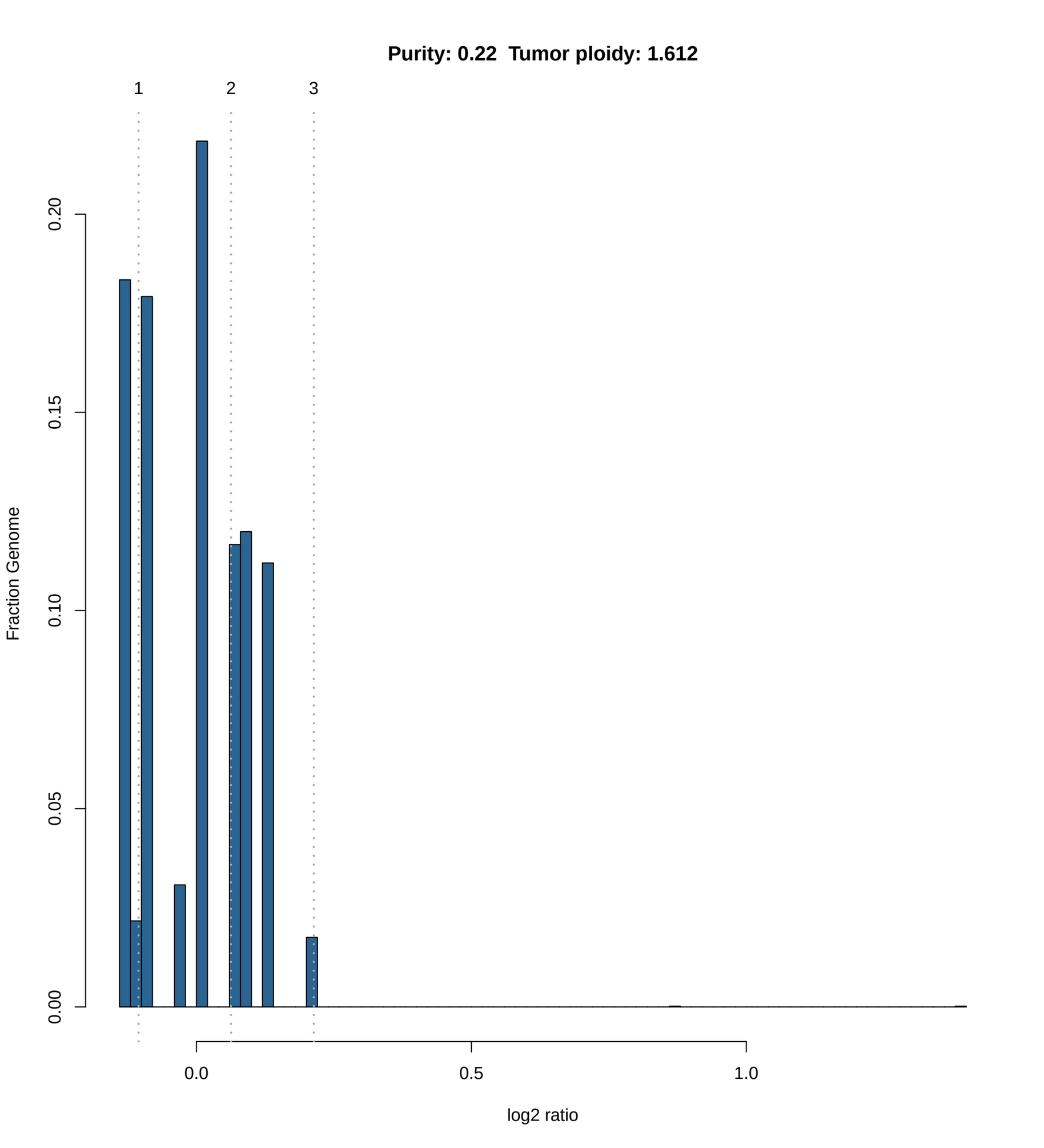
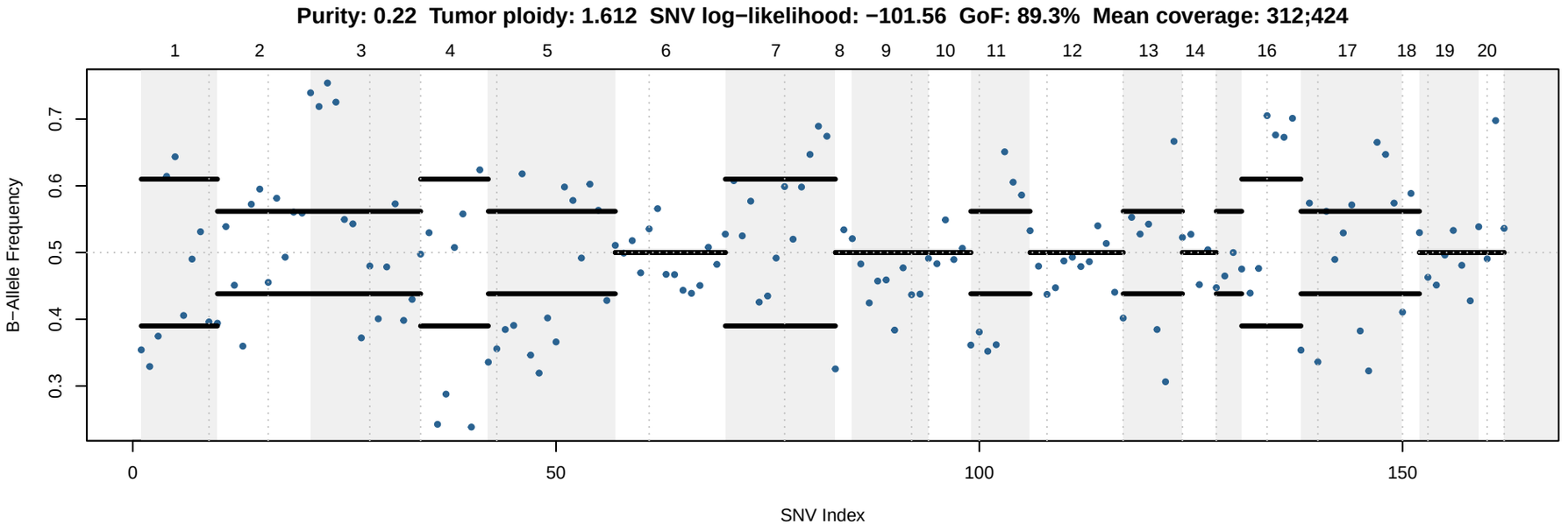
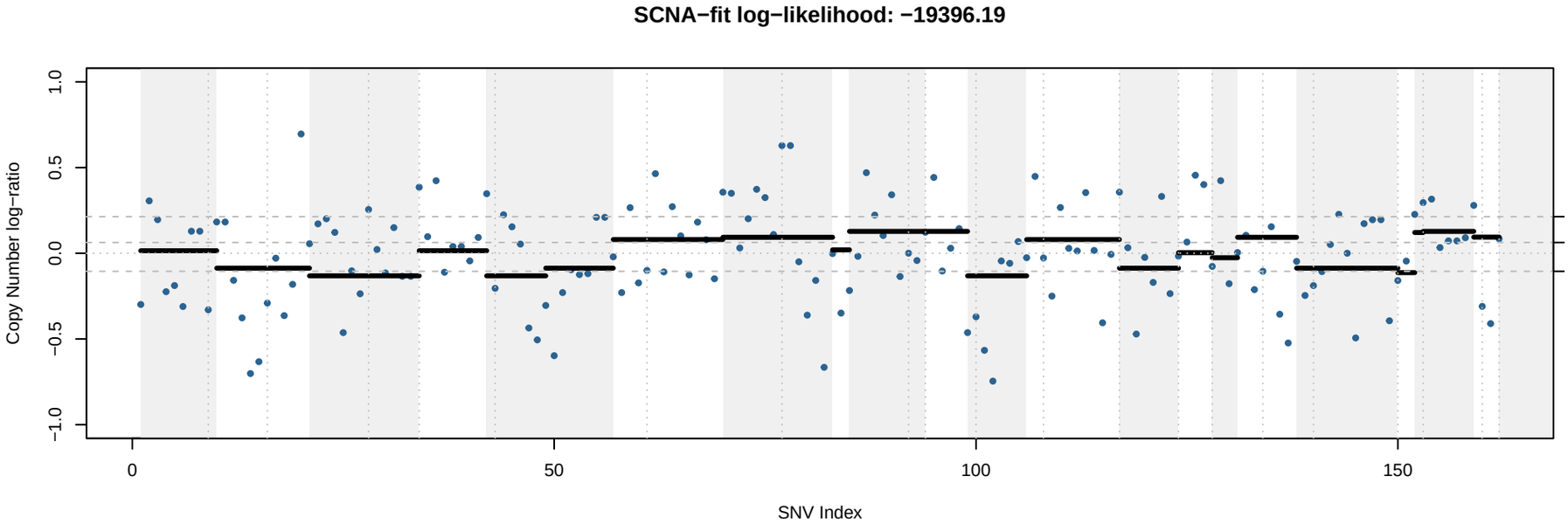
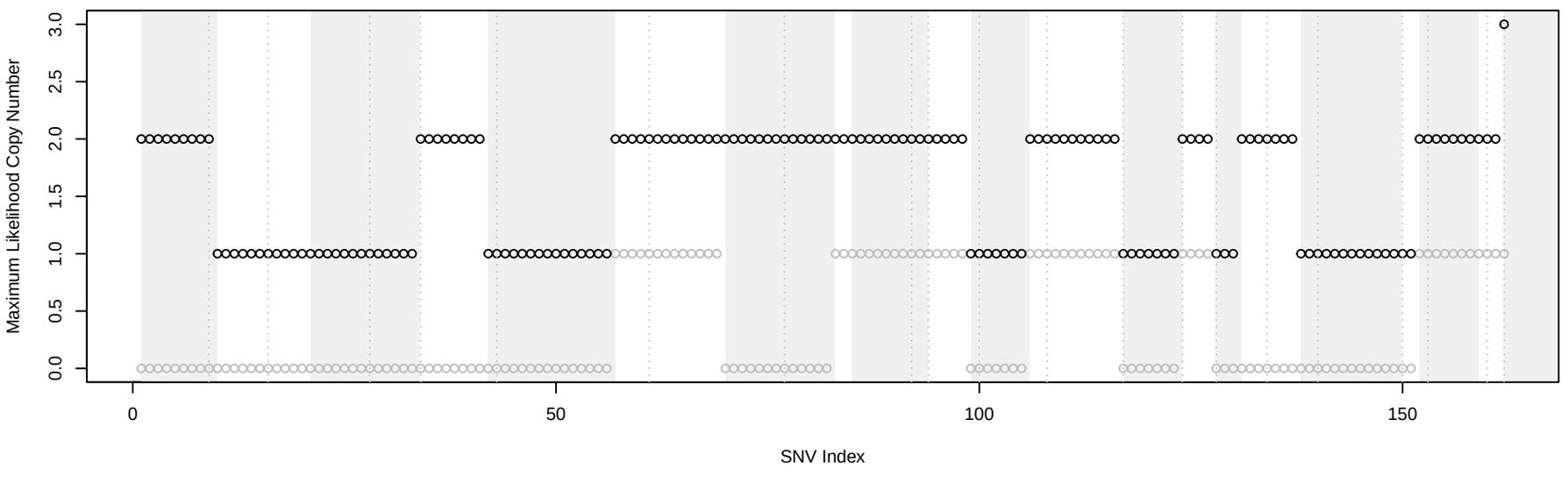
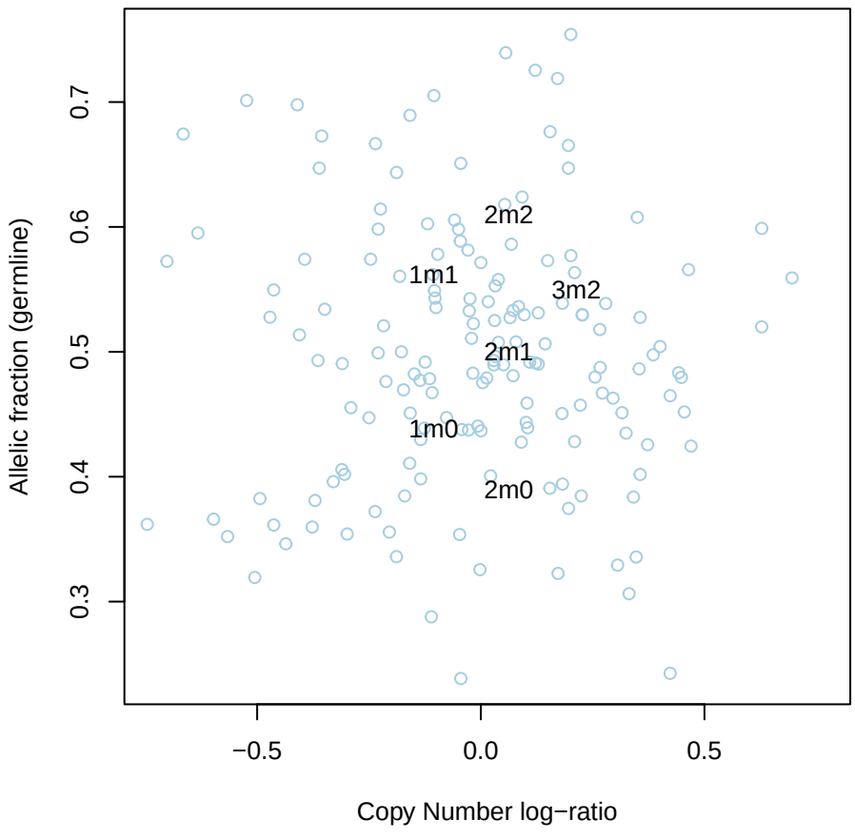
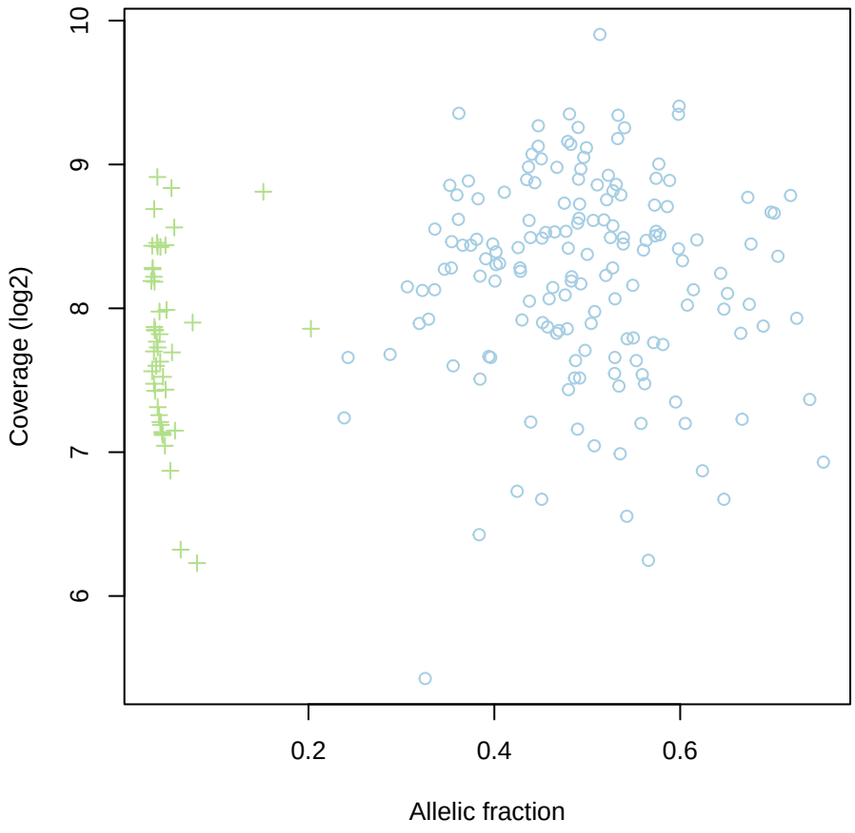

Purity: 0.22 Tumor ploidy: 1.612
1
2
3
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

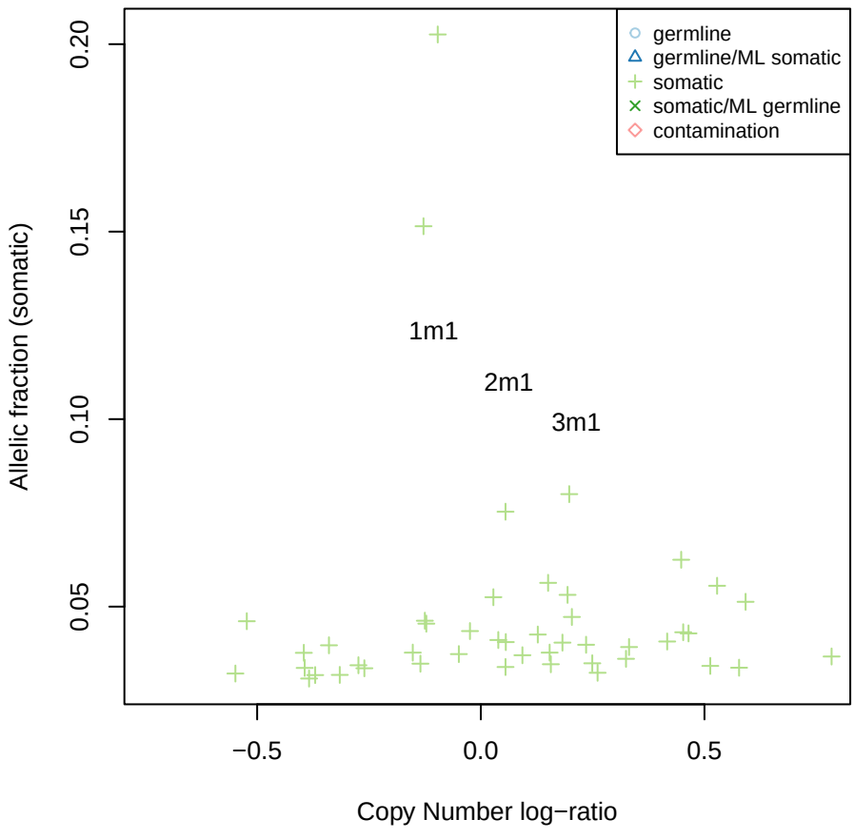

Purity: 0.22 Tumor ploidy: 1.612 SNV log−likelihood: −101.56 GoF: 89.3% Mean coverage: 312;424
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

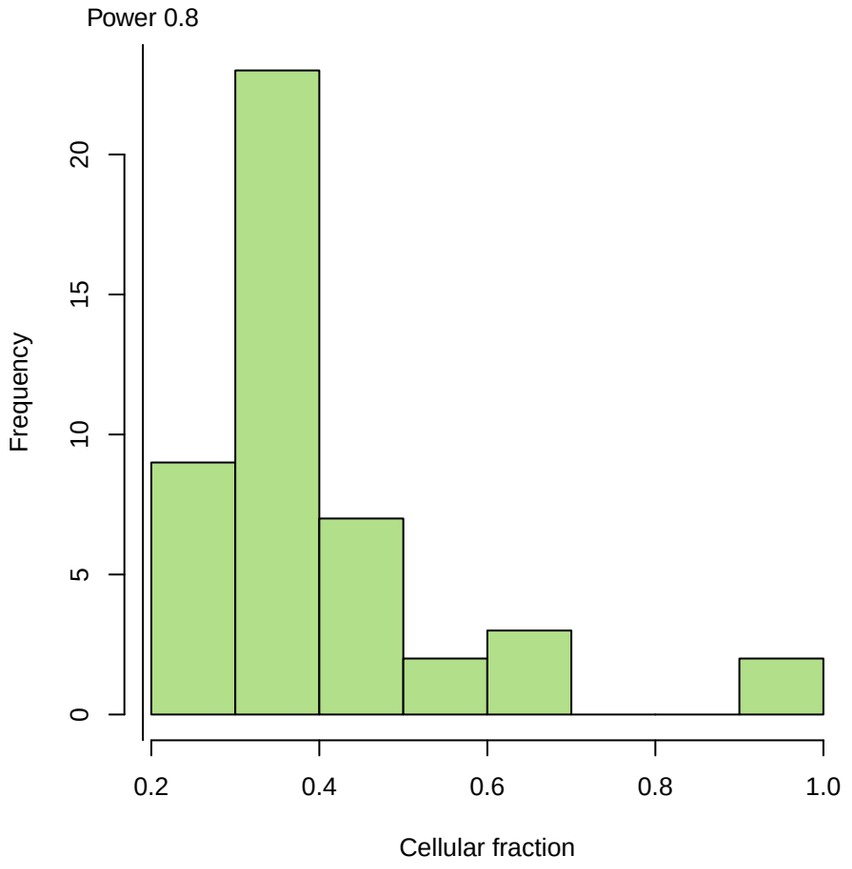

SCNA−fit log−likelihood: −19396.19
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3
0 50 100 150
SNV Index

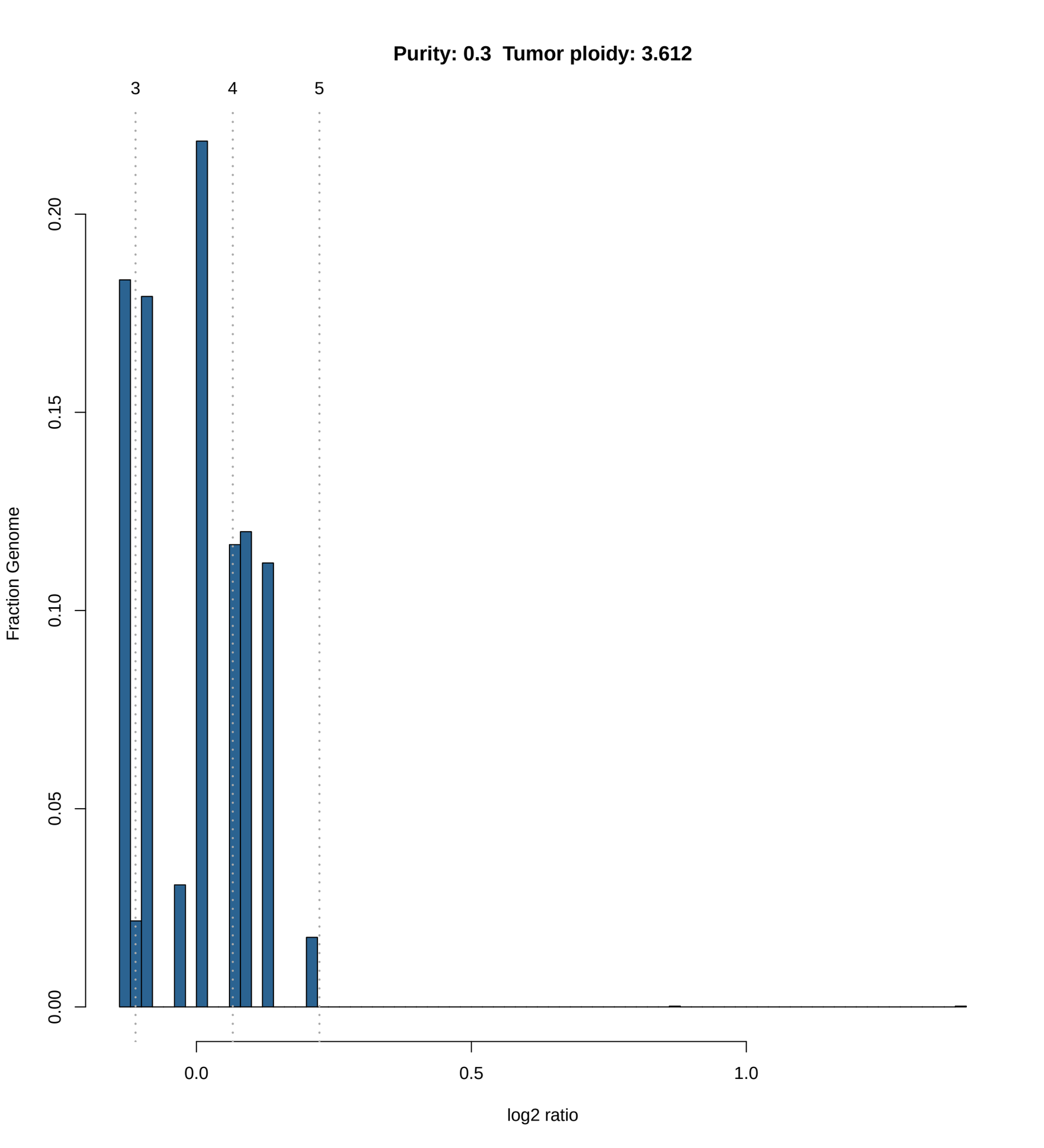

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

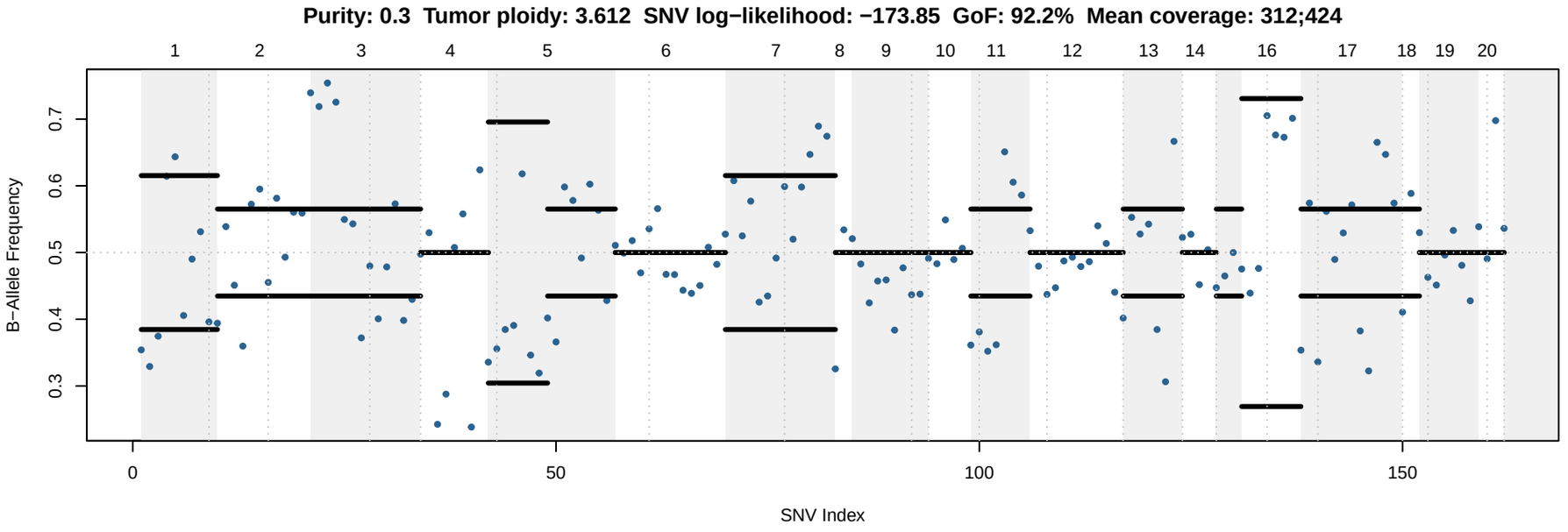

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
2m2
1m1
3m2
2m1
1m0
2m0
−0.5
0.0
0.5
Copy Number log−ratio

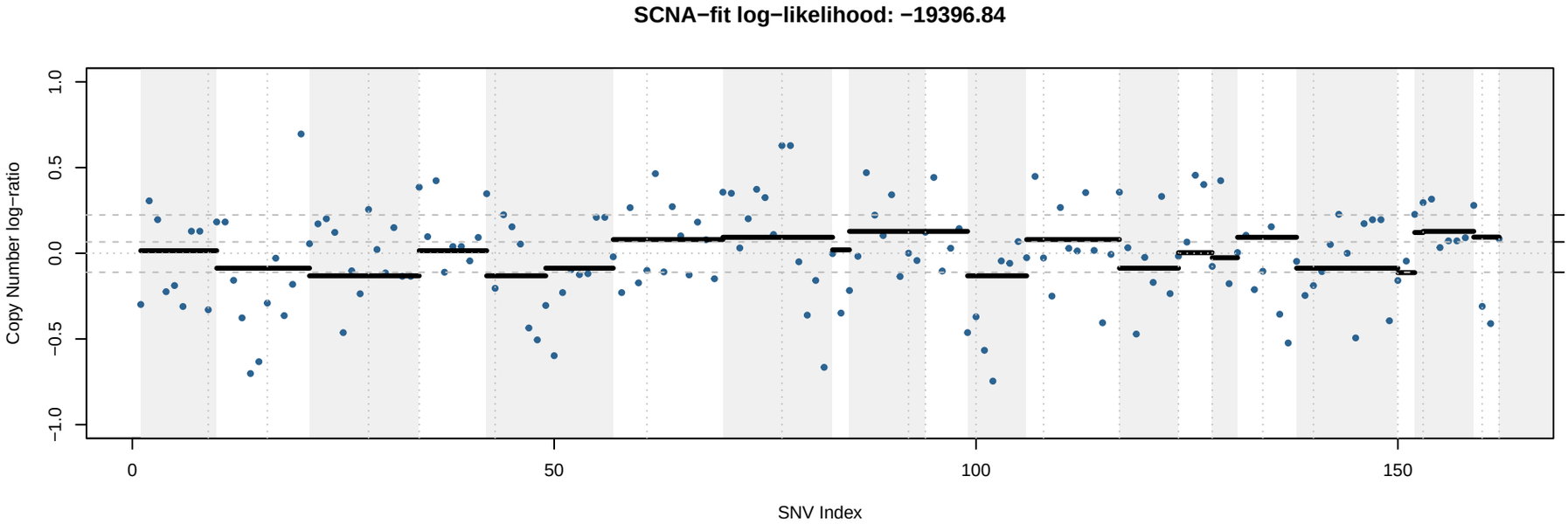

Coverage (log2)
6
7
8
9
10
0.2
0.4
0.6
Allelic fraction

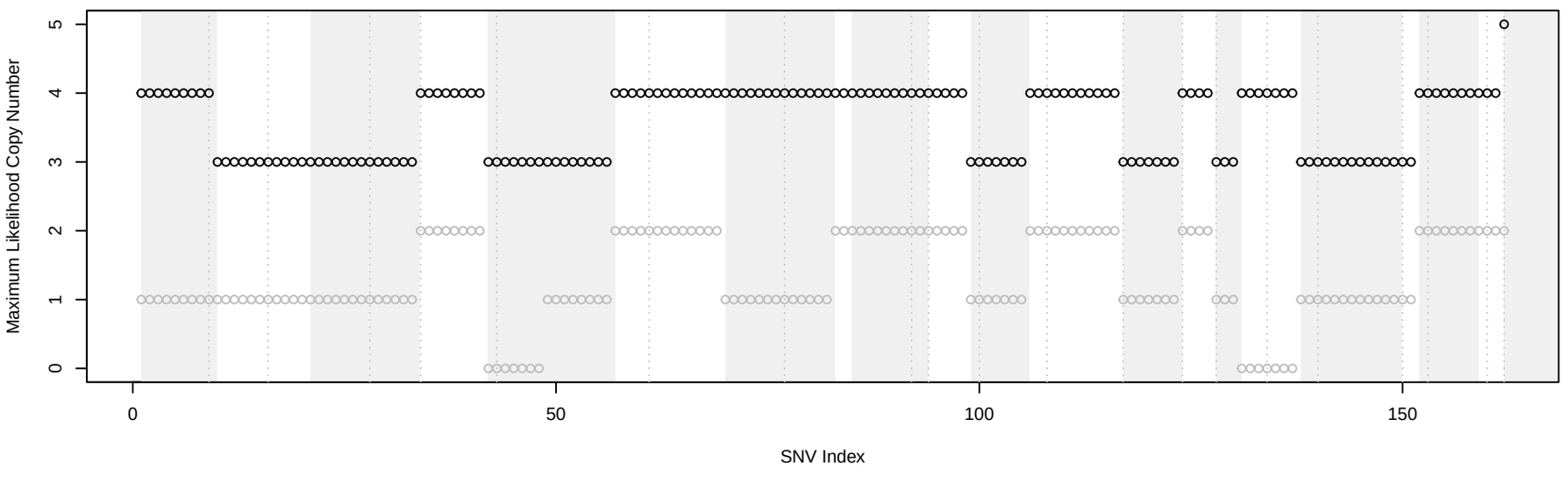

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
−0.5
0.0
0.5
Copy Number log−ratio

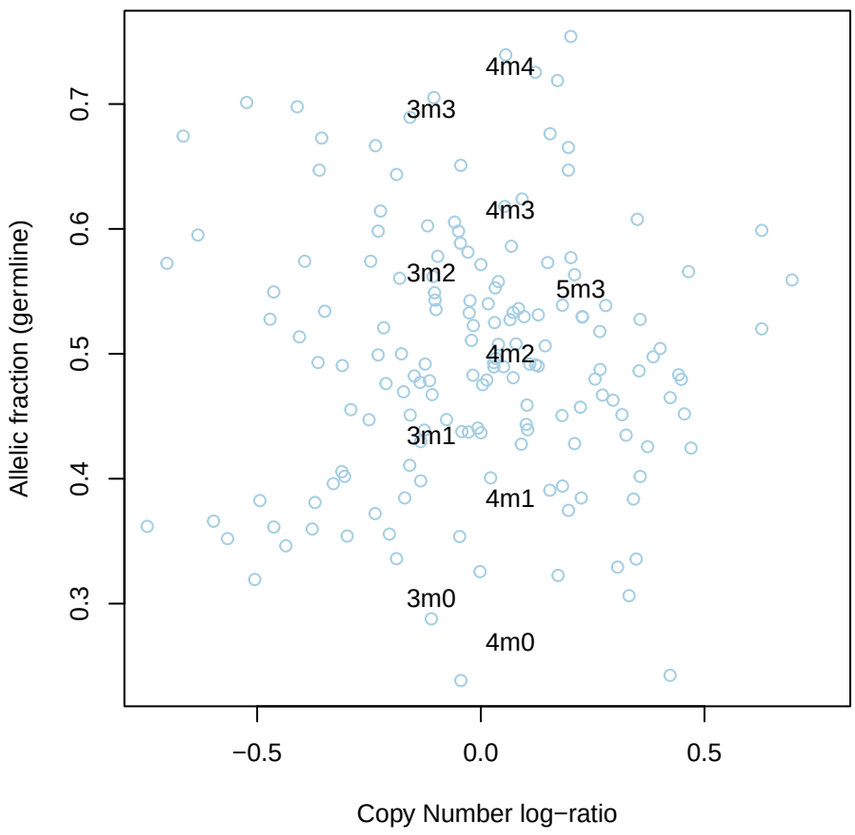

Power 0.8
Frequency
0
5
10
15
20
0.2
0.4
0.6
0.8
1.0
Cellular fraction

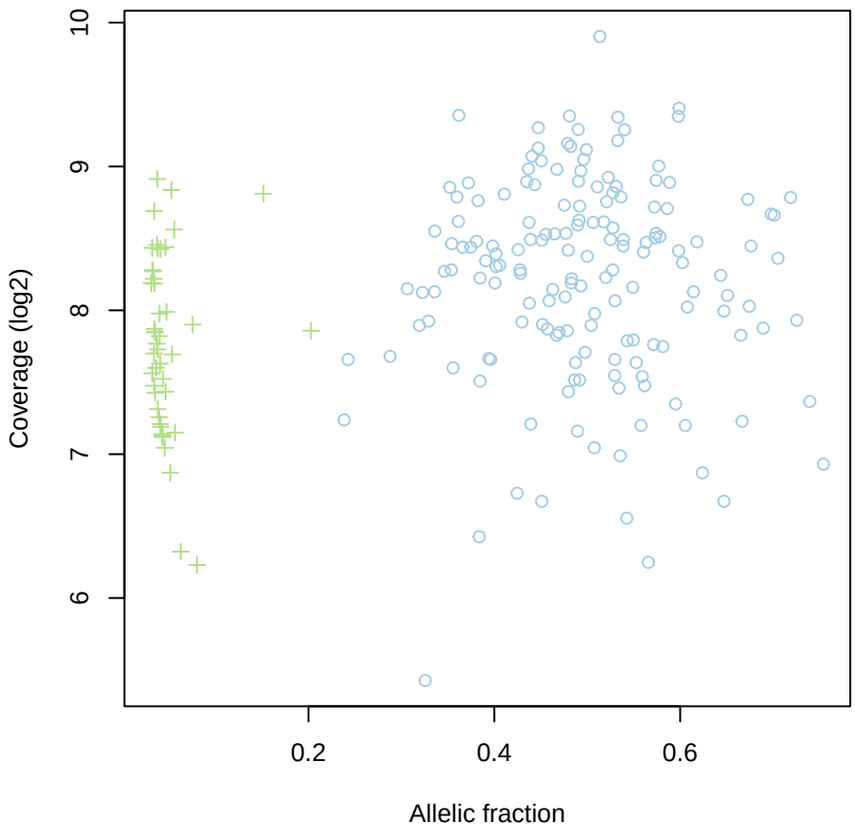

Purity: 0.3 Tumor ploidy: 3.612
3
4
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

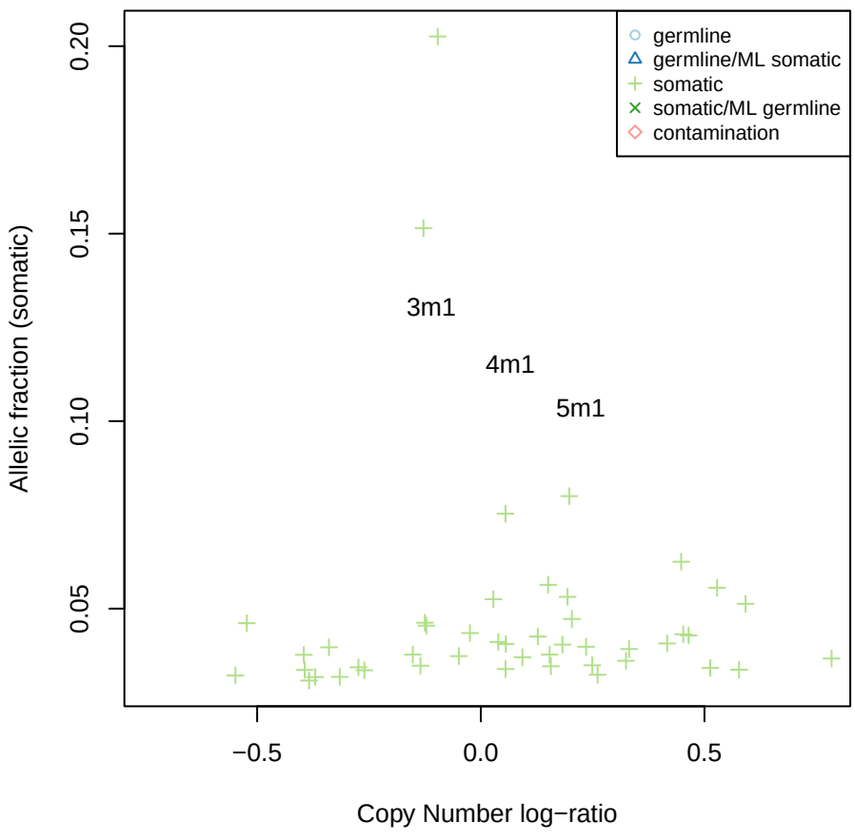

Purity: 0.3 Tumor ploidy: 3.612 SNV log−likelihood: −173.85 GoF: 92.2% Mean coverage: 312;424
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

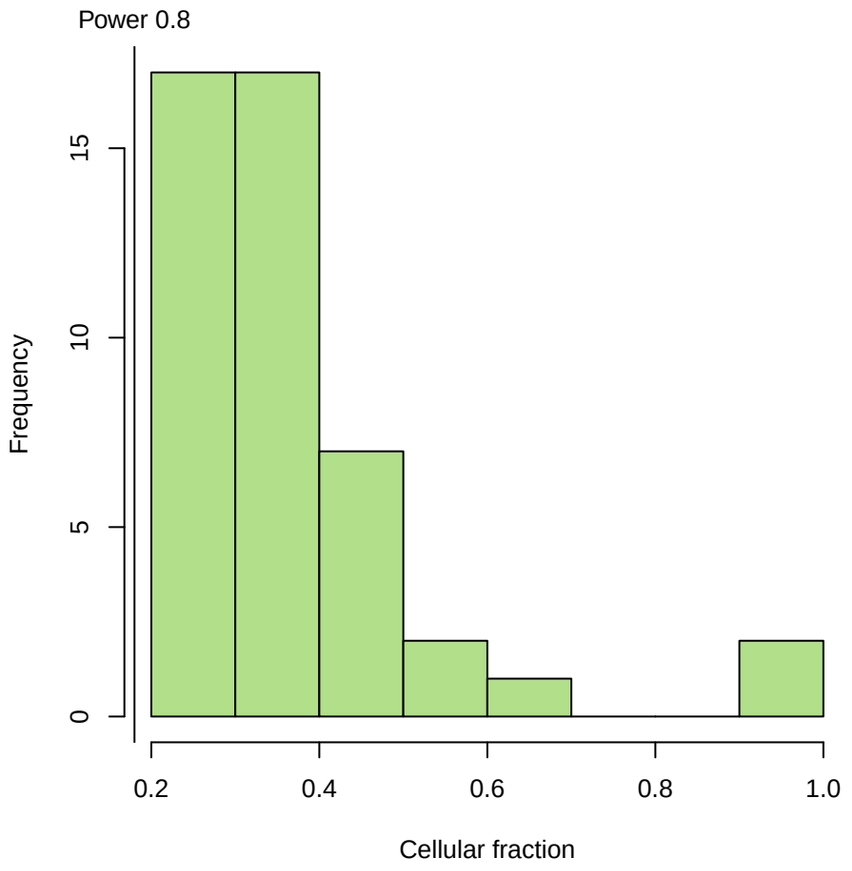

SCNA−fit log−likelihood: −19396.84
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5
0 50 100 150
SNV Index

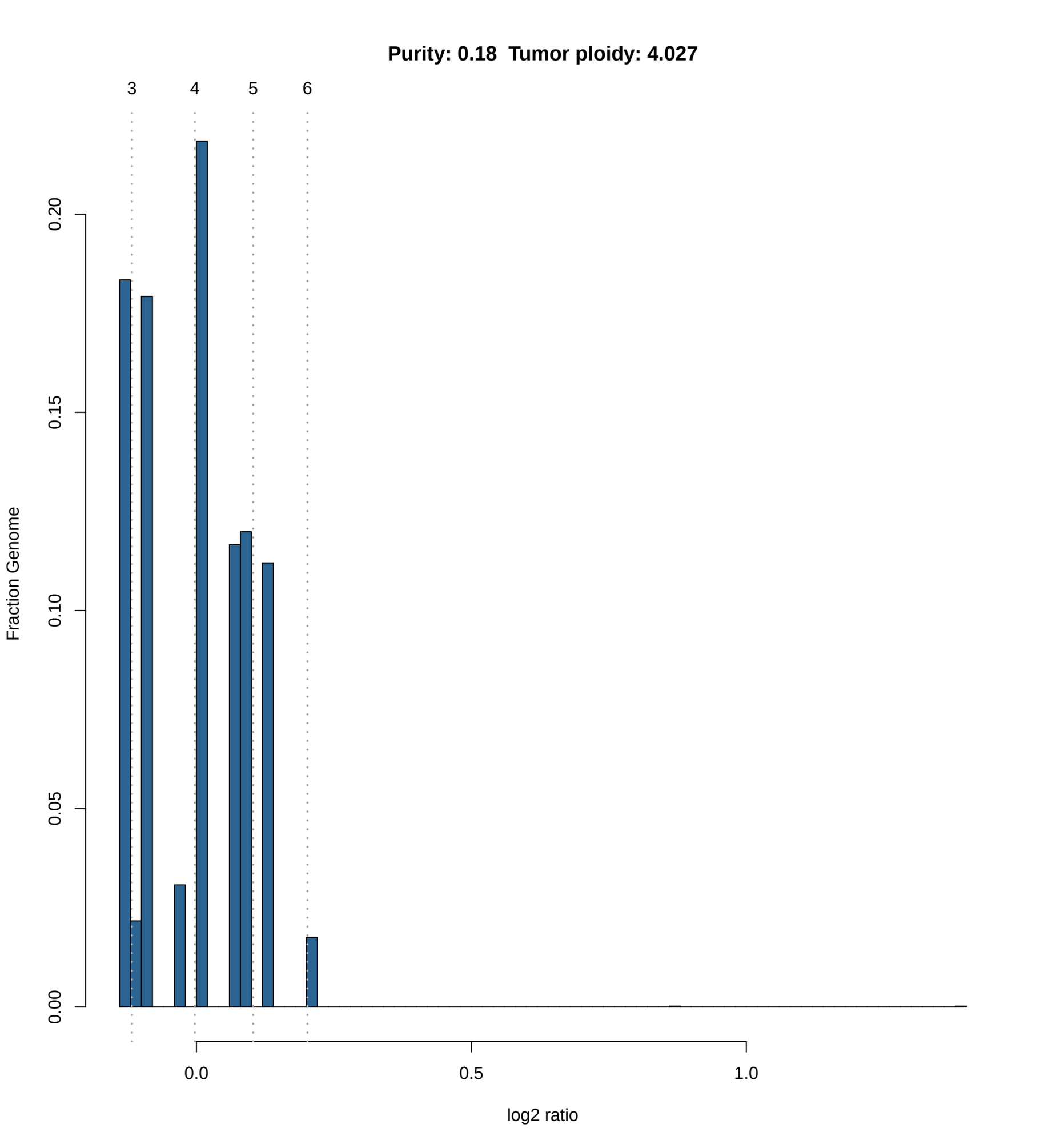

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

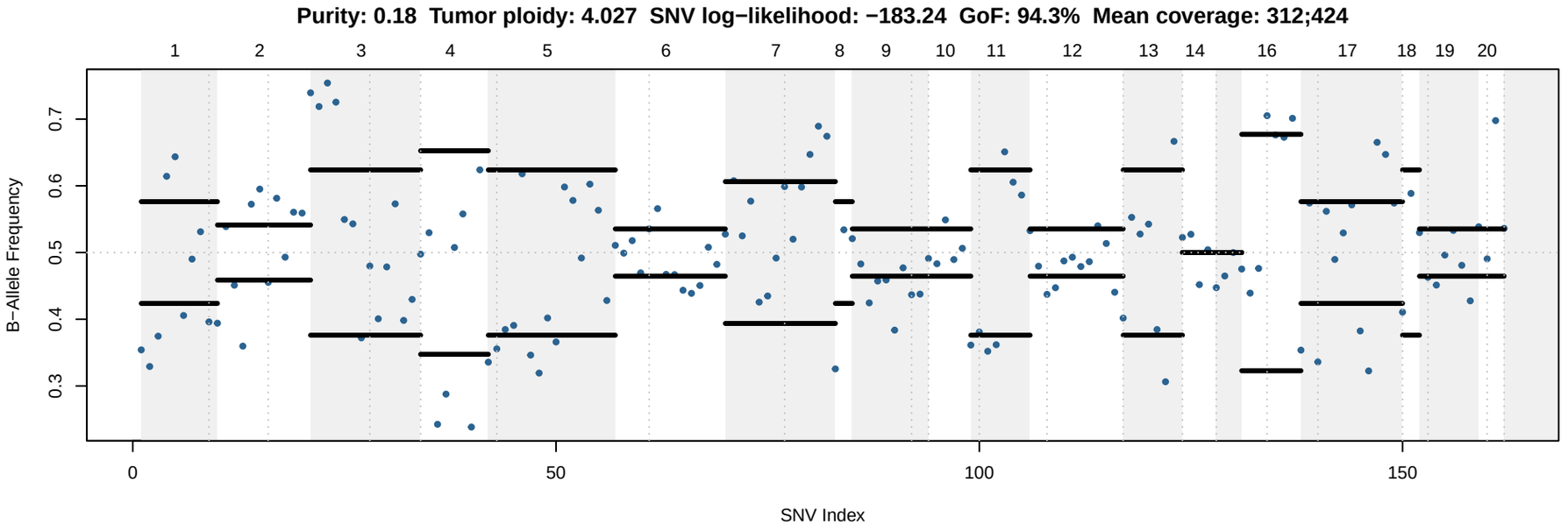

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
4m4
3m3
4m3
3m2
5m3
4m2
3m1
4m1
3m0
4m0
−0.5
0.0
0.5
Copy Number log−ratio

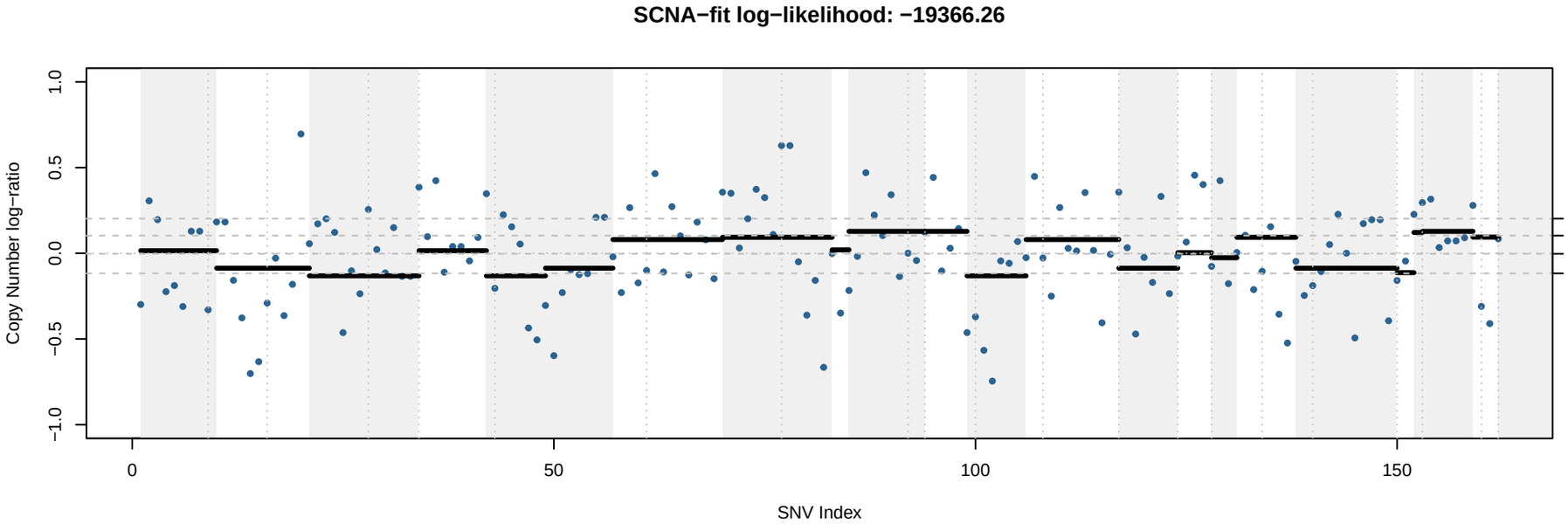

Coverage (log2)
6
7
8
9
10
0.2
0.4
0.6
Allelic fraction

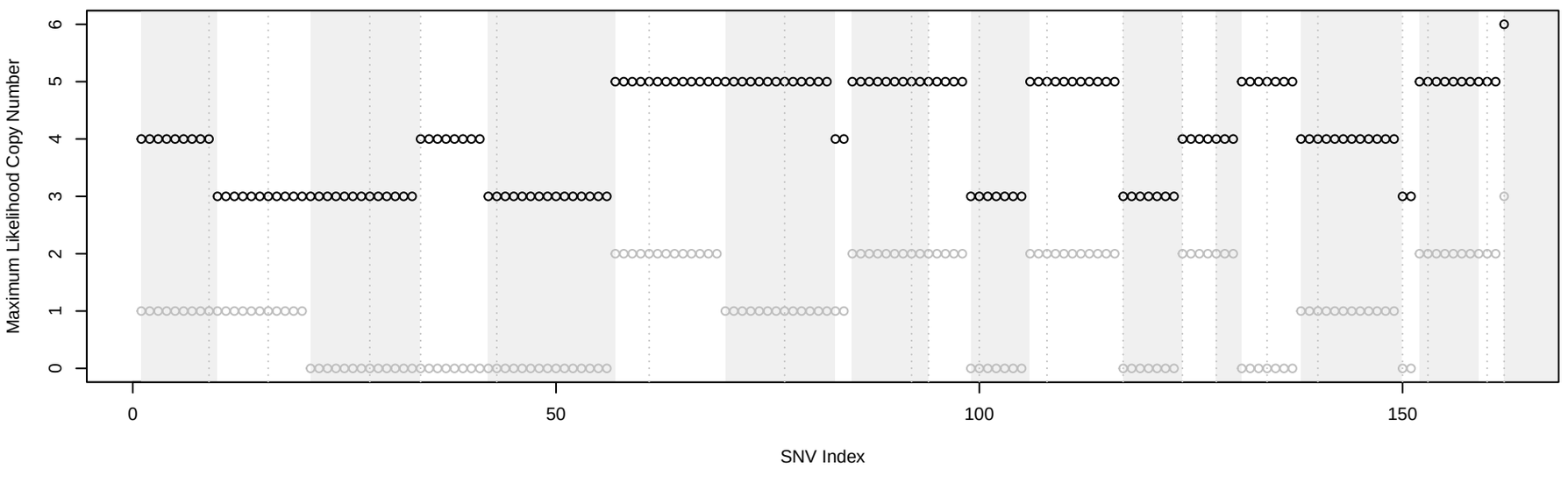

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
−0.5
0.0
0.5
Copy Number log−ratio

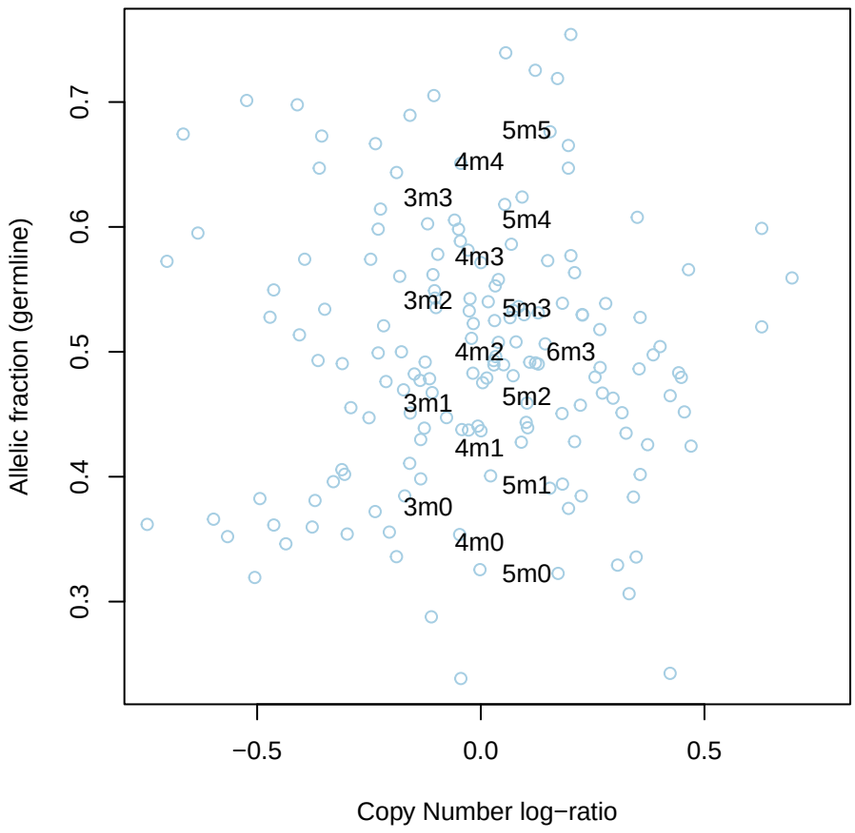

Power 0.8
Frequency
0
5
10
15
0.2
0.4
0.6
0.8
1.0
Cellular fraction

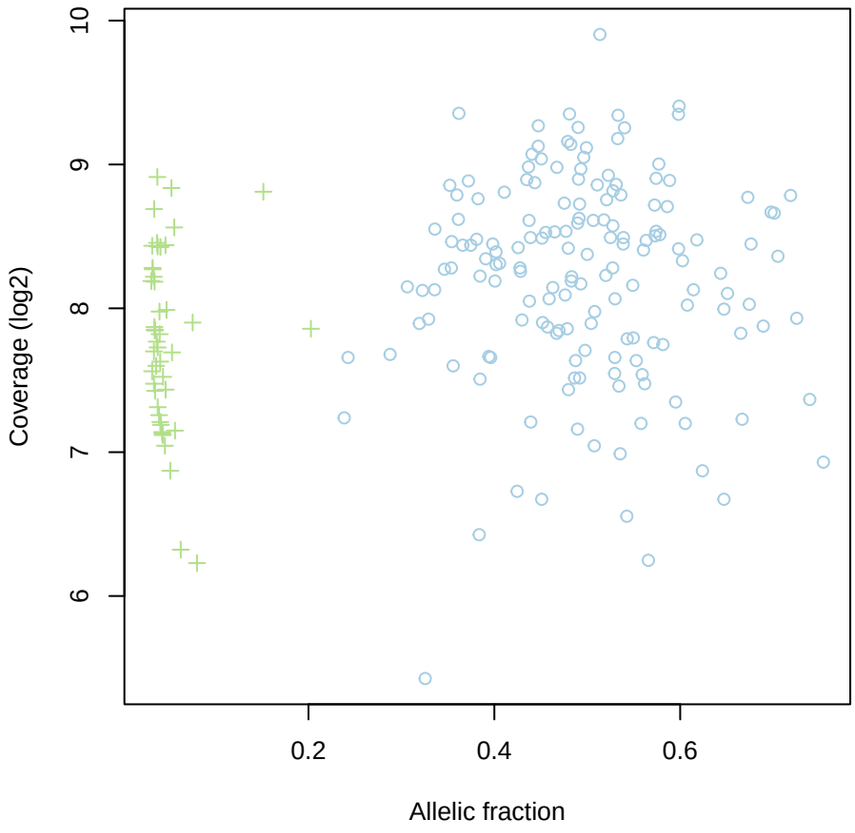

Purity: 0.18 Tumor ploidy: 4.027
3
4
5
6
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

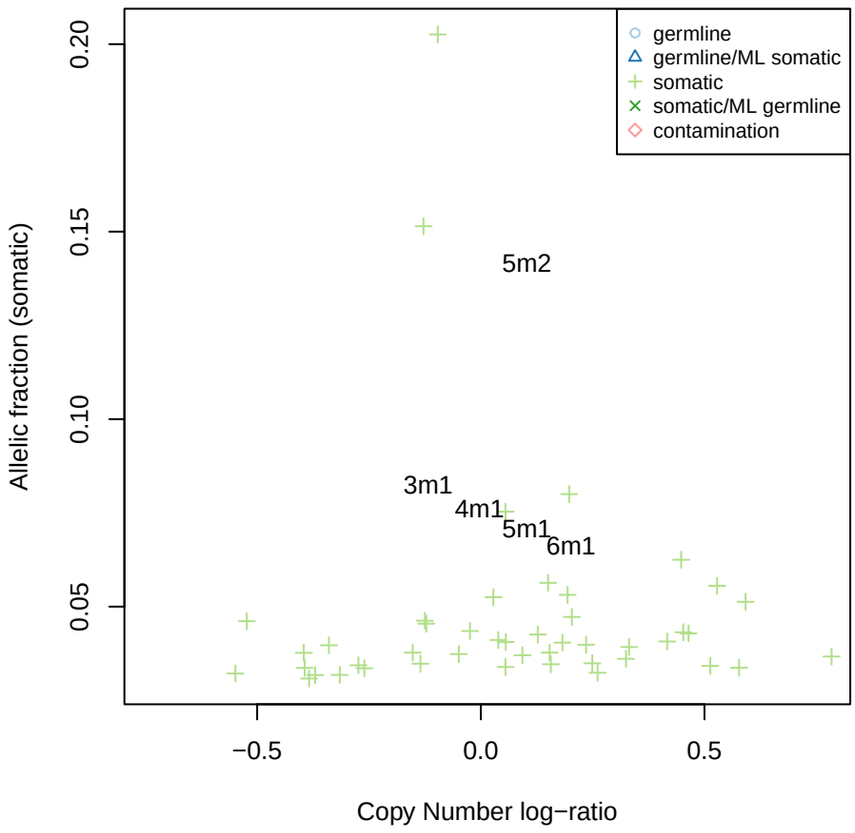

Purity: 0.18 Tumor ploidy: 4.027 SNV log−likelihood: −183.24 GoF: 94.3% Mean coverage: 312;424
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

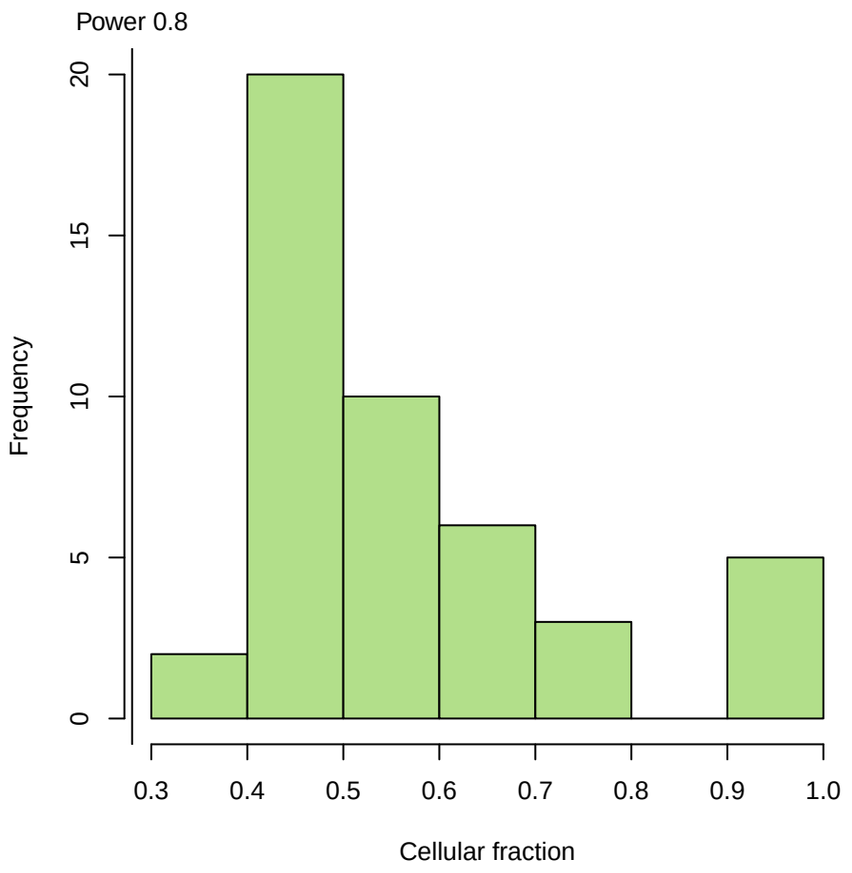

SCNA−fit log−likelihood: −19366.26
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 5
0 50 100 150
SNV Index

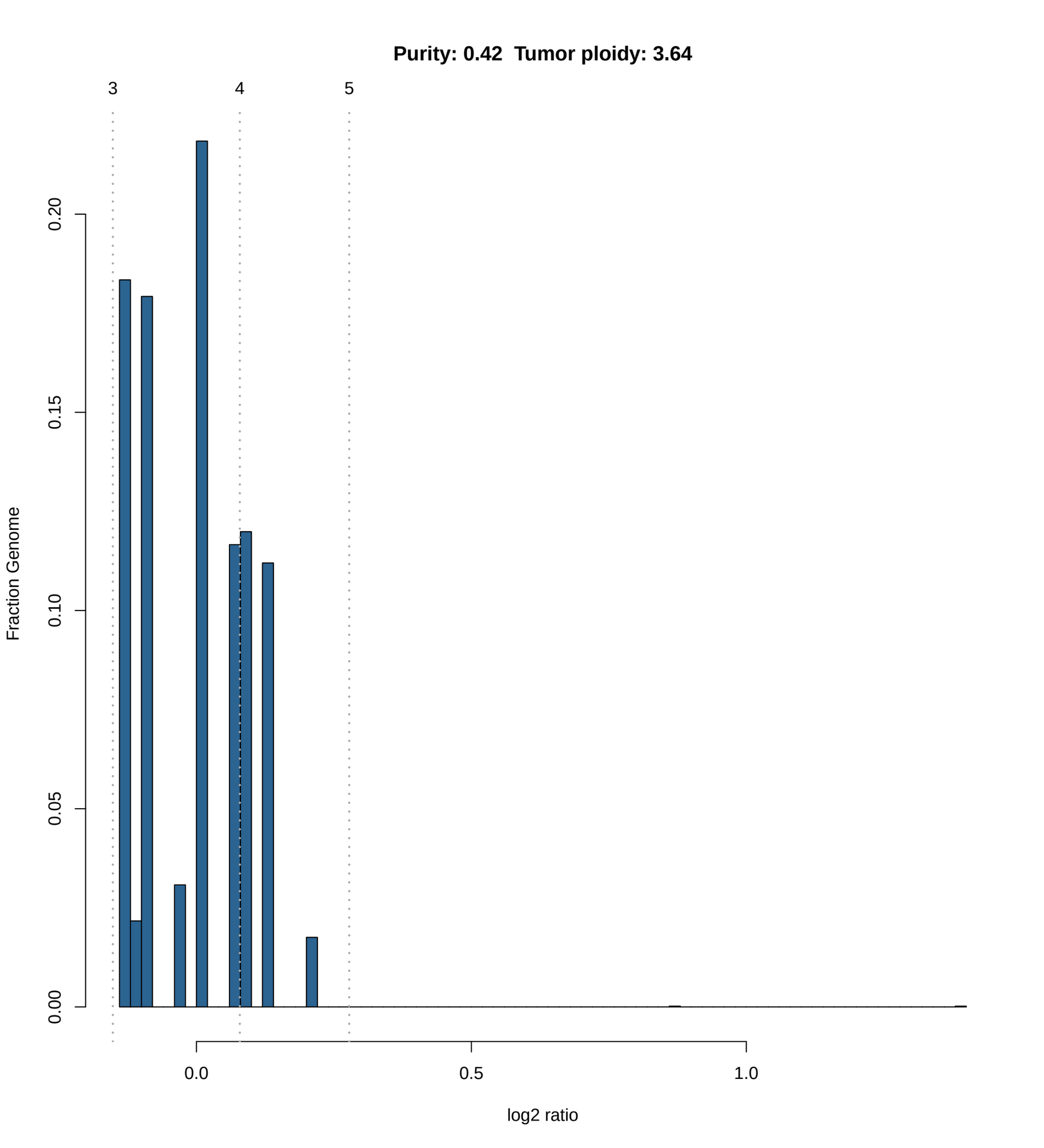

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

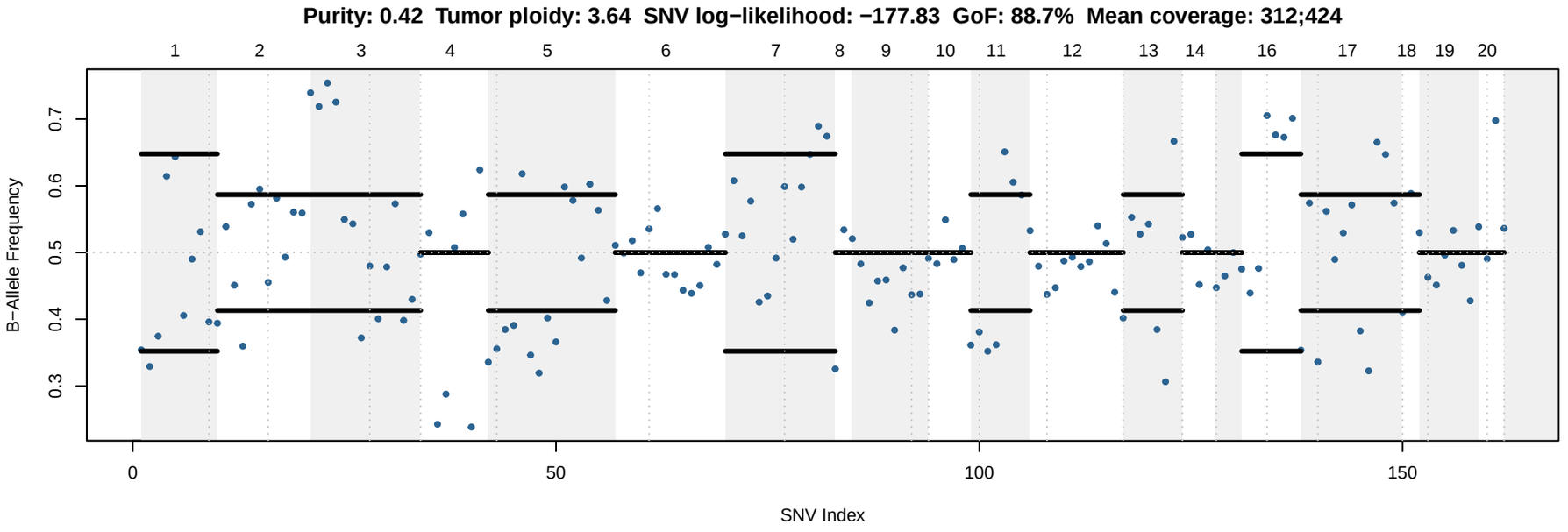

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
−0.5
0.0
0.5
Copy Number log−ratio
5m5
4m4
3m3
5m4
4m3
3m2
5m3
4m2
6m3
3m1
5m2
4m1
5m1
3m0
4m0
5m0

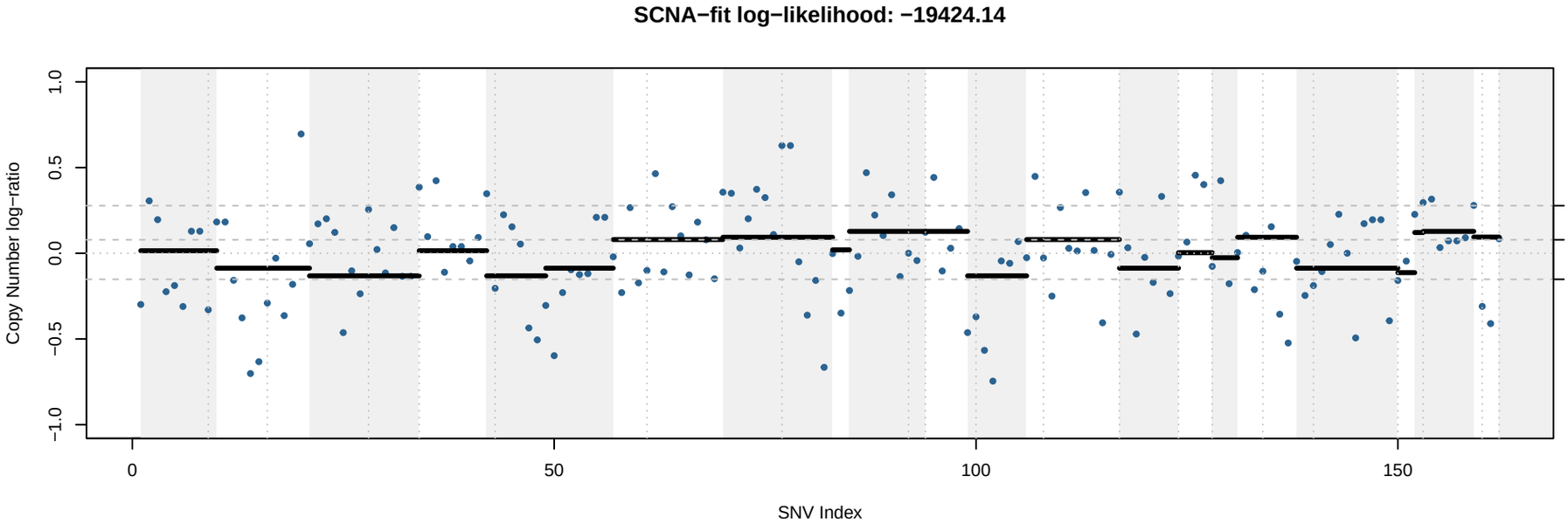

Coverage (log2)
6
7
8
9
10
0.2
0.4
0.6
Allelic fraction

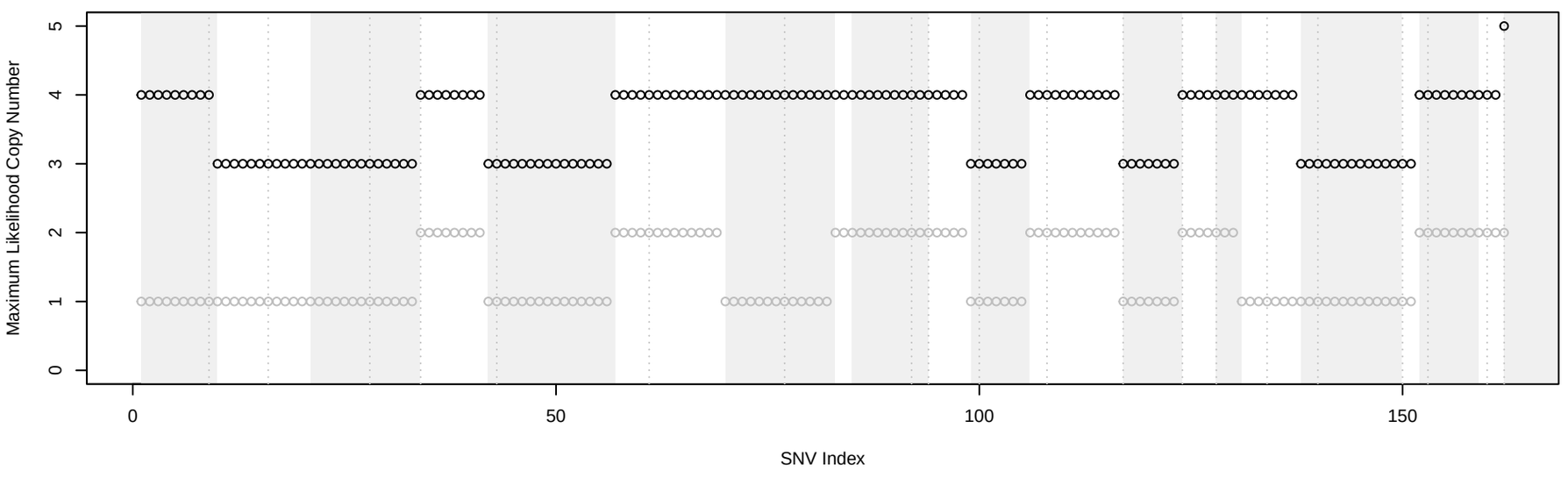

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
−0.5
0.0
0.5
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m2
3m1
4m1
5m1
6m1

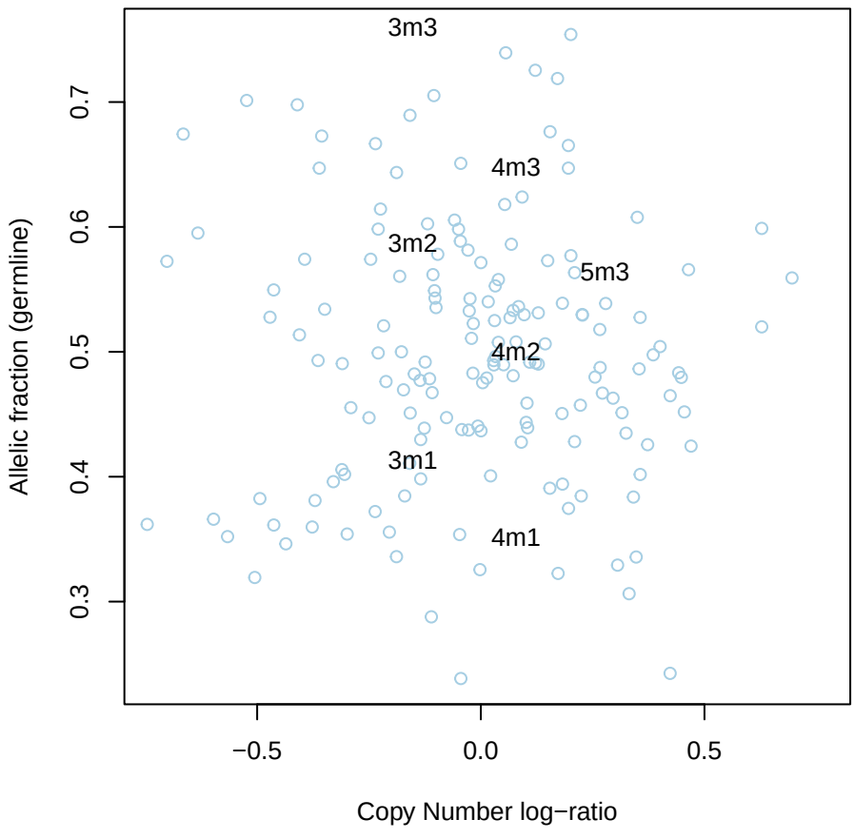

Power 0.8
Frequency
0
5
10
15
20
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

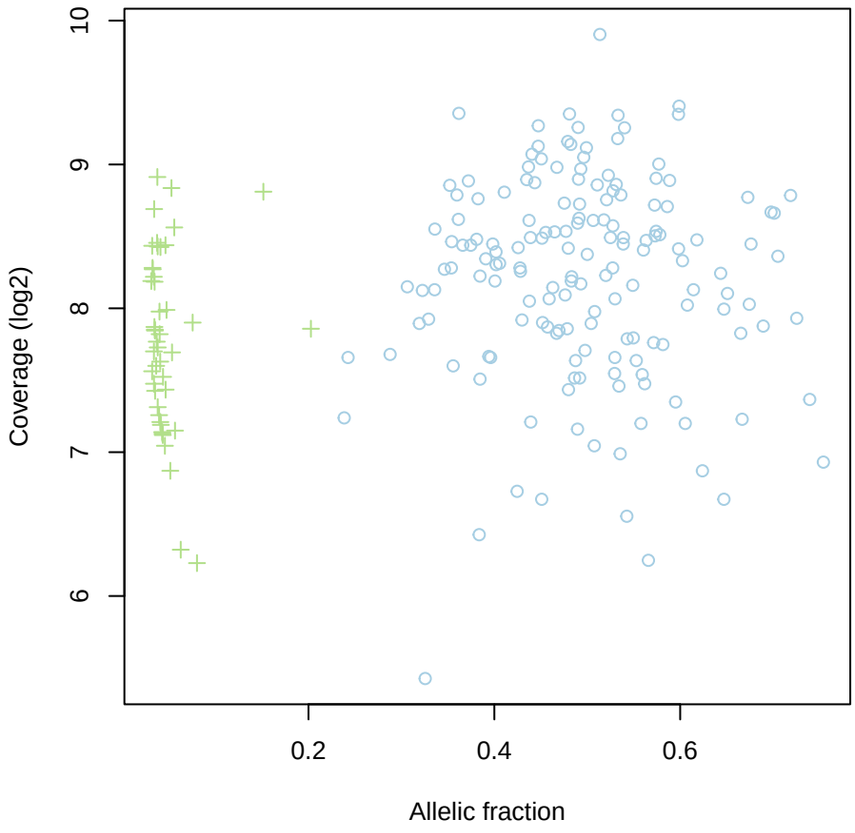

Purity: 0.42 Tumor ploidy: 3.64
3
4
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

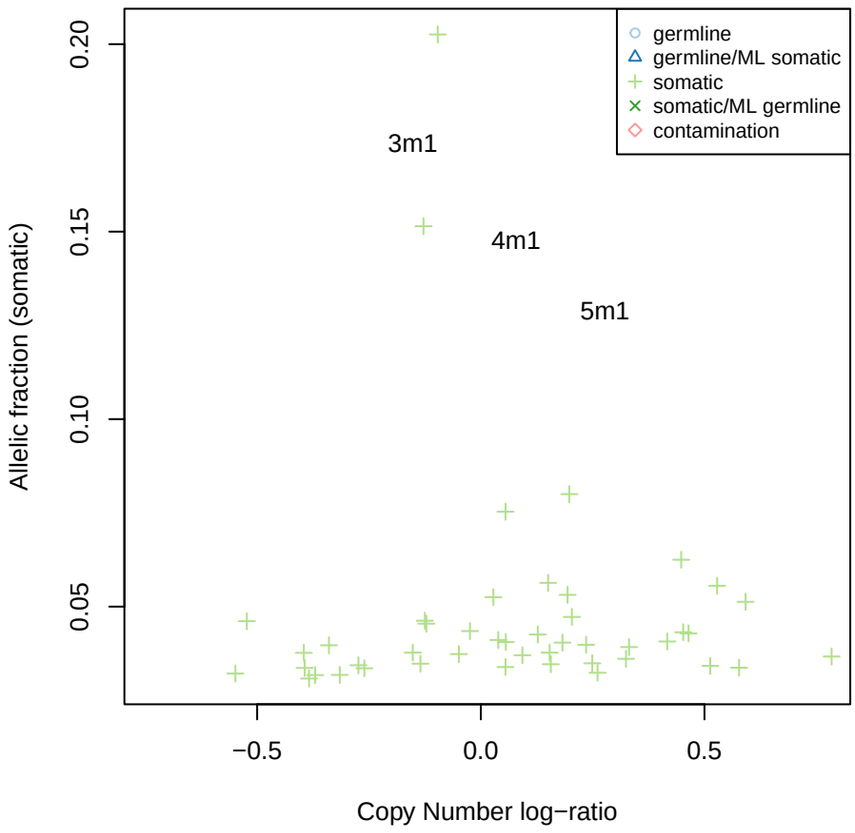

Purity: 0.42 Tumor ploidy: 3.64 SNV log−likelihood: −177.83 GoF: 88.7% Mean coverage: 312;424
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

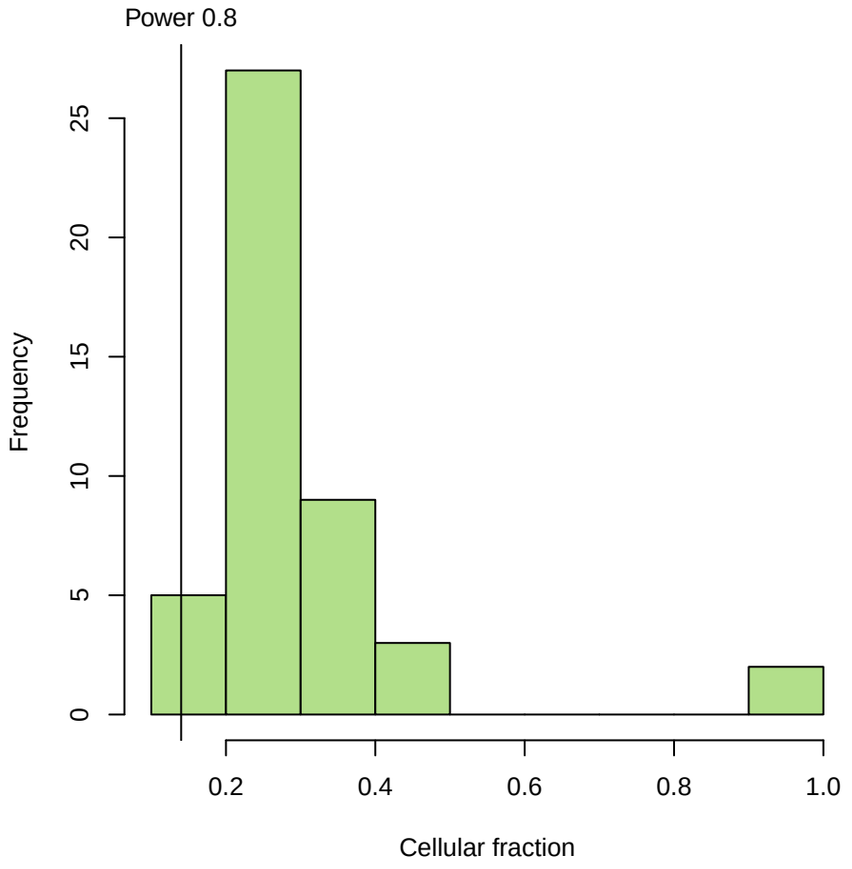

SCNA−fit log−likelihood: −19424.14
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5
0 50 100 150
SNV Index

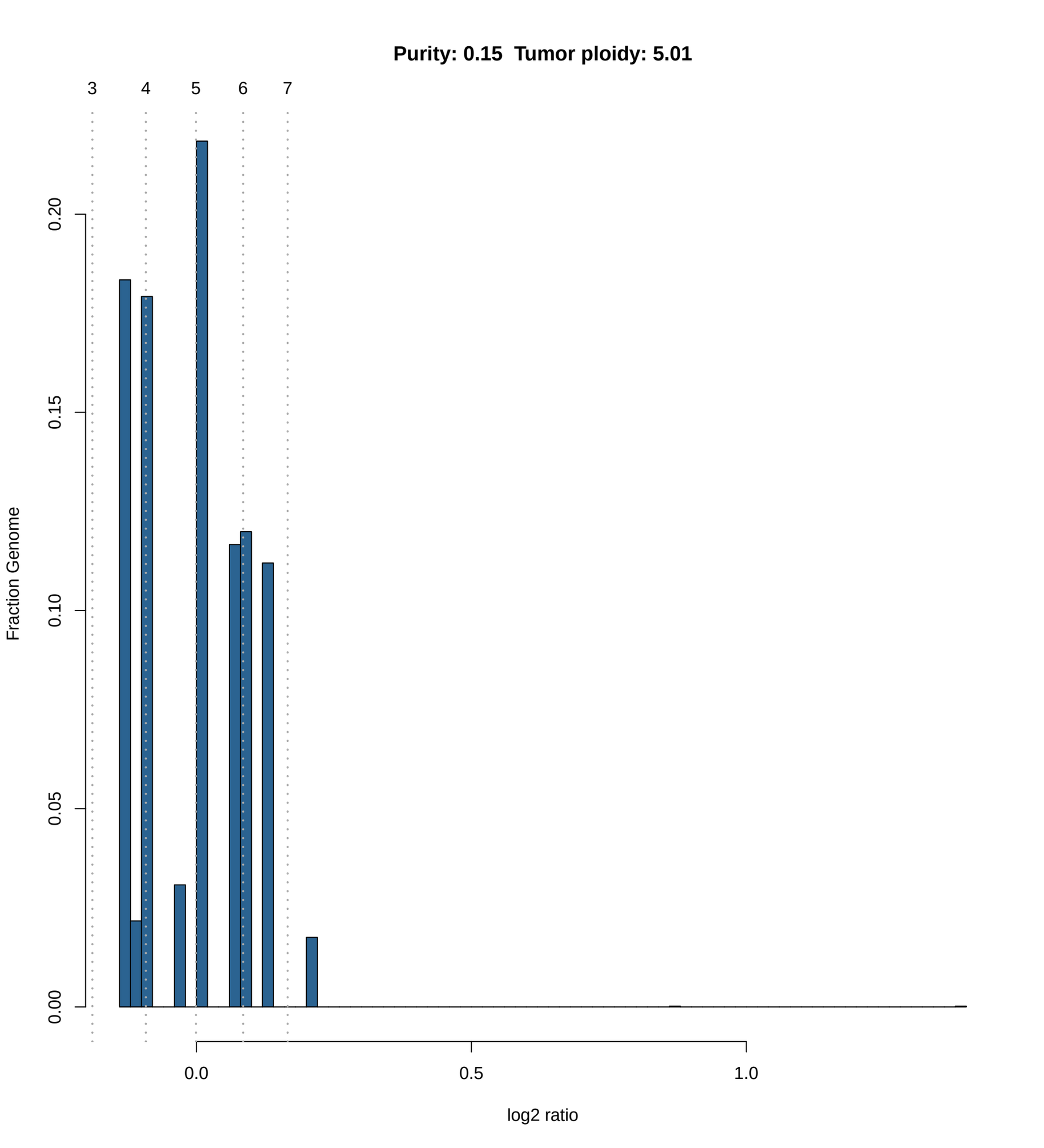

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

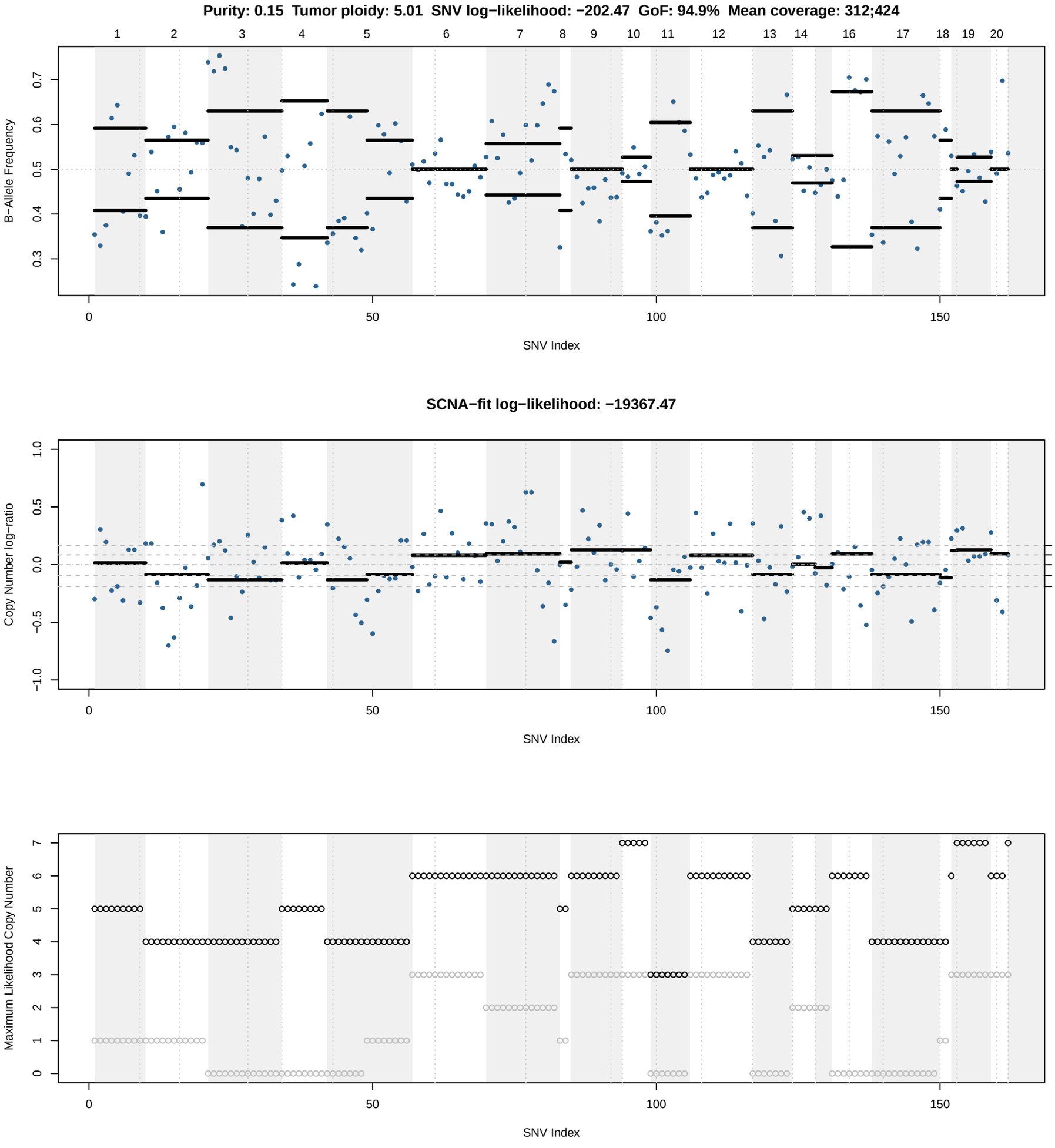

3m3
4m3
3m2
5m3
4m2
3m1
4m1
Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
−0.5
0.0
0.5
Copy Number log−ratio

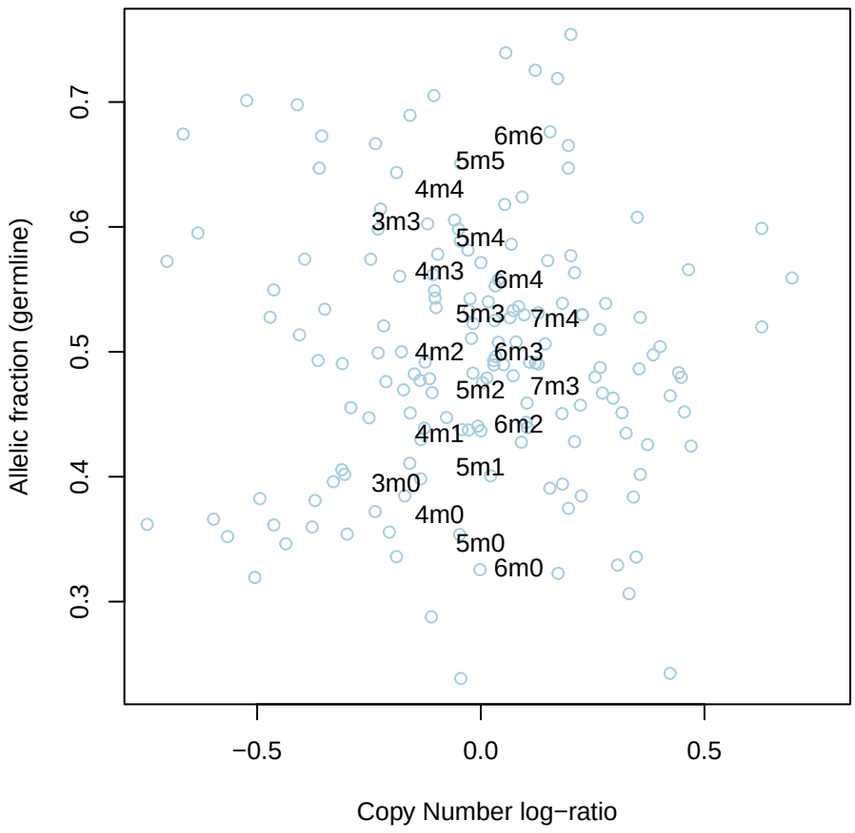

Coverage (log2)
6
7
8
9
10
0.2
0.4
0.6
Allelic fraction

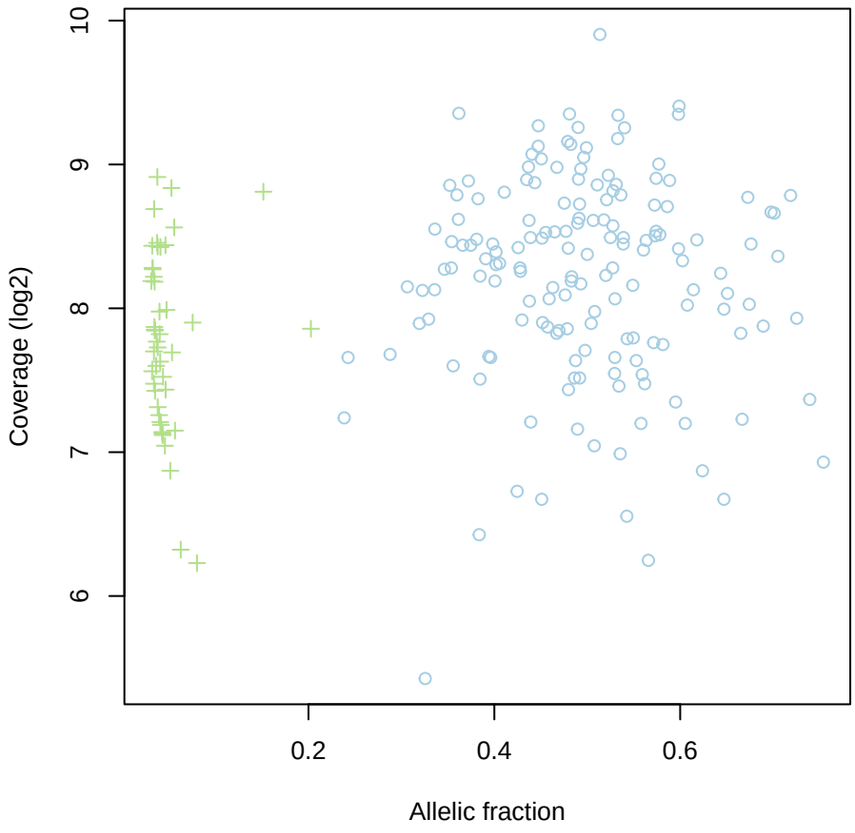

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
5m1
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
−0.5
0.0
0.5
Copy Number log−ratio

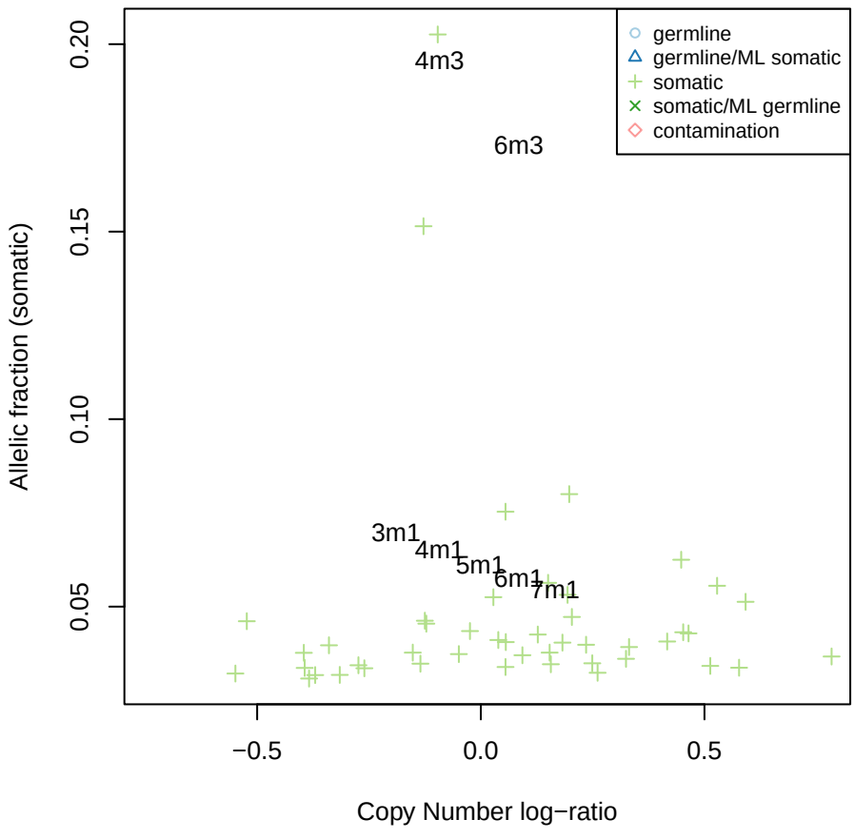

Power 0.8
Frequency
0
5
10
15
20
25
0.2
0.4
0.6
0.8
1.0
Cellular fraction

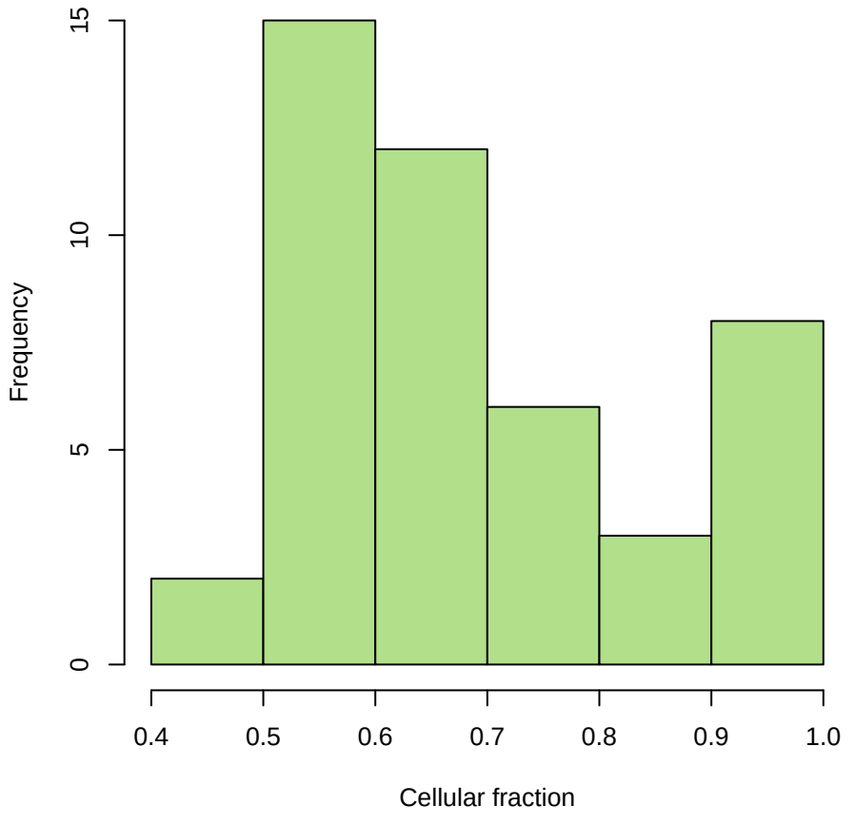

Purity: 0.15 Tumor ploidy: 5.01
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

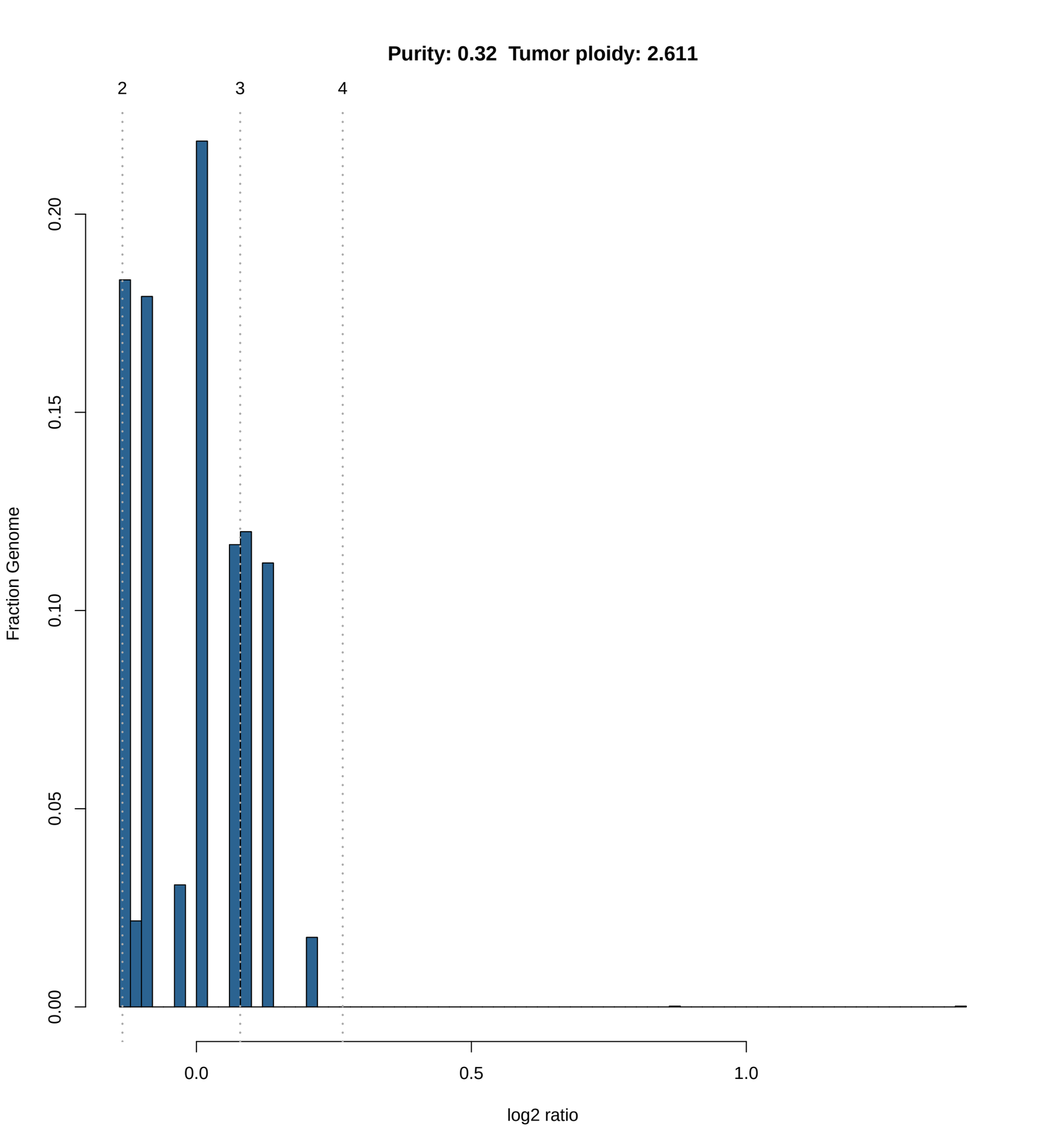

Purity: 0.15 Tumor ploidy: 5.01 SNV log−likelihood: −202.47 GoF: 94.9% Mean coverage: 312;424
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index
SCNA−fit log−likelihood: −19367.47
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 5 7
0 50 100 150
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

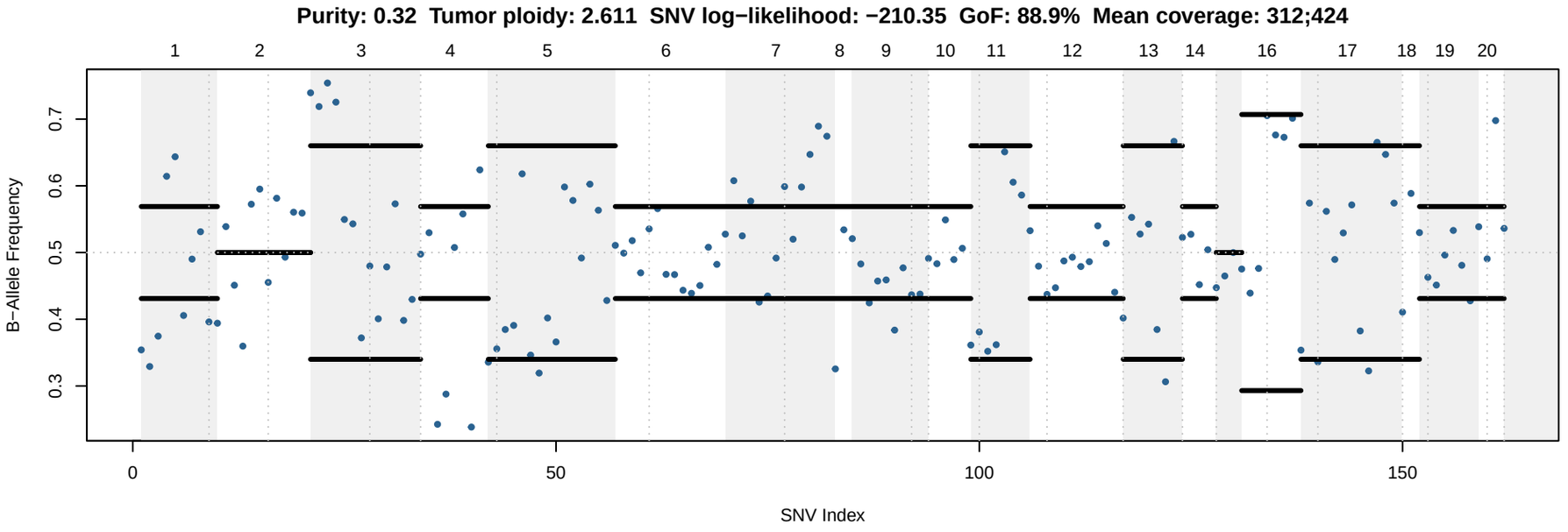

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
−0.5
0.0
0.5
Copy Number log−ratio
6m6
5m5
4m4
3m3
5m4
4m3
6m4
5m3
7m4
4m2
6m3
5m2
7m3
4m1
6m2
5m1
3m0
4m0
5m0
6m0

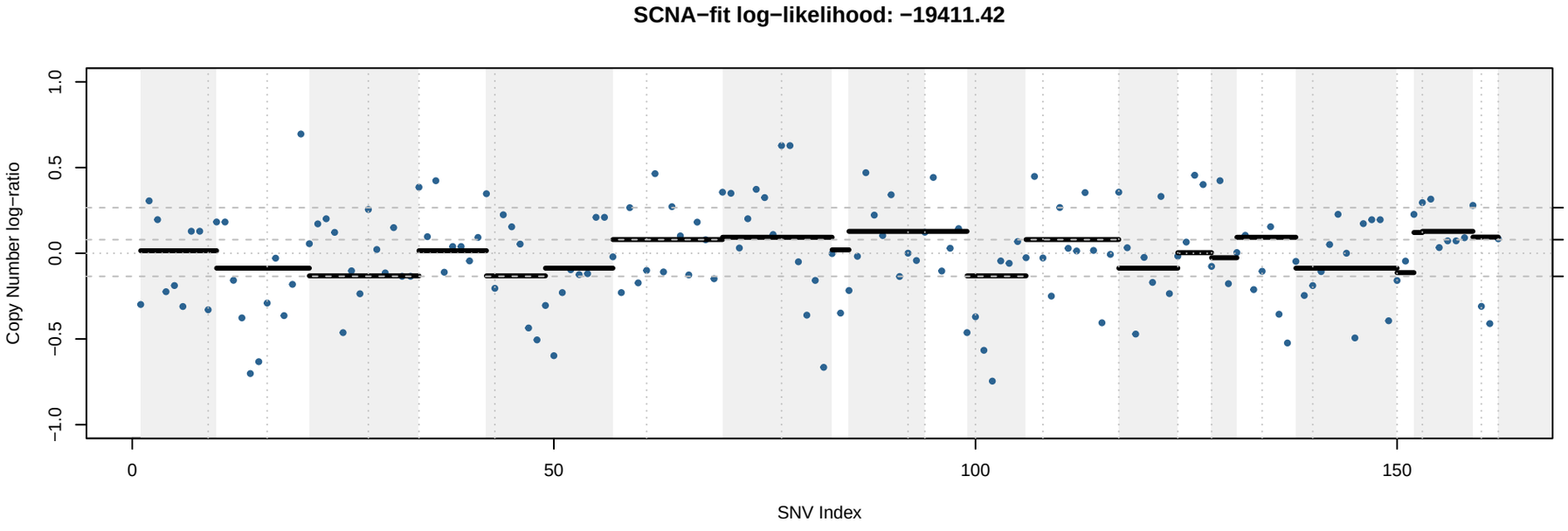

Coverage (log2)
6
7
8
9
10
0.2
0.4
0.6
Allelic fraction

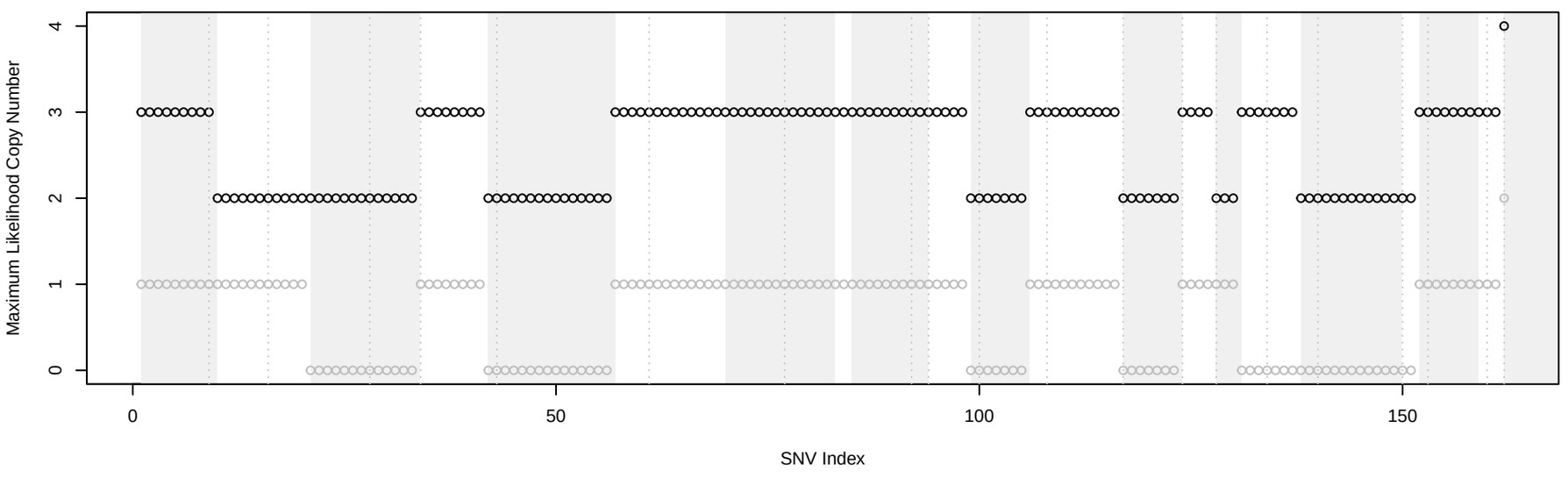

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
−0.5
0.0
0.5
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m3
6m3
3m1
4m1
5m1
6m1
7m1

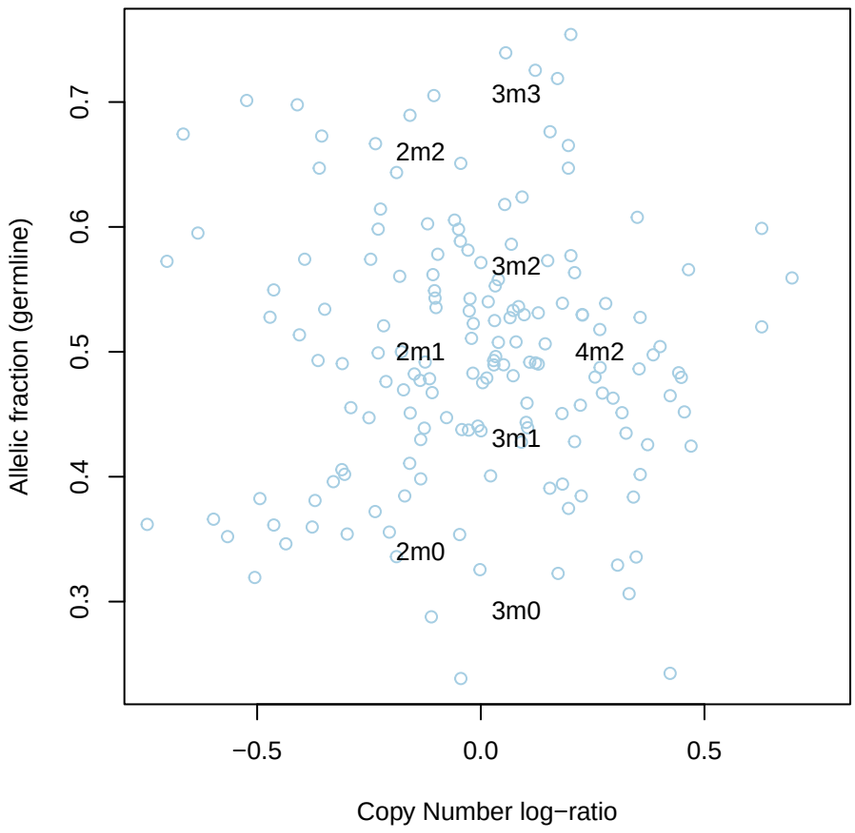

Frequency
0
5
10
15
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

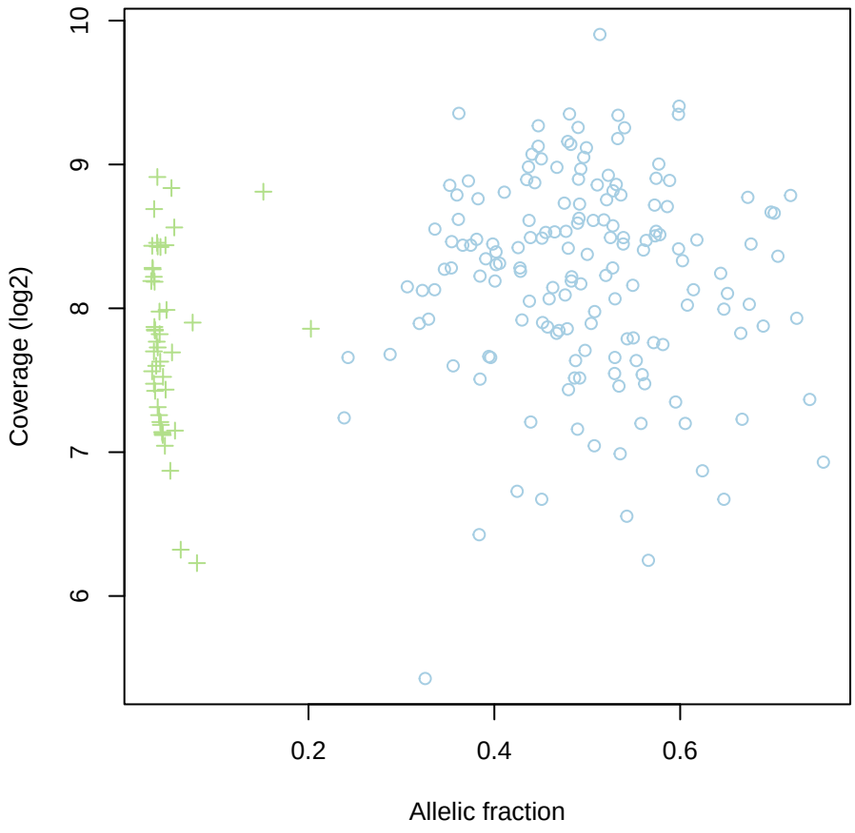

Purity: 0.32 Tumor ploidy: 2.611
2
3
4
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

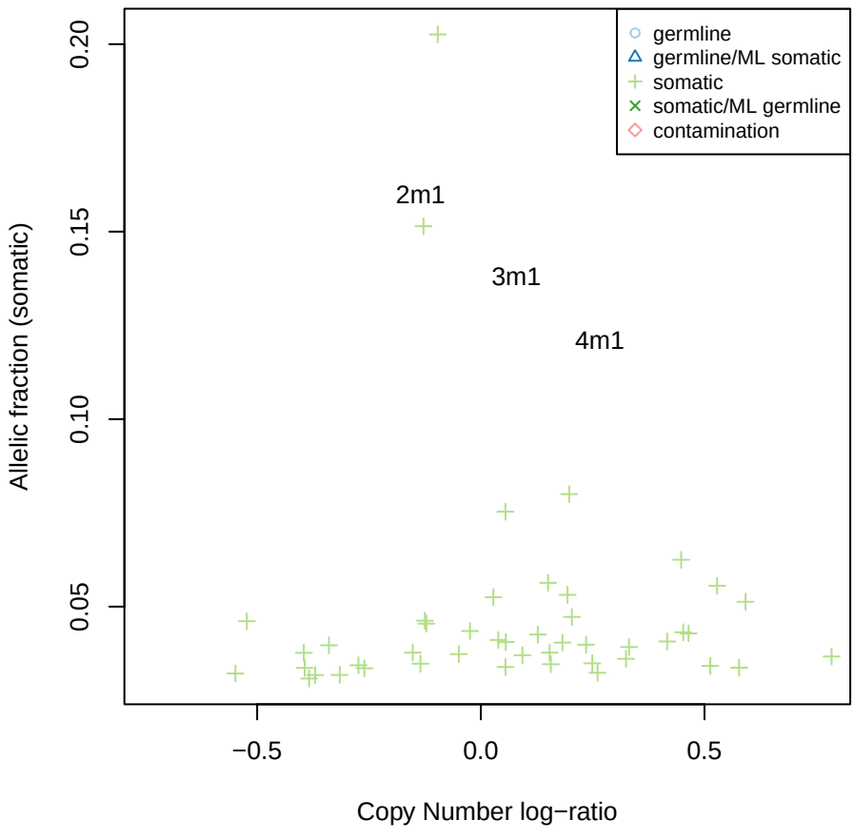

Purity: 0.32 Tumor ploidy: 2.611 SNV log−likelihood: −210.35 GoF: 88.9% Mean coverage: 312;424
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

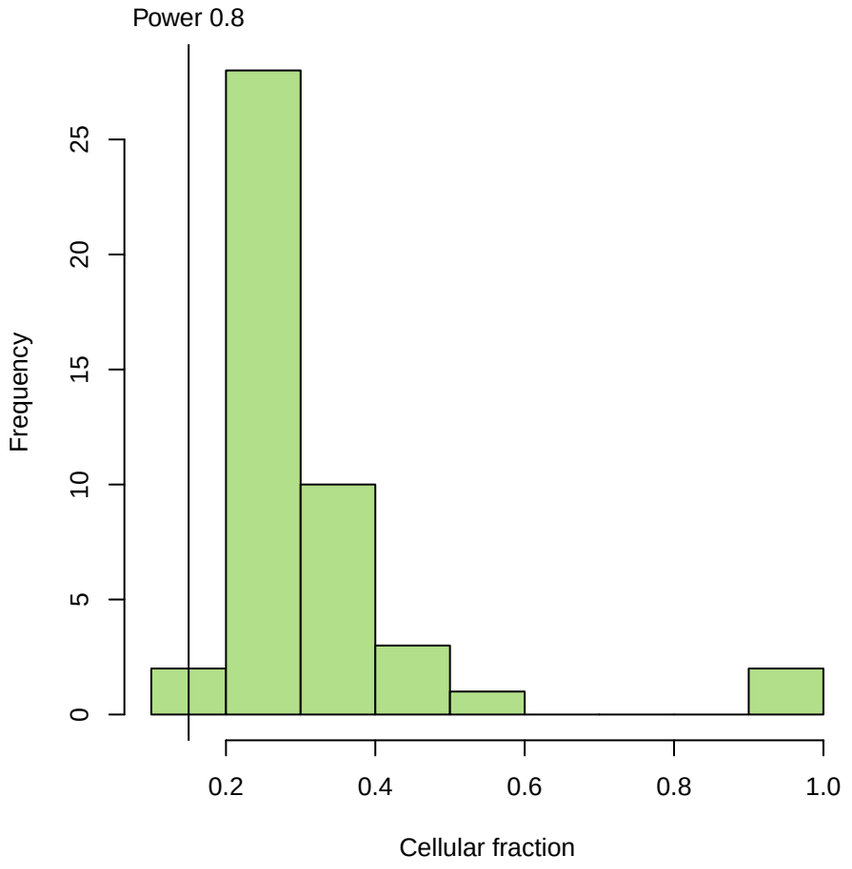

SCNA−fit log−likelihood: −19411.42
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4
0 50 100 150
SNV Index

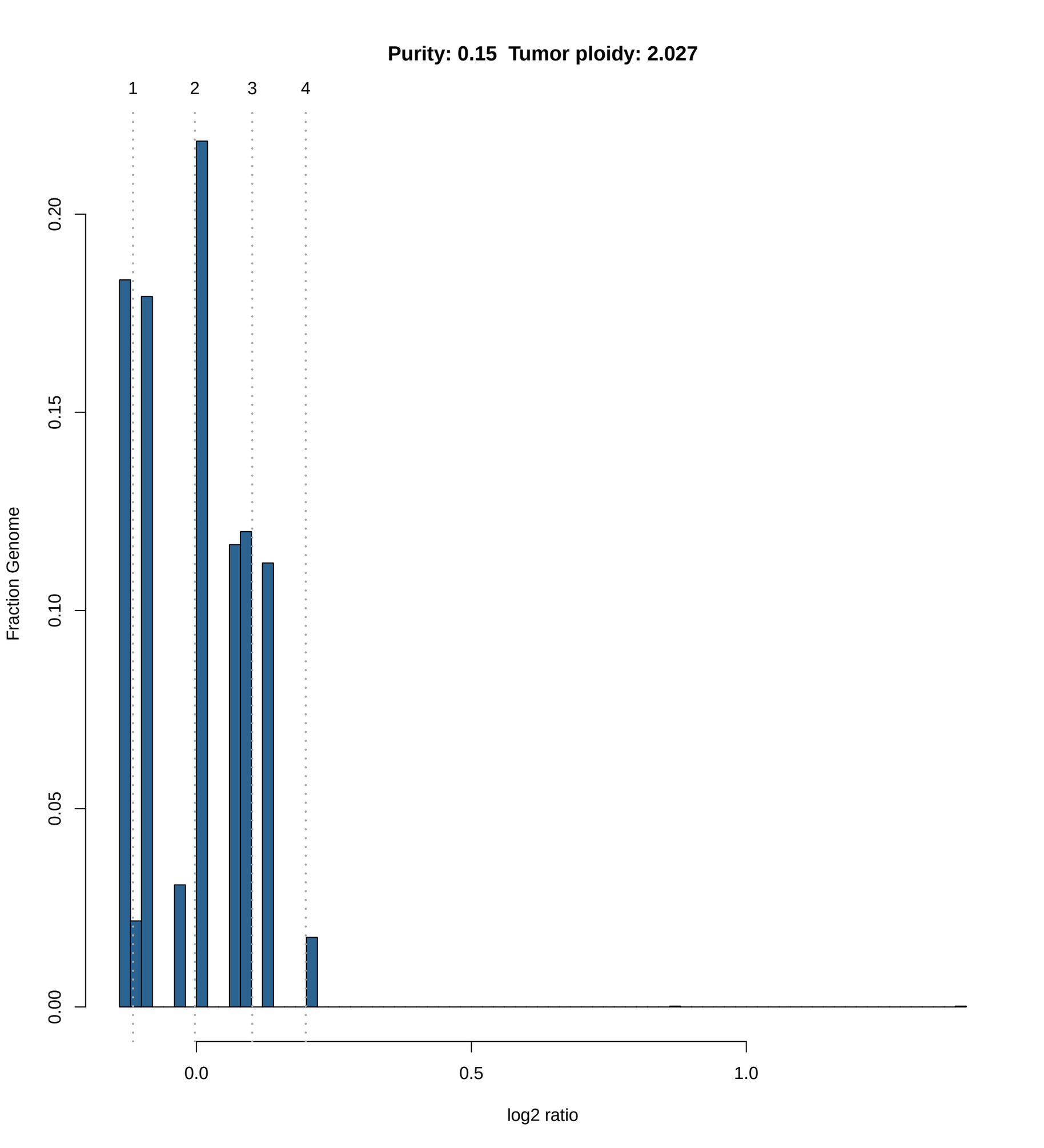

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

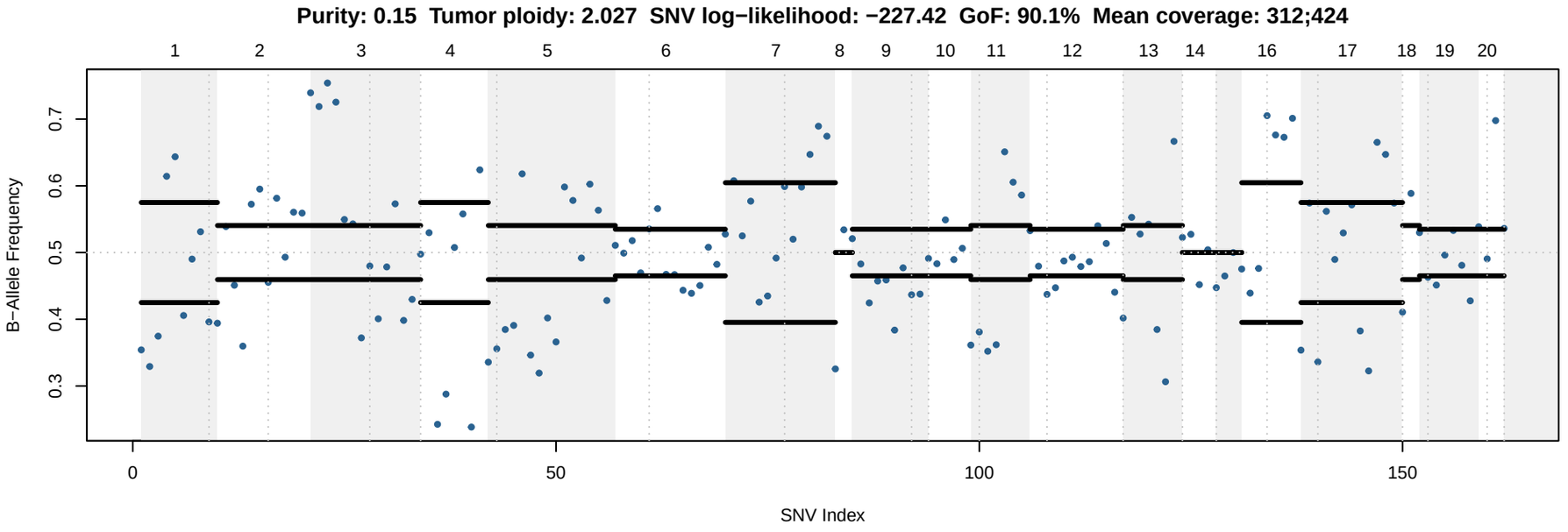

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
3m3
2m2
3m2
2m1
4m2
3m1
2m0
3m0
−0.5
0.0
0.5
Copy Number log−ratio

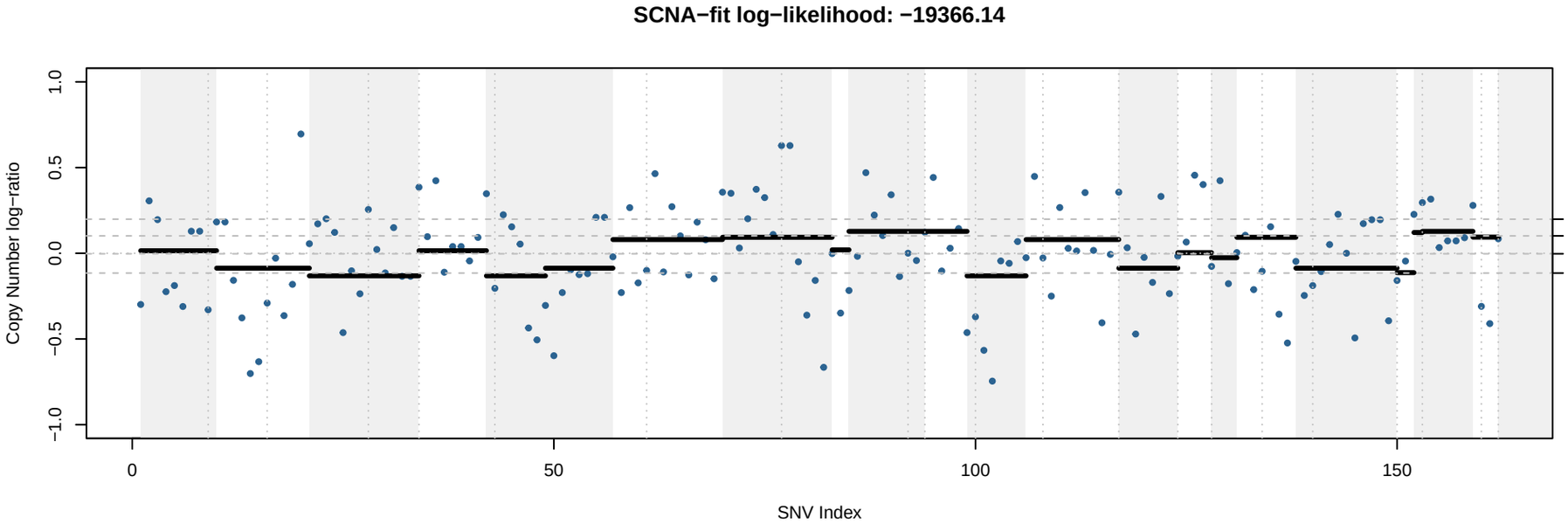

Coverage (log2)
6
7
8
9
10
0.2
0.4
0.6
Allelic fraction

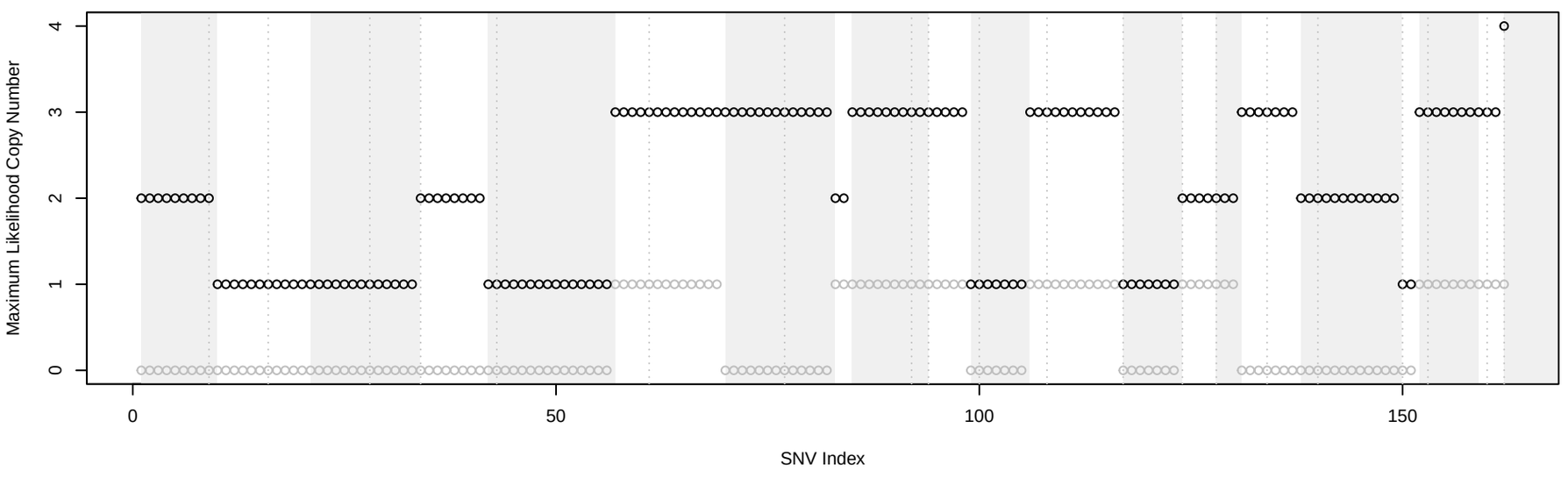

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
4m1
−0.5
0.0
0.5
Copy Number log−ratio

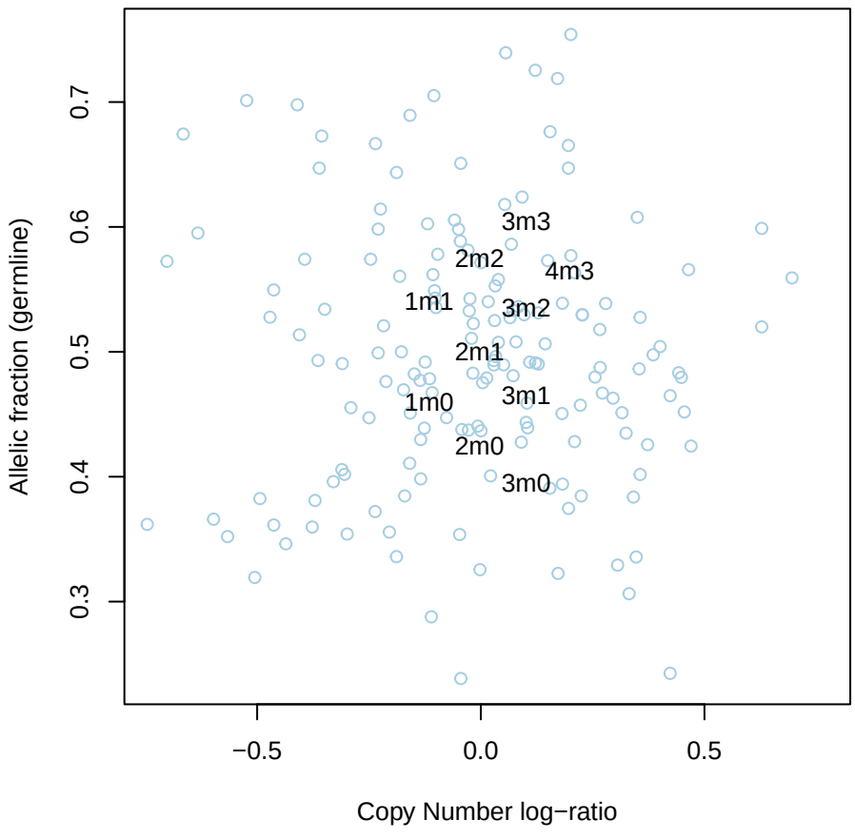

Power 0.8
Frequency
0
5
10
15
20
25
0.2
0.4
0.6
0.8
1.0
Cellular fraction

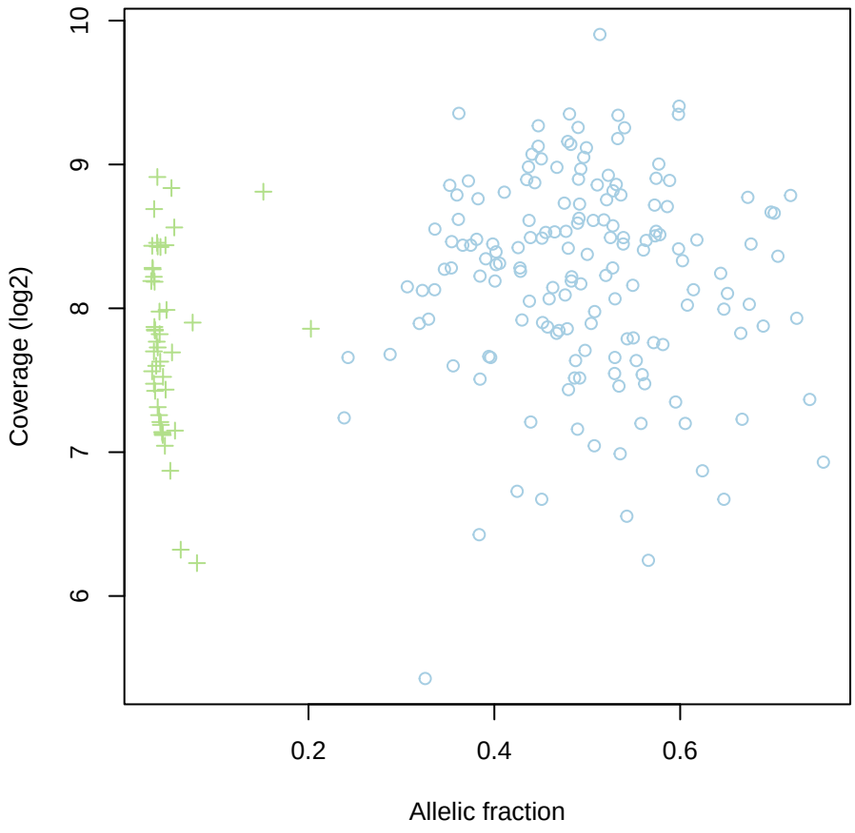

Purity: 0.15 Tumor ploidy: 2.027
1
2
3
4
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

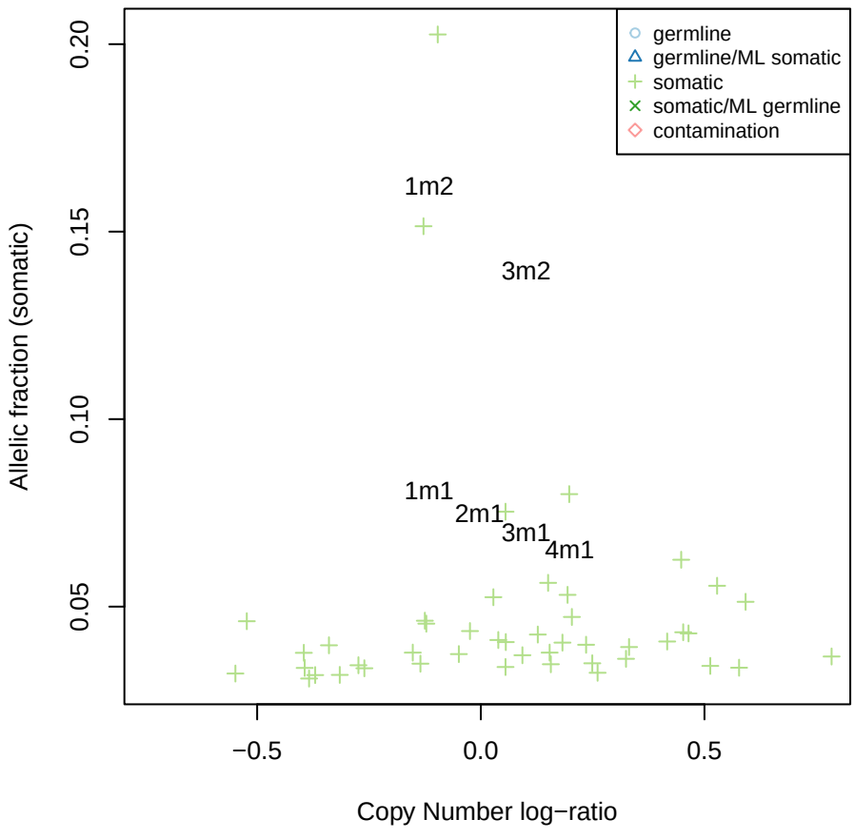

Purity: 0.15 Tumor ploidy: 2.027 SNV log−likelihood: −227.42 GoF: 90.1% Mean coverage: 312;424
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

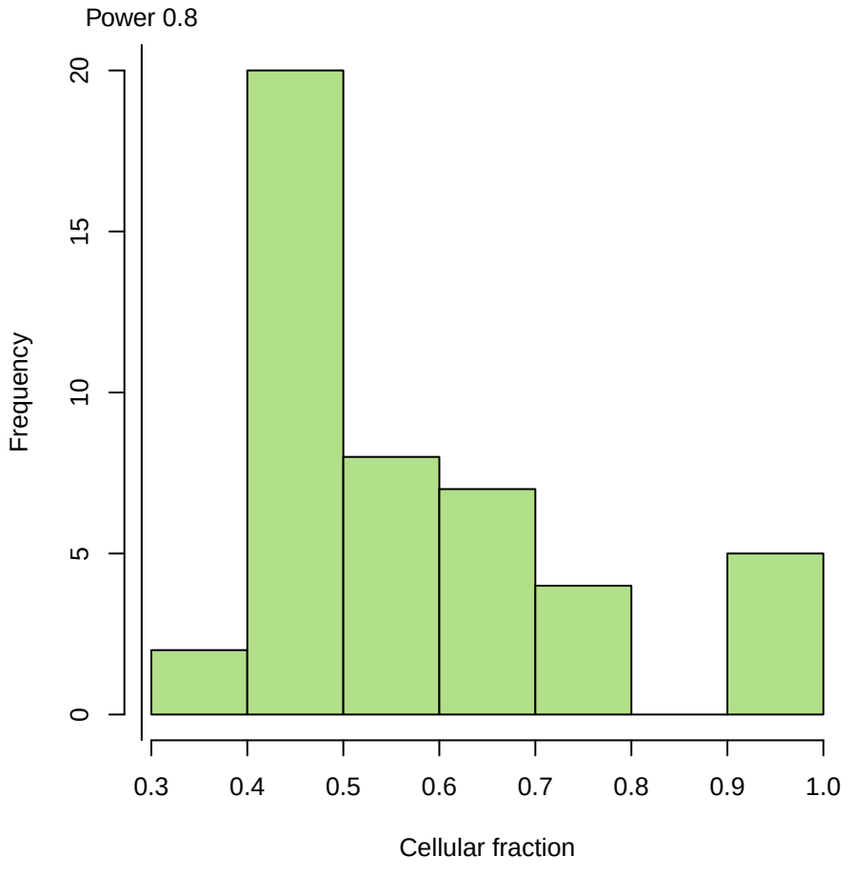

SCNA−fit log−likelihood: −19366.14
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 3
0 50 100 150
SNV Index

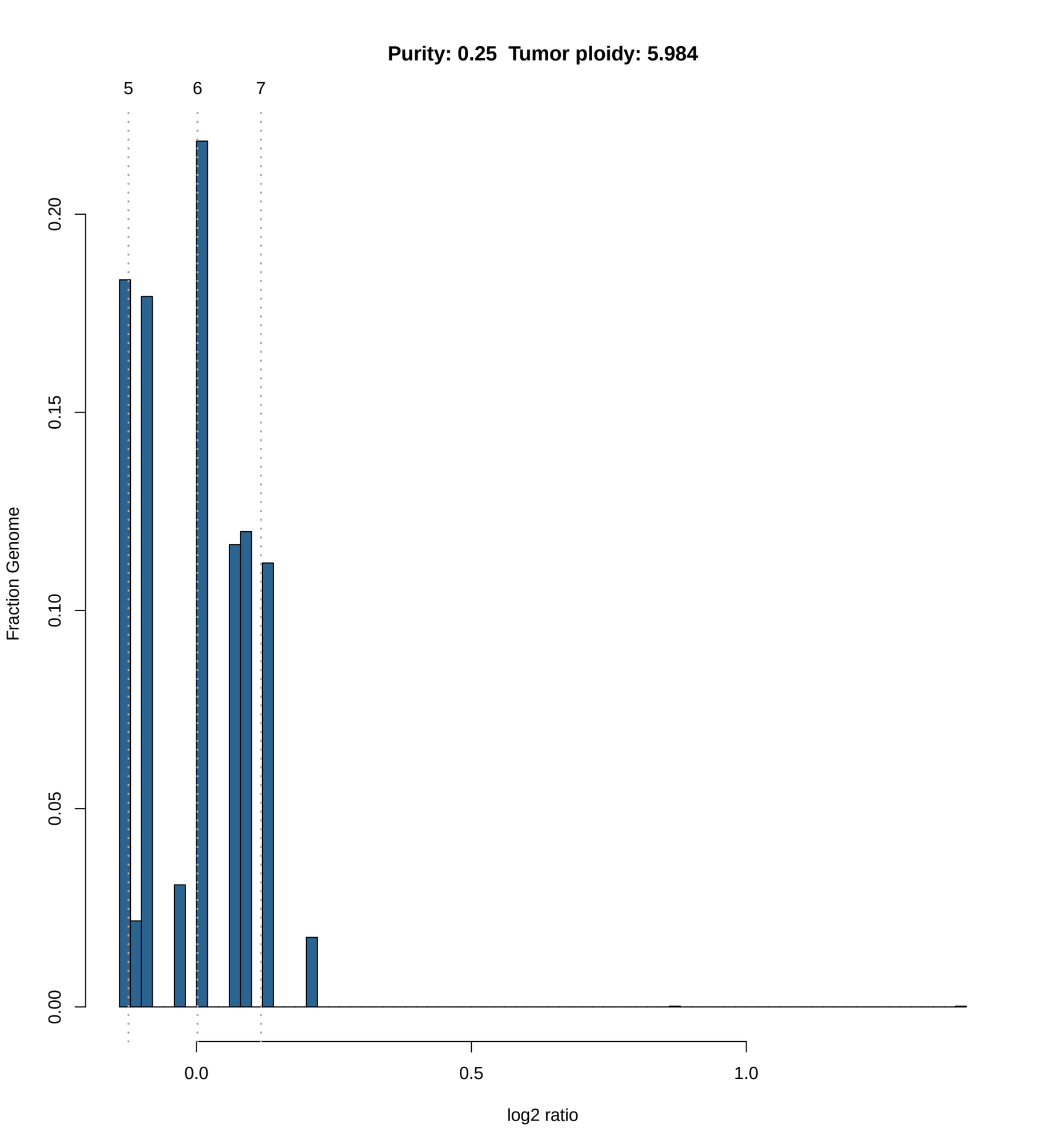

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

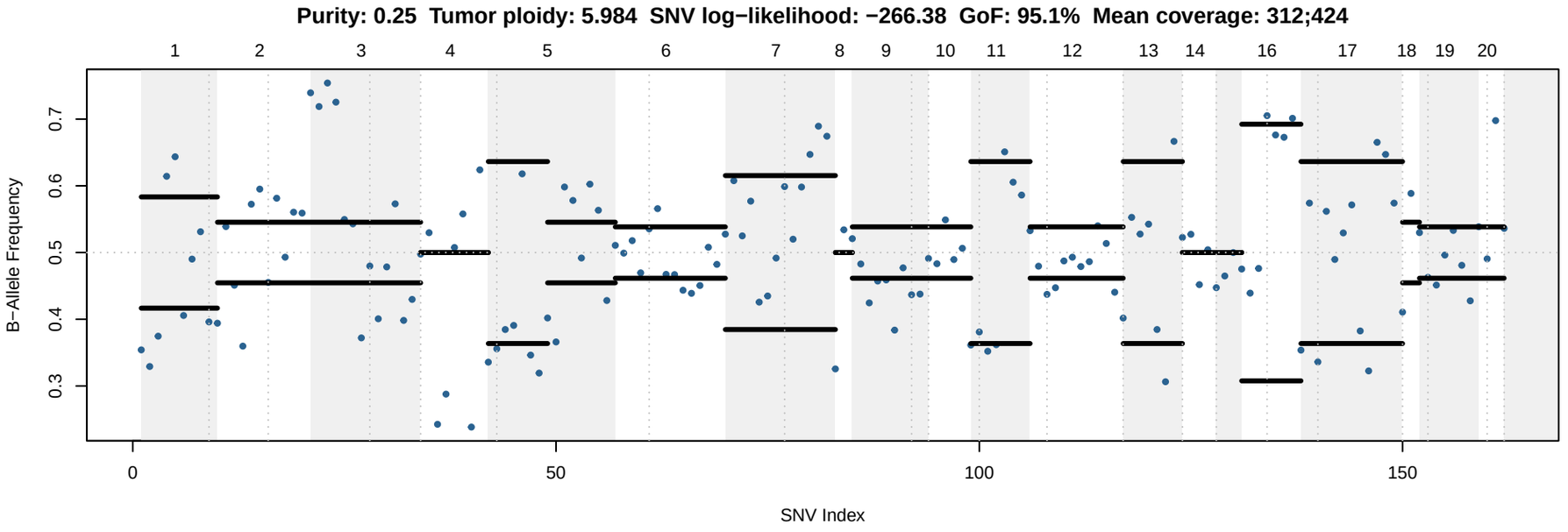

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
−0.5
0.0
0.5
Copy Number log−ratio
3m3
2m2
4m3
1m1
3m2
2m1
1m0
3m1
2m0
3m0

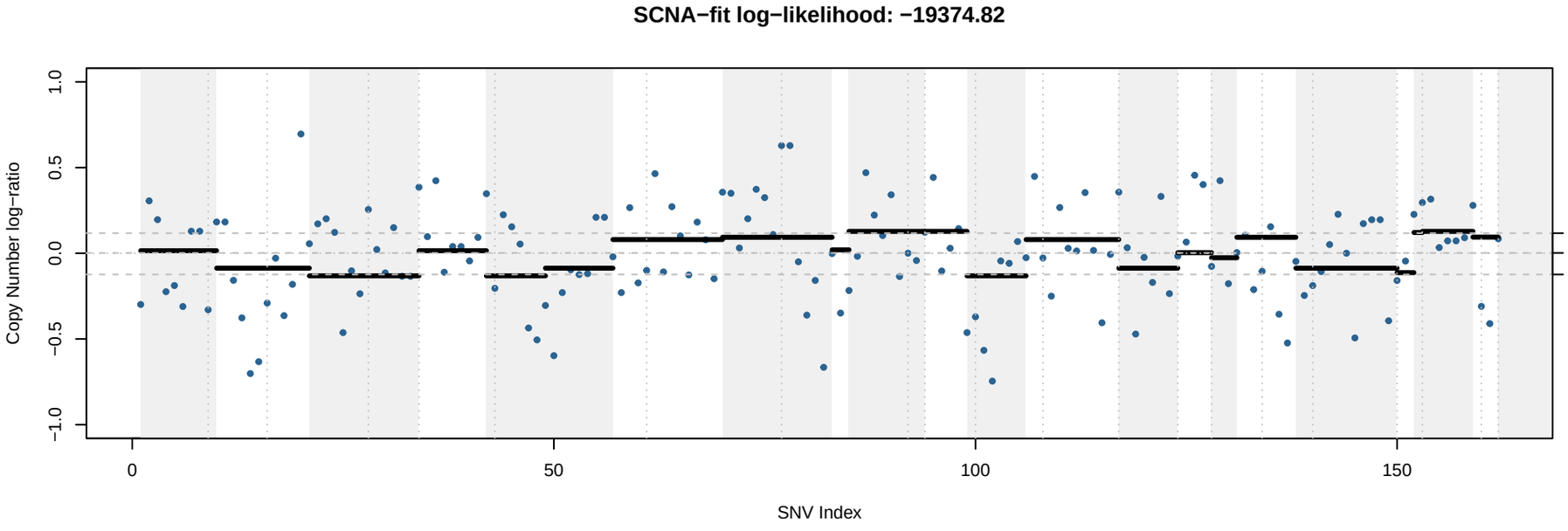

Coverage (log2)
6
7
8
9
10
0.2
0.4
0.6
Allelic fraction

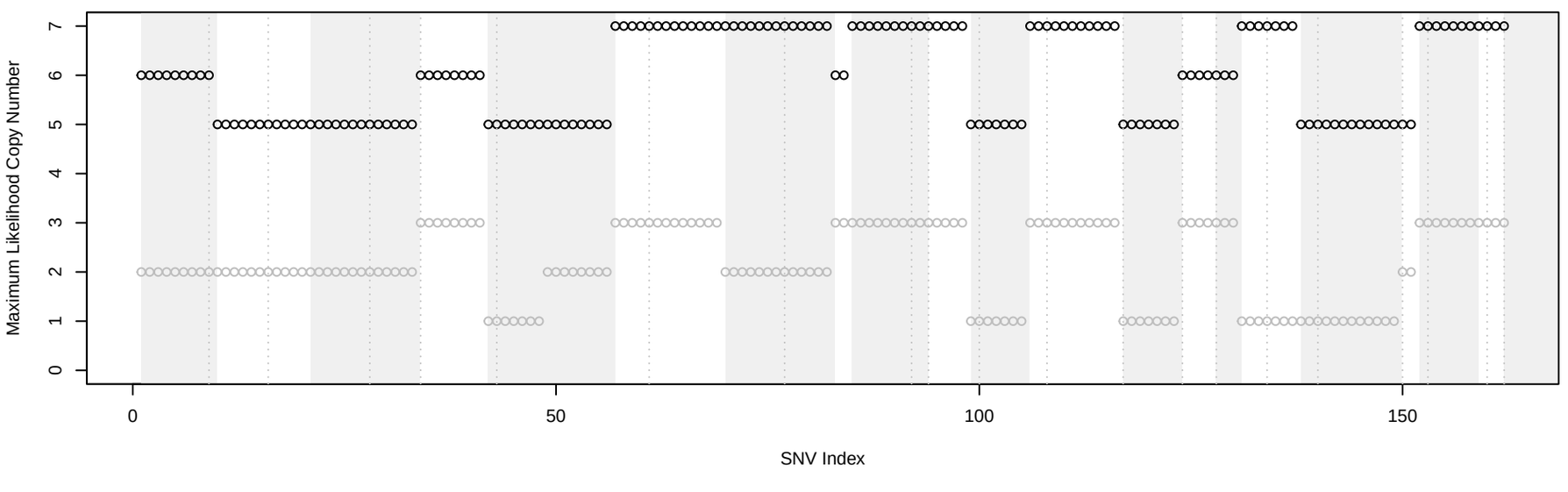

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
−0.5
0.0
0.5
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m2
3m2
1m1
2m1
3m1
4m1

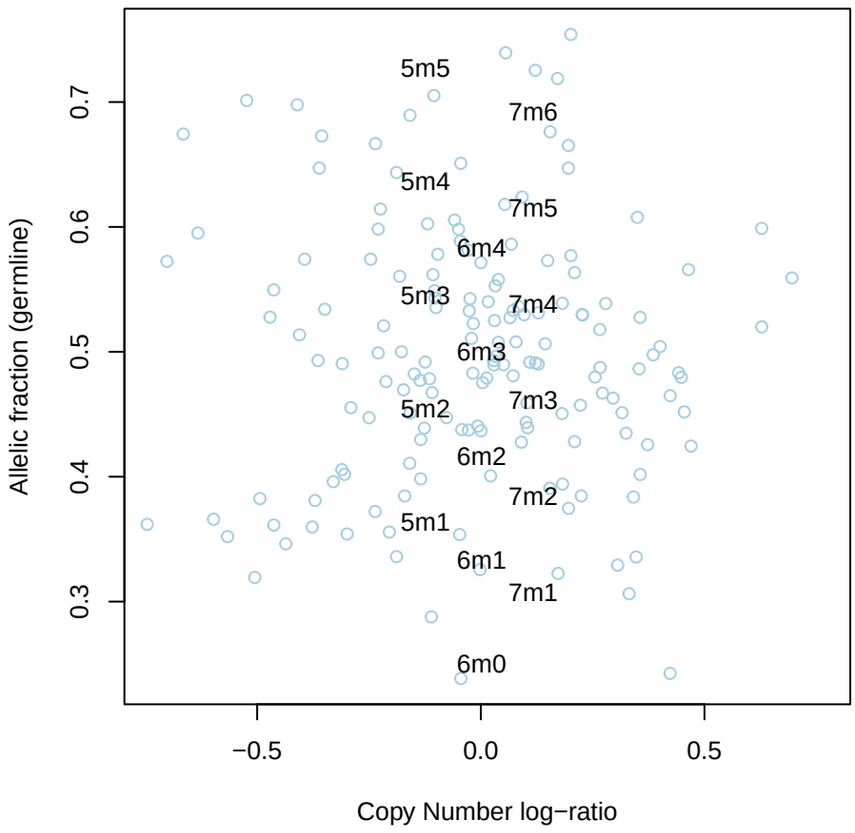

Power 0.8
Frequency
0
5
10
15
20
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

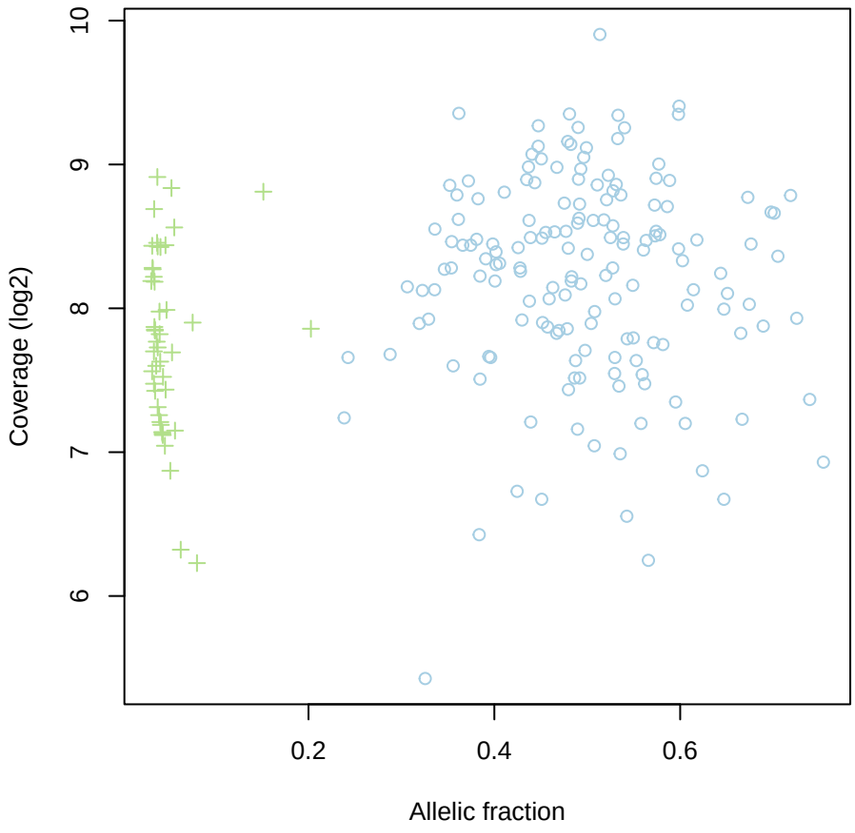

Purity: 0.25 Tumor ploidy: 5.984
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

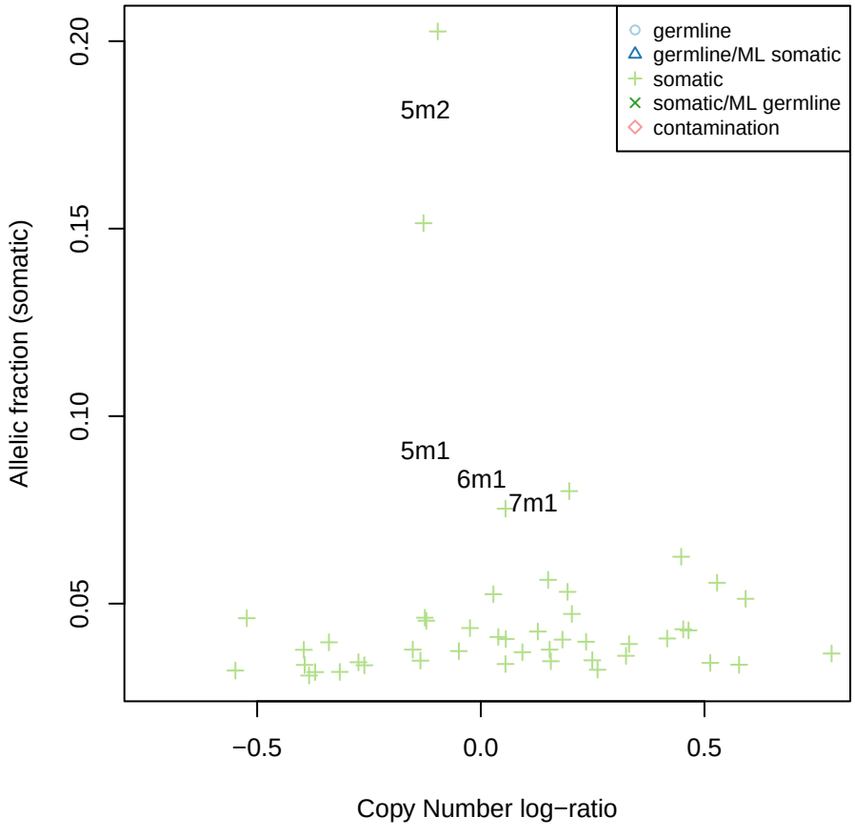

Purity: 0.25 Tumor ploidy: 5.984 SNV log−likelihood: −266.38 GoF: 95.1% Mean coverage: 312;424
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

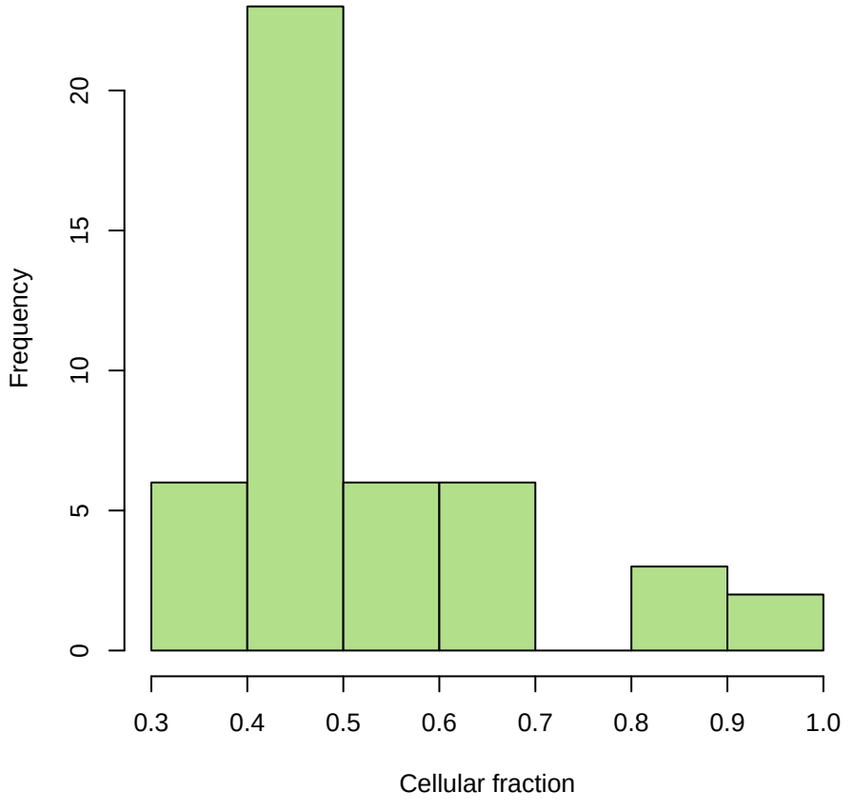

SCNA−fit log−likelihood: −19374.82
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
5 7
0 50 100 150
SNV Index

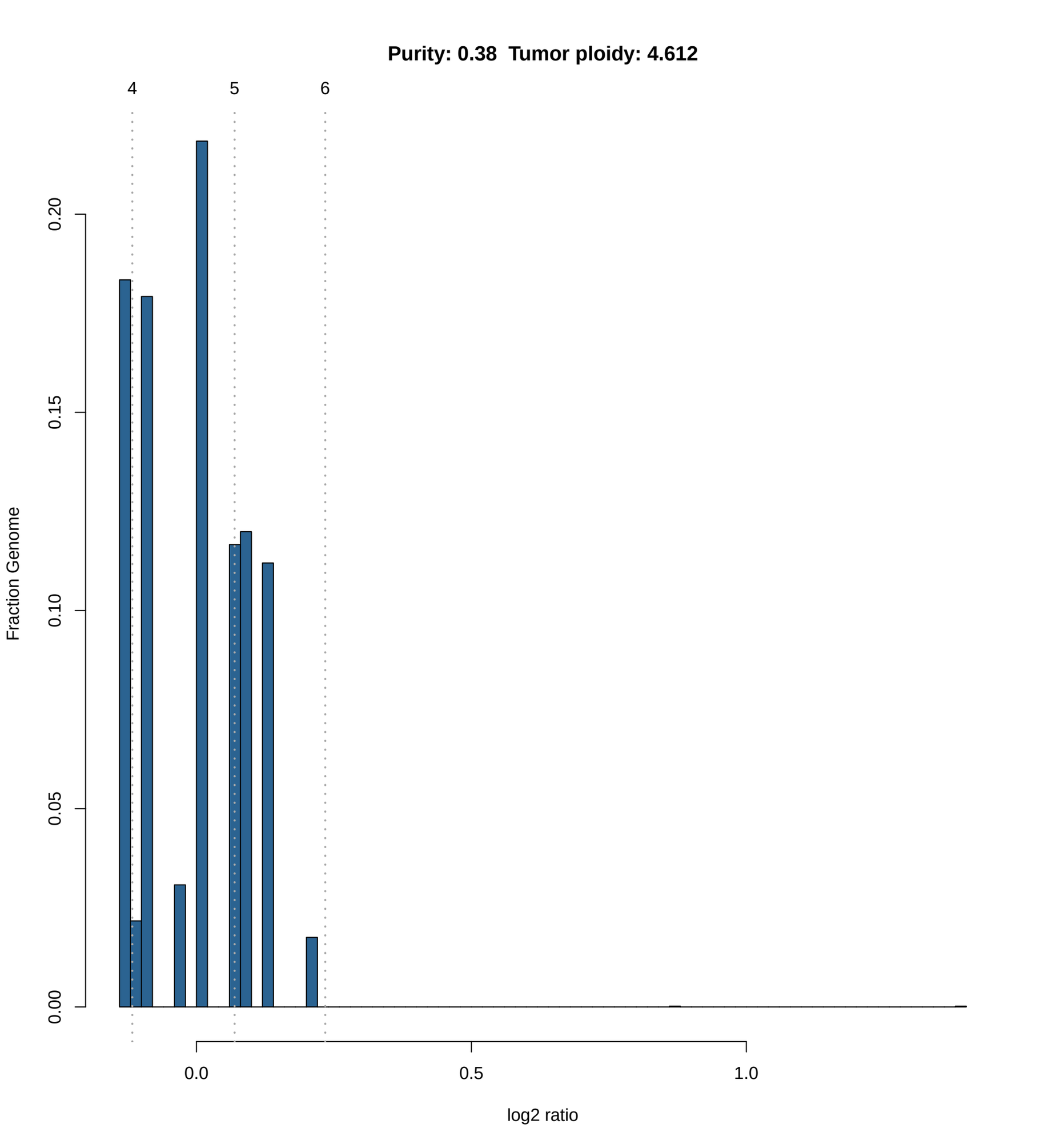

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

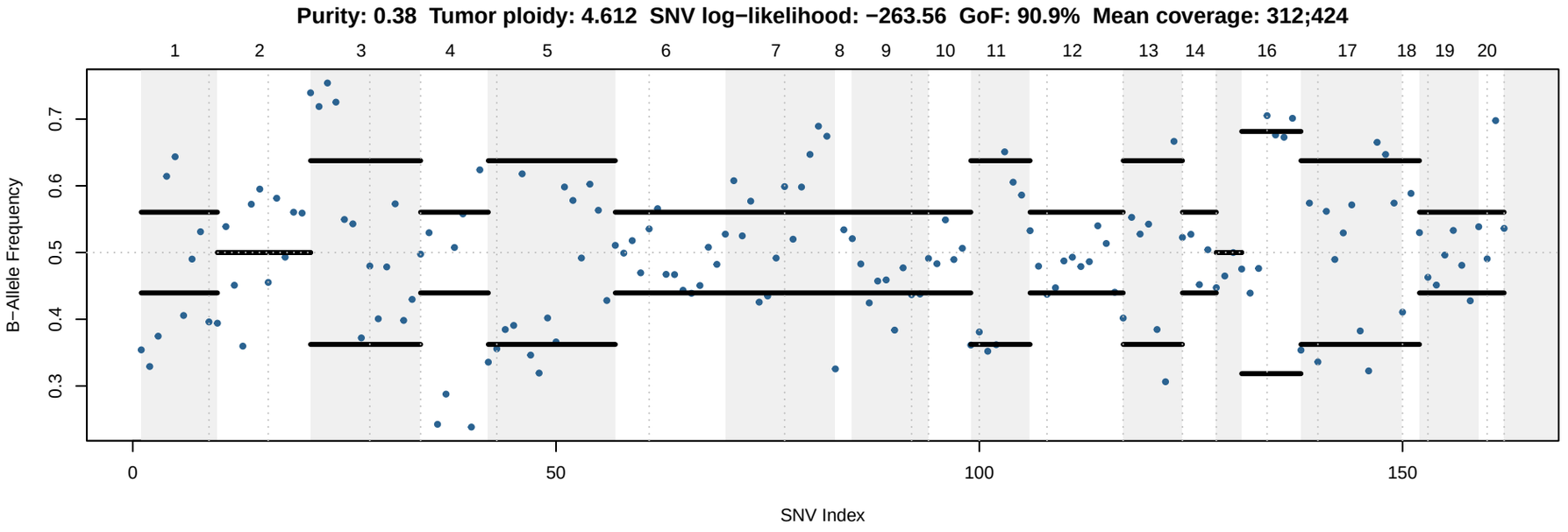

Allelic fraction (germline)
Copy Number log−ratio
5m5
7m6
5m4
7m5
6m4
5m3
7m4
6m3
5m2
7m3
6m2
7m2
5m1
6m1
7m1
6m0

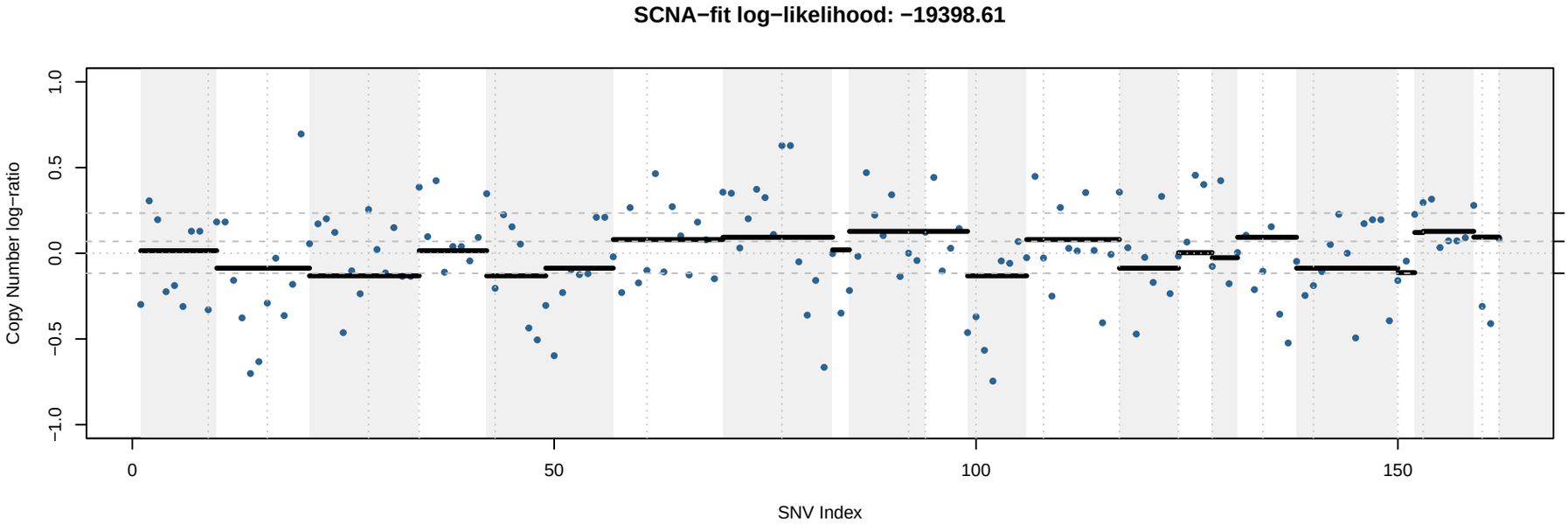

Coverage (log2)
Allelic fraction

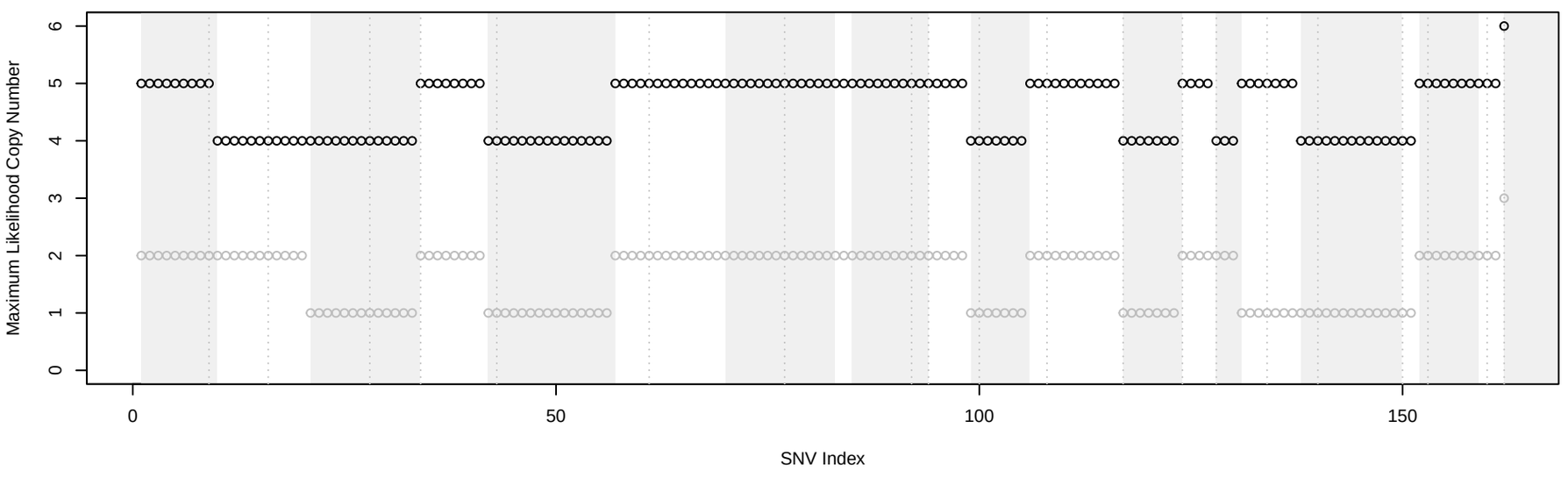

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m2
5m1
6m1
7m1

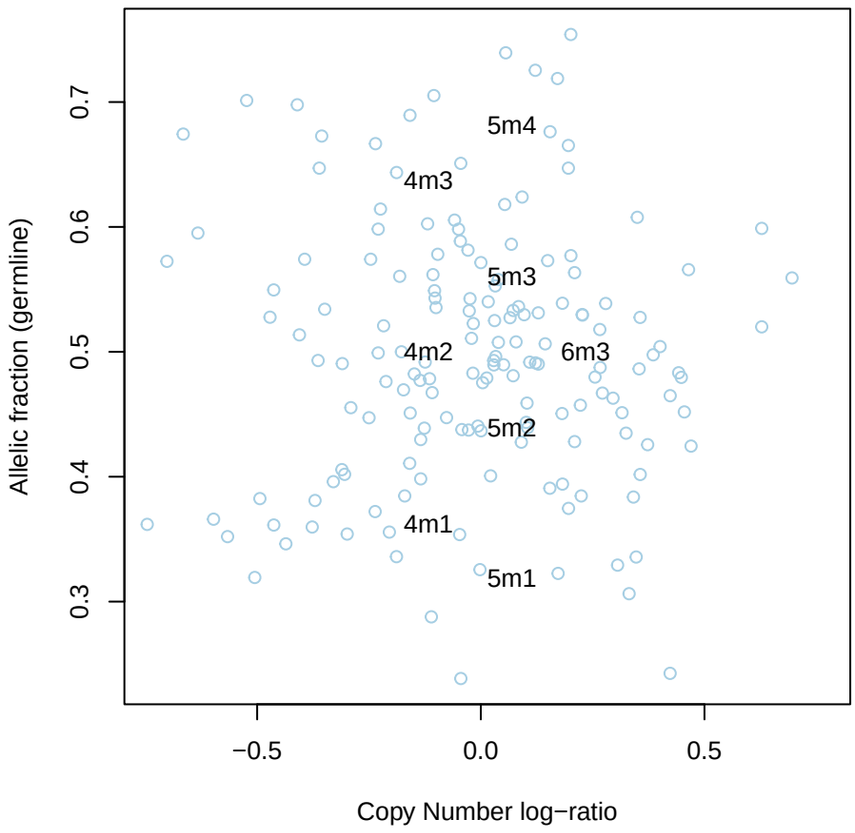

Frequency
Cellular fraction

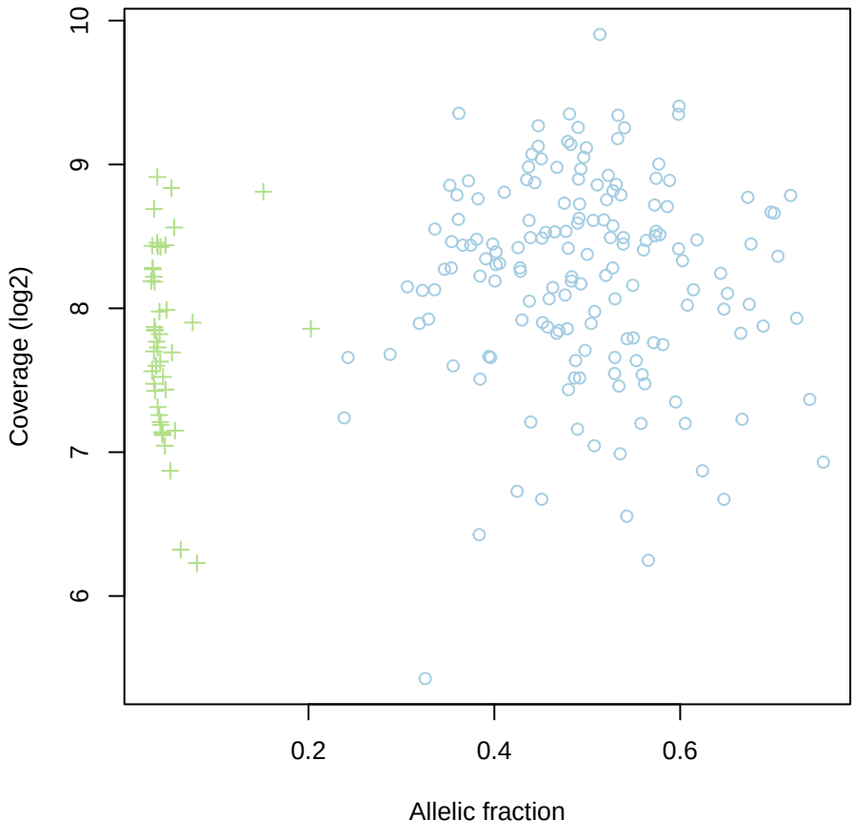

Purity: 0.38 Tumor ploidy: 4.612
4
5
6
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

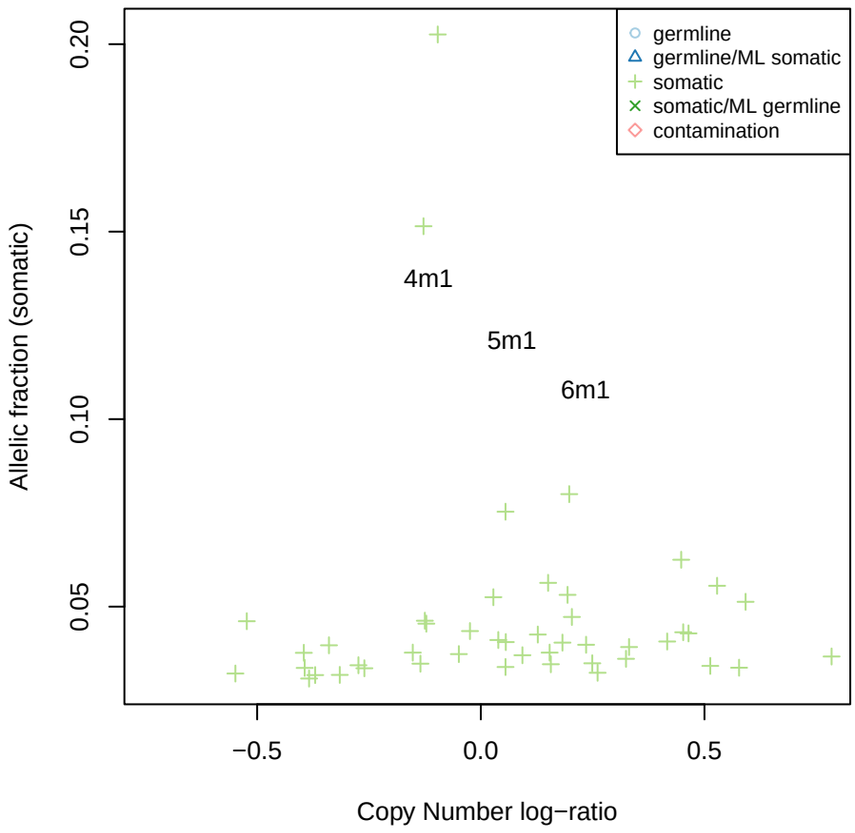

Purity: 0.38 Tumor ploidy: 4.612 SNV log−likelihood: −263.56 GoF: 90.9% Mean coverage: 312;424
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

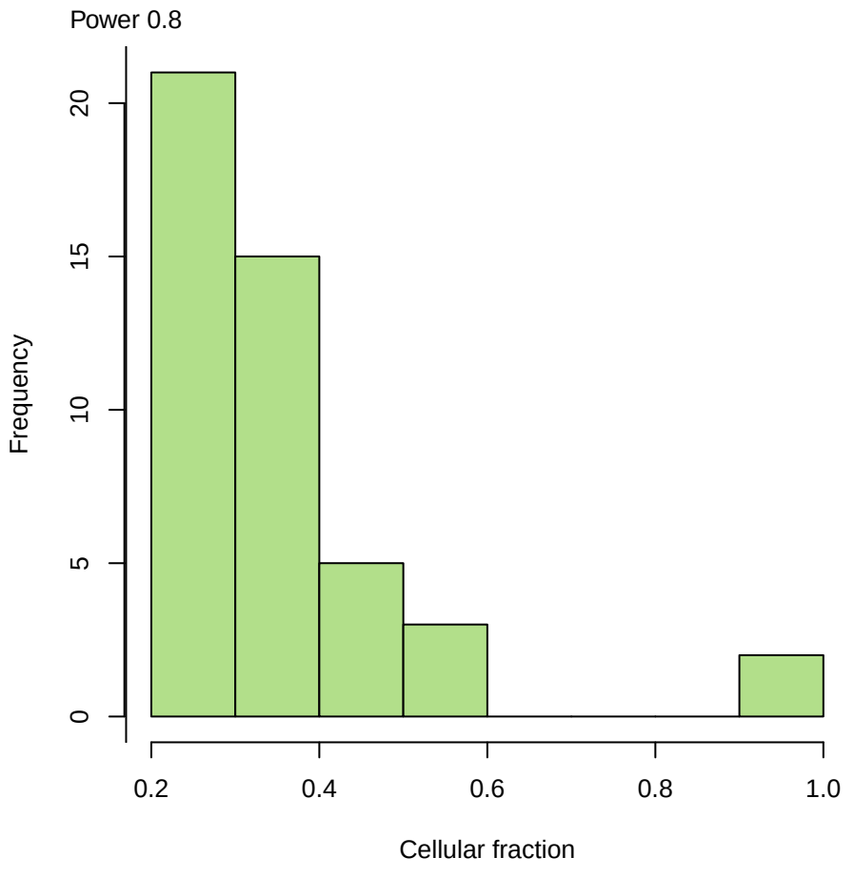

SCNA−fit log−likelihood: −19398.61
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5 6
0 50 100 150
SNV Index

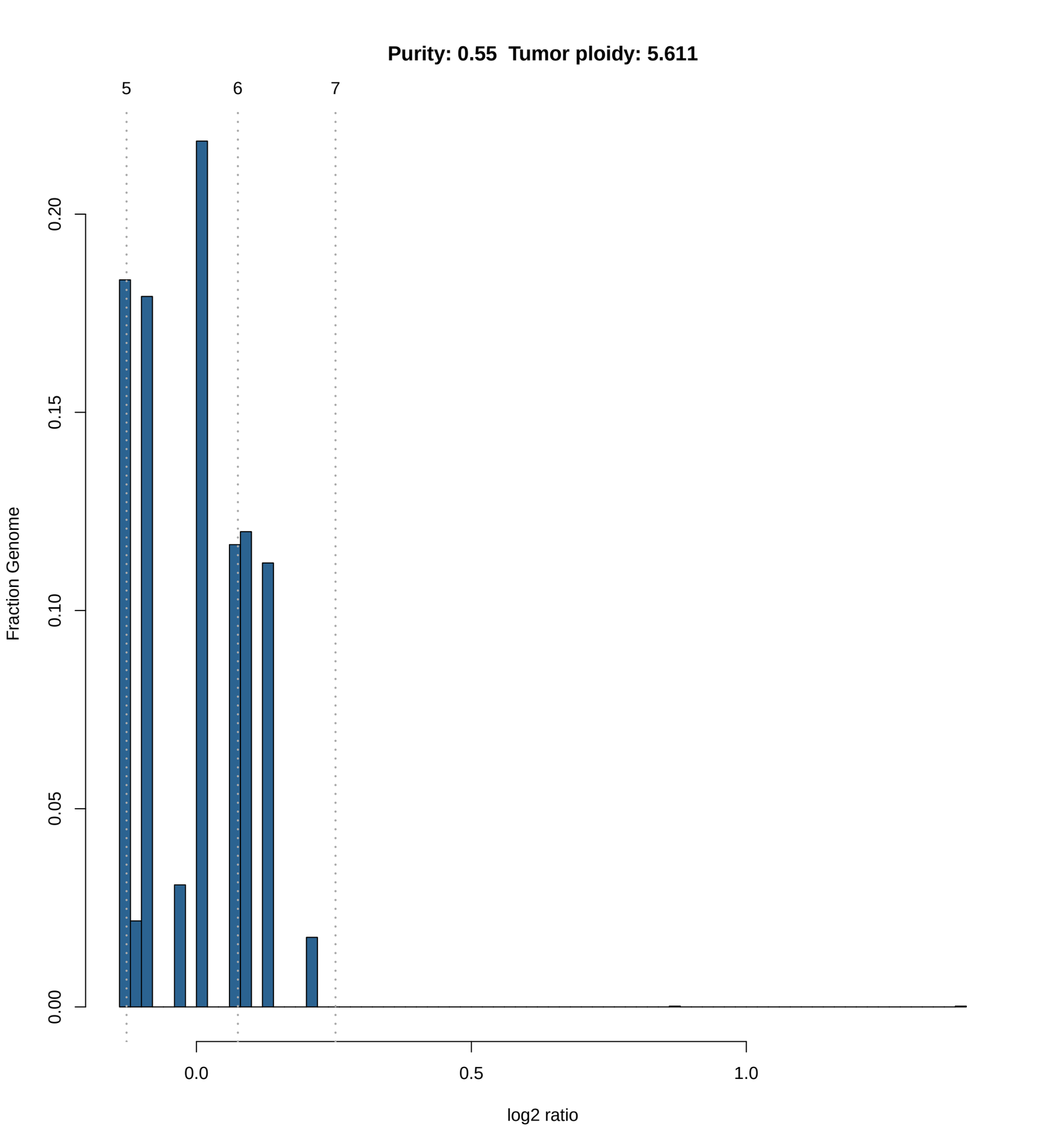

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

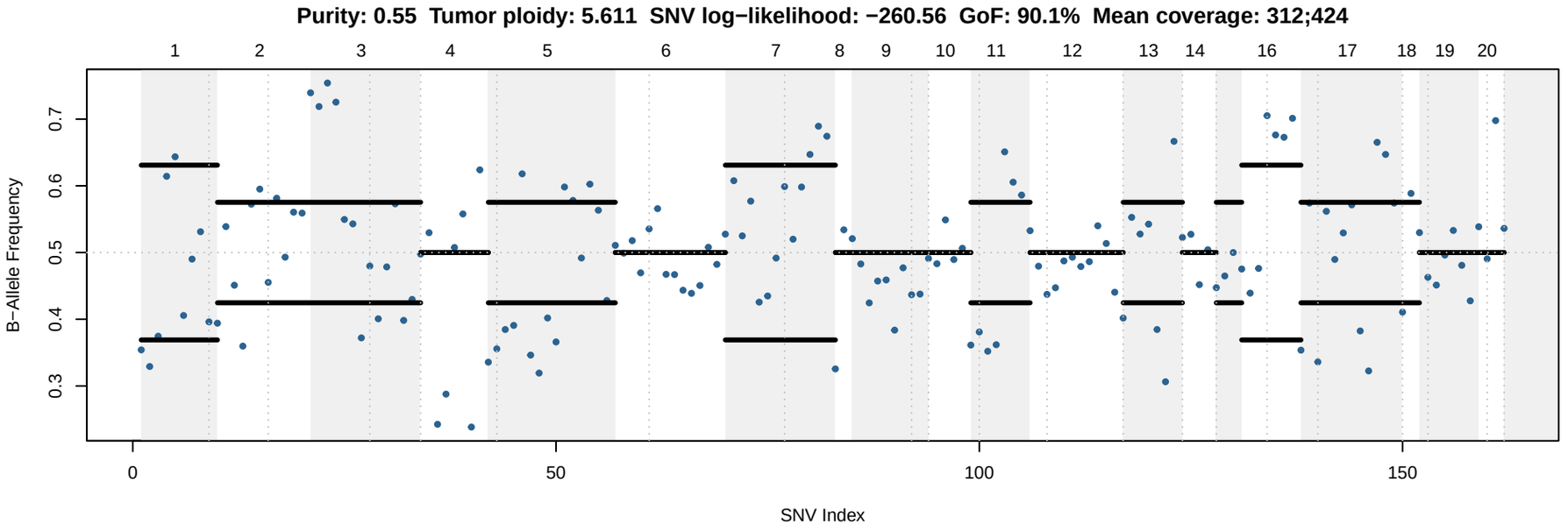

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
5m4
4m3
5m3
4m2
6m3
5m2
4m1
5m1
−0.5
0.0
0.5
Copy Number log−ratio

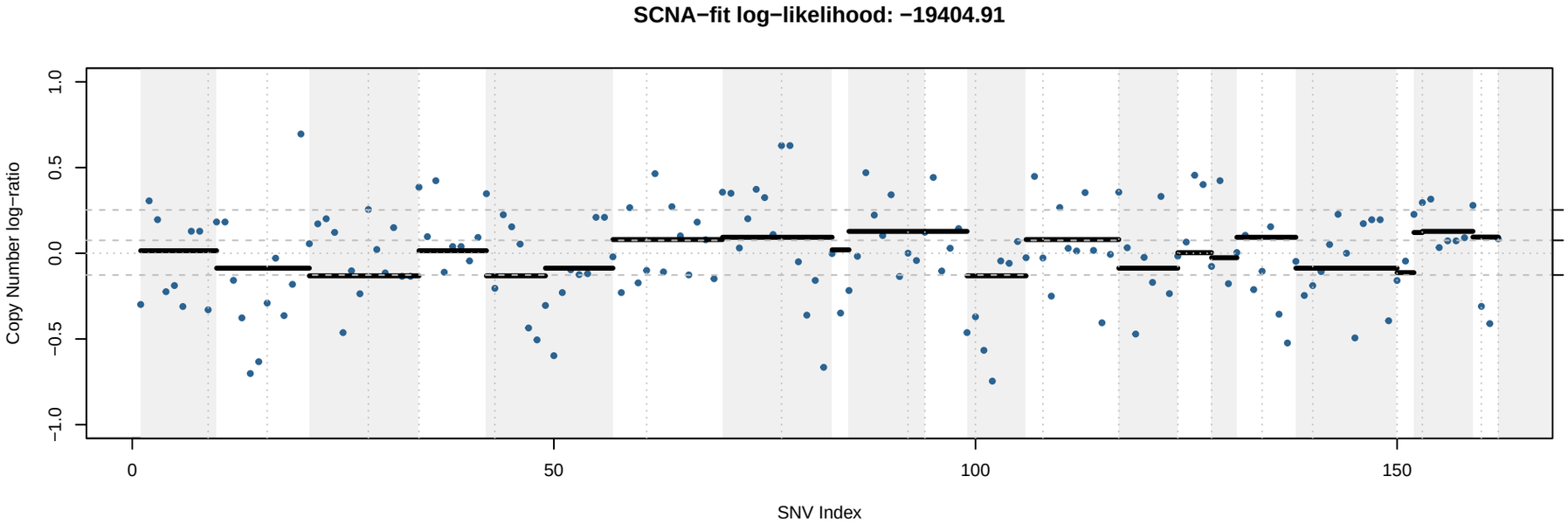

Coverage (log2)
6
7
8
9
10
0.2
0.4
0.6
Allelic fraction

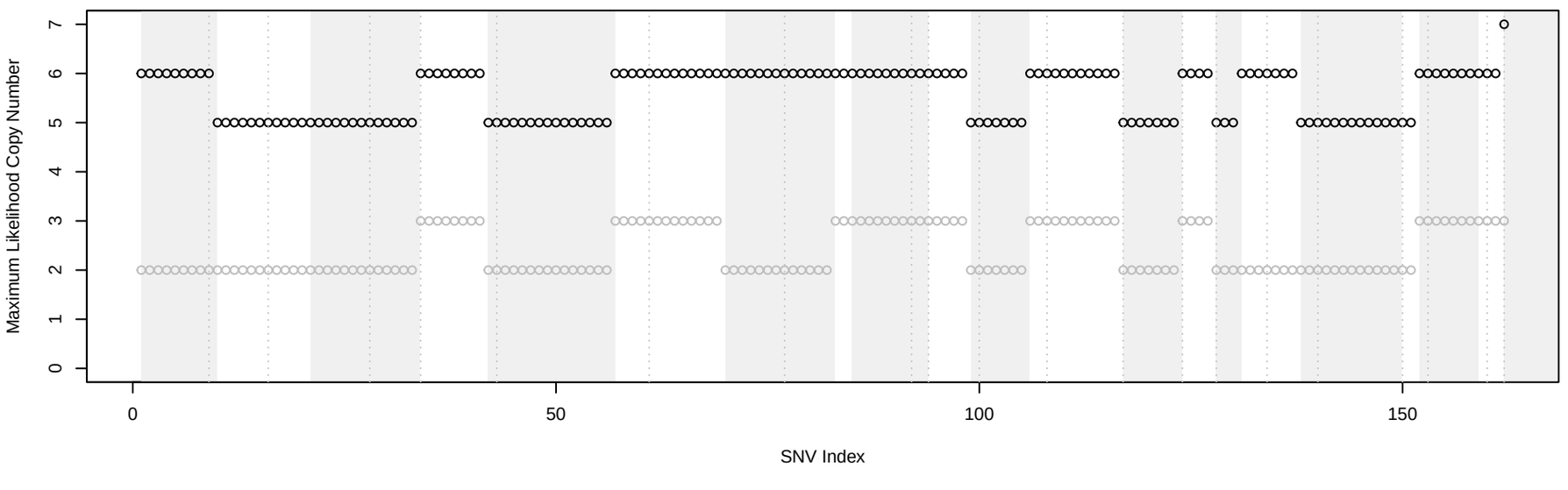

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
−0.5
0.0
0.5
Copy Number log−ratio


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

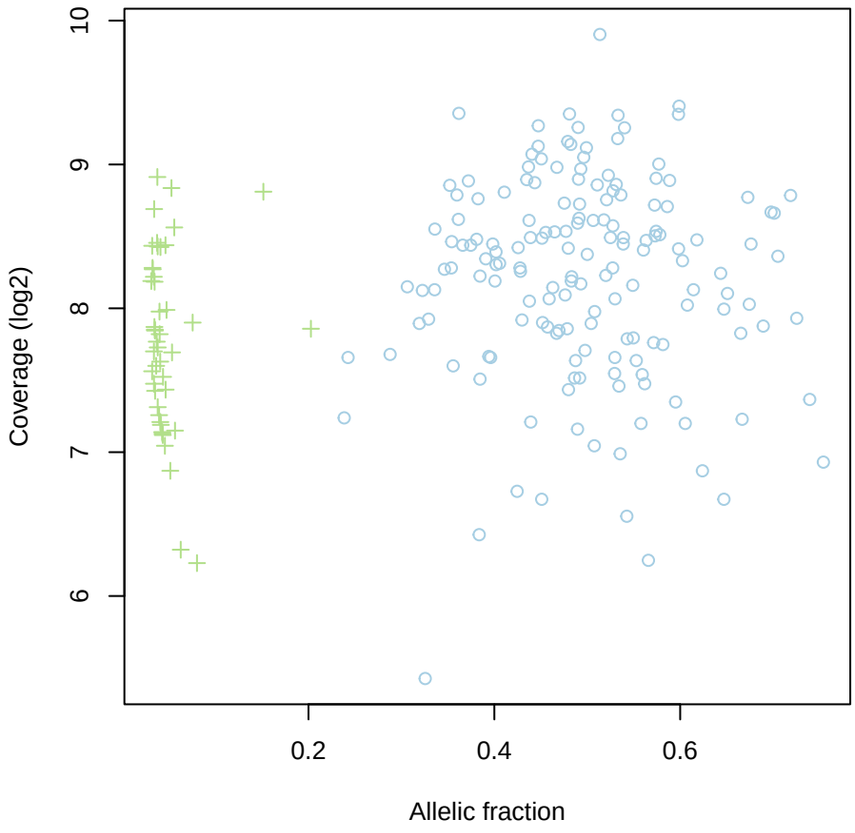

Purity: 0.55 Tumor ploidy: 5.611
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

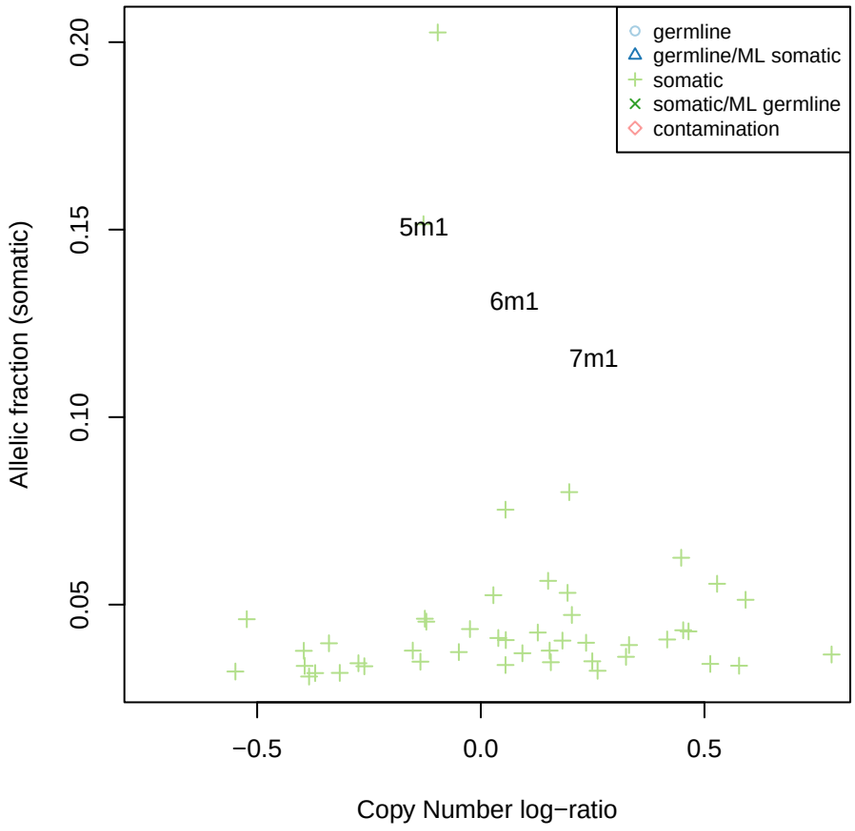

Purity: 0.55 Tumor ploidy: 5.611 SNV log−likelihood: −260.56 GoF: 90.1% Mean coverage: 312;424
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

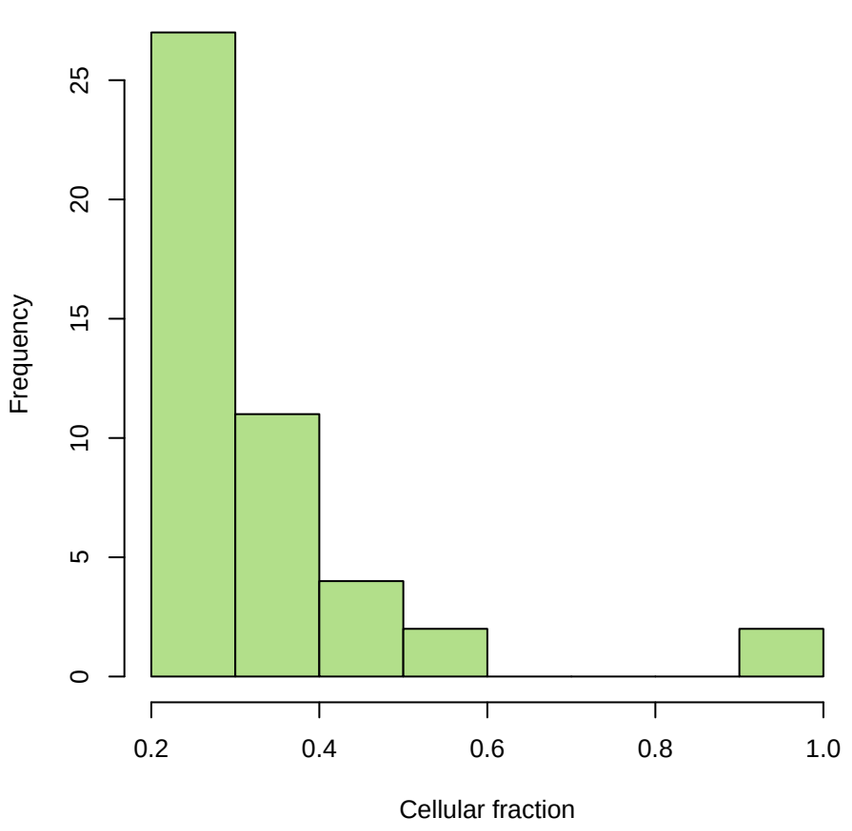

SCNA−fit log−likelihood: −19404.91
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
5 6 7
0 50 100 150
SNV Index

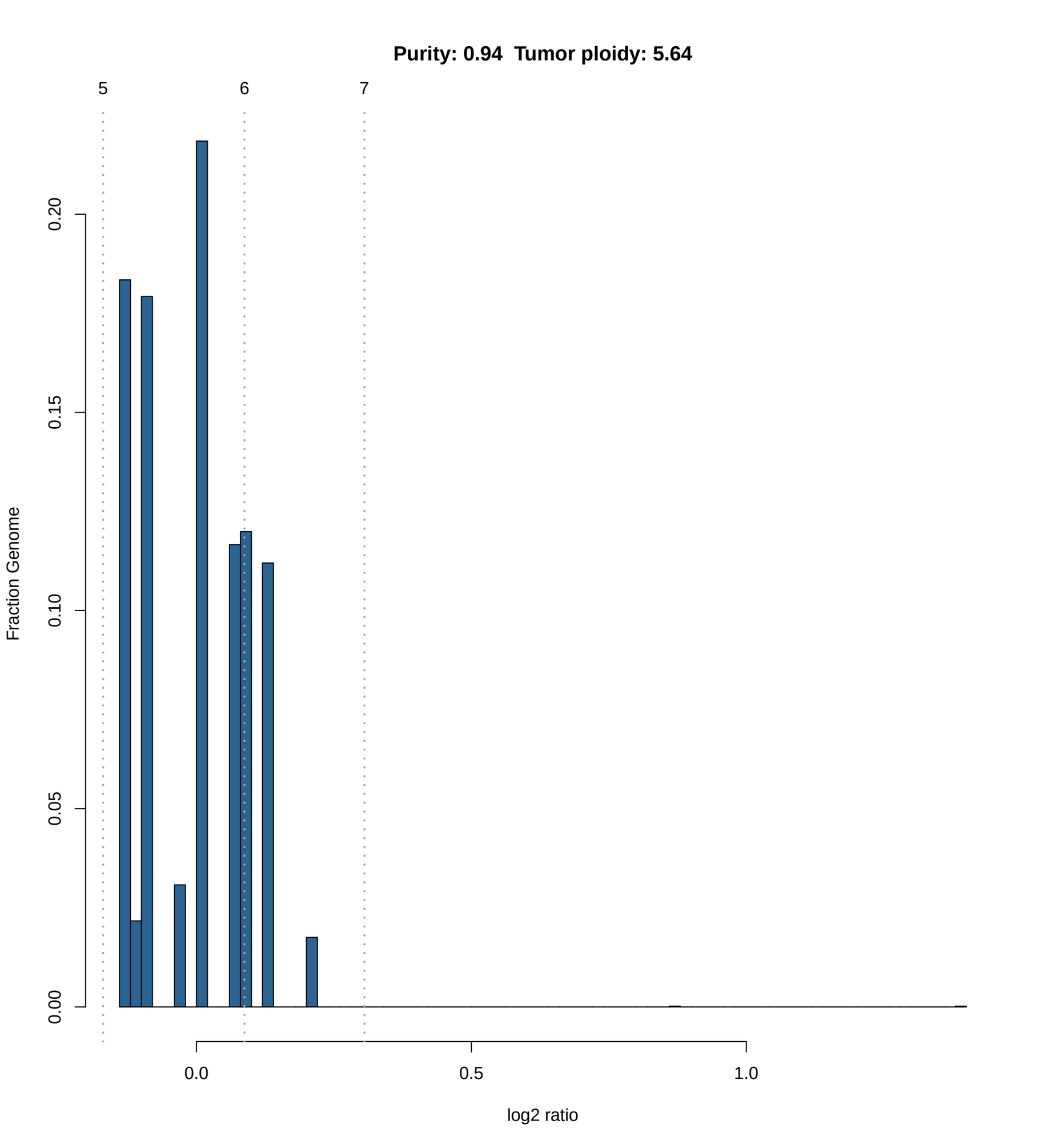

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

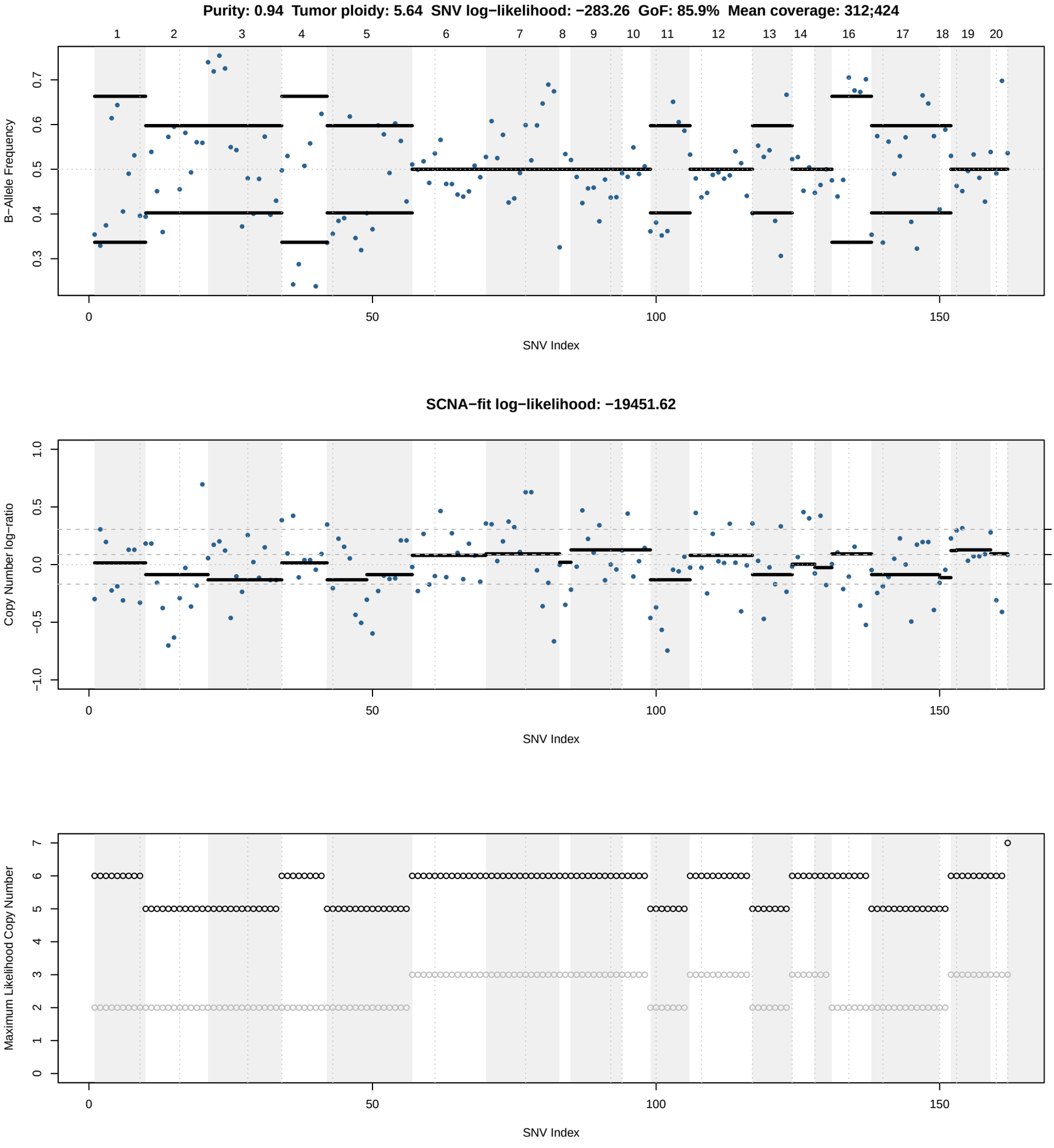
6m5
5m4
6m4
5m3
7m4
6m3
5m2
6m2
6m1
Allelic fraction (germline)
Copy Number log−ratio


Coverage (log2)
Allelic fraction

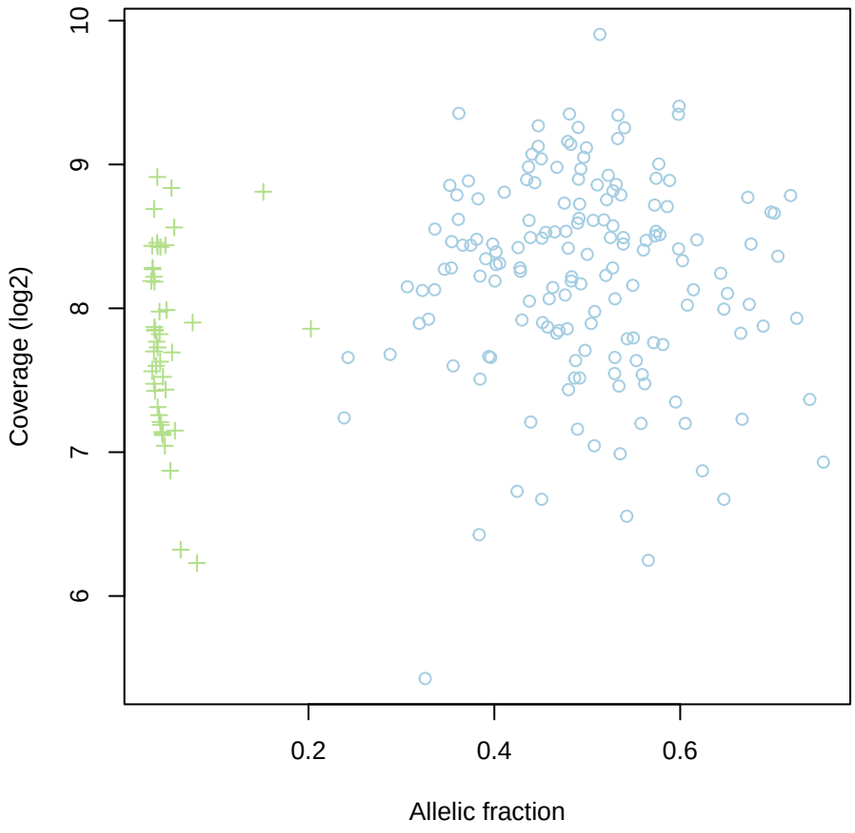

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

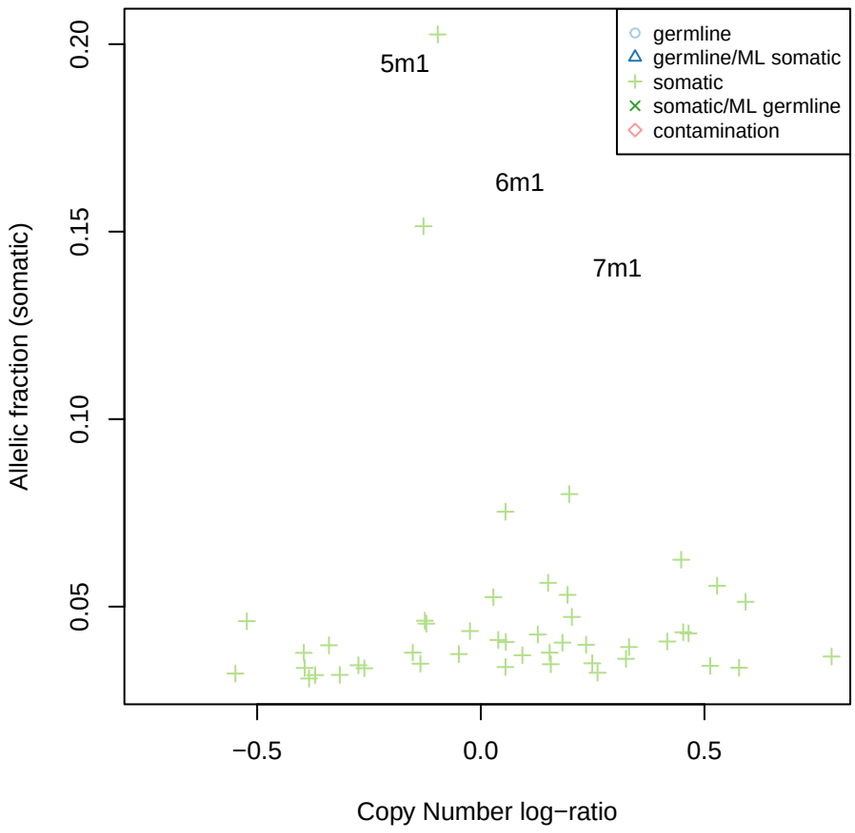

Frequency
Cellular fraction

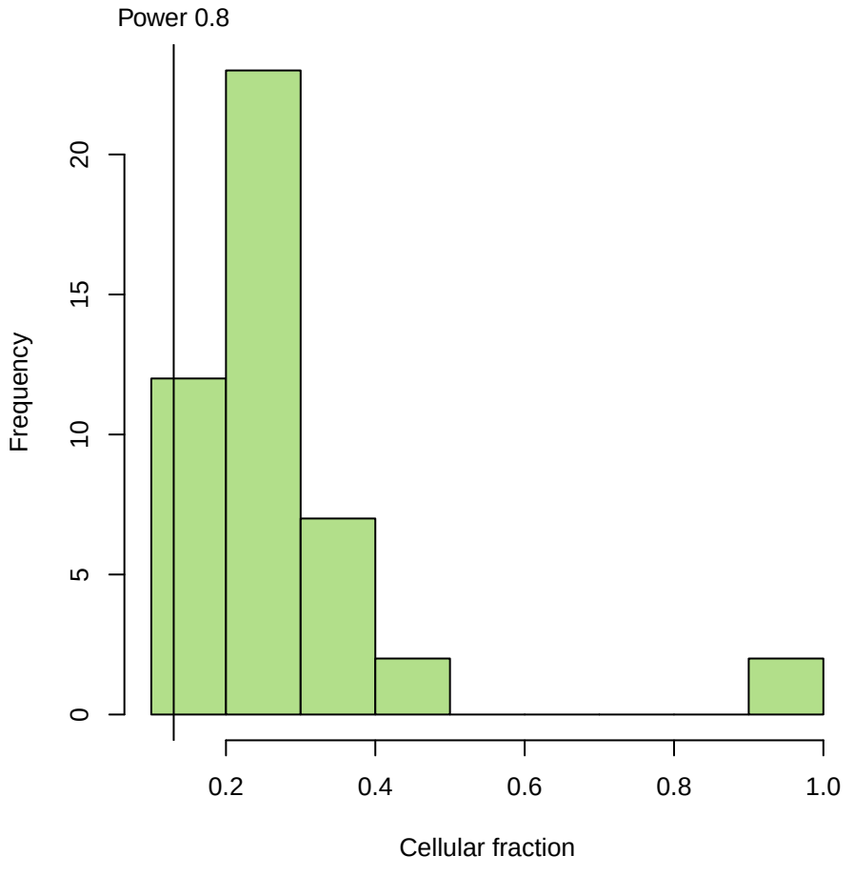

Purity: 0.94 Tumor ploidy: 5.64
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

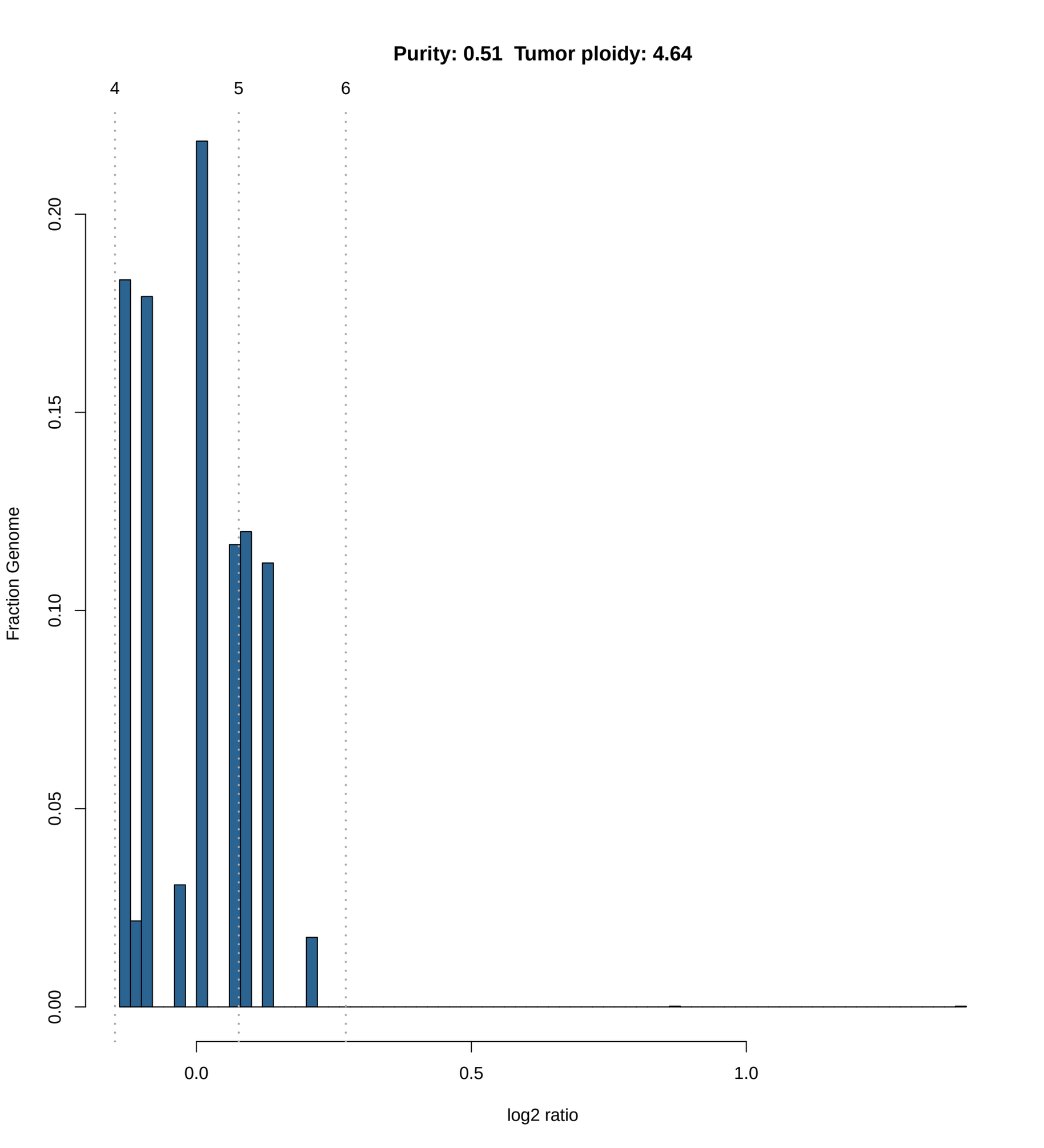

Purity: 0.94 Tumor ploidy: 5.64 SNV log−likelihood: −283.26 GoF: 85.9% Mean coverage: 312;424
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index
SCNA−fit log−likelihood: −19451.62
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
5 6 7
0 50 100 150
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

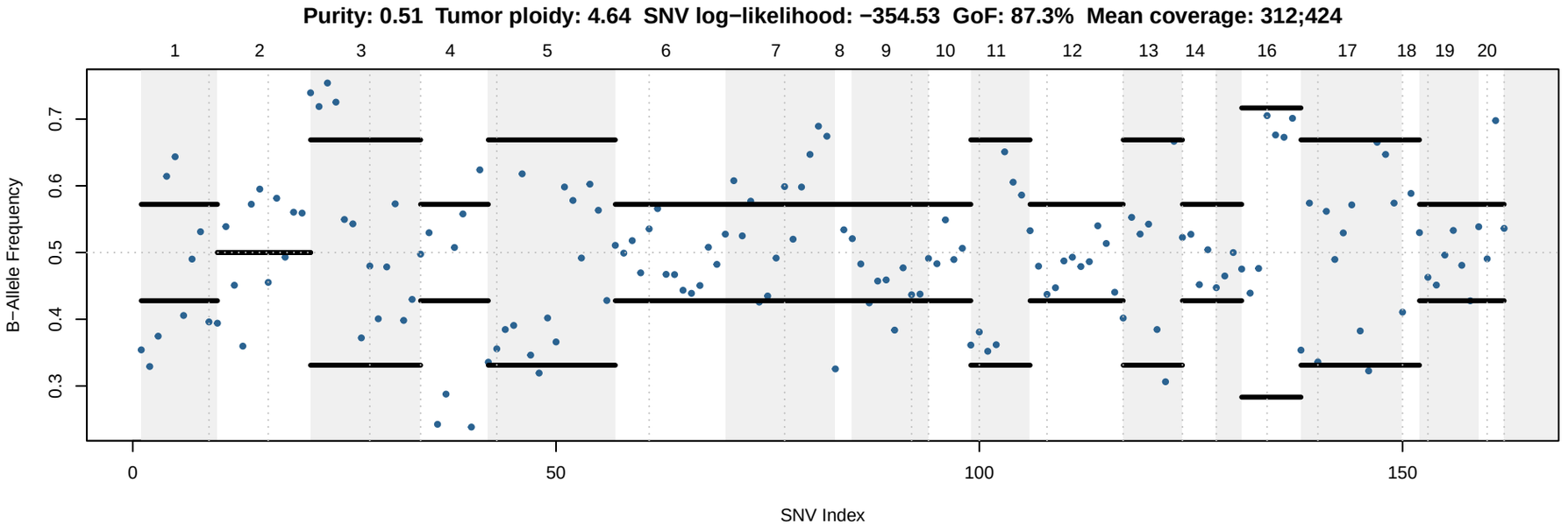
Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
6m4
5m3
7m4
6m3
5m2
6m2
−0.5
0.0
0.5
Copy Number log−ratio

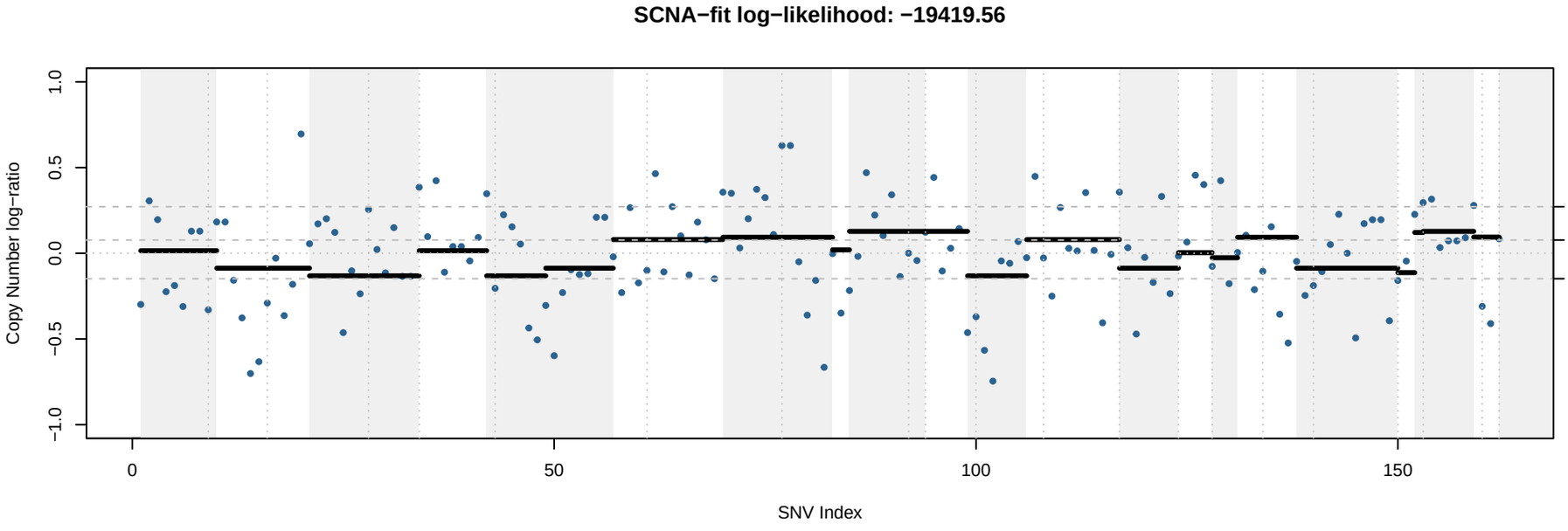

Coverage (log2)
6
7
8
9
10
0.2
0.4
0.6
Allelic fraction

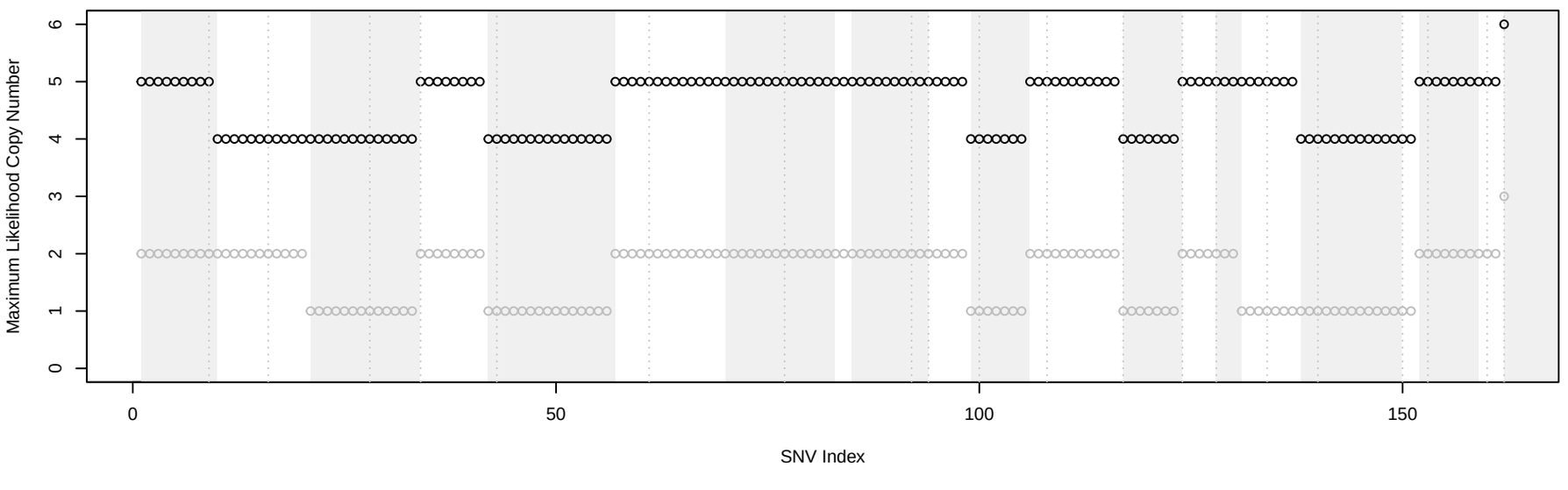

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
6m1
7m1
−0.5
0.0
0.5
Copy Number log−ratio

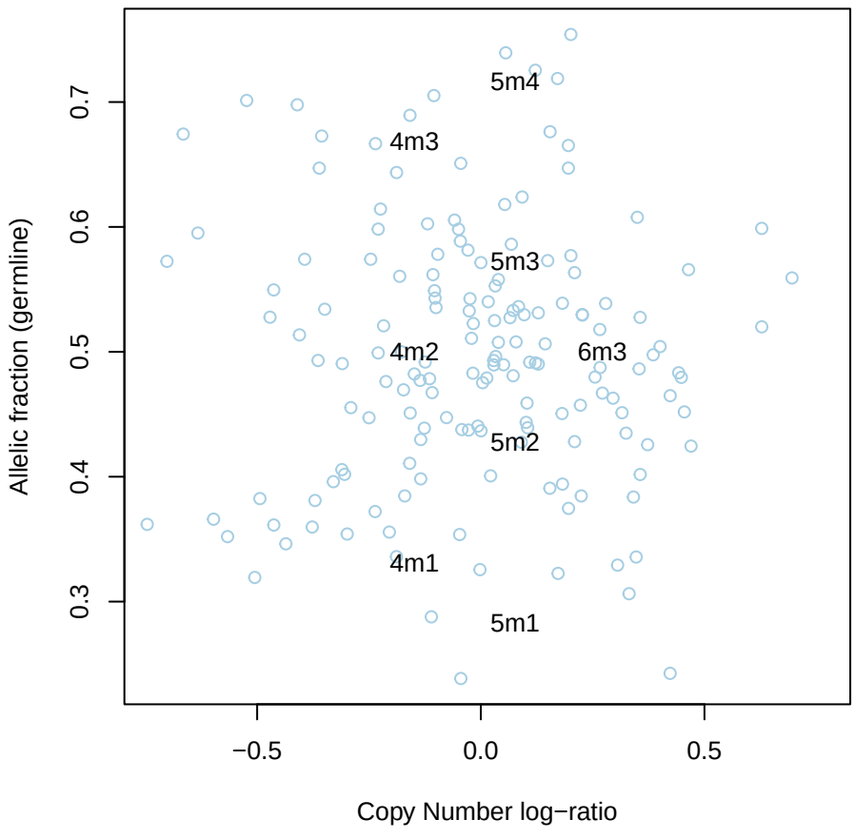

Power 0.8
Frequency
0
5
10
15
20
0.2
0.4
0.6
0.8
1.0
Cellular fraction

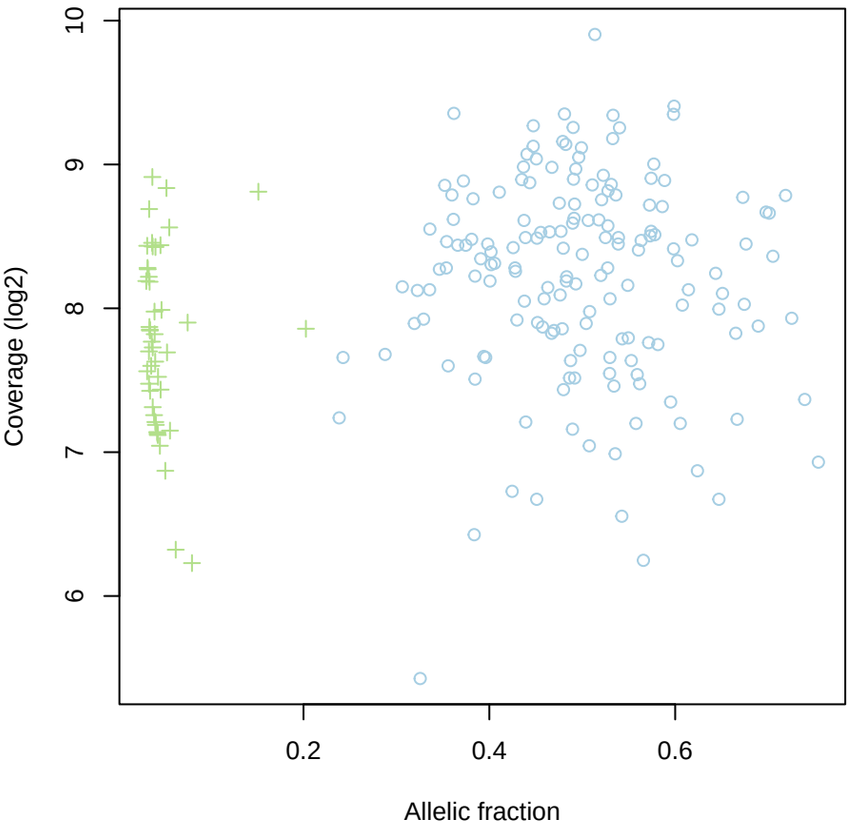

Purity: 0.51 Tumor ploidy: 4.64
4
5
6
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

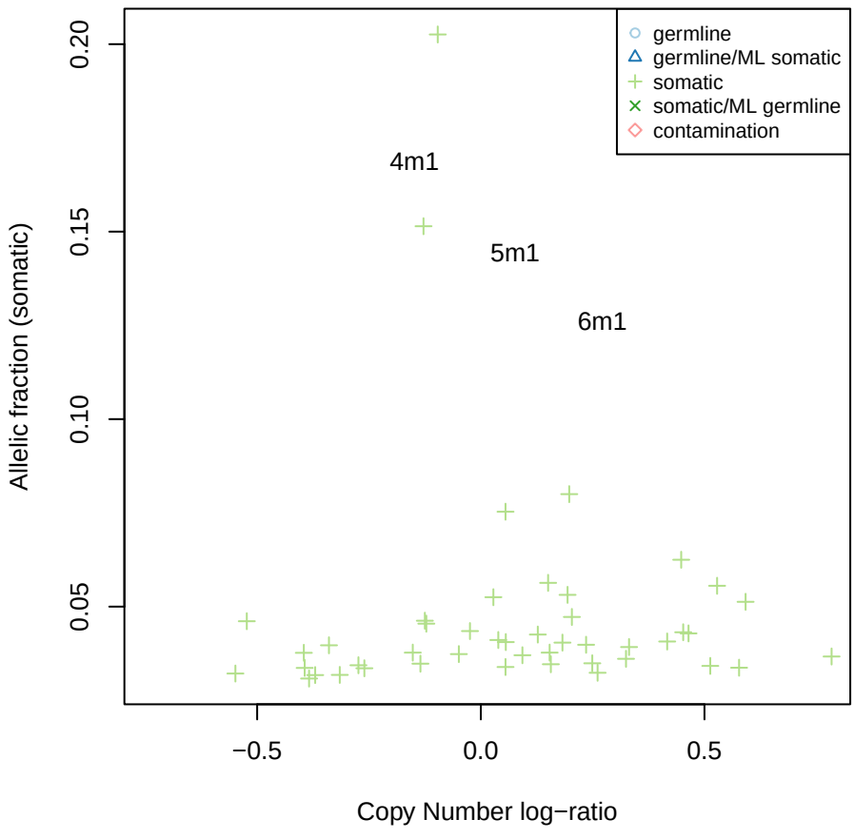

Purity: 0.51 Tumor ploidy: 4.64 SNV log−likelihood: −354.53 GoF: 87.3% Mean coverage: 312;424
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

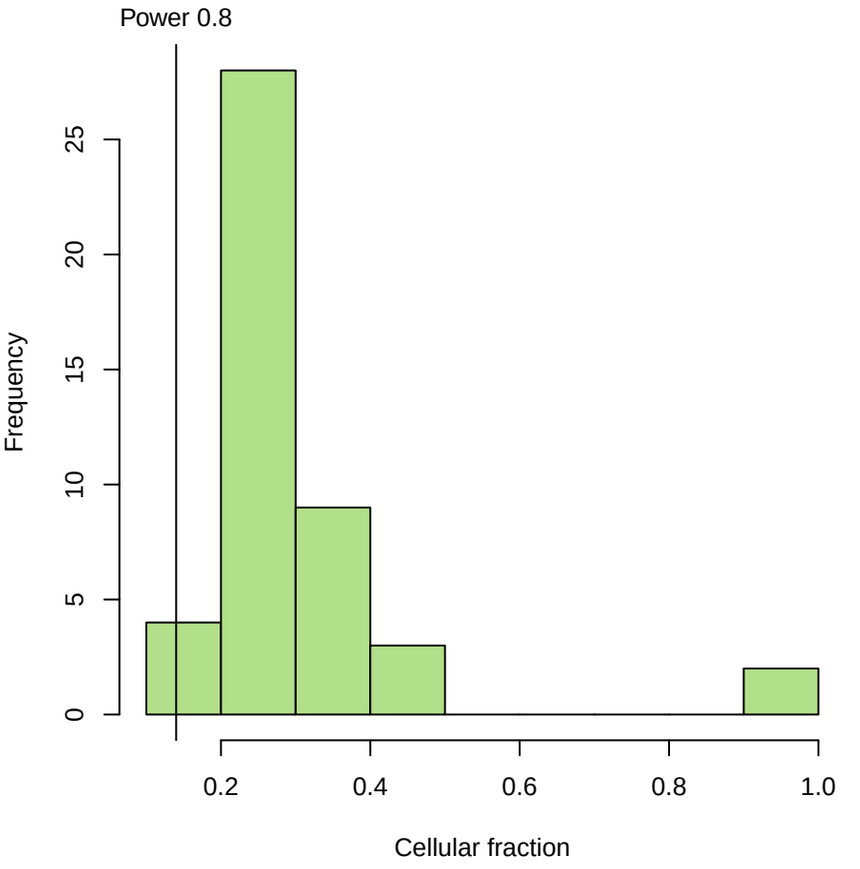

SCNA−fit log−likelihood: −19419.56
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5 6
0 50 100 150
SNV Index

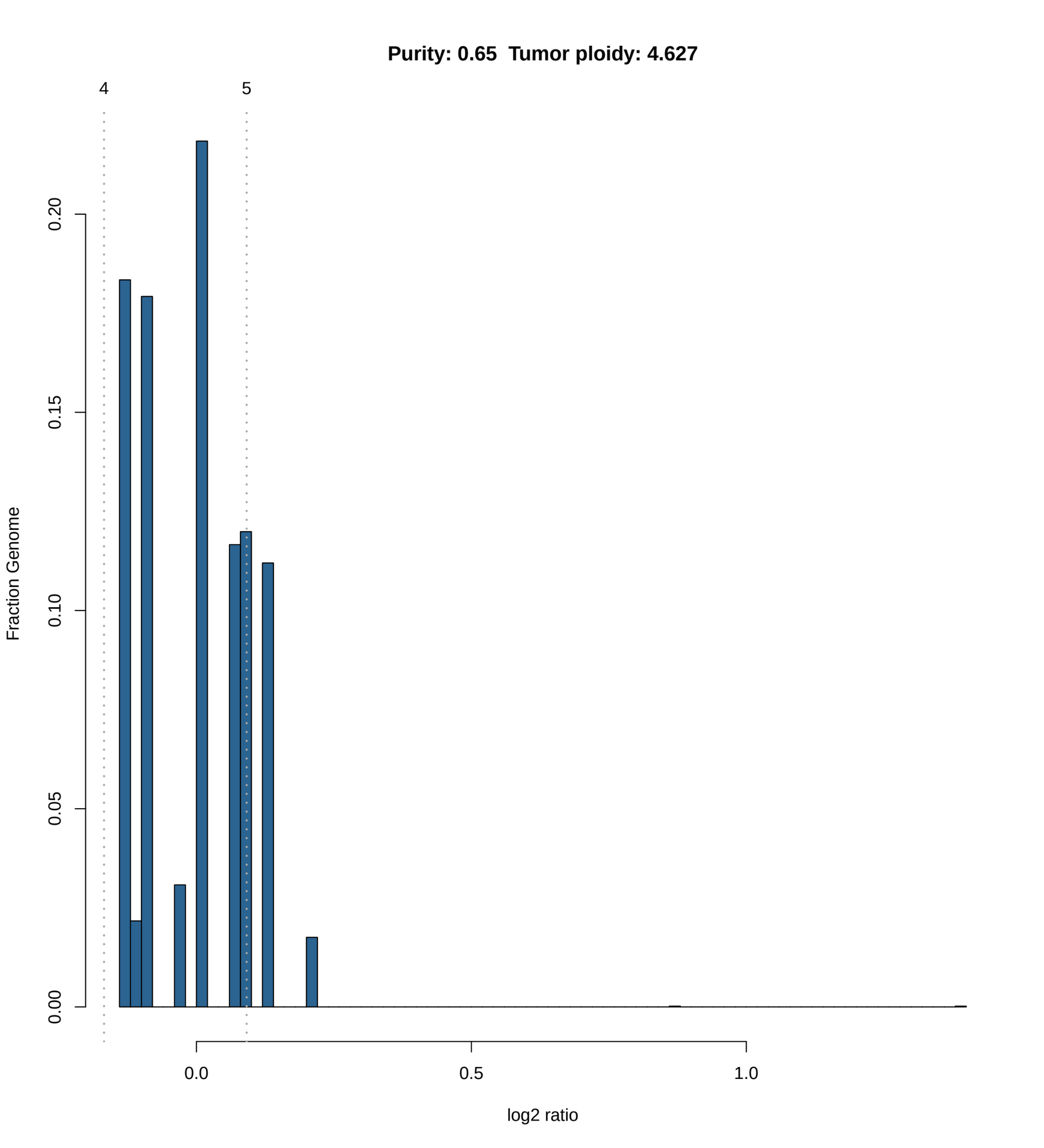

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

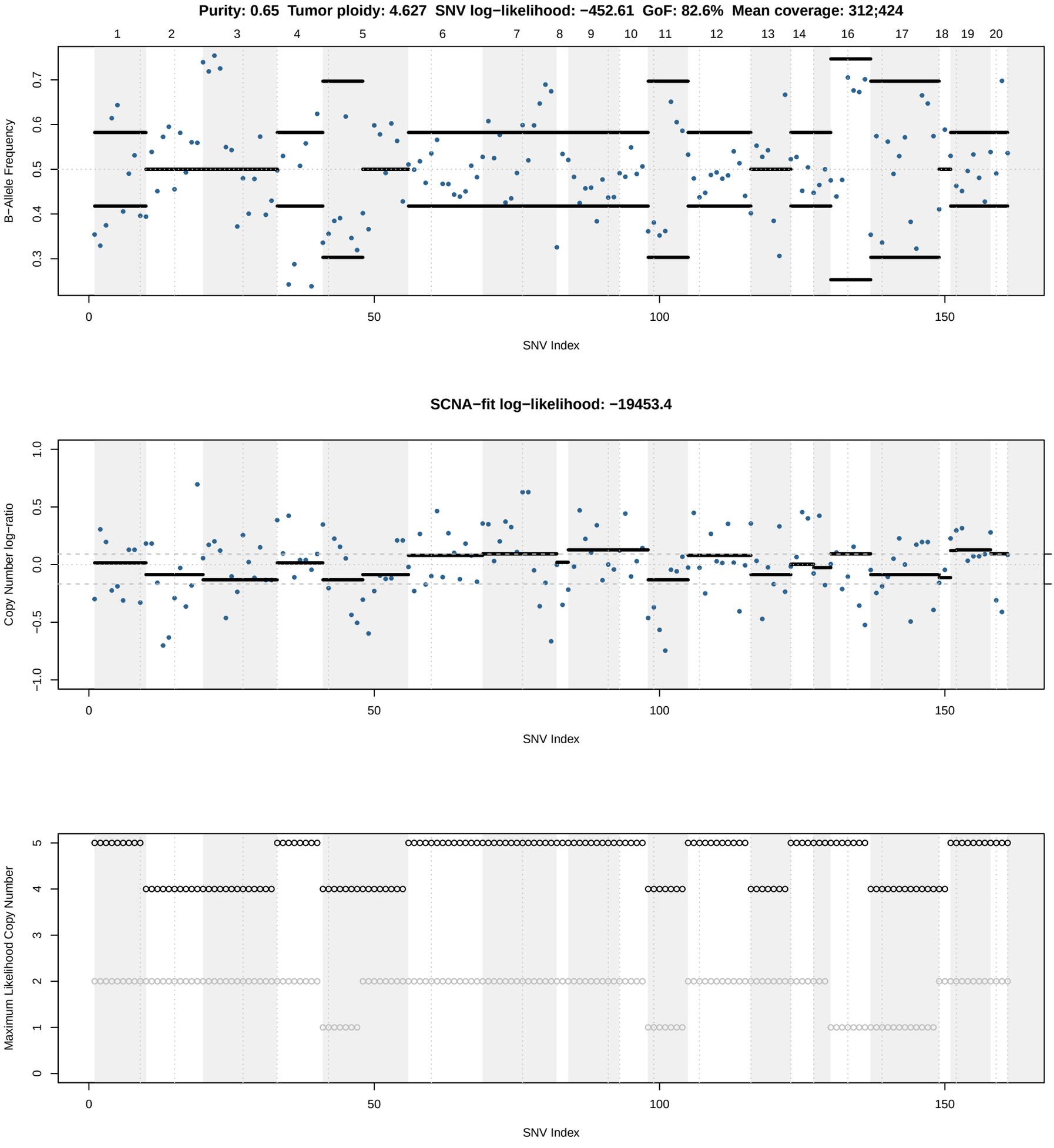

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
5m4
4m3
5m3
4m2
6m3
5m2
4m1
5m1
−0.5
0.0
0.5
Copy Number log−ratio


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

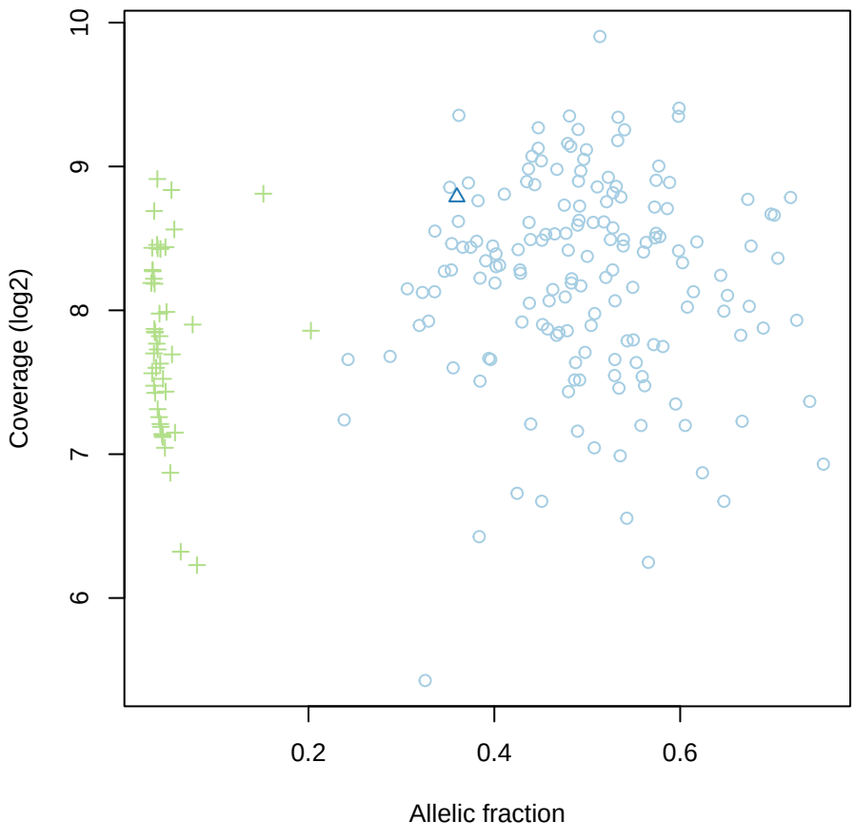

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
−0.5
0.0
0.5
Copy Number log−ratio

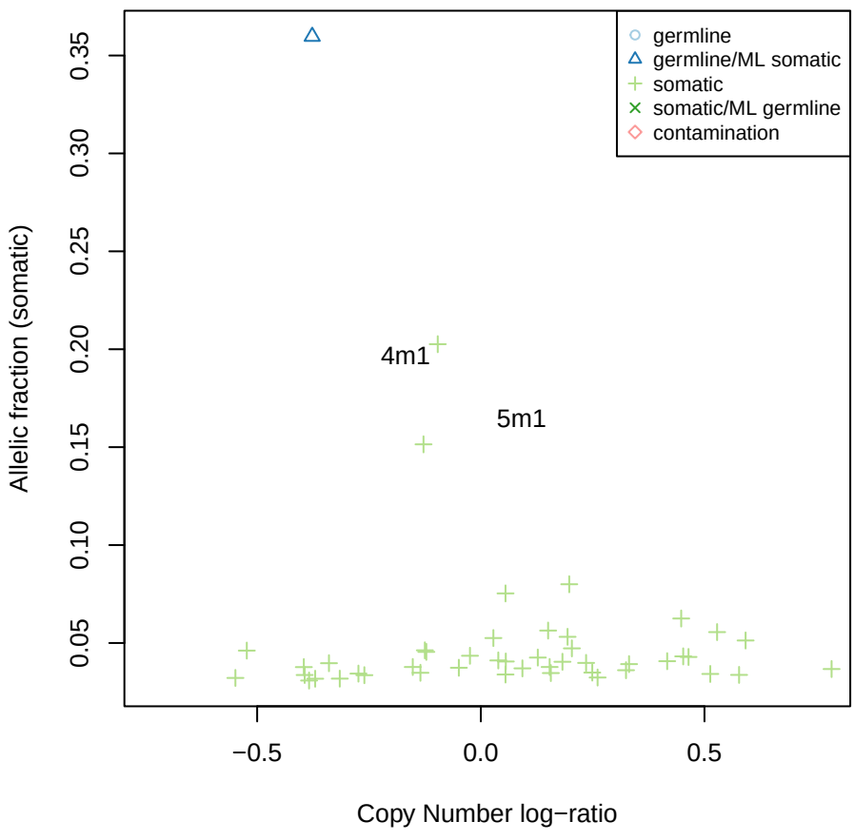

Power 0.8
Frequency
0
5
10
15
20
25
0.2
0.4
0.6
0.8
1.0
Cellular fraction

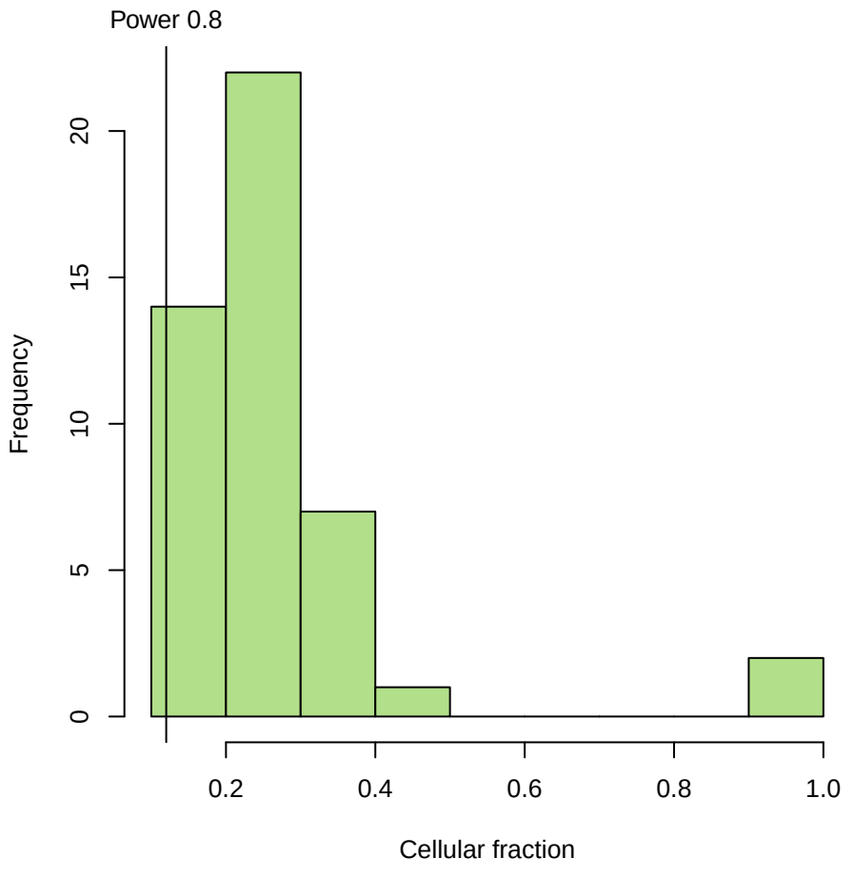

Purity: 0.65 Tumor ploidy: 4.627
4
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

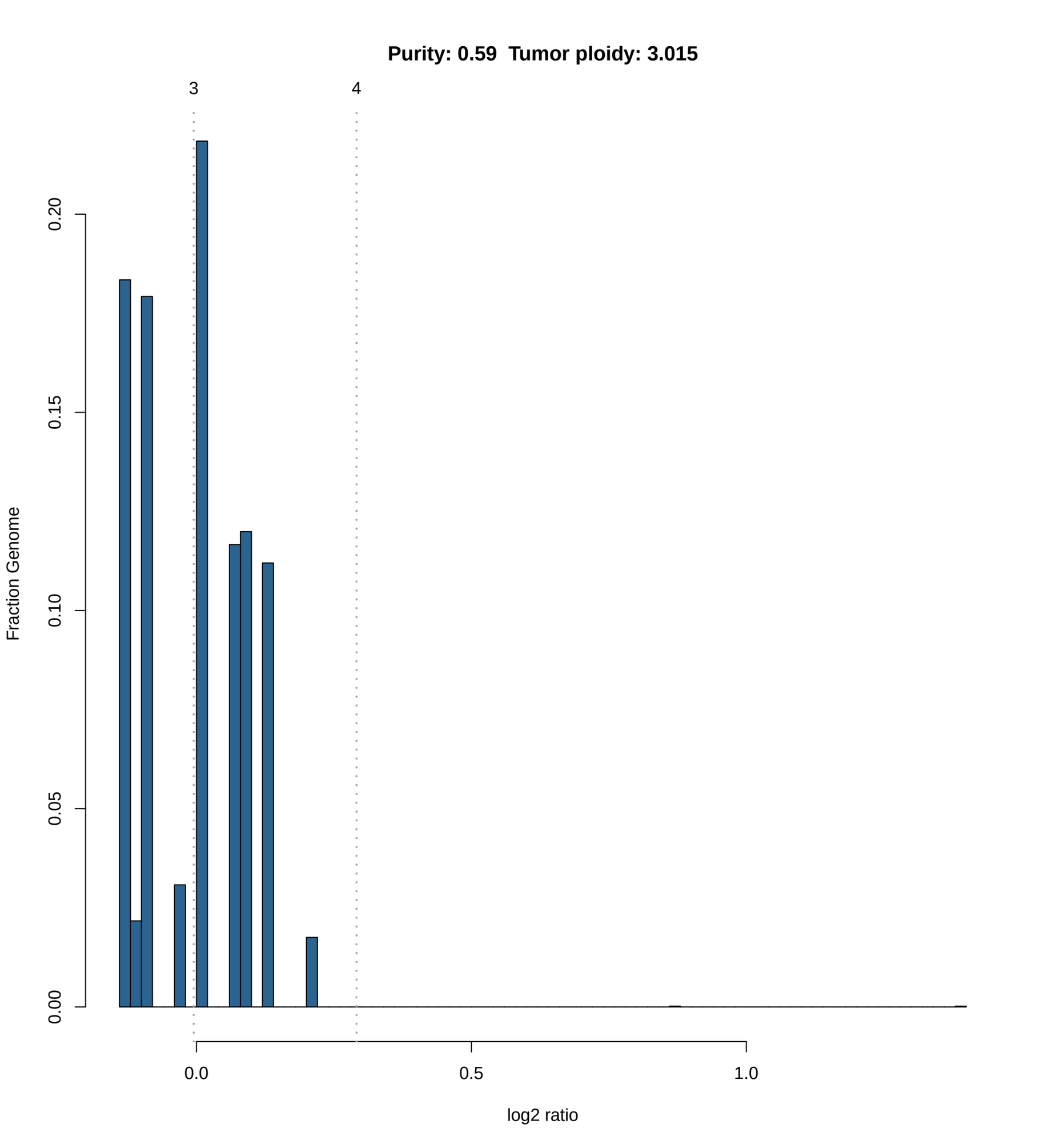

Purity: 0.65 Tumor ploidy: 4.627 SNV log−likelihood: −452.61 GoF: 82.6% Mean coverage: 312;424
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index
SCNA−fit log−likelihood: −19453.4
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
5
4
0 50 100 150
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

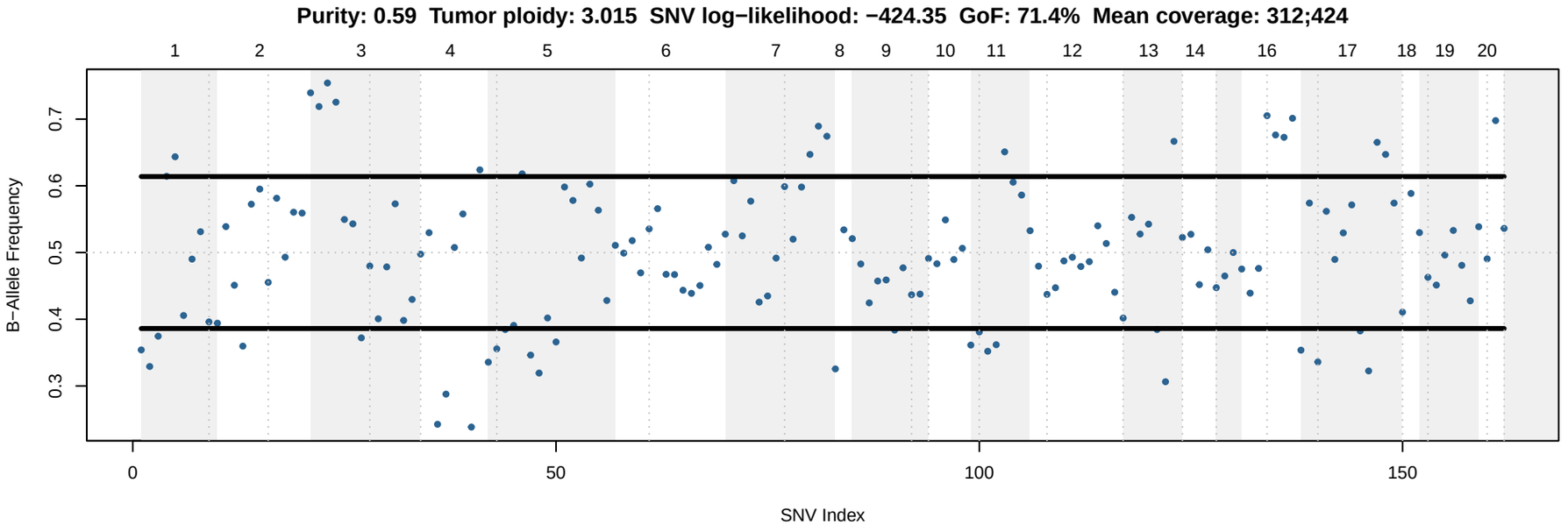
5m4
4m3
5m3
4m2
5m2
4m1
5m1
Allelic fraction (germline)
Copy Number log−ratio
0.3
0.4
0.5
0.6
0.7
−0.5
0.0
0.5

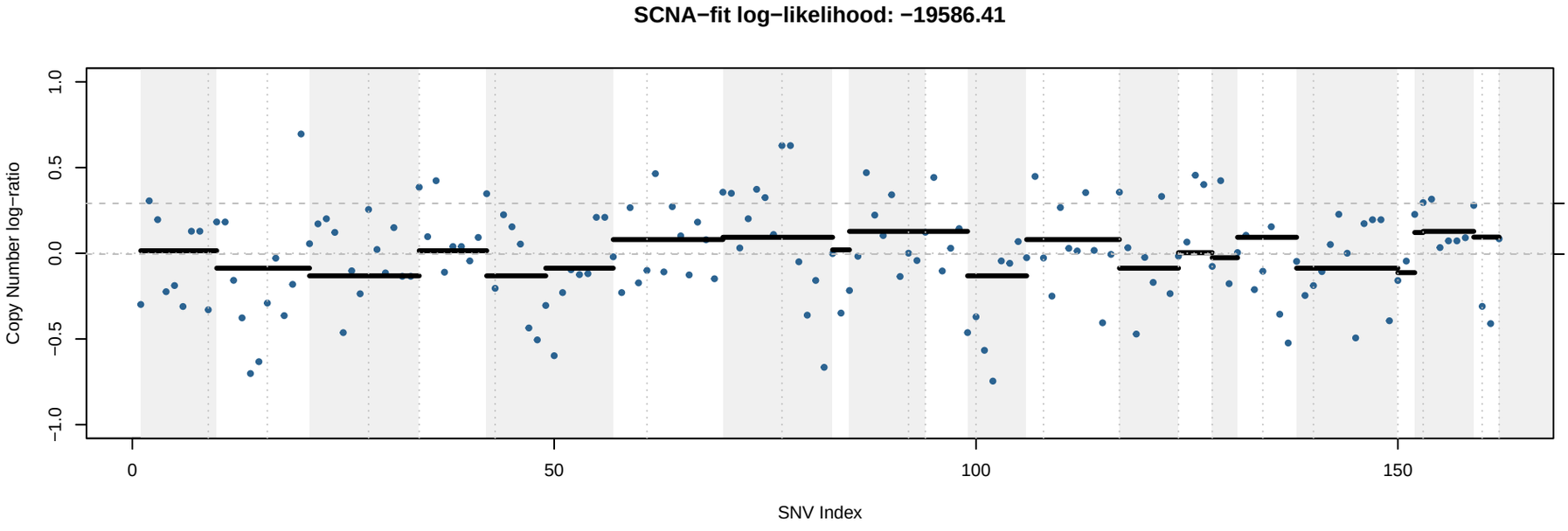

Coverage (log2)
Allelic fraction
6
7
8
9
10
0.2
0.4
0.6

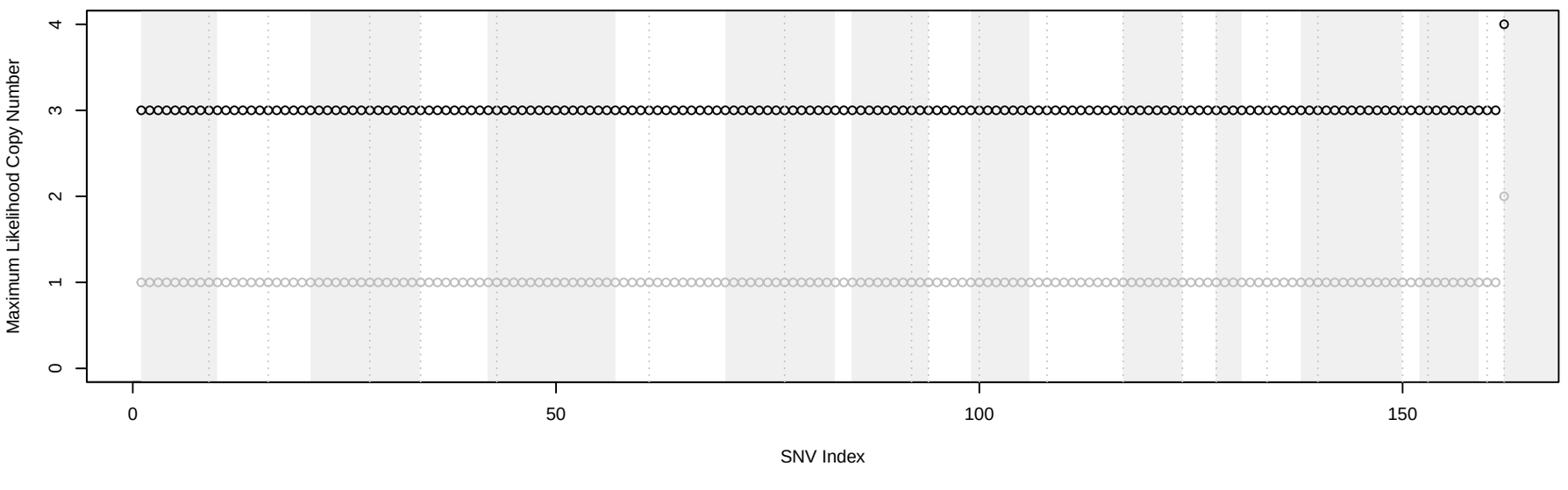

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
Allelic fraction (somatic)
Copy Number log−ratio
0.05
0.10
0.15
0.20
0.25
0.30
0.35
−0.5
0.0
0.5

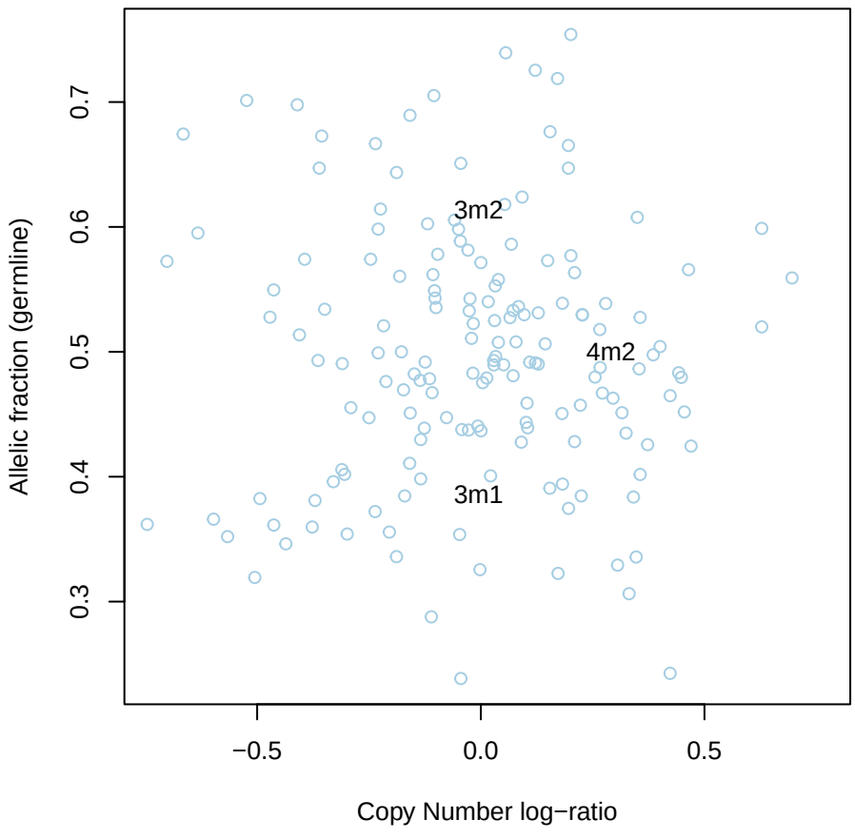

Power 0.8
Frequency
Cellular fraction
0
5
10
15
20
0.2
0.4
0.6
0.8
1.0

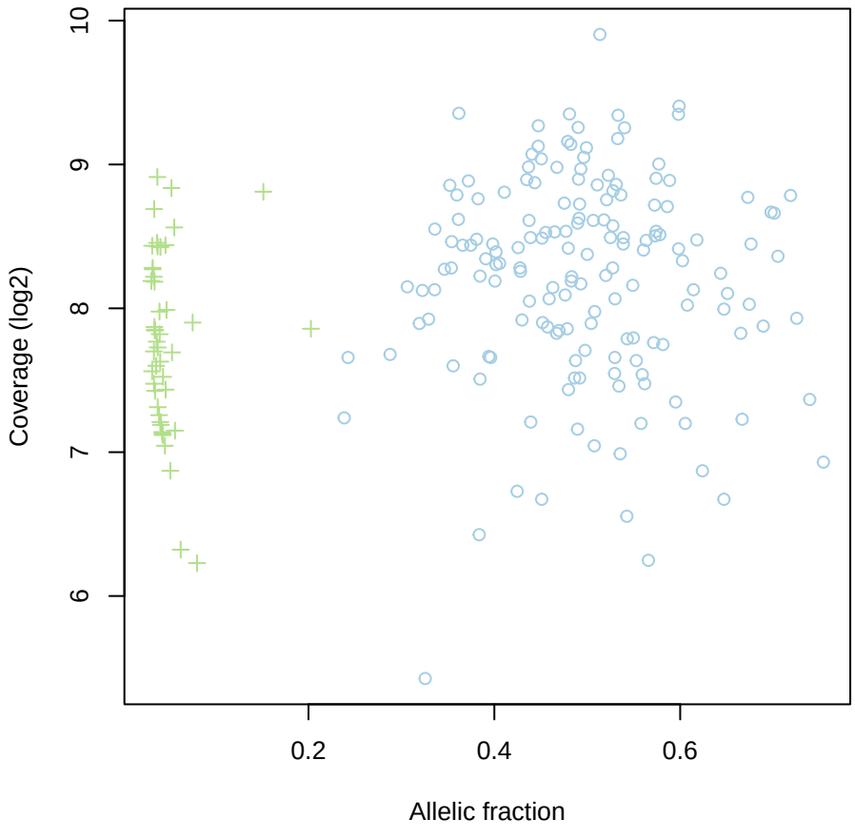

Purity: 0.59 Tumor ploidy: 3.015
3
4
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

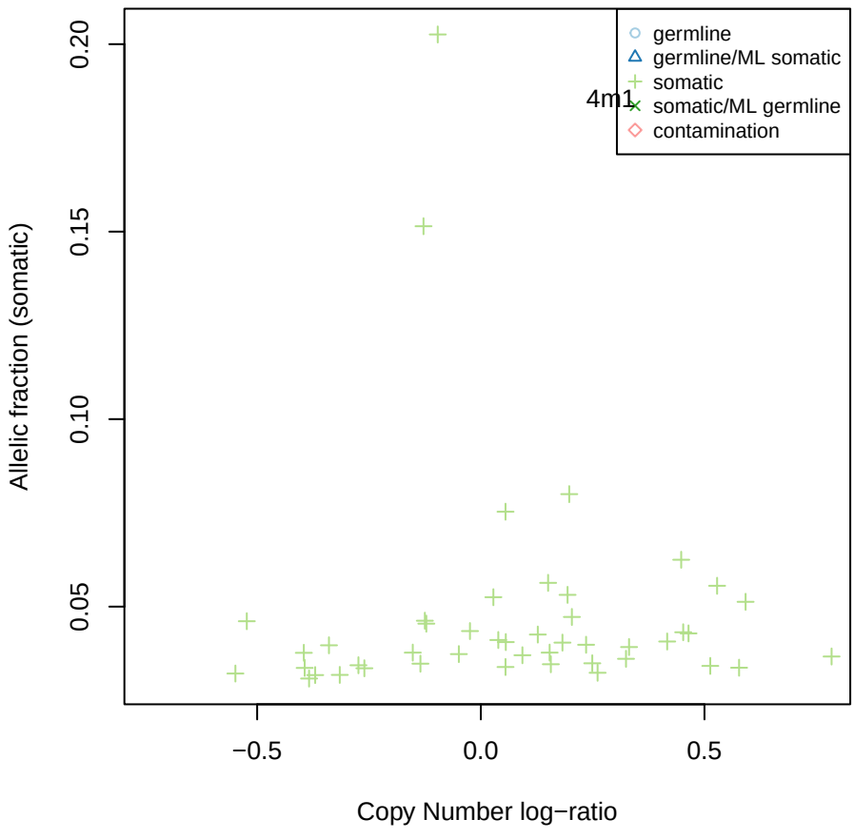

Purity: 0.59 Tumor ploidy: 3.015 SNV log−likelihood: −424.35 GoF: 71.4% Mean coverage: 312;424
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

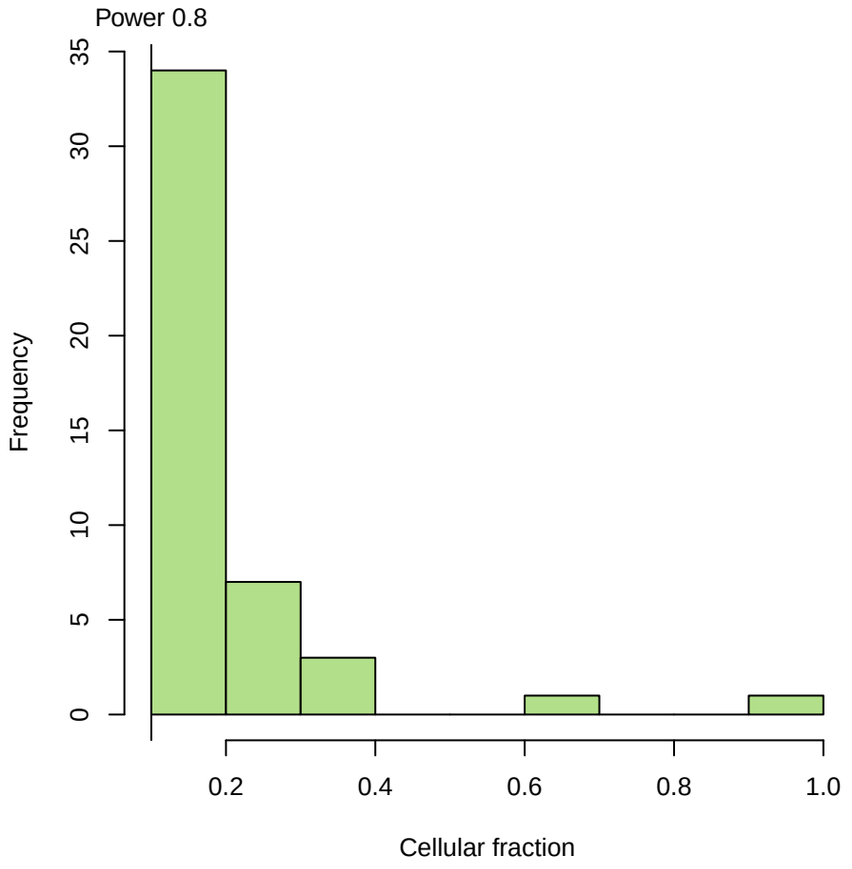

SCNA−fit log−likelihood: −19586.41
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4
0 50 100 150
SNV Index

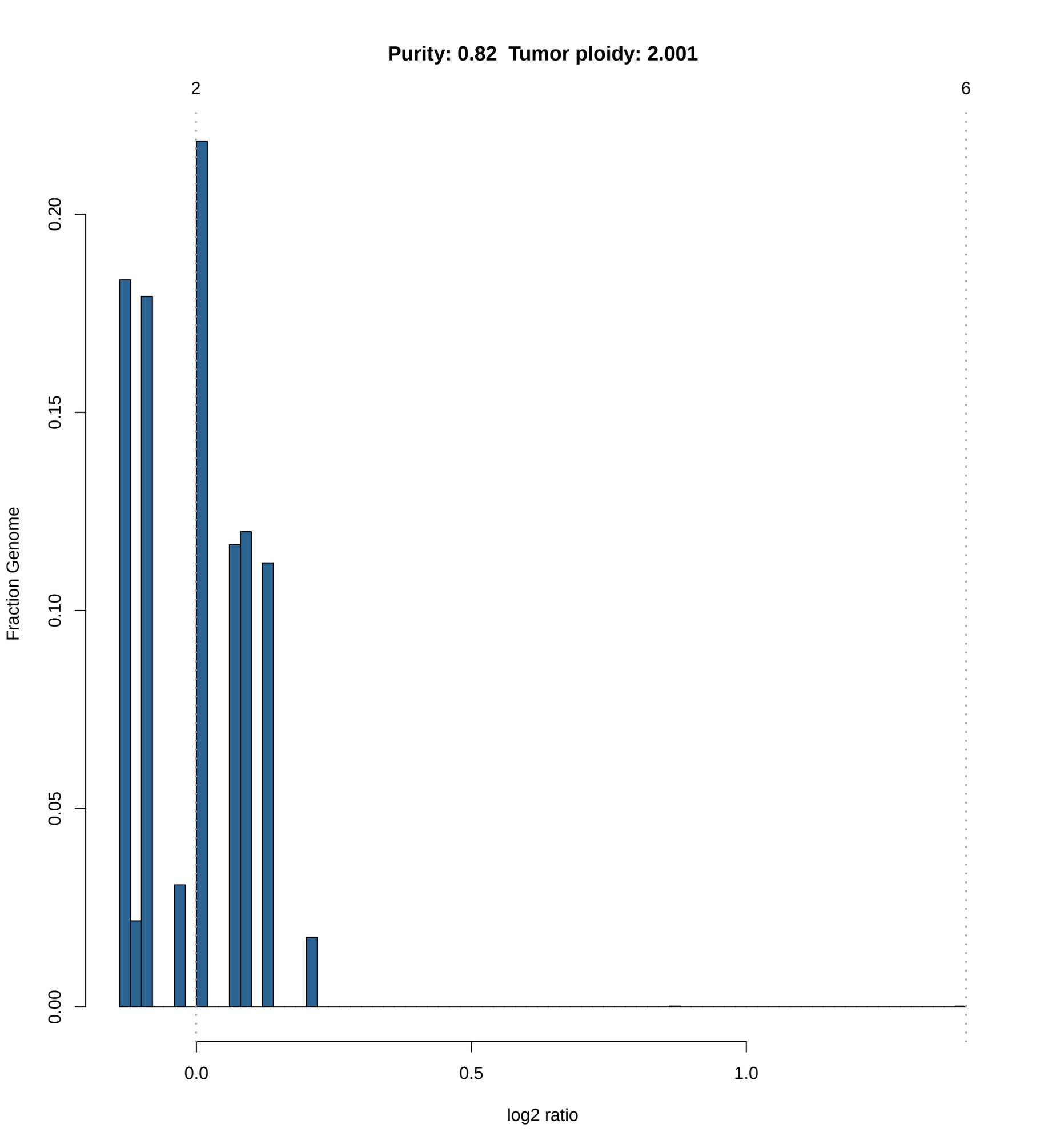

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

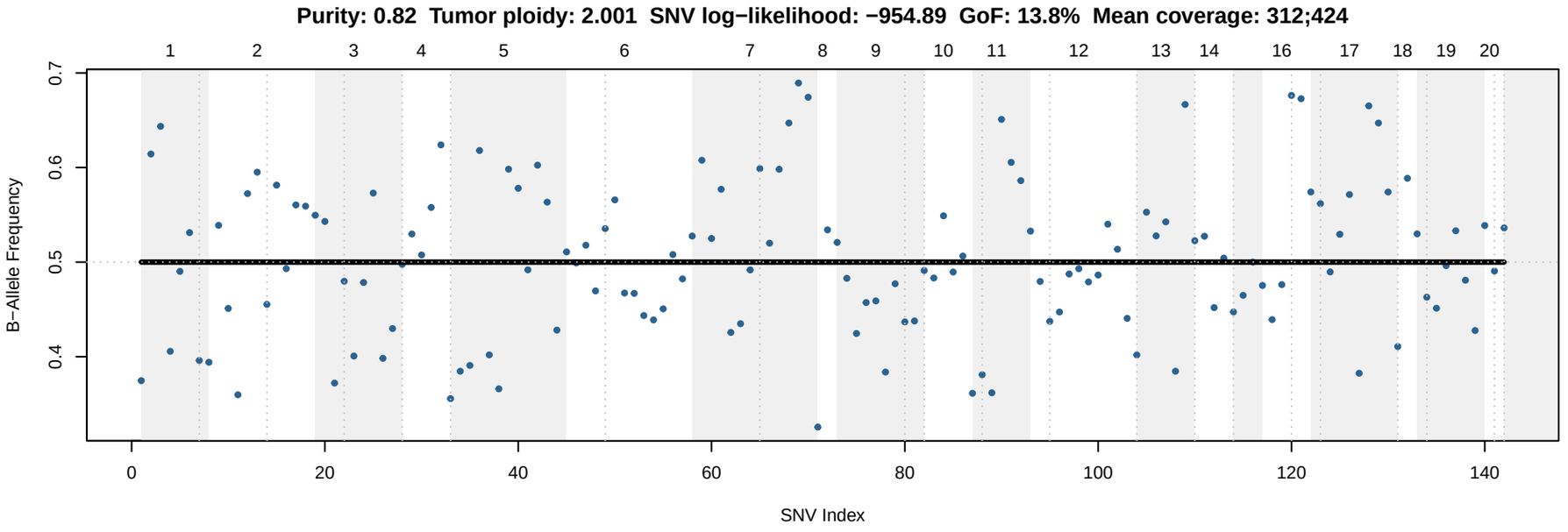

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
3m2
4m2
3m1
−0.5
0.0
0.5
Copy Number log−ratio

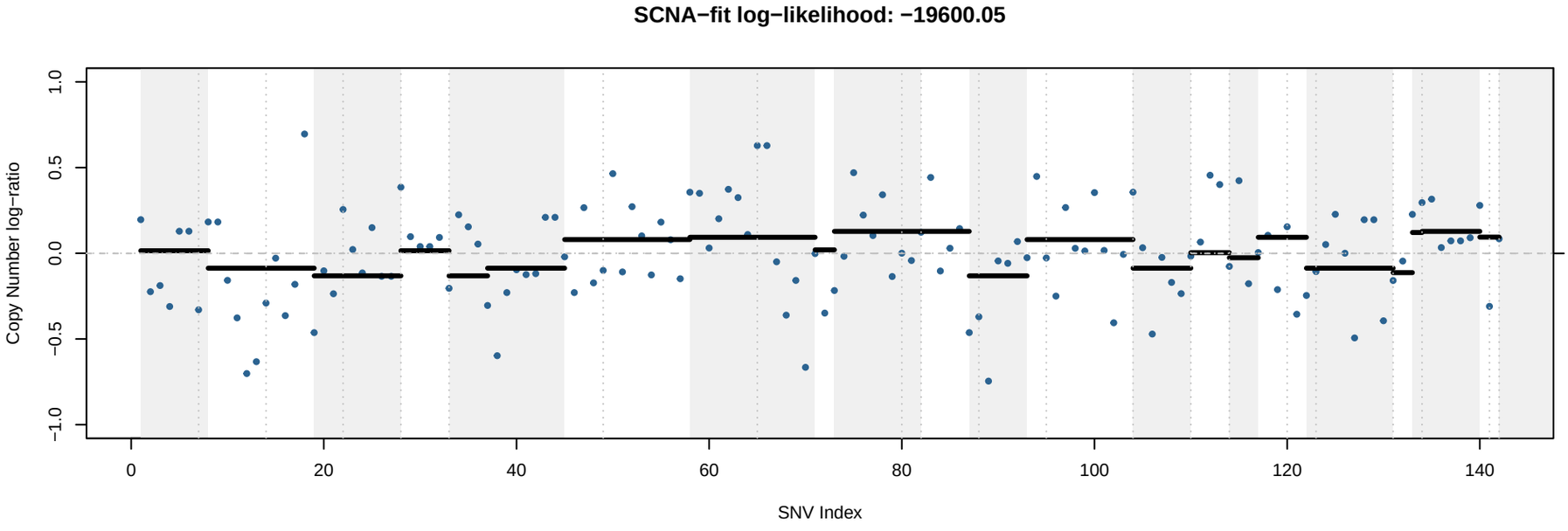

Coverage (log2)
6
7
8
9
10
0.2
0.4
0.6
Allelic fraction

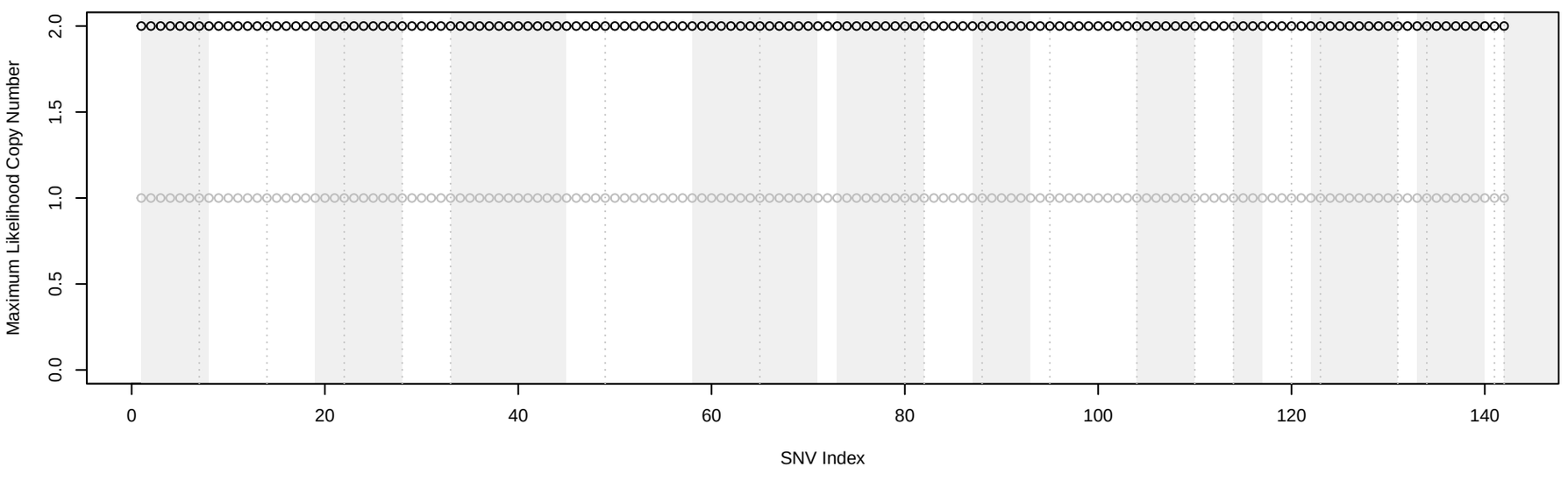

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
−0.5
0.0
0.5
Copy Number log−ratio

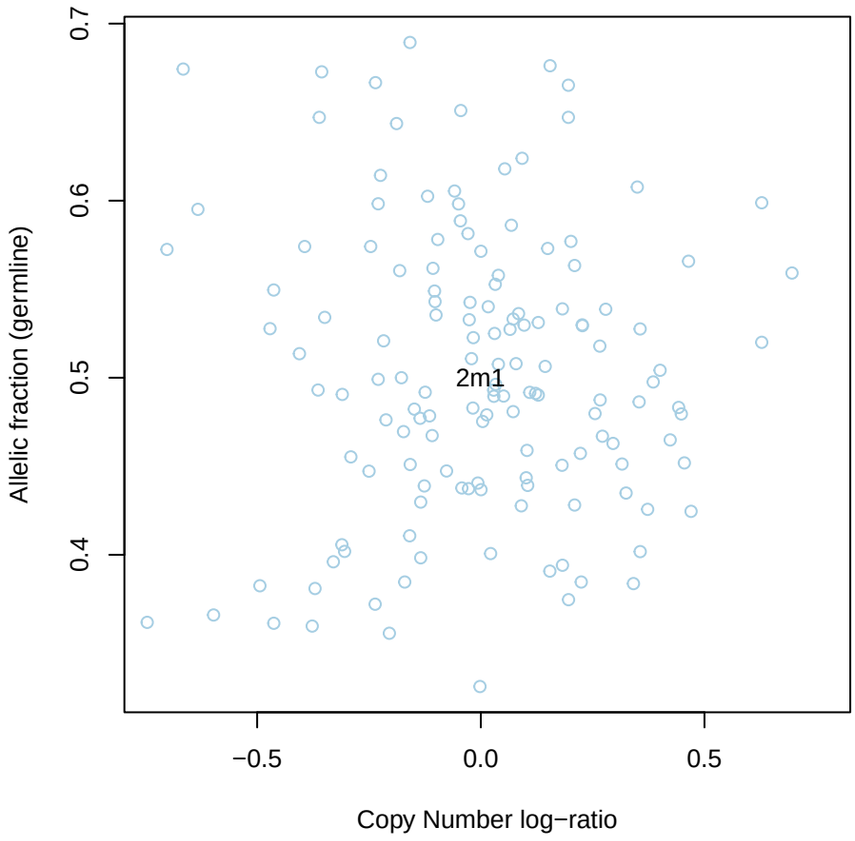

Power 0.8
Frequency
0
5
10
15
20
25
30
35
0.2
0.4
0.6
0.8
1.0
Cellular fraction

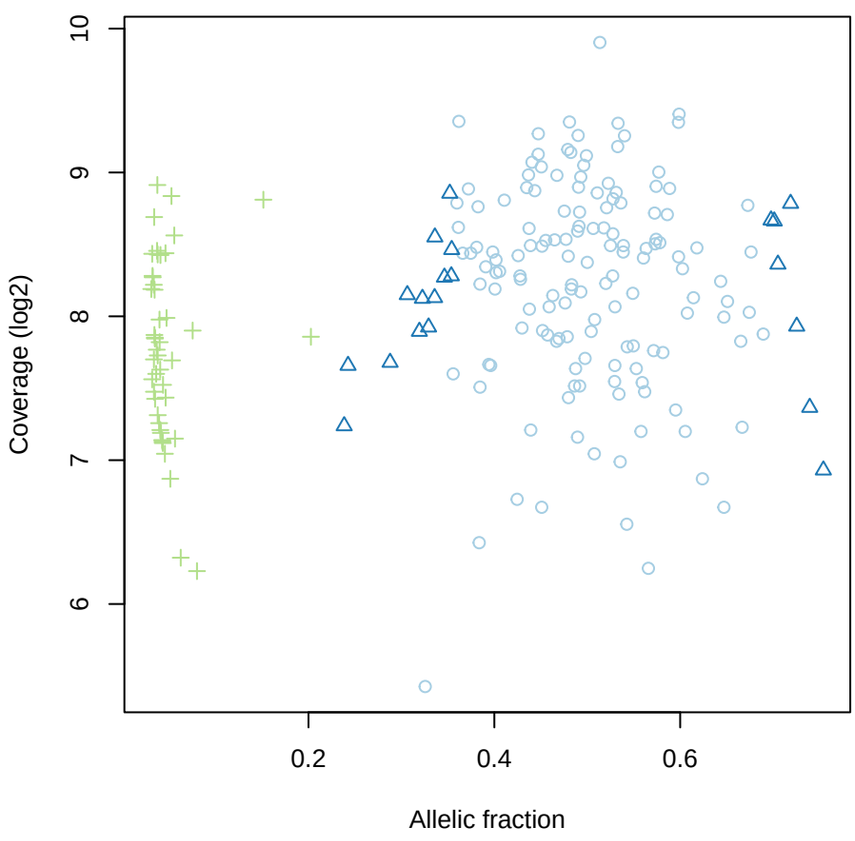

Purity: 0.82 Tumor ploidy: 2.001
2
6
0.20
0.15
0.10
0.05
0.00
Fraction Genome
0.0
0.5
1.0
log2 ratio

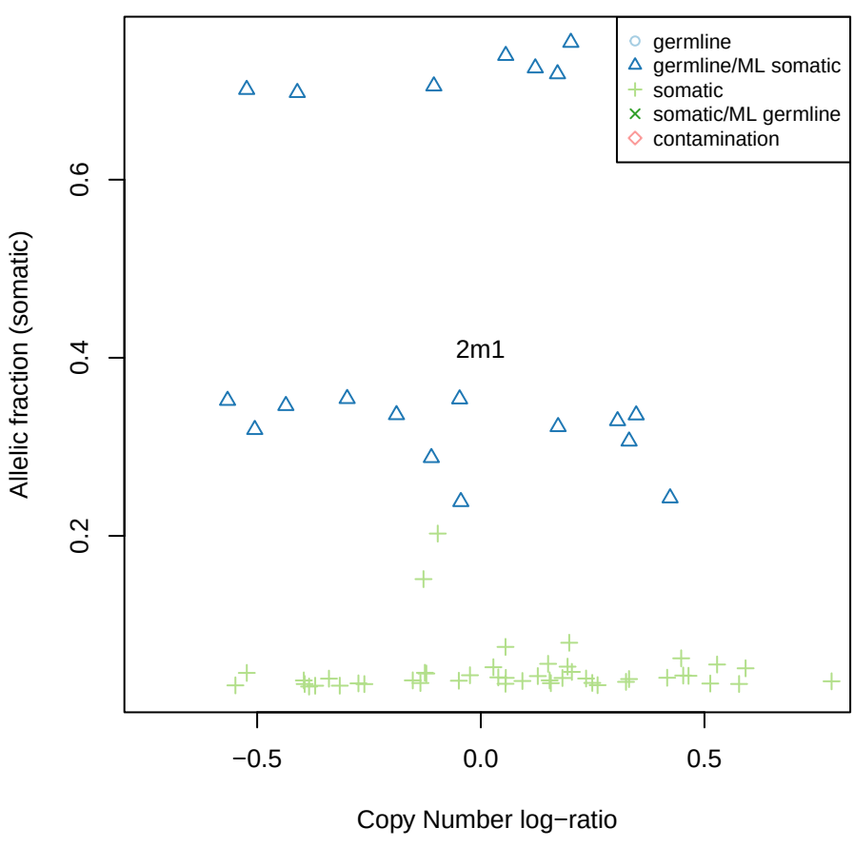

Purity: 0.82 Tumor ploidy: 2.001 SNV log−likelihood: −954.89 GoF: 13.8% Mean coverage: 312;424
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 18 19 20
B−Allele Frequency
0.4 0.5 0.6 0.7
0 20 40 60 80 100 120 140
SNV Index

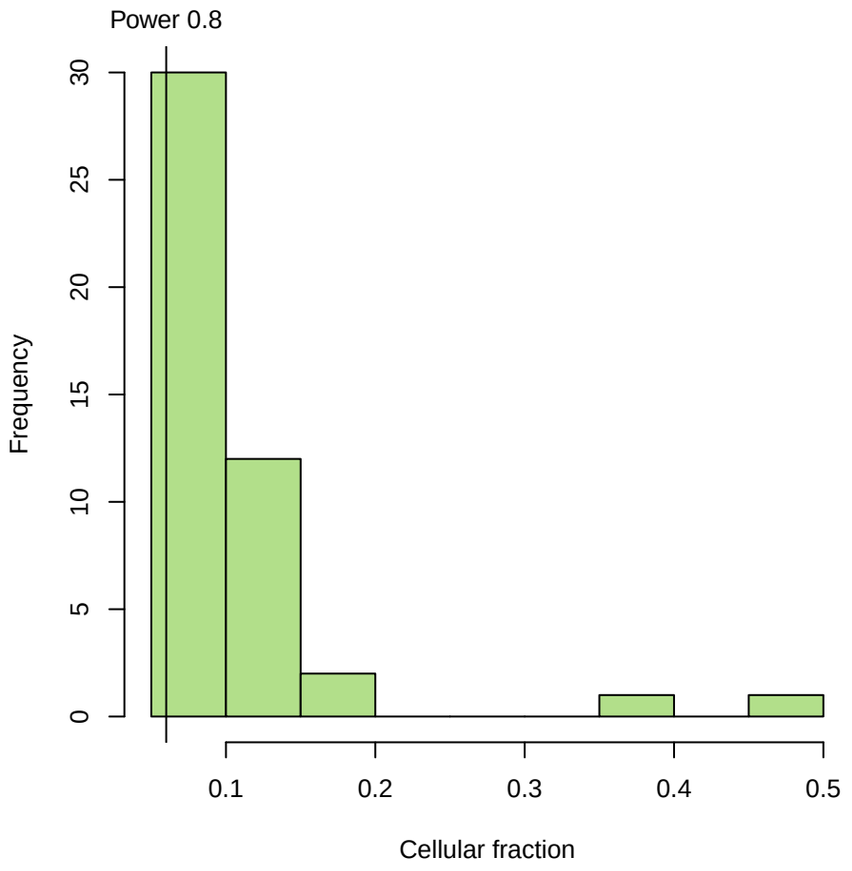

SCNA−fit log−likelihood: −19600.05
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2
0 20 40 60 80 100 120 140
SNV Index


Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0
0 20 40 60 80 100 120 140
SNV Index


Allelic fraction (germline)
0.4
0.5
0.6
0.7
2m1
−0.5
0.0
0.5
Copy Number log−ratio


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


Allelic fraction (somatic)
0.2
0.4
0.6
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
−0.5
0.0
0.5
Copy Number log−ratio


Power 0.8
Frequency
0
5
10
15
20
25
30
0.1
0.2
0.3
0.4
0.5
Cellular fraction