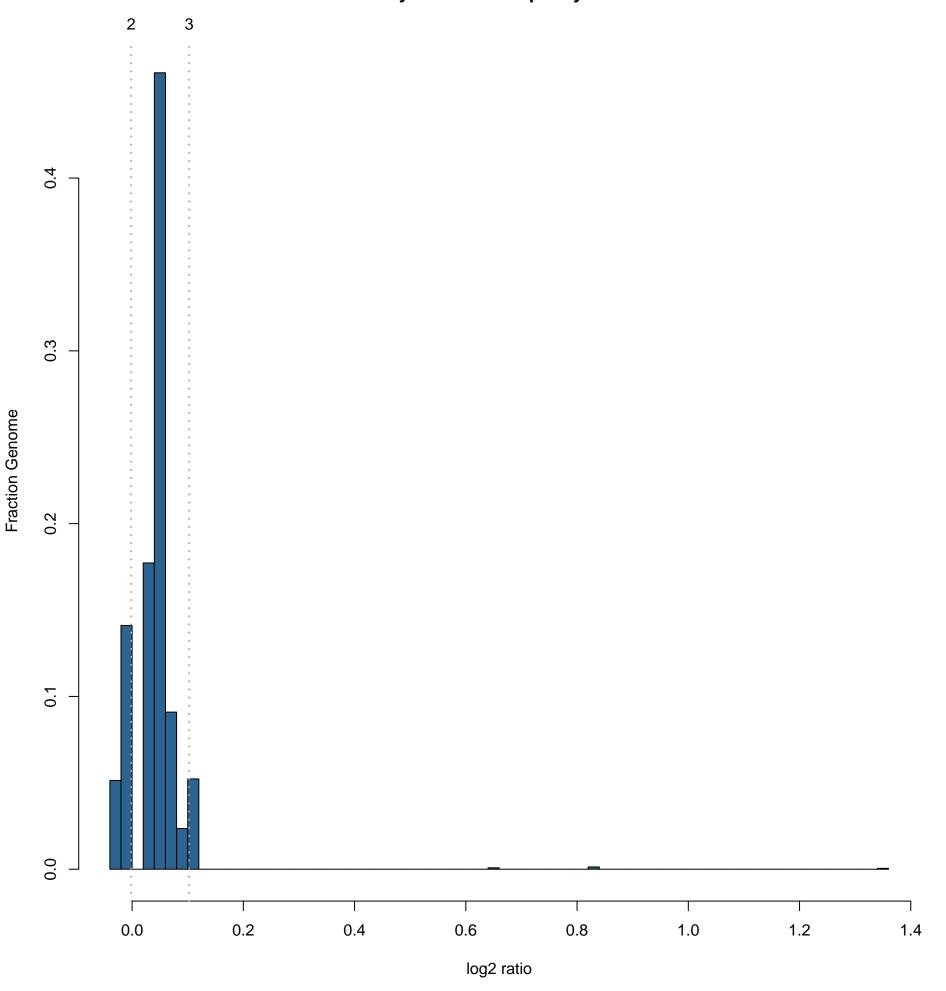
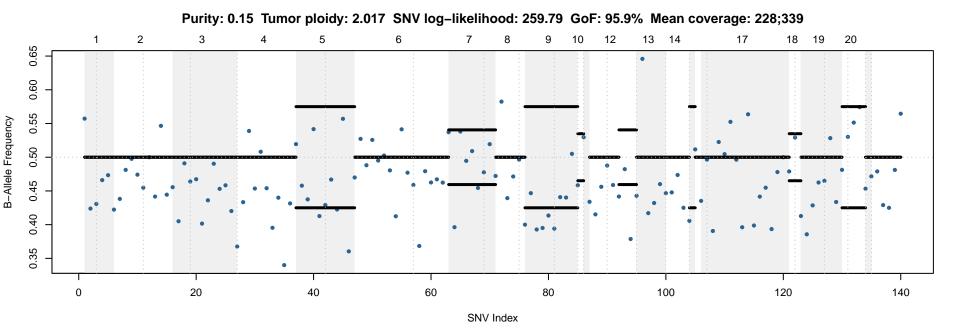
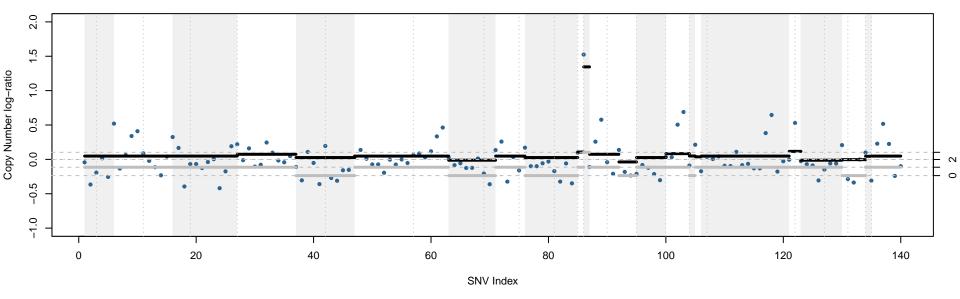
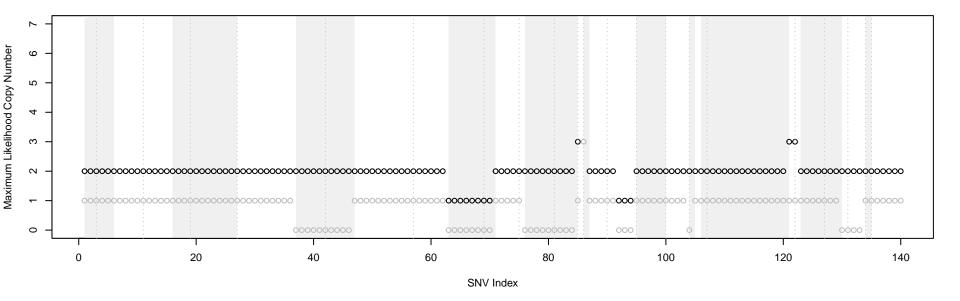
Purity: 0.15 Tumor ploidy: 2.017

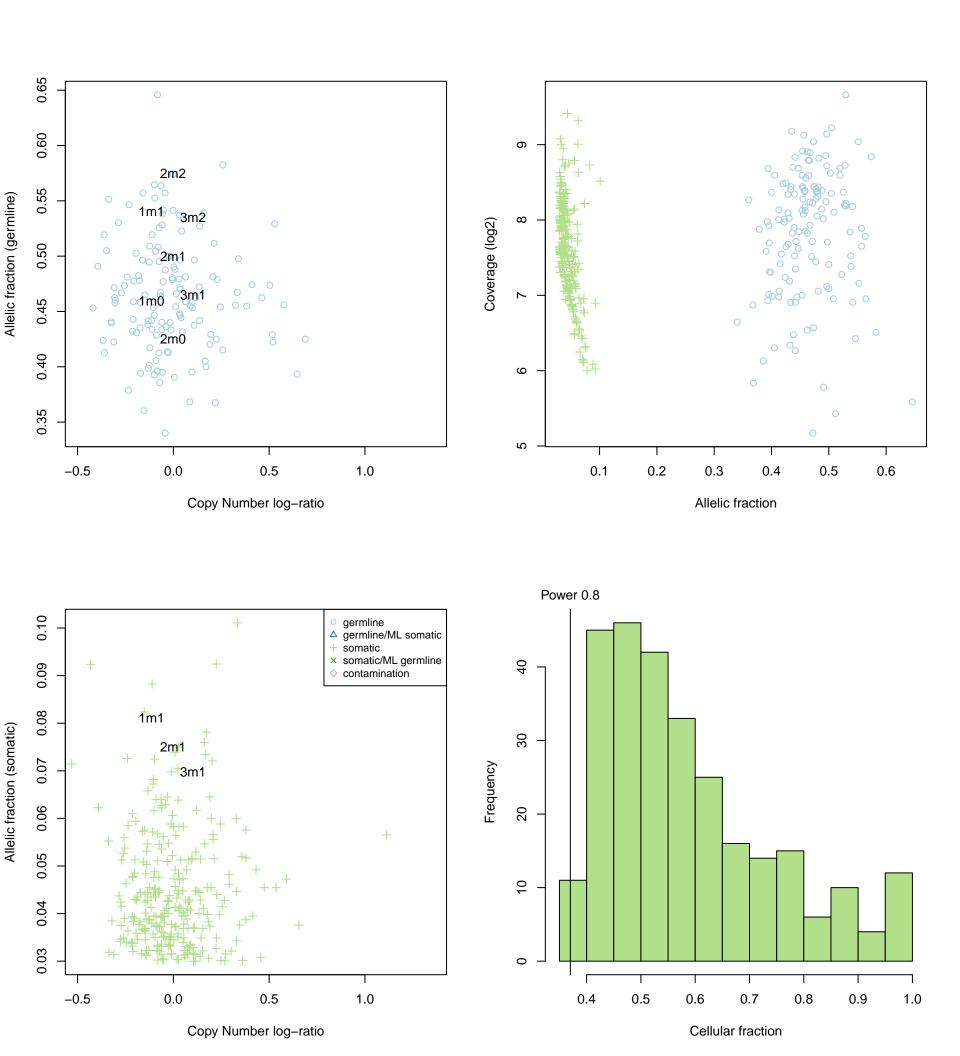




SCNA-fit log-likelihood: -4009.98

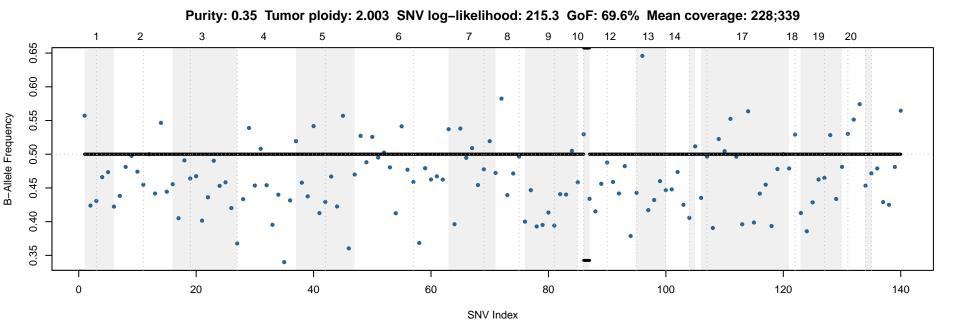




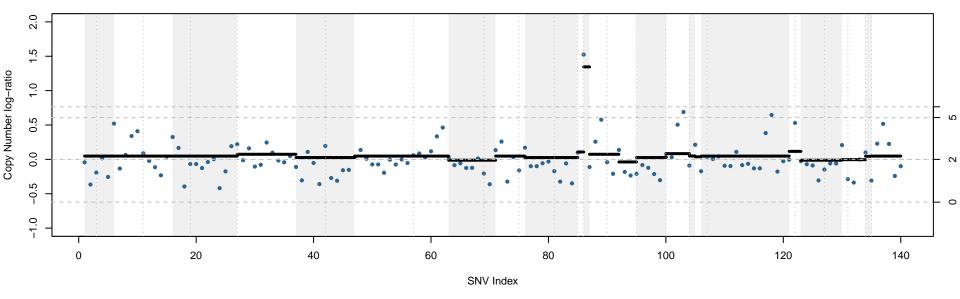


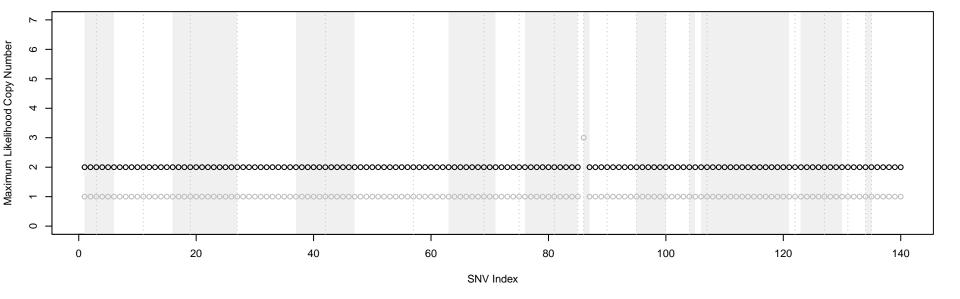
Purity: 0.35 Tumor ploidy: 2.003 0 2 6 Fraction Genome 0.2 0.1 0.0 -0.5 0.0 0.5 1.0

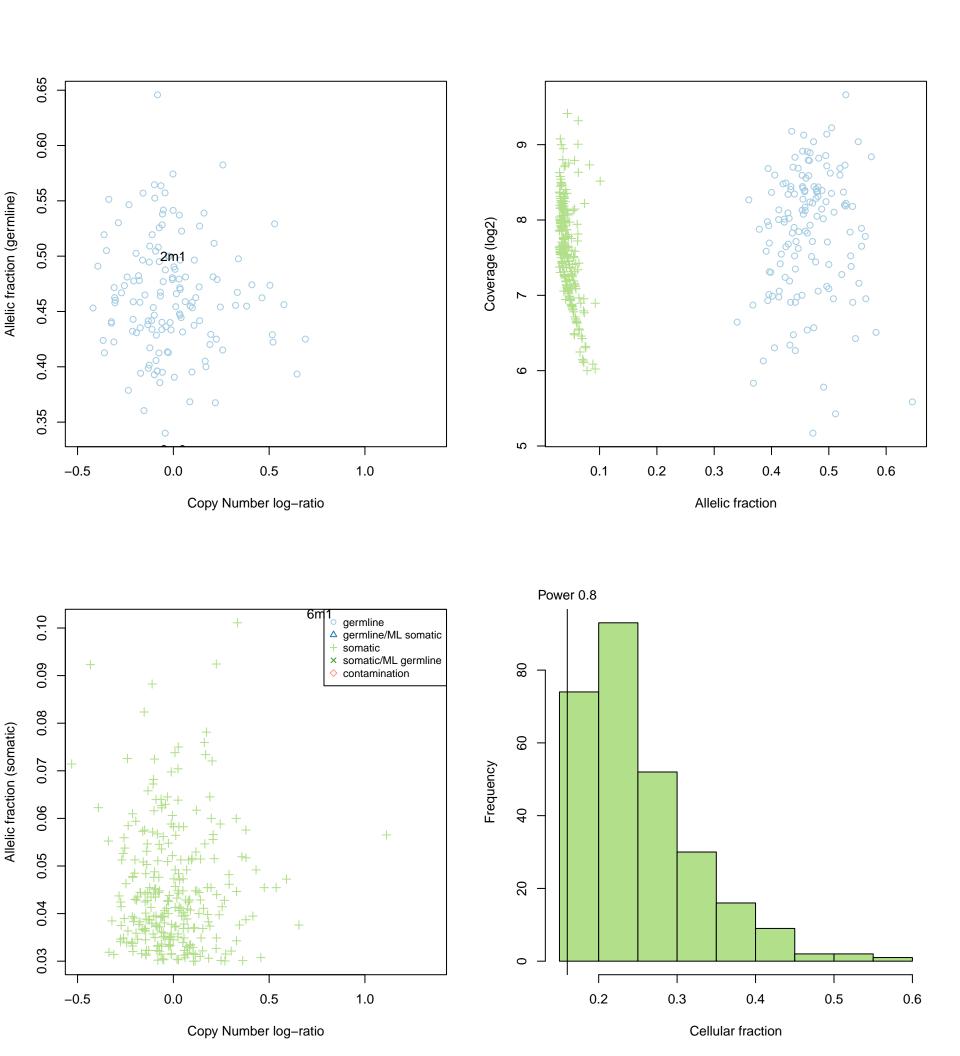
log2 ratio



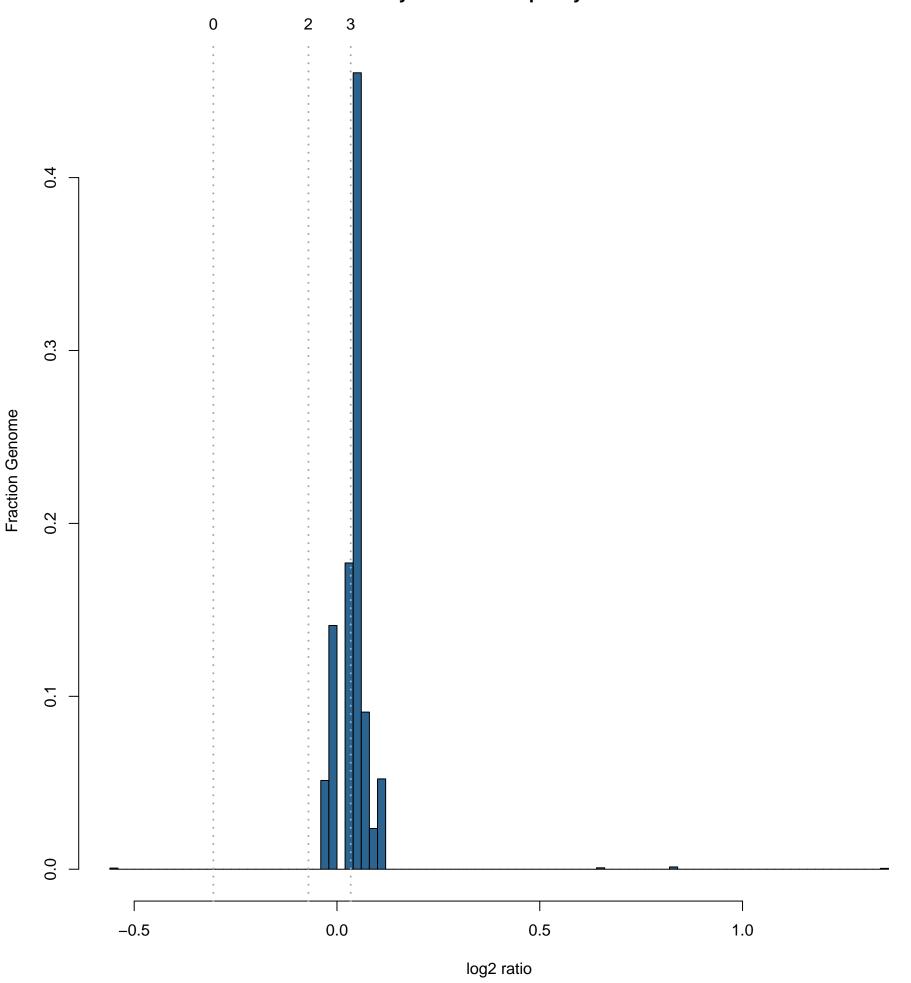
SCNA-fit log-likelihood: -3999.61

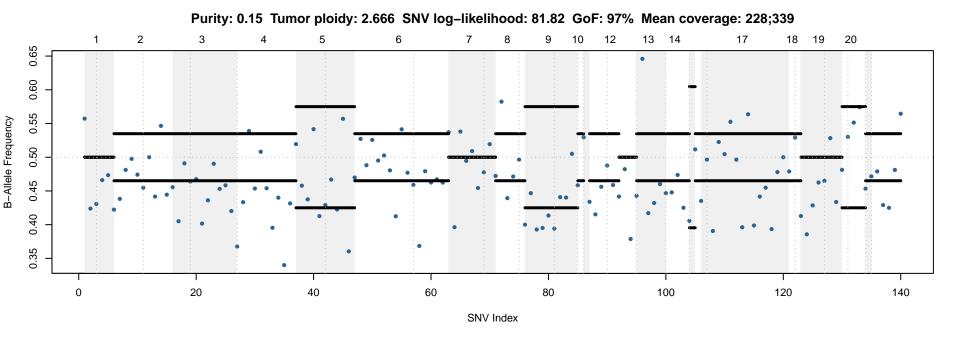




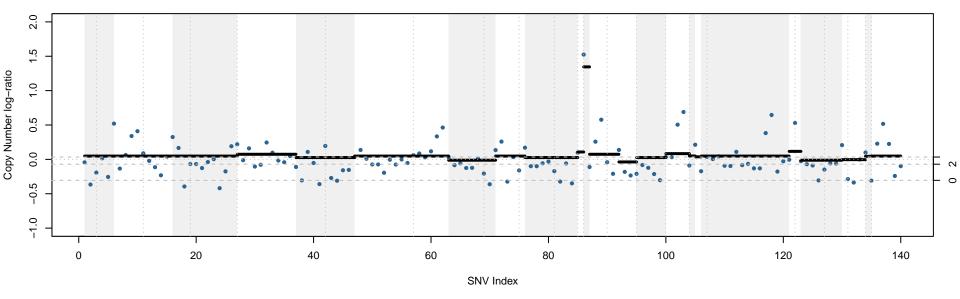


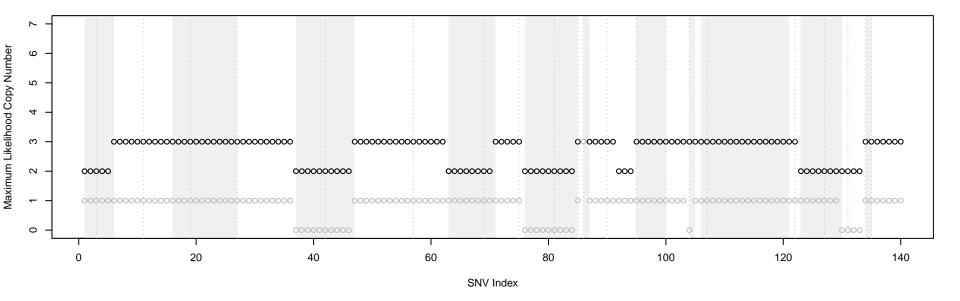
Purity: 0.15 Tumor ploidy: 2.666

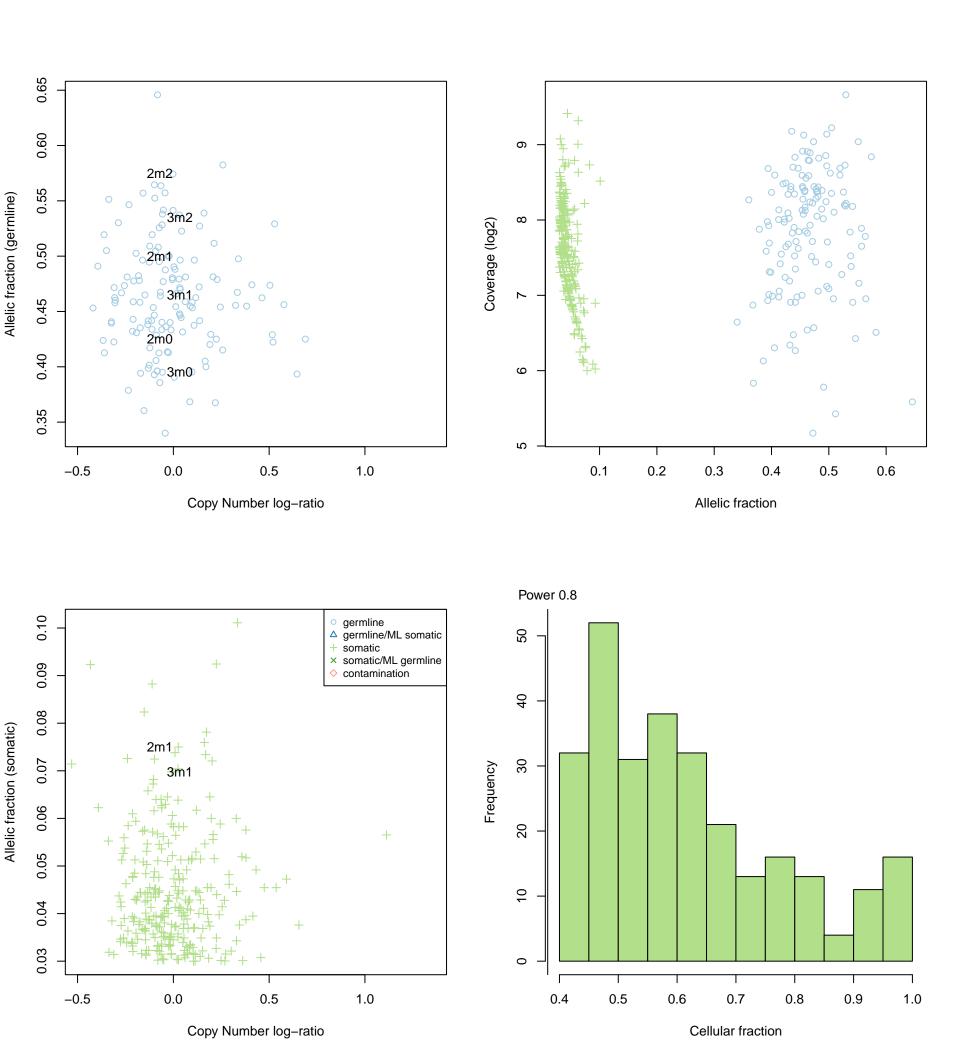




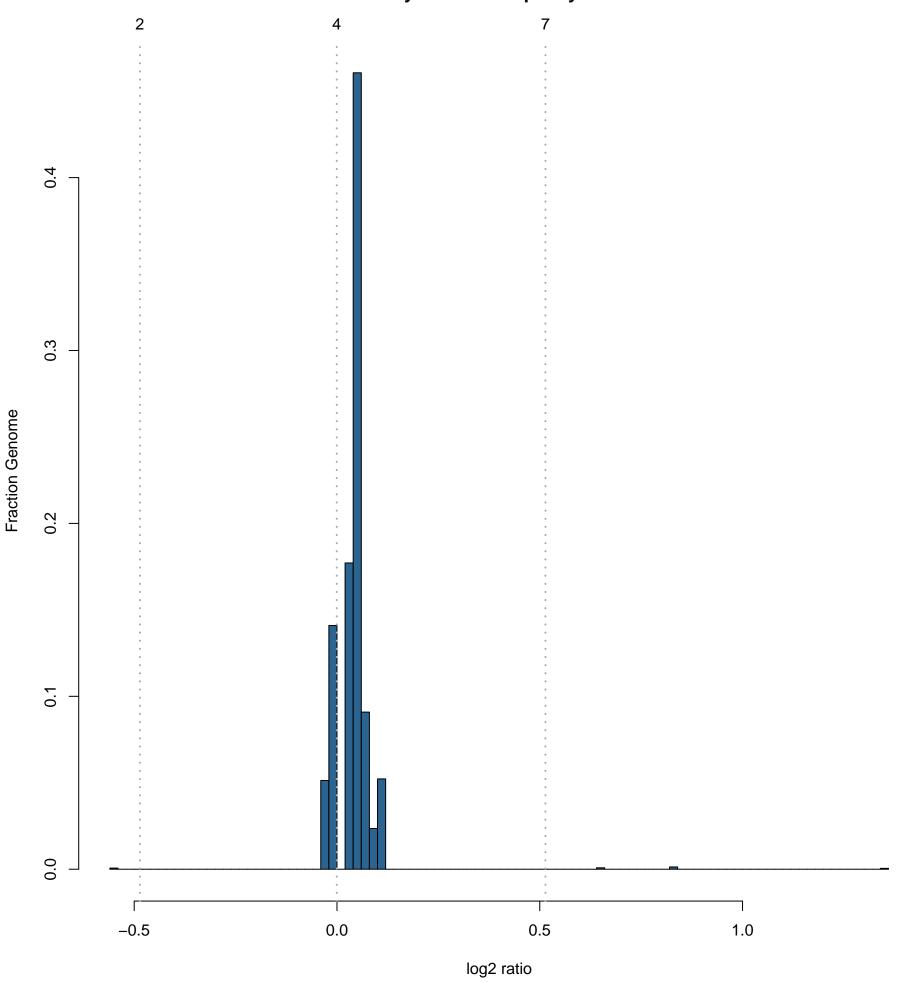
SCNA-fit log-likelihood: -4020.55

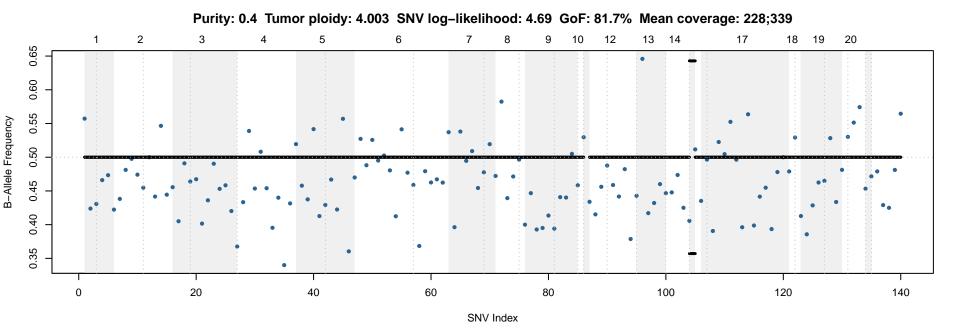




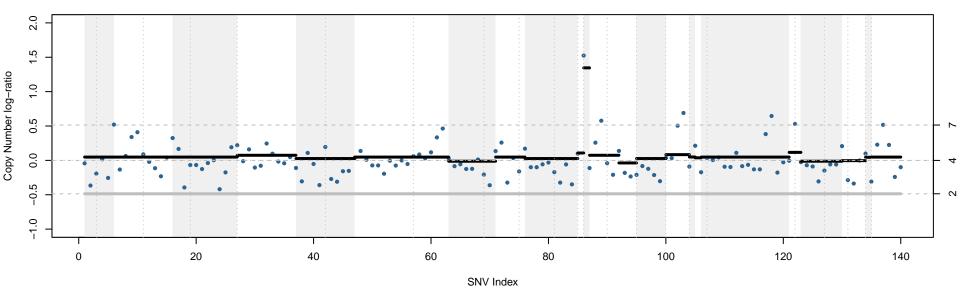


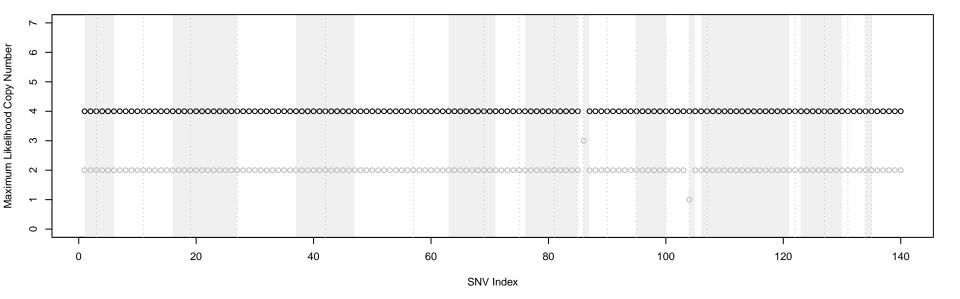
Purity: 0.4 Tumor ploidy: 4.003

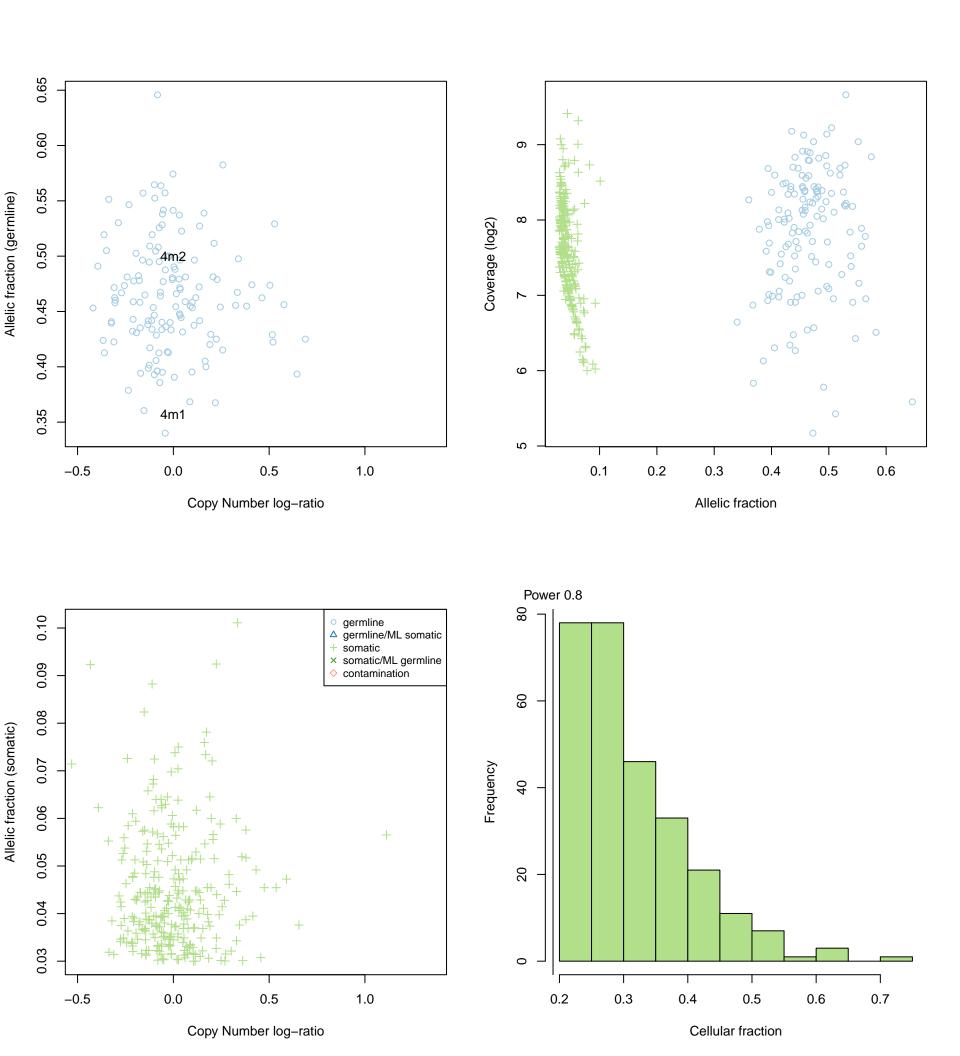




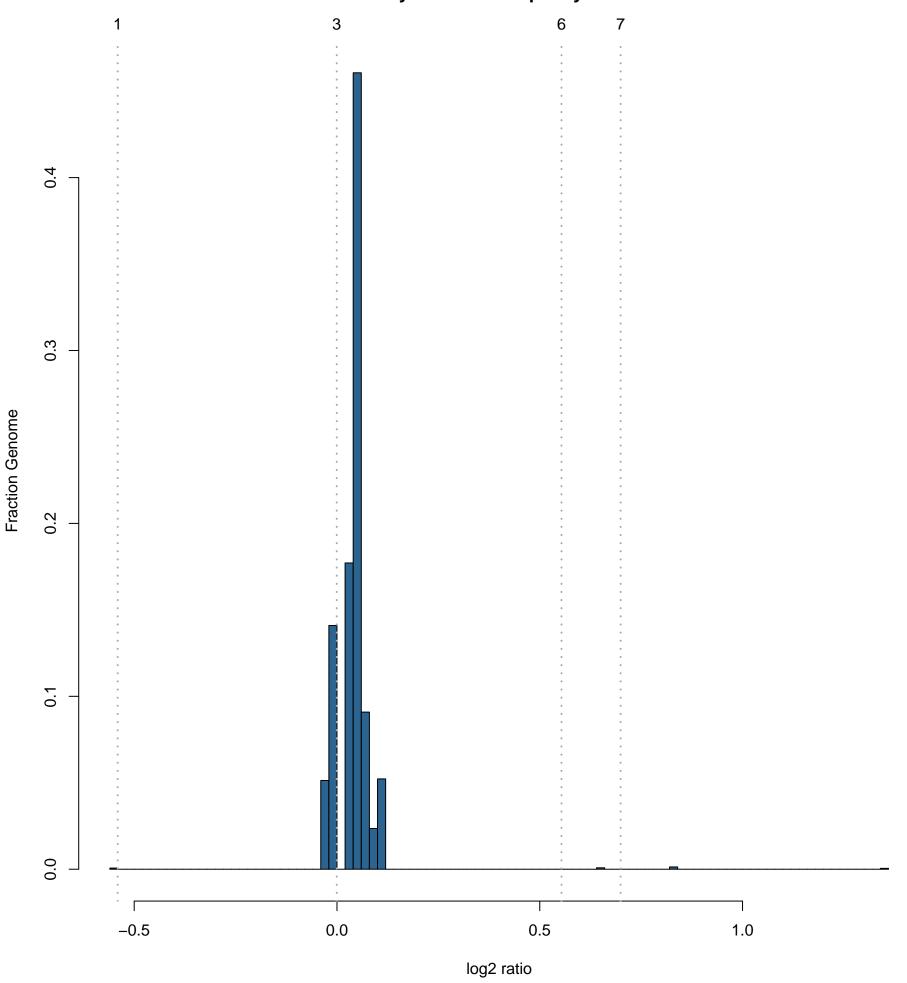
SCNA-fit log-likelihood: -4022.22

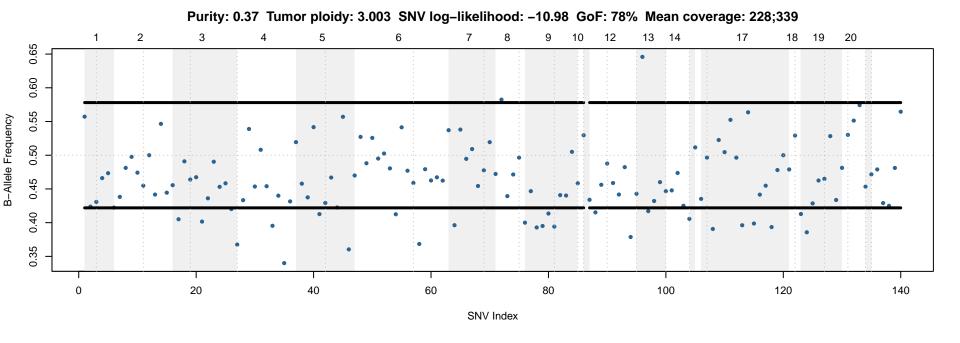




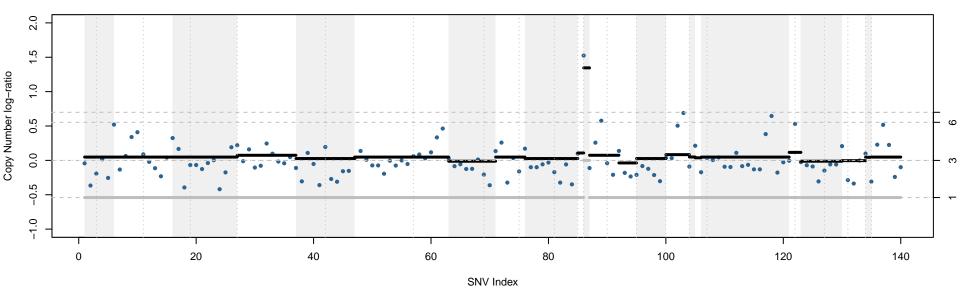


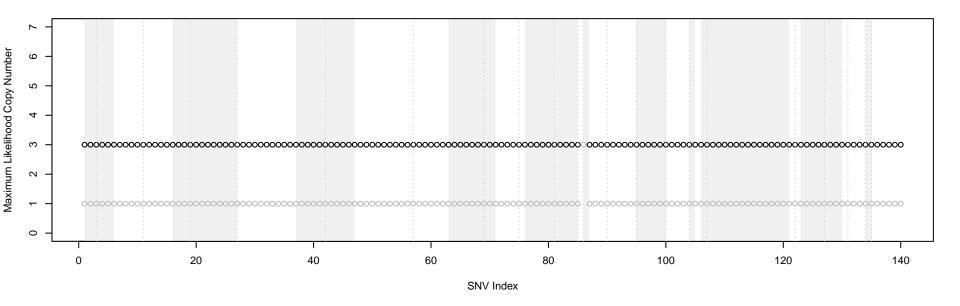
Purity: 0.37 Tumor ploidy: 3.003

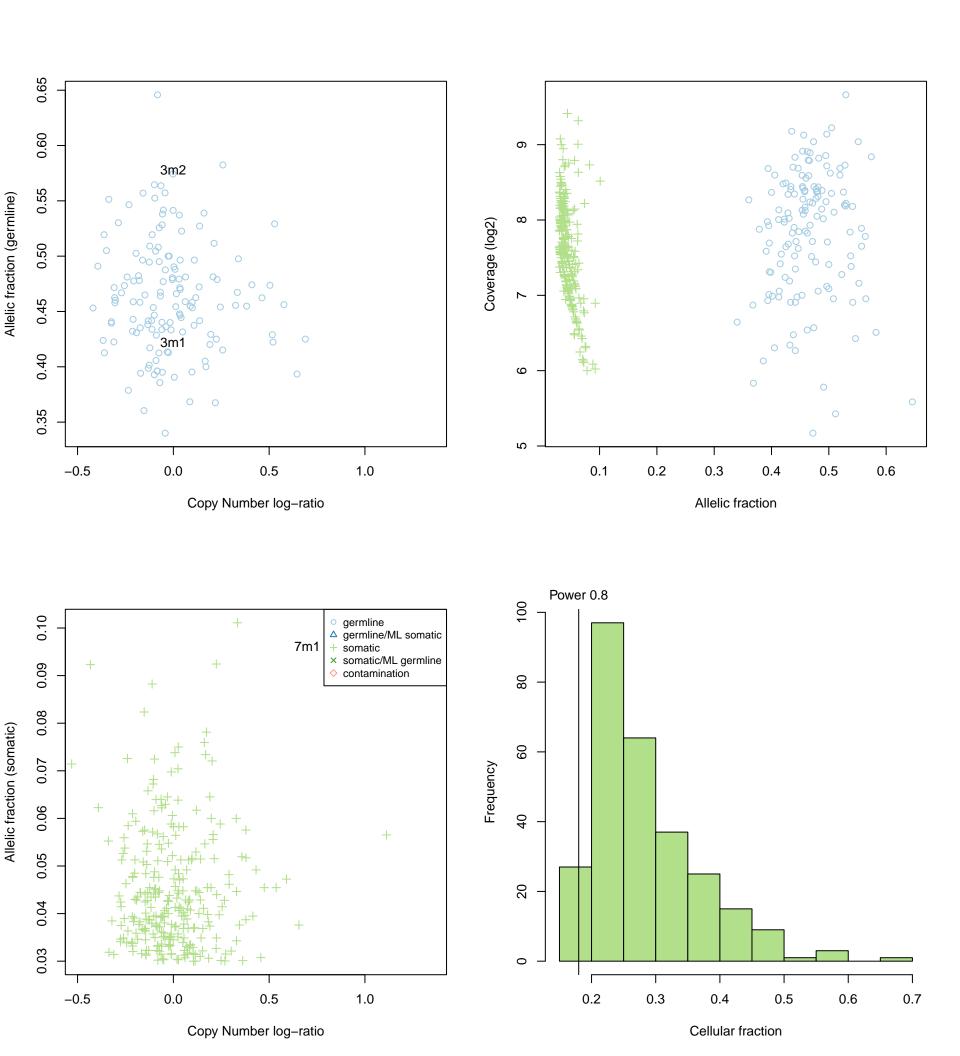




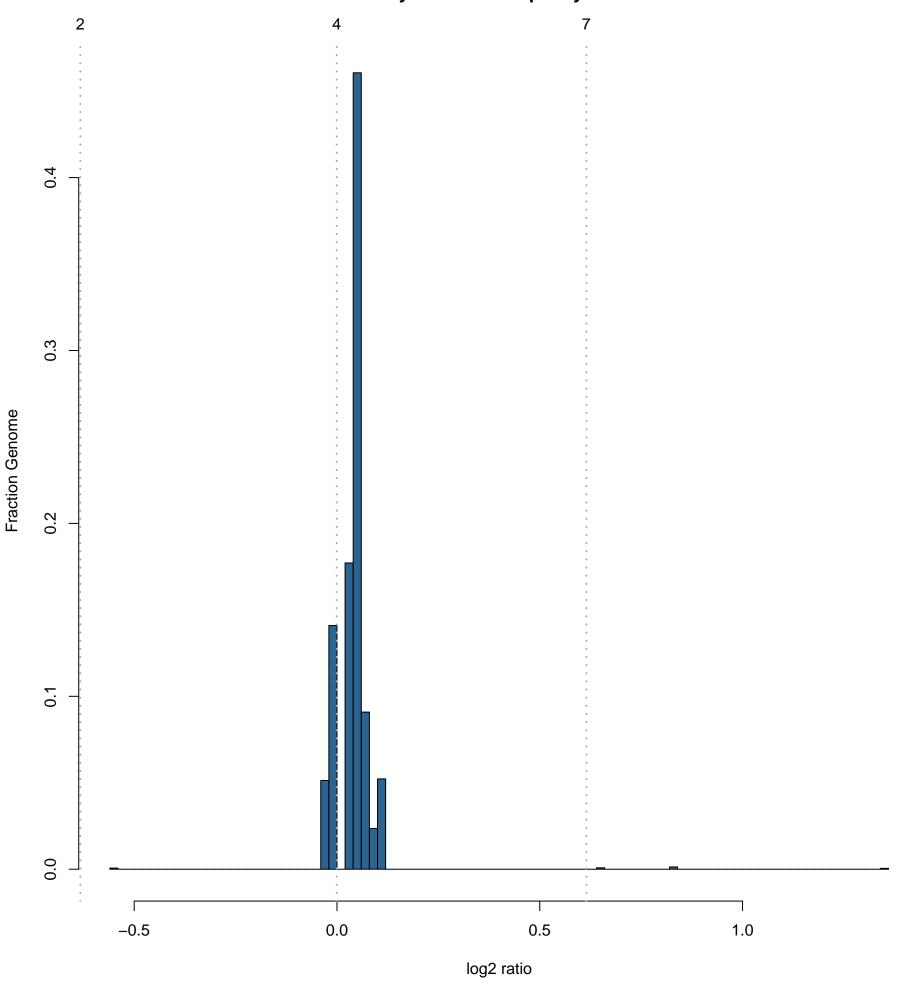
SCNA-fit log-likelihood: -3999.59

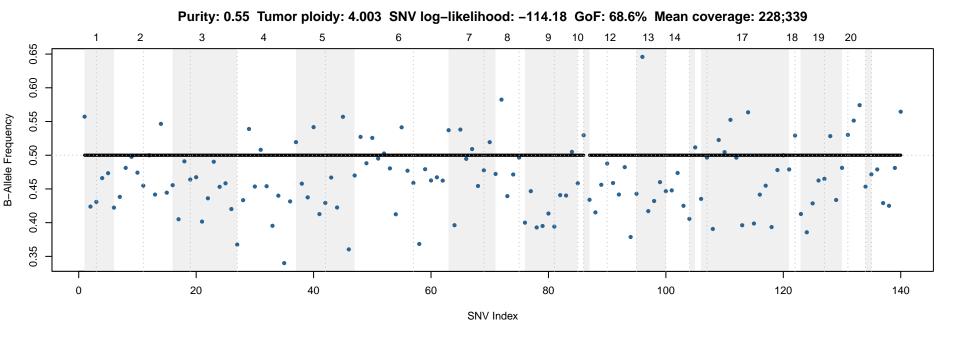




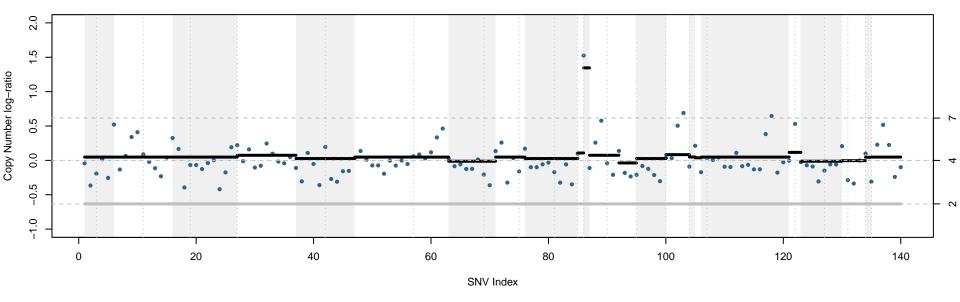


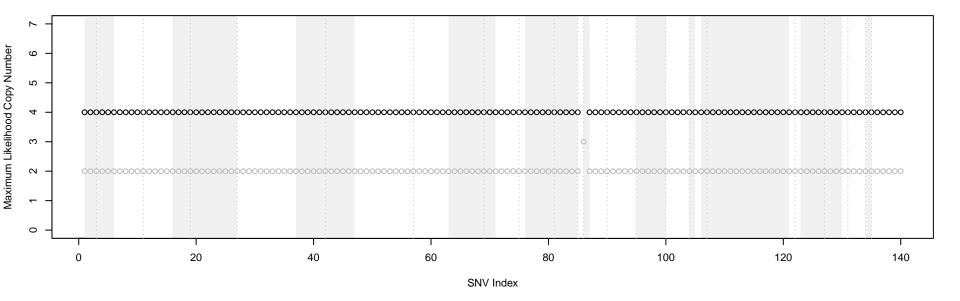
Purity: 0.55 Tumor ploidy: 4.003

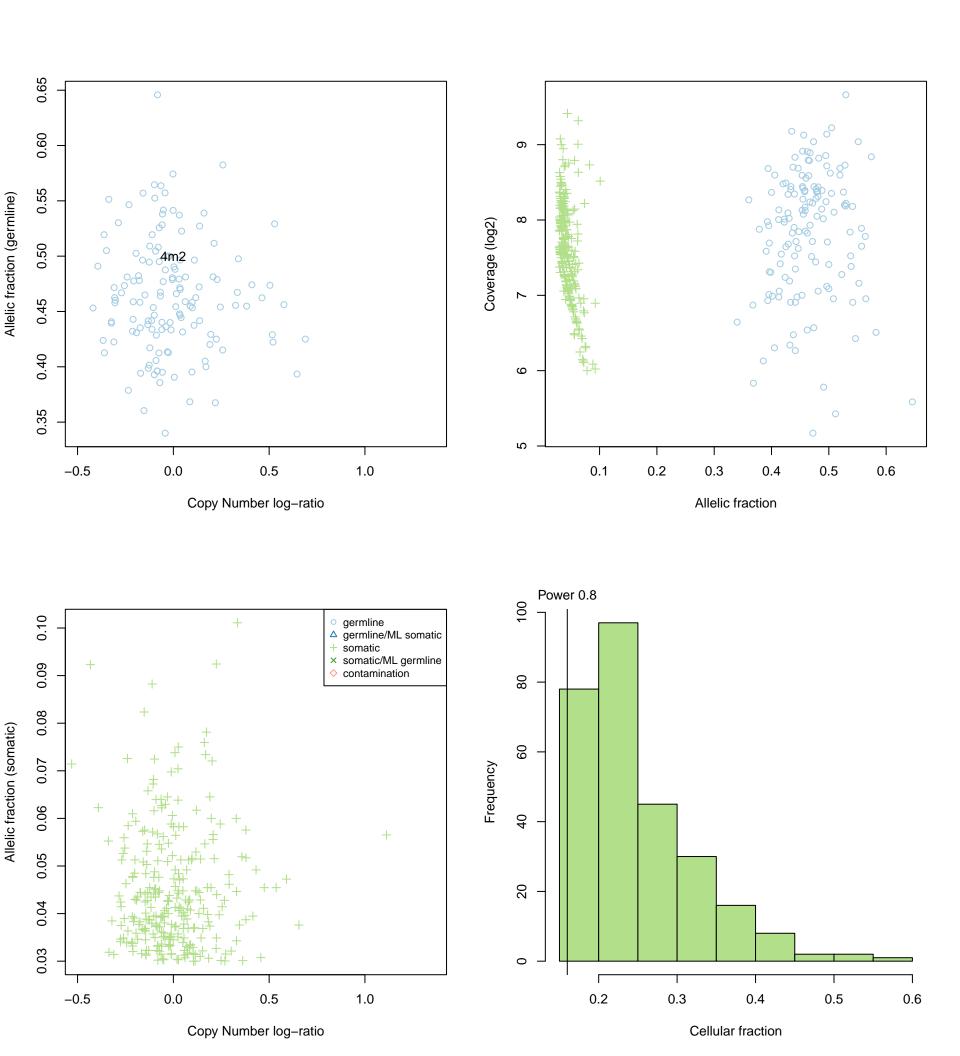




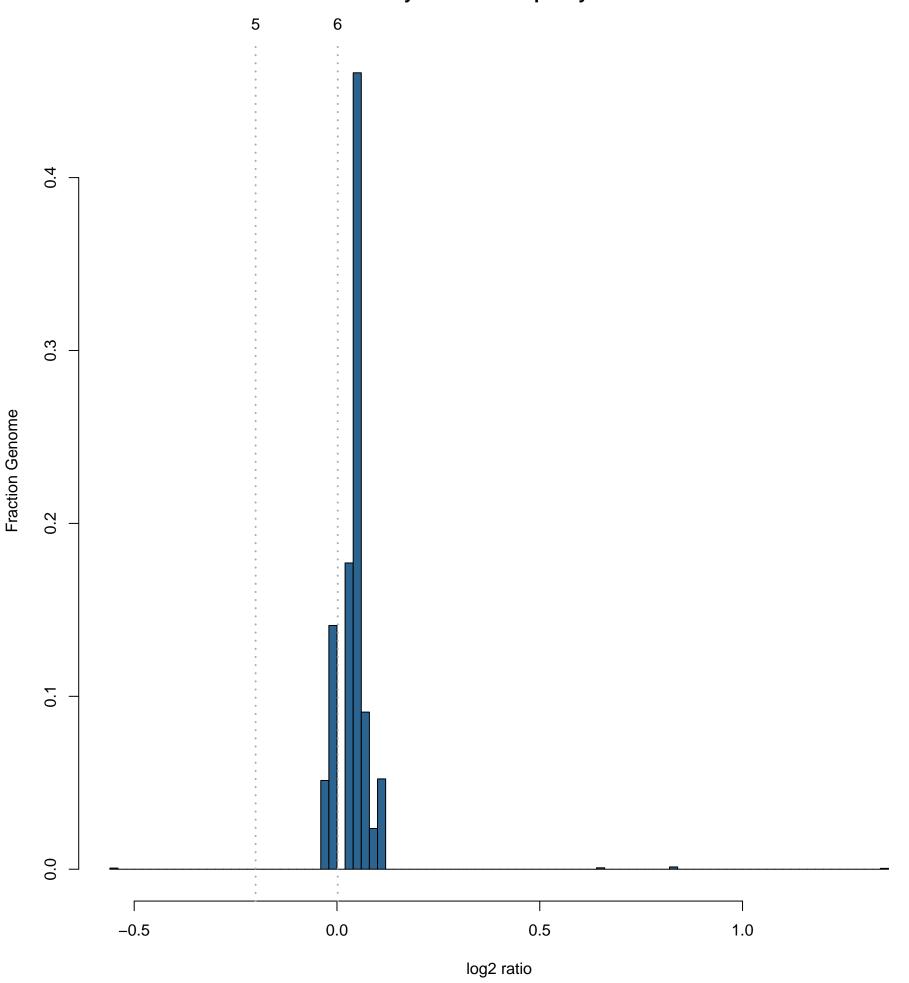
SCNA-fit log-likelihood: -4001.19

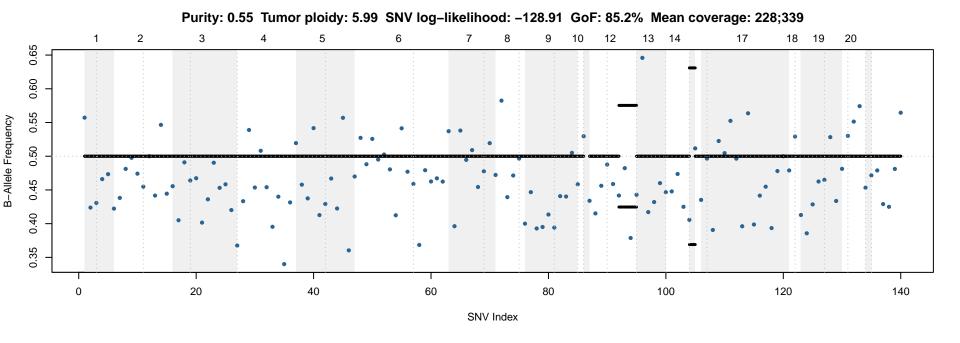




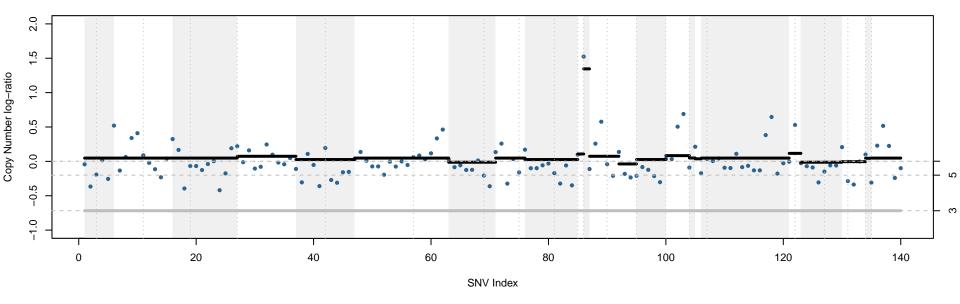


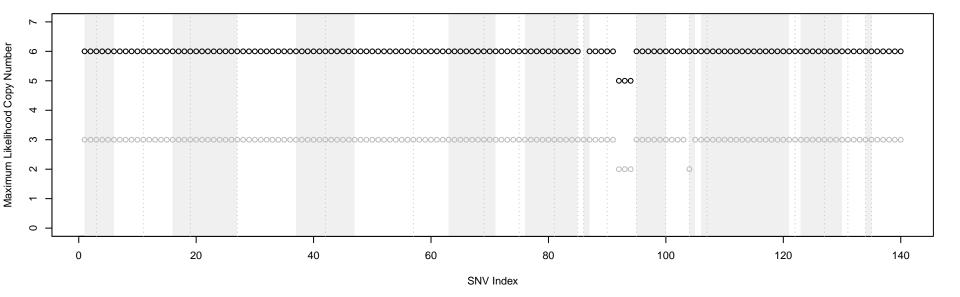
Purity: 0.55 Tumor ploidy: 5.99

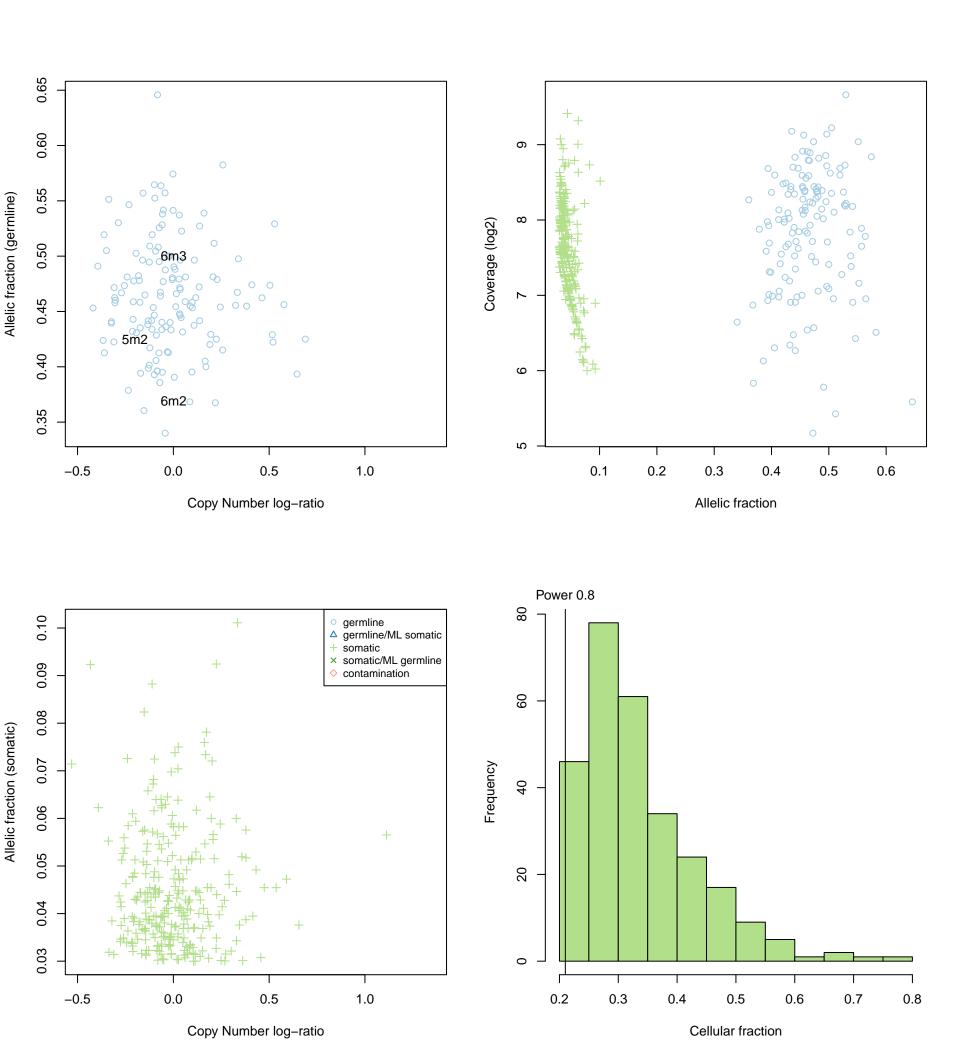




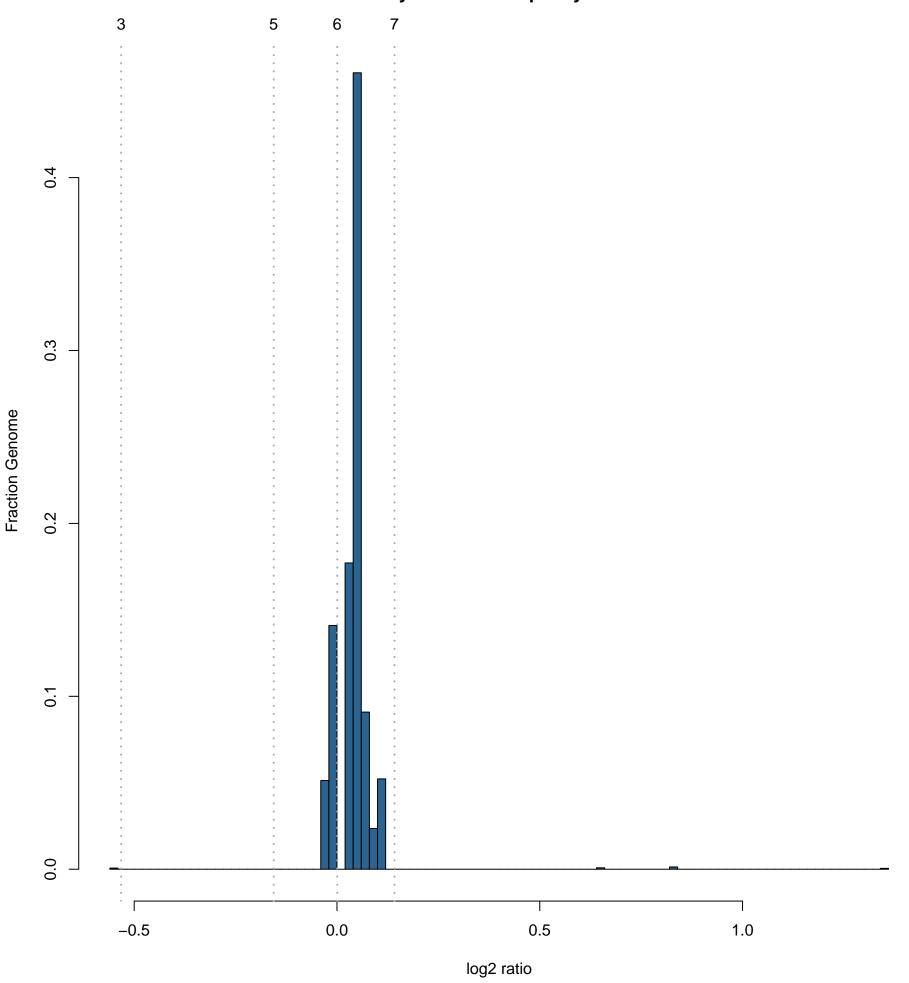
SCNA-fit log-likelihood: -4040.44

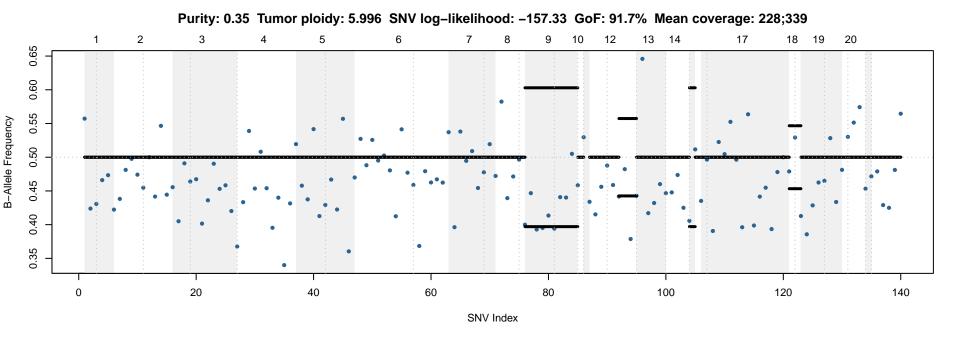




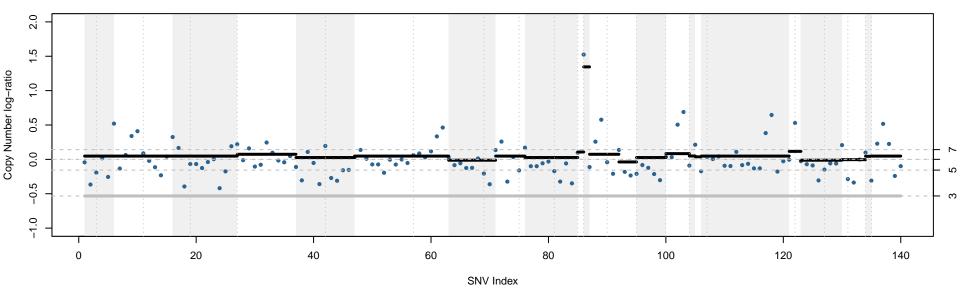


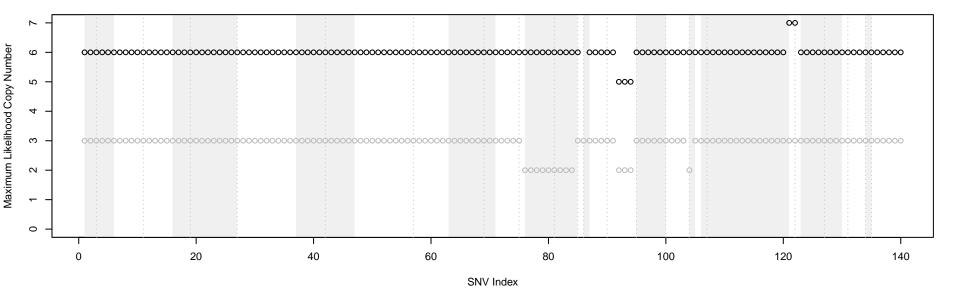
Purity: 0.35 Tumor ploidy: 5.996

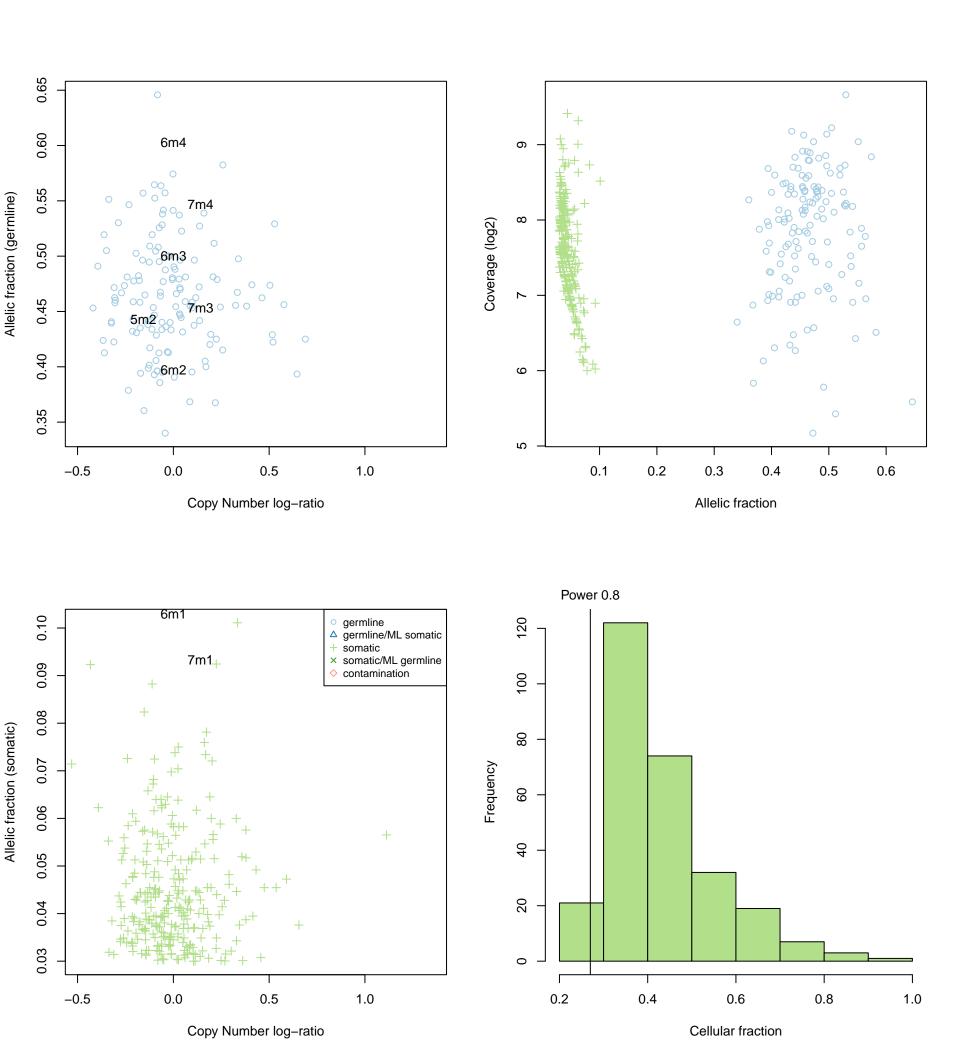




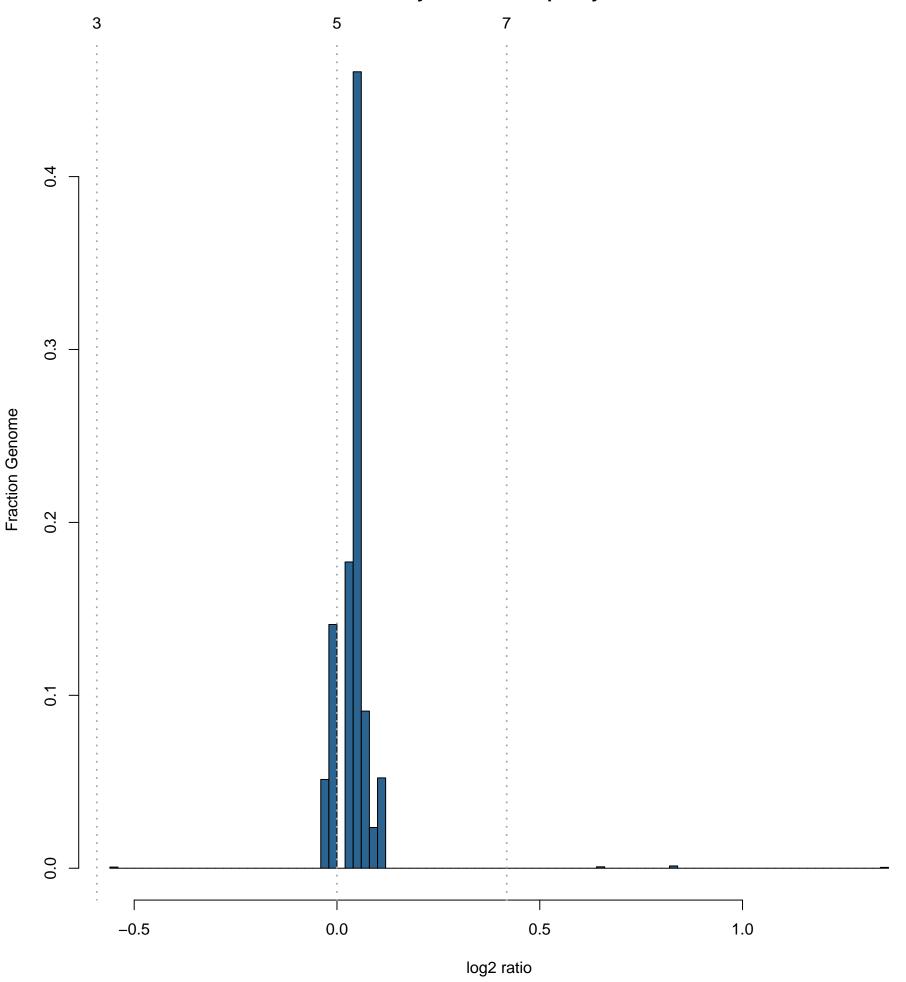
SCNA-fit log-likelihood: -4041.11

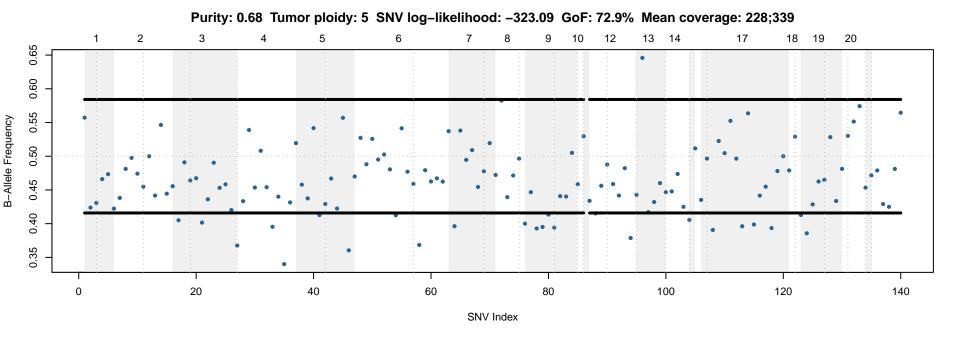




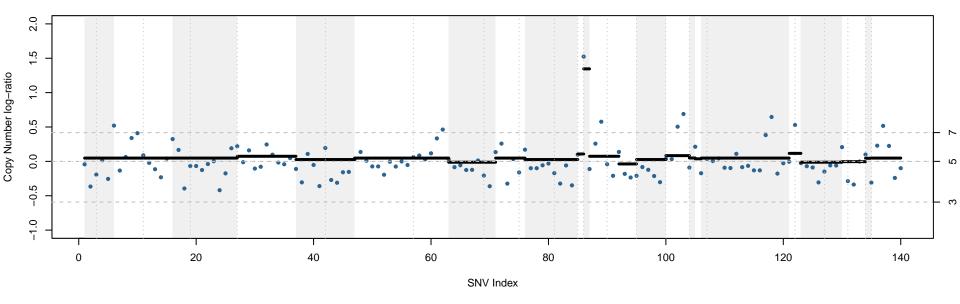


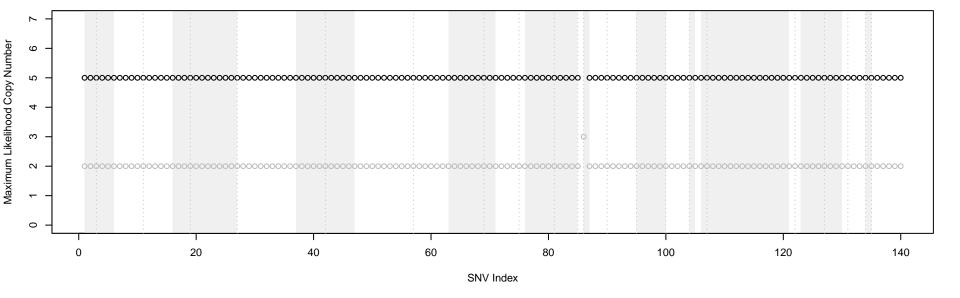
Purity: 0.68 Tumor ploidy: 5

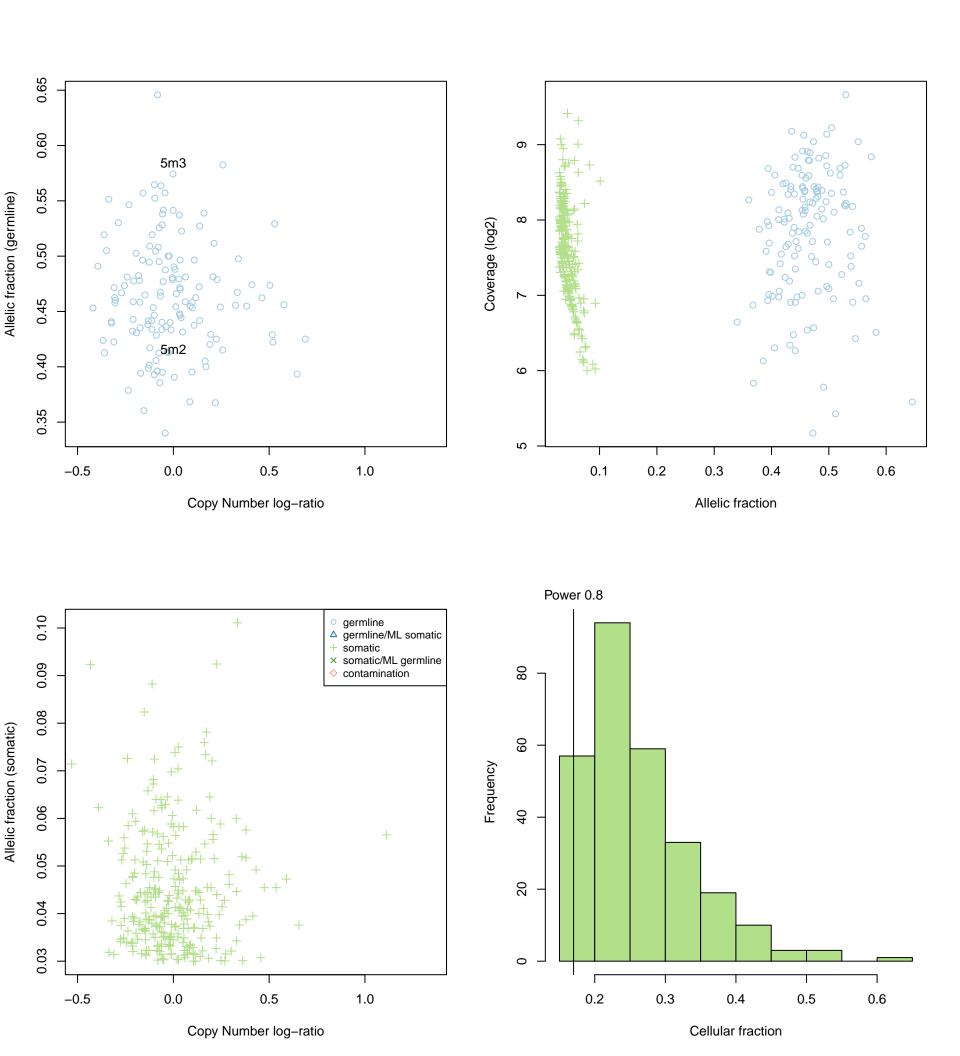




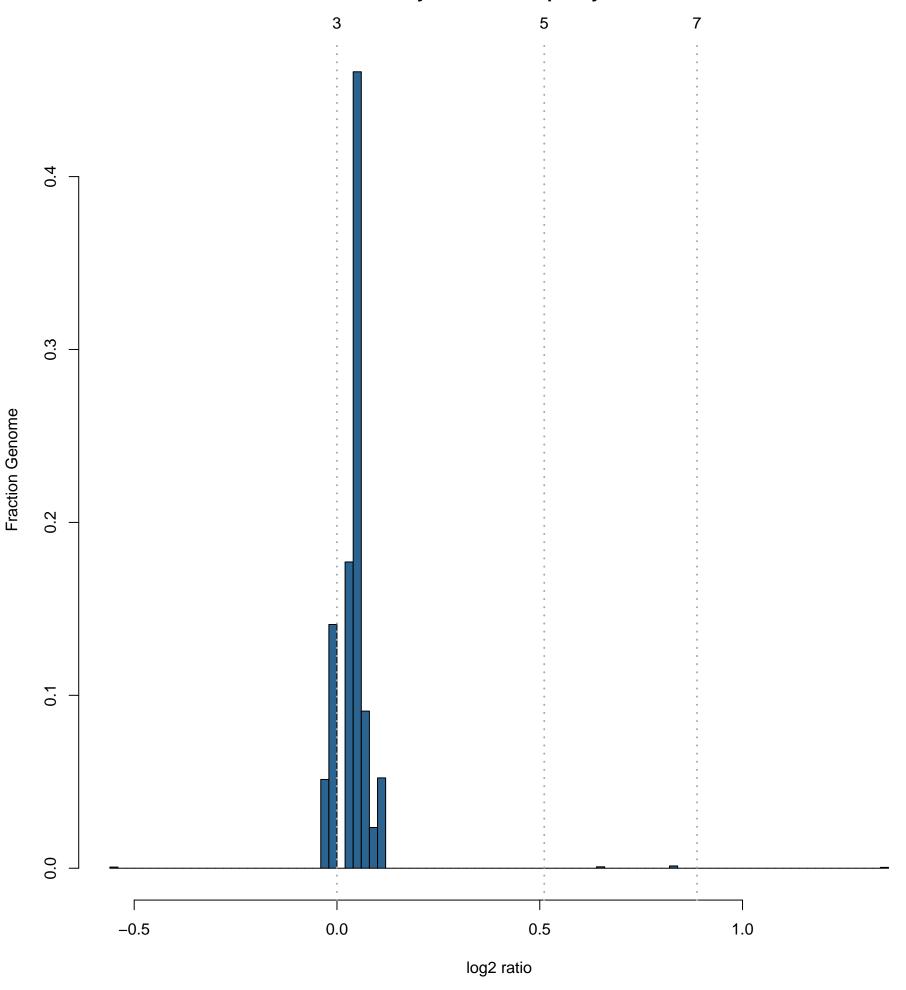
SCNA-fit log-likelihood: -4022.9

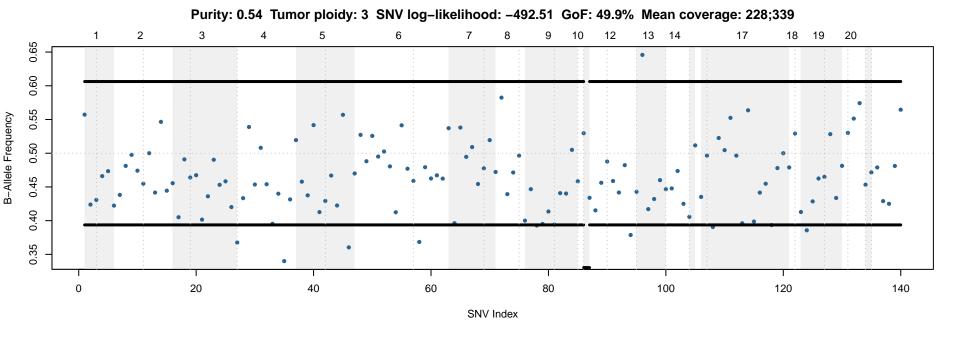




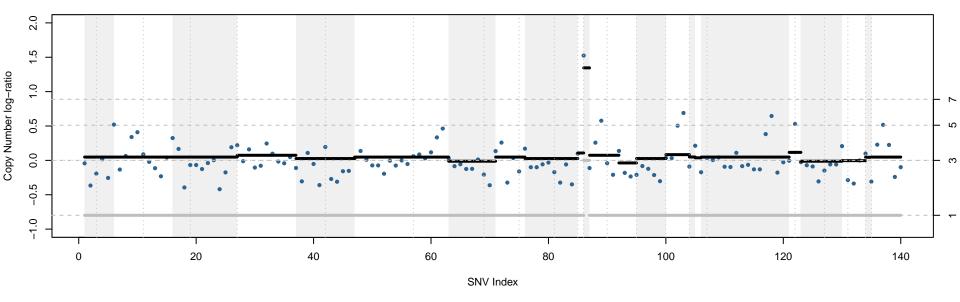


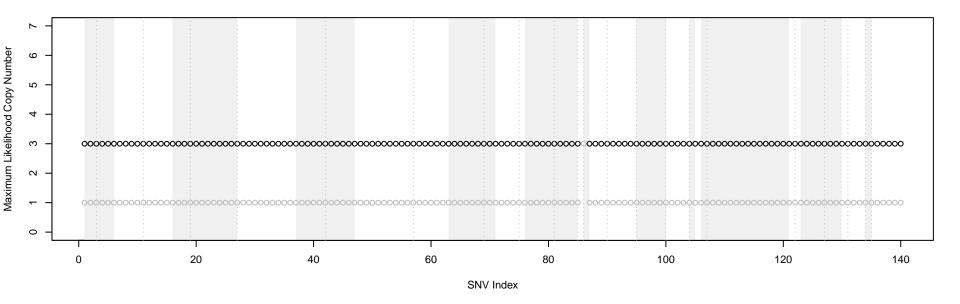
Purity: 0.54 Tumor ploidy: 3

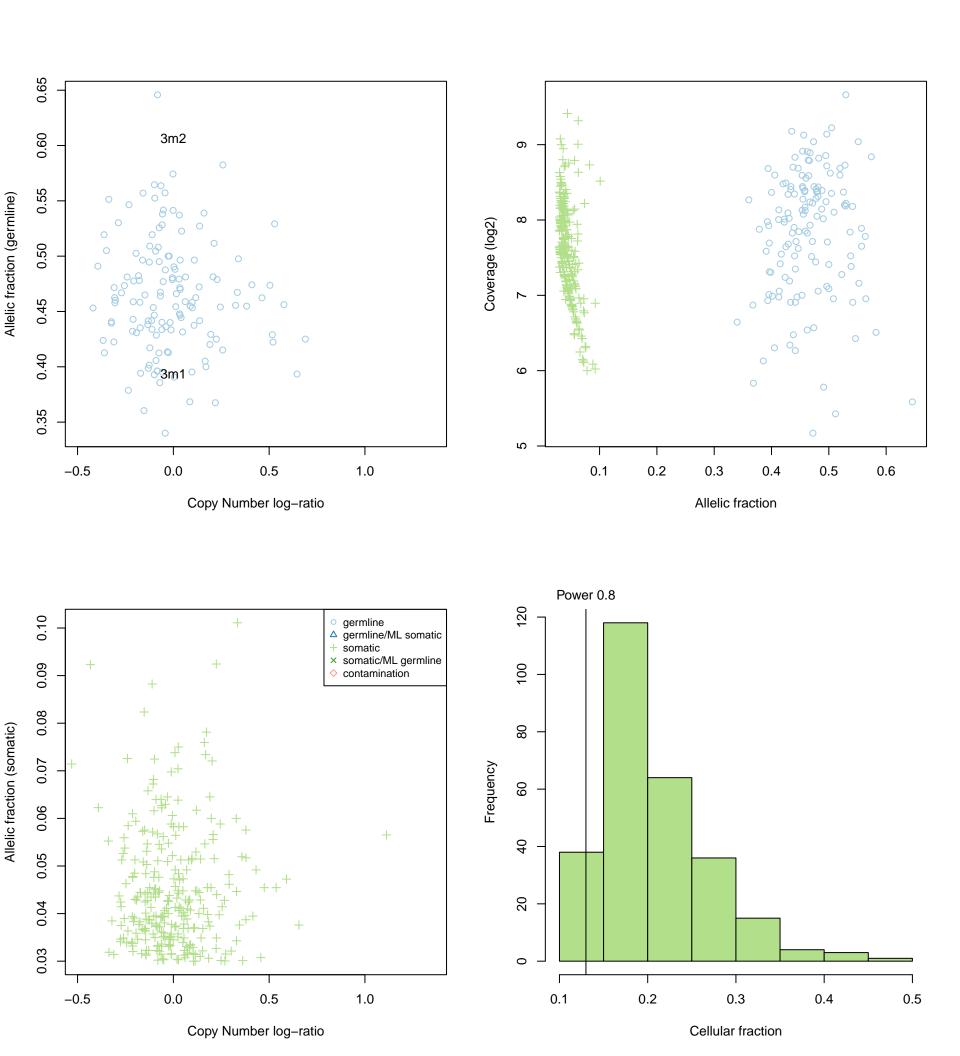




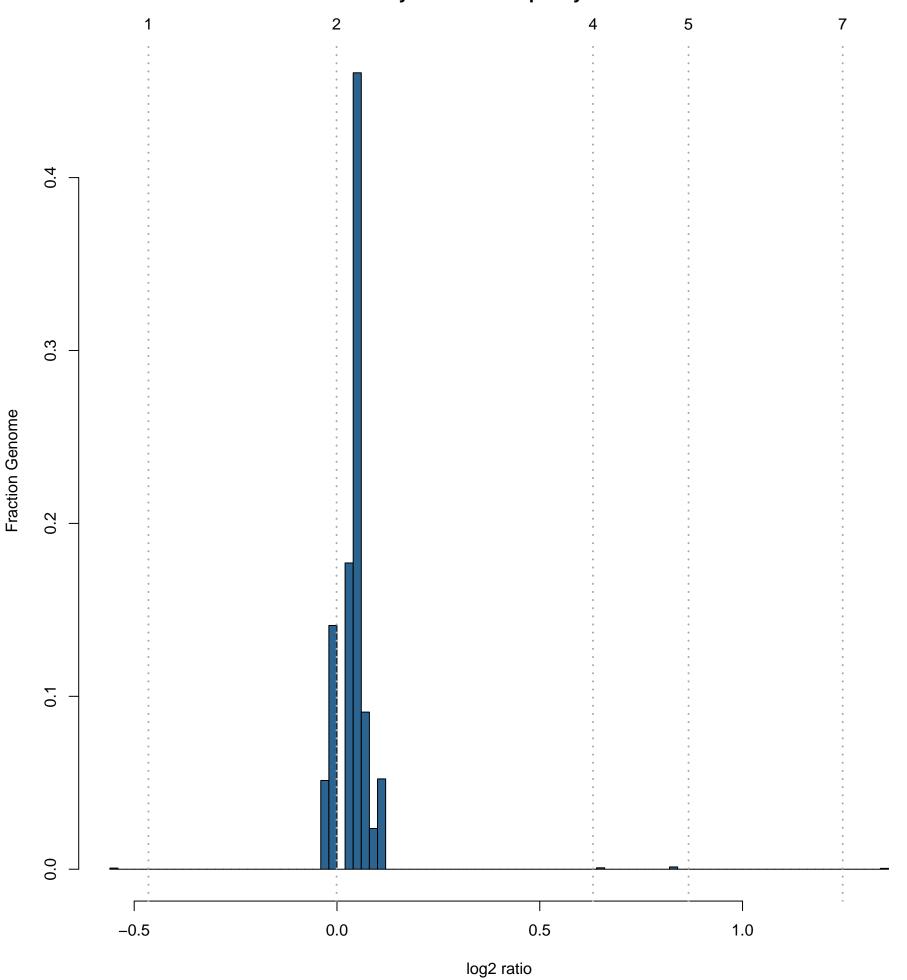
SCNA-fit log-likelihood: -4001.12

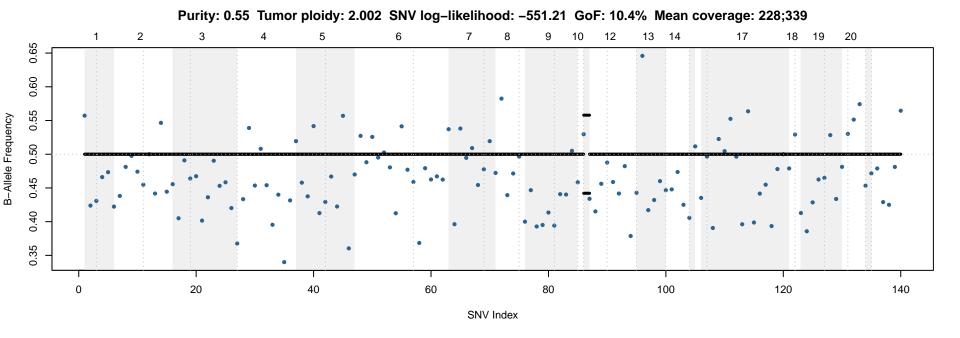




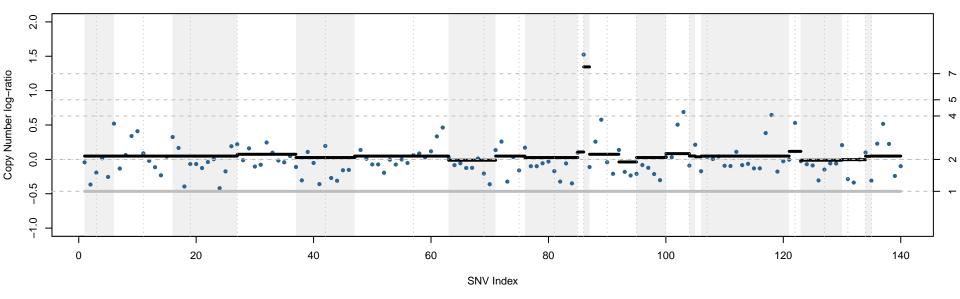


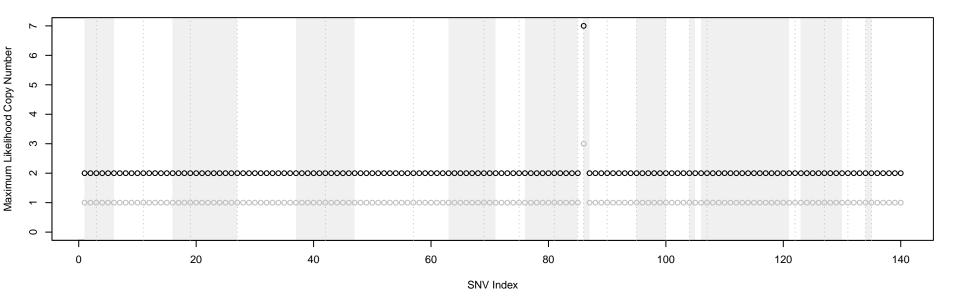
Purity: 0.55 Tumor ploidy: 2.002

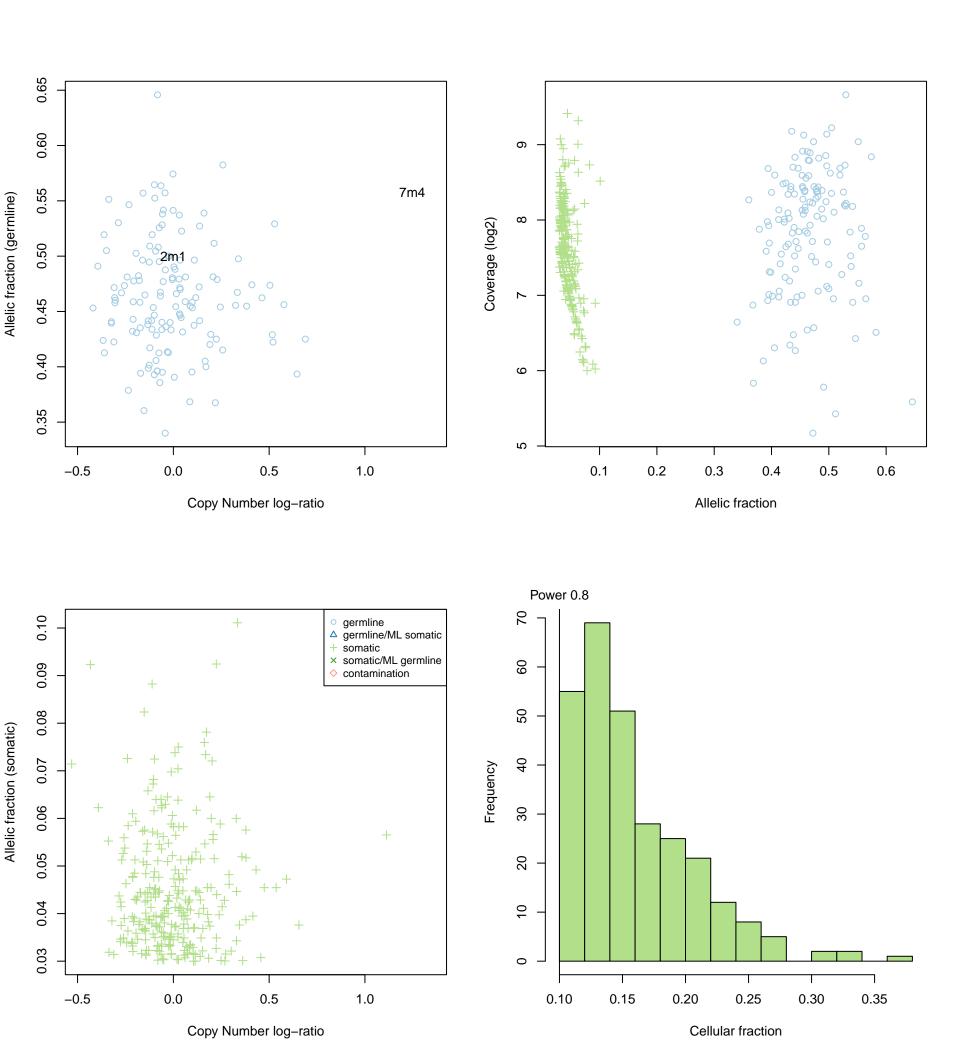




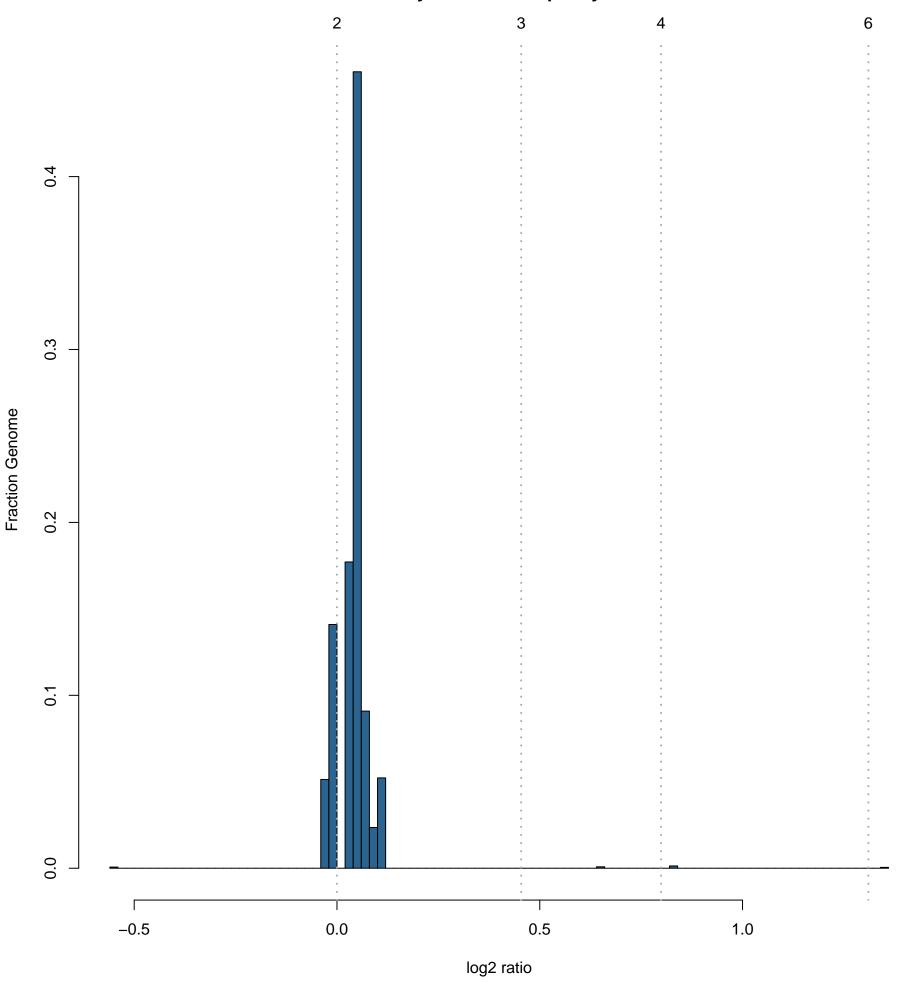
SCNA-fit log-likelihood: -3991.01

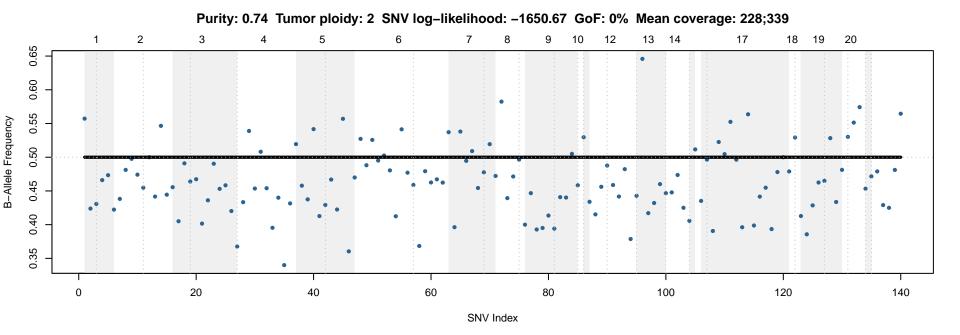




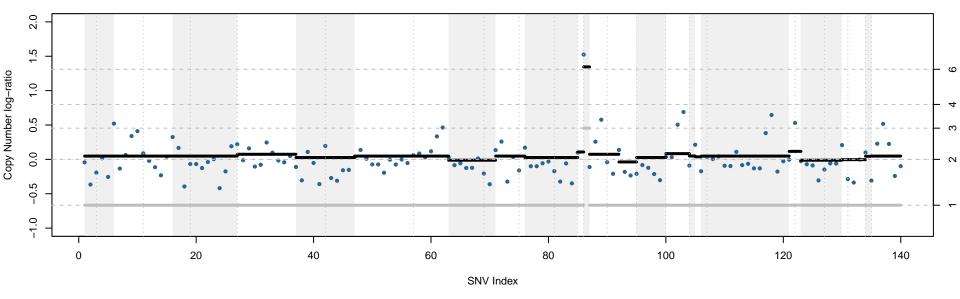


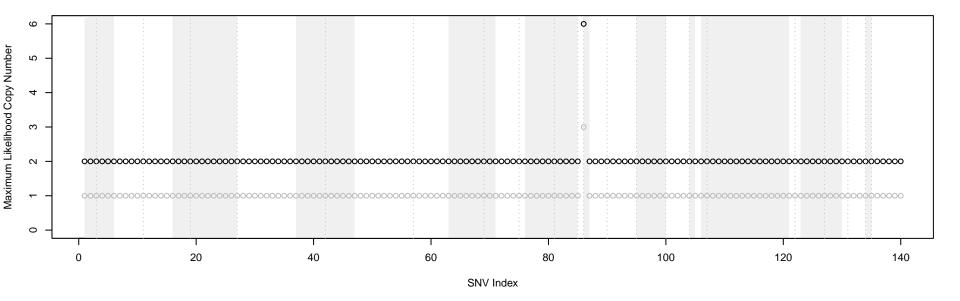
Purity: 0.74 Tumor ploidy: 2

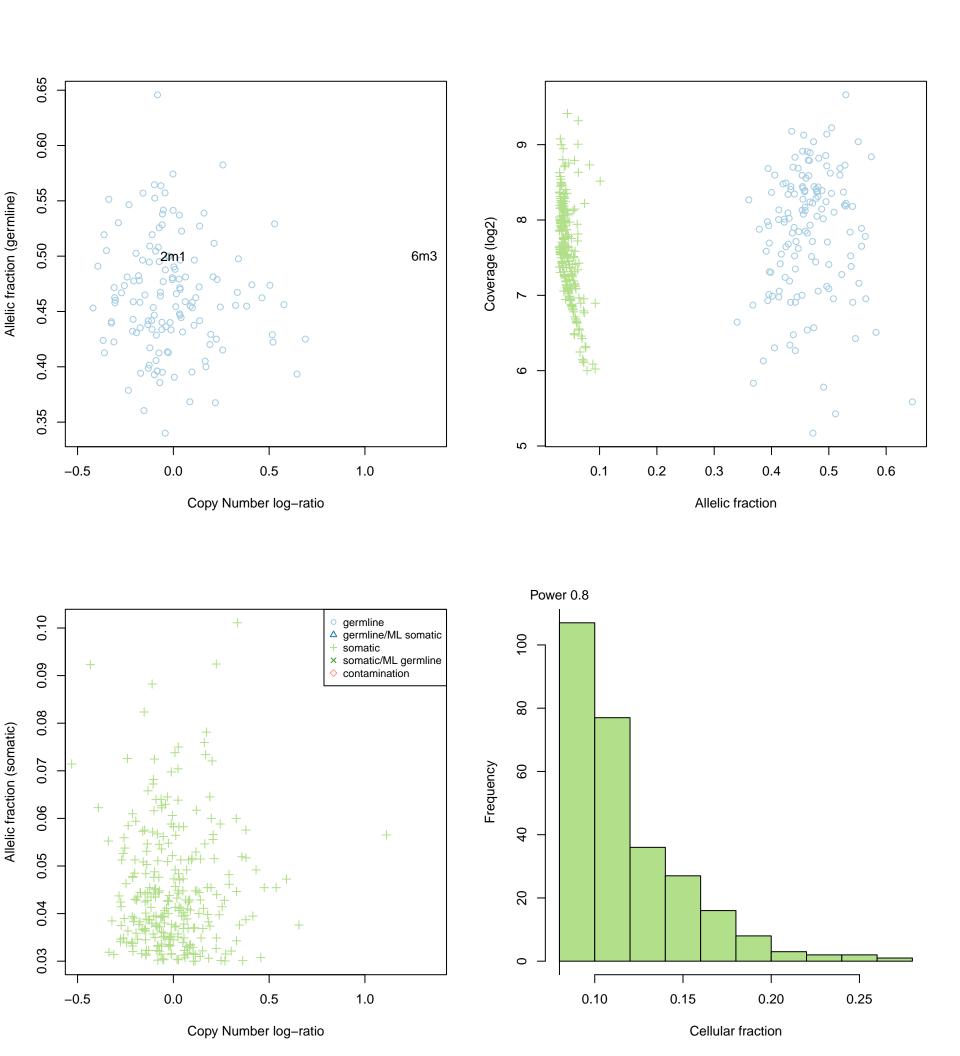




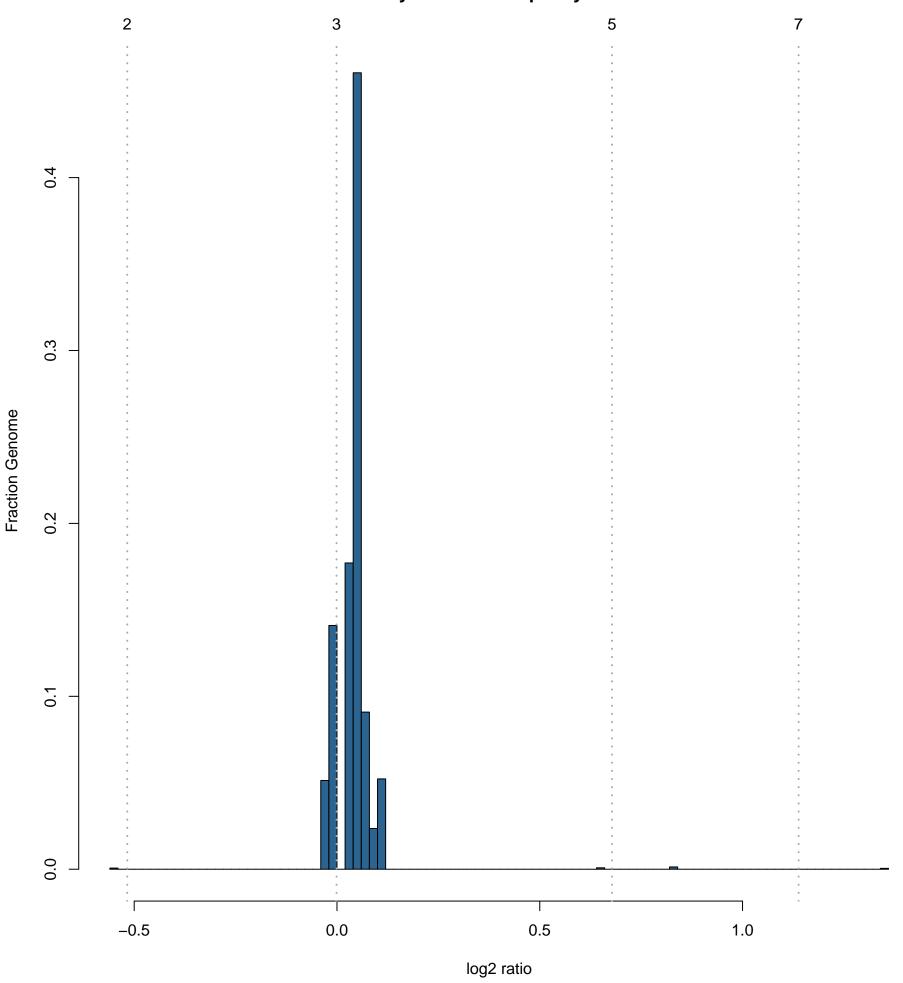
SCNA-fit log-likelihood: -3991.07

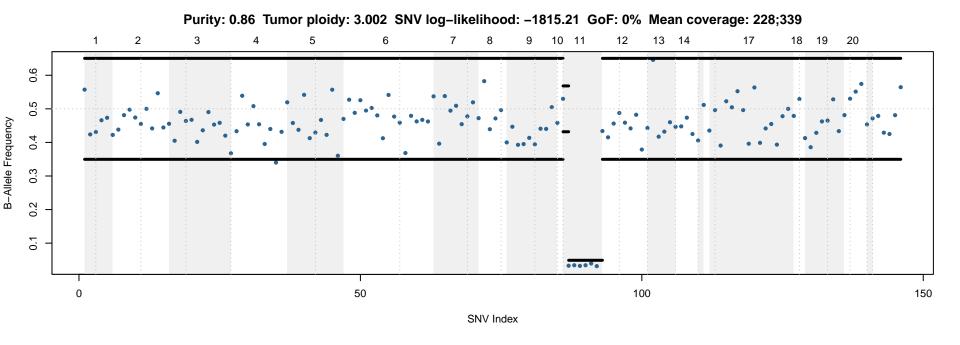






Purity: 0.86 Tumor ploidy: 3.002





SCNA-fit log-likelihood: -3991.89

