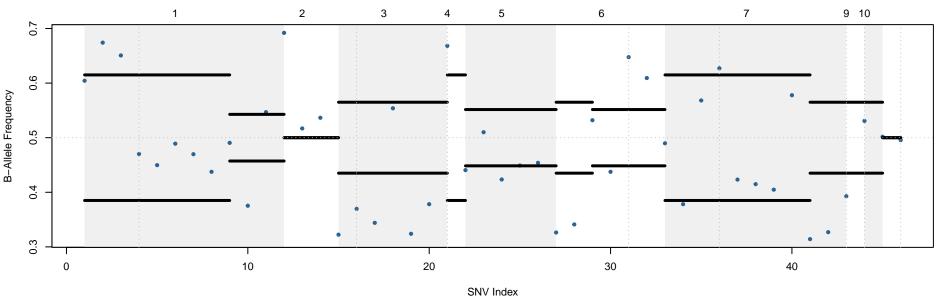
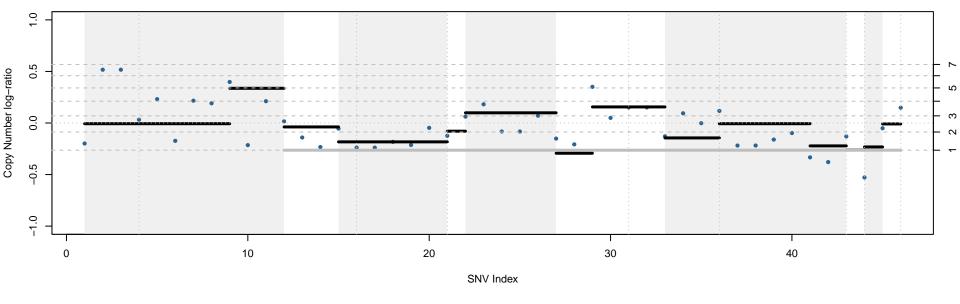
Purity: 0.23 Tumor ploidy: 2.544 2 3 6 7 5 Fraction Genome 0.05 0.00 -0.4 -0.2 0.0 0.2 0.4 0.6

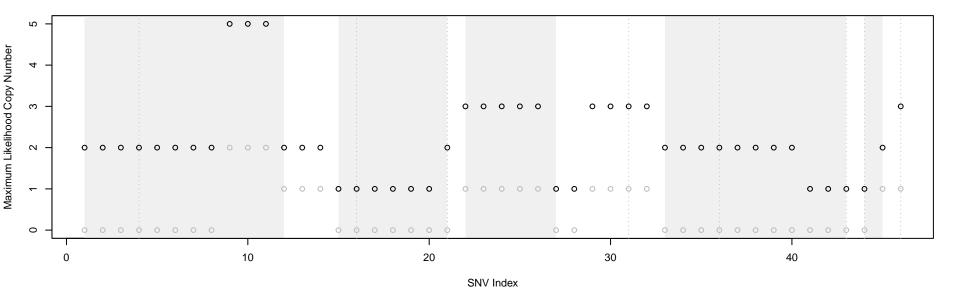
log2 ratio

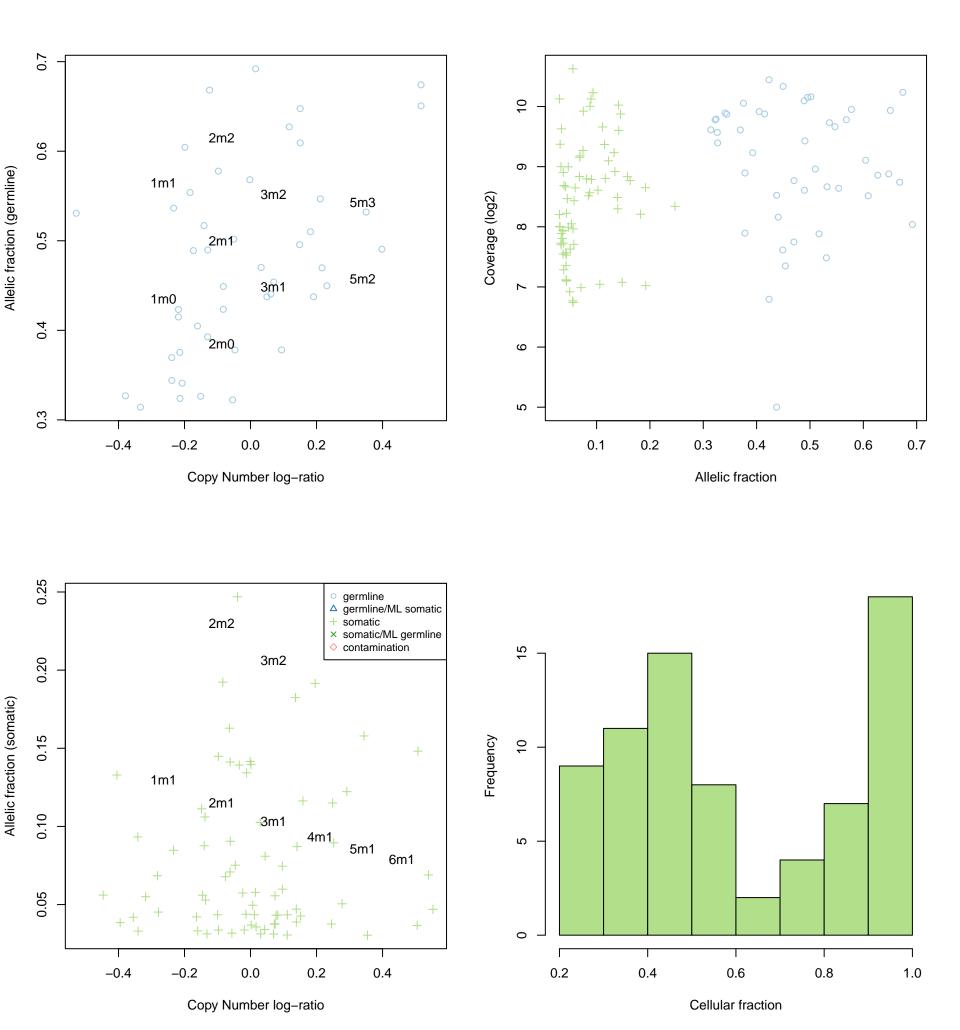
Purity: 0.23 Tumor ploidy: 2.544 SNV log-likelihood: -65.21 GoF: 91.7% Mean coverage: 542;511



SCNA-fit log-likelihood: -1802.82

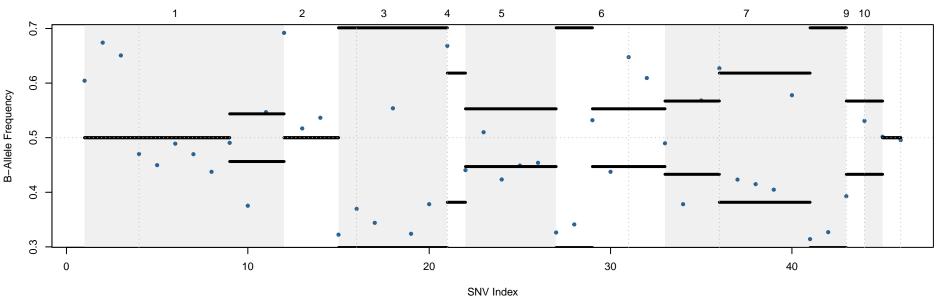




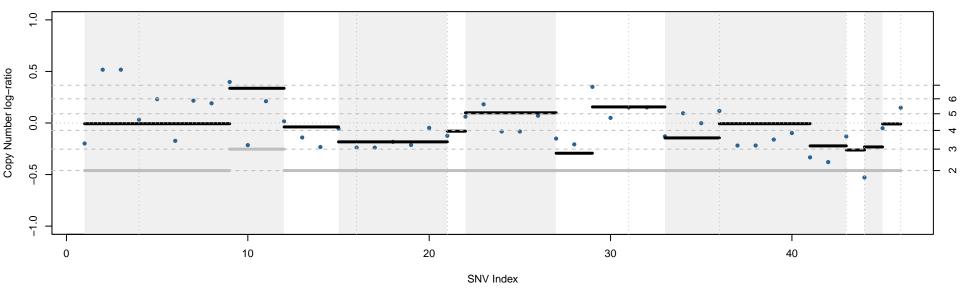


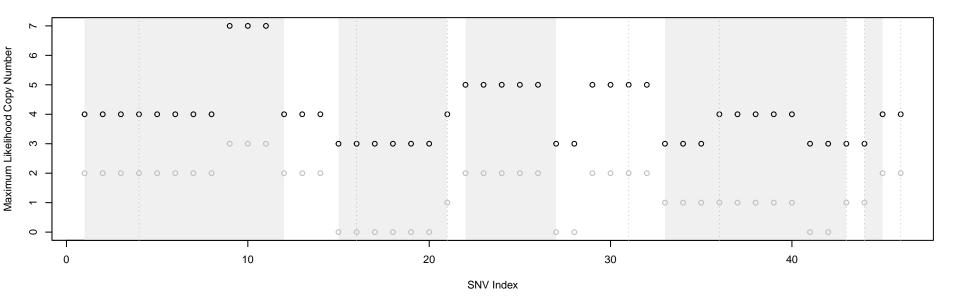
Purity: 0.31 Tumor ploidy: 4.431 2 3 5 6 7 Fraction Genome 0.05 0.00 -0.4 -0.2 0.0 0.2 0.4 0.6 log2 ratio

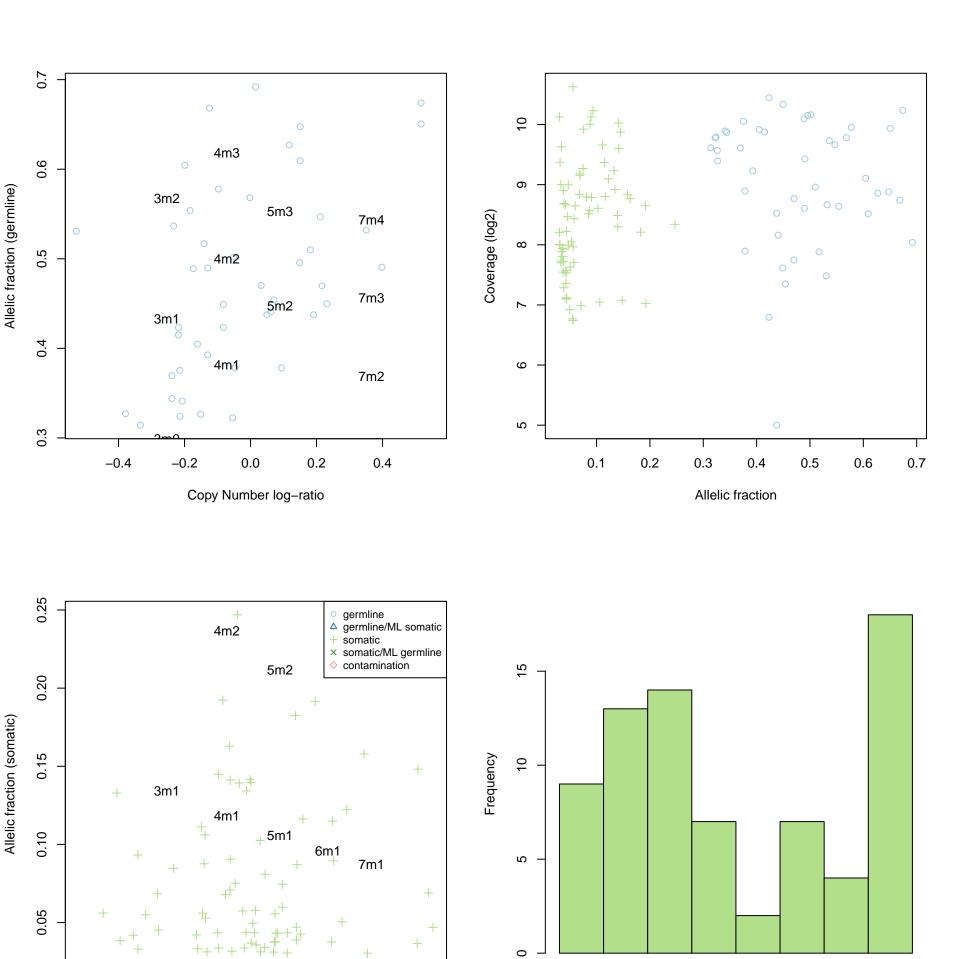
Purity: 0.31 Tumor ploidy: 4.431 SNV log-likelihood: -98.43 GoF: 93.1% Mean coverage: 542;511



SCNA-fit log-likelihood: -1819.39







0.2

0.4

-0.4

-0.2

0.0

Copy Number log-ratio

0.2

0.4

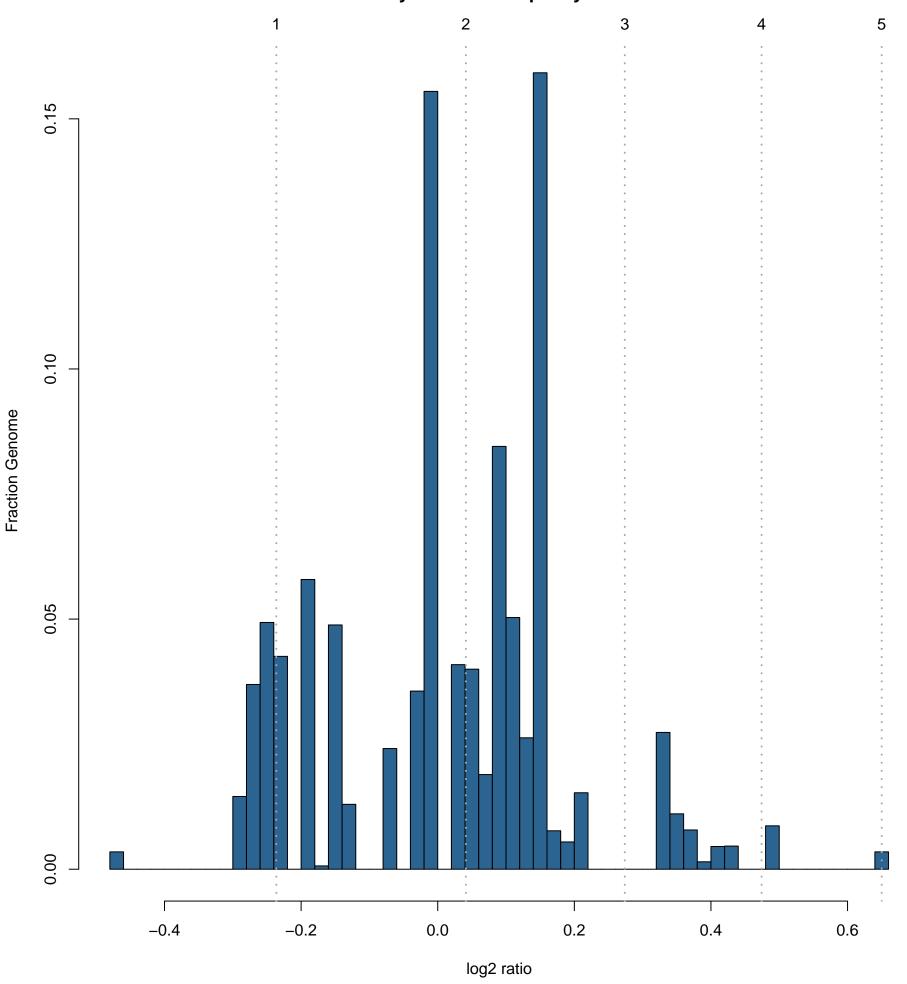
0.6

Cellular fraction

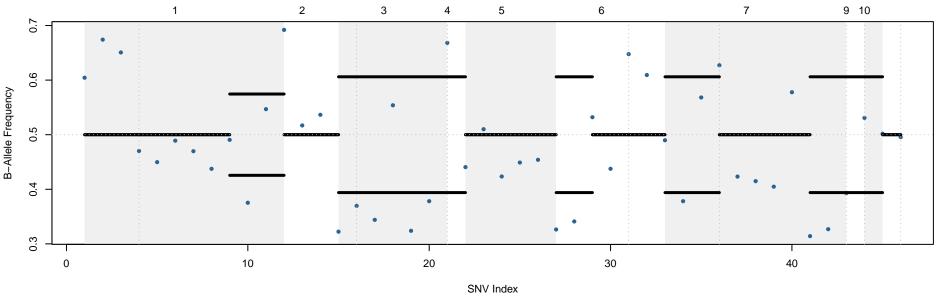
8.0

1.0

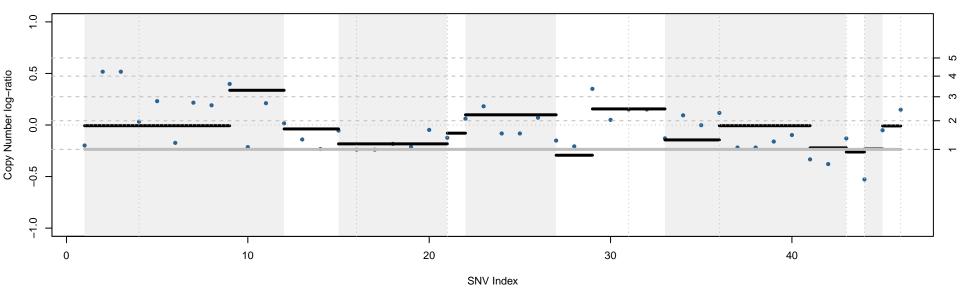
Purity: 0.35 Tumor ploidy: 1.839

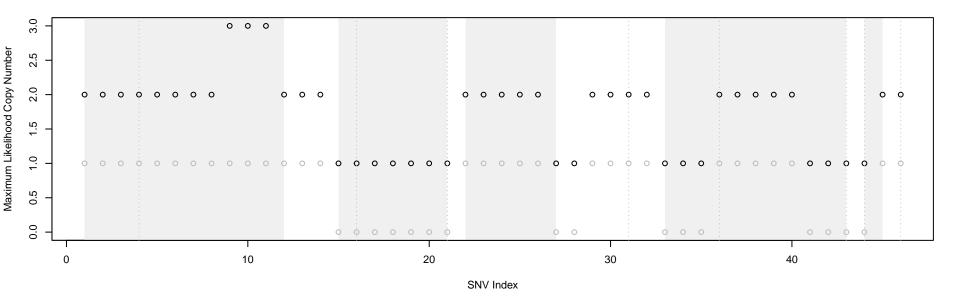


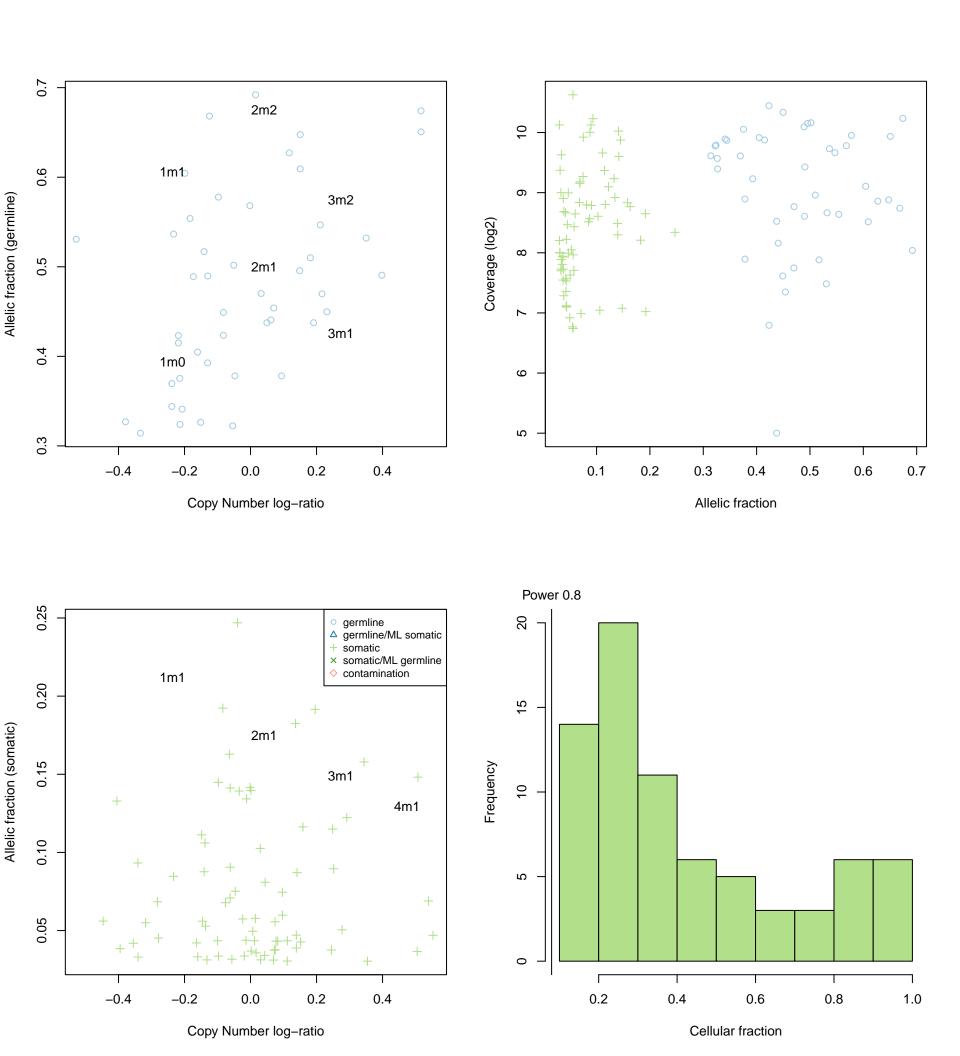




SCNA-fit log-likelihood: -1972.8

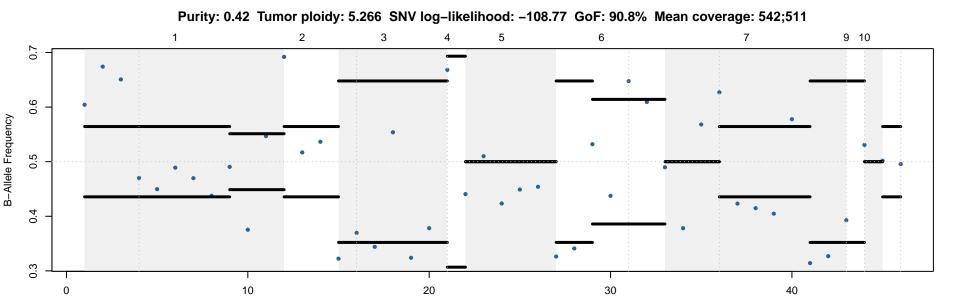






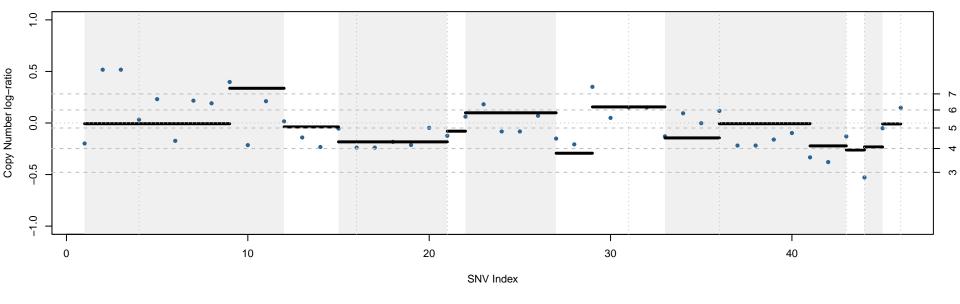
Purity: 0.42 Tumor ploidy: 5.266 3 5 6 Fraction Genome 0.05 0.00 -0.4 -0.2 0.0 0.2 0.4 0.6

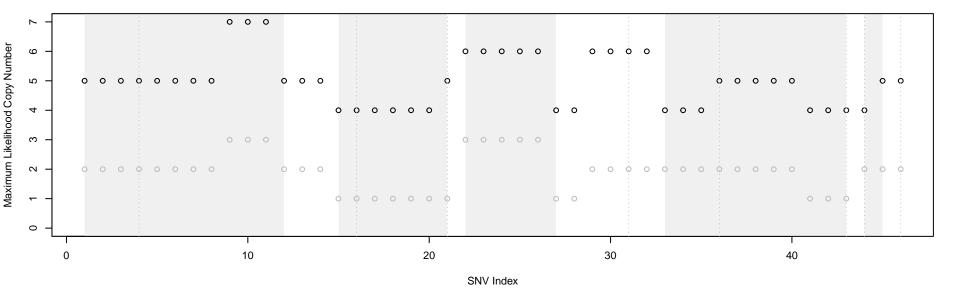
log2 ratio

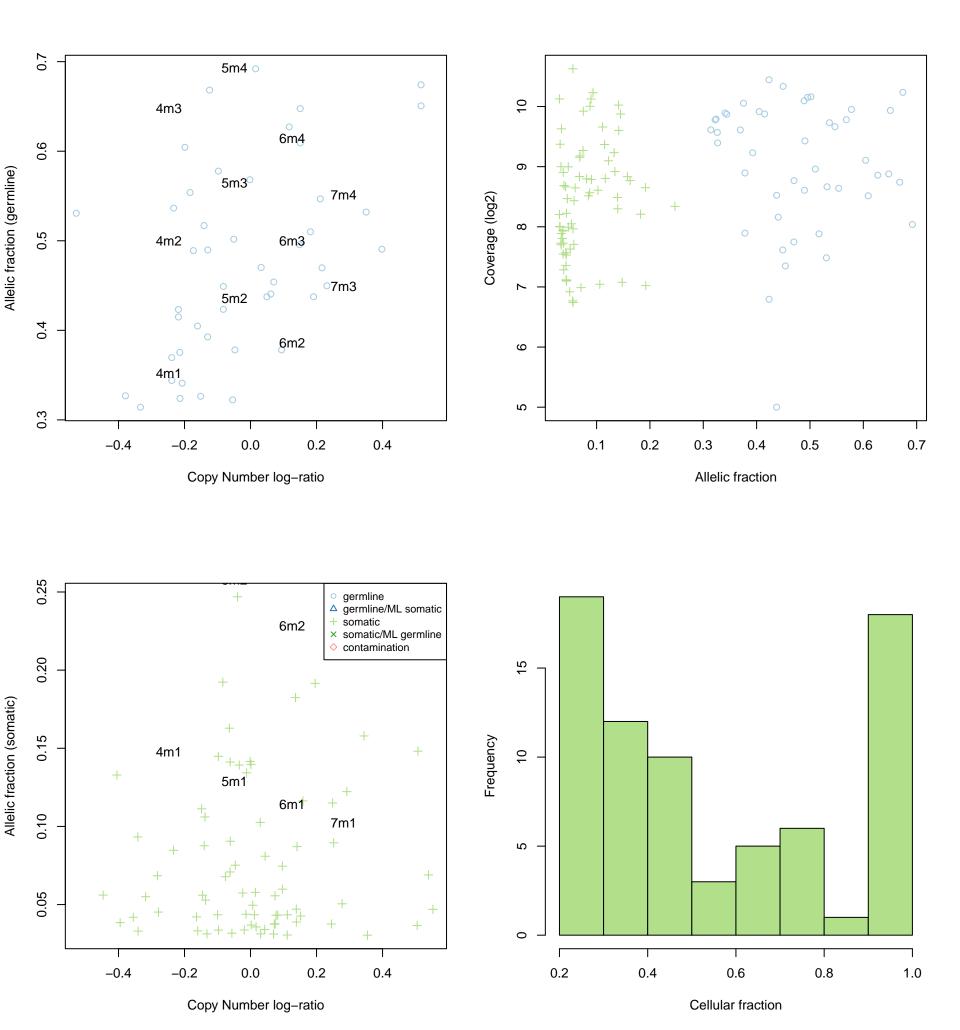


SCNA-fit log-likelihood: -1855.21

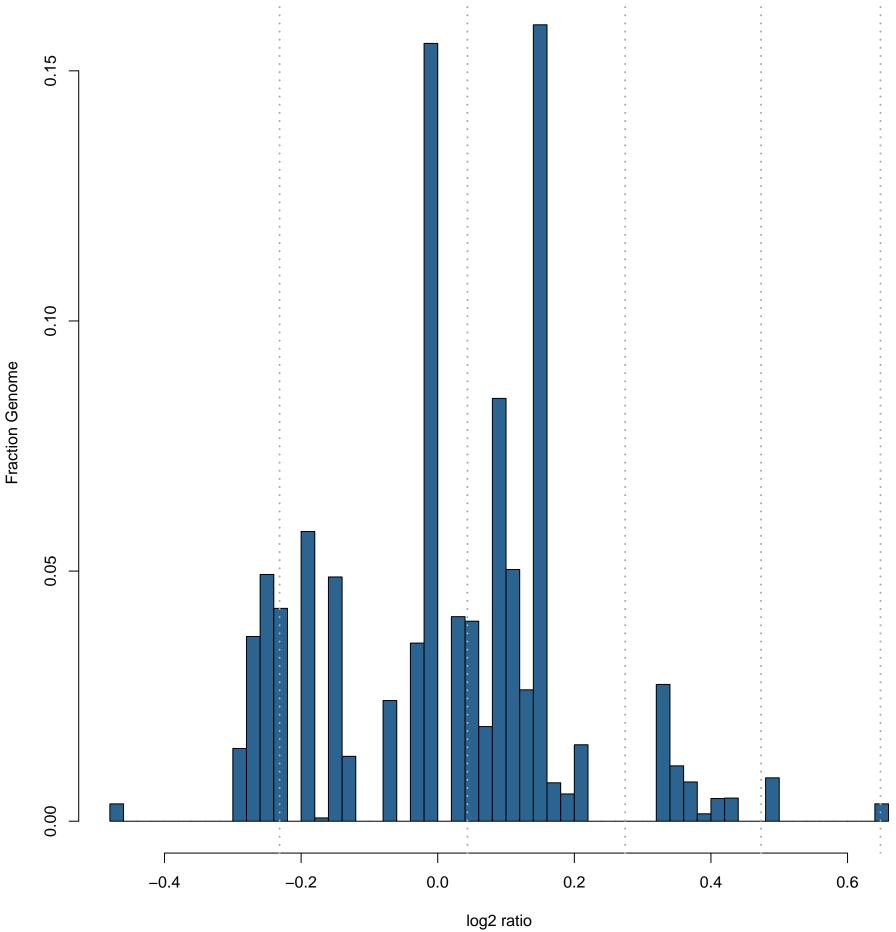
SNV Index

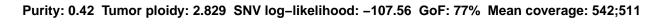


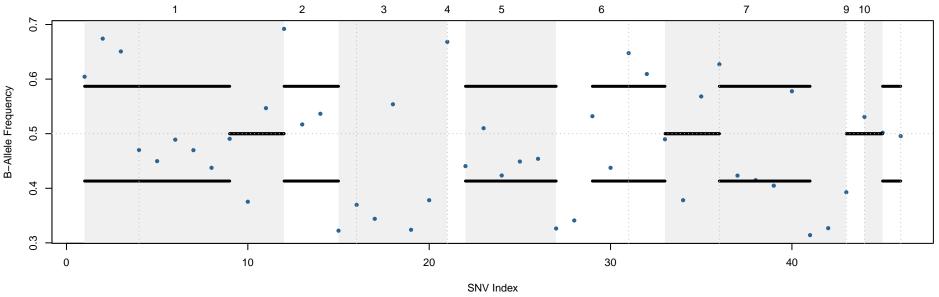




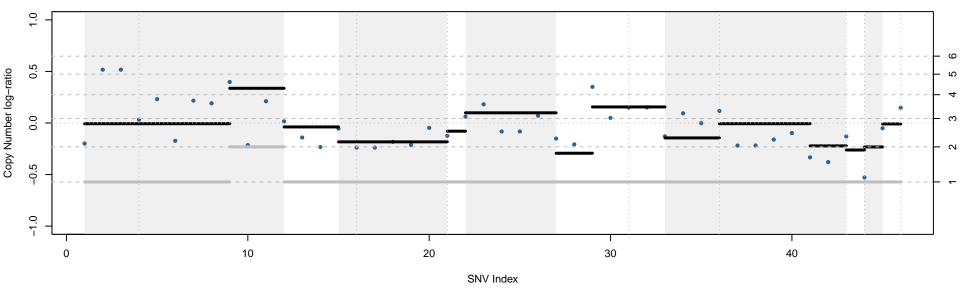
Purity: 0.42 Tumor ploidy: 2.829

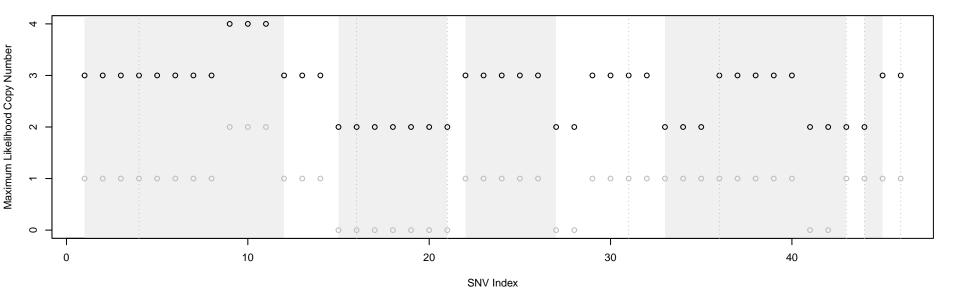


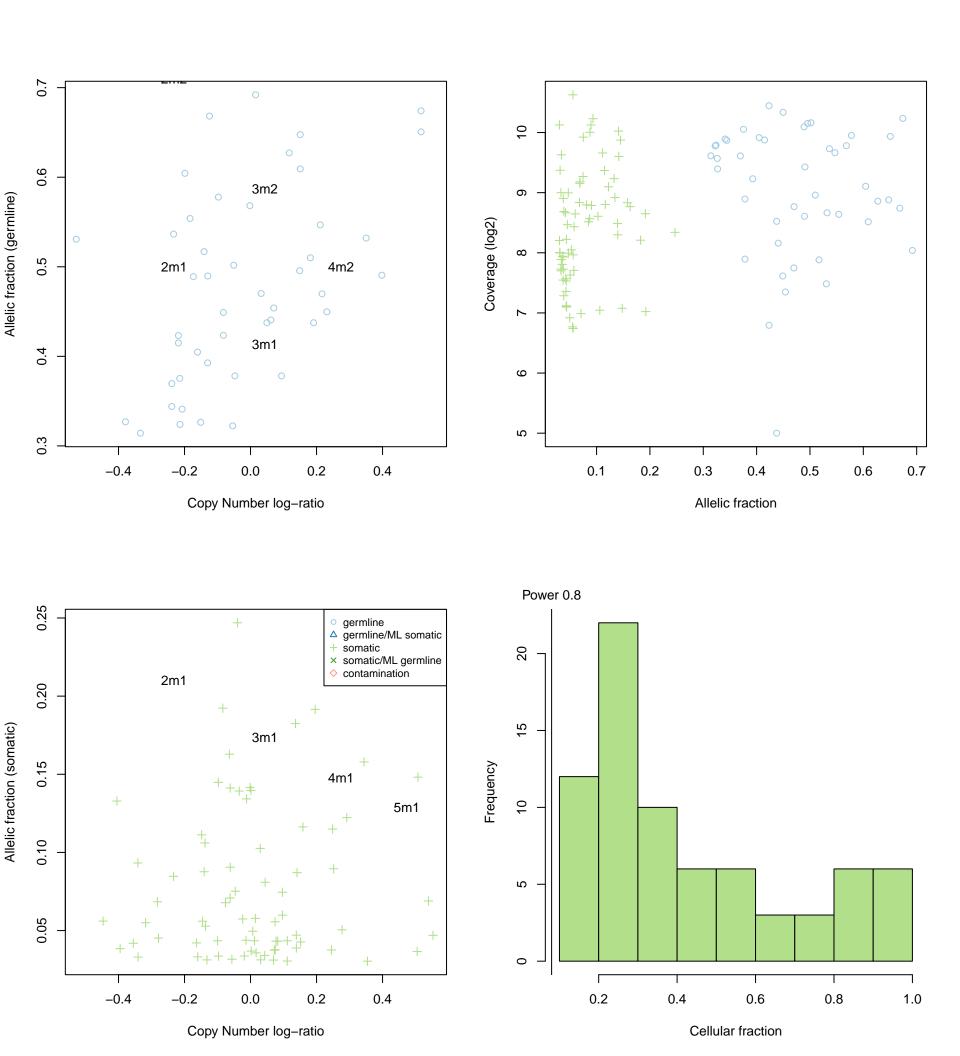




SCNA-fit log-likelihood: -1957.19

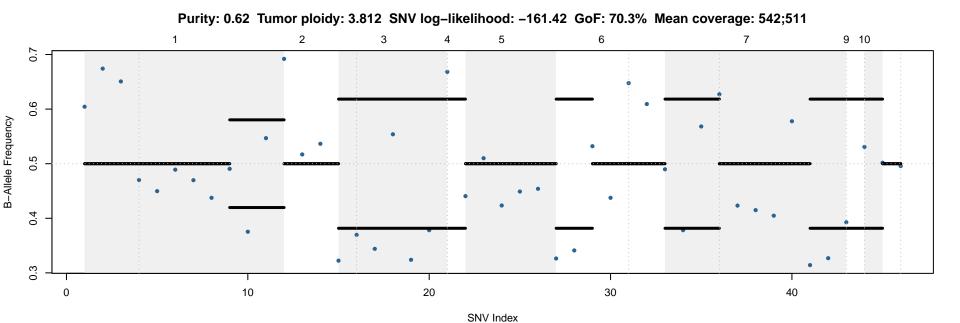




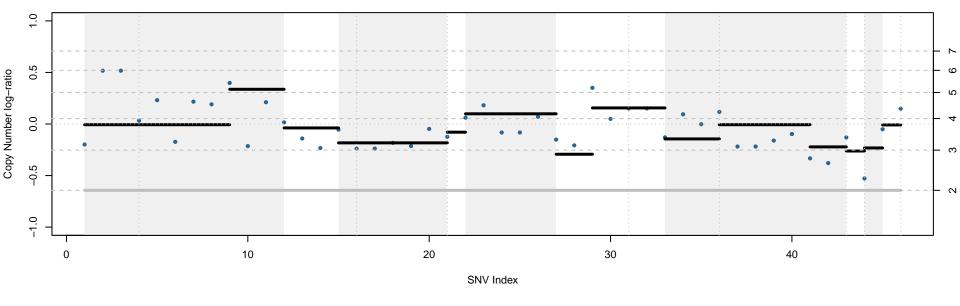


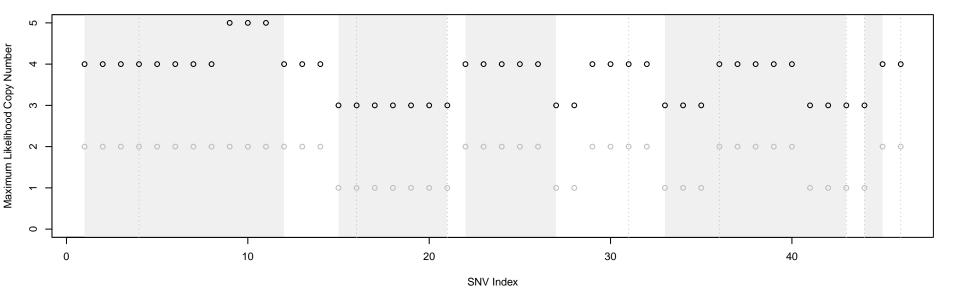
Purity: 0.62 Tumor ploidy: 3.812 3 6 5 Fraction Genome 0.05 0.00 -0.4 -0.2 0.0 0.2 0.4 0.6

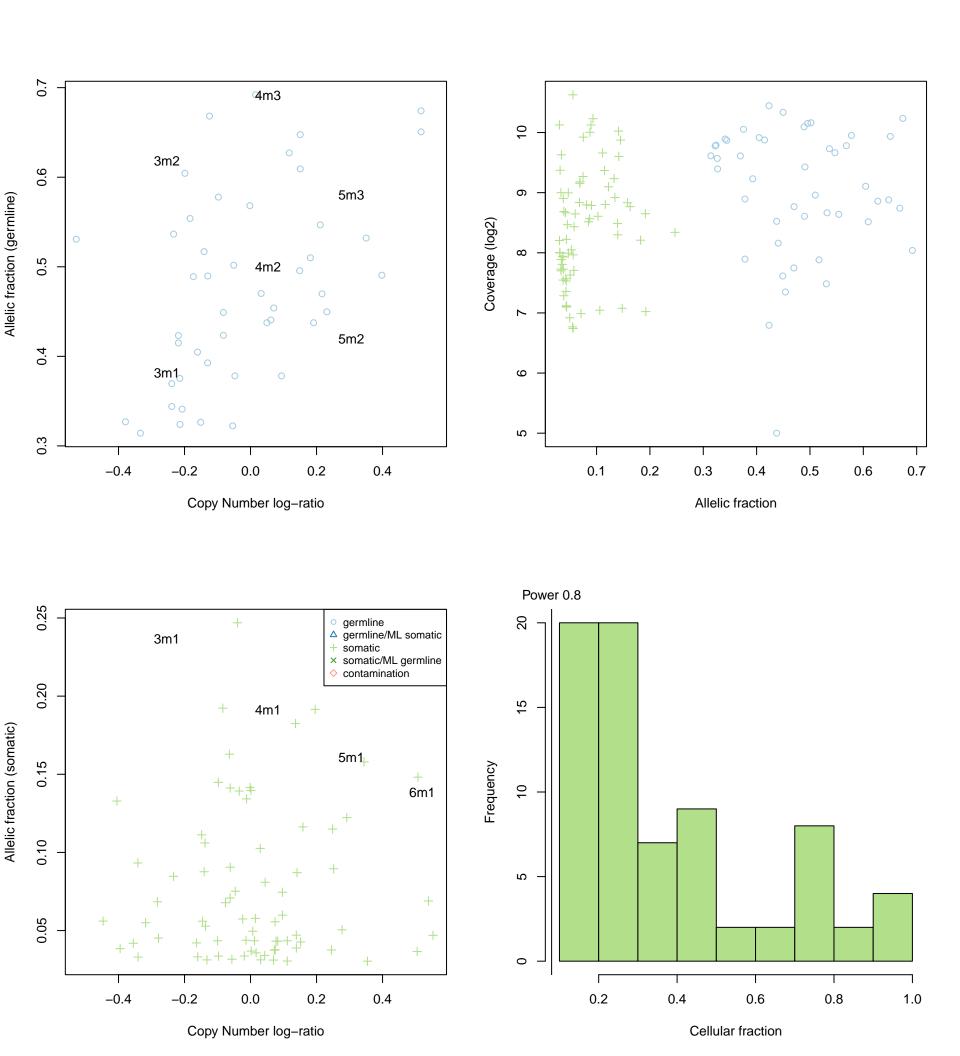
log2 ratio



SCNA-fit log-likelihood: -1984.44

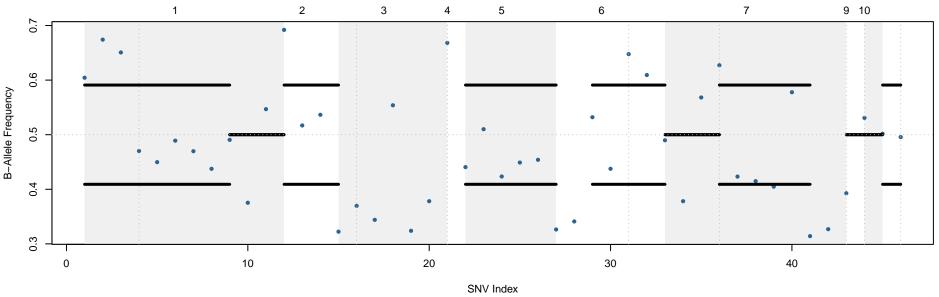




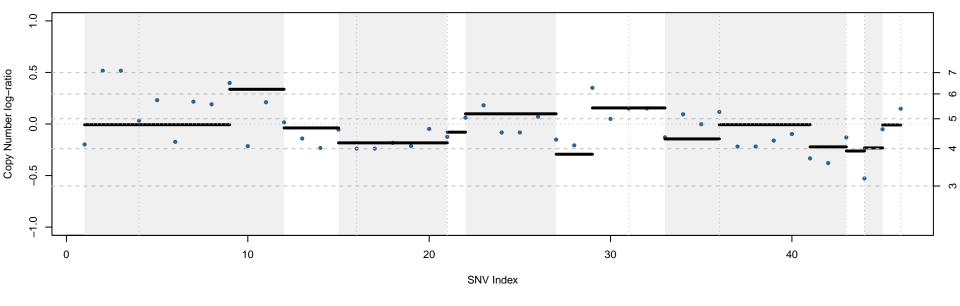


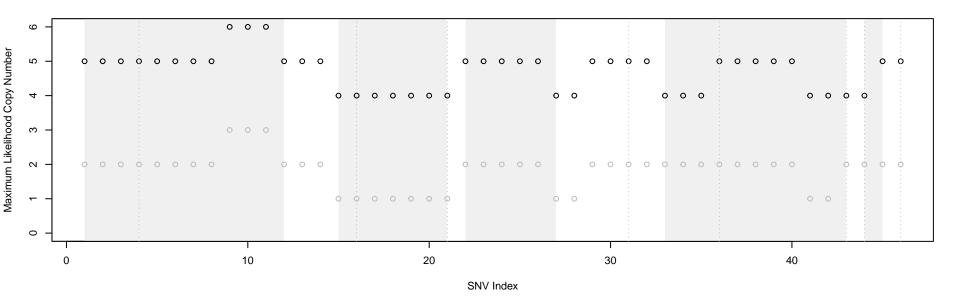
Purity: 0.8 Tumor ploidy: 4.81 6 7 5 4 Fraction Genome 0.05 0.00 -0.4 -0.2 0.0 0.2 0.4 0.6 log2 ratio

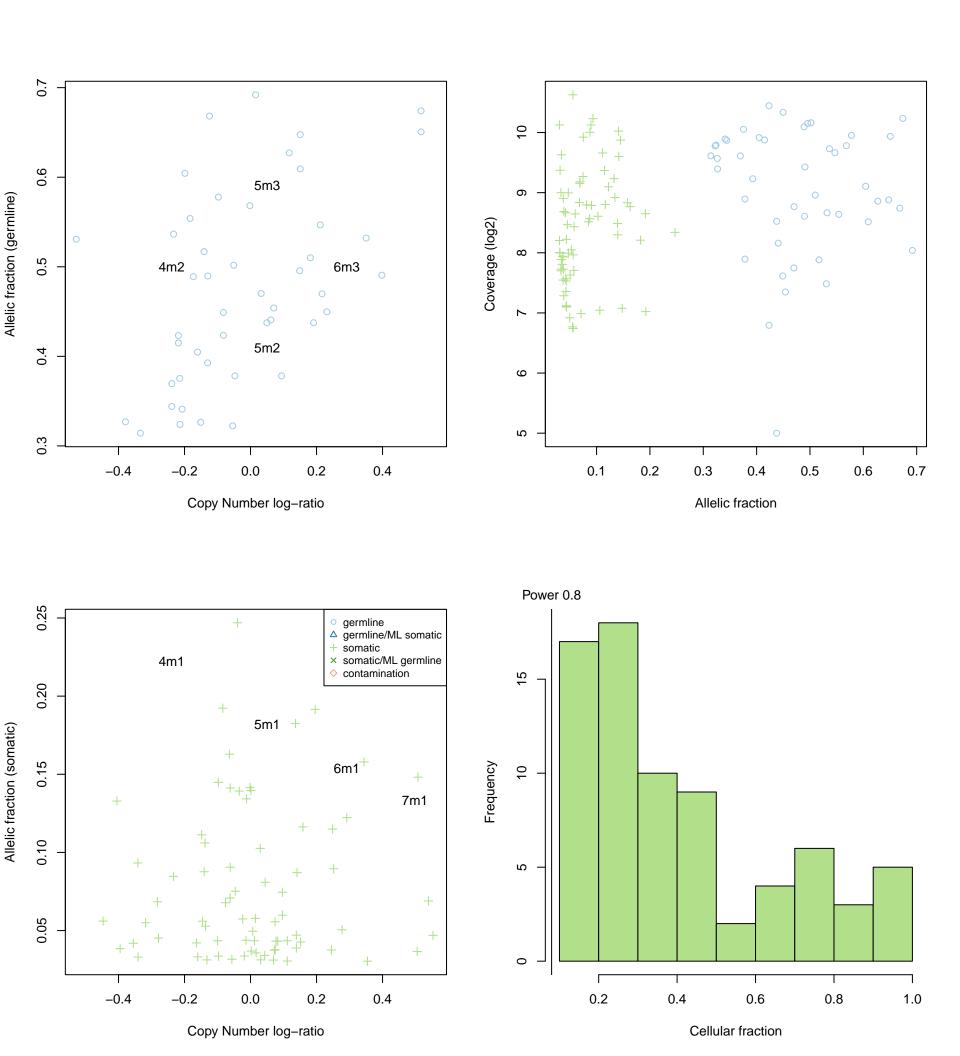
Purity: 0.8 Tumor ploidy: 4.81 SNV log-likelihood: -188.09 GoF: 73.6% Mean coverage: 542;511



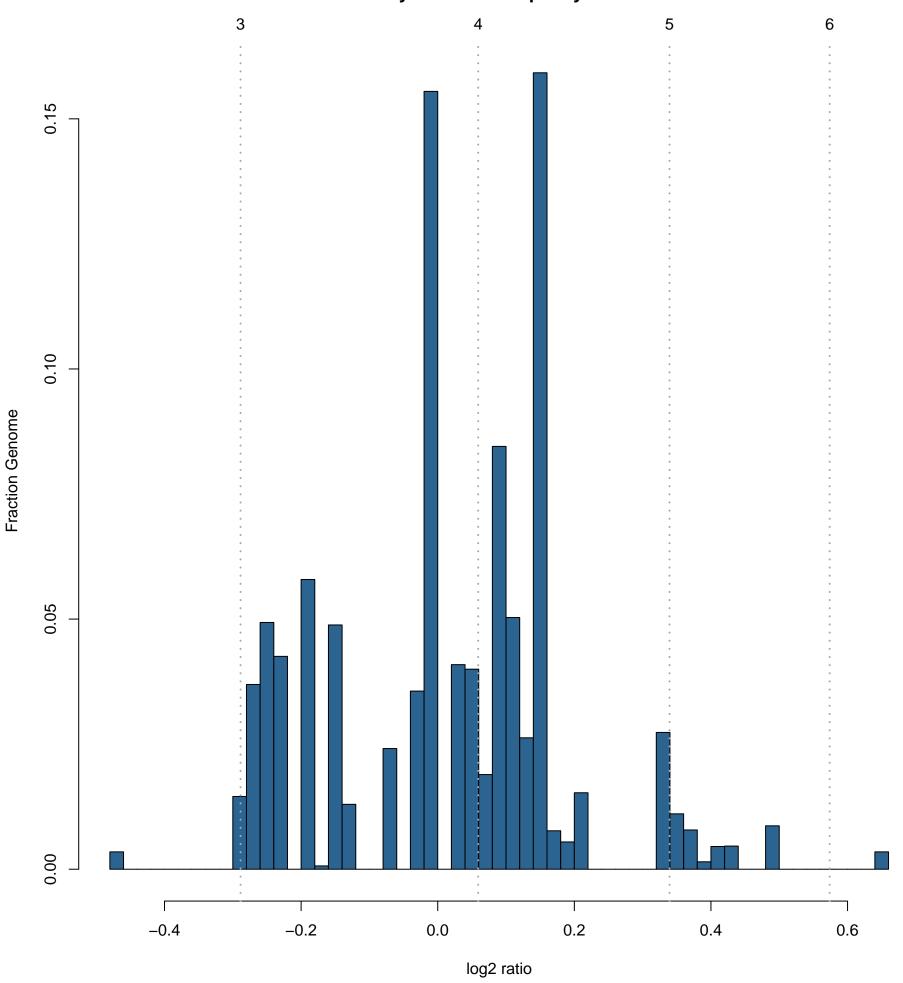
SCNA-fit log-likelihood: -1970.33

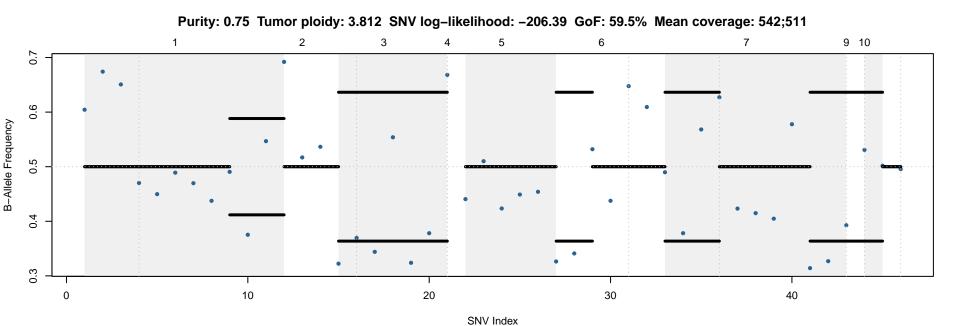




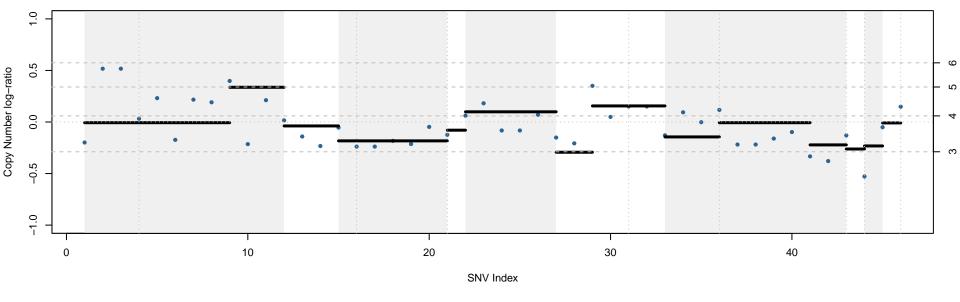


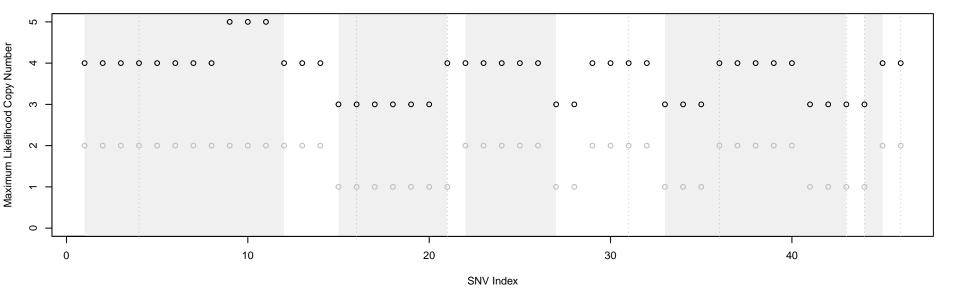
Purity: 0.75 Tumor ploidy: 3.812

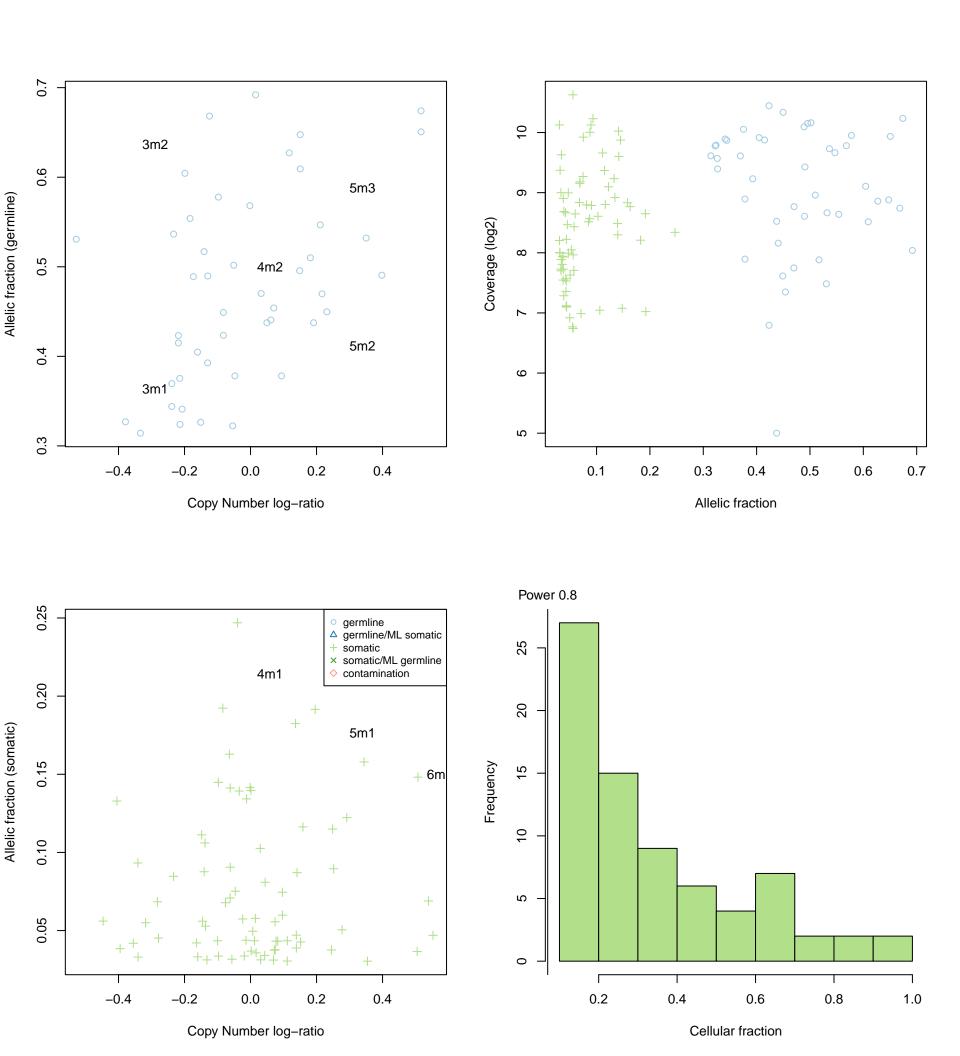




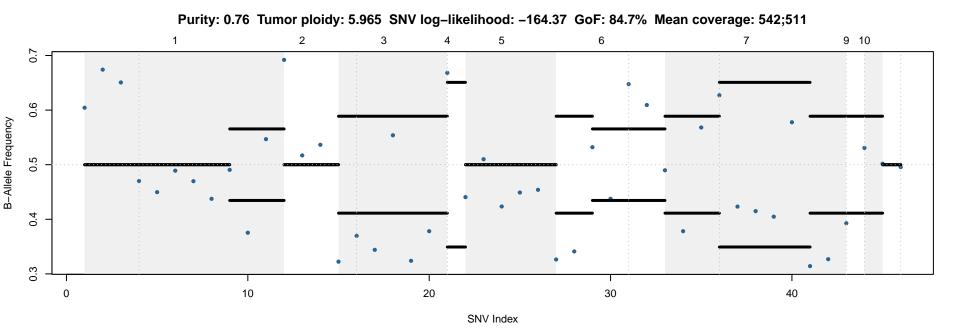
SCNA-fit log-likelihood: -2051.17



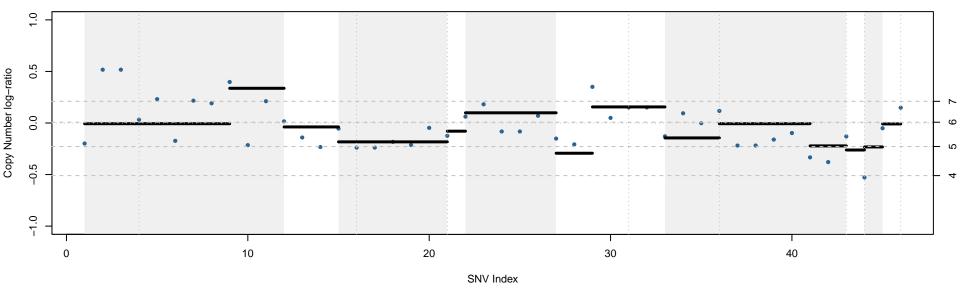


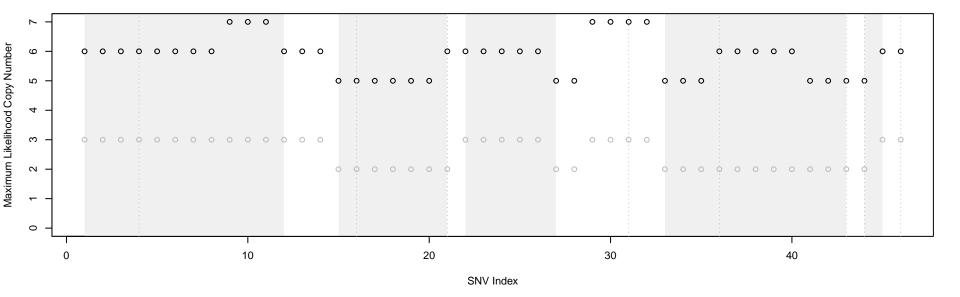


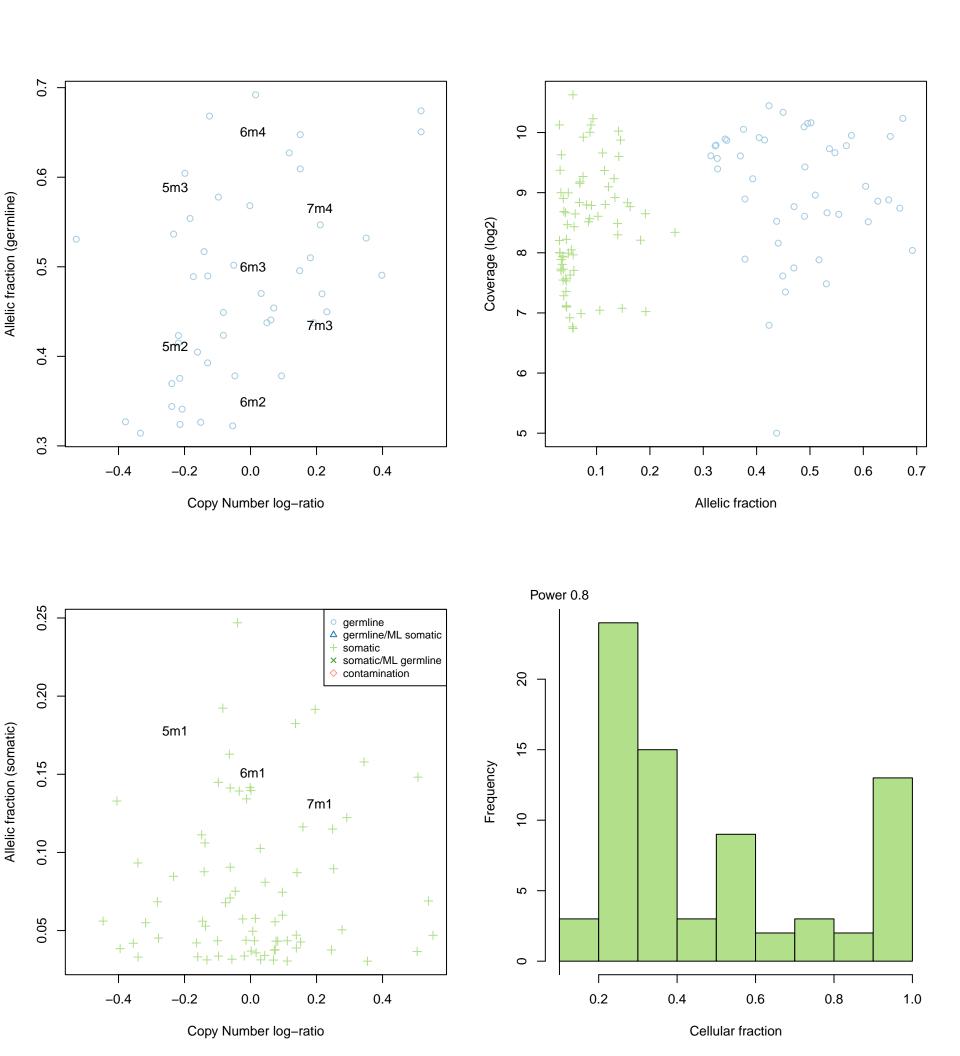
Purity: 0.76 Tumor ploidy: 5.965 5 4 6 Fraction Genome 0.05 0.00 -0.4 -0.2 0.0 0.2 0.4 0.6 log2 ratio



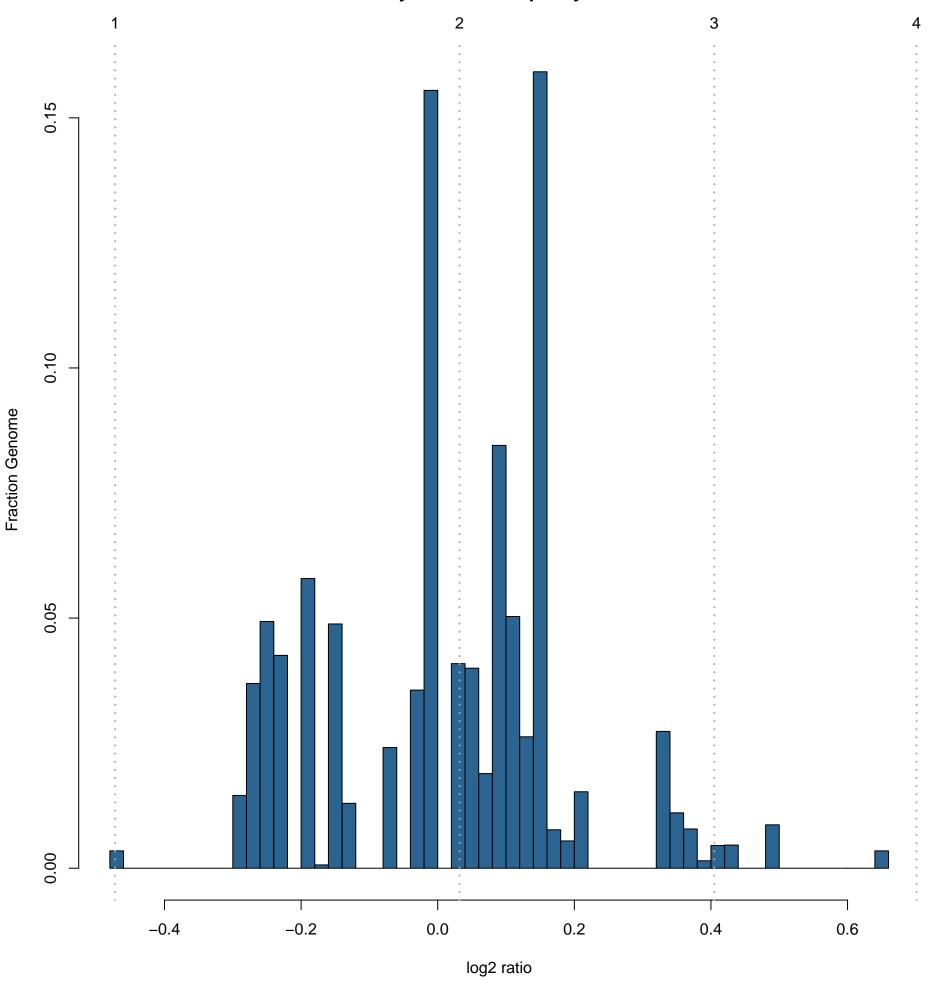
SCNA-fit log-likelihood: -2186.23



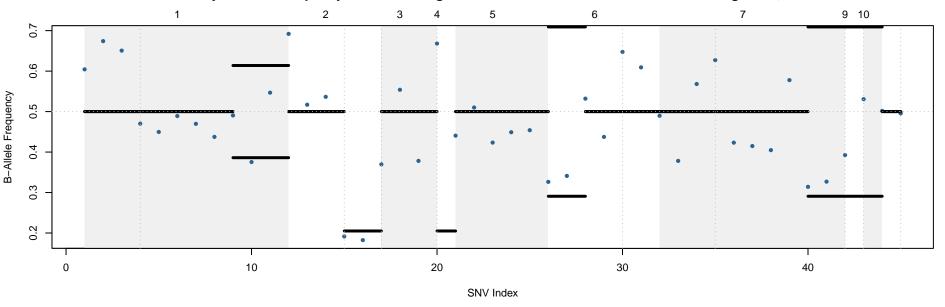




Purity: 0.59 Tumor ploidy: 1.926



Purity: 0.59 Tumor ploidy: 1.926 SNV log-likelihood: -361.92 GoF: 2.3% Mean coverage: 542;511



SCNA-fit log-likelihood: -2741.91

