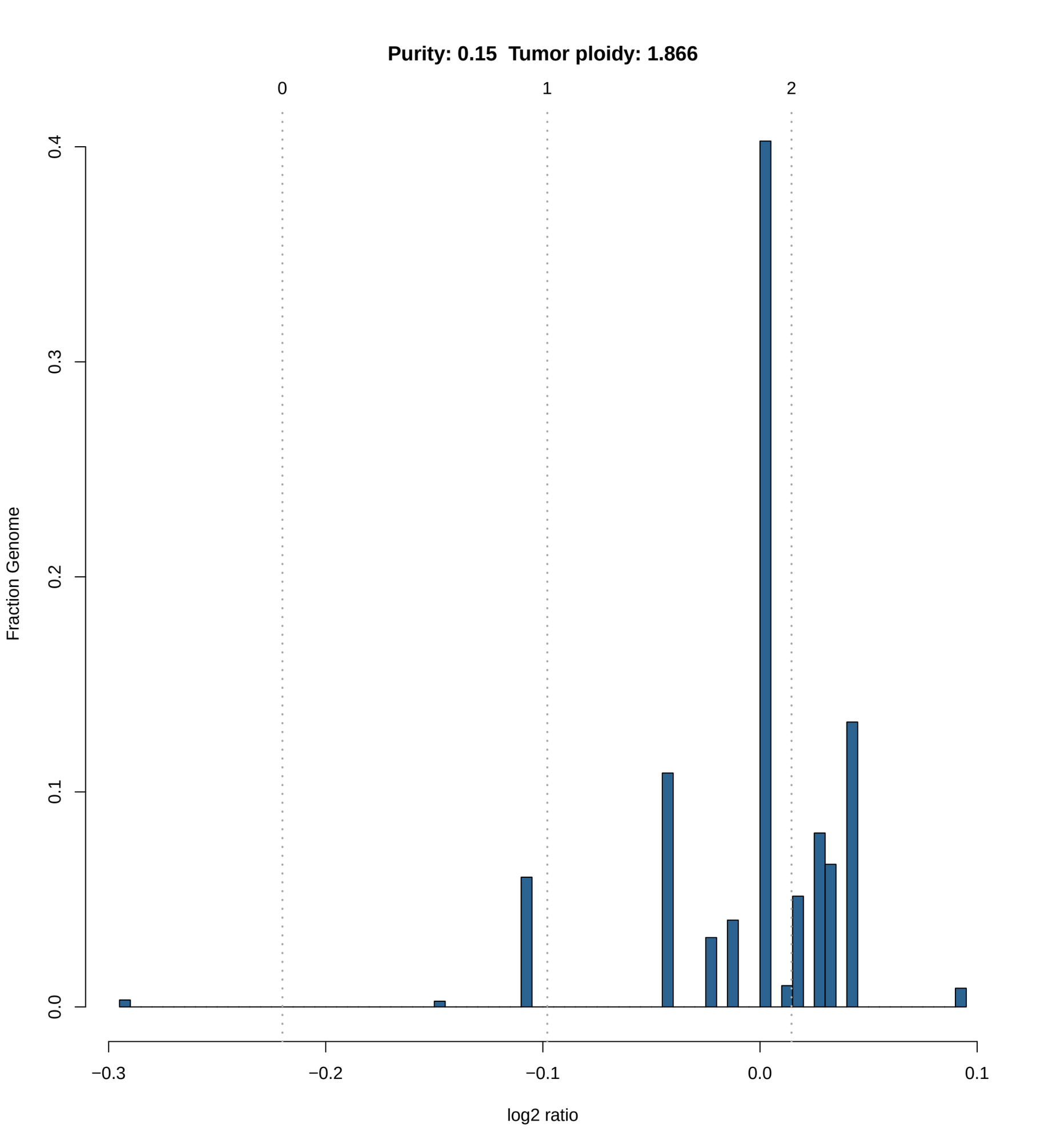
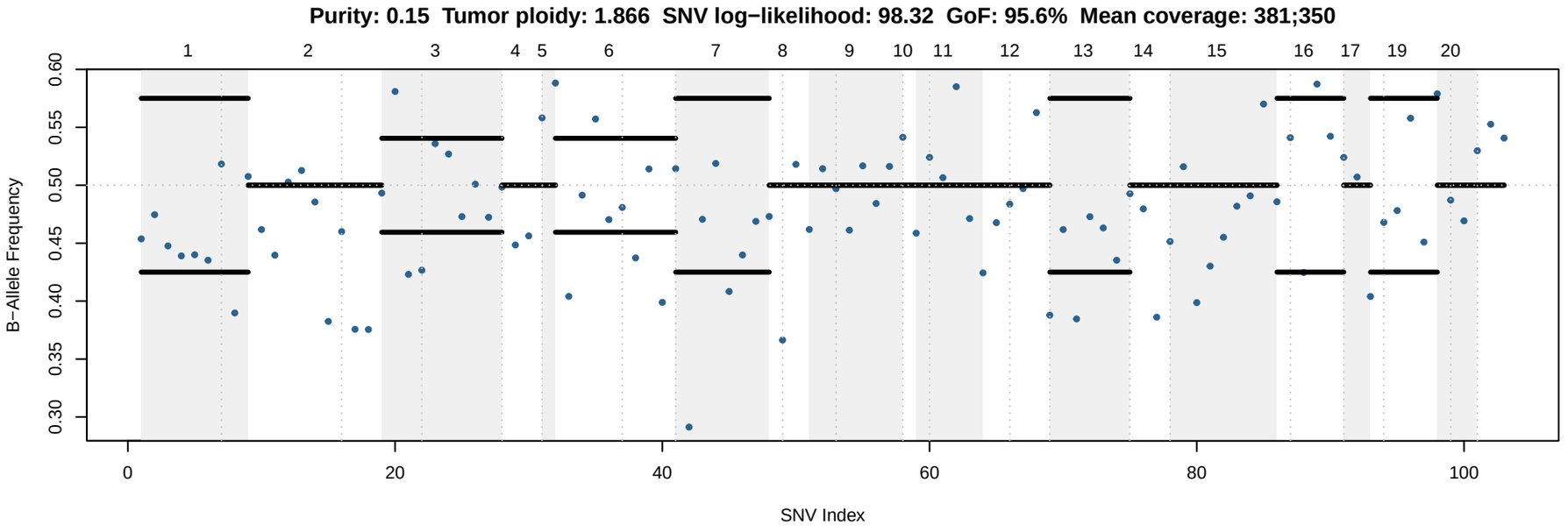
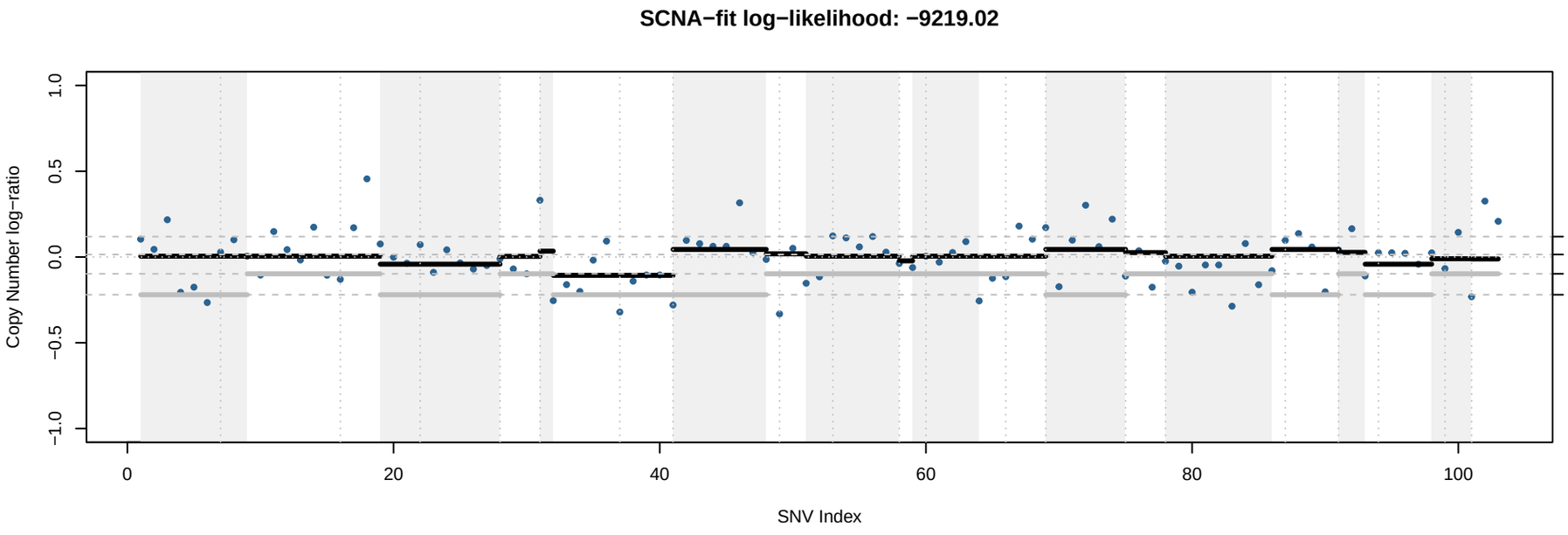
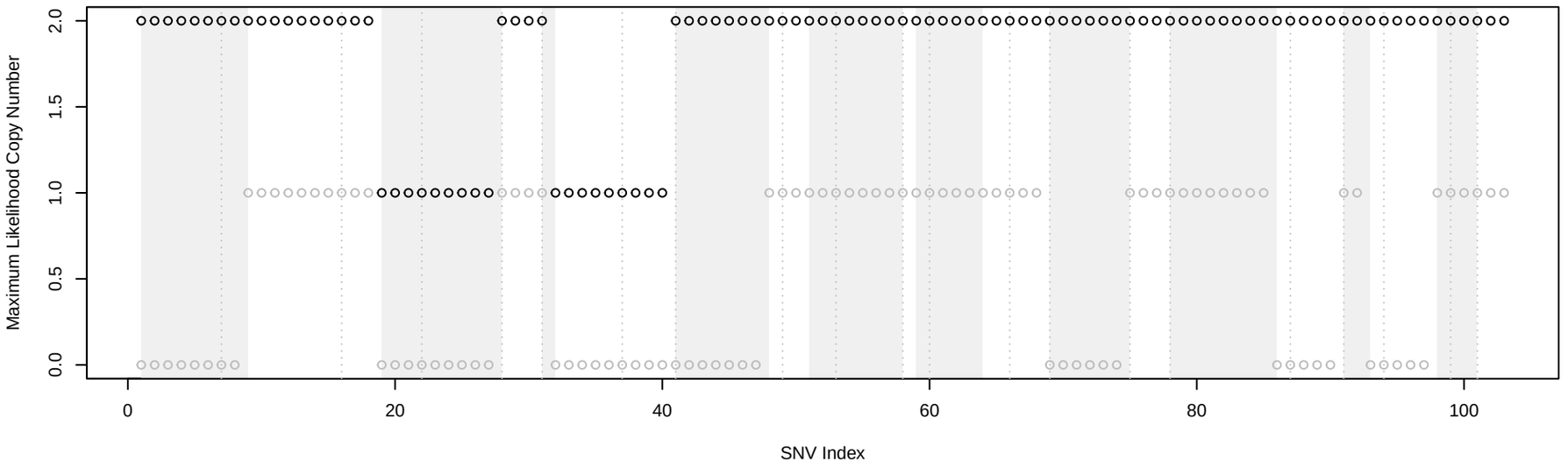
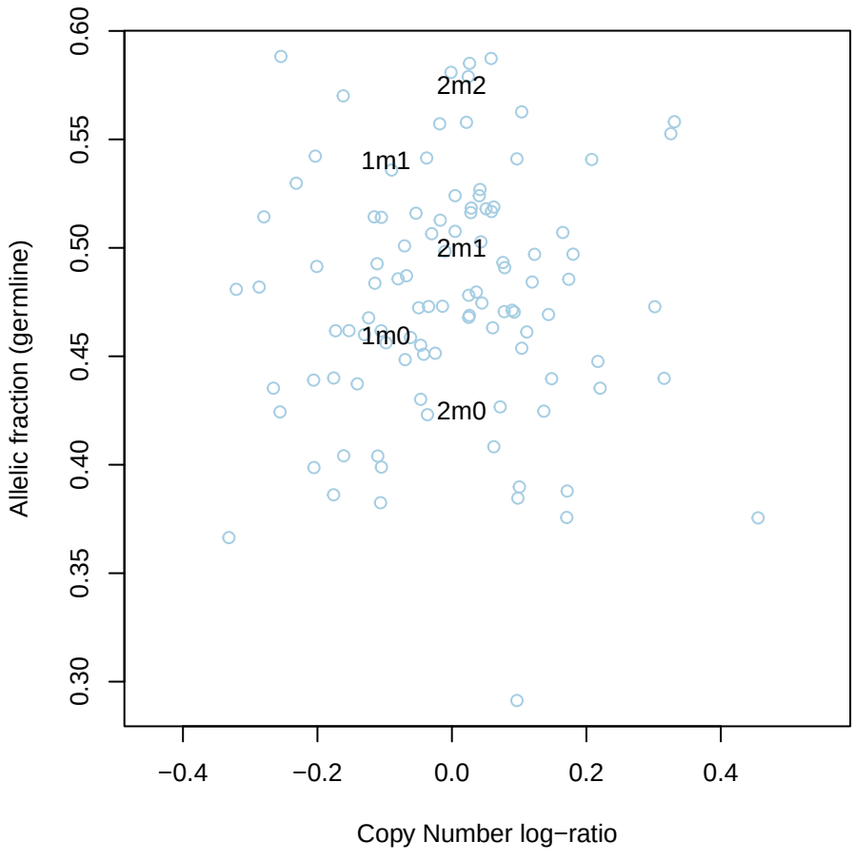
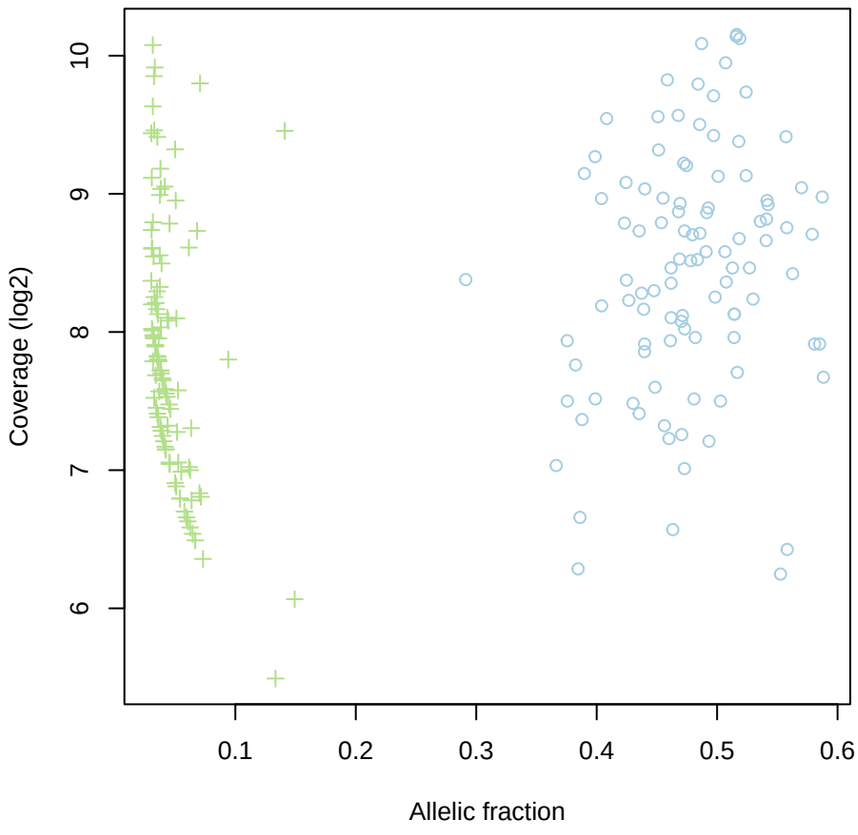

Purity: 0.15 Tumor ploidy: 1.866
0
1
2
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.3
−0.2
−0.1
0.0
0.1
log2 ratio

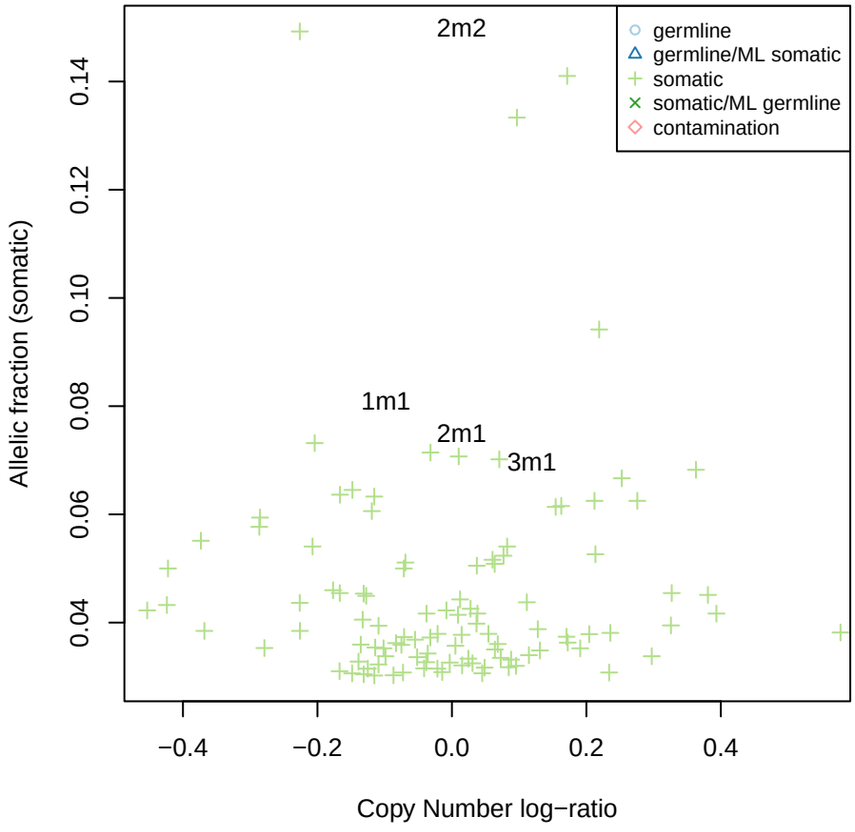

Purity: 0.15 Tumor ploidy: 1.866 SNV log−likelihood: 98.32 GoF: 95.6% Mean coverage: 381;350
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

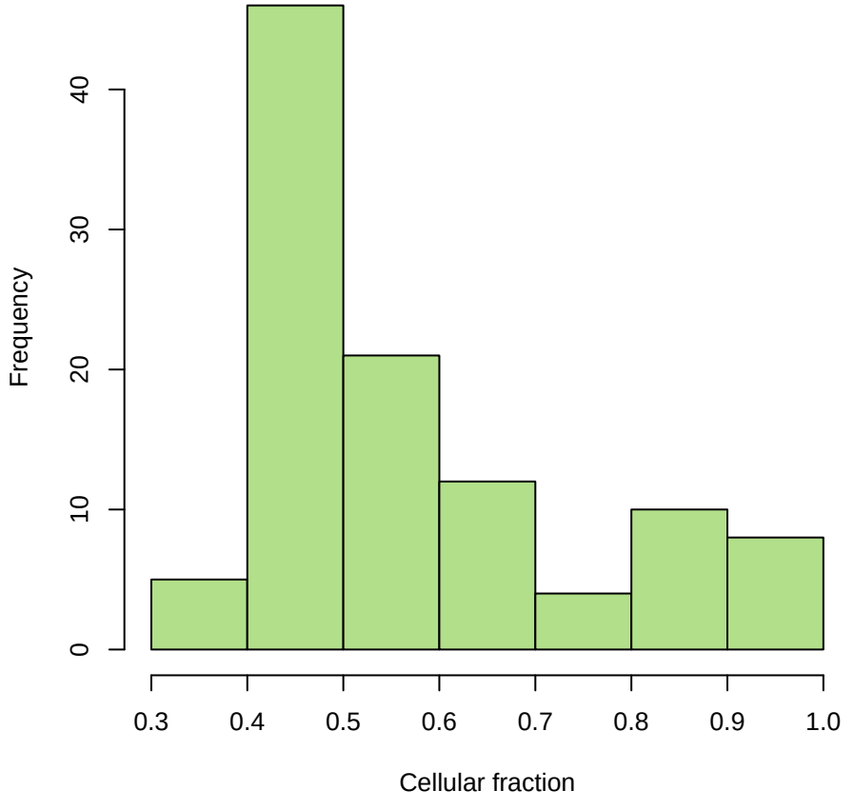

SCNA−fit log−likelihood: −9219.02
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2
0 20 40 60 80 100
SNV Index

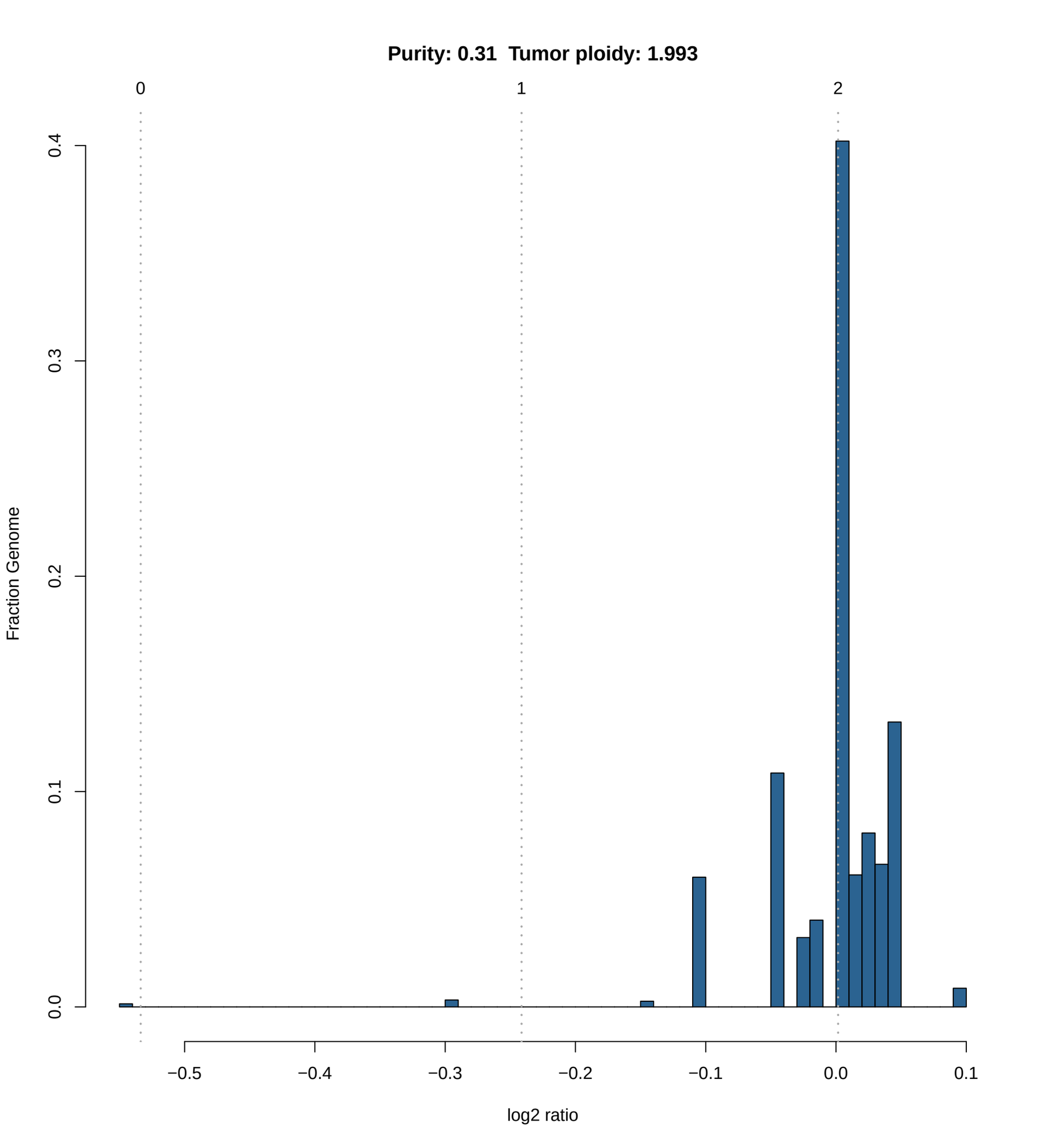

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 20 40 60 80 100
SNV Index

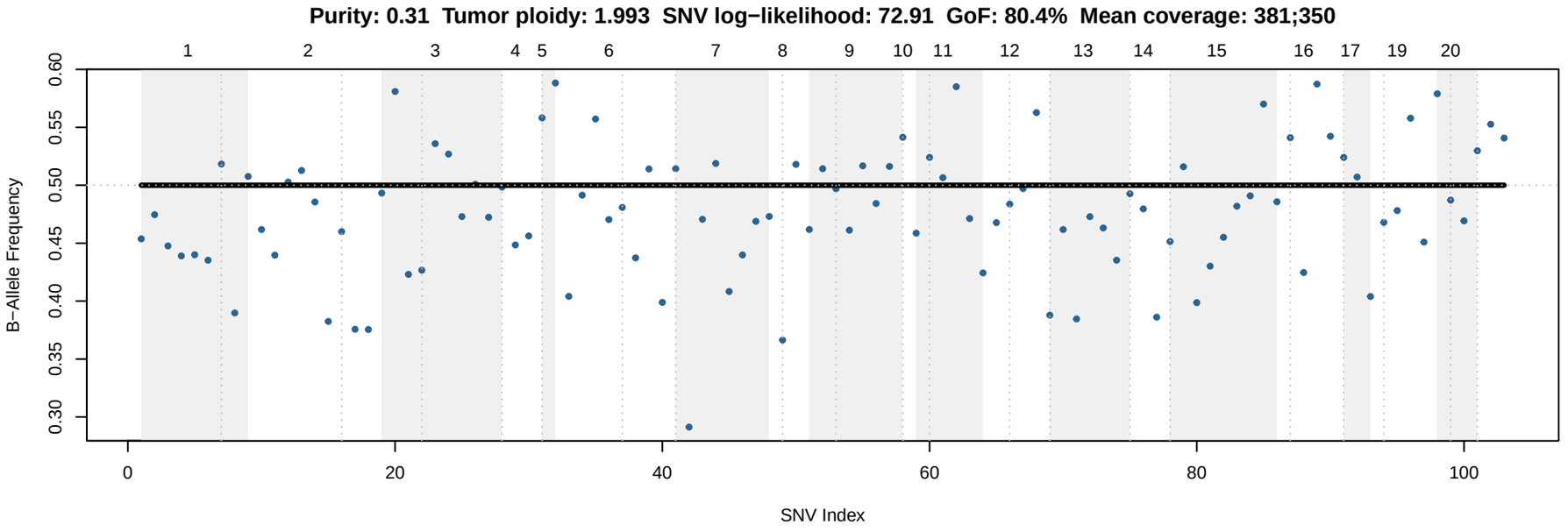

Allelic fraction (germline)
Copy Number log−ratio
2m2
1m1
2m1
1m0
2m0

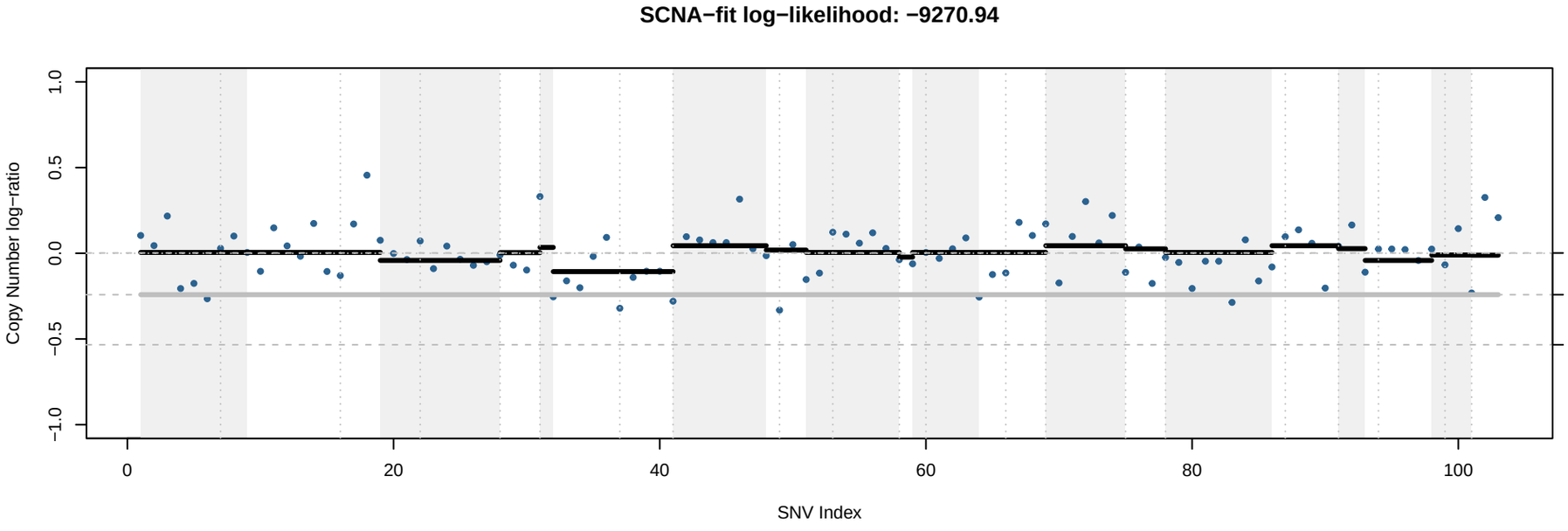

Coverage (log2)
Allelic fraction

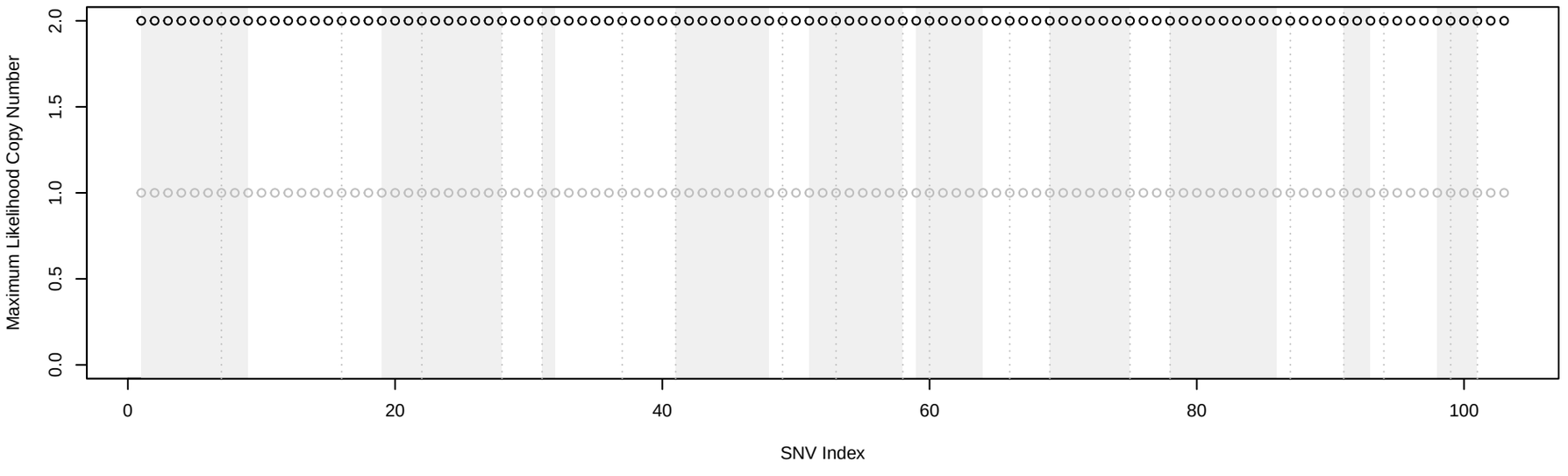

Allelic fraction (somatic)
Copy Number log−ratio
2m2
1m1
2m1
3m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

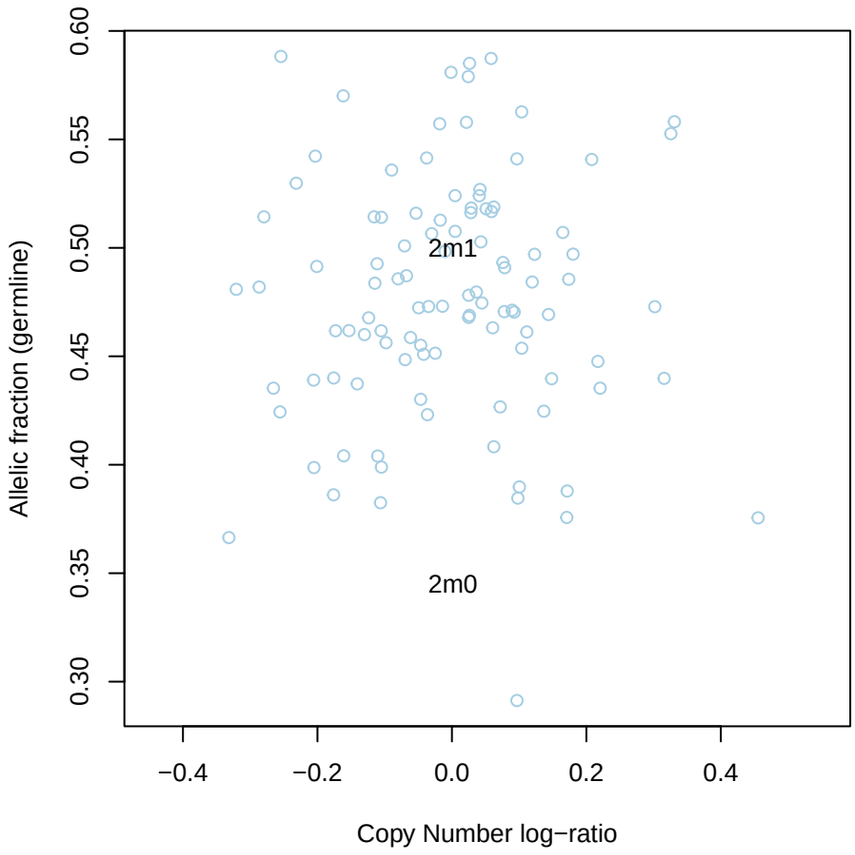

Frequency
Cellular fraction

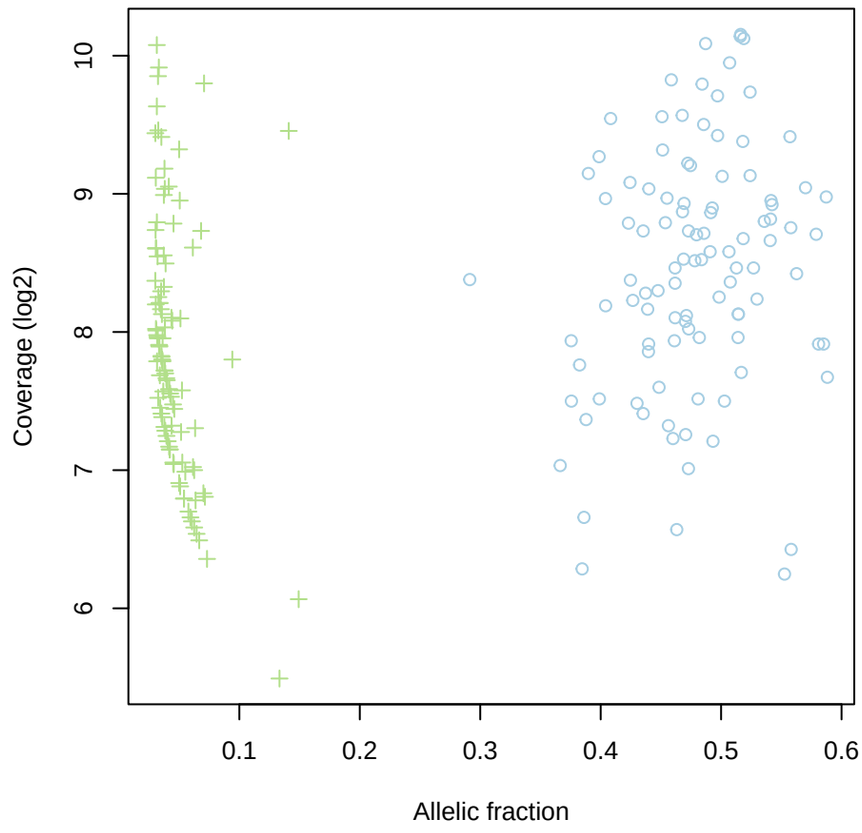

Purity: 0.31 Tumor ploidy: 1.993
0
1
2
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
−0.4
−0.3
−0.2
−0.1
0.0
0.1
log2 ratio

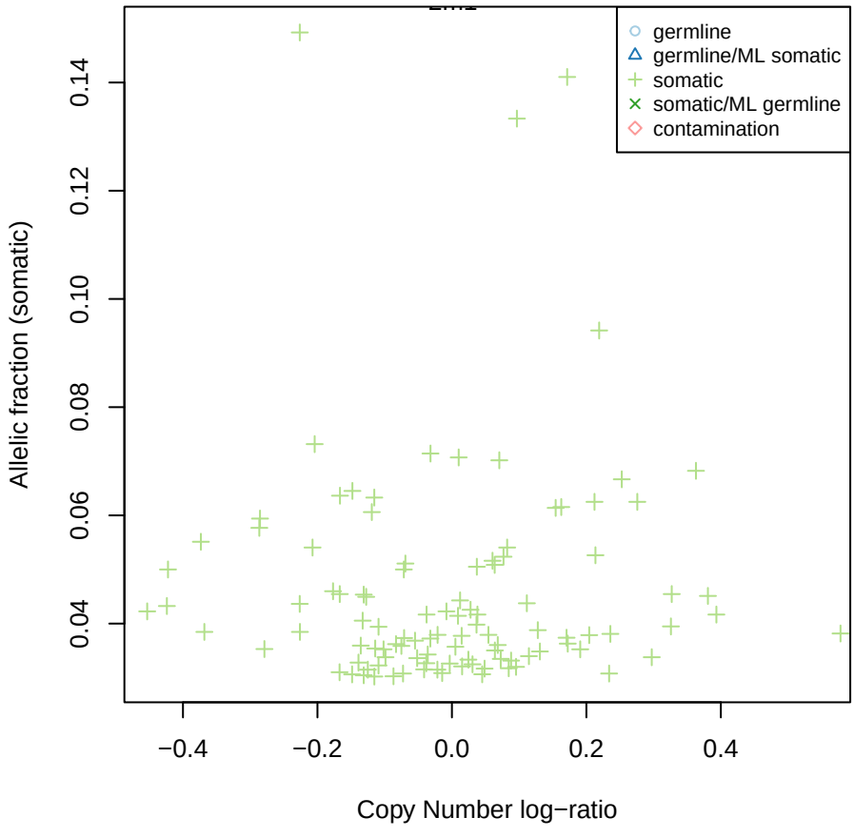

Purity: 0.31 Tumor ploidy: 1.993 SNV log−likelihood: 72.91 GoF: 80.4% Mean coverage: 381;350
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

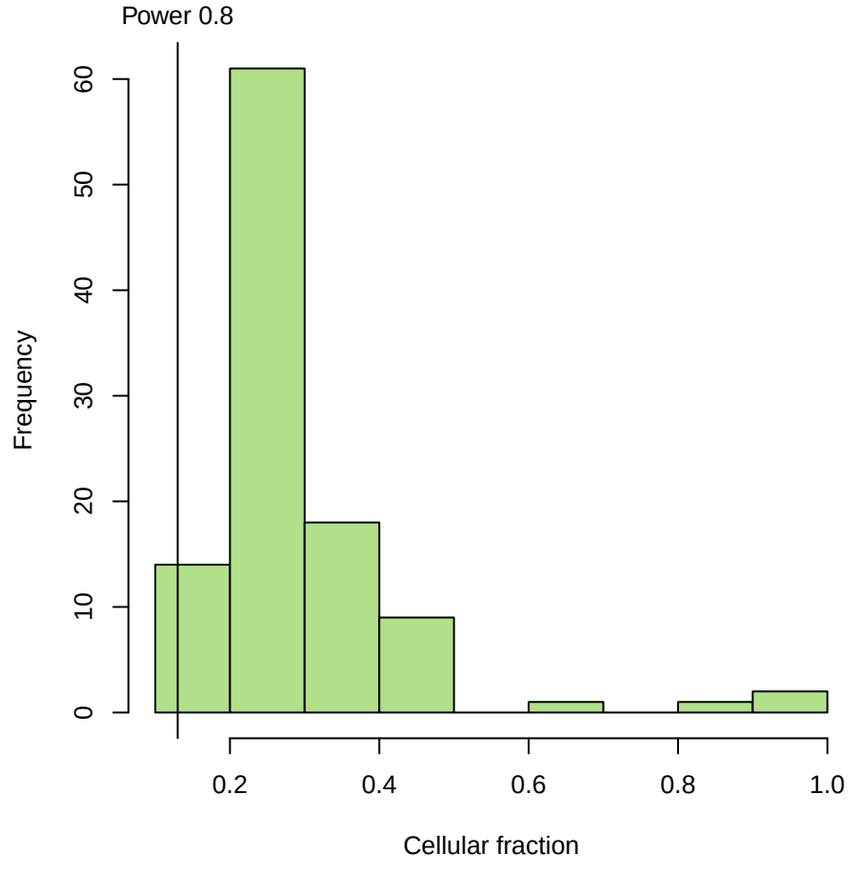

SCNA−fit log−likelihood: −9270.94
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2
0 20 40 60 80 100
SNV Index

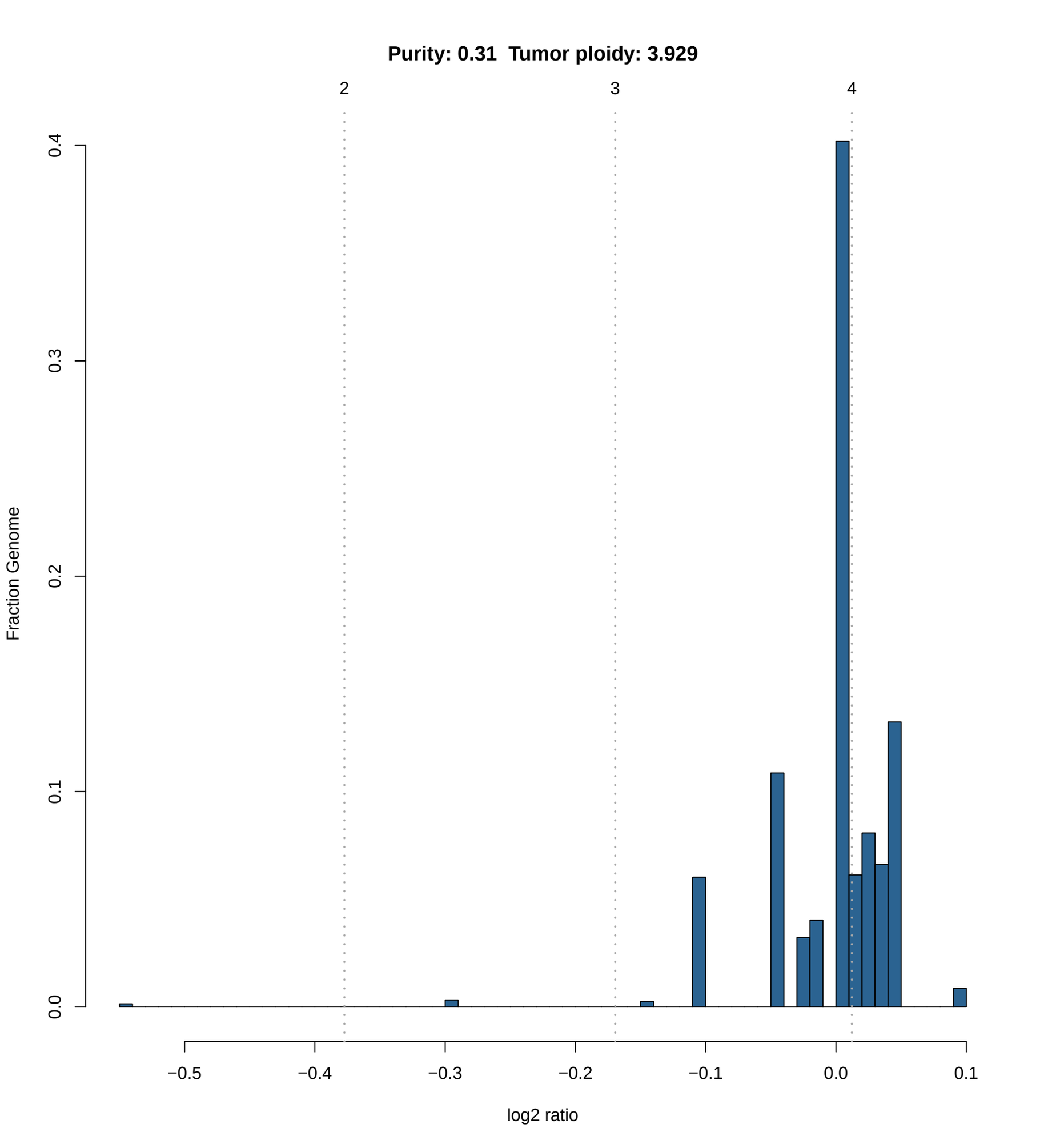

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 20 40 60 80 100
SNV Index

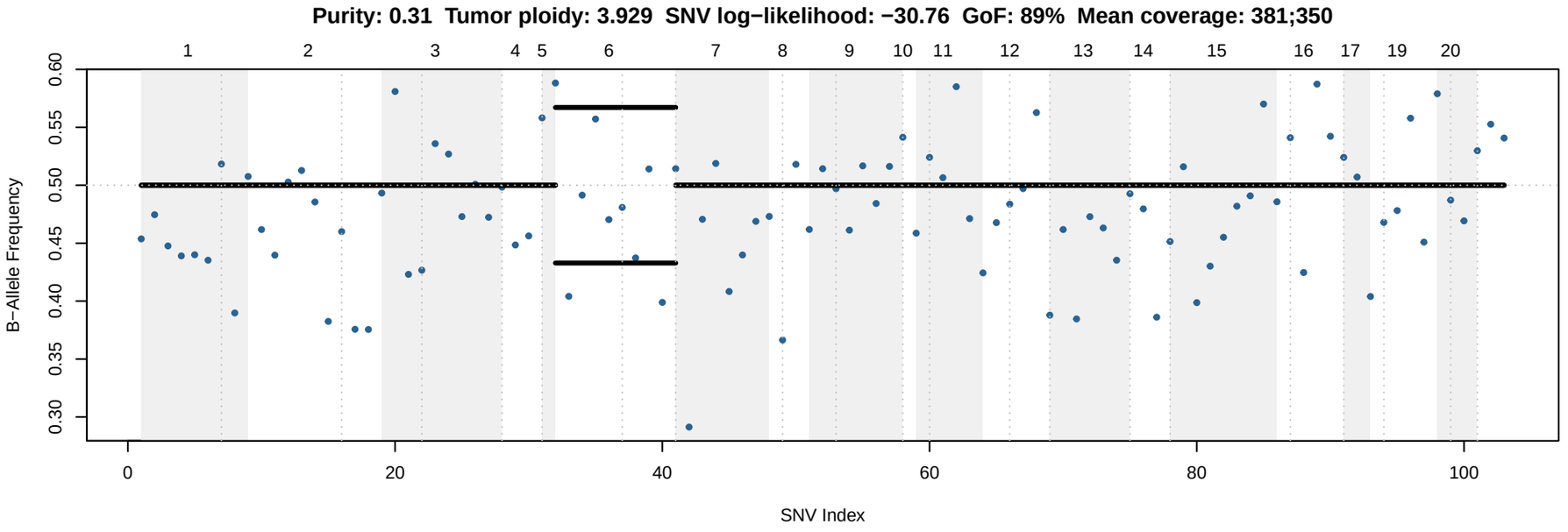

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
2m1
2m0
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

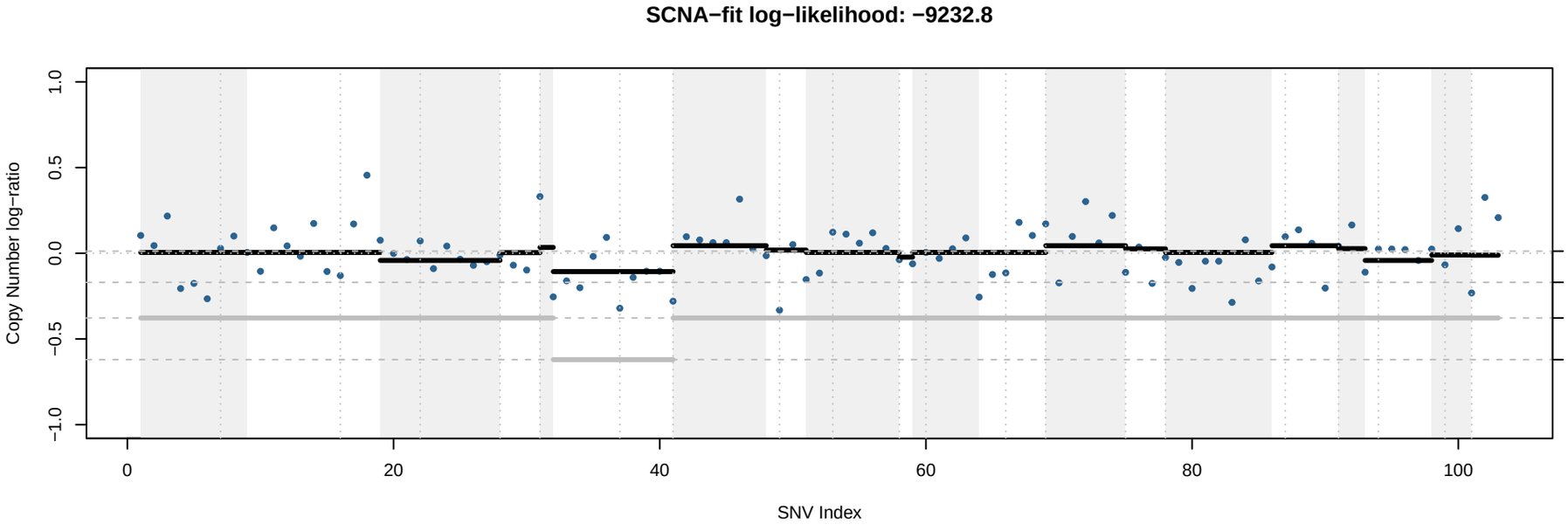

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

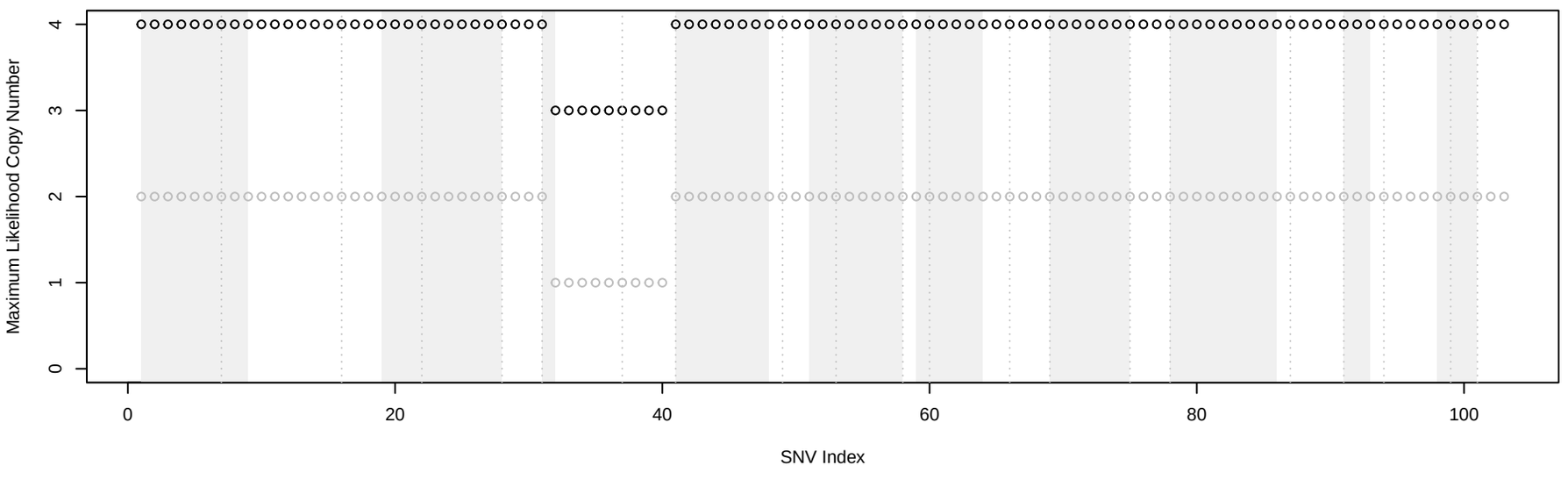

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

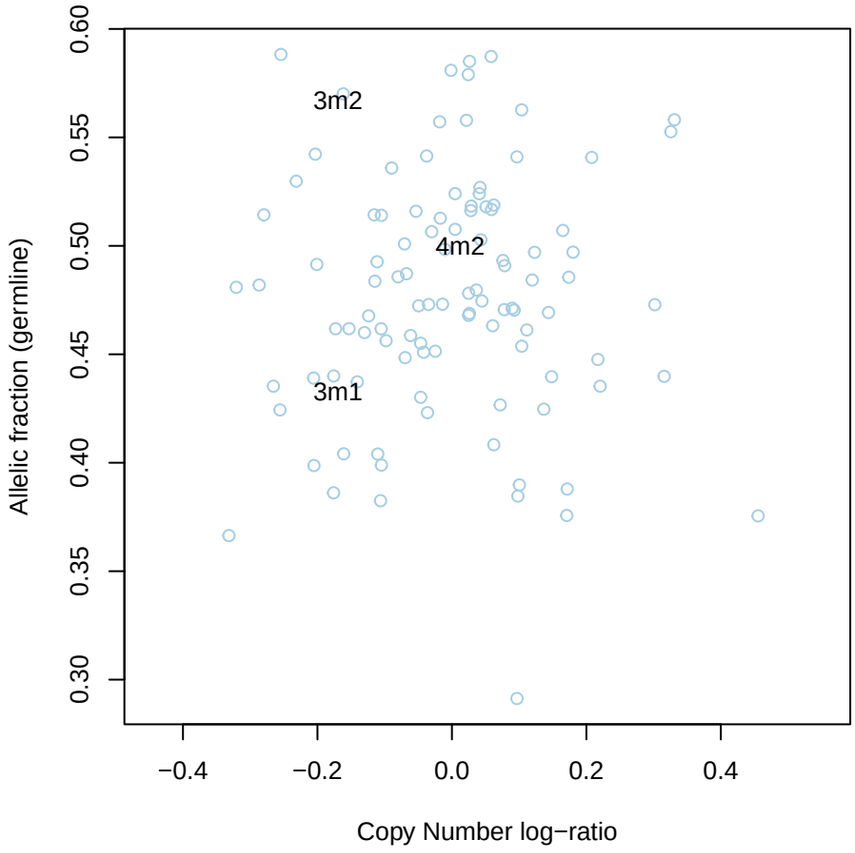

Power 0.8
Frequency
0
10
20
30
40
50
60
0.2
0.4
0.6
0.8
1.0
Cellular fraction

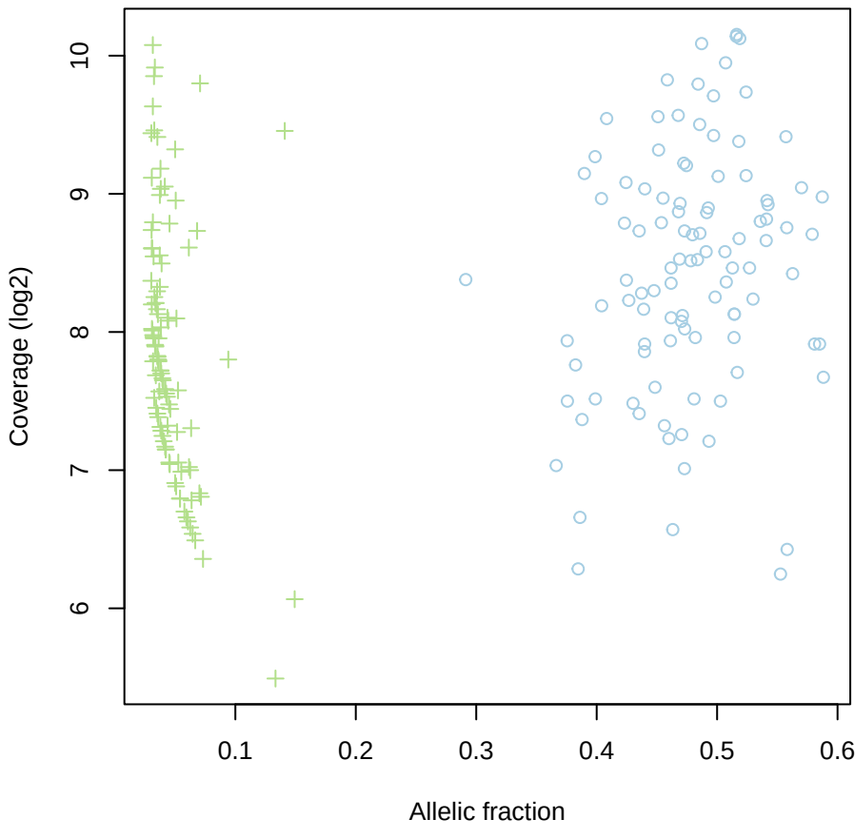

Purity: 0.31 Tumor ploidy: 3.929
2
3
4
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
−0.4
−0.3
−0.2
−0.1
0.0
0.1
log2 ratio

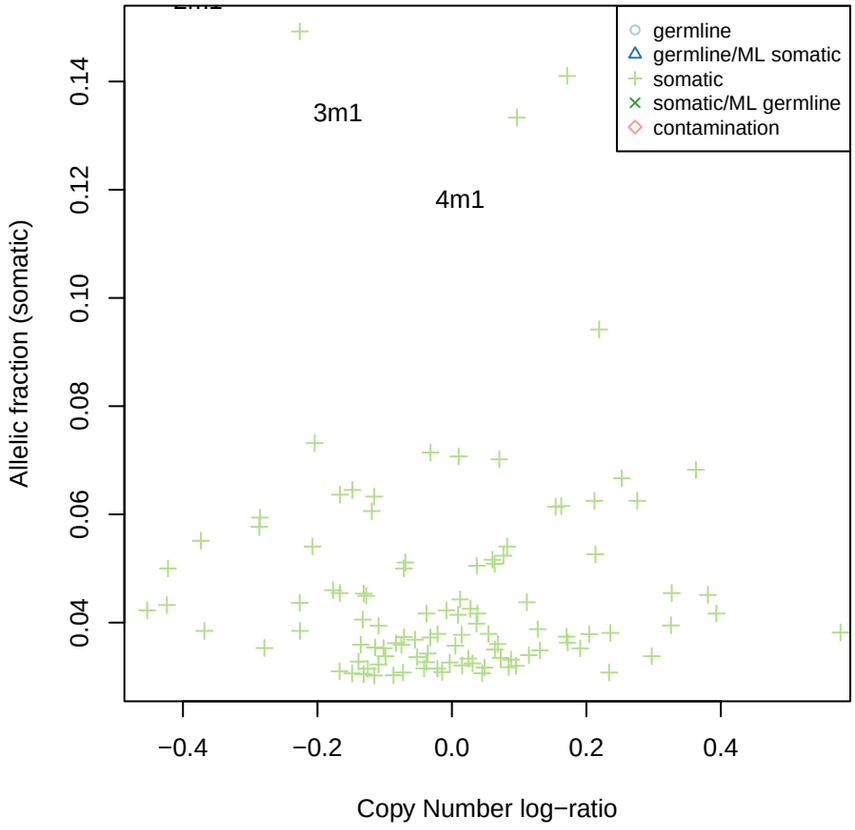

Purity: 0.31 Tumor ploidy: 3.929 SNV log−likelihood: −30.76 GoF: 89% Mean coverage: 381;350
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

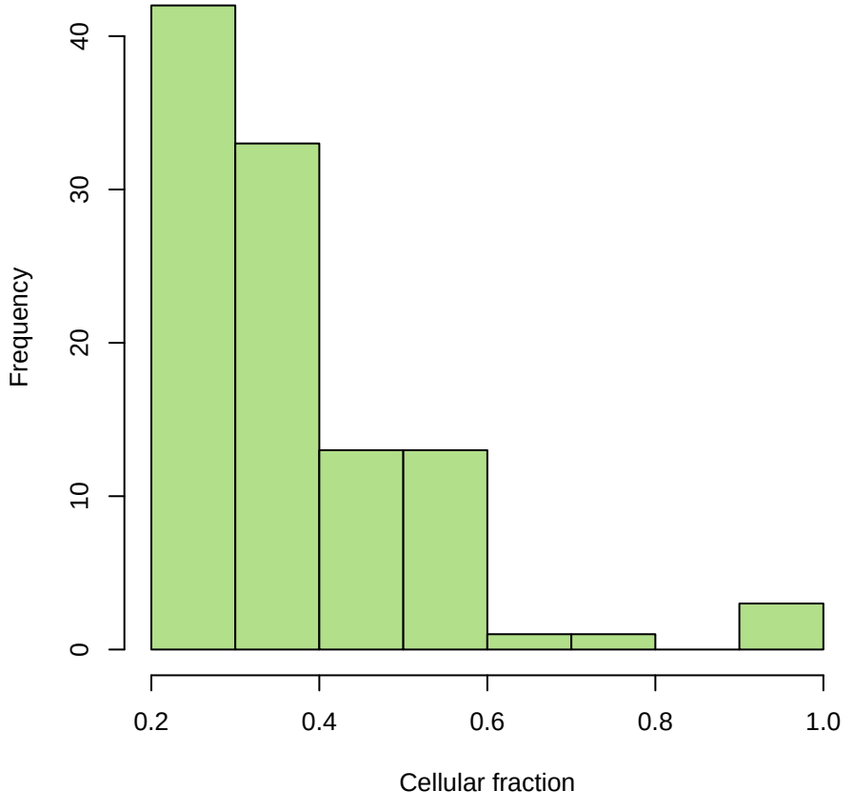

SCNA−fit log−likelihood: −9232.8
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4
0 20 40 60 80 100
SNV Index

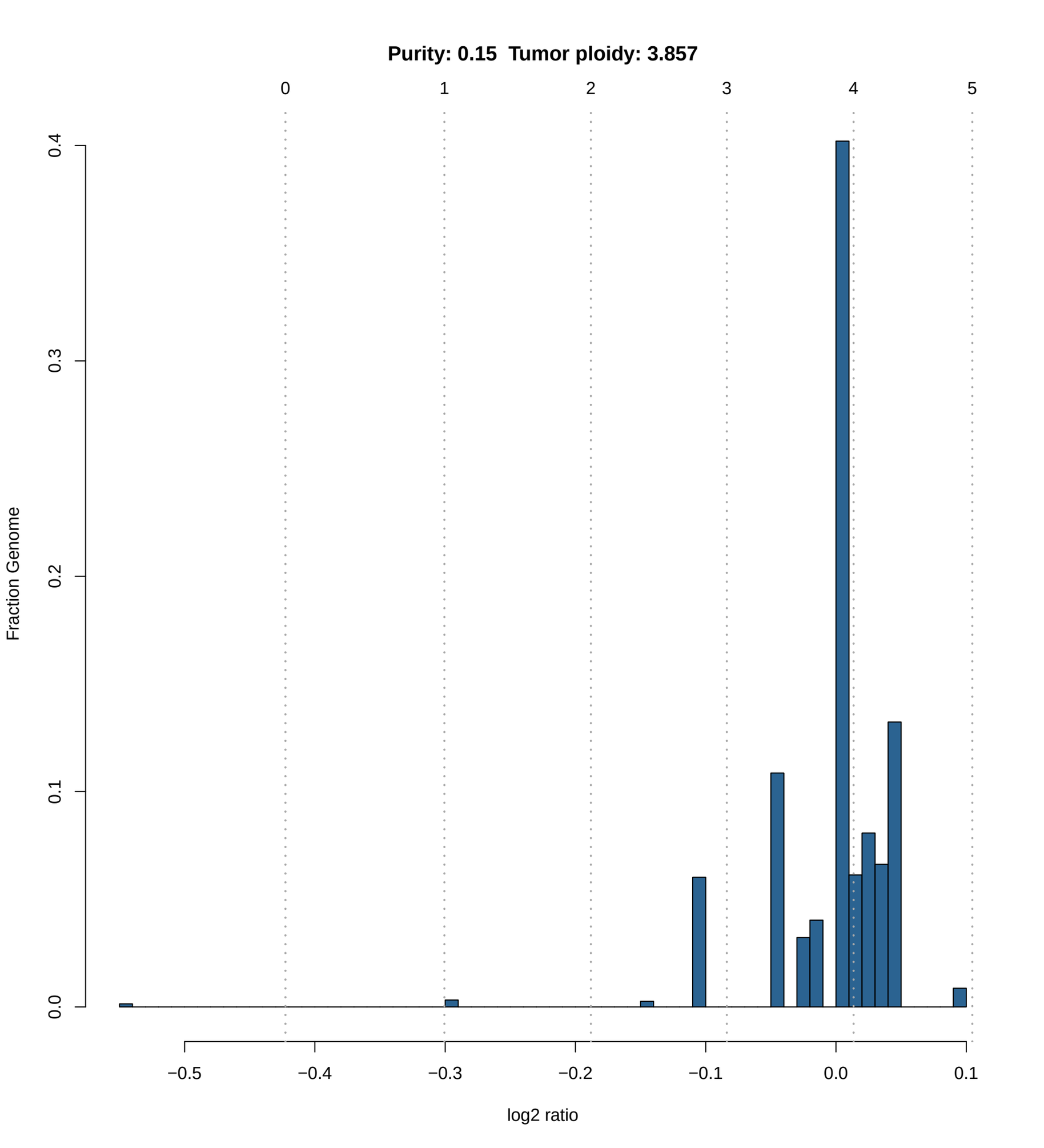

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100
SNV Index

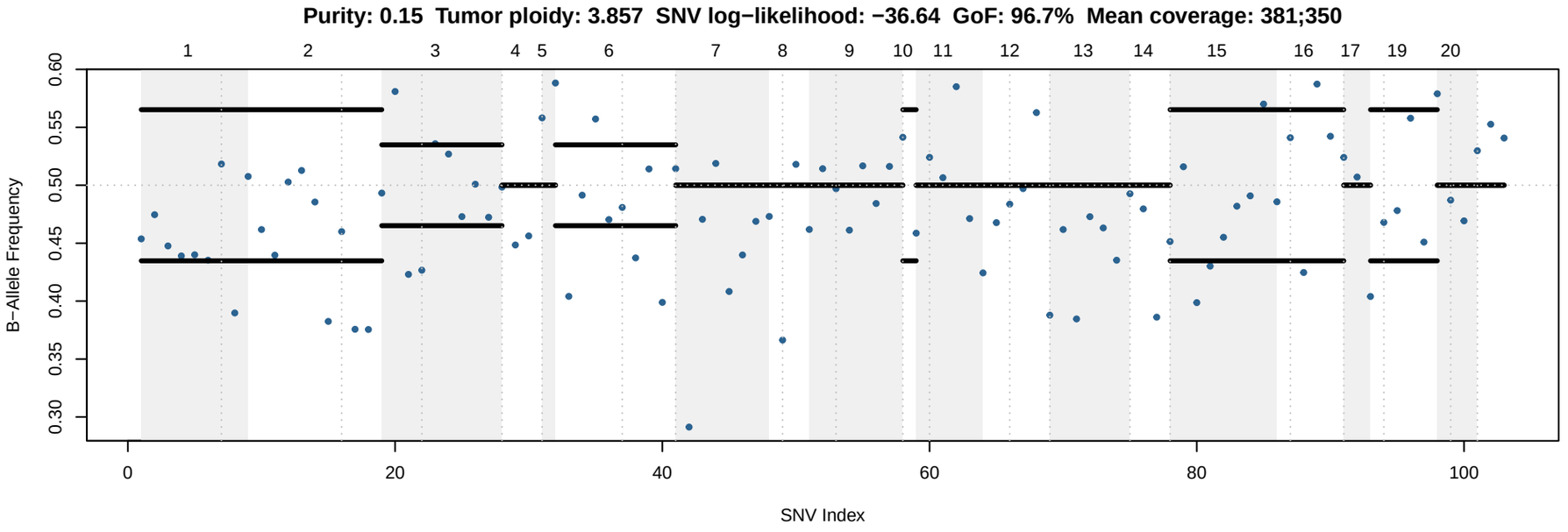

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
3m2
4m2
3m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

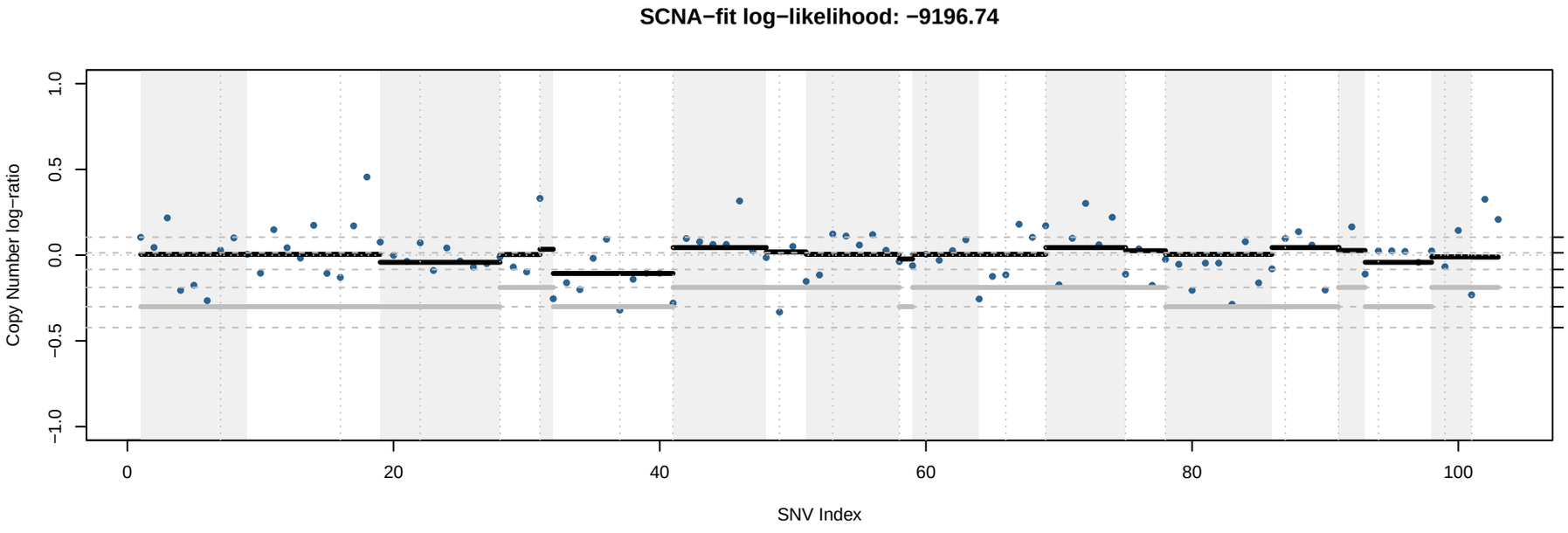

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

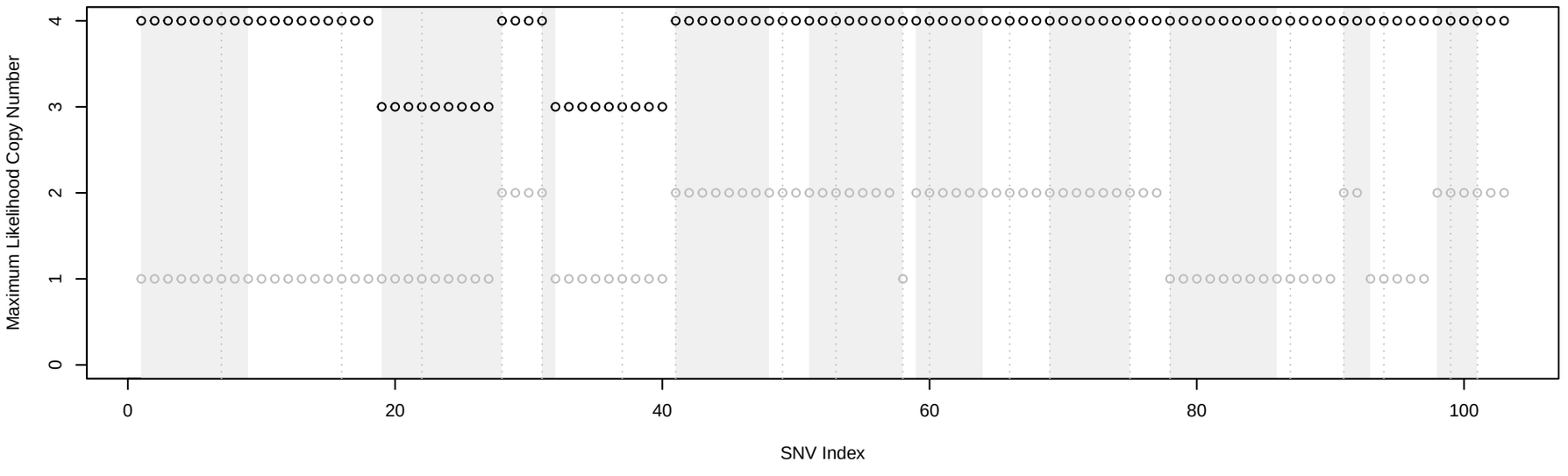

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
3m1
4m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

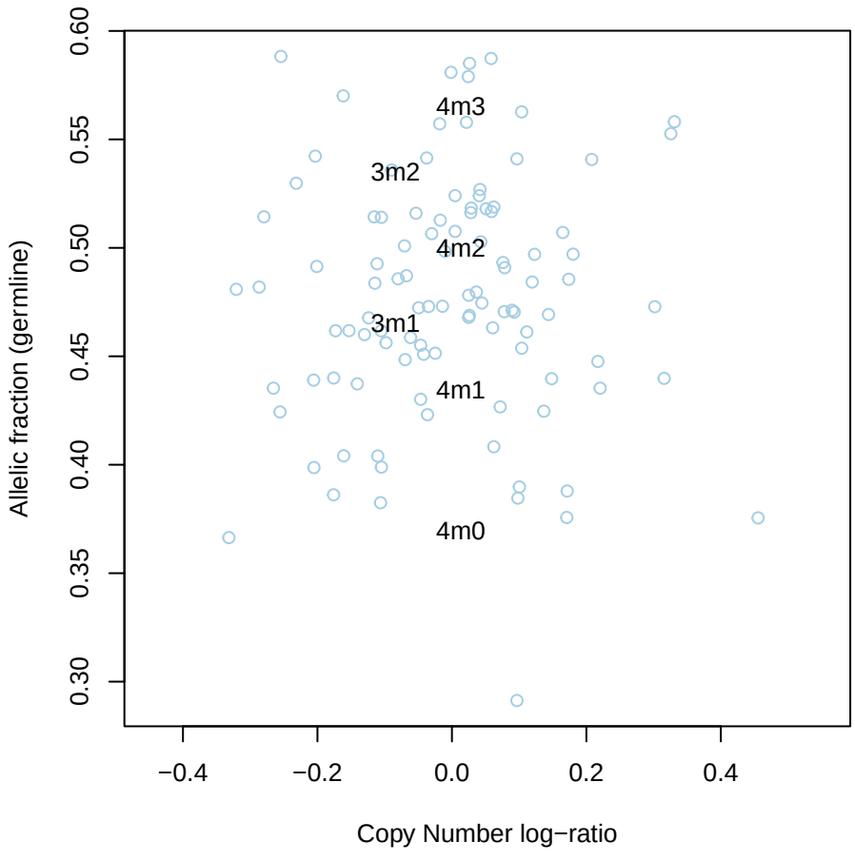

Frequency
0
10
20
30
40
0.2
0.4
0.6
0.8
1.0
Cellular fraction

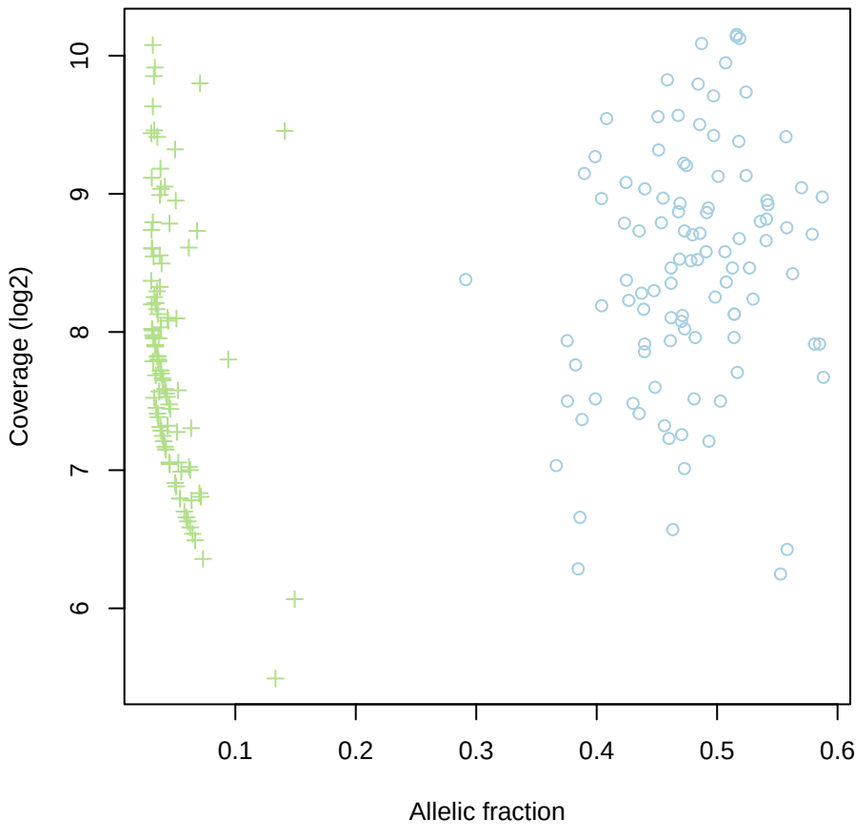

Purity: 0.15 Tumor ploidy: 3.857
0
1
2
3
4
5
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
−0.4
−0.3
−0.2
−0.1
0.0
0.1
log2 ratio

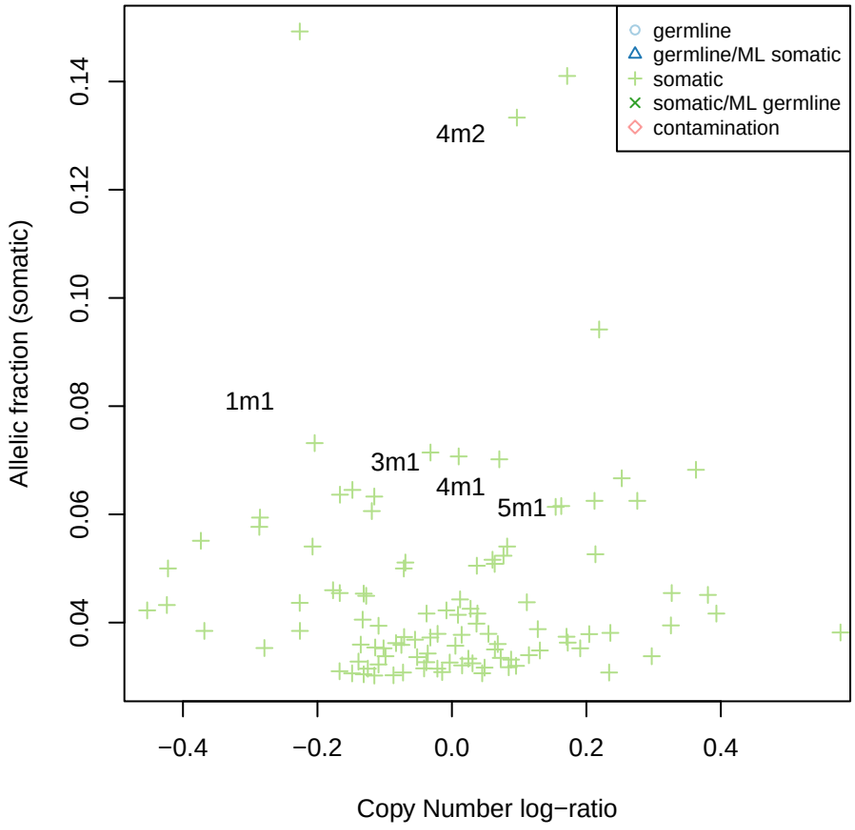

Purity: 0.15 Tumor ploidy: 3.857 SNV log−likelihood: −36.64 GoF: 96.7% Mean coverage: 381;350
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

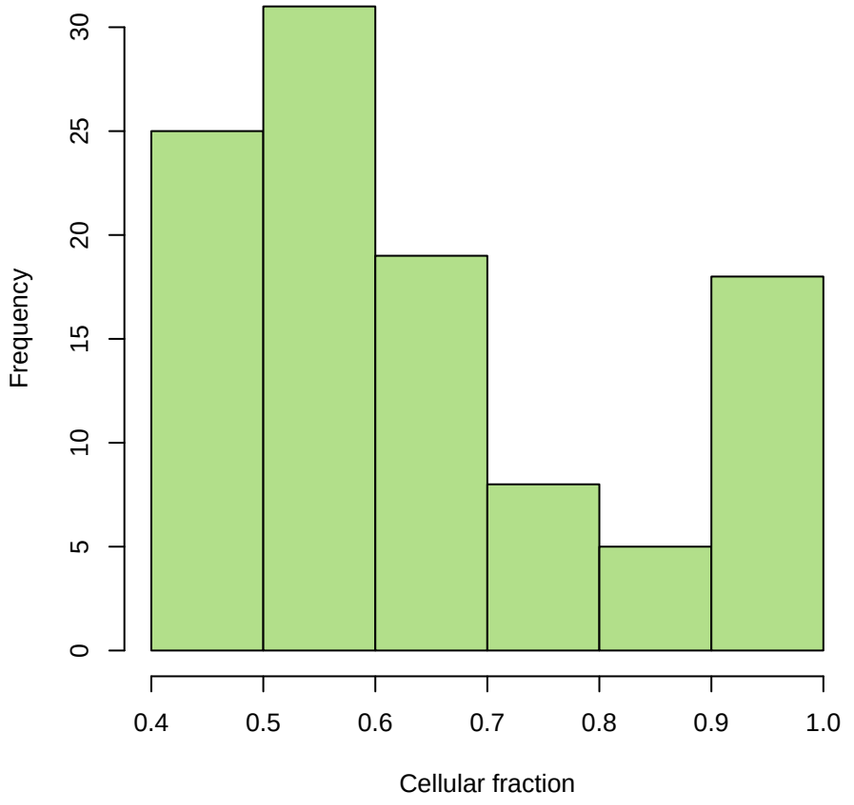

SCNA−fit log−likelihood: −9196.74
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4
0 20 40 60 80 100
SNV Index

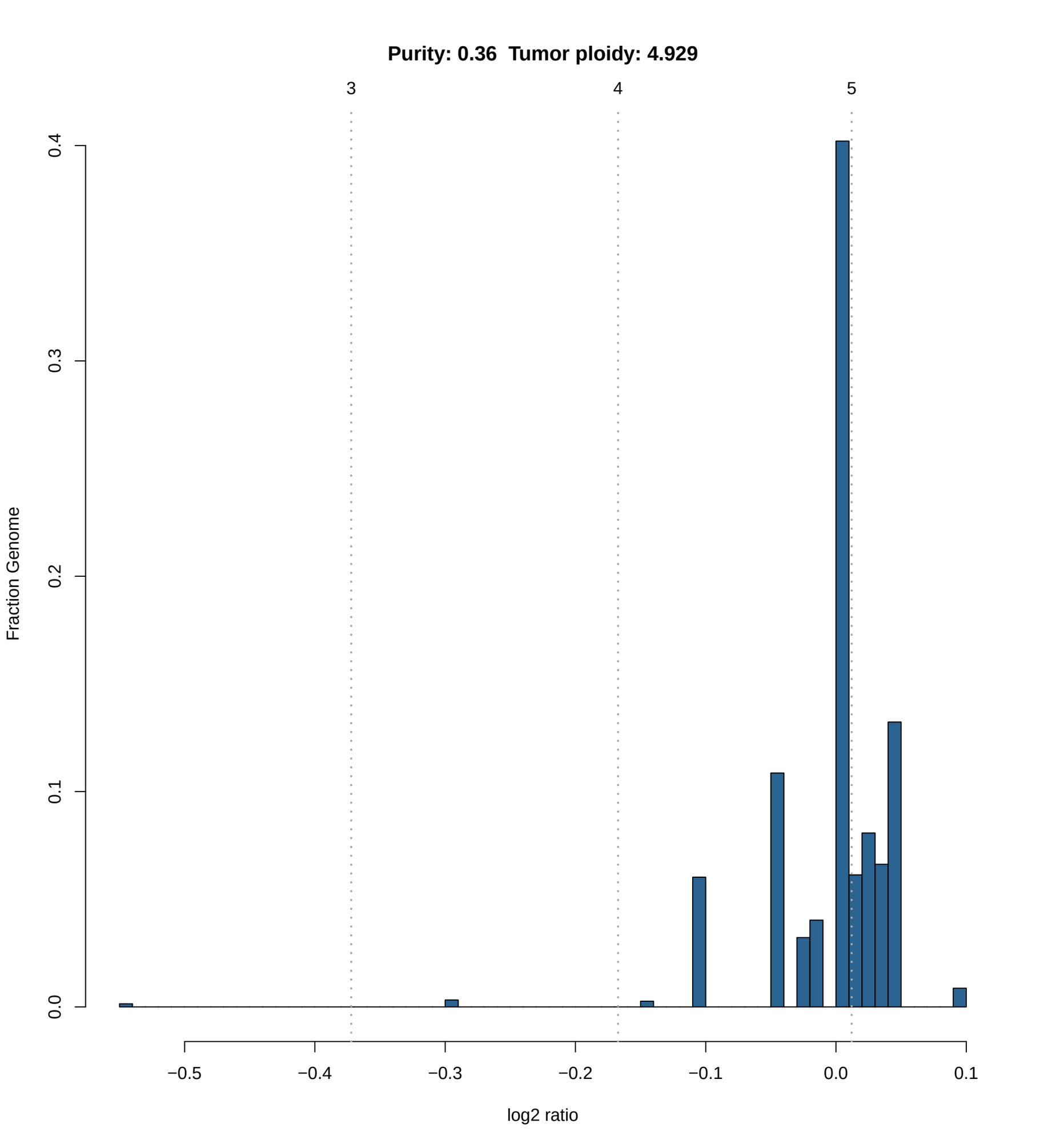

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100
SNV Index

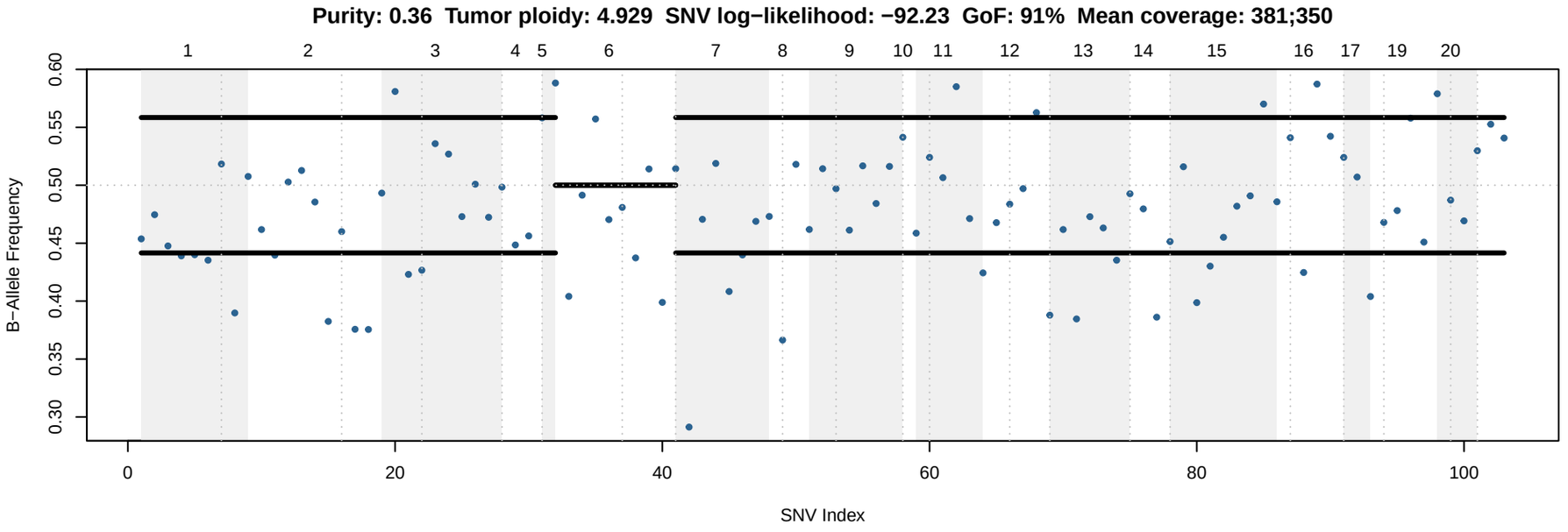

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
4m3
3m2
4m2
3m1
4m1
4m0
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

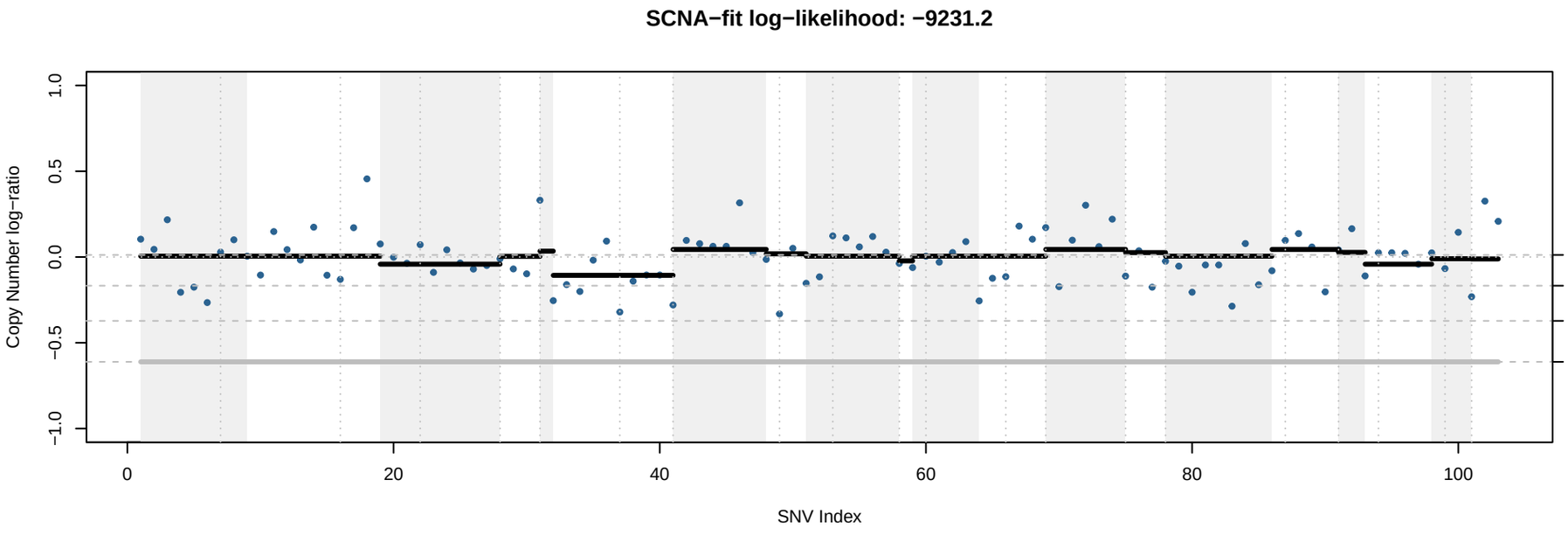

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

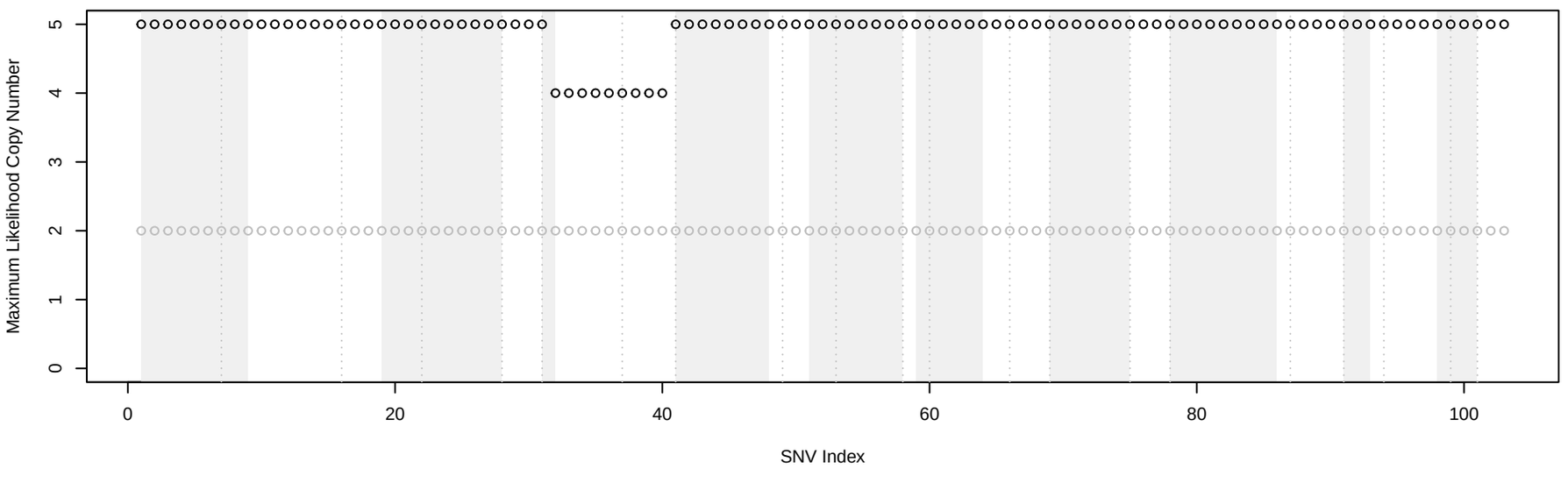

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
4m2
1m1
3m1
4m1
5m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

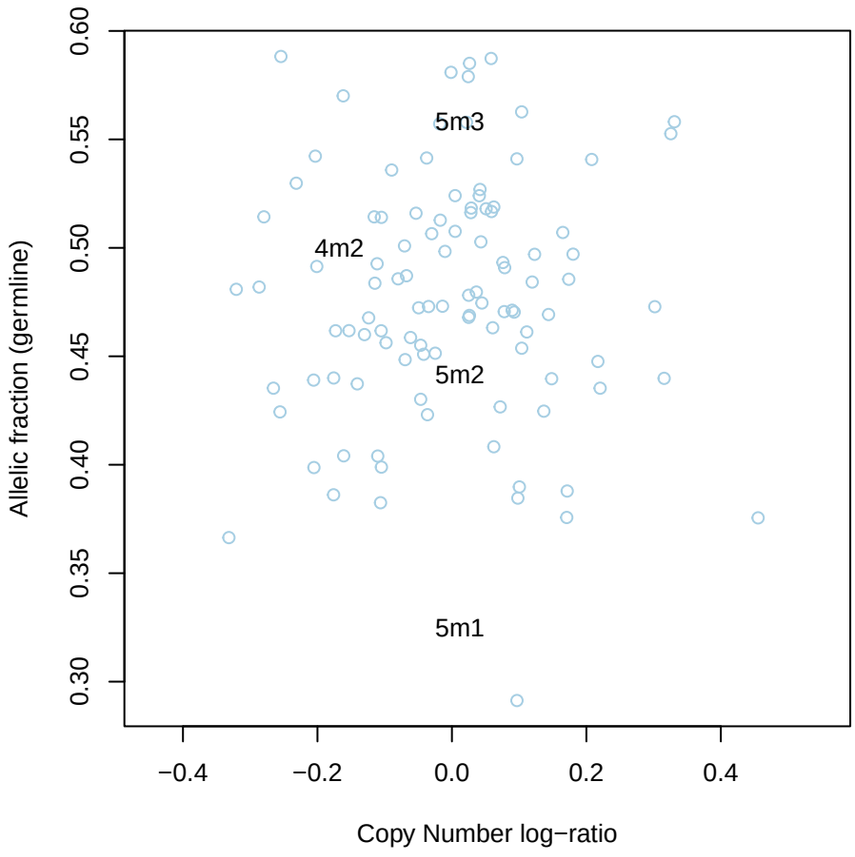

Frequency
0
5
10
15
20
25
30
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

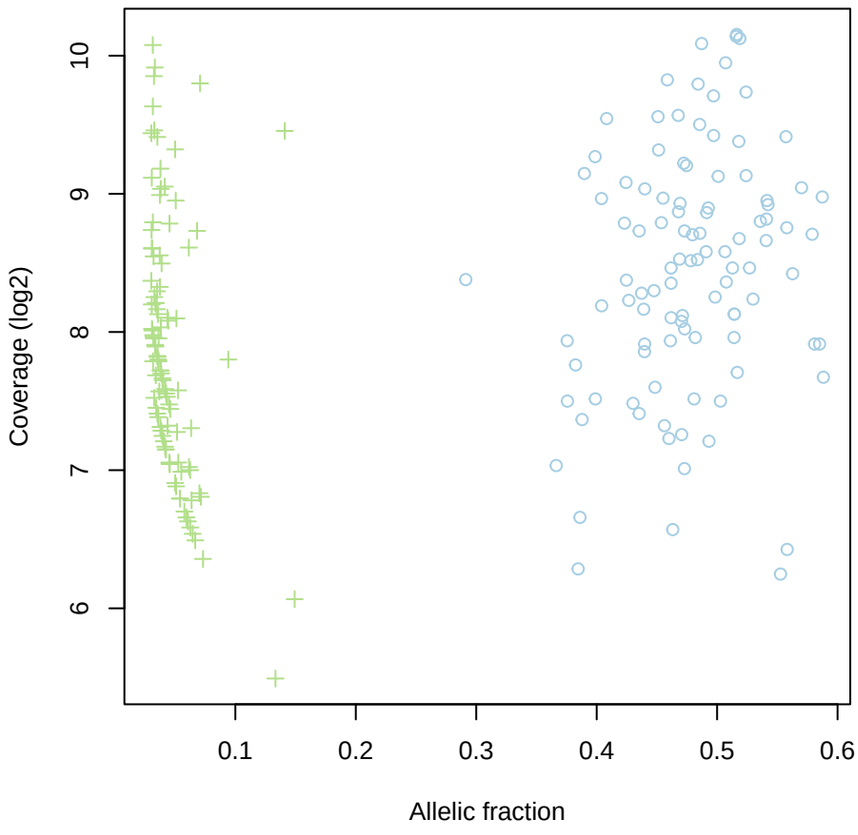

Purity: 0.36 Tumor ploidy: 4.929
3
4
5
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
−0.4
−0.3
−0.2
−0.1
0.0
0.1
log2 ratio

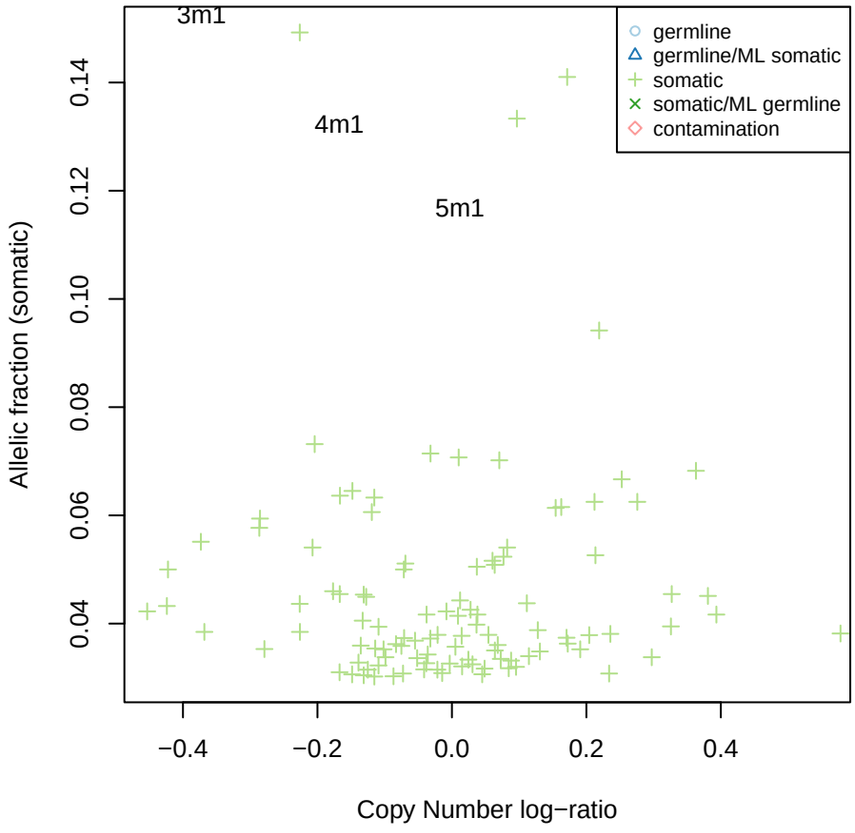

Purity: 0.36 Tumor ploidy: 4.929 SNV log−likelihood: −92.23 GoF: 91% Mean coverage: 381;350
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

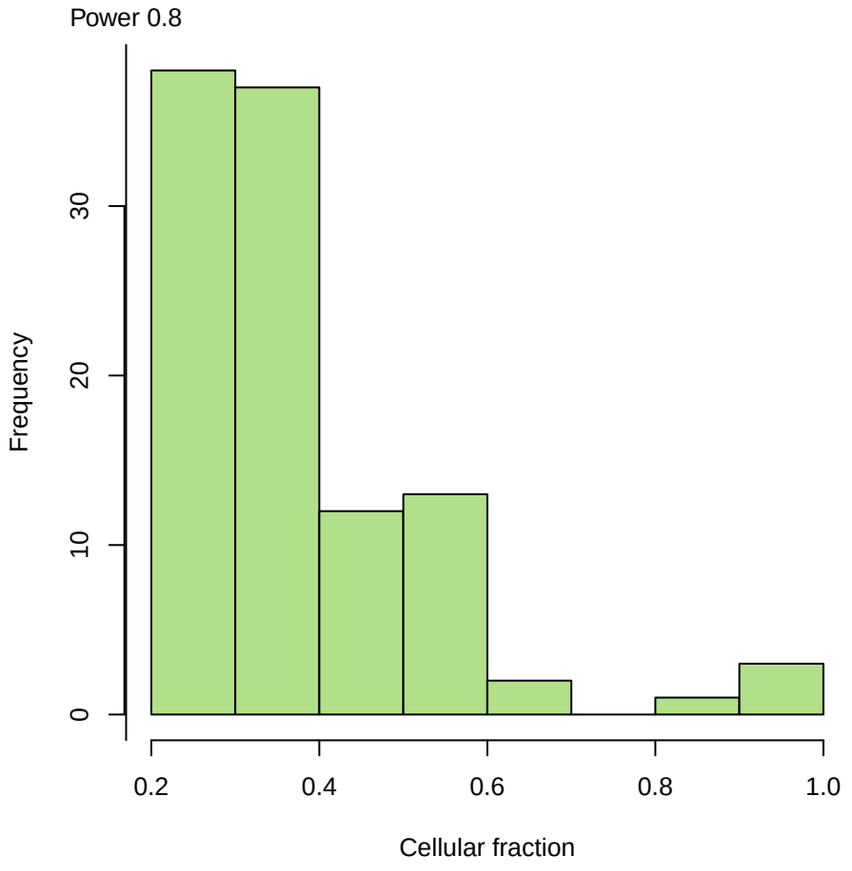

SCNA−fit log−likelihood: −9231.2
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5
0 20 40 60 80 100
SNV Index

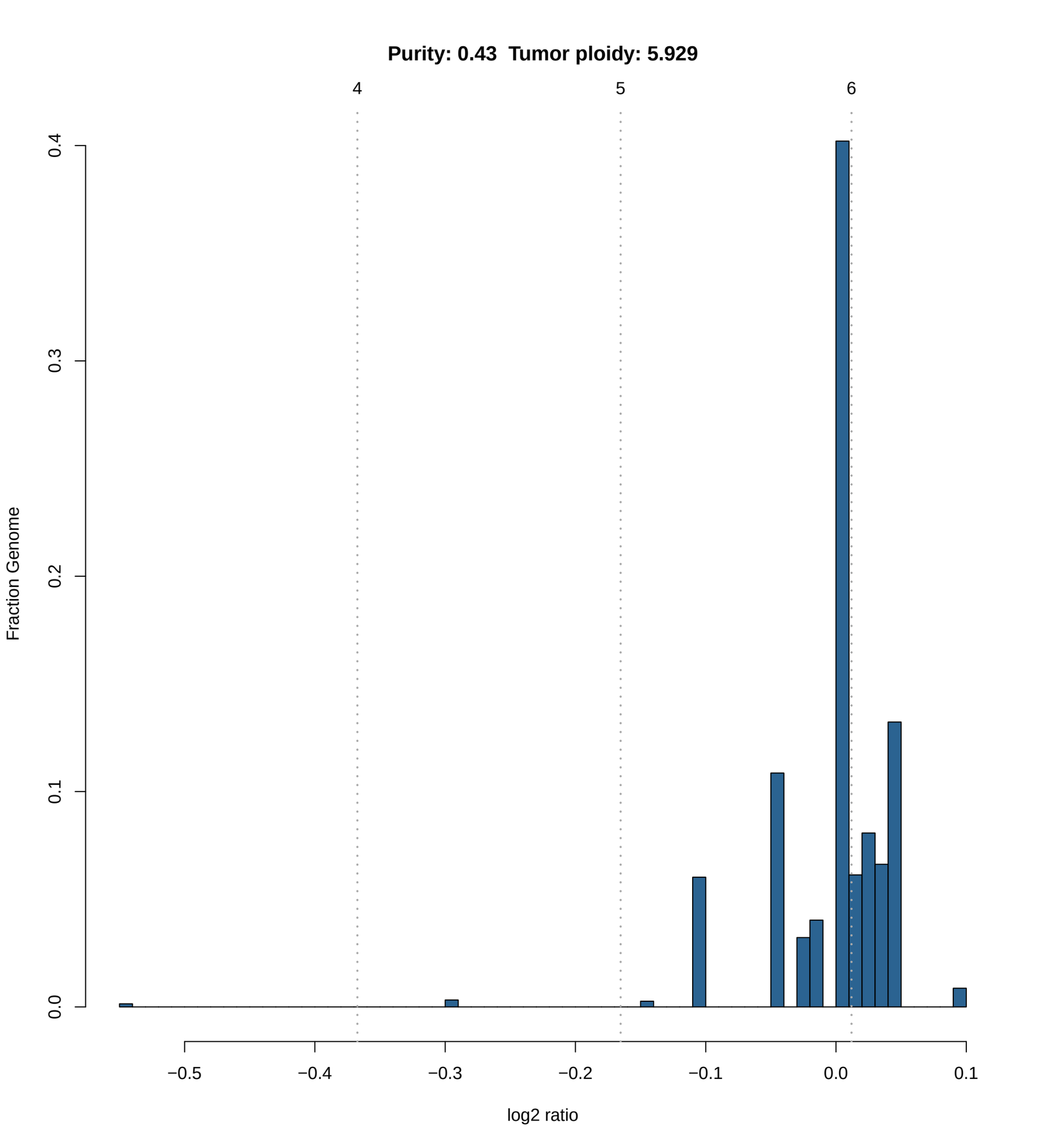

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100
SNV Index

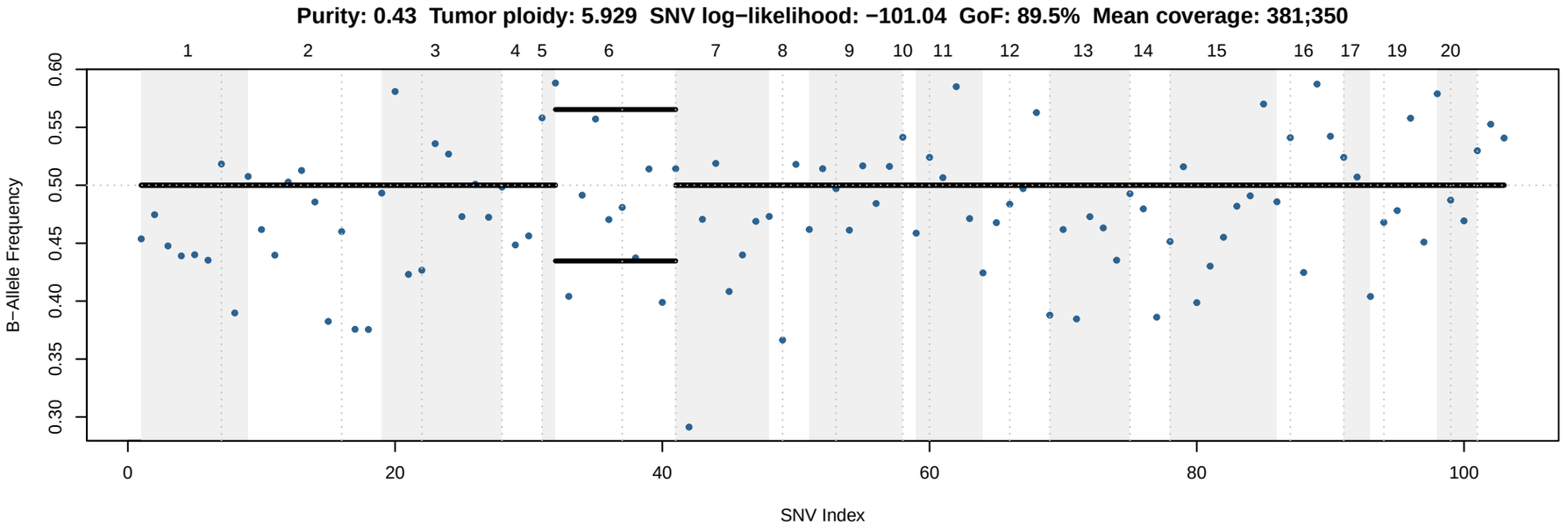

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
5m3
4m2
5m2
5m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

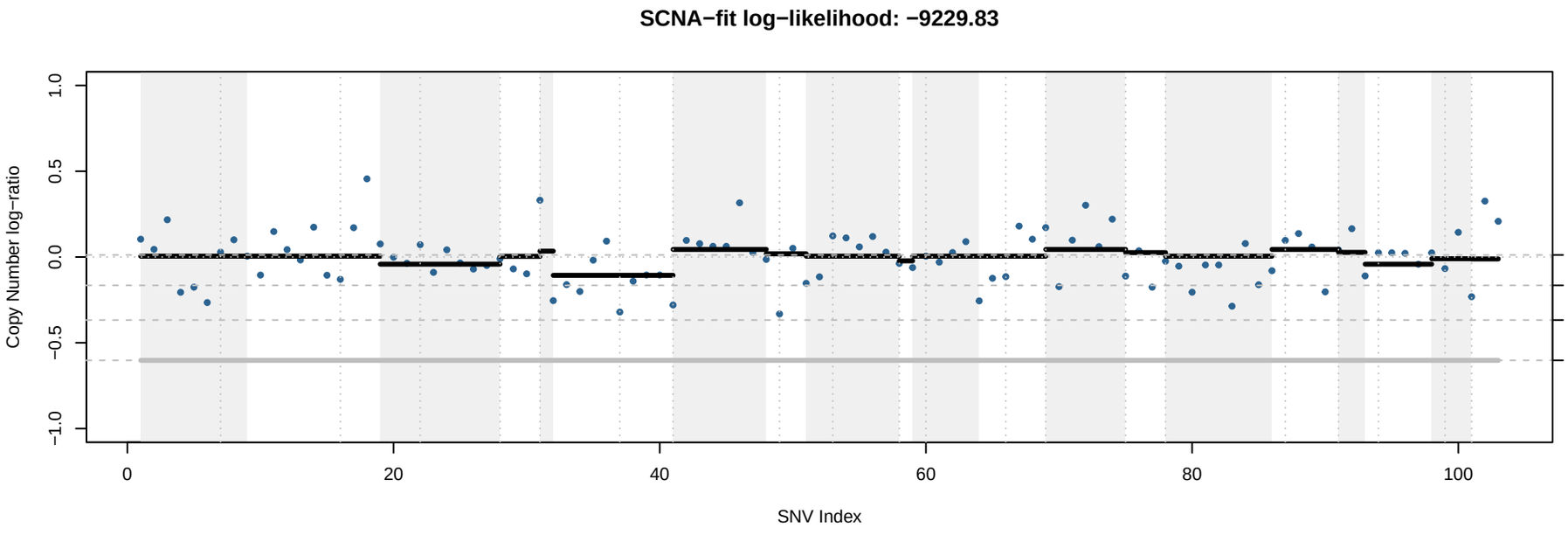

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

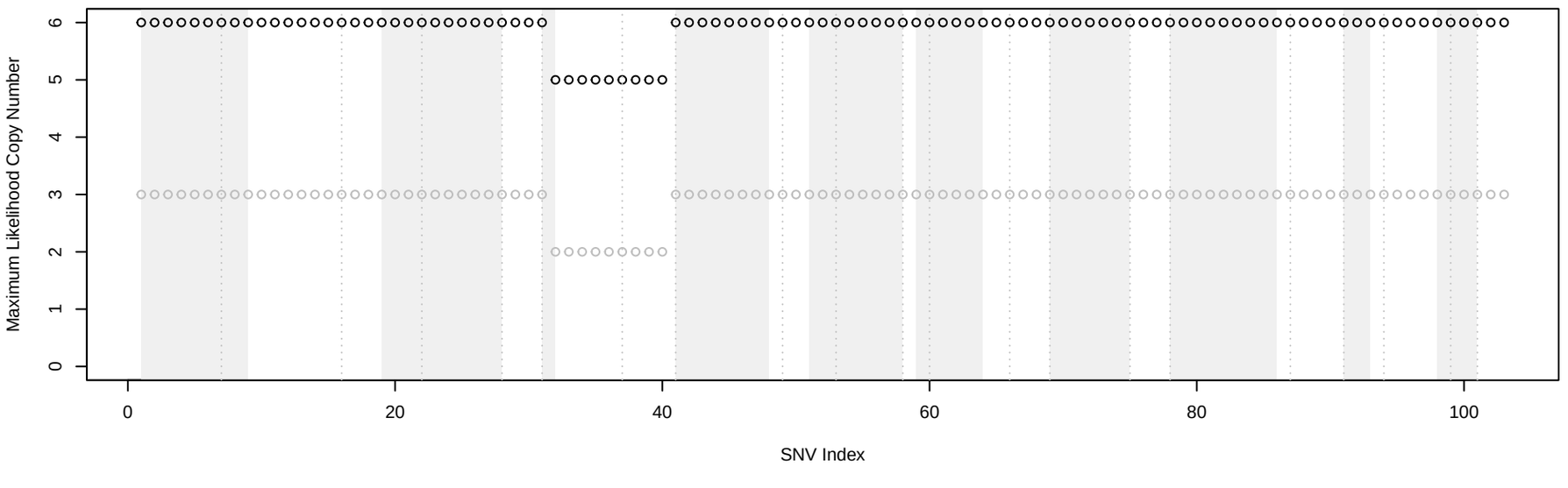

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
3m1
4m1
5m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

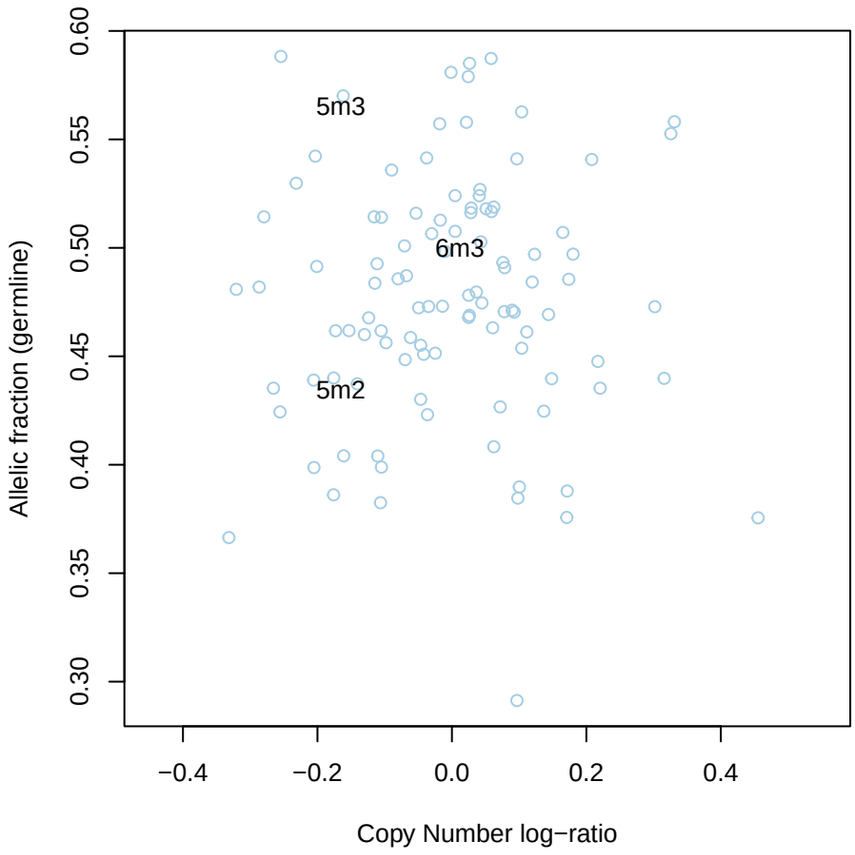

Power 0.8
Frequency
0
10
20
30
0.2
0.4
0.6
0.8
1.0
Cellular fraction

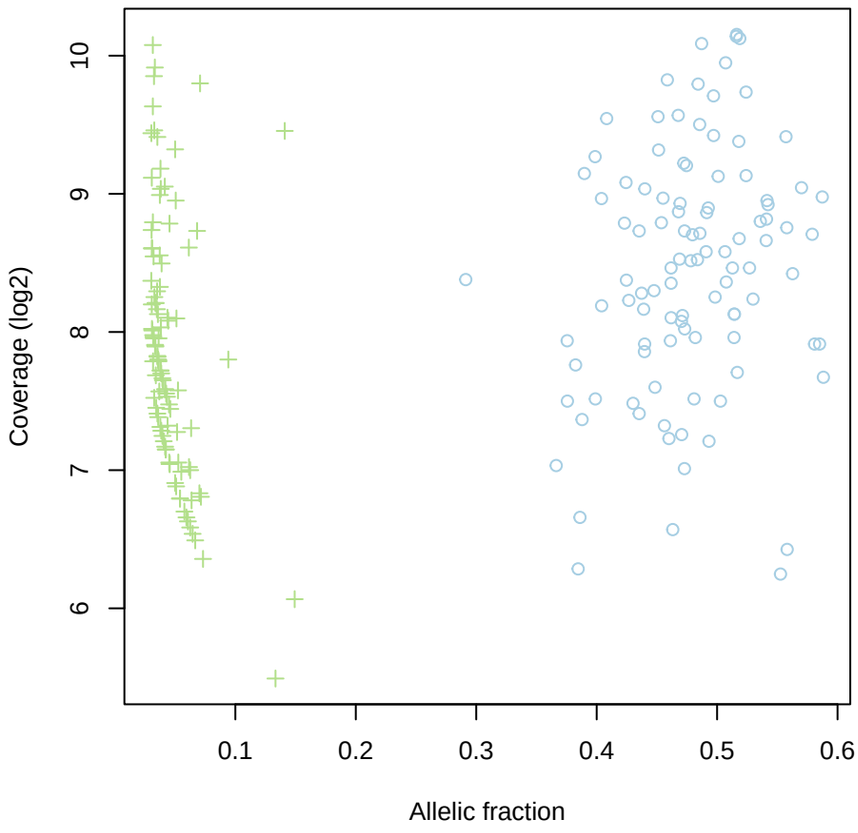

Purity: 0.43 Tumor ploidy: 5.929
4
5
6
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
−0.4
−0.3
−0.2
−0.1
0.0
0.1
log2 ratio

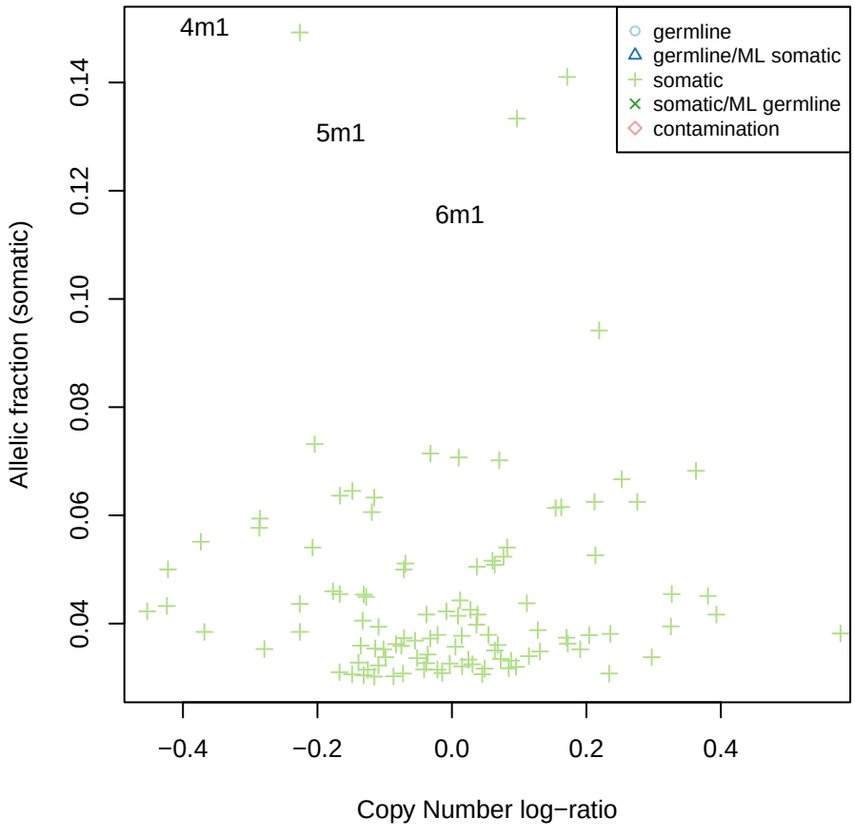

Purity: 0.43 Tumor ploidy: 5.929 SNV log−likelihood: −101.04 GoF: 89.5% Mean coverage: 381;350
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

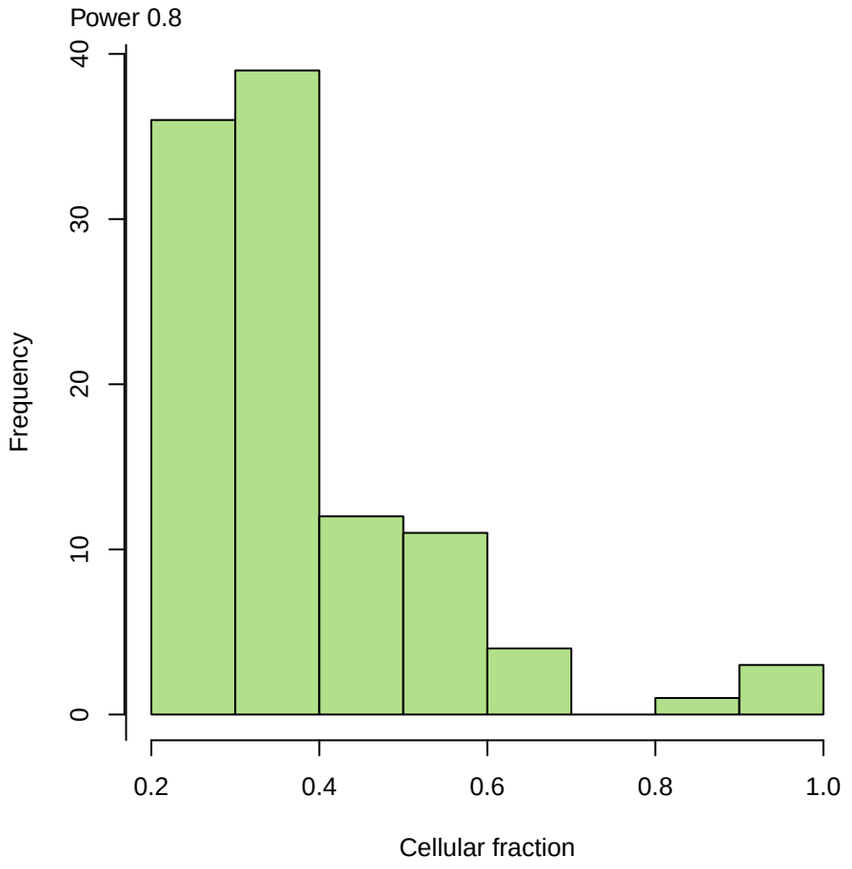

SCNA−fit log−likelihood: −9229.83
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6
0 20 40 60 80 100
SNV Index

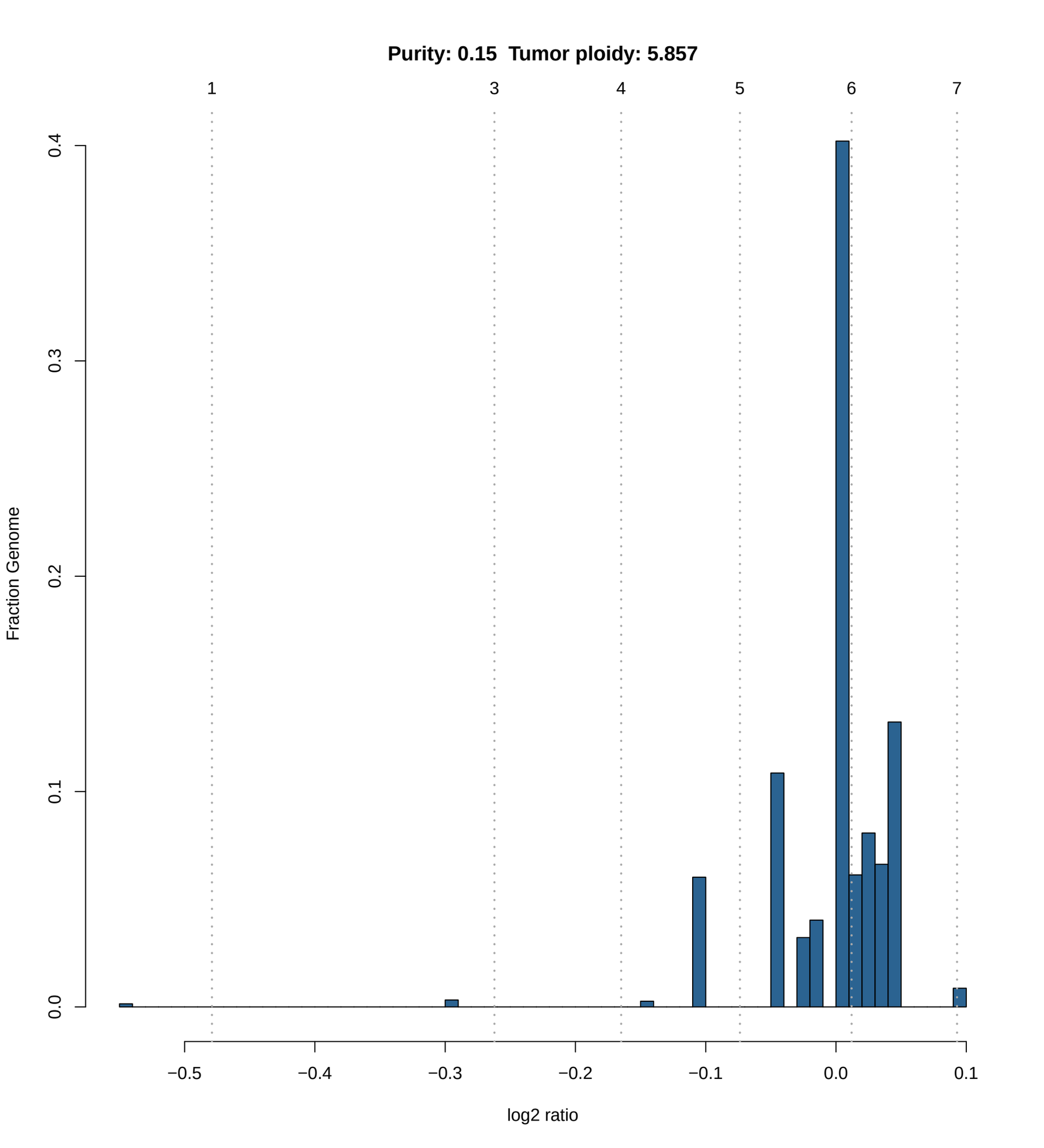

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100
SNV Index

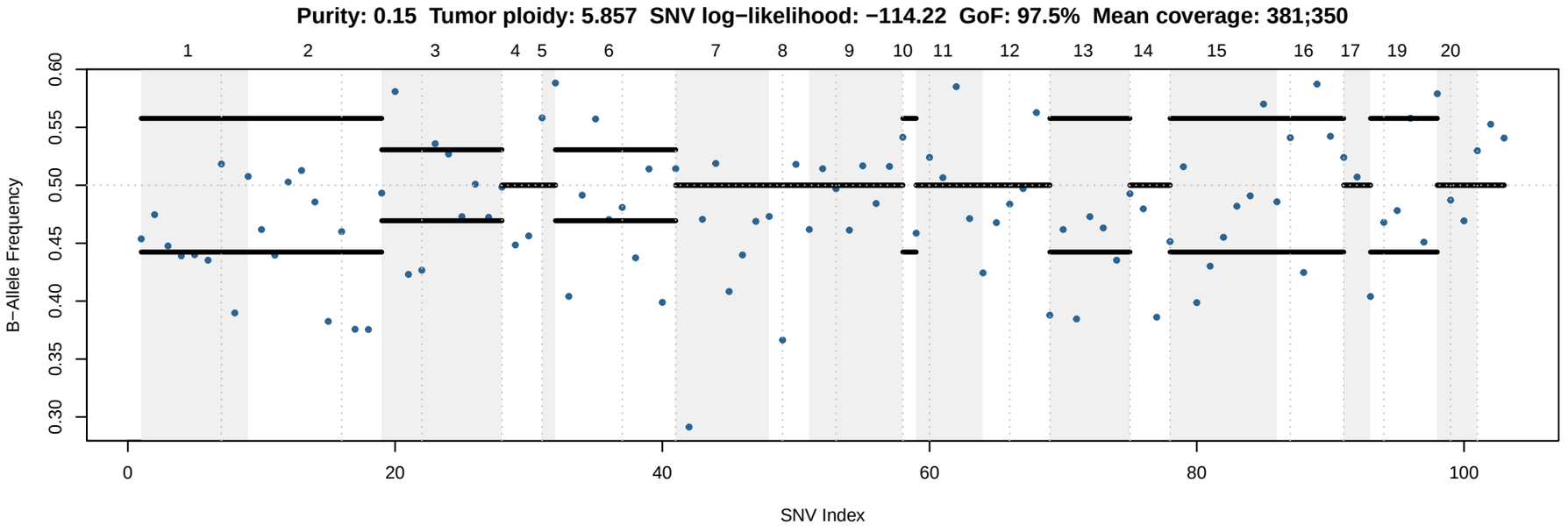

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
5m3
6m3
5m2
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

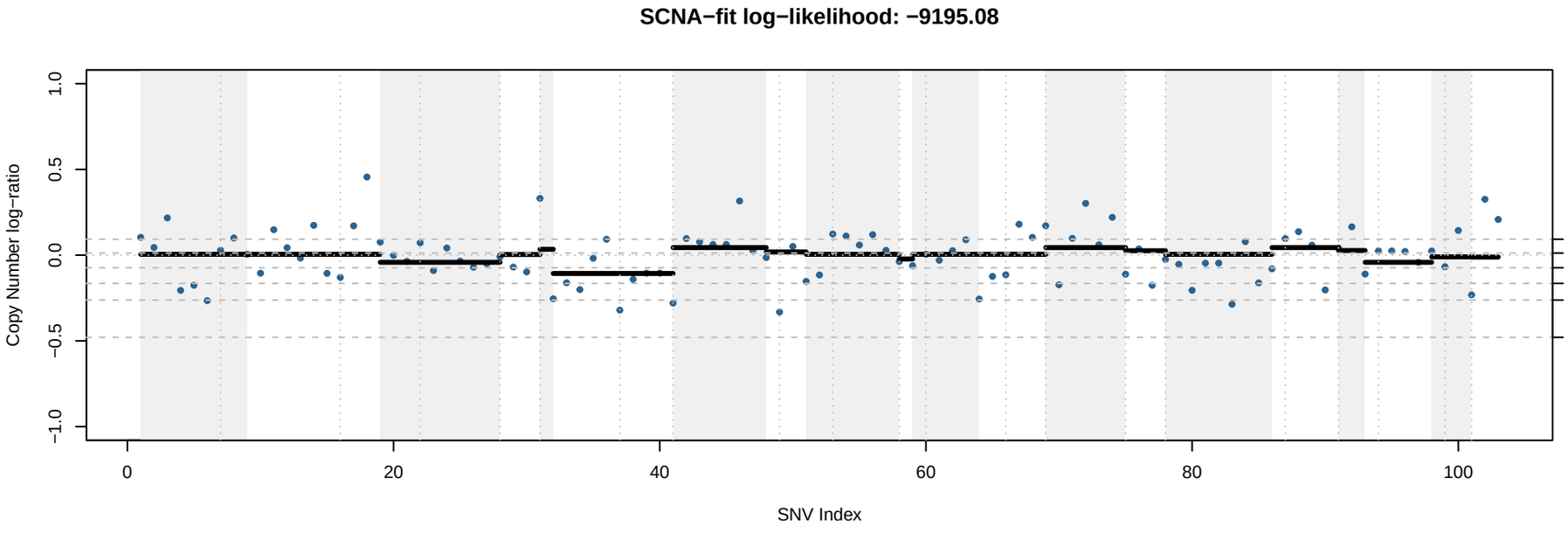

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

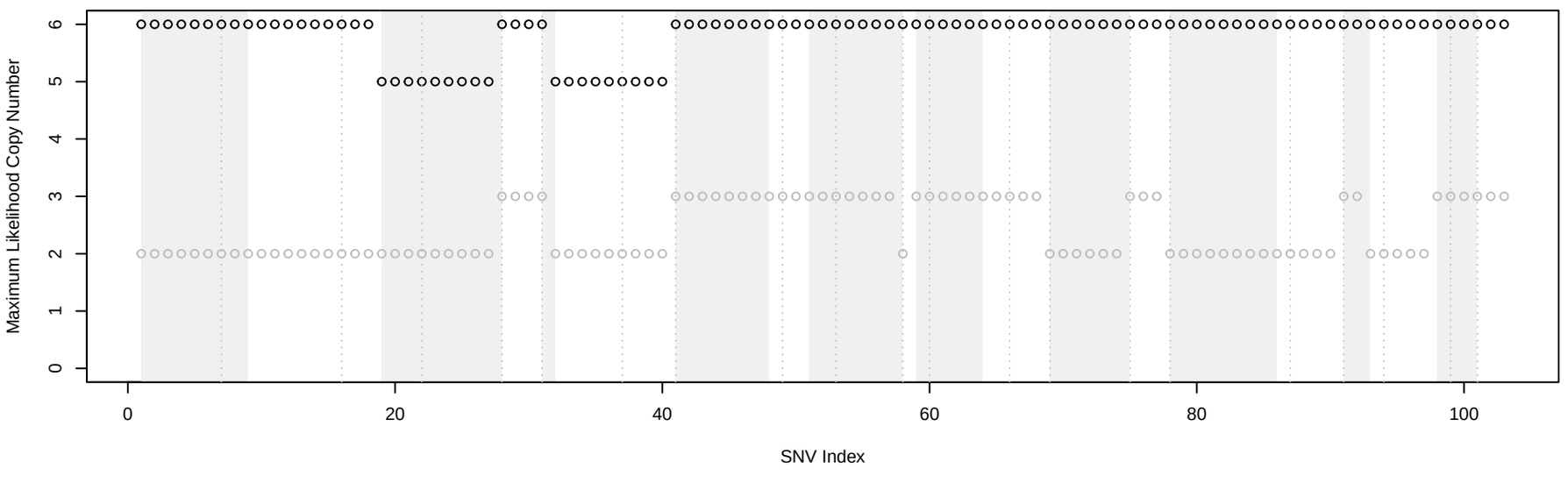

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
4m1
5m1
6m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

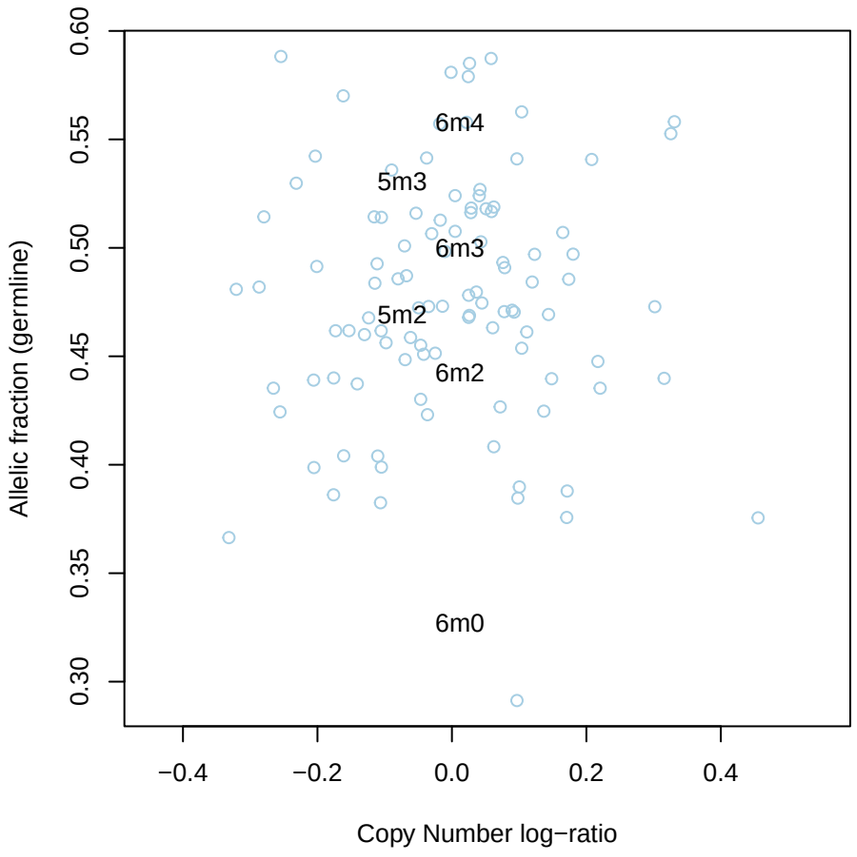

Power 0.8
Frequency
0
10
20
30
40
0.2
0.4
0.6
0.8
1.0
Cellular fraction

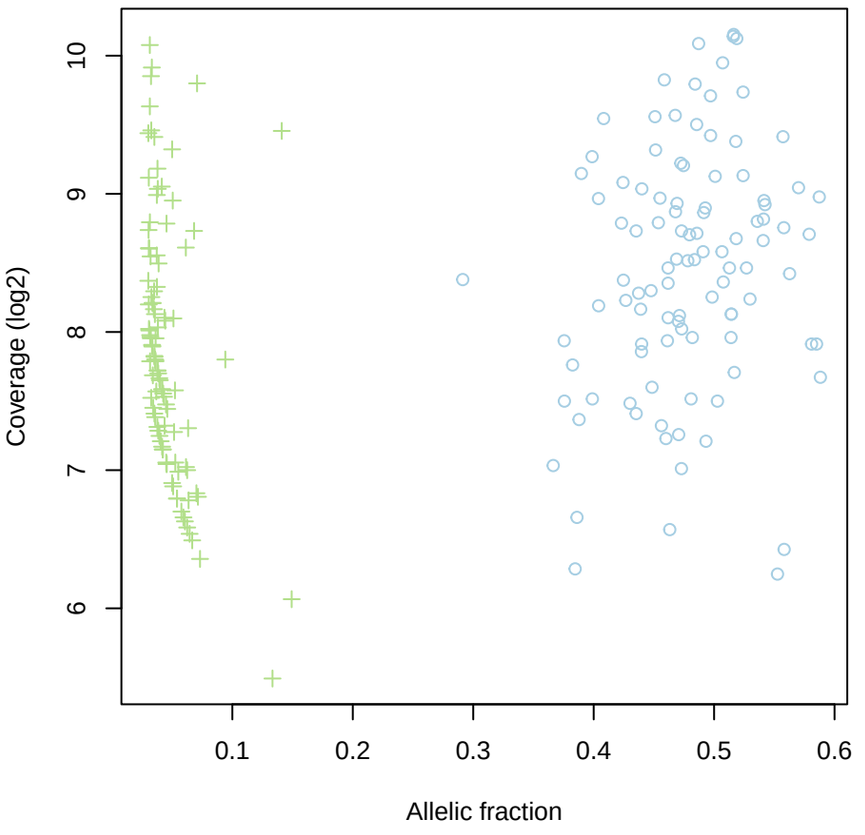

Purity: 0.15 Tumor ploidy: 5.857
1
3
4
5
6
7
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
−0.4
−0.3
−0.2
−0.1
0.0
0.1
log2 ratio

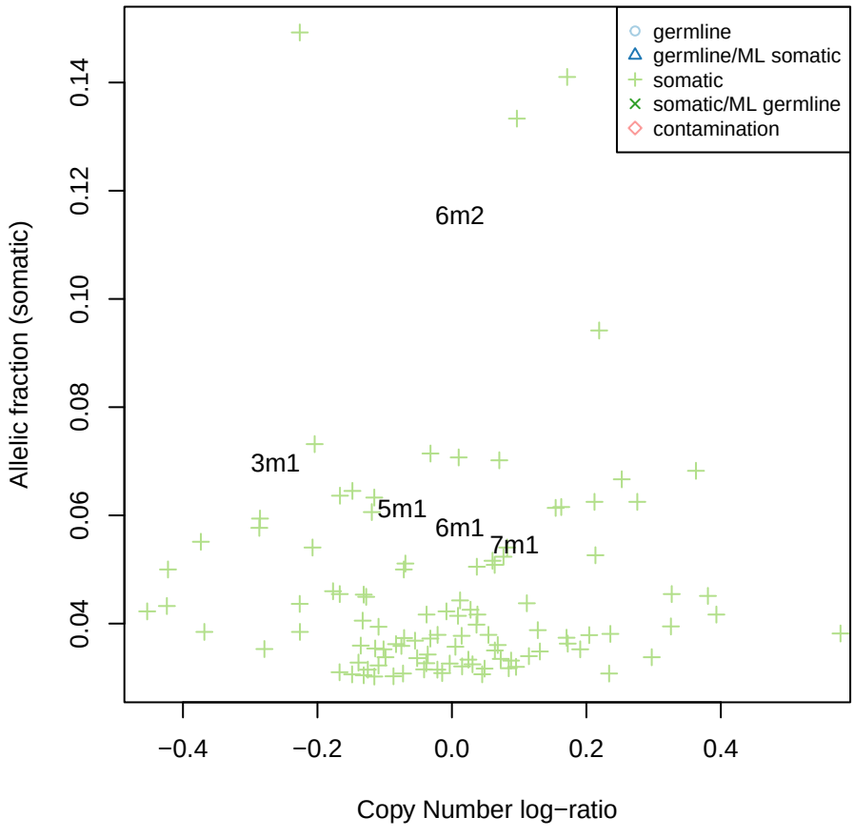

Purity: 0.15 Tumor ploidy: 5.857 SNV log−likelihood: −114.22 GoF: 97.5% Mean coverage: 381;350
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

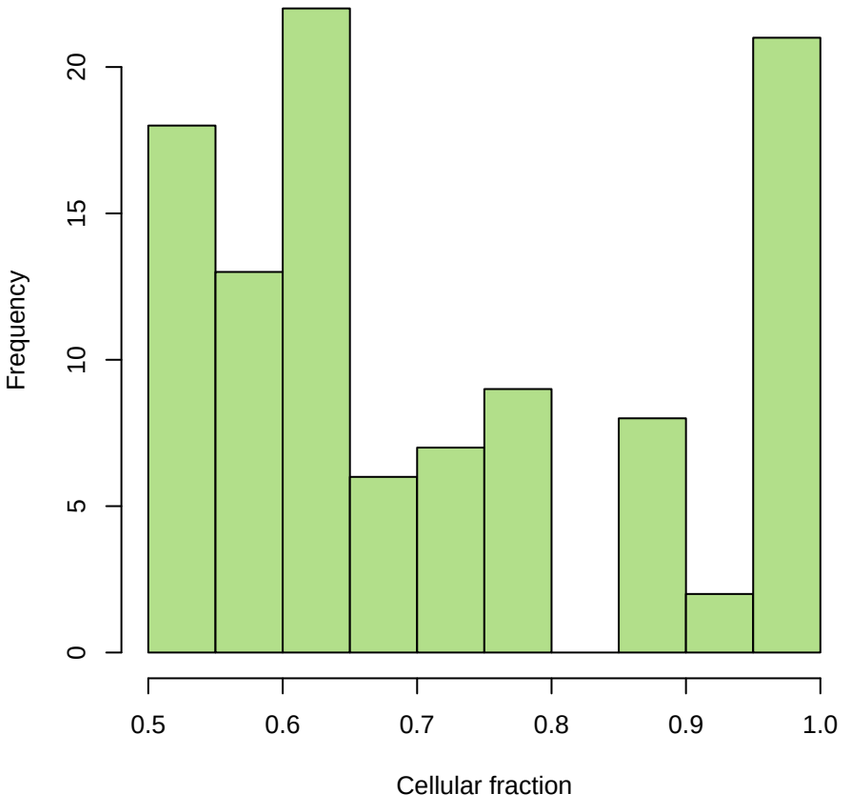

SCNA−fit log−likelihood: −9195.08
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 3 5 7
0 20 40 60 80 100
SNV Index

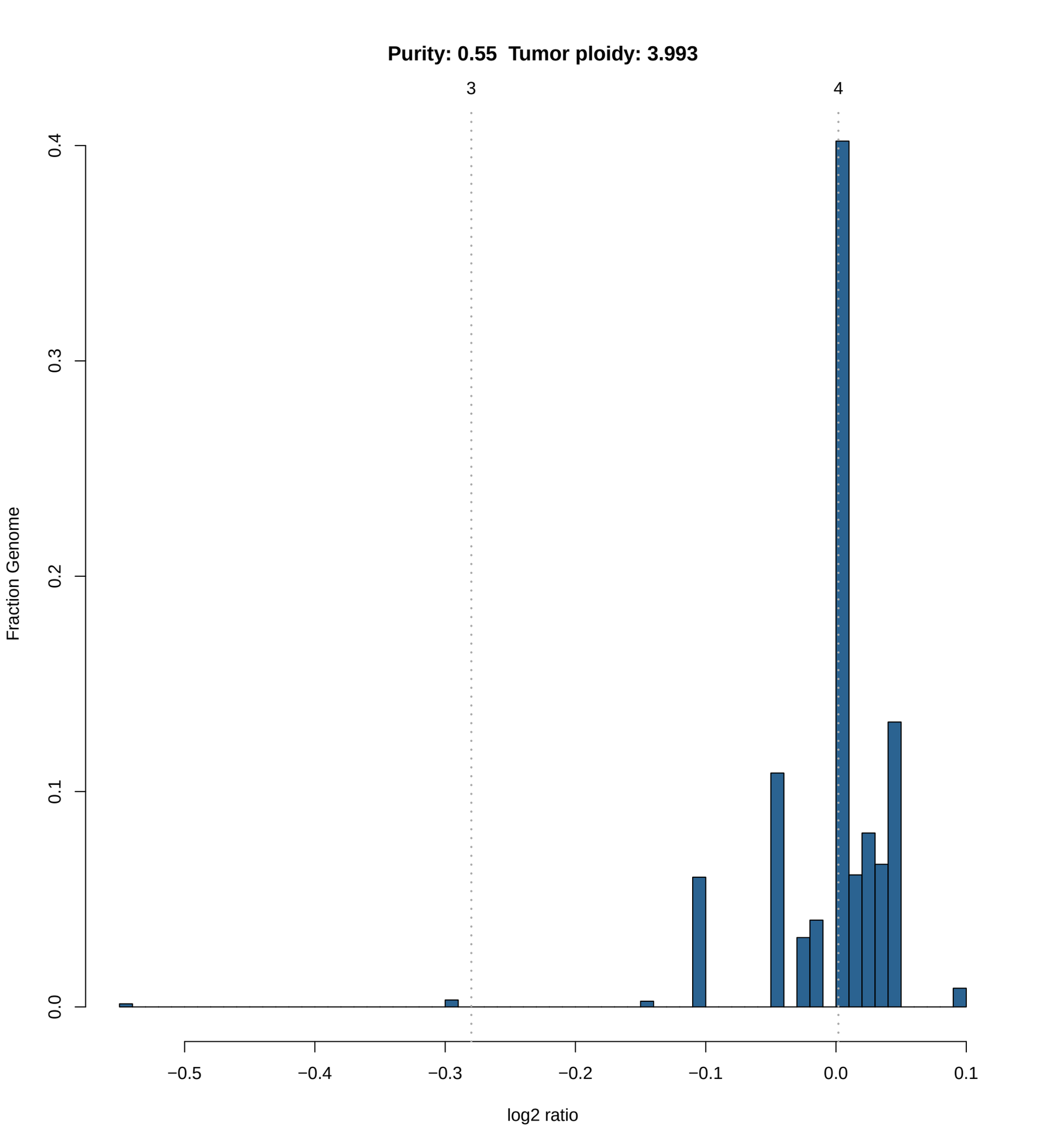

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100
SNV Index

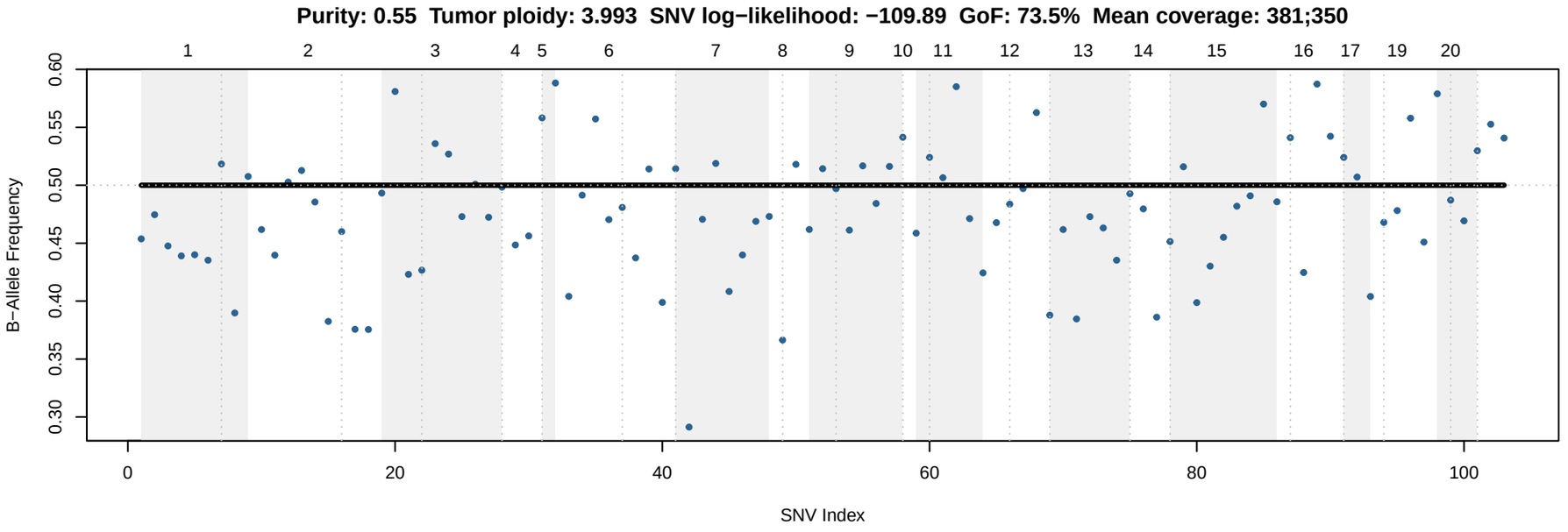

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
6m4
5m3
6m3
5m2
6m2
6m0
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

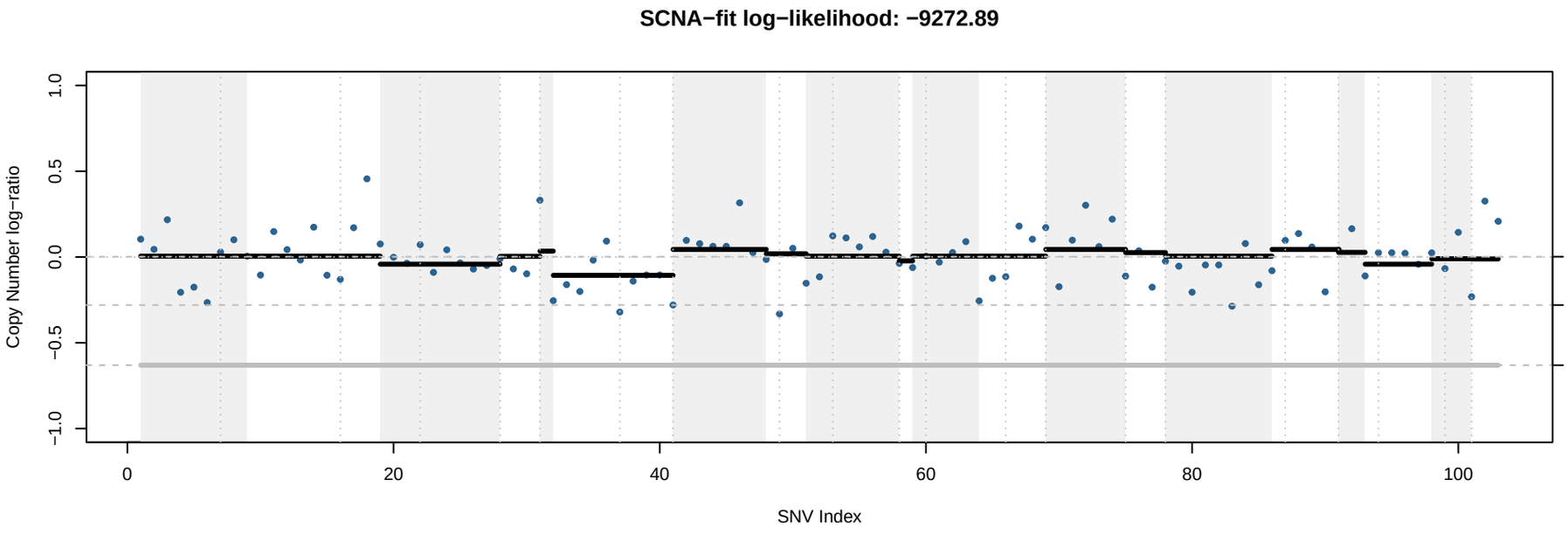

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

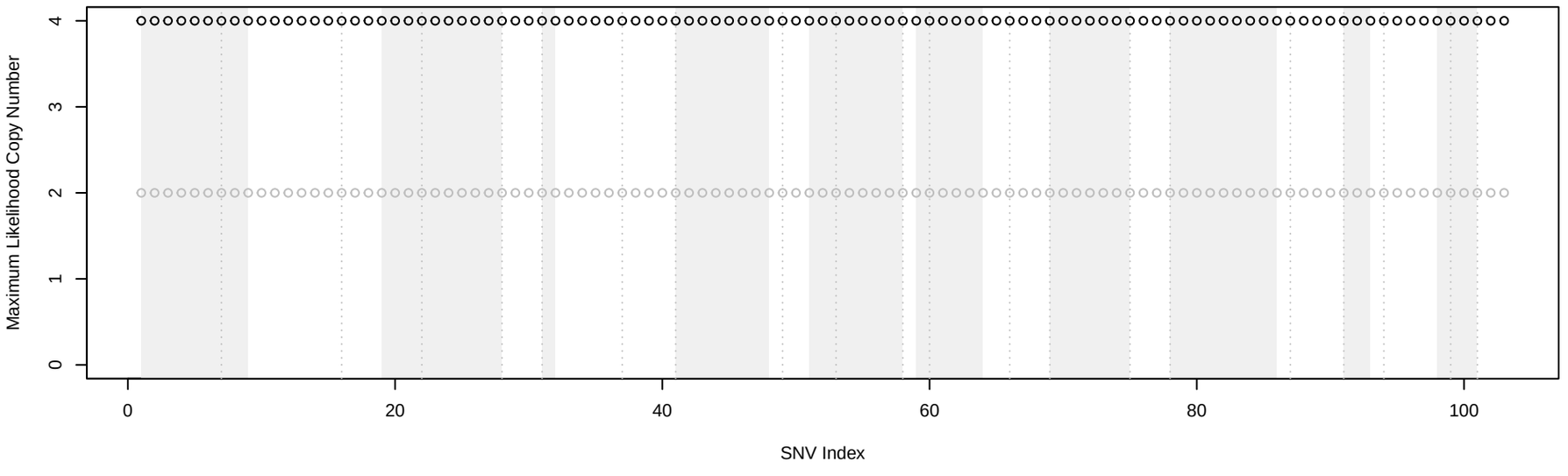

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
6m2
3m1
5m1
6m1
7m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

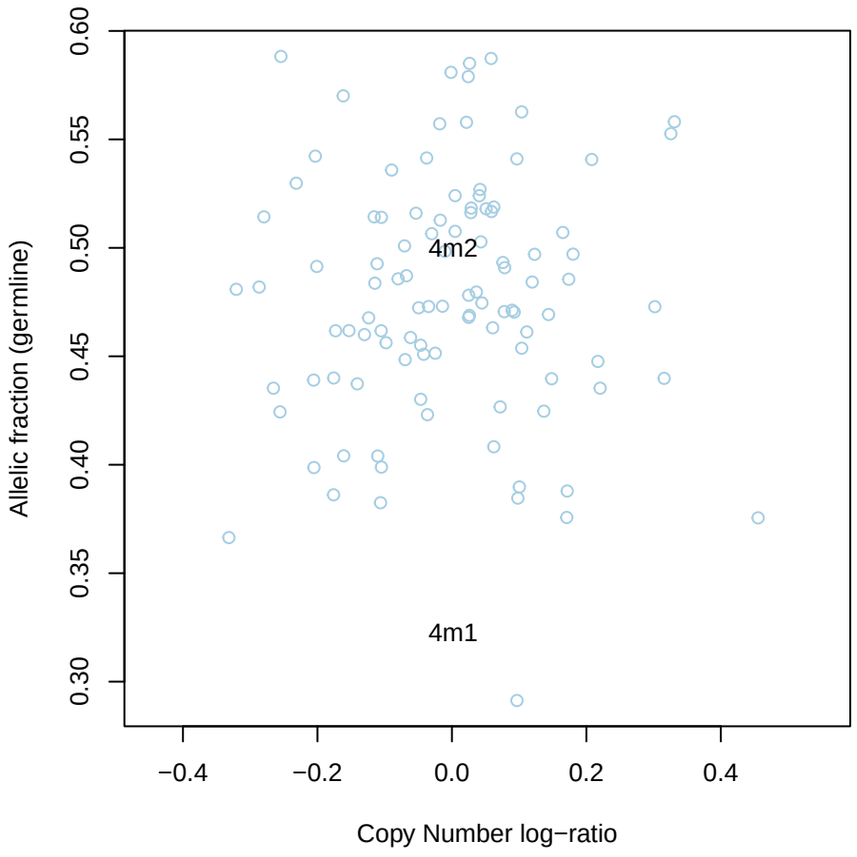

Frequency
0
5
10
15
20
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

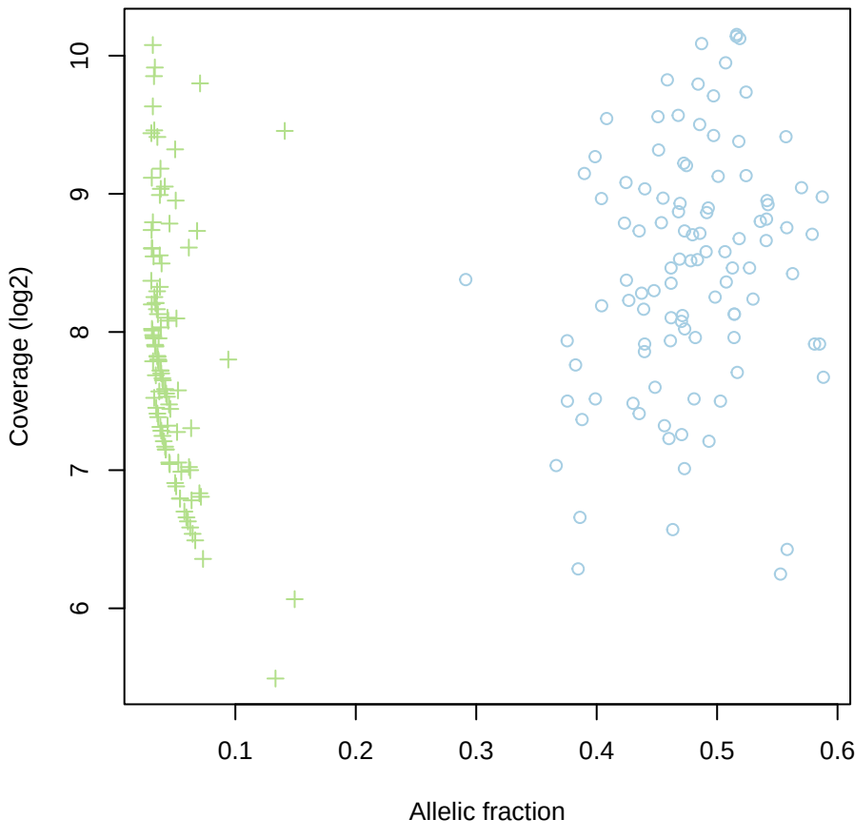

Purity: 0.55 Tumor ploidy: 3.993
3
4
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
−0.4
−0.3
−0.2
−0.1
0.0
0.1
log2 ratio

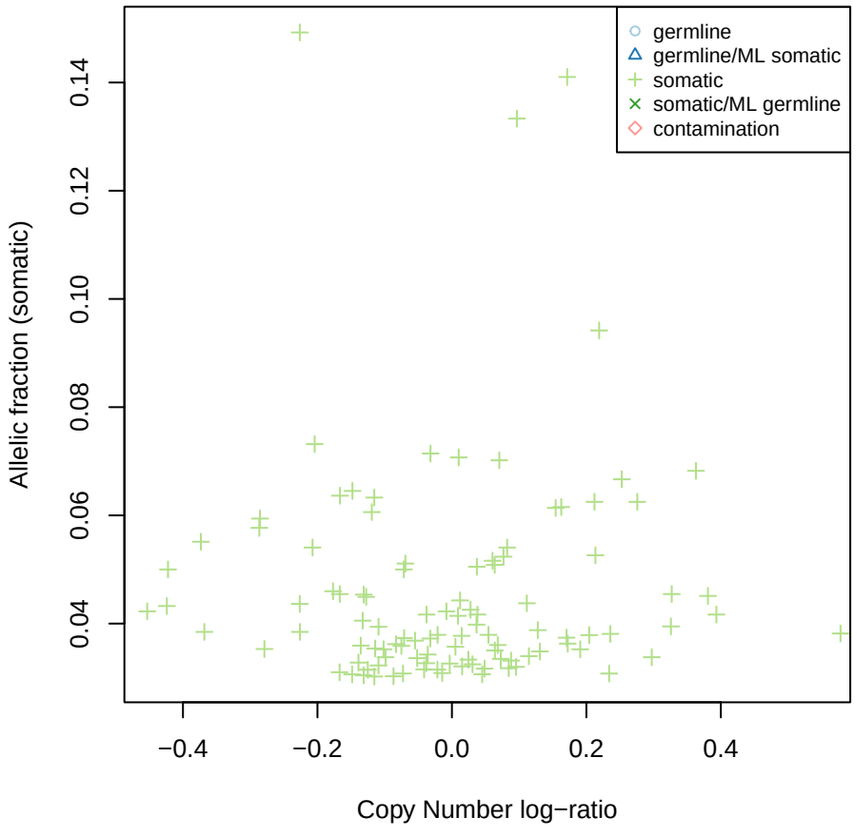

Purity: 0.55 Tumor ploidy: 3.993 SNV log−likelihood: −109.89 GoF: 73.5% Mean coverage: 381;350
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

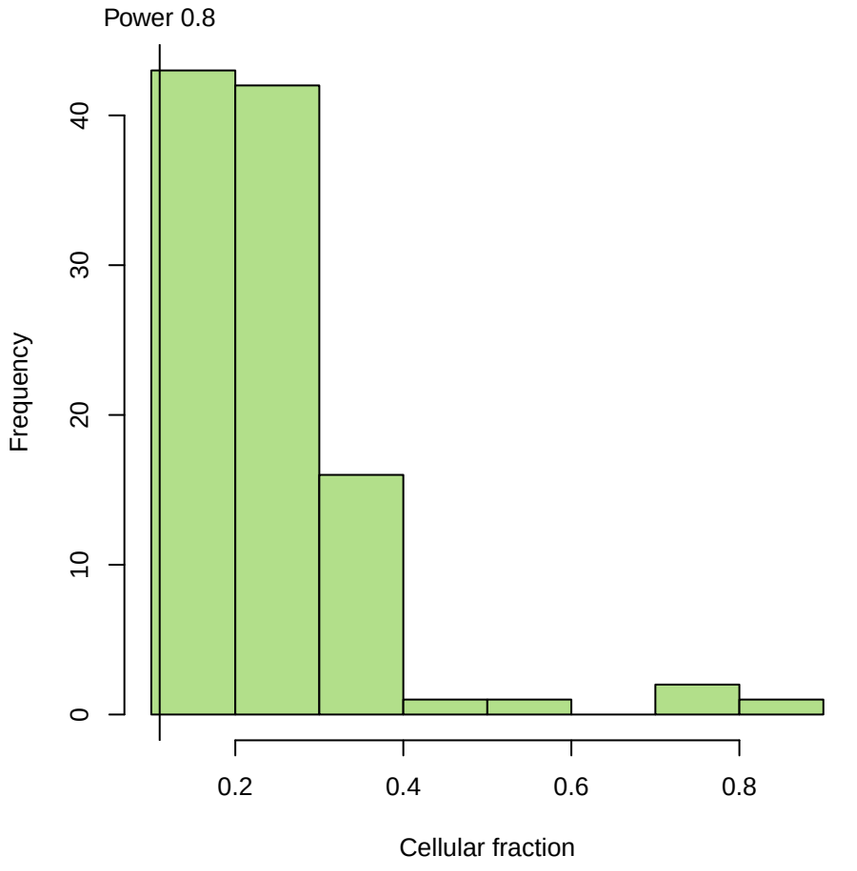

SCNA−fit log−likelihood: −9272.89
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4
0 20 40 60 80 100
SNV Index

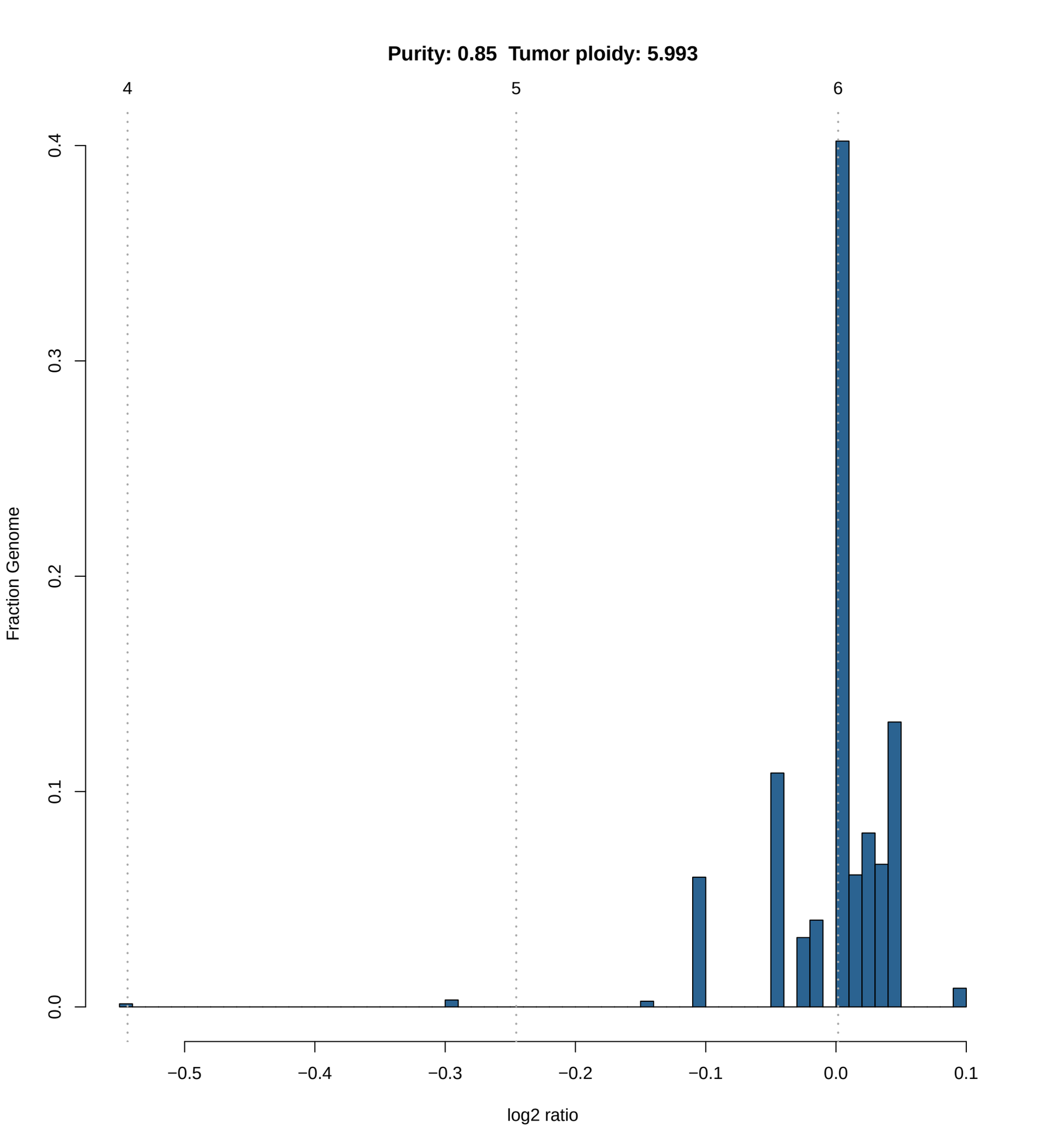

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100
SNV Index

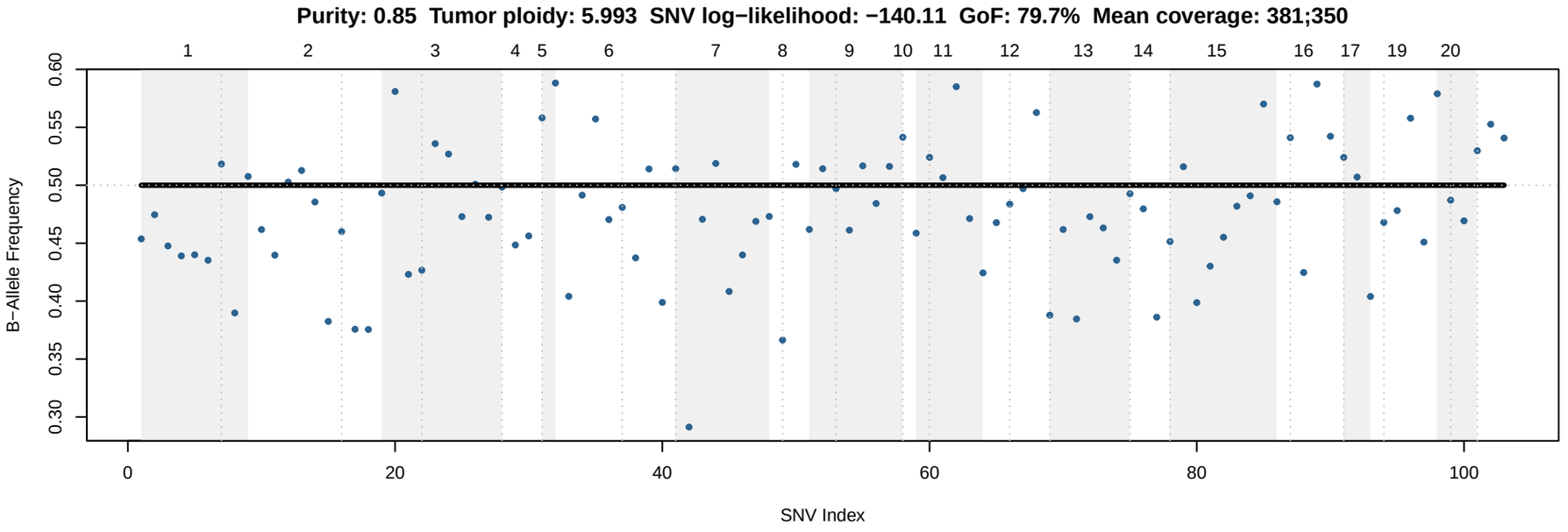

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
4m2
4m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

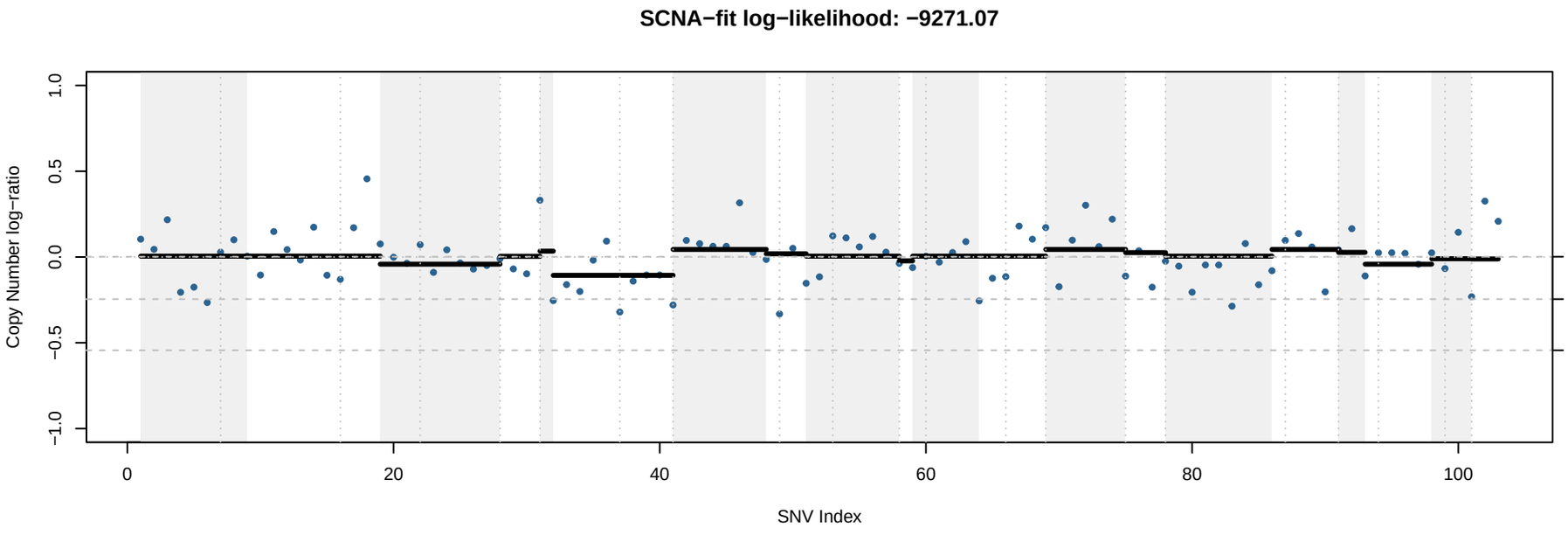

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

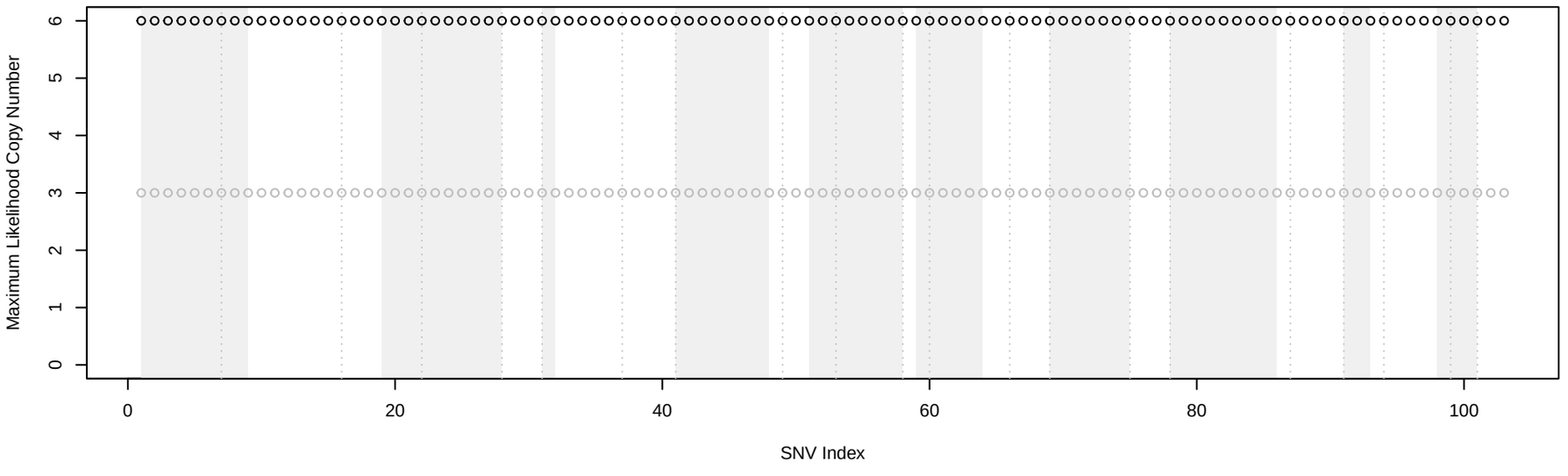

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

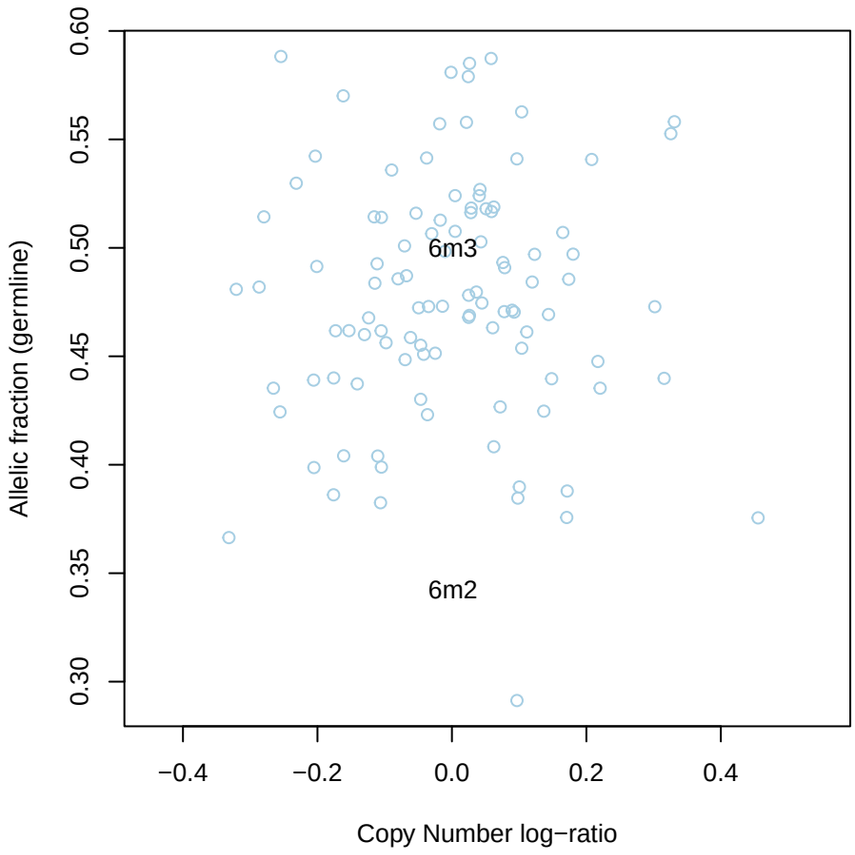

Power 0.8
Frequency
0
10
20
30
40
0.2
0.4
0.6
0.8
Cellular fraction

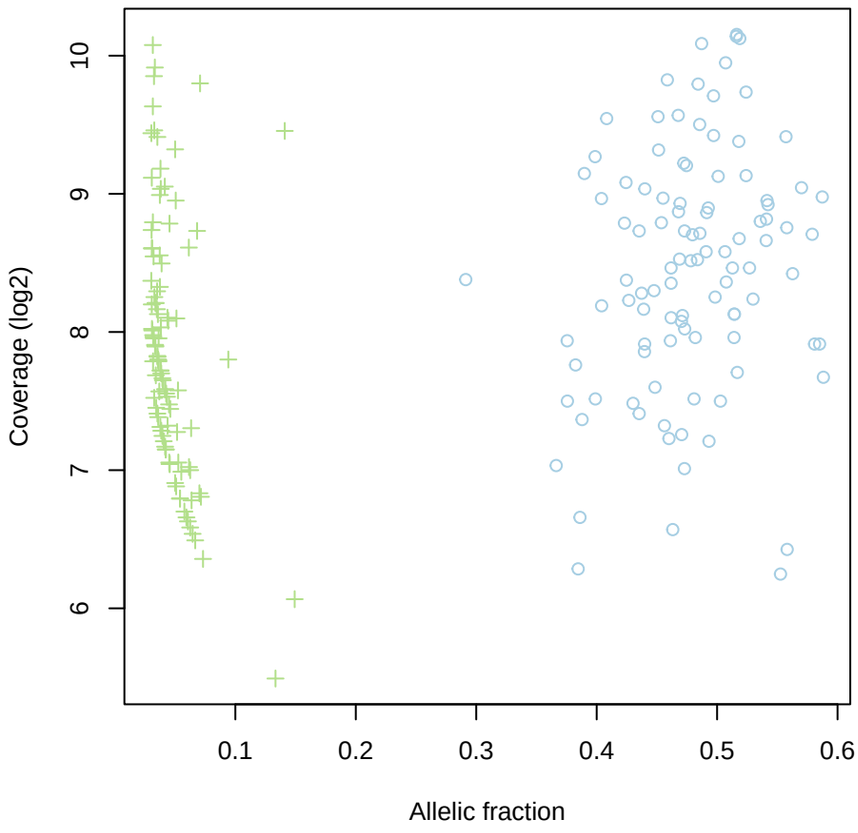

Purity: 0.85 Tumor ploidy: 5.993
4
5
6
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
−0.4
−0.3
−0.2
−0.1
0.0
0.1
log2 ratio

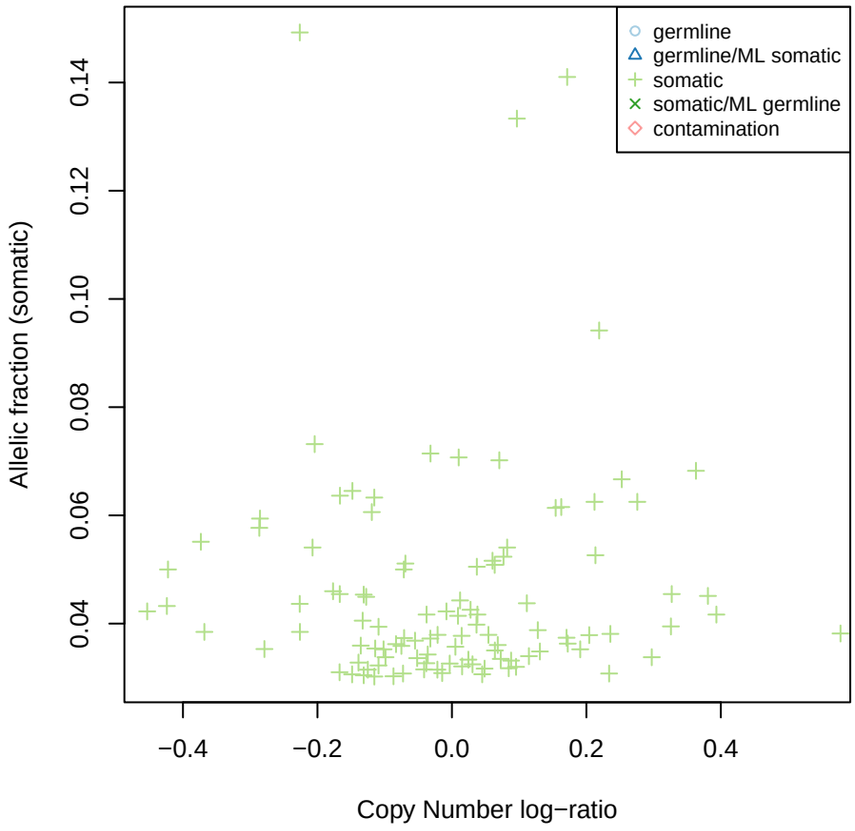

Purity: 0.85 Tumor ploidy: 5.993 SNV log−likelihood: −140.11 GoF: 79.7% Mean coverage: 381;350
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

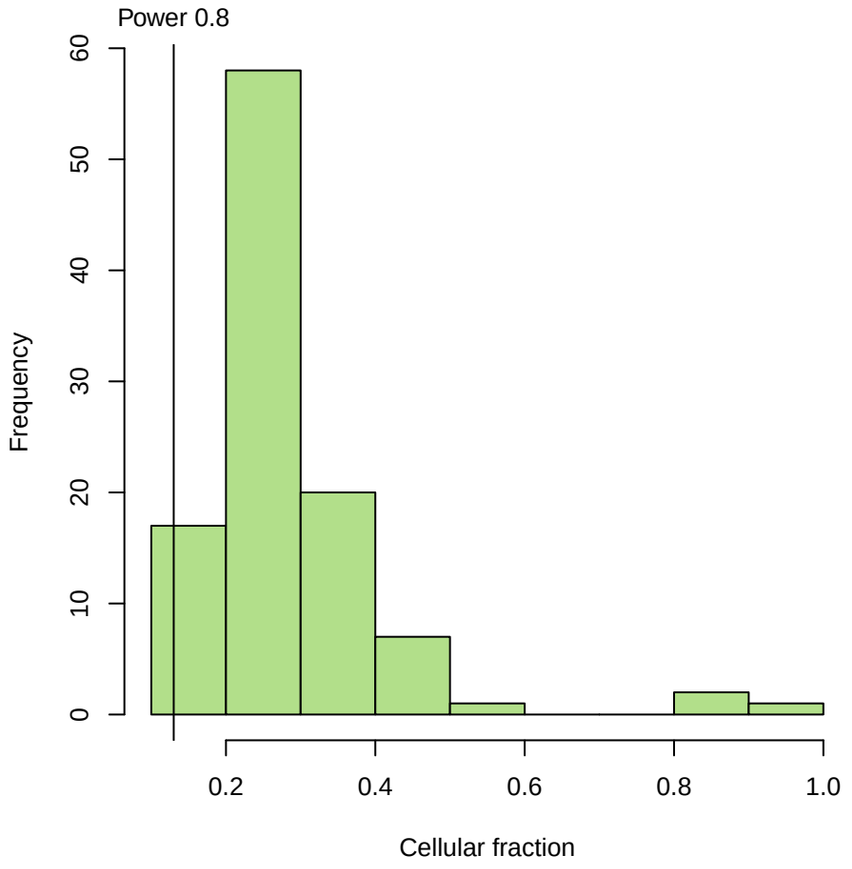

SCNA−fit log−likelihood: −9271.07
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5 6
0 20 40 60 80 100
SNV Index

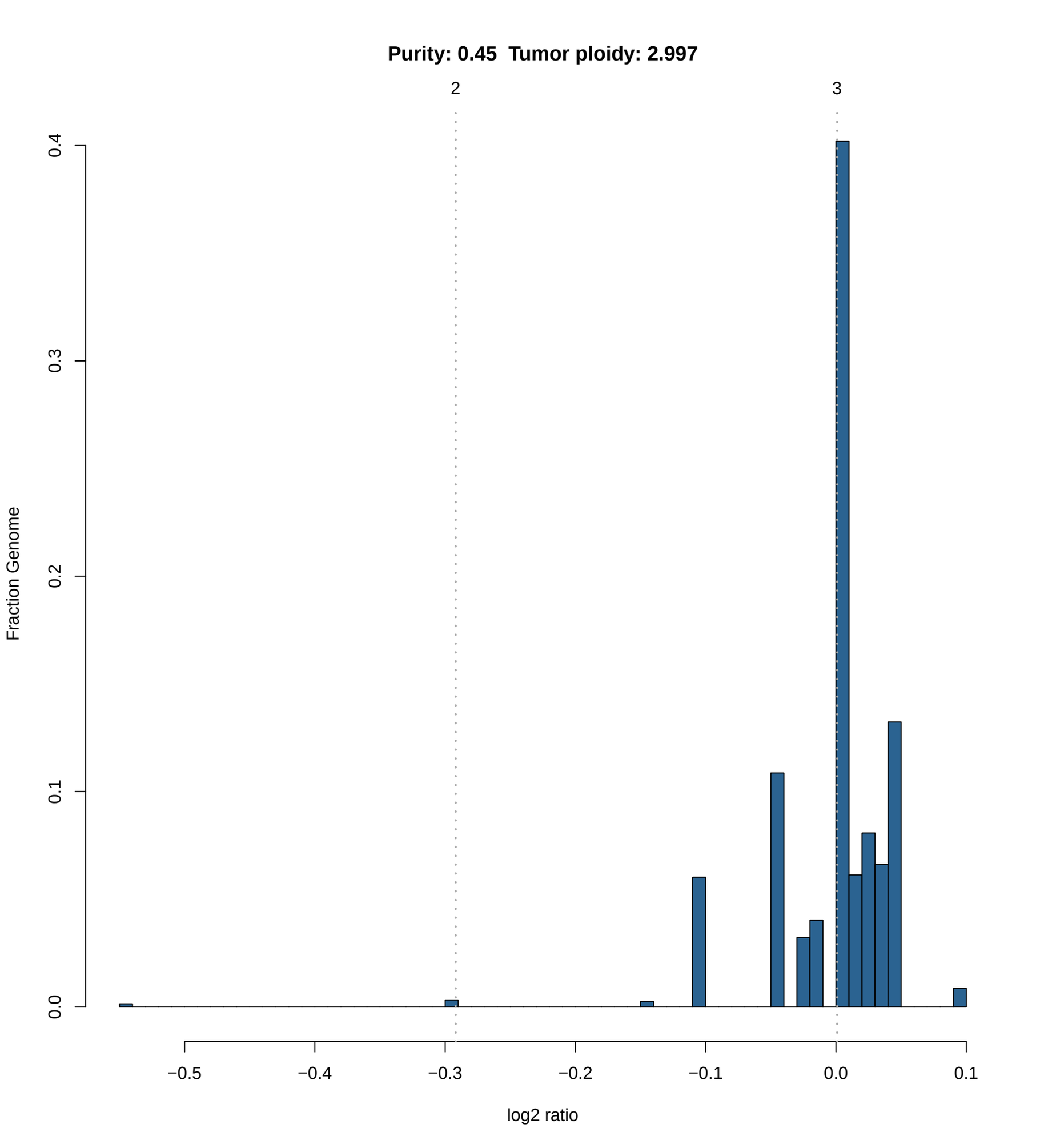

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100
SNV Index

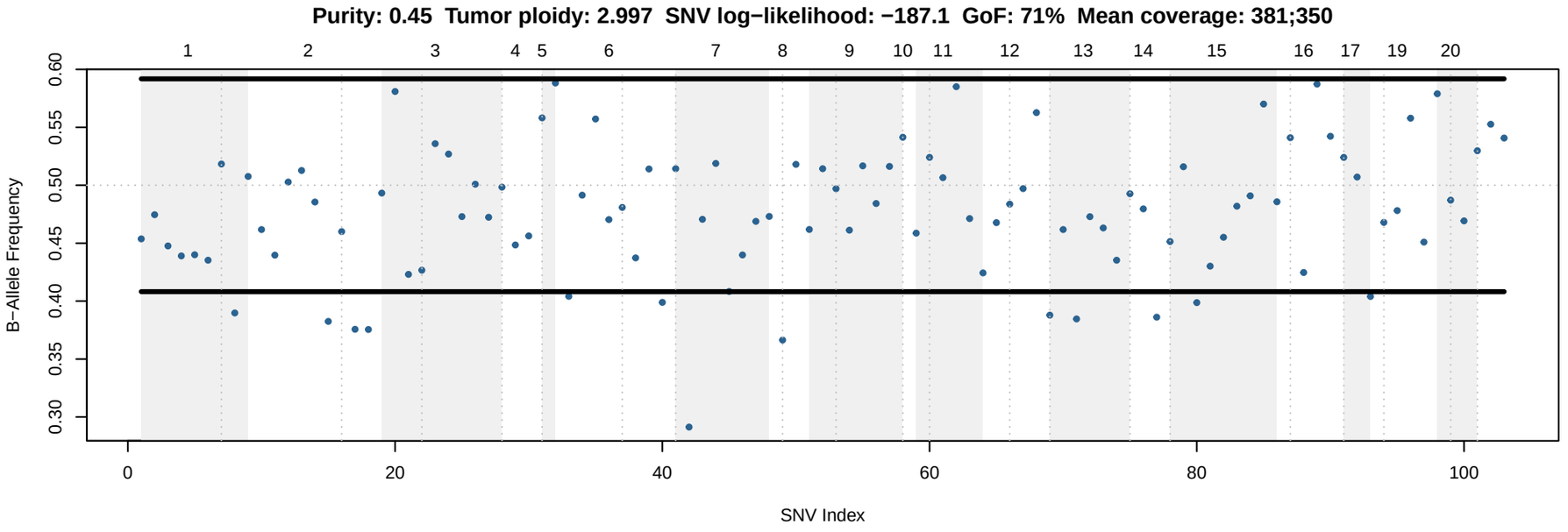

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
6m3
6m2
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

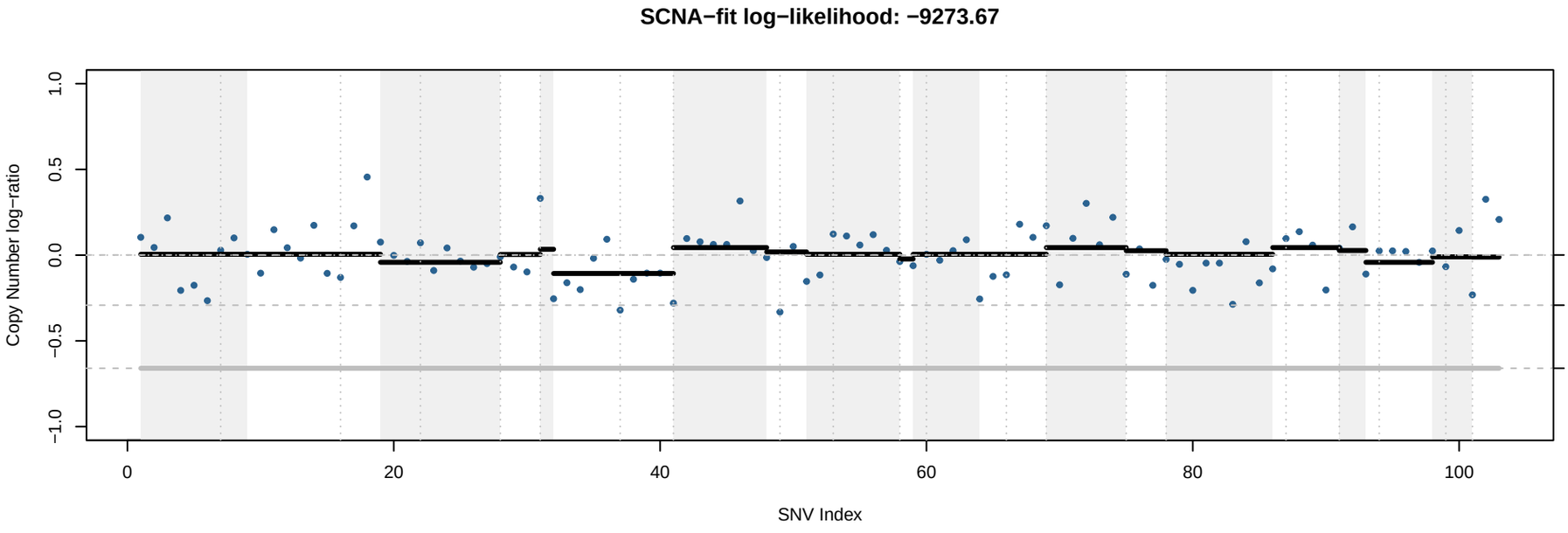

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

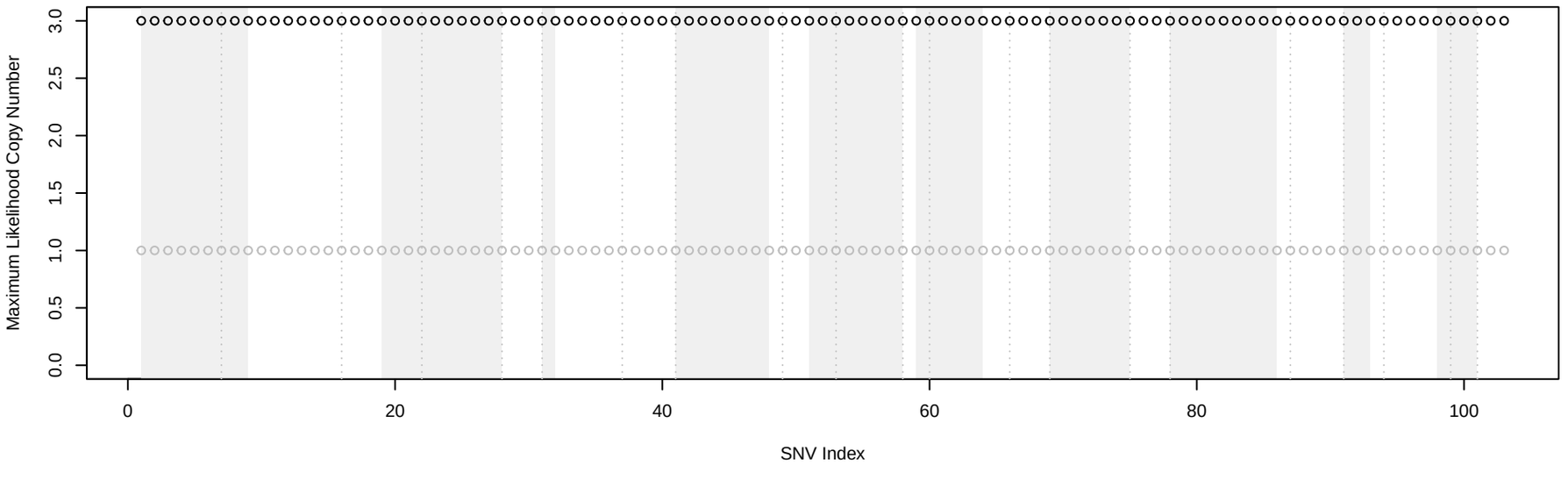

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

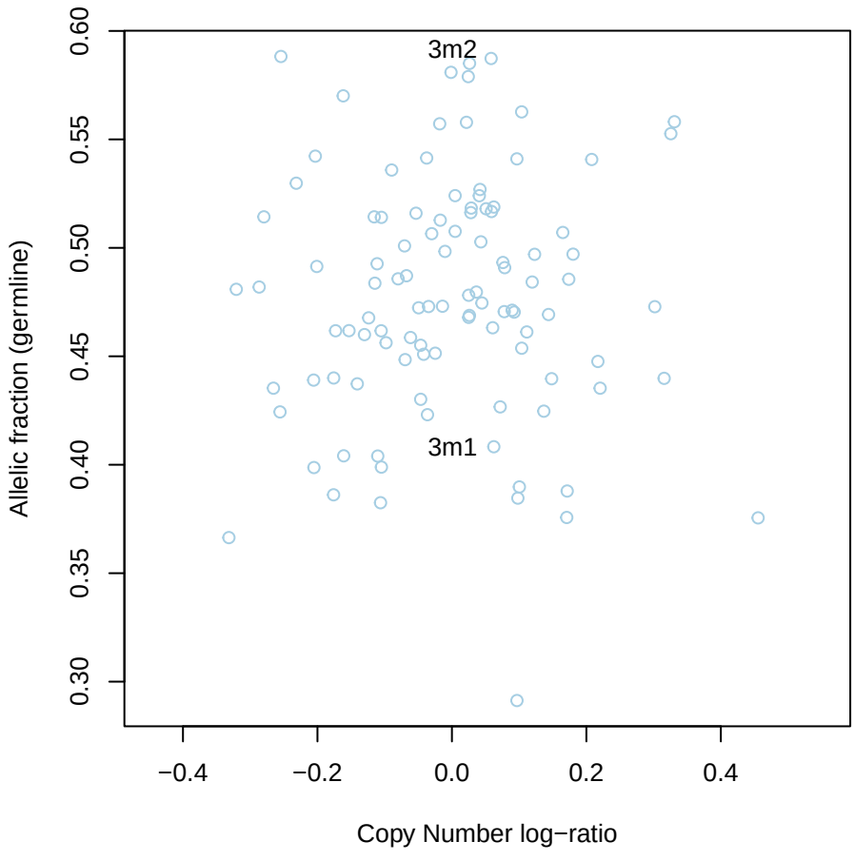

Power 0.8
Frequency
0
10
20
30
40
50
60
0.2
0.4
0.6
0.8
1.0
Cellular fraction

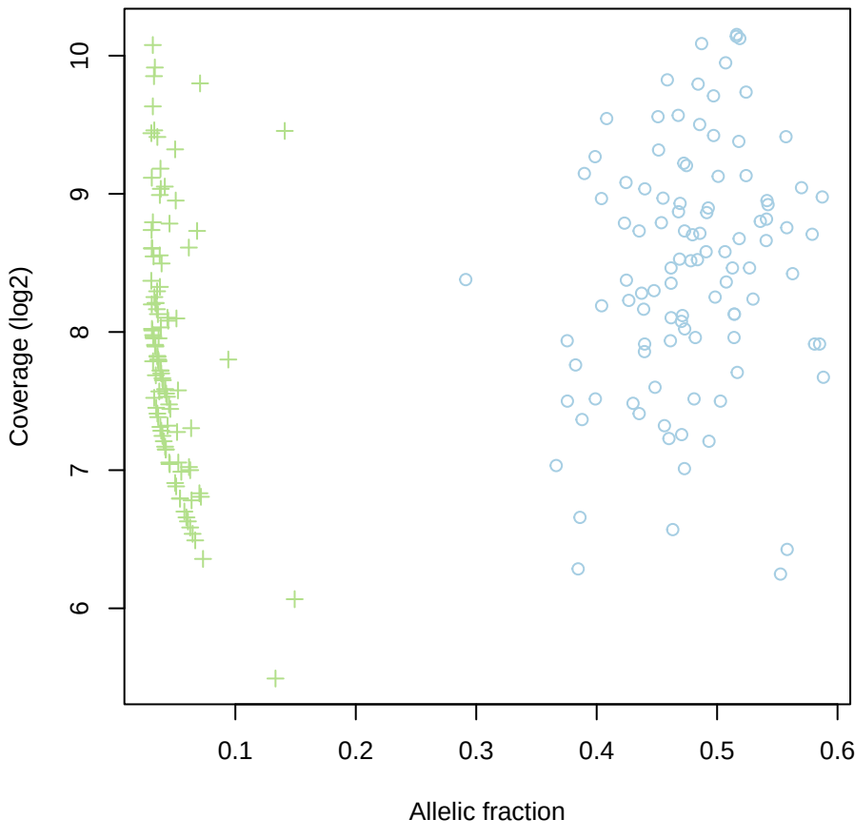

Purity: 0.45 Tumor ploidy: 2.997
2
3
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
−0.4
−0.3
−0.2
−0.1
0.0
0.1
log2 ratio

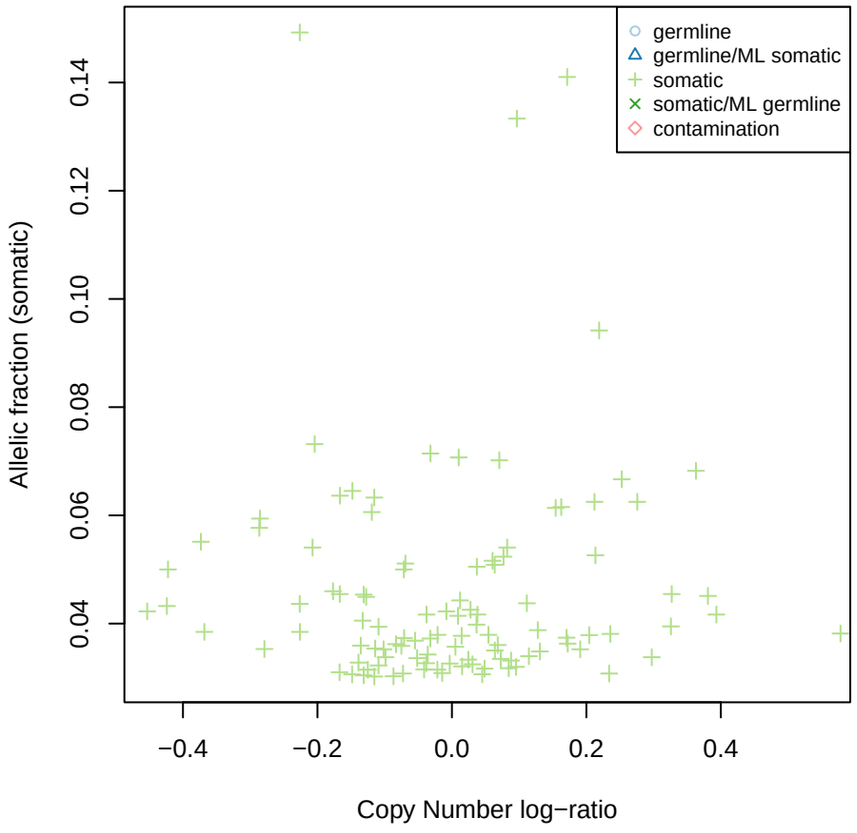

Purity: 0.45 Tumor ploidy: 2.997 SNV log−likelihood: −187.1 GoF: 71% Mean coverage: 381;350
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

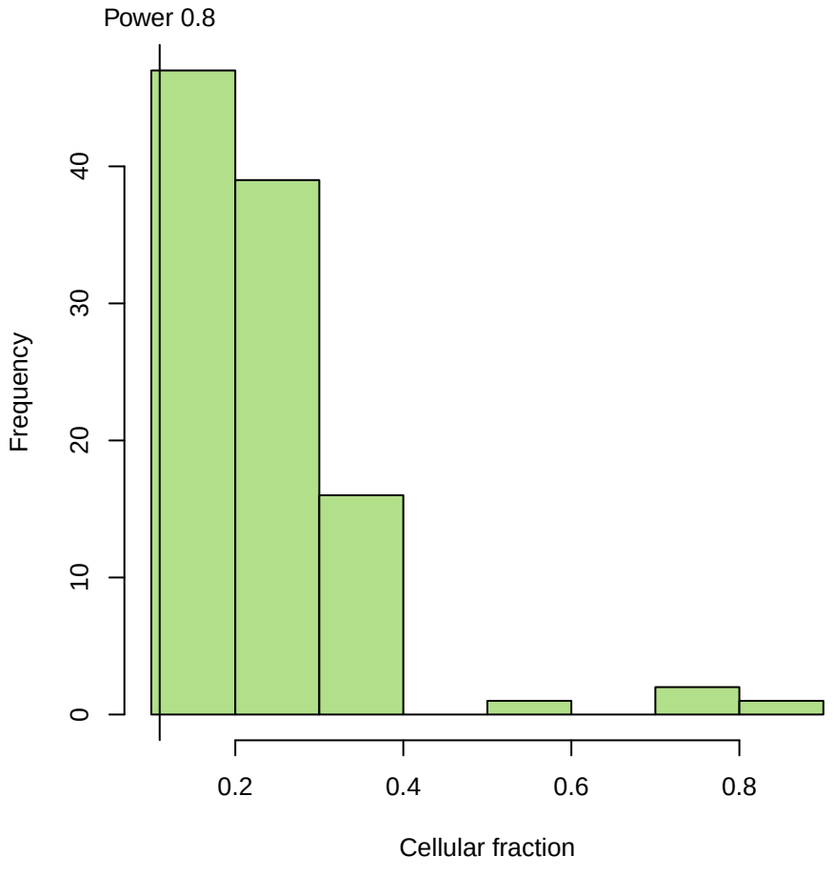

SCNA−fit log−likelihood: −9273.67
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3
0 20 40 60 80 100
SNV Index

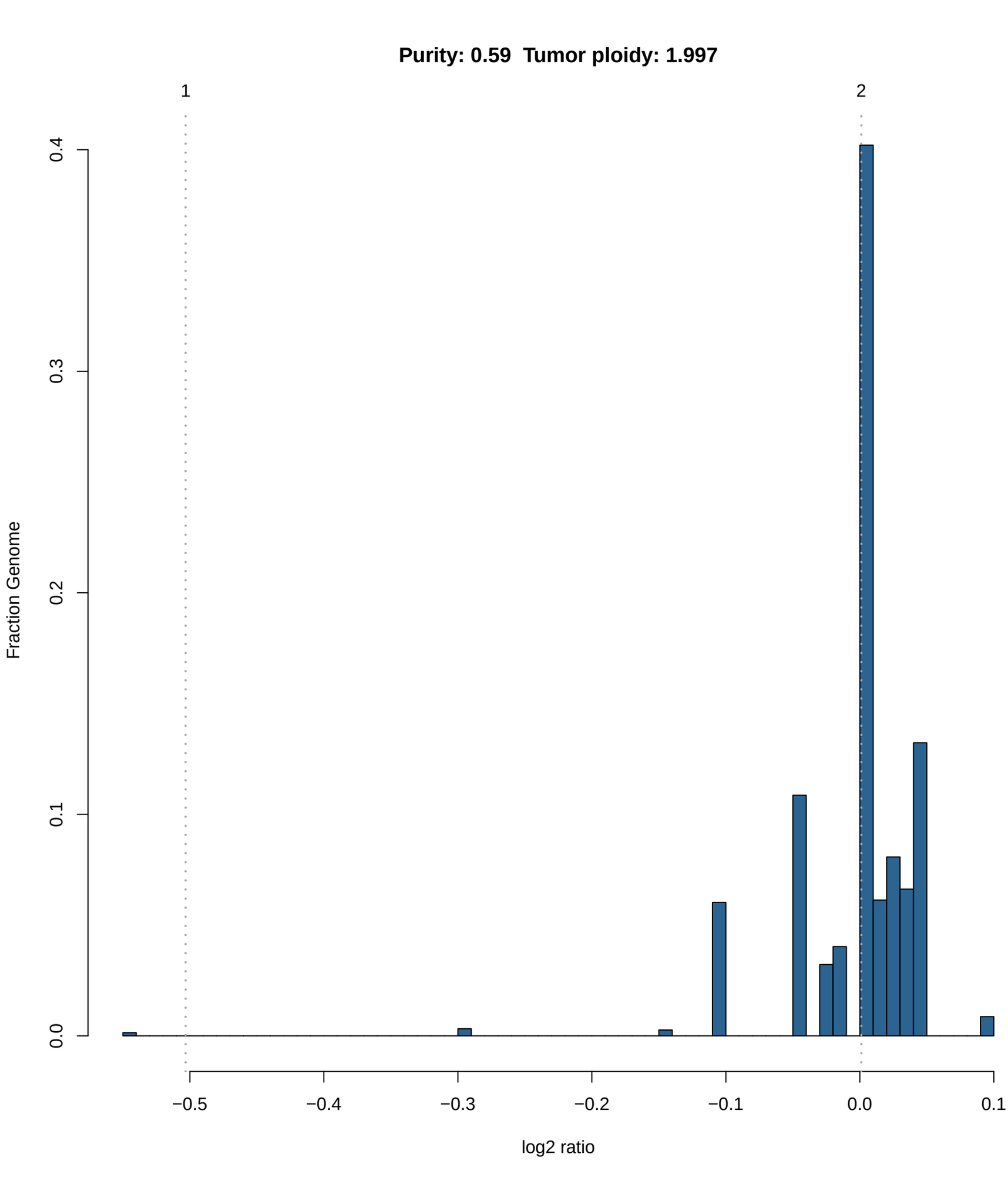

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100
SNV Index

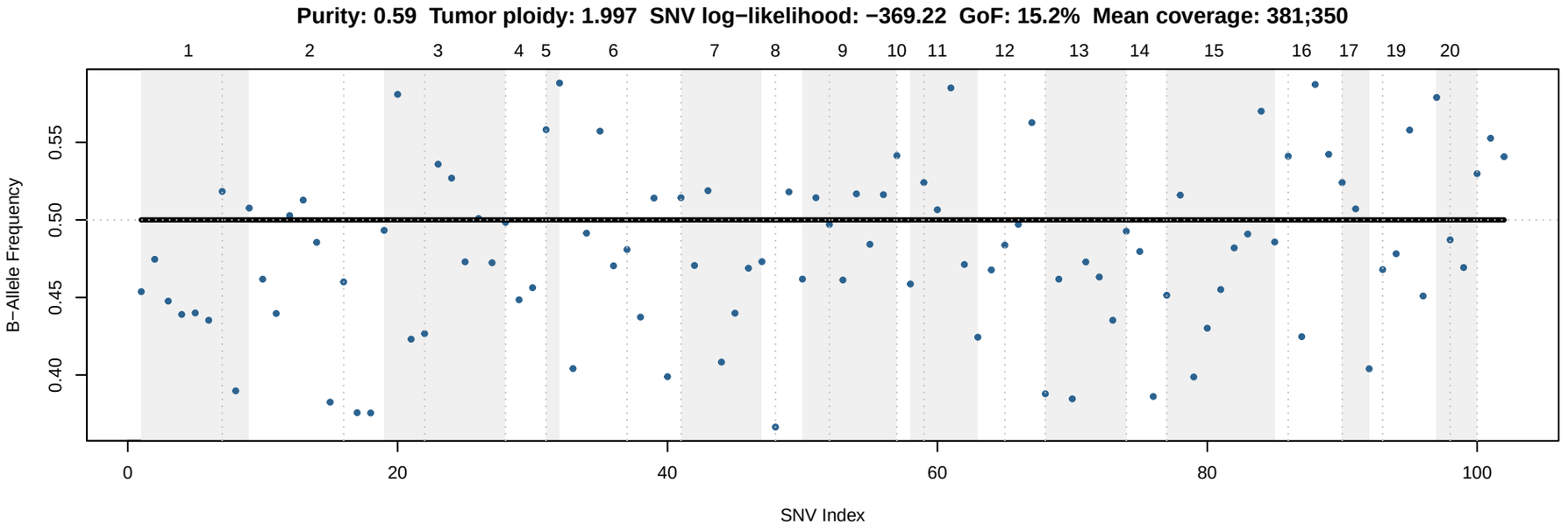

3m2
3m1
Allelic fraction (germline)
Copy Number log−ratio
0.30
0.35
0.40
0.45
0.50
0.55
0.60
−0.4
−0.2
0.0
0.2
0.4

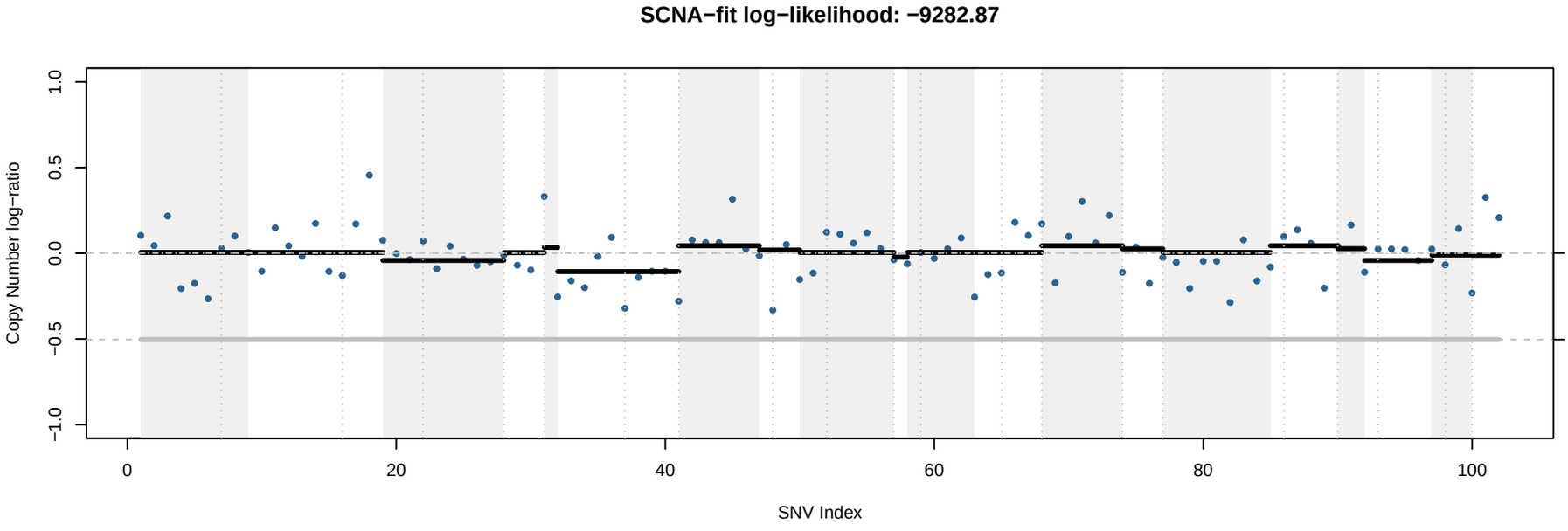

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

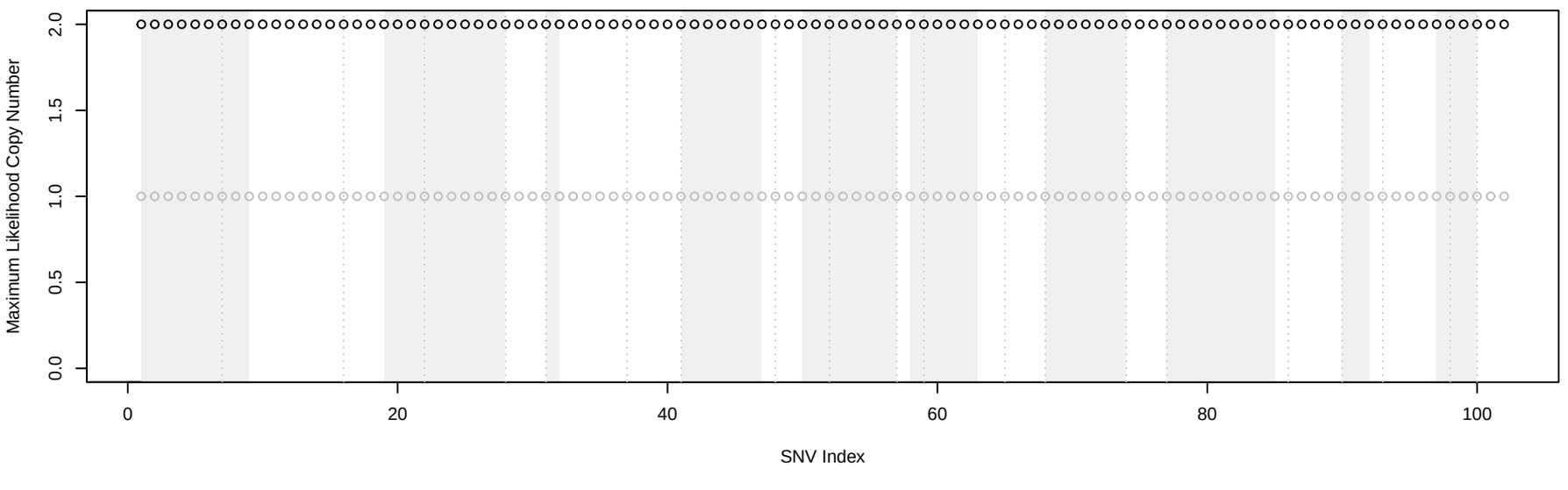

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
0.12
0.14
−0.4
−0.2
0.0
0.2
0.4

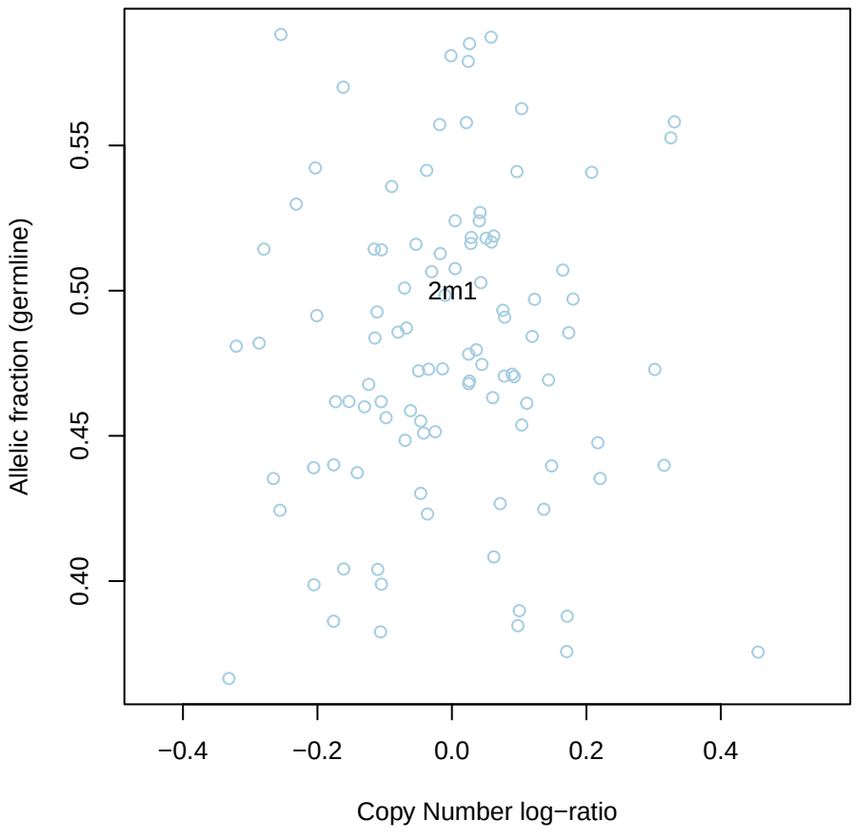

Power 0.8
Frequency
Cellular fraction
0
10
20
30
40
0.2
0.4
0.6
0.8

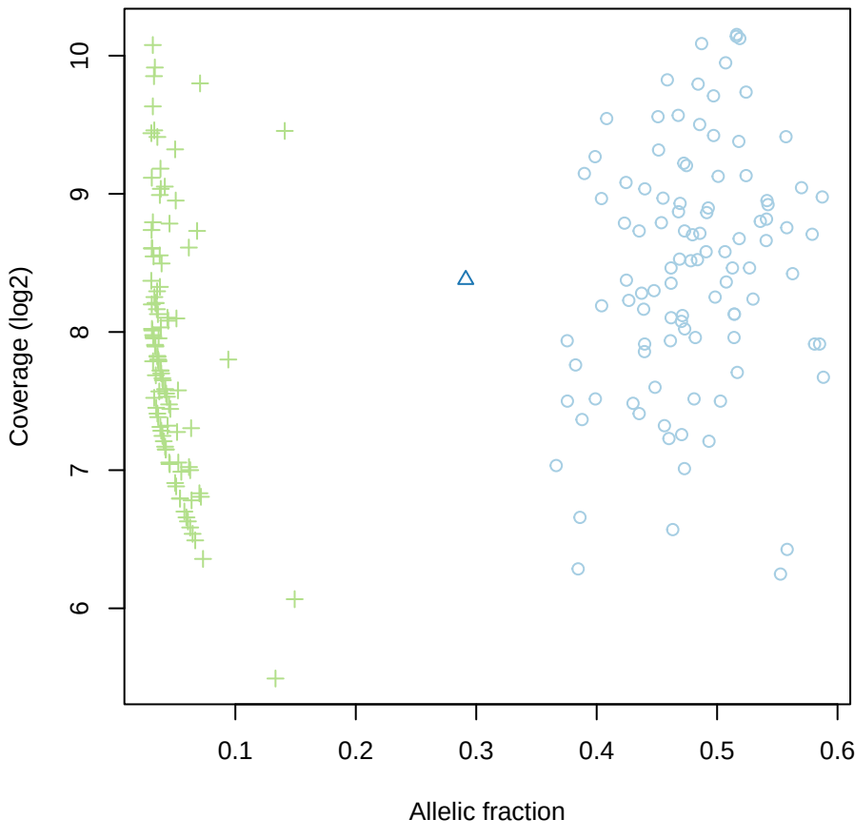

Purity: 0.59 Tumor ploidy: 1.997
1
2
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
−0.4
−0.3
−0.2
−0.1
0.0
0.1
log2 ratio

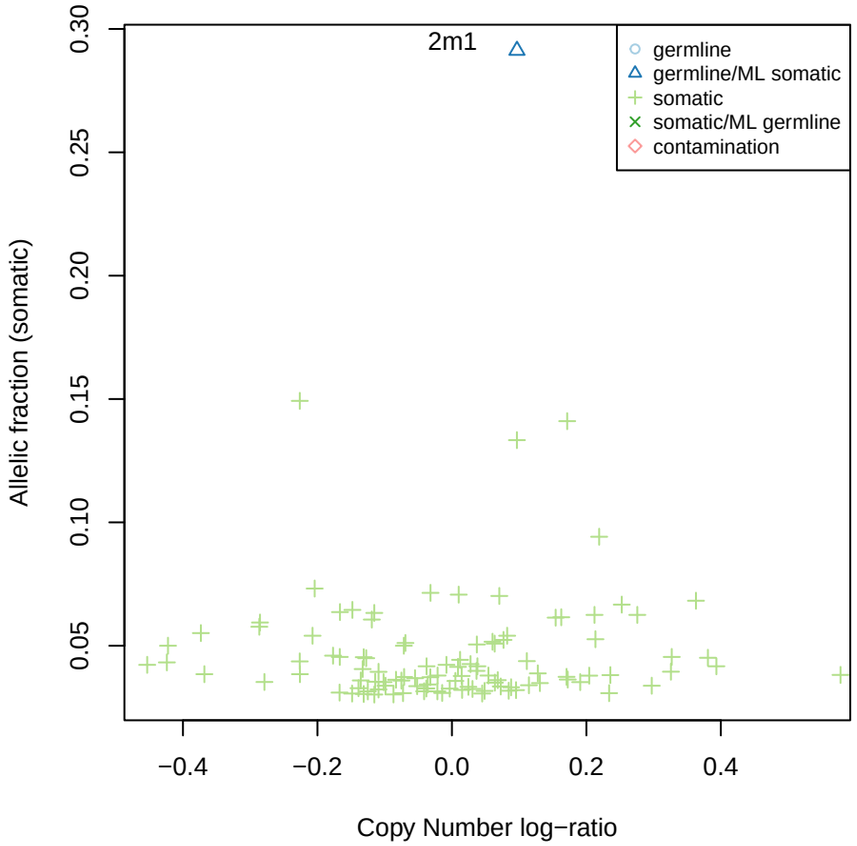

Purity: 0.59 Tumor ploidy: 1.997 SNV log−likelihood: −369.22 GoF: 15.2% Mean coverage: 381;350
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.40 0.45 0.50 0.55
0 20 40 60 80 100
SNV Index

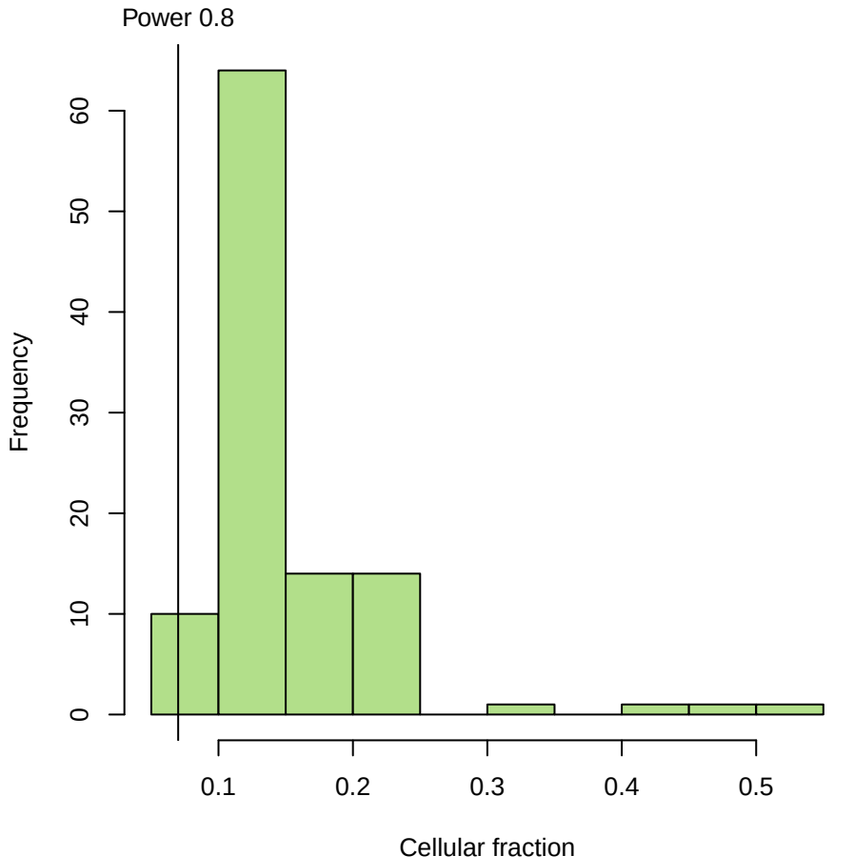

SCNA−fit log−likelihood: −9282.87
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2
0 20 40 60 80 100
SNV Index

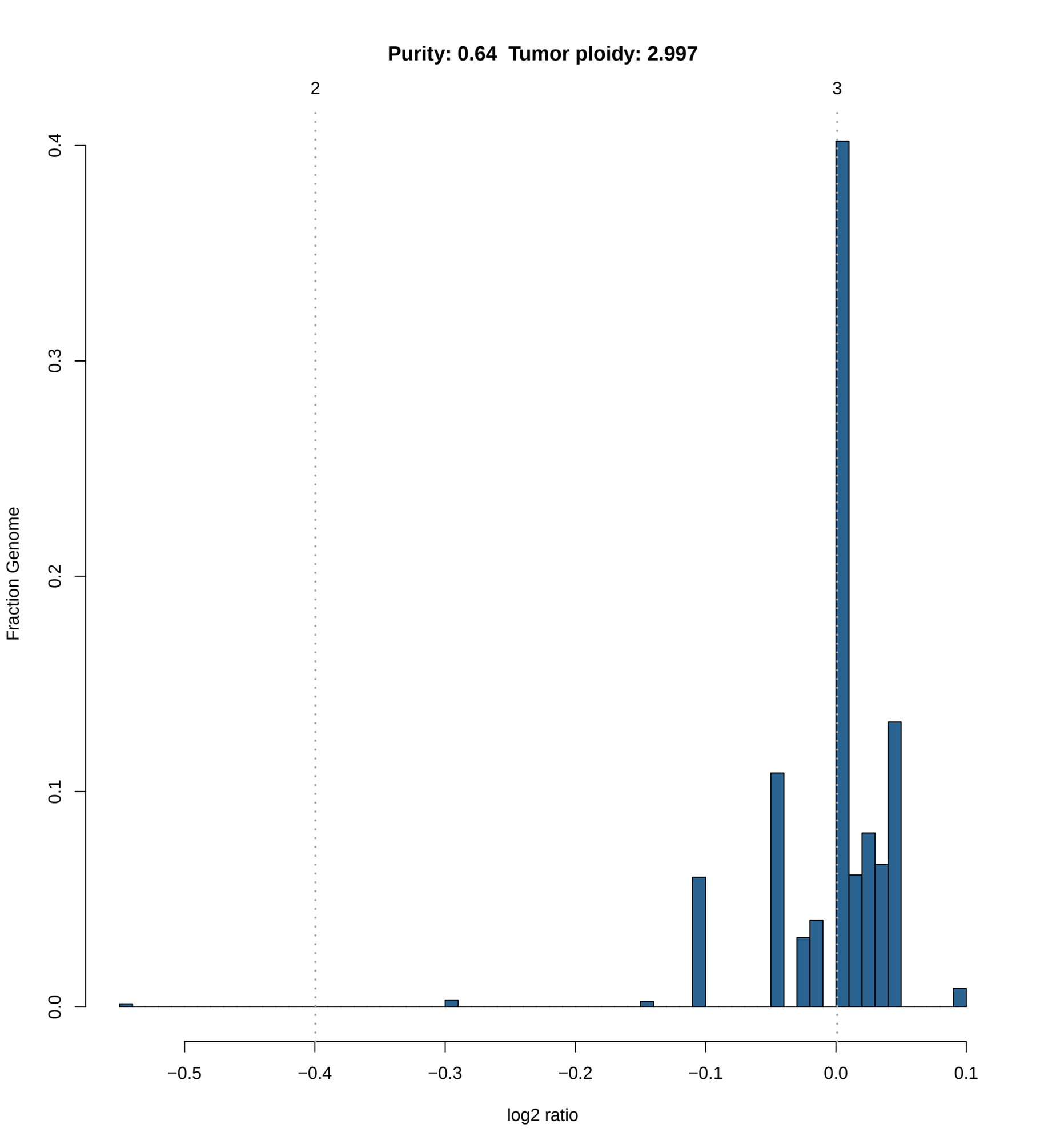

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 20 40 60 80 100
SNV Index

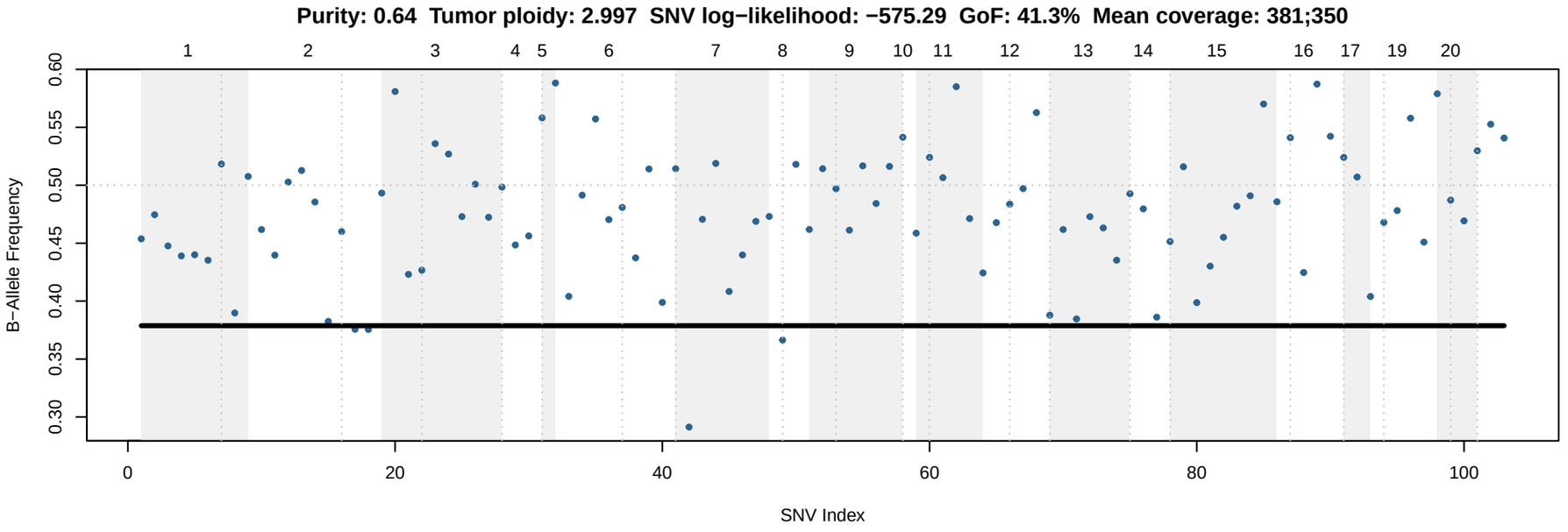

Allelic fraction (germline)
0.40
0.45
0.50
0.55
2m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

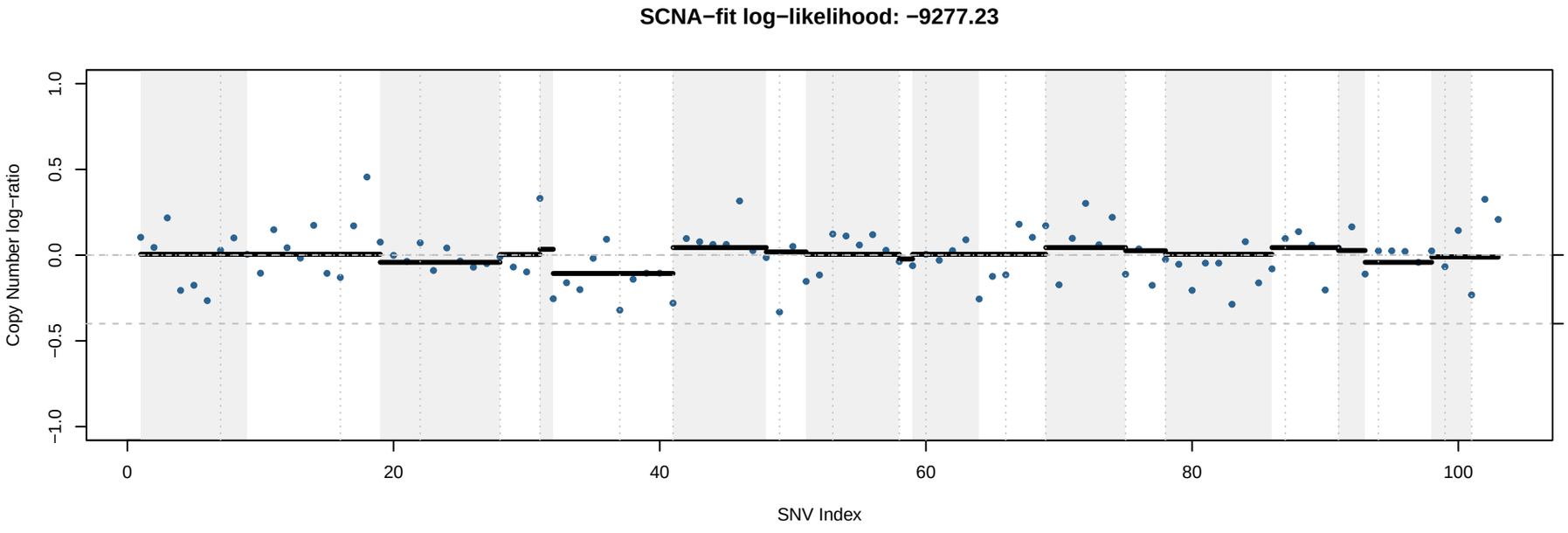

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

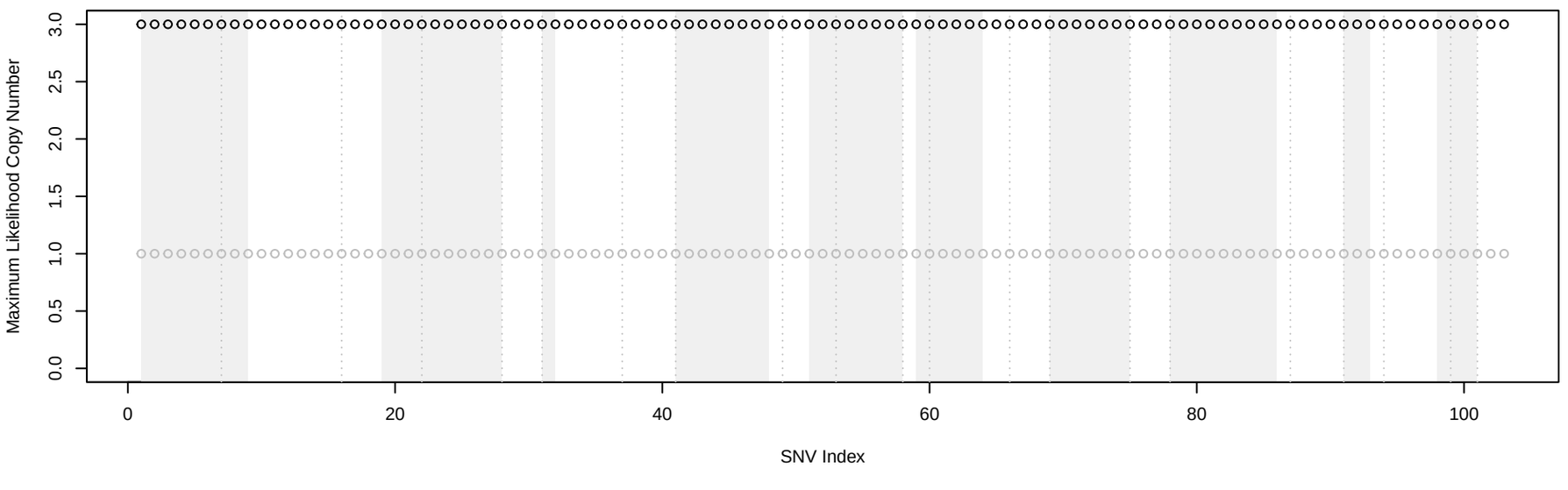

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
0.30
2m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

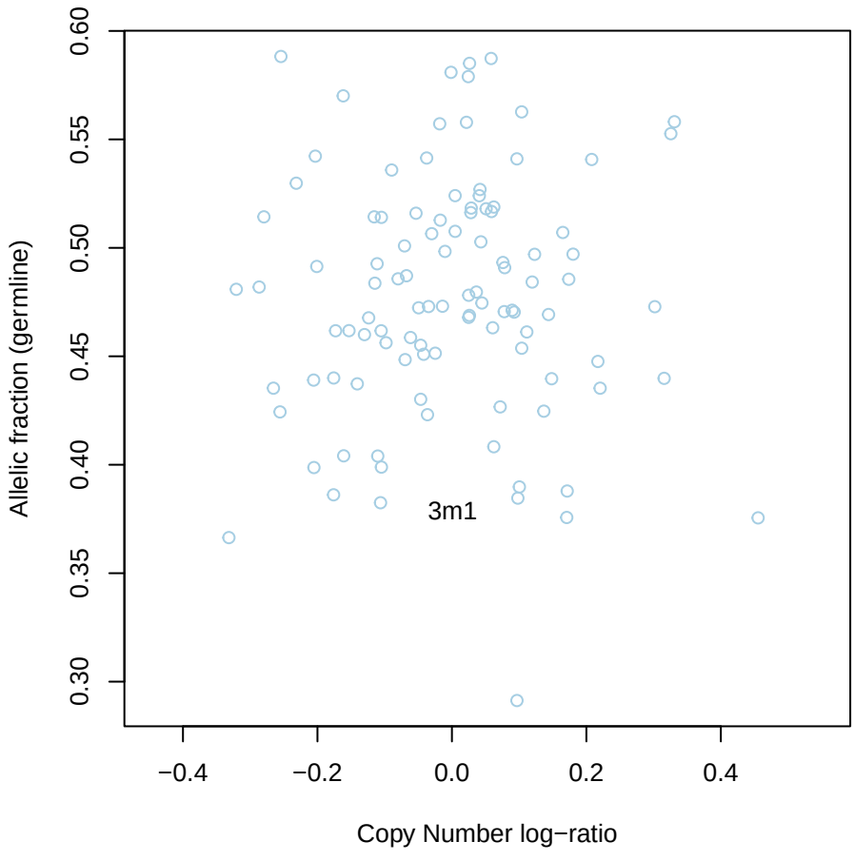

Power 0.8
Frequency
0
10
20
30
40
50
60
0.1
0.2
0.3
0.4
0.5
Cellular fraction

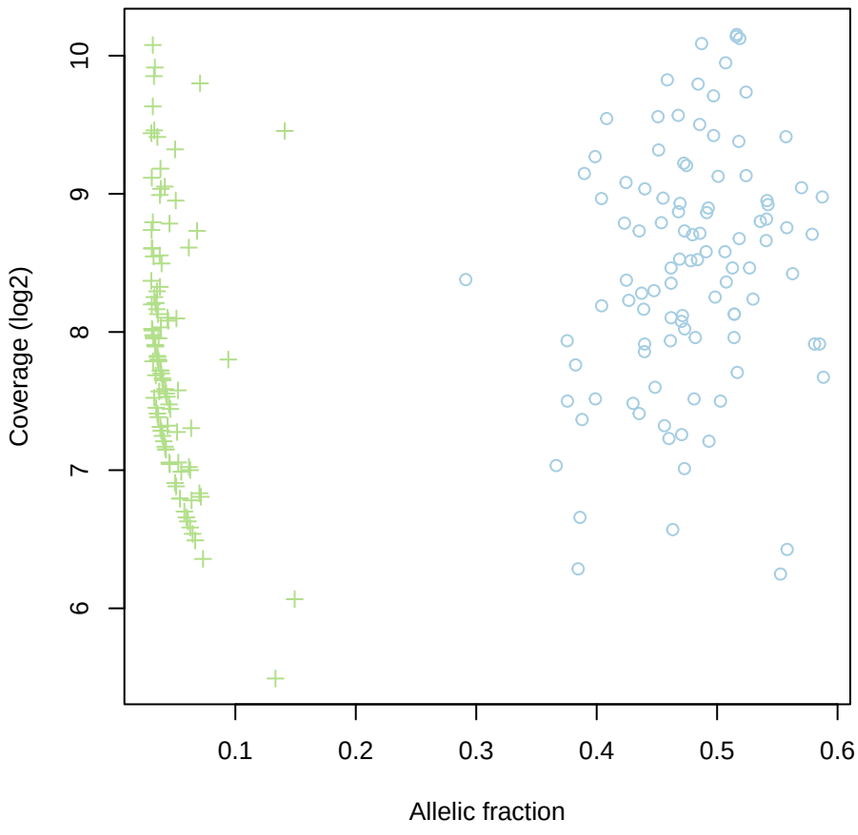

Purity: 0.64 Tumor ploidy: 2.997
2
3
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
−0.4
−0.3
−0.2
−0.1
0.0
0.1
log2 ratio

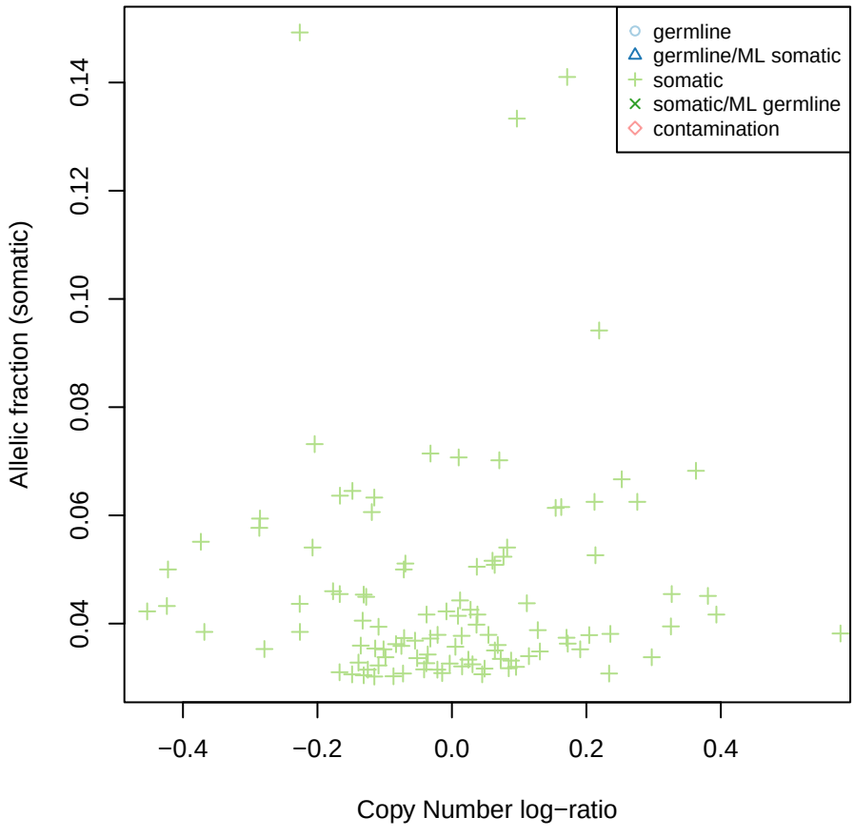

Purity: 0.64 Tumor ploidy: 2.997 SNV log−likelihood: −575.29 GoF: 41.3% Mean coverage: 381;350
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.30 0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80 100
SNV Index

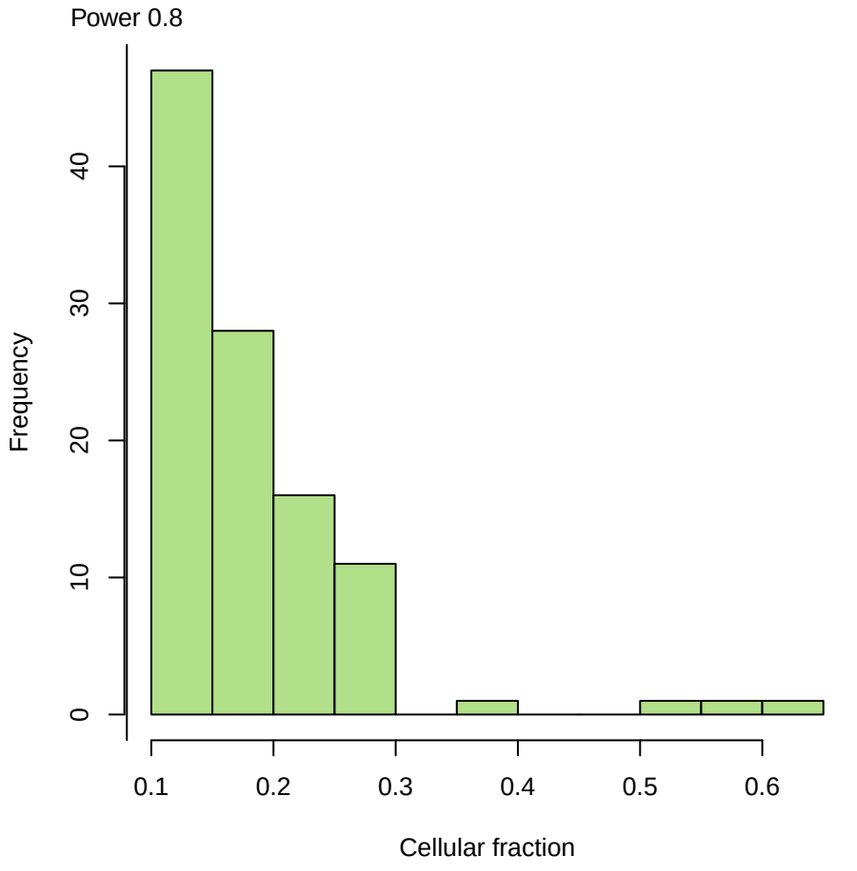

SCNA−fit log−likelihood: −9277.23
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3
0 20 40 60 80 100
SNV Index

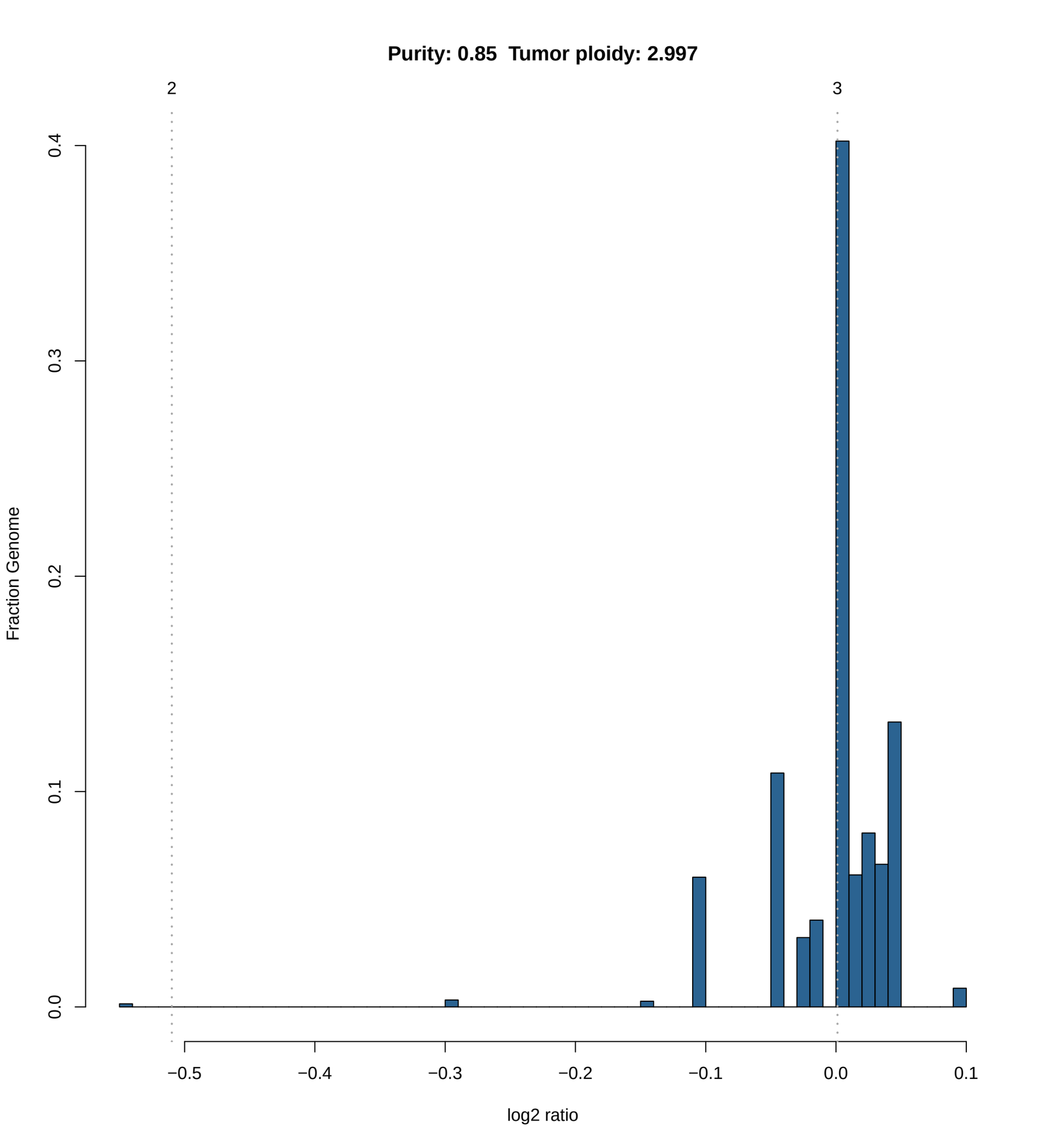

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100
SNV Index

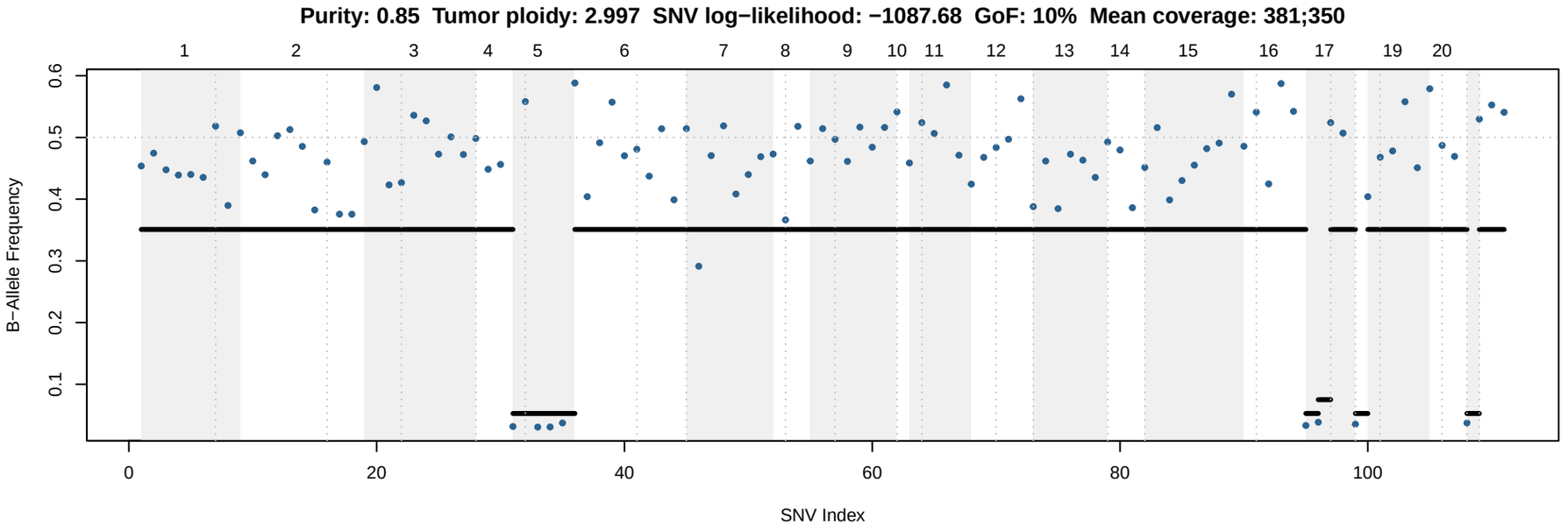

Allelic fraction (germline)
0.30
0.35
0.40
0.45
0.50
0.55
0.60
3m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

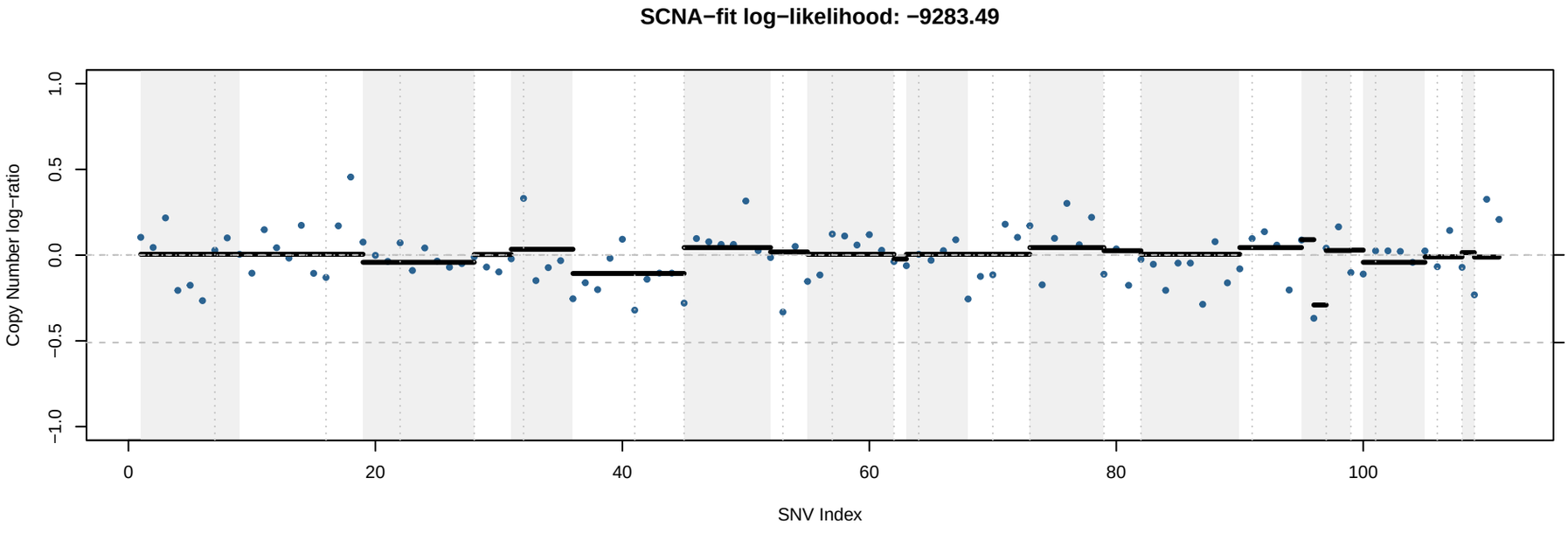

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

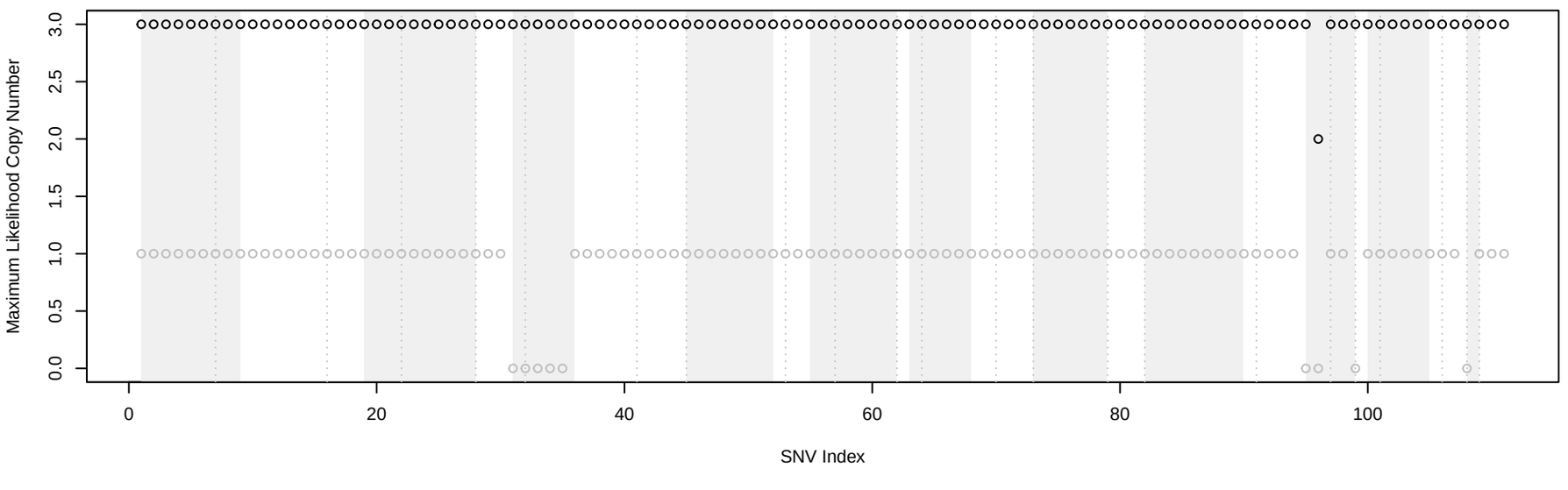

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

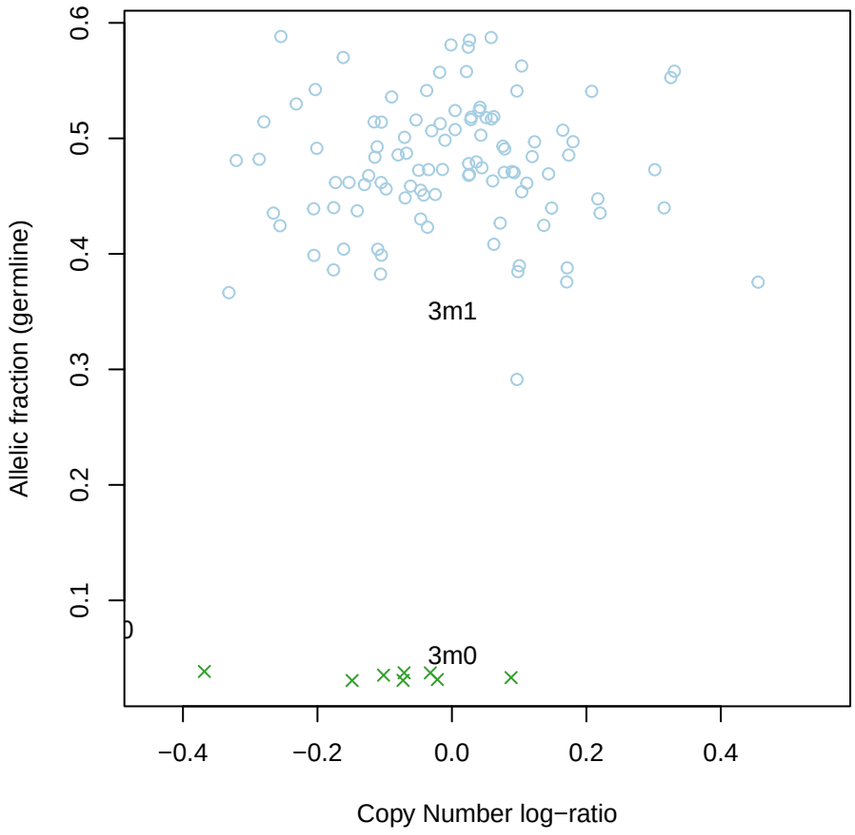

Power 0.8
Frequency
0
10
20
30
40
0.1
0.2
0.3
0.4
0.5
0.6
Cellular fraction

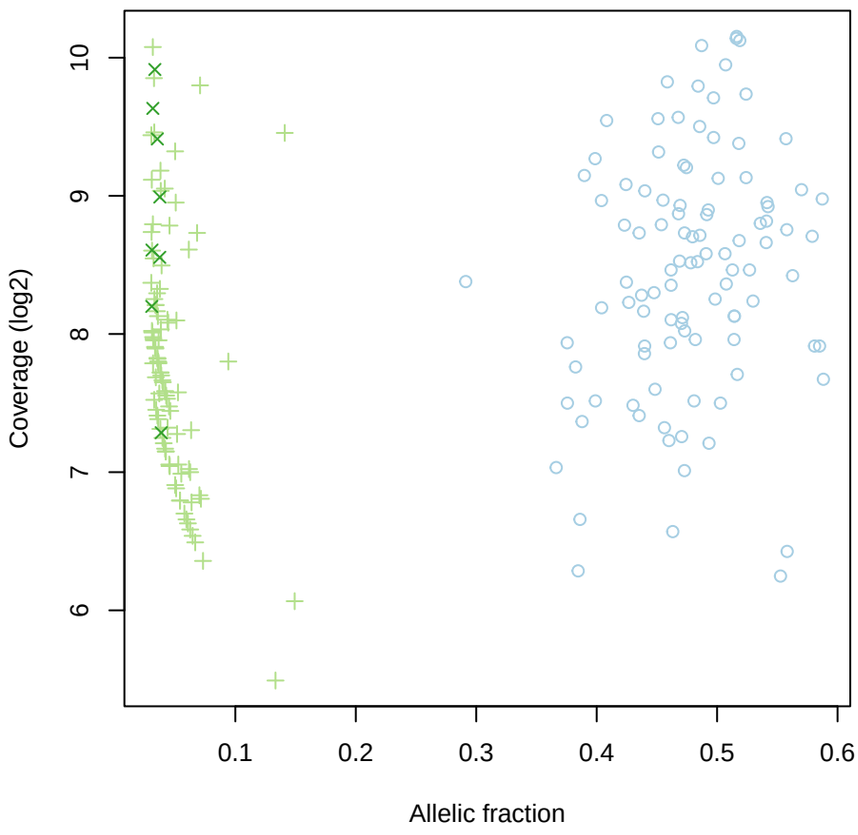

Purity: 0.85 Tumor ploidy: 2.997
2
3
0.4
0.3
0.2
0.1
0.0
Fraction Genome
−0.5
−0.4
−0.3
−0.2
−0.1
0.0
0.1
log2 ratio

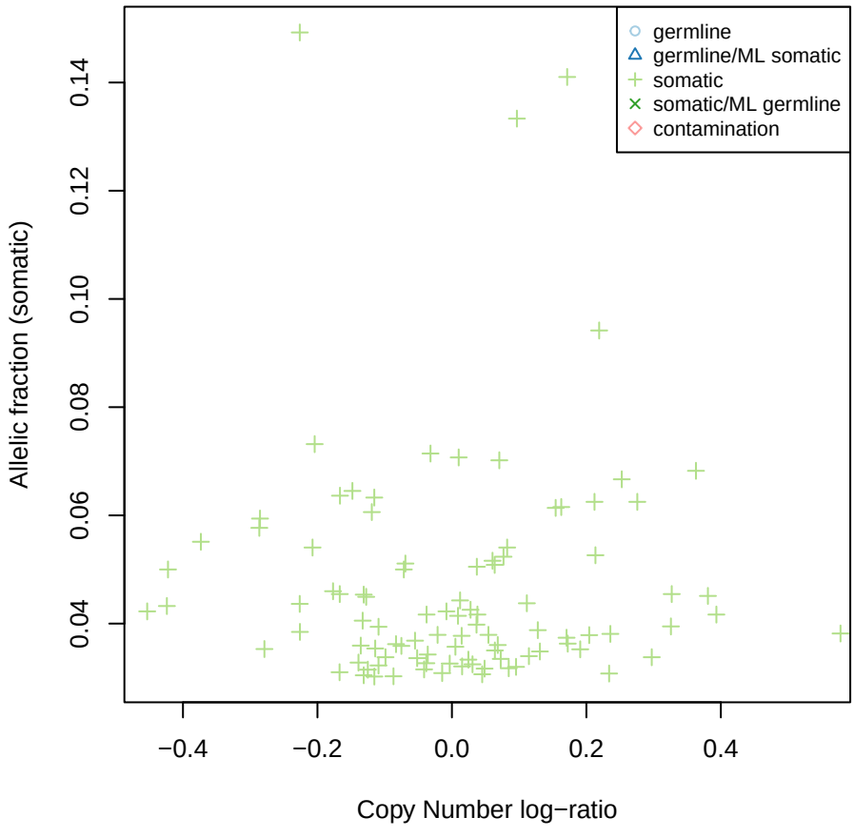

Purity: 0.85 Tumor ploidy: 2.997 SNV log−likelihood: −1087.68 GoF: 10% Mean coverage: 381;350
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 19 20
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6
0 20 40 60 80 100
SNV Index

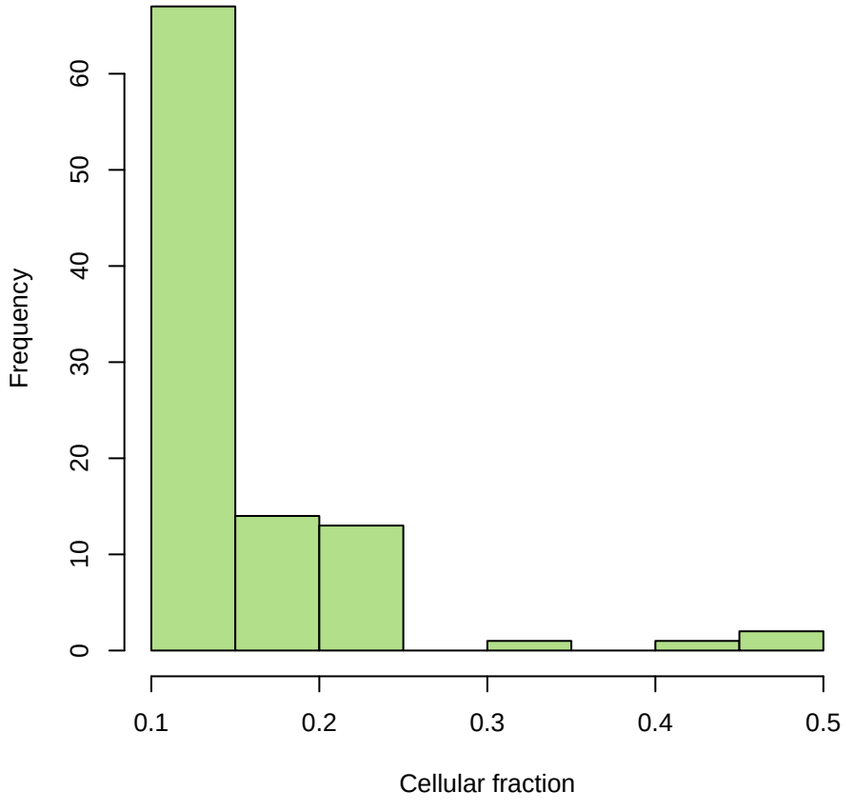

SCNA−fit log−likelihood: −9283.49
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3
0 20 40 60 80 100
SNV Index


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


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


Coverage (log2)
Allelic fraction


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


Frequency
Cellular fraction