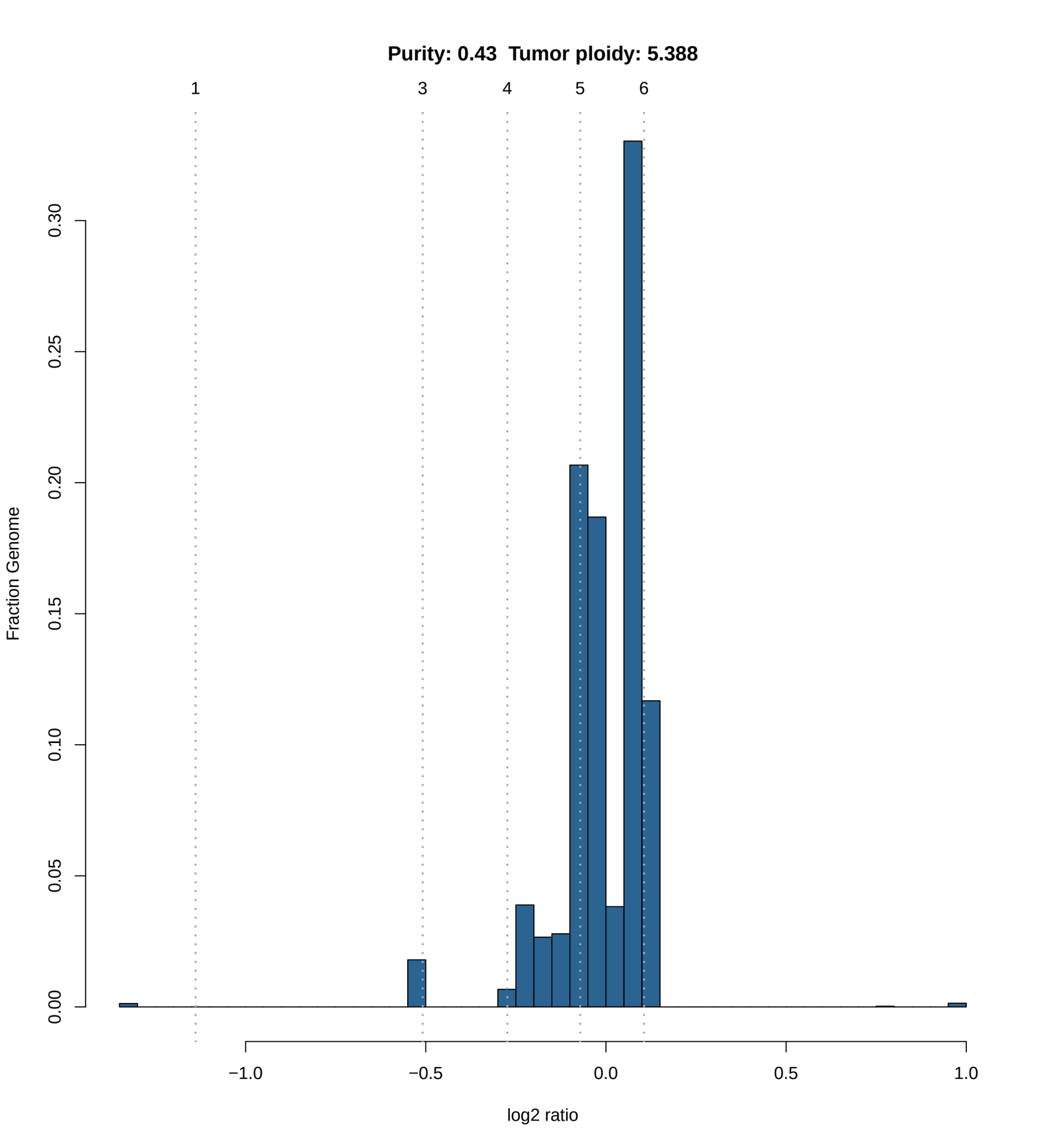
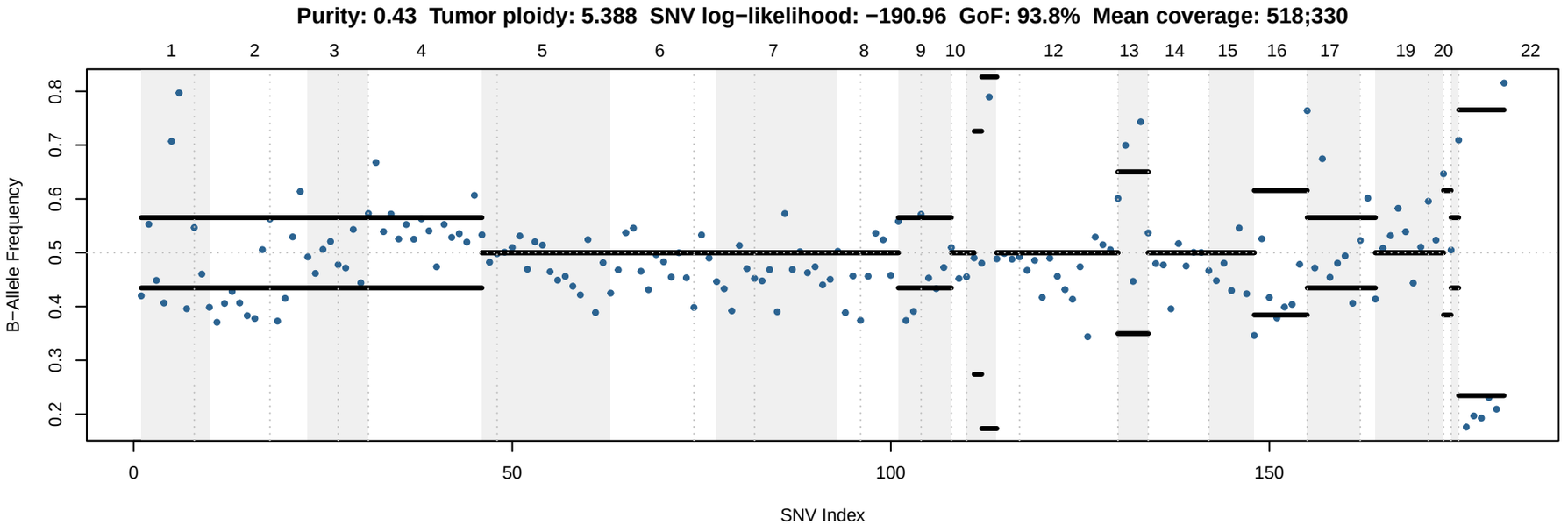
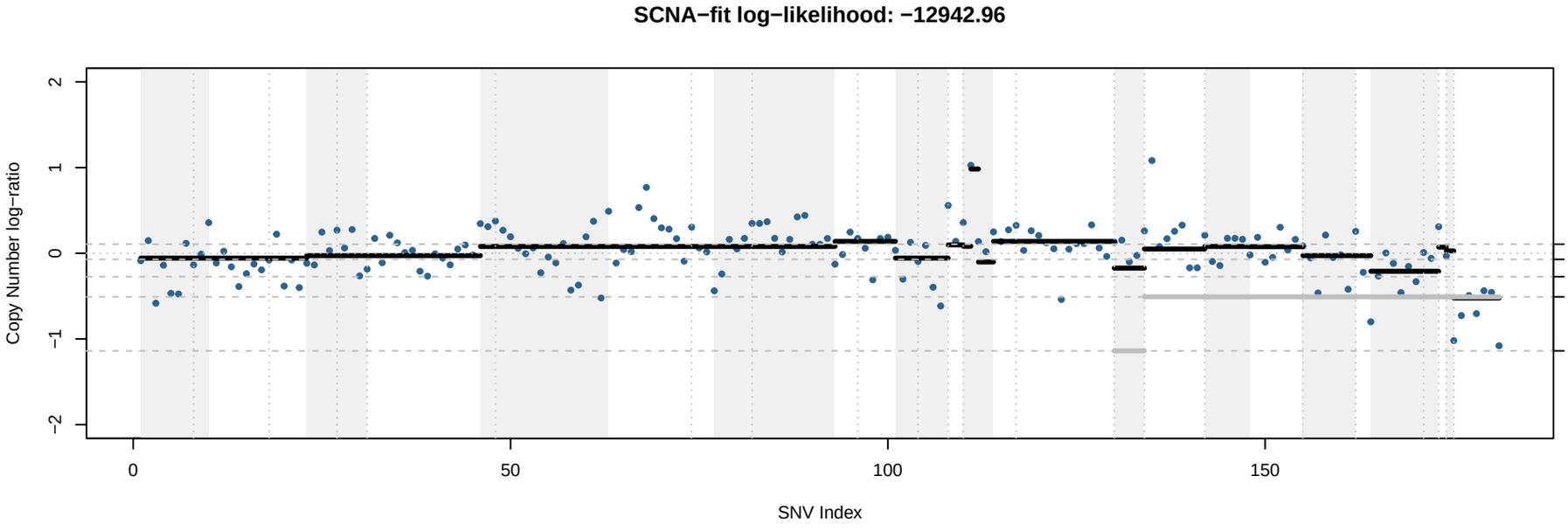
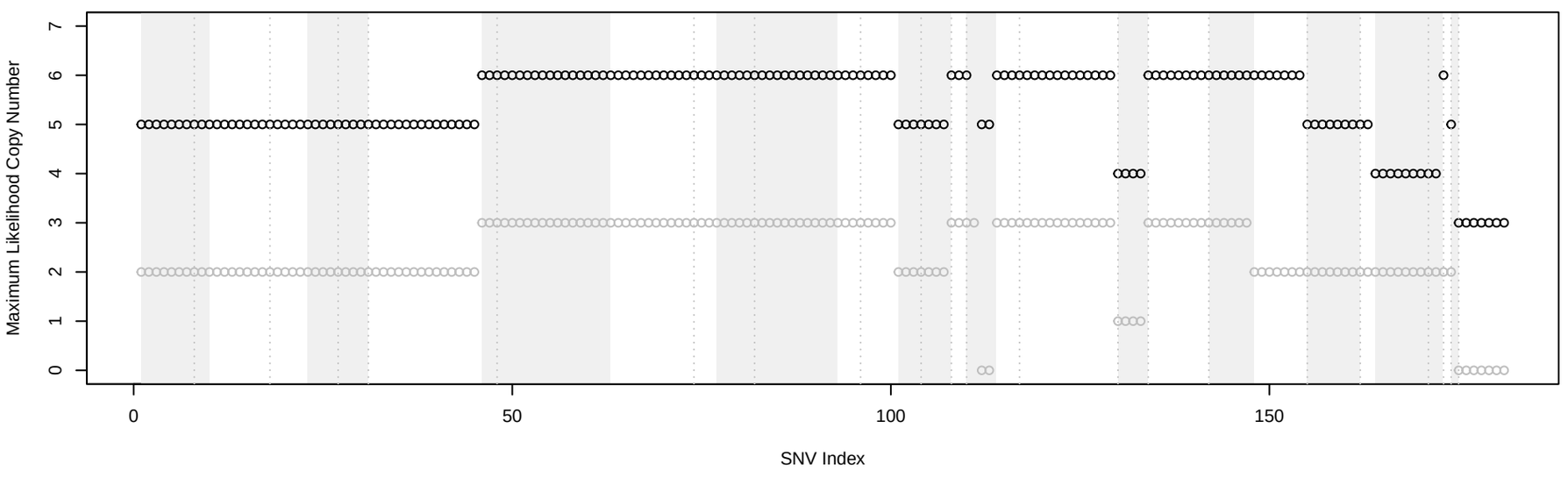
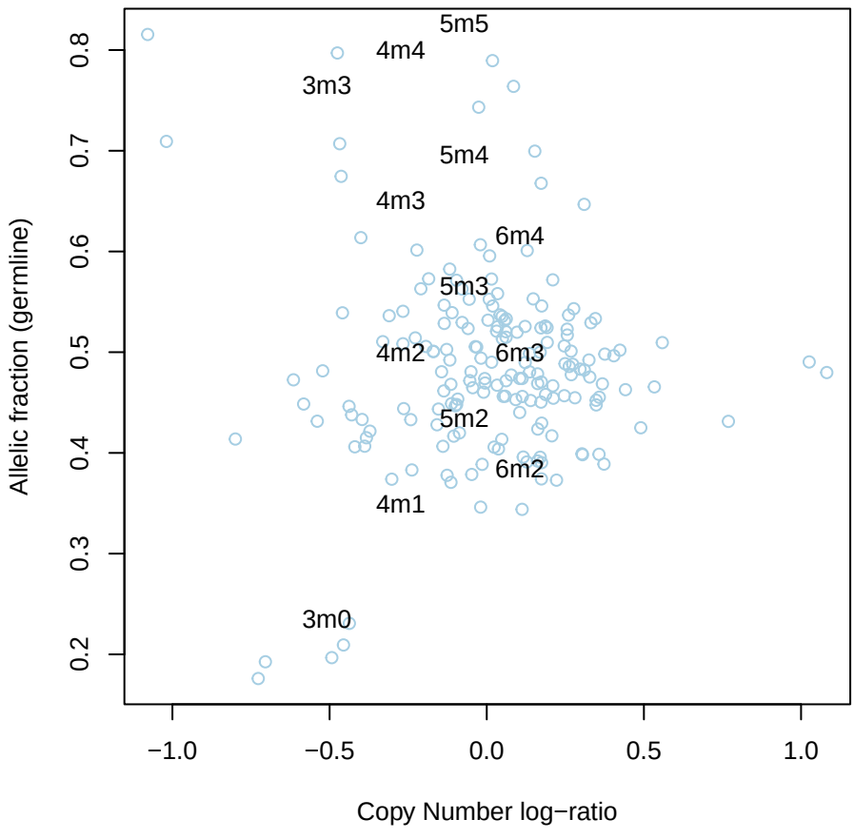
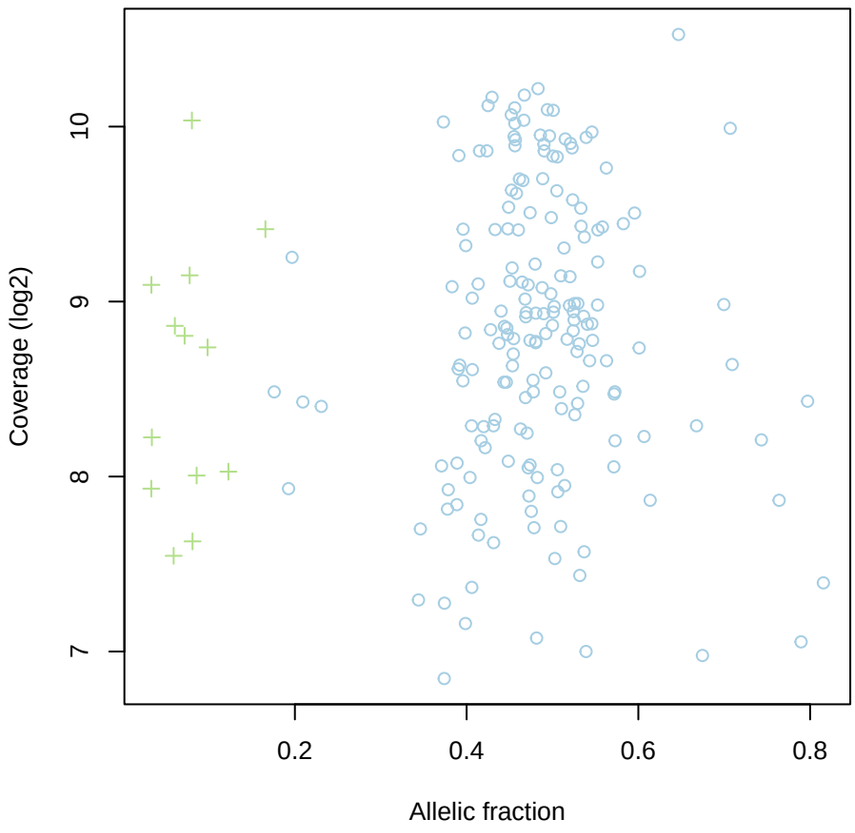

Purity: 0.43 Tumor ploidy: 5.388
1
3
4
5
6
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

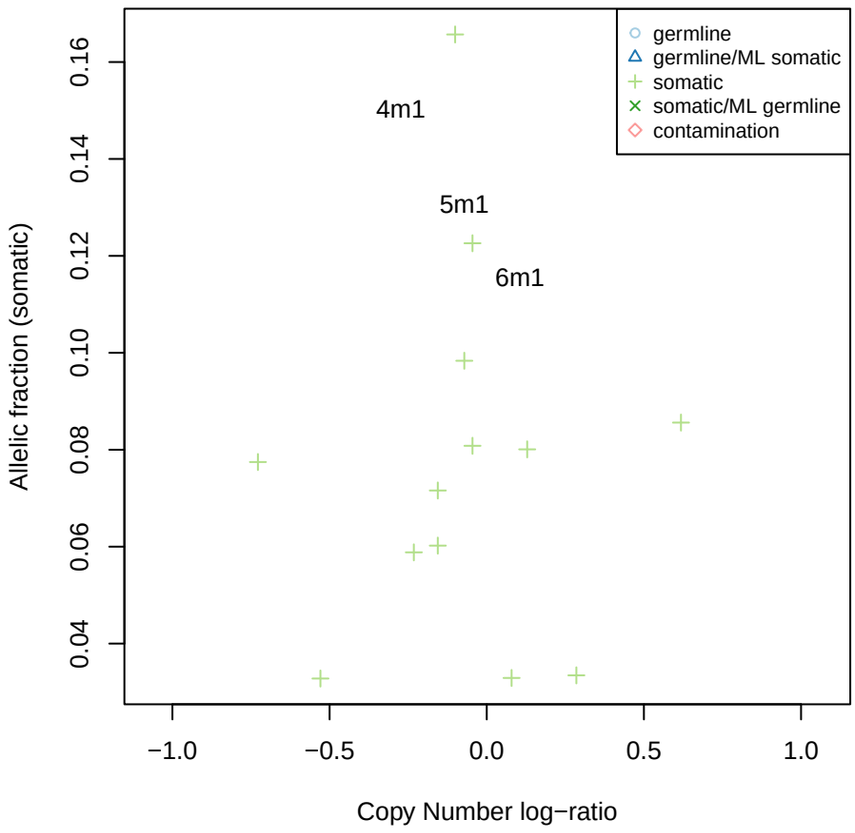

Purity: 0.43 Tumor ploidy: 5.388 SNV log−likelihood: −190.96 GoF: 93.8% Mean coverage: 518;330
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 19 20 22
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

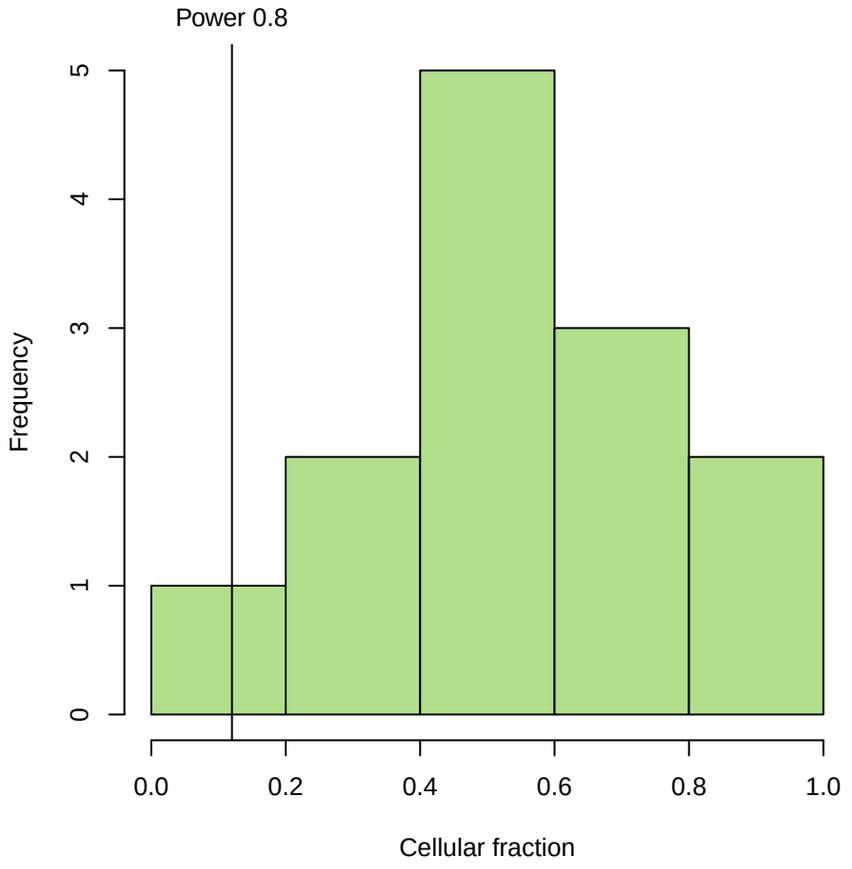

SCNA−fit log−likelihood: −12942.96
Copy Number log−ratio
−2 −1 0 1 2
1 3 5
0 50 100 150
SNV Index

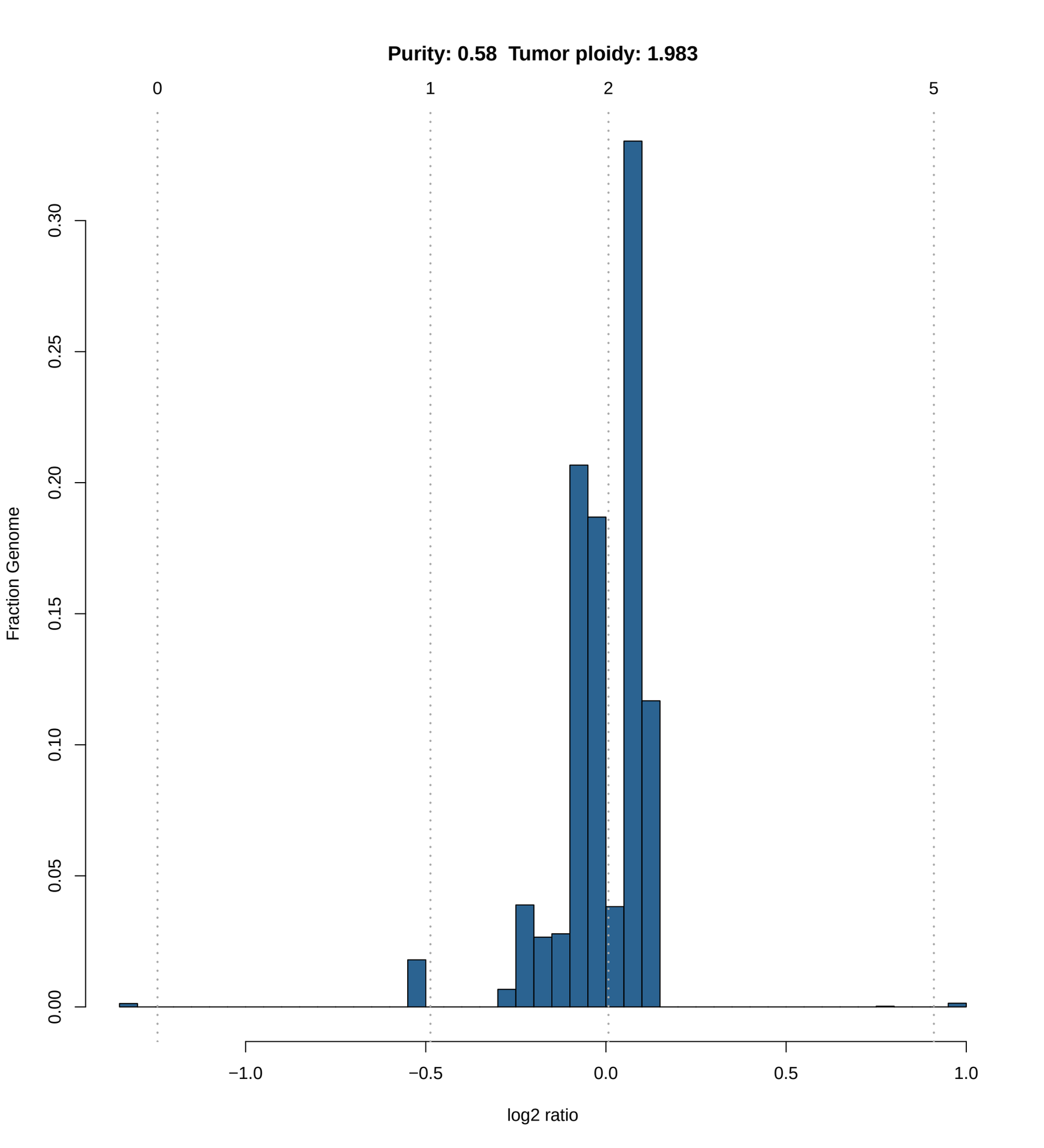

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

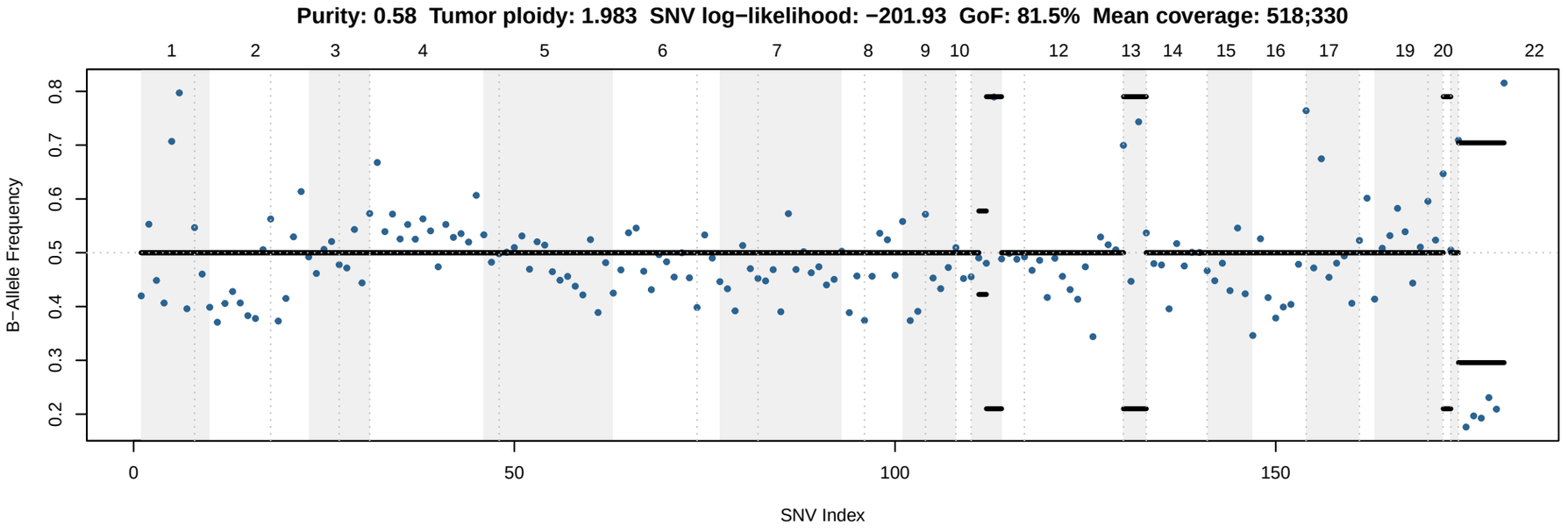

5m5
4m4
3m3
5m4
4m3
6m4
5m3
4m2
6m3
5m2
6m2
4m1
3m0
Allelic fraction (germline)
Copy Number log−ratio
0.2
0.3
0.4
0.5
0.6
0.7
0.8
−1.0
−0.5
0.0
0.5
1.0

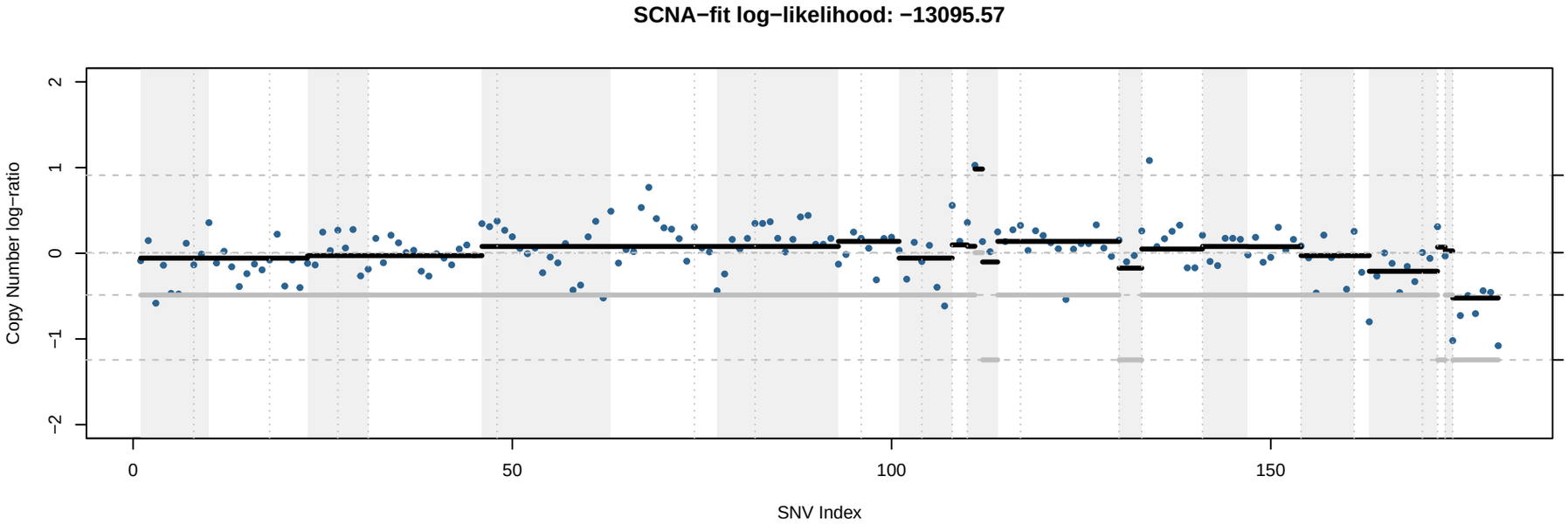

Coverage (log2)
Allelic fraction
7
8
9
10
0.2
0.4
0.6
0.8

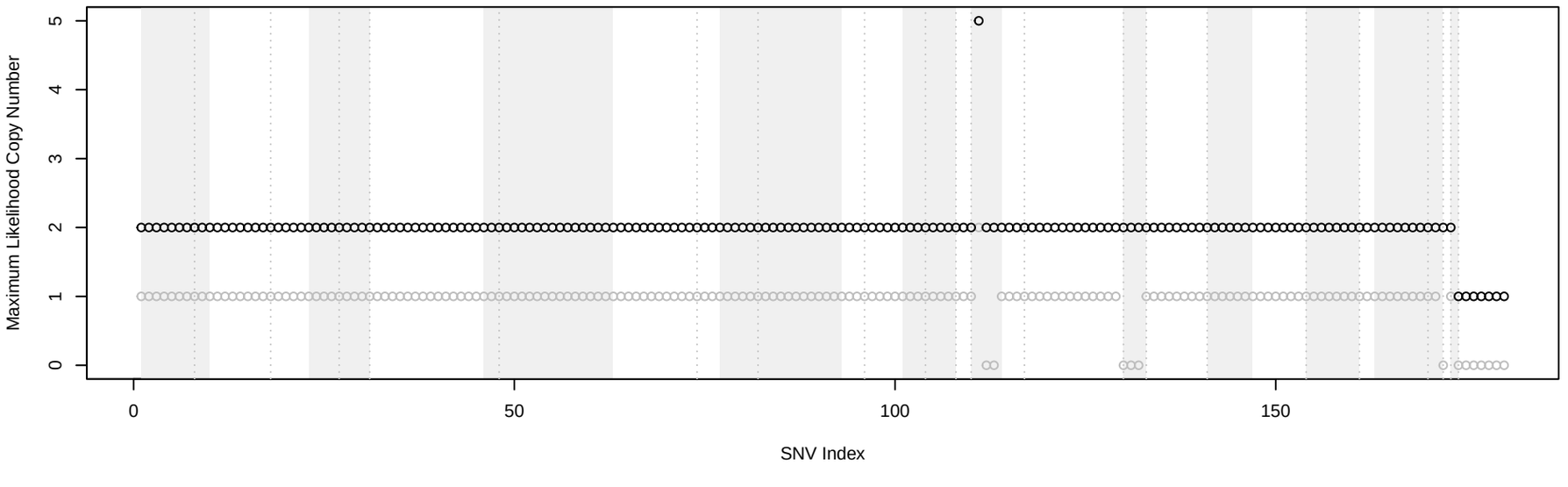

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
4m1
5m1
6m1
Allelic fraction (somatic)
Copy Number log−ratio
0.04
0.06
0.08
0.10
0.12
0.14
0.16
−1.0
−0.5
0.0
0.5
1.0

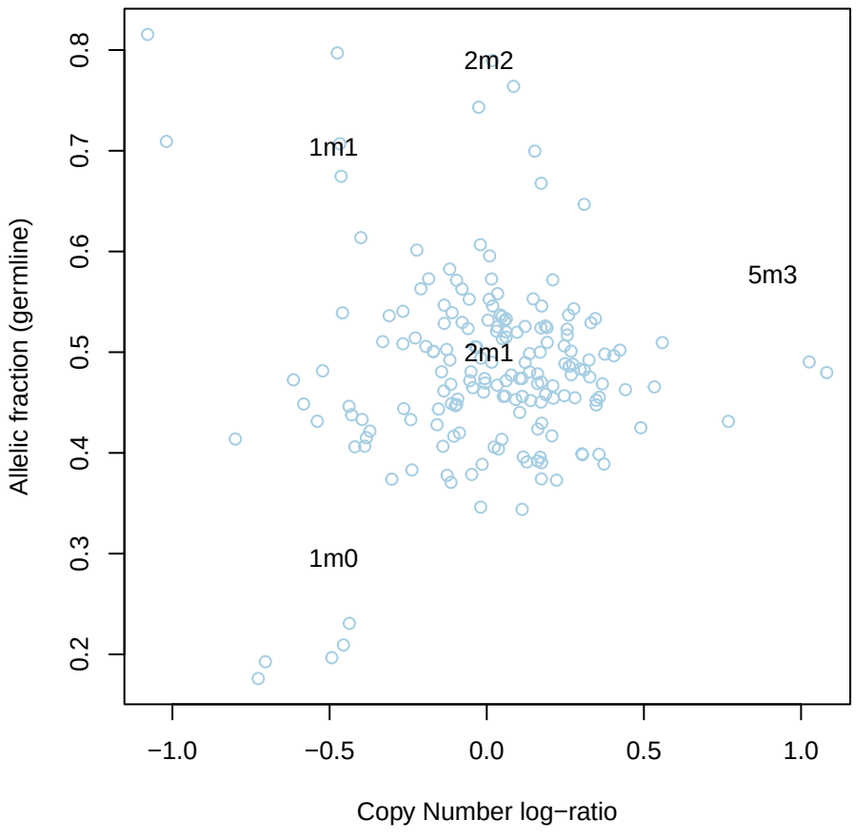

Power 0.8
Frequency
Cellular fraction
0
1
2
3
4
5
0.0
0.2
0.4
0.6
0.8
1.0

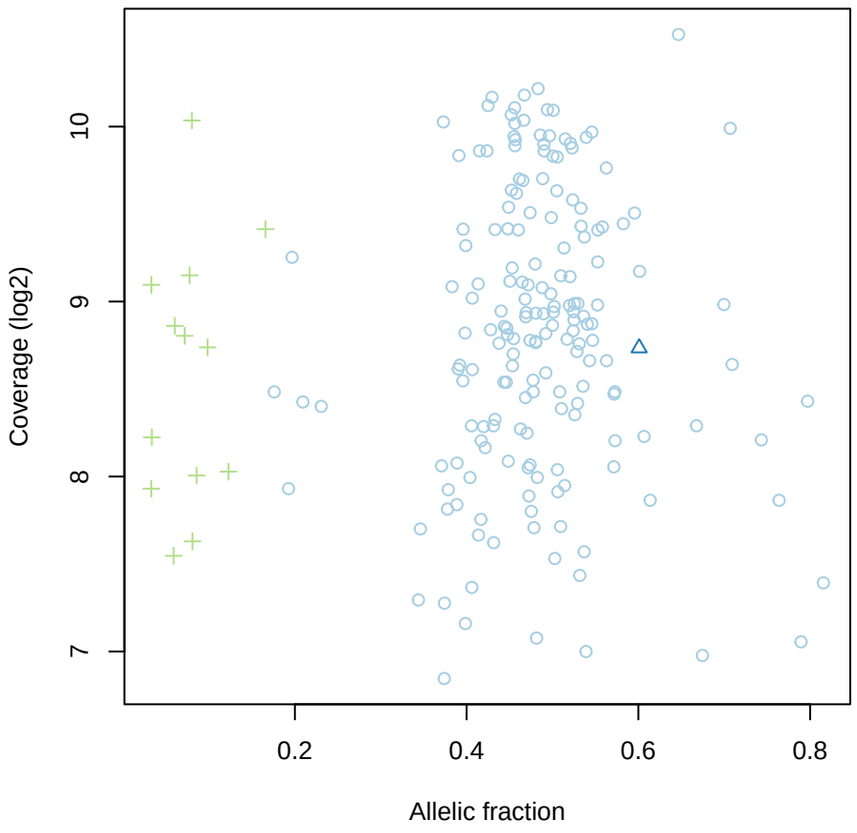

Purity: 0.58 Tumor ploidy: 1.983
0
1
2
5
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

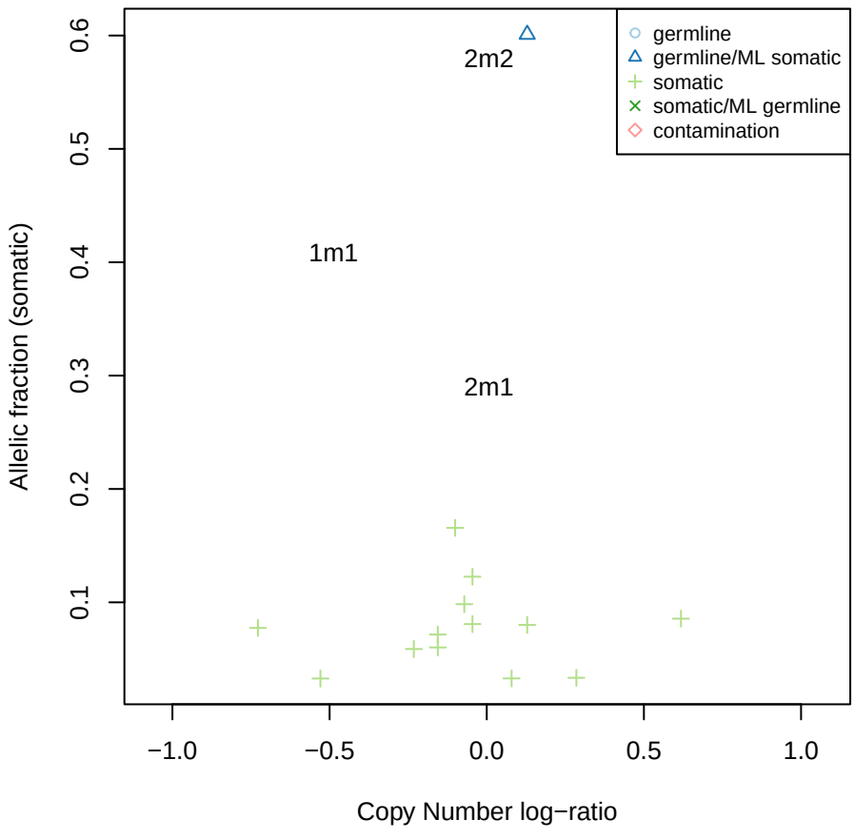

Purity: 0.58 Tumor ploidy: 1.983 SNV log−likelihood: −201.93 GoF: 81.5% Mean coverage: 518;330
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 19 20 22
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

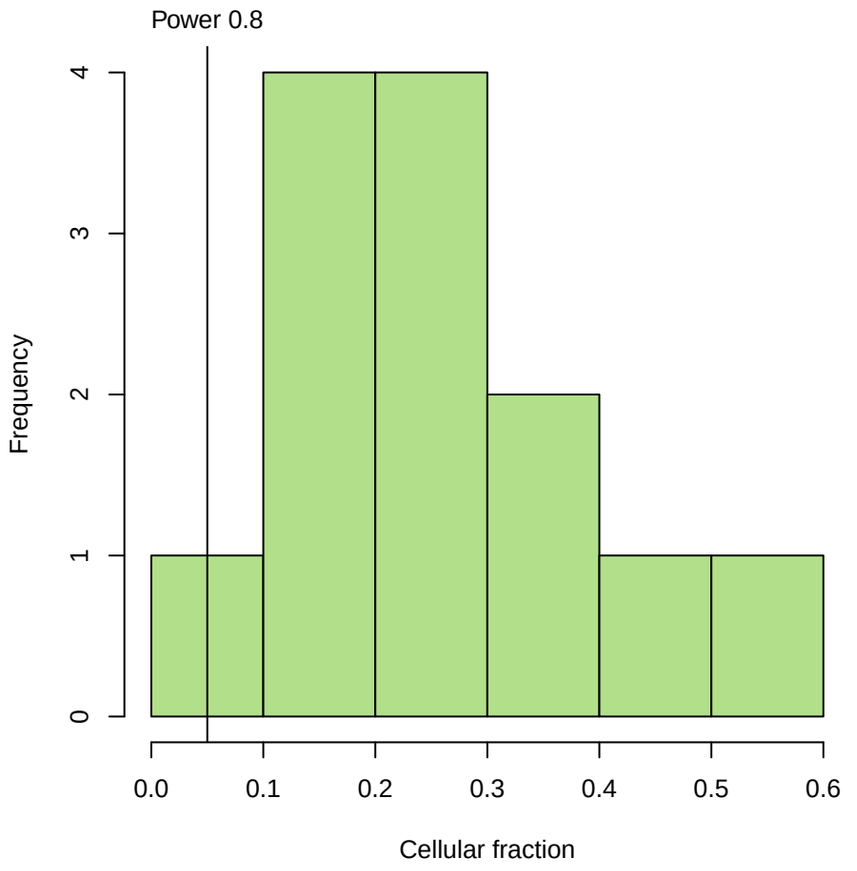

SCNA−fit log−likelihood: −13095.57
Copy Number log−ratio
−2 −1 0 1 2
0 1 2 5
0 50 100 150
SNV Index

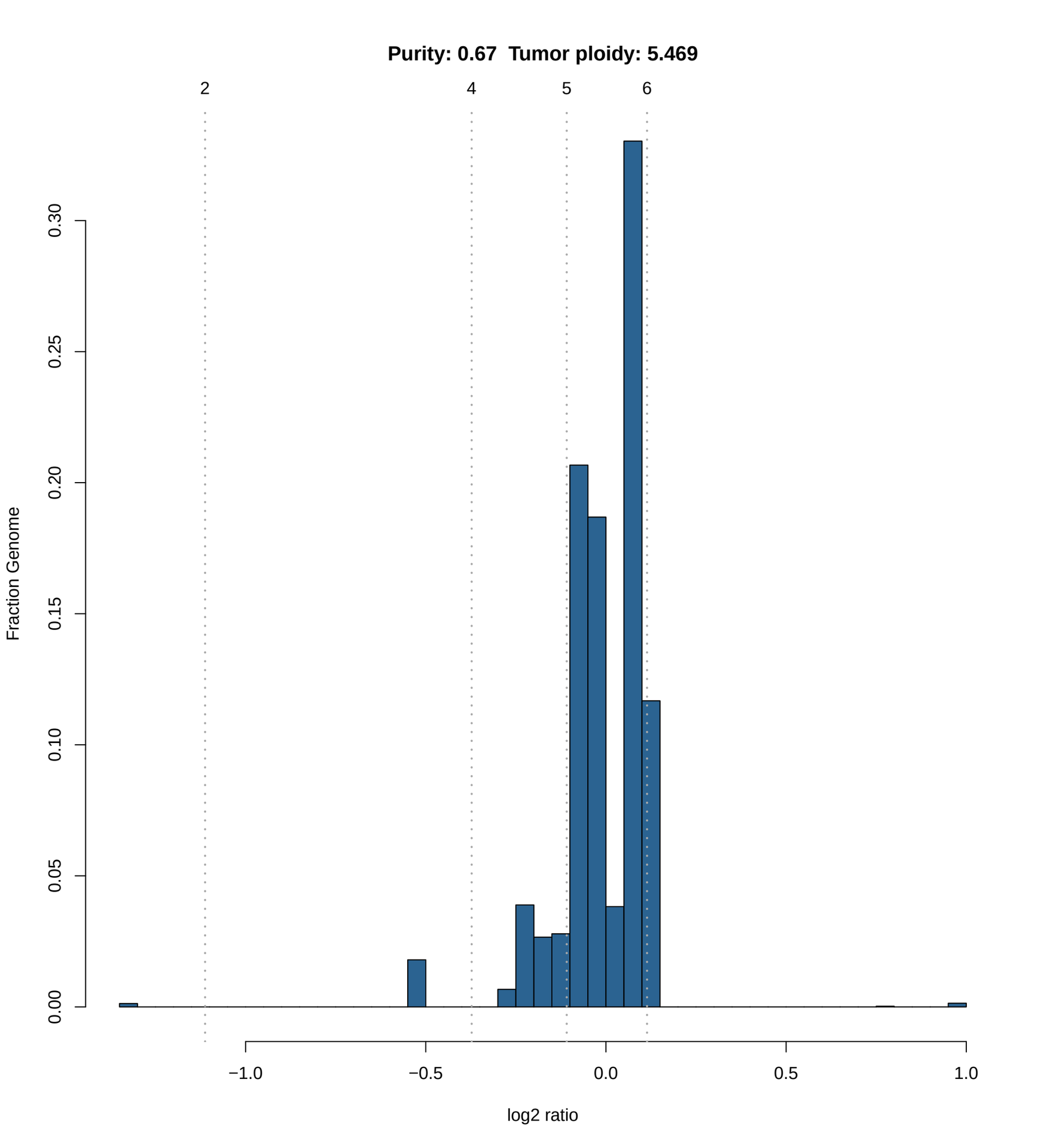

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

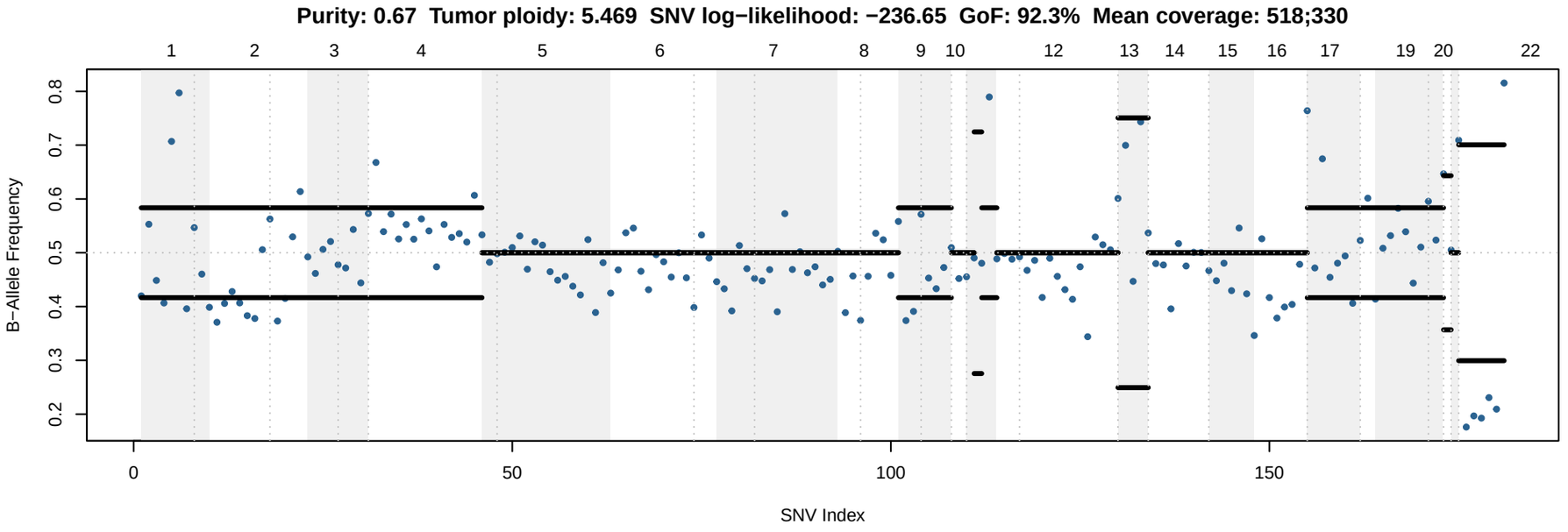

Allelic fraction (germline)
Copy Number log−ratio
2m2
1m1
5m3
2m1
1m0

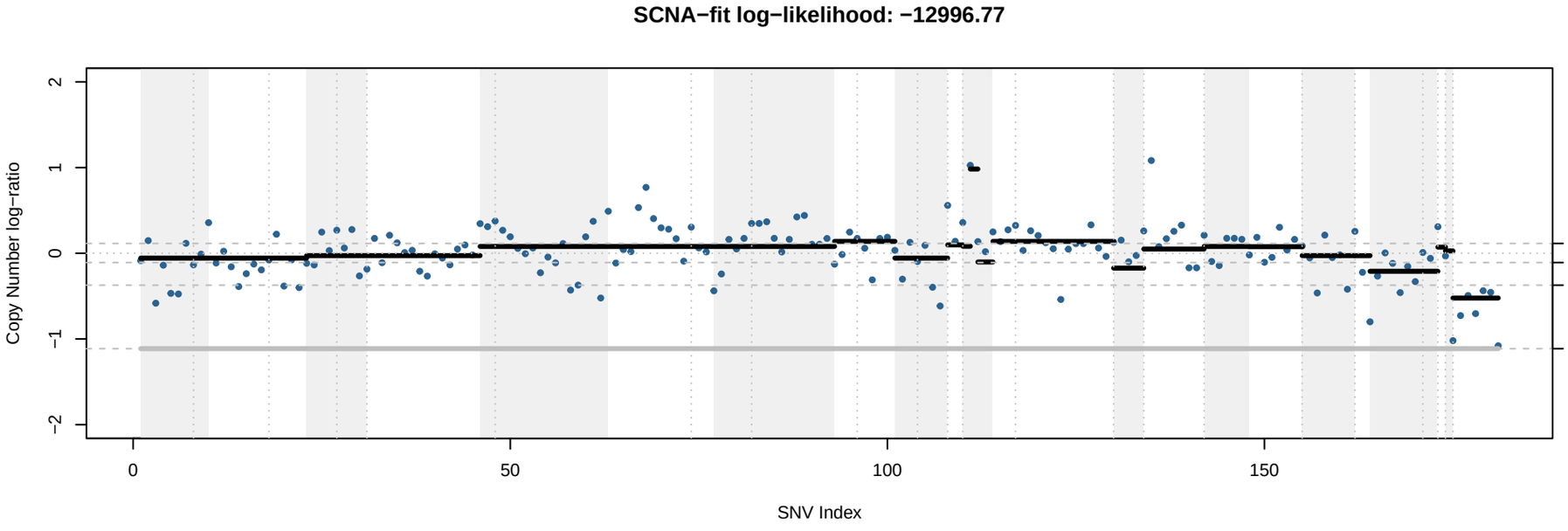

Coverage (log2)
Allelic fraction

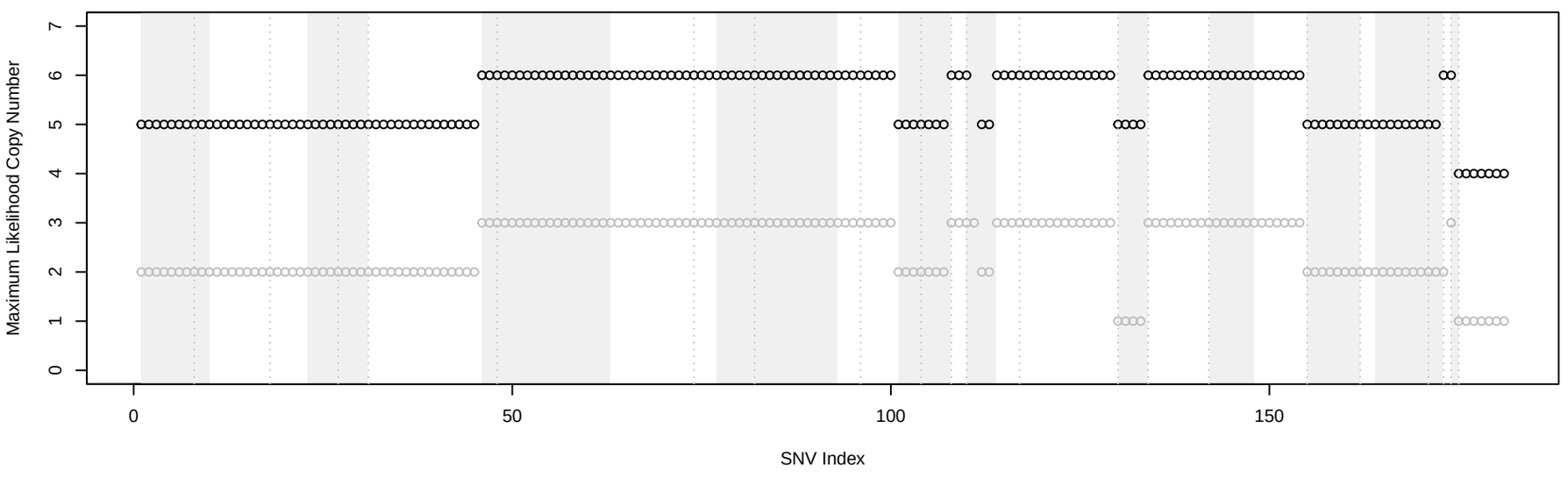

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
1m1
2m1

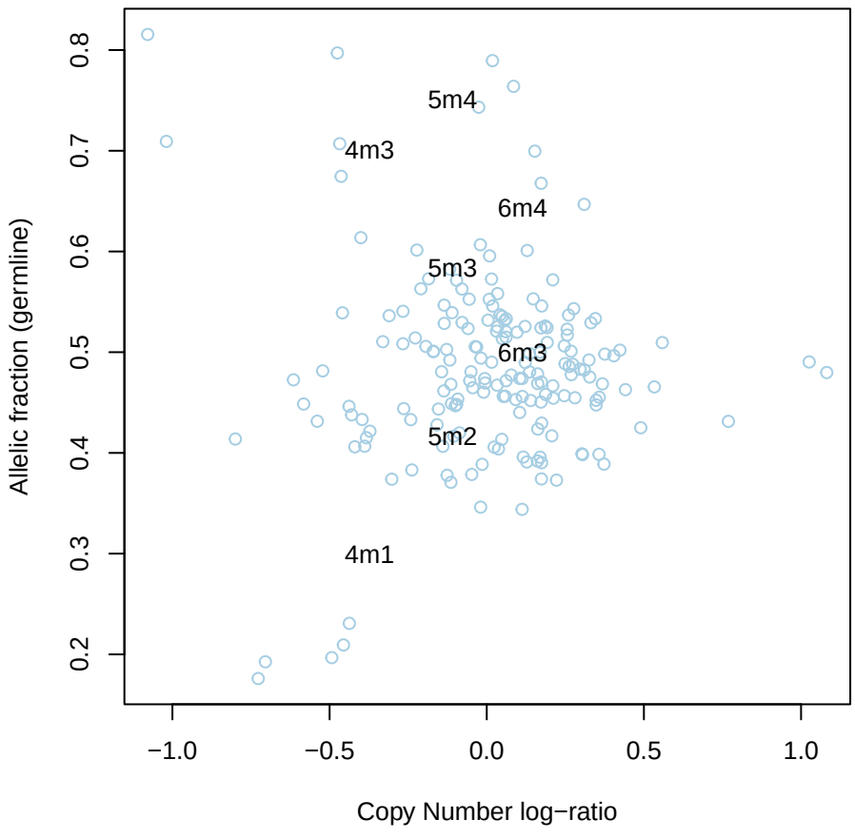

Power 0.8
Frequency
Cellular fraction

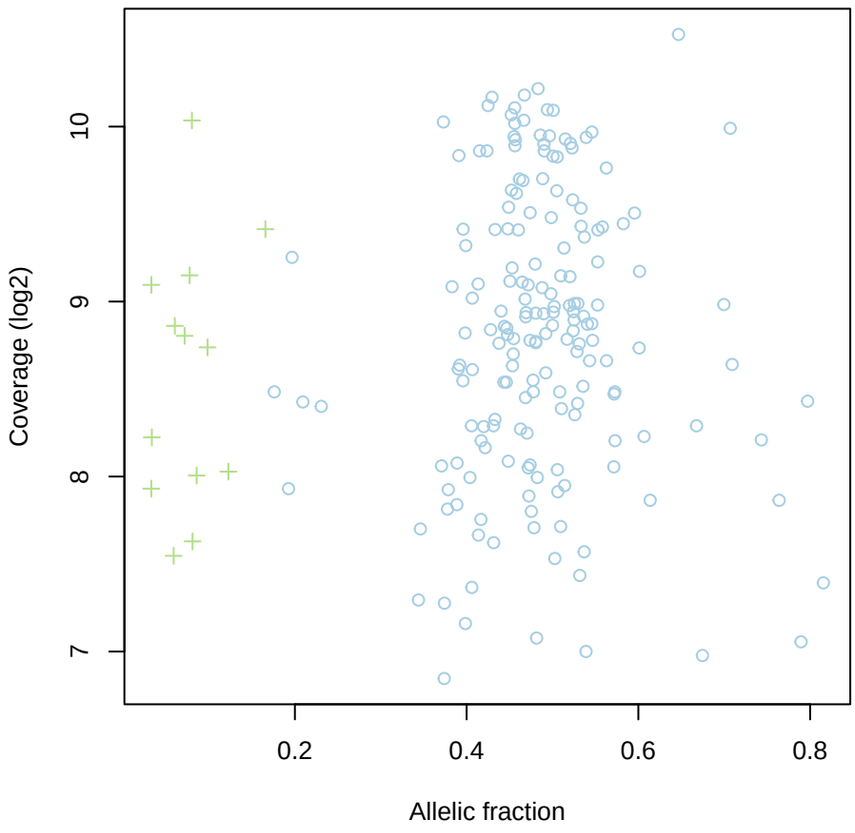

Purity: 0.67 Tumor ploidy: 5.469
2
4
5
6
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

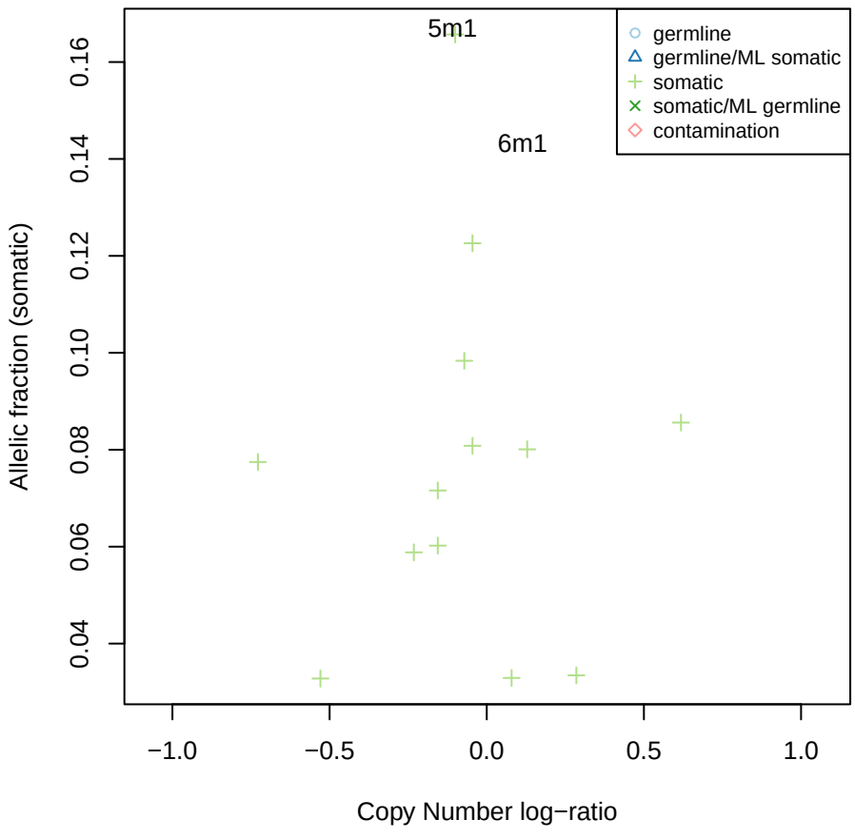

Purity: 0.67 Tumor ploidy: 5.469 SNV log−likelihood: −236.65 GoF: 92.3% Mean coverage: 518;330
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 19 20 22
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

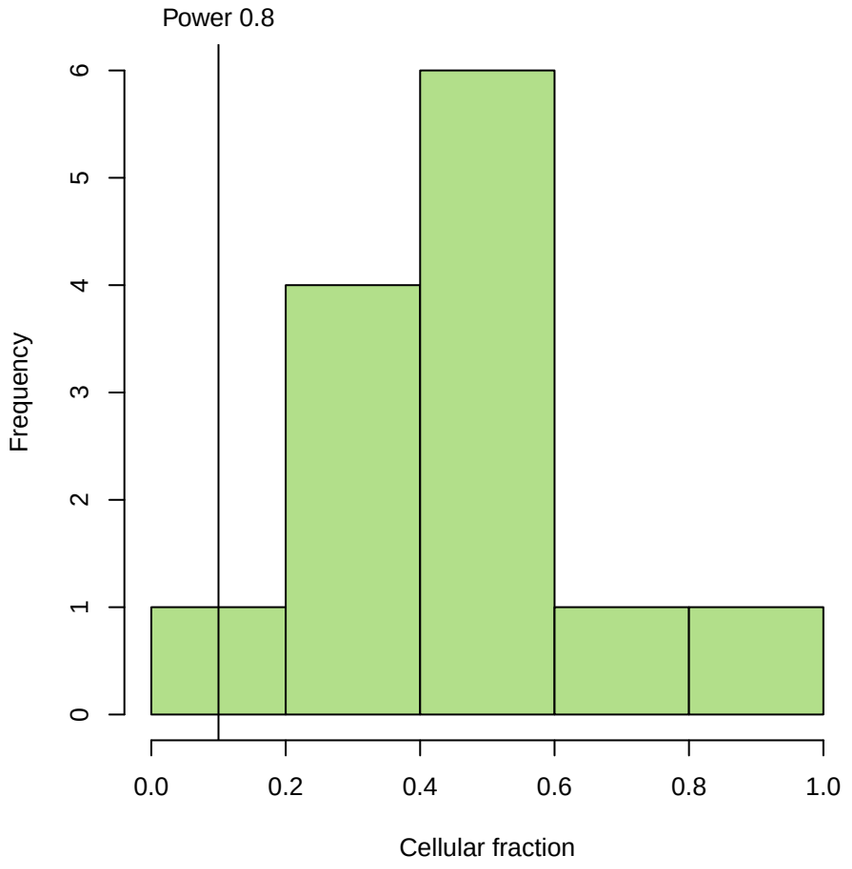

SCNA−fit log−likelihood: −12996.77
Copy Number log−ratio
2 1 0 −1 −2
2 4 6
0 50 100 150
SNV Index

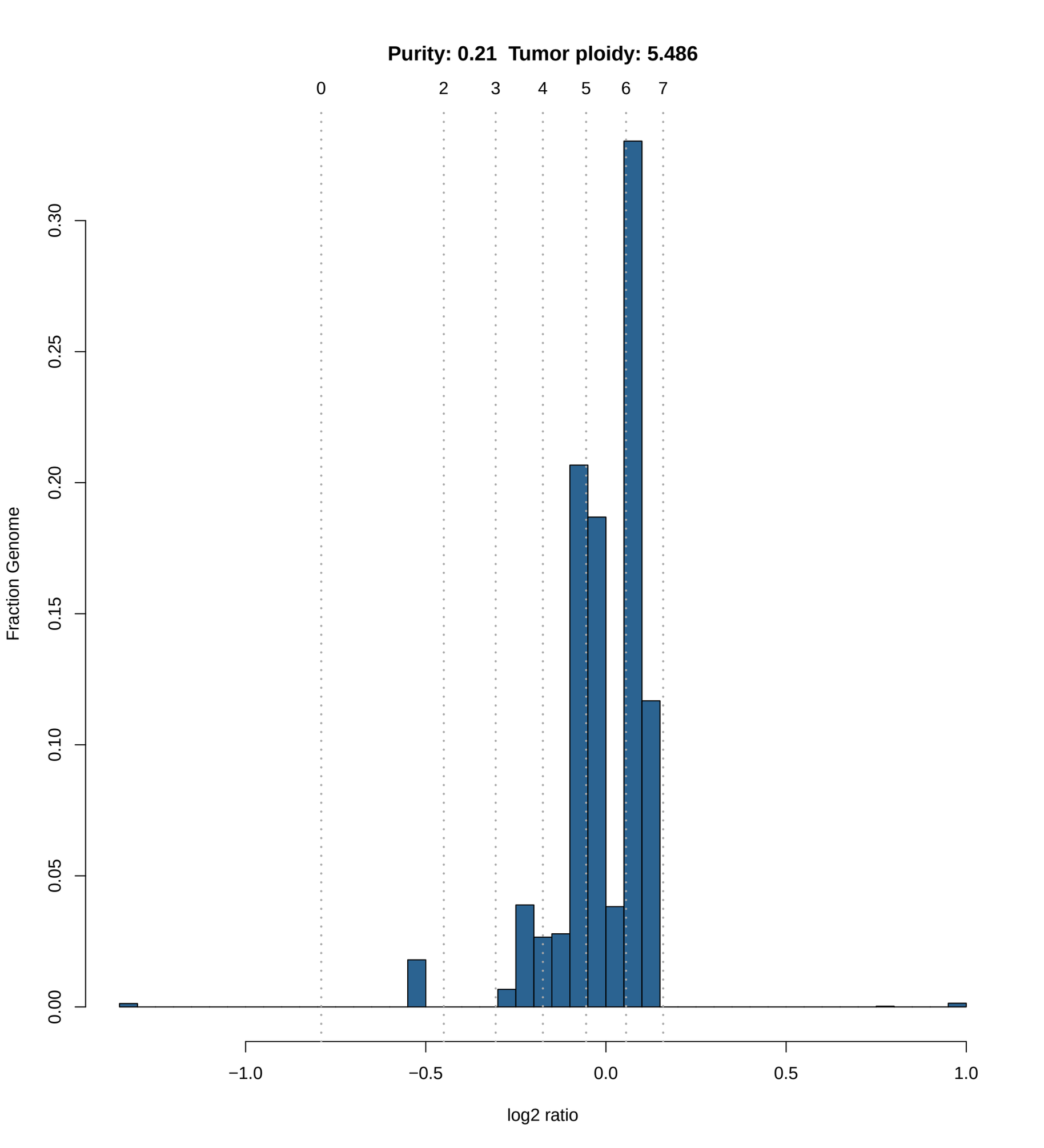

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

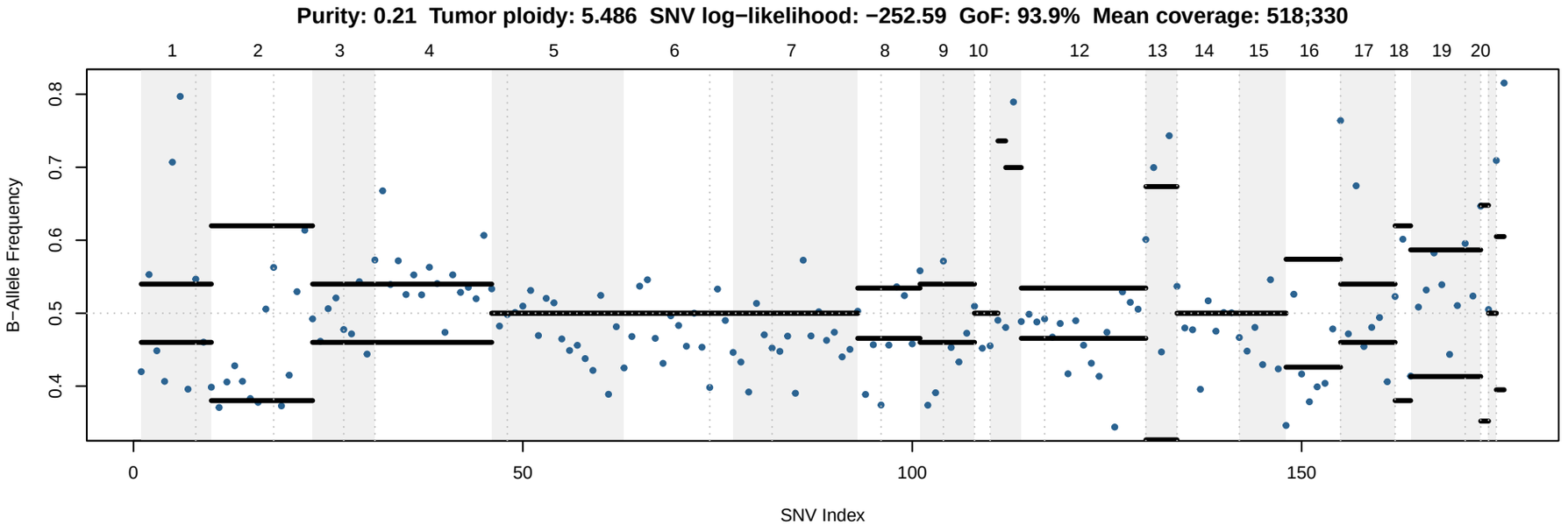

Allelic fraction (germline)
Copy Number log−ratio
5m4
4m3
6m4
5m3
6m3
5m2
4m1

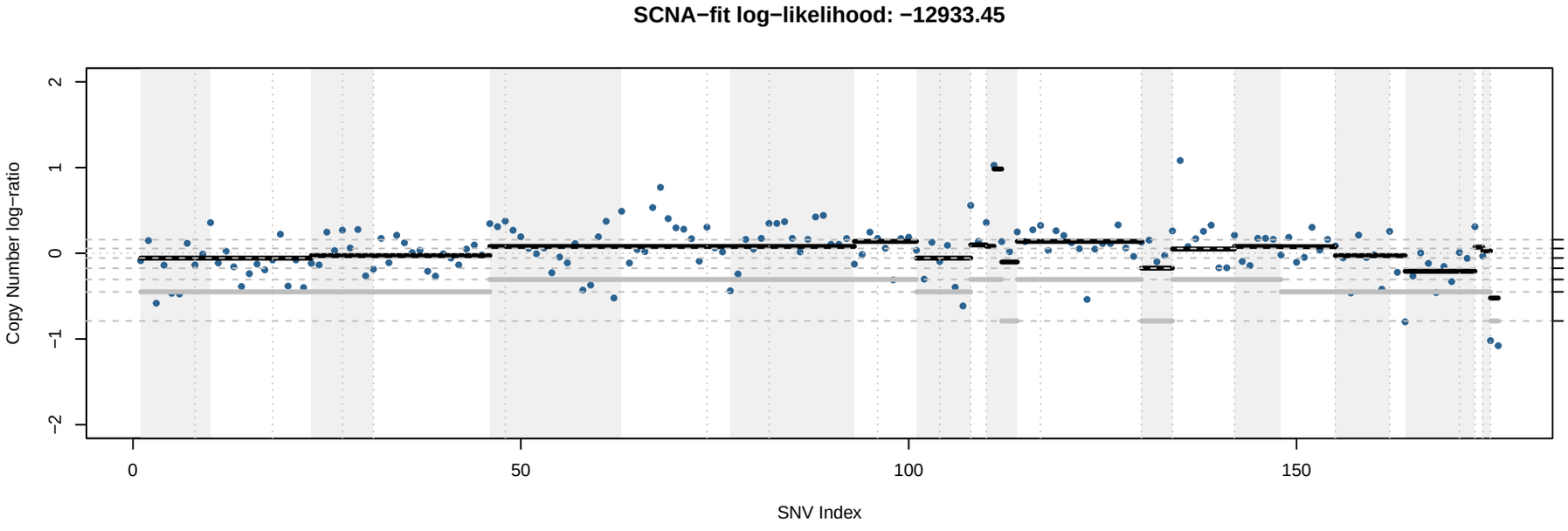

Coverage (log2)
Allelic fraction

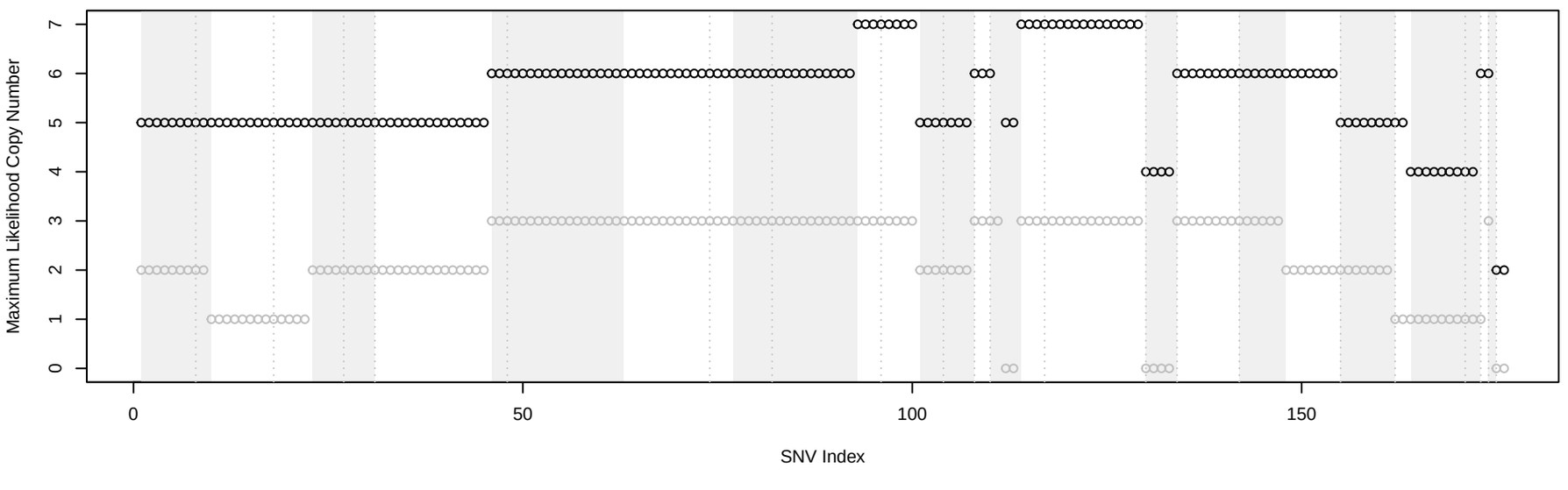

Allelic fraction (somatic)
Copy Number log−ratio
5m1
6m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

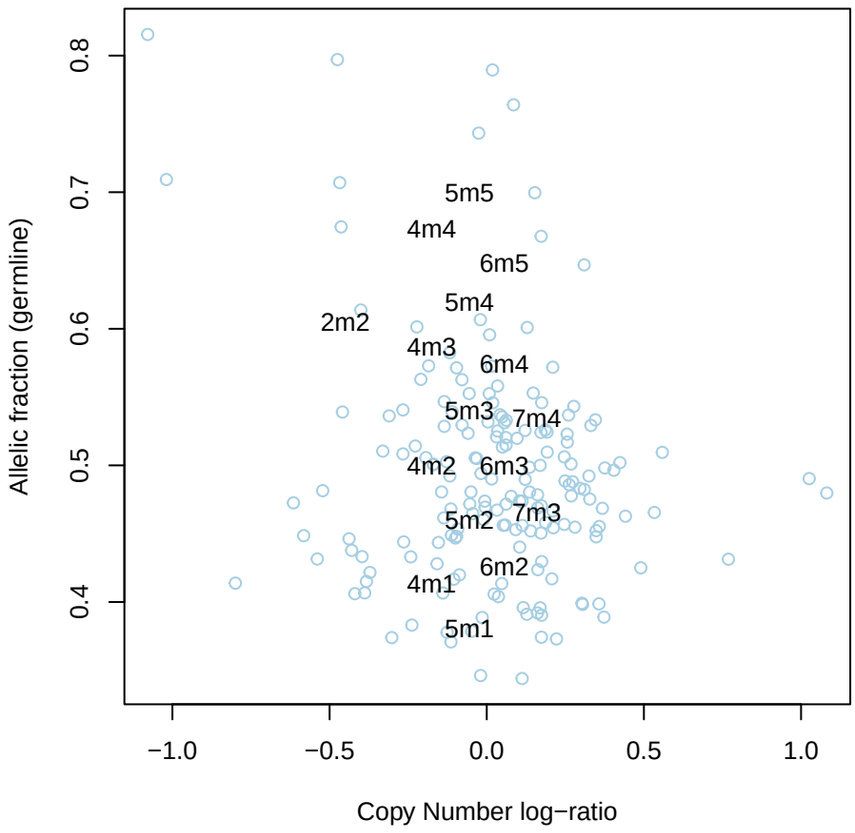

Power 0.8
Frequency
Cellular fraction

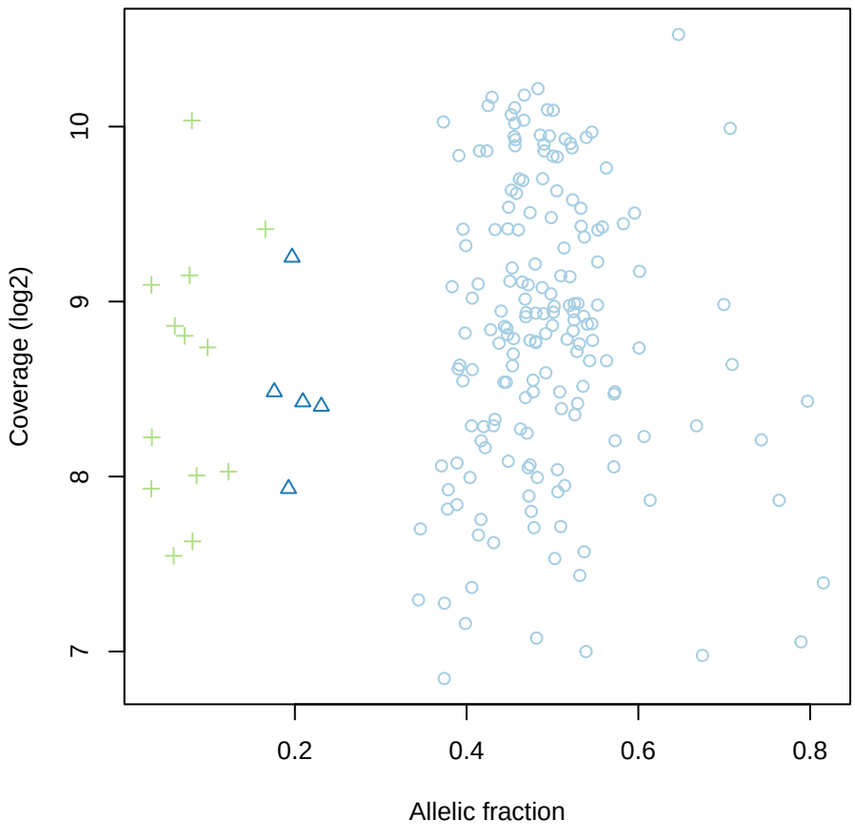

Purity: 0.21 Tumor ploidy: 5.486
0
2
3
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

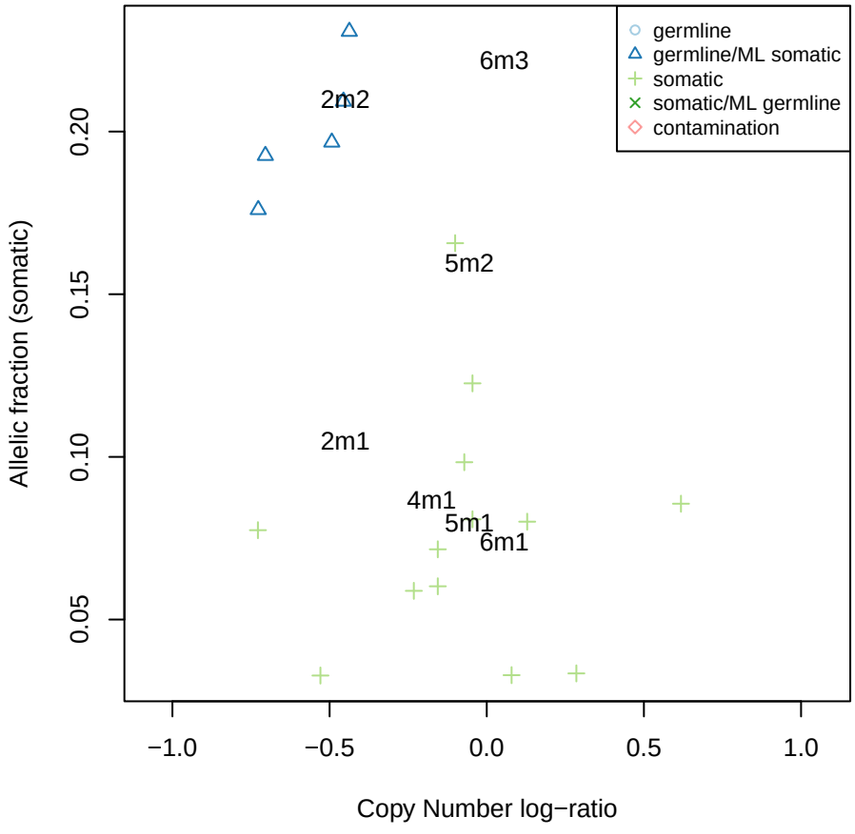

Purity: 0.21 Tumor ploidy: 5.486 SNV log−likelihood: −252.59 GoF: 93.9% Mean coverage: 518;330
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 18 19 20
B−Allele Frequency
0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

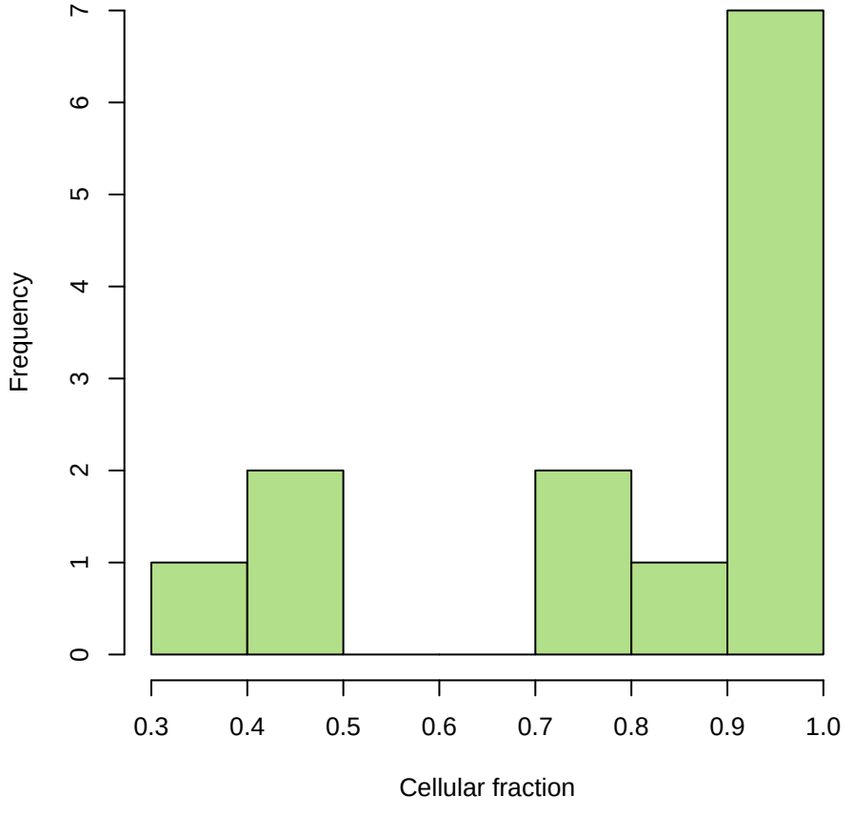

SCNA−fit log−likelihood: −12933.45
Copy Number log−ratio
−2 −1 0 1 2
0 2 5
0 50 100 150
SNV Index

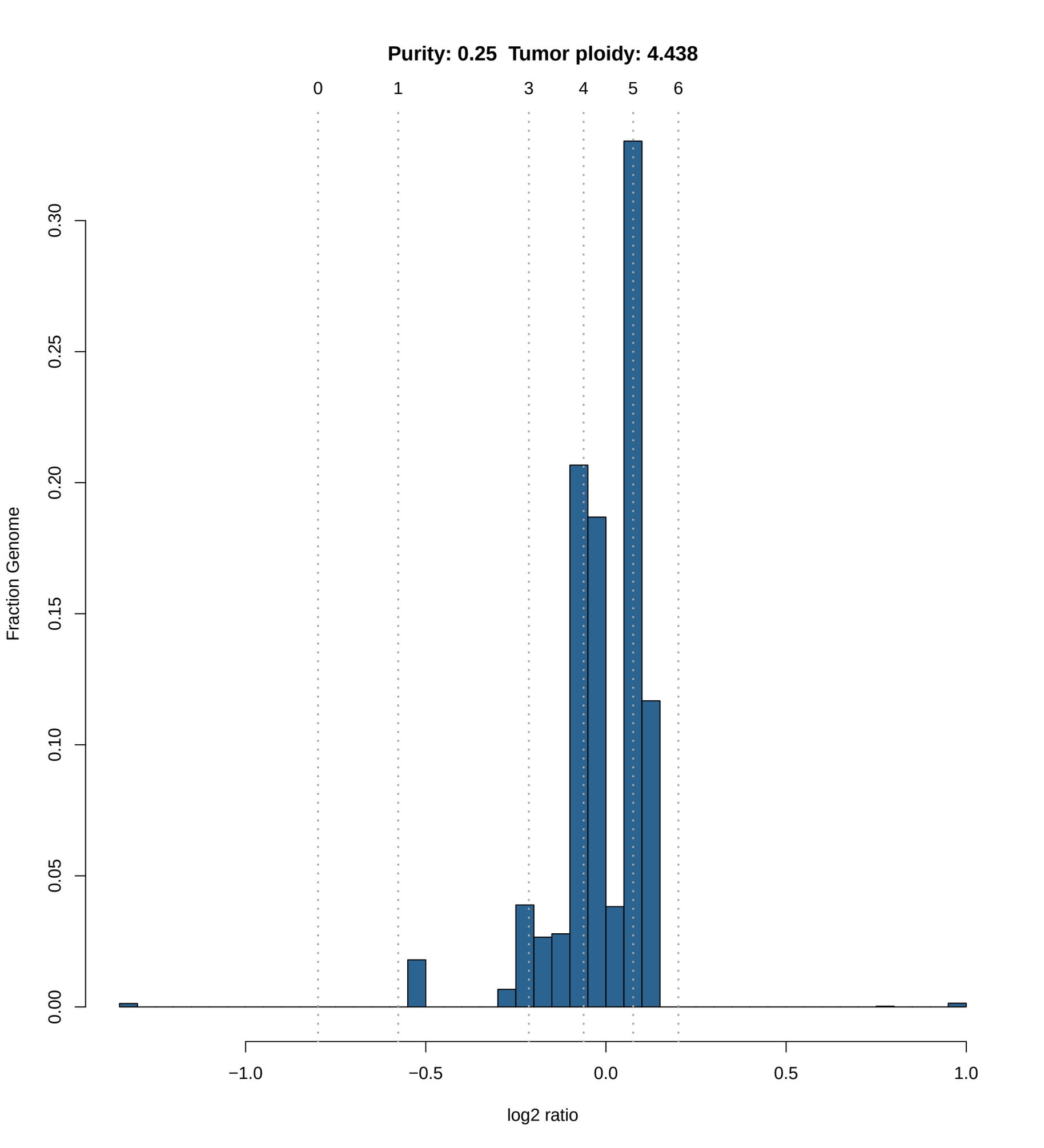

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

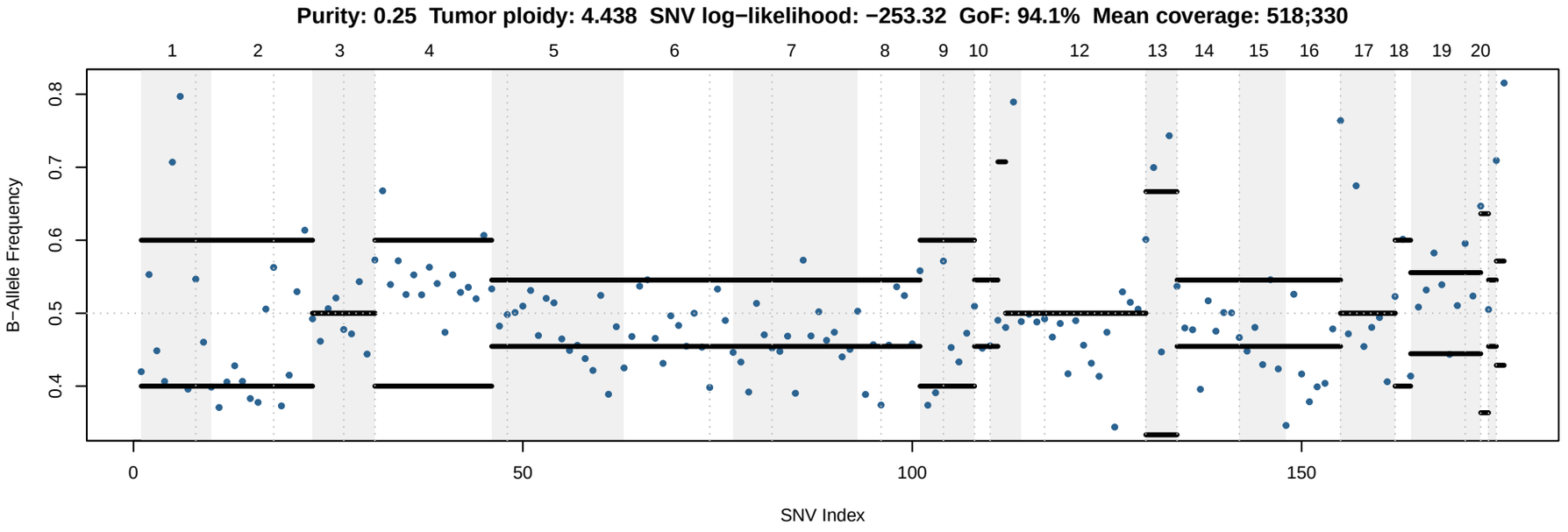

Allelic fraction (germline)
Copy Number log−ratio
5m5
4m4
6m5
5m4
2m2
4m3
6m4
5m3
7m4
4m2
6m3
5m2
7m3
6m2
4m1
5m1

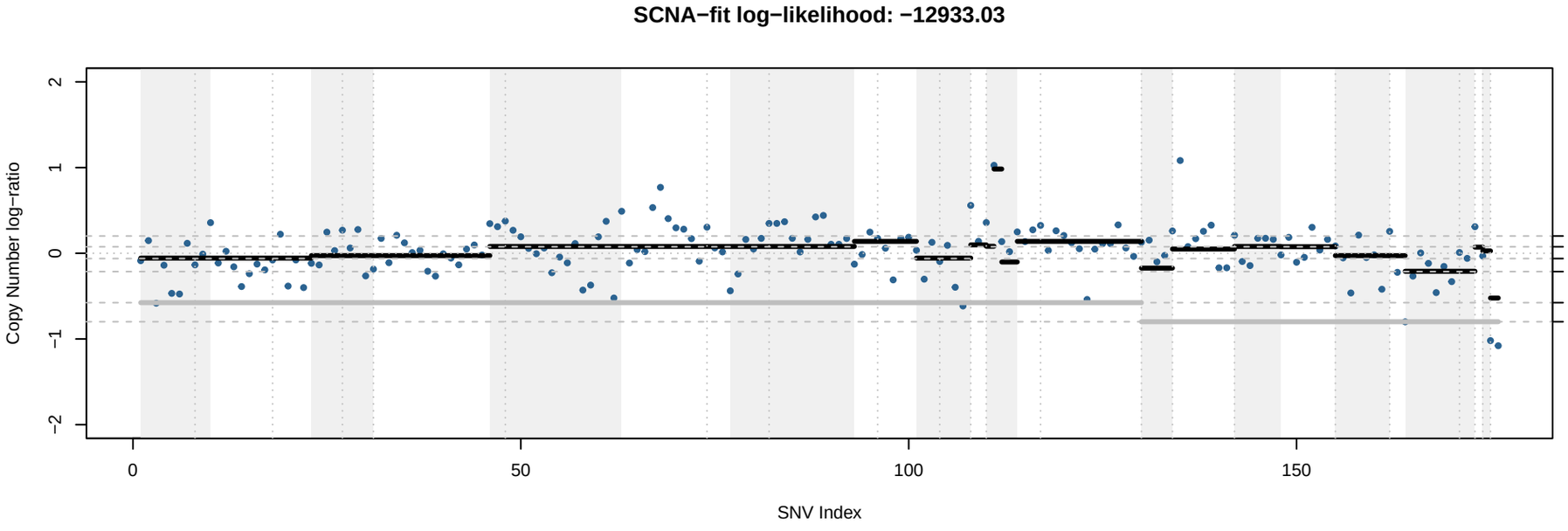

Coverage (log2)
Allelic fraction

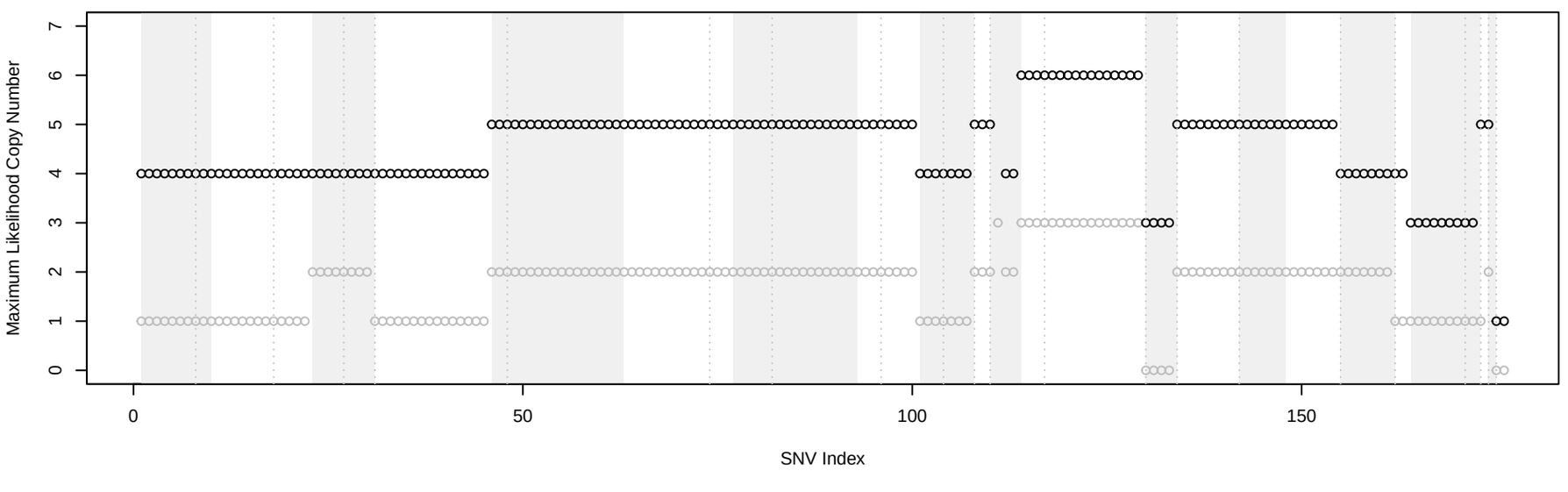

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
6m3
2m2
5m2
2m1
4m1
5m1
6m1

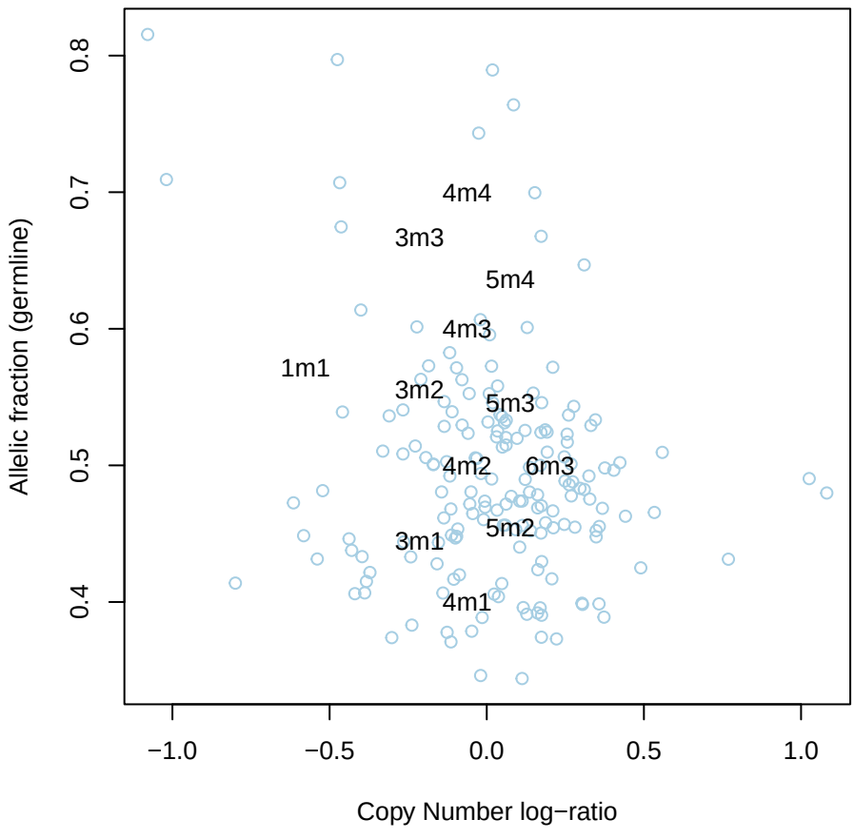

Frequency
Cellular fraction

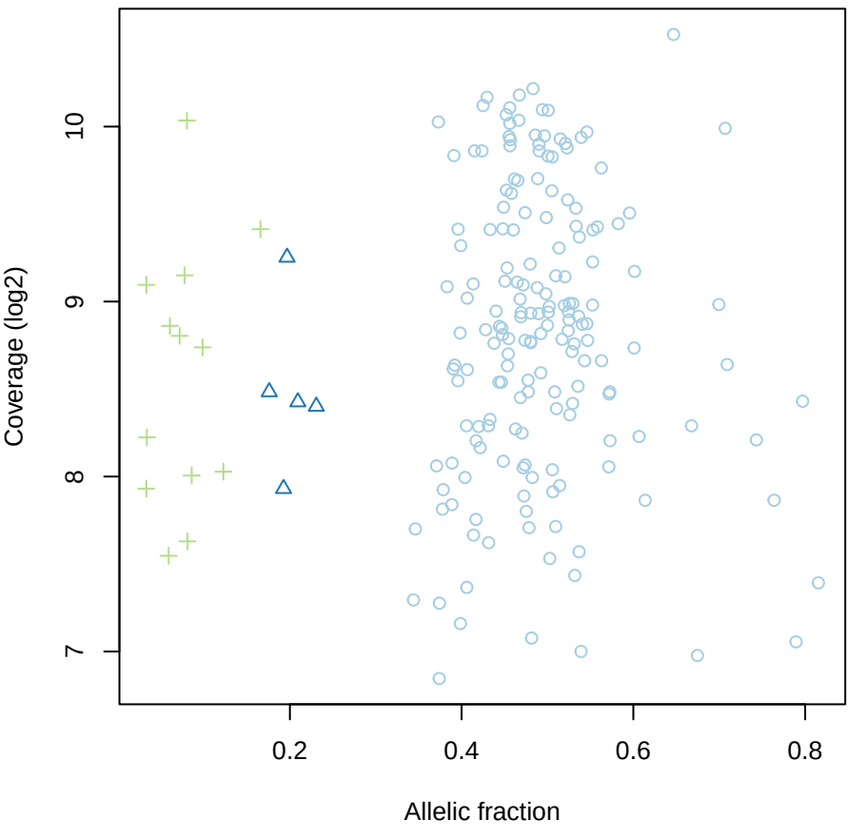

Purity: 0.25 Tumor ploidy: 4.438
0
1
3
4
5
6
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

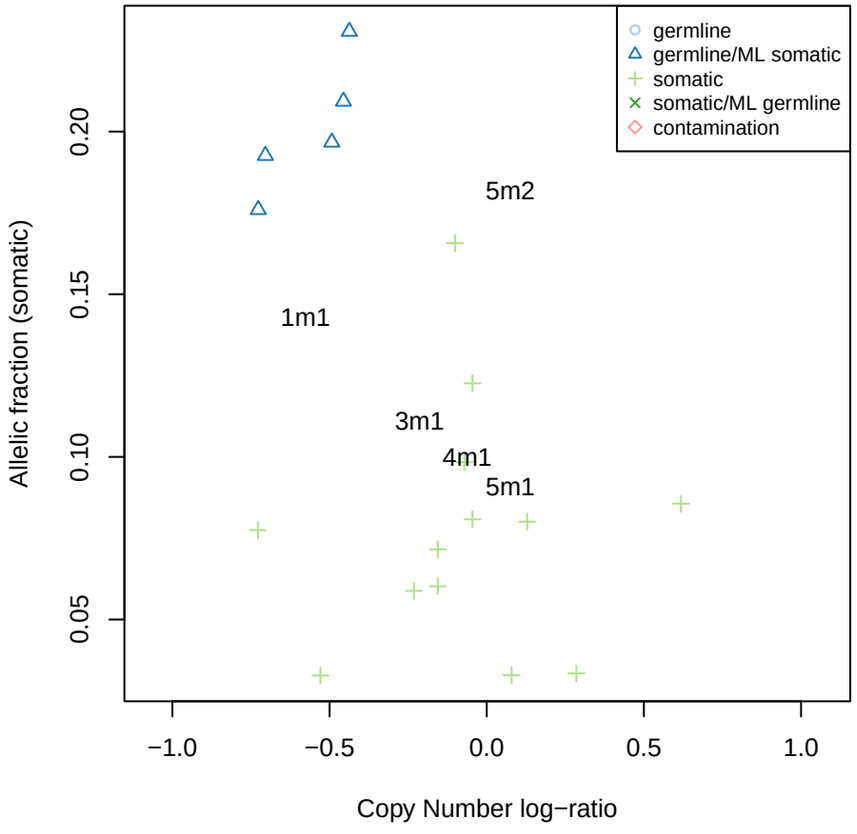

Purity: 0.25 Tumor ploidy: 4.438 SNV log−likelihood: −253.32 GoF: 94.1% Mean coverage: 518;330
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 18 19 20
B−Allele Frequency
0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

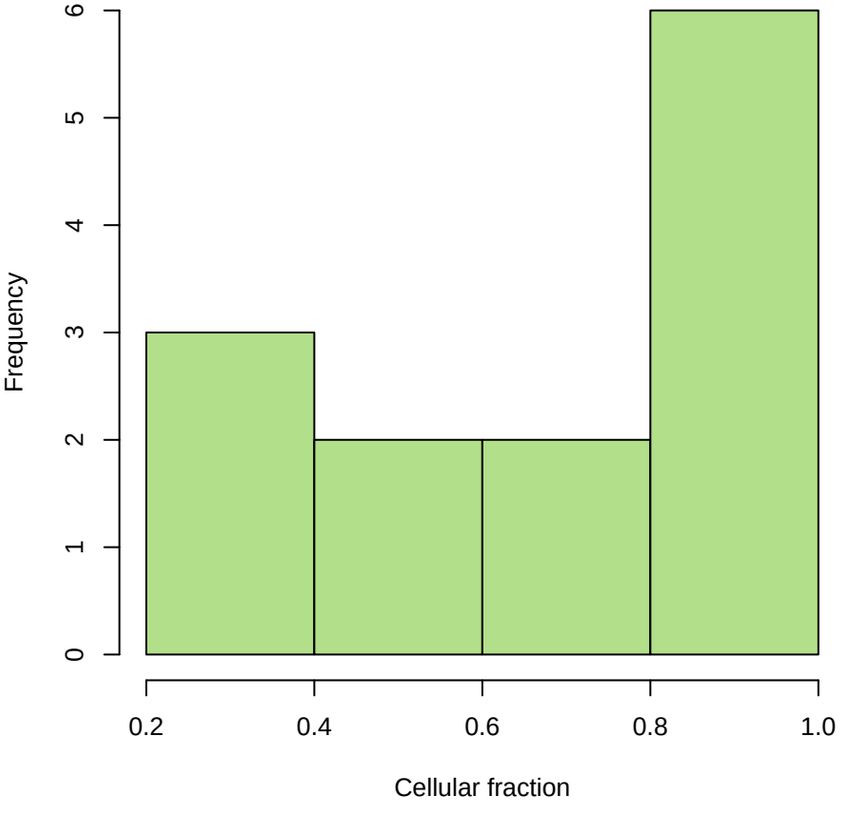

SCNA−fit log−likelihood: −12933.03
Copy Number log−ratio
−2 −1 0 1 2
0 3 5
0 50 100 150
SNV Index

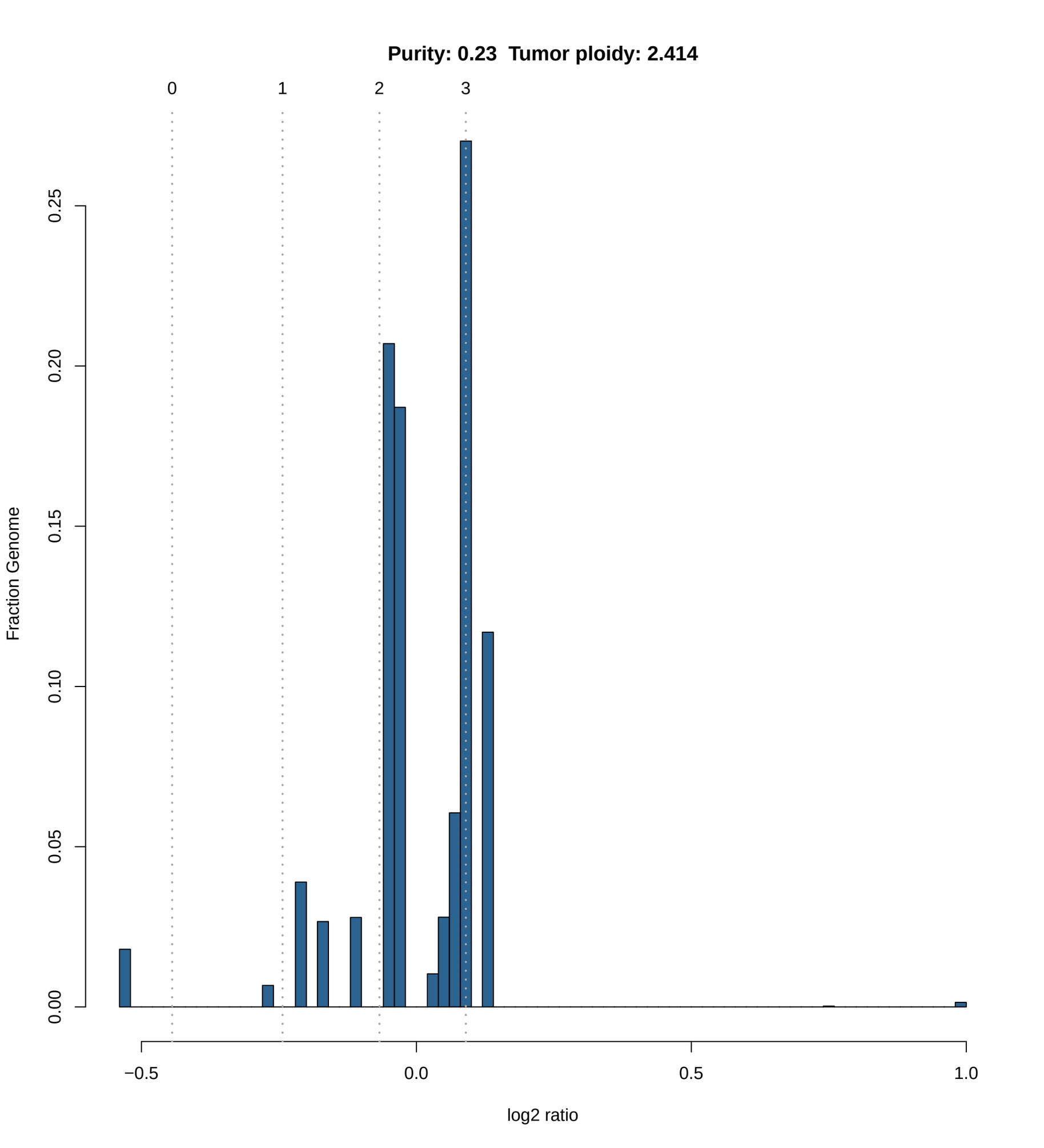

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

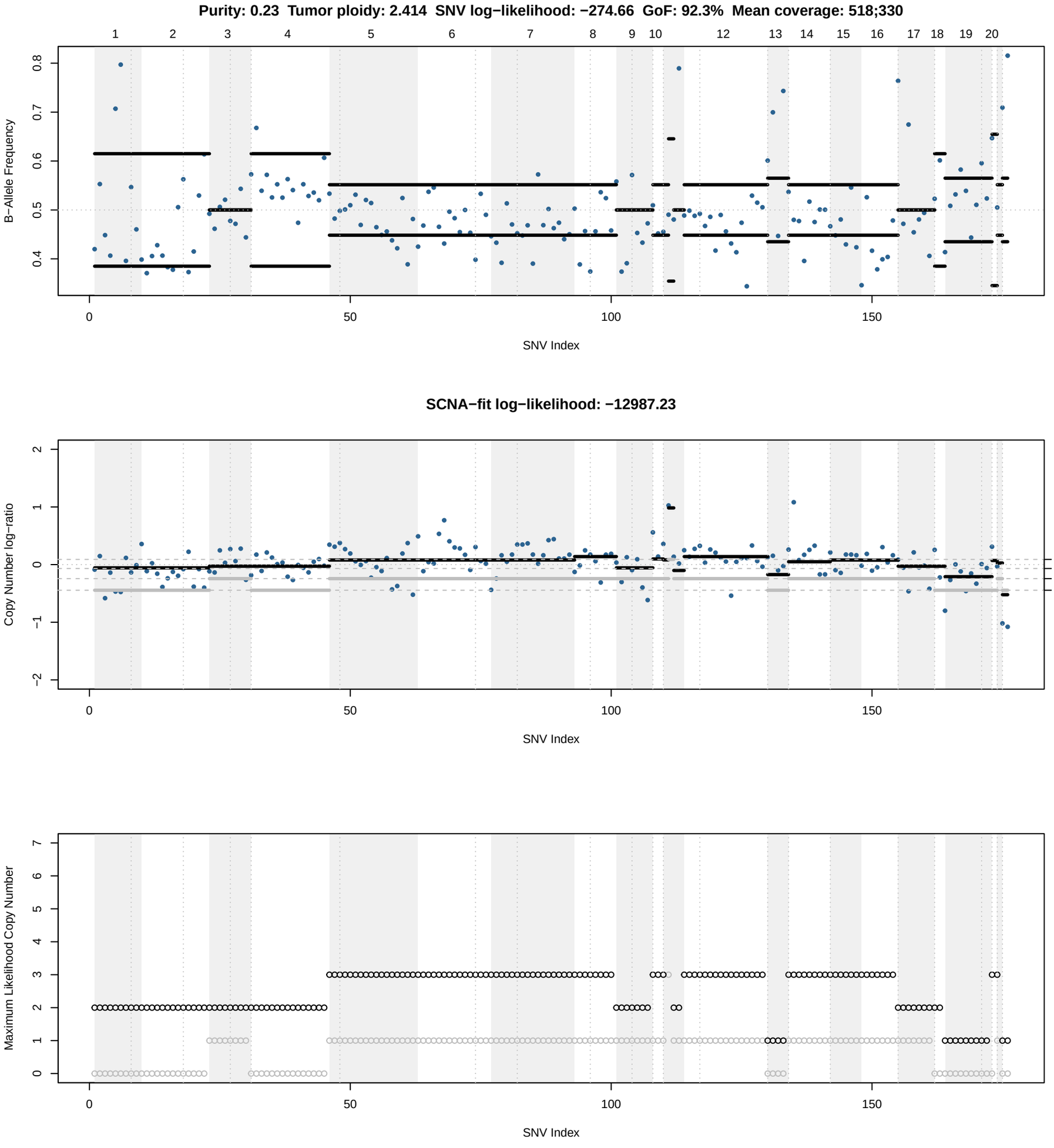

Allelic fraction (germline)
Copy Number log−ratio
4m4
3m3
5m4
4m3
1m1
3m2
5m3
4m2
6m3
5m2
3m1
4m1

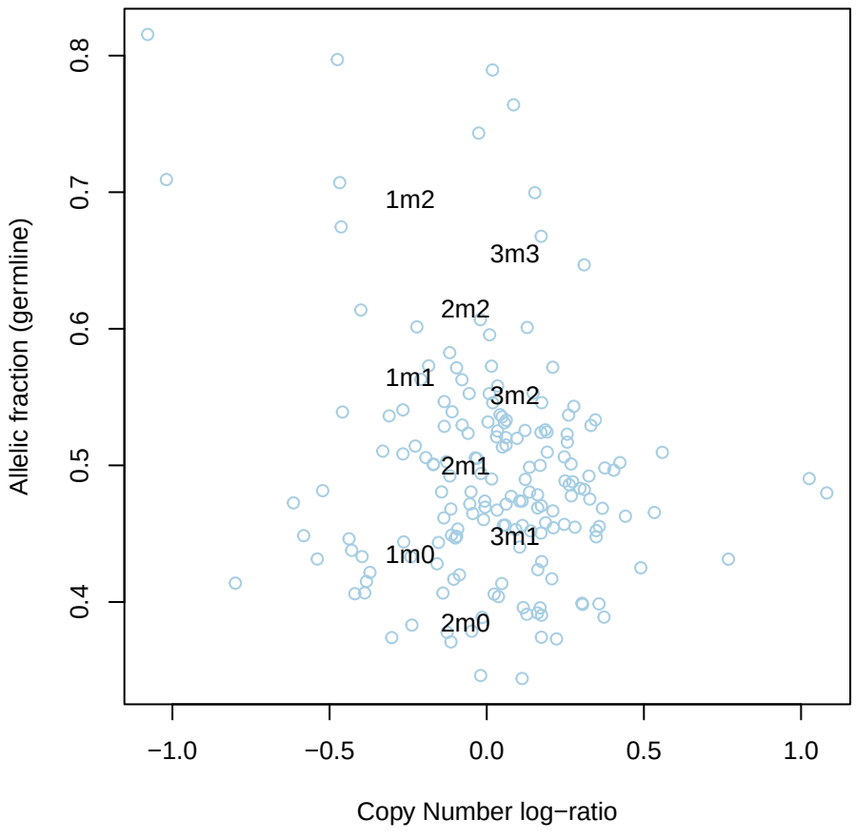

Coverage (log2)
Allelic fraction

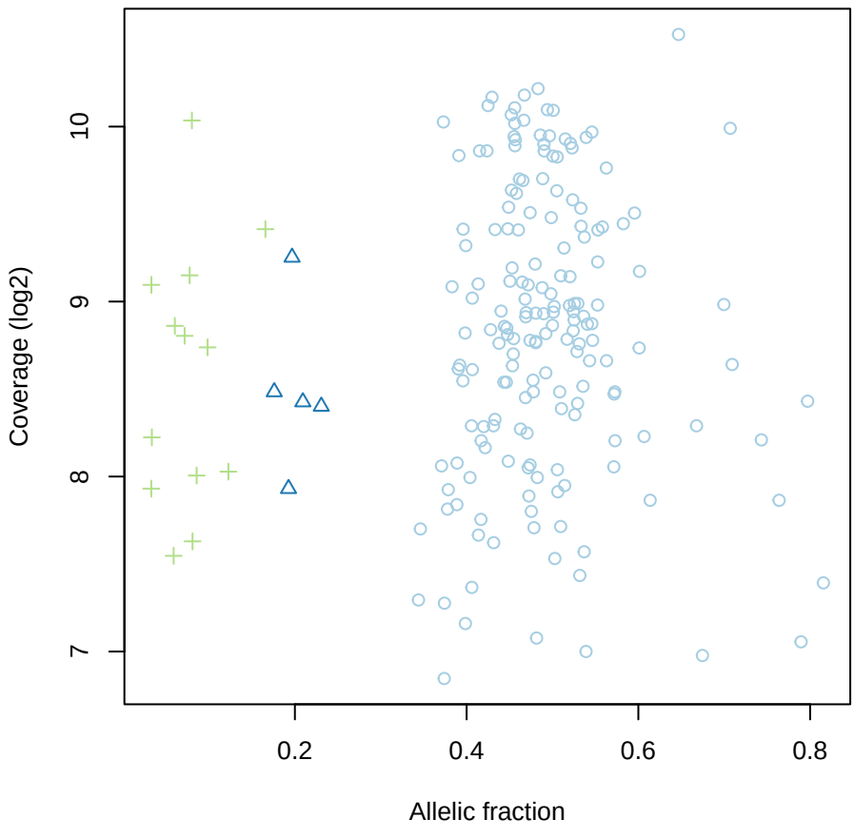

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
5m2
1m1
3m1
4m1
5m1

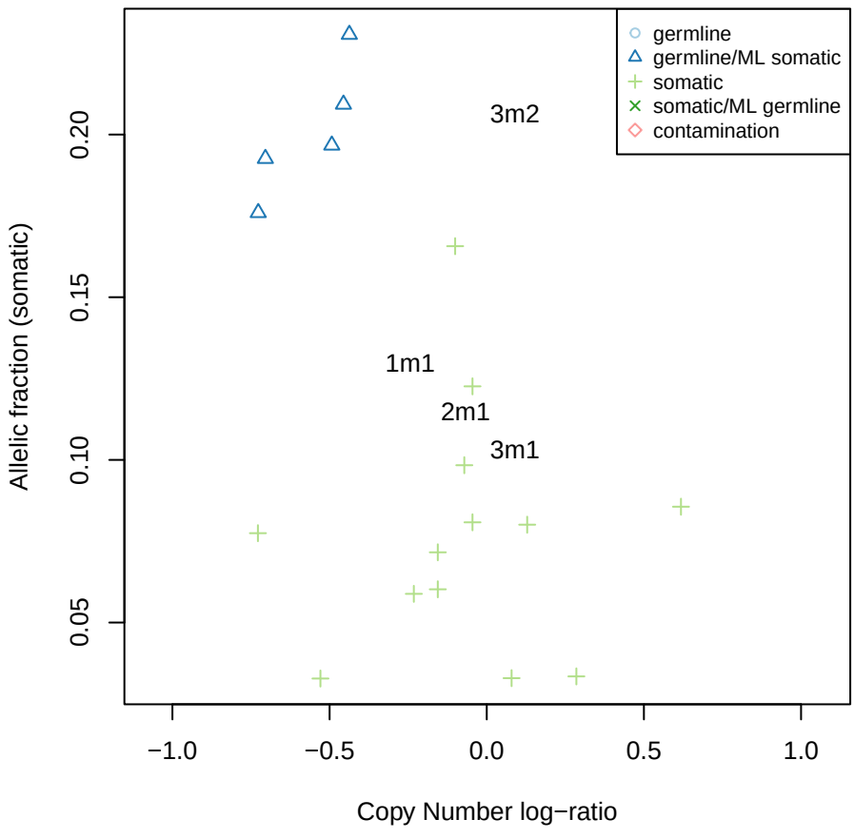

Frequency
Cellular fraction

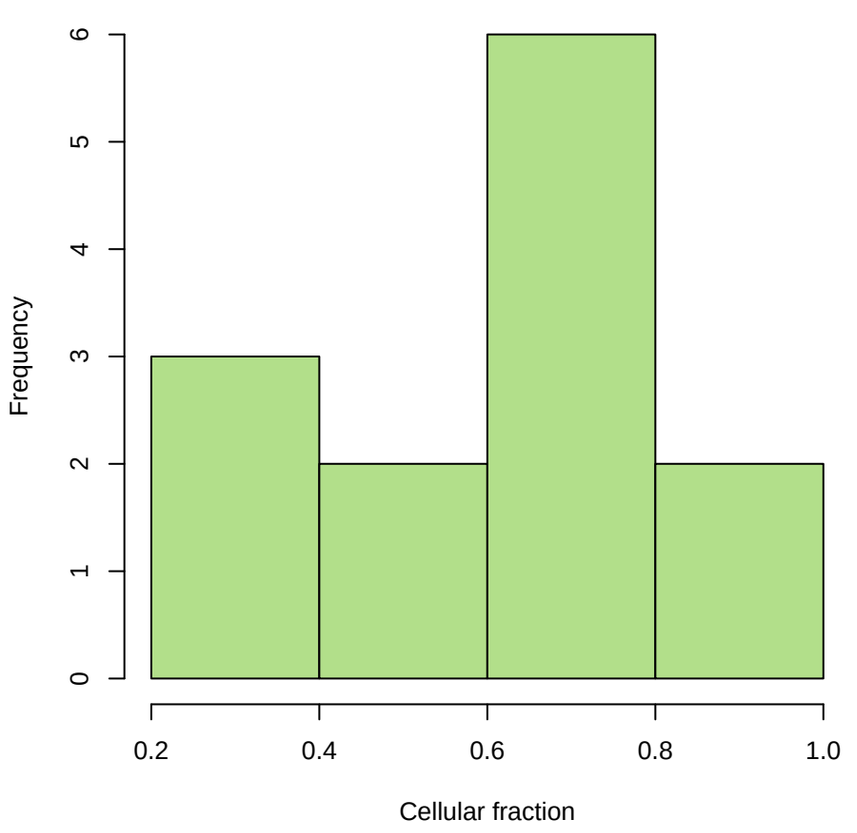

Purity: 0.23 Tumor ploidy: 2.414
0
1
2
3
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
1.0
log2 ratio

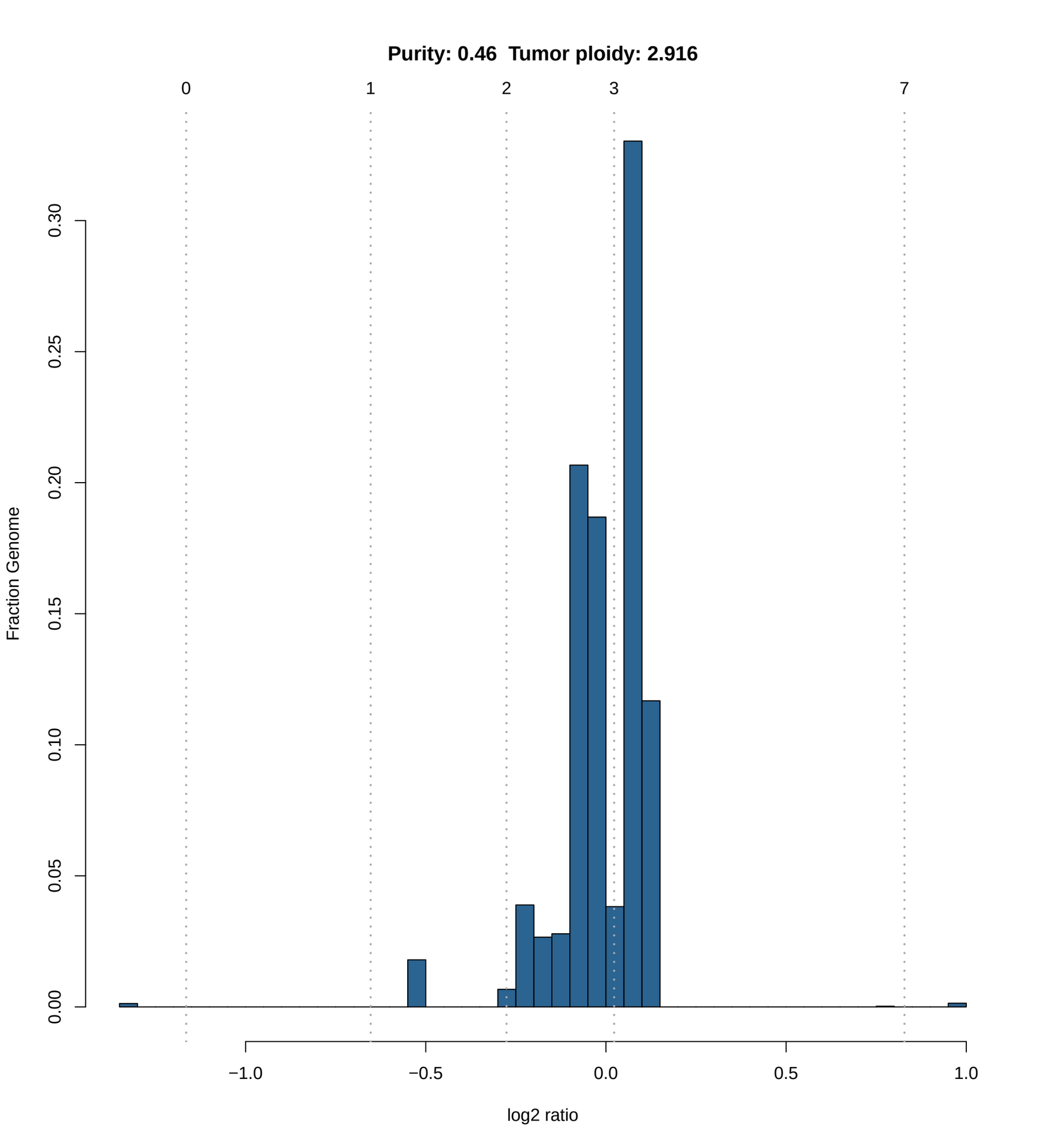

Purity: 0.23 Tumor ploidy: 2.414 SNV log−likelihood: −274.66 GoF: 92.3% Mean coverage: 518;330
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 18 19 20
B−Allele Frequency
0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index
SCNA−fit log−likelihood: −12987.23
Copy Number log−ratio
−2 −1 0 1 2
0 2
0 50 100 150
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

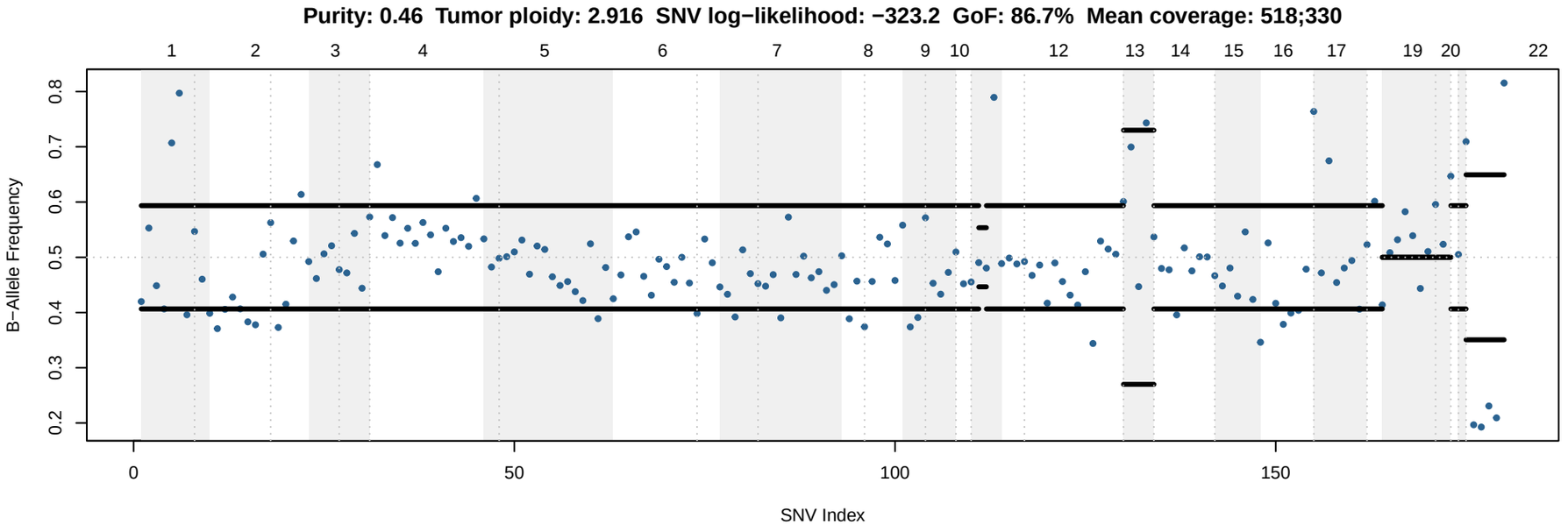

Allelic fraction (germline)
0.4
0.5
0.6
0.7
0.8
1m2
3m3
2m2
1m1
3m2
2m1
3m1
1m0
2m0
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

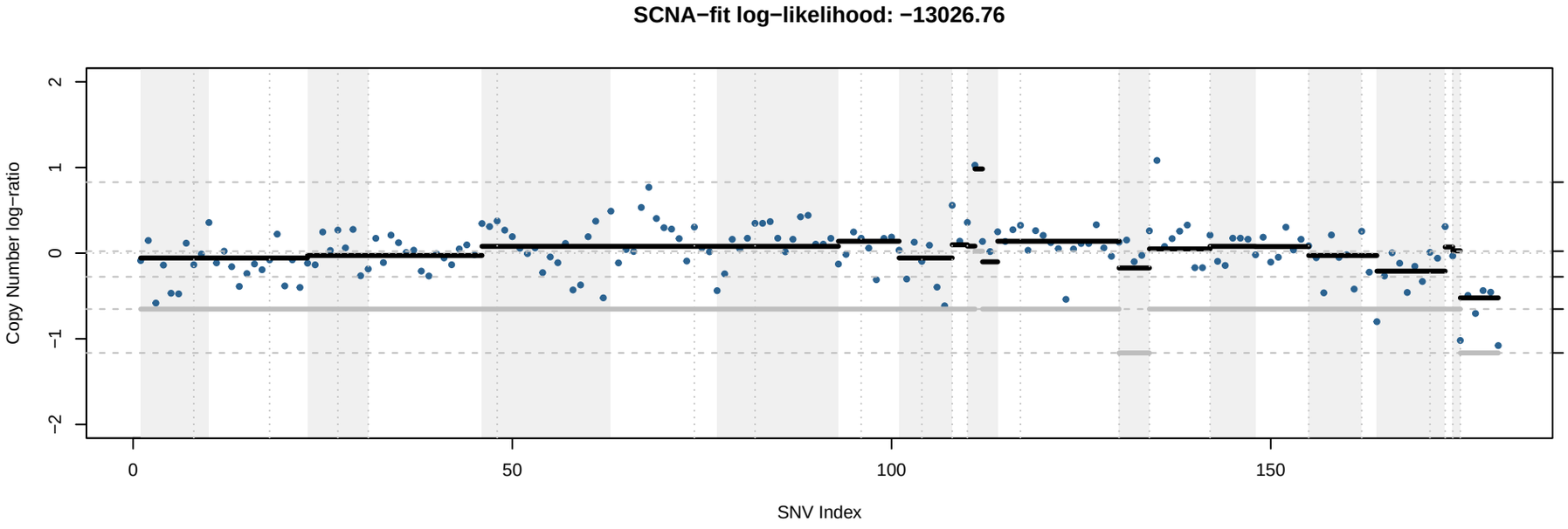

Coverage (log2)
7
8
9
10
0.2
0.4
0.6
0.8
Allelic fraction

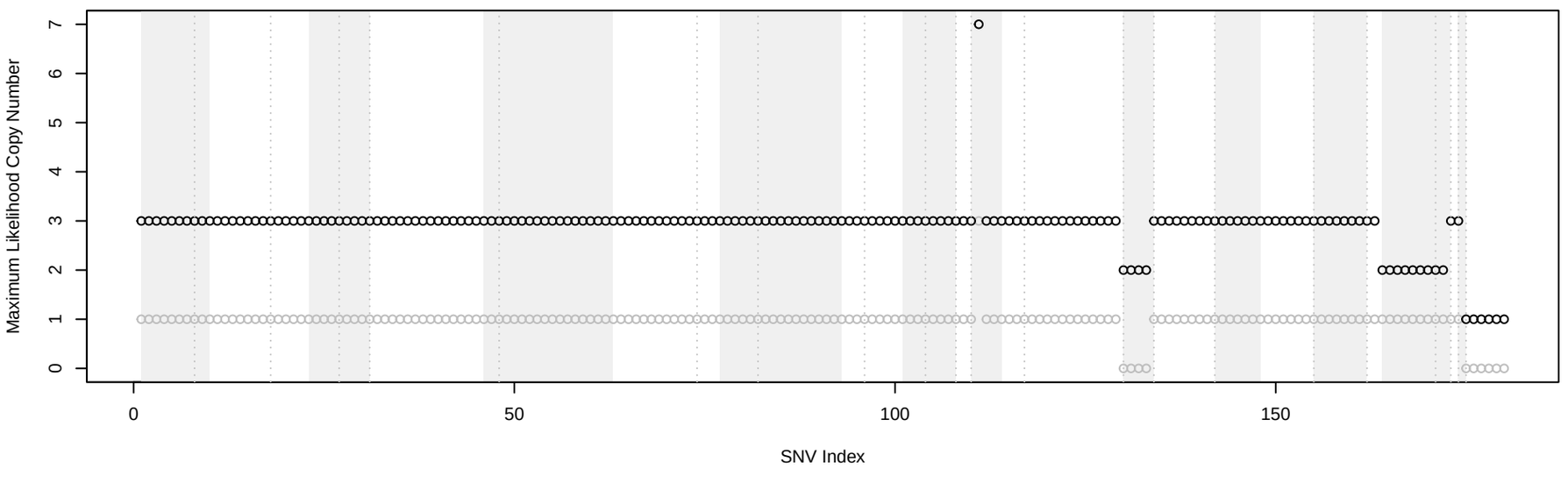

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0.20
3m2
1m1
2m1
3m1
−1.0
−0.5
0.0
0.5
1.0
Copy Number log−ratio

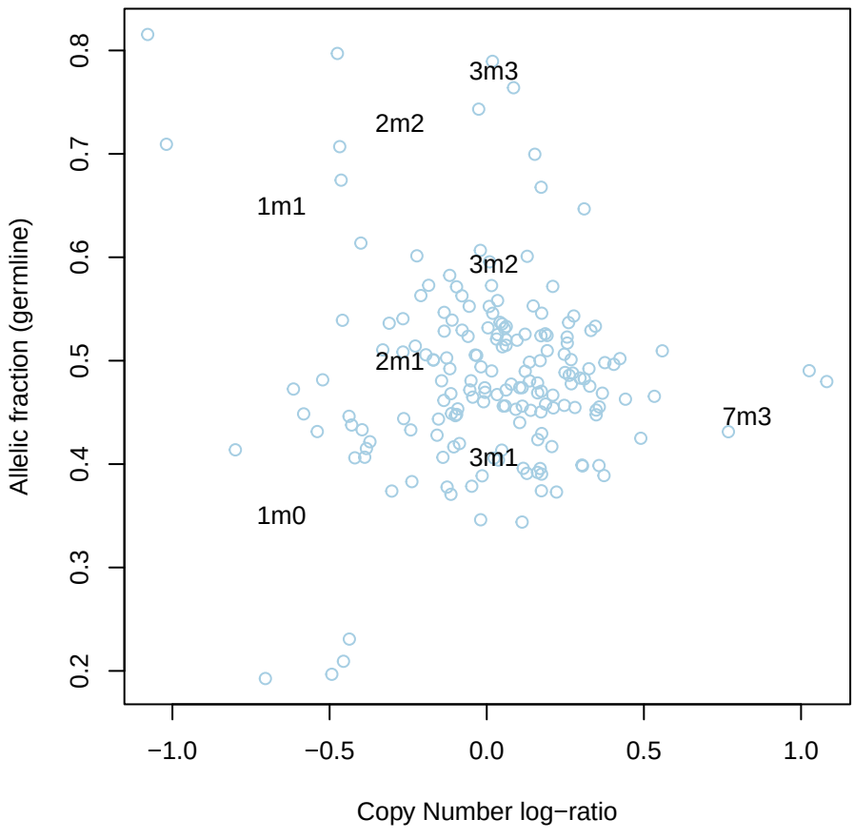

Frequency
0
1
2
3
4
5
6
0.2
0.4
0.6
0.8
1.0
Cellular fraction

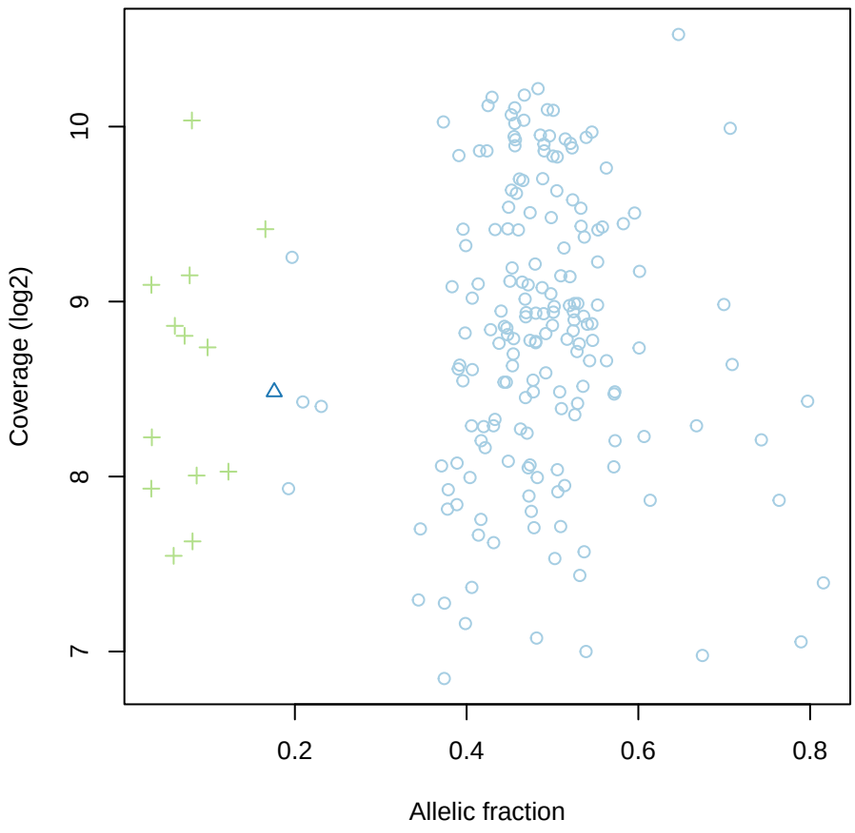

Purity: 0.46 Tumor ploidy: 2.916
0
1
2
3
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

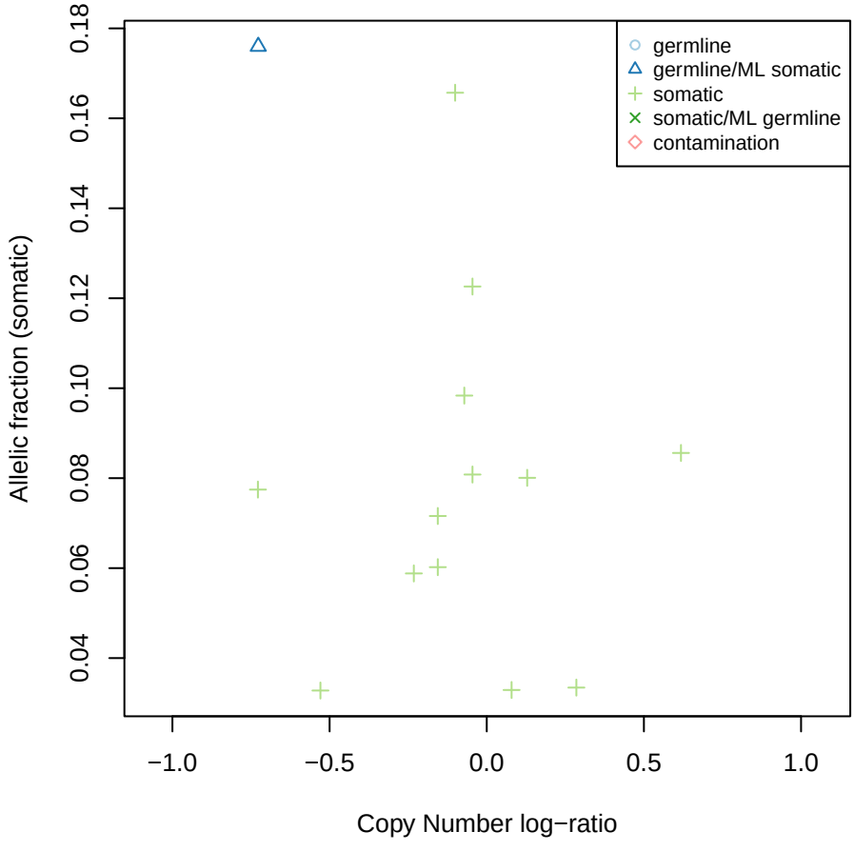

Purity: 0.46 Tumor ploidy: 2.916 SNV log−likelihood: −323.2 GoF: 86.7% Mean coverage: 518;330
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 19 20 22
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

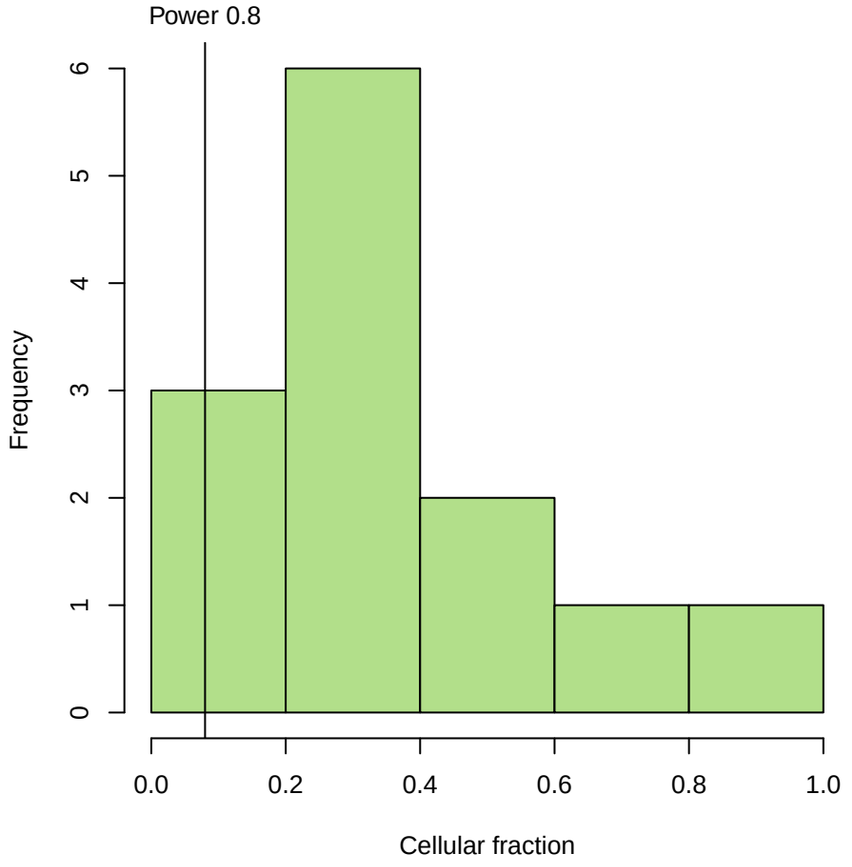

SCNA−fit log−likelihood: −13026.76
Copy Number log−ratio
−2 −1 0 1 2
0 1 2 3 7
0 50 100 150
SNV Index

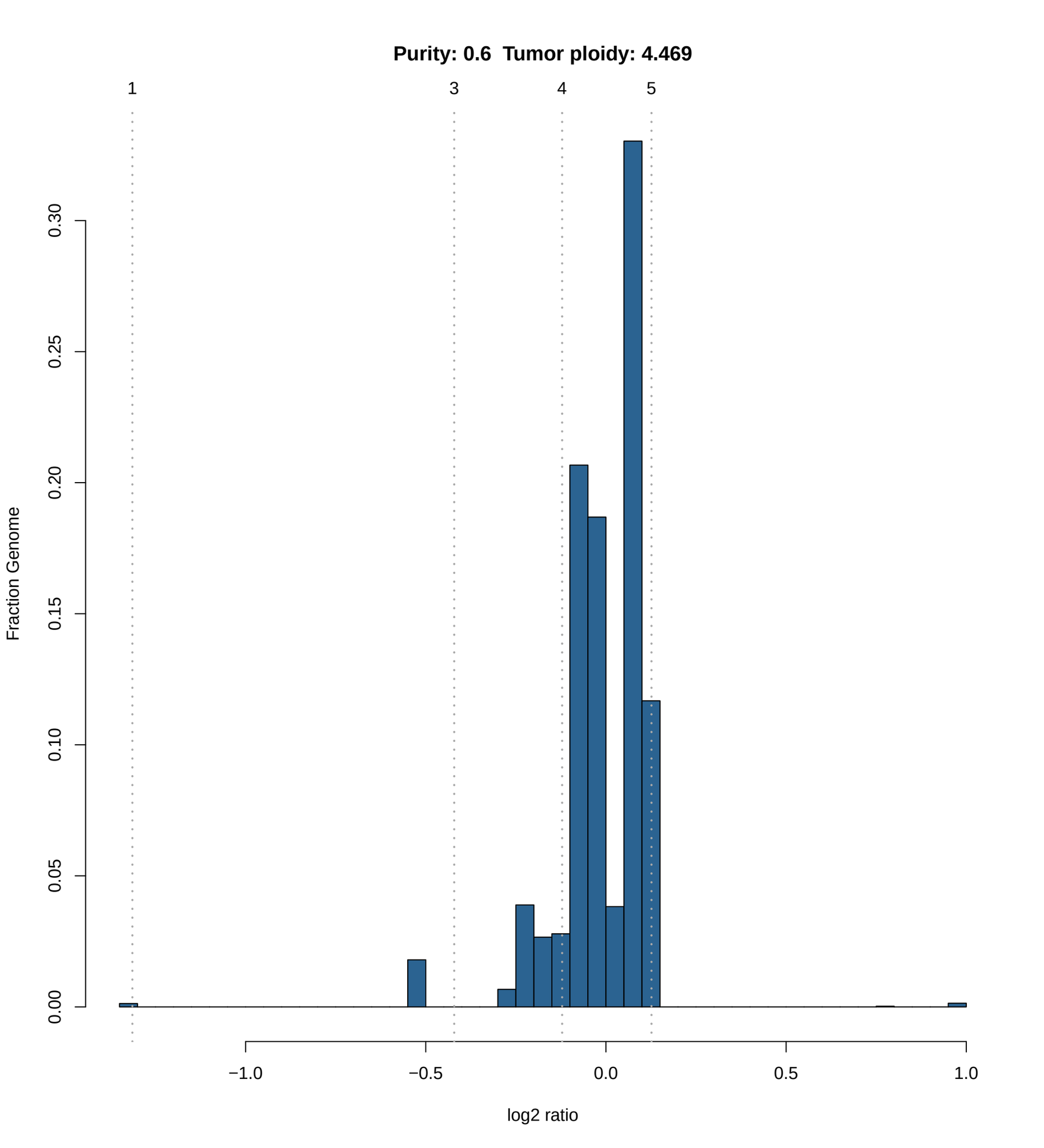

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

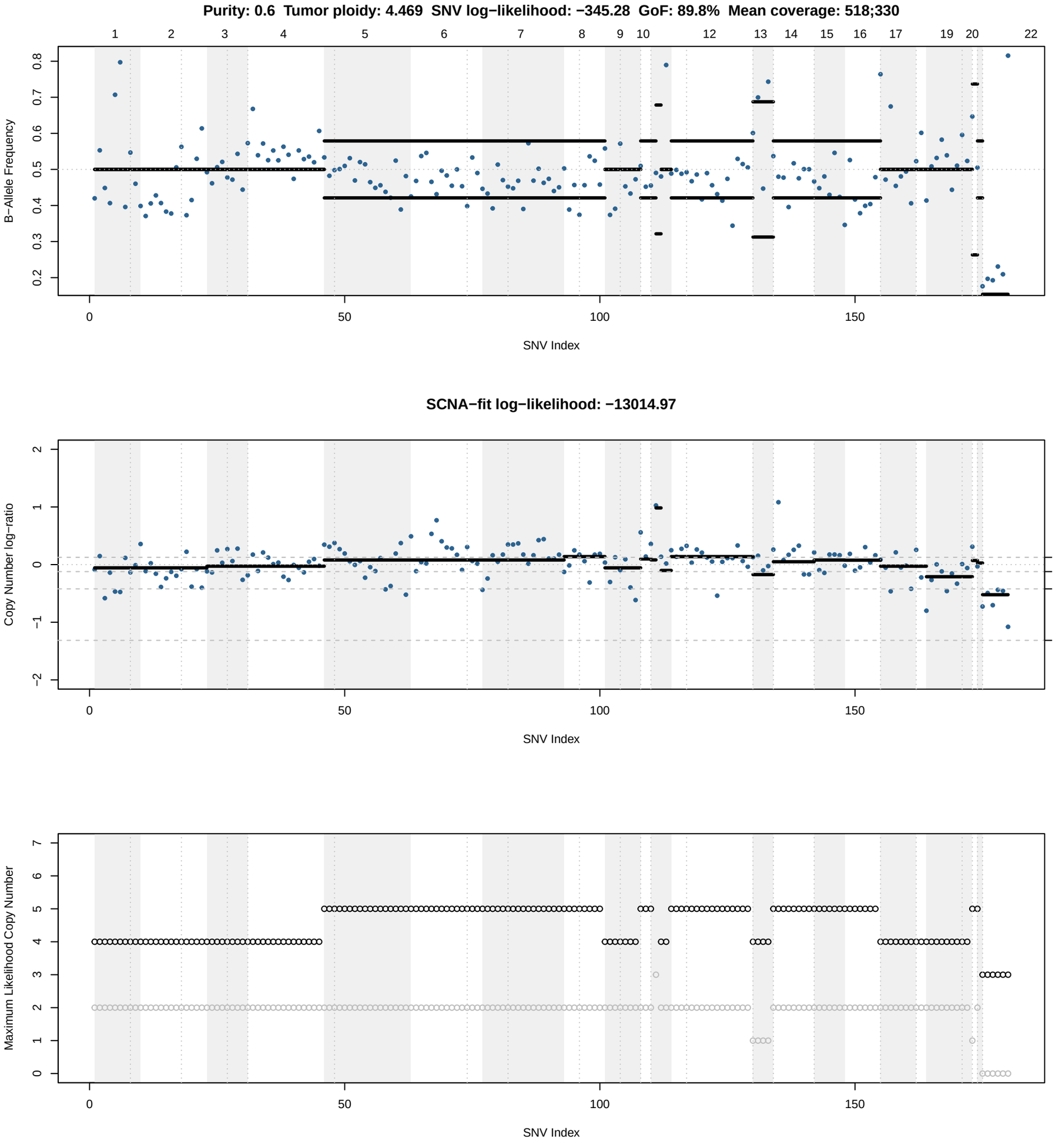

3m3
2m2
1m1
3m2
2m1
7m3
3m1
1m0
Allelic fraction (germline)
Copy Number log−ratio

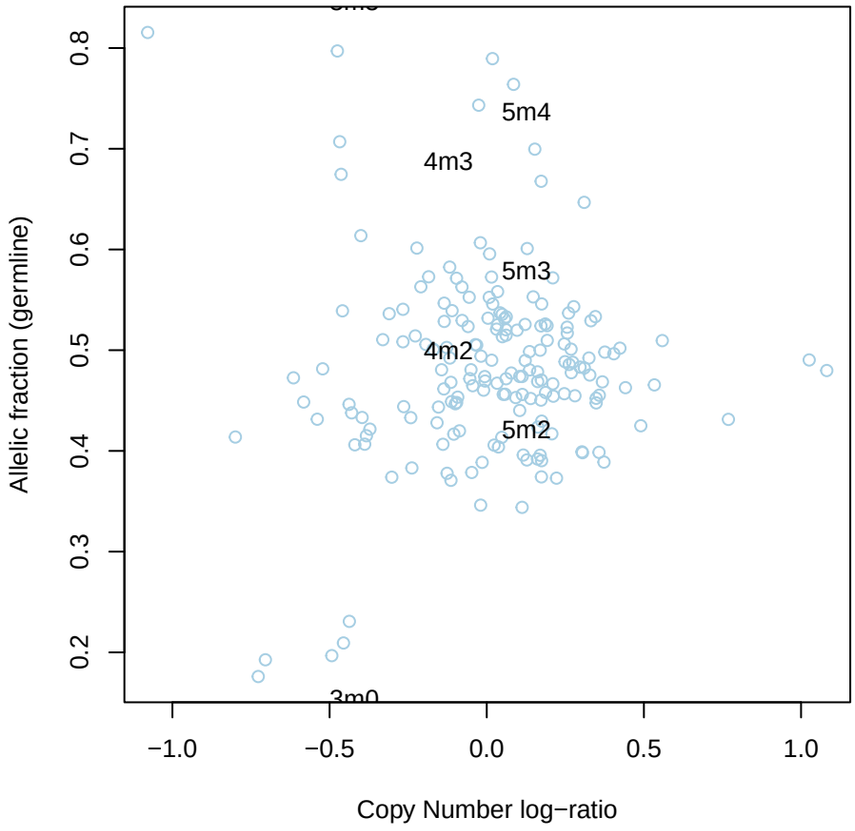

Coverage (log2)
Allelic fraction

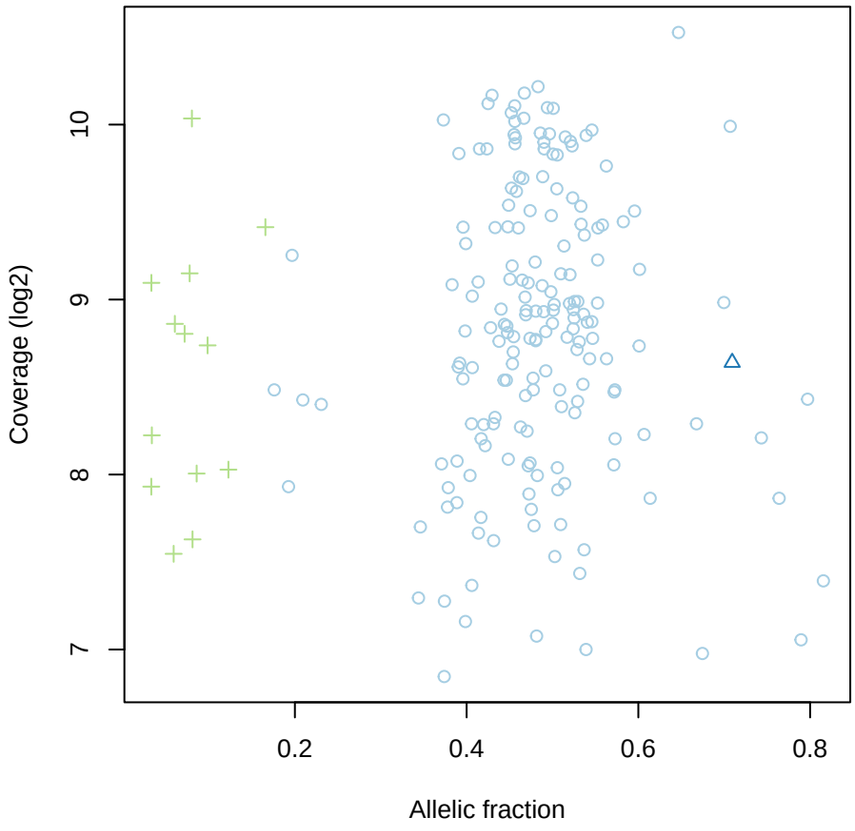

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio

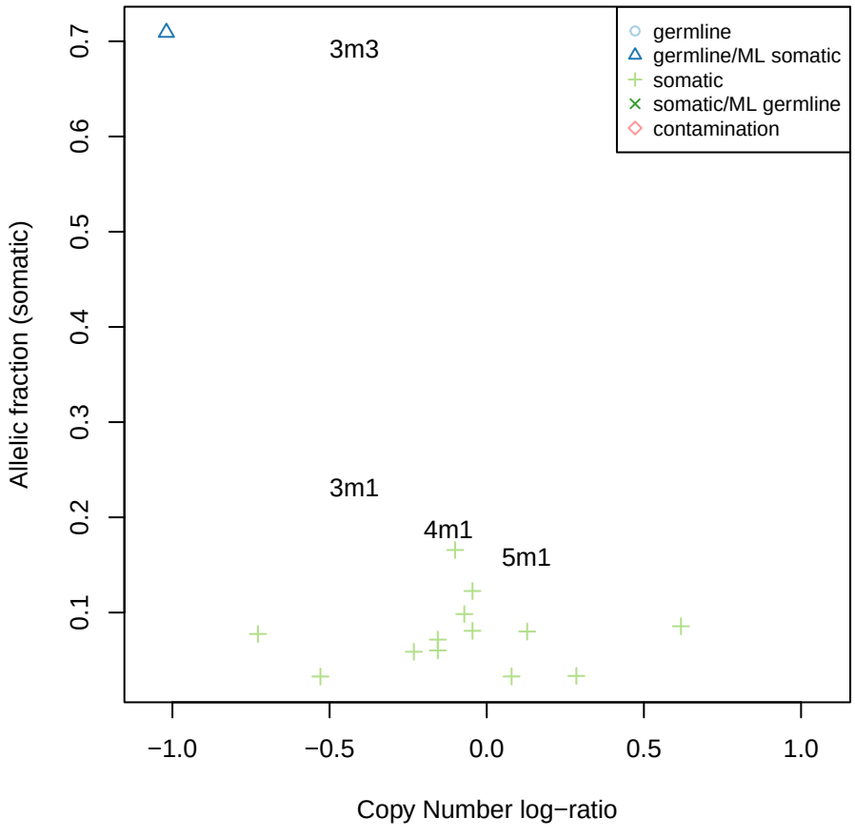

Power 0.8
Frequency
Cellular fraction

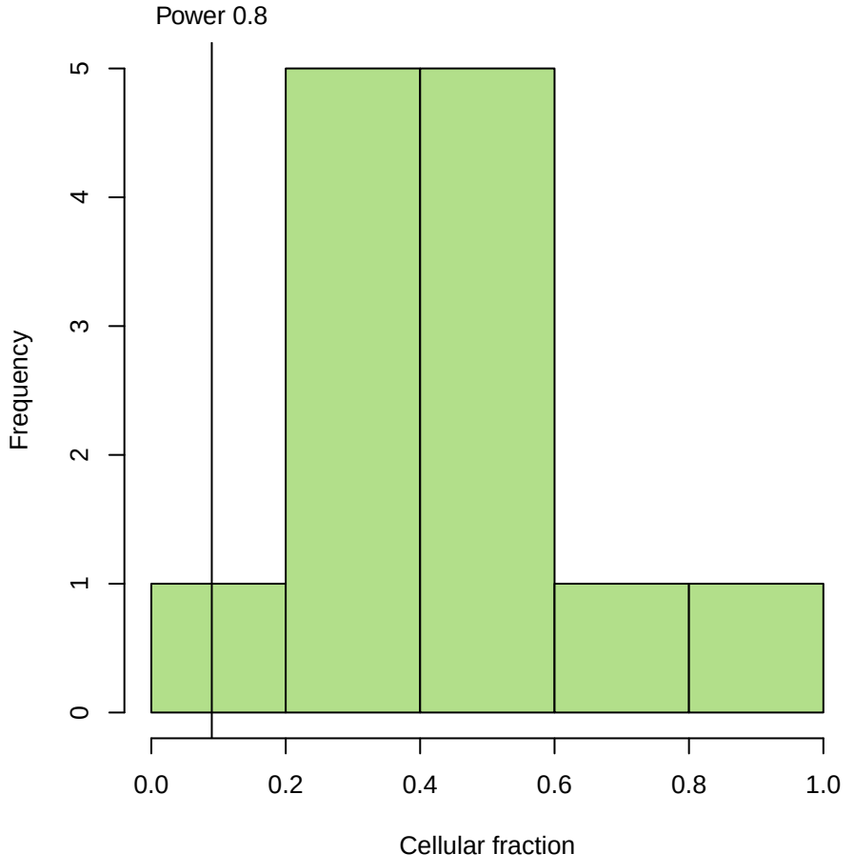

Purity: 0.6 Tumor ploidy: 4.469
1
3
4
5
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

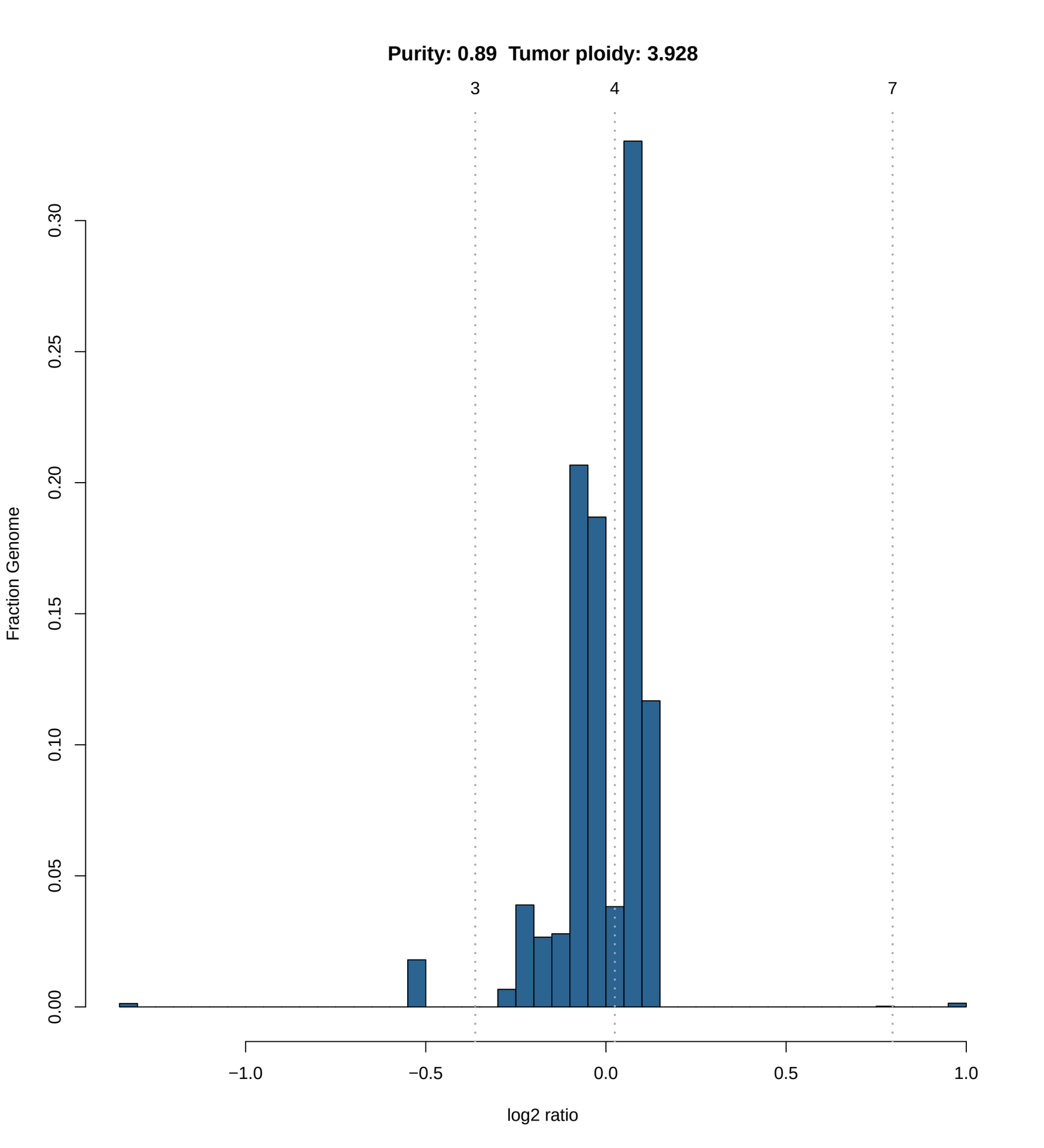

Purity: 0.6 Tumor ploidy: 4.469 SNV log−likelihood: −345.28 GoF: 89.8% Mean coverage: 518;330
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 19 20 22
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index
SCNA−fit log−likelihood: −13014.97
Copy Number log−ratio
−2 −1 0 1 2
1 3 4
0 50 100 150
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

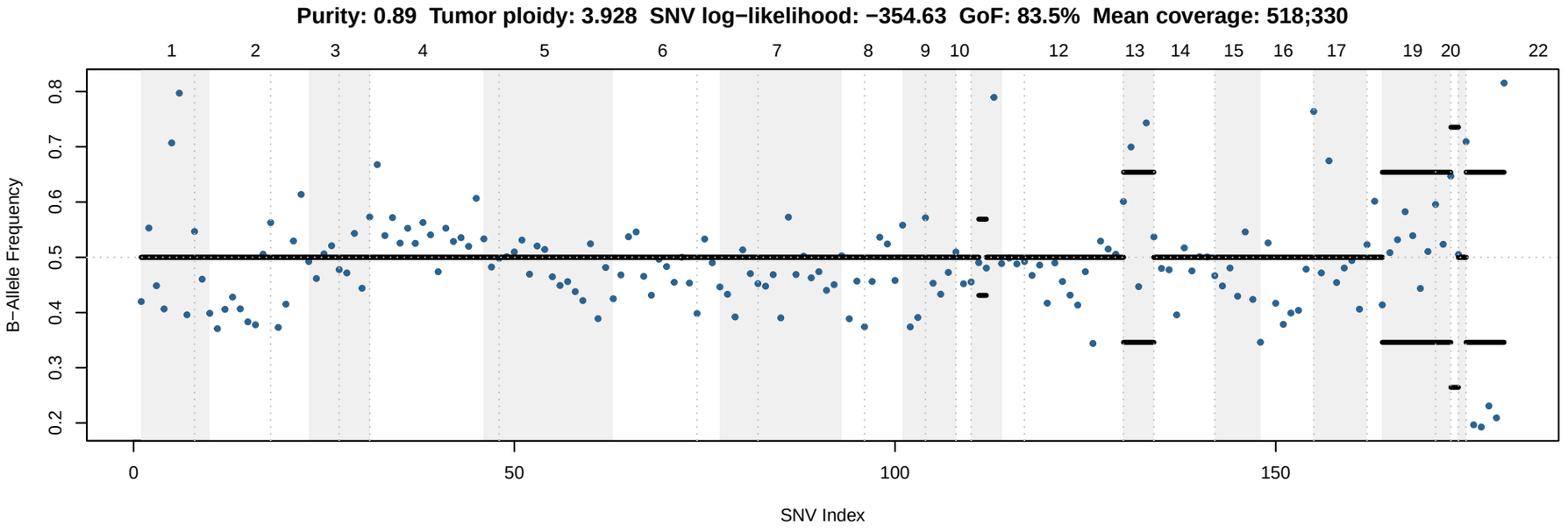

Allelic fraction (germline)
Copy Number log−ratio
5m4
4m3
5m3
4m2
5m2
3m0

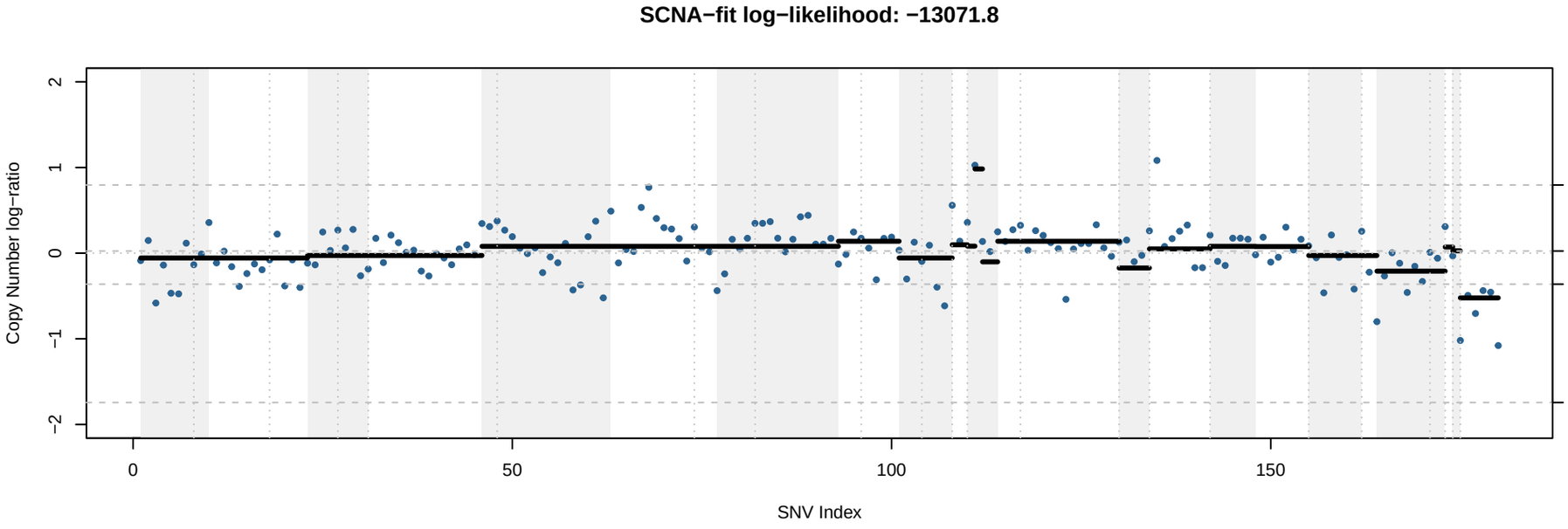

Coverage (log2)
Allelic fraction

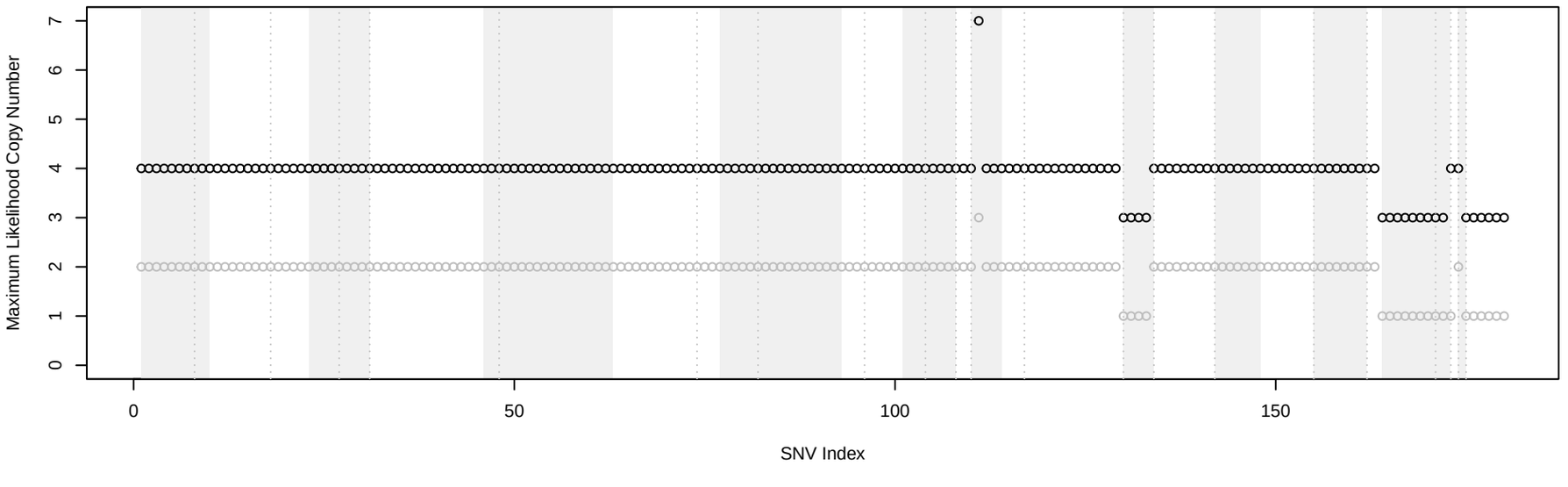

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m3
3m1
4m1
5m1

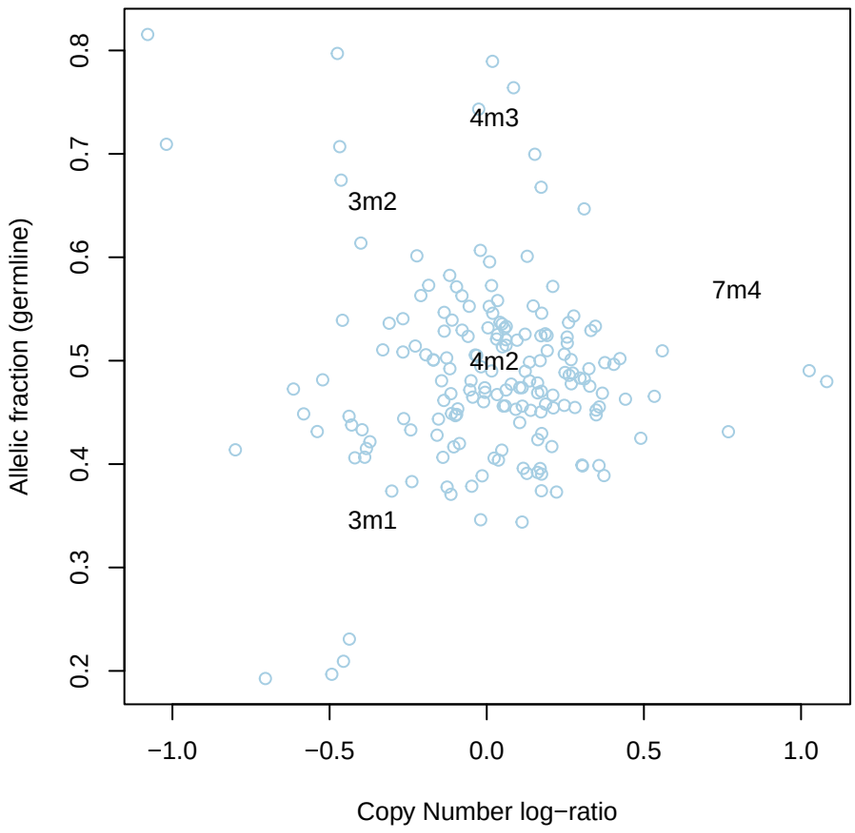

Power 0.8
Frequency
Cellular fraction

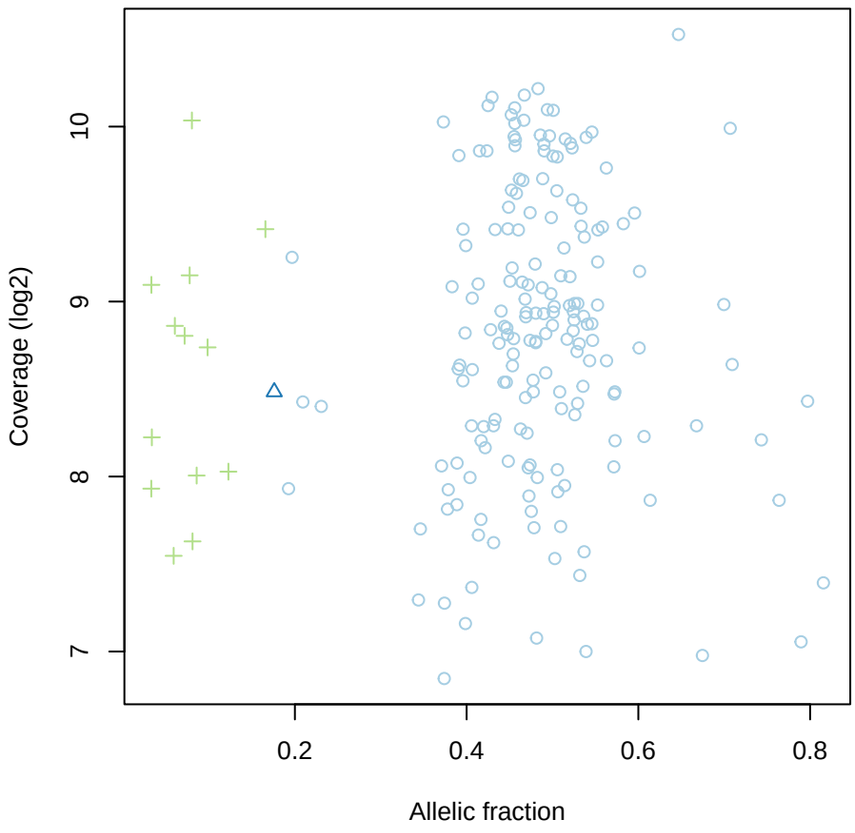

Purity: 0.89 Tumor ploidy: 3.928
3
4
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio

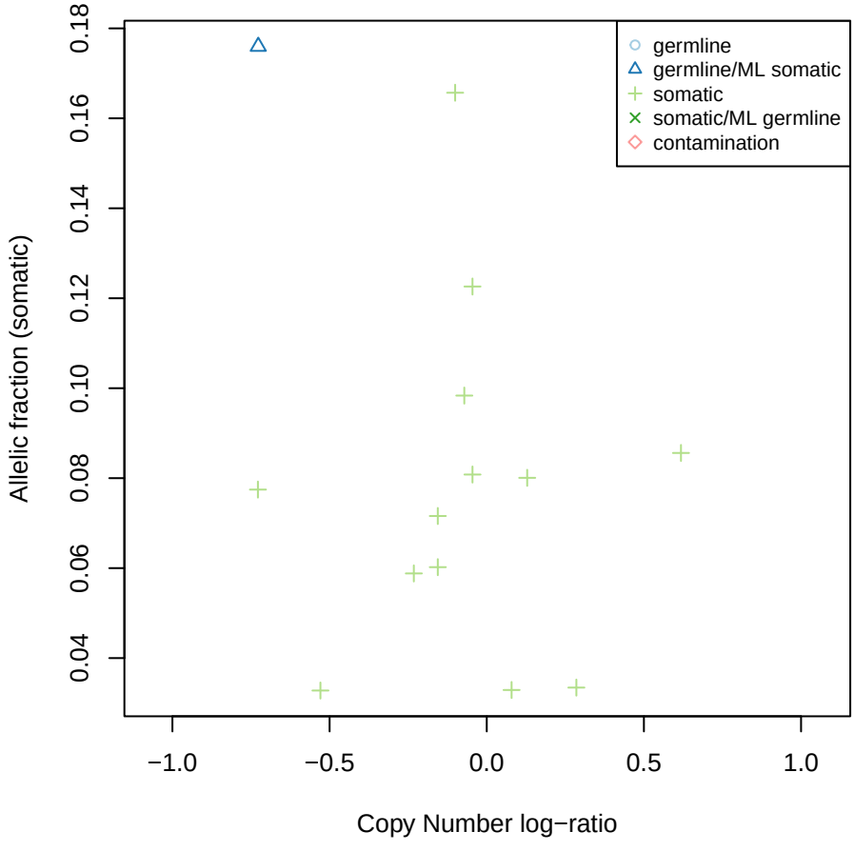

Purity: 0.89 Tumor ploidy: 3.928 SNV log−likelihood: −354.63 GoF: 83.5% Mean coverage: 518;330
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 19 20 22
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index

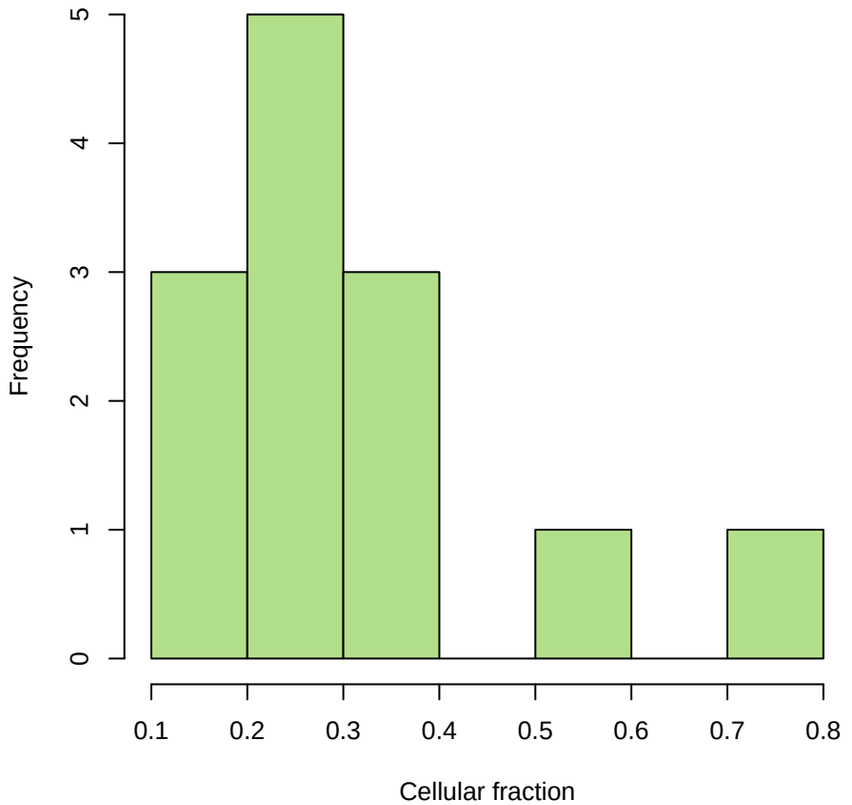

SCNA−fit log−likelihood: −13071.8
Copy Number log−ratio
2 1 0 −1 −2
7 4 3 1
0 50 100 150
SNV Index

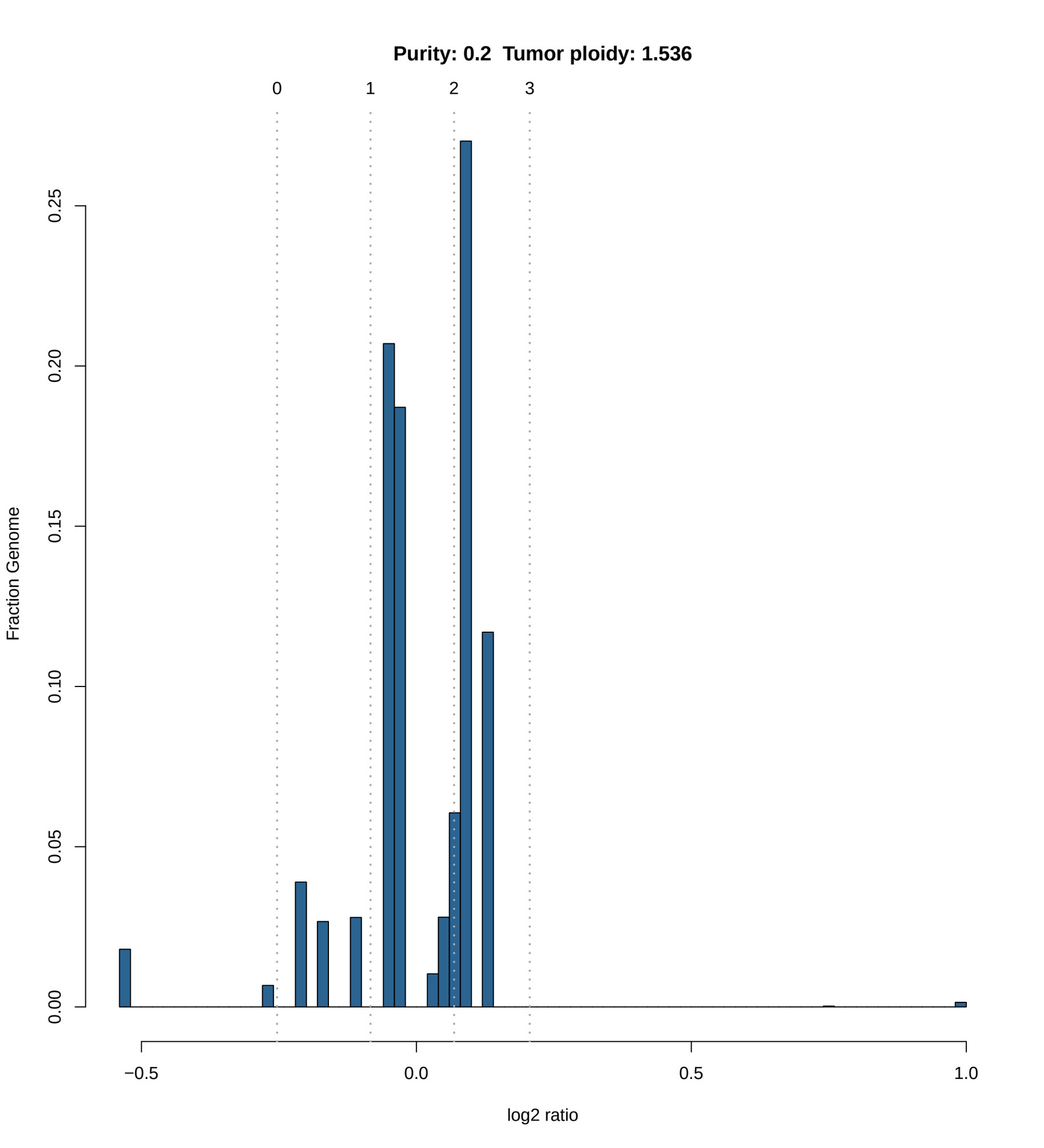

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

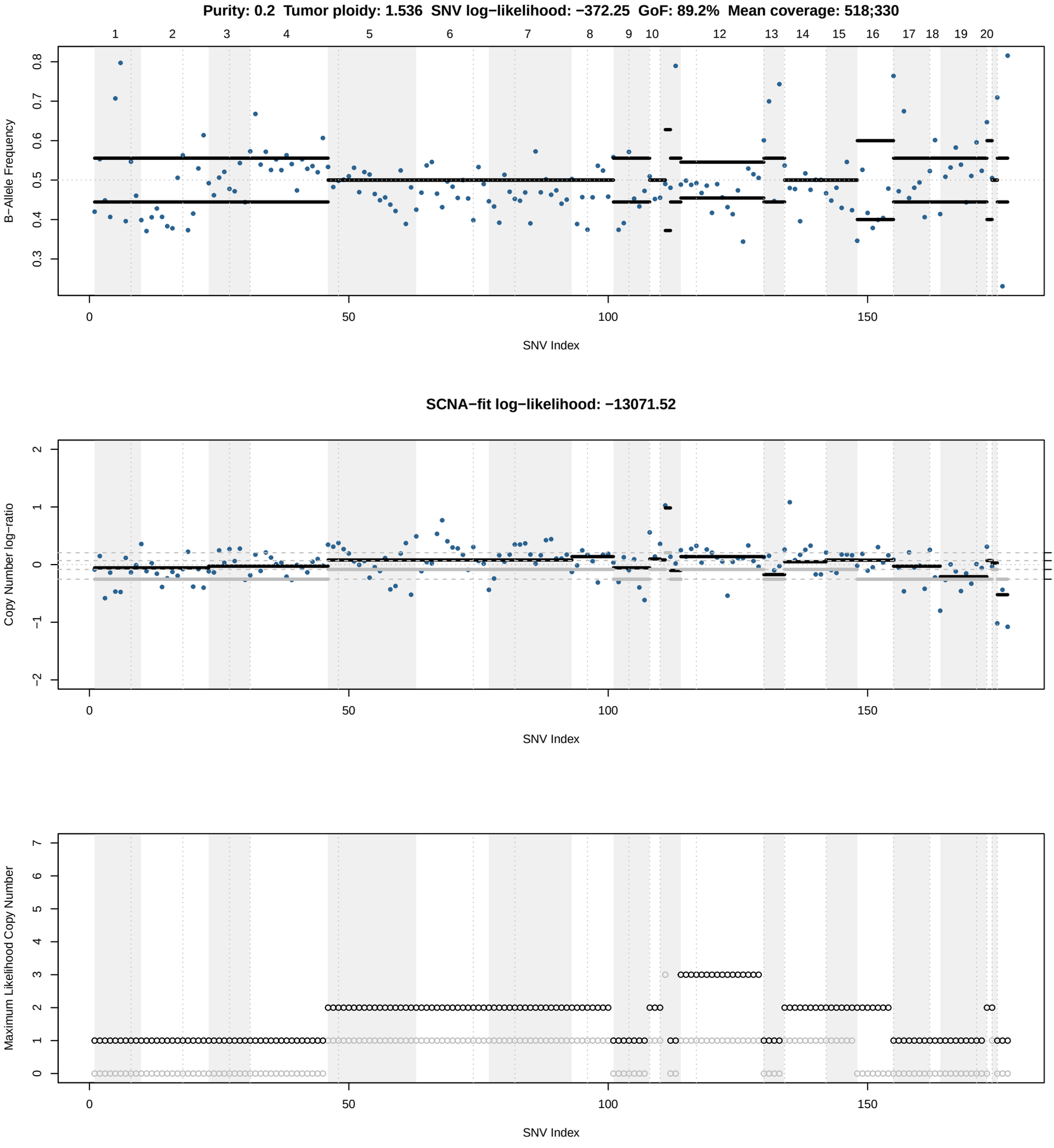

Allelic fraction (germline)
Copy Number log−ratio
4m3
3m2
7m4
4m2
3m1

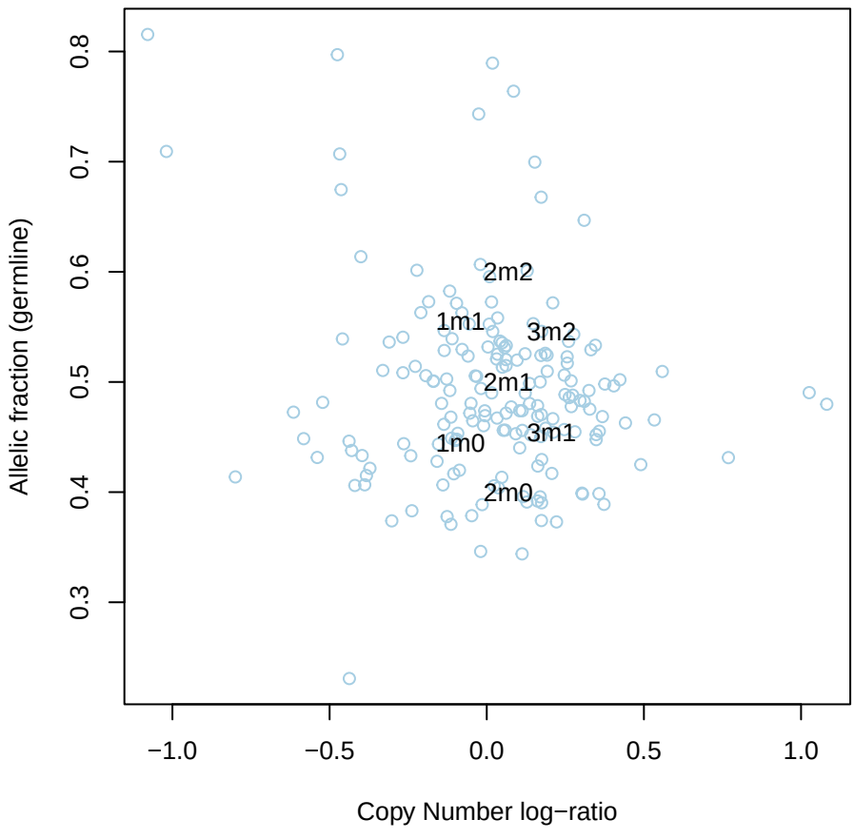

Coverage (log2)
Allelic fraction

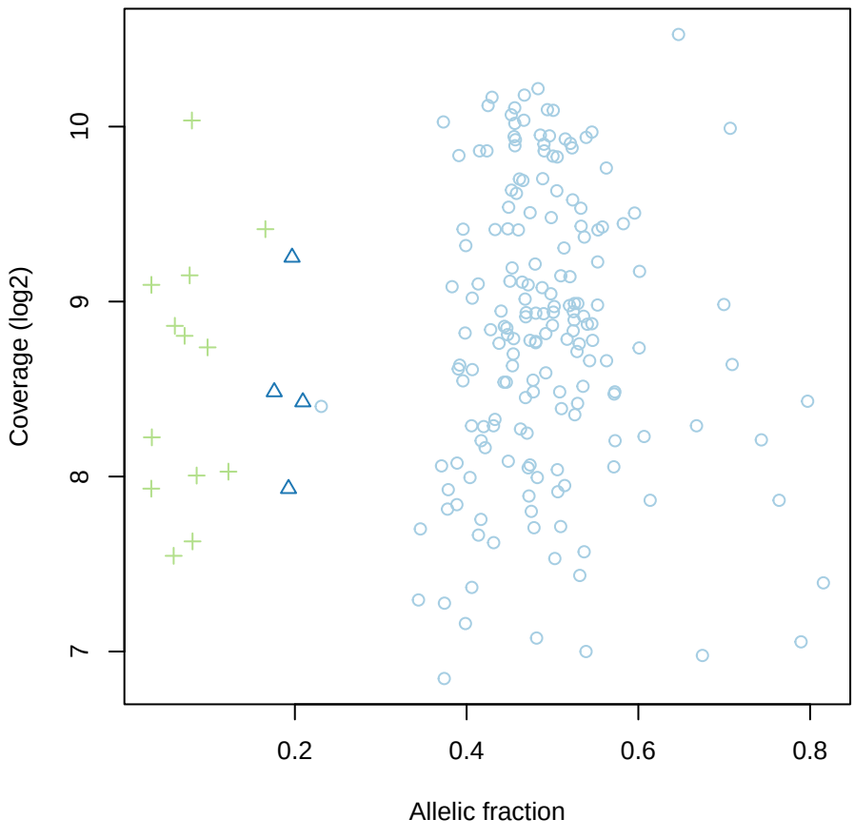

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

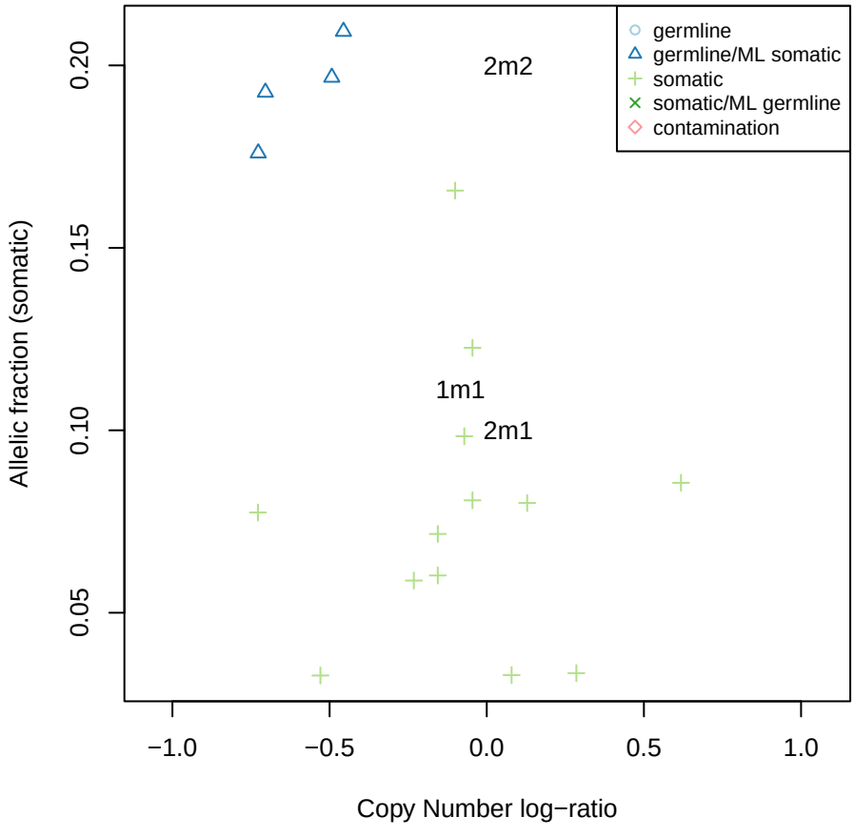

Frequency
Cellular fraction

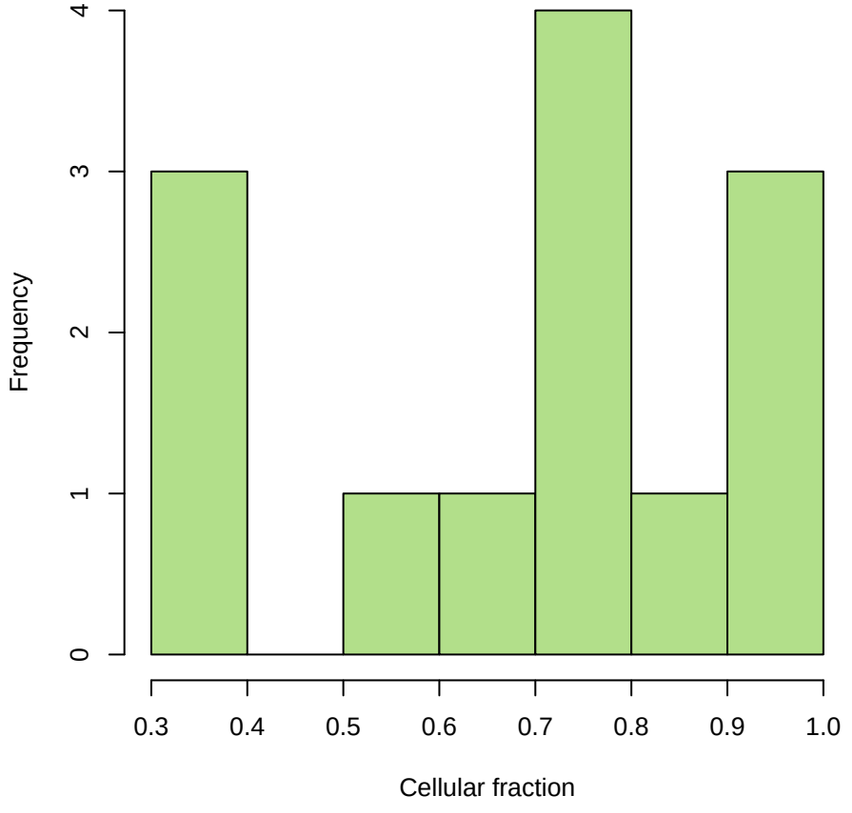

Purity: 0.2 Tumor ploidy: 1.536
0
1
2
3
Fraction Genome
0.00
0.05
0.10
0.15
0.20
0.25
−0.5
0.0
0.5
1.0
log2 ratio

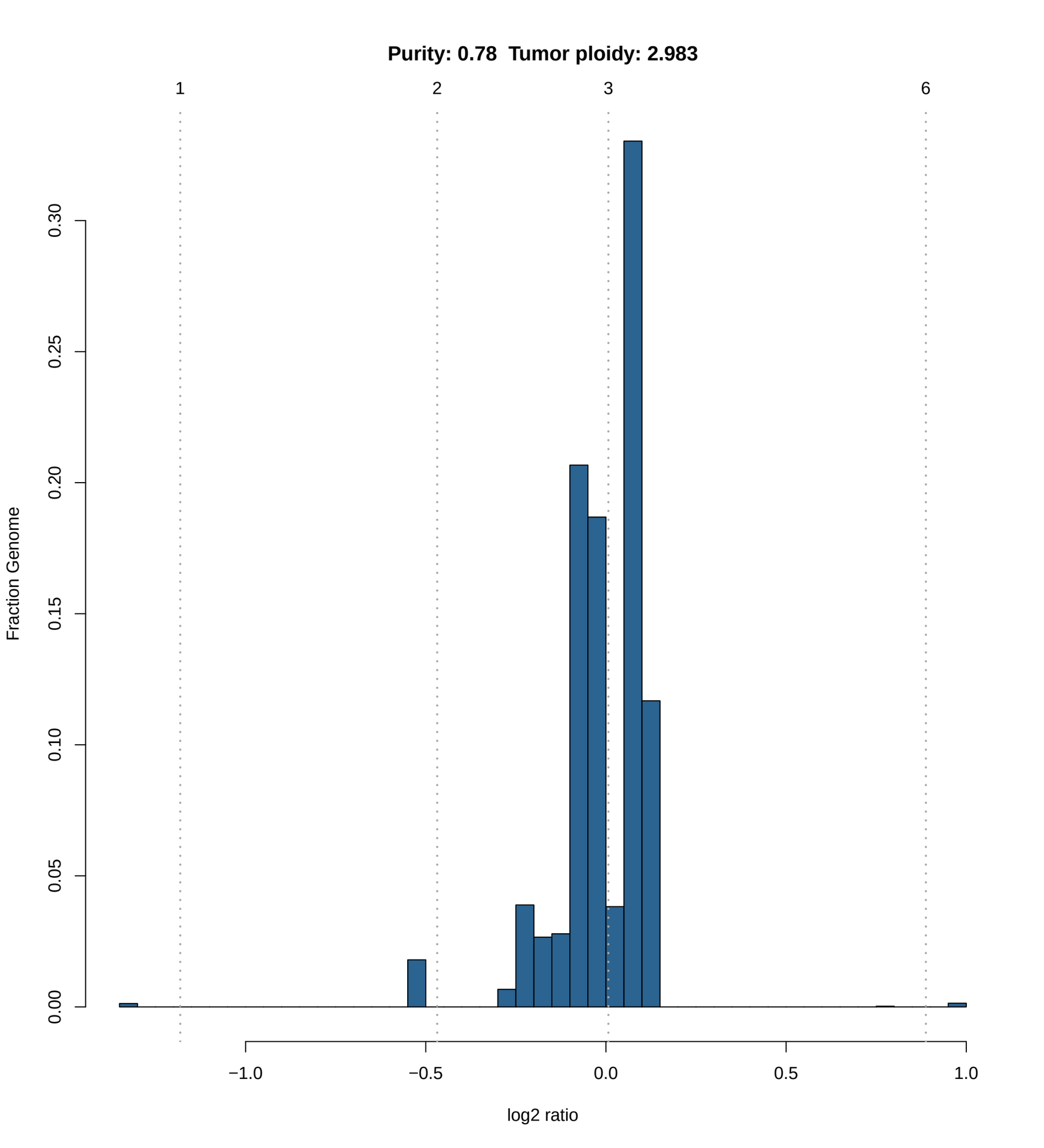

Purity: 0.2 Tumor ploidy: 1.536 SNV log−likelihood: −372.25 GoF: 89.2% Mean coverage: 518;330
1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7 0.8
0 50 100 150
SNV Index
SCNA−fit log−likelihood: −13071.52
Copy Number log−ratio
−2 −1 0 1 2
0 2
0 50 100 150
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 50 100 150
SNV Index

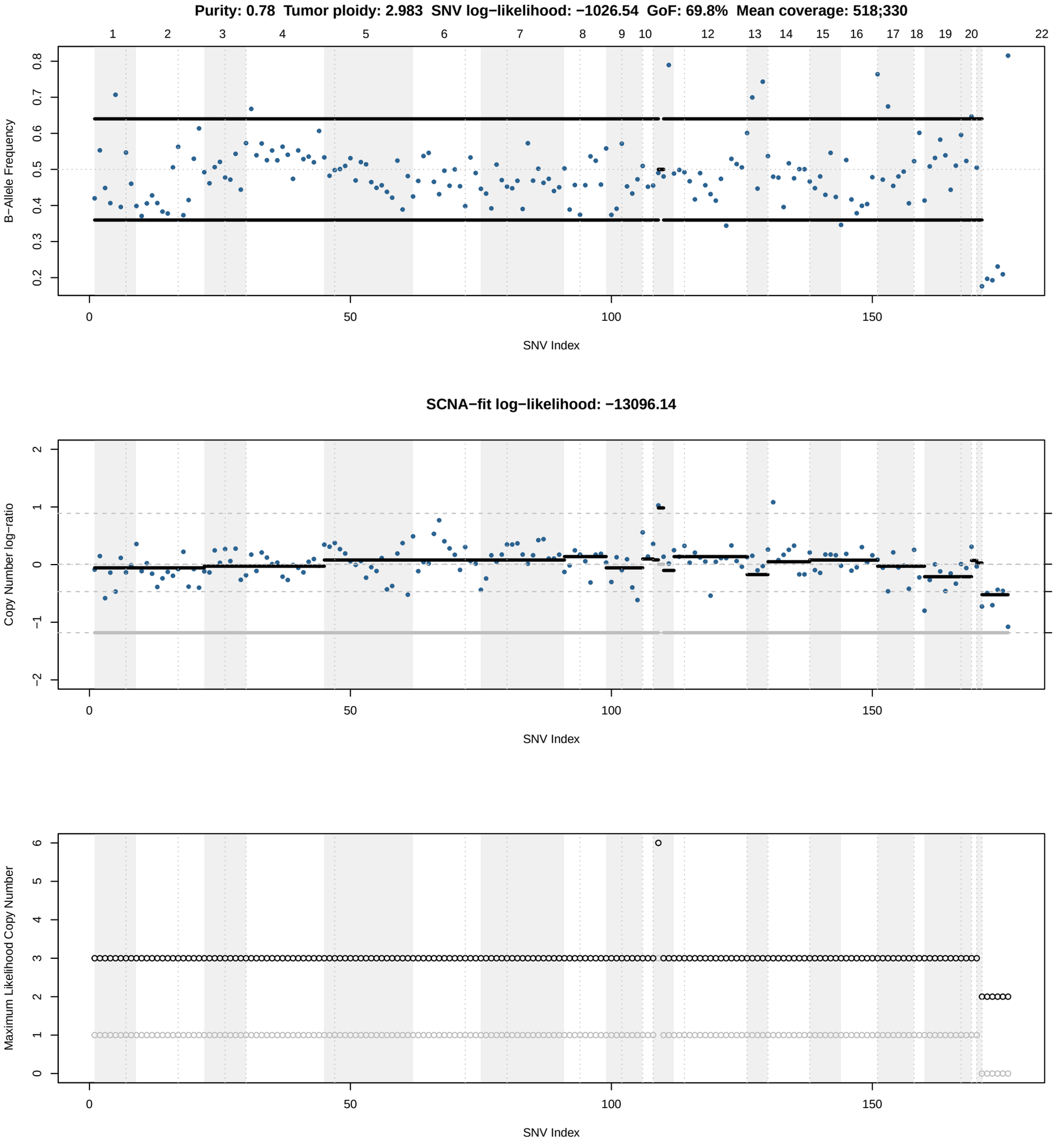

Allelic fraction (germline)
Copy Number log−ratio
2m2
1m1
3m2
2m1
3m1
1m0
2m0

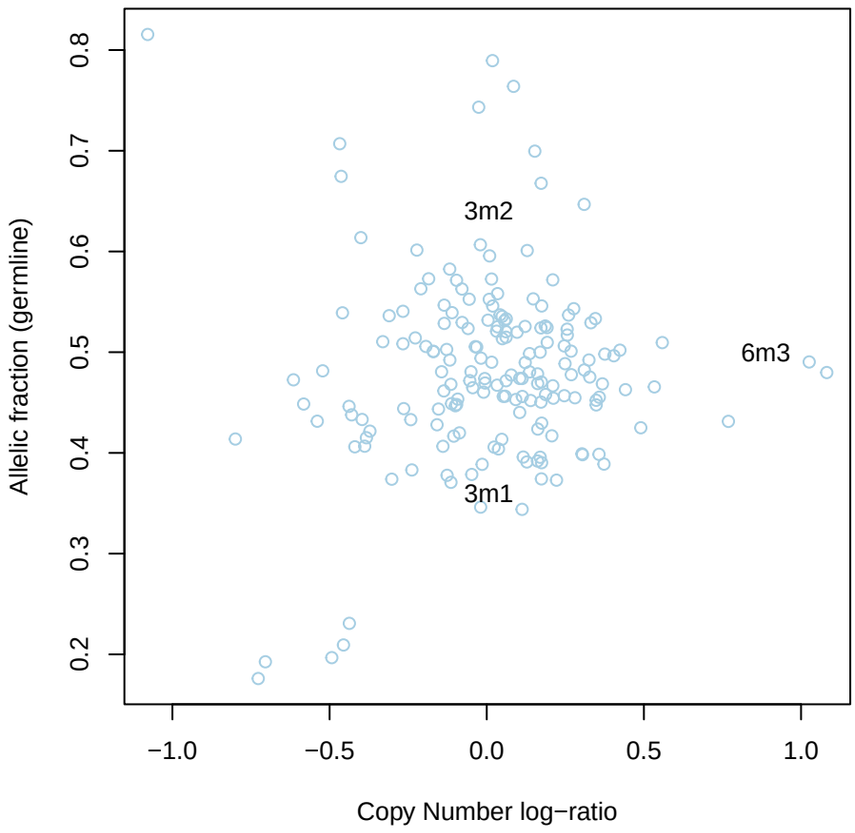

Coverage (log2)
Allelic fraction

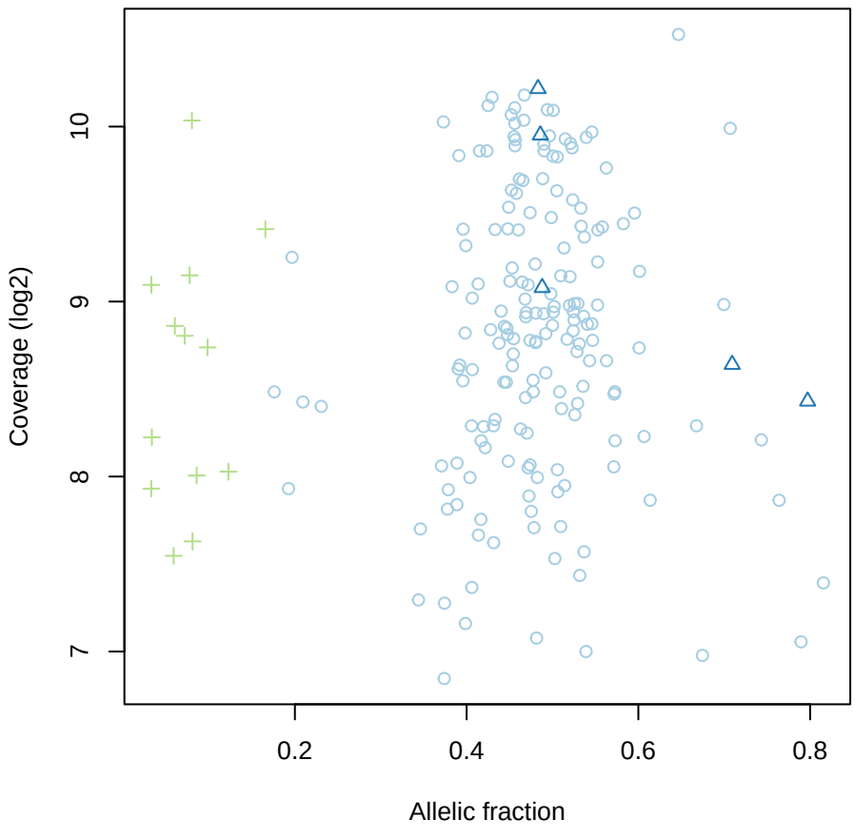

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m2
1m1
2m1

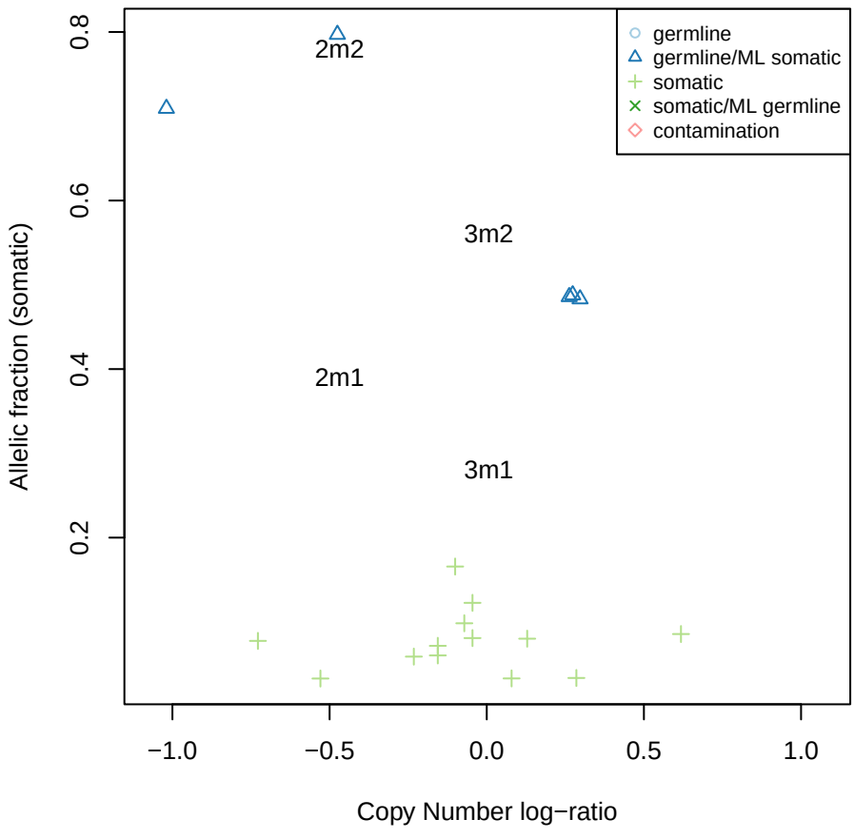

Frequency
Cellular fraction

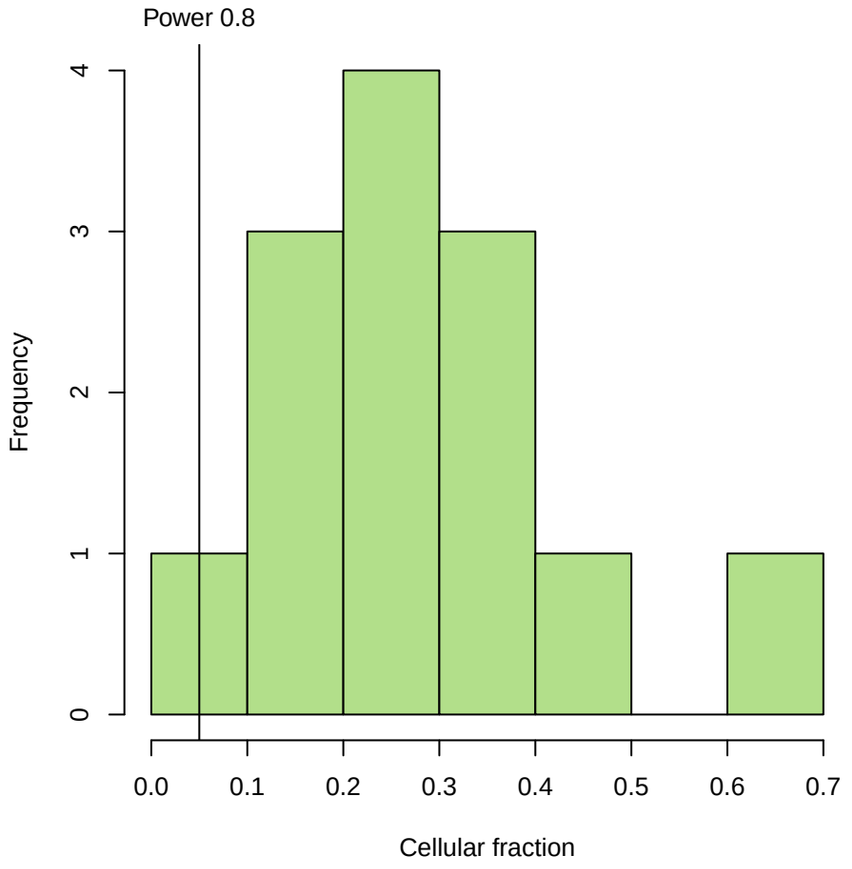

Purity: 0.78 Tumor ploidy: 2.983
1
2
3
6
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
1.0
log2 ratio


Purity: 0.78 Tumor ploidy: 2.983 SNV log−likelihood: −1026.54 GoF: 69.8% Mean coverage: 518;330
B−Allele Frequency
SNV Index
SCNA−fit log−likelihood: −13096.14
Copy Number log−ratio
SNV Index
Maximum Likelihood Copy Number
SNV Index


Allelic fraction (germline)
Copy Number log−ratio
3m2
6m3
3m1


Coverage (log2)
Allelic fraction


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


Power 0.8
Frequency
Cellular fraction