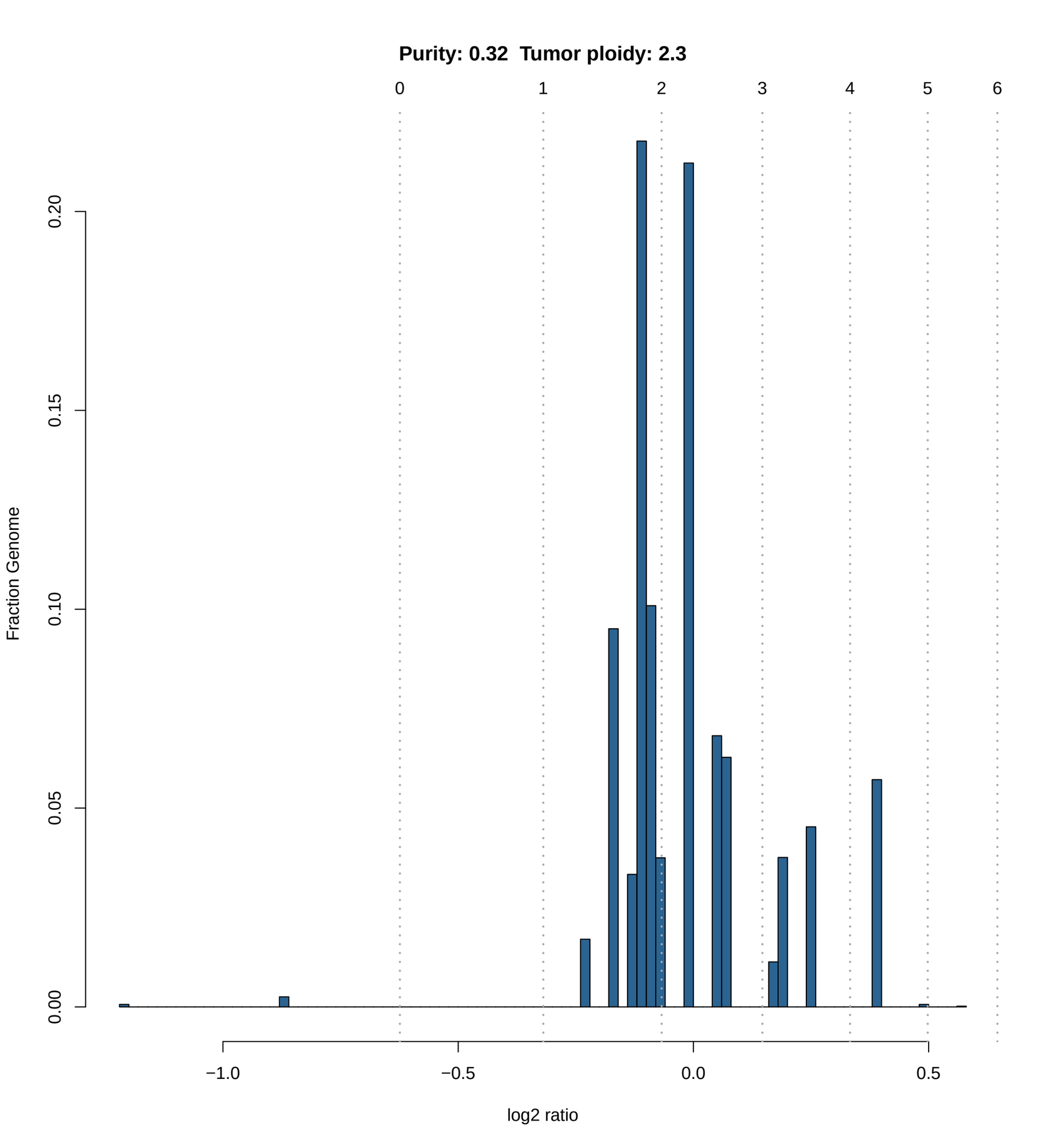
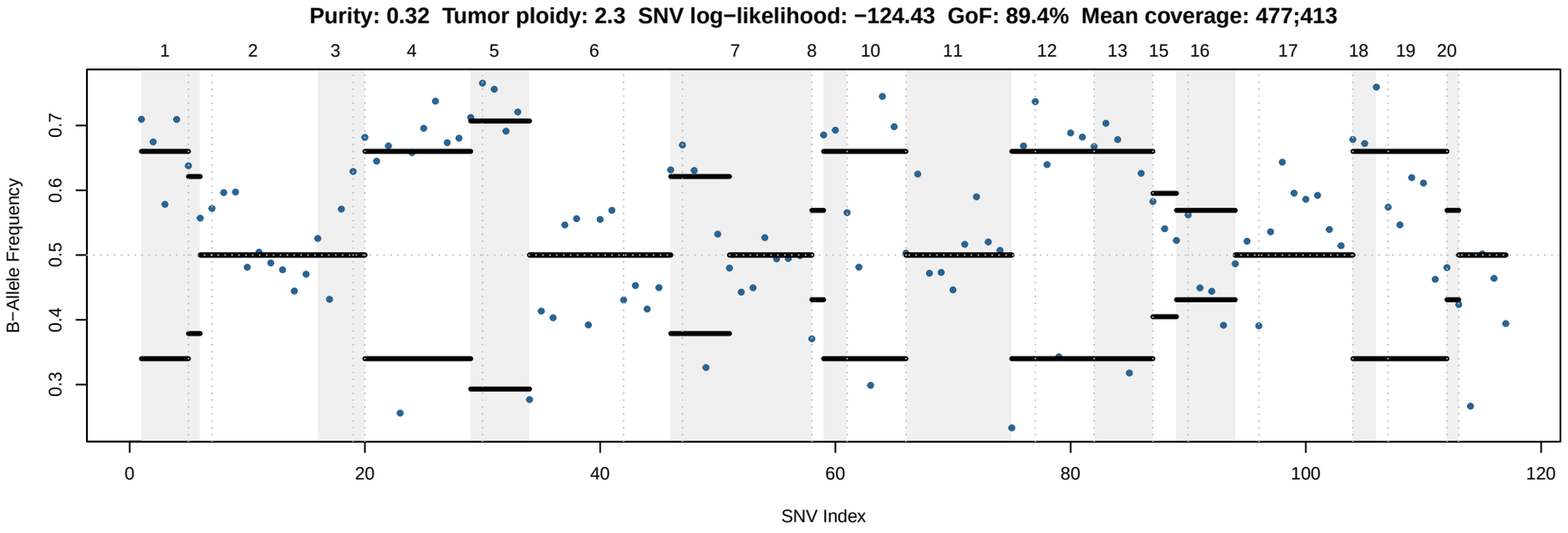
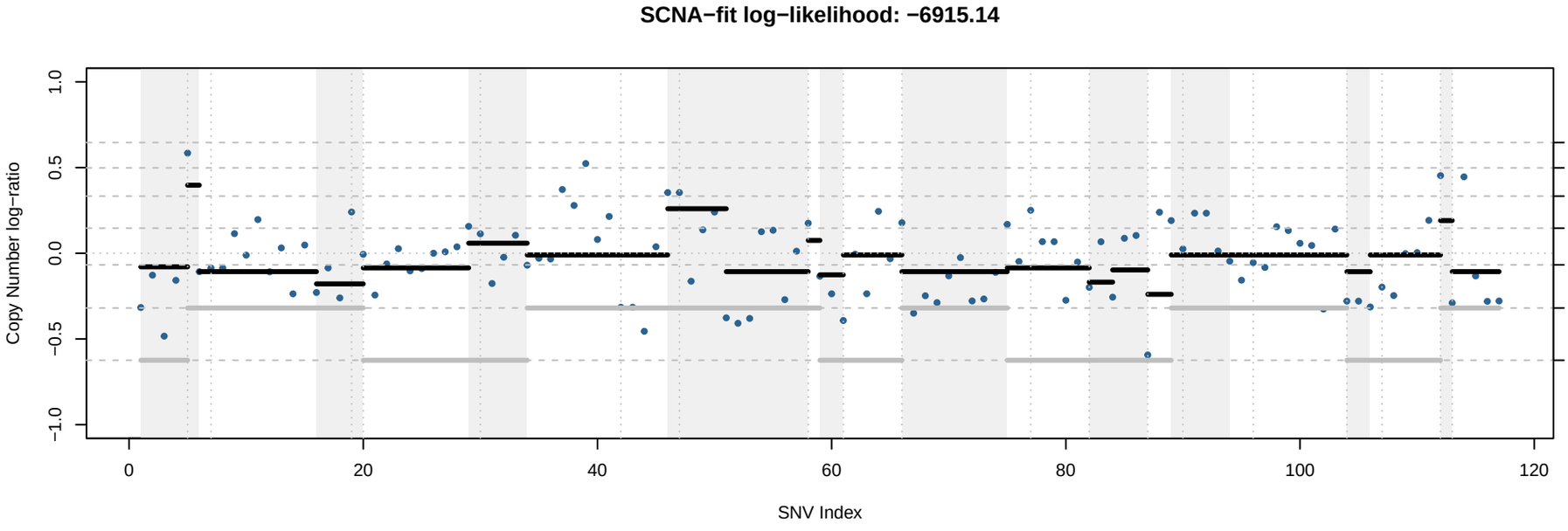
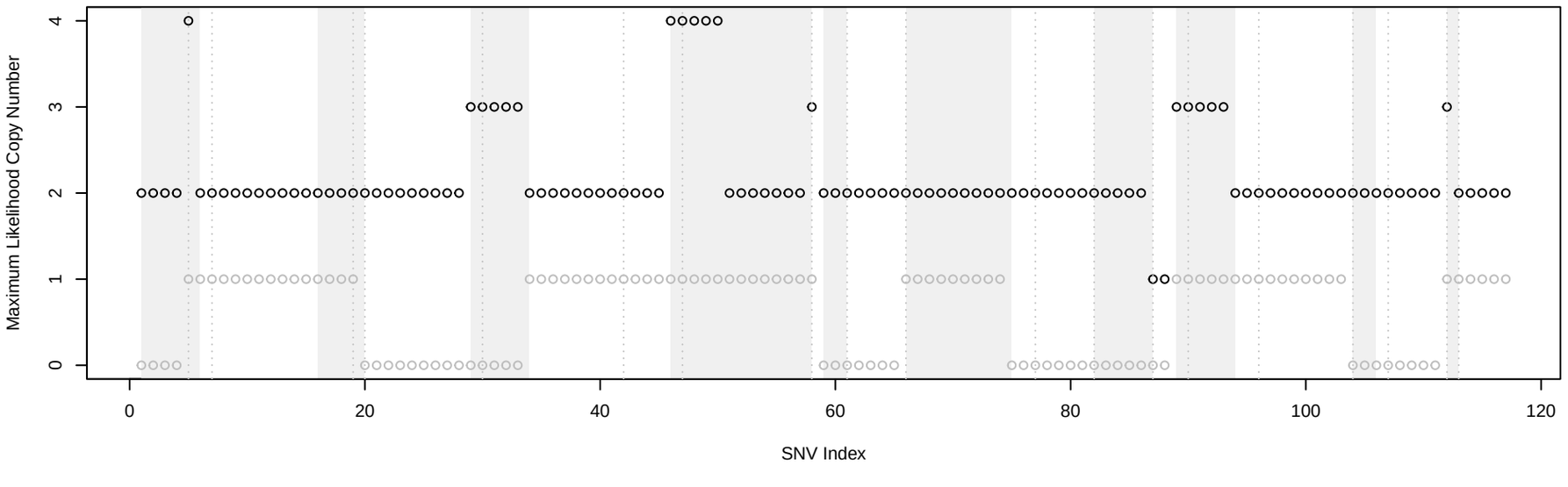
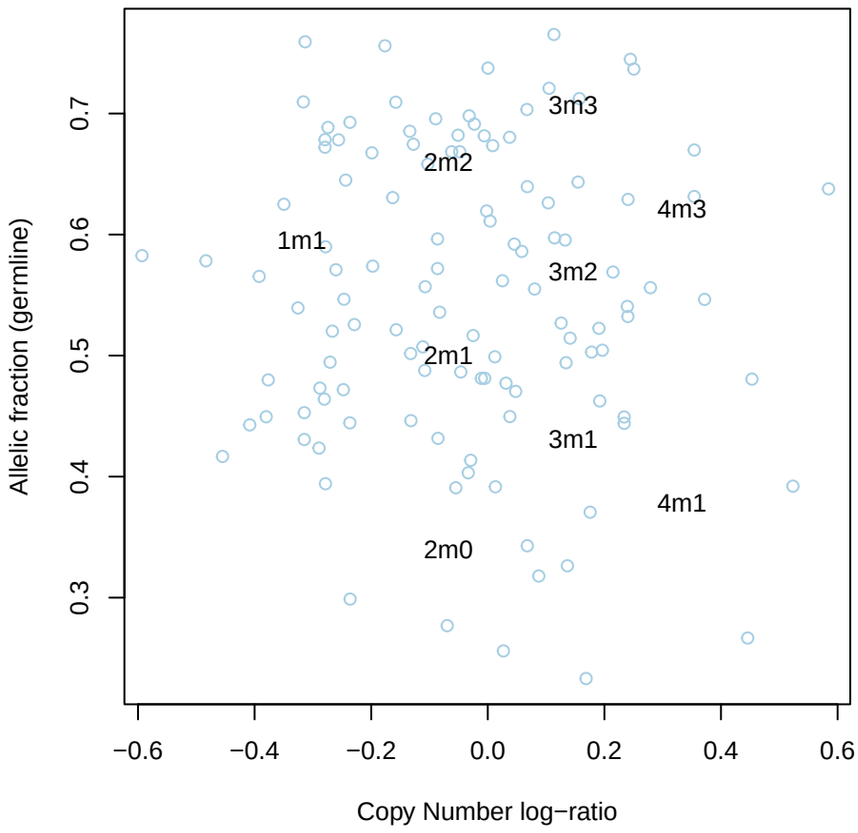
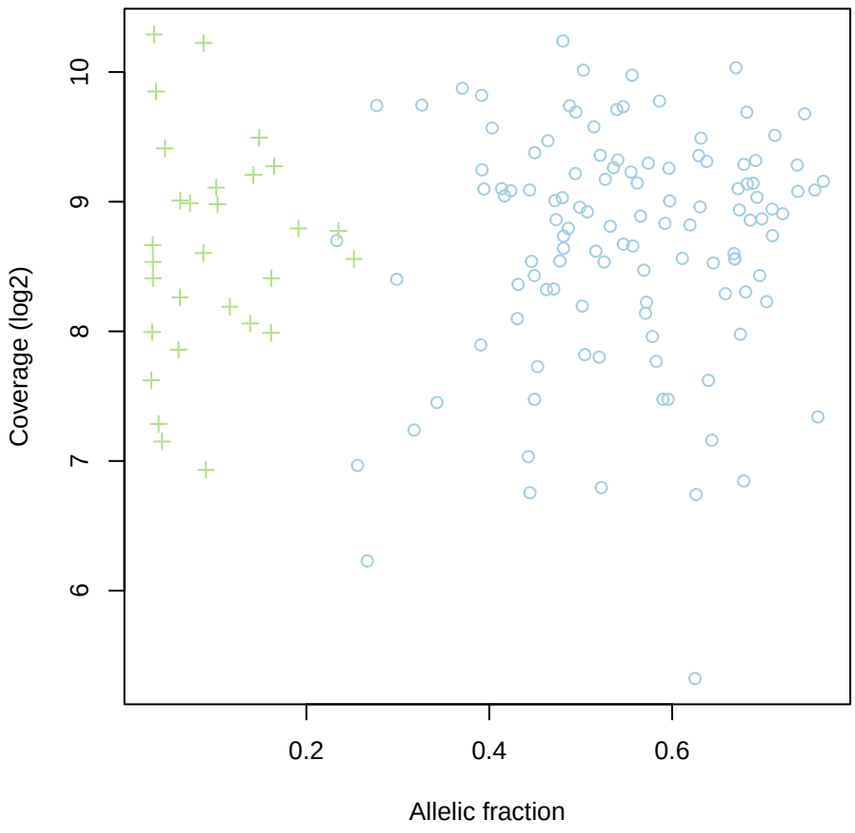

Purity: 0.32 Tumor ploidy: 2.3
0
1
2
3
4
5
6
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.0
−0.5
0.0
0.5
log2 ratio

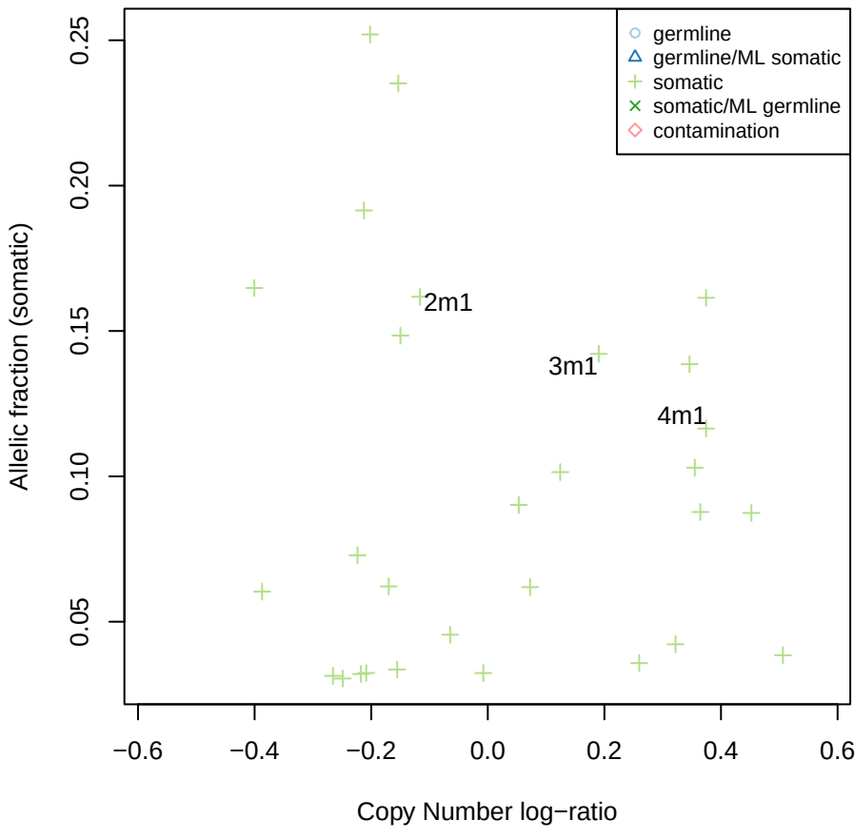

Purity: 0.32 Tumor ploidy: 2.3 SNV log−likelihood: −124.43 GoF: 89.4% Mean coverage: 477;413
1 2 3 4 5 6 7 8 10 11 12 13 15 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

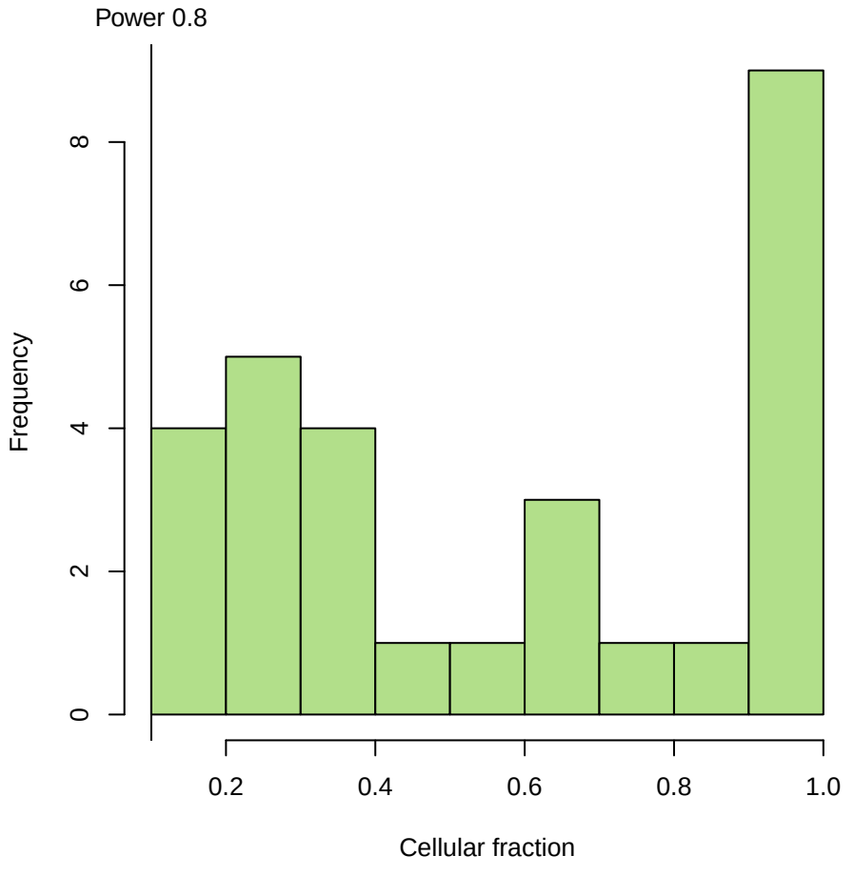

SCNA−fit log−likelihood: −6915.14
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 6
0 20 40 60 80 100 120
SNV Index

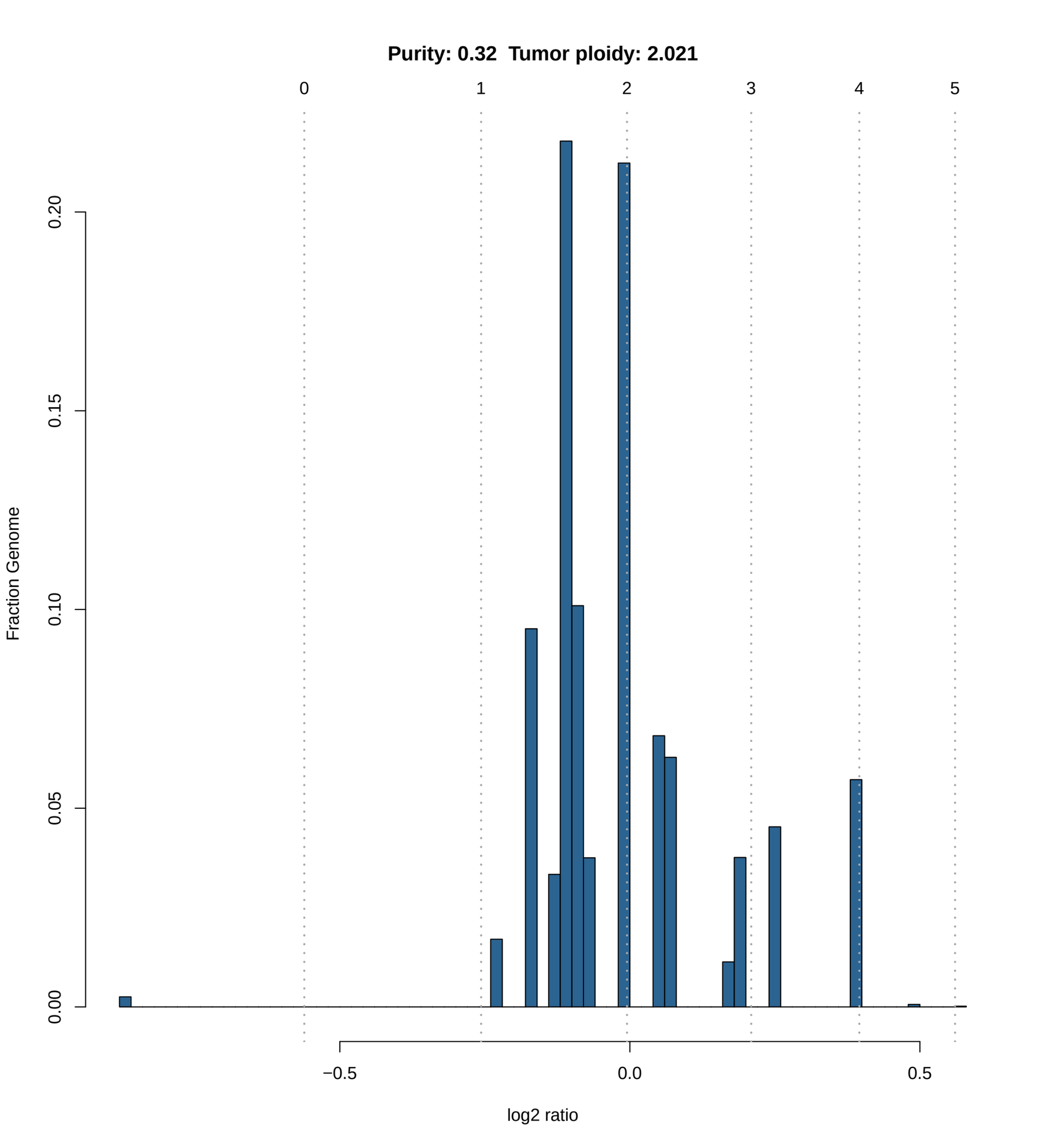

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120
SNV Index

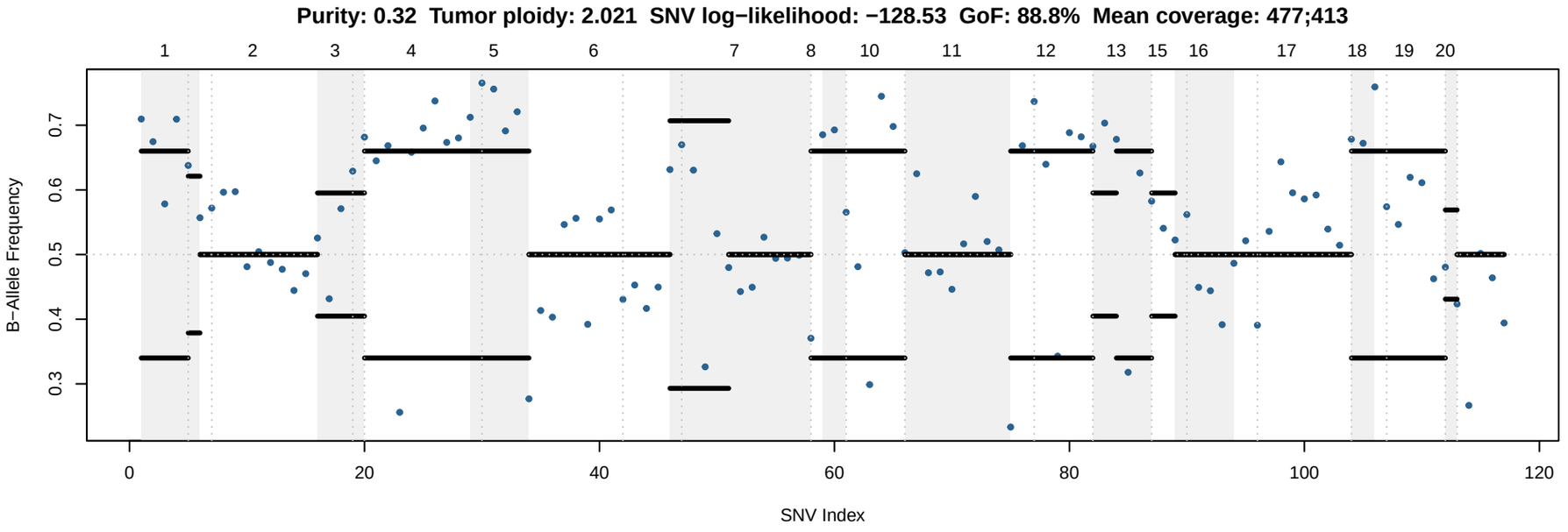

Allelic fraction (germline)
Copy Number log−ratio
3m3
2m2
4m3
1m1
3m2
2m1
3m1
4m1
2m0

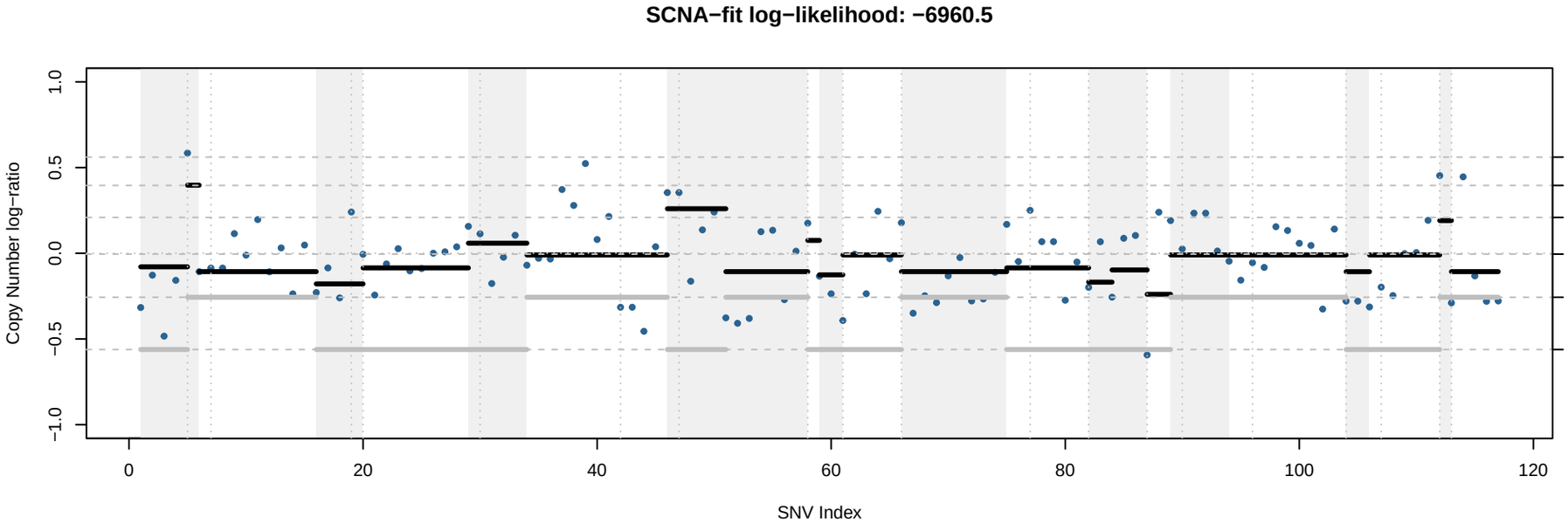

Coverage (log2)
Allelic fraction

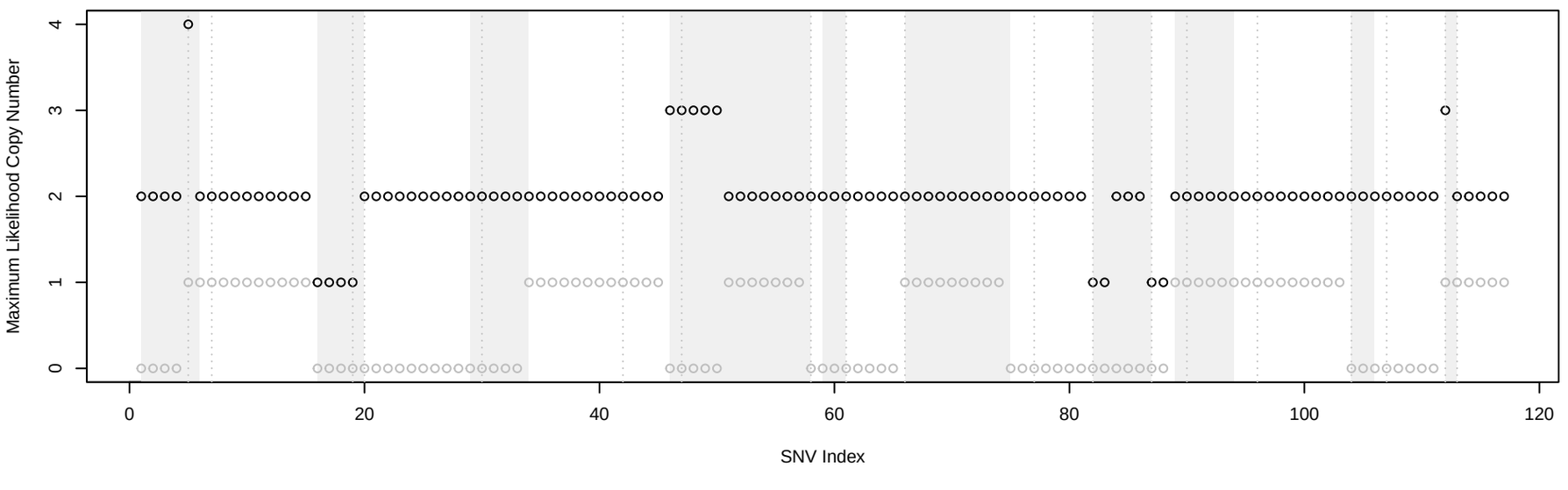

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m1
3m1
4m1

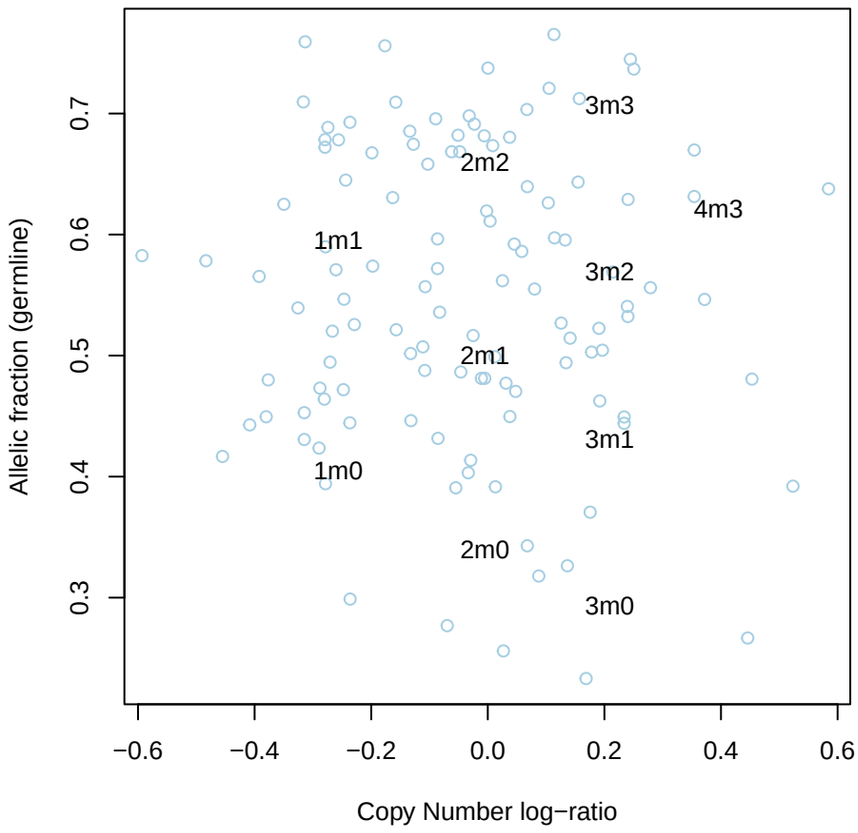

Power 0.8
Frequency
Cellular fraction

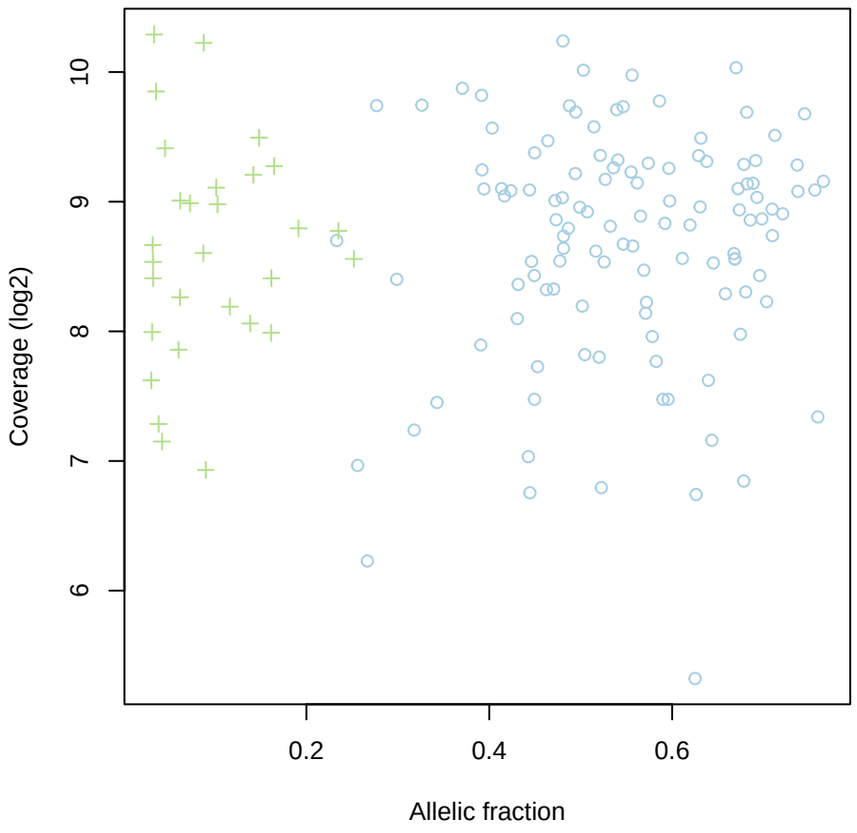

Purity: 0.32 Tumor ploidy: 2.021
0
1
2
3
4
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

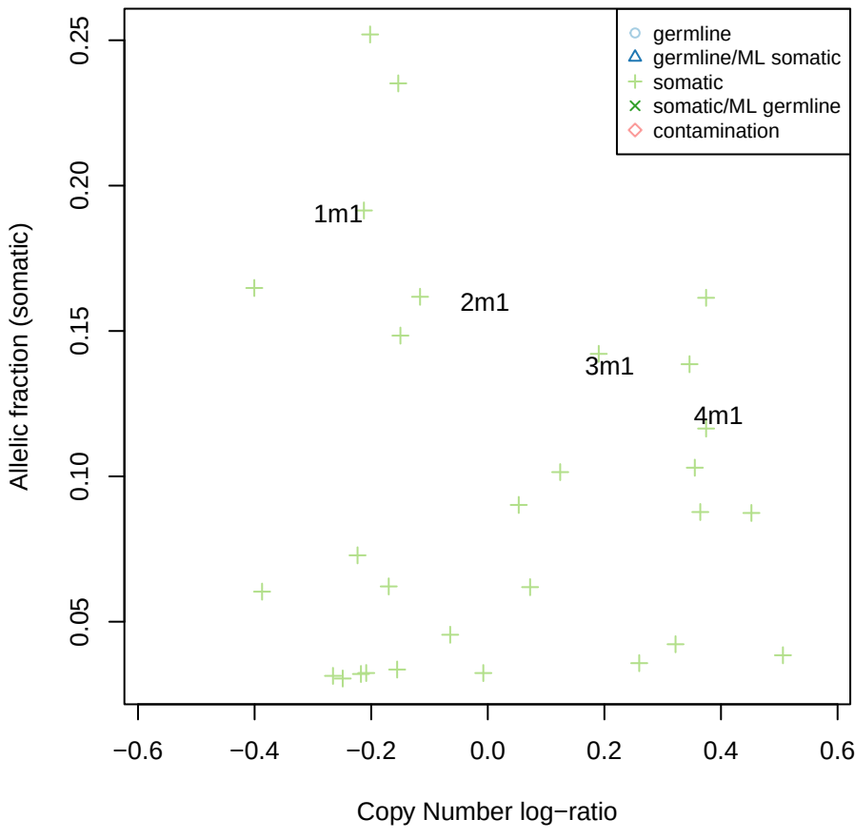

Purity: 0.32 Tumor ploidy: 2.021 SNV log−likelihood: −128.53 GoF: 88.8% Mean coverage: 477;413
1 2 3 4 5 6 7 8 10 11 12 13 15 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

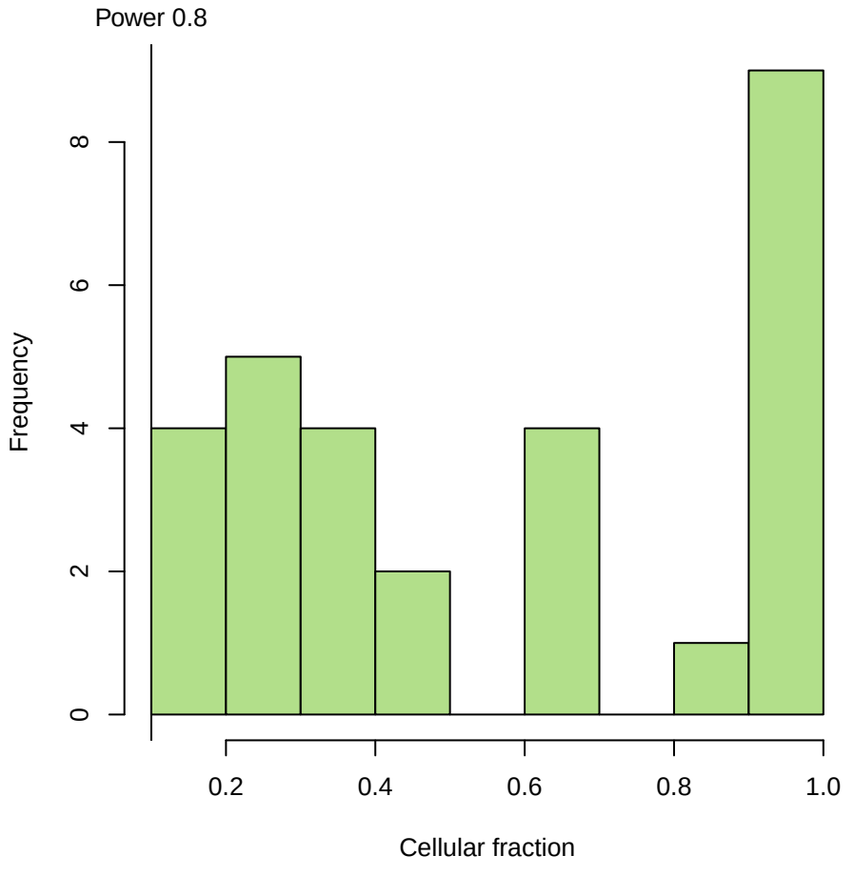

SCNA−fit log−likelihood: −6960.5
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5
0 20 40 60 80 100 120
SNV Index

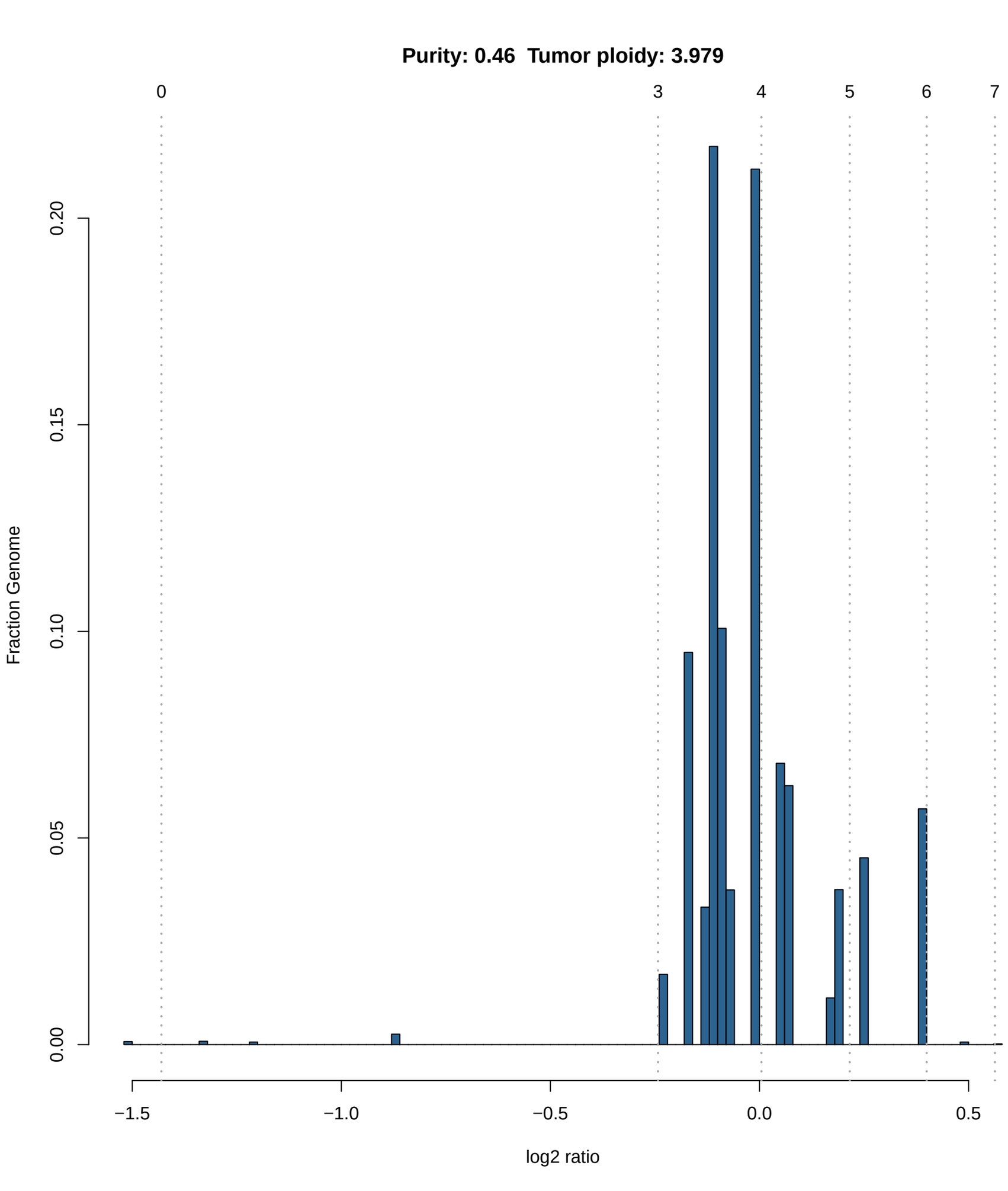

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120
SNV Index

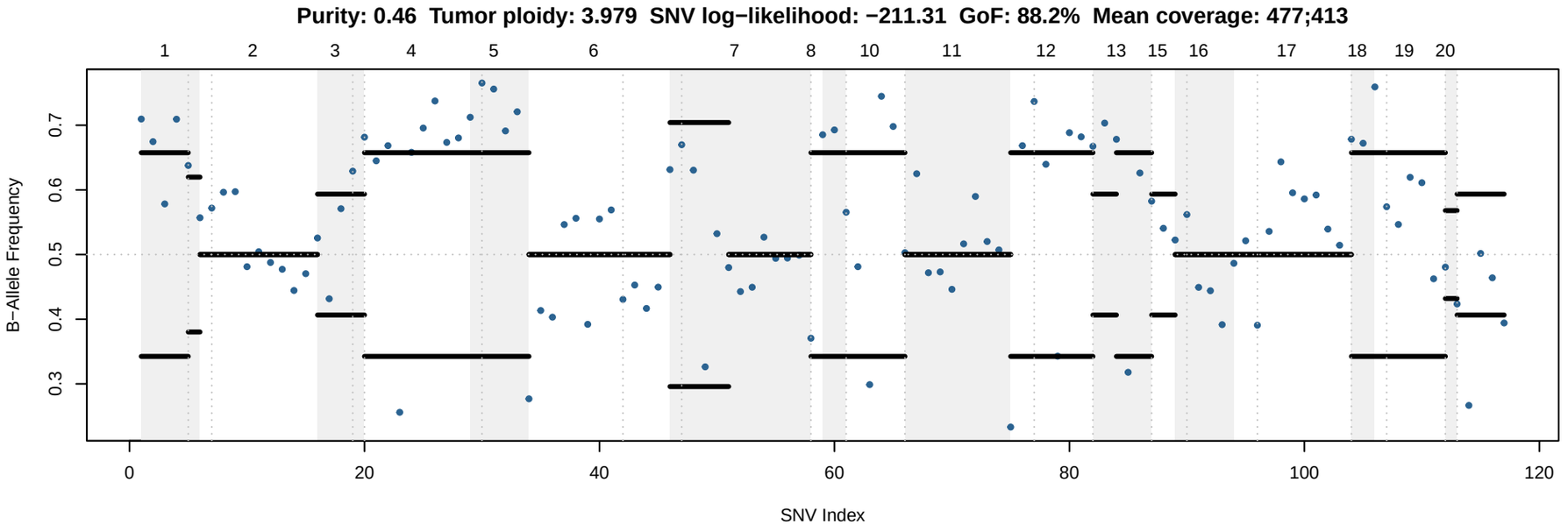

Allelic fraction (germline)
Copy Number log−ratio
1m1
2m2
3m3
4m3
3m2
2m1
3m1
1m0
2m0
3m0

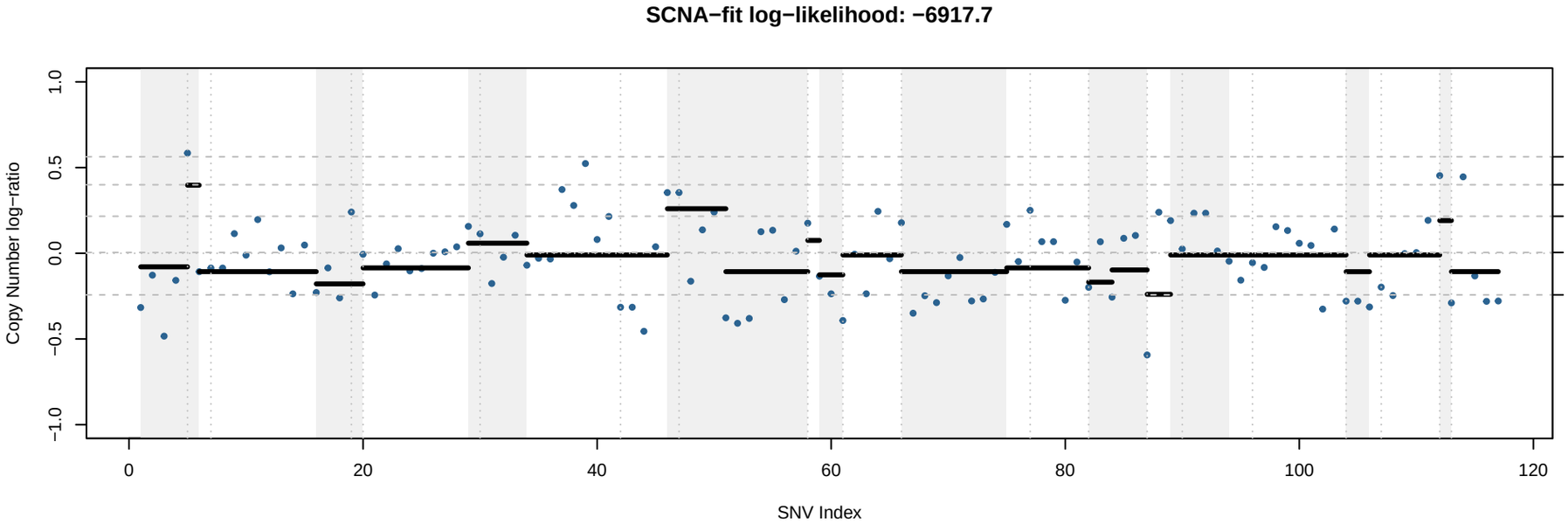

Coverage (log2)
Allelic fraction

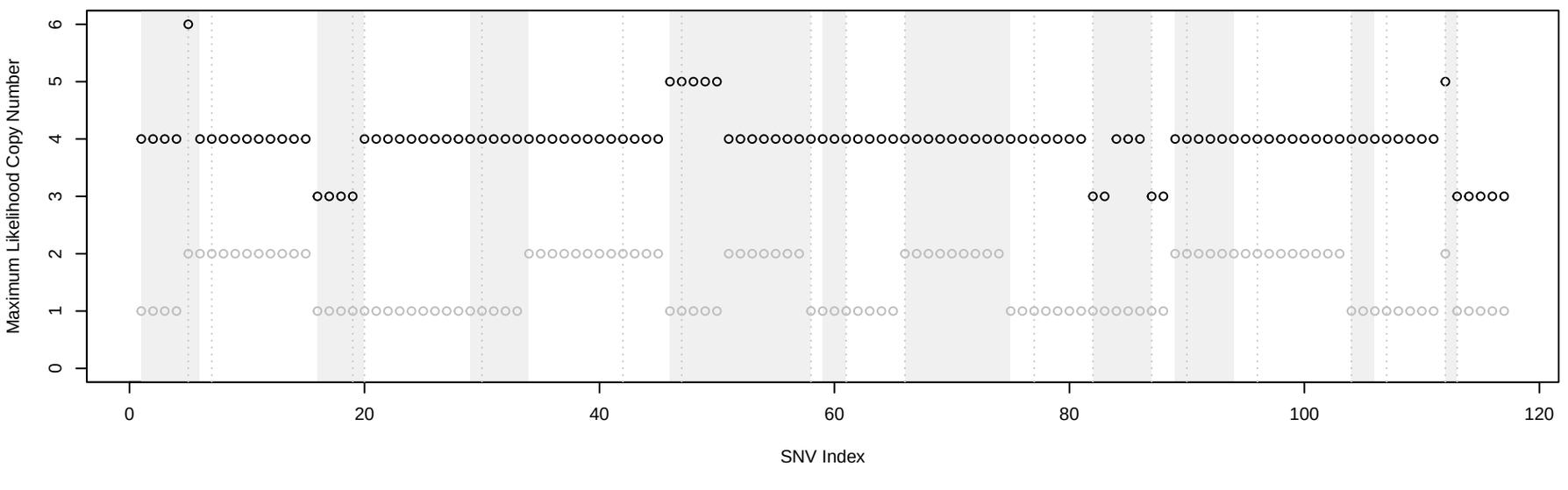

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1
3m1
4m1

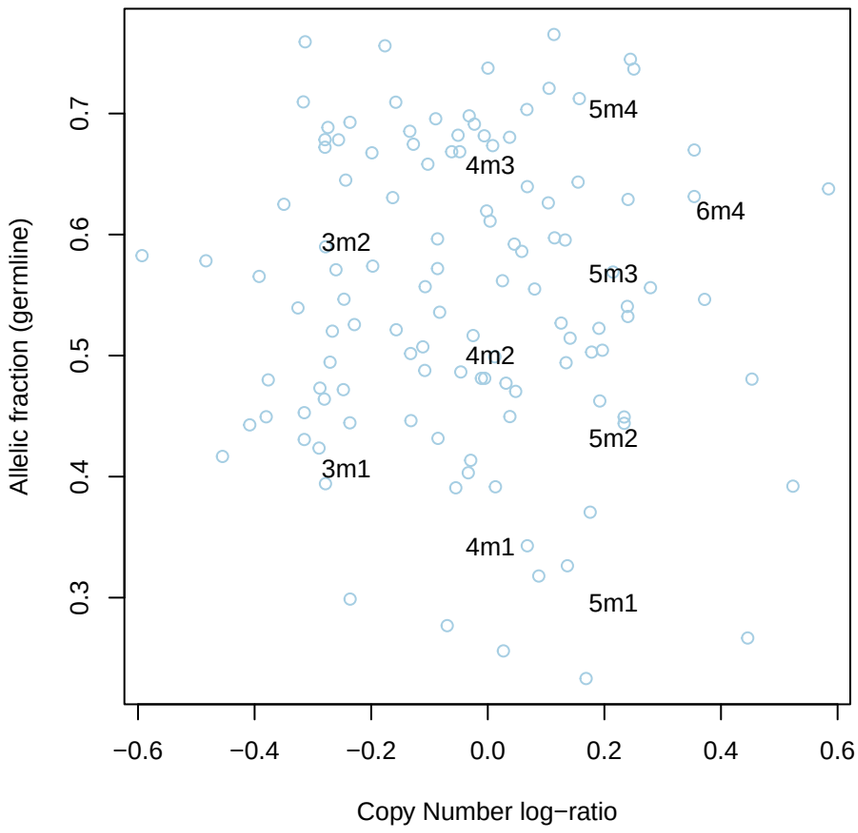

Power 0.8
Frequency
Cellular fraction

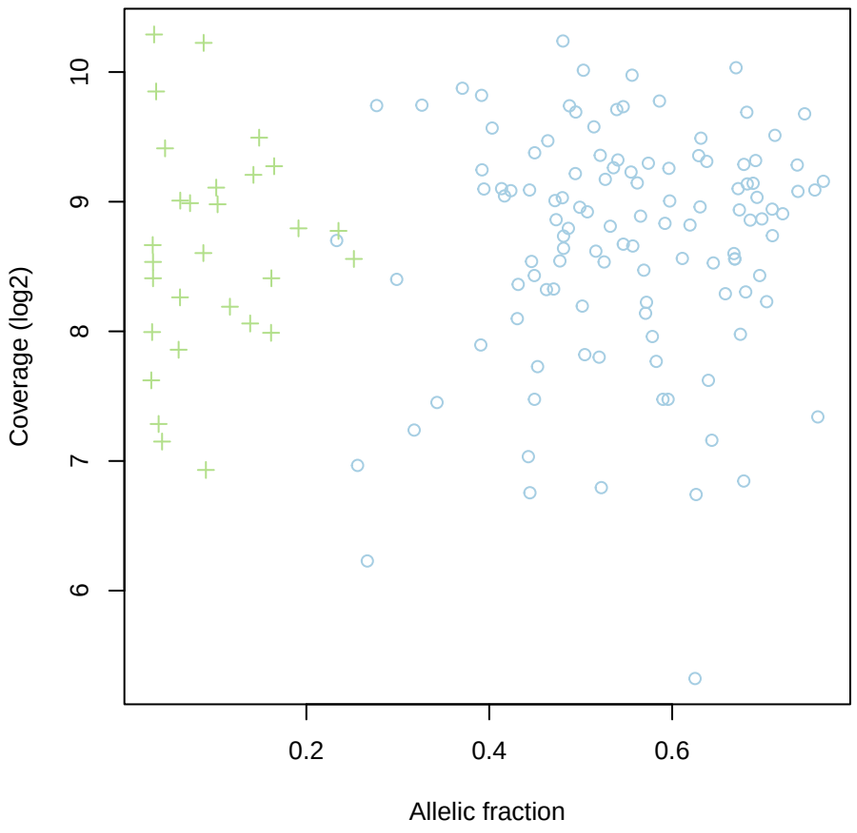

Purity: 0.46 Tumor ploidy: 3.979
0
3
4
5
6
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

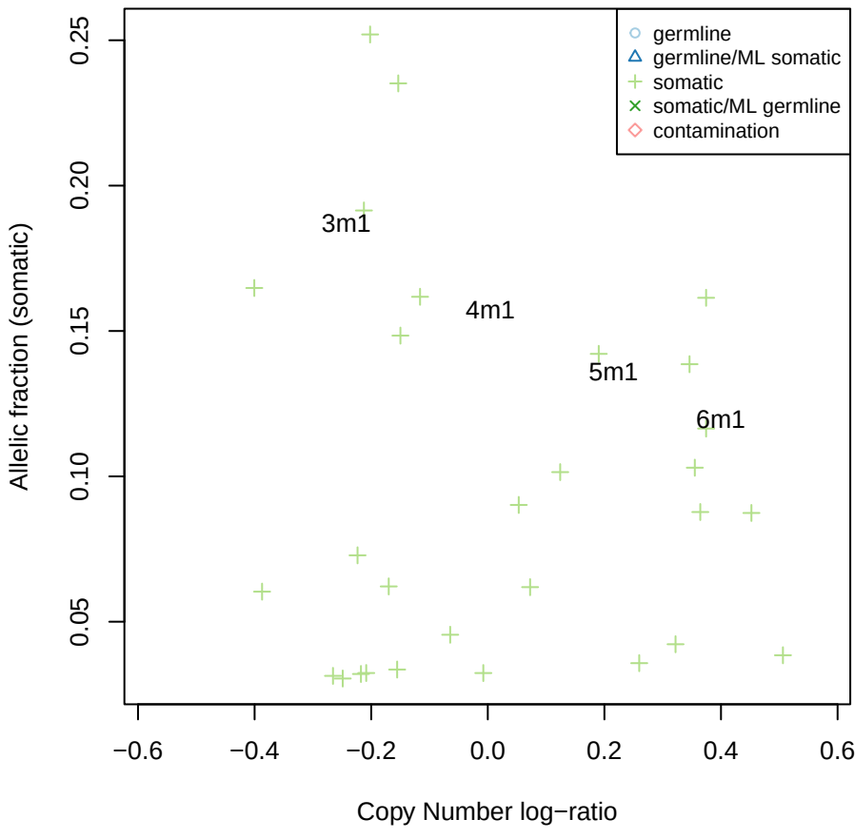

Purity: 0.46 Tumor ploidy: 3.979 SNV log−likelihood: −211.31 GoF: 88.2% Mean coverage: 477;413
1 2 3 4 5 6 7 8 10 11 12 13 15 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

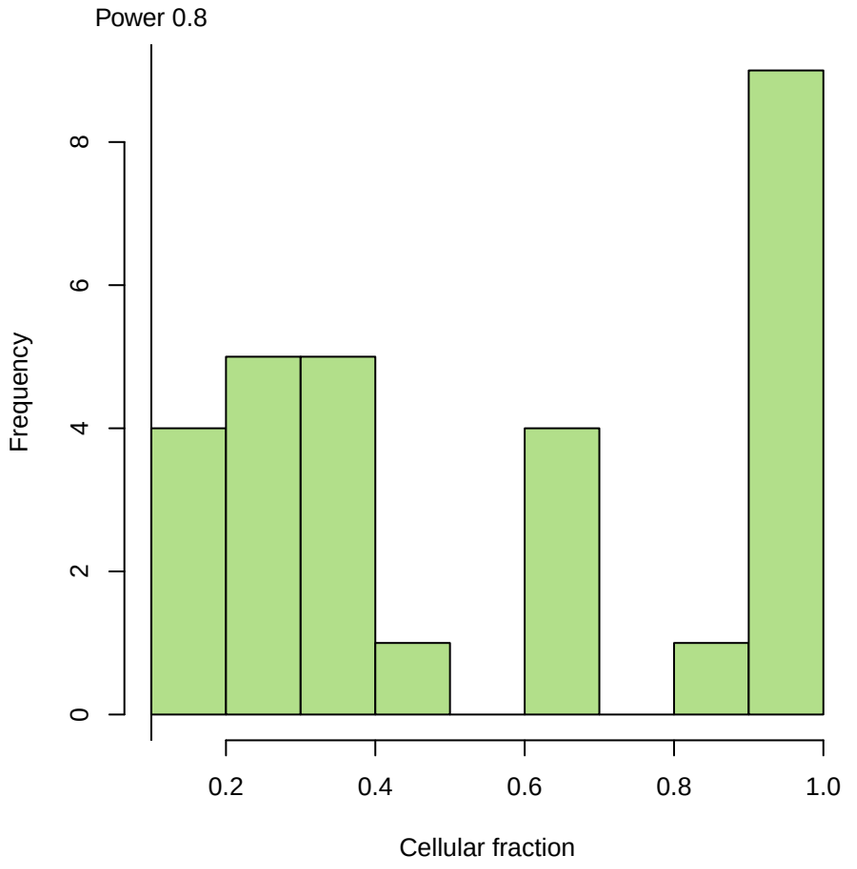

SCNA−fit log−likelihood: −6917.7
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

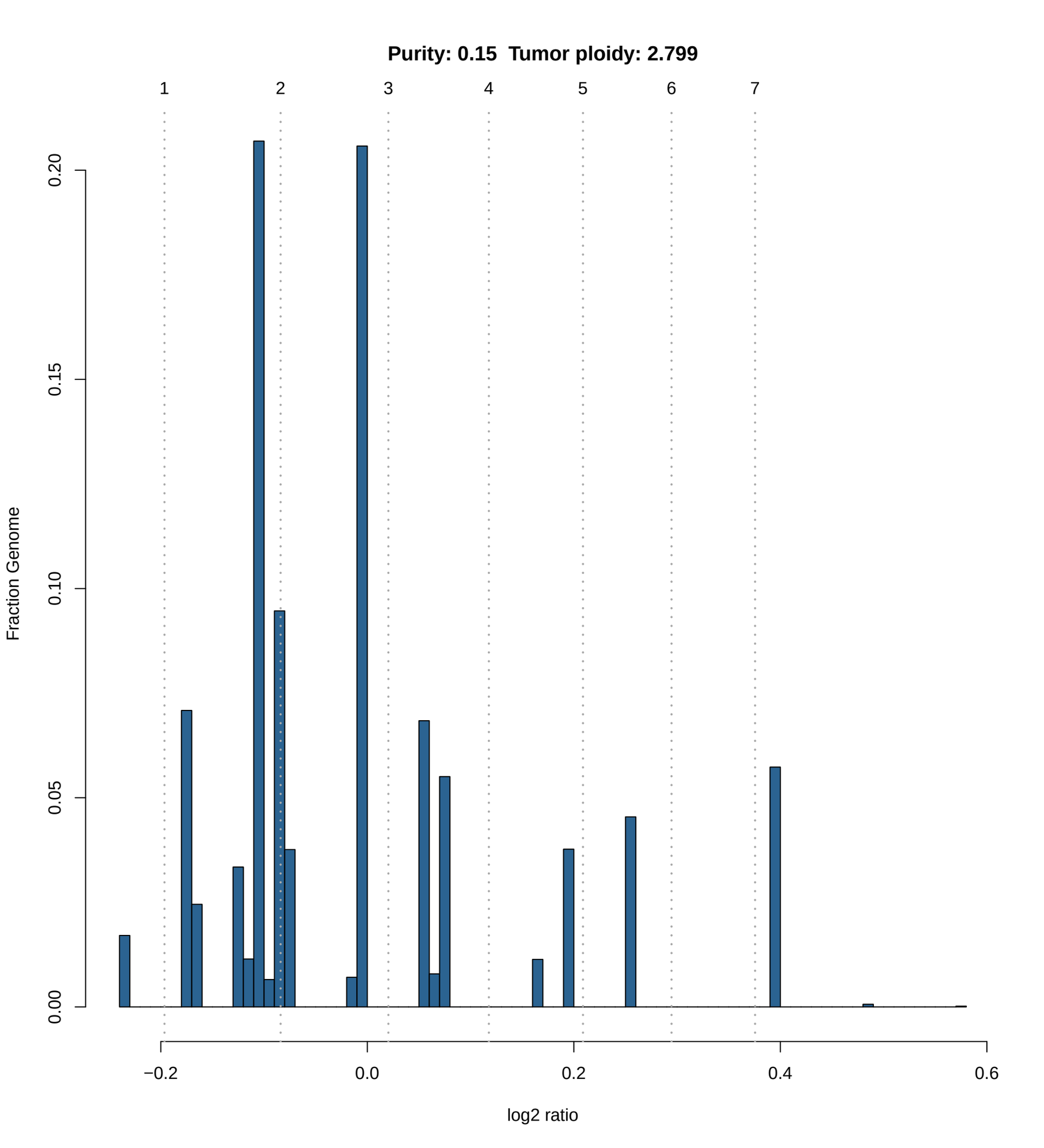

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100 120
SNV Index

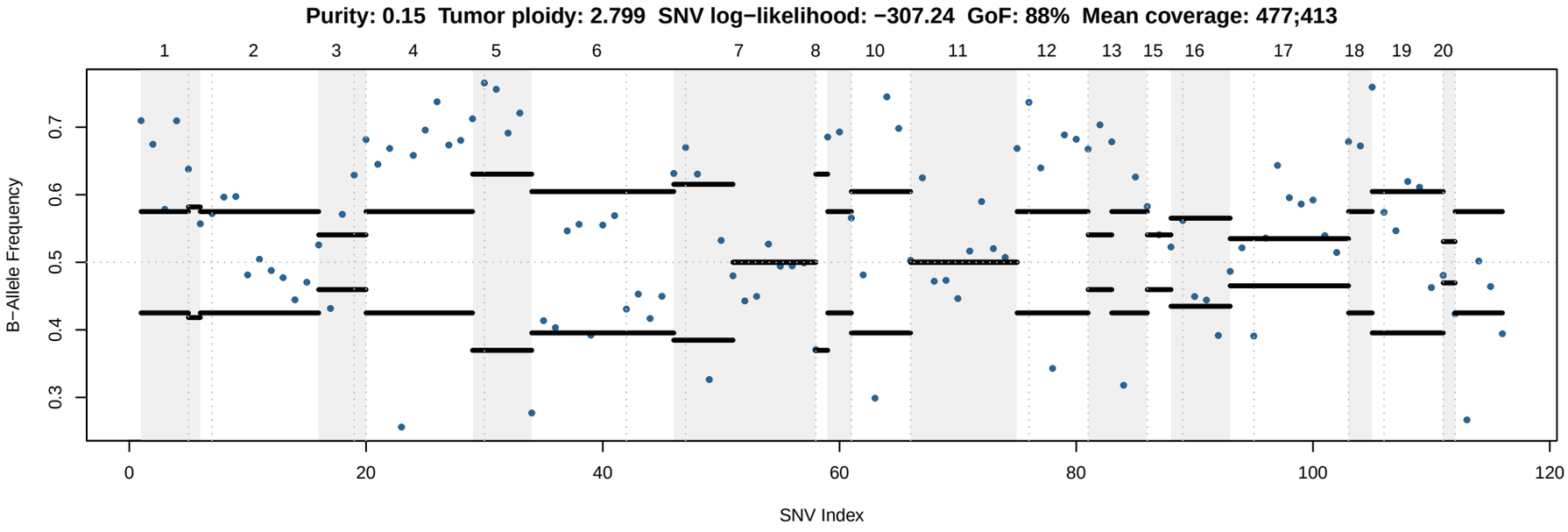

Allelic fraction (germline)
Copy Number log−ratio
5m4
4m3
6m4
3m2
5m3
4m2
5m2
3m1
4m1
5m1

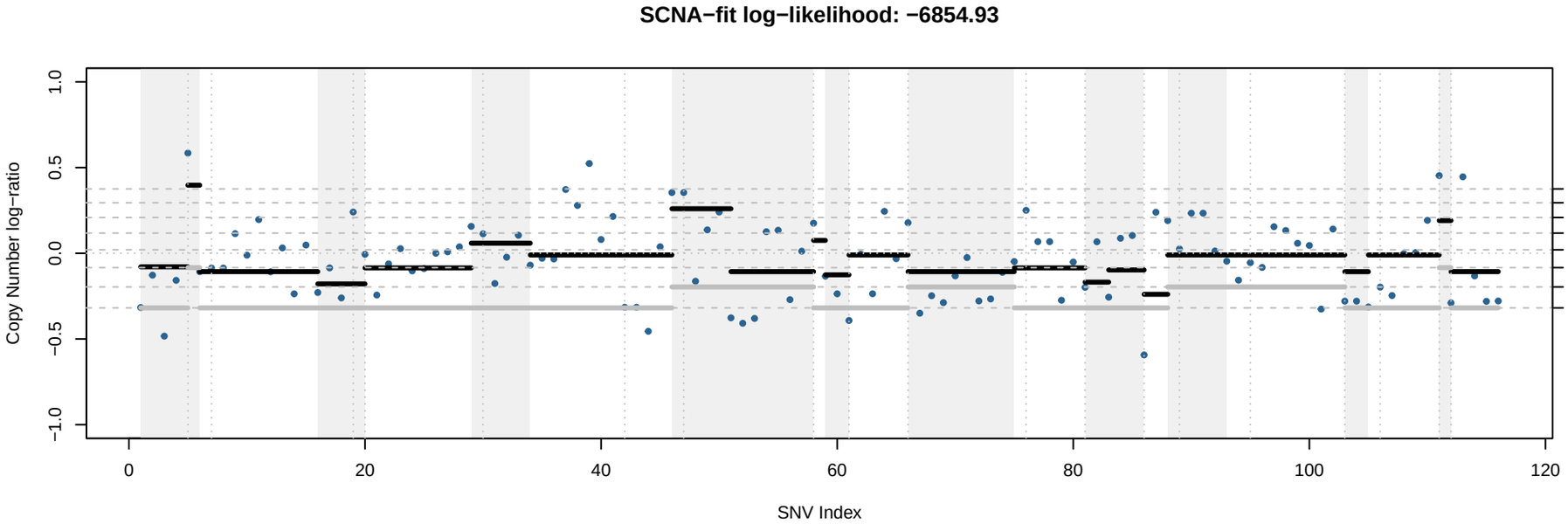

Coverage (log2)
Allelic fraction

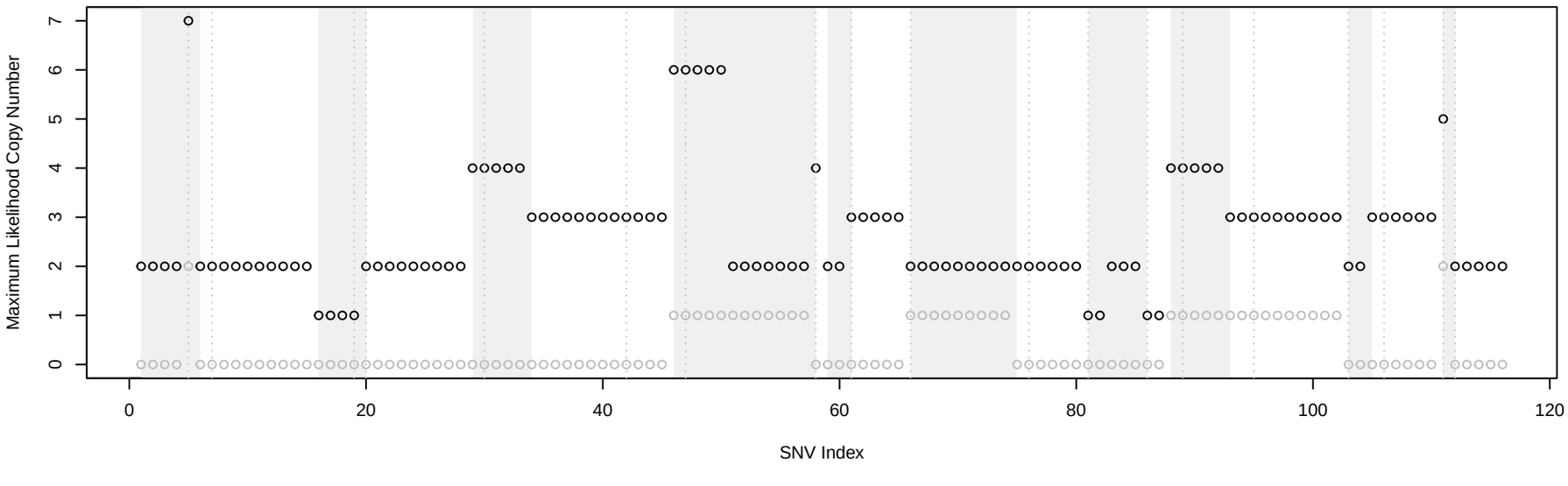

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m1
4m1
5m1
6m1

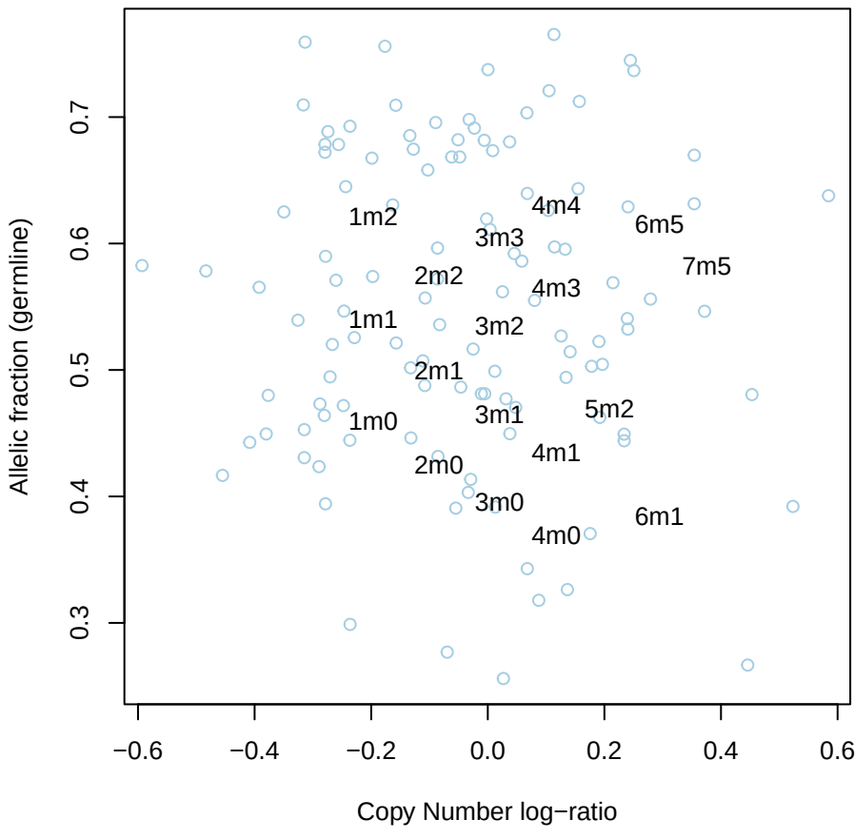

Power 0.8
Frequency
Cellular fraction

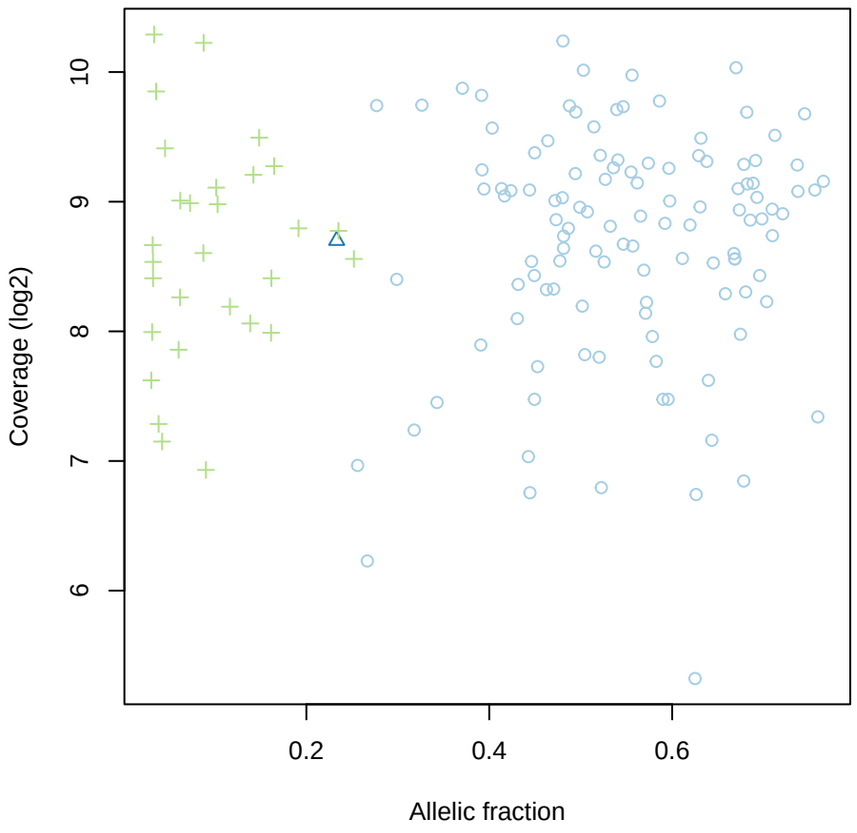

Purity: 0.15 Tumor ploidy: 2.799
1
2
3
4
5
6
7
0.00
0.05
0.10
0.15
0.20
Fraction Genome
−0.2
0.0
0.2
0.4
0.6
log2 ratio

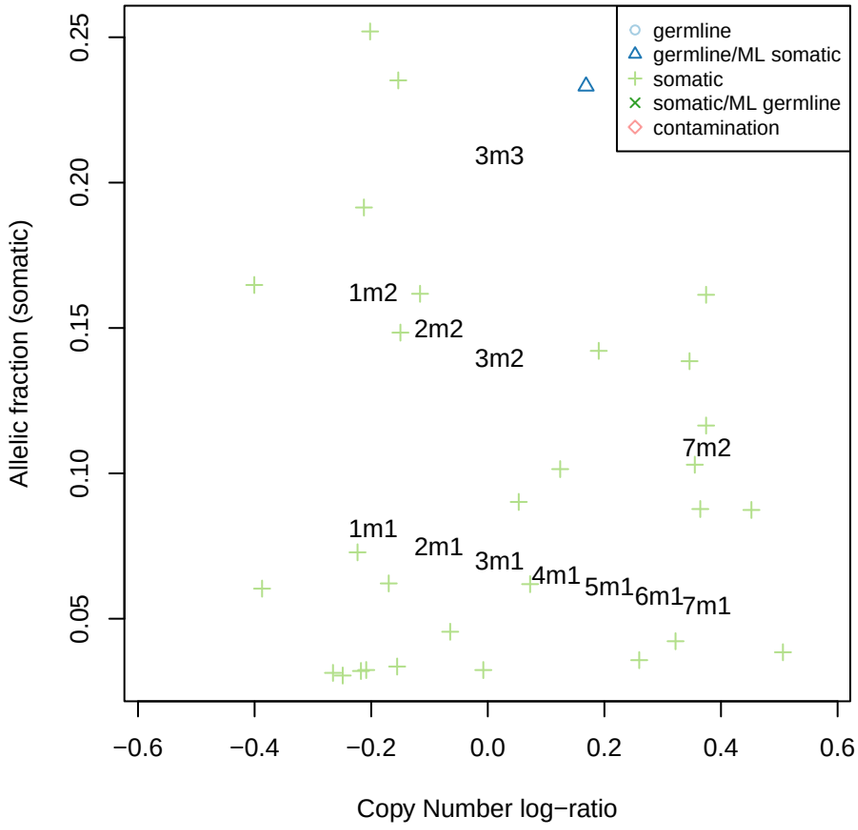

Purity: 0.15 Tumor ploidy: 2.799 SNV log−likelihood: −307.24 GoF: 88% Mean coverage: 477;413
1 2 3 4 5 6 7 8 10 11 12 13 15 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

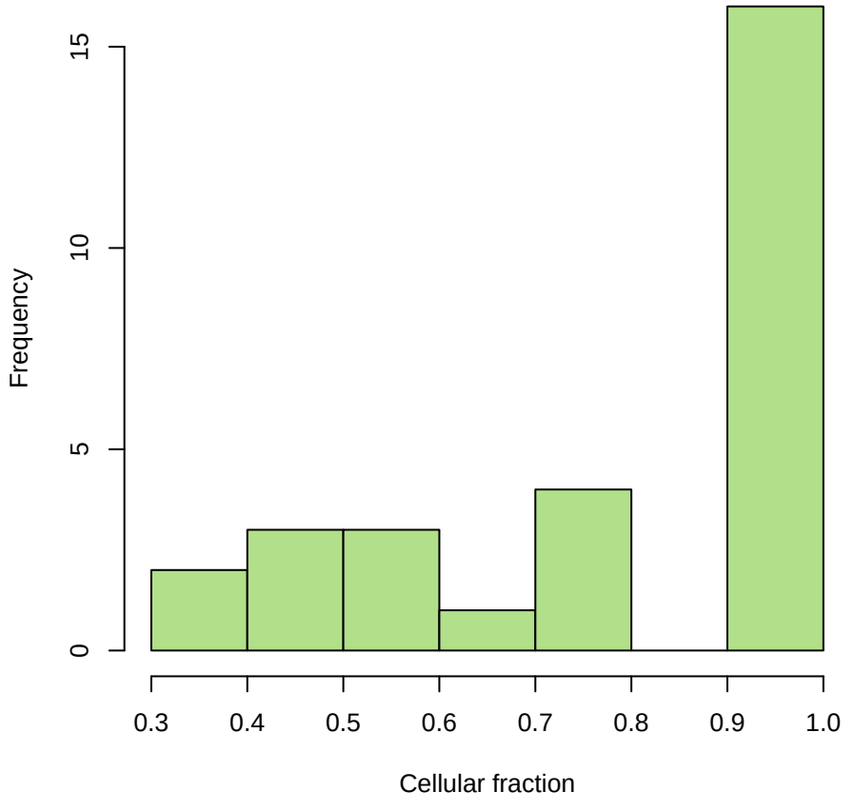

SCNA−fit log−likelihood: −6854.93
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4 6
0 20 40 60 80 100 120
SNV Index

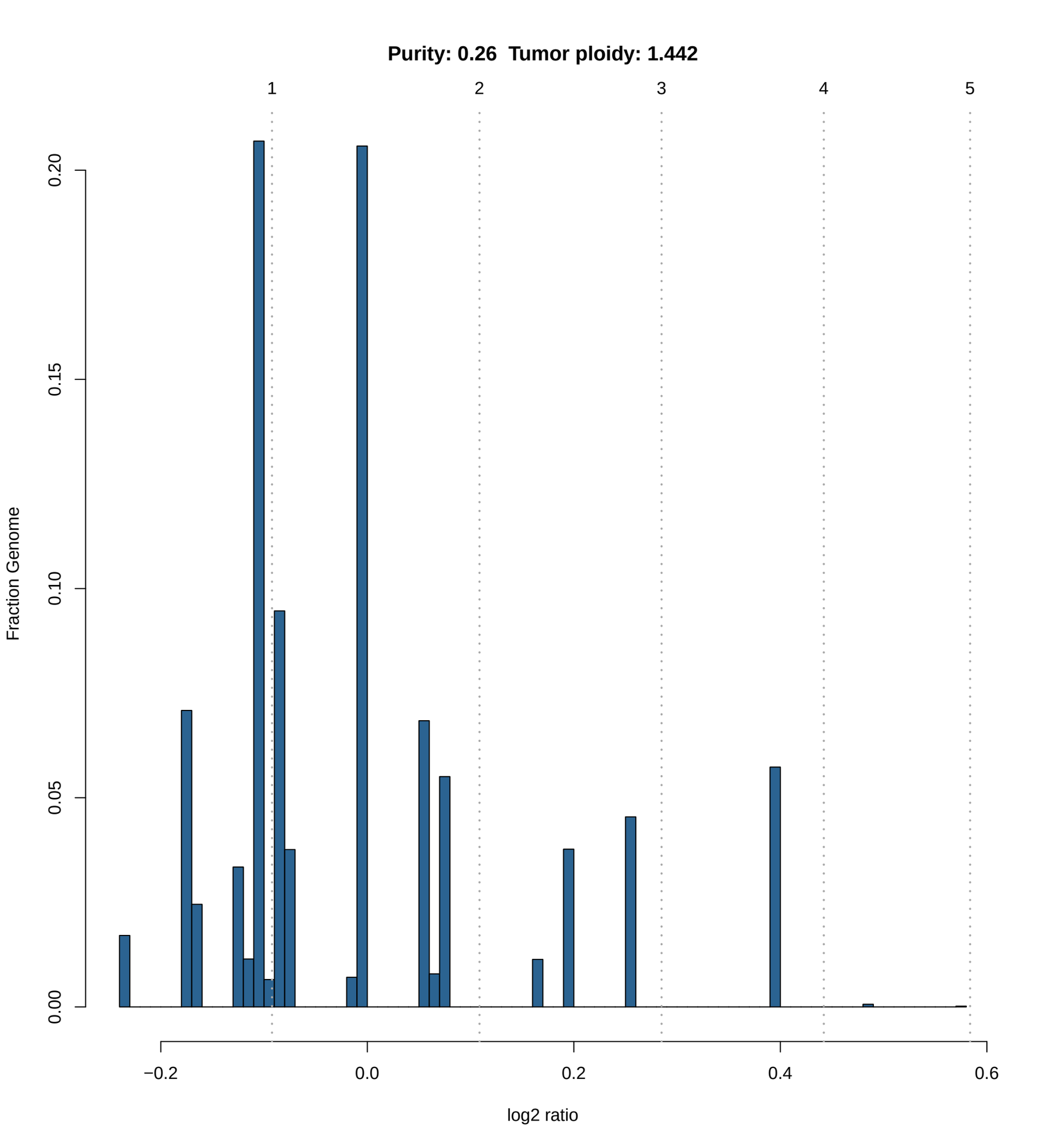

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100 120
SNV Index

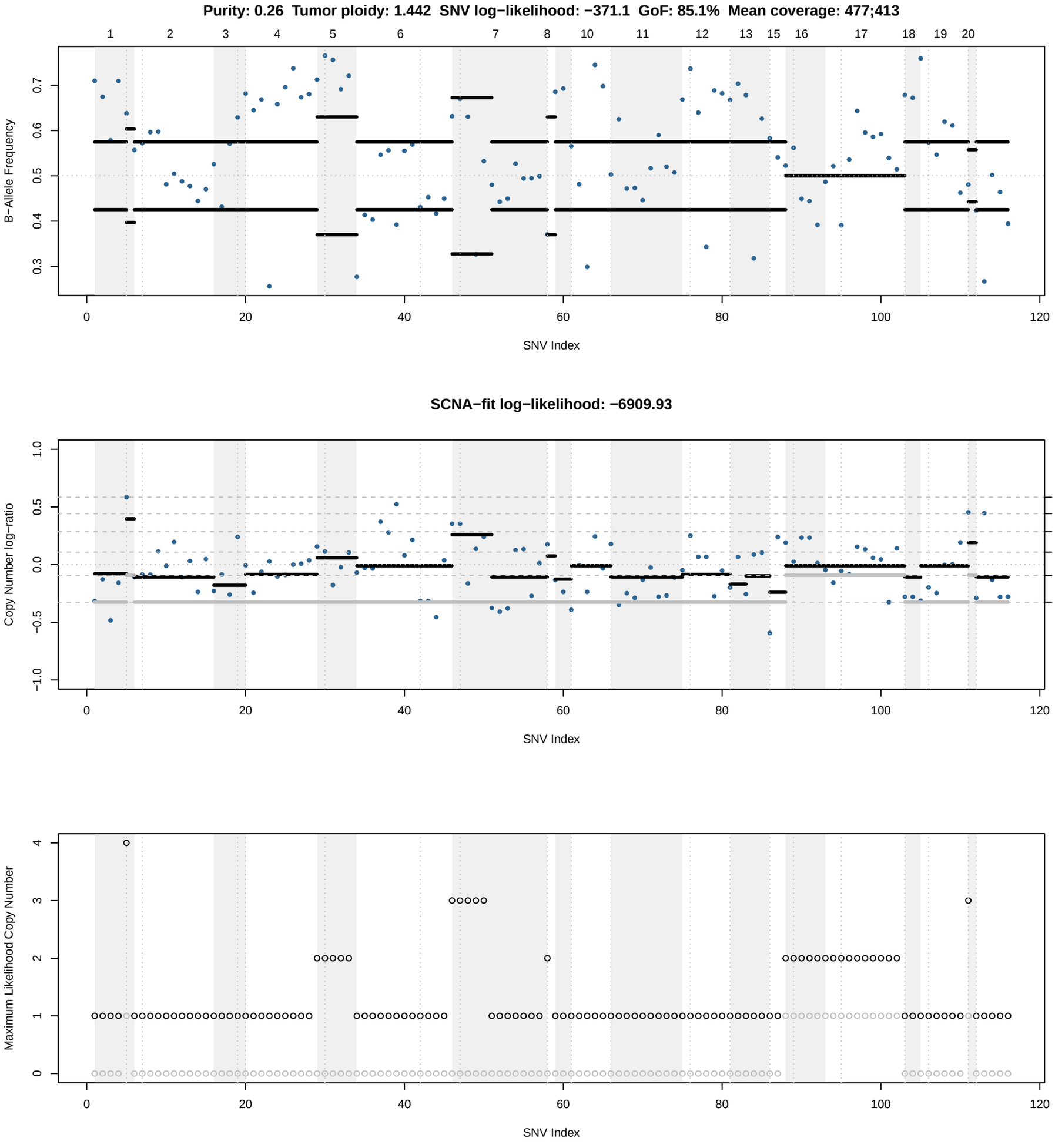

Allelic fraction (germline)
Copy Number log−ratio
1m2
4m4
6m5
3m3
7m5
2m2
4m3
1m1
3m2
2m1
5m2
1m0
3m1
4m1
2m0
3m0
6m1
4m0

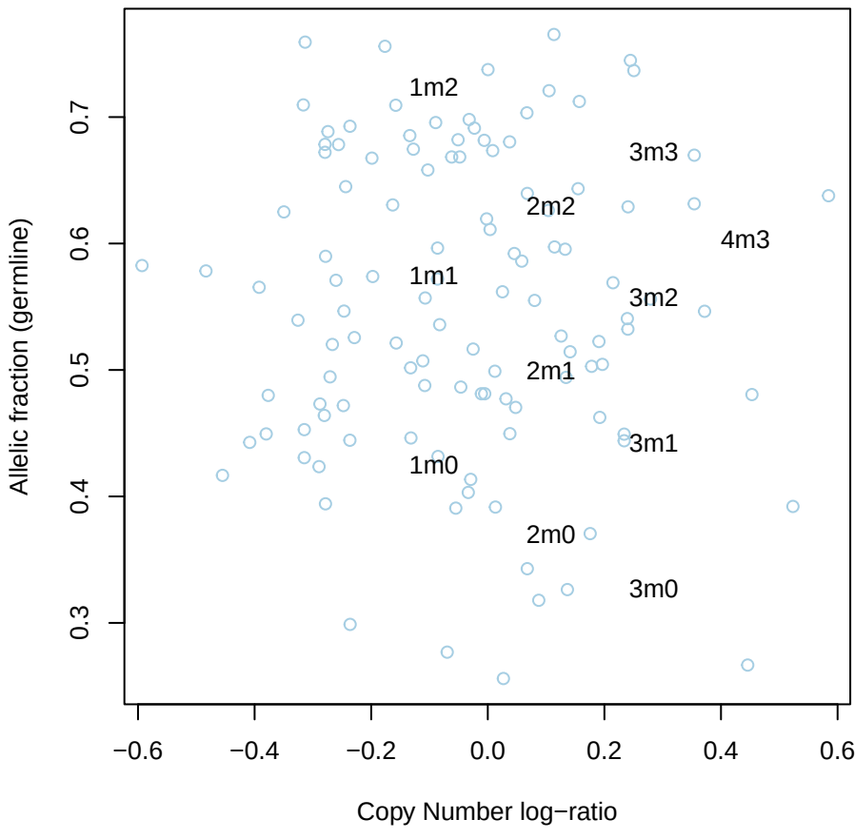

Coverage (log2)
Allelic fraction

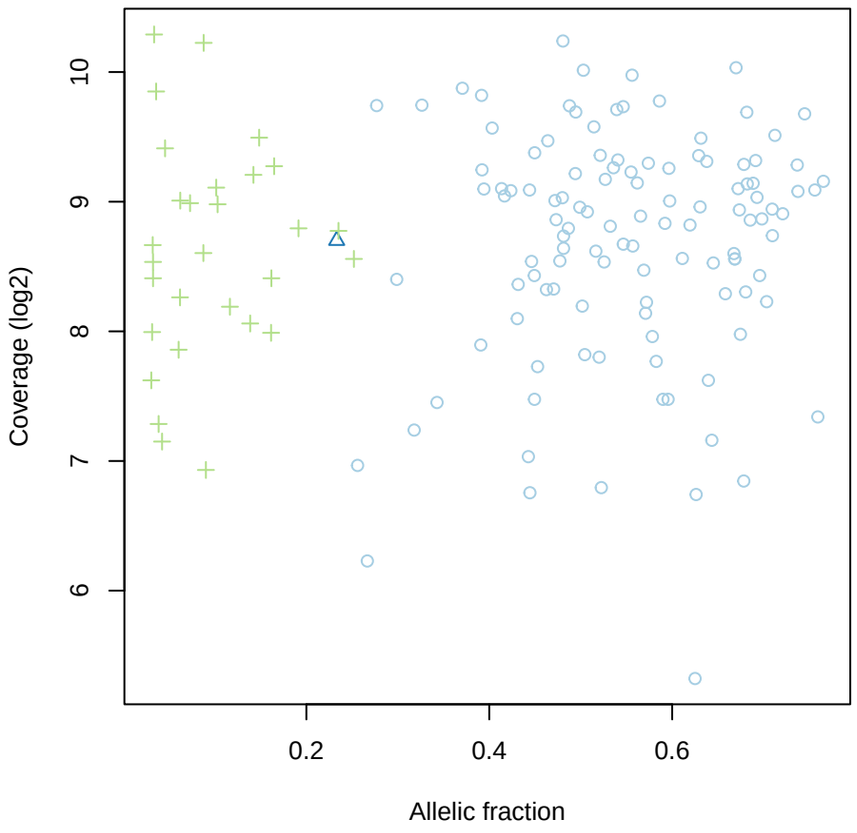

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m3
1m2
2m2
3m2
7m2
1m1
2m1
3m1
4m1
5m1
6m1
7m1

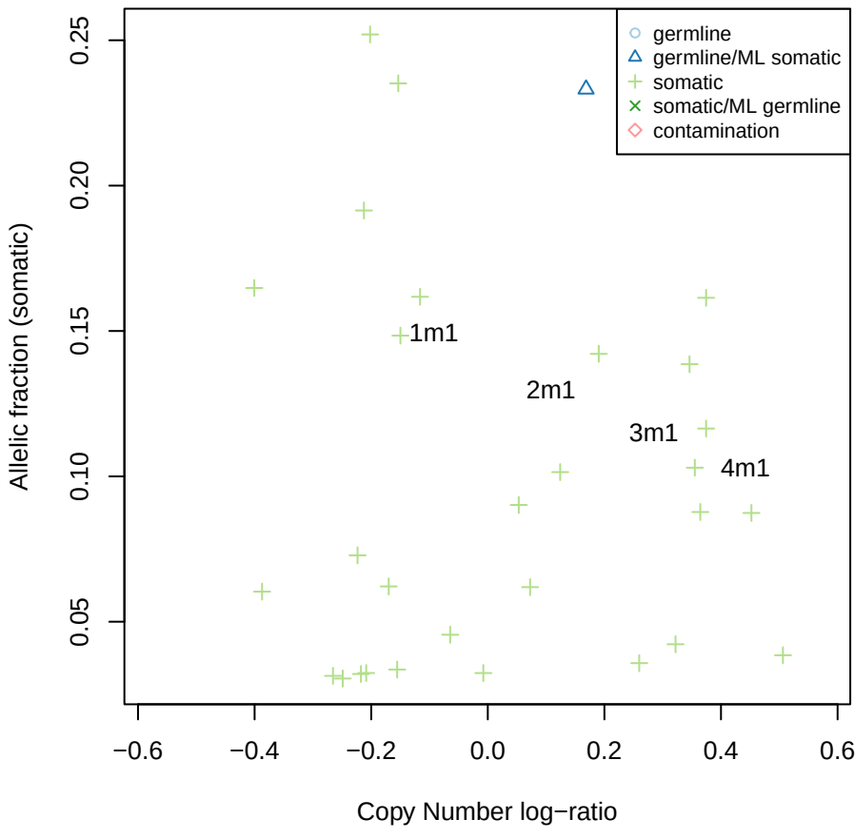

Frequency
Cellular fraction

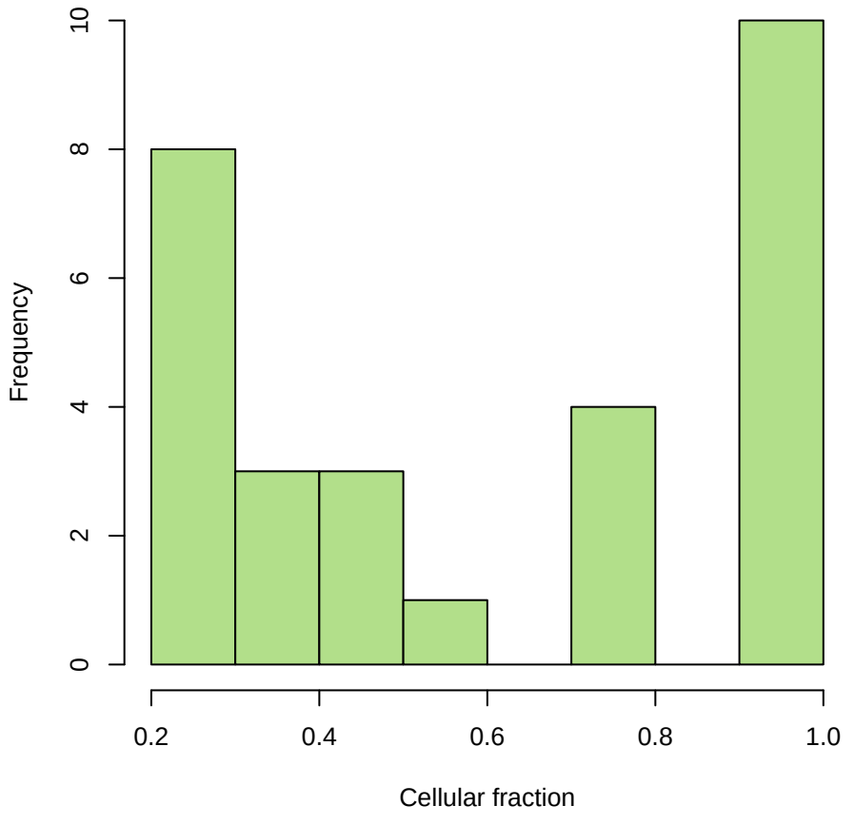

Purity: 0.26 Tumor ploidy: 1.442
1
2
3
4
5
0.00
0.05
0.10
0.15
0.20
Fraction Genome
−0.2
0.0
0.2
0.4
0.6
log2 ratio

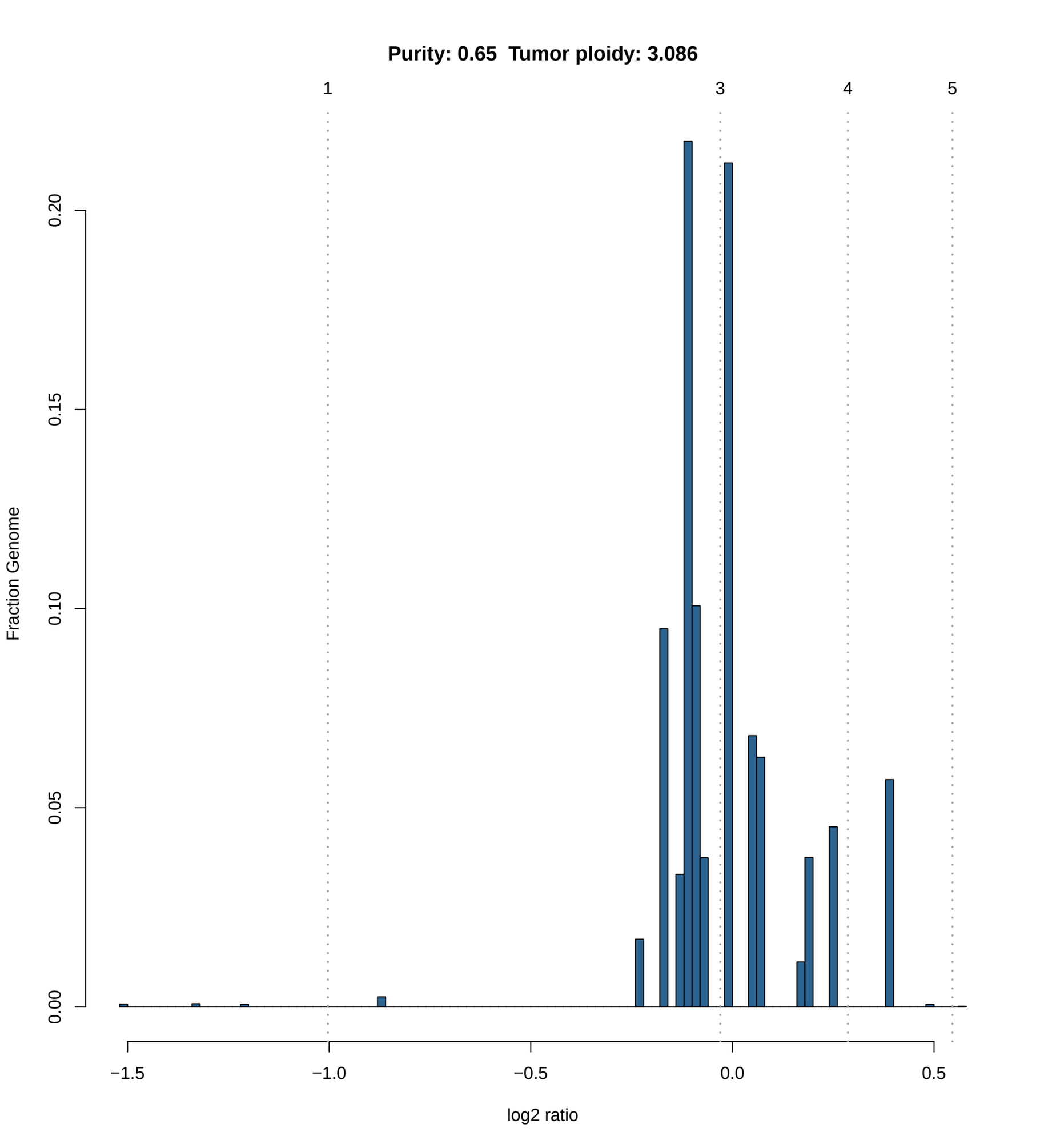

Purity: 0.26 Tumor ploidy: 1.442 SNV log−likelihood: −371.1 GoF: 85.1% Mean coverage: 477;413
1 2 3 4 5 6 7 8 10 11 12 13 15 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index
SCNA−fit log−likelihood: −6909.93
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4
0 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

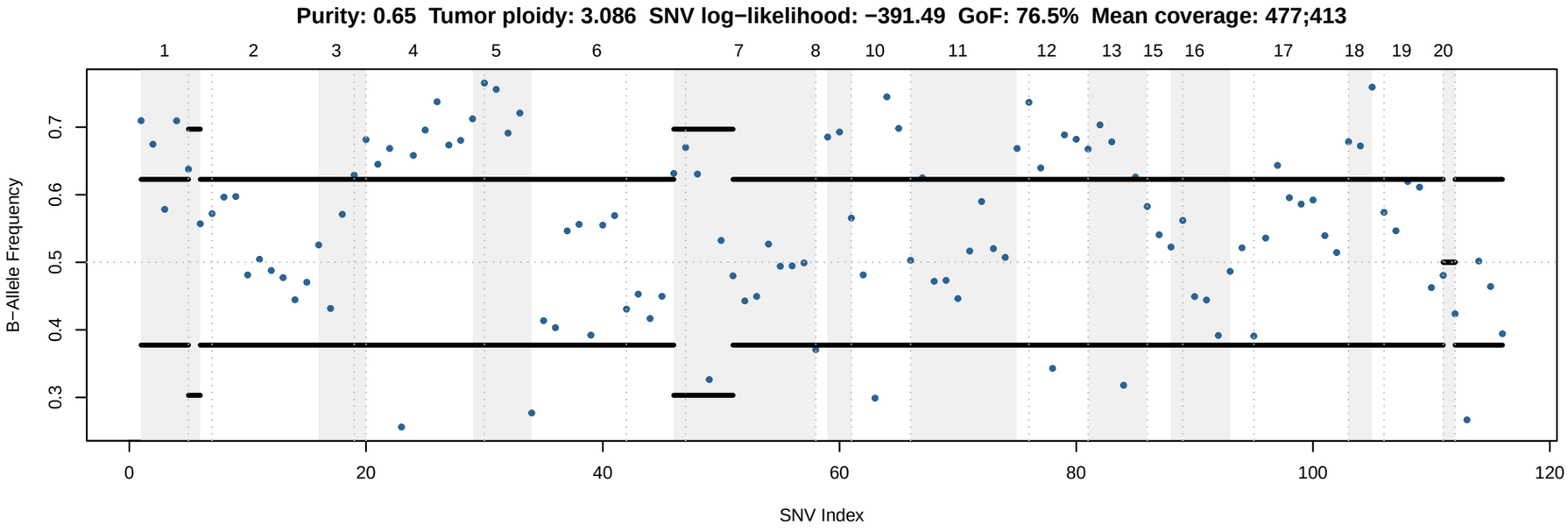

Allelic fraction (germline)
Copy Number log−ratio
1m2
3m3
2m2
4m3
1m1
3m2
2m1
3m1
1m0
2m0
3m0

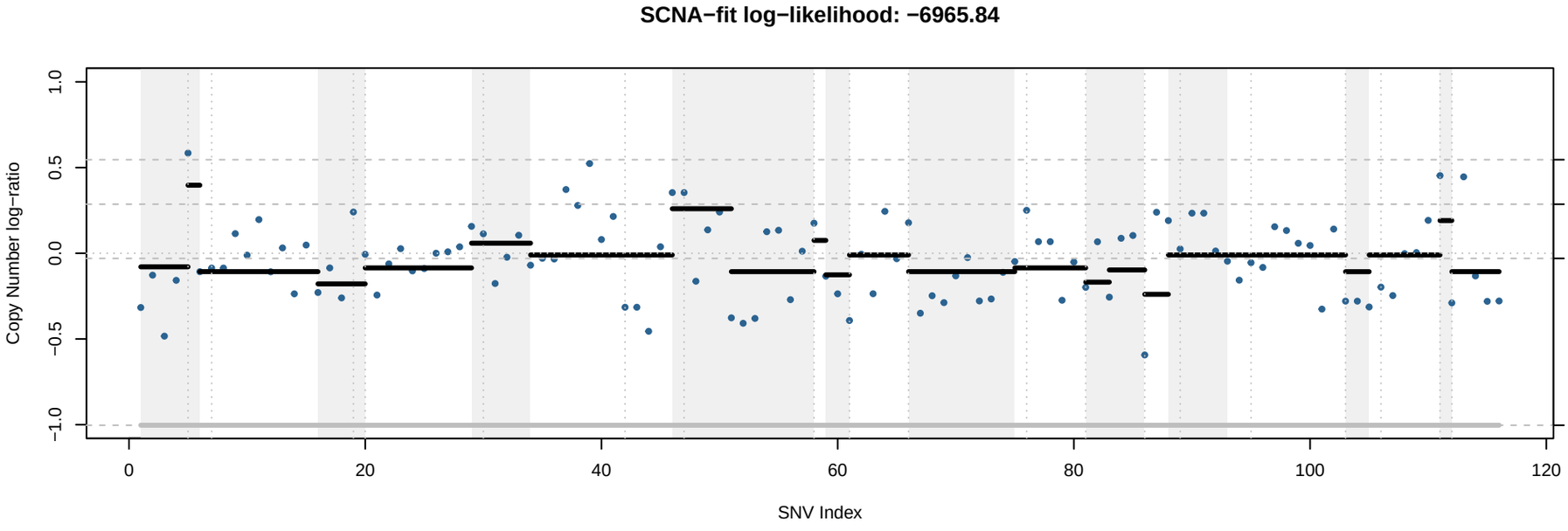

Coverage (log2)
Allelic fraction

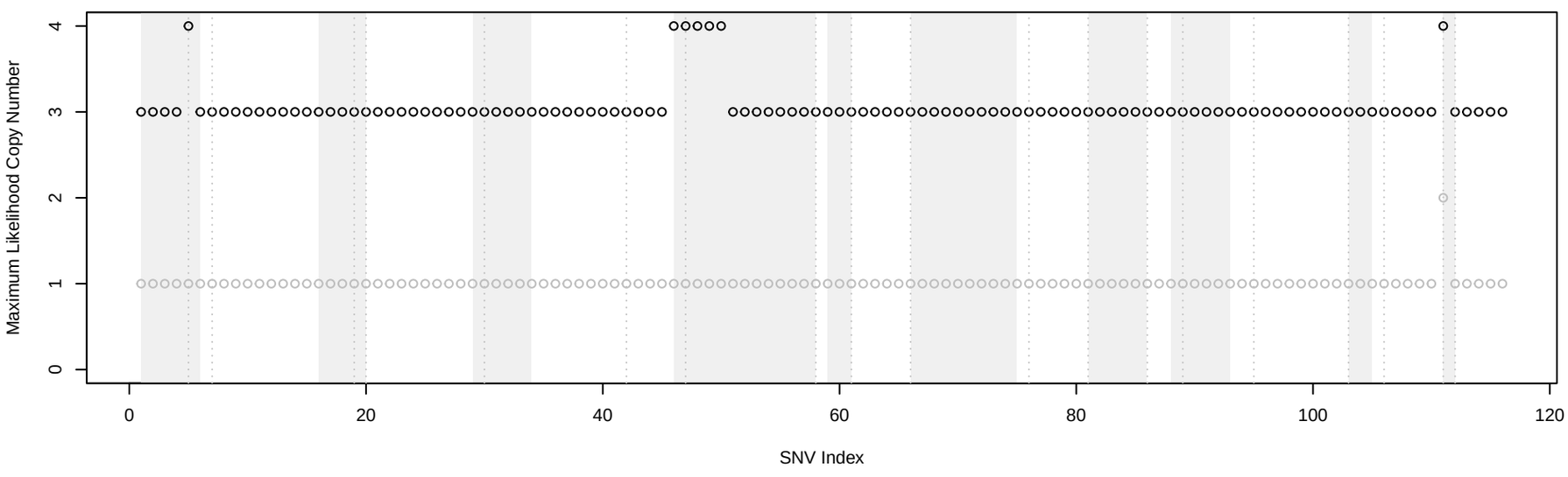

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1
3m1
4m1

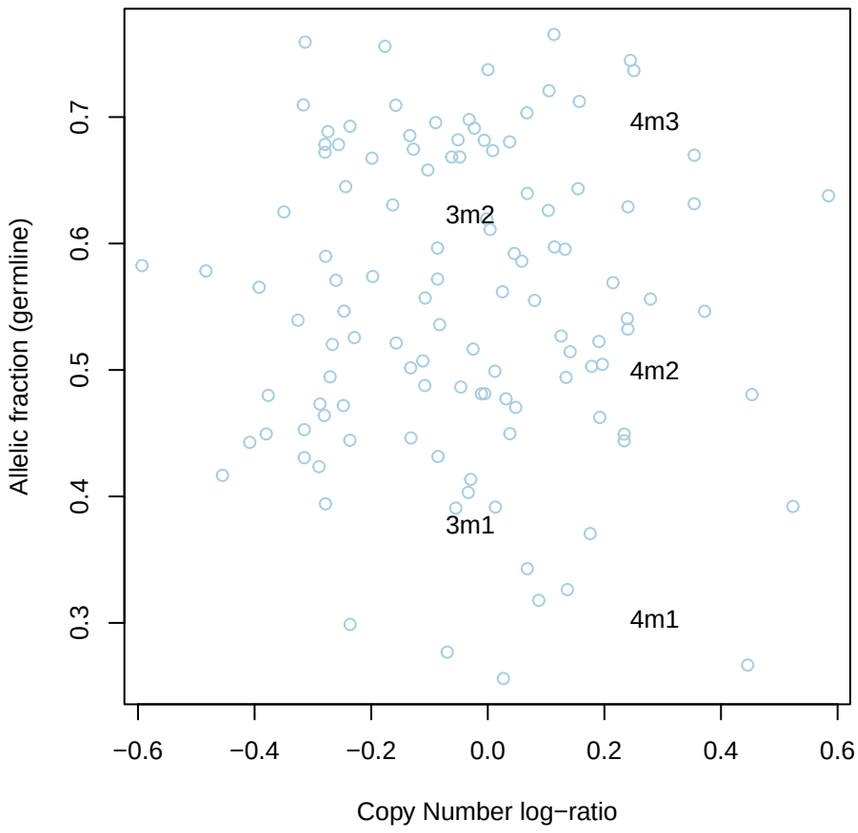

Frequency
Cellular fraction

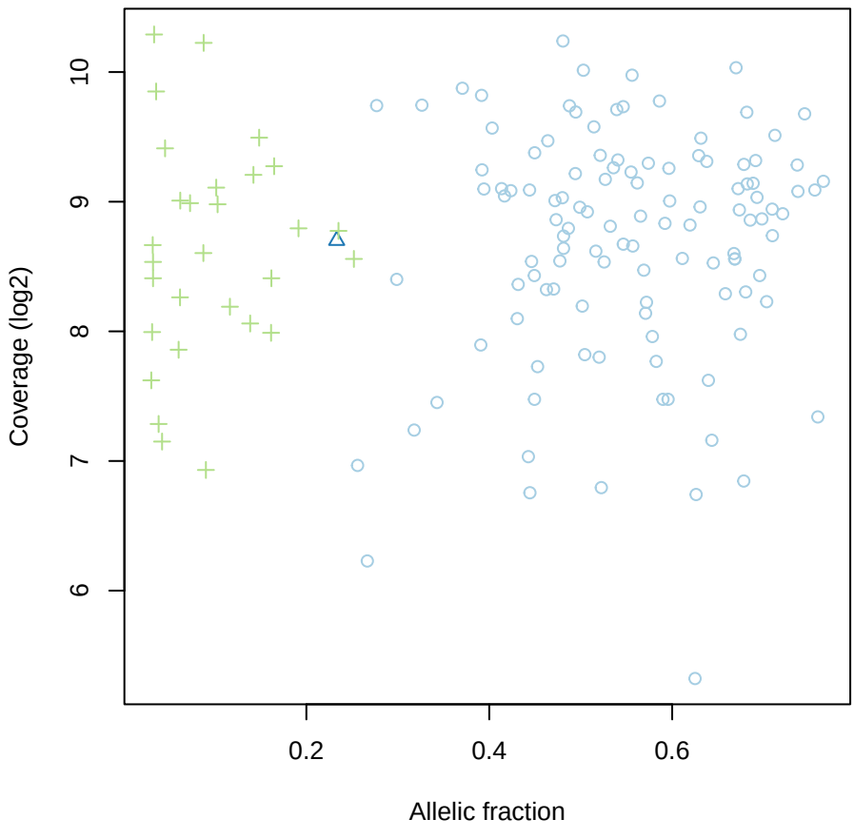

Purity: 0.65 Tumor ploidy: 3.086
1
3
4
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

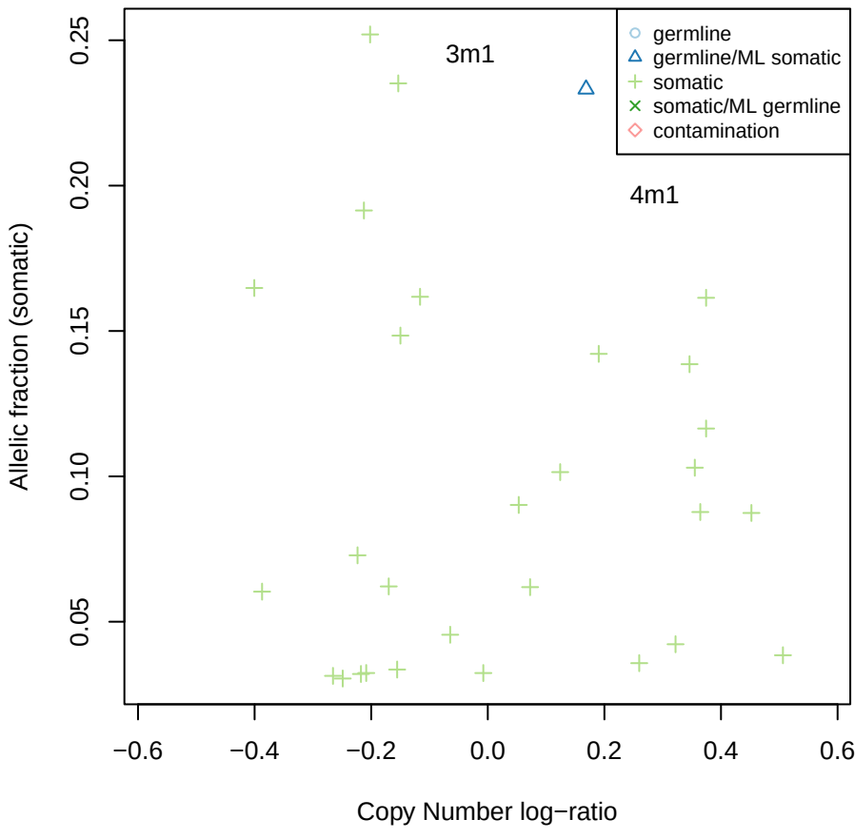

Purity: 0.65 Tumor ploidy: 3.086 SNV log−likelihood: −391.49 GoF: 76.5% Mean coverage: 477;413
1 2 3 4 5 6 7 8 10 11 12 13 15 16 17 18 19 20
B−Allele Frequency
0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

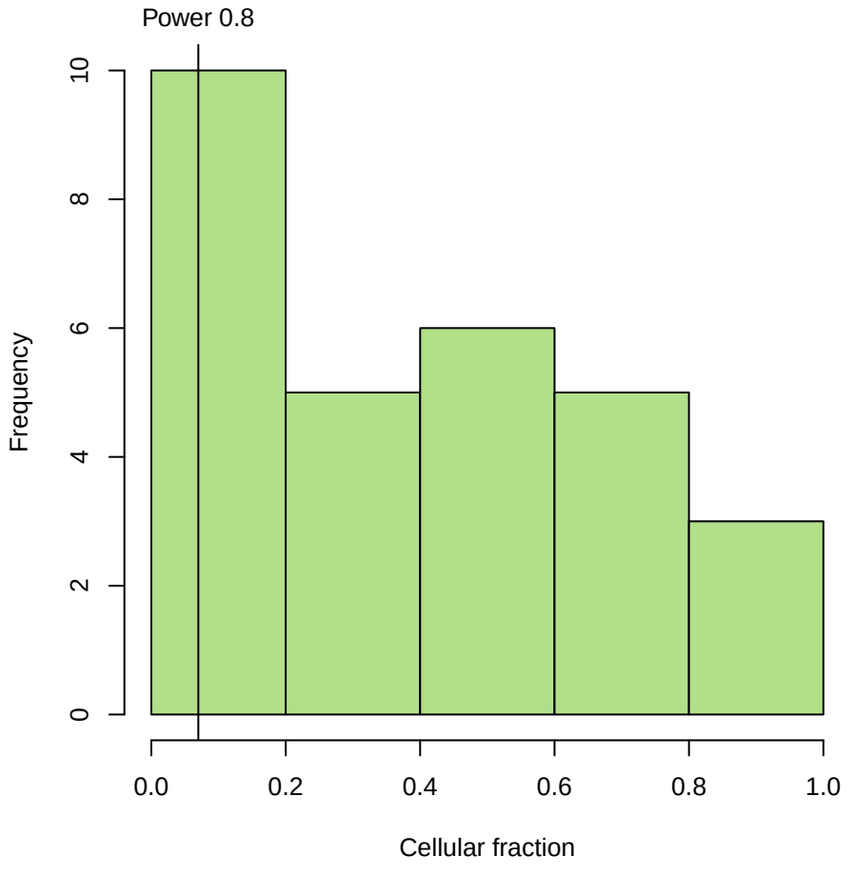

SCNA−fit log−likelihood: −6965.84
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 3 4 5
0 20 40 60 80 100 120
SNV Index

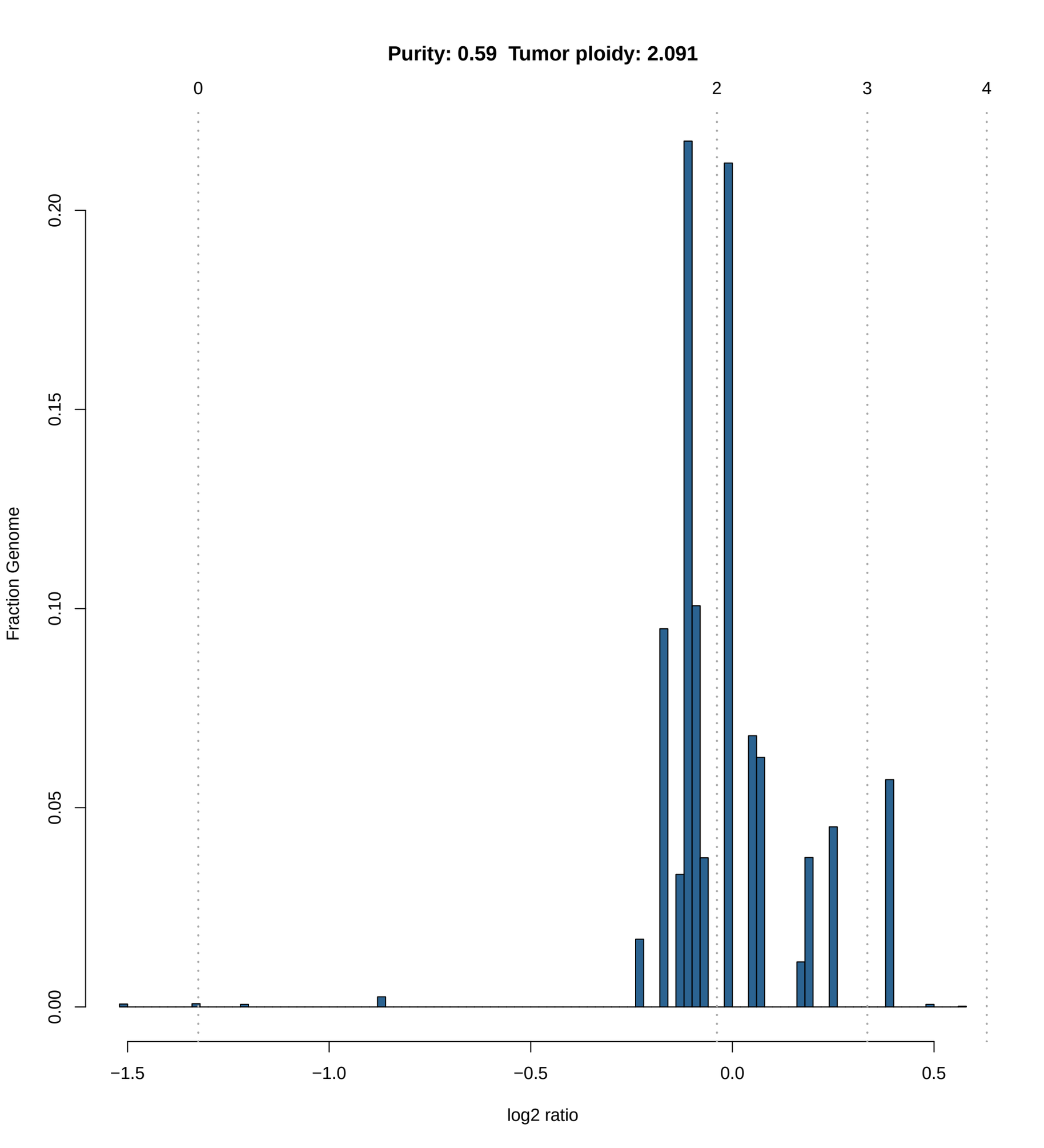

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100 120
SNV Index

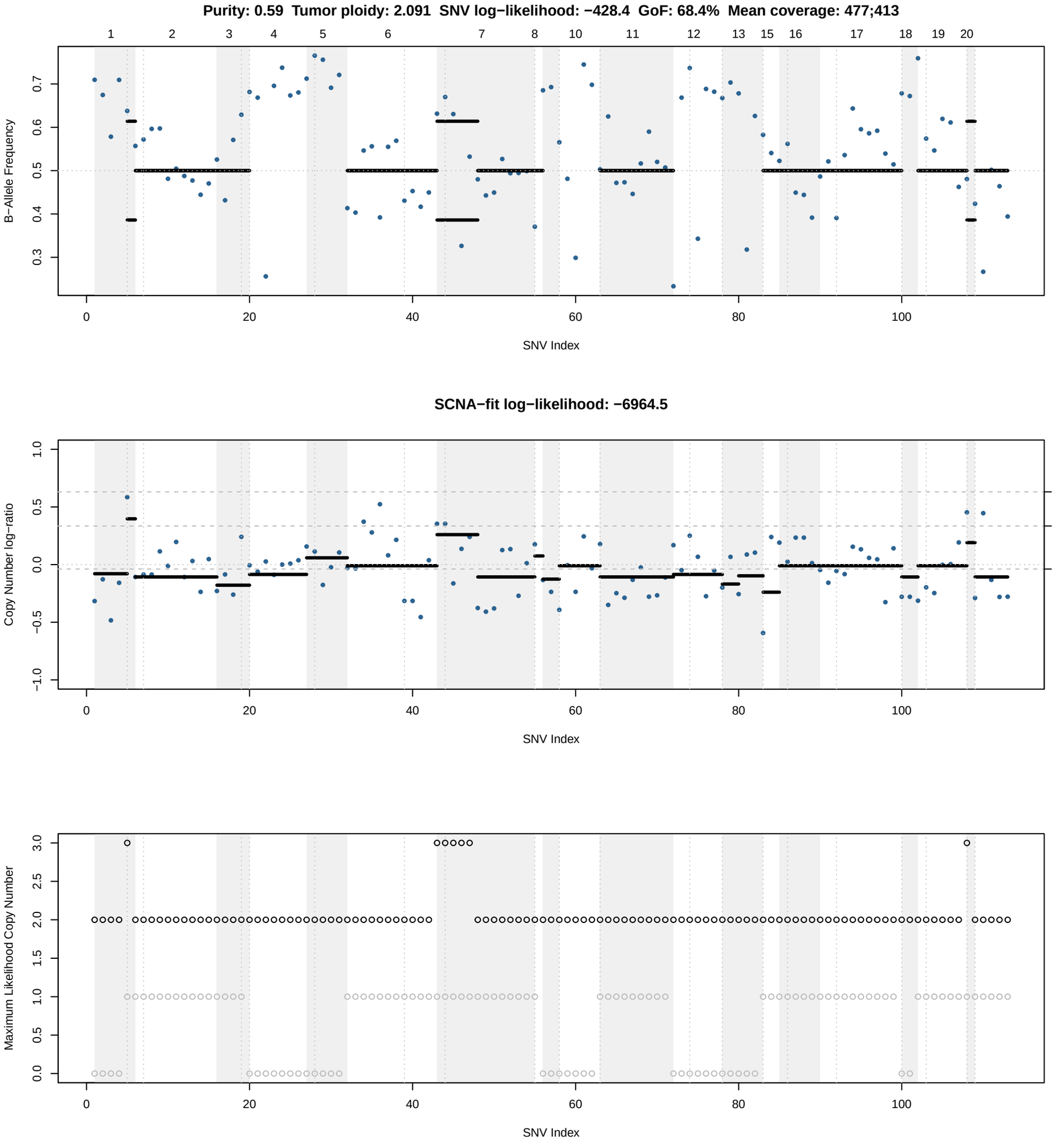

Allelic fraction (germline)
0.3
0.4
0.5
0.6
0.7
4m3
3m2
4m2
3m1
4m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

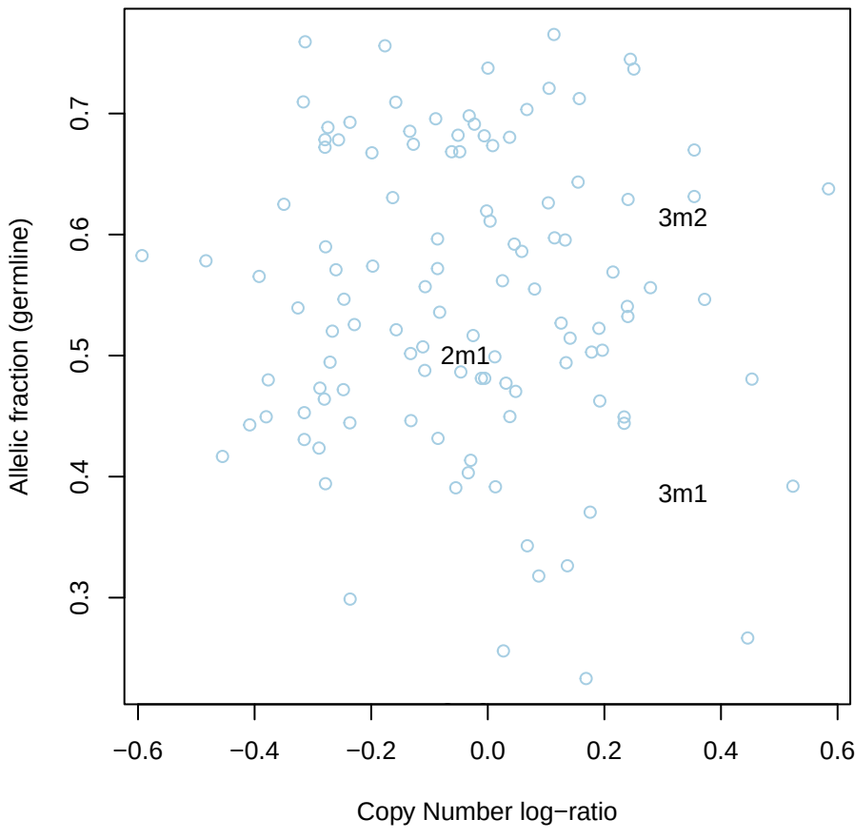

Coverage (log2)
6
7
8
9
10
0.2
0.4
0.6
Allelic fraction

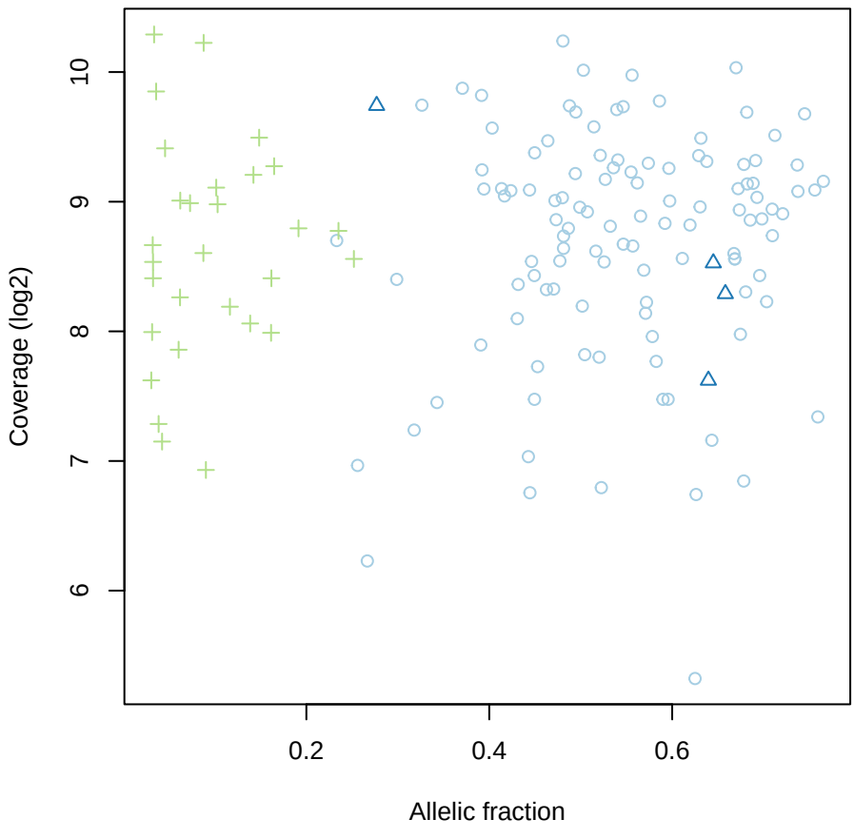

Allelic fraction (somatic)
0.05
0.10
0.15
0.20
0.25
3m1
4m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

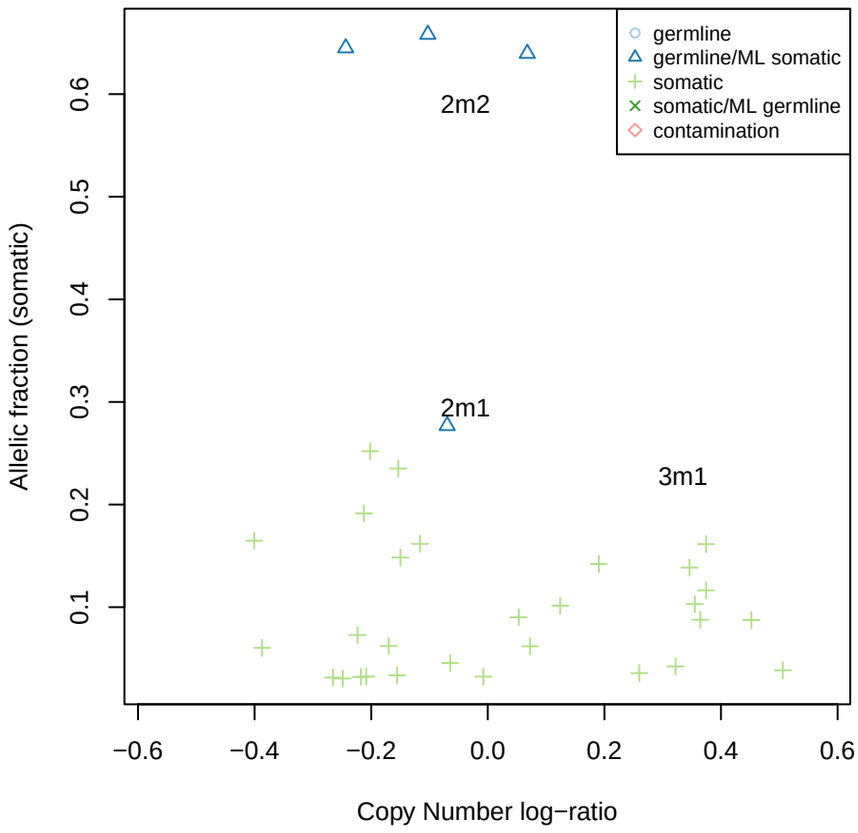

Power 0.8
Frequency
0
2
4
6
8
10
0.0
0.2
0.4
0.6
0.8
1.0
Cellular fraction

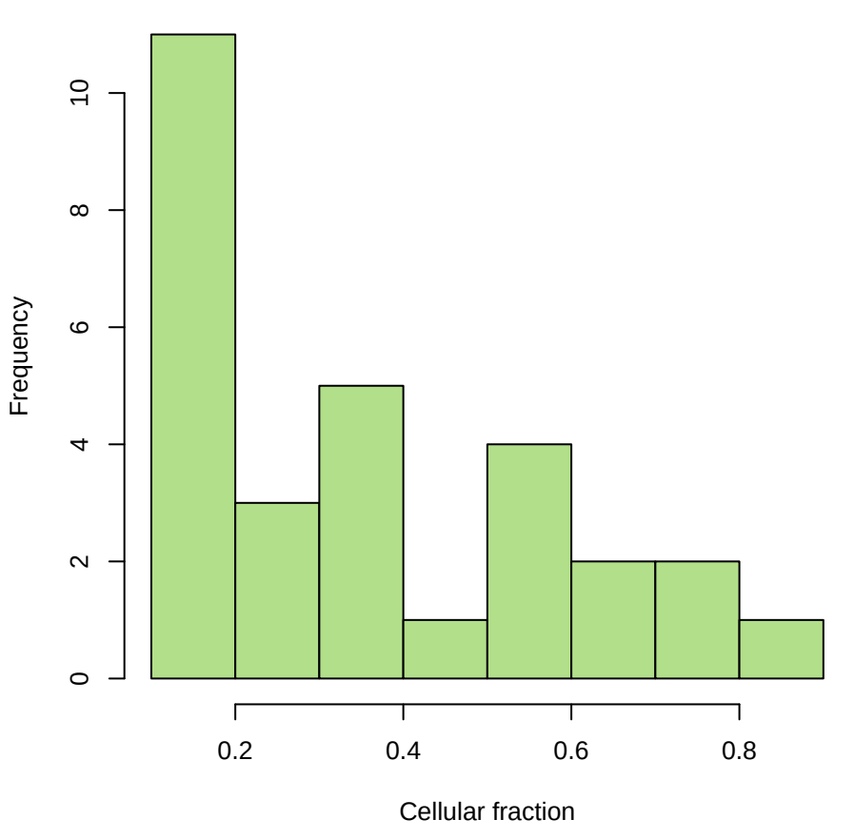

Purity: 0.59 Tumor ploidy: 2.091
0
2
3
4
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio


Purity: 0.59 Tumor ploidy: 2.091 SNV log−likelihood: −428.4 GoF: 68.4% Mean coverage: 477;413
1 2 3 4 5 6 7 8 10 11 12 13 15 16 17 18 19 20
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: −6964.5
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 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)
0.3
0.4
0.5
0.6
0.7
3m2
2m1
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio


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


Allelic fraction (somatic)
0.1
0.2
0.3
0.4
0.5
0.6
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
2m1
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio


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