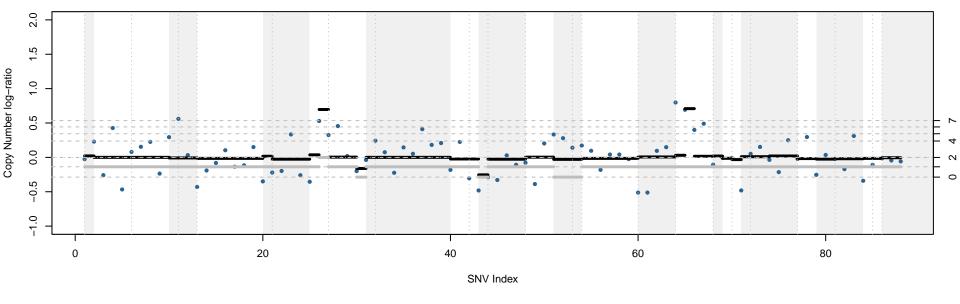
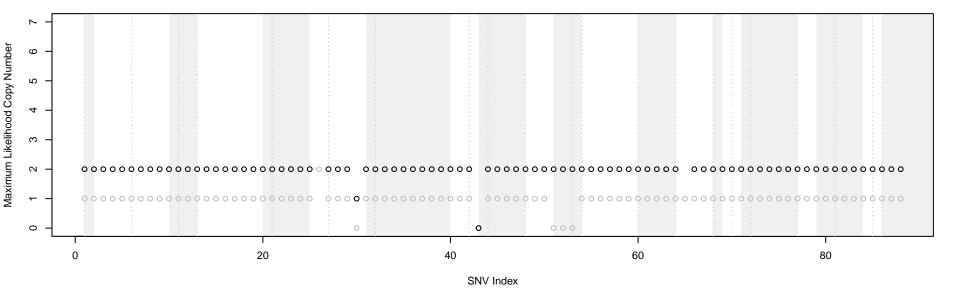
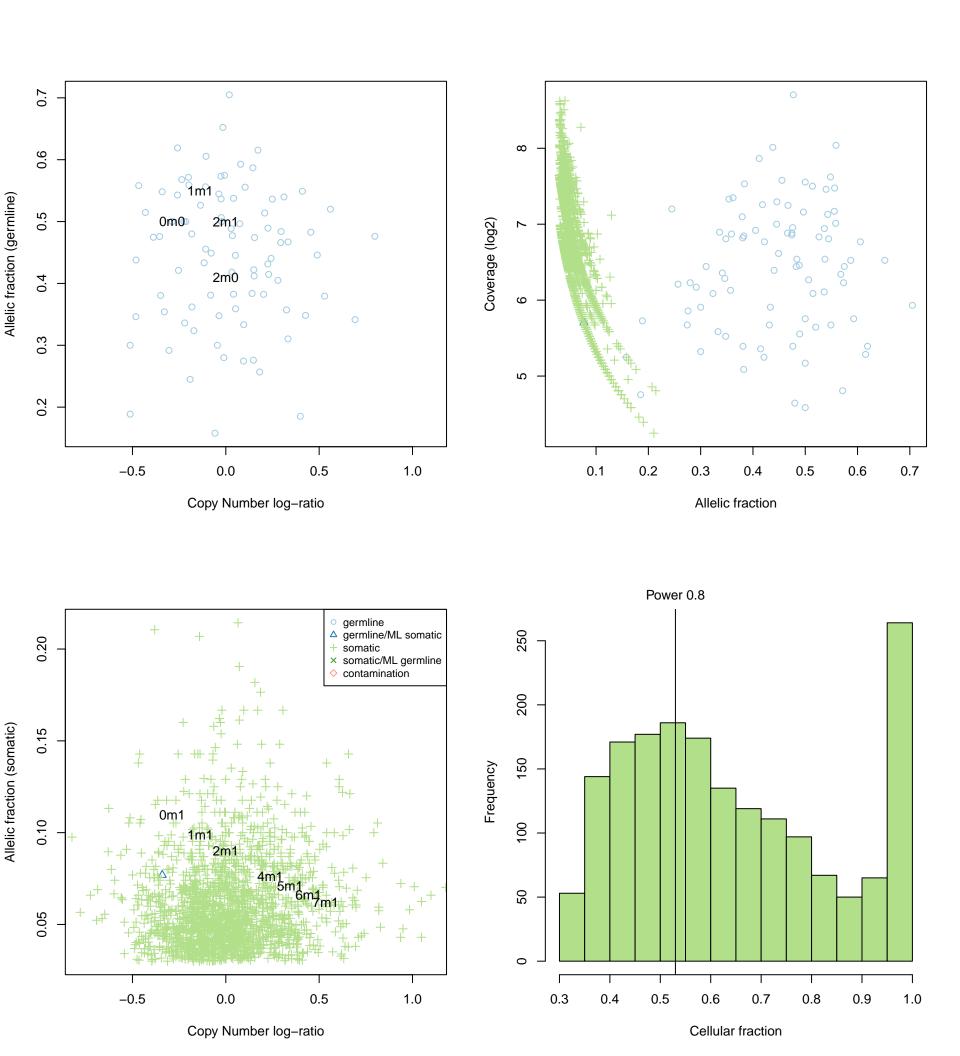
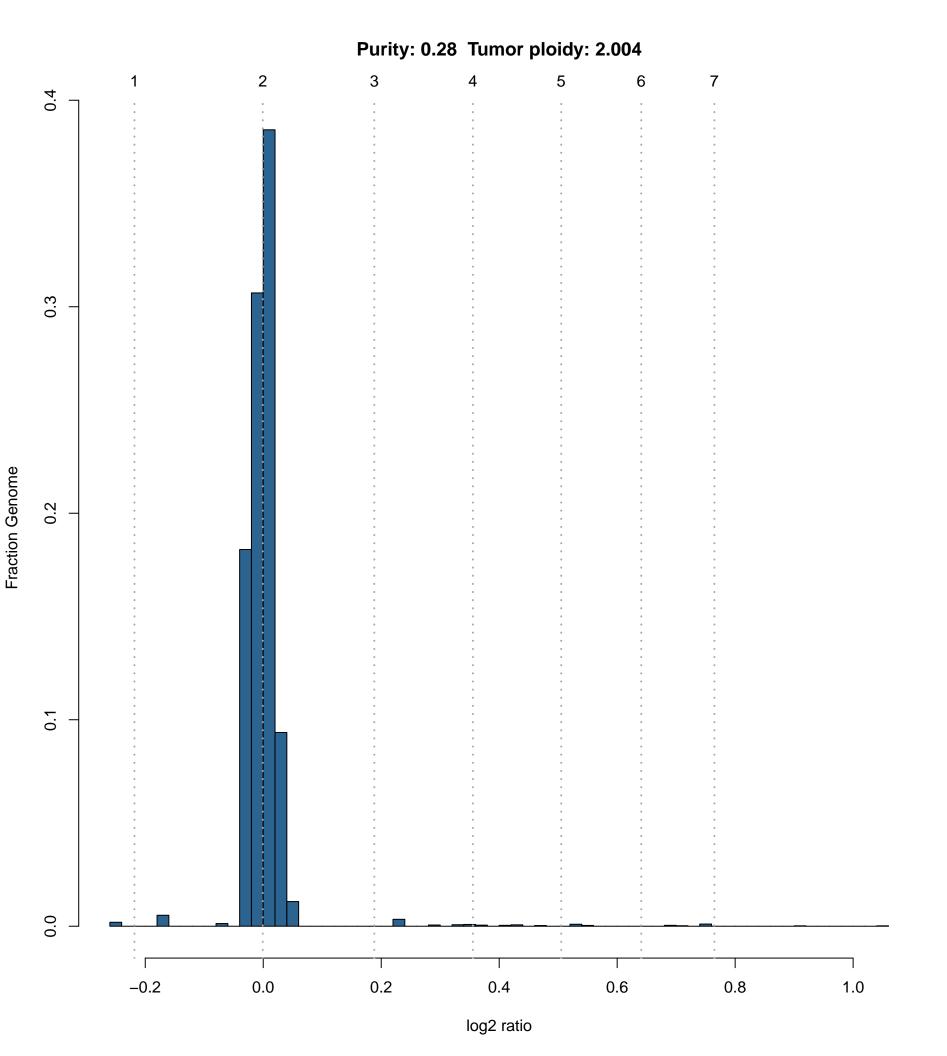


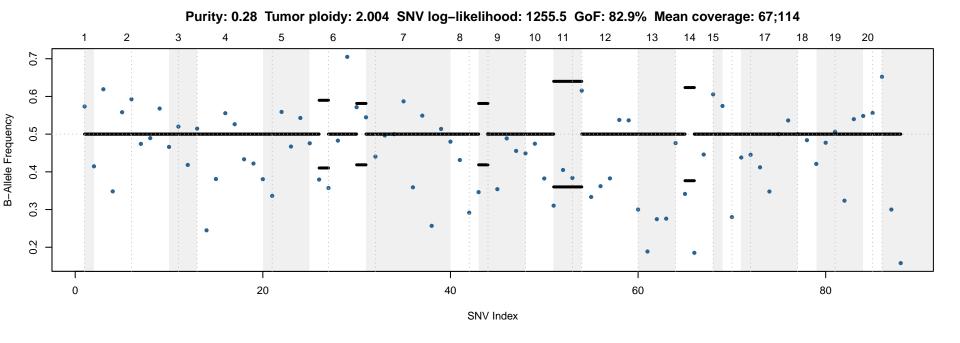
SCNA-fit log-likelihood: 1203.15



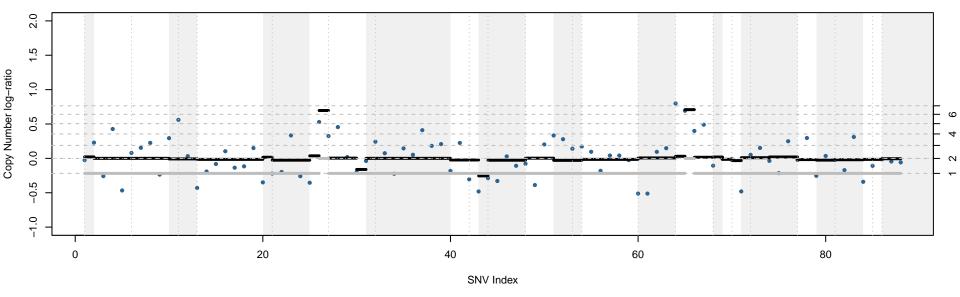


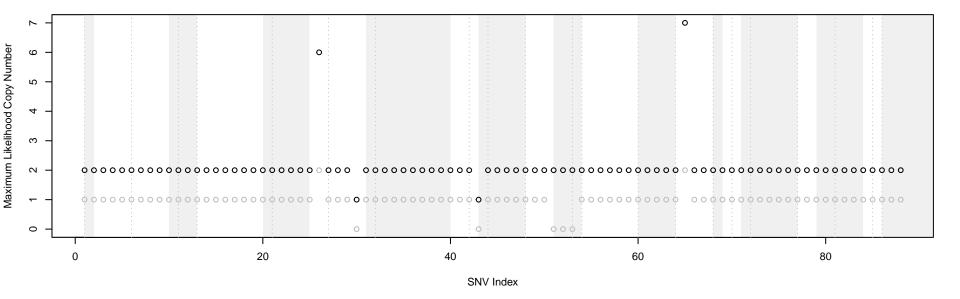


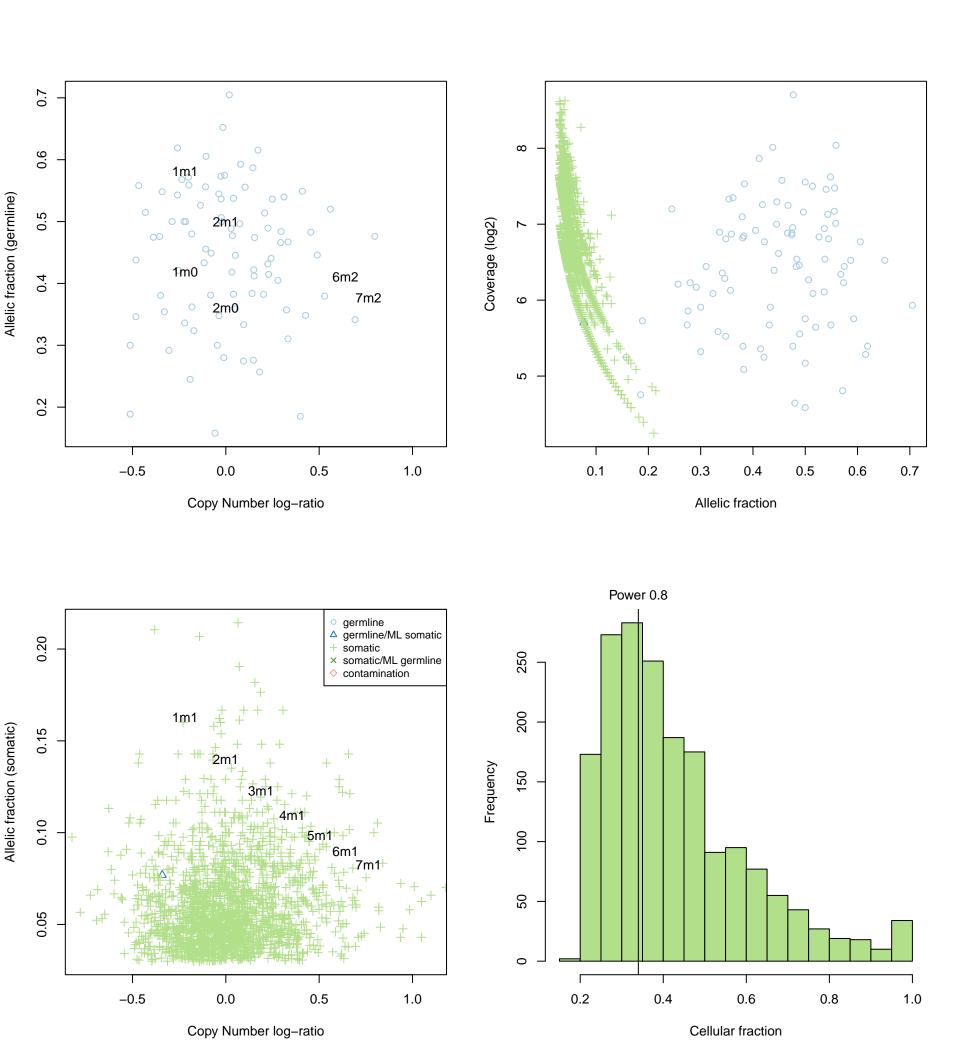


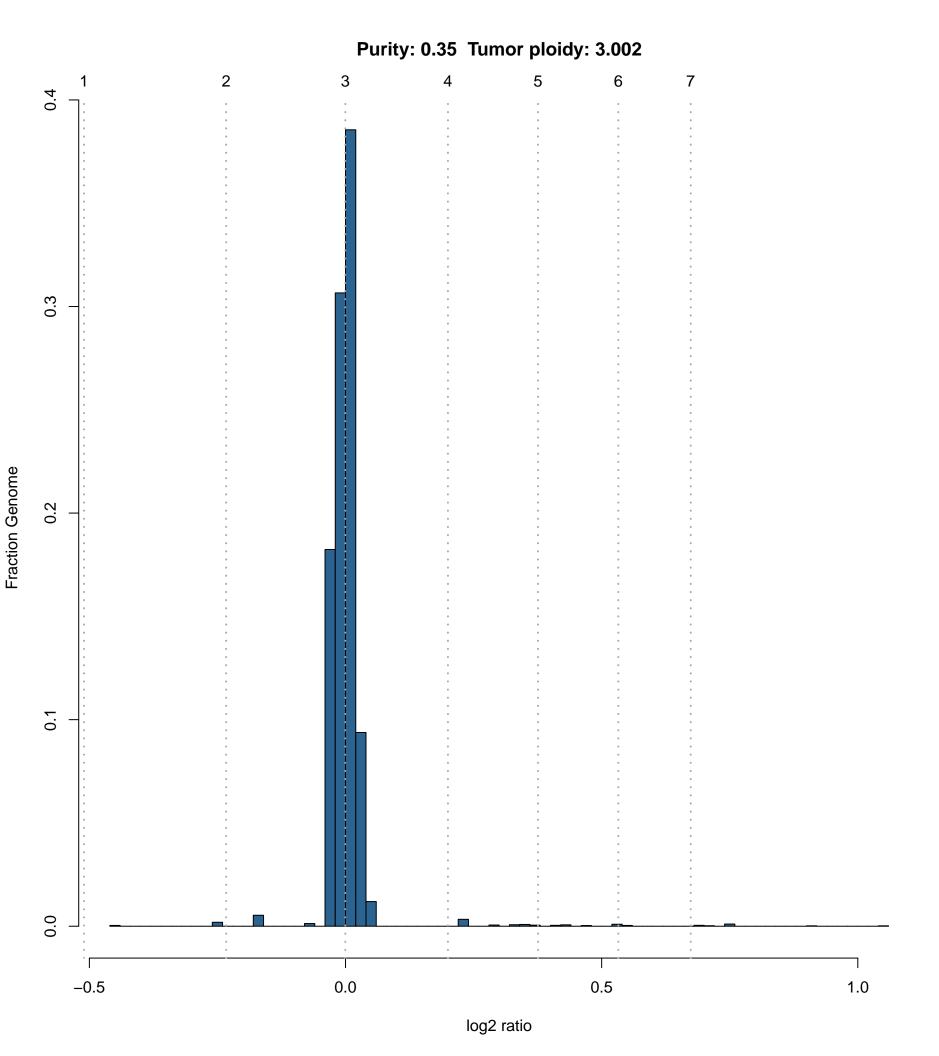


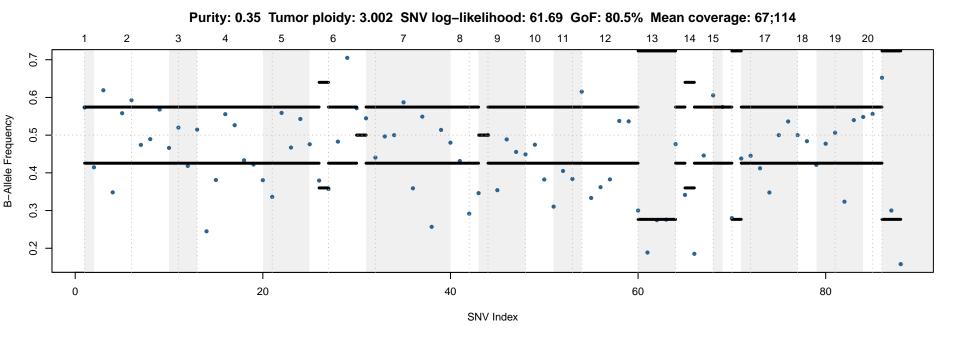
SCNA-fit log-likelihood: 1256.51



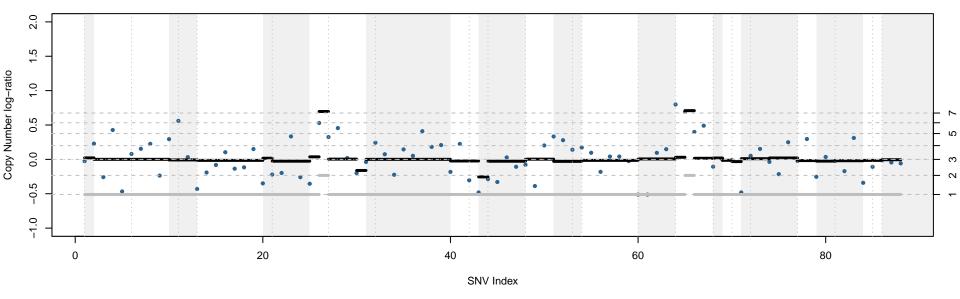


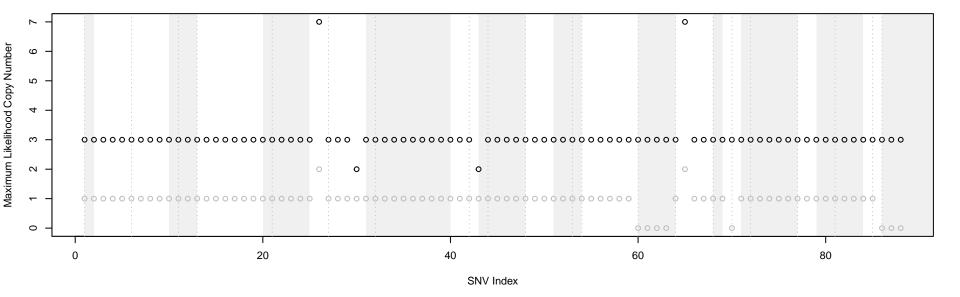


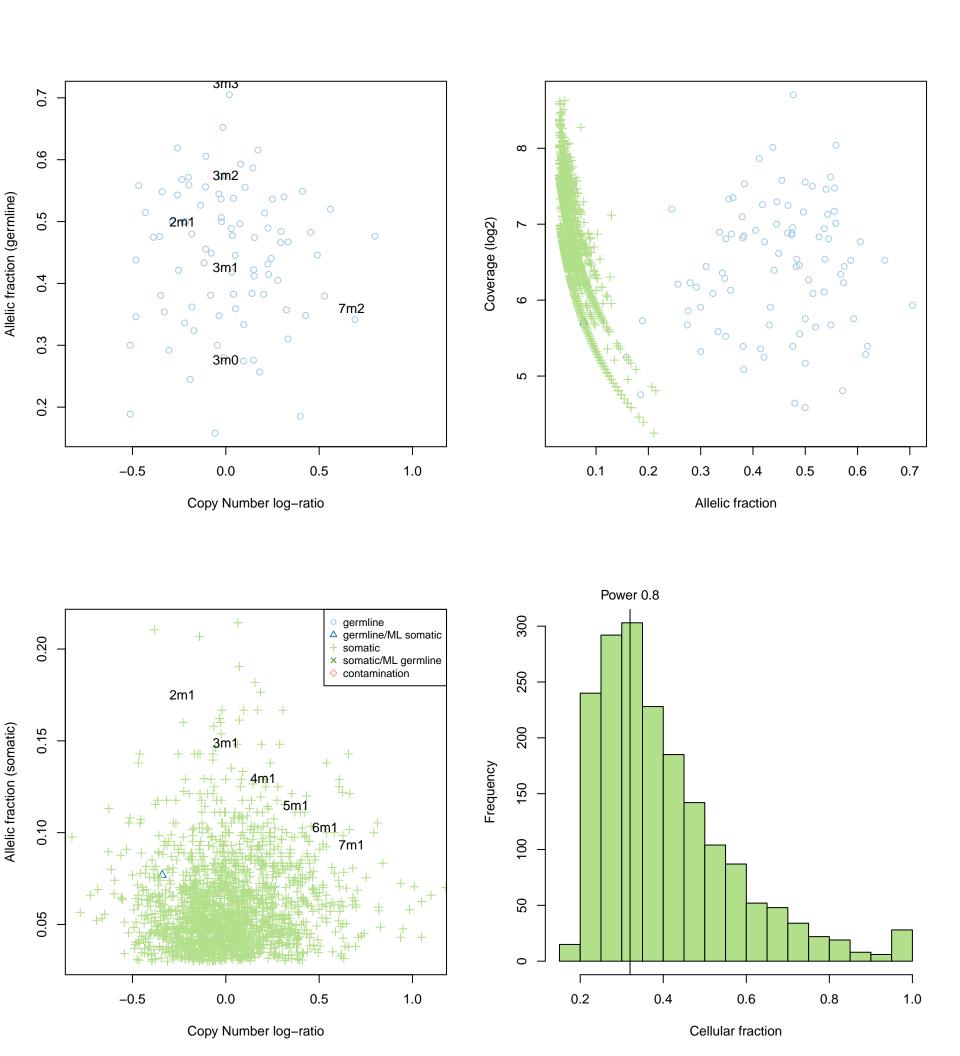


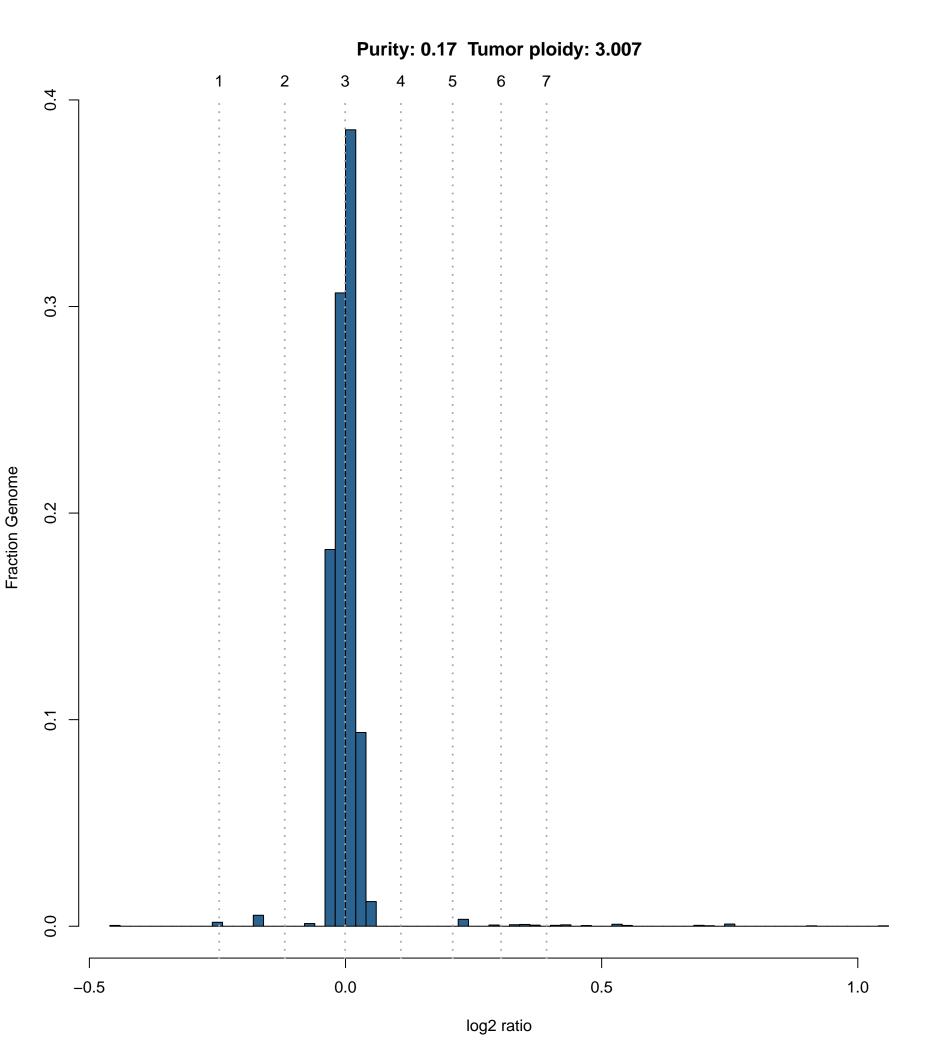


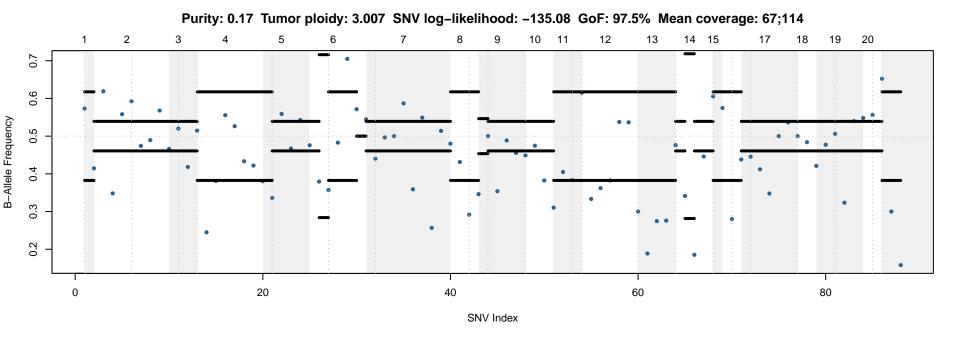
SCNA-fit log-likelihood: 1250.17



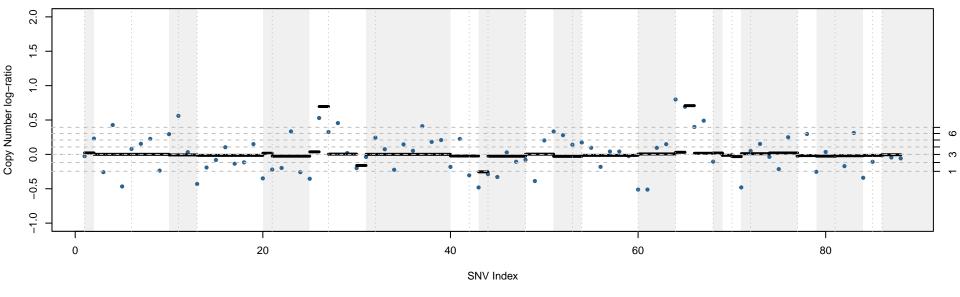


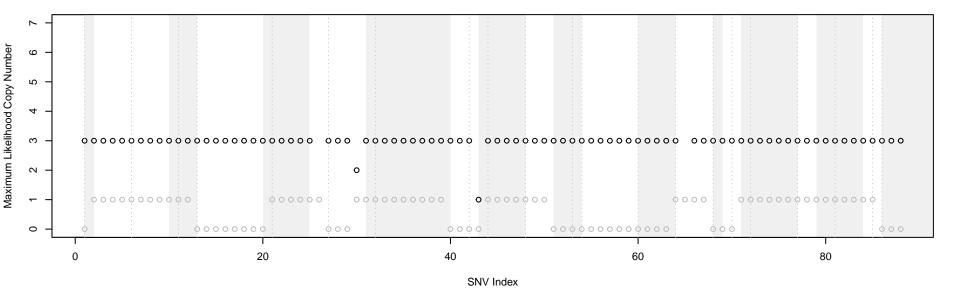


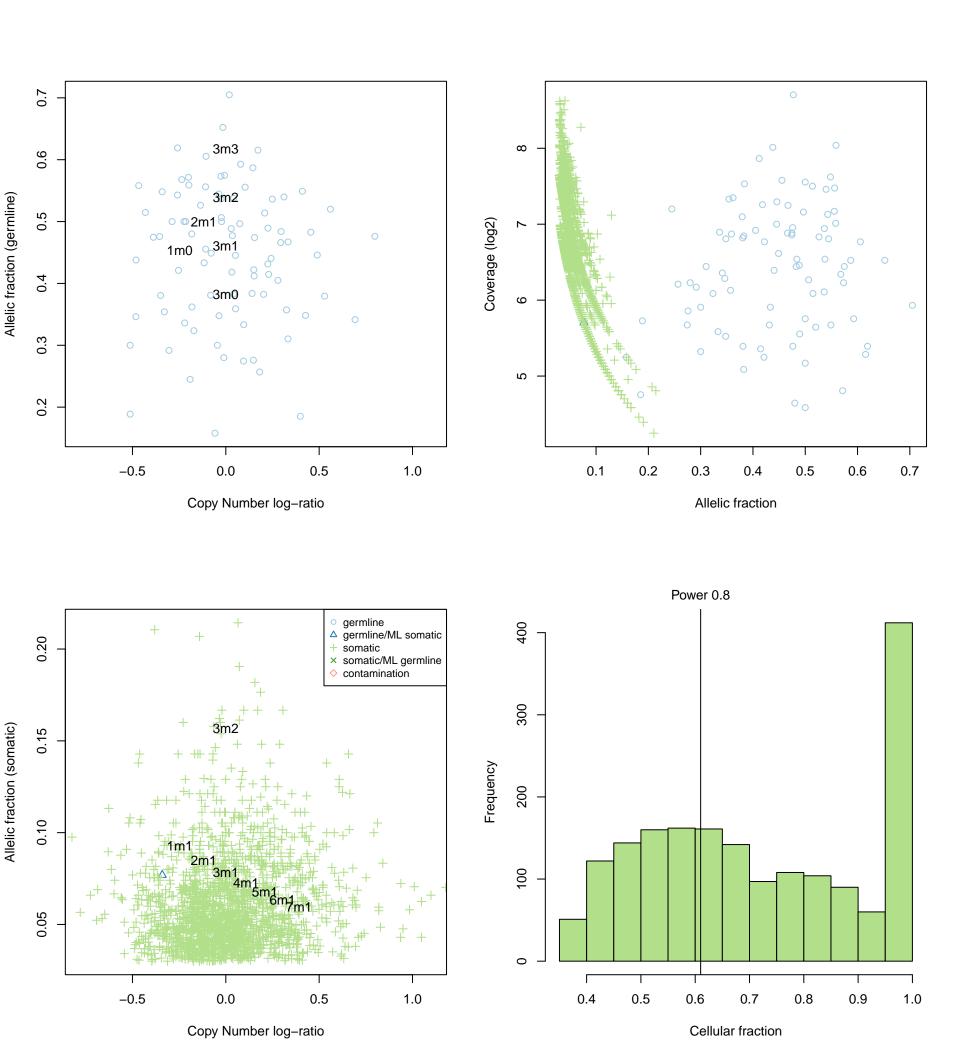




SCNA-fit log-likelihood: 1184.09



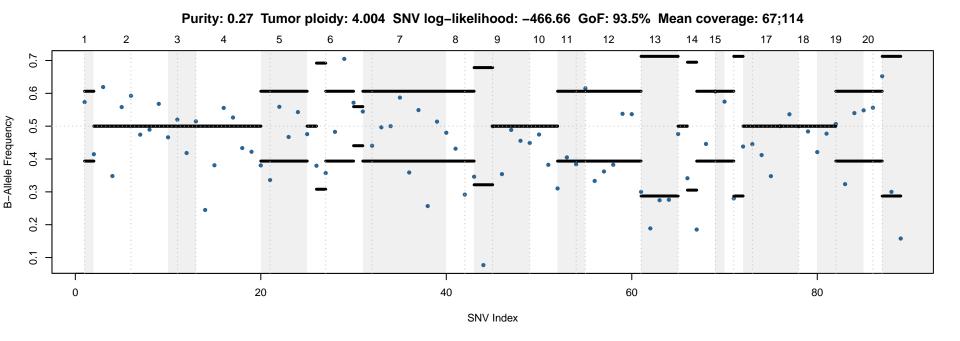




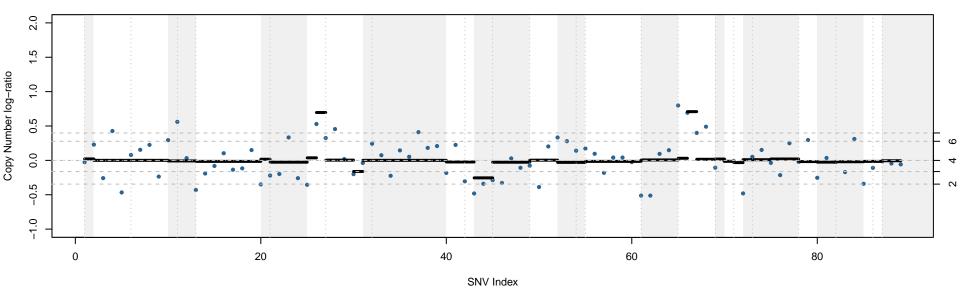
Purity: 0.27 Tumor ploidy: 4.004 6 2 3 0.3 0.1 0.0 -0.5 0.0 0.5 1.0

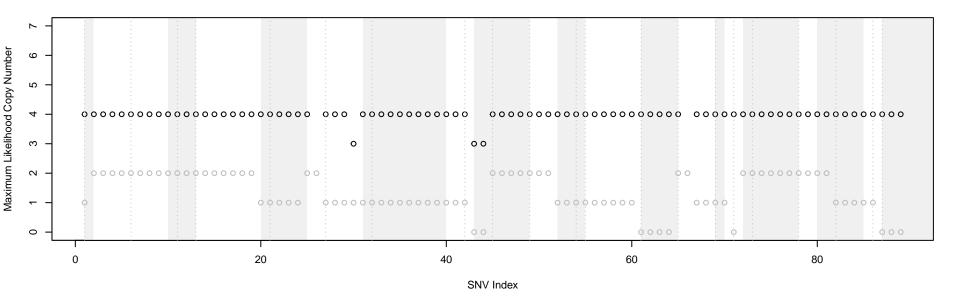
log2 ratio

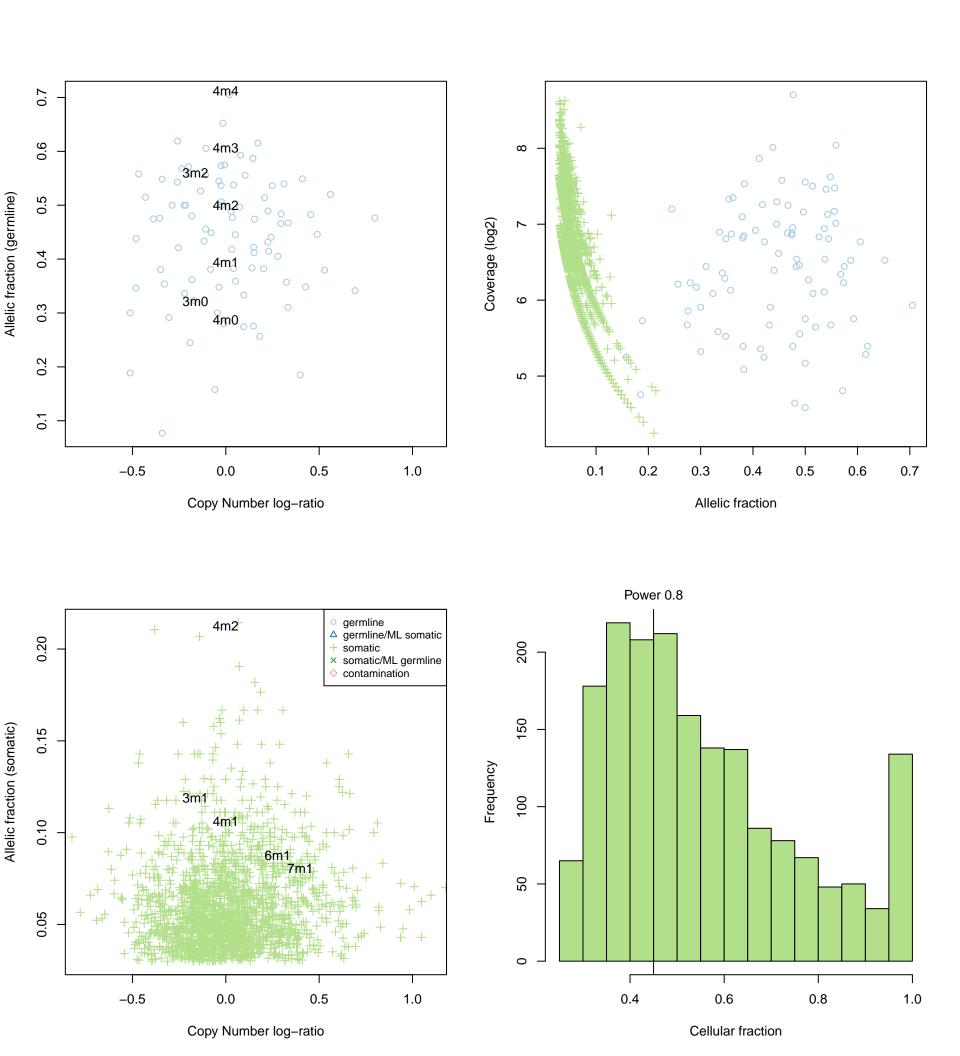
Fraction Genome

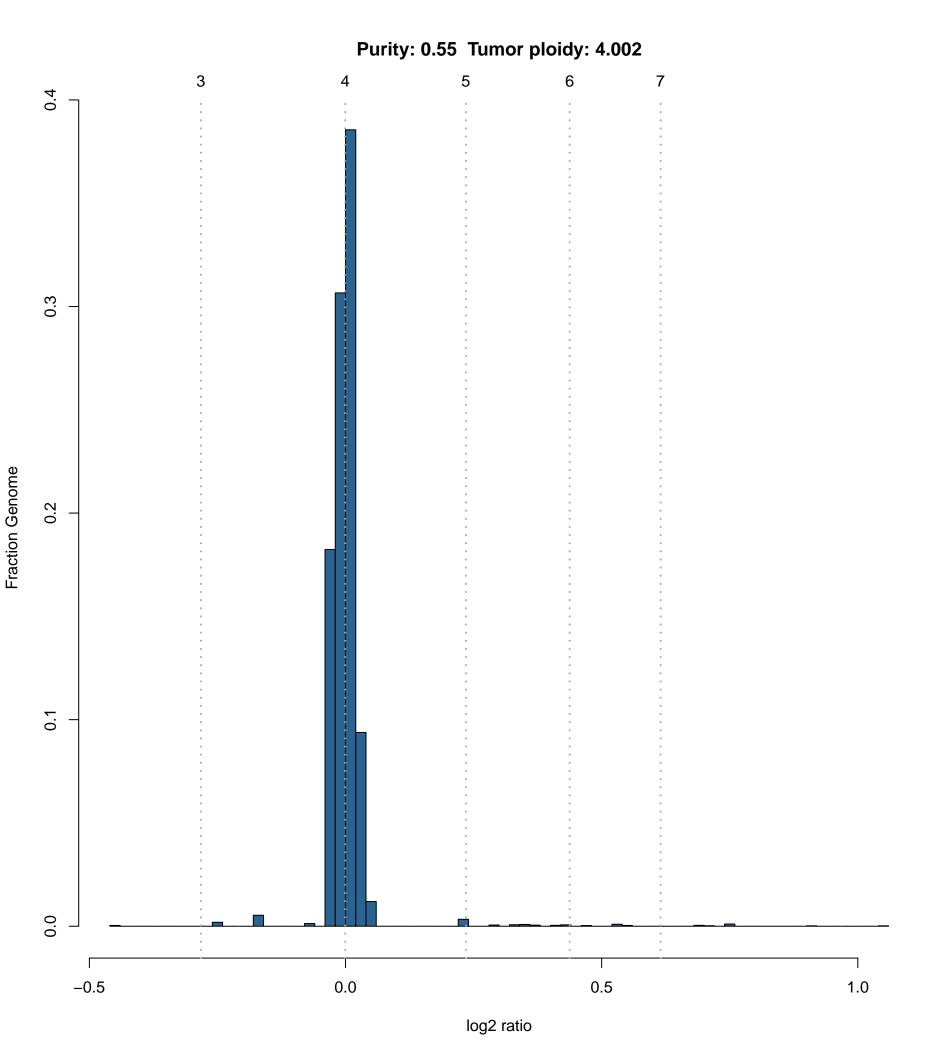


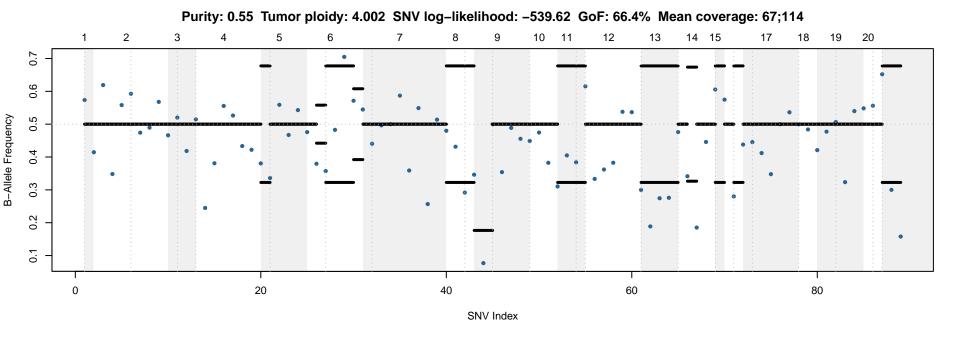
SCNA-fit log-likelihood: 1199.83



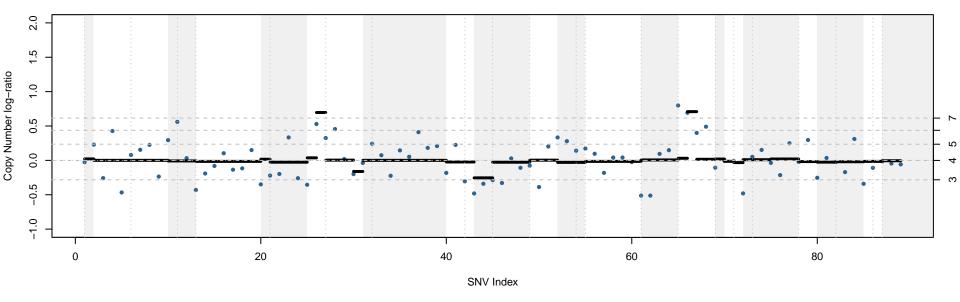


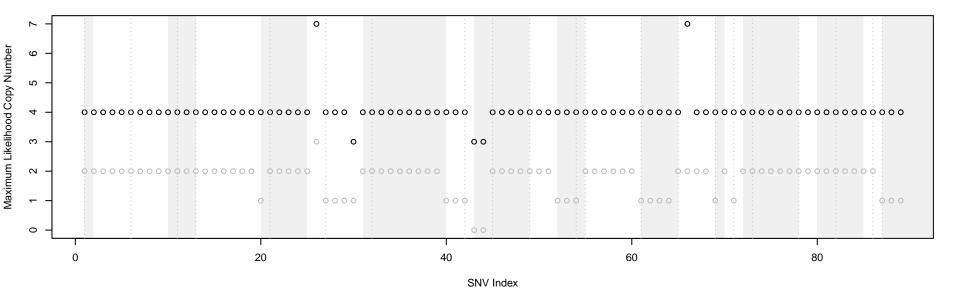


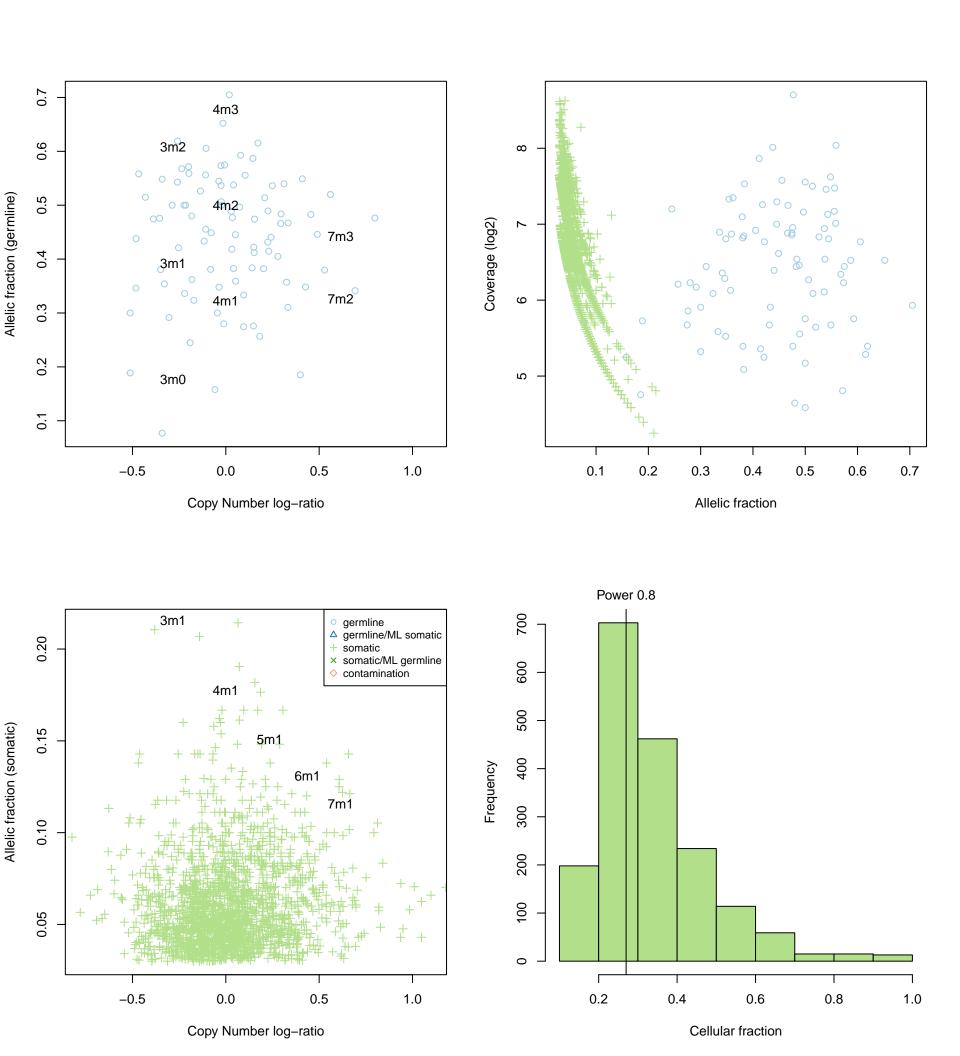


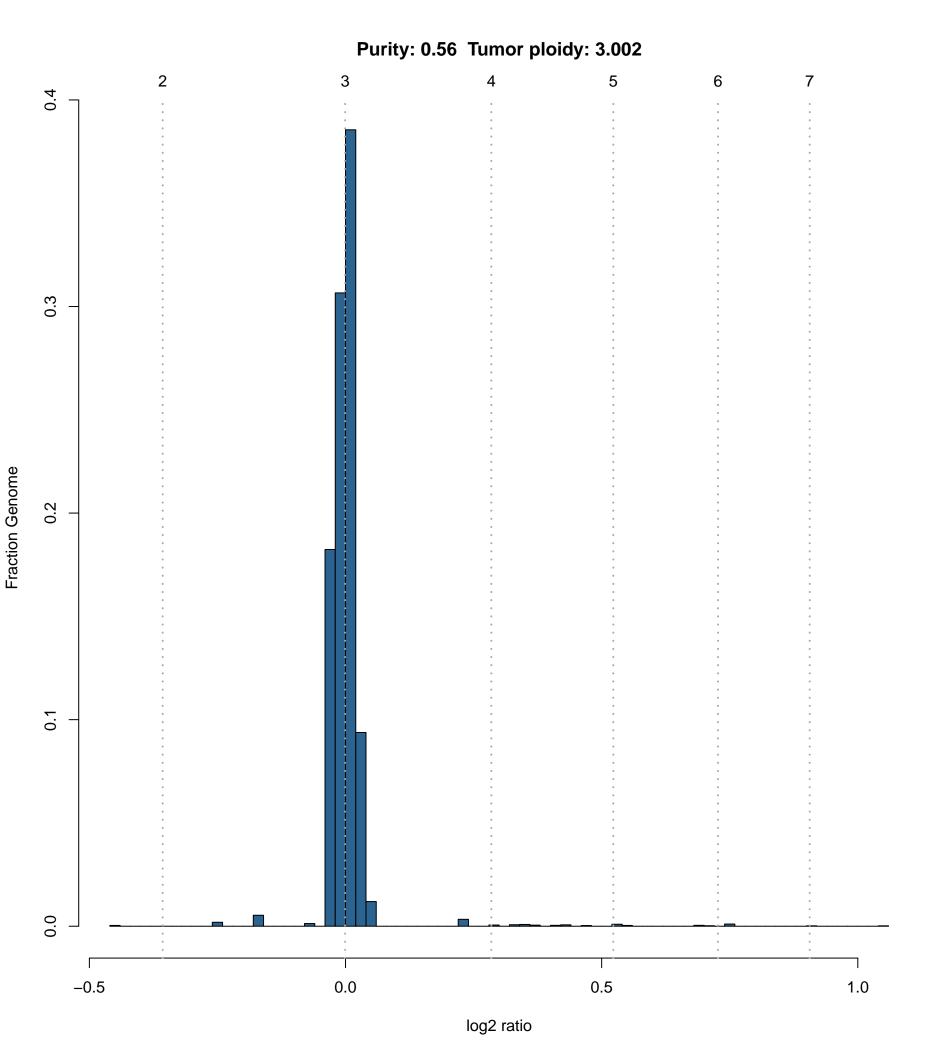


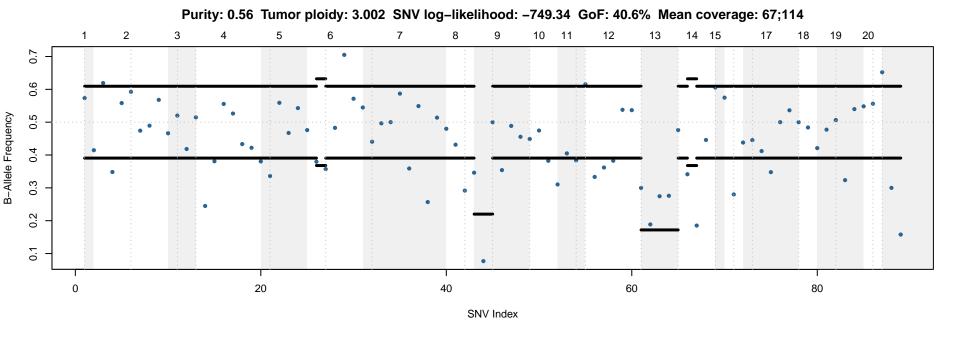
SCNA-fit log-likelihood: 1230.41



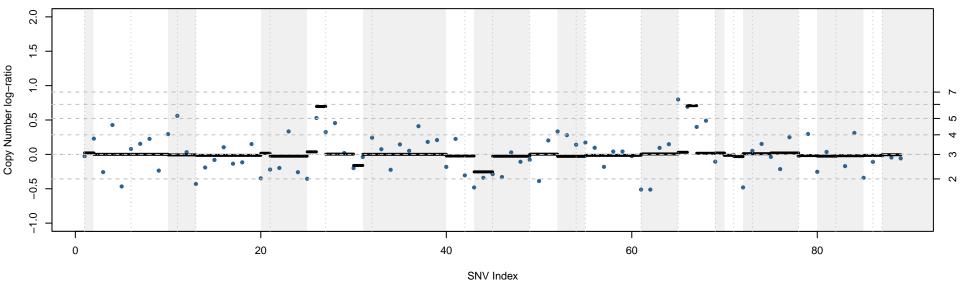


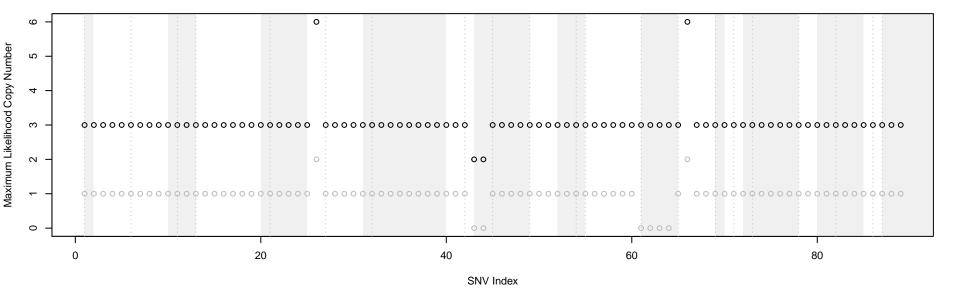


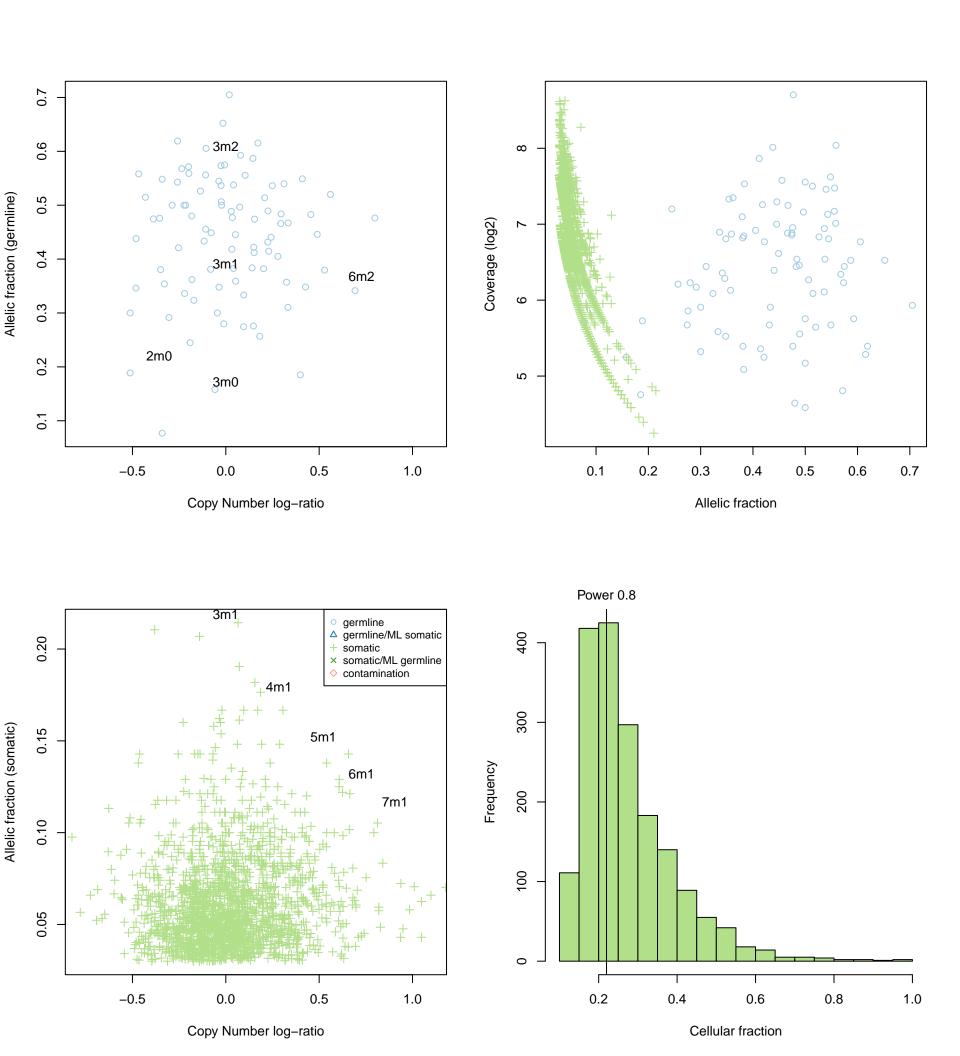




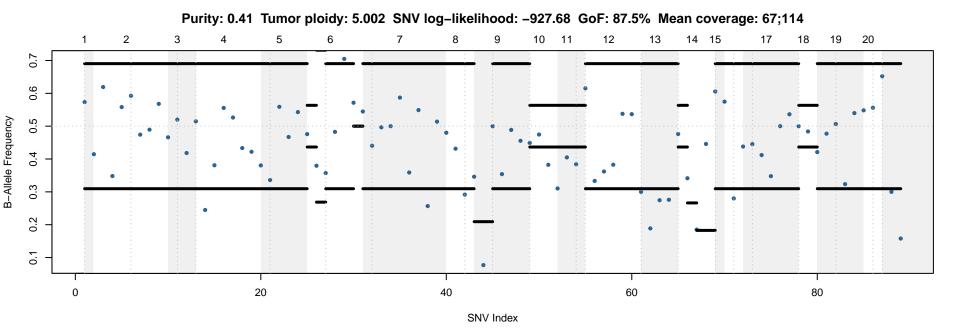
SCNA-fit log-likelihood: 1233.91



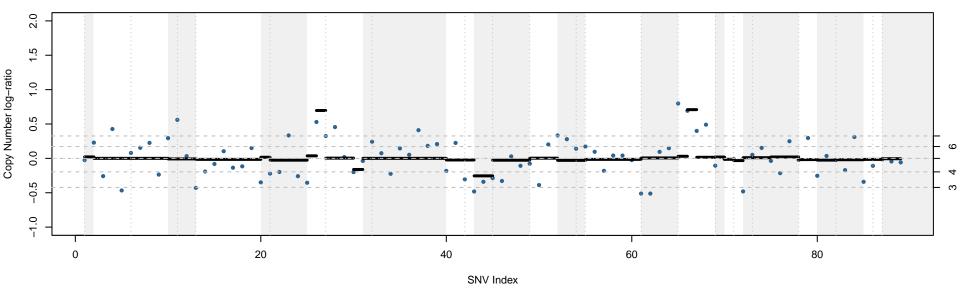


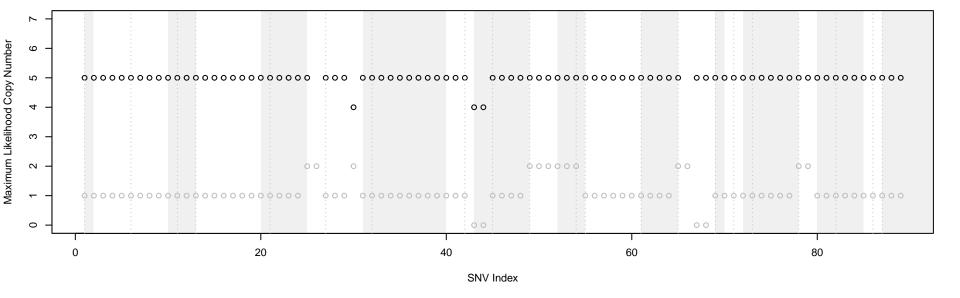


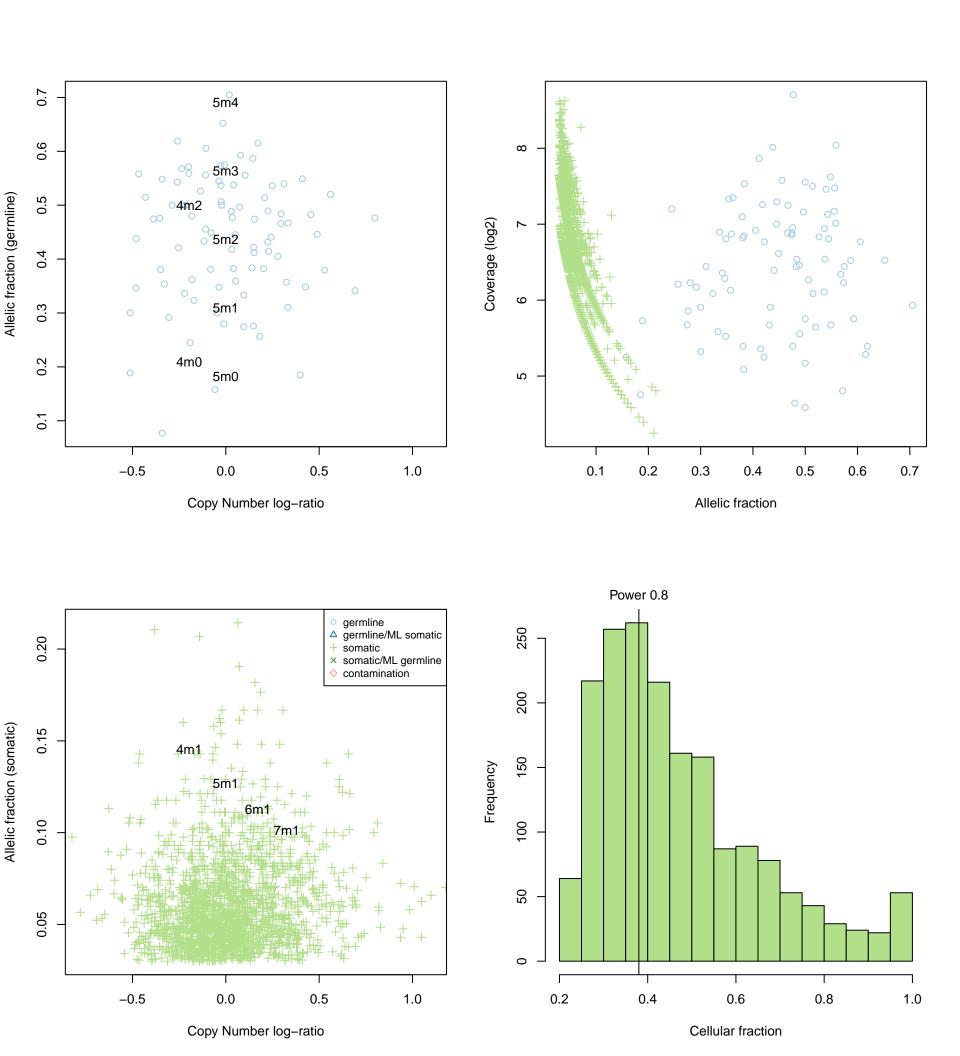
Purity: 0.41 Tumor ploidy: 5.002 3 6 0.3 Fraction Genome 0.1 0.0 -0.5 0.0 0.5 1.0 log2 ratio



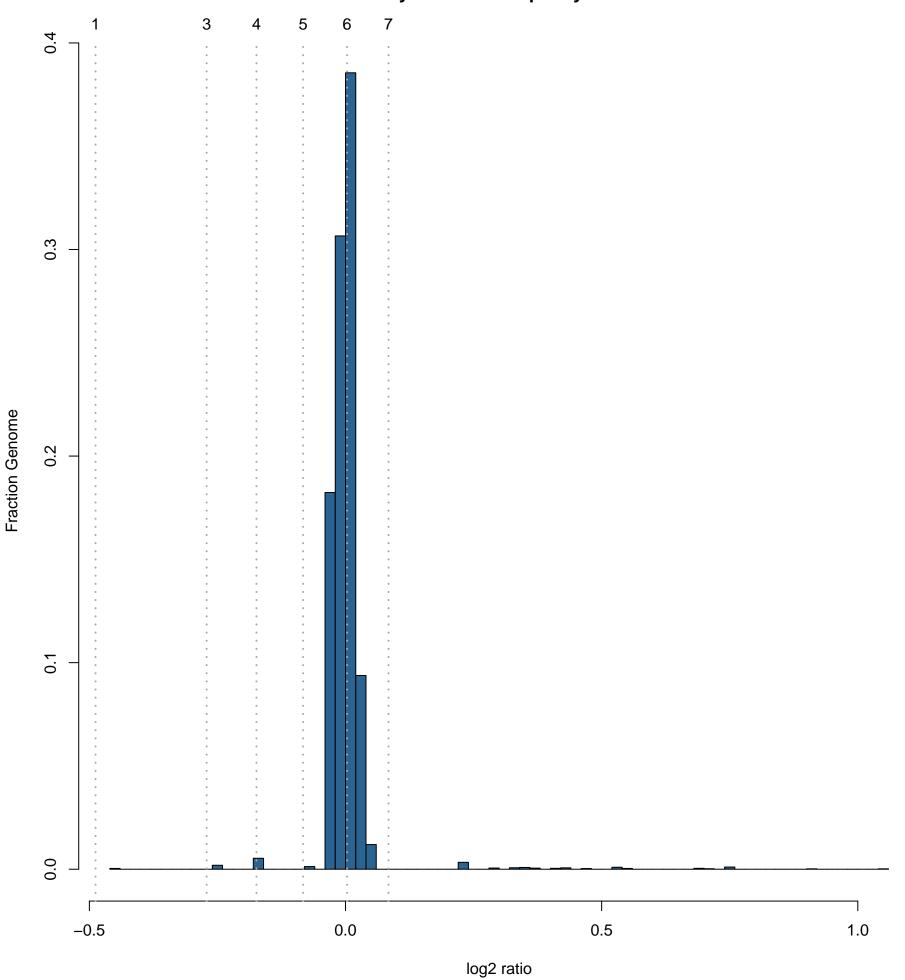
SCNA-fit log-likelihood: 1179.96

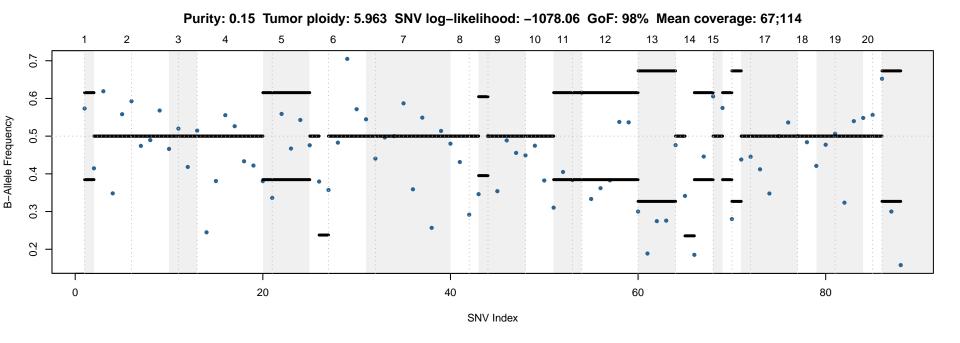




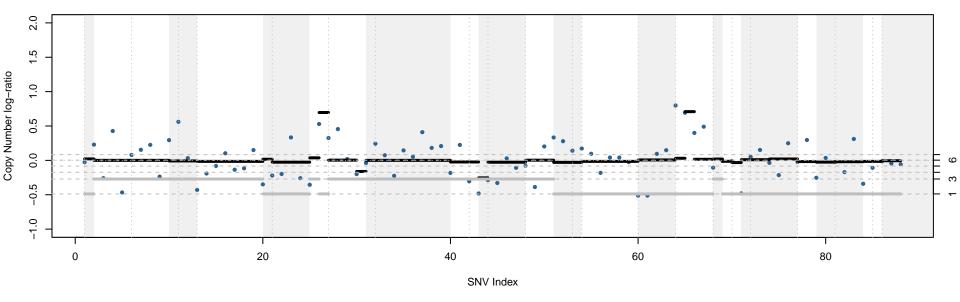


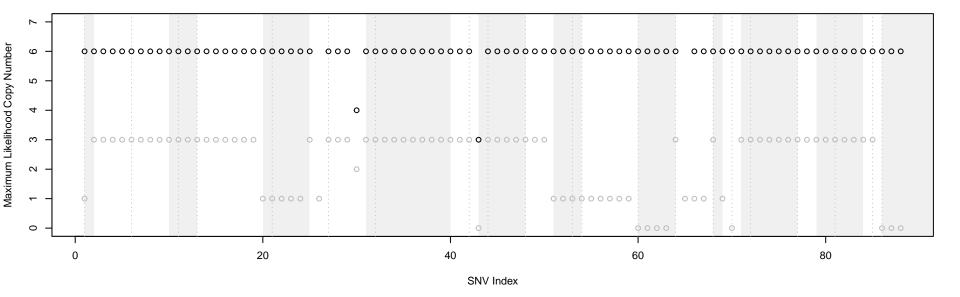
Purity: 0.15 Tumor ploidy: 5.963

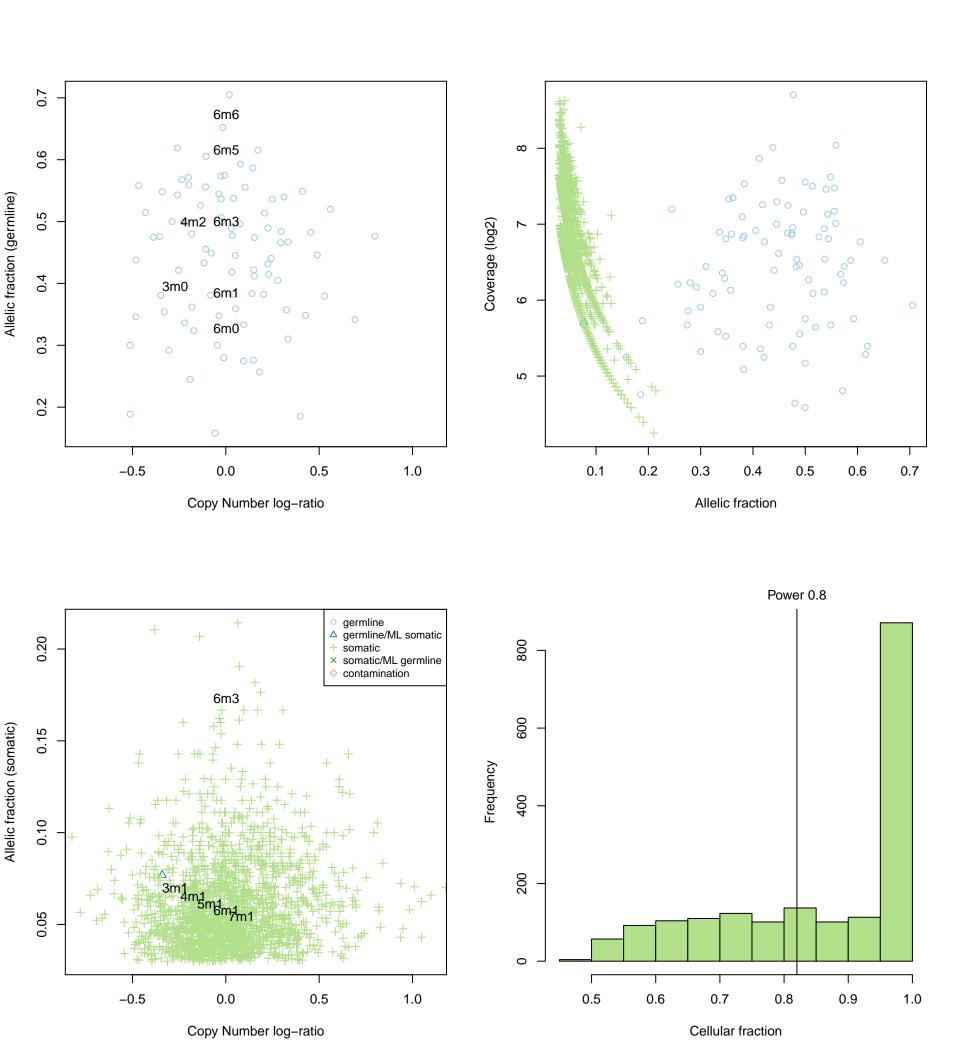




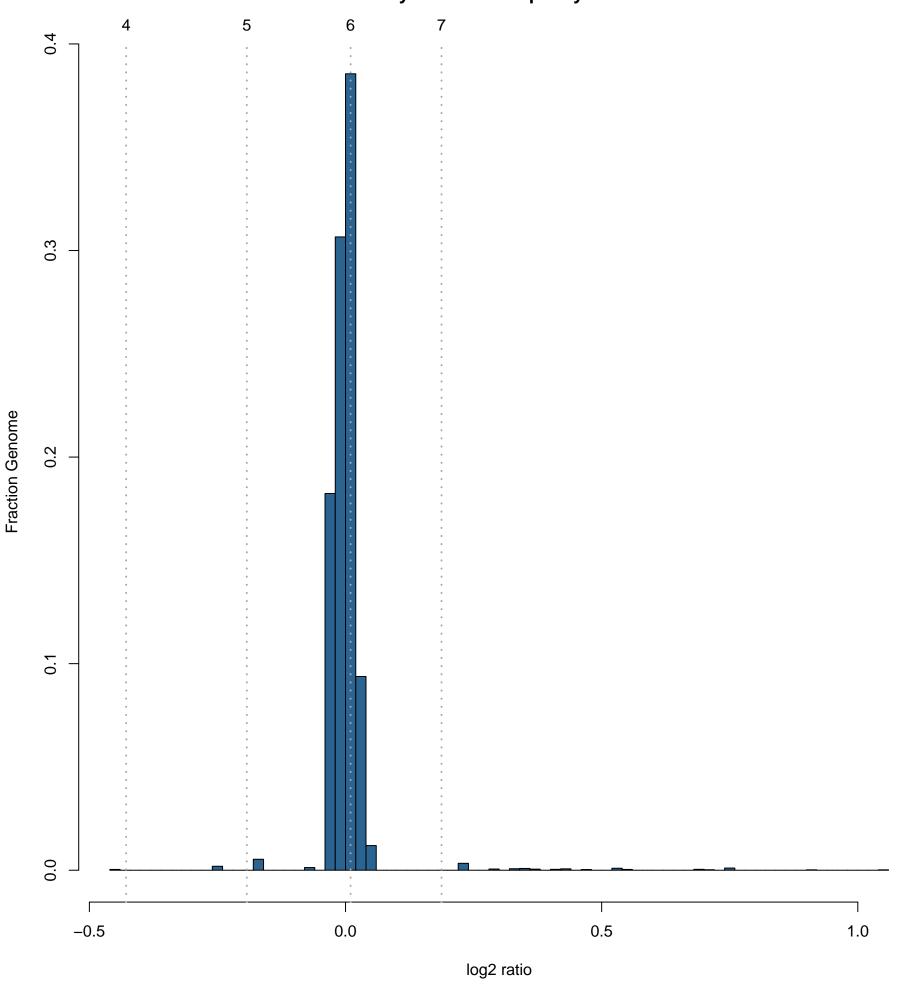
SCNA-fit log-likelihood: 906.9

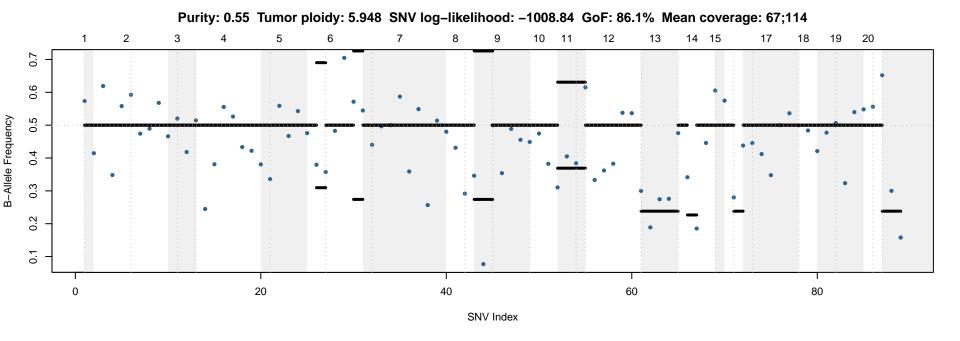




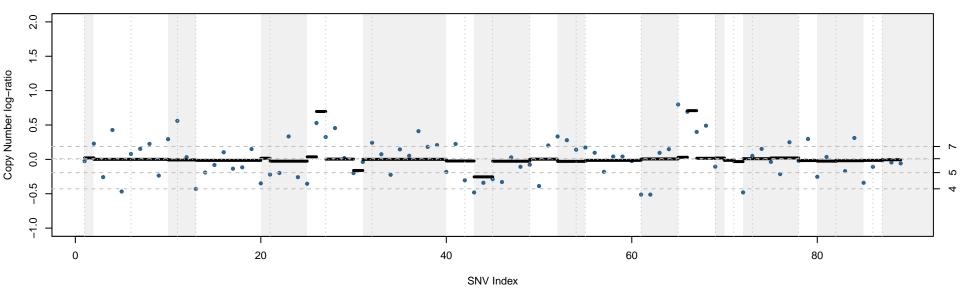


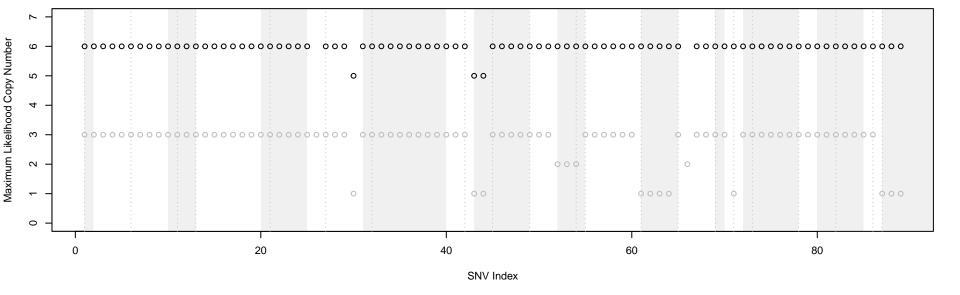
Purity: 0.55 Tumor ploidy: 5.948

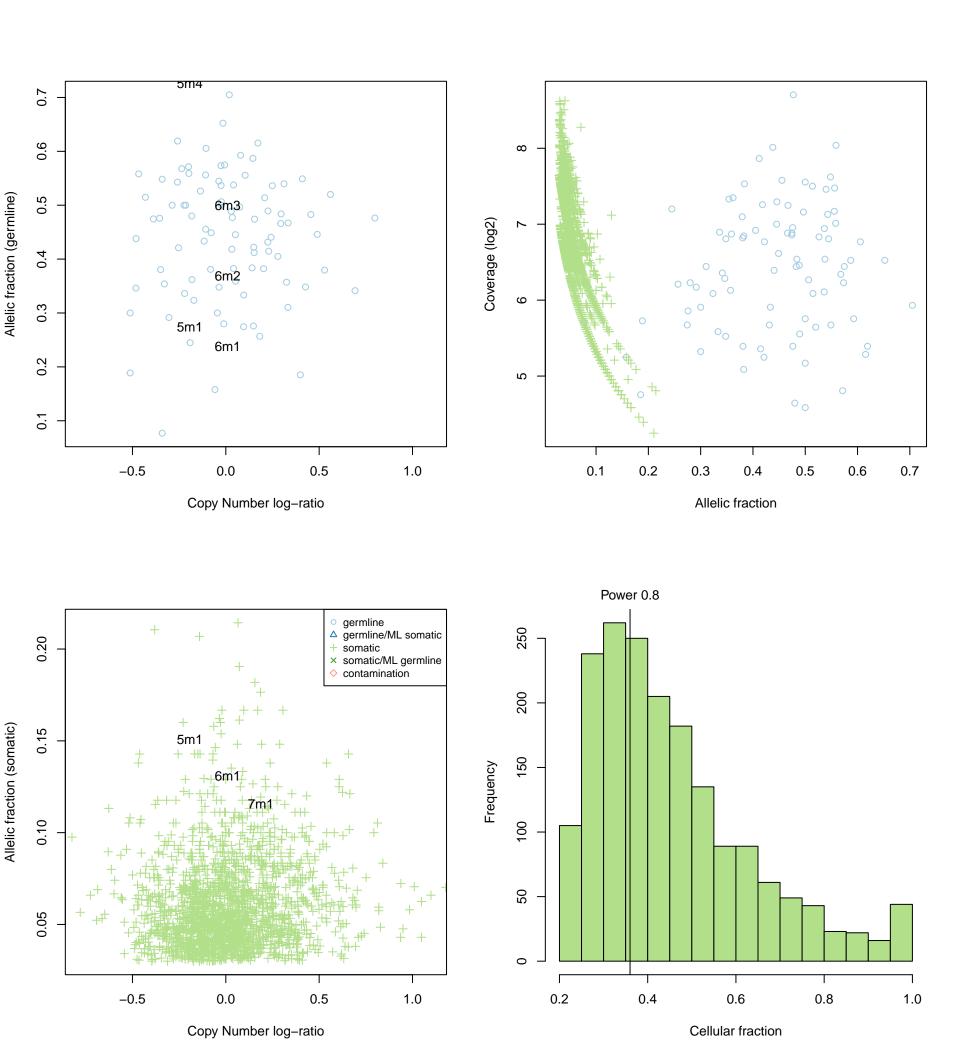




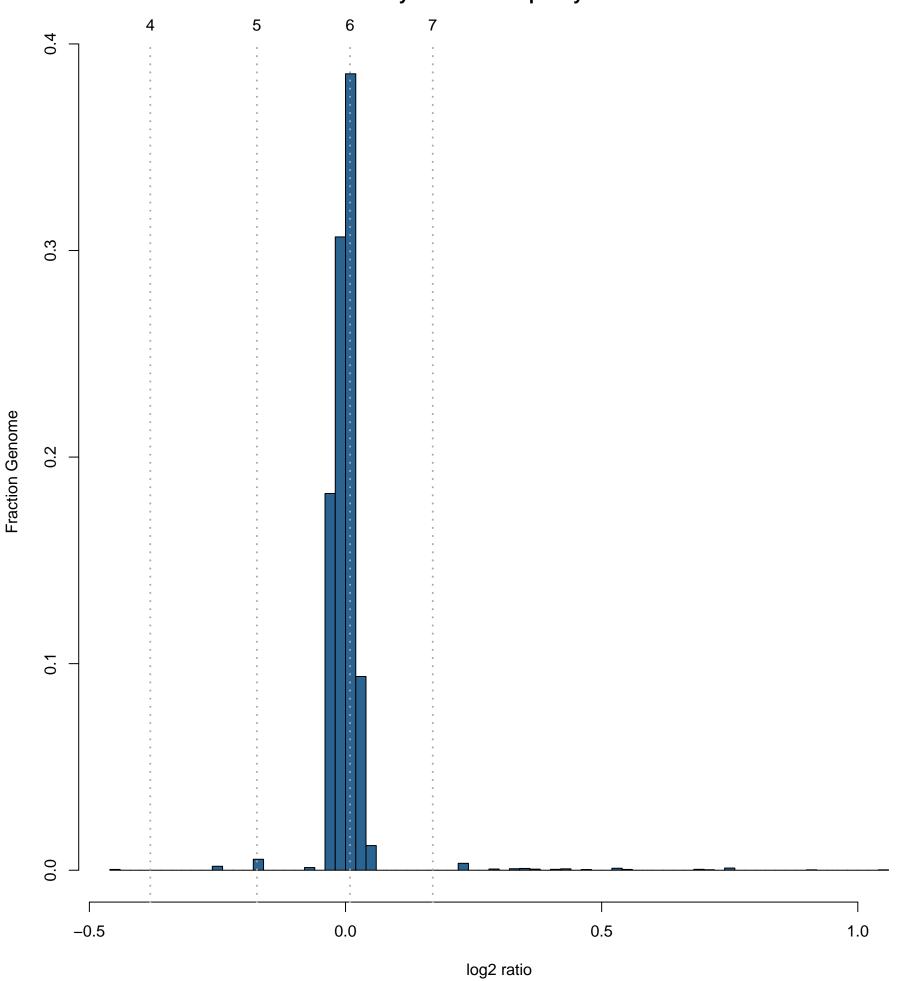
SCNA-fit log-likelihood: 656.07

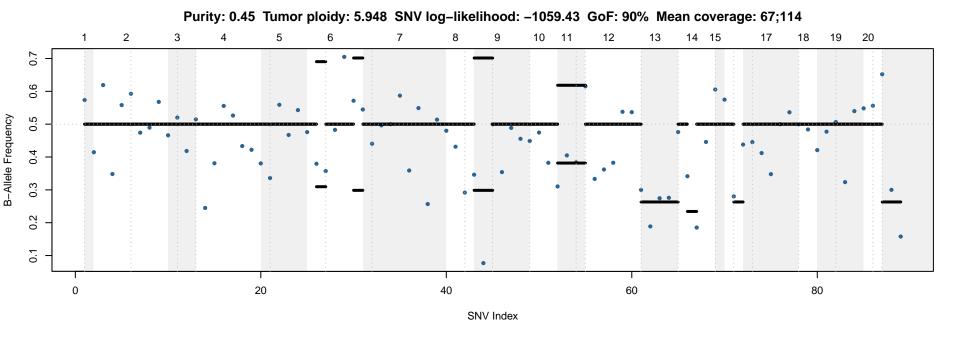




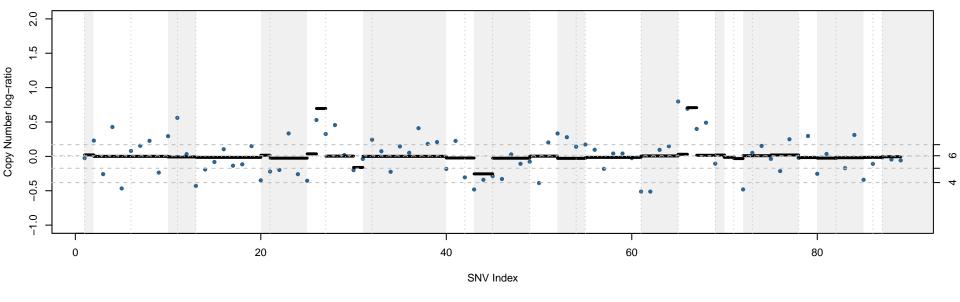


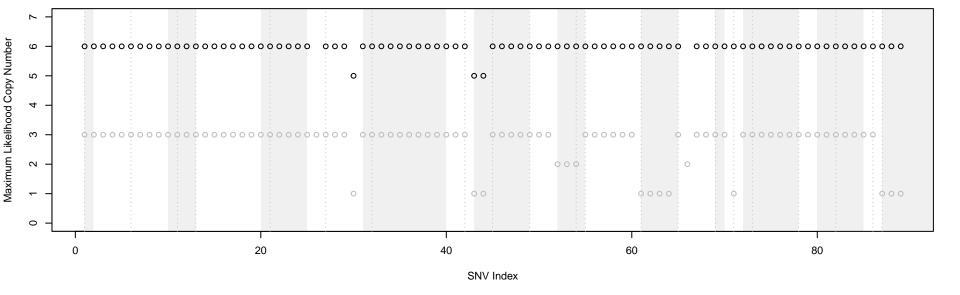
Purity: 0.45 Tumor ploidy: 5.948

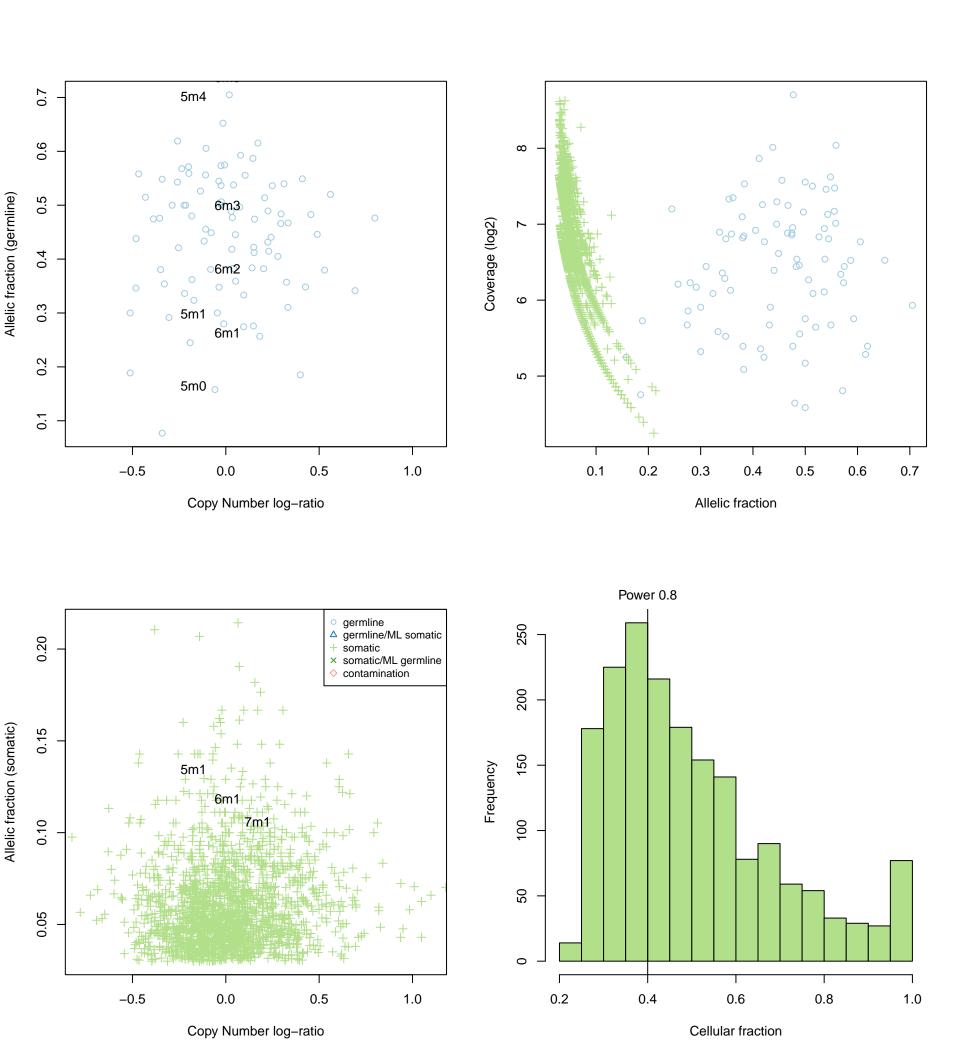




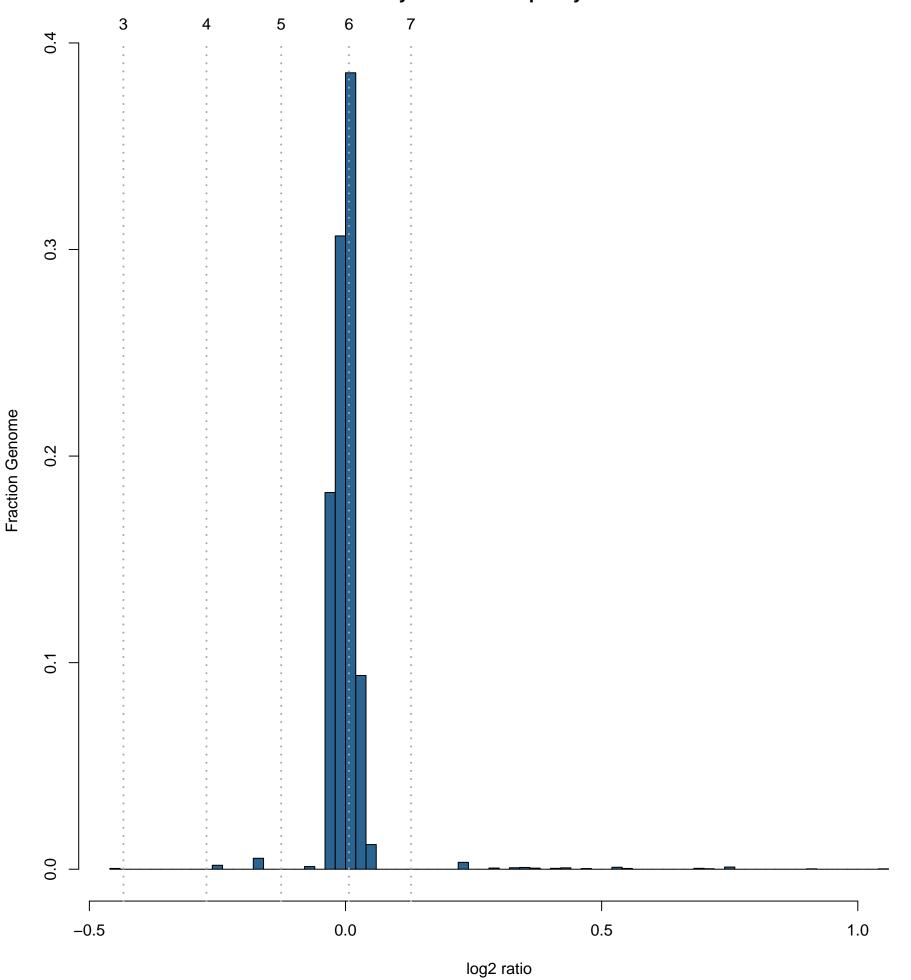
SCNA-fit log-likelihood: 735.73

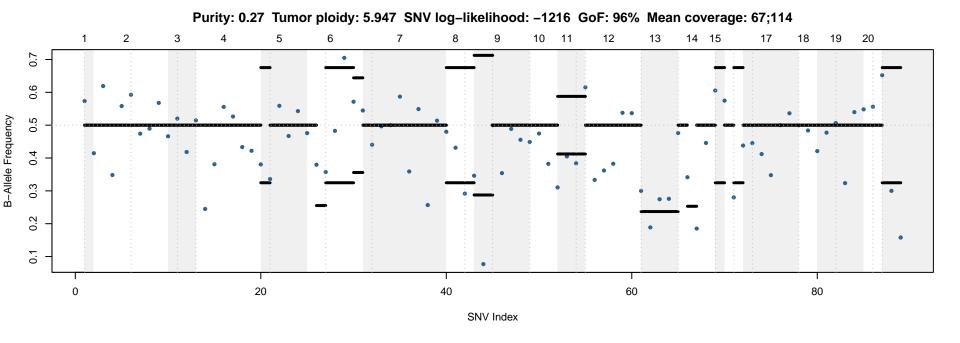




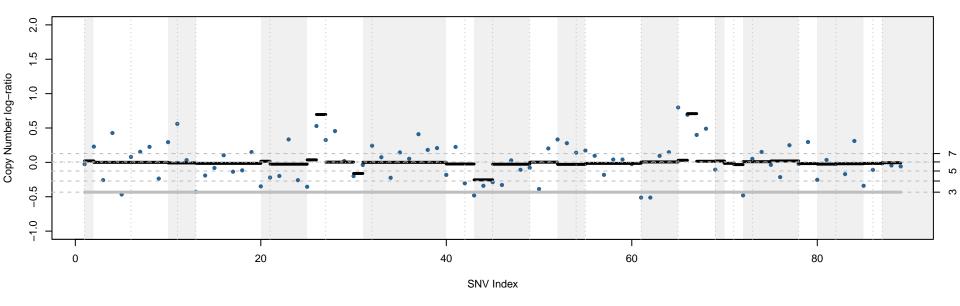


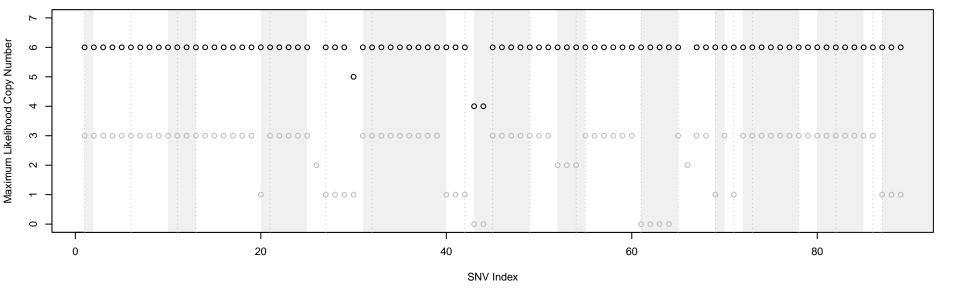
Purity: 0.27 Tumor ploidy: 5.947

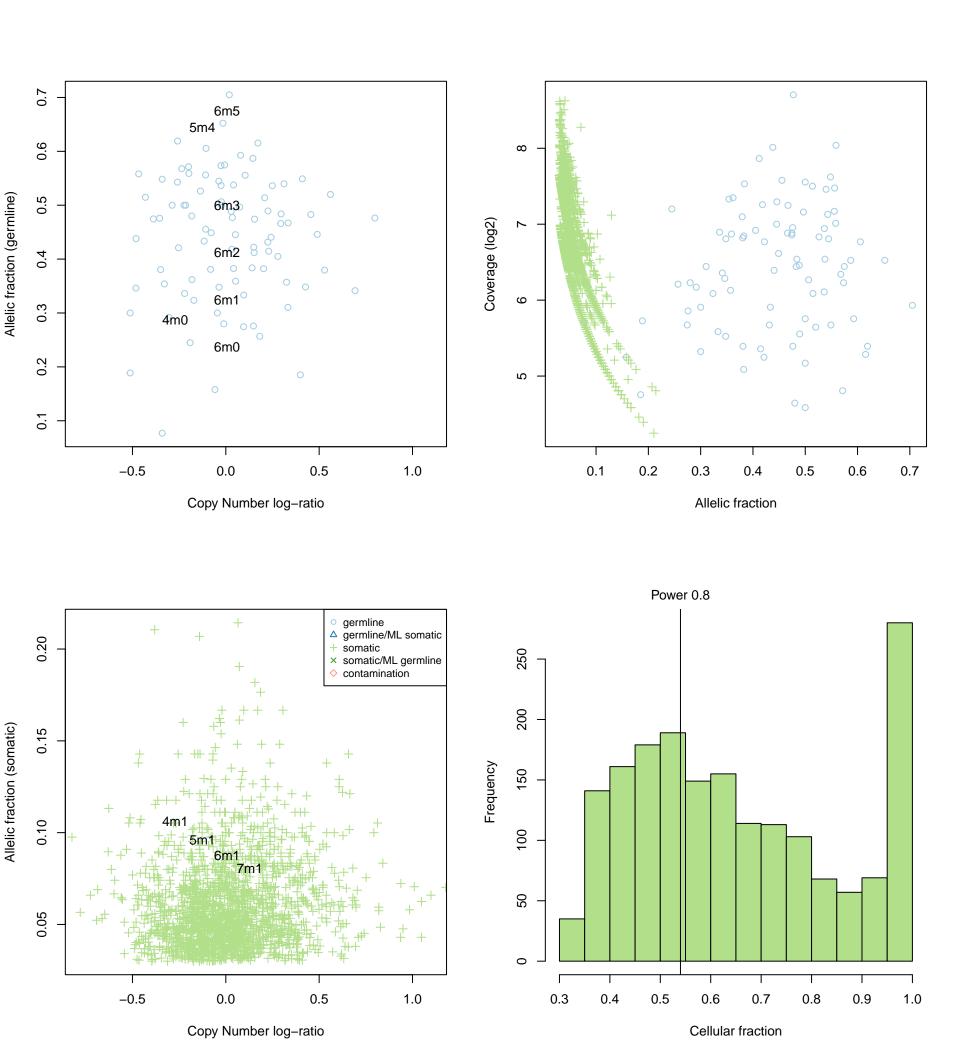








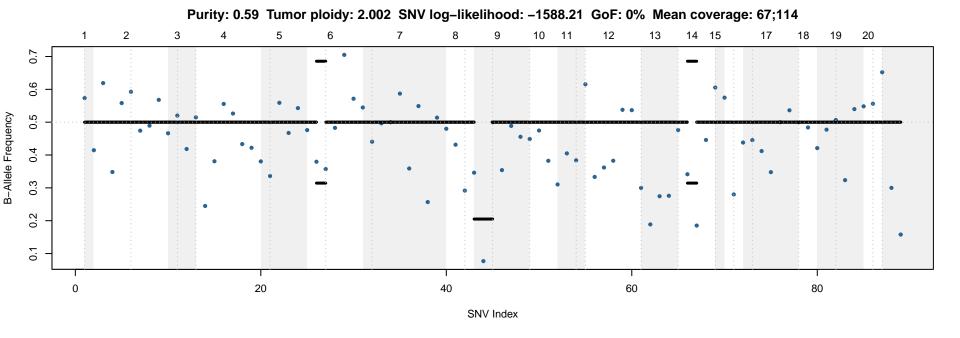




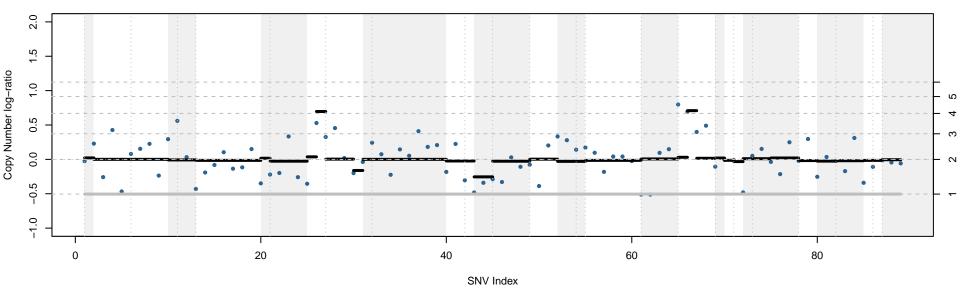
Purity: 0.59 Tumor ploidy: 2.002 5 0.3 0.2 0.1 0.0 -0.5 0.0 0.5 1.0

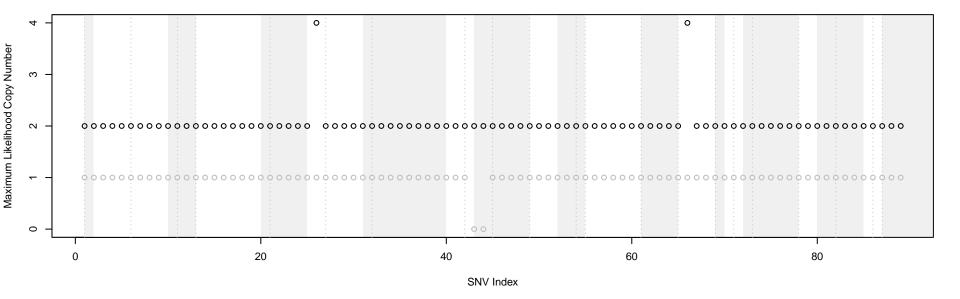
log2 ratio

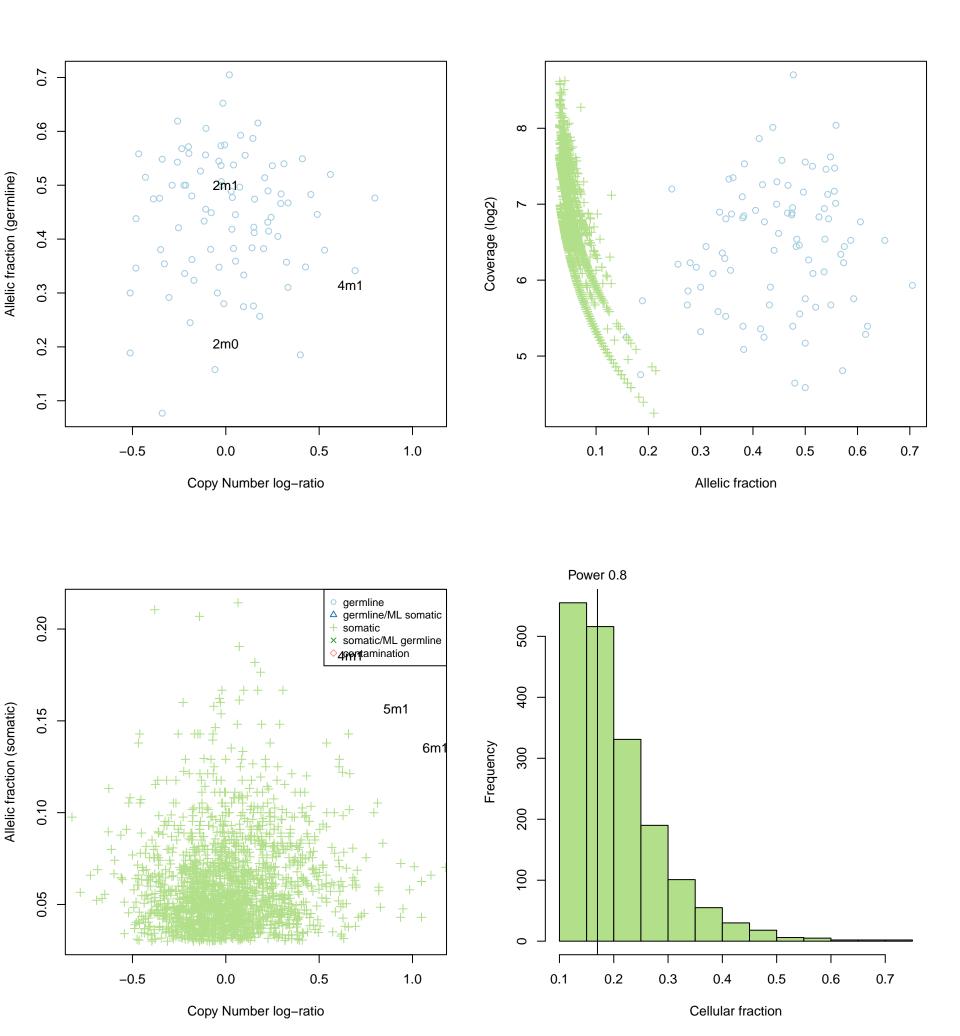
Fraction Genome



SCNA-fit log-likelihood: 1198.02

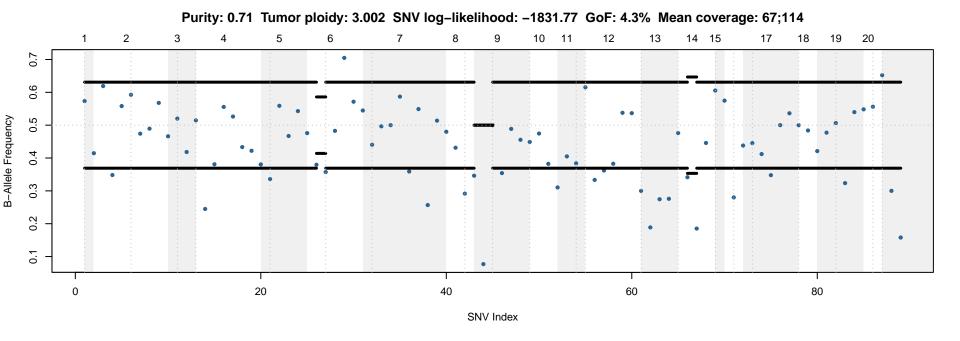




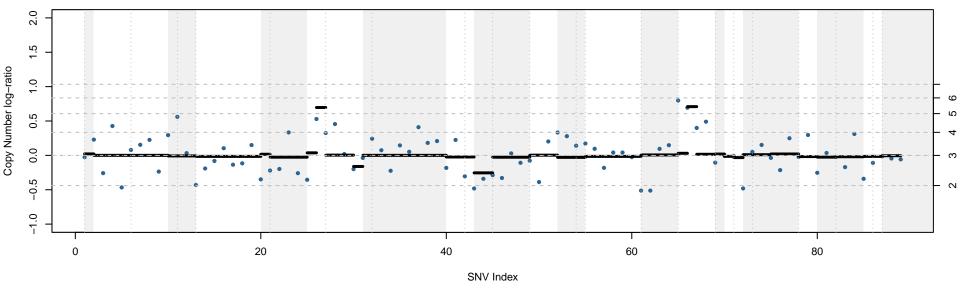


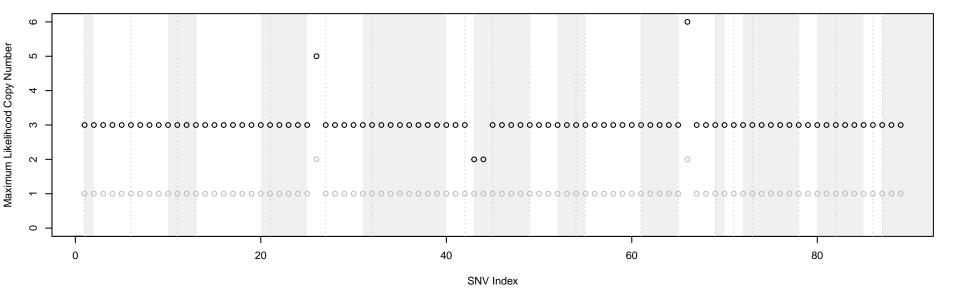
Purity: 0.71 Tumor ploidy: 3.002 2 5 6 7 0.3 Fraction Genome 0.1 0.0 -0.5 0.0 0.5 1.0

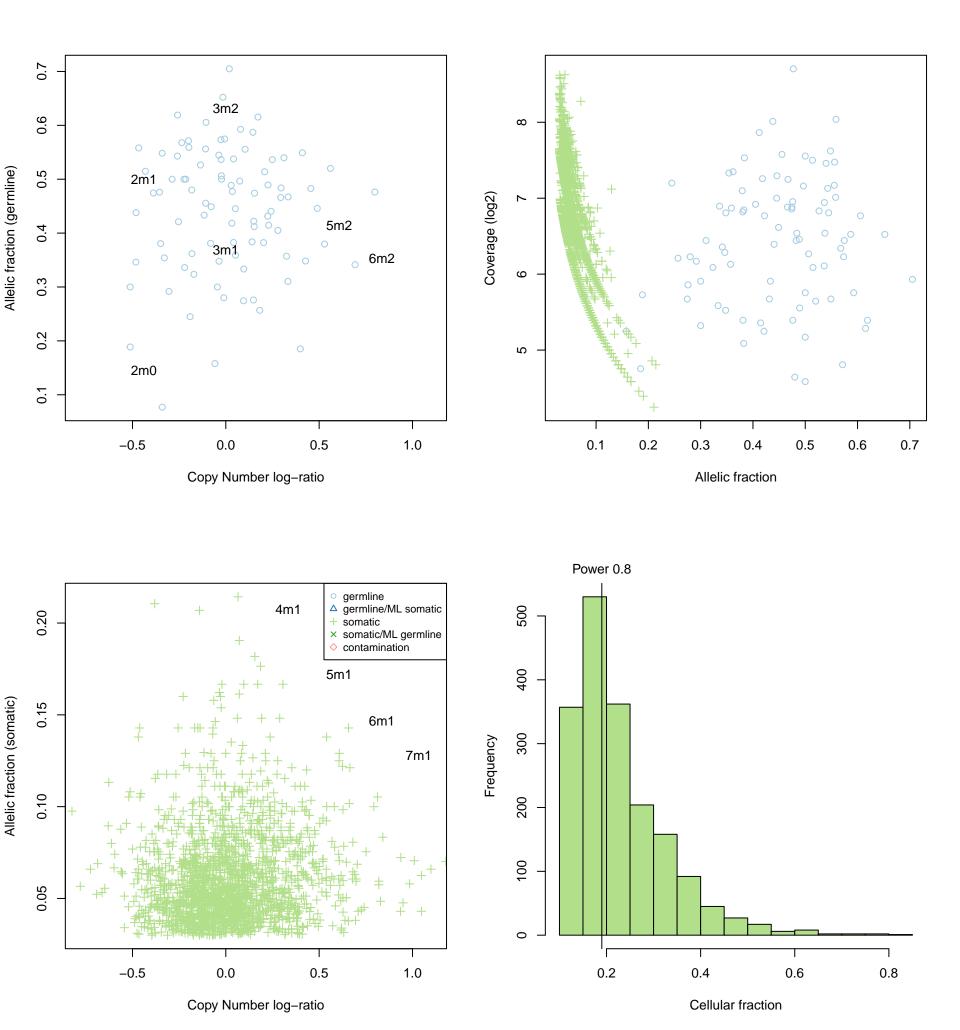
log2 ratio



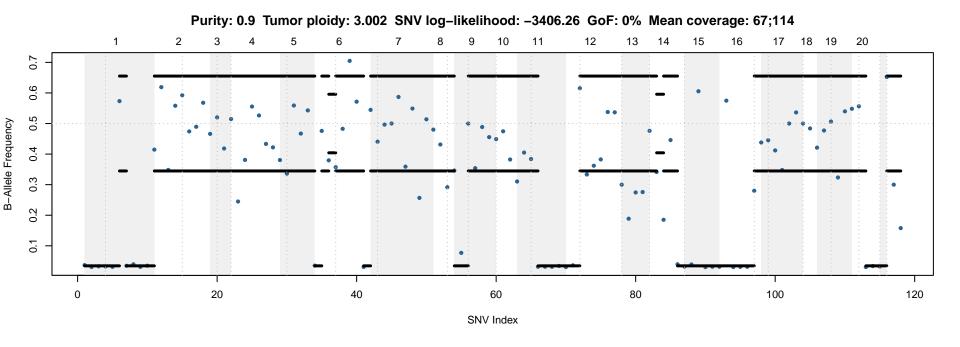
SCNA-fit log-likelihood: 1215.77







Purity: 0.9 Tumor ploidy: 3.002 3 5 6 0.3 Fraction Genome 0.1 0.0 -0.5 0.0 0.5 1.0 log2 ratio



SCNA-fit log-likelihood: 1190.5

