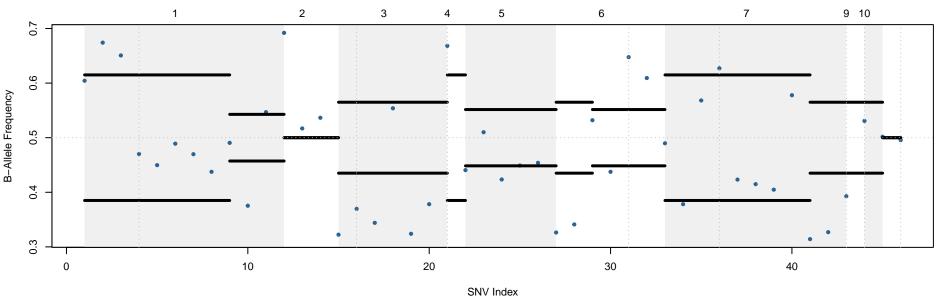
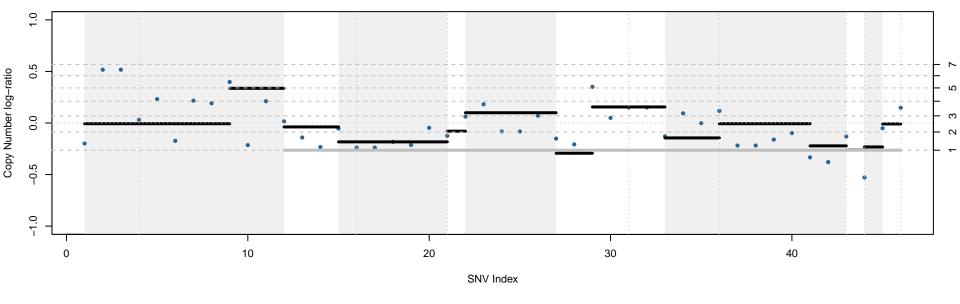
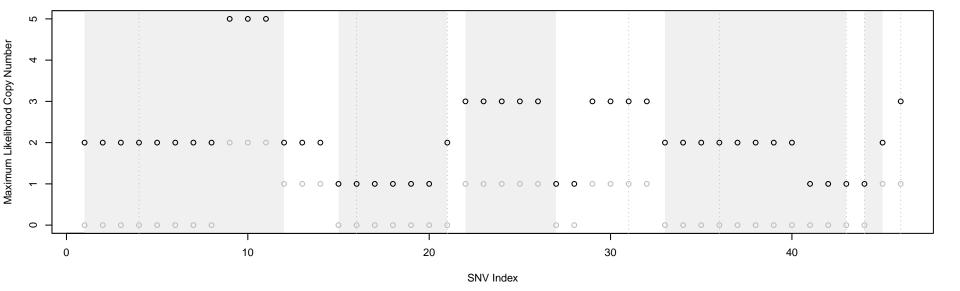
Purity: 0.23 Tumor ploidy: 2.544 2 3 6 7 5 Fraction Genome 0.05 0.00 -0.4 -0.2 0.0 0.2 0.4 0.6 log2 ratio

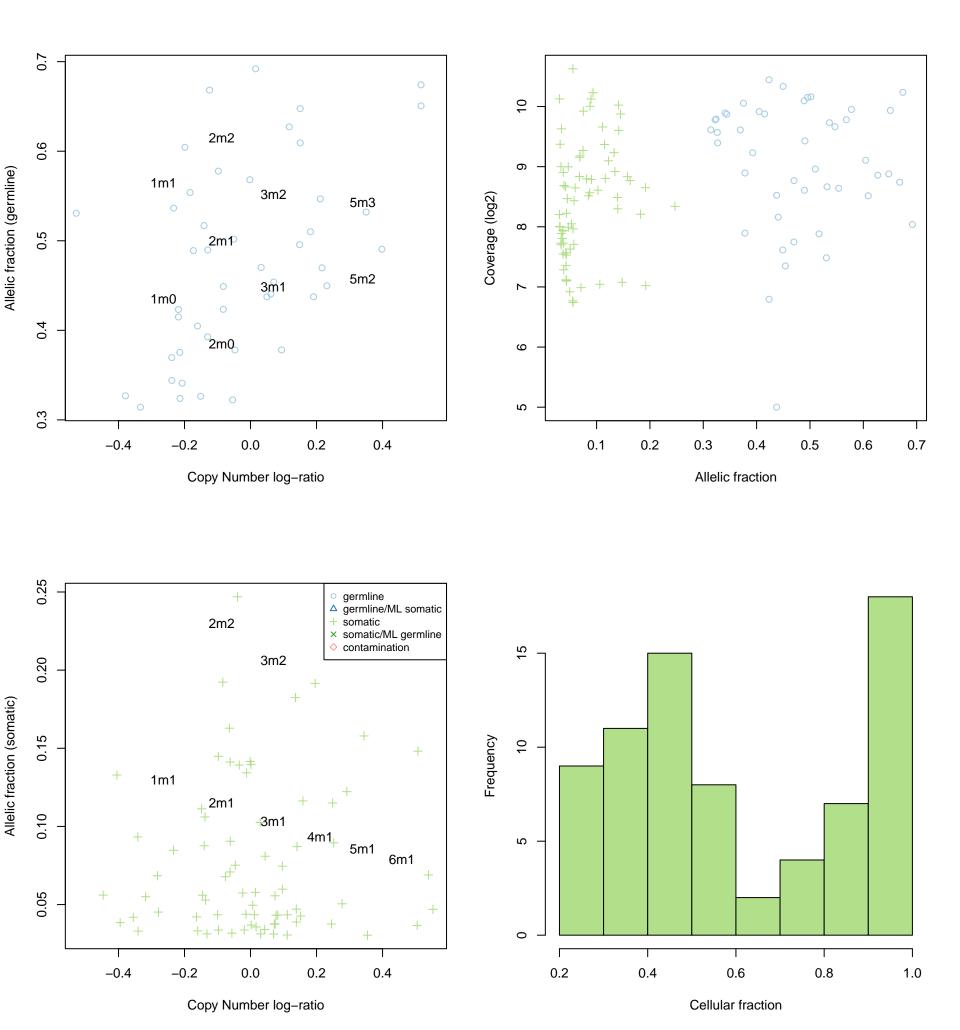
Purity: 0.23 Tumor ploidy: 2.544 SNV log-likelihood: -65.21 GoF: 91.7% Mean coverage: 542;511



SCNA-fit log-likelihood: -1803.15

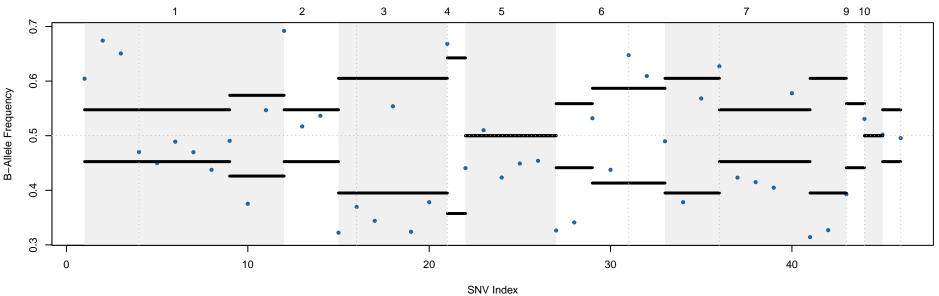




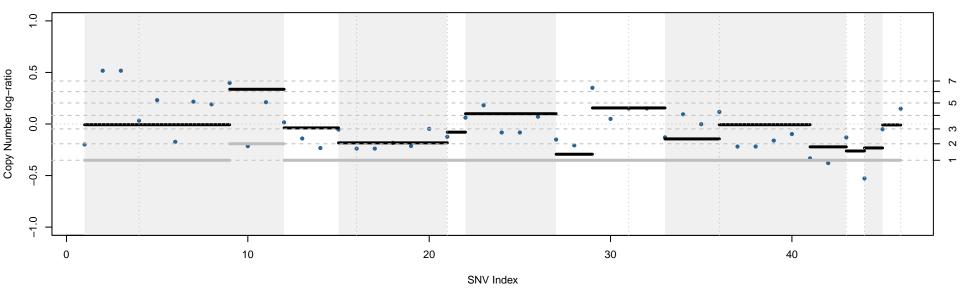


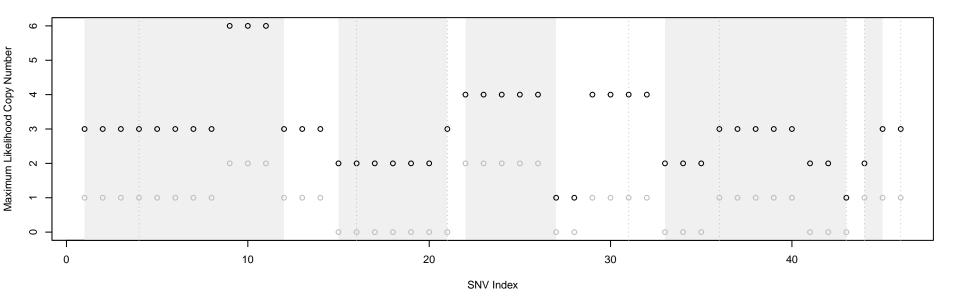
Purity: 0.21 Tumor ploidy: 3.353 2 3 5 6 7 Fraction Genome 0.05 0.00 -0.4 -0.2 0.0 0.2 0.4 0.6 log2 ratio

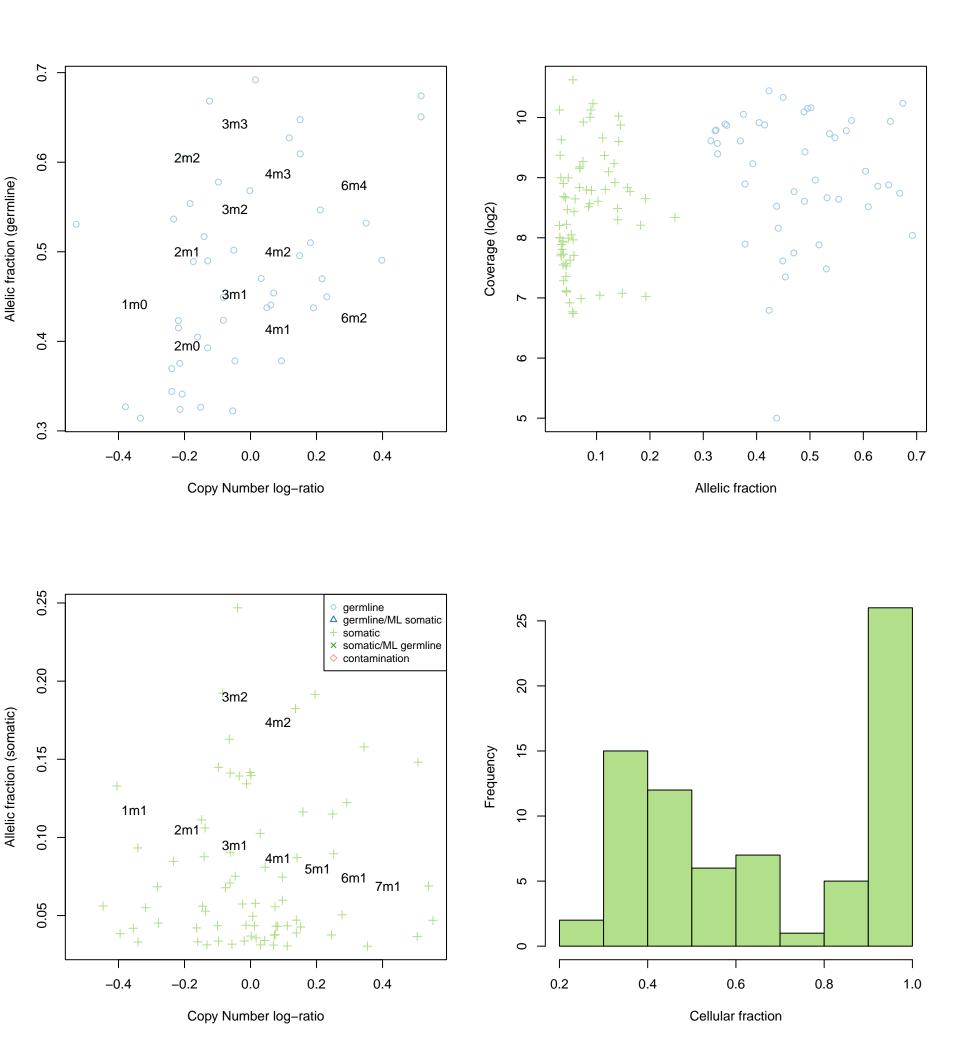




SCNA-fit log-likelihood: -1796.26

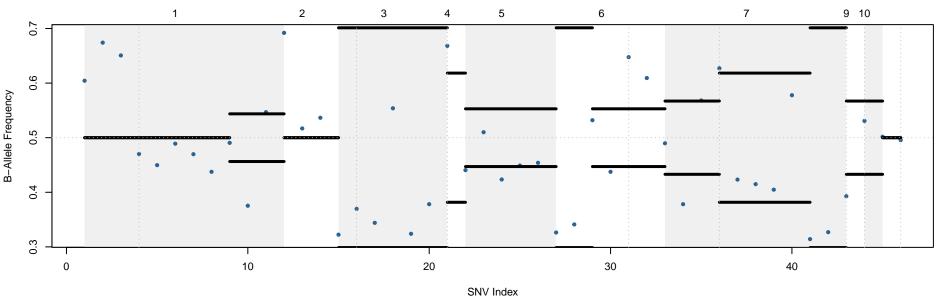




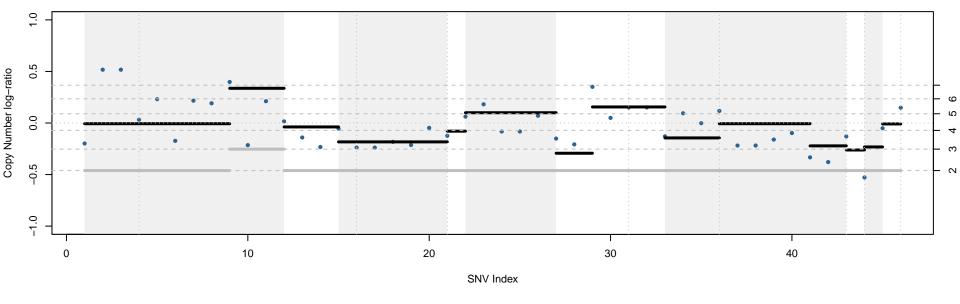


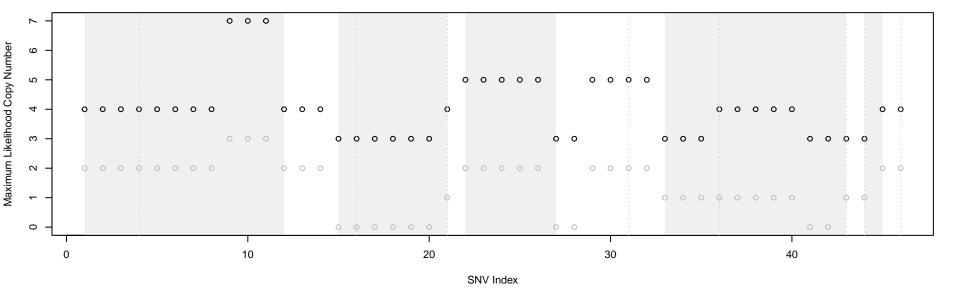
Purity: 0.31 Tumor ploidy: 4.431 2 3 5 6 7 Fraction Genome 0.05 0.00 -0.4 -0.2 0.0 0.2 0.4 0.6 log2 ratio

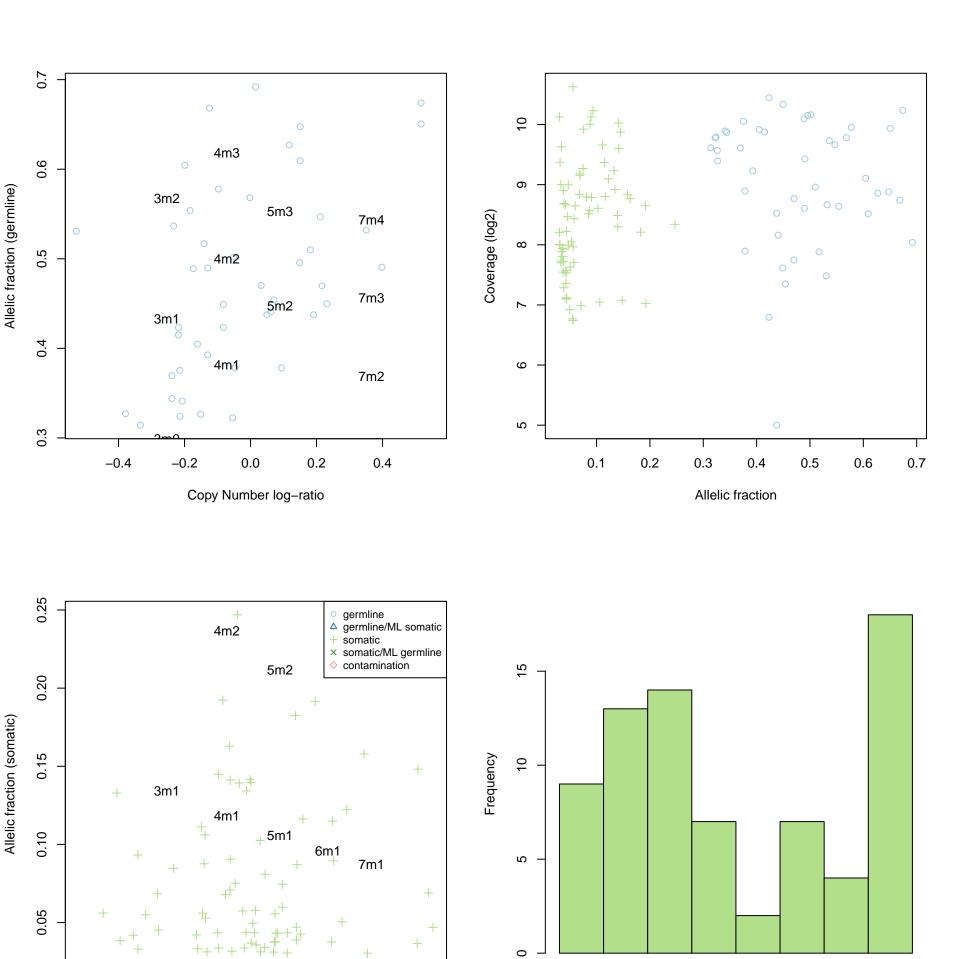
Purity: 0.31 Tumor ploidy: 4.431 SNV log-likelihood: -98.43 GoF: 93.1% Mean coverage: 542;511



SCNA-fit log-likelihood: -1819.59







0.2

0.4

-0.4

-0.2

0.0

Copy Number log-ratio

0.2

0.4

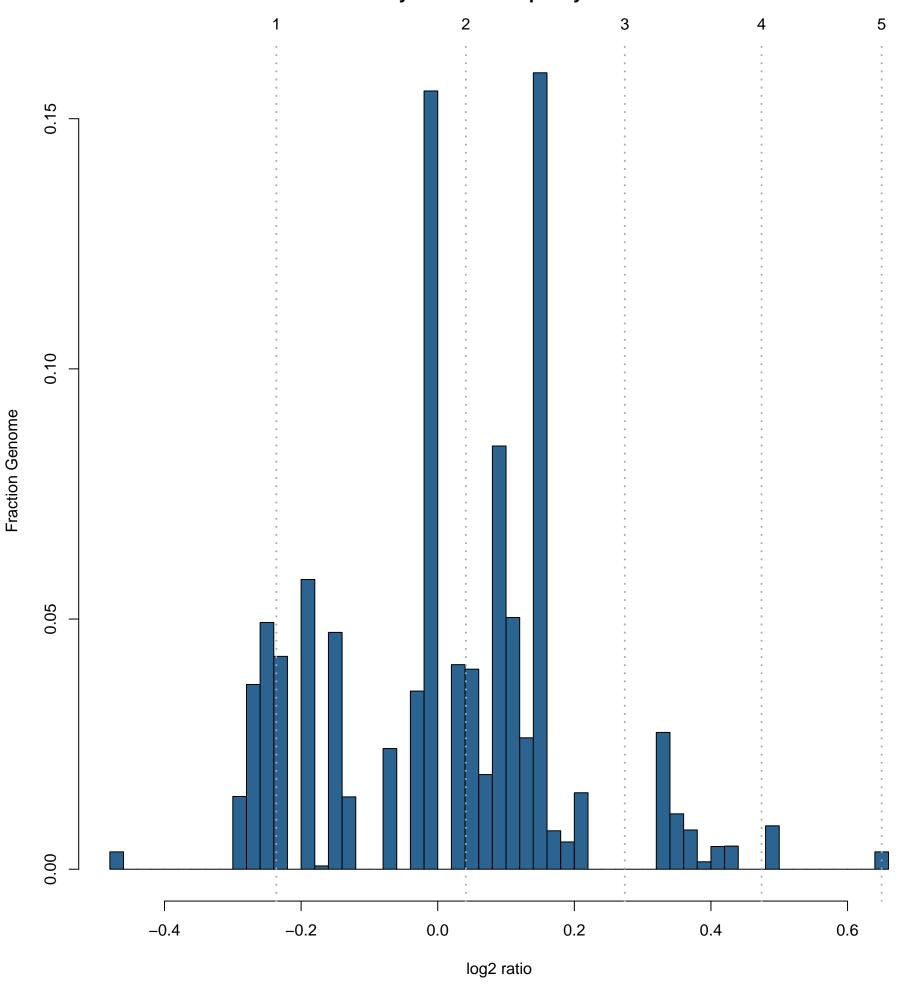
0.6

Cellular fraction

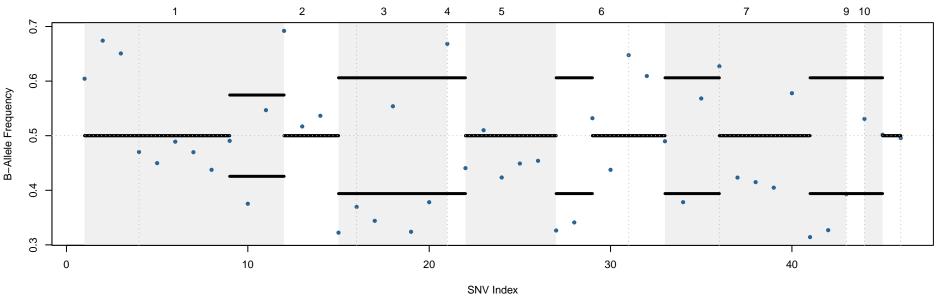
8.0

1.0

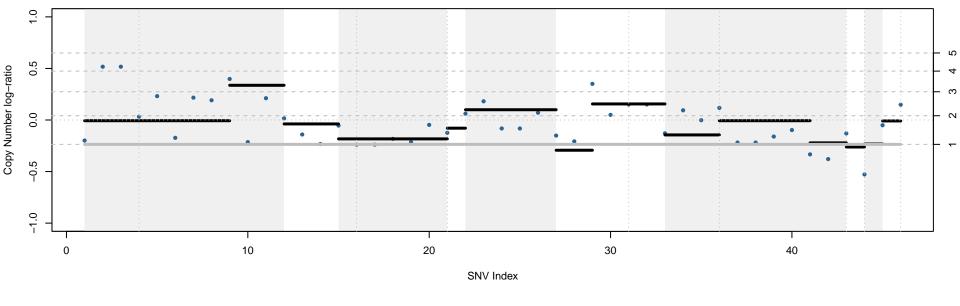
Purity: 0.35 Tumor ploidy: 1.839

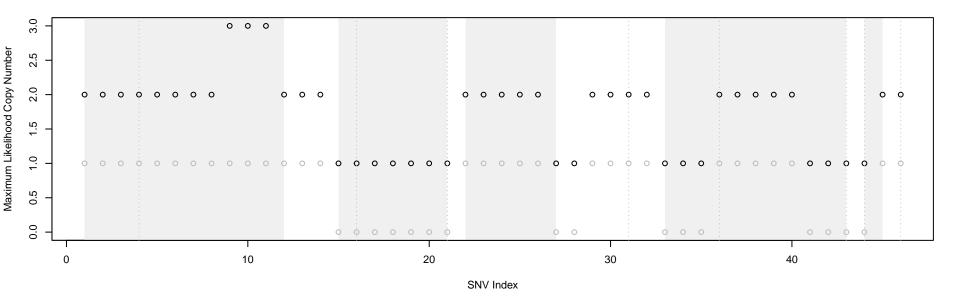


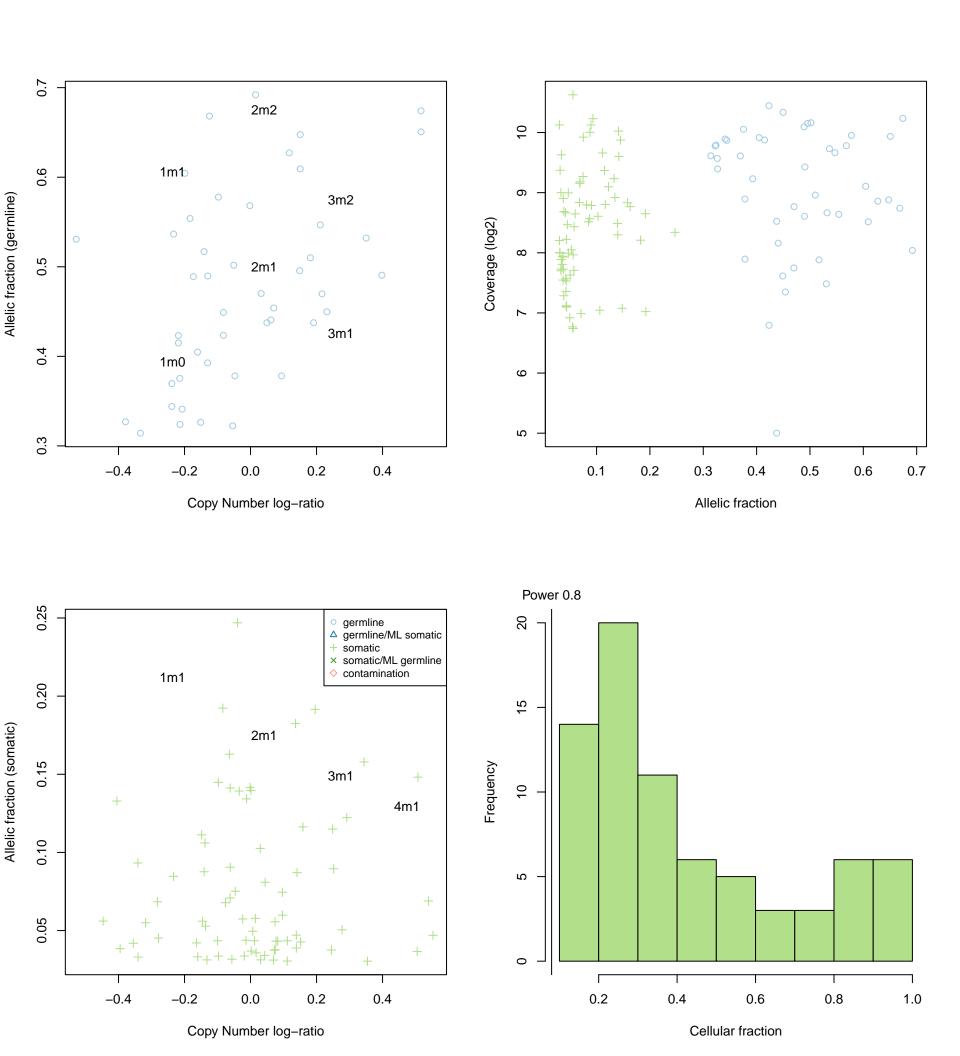




SCNA-fit log-likelihood: -1973.34

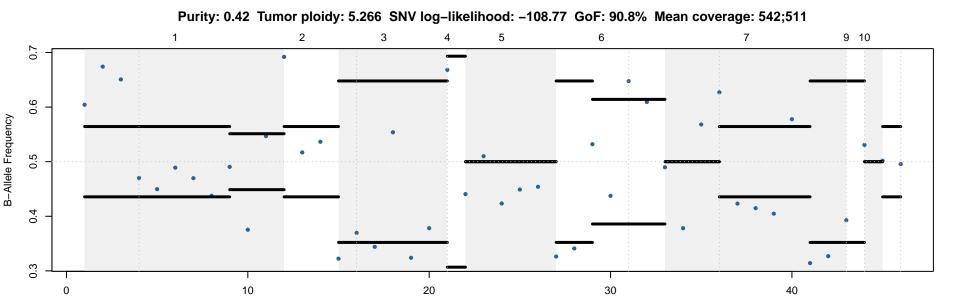






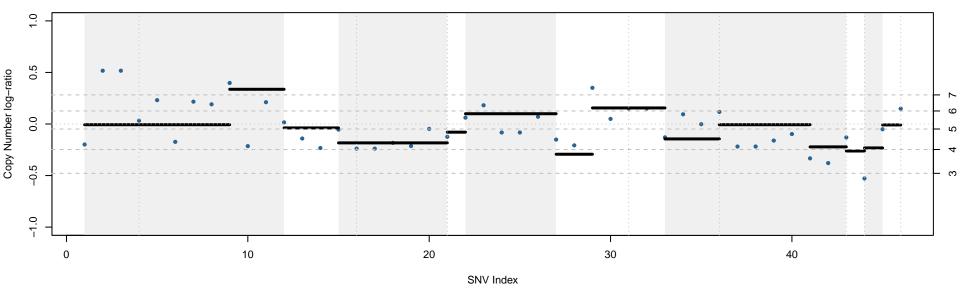
Purity: 0.42 Tumor ploidy: 5.266 3 5 6 Fraction Genome 0.05 0.00 -0.4 -0.2 0.0 0.2 0.4 0.6

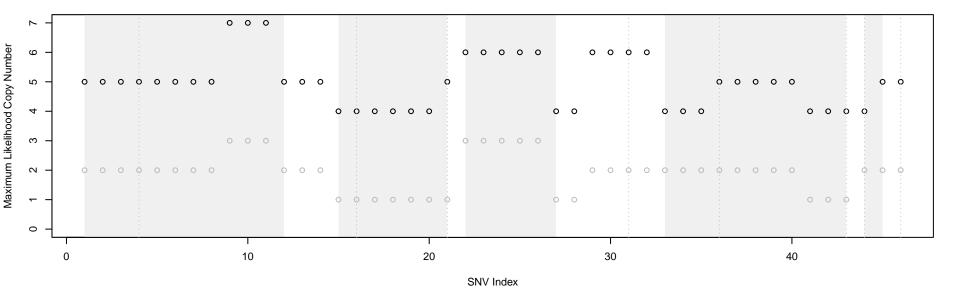
log2 ratio

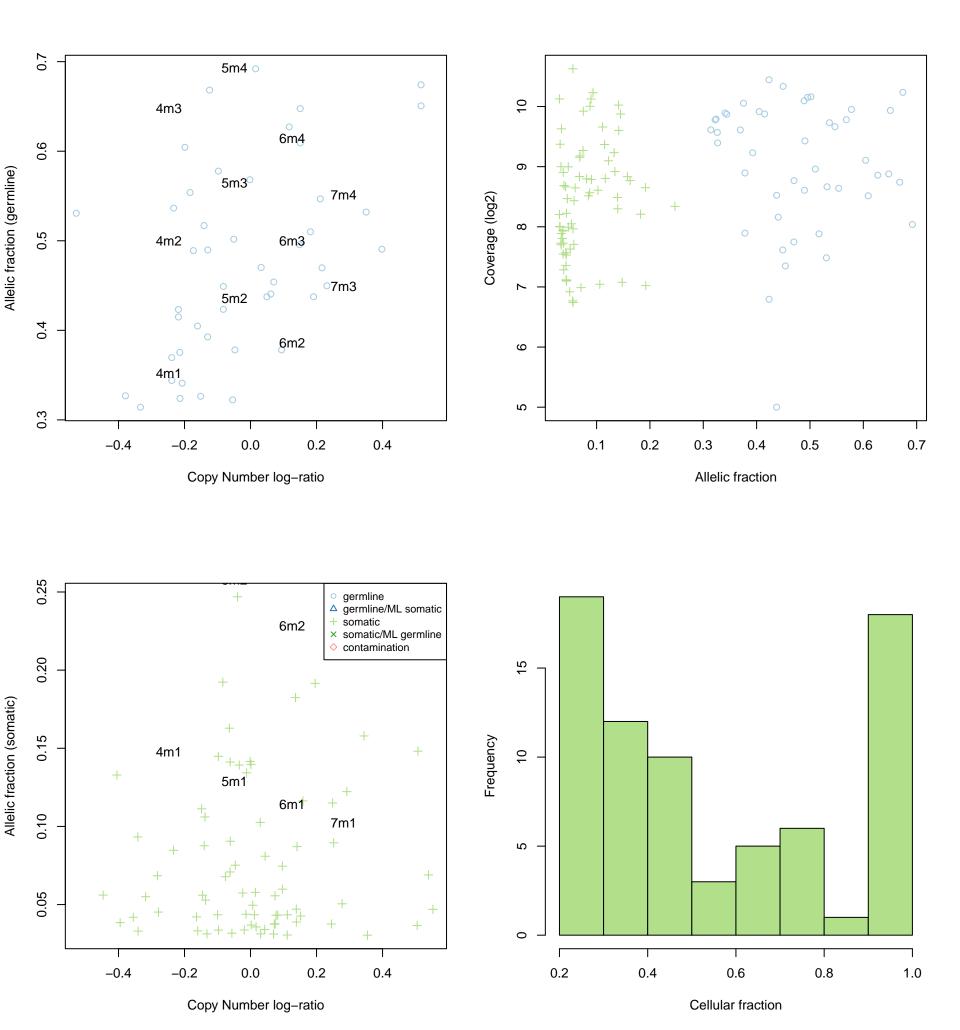


SCNA-fit log-likelihood: -1855.26

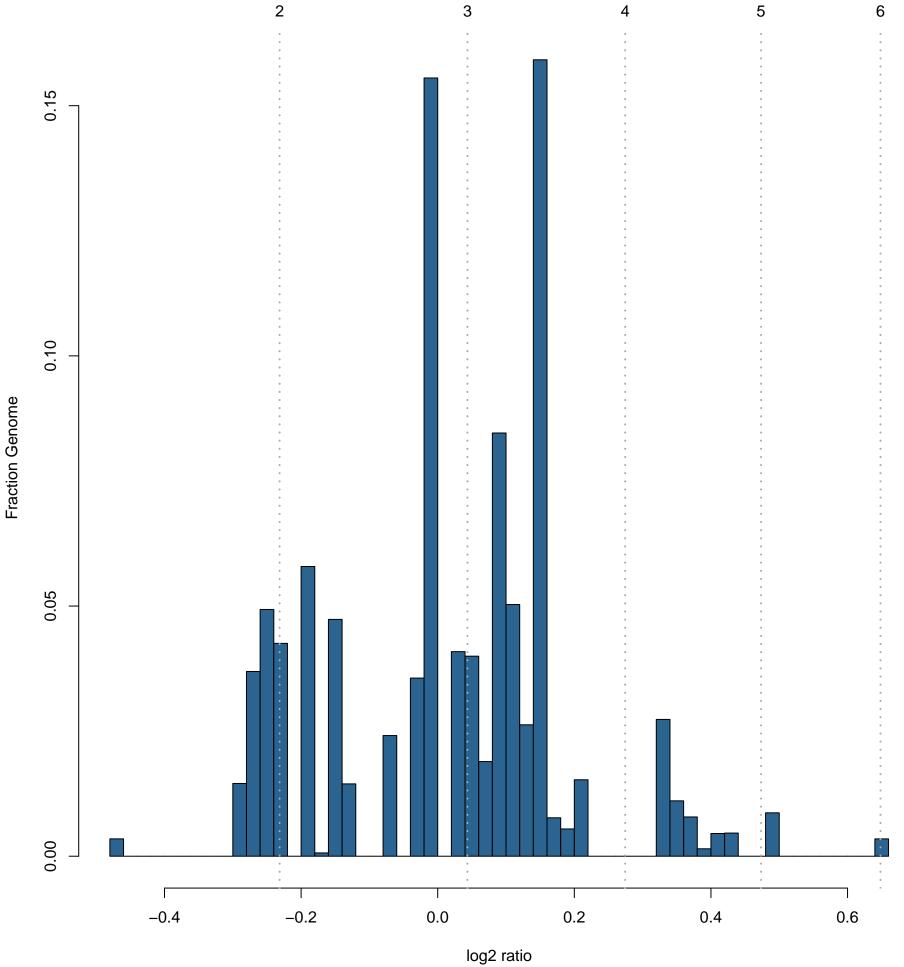
SNV Index



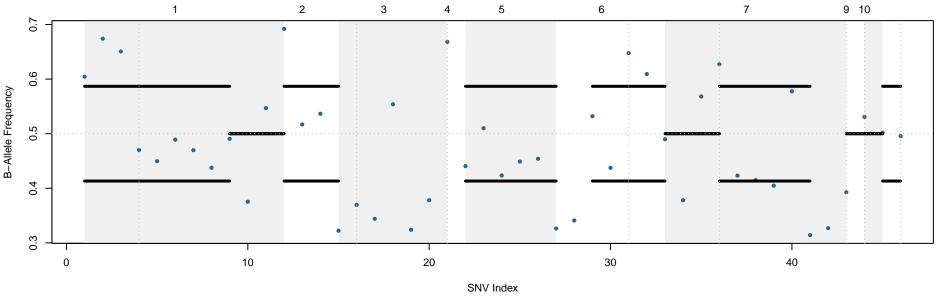




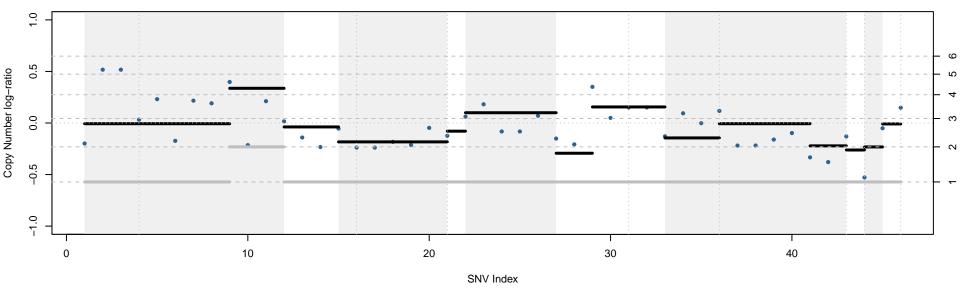
Purity: 0.42 Tumor ploidy: 2.829

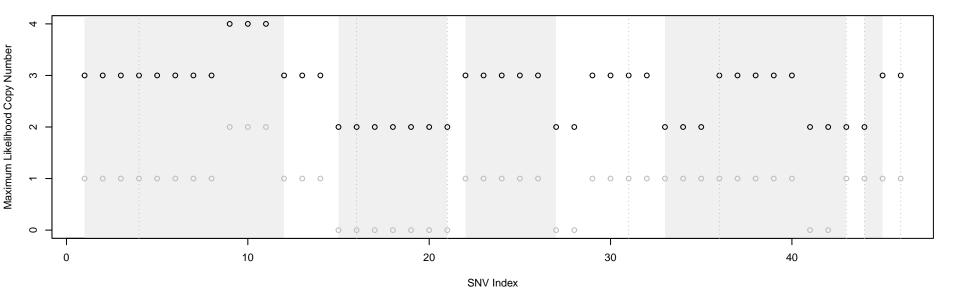


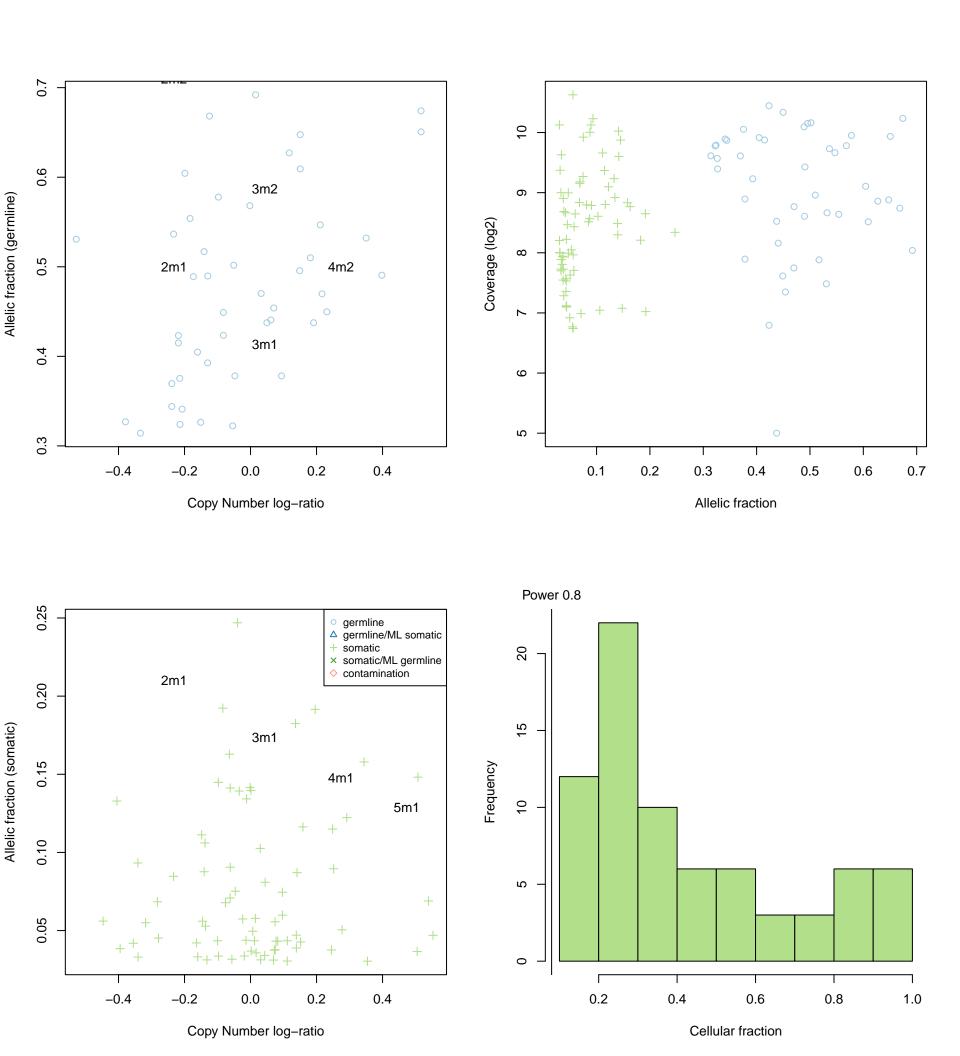
Purity: 0.42 Tumor ploidy: 2.829 SNV log-likelihood: -107.56 GoF: 77% Mean coverage: 542;511



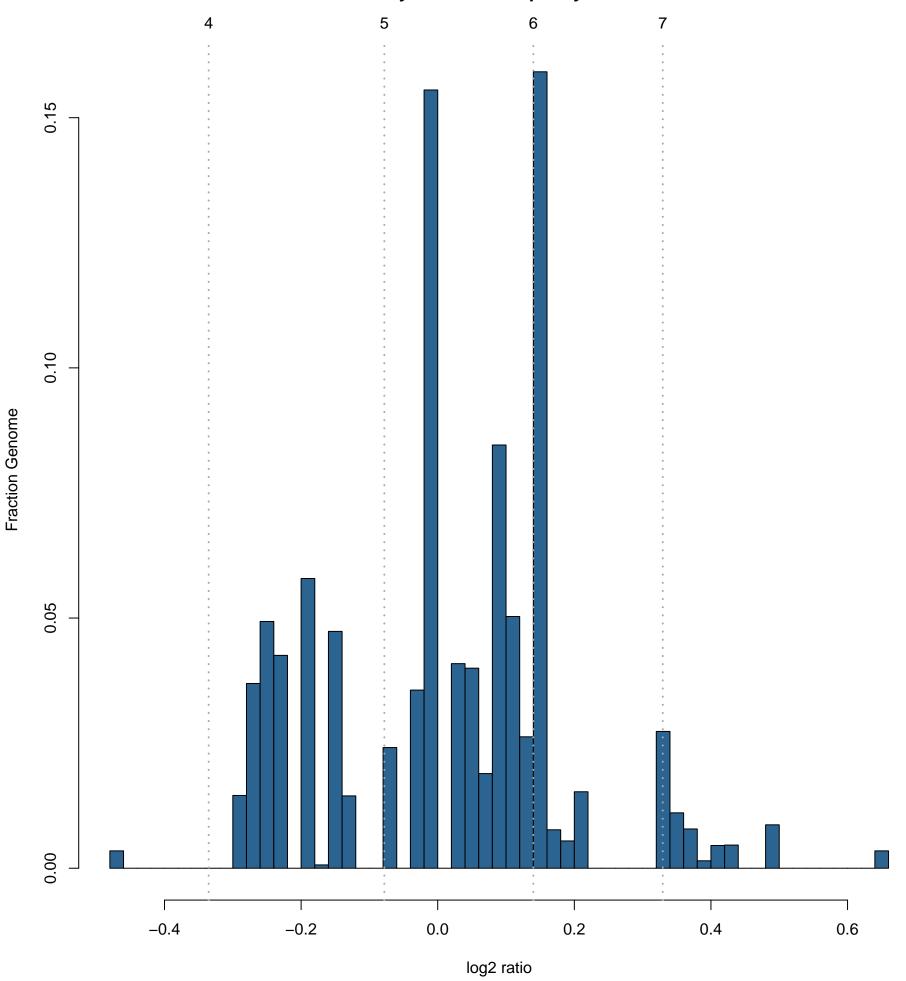
SCNA-fit log-likelihood: -1957.74

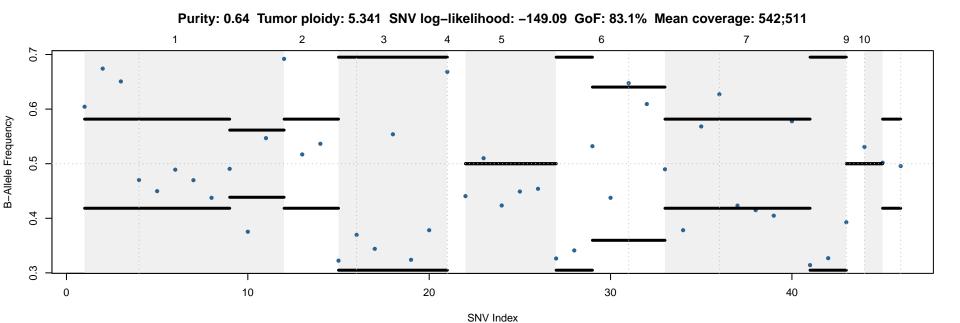




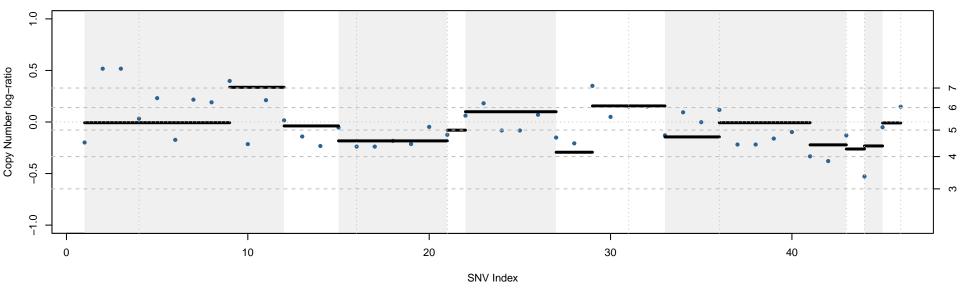


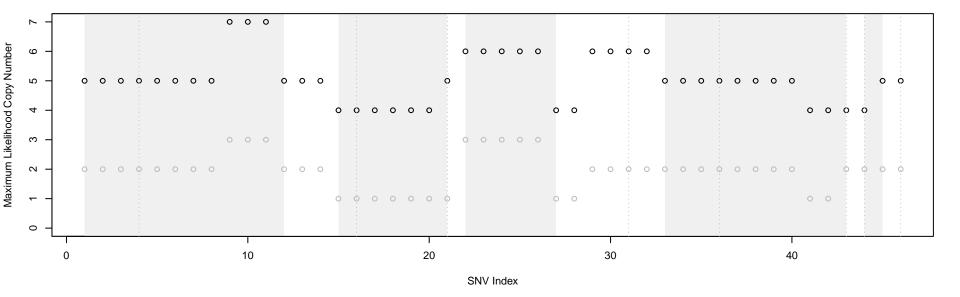
Purity: 0.64 Tumor ploidy: 5.341

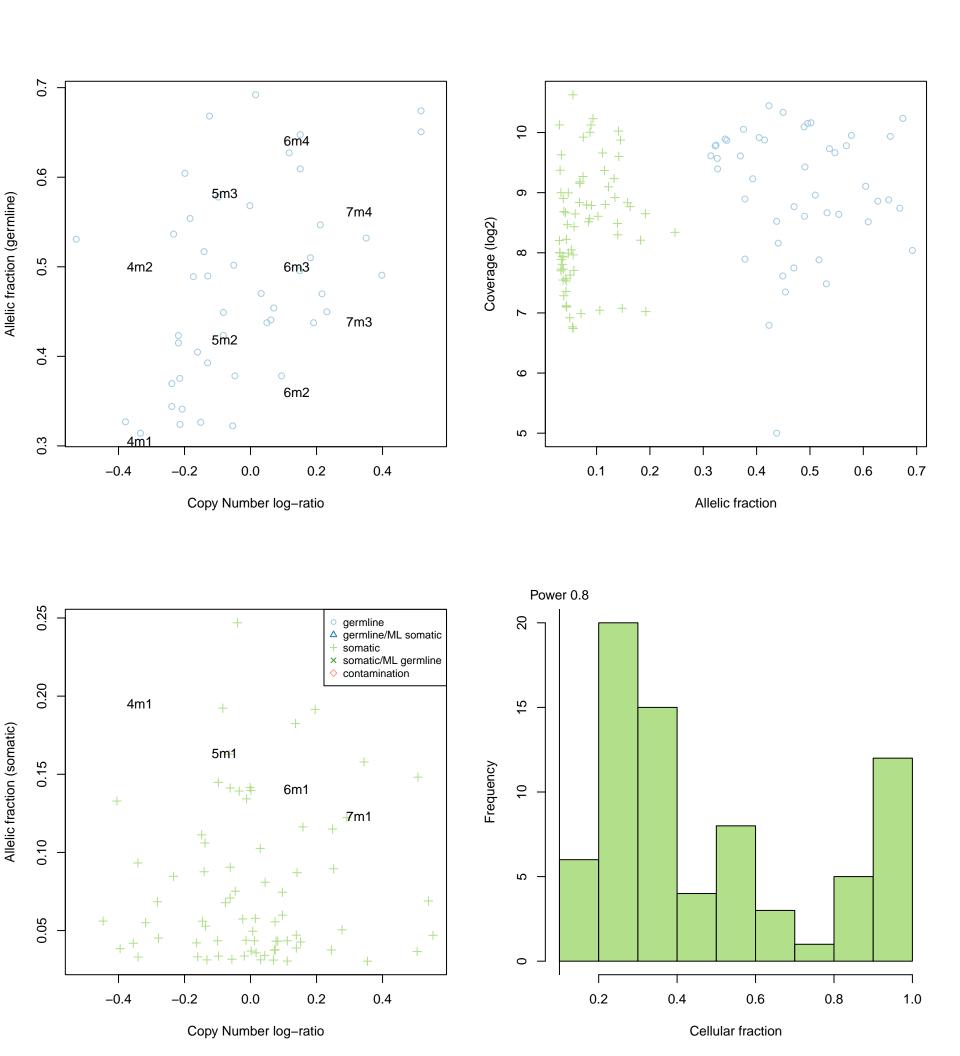




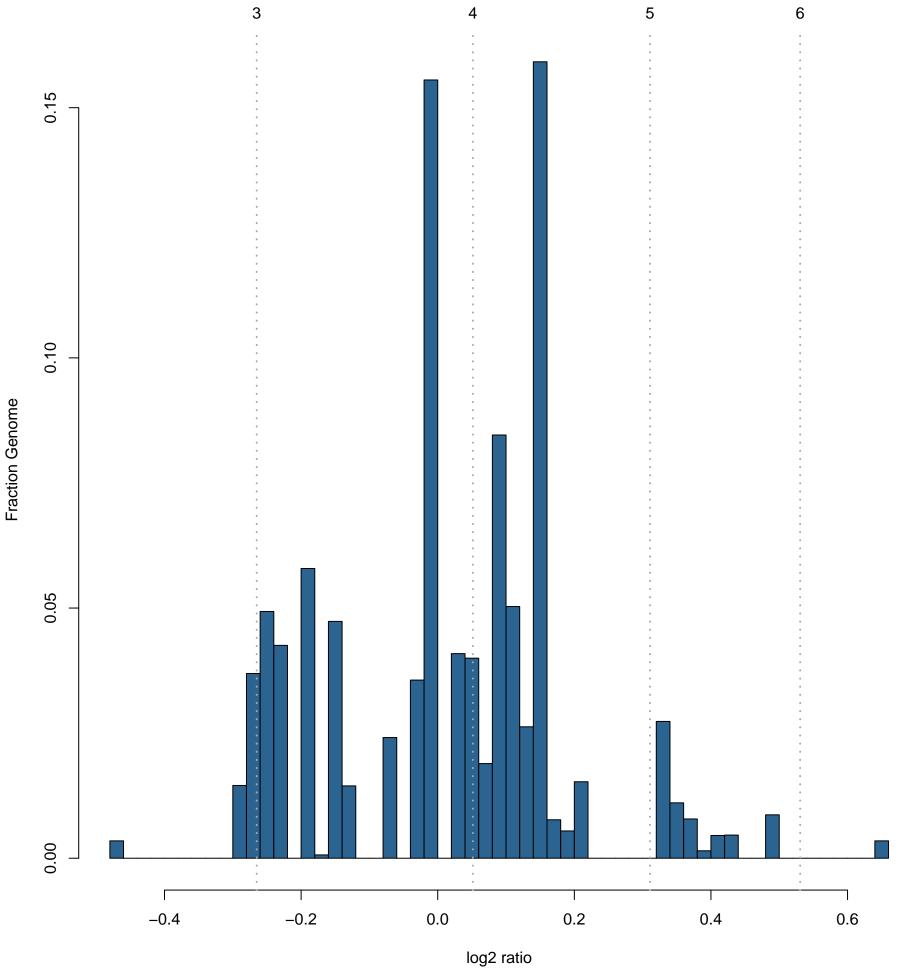
SCNA-fit log-likelihood: -1987.04

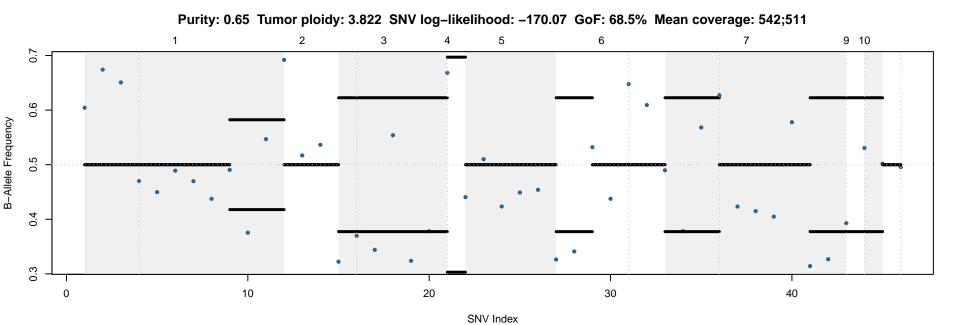




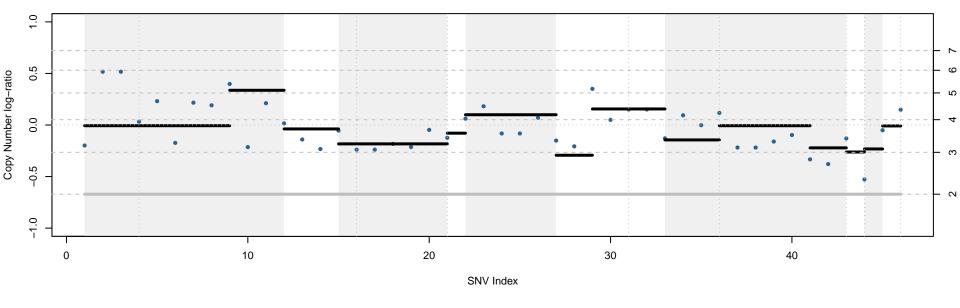


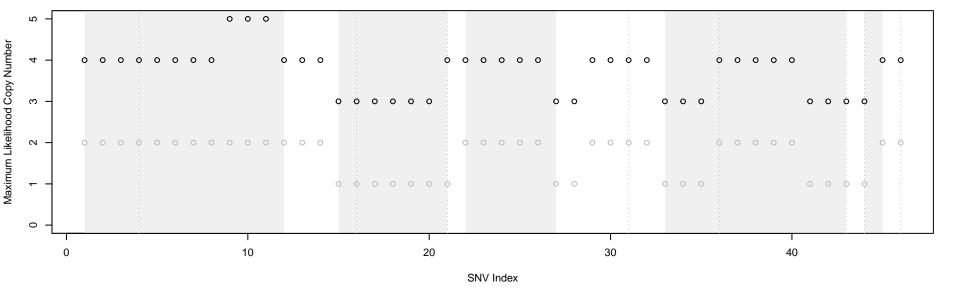
Purity: 0.65 Tumor ploidy: 3.822

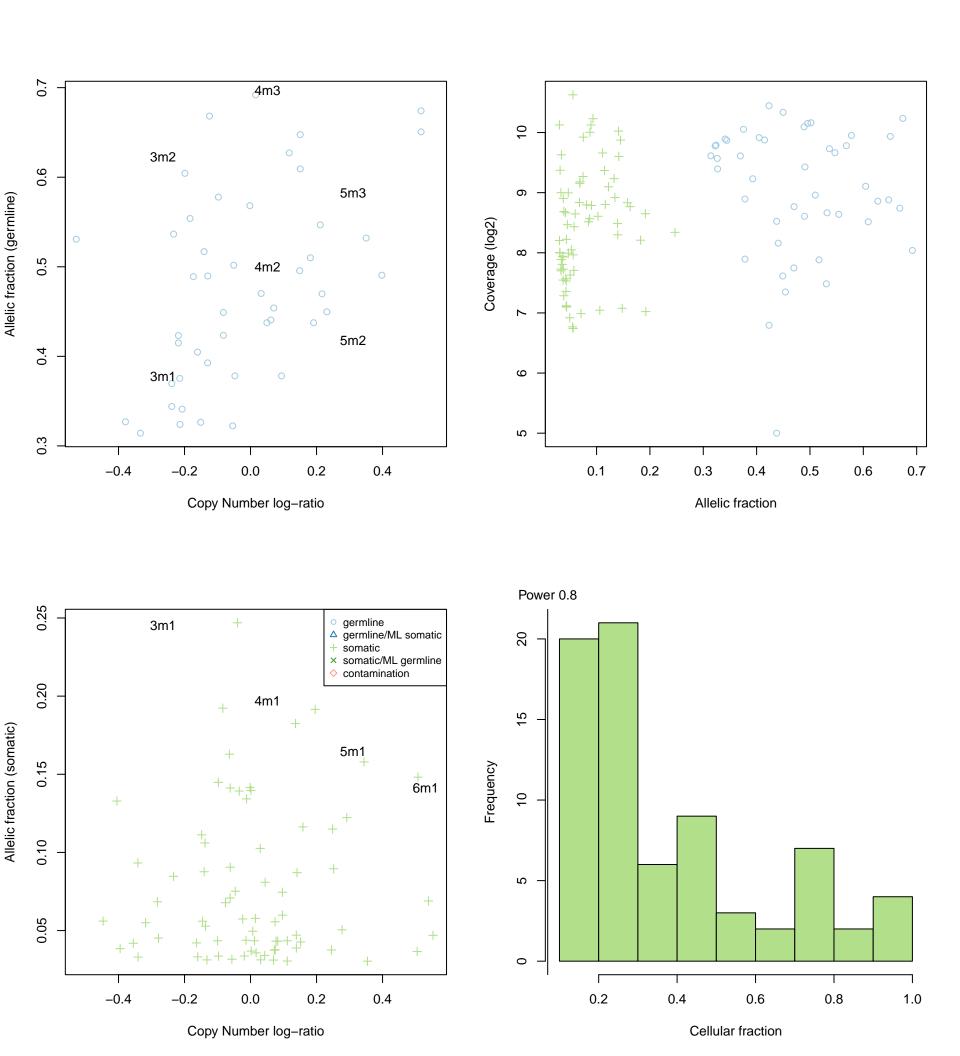




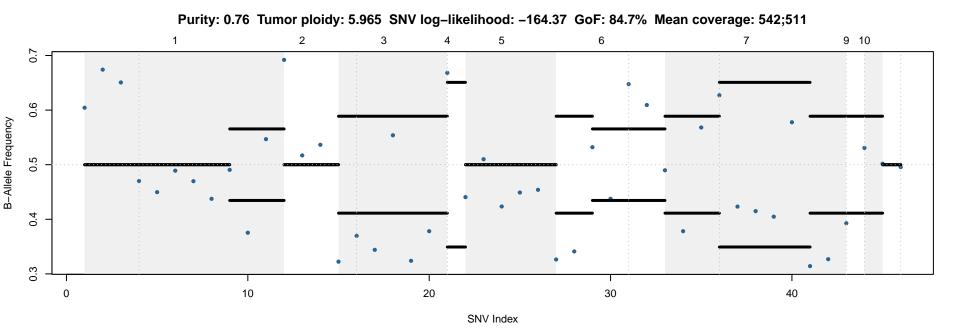
SCNA-fit log-likelihood: -1999.62



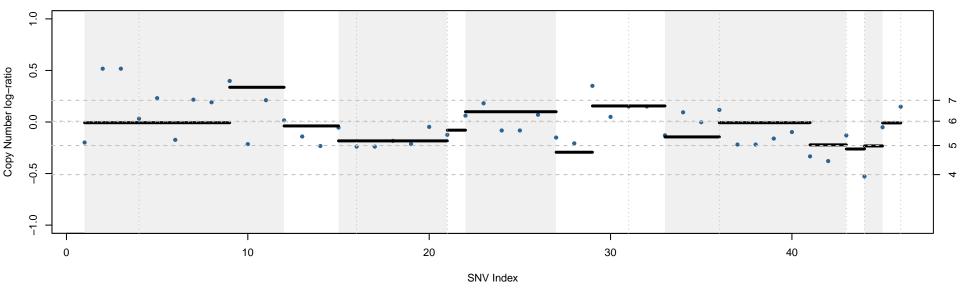


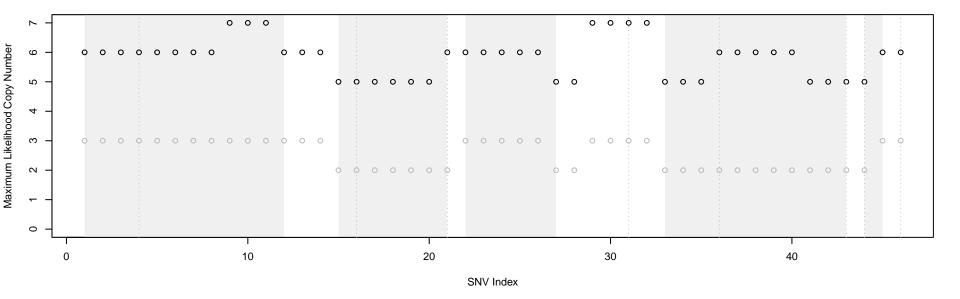


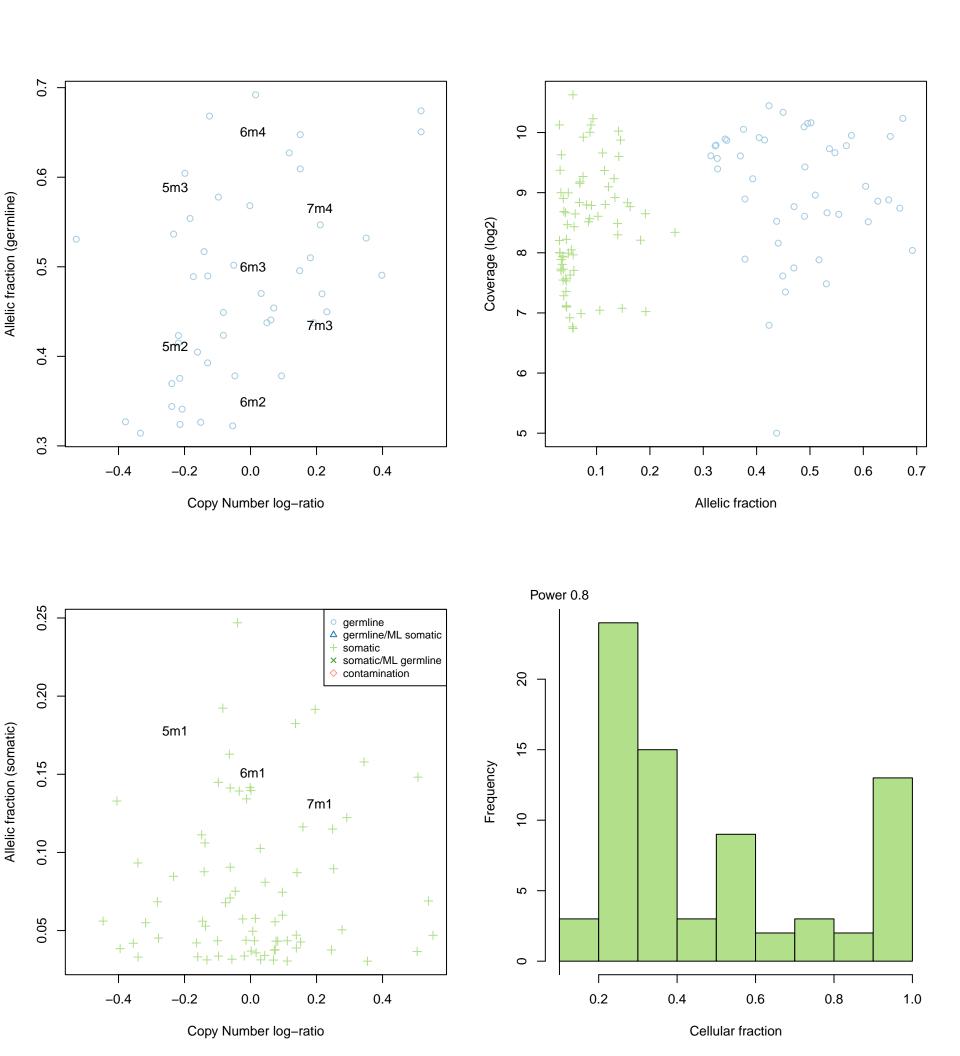
Purity: 0.76 Tumor ploidy: 5.965 5 4 6 Fraction Genome 0.05 0.00 -0.4 -0.2 0.0 0.2 0.4 0.6 log2 ratio



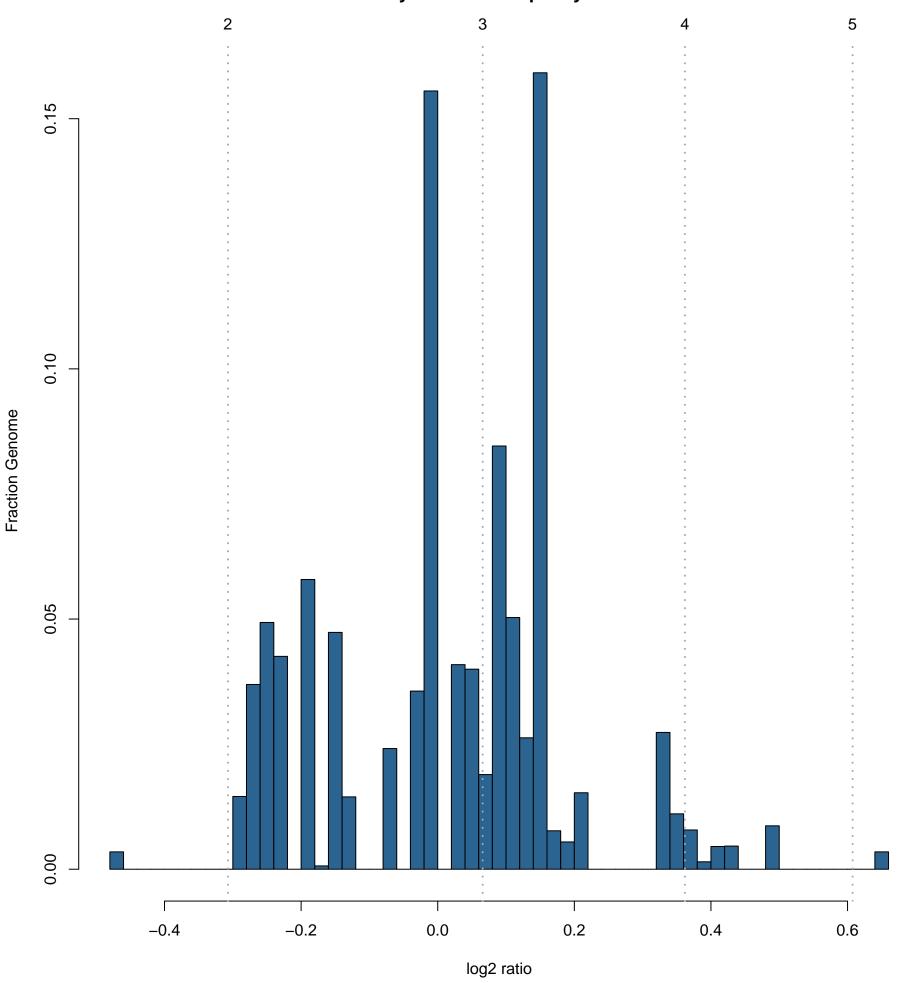
SCNA-fit log-likelihood: -2186.92

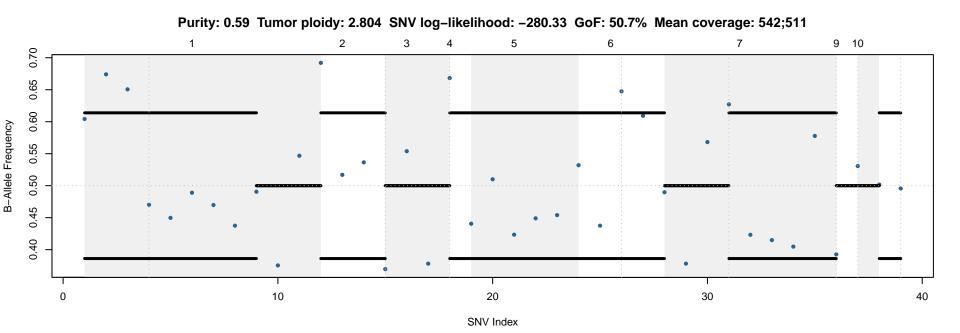






Purity: 0.59 Tumor ploidy: 2.804





SCNA-fit log-likelihood: -2109.38

