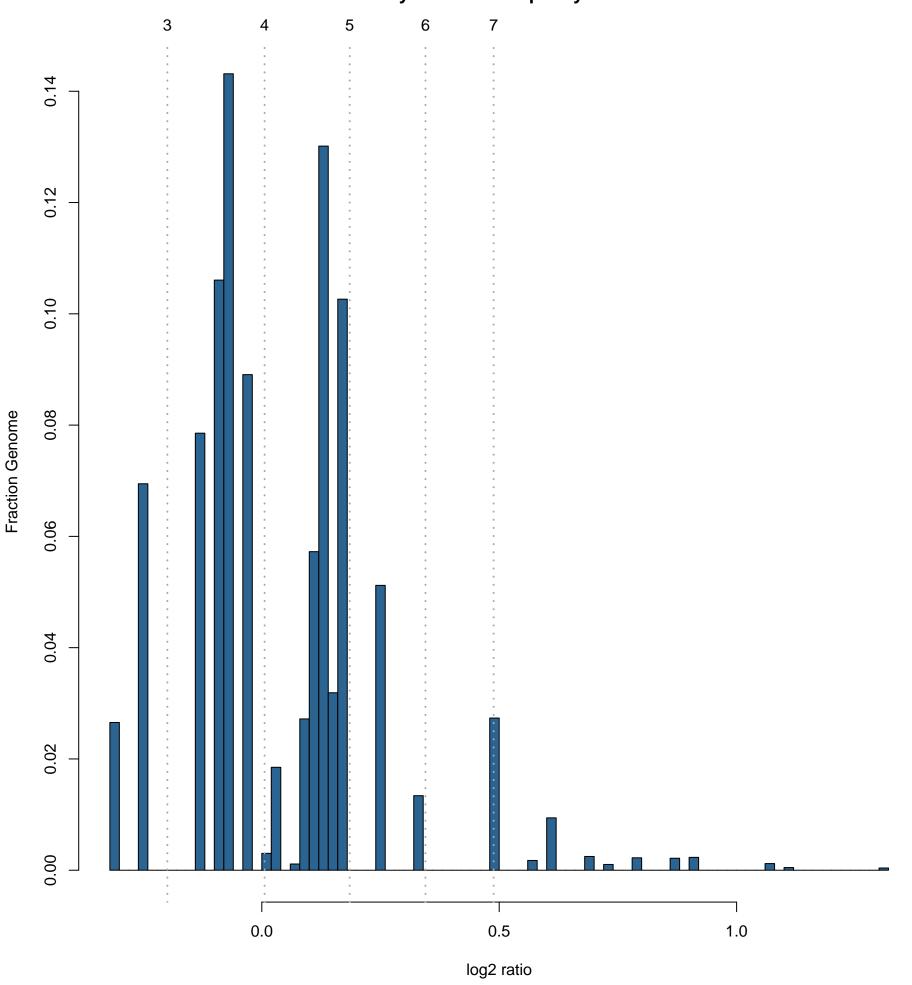
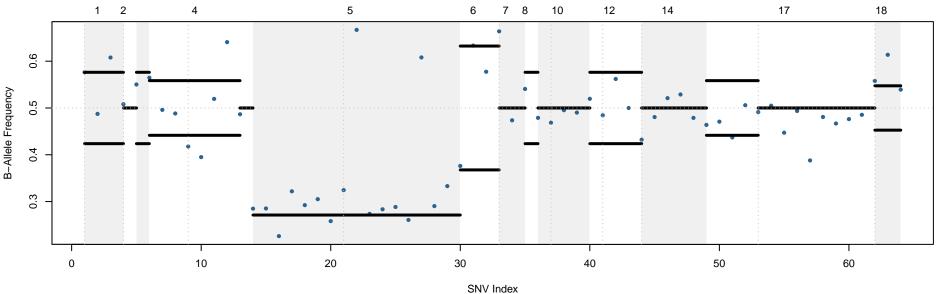
Purity: 0.36 Tumor ploidy: 3.969

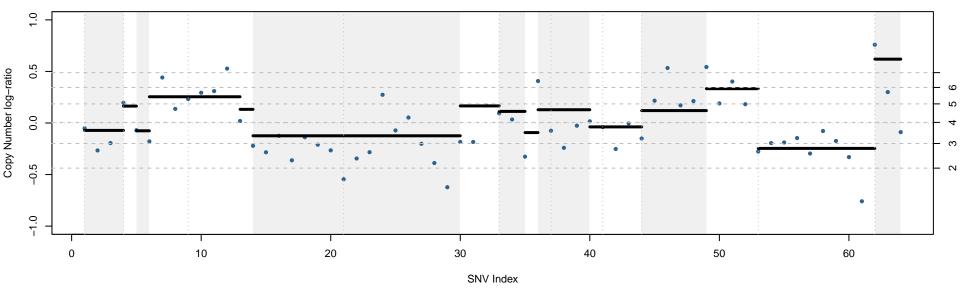


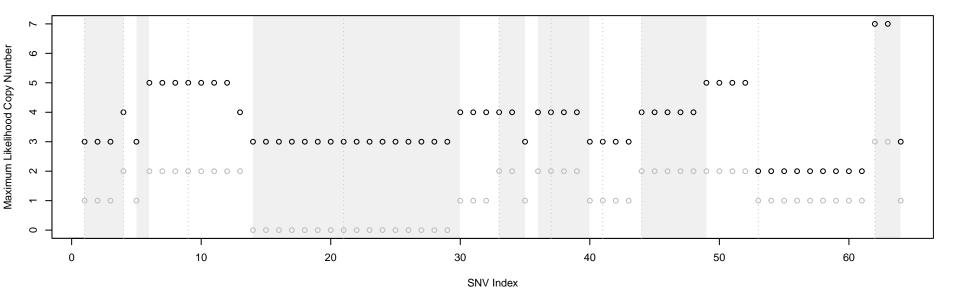
Purity: 0.36 Tumor ploidy: 3.969 SNV log-likelihood: -44.15 GoF: 94.3% Mean coverage: 586;641

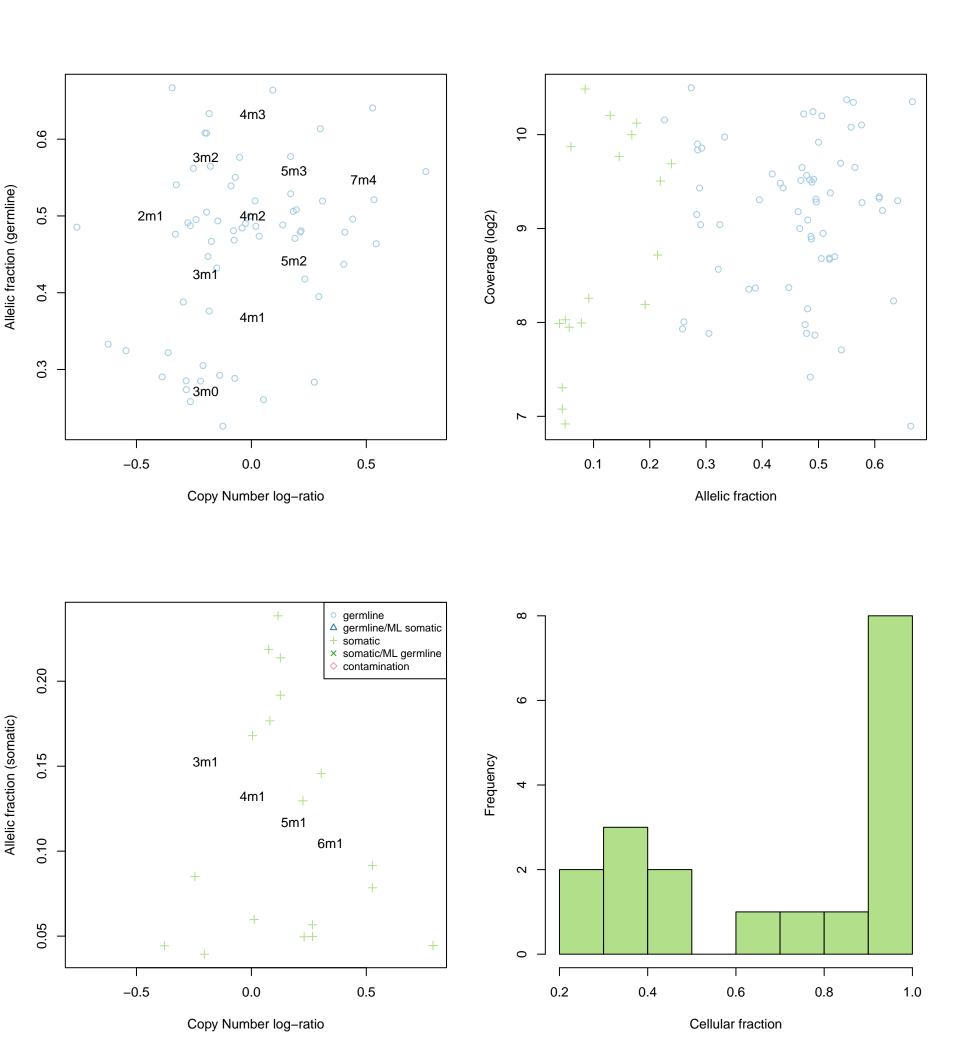
4 5 6 7 8 10 12 14 17



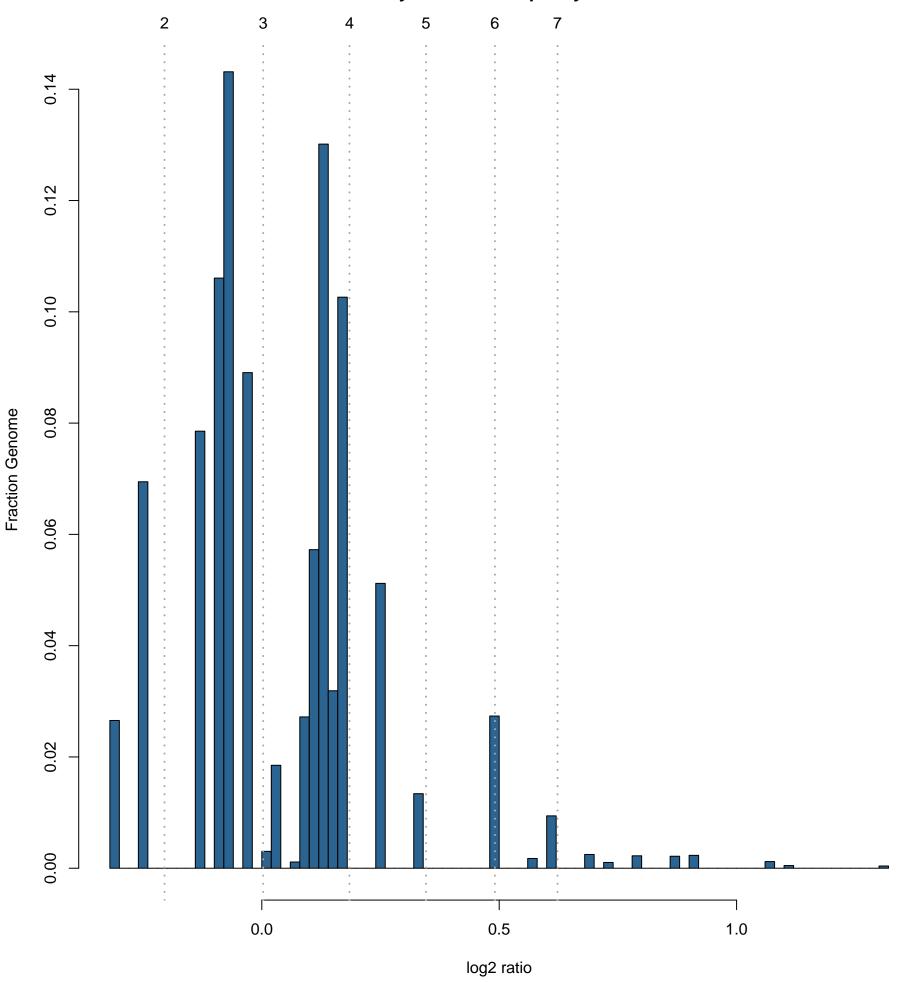
# SCNA-fit log-likelihood: -6967.6



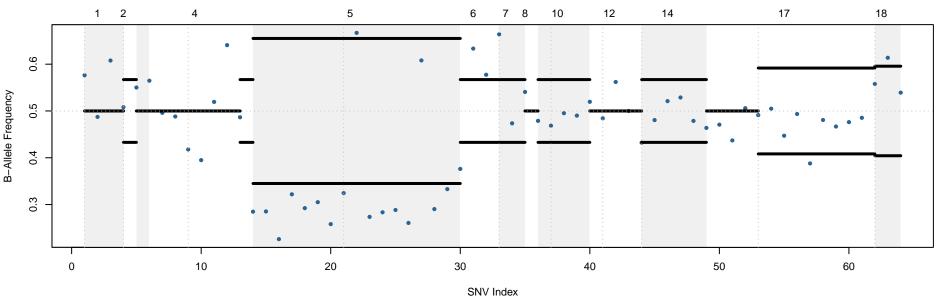




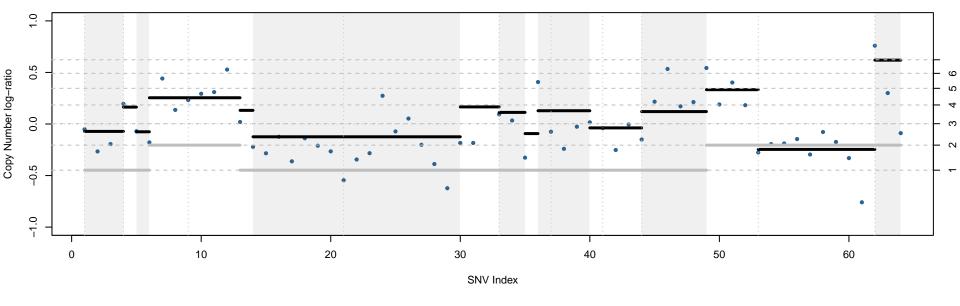
Purity: 0.31 Tumor ploidy: 2.985

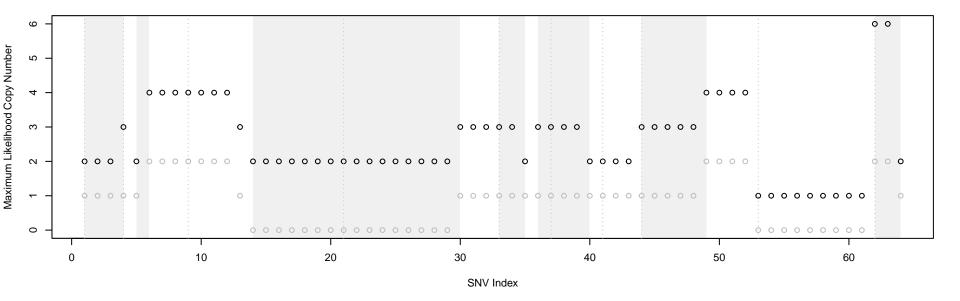


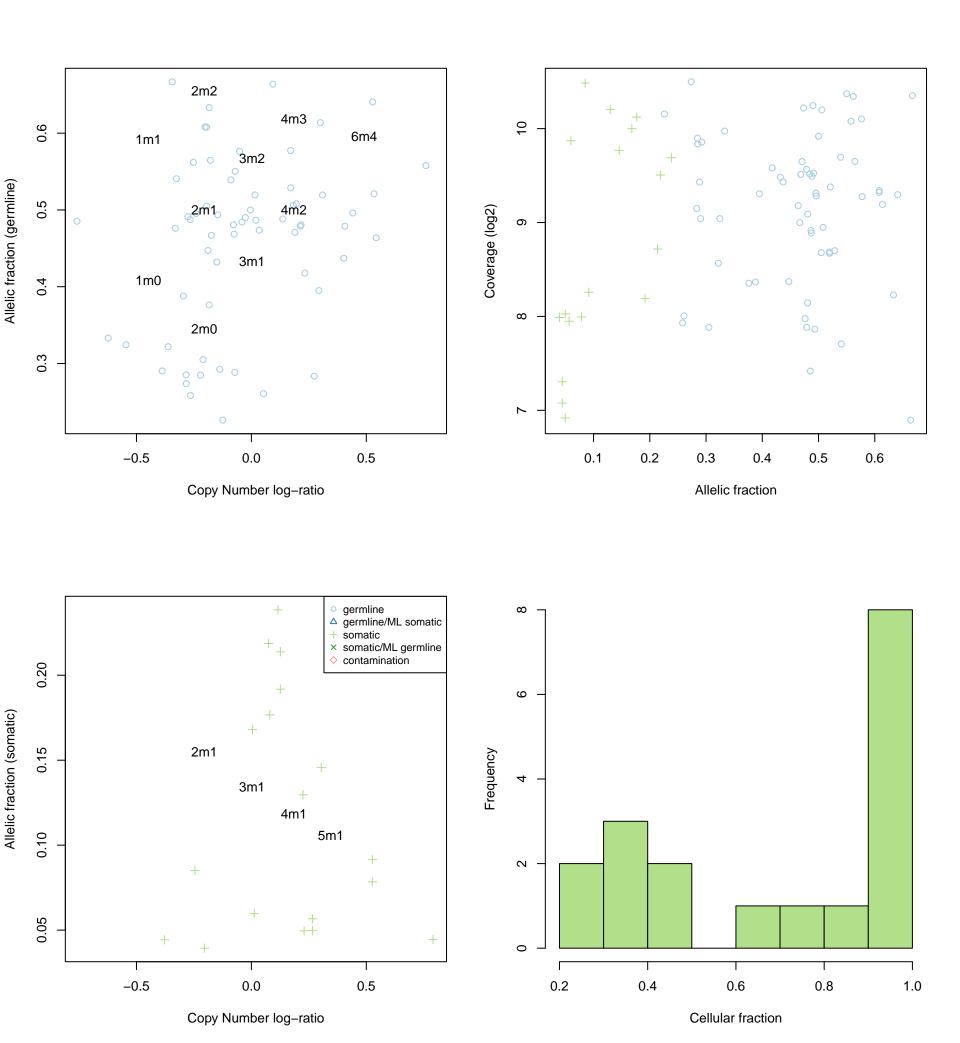




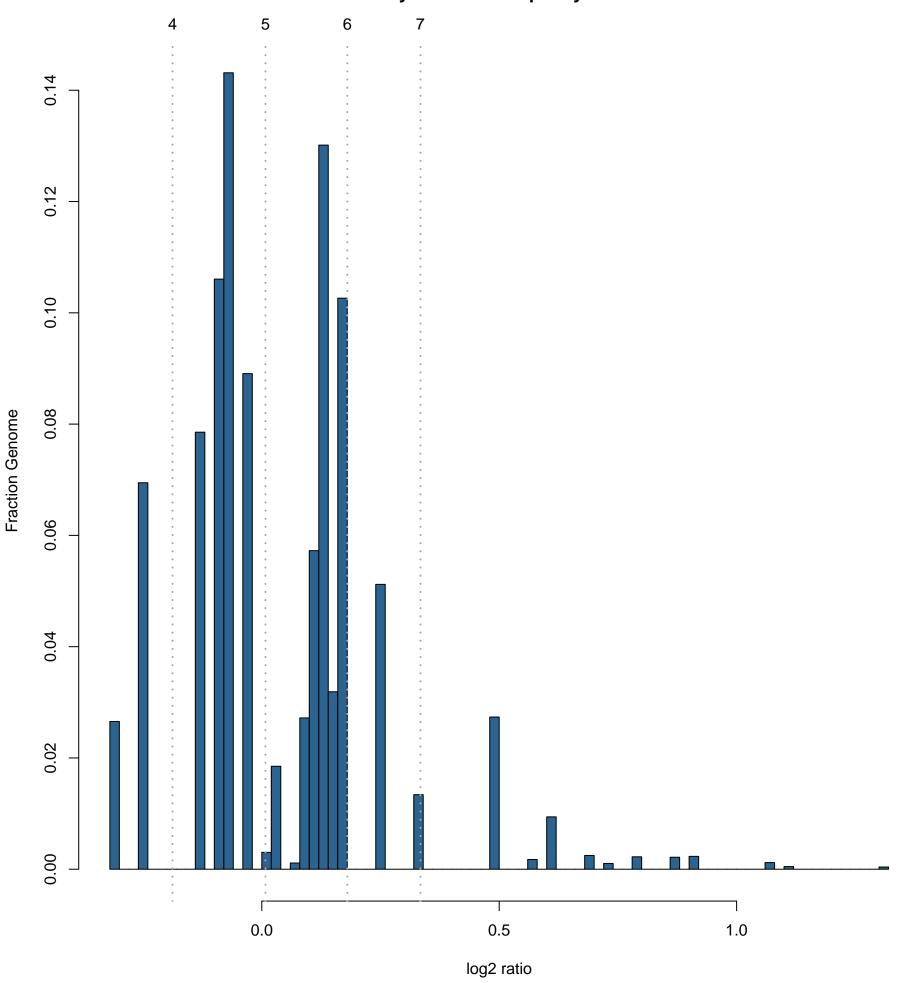
# SCNA-fit log-likelihood: -6943.15



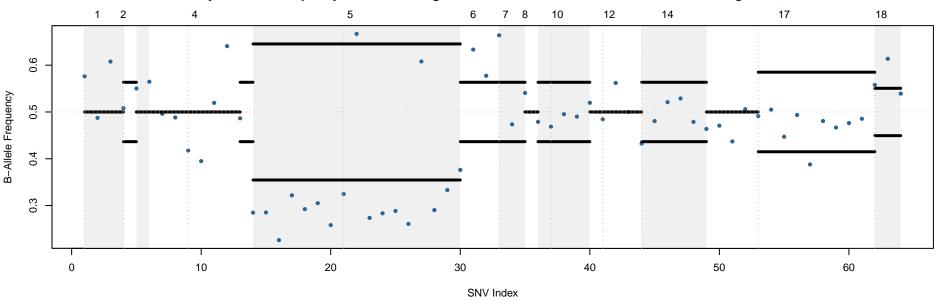




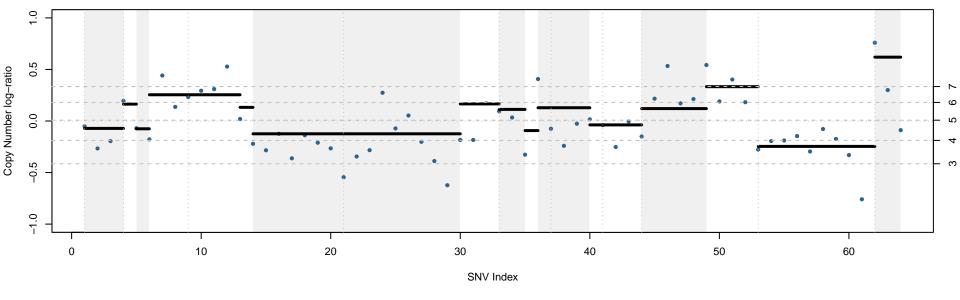
Purity: 0.41 Tumor ploidy: 4.958

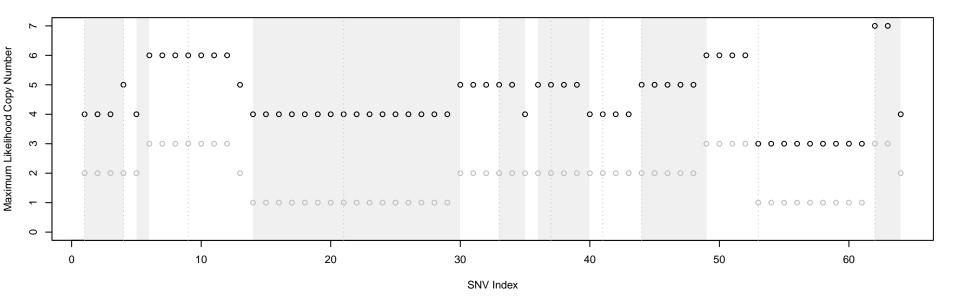


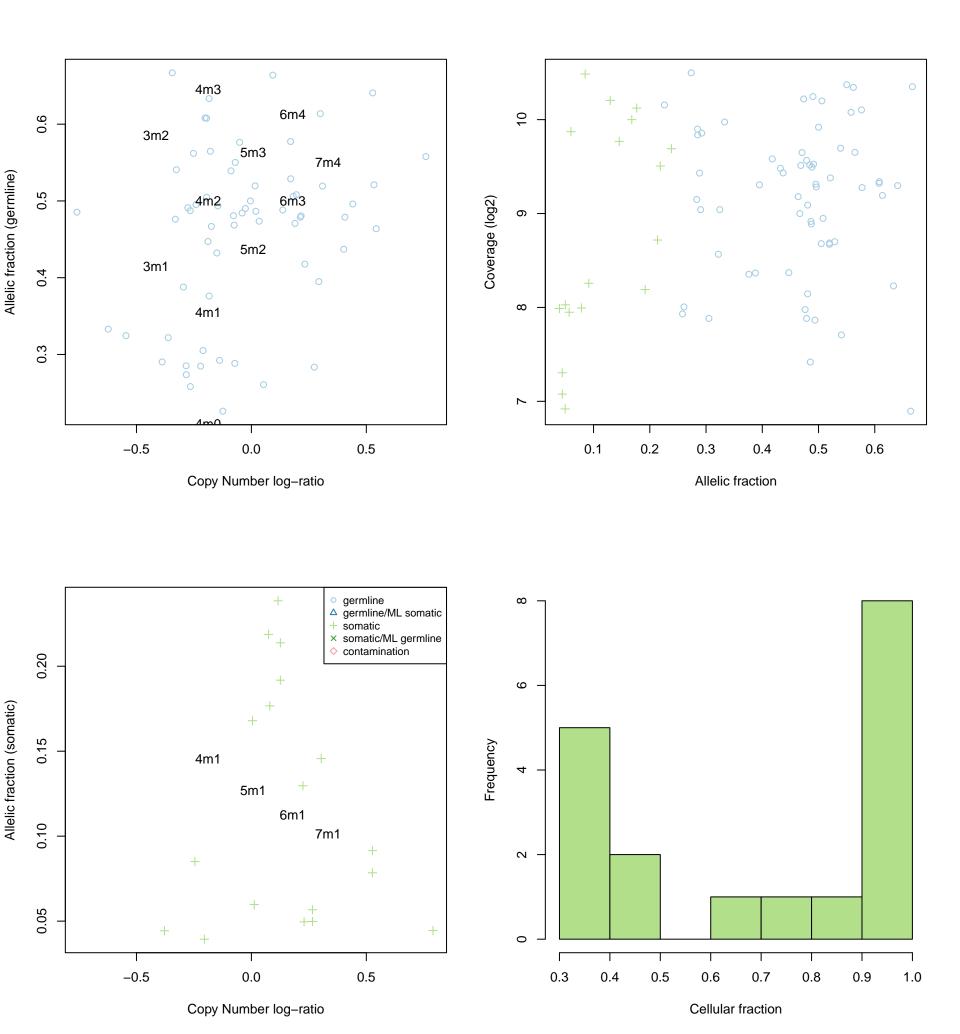




# SCNA-fit log-likelihood: -6983.44

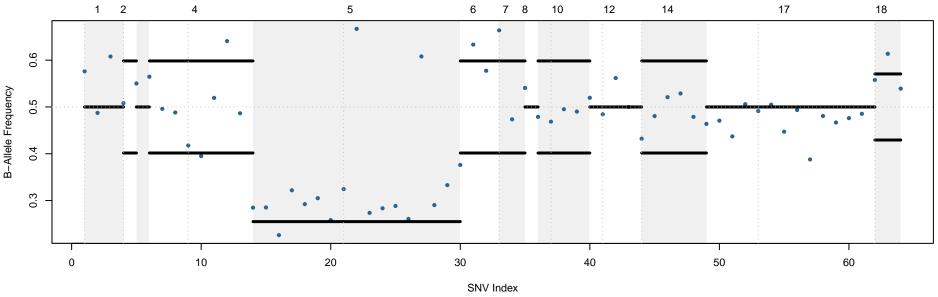




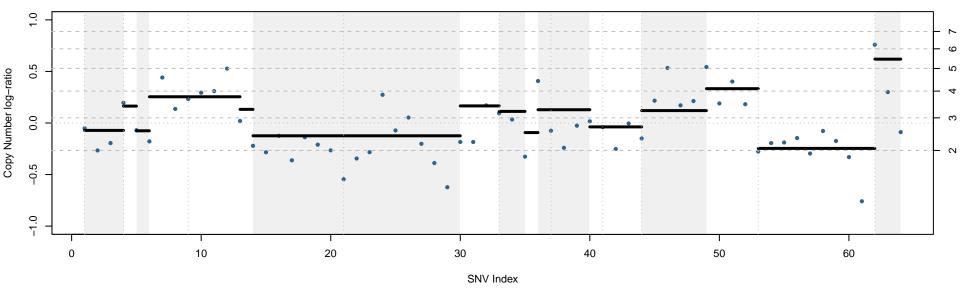


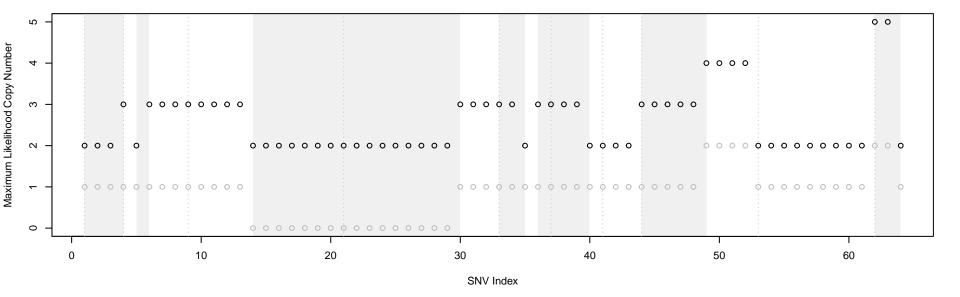
Purity: 0.49 Tumor ploidy: 2.827 2 7 3 5 0.12 0.08 Fraction Genome 90.0 0.04 0.02 0.00 0.0 0.5 1.0 log2 ratio

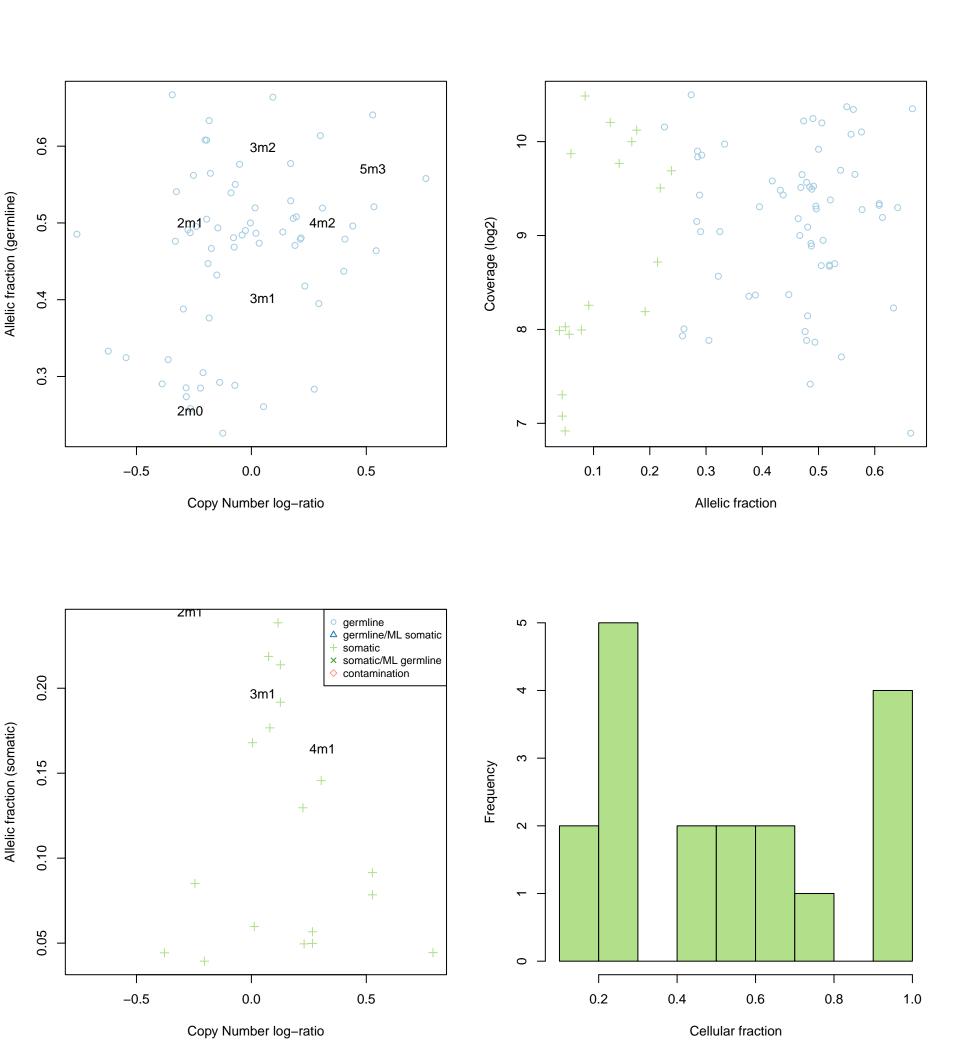




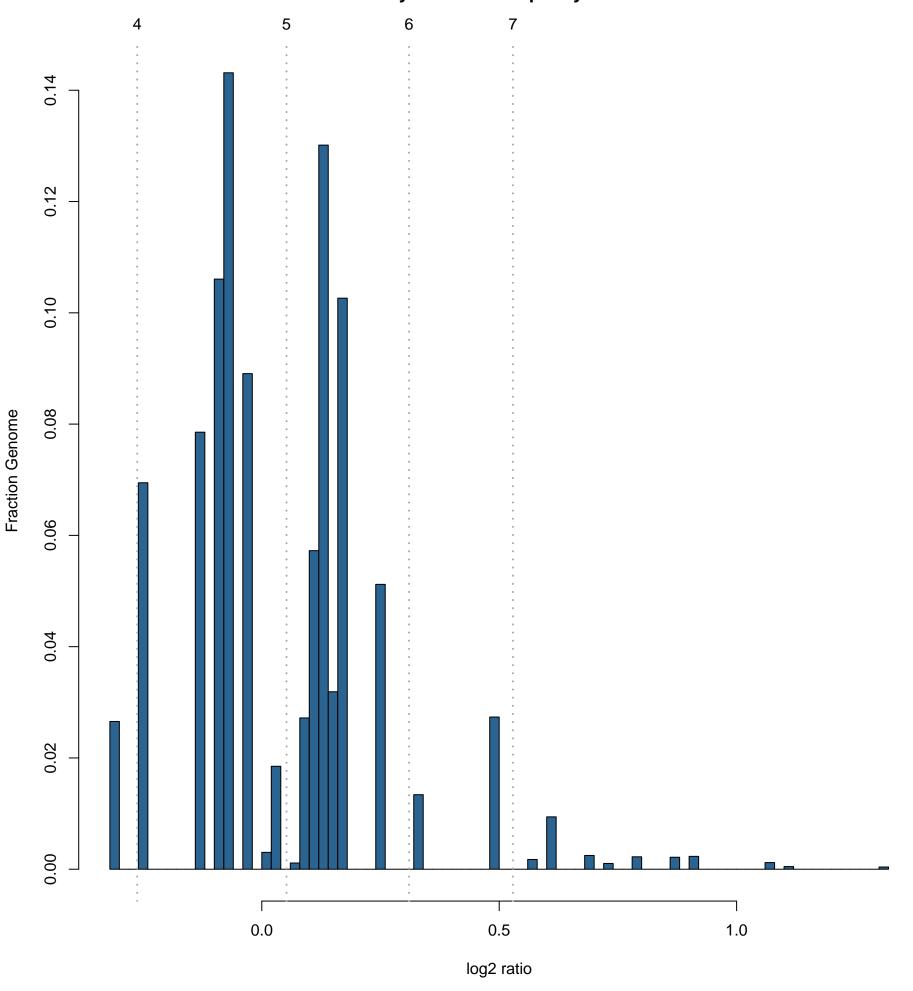
# SCNA-fit log-likelihood: -7043.48

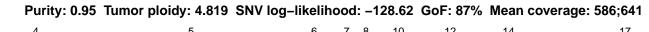


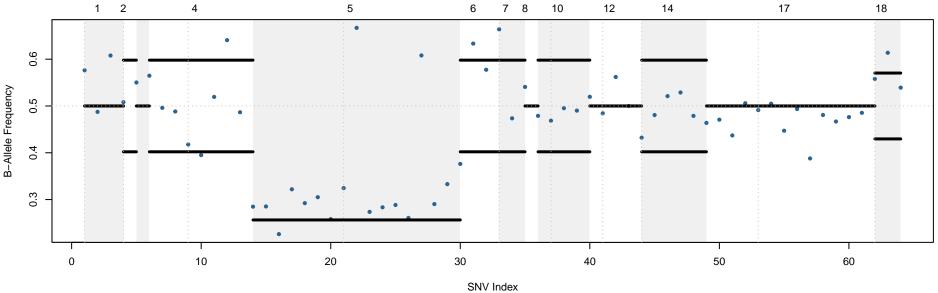




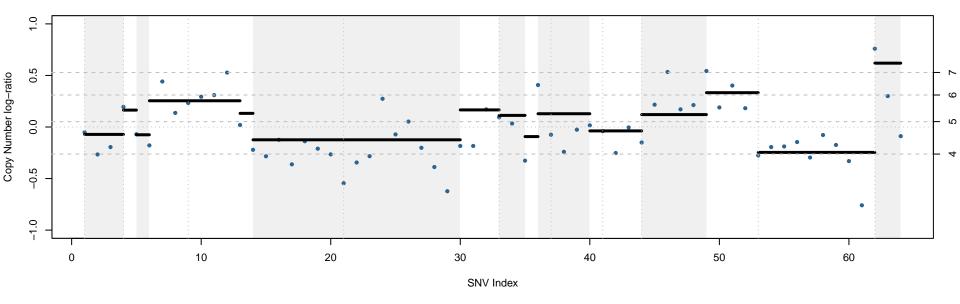
Purity: 0.95 Tumor ploidy: 4.819

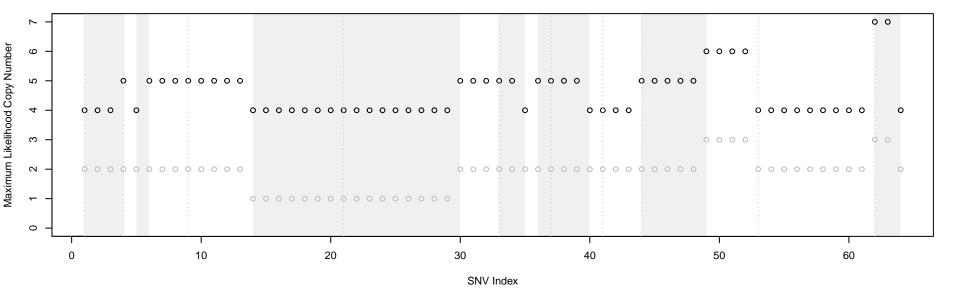


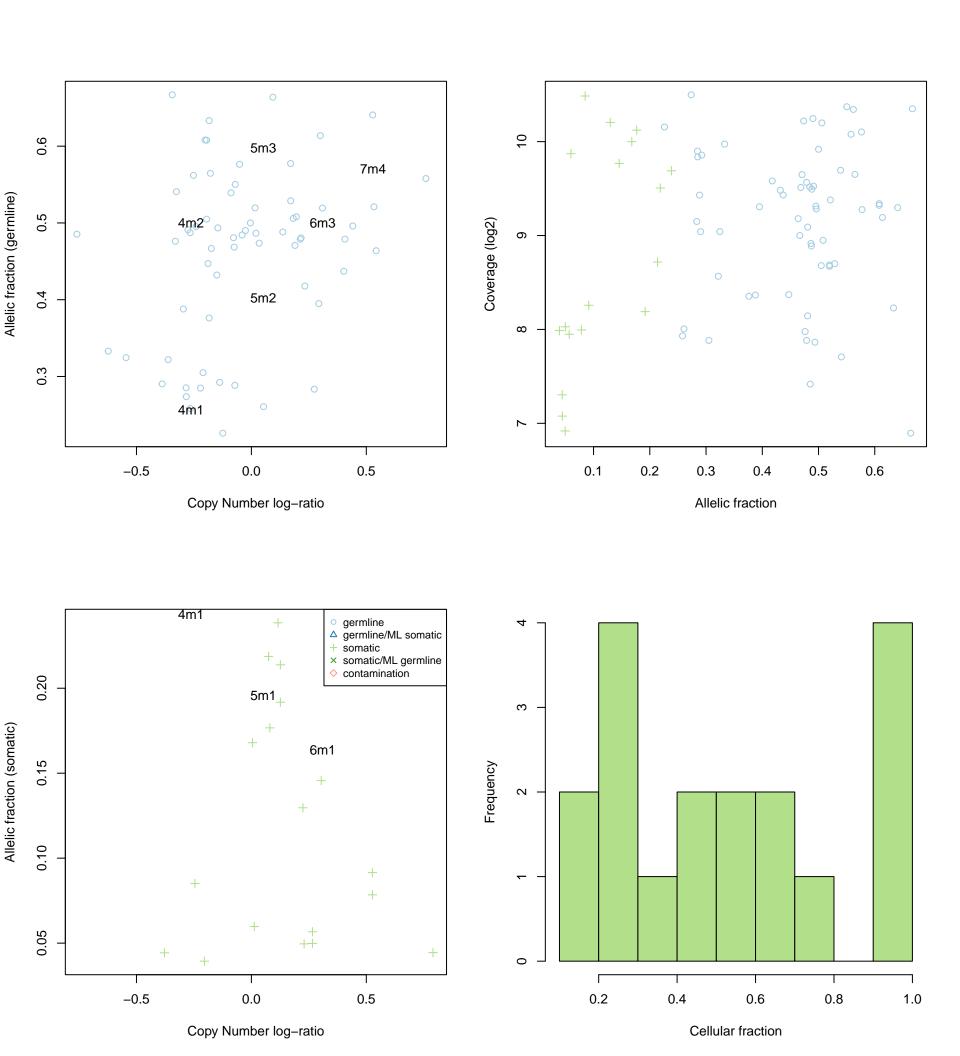




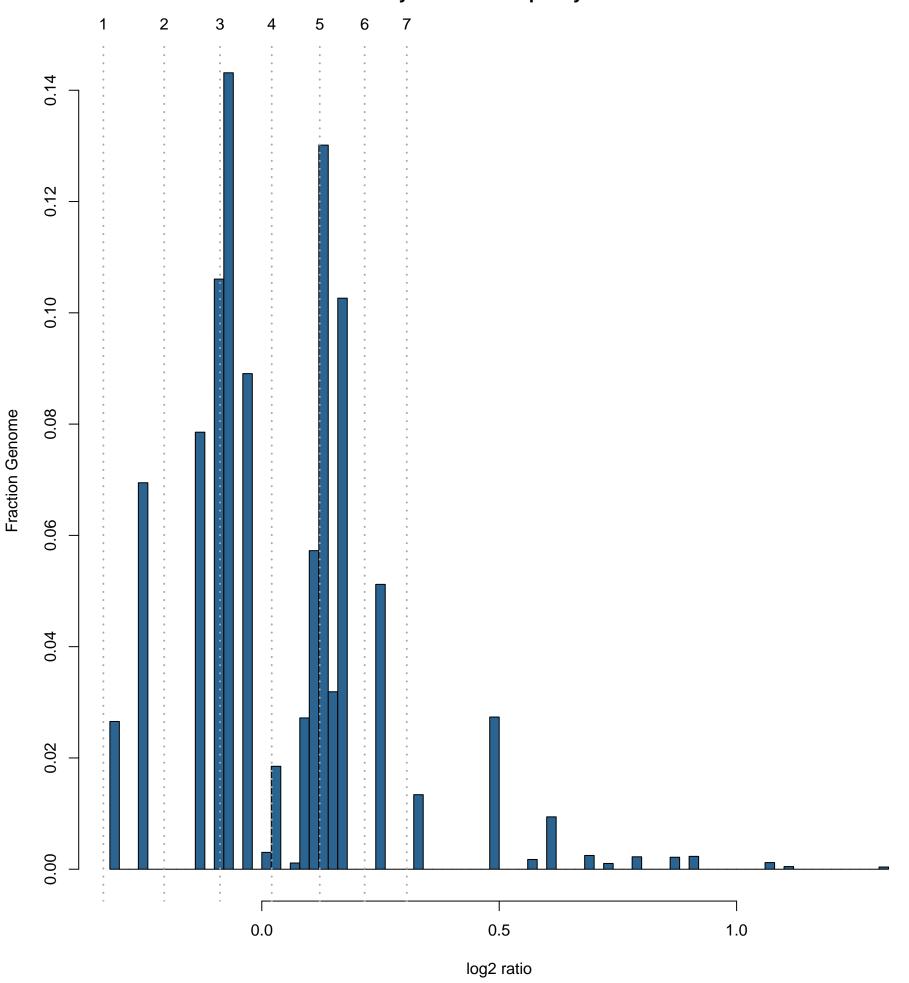
# SCNA-fit log-likelihood: -7086.61

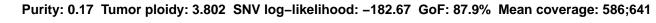


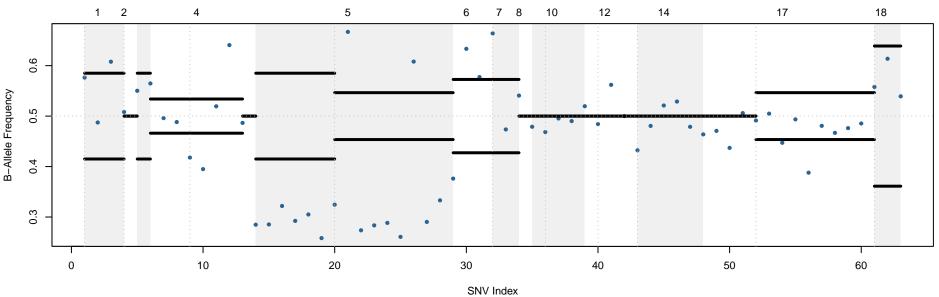




Purity: 0.17 Tumor ploidy: 3.802







# SCNA-fit log-likelihood: -7066.12

