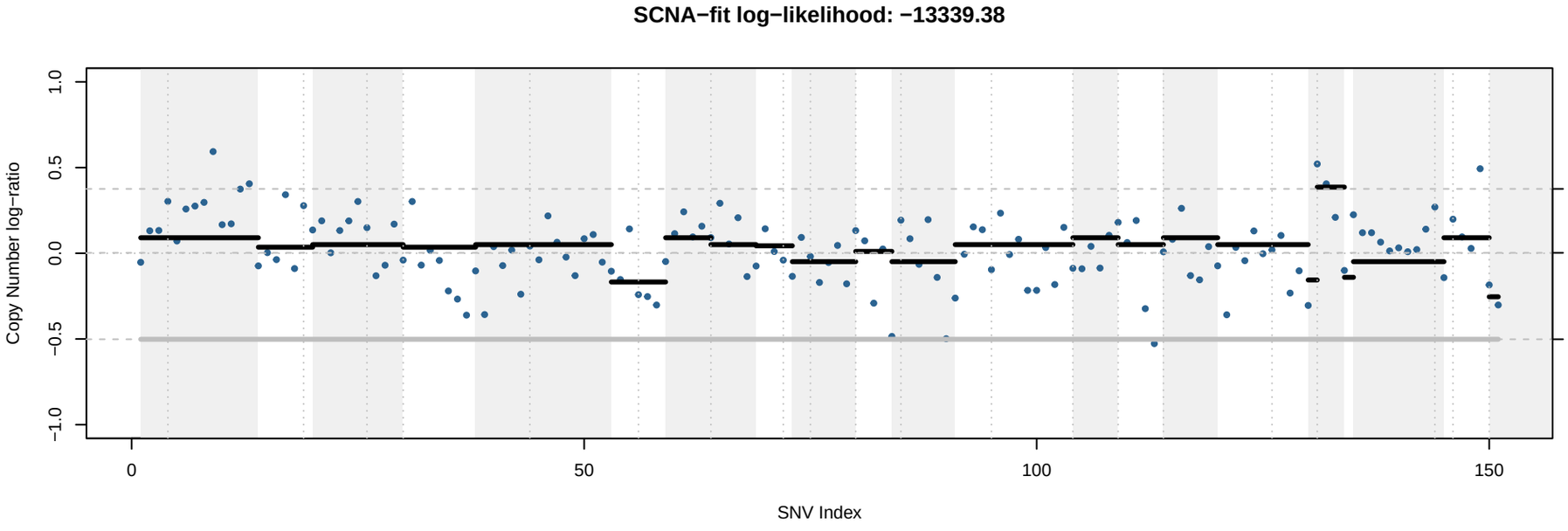

Coverage (log2)
Allelic fraction

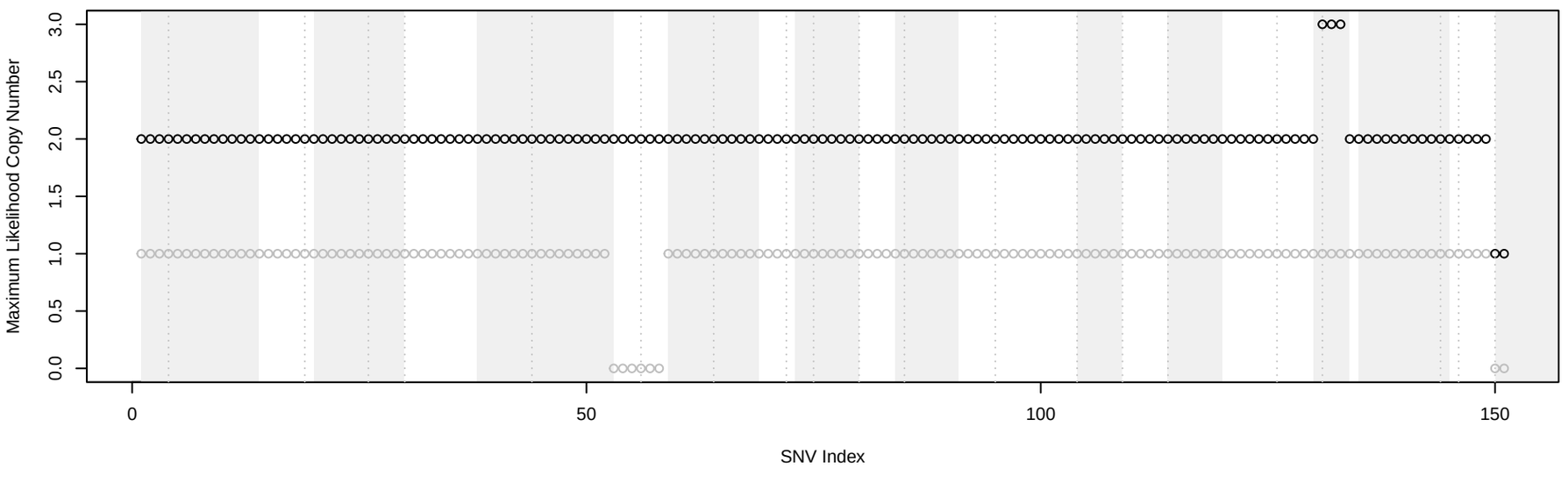

Allelic fraction (somatic)
Copy Number log−ratio
5m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

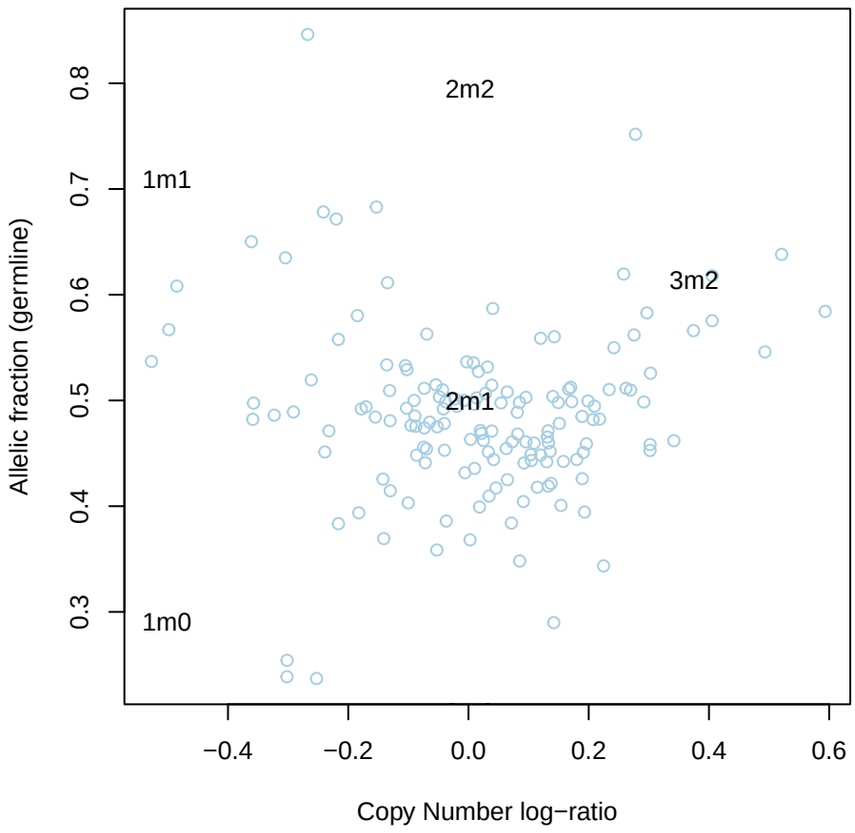

Power 0.8
Frequency
Cellular fraction

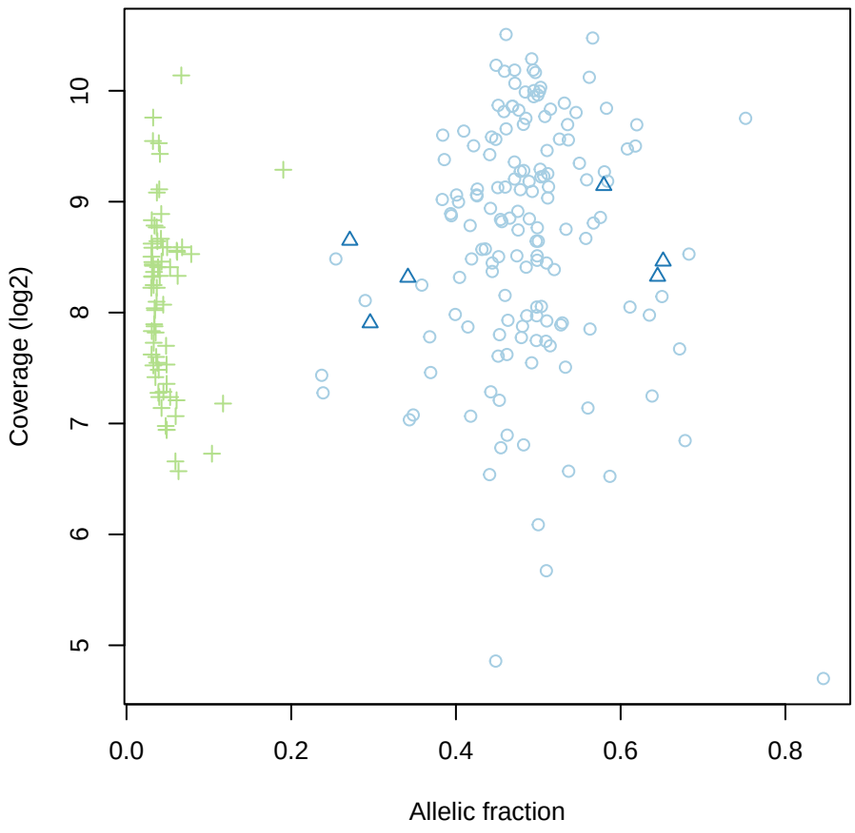

Purity: 0.59 Tumor ploidy: 1.994
1
2
3
Fraction Genome
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

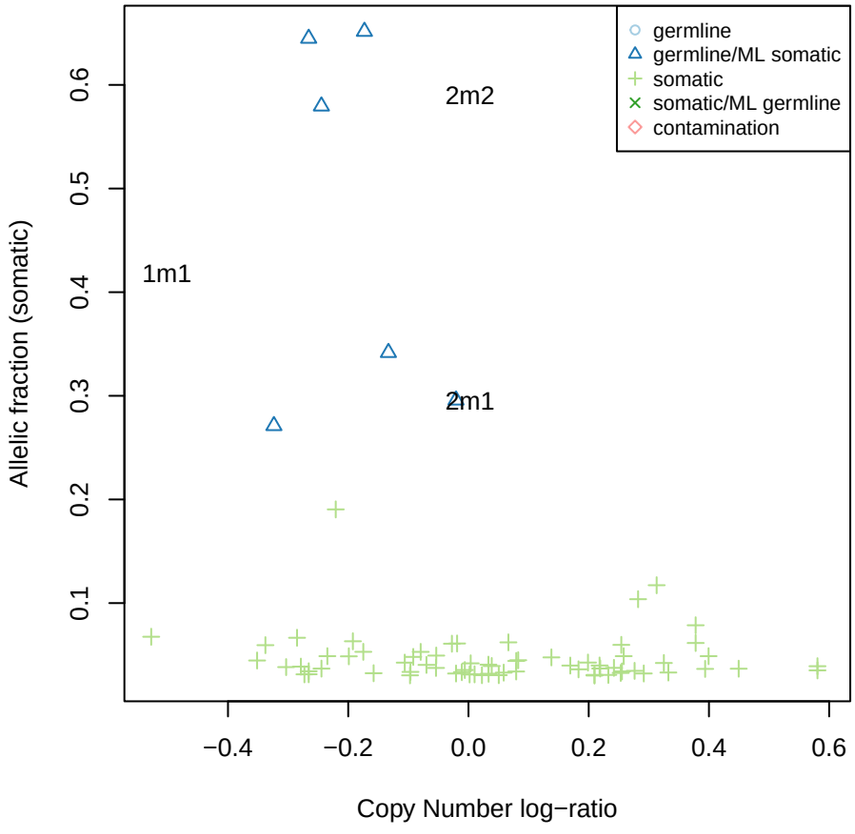

Purity: 0.59 Tumor ploidy: 1.994 SNV log−likelihood: −446.77 GoF: 42.9% Mean coverage: 558;453
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

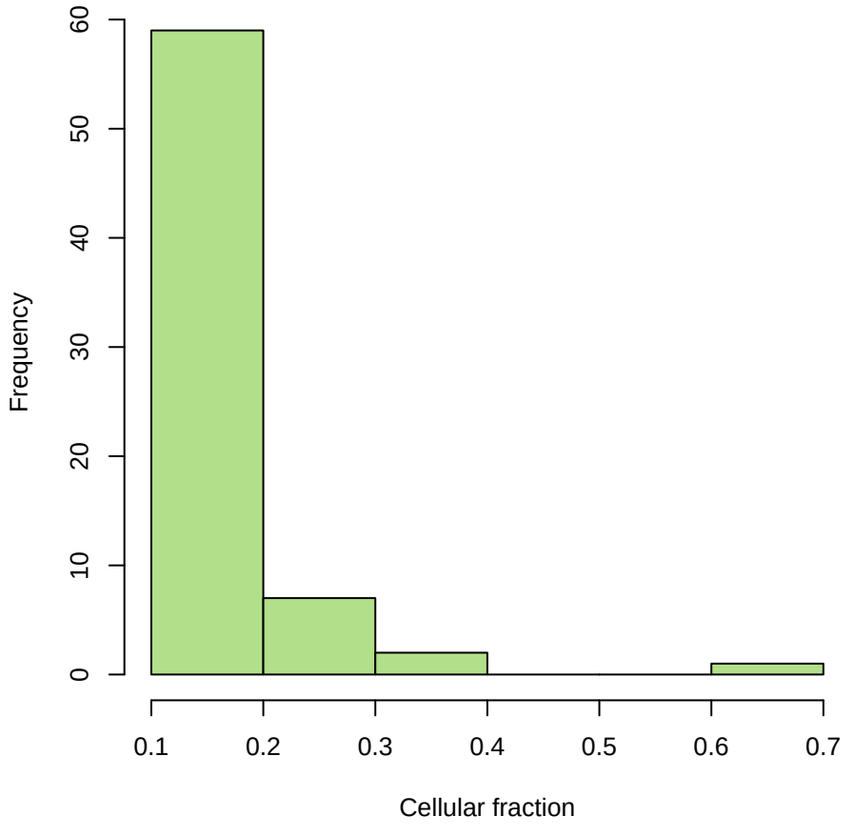

SCNA−fit log−likelihood: −13339.38
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3
0 50 100 150
SNV Index

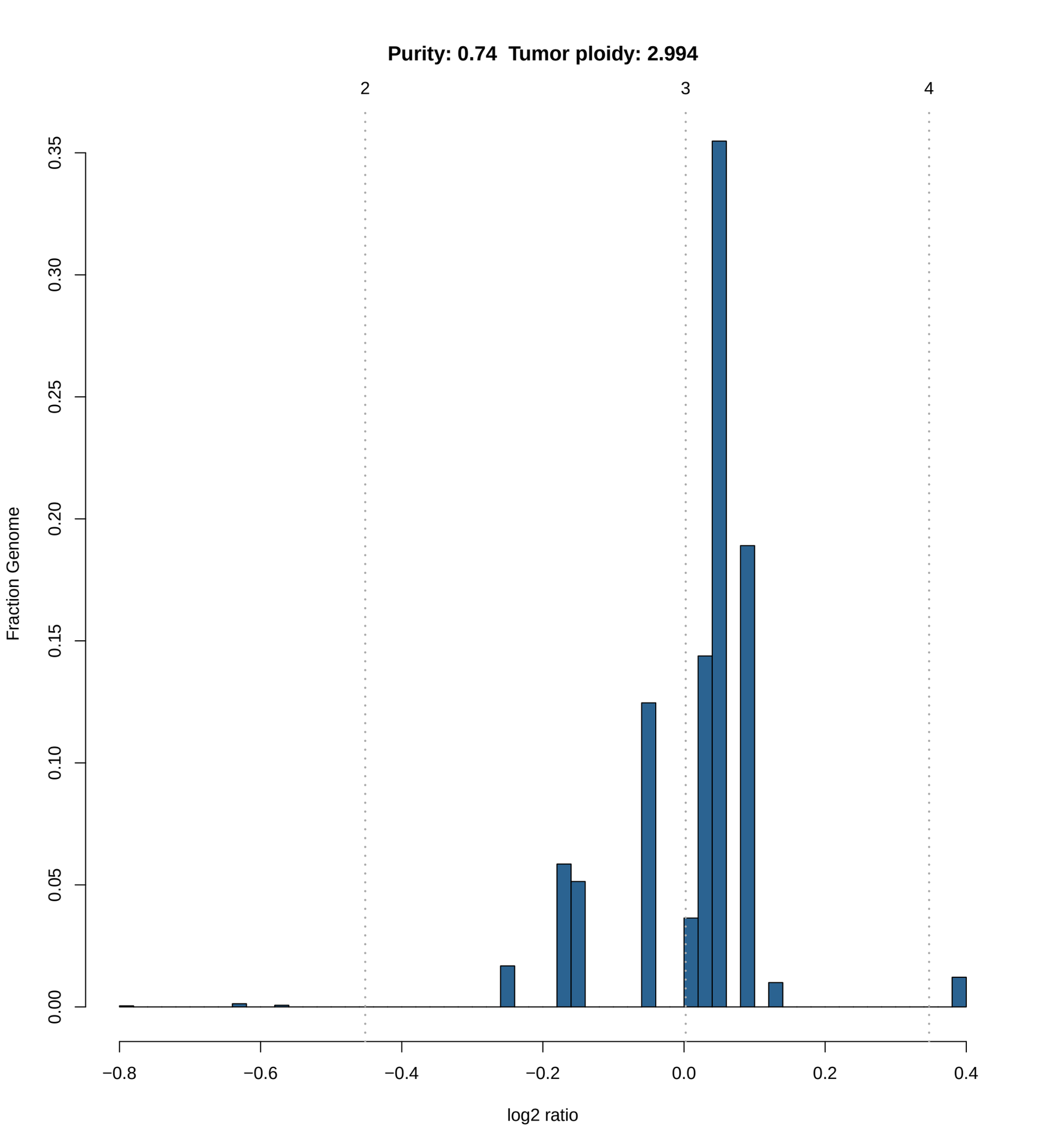

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

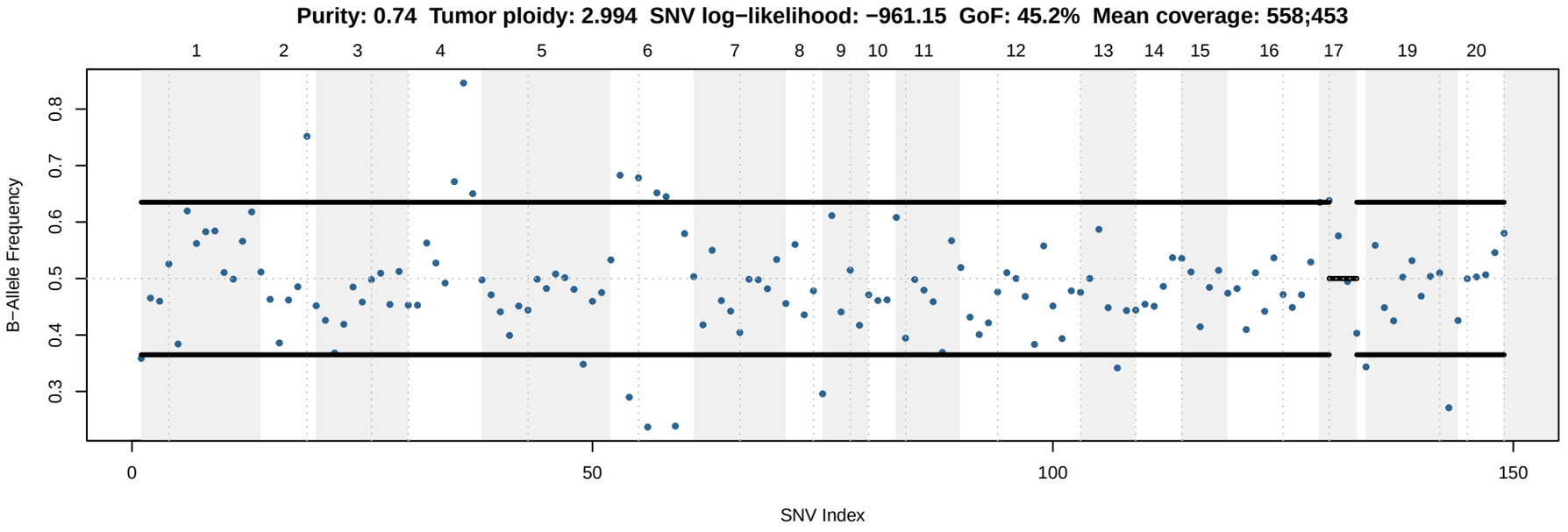

Allelic fraction (germline)
Copy Number log−ratio
1m1
2m2
3m2
2m1
1m0

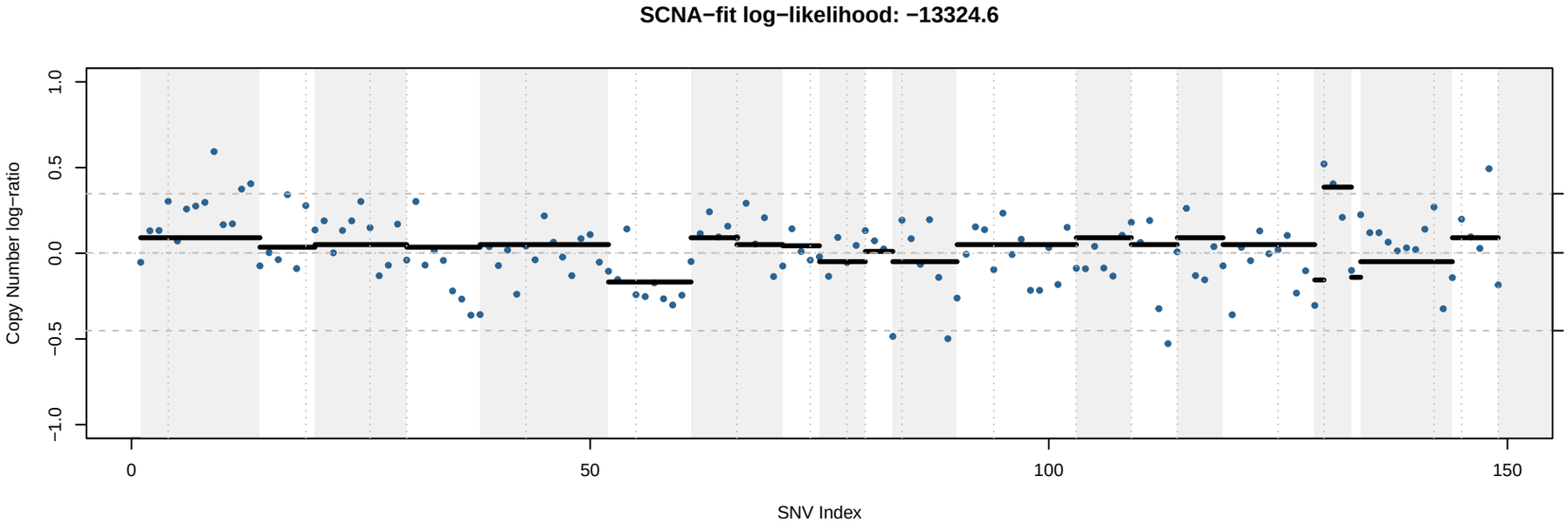

Coverage (log2)
Allelic fraction

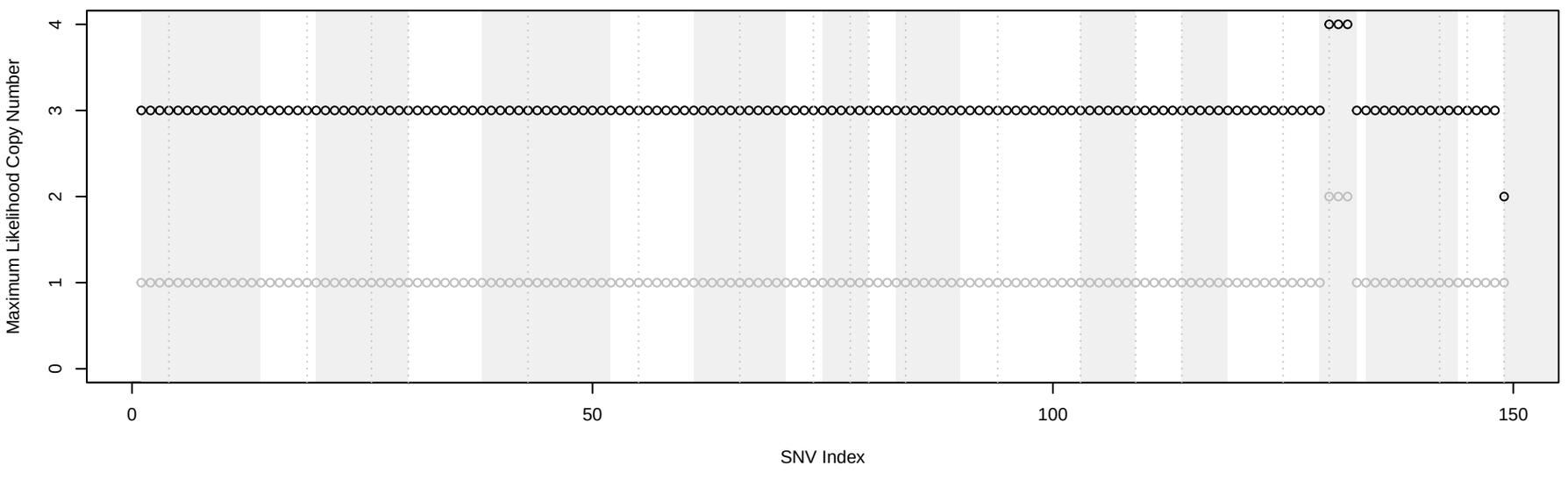

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m2
2m1

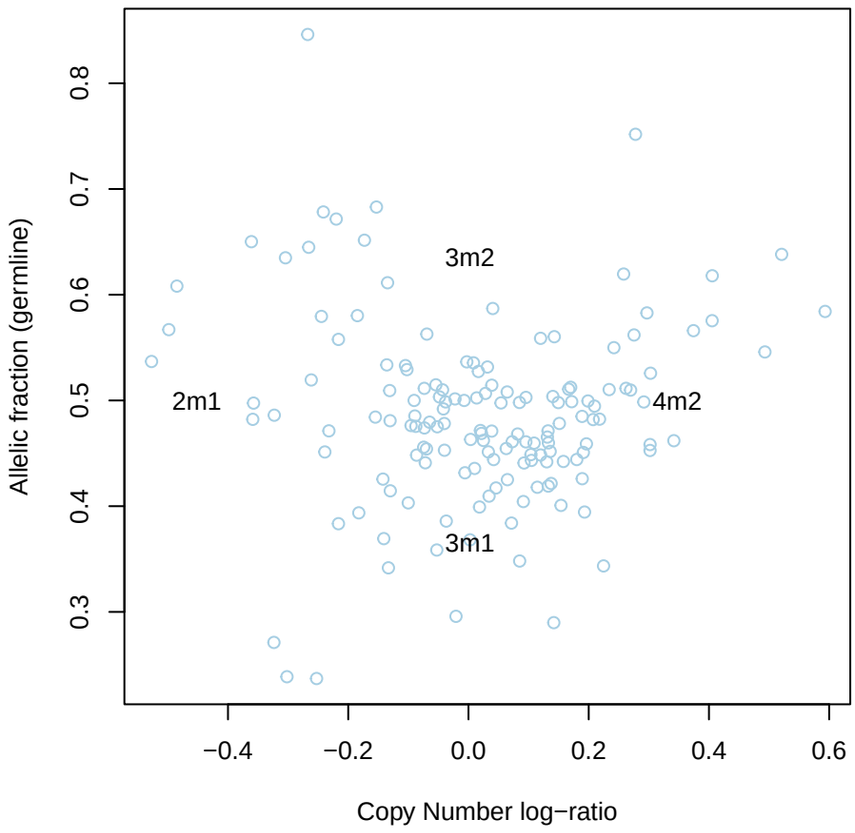

Frequency
Cellular fraction

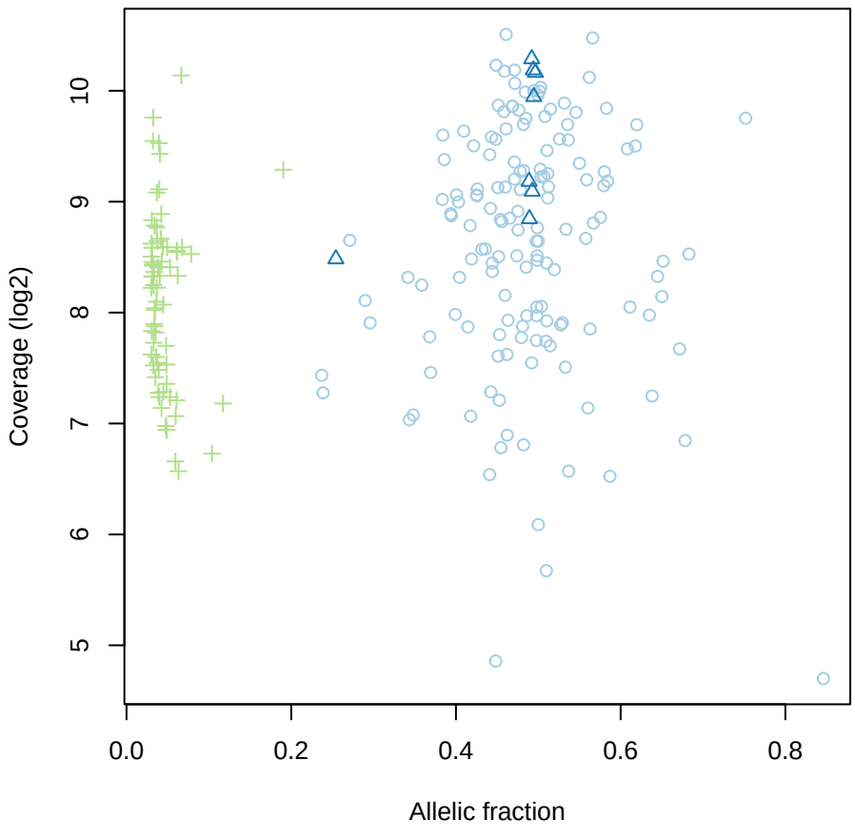

Purity: 0.74 Tumor ploidy: 2.994
2
3
4
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

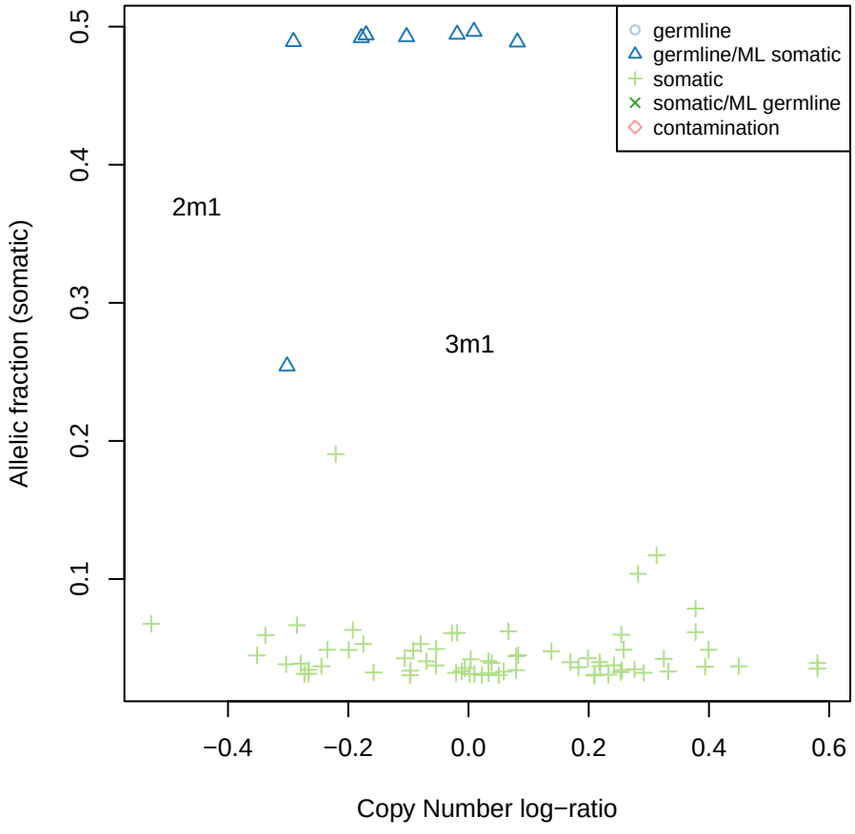

Purity: 0.74 Tumor ploidy: 2.994 SNV log−likelihood: −961.15 GoF: 45.2% Mean coverage: 558;453
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

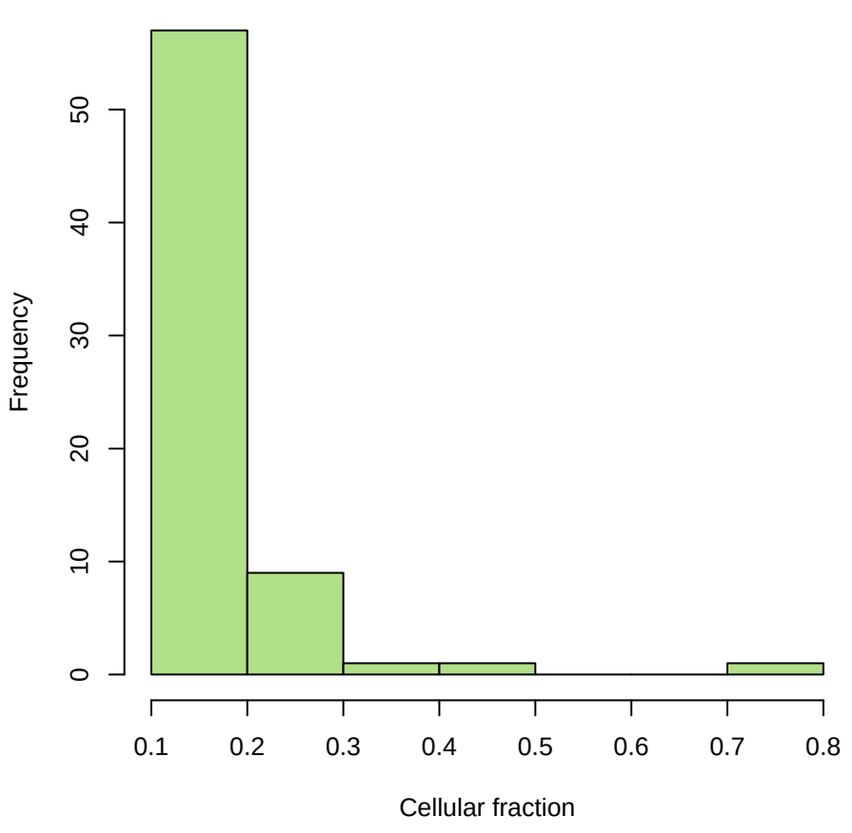

SCNA−fit log−likelihood: −13324.6
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4
0 50 100 150
SNV Index

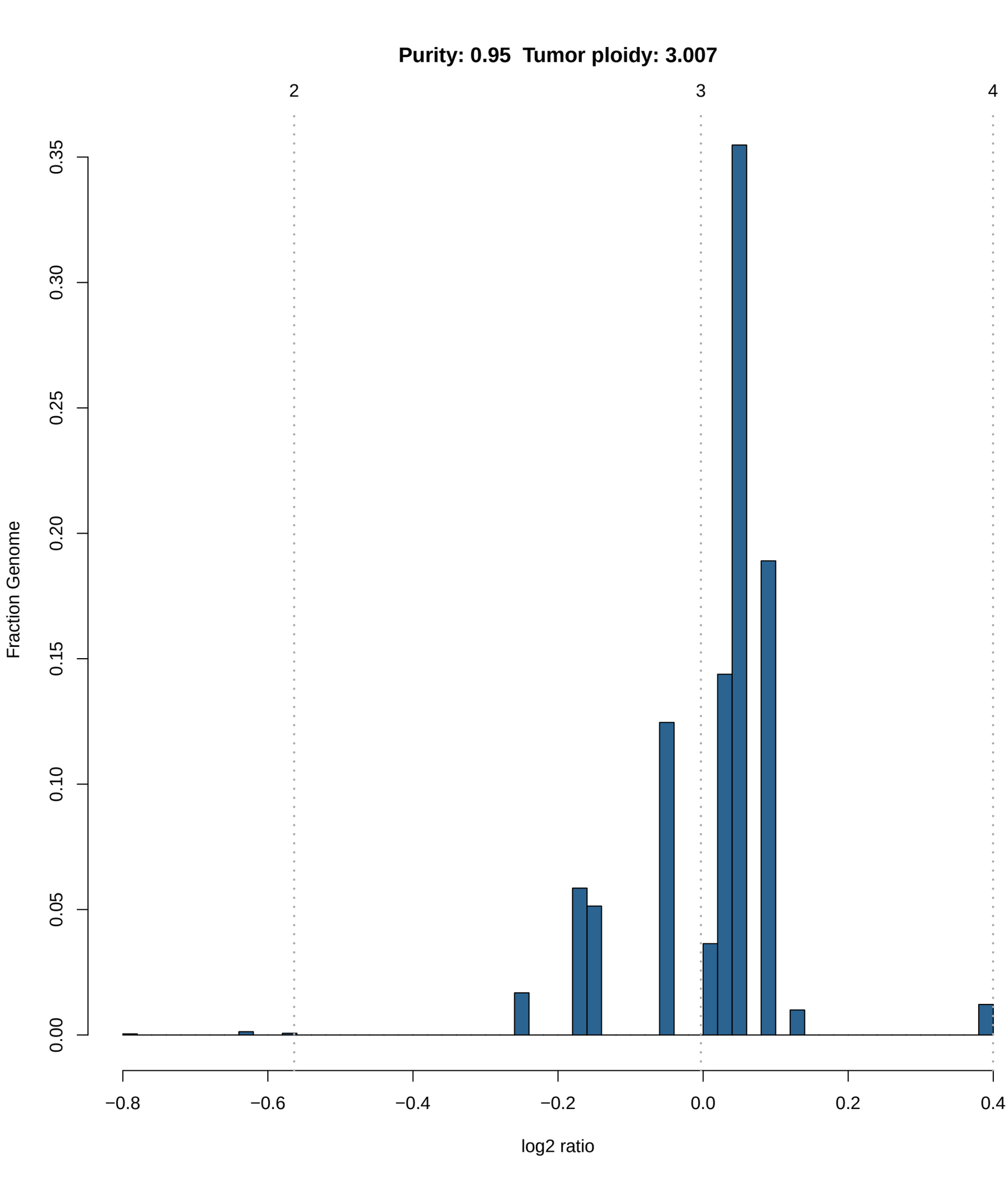

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

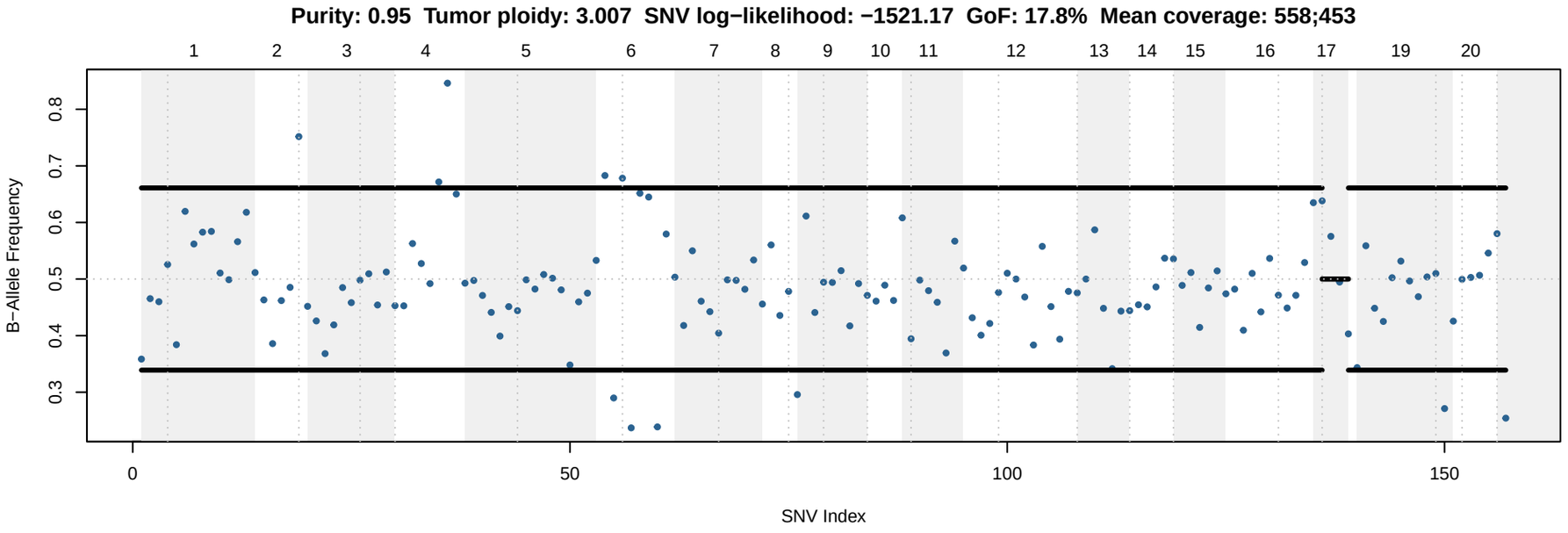

Allelic fraction (germline)
Copy Number log−ratio
2m1
3m2
4m2
3m1

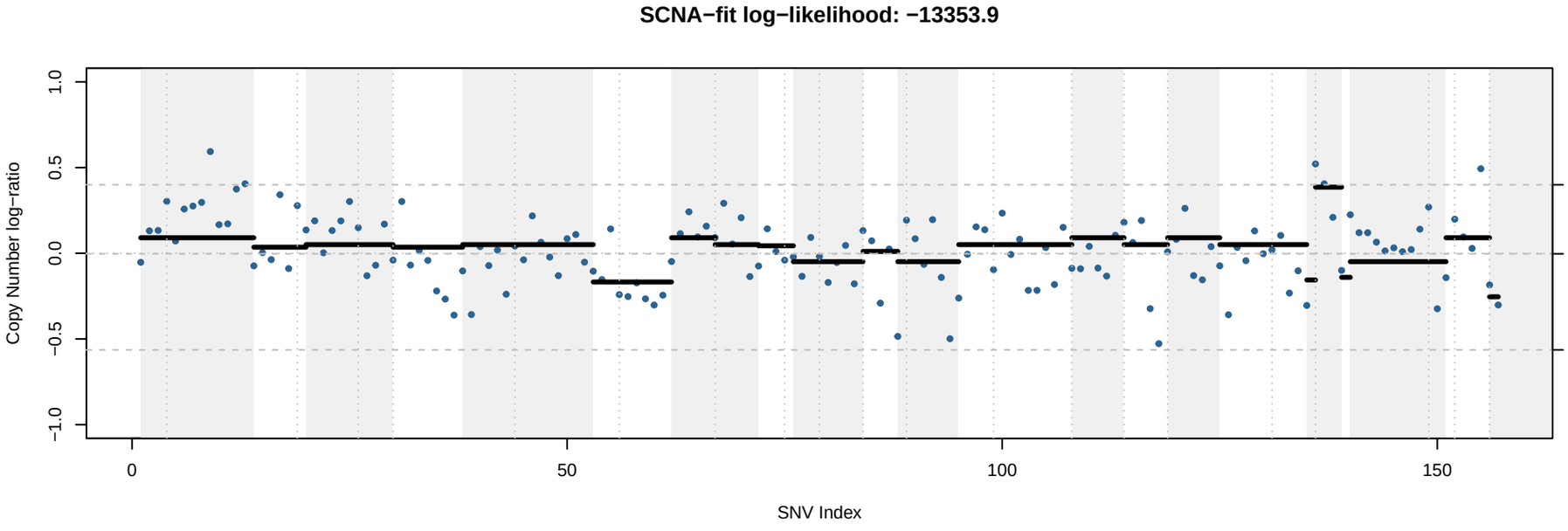

Coverage (log2)
Allelic fraction

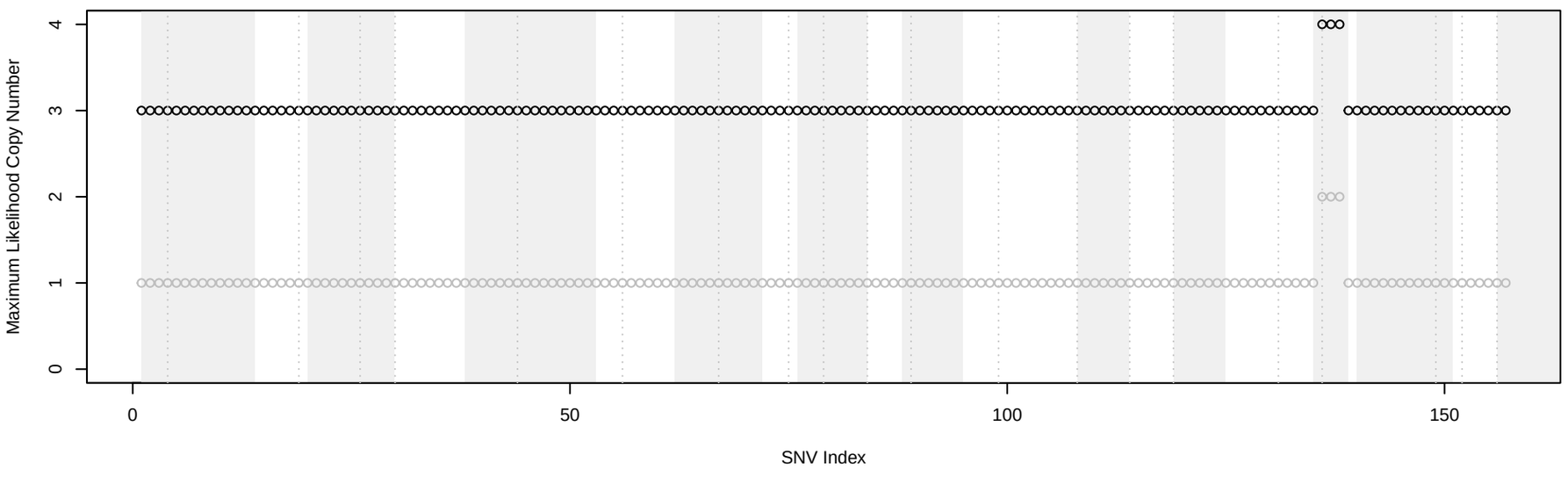

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1

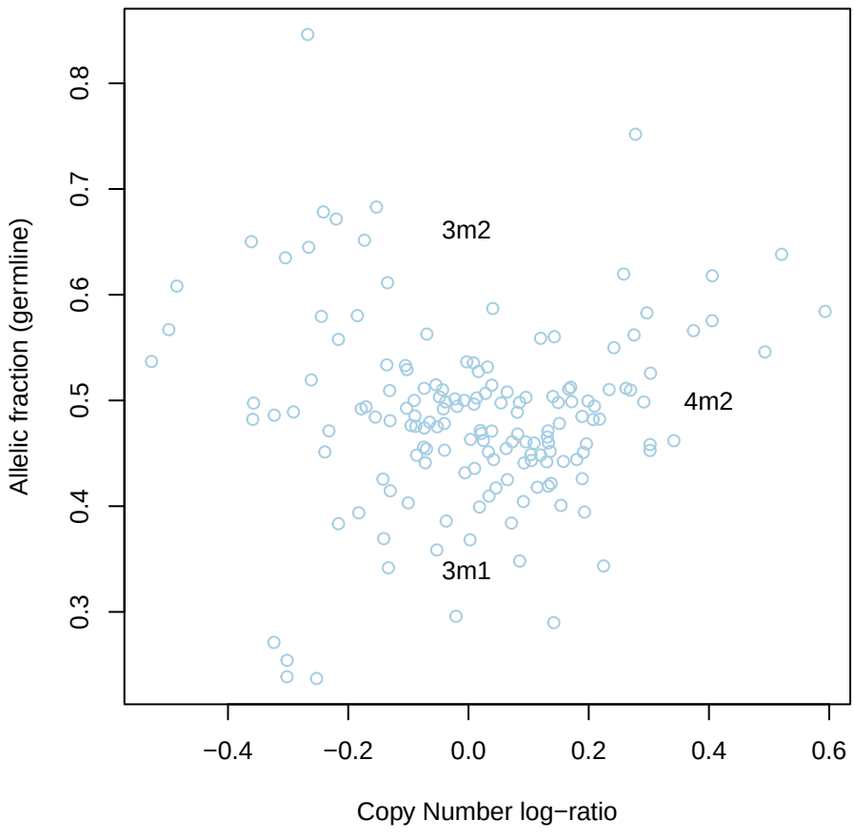

Frequency
Cellular fraction

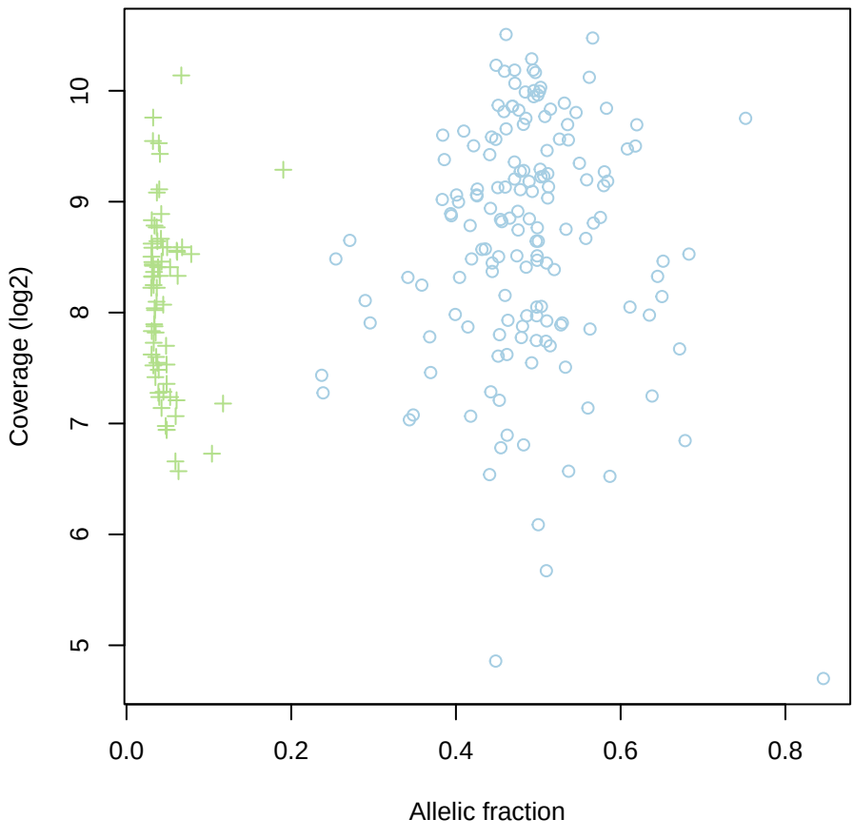

Purity: 0.95 Tumor ploidy: 3.007
2
3
4
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
log2 ratio

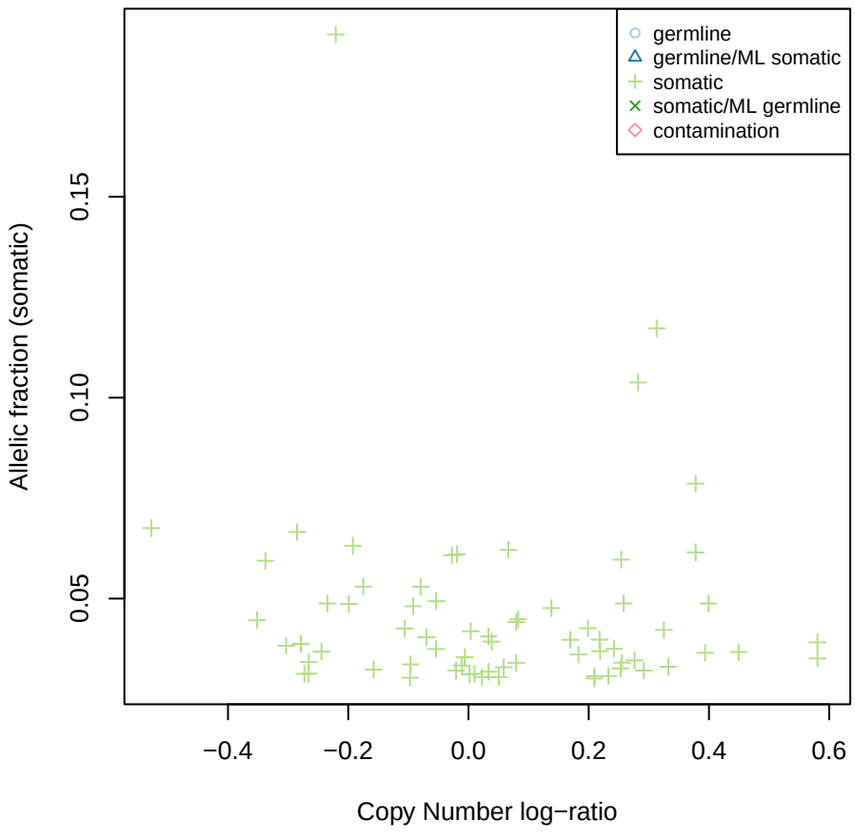

Purity: 0.95 Tumor ploidy: 3.007 SNV log−likelihood: −1521.17 GoF: 17.8% Mean coverage: 558;453
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

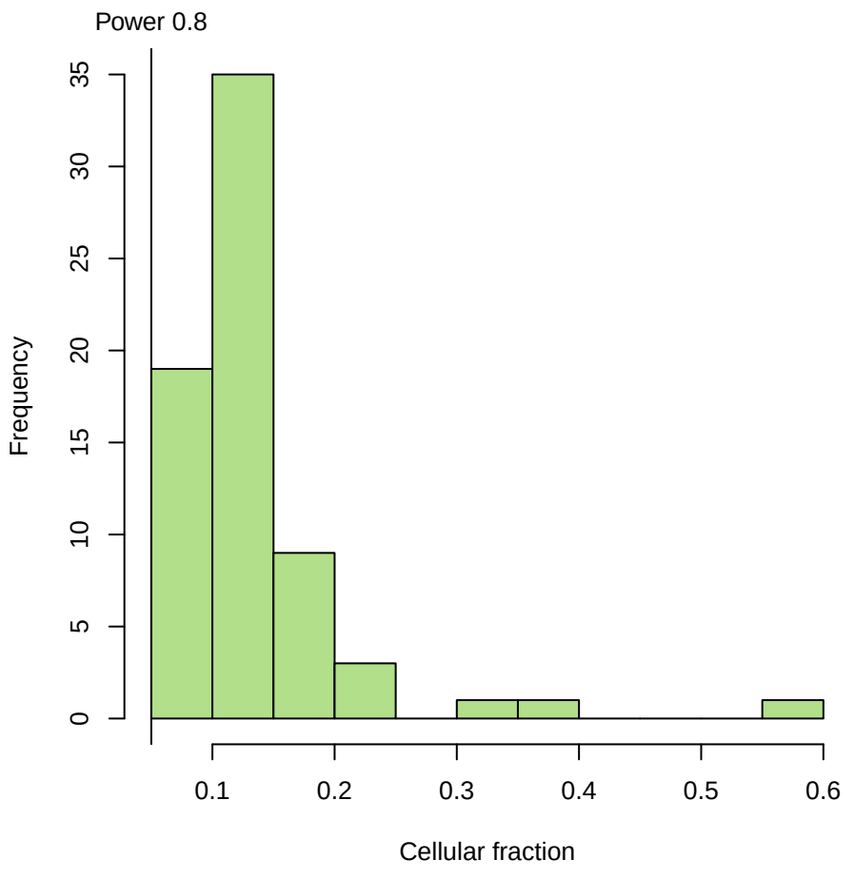

SCNA−fit log−likelihood: −13353.9
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4
0 50 100 150
SNV Index


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


Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
0.8
3m2
4m2
3m1
−0.4
−0.2
0.0
0.2
0.4
0.6
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
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio


Power 0.8
Frequency
0
5
10
15
20
25
30
35
0.1
0.2
0.3
0.4
0.5
0.6
Cellular fraction