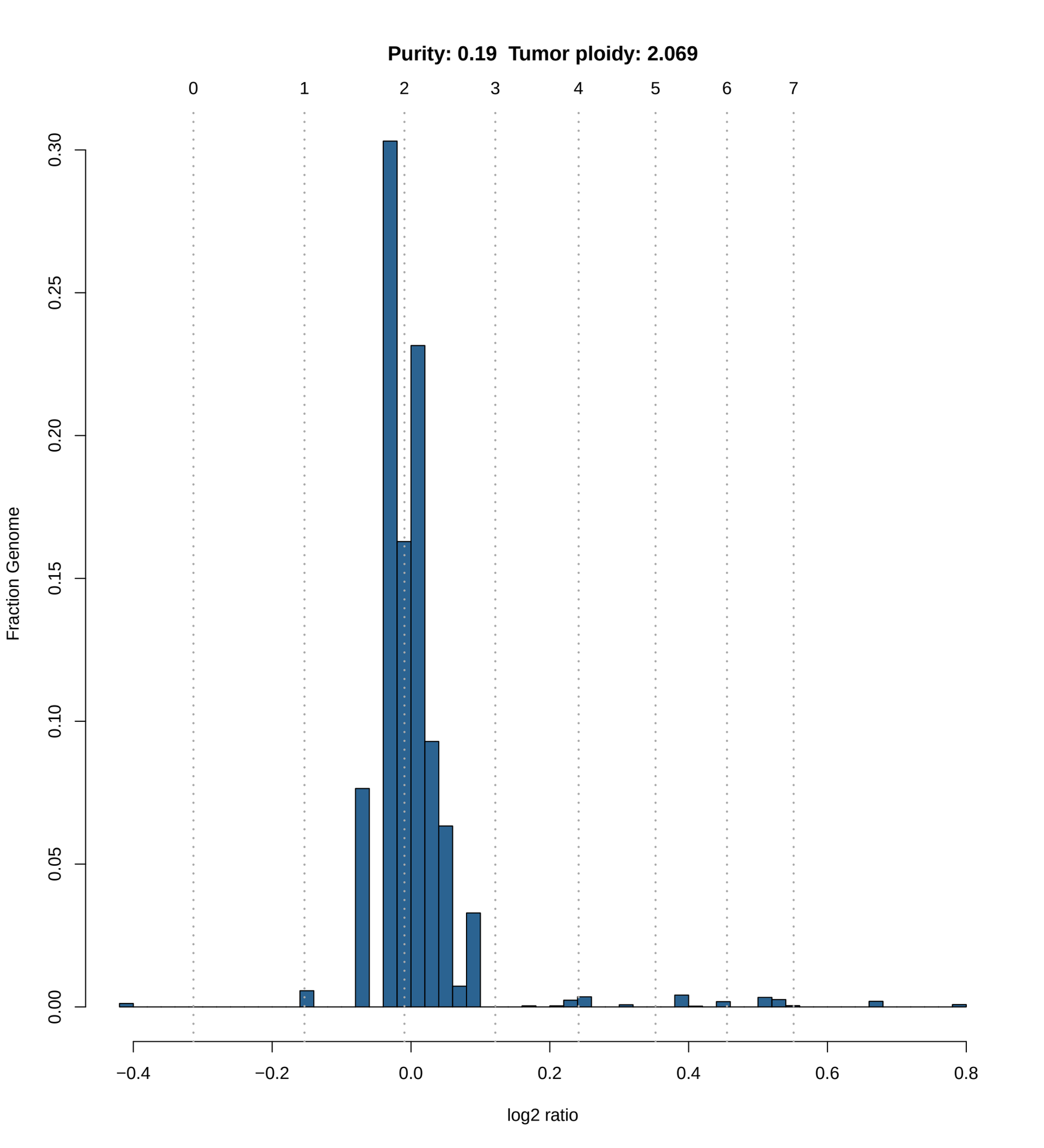
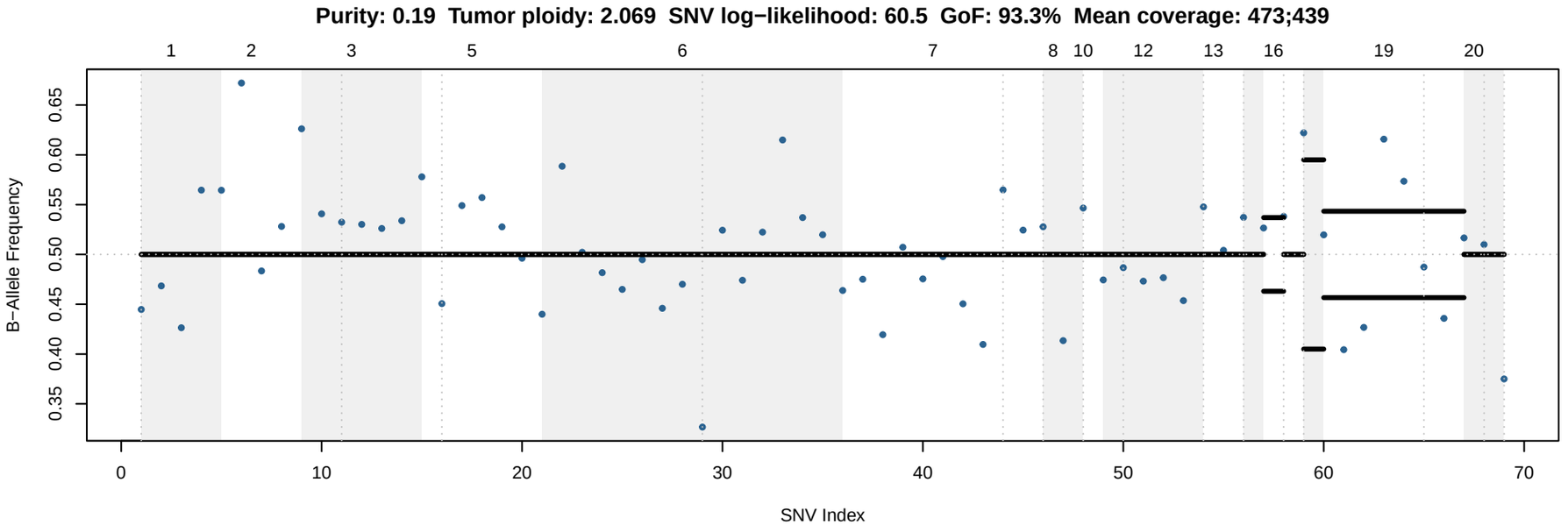
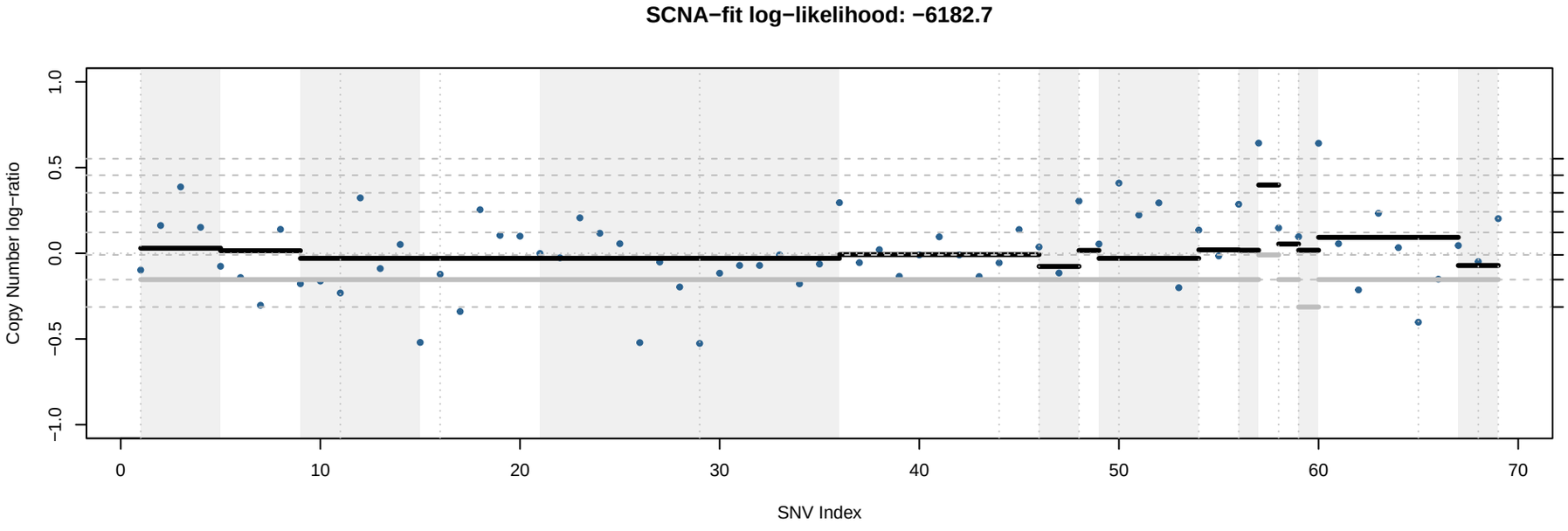
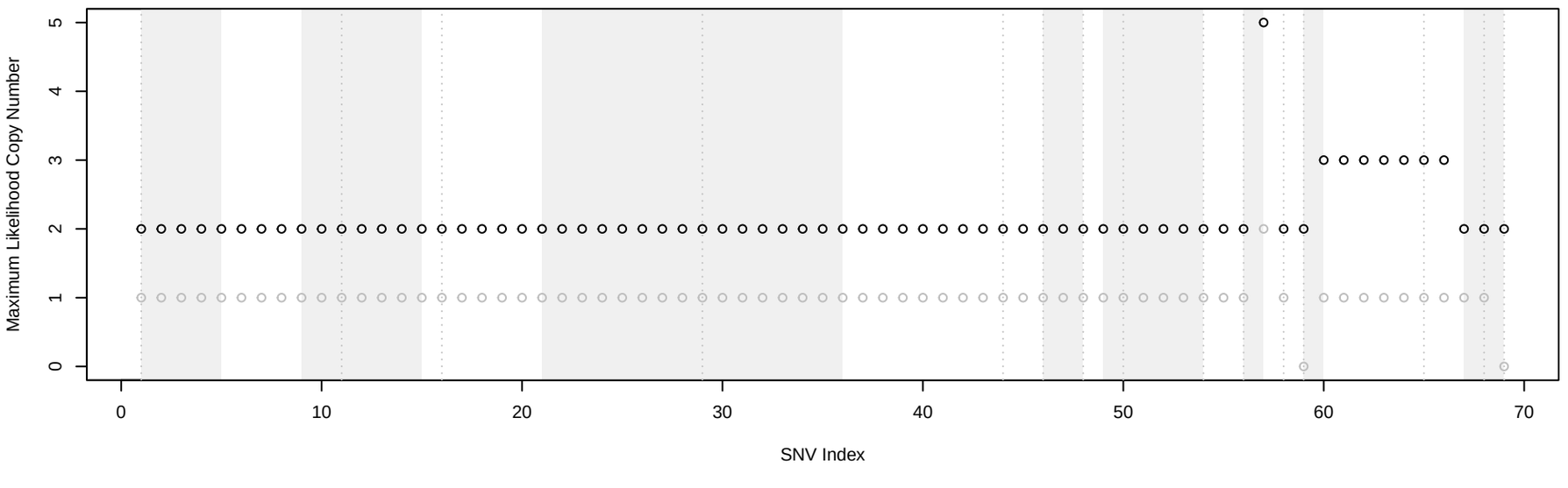
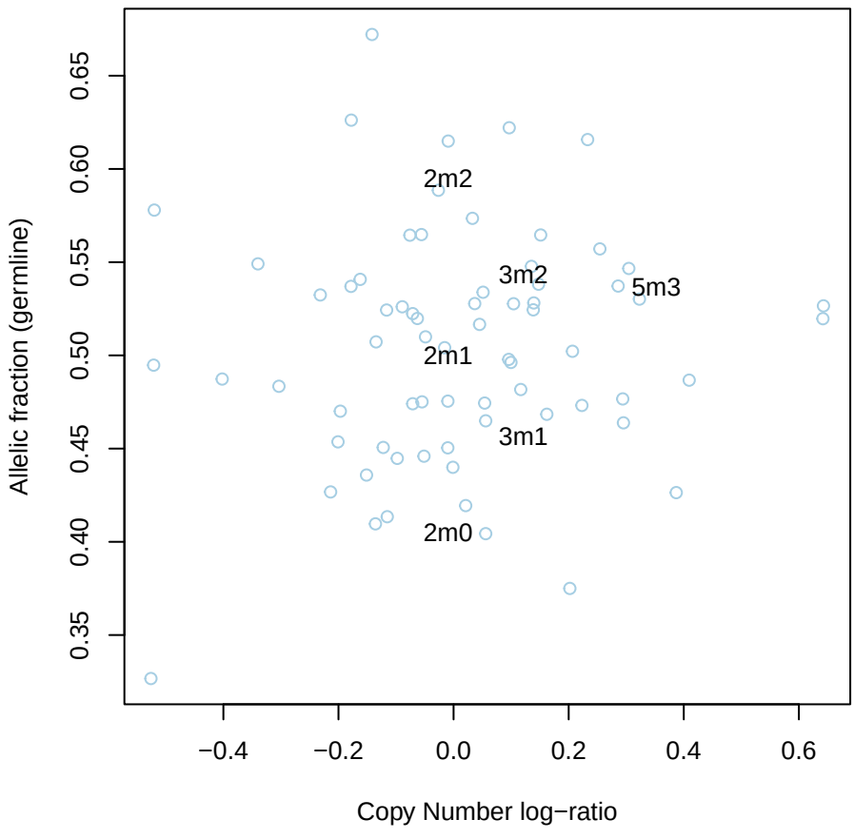
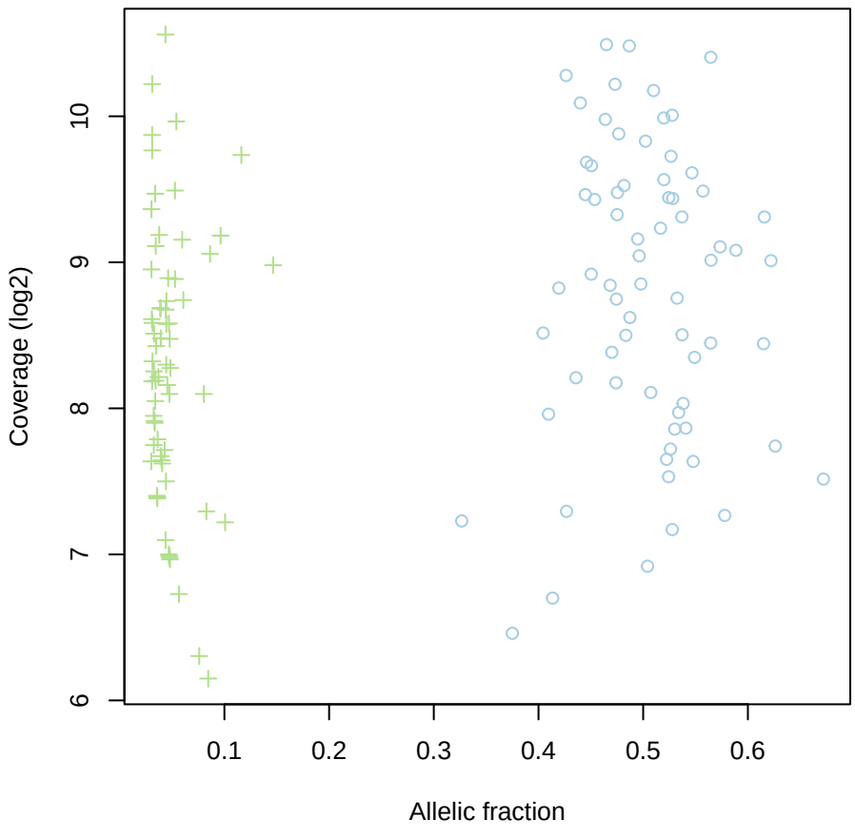

Purity: 0.19 Tumor ploidy: 2.069
0
1
2
3
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
log2 ratio

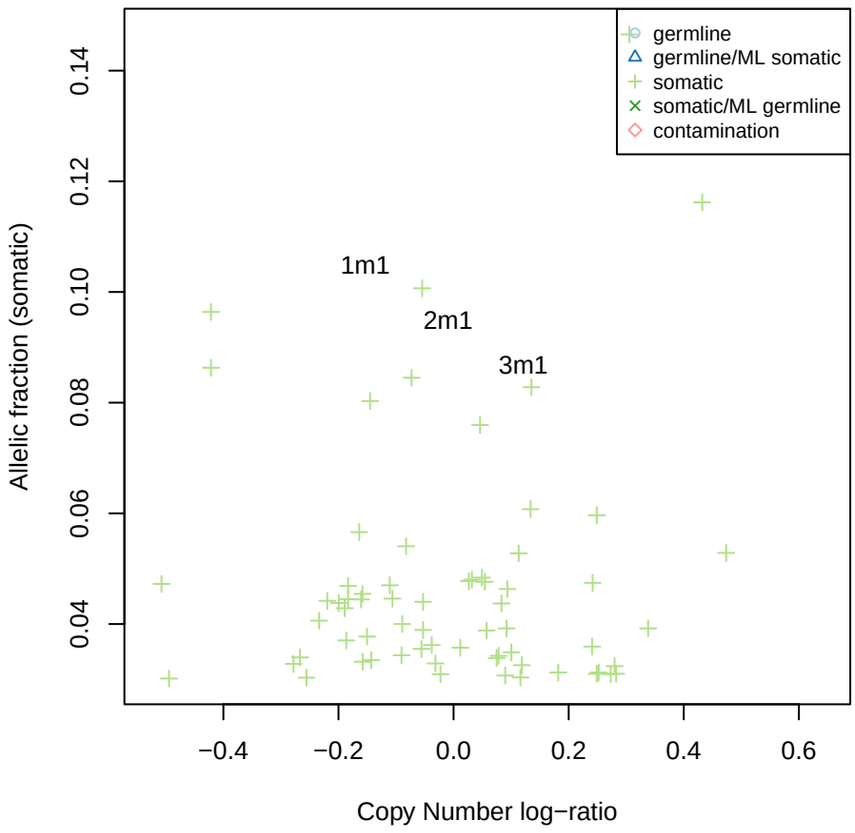

Purity: 0.19 Tumor ploidy: 2.069 SNV log−likelihood: 60.5 GoF: 93.3% Mean coverage: 473;439
1 2 3 5 6 7 8 10 12 13 16 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 10 20 30 40 50 60 70
SNV Index

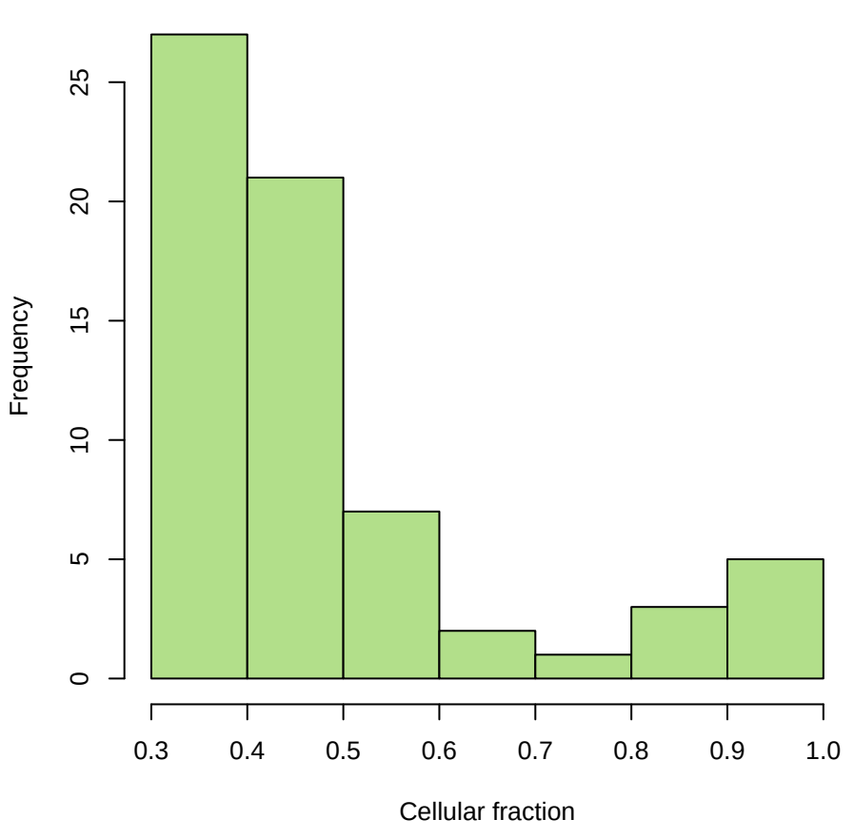

SCNA−fit log−likelihood: −6182.7
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 4 6
0 10 20 30 40 50 60 70
SNV Index

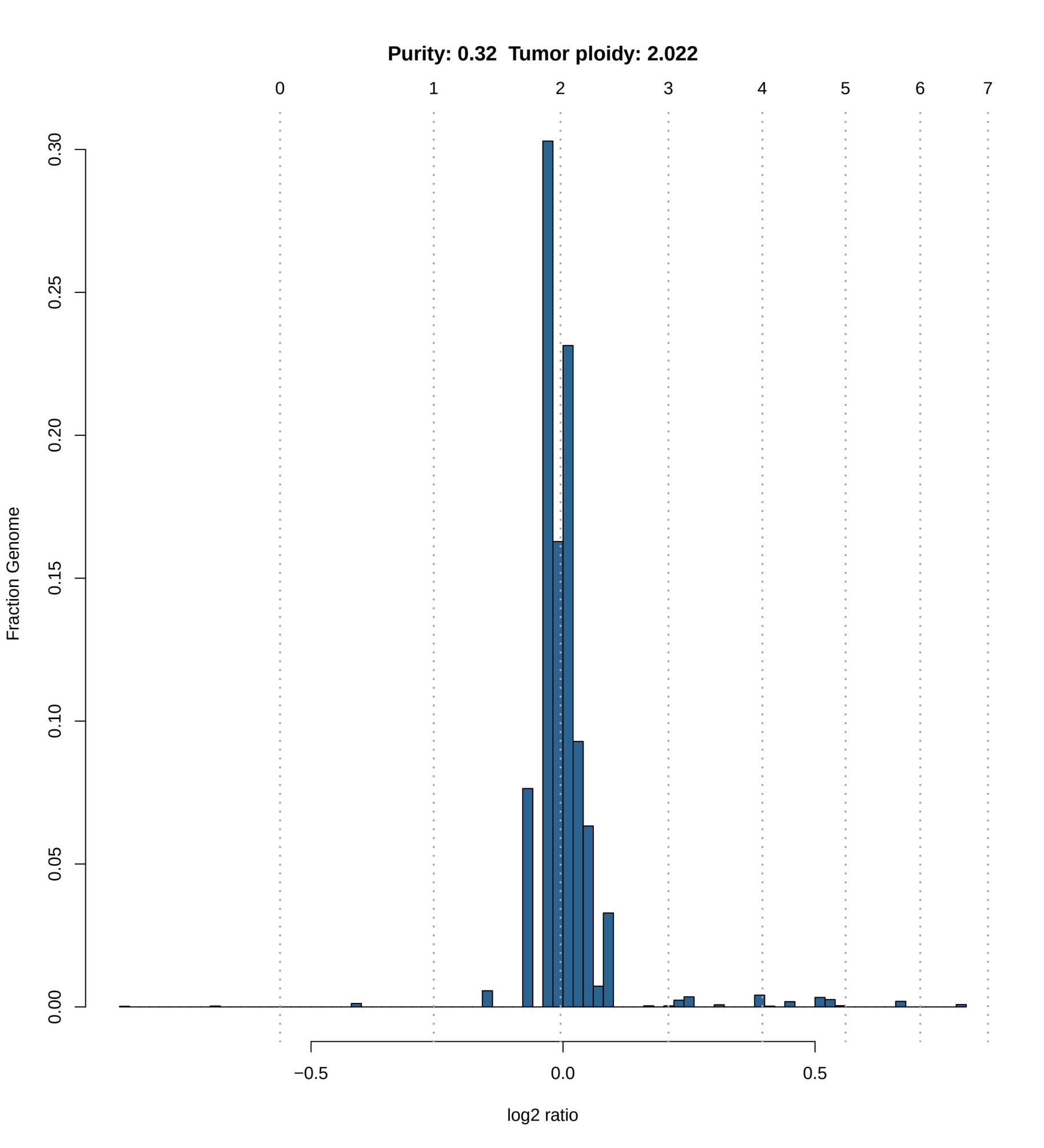

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 10 20 30 40 50 60 70
SNV Index

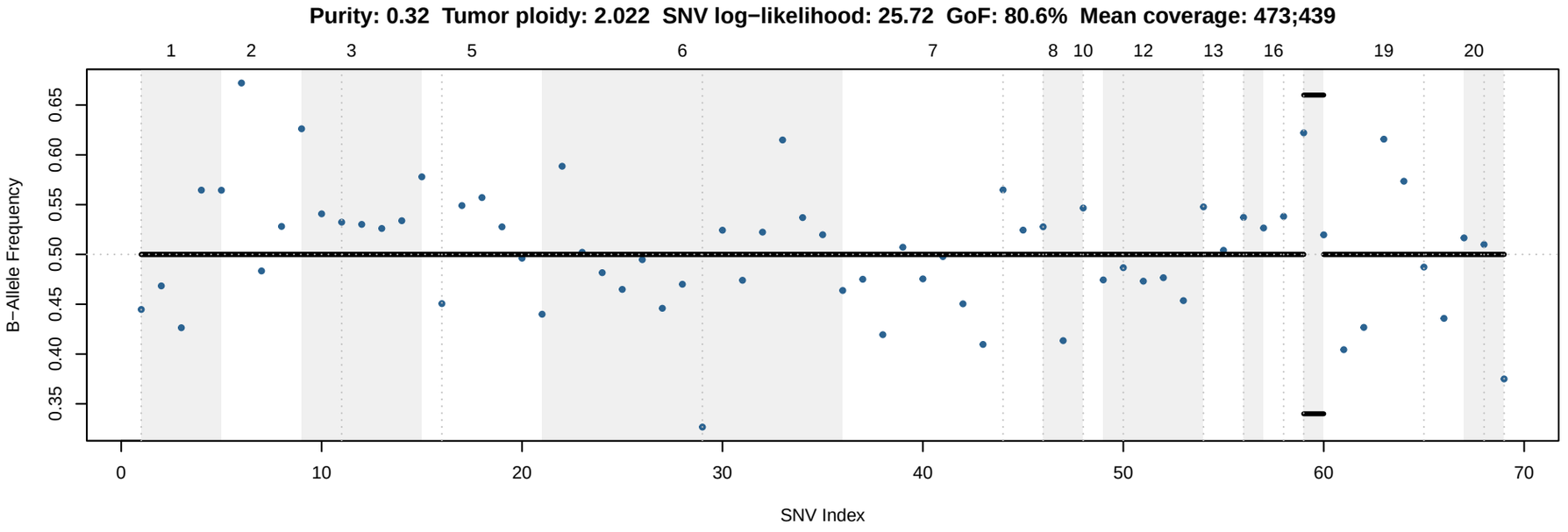

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
2m2
3m2
5m3
2m1
3m1
2m0
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

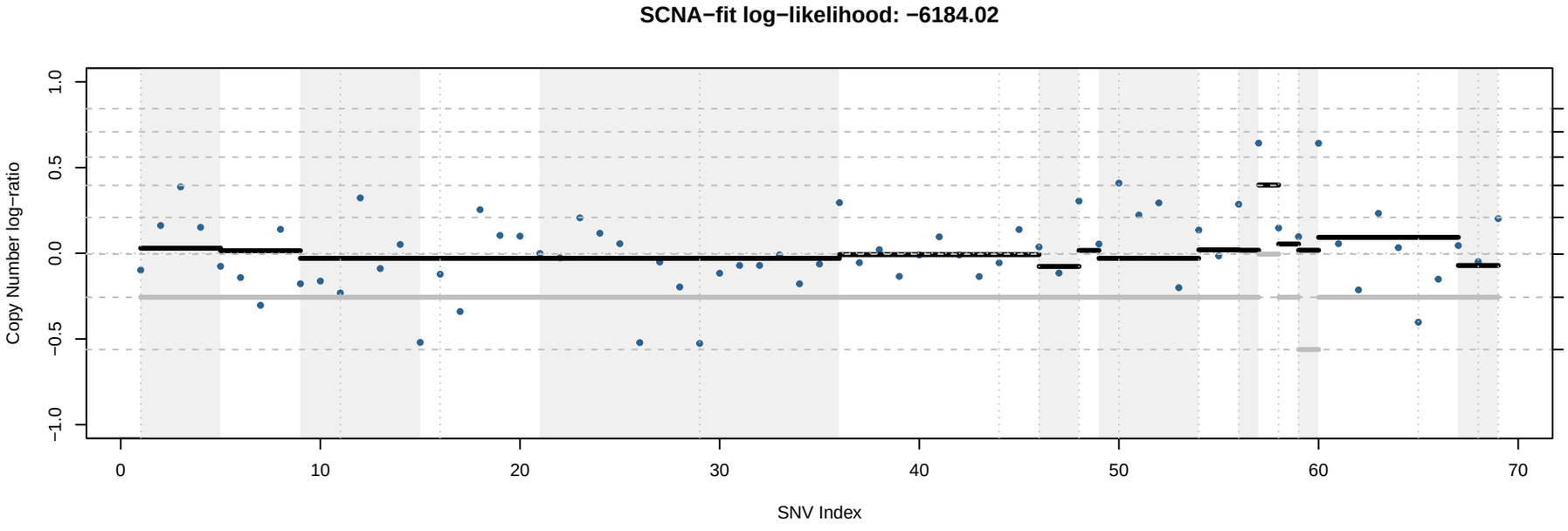

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

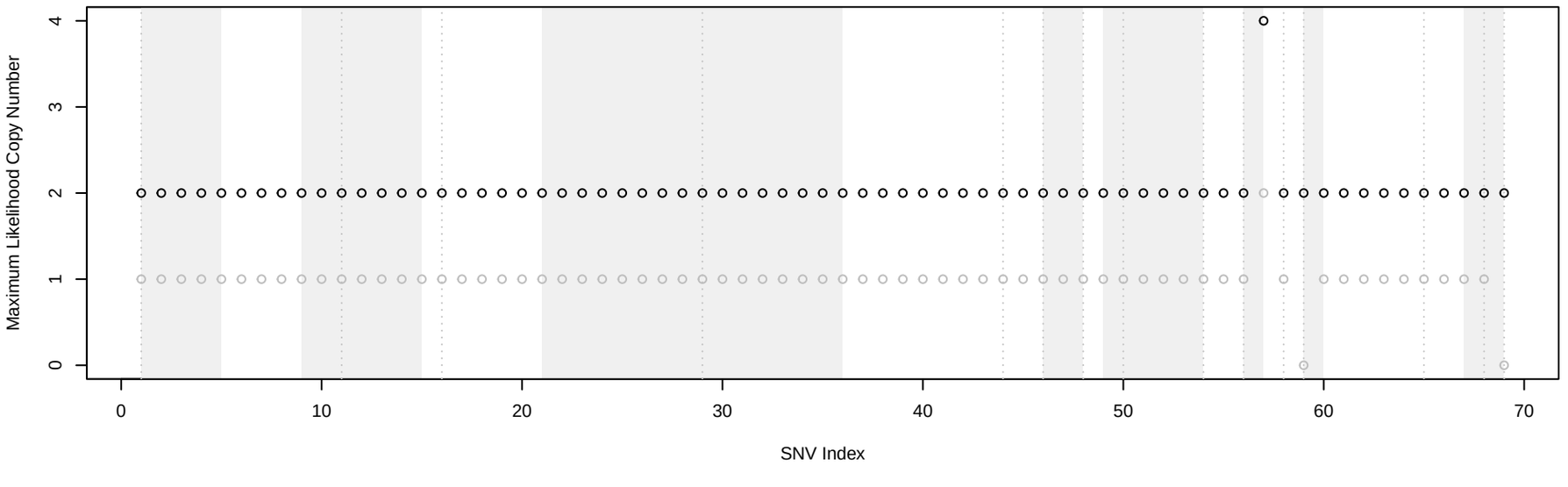

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
1m1
2m1
3m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

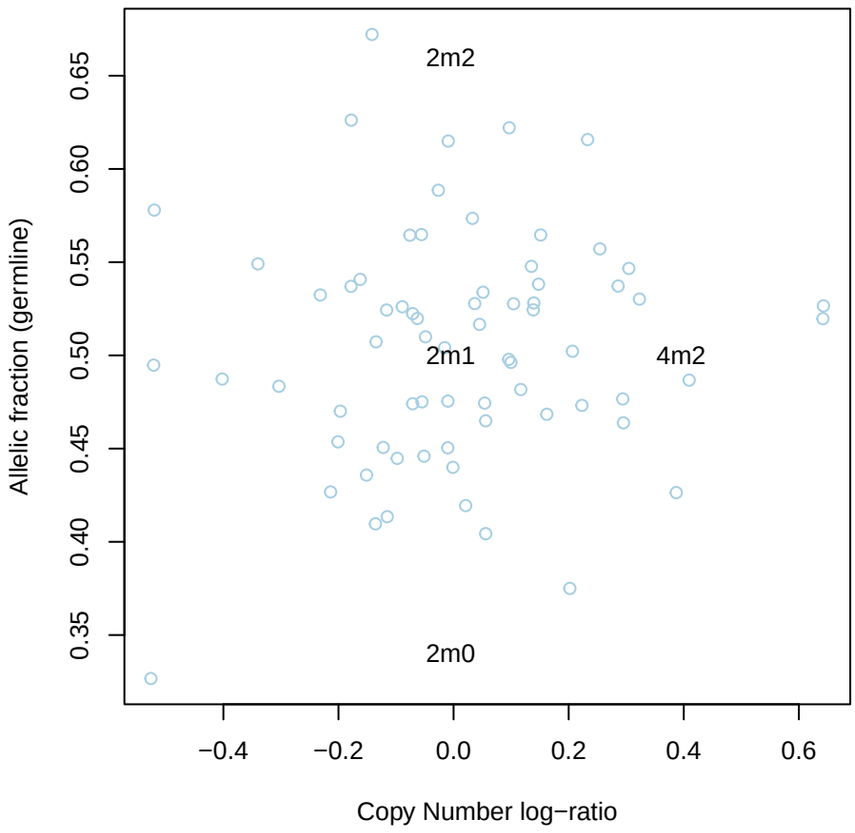

Frequency
0
5
10
15
20
25
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

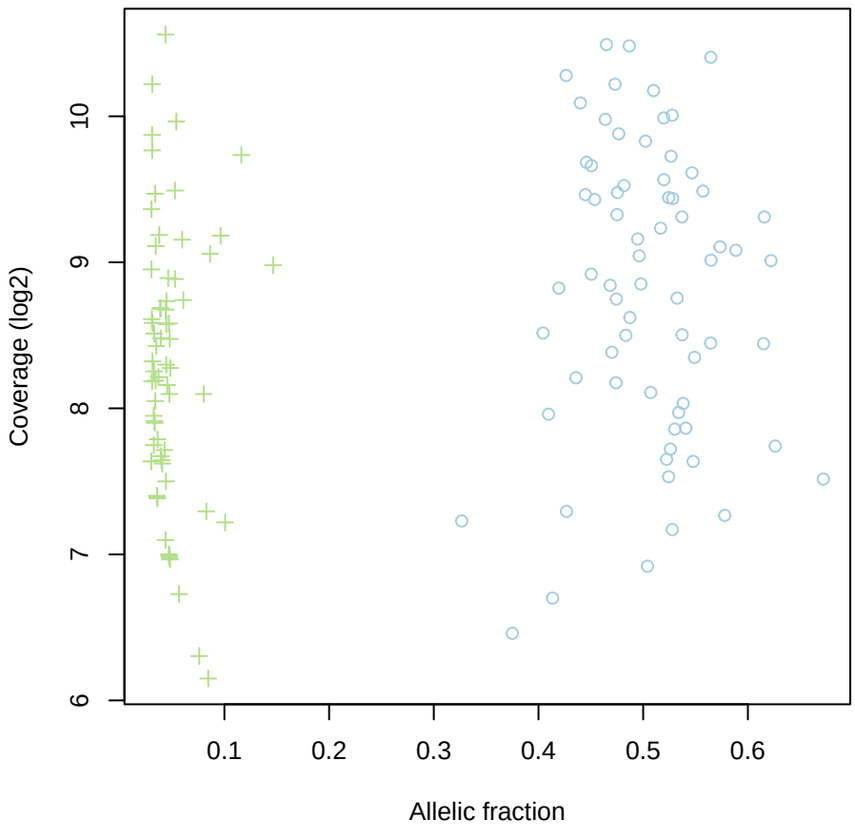

Purity: 0.32 Tumor ploidy: 2.022
0
1
2
3
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

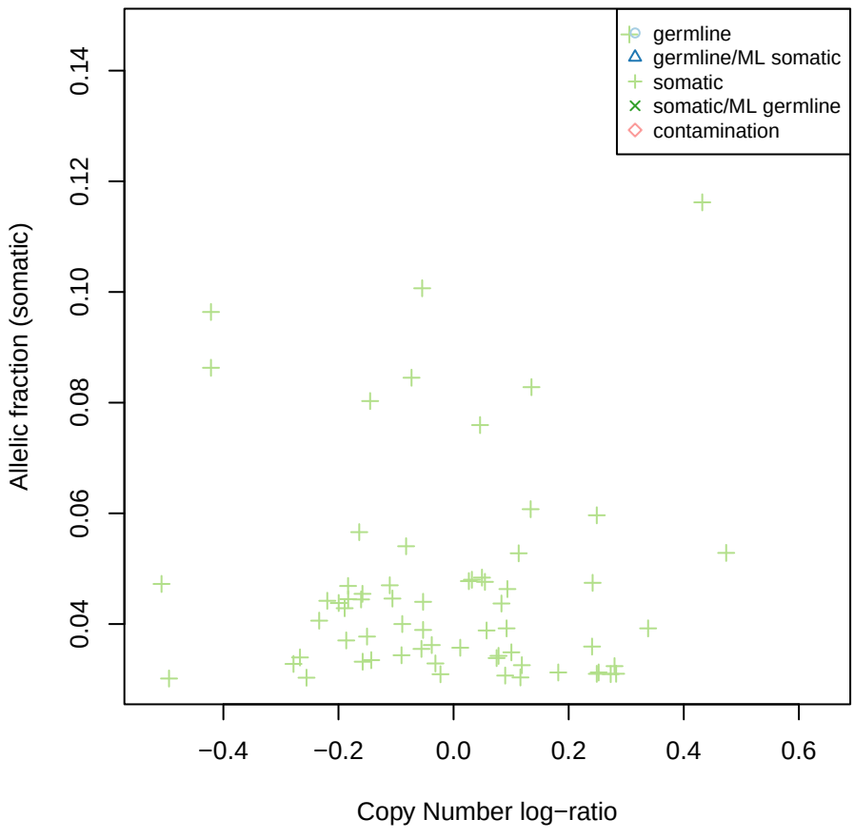

Purity: 0.32 Tumor ploidy: 2.022 SNV log−likelihood: 25.72 GoF: 80.6% Mean coverage: 473;439
1 2 3 5 6 7 8 10 12 13 16 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 10 20 30 40 50 60 70
SNV Index

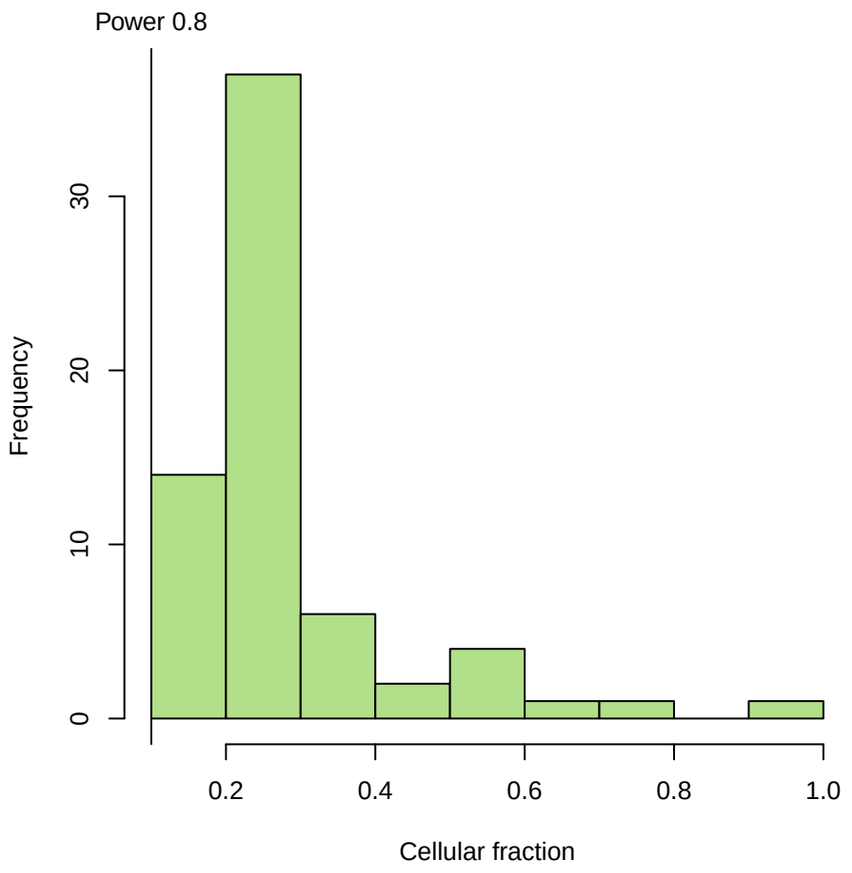

SCNA−fit log−likelihood: −6184.02
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 6
0 10 20 30 40 50 60 70
SNV Index

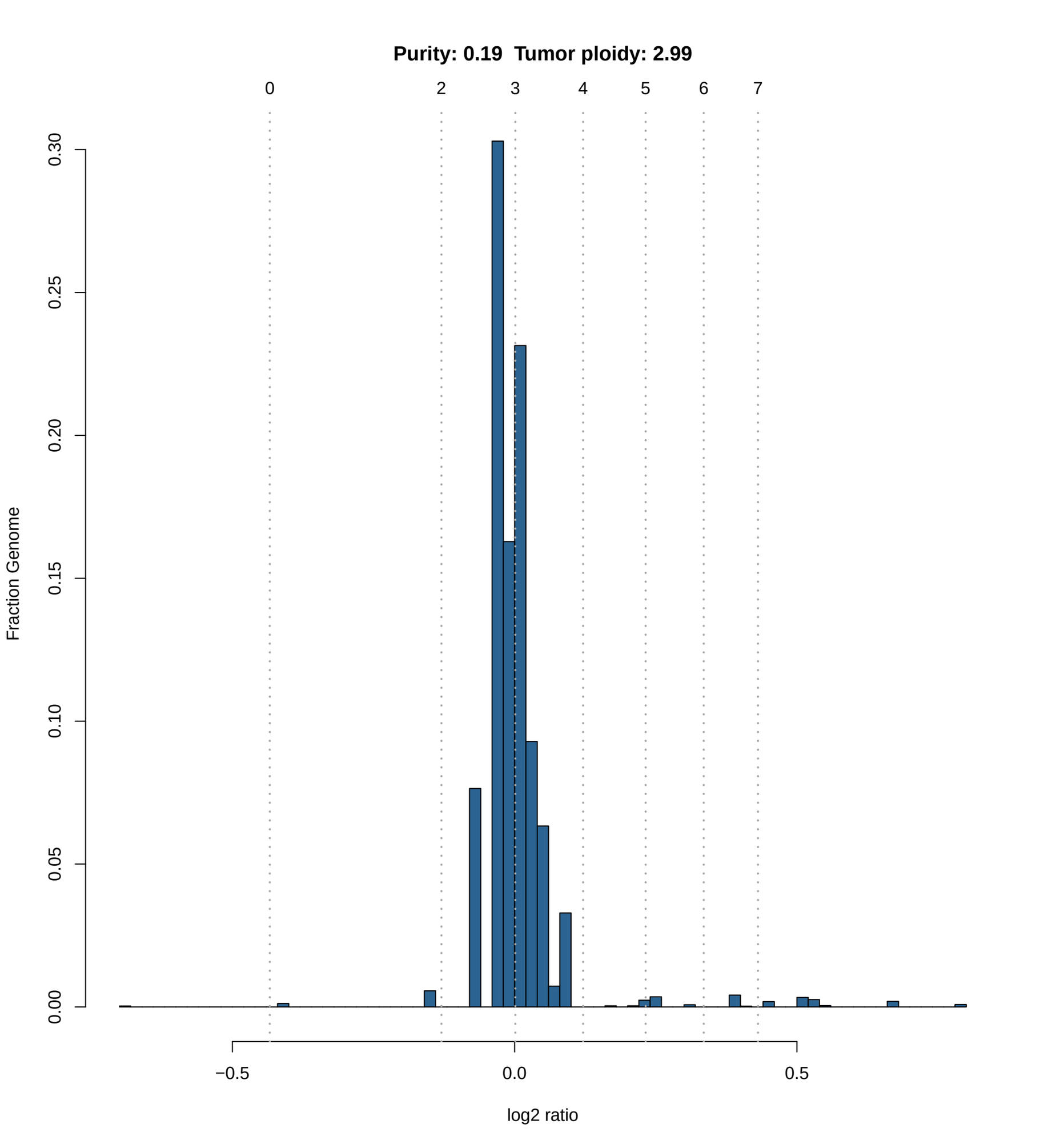

Maximum Likelihood Copy Number
0 1 2 3 4
0 10 20 30 40 50 60 70
SNV Index

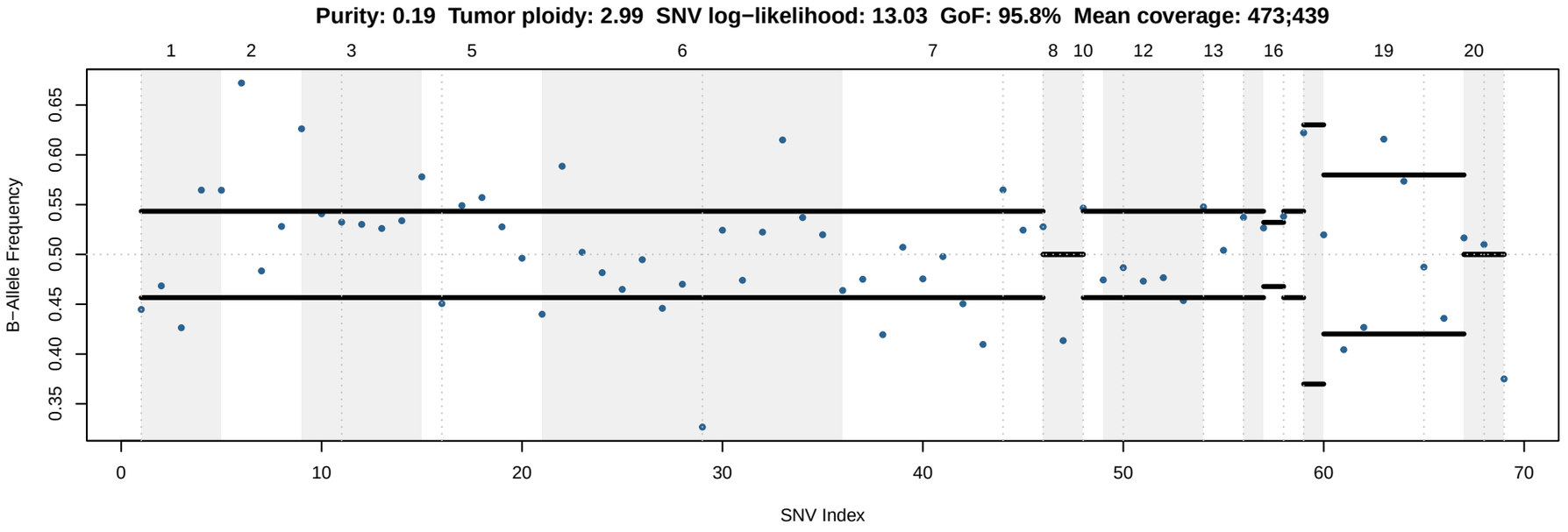

2m2
2m1
4m2
2m0
Allelic fraction (germline)
Copy Number log−ratio
0.35
0.40
0.45
0.50
0.55
0.60
0.65
−0.4
−0.2
0.0
0.2
0.4
0.6

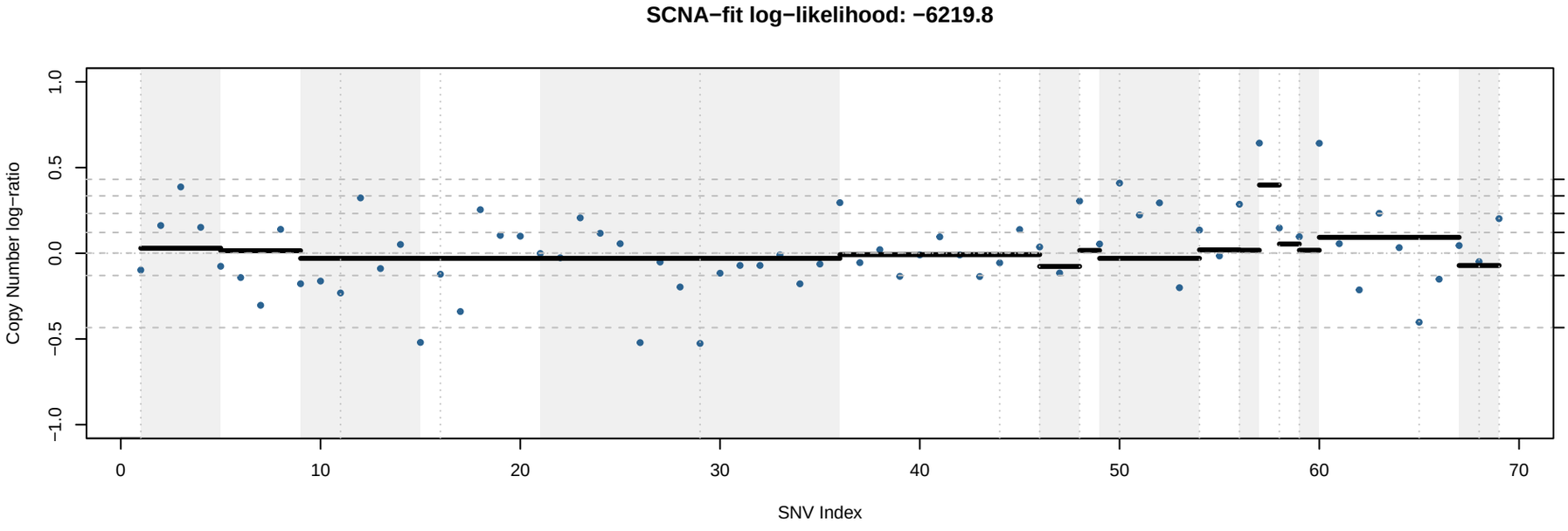

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

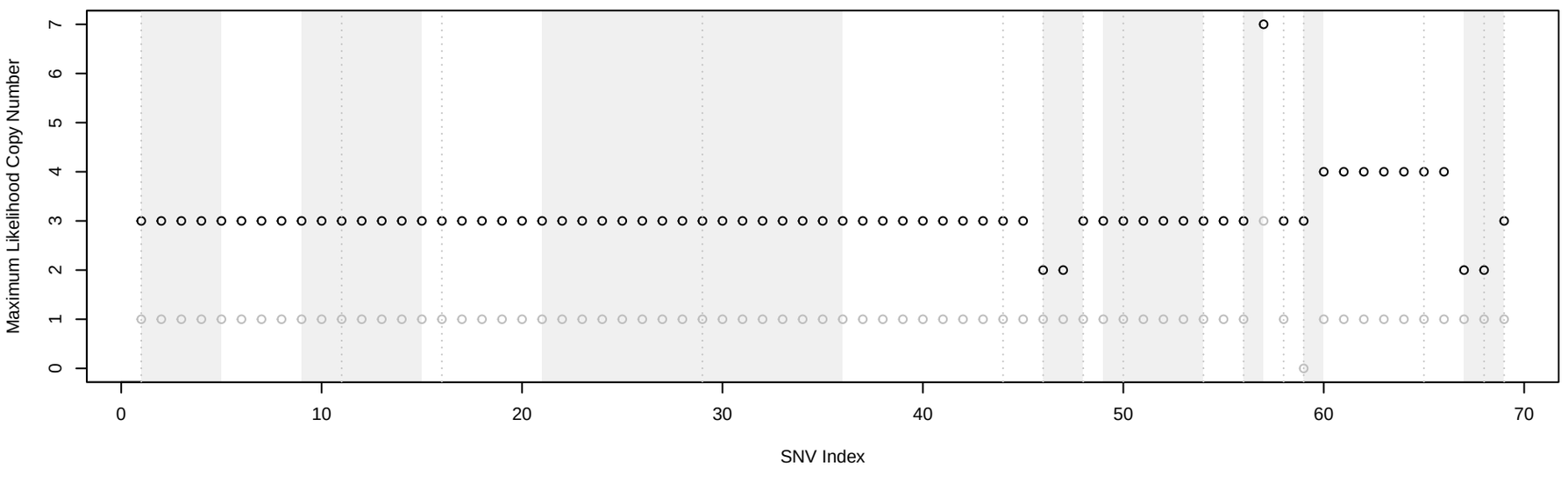

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
0.12
0.14
−0.4
−0.2
0.0
0.2
0.4
0.6

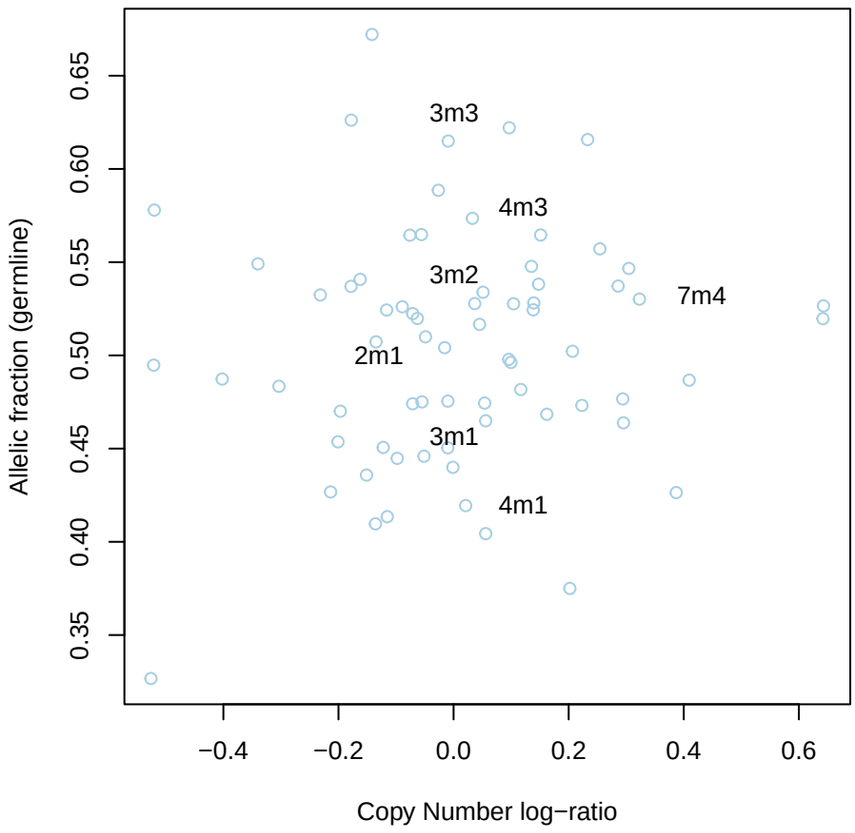

Power 0.8
Frequency
Cellular fraction
0
10
20
30
0.2
0.4
0.6
0.8
1.0

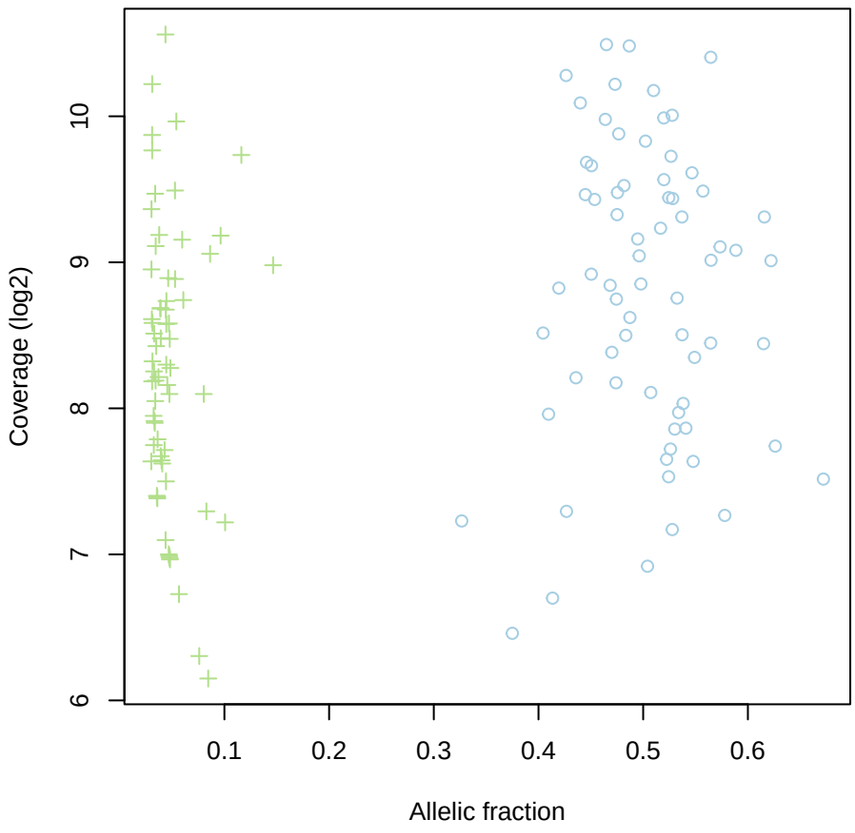

Purity: 0.19 Tumor ploidy: 2.99
0
2
3
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

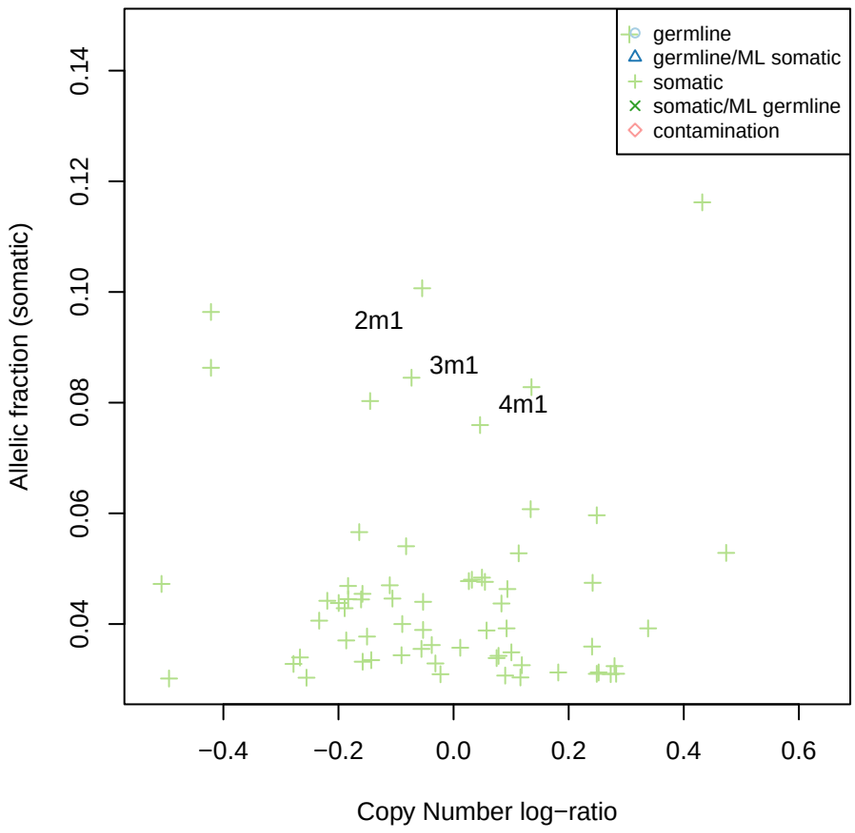

Purity: 0.19 Tumor ploidy: 2.99 SNV log−likelihood: 13.03 GoF: 95.8% Mean coverage: 473;439
1 2 3 5 6 7 8 10 12 13 16 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 10 20 30 40 50 60 70
SNV Index

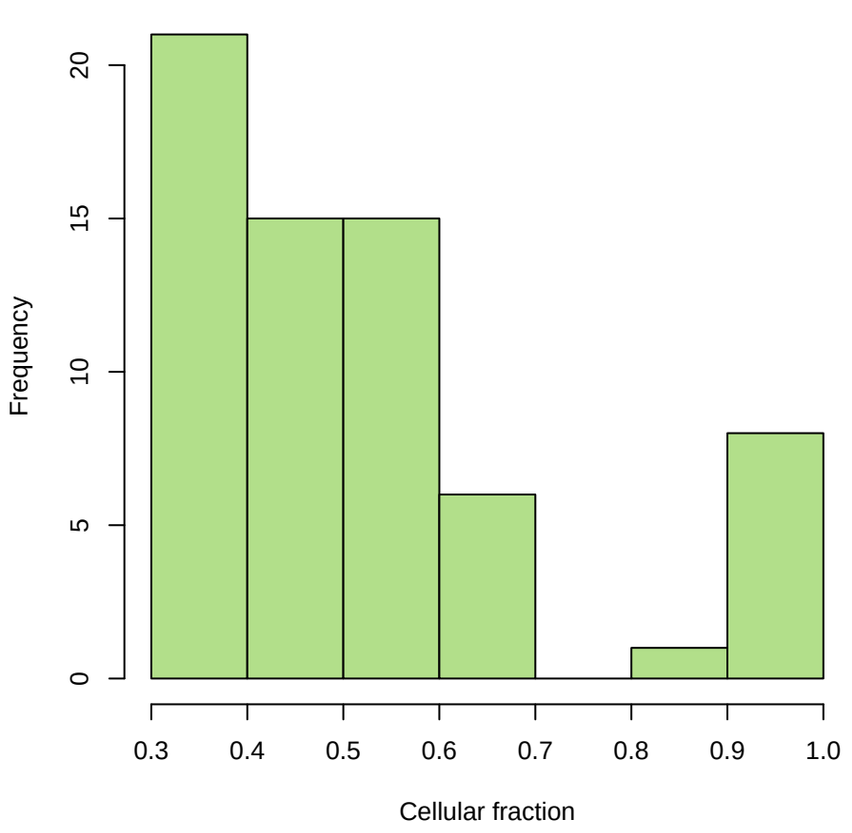

SCNA−fit log−likelihood: −6219.8
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4 6
0 10 20 30 40 50 60 70
SNV Index

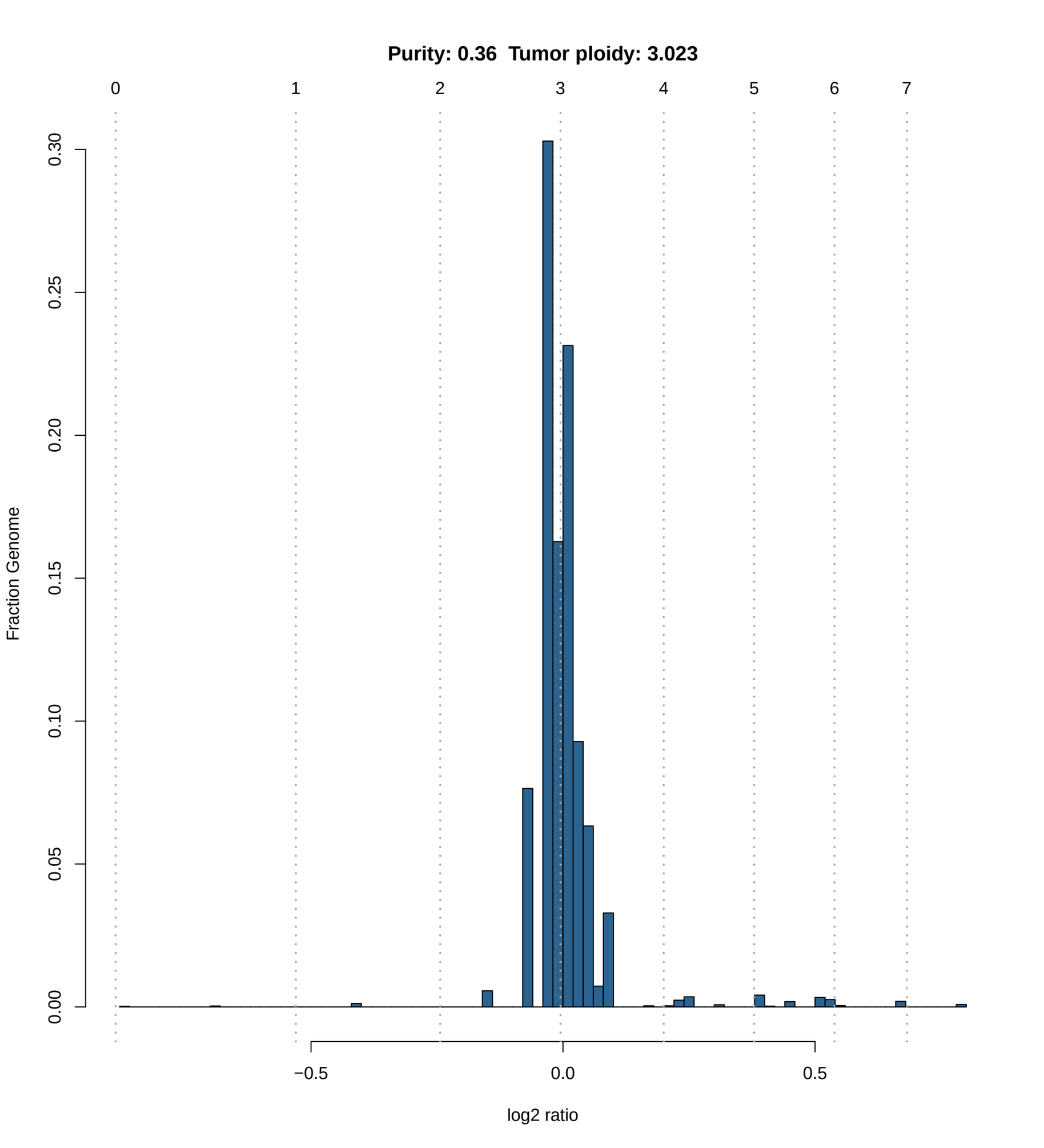

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 10 20 30 40 50 60 70
SNV Index

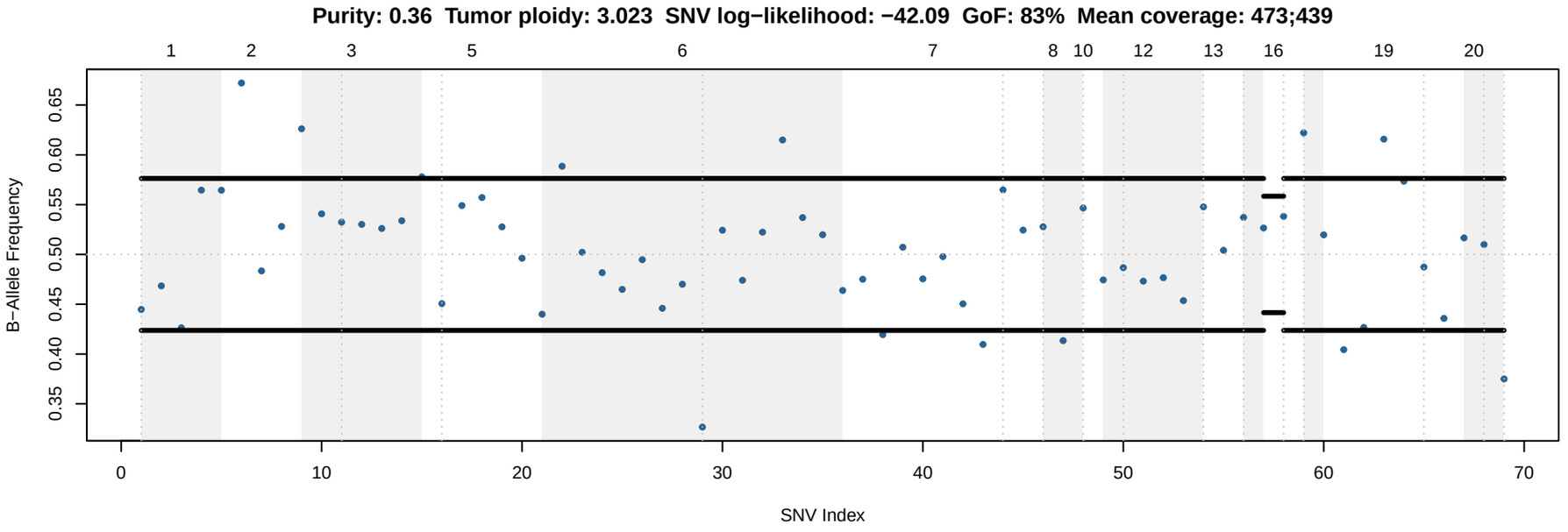

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
3m3
4m3
3m2
7m4
2m1
3m1
4m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

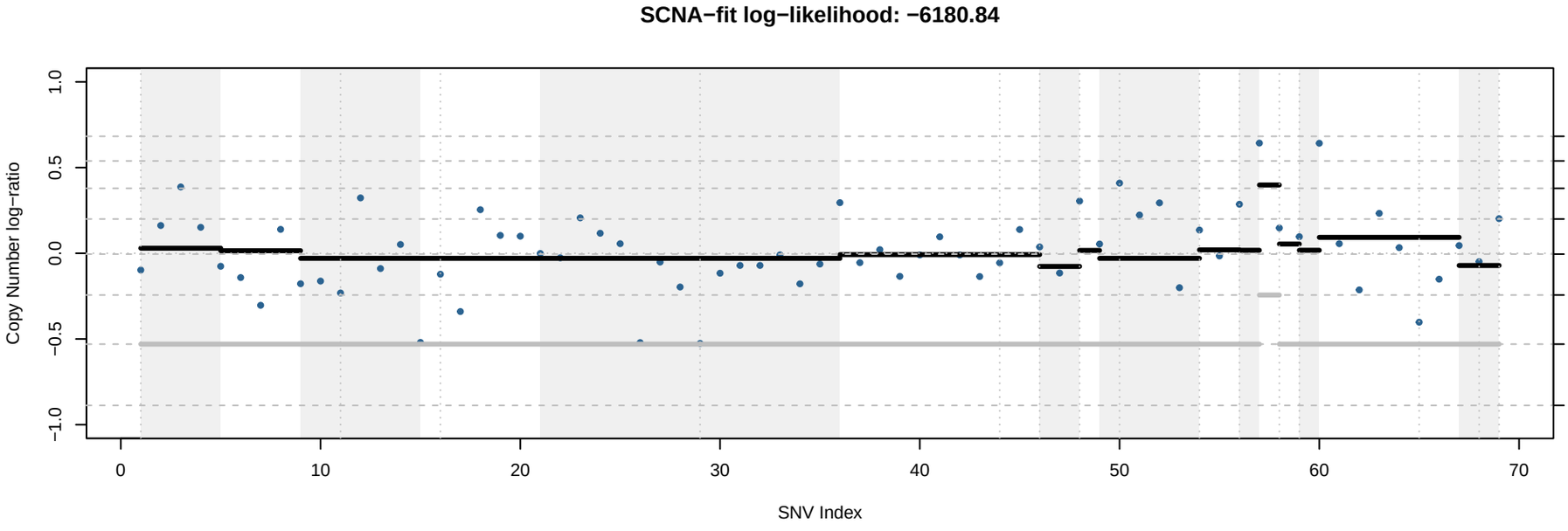

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

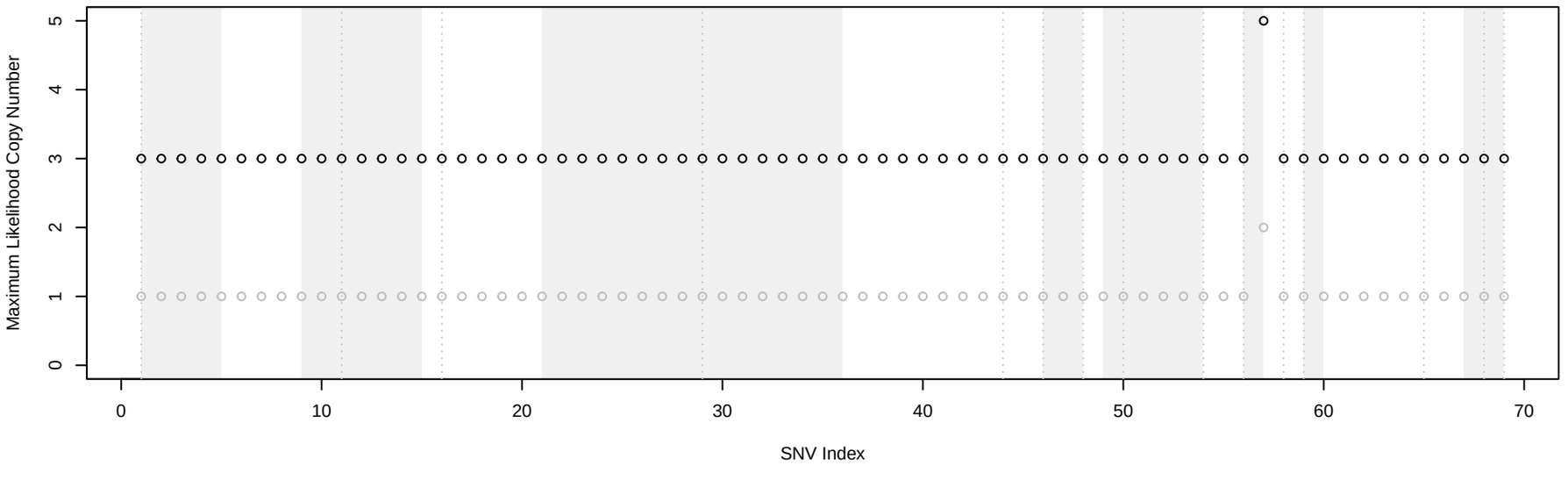

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
2m1
3m1
4m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

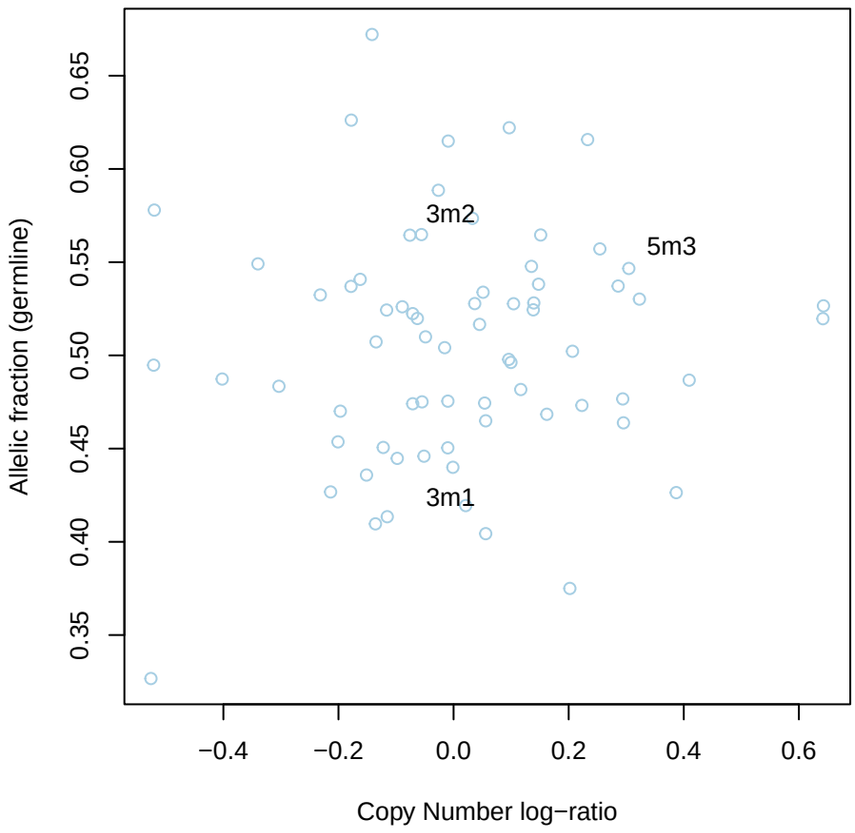

Frequency
0
5
10
15
20
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

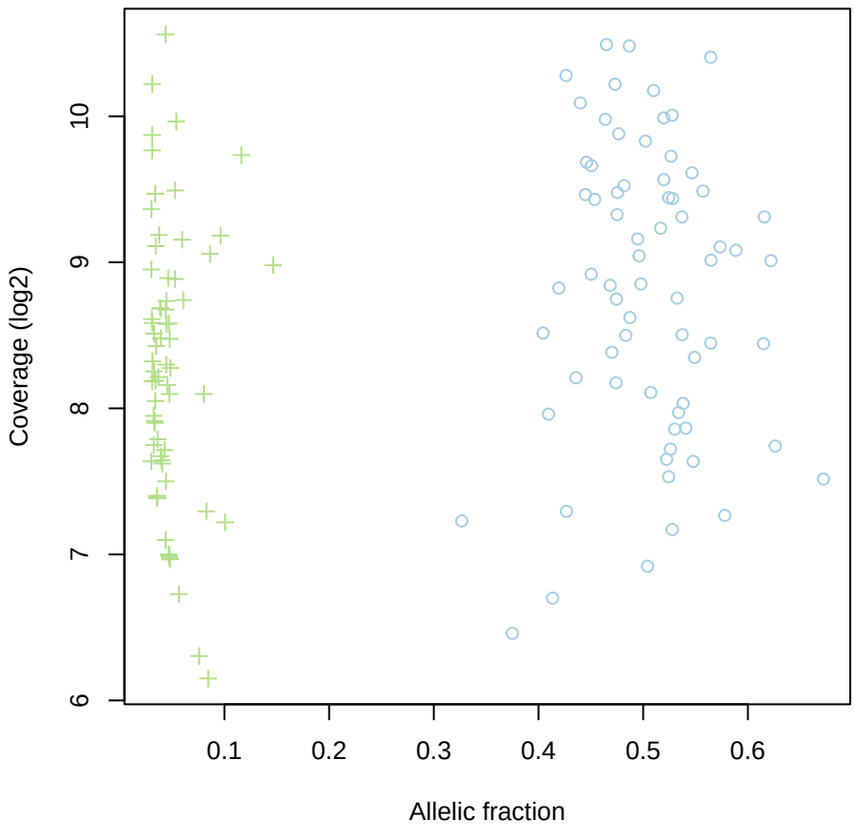

Purity: 0.36 Tumor ploidy: 3.023
0
1
2
3
4
5
6
7
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Fraction Genome
−0.5
0.0
0.5
log2 ratio

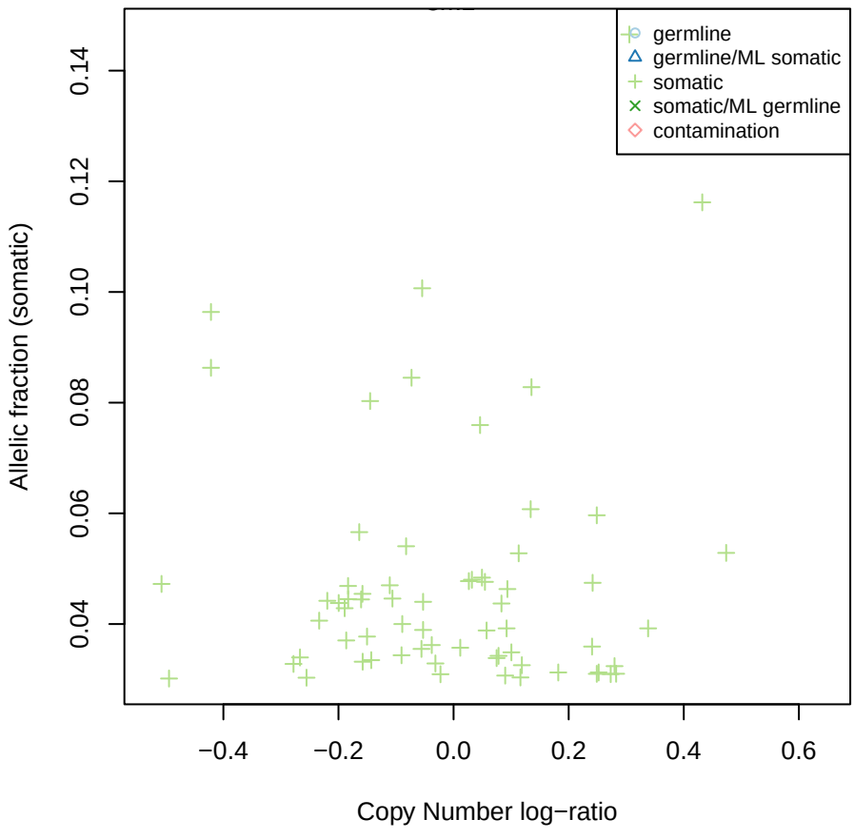

Purity: 0.36 Tumor ploidy: 3.023 SNV log−likelihood: −42.09 GoF: 83% Mean coverage: 473;439
1 2 3 5 6 7 8 10 12 13 16 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 10 20 30 40 50 60 70
SNV Index

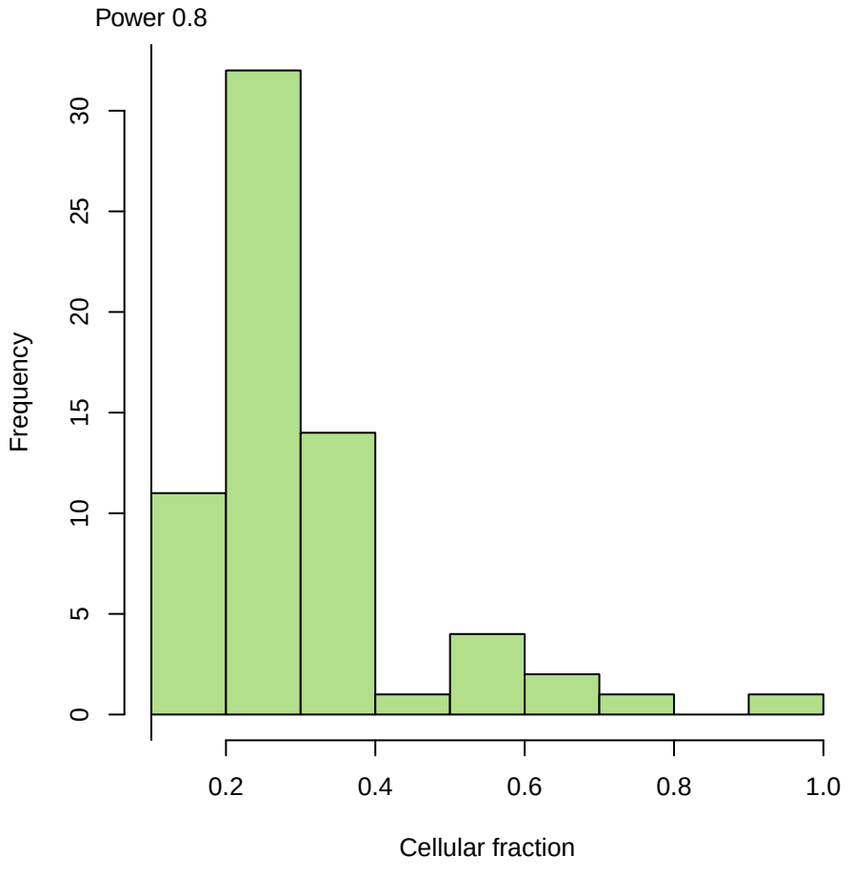

SCNA−fit log−likelihood: −6180.84
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 6
0 10 20 30 40 50 60 70
SNV Index

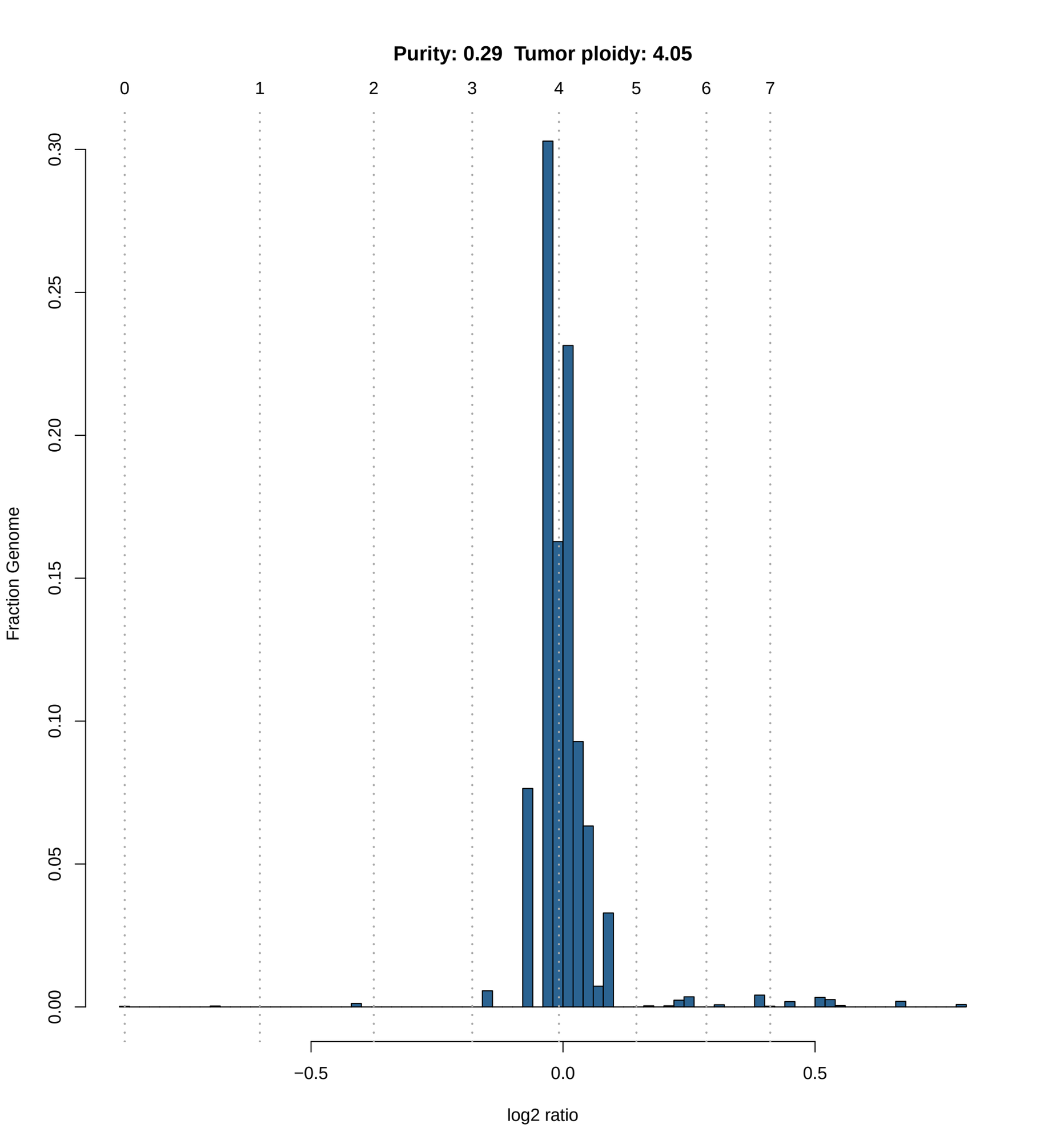

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 10 20 30 40 50 60 70
SNV Index

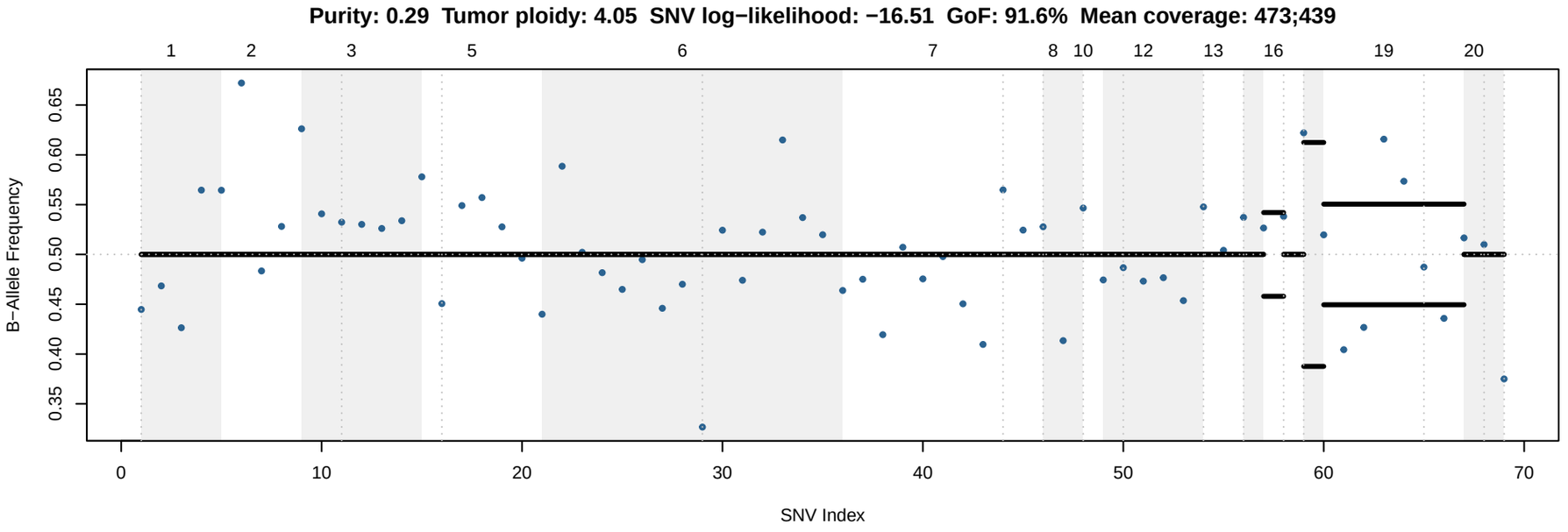

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
3m2
5m3
3m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

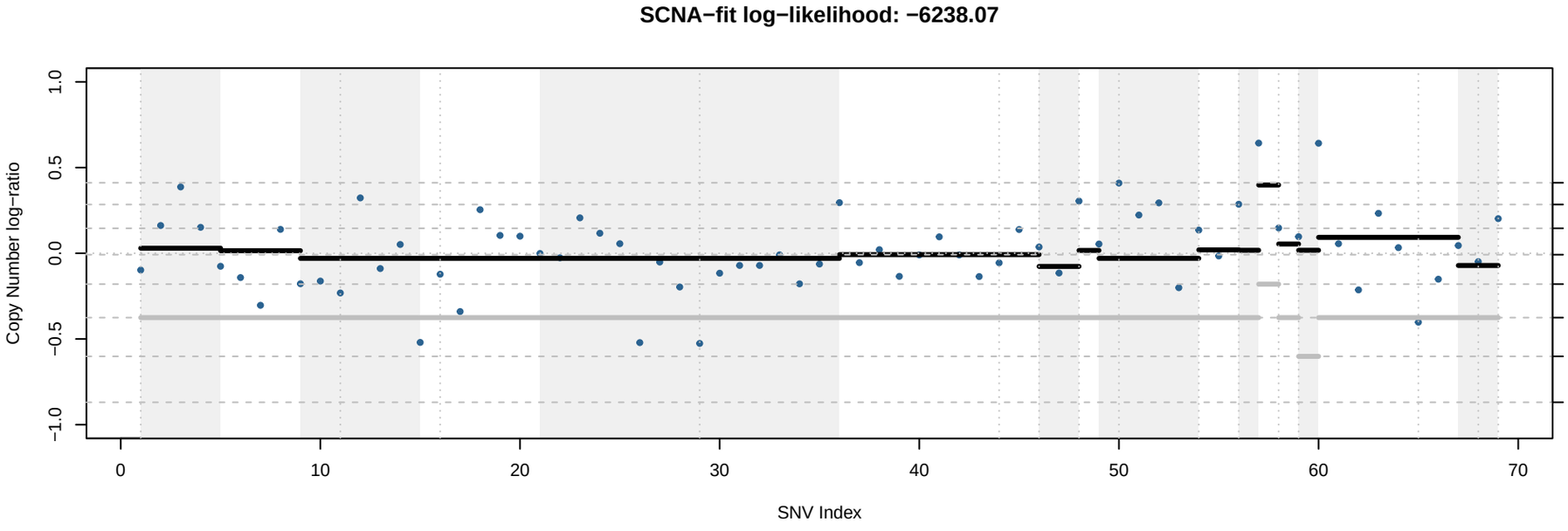

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

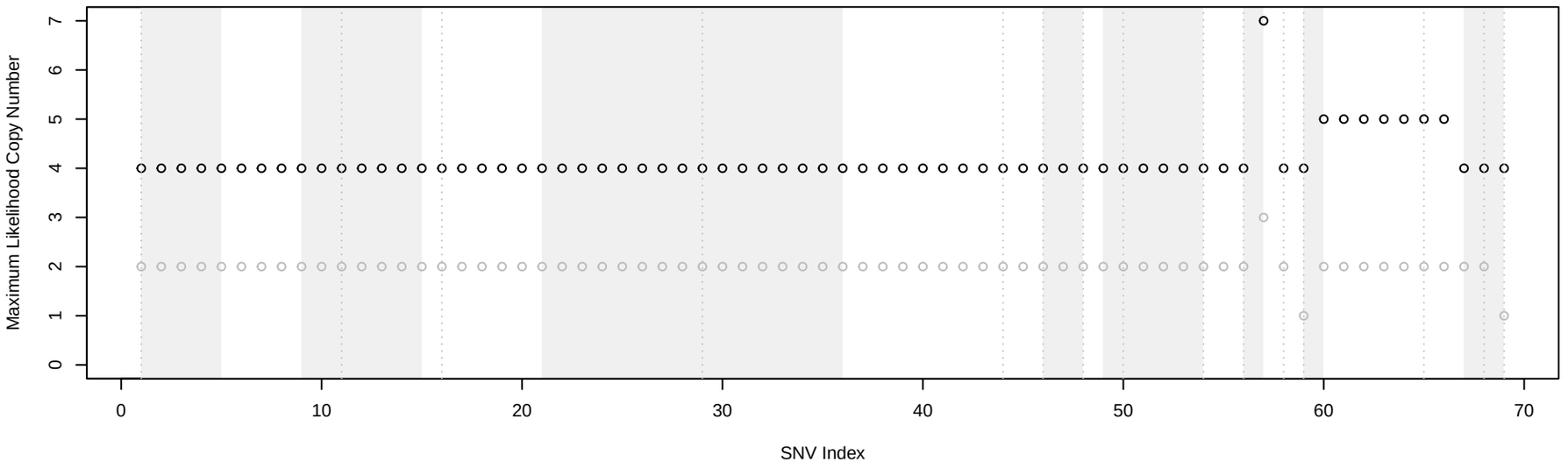

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

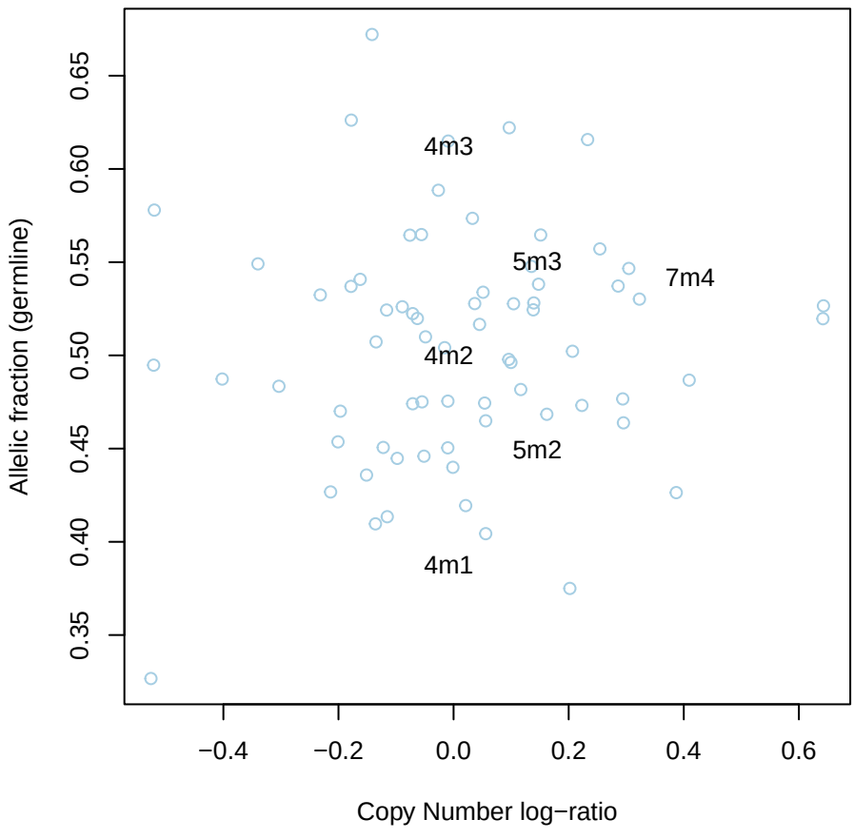

Power 0.8
Frequency
0
5
10
15
20
25
30
0.2
0.4
0.6
0.8
1.0
Cellular fraction

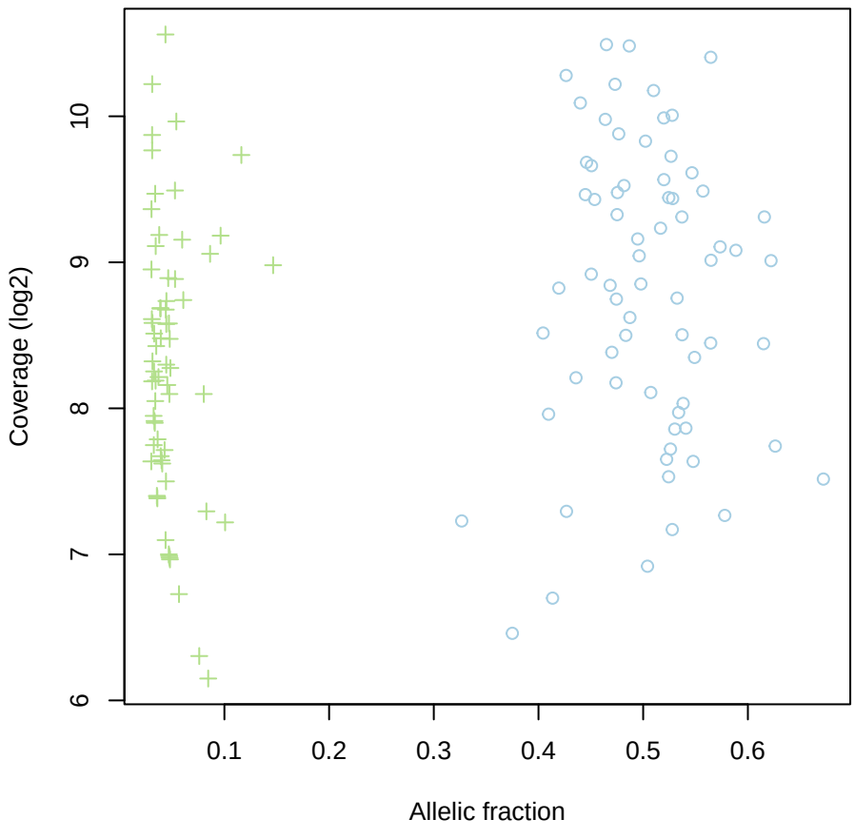

Purity: 0.29 Tumor ploidy: 4.05
0
1
2
3
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

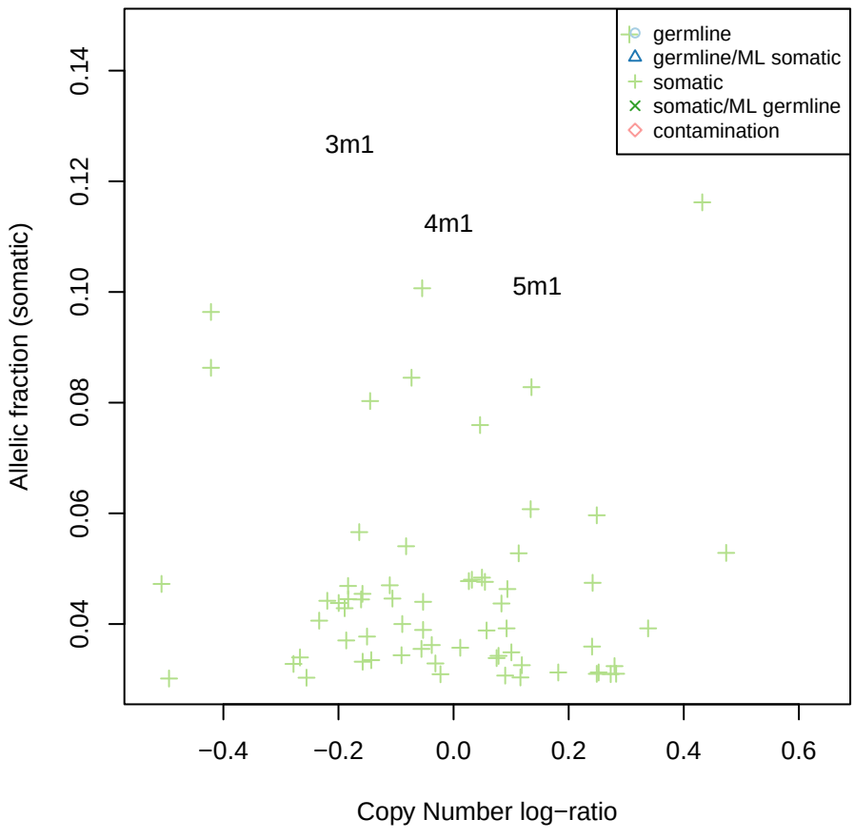

Purity: 0.29 Tumor ploidy: 4.05 SNV log−likelihood: −16.51 GoF: 91.6% Mean coverage: 473;439
1 2 3 5 6 7 8 10 12 13 16 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 10 20 30 40 50 60 70
SNV Index

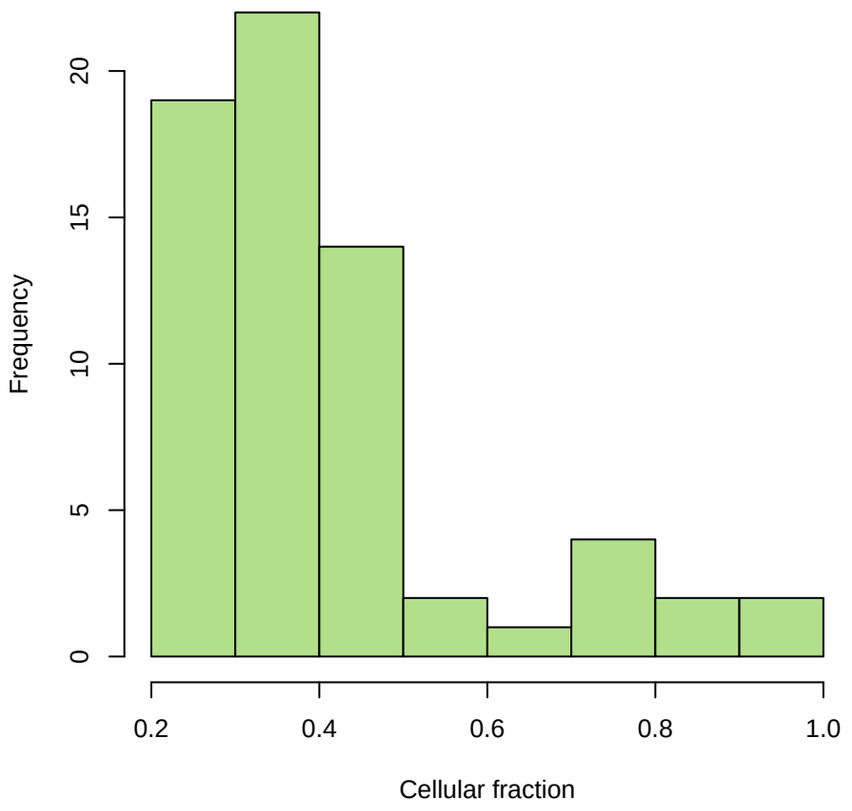

SCNA−fit log−likelihood: −6238.07
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 6 7
0 10 20 30 40 50 60 70
SNV Index

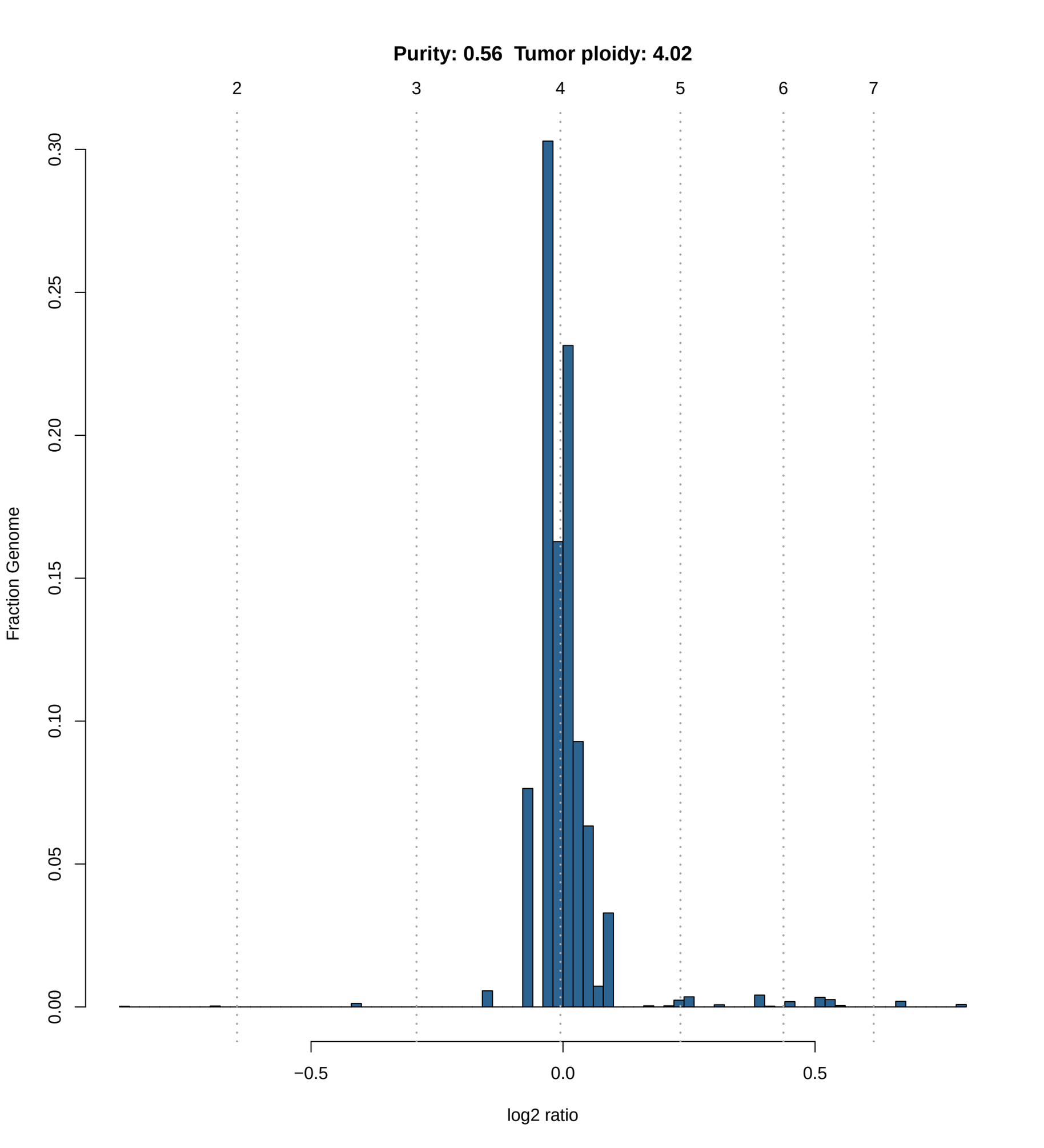

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 10 20 30 40 50 60 70
SNV Index

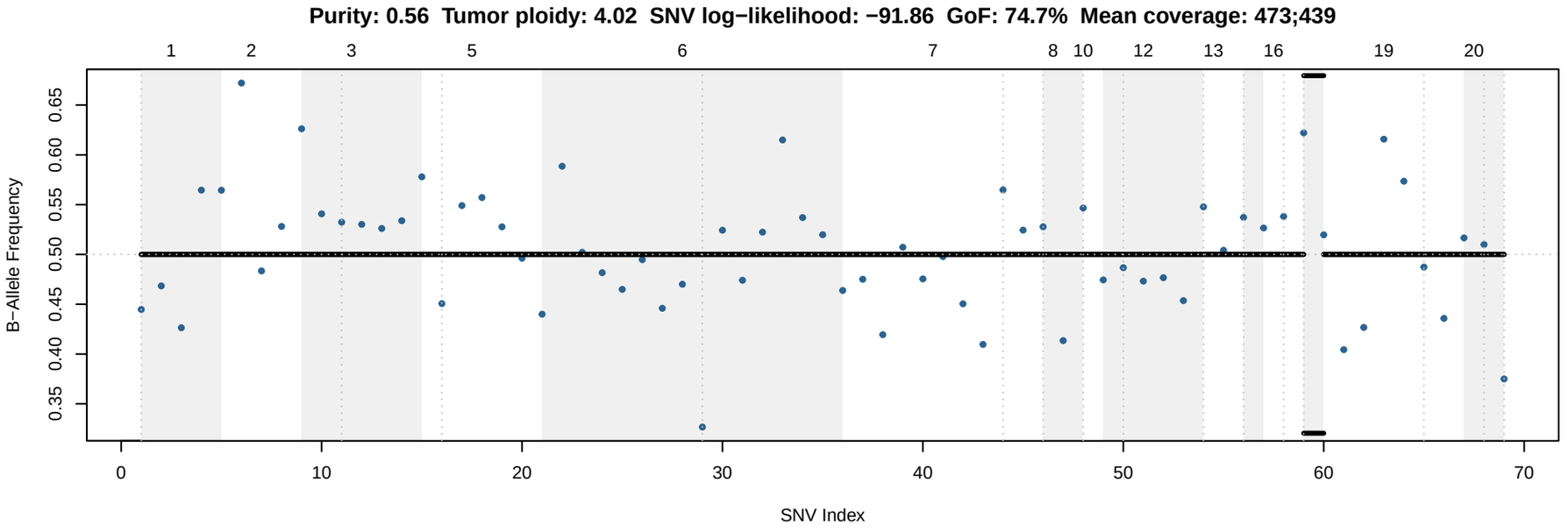

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
4m3
5m3
7m4
4m2
5m2
4m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

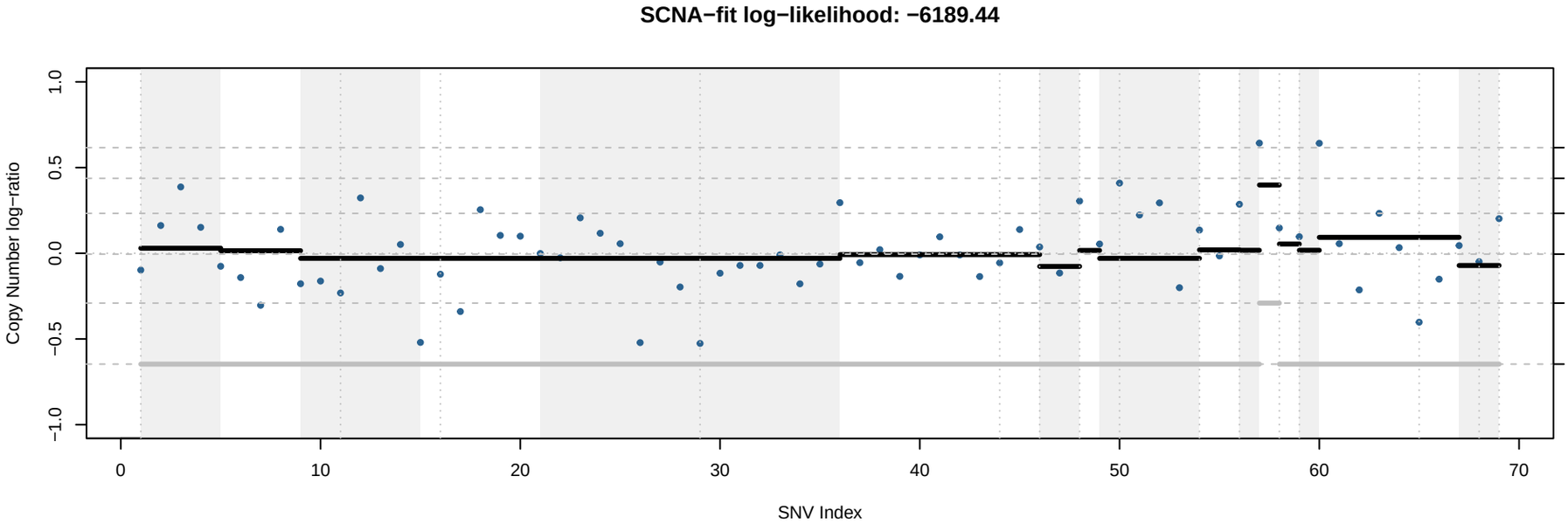

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

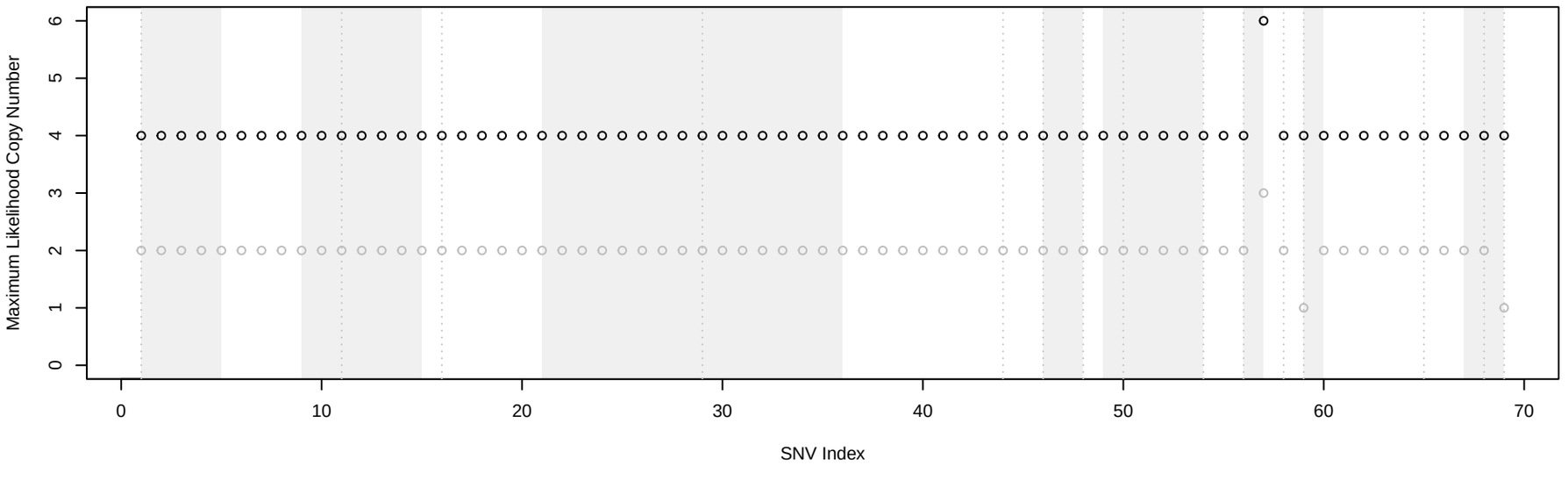

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
3m1
4m1
5m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

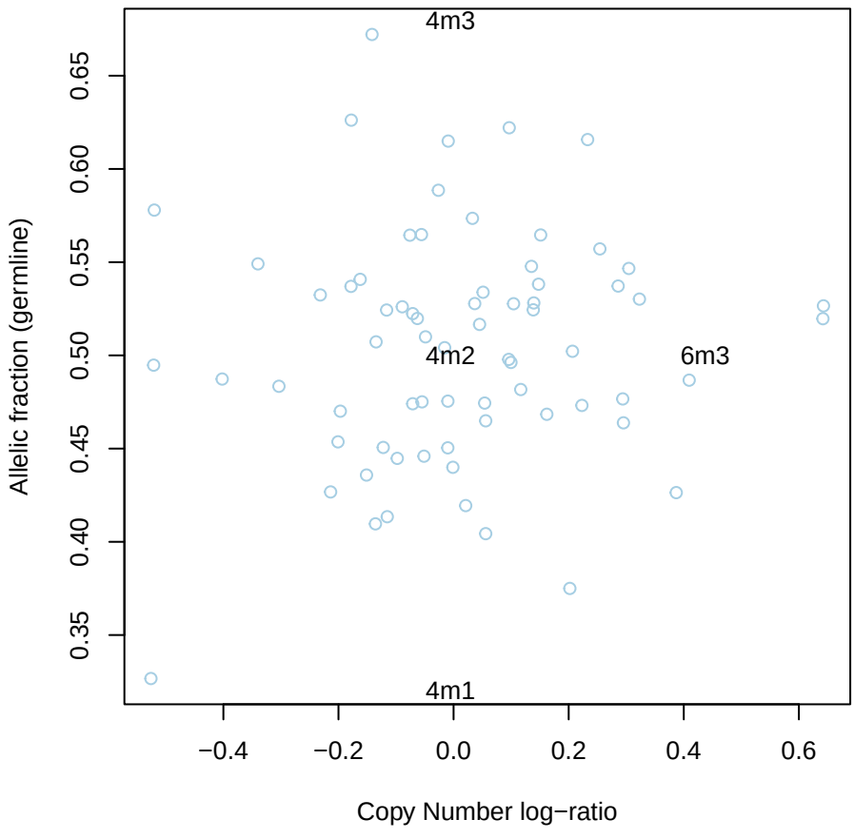

Frequency
0
5
10
15
20
0.2
0.4
0.6
0.8
1.0
Cellular fraction

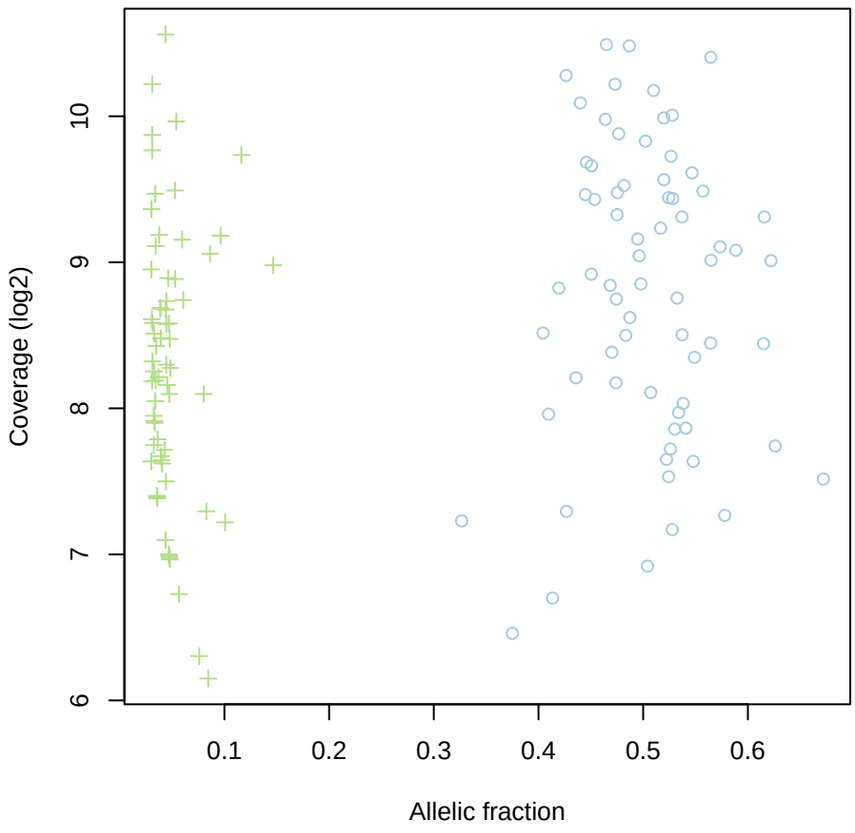

Purity: 0.56 Tumor ploidy: 4.02
2
3
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

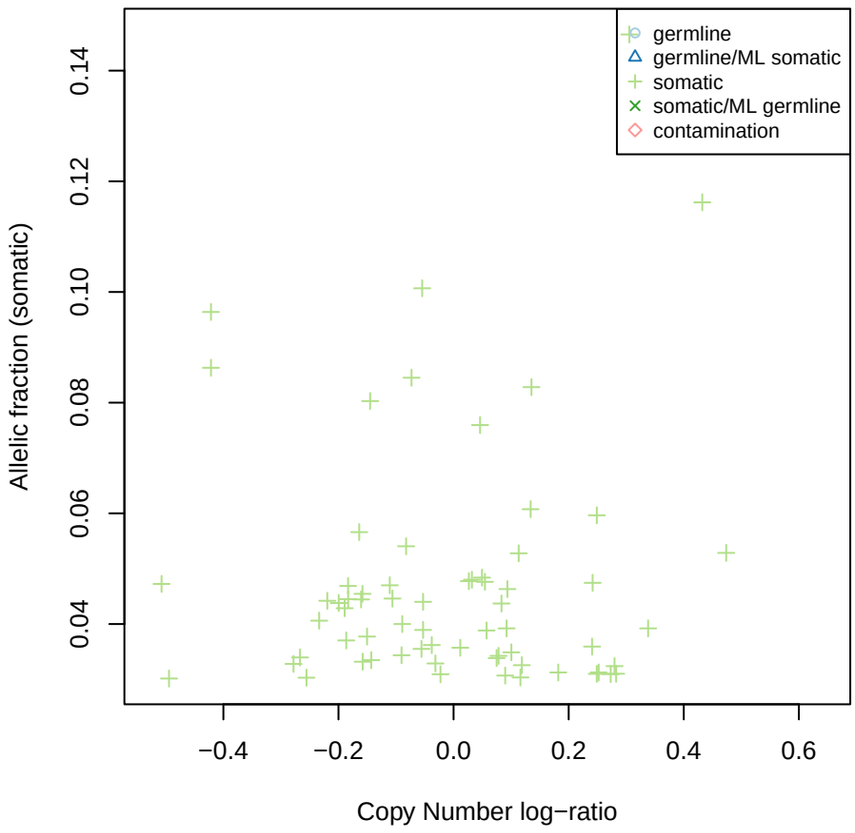

Purity: 0.56 Tumor ploidy: 4.02 SNV log−likelihood: −91.86 GoF: 74.7% Mean coverage: 473;439
1 2 3 5 6 7 8 10 12 13 16 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 10 20 30 40 50 60 70
SNV Index

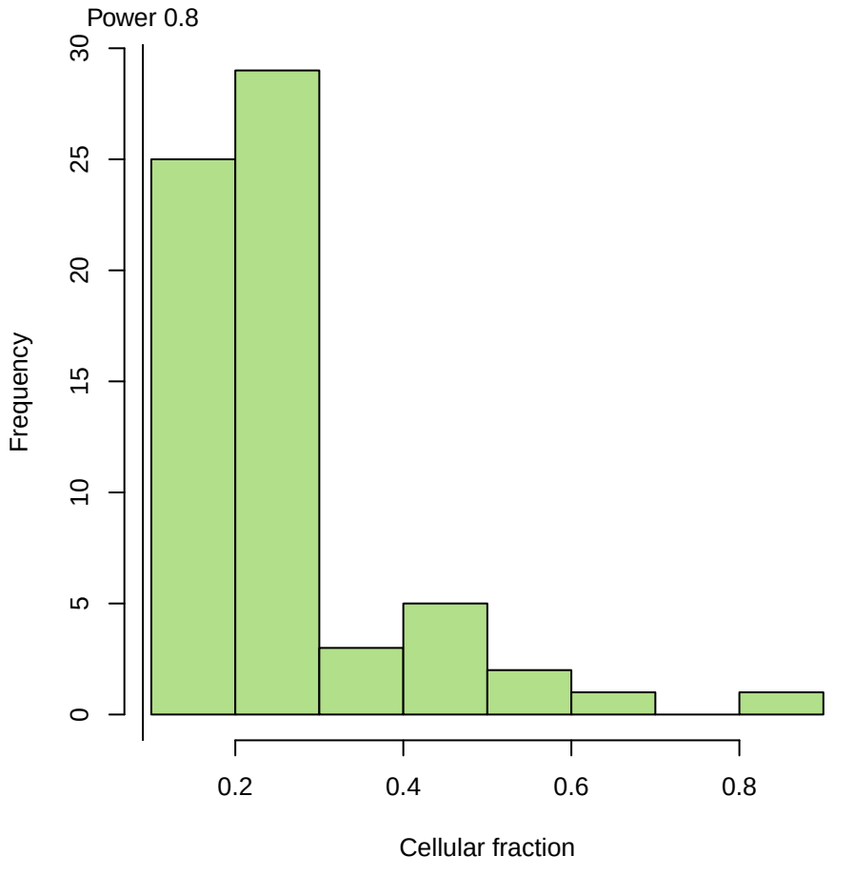

SCNA−fit log−likelihood: −6189.44
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 10 20 30 40 50 60 70
SNV Index

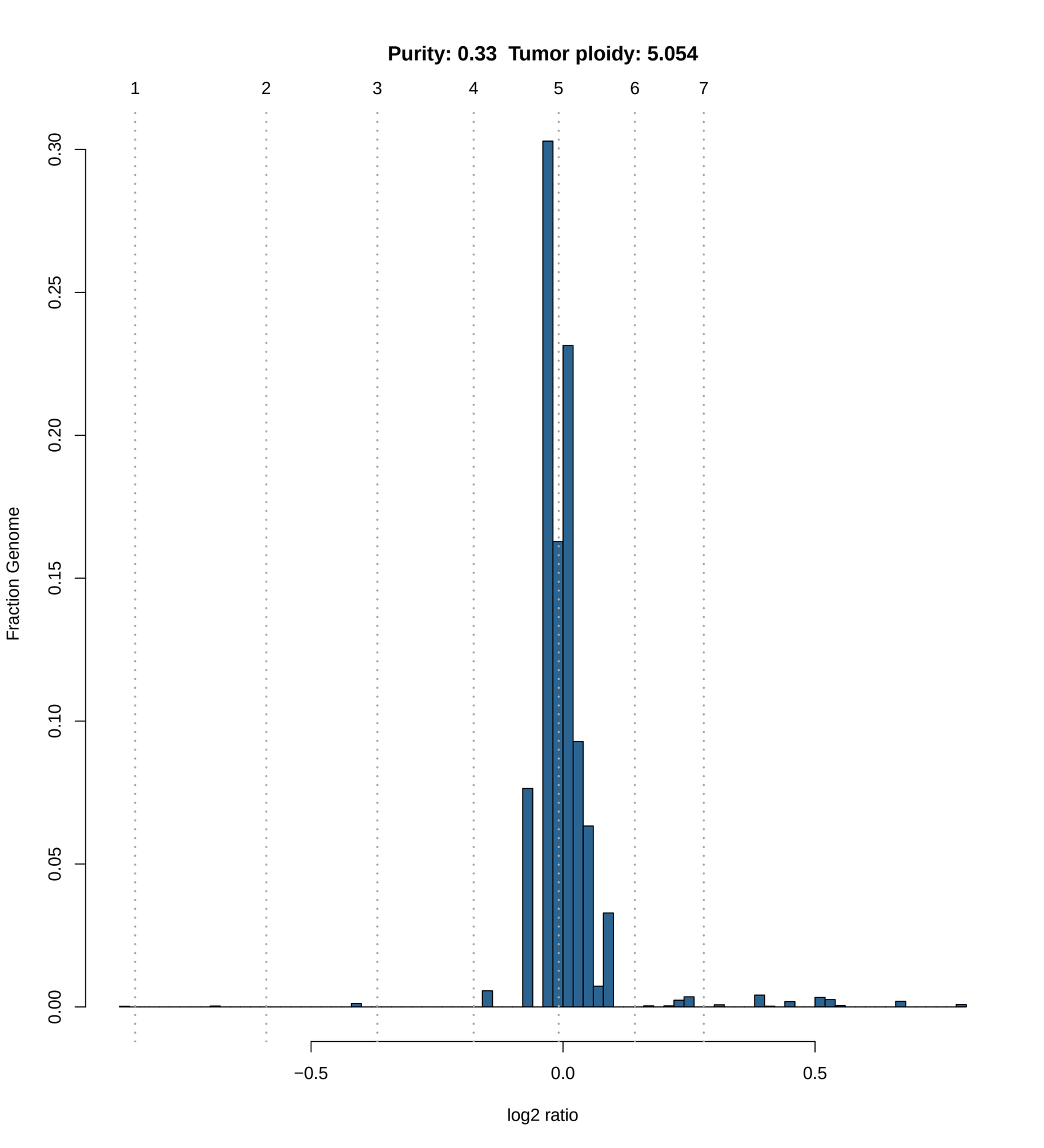

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 10 20 30 40 50 60 70
SNV Index

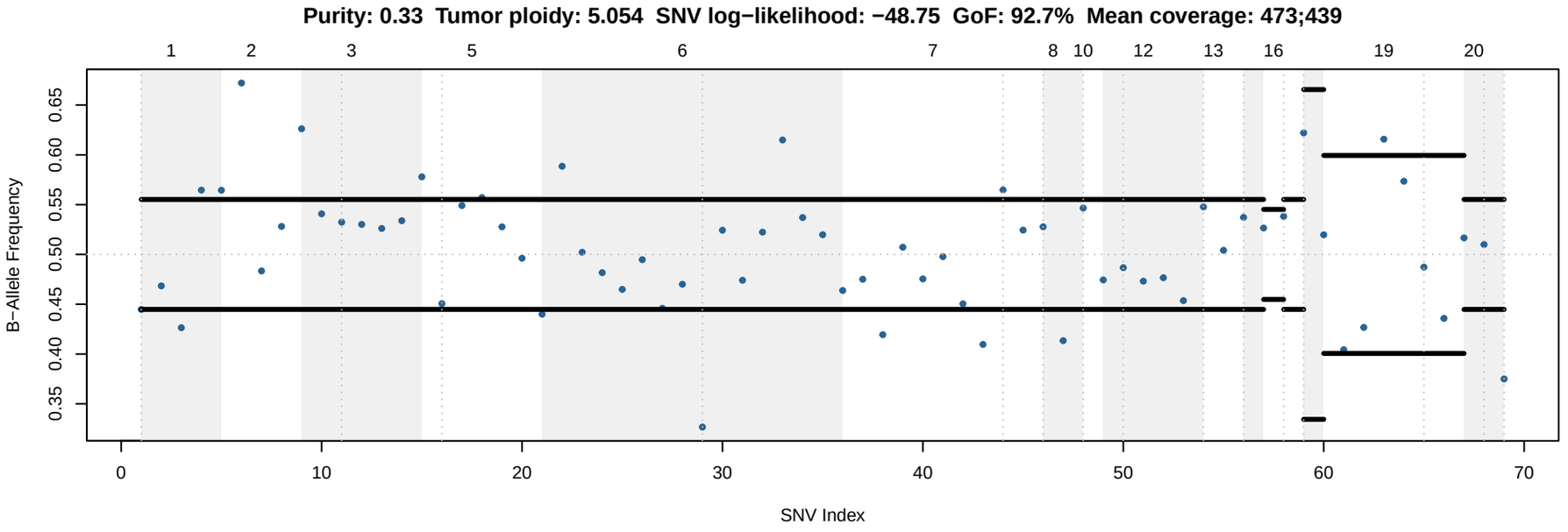

4m3
4m2
6m3
4m1
Allelic fraction (germline)
Copy Number log−ratio
0.35
0.40
0.45
0.50
0.55
0.60
0.65
−0.4
−0.2
0.0
0.2
0.4
0.6

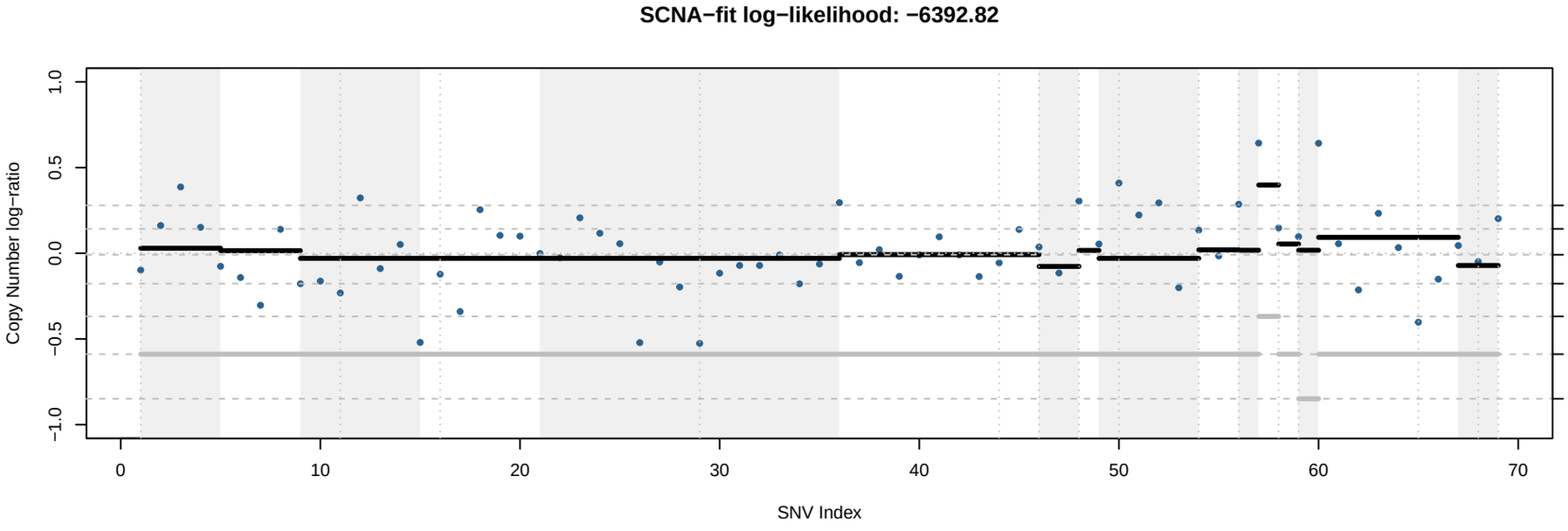

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6

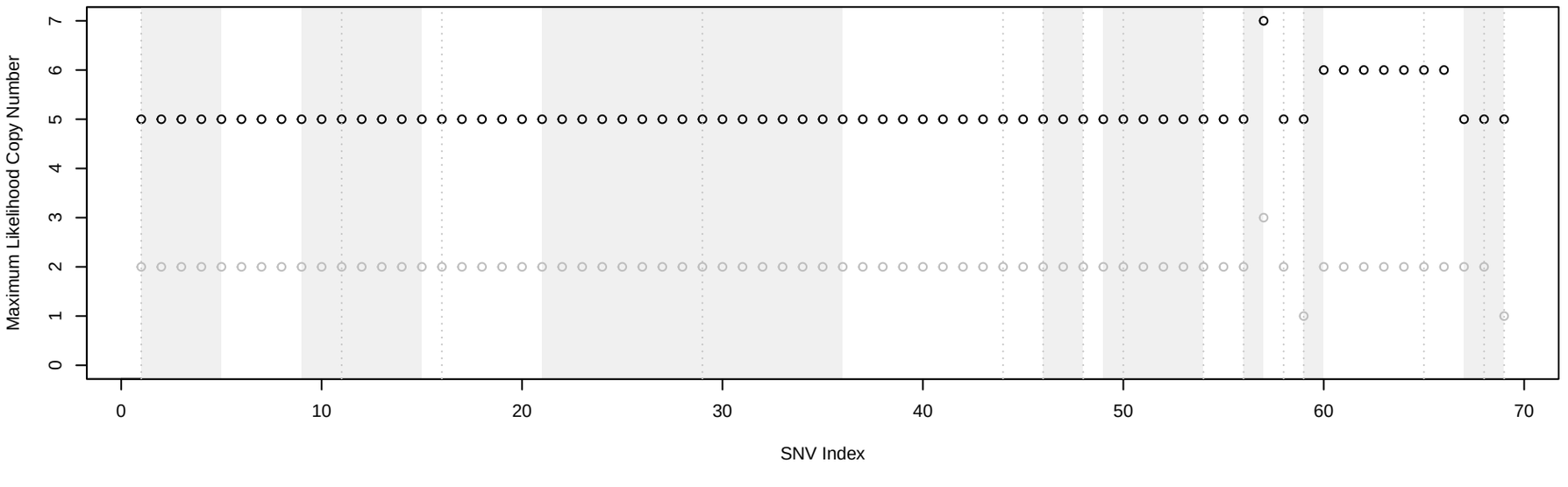

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
0.12
0.14
−0.4
−0.2
0.0
0.2
0.4
0.6

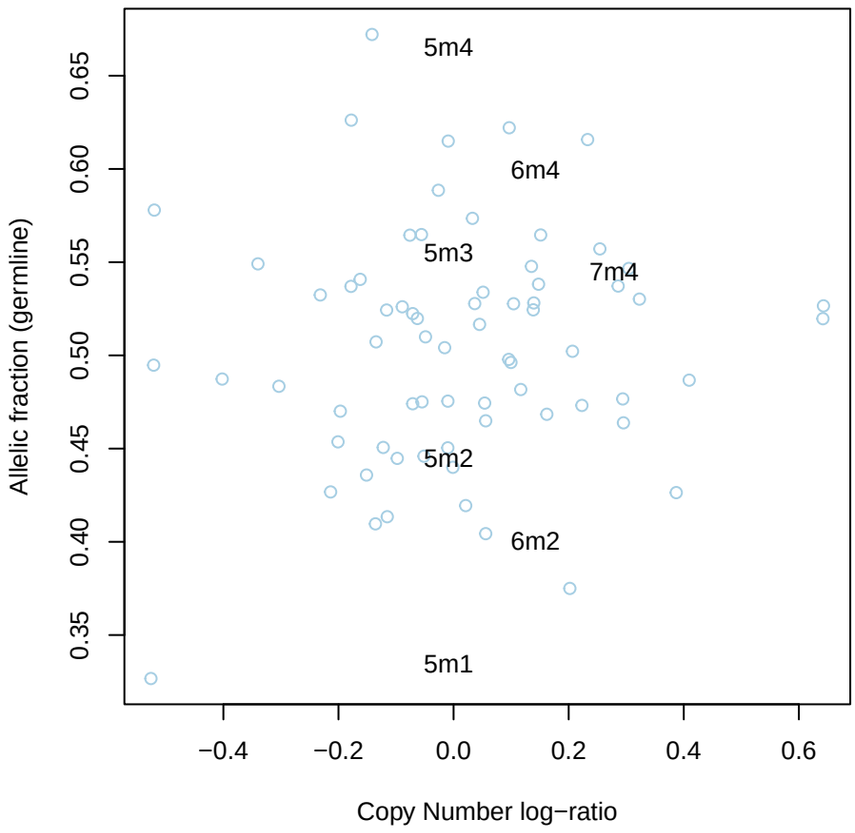

Power 0.8
Frequency
Cellular fraction
0
5
10
15
20
25
30
0.2
0.4
0.6
0.8

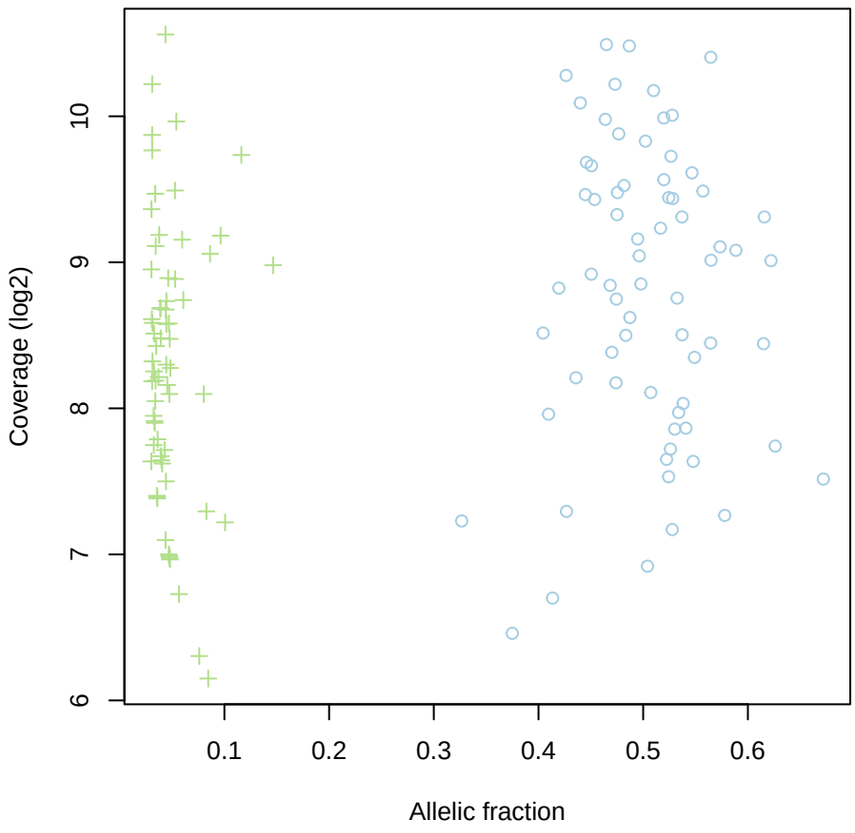

Purity: 0.33 Tumor ploidy: 5.054
1
2
3
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

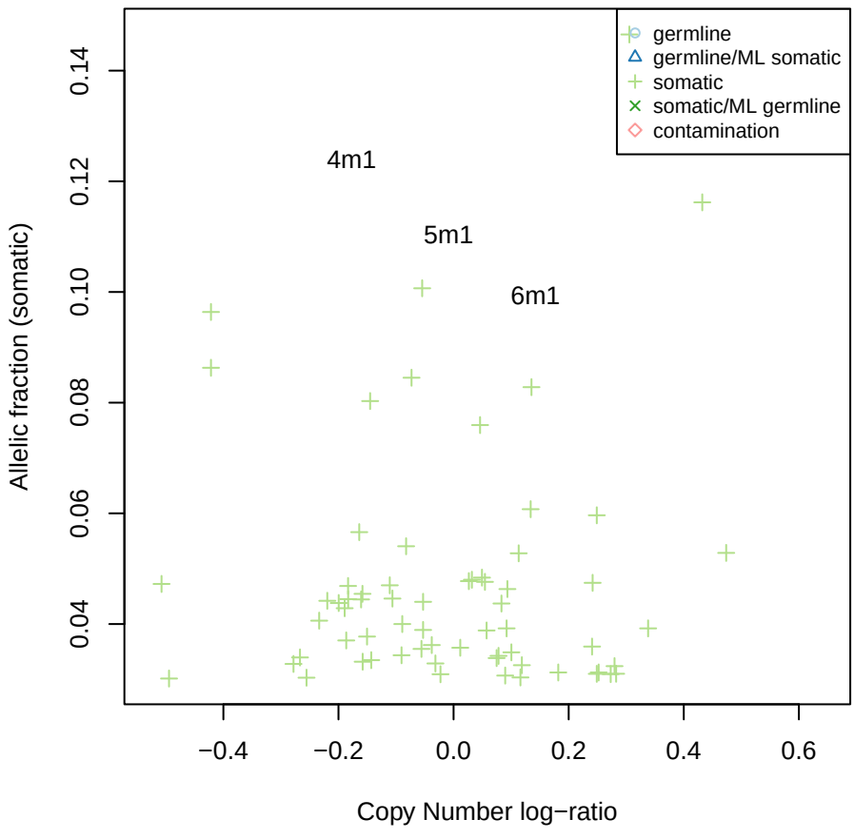

Purity: 0.33 Tumor ploidy: 5.054 SNV log−likelihood: −48.75 GoF: 92.7% Mean coverage: 473;439
1 2 3 5 6 7 8 10 12 13 16 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 10 20 30 40 50 60 70
SNV Index

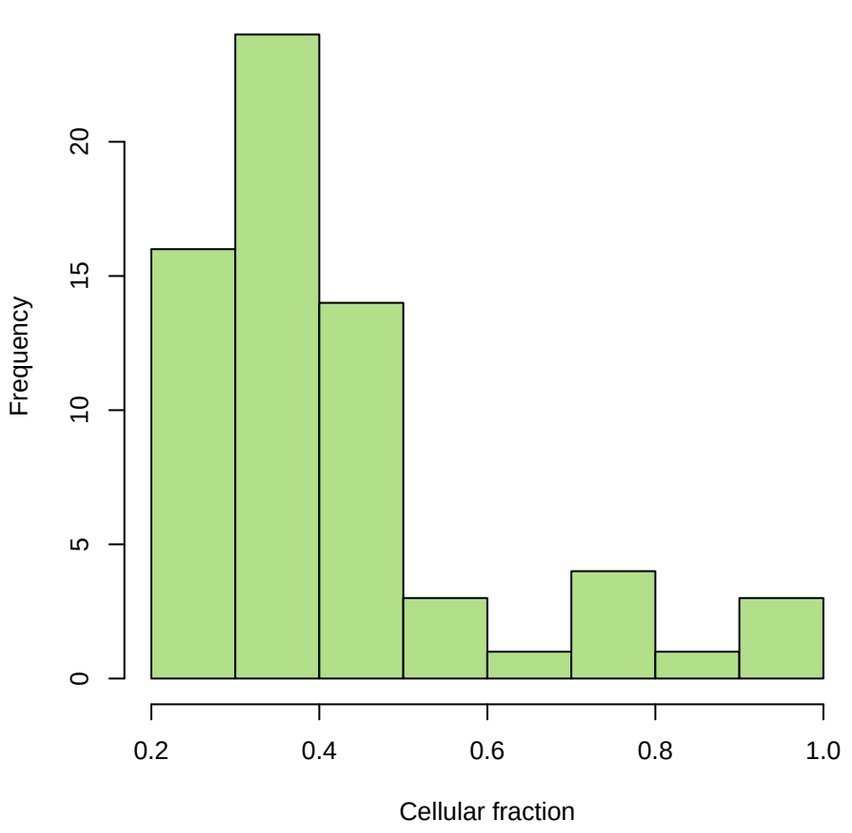

SCNA−fit log−likelihood: −6392.82
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
1 2 3 4 5 6
0 10 20 30 40 50 60 70
SNV Index

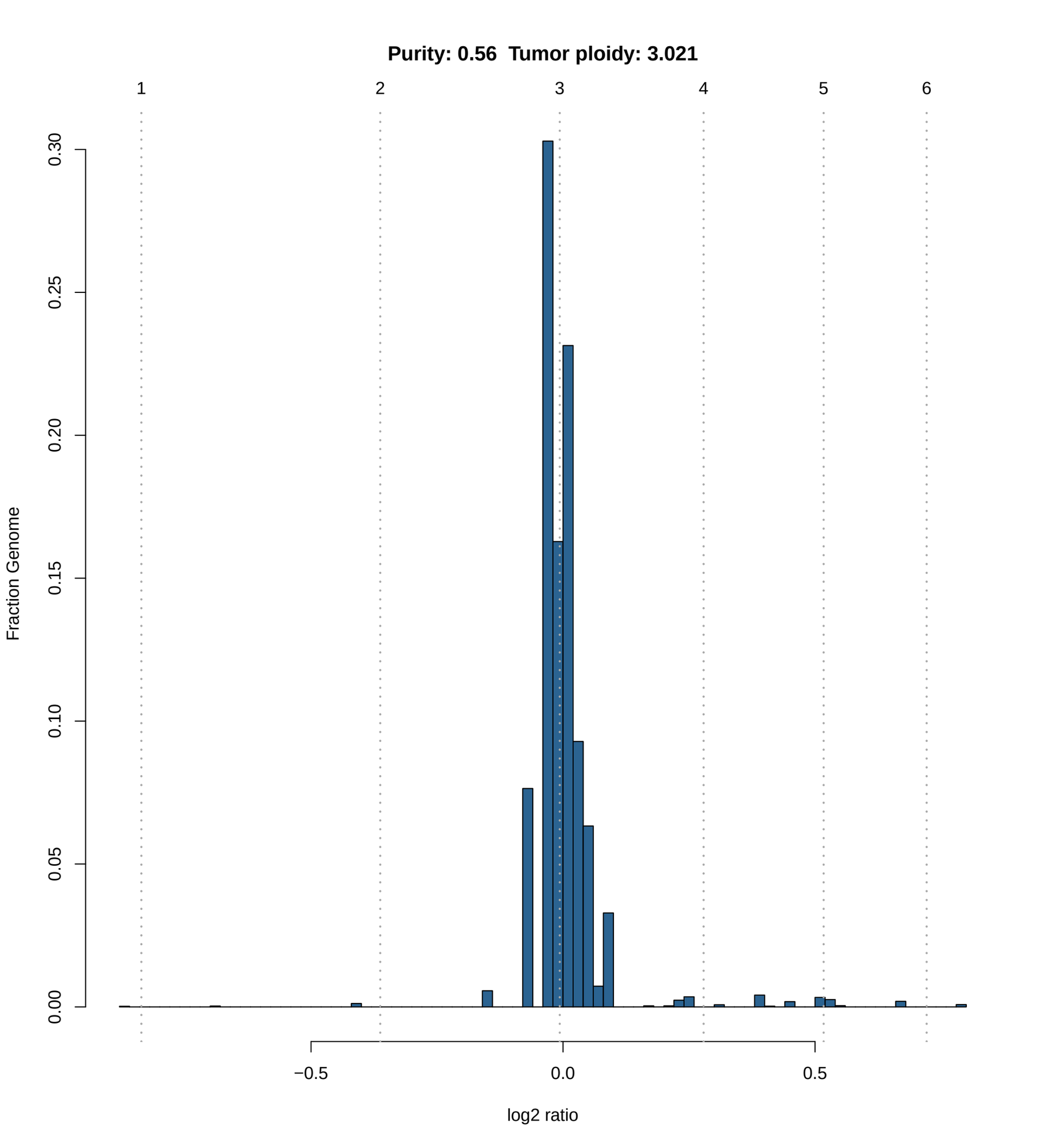

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 10 20 30 40 50 60 70
SNV Index

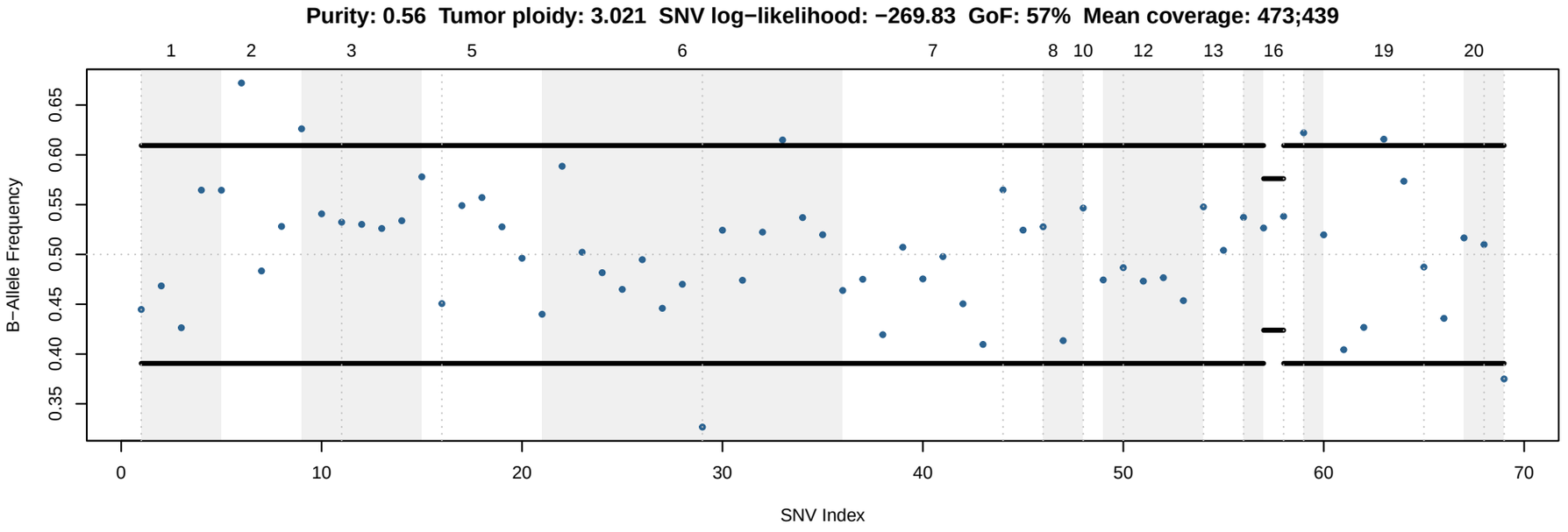

5m4
6m4
5m3
7m4
5m2
6m2
5m1
Allelic fraction (germline)
Copy Number log−ratio

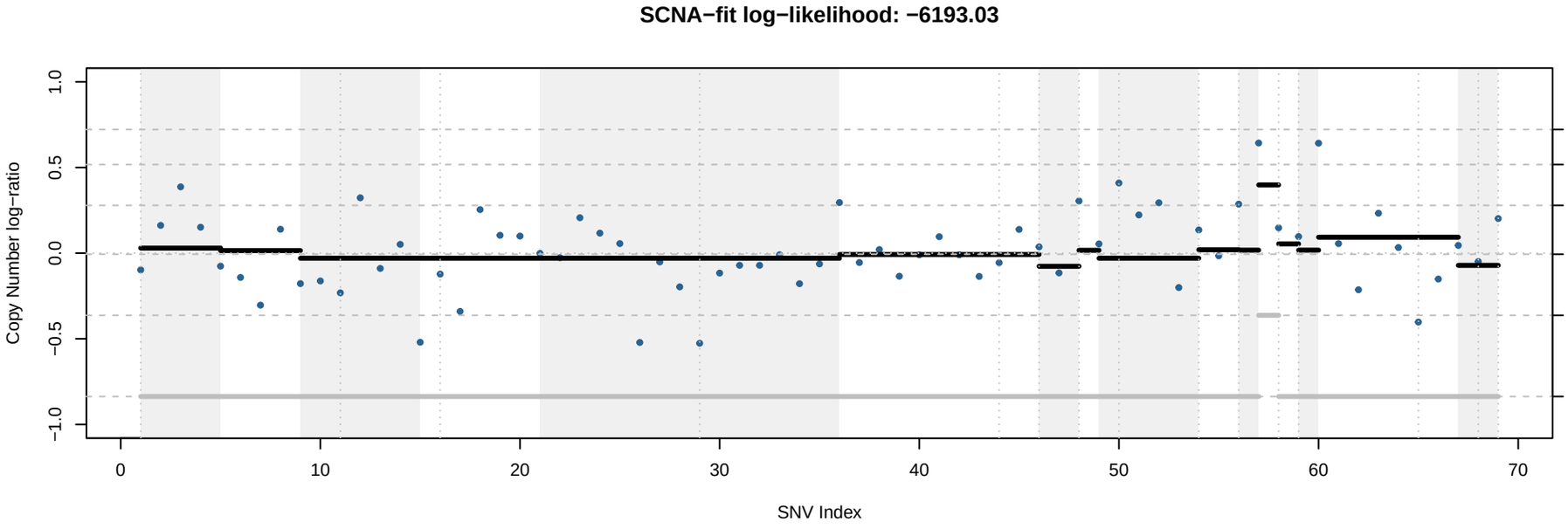

Coverage (log2)
Allelic fraction

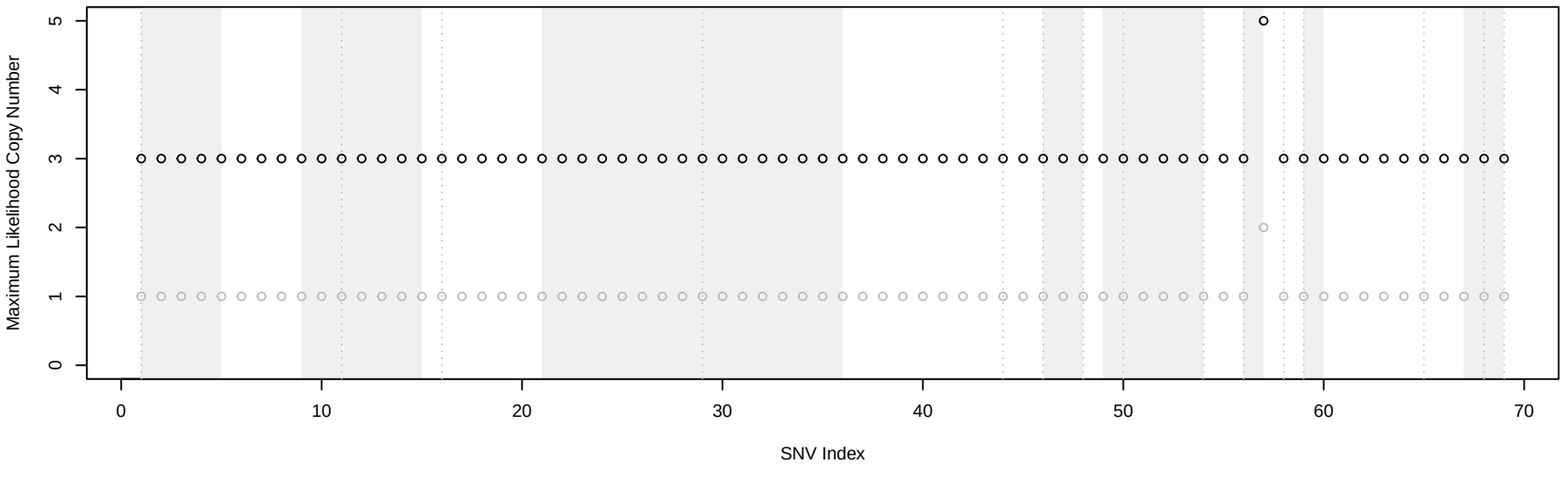

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio

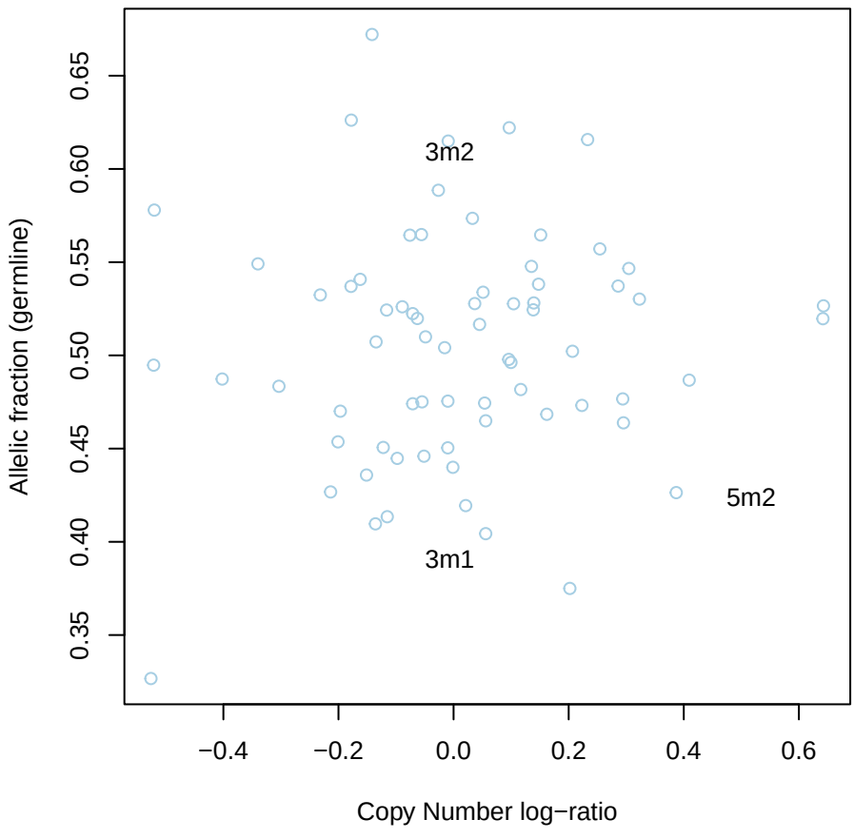

Frequency
Cellular fraction

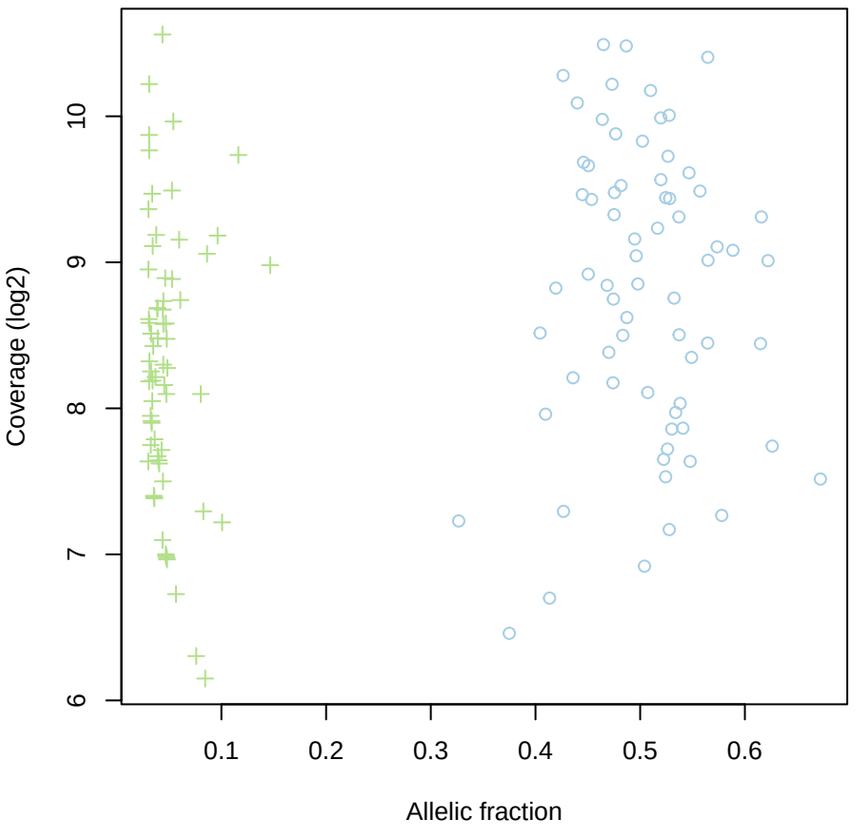

Purity: 0.56 Tumor ploidy: 3.021
1
2
3
4
5
6
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Fraction Genome
−0.5
0.0
0.5
log2 ratio

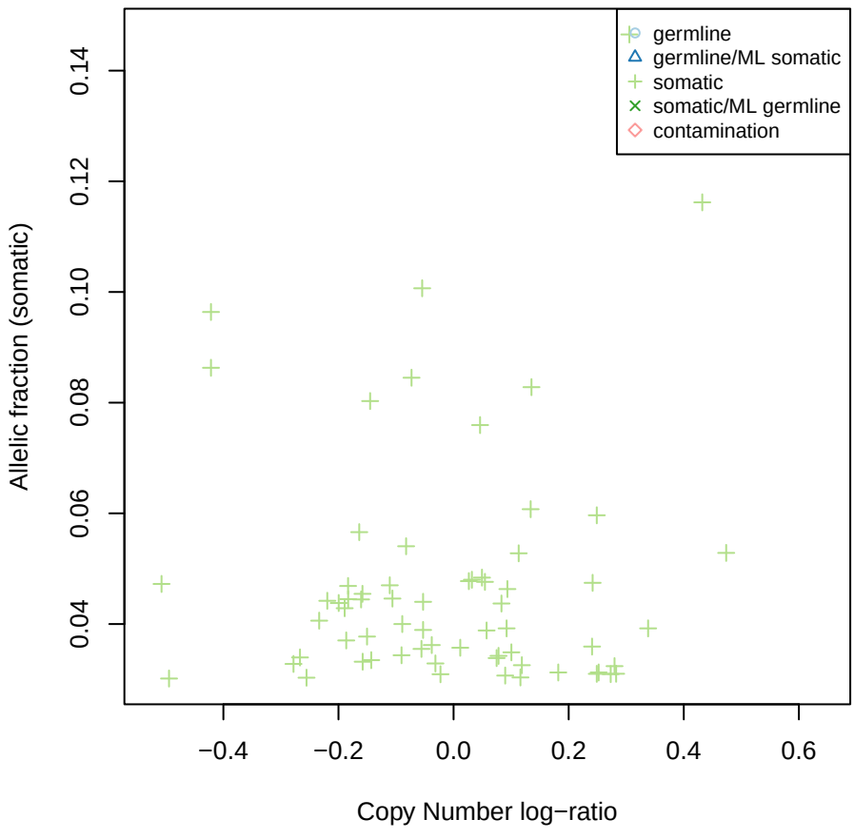

Purity: 0.56 Tumor ploidy: 3.021 SNV log−likelihood: −269.83 GoF: 57% Mean coverage: 473;439
1 2 3 5 6 7 8 10 12 13 16 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 10 20 30 40 50 60 70
SNV Index

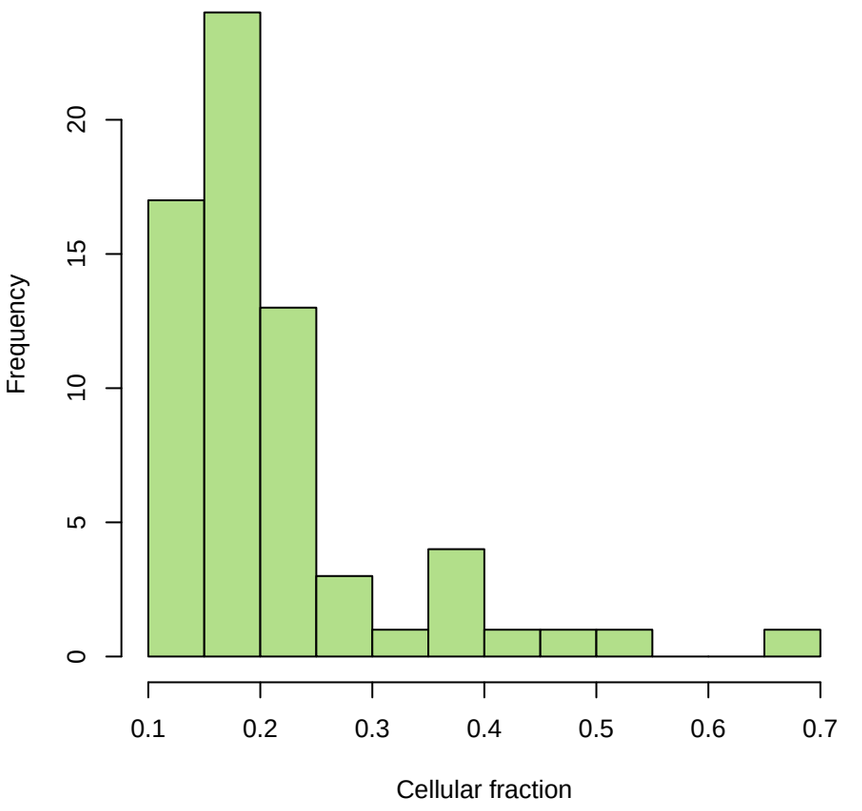

SCNA−fit log−likelihood: −6193.03
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6
0 10 20 30 40 50 60 70
SNV Index

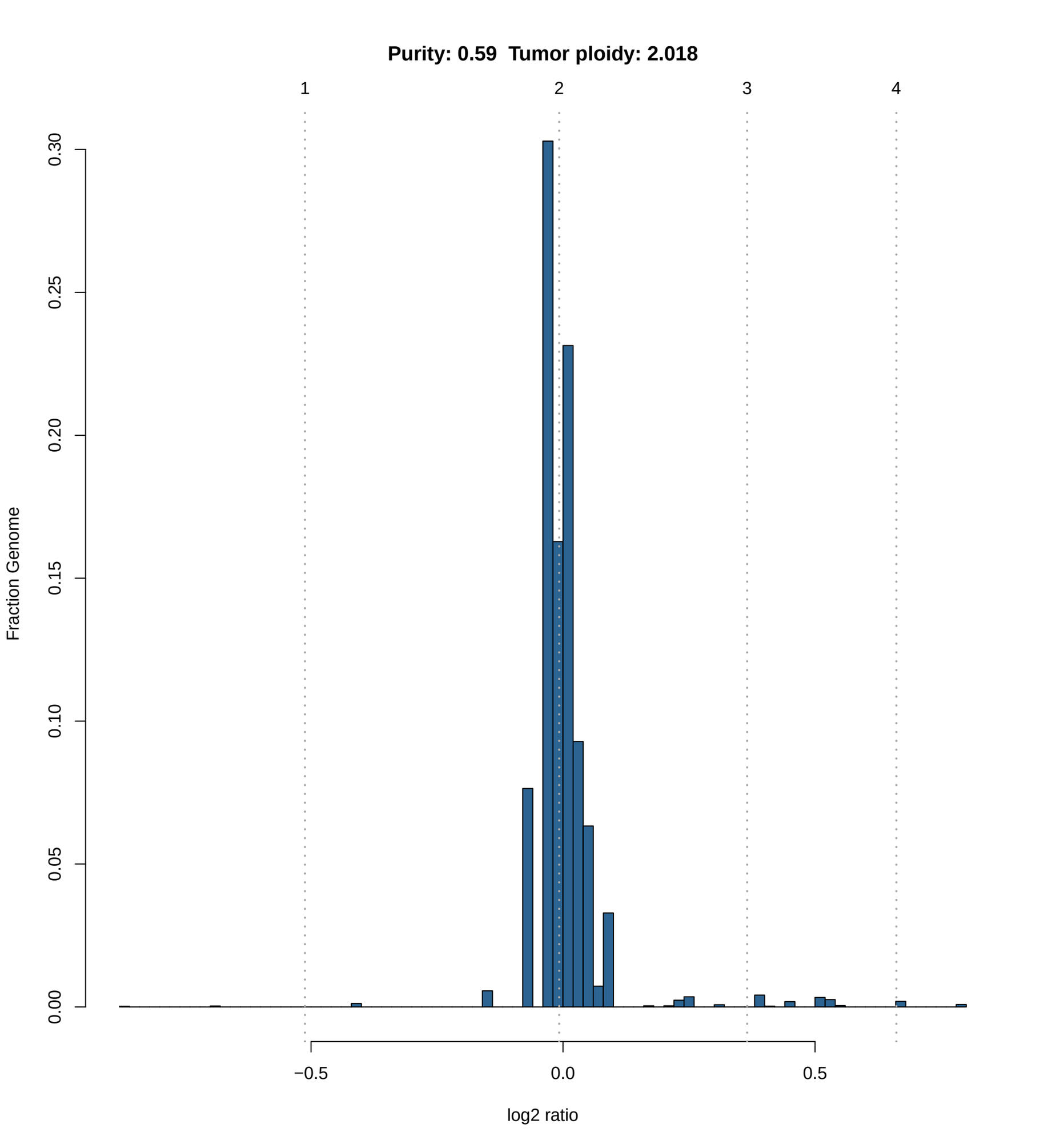

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 10 20 30 40 50 60 70
SNV Index

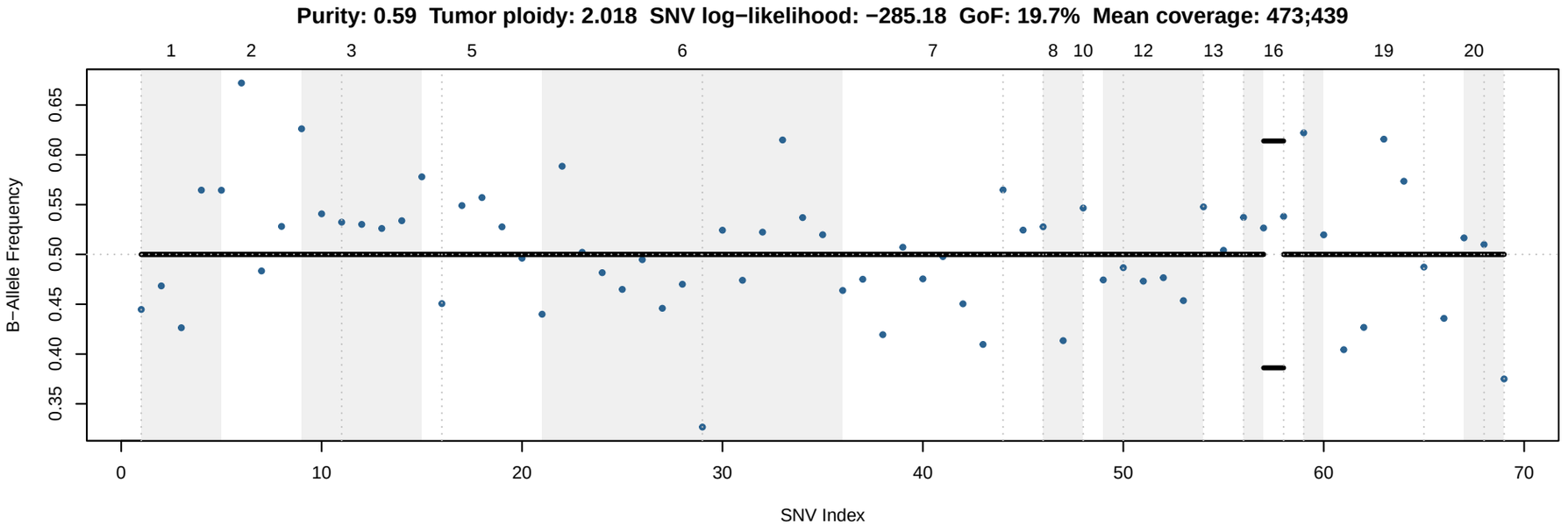

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
3m2
5m2
3m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

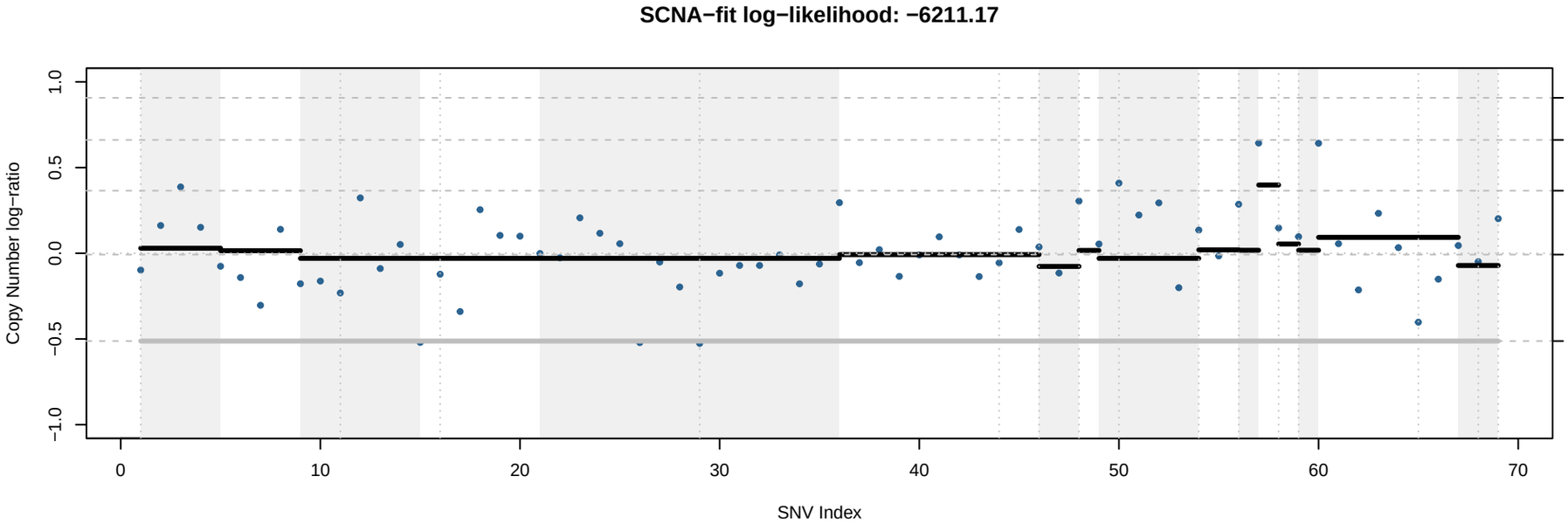

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

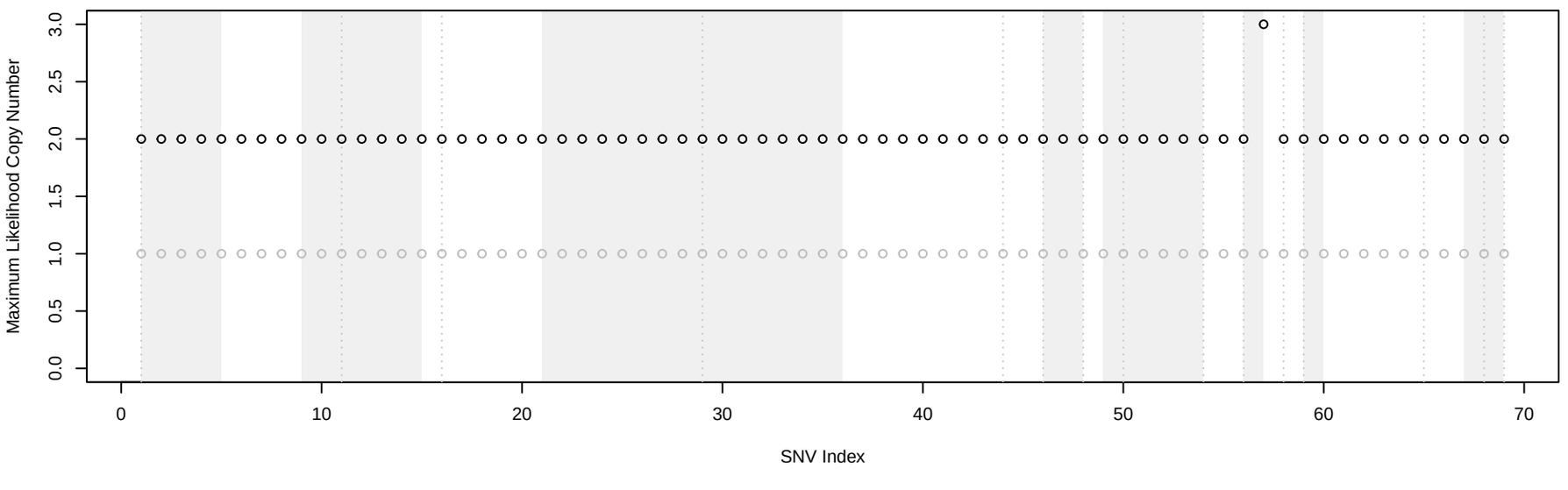

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

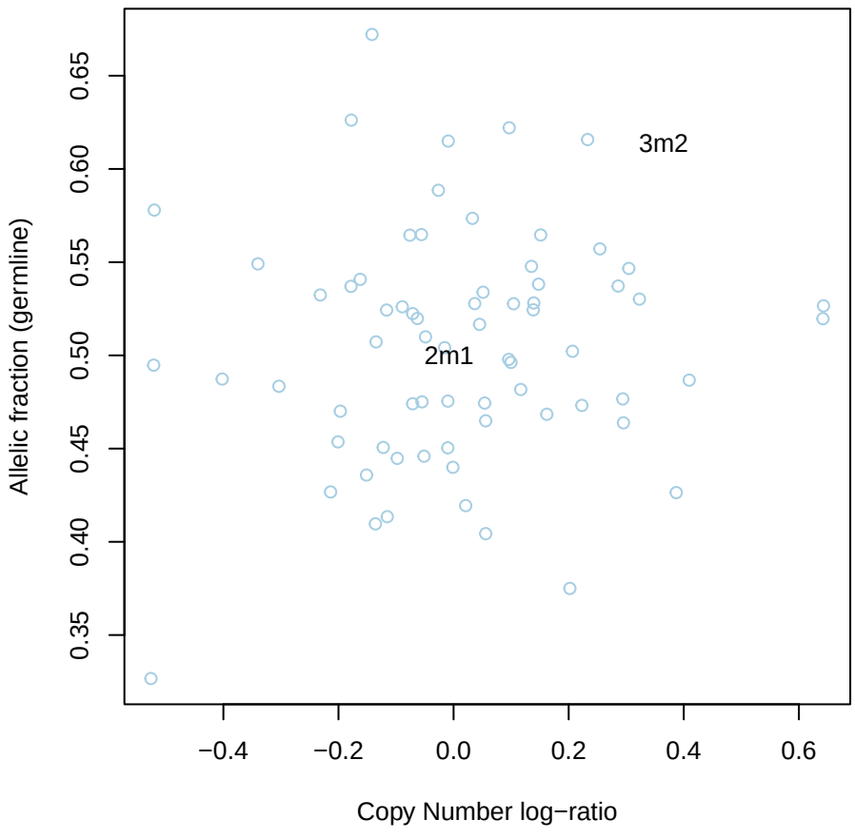

Frequency
0
5
10
15
20
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Cellular fraction

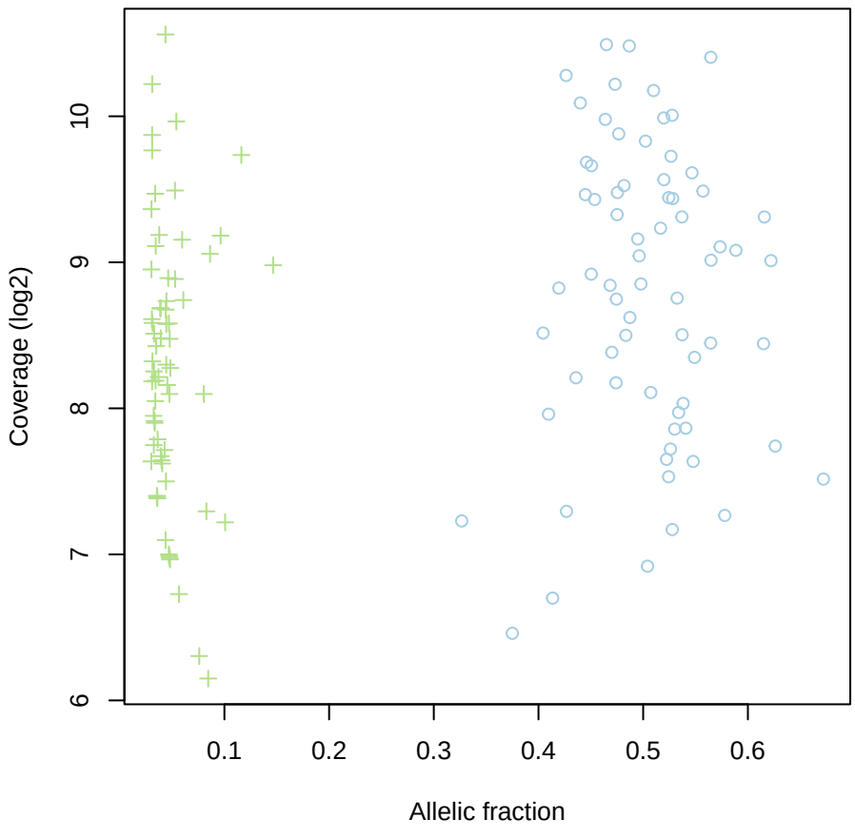

Purity: 0.59 Tumor ploidy: 2.018
1
2
3
4
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

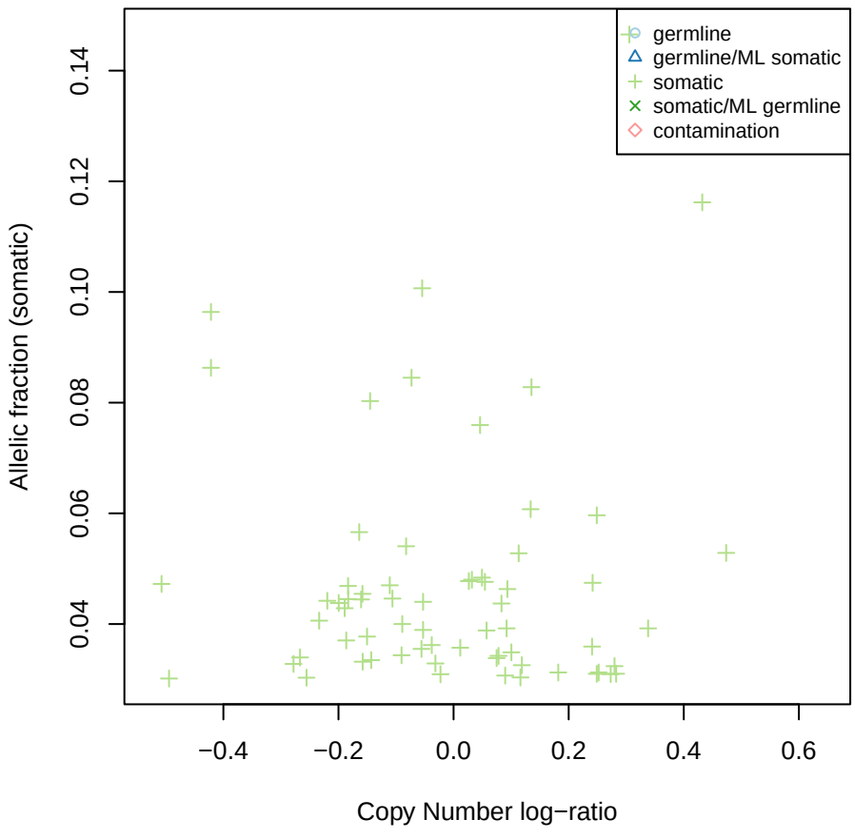

Purity: 0.59 Tumor ploidy: 2.018 SNV log−likelihood: −285.18 GoF: 19.7% Mean coverage: 473;439
1 2 3 5 6 7 8 10 12 13 16 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 10 20 30 40 50 60 70
SNV Index

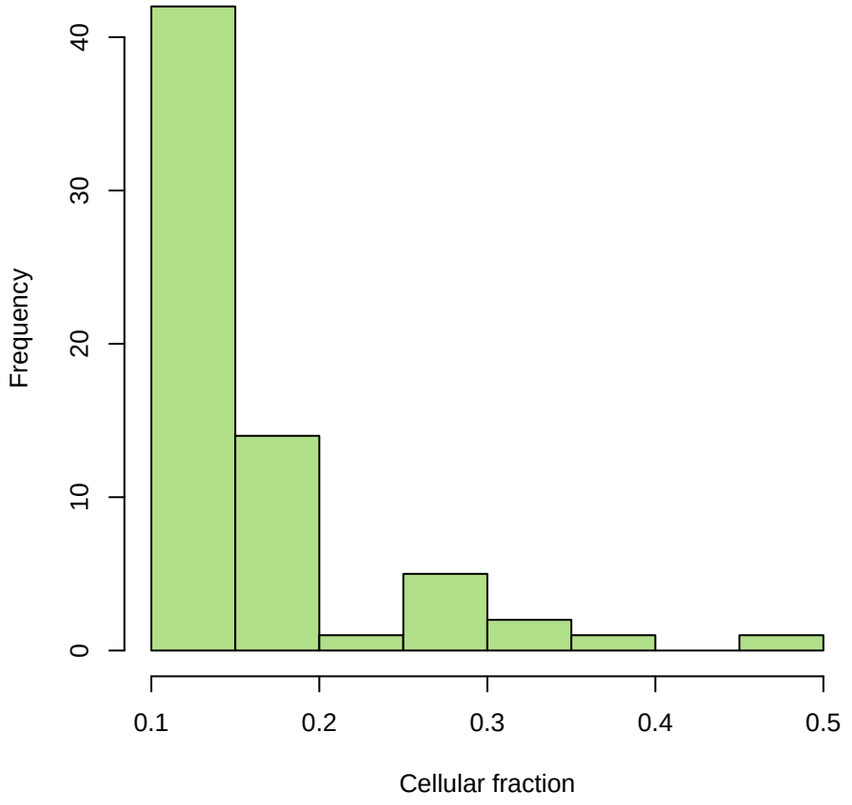

SCNA−fit log−likelihood: −6211.17
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5
0 10 20 30 40 50 60 70
SNV Index

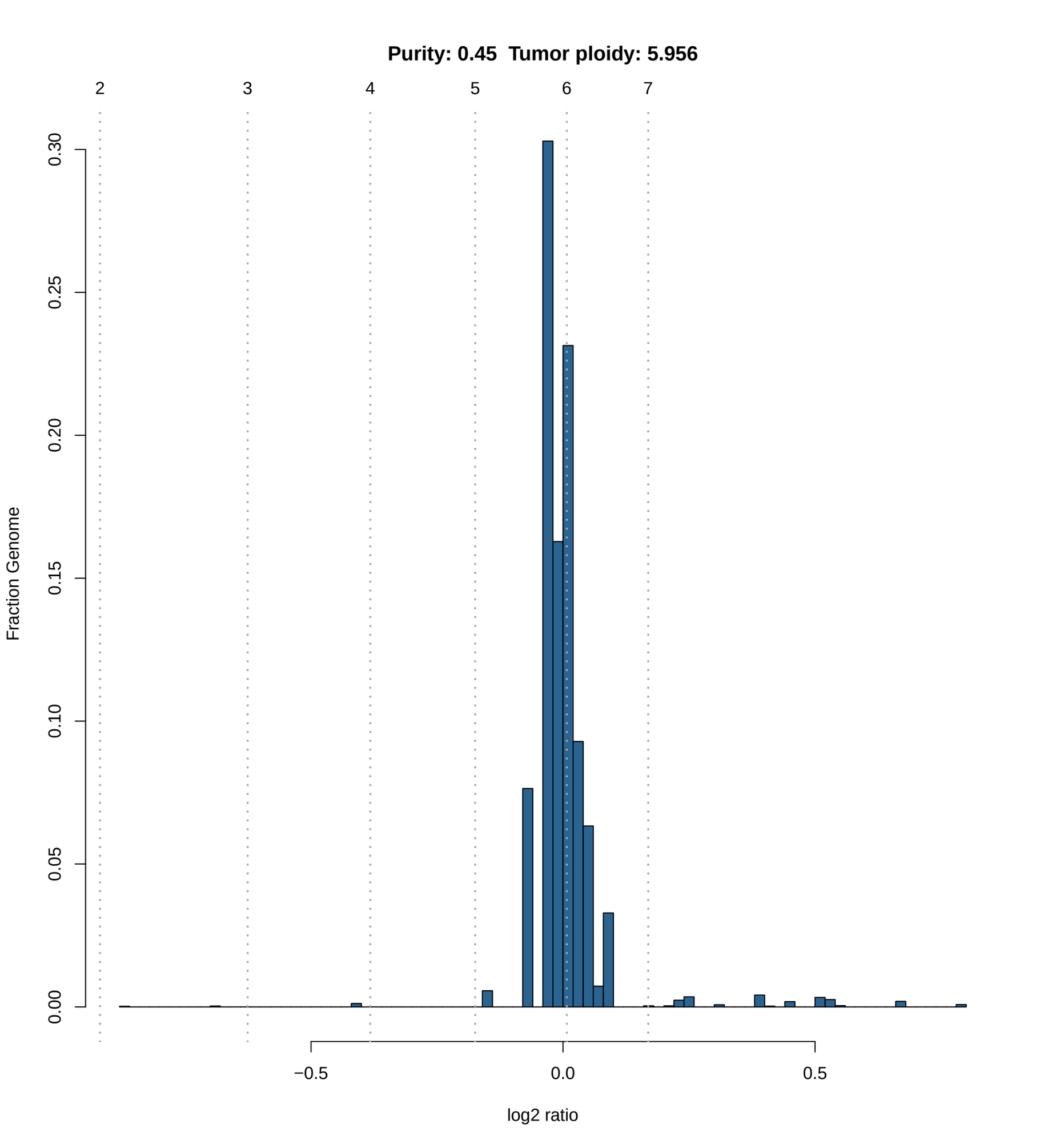

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 10 20 30 40 50 60 70
SNV Index

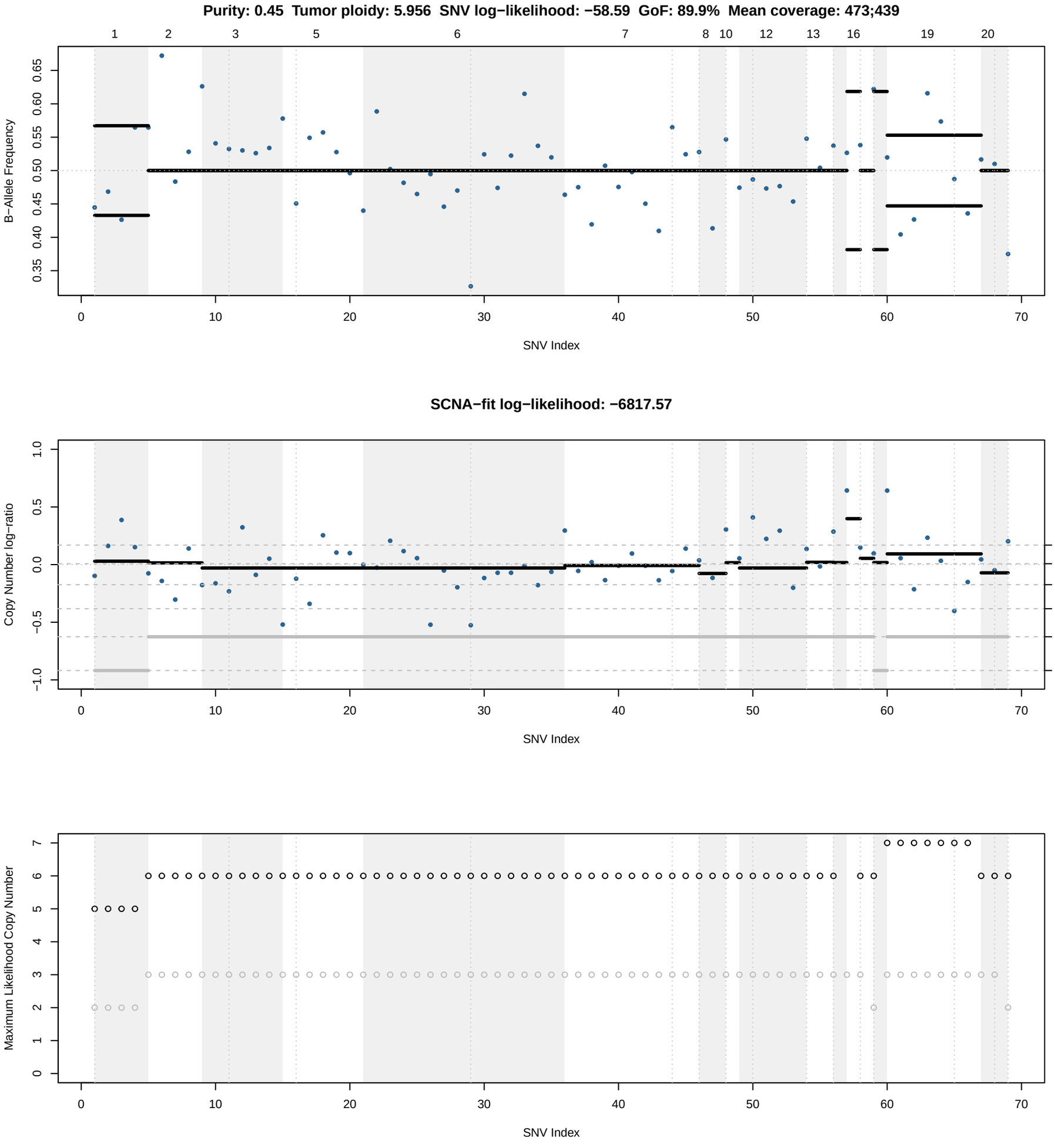

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
3m2
2m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

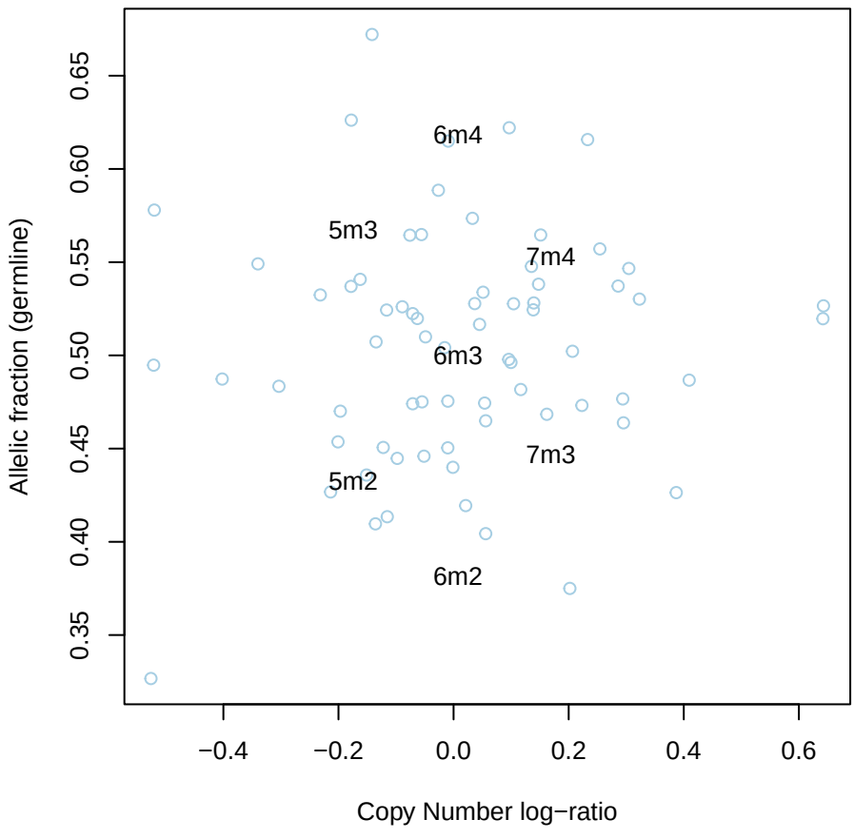

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

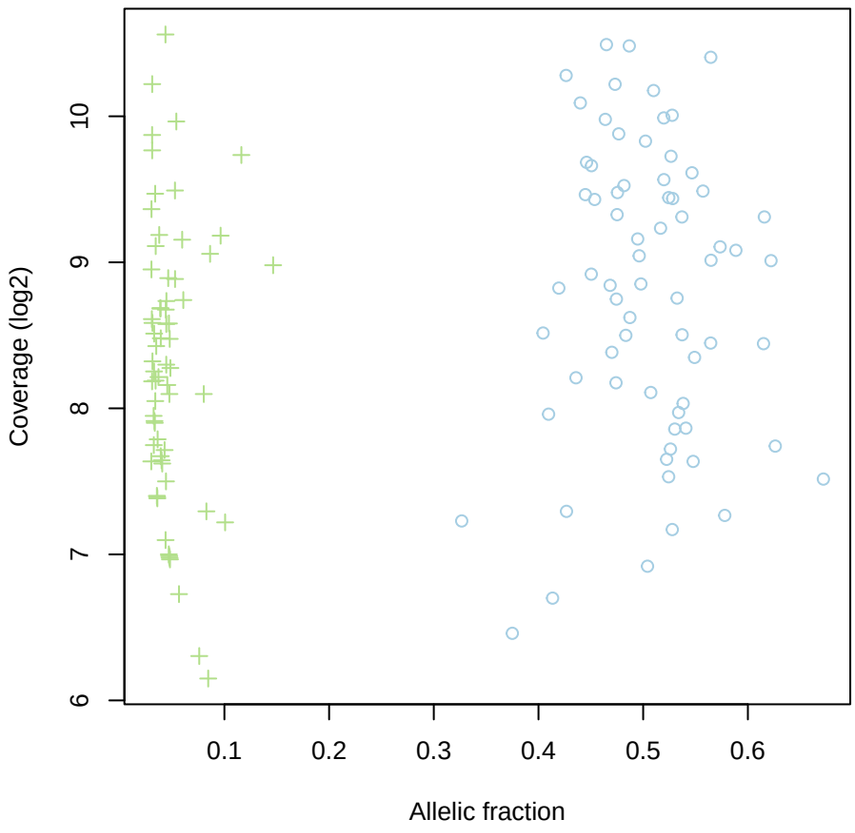

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

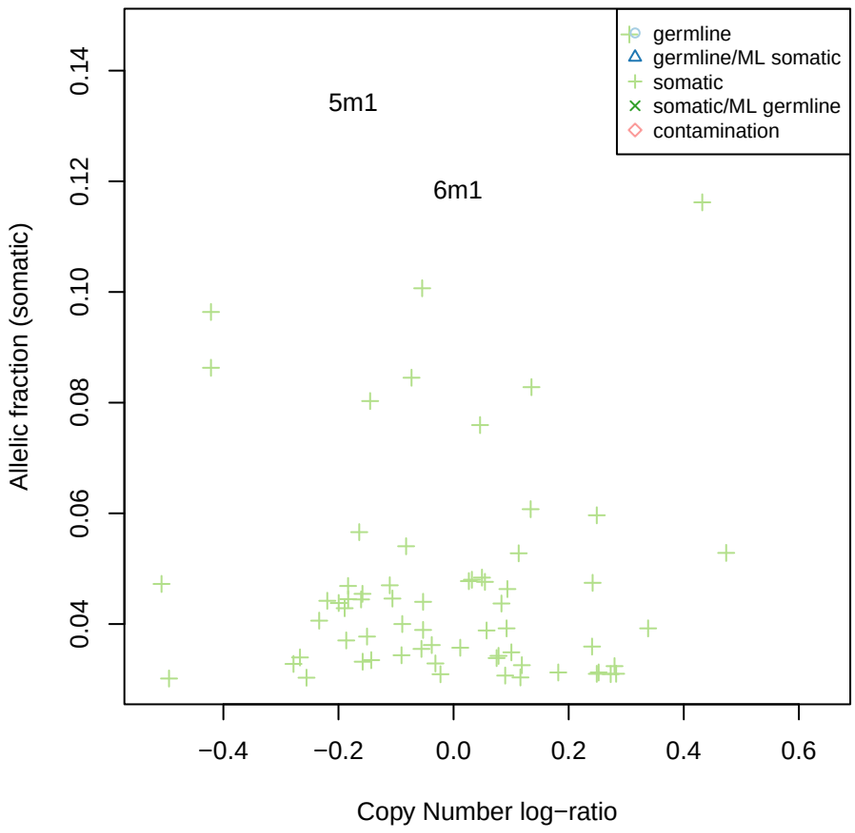

Frequency
0
10
20
30
40
0.1
0.2
0.3
0.4
0.5
Cellular fraction

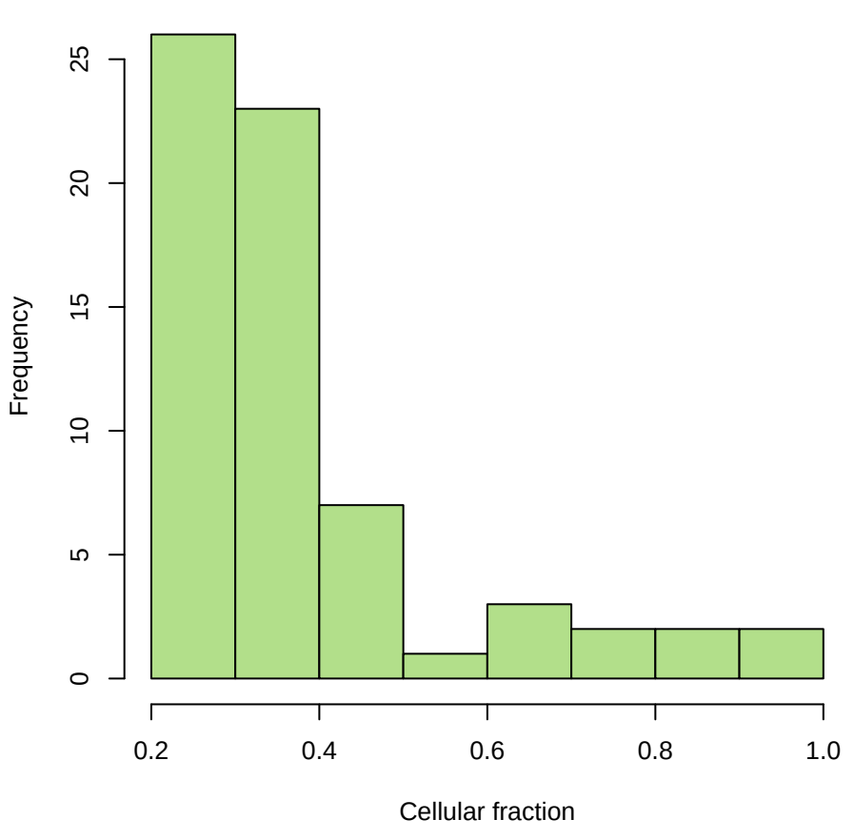

Purity: 0.45 Tumor ploidy: 5.956
2
3
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

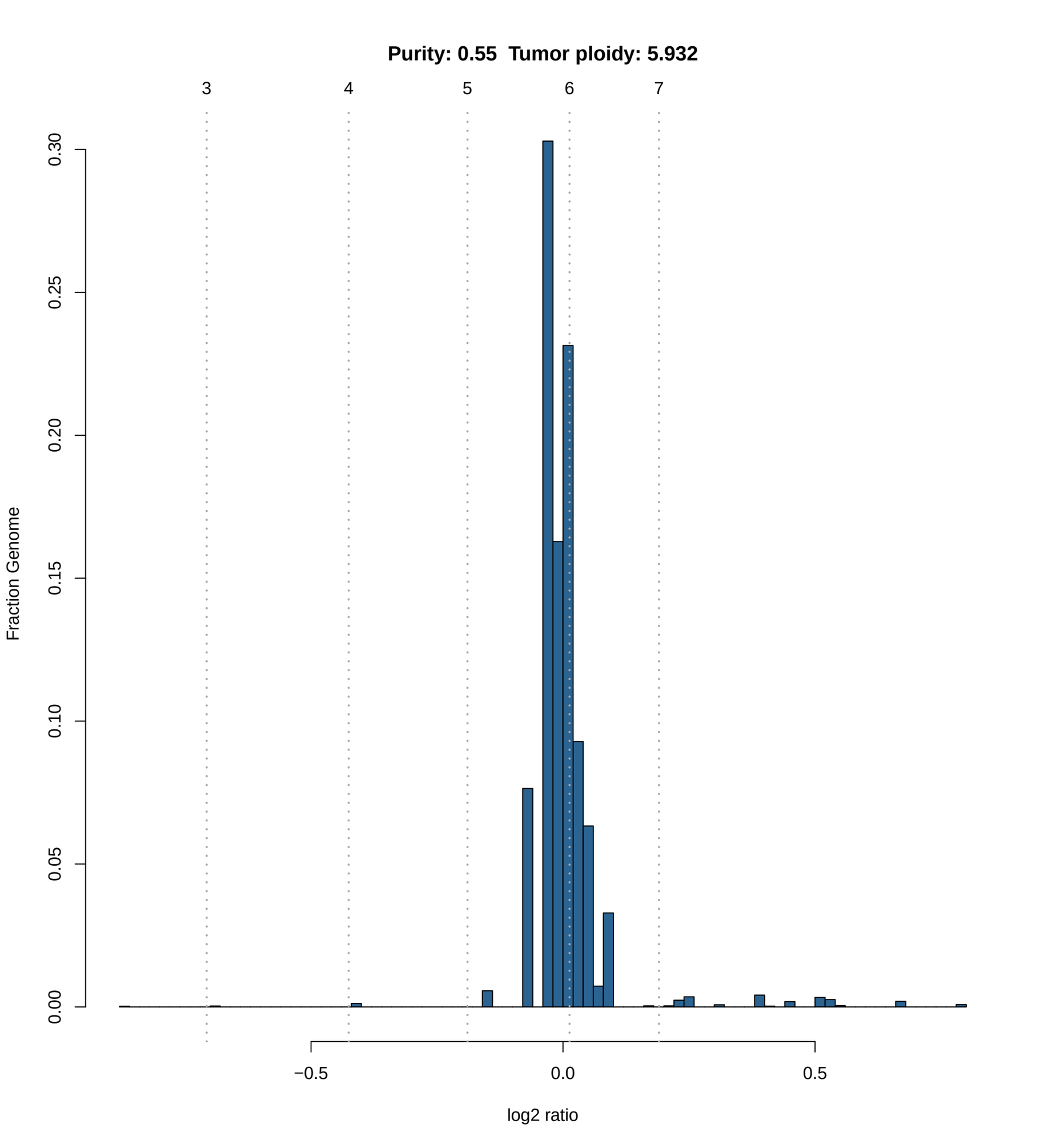

Purity: 0.45 Tumor ploidy: 5.956 SNV log−likelihood: −58.59 GoF: 89.9% Mean coverage: 473;439
1 2 3 5 6 7 8 10 12 13 16 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 10 20 30 40 50 60 70
SNV Index
SCNA−fit log−likelihood: −6817.57
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 10 20 30 40 50 60 70
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 10 20 30 40 50 60 70
SNV Index

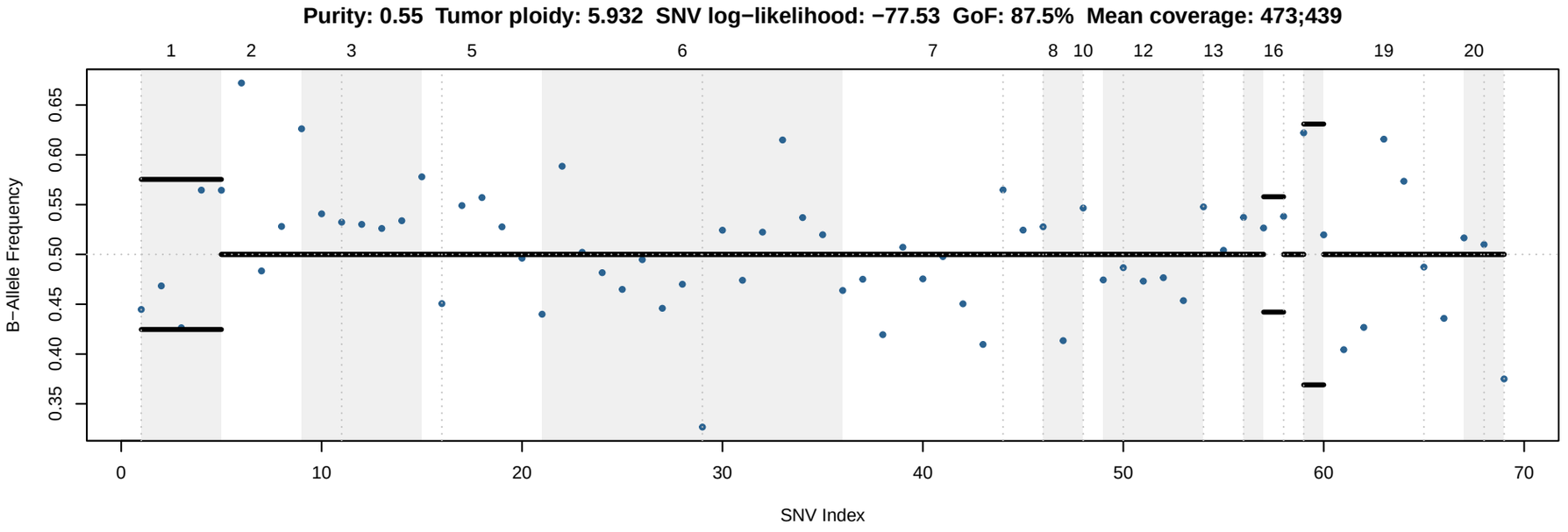

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
6m4
5m3
7m4
6m3
7m3
5m2
6m2
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

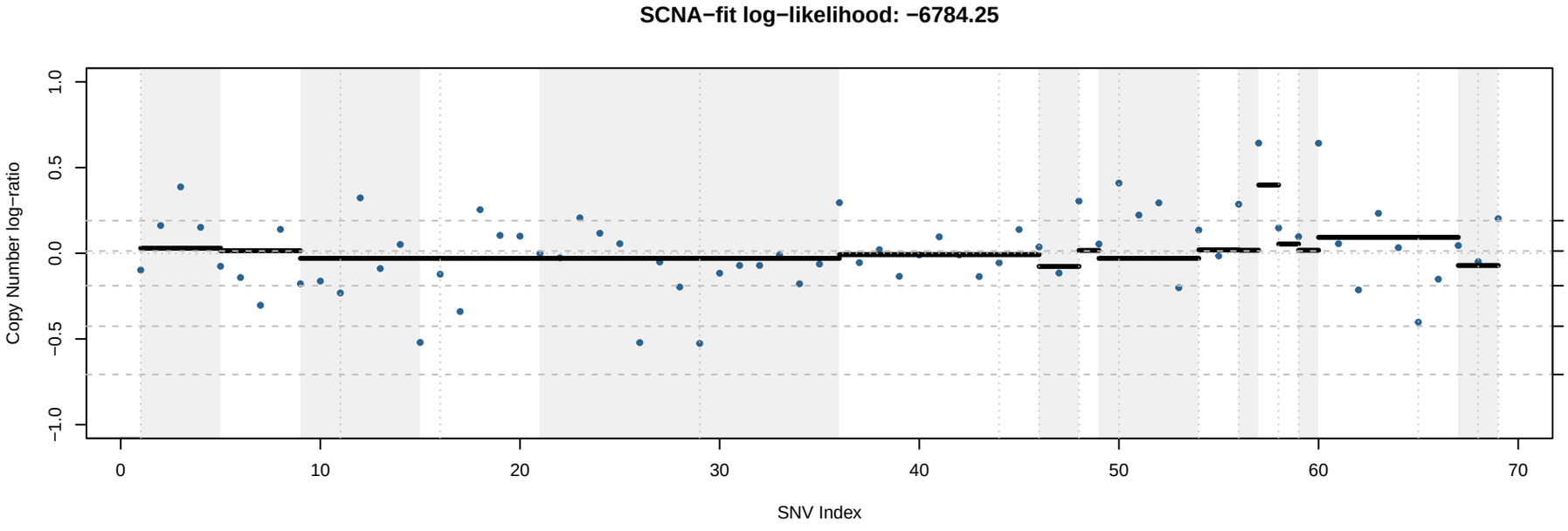

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

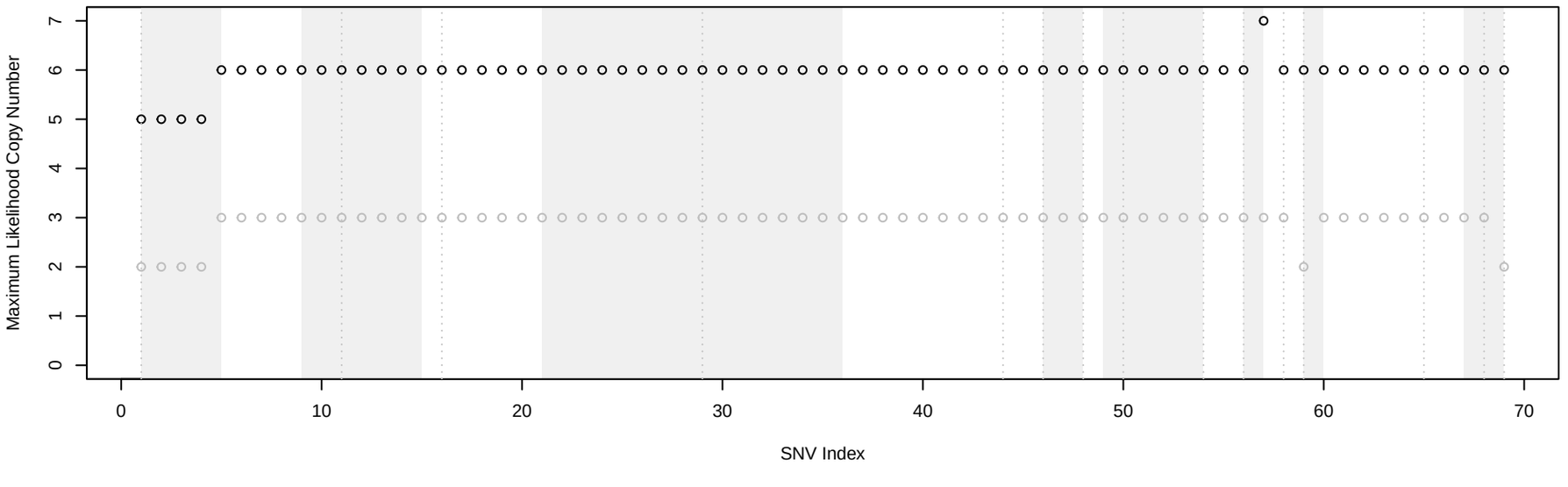

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
6m1
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

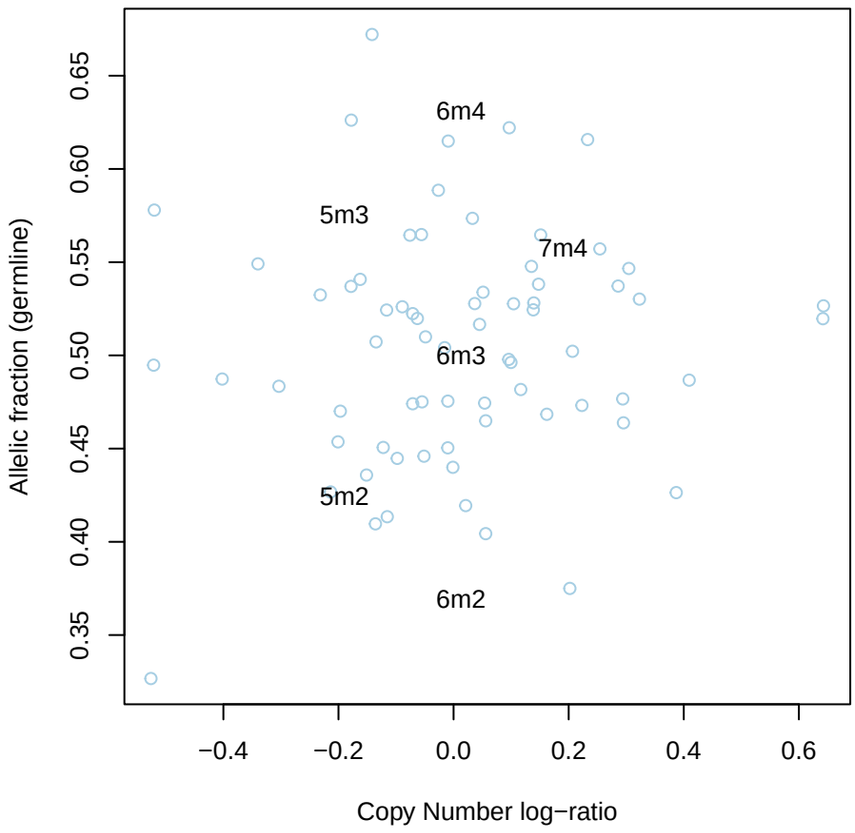

Frequency
0
5
10
15
20
25
0.2
0.4
0.6
0.8
1.0
Cellular fraction

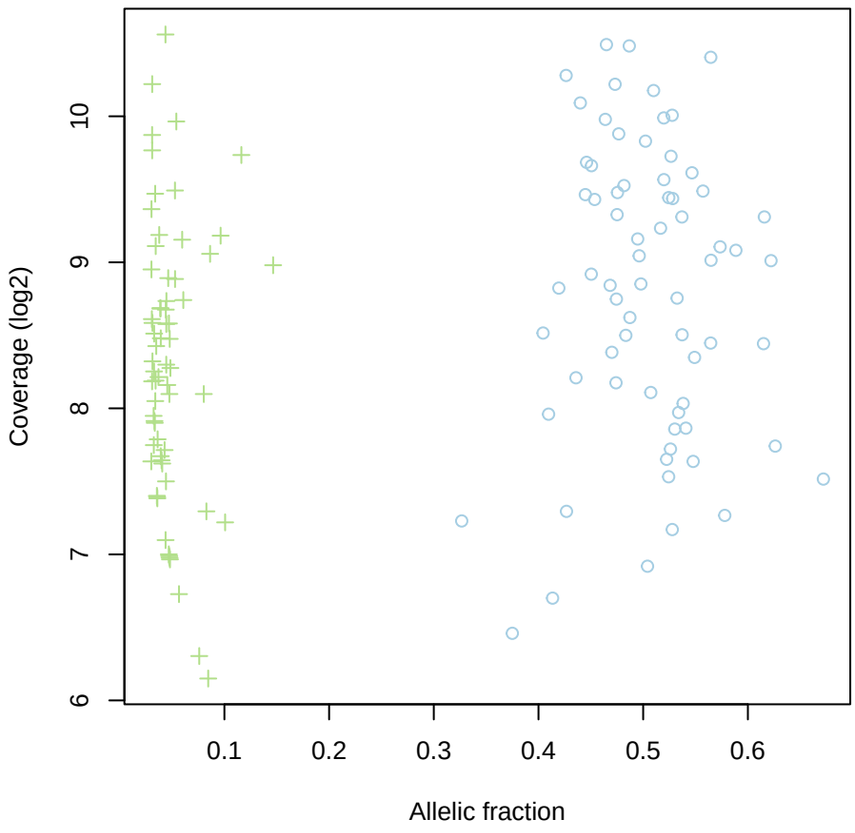

Purity: 0.55 Tumor ploidy: 5.932
3
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

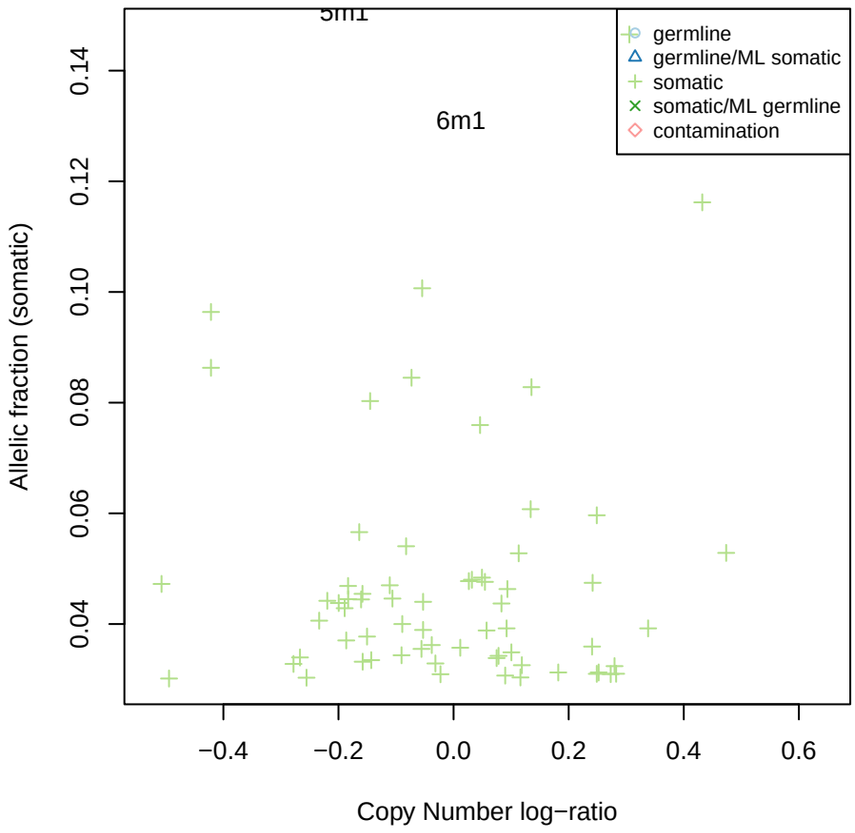

Purity: 0.55 Tumor ploidy: 5.932 SNV log−likelihood: −77.53 GoF: 87.5% Mean coverage: 473;439
1 2 3 5 6 7 8 10 12 13 16 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 10 20 30 40 50 60 70
SNV Index

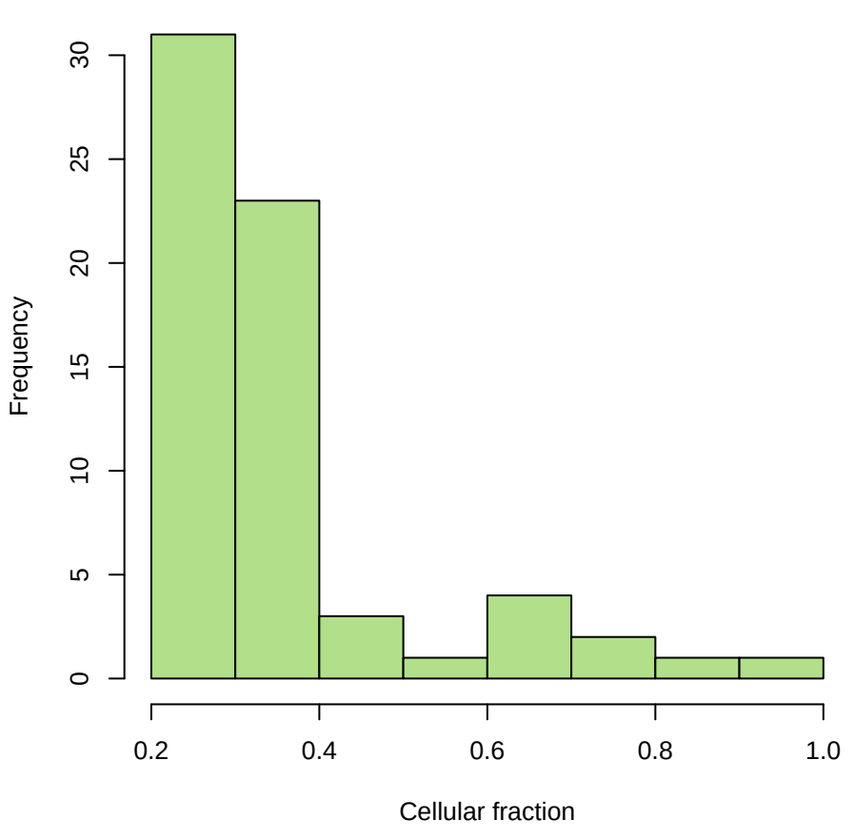

SCNA−fit log−likelihood: −6784.25
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 10 20 30 40 50 60 70
SNV Index

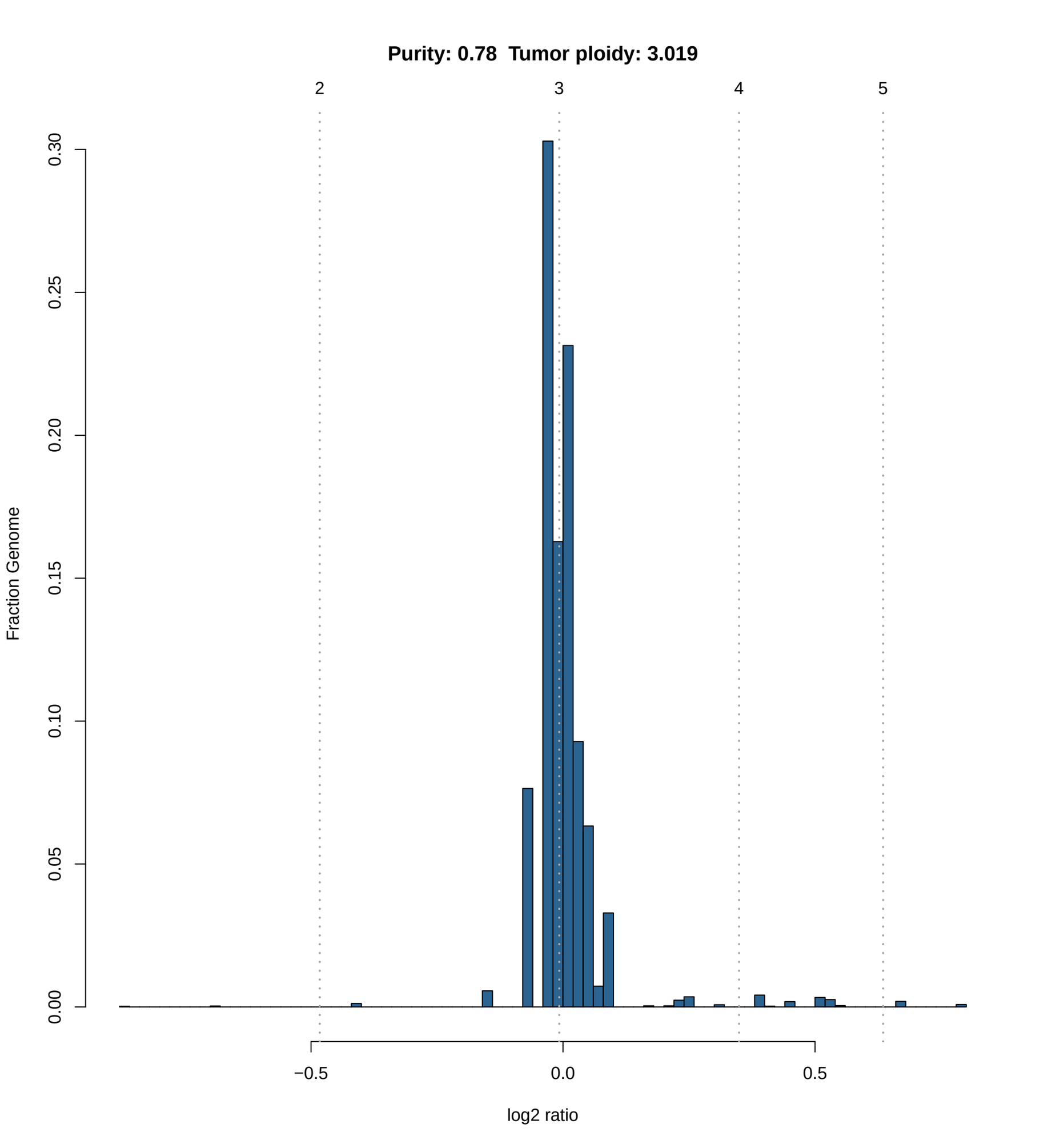

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 10 20 30 40 50 60 70
SNV Index

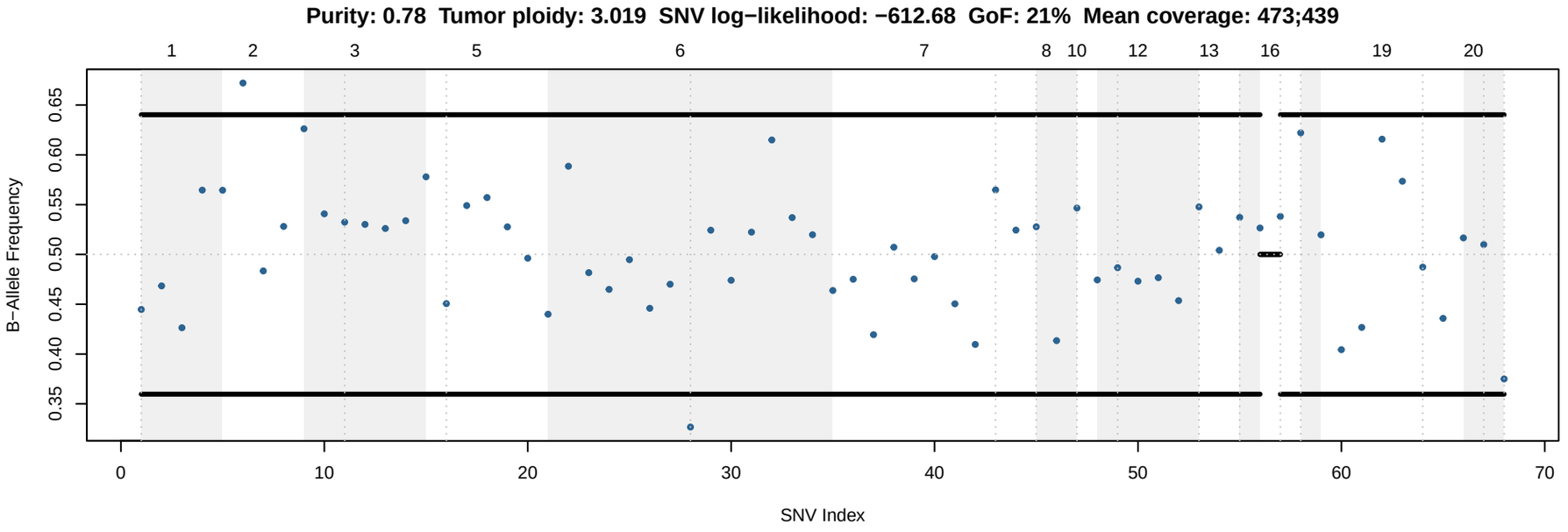

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
6m4
5m3
7m4
6m3
5m2
6m2
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

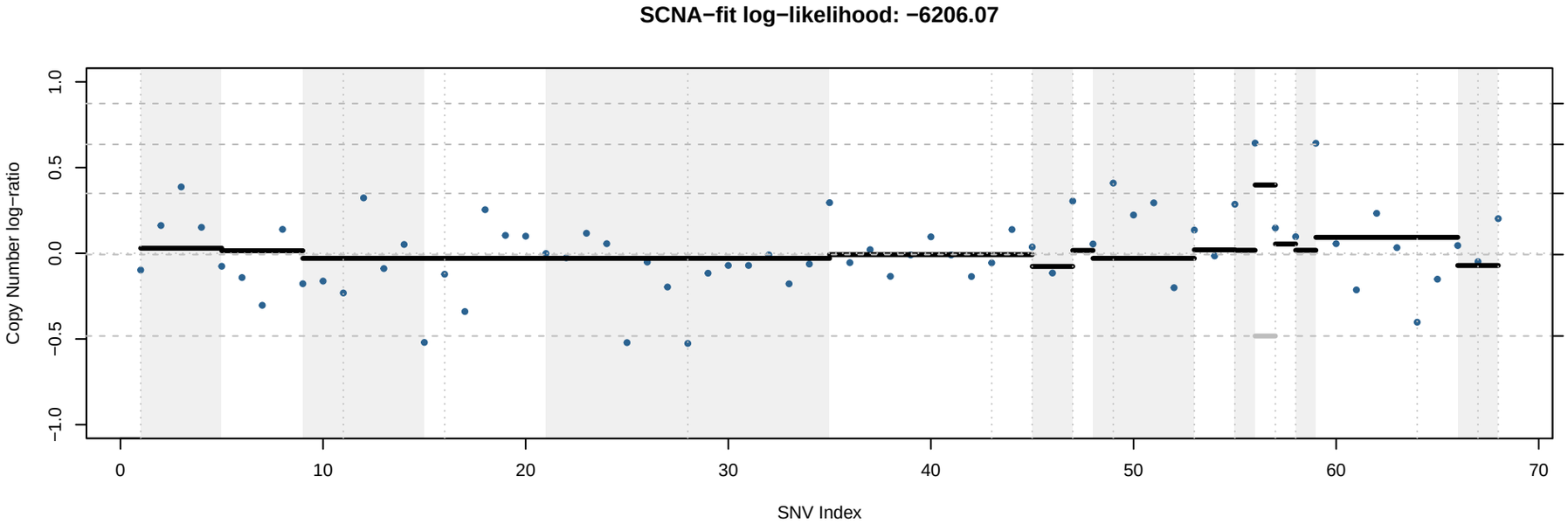

Coverage (log2)
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

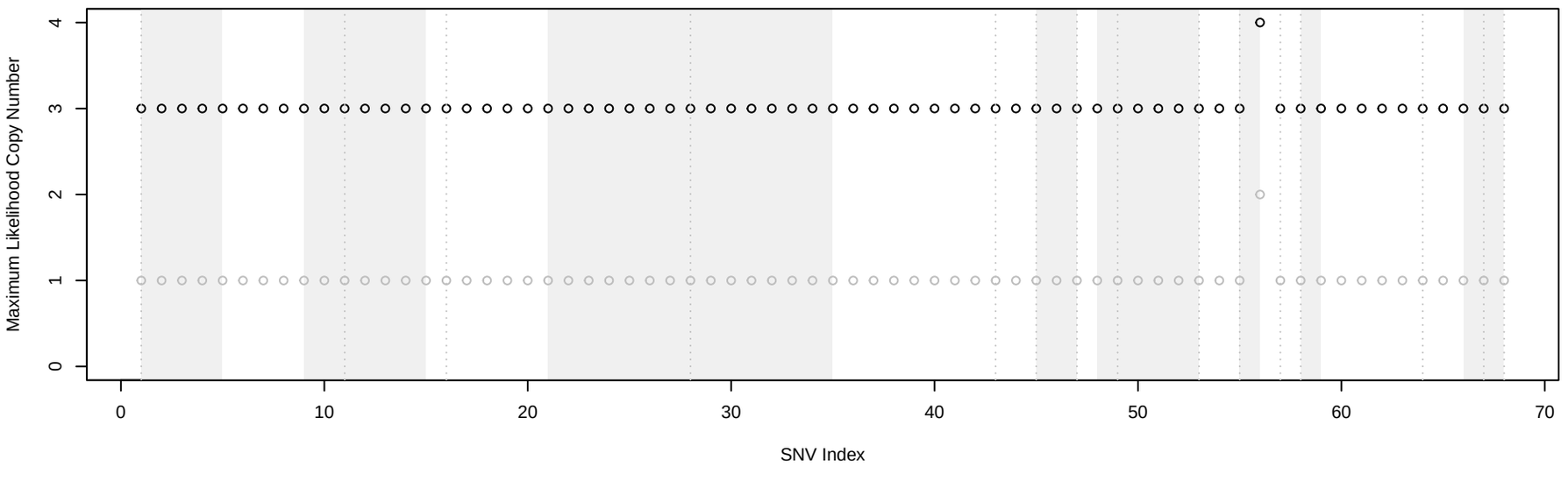

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
5m1
6m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

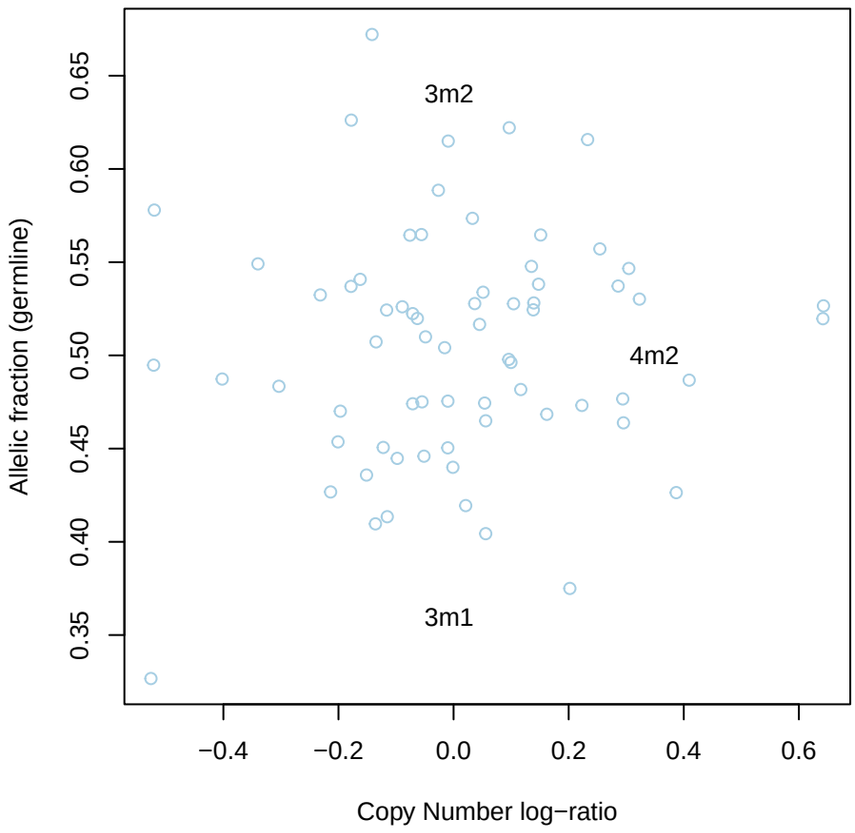

Frequency
0
5
10
15
20
25
30
0.2
0.4
0.6
0.8
1.0
Cellular fraction

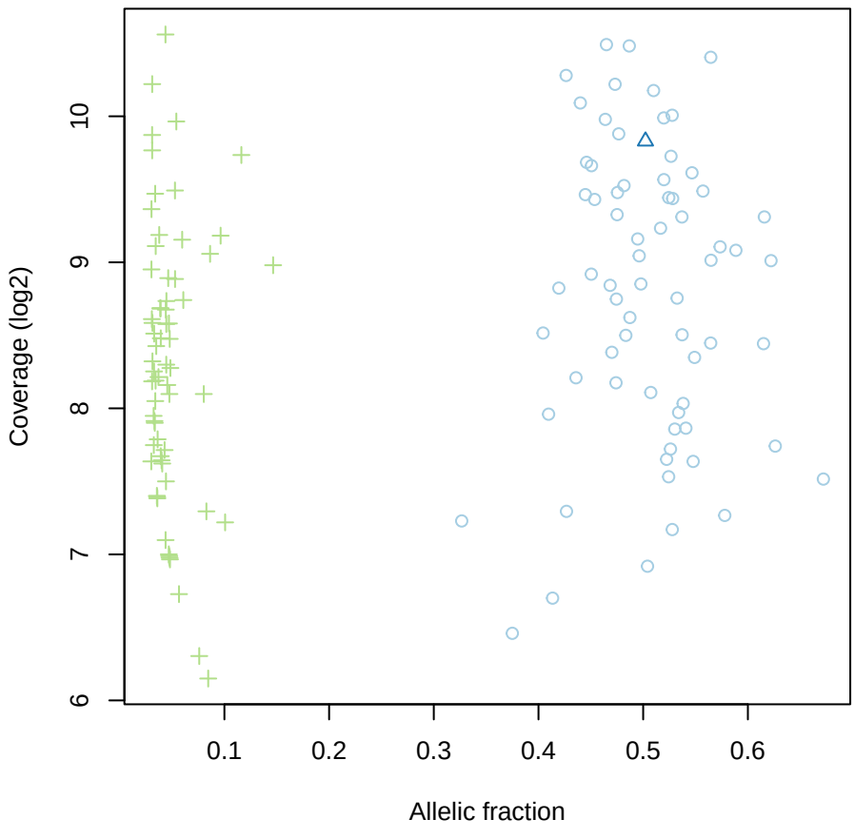

Purity: 0.78 Tumor ploidy: 3.019
2
3
4
5
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

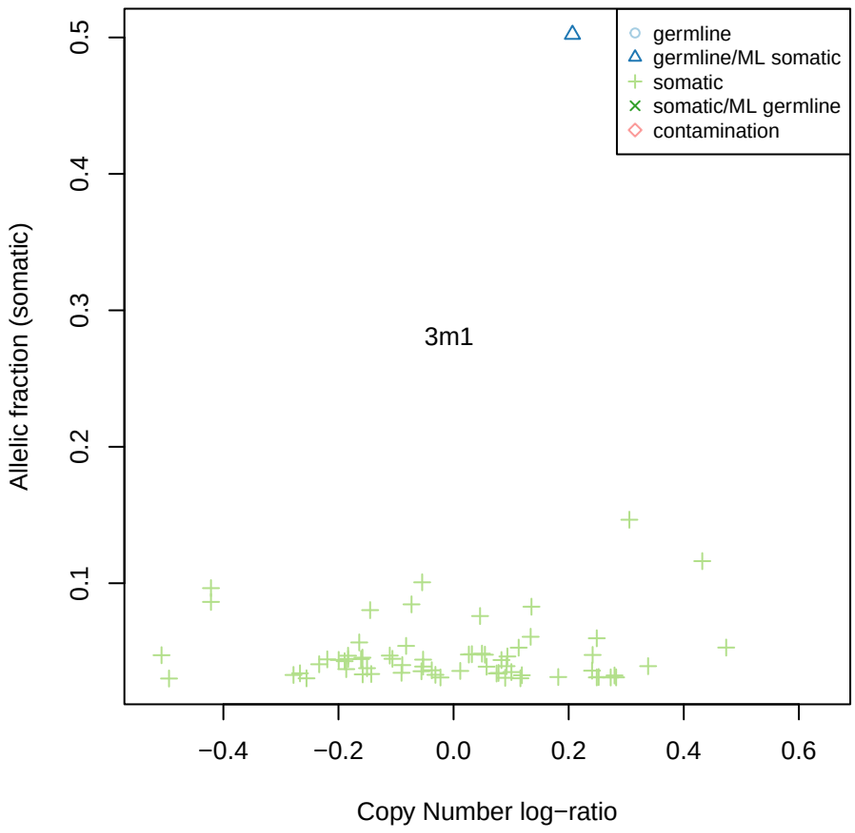

Purity: 0.78 Tumor ploidy: 3.019 SNV log−likelihood: −612.68 GoF: 21% Mean coverage: 473;439
1 2 3 5 6 7 8 10 12 13 16 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 10 20 30 40 50 60 70
SNV Index

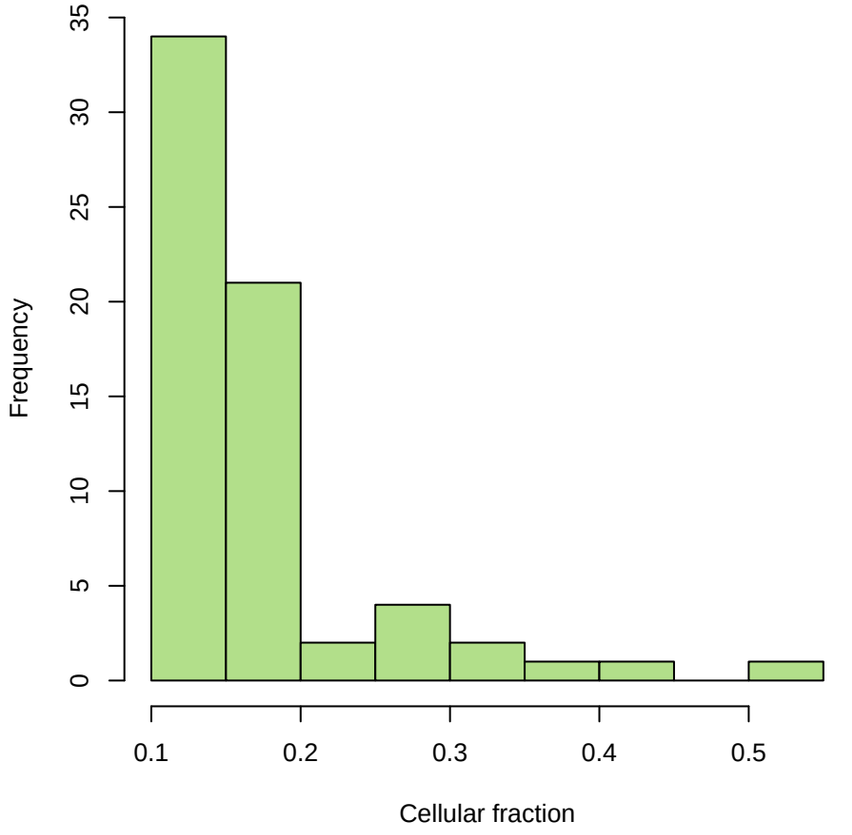

SCNA−fit log−likelihood: −6206.07
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6
0 10 20 30 40 50 60 70
SNV Index


Maximum Likelihood Copy Number
0 1 2 3 4
0 10 20 30 40 50 60 70
SNV Index


3m2
4m2
3m1
Allelic fraction (germline)
Copy Number log−ratio
0.35
0.40
0.45
0.50
0.55
0.60
0.65
−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
3m1
Allelic fraction (somatic)
Copy Number log−ratio
0.1
0.2
0.3
0.4
0.5
−0.4
−0.2
0.0
0.2
0.4
0.6


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