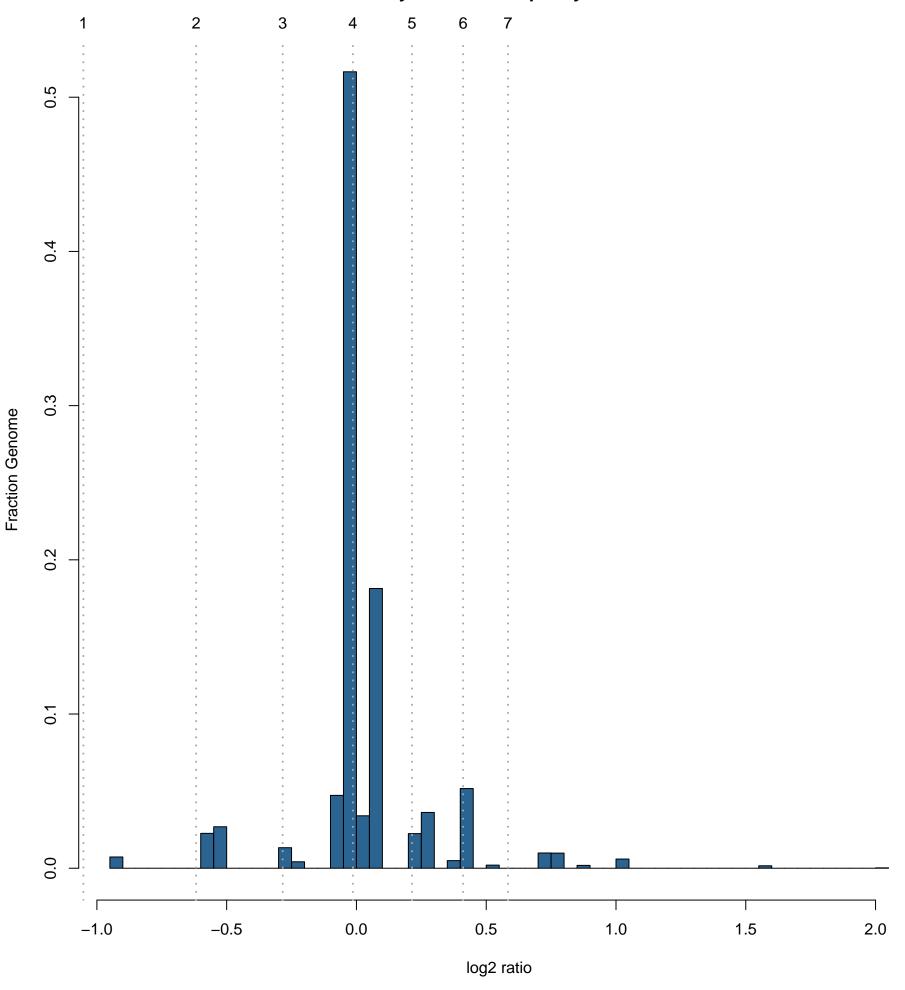
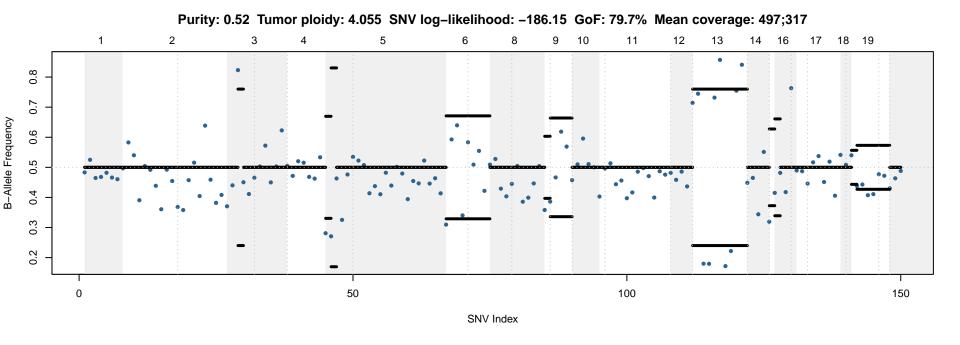
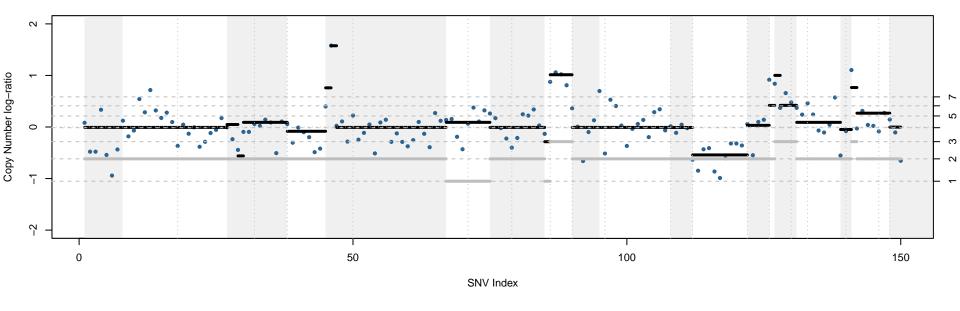
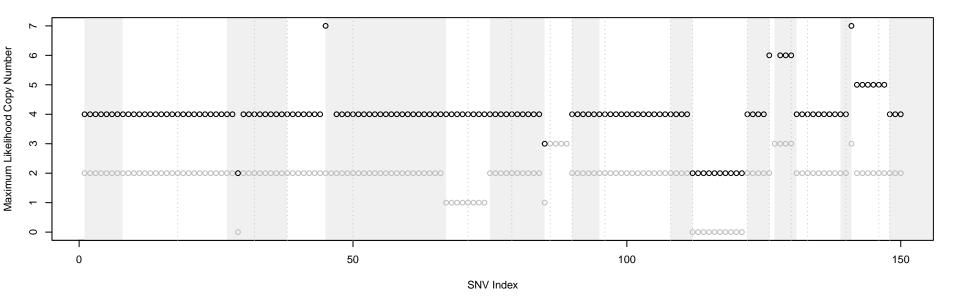
Purity: 0.52 Tumor ploidy: 4.055

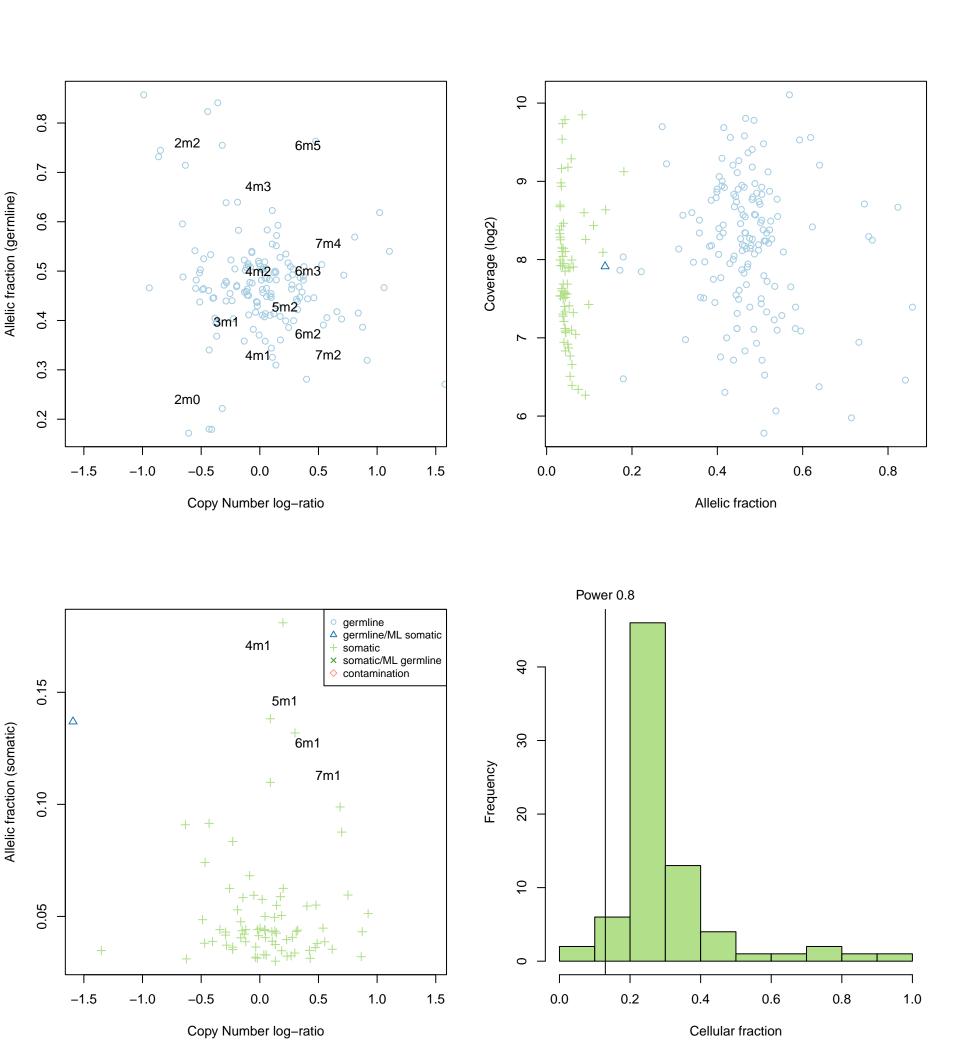




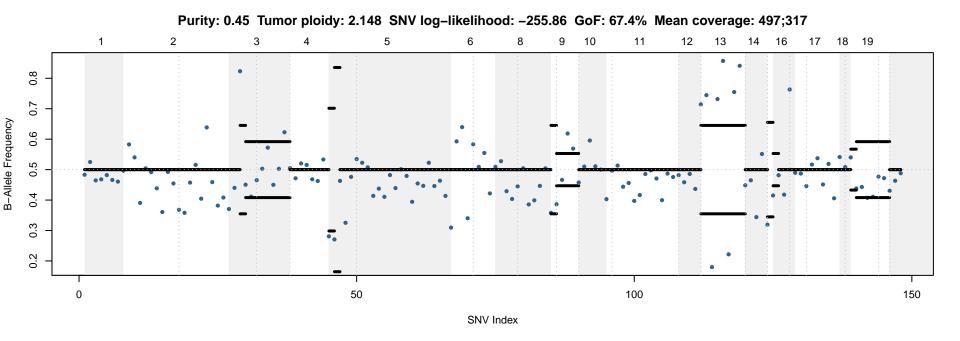
### SCNA-fit log-likelihood: -7744.99



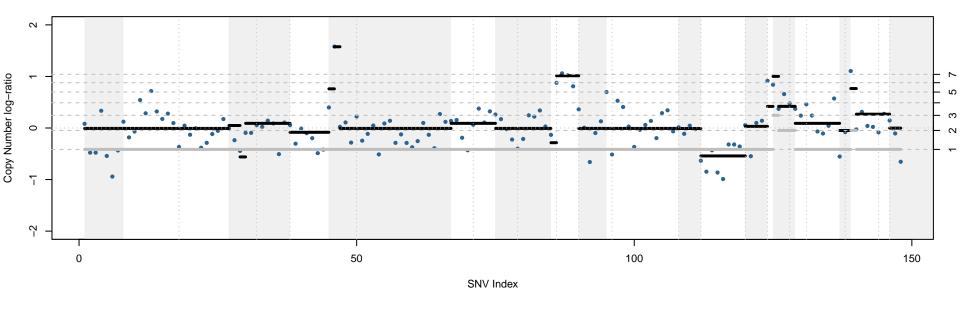


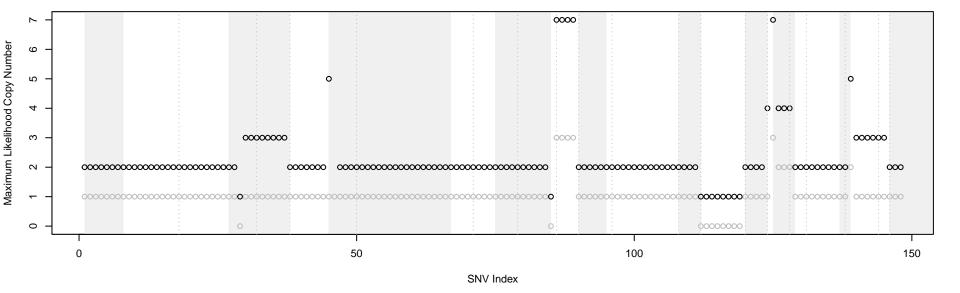


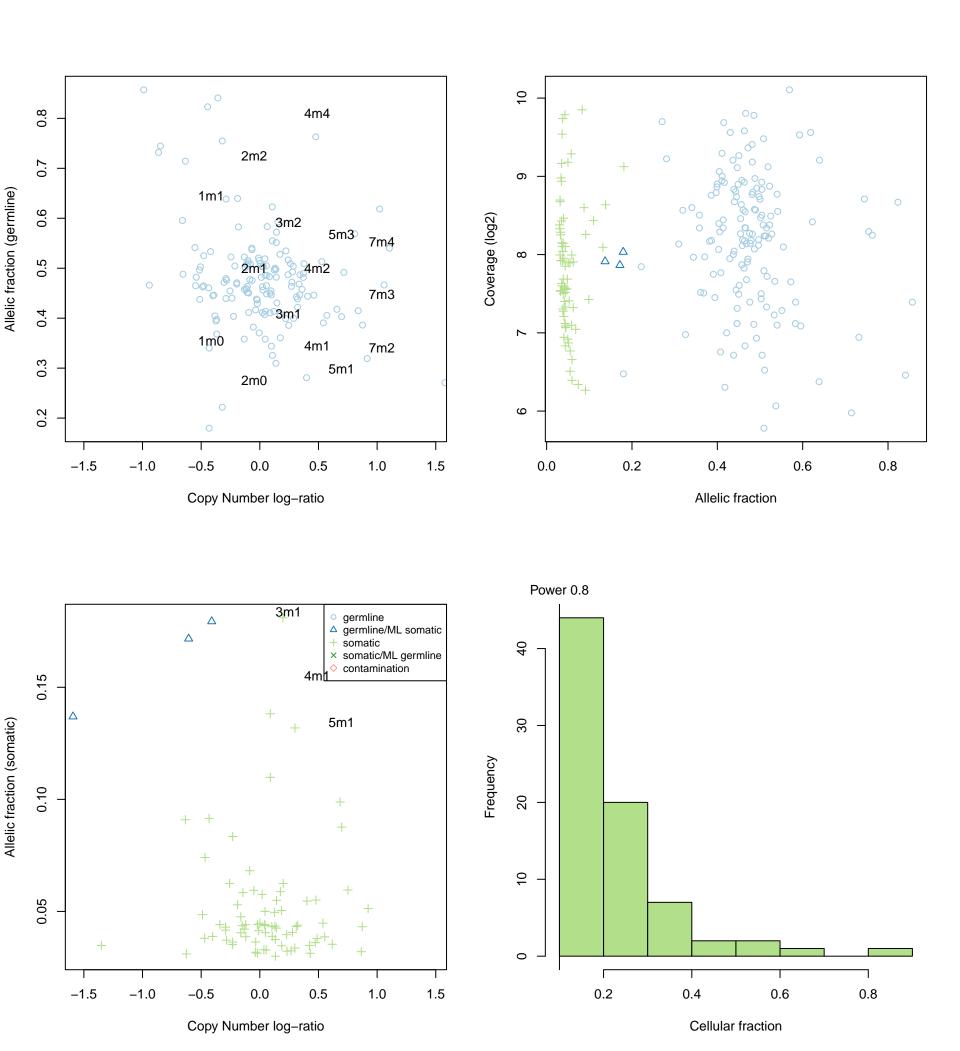
Purity: 0.45 Tumor ploidy: 2.148 2 3 5 6 1 0.5 Fraction Genome 0.2 0.1 0.0 -0.5 0.0 0.5 1.0 1.5 2.0 log2 ratio



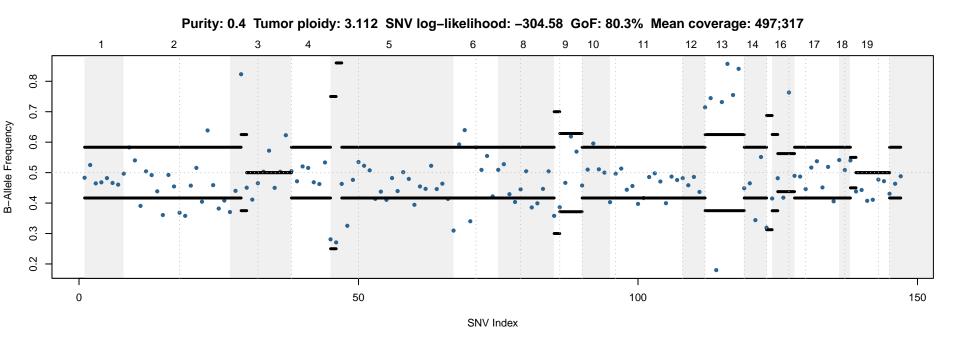
## SCNA-fit log-likelihood: -7772.06



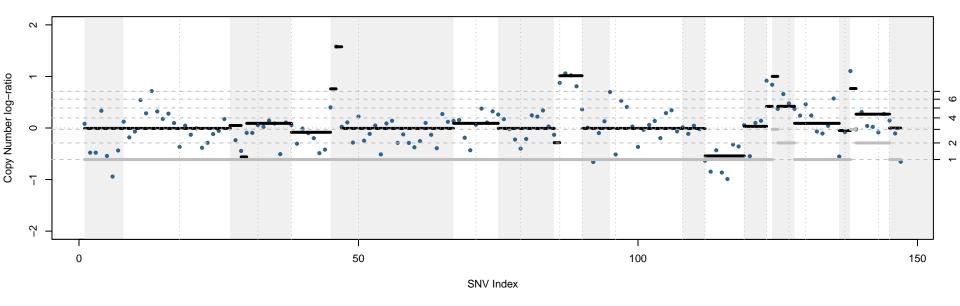


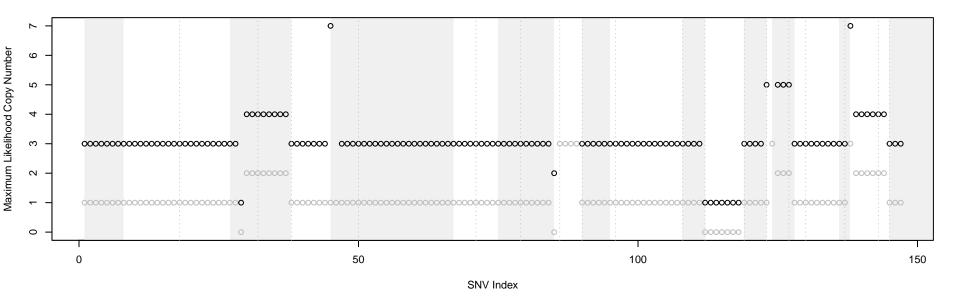


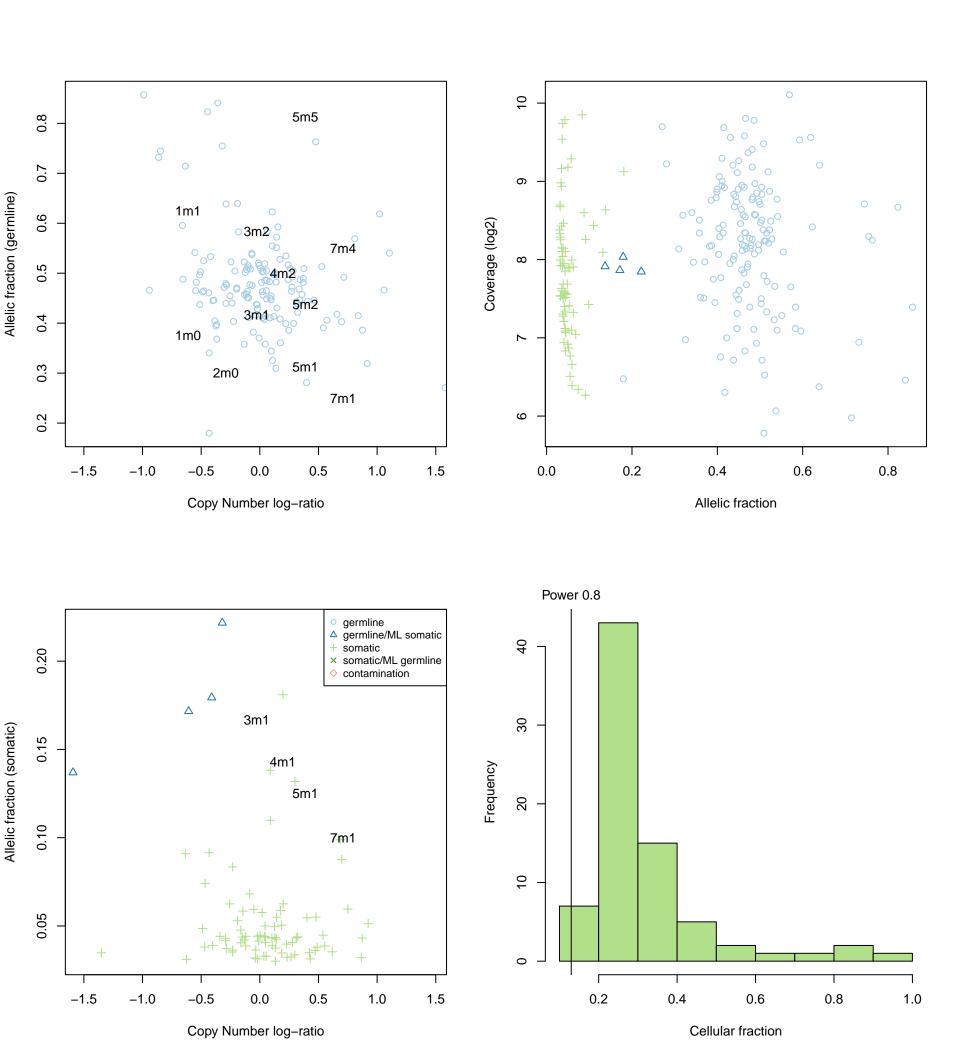
Purity: 0.4 Tumor ploidy: 3.112 2 3 5 6 7 Fraction Genome 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0 1.5 2.0 log2 ratio



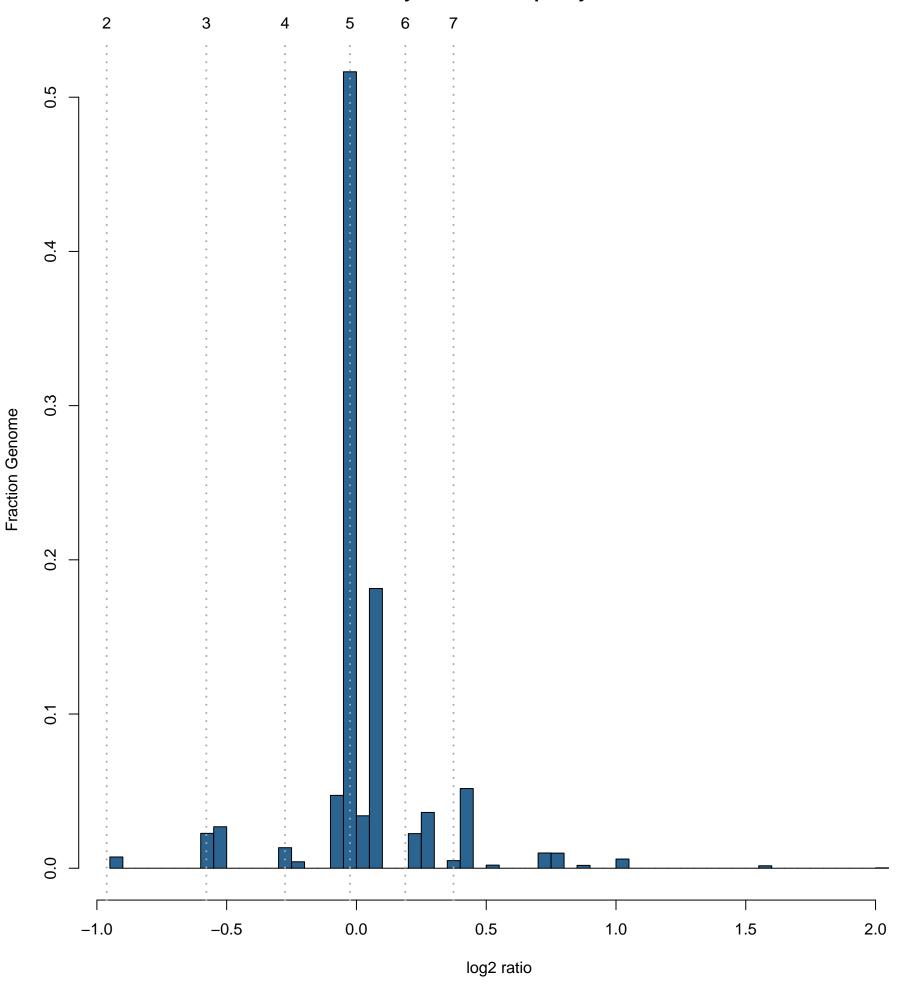
# SCNA-fit log-likelihood: -7734.91

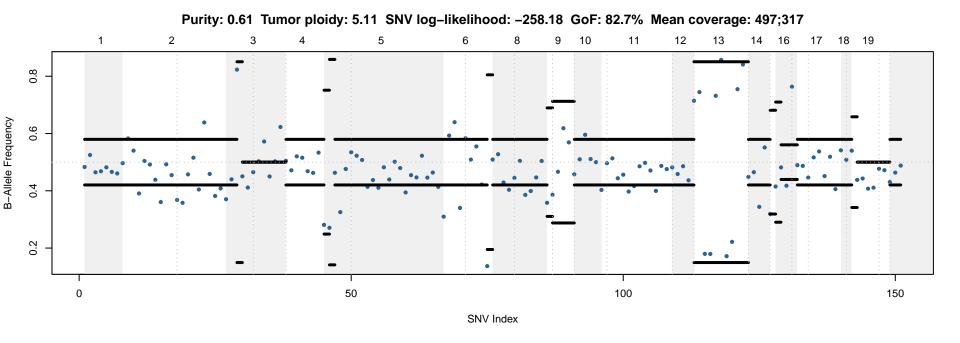




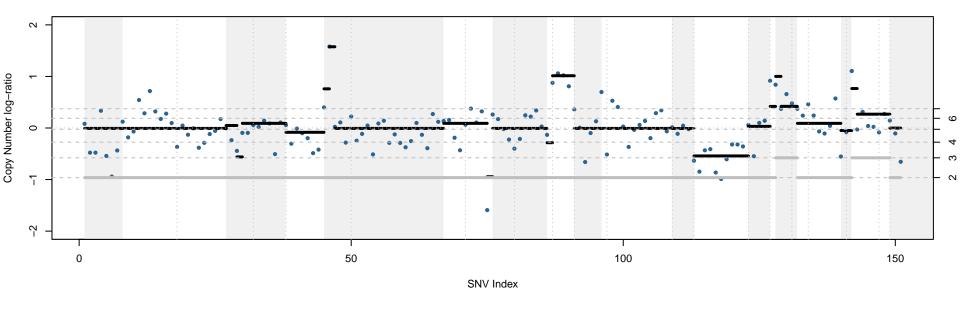


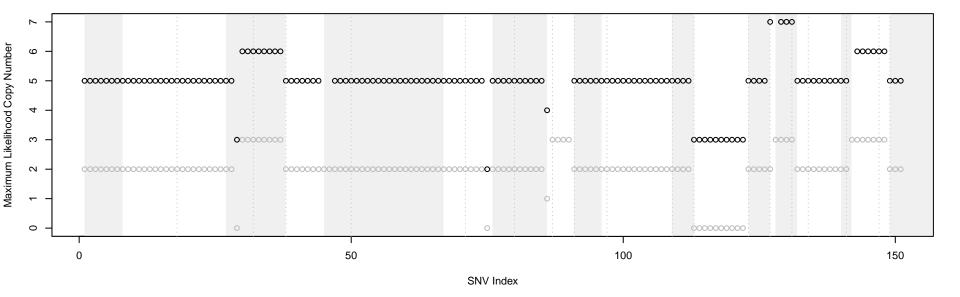
Purity: 0.61 Tumor ploidy: 5.11

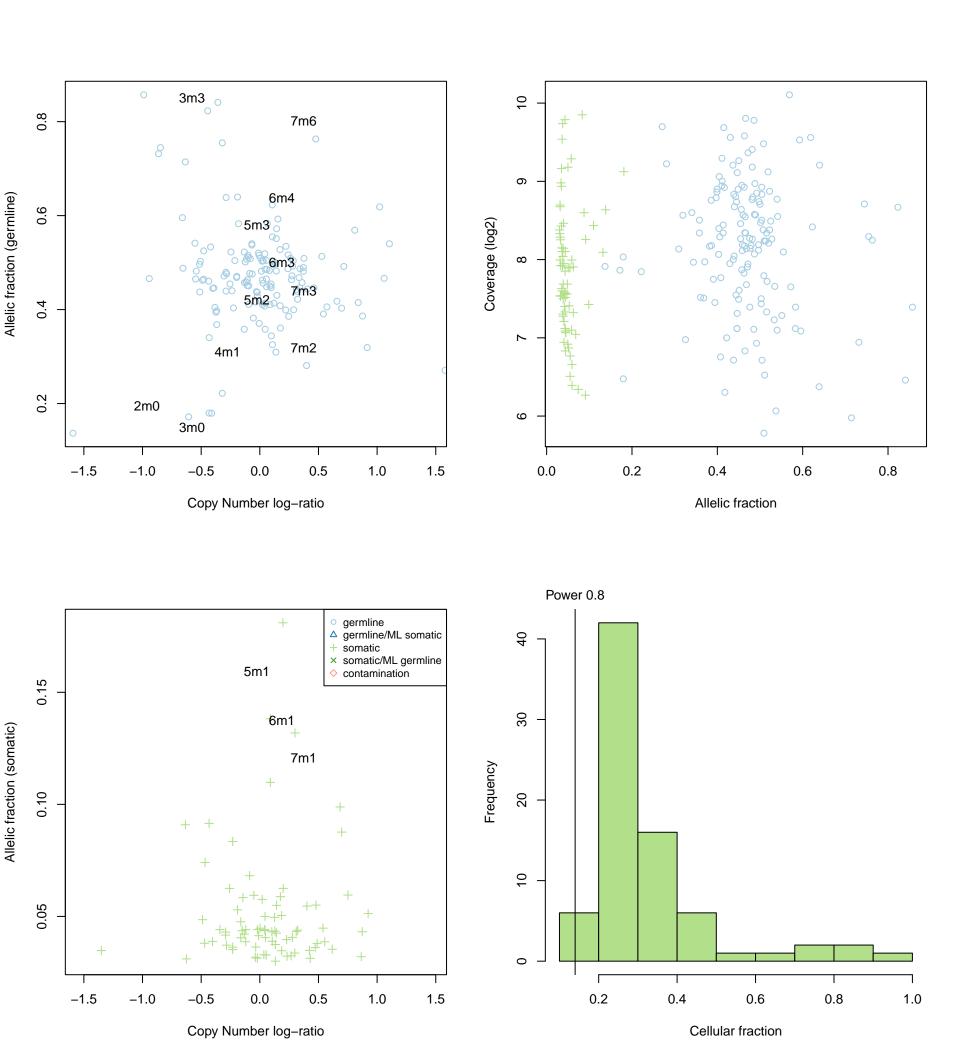




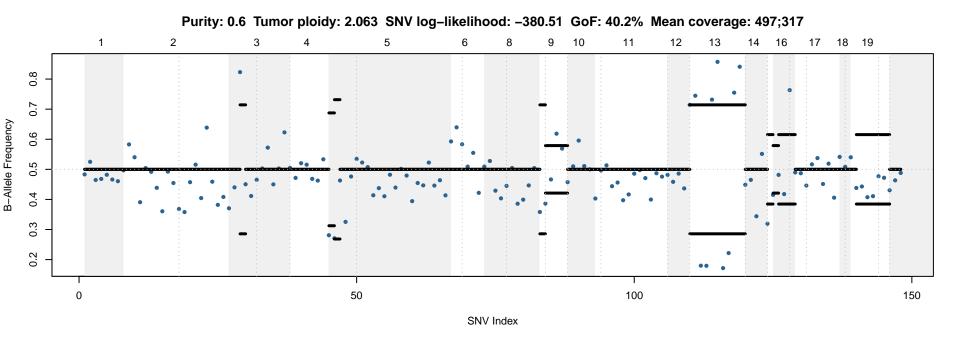
## SCNA-fit log-likelihood: -7882.64



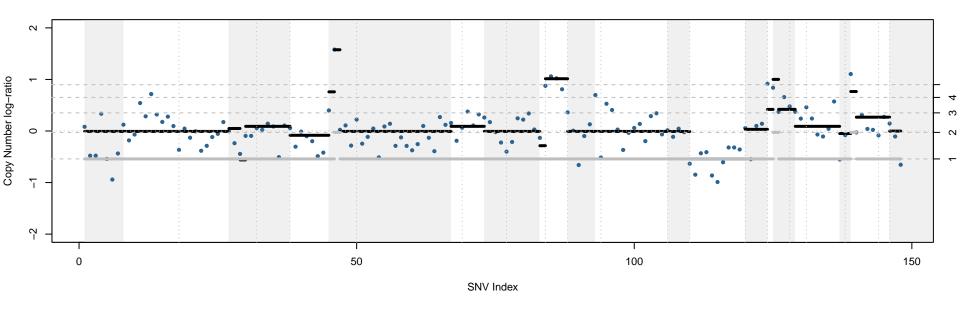


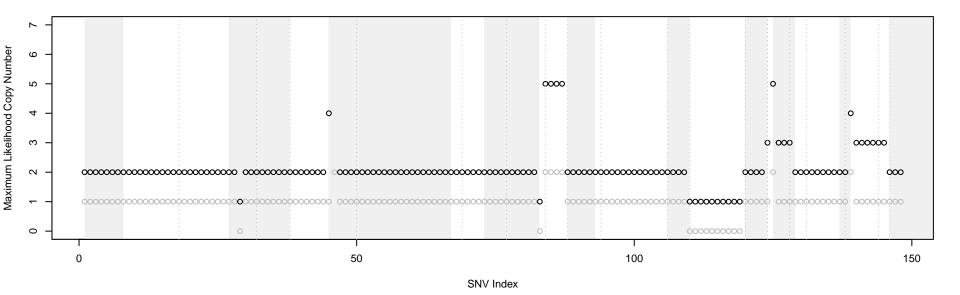


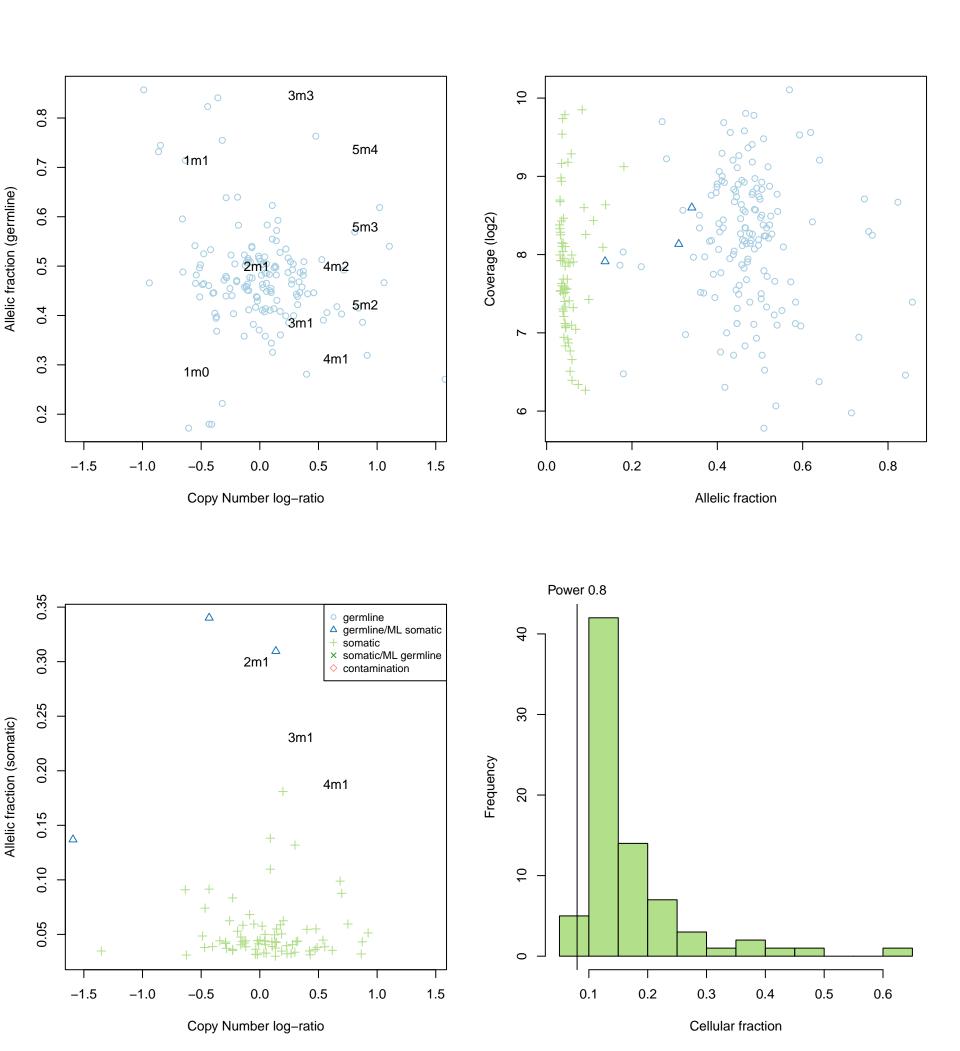
Purity: 0.6 Tumor ploidy: 2.063 2 1 Fraction Genome 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0 1.5 2.0 log2 ratio



## SCNA-fit log-likelihood: -7730.03

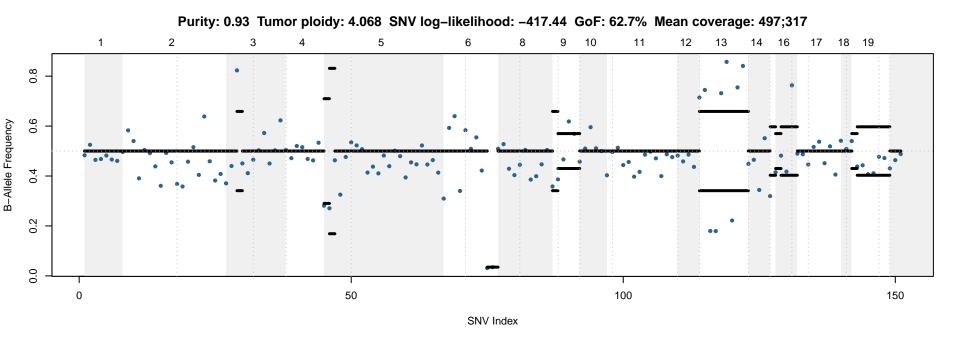




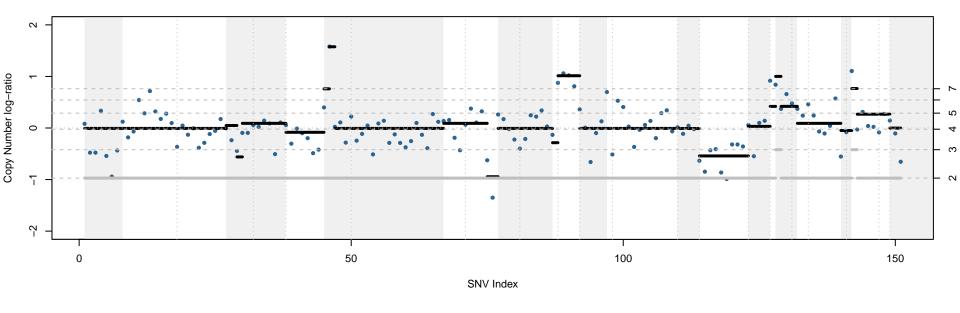


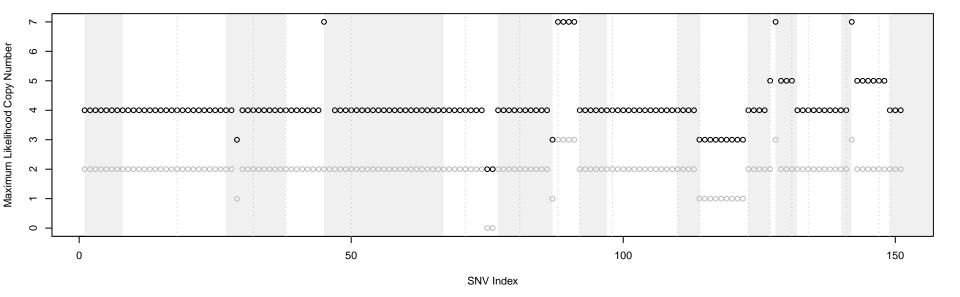
Purity: 0.93 Tumor ploidy: 4.068 2 7 3 5 6 0.3 Fraction Genome 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0 1.5 2.0

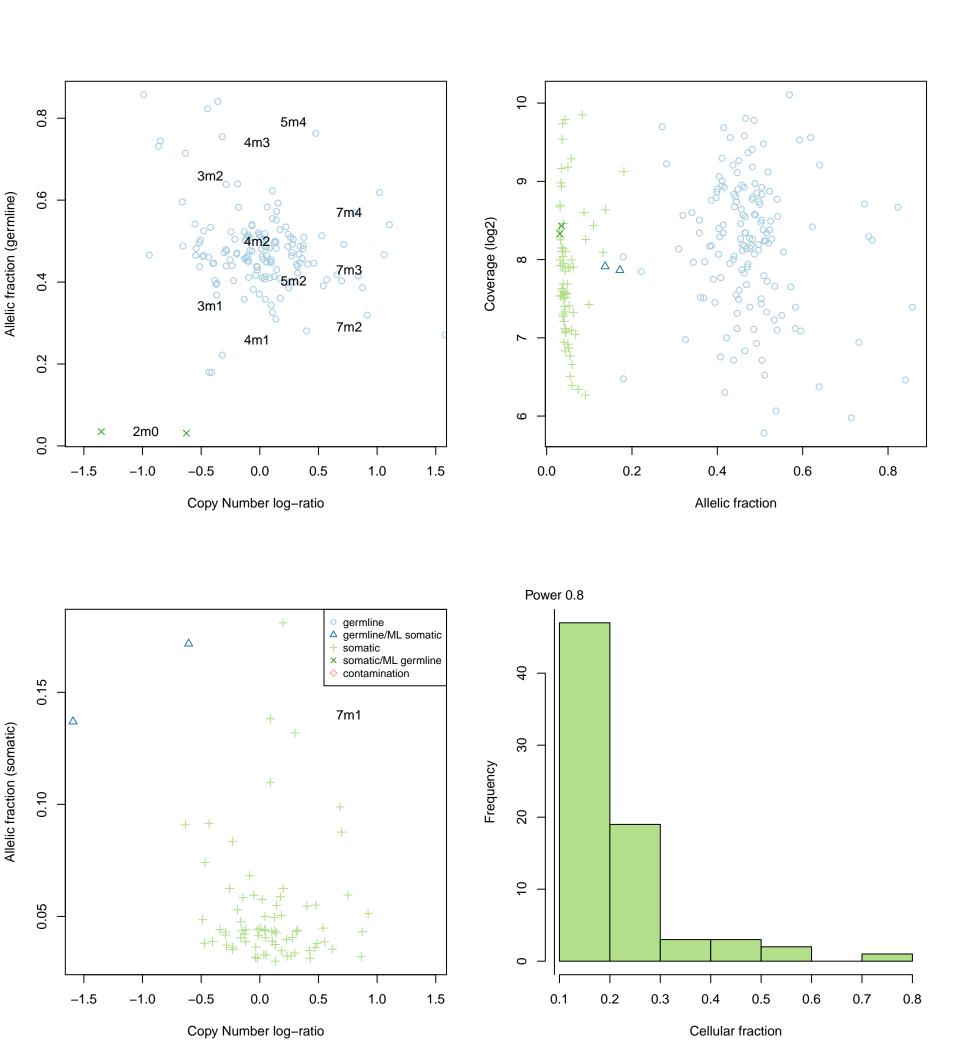
log2 ratio



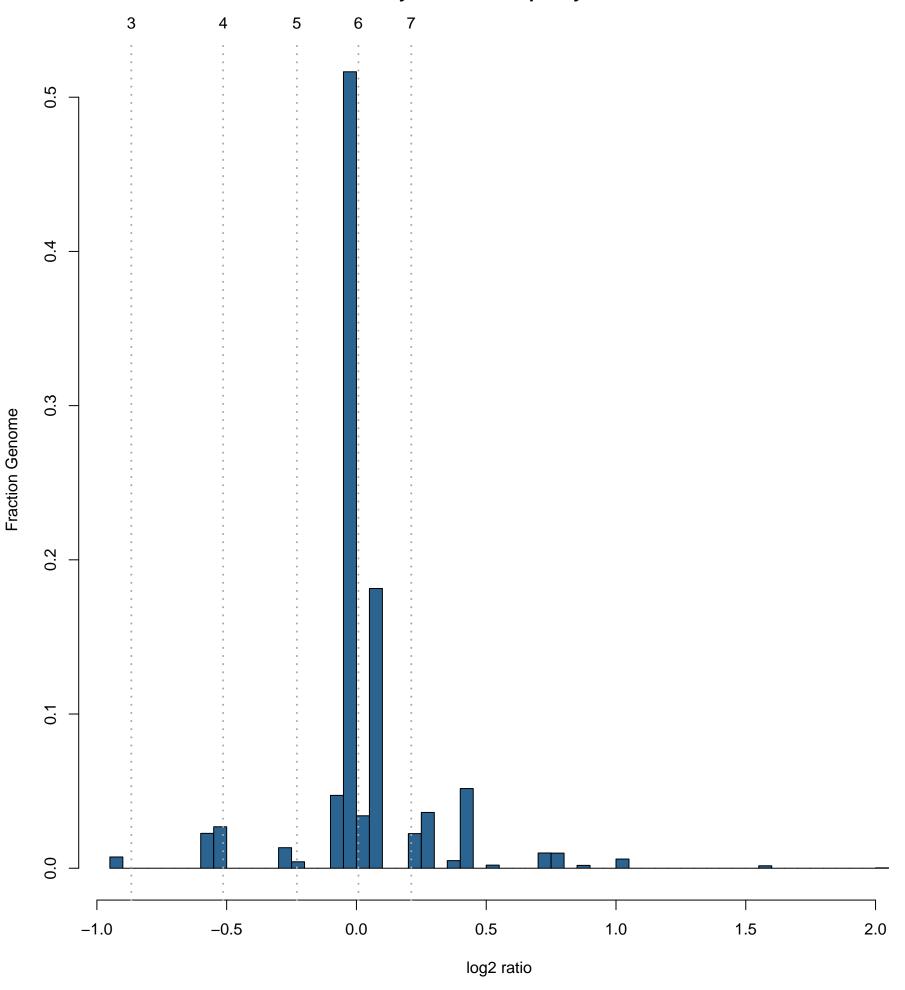
## SCNA-fit log-likelihood: -7703.63

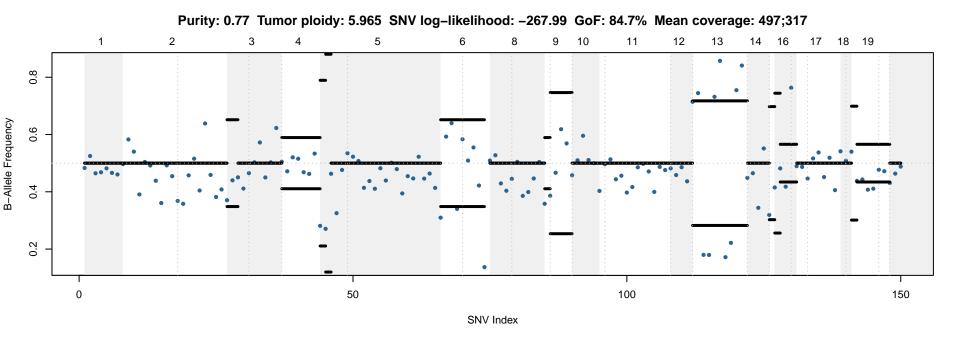




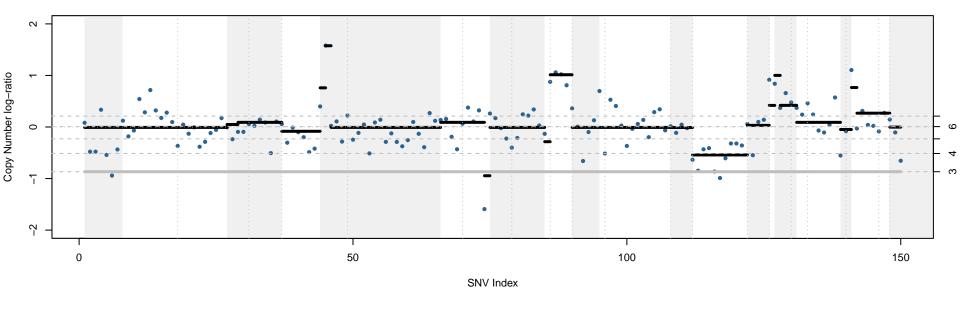


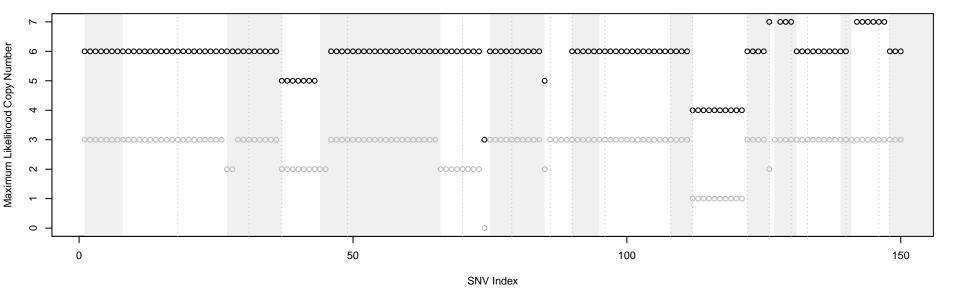
Purity: 0.77 Tumor ploidy: 5.965

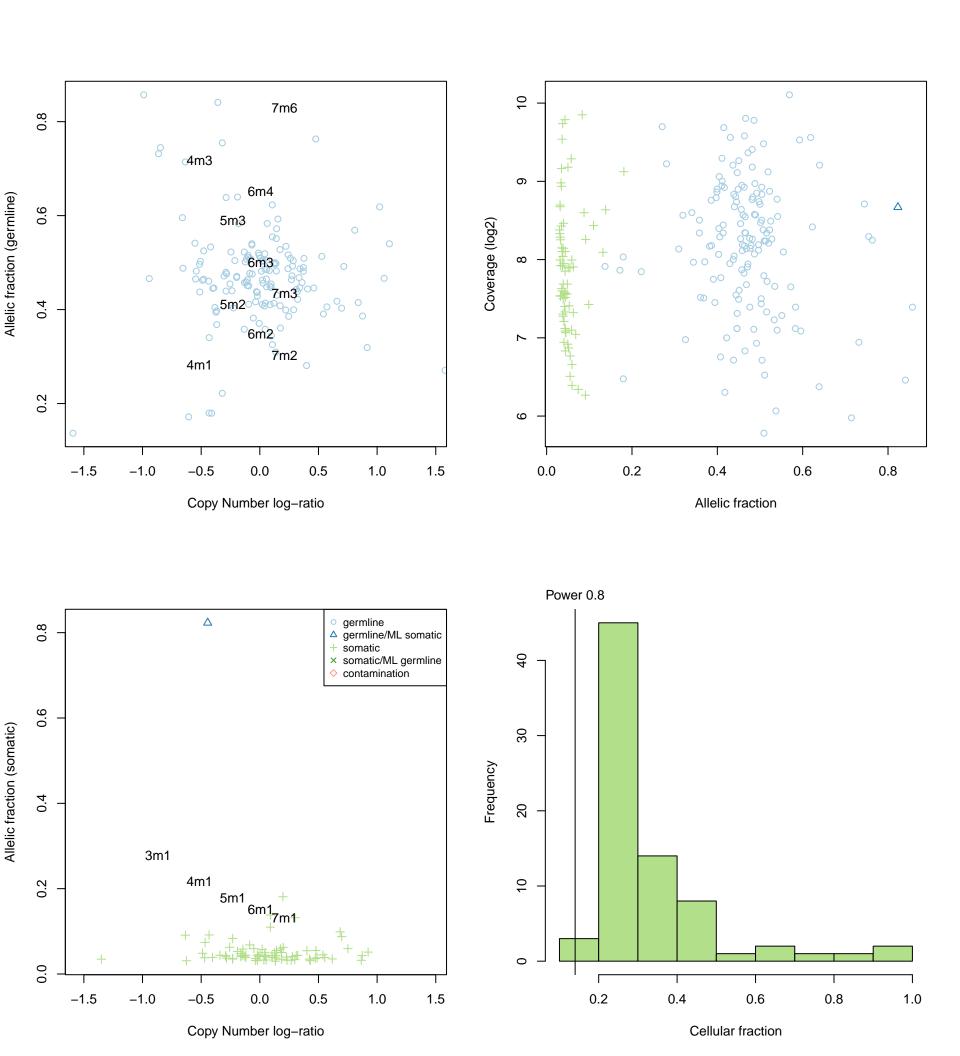




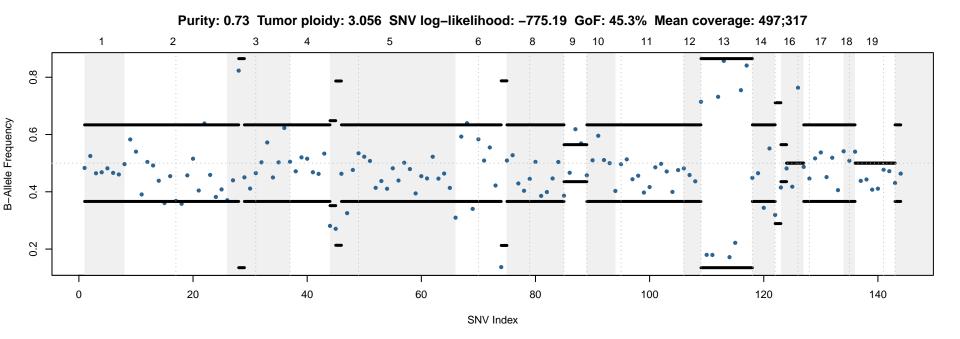
## SCNA-fit log-likelihood: -7985.64







Purity: 0.73 Tumor ploidy: 3.056 6 2 3 5 Fraction Genome 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0 1.5 2.0 log2 ratio



## SCNA-fit log-likelihood: -7690.38

