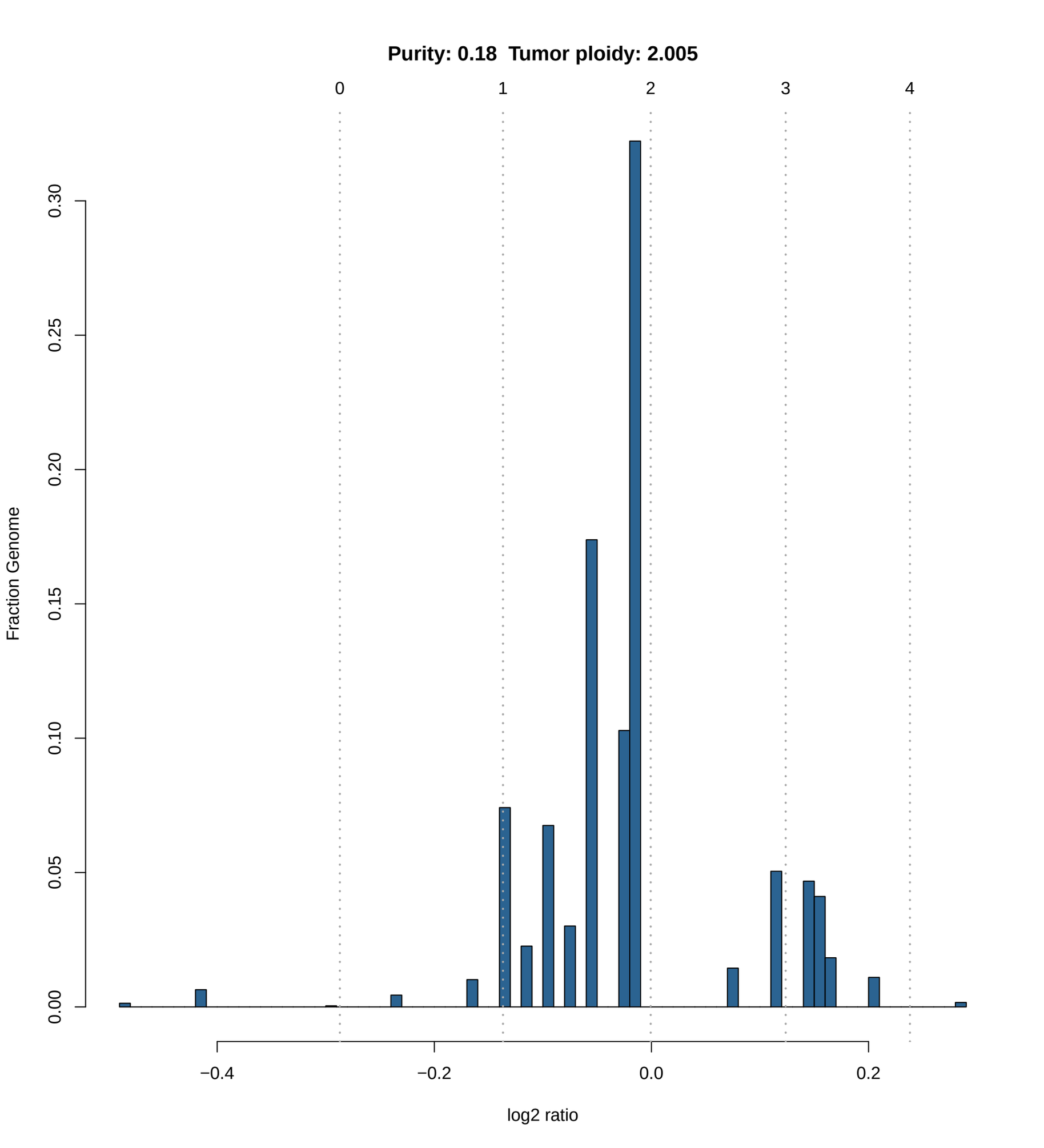
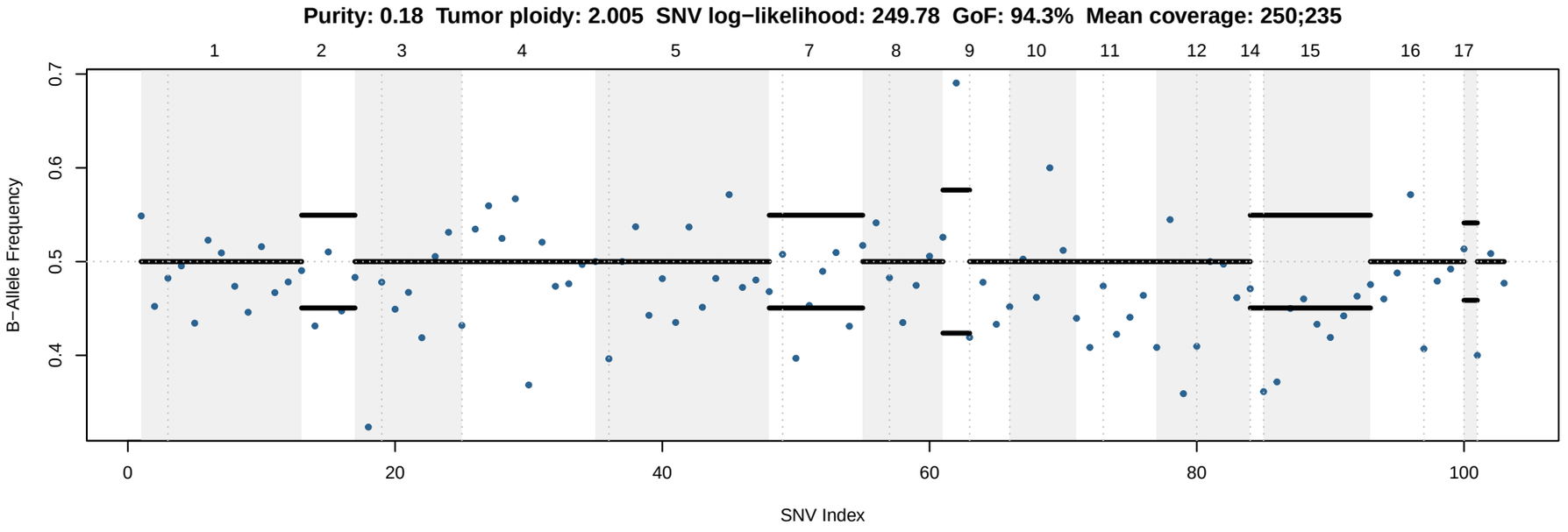
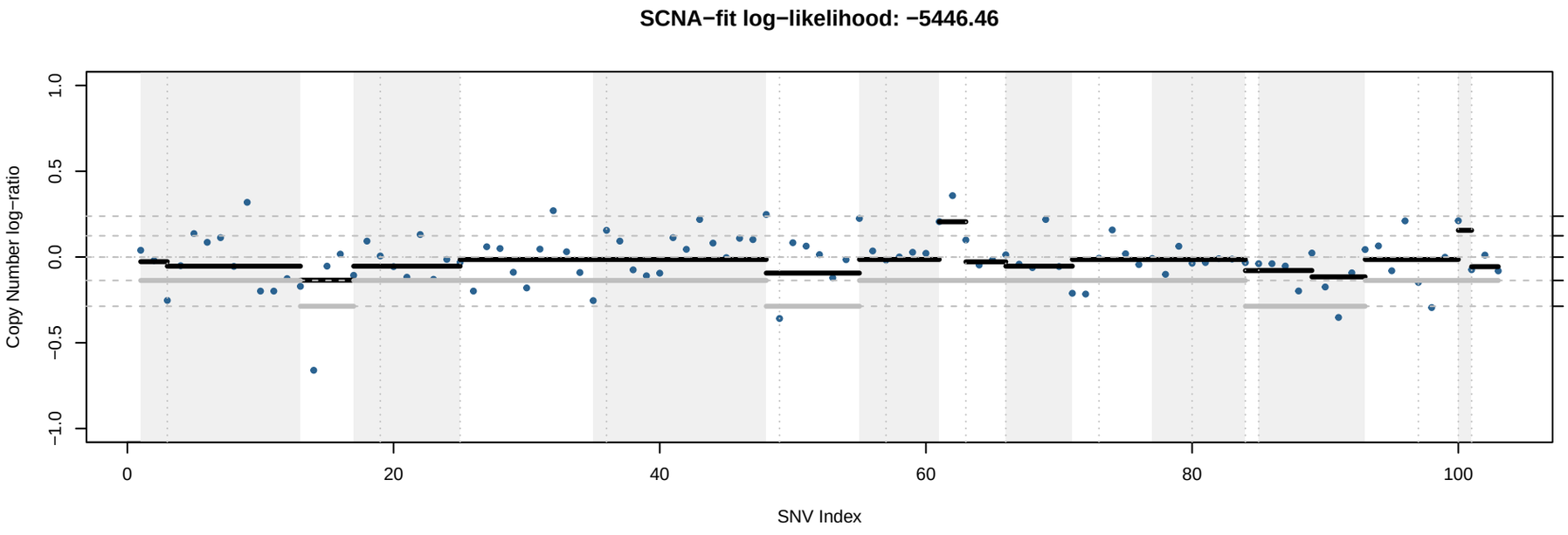
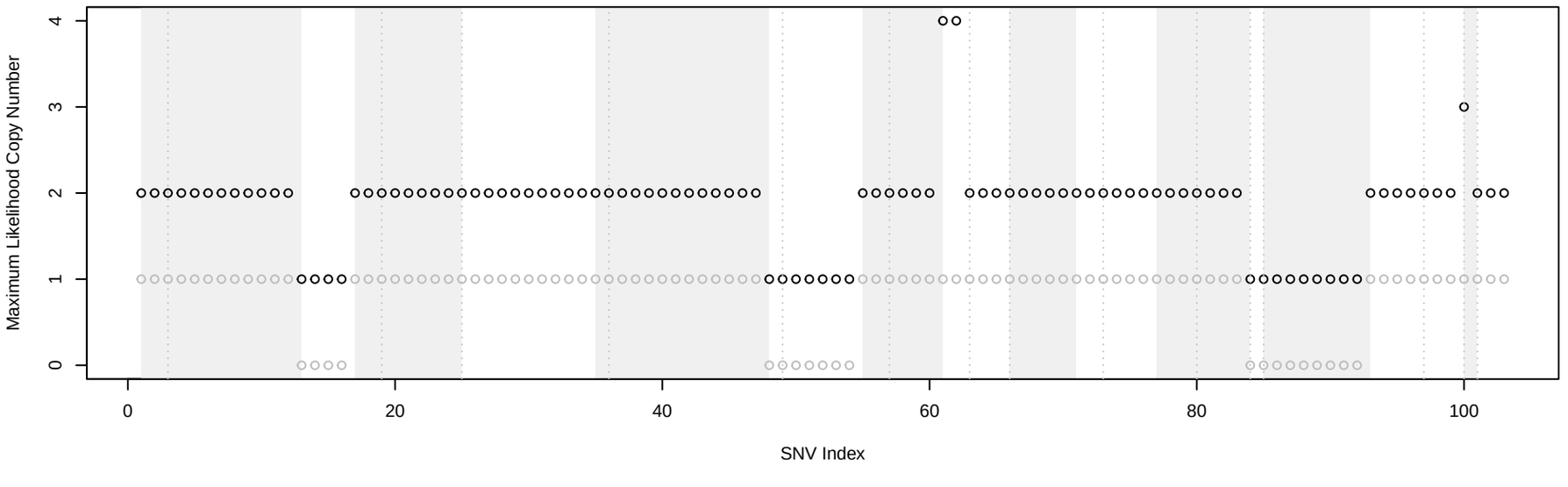
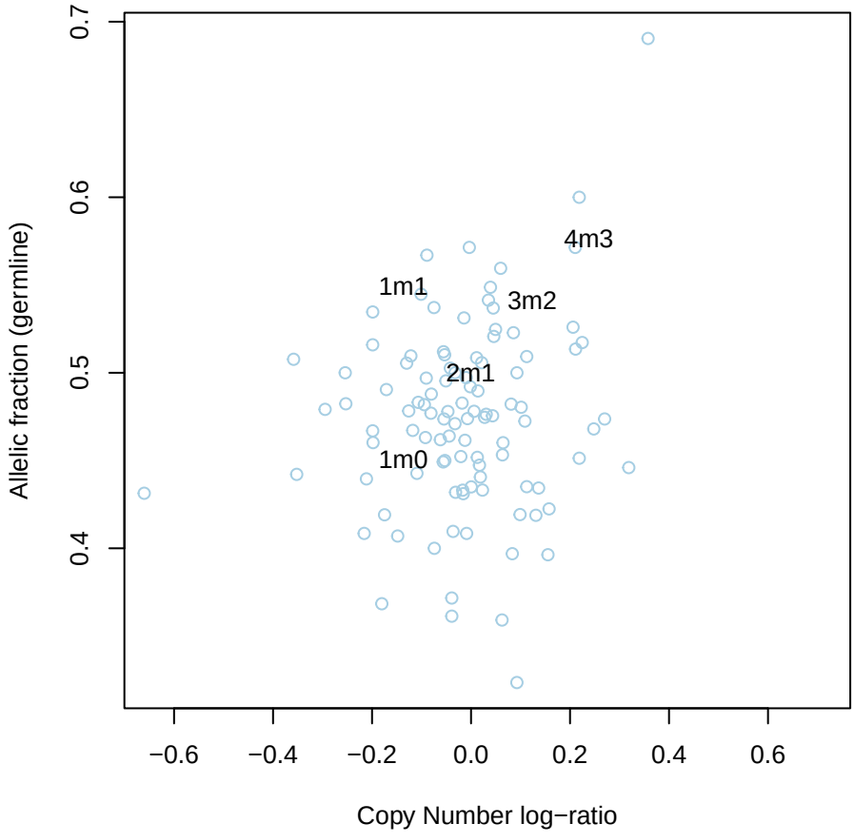
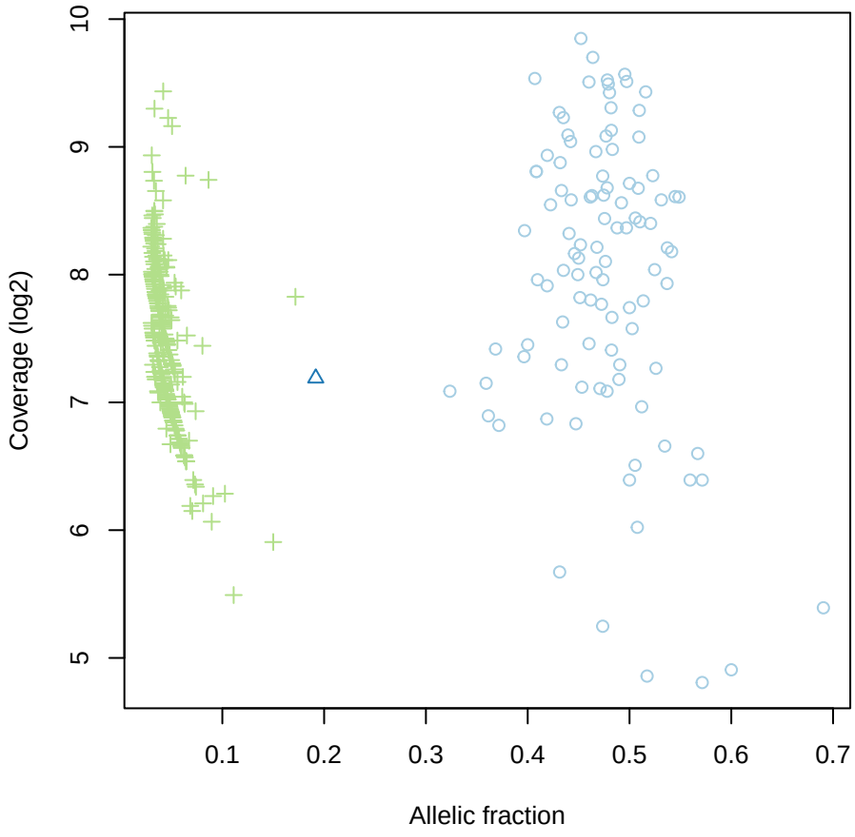

Purity: 0.18 Tumor ploidy: 2.005
0
1
2
3
4
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
log2 ratio

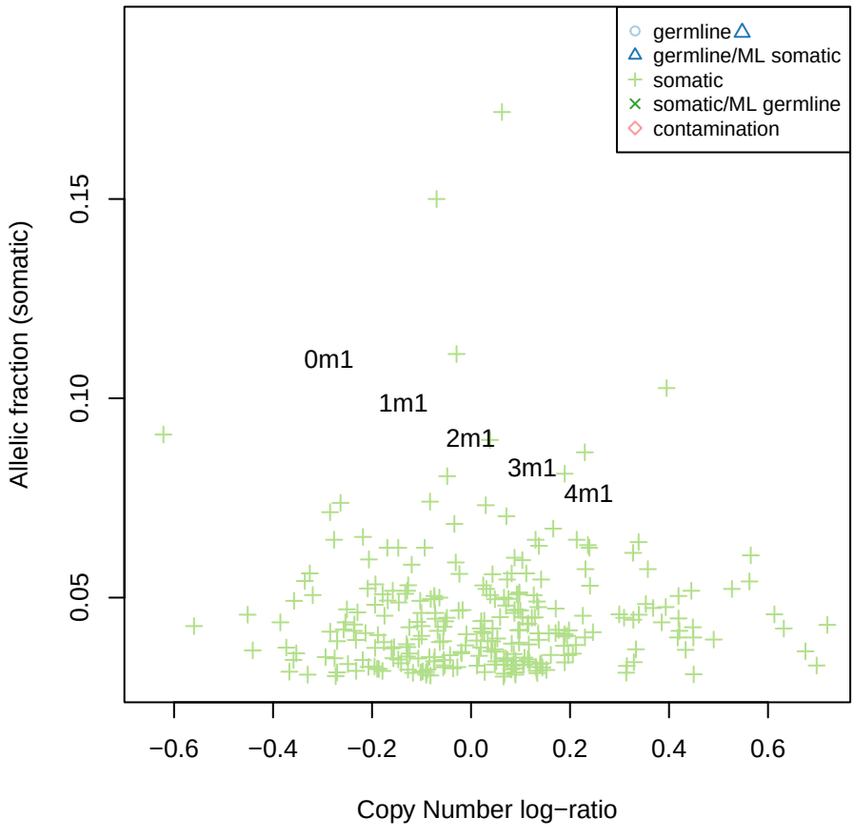

Purity: 0.18 Tumor ploidy: 2.005 SNV log−likelihood: 249.78 GoF: 94.3% Mean coverage: 250;235
1 2 3 4 5 7 8 9 10 11 12 14 15 16 17
B−Allele Frequency
0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

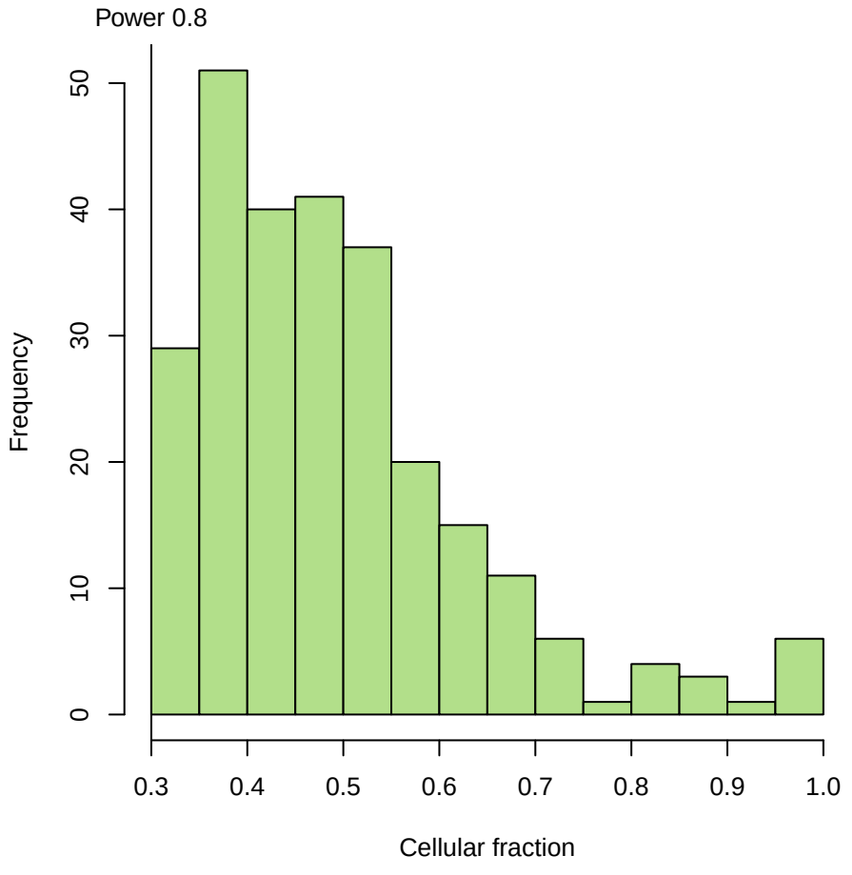

SCNA−fit log−likelihood: −5446.46
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 3
0 20 40 60 80 100
SNV Index

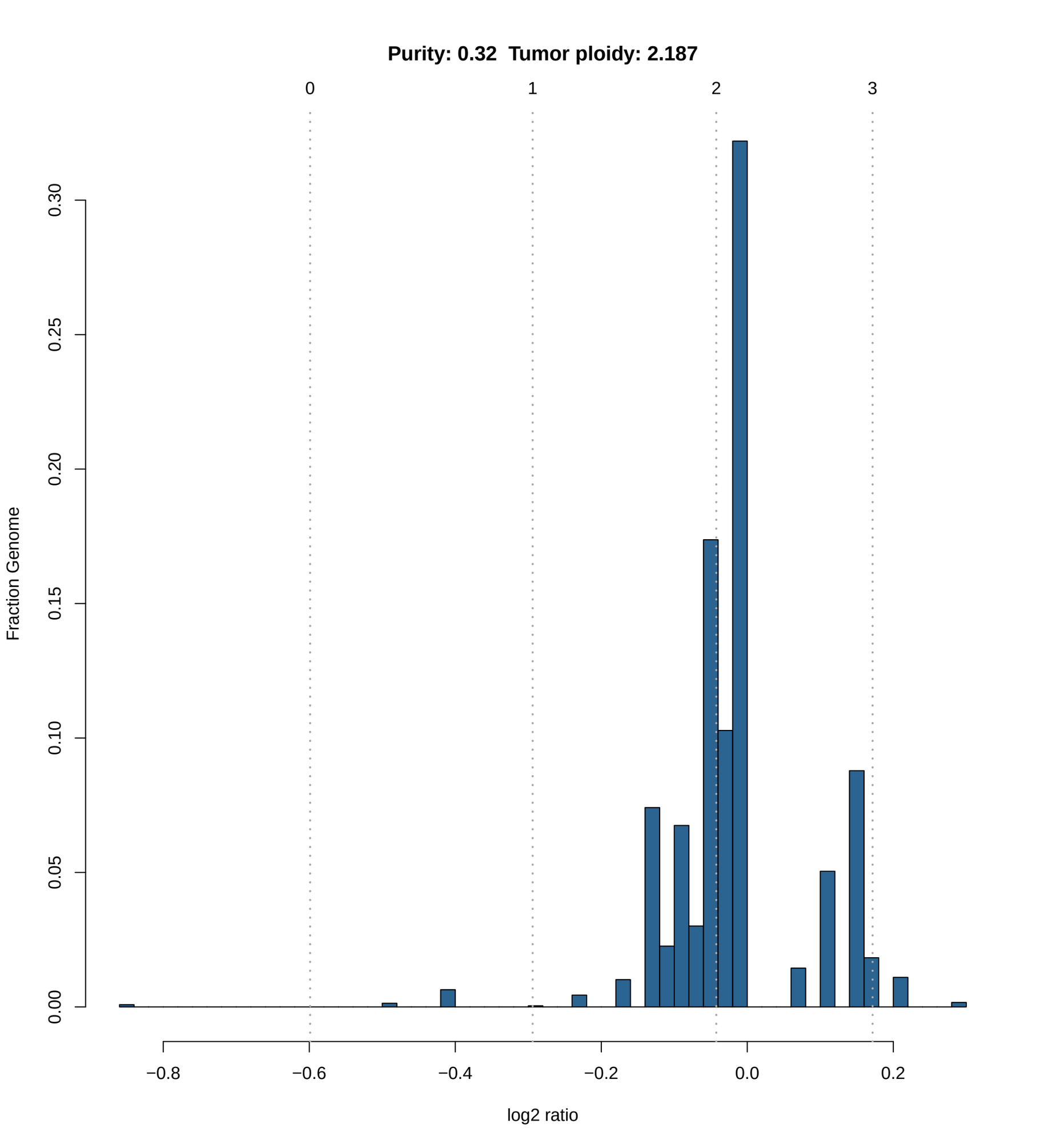

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100
SNV Index

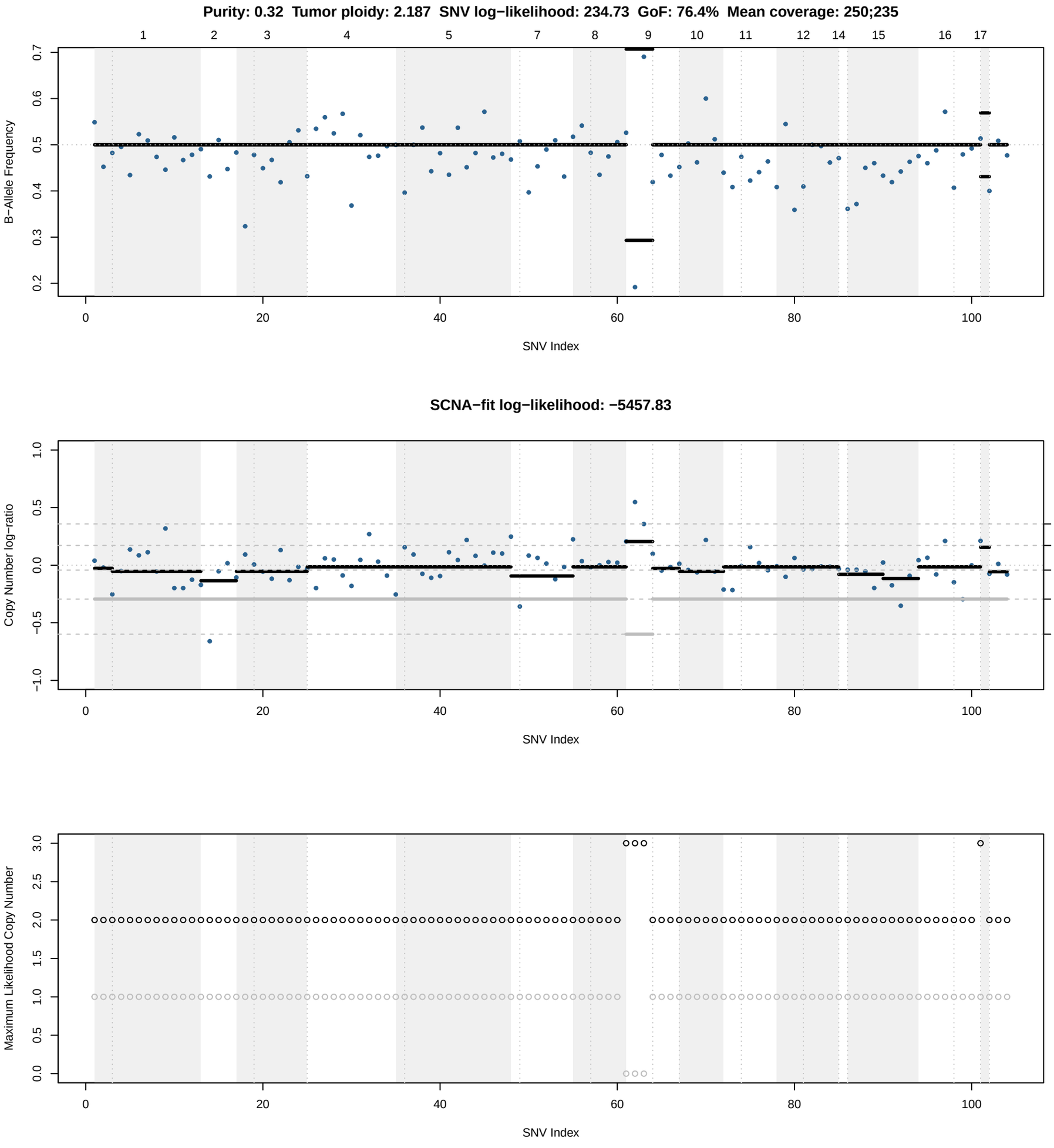

Allelic fraction (germline)
0.4
0.5
0.6
0.7
4m3
1m1
3m2
2m1
1m0
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

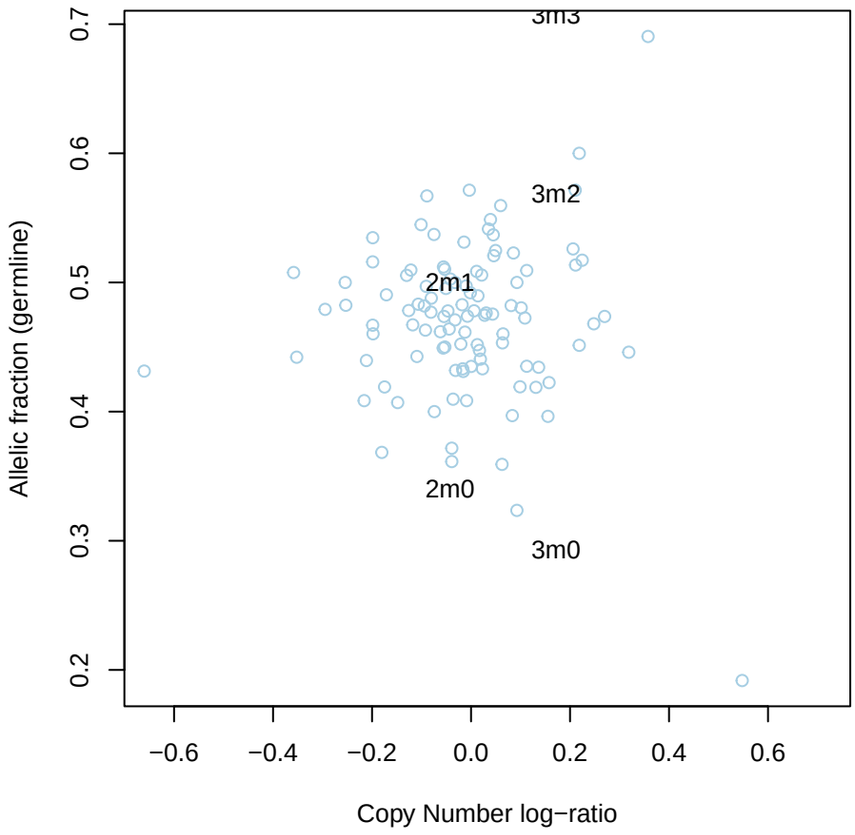

Coverage (log2)
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

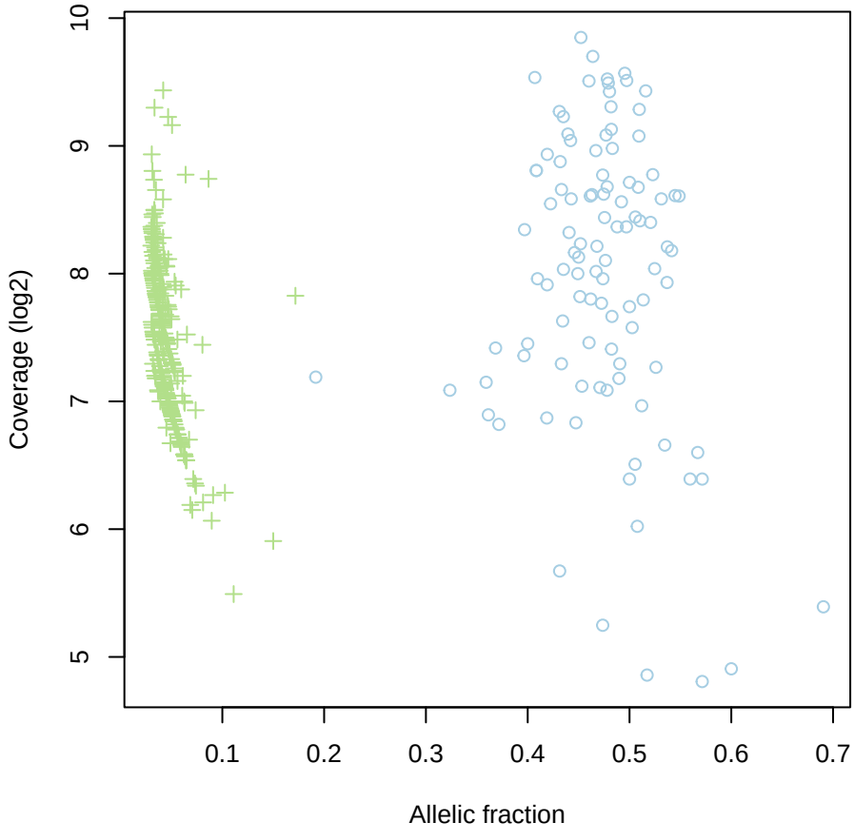

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
0m1
1m1
2m1
3m1
4m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

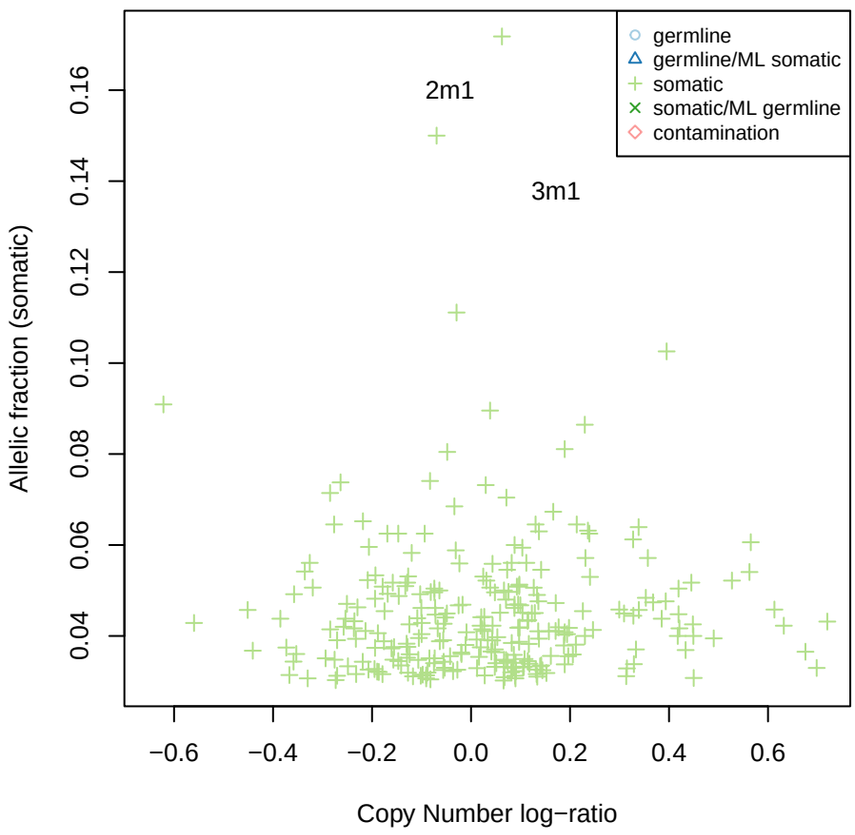

Power 0.8
Frequency
0
10
20
30
40
50
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Cellular fraction

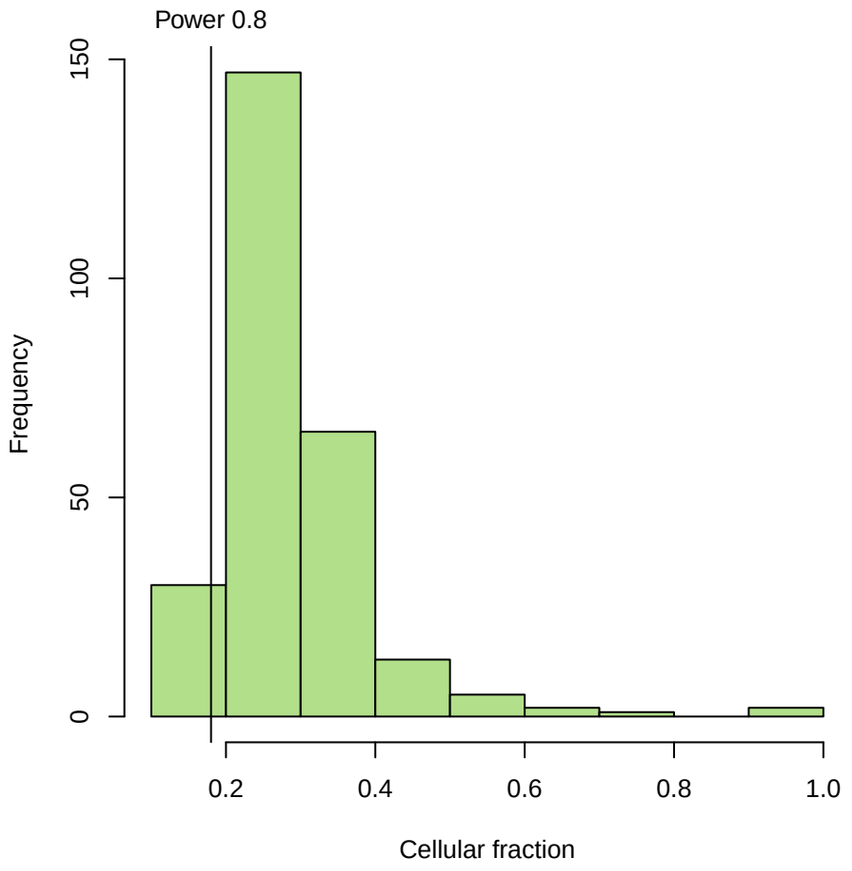

Purity: 0.32 Tumor ploidy: 2.187
0
1
2
3
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

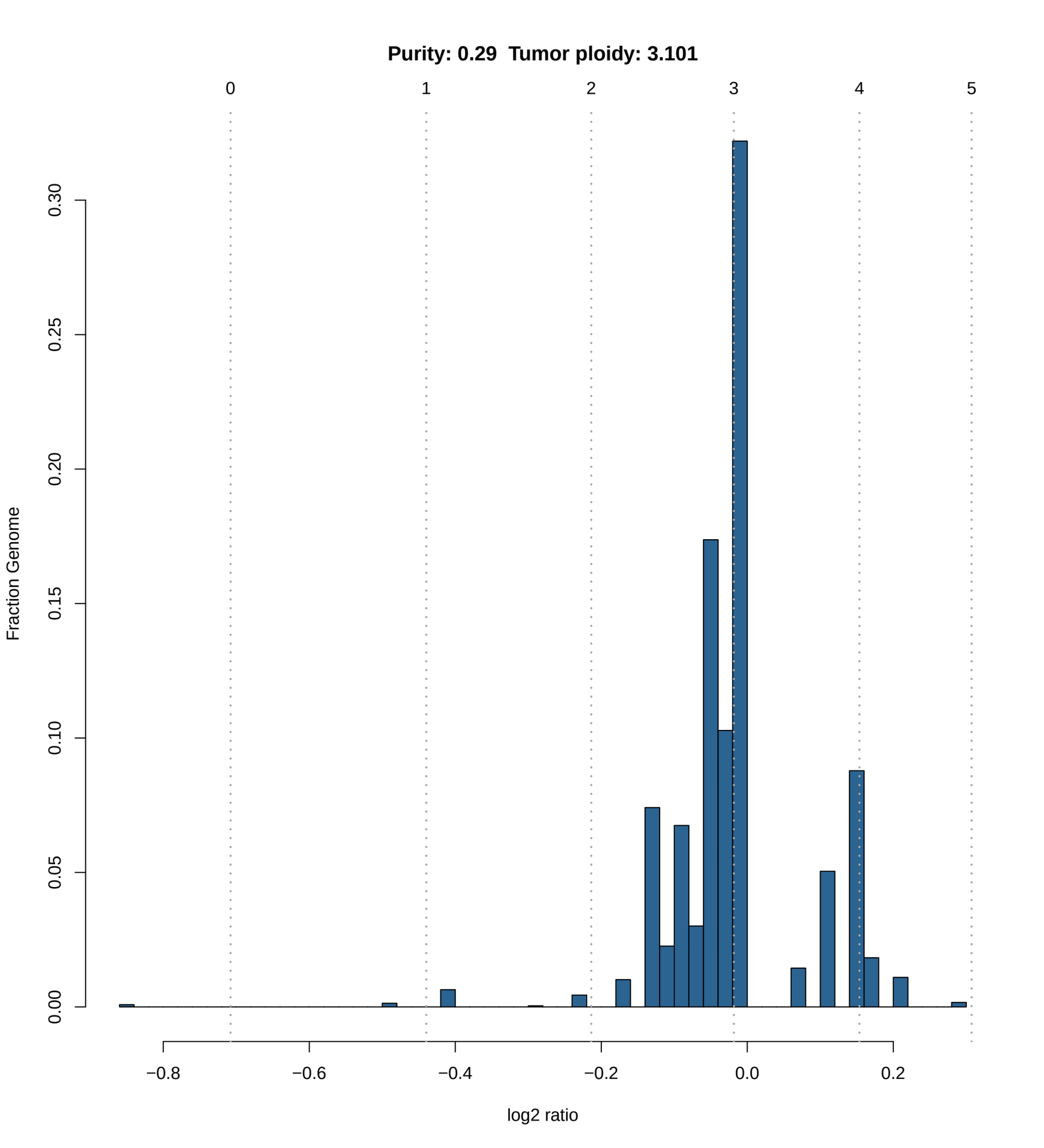

Purity: 0.32 Tumor ploidy: 2.187 SNV log−likelihood: 234.73 GoF: 76.4% Mean coverage: 250;235
1 2 3 4 5 7 8 9 10 11 12 14 15 16 17
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index
SCNA−fit log−likelihood: −5457.83
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4
0 20 40 60 80 100
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

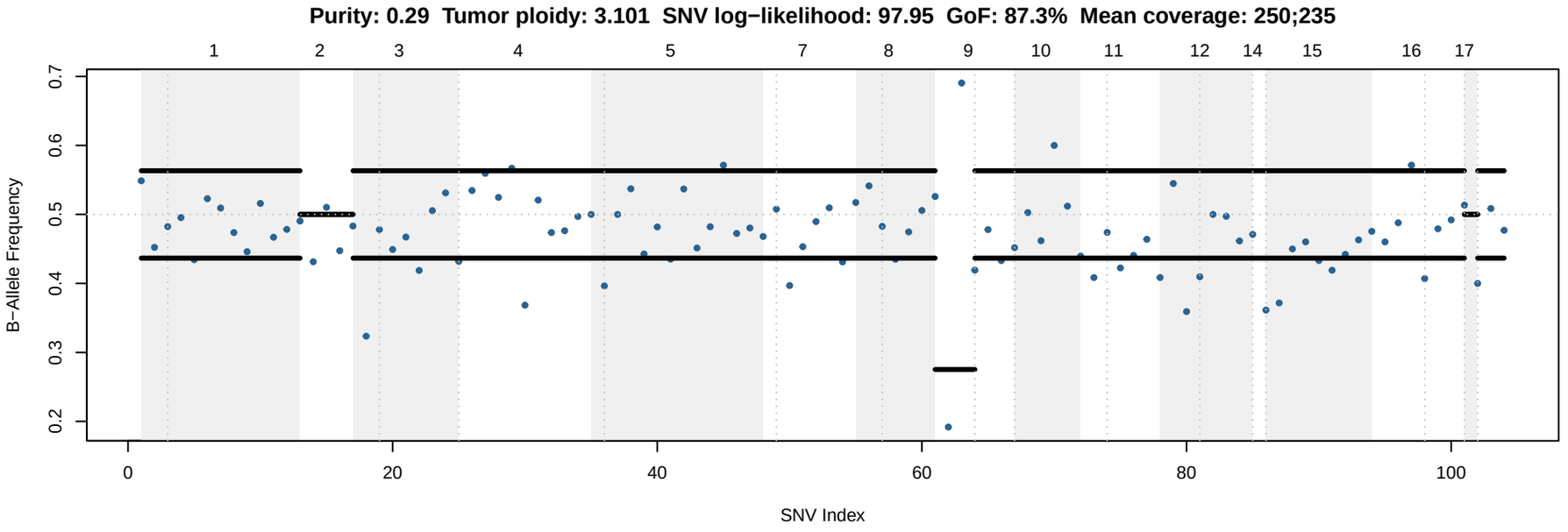

3m3
3m2
2m1
2m0
3m0
Allelic fraction (germline)
Copy Number log−ratio

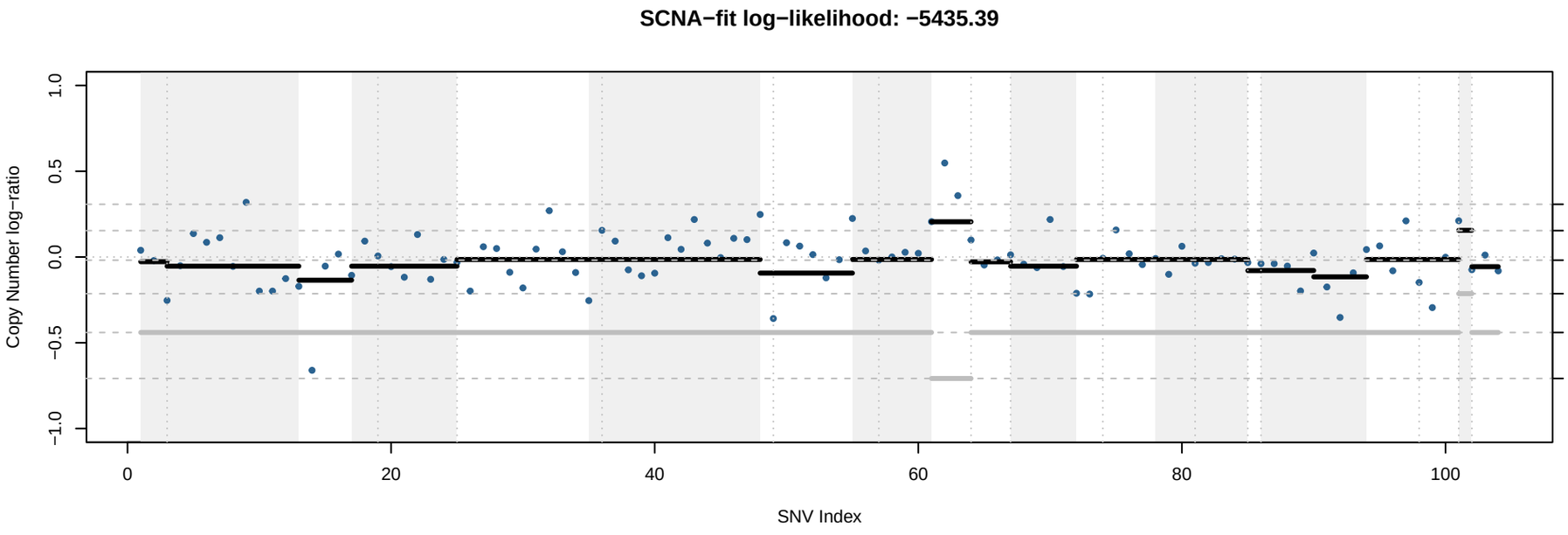

Coverage (log2)
Allelic fraction

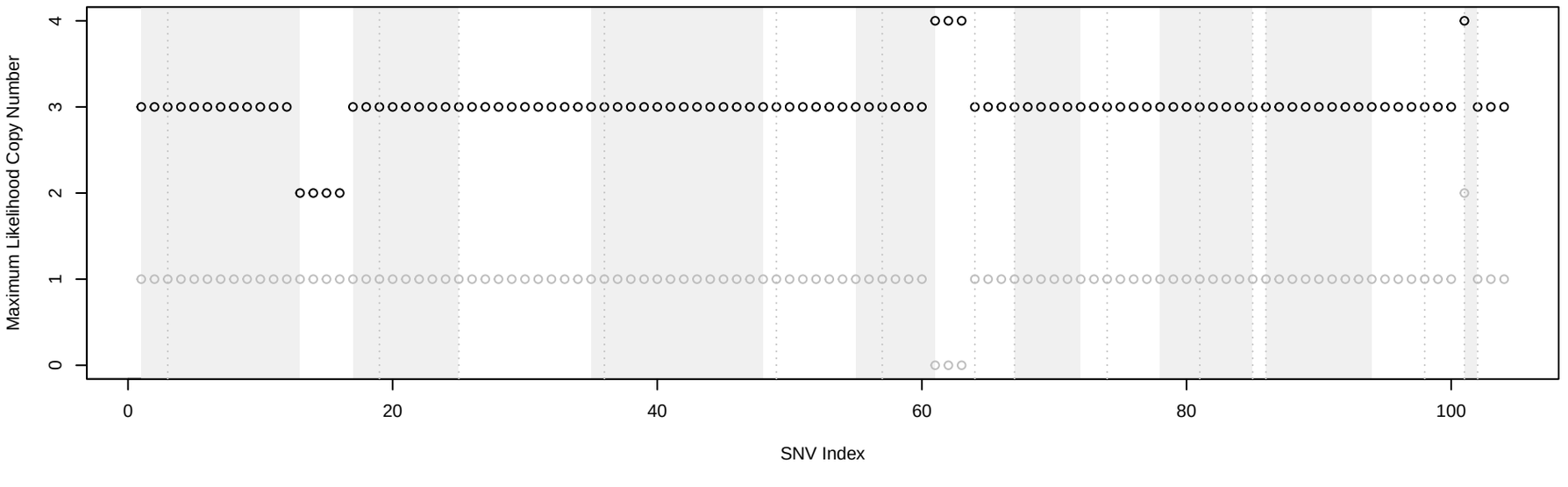

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
2m1
3m1
Allelic fraction (somatic)
Copy Number log−ratio

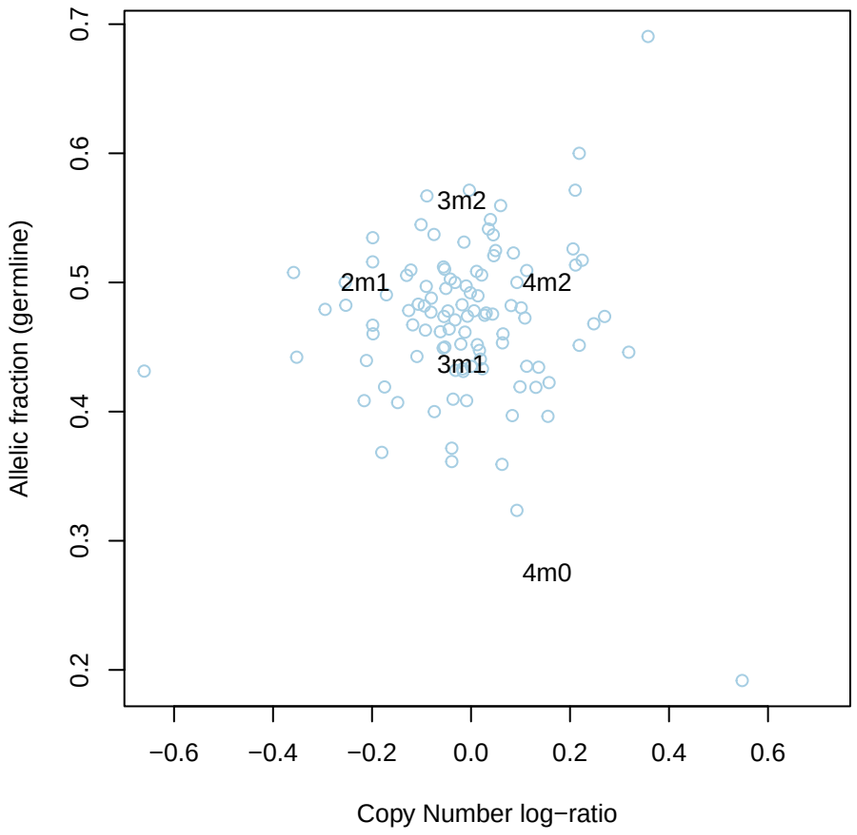

Power 0.8
Frequency
Cellular fraction

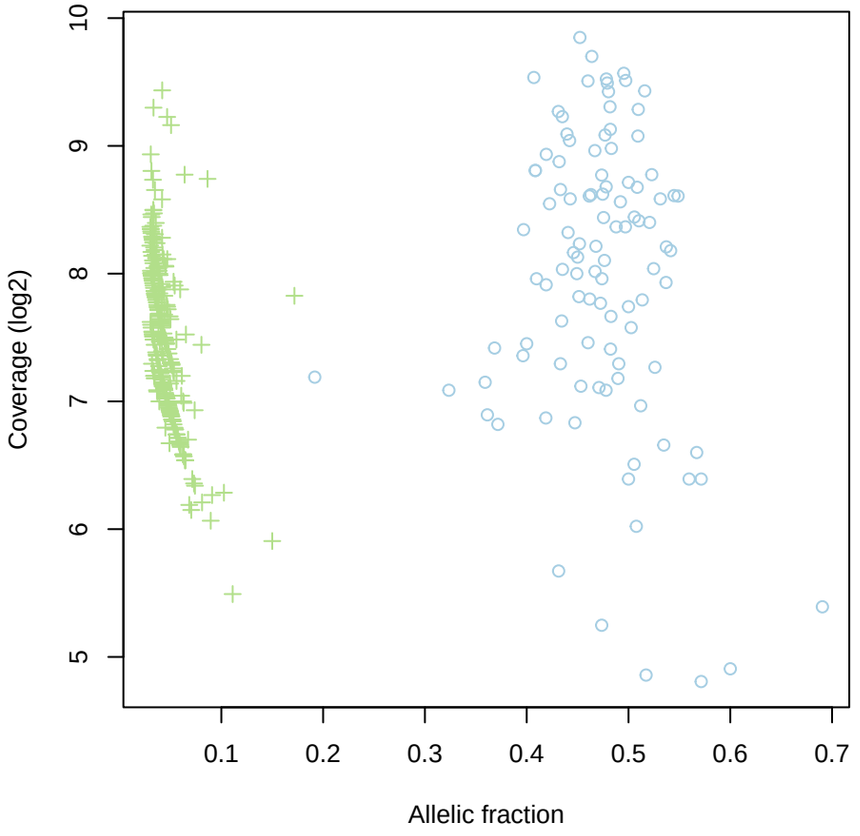

Purity: 0.29 Tumor ploidy: 3.101
0
1
2
3
4
5
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

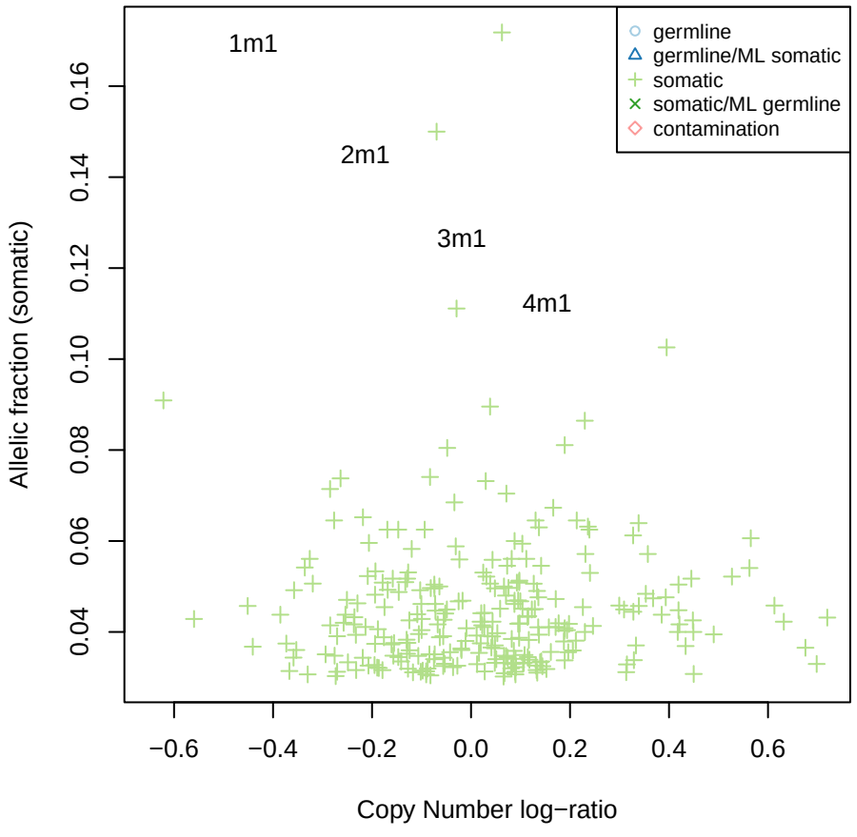

Purity: 0.29 Tumor ploidy: 3.101 SNV log−likelihood: 97.95 GoF: 87.3% Mean coverage: 250;235
1 2 3 4 5 7 8 9 10 11 12 14 15 16 17
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

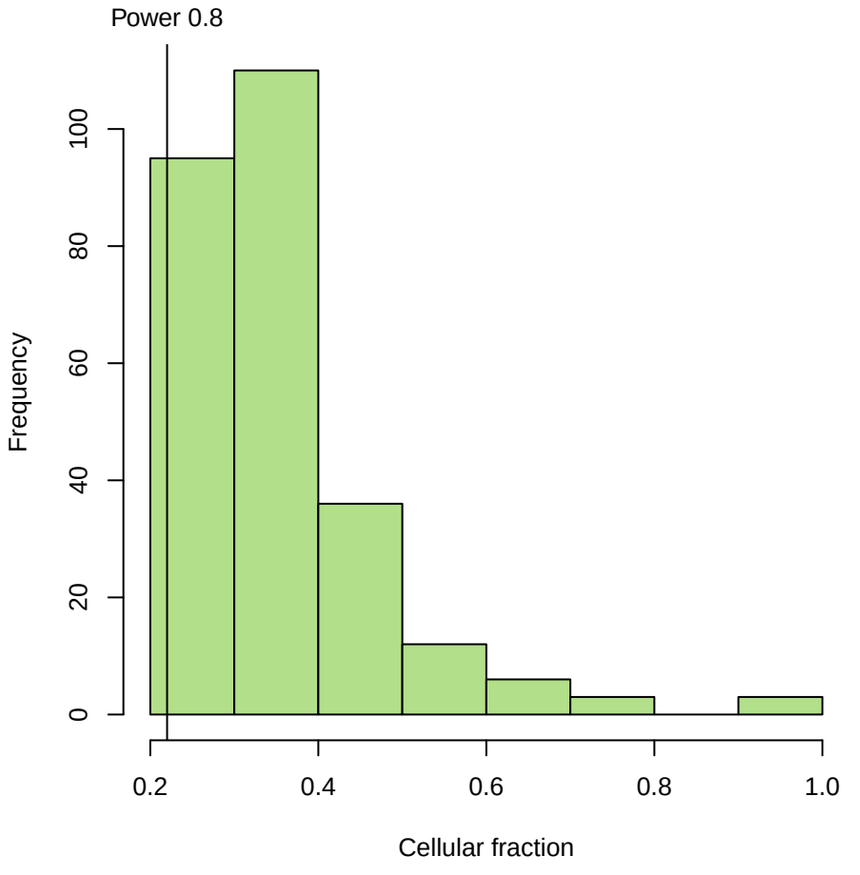

SCNA−fit log−likelihood: −5435.39
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 1 2 3 4 5
0 20 40 60 80 100
SNV Index

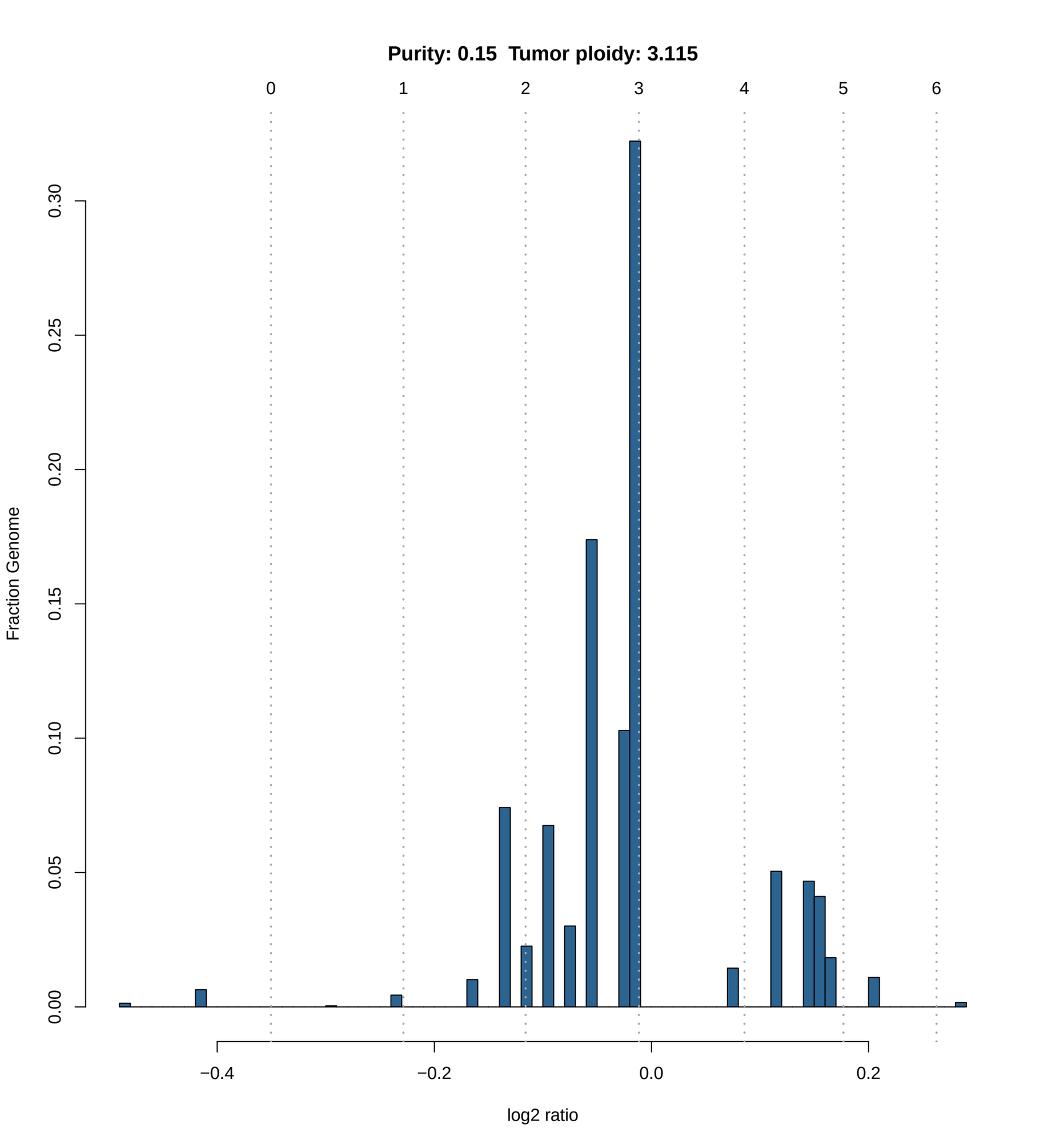

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100
SNV Index

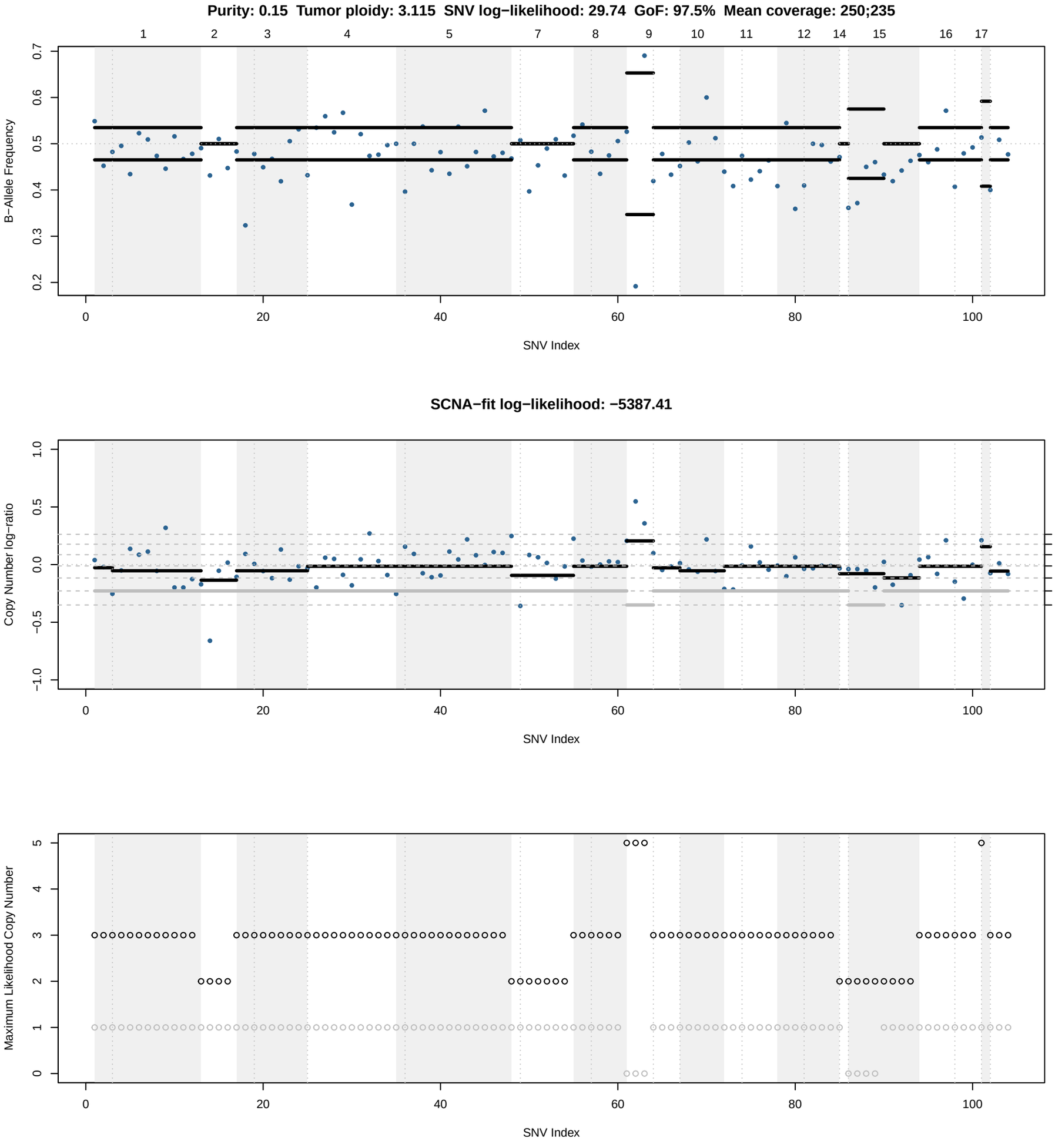

Allelic fraction (germline)
Copy Number log−ratio
3m2
2m1
4m2
3m1
4m0

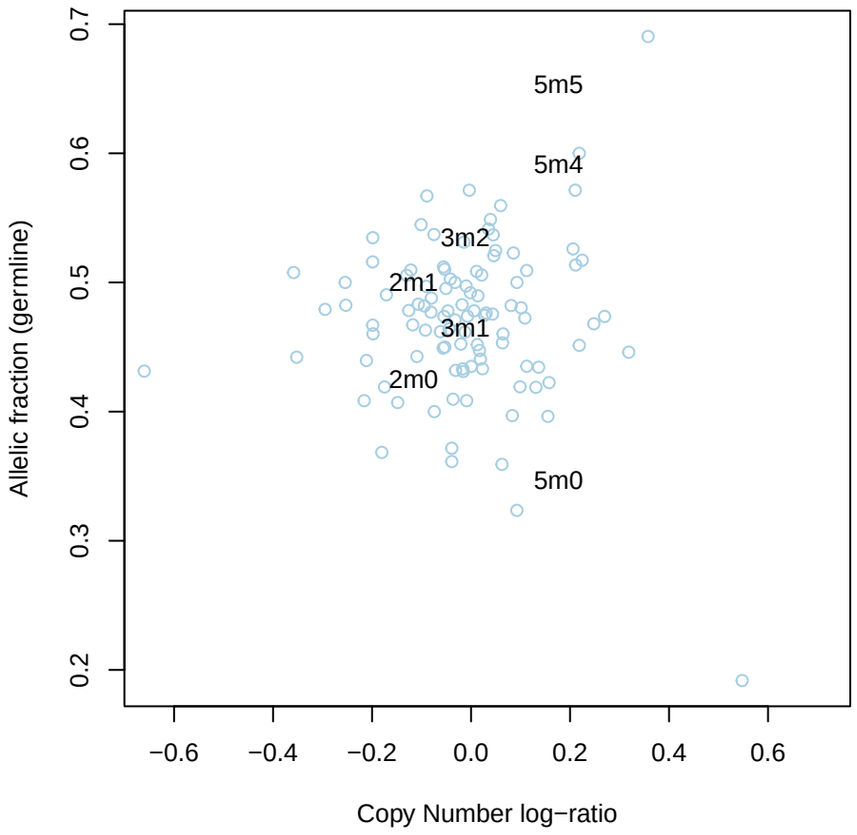

Coverage (log2)
Allelic fraction

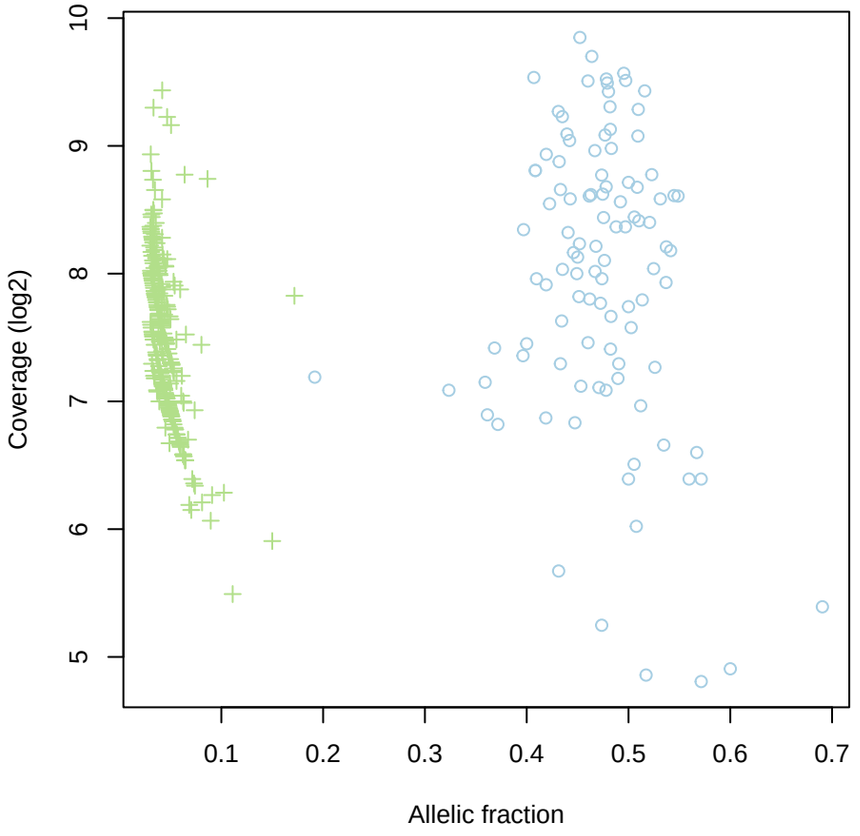

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
1m1
2m1
3m1
4m1

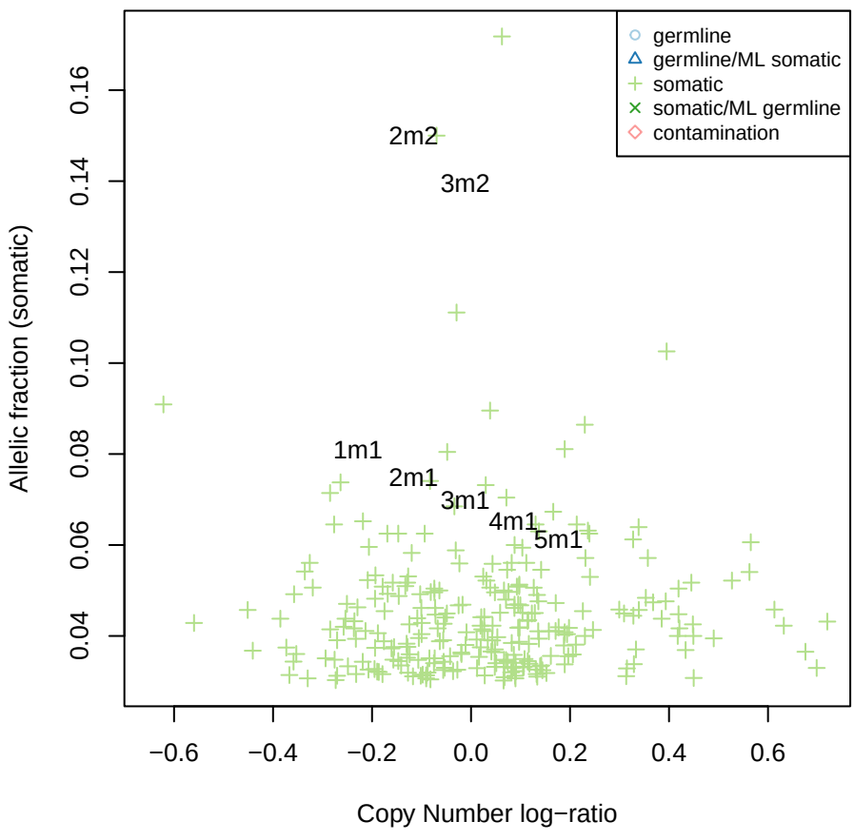

Power 0.8
Frequency
Cellular fraction

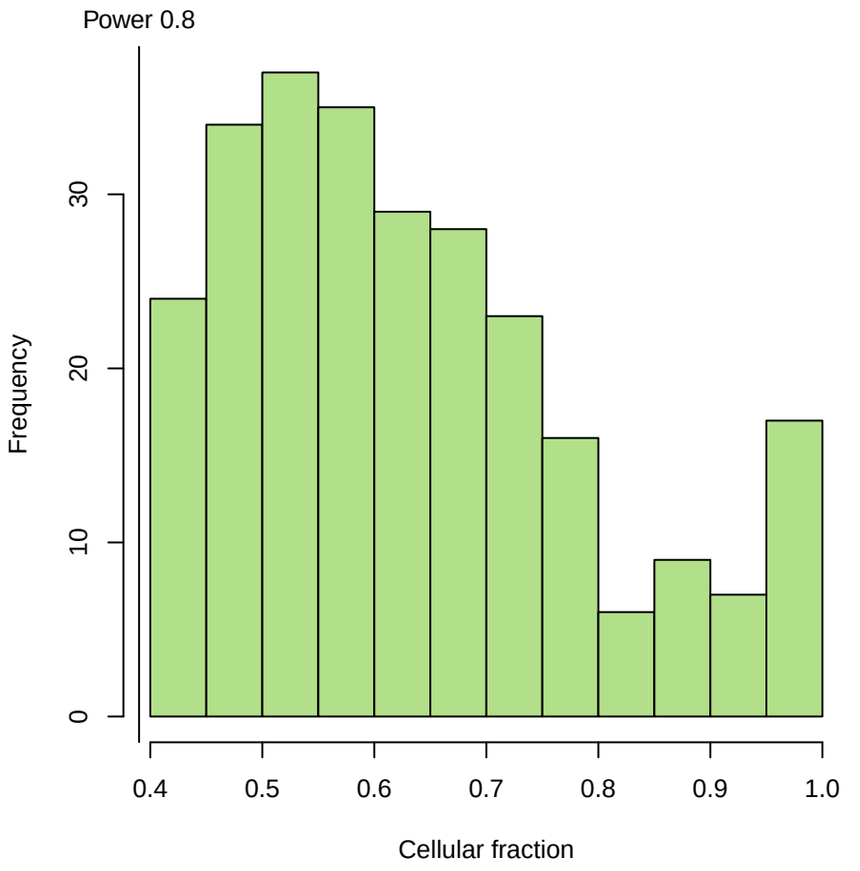

Purity: 0.15 Tumor ploidy: 3.115
0
1
2
3
4
5
6
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.4
−0.2
0.0
0.2
log2 ratio

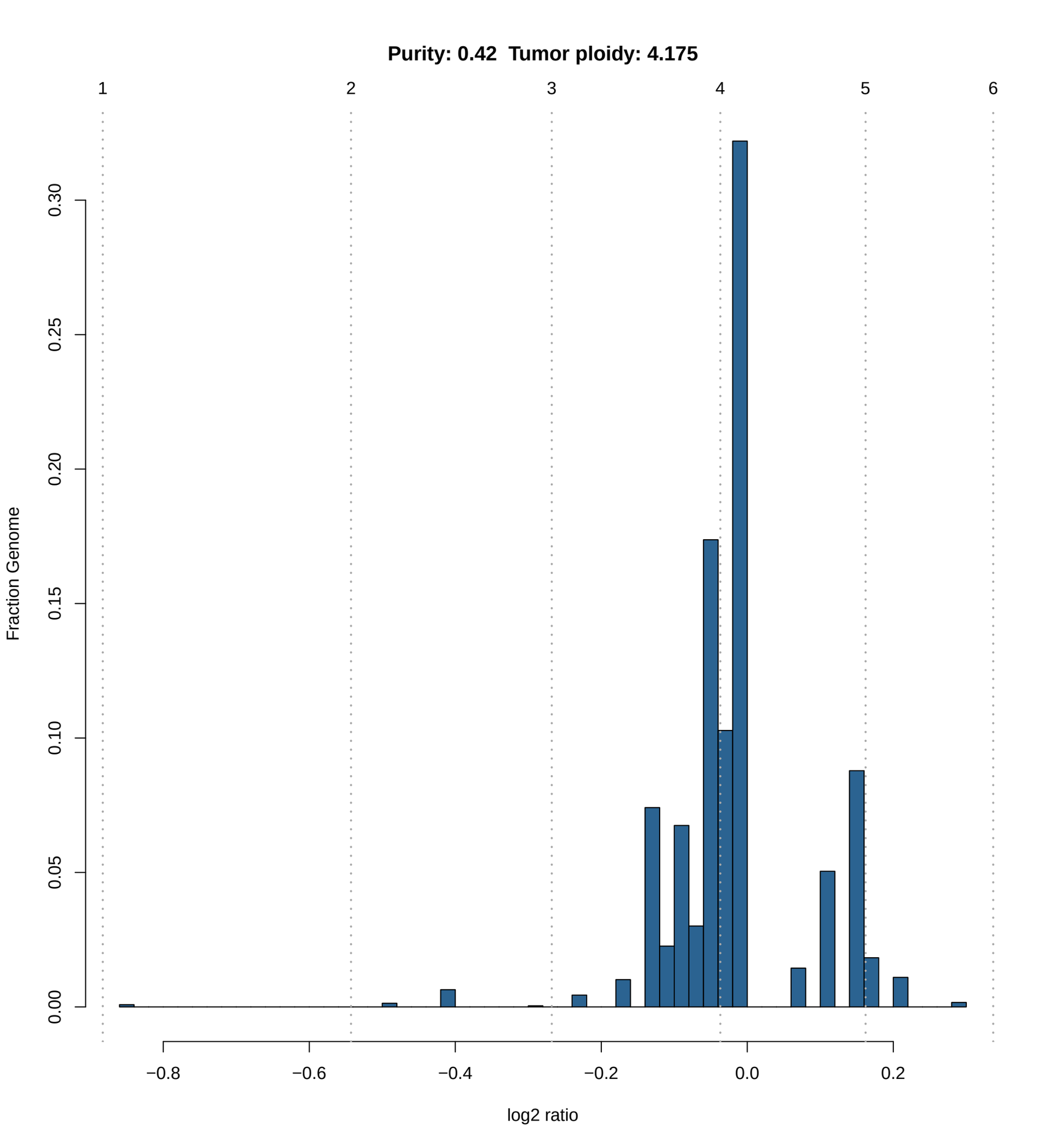

Purity: 0.15 Tumor ploidy: 3.115 SNV log−likelihood: 29.74 GoF: 97.5% Mean coverage: 250;235
1 2 3 4 5 7 8 9 10 11 12 14 15 16 17
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index
SCNA−fit log−likelihood: −5387.41
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4 6
0 20 40 60 80 100
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100
SNV Index

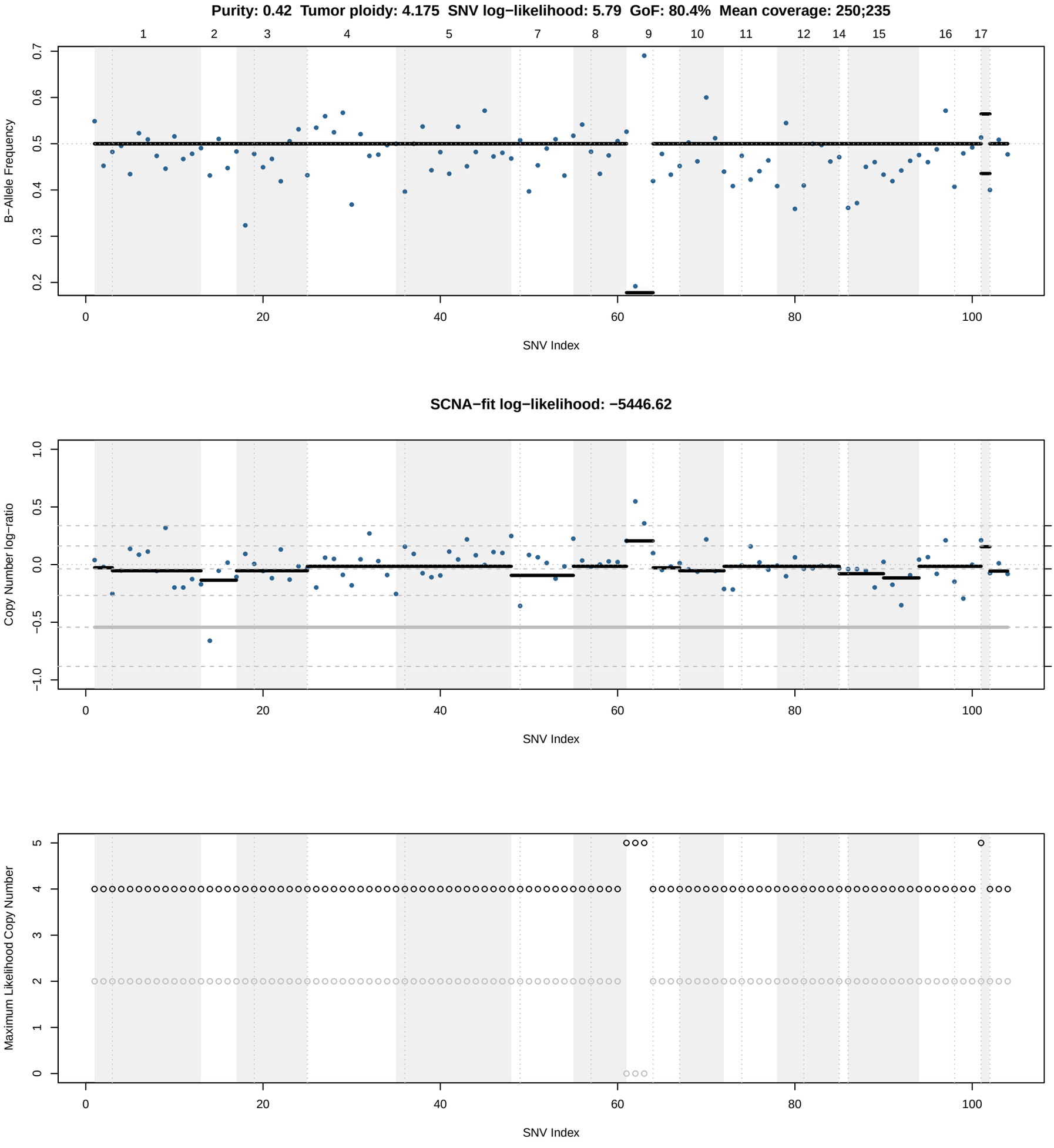

Allelic fraction (germline)
Copy Number log−ratio
5m5
5m4
3m2
2m1
3m1
2m0
5m0

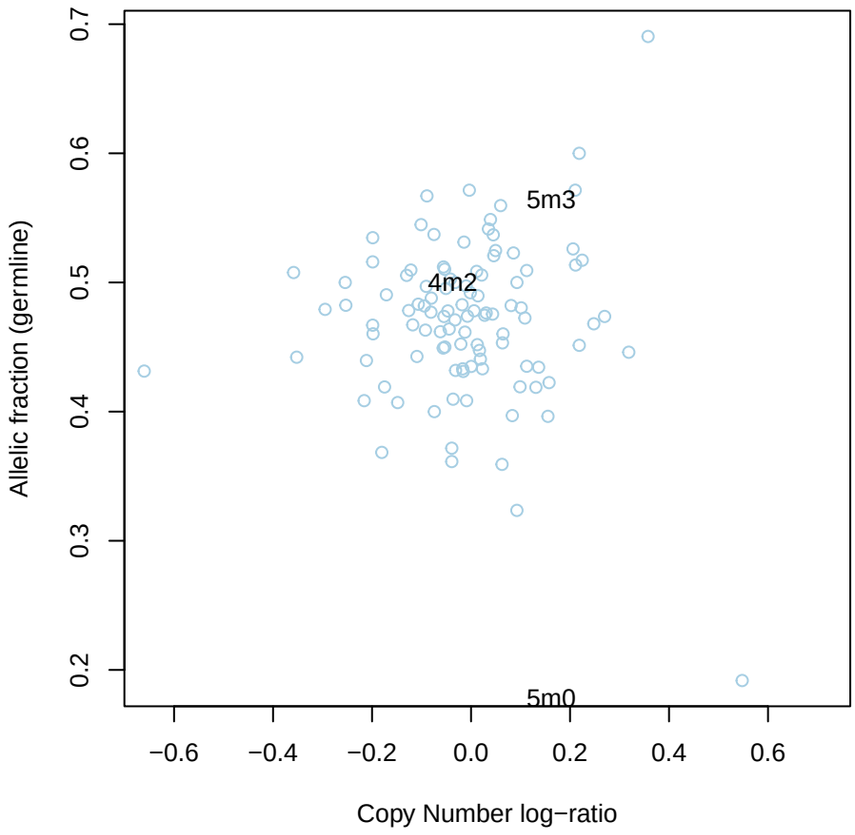

Coverage (log2)
Allelic fraction

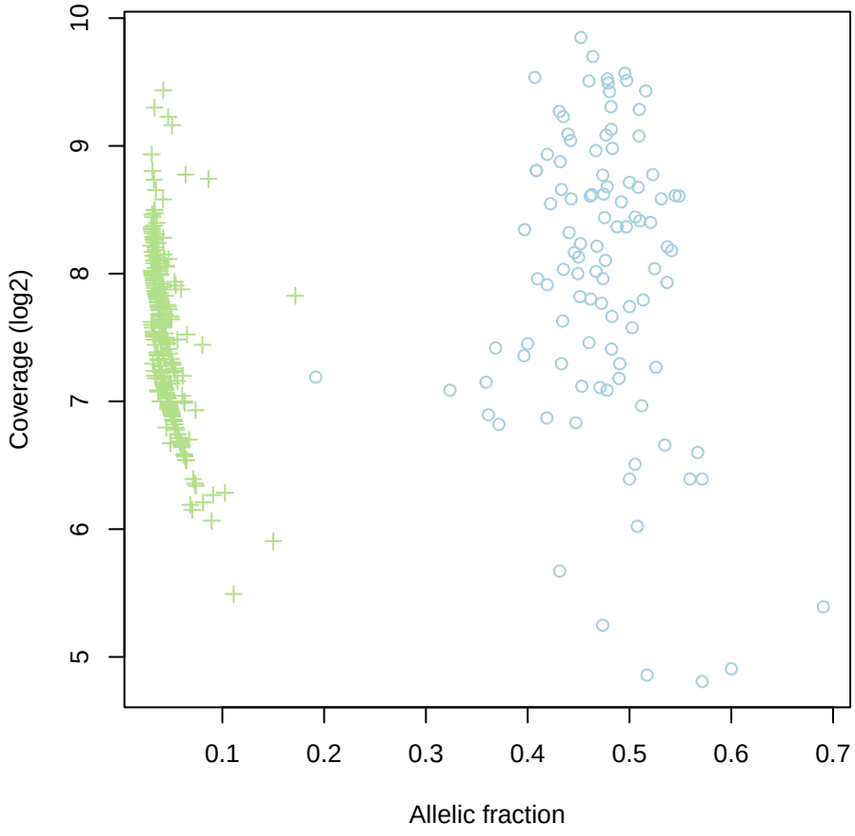

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
2m2
3m2
1m1
2m1
3m1
4m1
5m1

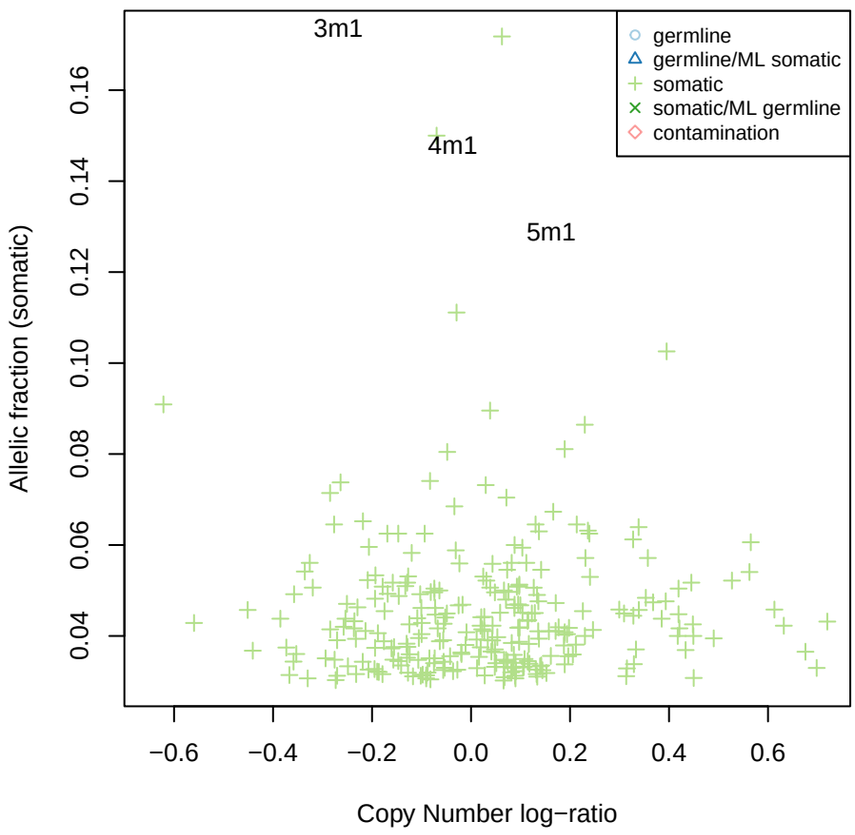

Power 0.8
Frequency
Cellular fraction

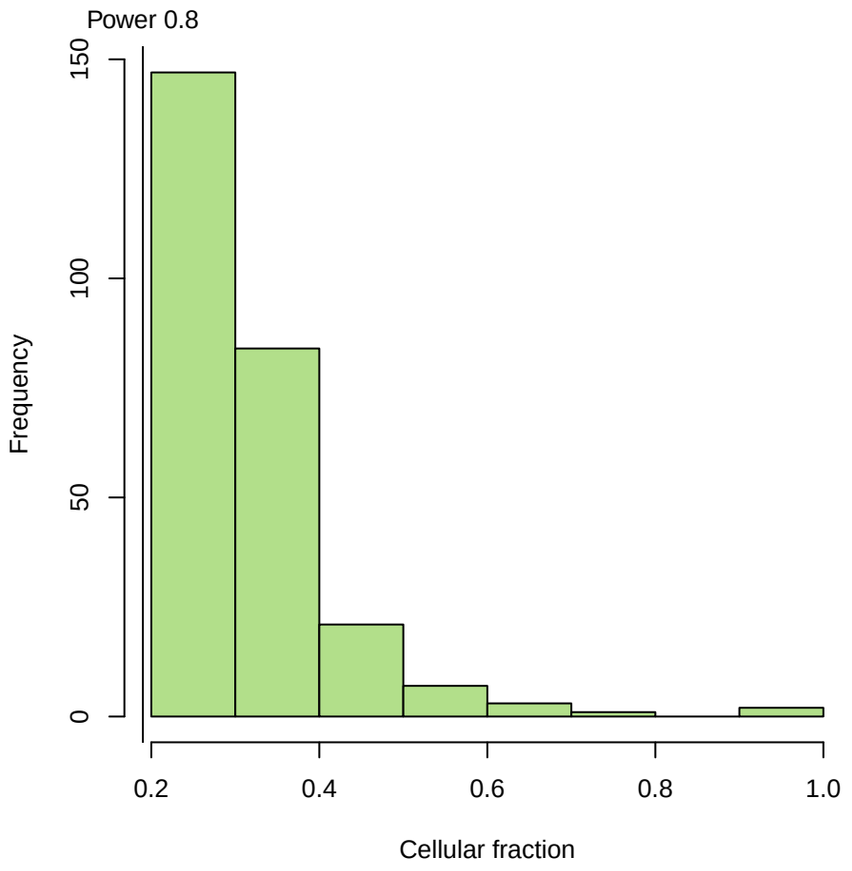

Purity: 0.42 Tumor ploidy: 4.175
1
2
3
4
5
6
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

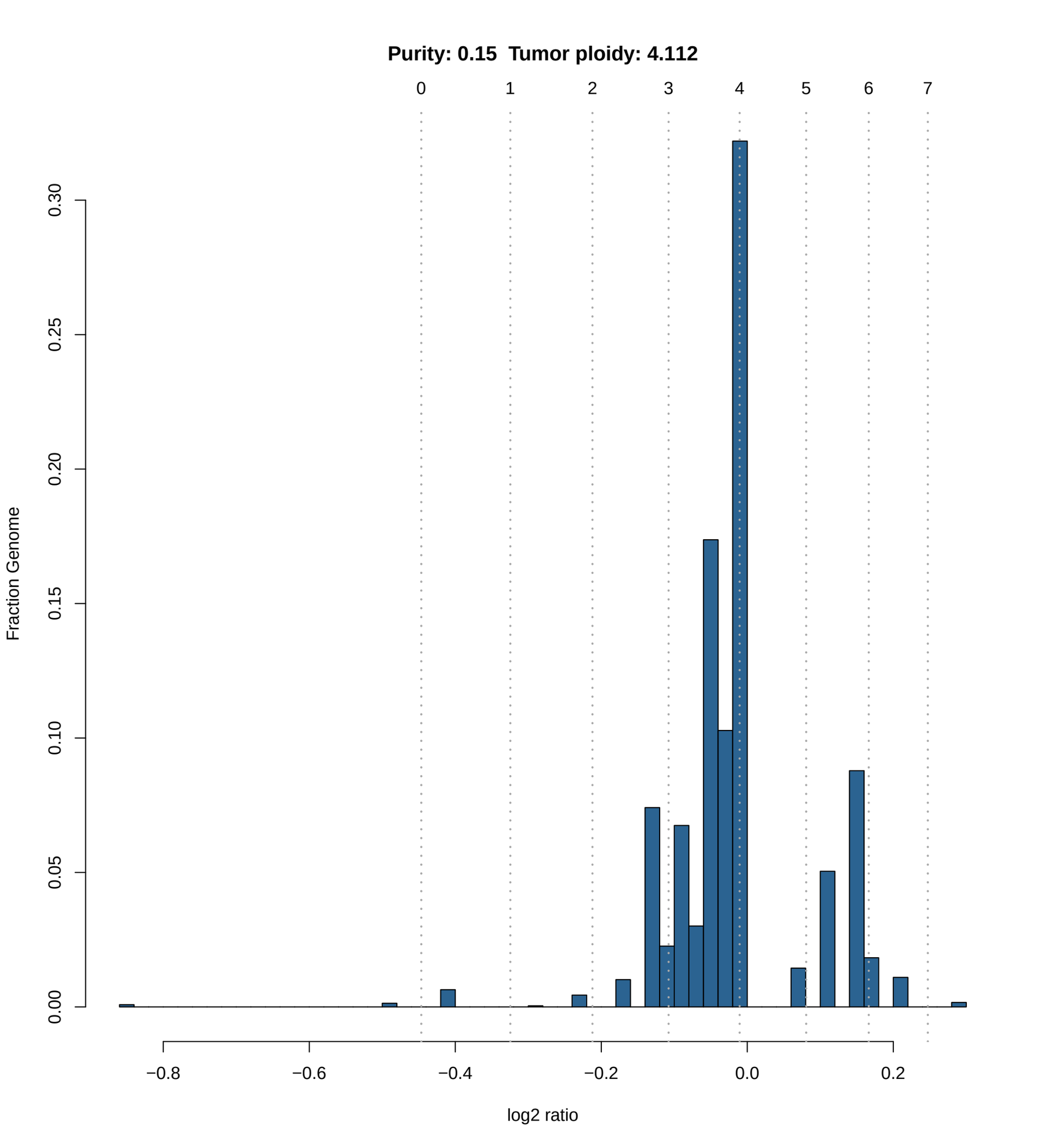

Purity: 0.42 Tumor ploidy: 4.175 SNV log−likelihood: 5.79 GoF: 80.4% Mean coverage: 250;235
1 2 3 4 5 7 8 9 10 11 12 14 15 16 17
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index
SCNA−fit log−likelihood: −5446.62
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4 5 6
0 20 40 60 80 100
SNV Index
Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100
SNV Index

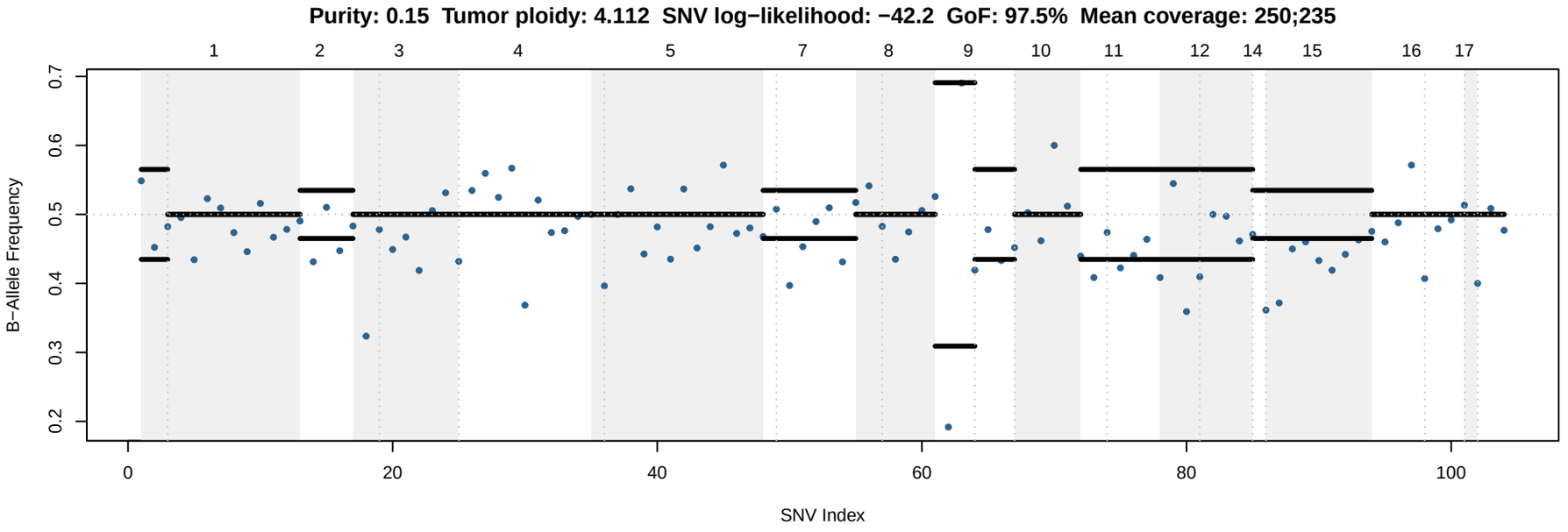

Allelic fraction (germline)
Copy Number log−ratio
5m3
4m2
5m0

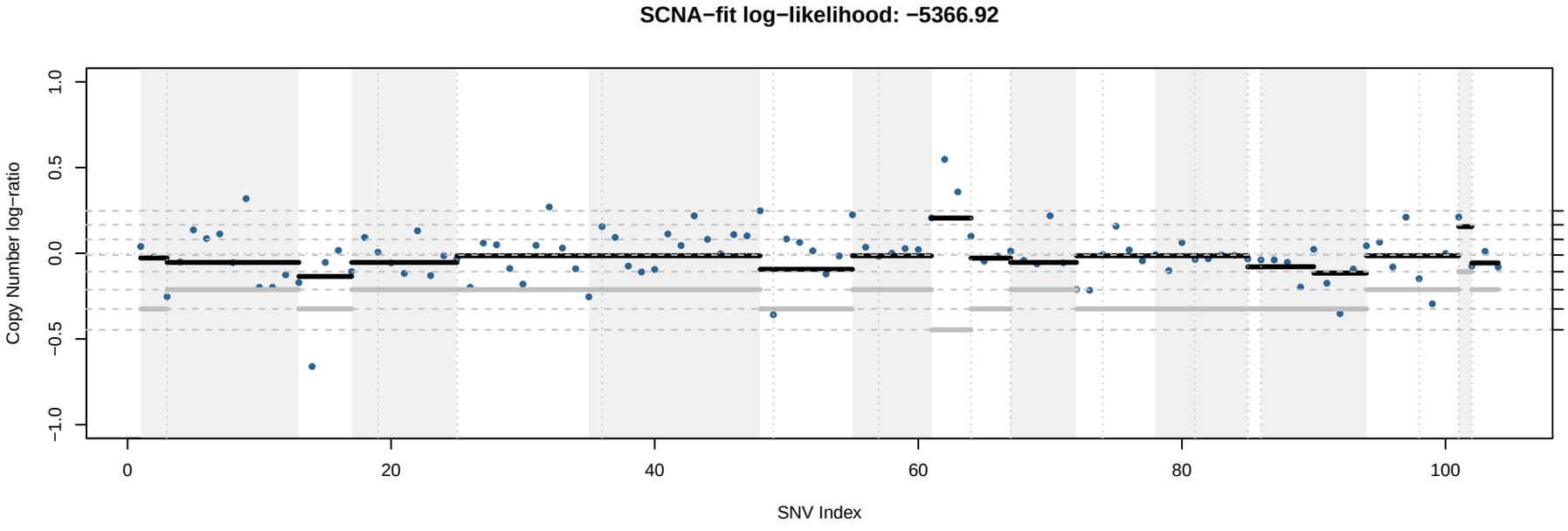

Coverage (log2)
Allelic fraction

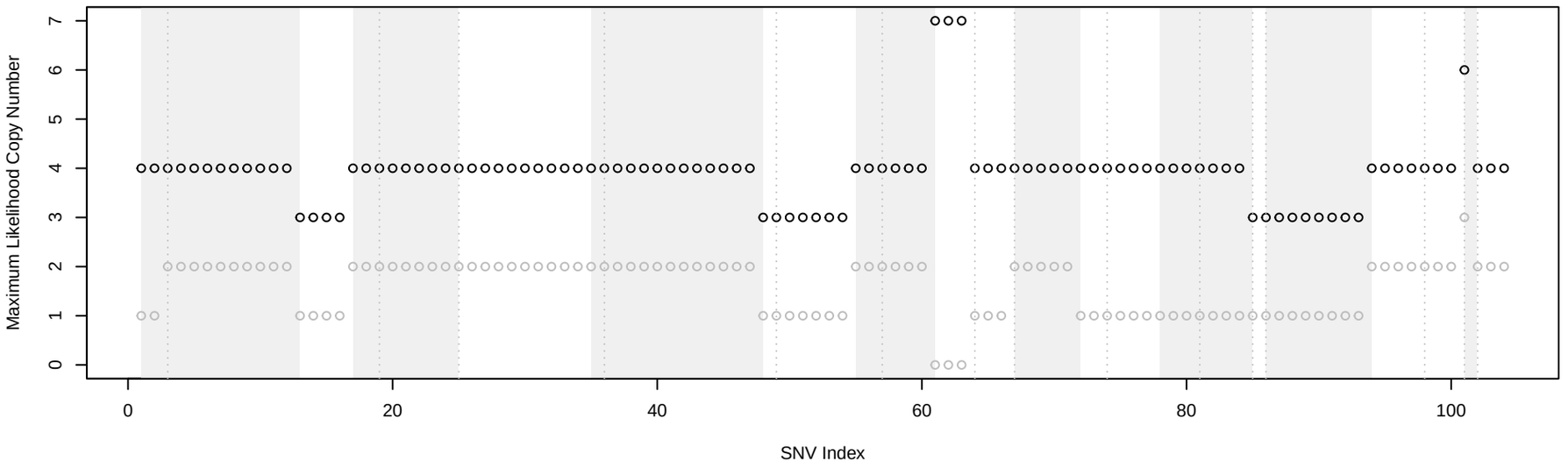

Allelic fraction (somatic)
Copy Number log−ratio
3m1
4m1
5m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

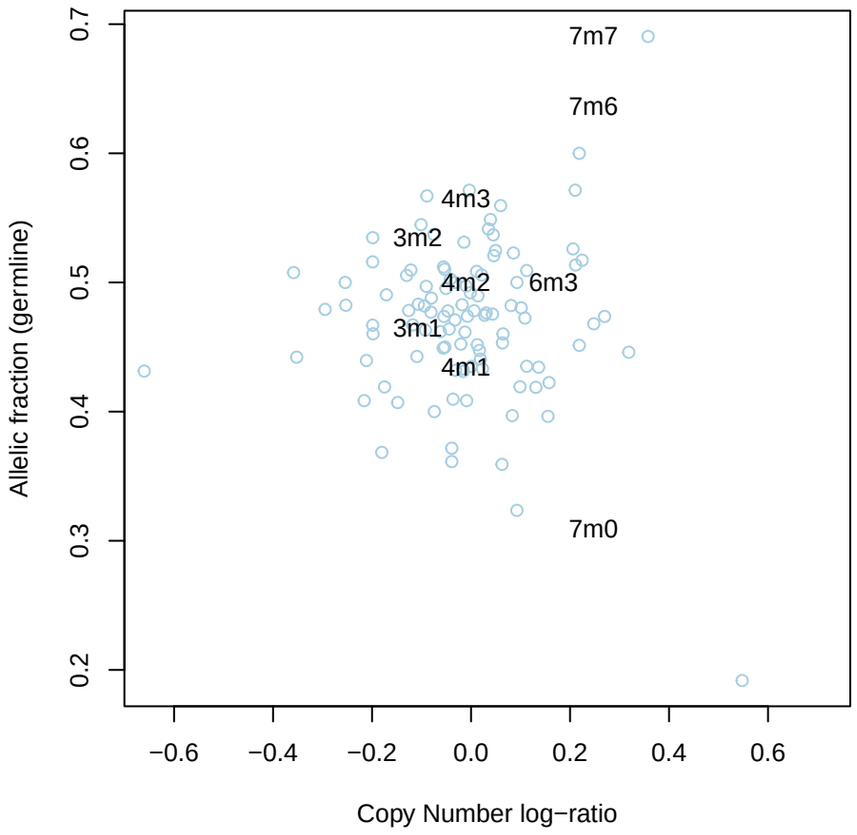

Power 0.8
Frequency
Cellular fraction

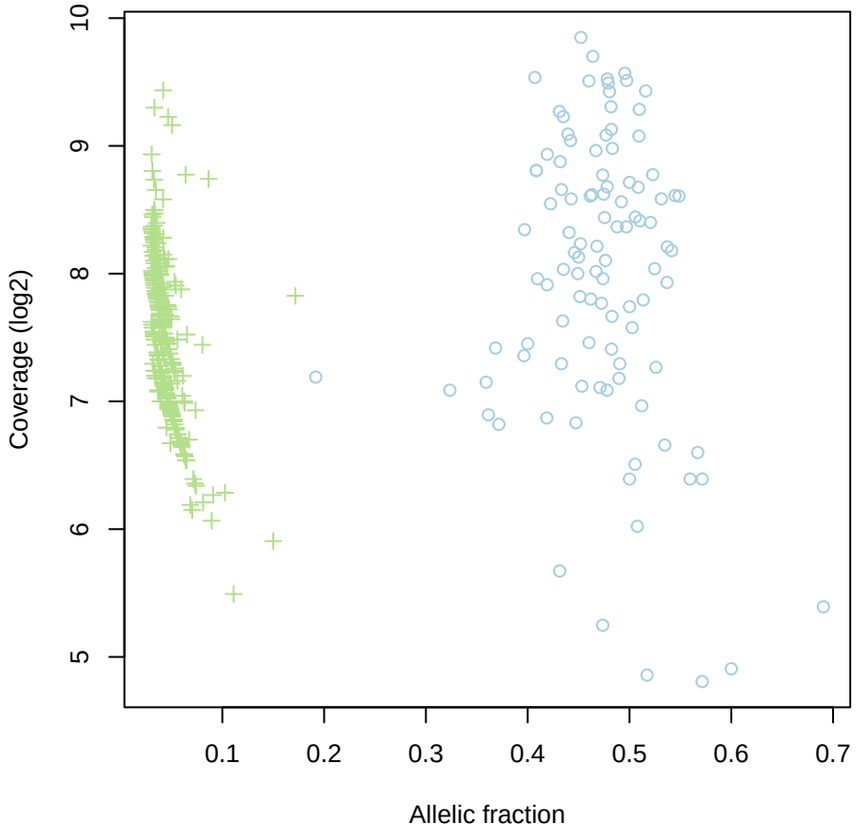

Purity: 0.15 Tumor ploidy: 4.112
0
1
2
3
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

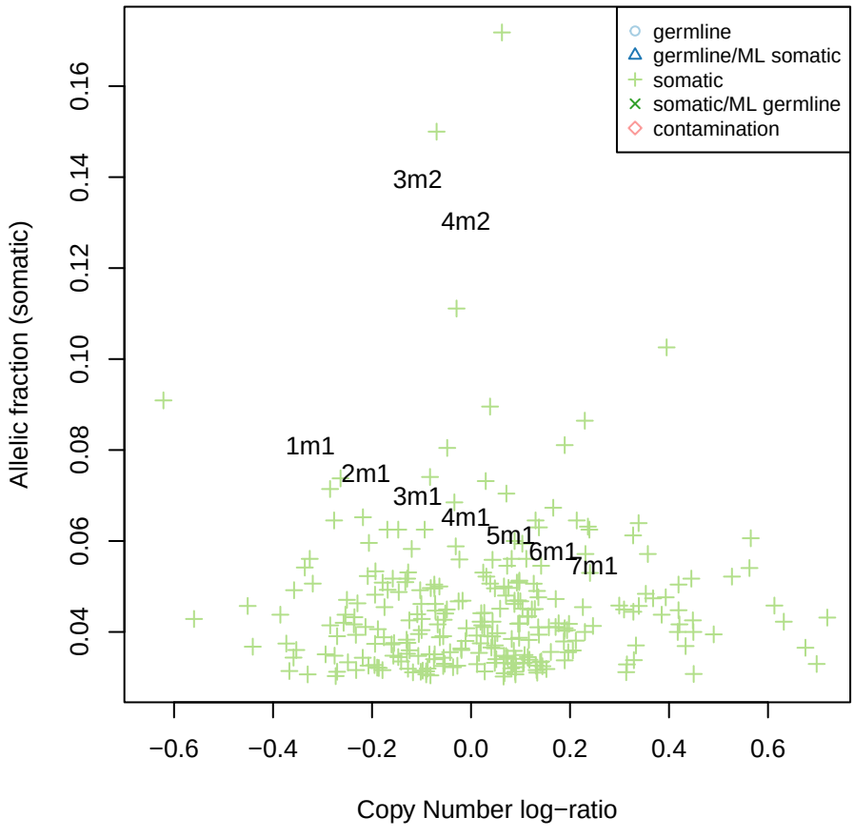

Purity: 0.15 Tumor ploidy: 4.112 SNV log−likelihood: −42.2 GoF: 97.5% Mean coverage: 250;235
1 2 3 4 5 7 8 9 10 11 12 14 15 16 17
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

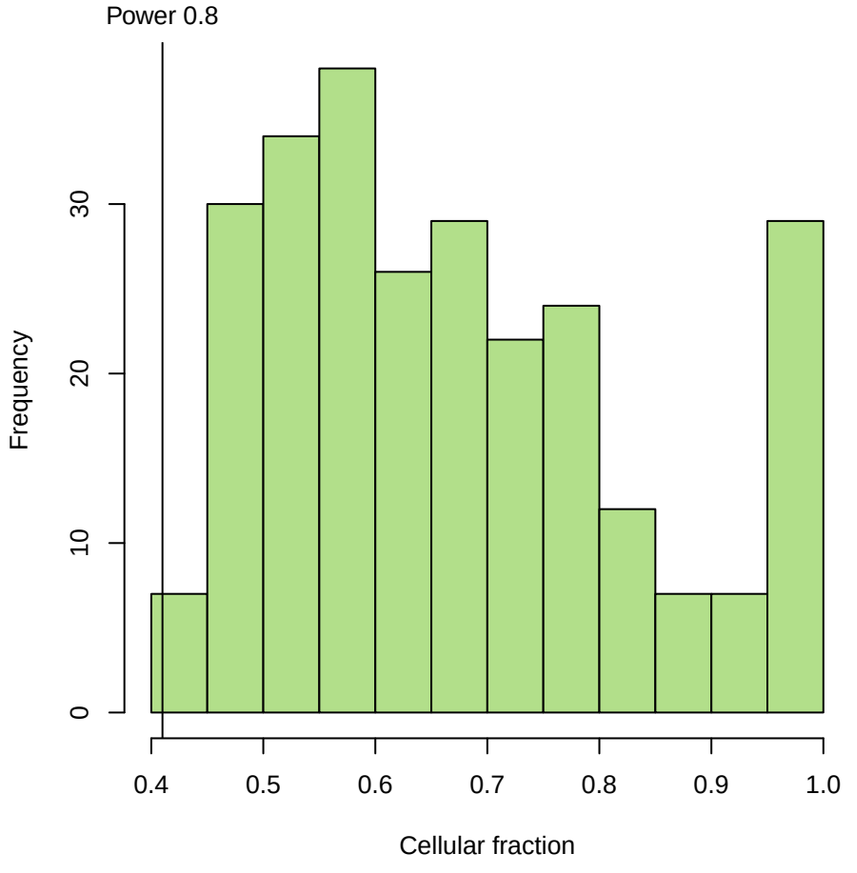

SCNA−fit log−likelihood: −5366.92
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
0 2 4 6
0 20 40 60 80 100
SNV Index

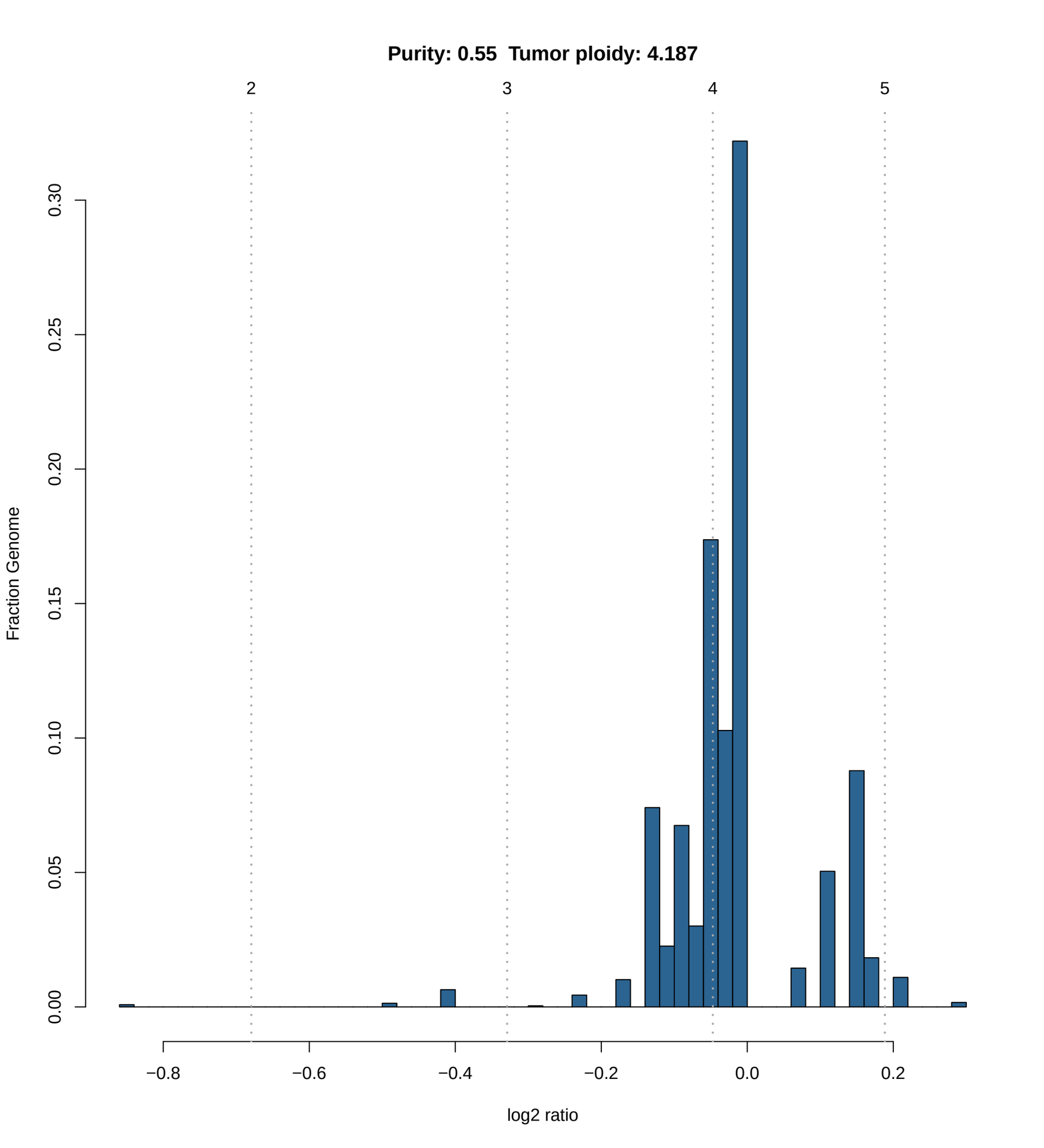

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

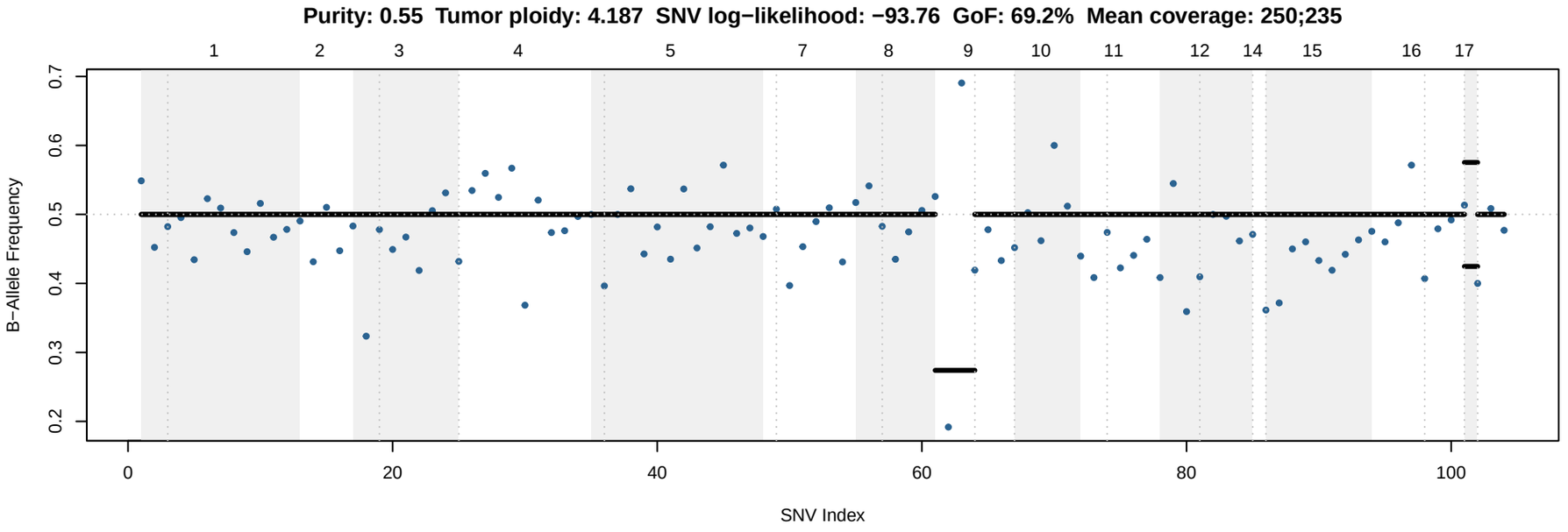

Allelic fraction (germline)
Copy Number log−ratio
7m7
7m6
4m3
3m2
4m2
6m3
3m1
4m1
7m0

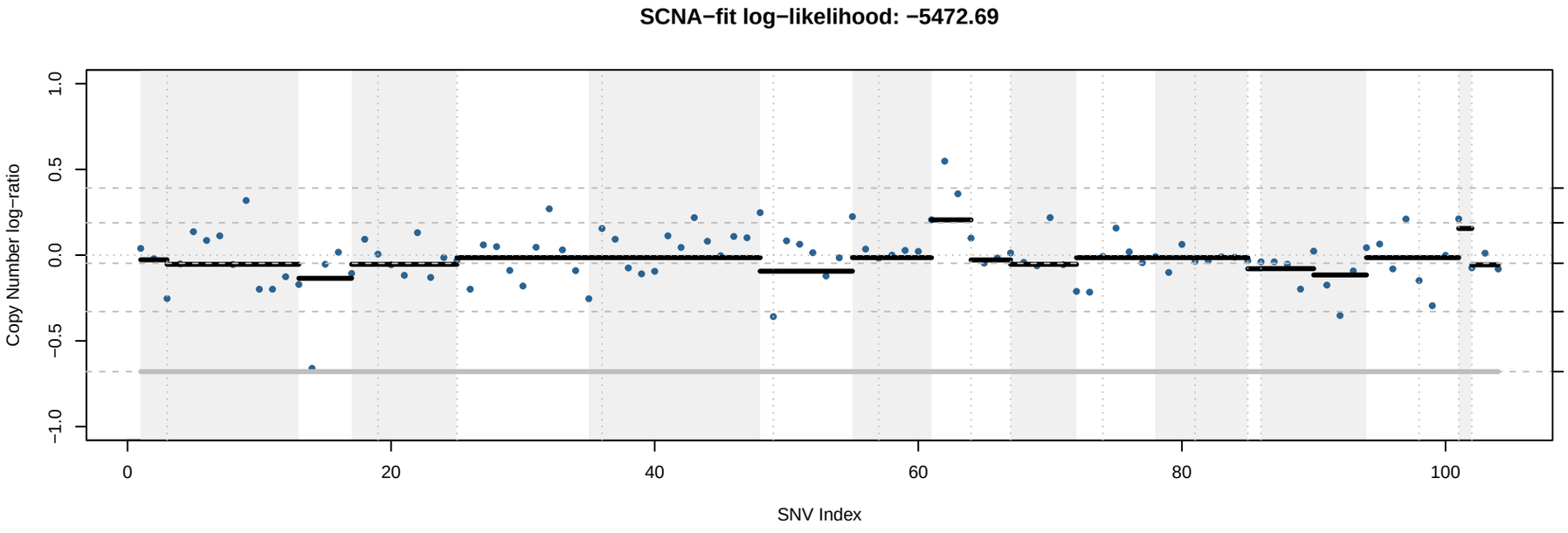

Coverage (log2)
Allelic fraction

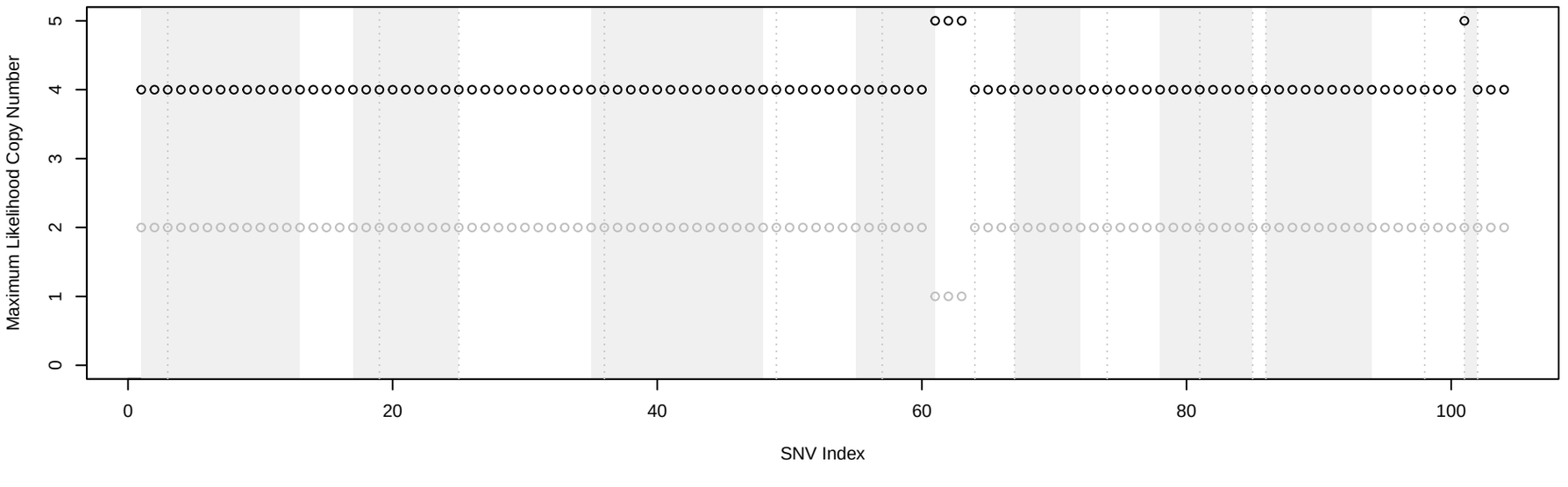

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m2
4m2
1m1
2m1
3m1
4m1
5m1
6m1
7m1

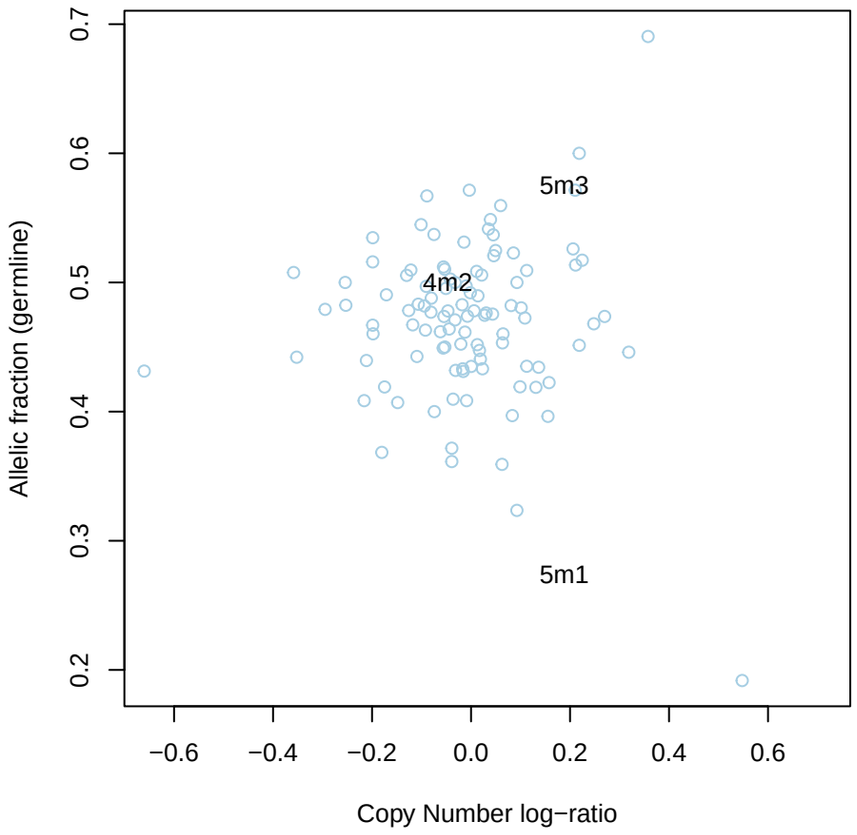

Power 0.8
Frequency
Cellular fraction

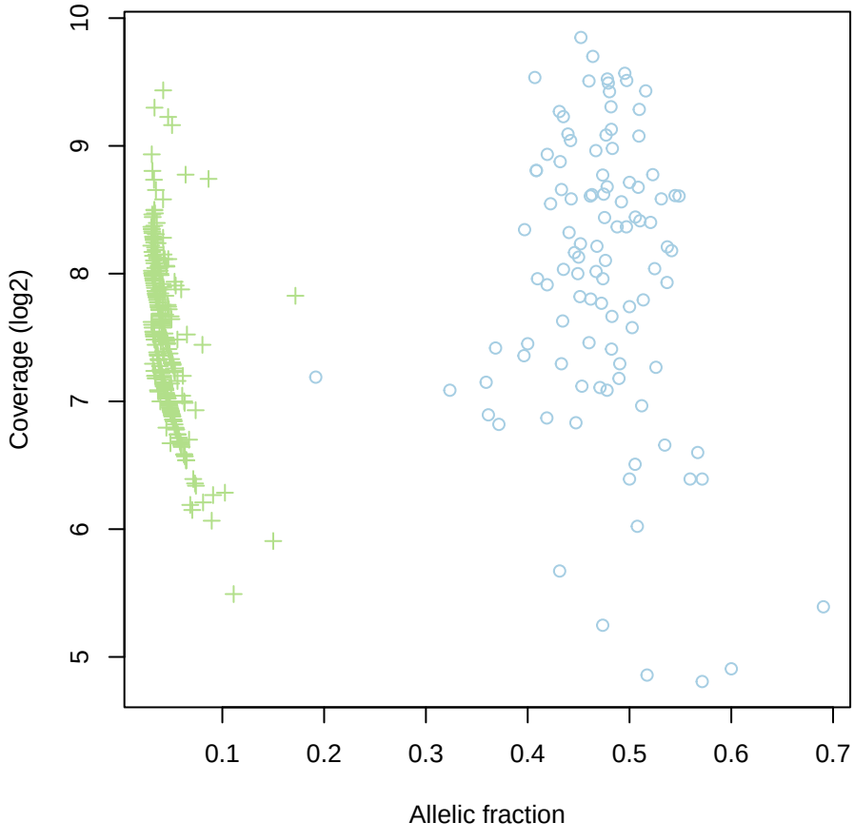

Purity: 0.55 Tumor ploidy: 4.187
2
3
4
5
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

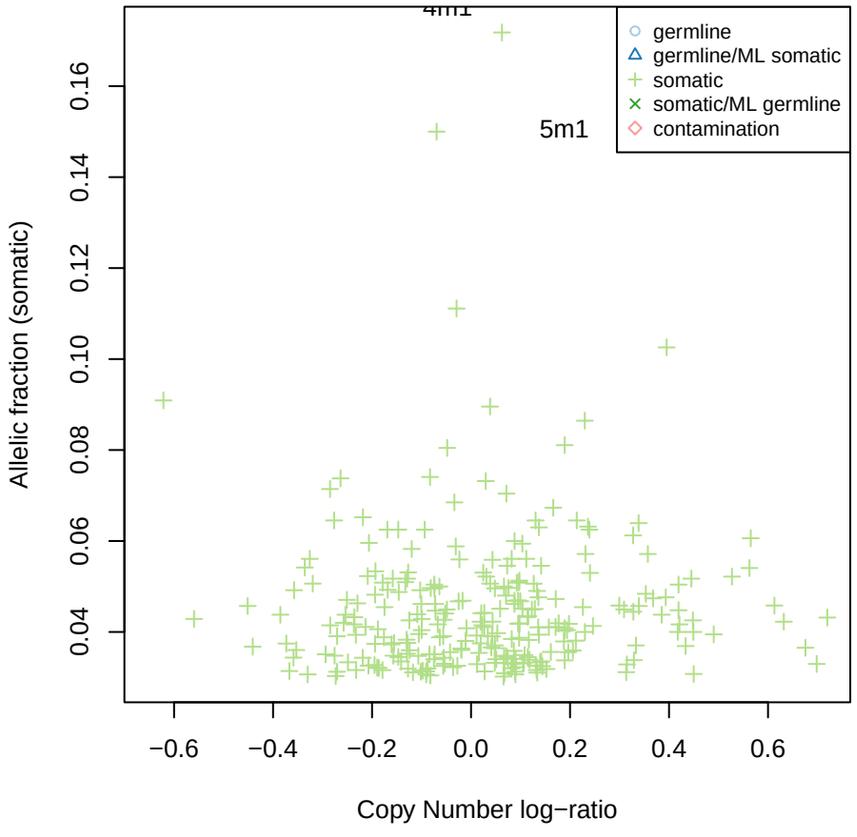

Purity: 0.55 Tumor ploidy: 4.187 SNV log−likelihood: −93.76 GoF: 69.2% Mean coverage: 250;235
1 2 3 4 5 7 8 9 10 11 12 14 15 16 17
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

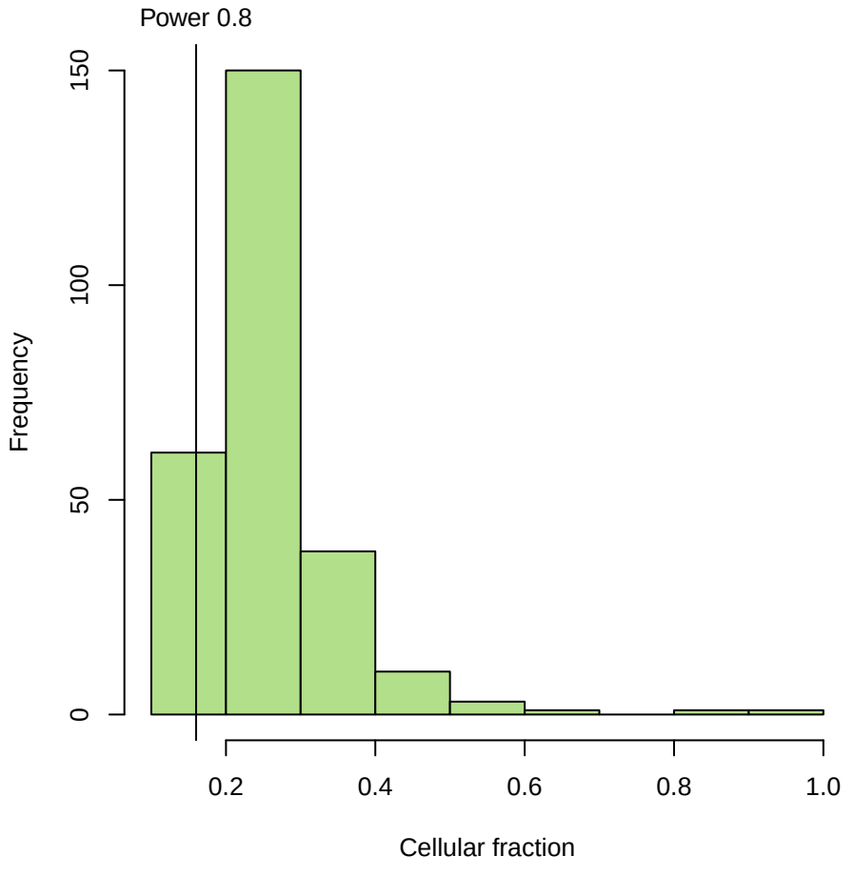

SCNA−fit log−likelihood: −5472.69
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6
0 20 40 60 80 100
SNV Index

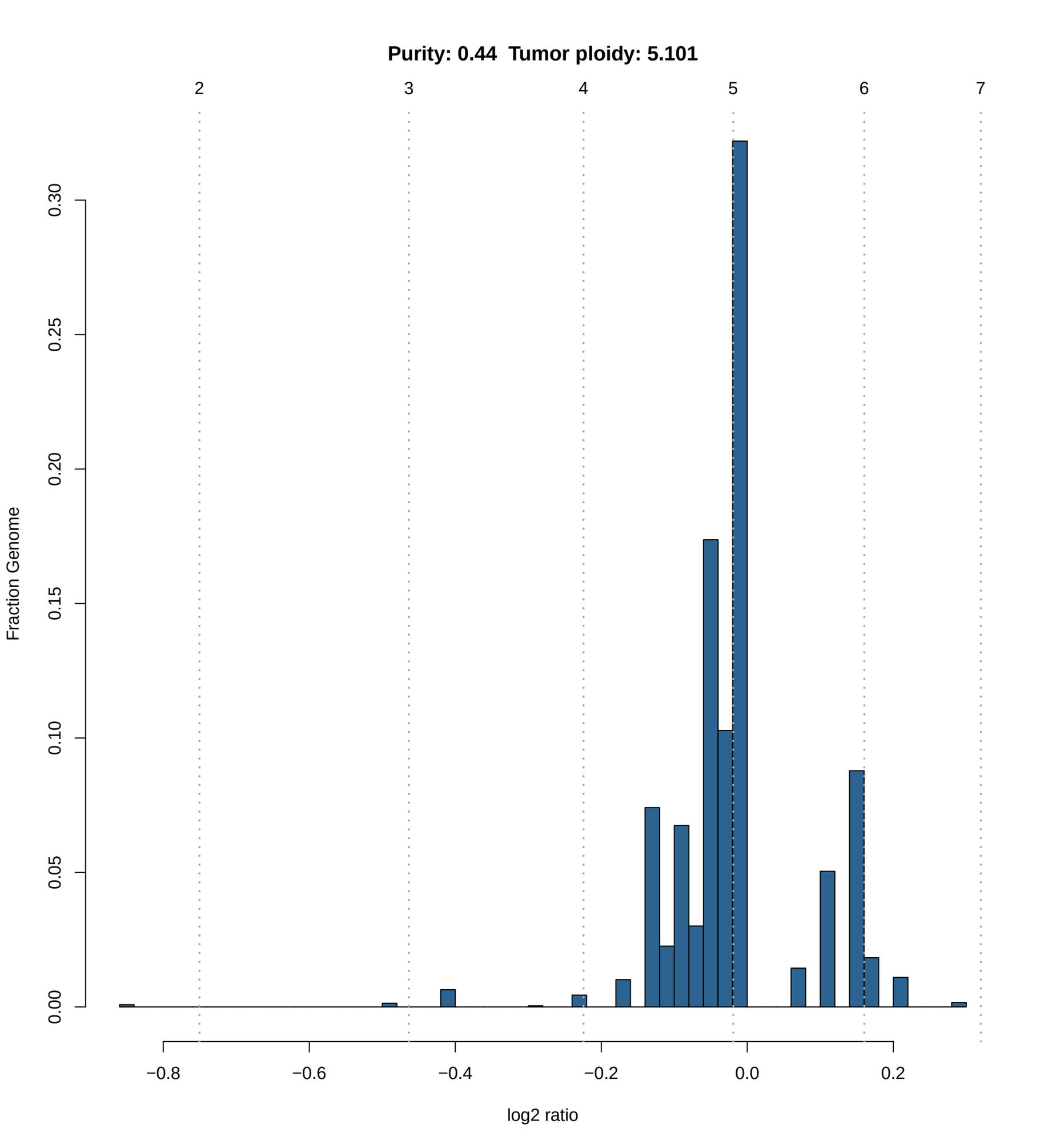

Maximum Likelihood Copy Number
0 1 2 3 4 5
0 20 40 60 80 100
SNV Index

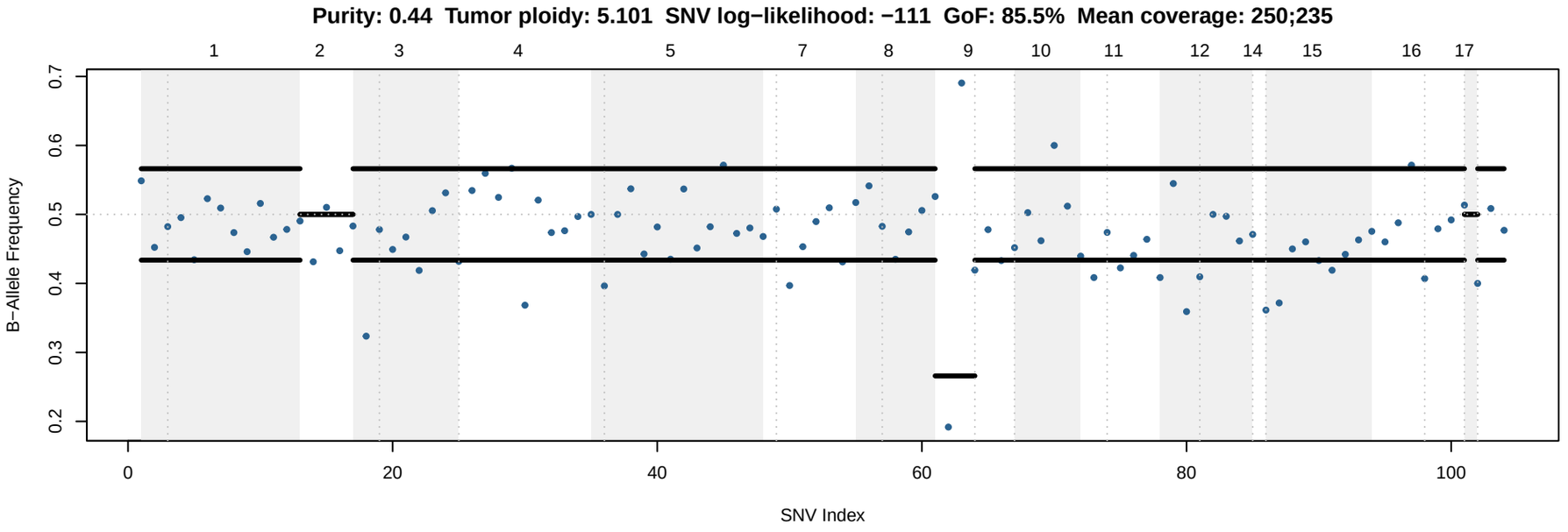

Allelic fraction (germline)
Copy Number log−ratio
5m3
4m2
5m1

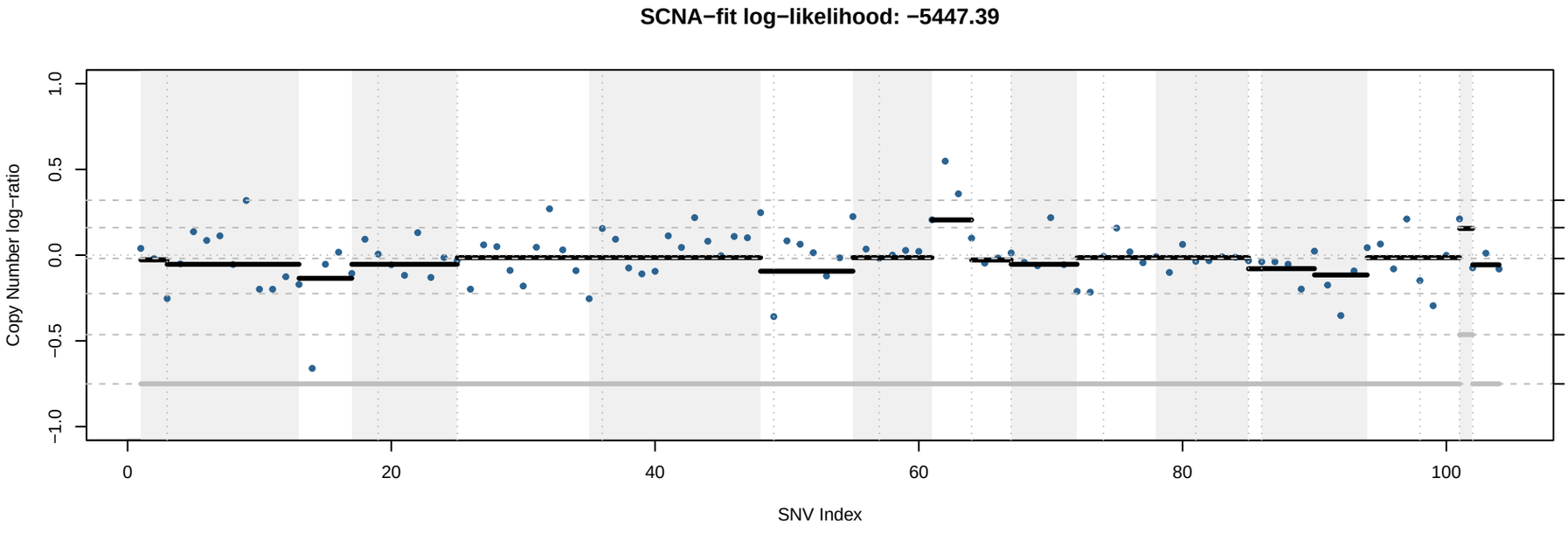

Coverage (log2)
Allelic fraction

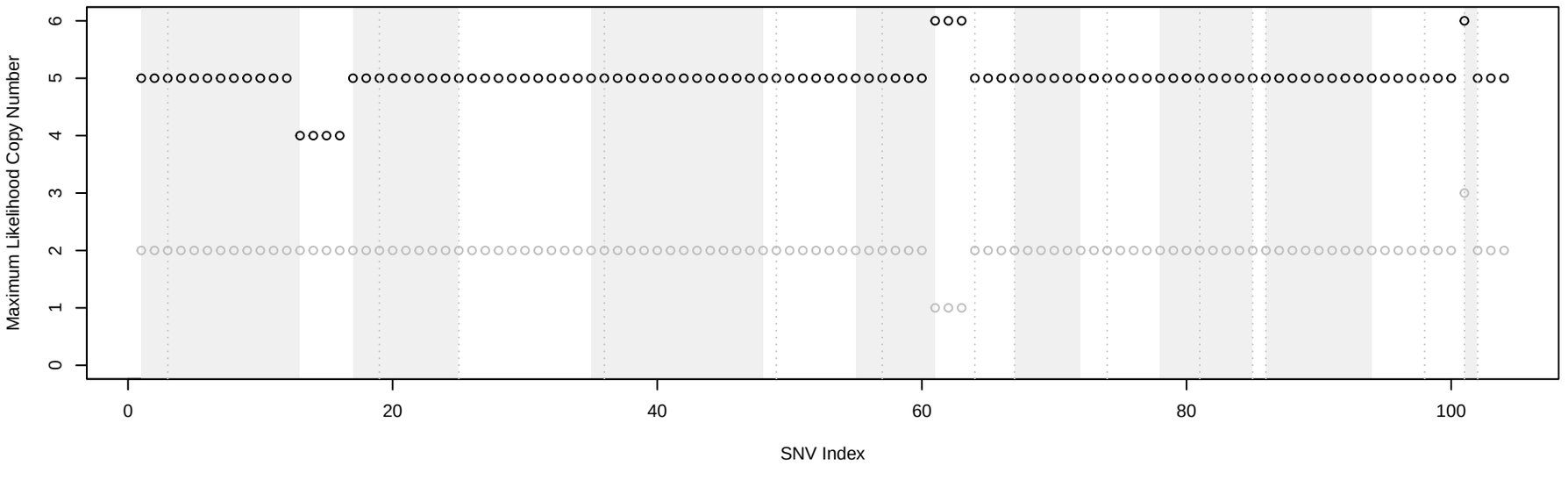

Allelic fraction (somatic)
Copy Number log−ratio
5m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

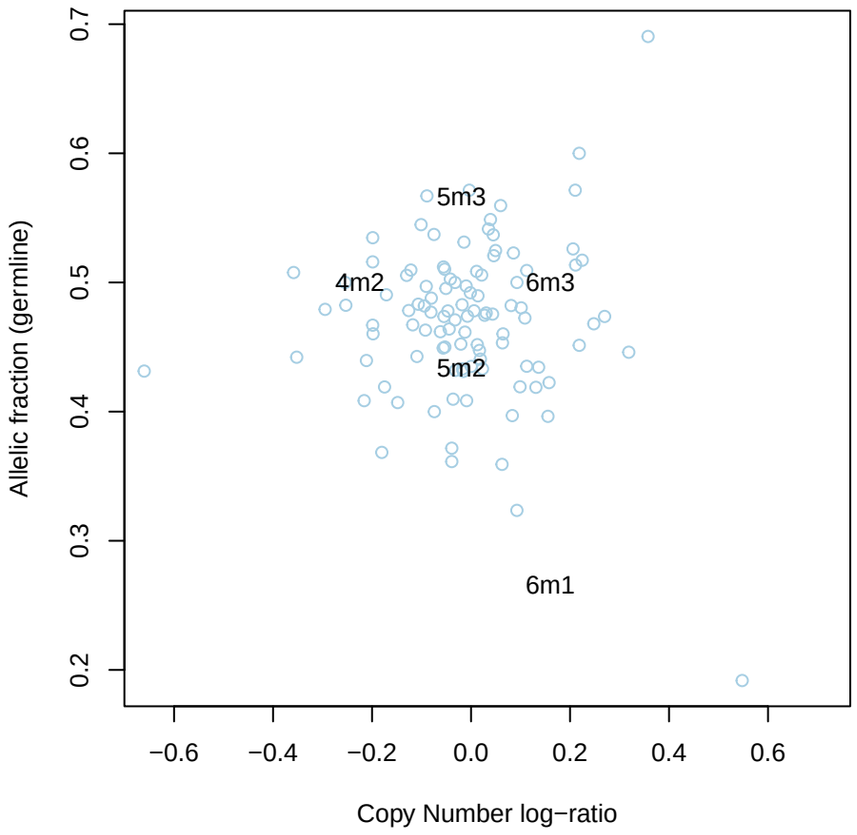

Power 0.8
Frequency
Cellular fraction

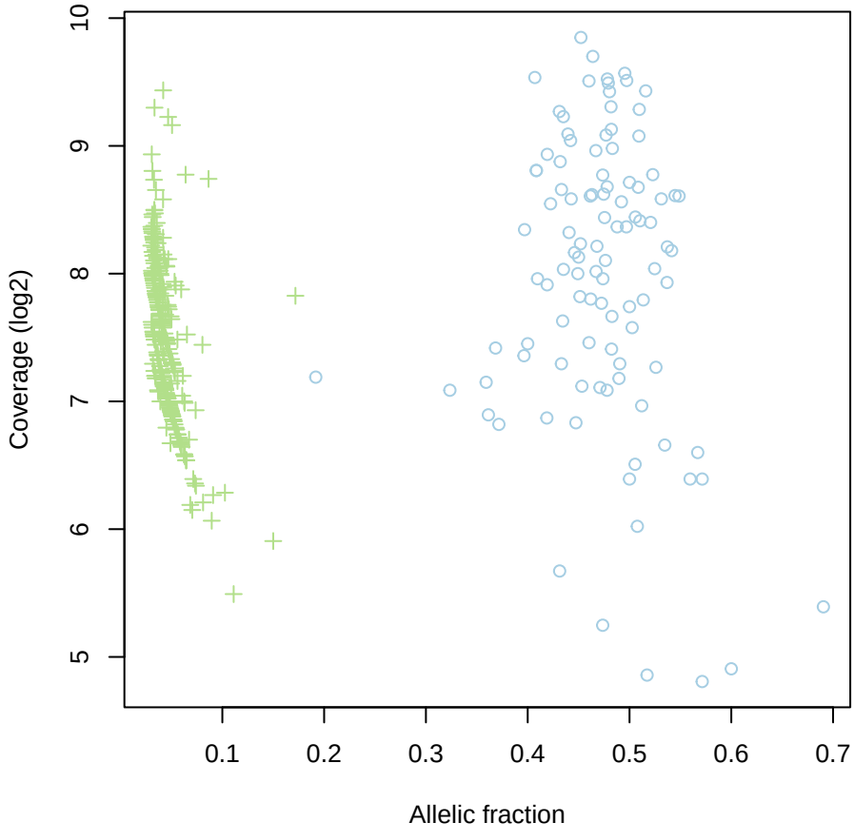

Purity: 0.44 Tumor ploidy: 5.101
2
3
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

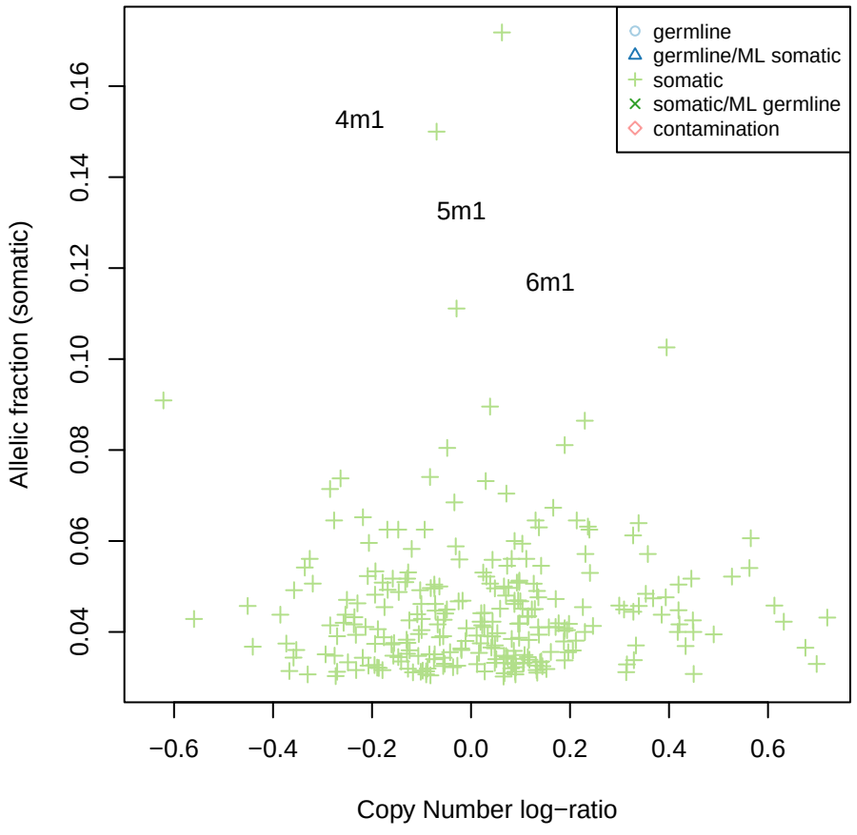

Purity: 0.44 Tumor ploidy: 5.101 SNV log−likelihood: −111 GoF: 85.5% Mean coverage: 250;235
1 2 3 4 5 7 8 9 10 11 12 14 15 16 17
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

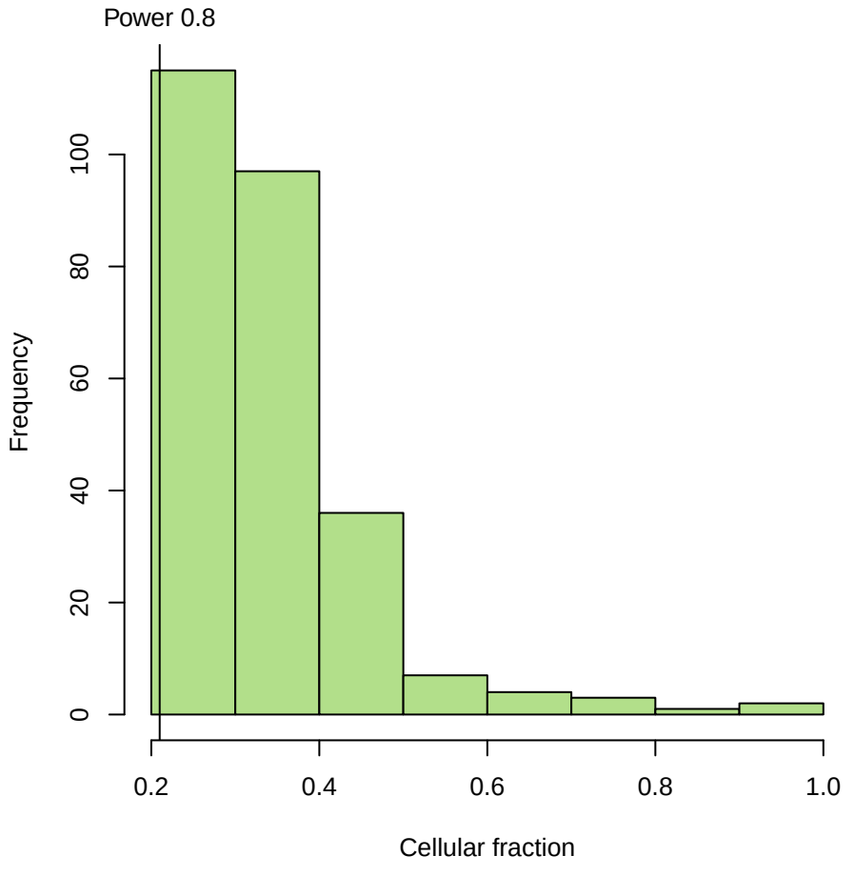

SCNA−fit log−likelihood: −5447.39
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

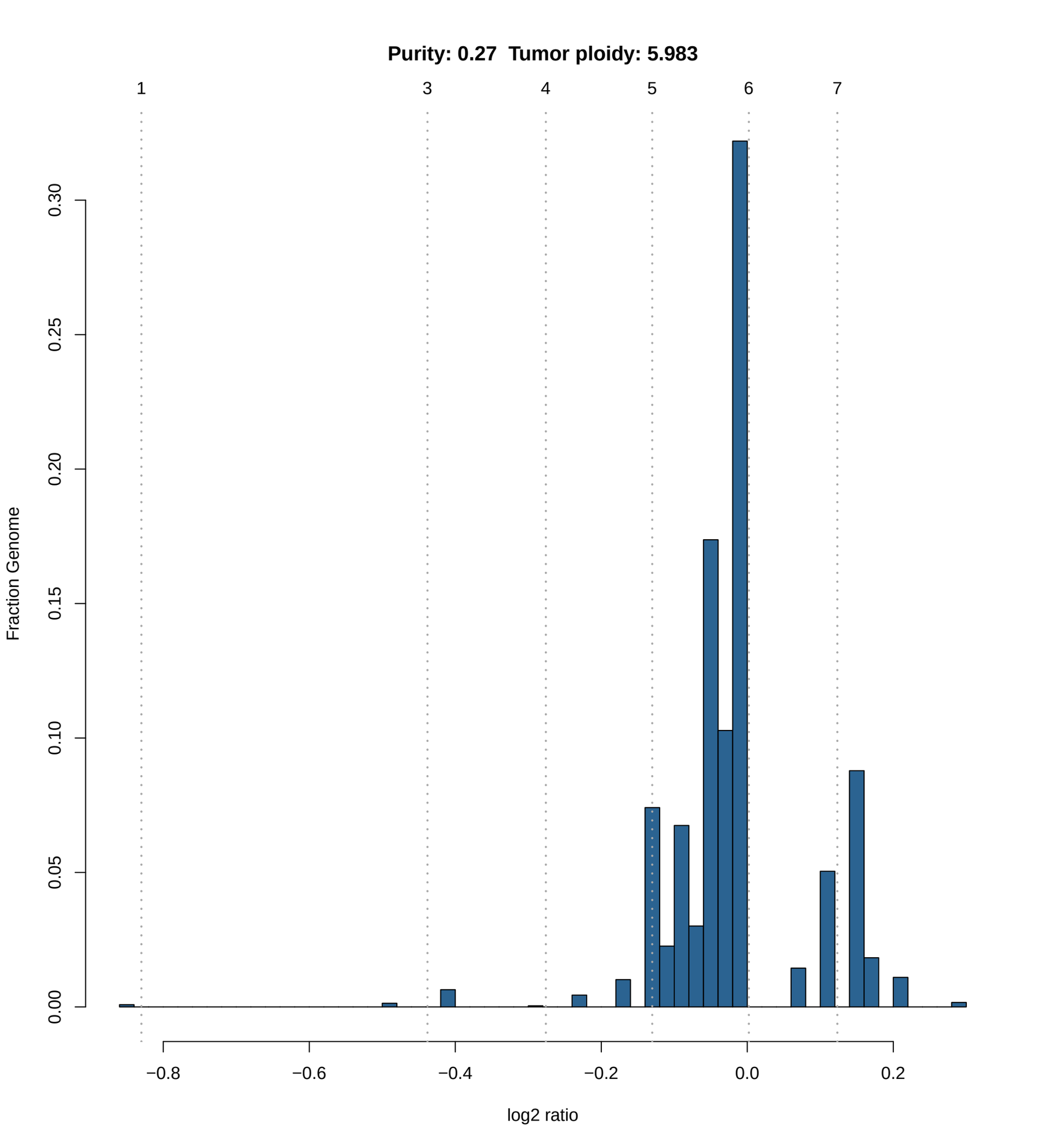

Maximum Likelihood Copy Number
0 1 2 3 4 5 6
0 20 40 60 80 100
SNV Index

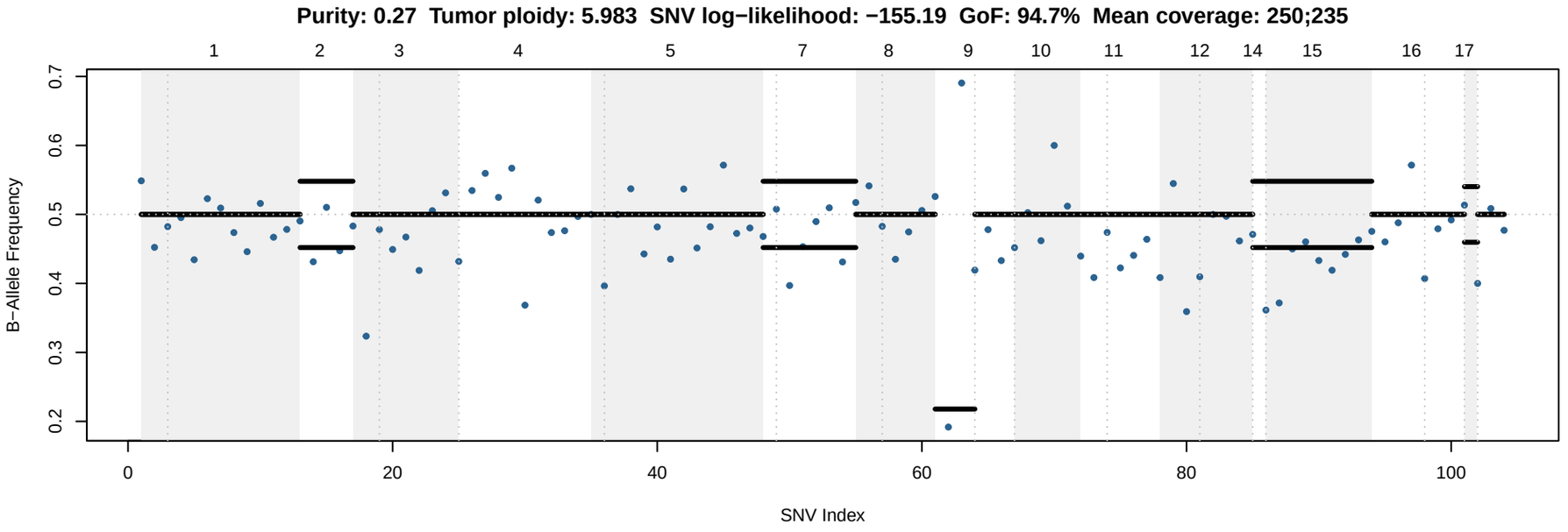

Allelic fraction (germline)
Copy Number log−ratio
5m3
4m2
6m3
5m2
6m1

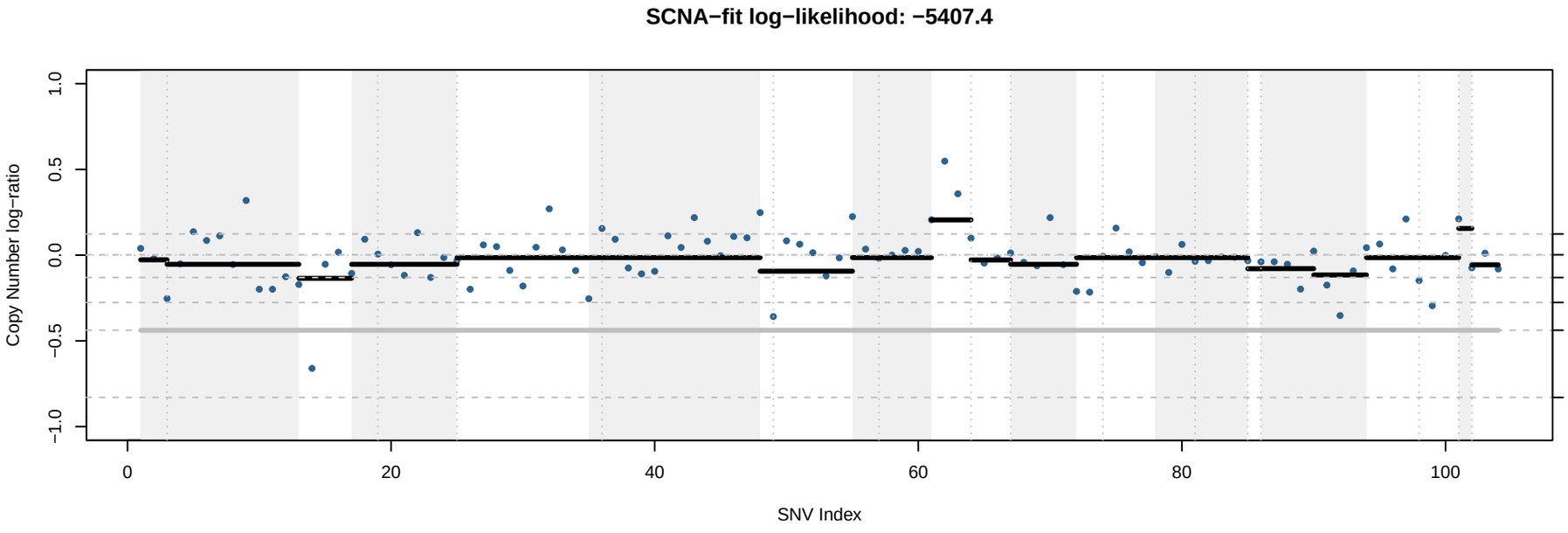

Coverage (log2)
Allelic fraction

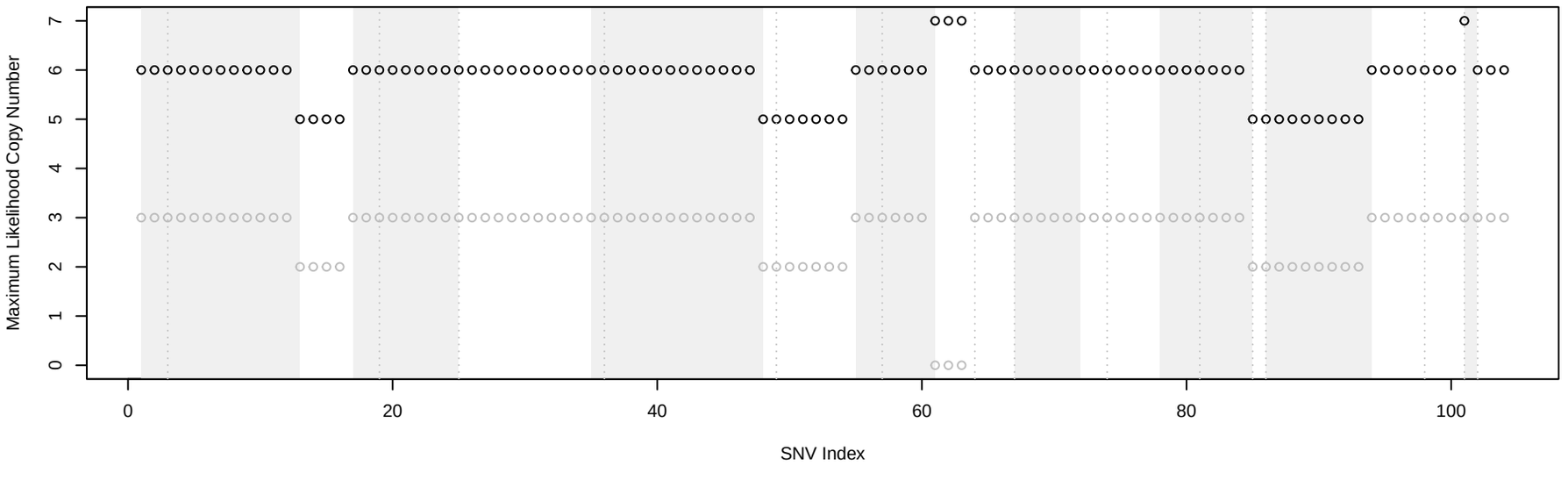

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
4m1
5m1
6m1

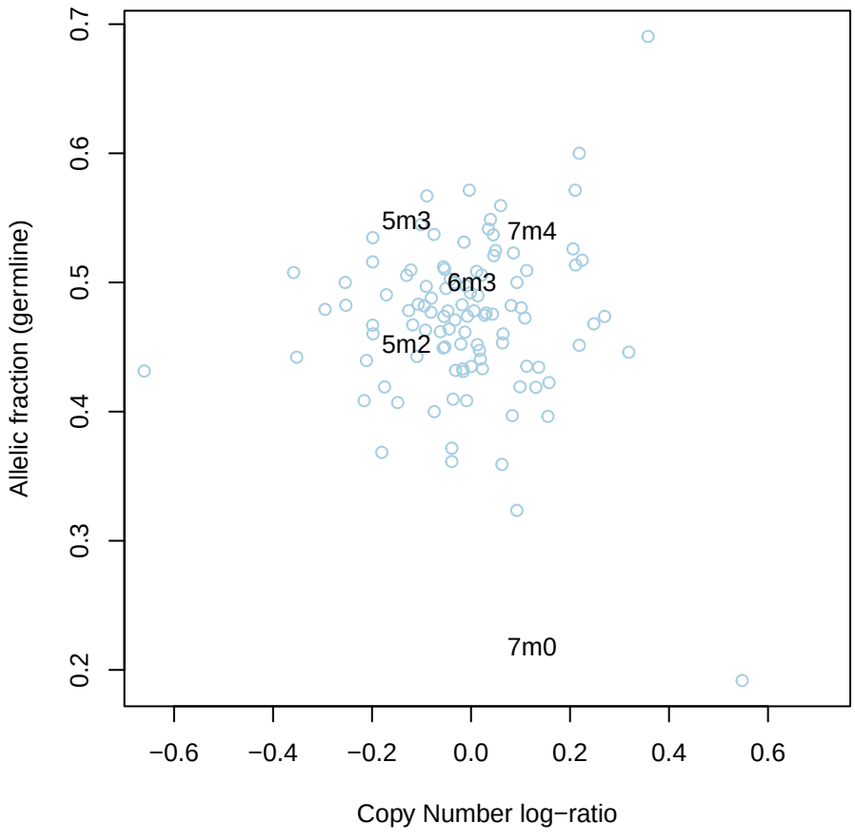

Power 0.8
Frequency
Cellular fraction

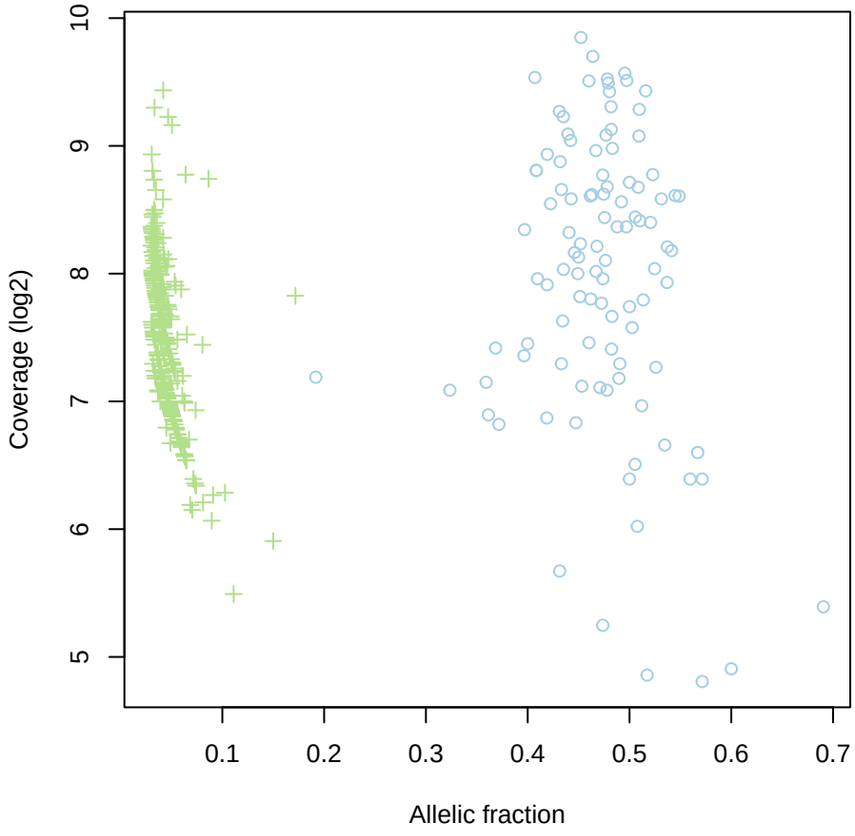

Purity: 0.27 Tumor ploidy: 5.983
1
3
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

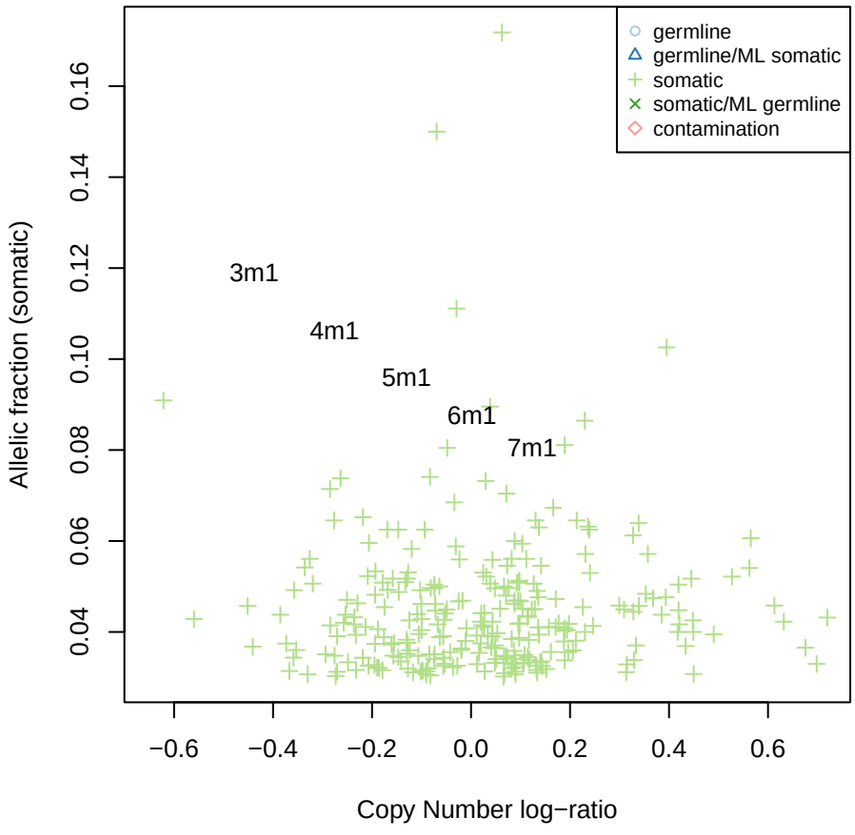

Purity: 0.27 Tumor ploidy: 5.983 SNV log−likelihood: −155.19 GoF: 94.7% Mean coverage: 250;235
1 2 3 4 5 7 8 9 10 11 12 14 15 16 17
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

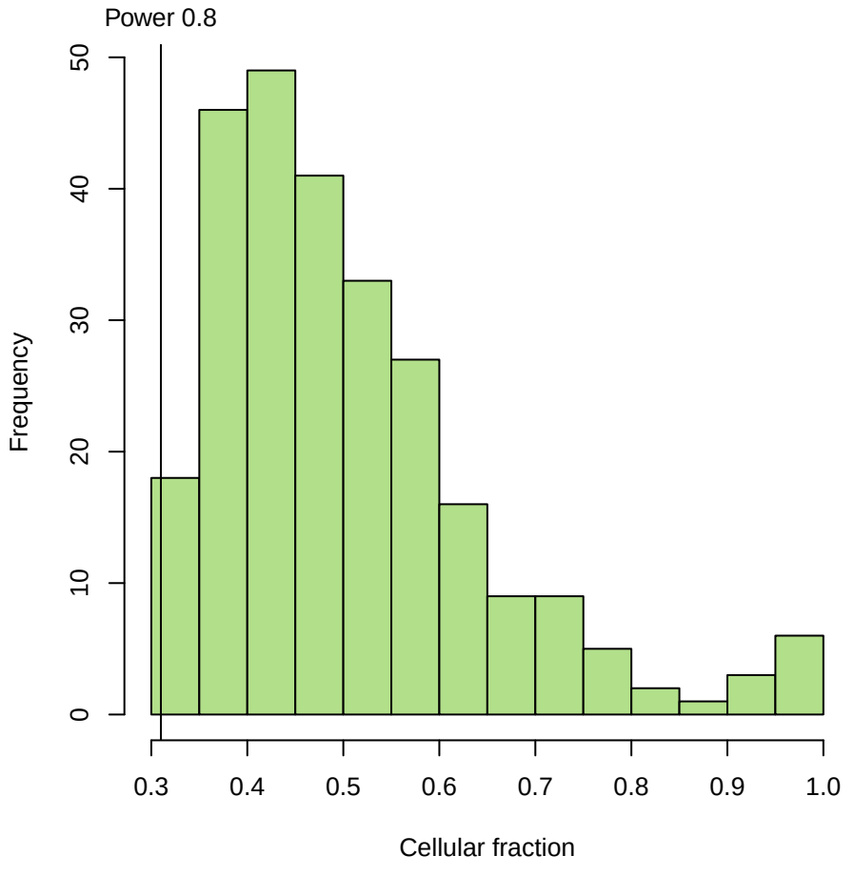

SCNA−fit log−likelihood: −5407.4
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 3 4 5 7
0 20 40 60 80 100
SNV Index

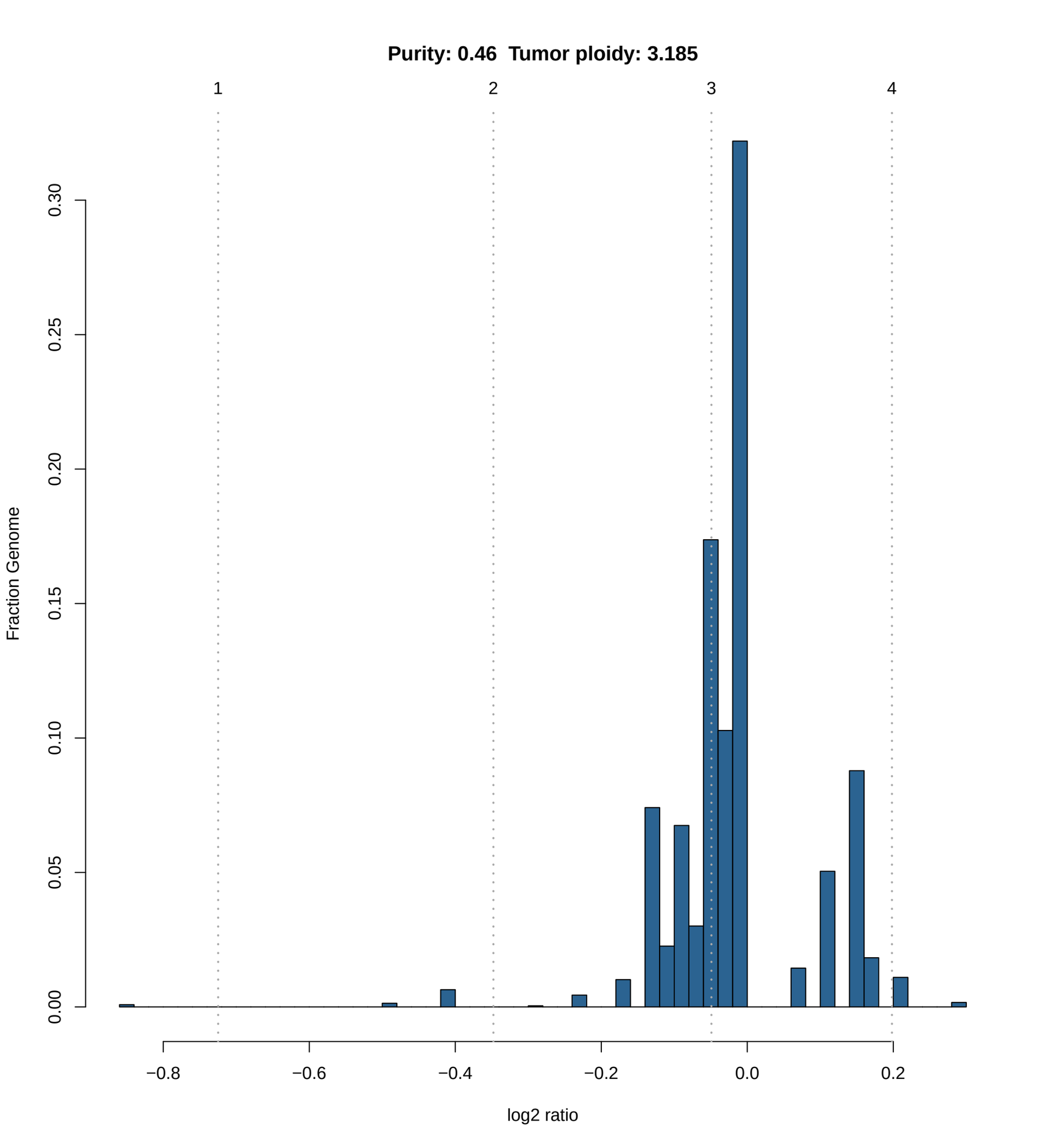

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

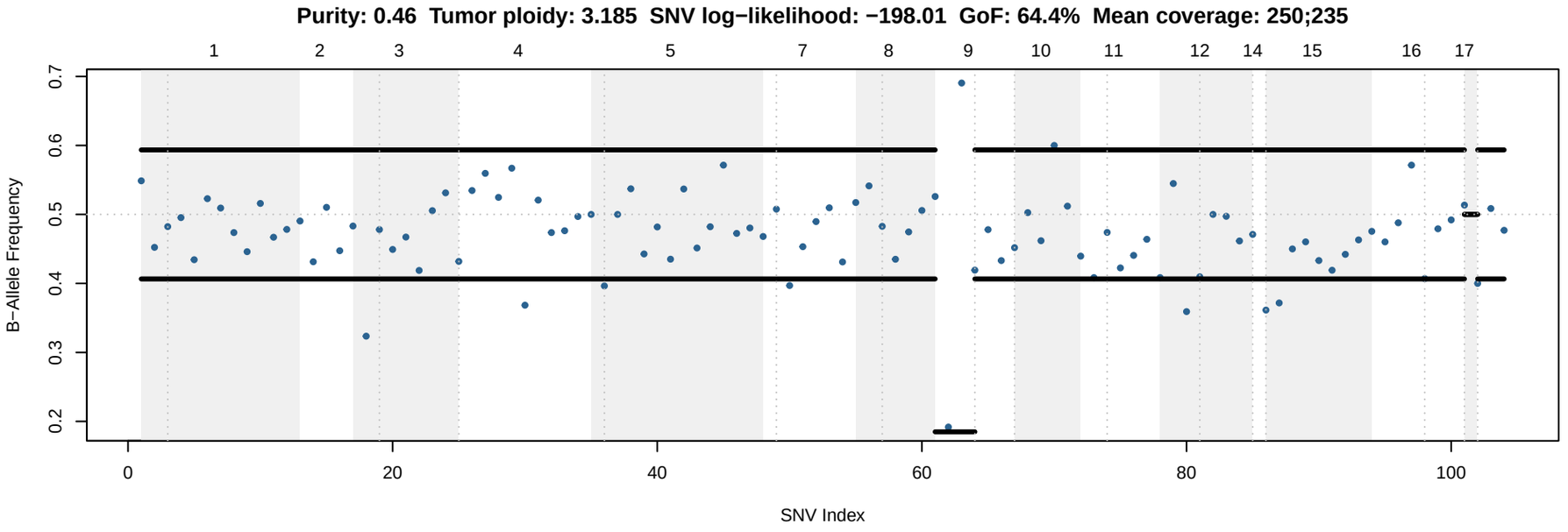

Allelic fraction (germline)
Copy Number log−ratio
5m3
7m4
6m3
5m2
7m0

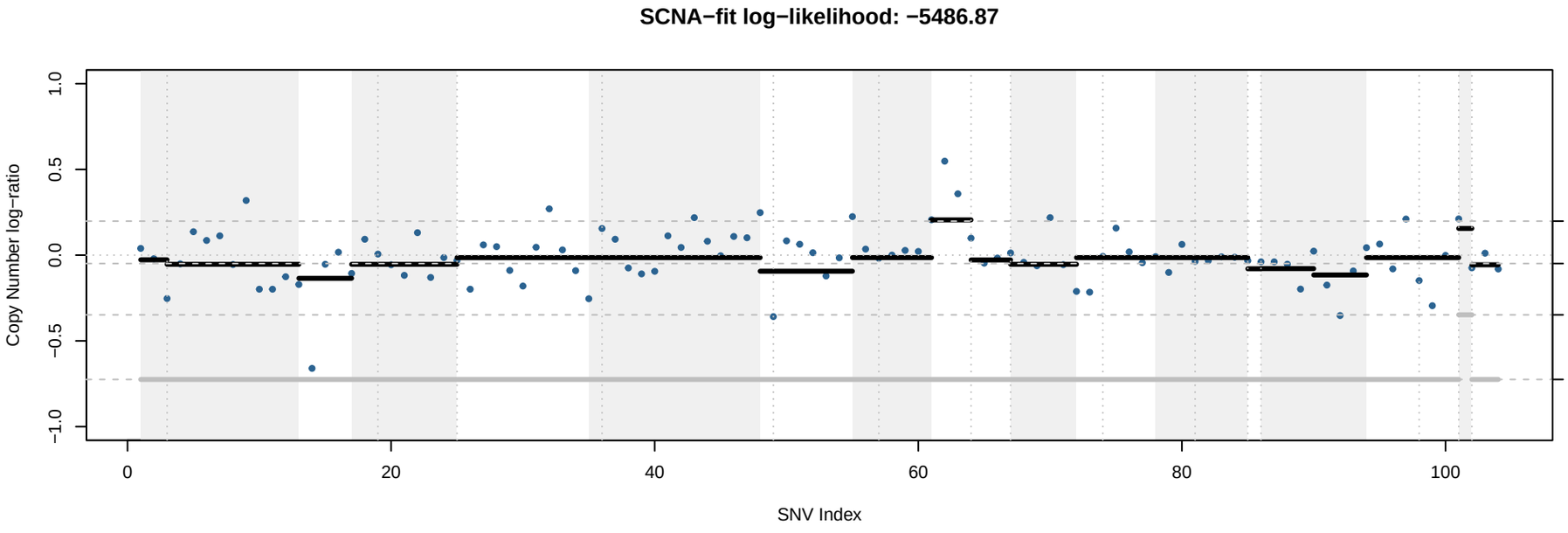

Coverage (log2)
Allelic fraction

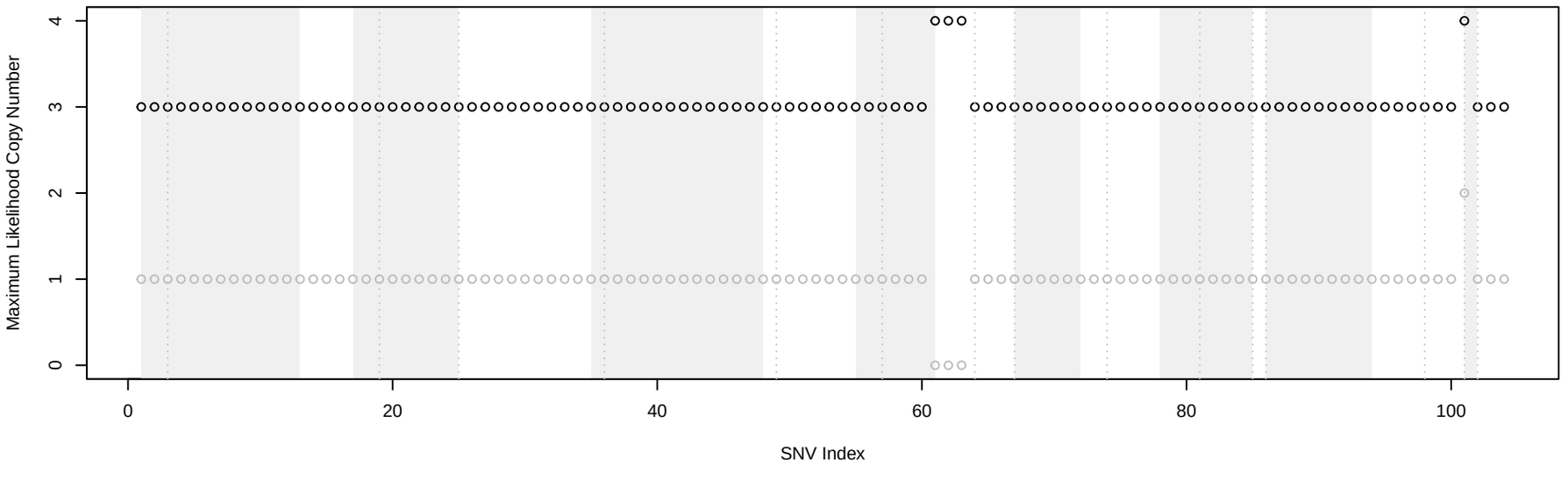

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
3m1
4m1
5m1
6m1
7m1

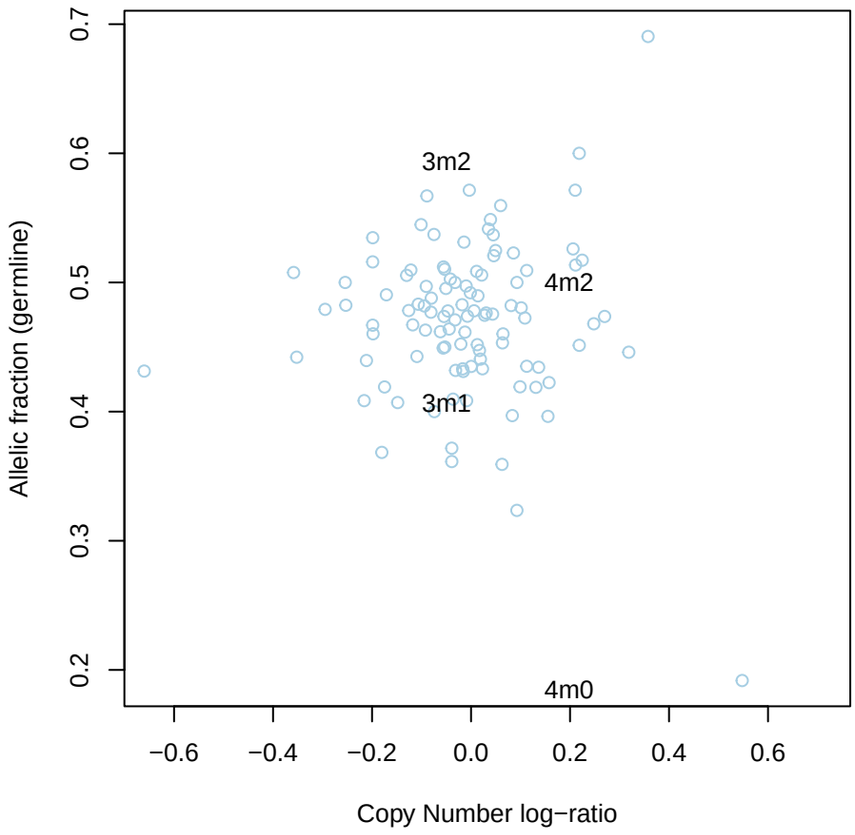

Power 0.8
Frequency
Cellular fraction

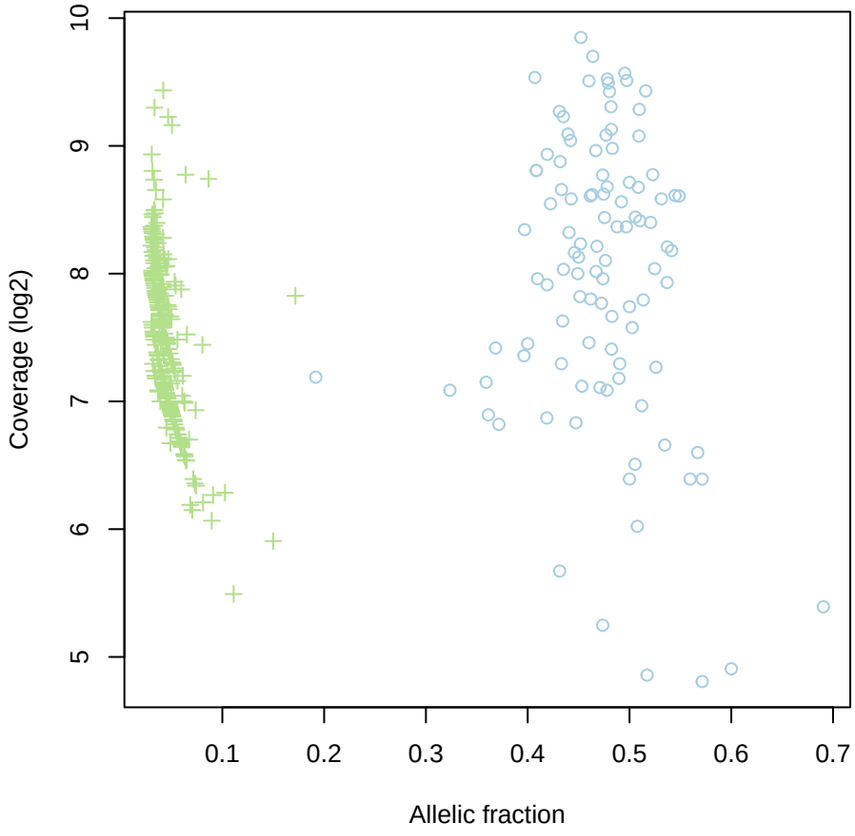

Purity: 0.46 Tumor ploidy: 3.185
1
2
3
4
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

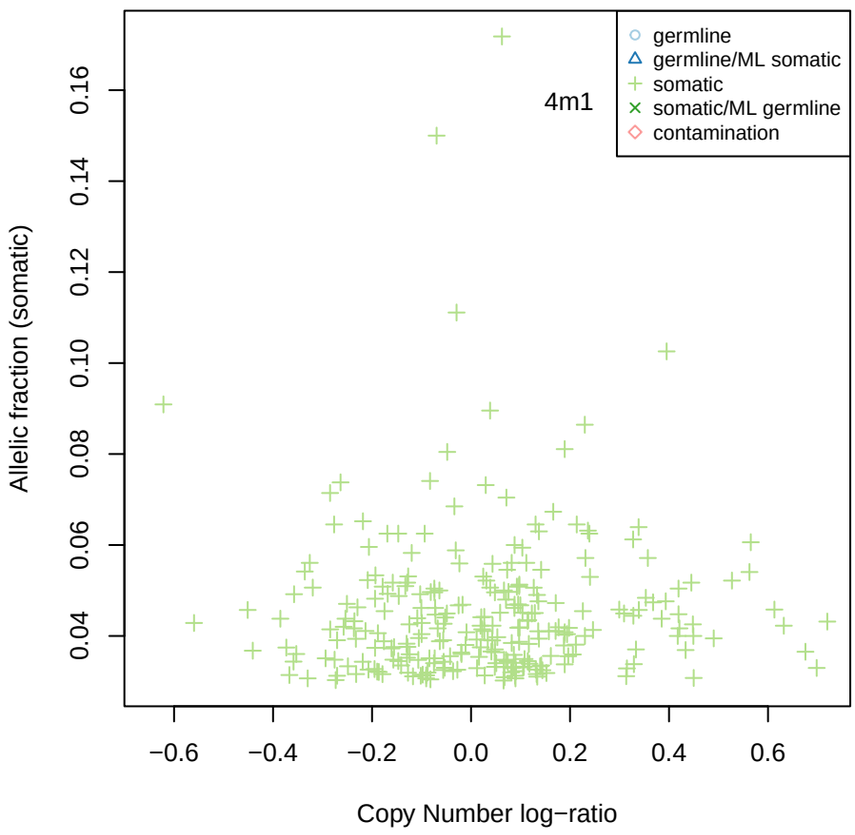

Purity: 0.46 Tumor ploidy: 3.185 SNV log−likelihood: −198.01 GoF: 64.4% Mean coverage: 250;235
1 2 3 4 5 7 8 9 10 11 12 14 15 16 17
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

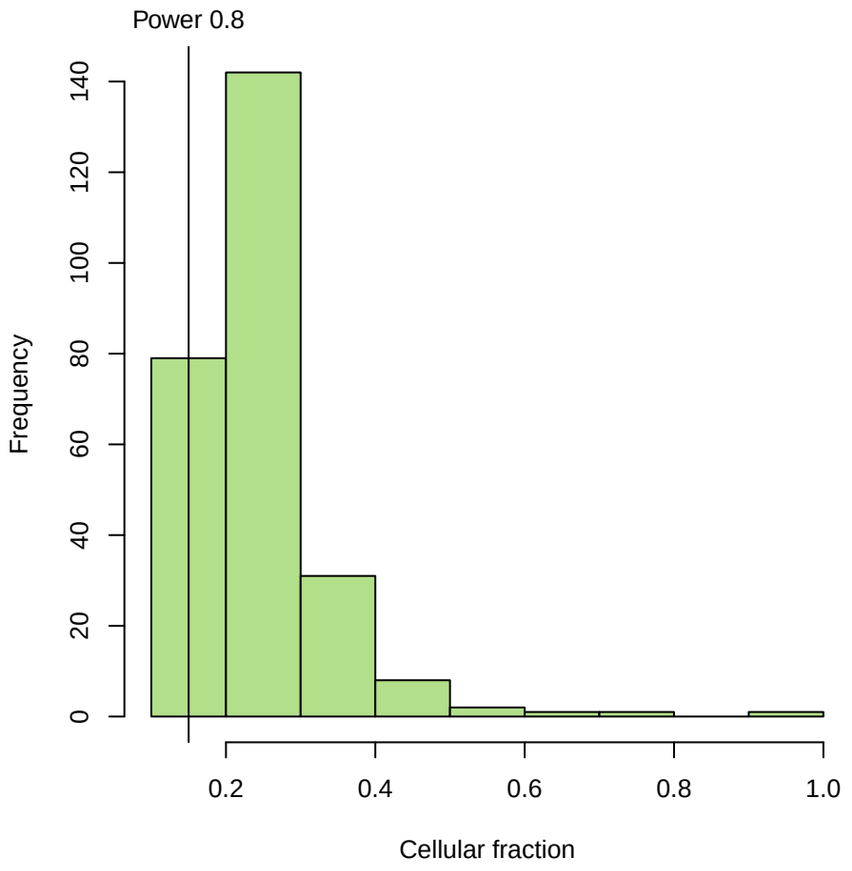

SCNA−fit log−likelihood: −5486.87
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4
0 20 40 60 80 100
SNV Index

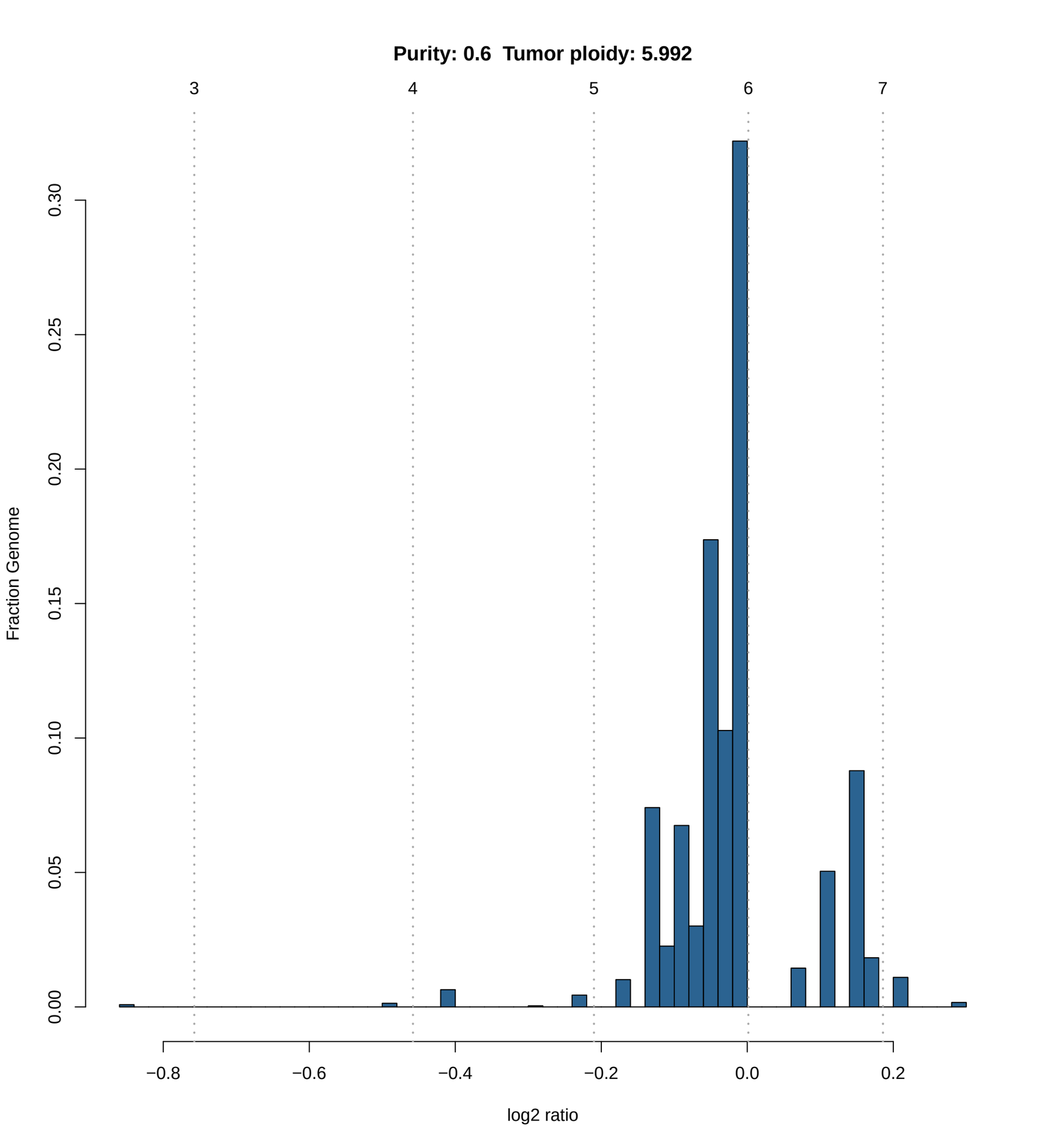

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100
SNV Index

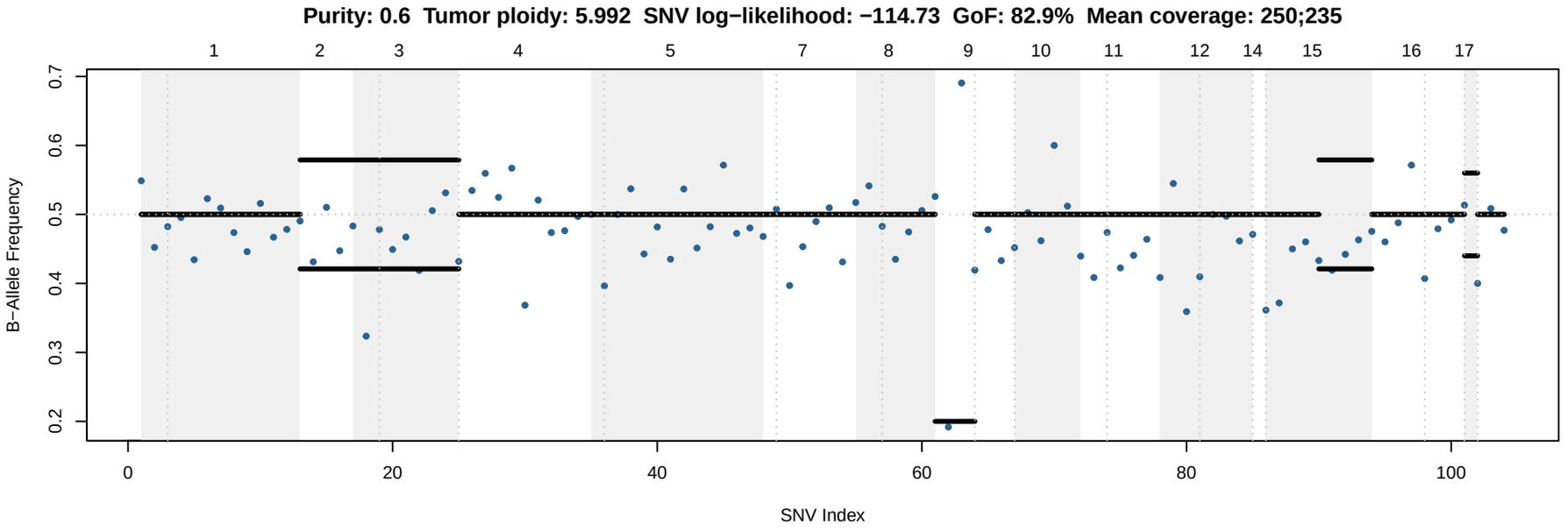

Allelic fraction (germline)
Copy Number log−ratio
3m2
4m2
3m1
4m0

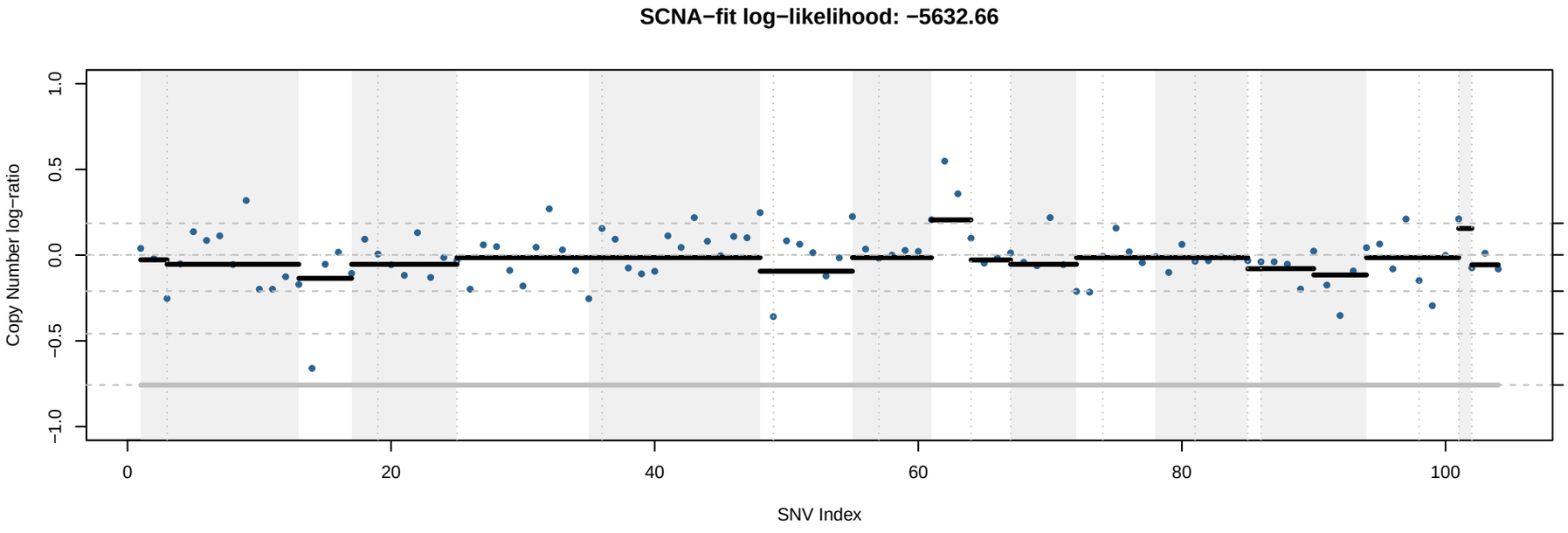

Coverage (log2)
Allelic fraction

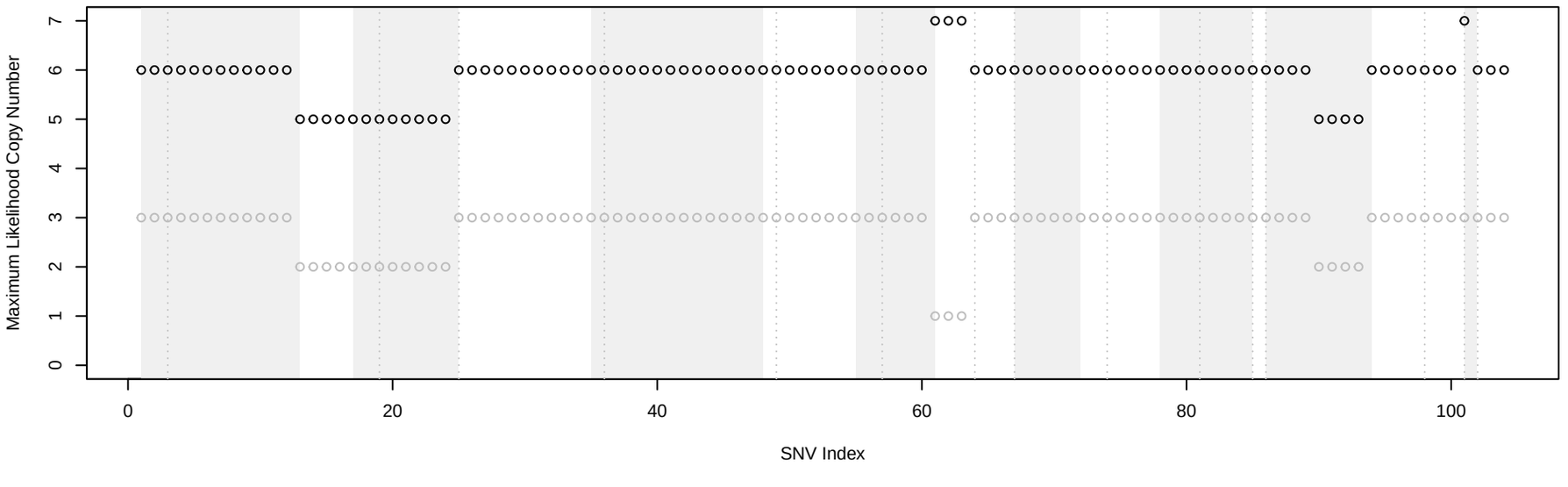

Allelic fraction (somatic)
Copy Number log−ratio
4m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

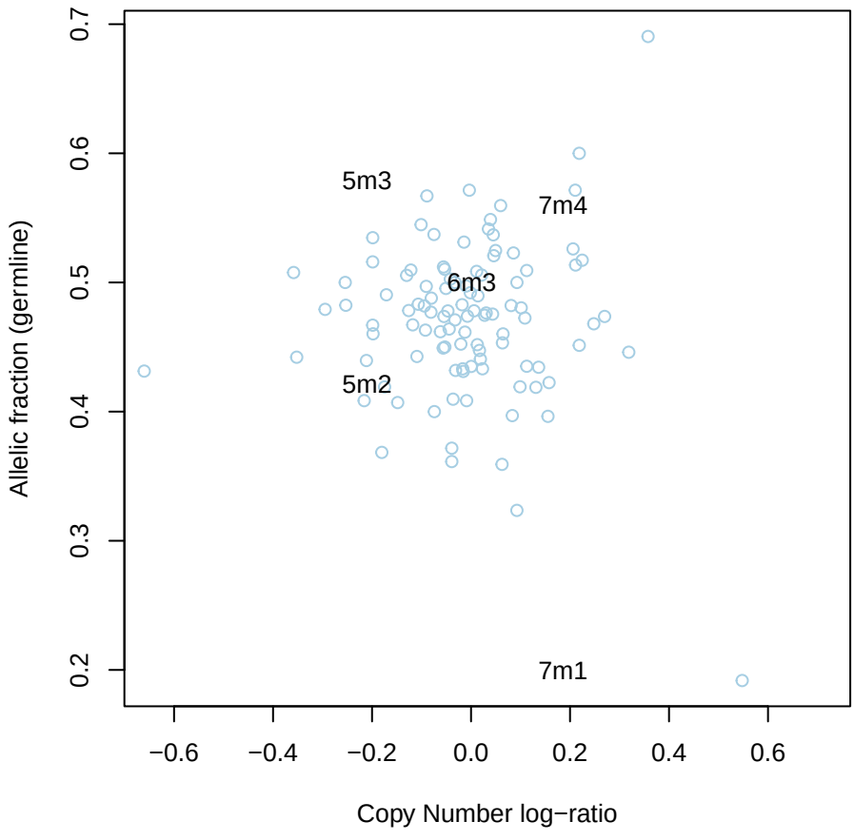

Power 0.8
Frequency
Cellular fraction

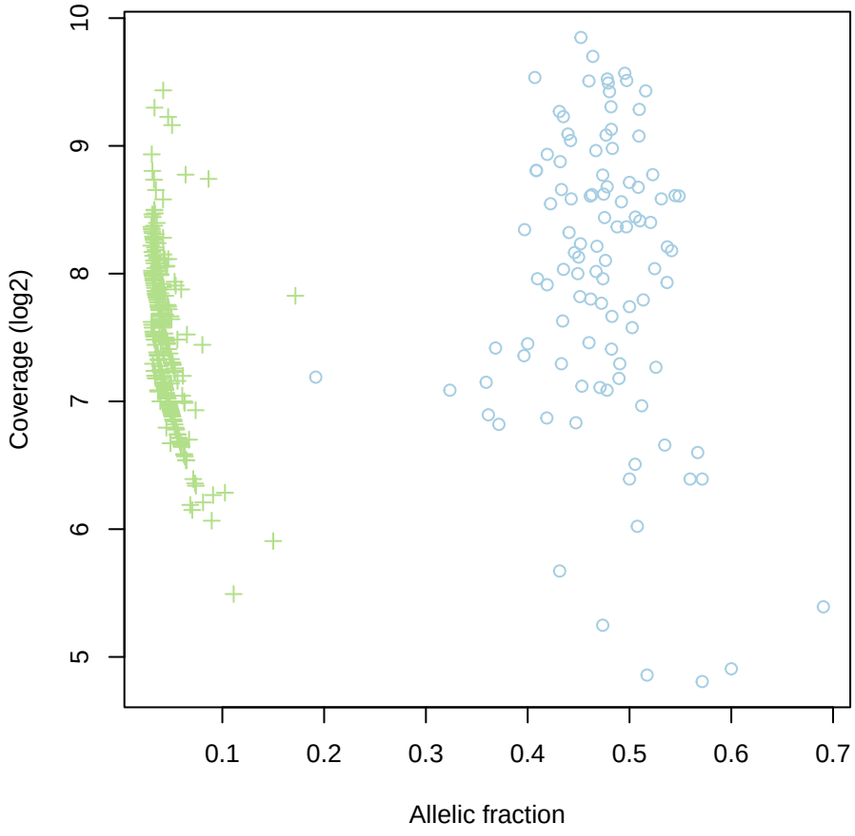

Purity: 0.6 Tumor ploidy: 5.992
3
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

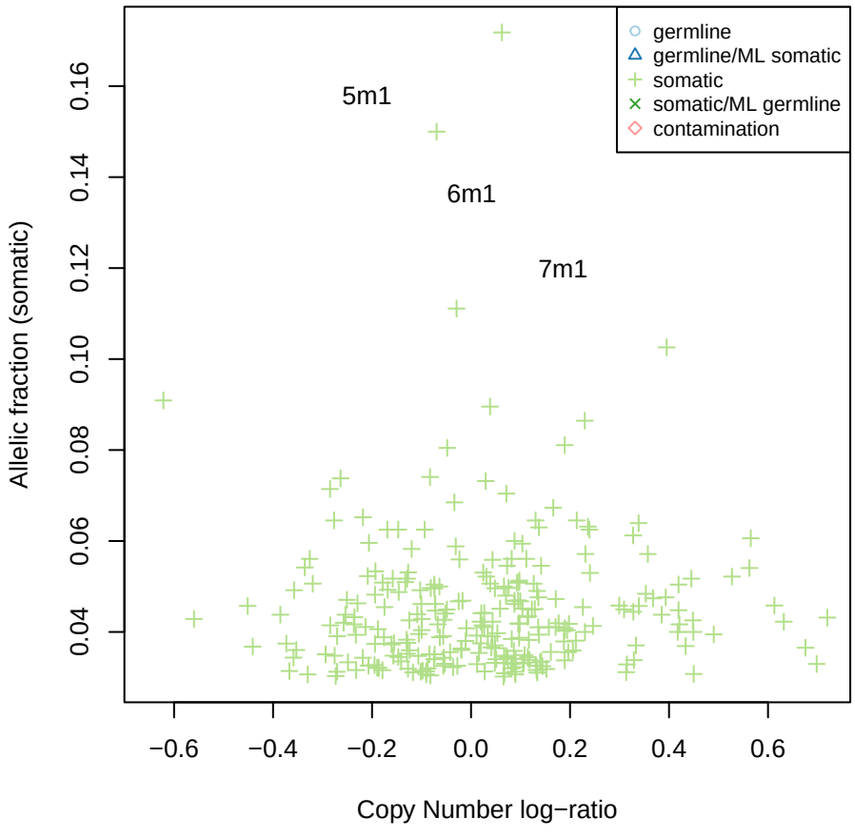

Purity: 0.6 Tumor ploidy: 5.992 SNV log−likelihood: −114.73 GoF: 82.9% Mean coverage: 250;235
1 2 3 4 5 7 8 9 10 11 12 14 15 16 17
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

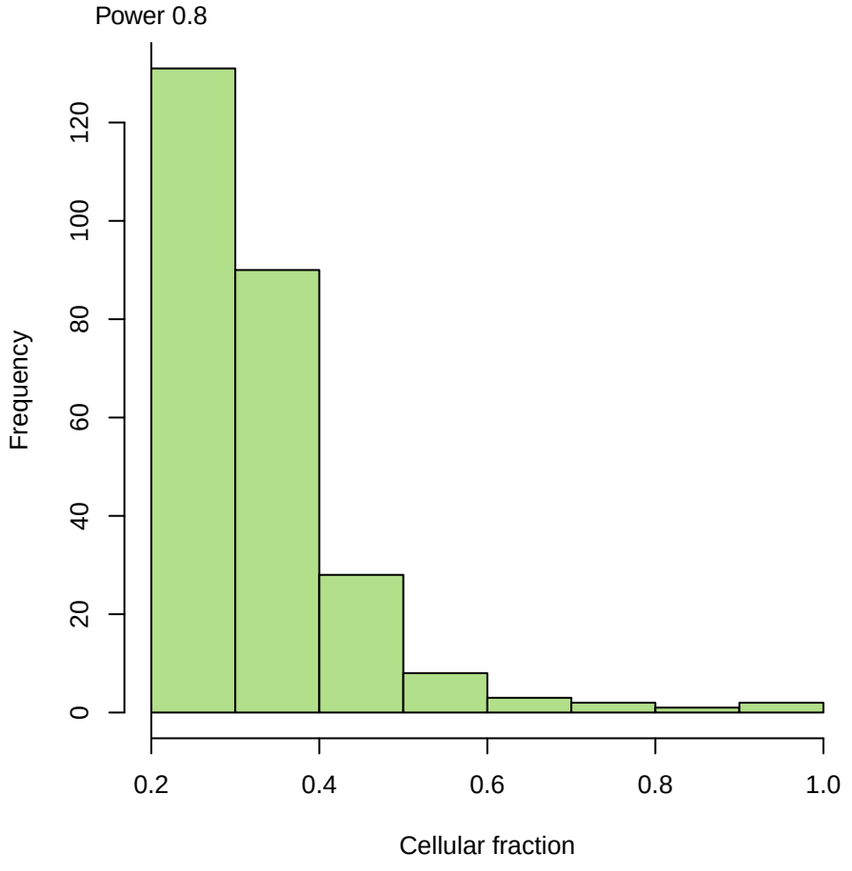

SCNA−fit log−likelihood: −5632.66
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 20 40 60 80 100
SNV Index

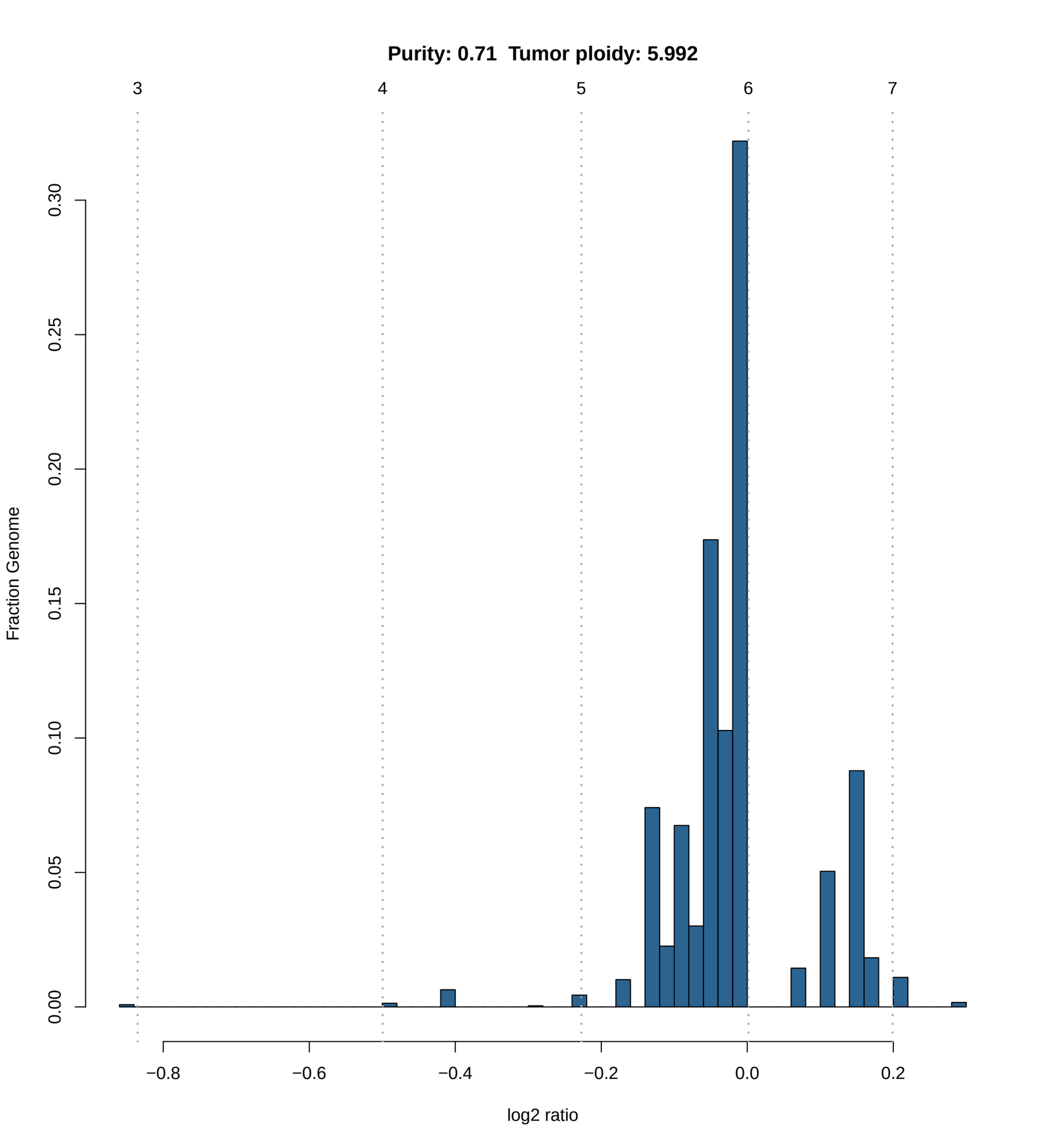

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

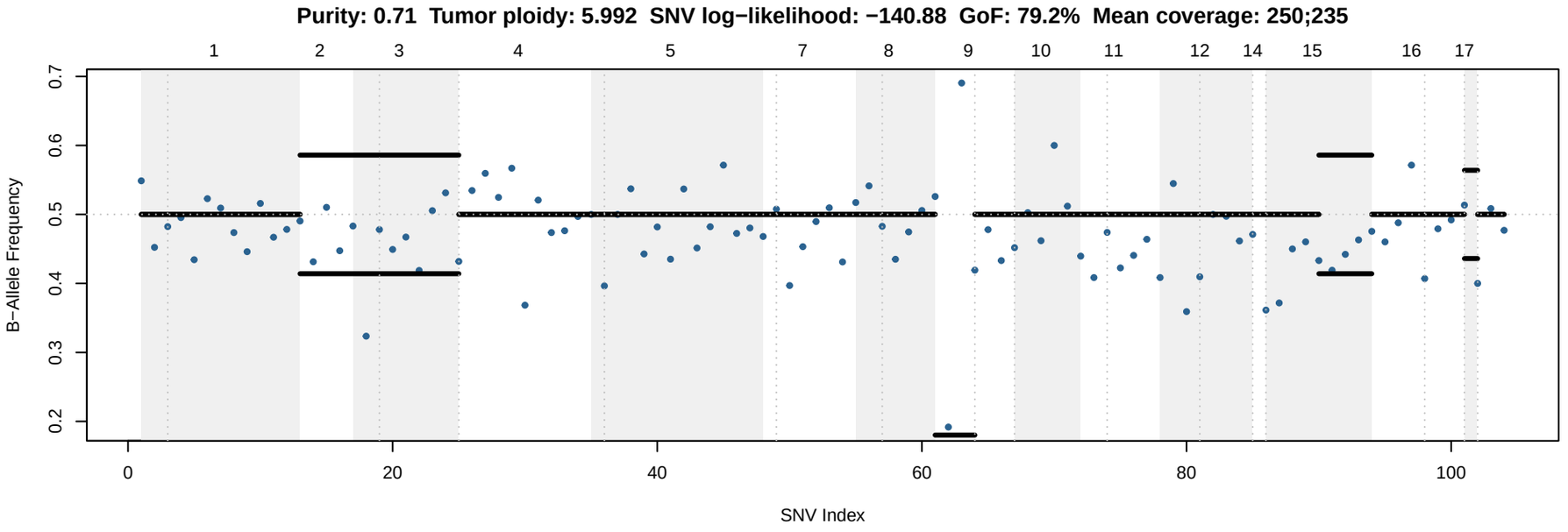

Allelic fraction (germline)
Copy Number log−ratio
5m3
7m4
6m3
5m2
7m1

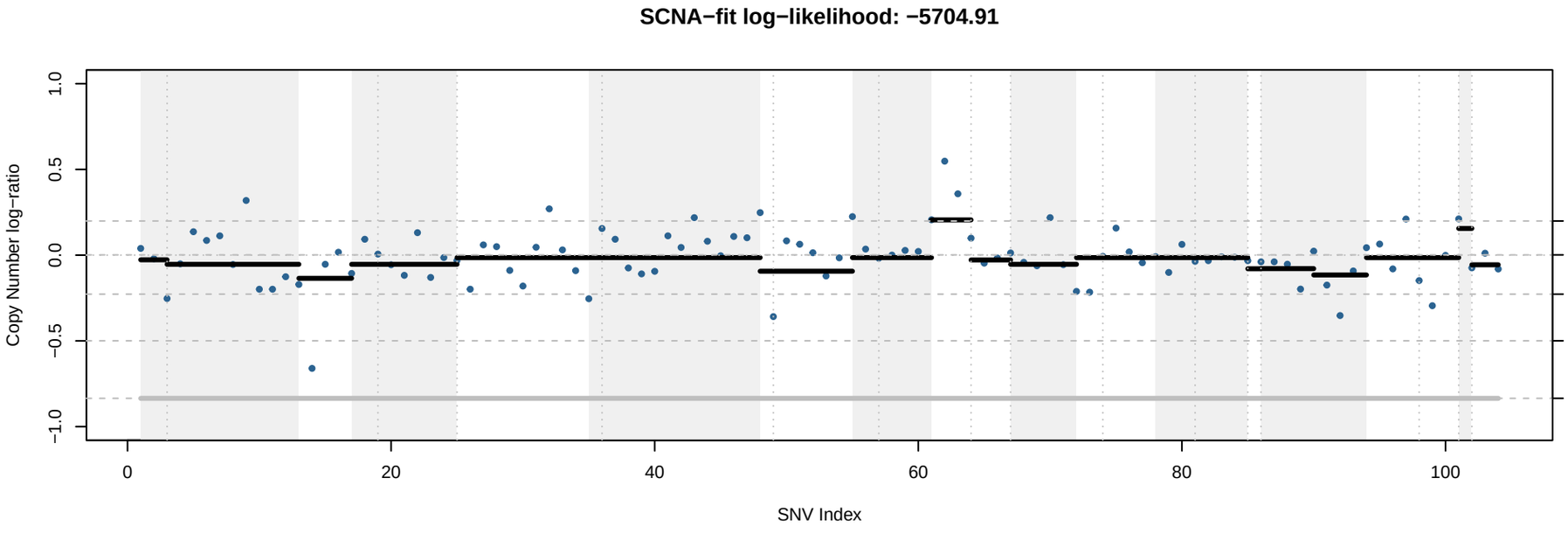

Coverage (log2)
Allelic fraction

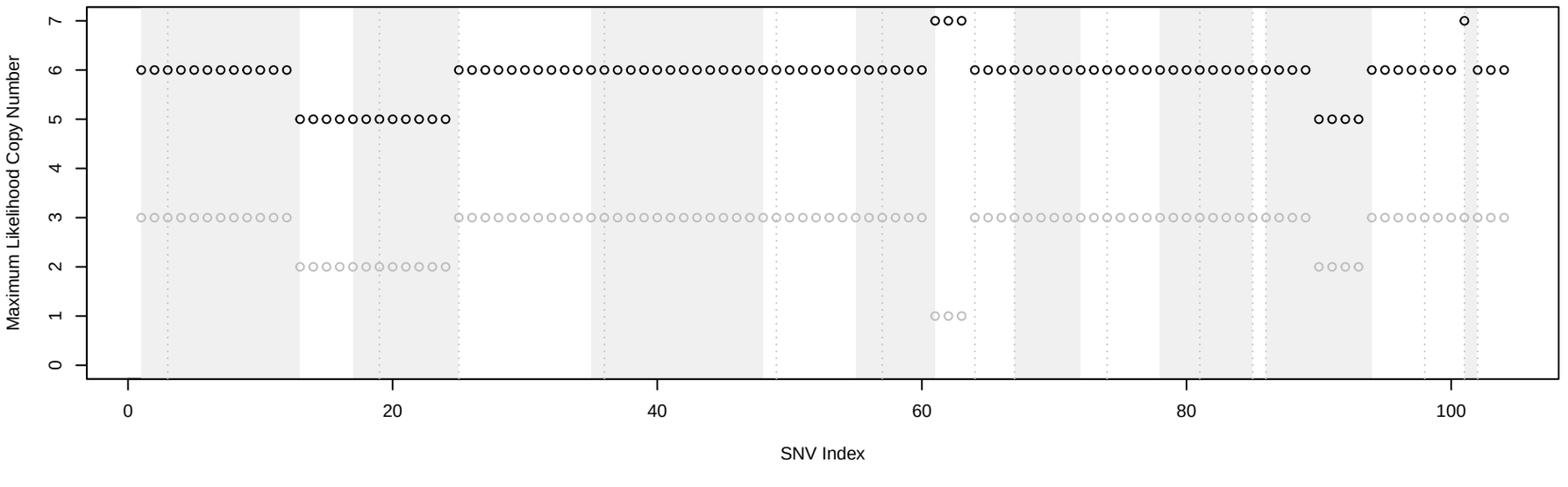

germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
Copy Number log−ratio
5m1
6m1
7m1

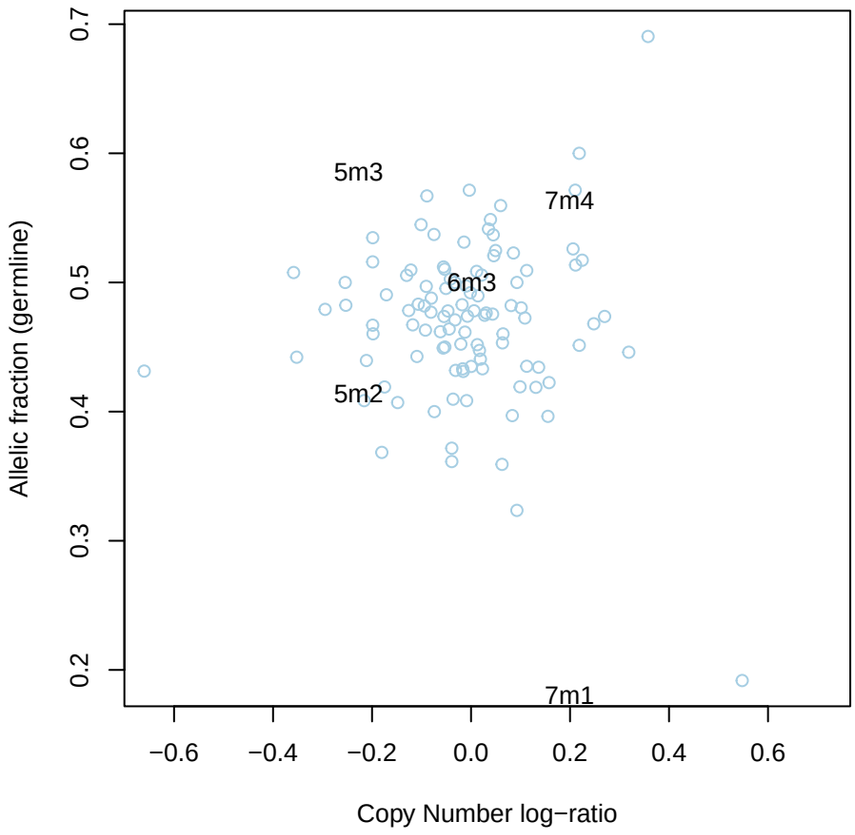

Power 0.8
Frequency
Cellular fraction

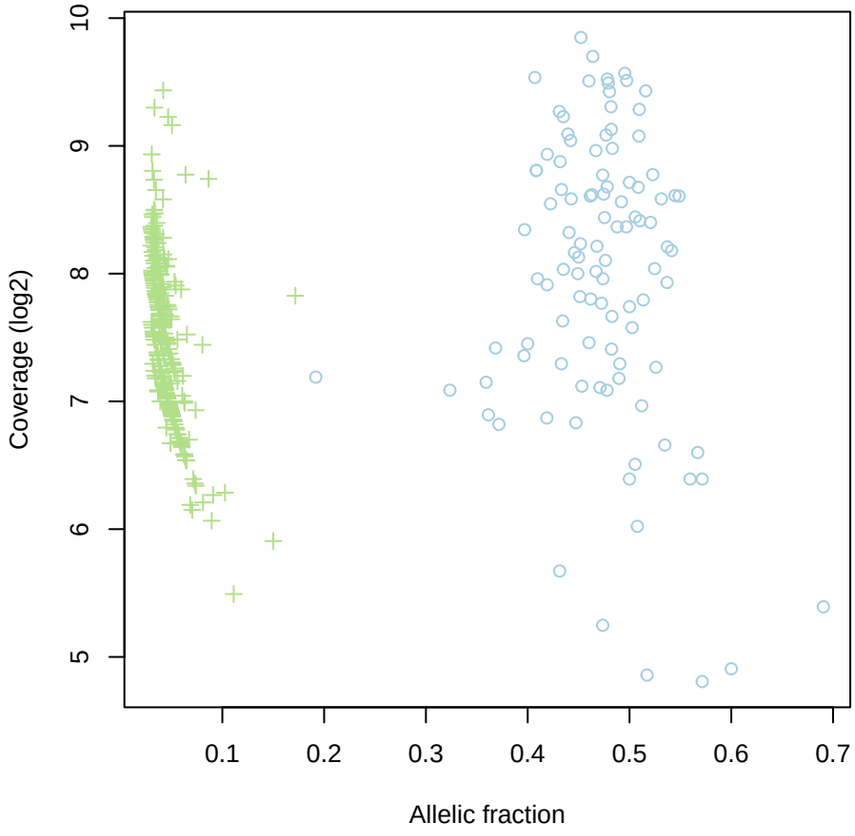

Purity: 0.71 Tumor ploidy: 5.992
3
4
5
6
7
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

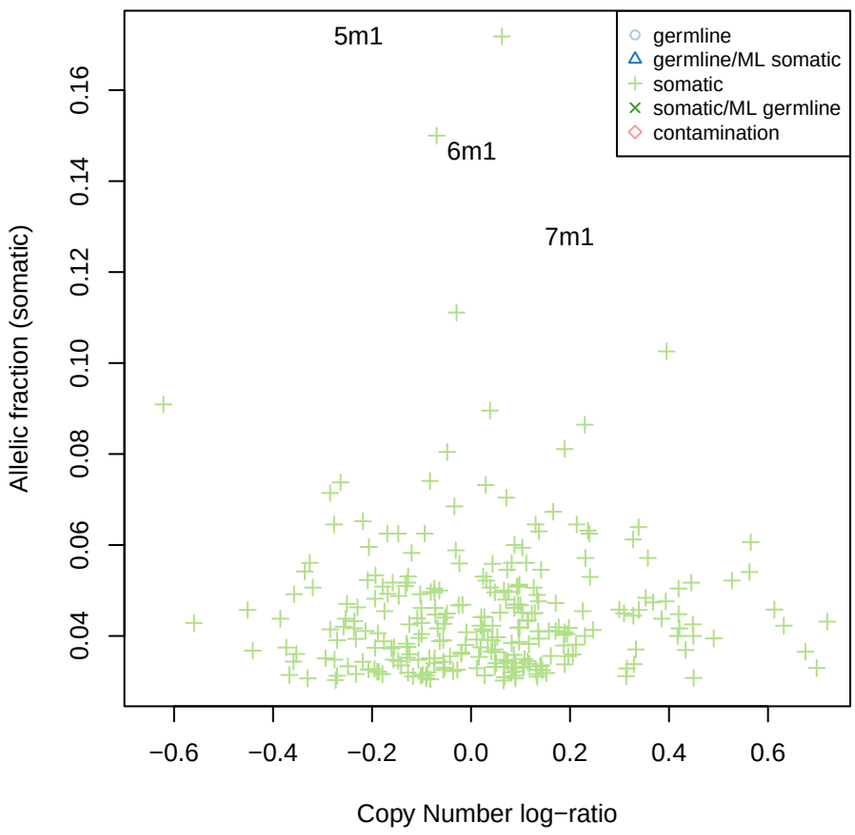

Purity: 0.71 Tumor ploidy: 5.992 SNV log−likelihood: −140.88 GoF: 79.2% Mean coverage: 250;235
1 2 3 4 5 7 8 9 10 11 12 14 15 16 17
B−Allele Frequency
0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

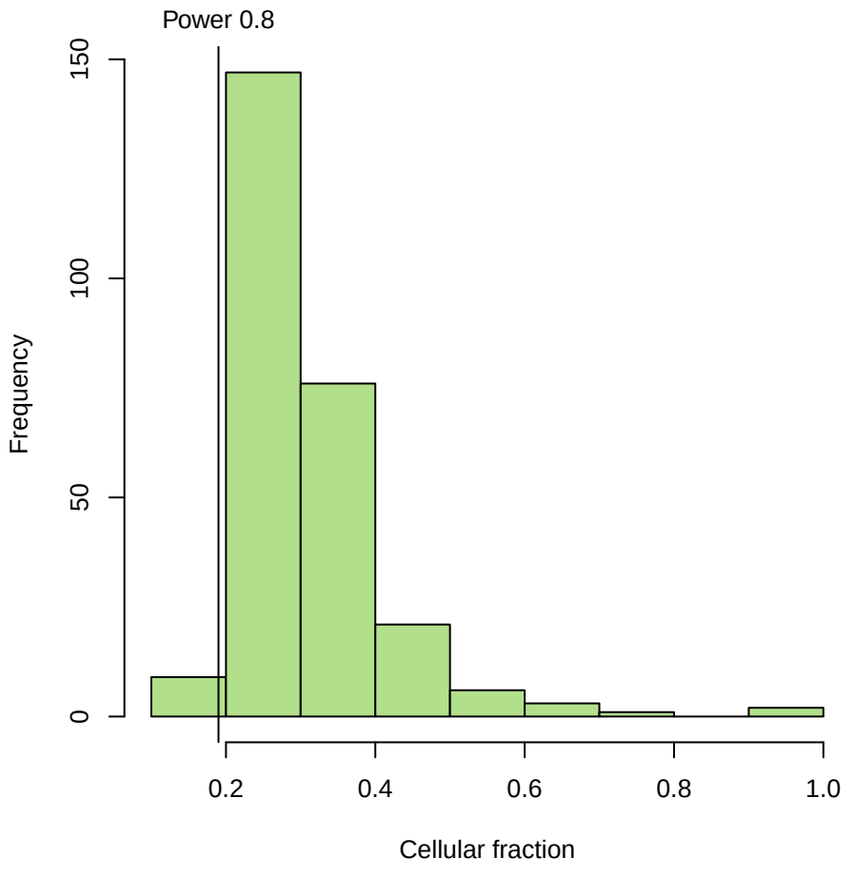

SCNA−fit log−likelihood: −5704.91
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
3 4 5 6 7
0 20 40 60 80 100
SNV Index

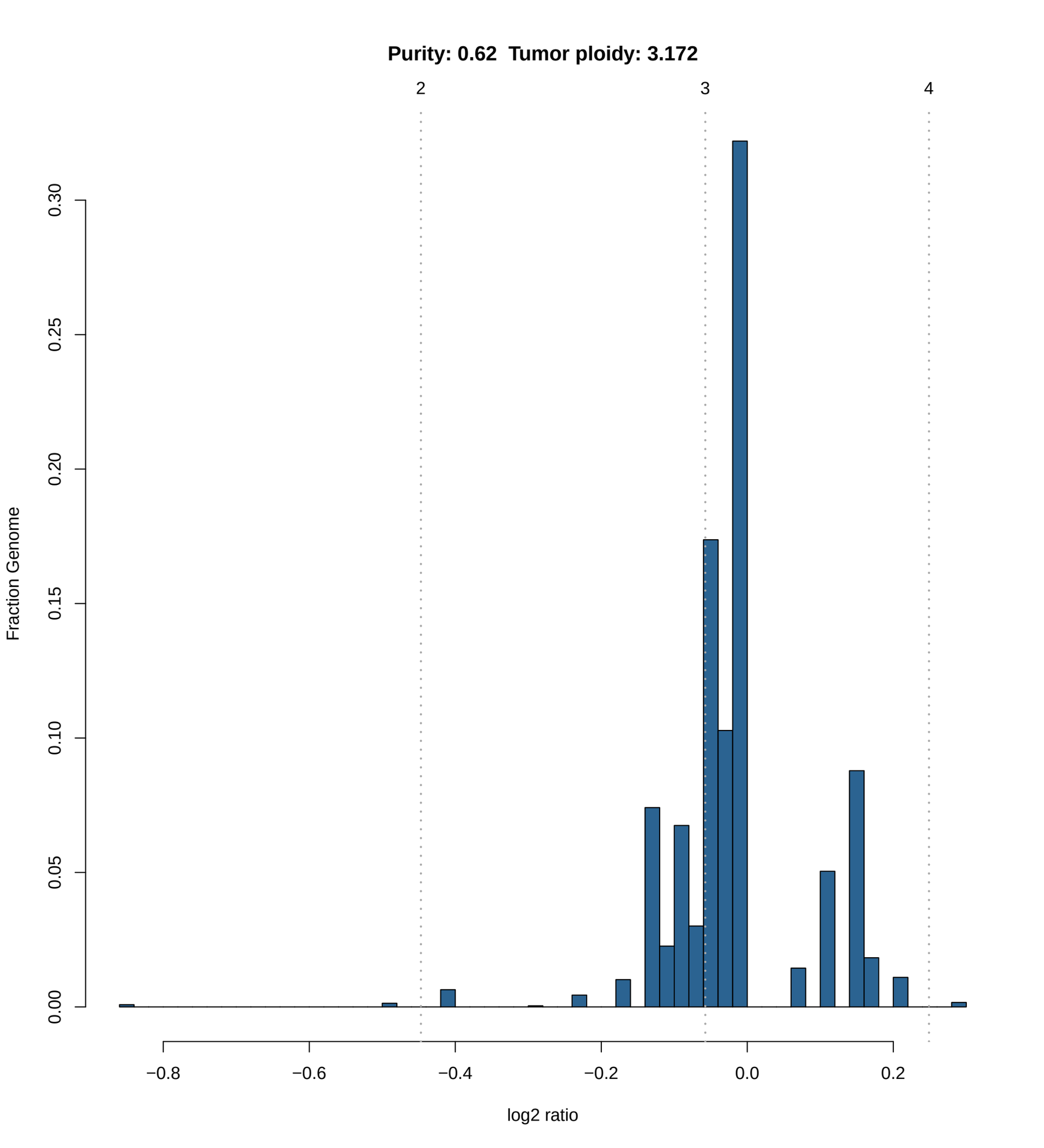

Maximum Likelihood Copy Number
0 1 2 3 4 5 6 7
0 20 40 60 80 100
SNV Index

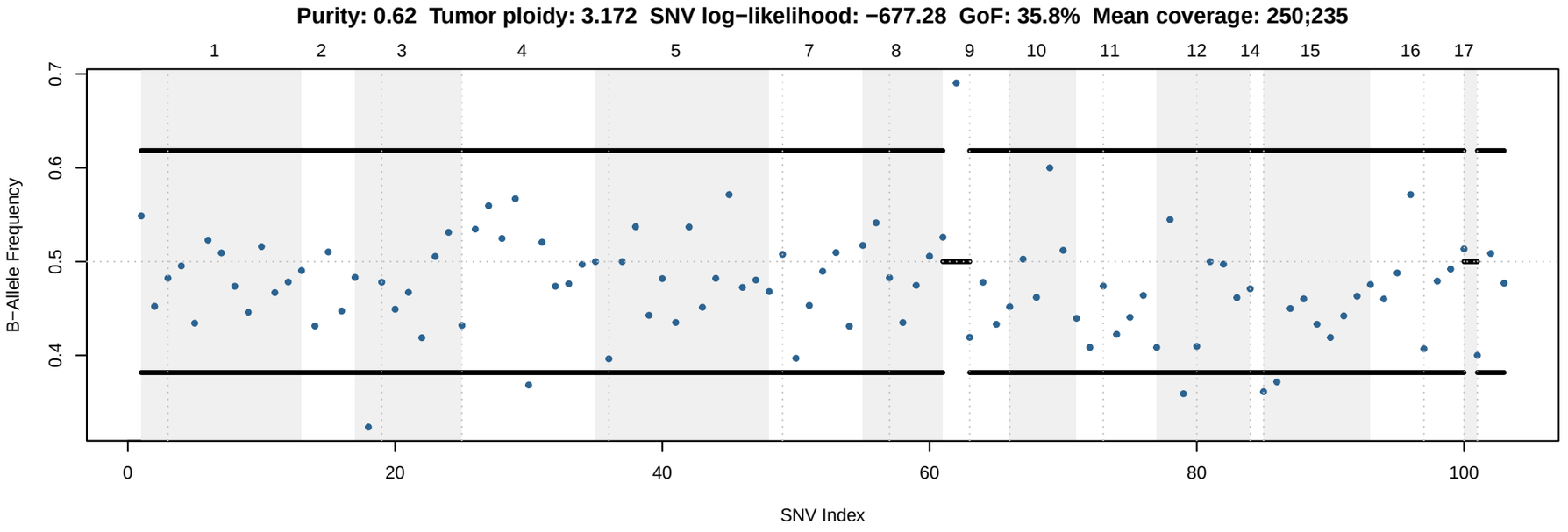

Allelic fraction (germline)
Copy Number log−ratio
5m3
7m4
6m3
5m2
7m1

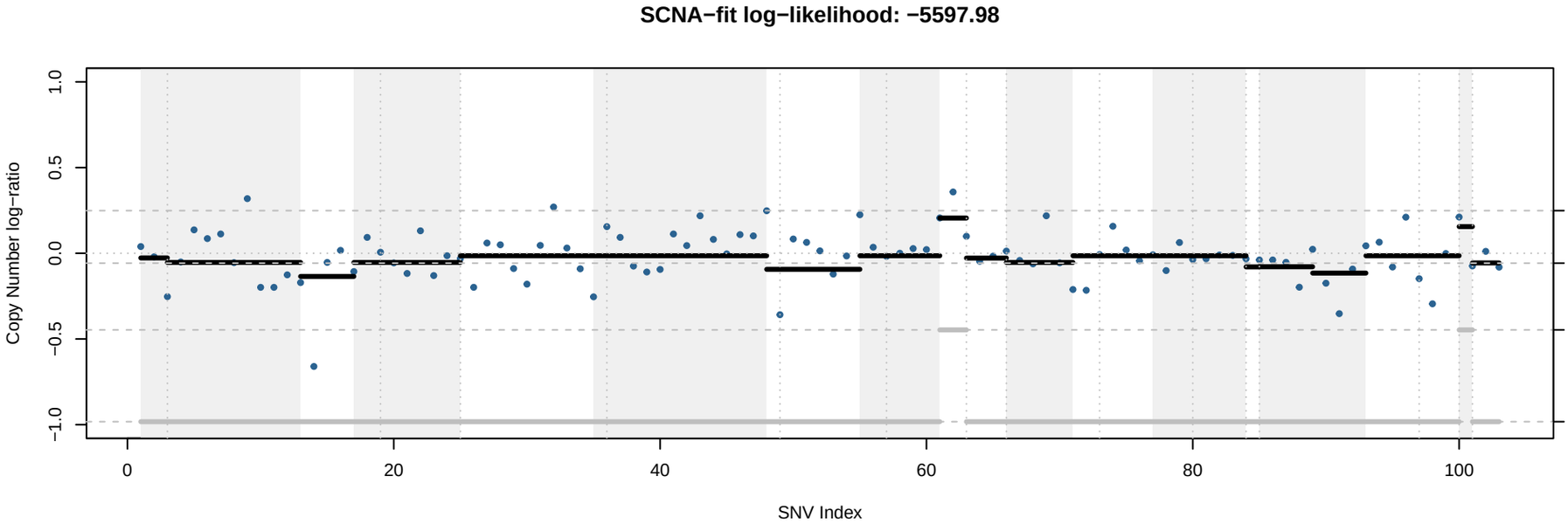

Coverage (log2)
Allelic fraction

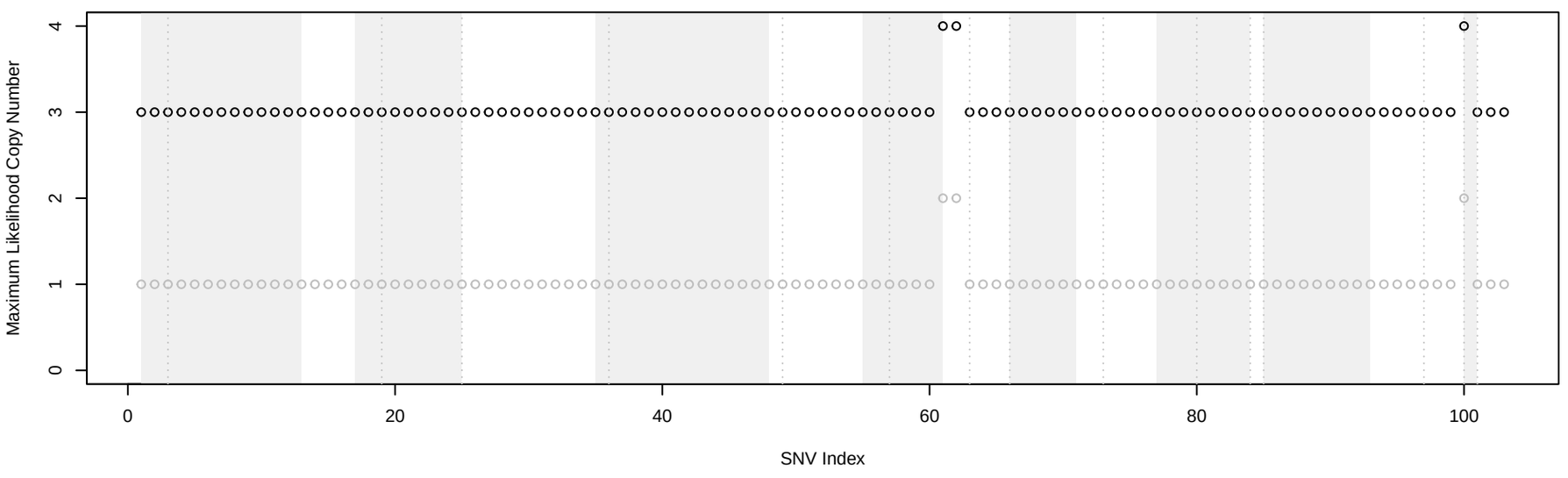

Allelic fraction (somatic)
Copy Number log−ratio
5m1
6m1
7m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

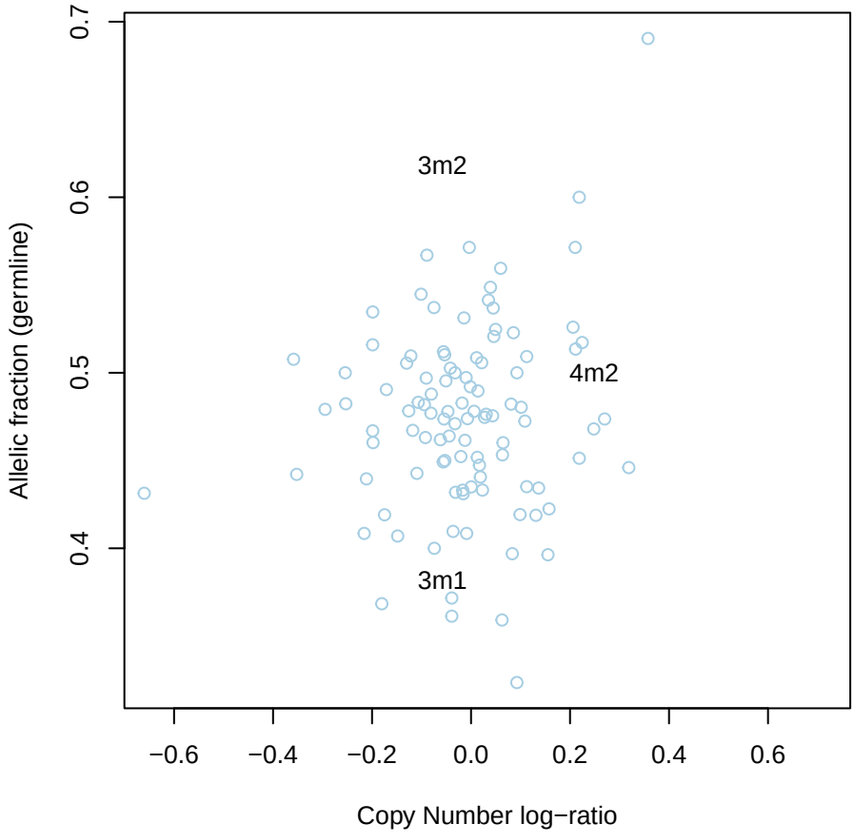

Power 0.8
Frequency
Cellular fraction

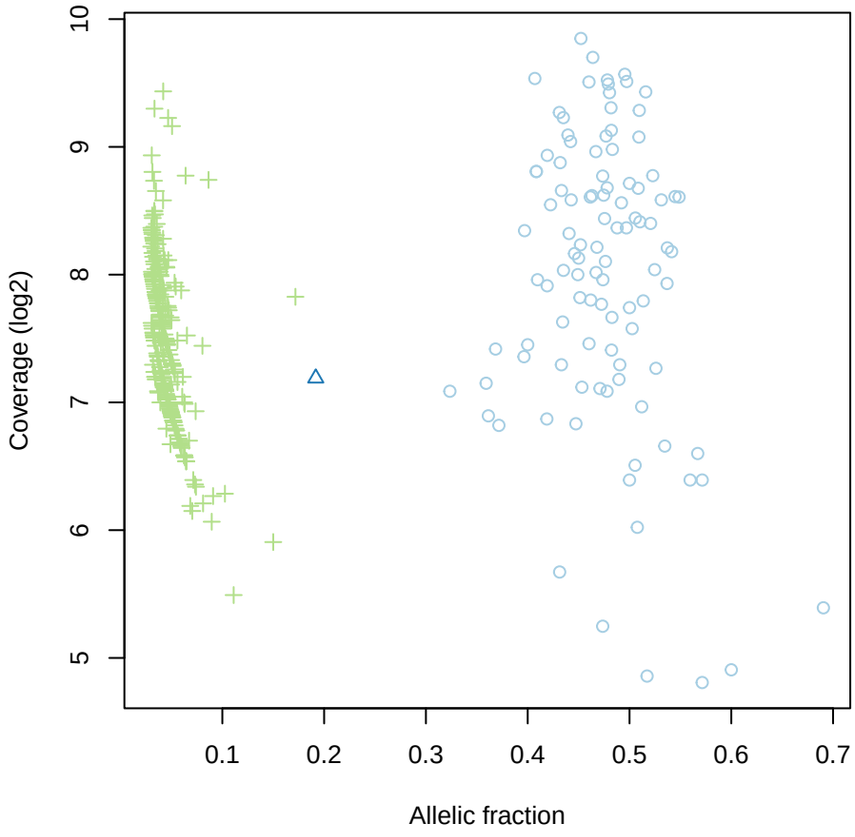

Purity: 0.62 Tumor ploidy: 3.172
2
3
4
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

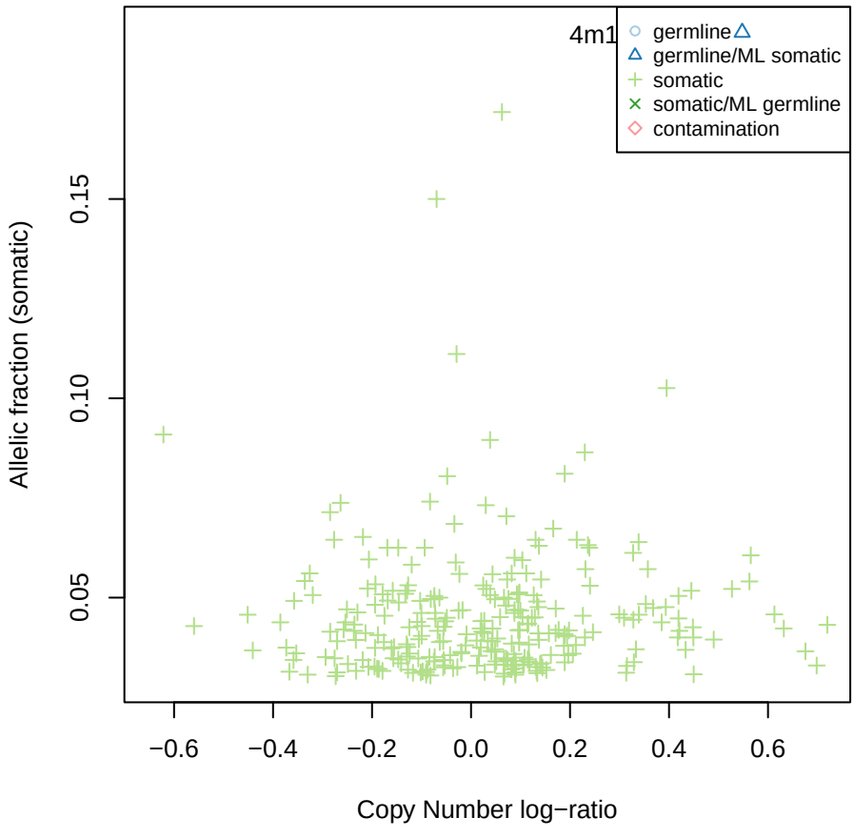

Purity: 0.62 Tumor ploidy: 3.172 SNV log−likelihood: −677.28 GoF: 35.8% Mean coverage: 250;235
1 2 3 4 5 7 8 9 10 11 12 14 15 16 17
B−Allele Frequency
0.4 0.5 0.6 0.7
0 20 40 60 80 100
SNV Index

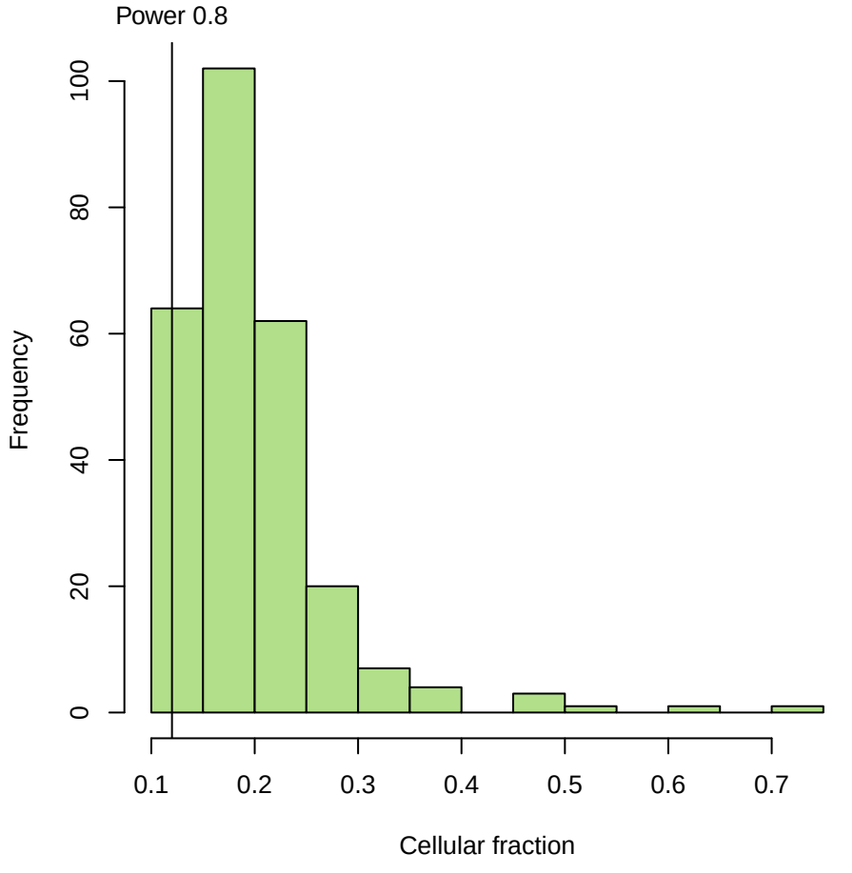

SCNA−fit log−likelihood: −5597.98
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
1 2 3 4
0 20 40 60 80 100
SNV Index

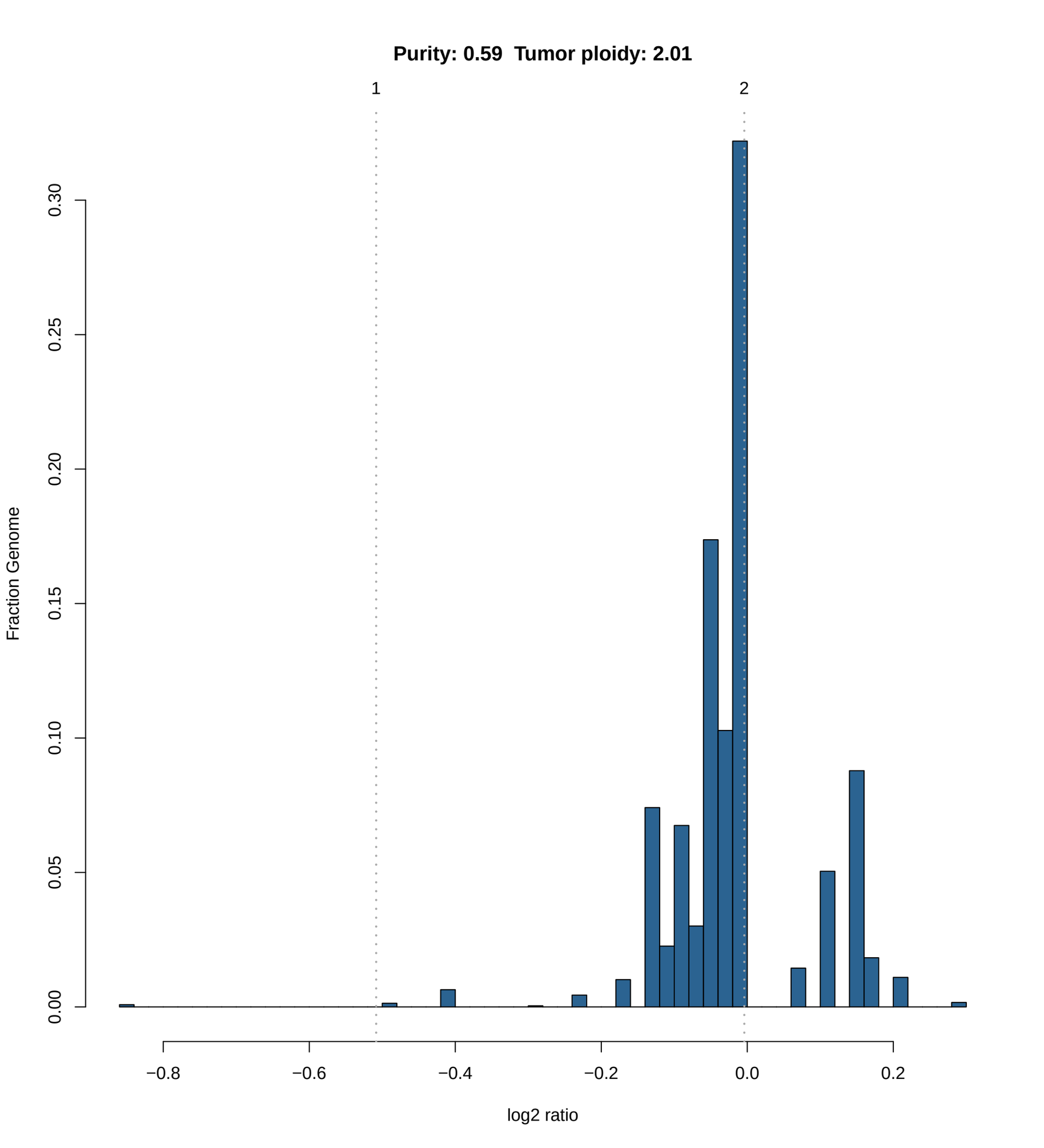

Maximum Likelihood Copy Number
0 1 2 3 4
0 20 40 60 80 100
SNV Index

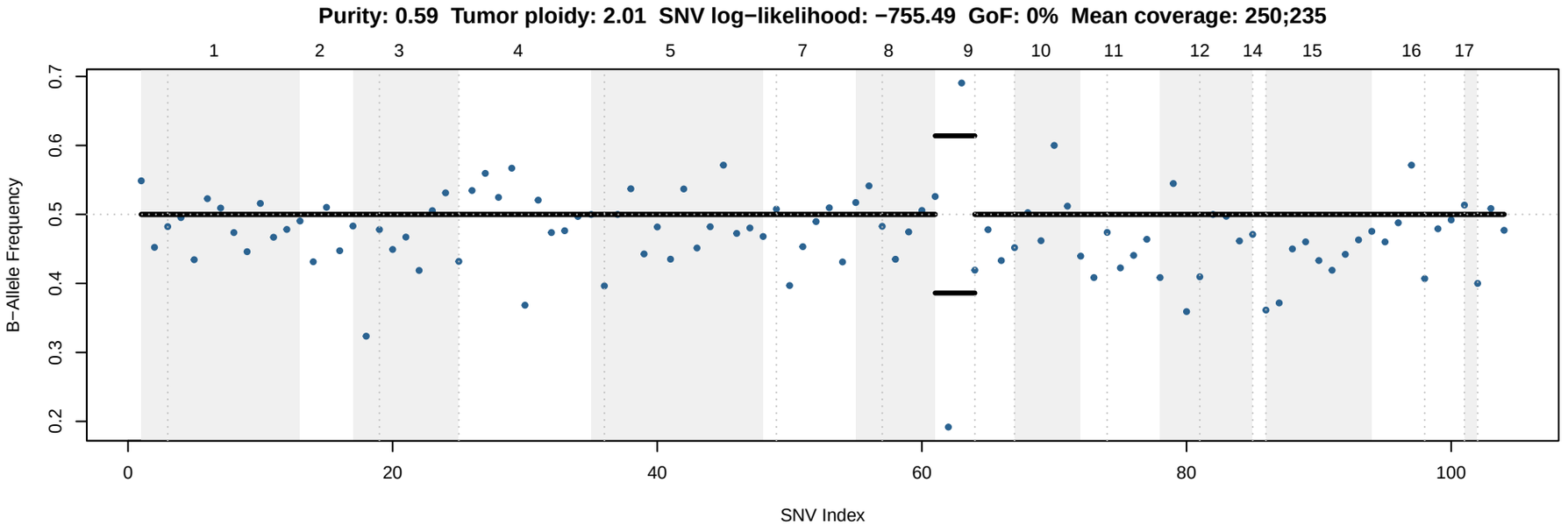

Allelic fraction (germline)
0.4
0.5
0.6
0.7
3m2
4m2
3m1
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

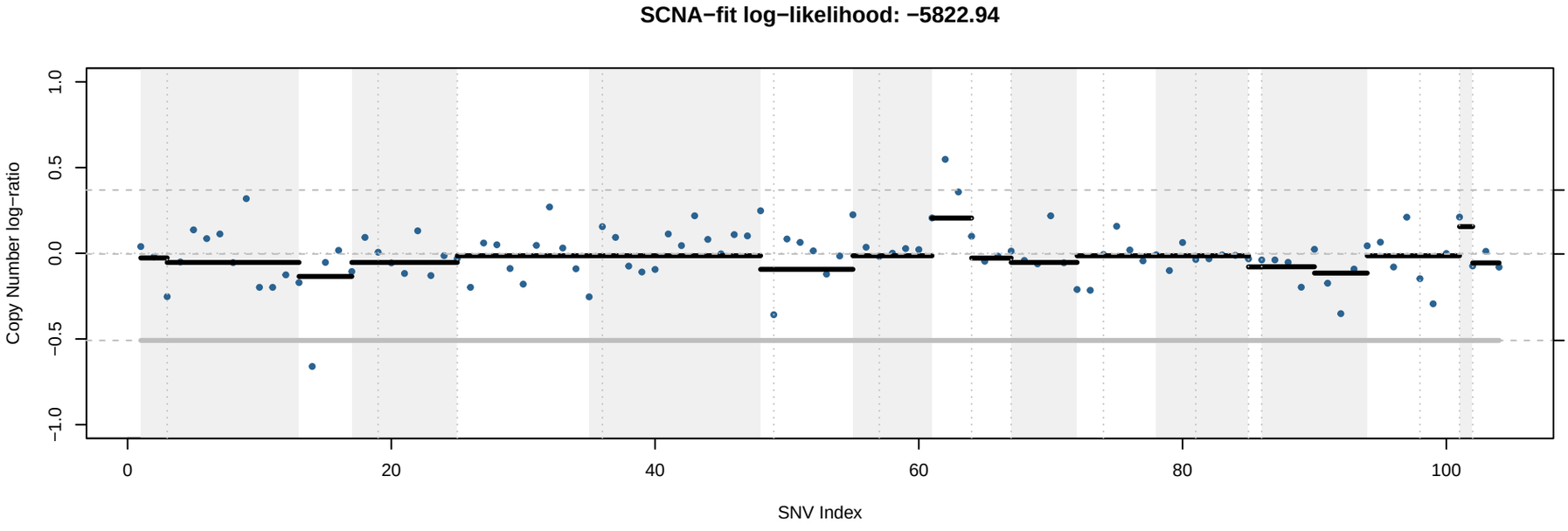

Coverage (log2)
5
6
7
8
9
10
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Allelic fraction

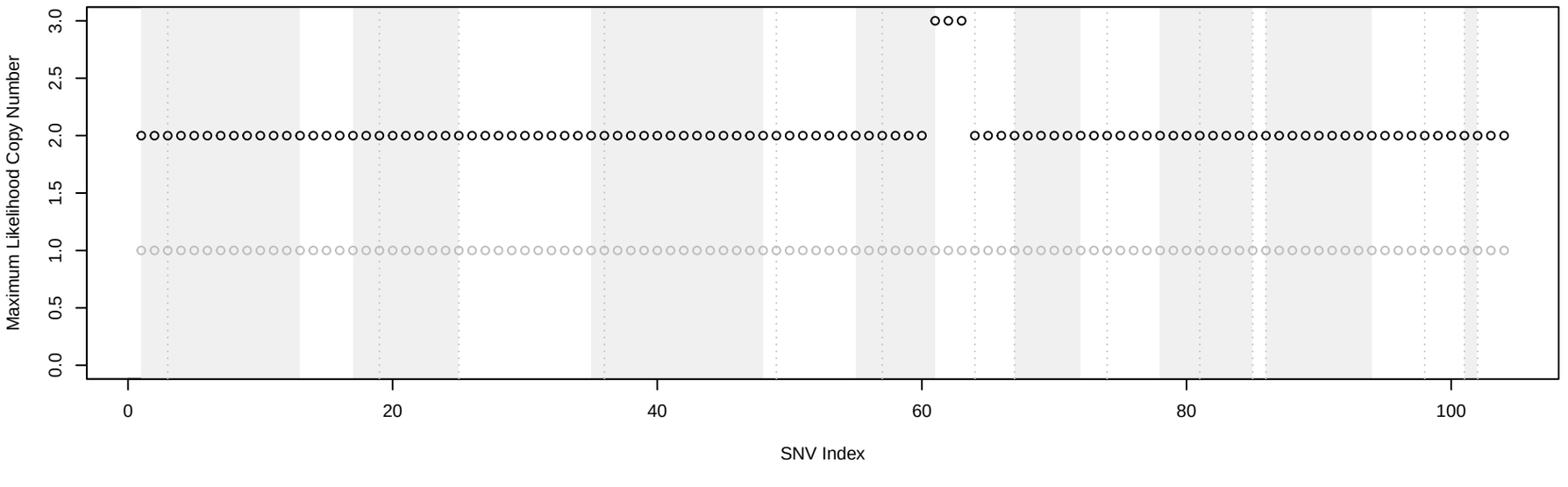

4m1
germline
germline/ML somatic
somatic
somatic/ML germline
contamination
Allelic fraction (somatic)
0.05
0.10
0.15
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Copy Number log−ratio

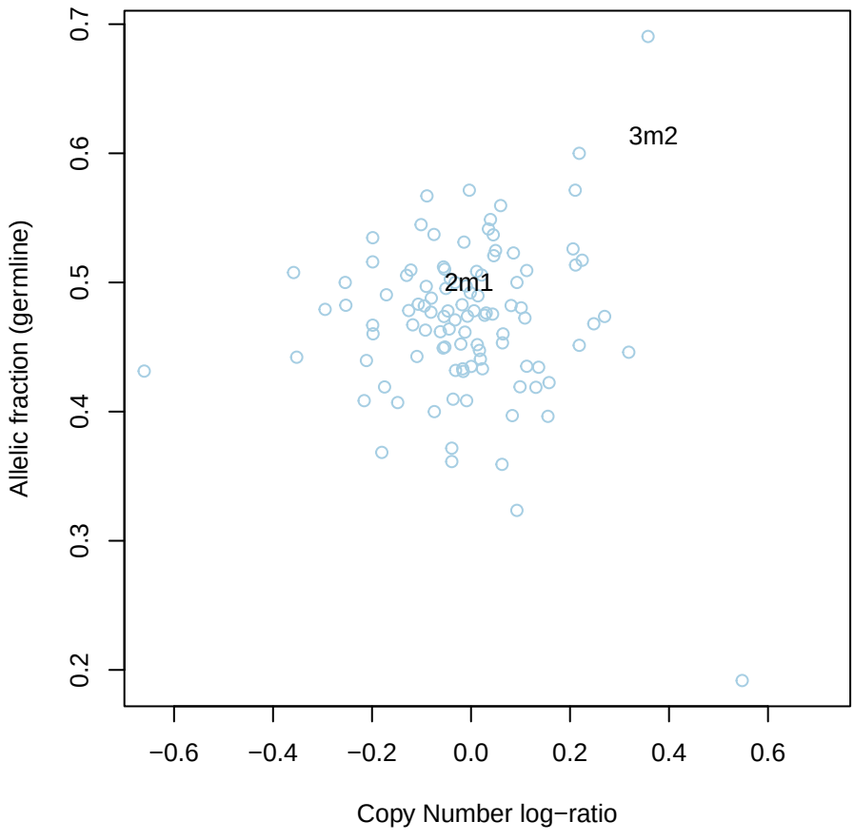

Power 0.8
Frequency
0
20
40
60
80
100
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Cellular fraction

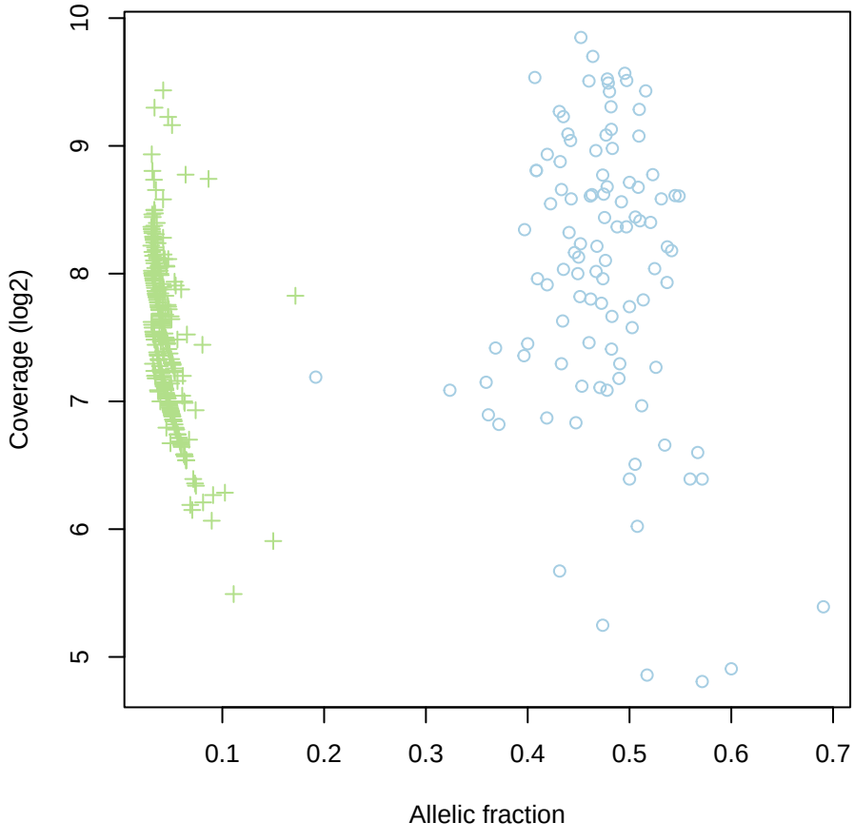

Purity: 0.59 Tumor ploidy: 2.01
1
2
Fraction Genome
0.00
0.05
0.10
0.15
0.20
0.25
0.30
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

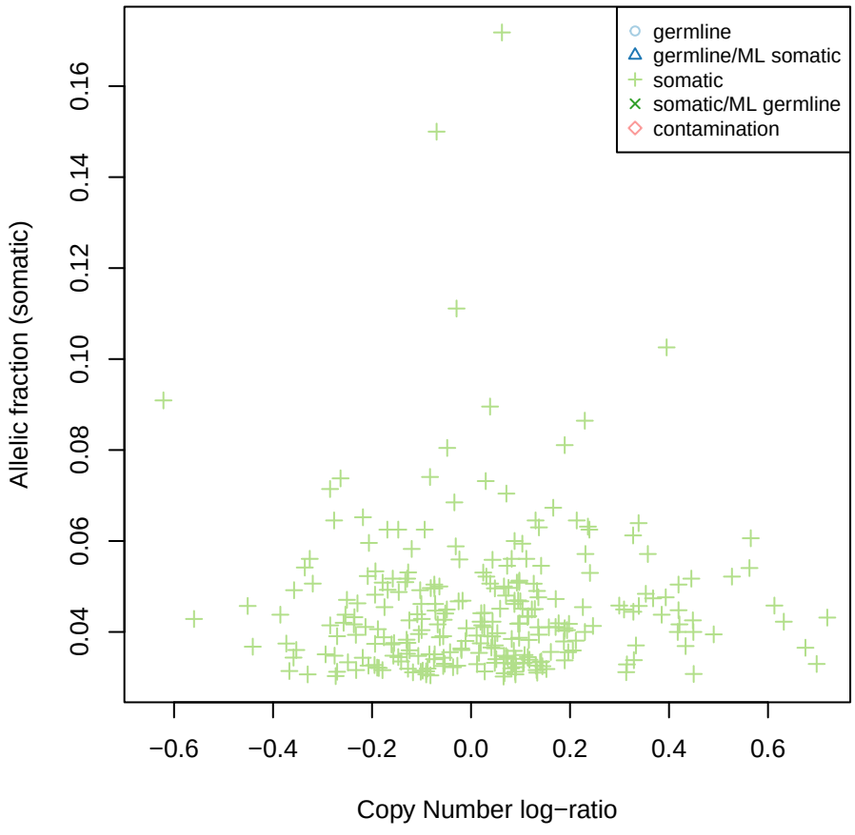

Purity: 0.59 Tumor ploidy: 2.01 SNV log−likelihood: −755.49 GoF: 0% Mean coverage: 250;235
1
2
3
4
5
7
8
9
10
11
12
14
15
16
17
B−Allele Frequency
0.2
0.3
0.4
0.5
0.6
0.7
0
20
40
60
80
100
SNV Index

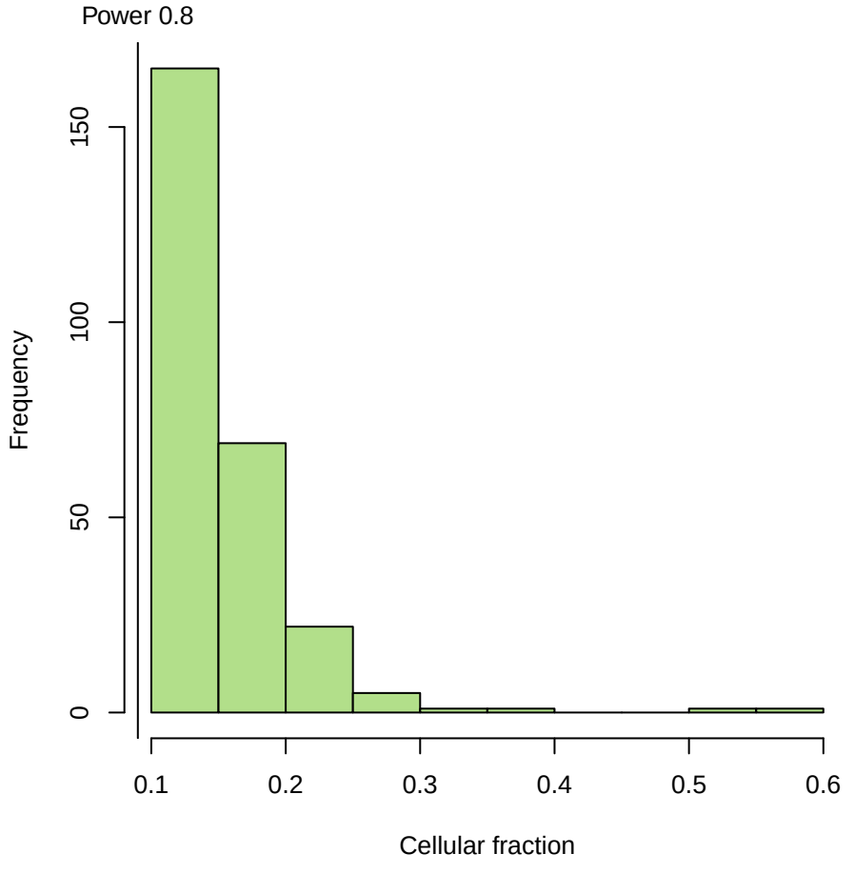

SCNA−fit log−likelihood: −5822.94
Copy Number log−ratio
−1.0
−0.5
0.0
0.5
1.0
1
2
3
0
20
40
60
80
100
SNV Index

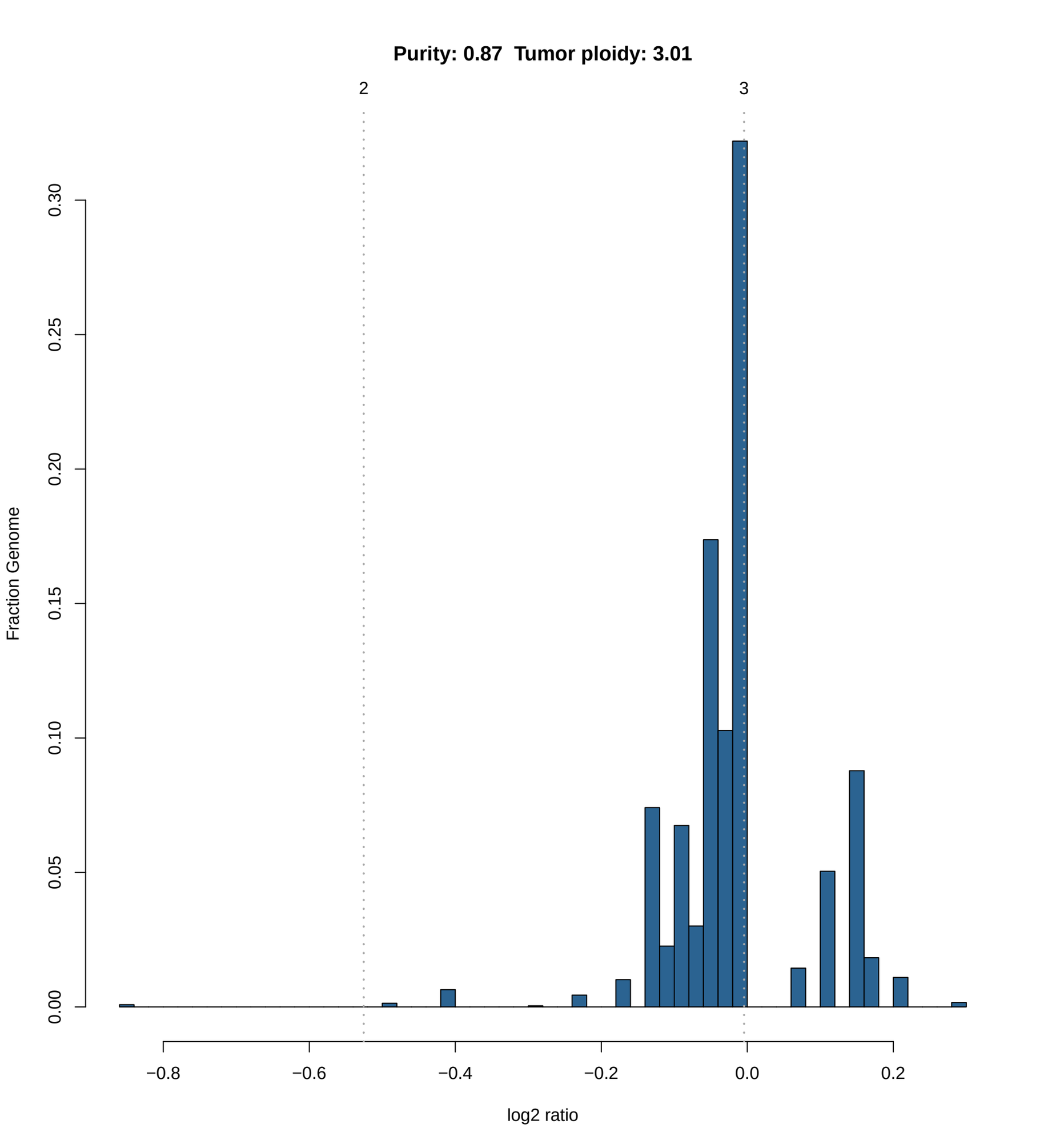

Maximum Likelihood Copy Number
0.0
0.5
1.0
1.5
2.0
2.5
3.0
0
20
40
60
80
100
SNV Index

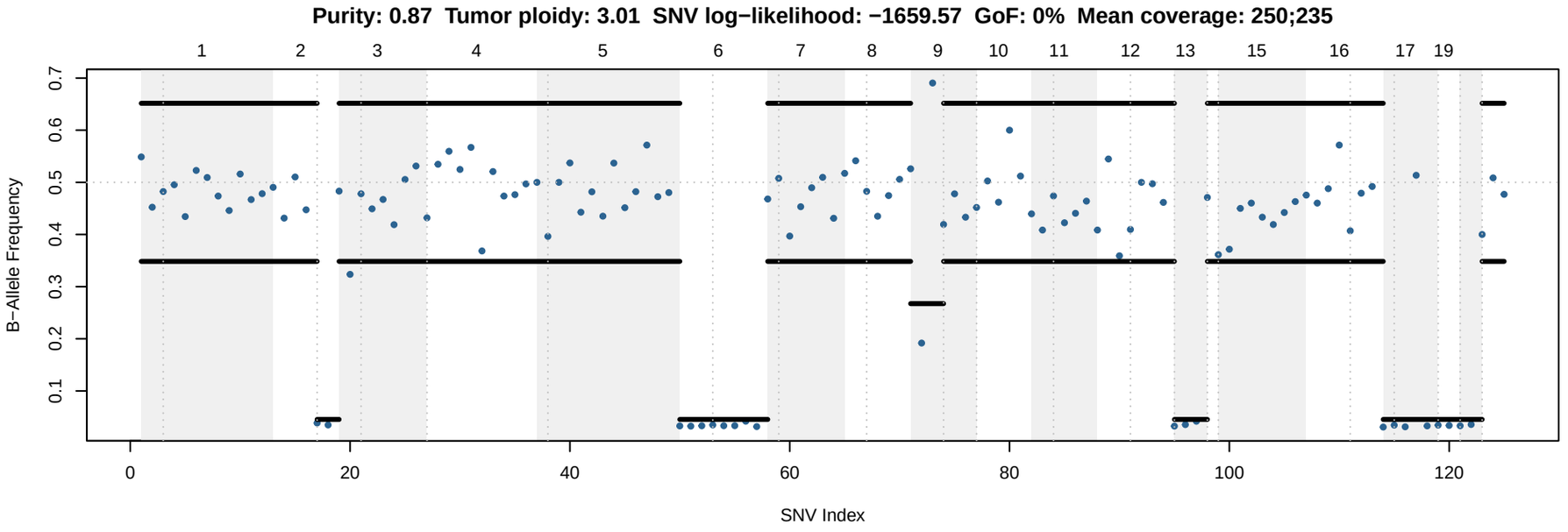

Allelic fraction (germline)
Copy Number log−ratio
3m2
2m1

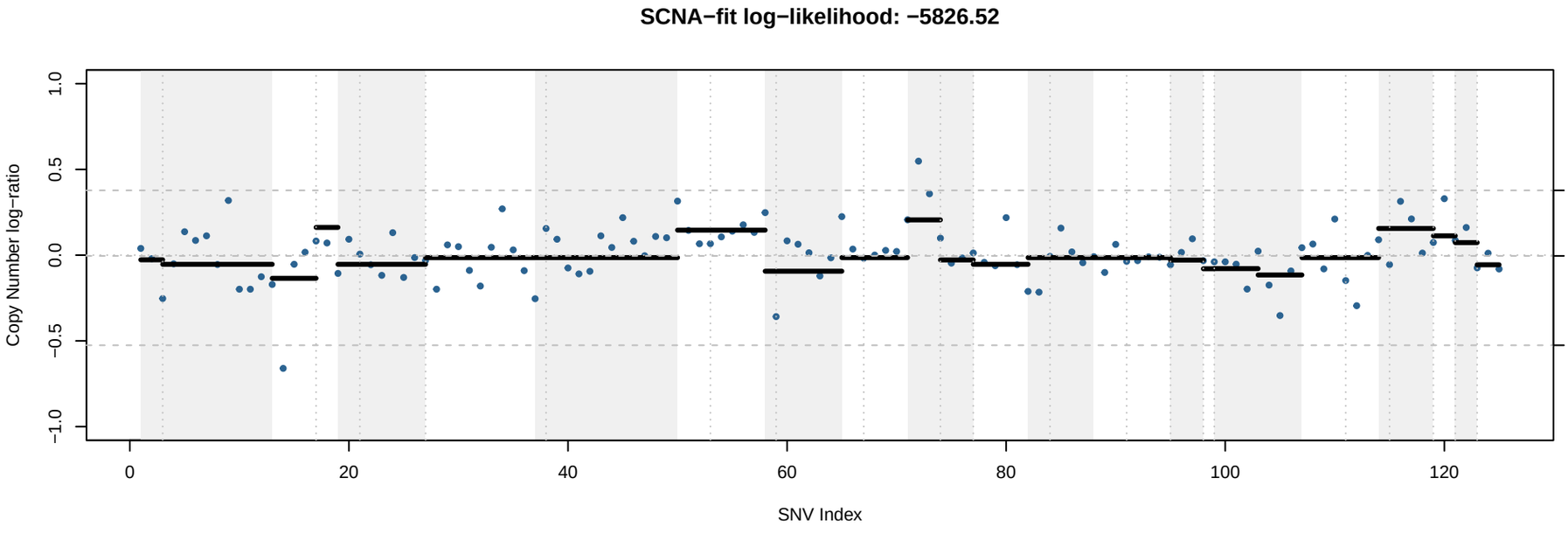

Coverage (log2)
Allelic fraction

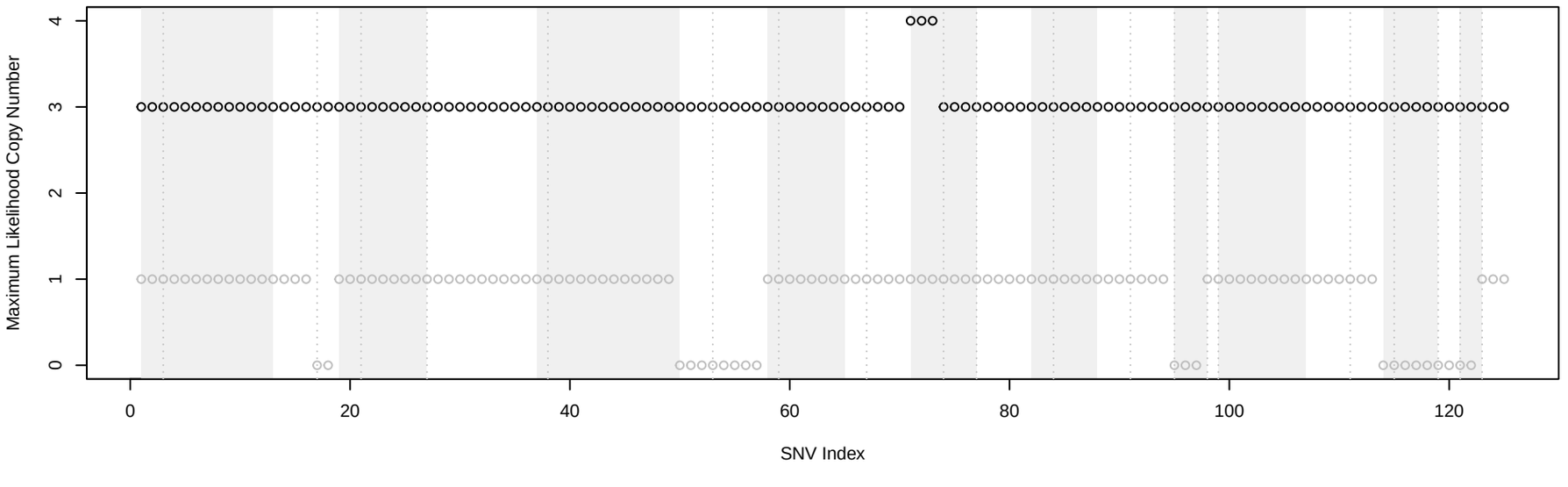

Allelic fraction (somatic)
Copy Number log−ratio
germline
germline/ML somatic
somatic
somatic/ML germline
contamination

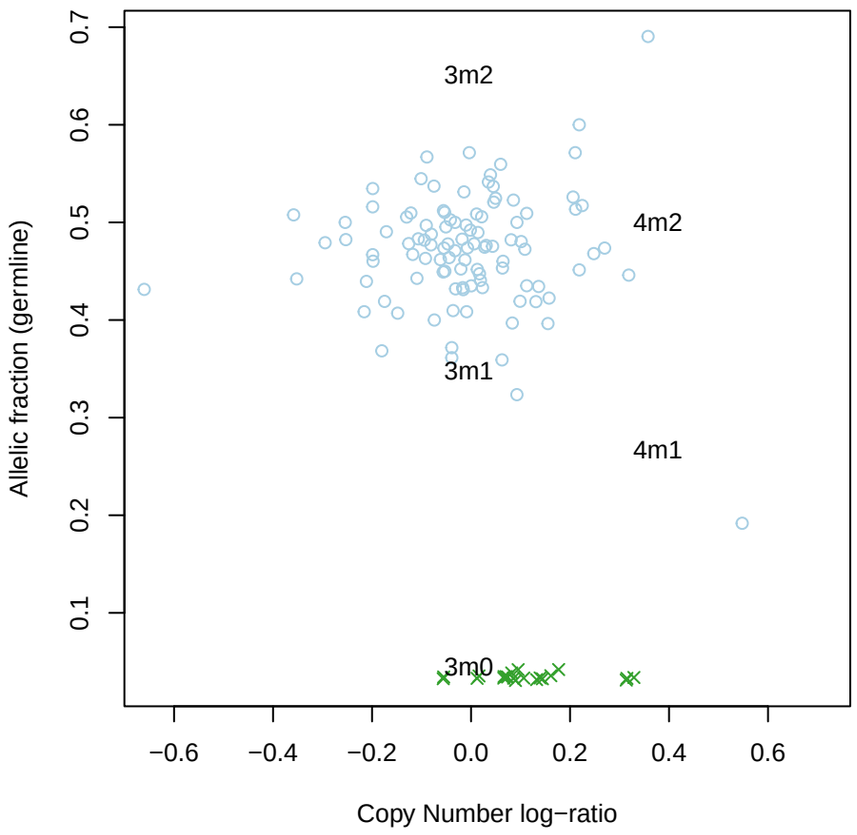

Power 0.8
Frequency
Cellular fraction

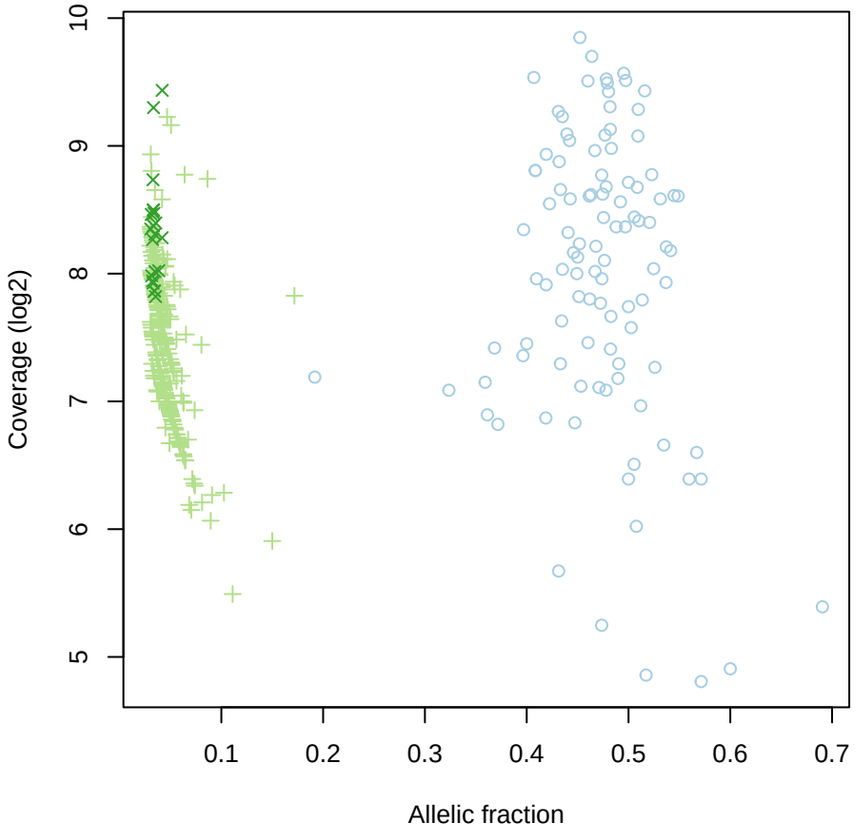

Purity: 0.87 Tumor ploidy: 3.01
2
3
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Fraction Genome
−0.8
−0.6
−0.4
−0.2
0.0
0.2
log2 ratio

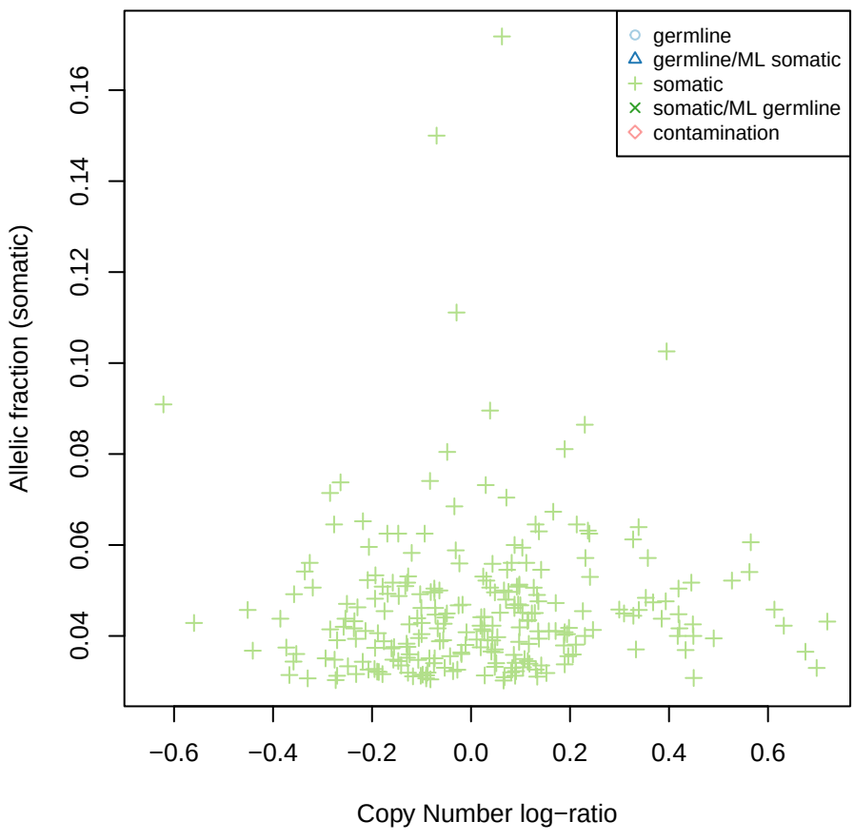

Purity: 0.87 Tumor ploidy: 3.01 SNV log−likelihood: −1659.57 GoF: 0% Mean coverage: 250;235
1 2 3 4 5 6 7 8 9 10 11 12 13 15 16 17 19
B−Allele Frequency
0.1 0.2 0.3 0.4 0.5 0.6 0.7
0 20 40 60 80 100 120
SNV Index

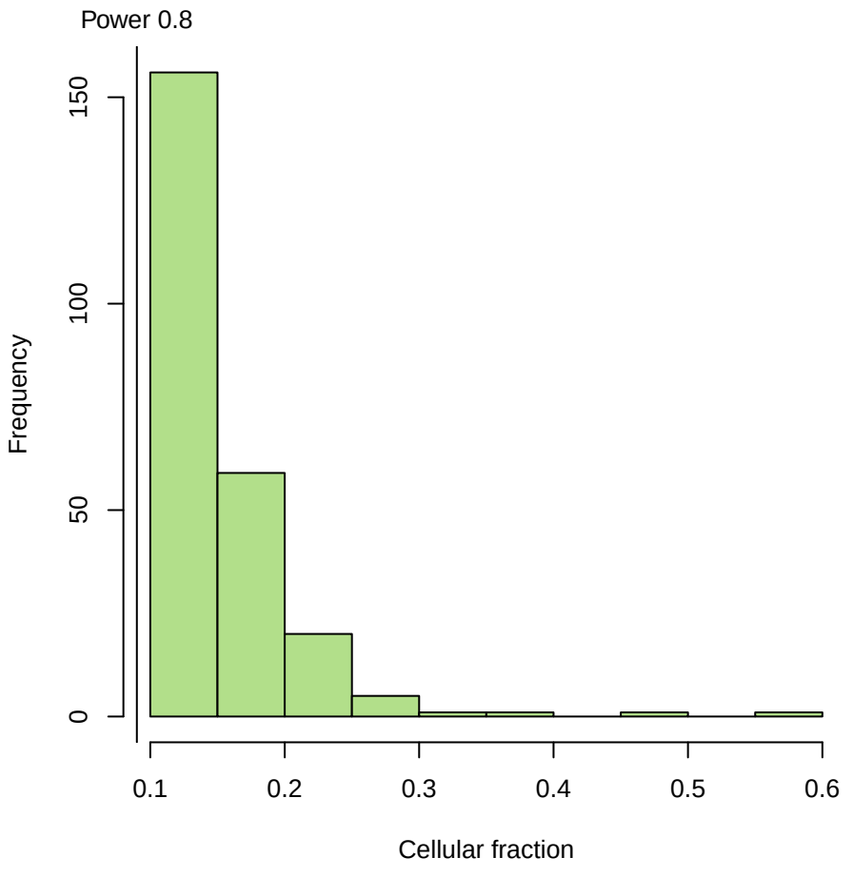

SCNA−fit log−likelihood: −5826.52
Copy Number log−ratio
−1.0 −0.5 0.0 0.5 1.0
2 3 4
0 20 40 60 80 100 120
SNV Index


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


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


Coverage (log2)
Allelic fraction


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


Power 0.8
Frequency
Cellular fraction