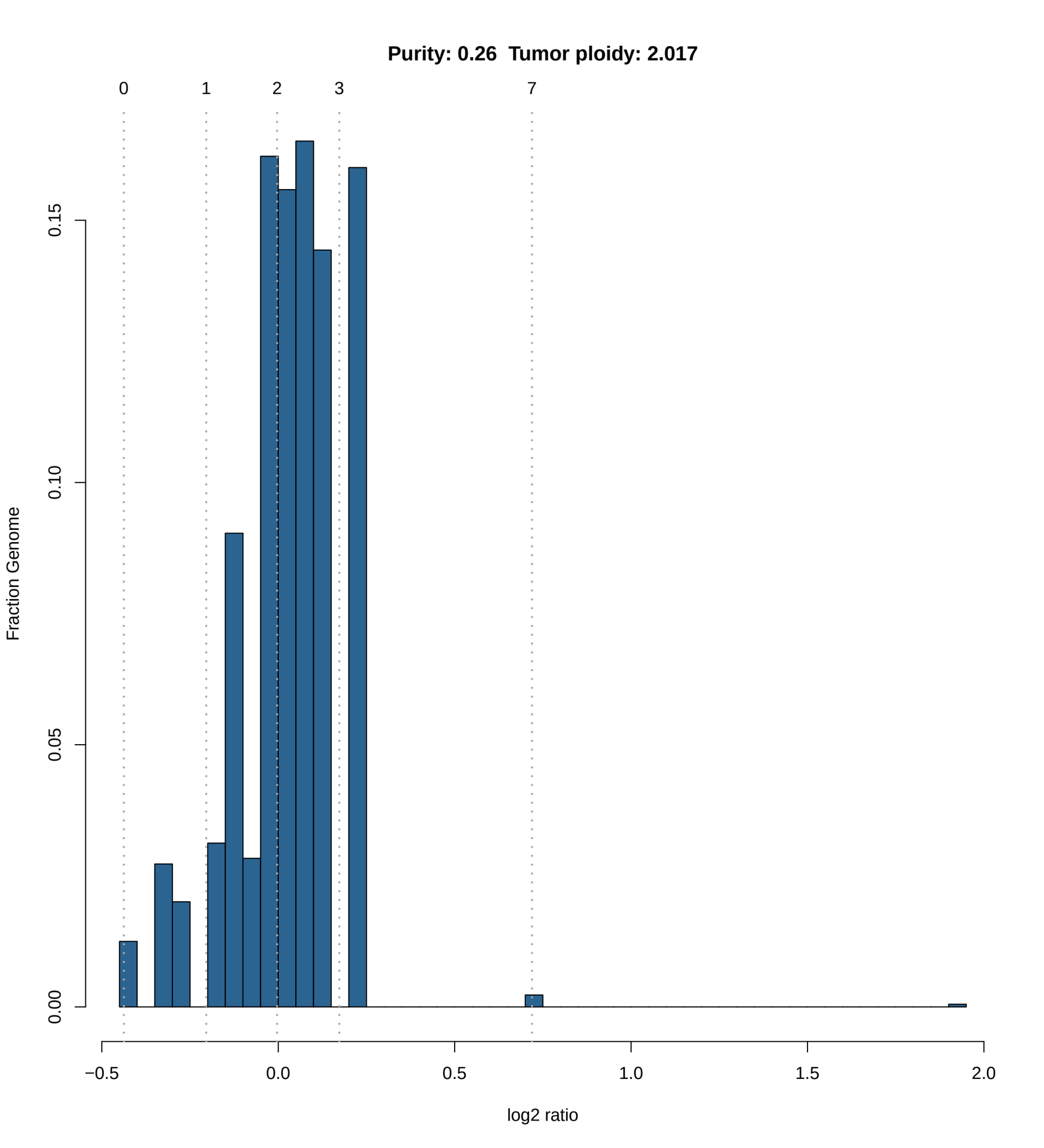
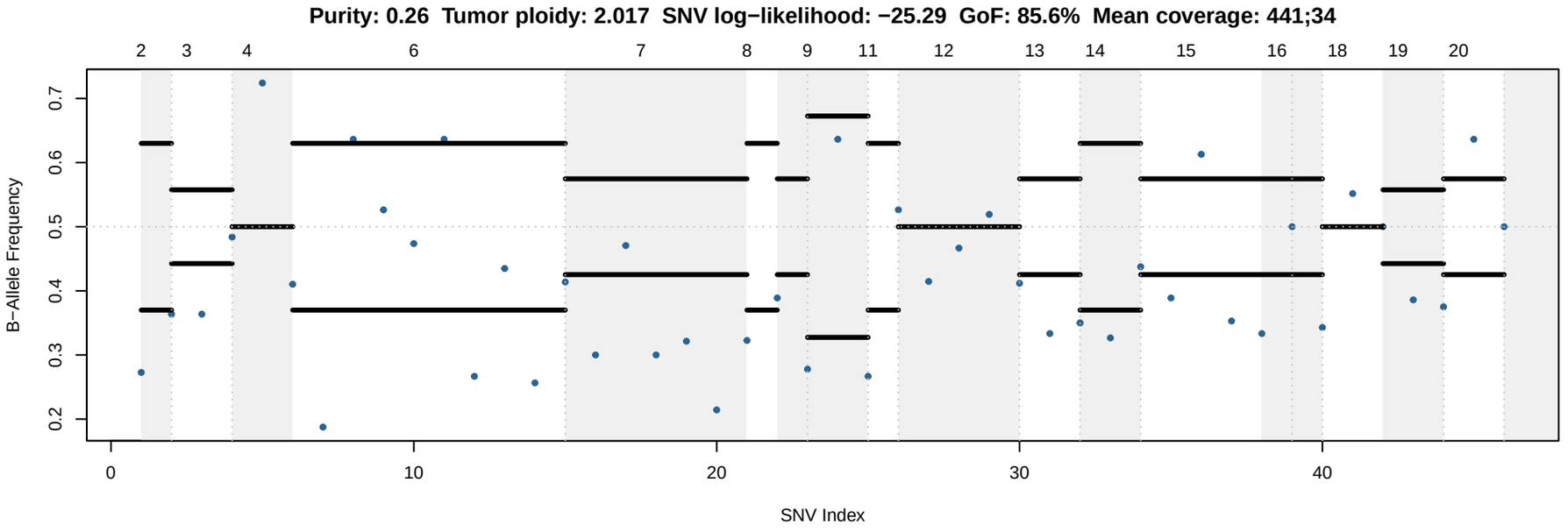
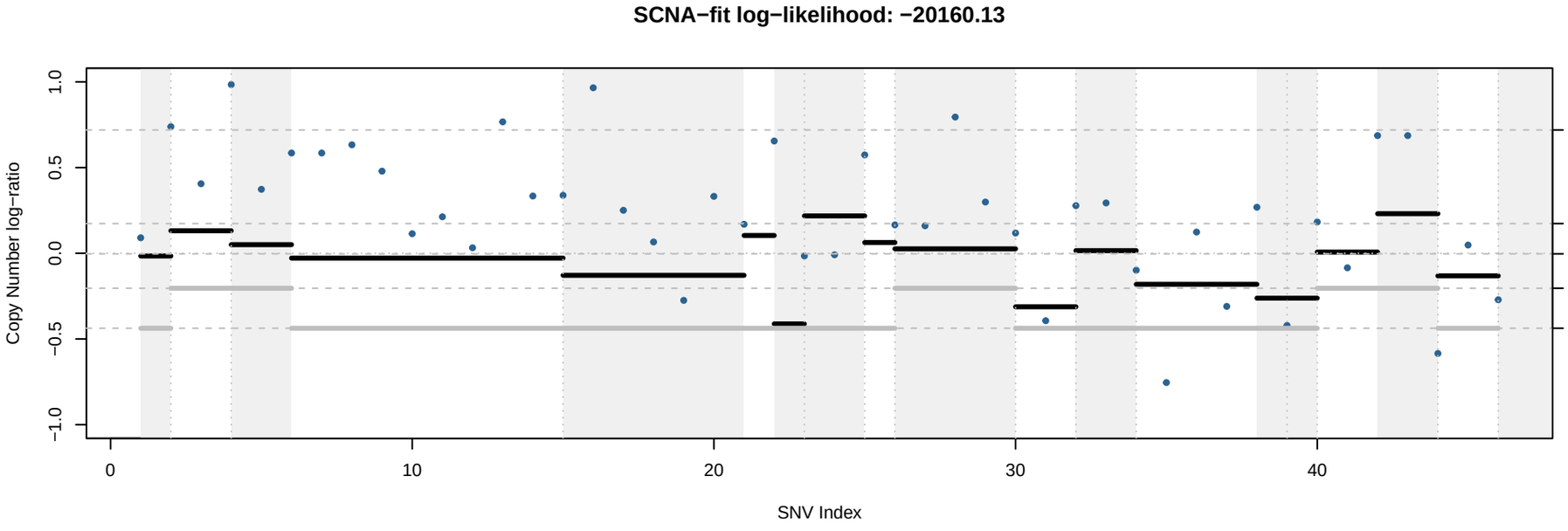
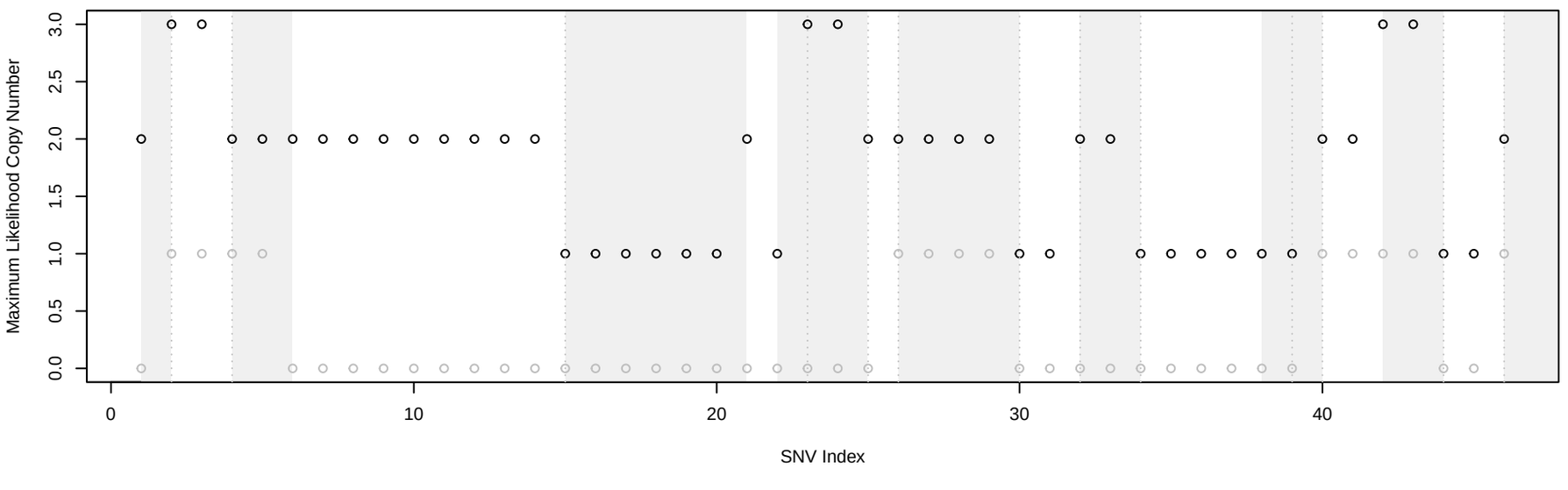
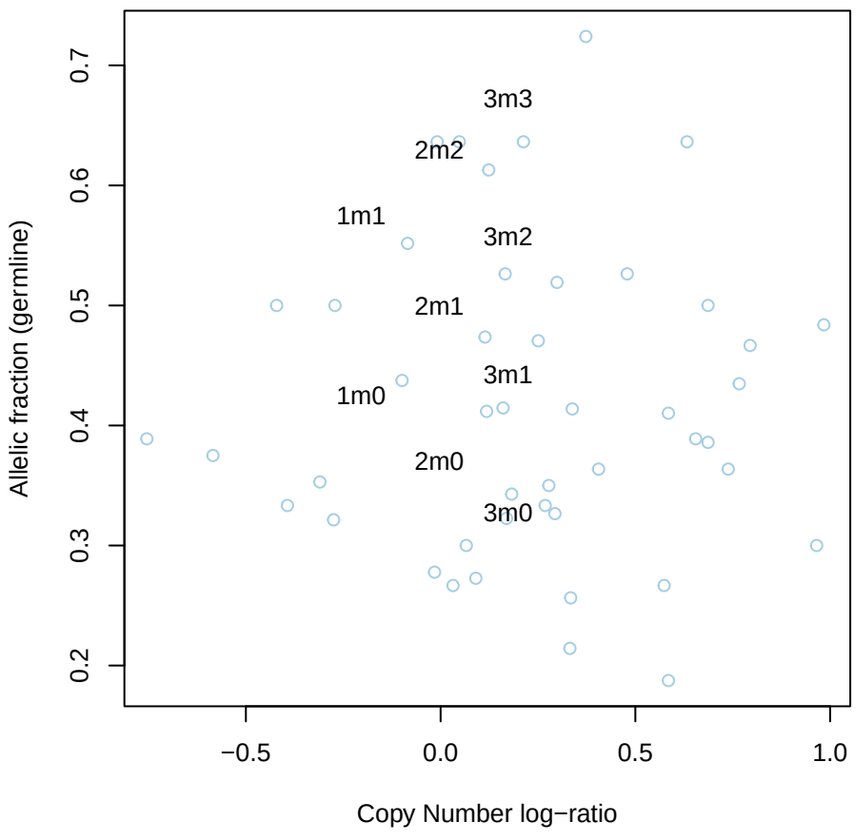
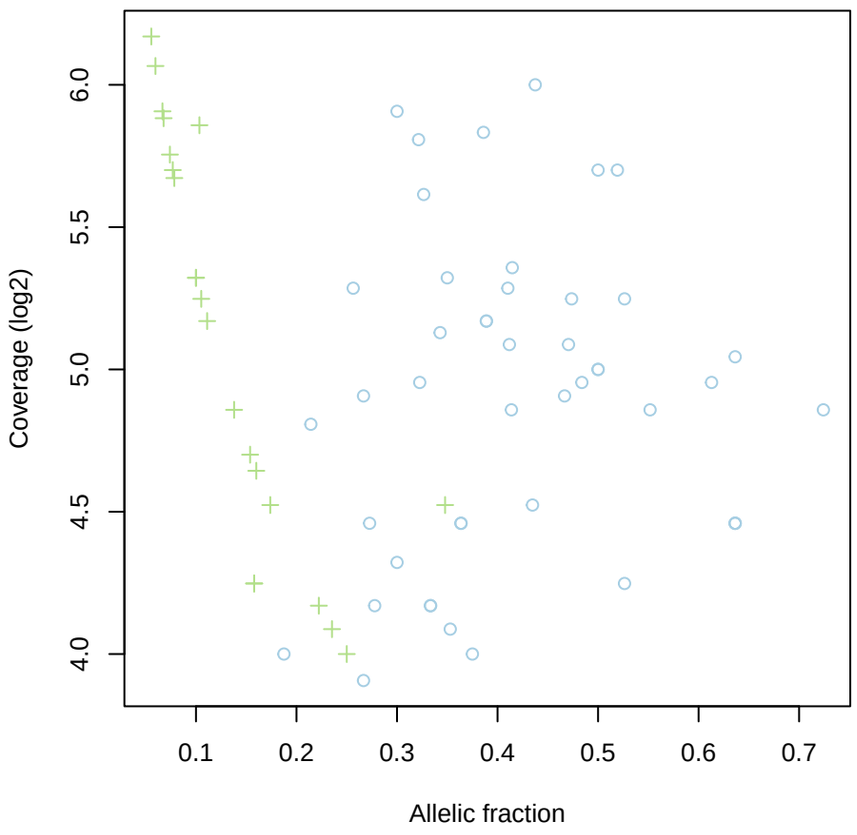

Purity: 0.26 Tumor ploidy: 2.017
0
1
2
3
7
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

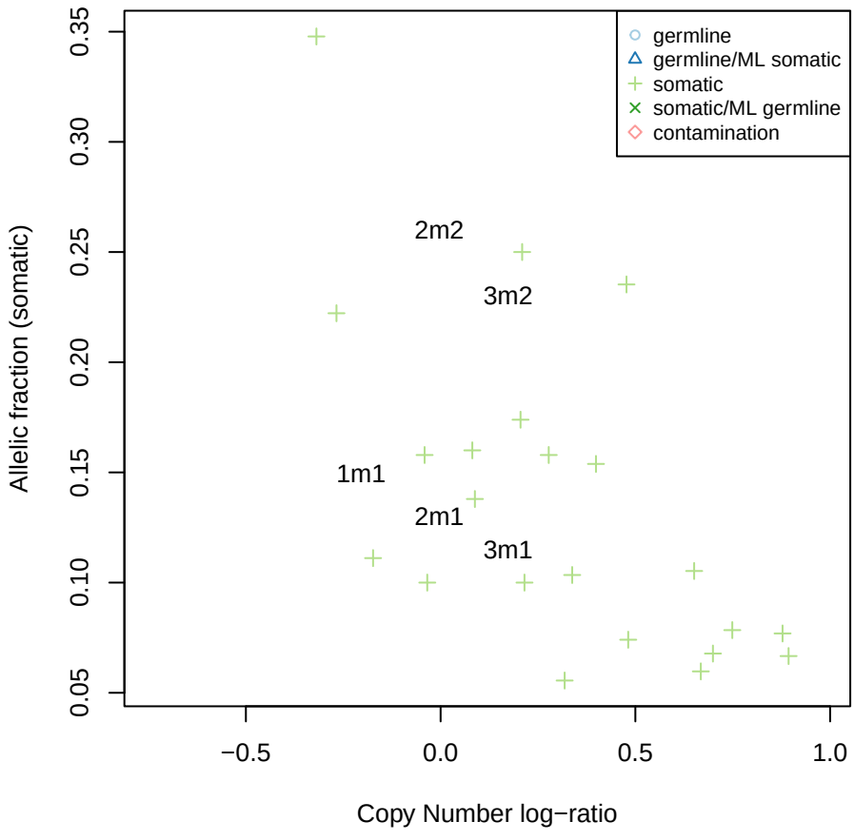

Purity: 0.26 Tumor ploidy: 2.017 SNV log−likelihood: −25.29 GoF: 85.6% Mean coverage: 441;34
2 3 4 6 7 8 9 11 12 13 14 15 16 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 10 20 30 40
SNV Index

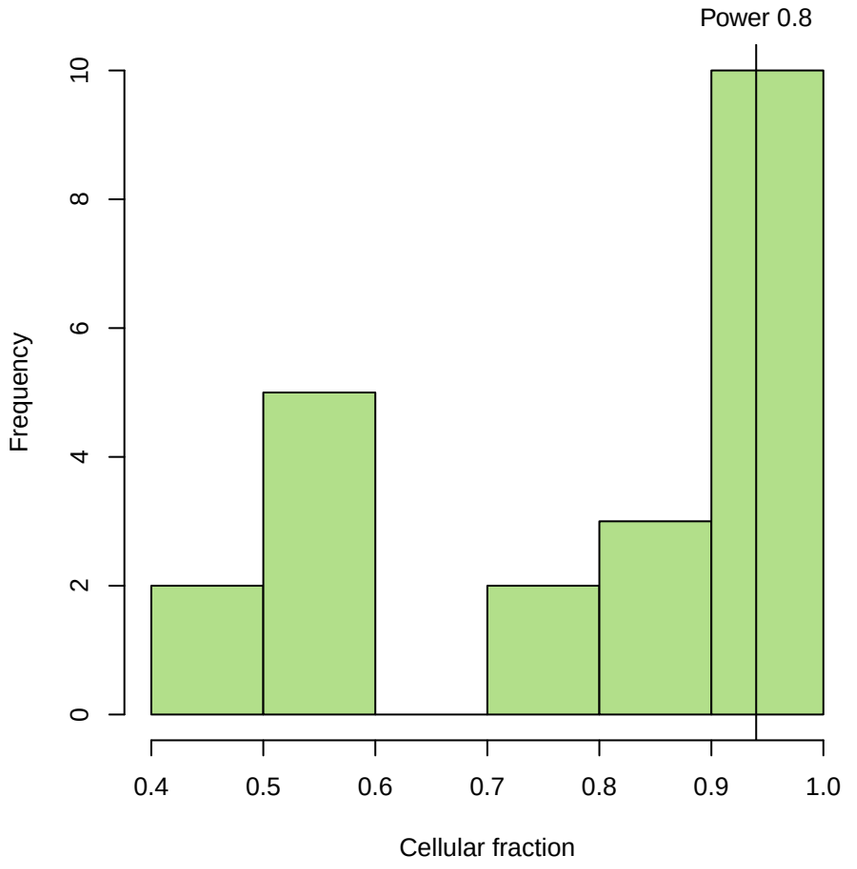

SCNA−fit log−likelihood: −20160.13
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 7
0 10 20 30 40
SNV Index

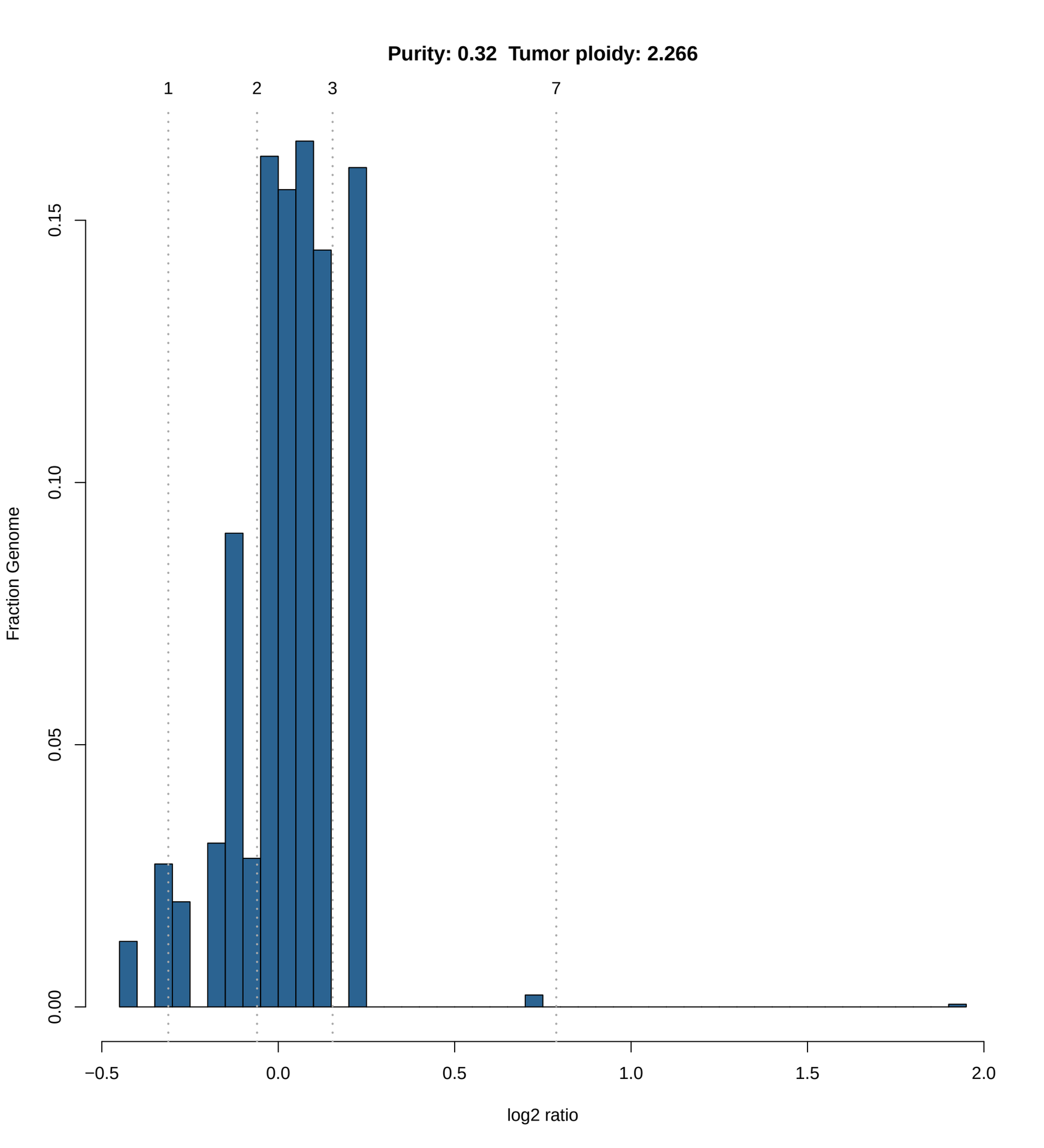

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 10 20 30 40
SNV Index

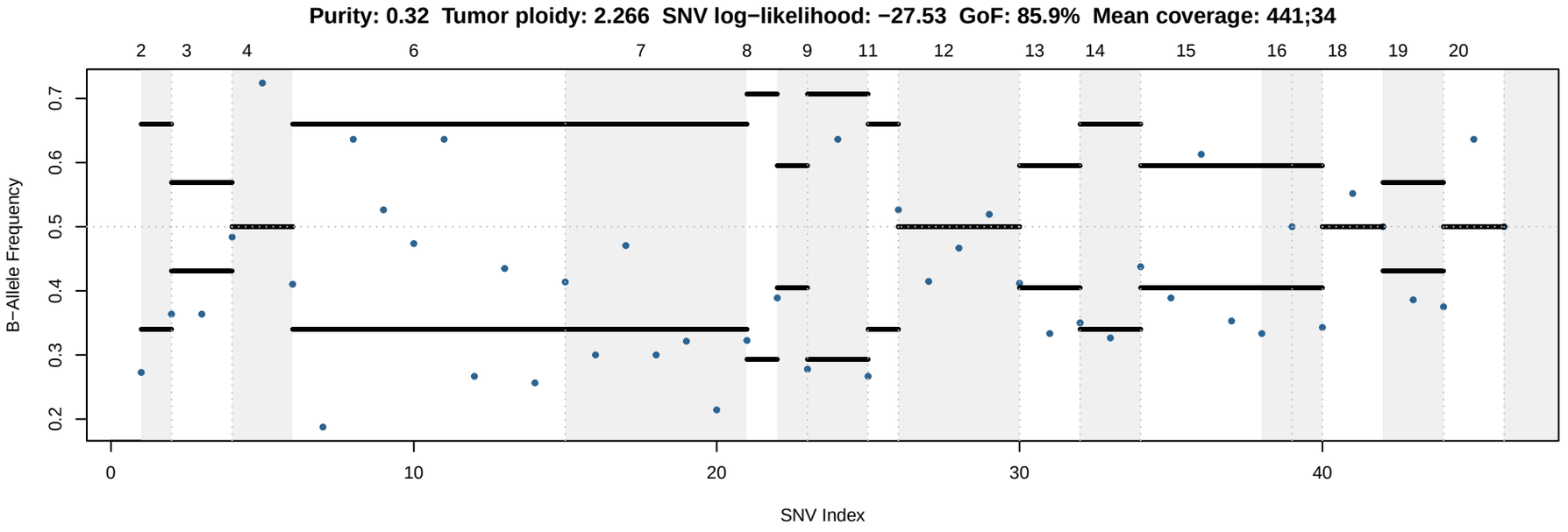

Allelic fraction (germline)
Copy Number log−ratio
3m3
2m2
1m1
3m2
2m1
3m1
1m0
2m0
3m0

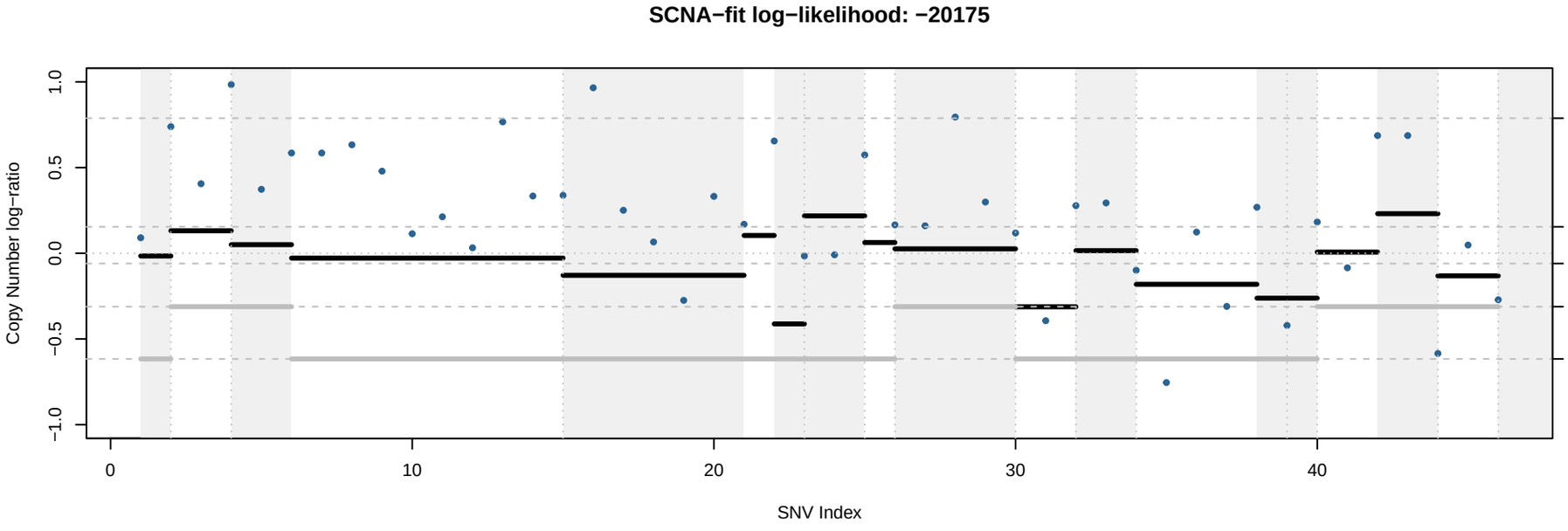

Coverage (log2)
Allelic fraction

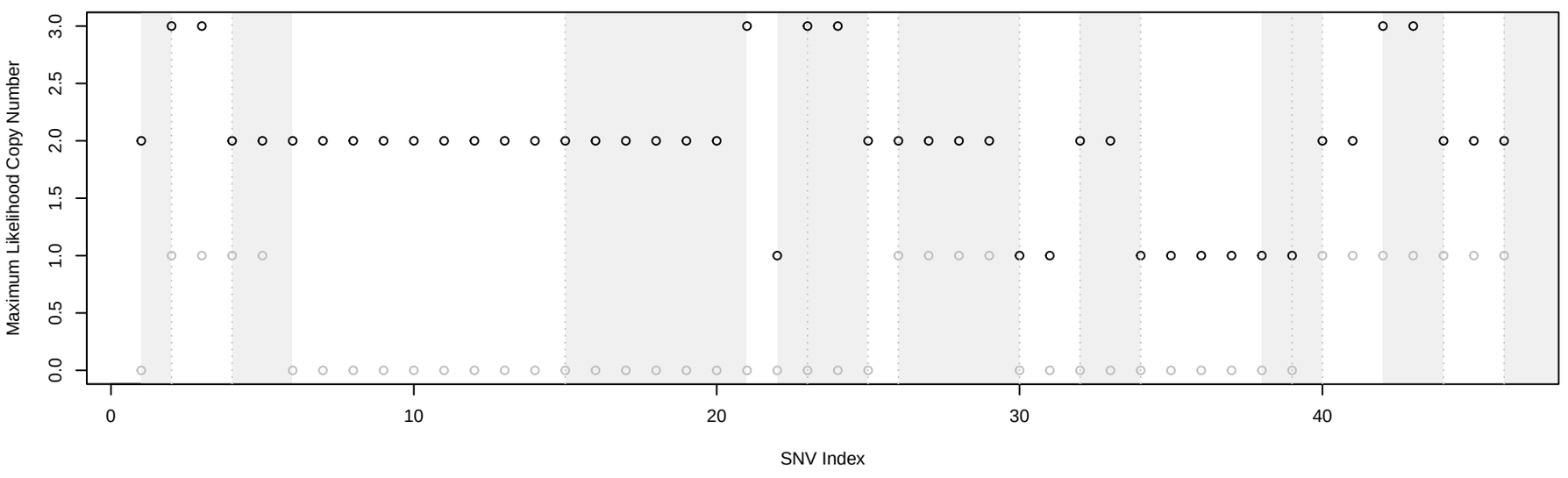

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
3m2
1m1
2m1
3m1

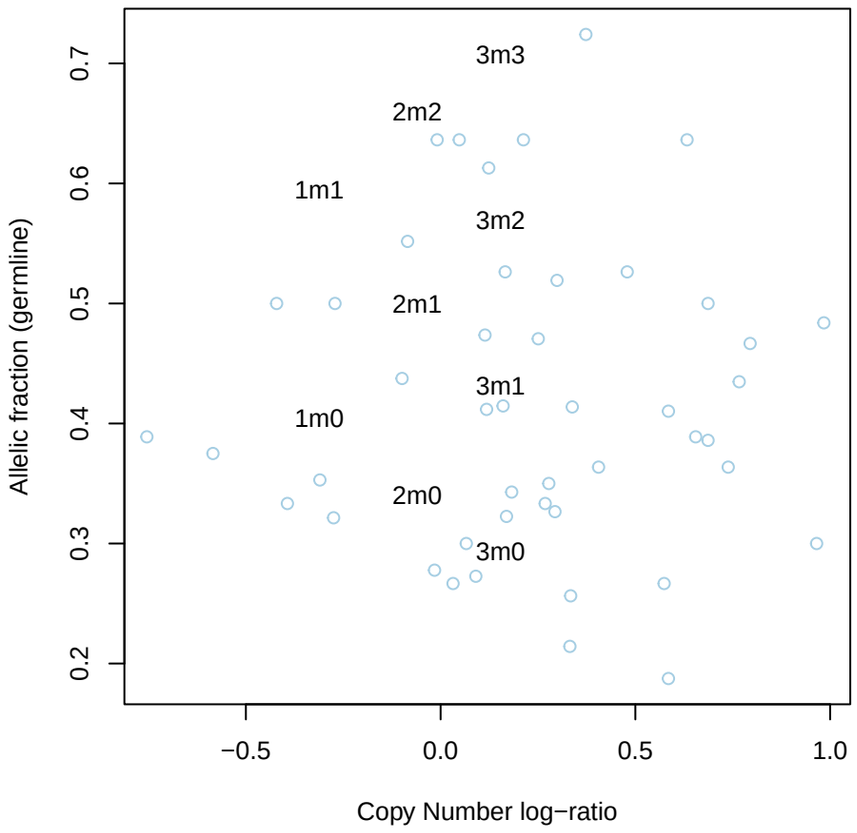

Power 0.8
Frequency
Cellular fraction

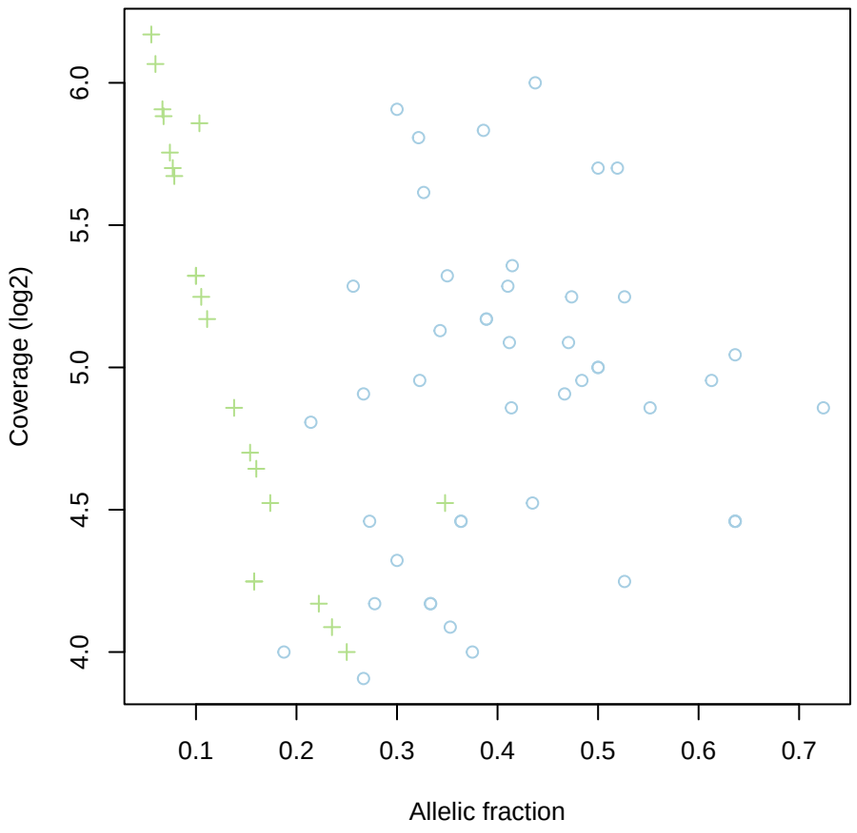

Purity: 0.32 Tumor ploidy: 2.266
1
2
3
7
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

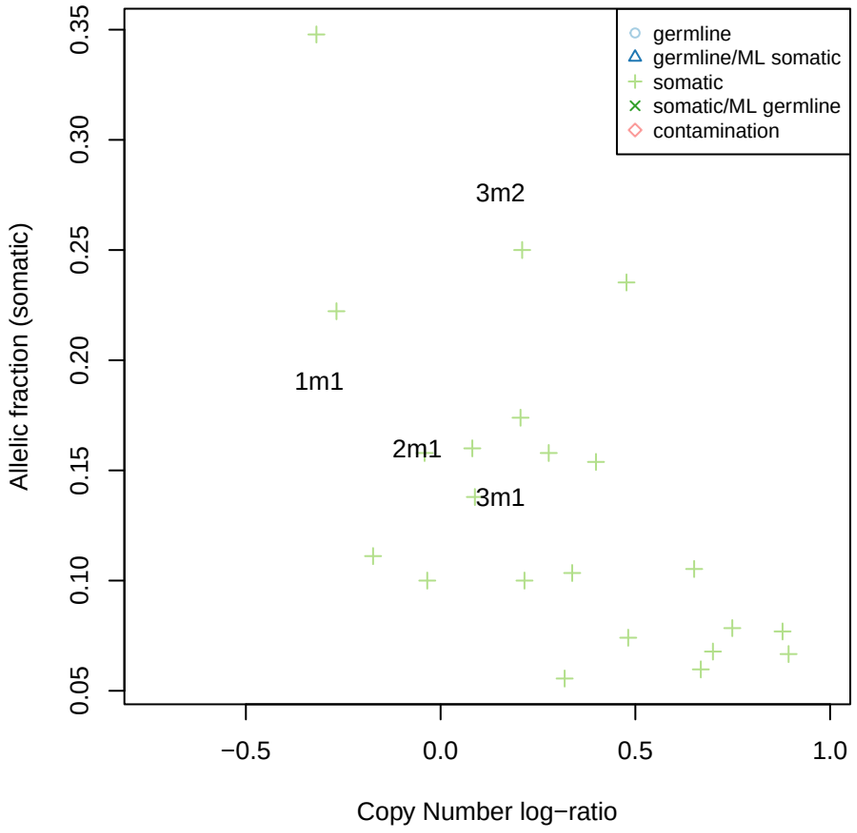

Purity: 0.32 Tumor ploidy: 2.266 SNV log−likelihood: −27.53 GoF: 85.9% Mean coverage: 441;34
2 3 4 6 7 8 9 11 12 13 14 15 16 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 10 20 30 40
SNV Index

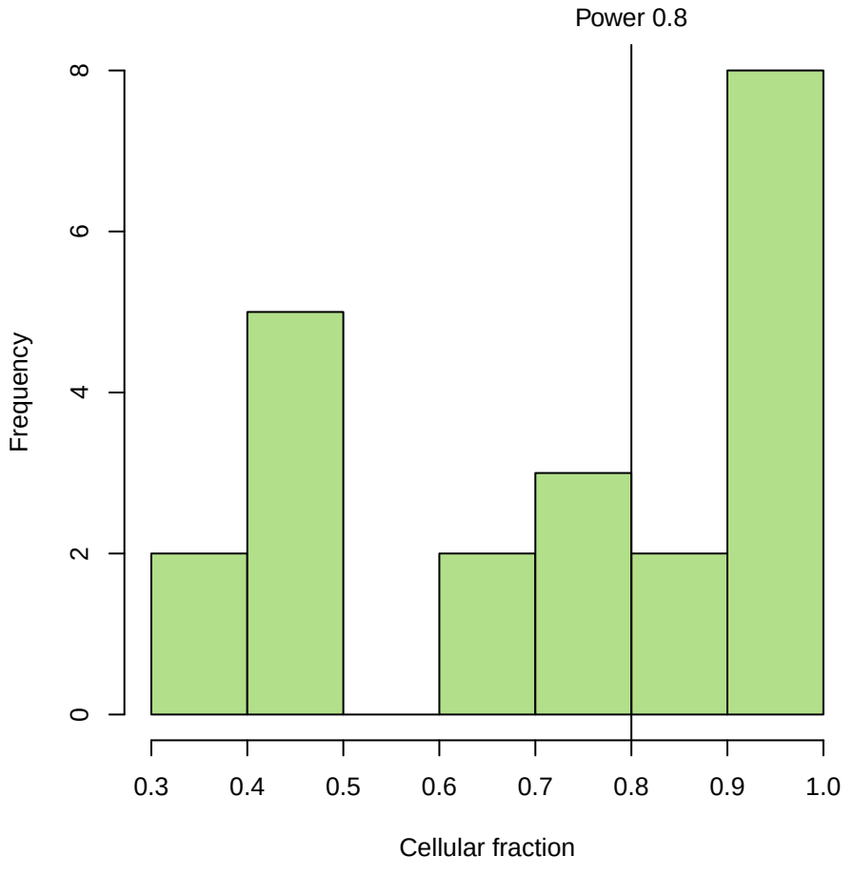

SCNA−fit log−likelihood: −20175
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 7
0 10 20 30 40
SNV Index

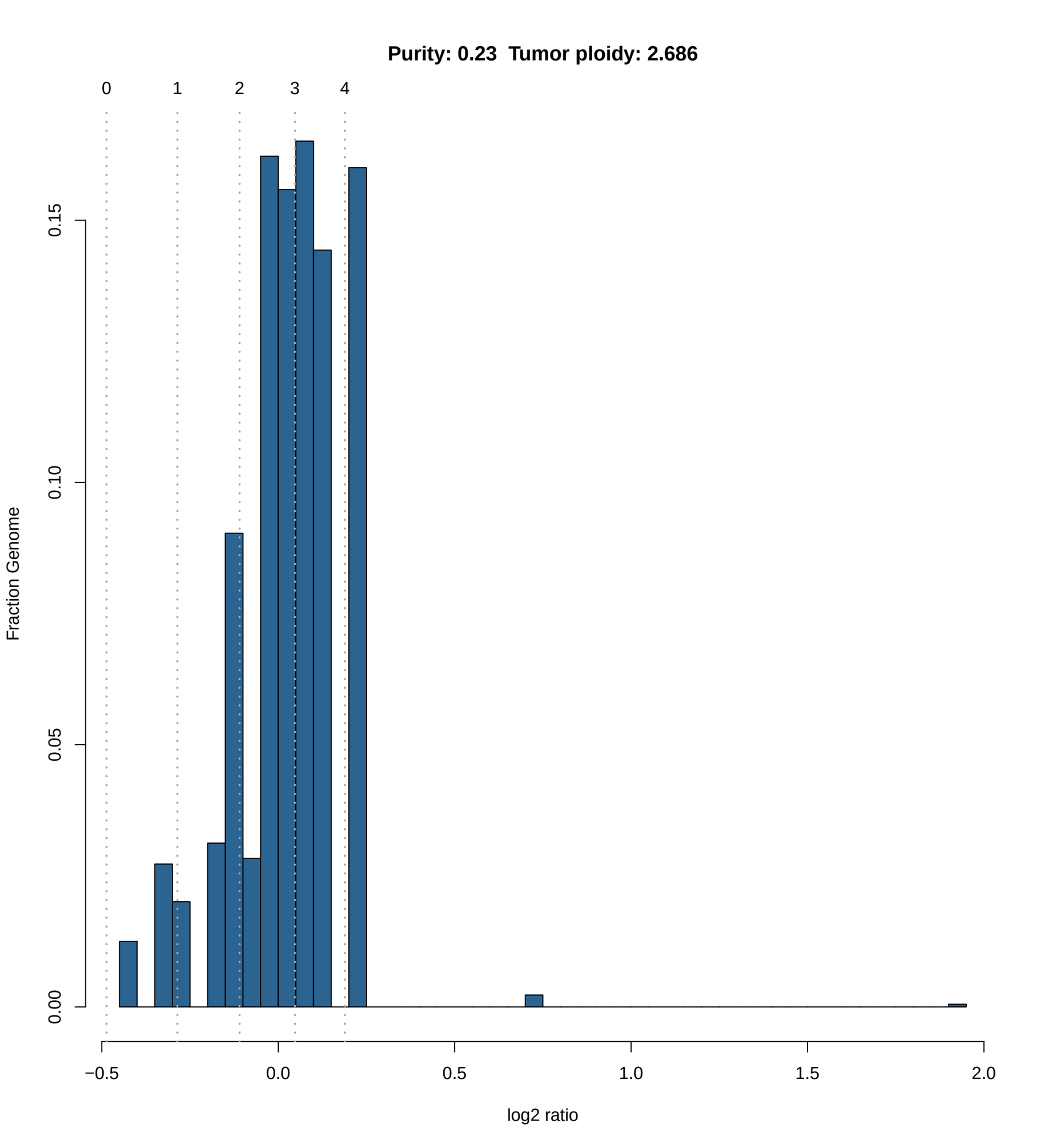

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 10 20 30 40
SNV Index

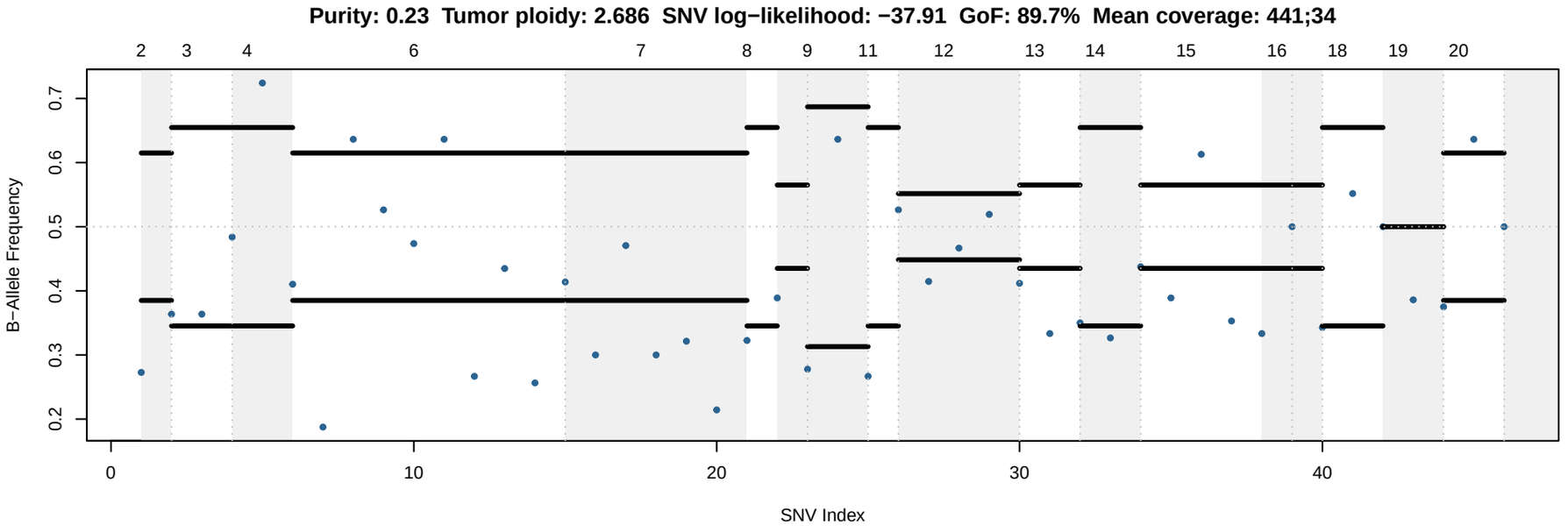

Allelic fraction (germline)
Copy Number log−ratio
3m3
2m2
1m1
3m2
2m1
3m1
1m0
2m0
3m0

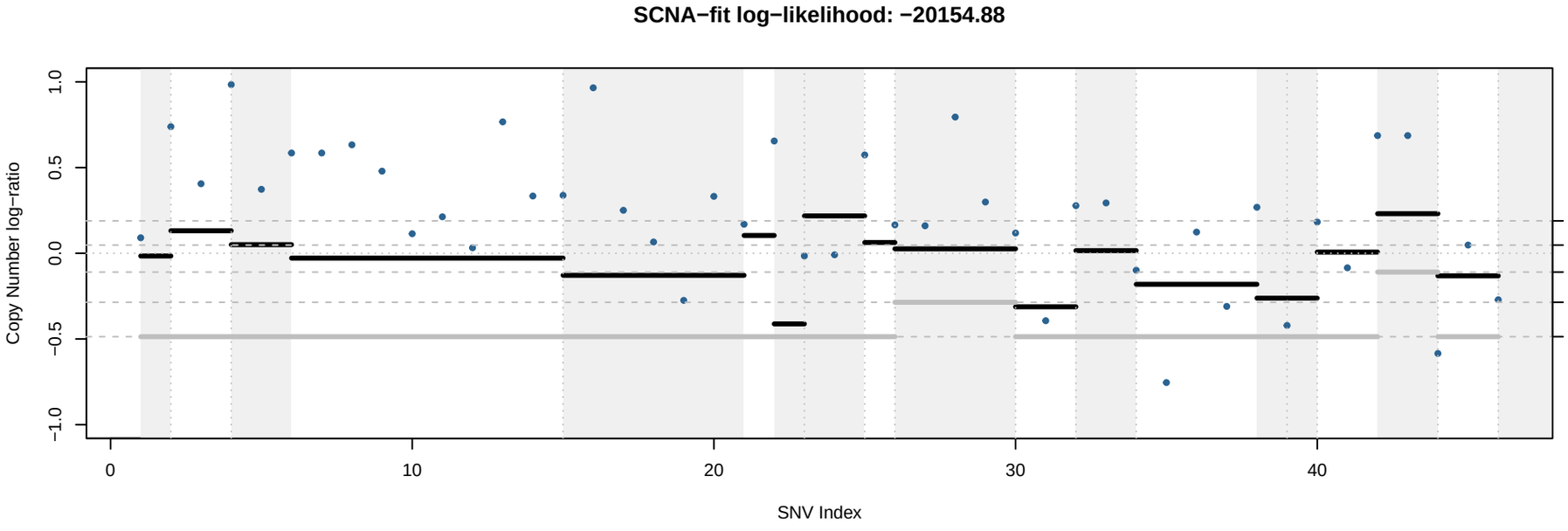

Coverage (log2)
Allelic fraction

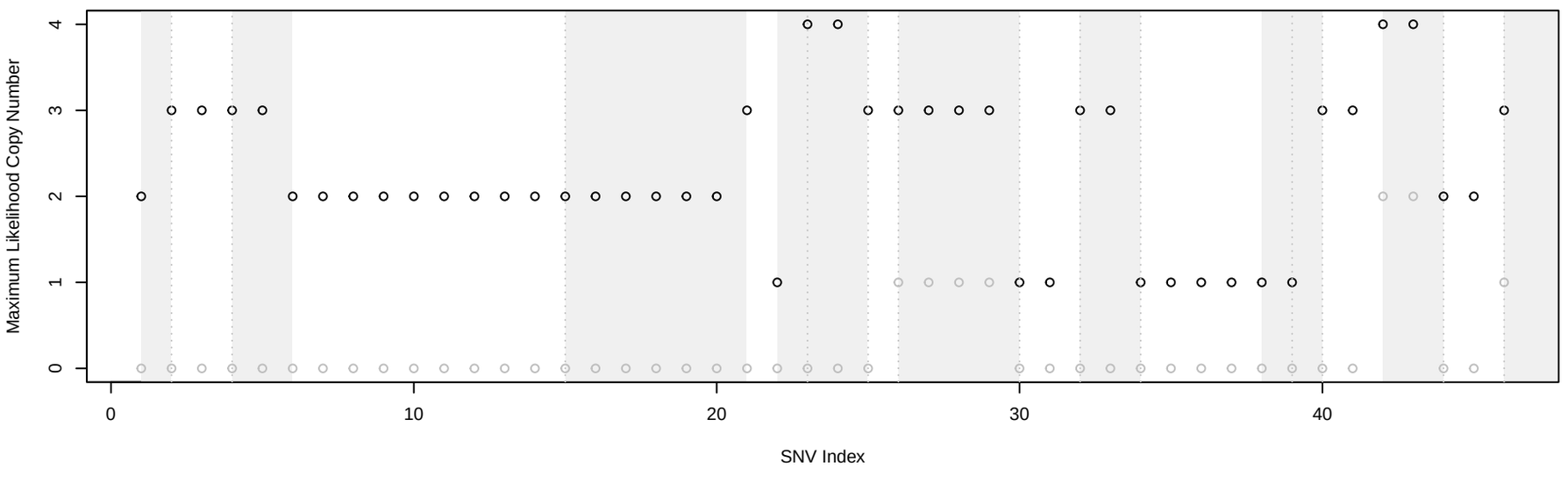

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m2
1m1
2m1
3m1

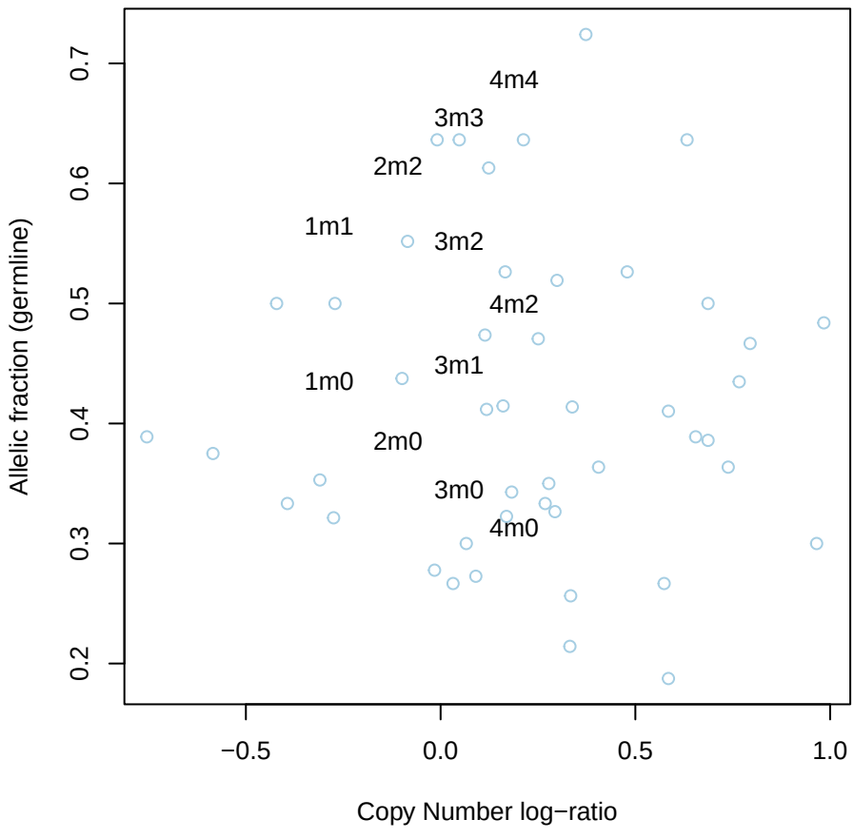

Power 0.8
Frequency
Cellular fraction

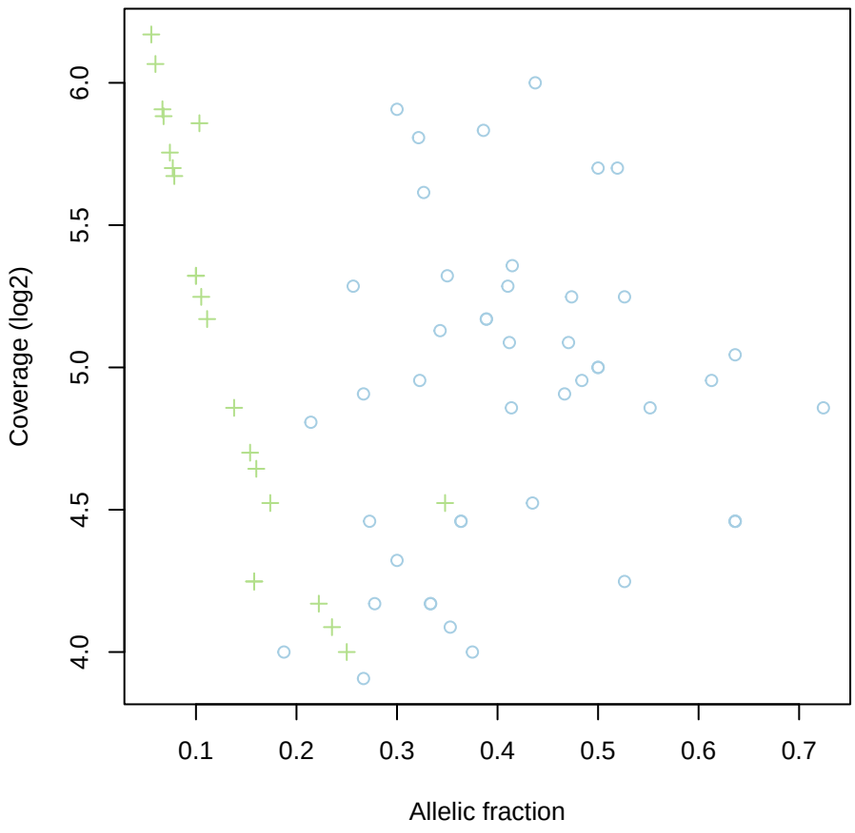

Purity: 0.23 Tumor ploidy: 2.686
0
1
2
3
4
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

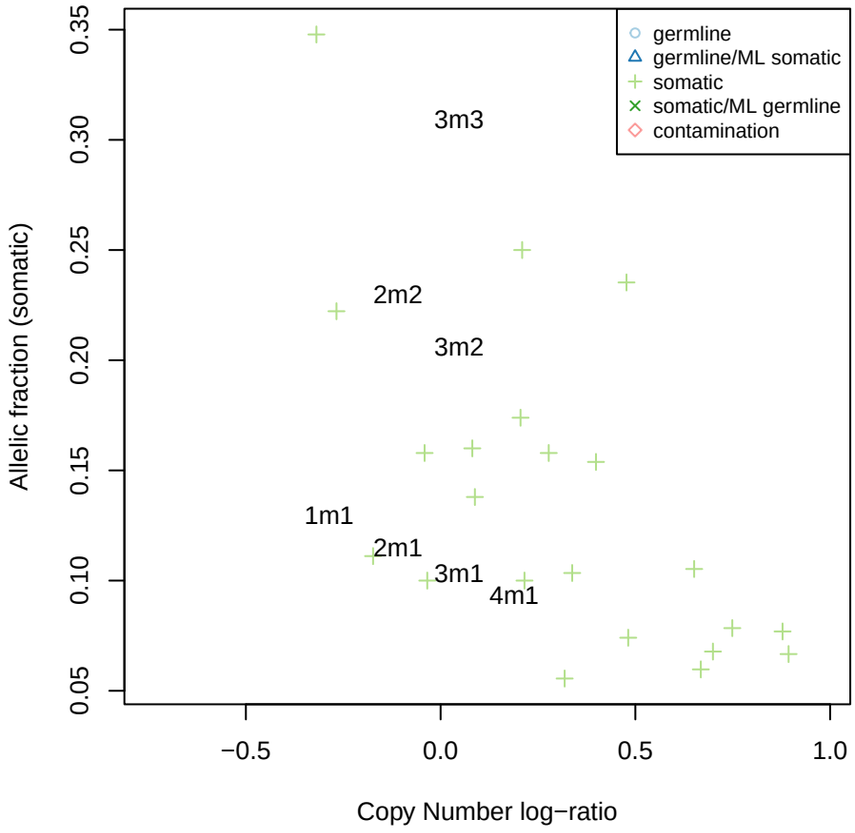

Purity: 0.23 Tumor ploidy: 2.686 SNV log−likelihood: −37.91 GoF: 89.7% Mean coverage: 441;34
2 3 4 6 7 8 9 11 12 13 14 15 16 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 10 20 30 40
SNV Index

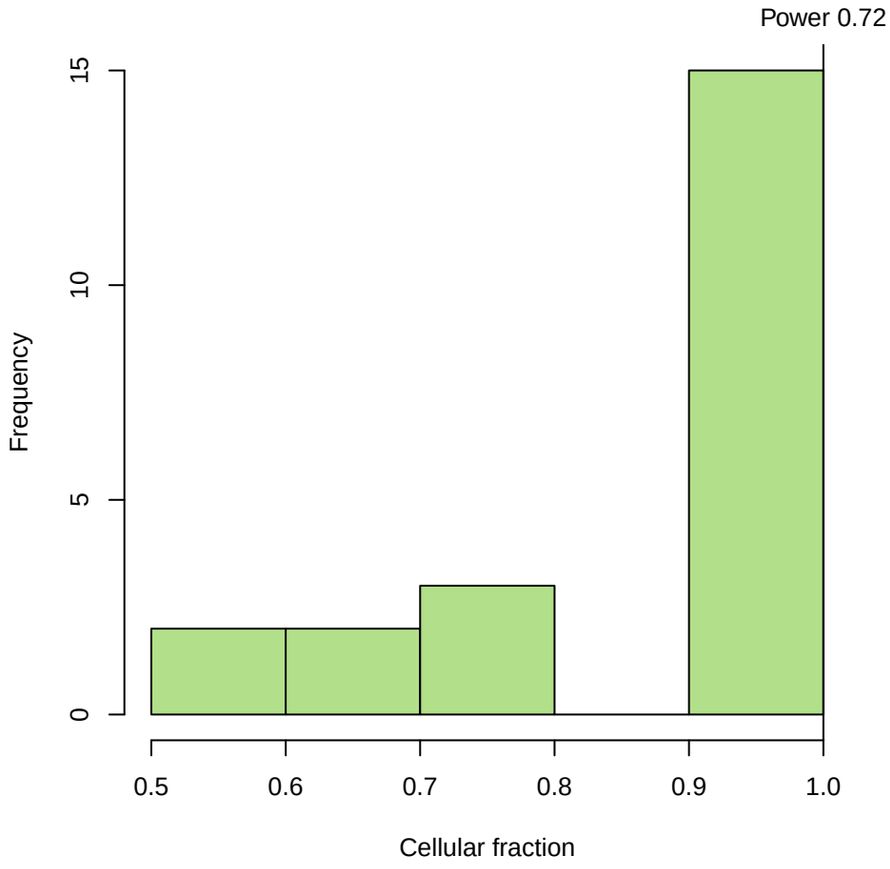

SCNA−fit log−likelihood: −20154.88
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3
0 10 20 30 40
SNV Index

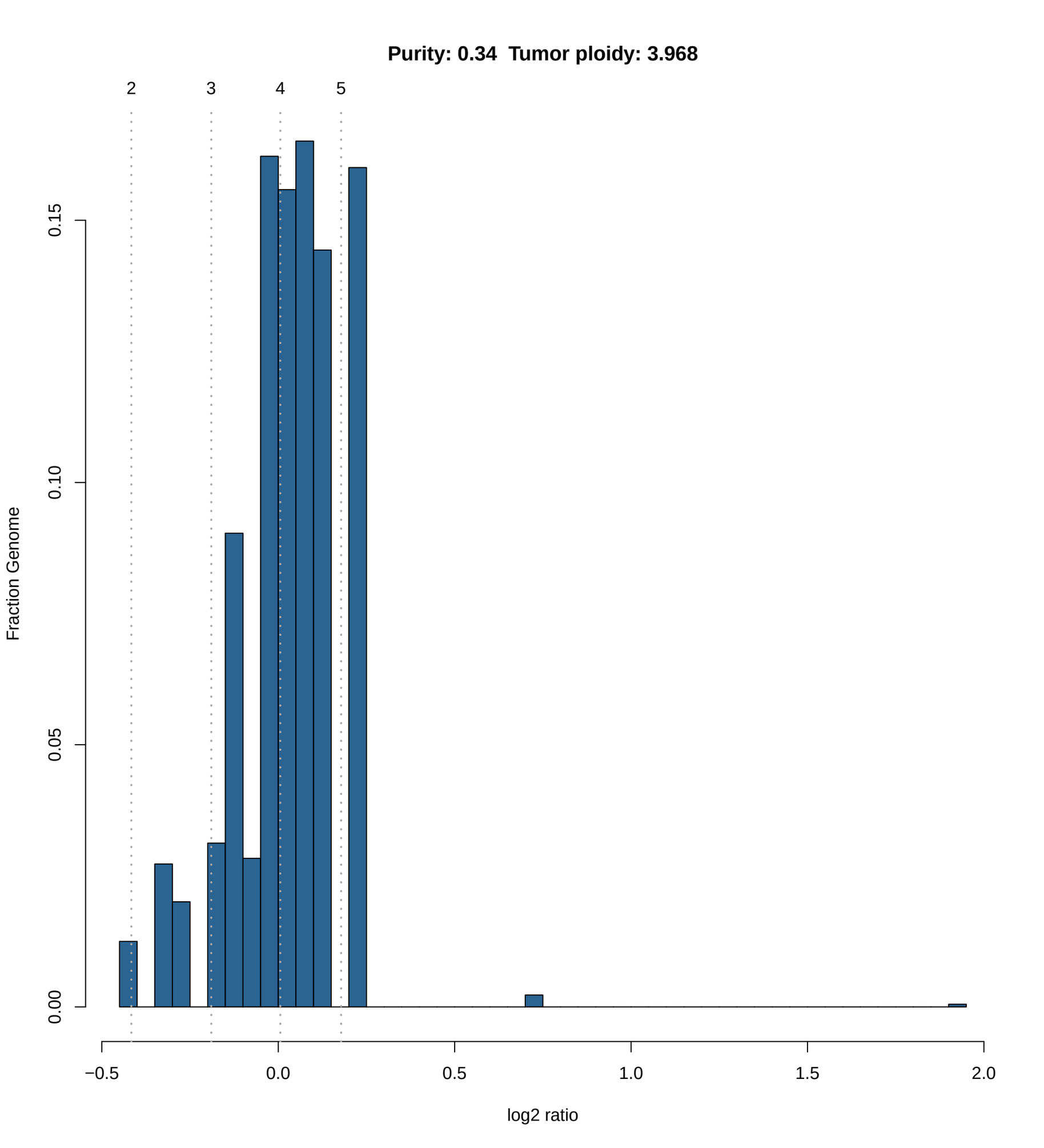

Maximum Likelihood Copy Number
0 1 2 3 4
0 10 20 30 40
SNV Index

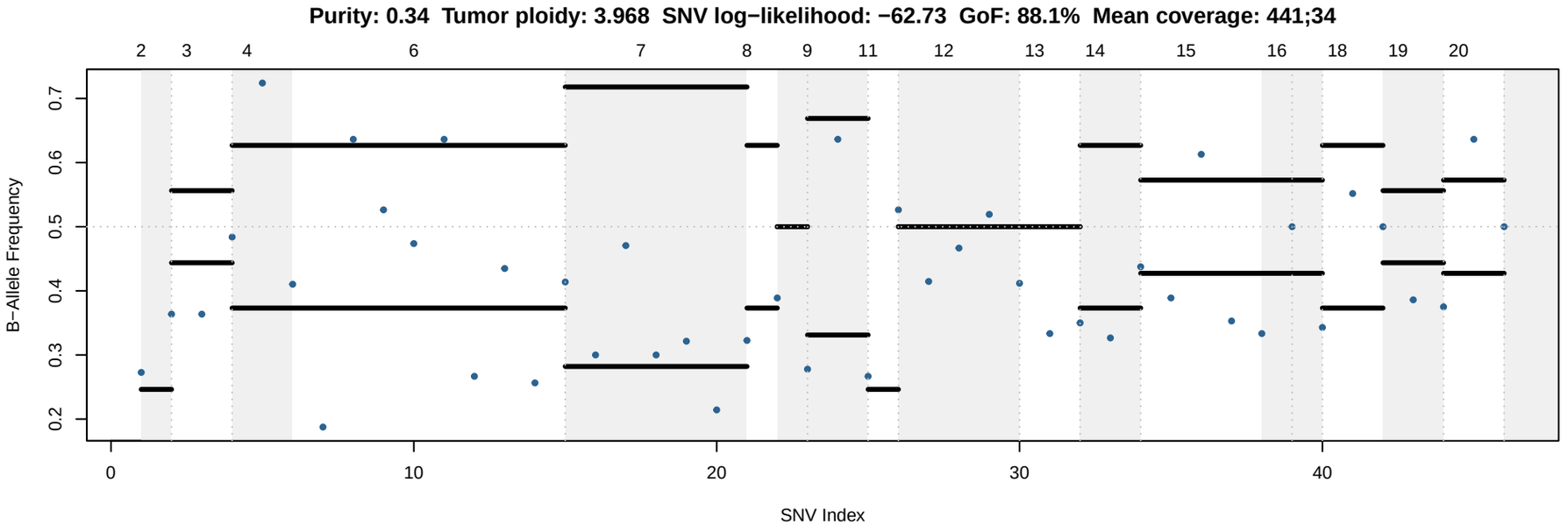

Allelic fraction (germline)
Copy Number log−ratio
4m4
3m3
2m2
1m1
3m2
4m2
3m1
1m0
2m0
3m0
4m0

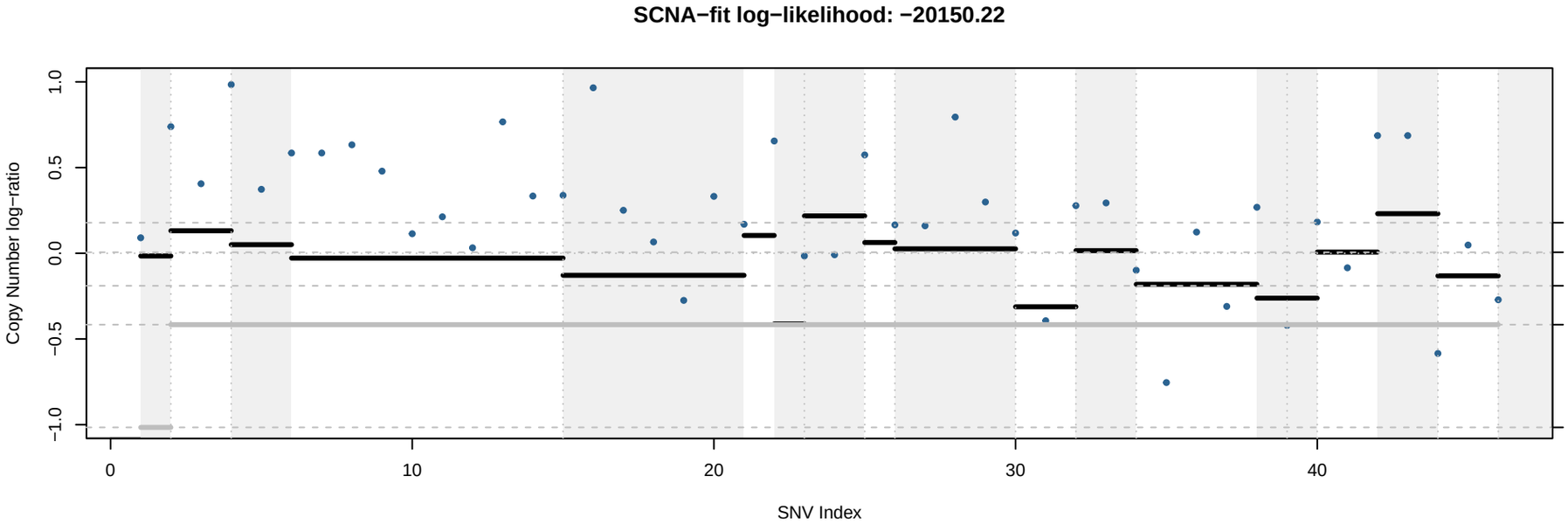

Coverage (log2)
Allelic fraction

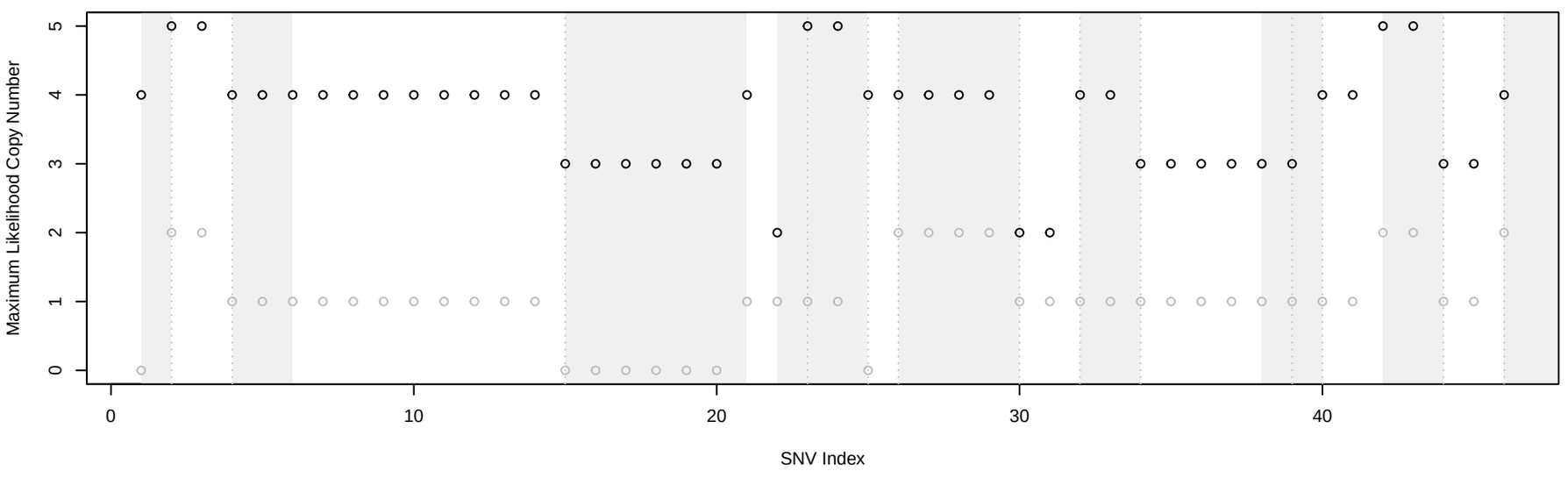

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m3
2m2
3m2
1m1
2m1
3m1
4m1

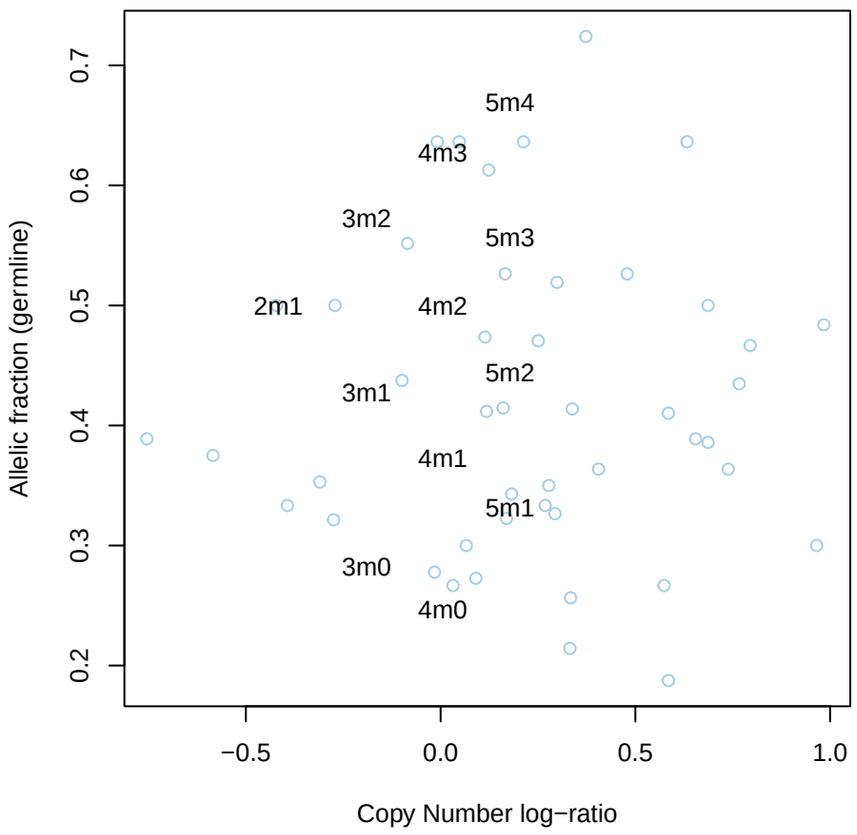

Power 0.72
Frequency
Cellular fraction

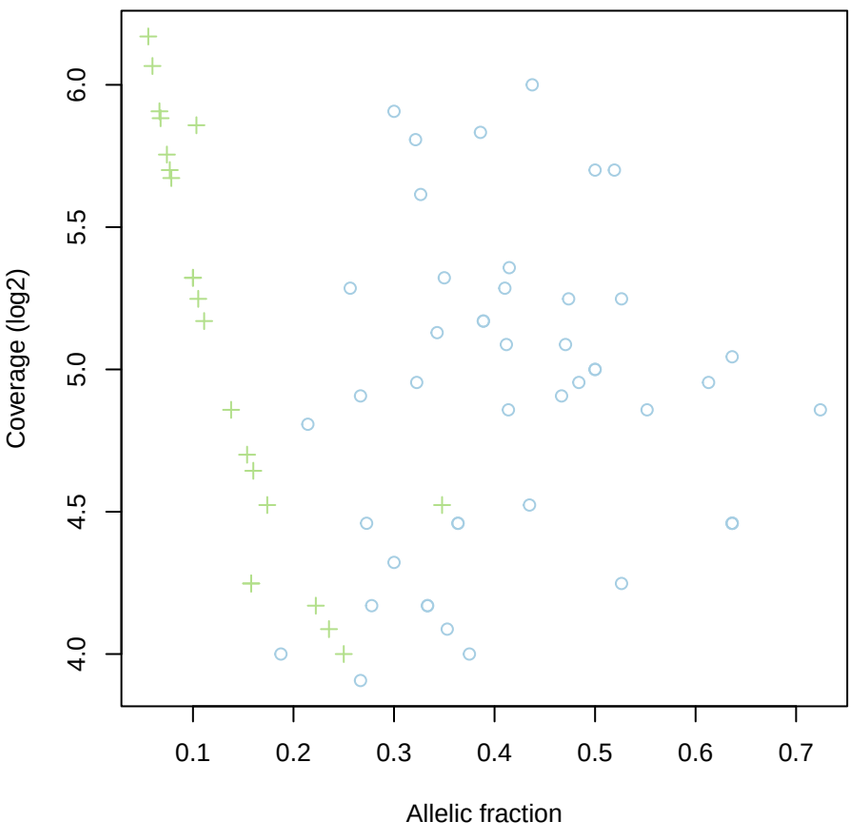

Purity: 0.34 Tumor ploidy: 3.968
2
3
4
5
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

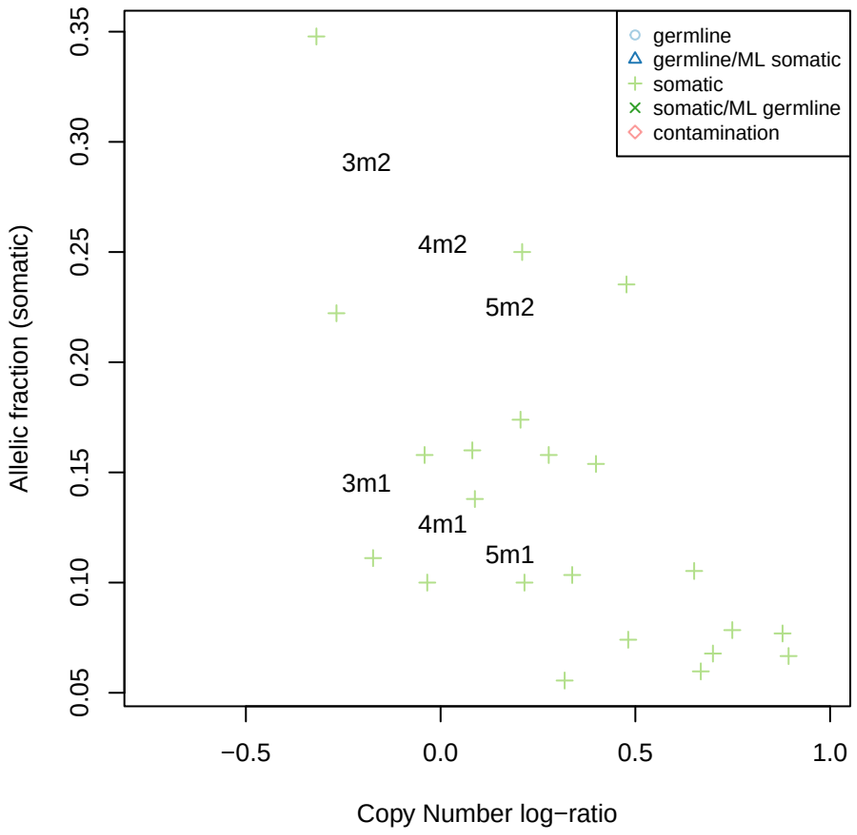

Purity: 0.34 Tumor ploidy: 3.968 SNV log−likelihood: −62.73 GoF: 88.1% Mean coverage: 441;34
2 3 4 6 7 8 9 11 12 13 14 15 16 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 10 20 30 40
SNV Index

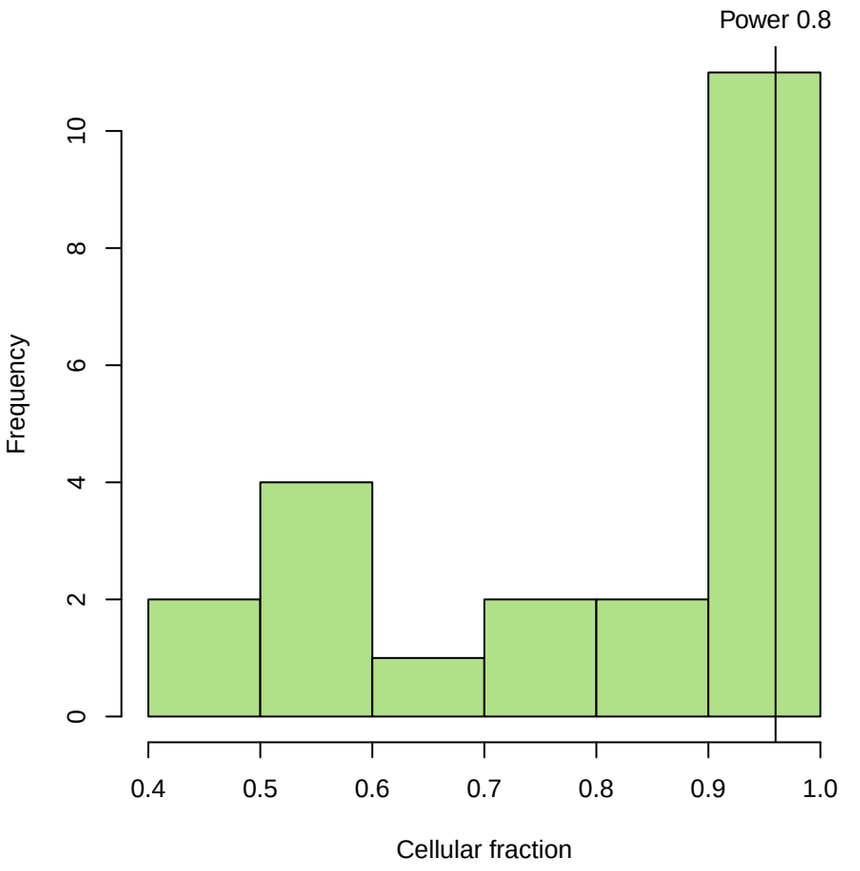

SCNA−fit log−likelihood: −20150.22
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 3 4 5
0 10 20 30 40
SNV Index

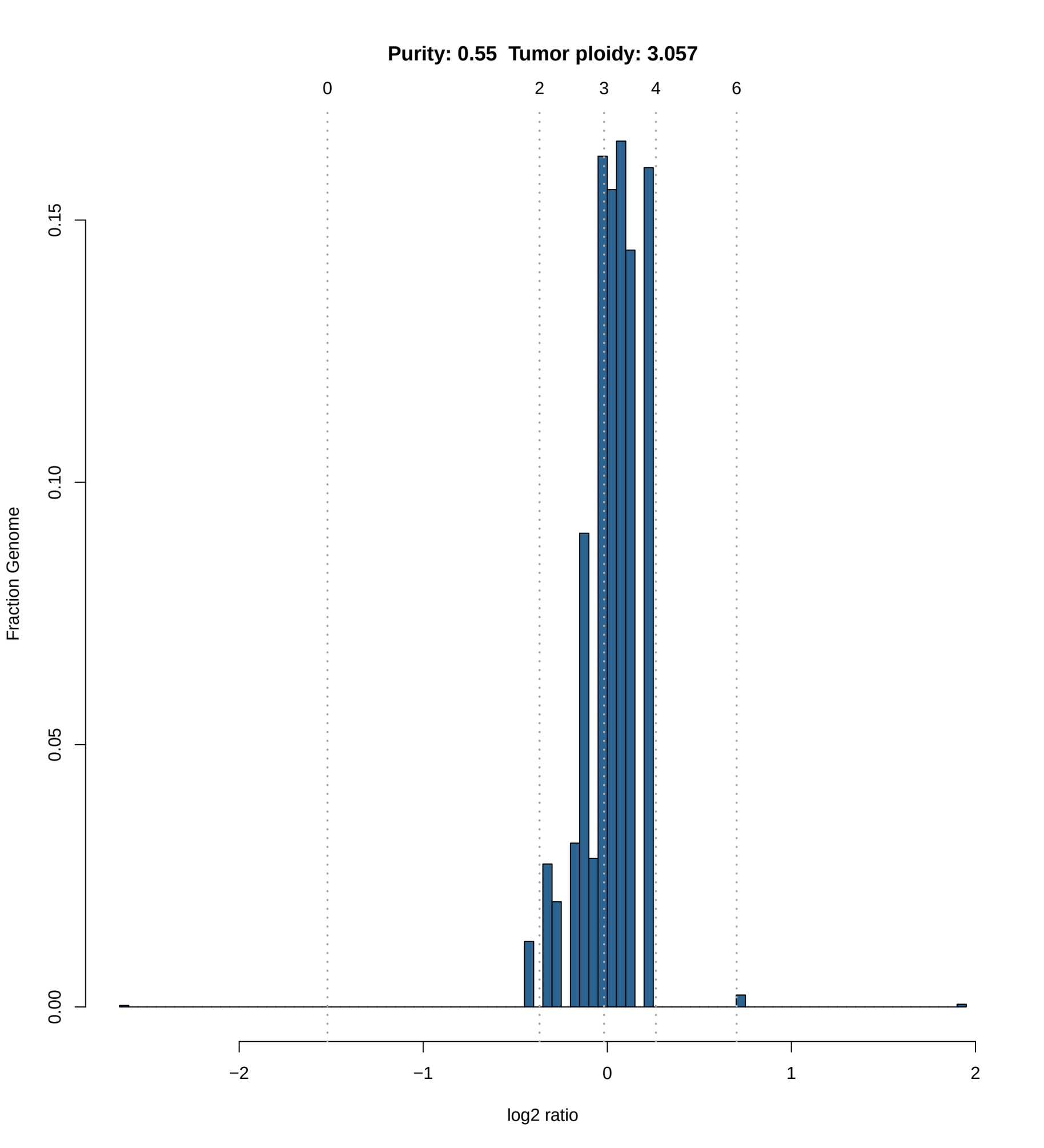

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 10 20 30 40
SNV Index

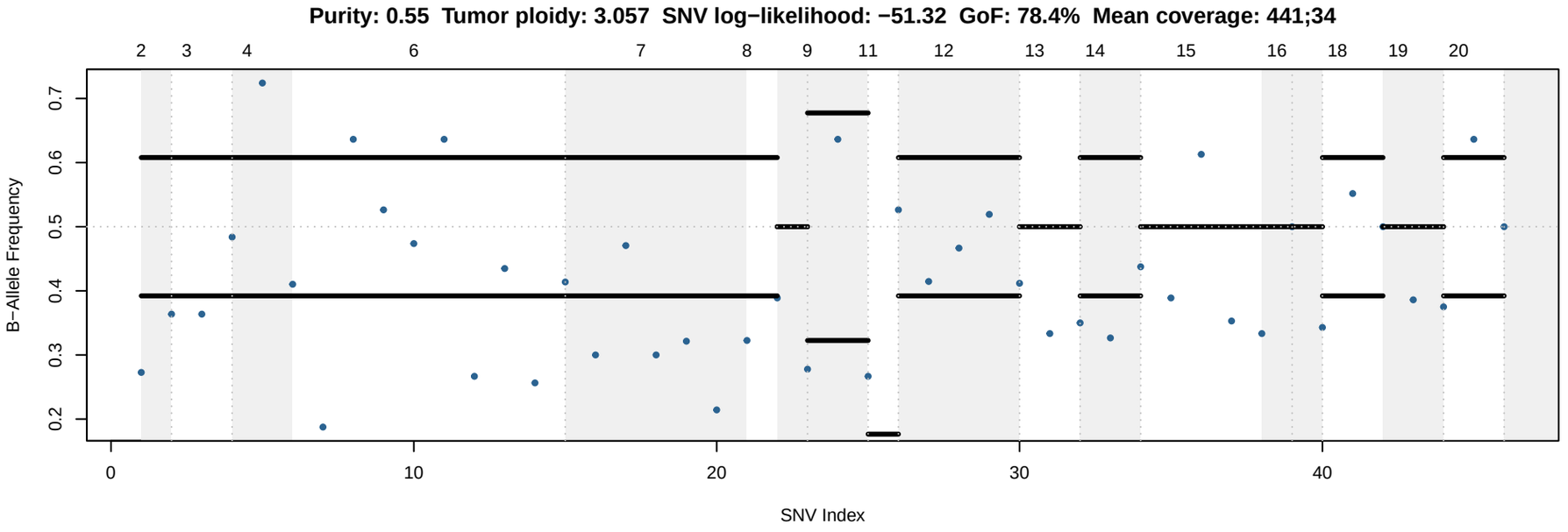

Allelic fraction (germline)
Copy Number log−ratio
5m4
4m3
3m2
5m3
2m1
4m2
5m2
3m1
4m1
5m1
3m0
4m0

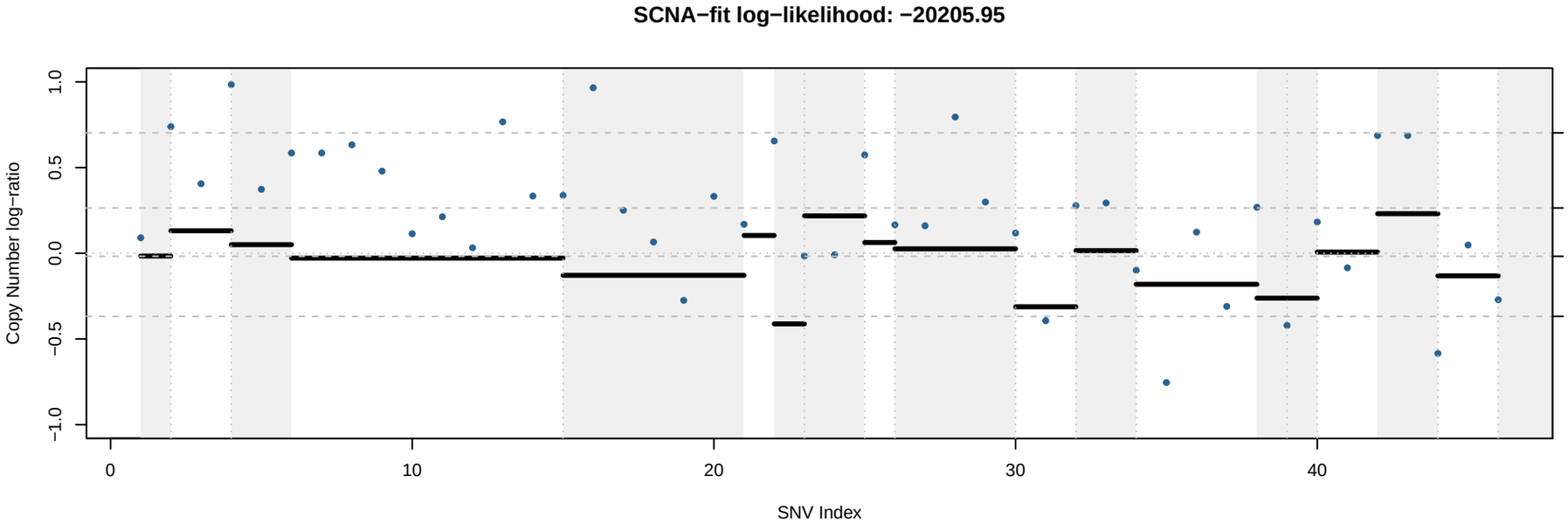

Coverage (log2)
Allelic fraction

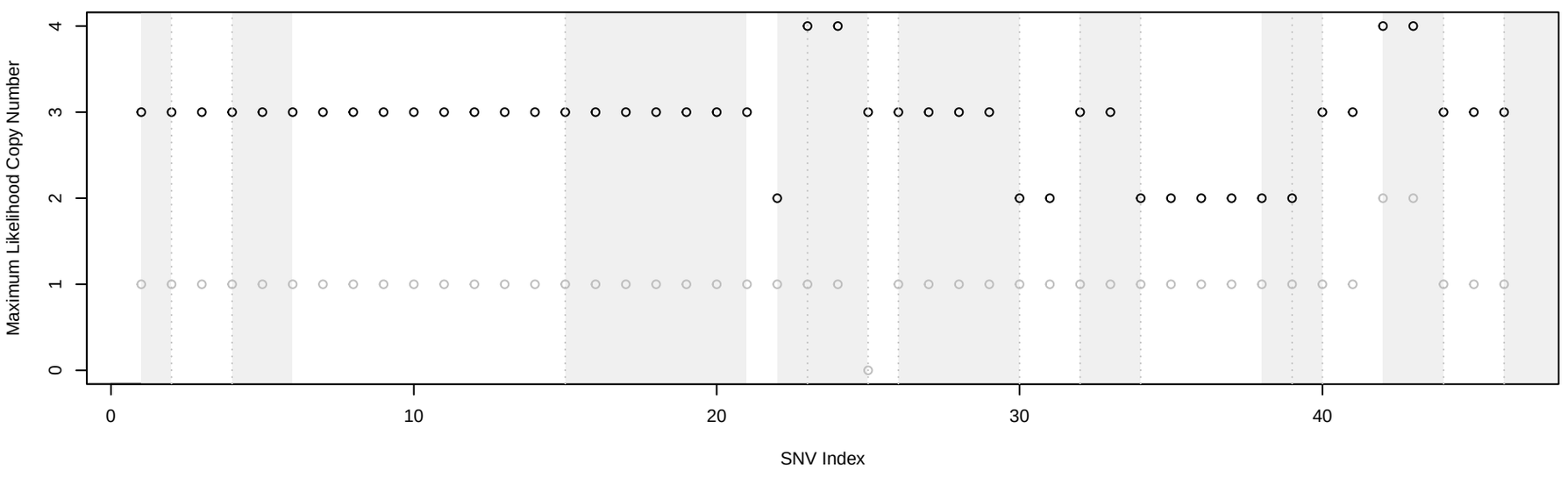

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m2
4m2
5m2
3m1
4m1
5m1

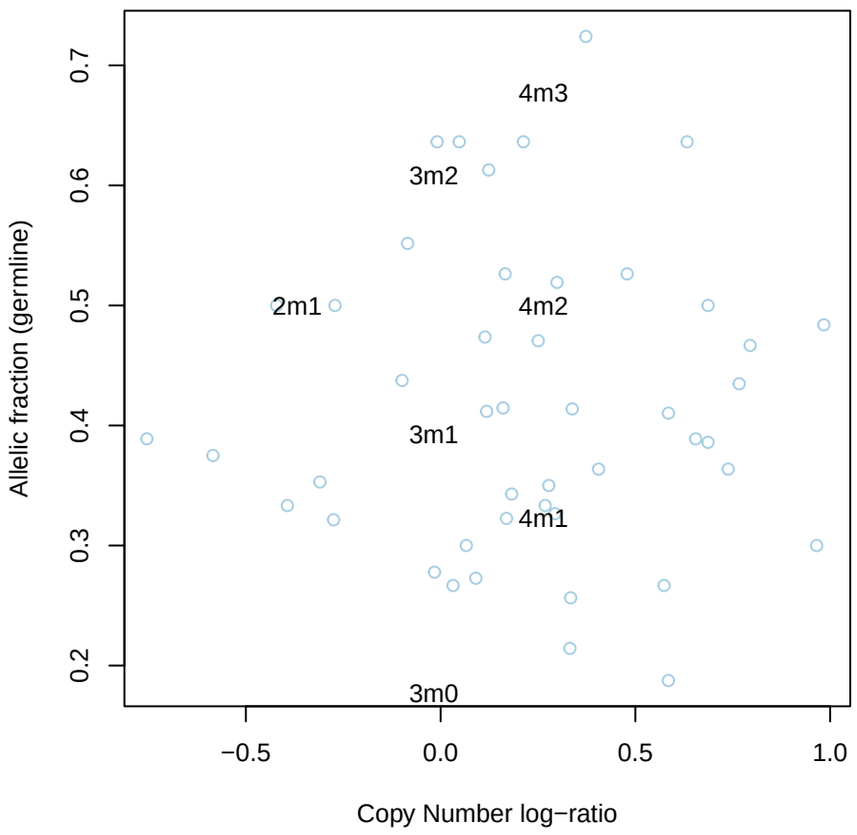

Power 0.8
Frequency
Cellular fraction

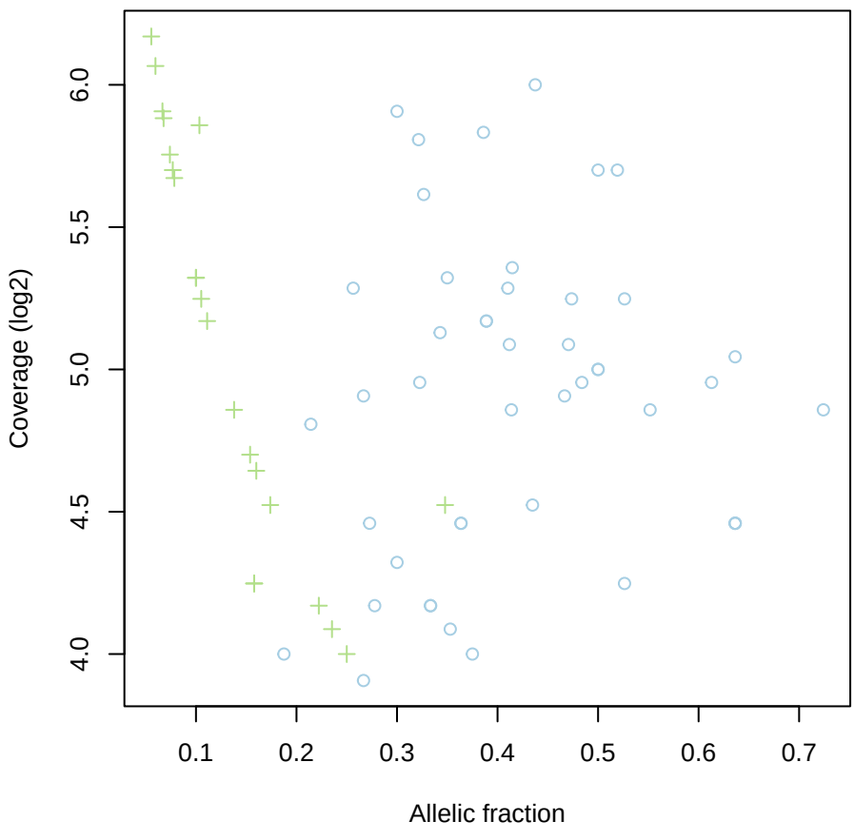

Purity: 0.55 Tumor ploidy: 3.057
0
2
3
4
6
0.15
0.10
0.05
0.00
Fraction Genome
−2
−1
0
1
2
log2 ratio

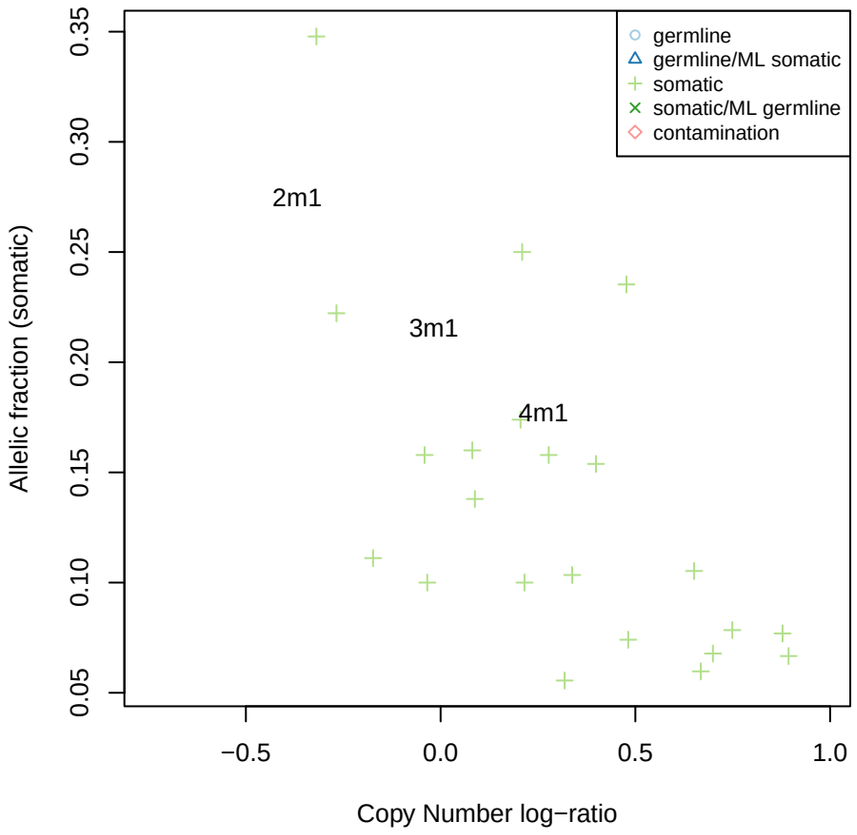

Purity: 0.55 Tumor ploidy: 3.057 SNV log−likelihood: −51.32 GoF: 78.4% Mean coverage: 441;34
2 3 4 6 7 8 9 11 12 13 14 15 16 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 10 20 30 40
SNV Index

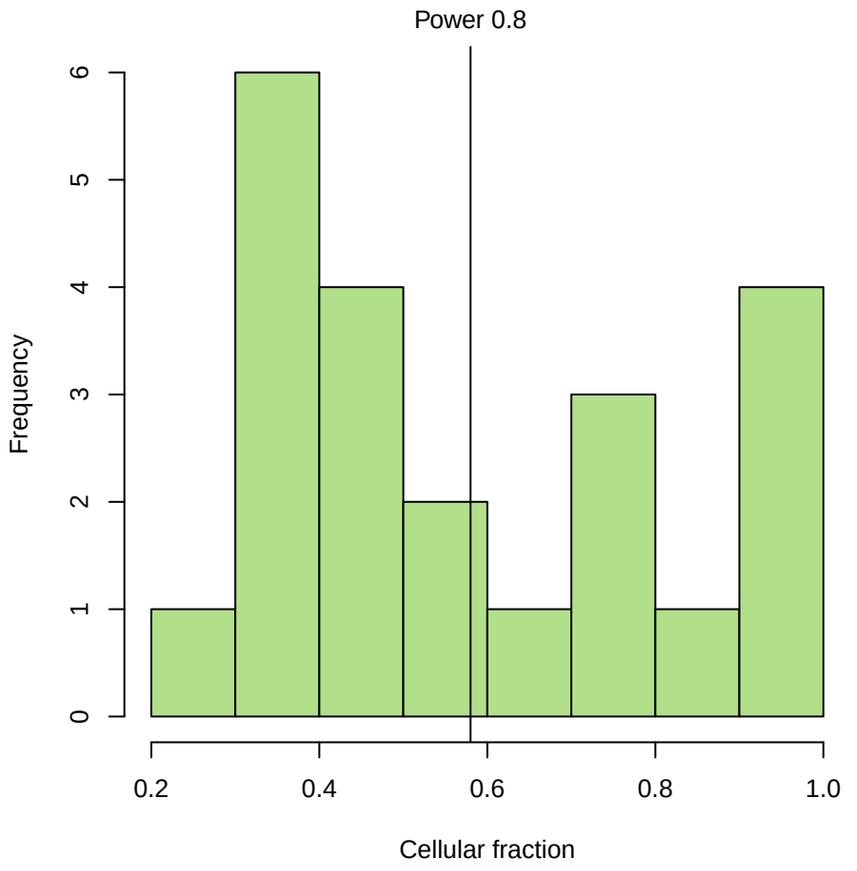

SCNA−fit log−likelihood: −20205.95
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 6
0 10 20 30 40
SNV Index

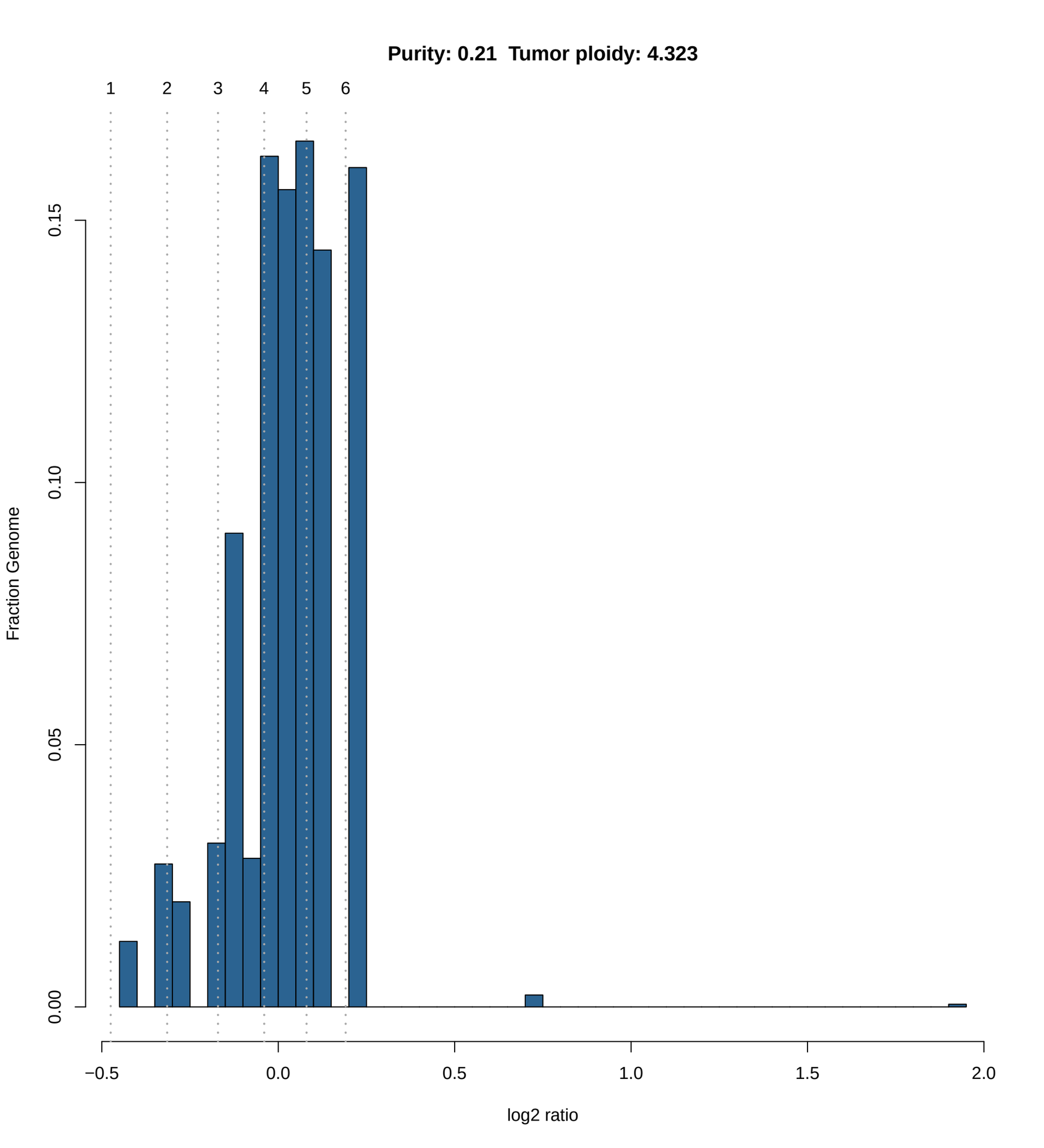

Maximum Likelihood Copy Number
0 1 2 3 4
0 10 20 30 40
SNV Index

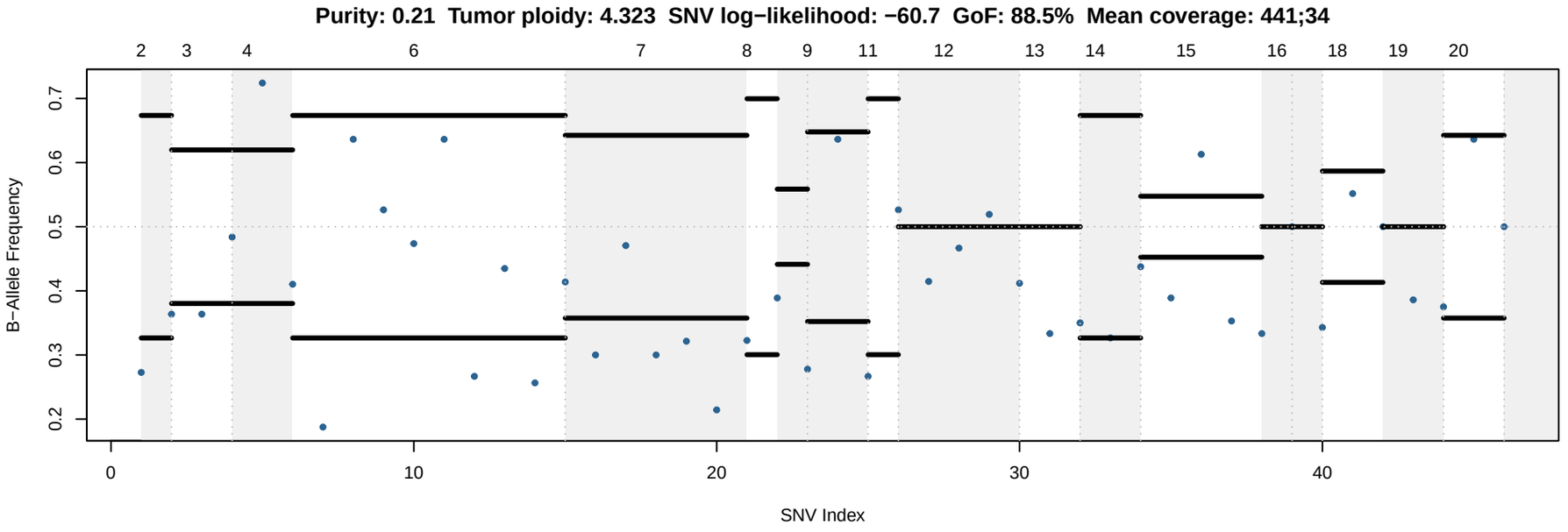

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
2m1
4m2
3m1
4m1
3m0

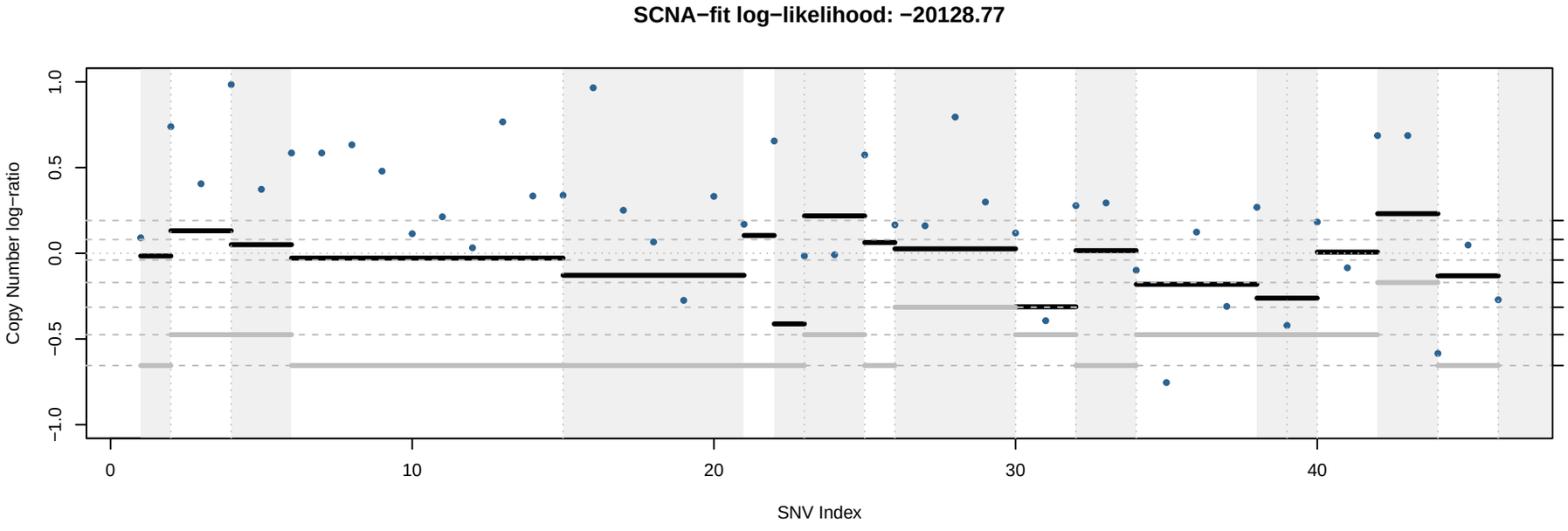

Coverage (log2)
Allelic fraction

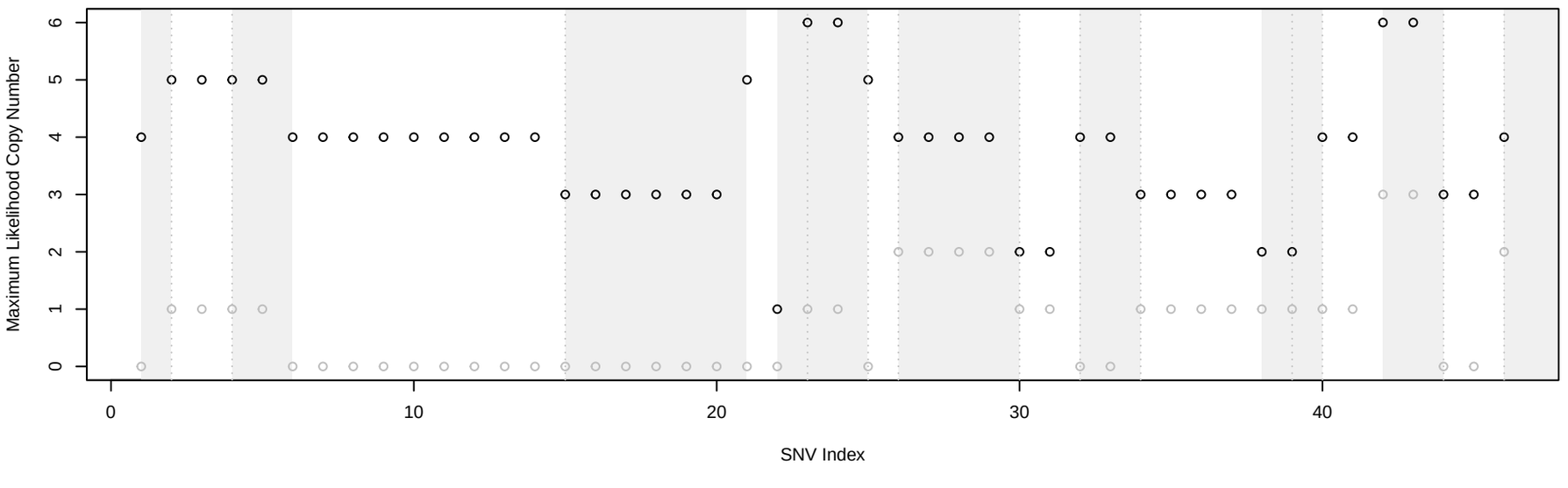

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m1
3m1
4m1

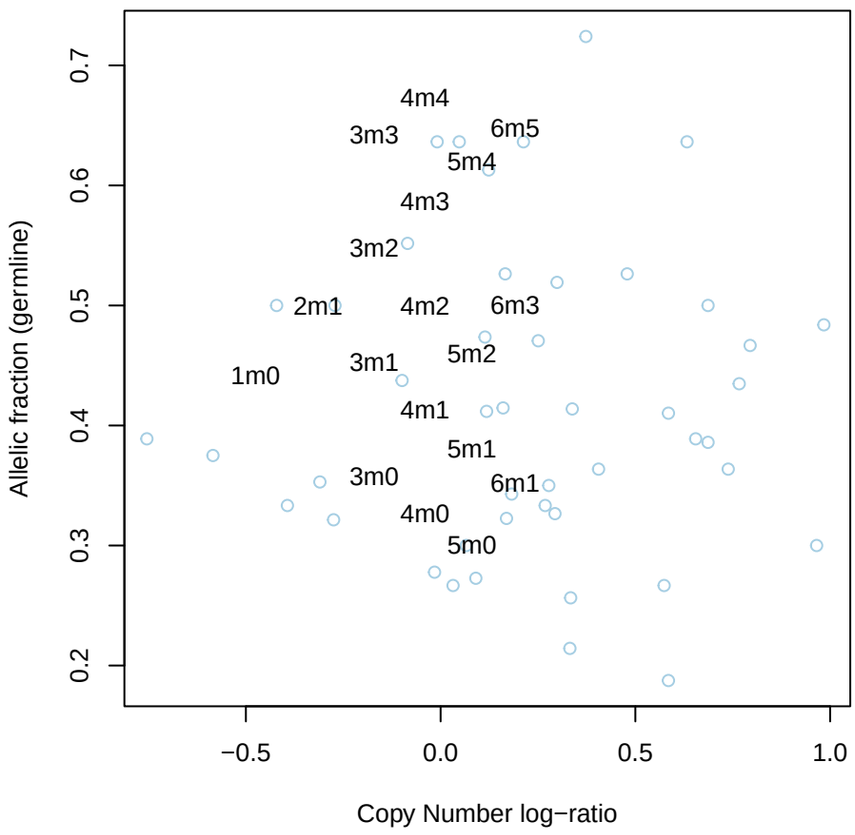

Power 0.8
Frequency
Cellular fraction

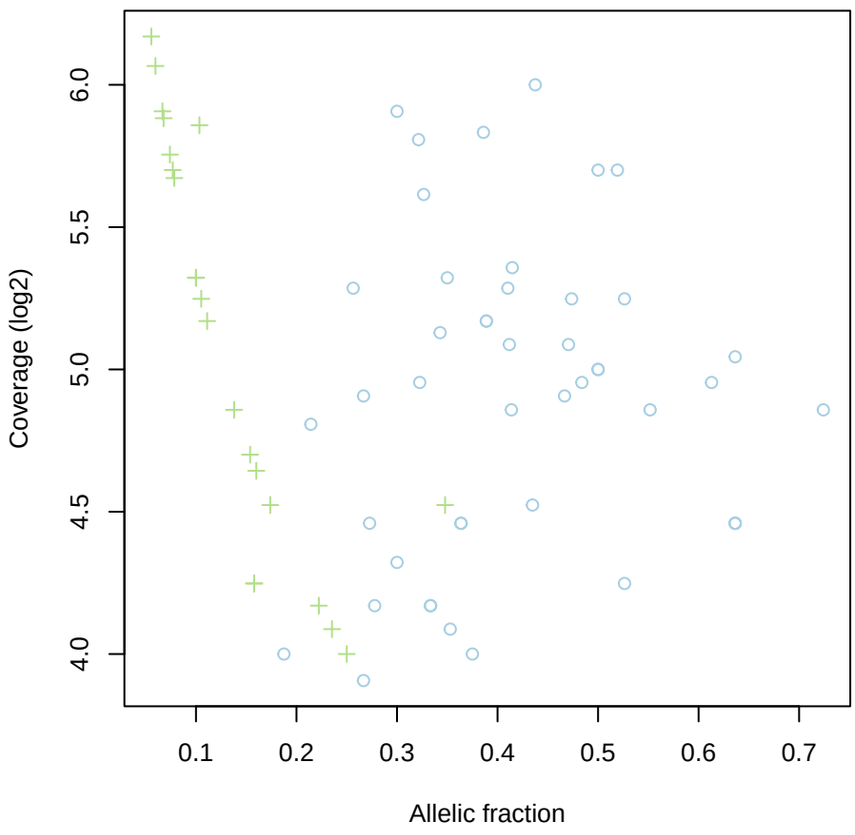

Purity: 0.21 Tumor ploidy: 4.323
1
2
3
4
5
6
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

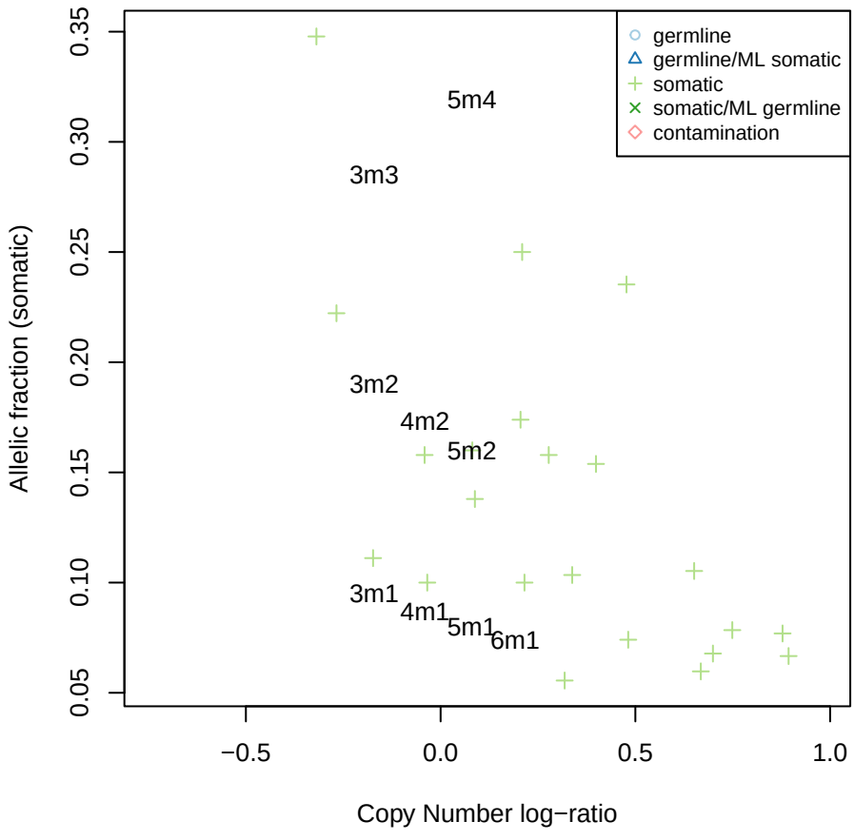

Purity: 0.21 Tumor ploidy: 4.323 SNV log−likelihood: −60.7 GoF: 88.5% Mean coverage: 441;34
2 3 4 6 7 8 9 11 12 13 14 15 16 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 10 20 30 40
SNV Index

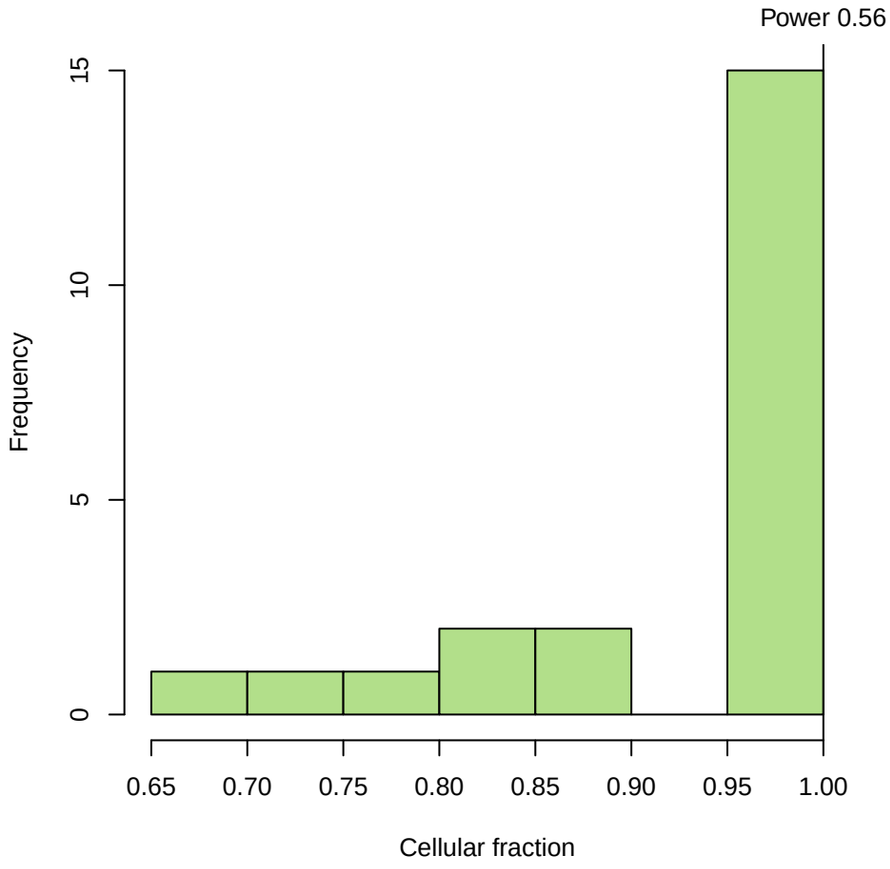

SCNA−fit log−likelihood: −20128.77
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 5
0 10 20 30 40
SNV Index

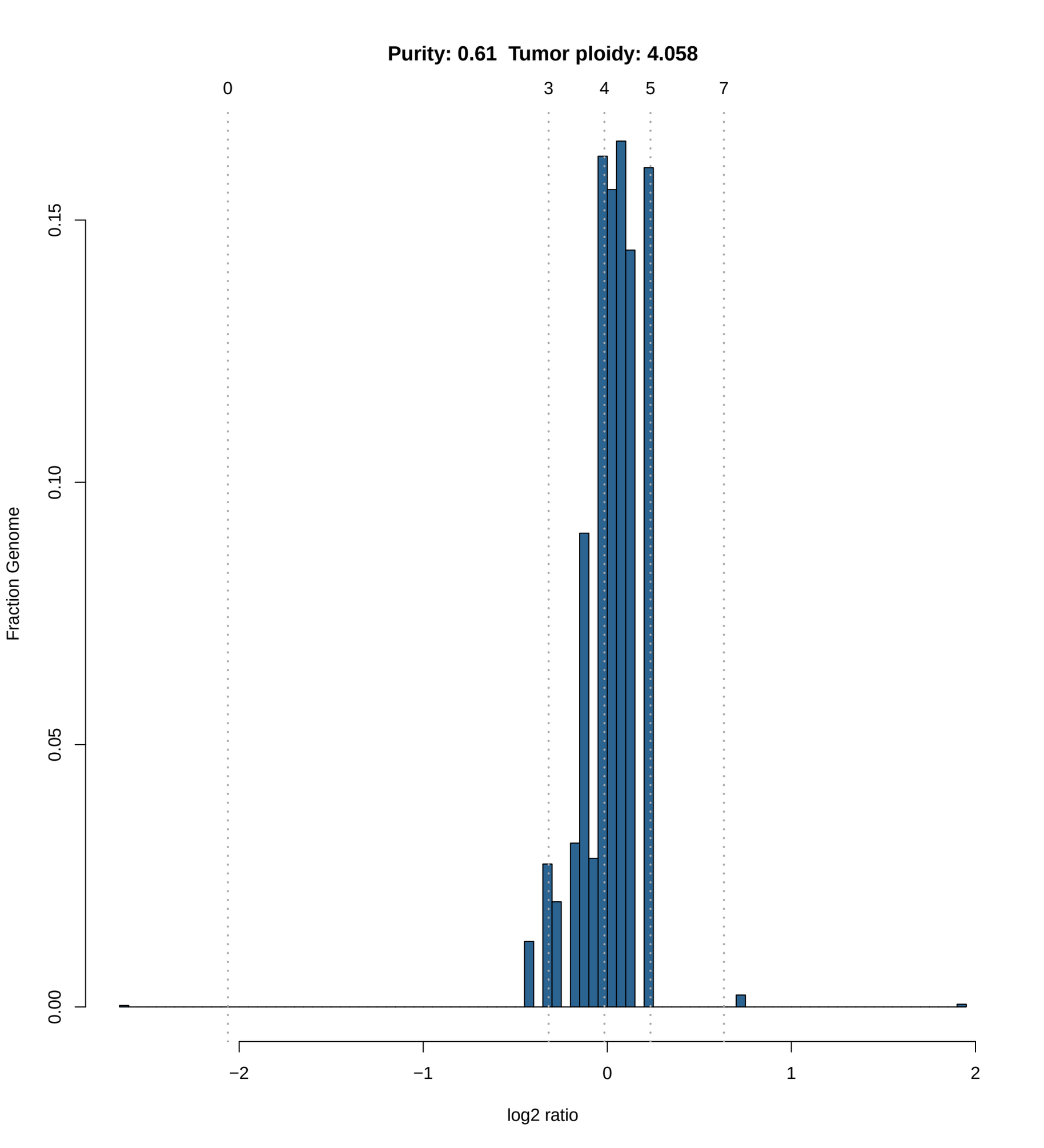

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 10 20 30 40
SNV Index

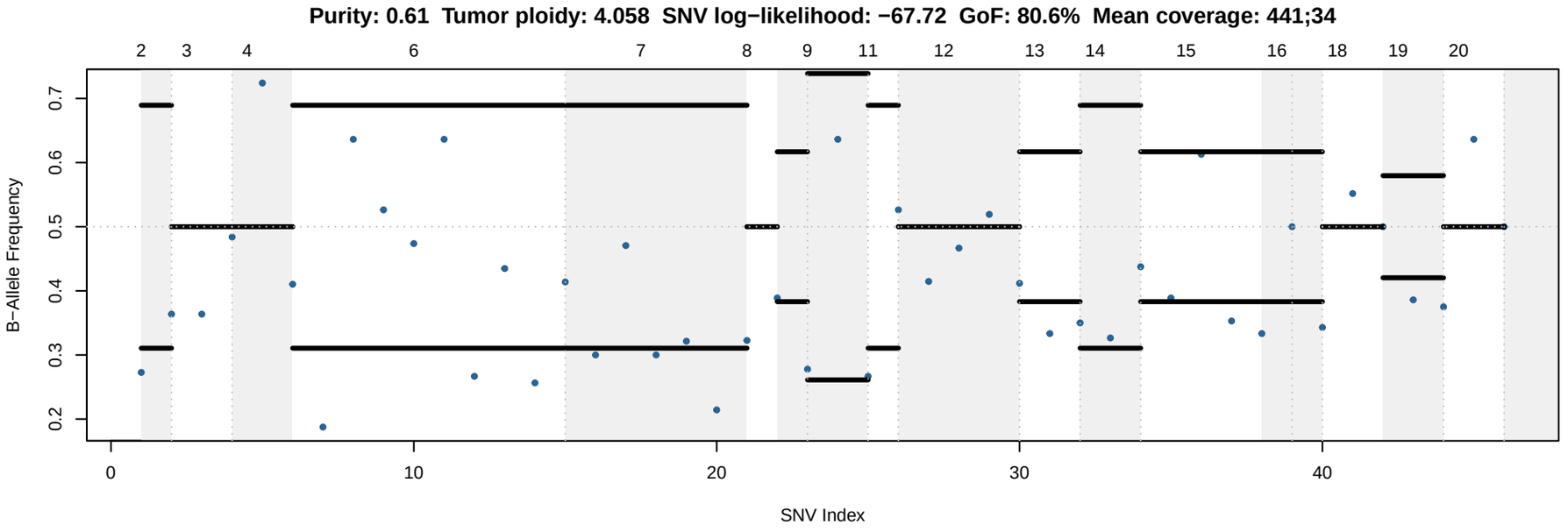

Allelic fraction (germline)
Copy Number log−ratio
4m4
3m3
6m5
5m4
4m3
3m2
2m1
4m2
6m3
5m2
1m0
3m1
4m1
5m1
3m0
6m1
4m0
5m0

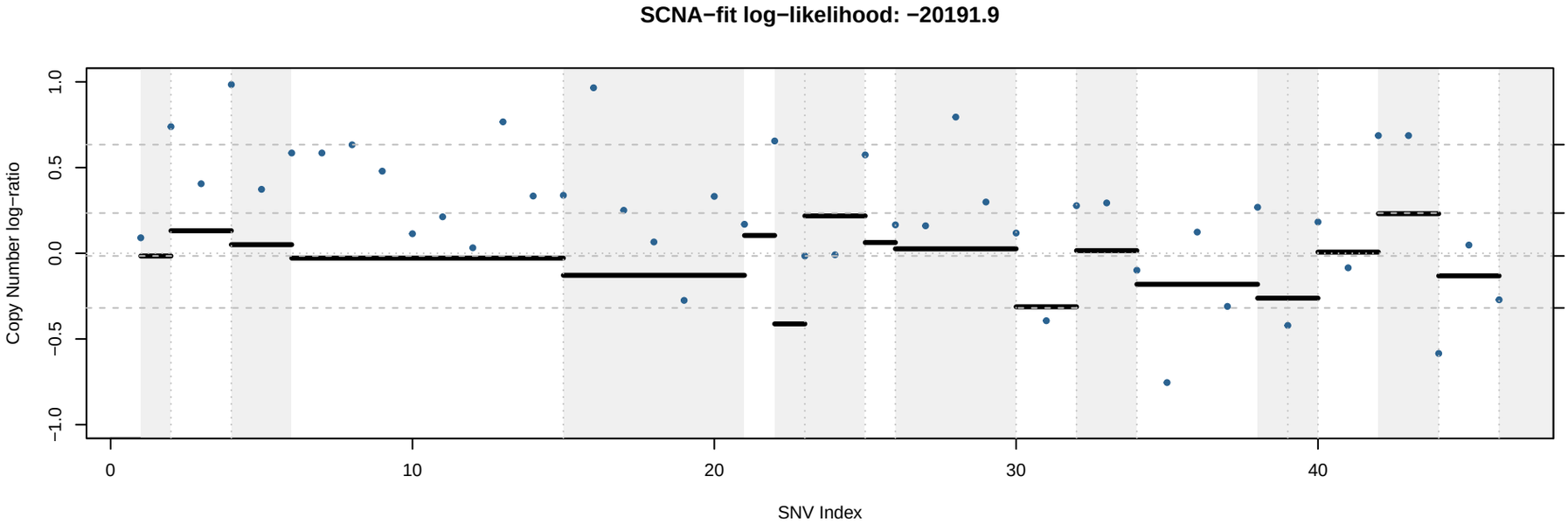

Coverage (log2)
Allelic fraction

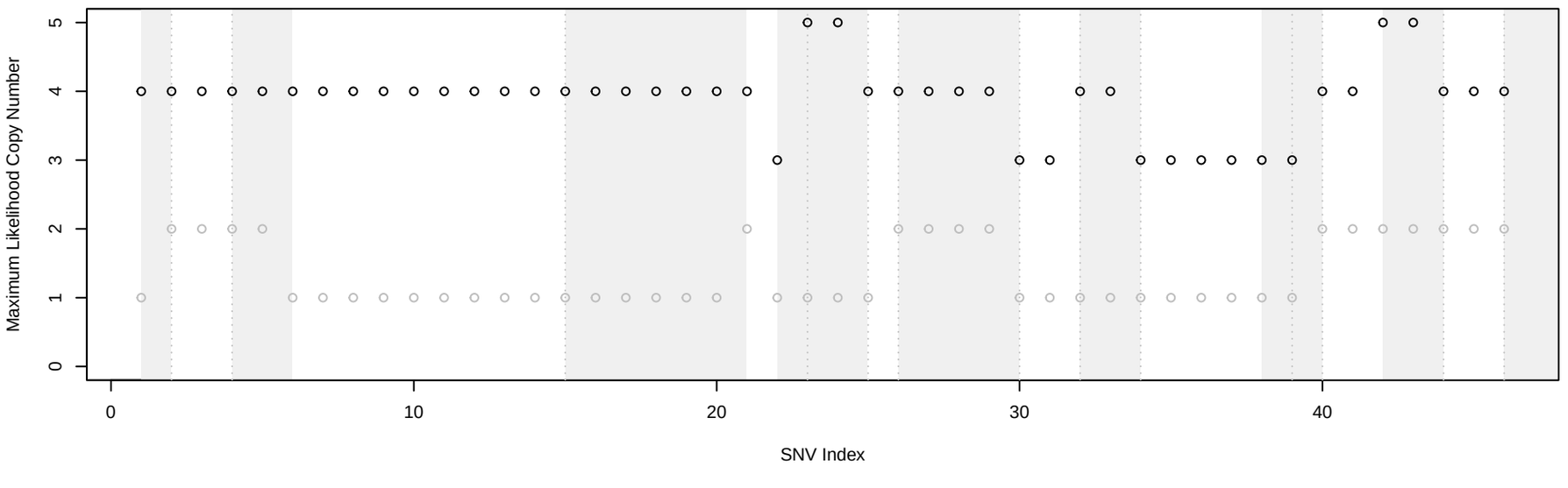

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m4
3m3
3m2
4m2
5m2
3m1
4m1
5m1
6m1

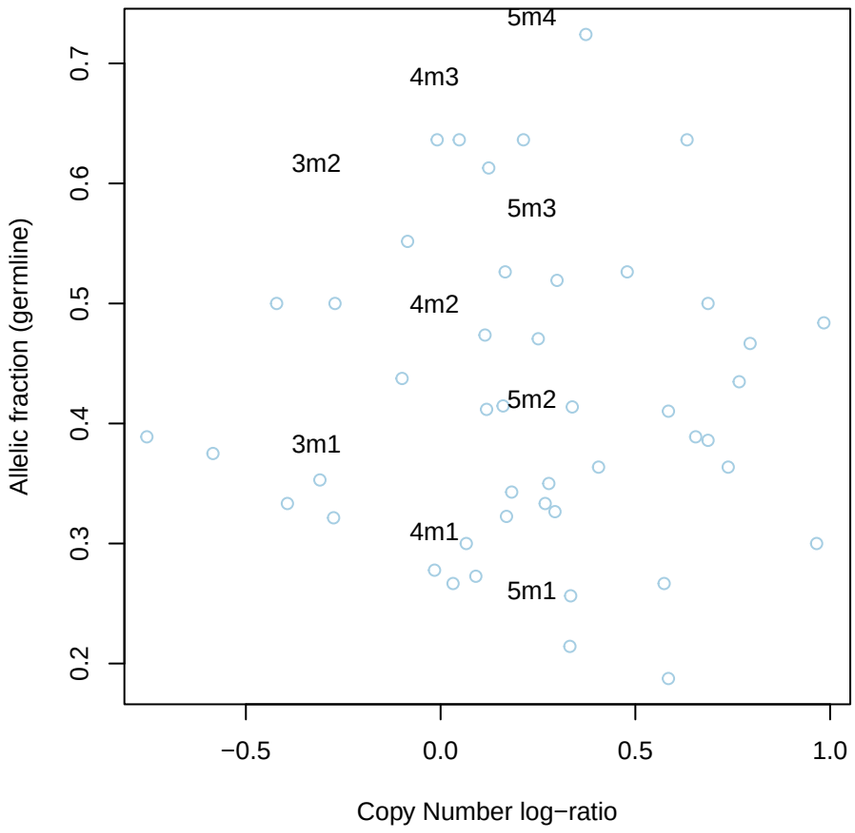

Power 0.56
Frequency
Cellular fraction

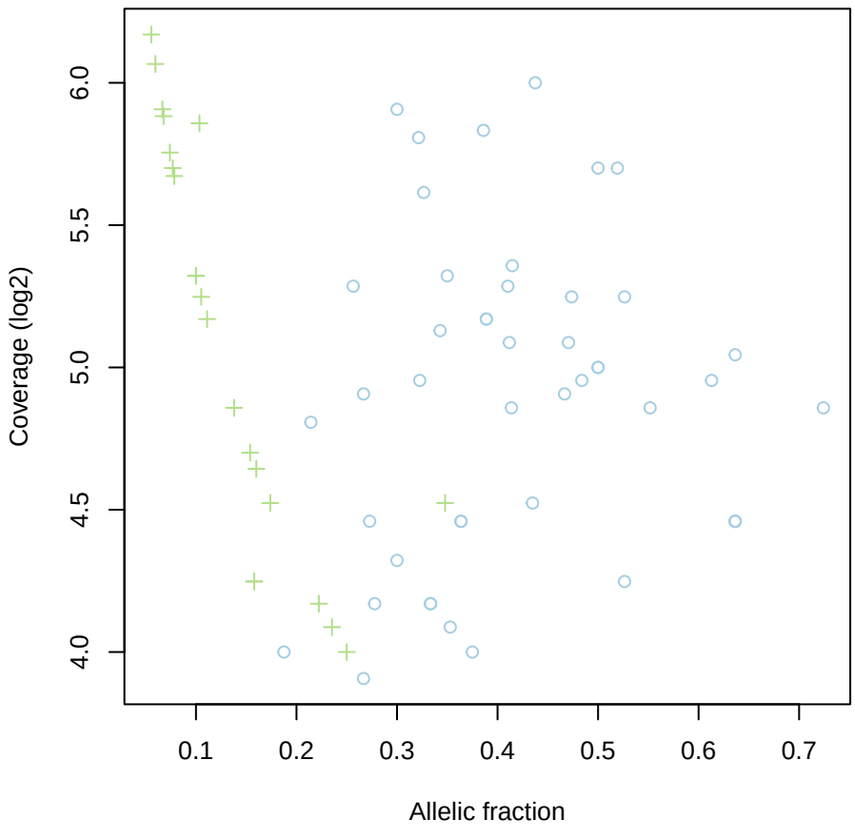

Purity: 0.61 Tumor ploidy: 4.058
0
3
4
5
7
0.15
0.10
0.05
0.00
Fraction Genome
−2
−1
0
1
2
log2 ratio

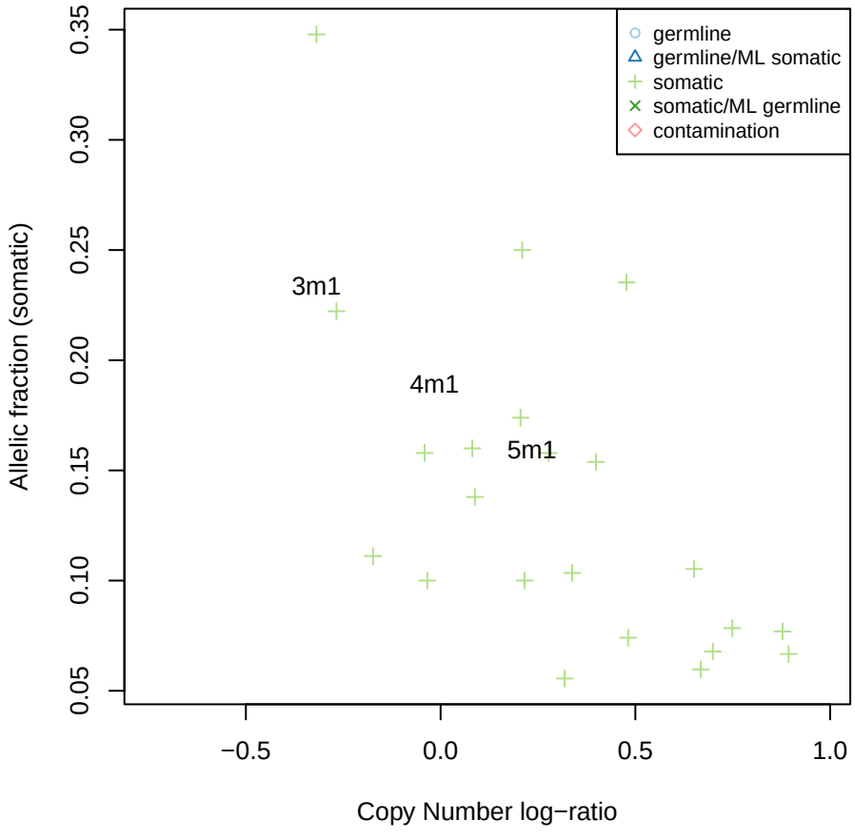

Purity: 0.61 Tumor ploidy: 4.058 SNV log−likelihood: −67.72 GoF: 80.6% Mean coverage: 441;34
2 3 4 6 7 8 9 11 12 13 14 15 16 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 10 20 30 40
SNV Index

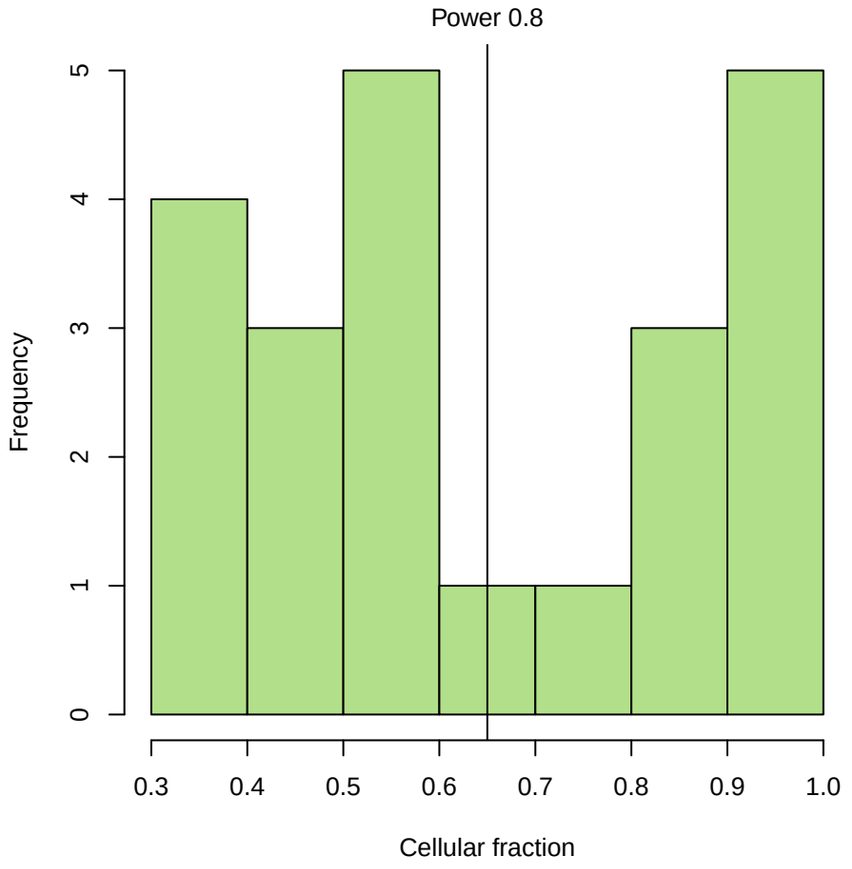

SCNA−fit log−likelihood: −20191.9
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 7
0 10 20 30 40
SNV Index

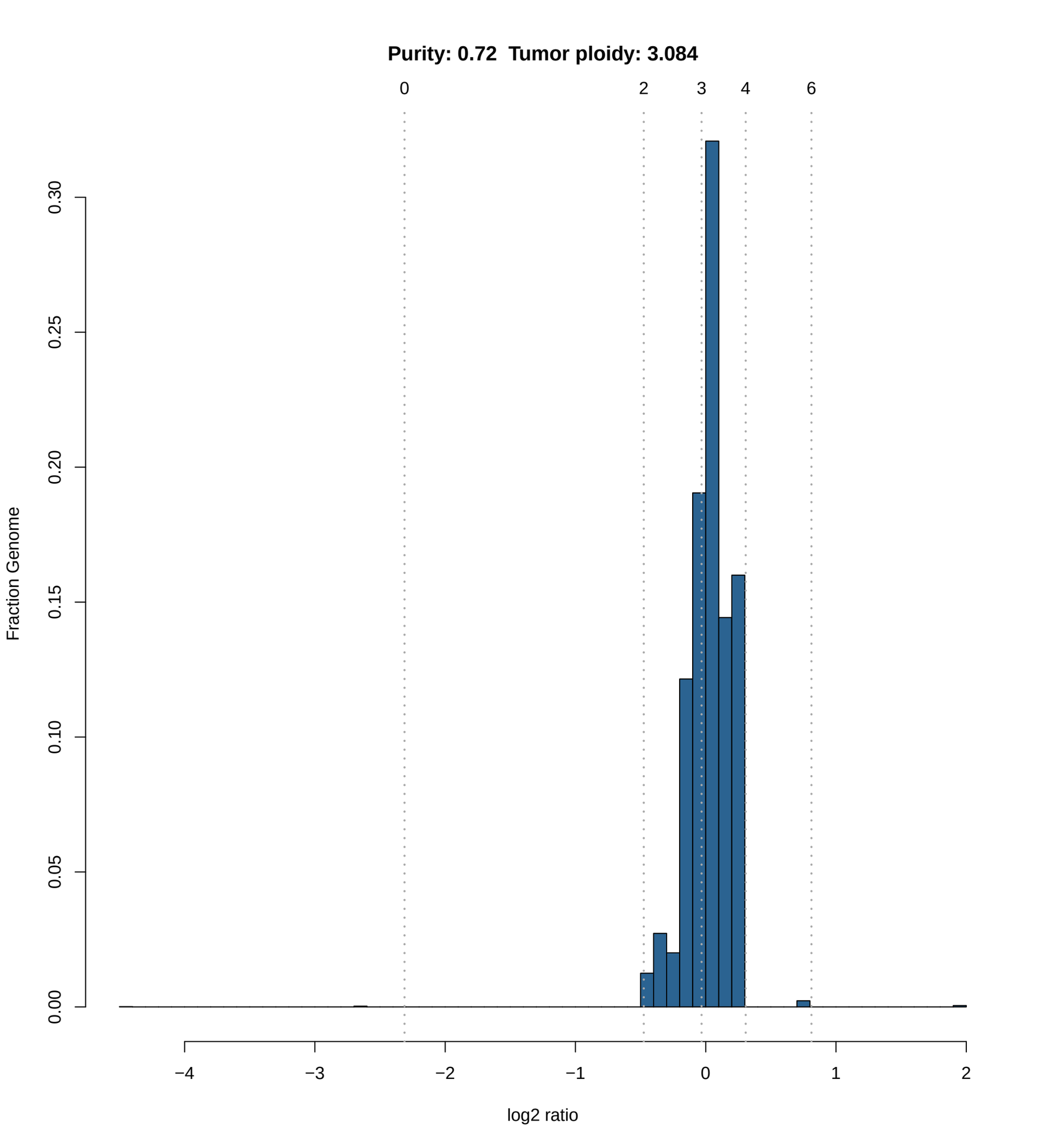

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 10 20 30 40
SNV Index

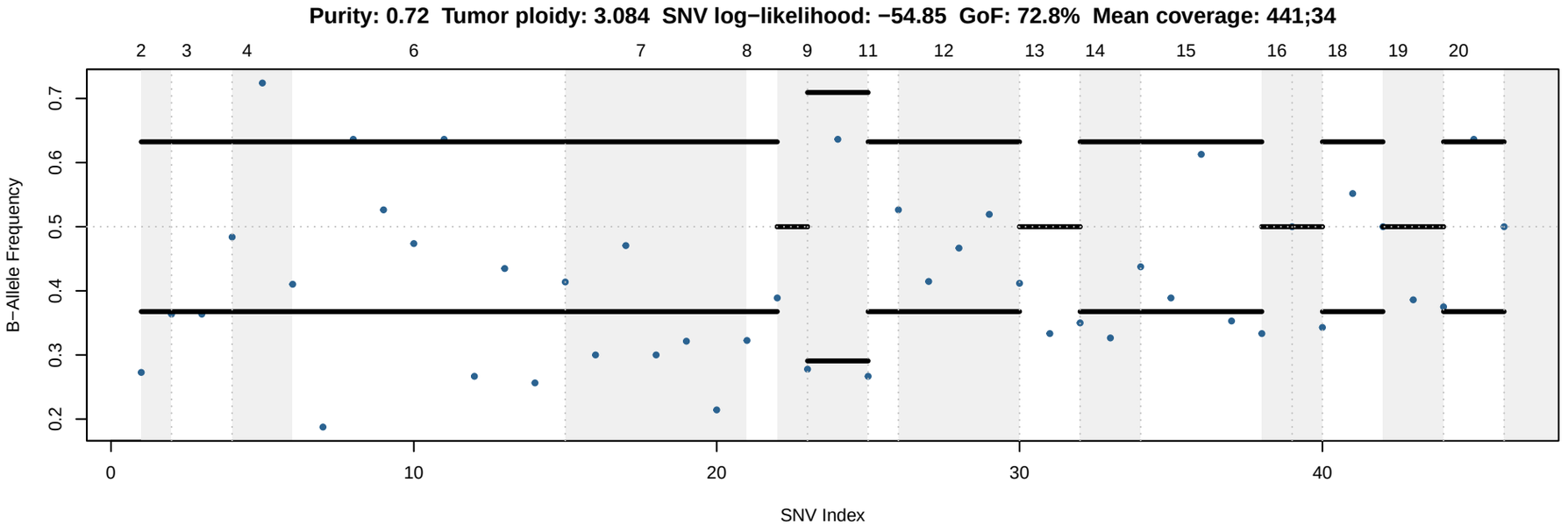

5m4
4m3
3m2
5m3
4m2
5m2
3m1
4m1
5m1
Allelic fraction (germline)
Copy Number log−ratio
0.2
0.3
0.4
0.5
0.6
0.7
−0.5
0.0
0.5
1.0

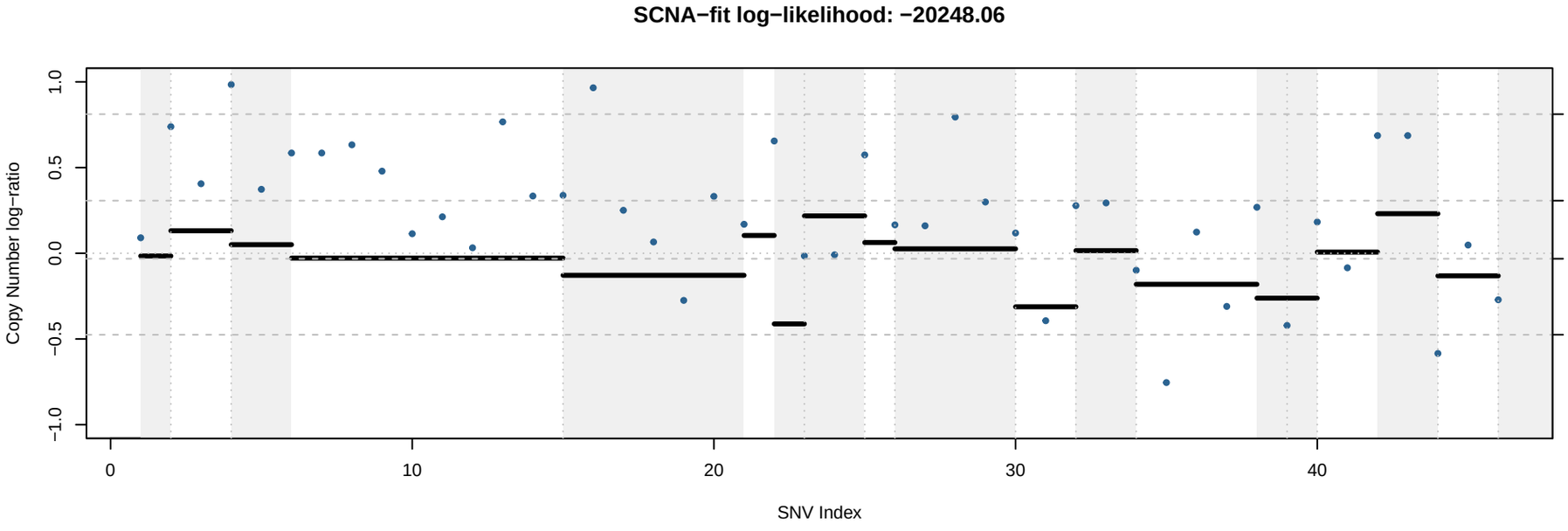

Coverage (log2)
Allelic fraction
4.0
4.5
5.0
5.5
6.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7

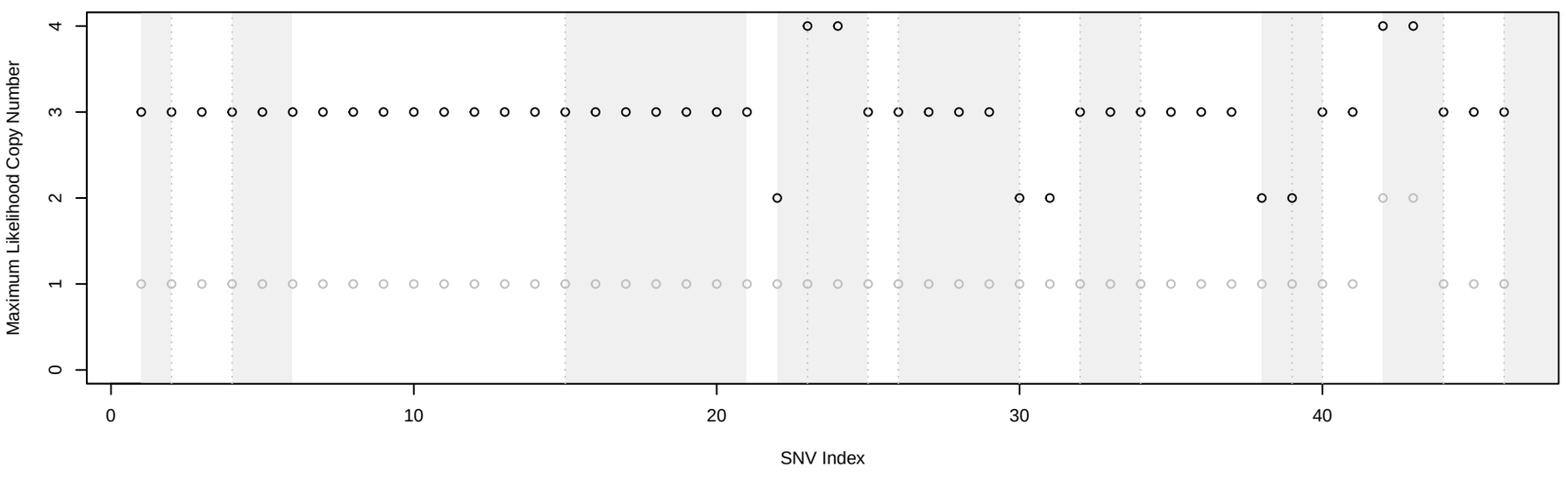

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
0.25
0.30
0.35
−0.5
0.0
0.5
1.0

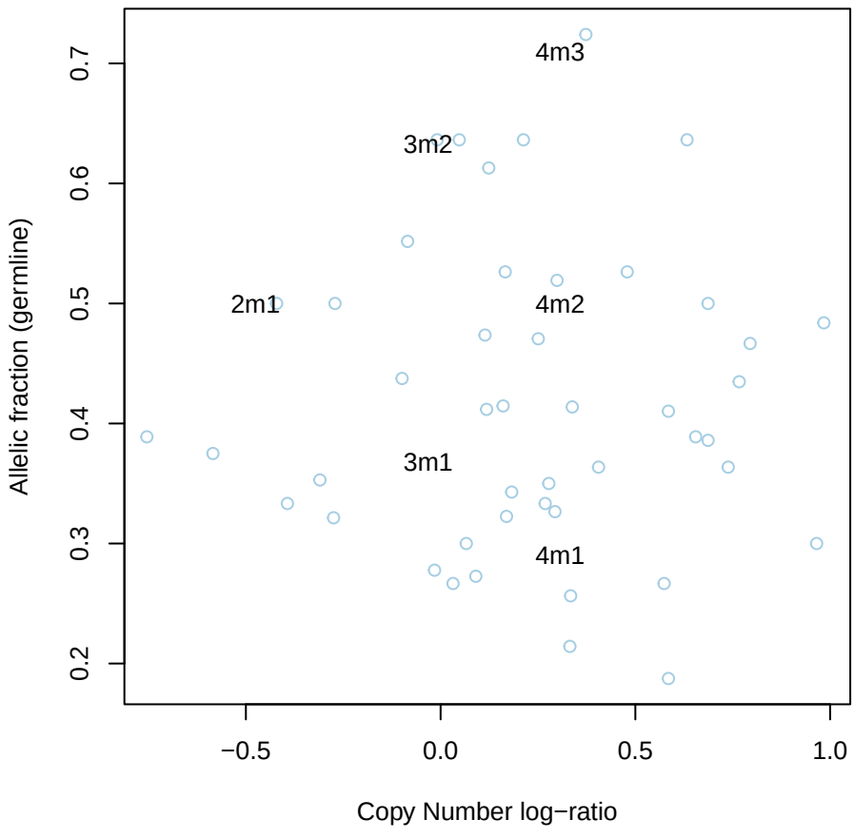

Power 0.8
Frequency
Cellular fraction
0
1
2
3
4
5
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0

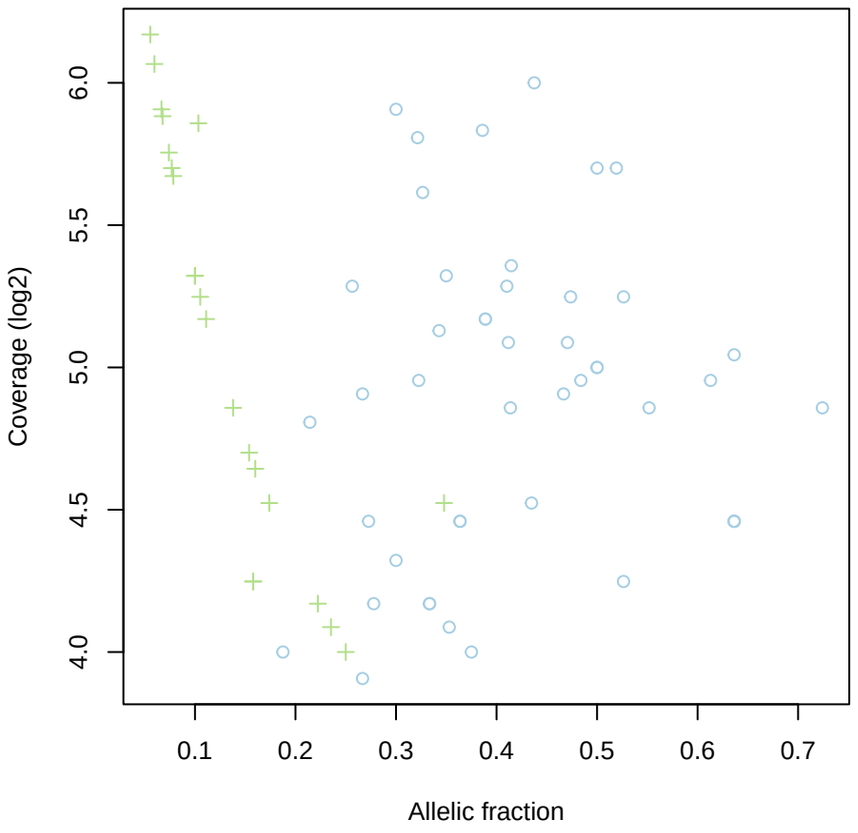

Purity: 0.72 Tumor ploidy: 3.084
0
2
3
4
6
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−4
−3
−2
−1
0
1
2
log2 ratio

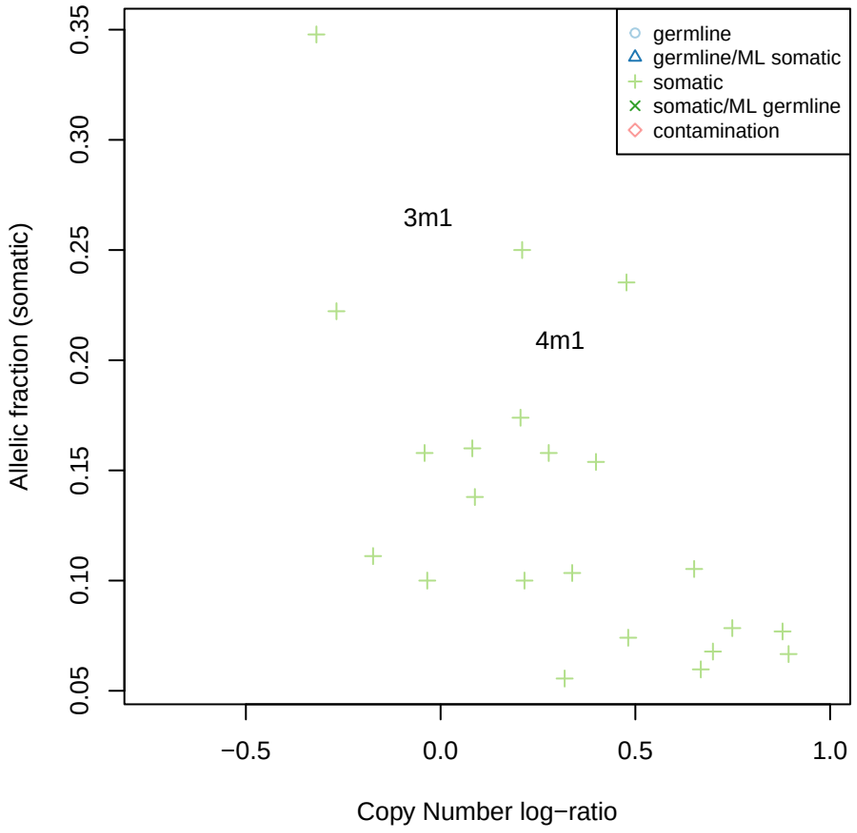

Purity: 0.72 Tumor ploidy: 3.084 SNV log−likelihood: −54.85 GoF: 72.8% Mean coverage: 441;34
2 3 4 6 7 8 9 11 12 13 14 15 16 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 10 20 30 40
SNV Index

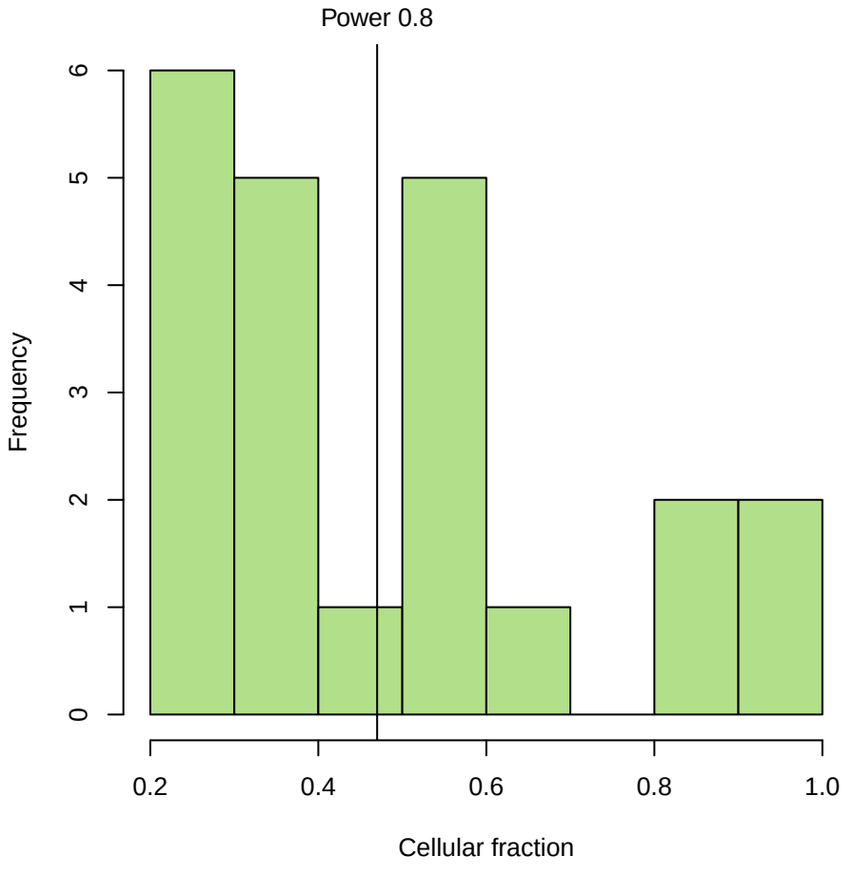

SCNA−fit log−likelihood: −20248.06
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 6
0 10 20 30 40
SNV Index

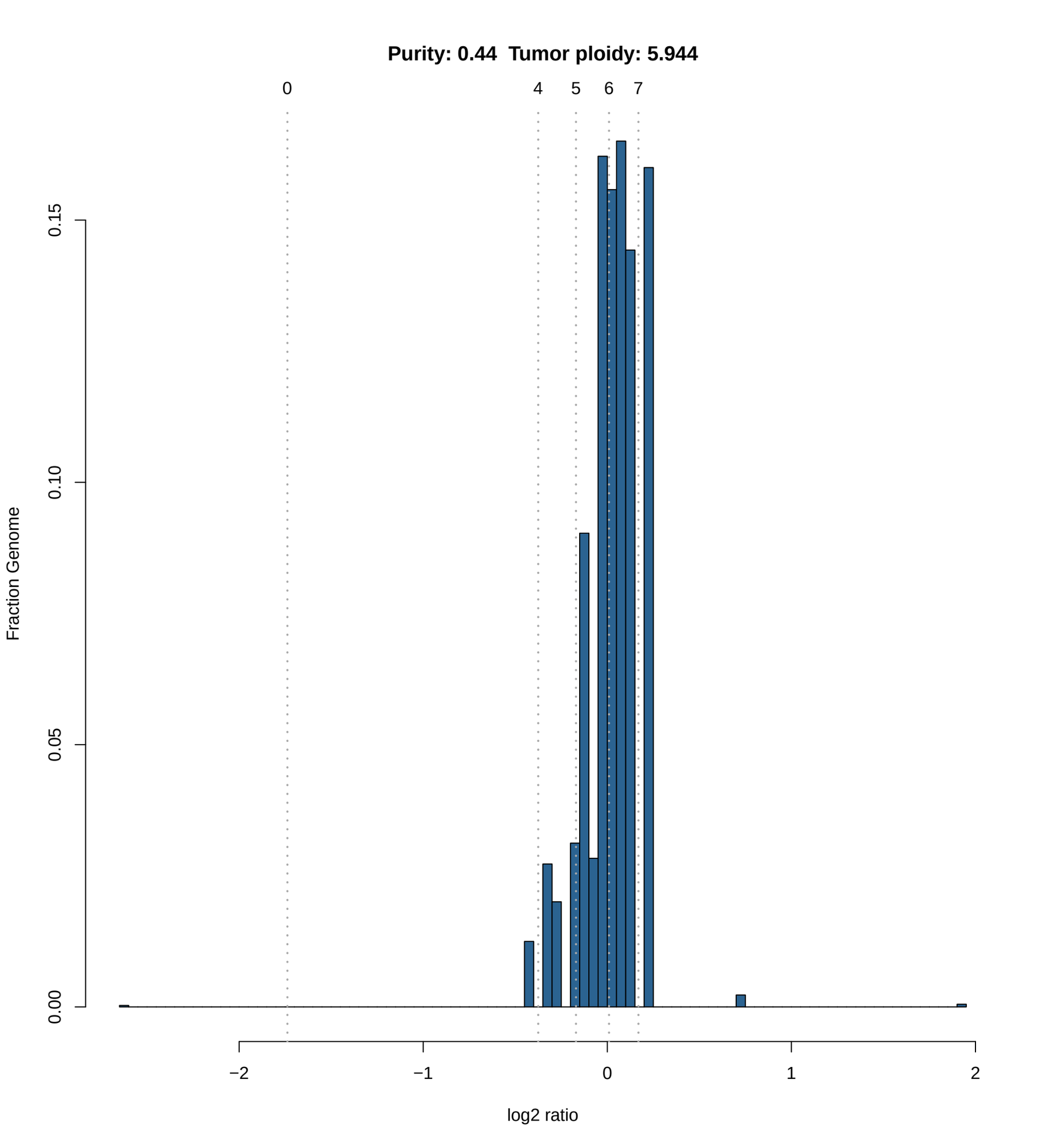

Maximum Likelihood Copy Number
0 1 2 3 4
0 10 20 30 40
SNV Index

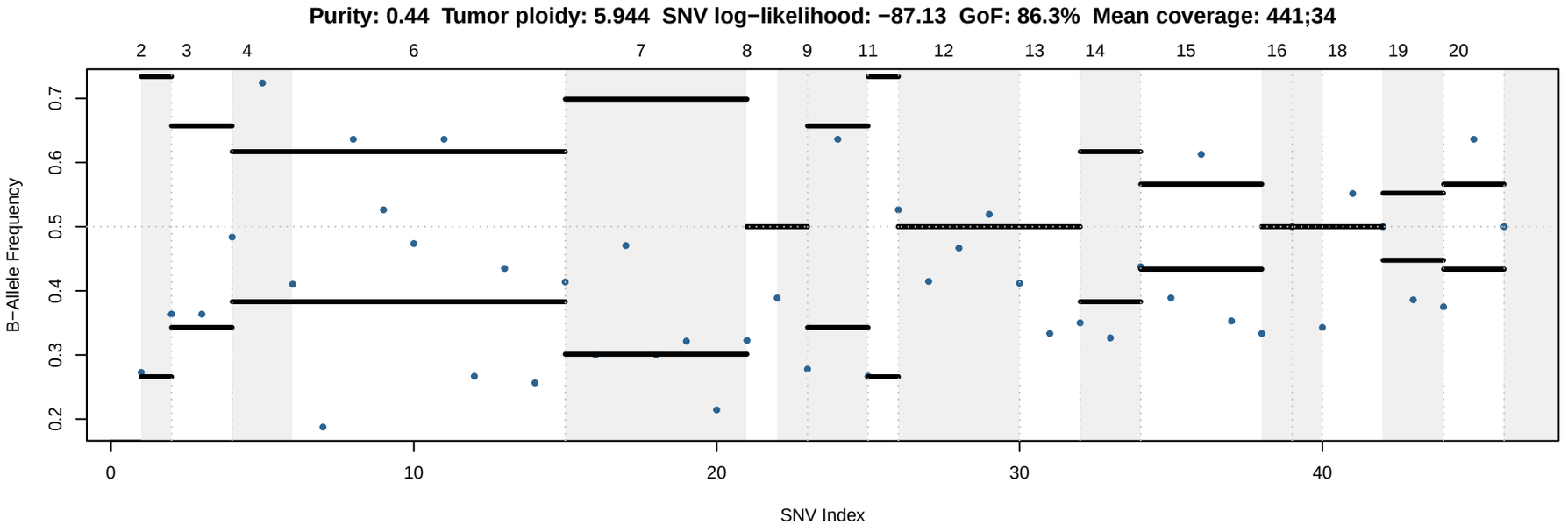

4m3
3m2
2m1
4m2
3m1
4m1
Allelic fraction (germline)
Copy Number log−ratio

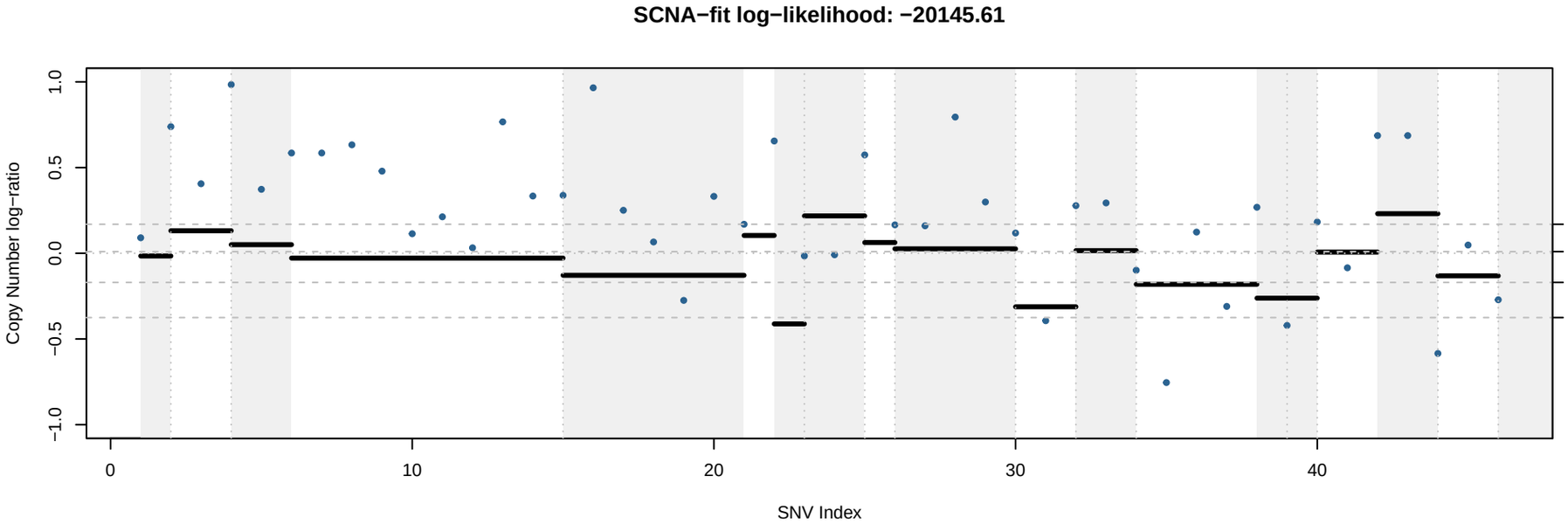

Coverage (log2)
Allelic fraction

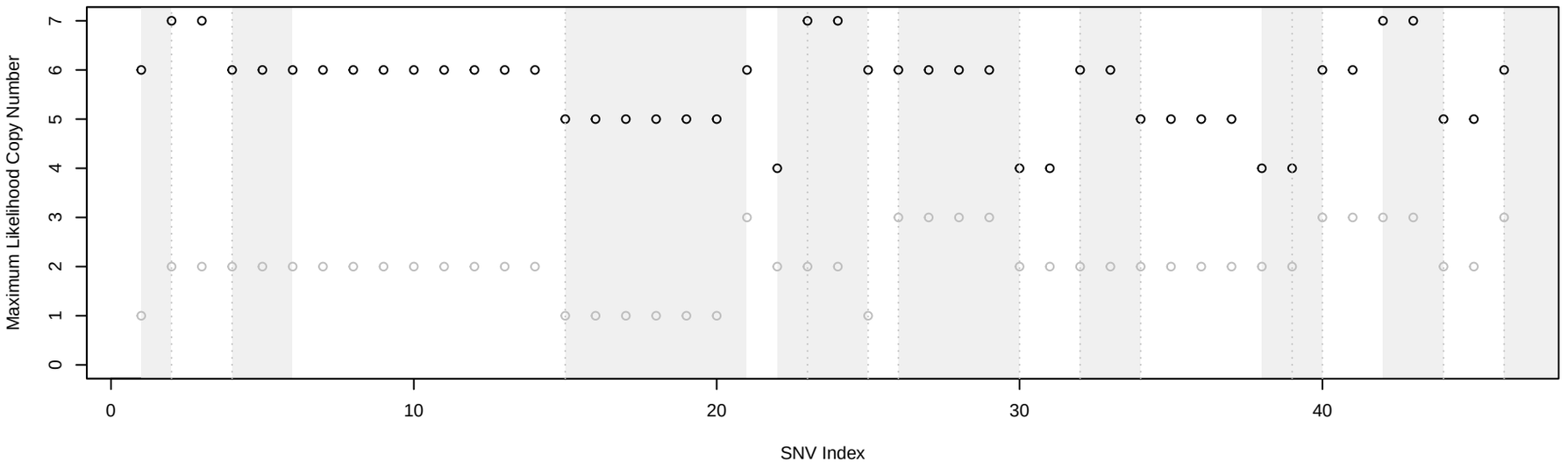

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
Allelic fraction (somatic)
Copy Number log−ratio

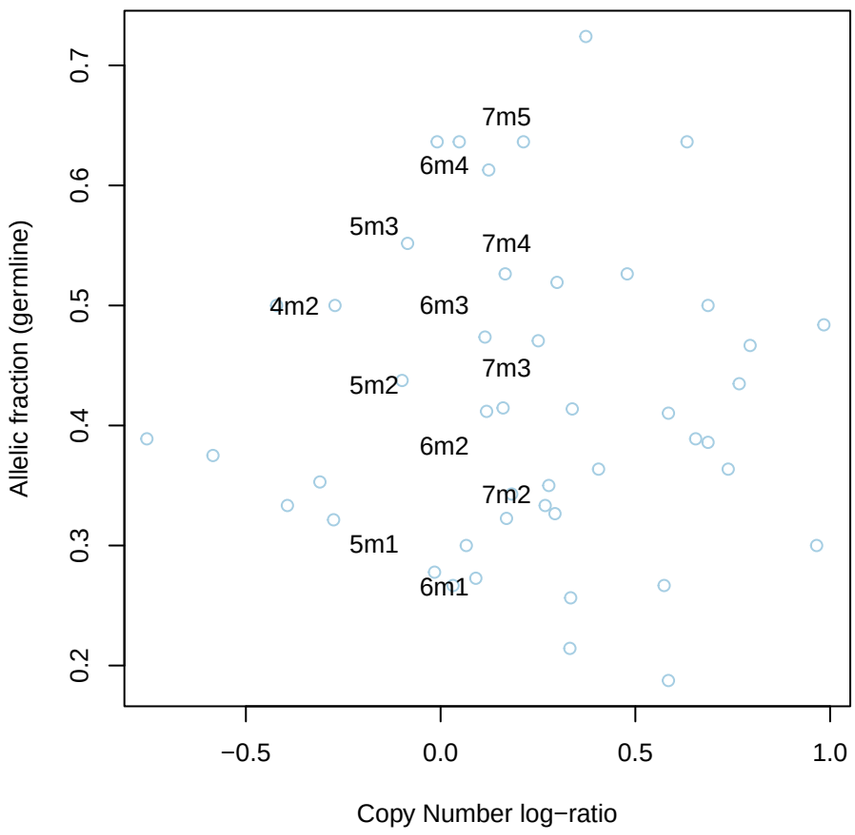

Power 0.8
Frequency
Cellular fraction

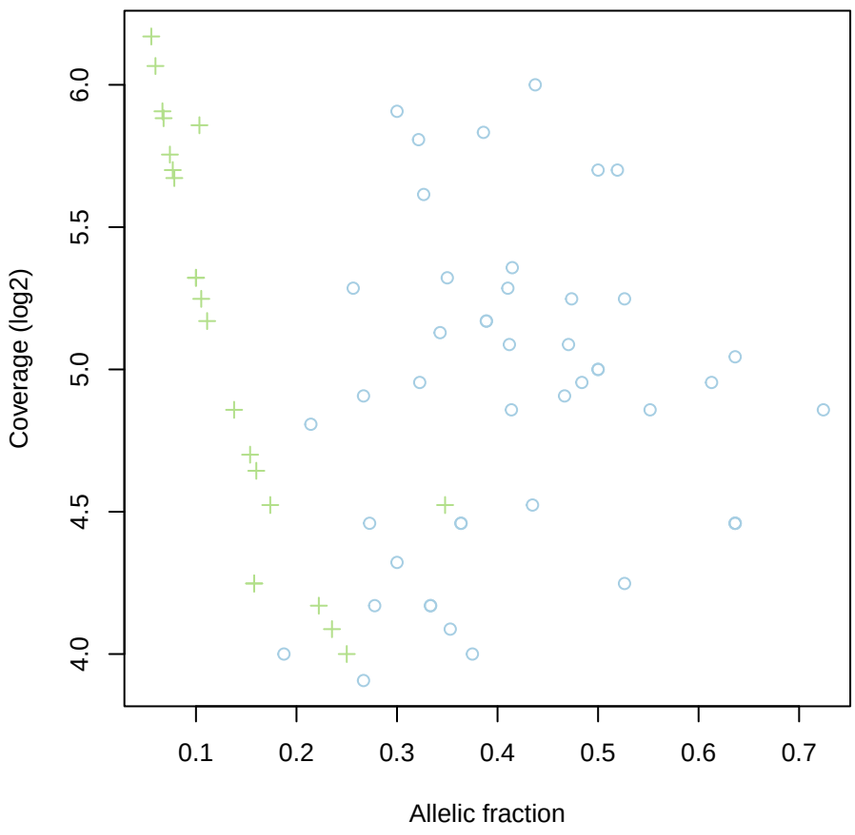

Purity: 0.44 Tumor ploidy: 5.944
0
4
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−2
−1
0
1
2
log2 ratio

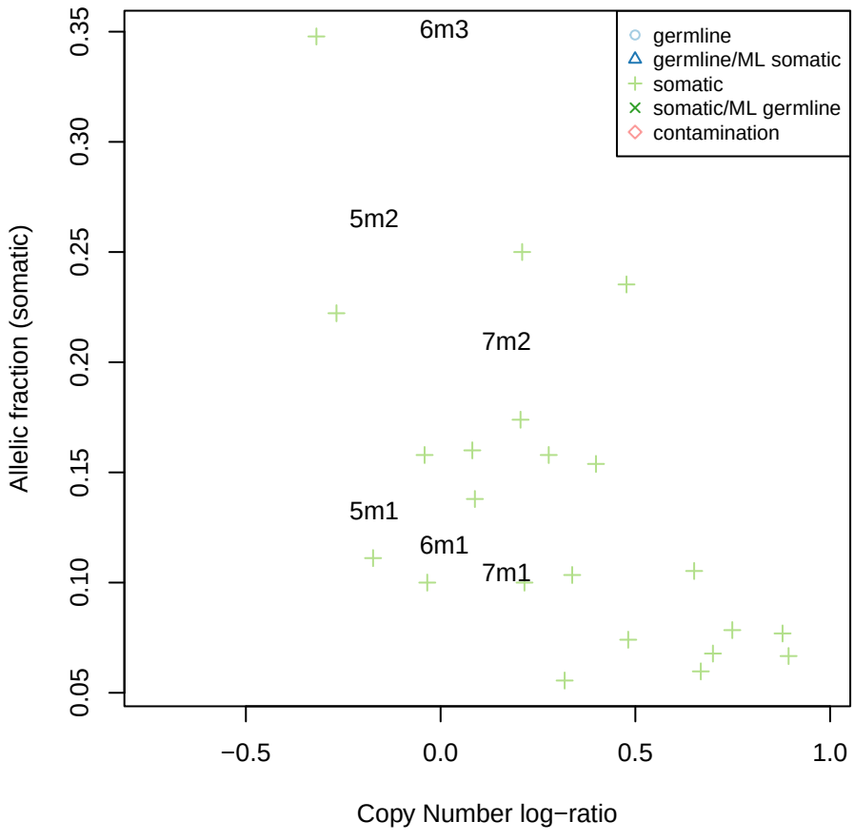

Purity: 0.44 Tumor ploidy: 5.944 SNV log−likelihood: −87.13 GoF: 86.3% Mean coverage: 441;34
2 3 4 6 7 8 9 11 12 13 14 15 16 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 10 20 30 40
SNV Index

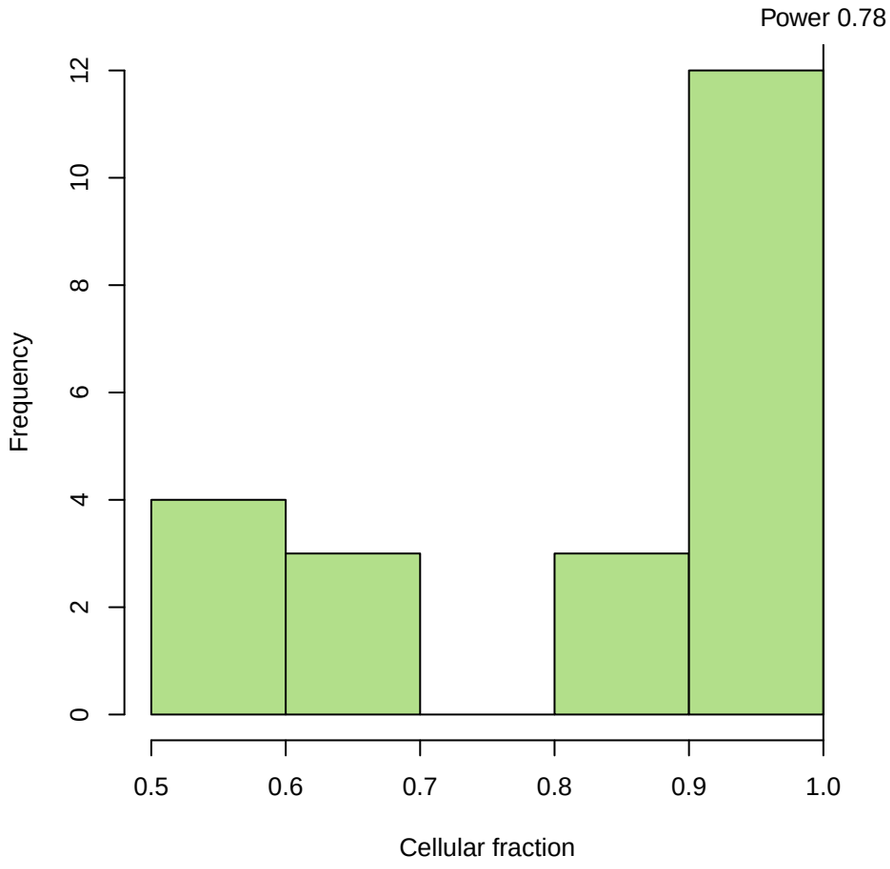

SCNA−fit log−likelihood: −20145.61
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5 6 7
0 10 20 30 40
SNV Index

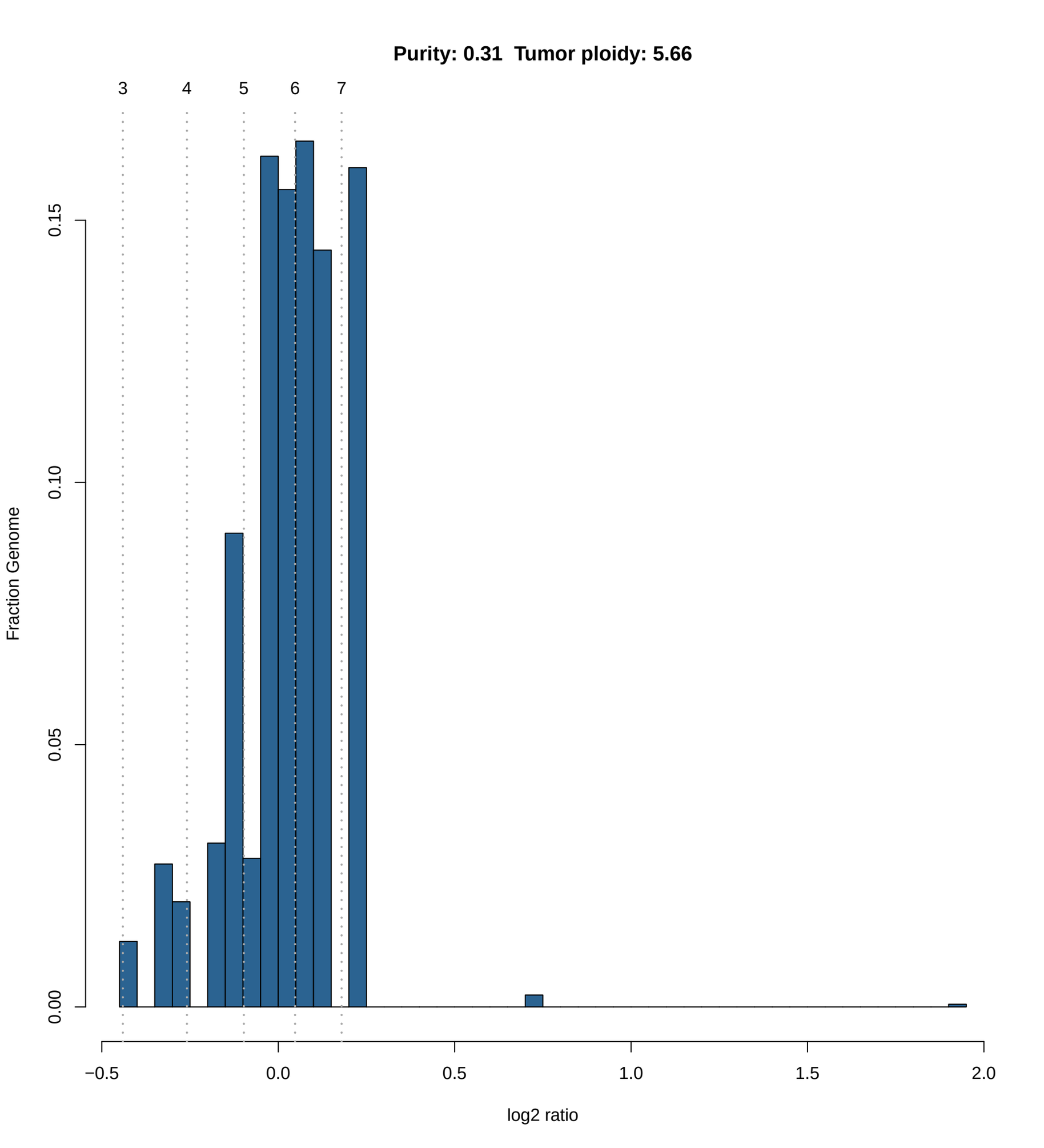

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 10 20 30 40
SNV Index

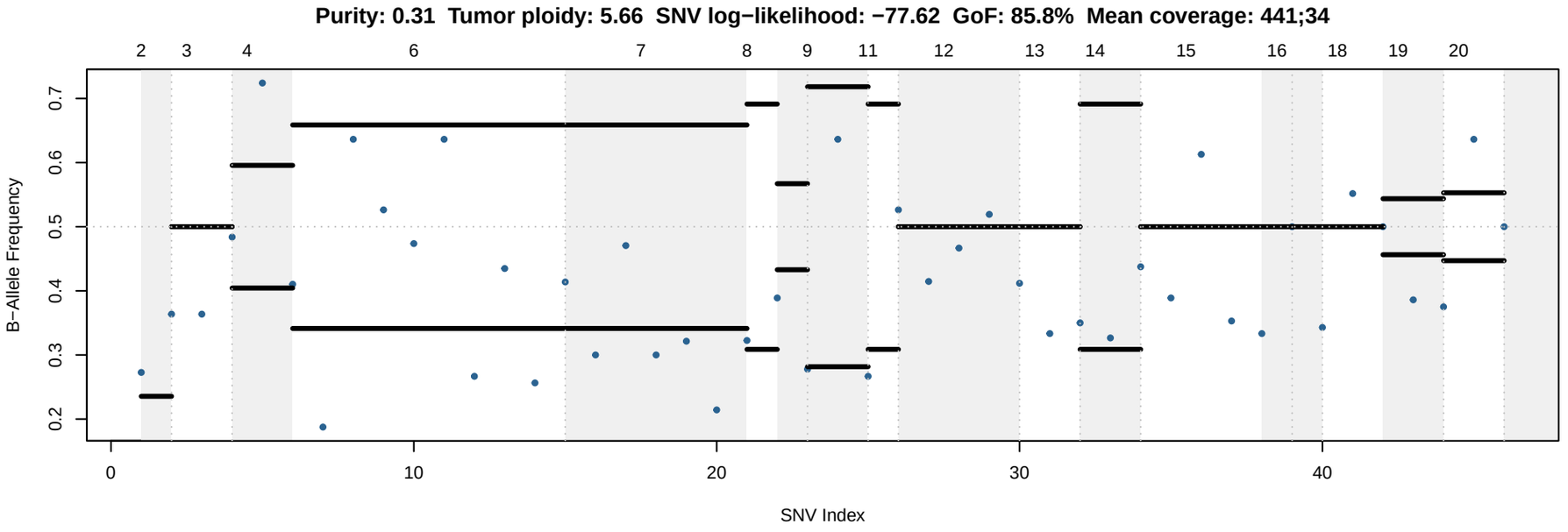

Allelic fraction (germline)
Copy Number log−ratio
7m5
6m4
5m3
7m4
4m2
6m3
7m3
5m2
6m2
7m2
5m1
6m1

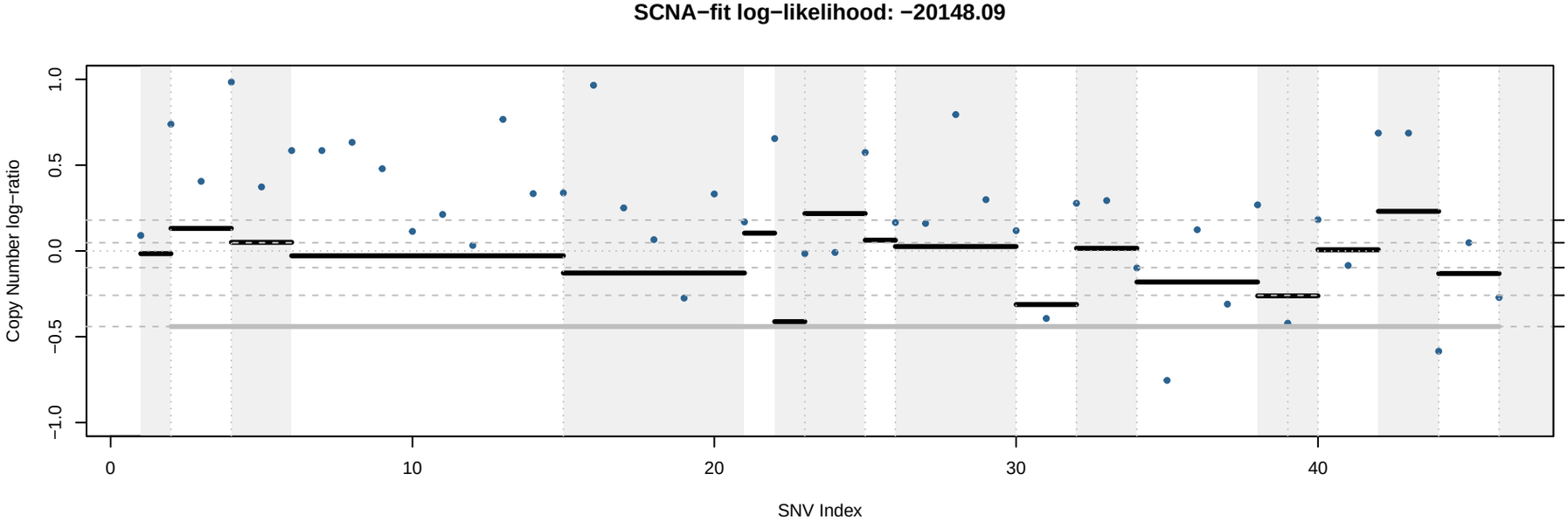

Coverage (log2)
Allelic fraction

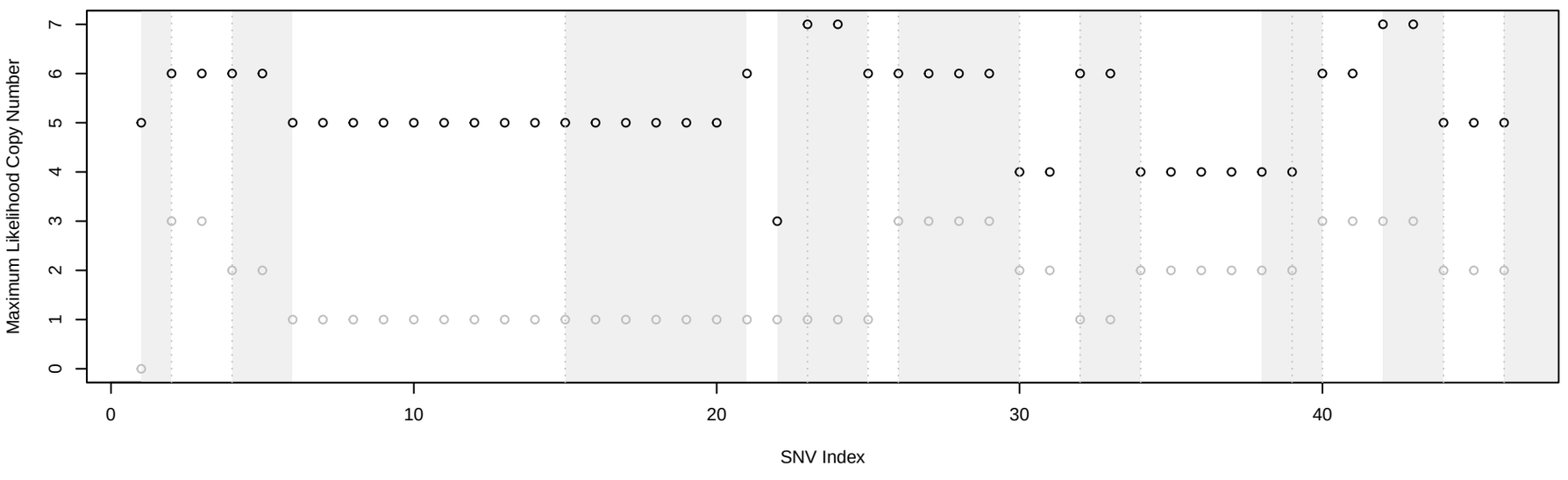

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m3
5m2
7m2
5m1
6m1
7m1

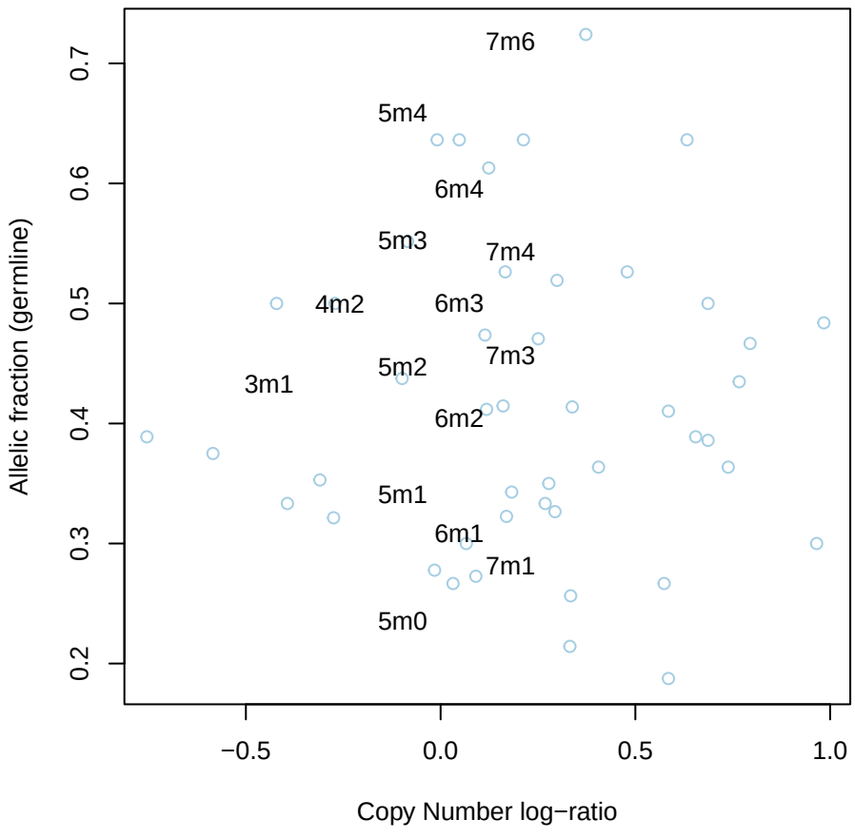

Power 0.78
Frequency
Cellular fraction

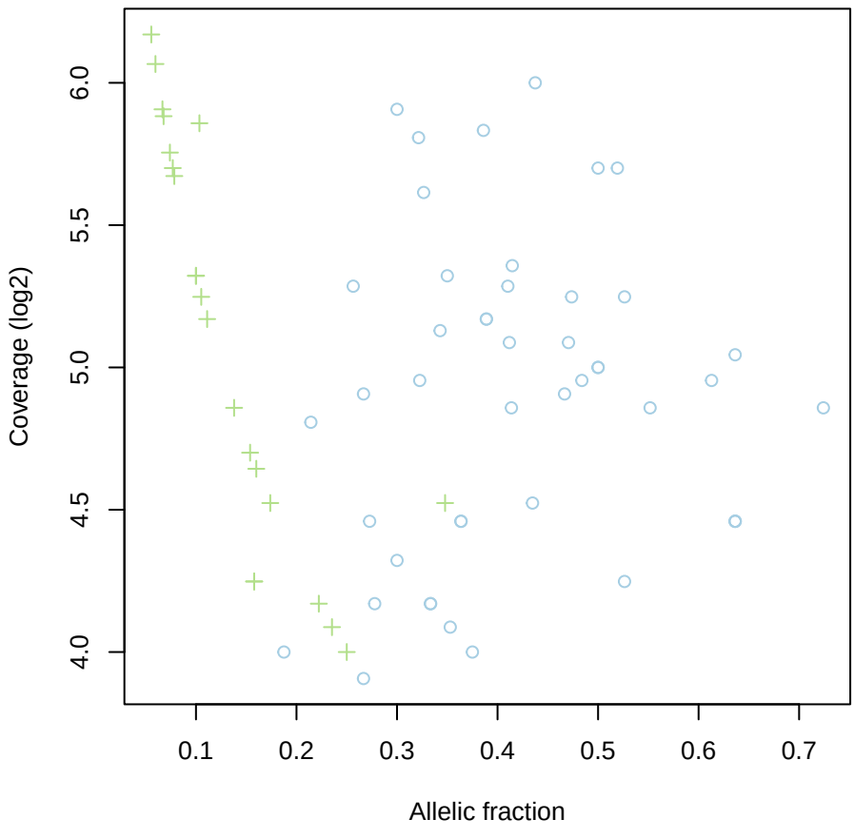

Purity: 0.31 Tumor ploidy: 5.66
3
4
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
1.5
2.0
log2 ratio

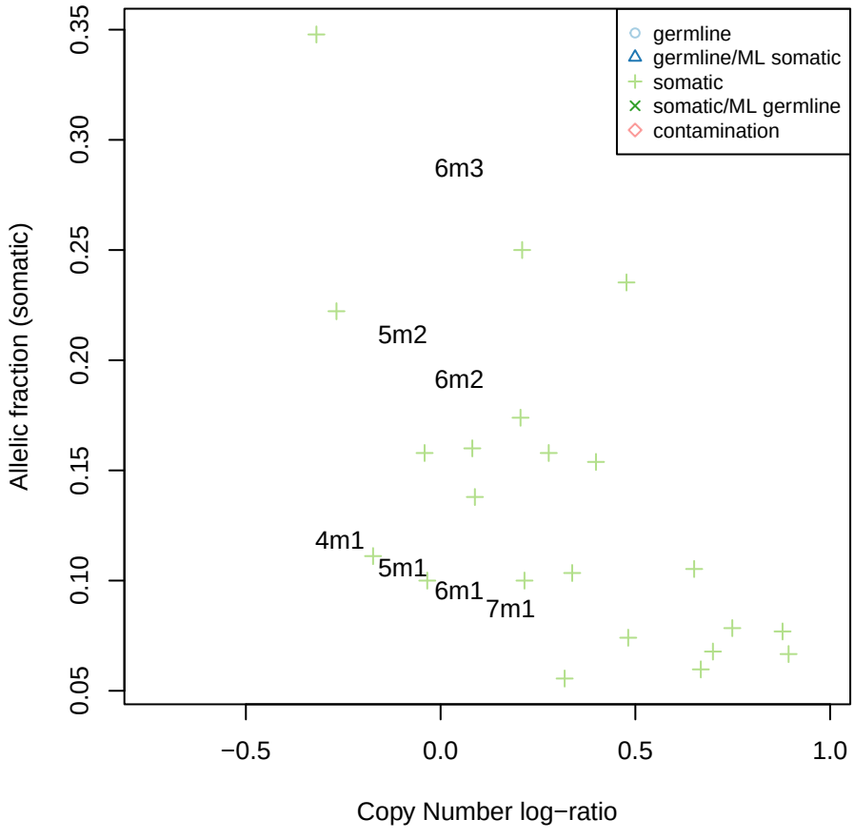

Purity: 0.31 Tumor ploidy: 5.66 SNV log−likelihood: −77.62 GoF: 85.8% Mean coverage: 441;34
2 3 4 6 7 8 9 11 12 13 14 15 16 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 10 20 30 40
SNV Index

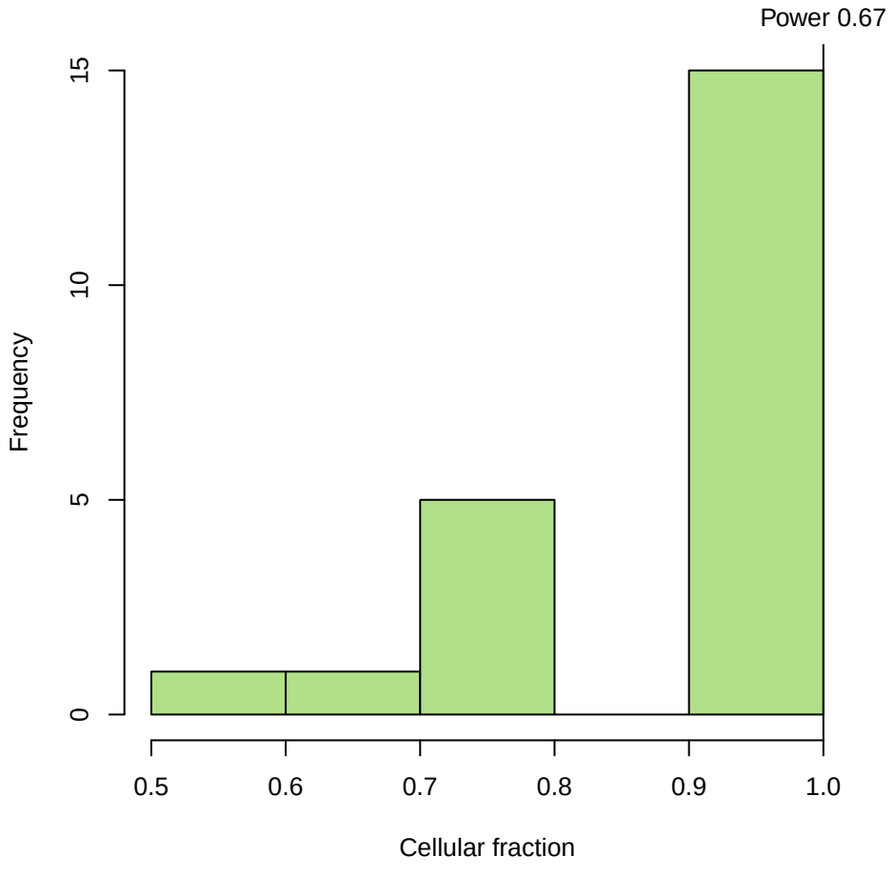

SCNA−fit log−likelihood: −20148.09
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6
0 10 20 30 40
SNV Index

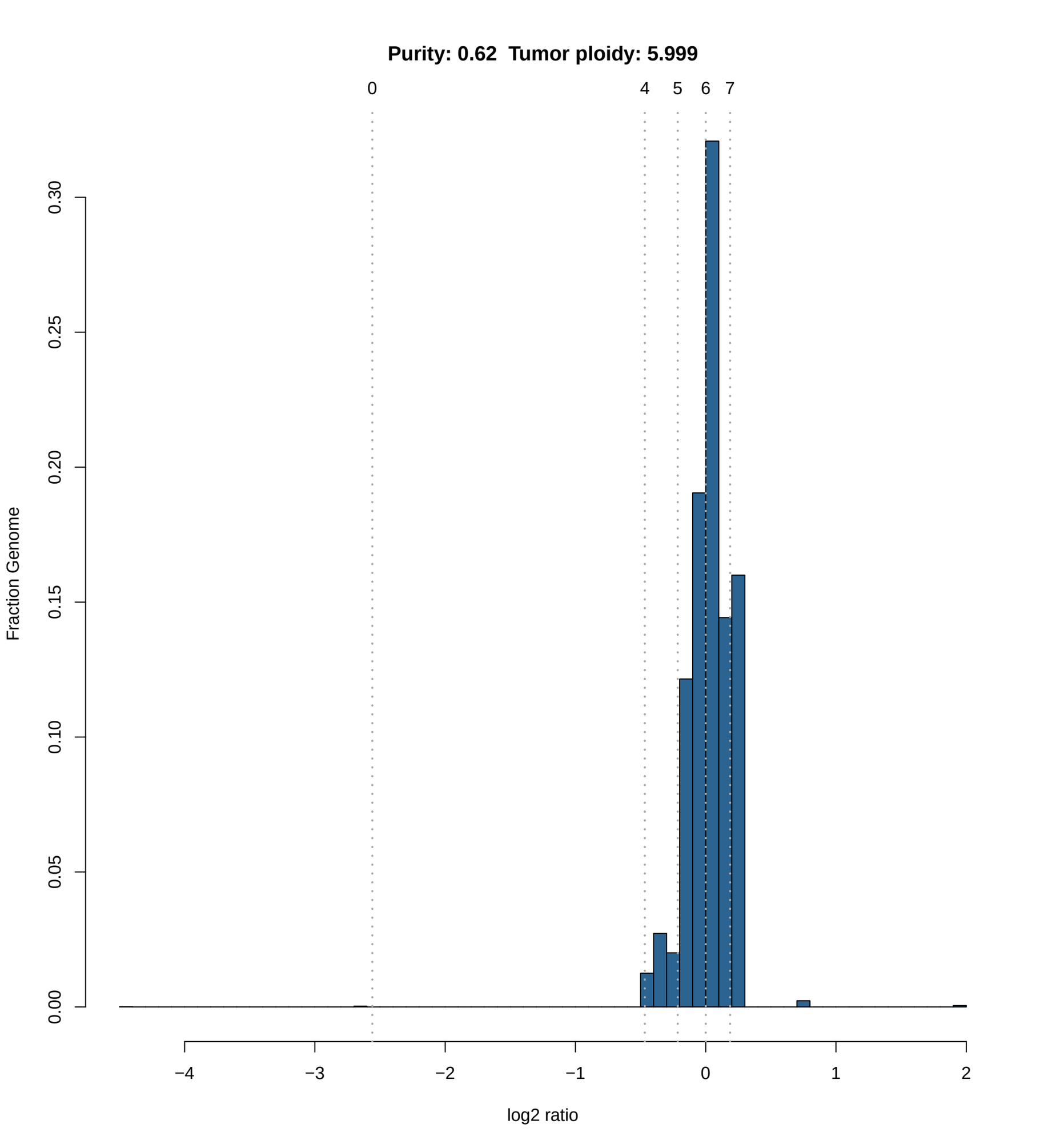

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 10 20 30 40
SNV Index

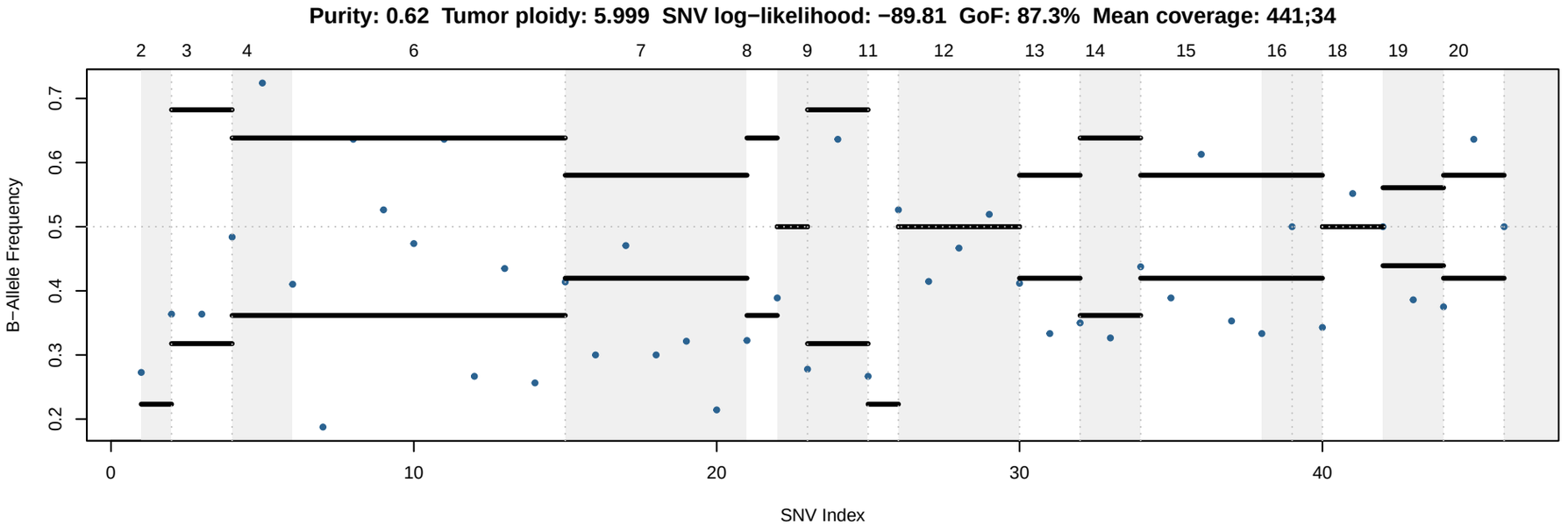

7m6
5m4
6m4
5m3
7m4
4m2
6m3
7m3
5m2
3m1
6m2
5m1
6m1
7m1
5m0
Allelic fraction (germline)
Copy Number log−ratio

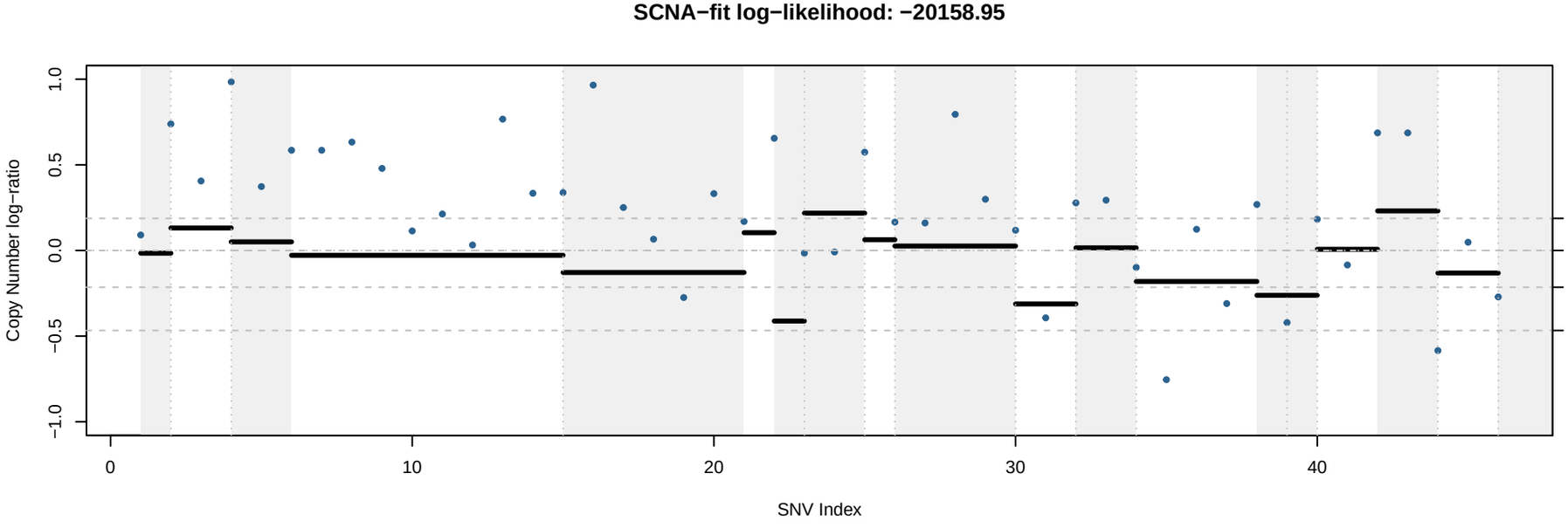

Coverage (log2)
Allelic fraction

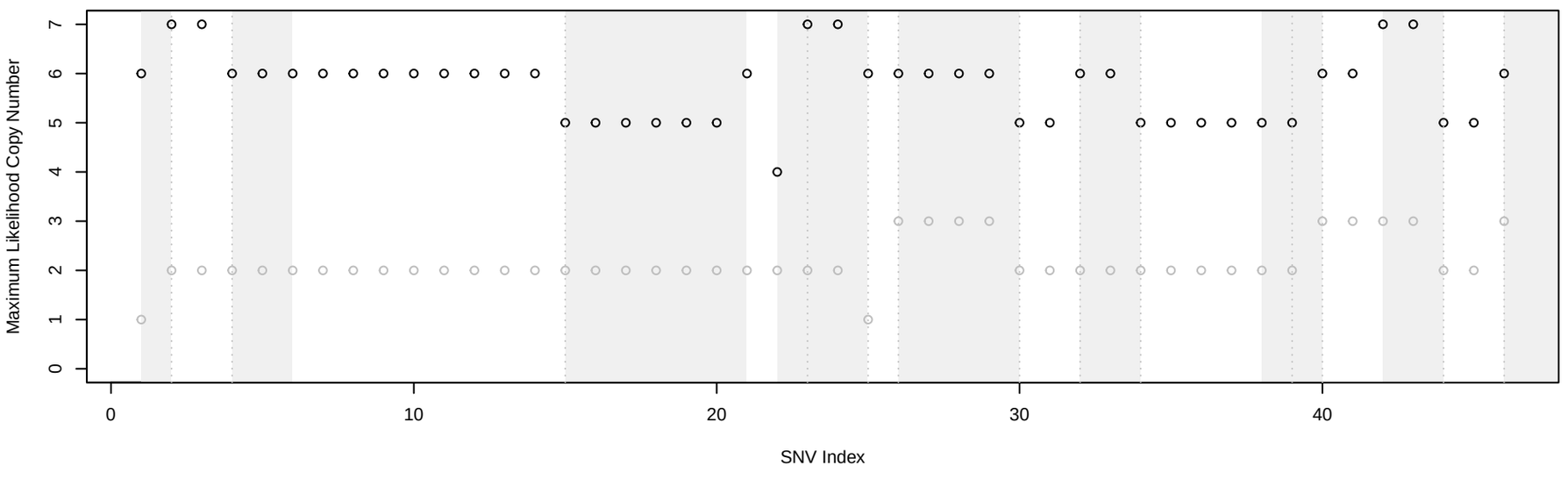

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m3
5m2
6m2
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

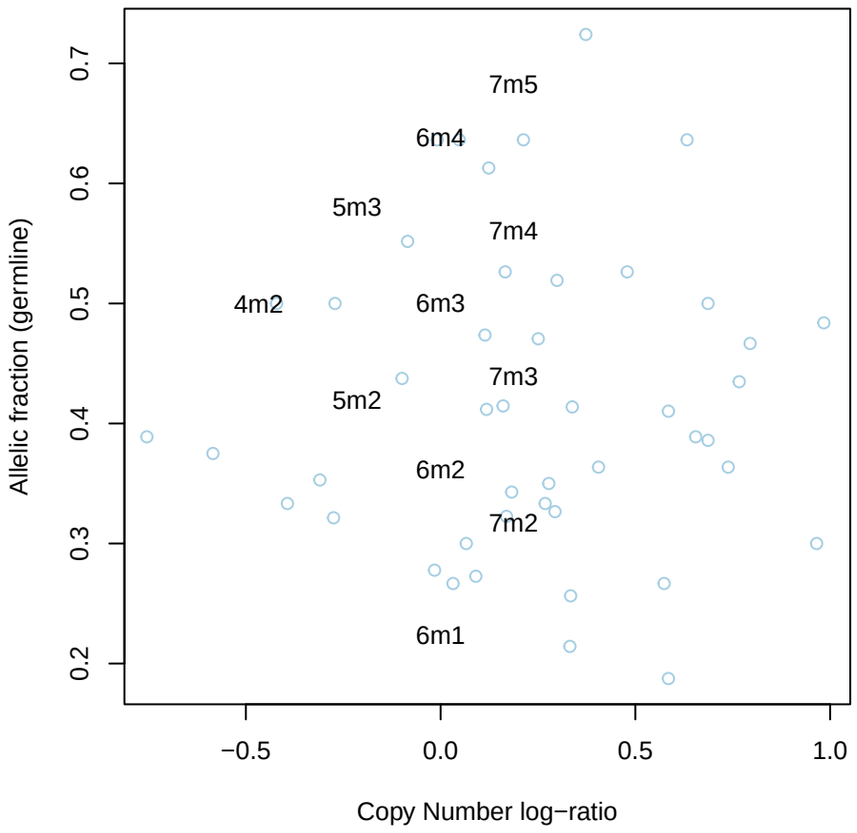

Power 0.67
Frequency
Cellular fraction

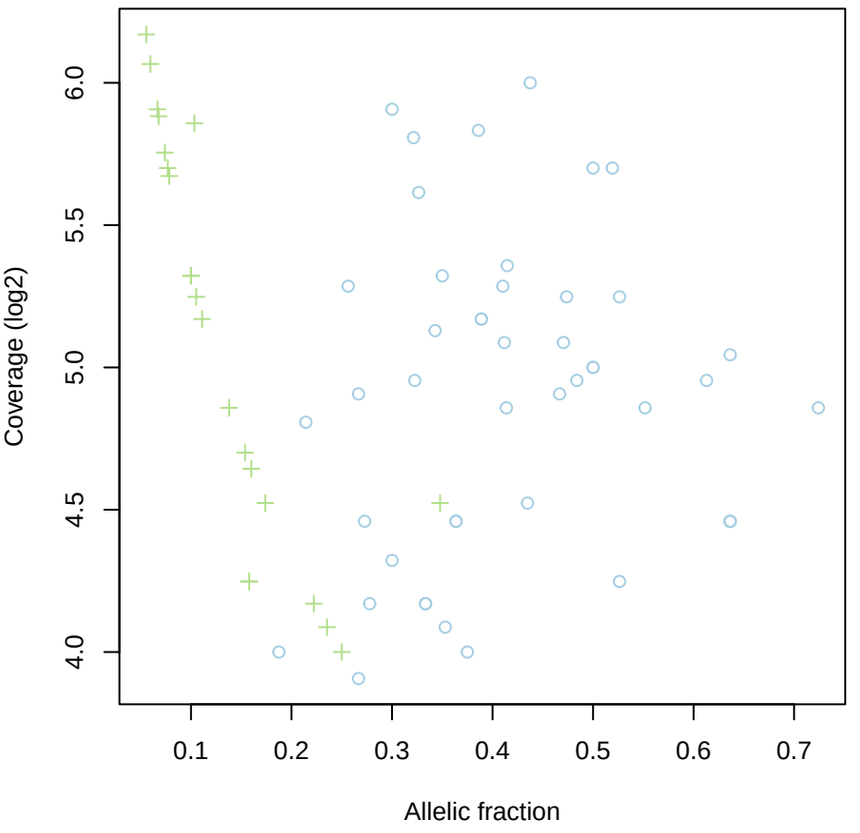

Purity: 0.62 Tumor ploidy: 5.999
0
4
5
6
7
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Fraction Genome
−4
−3
−2
−1
0
1
2
log2 ratio

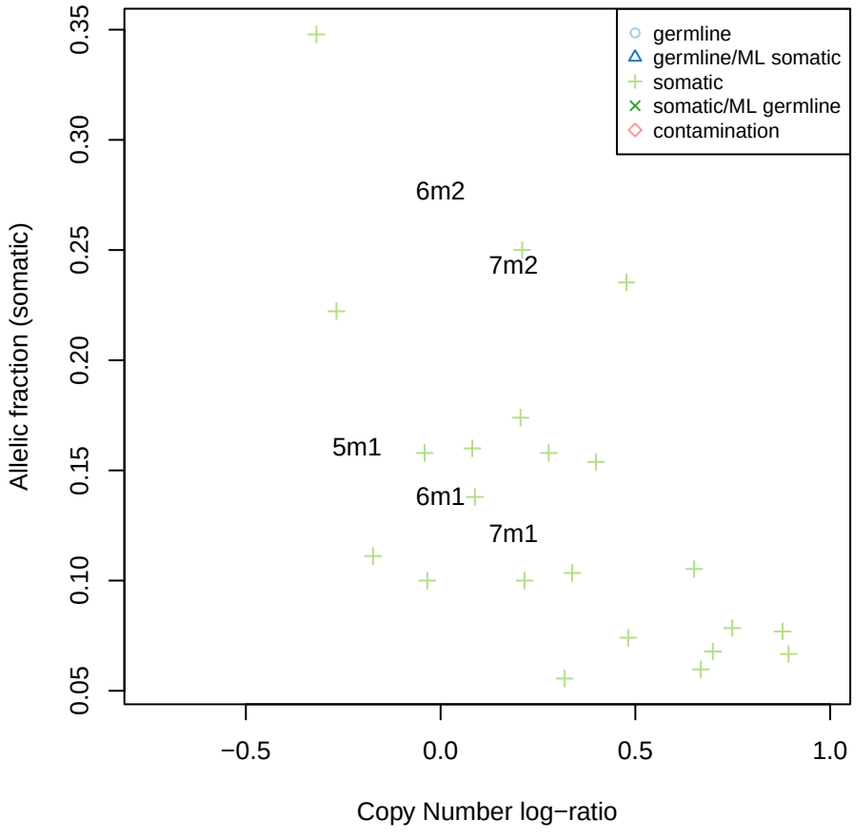

Purity: 0.62 Tumor ploidy: 5.999 SNV log−likelihood: −89.81 GoF: 87.3% Mean coverage: 441;34
2 3 4 6 7 8 9 11 12 13 14 15 16 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 10 20 30 40
SNV Index

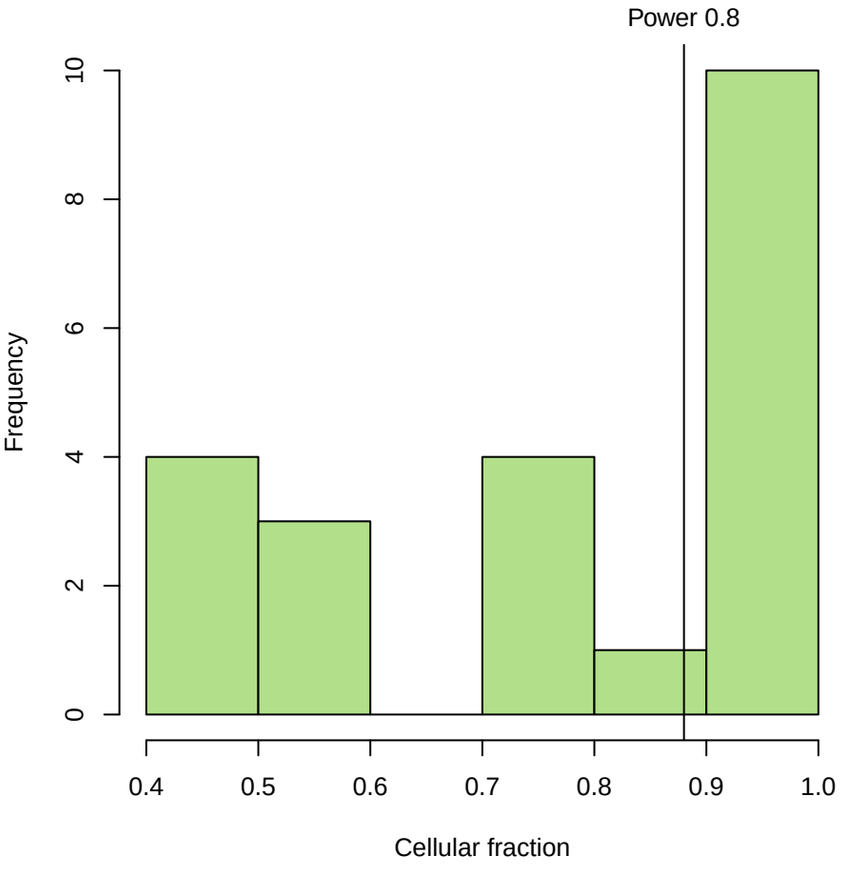

SCNA−fit log−likelihood: −20158.95
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5 6 7
0 10 20 30 40
SNV Index

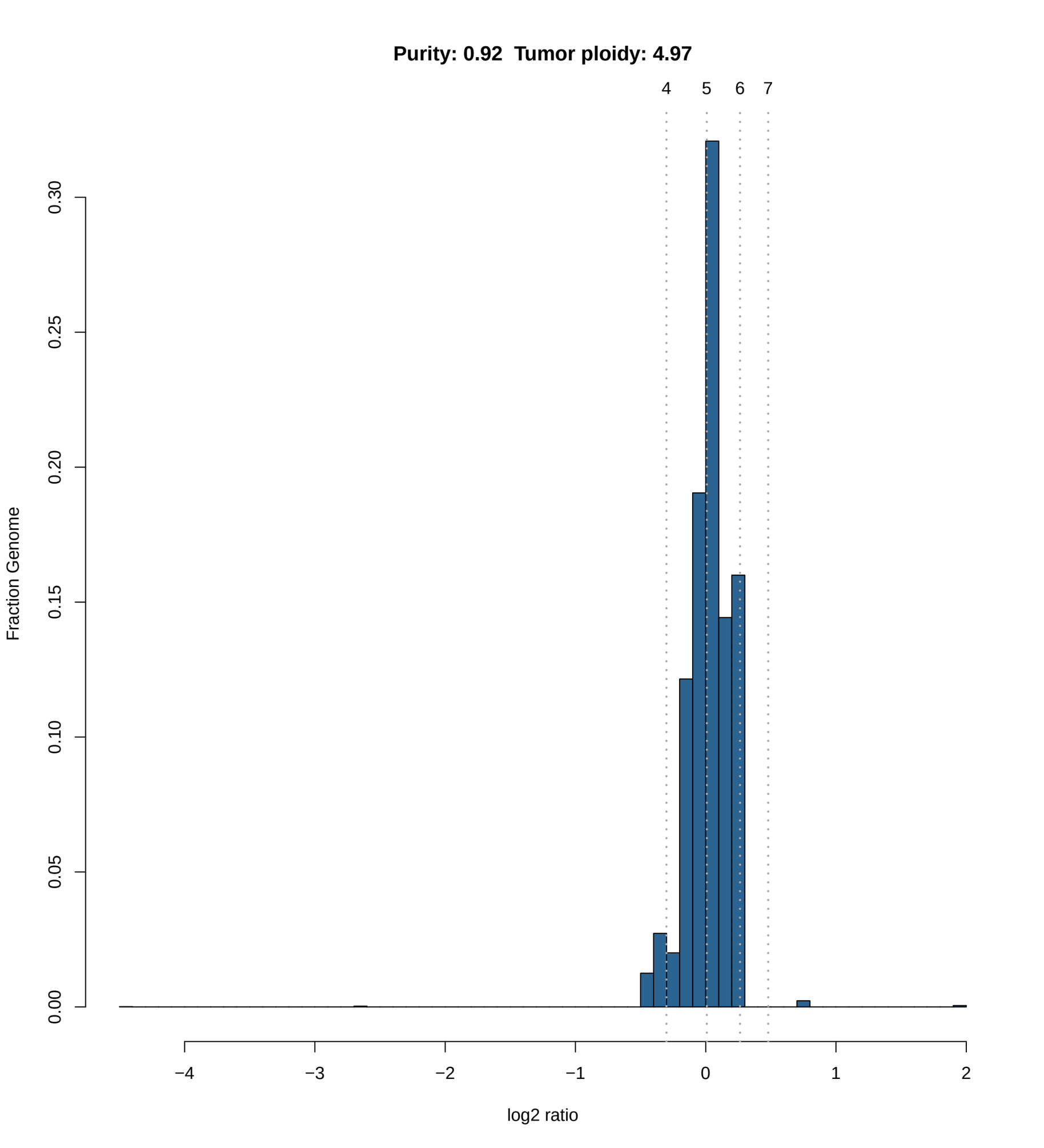

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 10 20 30 40
SNV Index

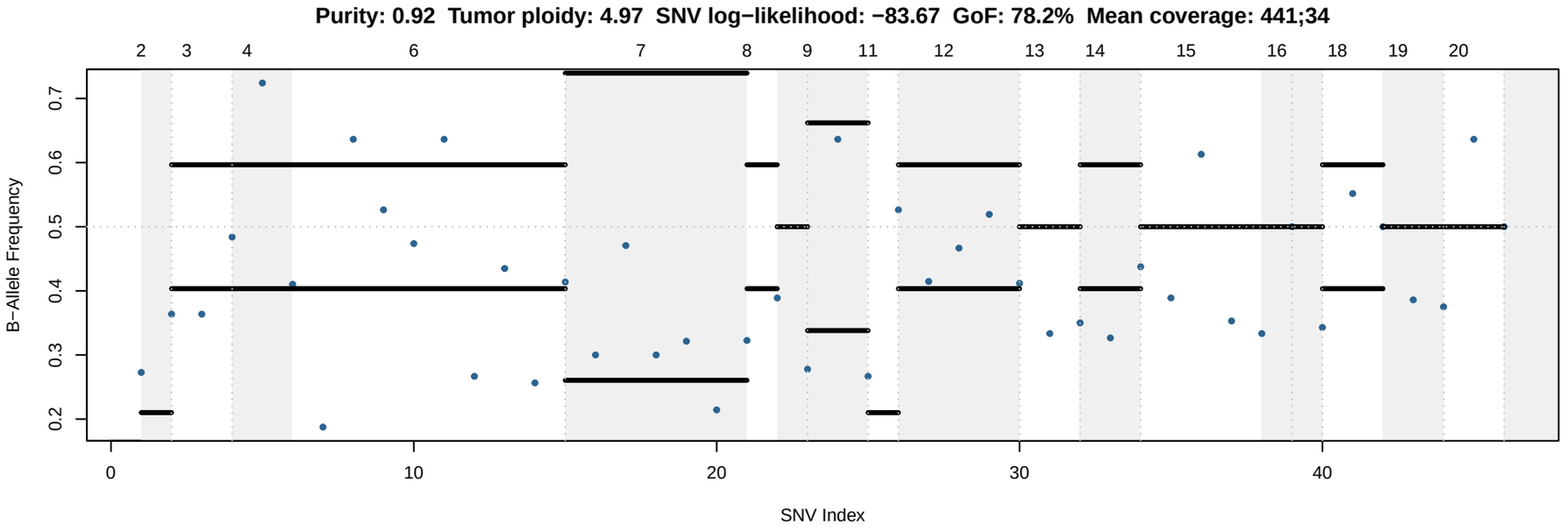

Allelic fraction (germline)
Copy Number log−ratio
7m5
6m4
5m3
7m4
4m2
6m3
7m3
5m2
6m2
7m2
6m1

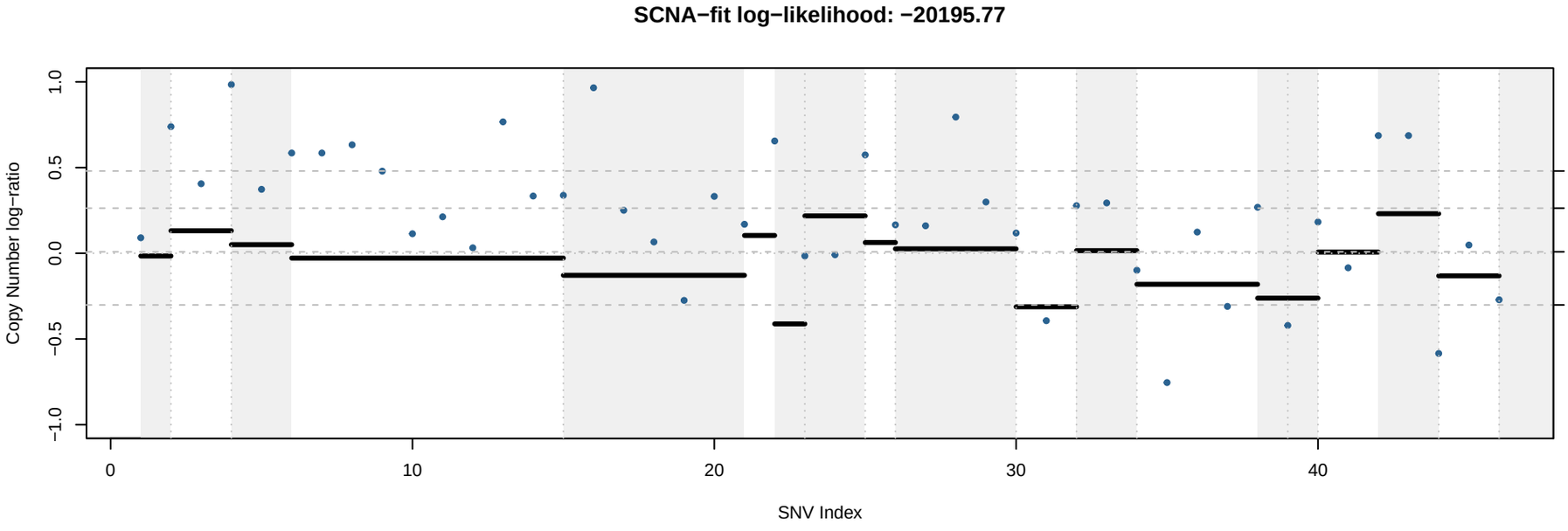

Coverage (log2)
Allelic fraction

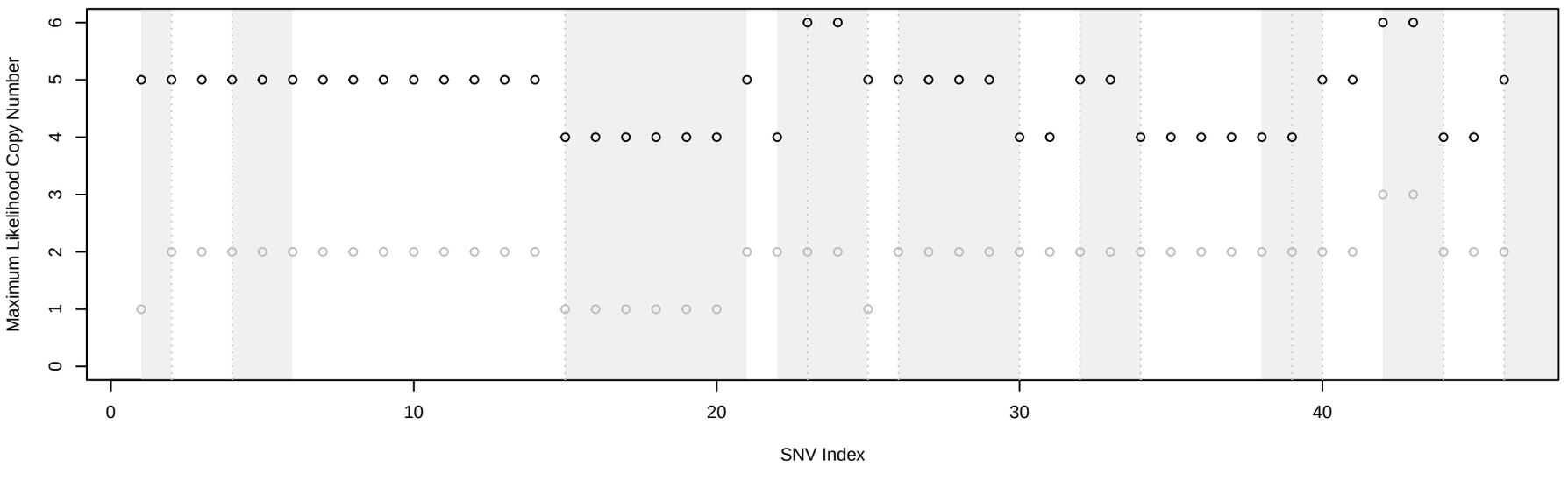

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m2
7m2
5m1
6m1
7m1

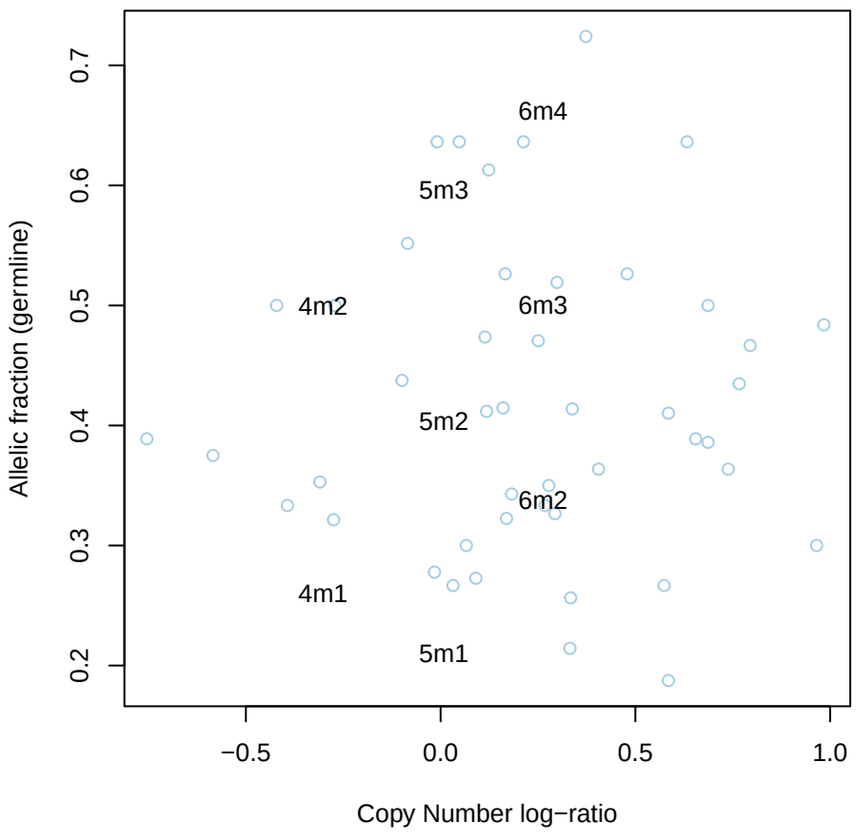

Power 0.8
Frequency
Cellular fraction

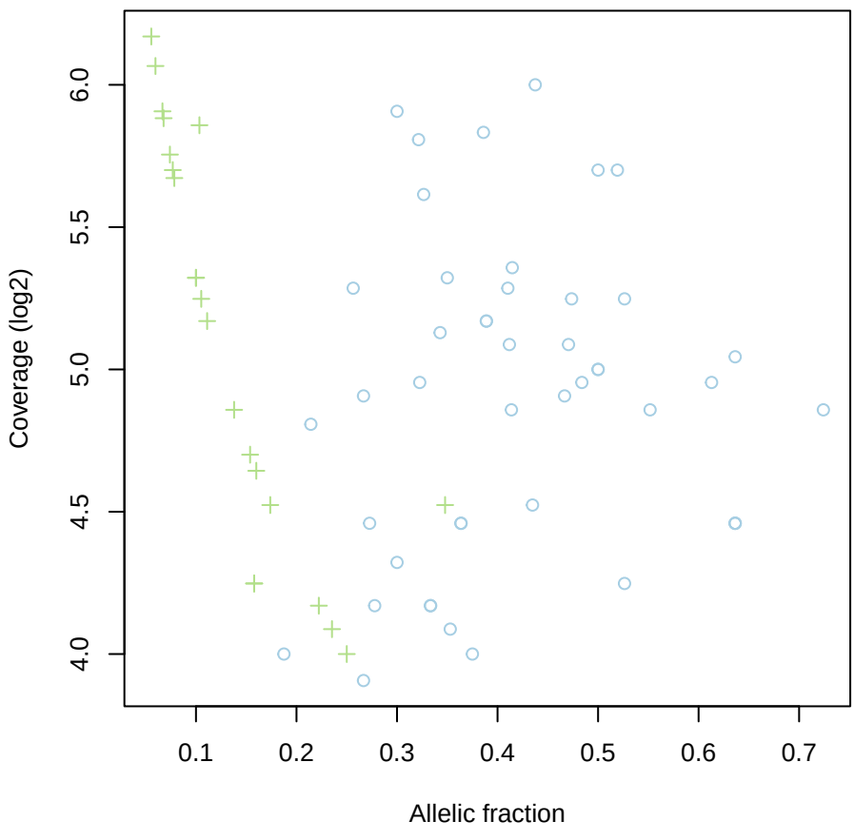

Purity: 0.92 Tumor ploidy: 4.97
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−4
−3
−2
−1
0
1
2
log2 ratio

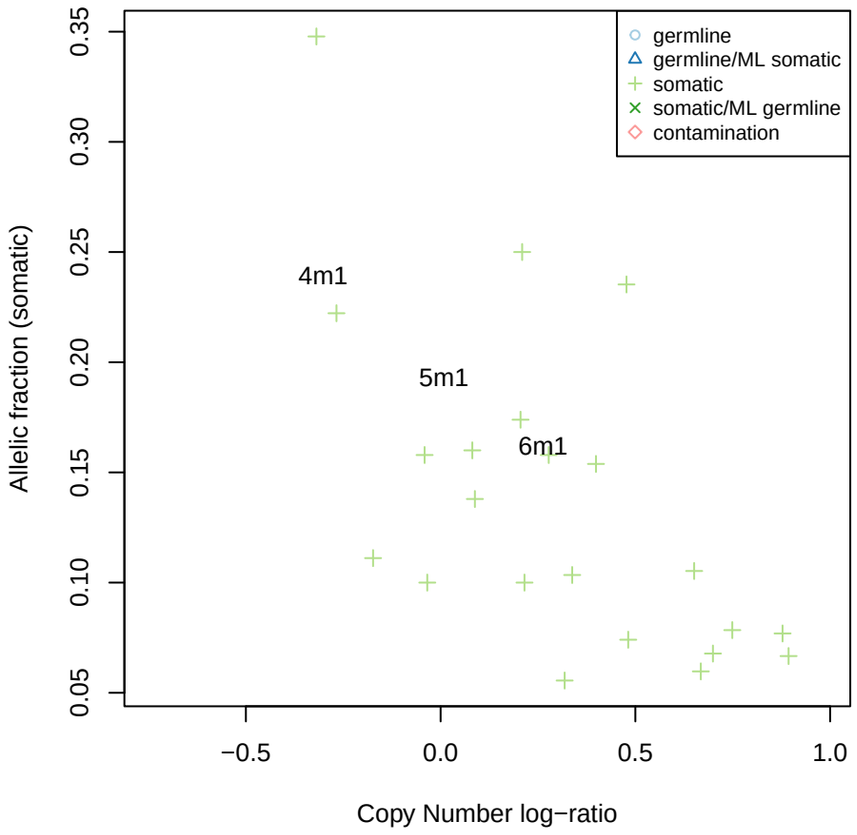

Purity: 0.92 Tumor ploidy: 4.97 SNV log−likelihood: −83.67 GoF: 78.2% Mean coverage: 441;34
2 3 4 6 7 8 9 11 12 13 14 15 16 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 10 20 30 40
SNV Index

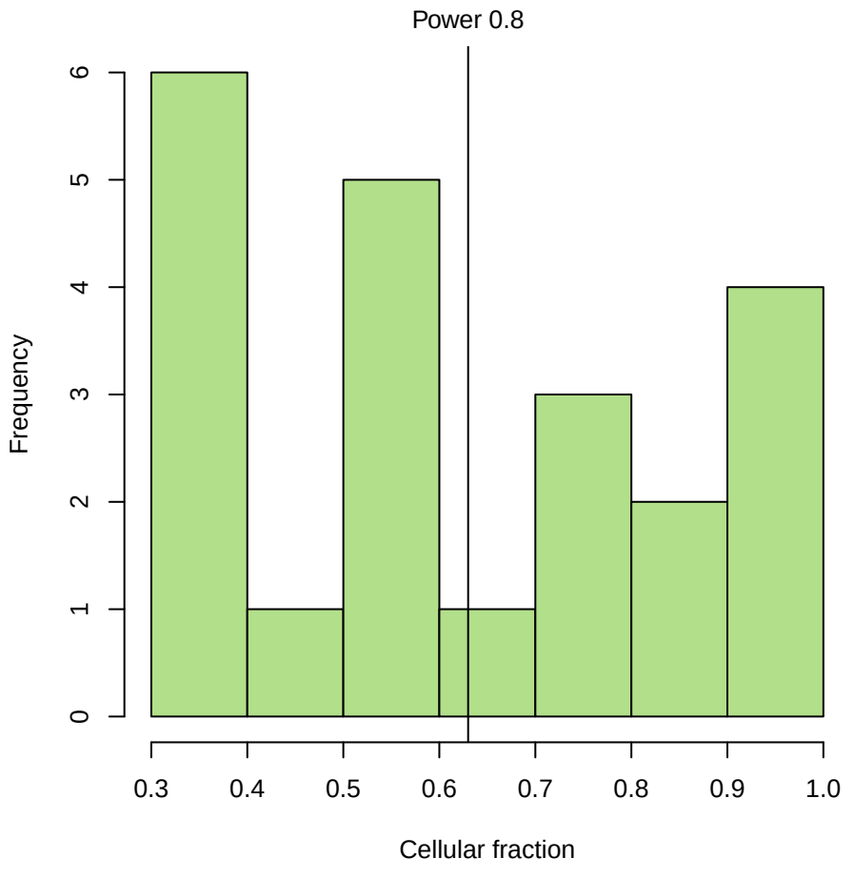

SCNA−fit log−likelihood: −20195.77
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5 6 7
0 10 20 30 40
SNV Index

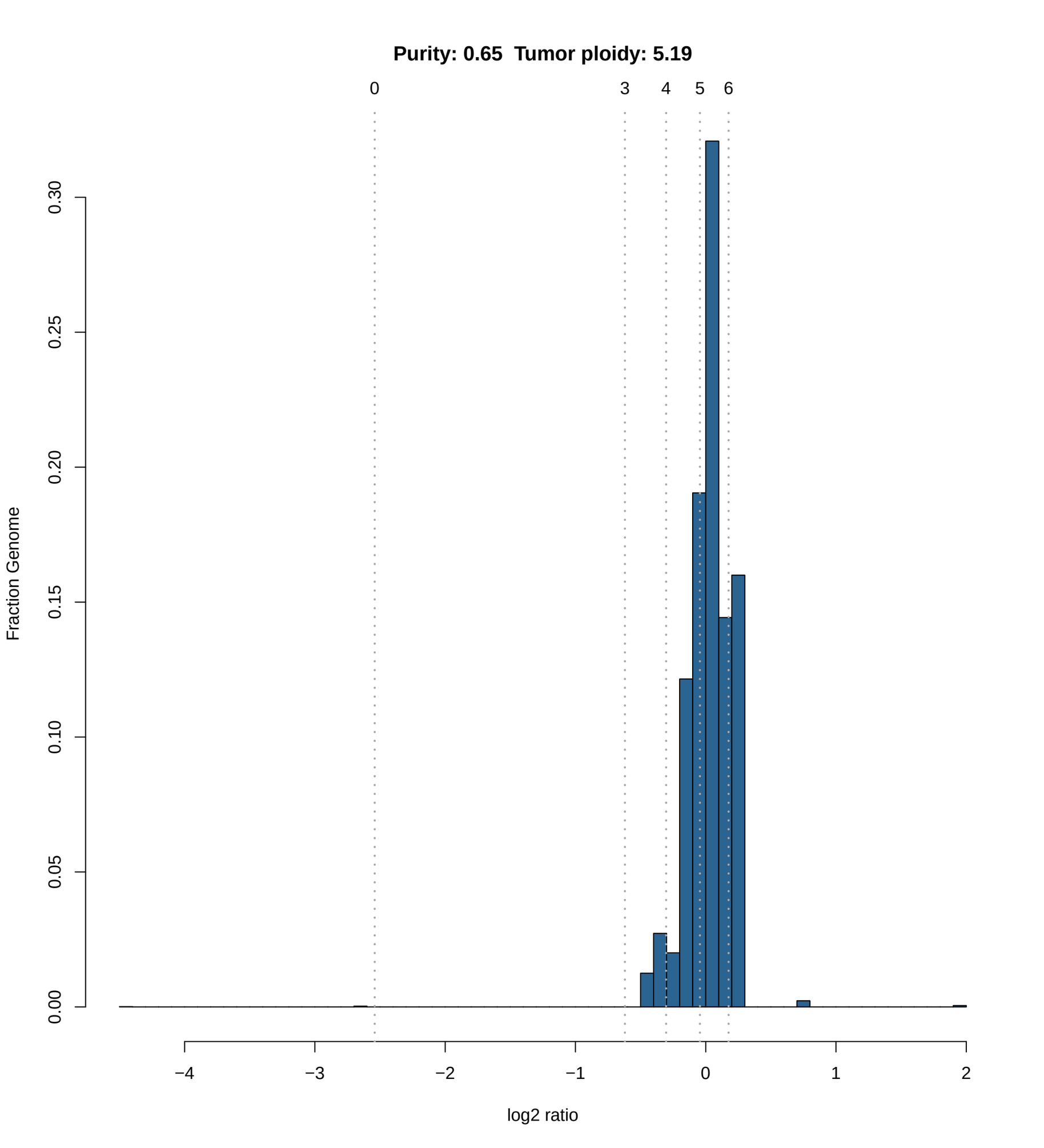

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 10 20 30 40
SNV Index

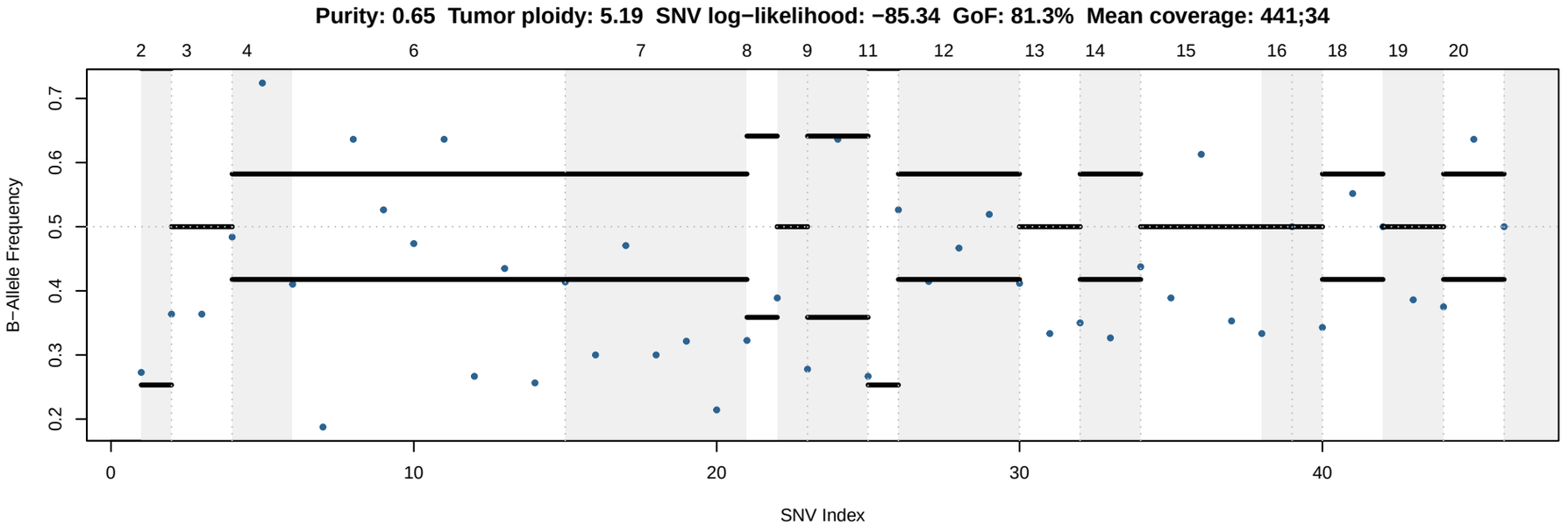

Allelic fraction (germline)
Copy Number log−ratio
6m4
5m3
4m2
6m3
5m2
6m2
4m1
5m1

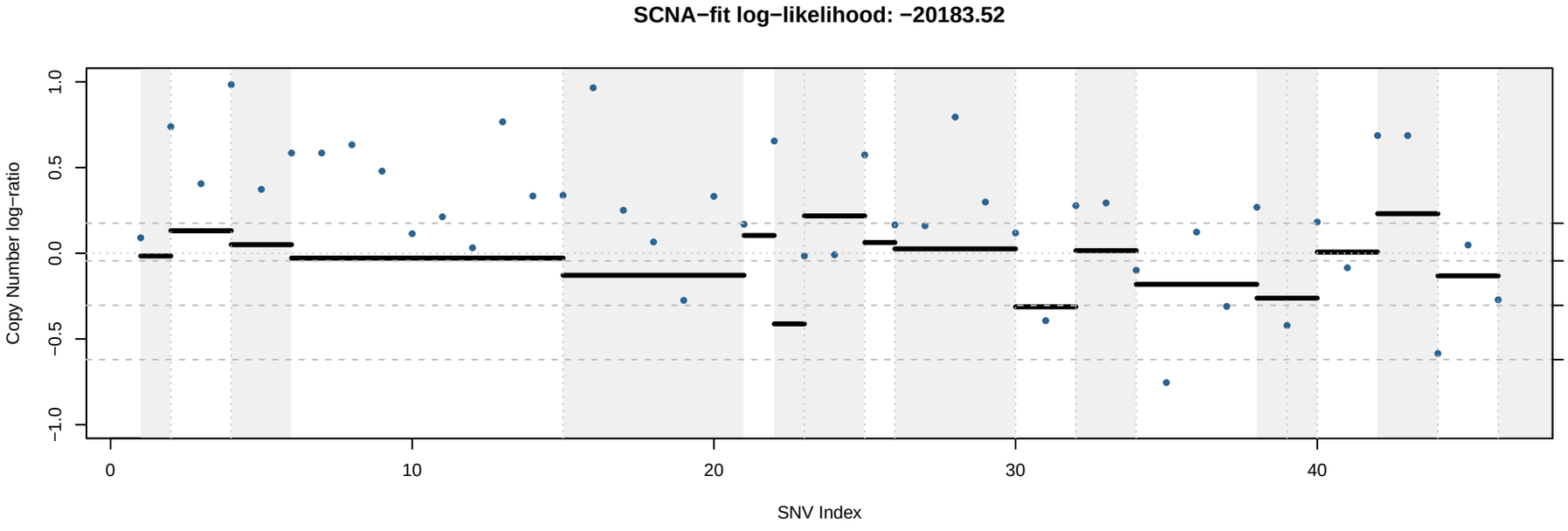

Coverage (log2)
Allelic fraction

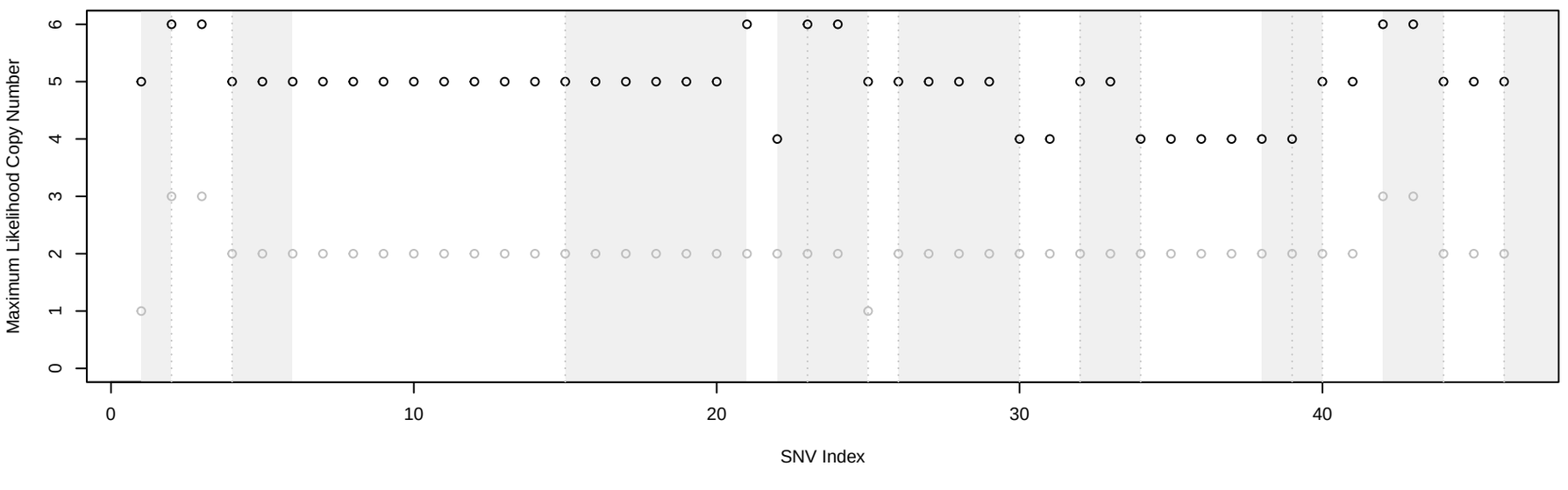

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1

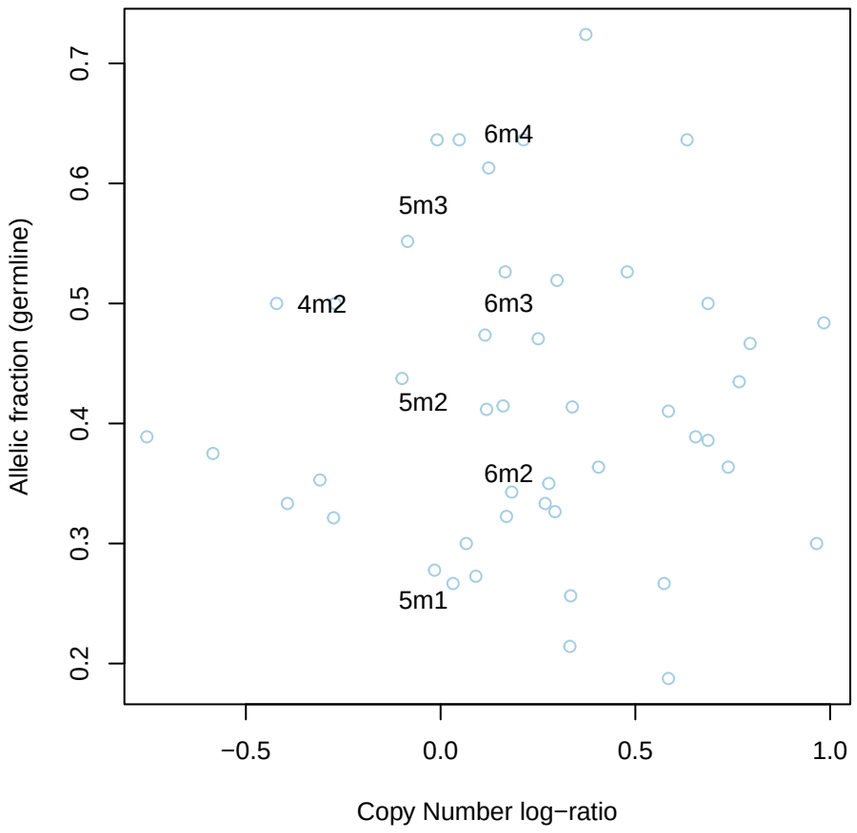

Power 0.8
Frequency
Cellular fraction

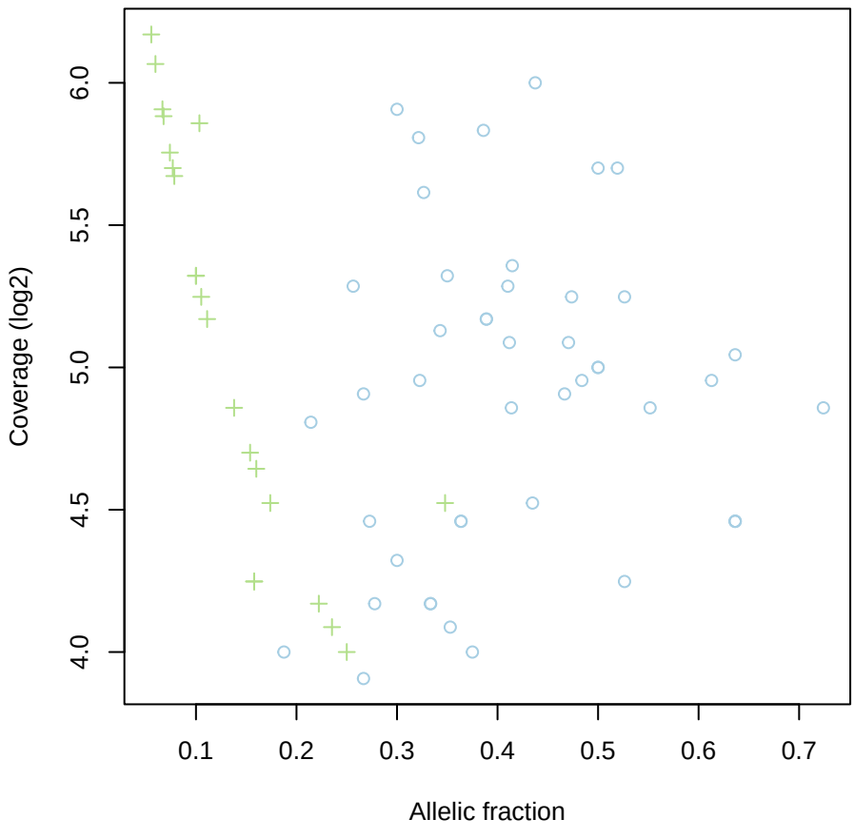

Purity: 0.65 Tumor ploidy: 5.19
0
3
4
5
6
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−4
−3
−2
−1
0
1
2
log2 ratio

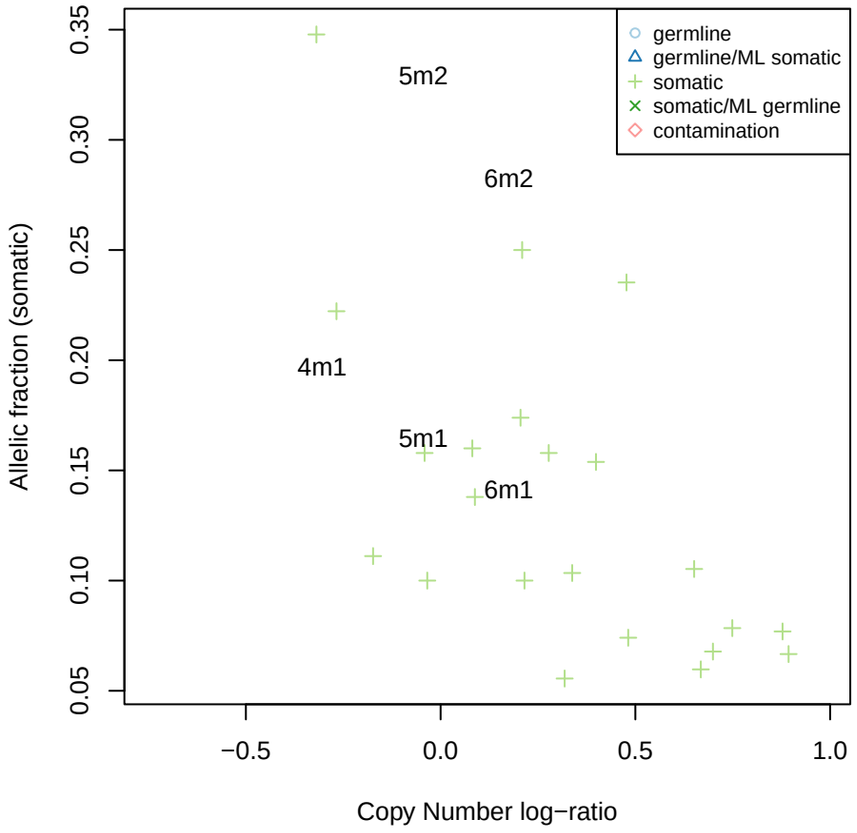

Purity: 0.65 Tumor ploidy: 5.19 SNV log−likelihood: −85.34 GoF: 81.3% Mean coverage: 441;34
2 3 4 6 7 8 9 11 12 13 14 15 16 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 10 20 30 40
SNV Index

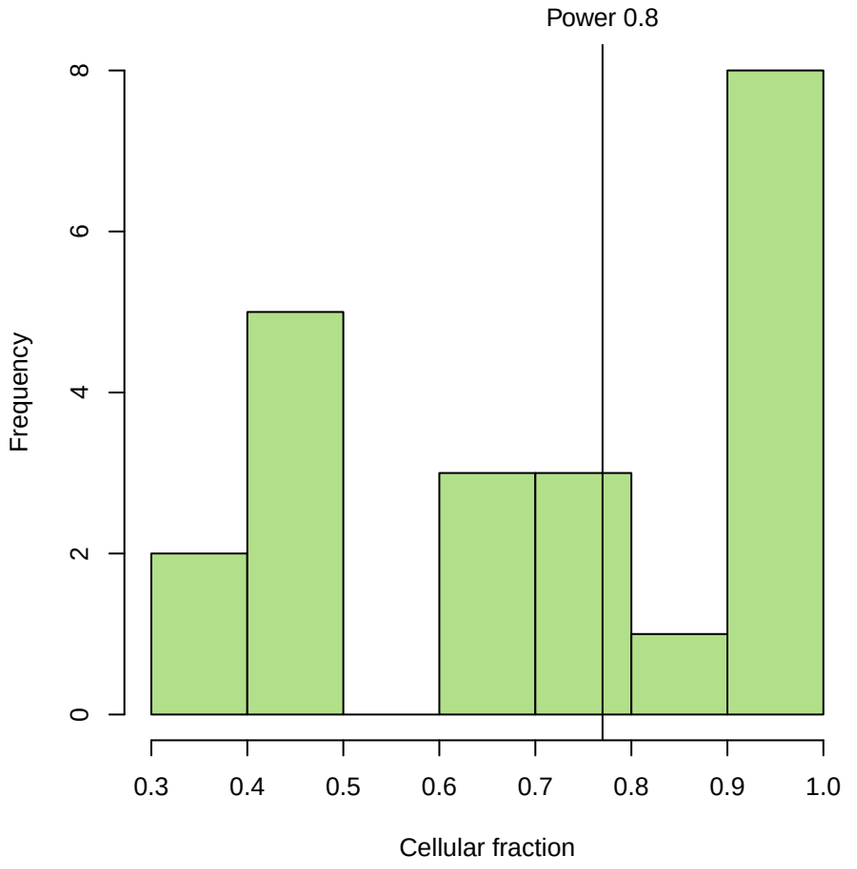

SCNA−fit log−likelihood: −20183.52
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6
0 10 20 30 40
SNV Index

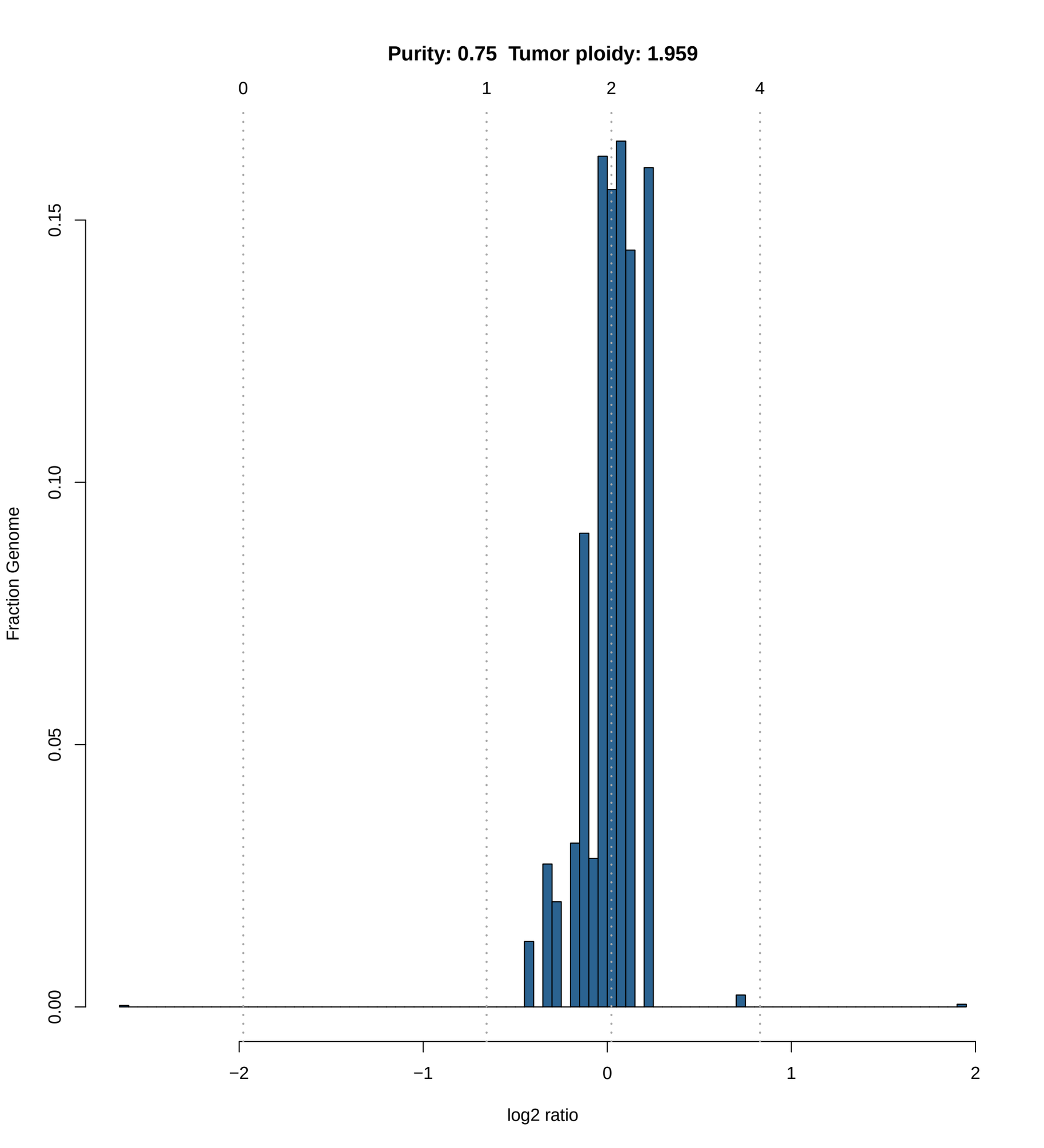

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 10 20 30 40
SNV Index

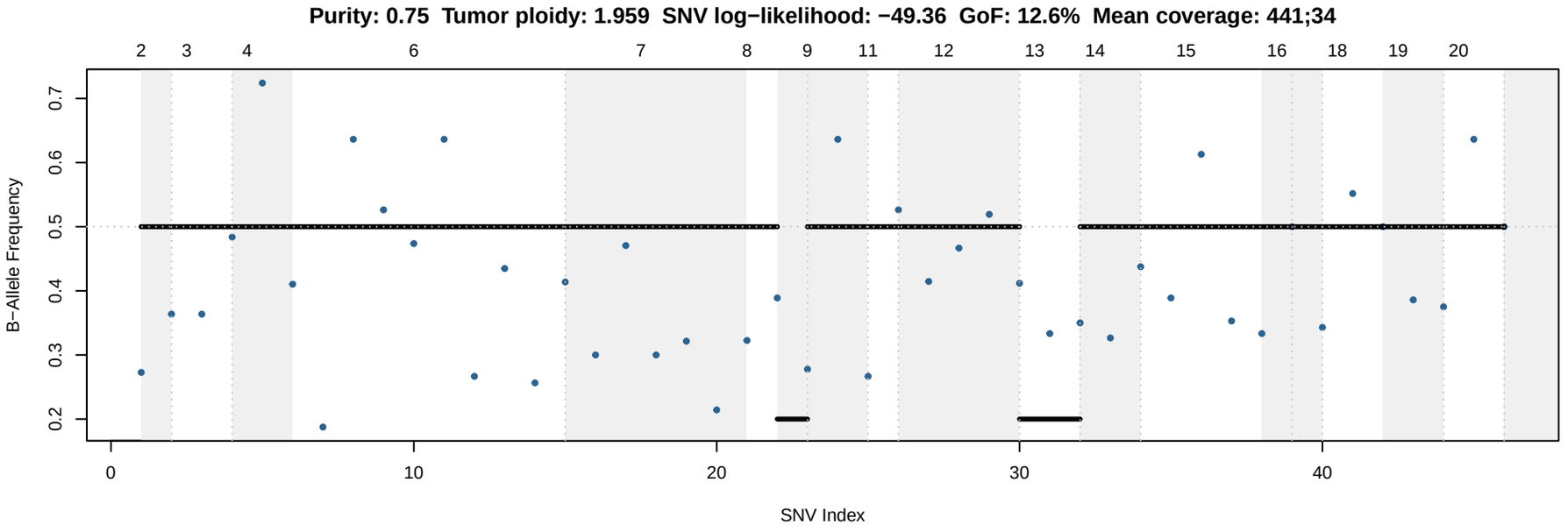

Allelic fraction (germline)
Copy Number log−ratio
6m4
5m3
4m2
6m3
5m2
6m2
5m1

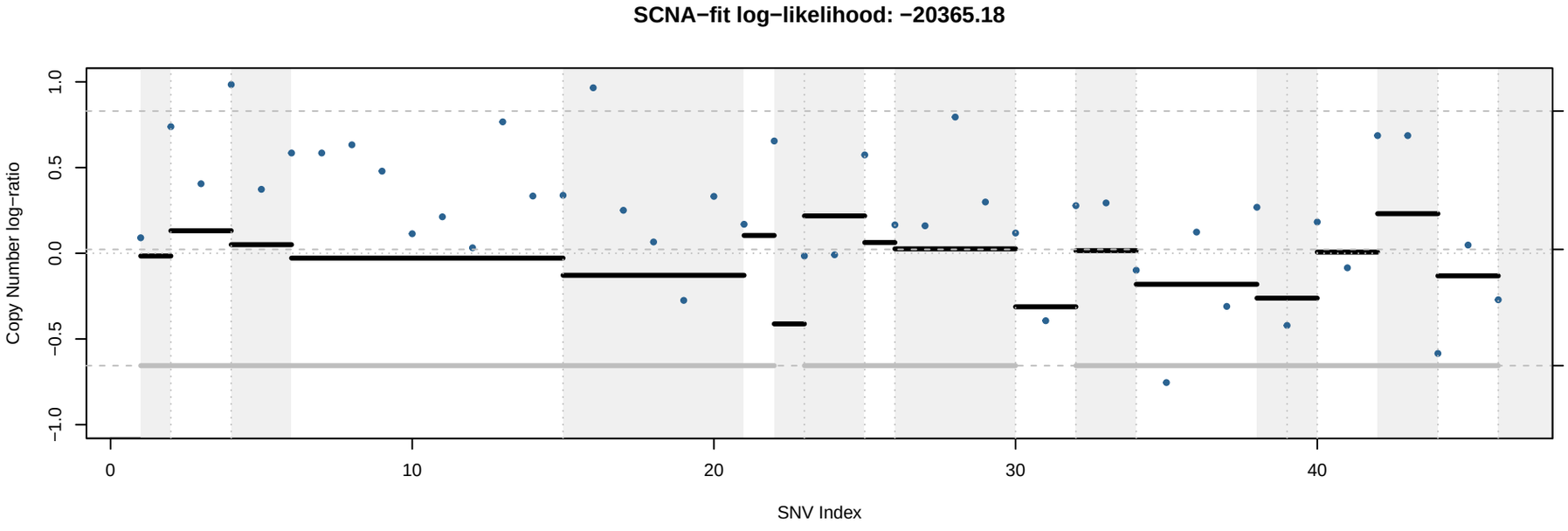

Coverage (log2)
Allelic fraction

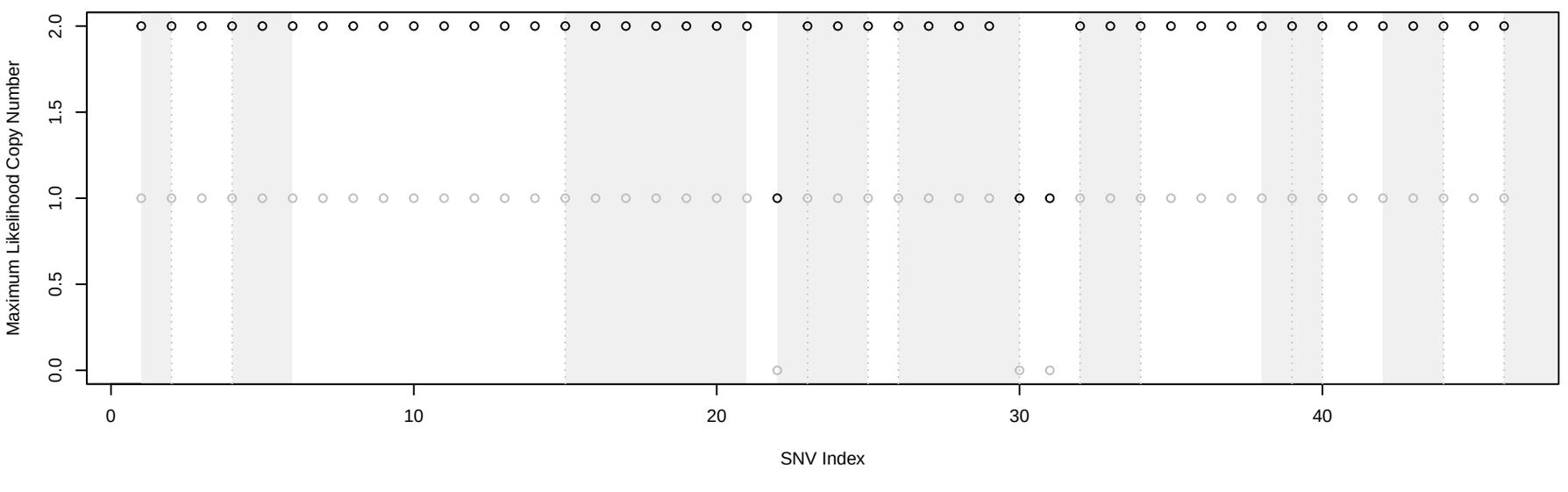

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m2
6m2
4m1
5m1
6m1

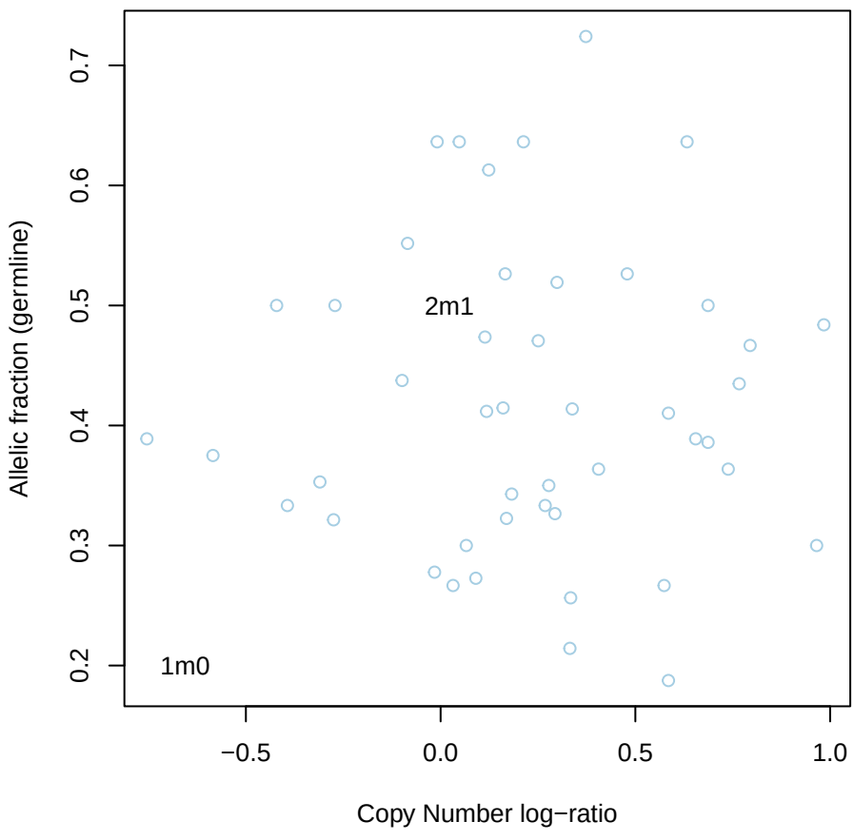

Power 0.8
Frequency
Cellular fraction

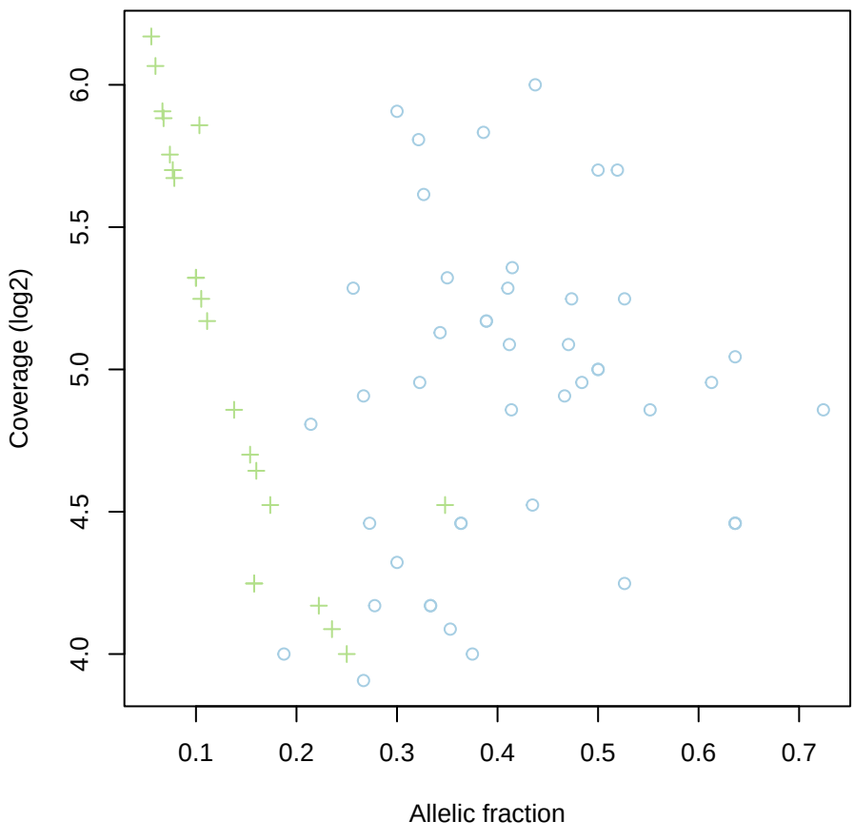

Purity: 0.75 Tumor ploidy: 1.959
0
1
2
4
0.15
0.10
0.05
0.00
Fraction Genome
−2
−1
0
1
2
log2 ratio

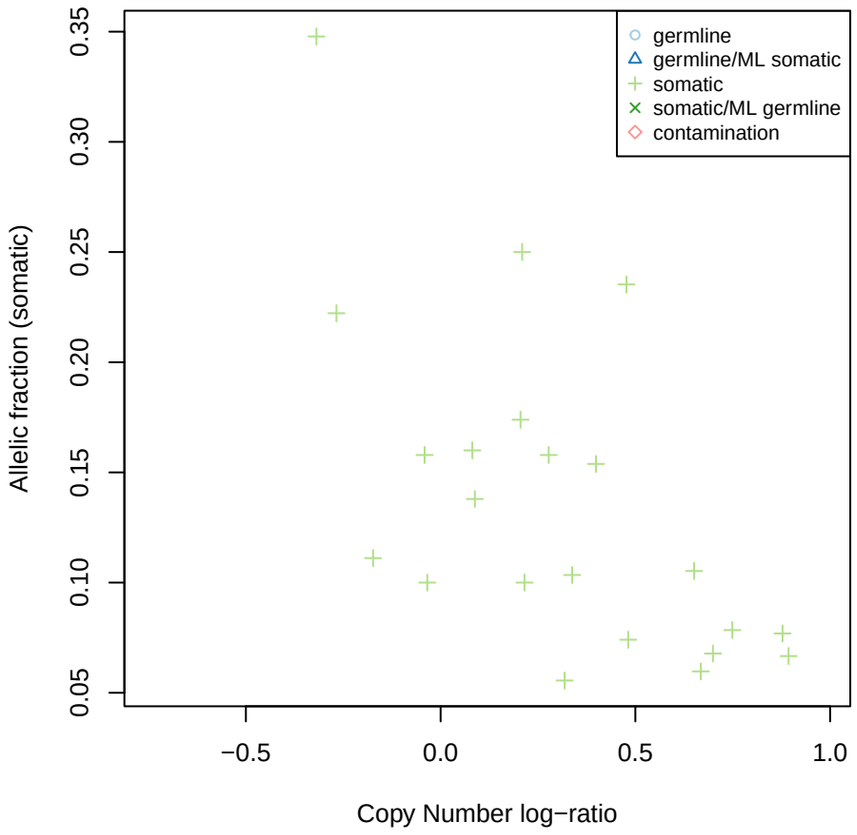

Purity: 0.75 Tumor ploidy: 1.959 SNV log−likelihood: −49.36 GoF: 12.6% Mean coverage: 441;34
2 3 4 6 7 8 9 11 12 13 14 15 16 18 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 10 20 30 40
SNV Index

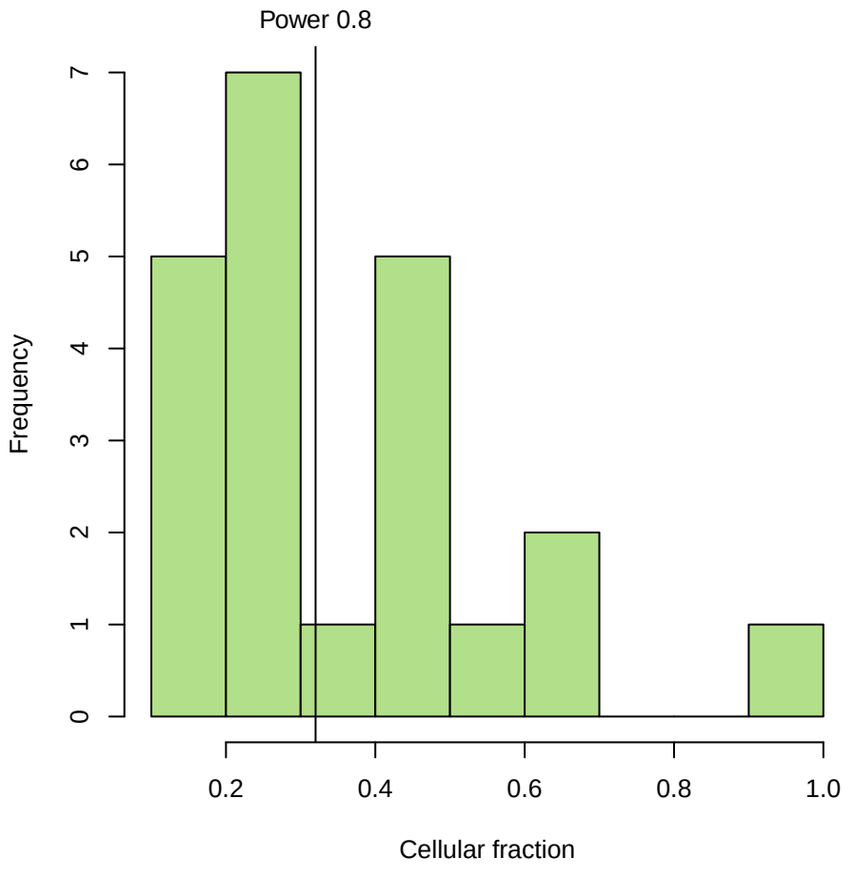

SCNA−fit log−likelihood: −20365.18
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 4
0 10 20 30 40
SNV Index


Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 10 20 30 40
SNV Index


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


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