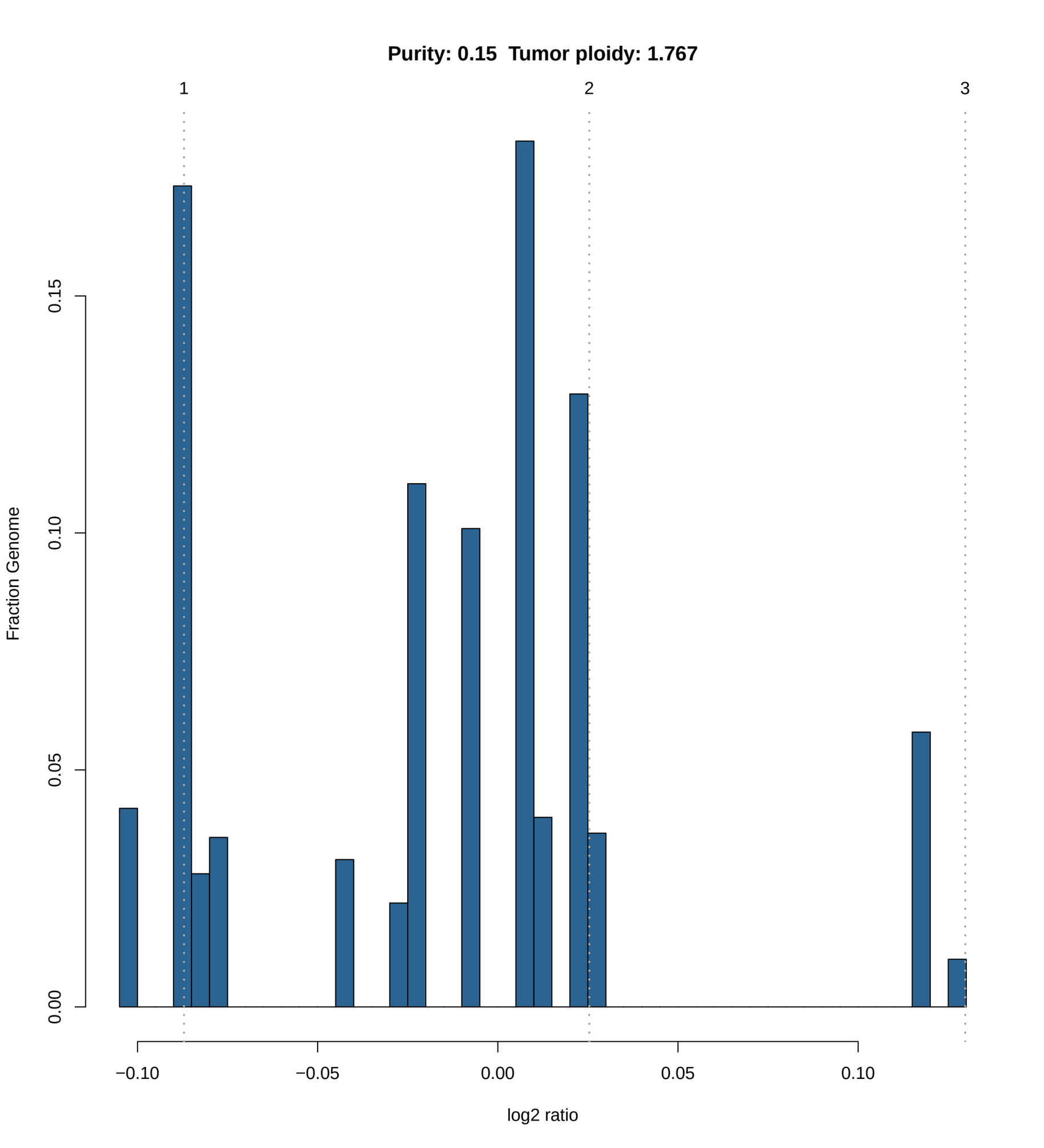
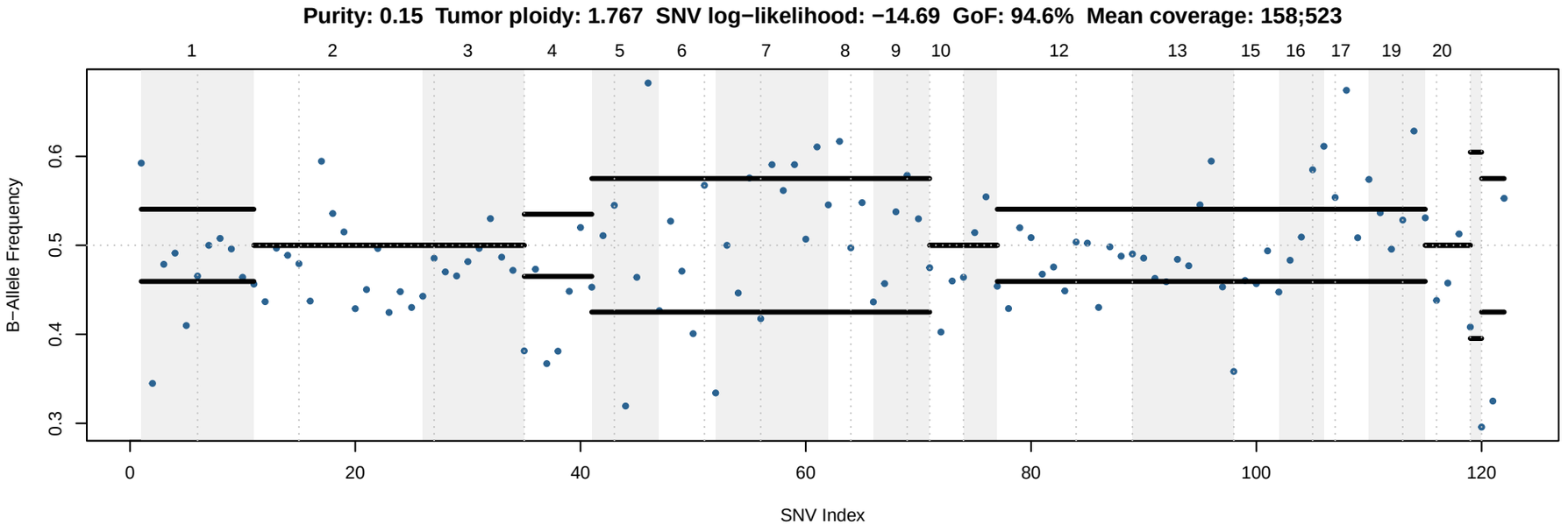
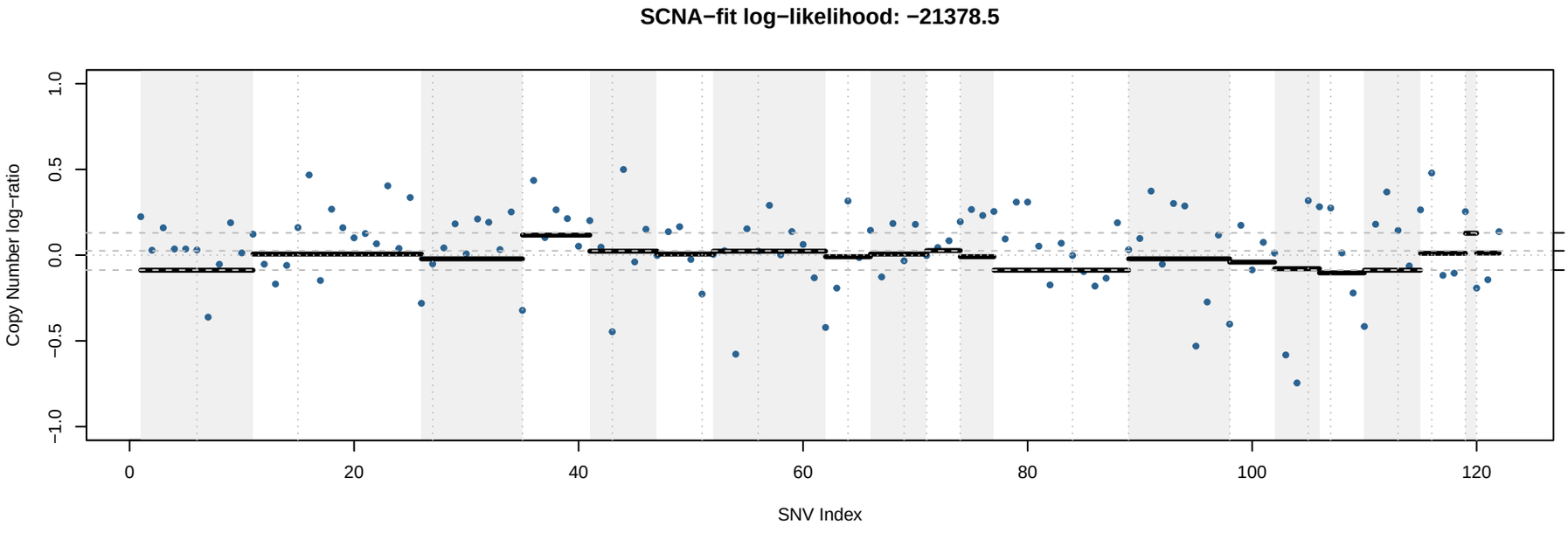
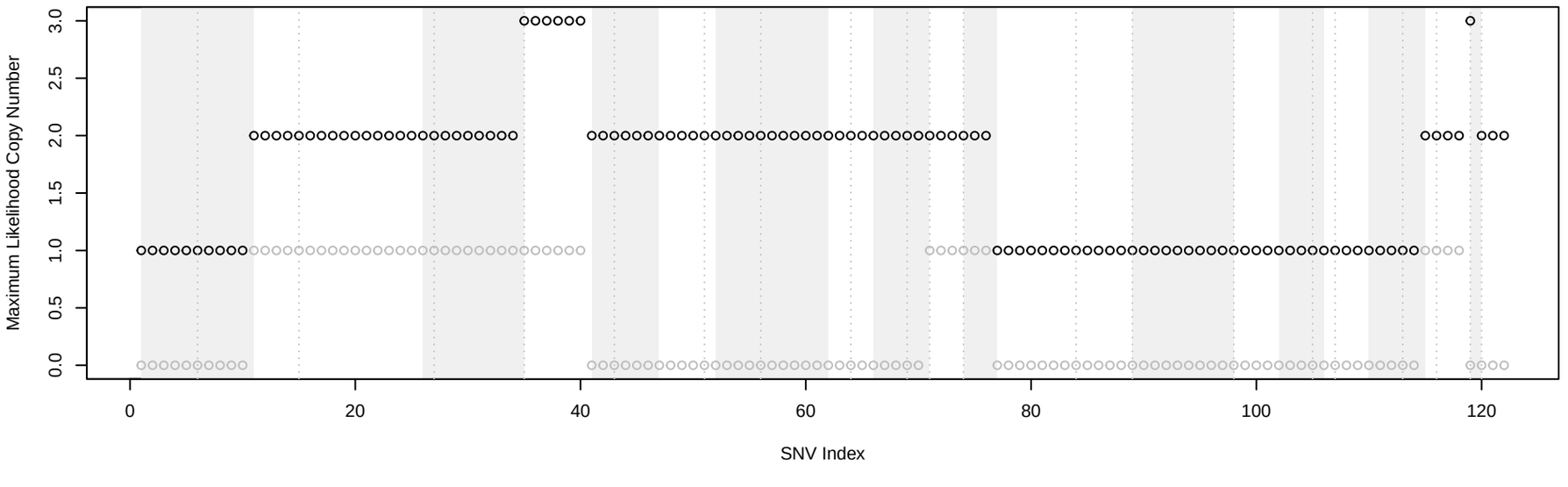
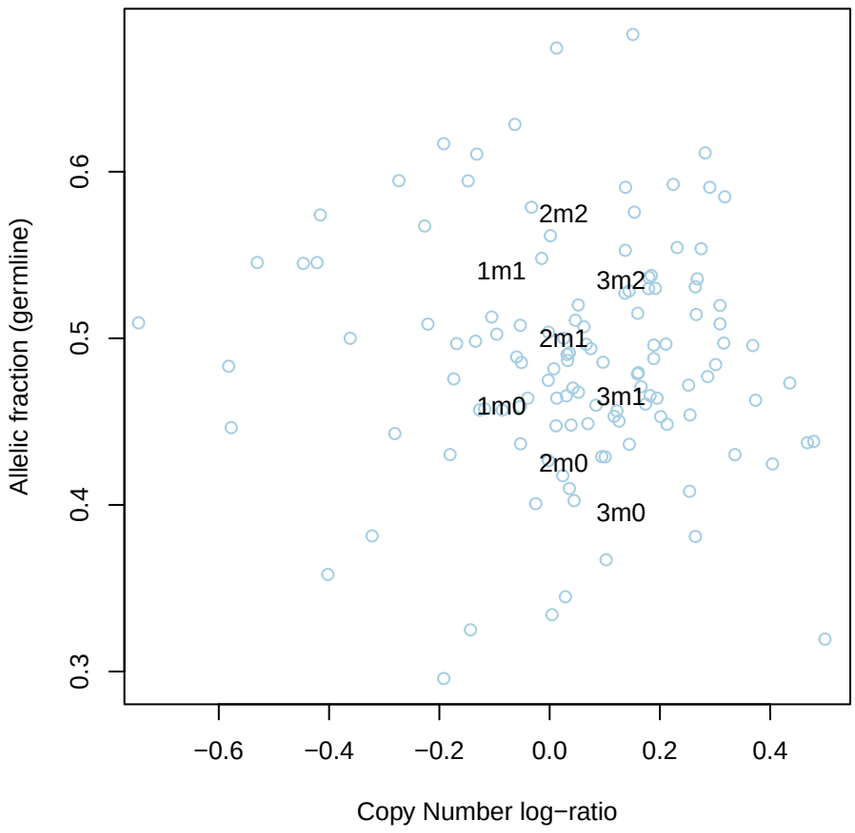
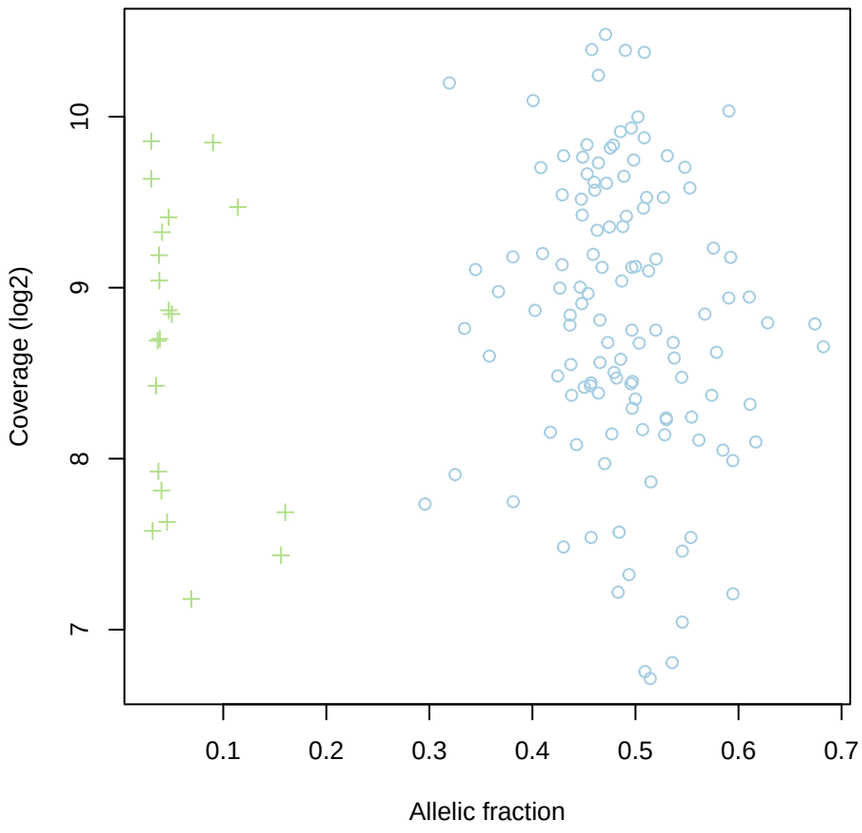

Purity: 0.15 Tumor ploidy: 1.767
1
2
3
0.15
0.10
0.05
0.00
Fraction Genome
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

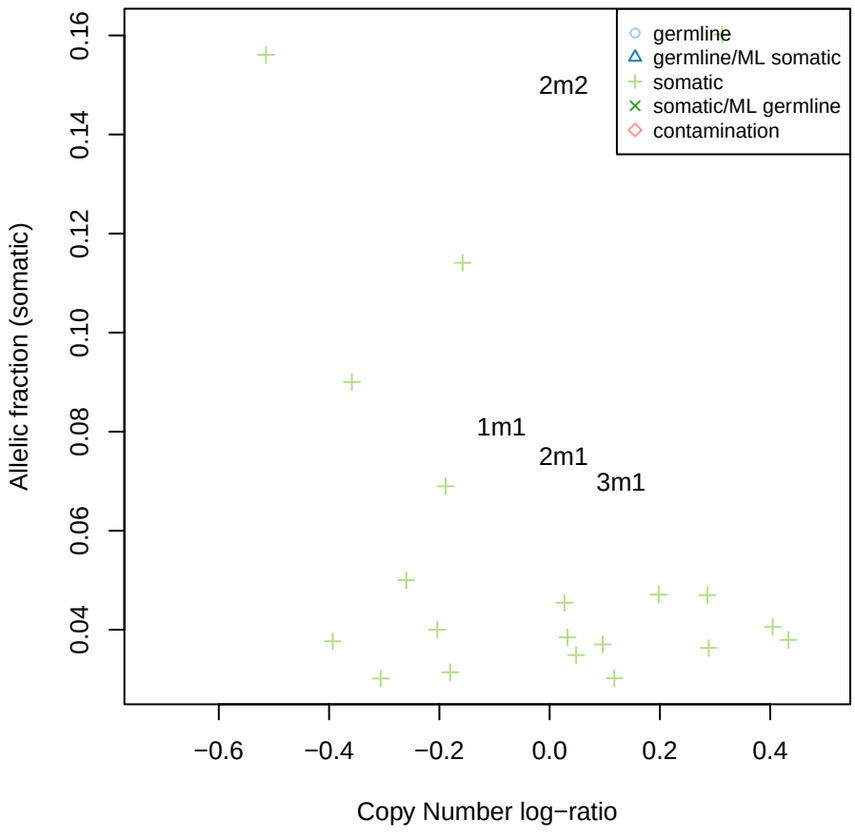

Purity: 0.15 Tumor ploidy: 1.767 SNV log−likelihood: −14.69 GoF: 94.6% Mean coverage: 158;523
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6
0 20 40 60 80 100 120
SNV Index

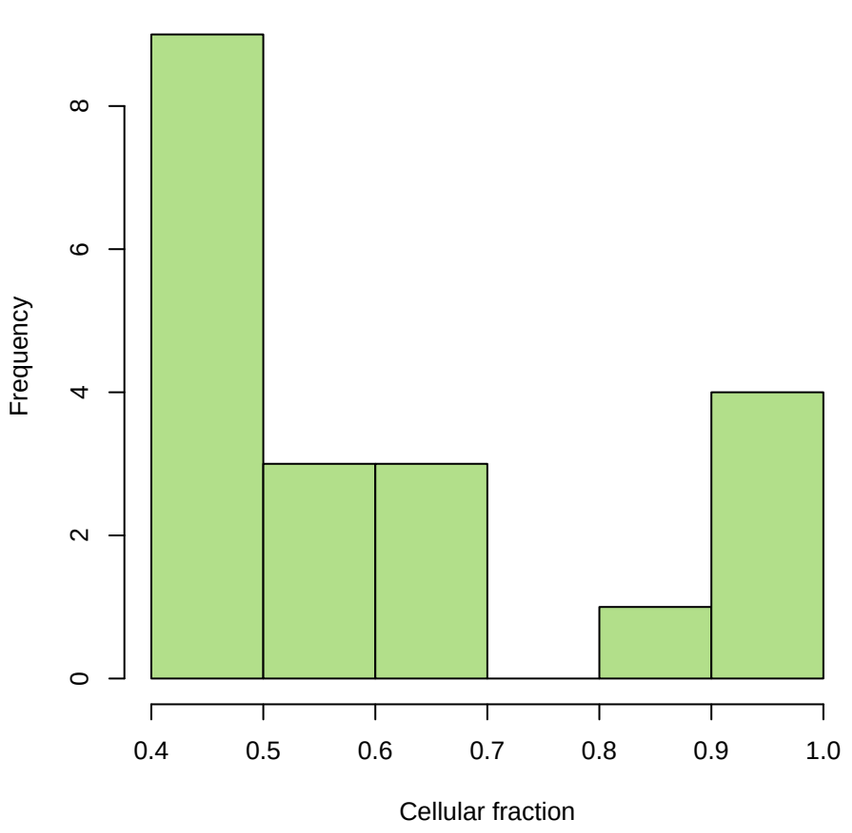

SCNA−fit log−likelihood: −21378.5
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 3
0 20 40 60 80 100 120
SNV Index

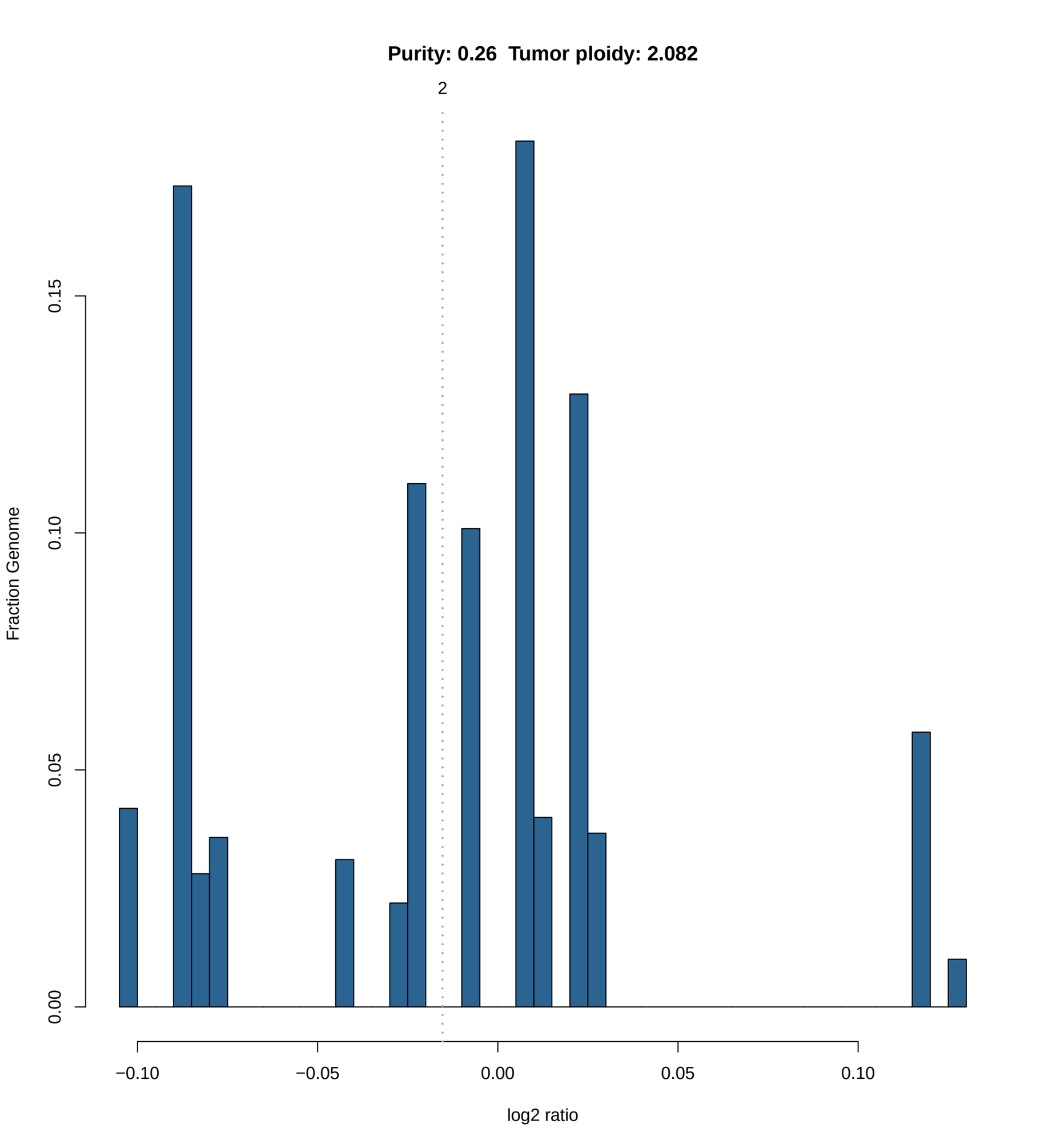

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120
SNV Index

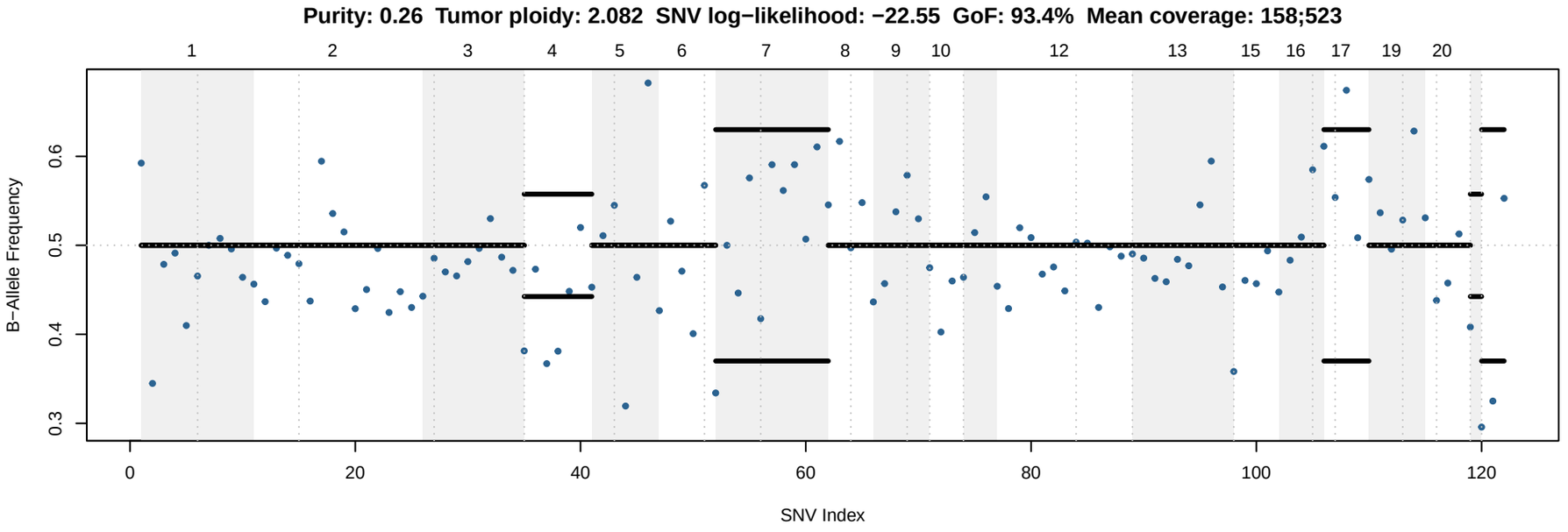

Allelic fraction (germline)
0.3
0.4
0.5
0.6
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio
2m2
1m1
3m2
2m1
1m0
3m1
2m0
3m0

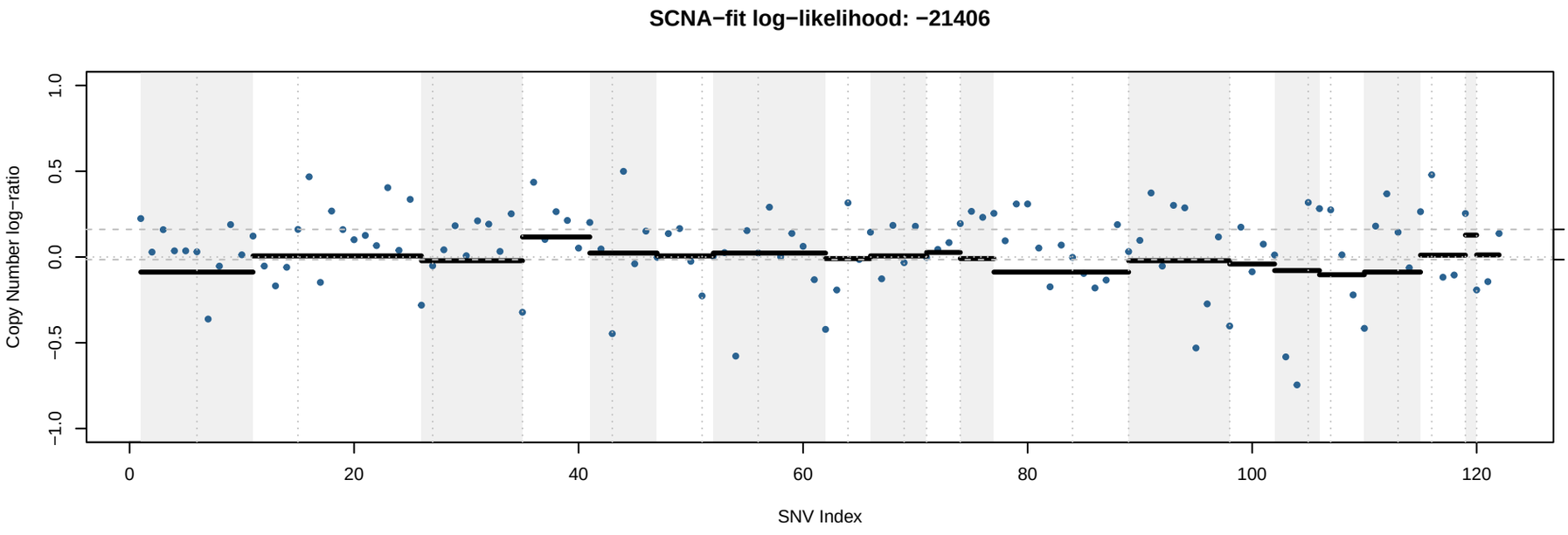

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

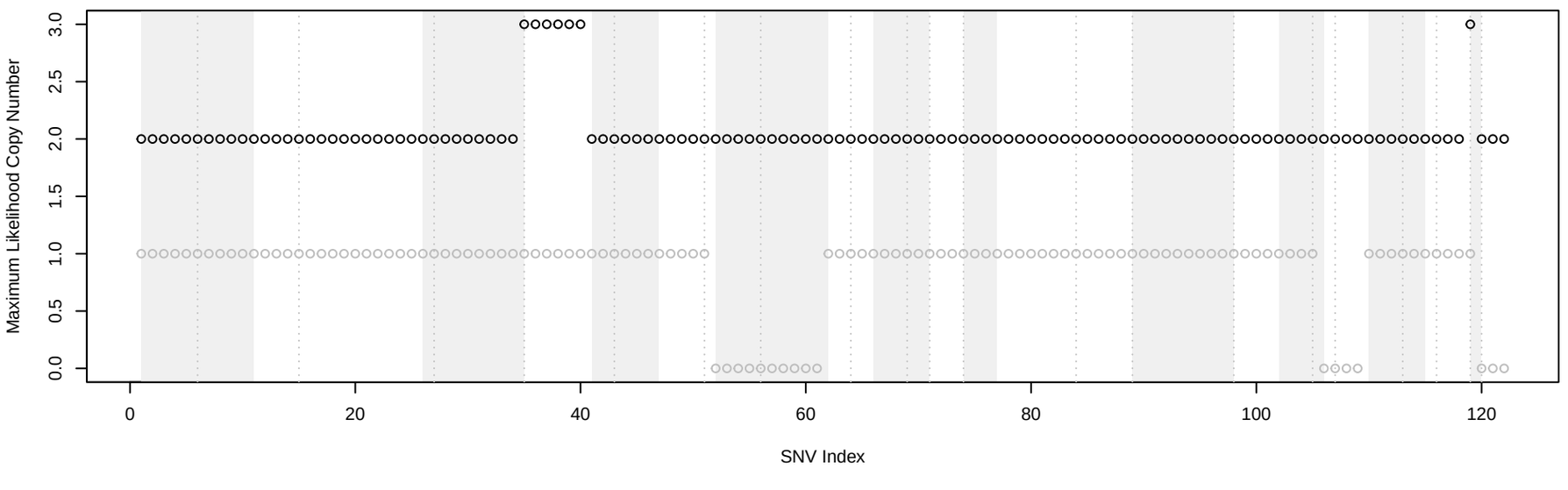

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
1m1
2m1
3m1

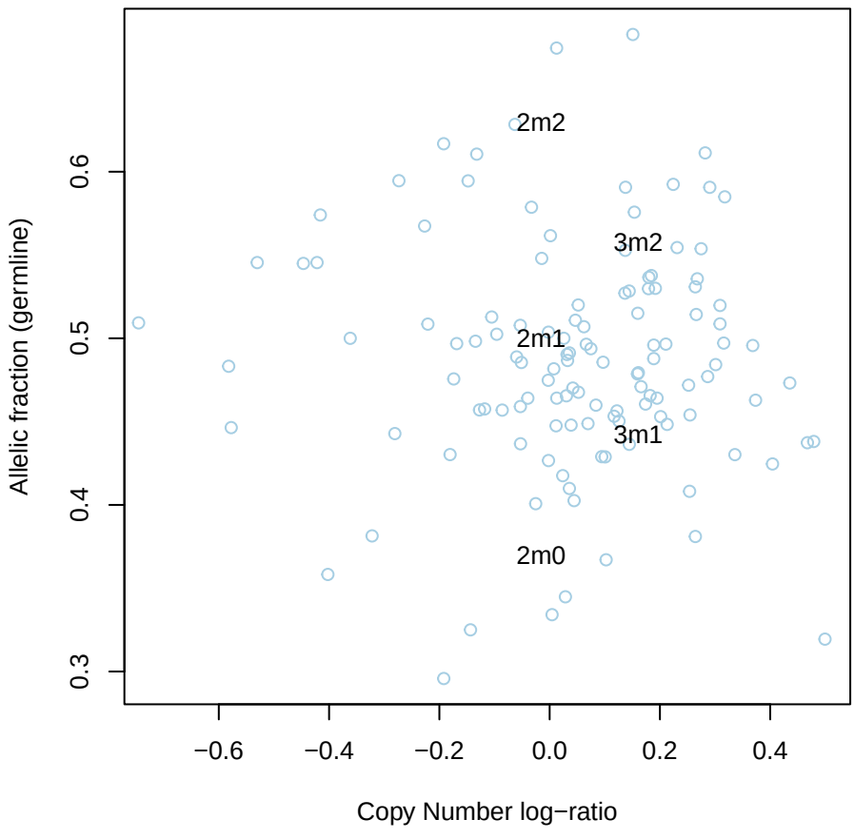

Frequency
0
2
4
6
8
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

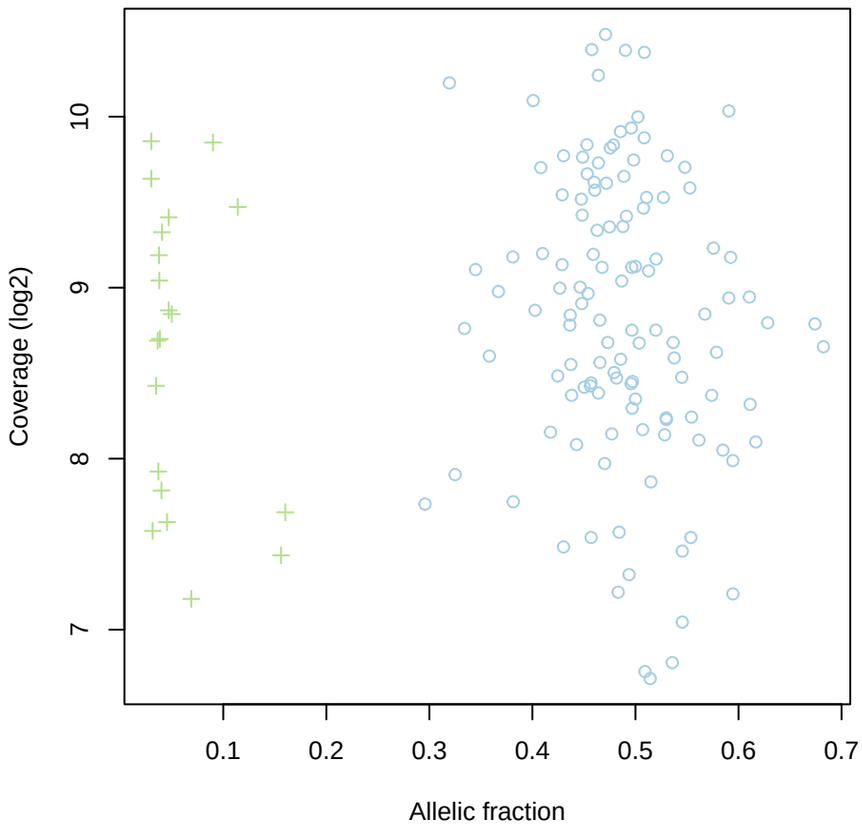

Purity: 0.26 Tumor ploidy: 2.082
2
0.15
0.10
0.05
0.00
Fraction Genome
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

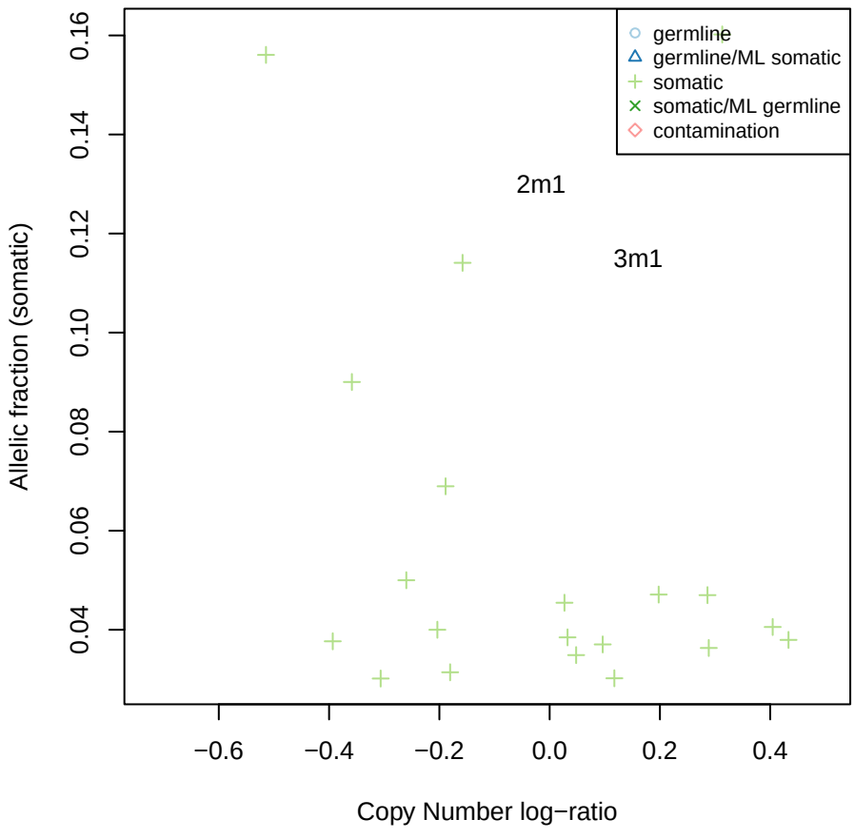

Purity: 0.26 Tumor ploidy: 2.082 SNV log−likelihood: −22.55 GoF: 93.4% Mean coverage: 158;523
1
2
3
4
5
6
7
8
9
10
12
13
15
16
17
19
20
B−Allele Frequency
0.3
0.4
0.5
0.6
0
20
40
60
80
100
120
SNV Index

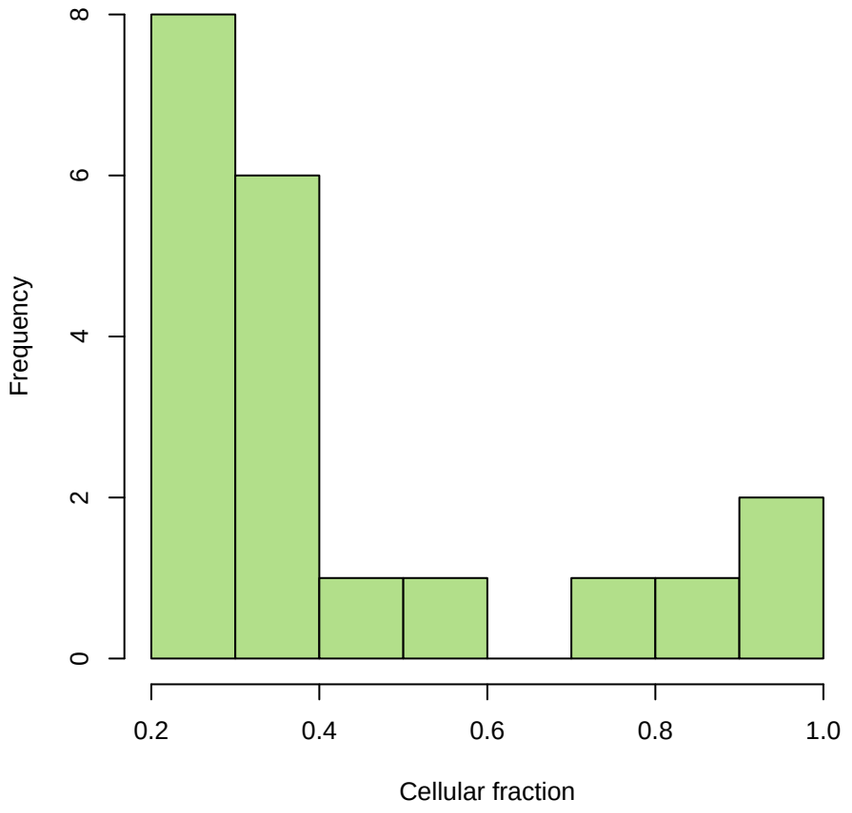

SCNA−fit log−likelihood: −21406
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
2
3
0
20
40
60
80
100
120
SNV Index

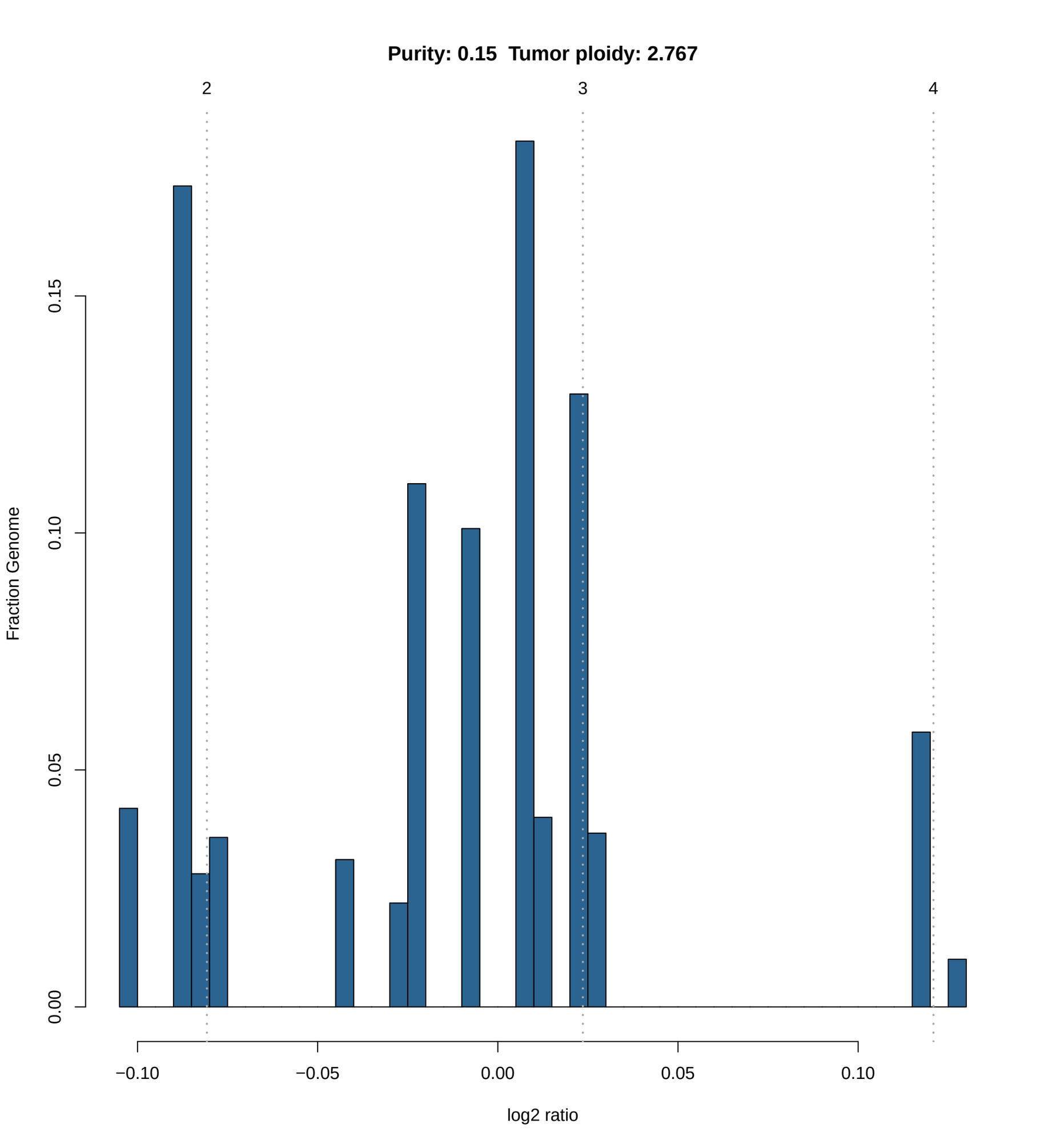

Maximum Likelihood Copy Number
0.0
0.5
1.0
1.5
2.0
2.5
3.0
0
20
40
60
80
100
120
SNV Index

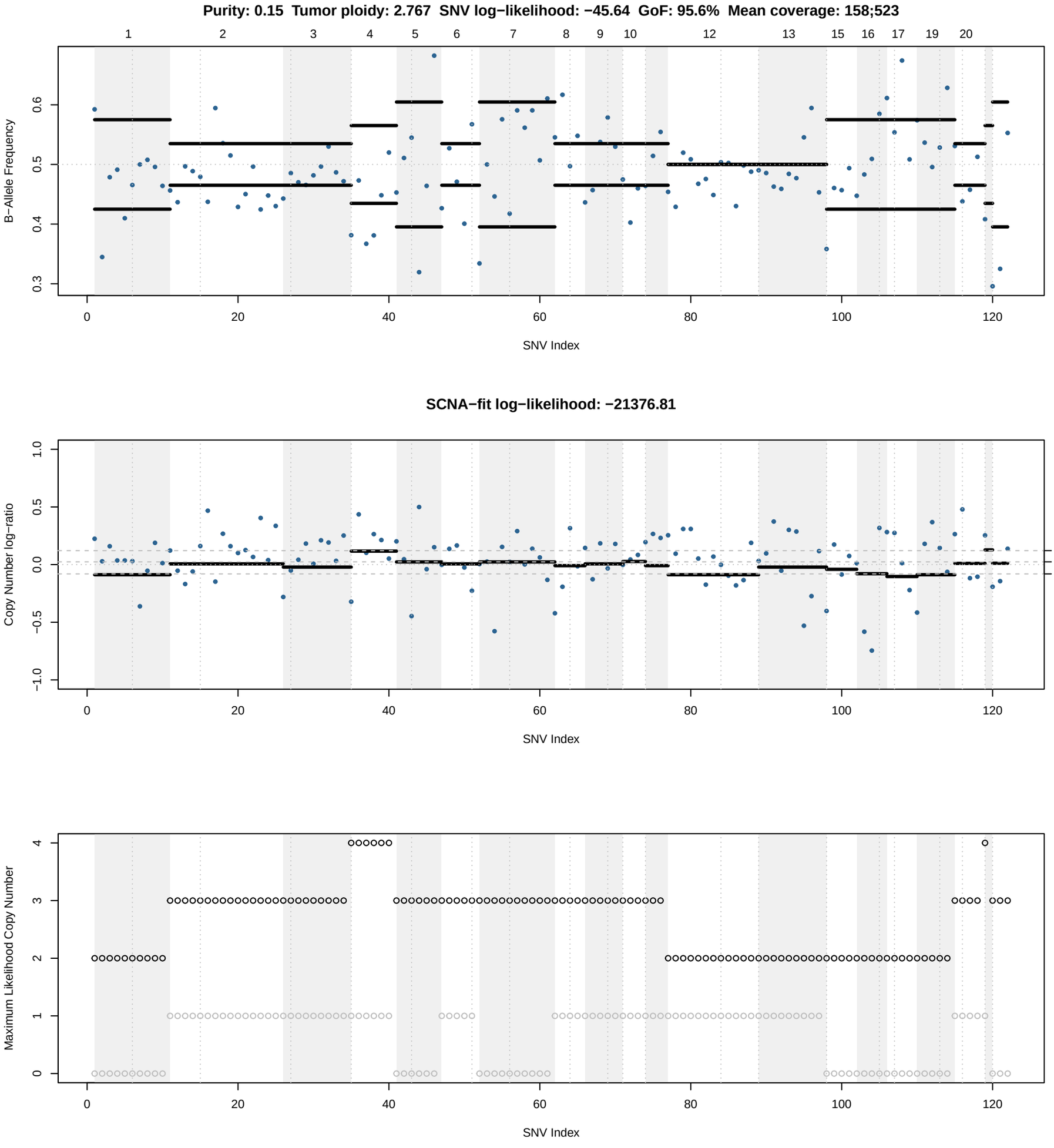

Allelic fraction (germline)
0.3
0.4
0.5
0.6
2m2
3m2
2m1
3m1
2m0
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

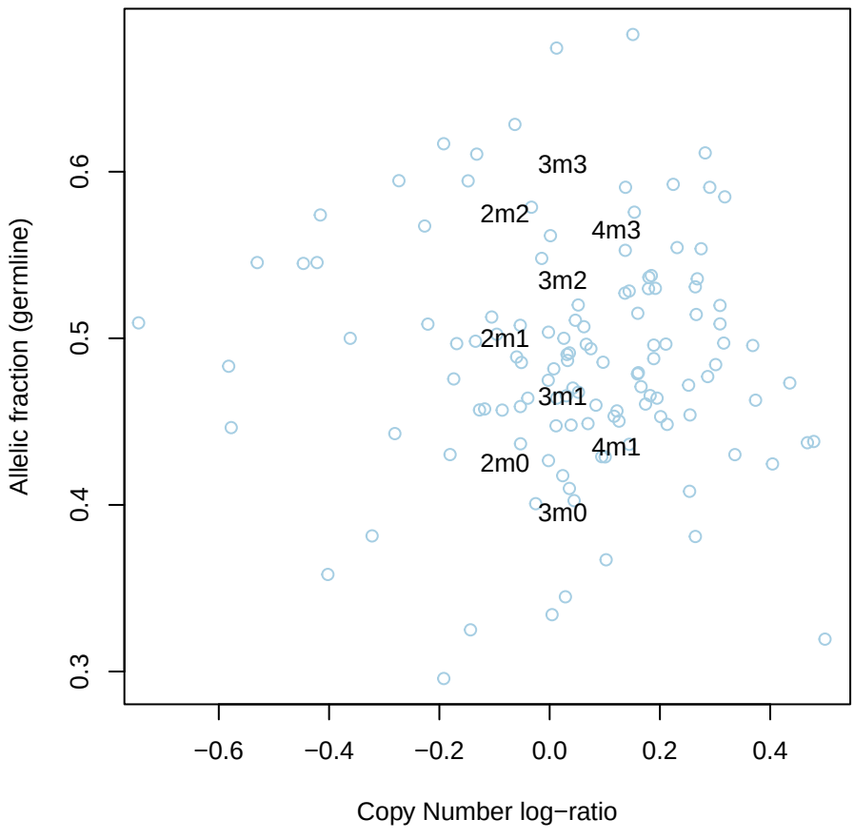

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

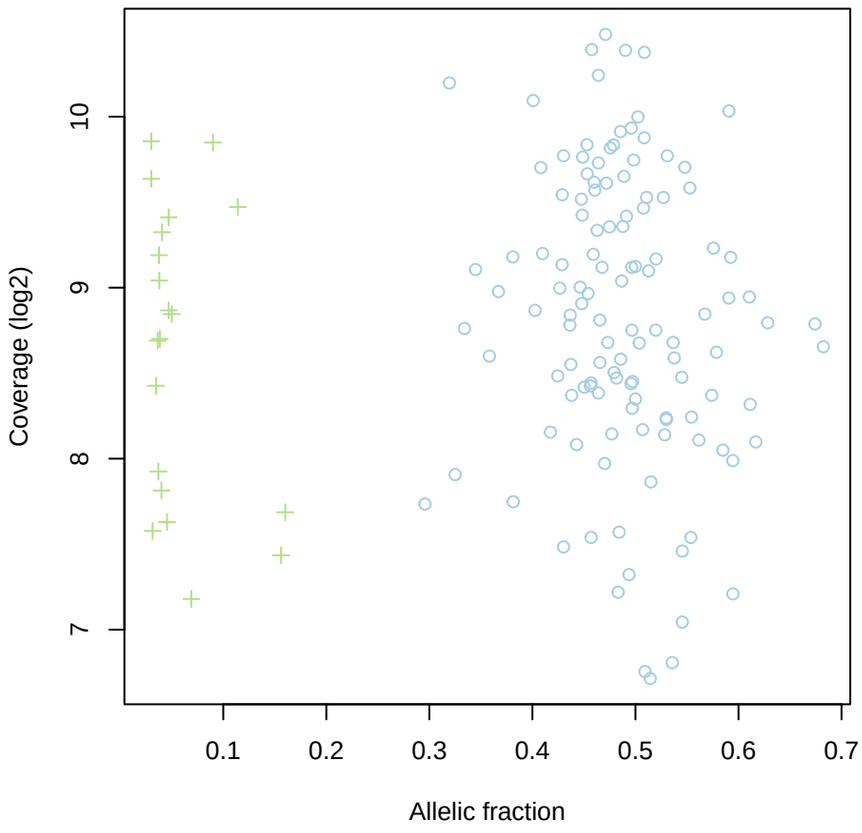

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
2m1
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

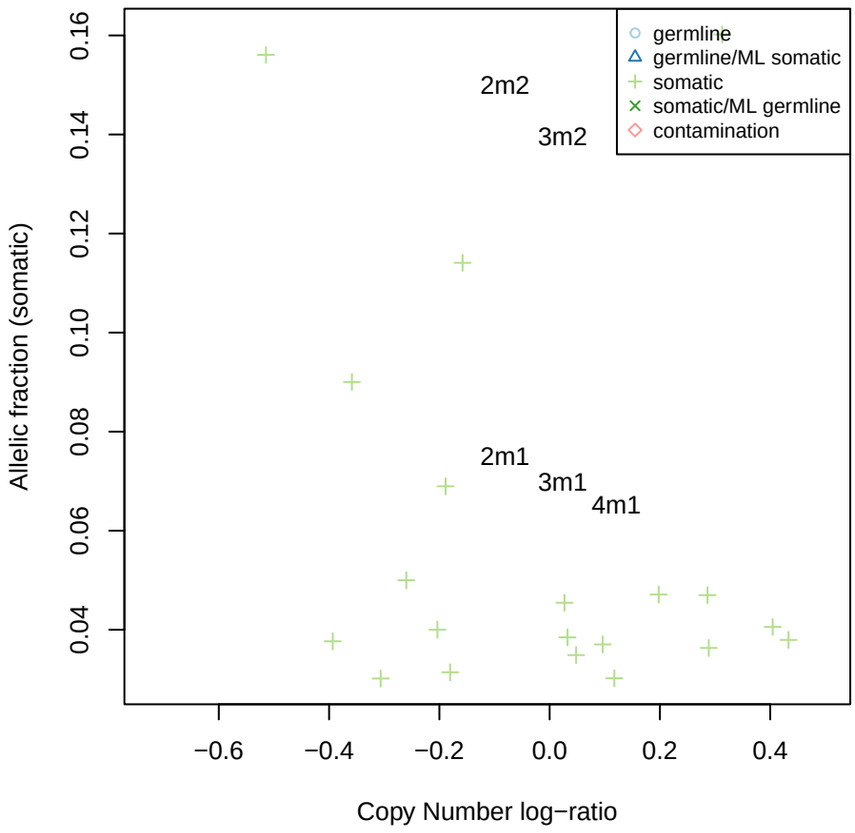

Frequency
0
2
4
6
8
0.2
0.4
0.6
0.8
1.0
Cellular fraction

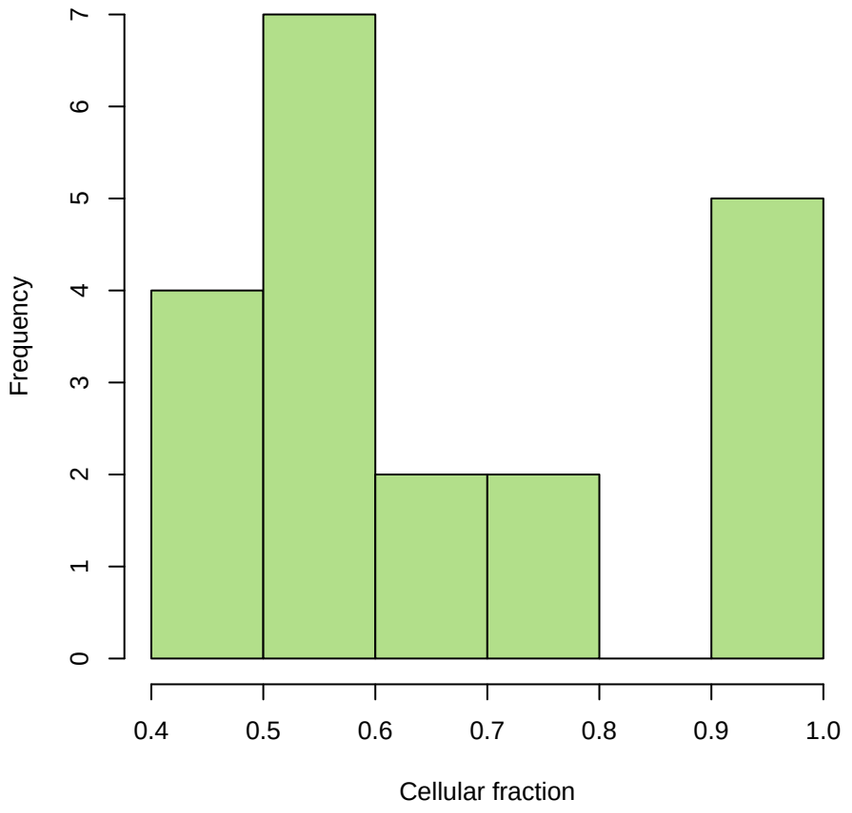

Purity: 0.15 Tumor ploidy: 2.767
2
3
4
0.15
0.10
0.05
0.00
Fraction Genome
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

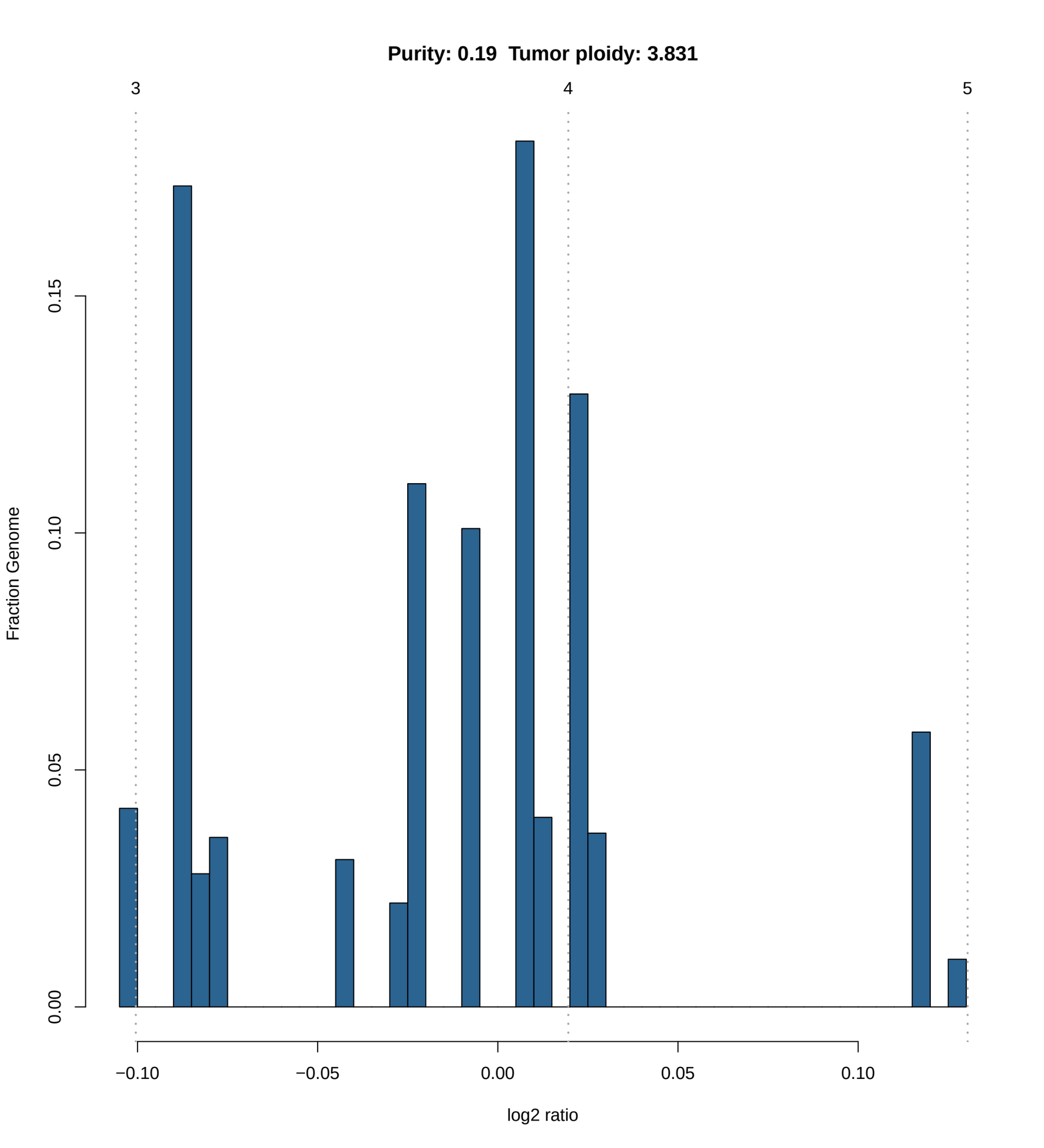

Purity: 0.15 Tumor ploidy: 2.767 SNV log−likelihood: −45.64 GoF: 95.6% Mean coverage: 158;523
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6
0 20 40 60 80 100 120
SNV Index
SCNA−fit log−likelihood: −21376.81
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 4
0 20 40 60 80 100 120
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120
SNV Index

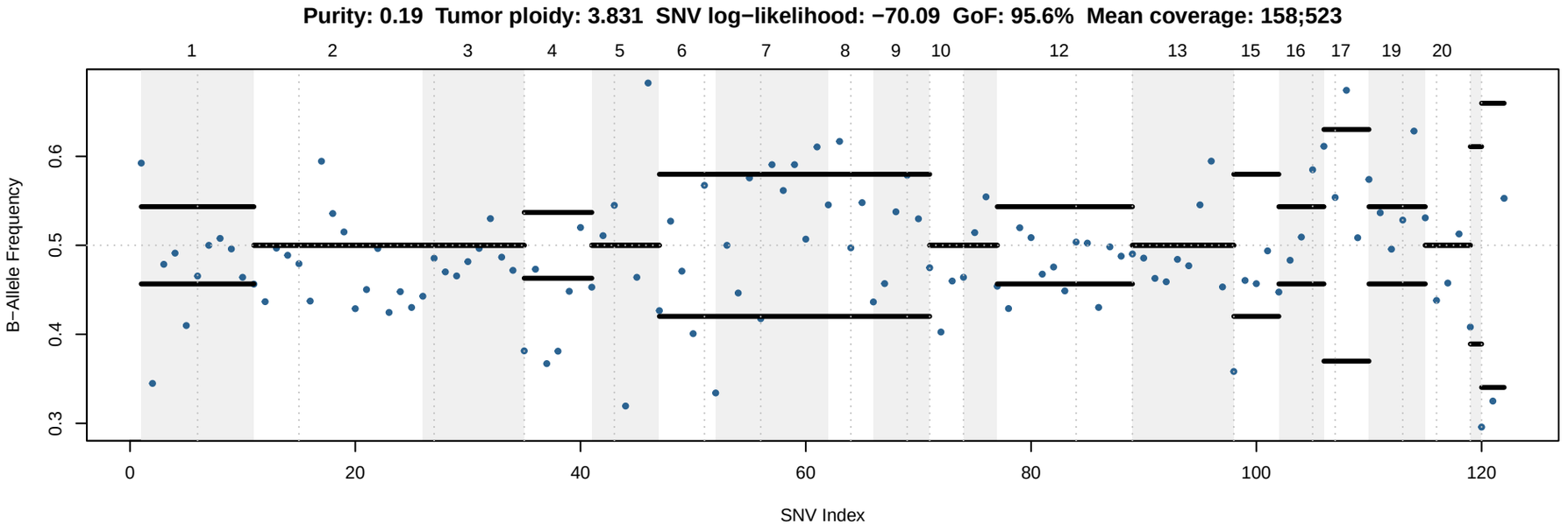

Allelic fraction (germline)
0.3
0.4
0.5
0.6
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio
3m3
2m2
4m3
3m2
2m1
3m1
4m1
2m0
3m0

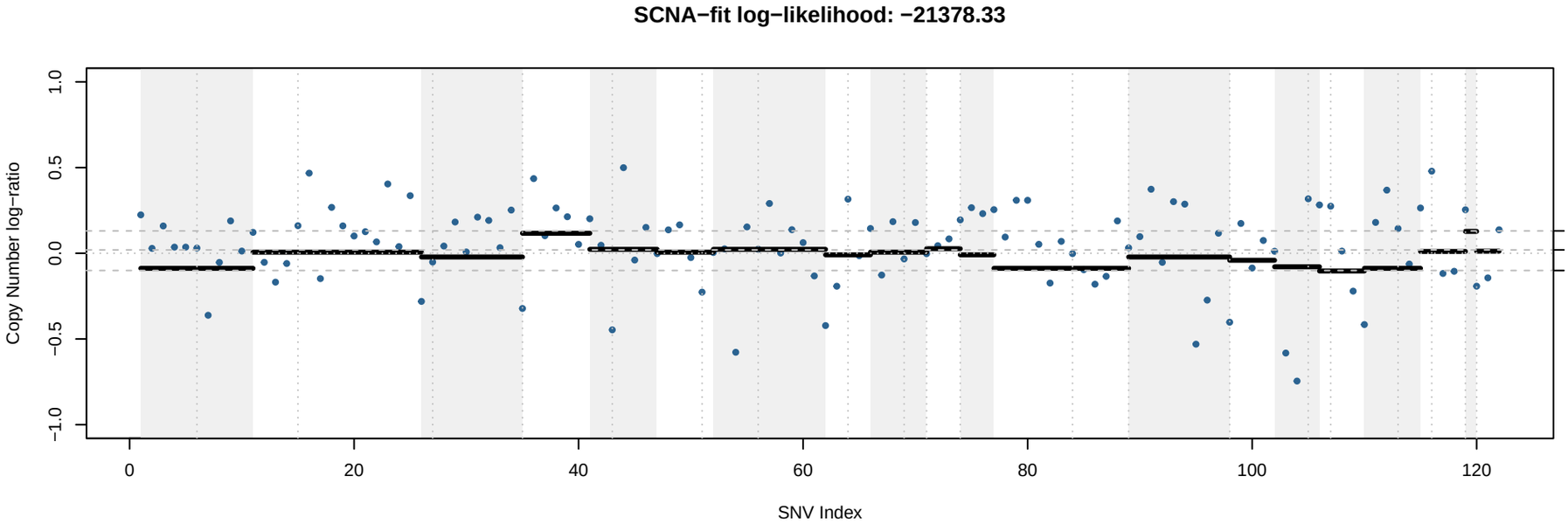

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

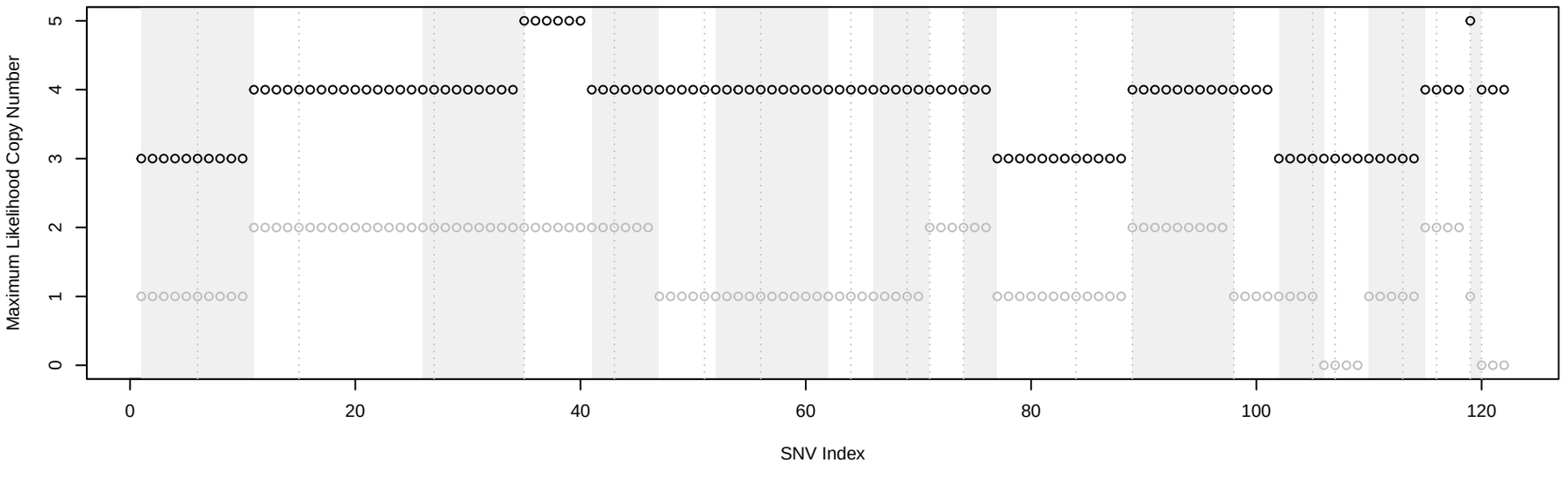

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
3m2
2m1
3m1
4m1

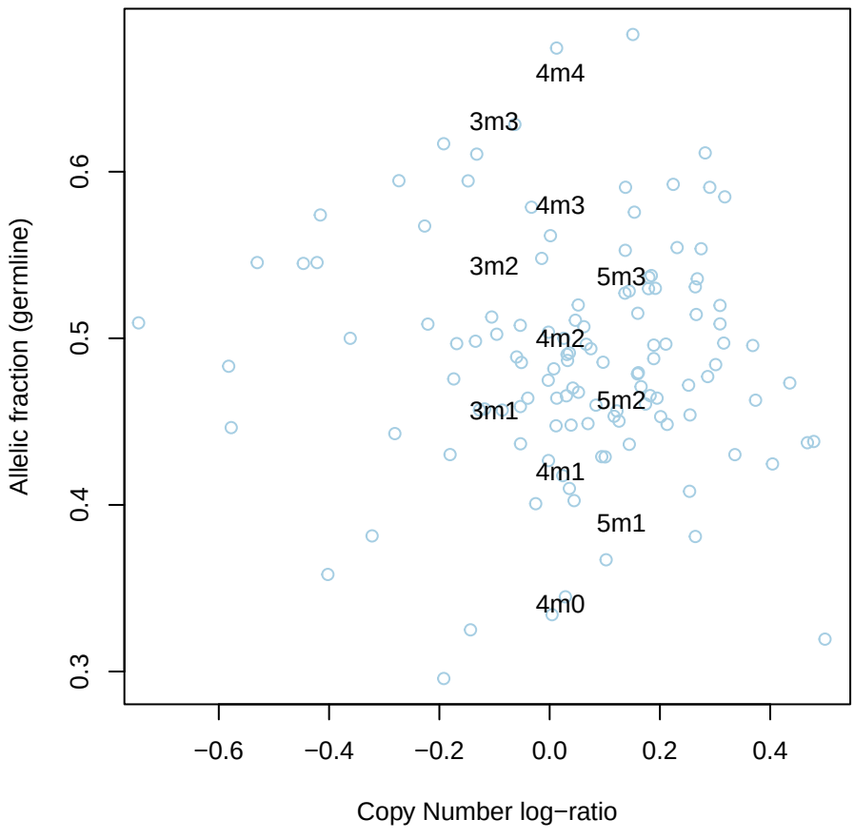

Frequency
0
1
2
3
4
5
6
7
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

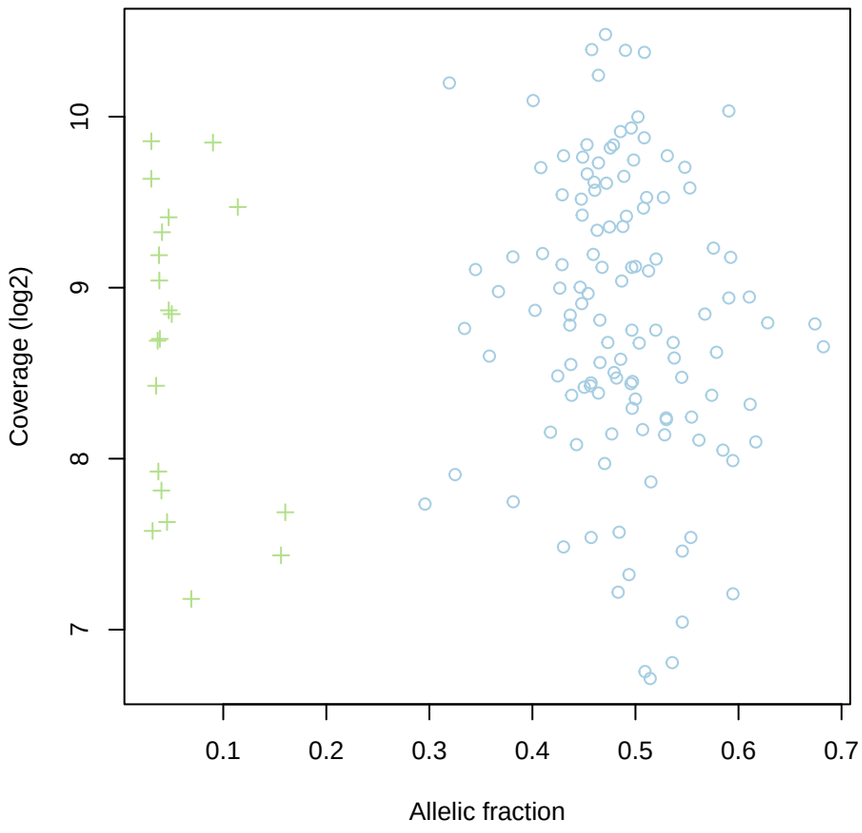

Purity: 0.19 Tumor ploidy: 3.831
3
4
5
0.15
0.10
0.05
0.00
Fraction Genome
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

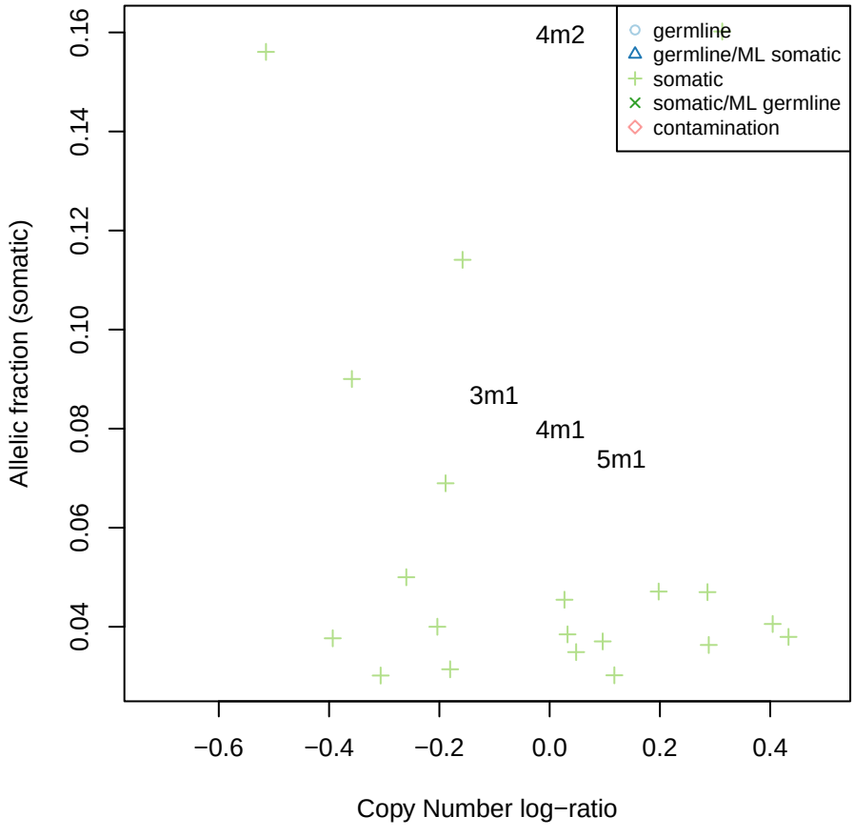

Purity: 0.19 Tumor ploidy: 3.831 SNV log−likelihood: −70.09 GoF: 95.6% Mean coverage: 158;523
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6
0 20 40 60 80 100 120
SNV Index

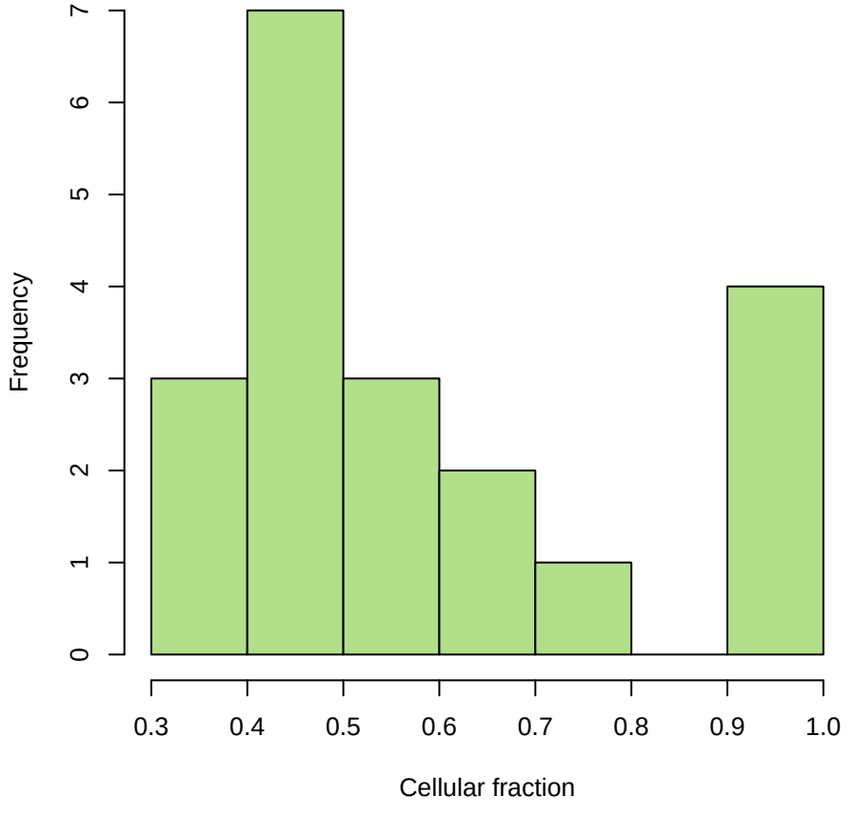

SCNA−fit log−likelihood: −21378.33
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 5
0 20 40 60 80 100 120
SNV Index

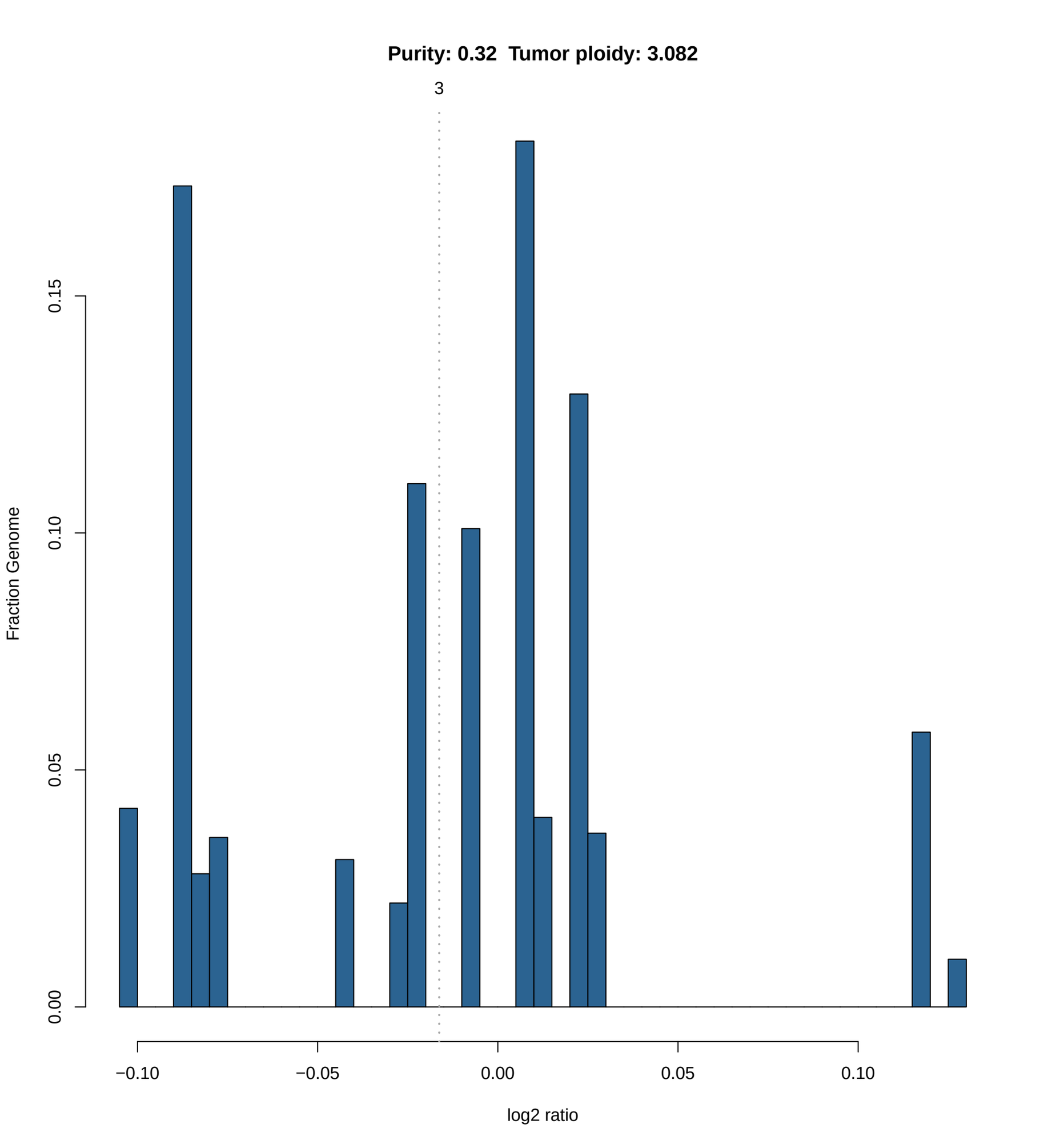

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100 120
SNV Index

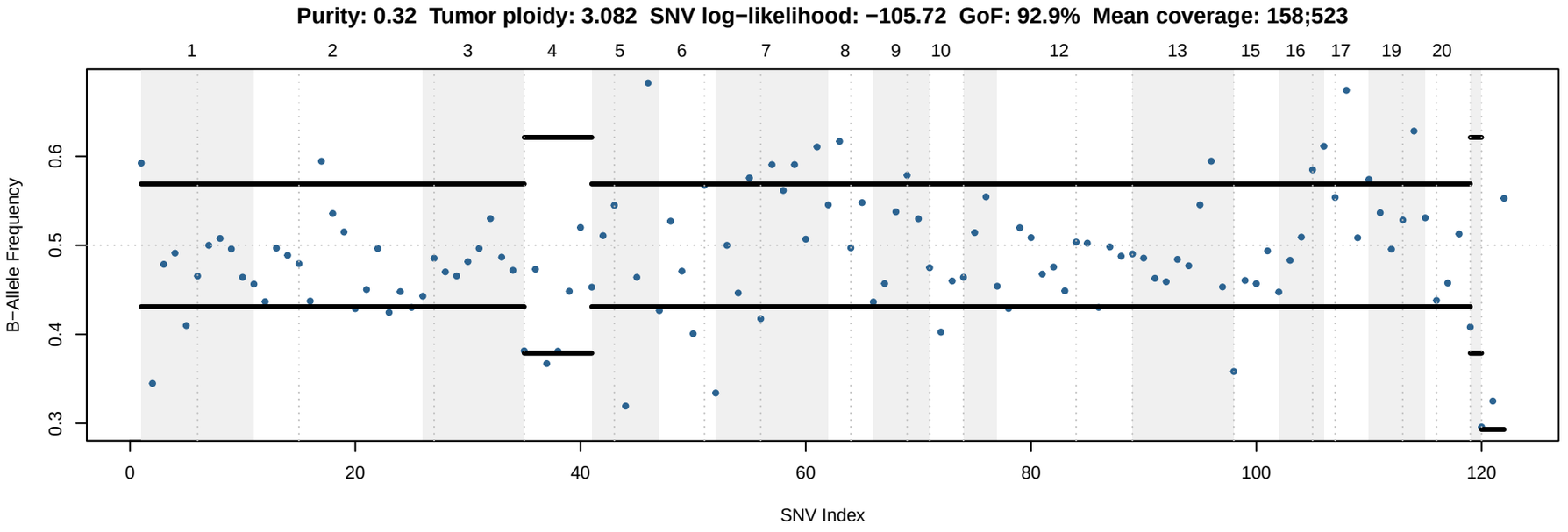

Allelic fraction (germline)
Copy Number log−ratio
4m4
3m3
4m3
3m2
5m3
4m2
5m2
3m1
4m1
5m1
4m0

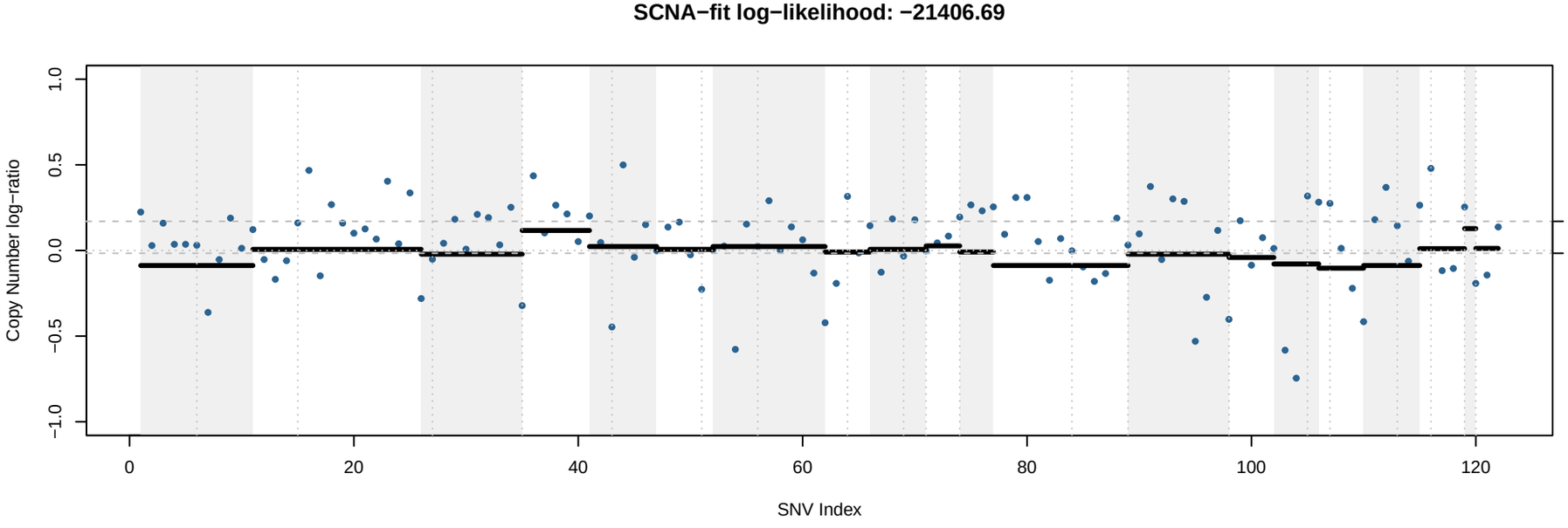

Coverage (log2)
Allelic fraction

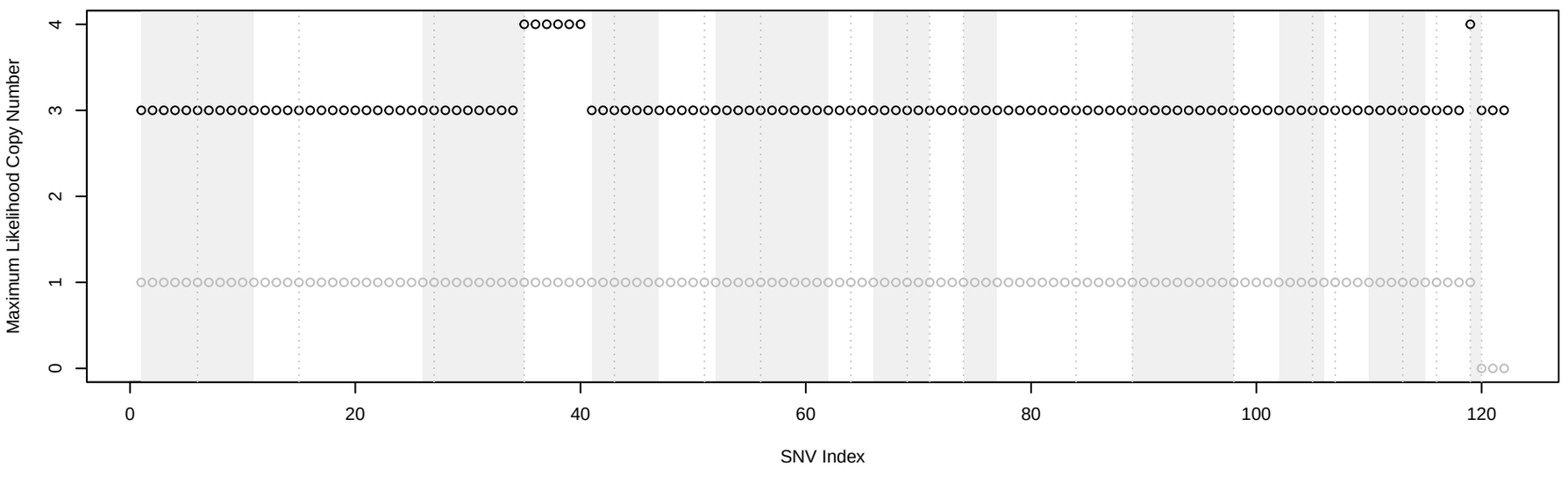

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m2
3m1
4m1
5m1

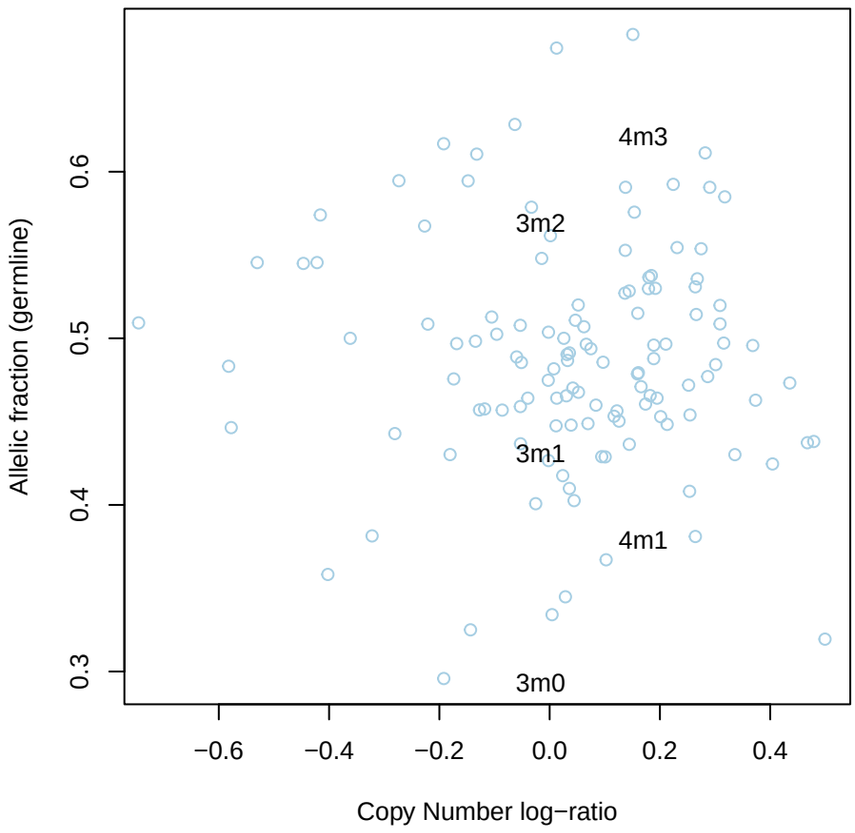

Frequency
Cellular fraction

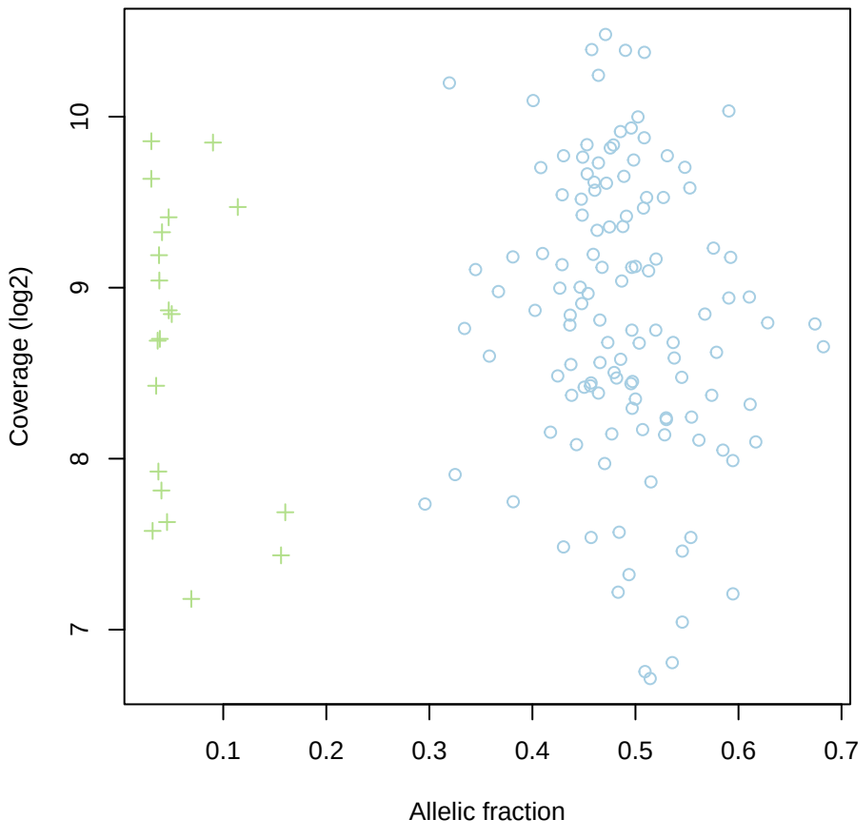

Purity: 0.32 Tumor ploidy: 3.082
3
Fraction Genome
0.00
0.05
0.10
0.15
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

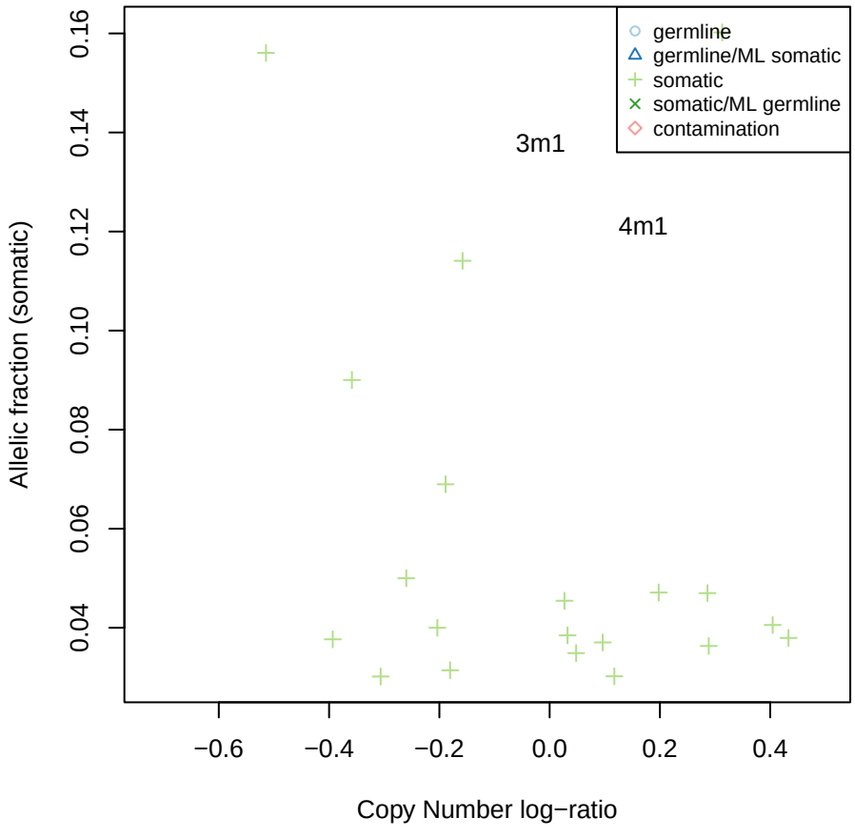

Purity: 0.32 Tumor ploidy: 3.082 SNV log−likelihood: −105.72 GoF: 92.9% Mean coverage: 158;523
1
2
3
4
5
6
7
8
9
10
12
13
15
16
17
19
20
B−Allele Frequency
0.3
0.4
0.5
0.6
0
20
40
60
80
100
120
SNV Index

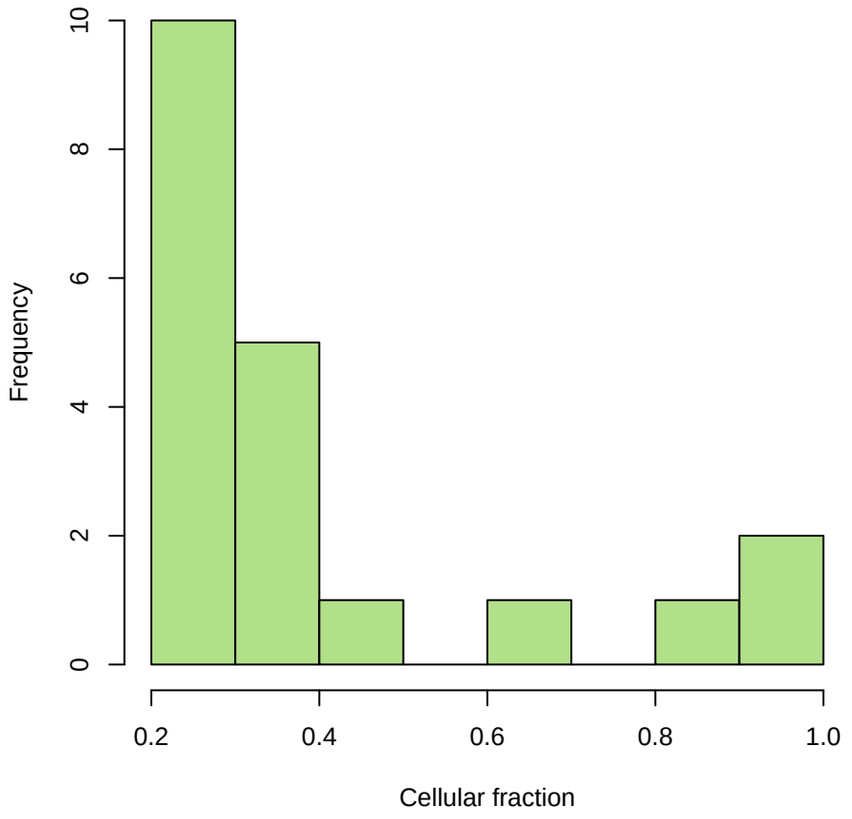

SCNA−fit log−likelihood: −21406.69
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
3
4
0
20
40
60
80
100
120
SNV Index

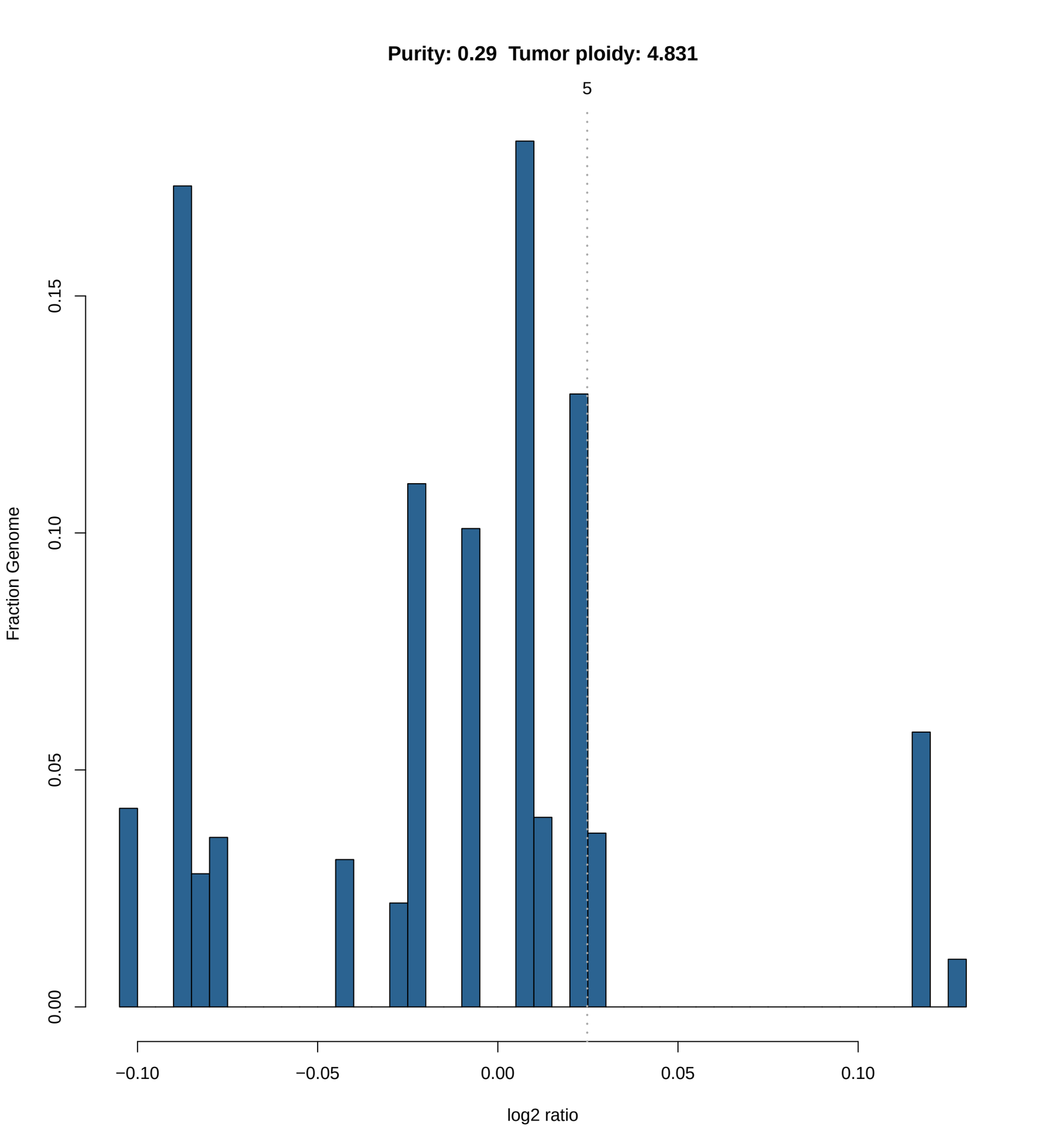

Maximum Likelihood Copy Number
0
1
2
3
4
0
20
40
60
80
100
120
SNV Index

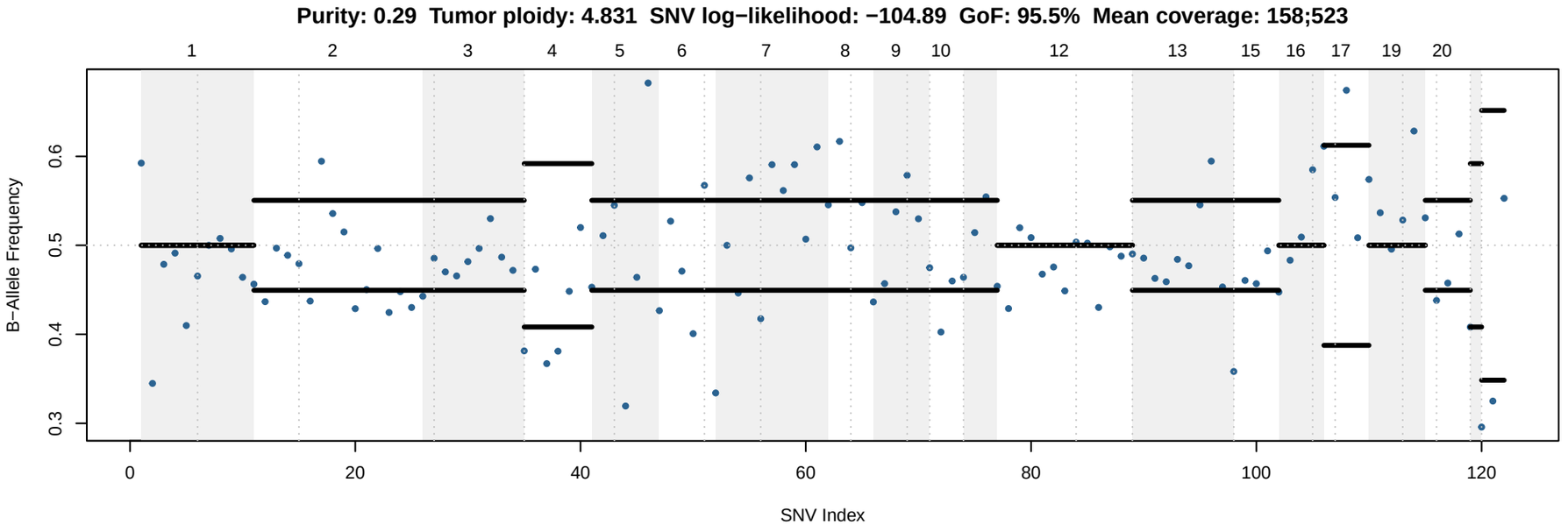

Allelic fraction (germline)
0.3
0.4
0.5
0.6
4m3
3m2
3m1
4m1
3m0
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

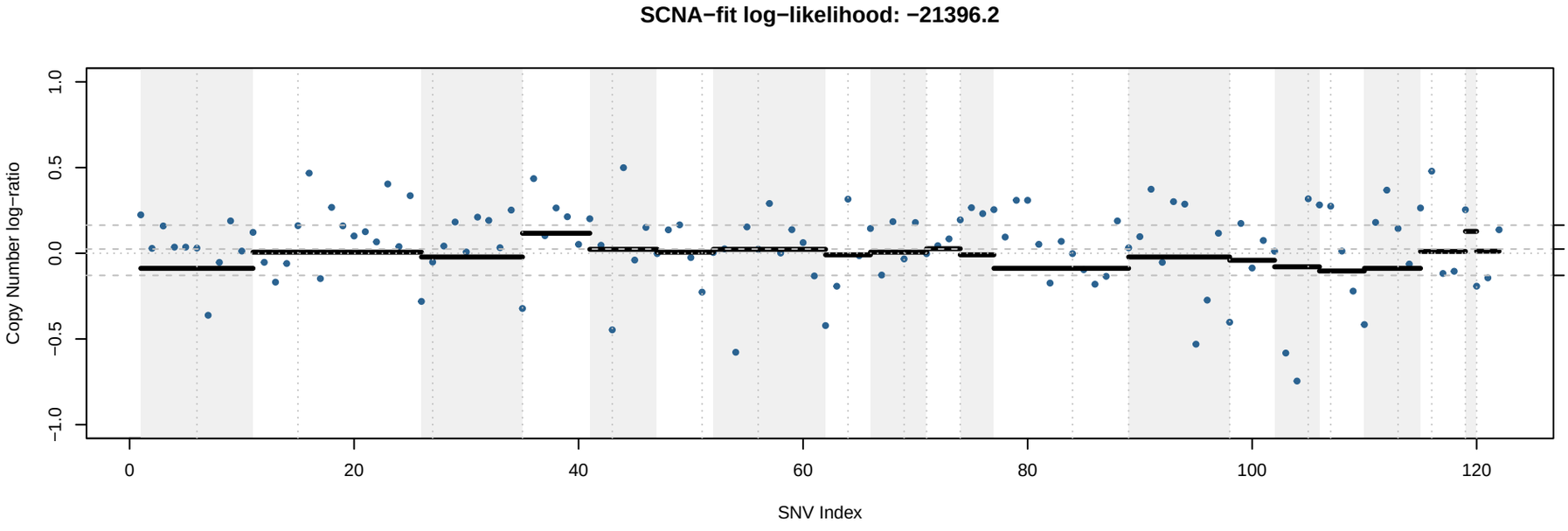

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

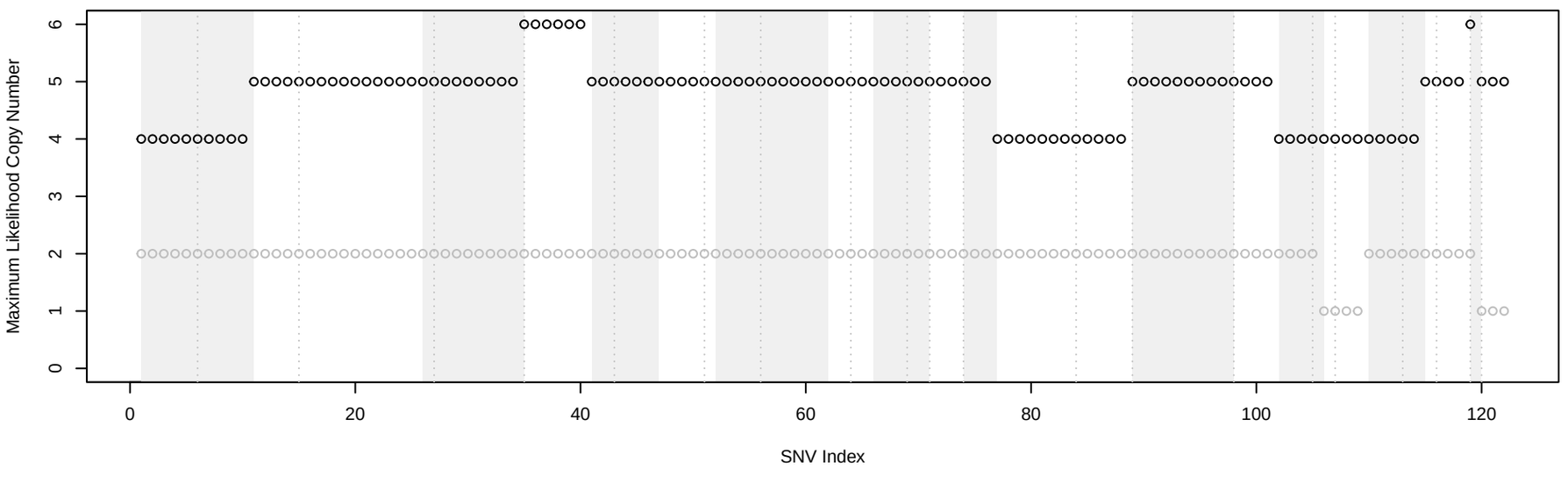

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
4m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

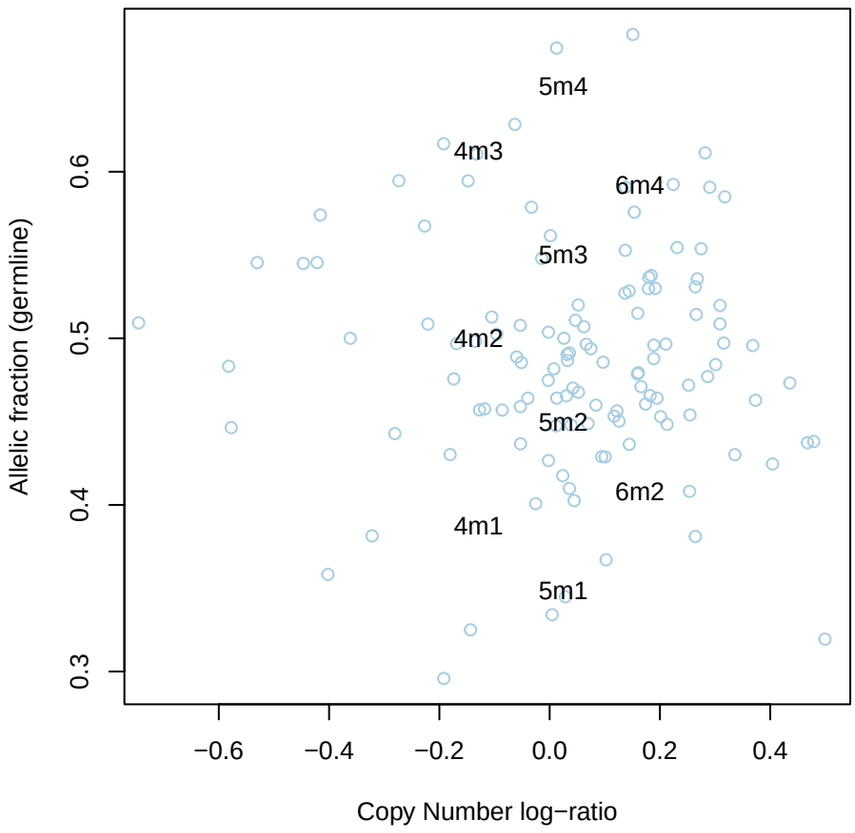

Frequency
0
2
4
6
8
10
0.2
0.4
0.6
0.8
1.0
Cellular fraction

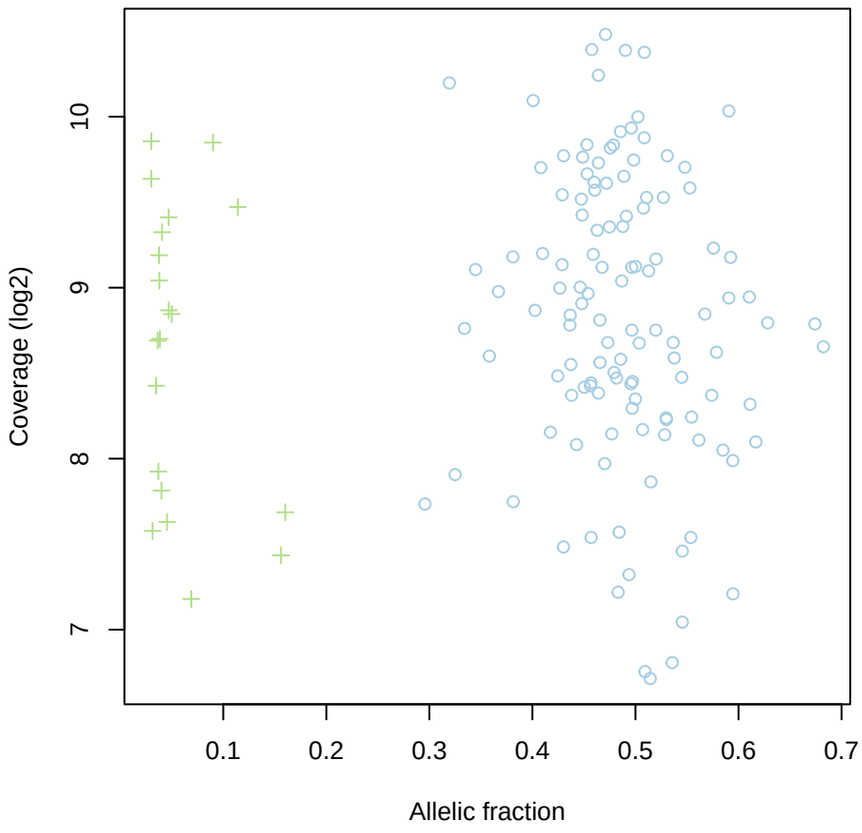

Purity: 0.29 Tumor ploidy: 4.831
5
0.15
0.10
0.05
0.00
Fraction Genome
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

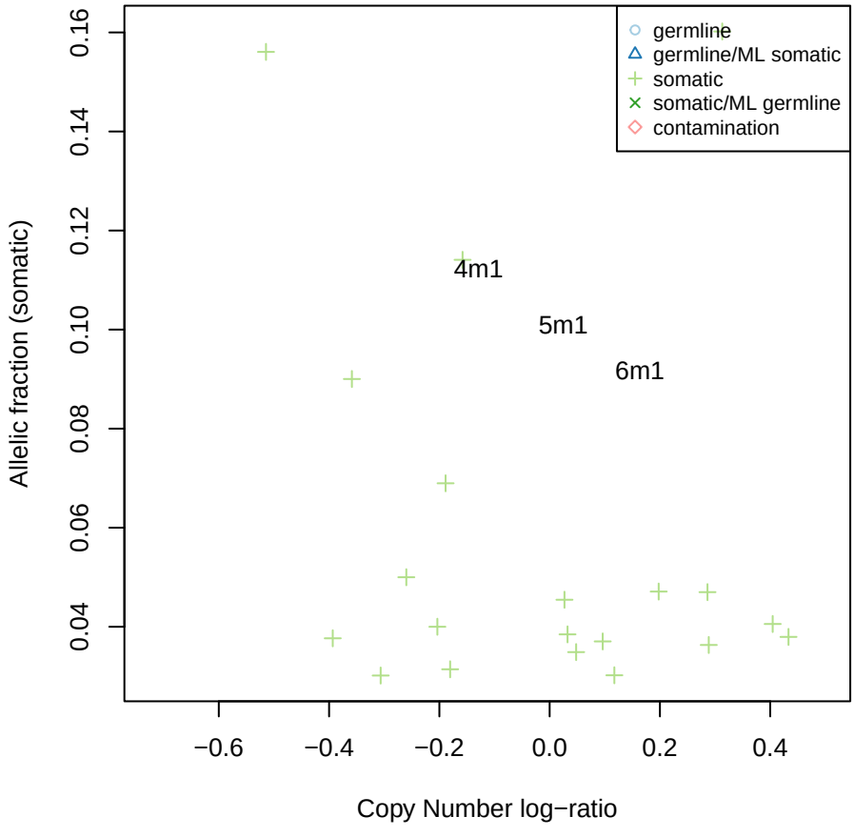

Purity: 0.29 Tumor ploidy: 4.831 SNV log−likelihood: −104.89 GoF: 95.5% Mean coverage: 158;523
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6
0 20 40 60 80 100 120
SNV Index

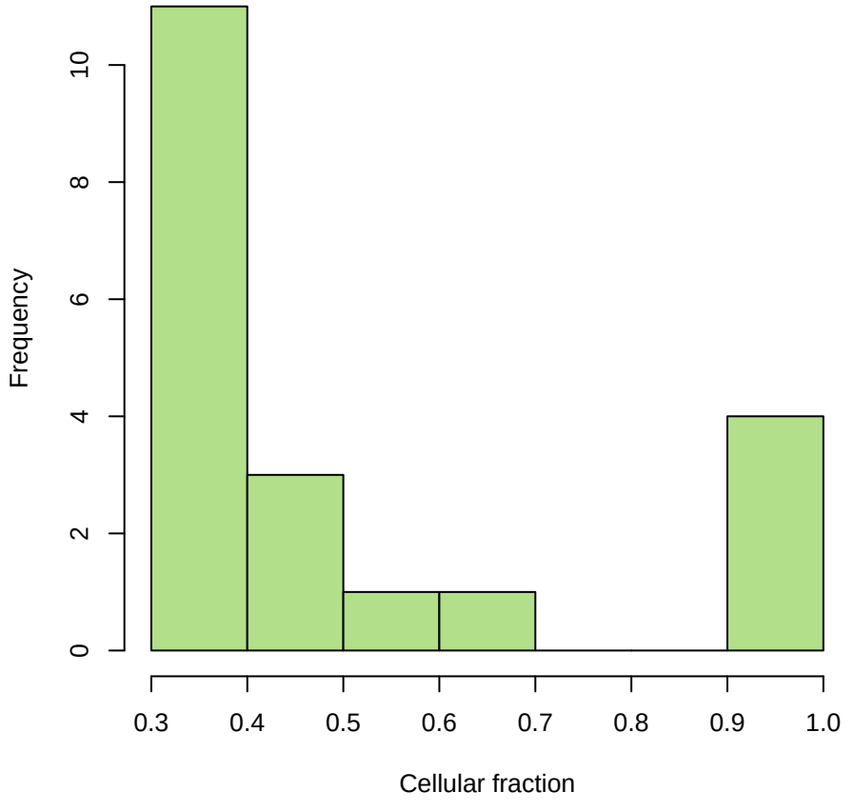

SCNA−fit log−likelihood: −21396.2
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
4 5
0 20 40 60 80 100 120
SNV Index

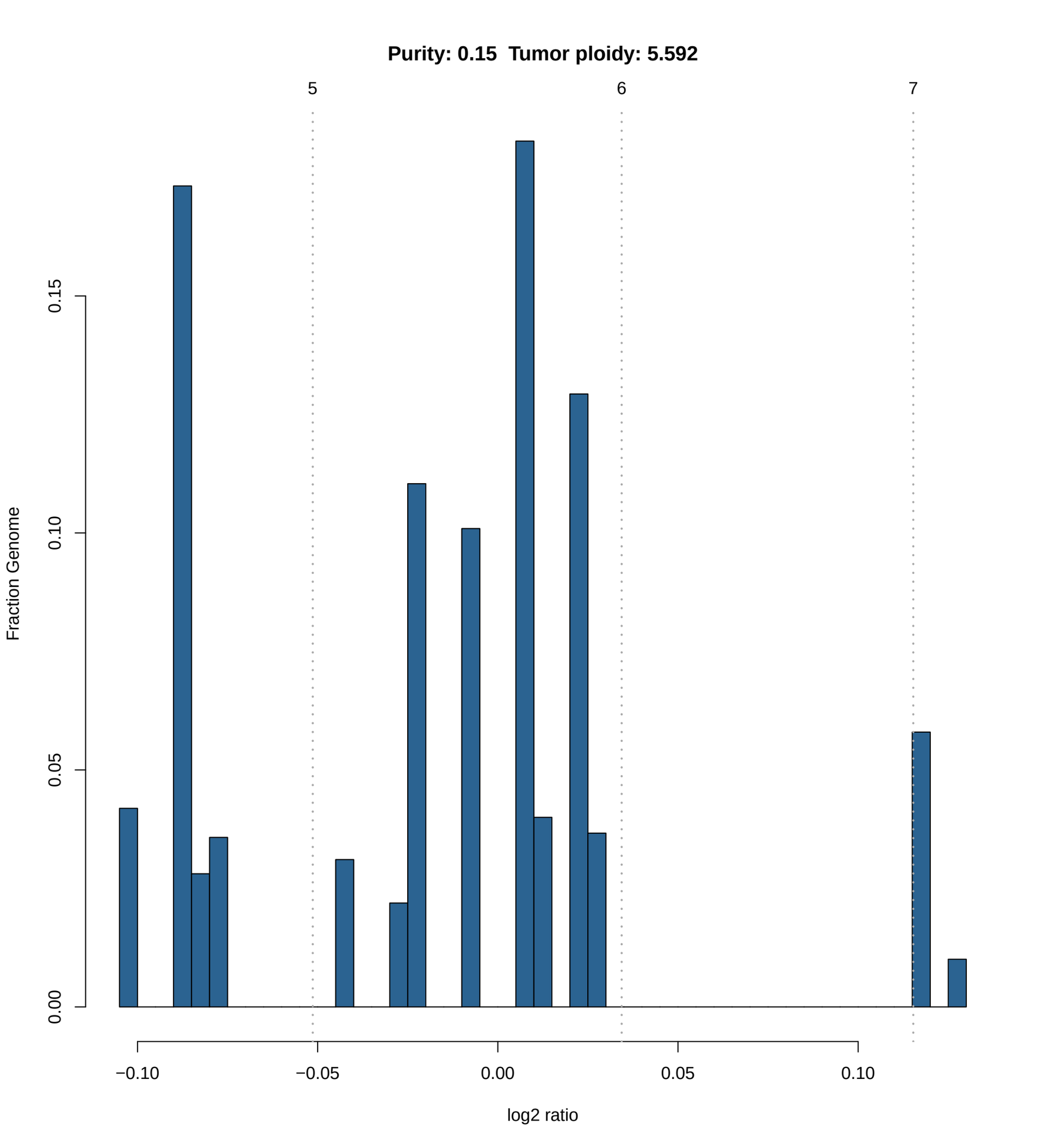

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120
SNV Index

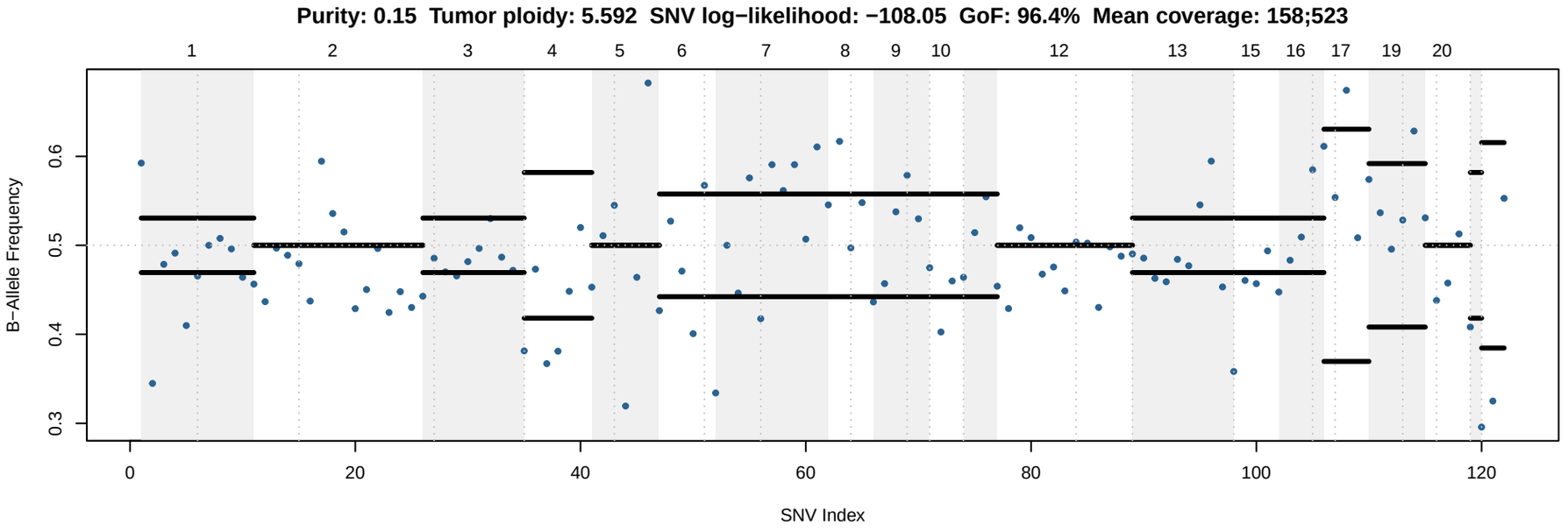

5m4
4m3
6m4
5m3
4m2
5m2
6m2
4m1
5m1
Allelic fraction (germline)
Copy Number log−ratio

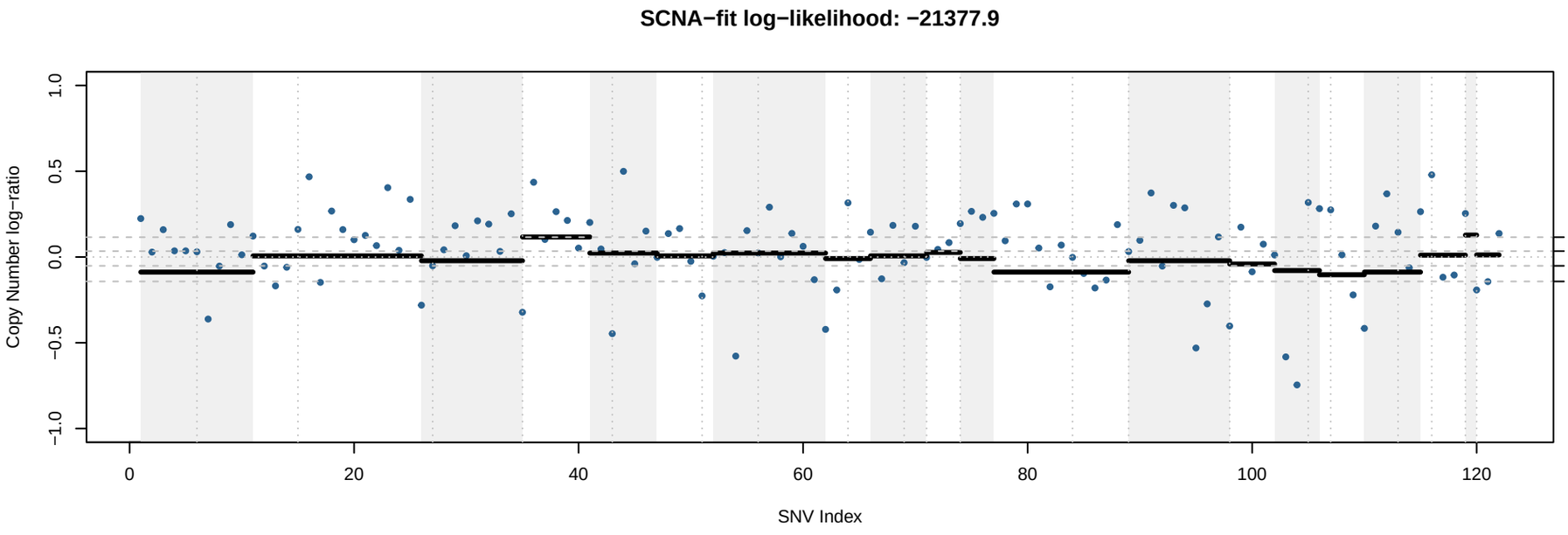

Coverage (log2)
Allelic fraction

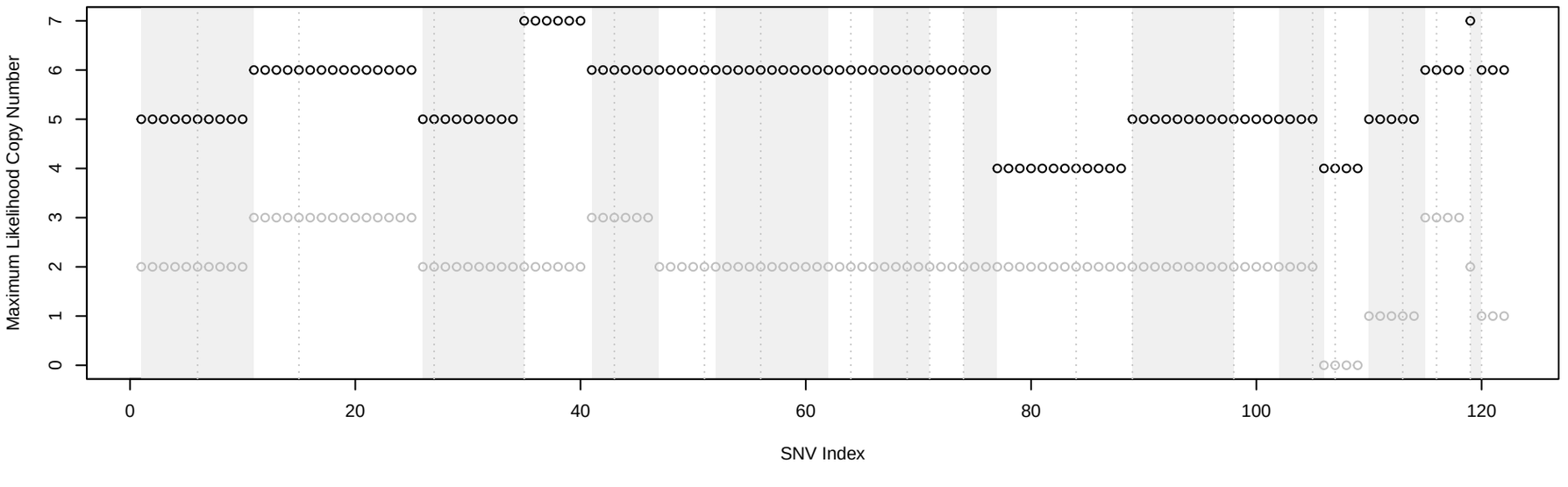

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio

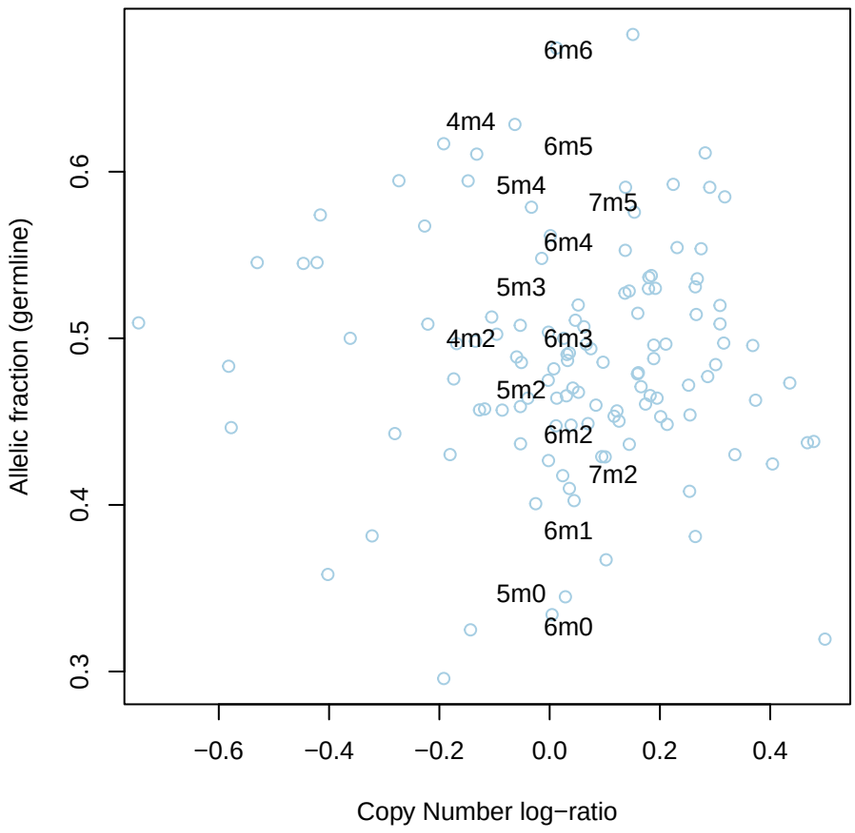

Frequency
Cellular fraction

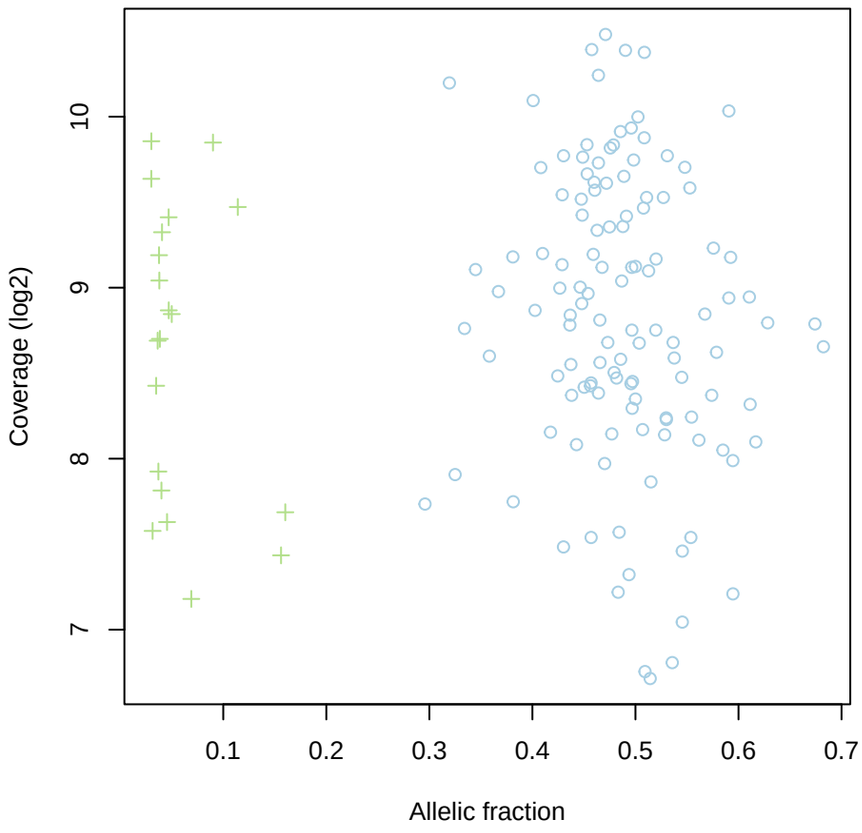

Purity: 0.15 Tumor ploidy: 5.592
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

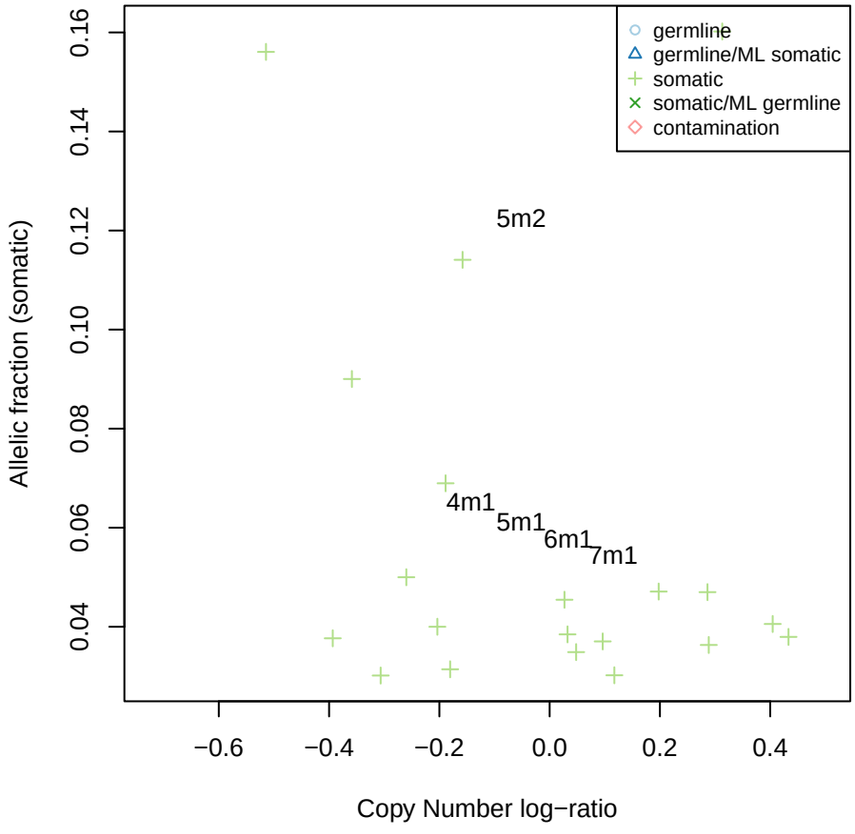

Purity: 0.15 Tumor ploidy: 5.592 SNV log−likelihood: −108.05 GoF: 96.4% Mean coverage: 158;523
1
2
3
4
5
6
7
8
9
10
12
13
15
16
17
19
20
B−Allele Frequency
0.3
0.4
0.5
0.6
0
20
40
60
80
100
120
SNV Index

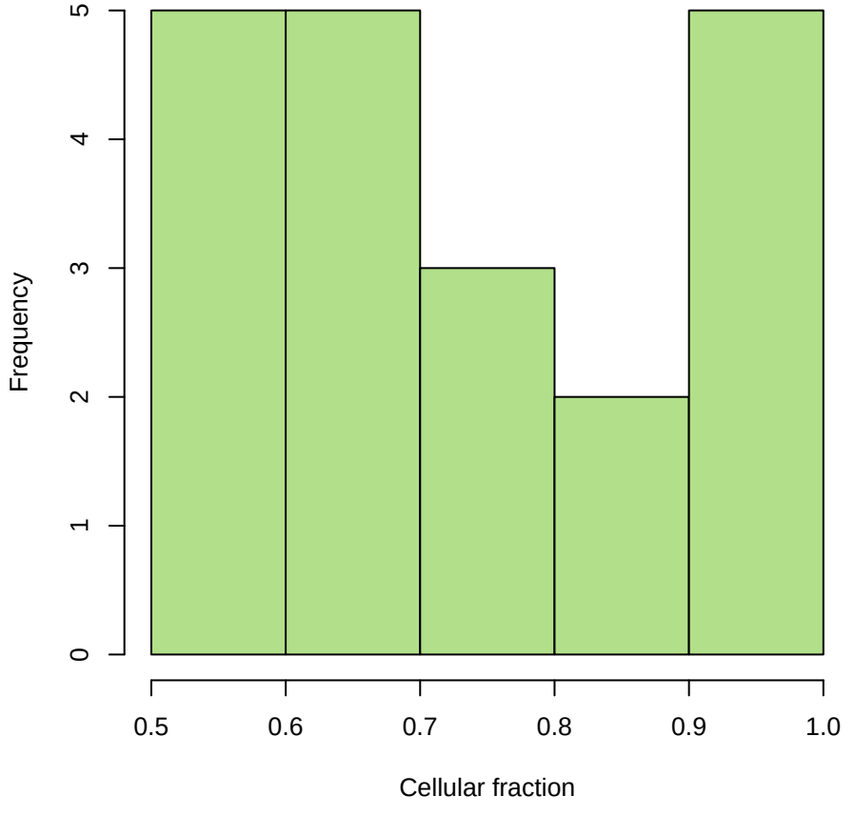

SCNA−fit log−likelihood: −21377.9
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
4
6
0
20
40
60
80
100
120
SNV Index

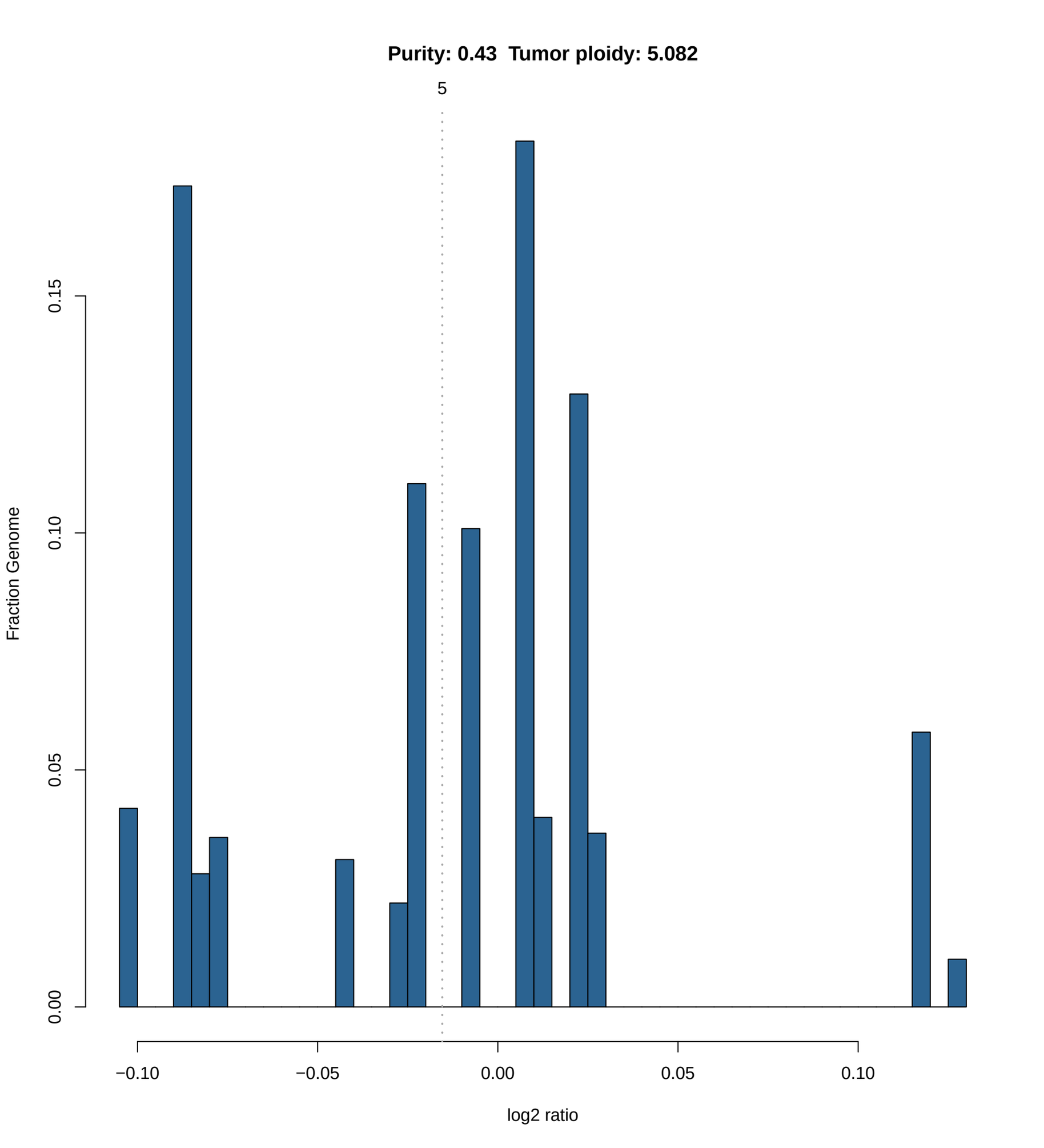

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
7
0
20
40
60
80
100
120
SNV Index

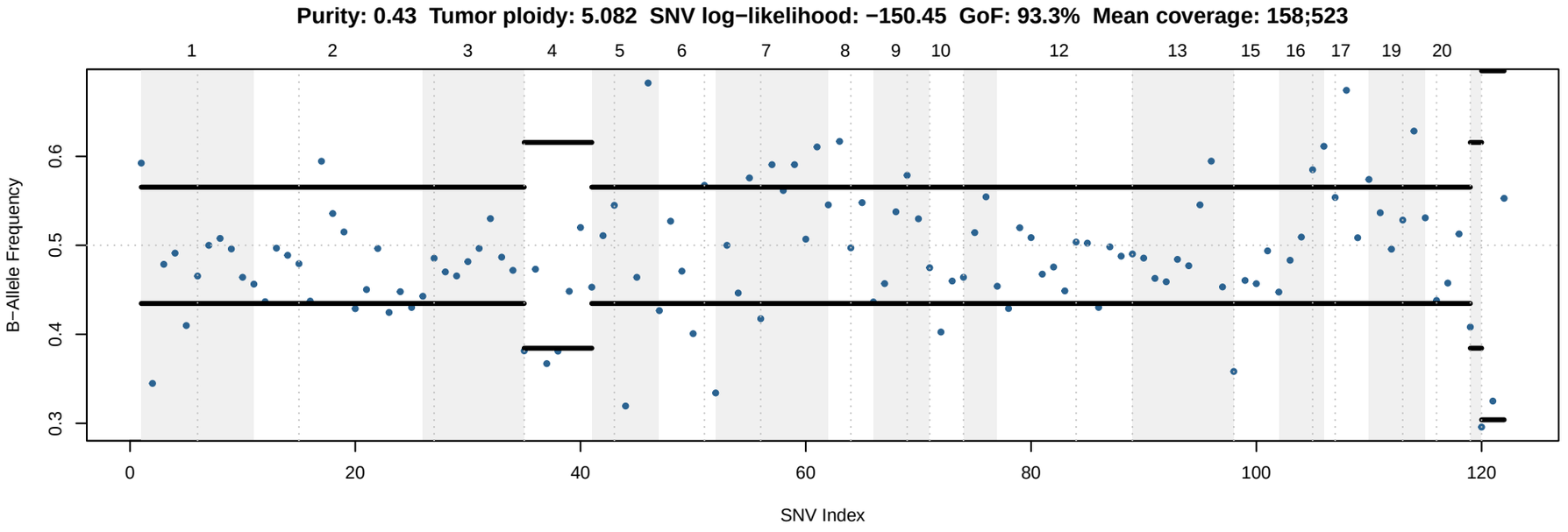

6m6
4m4
6m5
5m4
7m5
6m4
5m3
4m2
6m3
5m2
6m2
7m2
6m1
5m0
6m0
Allelic fraction (germline)
Copy Number log−ratio

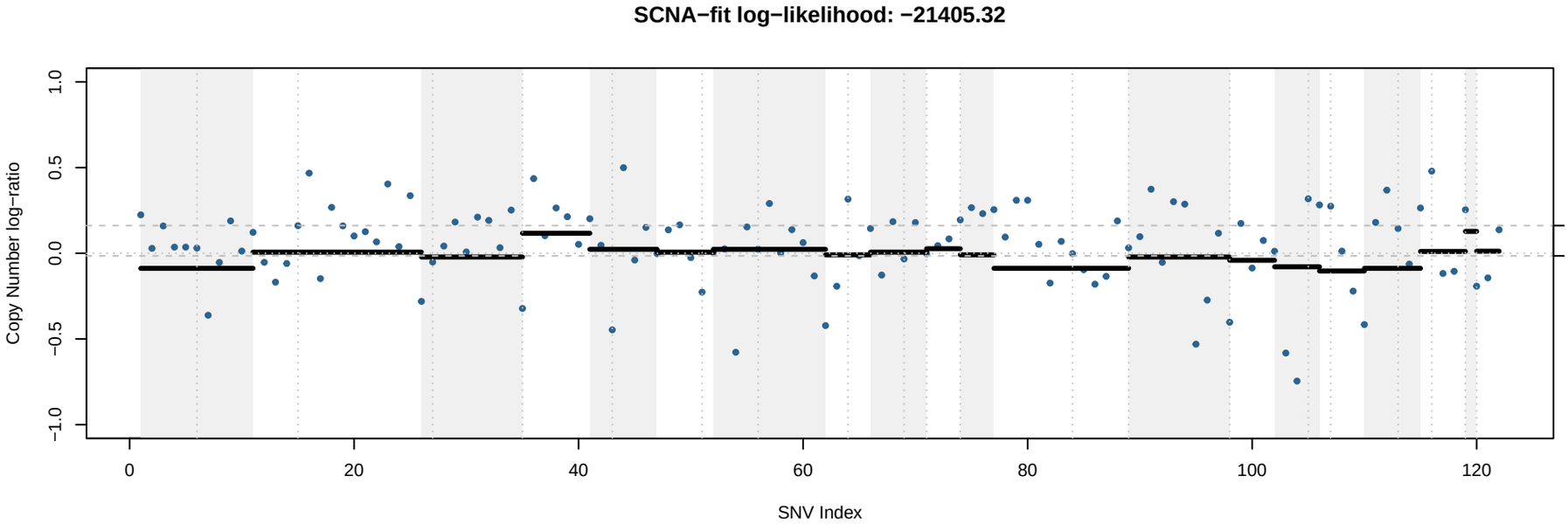

Coverage (log2)
Allelic fraction

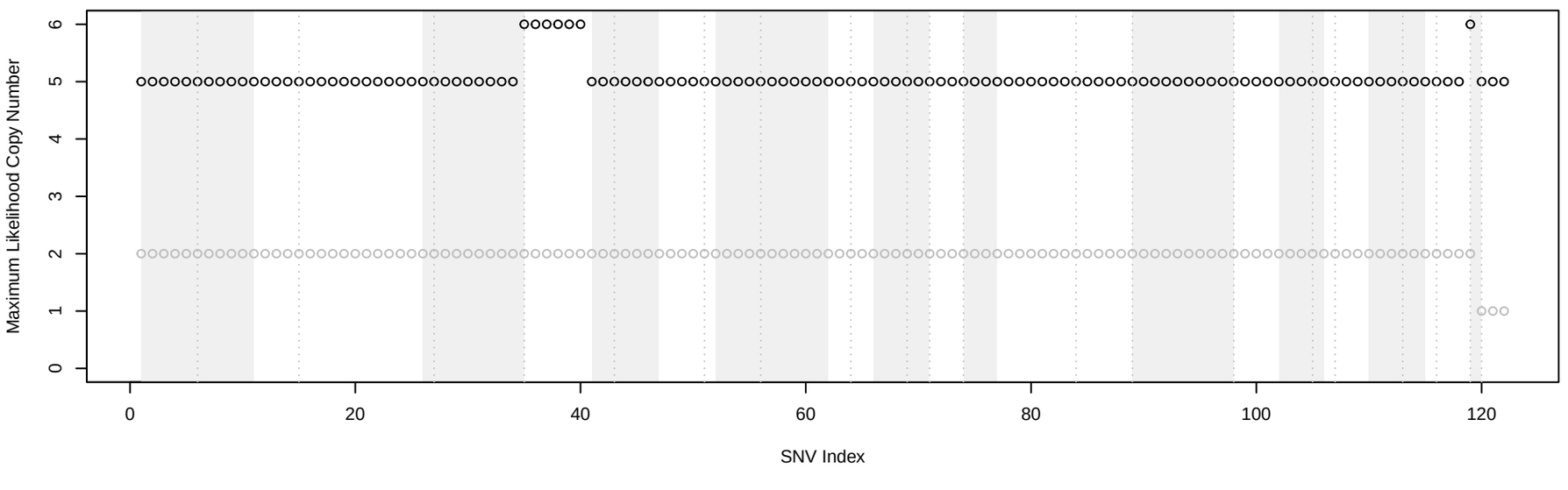

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m2
4m1
5m1
6m1
7m1
Allelic fraction (somatic)
Copy Number log−ratio

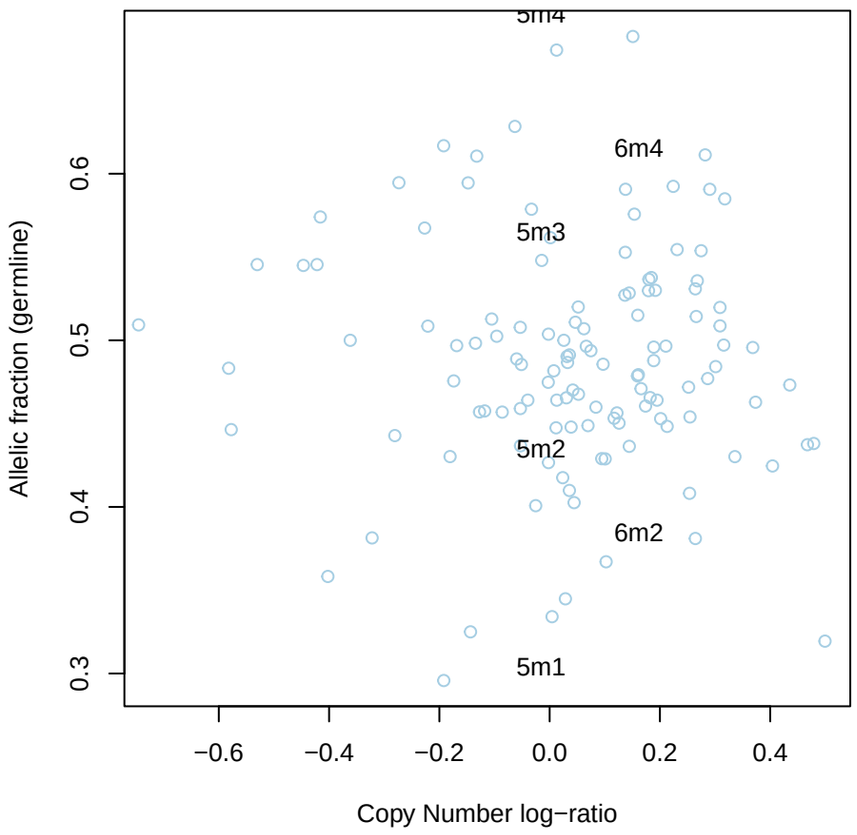

Frequency
Cellular fraction

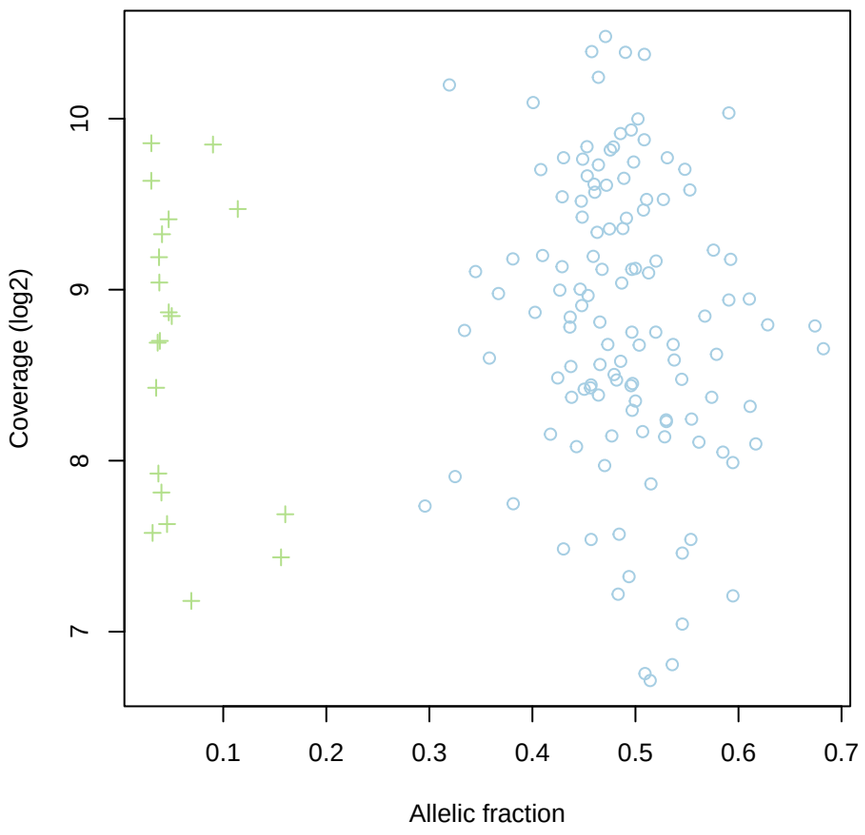

Purity: 0.43 Tumor ploidy: 5.082
5
Fraction Genome
0.00
0.05
0.10
0.15
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

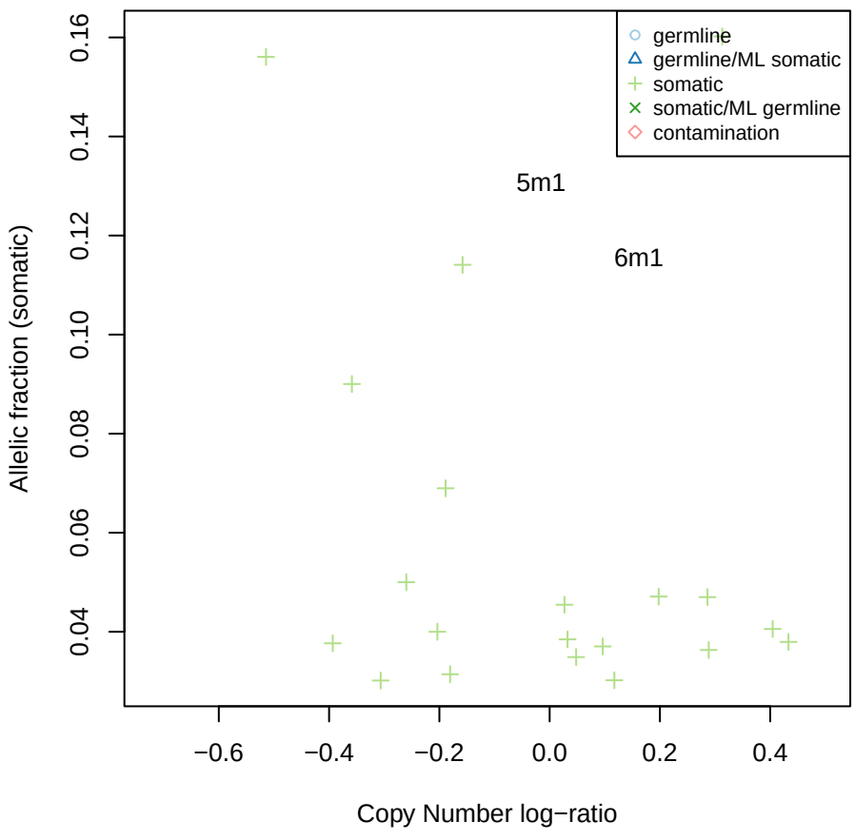

Purity: 0.43 Tumor ploidy: 5.082 SNV log−likelihood: −150.45 GoF: 93.3% Mean coverage: 158;523
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6
0 20 40 60 80 100 120
SNV Index

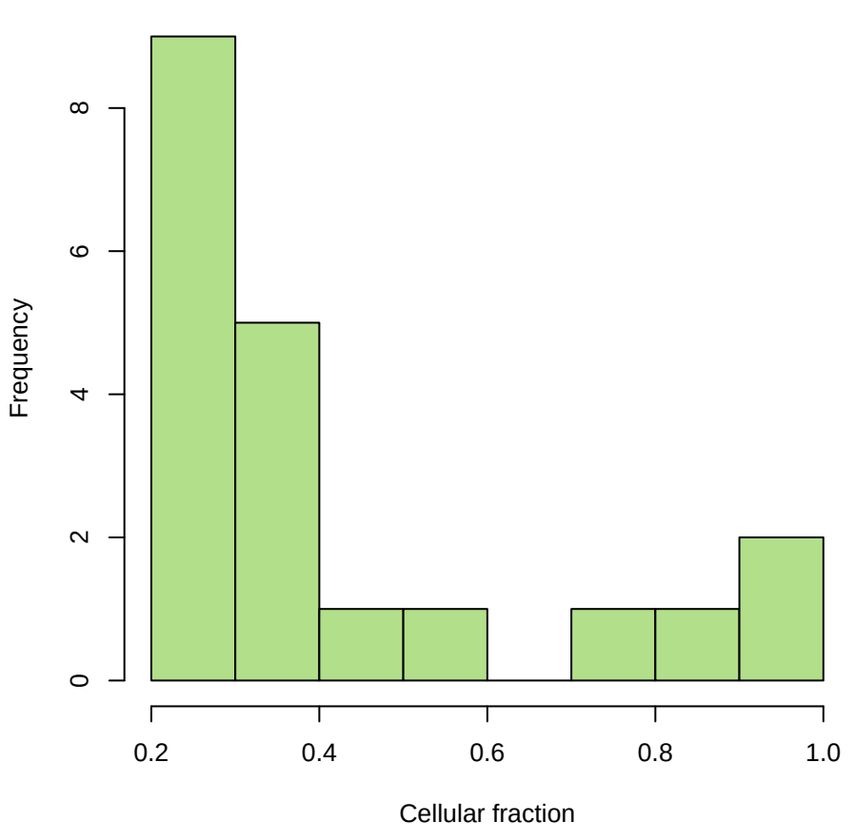

SCNA−fit log−likelihood: −21405.32
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
5 6
0 20 40 60 80 100 120
SNV Index

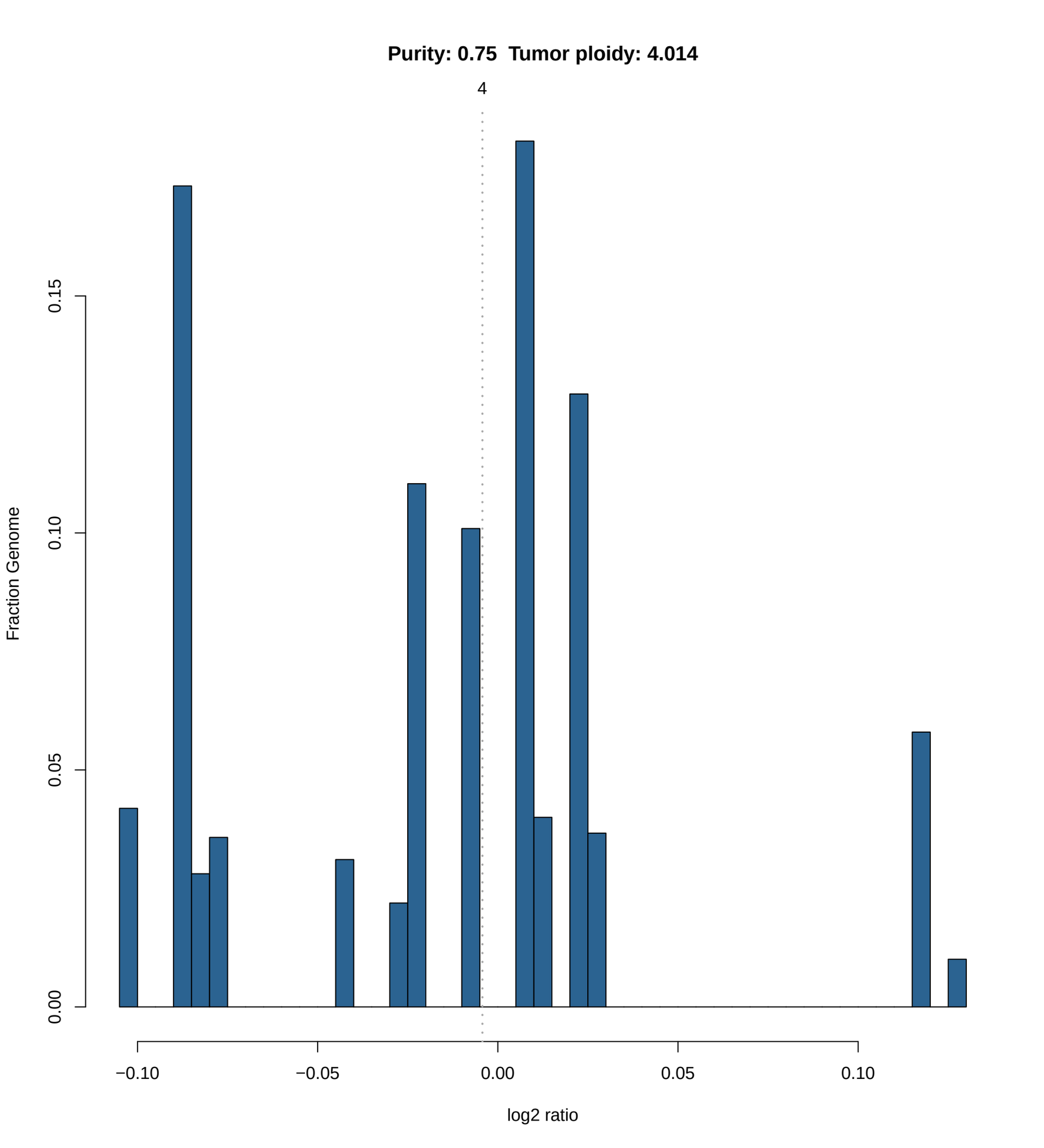

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120
SNV Index

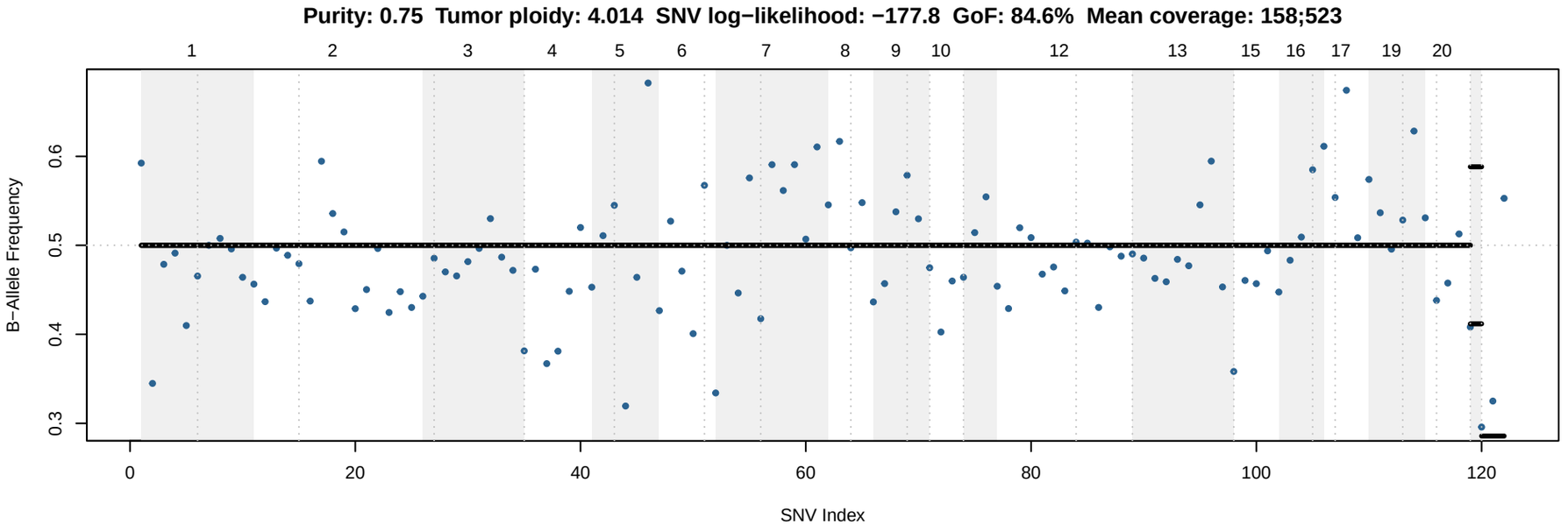

5m4
6m4
5m3
5m2
6m2
5m1
Allelic fraction (germline)
Copy Number log−ratio

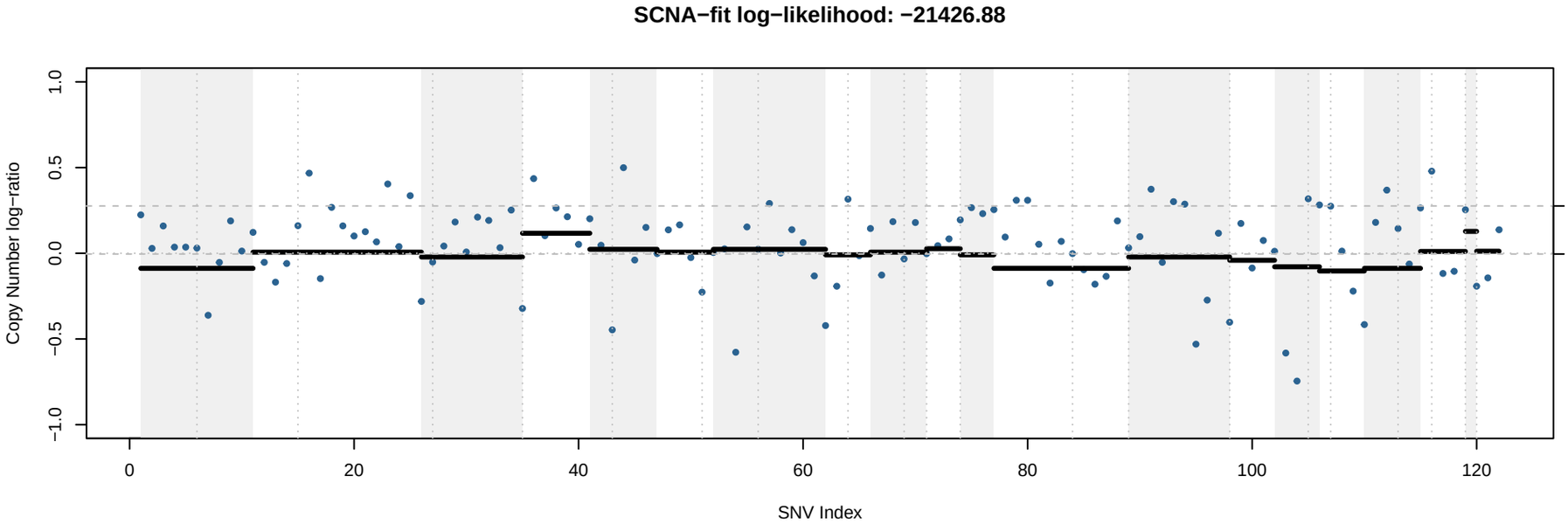

Coverage (log2)
Allelic fraction

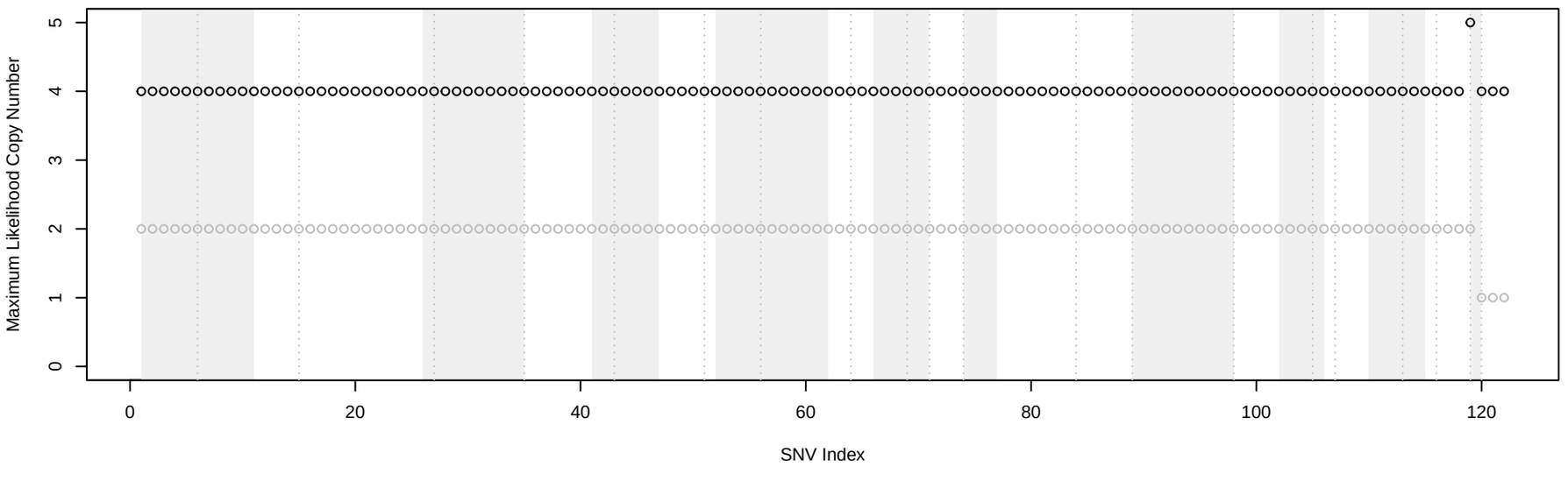

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio

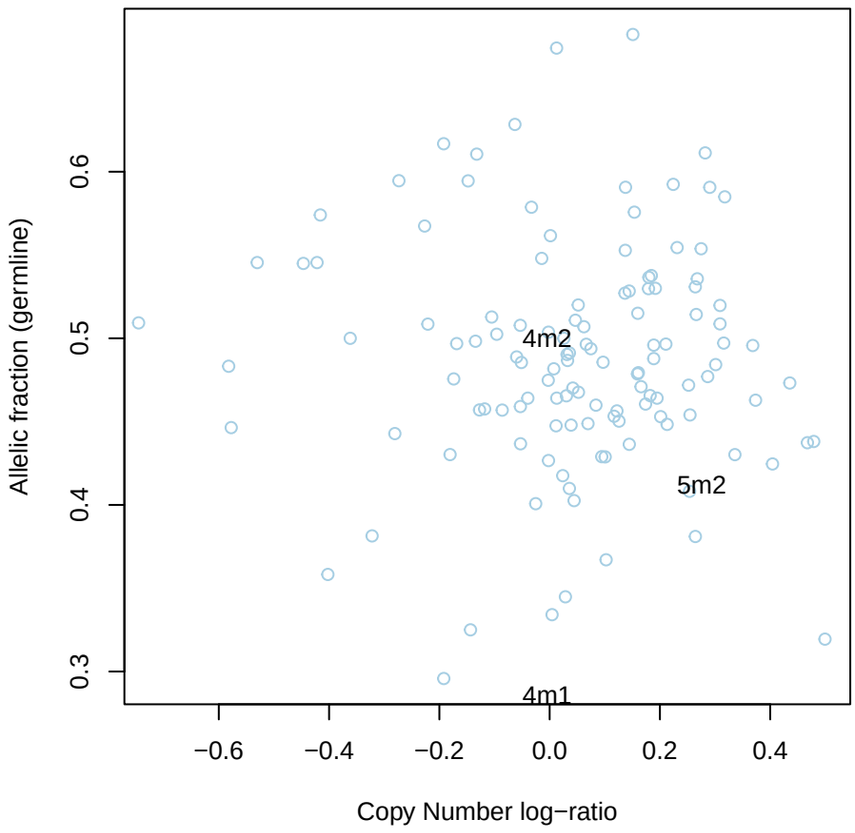

Frequency
Cellular fraction

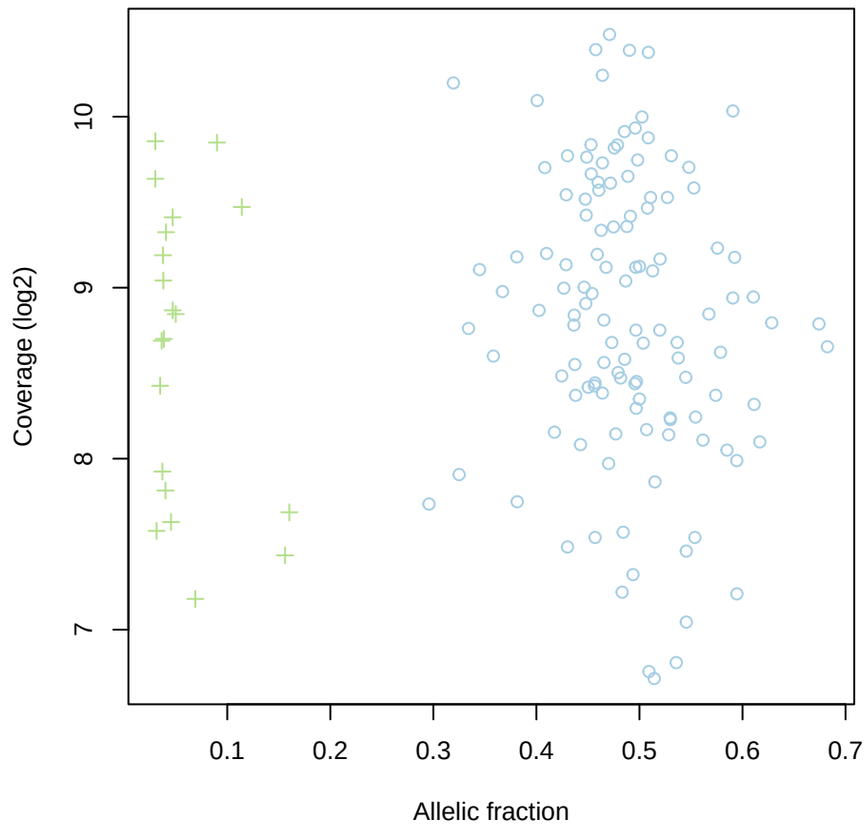

Purity: 0.75 Tumor ploidy: 4.014
4
Fraction Genome
0.00
0.05
0.10
0.15
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

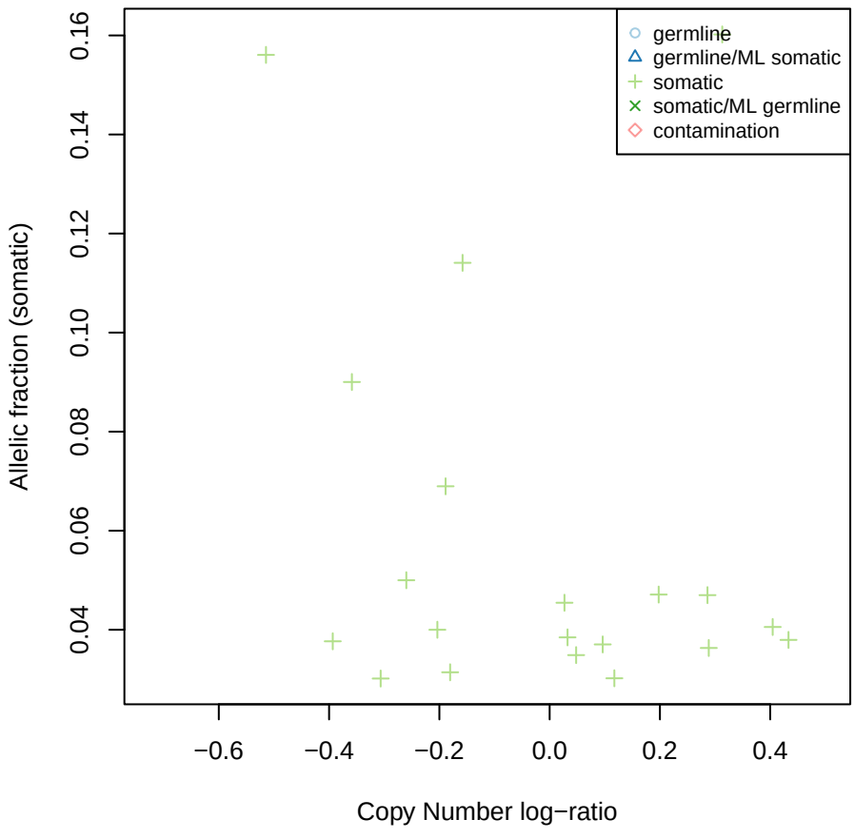

Purity: 0.75 Tumor ploidy: 4.014 SNV log−likelihood: −177.8 GoF: 84.6% Mean coverage: 158;523
1
2
3
4
5
6
7
8
9
10
12
13
15
16
17
19
20
B−Allele Frequency
0.3
0.4
0.5
0.6
0
20
40
60
80
100
120
SNV Index

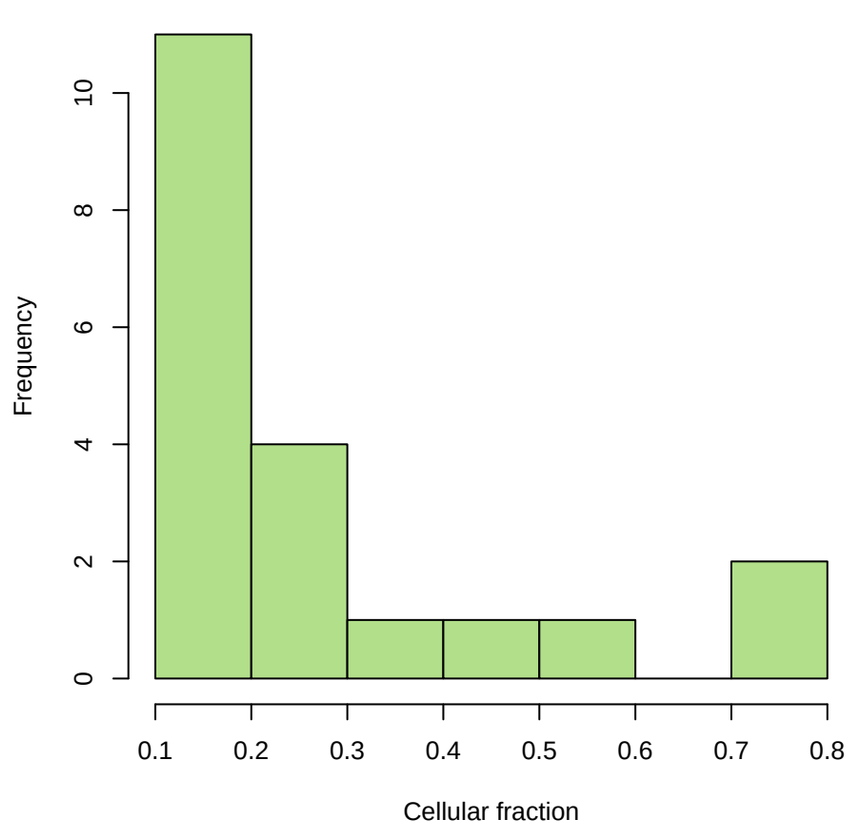

SCNA−fit log−likelihood: −21426.88
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
4
5
0
20
40
60
80
100
120
SNV Index

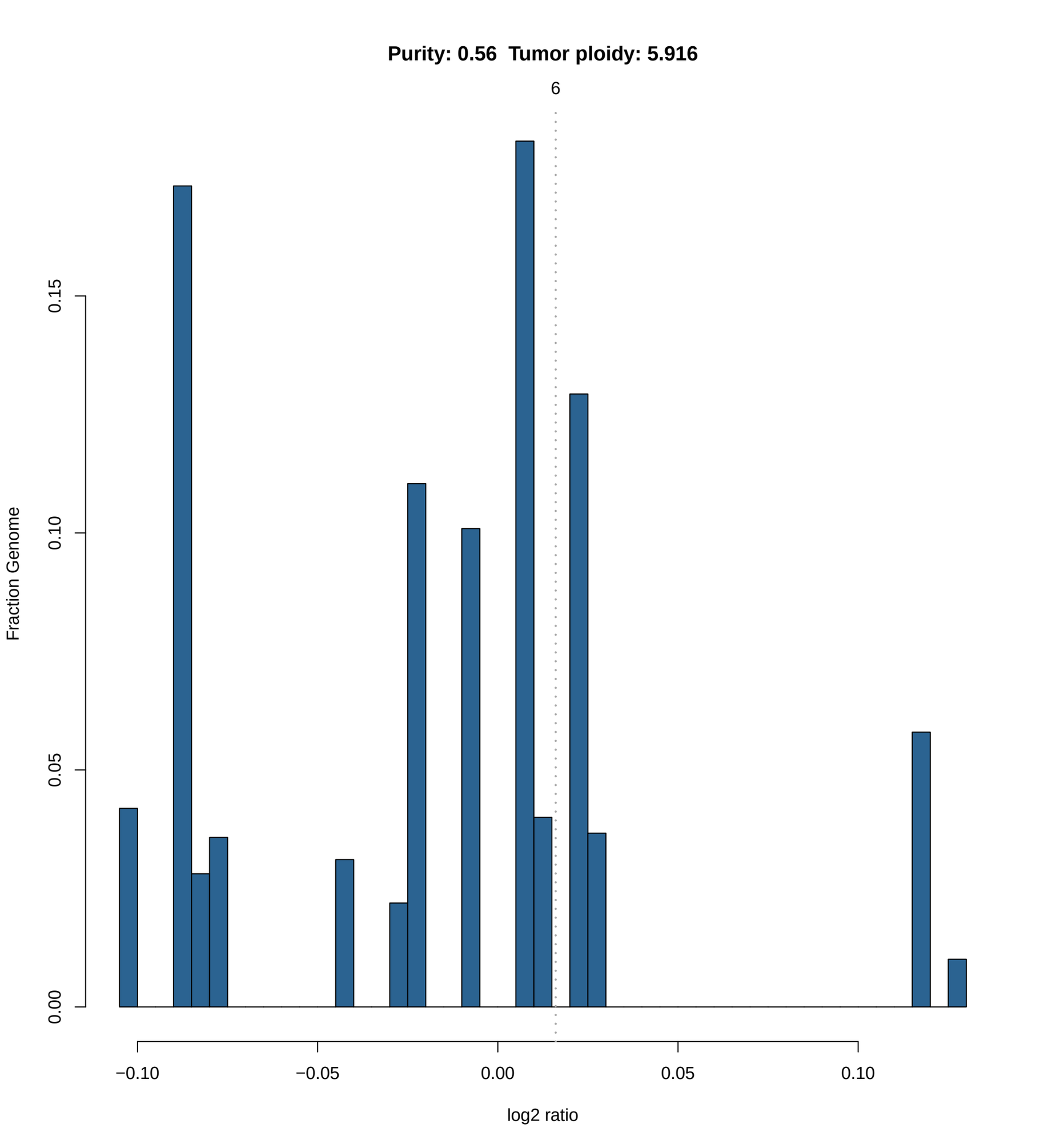

Maximum Likelihood Copy Number
0
1
2
3
4
5
0
20
40
60
80
100
120
SNV Index

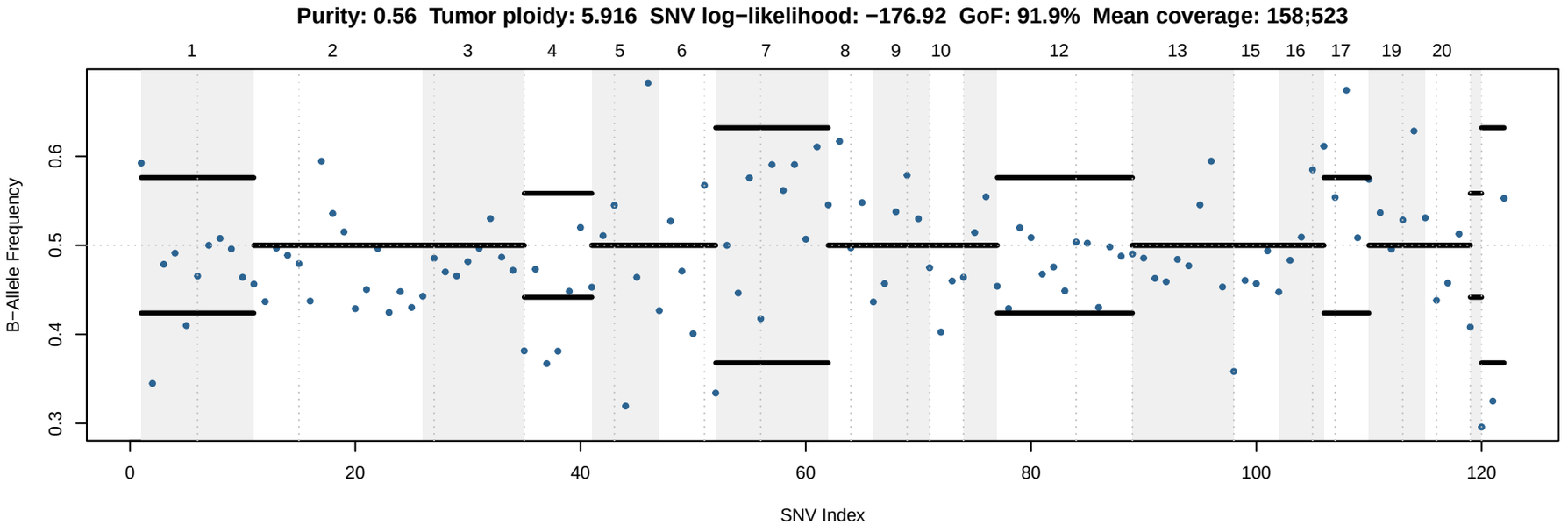

Allelic fraction (germline)
0.3
0.4
0.5
0.6
4m2
5m2
4m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

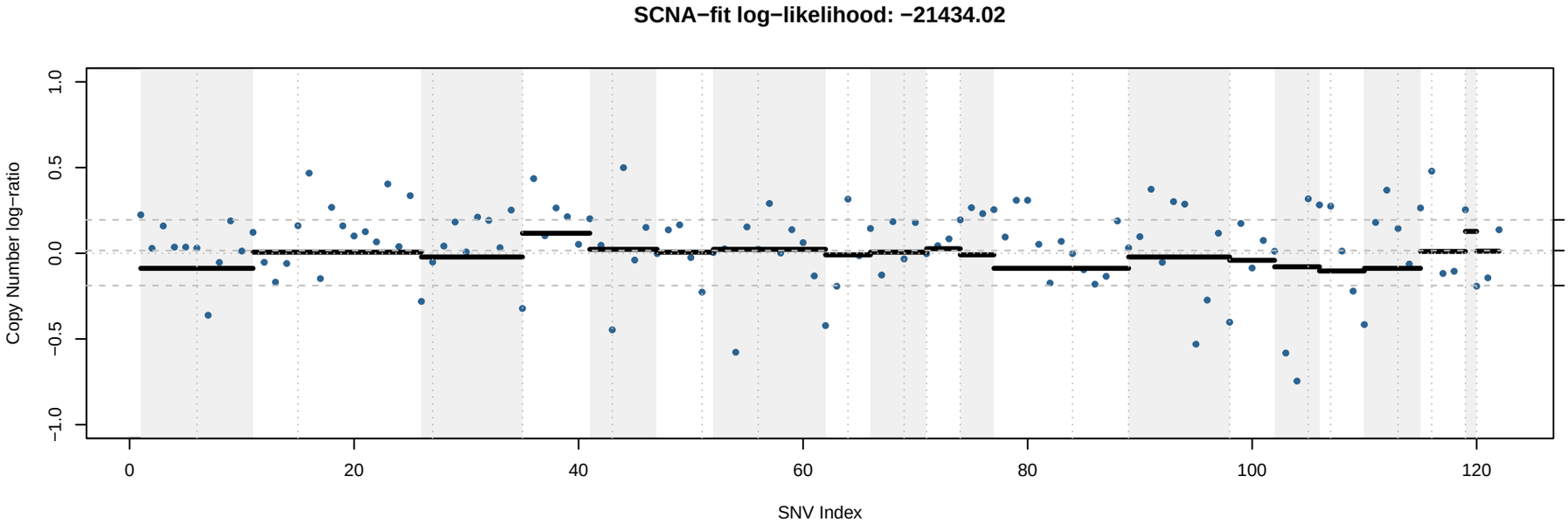

Coverage (log2)
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

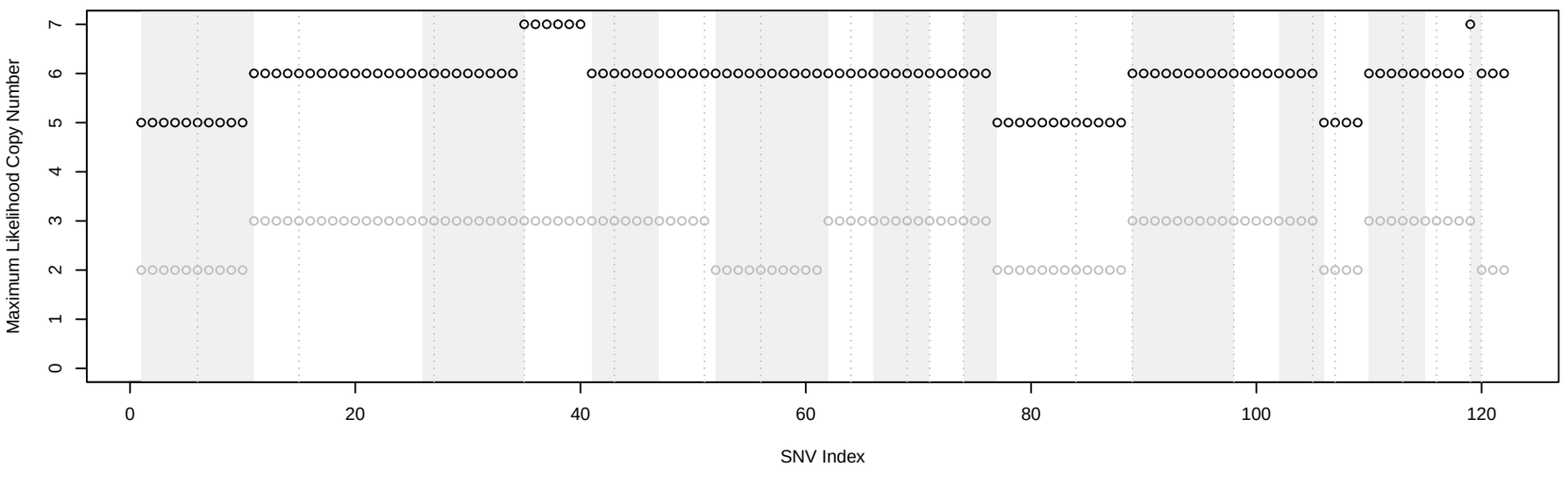

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
−0.6
−0.4
−0.2
0.0
0.2
0.4
Copy Number log−ratio

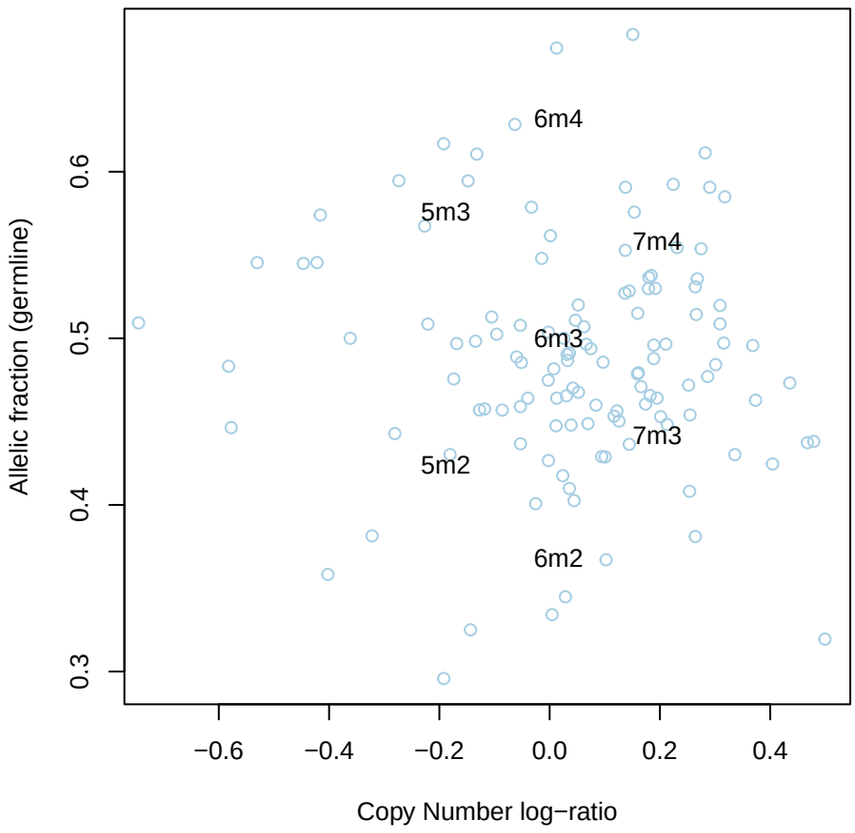

Frequency
0
2
4
6
8
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
Cellular fraction

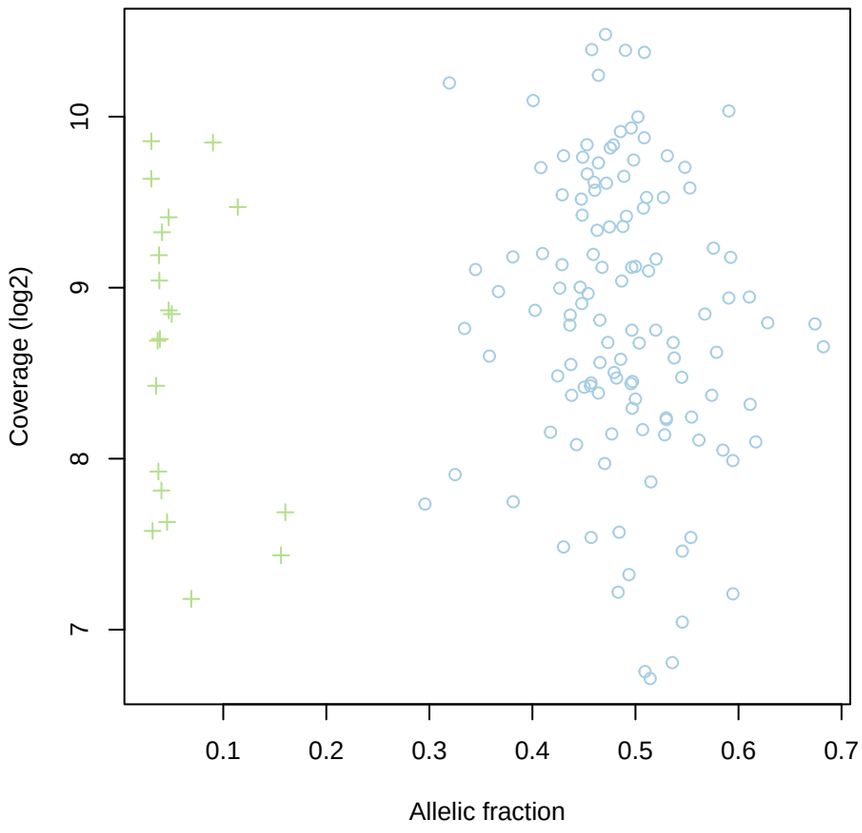

Purity: 0.56 Tumor ploidy: 5.916
6
Fraction Genome
0.00
0.05
0.10
0.15
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

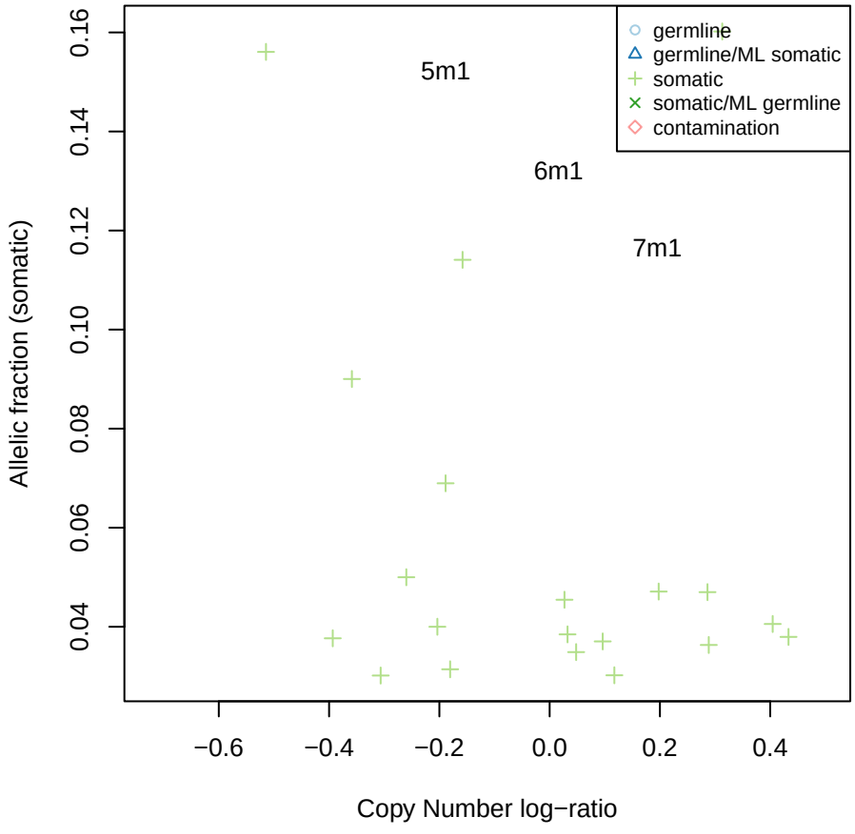

Purity: 0.56 Tumor ploidy: 5.916 SNV log−likelihood: −176.92 GoF: 91.9% Mean coverage: 158;523
1
2
3
4
5
6
7
8
9
10
12
13
15
16
17
19
20
B−Allele Frequency
0.3
0.4
0.5
0.6
0
20
40
60
80
100
120
SNV Index

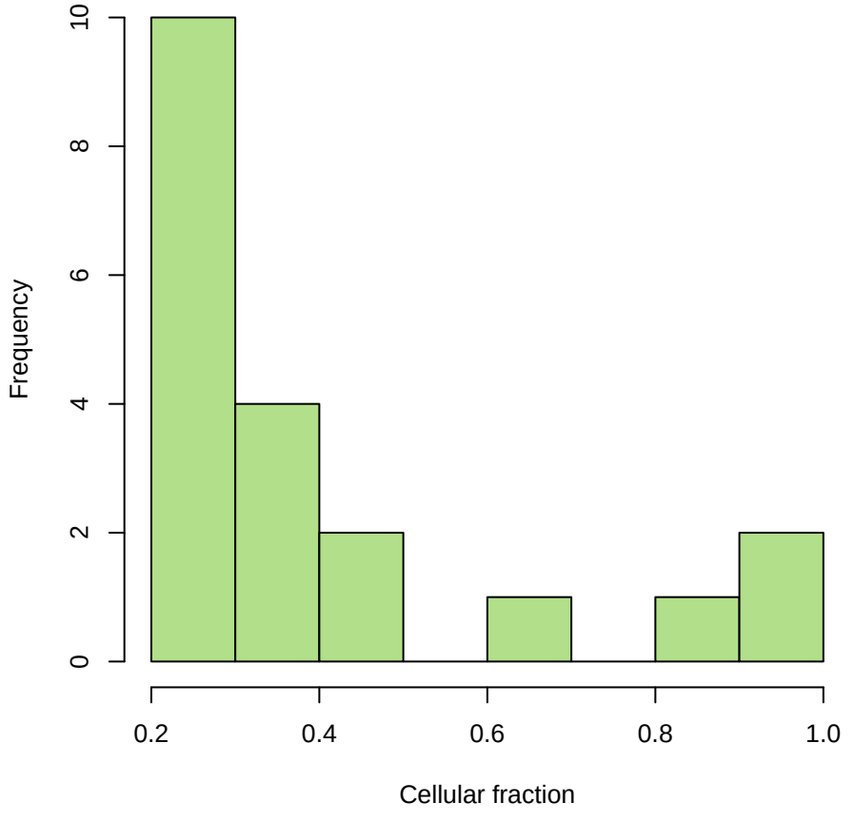

SCNA−fit log−likelihood: −21434.02
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
5
6
7
0
20
40
60
80
100
120
SNV Index

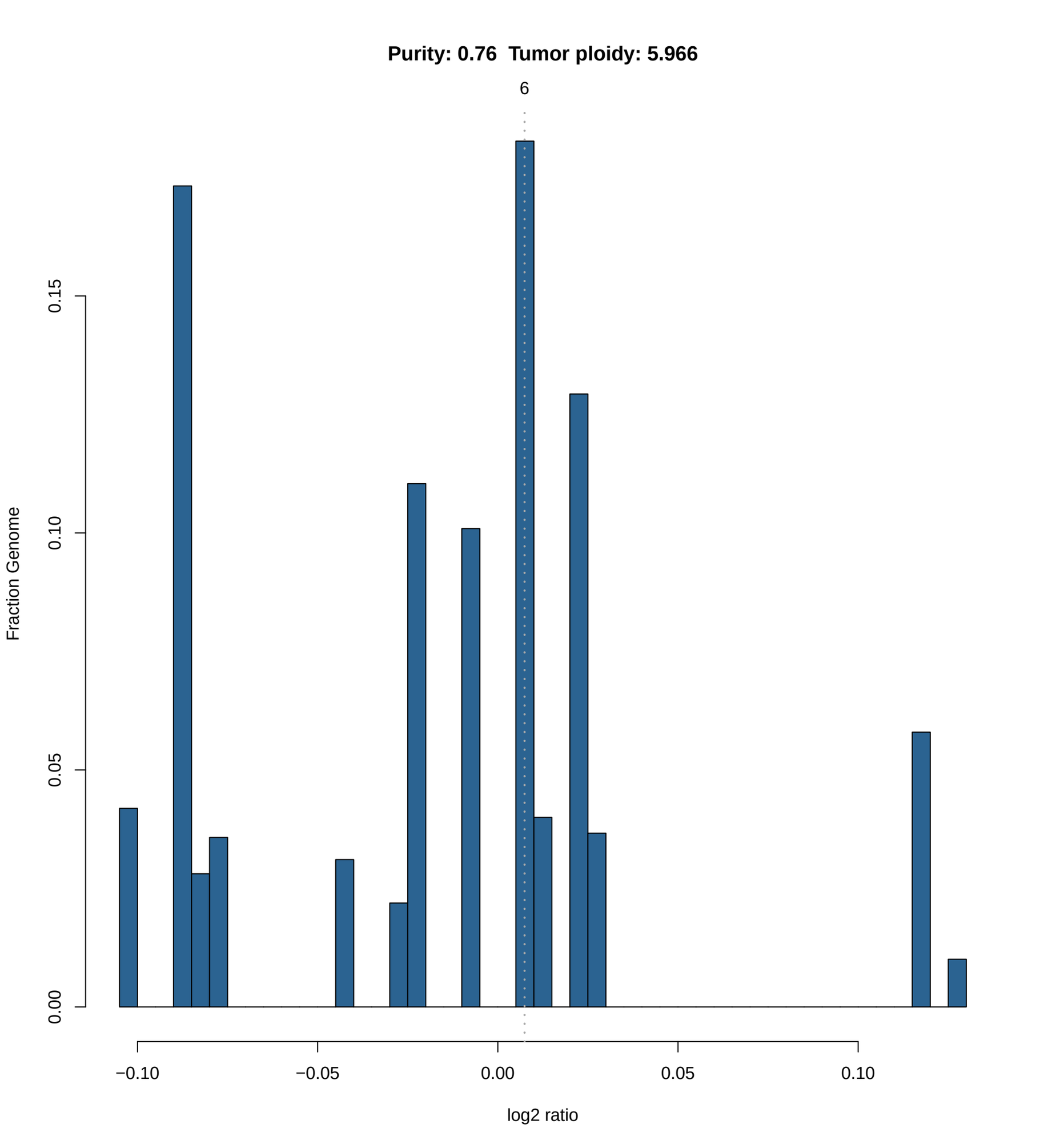

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
7
0
20
40
60
80
100
120
SNV Index

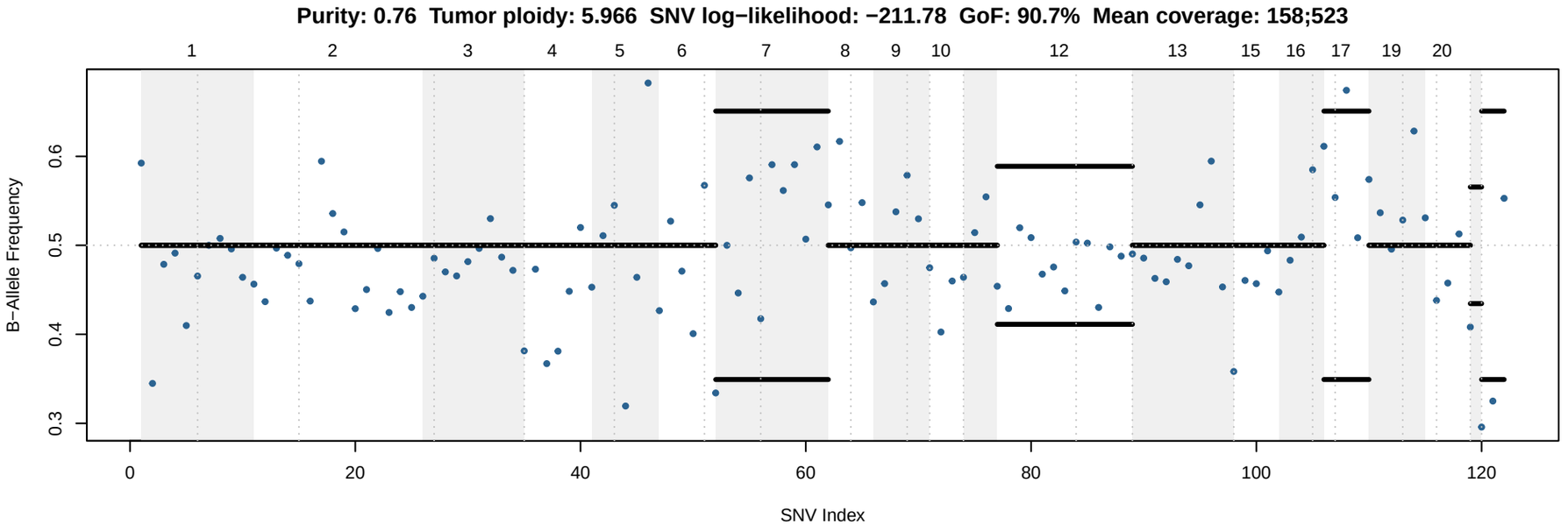

Allelic fraction (germline)
Copy Number log−ratio
6m4
5m3
7m4
6m3
7m3
5m2
6m2

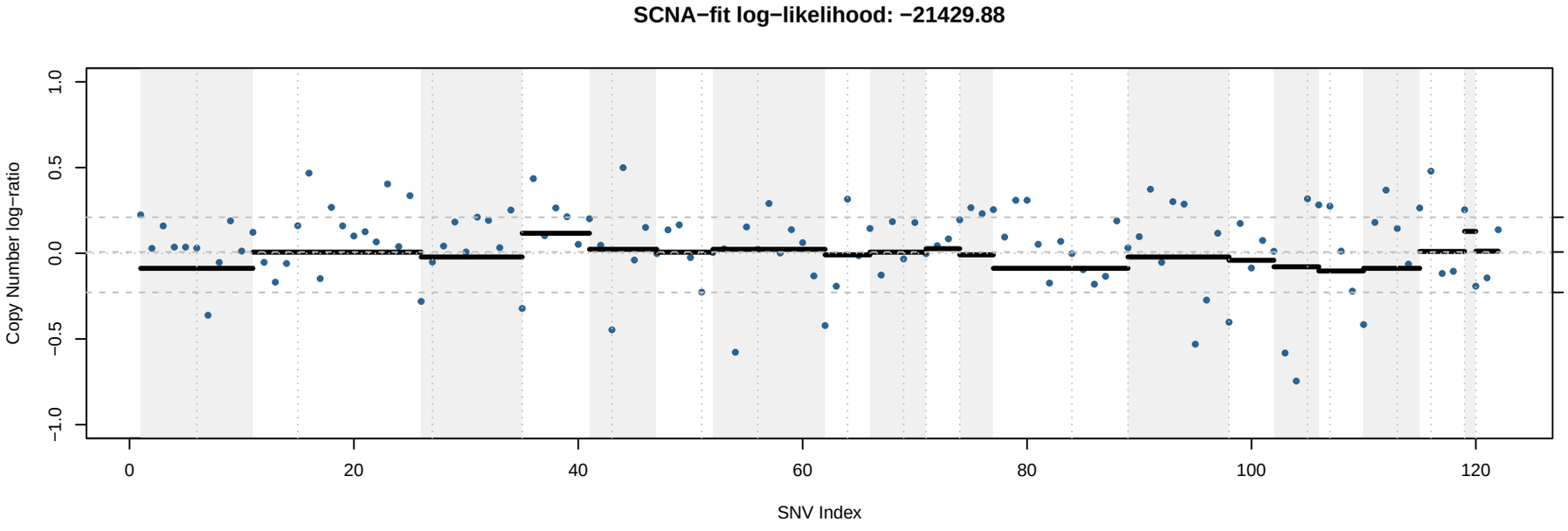

Coverage (log2)
Allelic fraction

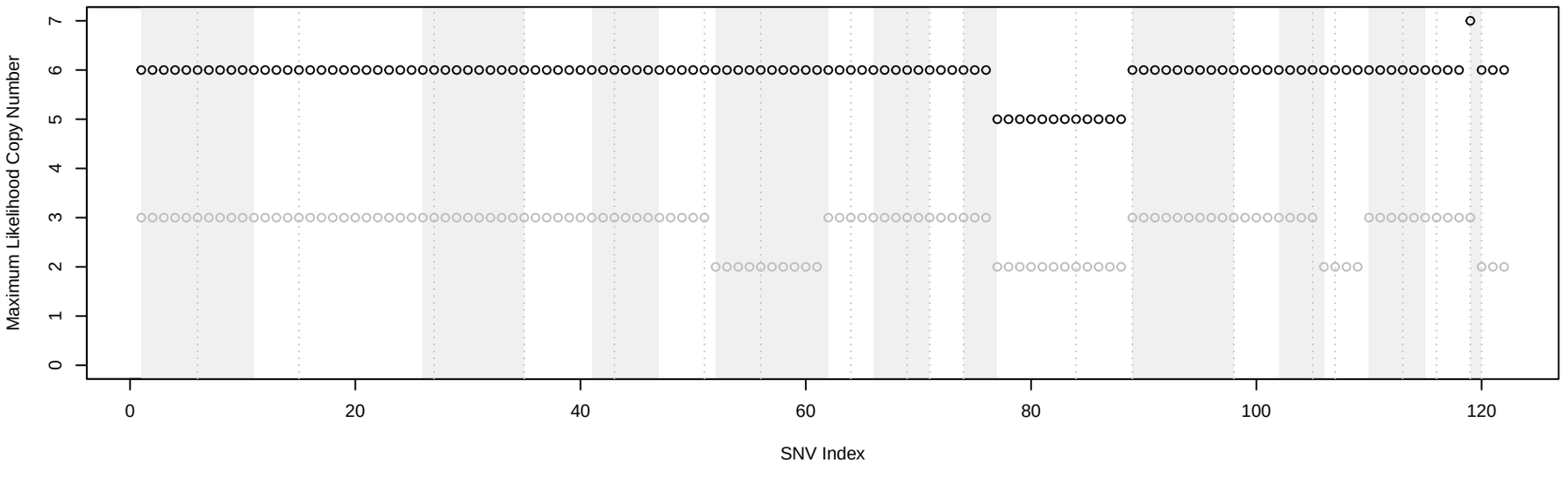

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
5m1
6m1
7m1

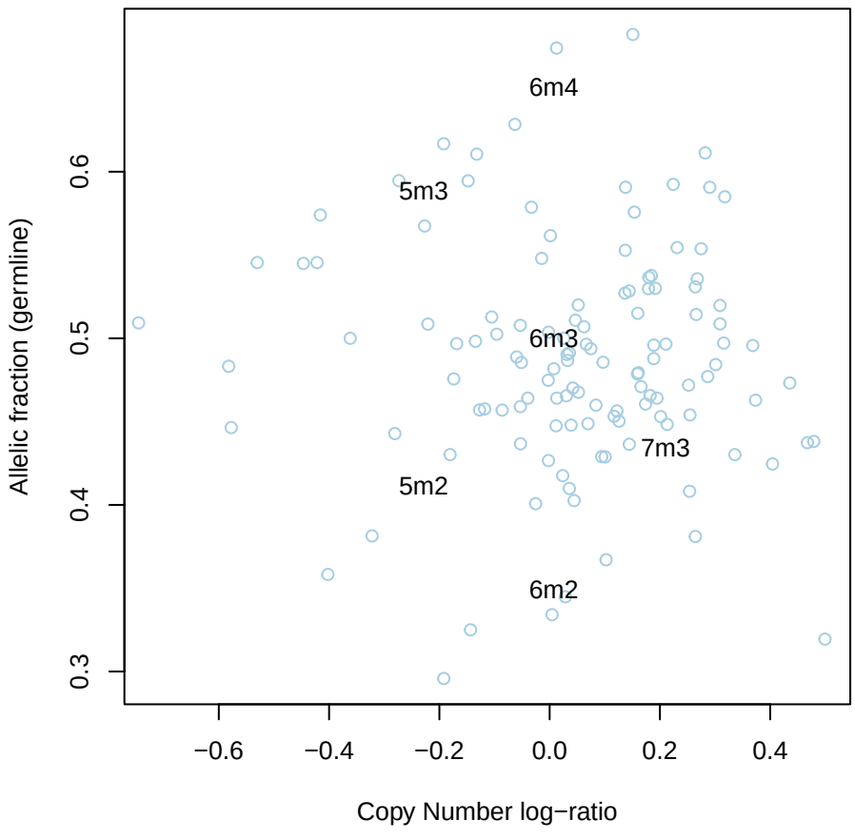

Frequency
Cellular fraction

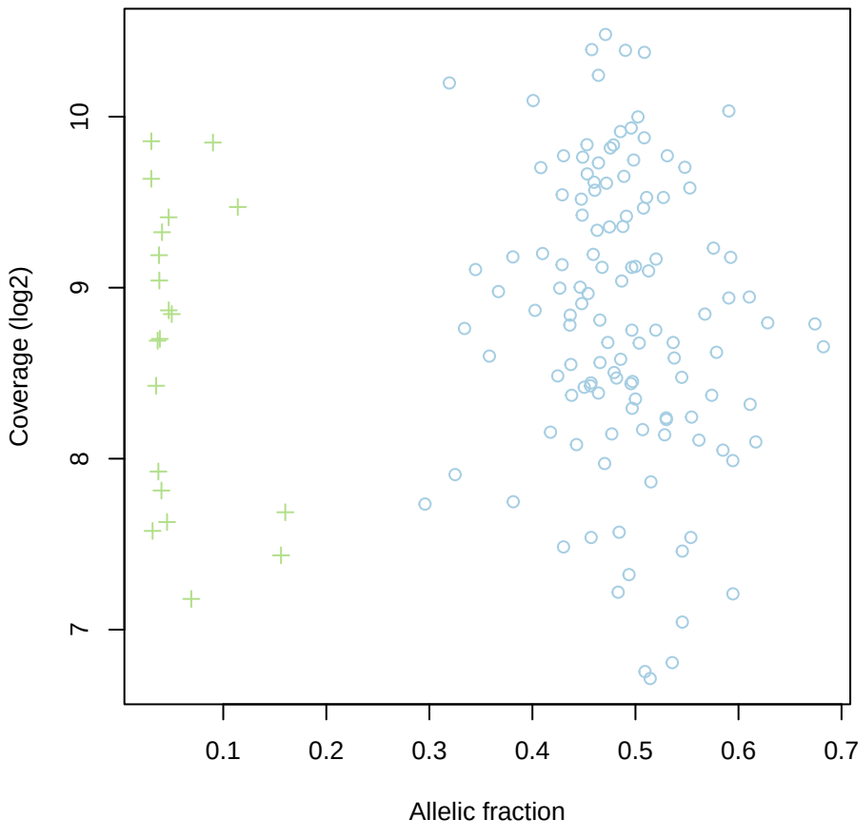

Purity: 0.76 Tumor ploidy: 5.966
6
Fraction Genome
0.00
0.05
0.10
0.15
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

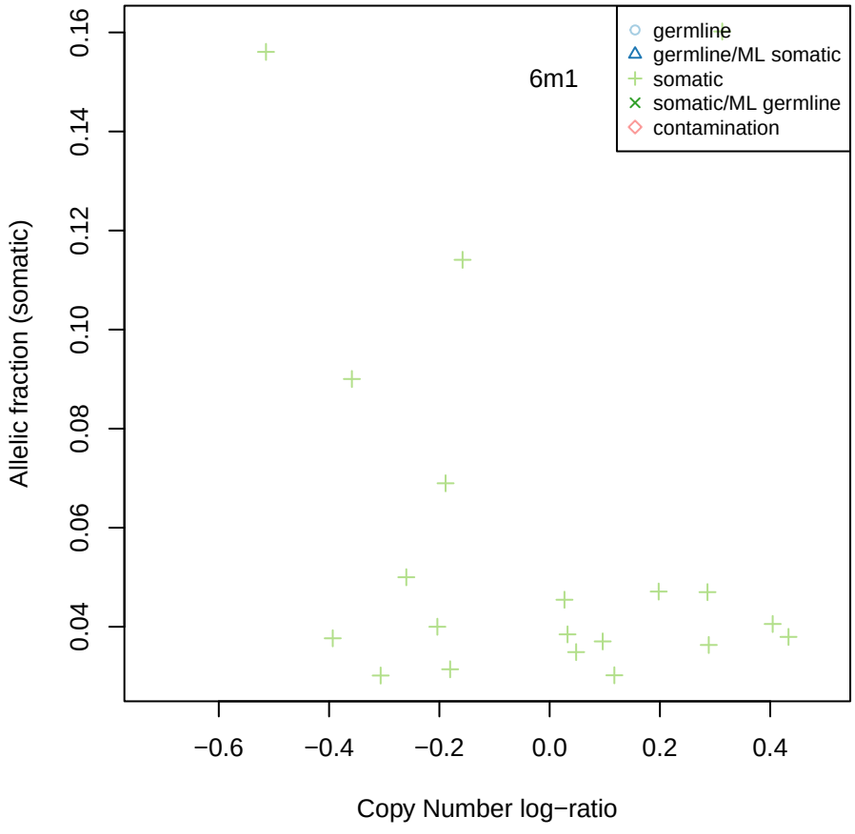

Purity: 0.76 Tumor ploidy: 5.966 SNV log−likelihood: −211.78 GoF: 90.7% Mean coverage: 158;523
1
2
3
4
5
6
7
8
9
10
12
13
15
16
17
19
20
B−Allele Frequency
0.3
0.4
0.5
0.6
0
20
40
60
80
100
120
SNV Index

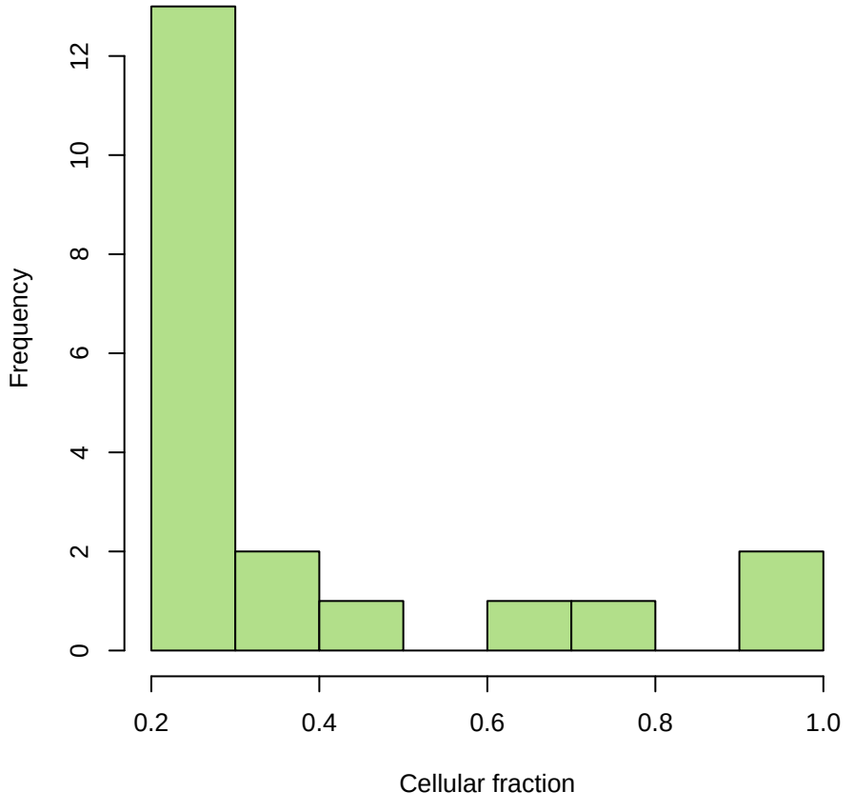

SCNA−fit log−likelihood: −21429.88
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
5
6
7
0
20
40
60
80
100
120
SNV Index

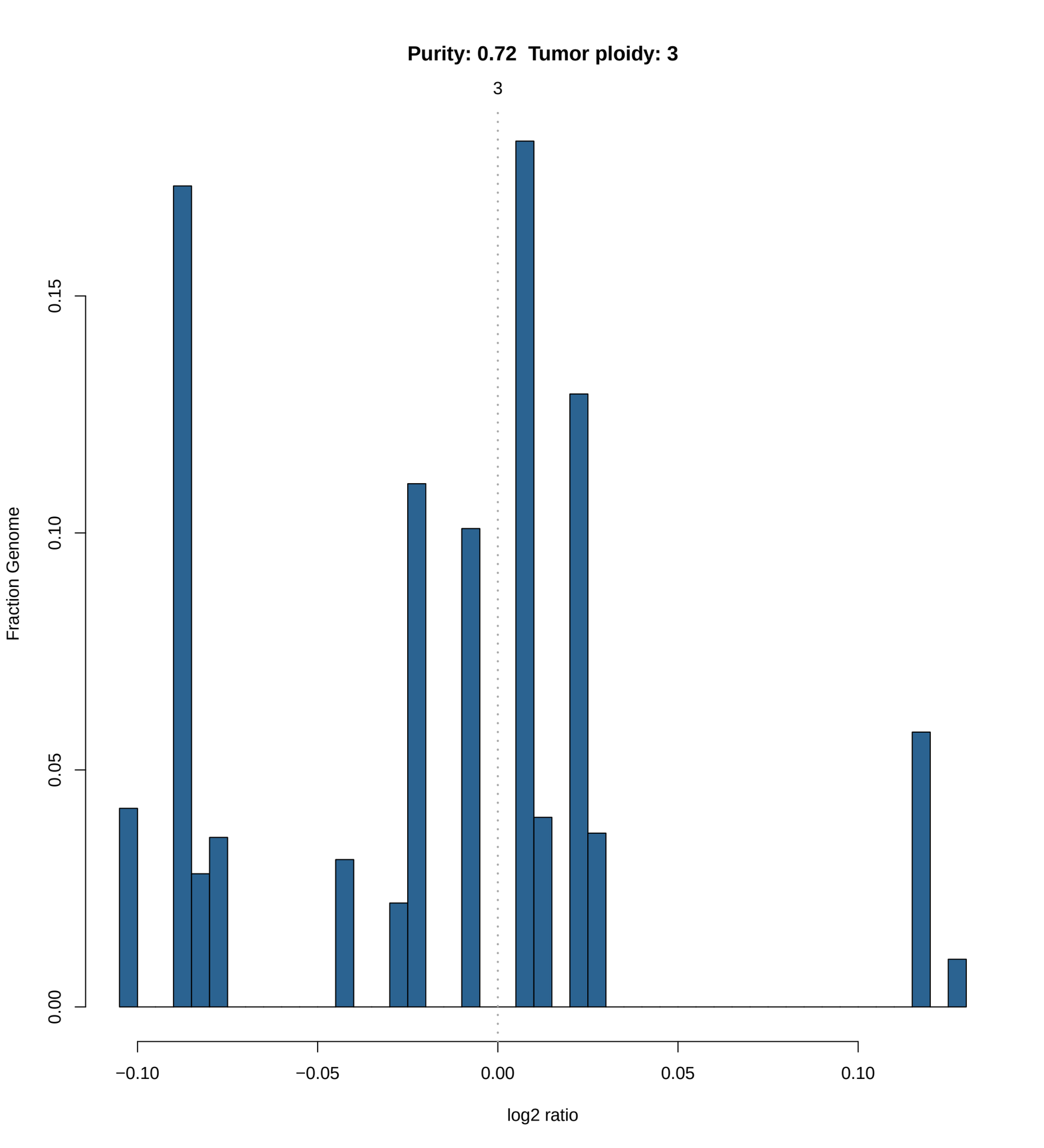

Maximum Likelihood Copy Number
0
1
2
3
4
5
6
7
0
20
40
60
80
100
120
SNV Index

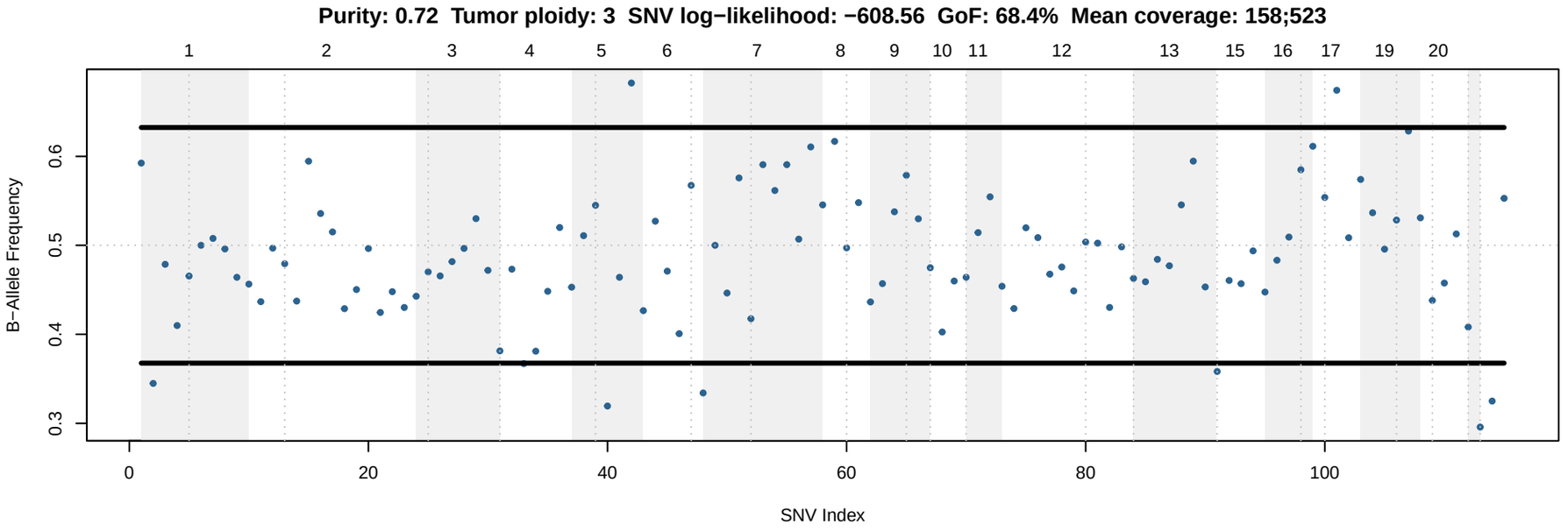

6m4
5m3
6m3
7m3
5m2
6m2
Allelic fraction (germline)
Copy Number log−ratio

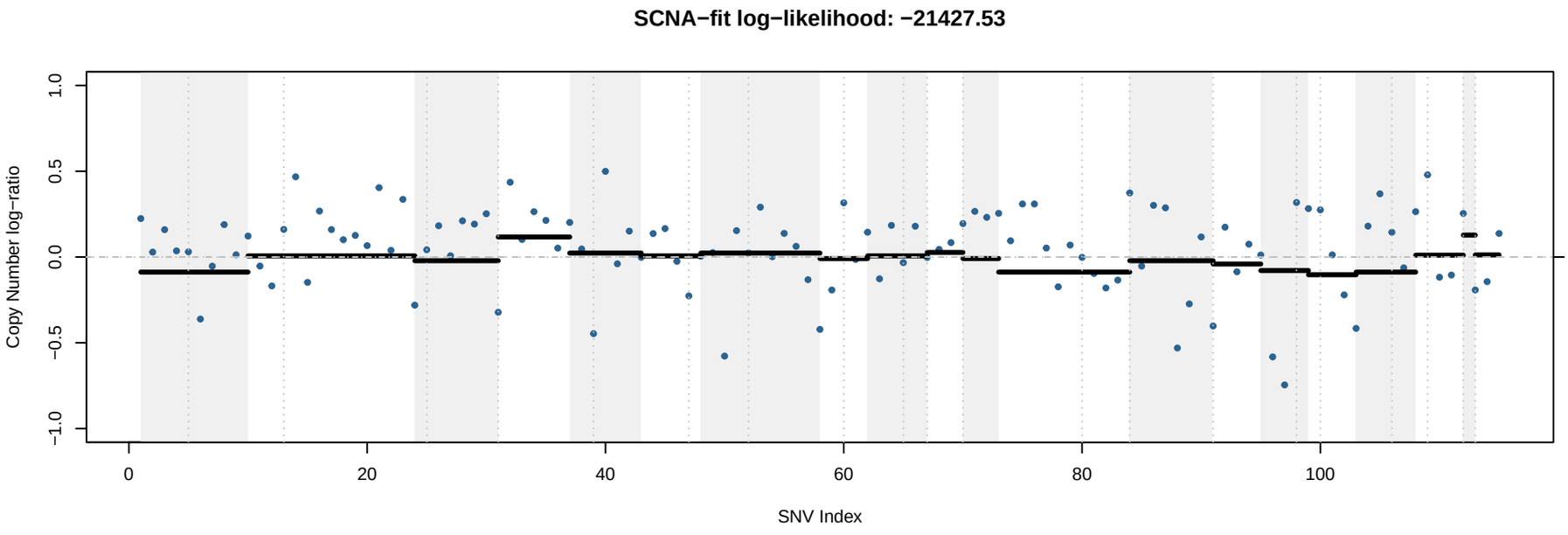

Coverage (log2)
Allelic fraction

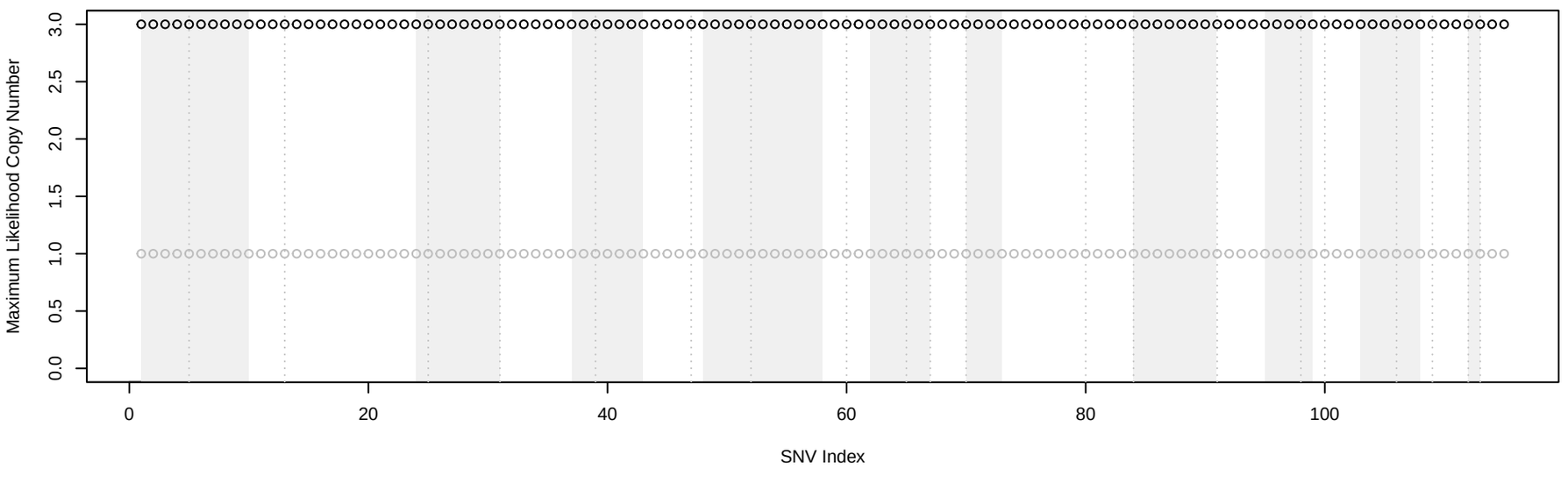

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
6m1
Allelic fraction (somatic)
Copy Number log−ratio

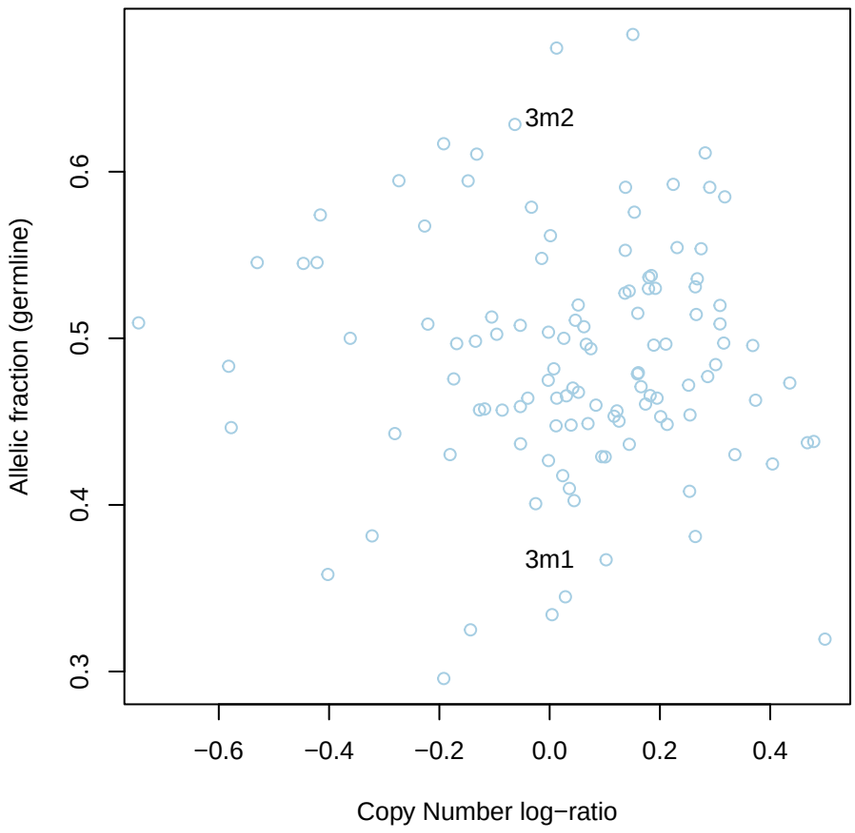

Frequency
Cellular fraction

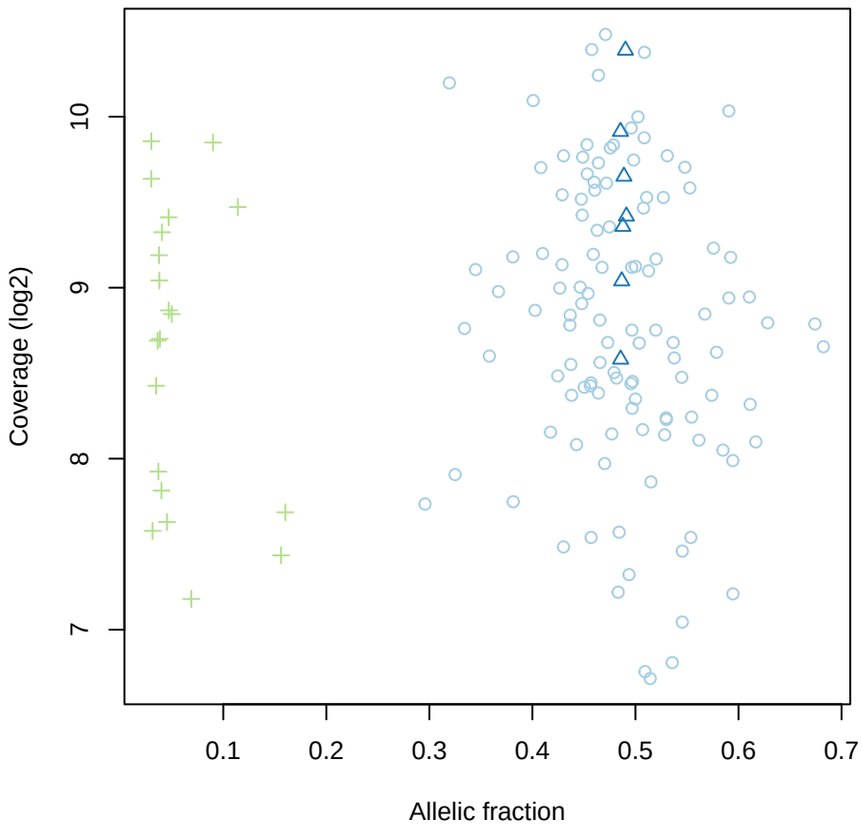

Purity: 0.72 Tumor ploidy: 3
3
Fraction Genome
0.00
0.05
0.10
0.15
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

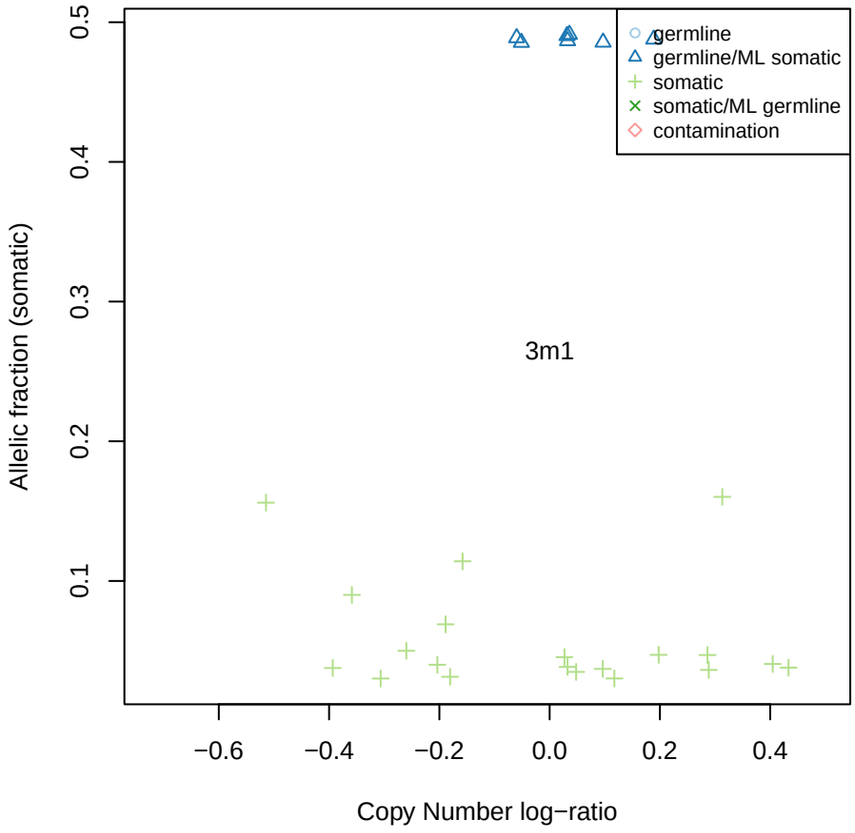

Purity: 0.72 Tumor ploidy: 3 SNV log−likelihood: −608.56 GoF: 68.4% Mean coverage: 158;523
1
2
3
4
5
6
7
8
9
10
11
12
13
15
16
17
19
20
B−Allele Frequency
0.3
0.4
0.5
0.6
0
20
40
60
80
100
SNV Index

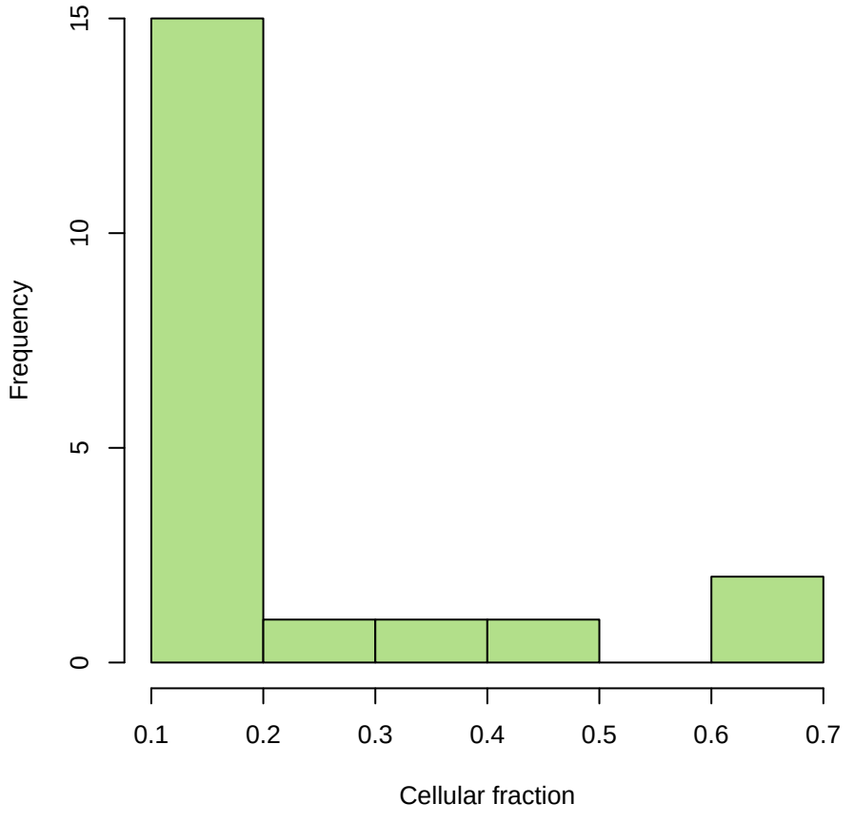

SCNA−fit log−likelihood: −21427.53
Copy Number log−ratio
1.0
0.5
0.0
−0.5
−1.0
3
0
20
40
60
80
100
SNV Index

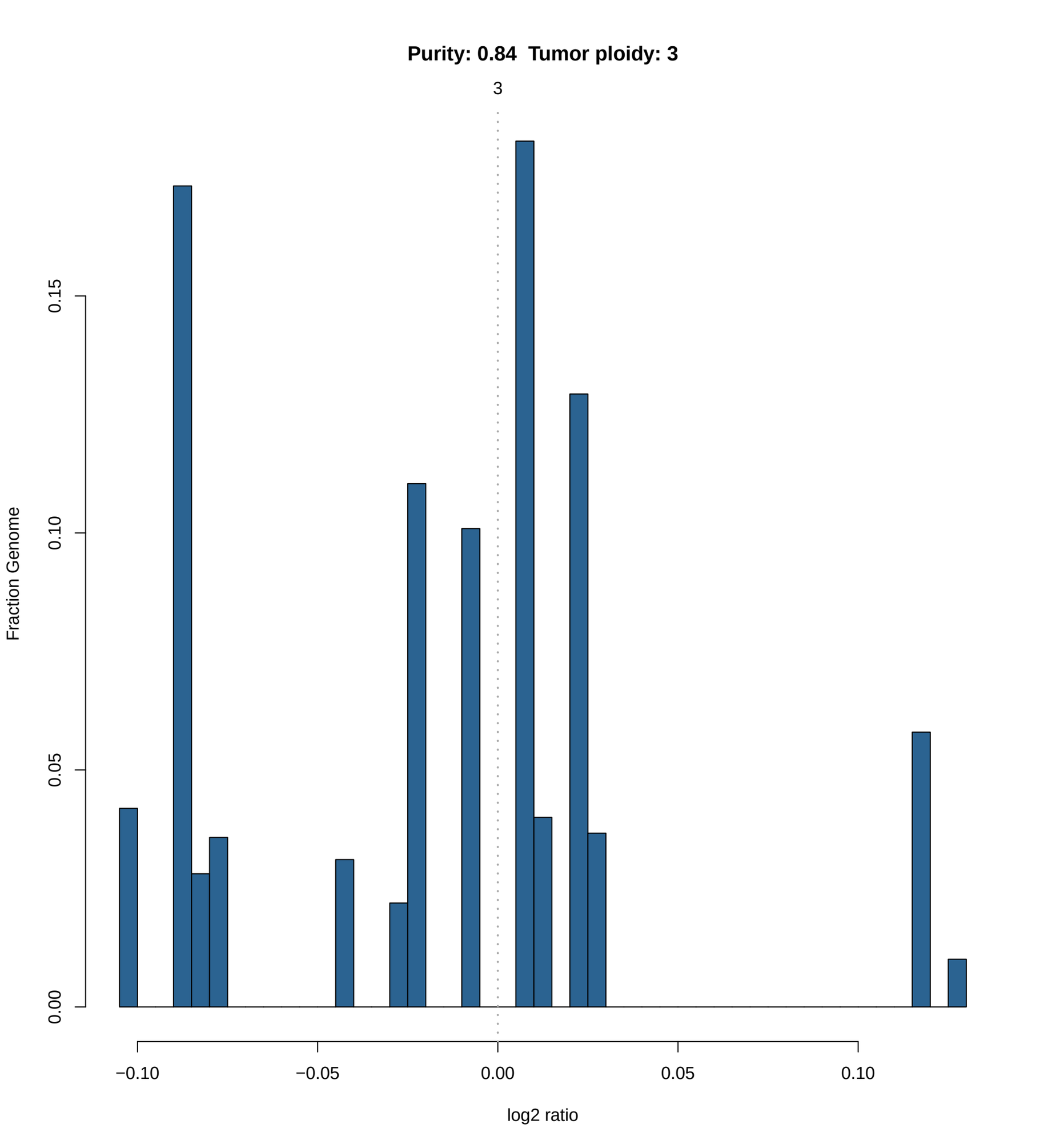

Maximum Likelihood Copy Number
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0
20
40
60
80
100
SNV Index

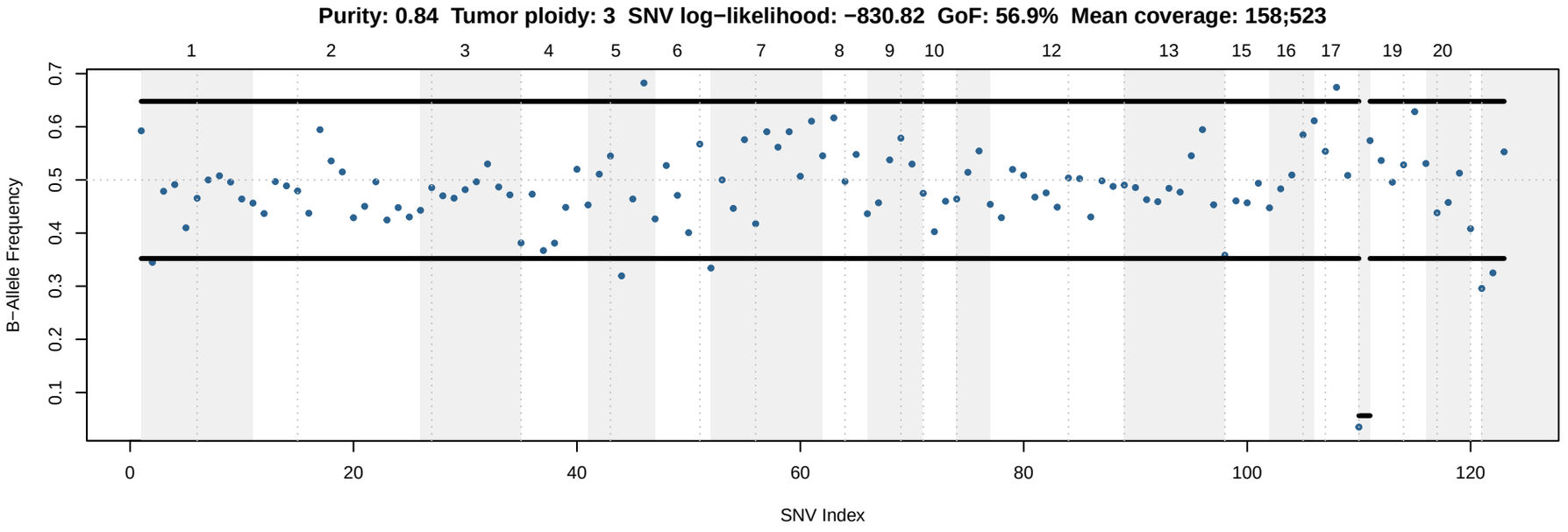

3m2
3m1
Allelic fraction (germline)
Copy Number log−ratio
0.3
0.4
0.5
0.6
−0.6
−0.4
−0.2
0.0
0.2
0.4

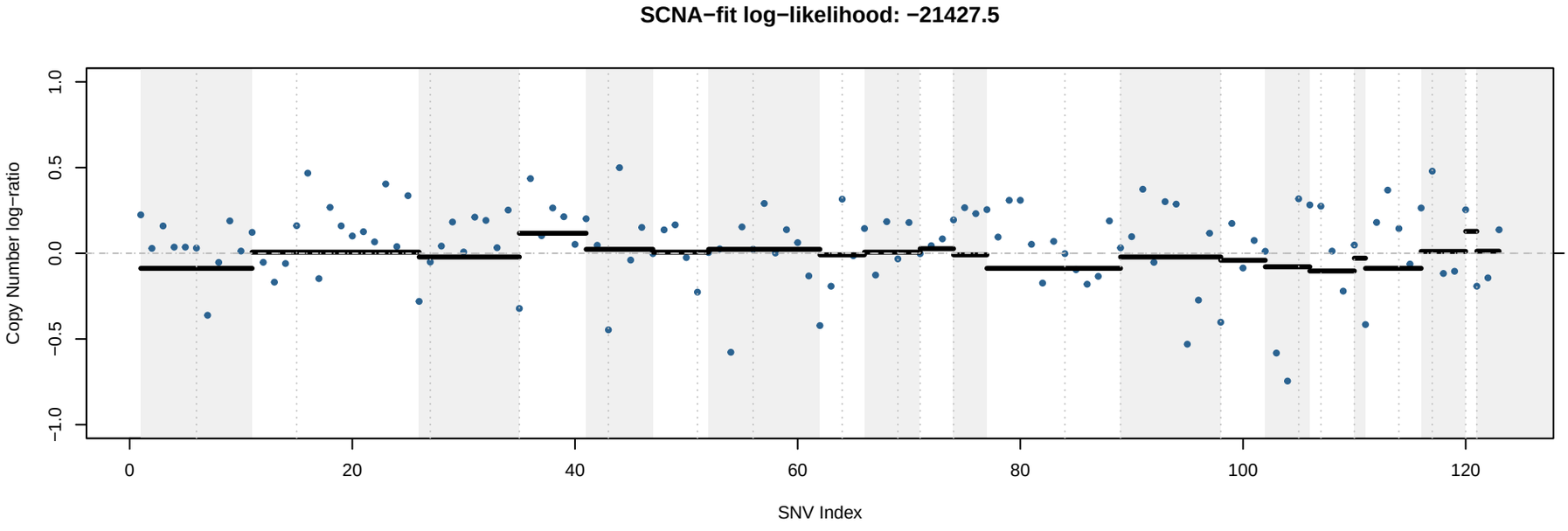

Coverage (log2)
Allelic fraction
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7

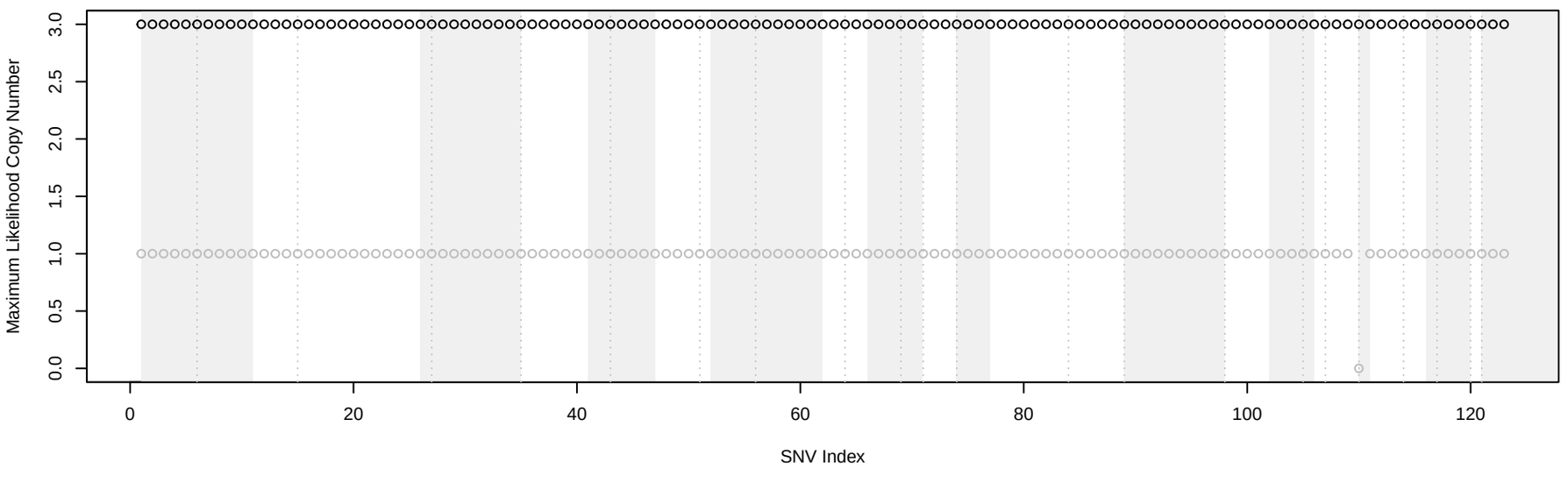

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m1
Allelic fraction (somatic)
Copy Number log−ratio
0.1
0.2
0.3
0.4
0.5
−0.6
−0.4
−0.2
0.0
0.2
0.4

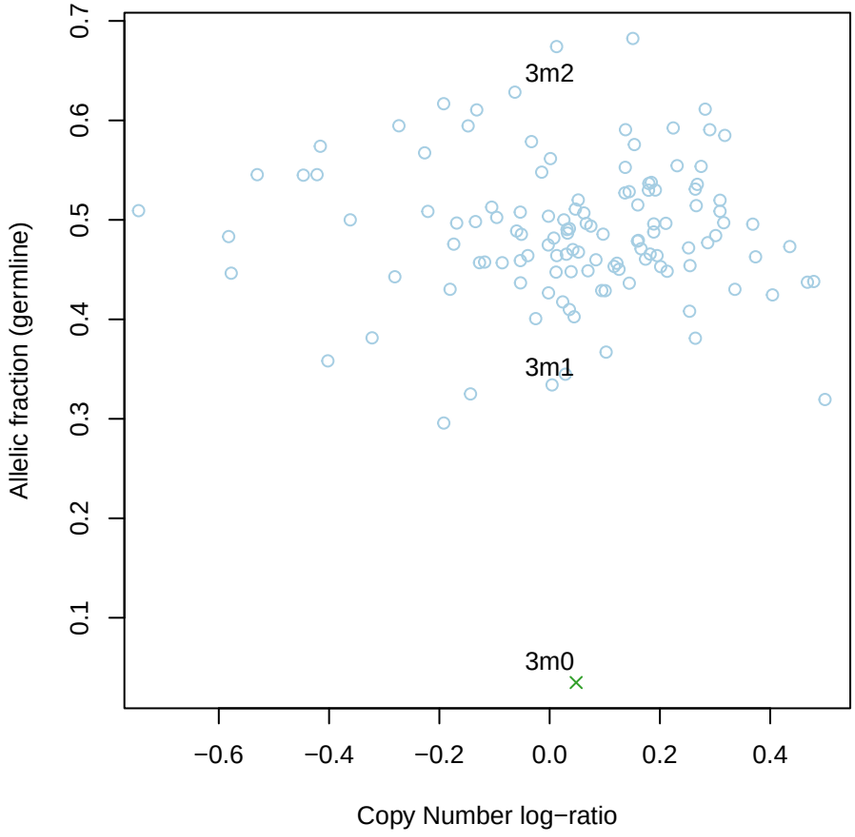

Frequency
Cellular fraction
0
5
10
15
0.1
0.2
0.3
0.4
0.5
0.6
0.7

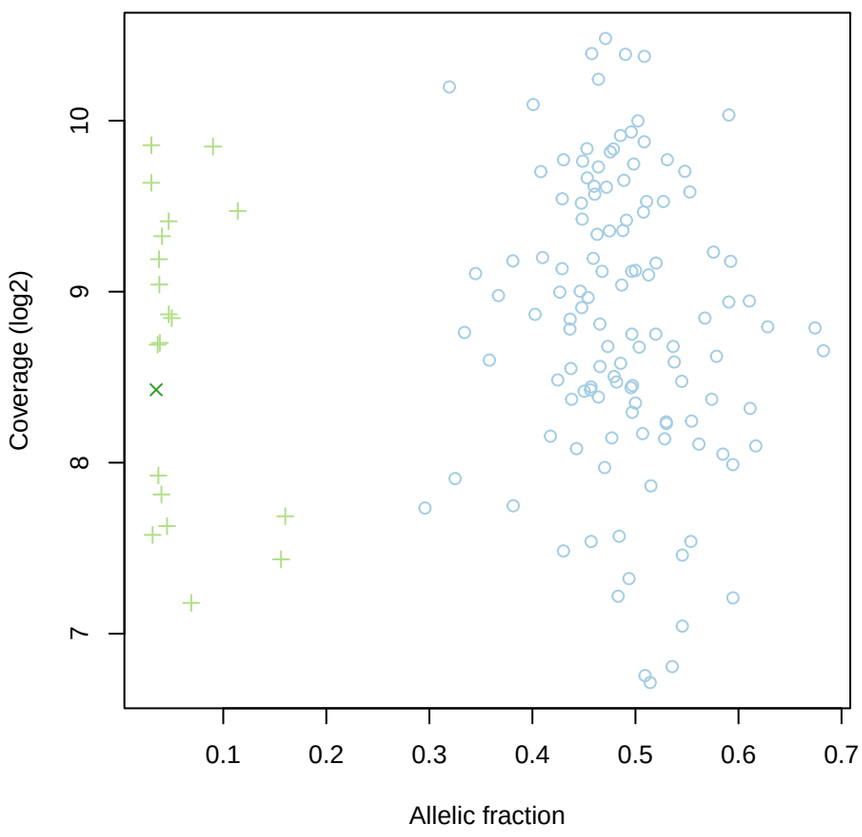

Purity: 0.84 Tumor ploidy: 3
3
0.15
0.10
0.05
0.00
Fraction Genome
−0.10
−0.05
0.00
0.05
0.10
log2 ratio

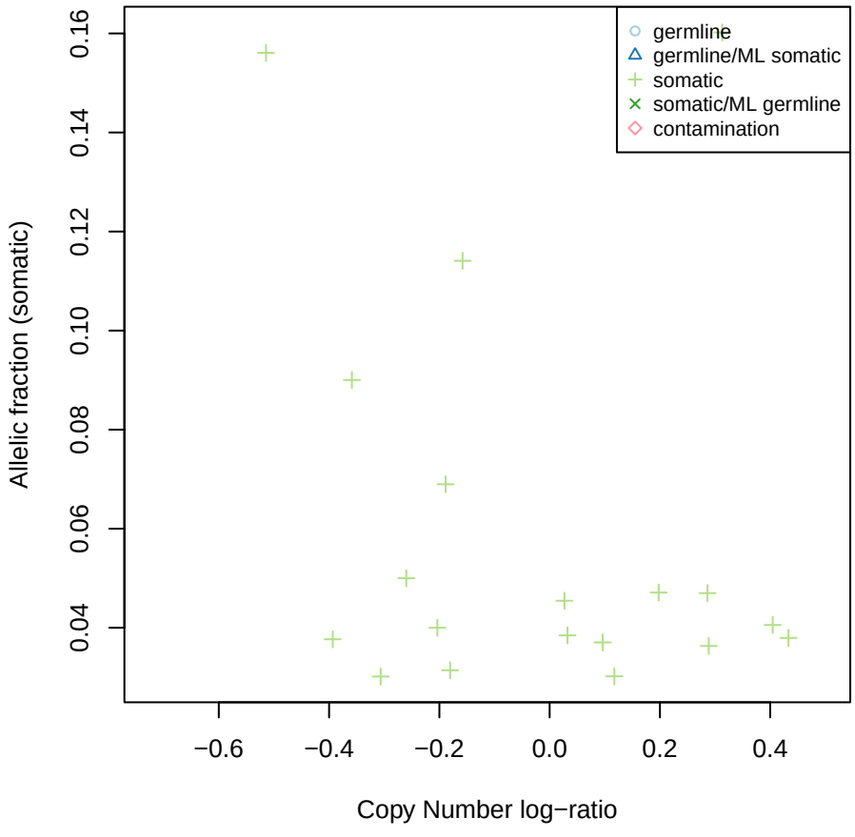

Purity: 0.84 Tumor ploidy: 3 SNV log−likelihood: −830.82 GoF: 56.9% Mean coverage: 158;523
1 2 3 4 5 6 7 8 9 10 12 13 15 16 17 19 20
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

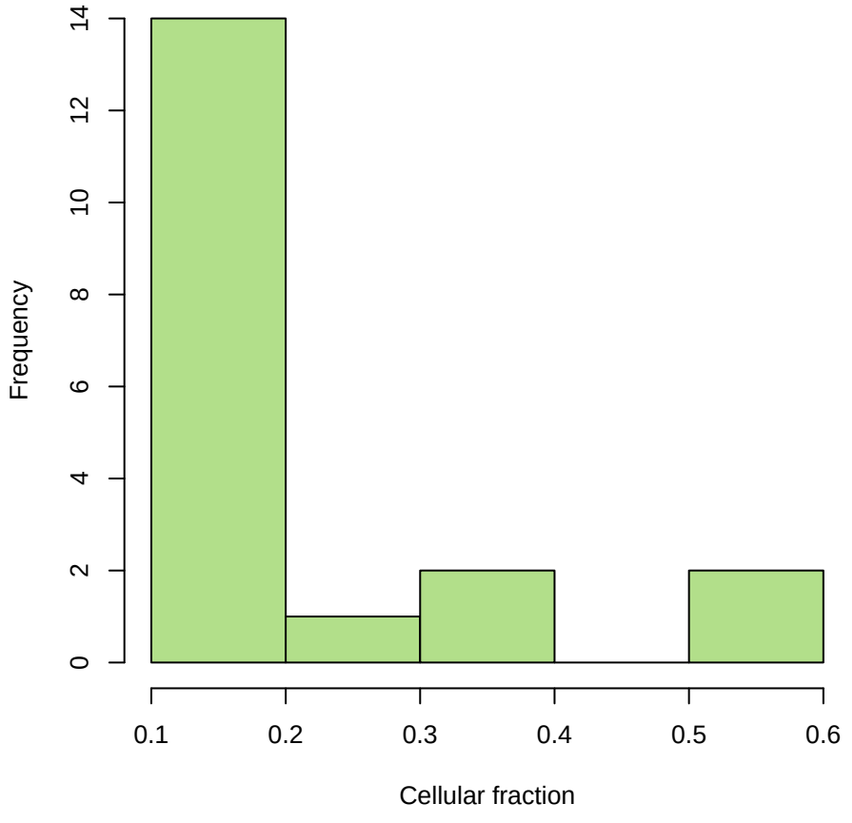

SCNA−fit log−likelihood: −21427.5
Copy Number log−ratio
1.0 0.5 0.0 −0.5 −1.0
3
0 20 40 60 80 100 120
SNV Index


Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100 120
SNV Index


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


Coverage (log2)
Allelic fraction


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


Frequency
Cellular fraction