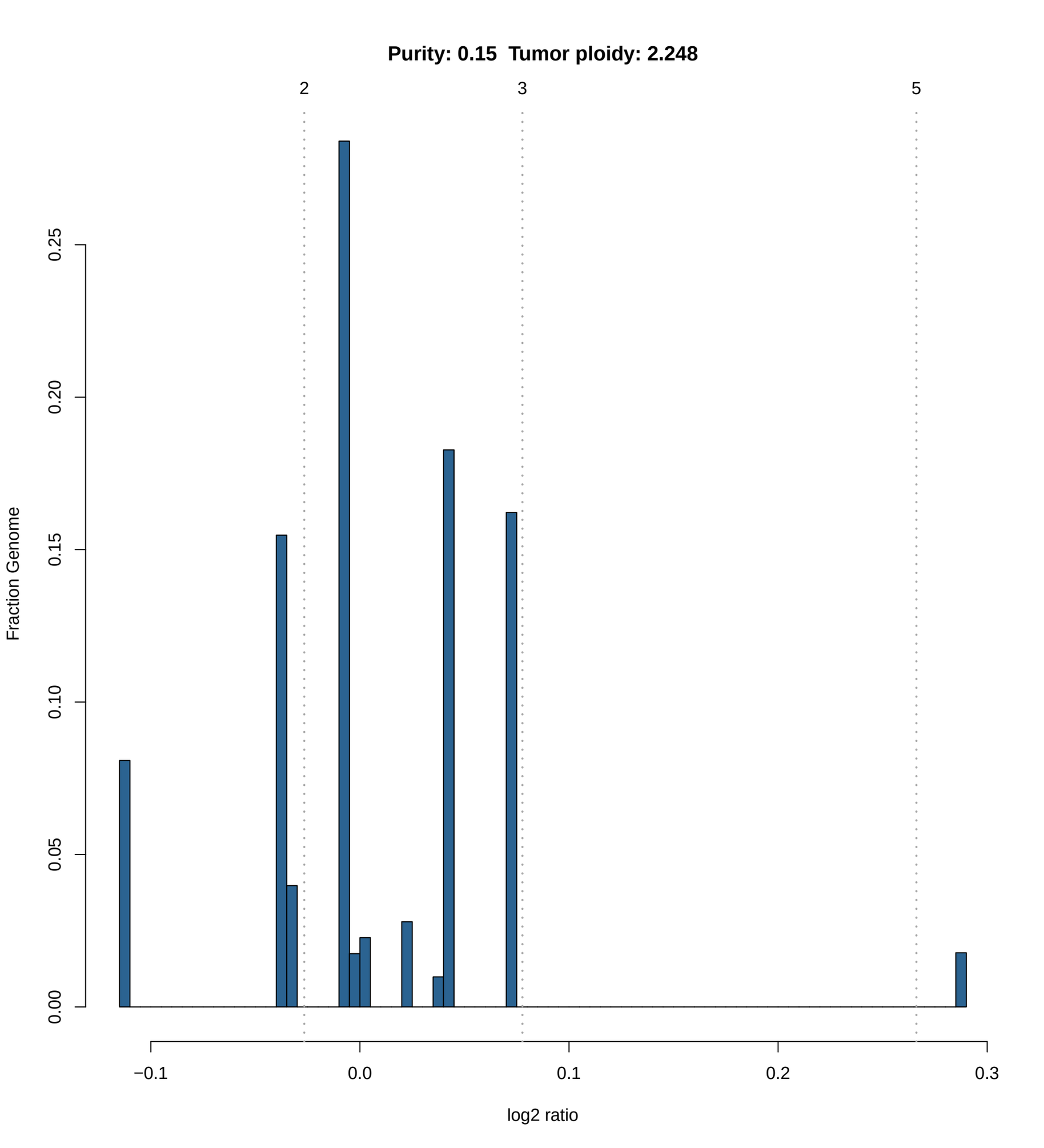
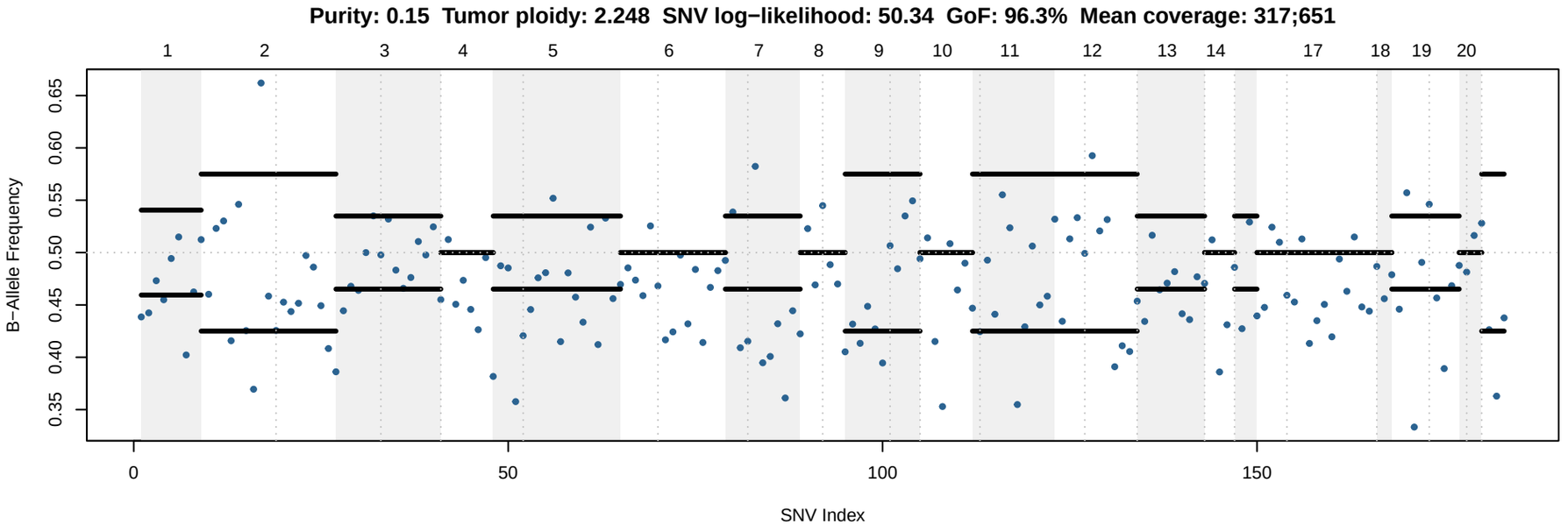
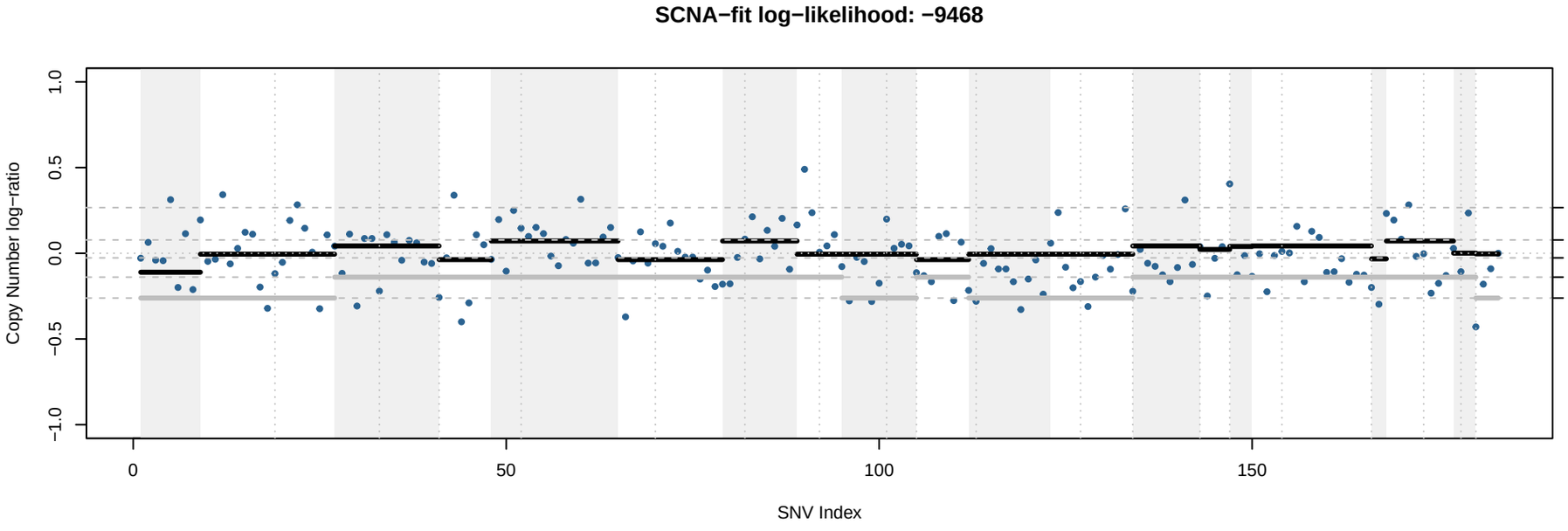
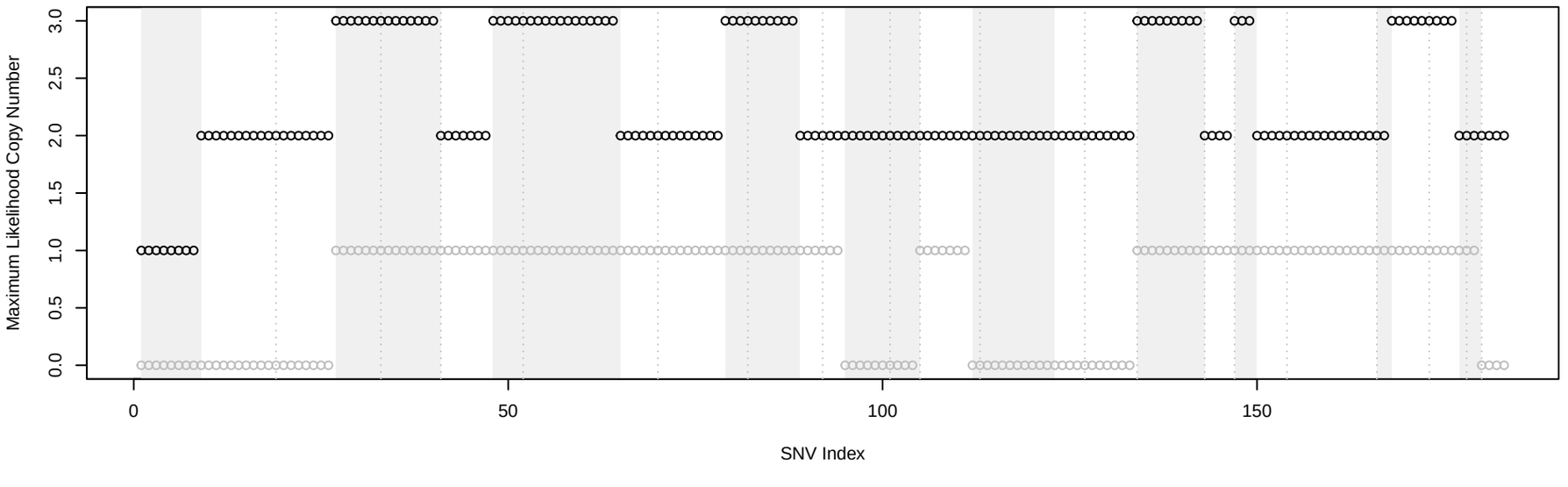
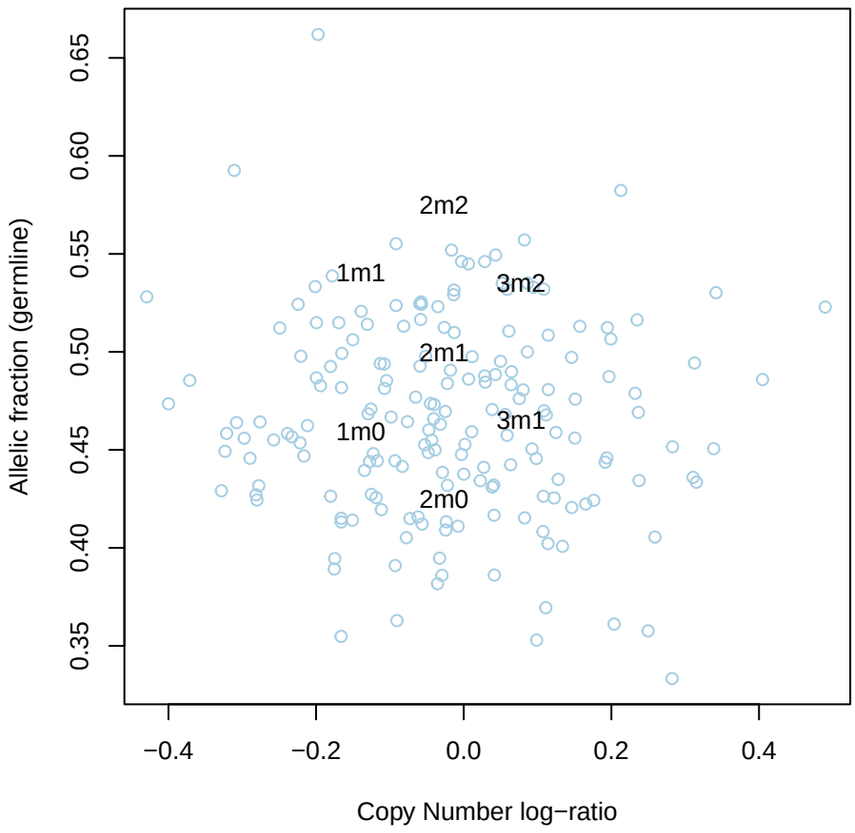
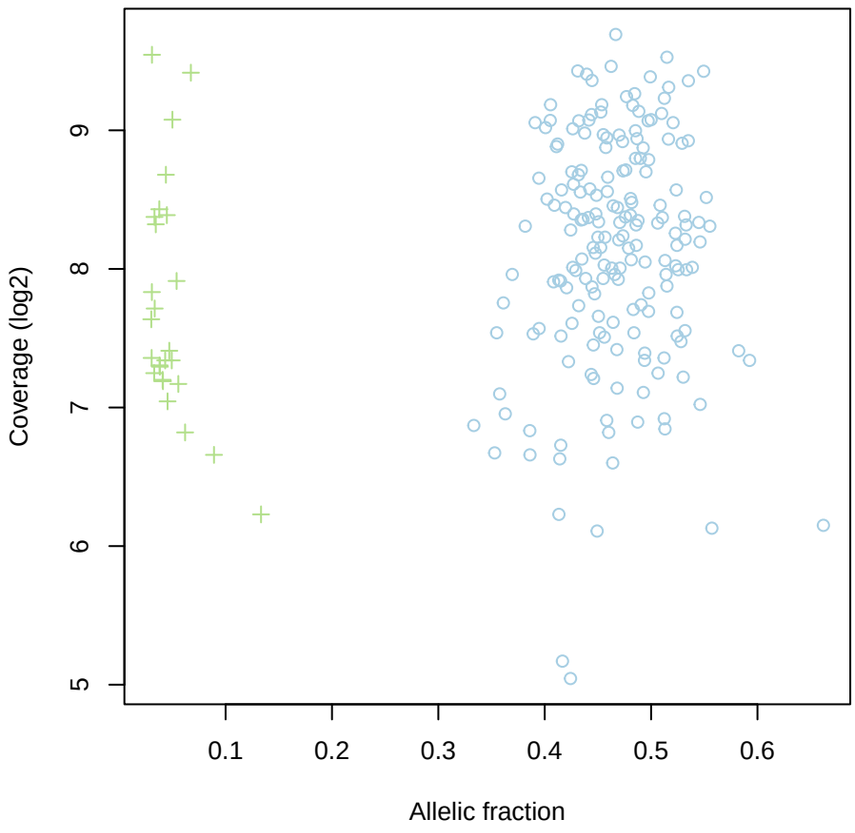

Purity: 0.15 Tumor ploidy: 2.248
2
3
5
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.1
0.0
0.1
0.2
0.3
log2 ratio

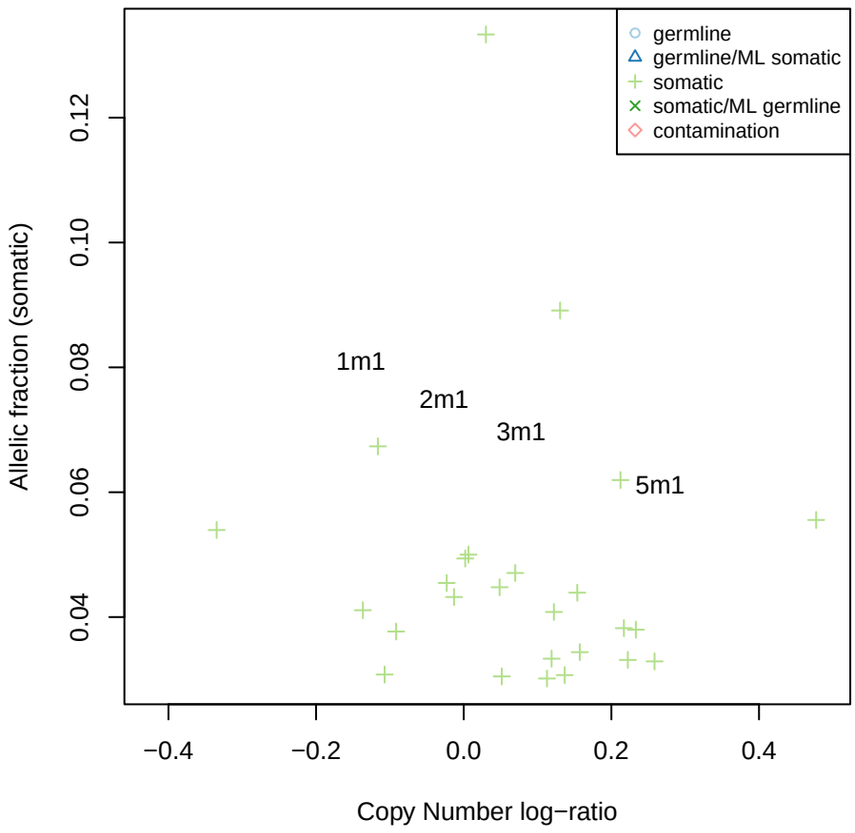

Purity: 0.15 Tumor ploidy: 2.248 SNV log−likelihood: 50.34 GoF: 96.3% Mean coverage: 317;651
1
2
3
4
5
6
7
8
9
10
11
12
13
14
17
18
19
20
B−Allele Frequency
0.35
0.40
0.45
0.50
0.55
0.60
0.65
0
50
100
150
SNV Index

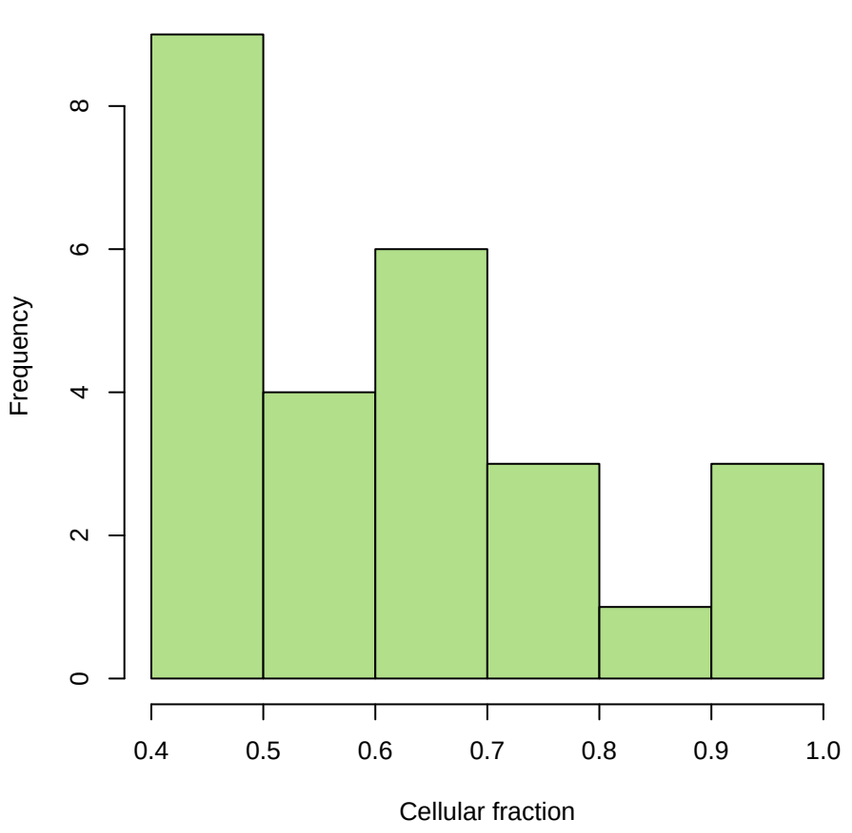

SCNA−fit log−likelihood: −9468
Copy Number log−ratio
1.0
0.5
0.0
−0.5
−1.0
0
2
5
0
50
100
150
SNV Index

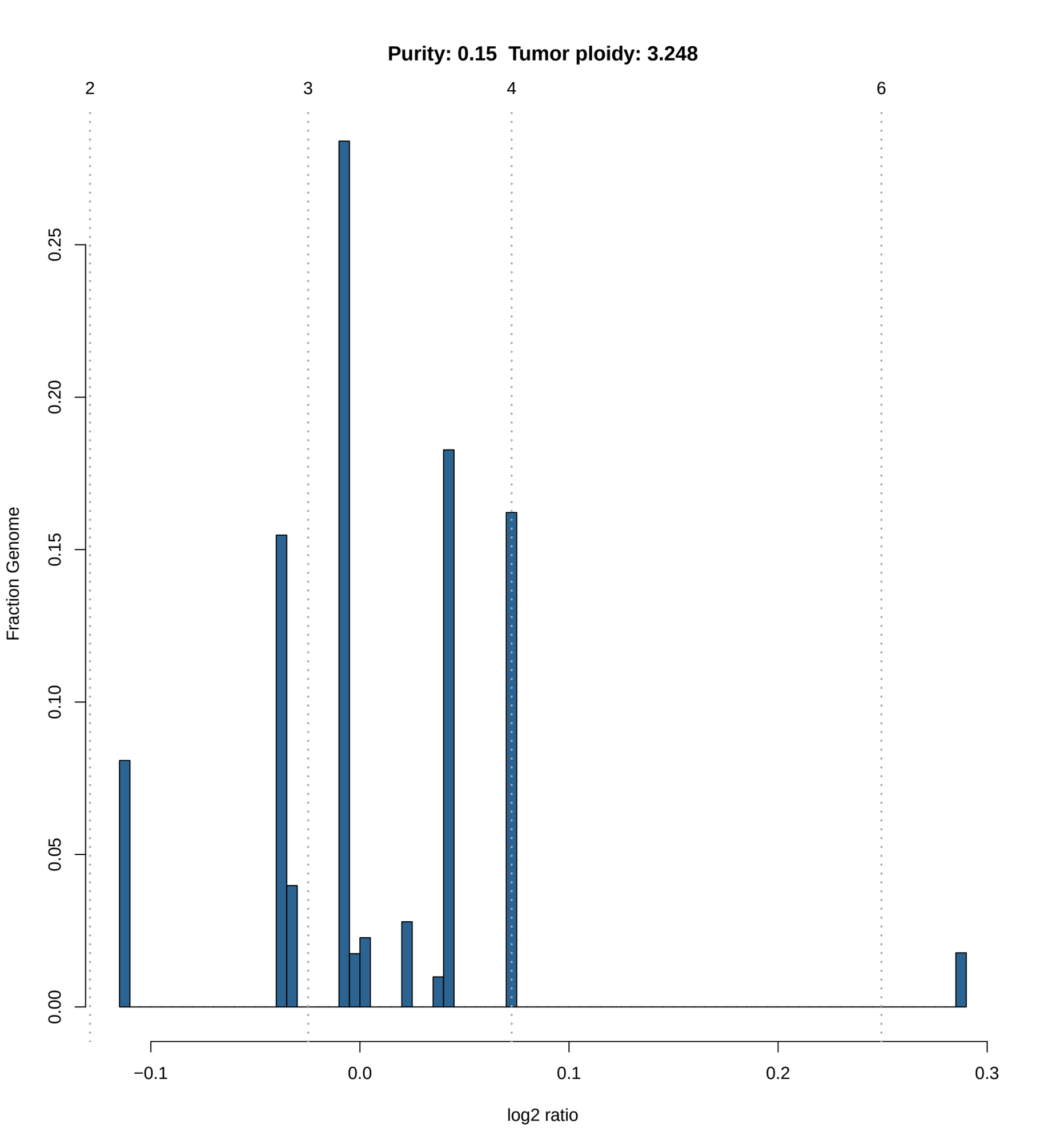

Maximum Likelihood Copy Number
0.0
0.5
1.0
1.5
2.0
2.5
3.0
0
50
100
150
SNV Index

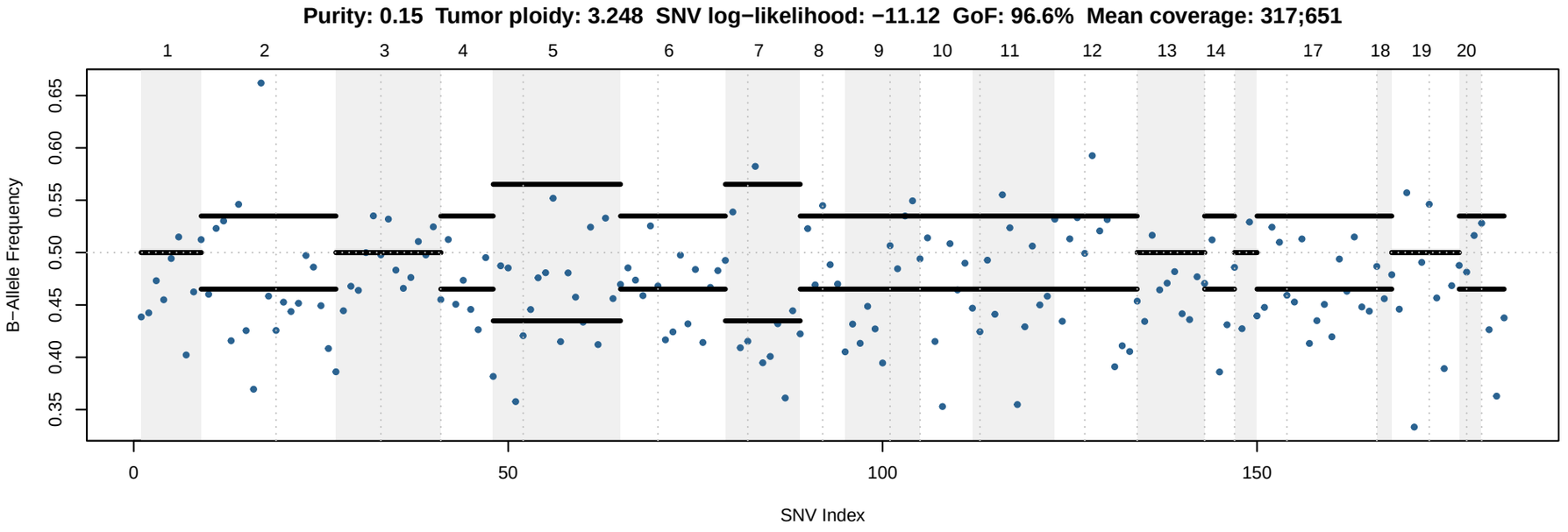

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
2m2
1m1
3m2
2m1
1m0
3m1
2m0
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

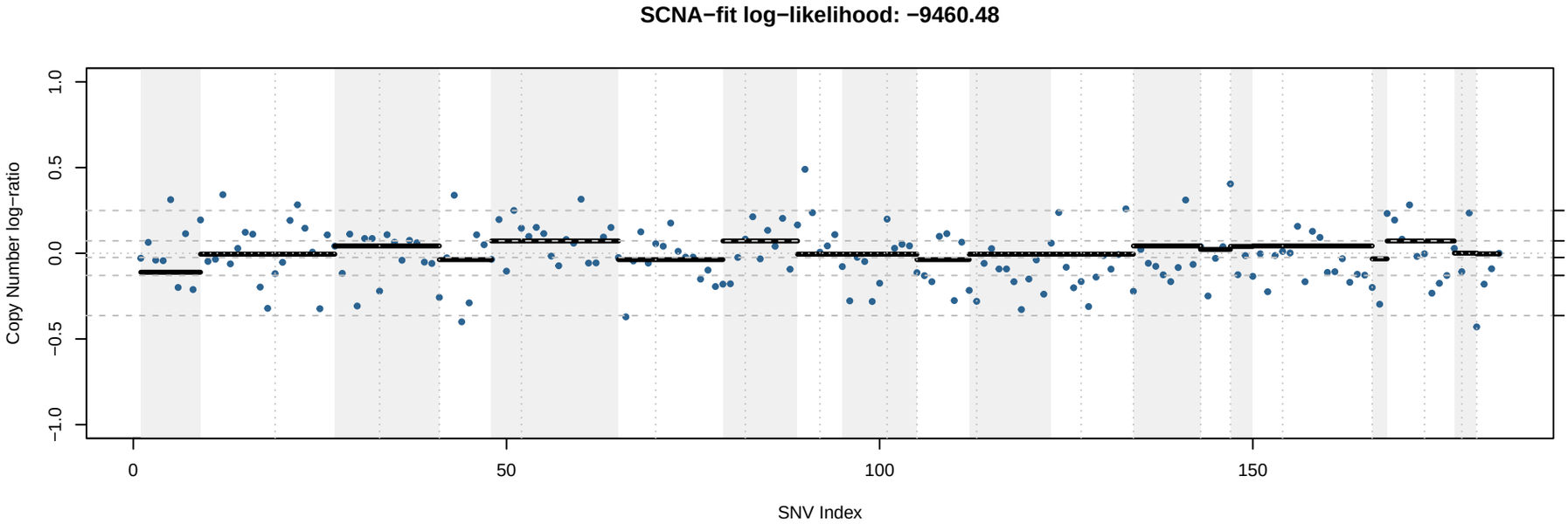

Coverage (log2)
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

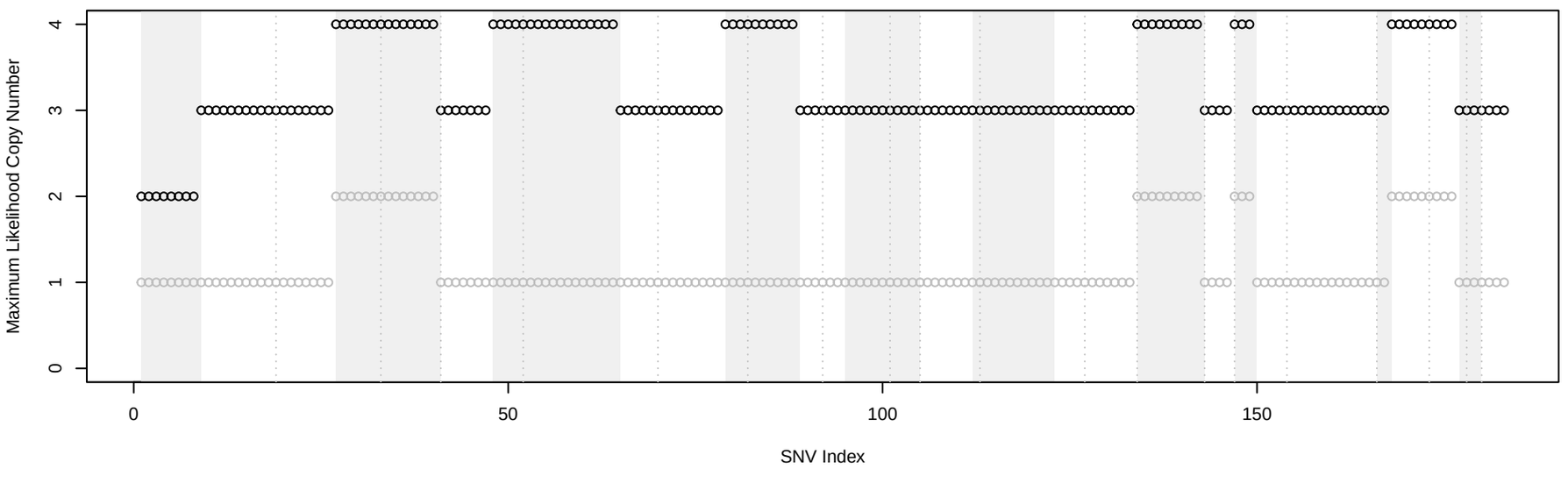

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
1m1
2m1
3m1
5m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

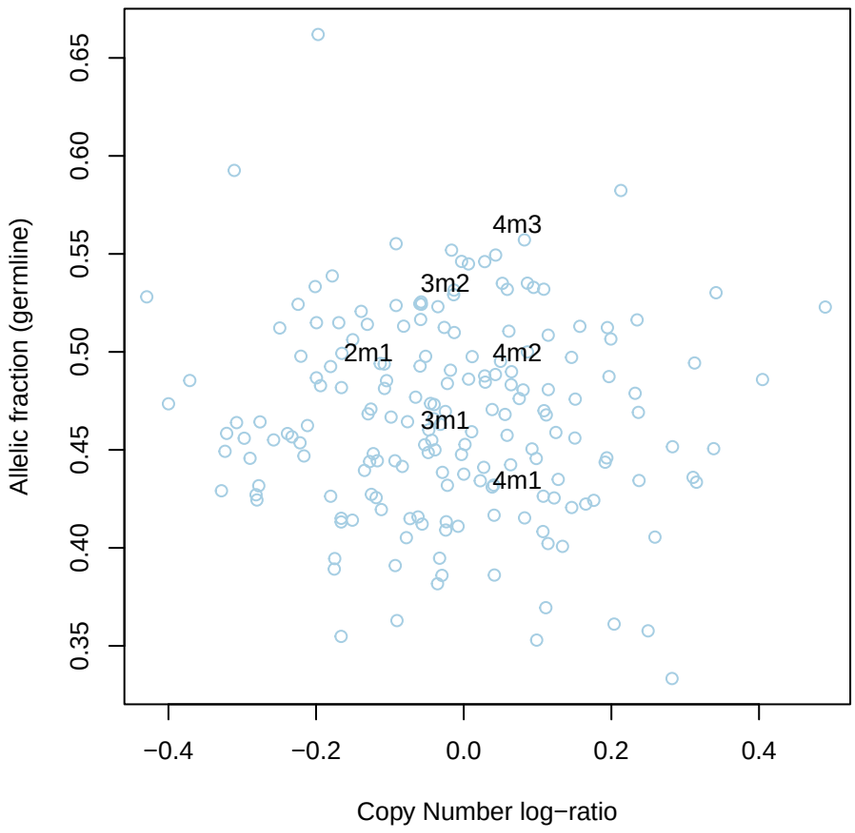

Frequency
0
2
4
6
8
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

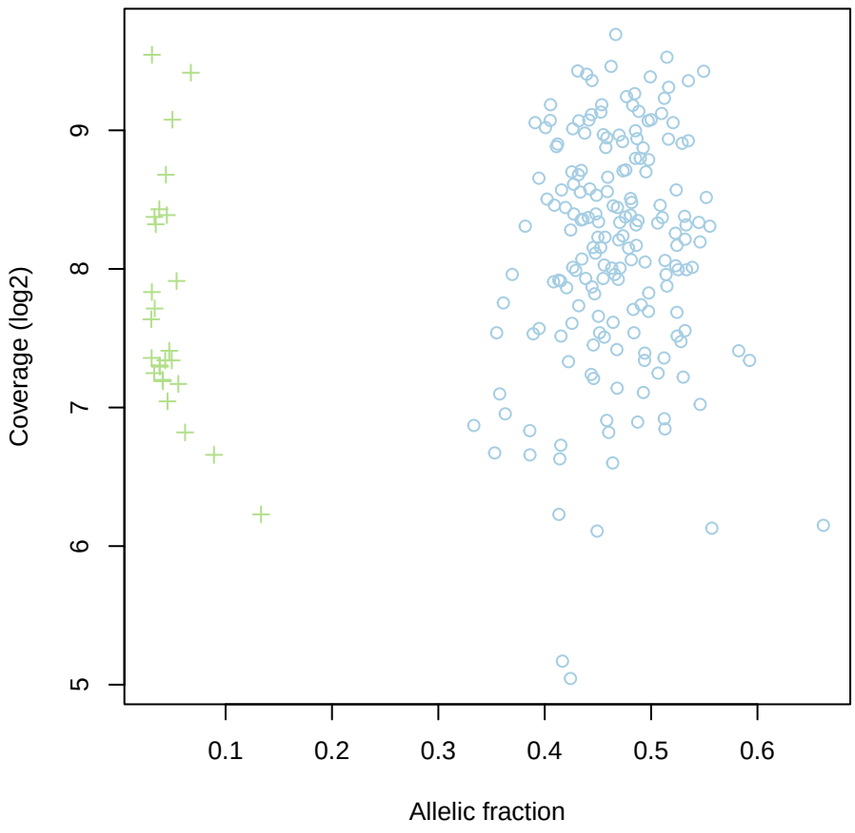

Purity: 0.15 Tumor ploidy: 3.248
2
3
4
6
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.1
0.0
0.1
0.2
0.3
log2 ratio

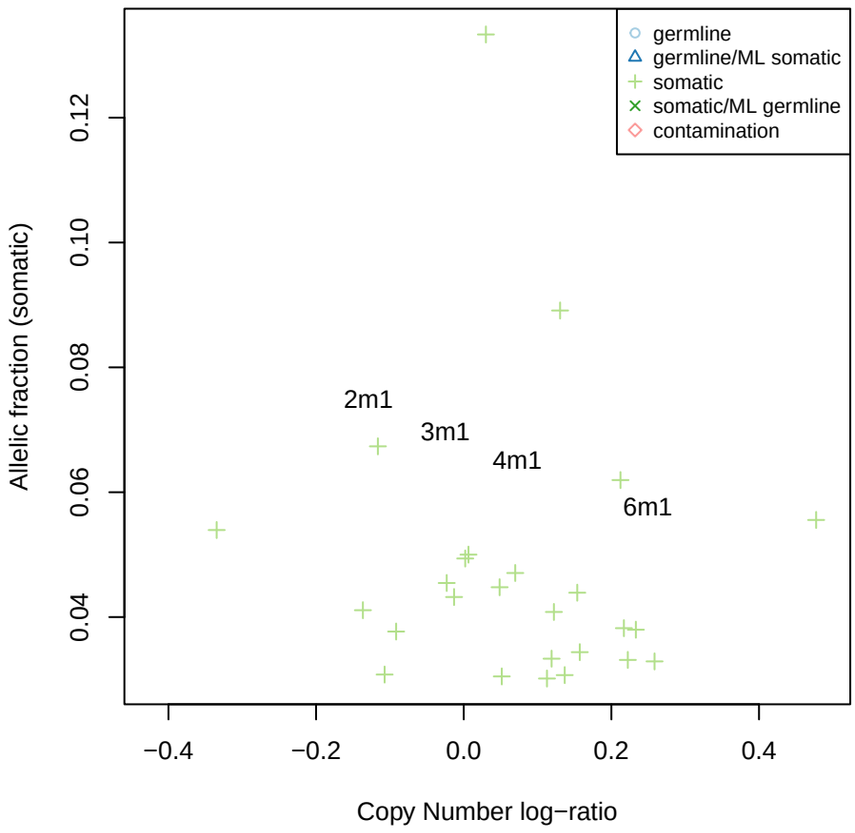

Purity: 0.15 Tumor ploidy: 3.248 SNV log−likelihood: −11.12 GoF: 96.6% Mean coverage: 317;651
1 2 3 4 5 6 7 8 9 10 11 12 13 14 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 50 100 150
SNV Index

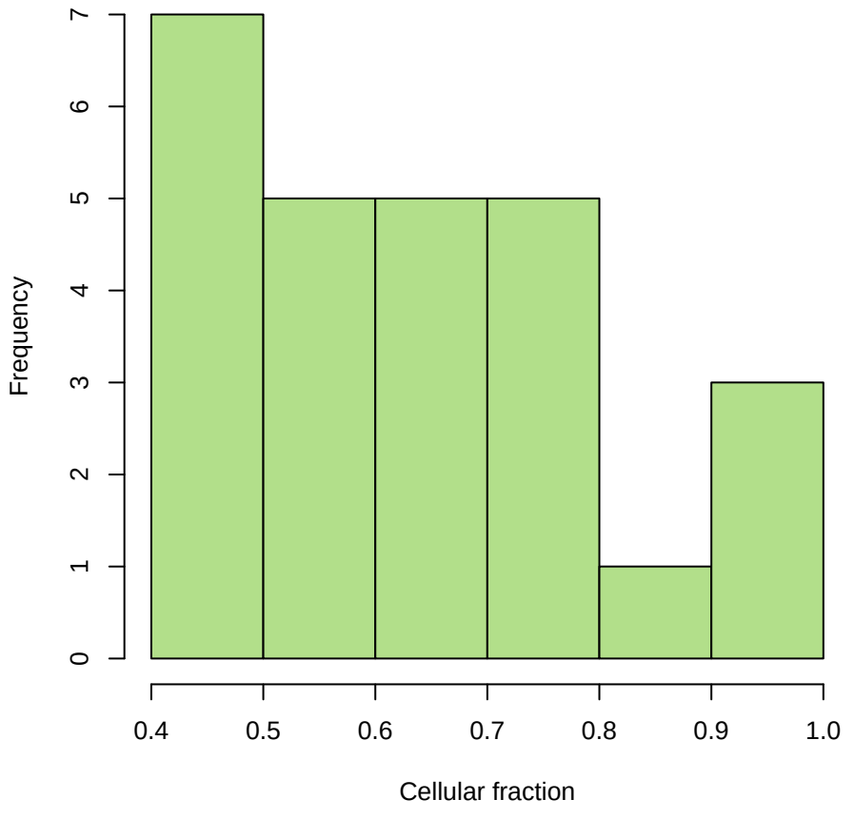

SCNA−fit log−likelihood: −9460.48
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4 6
0 50 100 150
SNV Index

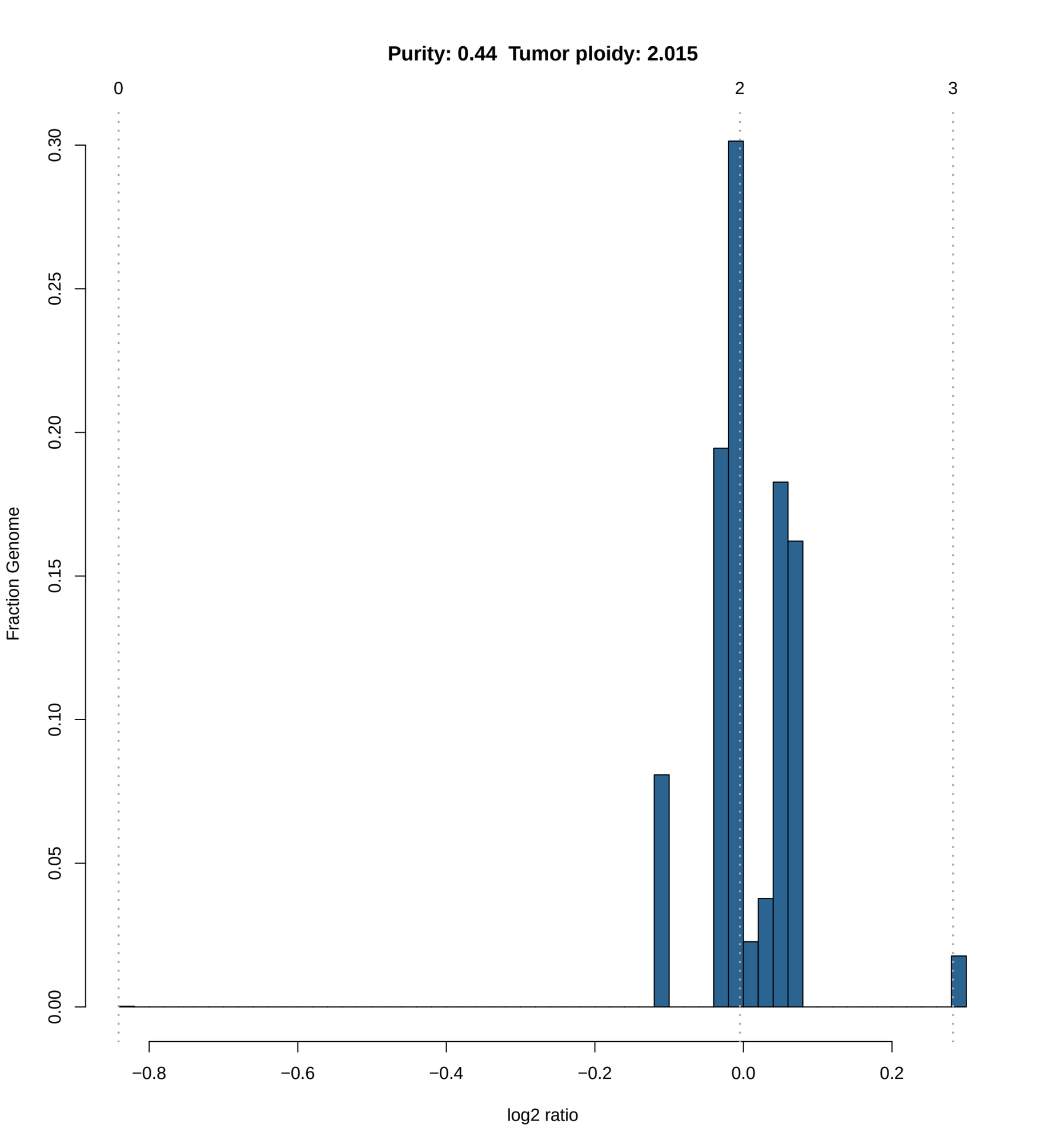

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

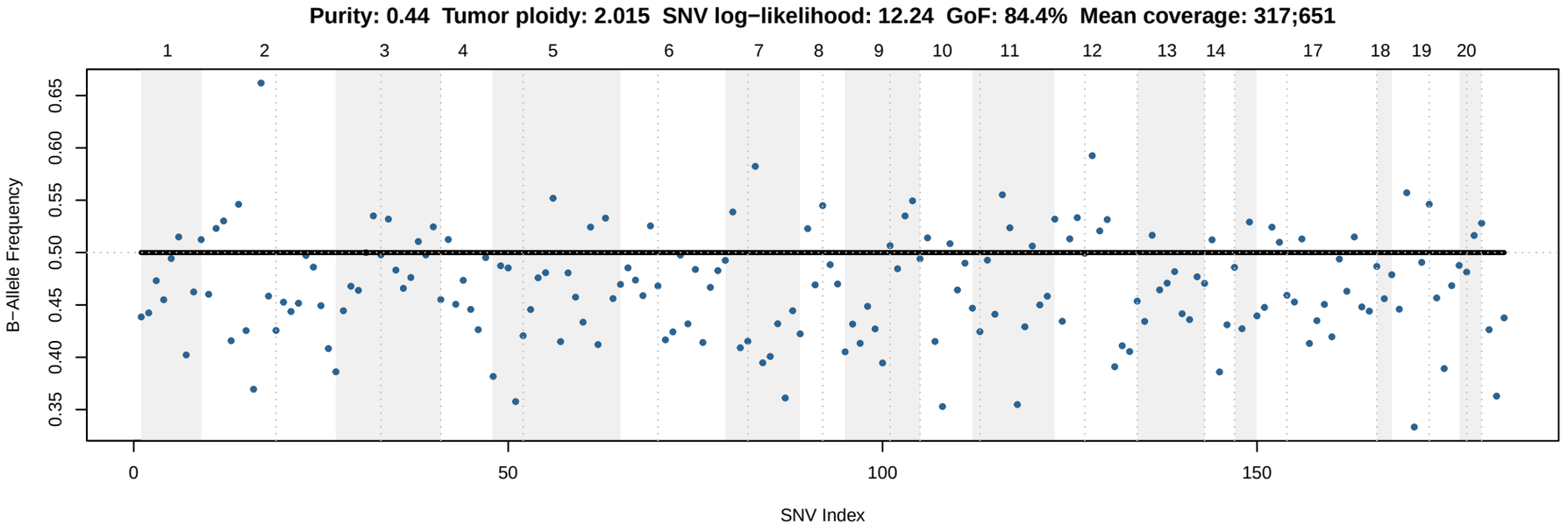

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio
4m3
3m2
2m1
4m2
3m1
4m1

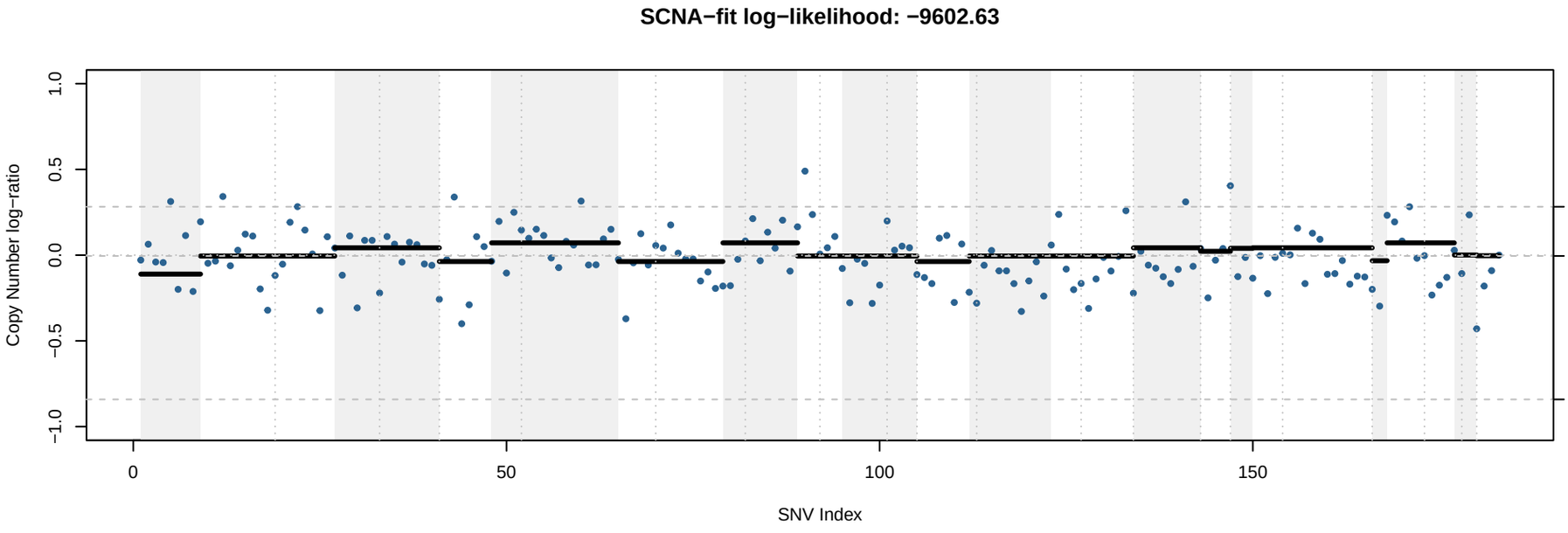

Coverage (log2)
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

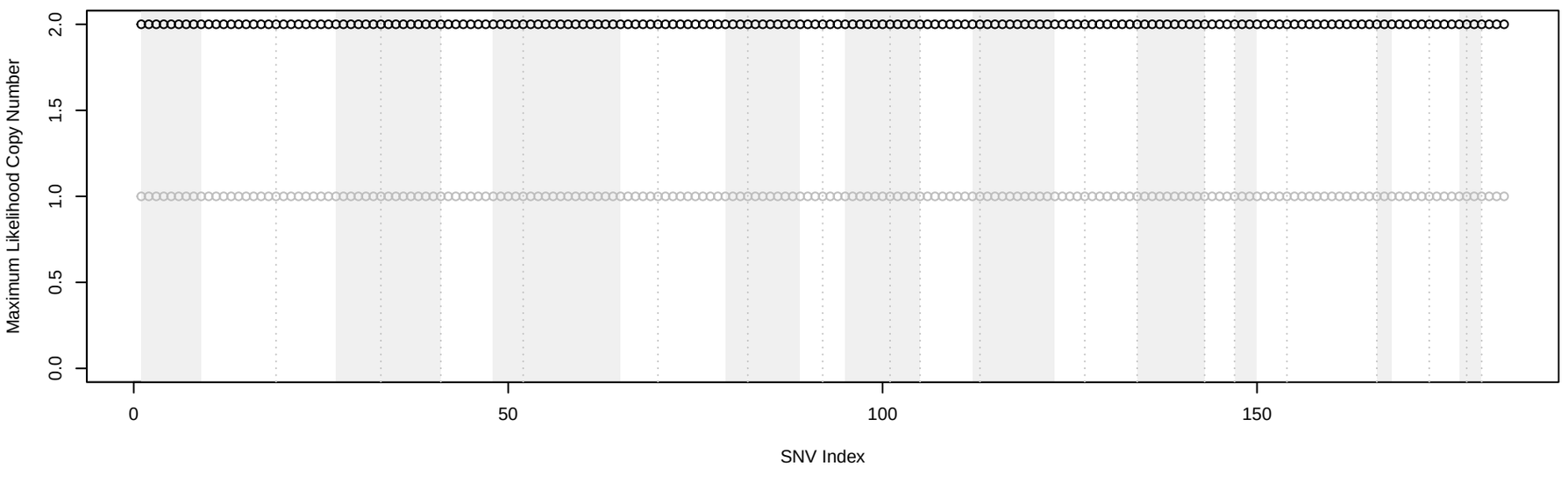

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1
6m1

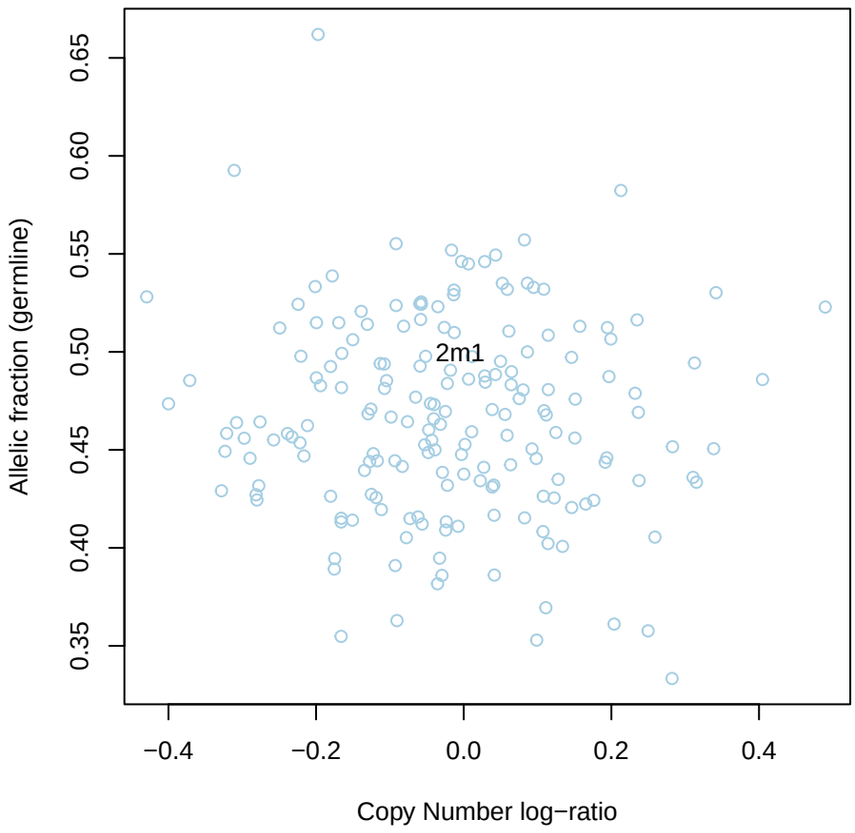

Frequency
0
1
2
3
4
5
6
7
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

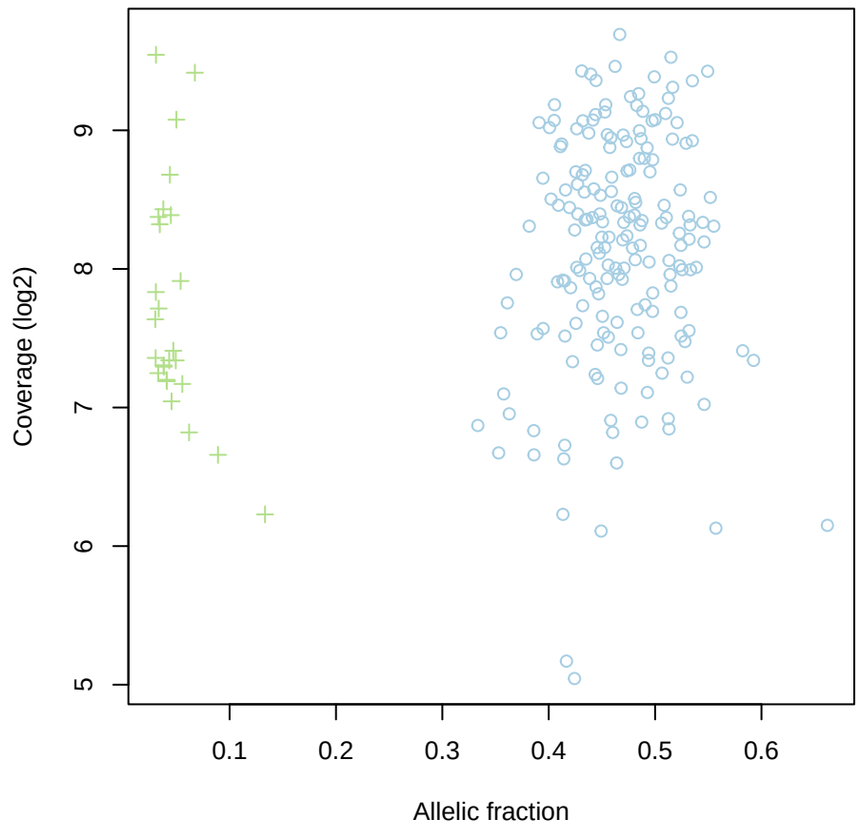

Purity: 0.44 Tumor ploidy: 2.015
0
2
3
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

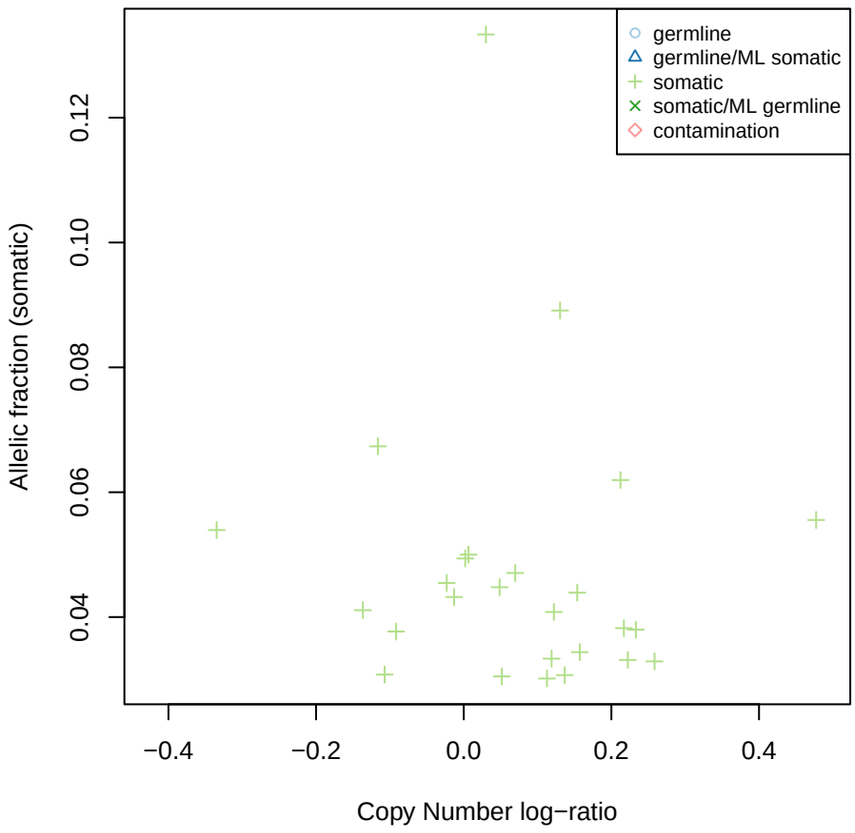

Purity: 0.44 Tumor ploidy: 2.015 SNV log−likelihood: 12.24 GoF: 84.4% Mean coverage: 317;651
1
2
3
4
5
6
7
8
9
10
11
12
13
14
17
18
19
20
B−Allele Frequency
0.35
0.40
0.45
0.50
0.55
0.60
0.65
0
50
100
150
SNV Index

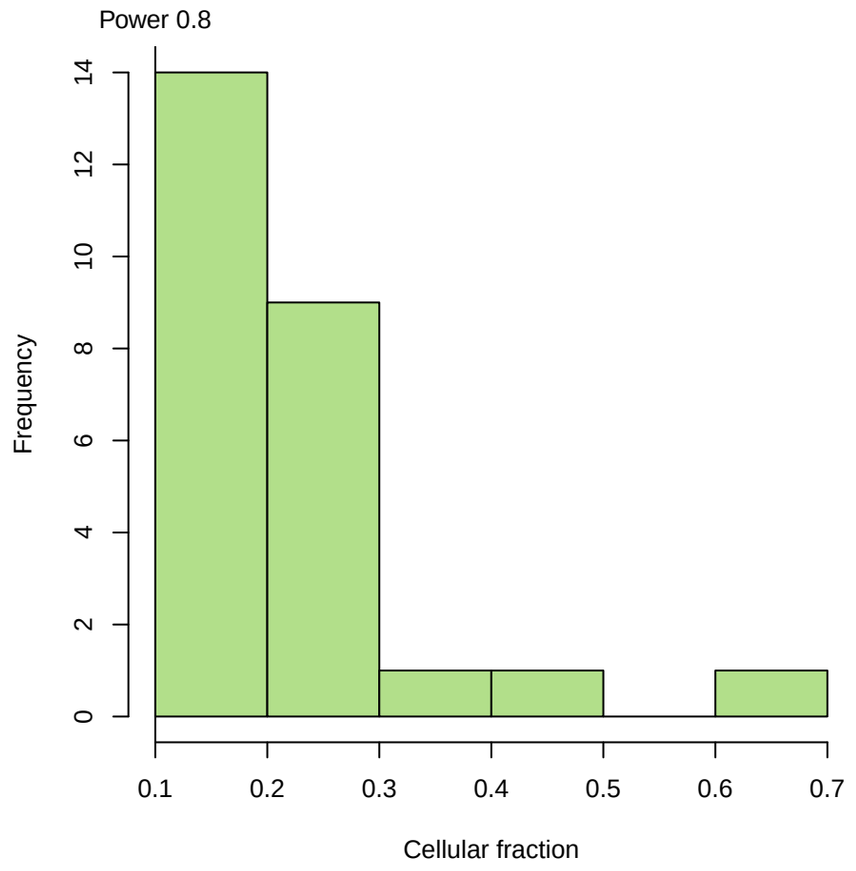

SCNA−fit log−likelihood: −9602.63
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
0
2
3
0
50
100
150
SNV Index

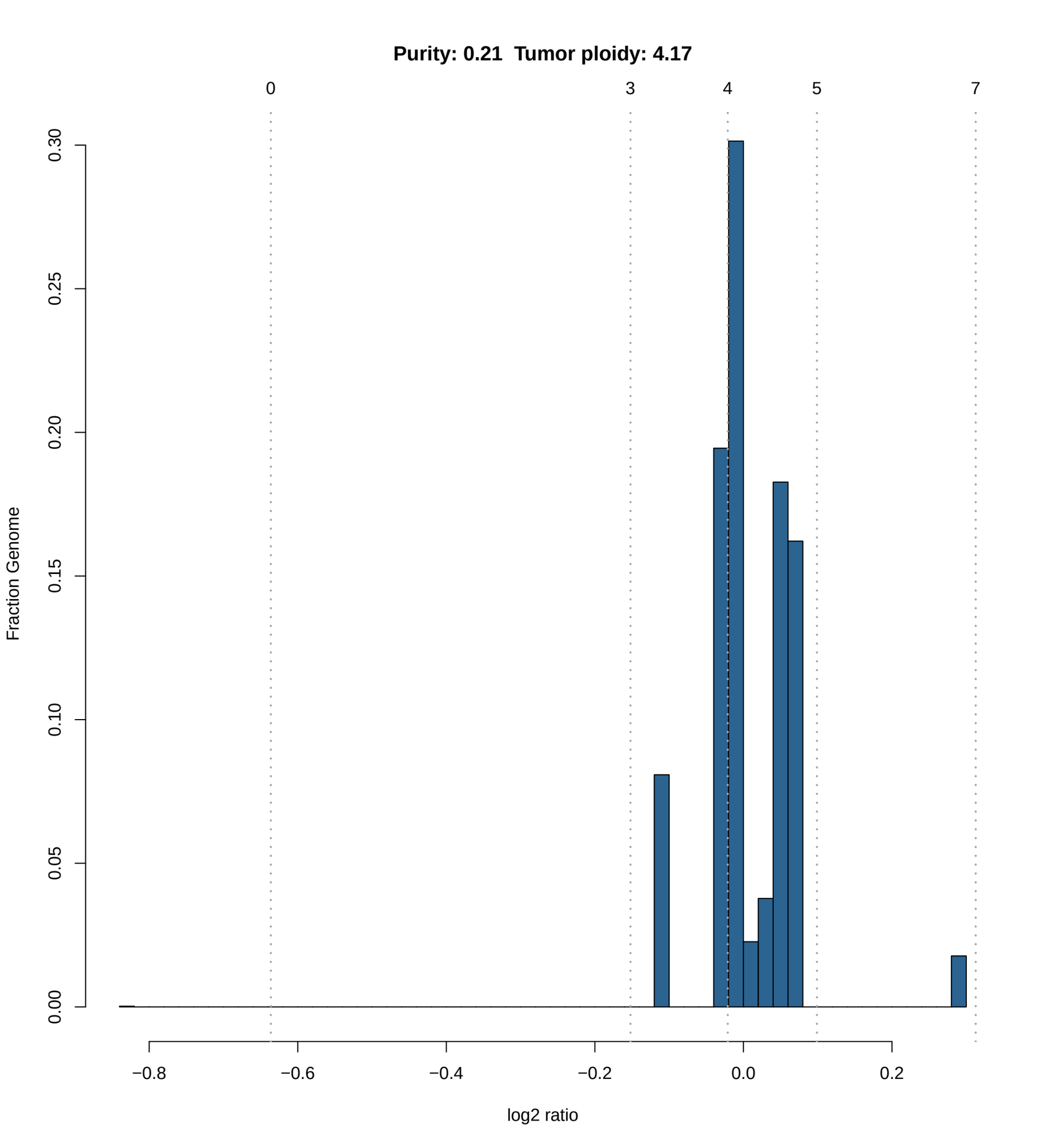

Maximum Likelihood Copy Number
0.0
0.5
1.0
1.5
2.0
0
50
100
150
SNV Index

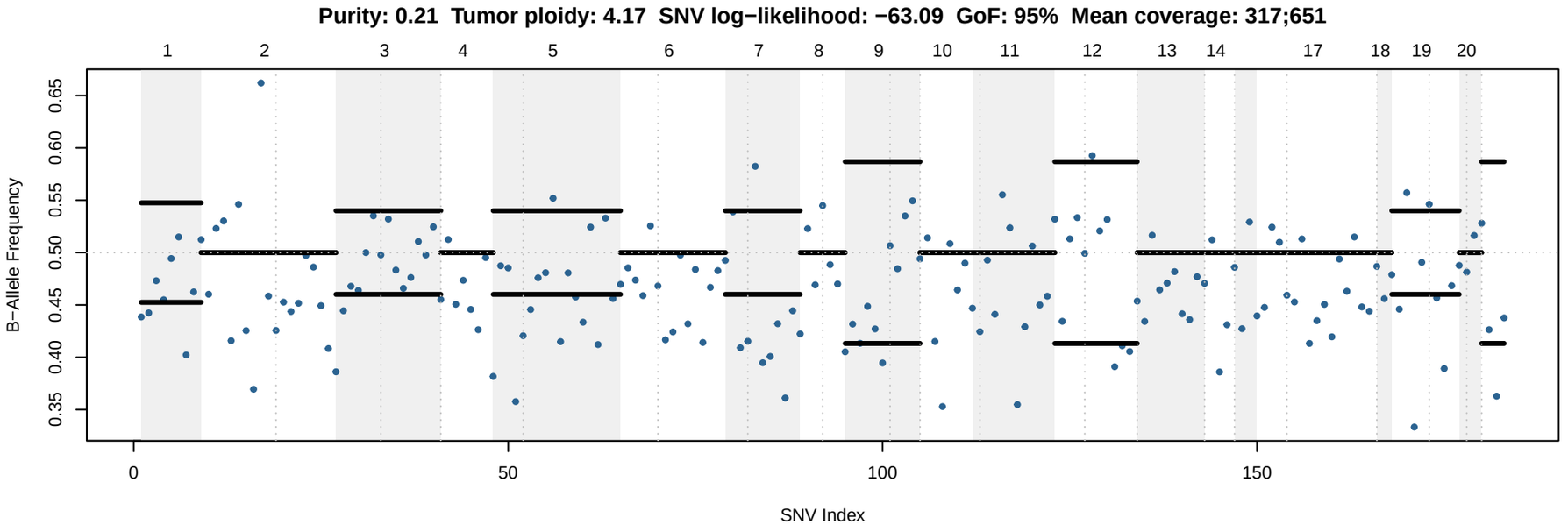

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
2m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

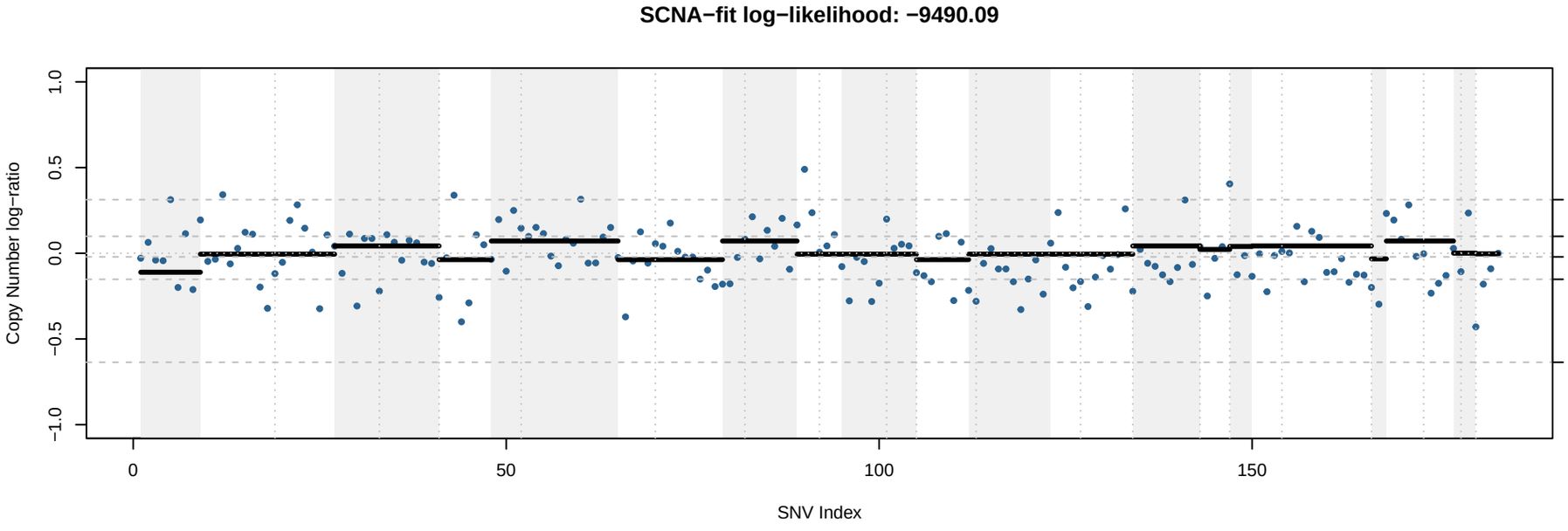

Coverage (log2)
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

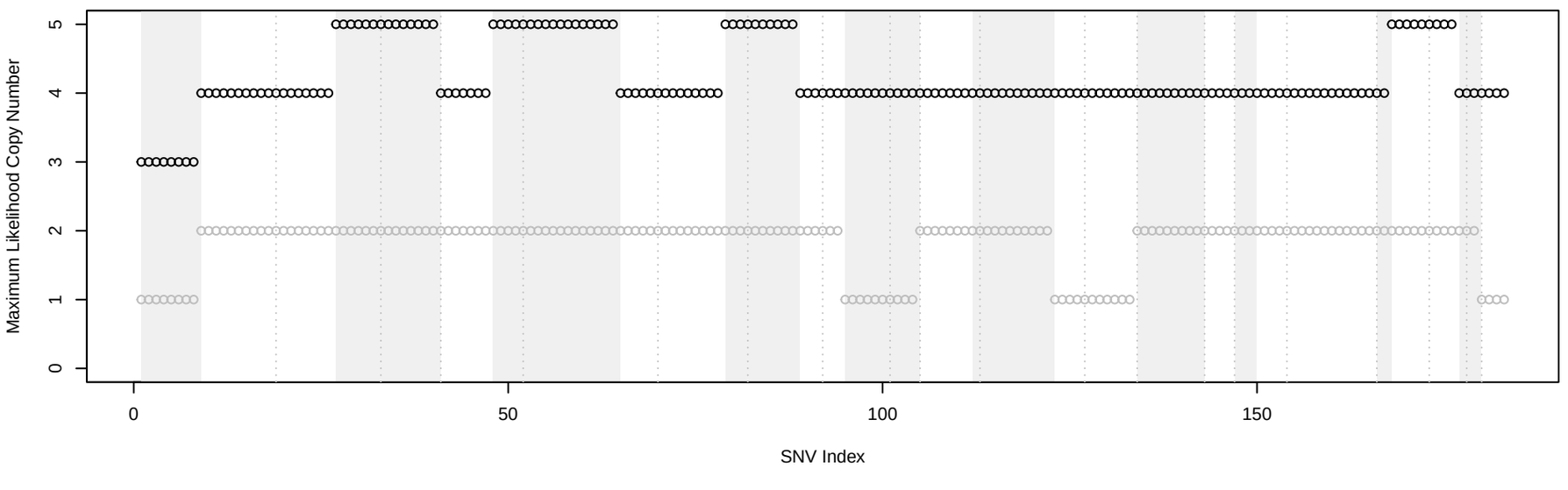

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

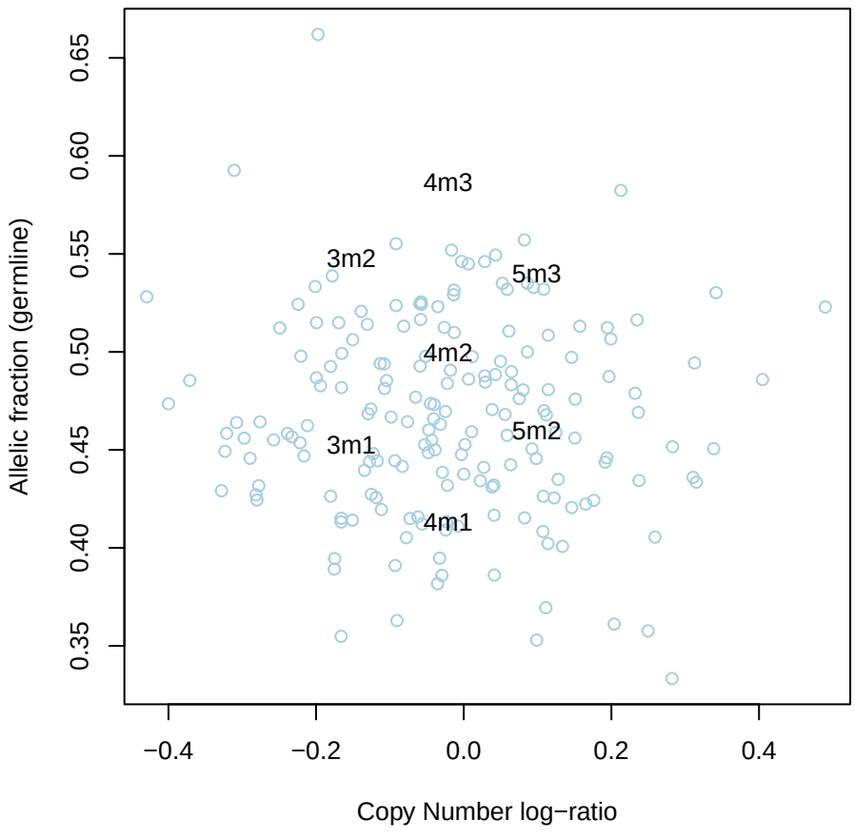

Power 0.8
Frequency
0
2
4
6
8
10
12
14
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Cellular fraction

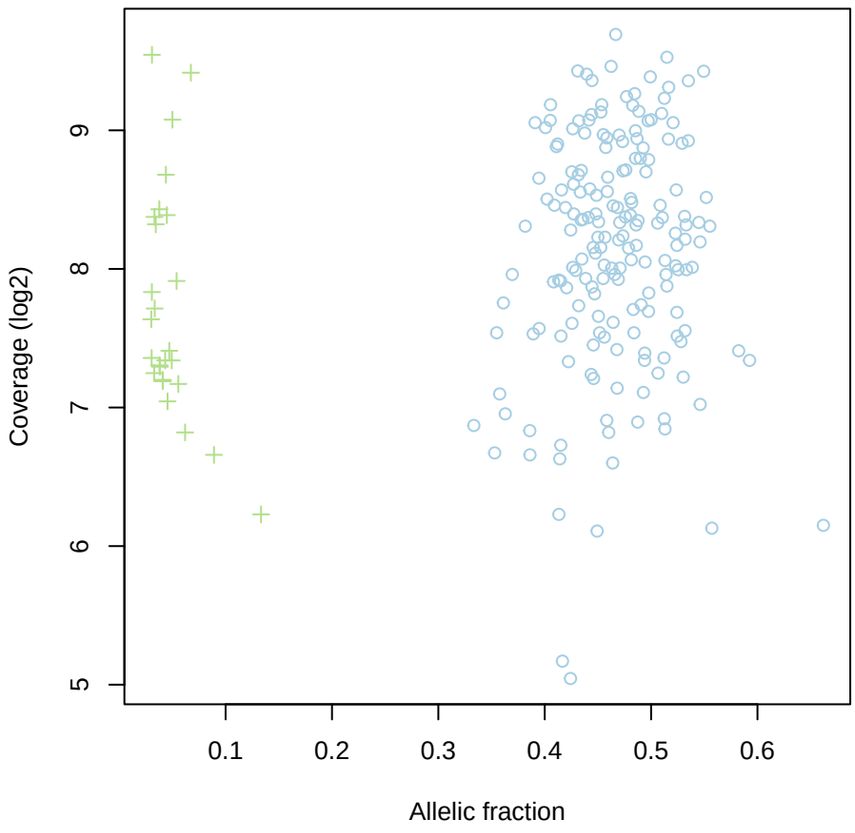

Purity: 0.21 Tumor ploidy: 4.17
0
3
4
5
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

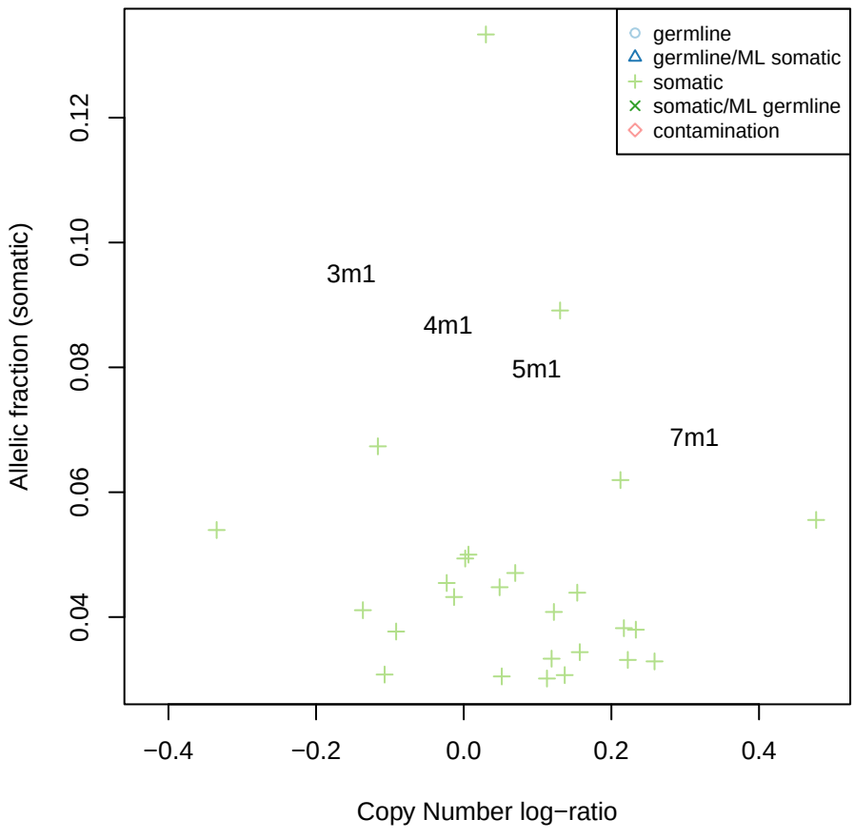

Purity: 0.21 Tumor ploidy: 4.17 SNV log−likelihood: −63.09 GoF: 95% Mean coverage: 317;651
1 2 3 4 5 6 7 8 9 10 11 12 13 14 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 50 100 150
SNV Index

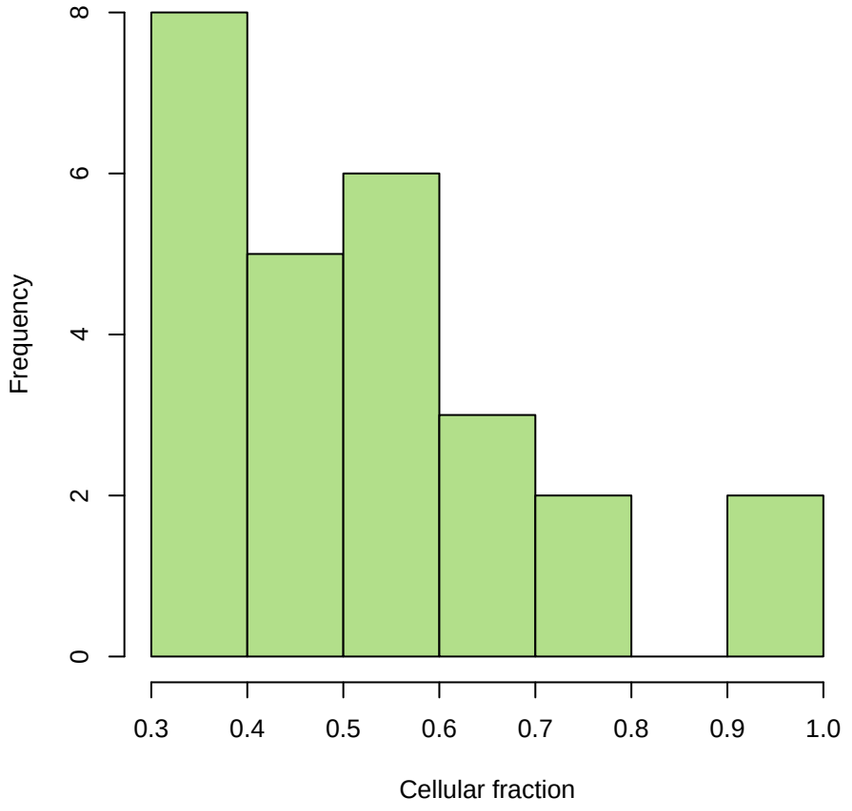

SCNA−fit log−likelihood: −9490.09
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
0 3 5 7
0 50 100 150
SNV Index

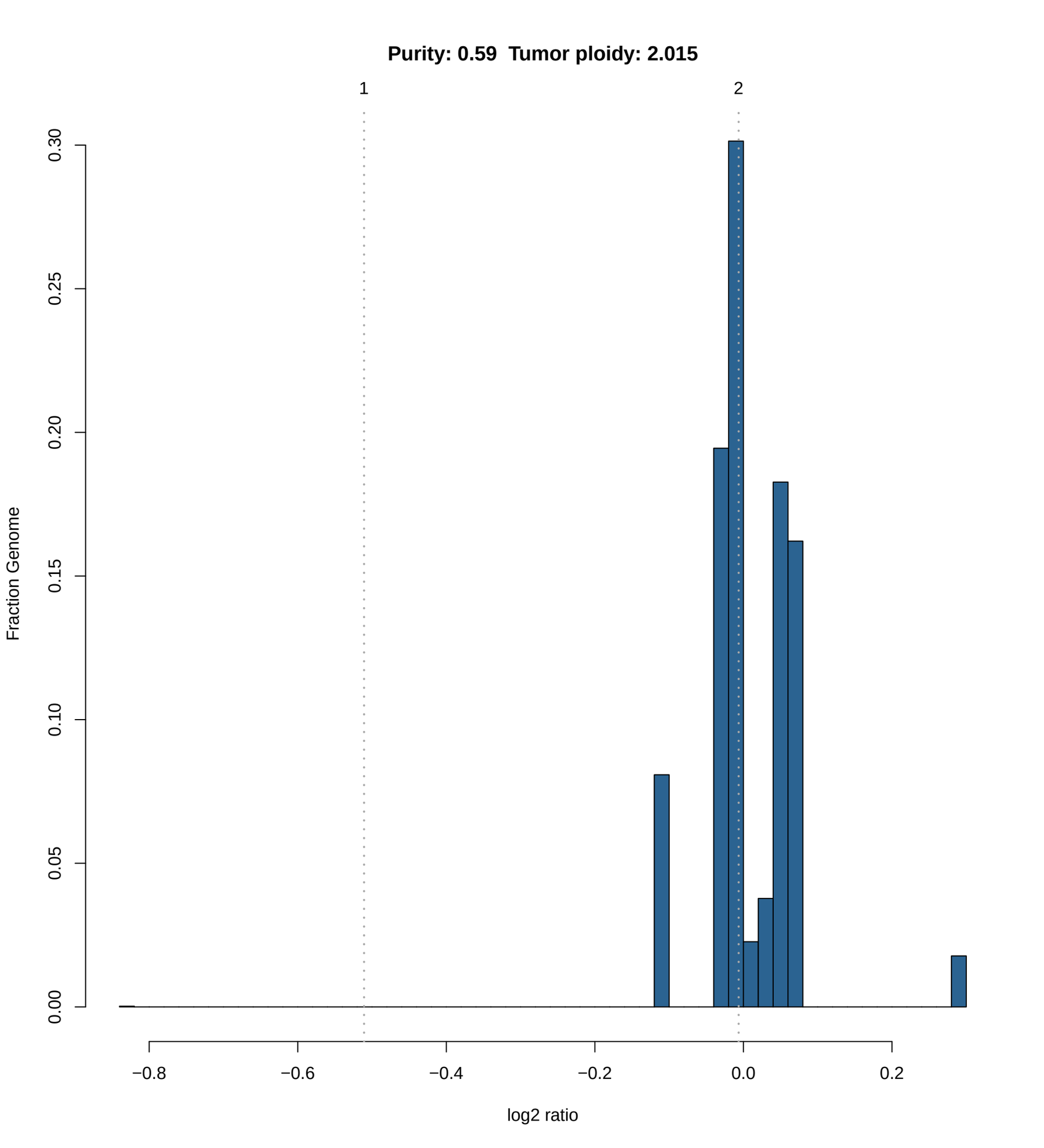

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

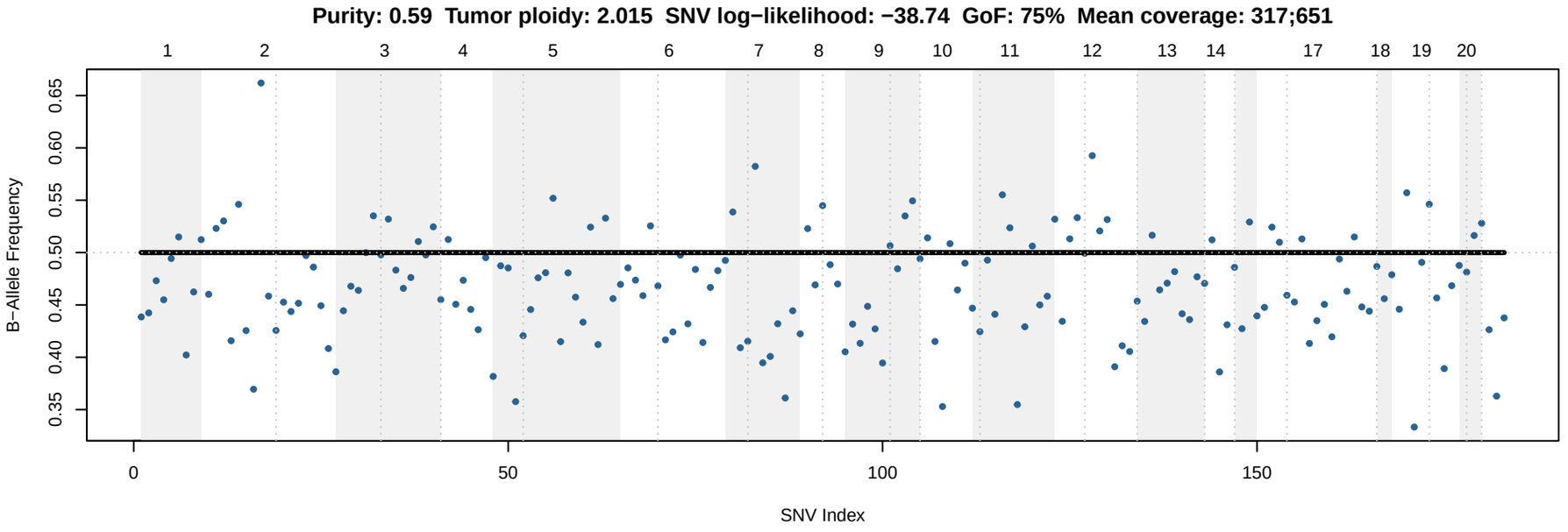

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
4m3
3m2
5m3
4m2
5m2
3m1
4m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

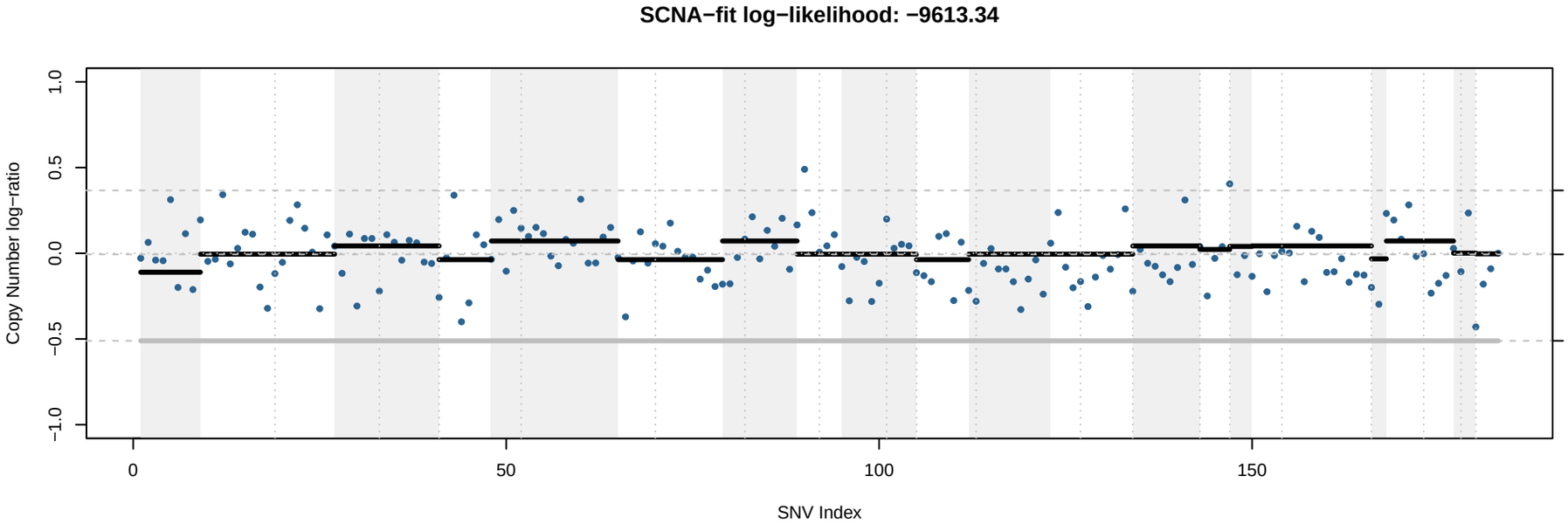

Coverage (log2)
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

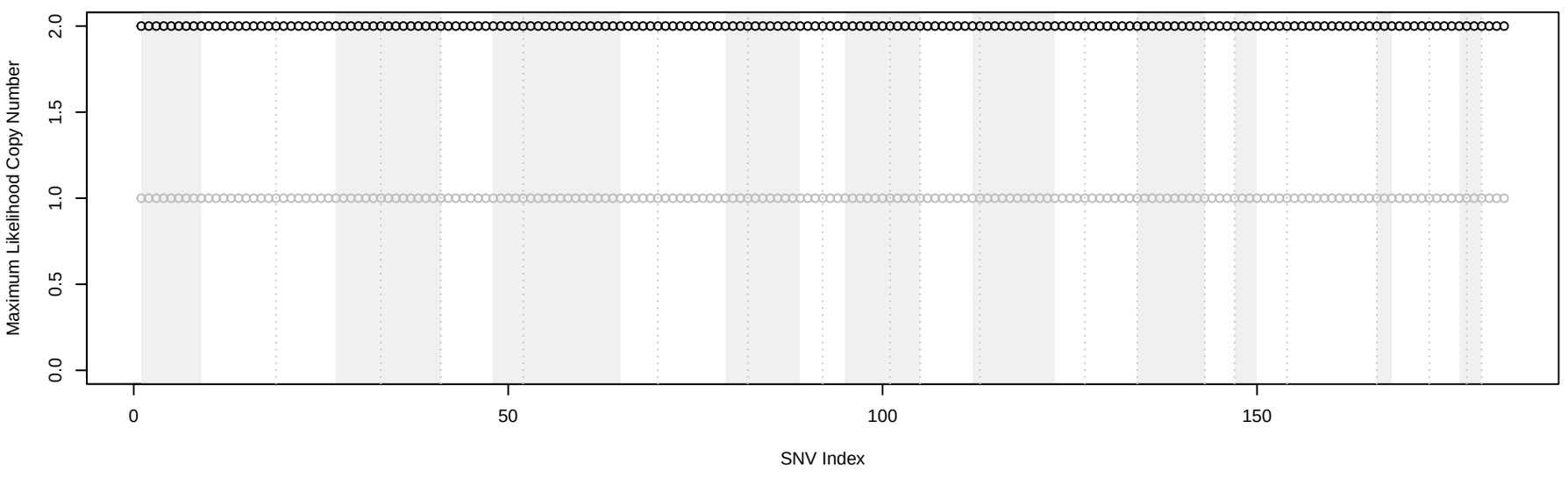

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
3m1
4m1
5m1
7m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

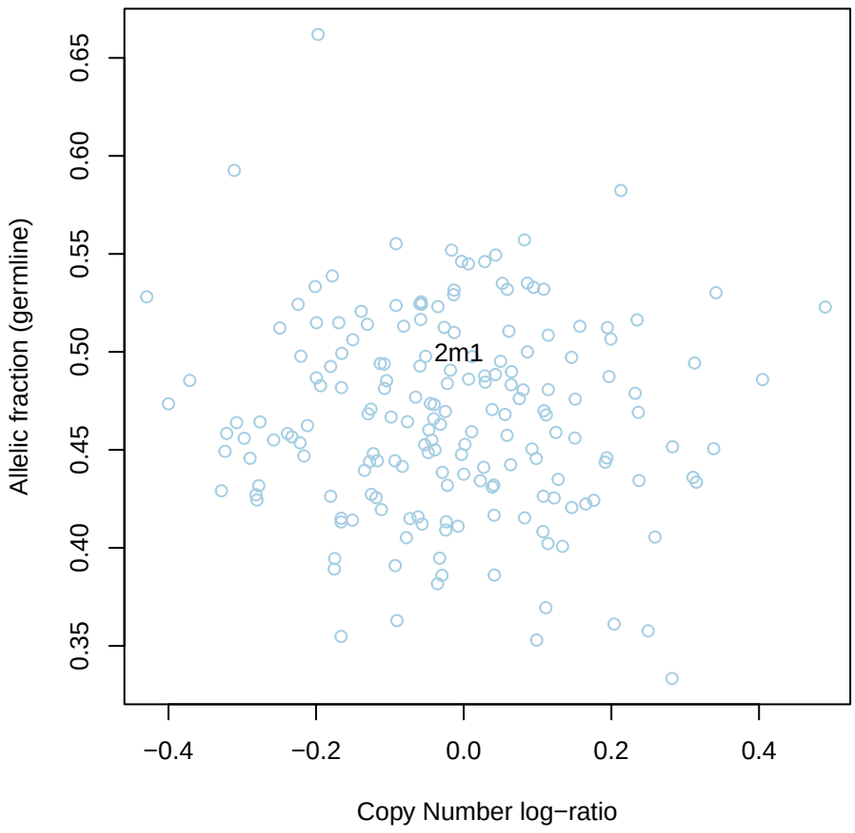

Frequency
0
2
4
6
8
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

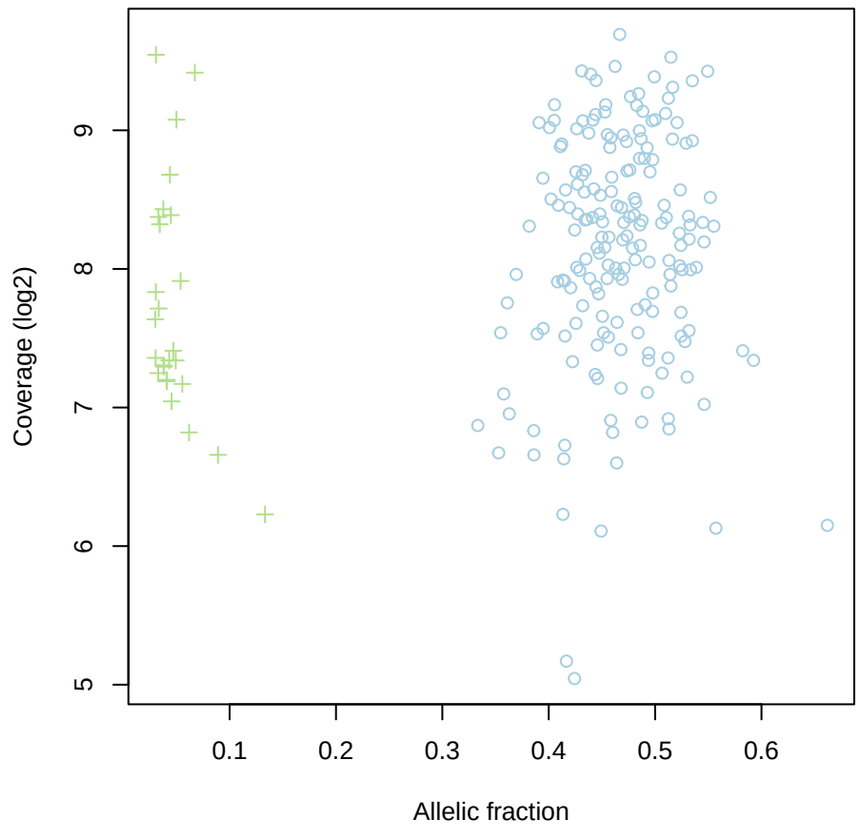

Purity: 0.59 Tumor ploidy: 2.015
1
2
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

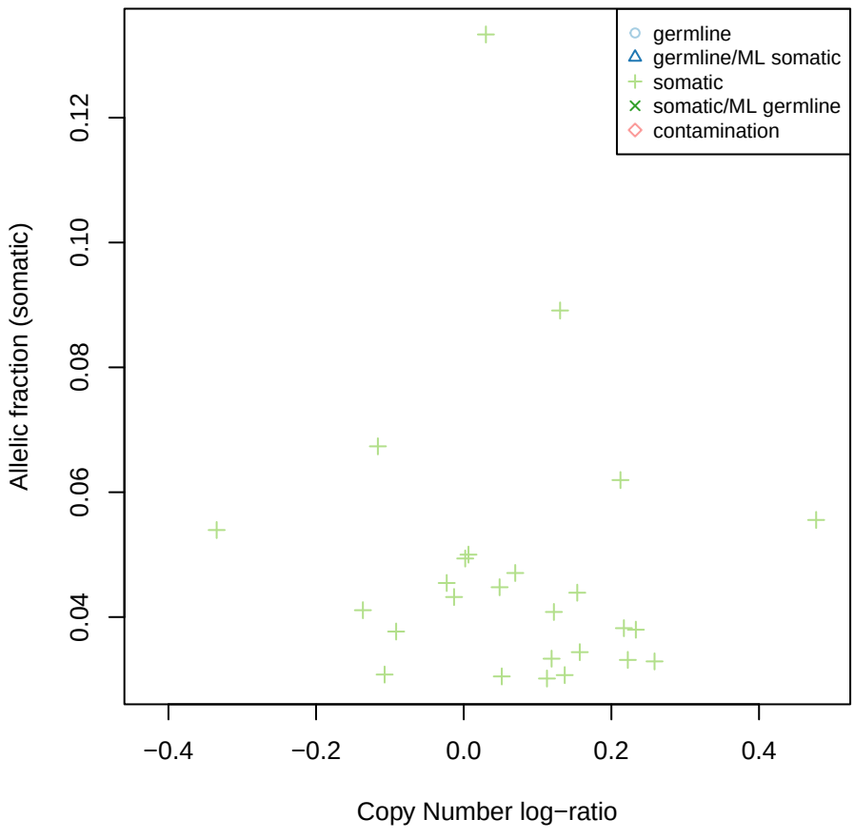

Purity: 0.59 Tumor ploidy: 2.015 SNV log−likelihood: −38.74 GoF: 75% Mean coverage: 317;651
1
2
3
4
5
6
7
8
9
10
11
12
13
14
17
18
19
20
B−Allele Frequency
0.35
0.40
0.45
0.50
0.55
0.60
0.65
0
50
100
150
SNV Index

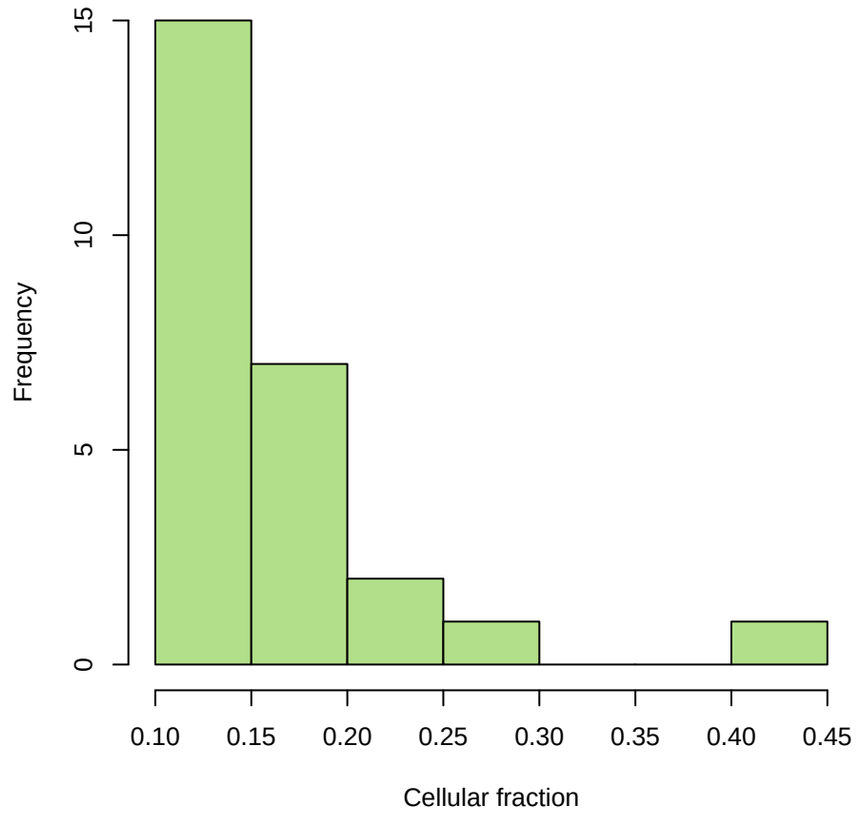

SCNA−fit log−likelihood: −9613.34
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1
2
3
0
50
100
150
SNV Index

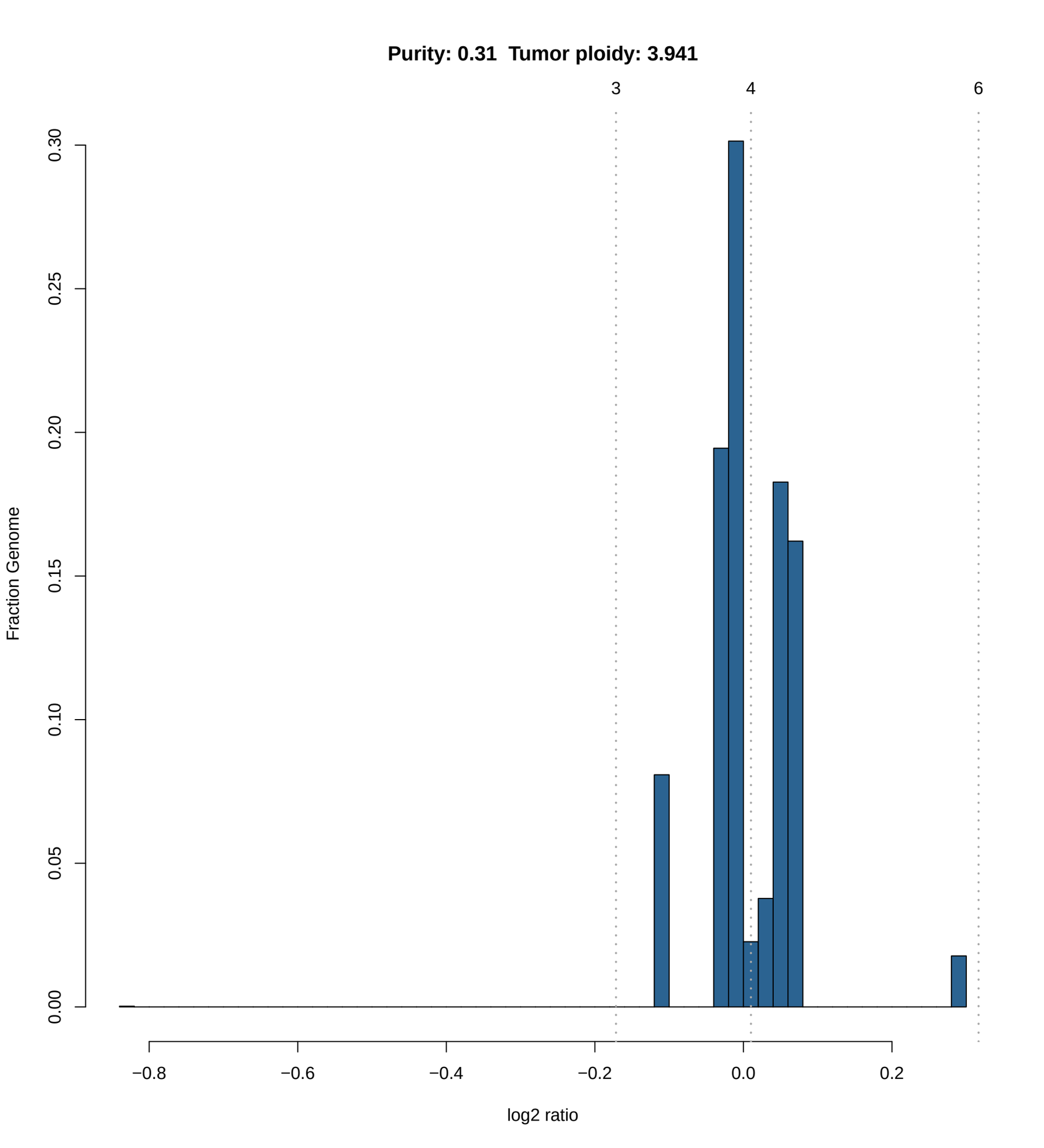

Maximum Likelihood Copy Number
0.0
0.5
1.0
1.5
2.0
0
50
100
150
SNV Index

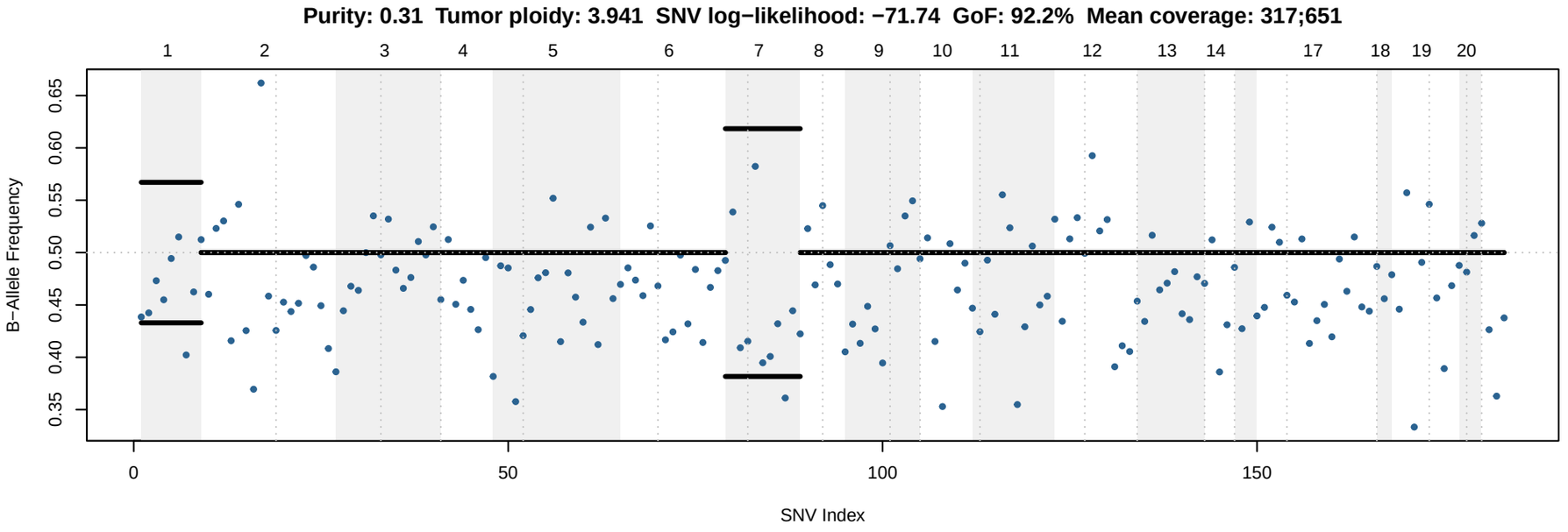

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
2m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

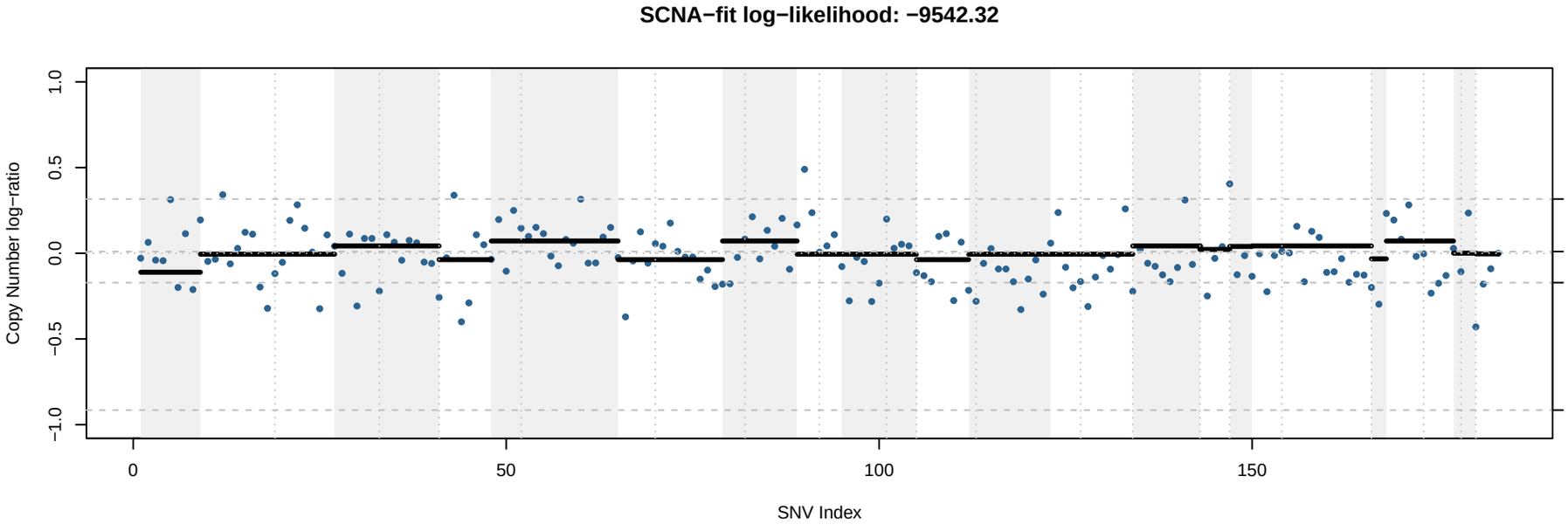

Coverage (log2)
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

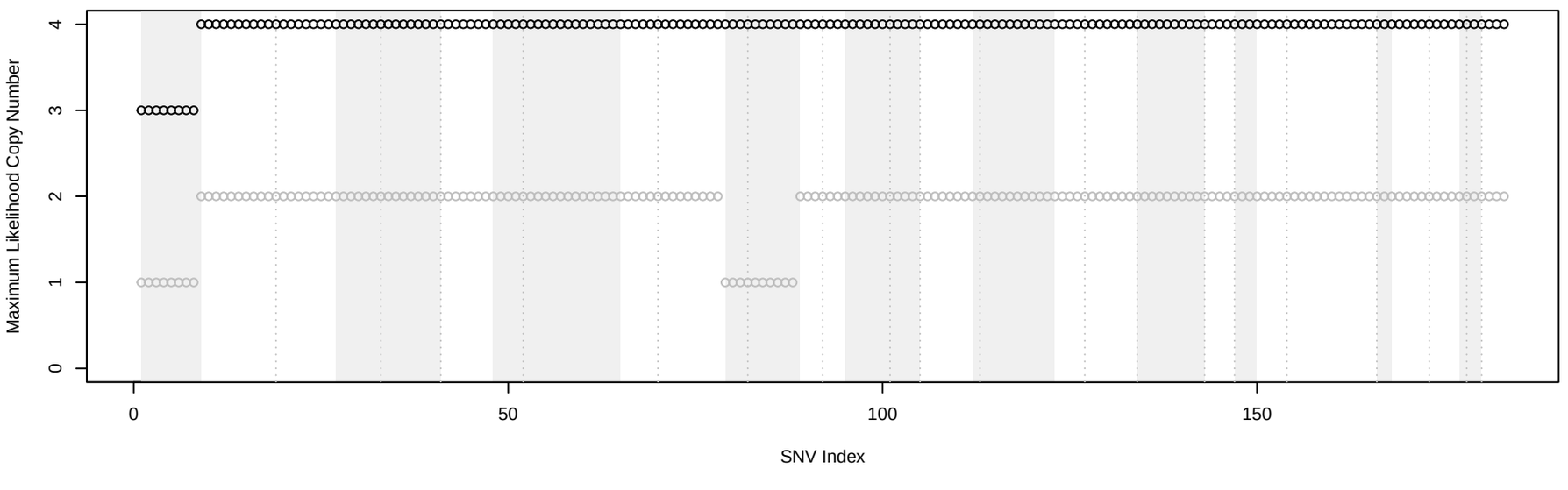

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

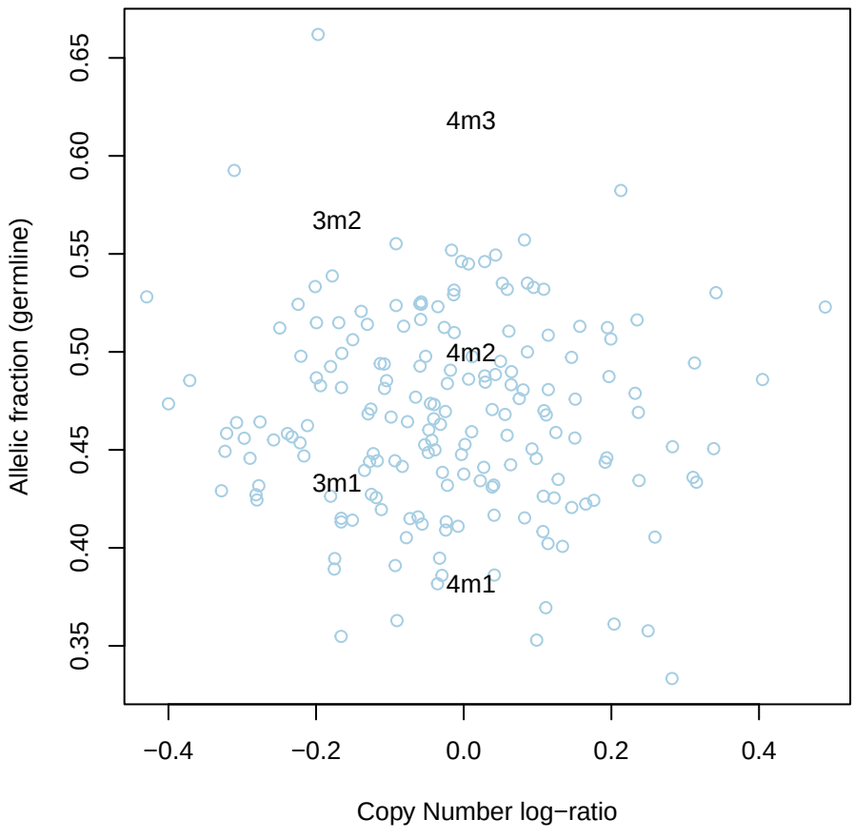

Frequency
0
5
10
15
0.10
0.15
0.20
0.25
0.30
0.35
0.40
0.45
Cellular fraction

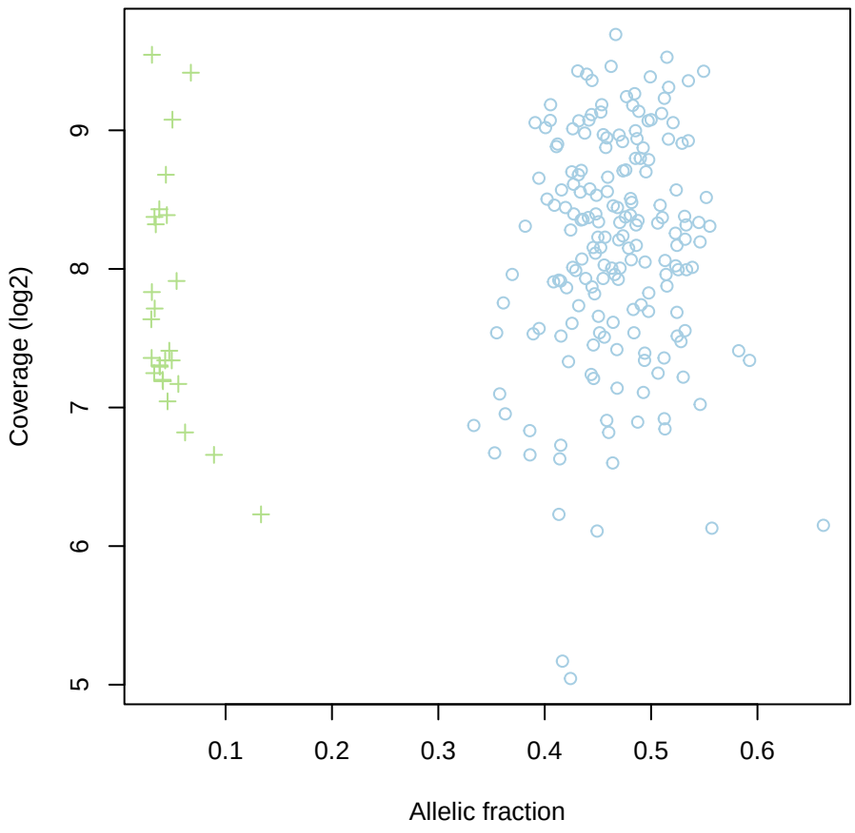

Purity: 0.31 Tumor ploidy: 3.941
3
4
6
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

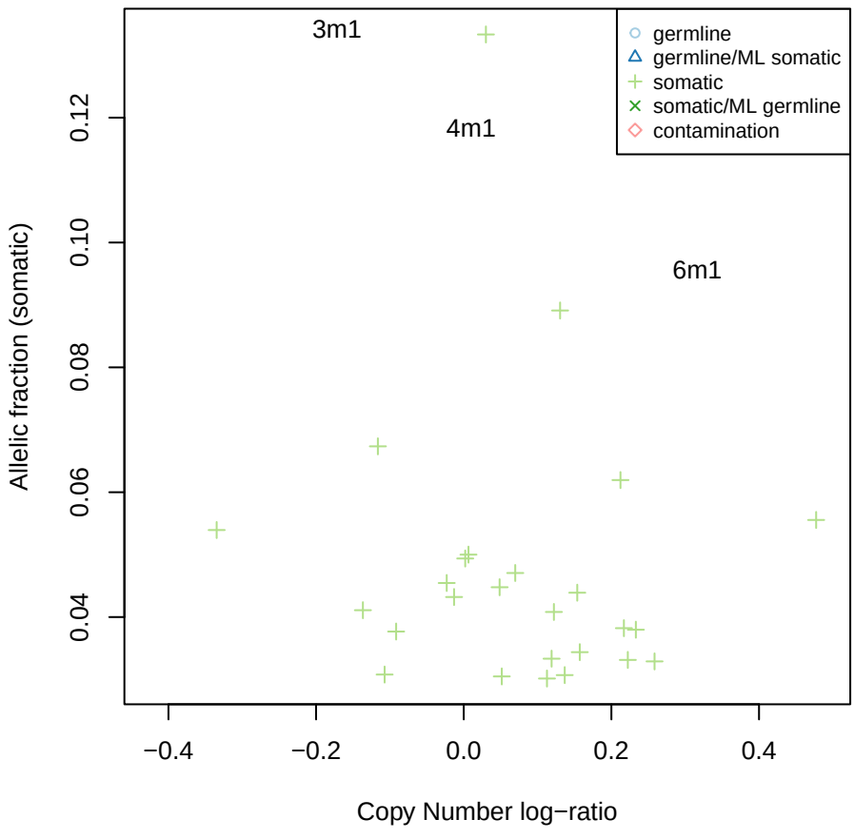

Purity: 0.31 Tumor ploidy: 3.941 SNV log−likelihood: −71.74 GoF: 92.2% Mean coverage: 317;651
1
2
3
4
5
6
7
8
9
10
11
12
13
14
17
18
19
20
B−Allele Frequency
0.35
0.40
0.45
0.50
0.55
0.60
0.65
0
50
100
150
SNV Index

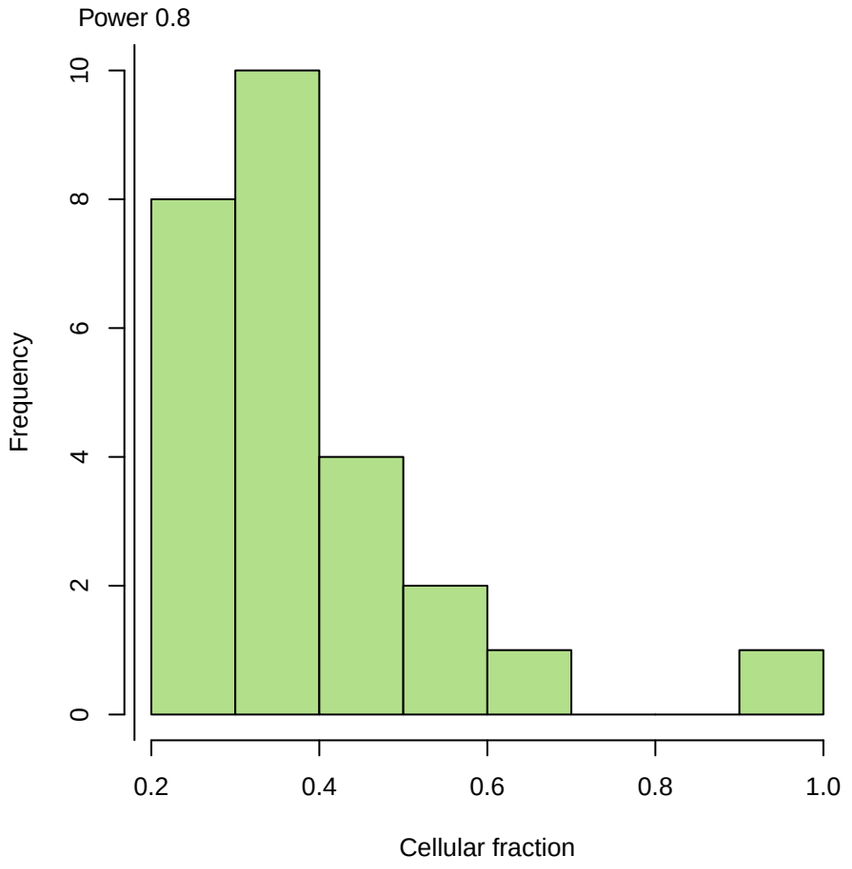

SCNA−fit log−likelihood: −9542.32
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
0
3
4
6
0
50
100
150
SNV Index

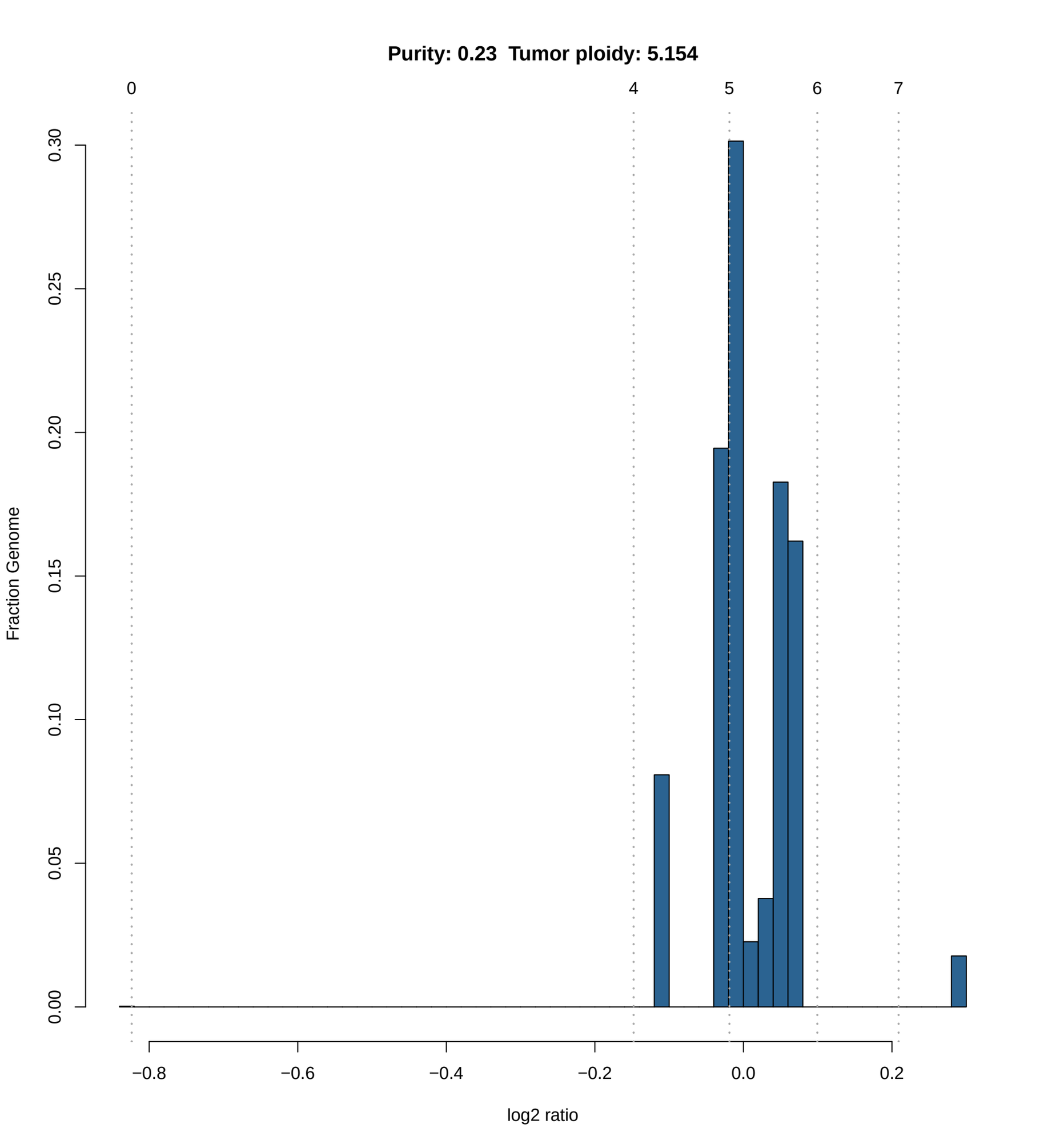

Maximum Likelihood Copy Number
0
1
2
3
4
0
50
100
150
SNV Index

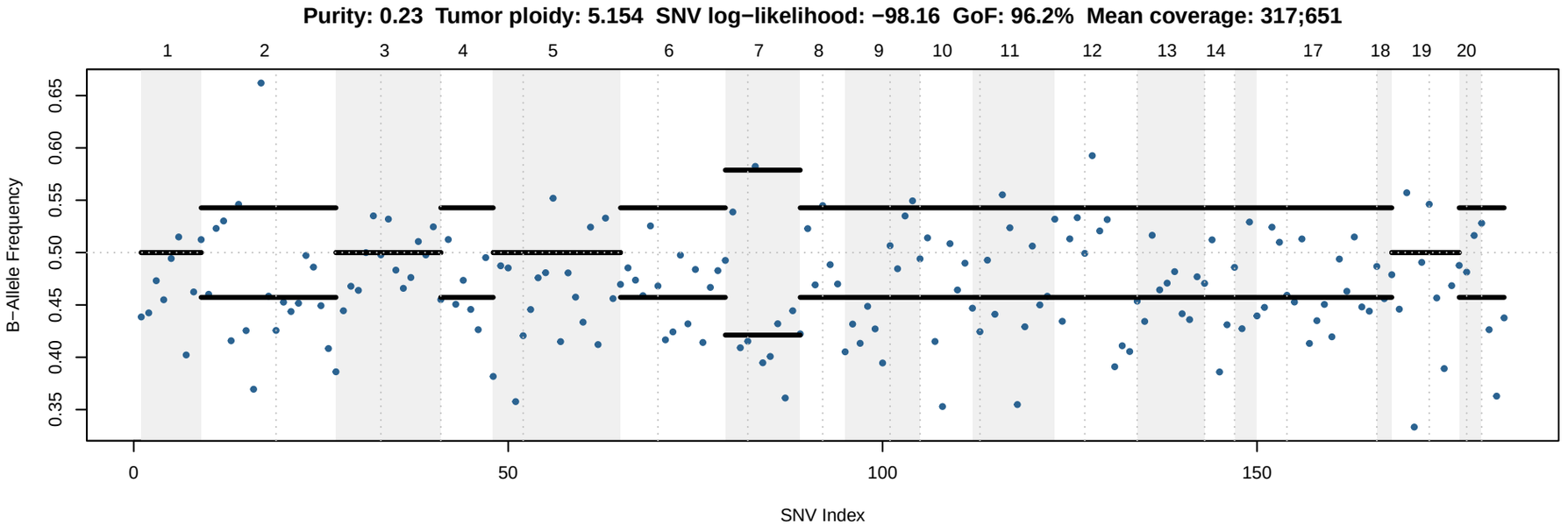

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
4m3
3m2
4m2
3m1
4m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

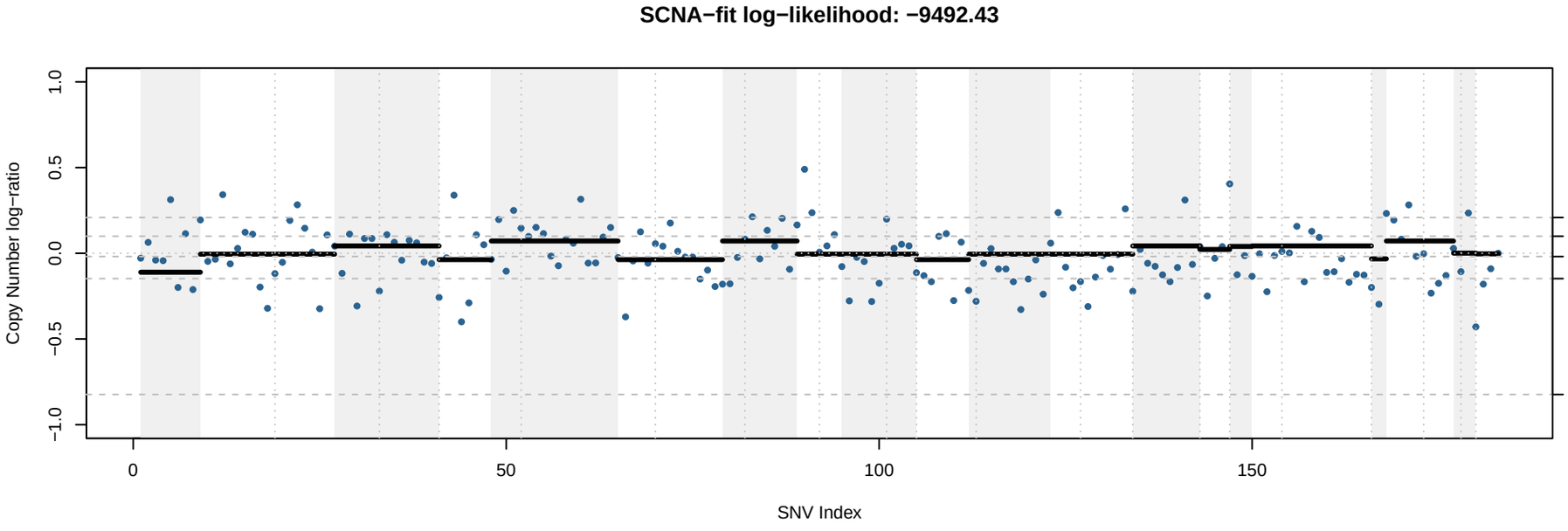

Coverage (log2)
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

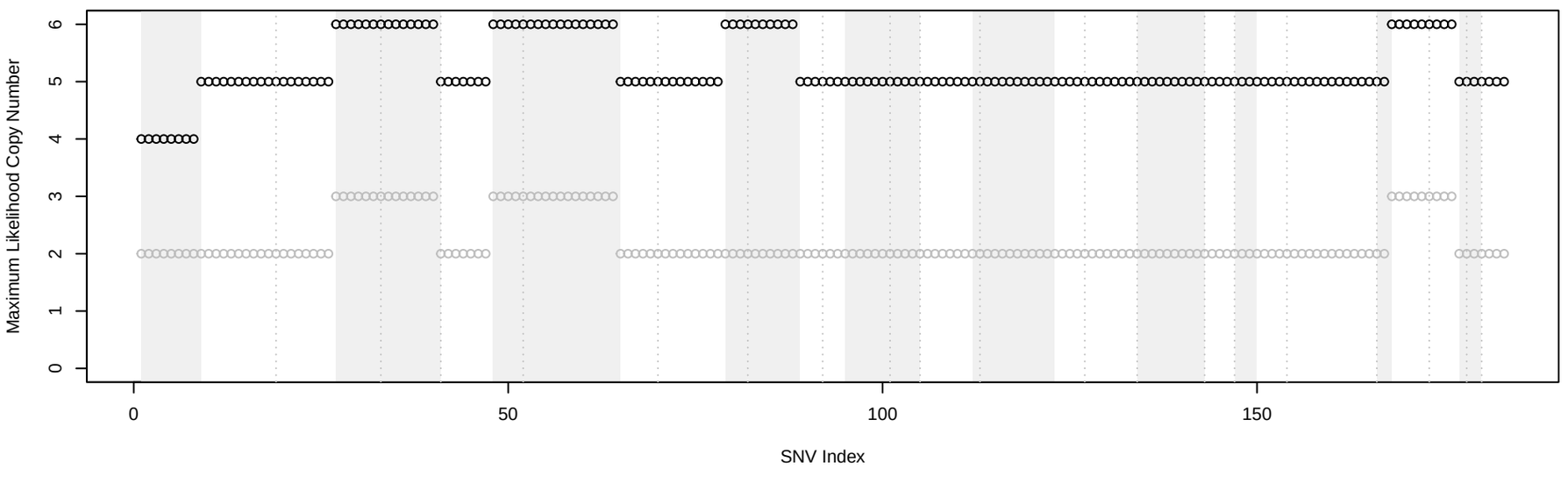

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
3m1
4m1
6m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

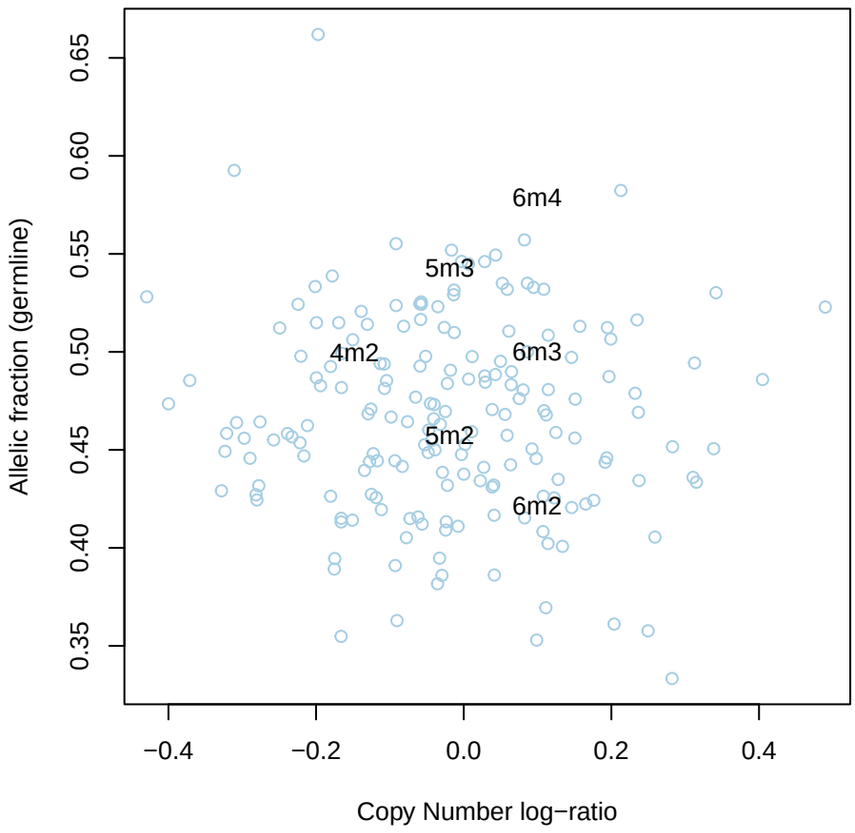

Power 0.8
Frequency
0
2
4
6
8
10
0.2
0.4
0.6
0.8
1.0
Cellular fraction

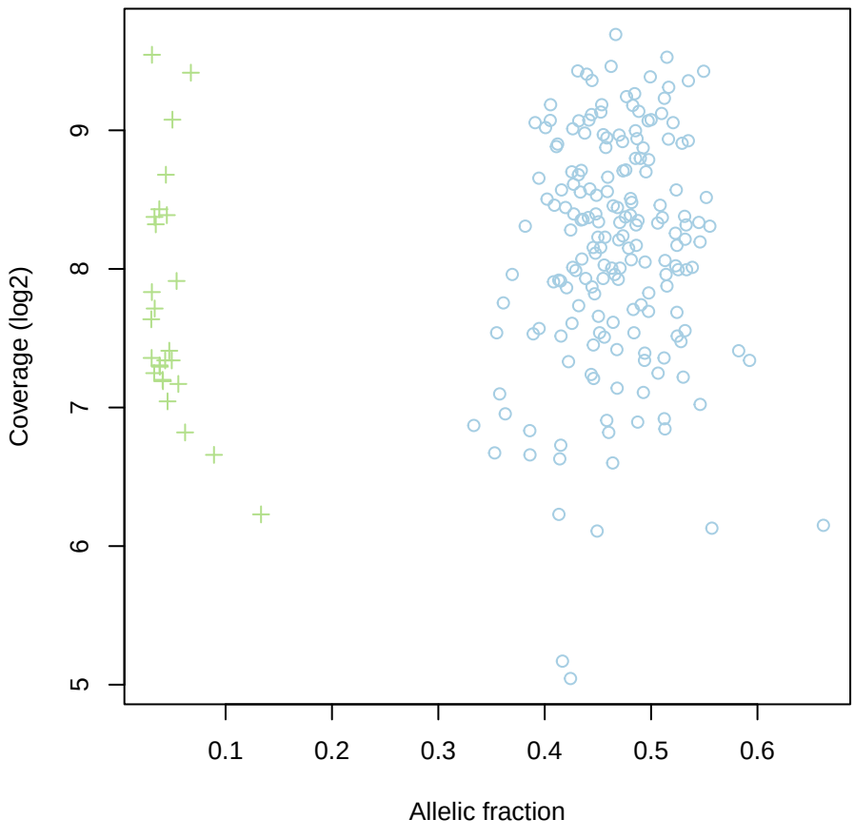

Purity: 0.23 Tumor ploidy: 5.154
0
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

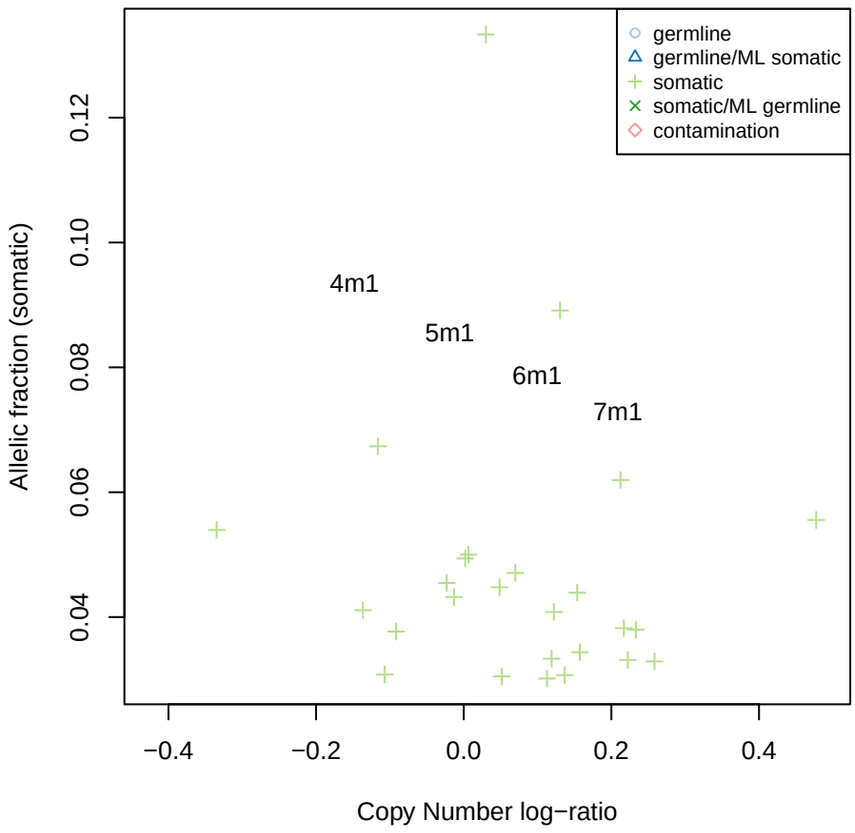

Purity: 0.23 Tumor ploidy: 5.154 SNV log−likelihood: −98.16 GoF: 96.2% Mean coverage: 317;651
1
2
3
4
5
6
7
8
9
10
11
12
13
14
17
18
19
20
B−Allele Frequency
0.35
0.40
0.45
0.50
0.55
0.60
0.65
0
50
100
150
SNV Index

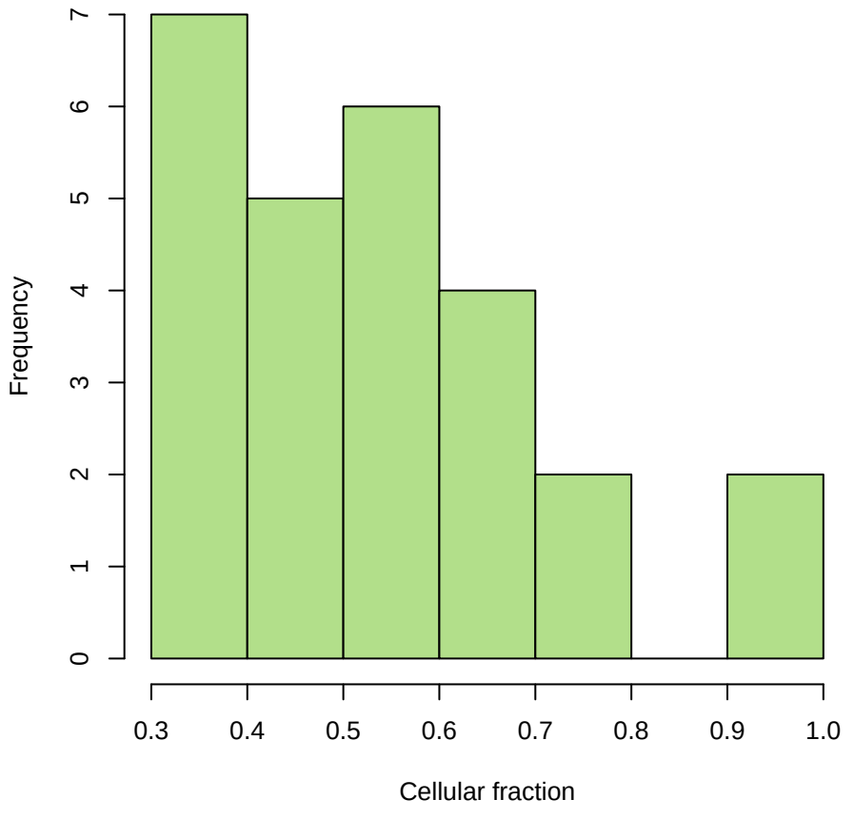

SCNA−fit log−likelihood: −9492.43
Copy Number log−ratio
1.0
0.5
0.0
−0.5
−1.0
6
4
0
0
50
100
150
SNV Index

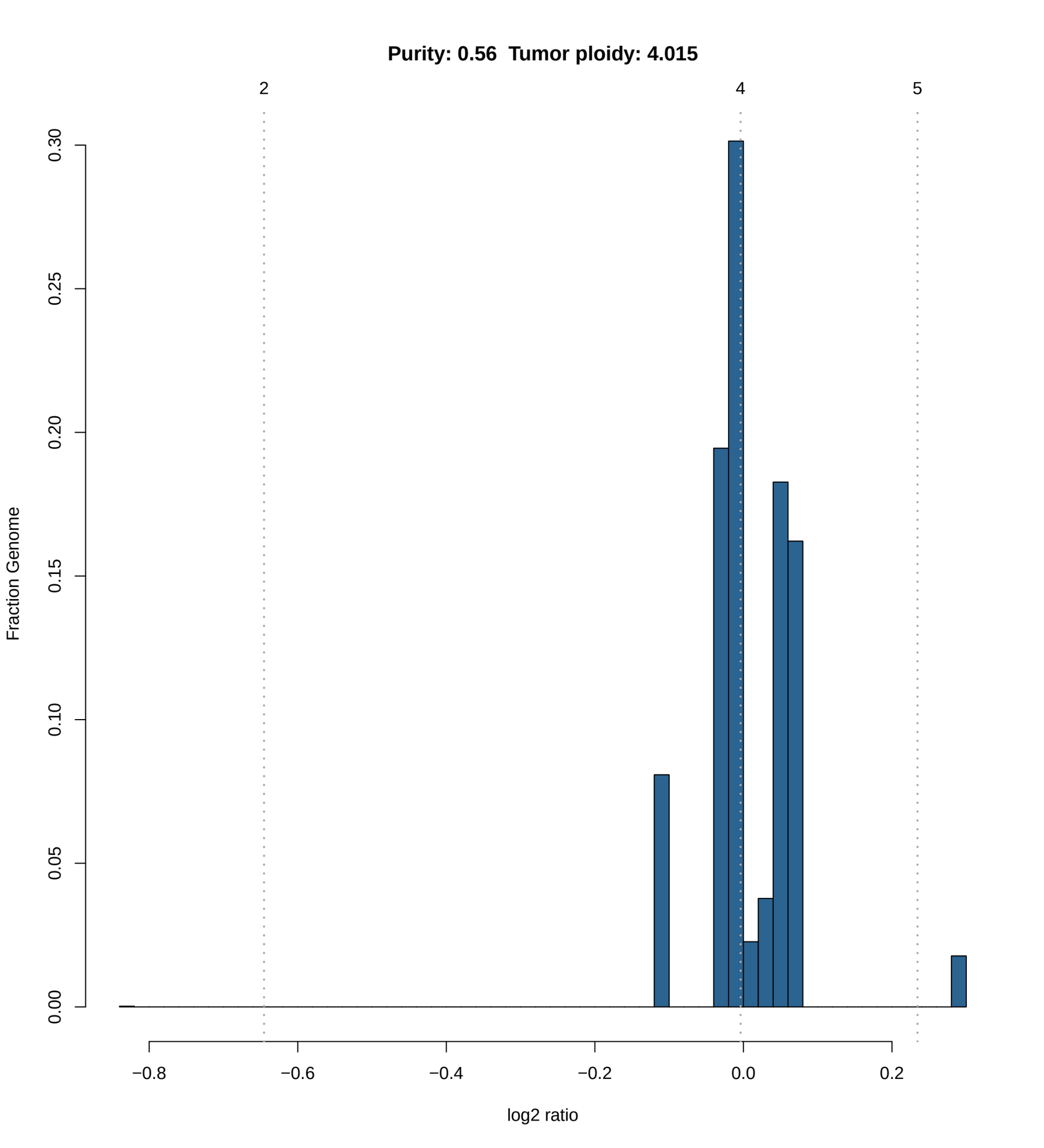

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
0
50
100
150
SNV Index

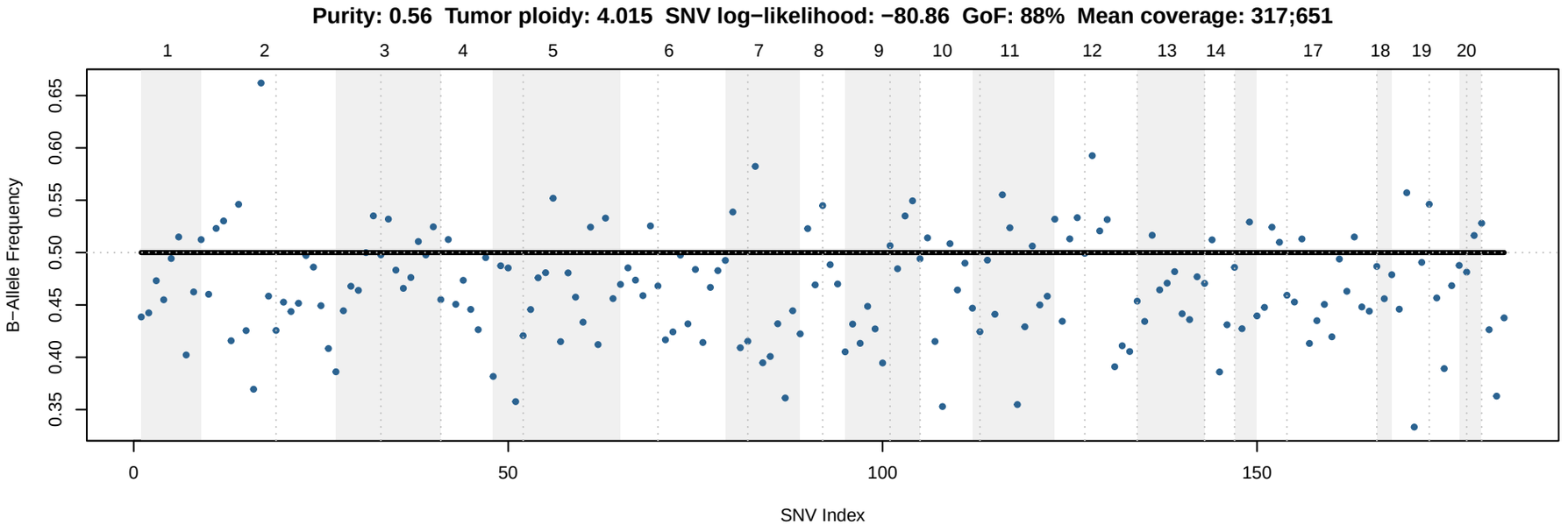

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
6m4
5m3
4m2
6m3
5m2
6m2
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

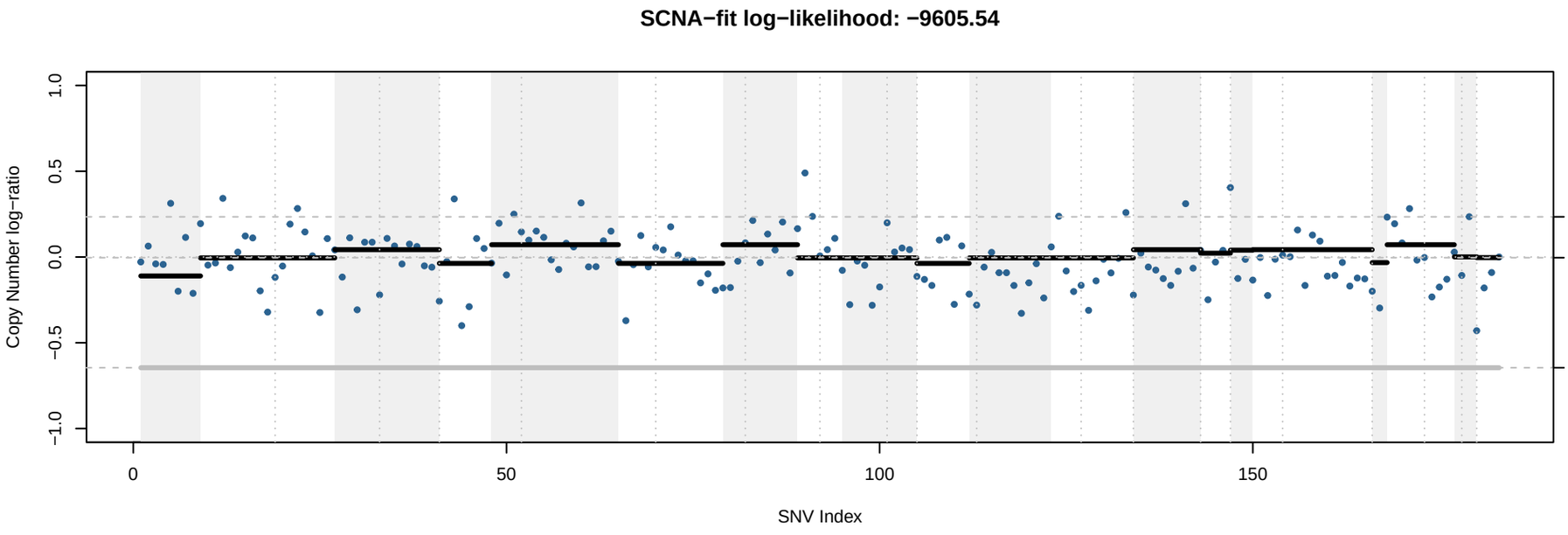

Coverage (log2)
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

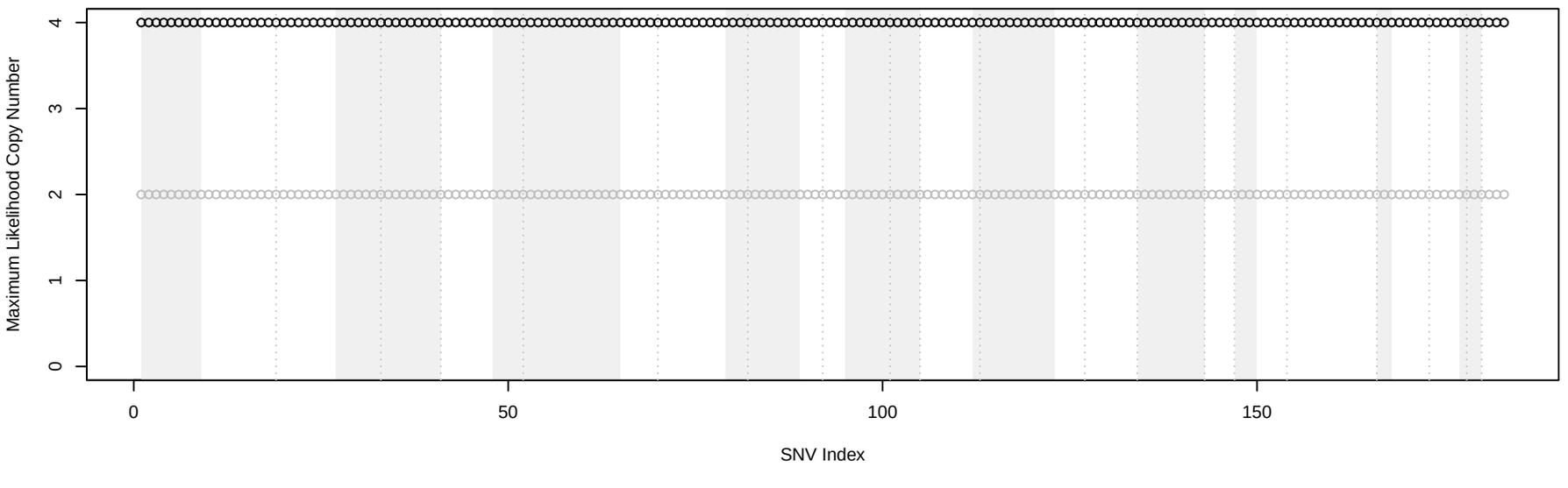

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
4m1
5m1
6m1
7m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

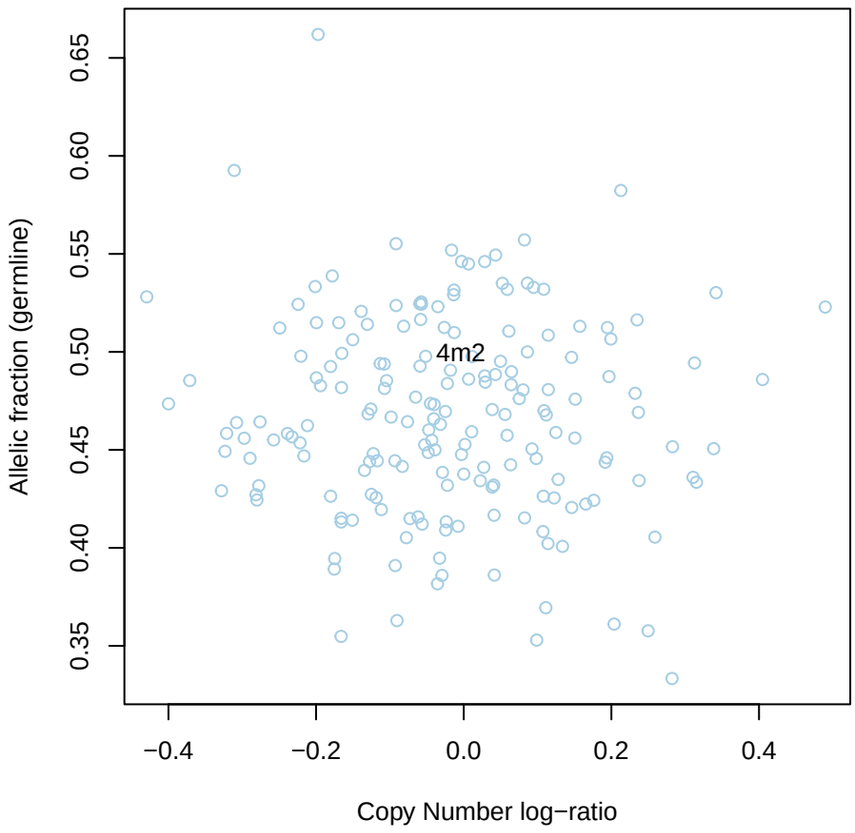

Frequency
0
1
2
3
4
5
6
7
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

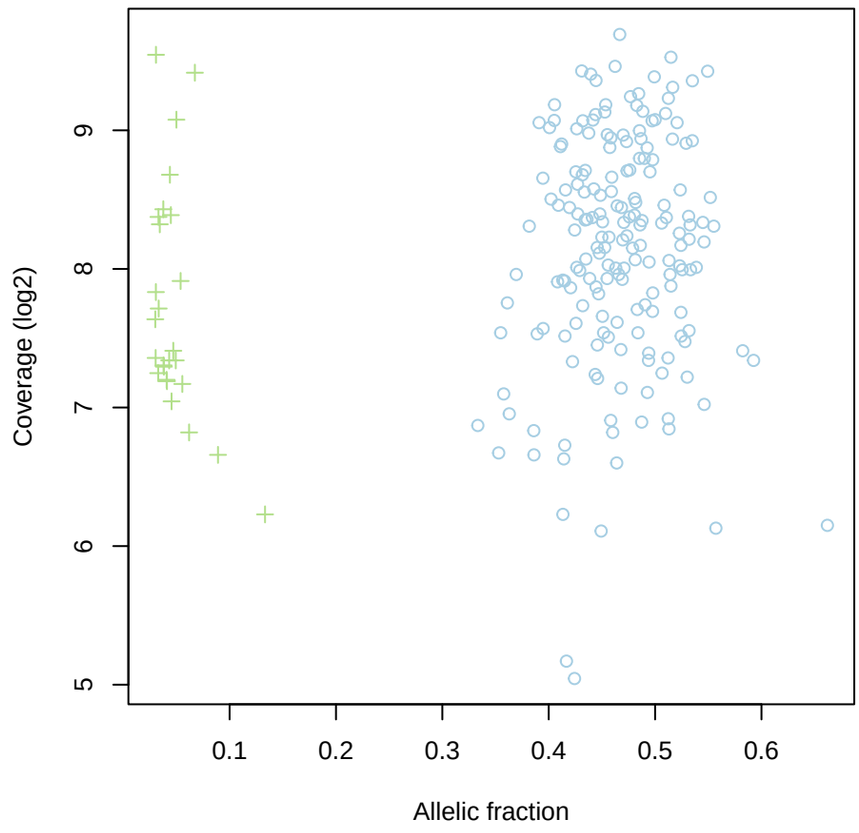

Purity: 0.56 Tumor ploidy: 4.015
2
4
5
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

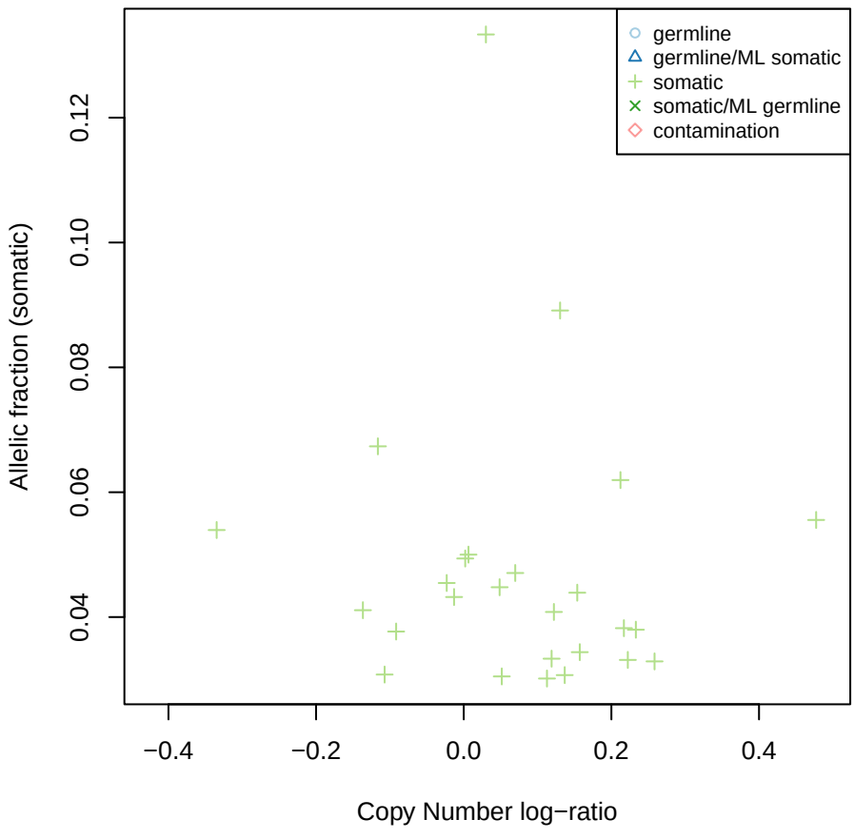

Purity: 0.56 Tumor ploidy: 4.015 SNV log−likelihood: −80.86 GoF: 88% Mean coverage: 317;651
1 2 3 4 5 6 7 8 9 10 11 12 13 14 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 50 100 150
SNV Index

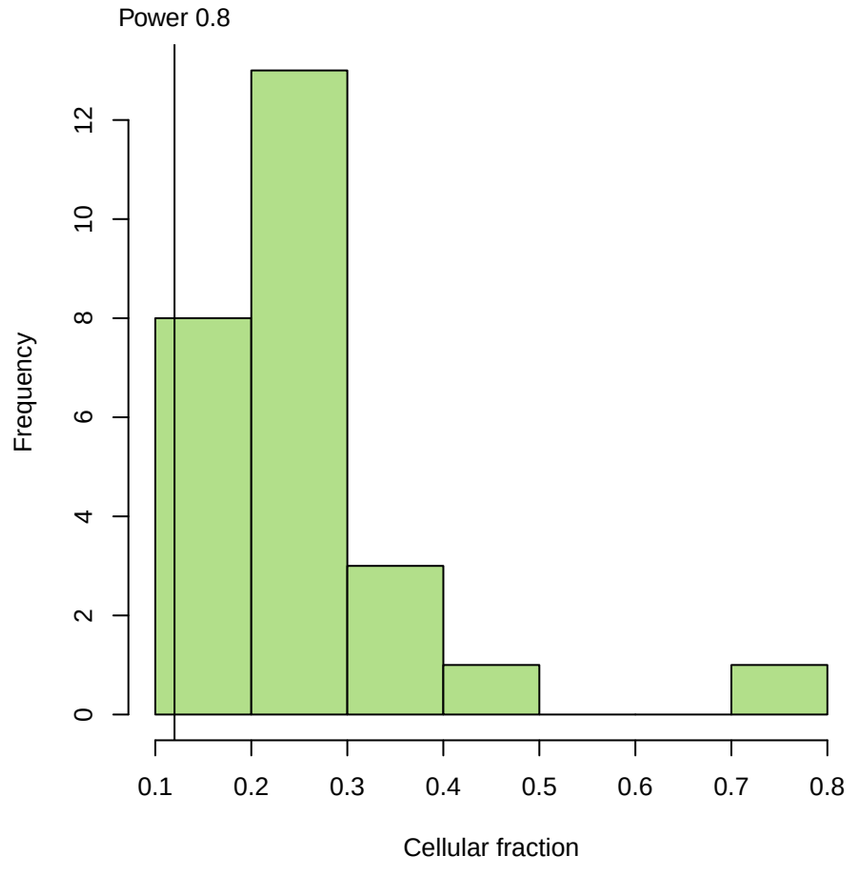

SCNA−fit log−likelihood: −9605.54
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 4 5
0 50 100 150
SNV Index

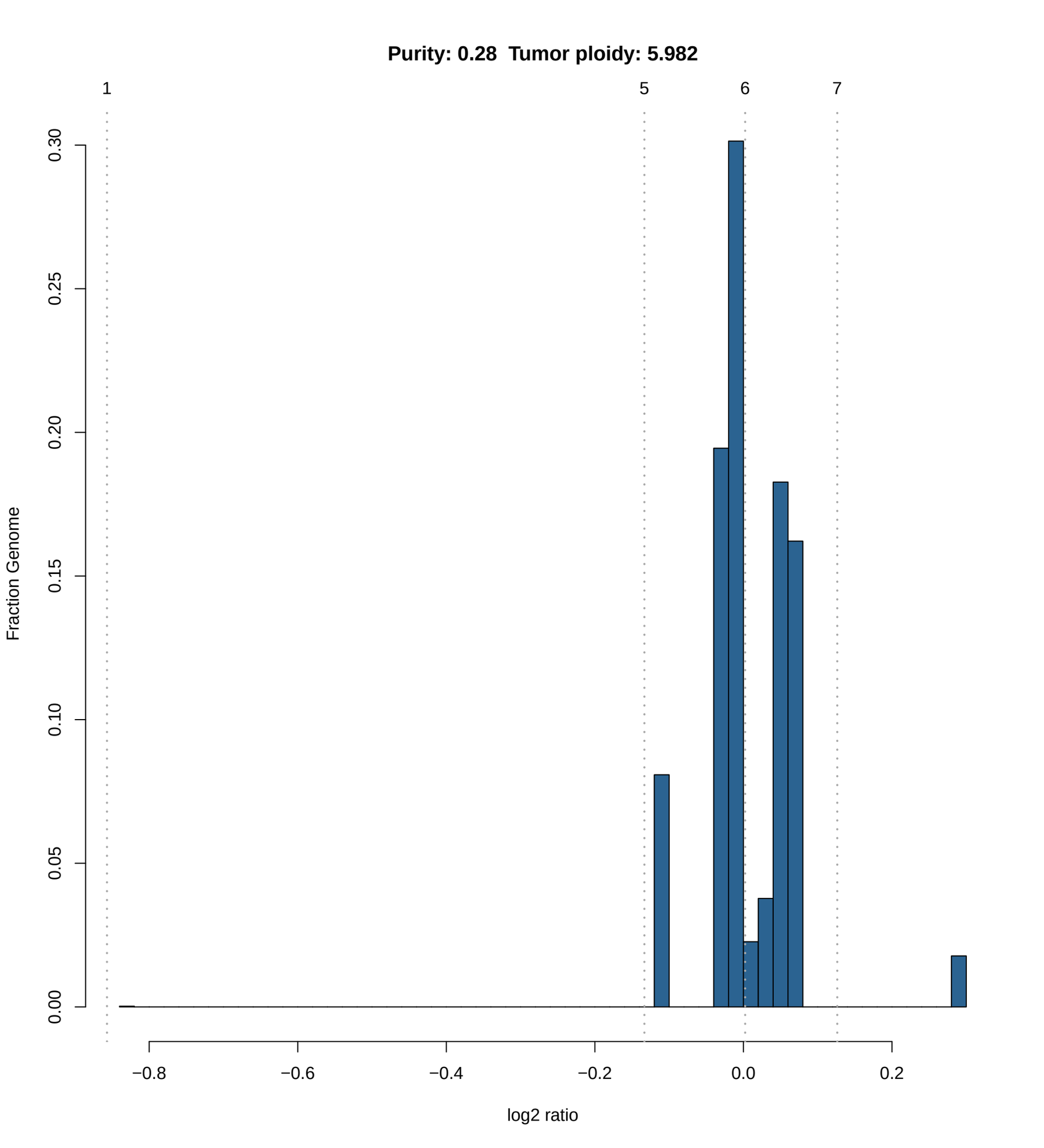

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

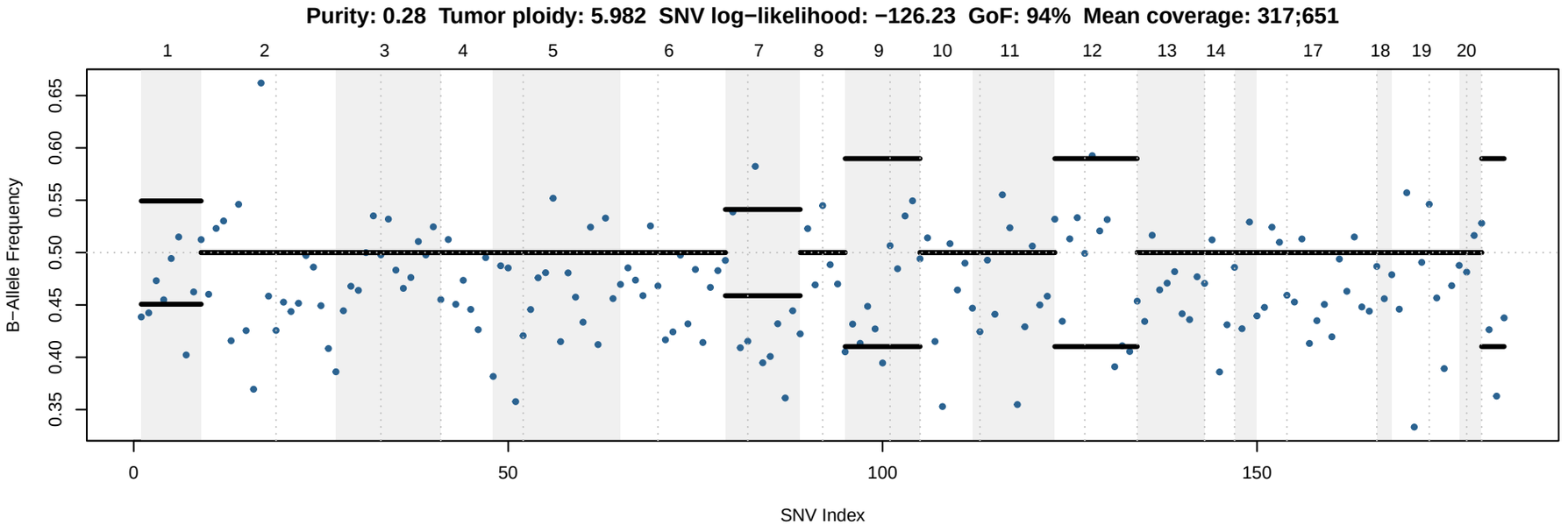

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
4m2
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

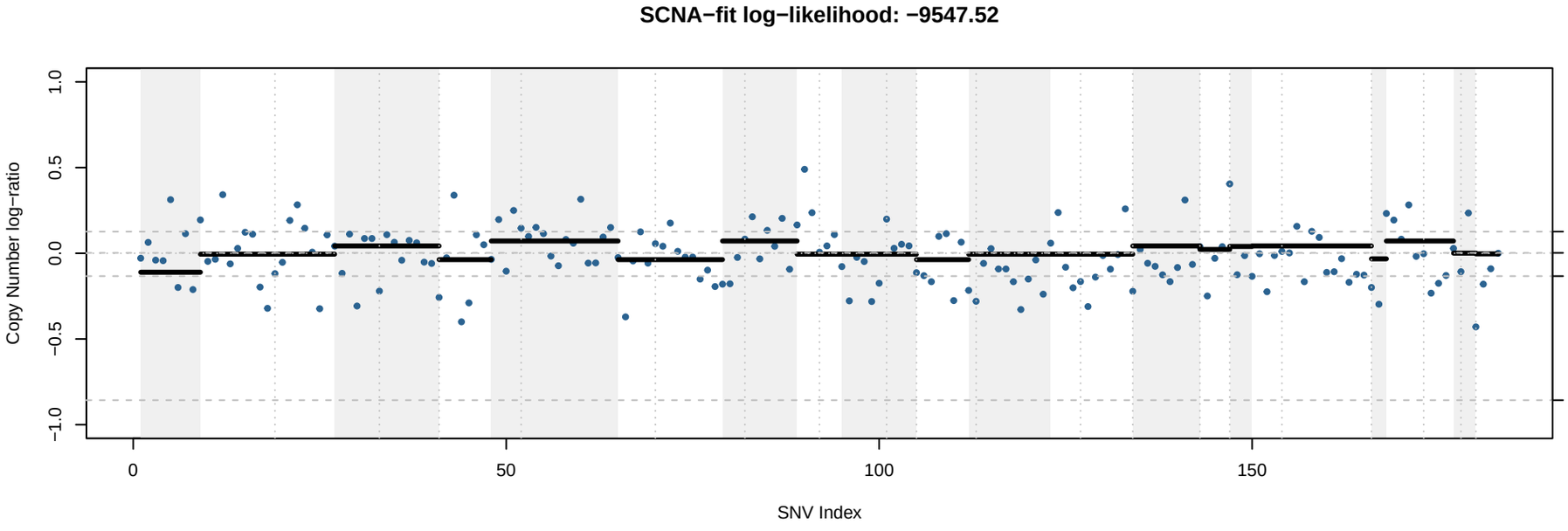

Coverage (log2)
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

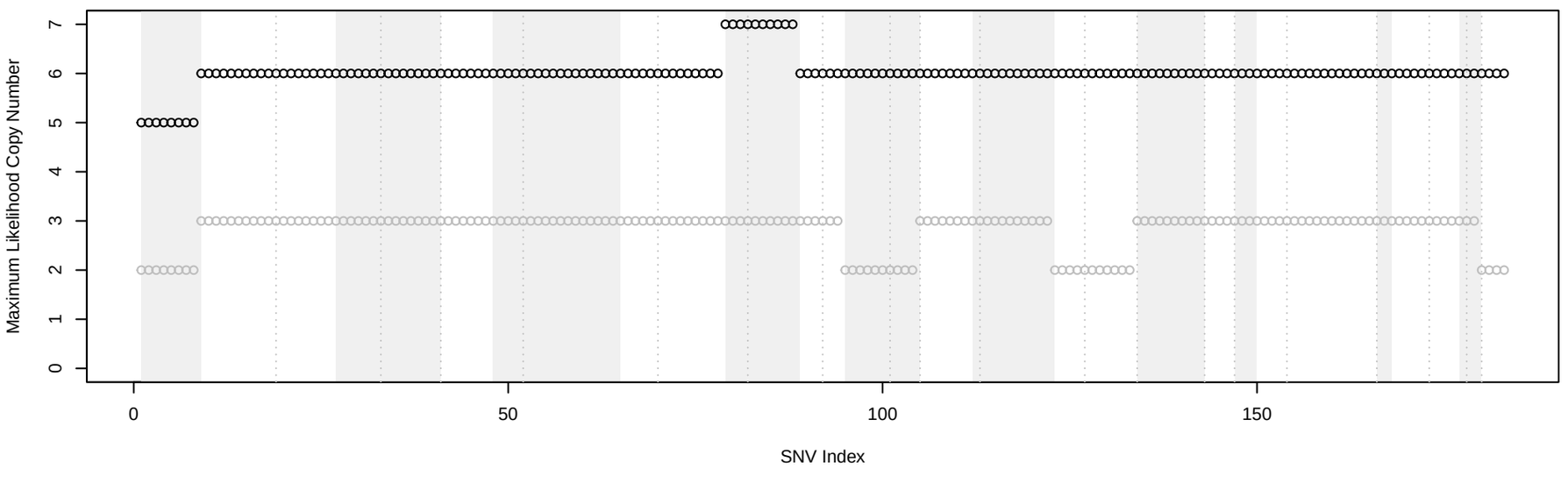

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

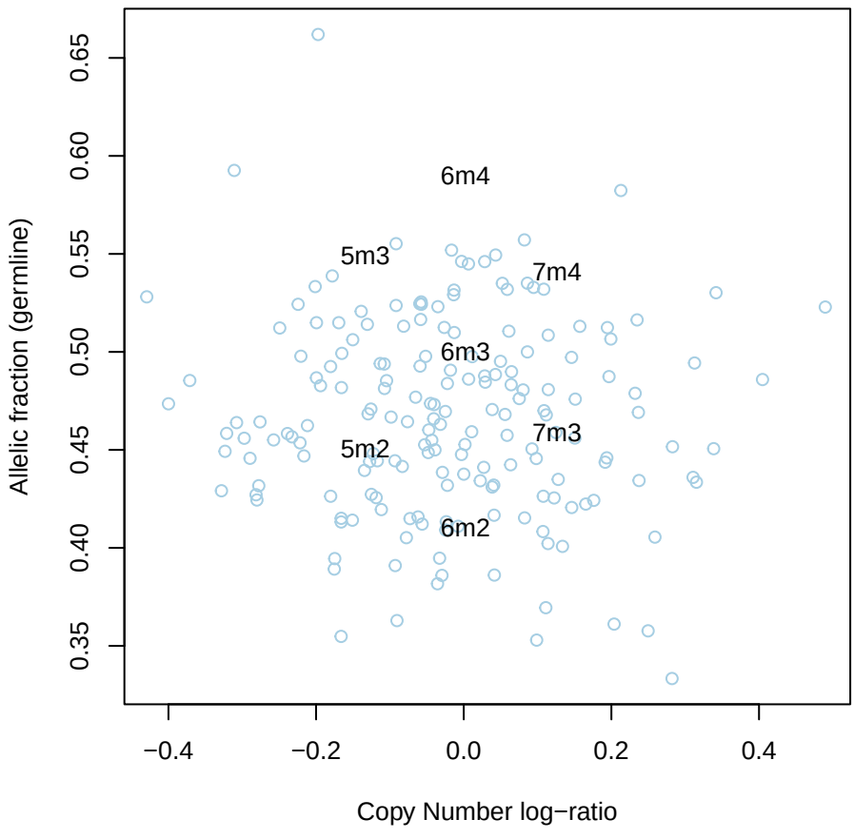

Power 0.8
Frequency
0
2
4
6
8
10
12
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
Cellular fraction

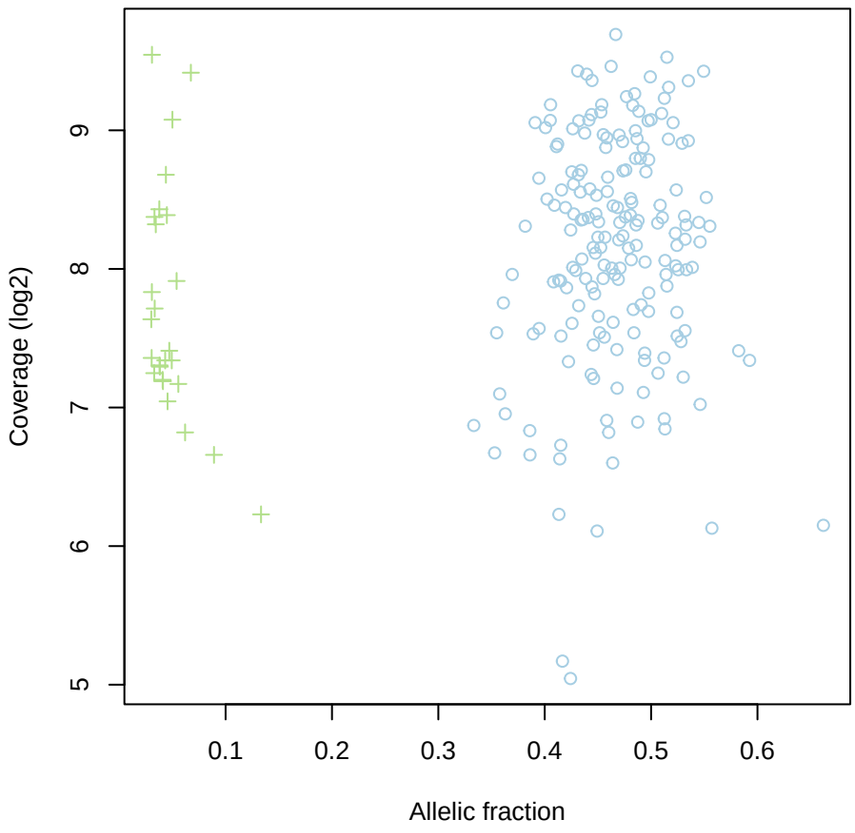

Purity: 0.28 Tumor ploidy: 5.982
1
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

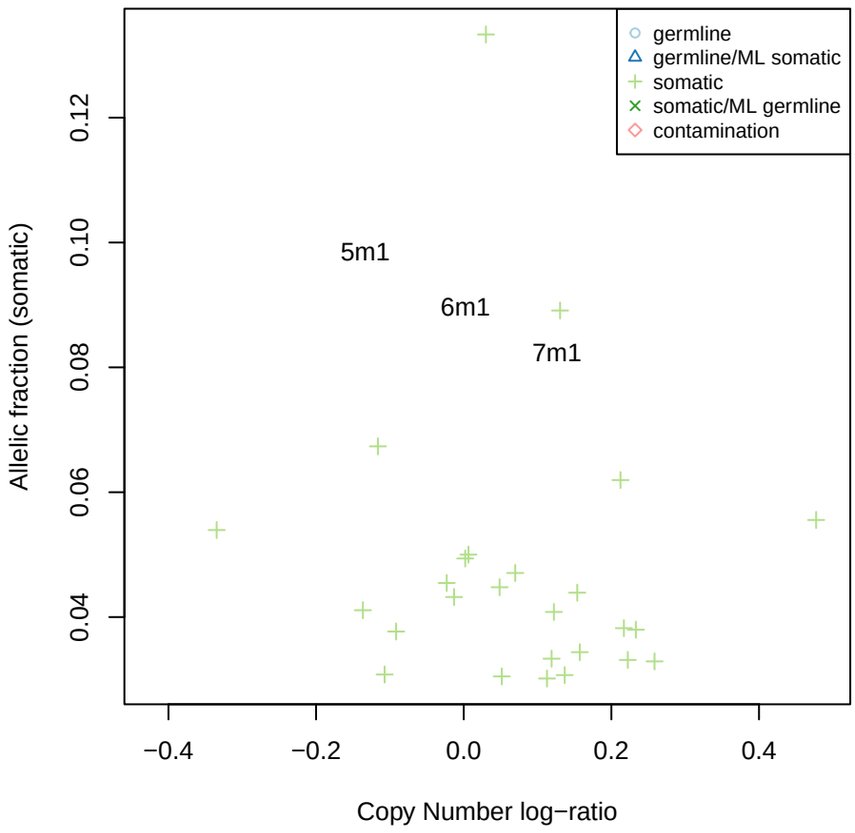

Purity: 0.28 Tumor ploidy: 5.982 SNV log−likelihood: −126.23 GoF: 94% Mean coverage: 317;651
1
2
3
4
5
6
7
8
9
10
11
12
13
14
17
18
19
20
B−Allele Frequency
0.35
0.40
0.45
0.50
0.55
0.60
0.65
0
50
100
150
SNV Index

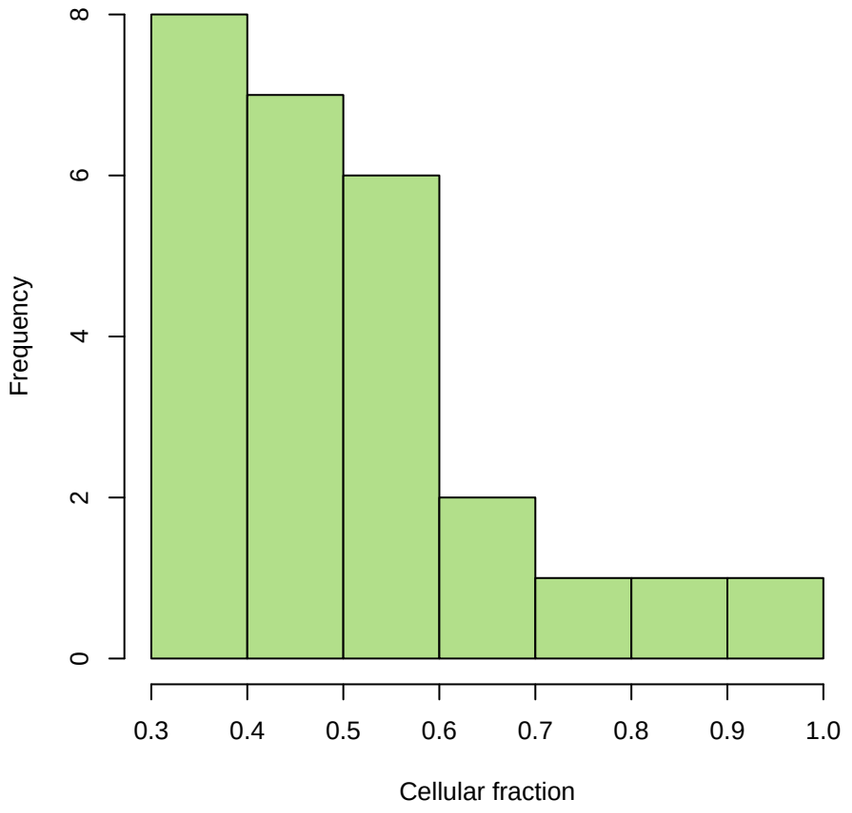

SCNA−fit log−likelihood: −9547.52
Copy Number log−ratio
1.0
0.5
0.0
−0.5
−1.0
7
5
1
0
50
100
150
SNV Index

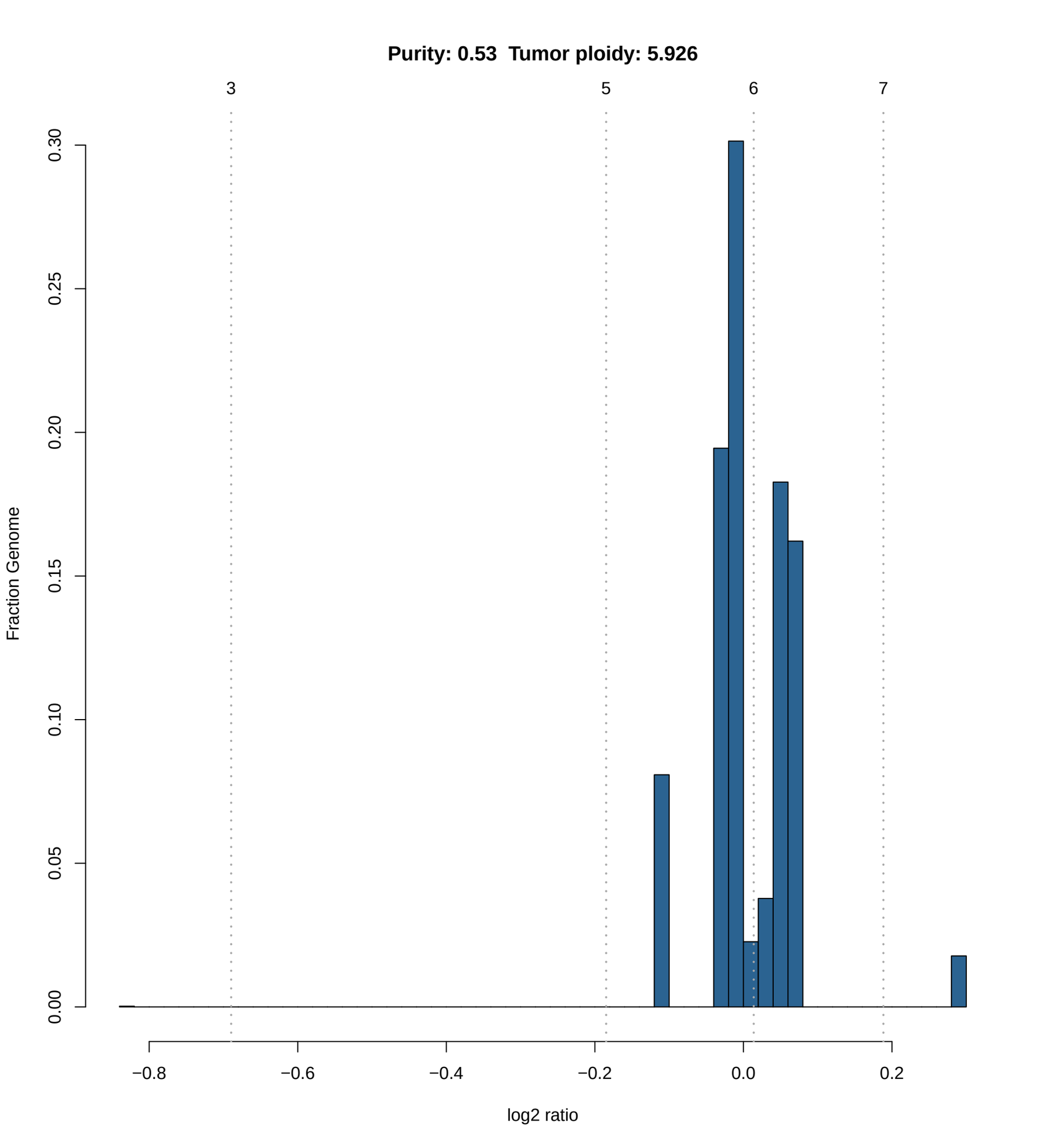

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
7
0
50
100
150
SNV Index

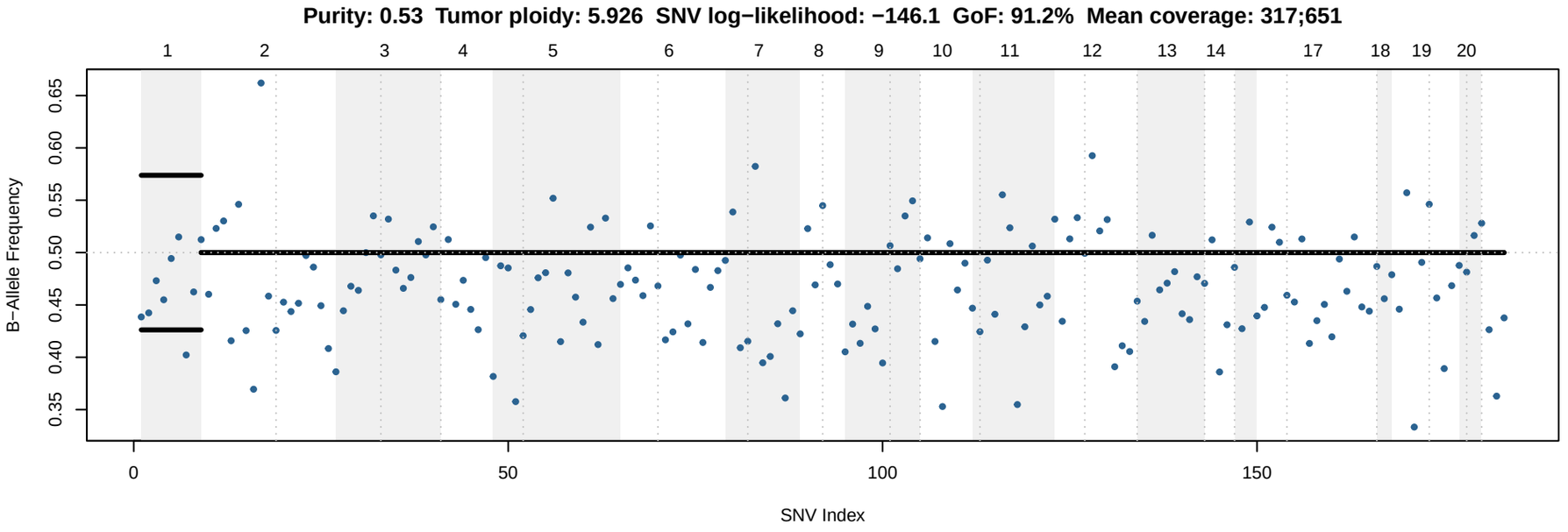

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
6m4
5m3
7m4
6m3
7m3
5m2
6m2
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

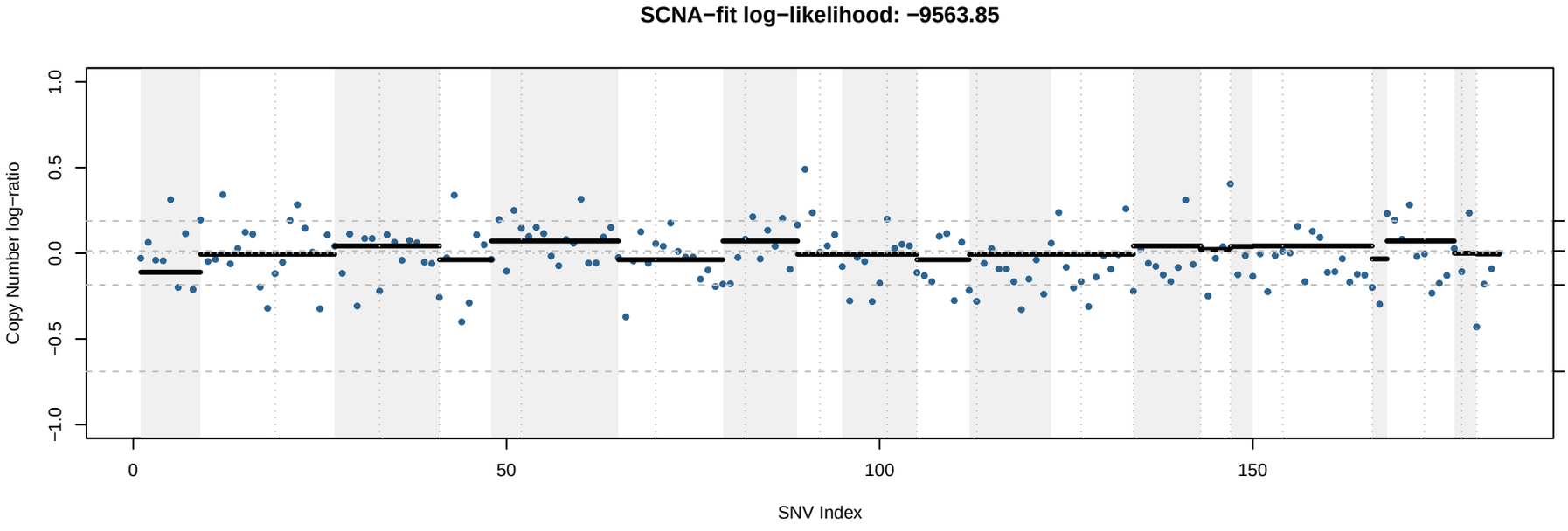

Coverage (log2)
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

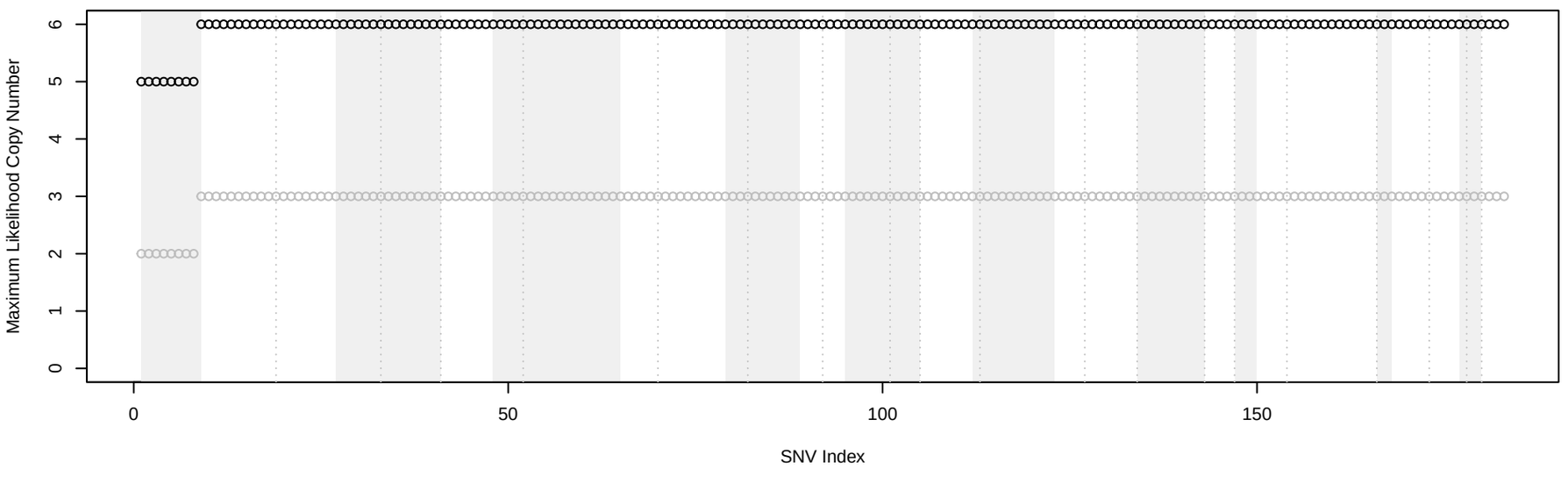

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
5m1
6m1
7m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

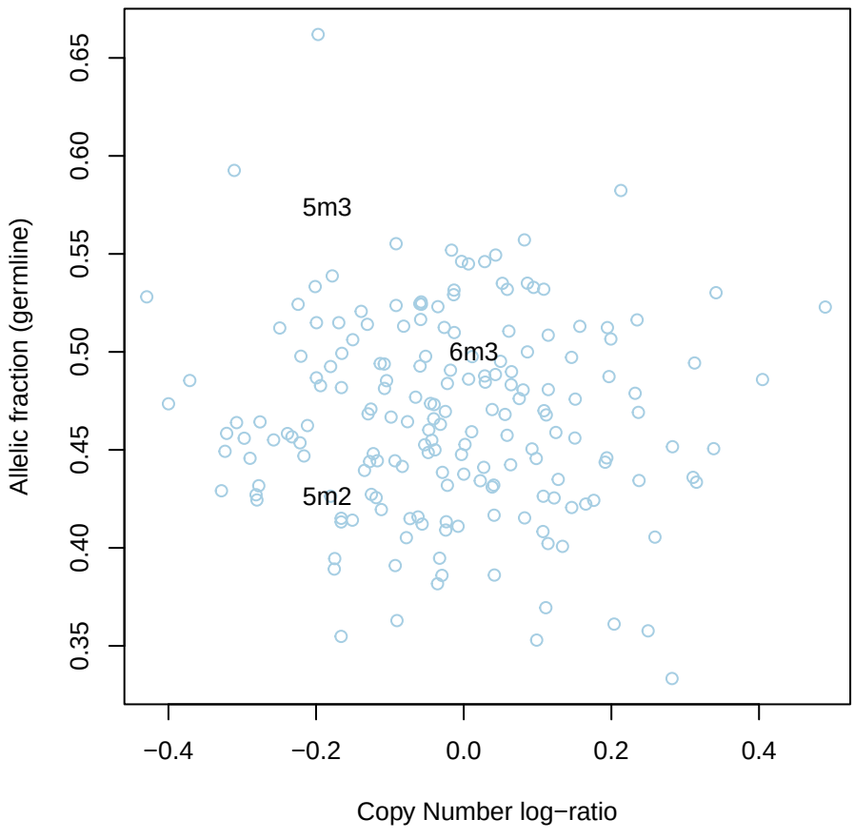

Frequency
0
2
4
6
8
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

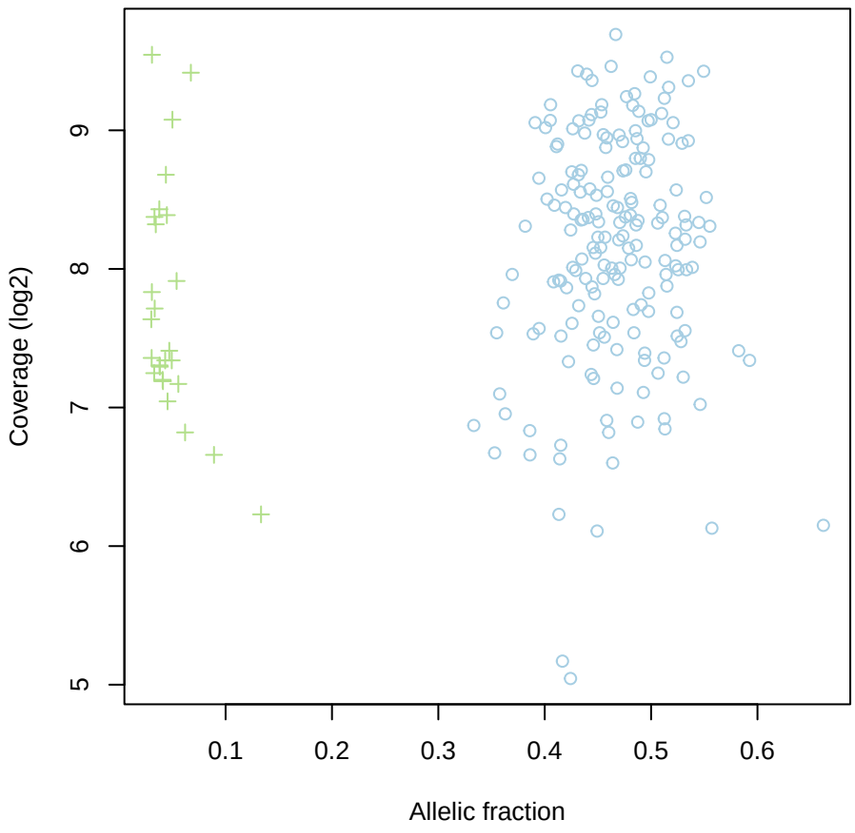

Purity: 0.53 Tumor ploidy: 5.926
3
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

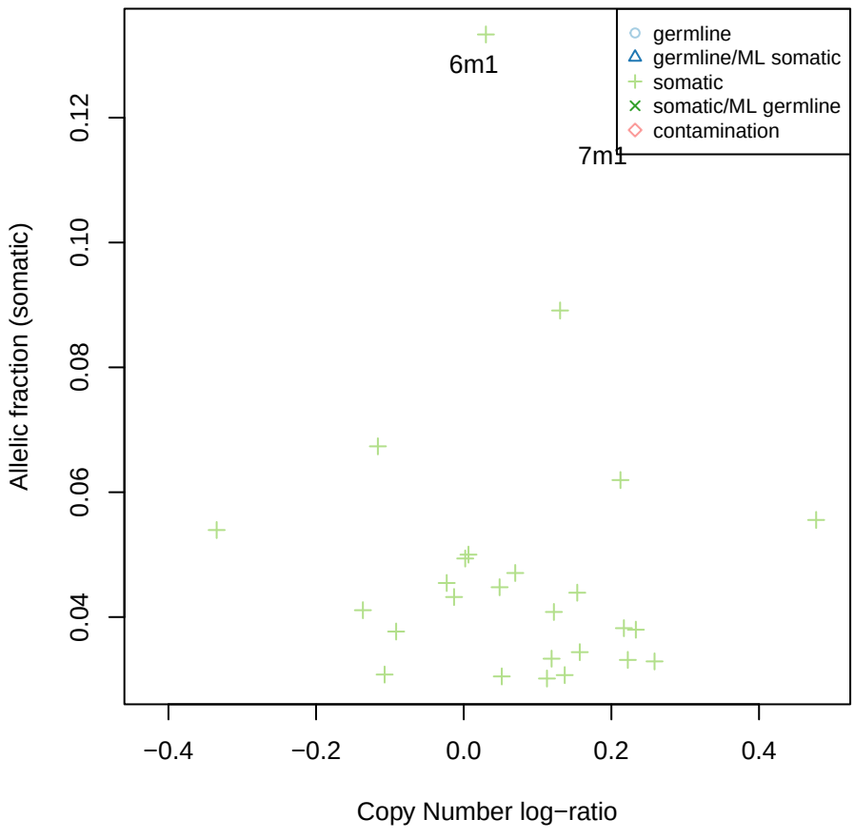

Purity: 0.53 Tumor ploidy: 5.926 SNV log−likelihood: −146.1 GoF: 91.2% Mean coverage: 317;651
1 2 3 4 5 6 7 8 9 10 11 12 13 14 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 50 100 150
SNV Index

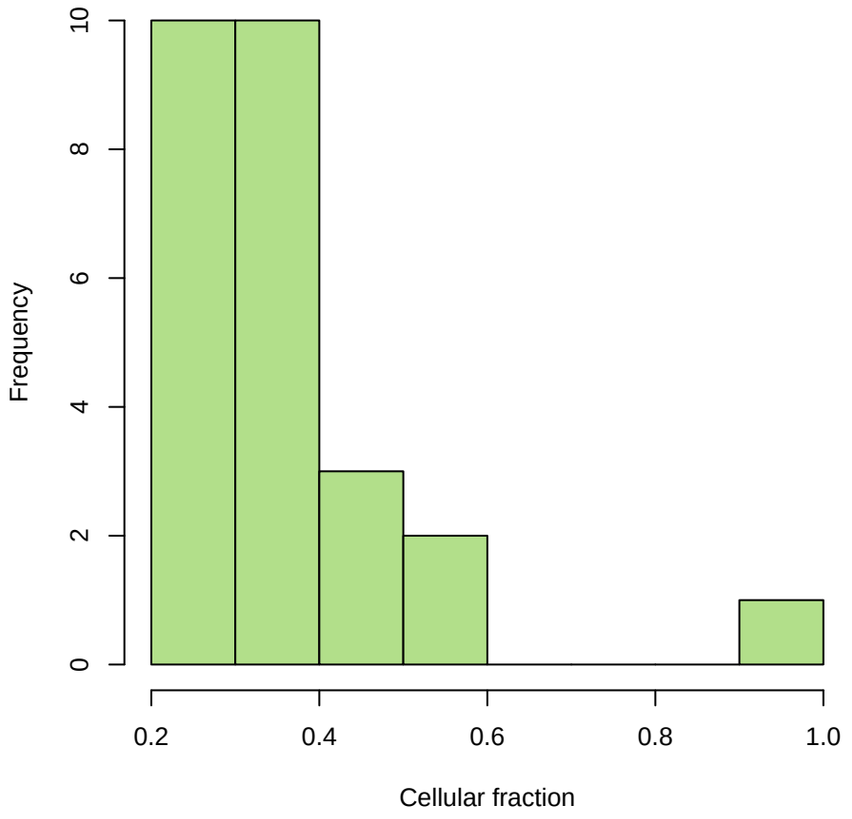

SCNA−fit log−likelihood: −9563.85
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
7 6 5 3
0 50 100 150
SNV Index

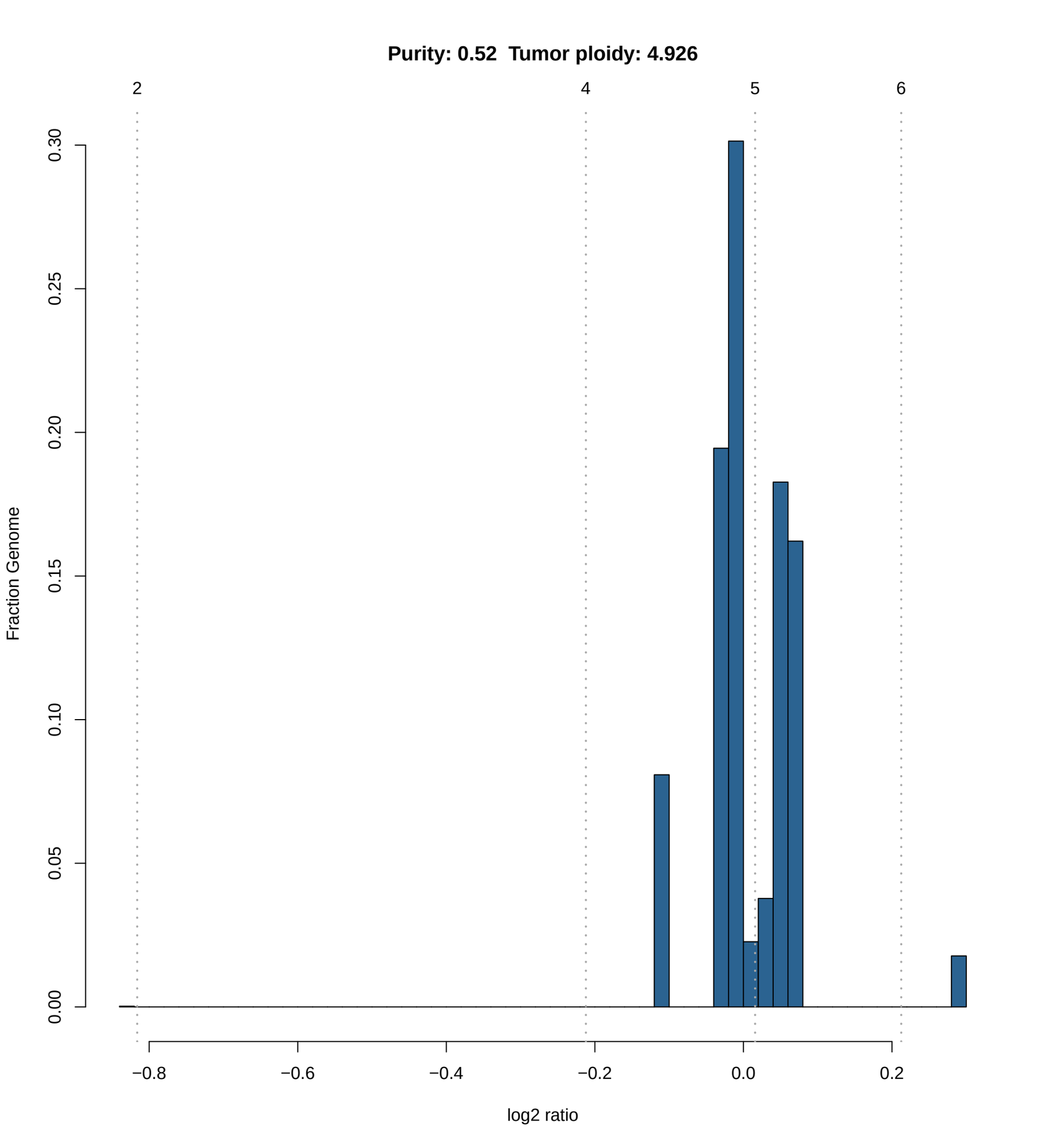

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

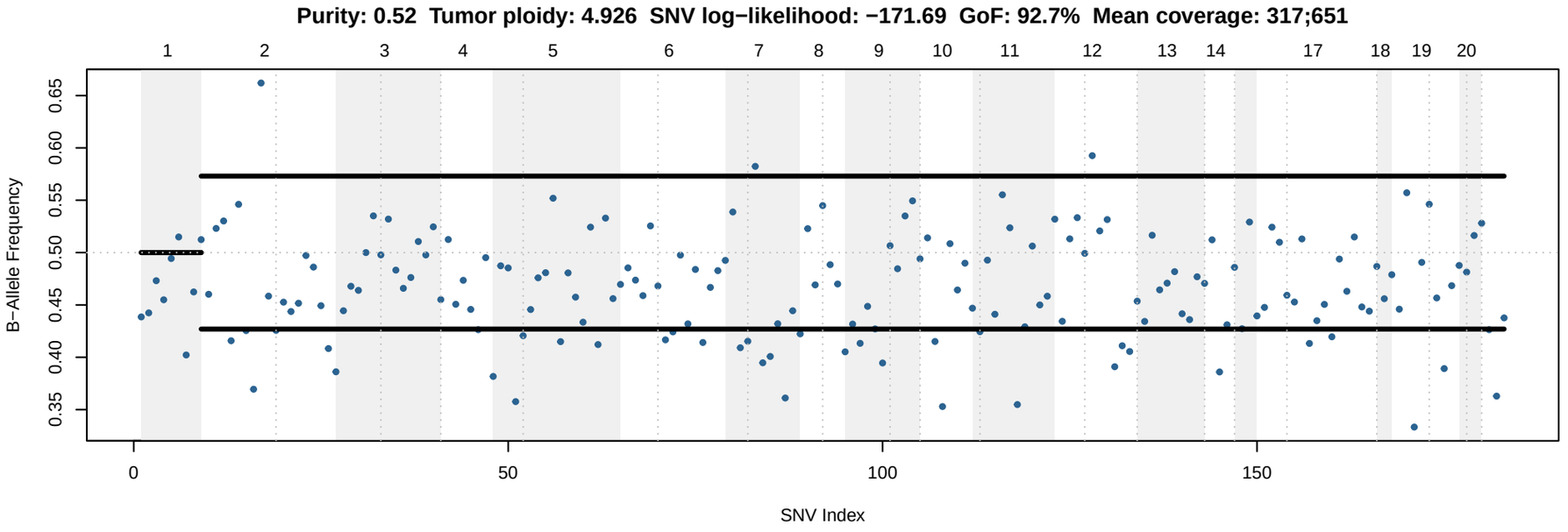

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
5m3
6m3
5m2
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

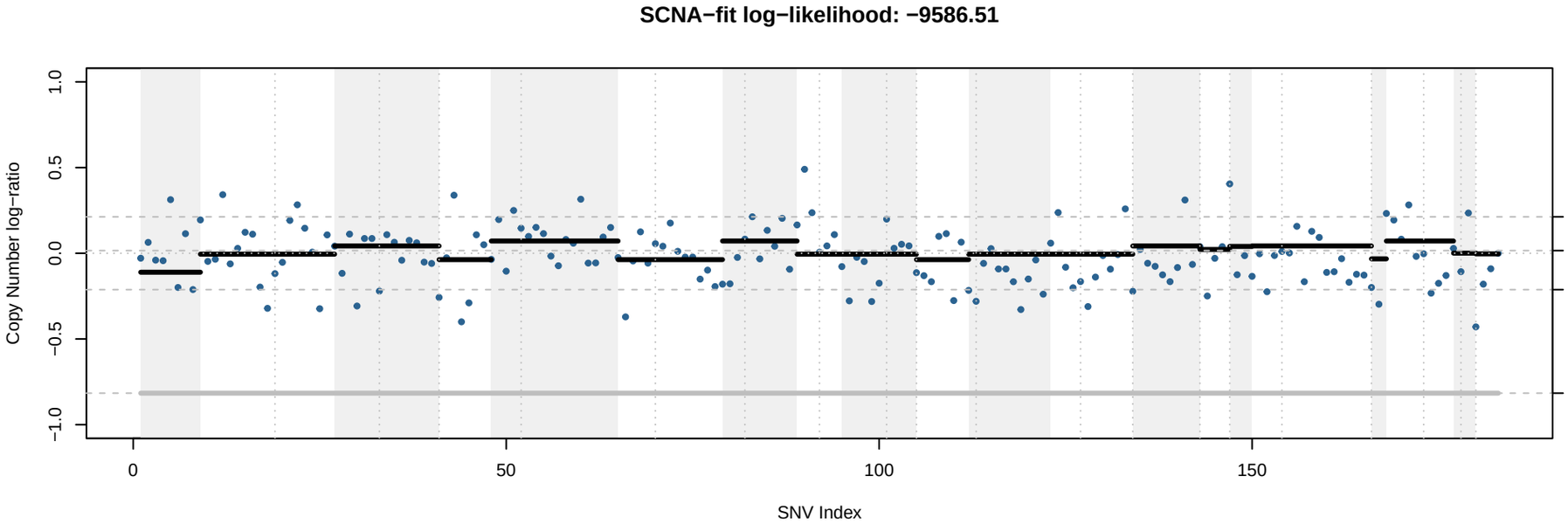

Coverage (log2)
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

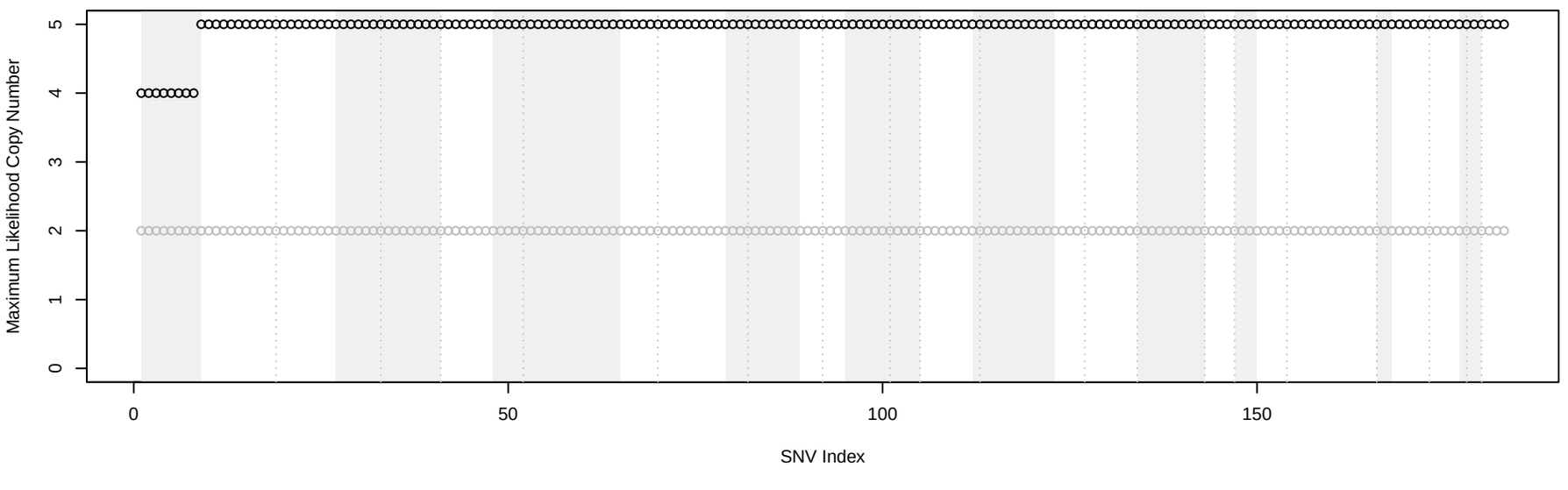

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m1
7m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

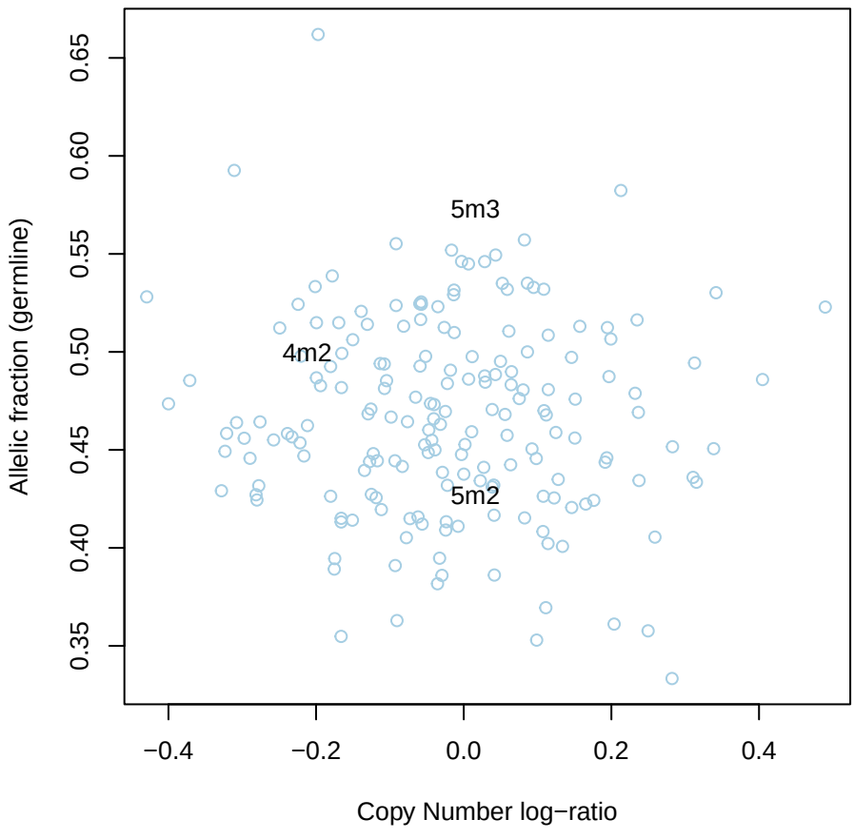

Frequency
0
2
4
6
8
10
0.2
0.4
0.6
0.8
1.0
Cellular fraction

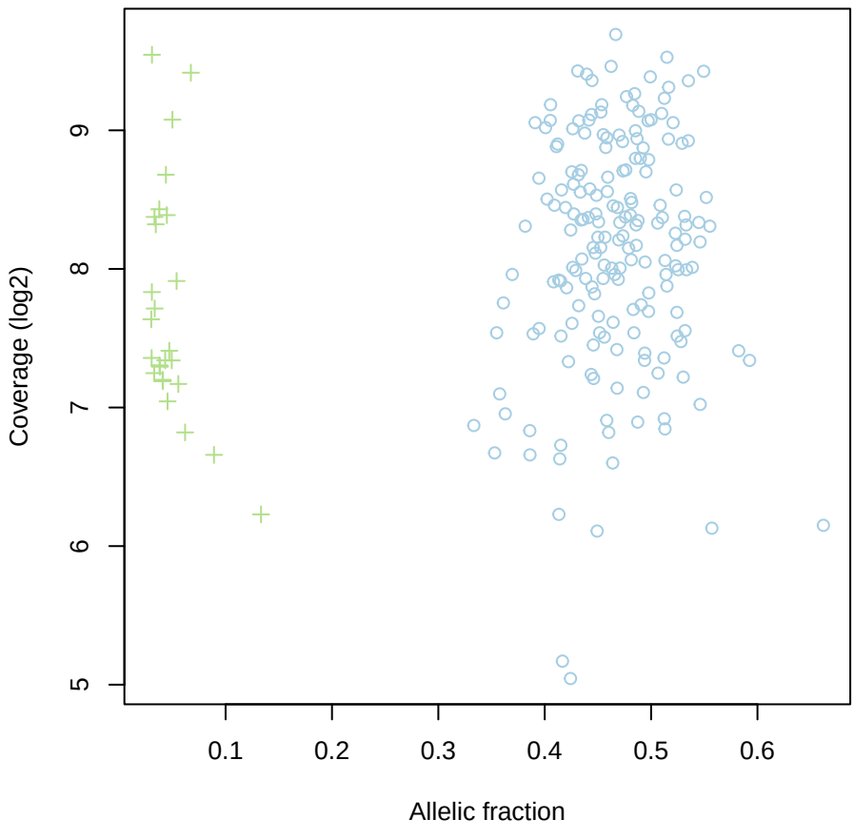

Purity: 0.52 Tumor ploidy: 4.926
2
4
5
6
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

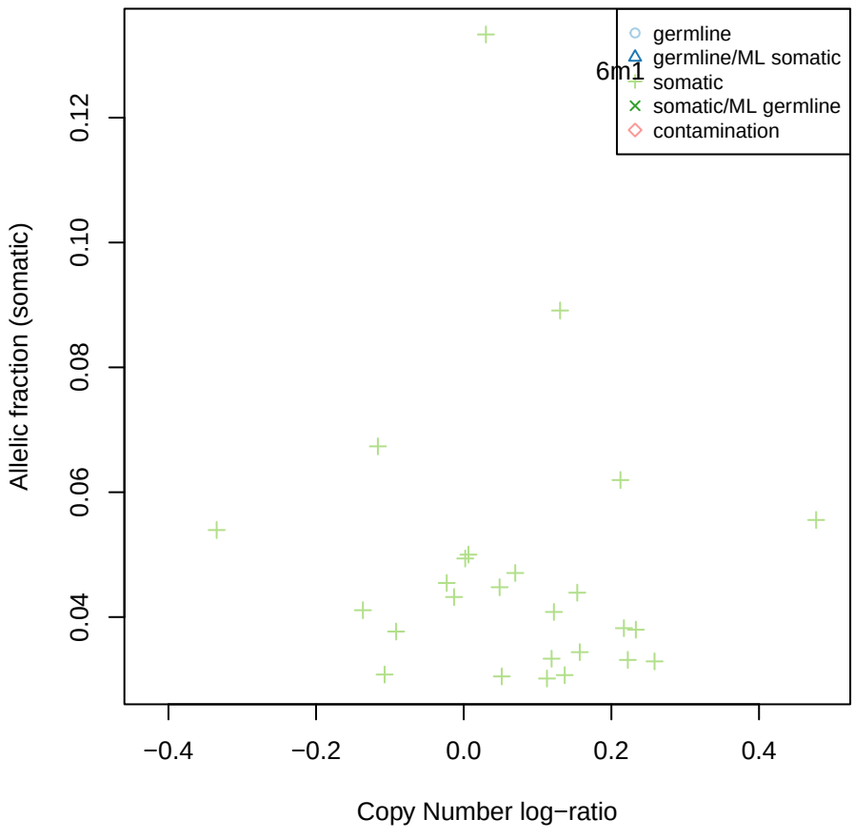

Purity: 0.52 Tumor ploidy: 4.926 SNV log−likelihood: −171.69 GoF: 92.7% Mean coverage: 317;651
1
2
3
4
5
6
7
8
9
10
11
12
13
14
17
18
19
20
B−Allele Frequency
0.35
0.40
0.45
0.50
0.55
0.60
0.65
0
50
100
150
SNV Index

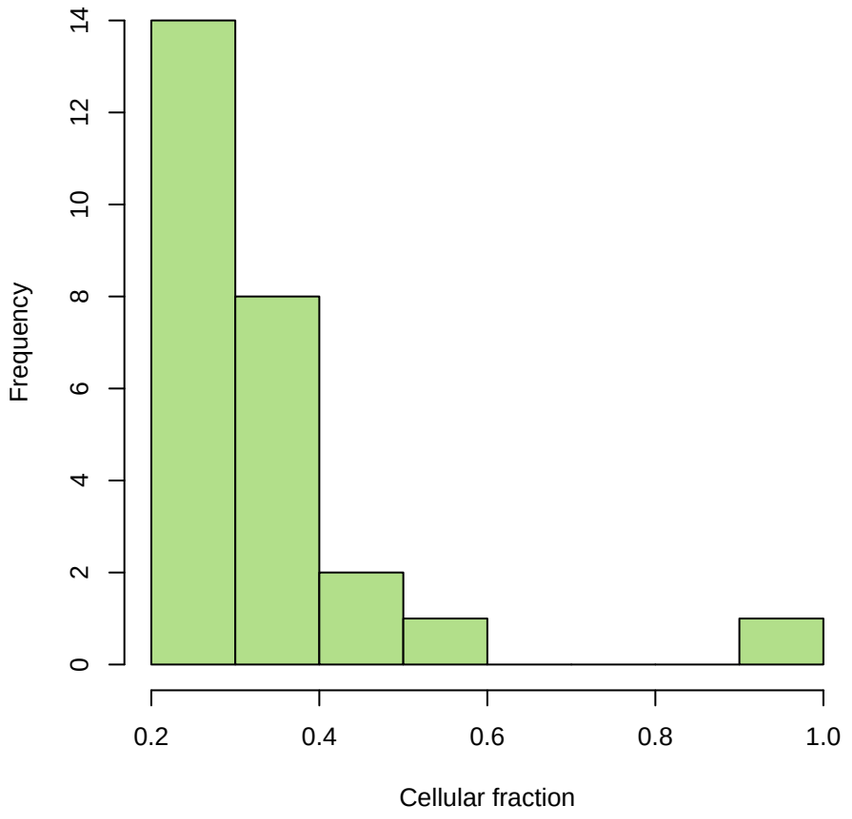

SCNA−fit log−likelihood: −9586.51
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
2
4
5
6
0
50
100
150
SNV Index

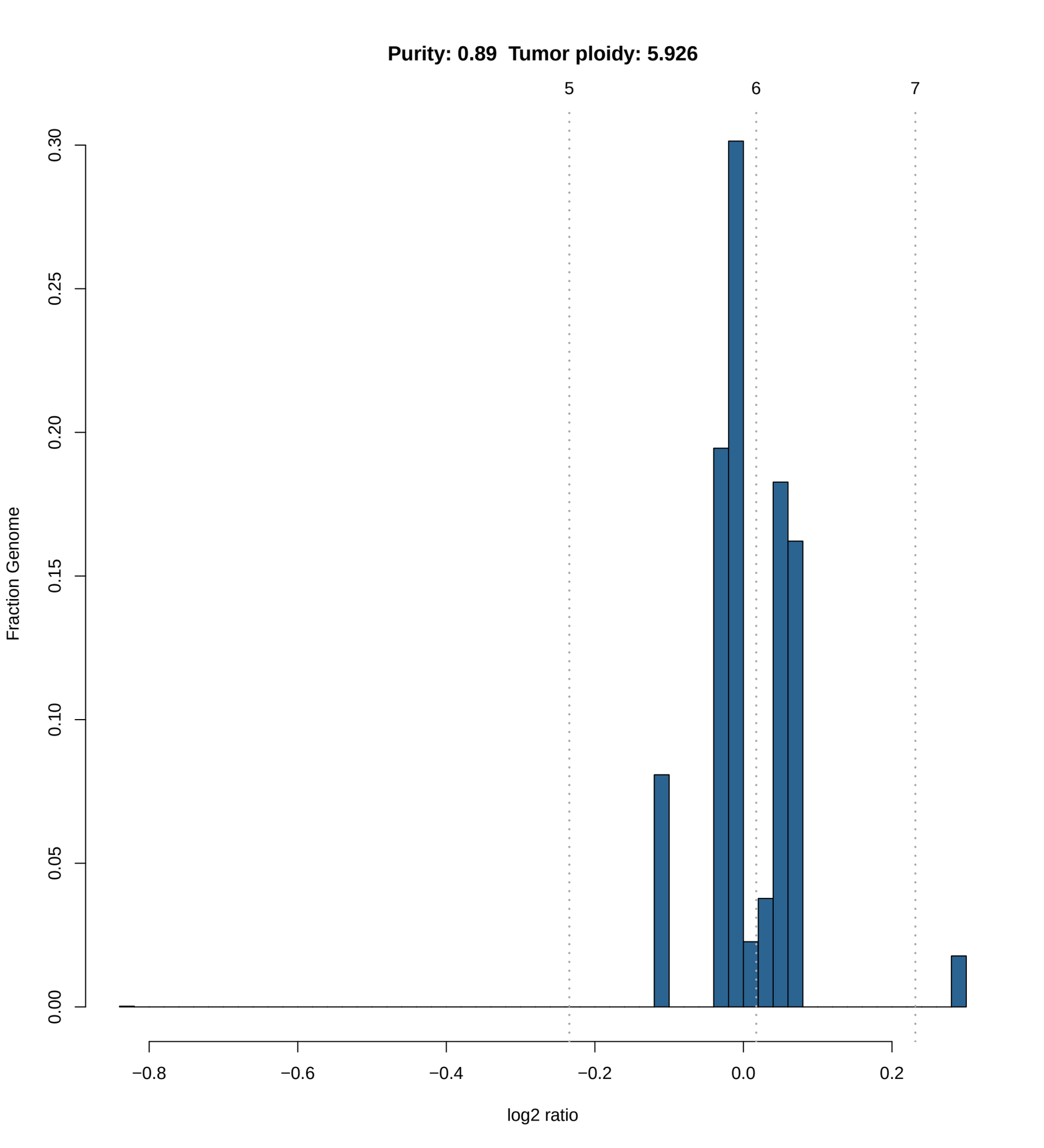

Maximum Likelihood Copy Number
0
1
2
3
4
5
0
50
100
150
SNV Index

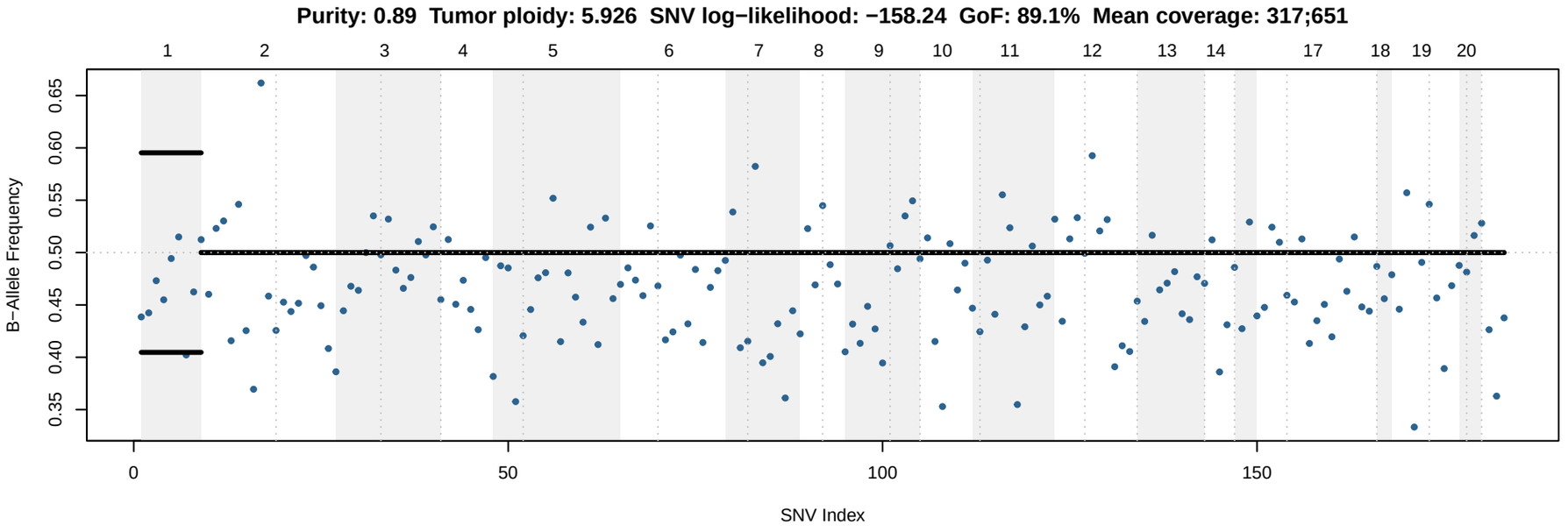

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
5m3
4m2
5m2
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

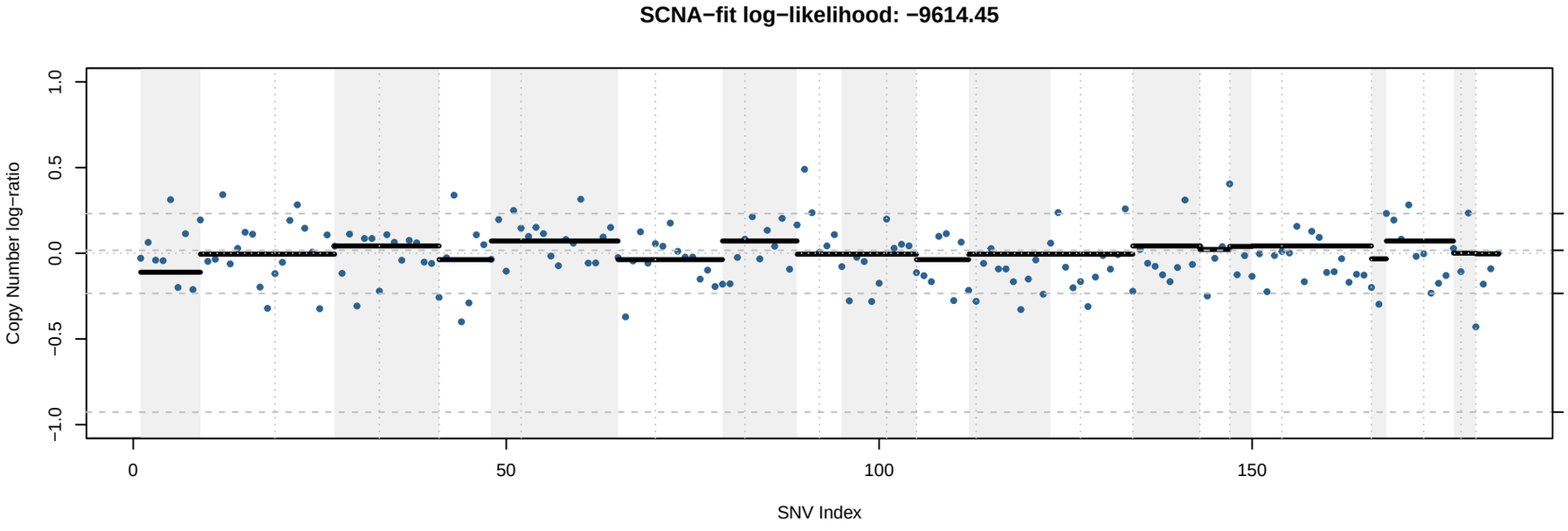

Coverage (log2)
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

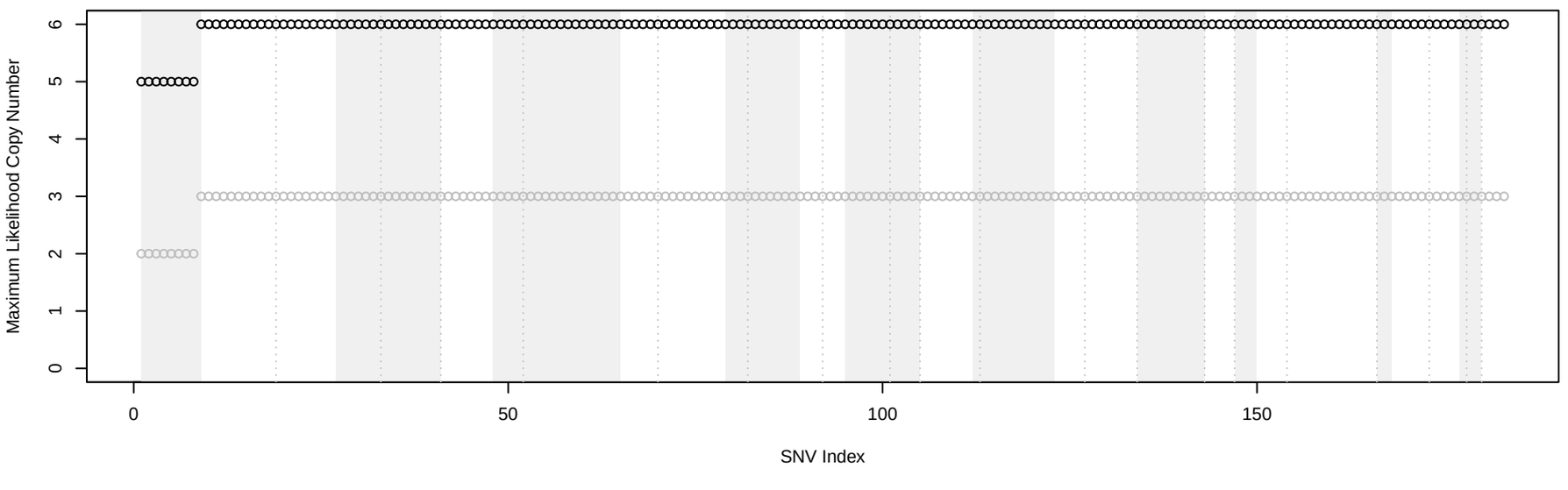

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m1
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

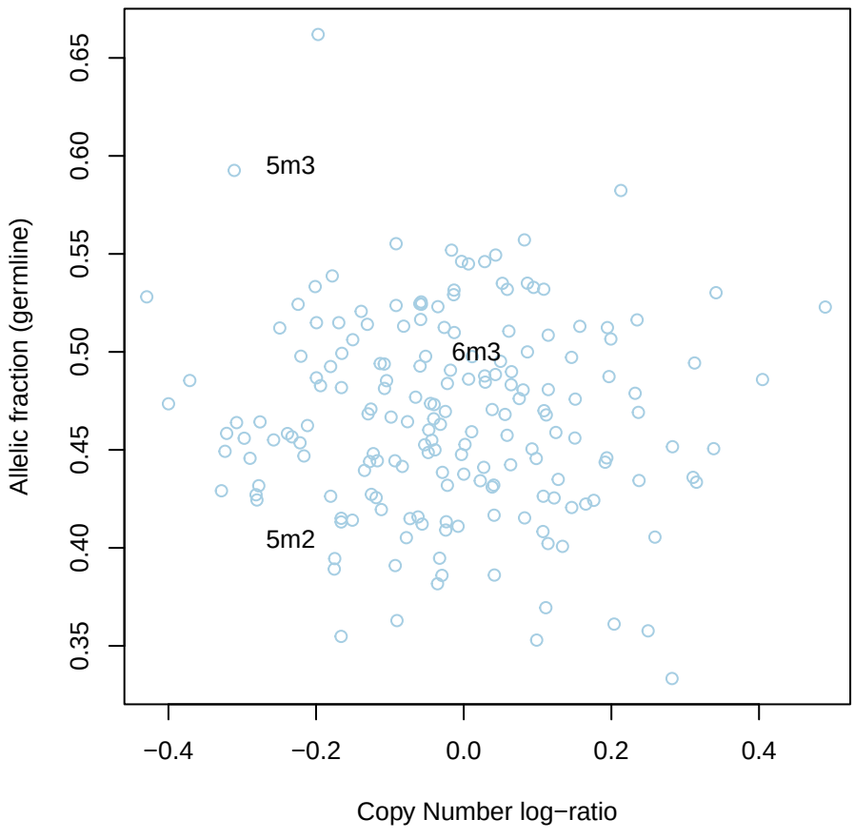

Frequency
0
2
4
6
8
10
12
14
0.2
0.4
0.6
0.8
1.0
Cellular fraction

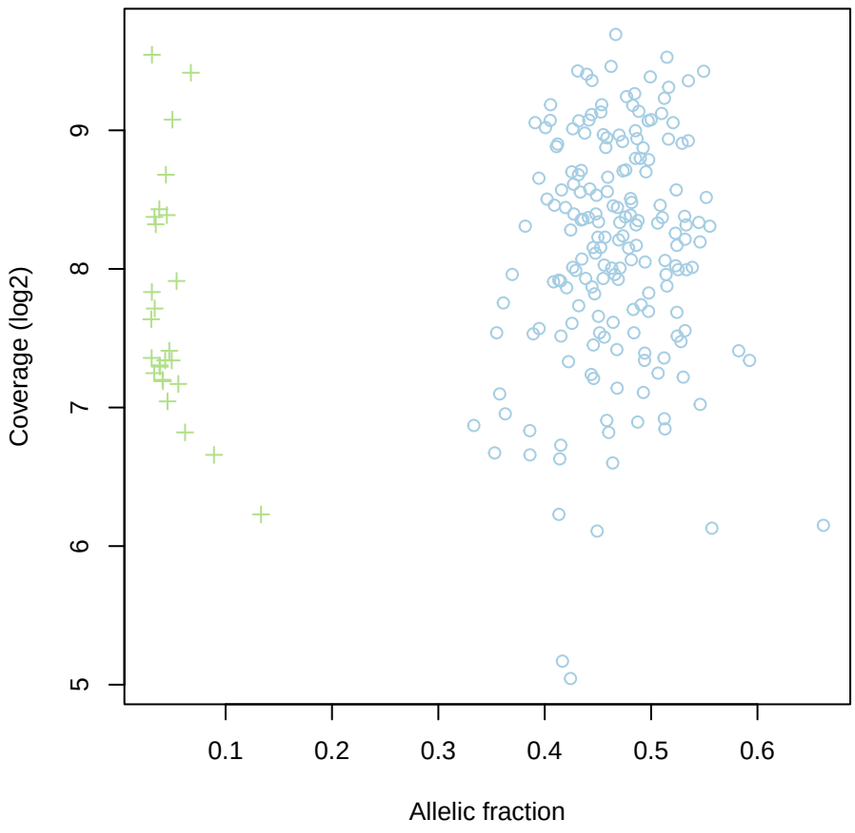

Purity: 0.89 Tumor ploidy: 5.926
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

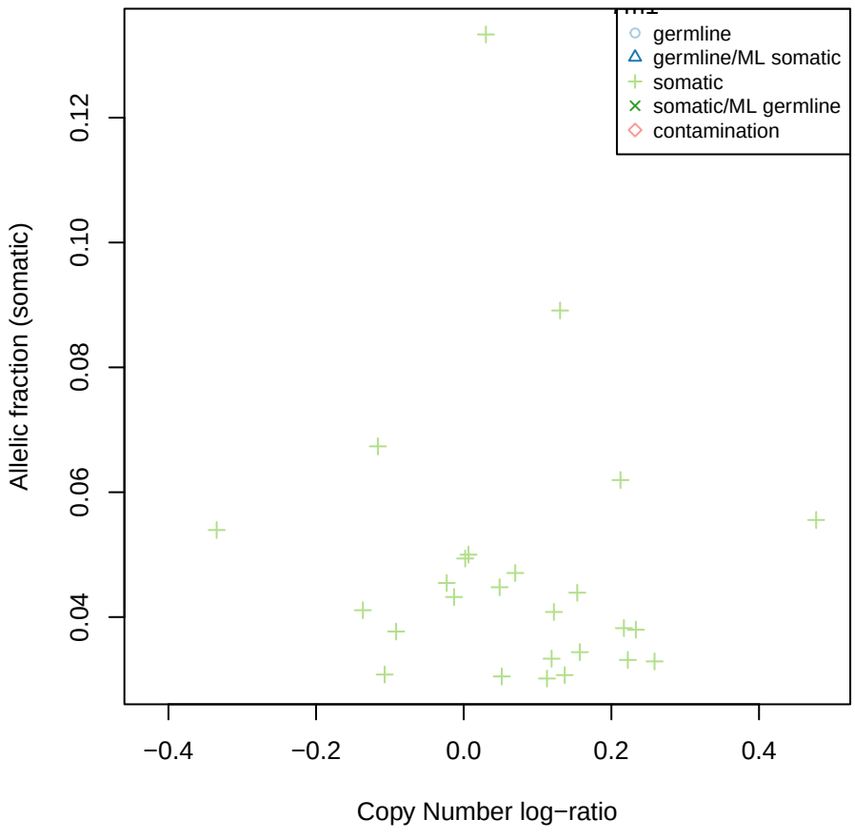

Purity: 0.89 Tumor ploidy: 5.926 SNV log−likelihood: −158.24 GoF: 89.1% Mean coverage: 317;651
1 2 3 4 5 6 7 8 9 10 11 12 13 14 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 50 100 150
SNV Index

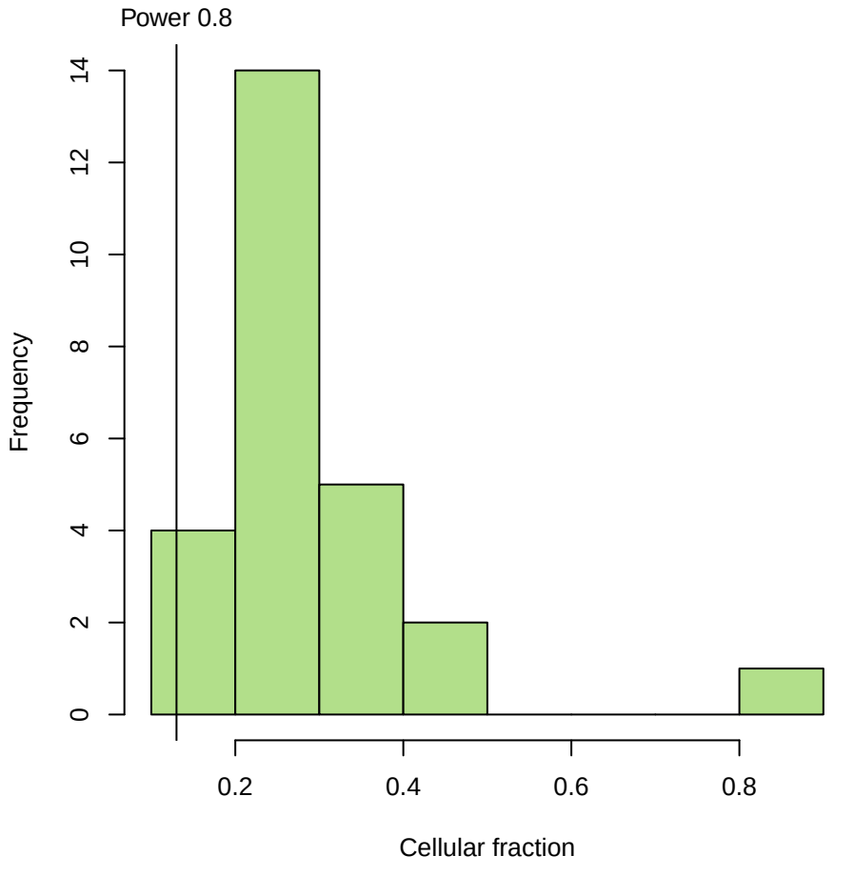

SCNA−fit log−likelihood: −9614.45
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 5 6 7
0 50 100 150
SNV Index

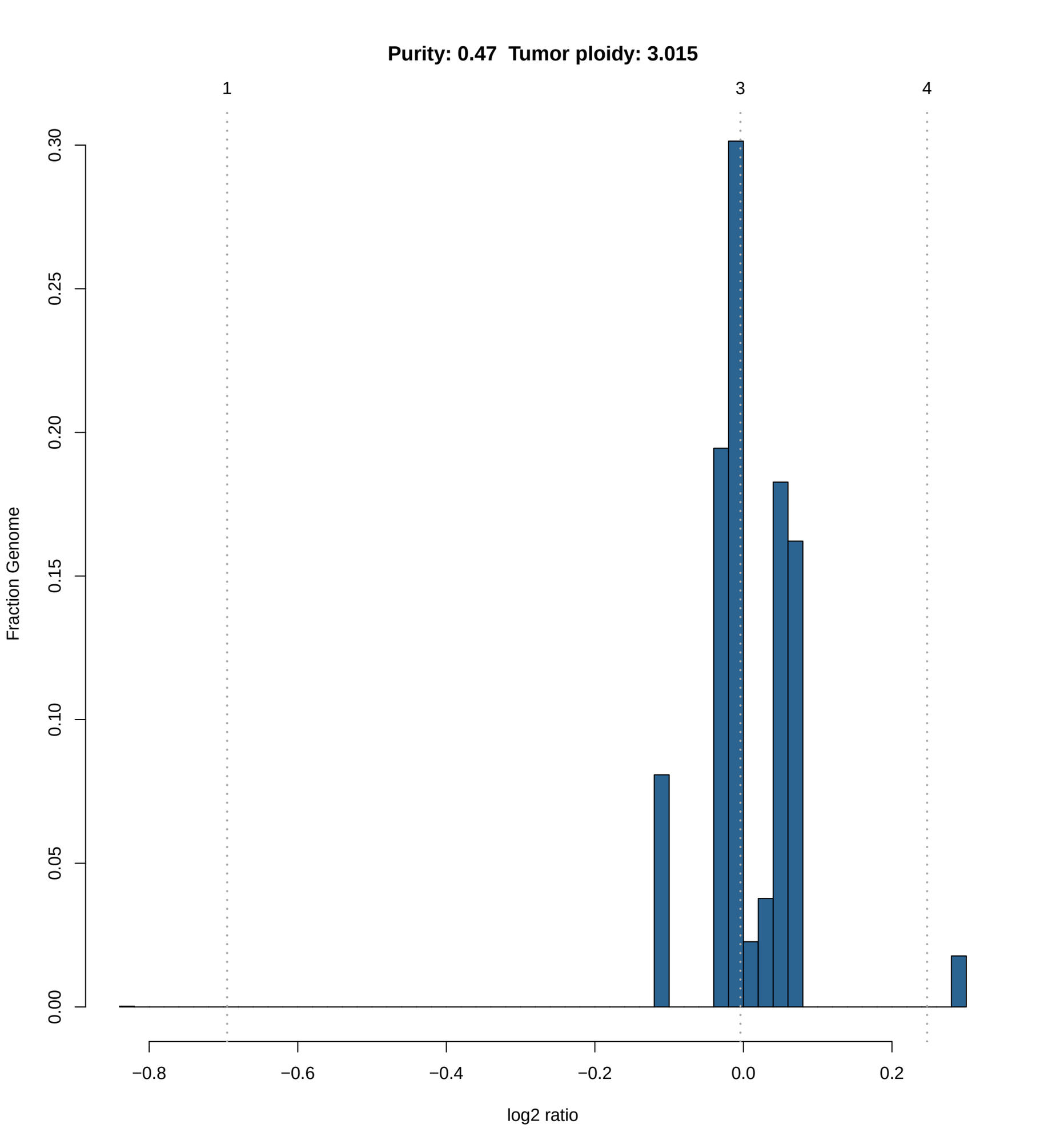

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

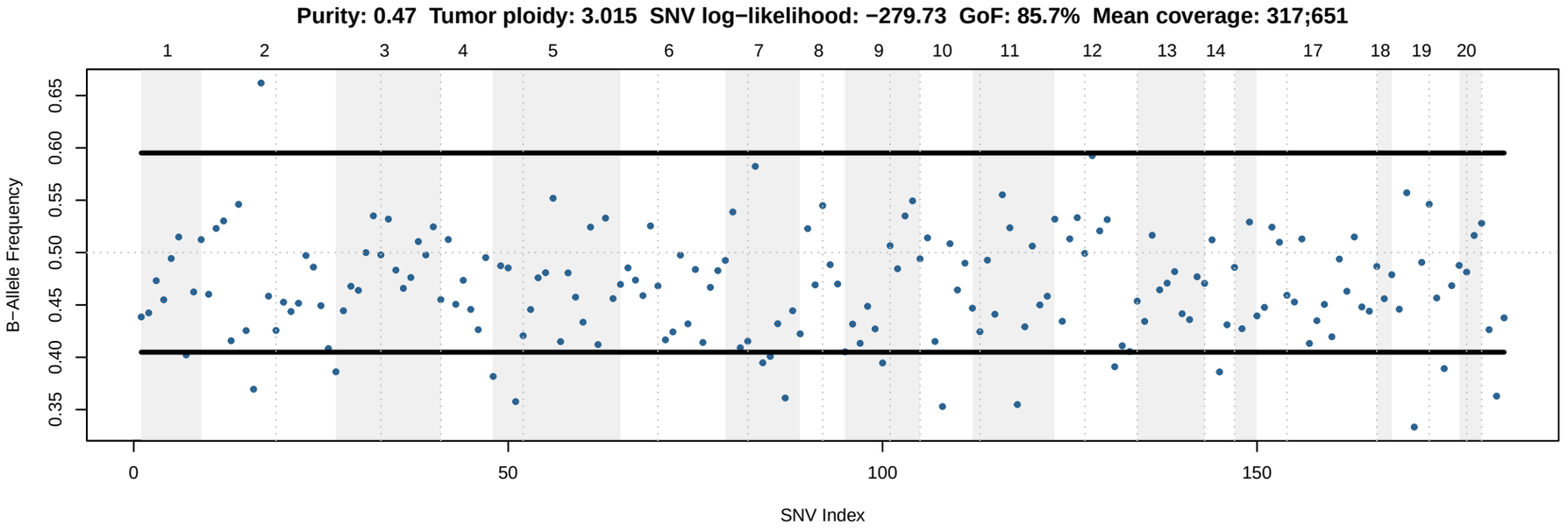

Allelic fraction (germline)
0.35
0.40
0.45
0.50
0.55
0.60
0.65
5m3
6m3
5m2
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

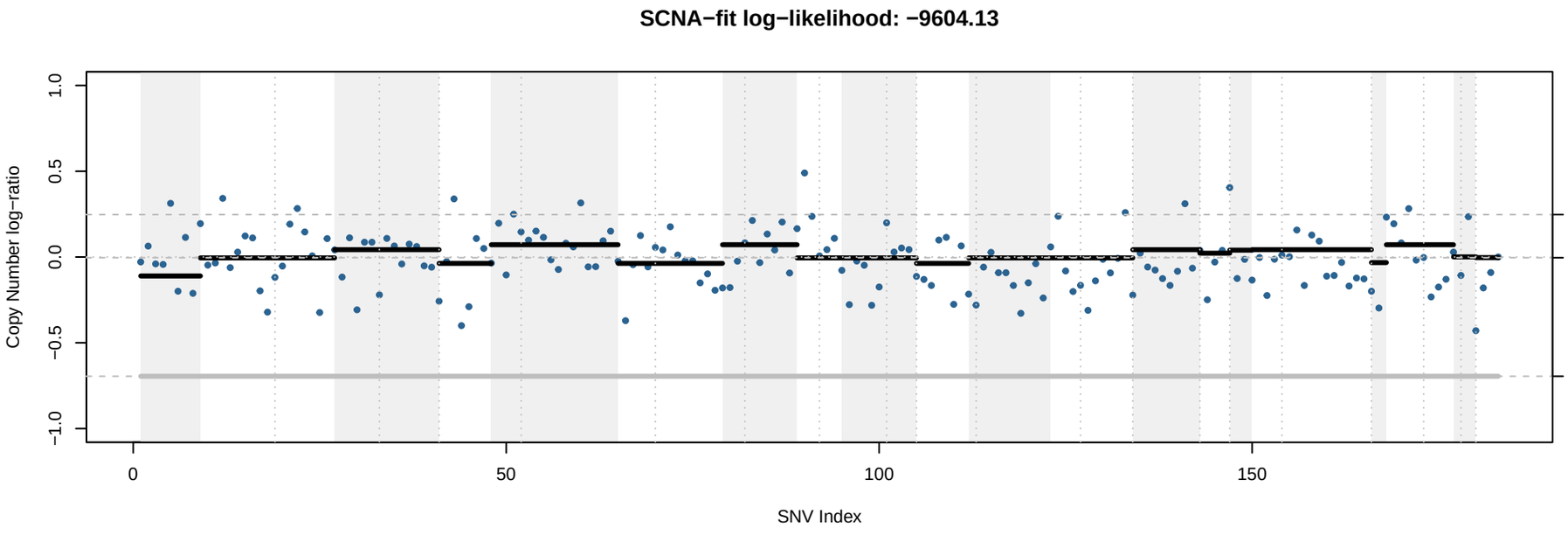

Coverage (log2)
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
Allelic fraction

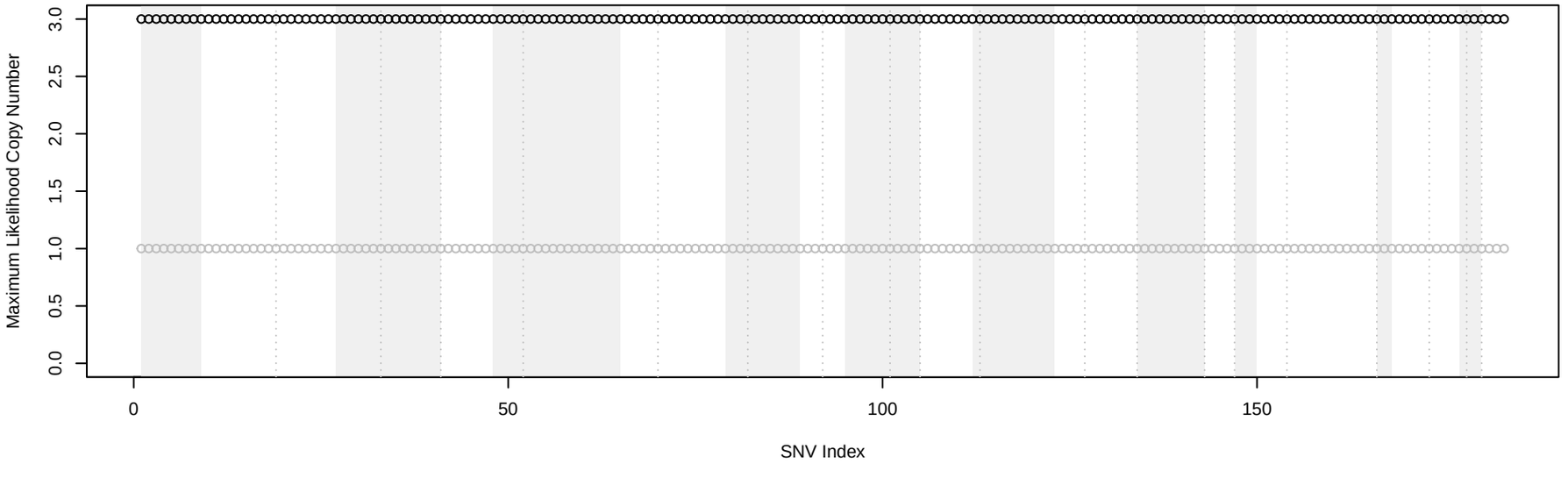

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

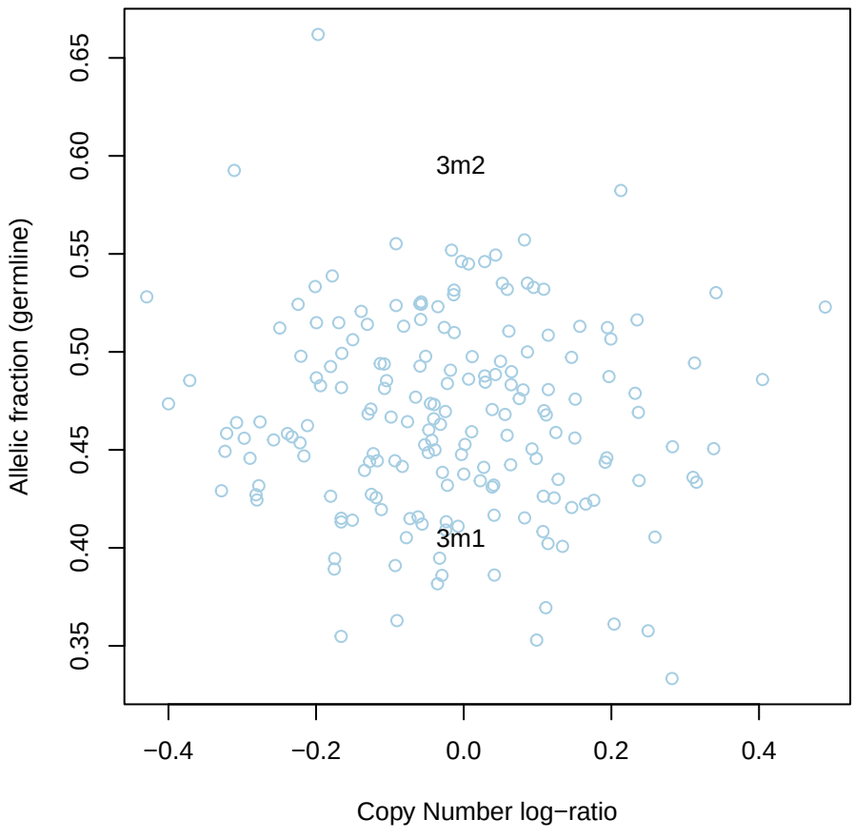

Power 0.8
Frequency
0
2
4
6
8
10
12
14
0.2
0.4
0.6
0.8
Cellular fraction

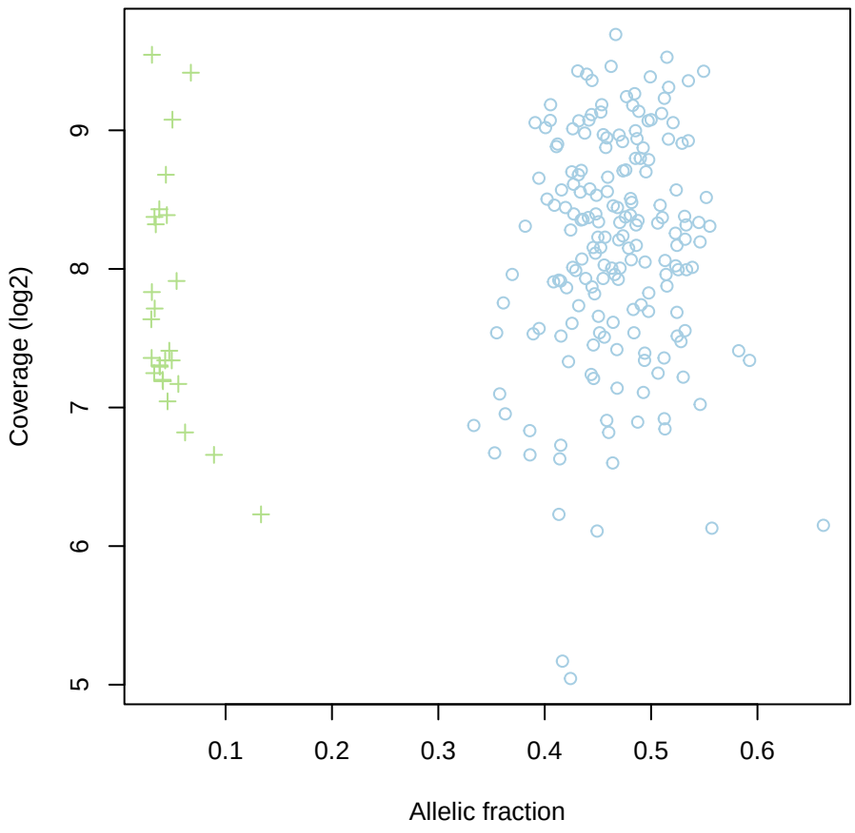

Purity: 0.47 Tumor ploidy: 3.015
1
3
4
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

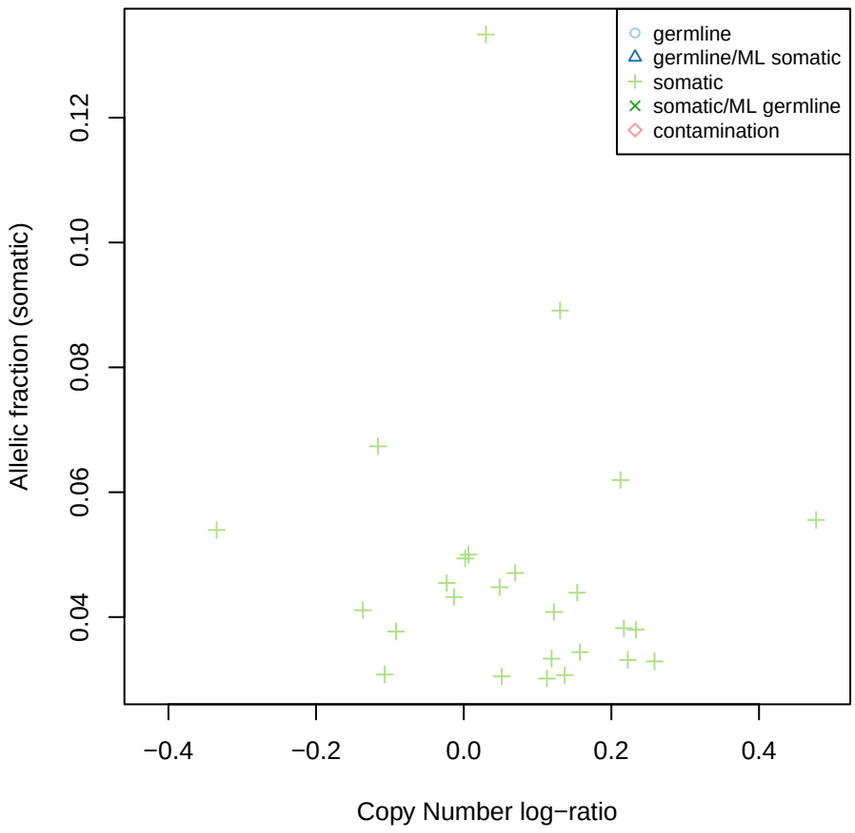

Purity: 0.47 Tumor ploidy: 3.015 SNV log−likelihood: −279.73 GoF: 85.7% Mean coverage: 317;651
1 2 3 4 5 6 7 8 9 10 11 12 13 14 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 50 100 150
SNV Index

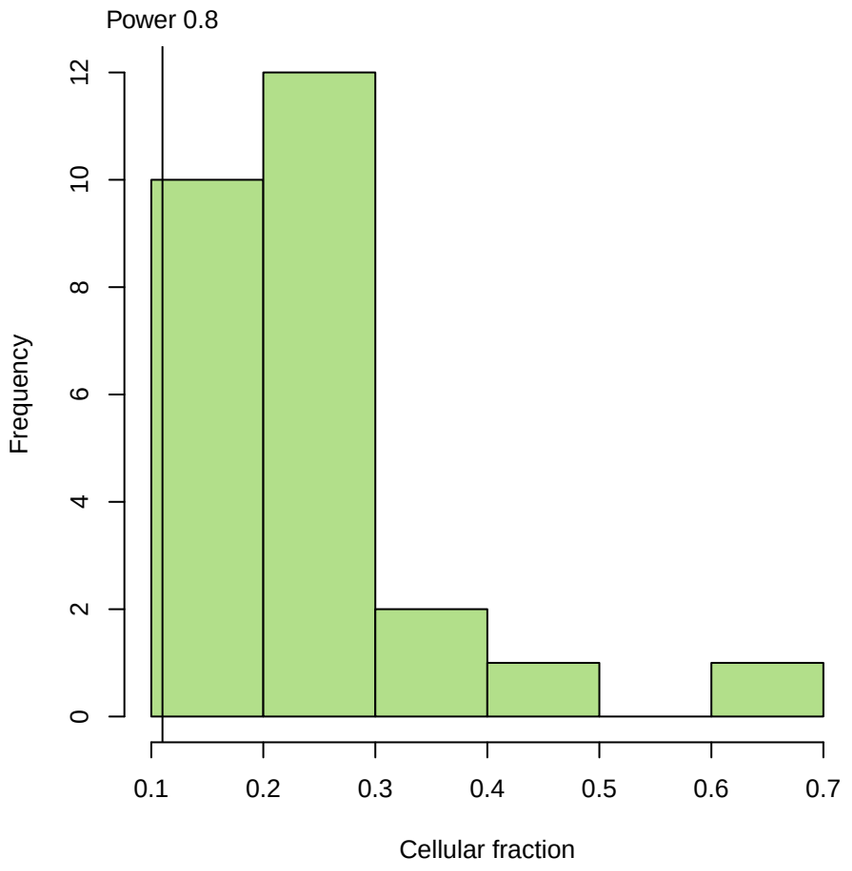

SCNA−fit log−likelihood: −9604.13
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 3 4
0 50 100 150
SNV Index

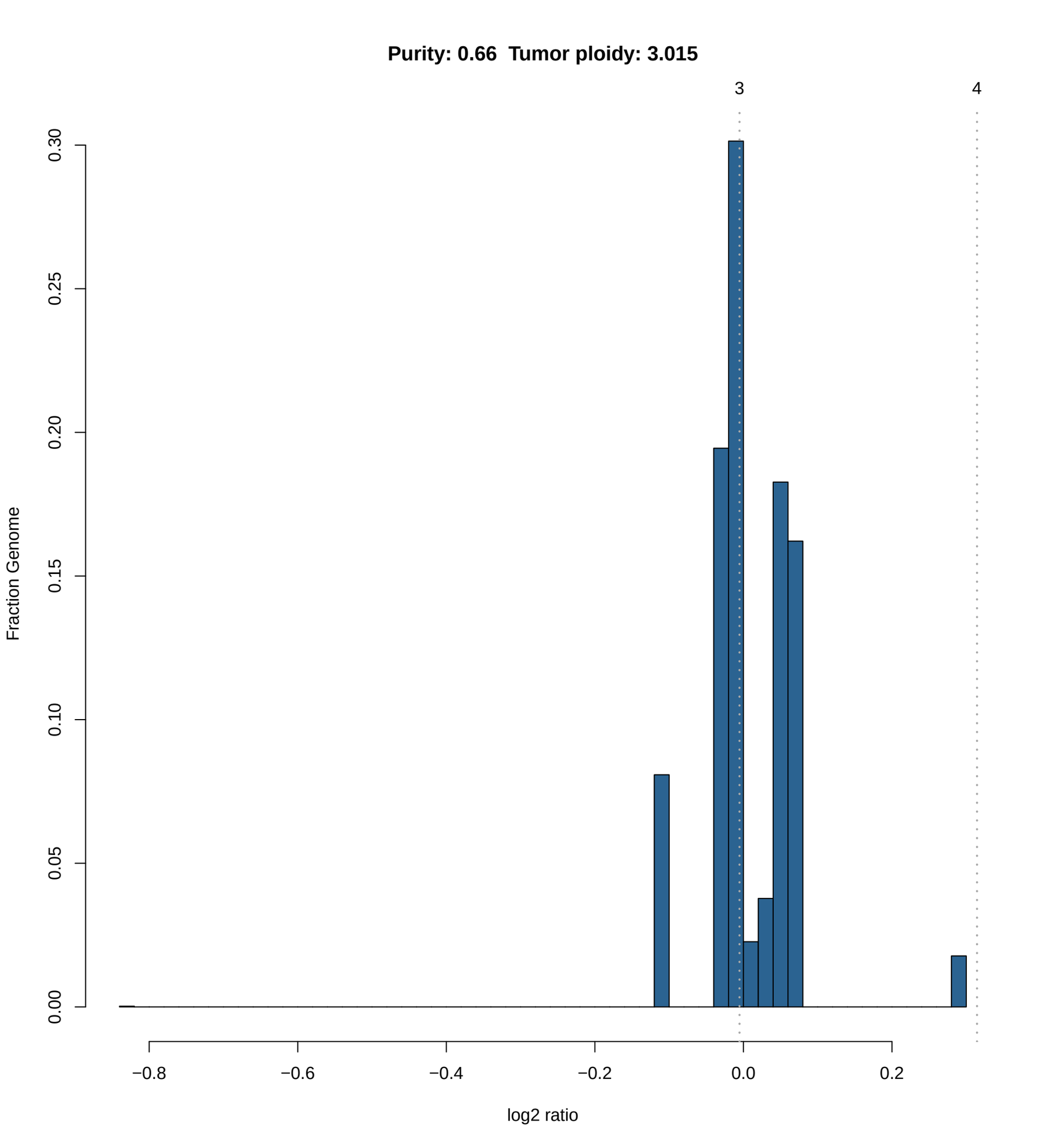

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

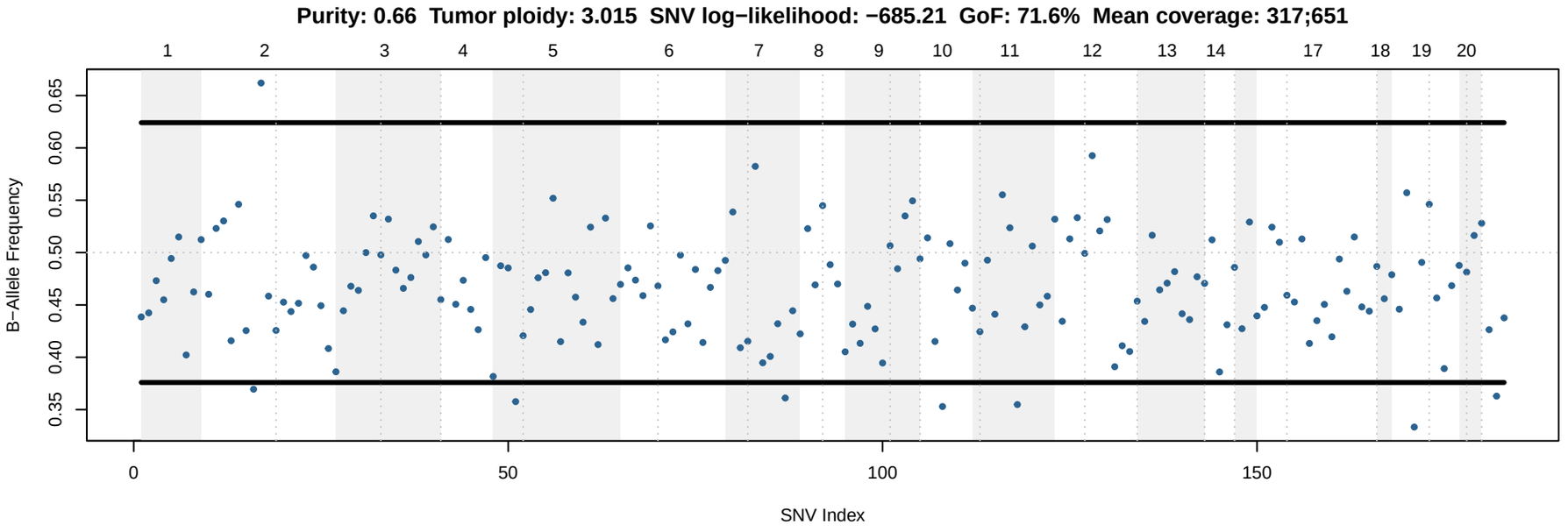

3m2
3m1
Allelic fraction (germline)
Copy Number log−ratio
0.35
0.40
0.45
0.50
0.55
0.60
0.65
−0.4
−0.2
0.0
0.2
0.4

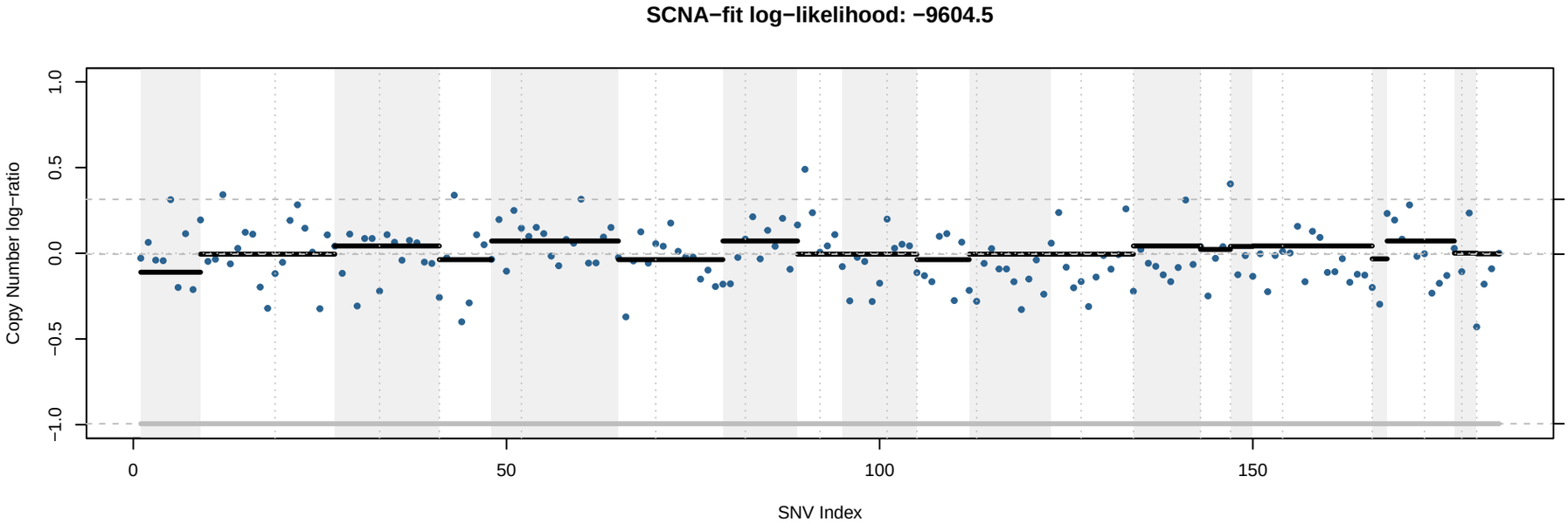

Coverage (log2)
Allelic fraction
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6

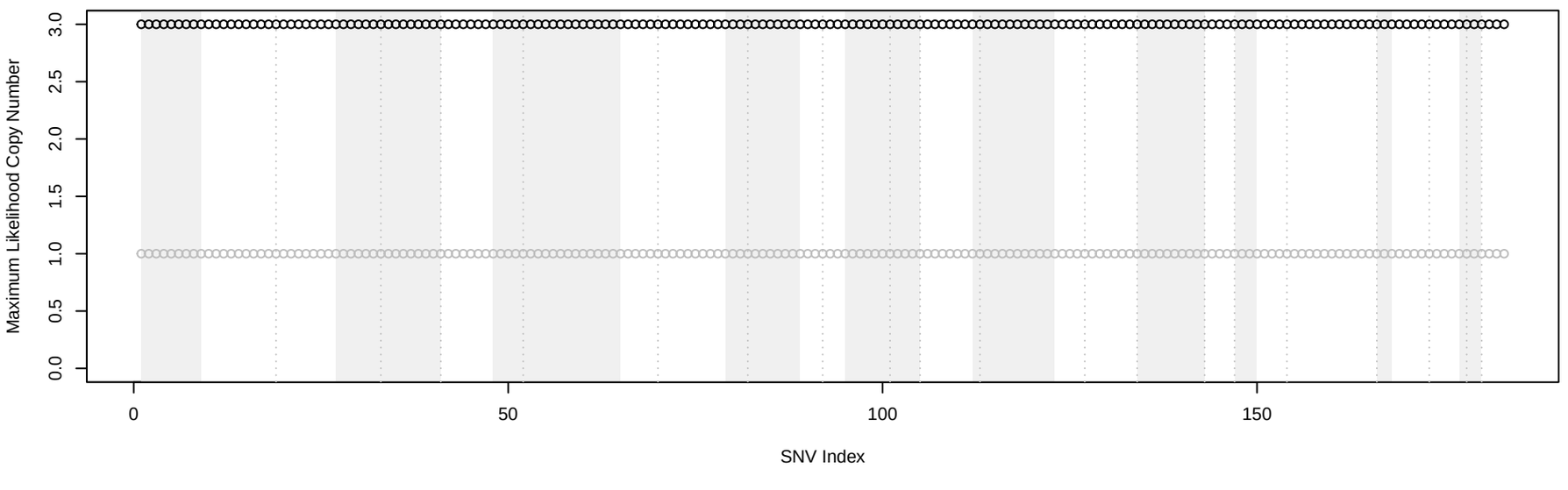

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
0.12
−0.4
−0.2
0.0
0.2
0.4

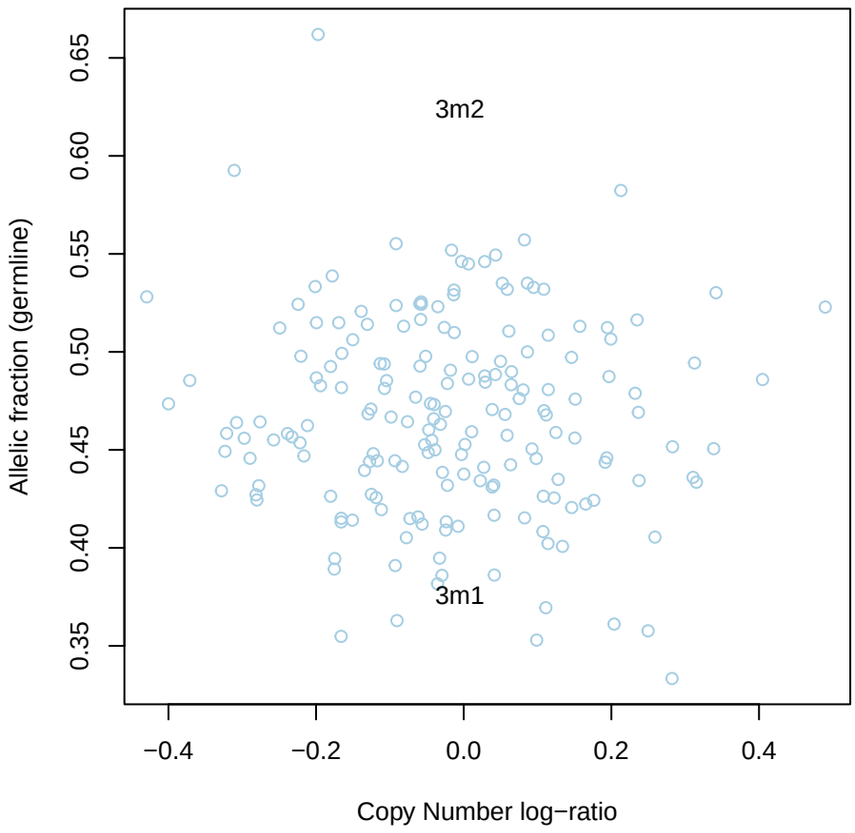

Power 0.8
Frequency
Cellular fraction
0
2
4
6
8
10
12
0.1
0.2
0.3
0.4
0.5
0.6
0.7

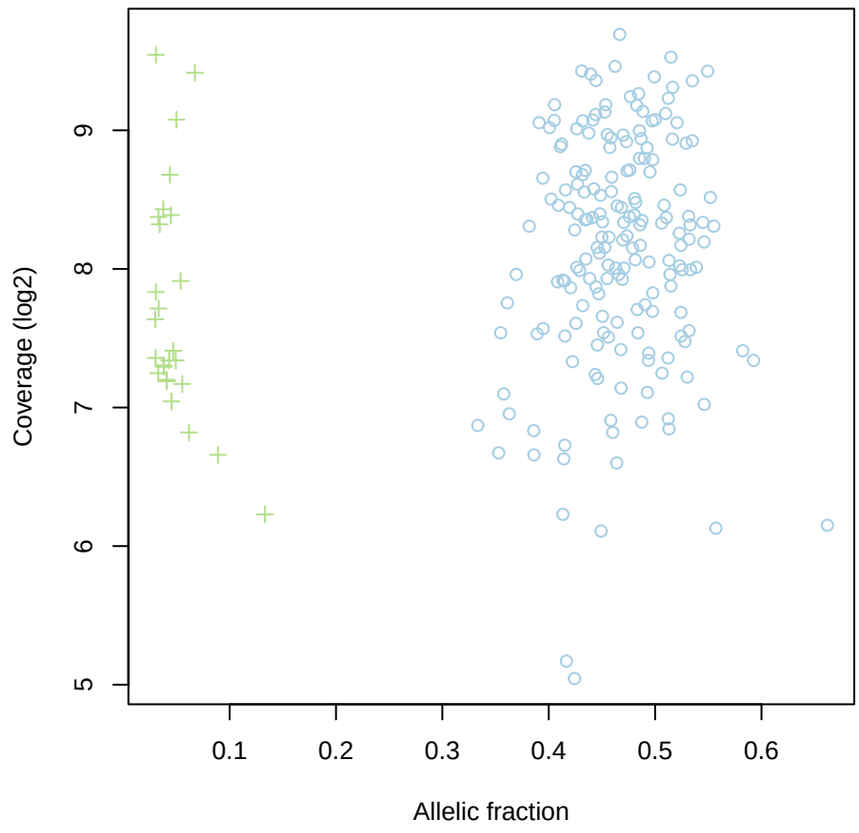

Purity: 0.66 Tumor ploidy: 3.015
3
4
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

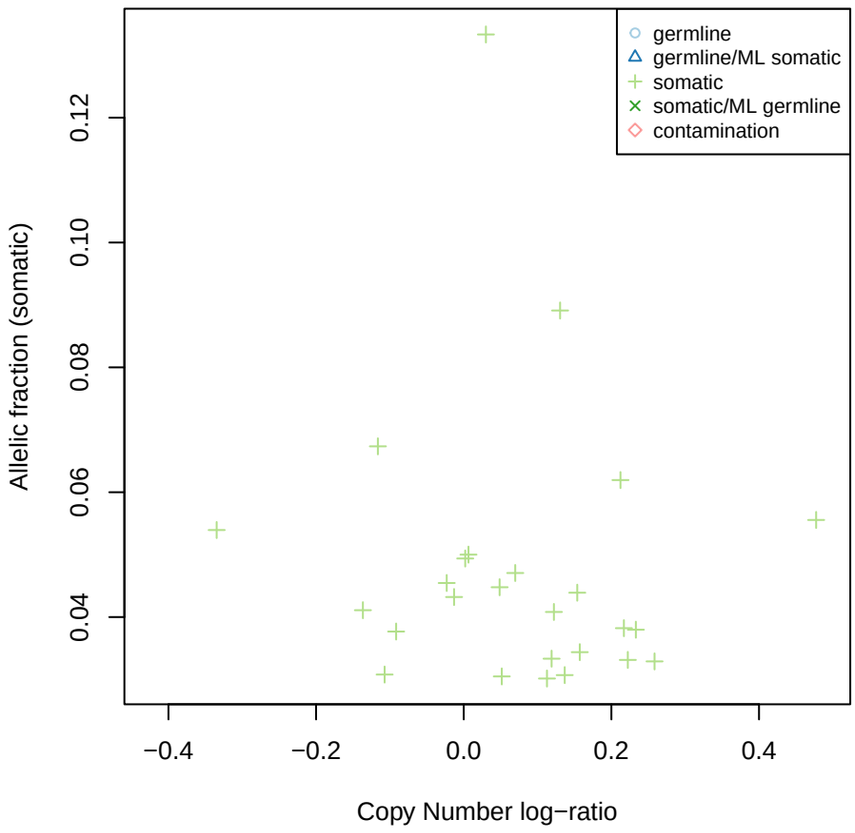

Purity: 0.66 Tumor ploidy: 3.015 SNV log−likelihood: −685.21 GoF: 71.6% Mean coverage: 317;651
1 2 3 4 5 6 7 8 9 10 11 12 13 14 17 18 19 20
B−Allele Frequency
0.35 0.40 0.45 0.50 0.55 0.60 0.65
0 50 100 150
SNV Index

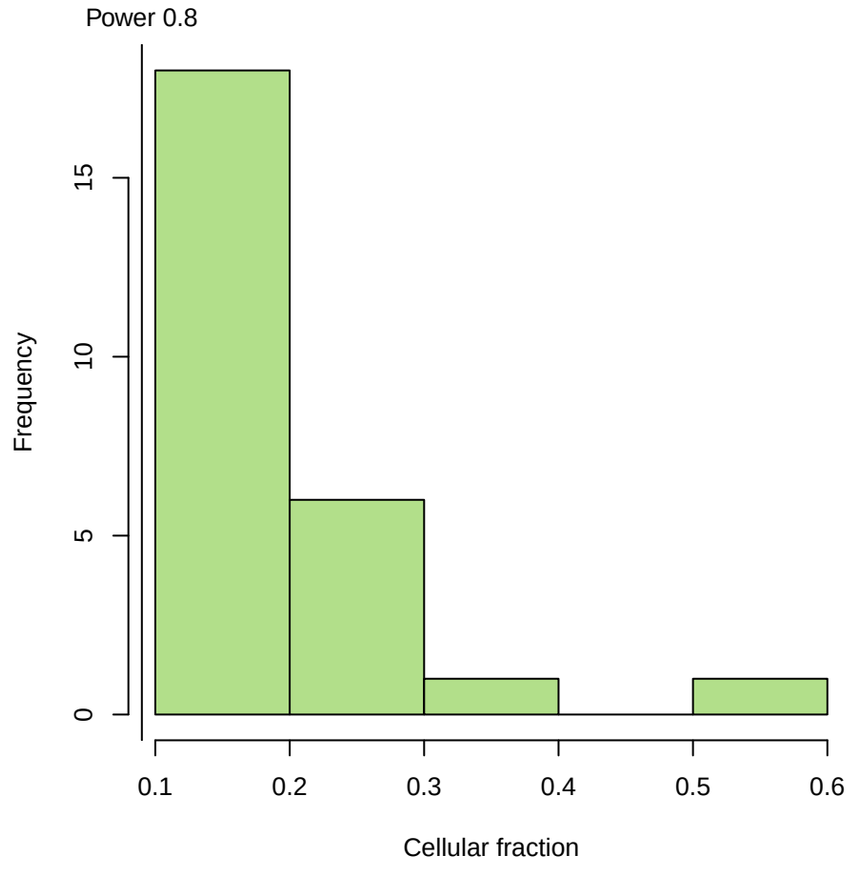

SCNA−fit log−likelihood: −9604.5
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 3 4
0 50 100 150
SNV Index


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


3m2
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


Coverage (log2)
Allelic fraction
5
6
7
8
9
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
−0.4
−0.2
0.0
0.2
0.4


Power 0.8
Frequency
Cellular fraction
0
5
10
15
0.1
0.2
0.3
0.4
0.5
0.6