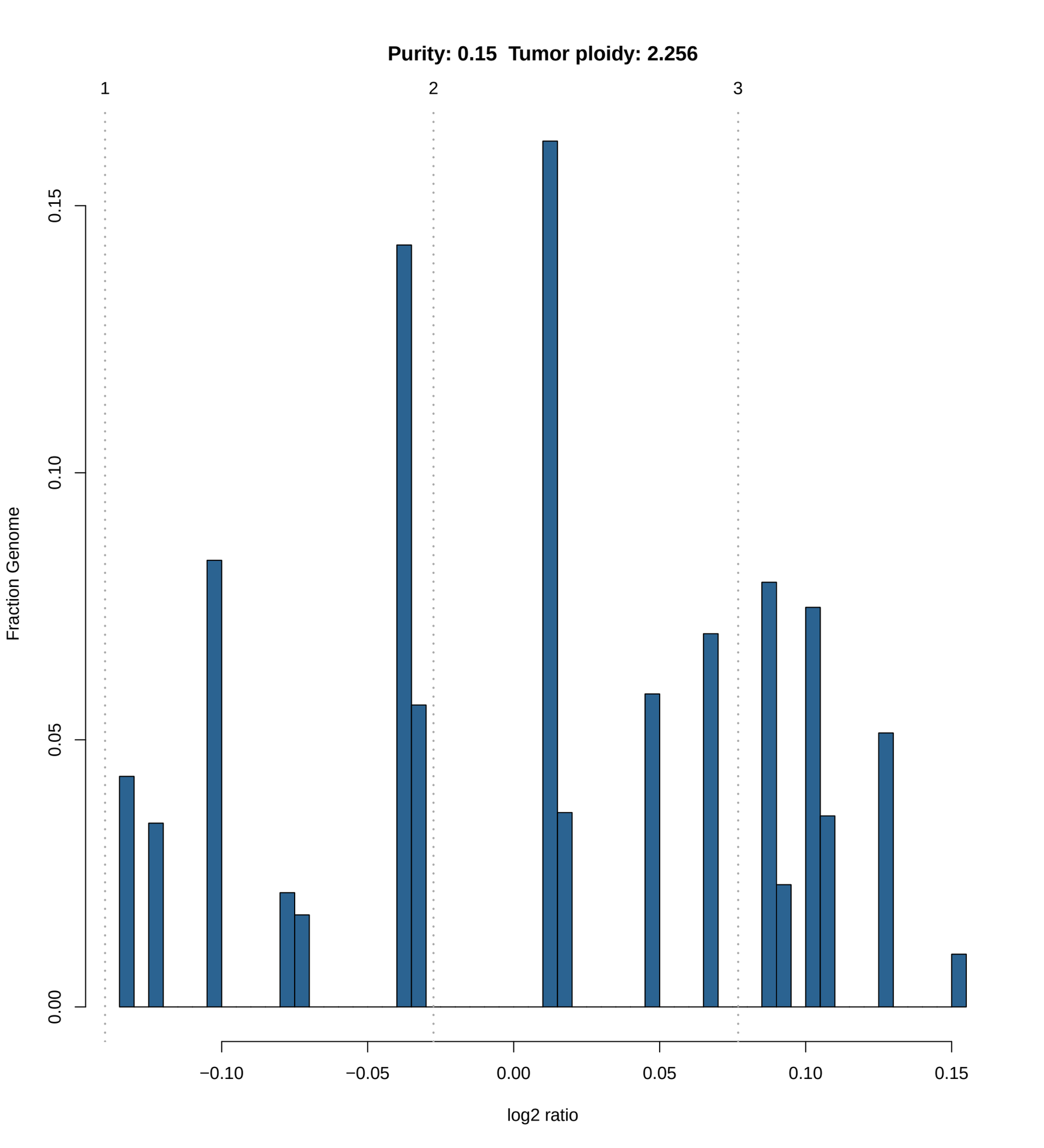
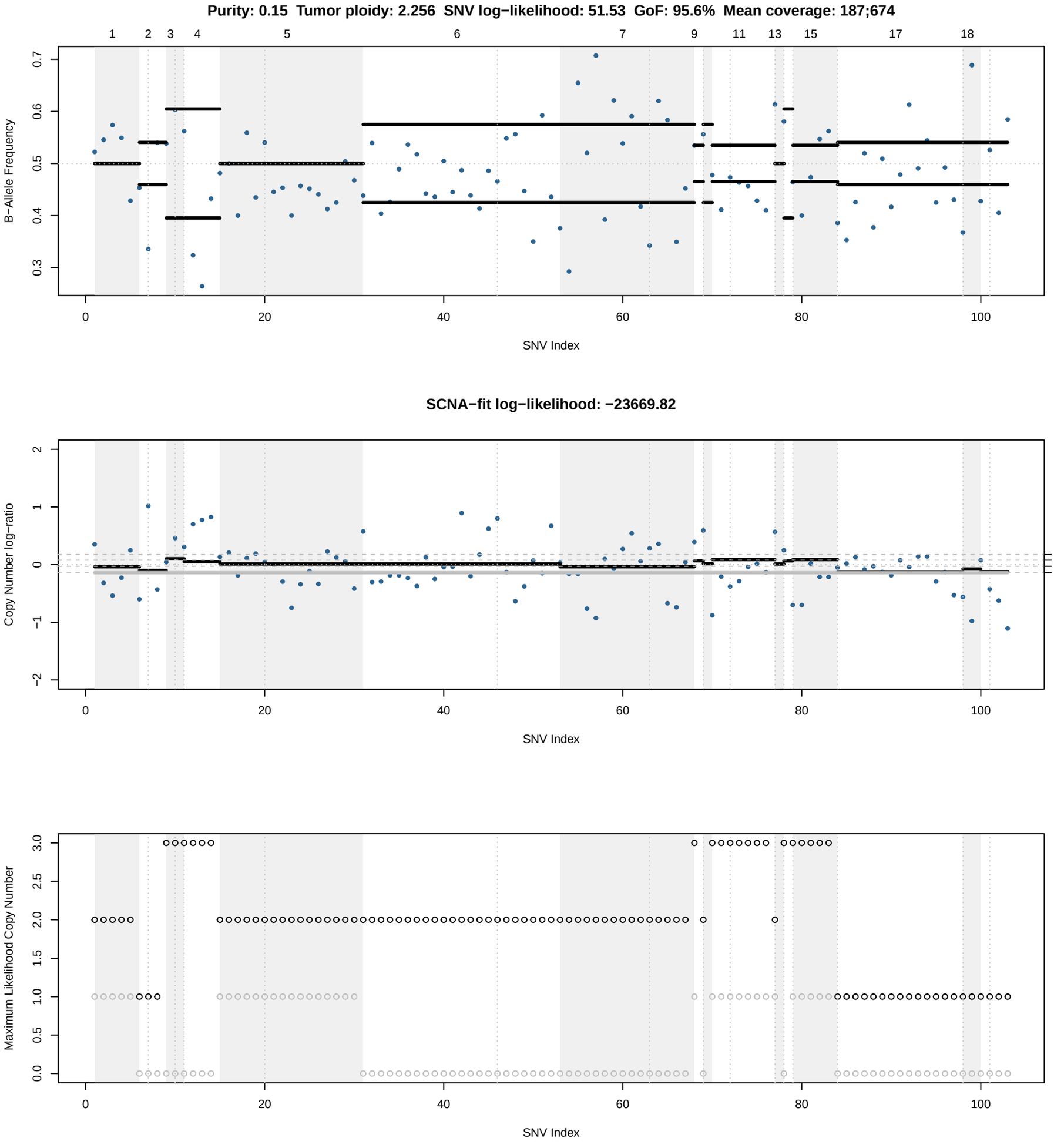
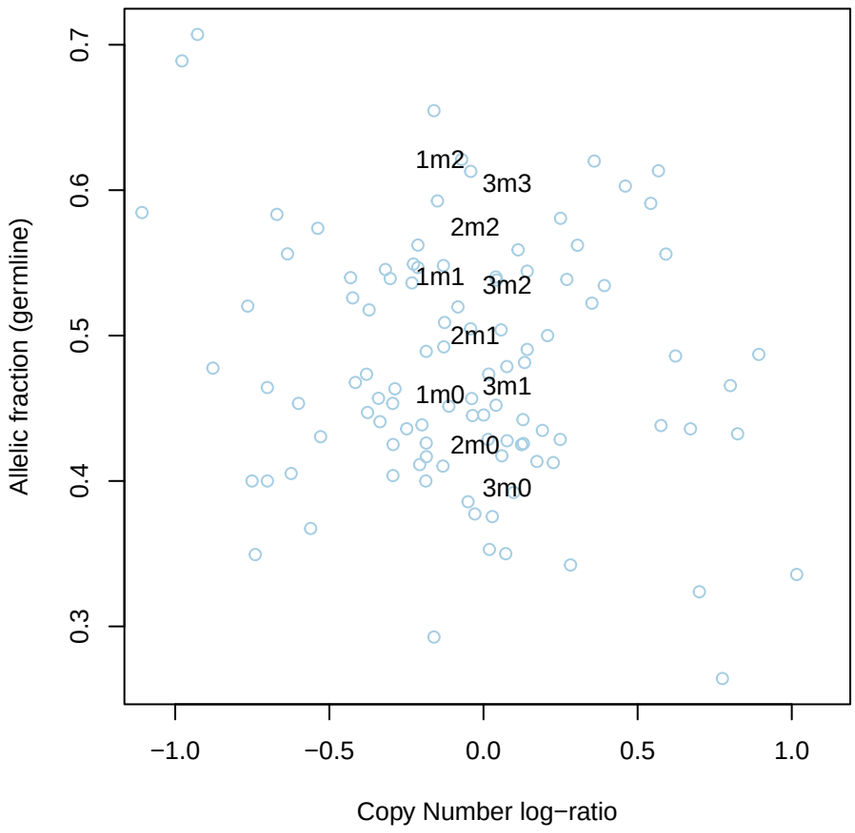
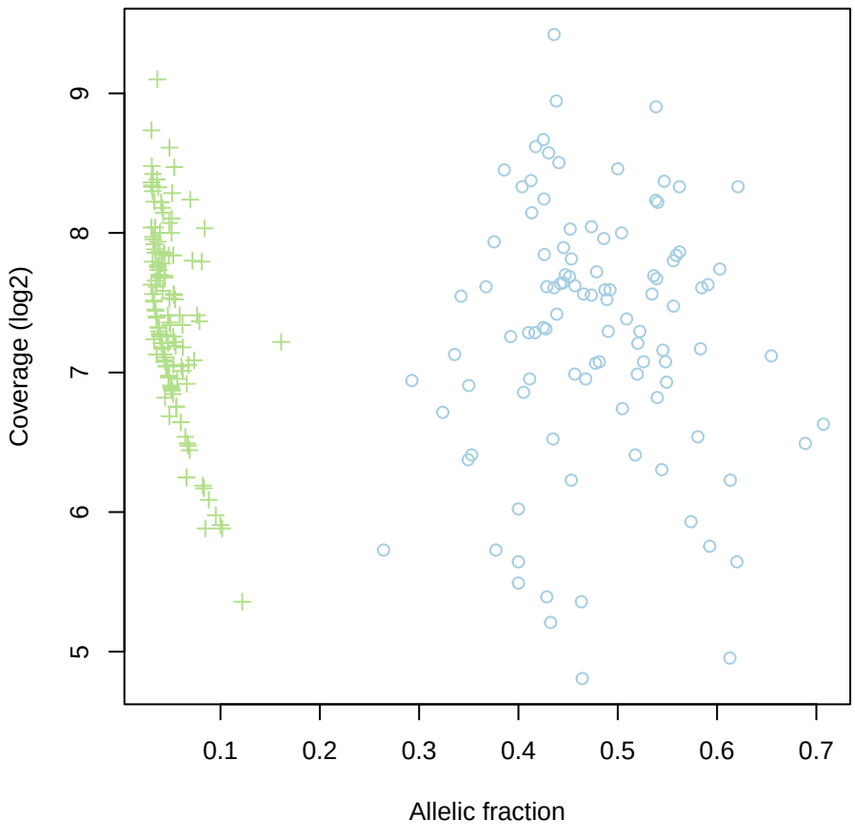
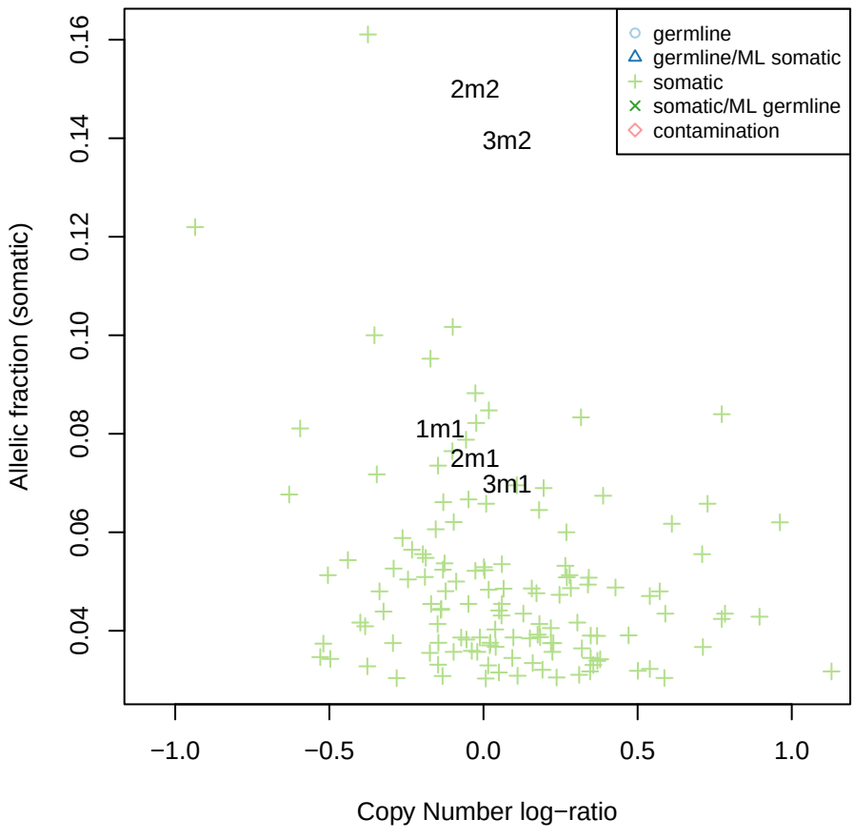
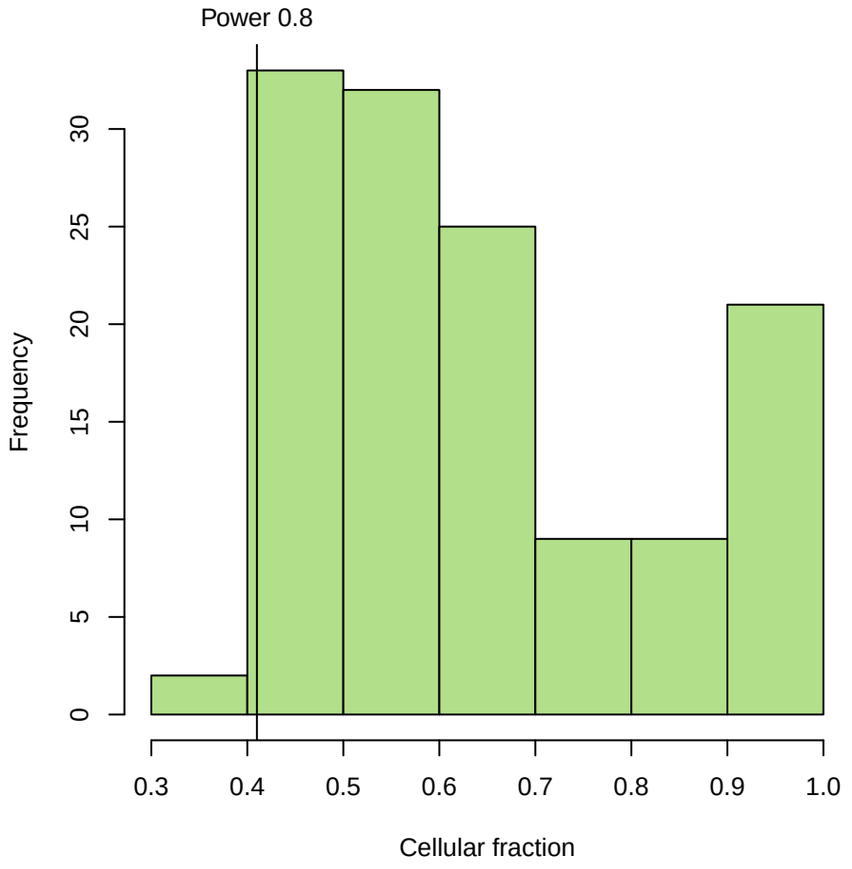

Purity: 0.15  Tumor ploidy: 2.256
1
2
3
0.15
0.10
0.05
0.00
Fraction Genome
−0.10
−0.05
0.00
0.05
0.10
0.15
log2 ratio

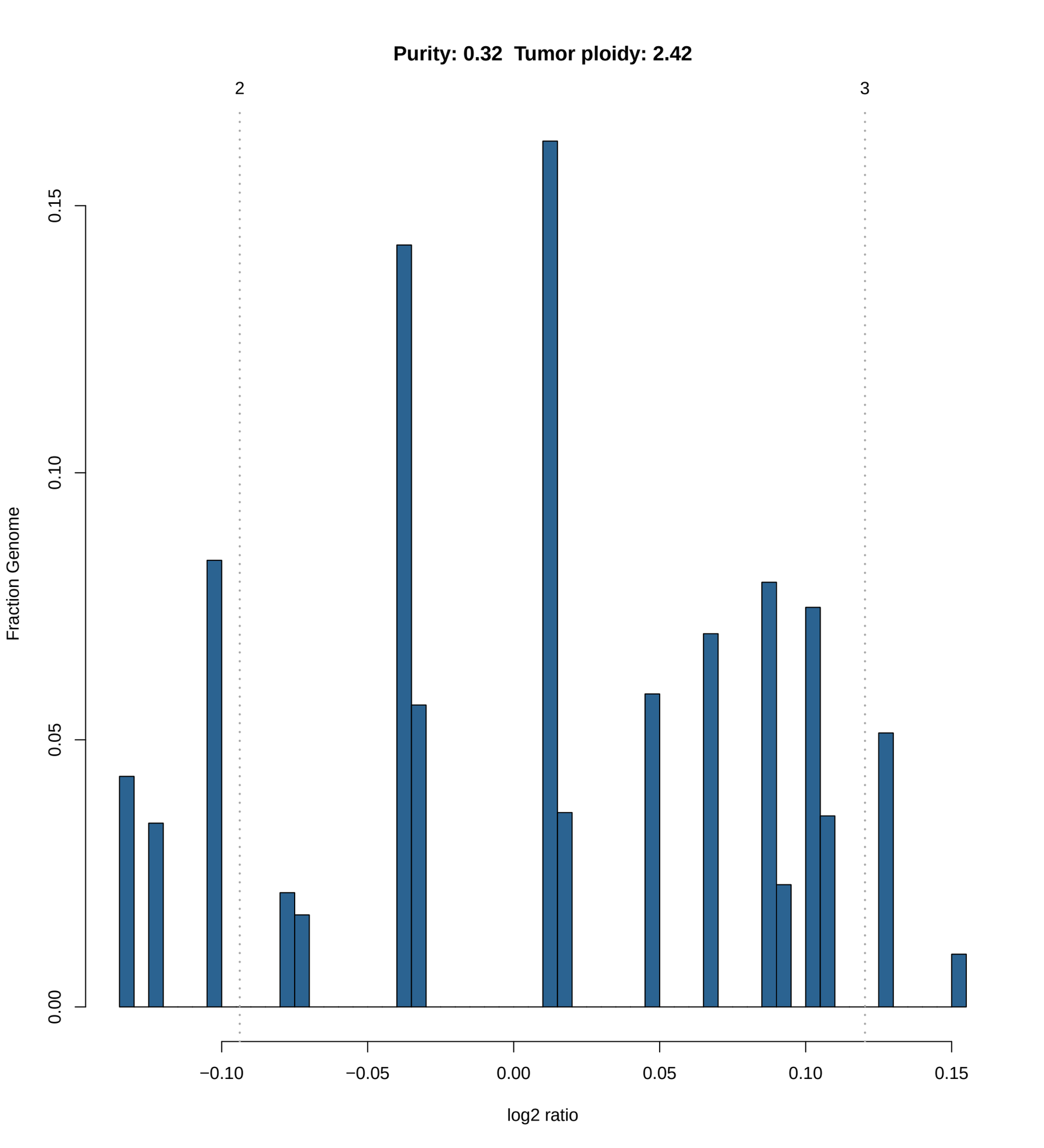

Purity: 0.15 Tumor ploidy: 2.256 SNV log−likelihood: 51.53 GoF: 95.6% Mean coverage: 187;674
1 2 3 4 5 6 7 9 11 13 15 17 18
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index
SCNA−fit log−likelihood: −23669.82
Copy Number log−ratio
−2 −1 0 1 2
1 4
0 20 40 60 80 100
SNV Index
Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100
SNV Index

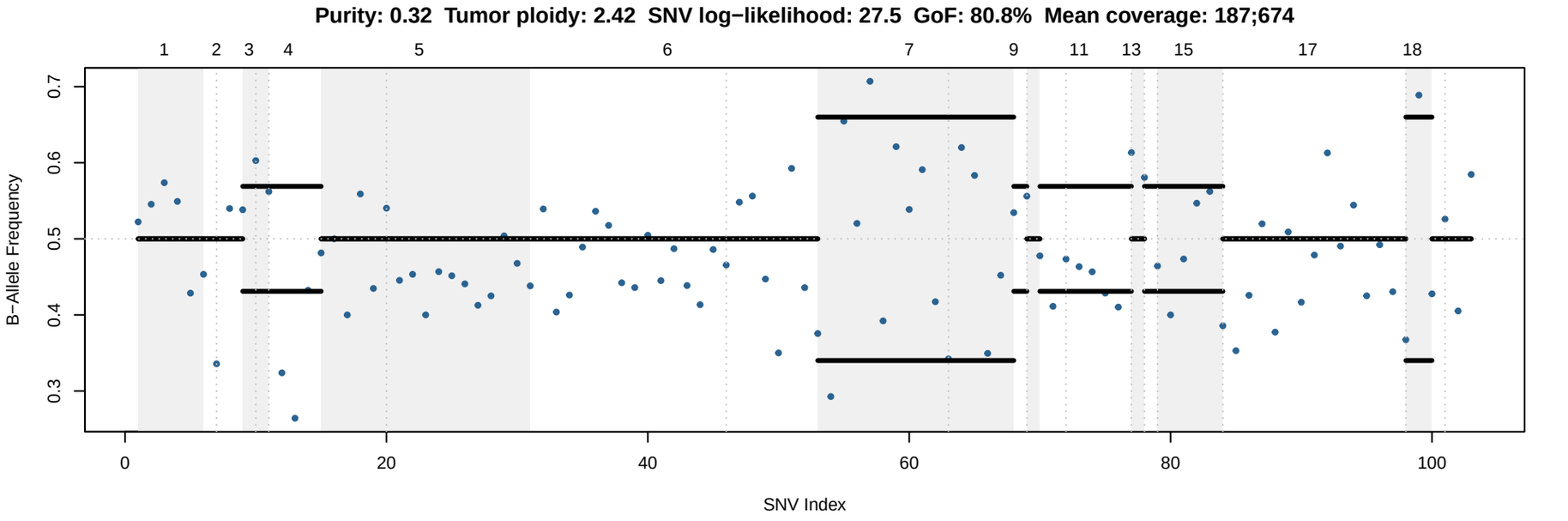

Allelic fraction (germline)
Copy Number log−ratio
1m2
3m3
2m2
1m1
3m2
2m1
1m0
3m1
2m0
3m0

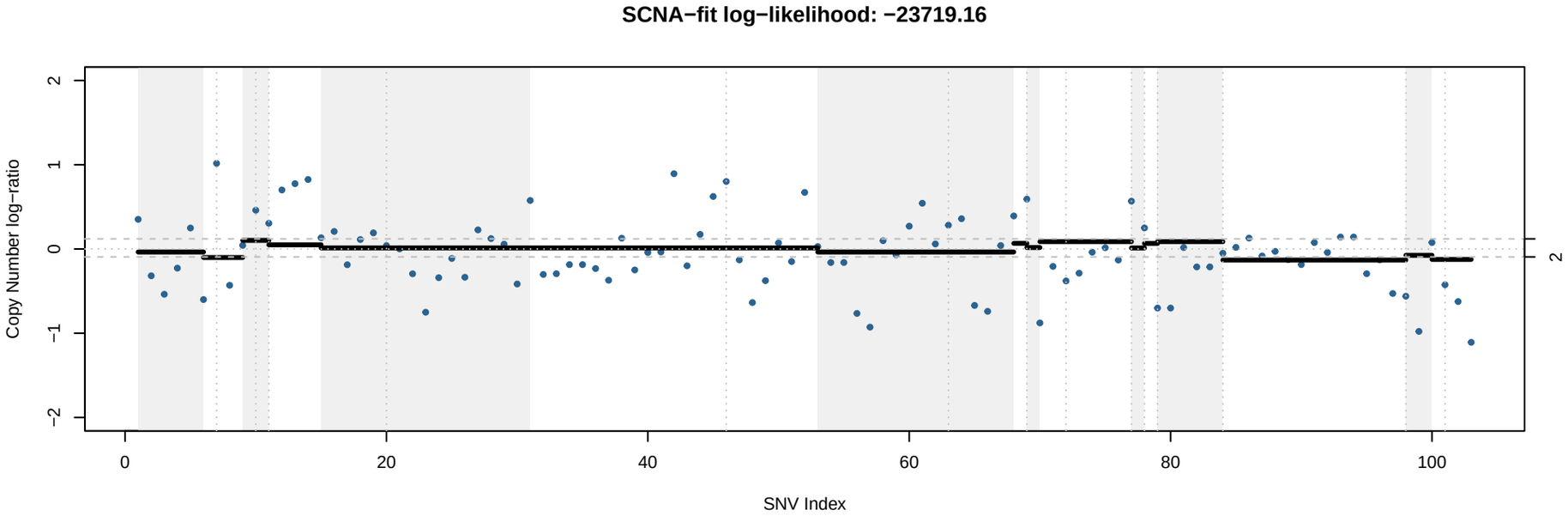

Coverage (log2)
Allelic fraction

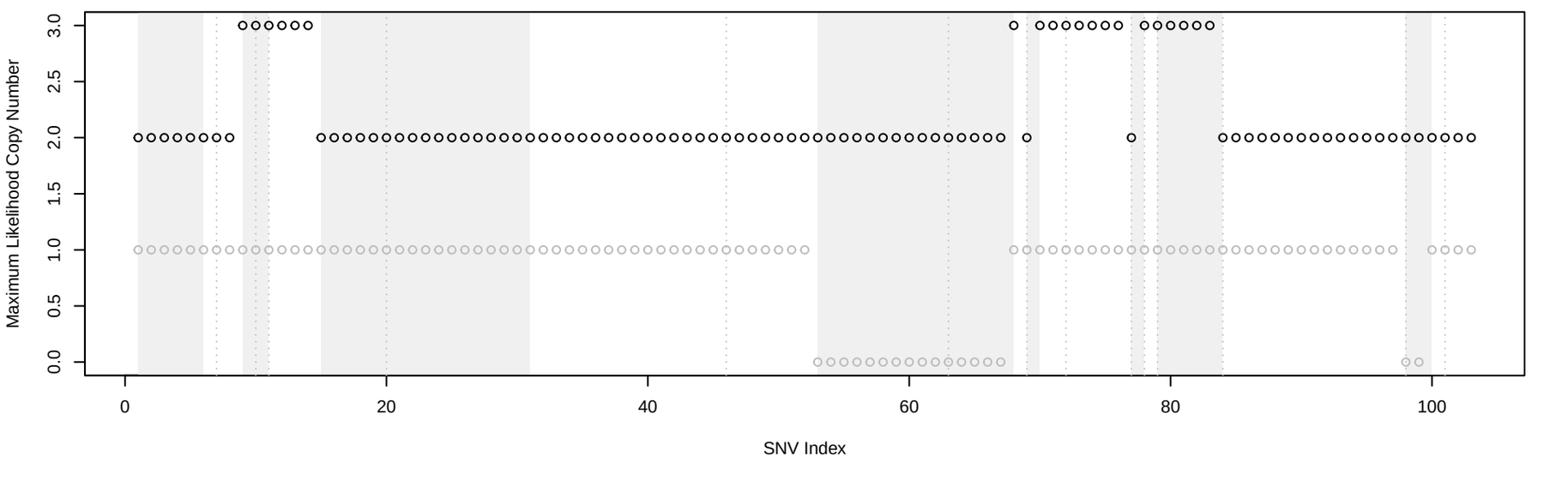

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
3m2
1m1
2m1
3m1

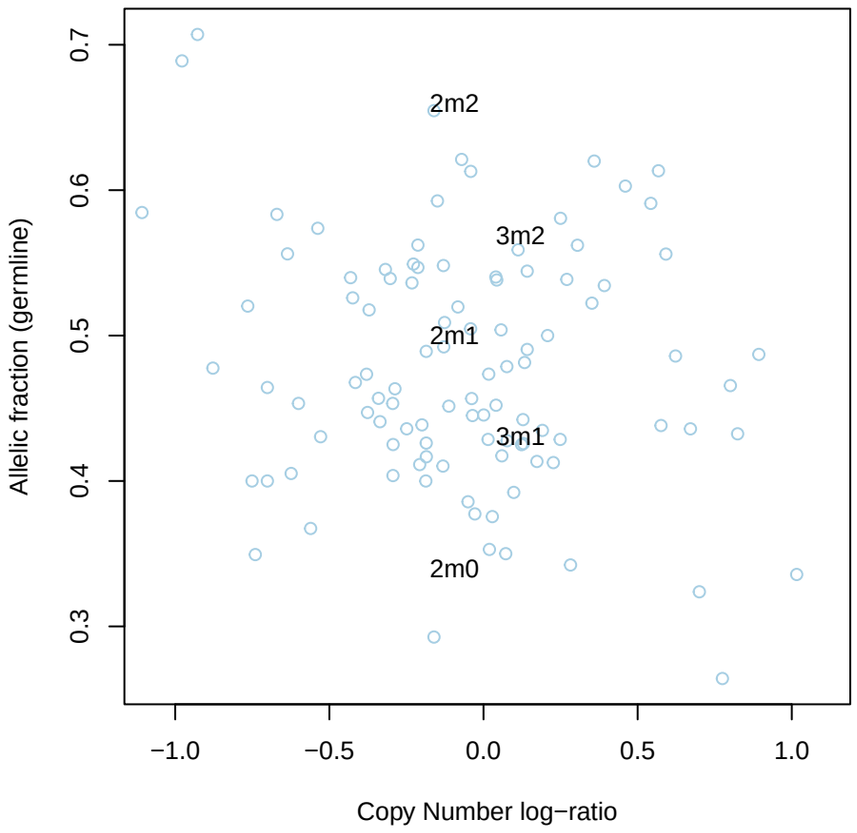

Power 0.8
Frequency
Cellular fraction

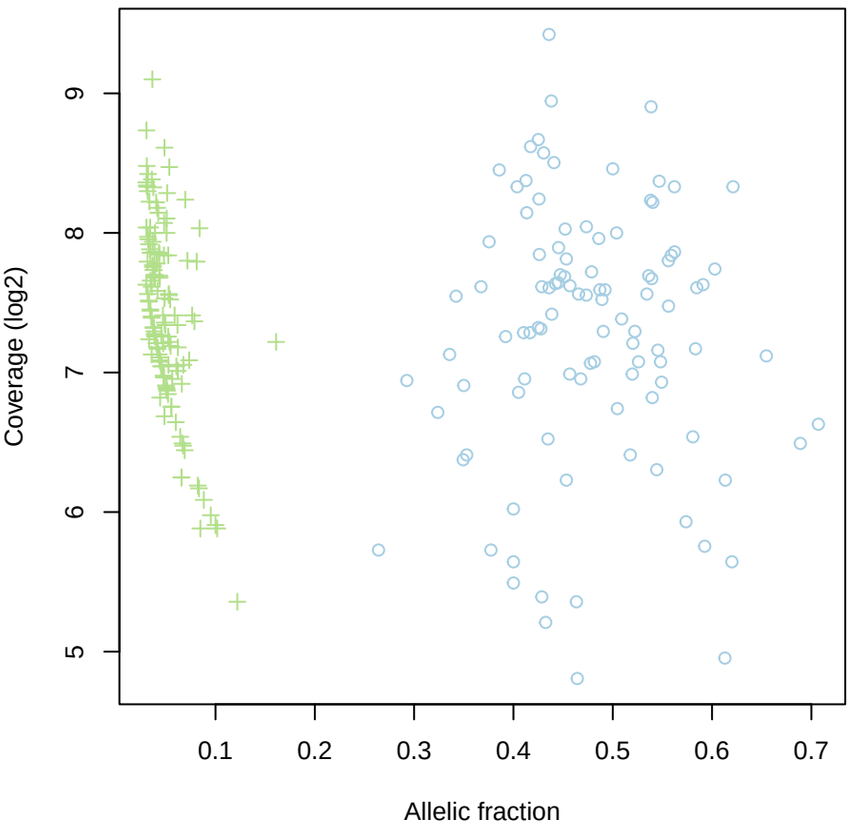

Purity: 0.32  Tumor ploidy: 2.42
2
3
0.15
0.10
0.05
0.00
Fraction Genome
−0.10
−0.05
0.00
0.05
0.10
0.15
log2 ratio

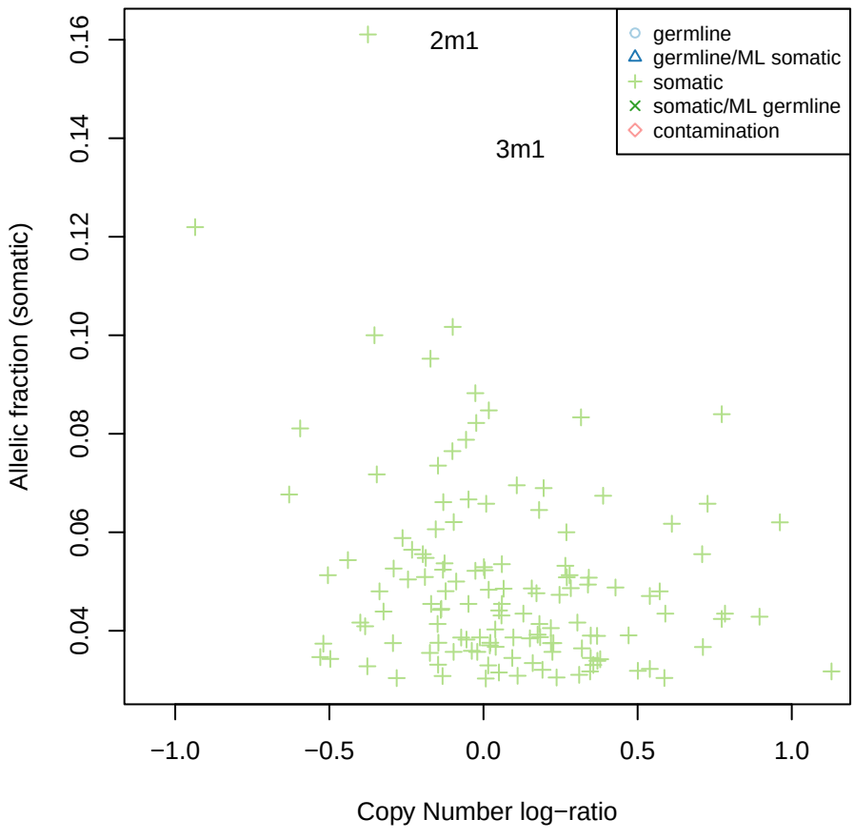

Purity: 0.32 Tumor ploidy: 2.42 SNV log−likelihood: 27.5 GoF: 80.8% Mean coverage: 187;674
1 2 3 4 5 6 7 9 11 13 15 17 18
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

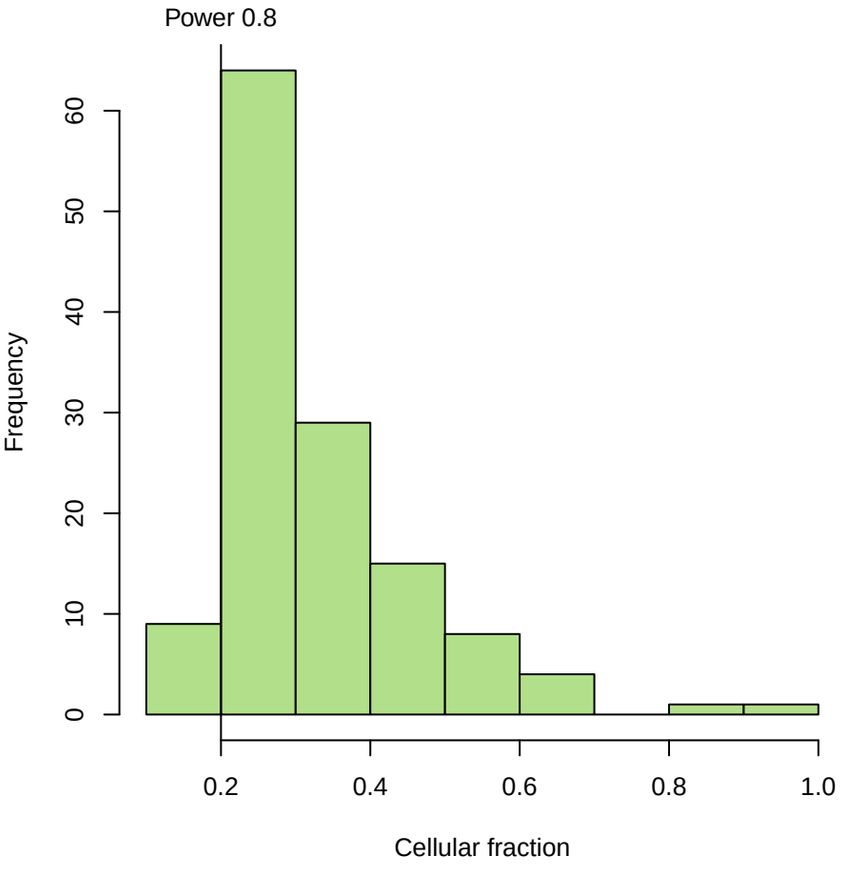

SCNA−fit log−likelihood: −23719.16
Copy Number log−ratio
−2 −1 0 1 2
2
0 20 40 60 80 100
SNV Index

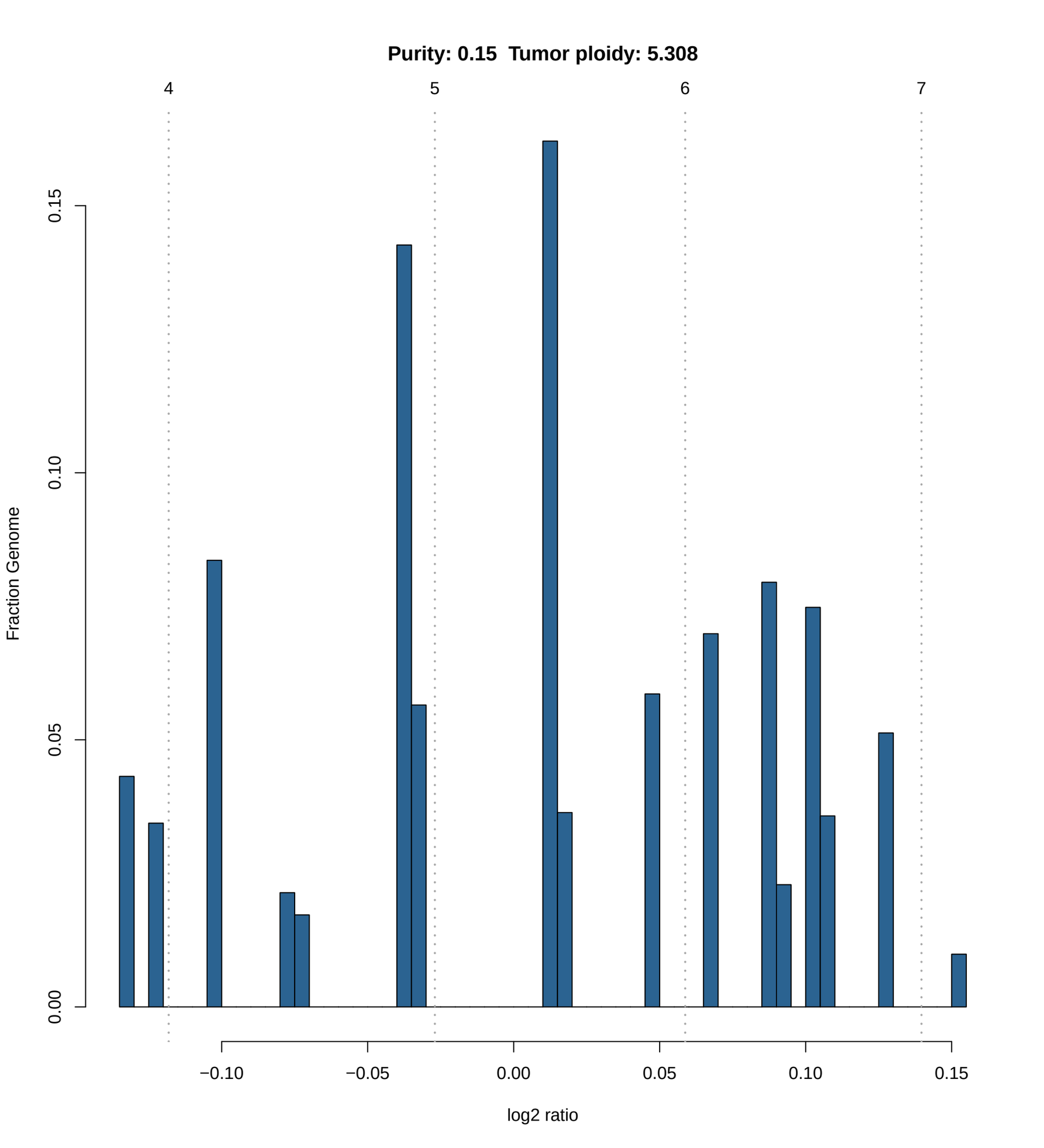

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100
SNV Index

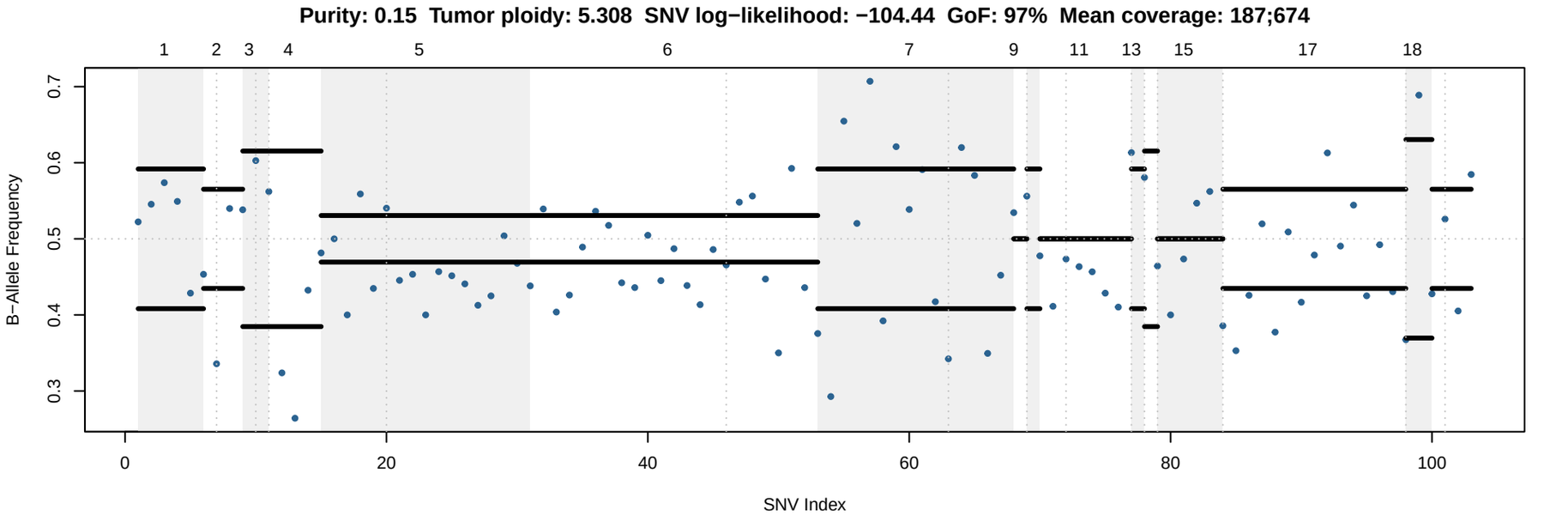

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
2m2
3m2
2m1
3m1
2m0
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

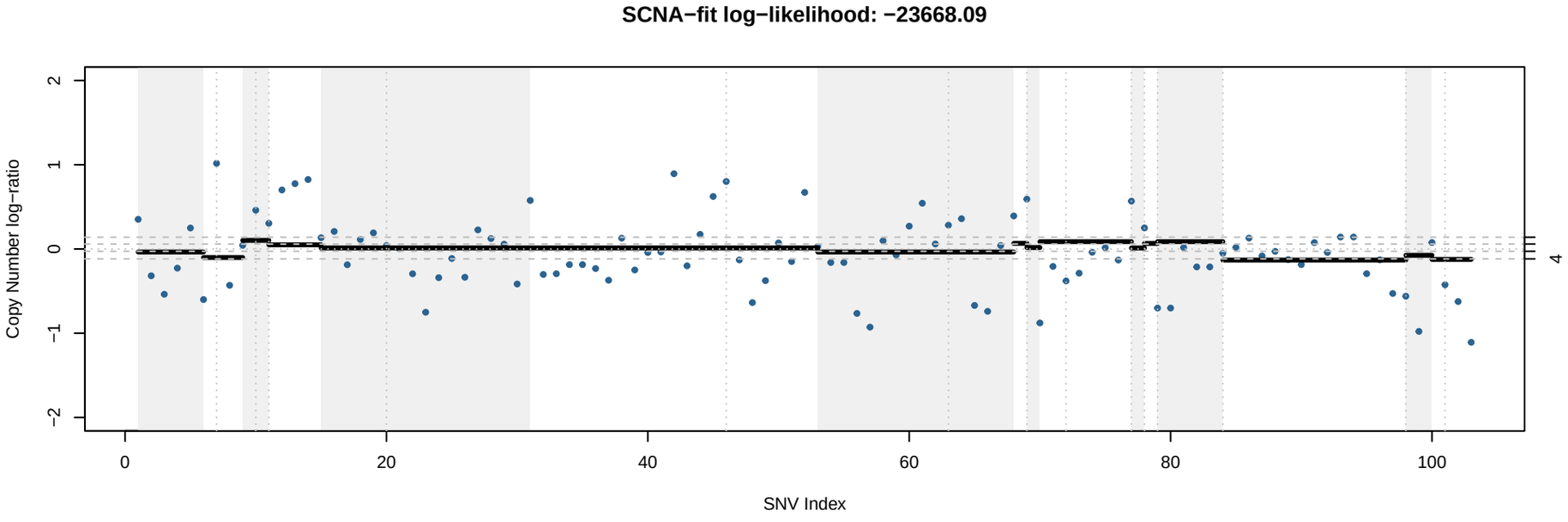

Coverage (log2)
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

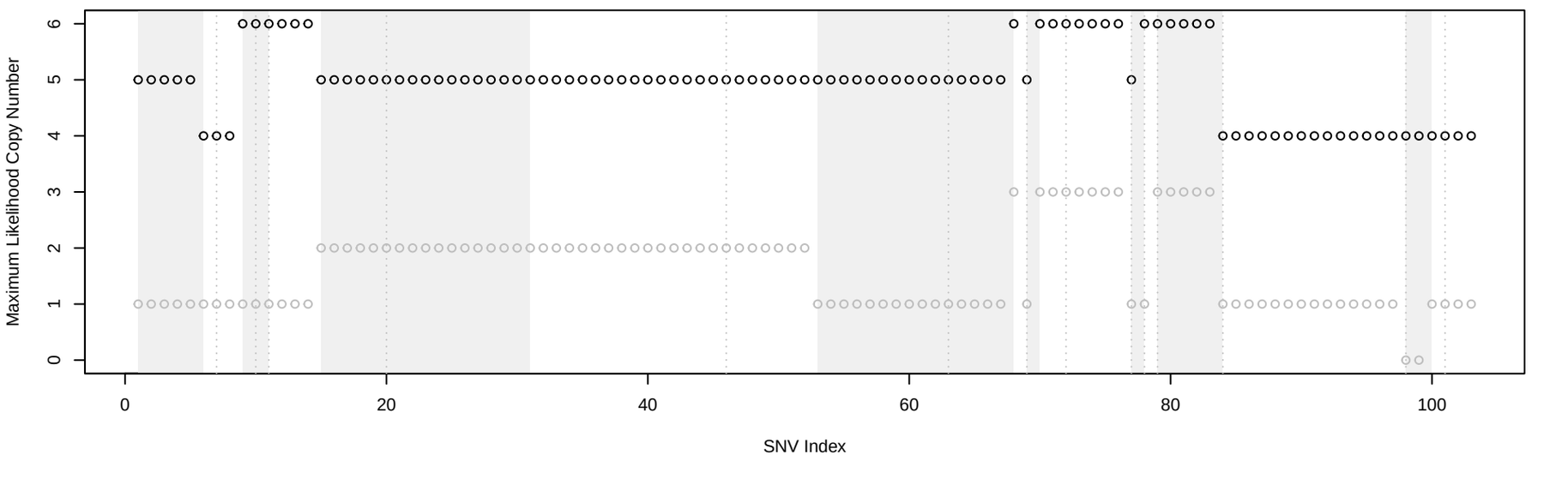

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
2m1
3m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

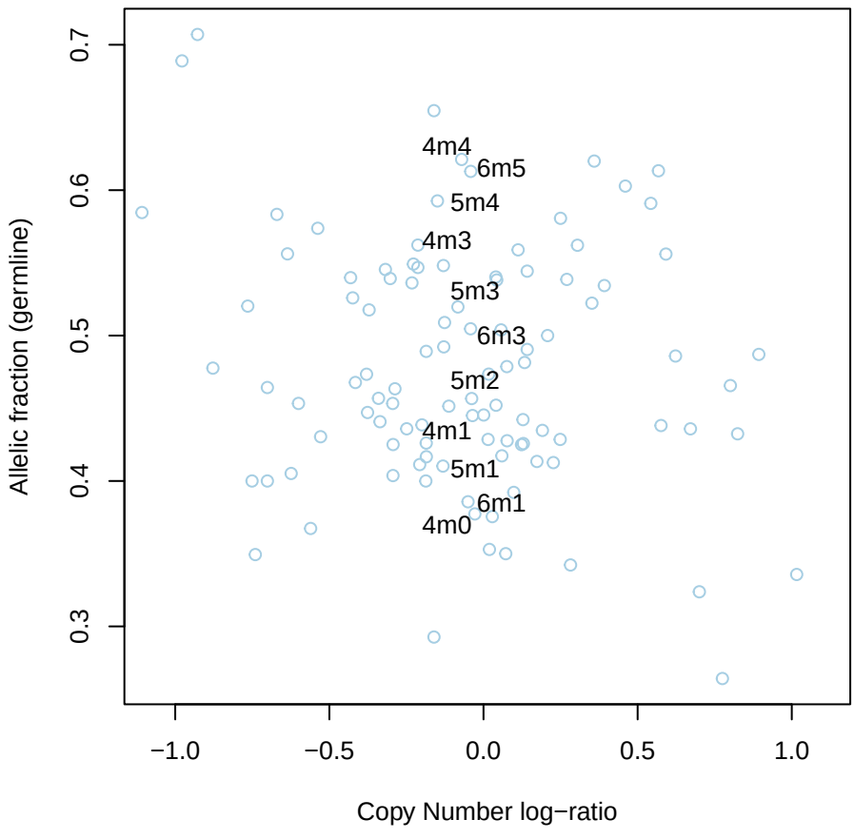

Power 0.8
Frequency
0
10
20
30
40
50
60
0.2
0.4
0.6
0.8
1.0
Cellular fraction

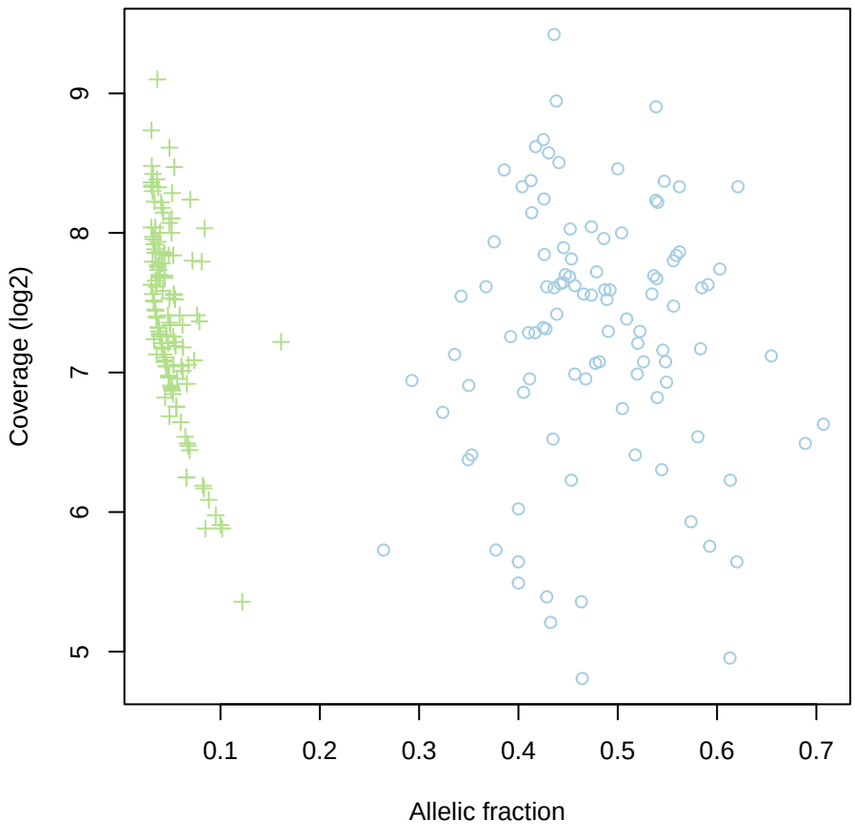

Purity: 0.15  Tumor ploidy: 5.308
4
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−0.10
−0.05
0.00
0.05
0.10
0.15
log2 ratio

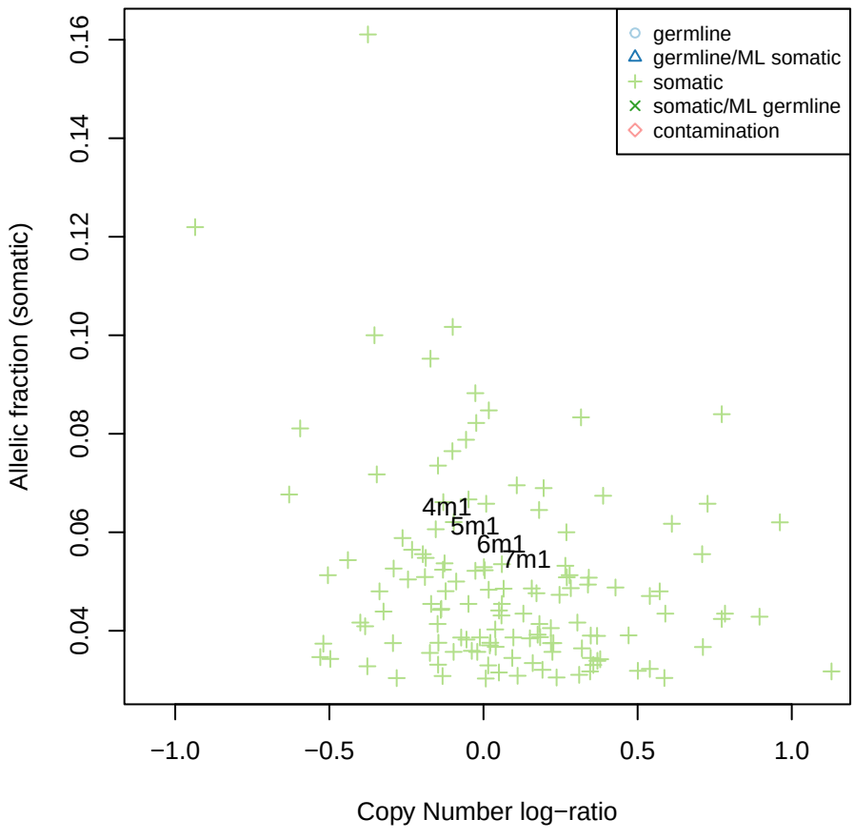

Purity: 0.15 Tumor ploidy: 5.308 SNV log−likelihood: −104.44 GoF: 97% Mean coverage: 187;674
1 2 3 4 5 6 7 9 11 13 15 17 18
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

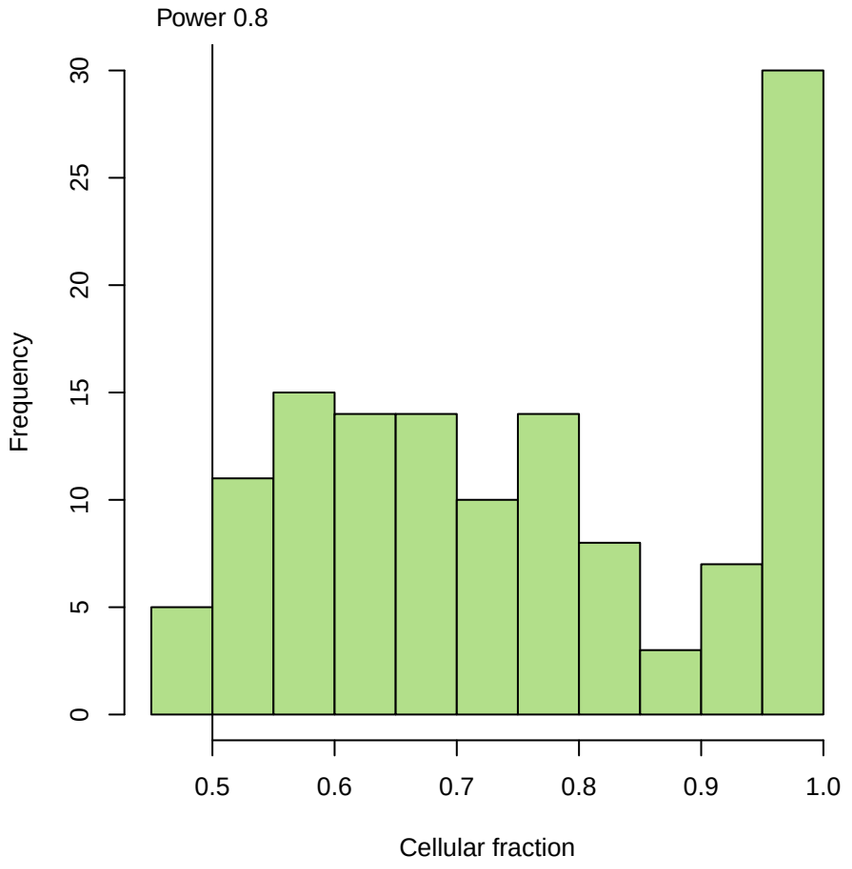

SCNA−fit log−likelihood: −23668.09
Copy Number log−ratio
−2 −1 0 1 2
4
0 20 40 60 80 100
SNV Index

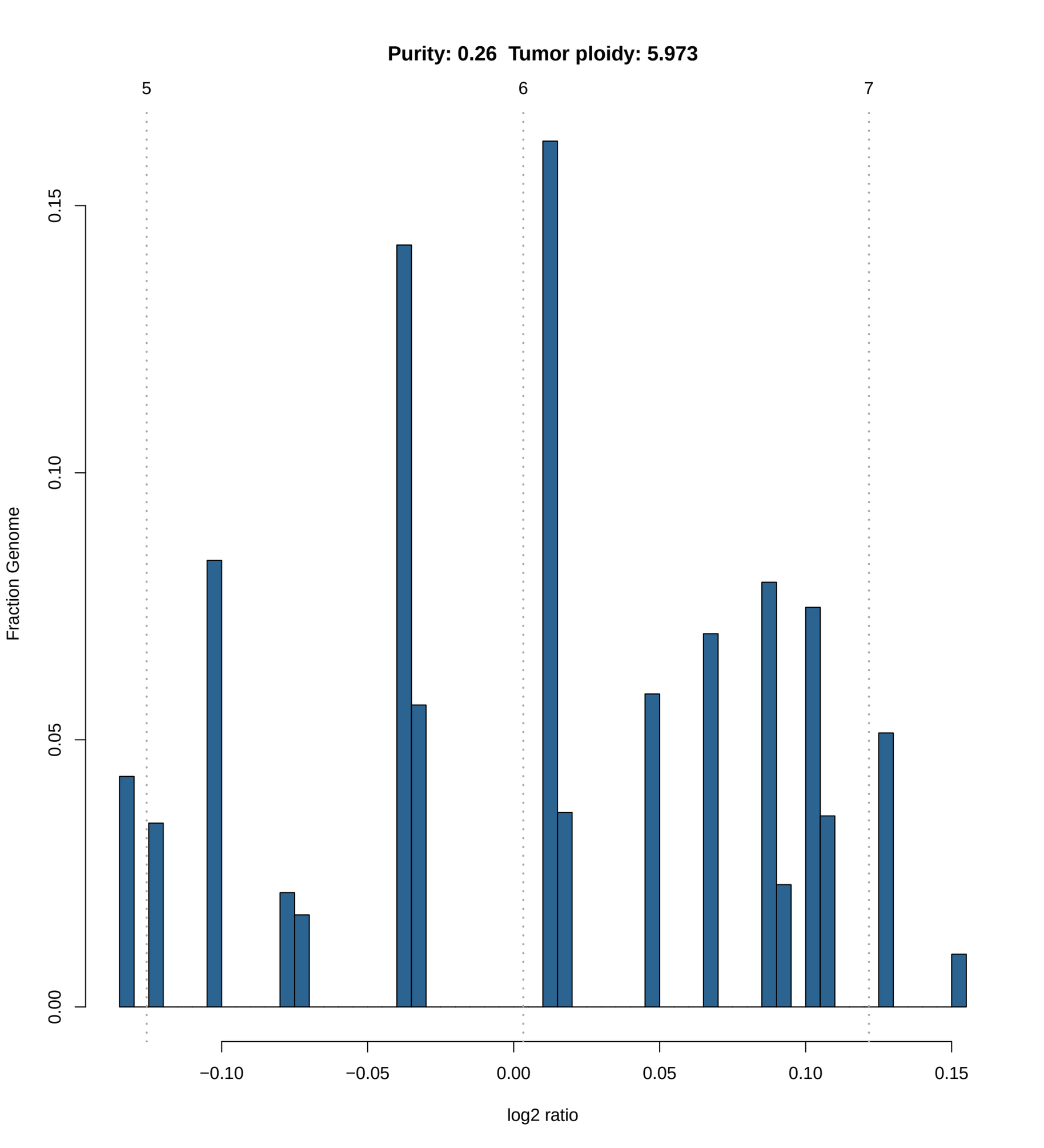

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100
SNV Index

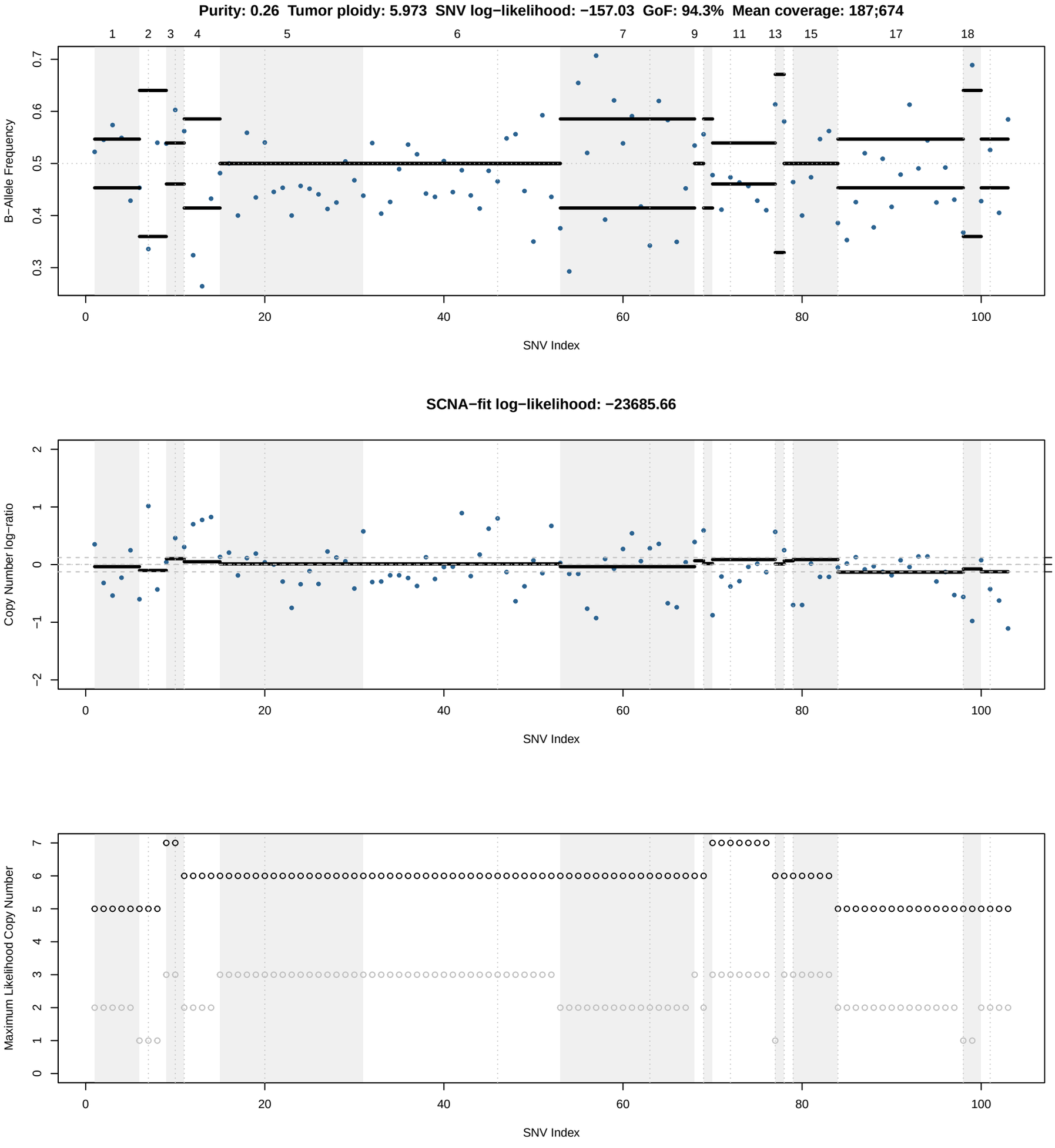

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
4m4
6m5
5m4
4m3
5m3
6m3
5m2
4m1
5m1
6m1
4m0
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

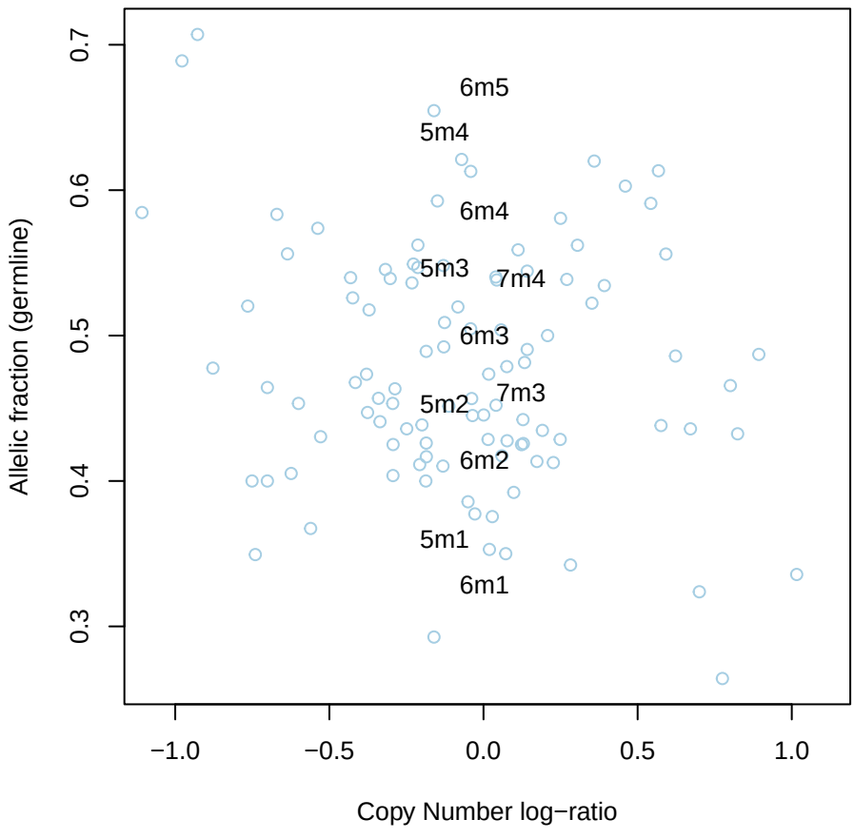

Coverage (log2)
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

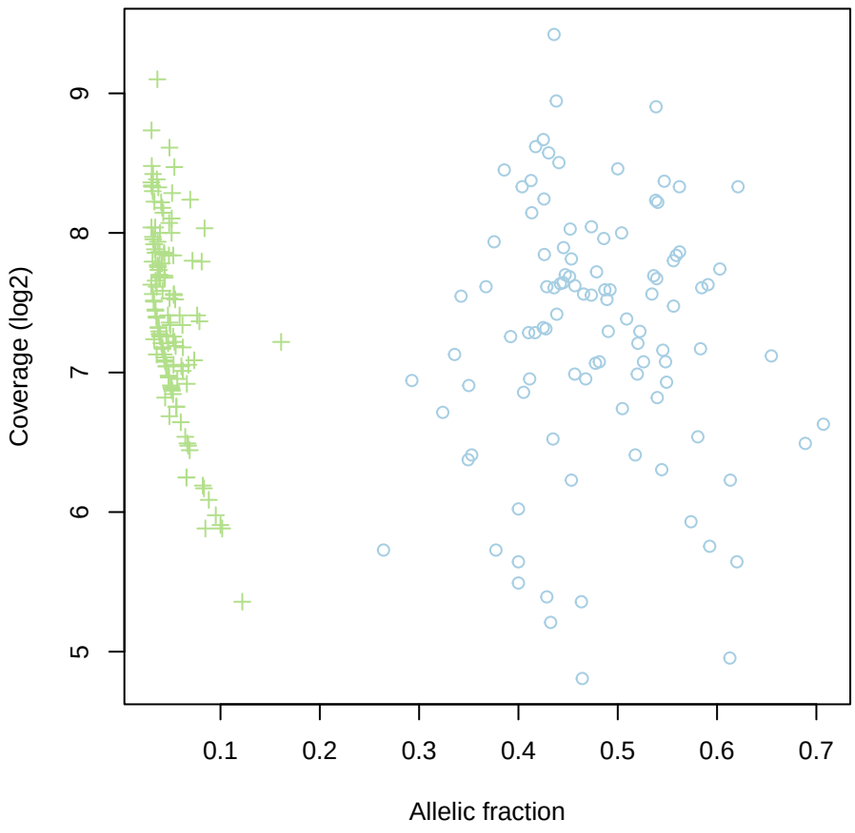

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
4m1
5m1
6m1
7m1
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

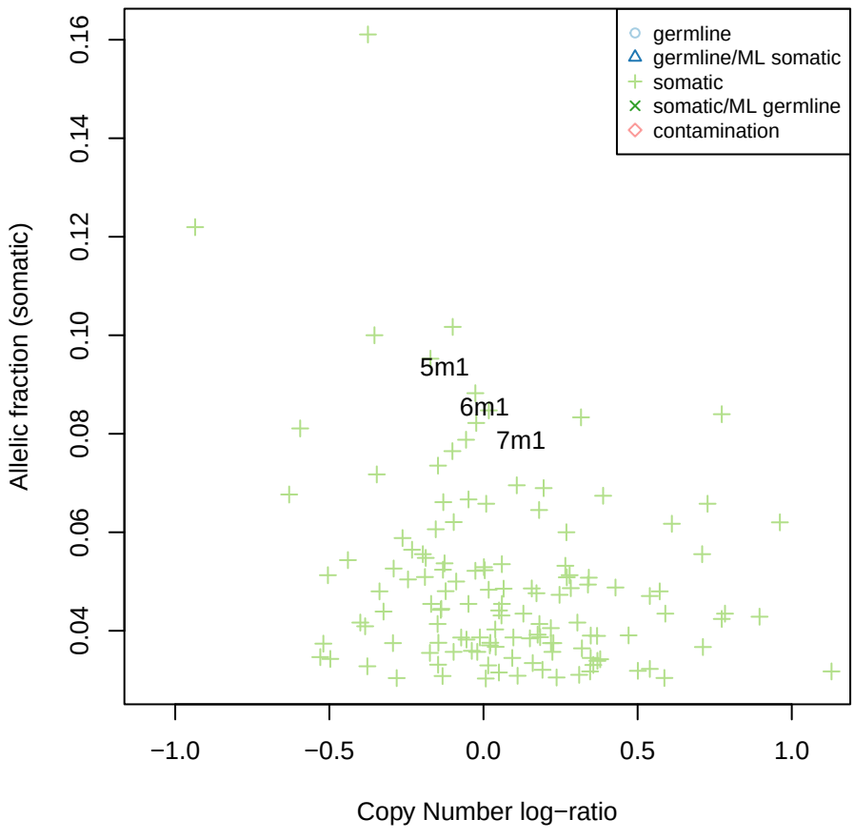

Power 0.8
Frequency
0
5
10
15
20
25
30
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

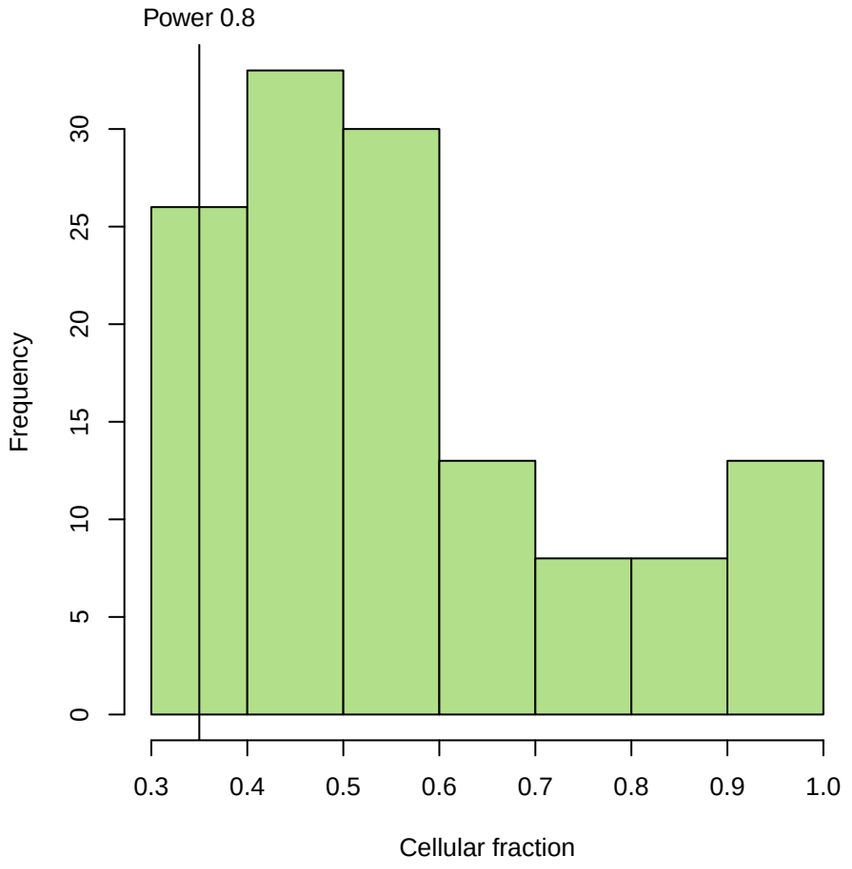

Purity: 0.26  Tumor ploidy: 5.973
5
6
7
0.15
0.10
0.05
0.00
Fraction Genome
−0.10
−0.05
0.00
0.05
0.10
0.15
log2 ratio

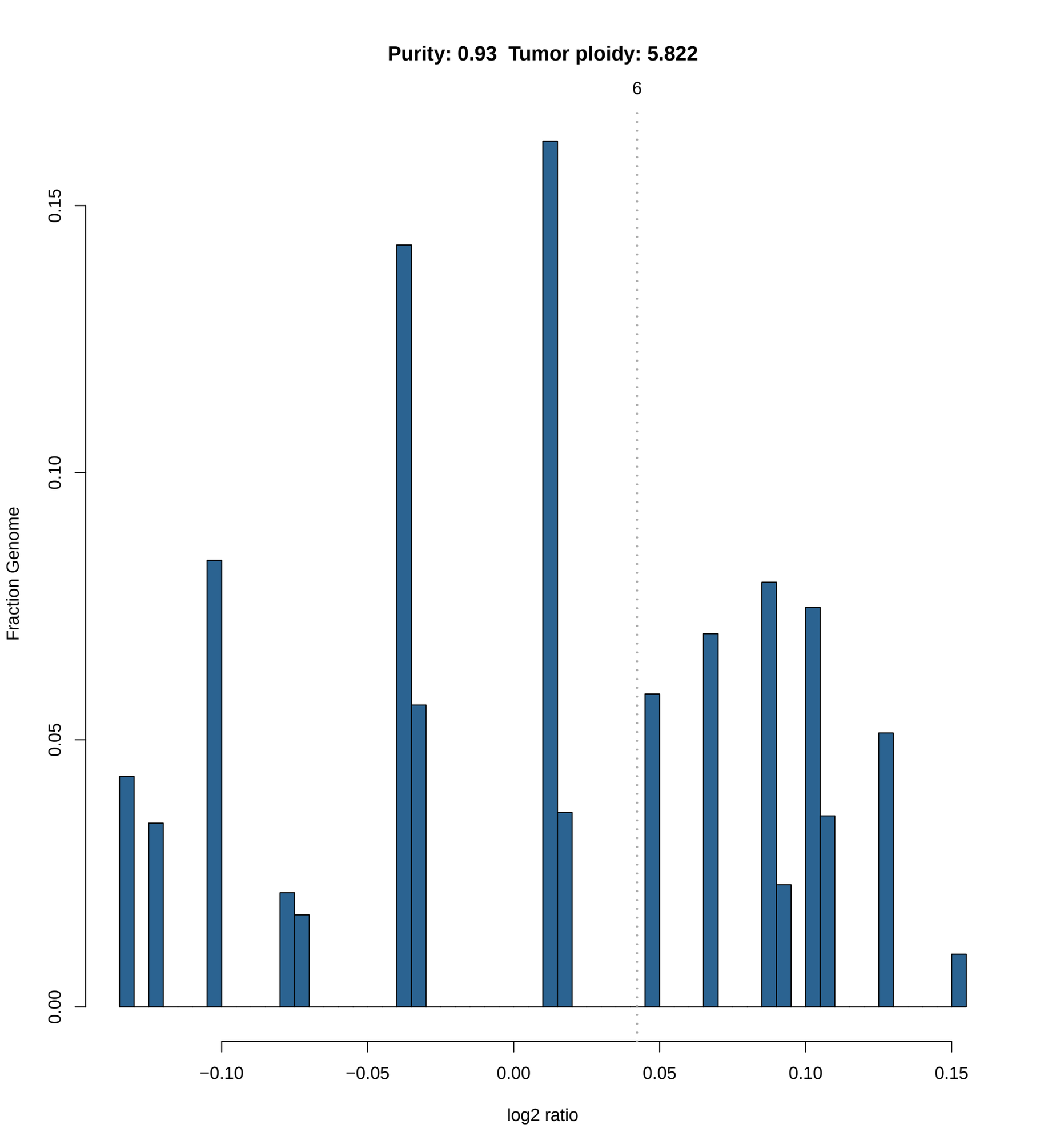

Purity: 0.26 Tumor ploidy: 5.973 SNV log−likelihood: −157.03 GoF: 94.3% Mean coverage: 187;674
1 2 3 4 5 6 7 9 11 13 15 17 18
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index
SCNA−fit log−likelihood: −23685.66
Copy Number log−ratio
−2 −1 0 1 2
5
0 20 40 60 80 100
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

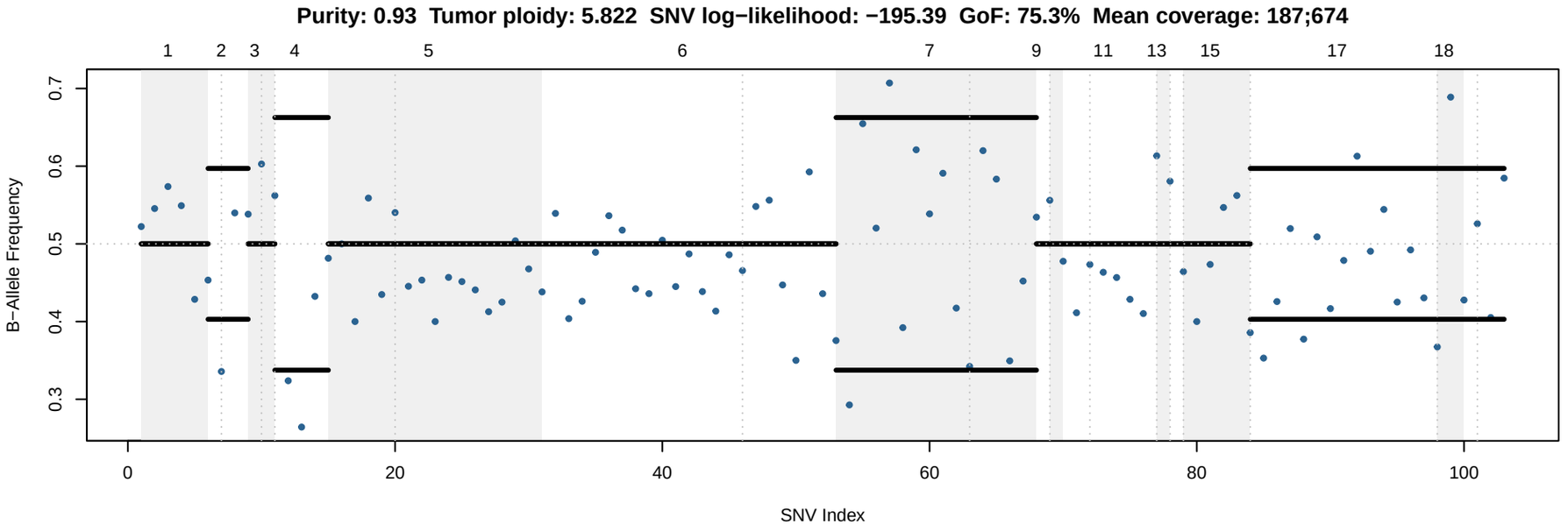

Allelic fraction (germline)
Copy Number log−ratio
6m5
5m4
6m4
5m3
7m4
6m3
5m2
7m3
6m2
5m1
6m1

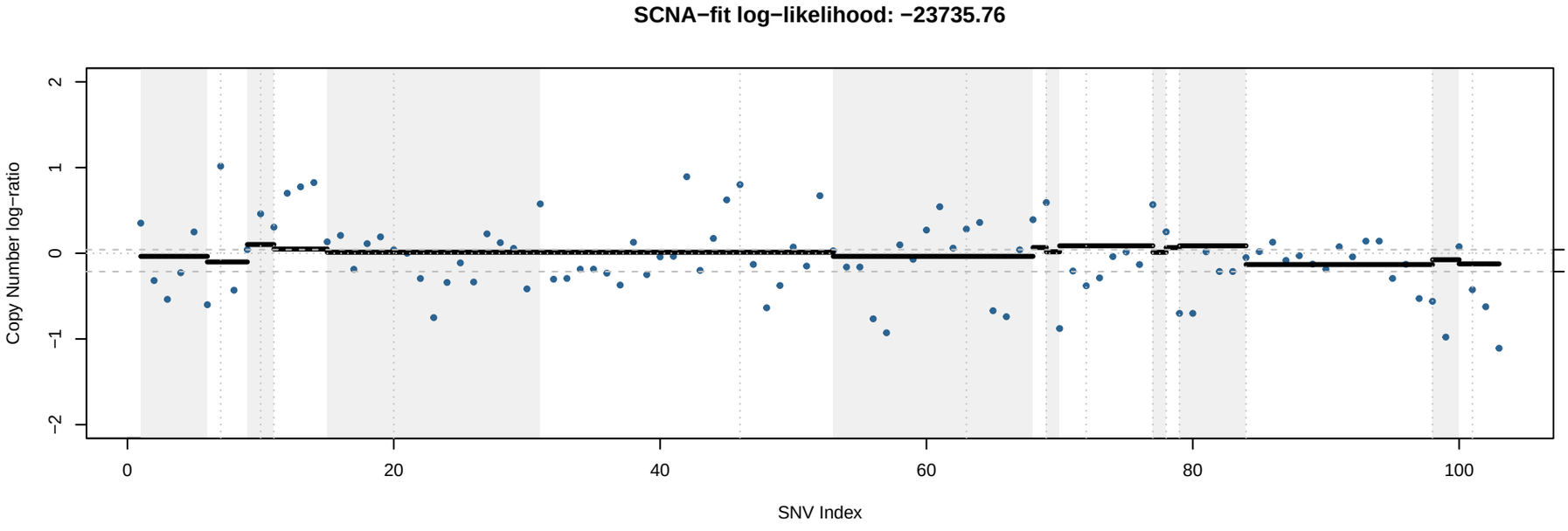

Coverage (log2)
Allelic fraction

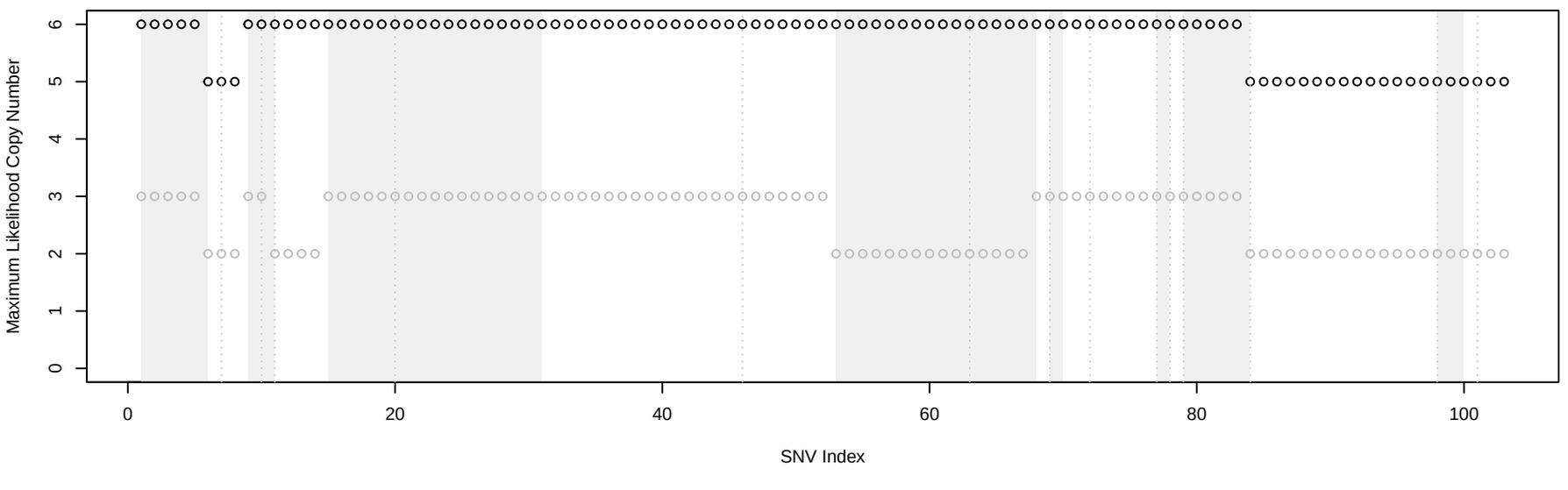

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
5m1
6m1
7m1

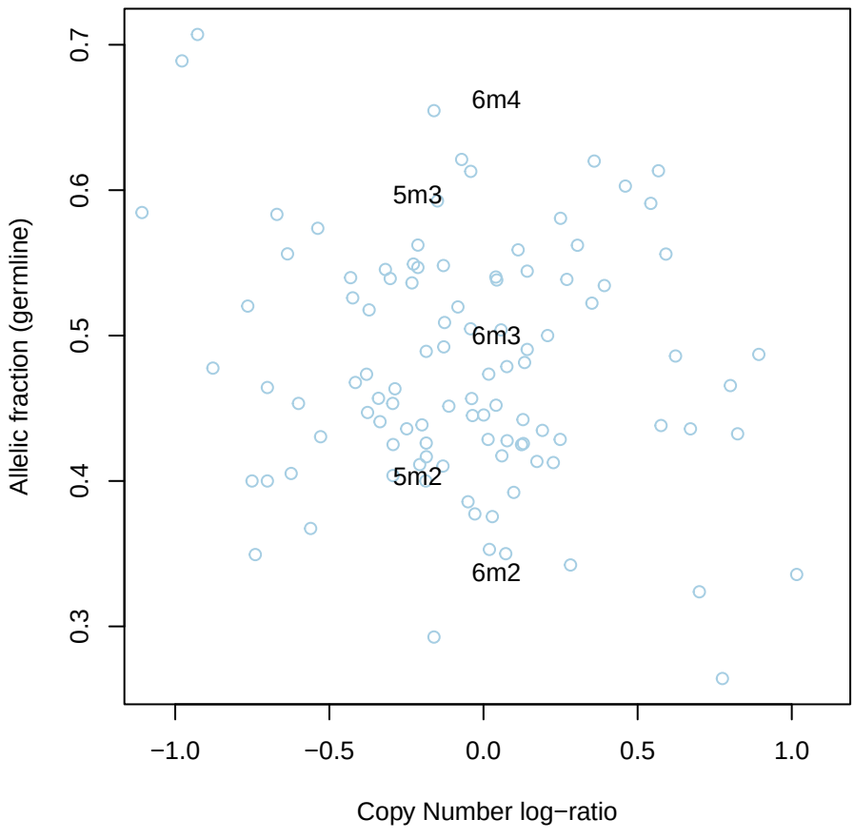

Power 0.8
Frequency
Cellular fraction

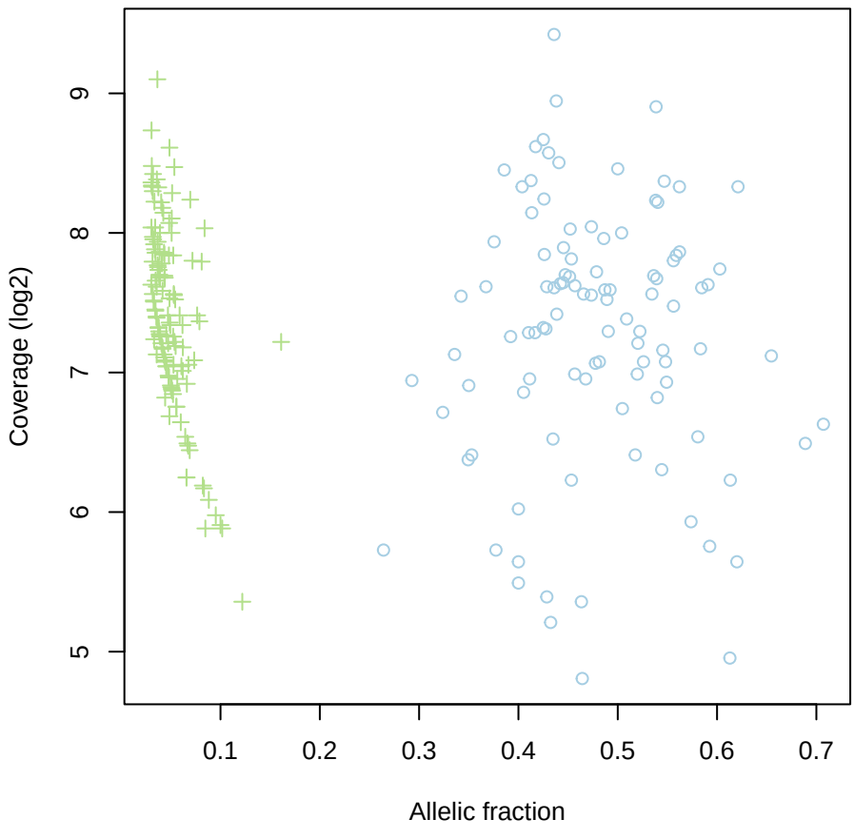

Purity: 0.93  Tumor ploidy: 5.822
6
0.15
0.10
0.05
0.00
Fraction Genome
−0.10
−0.05
0.00
0.05
0.10
0.15
log2 ratio

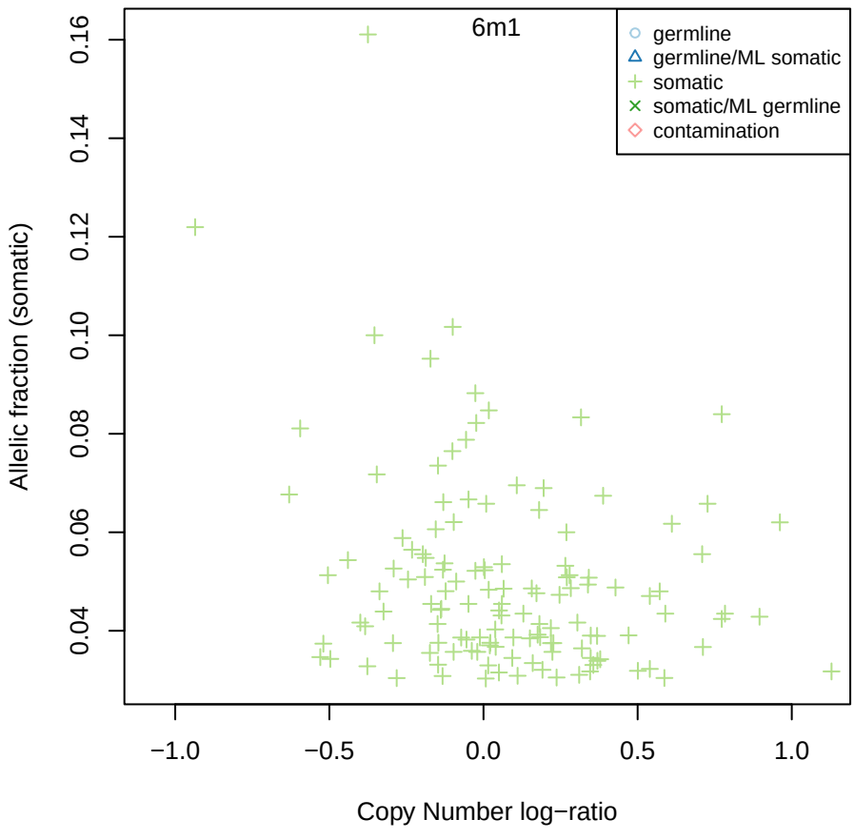

Purity: 0.93 Tumor ploidy: 5.822 SNV log−likelihood: −195.39 GoF: 75.3% Mean coverage: 187;674
1 2 3 4 5 6 7 9 11 13 15 17 18
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

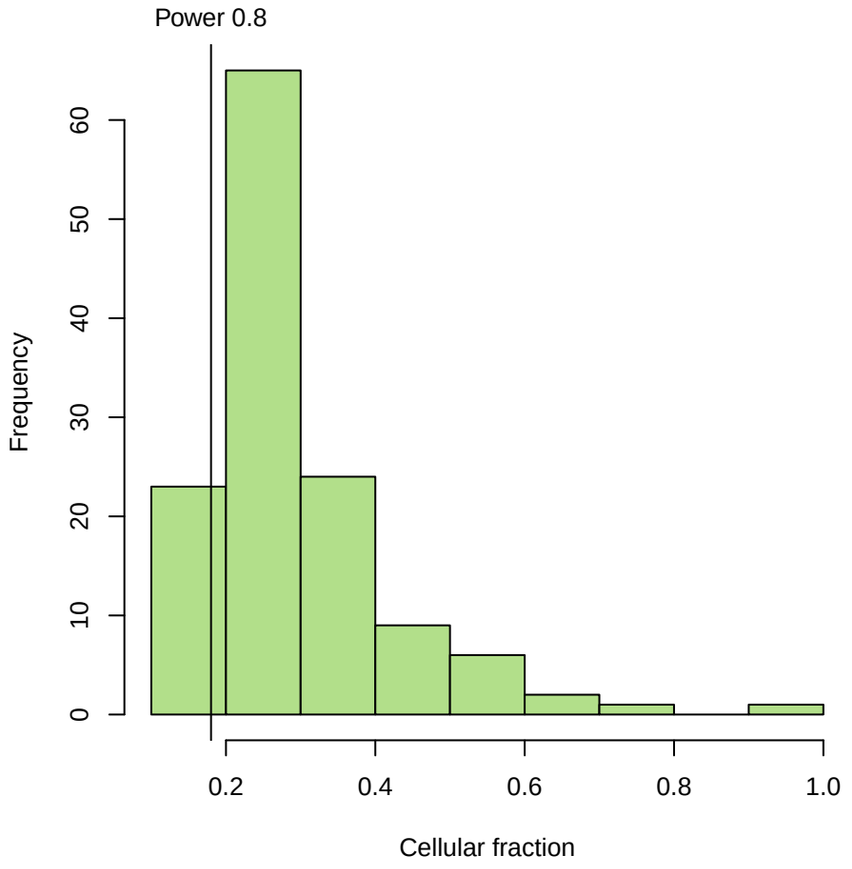

SCNA−fit log−likelihood: −23735.76
Copy Number log−ratio
−2 −1 0 1 2
5
0 20 40 60 80 100
SNV Index

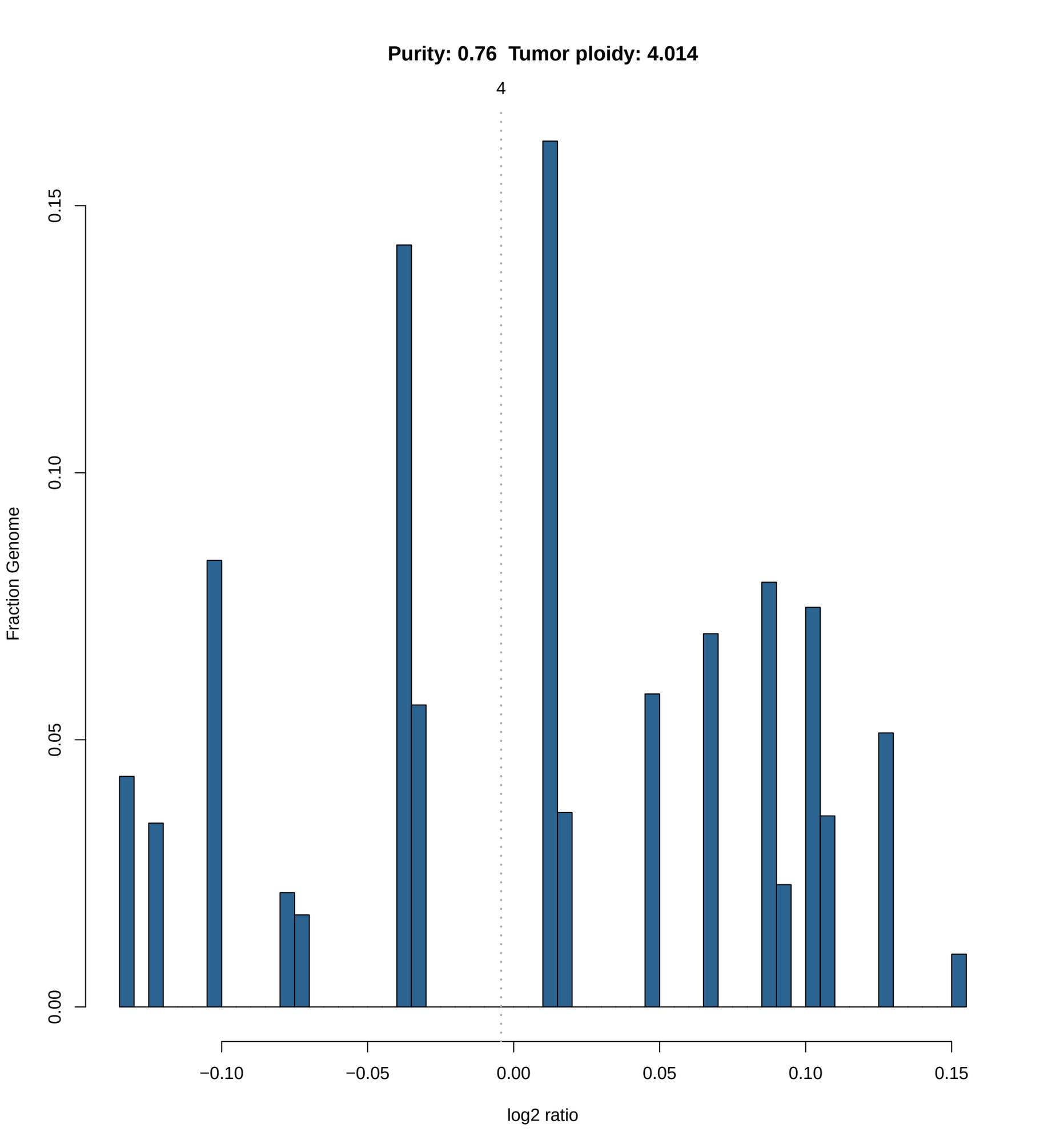

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100
SNV Index

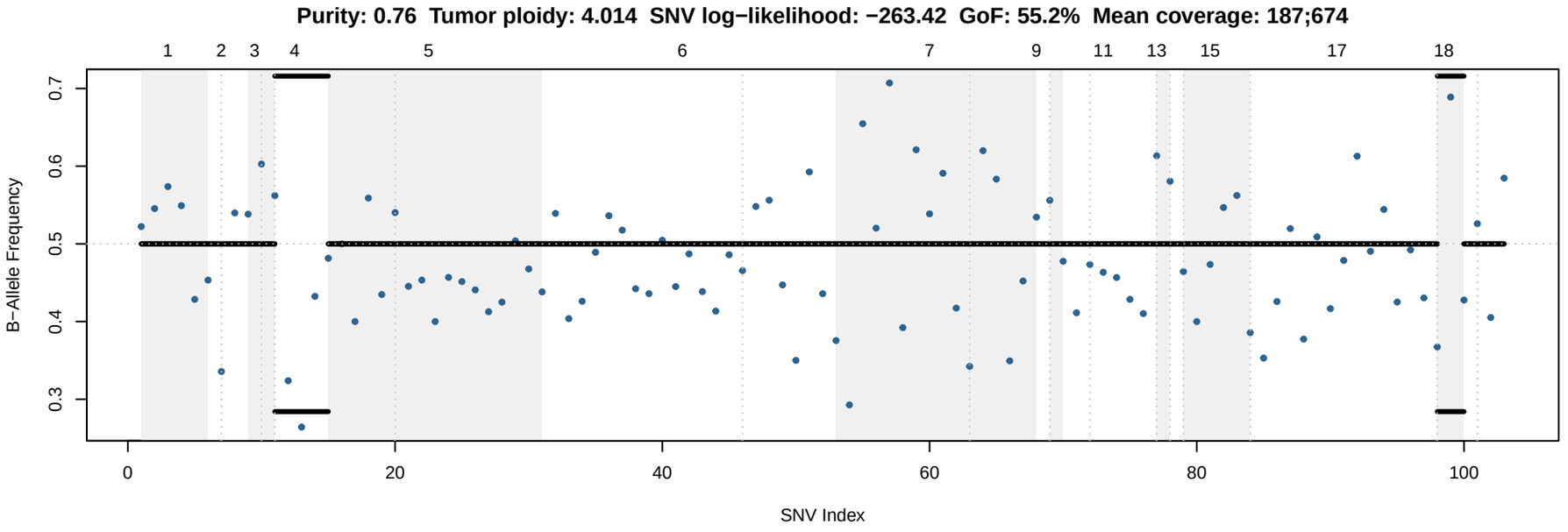

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
6m4
5m3
6m3
5m2
6m2
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

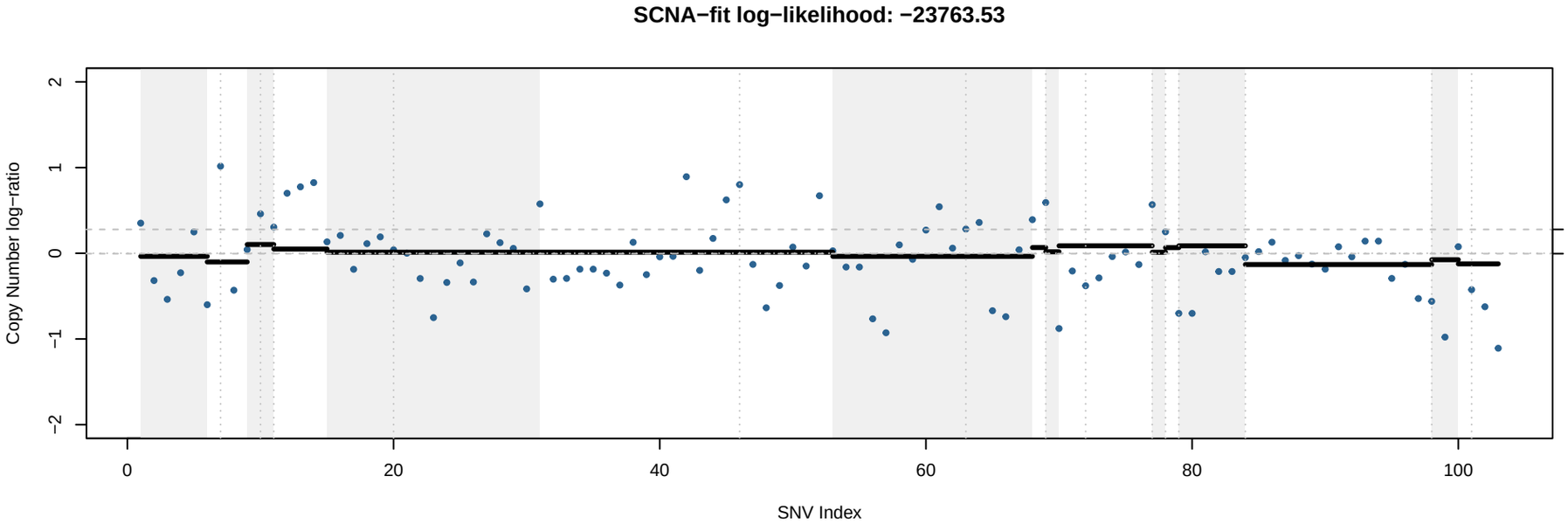

Coverage (log2)
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

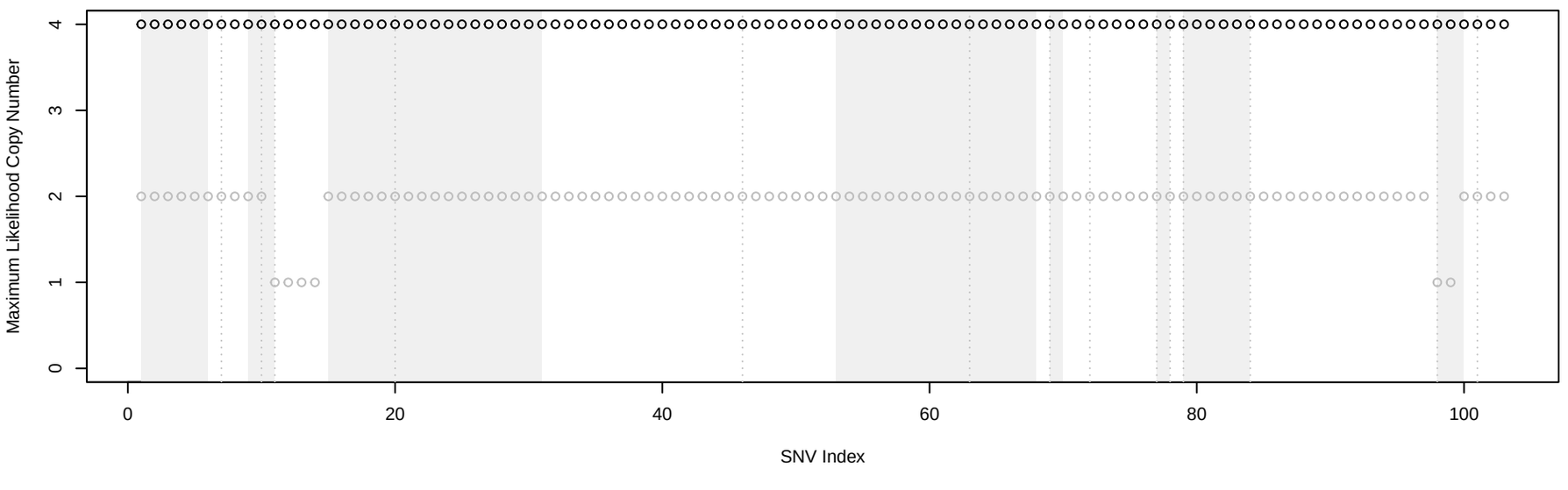

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
6m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

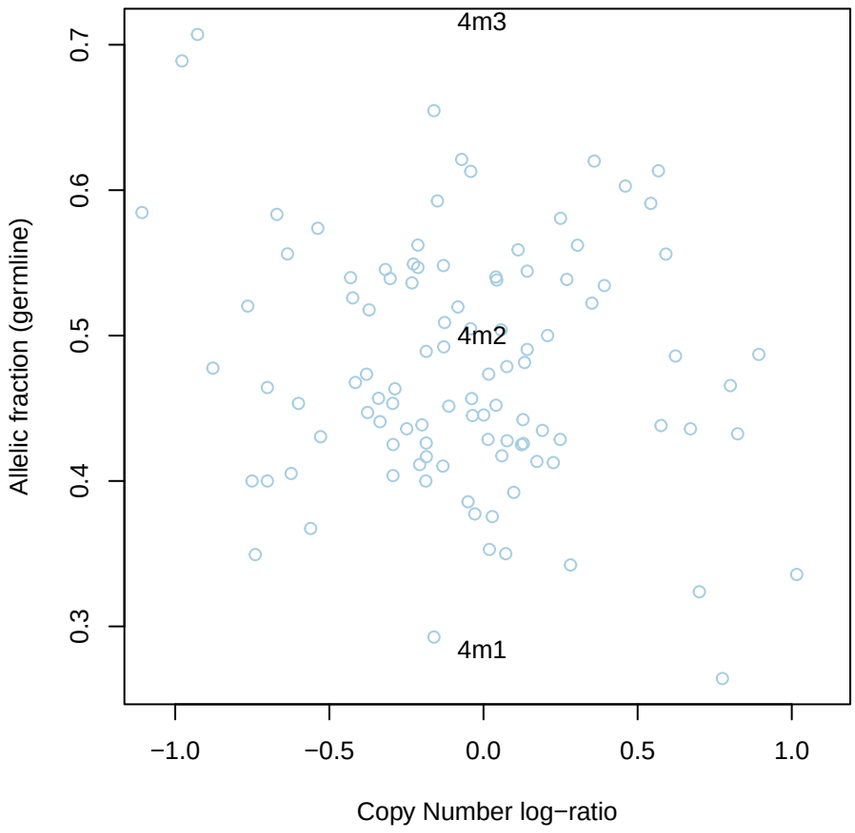

Power 0.8
Frequency
0
10
20
30
40
50
60
0.2
0.4
0.6
0.8
1.0
Cellular fraction

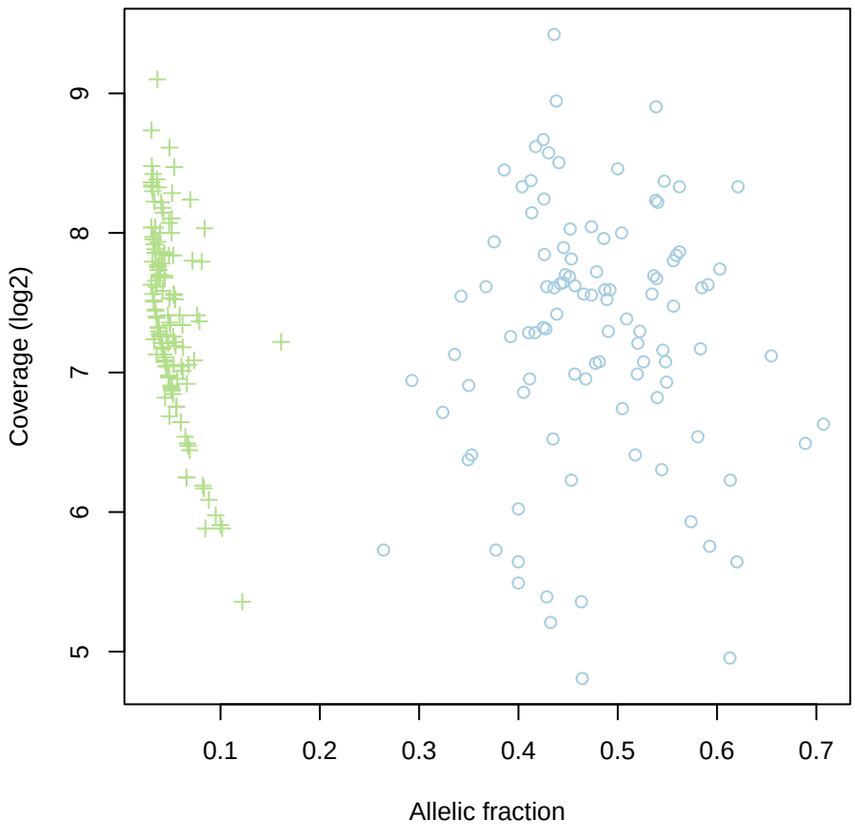

Purity: 0.76  Tumor ploidy: 4.014
4
Fraction Genome
0.00
0.05
0.10
0.15
−0.10
−0.05
0.00
0.05
0.10
0.15
log2 ratio

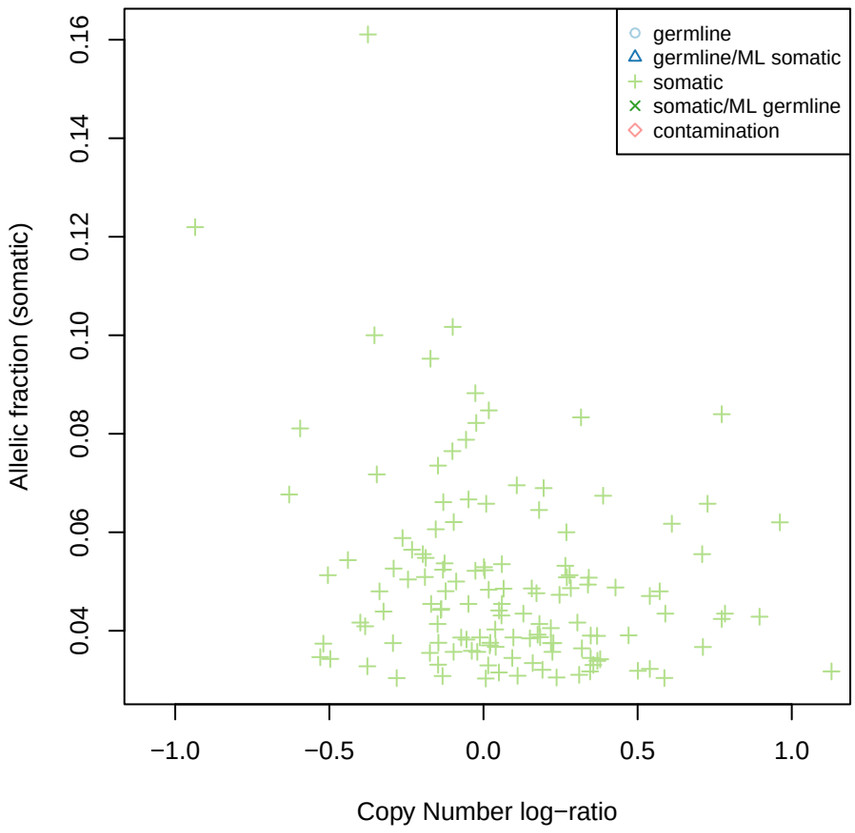

Purity: 0.76 Tumor ploidy: 4.014 SNV log−likelihood: −263.42 GoF: 55.2% Mean coverage: 187;674
1 2 3 4 5 6 7 9 11 13 15 17 18
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

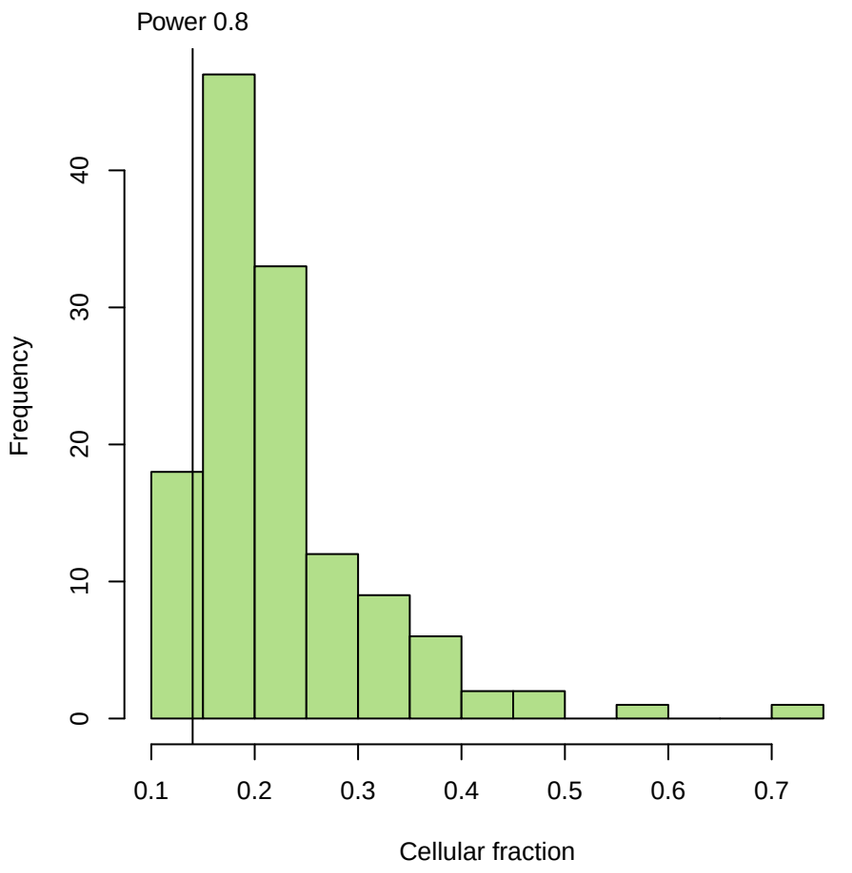

SCNA−fit log−likelihood: −23763.53
Copy Number log−ratio
−2 −1 0 1 2
4
0 20 40 60 80 100
SNV Index

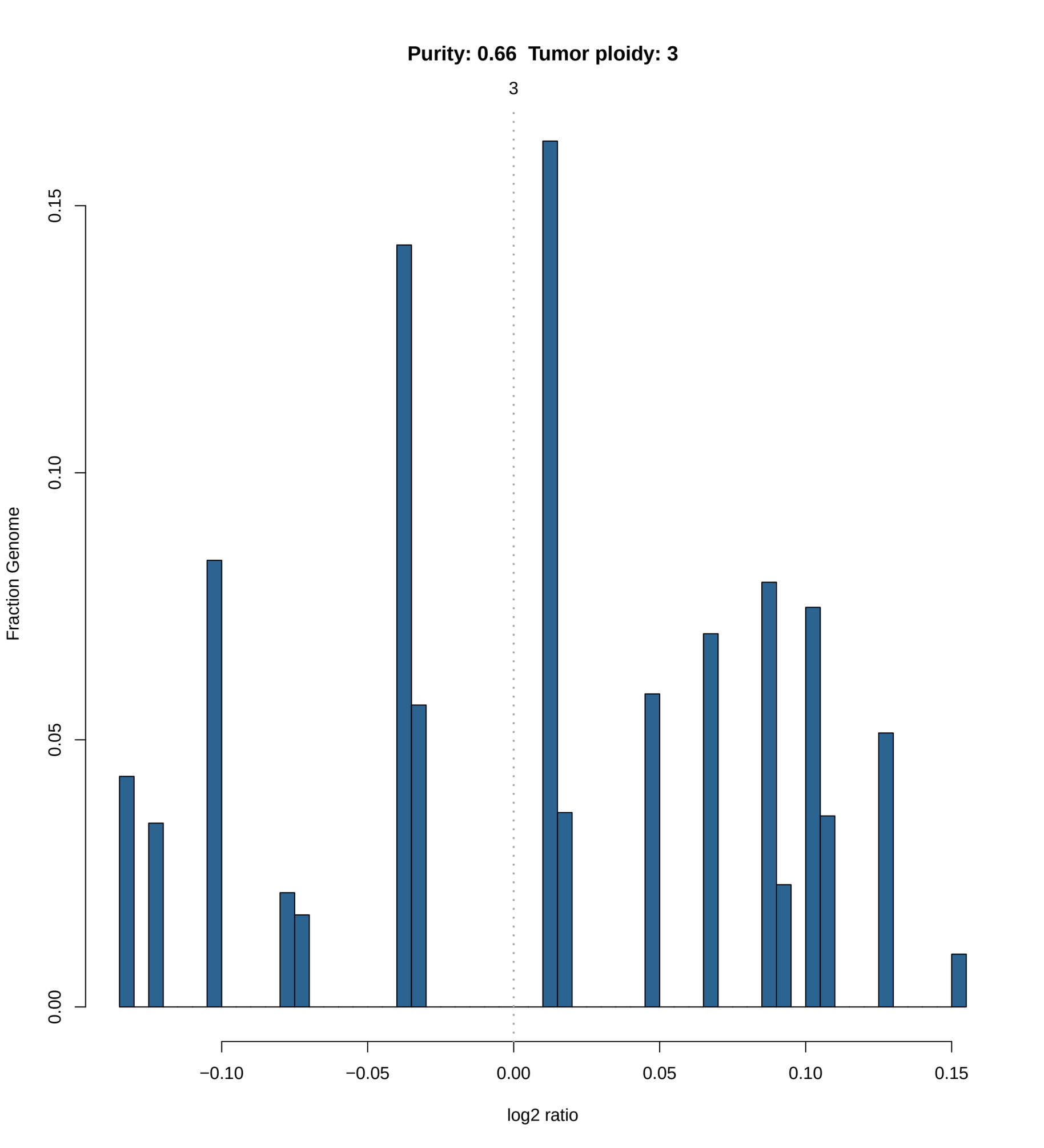

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100
SNV Index

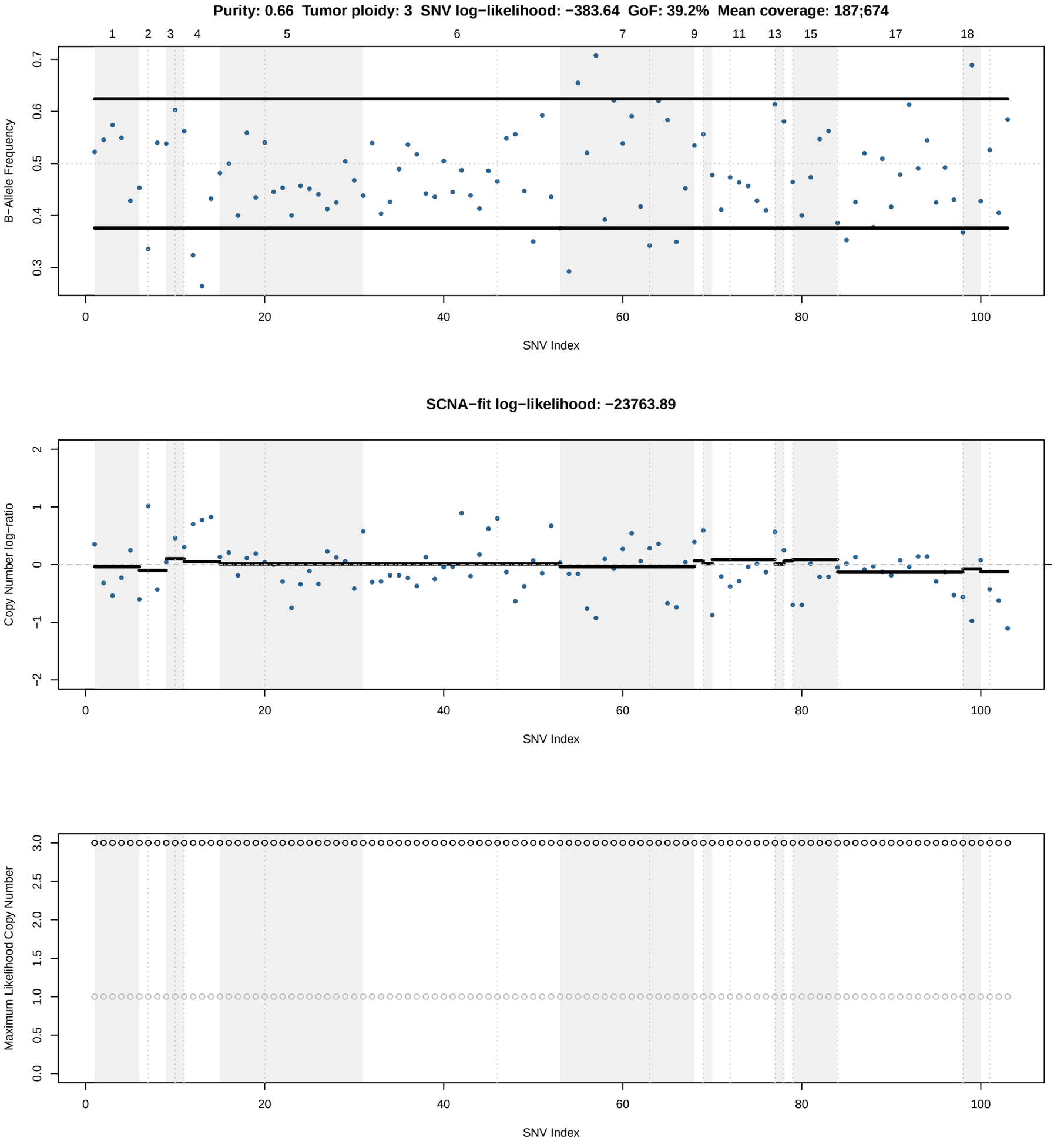

4m3
4m2
4m1
Allelic fraction (germline)
Copy Number log−ratio
0.3
0.4
0.5
0.6
0.7
−1.0
−0.5
0.0
0.5
1.0

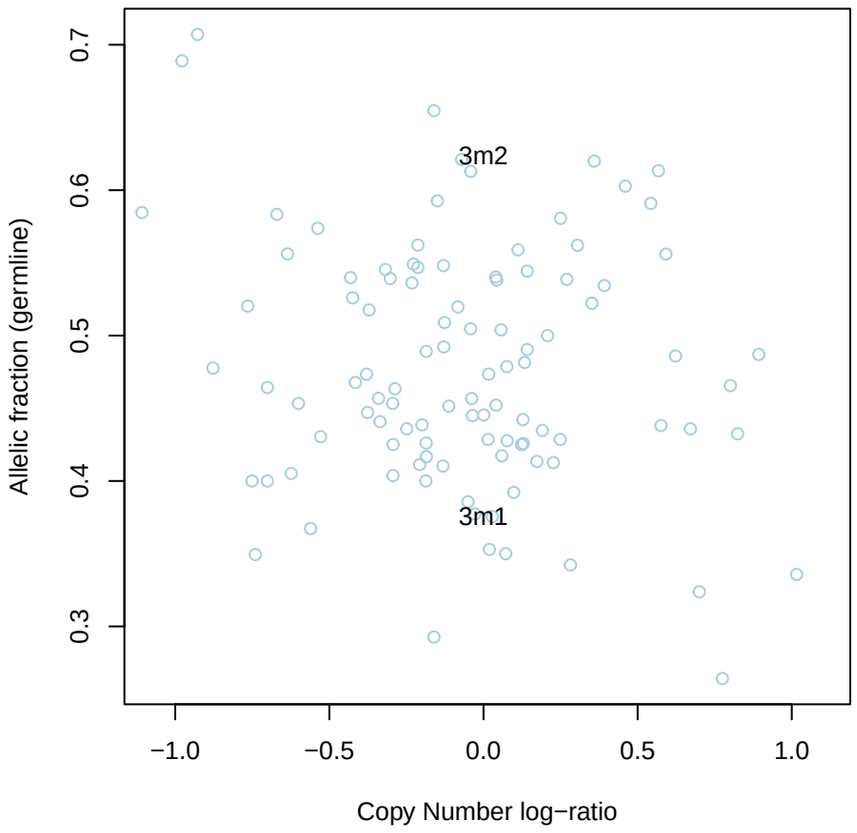

Coverage (log2)
Allelic fraction
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
0.7

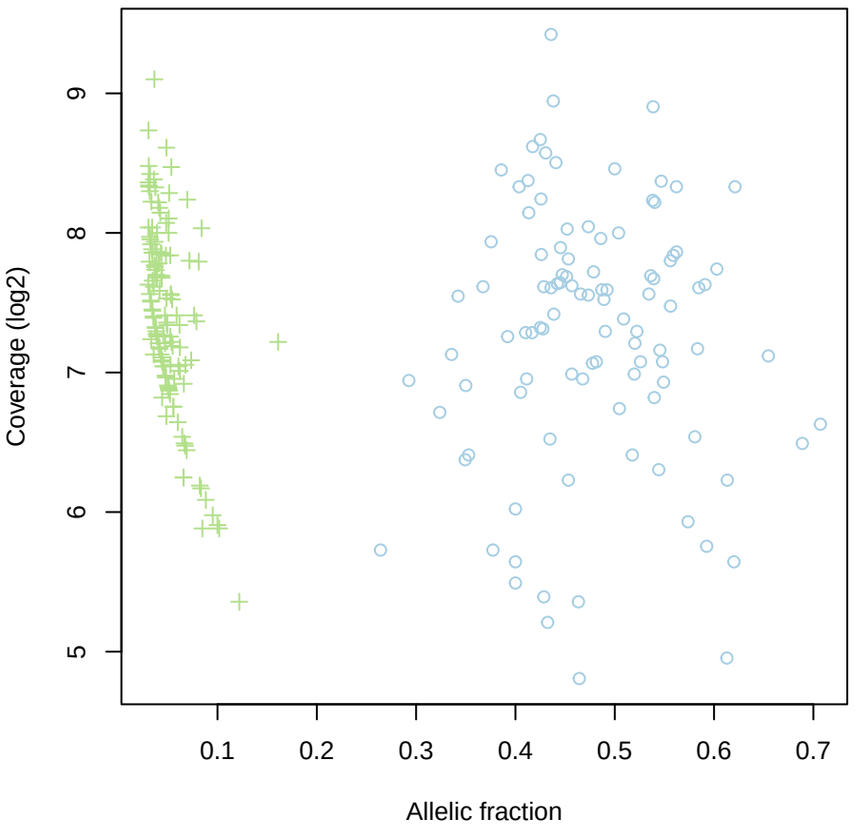

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
0.12
0.14
0.16
−1.0
−0.5
0.0
0.5
1.0

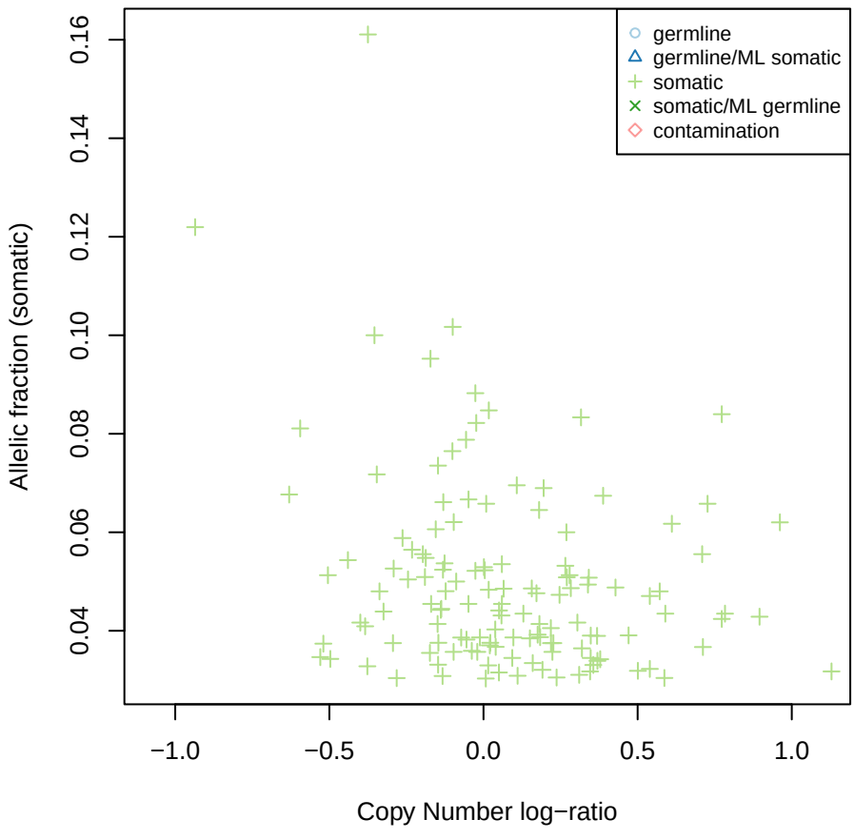

Power 0.8
Frequency
Cellular fraction
0
10
20
30
40
0.1
0.2
0.3
0.4
0.5
0.6
0.7

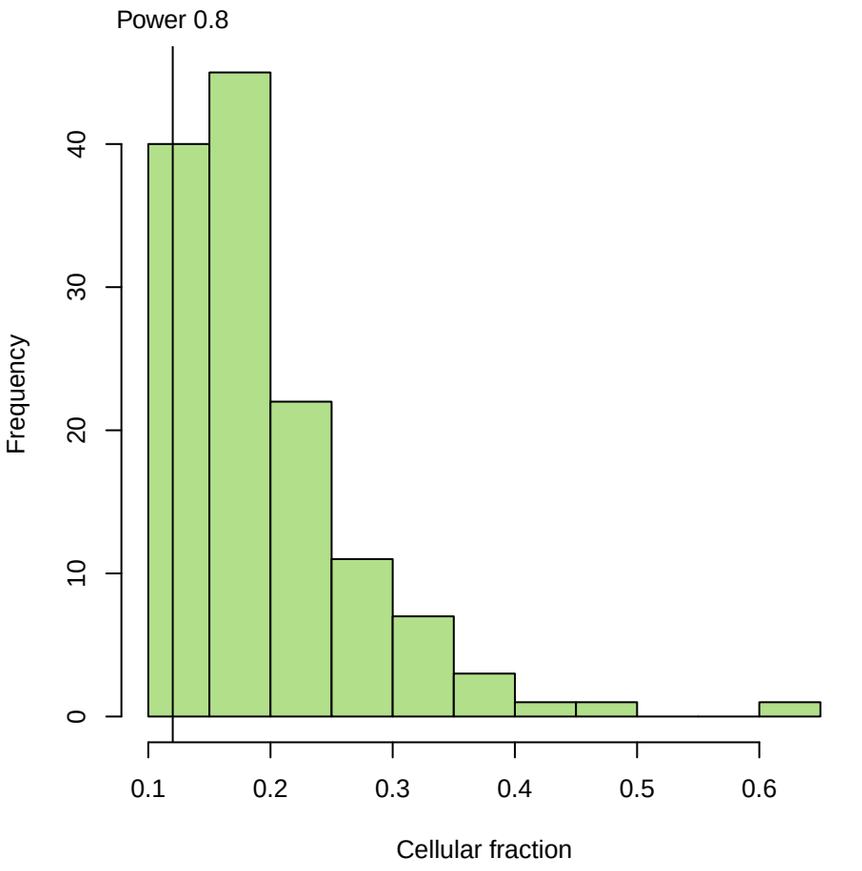

Purity: 0.66  Tumor ploidy: 3
3
0.15
0.10
0.05
0.00
Fraction Genome
−0.10
−0.05
0.00
0.05
0.10
0.15
log2 ratio

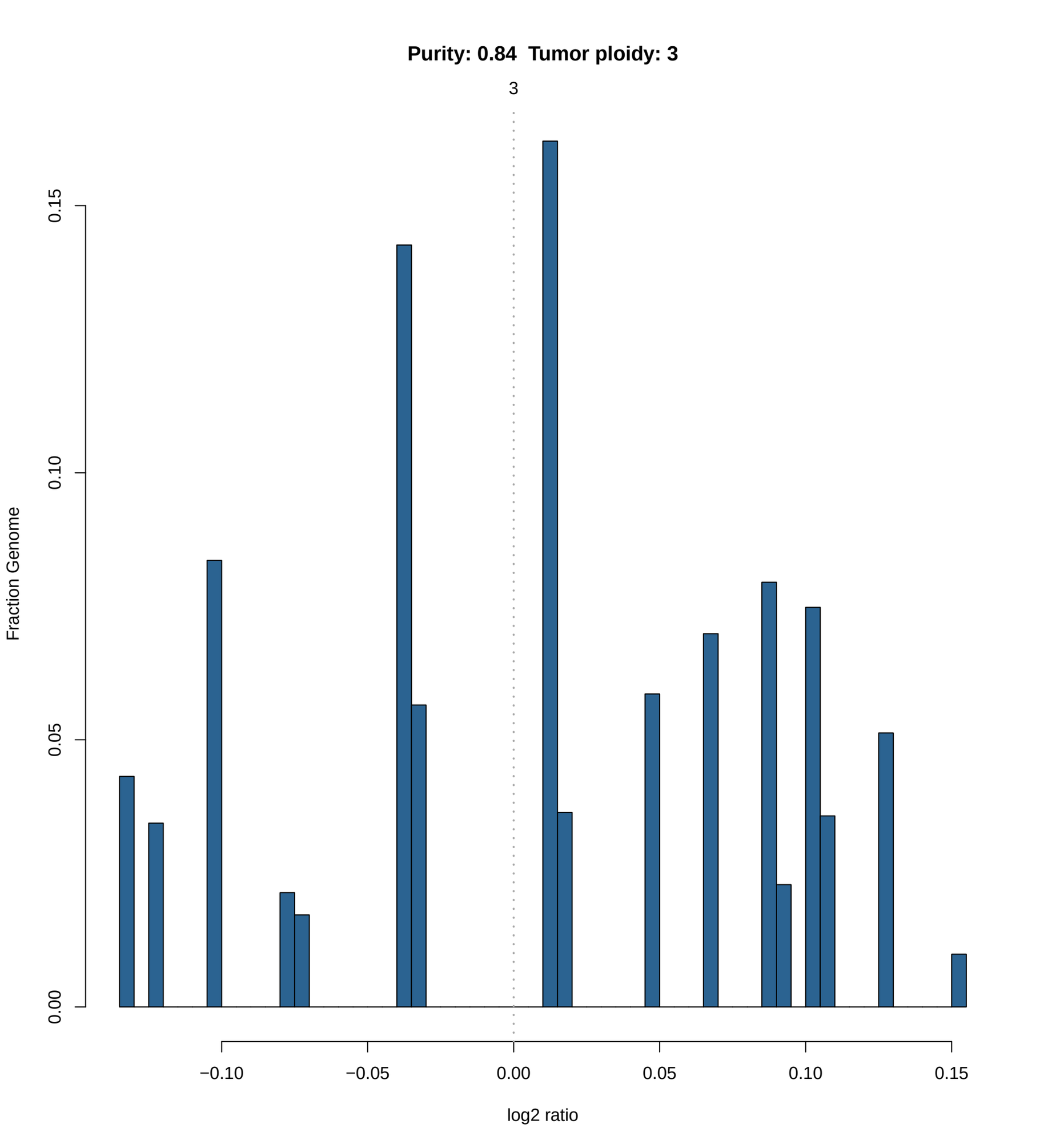

Purity: 0.66 Tumor ploidy: 3 SNV log−likelihood: −383.64 GoF: 39.2% Mean coverage: 187;674
1 2 3 4 5 6 7 9 11 13 15 17 18
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index
SCNA−fit log−likelihood: −23763.89
Copy Number log−ratio
−2 −1 0 1 2
3
0 20 40 60 80 100
SNV Index
Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 20 40 60 80 100
SNV Index

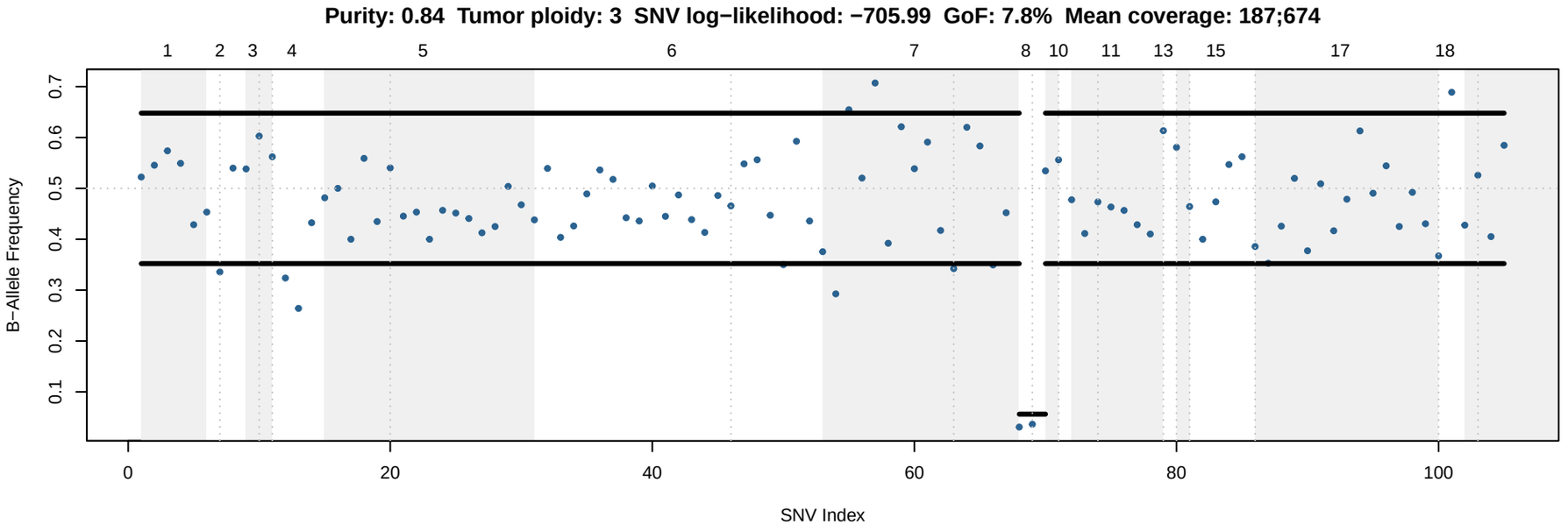

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
3m2
3m1
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

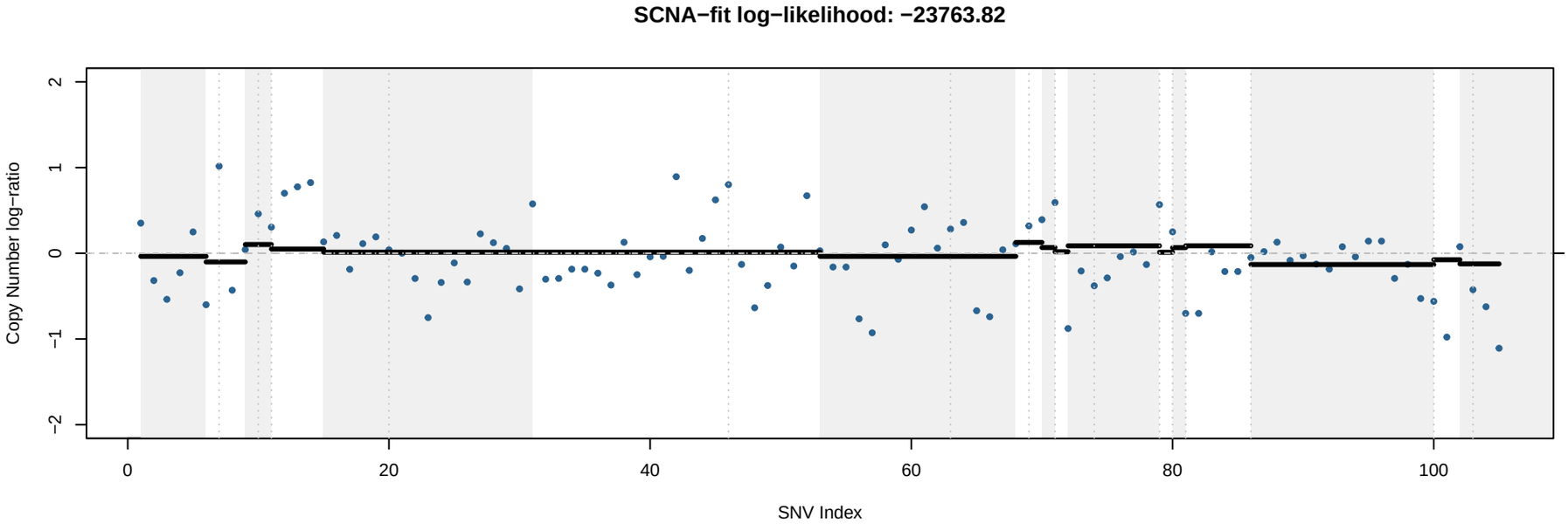

Coverage (log2)
5
6
7
8
9
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

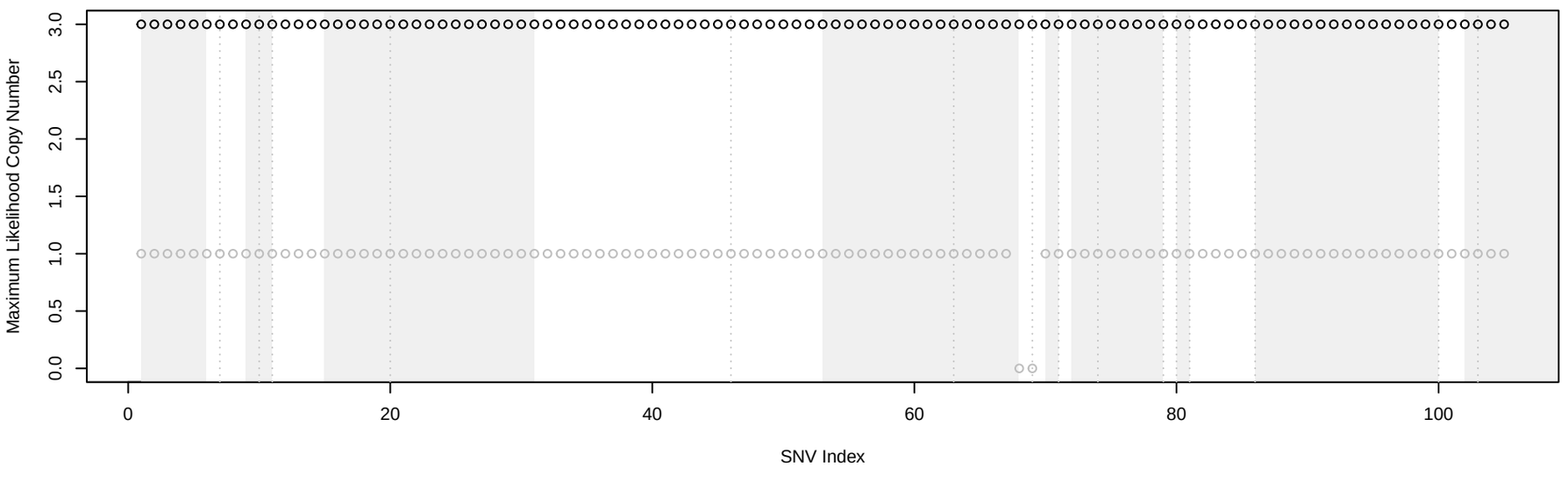

Allelic fraction (somatic)
0.04
0.06
0.08
0.10
0.12
0.14
0.16
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

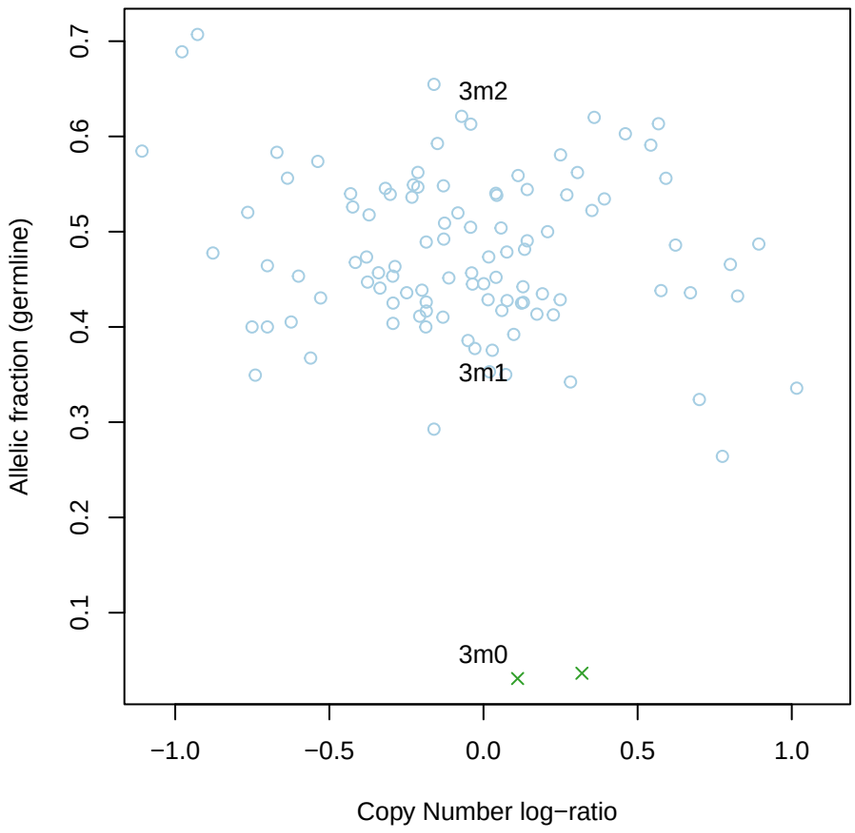

Power 0.8
Frequency
0
10
20
30
40
0.1
0.2
0.3
0.4
0.5
0.6
Cellular fraction

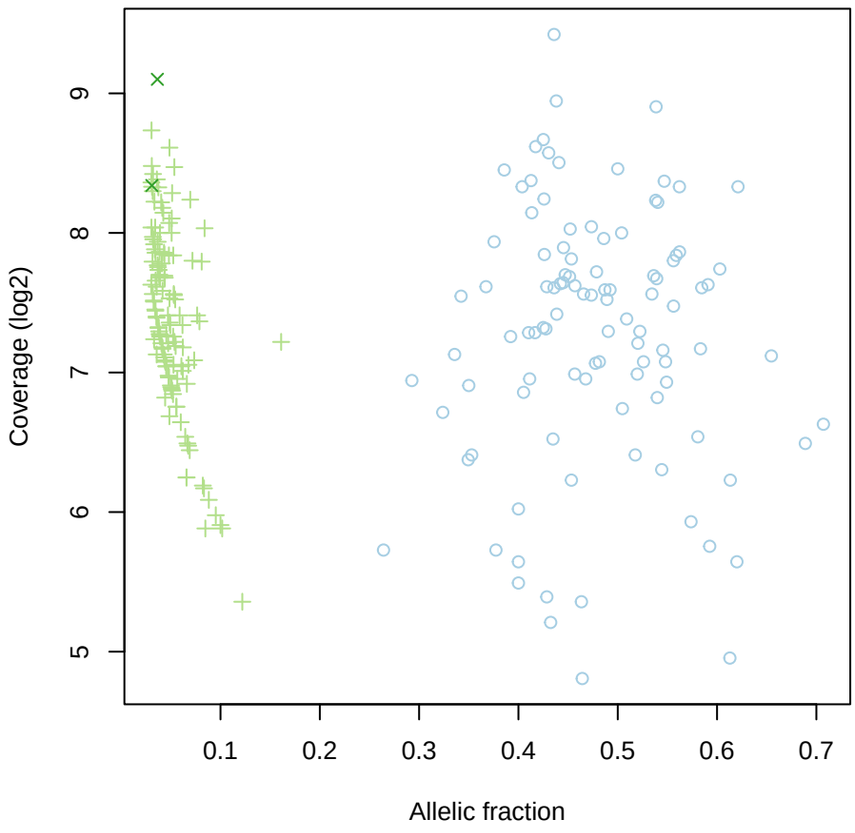

Purity: 0.84  Tumor ploidy: 3
3
0.15
0.10
0.05
0.00
Fraction Genome
−0.10
−0.05
0.00
0.05
0.10
0.15
log2 ratio

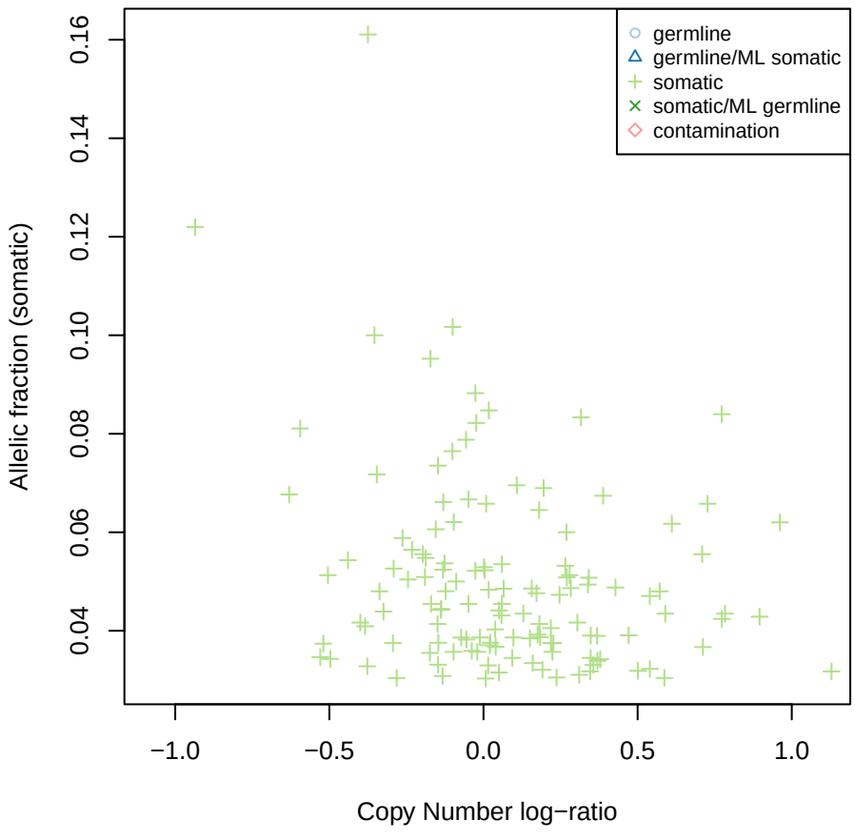

Purity: 0.84 Tumor ploidy: 3 SNV log−likelihood: −705.99 GoF: 7.8% Mean coverage: 187;674
1 2 3 4 5 6 7 8 10 11 13 15 17 18
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

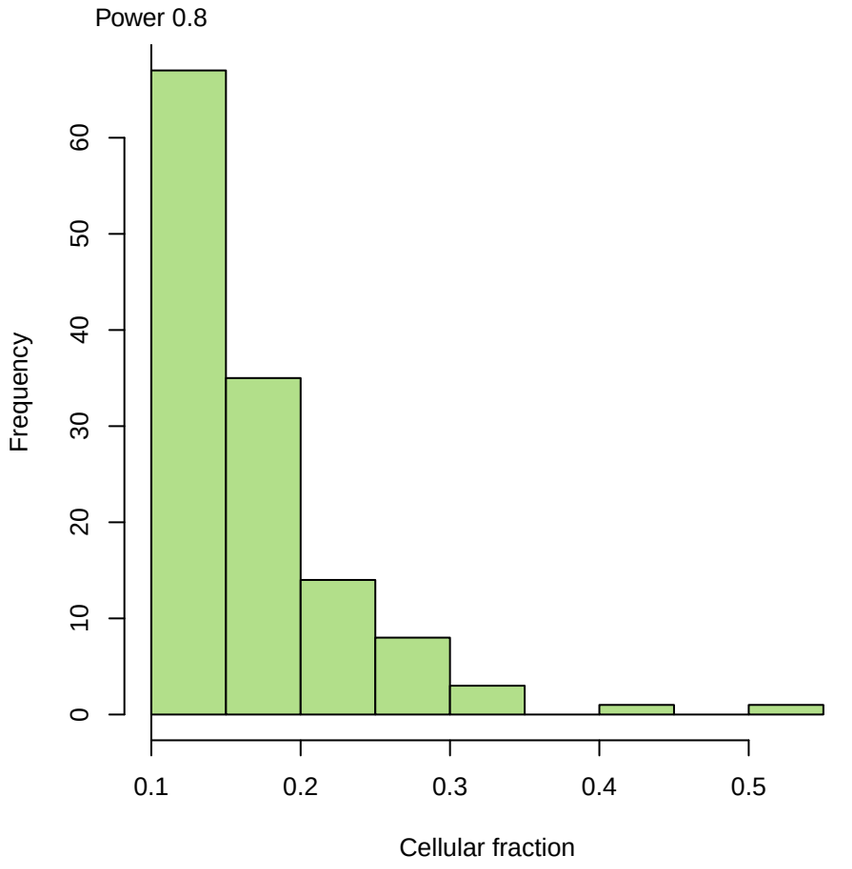

SCNA−fit log−likelihood: −23763.82
Copy Number log−ratio
−2 −1 0 1 2
3
0 20 40 60 80 100
SNV Index


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


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


Coverage (log2)
Allelic fraction


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


Power 0.8
Frequency
Cellular fraction