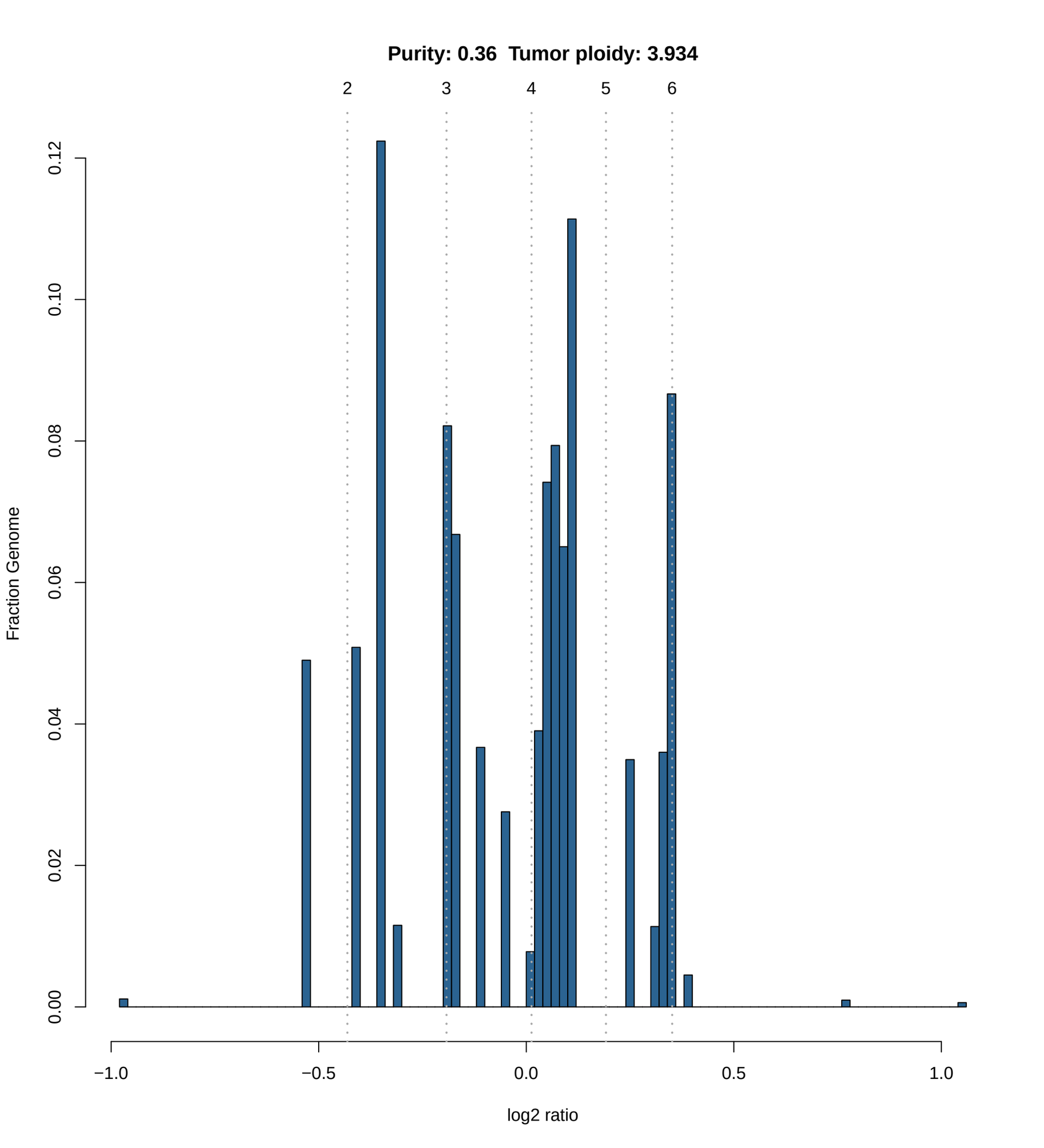
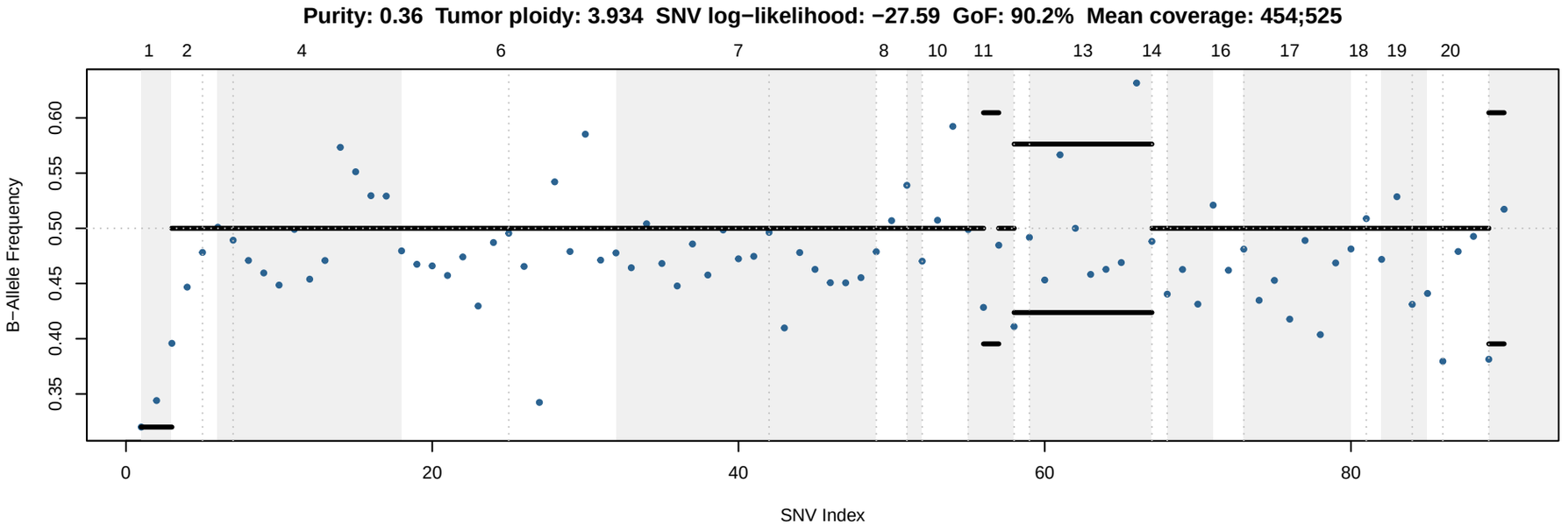
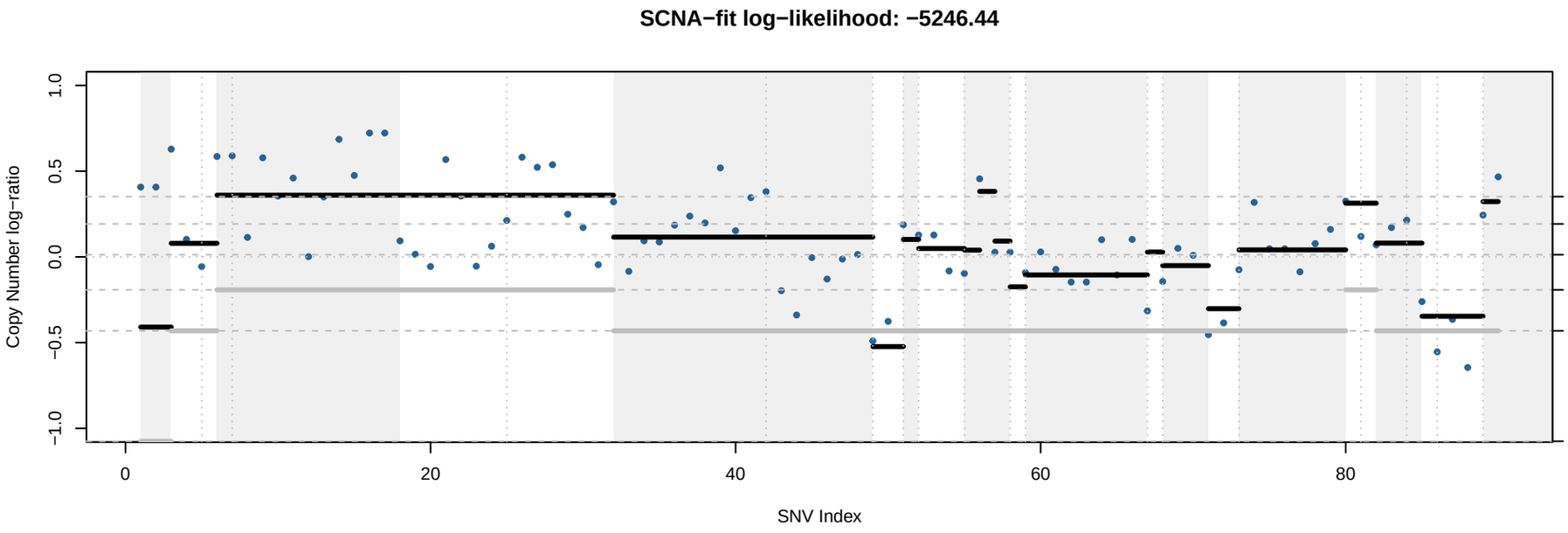
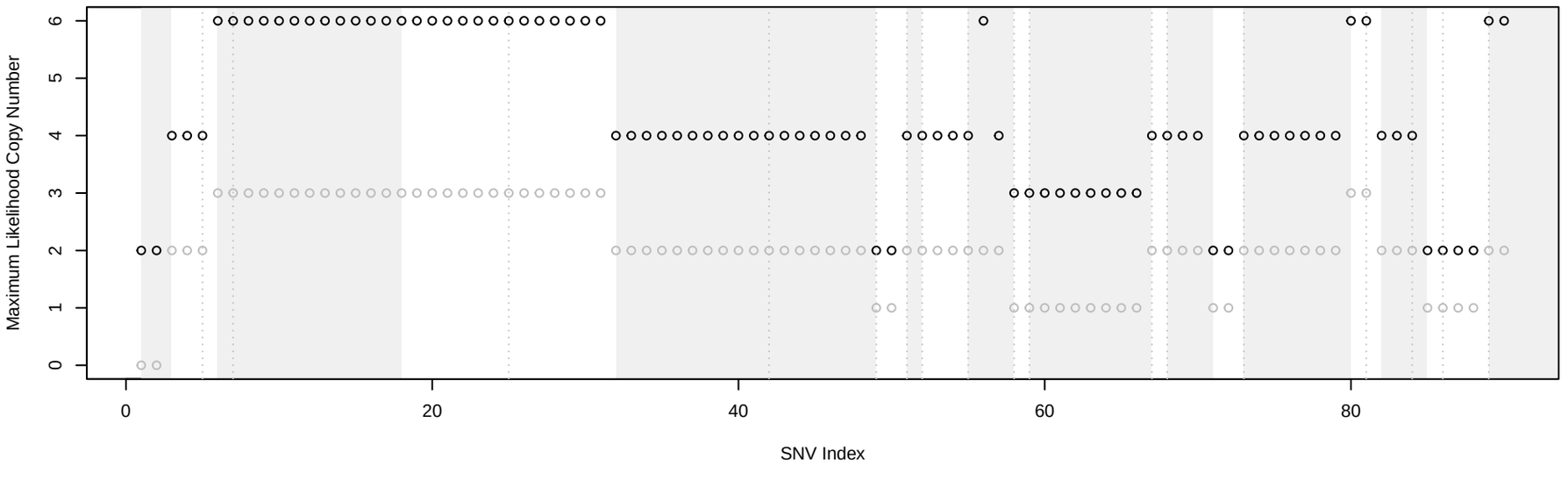
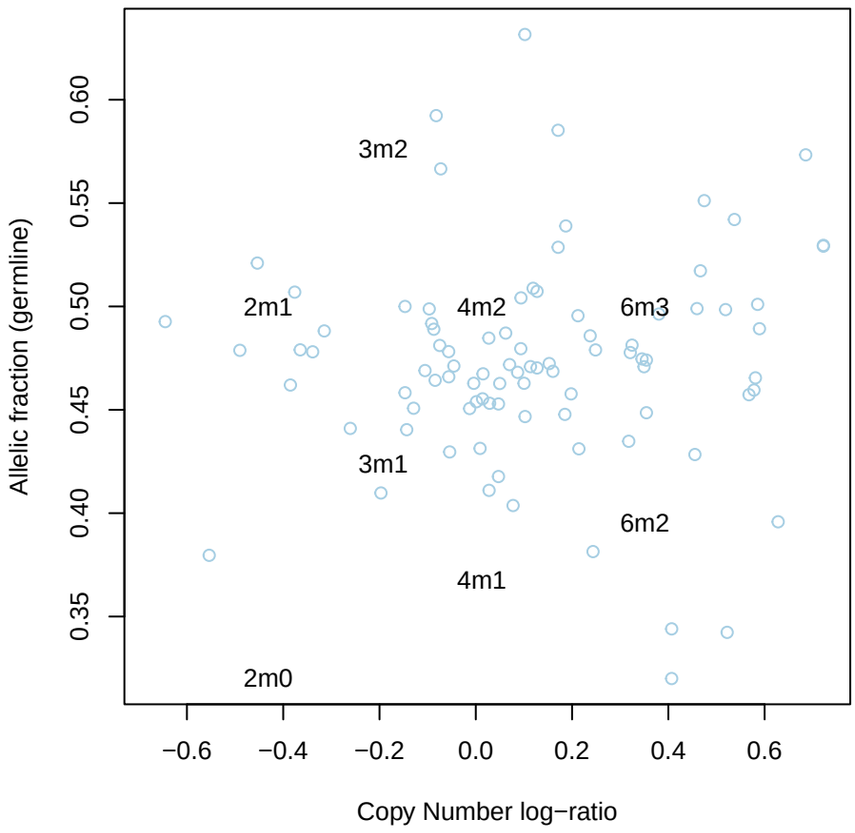
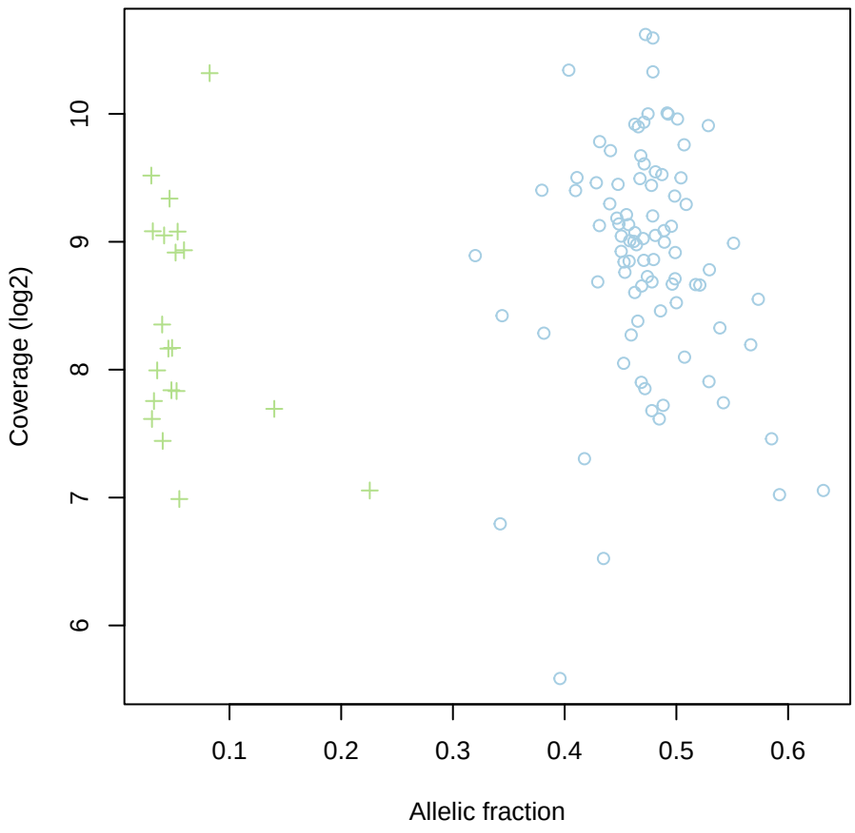

Purity: 0.36 Tumor ploidy: 3.934
2
3
4
5
6
0.12
0.10
0.08
0.06
0.04
0.02
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

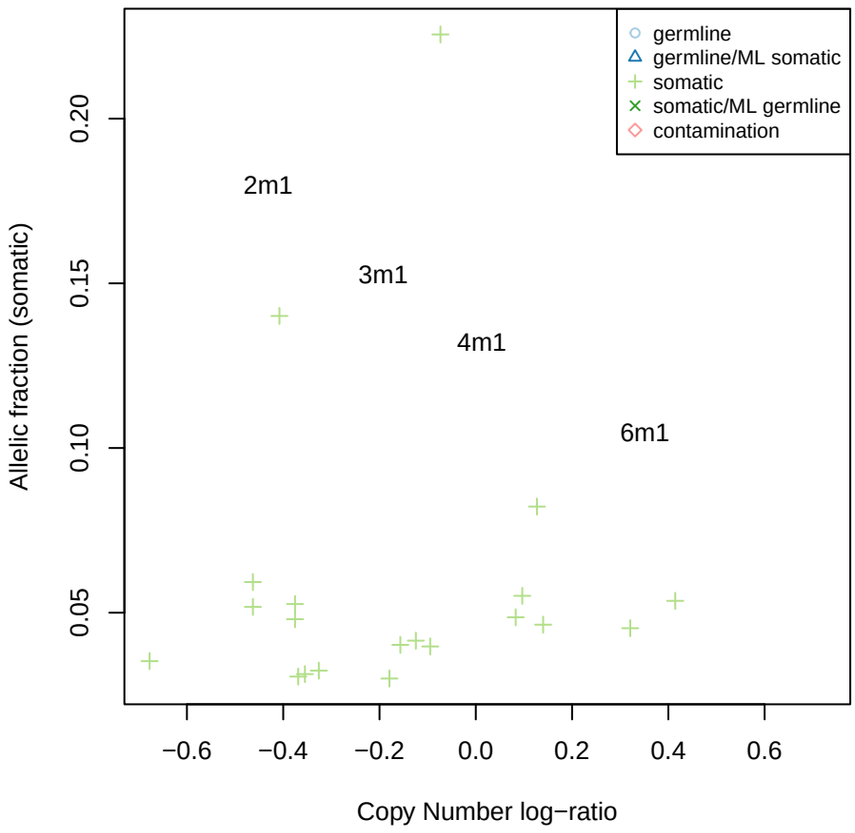

Purity: 0.36 Tumor ploidy: 3.934 SNV log−likelihood: −27.59 GoF: 90.2% Mean coverage: 454;525
1 2 4 6 7 8 10 11 13 14 16 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

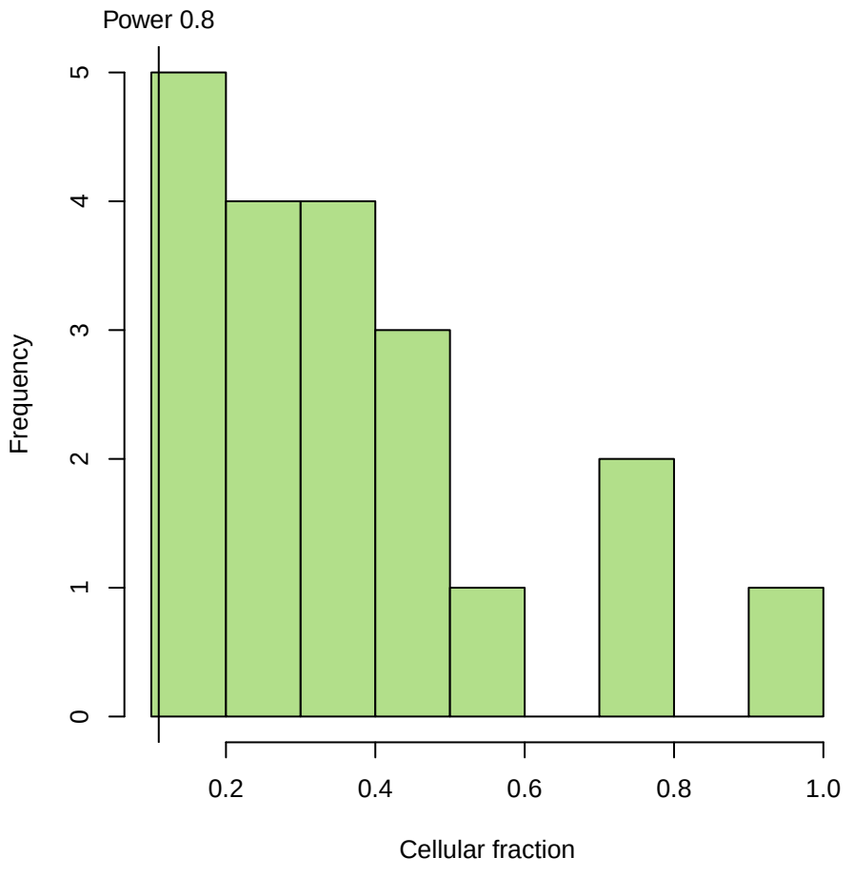

SCNA−fit log−likelihood: −5246.44
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 3 4 5 6
0 20 40 60 80
SNV Index

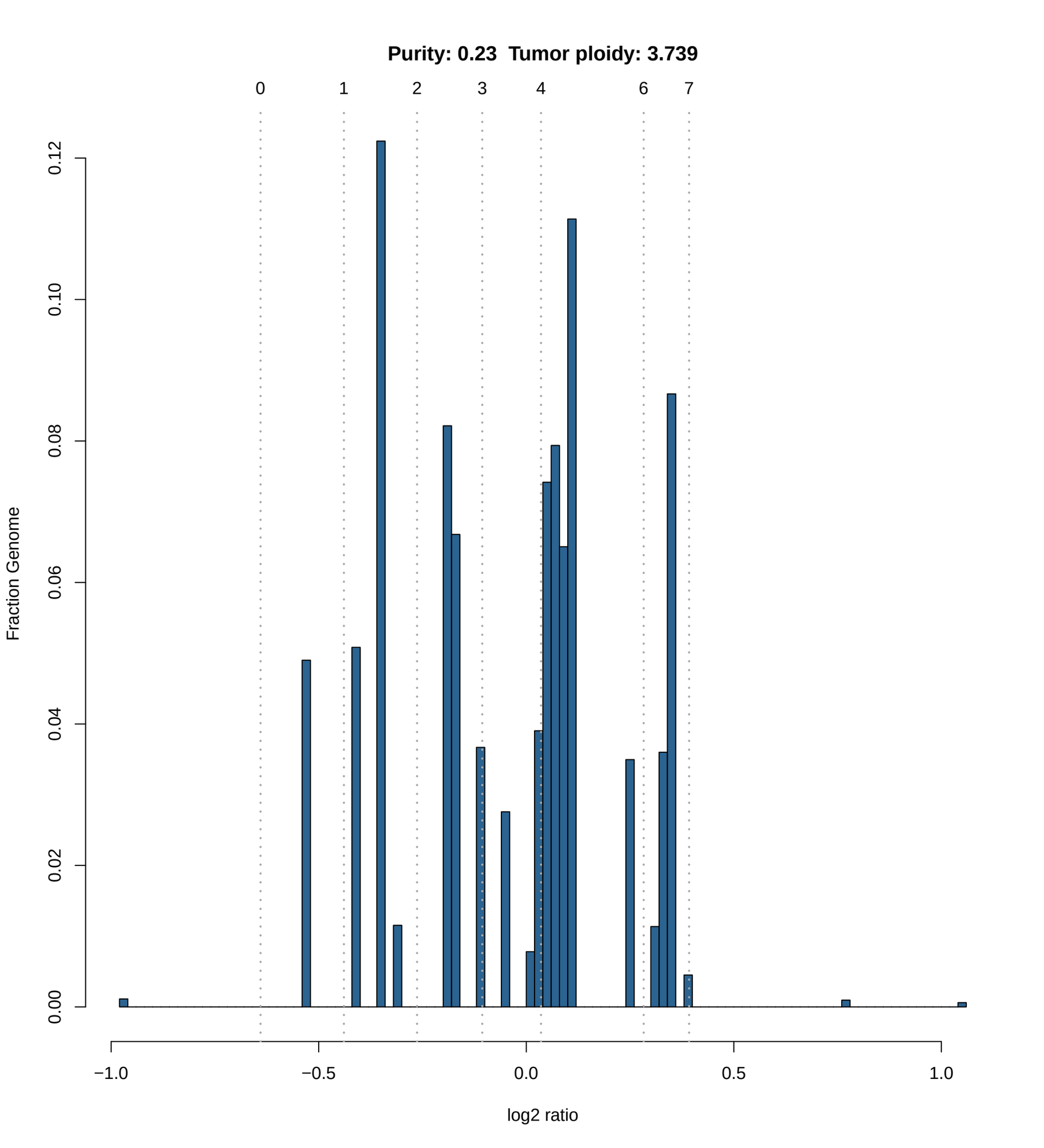

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80
SNV Index

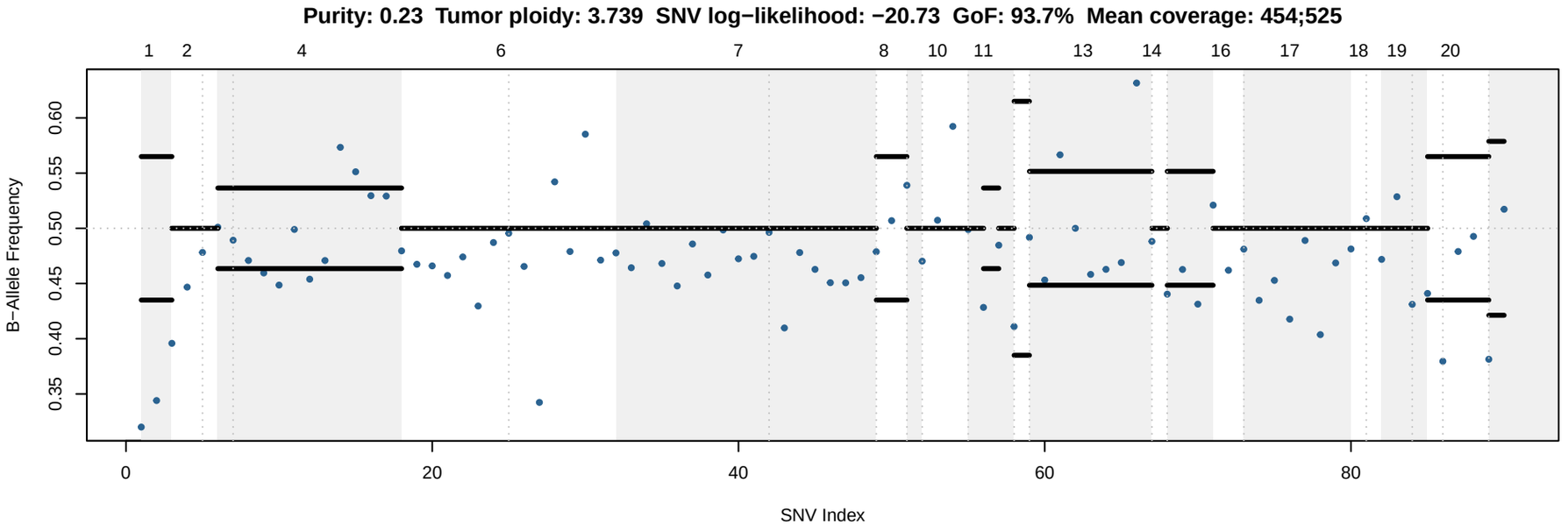

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
3m2
2m1
4m2
6m3
3m1
6m2
4m1
2m0
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

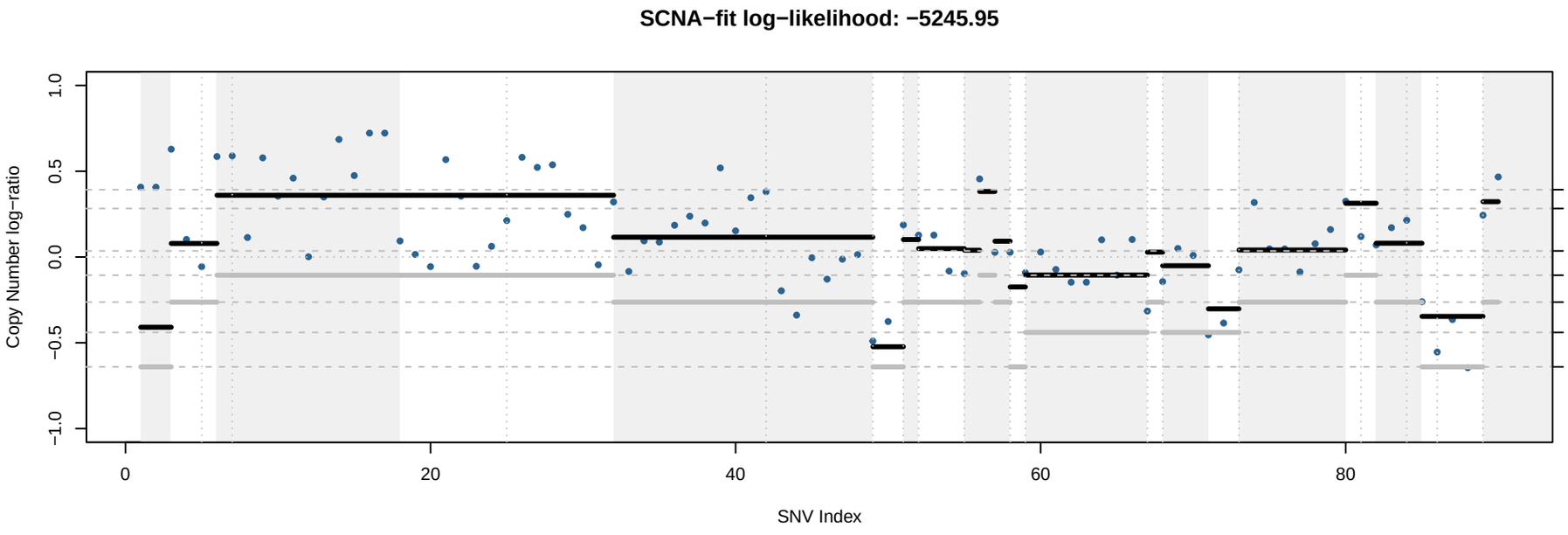

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

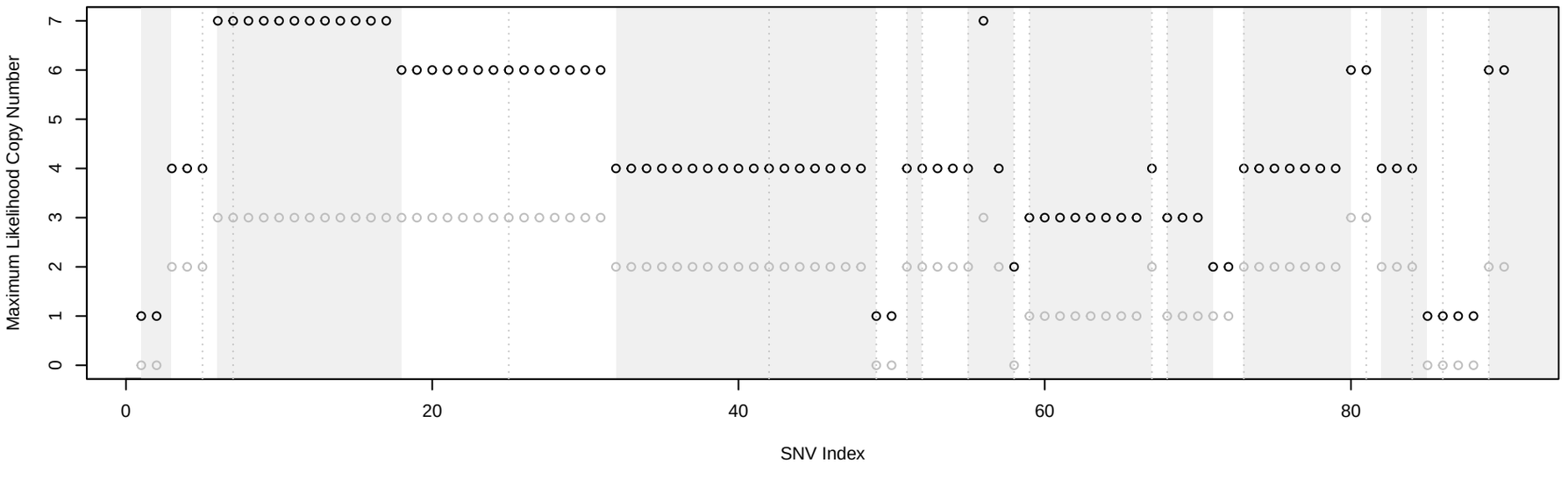

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
2m1
3m1
4m1
6m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

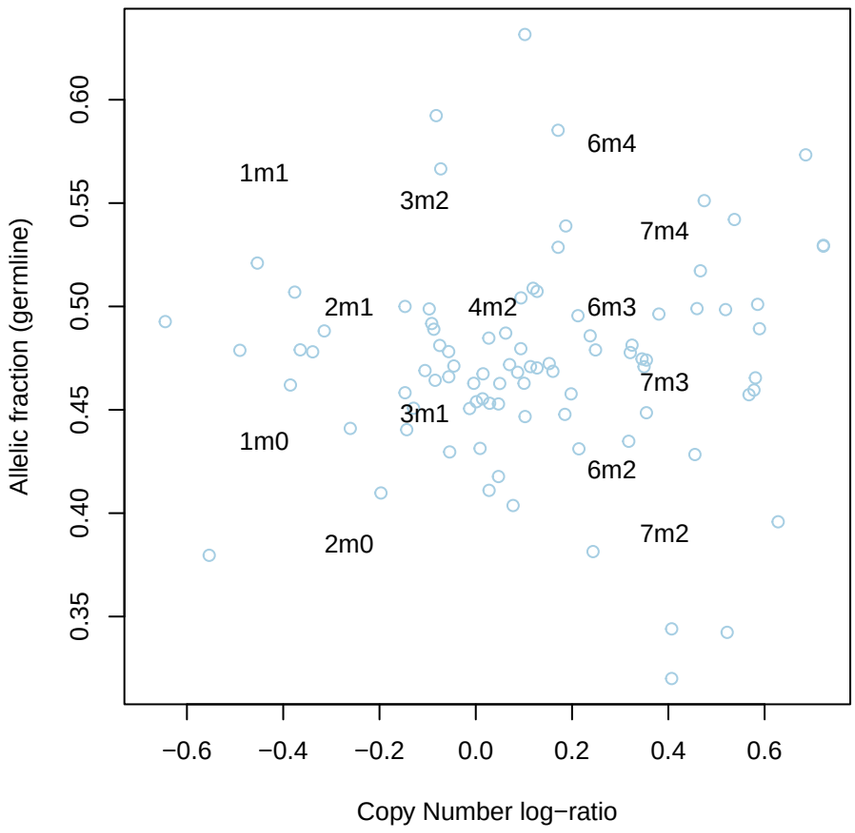

Power 0.8
Frequency
0
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0
Cellular fraction

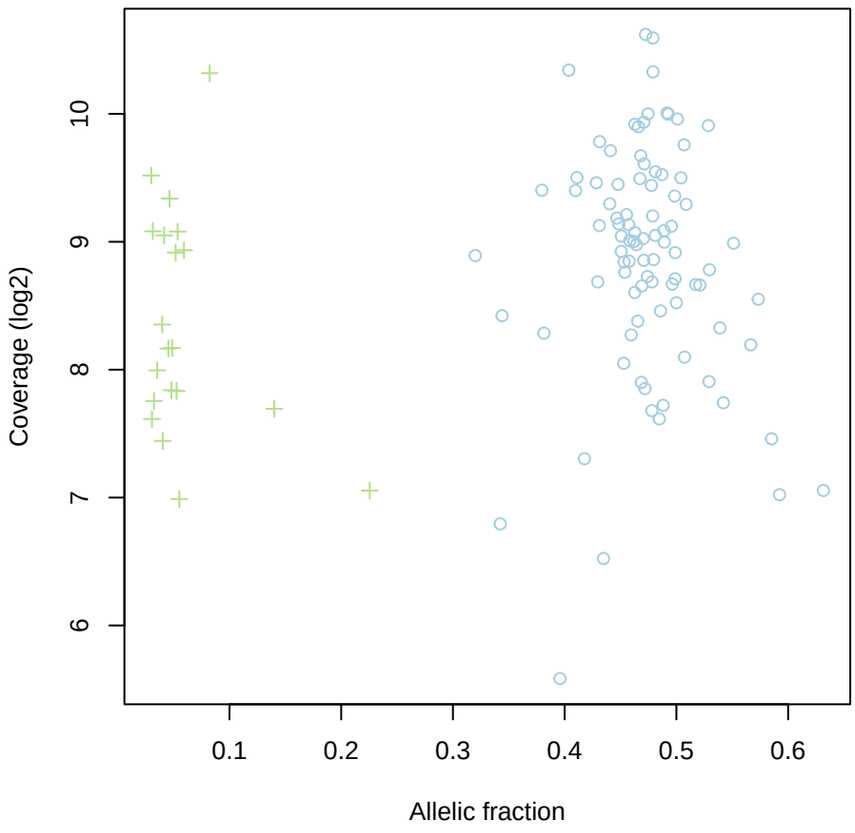

Purity: 0.23 Tumor ploidy: 3.739
0
1
2
3
4
6
7
0.12
0.10
0.08
0.06
0.04
0.02
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

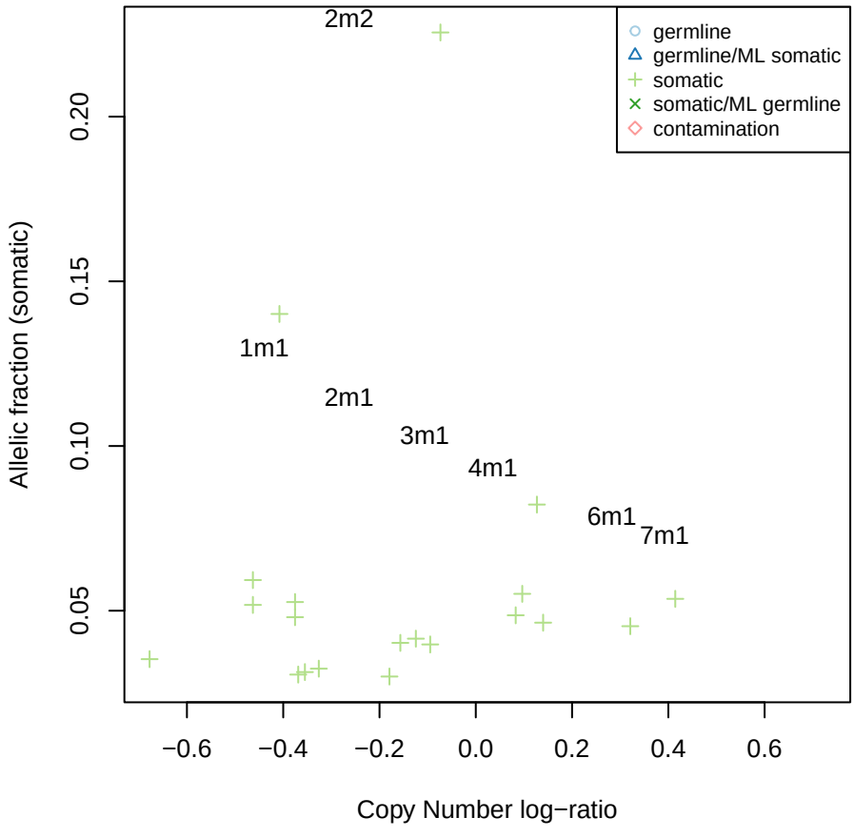

Purity: 0.23 Tumor ploidy: 3.739 SNV log−likelihood: −20.73 GoF: 93.7% Mean coverage: 454;525
1 2 4 6 7 8 10 11 13 14 16 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

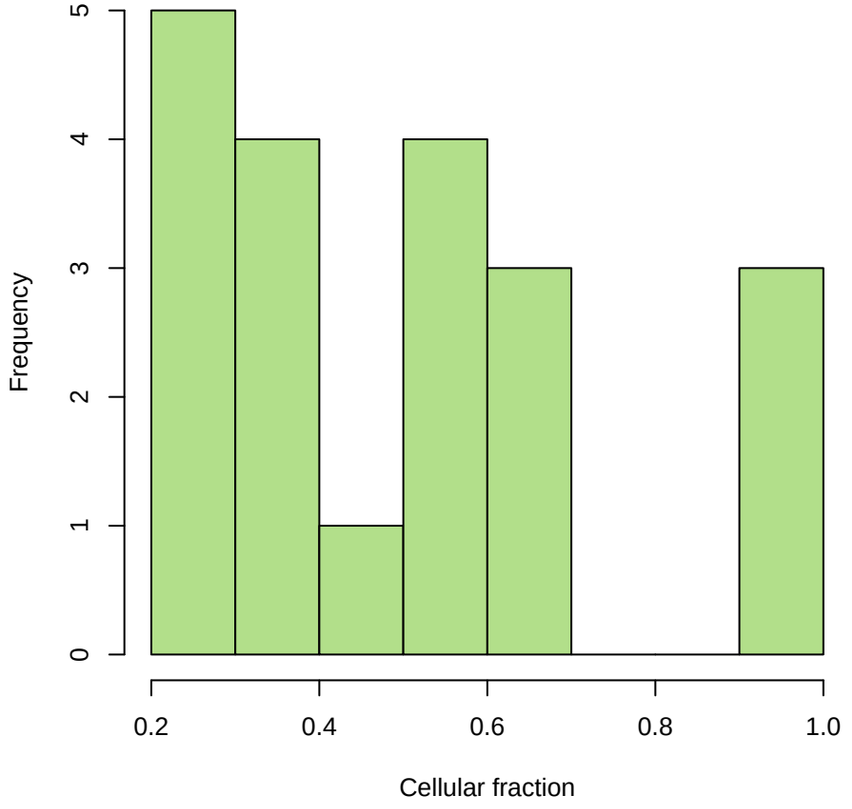

SCNA−fit log−likelihood: −5245.95
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 6
0 20 40 60 80
SNV Index

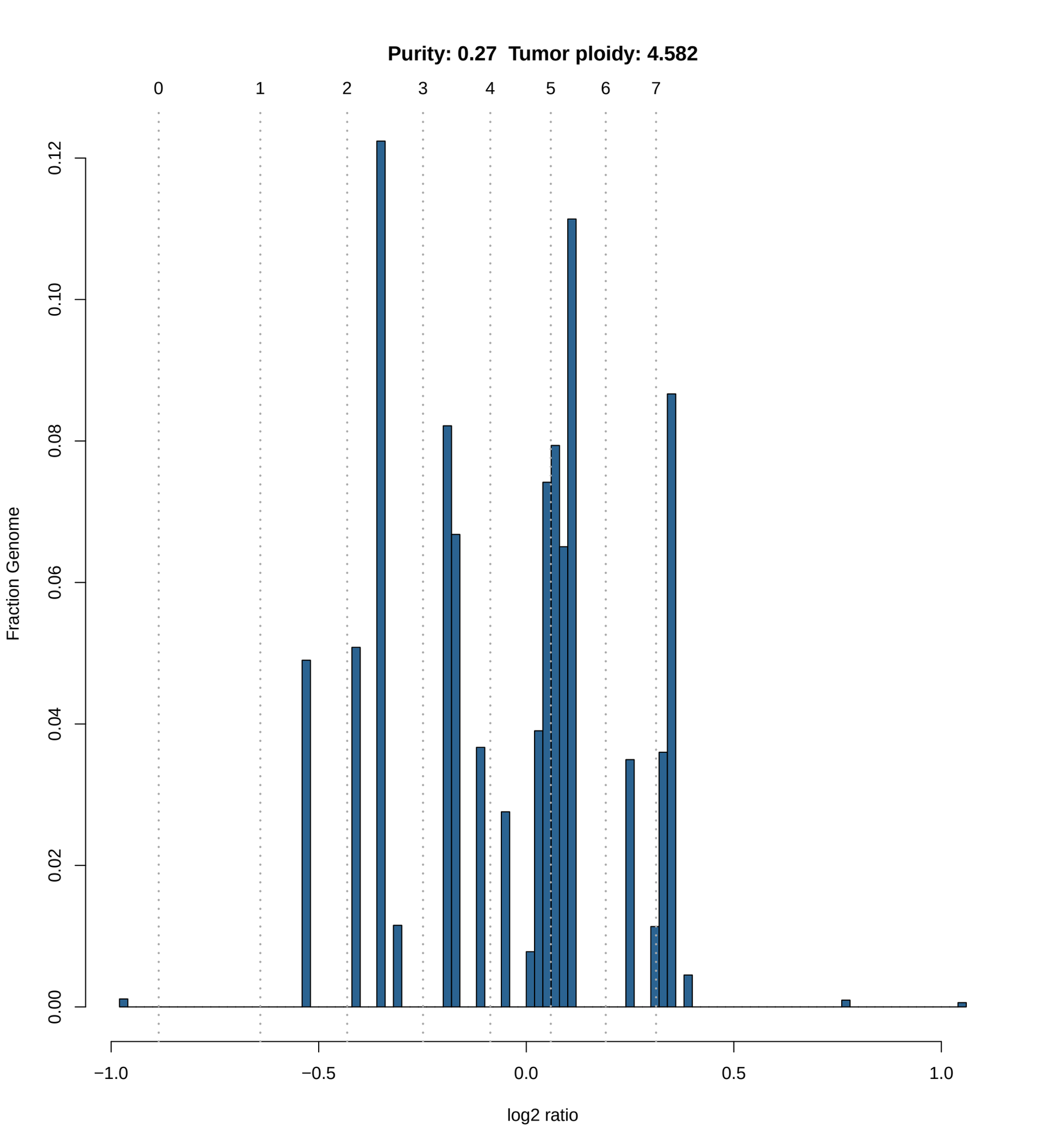

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

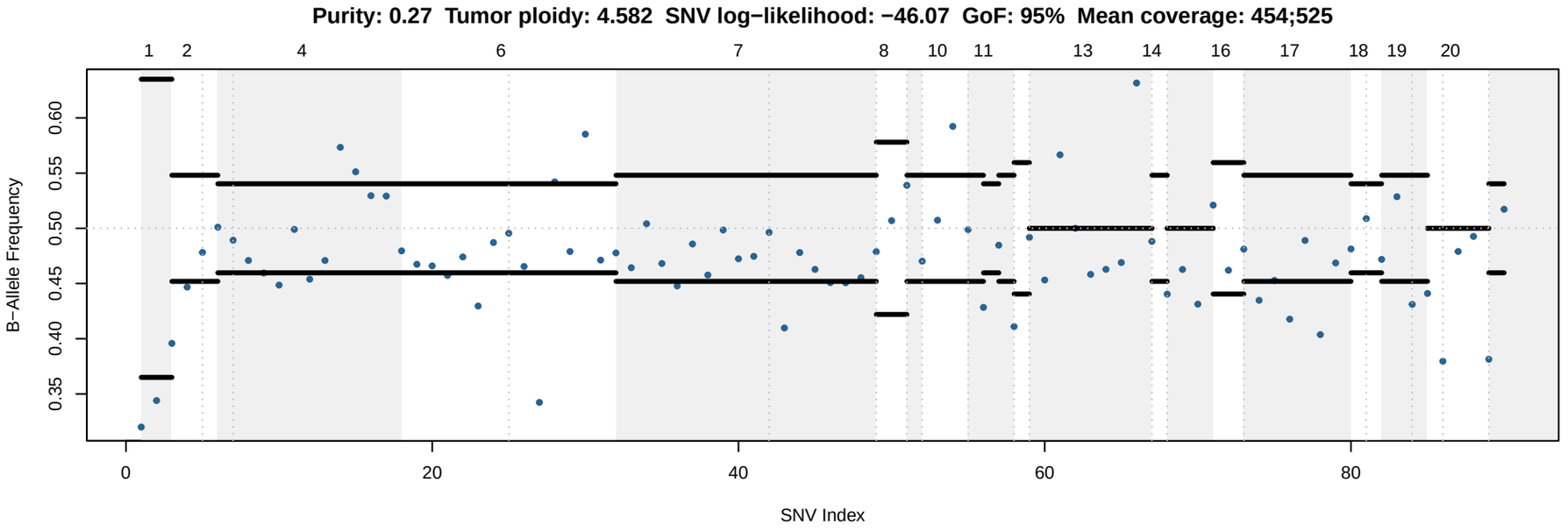

Allelic fraction (germline)
Copy Number log−ratio
1m1
2m0
2m1
3m1
3m2
4m2
6m2
6m3
6m4
7m2
7m3
7m4
1m0

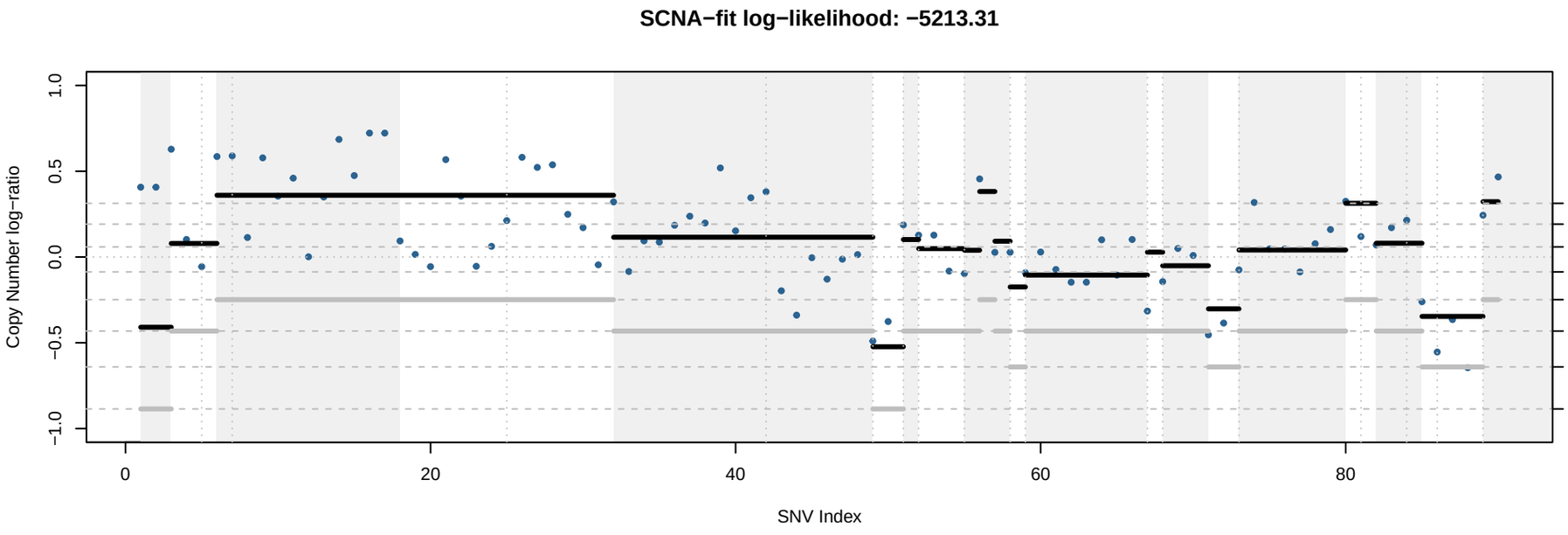

Coverage (log2)
Allelic fraction

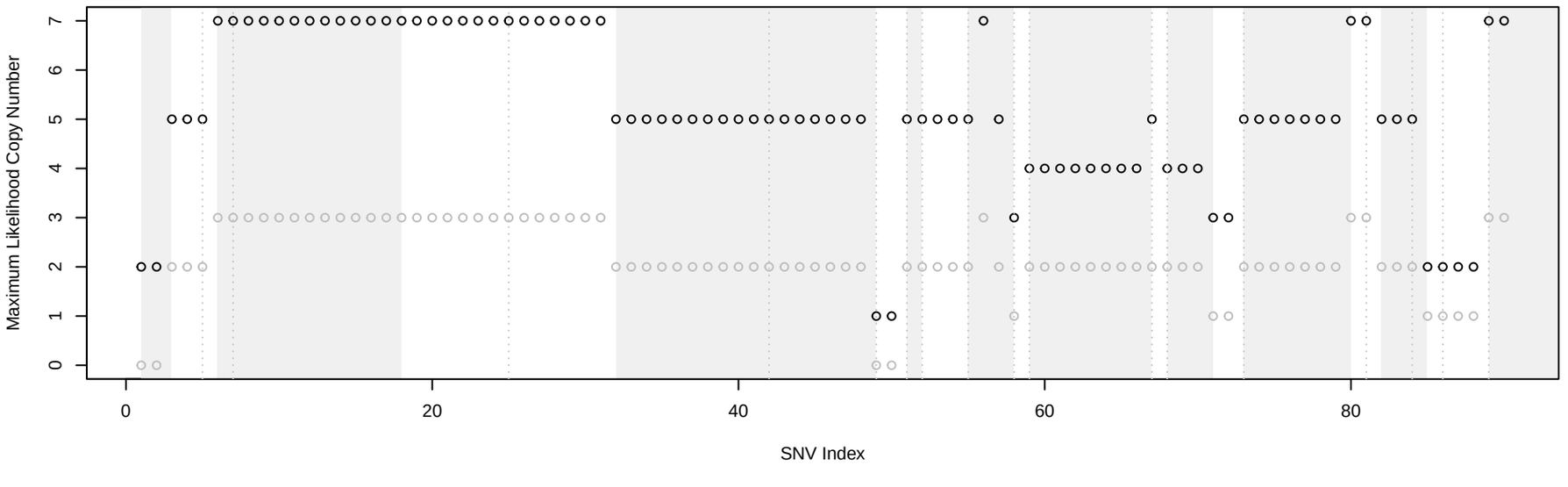

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
2m2
3m1
4m1
6m1
7m1

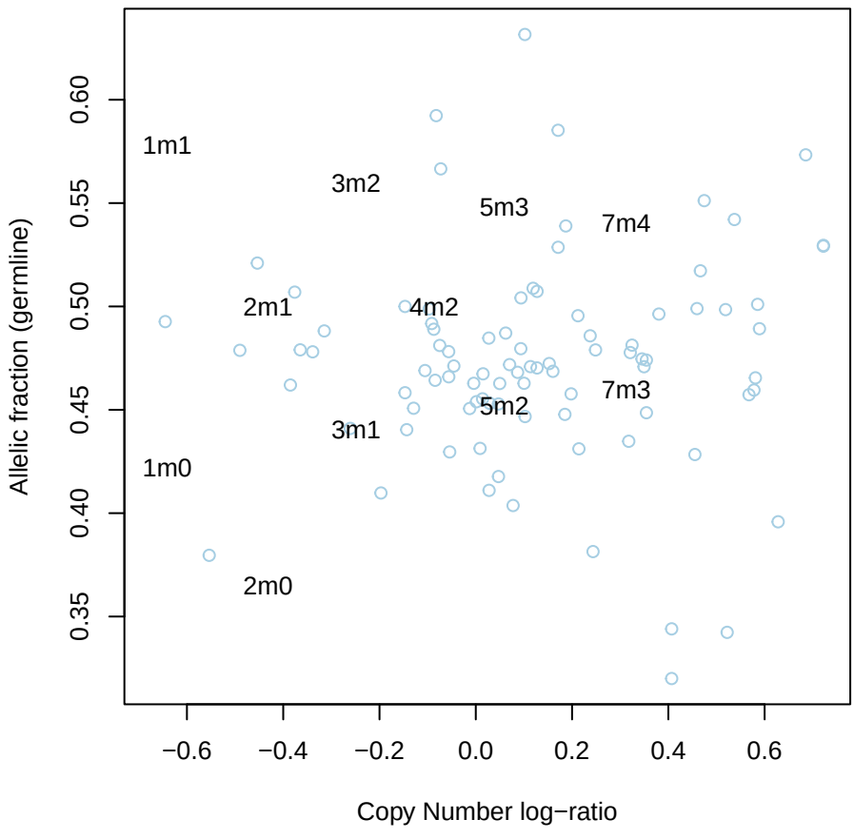

Frequency
Cellular fraction

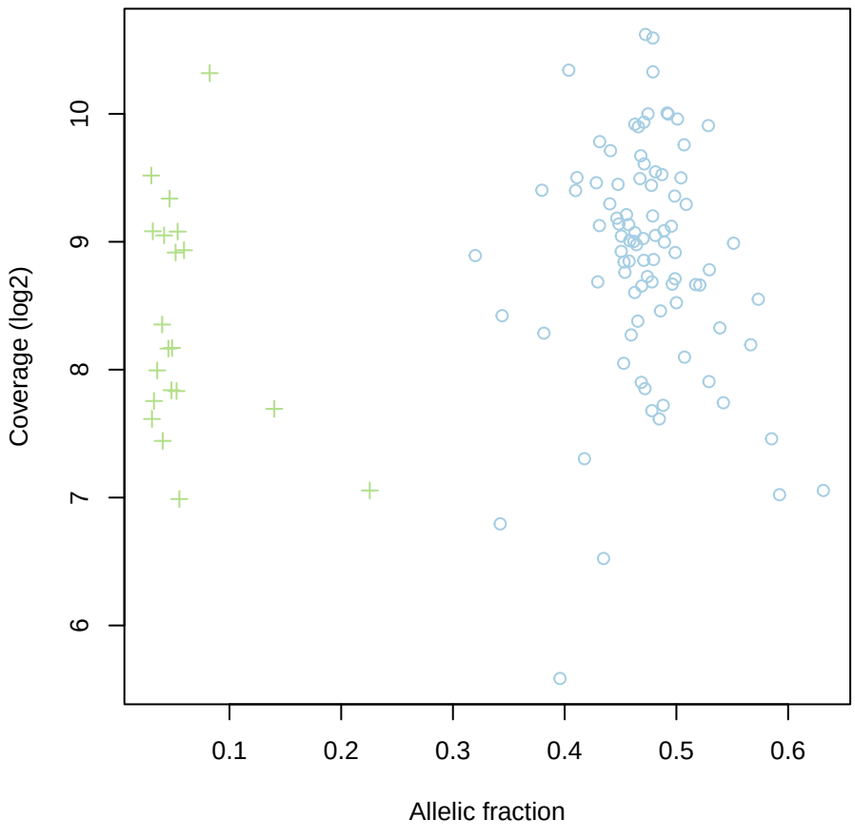

Purity: 0.27 Tumor ploidy: 4.582
0
1
2
3
4
5
6
7
0.12
0.10
0.08
0.06
0.04
0.02
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

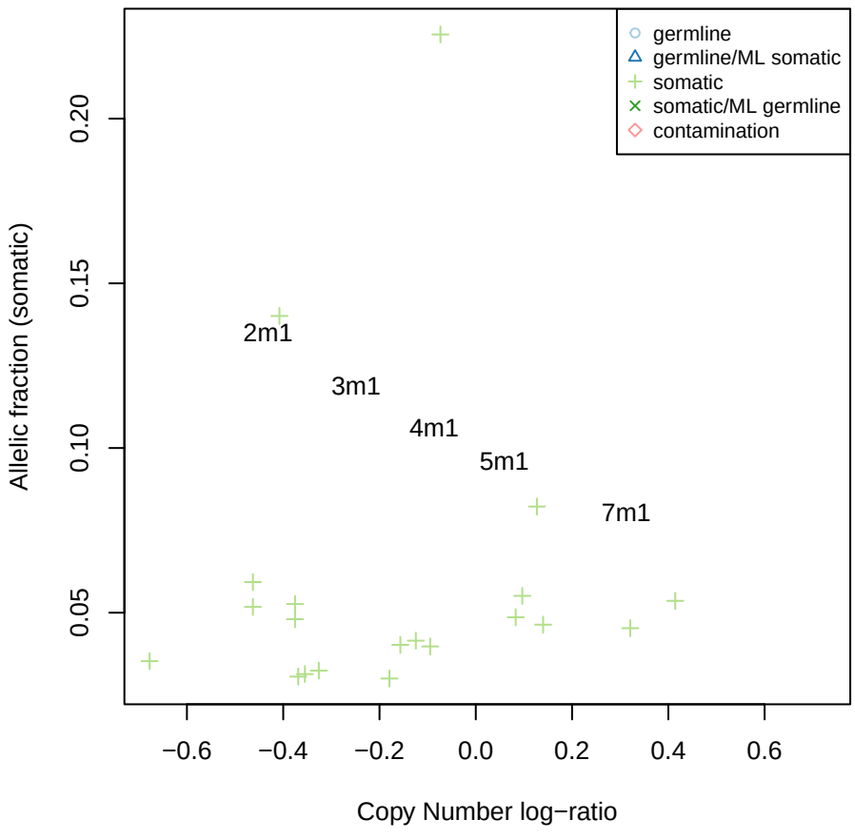

Purity: 0.27 Tumor ploidy: 4.582 SNV log−likelihood: −46.07 GoF: 95% Mean coverage: 454;525
1 2 4 6 7 8 10 11 13 14 16 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

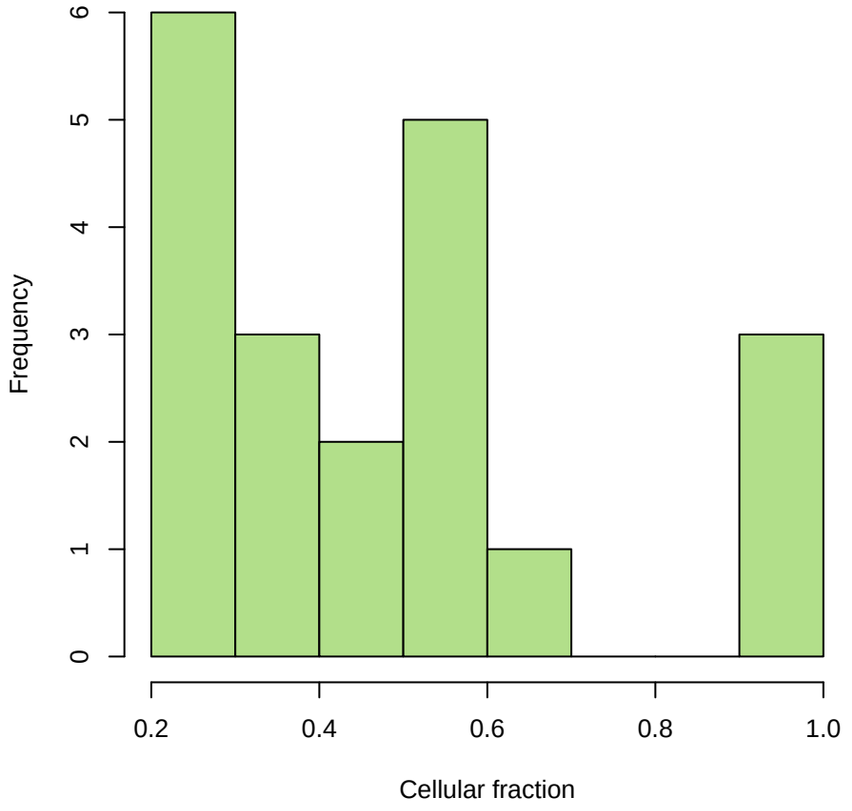

SCNA−fit log−likelihood: −5213.31
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 7
0 20 40 60 80
SNV Index

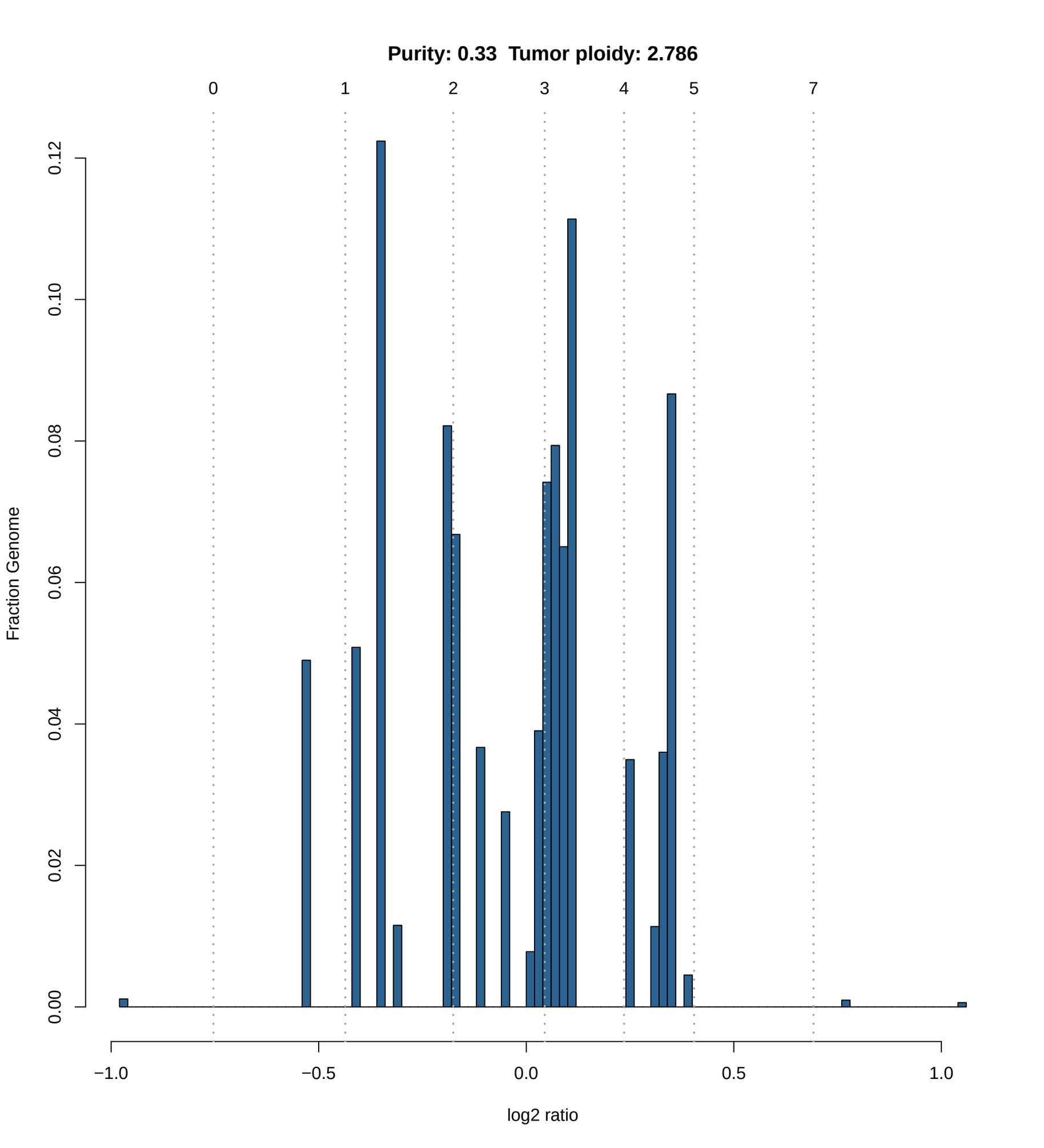

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

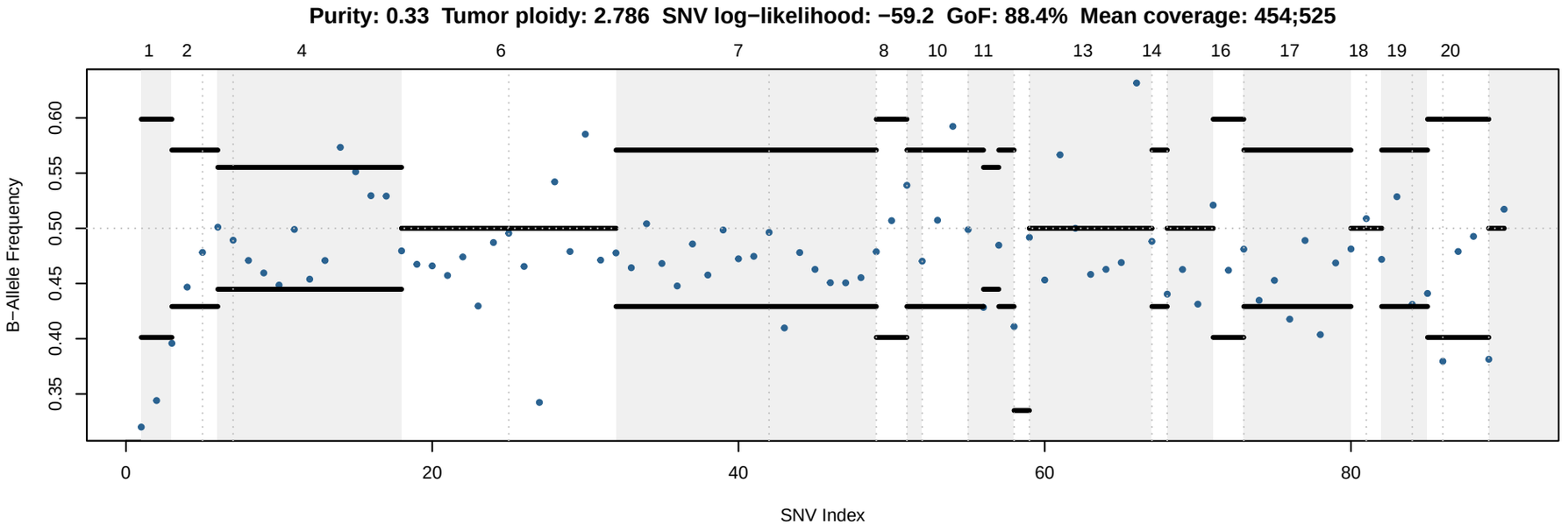

Allelic fraction (germline)
Copy Number log−ratio
1m1
3m2
5m3
7m4
2m1
4m2
7m3
5m2
3m1
1m0
2m0

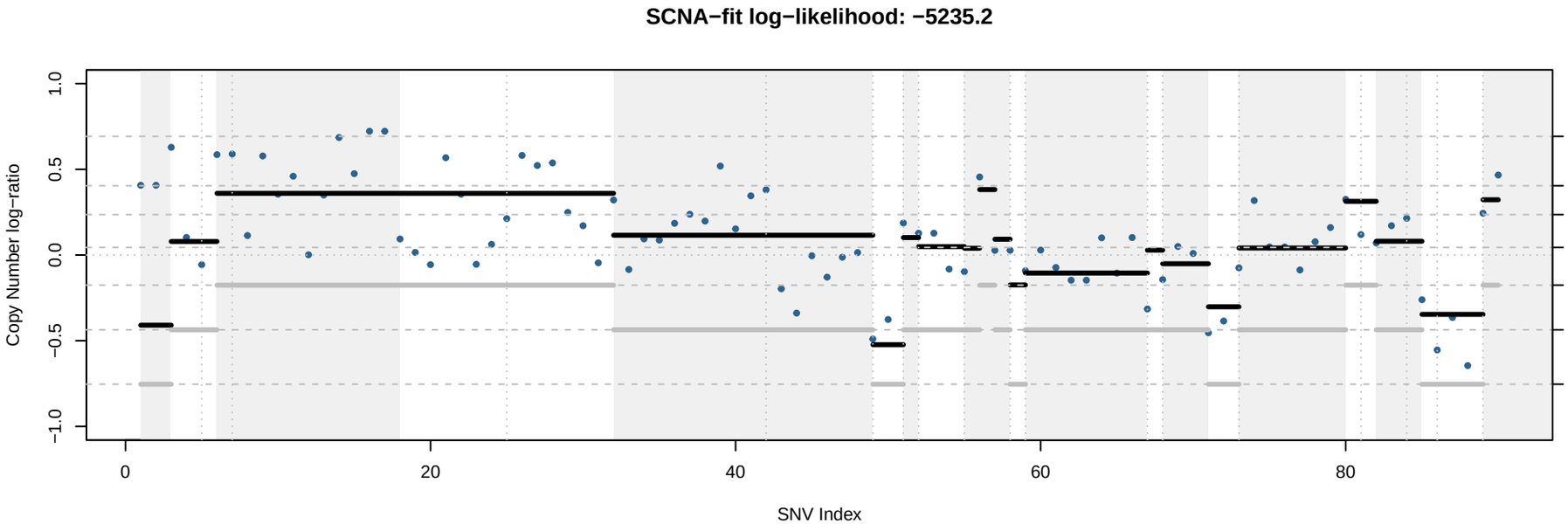

Coverage (log2)
Allelic fraction

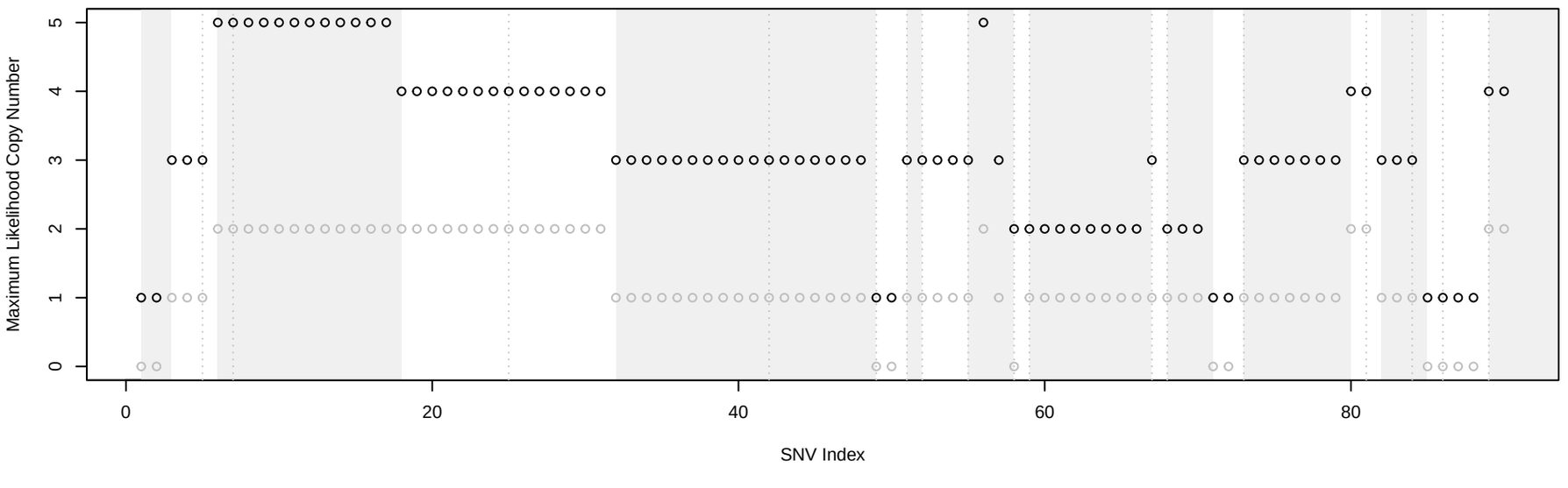

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m1
3m1
4m1
5m1
7m1

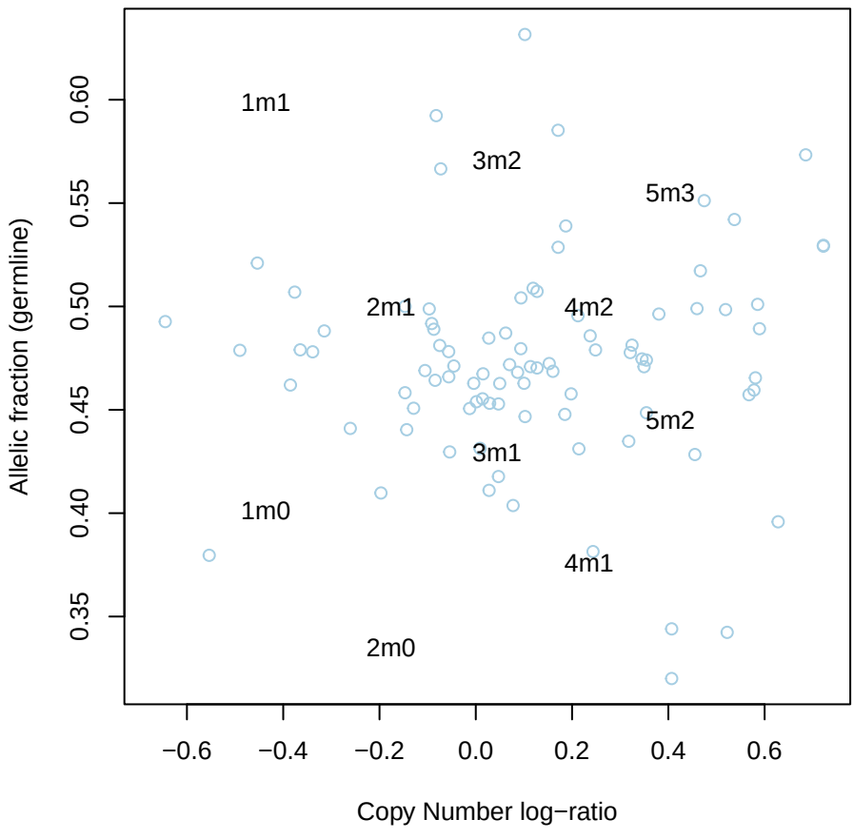

Frequency
Cellular fraction

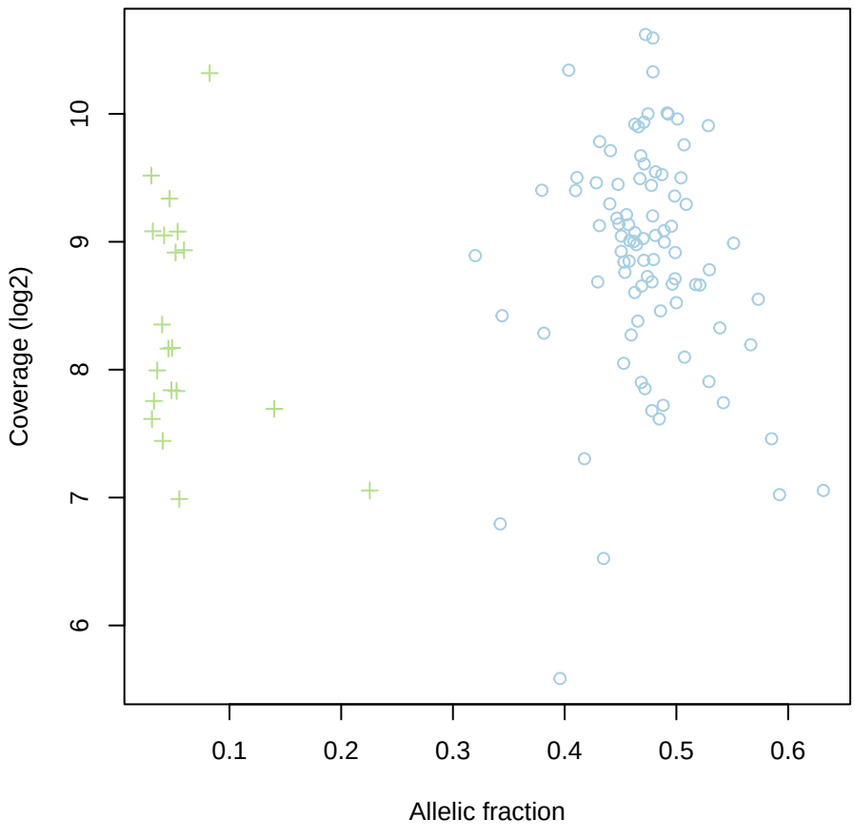

Purity: 0.33 Tumor ploidy: 2.786
0
1
2
3
4
5
7
0.12
0.10
0.08
0.06
0.04
0.02
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

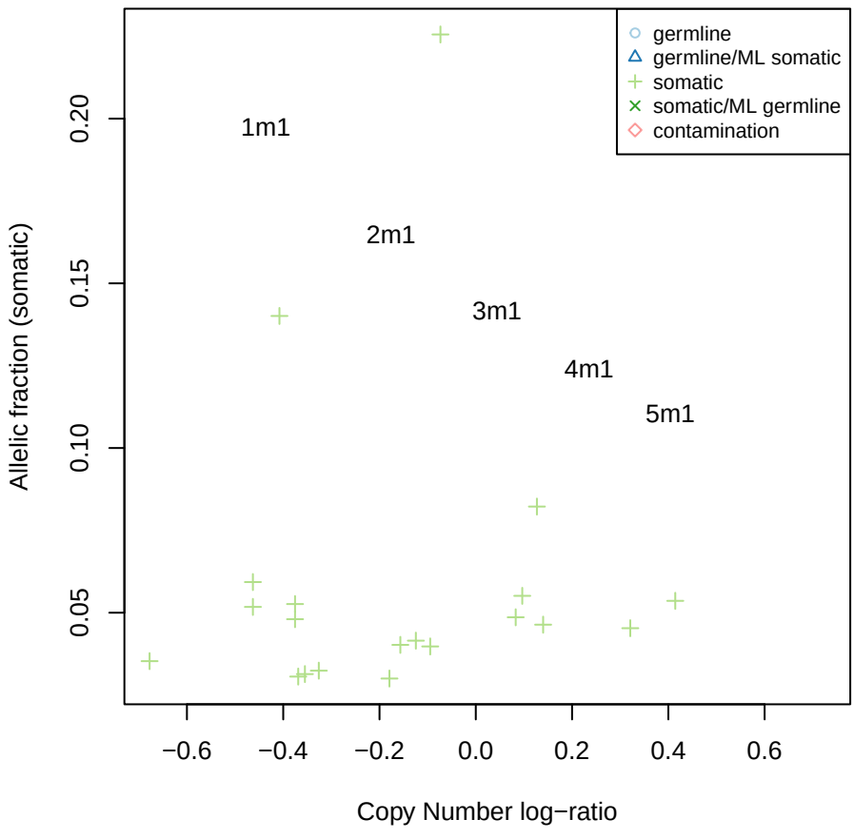

Purity: 0.33 Tumor ploidy: 2.786 SNV log−likelihood: −59.2 GoF: 88.4% Mean coverage: 454;525
1 2 4 6 7 8 10 11 13 14 16 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

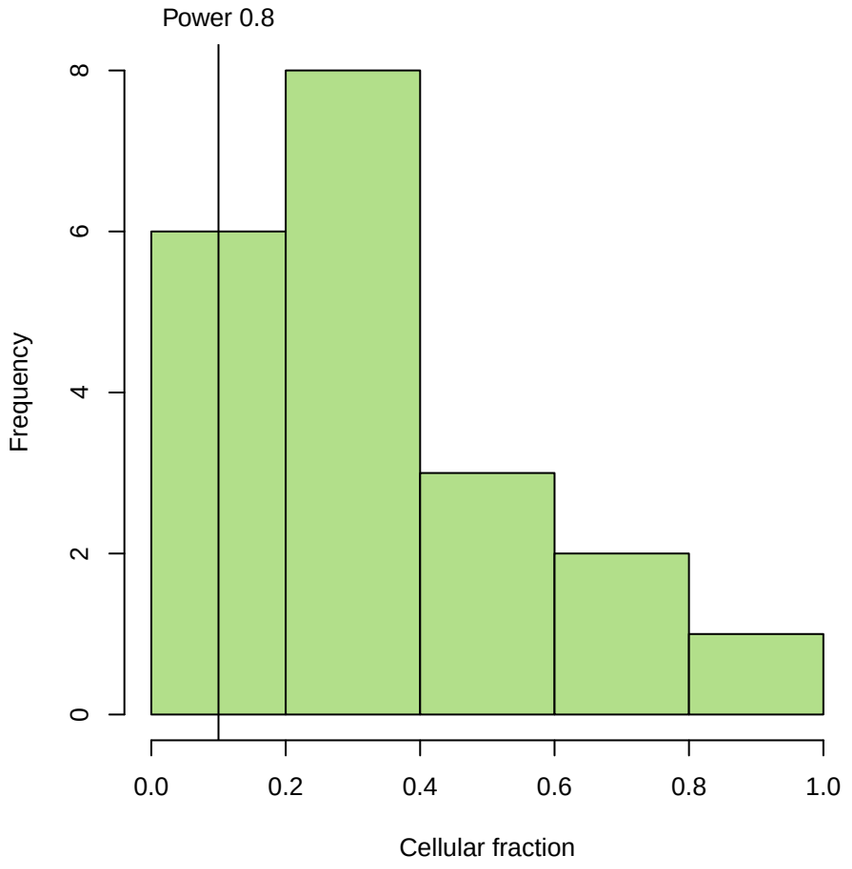

SCNA−fit log−likelihood: −5235.2
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 7
0 20 40 60 80
SNV Index

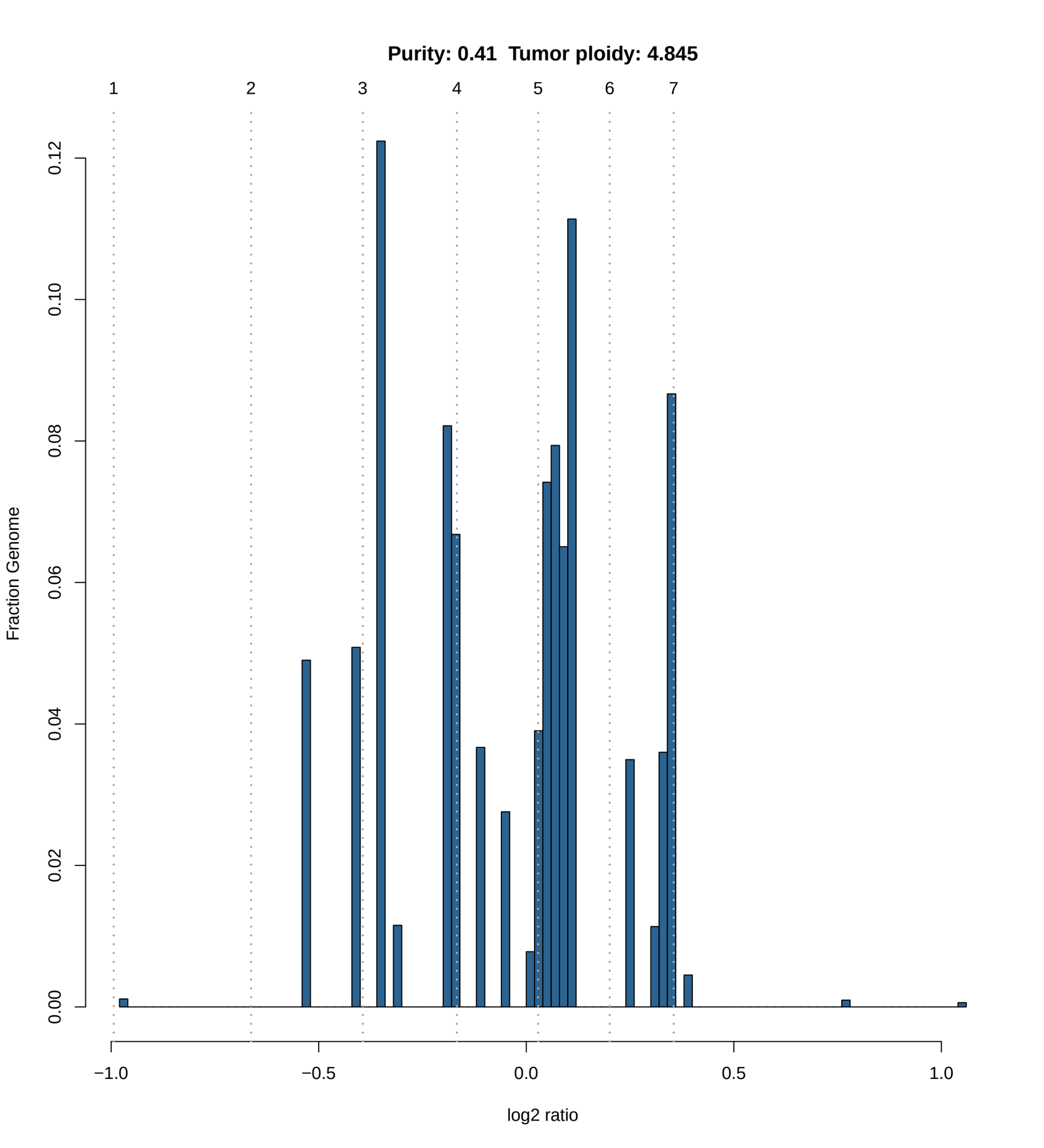

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80
SNV Index

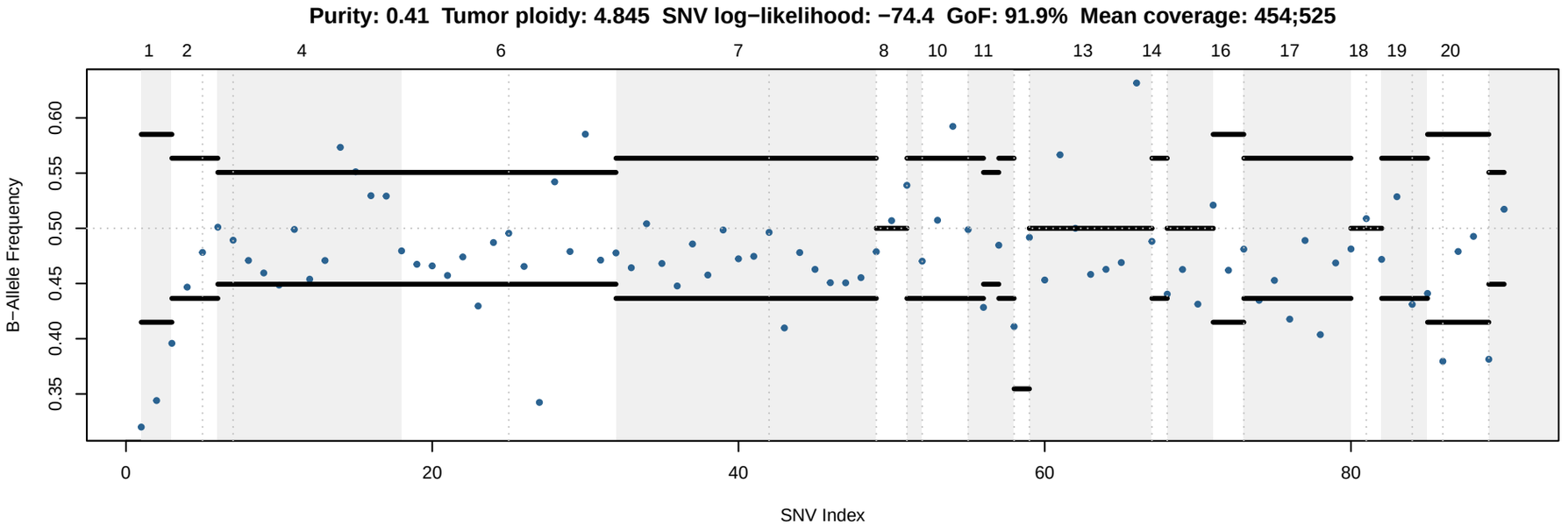

Allelic fraction (germline)
Copy Number log−ratio
1m1
3m2
5m3
2m1
4m2
5m2
3m1
1m0
4m1
2m0

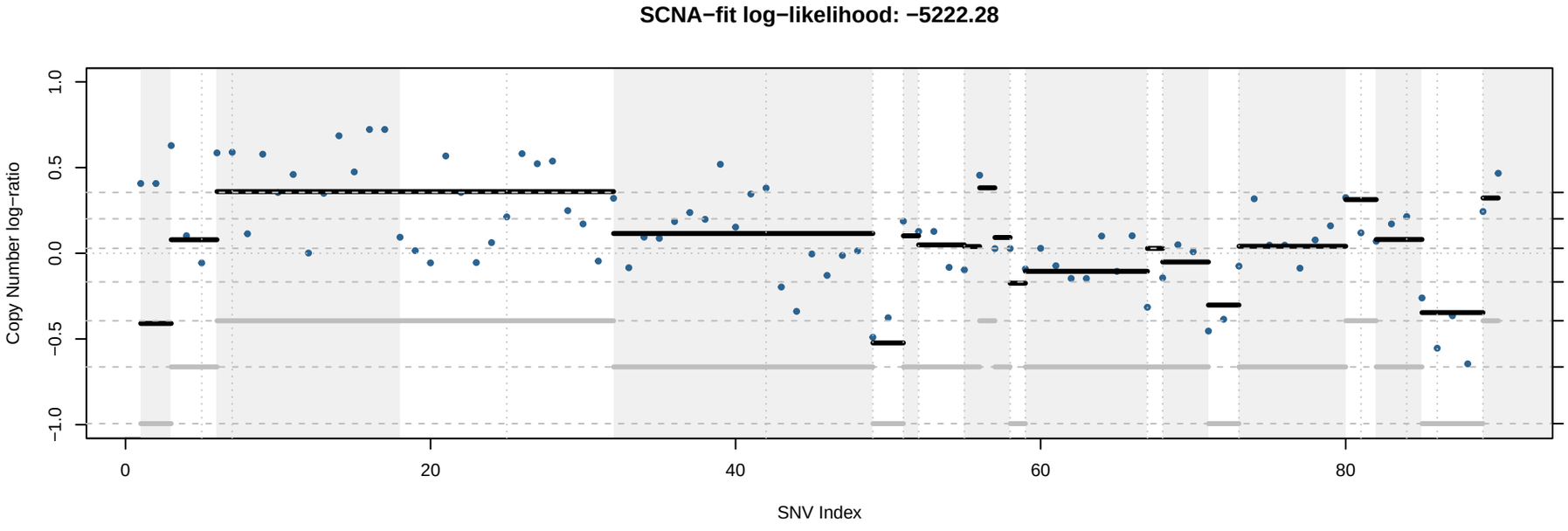

Coverage (log2)
Allelic fraction

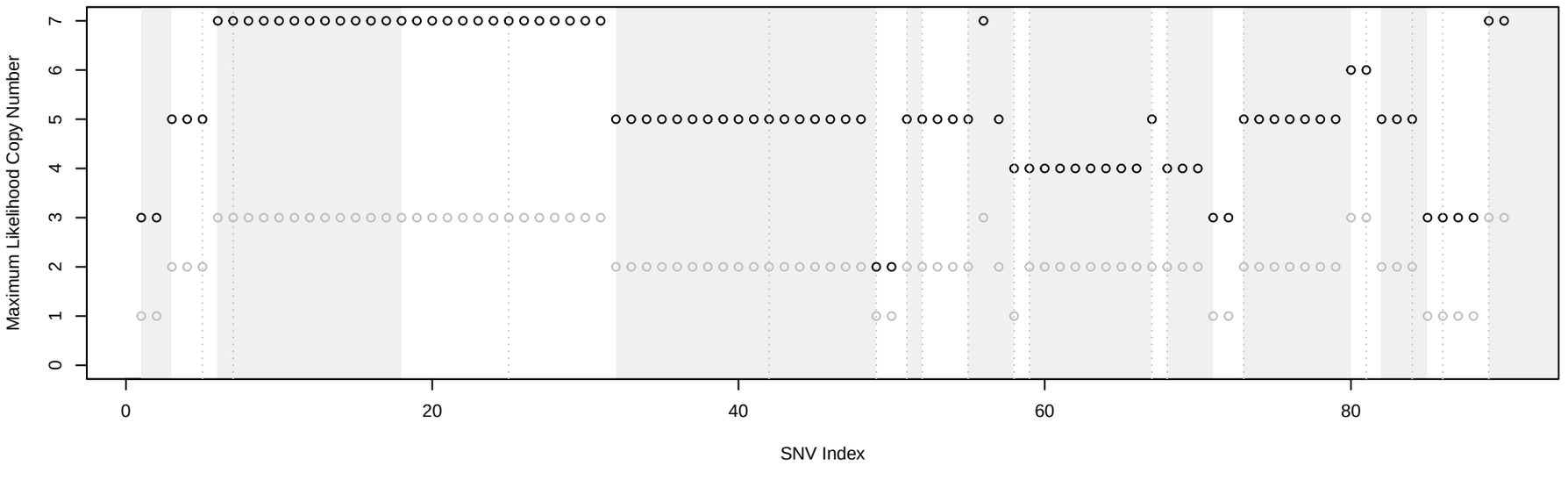

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1
3m1
4m1
5m1

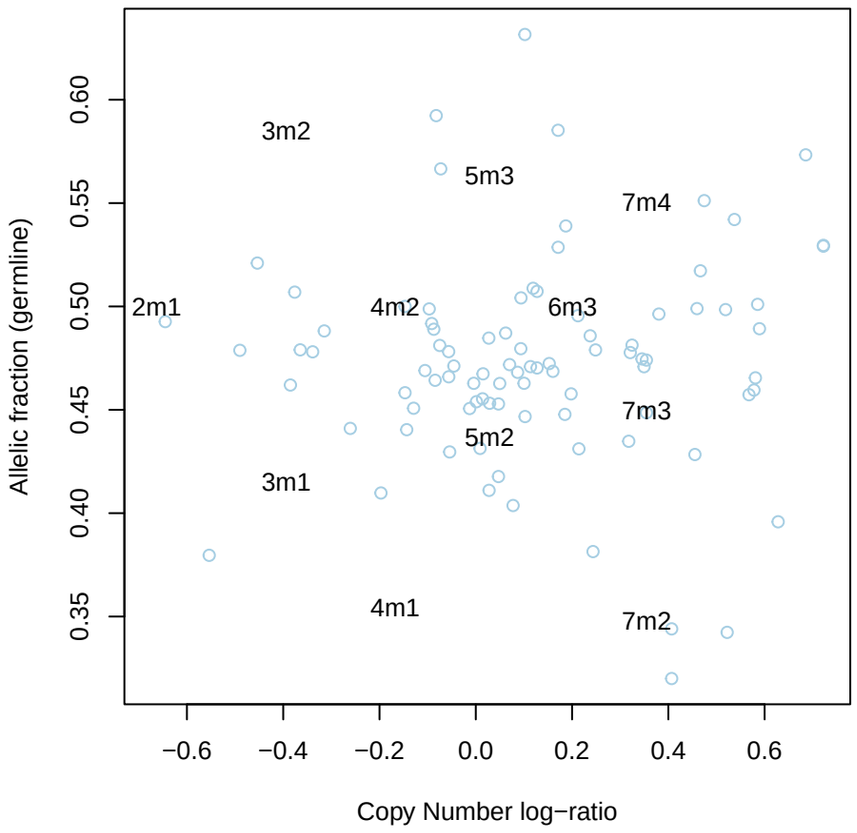

Power 0.8
Frequency
Cellular fraction

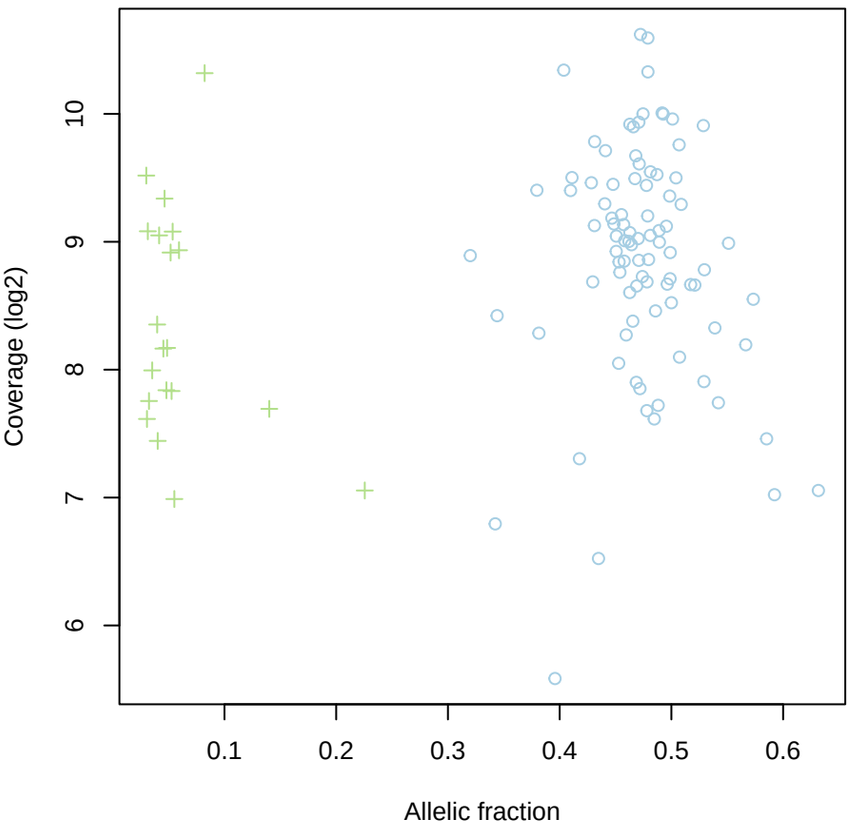

Purity: 0.41 Tumor ploidy: 4.845
1
2
3
4
5
6
7
0.00
0.02
0.04
0.06
0.08
0.10
0.12
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

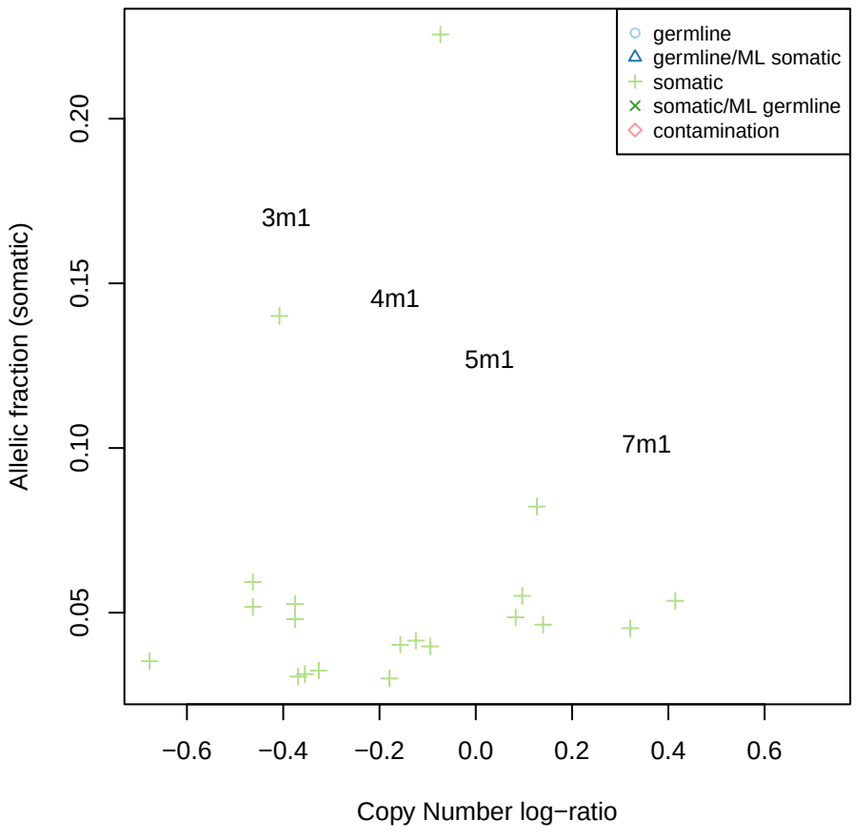

Purity: 0.41 Tumor ploidy: 4.845 SNV log−likelihood: −74.4 GoF: 91.9% Mean coverage: 454;525
1 2 4 6 7 8 10 11 13 14 16 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

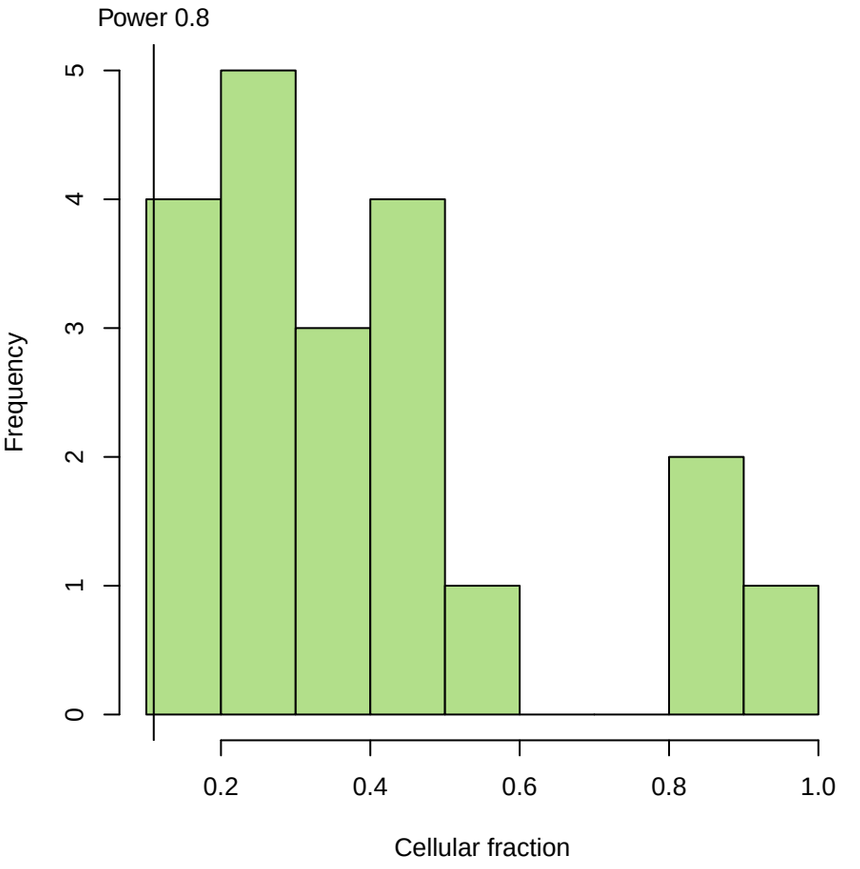

SCNA−fit log−likelihood: −5222.28
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

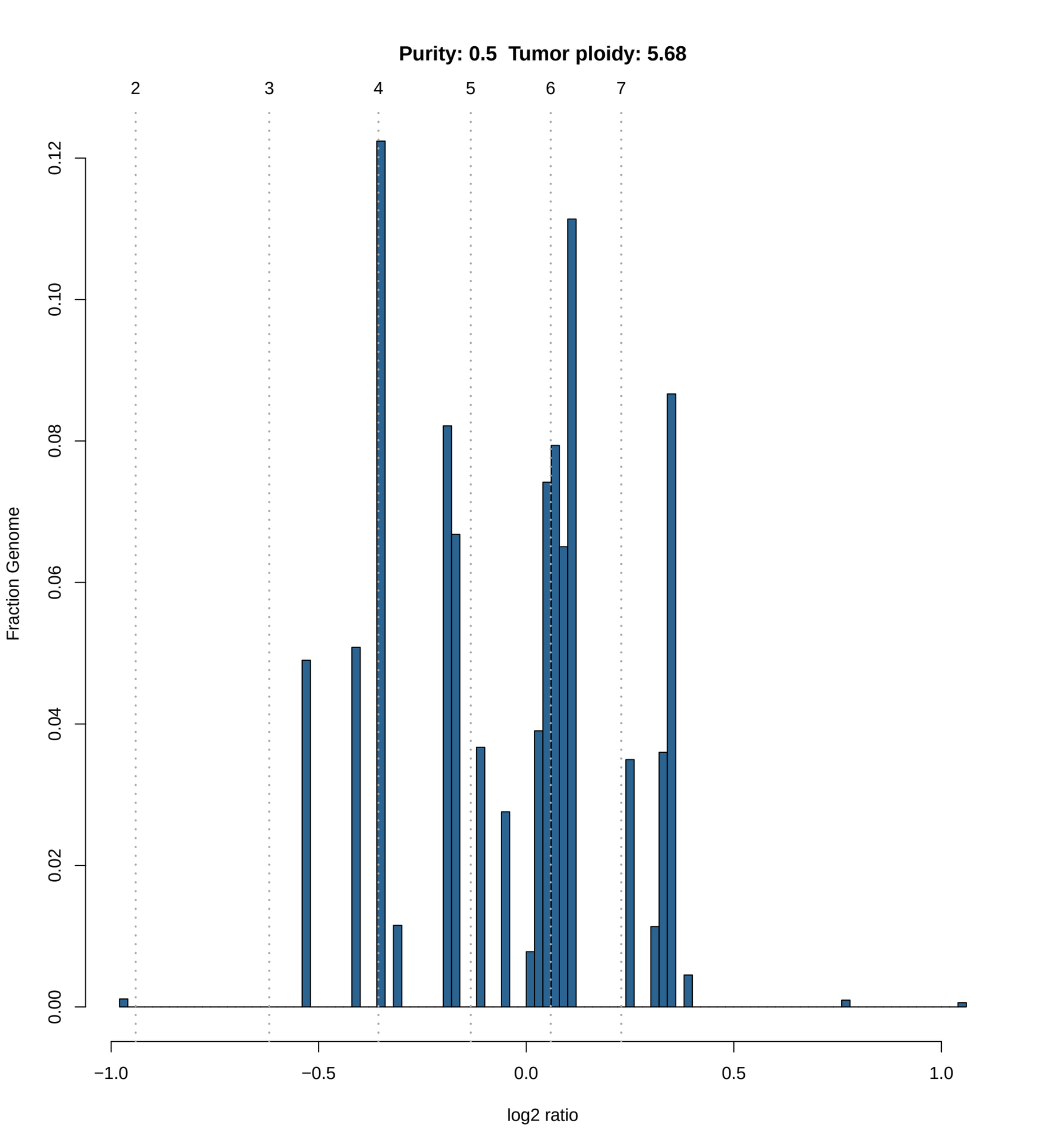

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

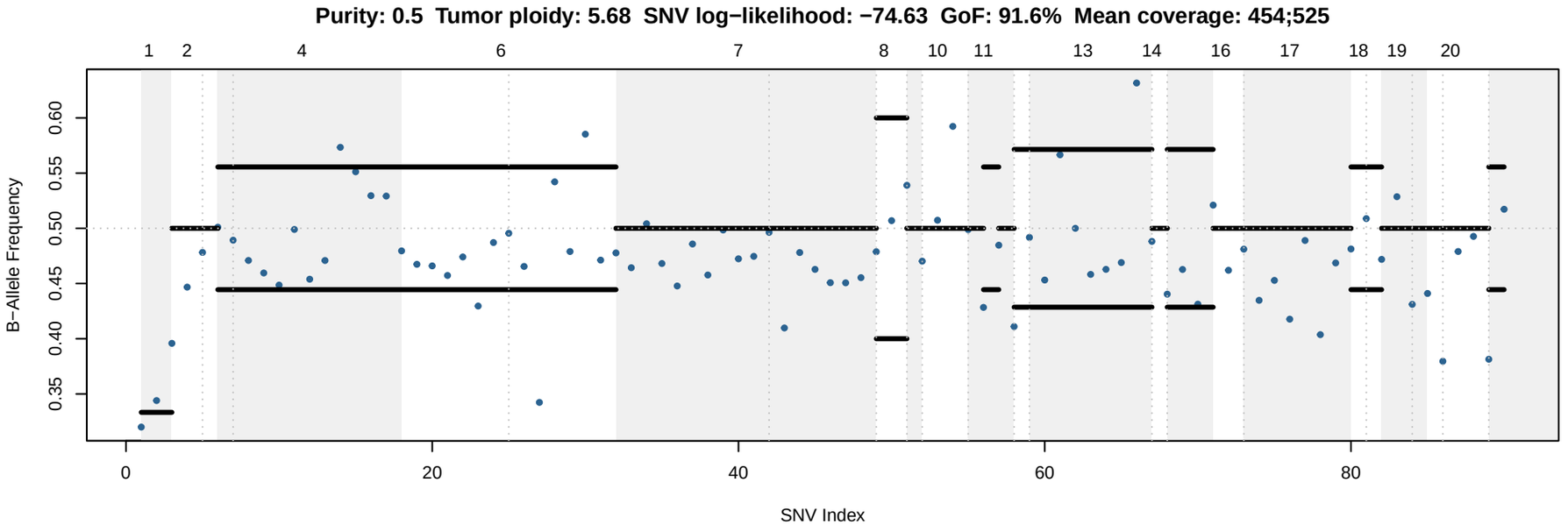

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
3m2
5m3
7m4
2m1
4m2
6m3
7m3
5m2
3m1
4m1
7m2
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

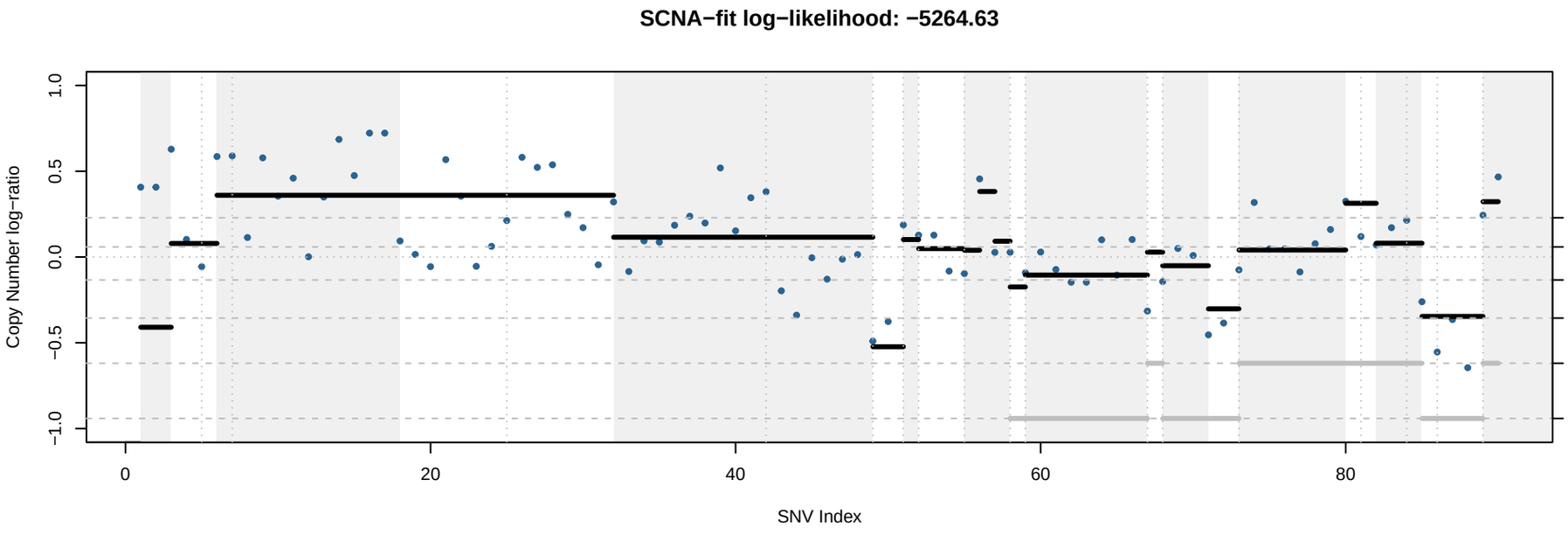

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

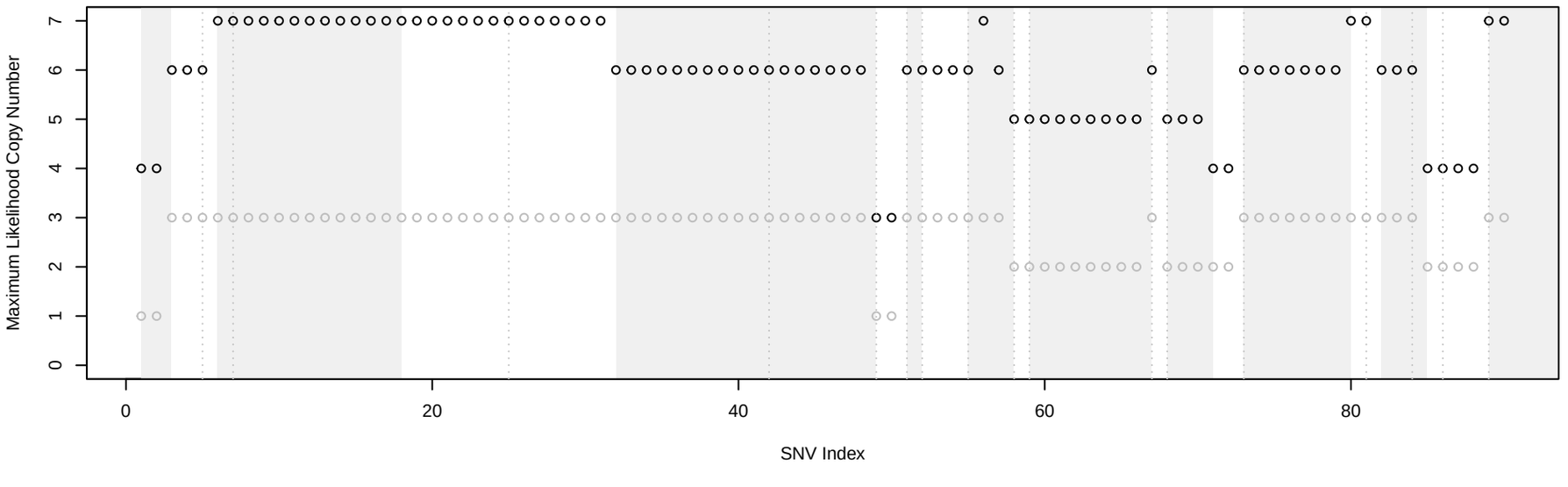

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
3m1
4m1
5m1
7m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

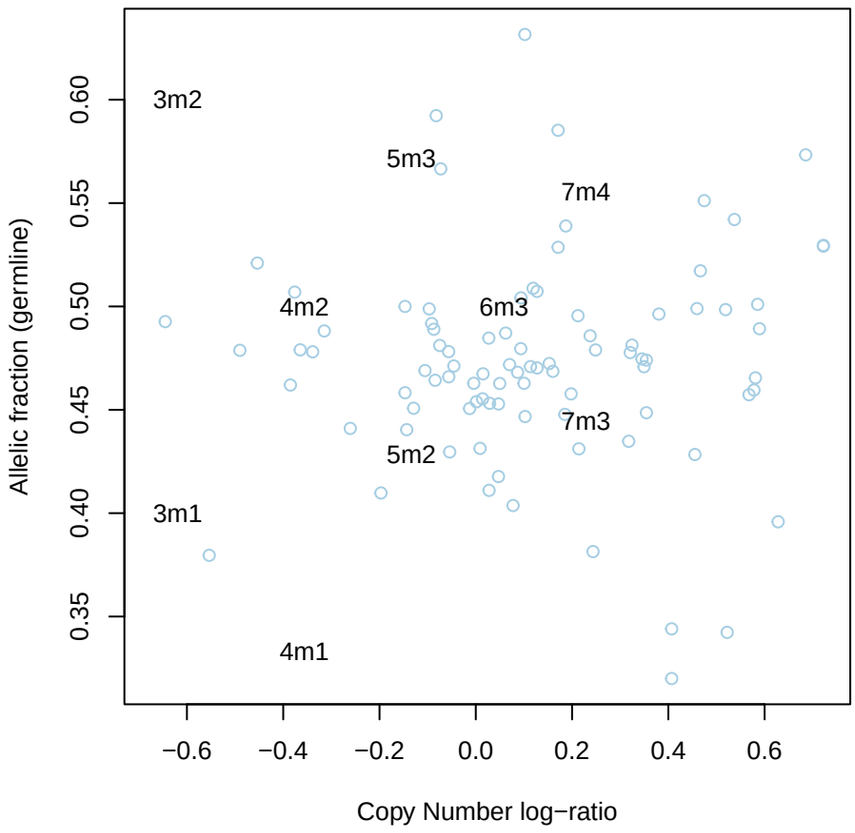

Power 0.8
Frequency
0
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0
Cellular fraction

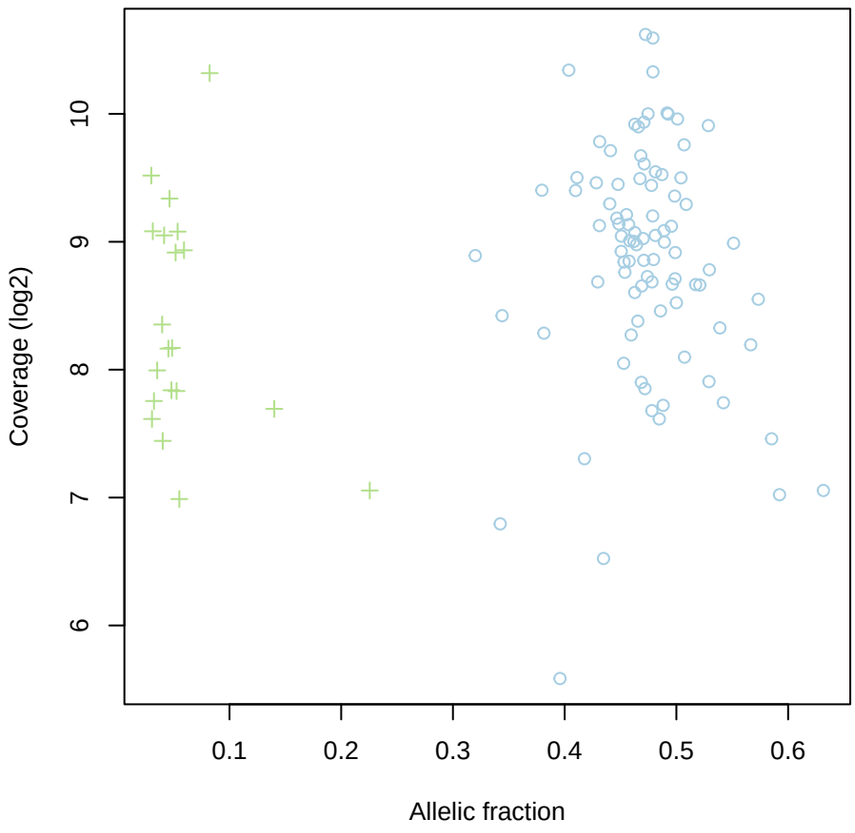

Purity: 0.5 Tumor ploidy: 5.68
2
3
4
5
6
7
0.00
0.02
0.04
0.06
0.08
0.10
0.12
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

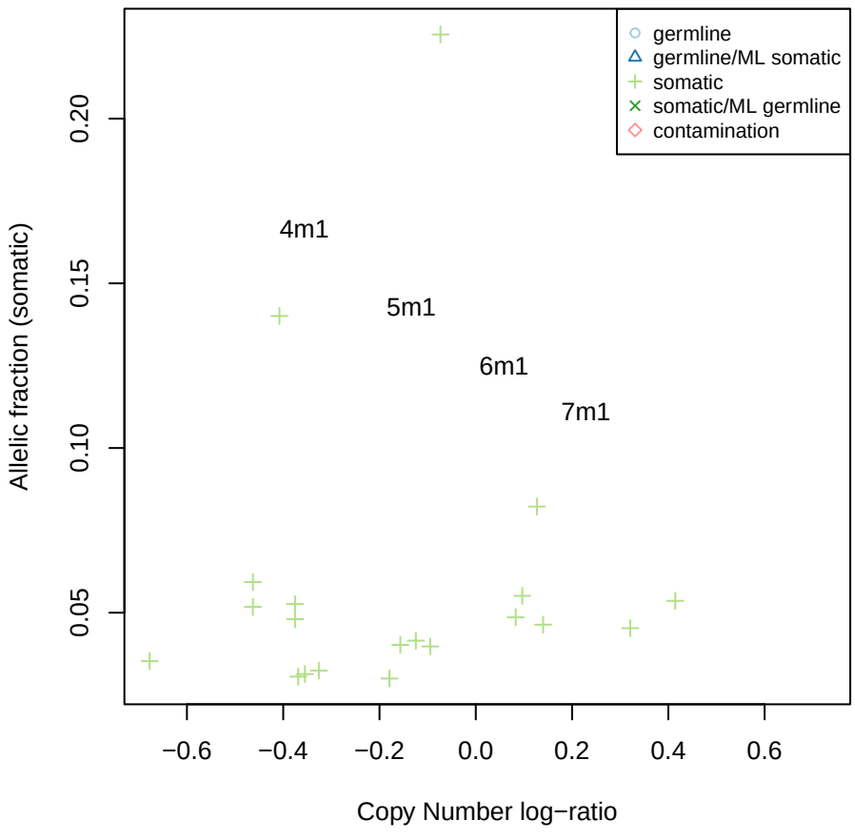

Purity: 0.5 Tumor ploidy: 5.68 SNV log−likelihood: −74.63 GoF: 91.6% Mean coverage: 454;525
1 2 4 6 7 8 10 11 13 14 16 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

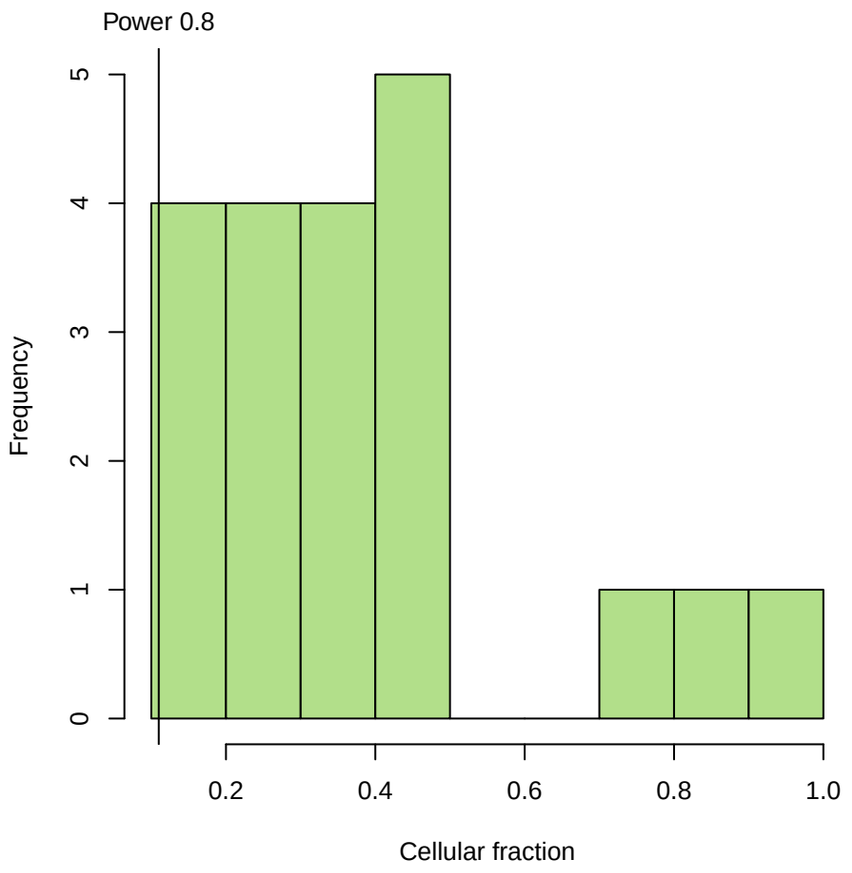

SCNA−fit log−likelihood: −5264.63
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 20 40 60 80
SNV Index

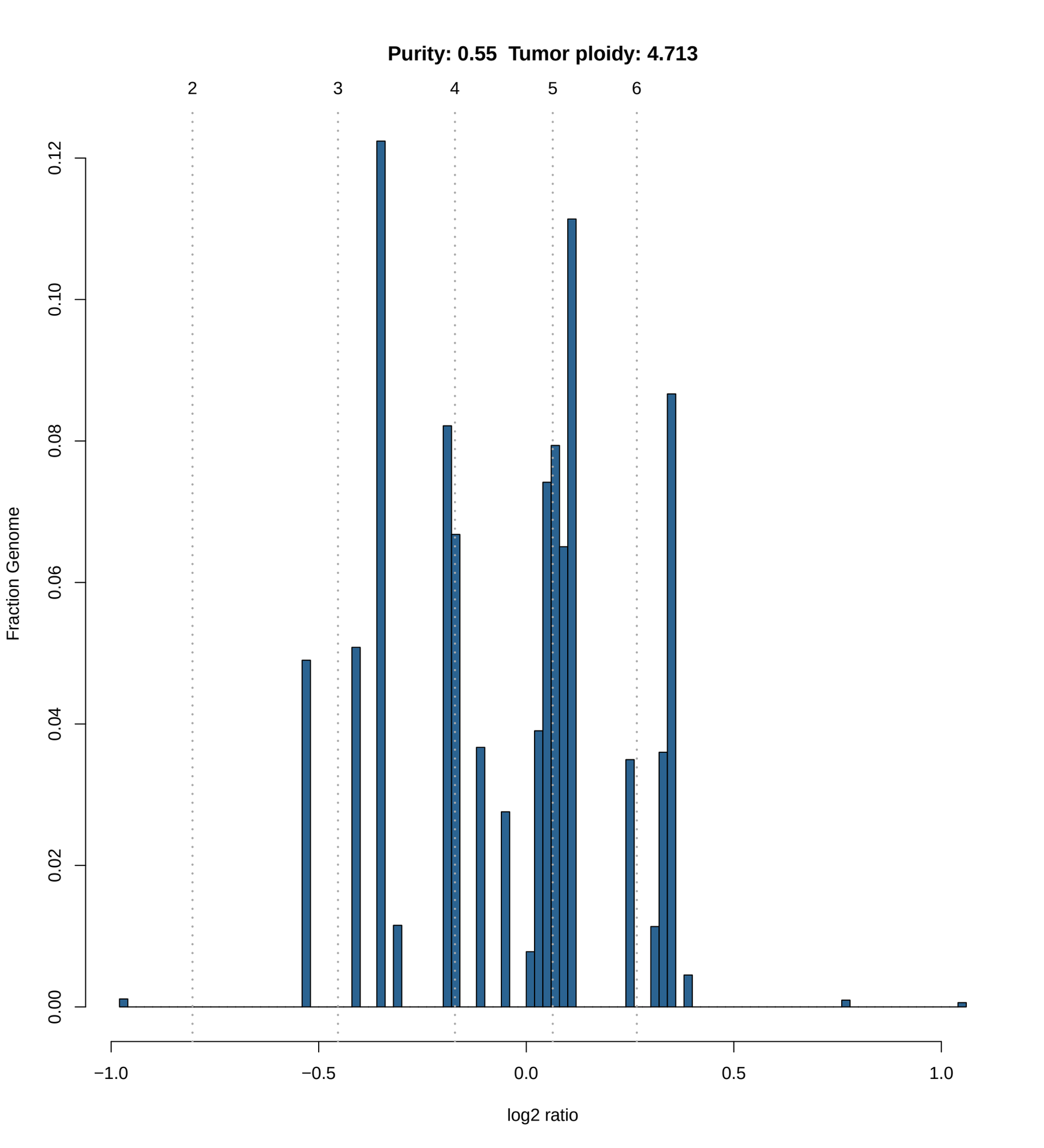

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80
SNV Index

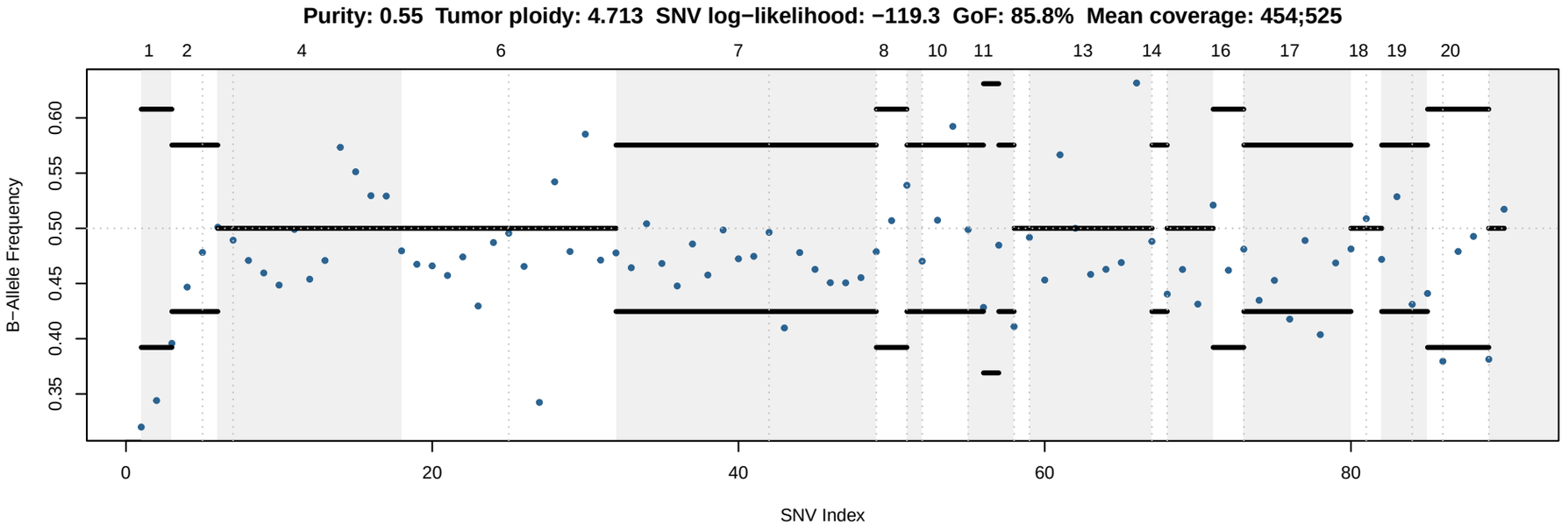

3m2
5m3
7m4
4m2
6m3
7m3
5m2
3m1
4m1
Allelic fraction (germline)
Copy Number log−ratio
0.35
0.40
0.45
0.50
0.55
0.60
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6

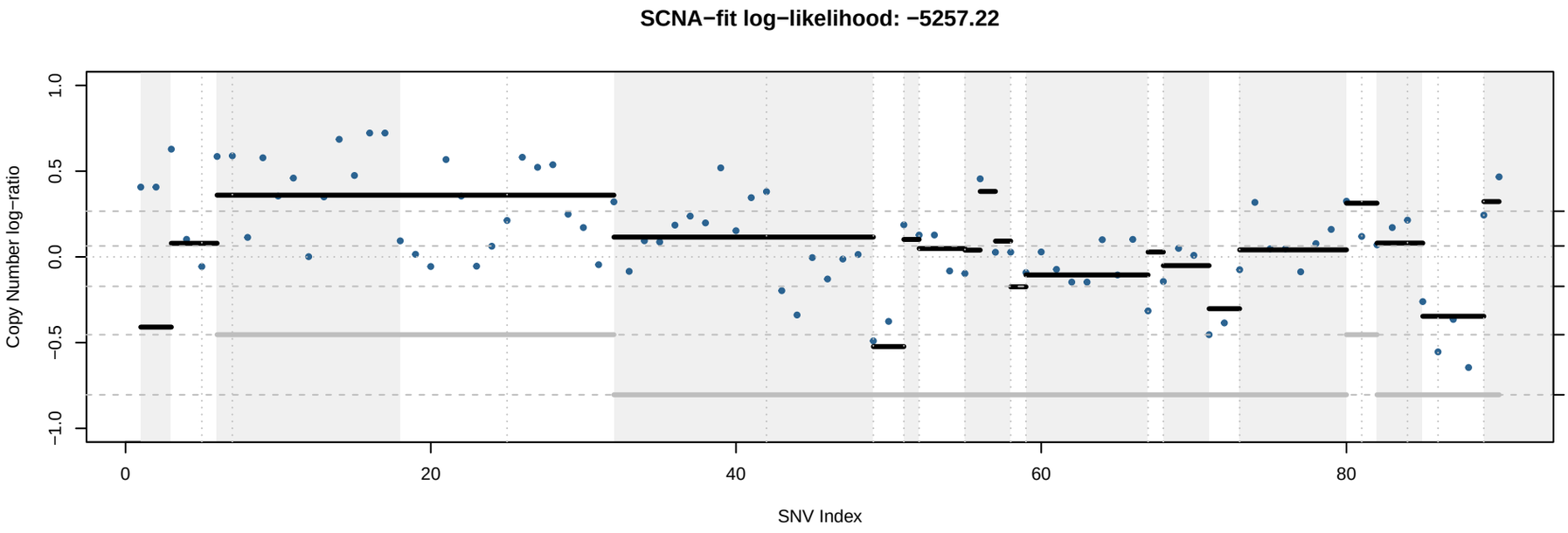

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

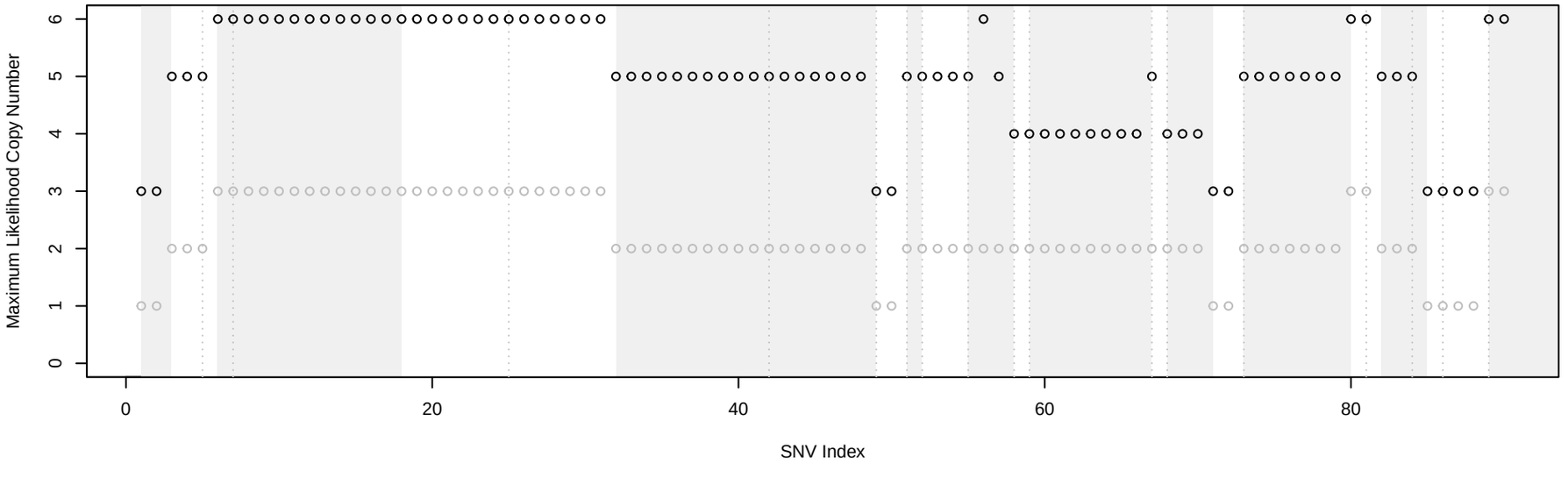

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6

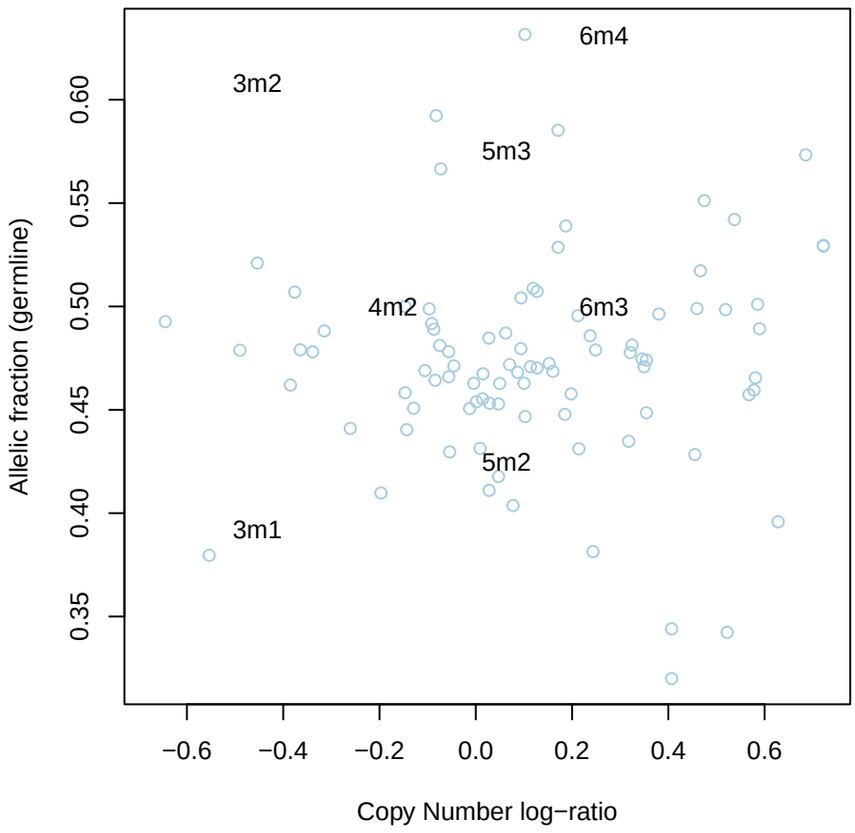

Power 0.8
Frequency
Cellular fraction
0
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0

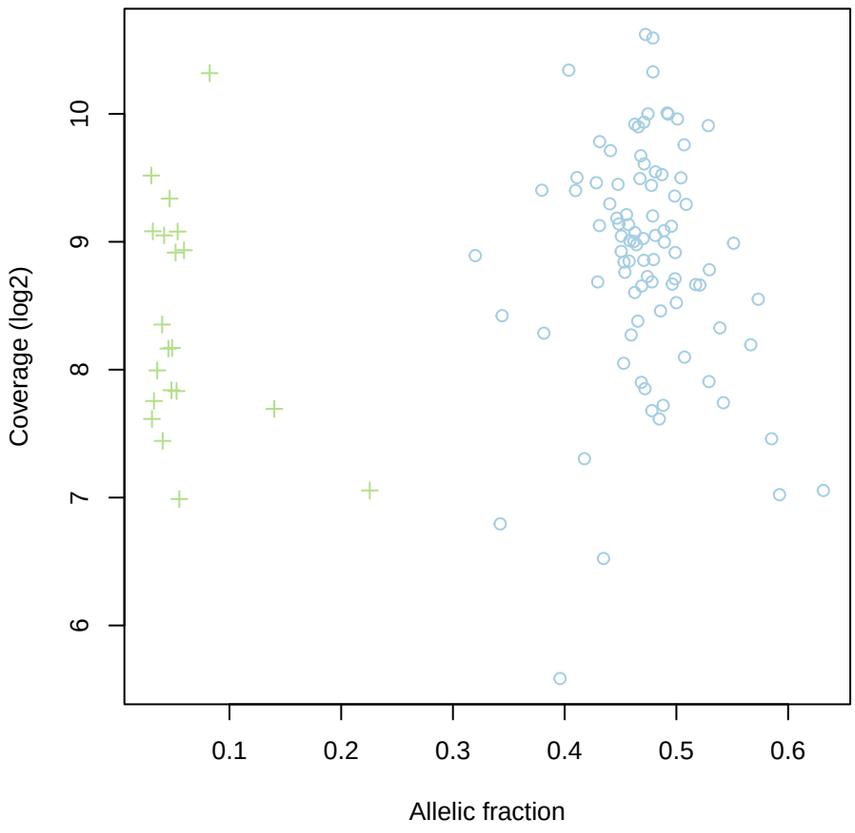

Purity: 0.55 Tumor ploidy: 4.713
2
3
4
5
6
0.00
0.02
0.04
0.06
0.08
0.10
0.12
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

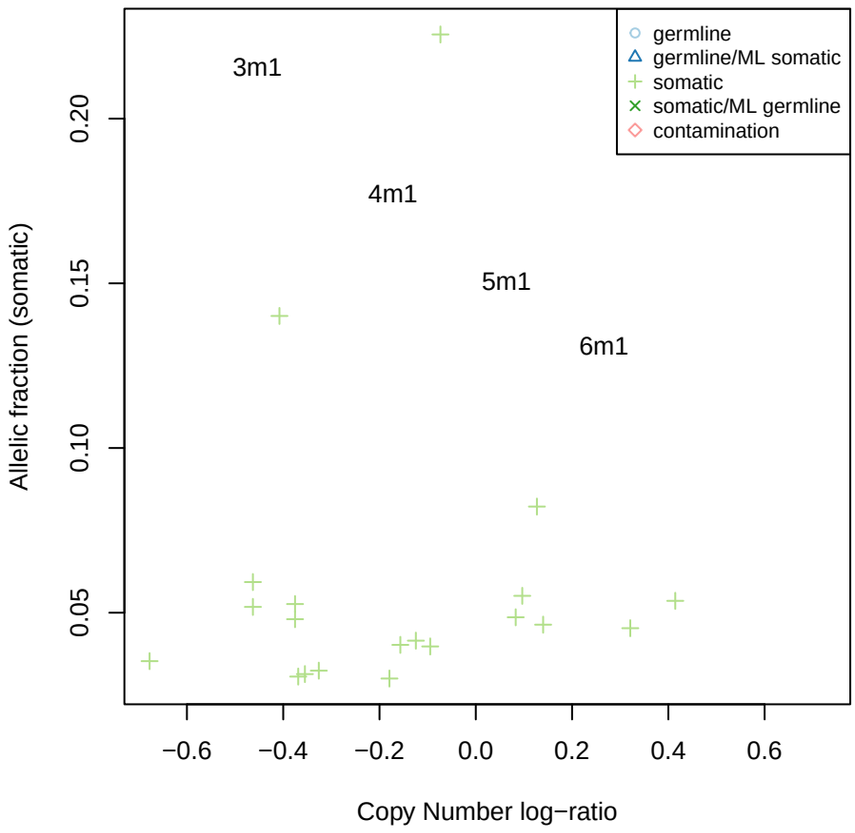

Purity: 0.55 Tumor ploidy: 4.713 SNV log−likelihood: −119.3 GoF: 85.8% Mean coverage: 454;525
1 2 4 6 7 8 10 11 13 14 16 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

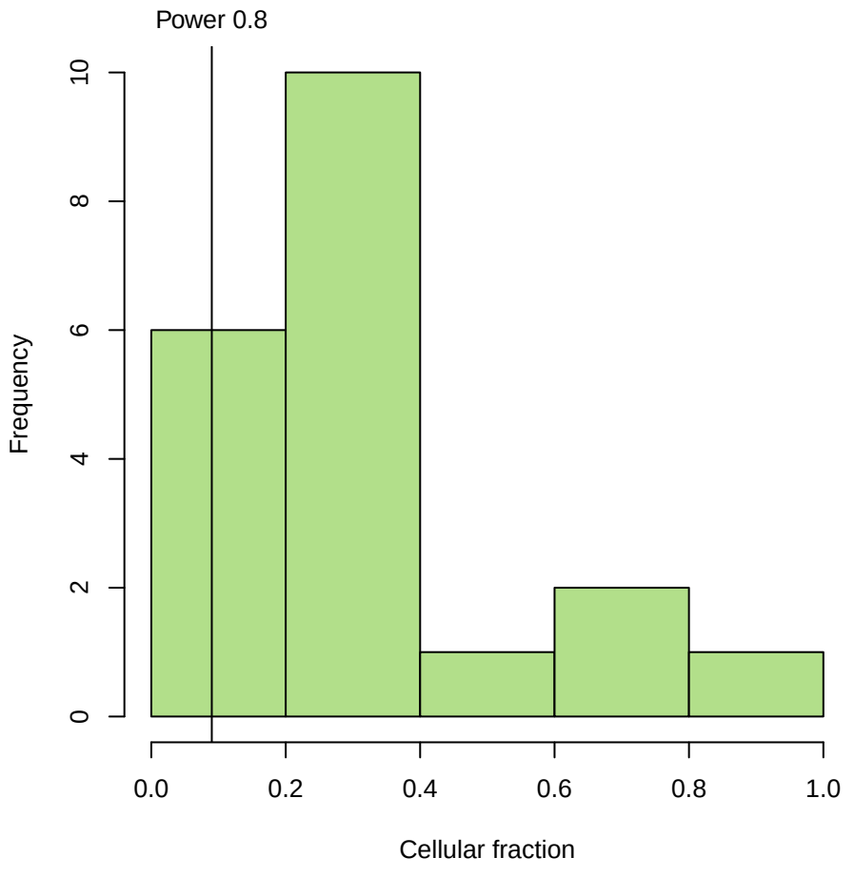

SCNA−fit log−likelihood: −5257.22
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6
0 20 40 60 80
SNV Index

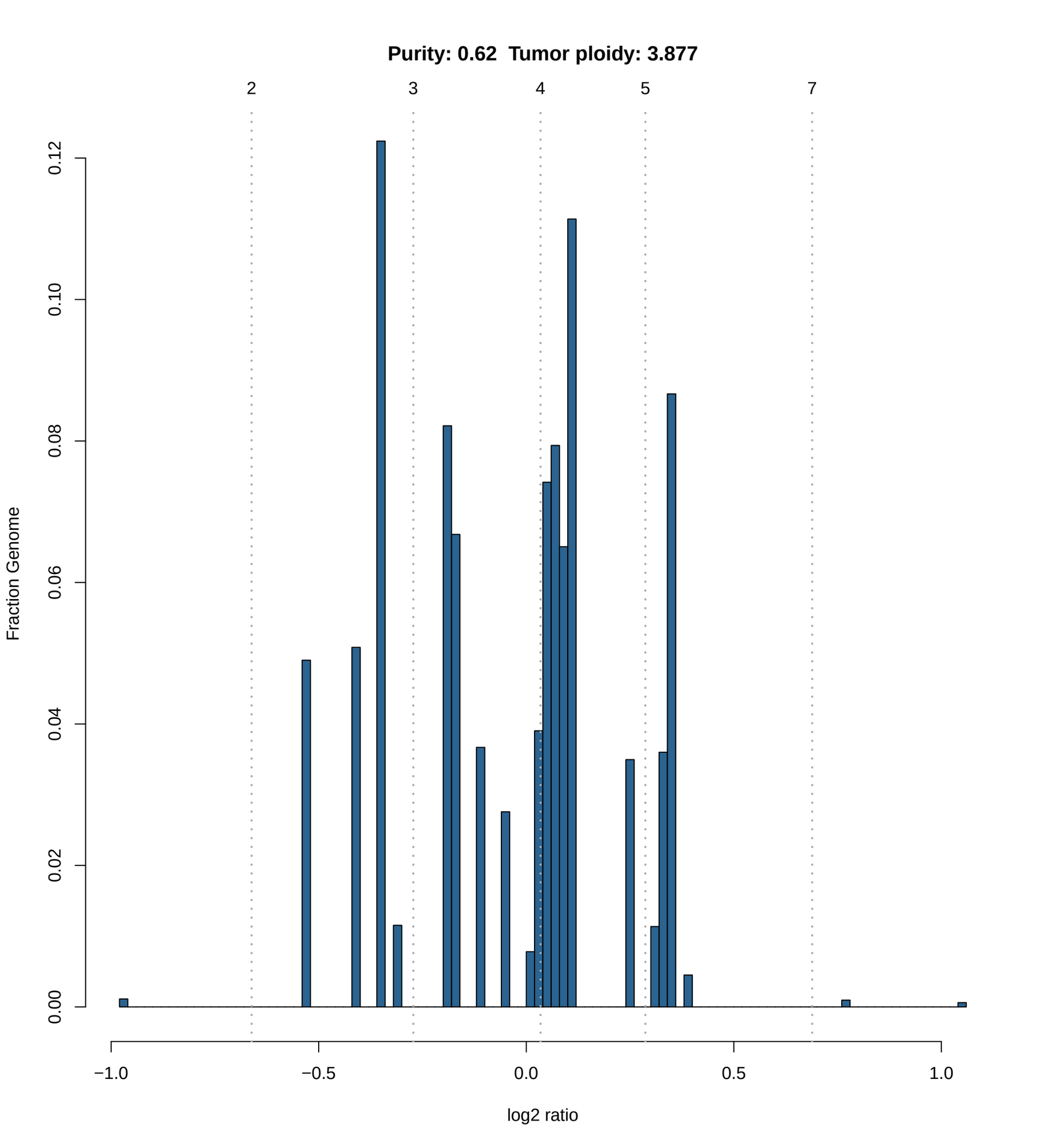

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80
SNV Index

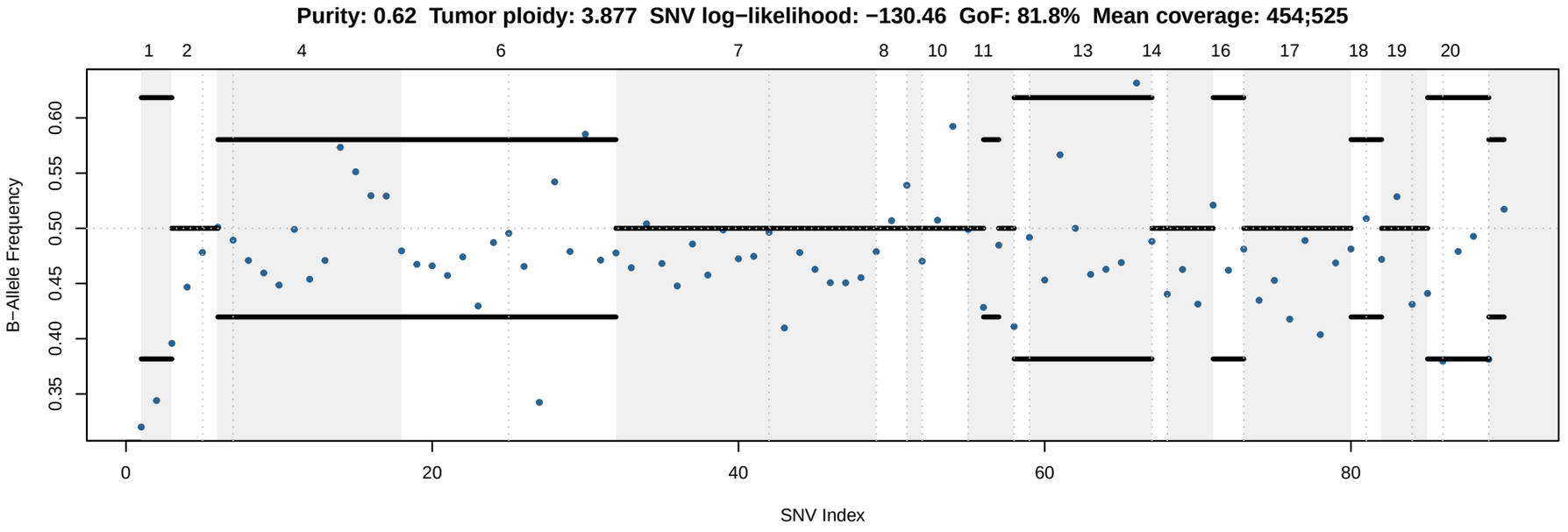

6m4
3m2
5m3
4m2
6m3
5m2
3m1
Allelic fraction (germline)
Copy Number log−ratio

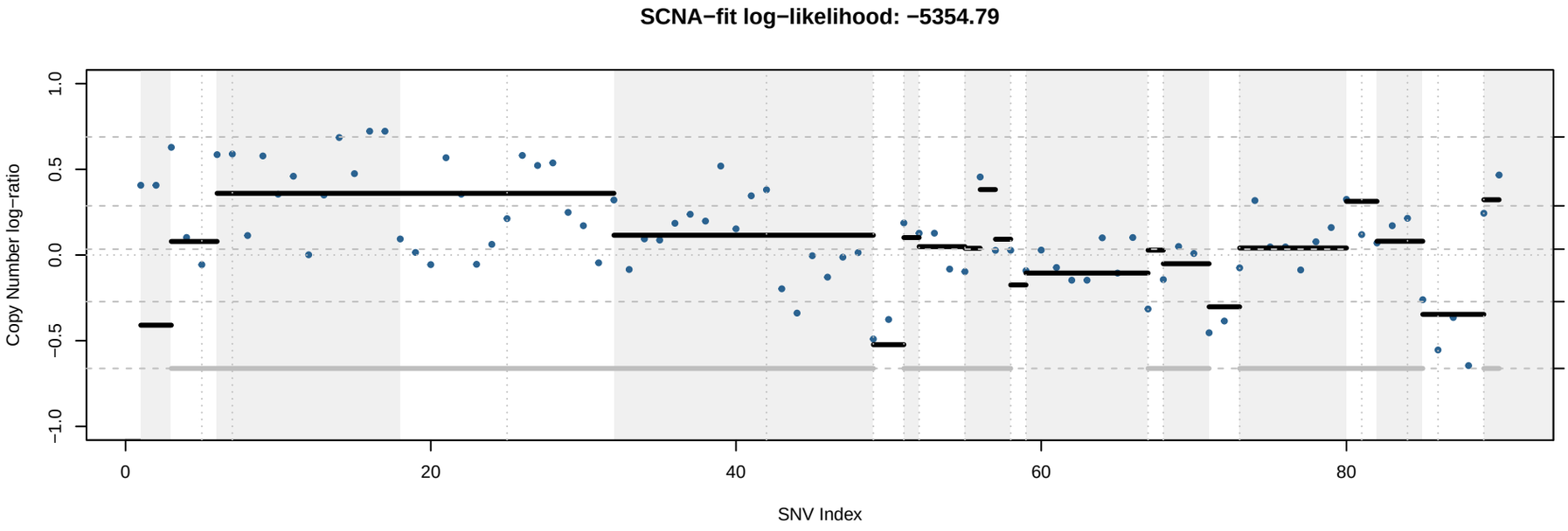

Coverage (log2)
Allelic fraction

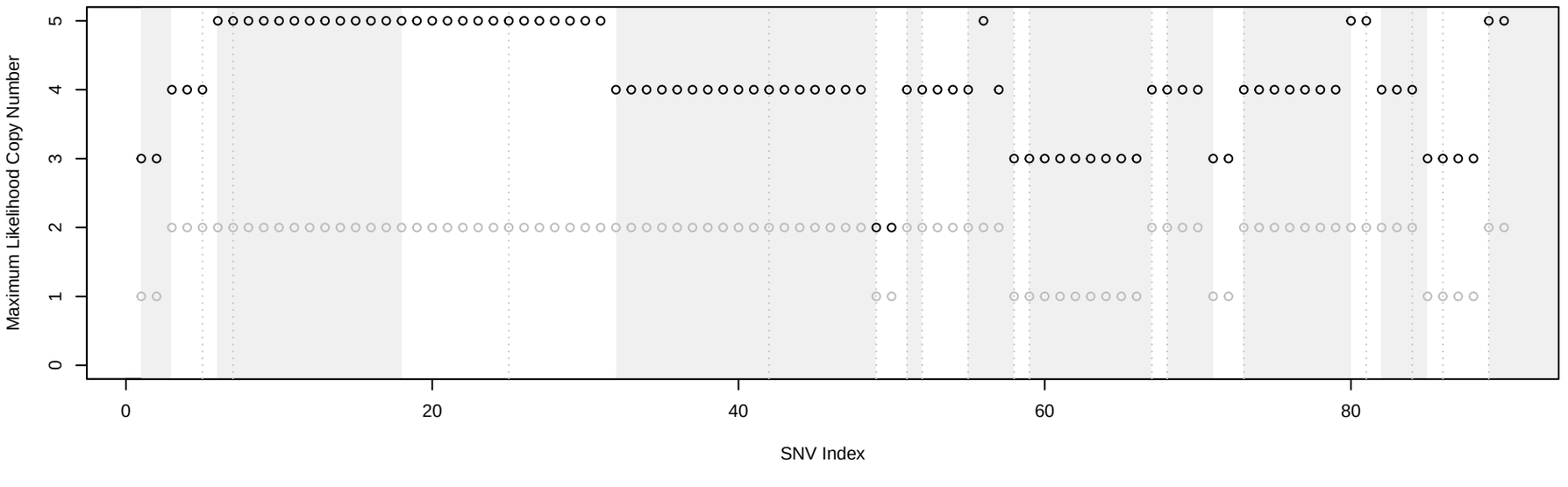

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio

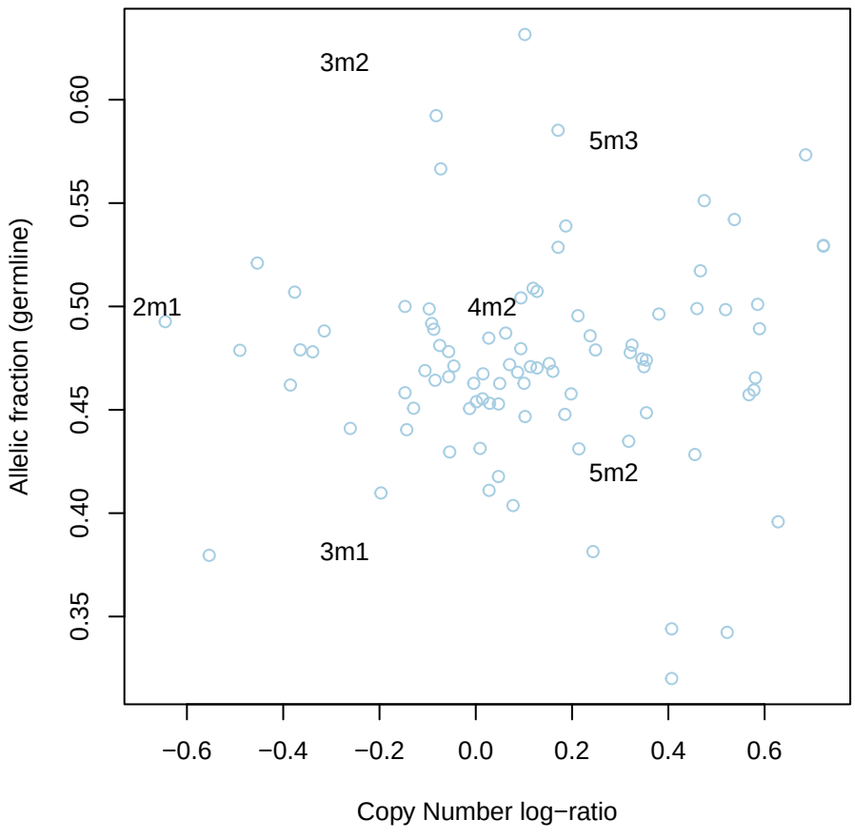

Power 0.8
Frequency
Cellular fraction

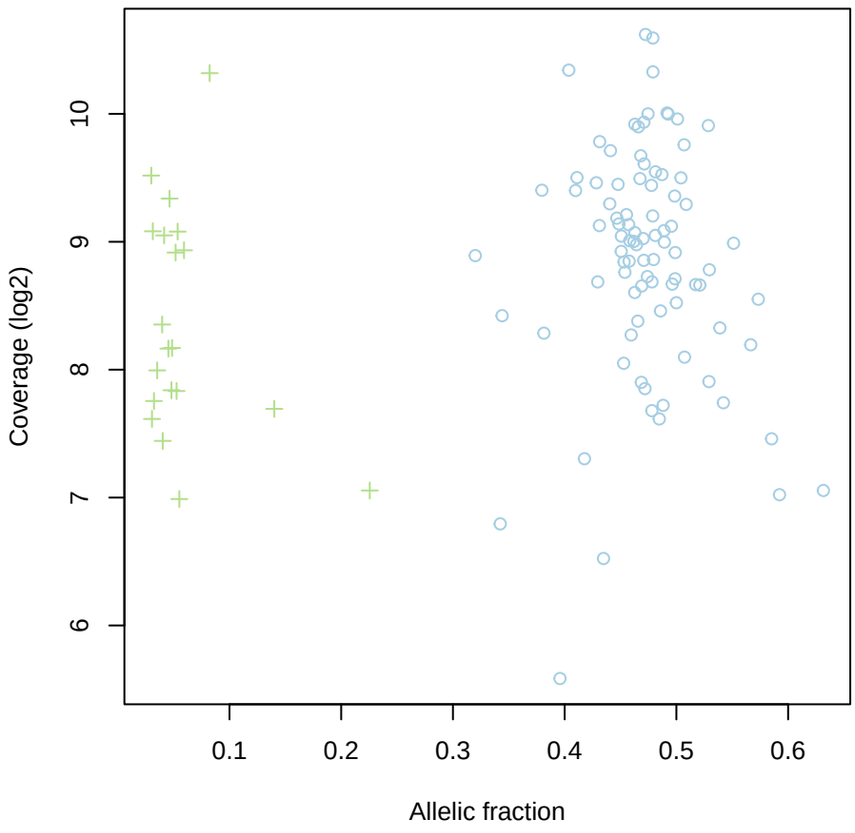

Purity: 0.62 Tumor ploidy: 3.877
2
3
4
5
7
0.12
0.10
0.08
0.06
0.04
0.02
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

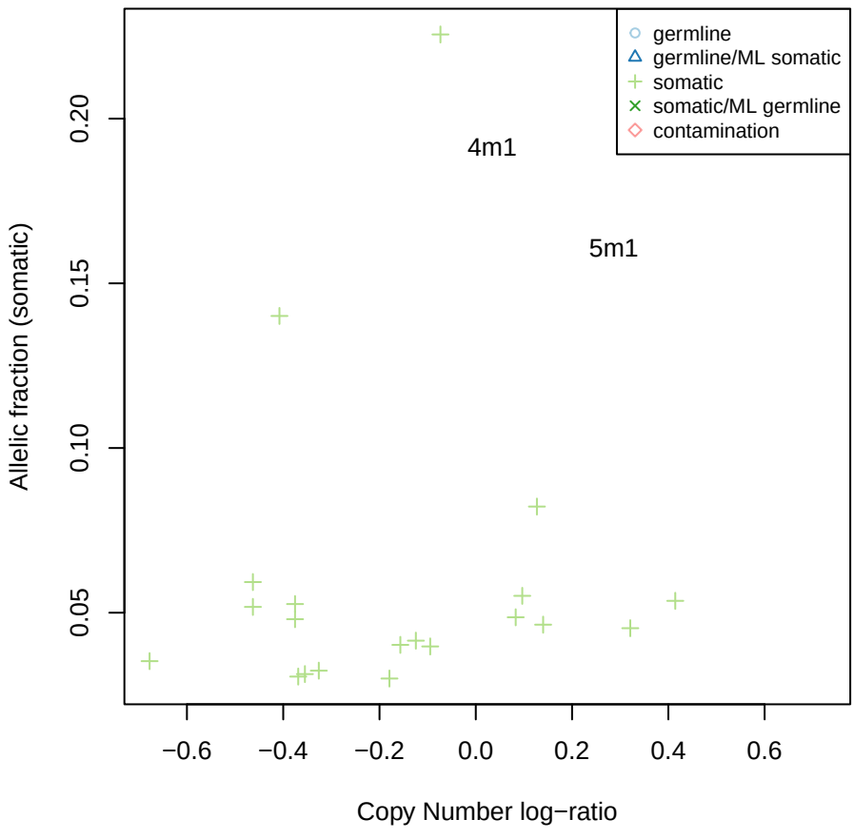

Purity: 0.62 Tumor ploidy: 3.877 SNV log−likelihood: −130.46 GoF: 81.8% Mean coverage: 454;525
1 2 4 6 7 8 10 11 13 14 16 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

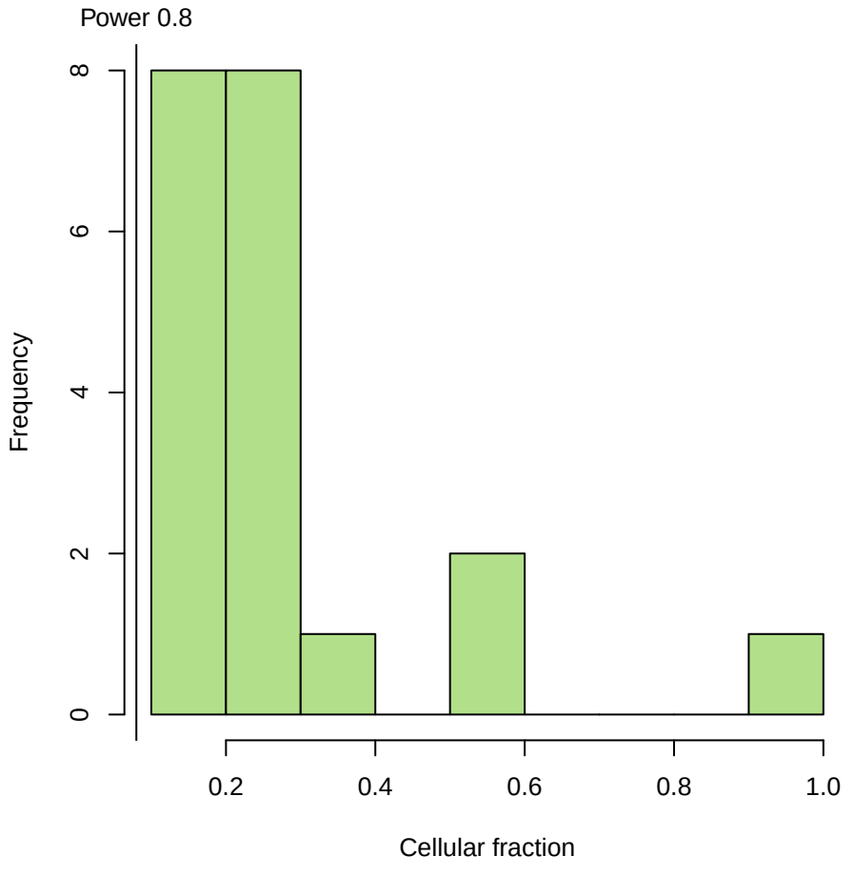

SCNA−fit log−likelihood: −5354.79
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 7
0 20 40 60 80
SNV Index

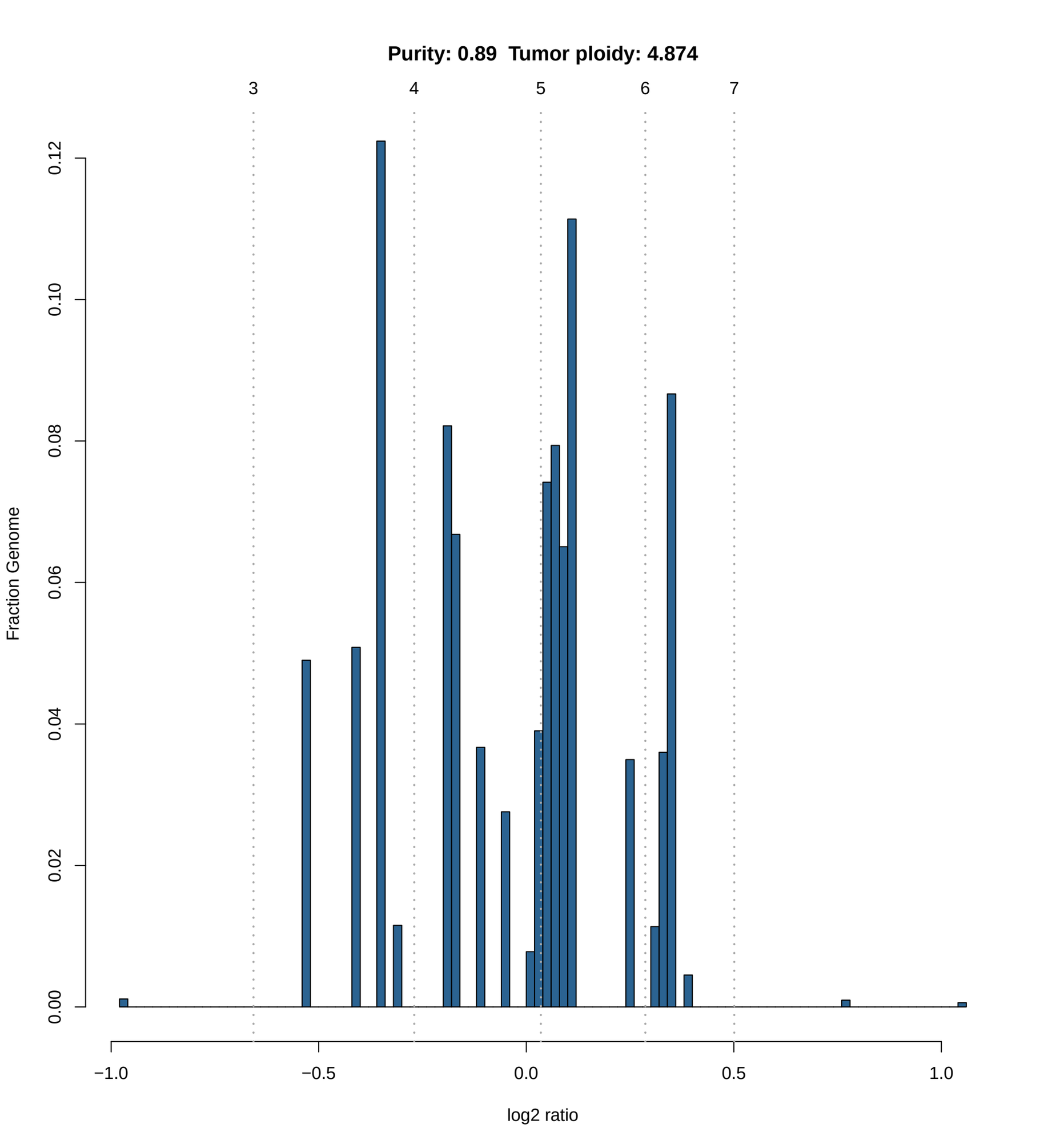

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80
SNV Index

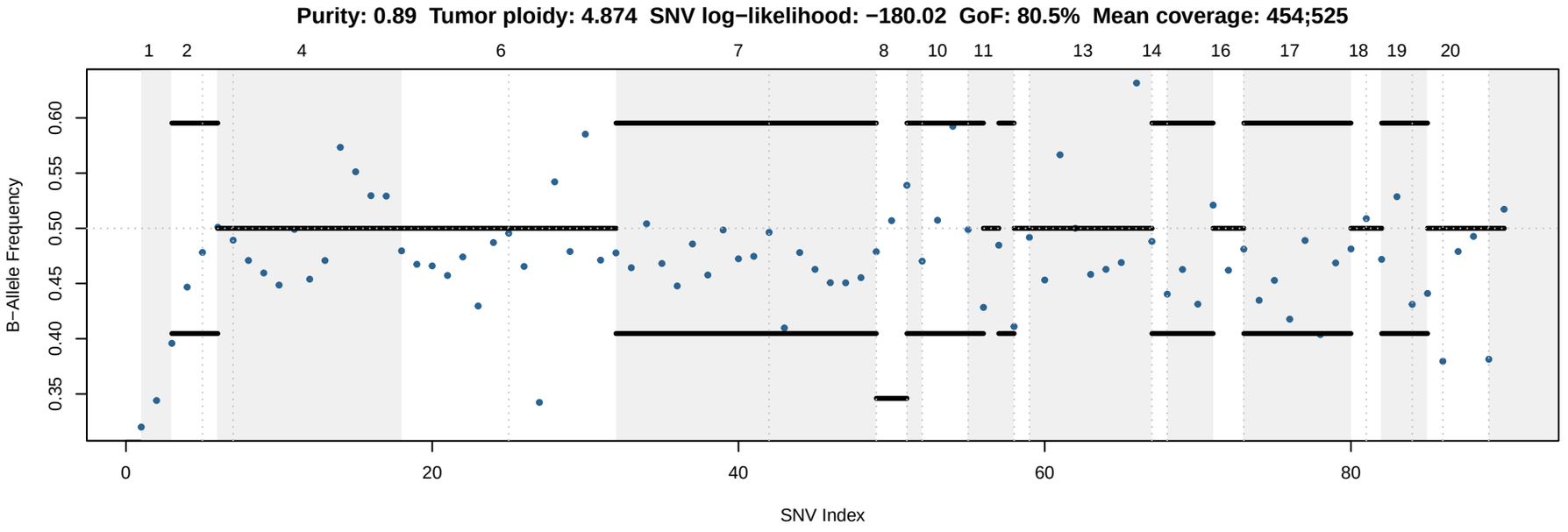

3m2
5m3
2m1
4m2
5m2
3m1
Allelic fraction (germline)
Copy Number log−ratio

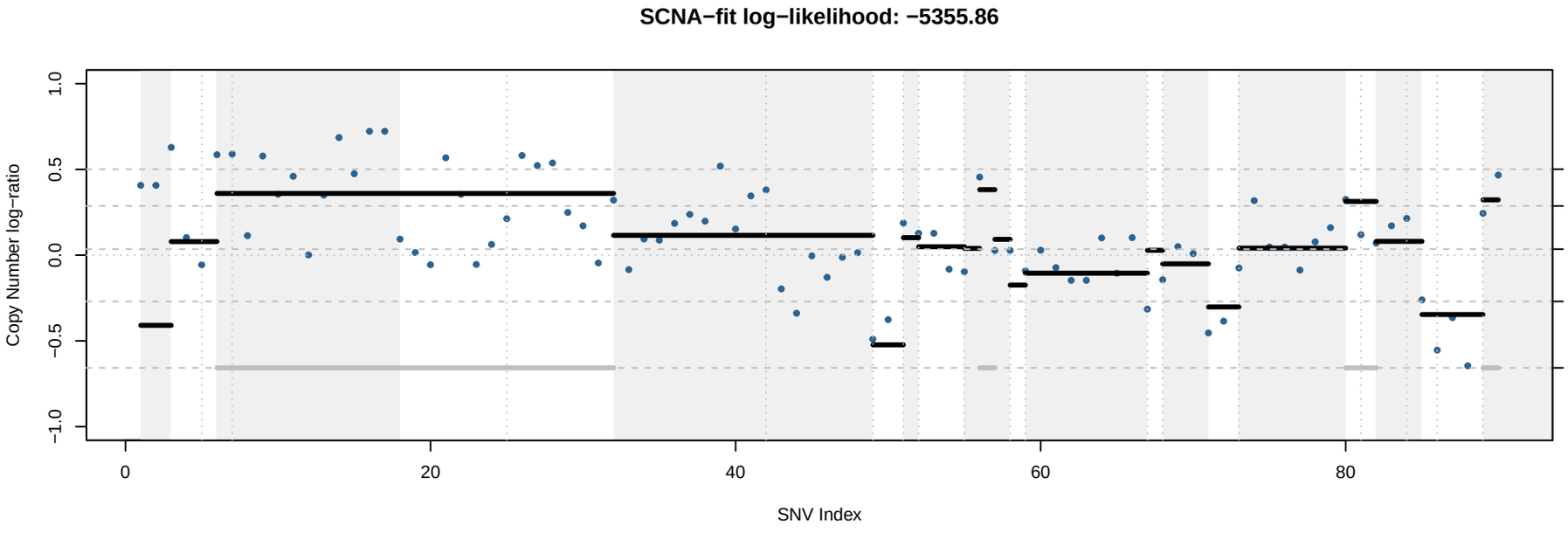

Coverage (log2)
Allelic fraction

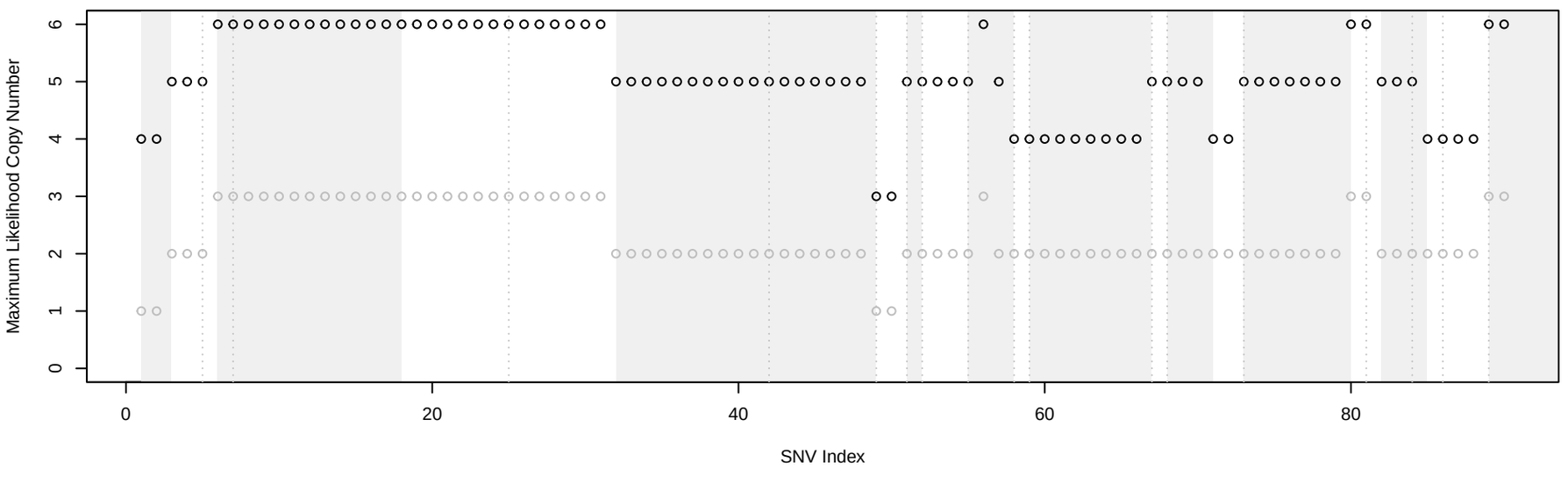

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
Allelic fraction (somatic)
Copy Number log−ratio

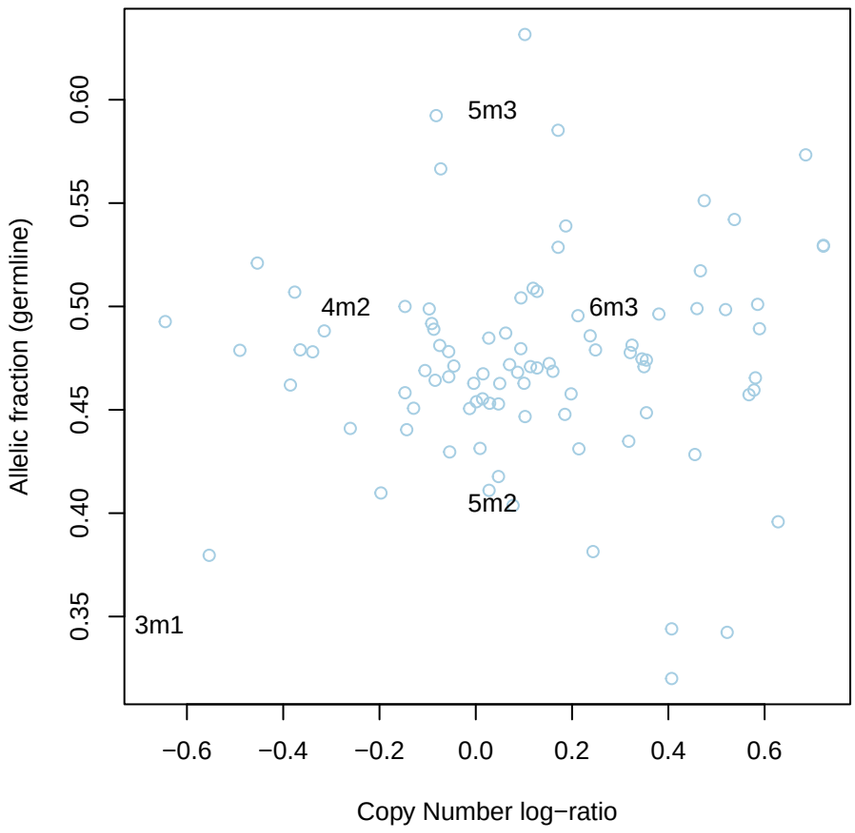

Power 0.8
Frequency
Cellular fraction

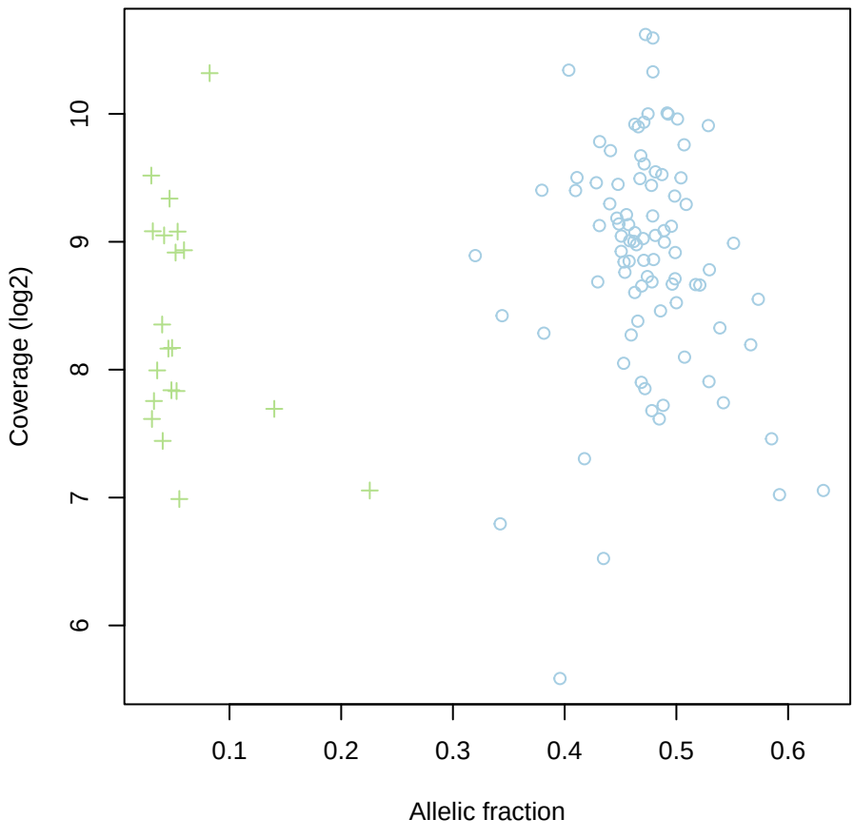

Purity: 0.89 Tumor ploidy: 4.874
3
4
5
6
7
0.12
0.10
0.08
0.06
0.04
0.02
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

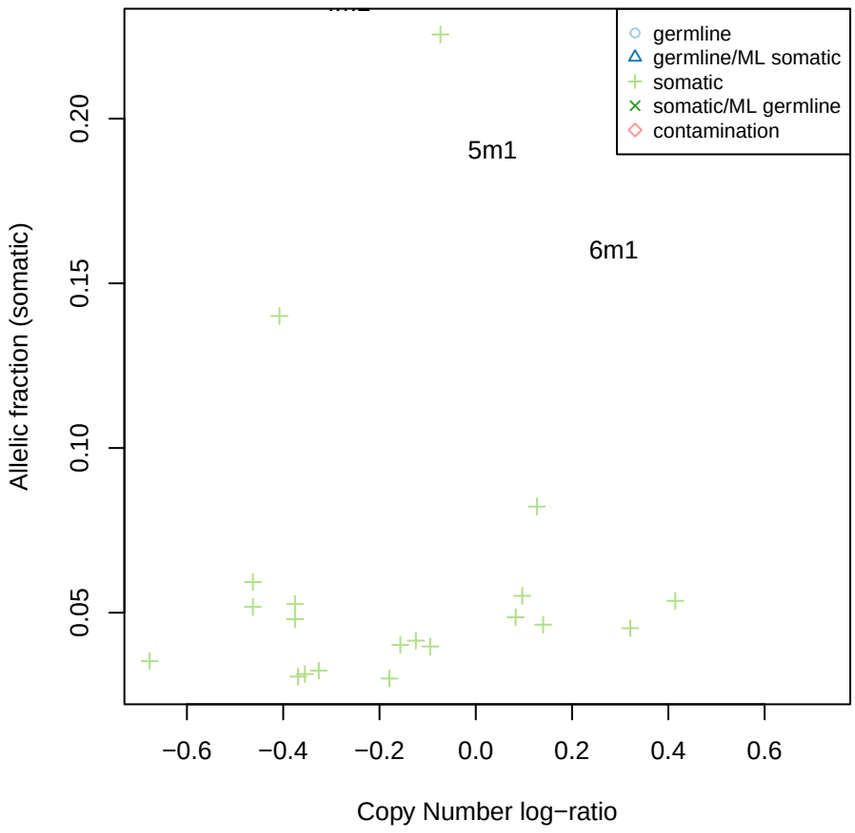

Purity: 0.89 Tumor ploidy: 4.874 SNV log−likelihood: −180.02 GoF: 80.5% Mean coverage: 454;525
1 2 4 6 7 8 10 11 13 14 16 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

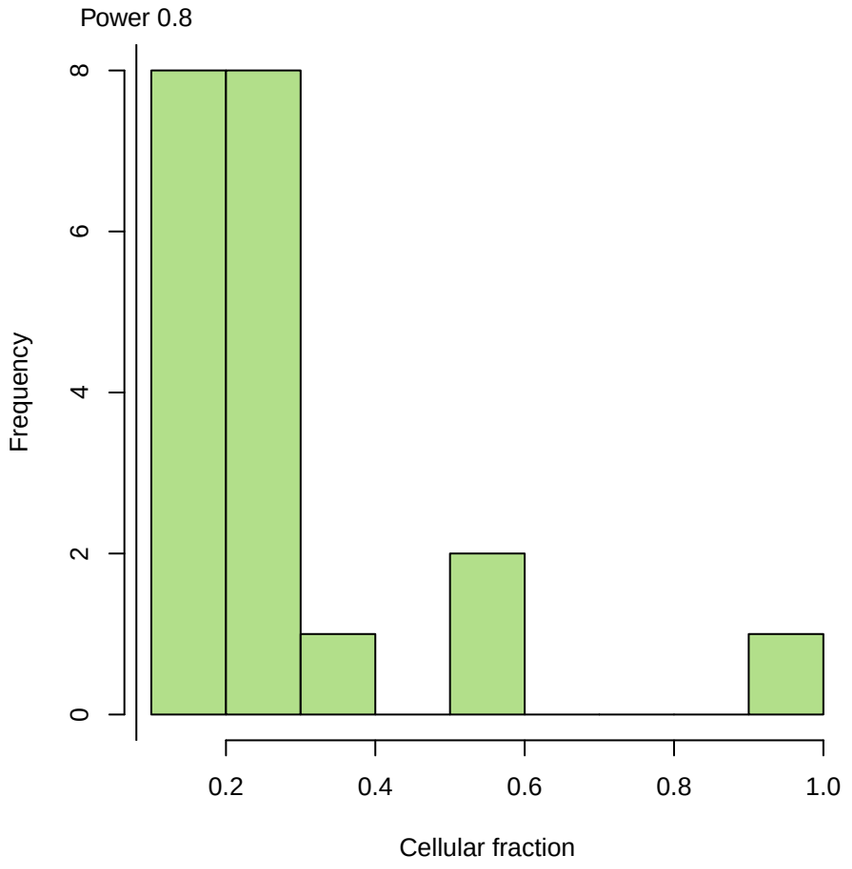

SCNA−fit log−likelihood: −5355.86
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 20 40 60 80
SNV Index

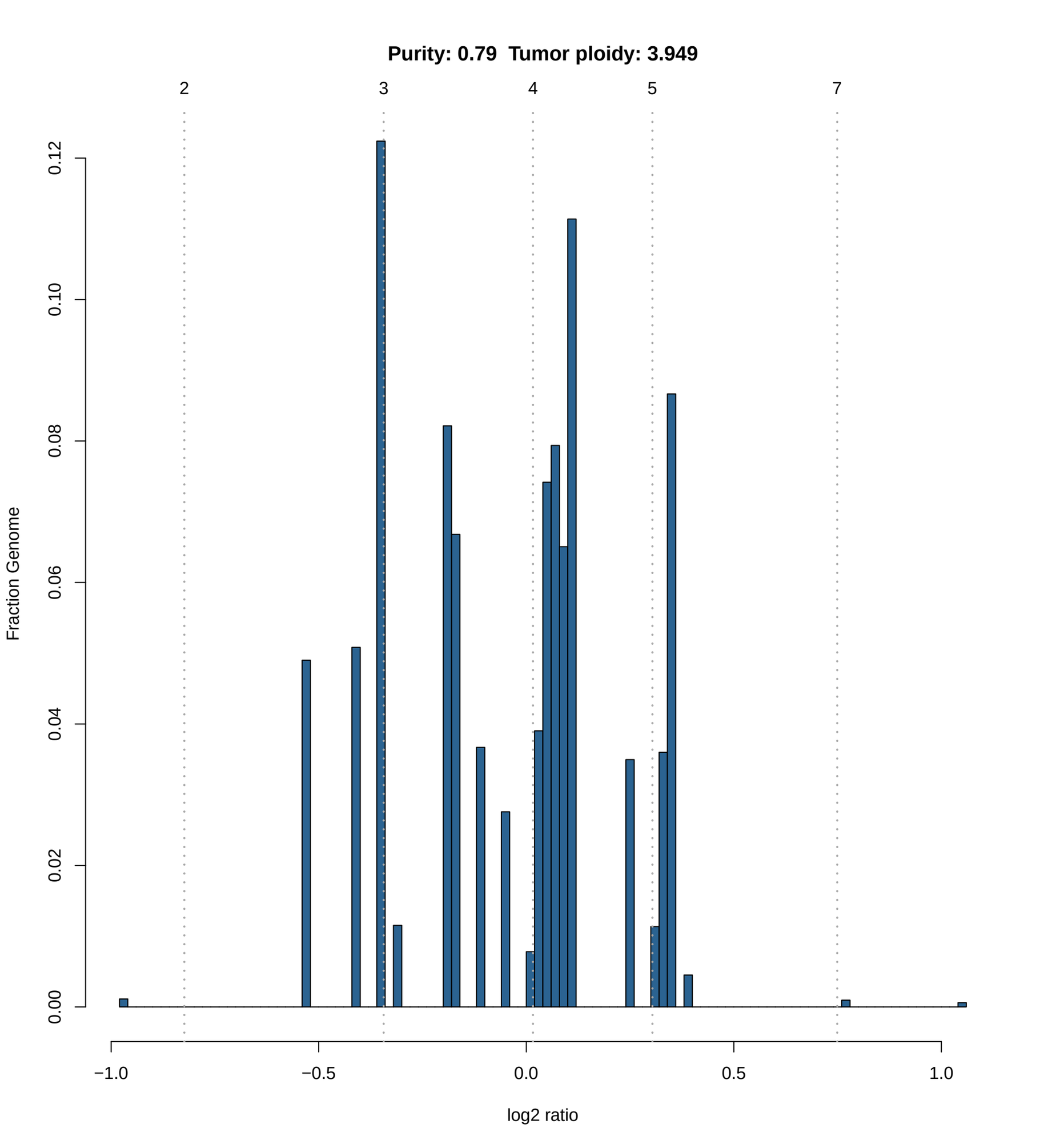

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80
SNV Index

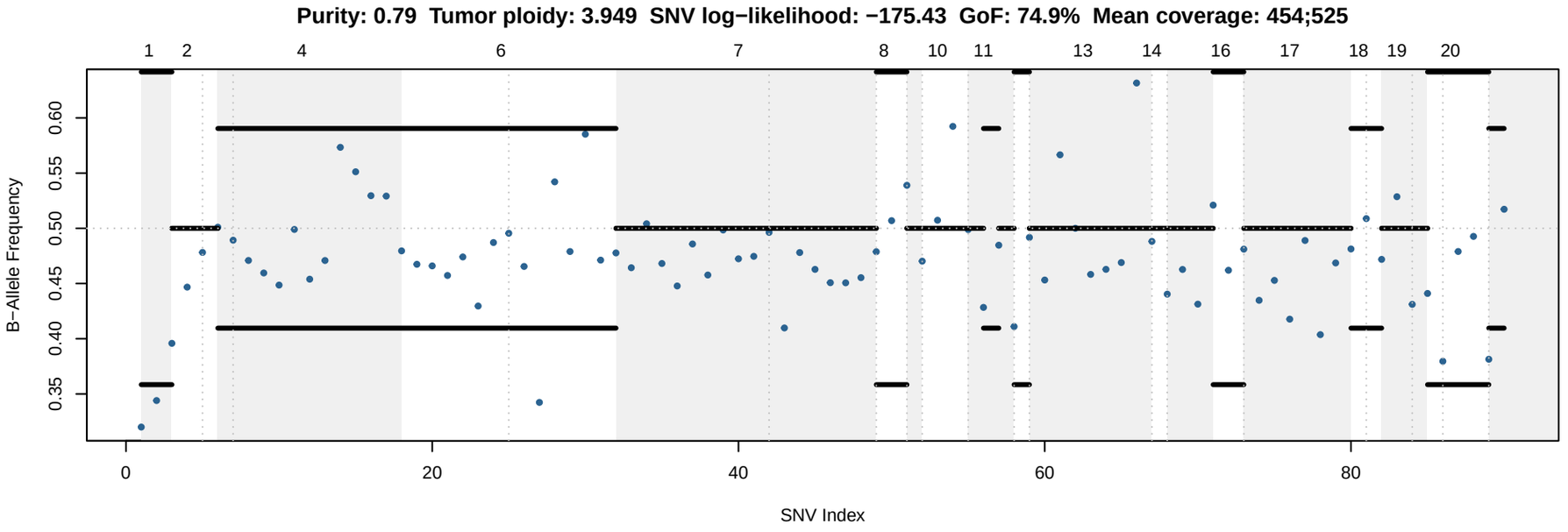

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
5m3
4m2
6m3
5m2
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

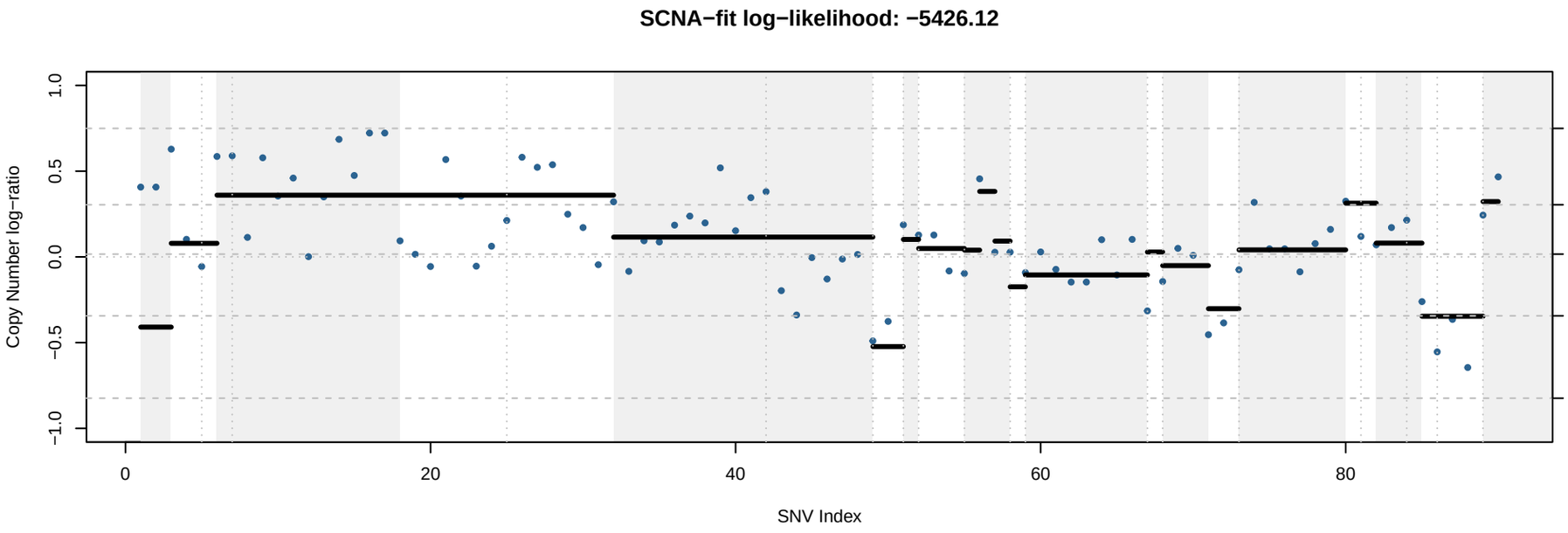

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

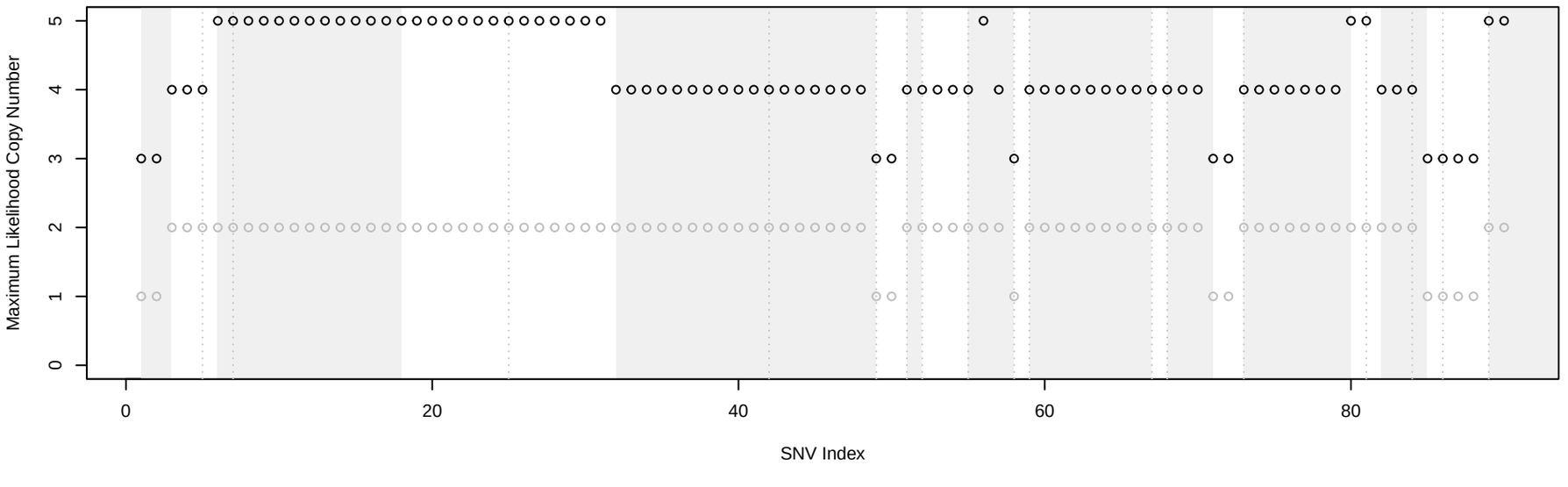

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
5m1
6m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

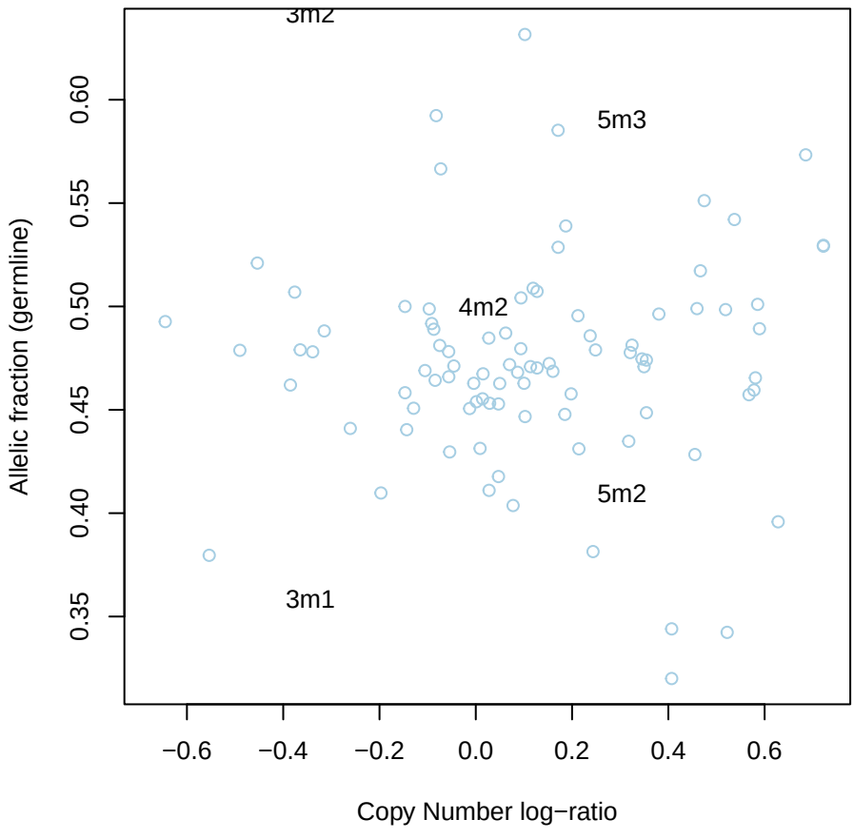

Power 0.8
Frequency
0
2
4
6
8
0.2
0.4
0.6
0.8
1.0
Cellular fraction

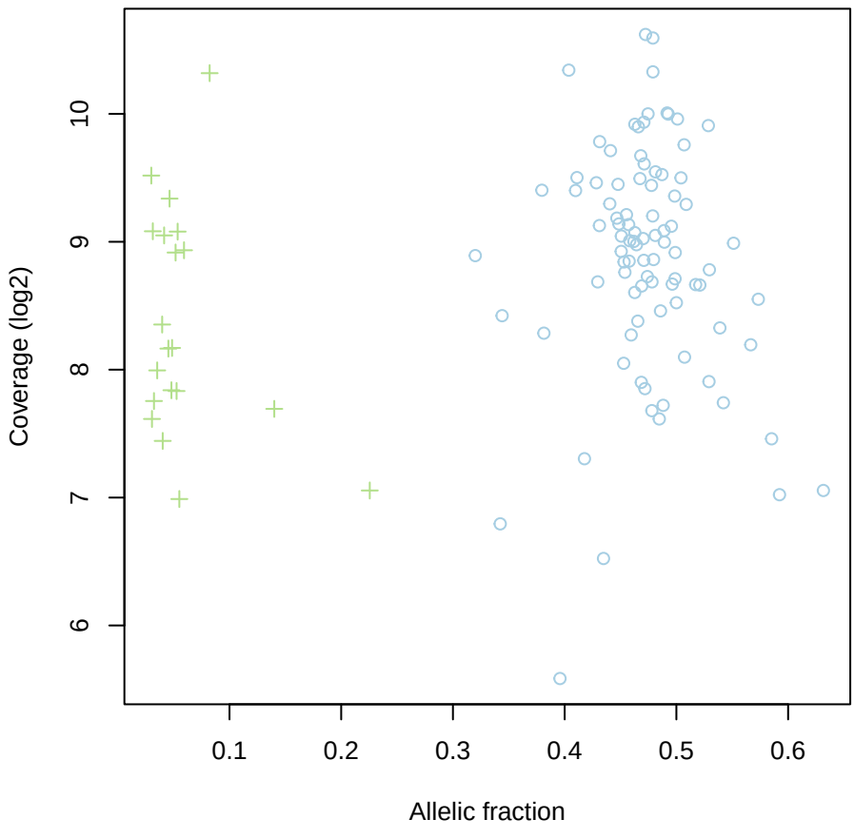

Purity: 0.79 Tumor ploidy: 3.949
2
3
4
5
7
0.00
0.02
0.04
0.06
0.08
0.10
0.12
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

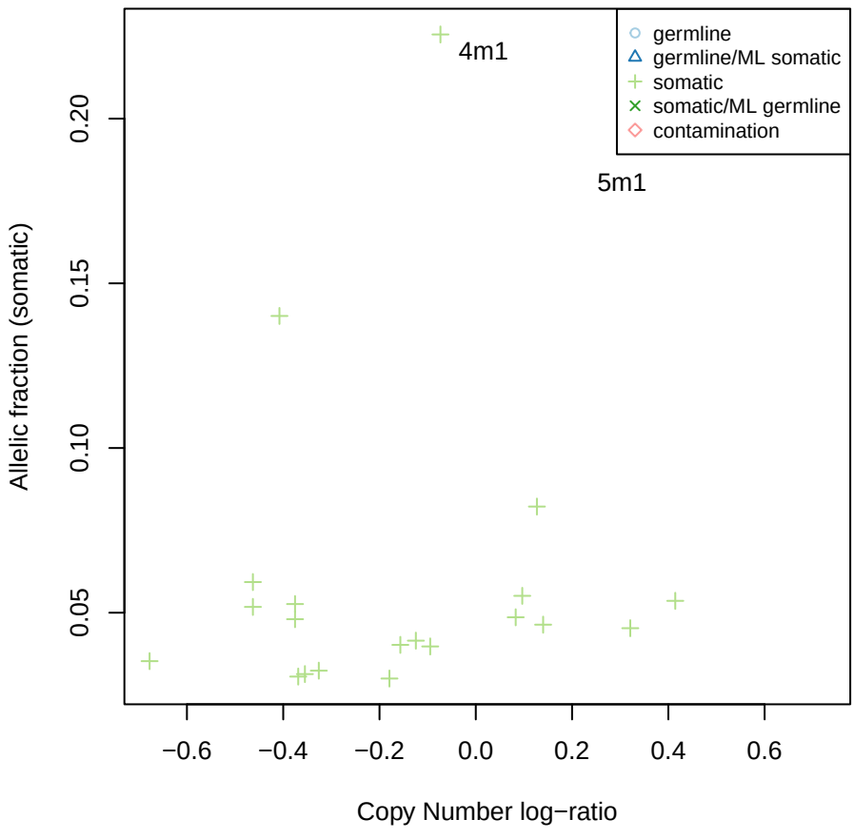

Purity: 0.79 Tumor ploidy: 3.949 SNV log−likelihood: −175.43 GoF: 74.9% Mean coverage: 454;525
1 2 4 6 7 8 10 11 13 14 16 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

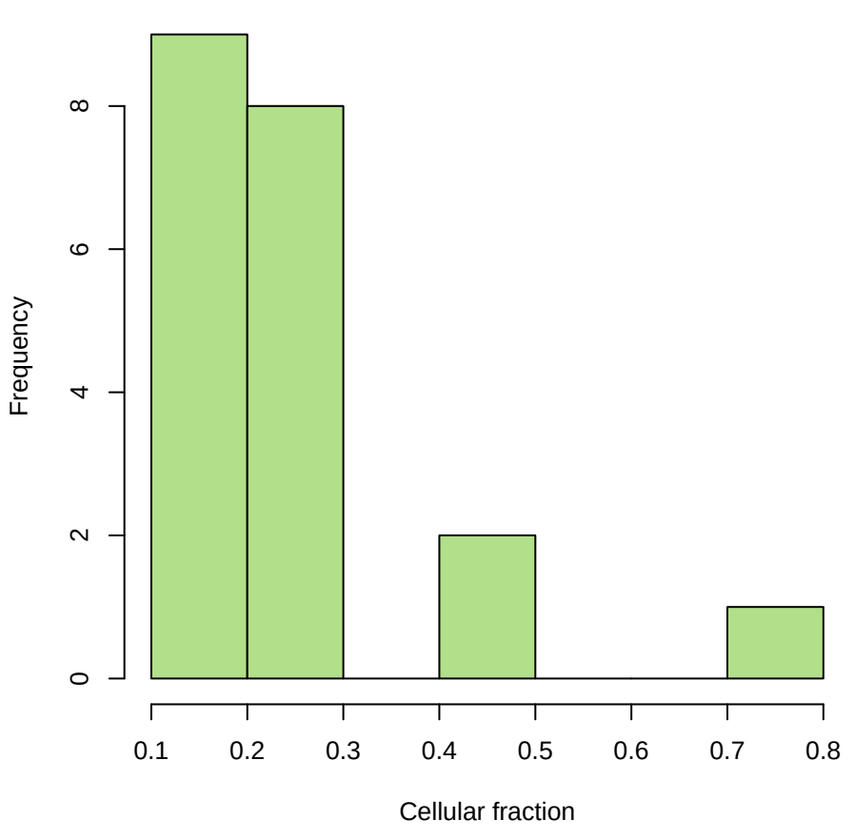

SCNA−fit log−likelihood: −5426.12
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 7
0 20 40 60 80
SNV Index

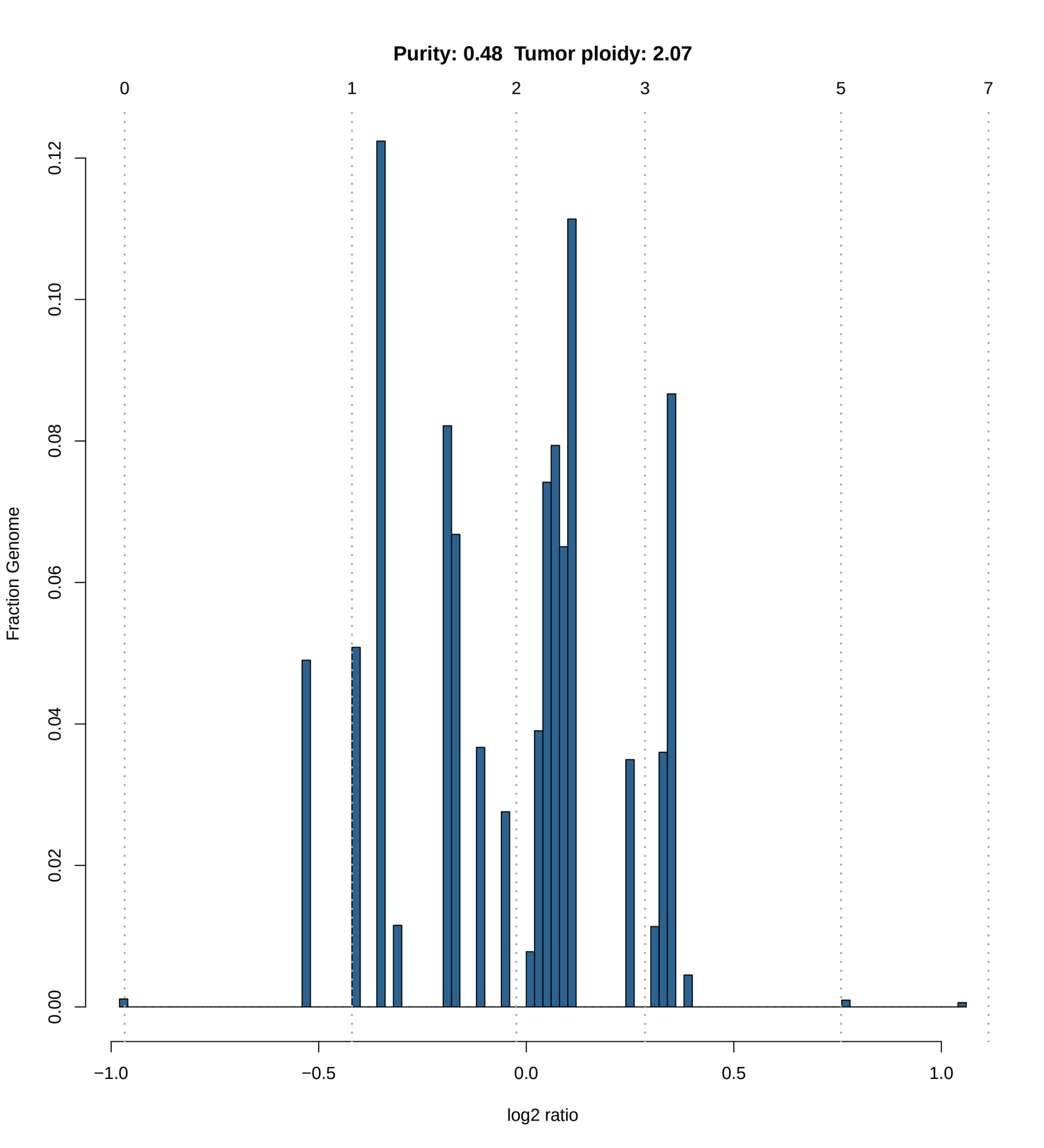

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80
SNV Index

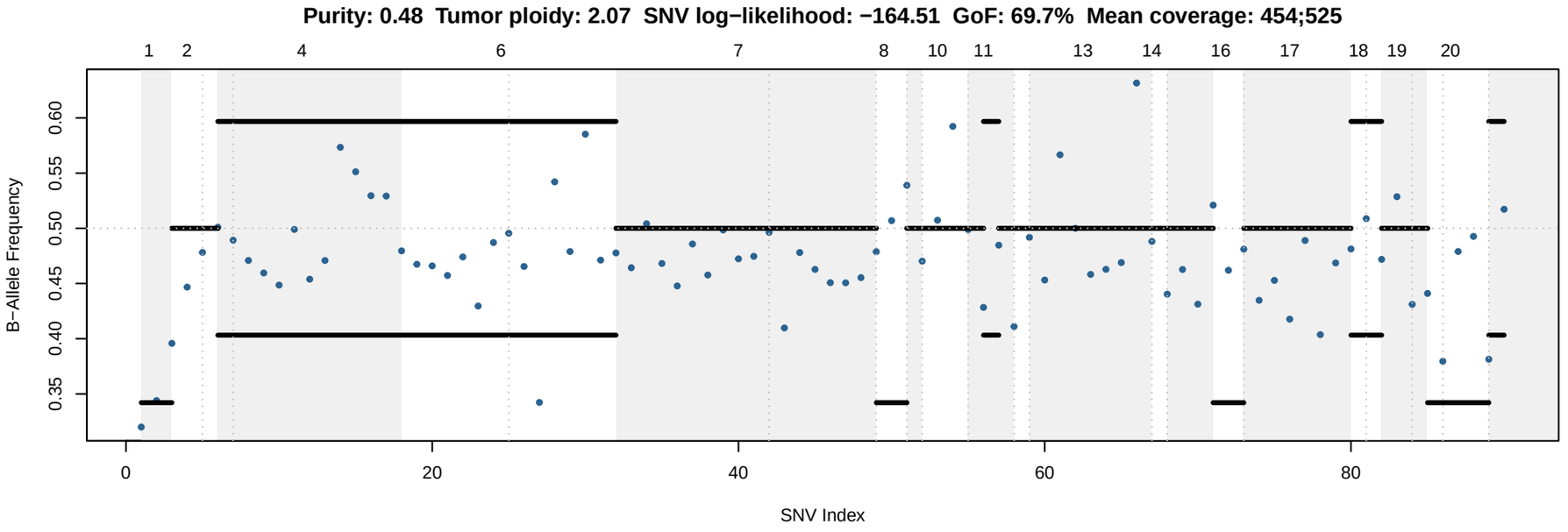

3m2
5m3
4m2
5m2
3m1
Allelic fraction (germline)
Copy Number log−ratio

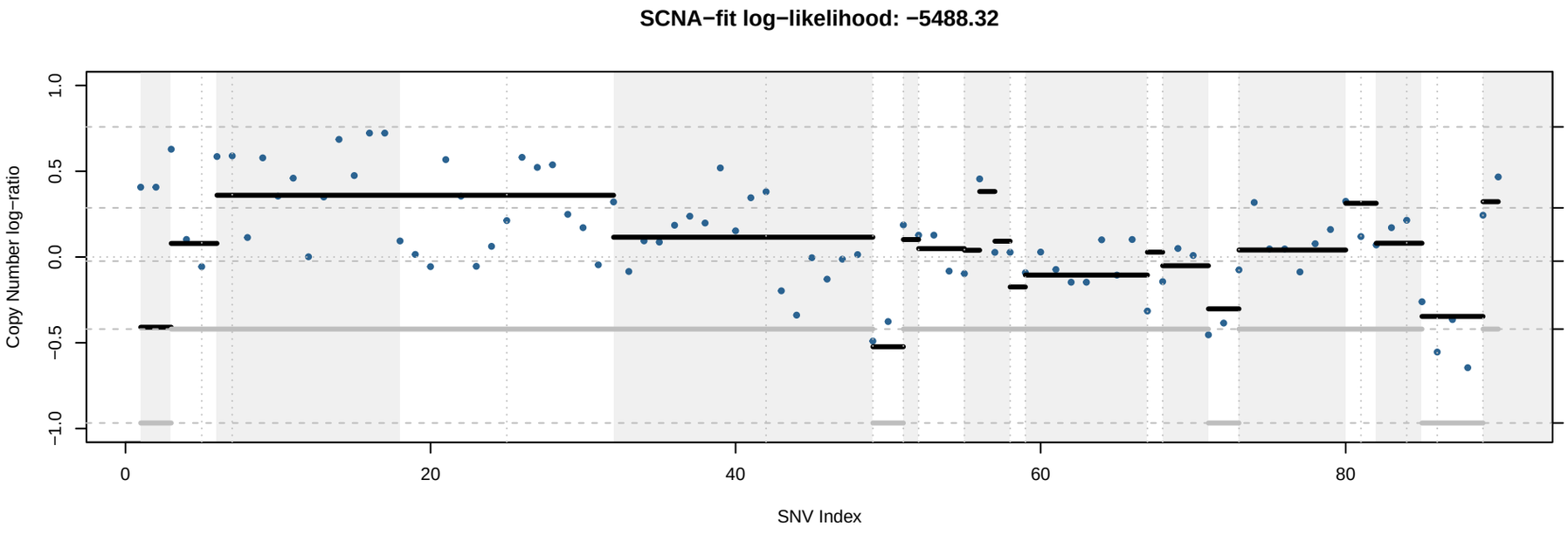

Coverage (log2)
Allelic fraction

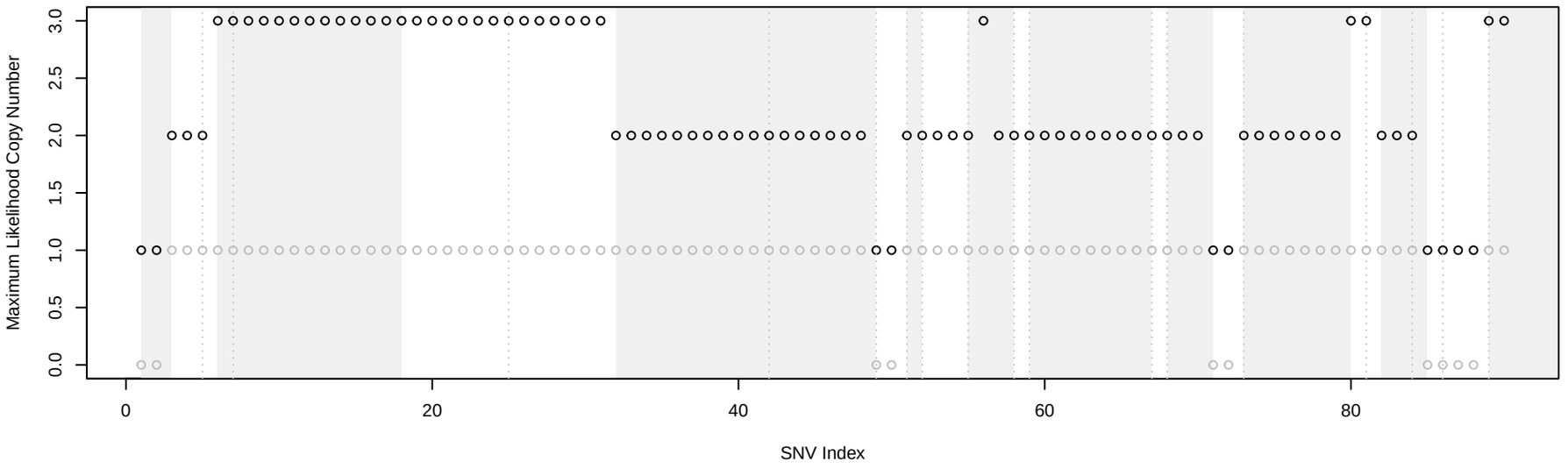

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
Allelic fraction (somatic)
Copy Number log−ratio

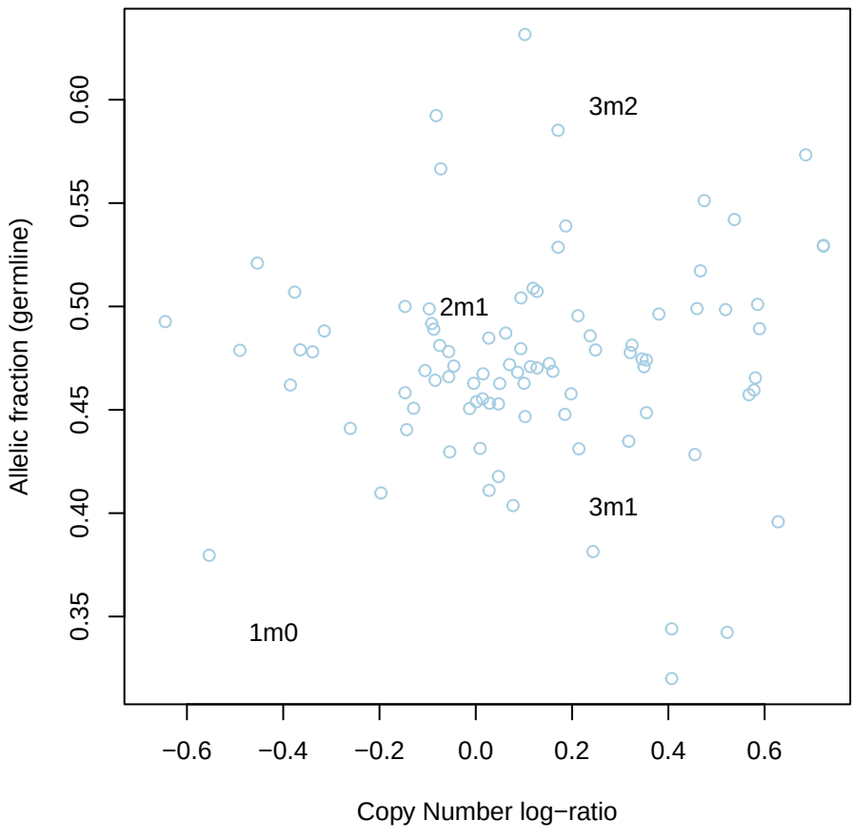

Frequency
Cellular fraction

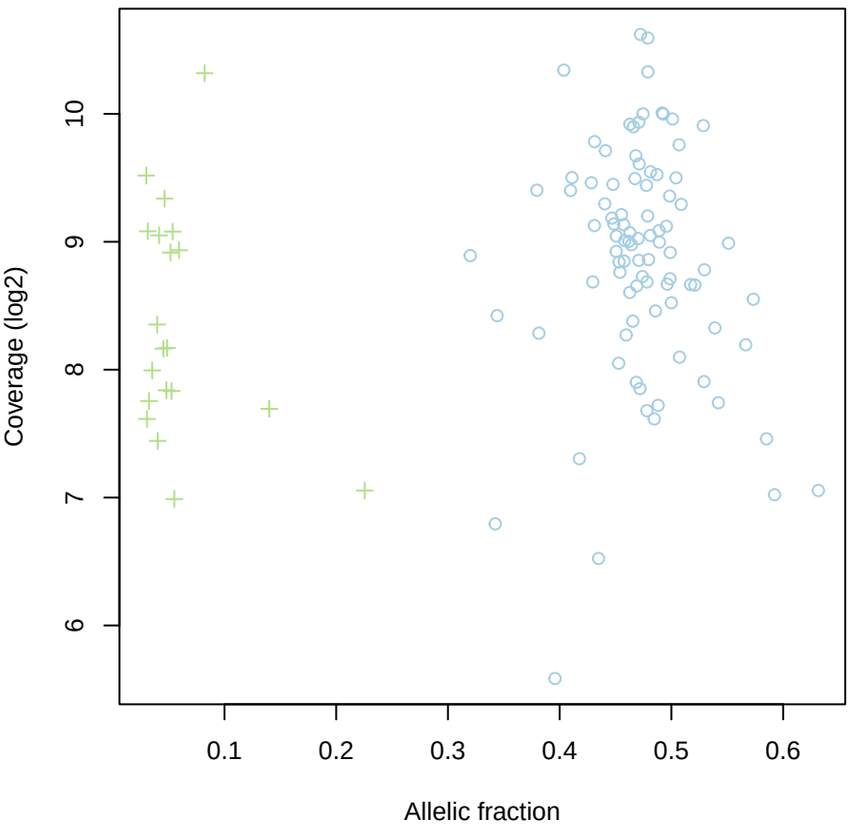

Purity: 0.48 Tumor ploidy: 2.07
0
1
2
3
5
7
0.12
0.10
0.08
0.06
0.04
0.02
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

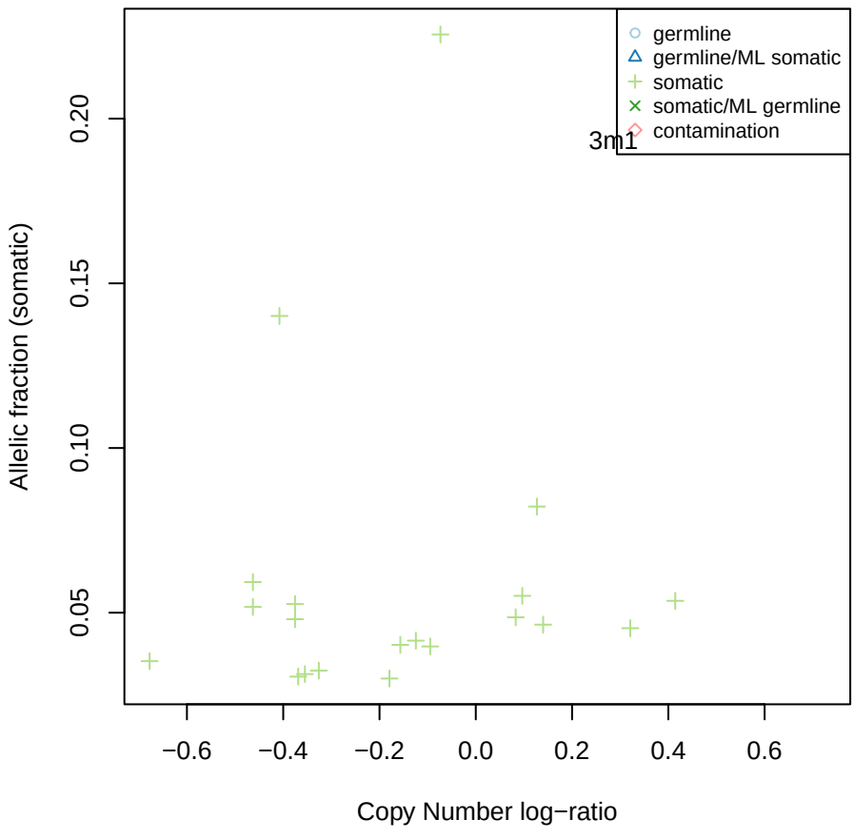

Purity: 0.48 Tumor ploidy: 2.07 SNV log−likelihood: −164.51 GoF: 69.7% Mean coverage: 454;525
1 2 4 6 7 8 10 11 13 14 16 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

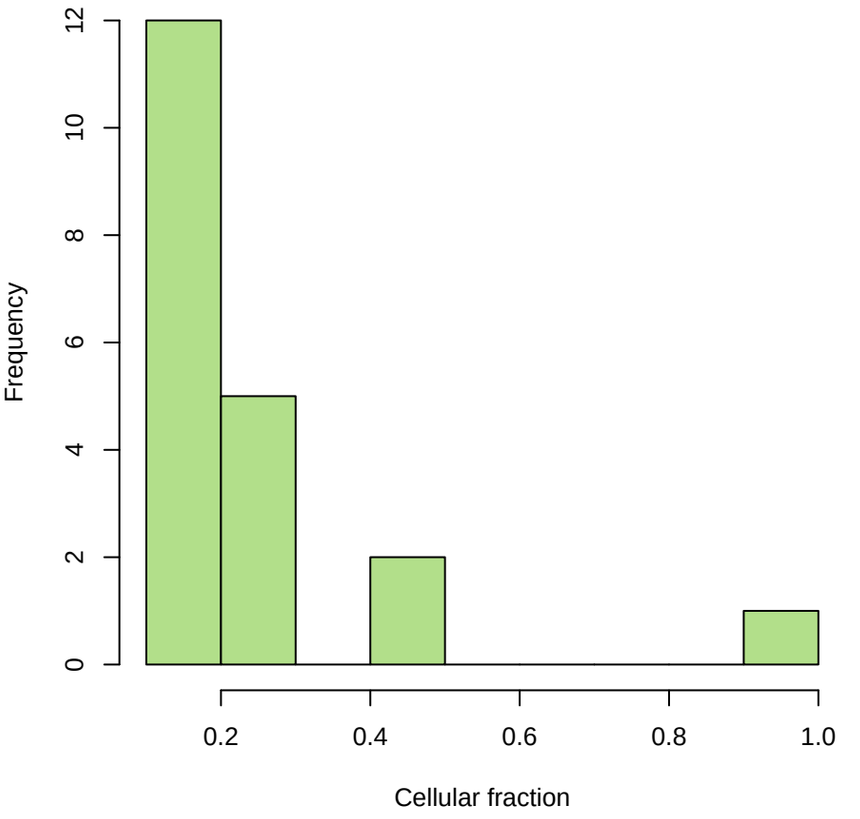

SCNA−fit log−likelihood: −5488.32
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 5
0 20 40 60 80
SNV Index

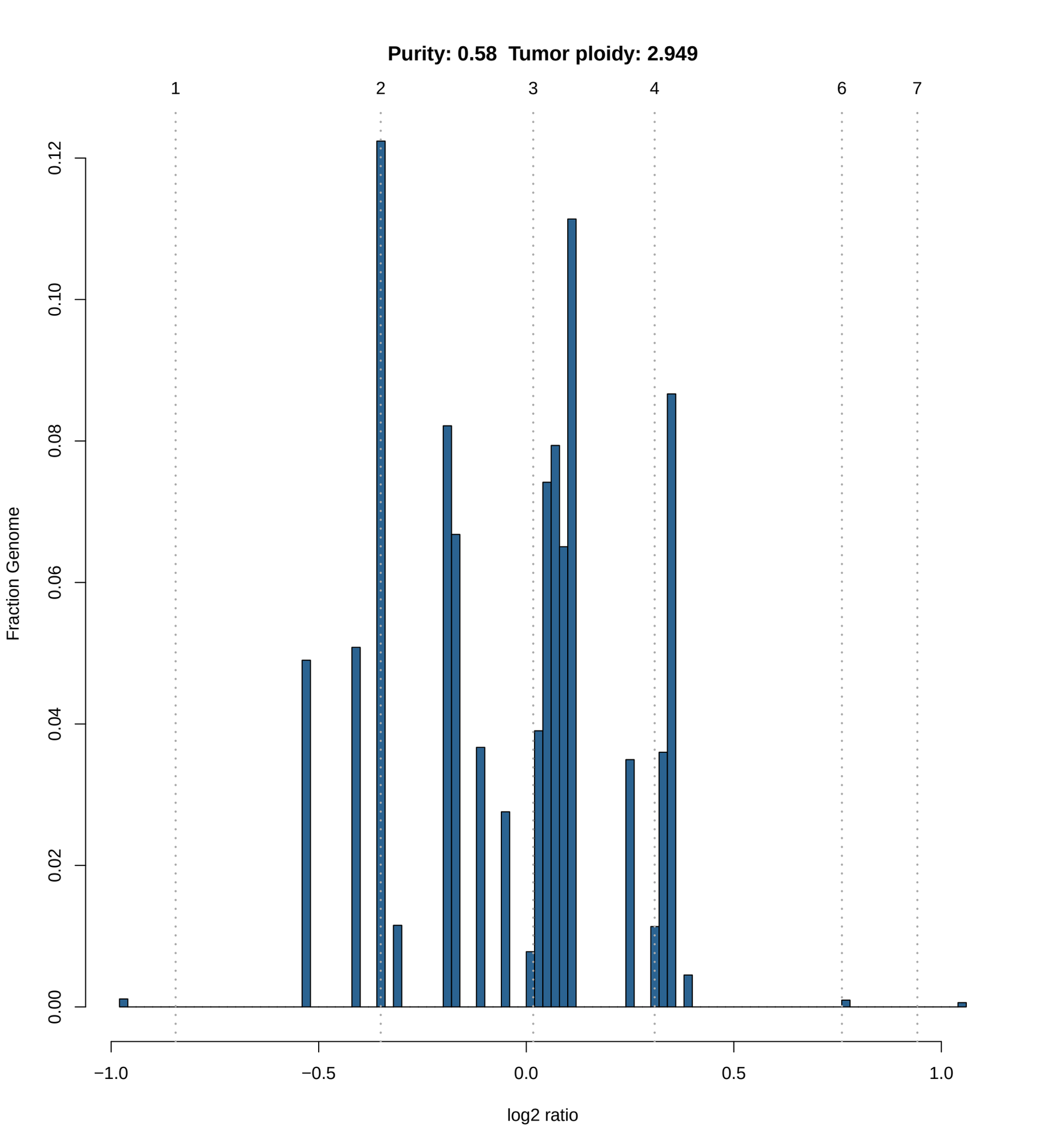

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80
SNV Index

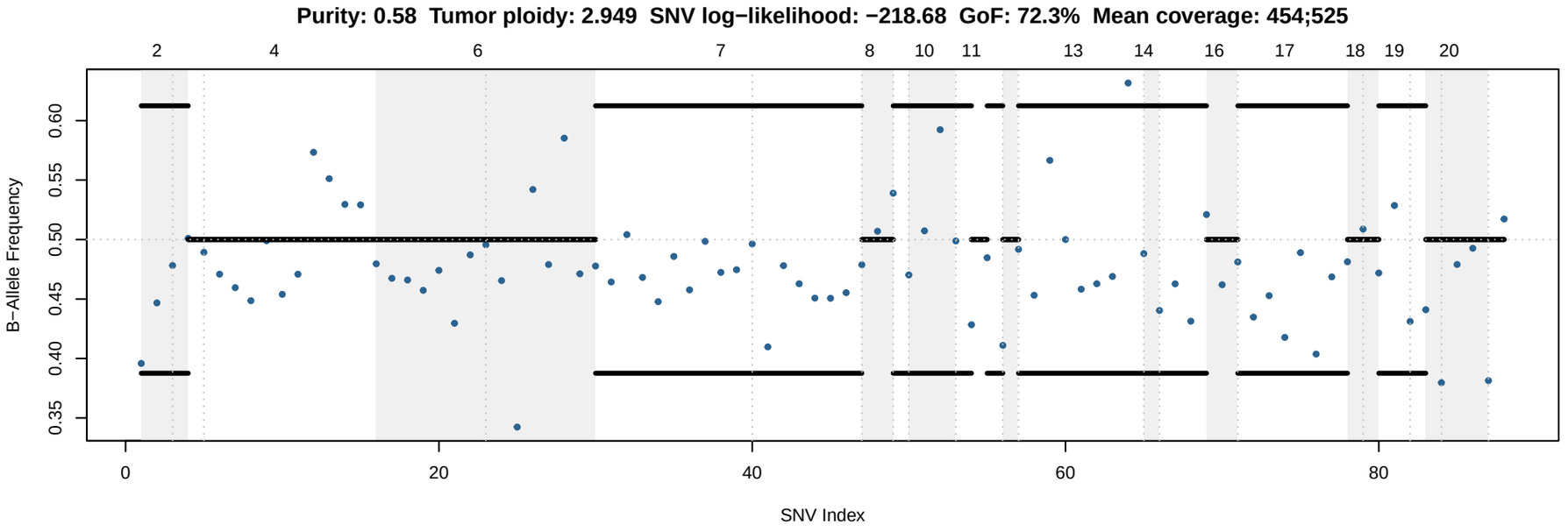

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
3m2
2m1
3m1
1m0
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

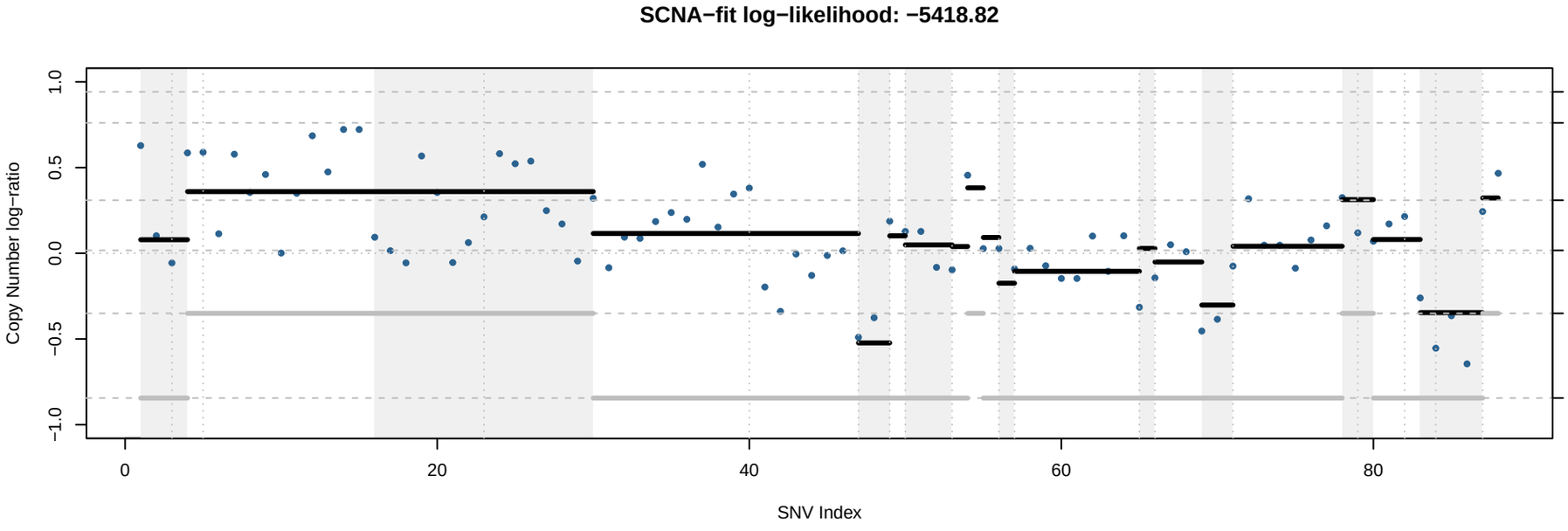

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

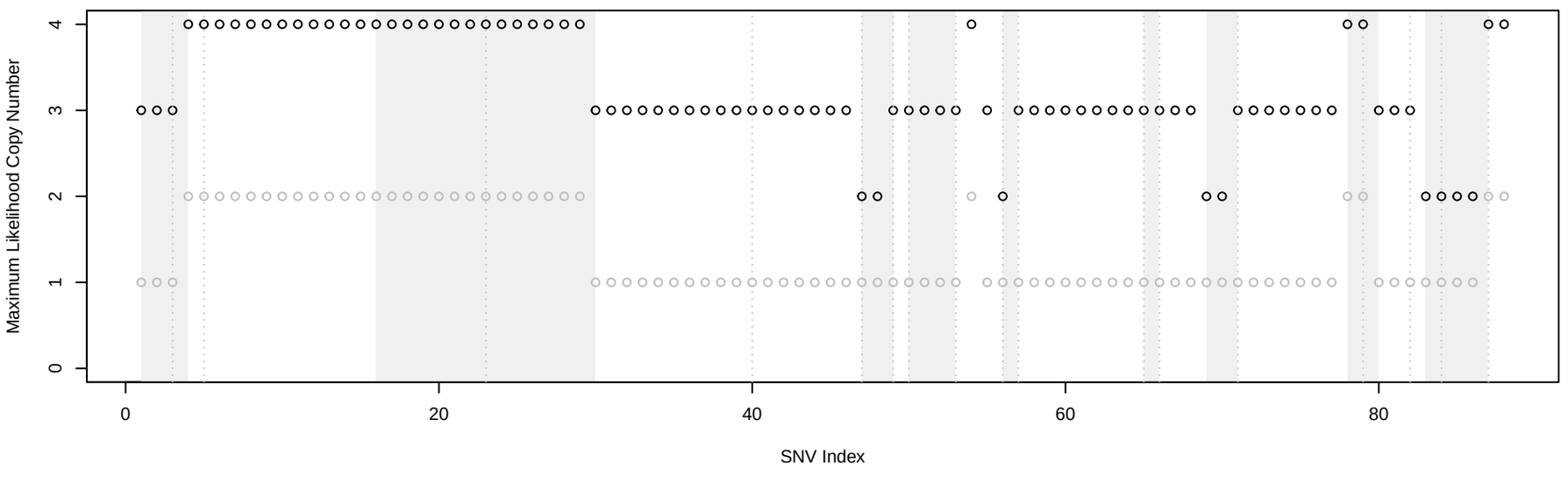

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

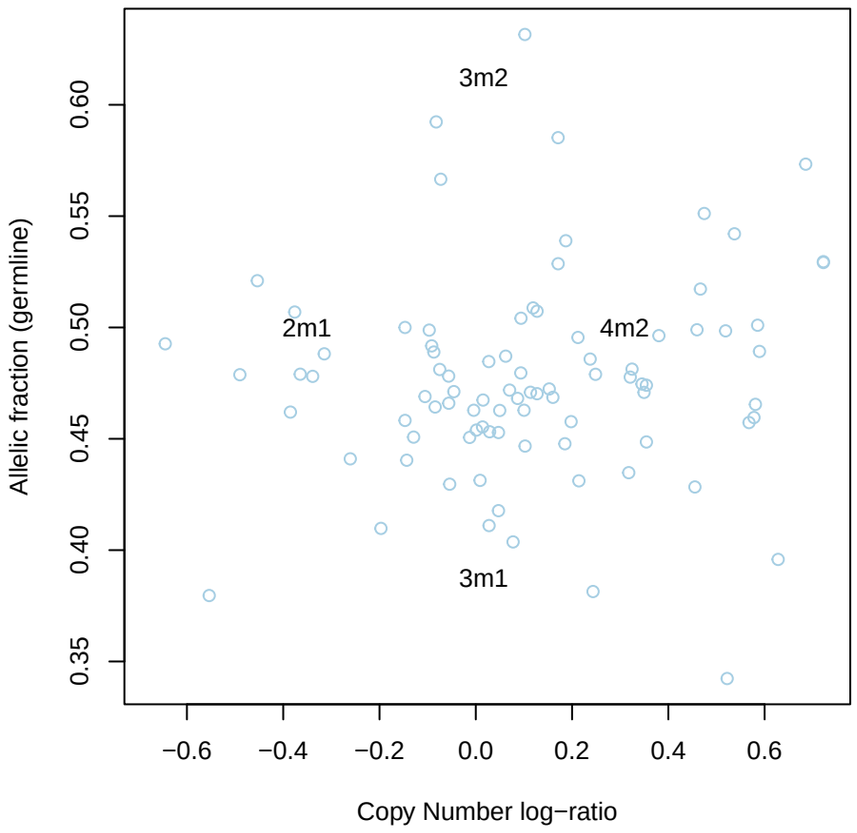

Frequency
0
2
4
6
8
10
12
0.2
0.4
0.6
0.8
1.0
Cellular fraction

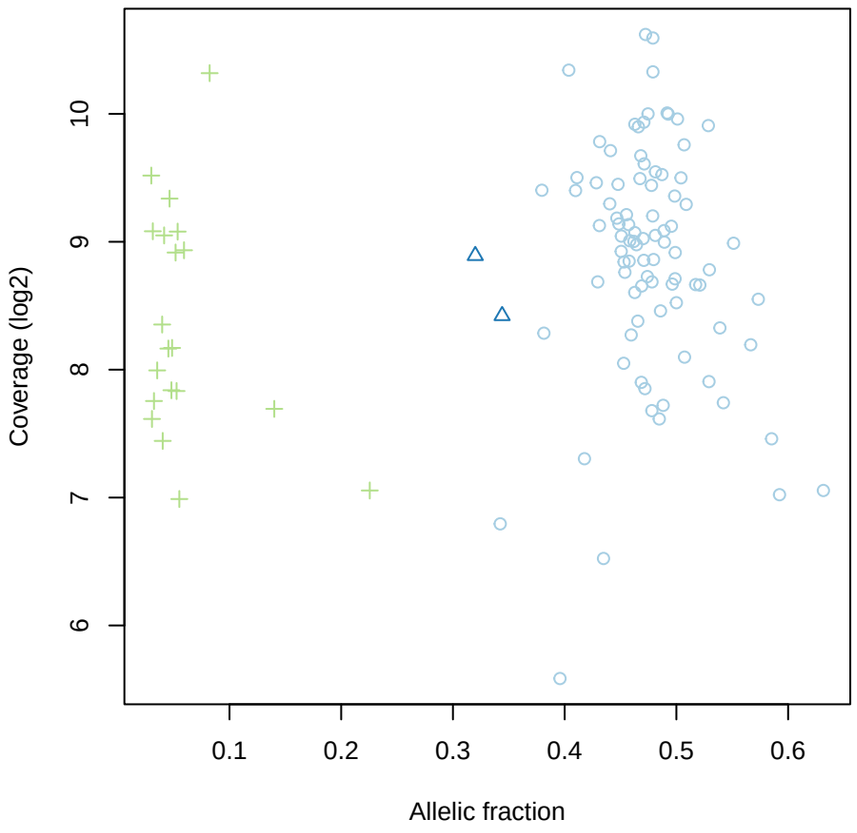

Purity: 0.58 Tumor ploidy: 2.949
1
2
3
4
6
7
0.12
0.10
0.08
0.06
0.04
0.02
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

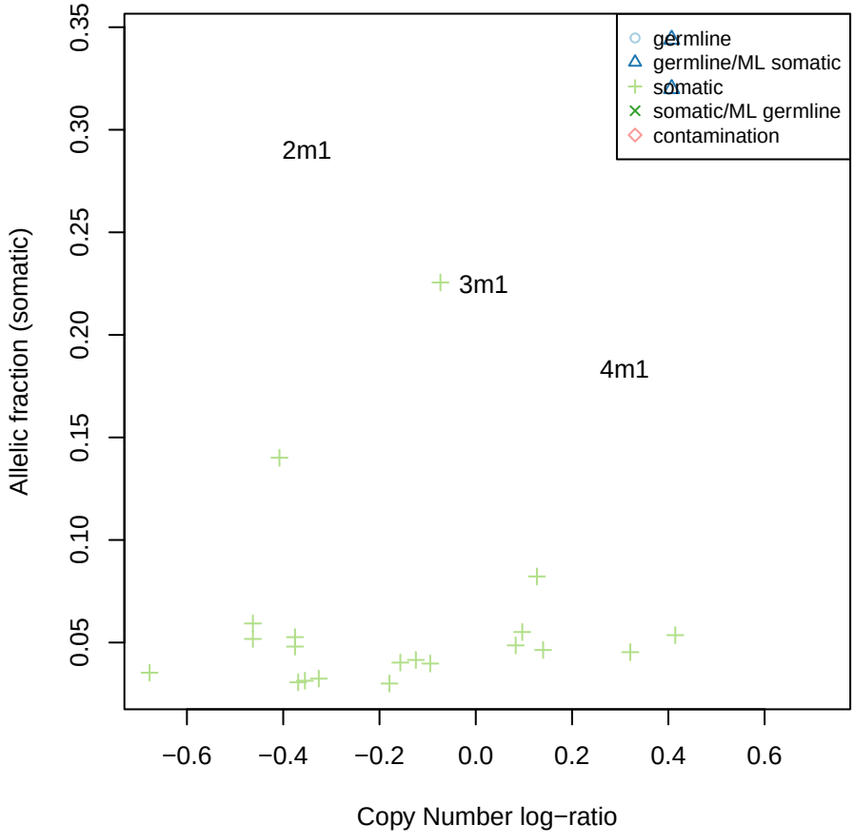

Purity: 0.58 Tumor ploidy: 2.949 SNV log−likelihood: −218.68 GoF: 72.3% Mean coverage: 454;525
2 4 6 7 8 10 11 13 14 16 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

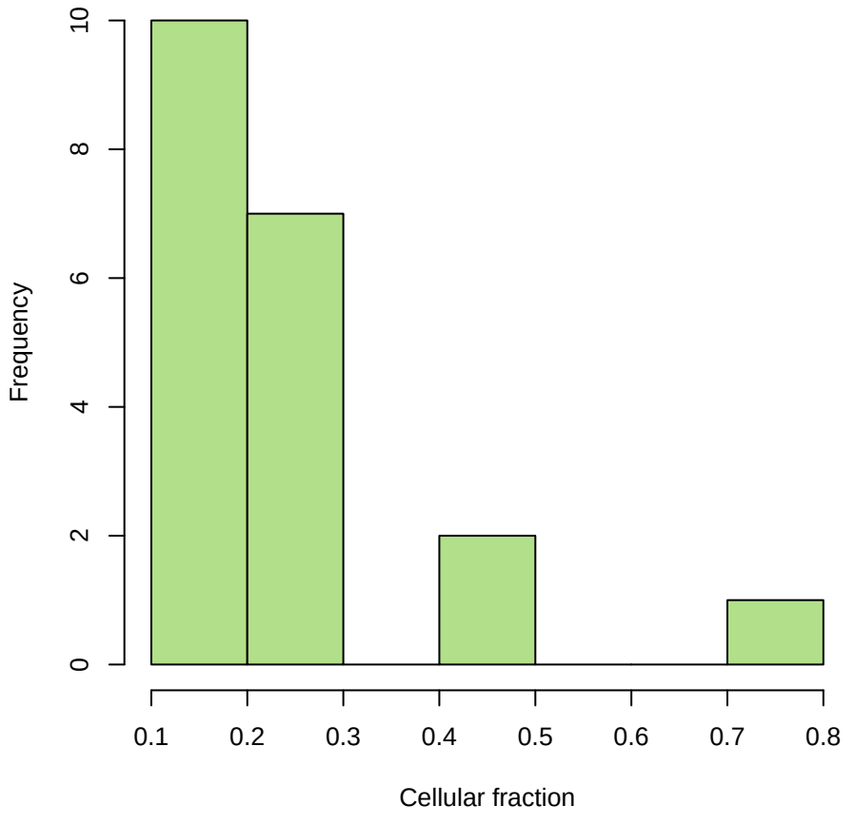

SCNA−fit log−likelihood: −5418.82
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 6 7
0 20 40 60 80
SNV Index

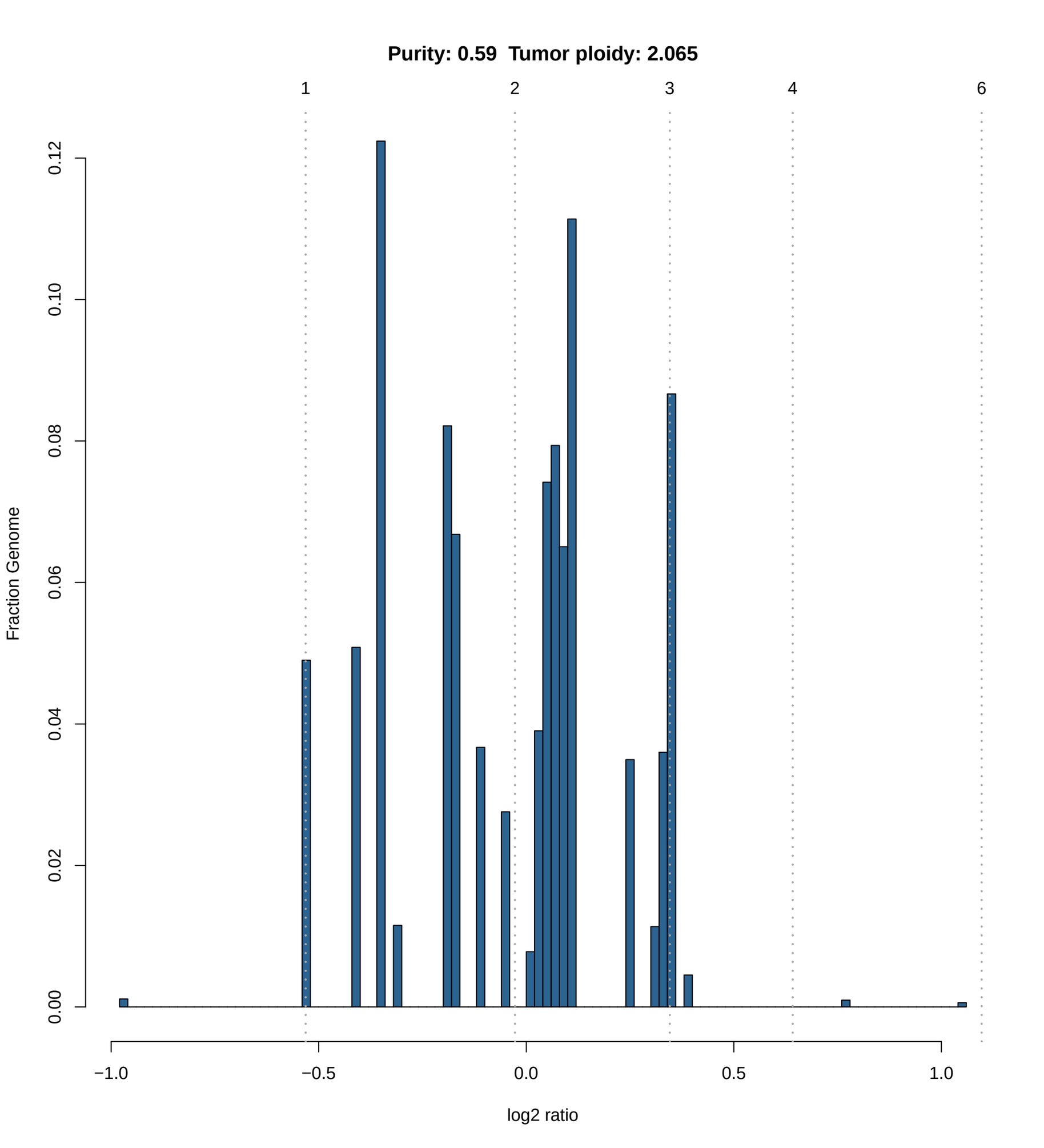

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80
SNV Index

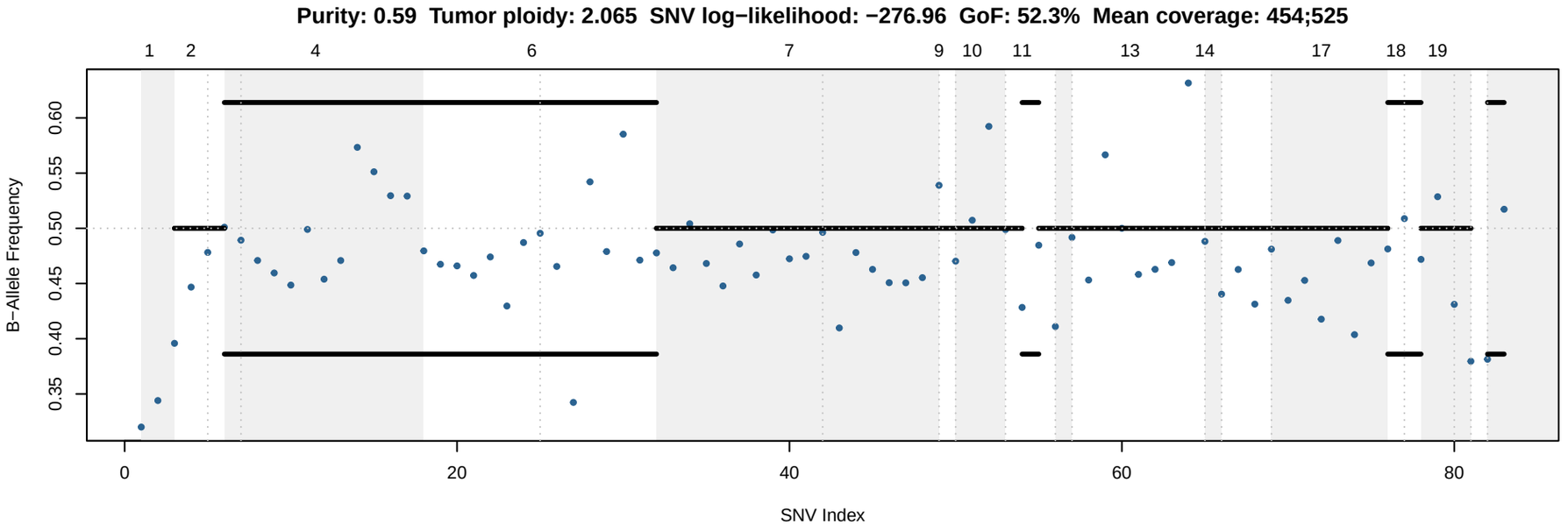

3m2
2m1
4m2
3m1
Allelic fraction (germline)
Copy Number log−ratio

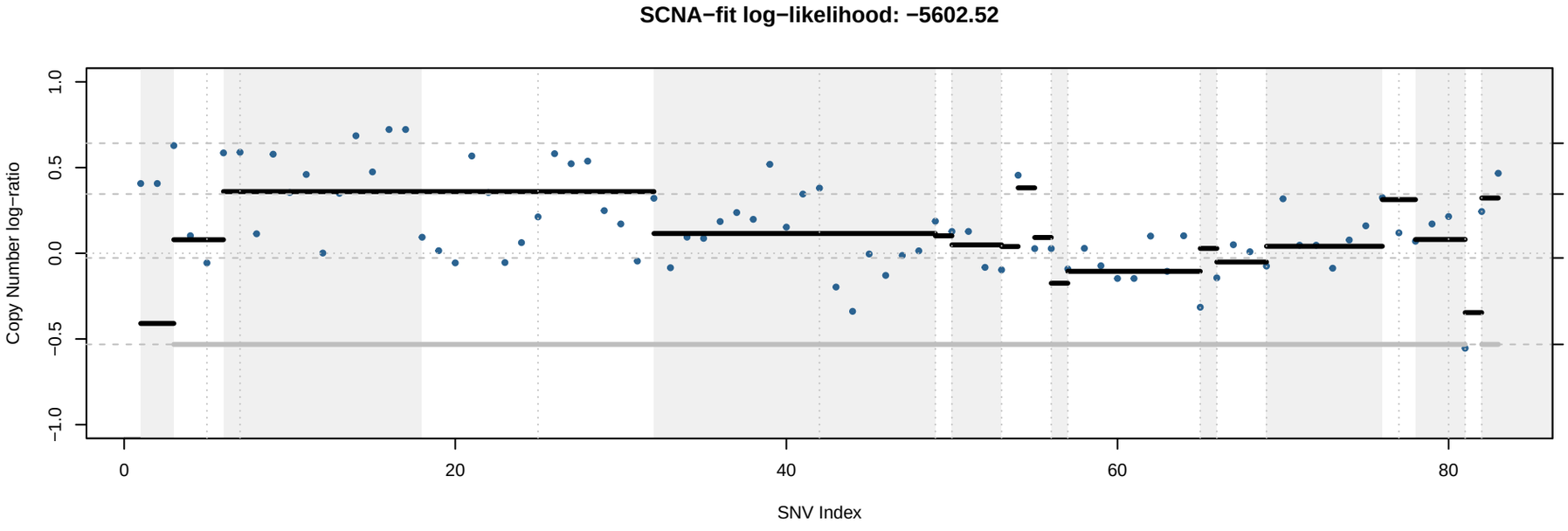

Coverage (log2)
Allelic fraction

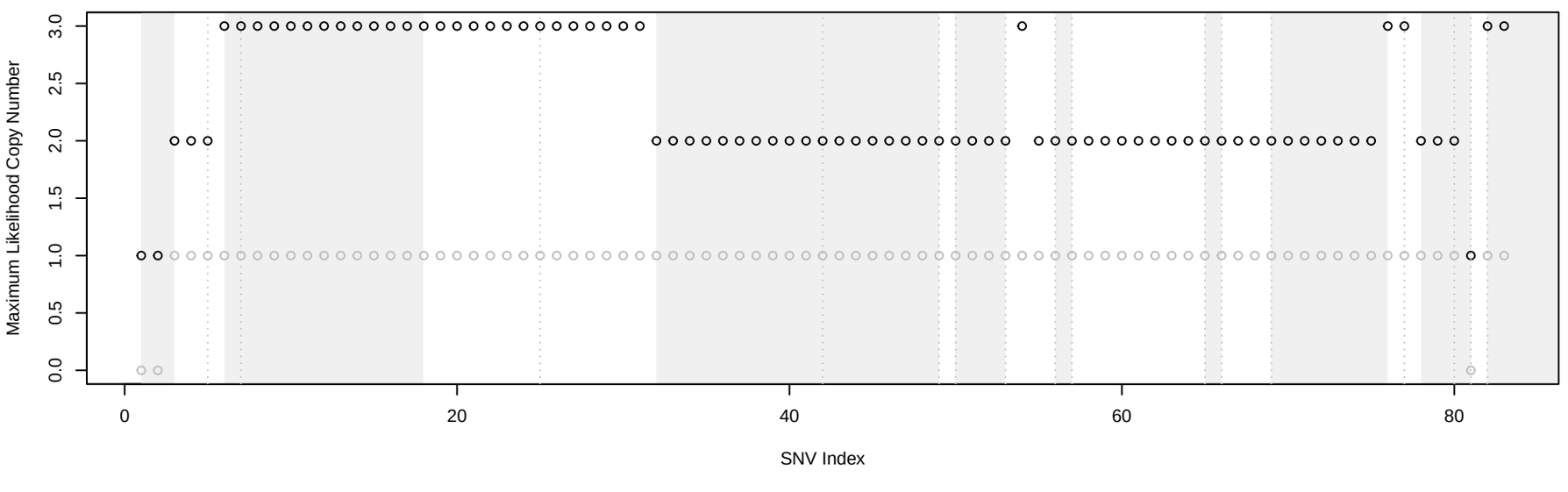

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1
Allelic fraction (somatic)
Copy Number log−ratio

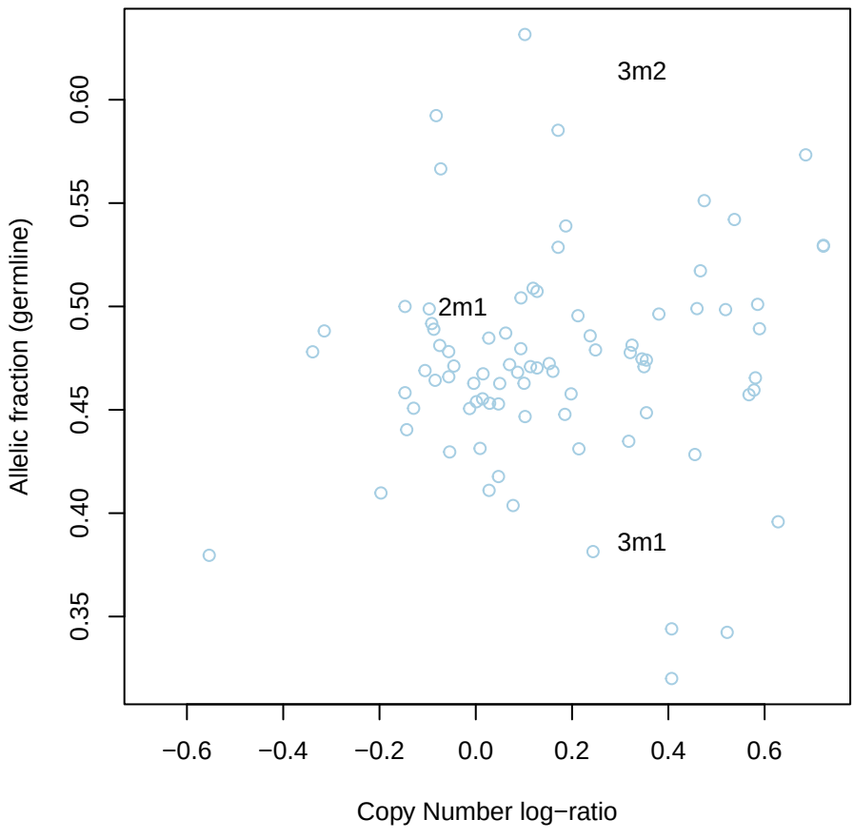

Frequency
Cellular fraction

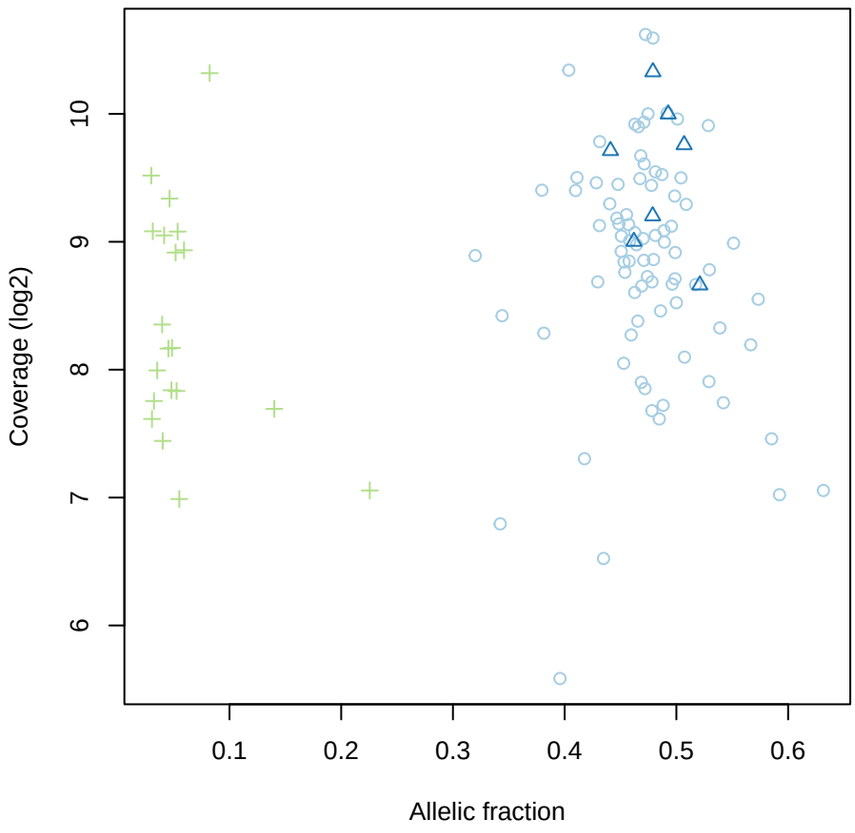

Purity: 0.59 Tumor ploidy: 2.065
1
2
3
4
6
0.12
0.10
0.08
0.06
0.04
0.02
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

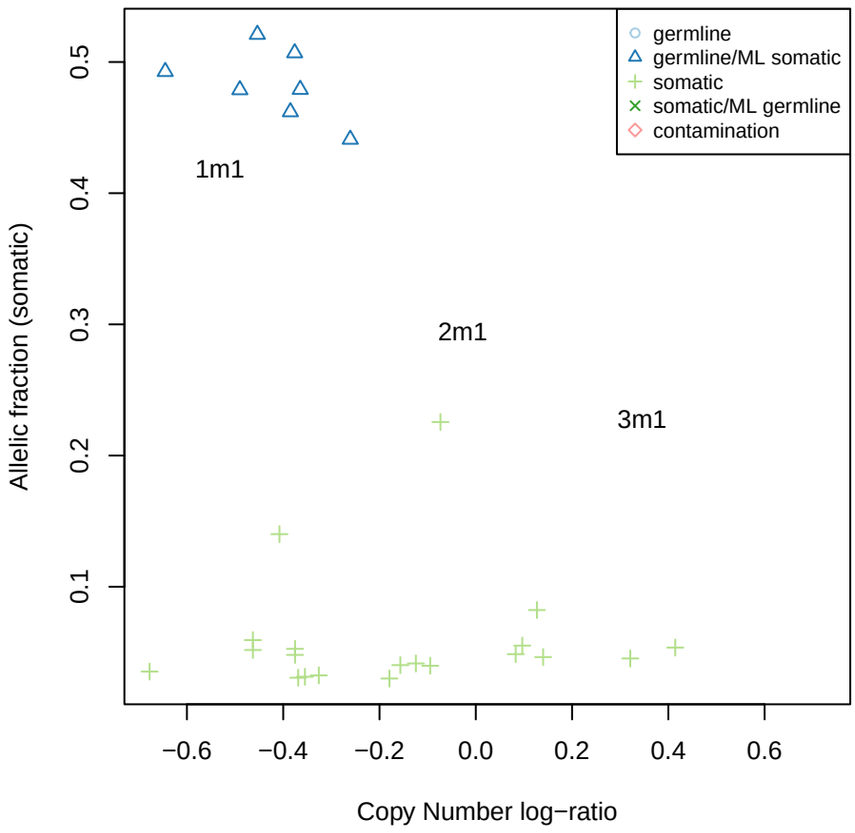

Purity: 0.59 Tumor ploidy: 2.065 SNV log−likelihood: −276.96 GoF: 52.3% Mean coverage: 454;525
1 2 4 6 7 9 10 11 13 14 17 18 19
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60
0 20 40 60 80
SNV Index

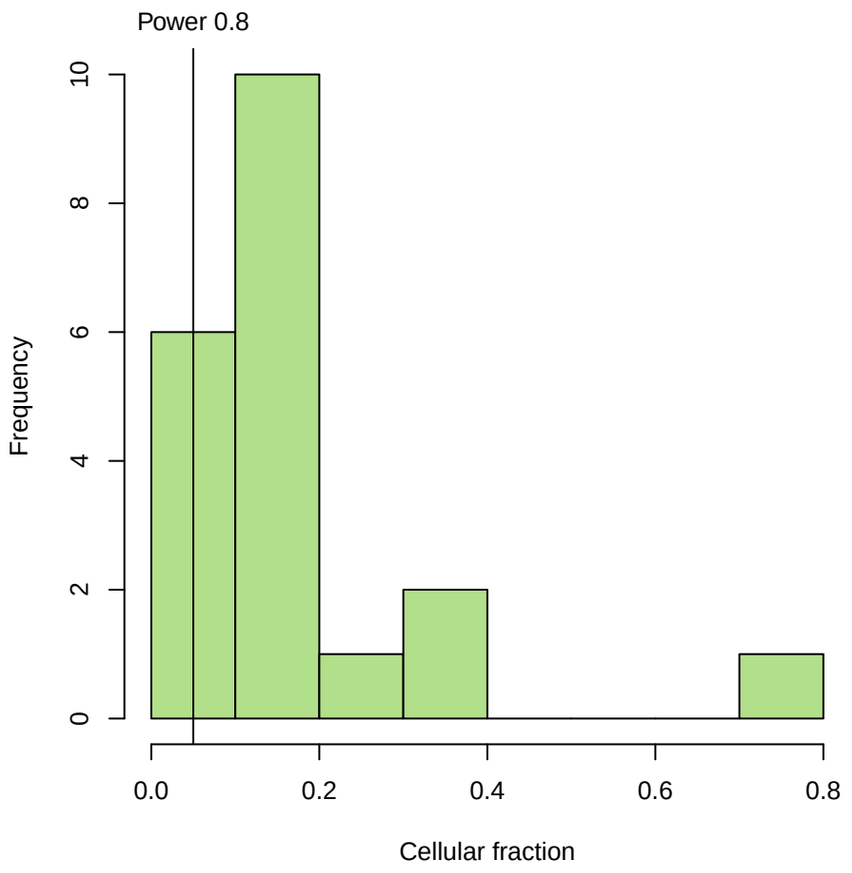

SCNA−fit log−likelihood: −5602.52
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4
0 20 40 60 80
SNV Index


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


3m2
2m1
3m1
Allelic fraction (germline)
Copy Number log−ratio
0.35
0.40
0.45
0.50
0.55
0.60
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6


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
1m1
2m1
3m1
Allelic fraction (somatic)
Copy Number log−ratio
0.1
0.2
0.3
0.4
0.5
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6


Power 0.8
Frequency
Cellular fraction
0
2
4
6
8
10
0.0
0.2
0.4
0.6
0.8