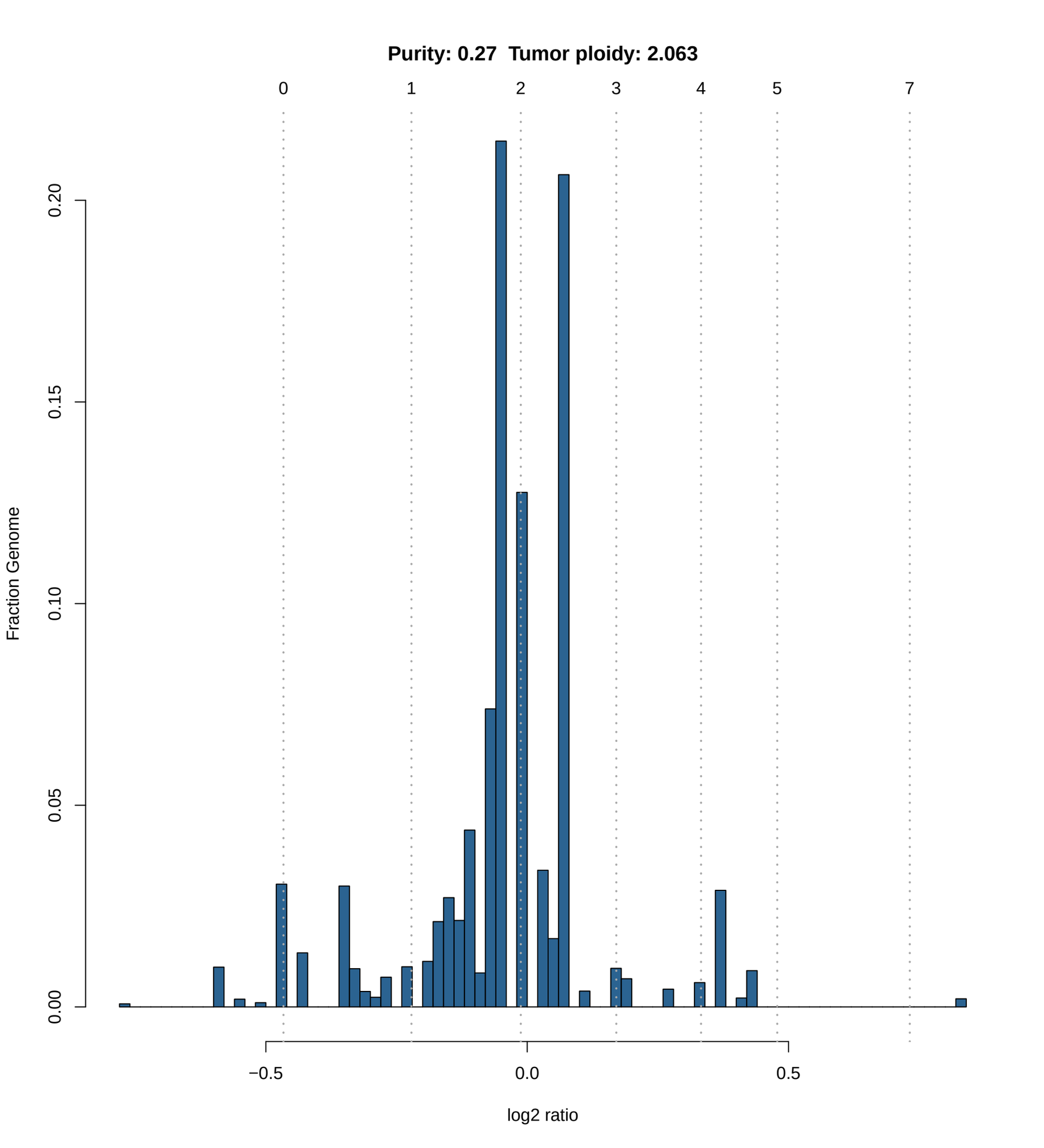
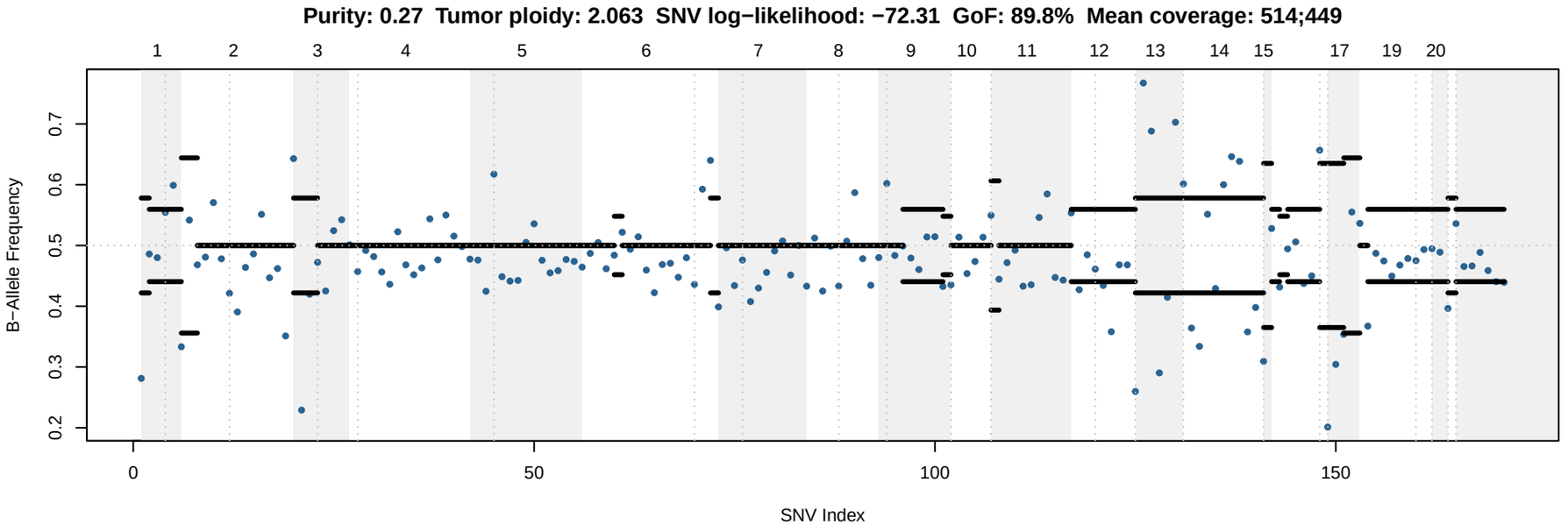
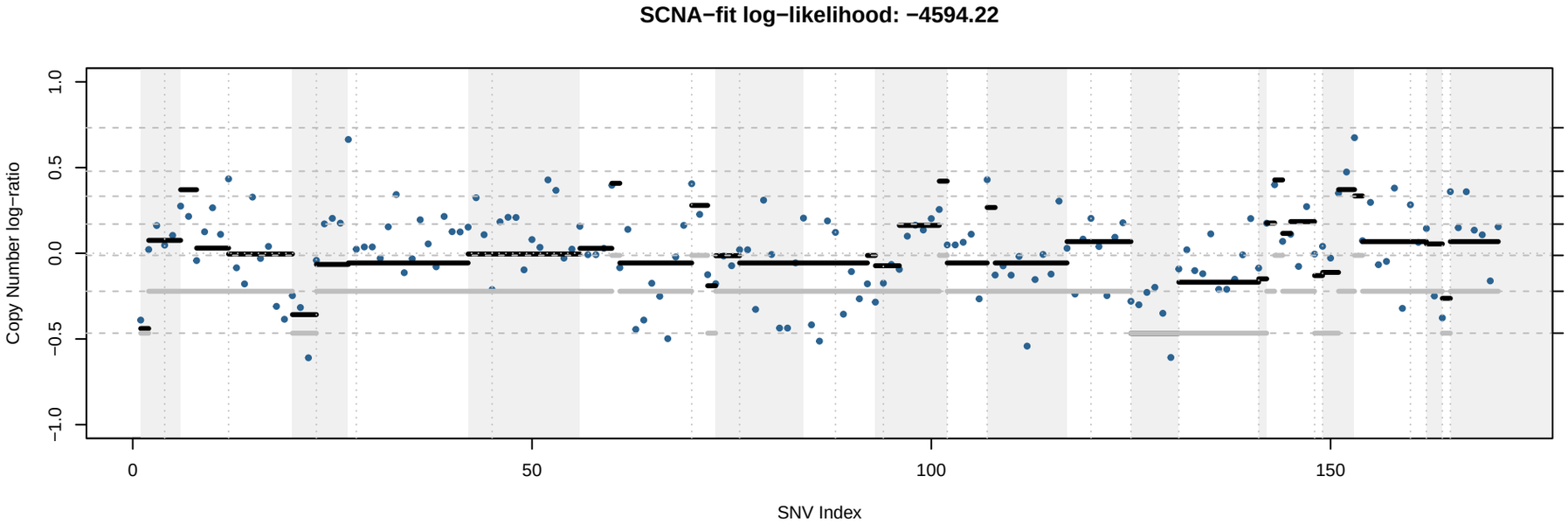
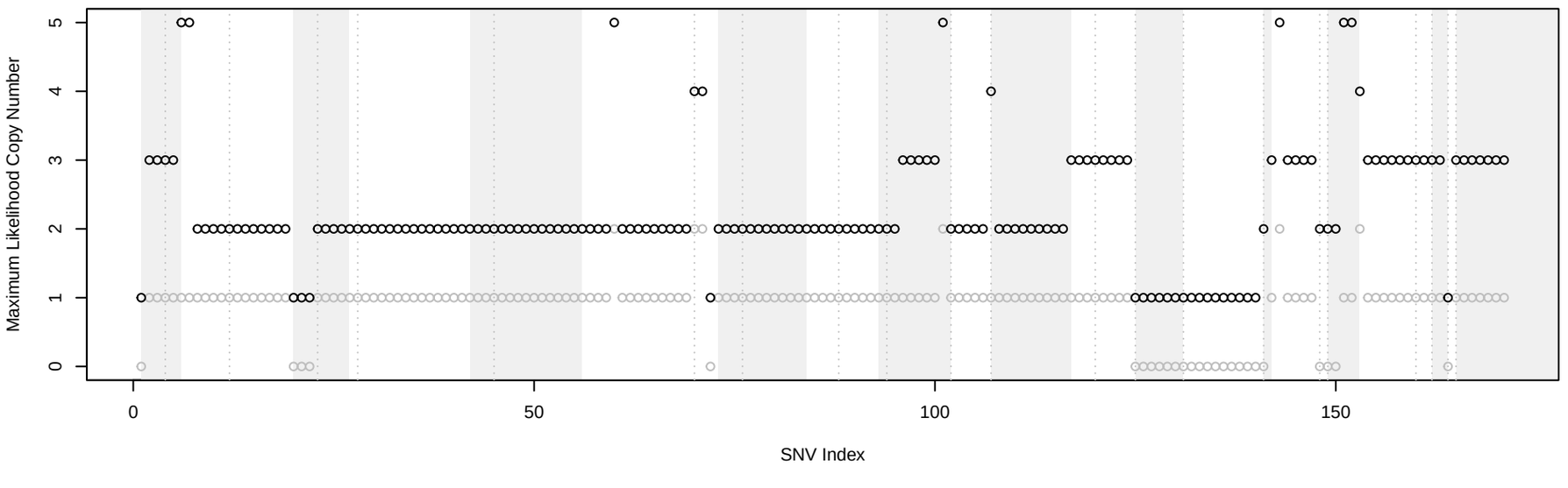
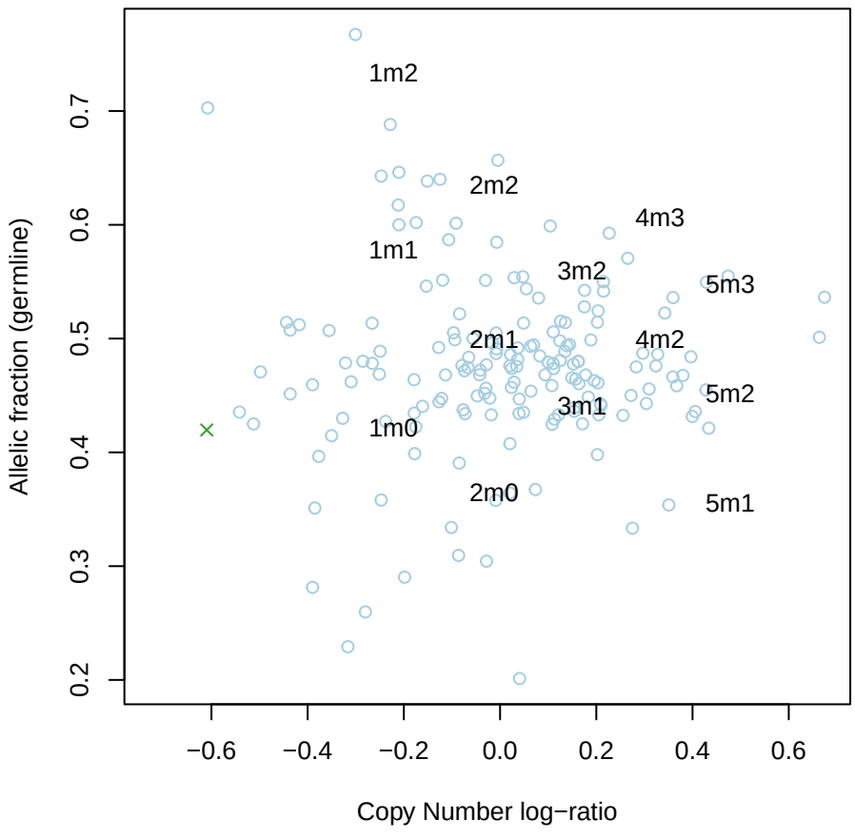
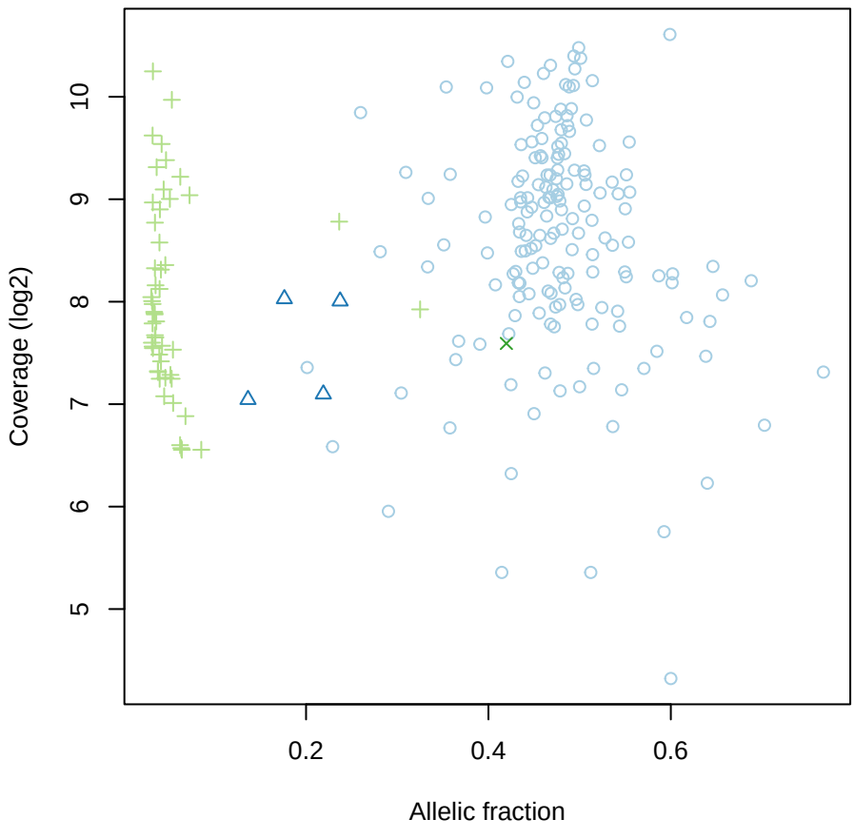

Purity: 0.27 Tumor ploidy: 2.063
0
1
2
3
4
5
7
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

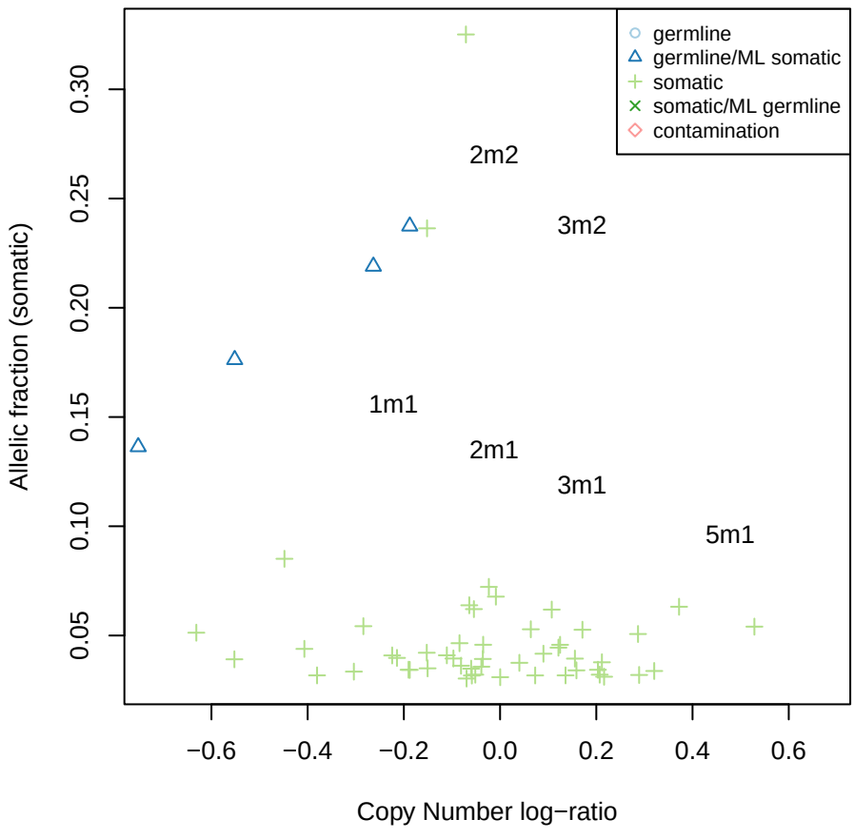

Purity: 0.27 Tumor ploidy: 2.063 SNV log−likelihood: −72.31 GoF: 89.8% Mean coverage: 514;449
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

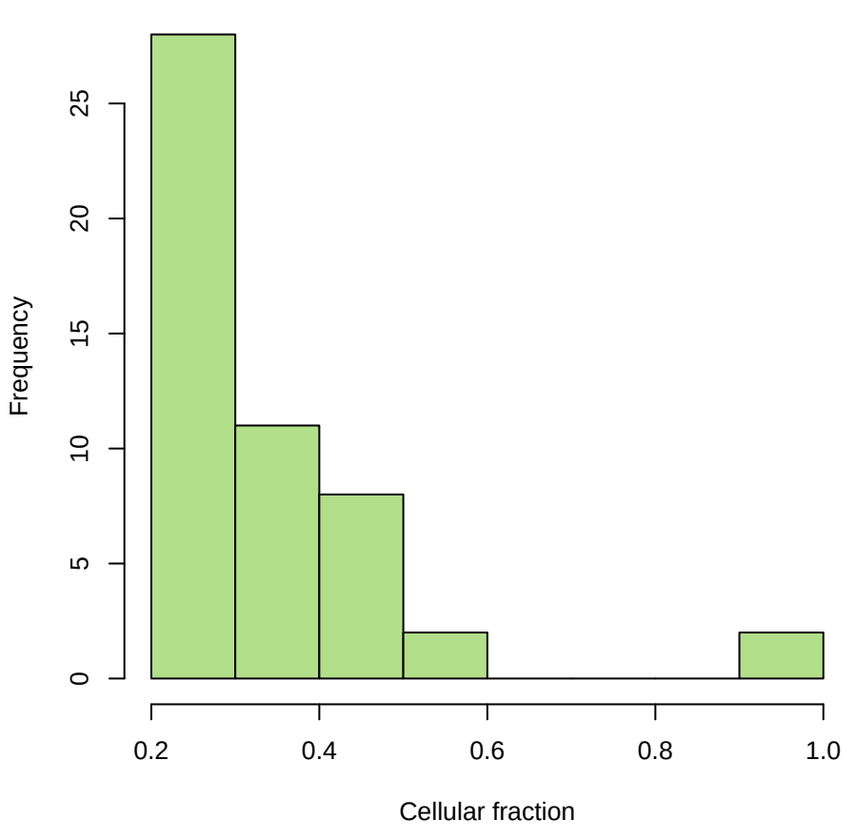

SCNA−fit log−likelihood: −4594.22
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5 7
0 50 100 150
SNV Index

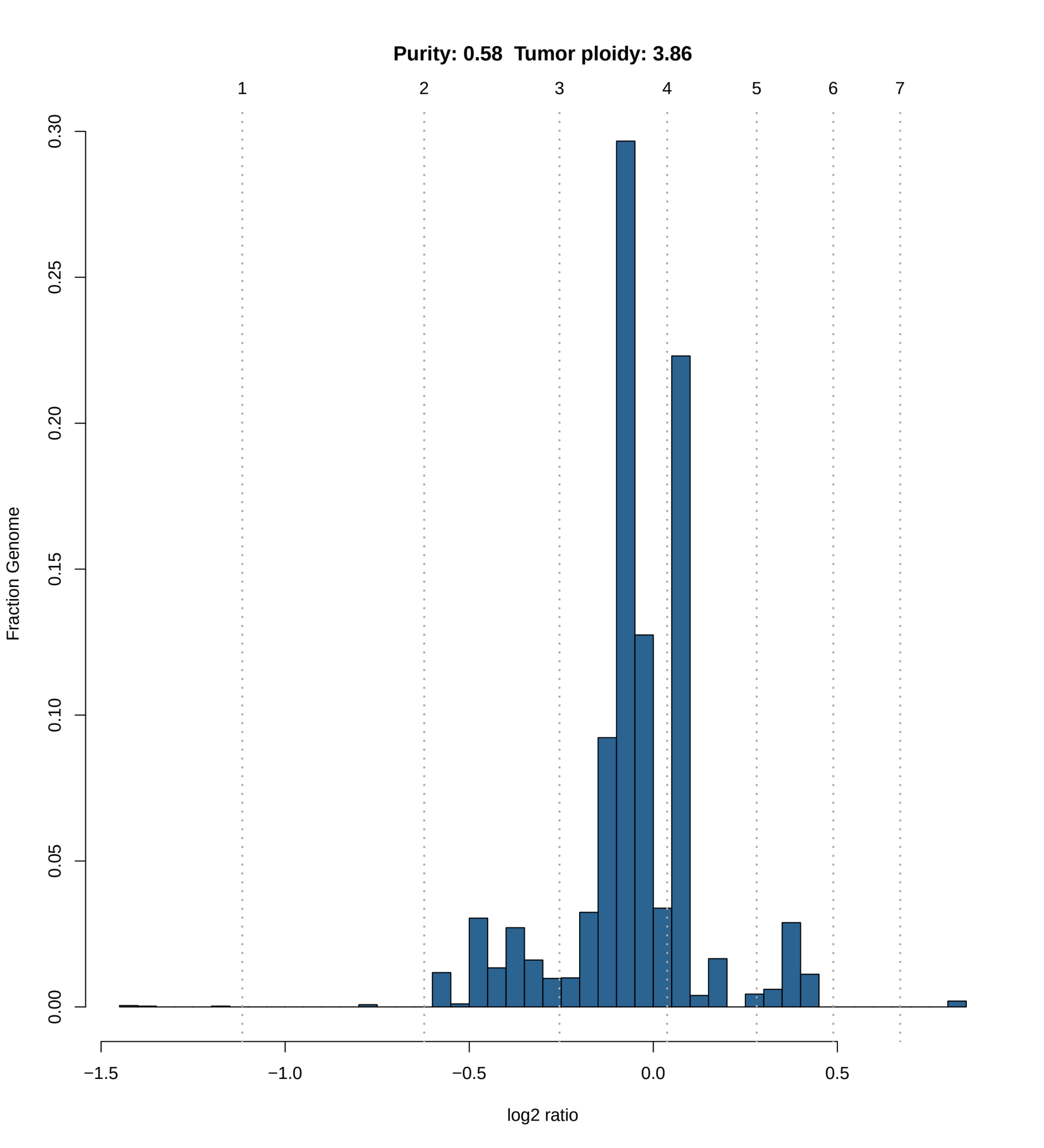

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 50 100 150
SNV Index

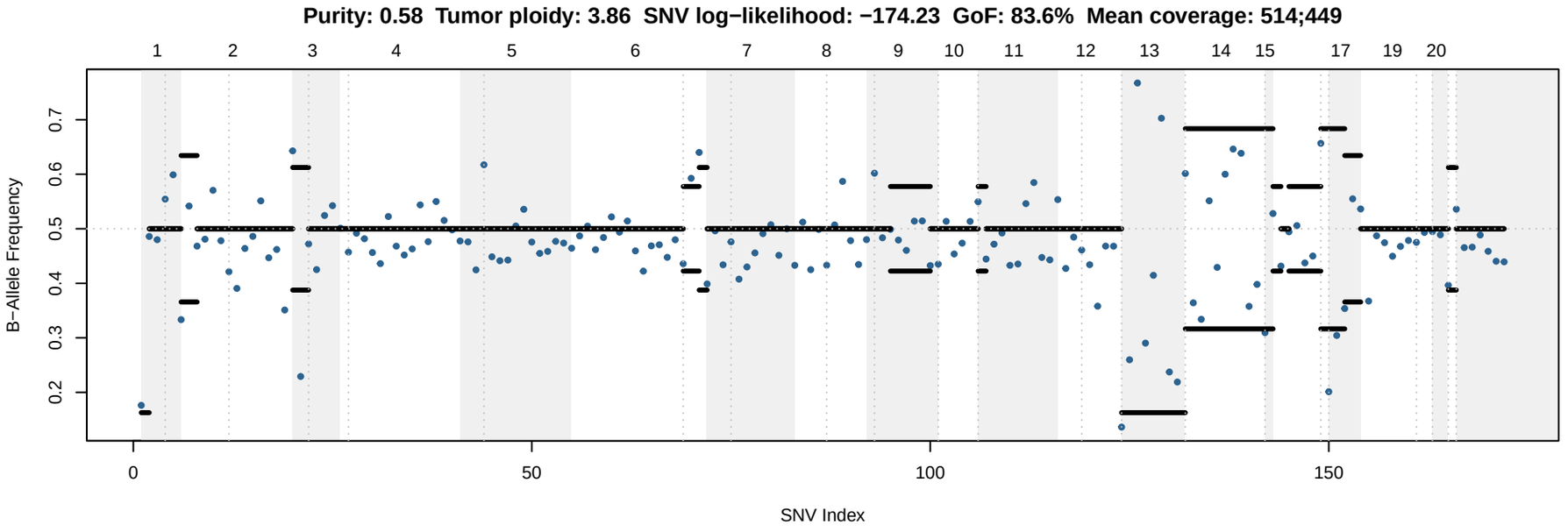

1m2
2m2
4m3
1m1
3m2
5m3
2m1
4m2
5m2
3m1
1m0
2m0
5m1
Allelic fraction (germline)
Copy Number log−ratio

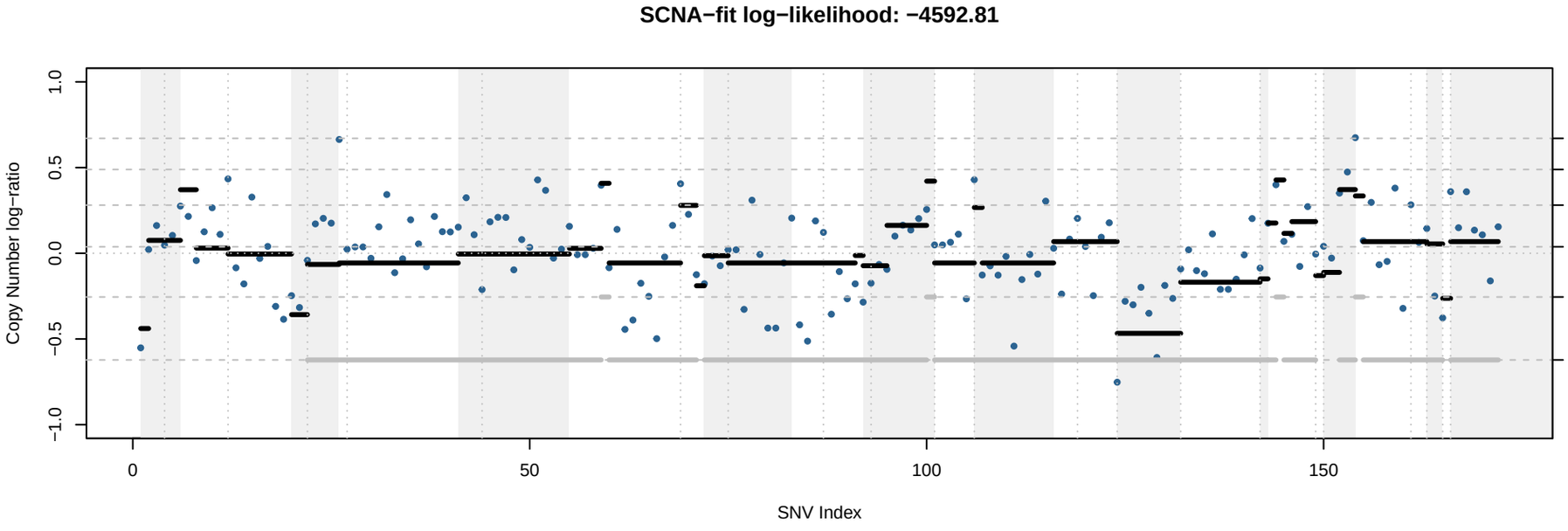

Coverage (log2)
Allelic fraction

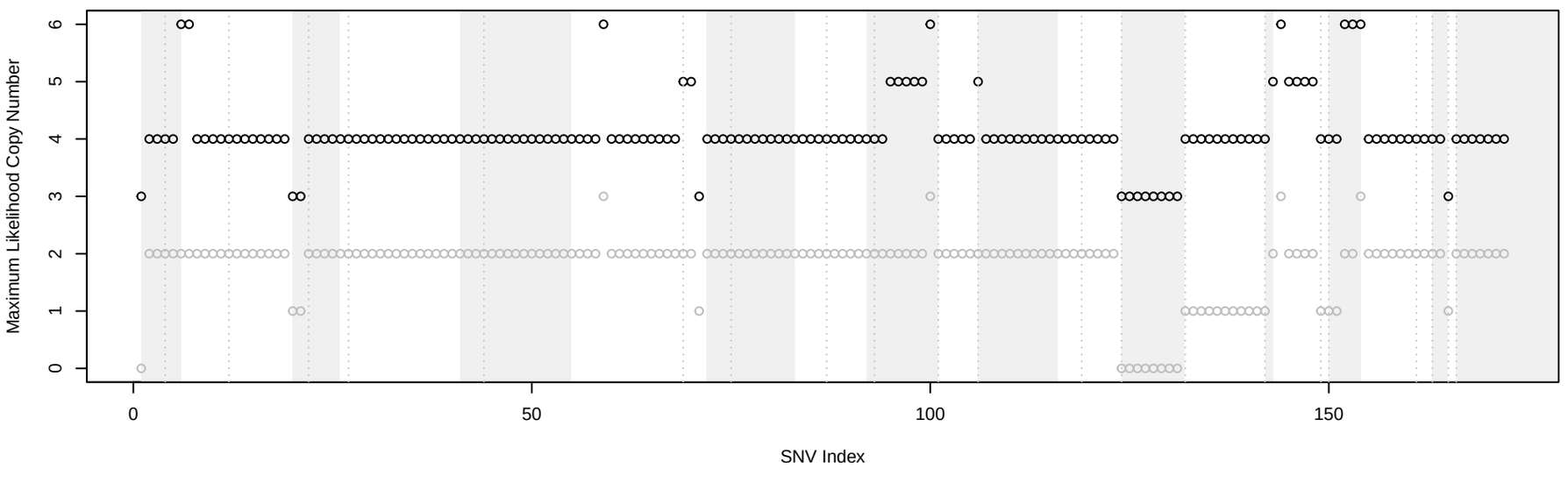

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m2
3m2
1m1
2m1
3m1
5m1
Allelic fraction (somatic)
Copy Number log−ratio

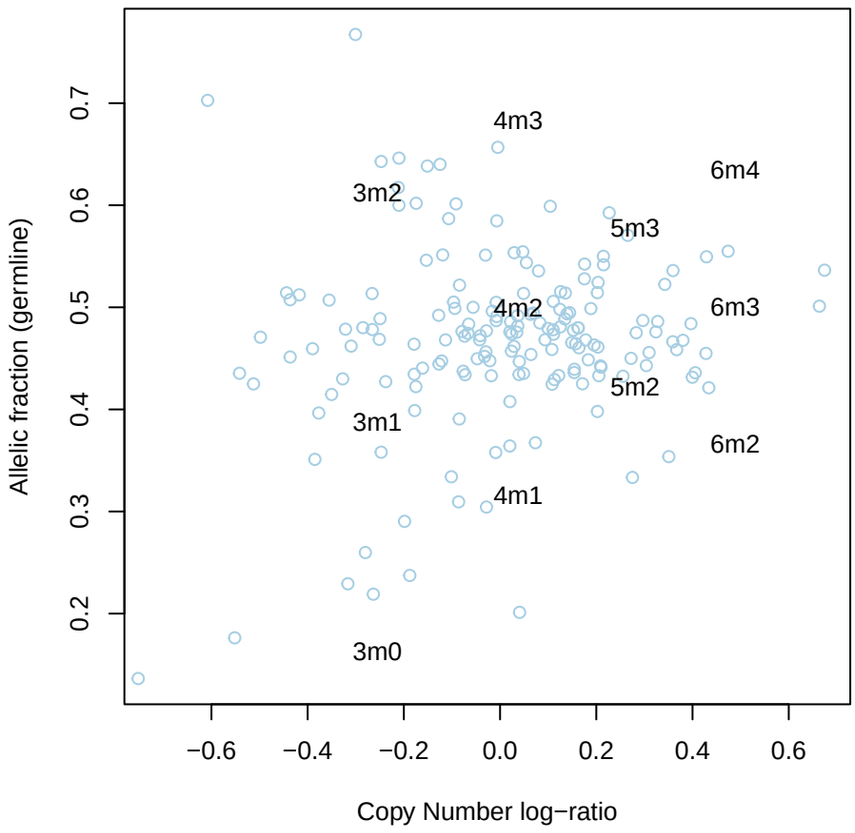

Frequency
Cellular fraction

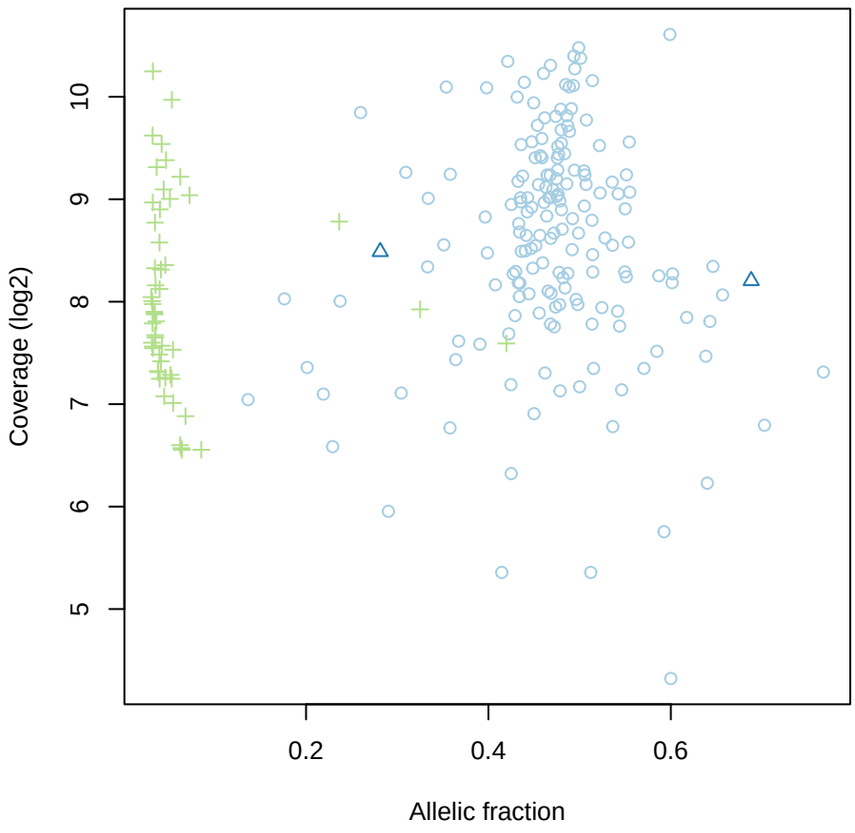

Purity: 0.58 Tumor ploidy: 3.86
1
2
3
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

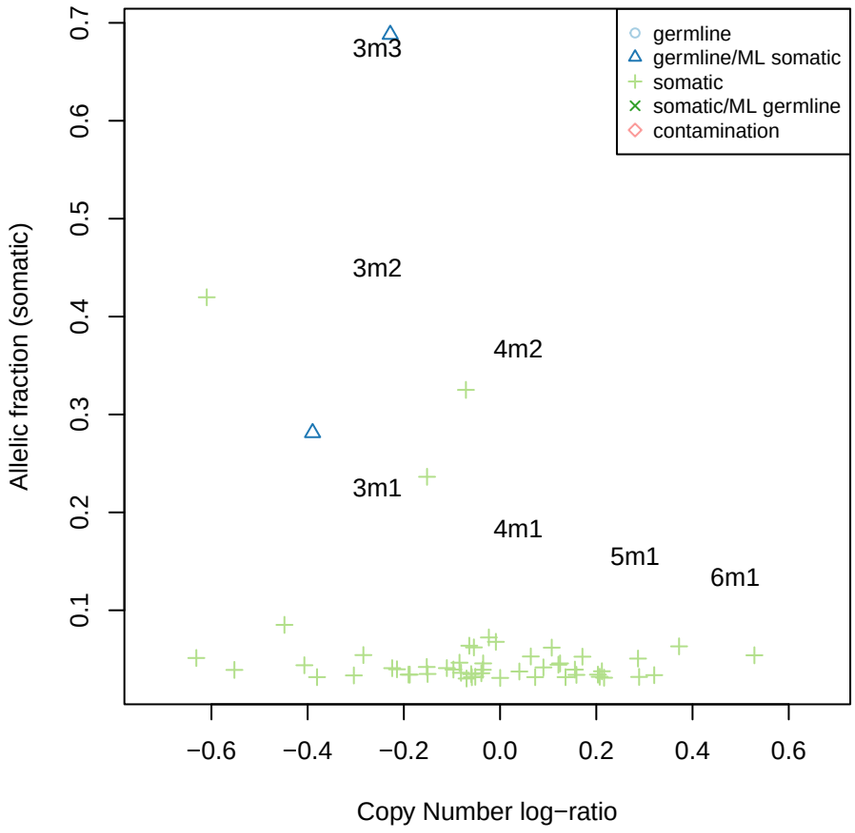

Purity: 0.58 Tumor ploidy: 3.86 SNV log−likelihood: −174.23 GoF: 83.6% Mean coverage: 514;449
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

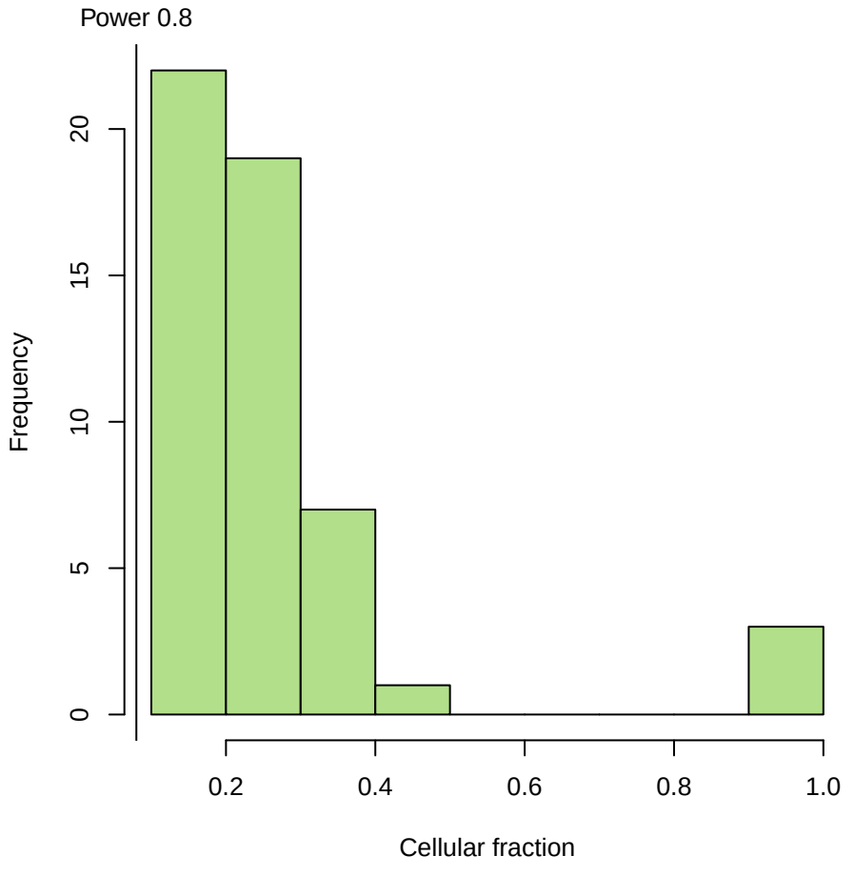

SCNA−fit log−likelihood: −4592.81
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 50 100 150
SNV Index

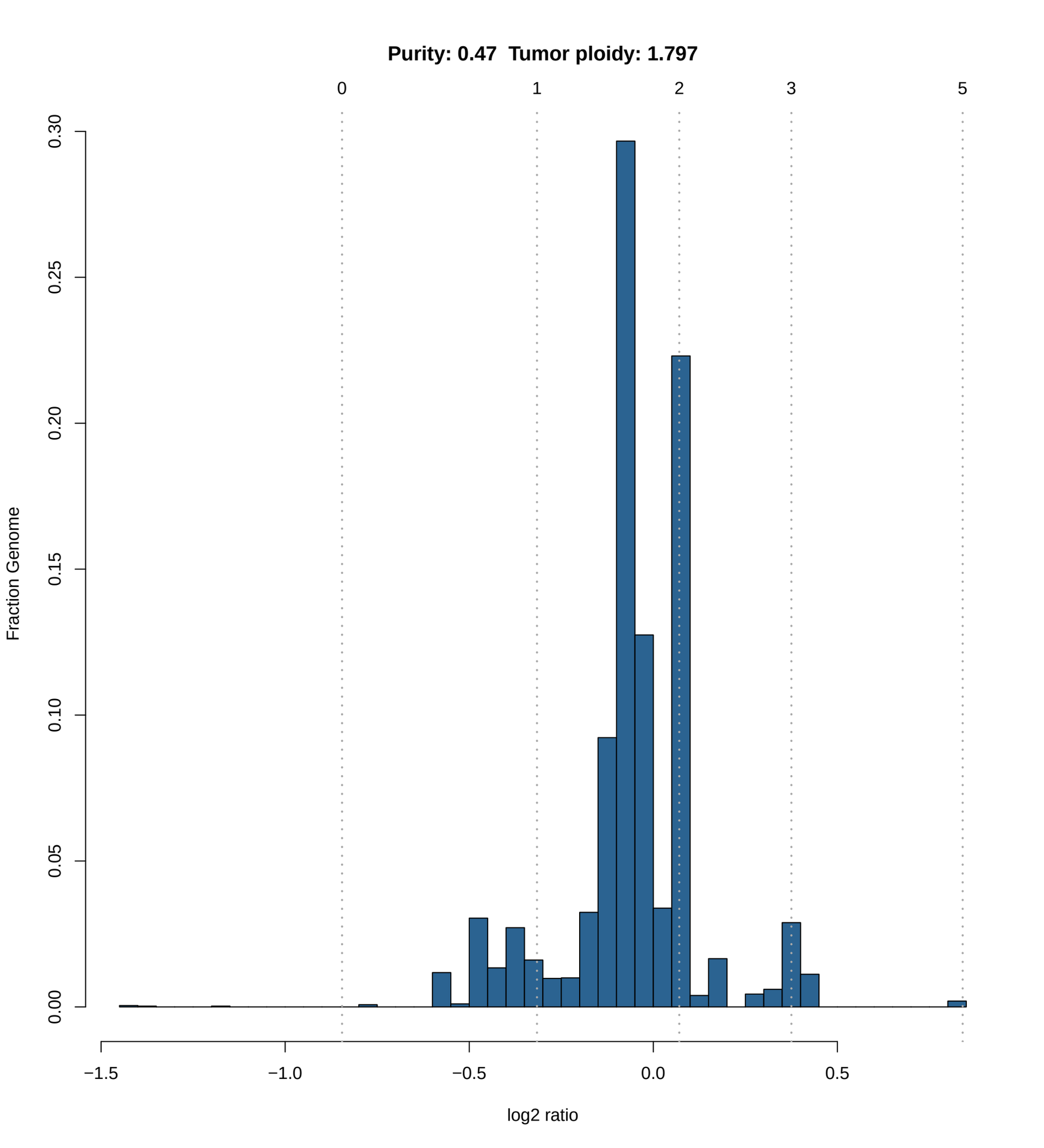

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 50 100 150
SNV Index

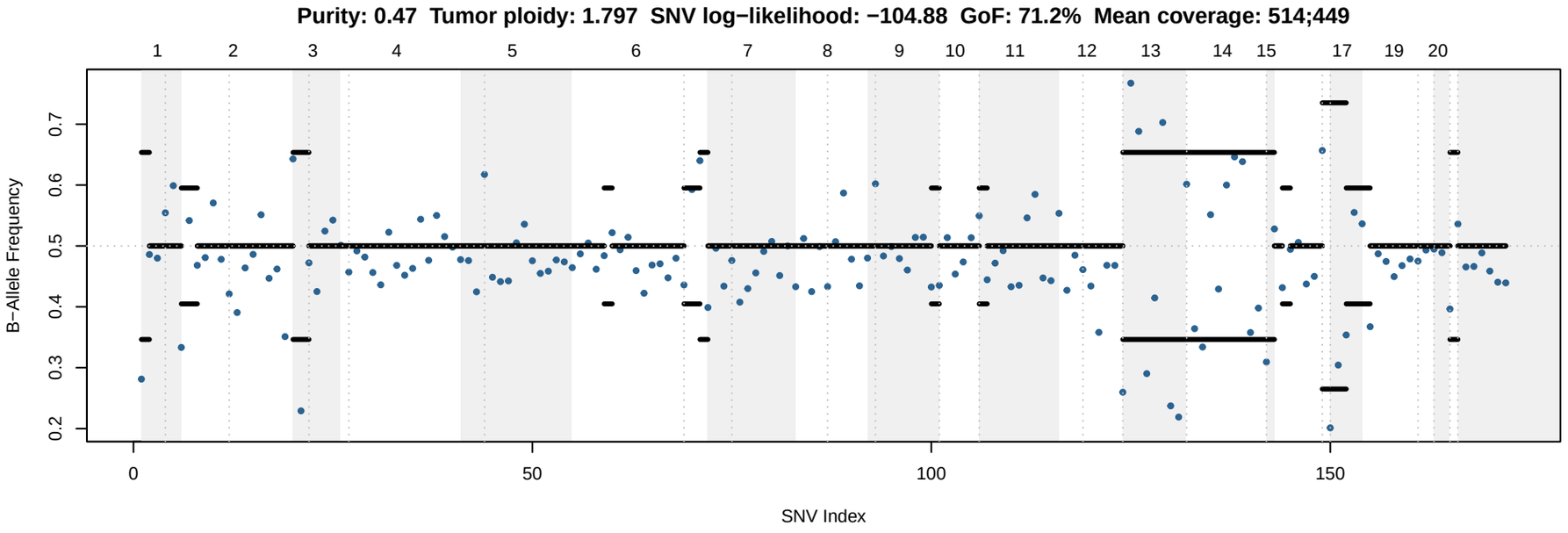

Allelic fraction (germline)
Copy Number log−ratio
4m3
6m4
3m2
5m3
4m2
6m3
5m2
3m1
6m2
4m1
3m0

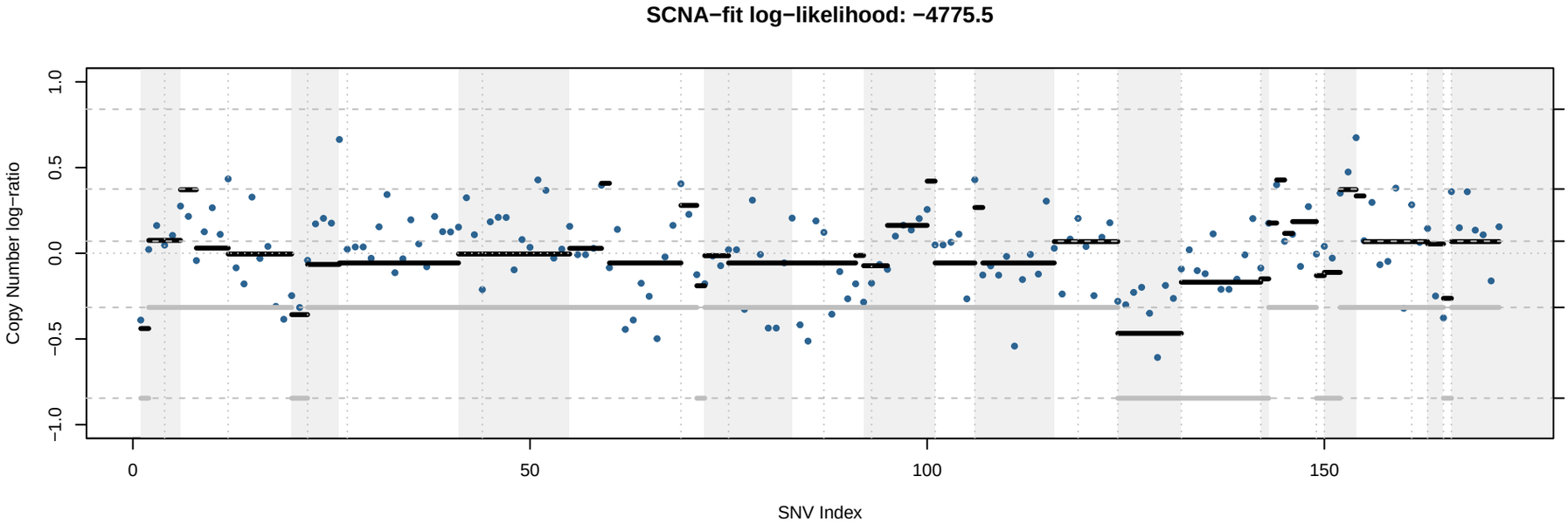

Coverage (log2)
Allelic fraction

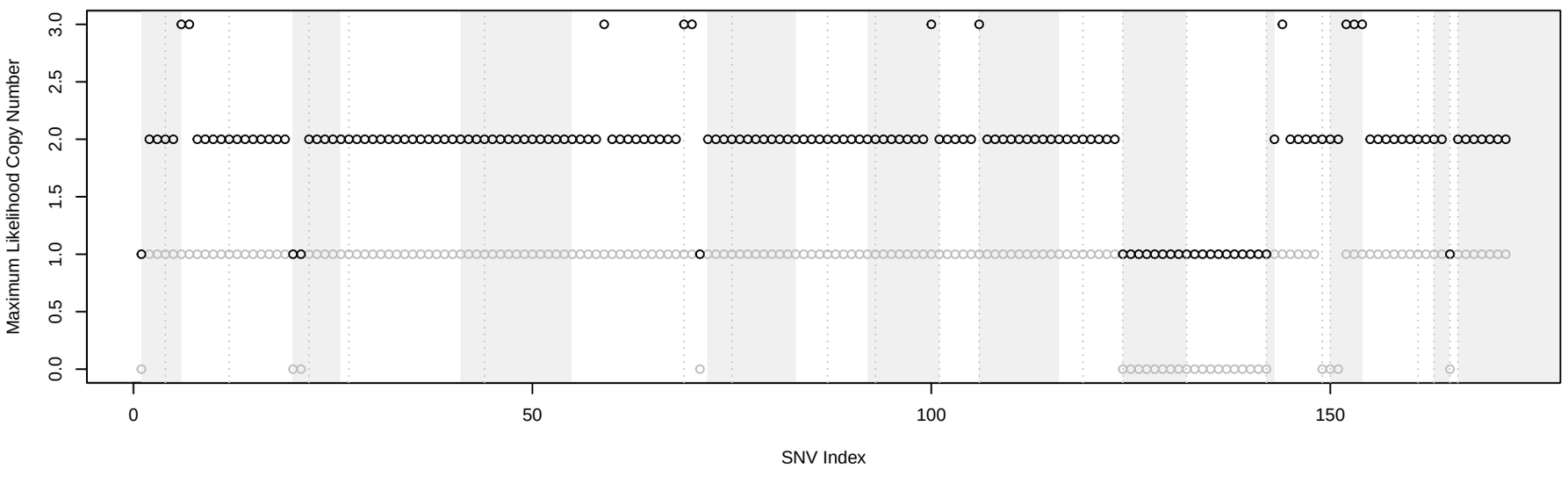

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m3
3m2
4m2
3m1
4m1
5m1
6m1

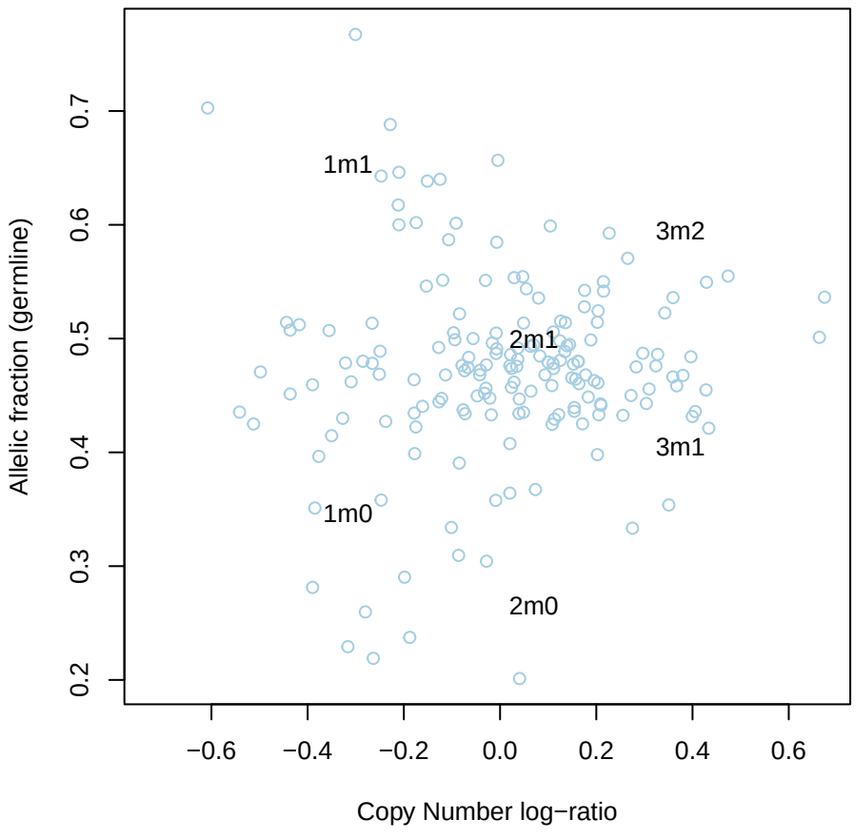

Power 0.8
Frequency
Cellular fraction

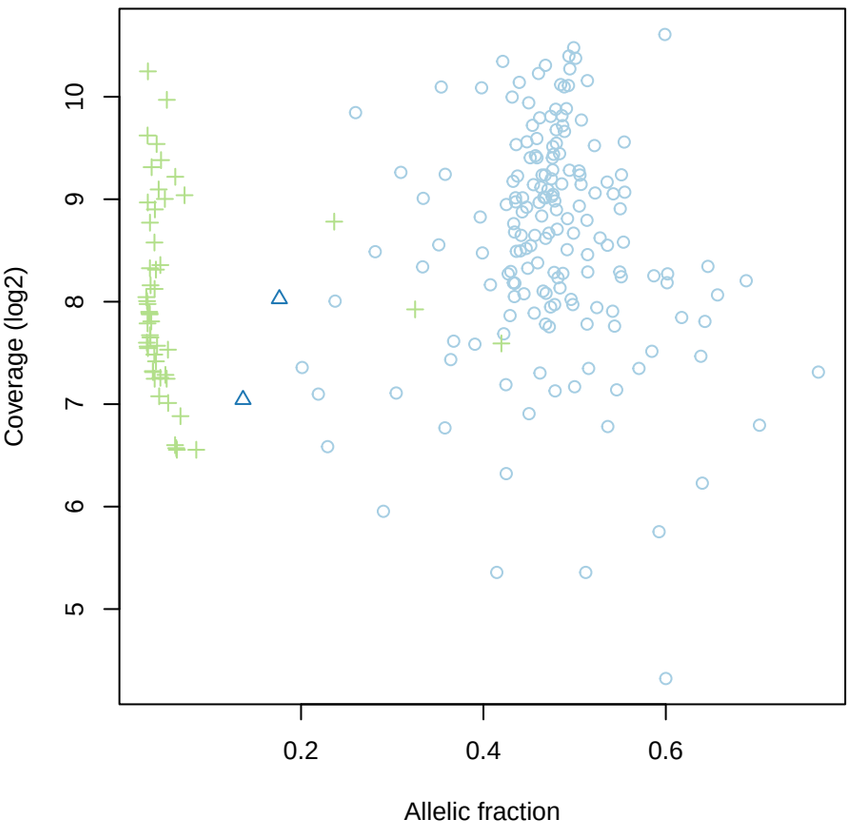

Purity: 0.47 Tumor ploidy: 1.797
0
1
2
3
5
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

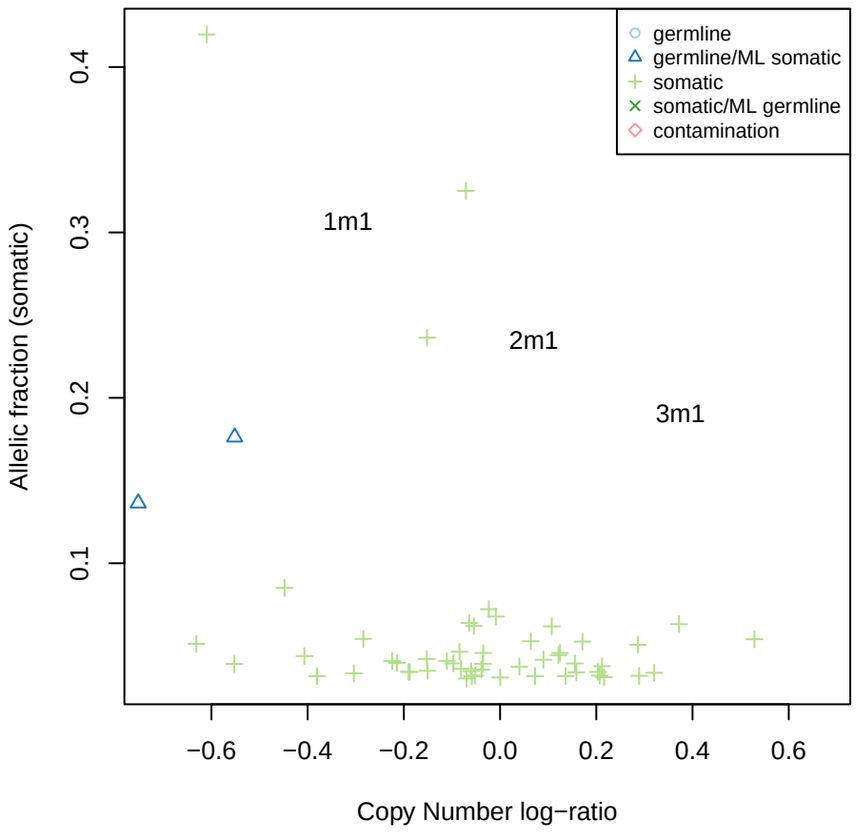

Purity: 0.47 Tumor ploidy: 1.797 SNV log−likelihood: −104.88 GoF: 71.2% Mean coverage: 514;449
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

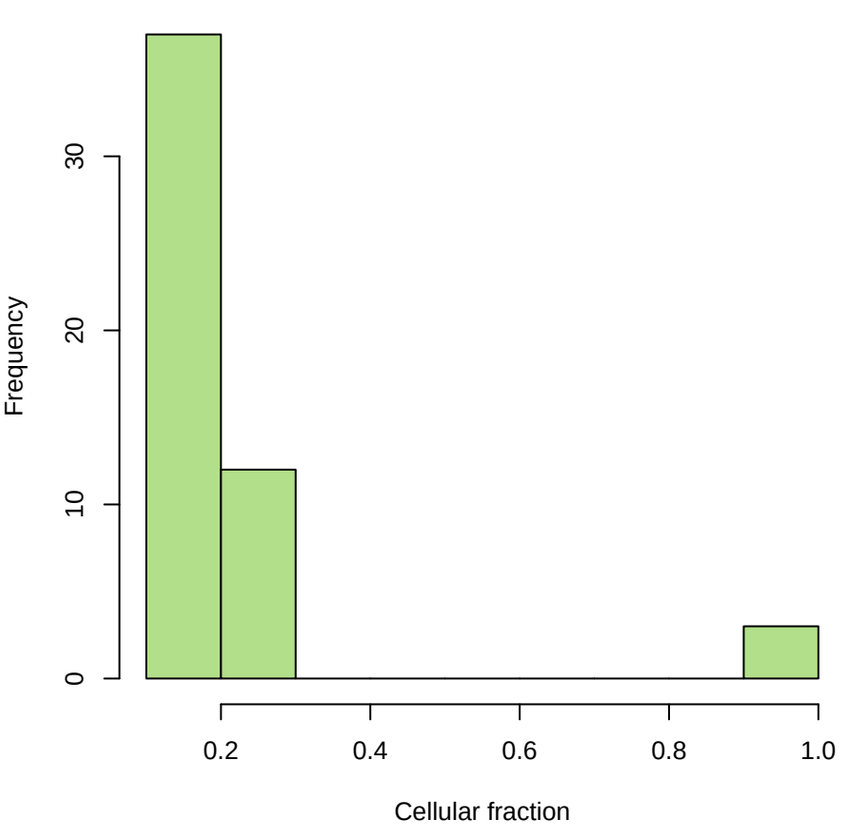

SCNA−fit log−likelihood: −4775.5
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 5
0 50 100 150
SNV Index

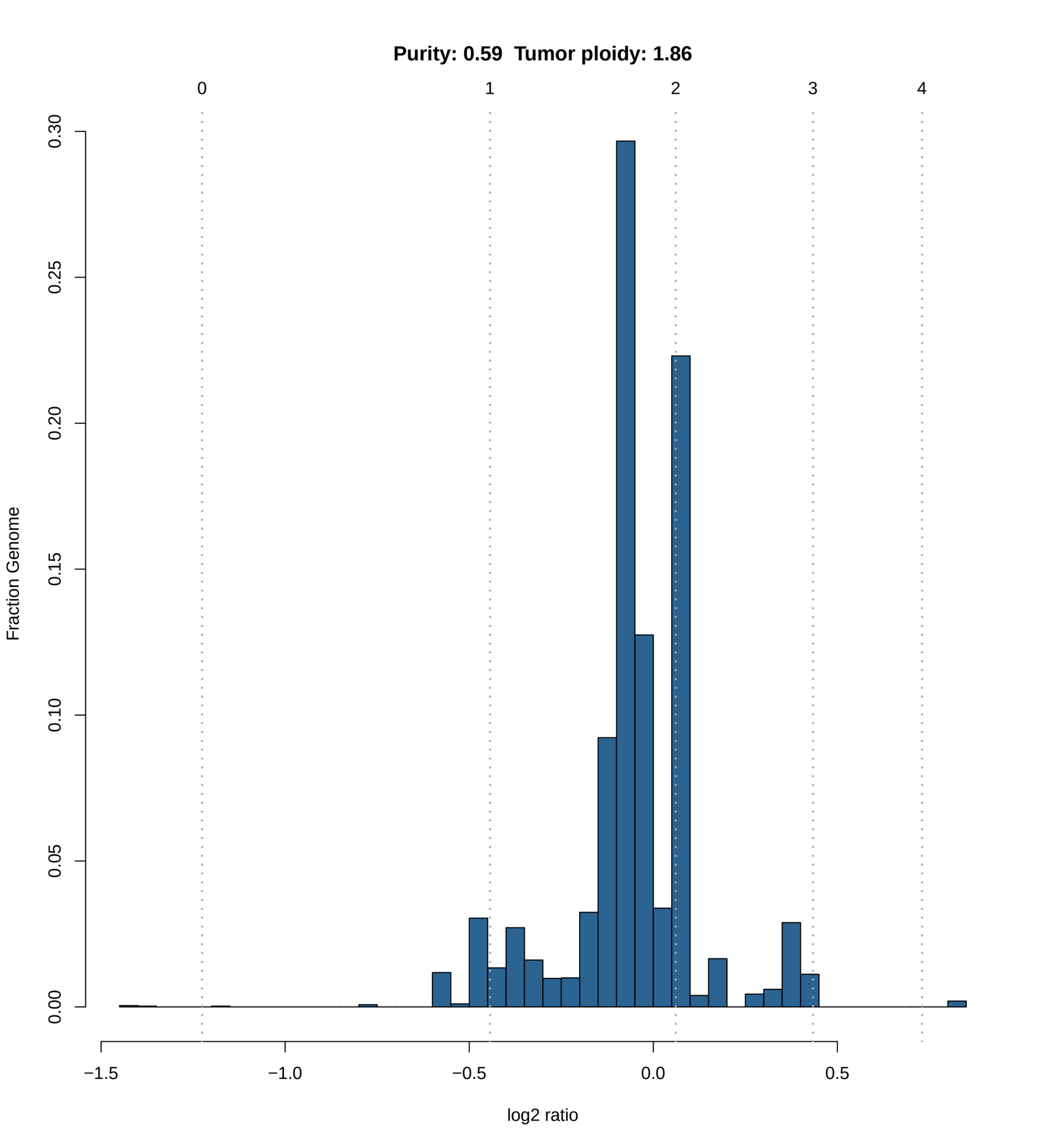

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

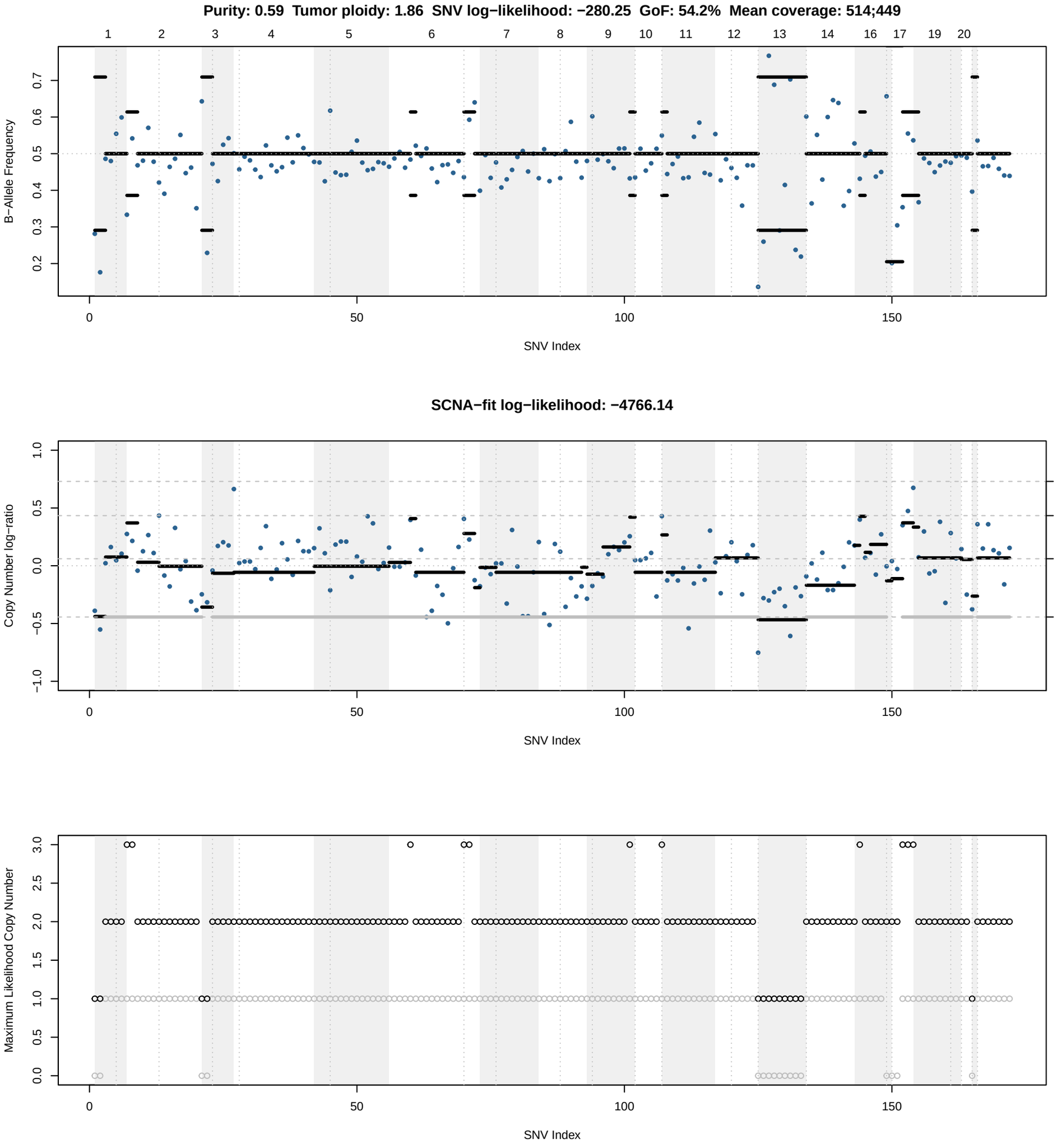

Allelic fraction (germline)
Copy Number log−ratio
1m1
3m2
2m1
3m1
1m0
2m0

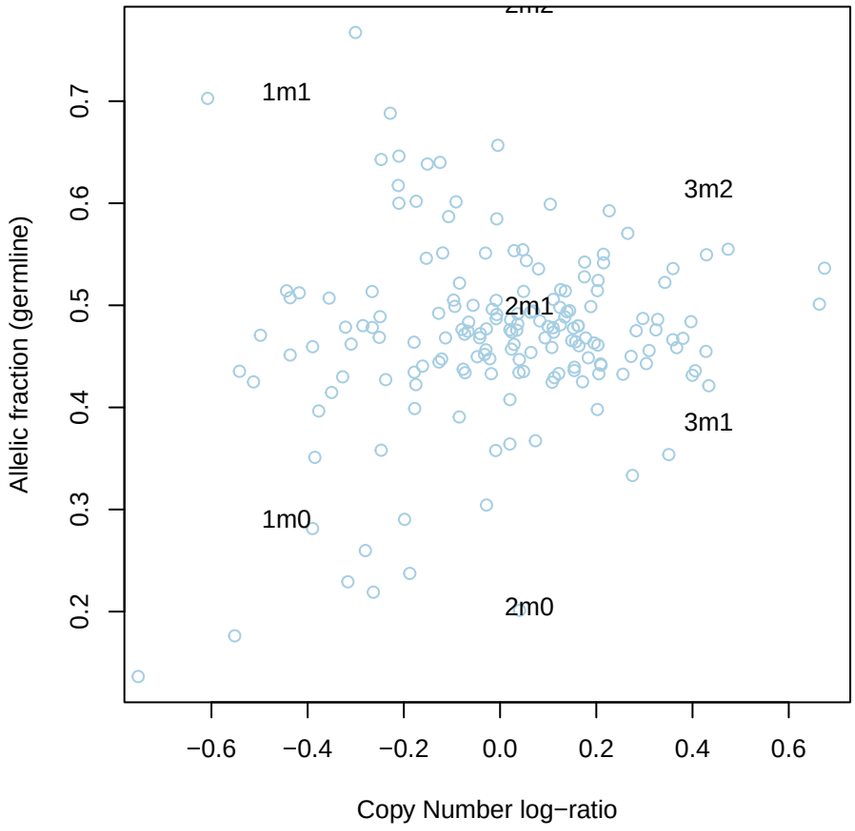

Coverage (log2)
Allelic fraction

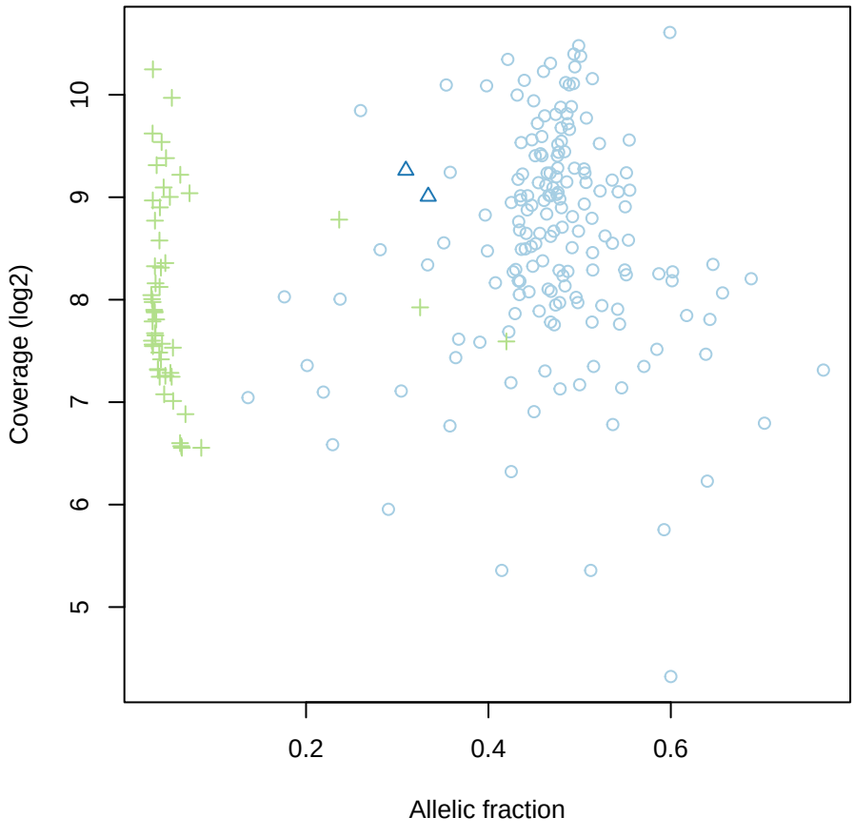

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1
3m1

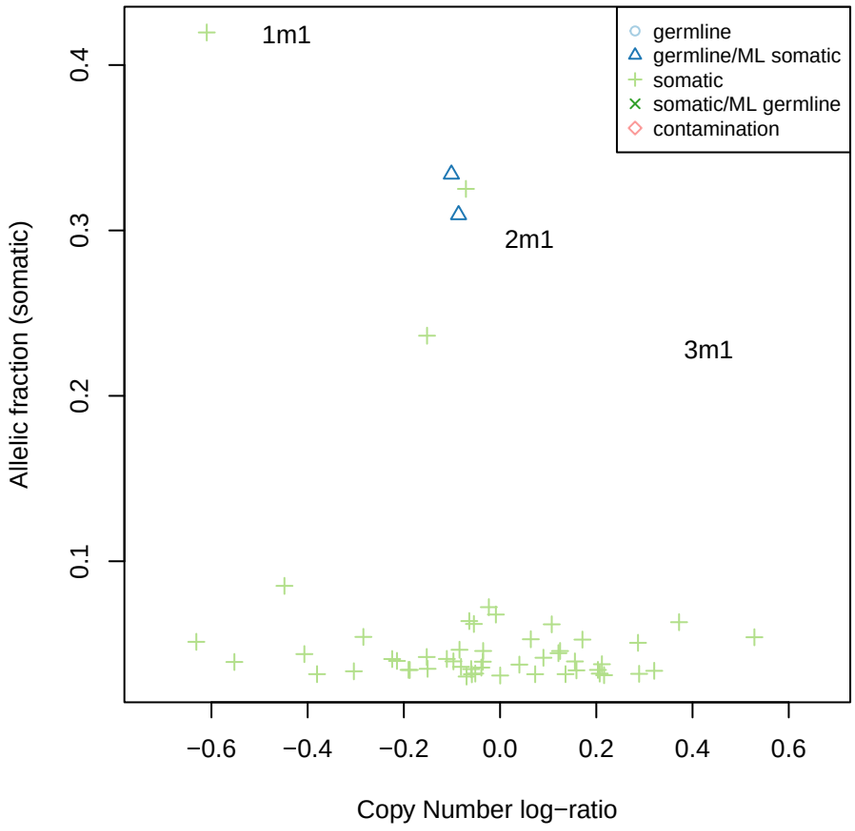

Frequency
Cellular fraction

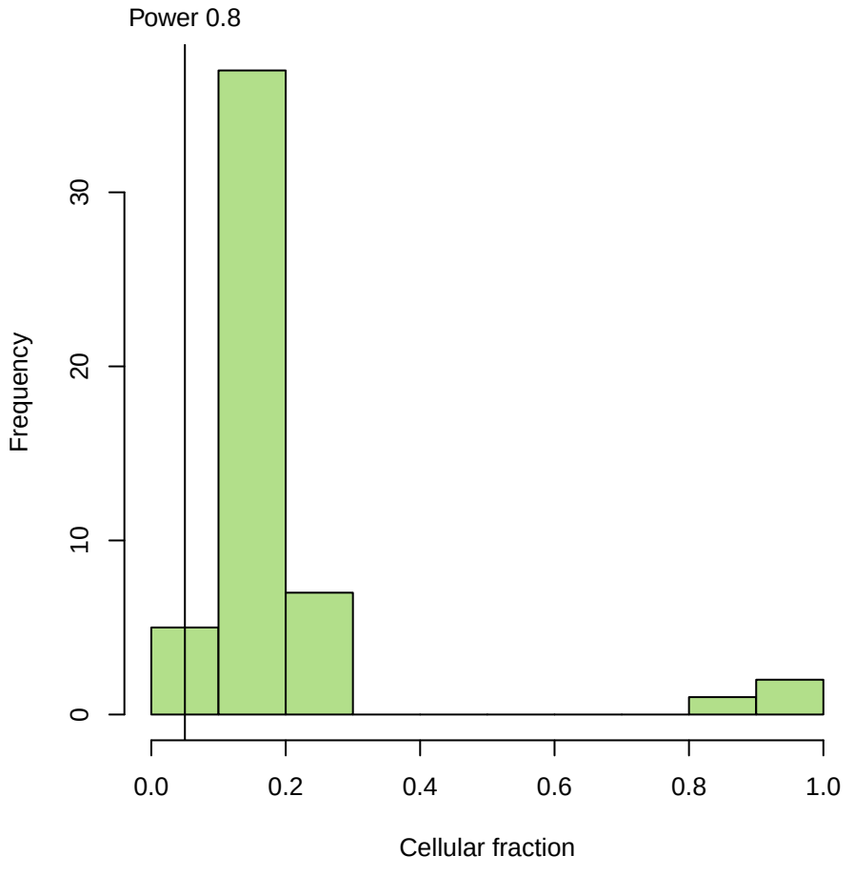

Purity: 0.59 Tumor ploidy: 1.86
0
1
2
3
4
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

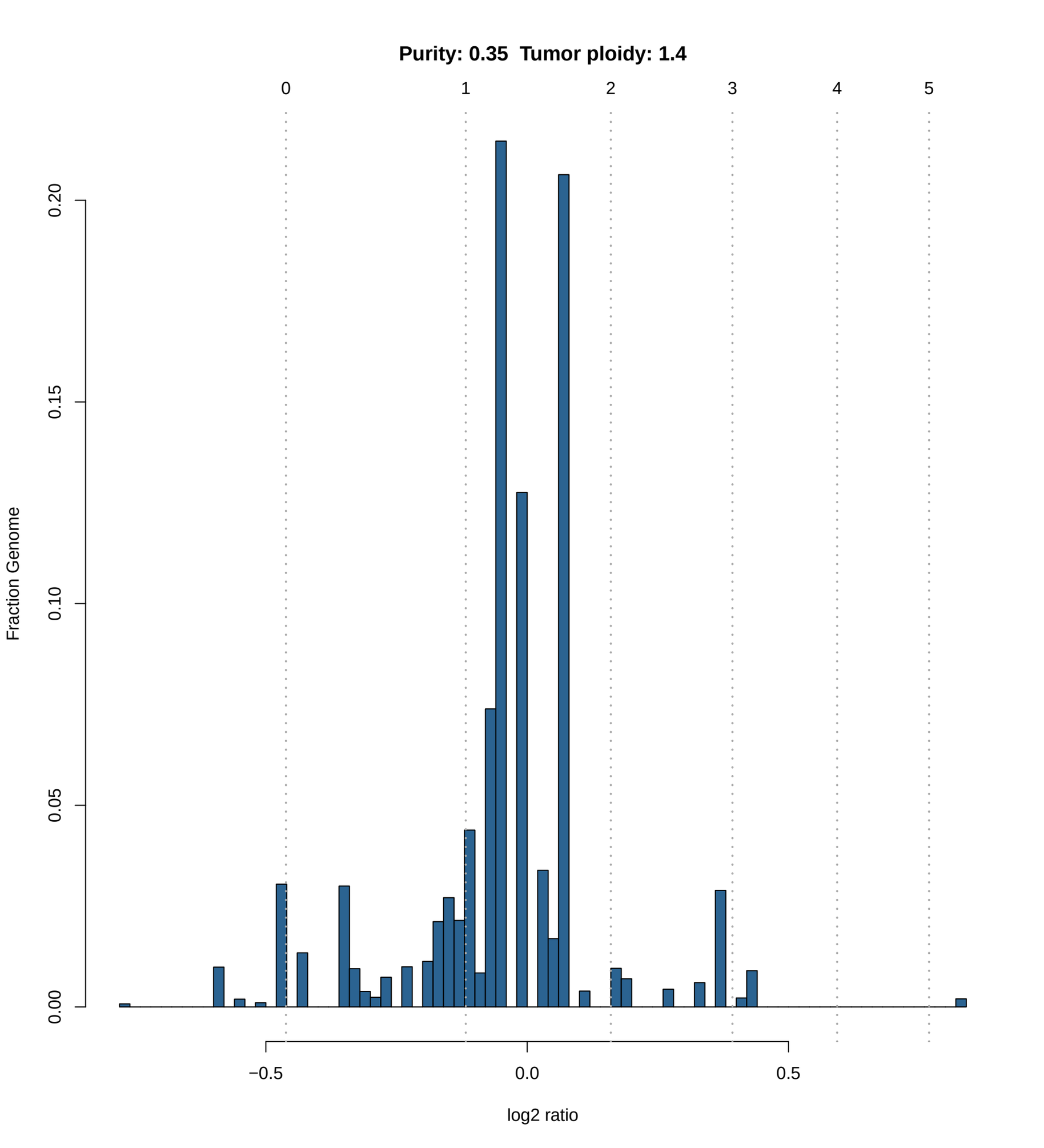

Purity: 0.59 Tumor ploidy: 1.86 SNV log−likelihood: −280.25 GoF: 54.2% Mean coverage: 514;449
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index
SCNA−fit log−likelihood: −4766.14
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4
0 50 100 150
SNV Index
Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

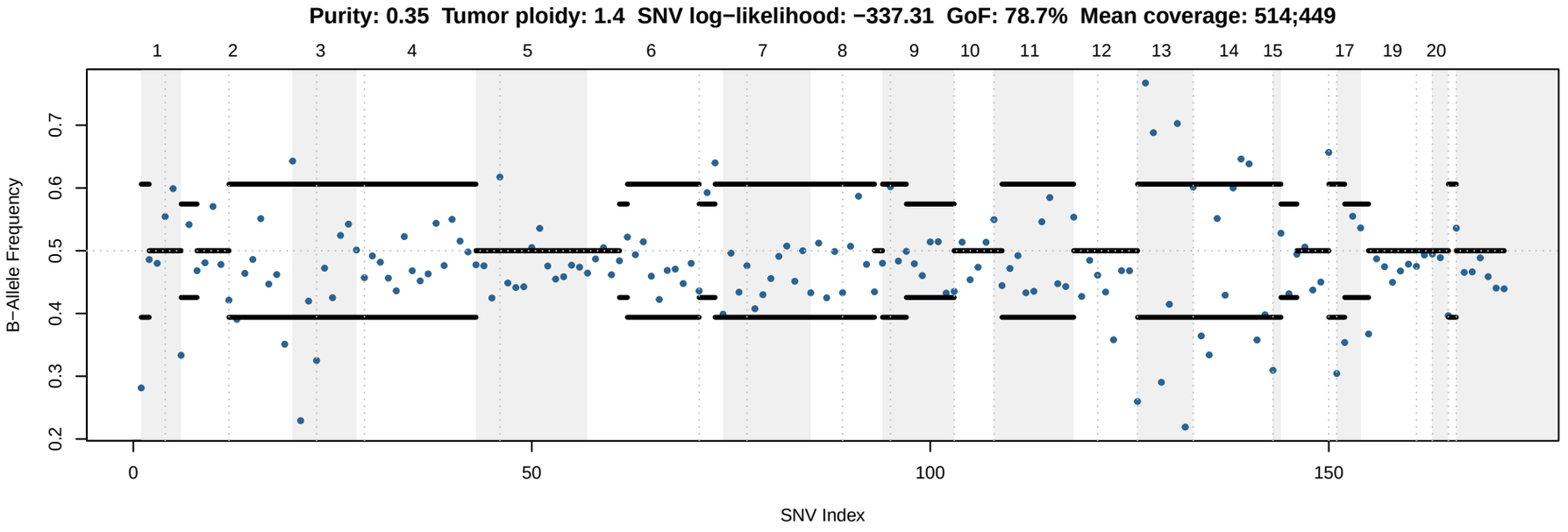

1m1
3m2
2m1
3m1
1m0
2m0
Allelic fraction (germline)
Copy Number log−ratio

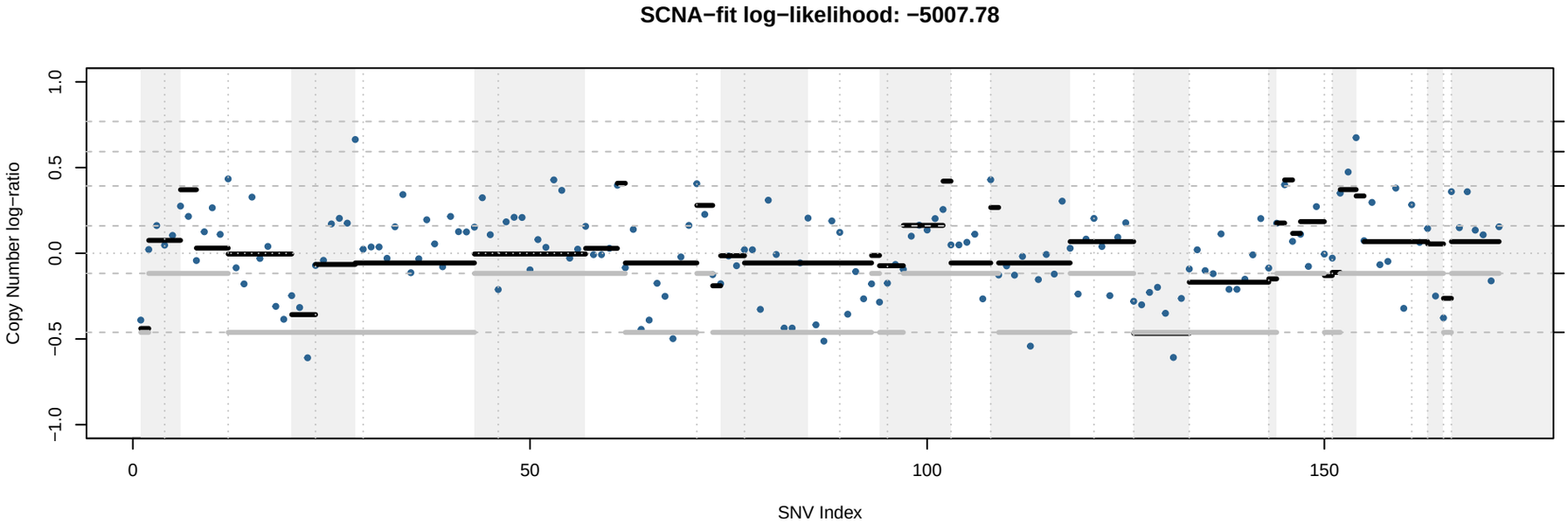

Coverage (log2)
Allelic fraction

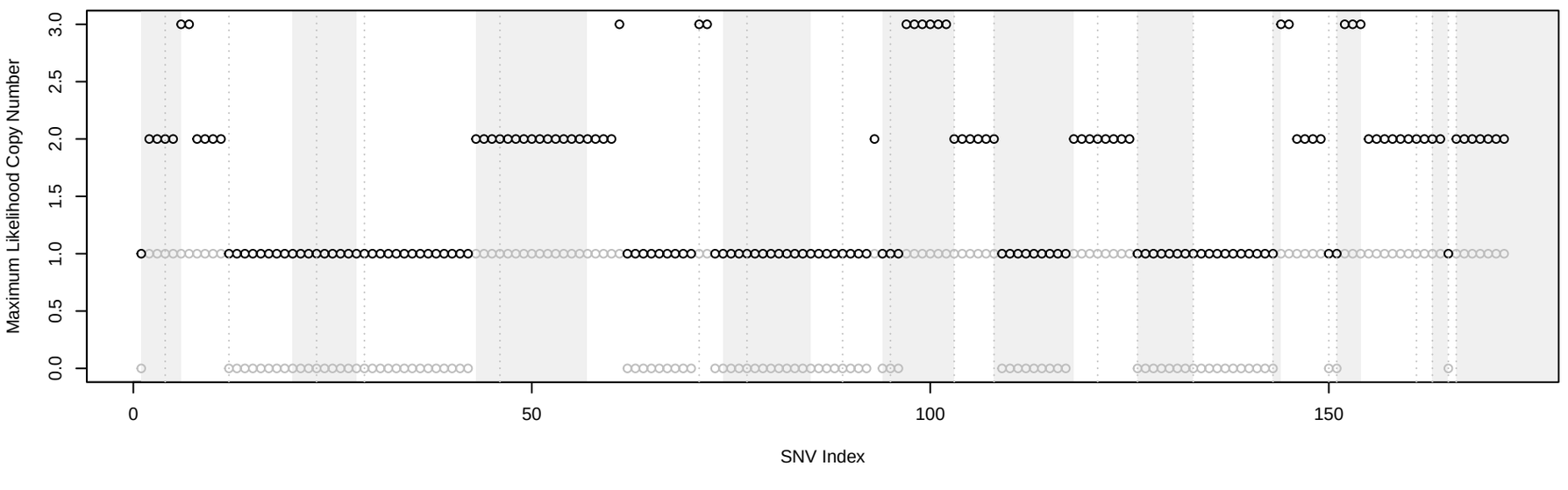

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
Allelic fraction (somatic)
Copy Number log−ratio

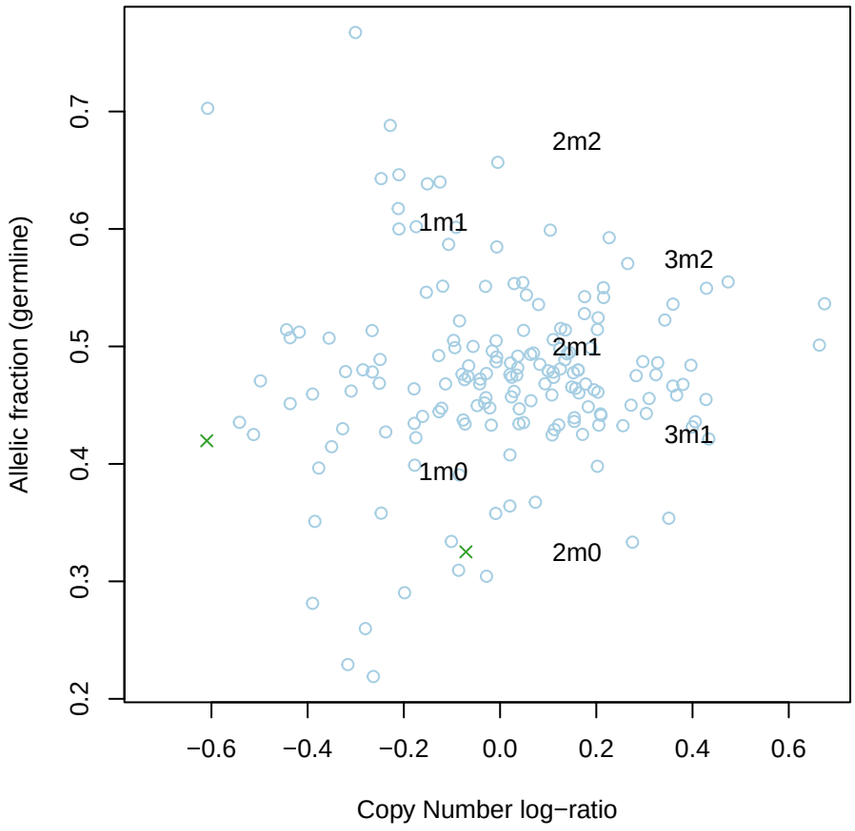

Power 0.8
Frequency
Cellular fraction

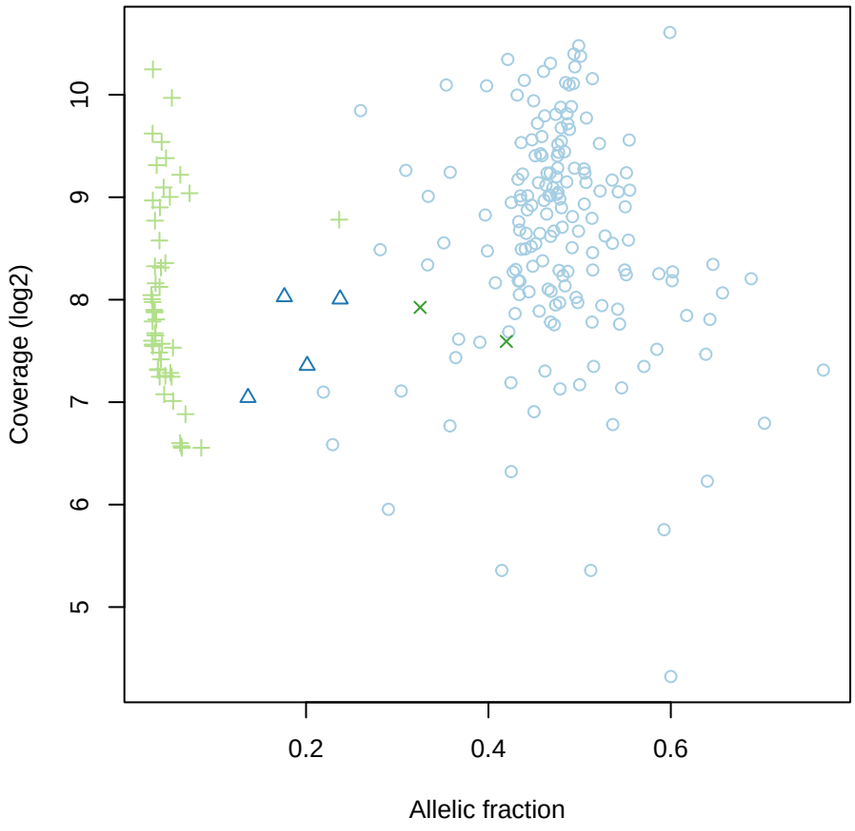

Purity: 0.35 Tumor ploidy: 1.4
0
1
2
3
4
5
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.5
0.0
0.5
log2 ratio

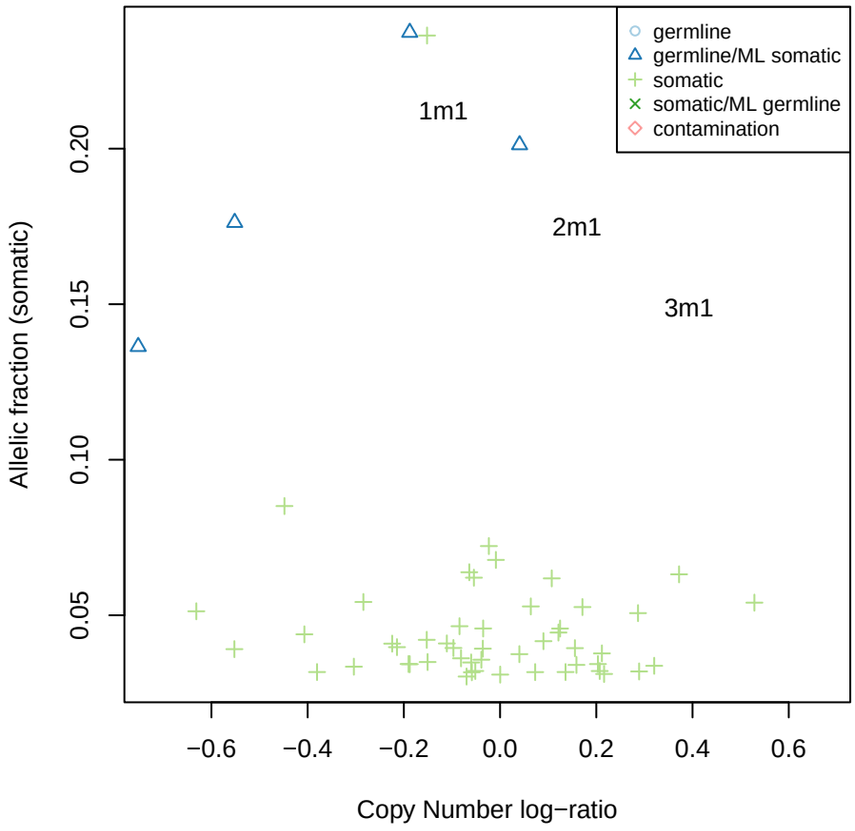

Purity: 0.35 Tumor ploidy: 1.4 SNV log−likelihood: −337.31 GoF: 78.7% Mean coverage: 514;449
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

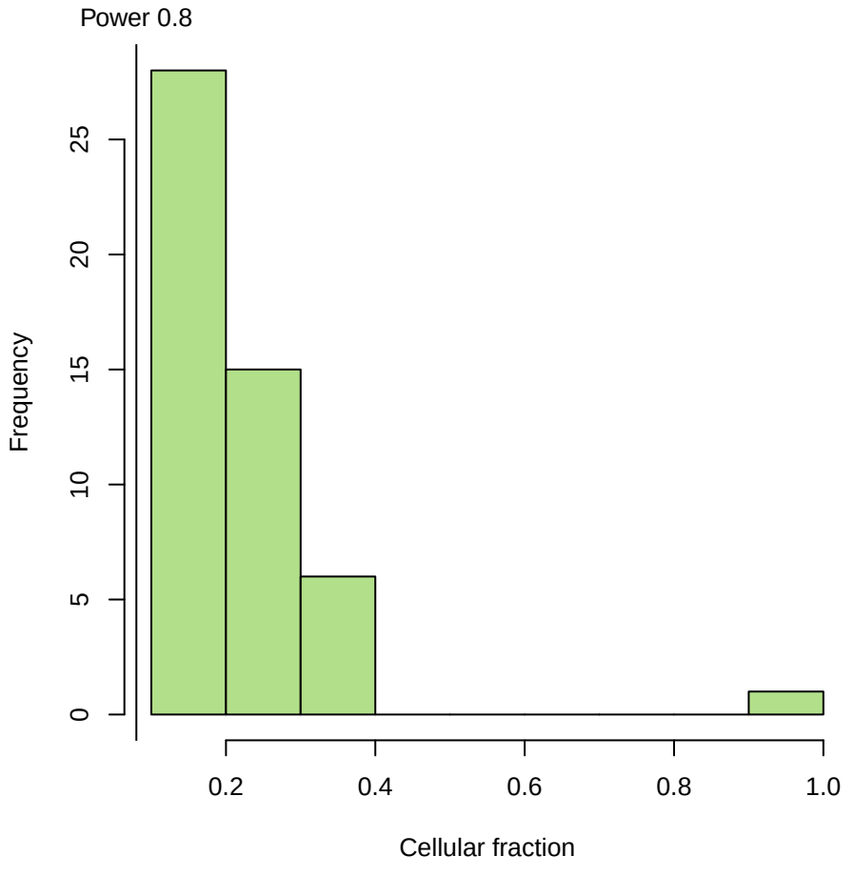

SCNA−fit log−likelihood: −5007.78
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5
0 50 100 150
SNV Index

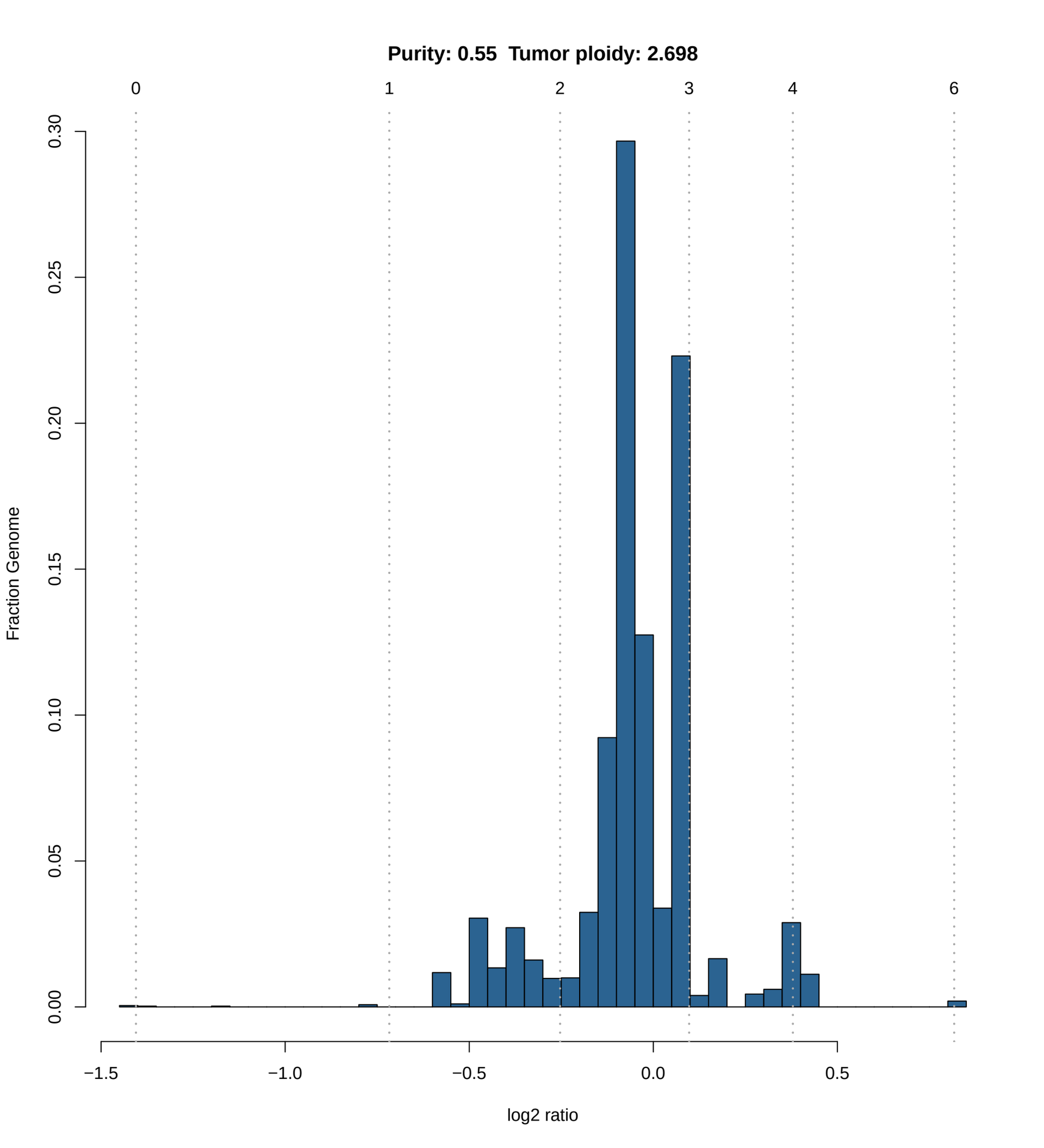

Maximum Likelihood Copy Number
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 50 100 150
SNV Index

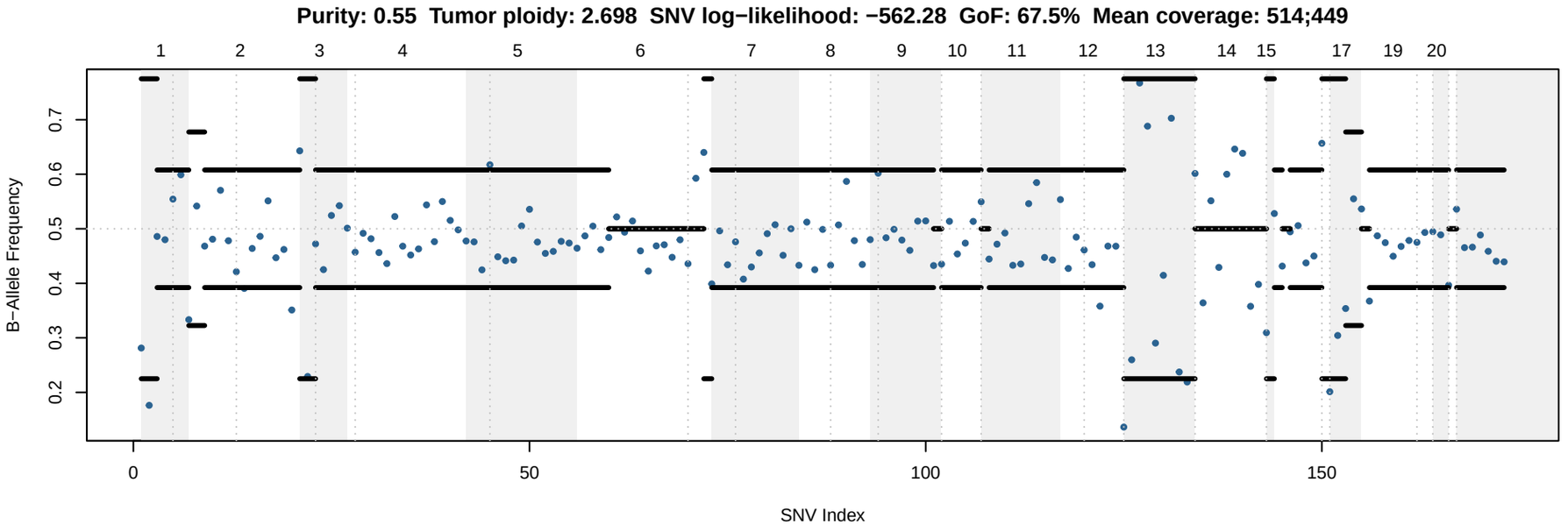

Allelic fraction (germline)
Copy Number log−ratio
2m2
1m1
3m2
2m1
3m1
1m0
2m0

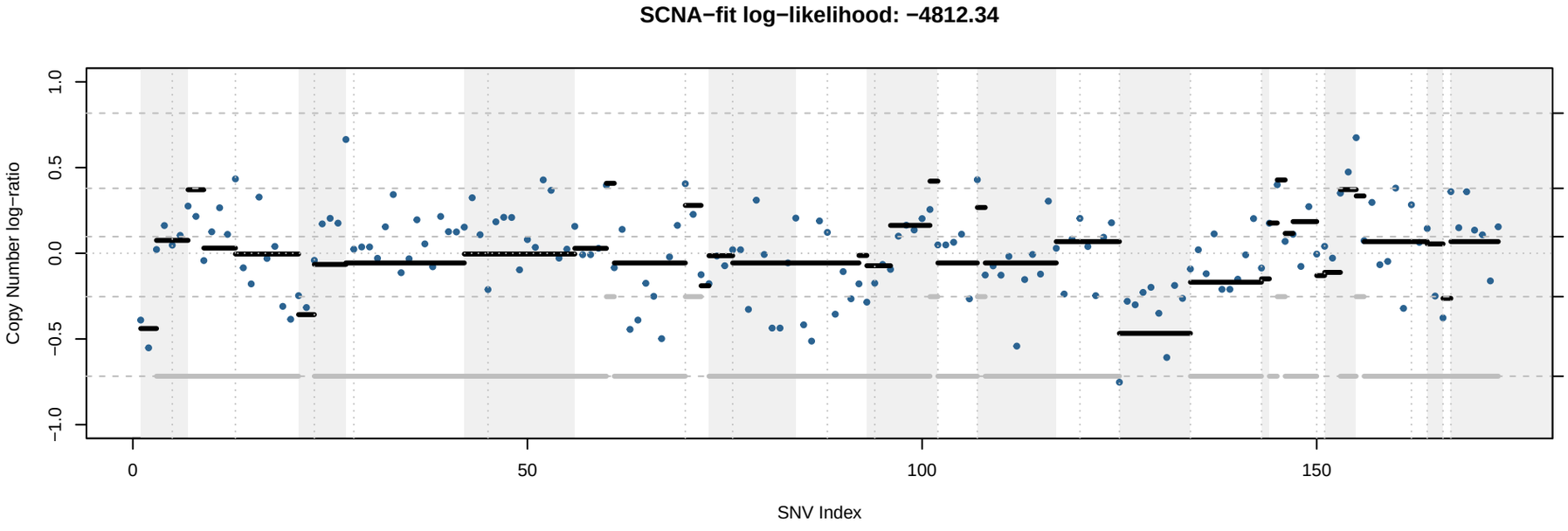

Coverage (log2)
Allelic fraction

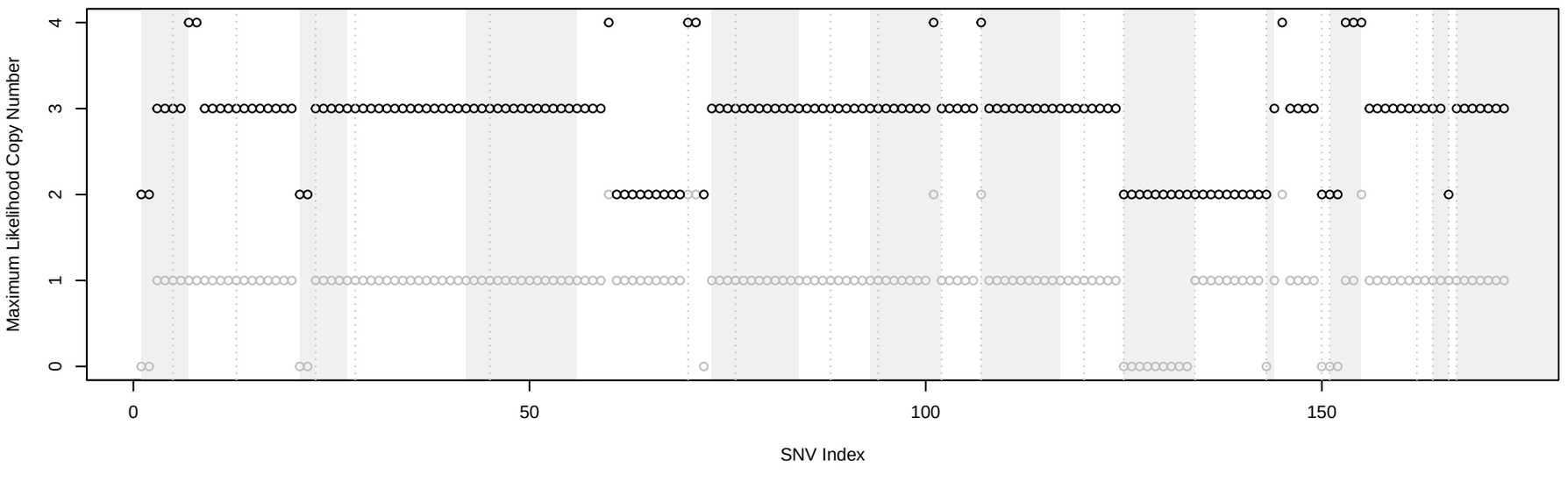

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
1m1
2m1
3m1

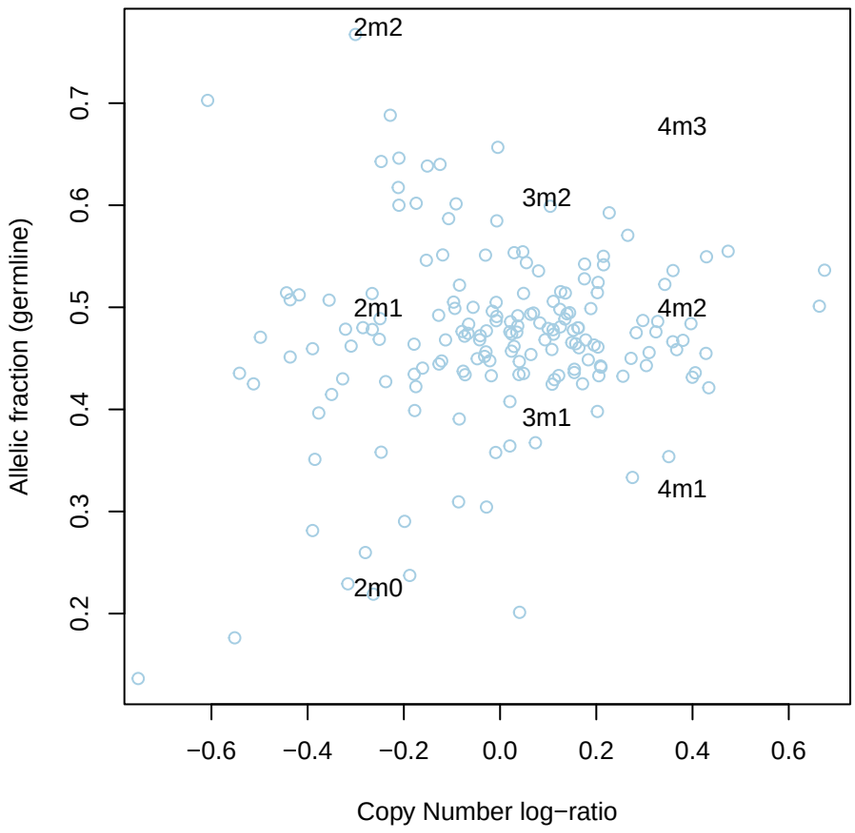

Power 0.8
Frequency
Cellular fraction

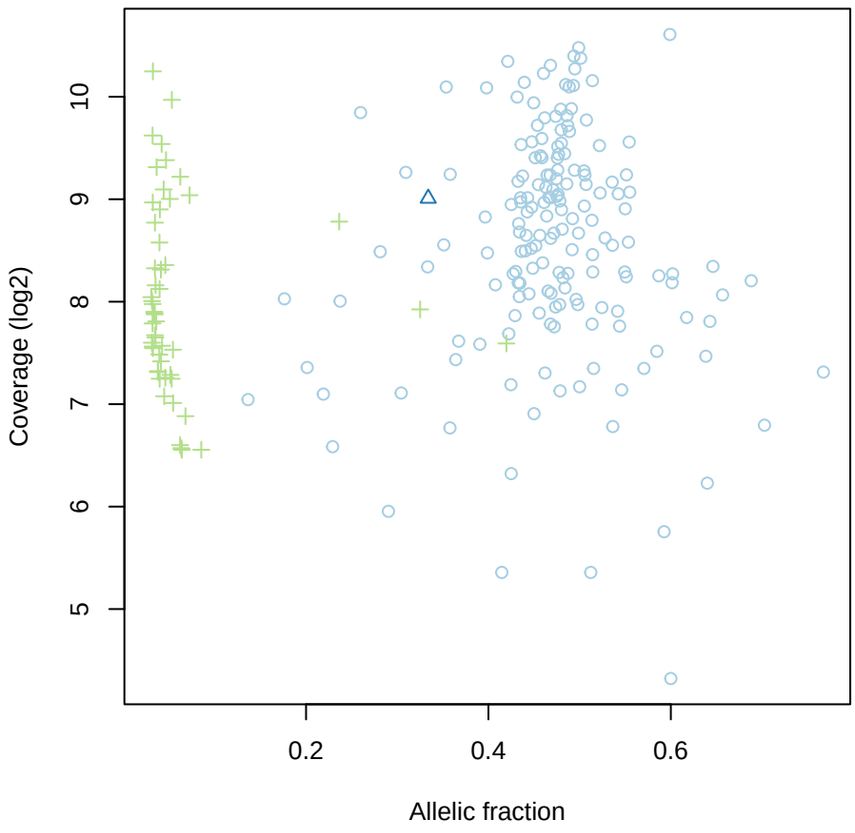

Purity: 0.55 Tumor ploidy: 2.698
0
1
2
3
4
6
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−1.5
−1.0
−0.5
0.0
0.5
log2 ratio

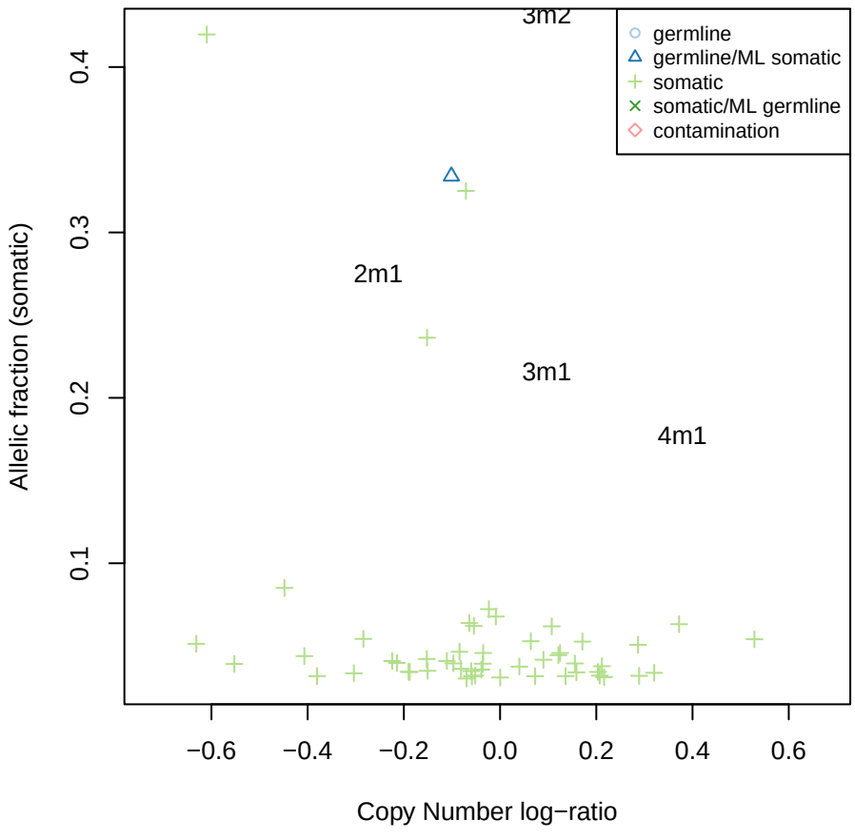

Purity: 0.55 Tumor ploidy: 2.698 SNV log−likelihood: −562.28 GoF: 67.5% Mean coverage: 514;449
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 19 20
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index

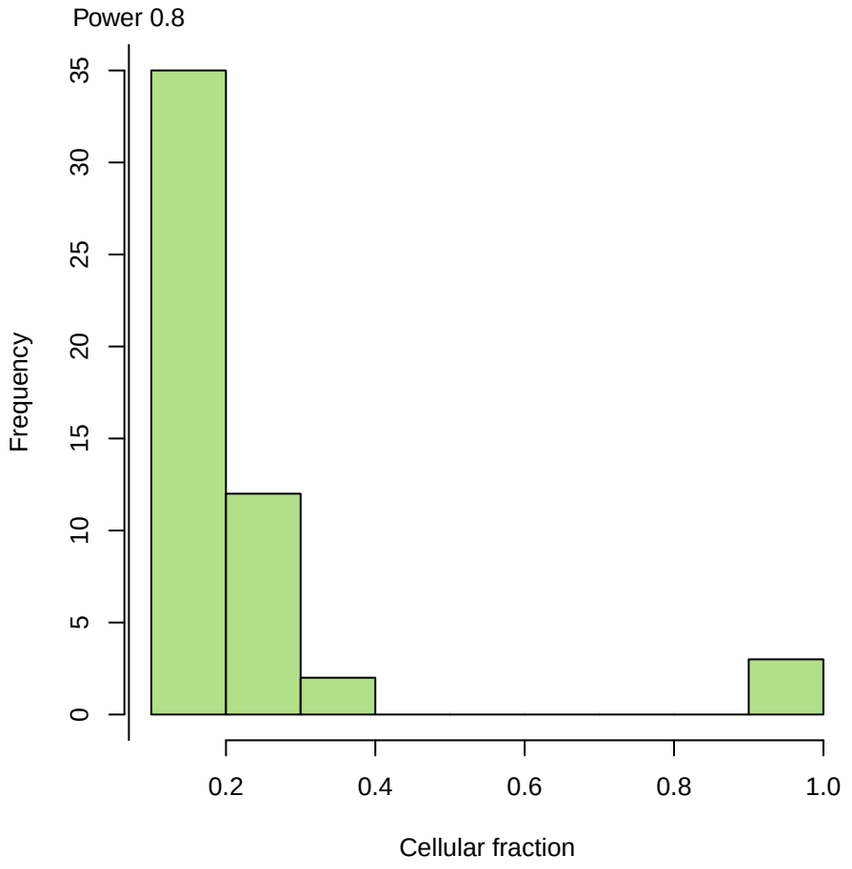

SCNA−fit log−likelihood: −4812.34
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 6
0 50 100 150
SNV Index

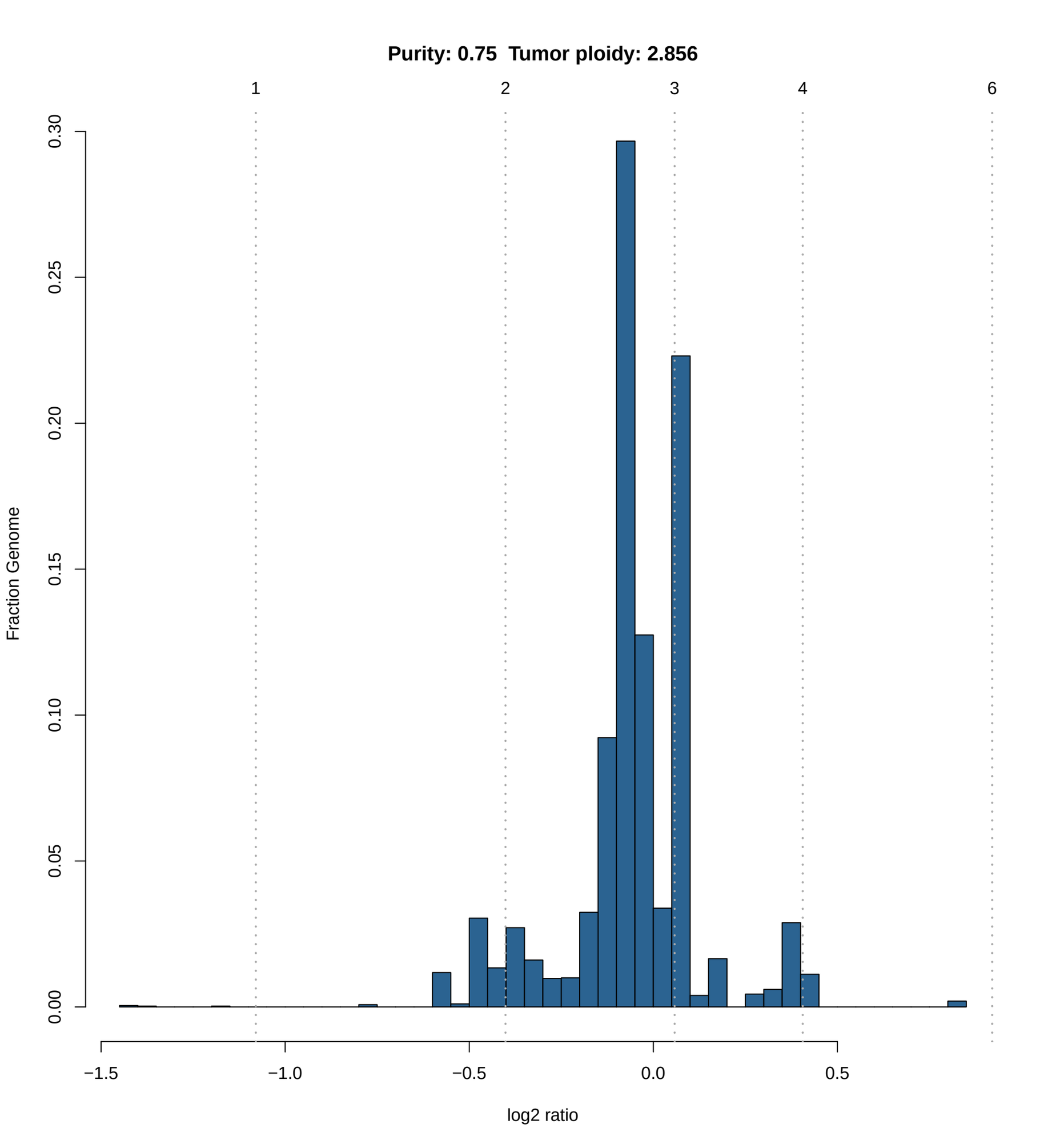

Maximum Likelihood Copy Number
0 1 2 3 4
0 50 100 150
SNV Index

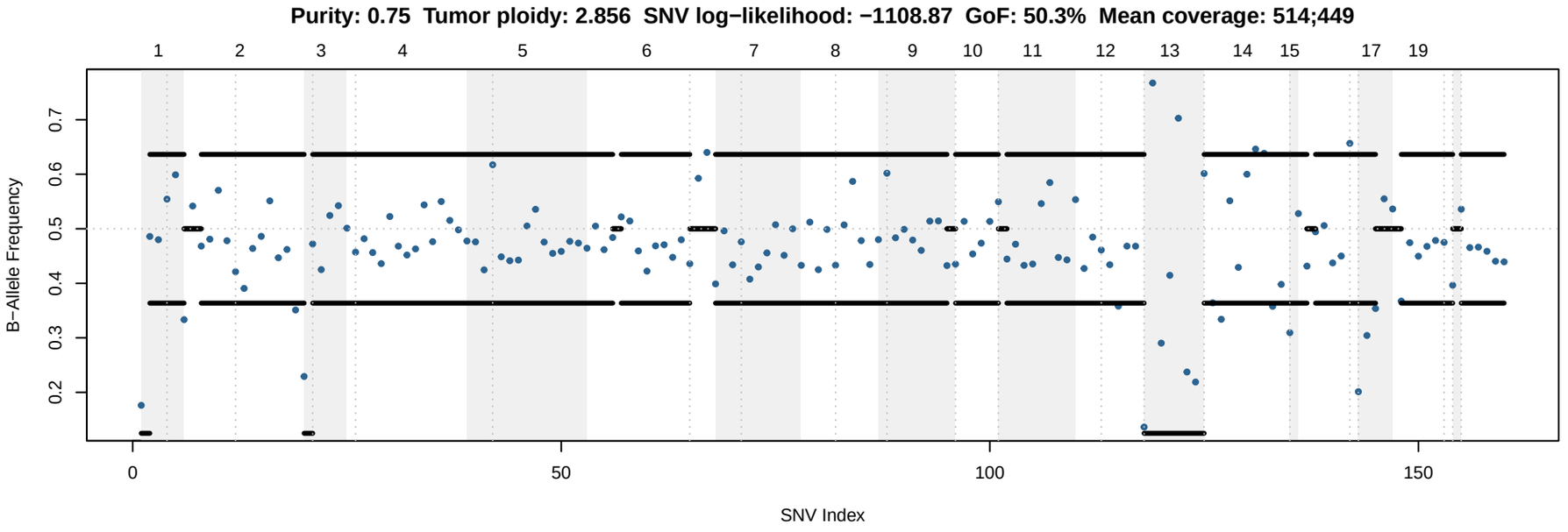

2m2
4m3
3m2
2m1
4m2
3m1
4m1
2m0
Allelic fraction (germline)
Copy Number log−ratio

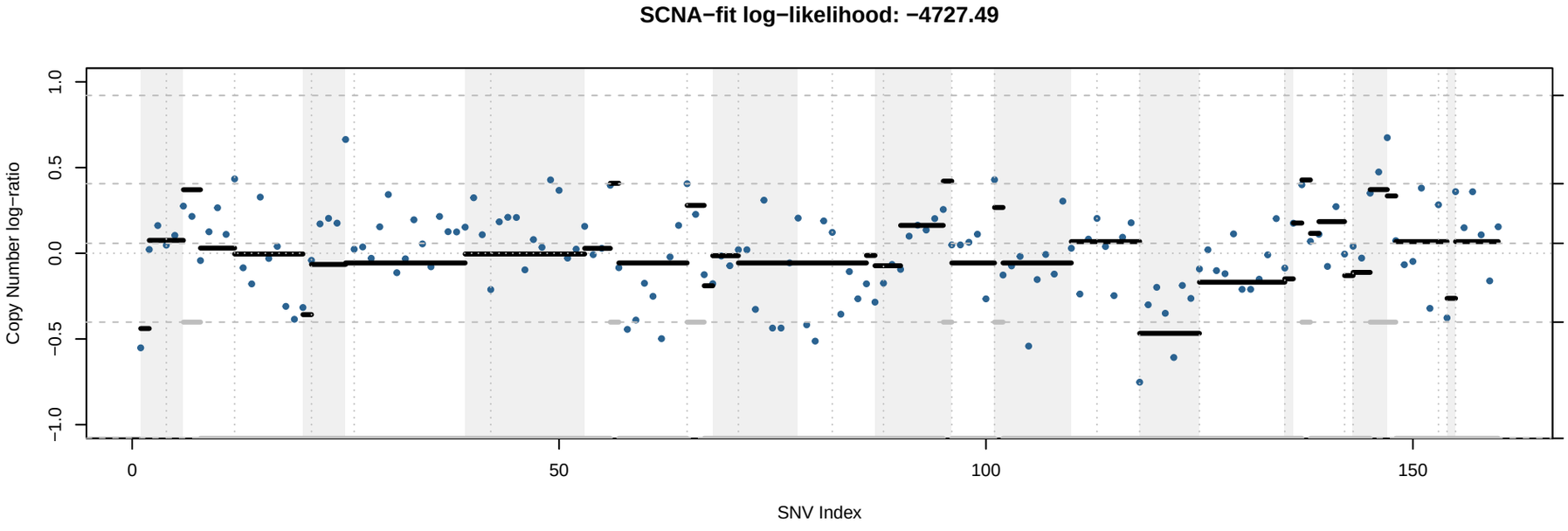

Coverage (log2)
Allelic fraction


germline
germline/ML somatic
somatic
somatic/ML germline
contamination
3m2
2m1
3m1
4m1
Allelic fraction (somatic)
Copy Number log−ratio


Power 0.8
Frequency
Cellular fraction


Purity: 0.75 Tumor ploidy: 2.856
1
2
3
4
6
0.30
0.25
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: 0.75 Tumor ploidy: 2.856 SNV log−likelihood: −1108.87 GoF: 50.3% Mean coverage: 514;449
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 19
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 50 100 150
SNV Index


SCNA−fit log−likelihood: −4727.49
Copy Number log−ratio
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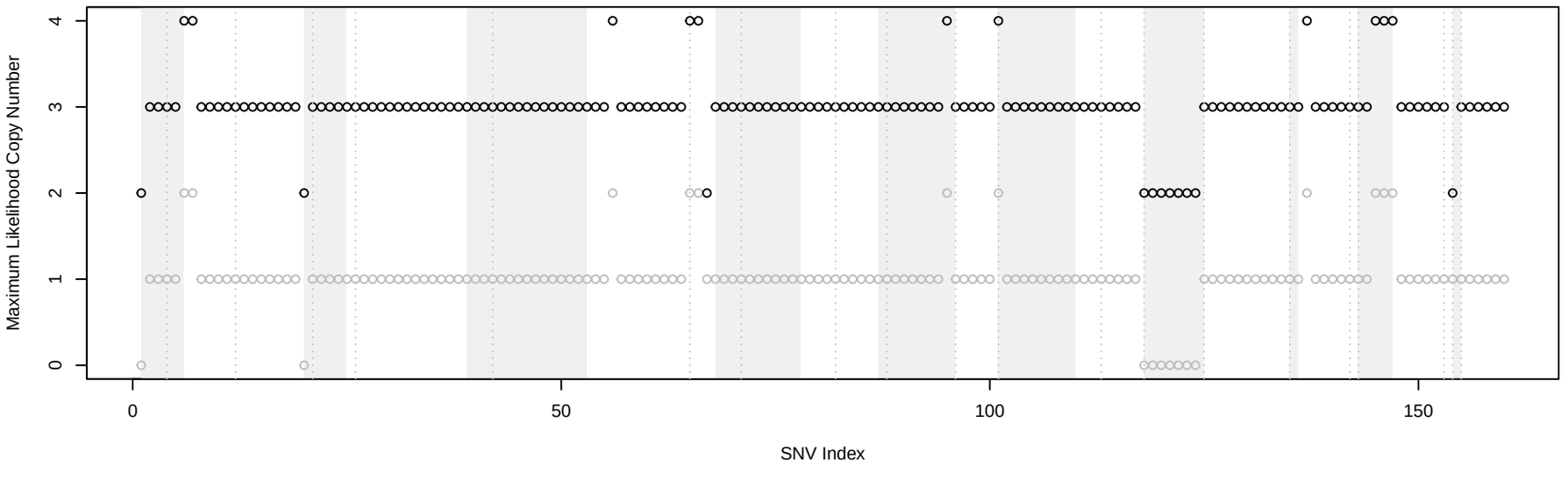
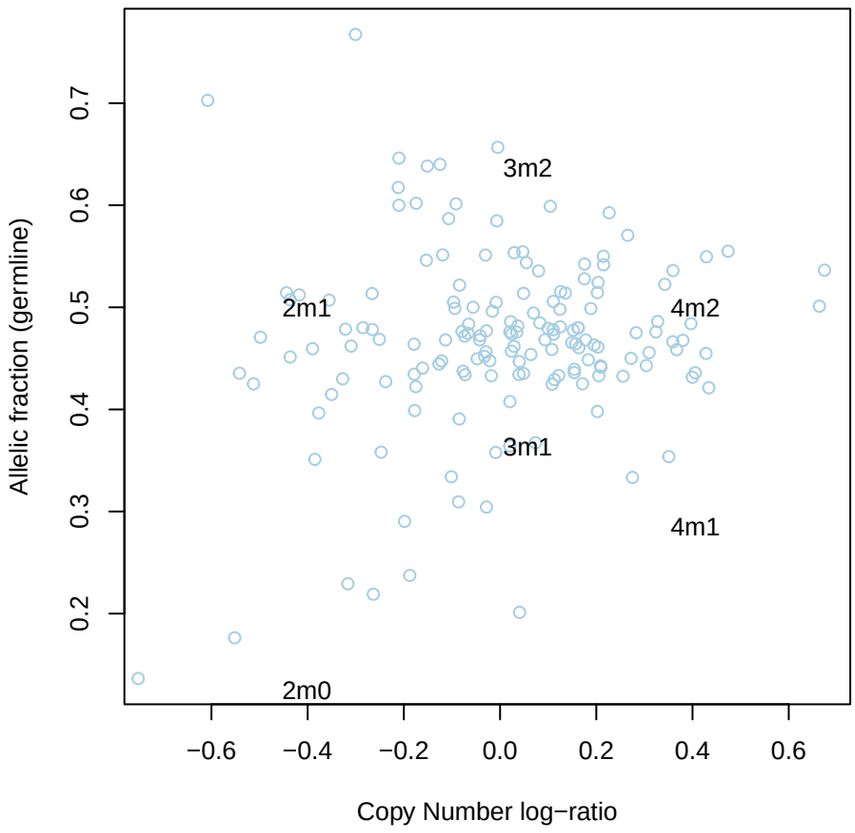
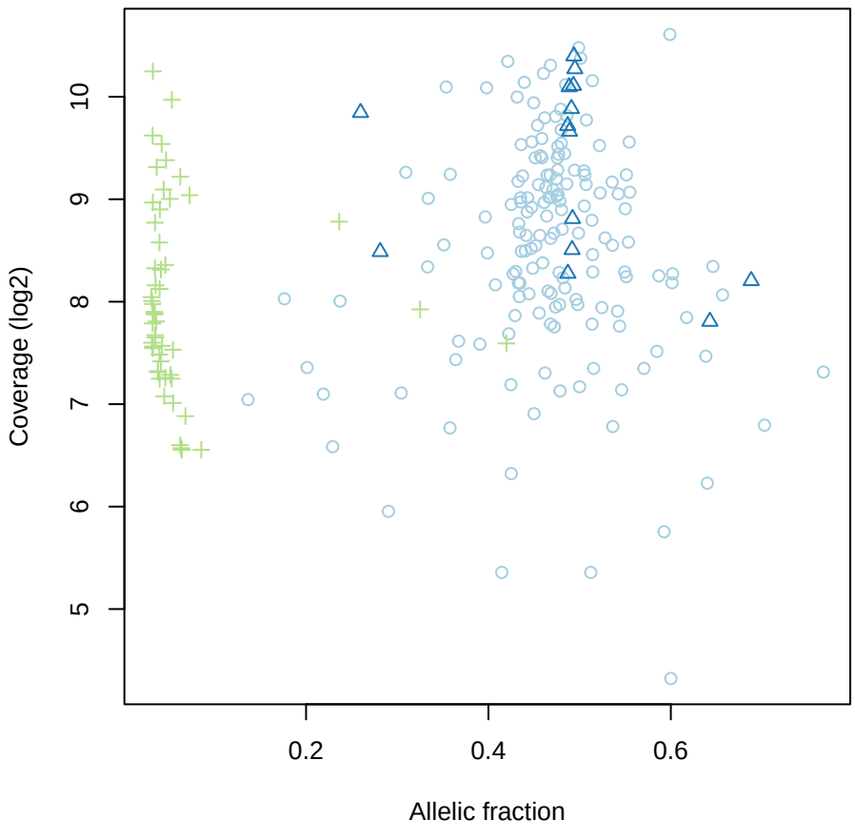
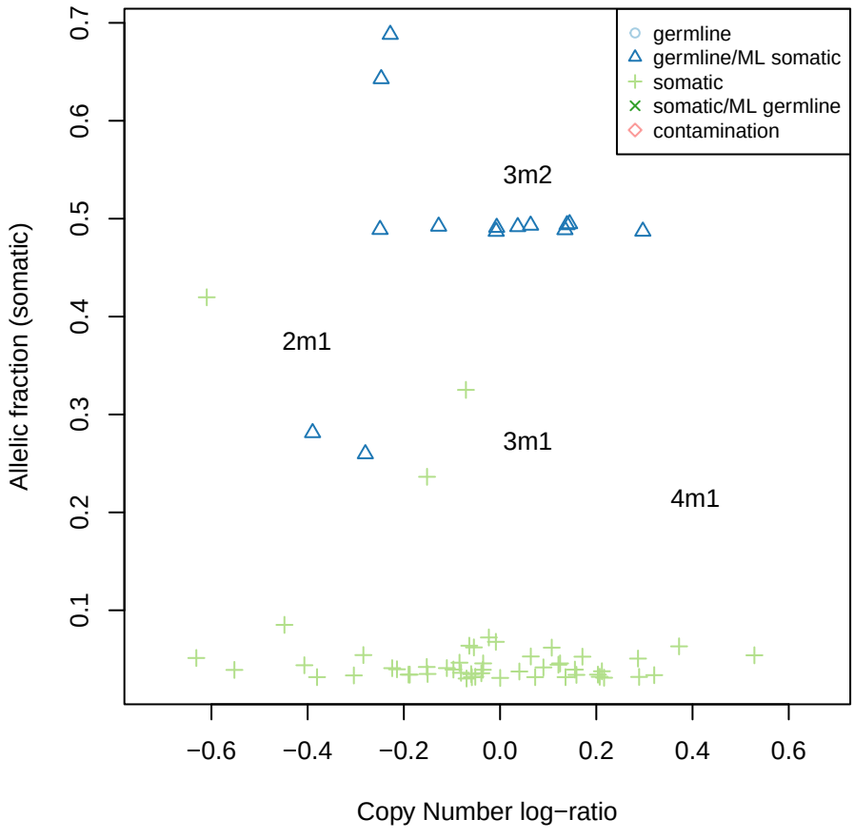
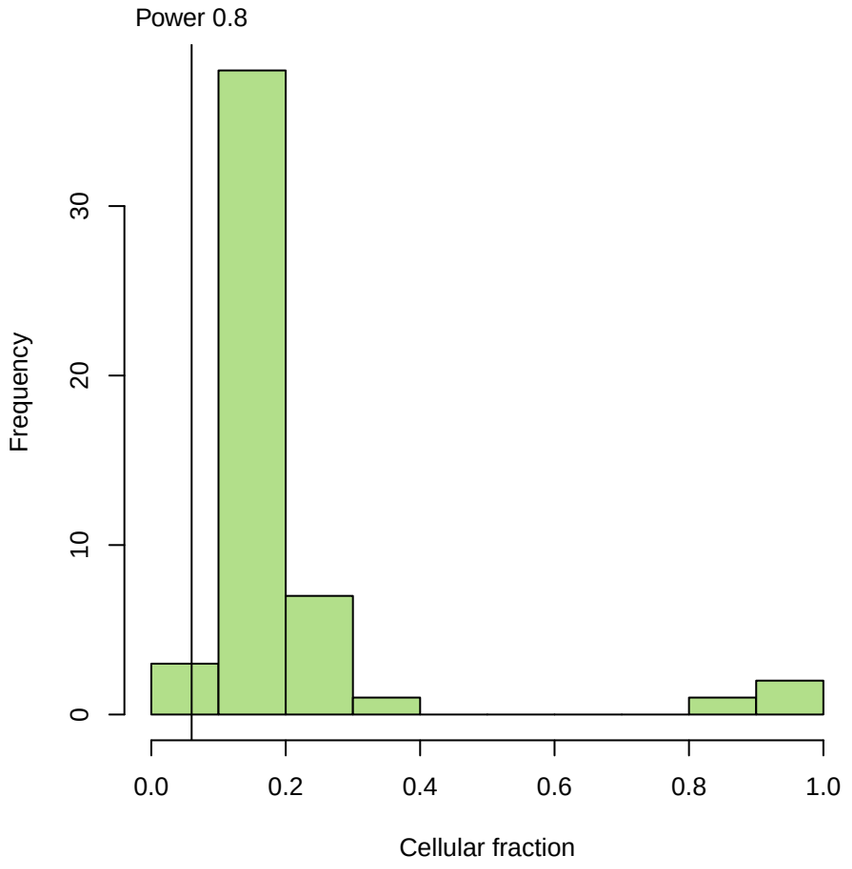
1 2 3 4 6
0 50 100 150
SNV Index


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


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


Coverage (log2)
Allelic fraction


Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m2
3m1
4m1


Power 0.8
Frequency
Cellular fraction