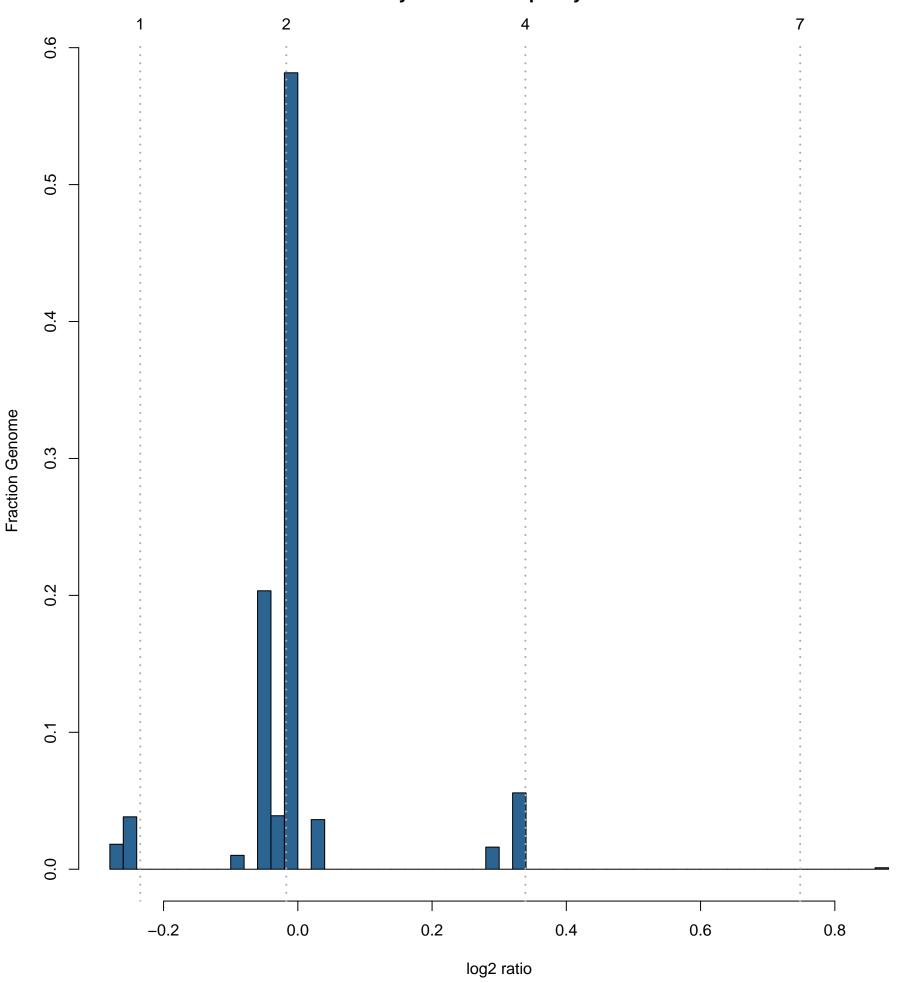
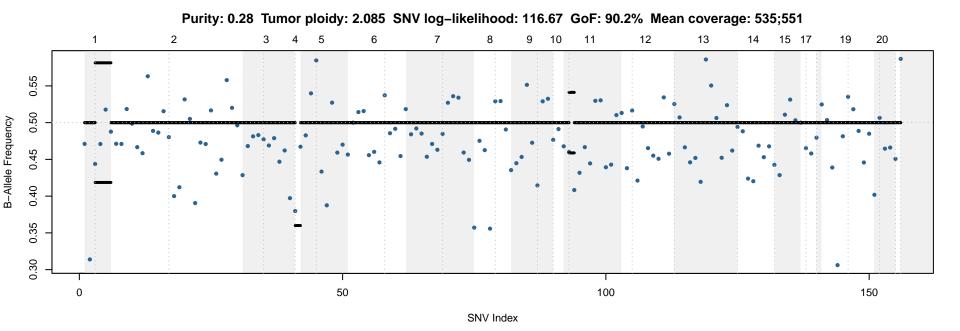
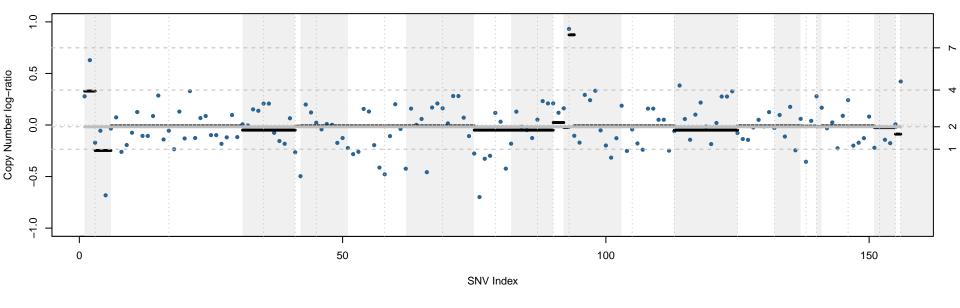
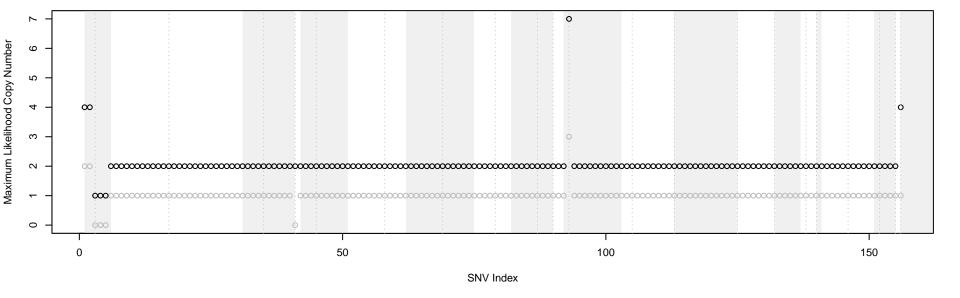
Purity: 0.28 Tumor ploidy: 2.085

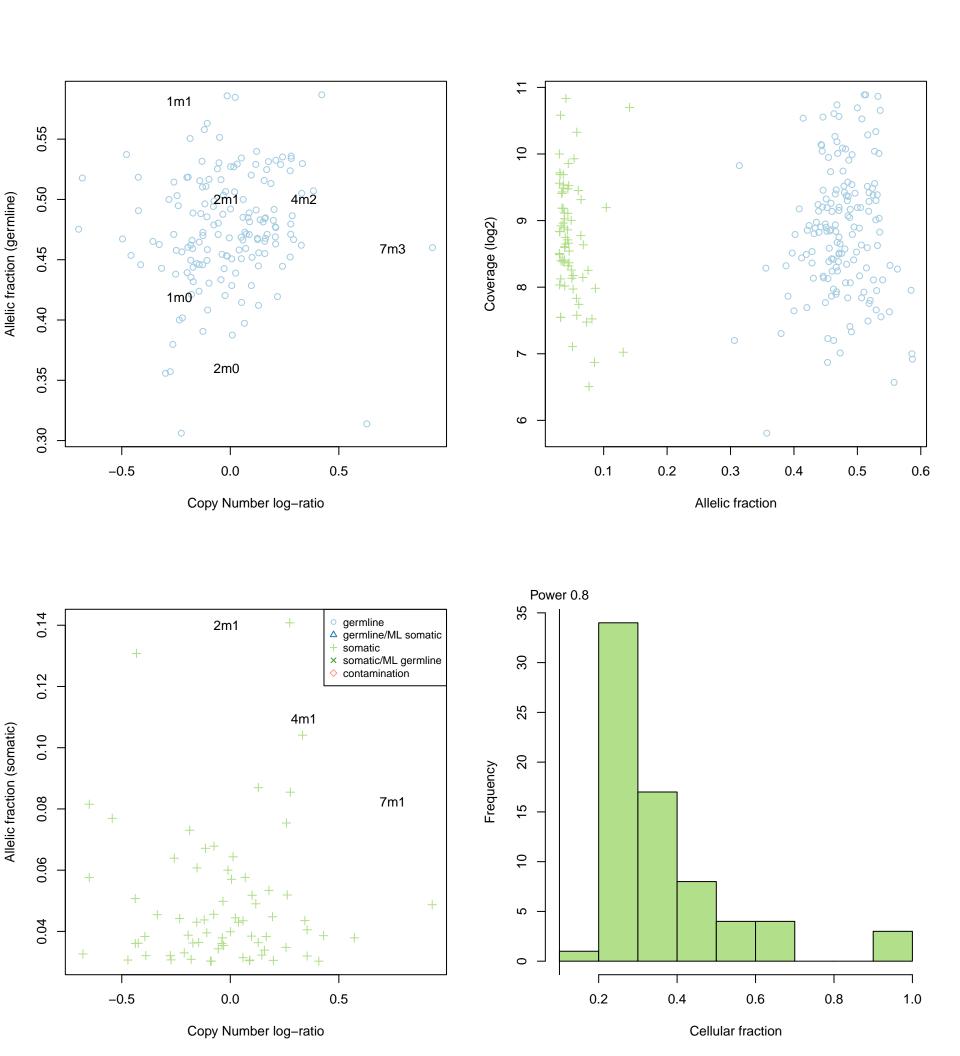




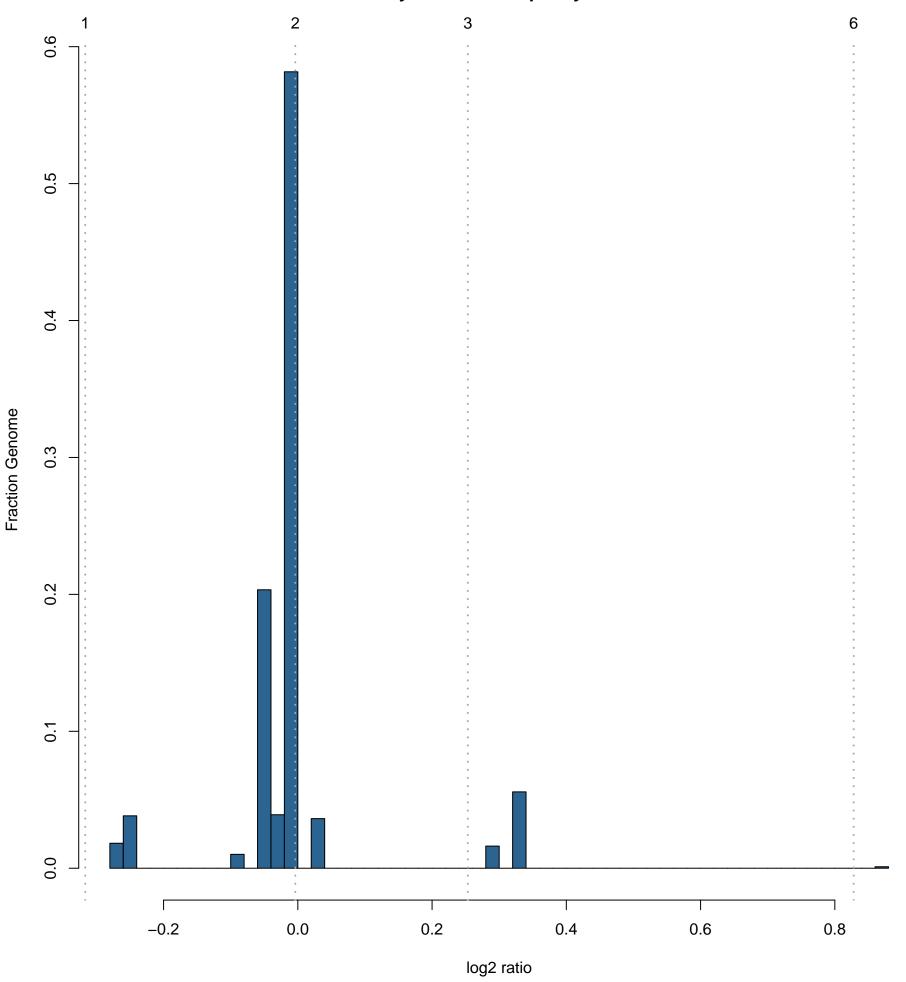
SCNA-fit log-likelihood: -10740.32

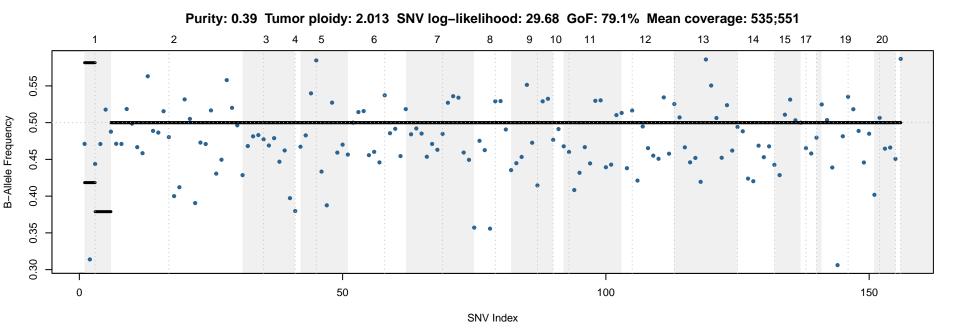




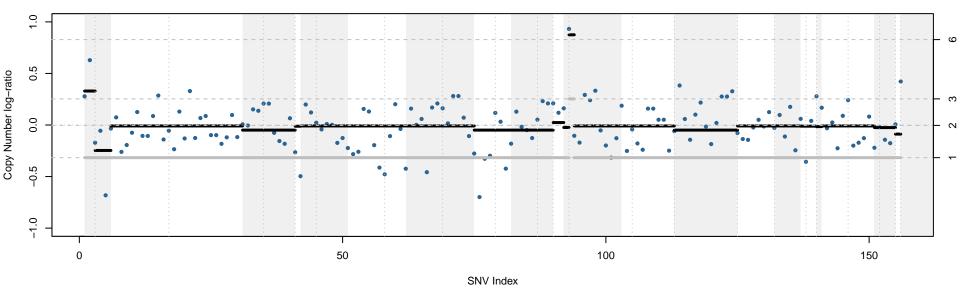


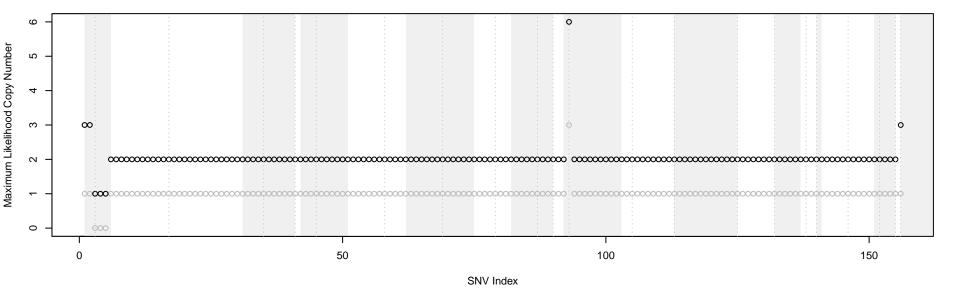
Purity: 0.39 Tumor ploidy: 2.013

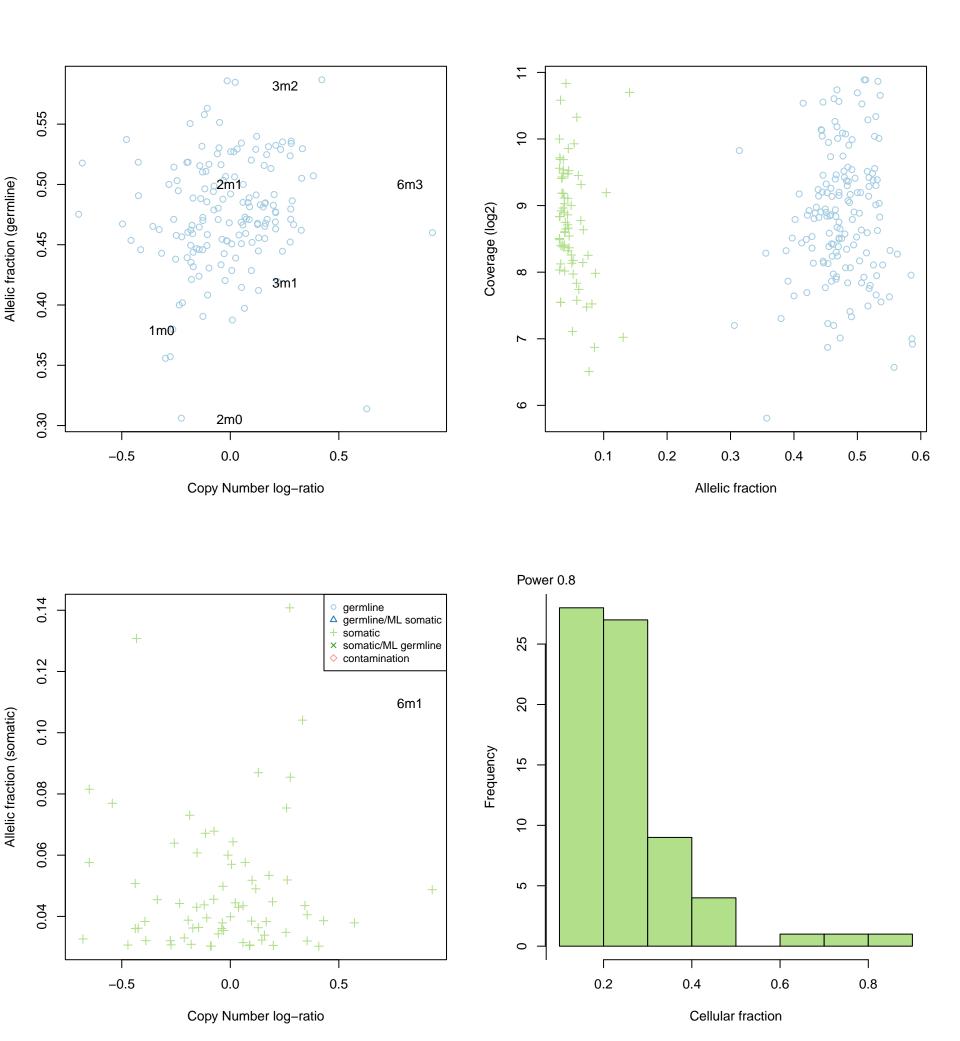




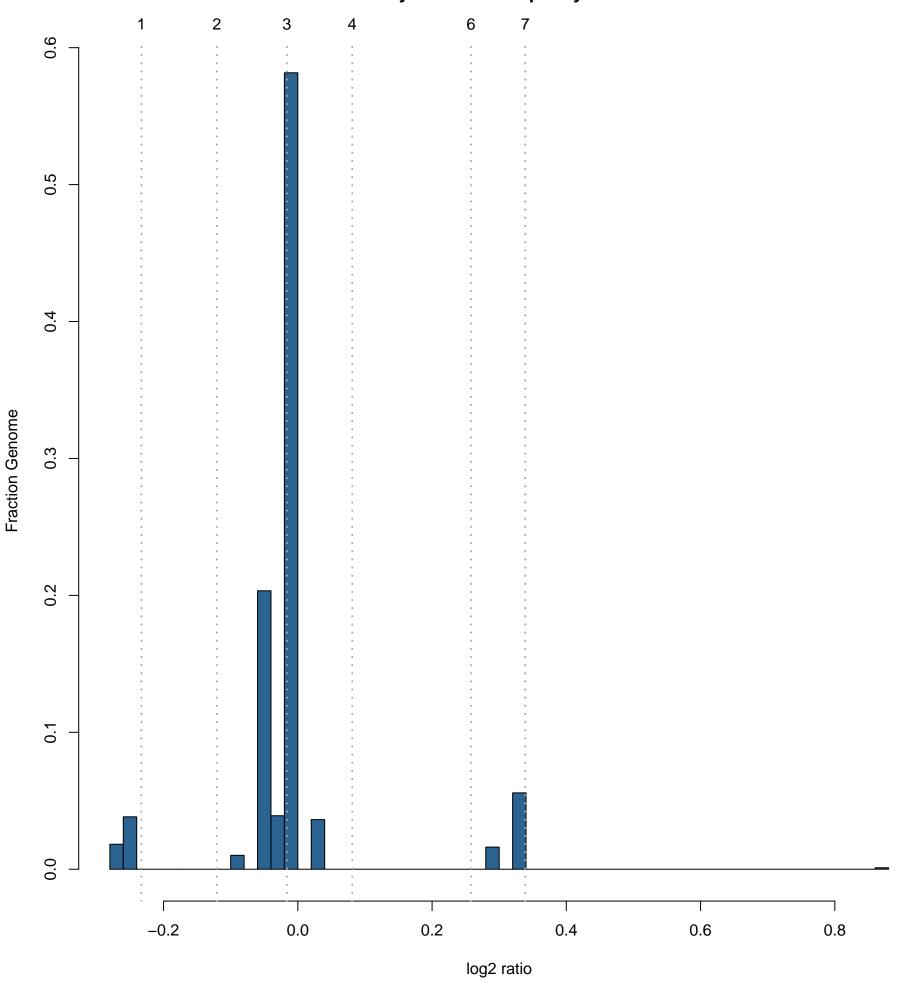
SCNA-fit log-likelihood: -10779.81

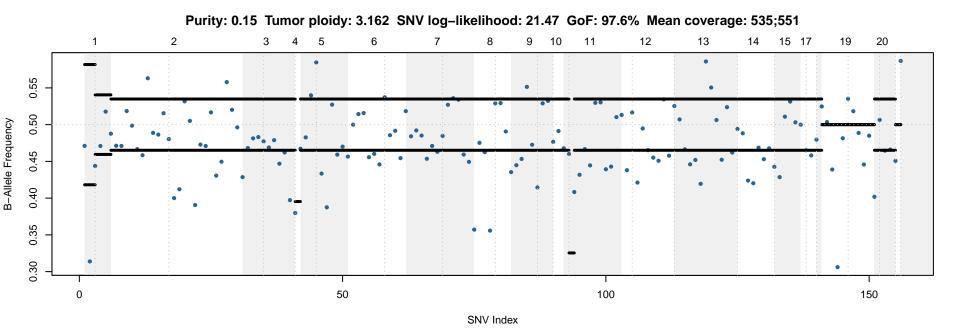




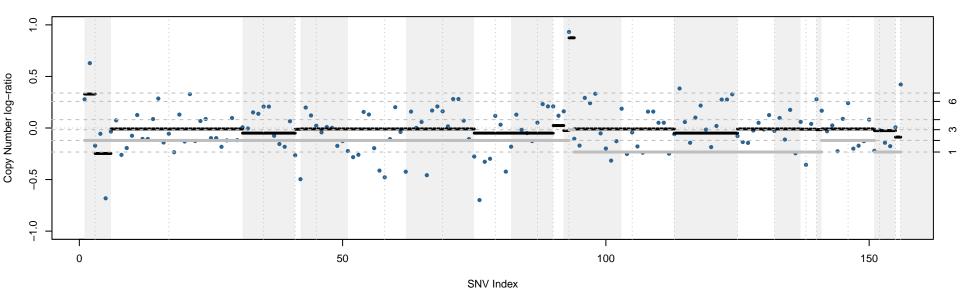


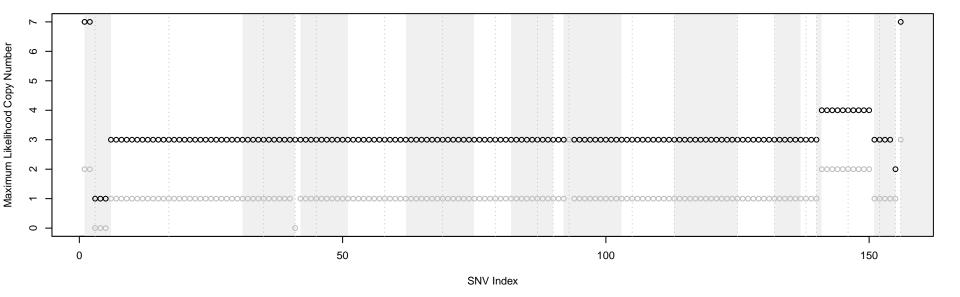
Purity: 0.15 Tumor ploidy: 3.162

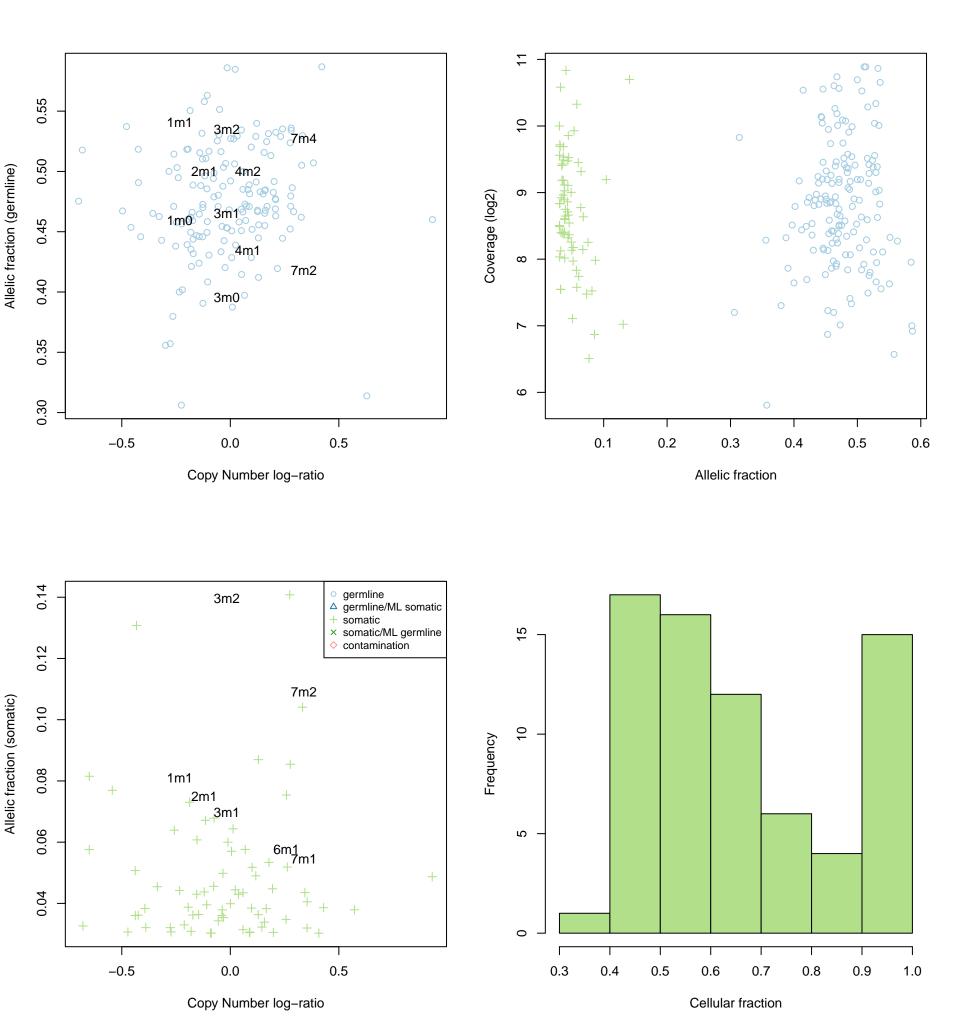




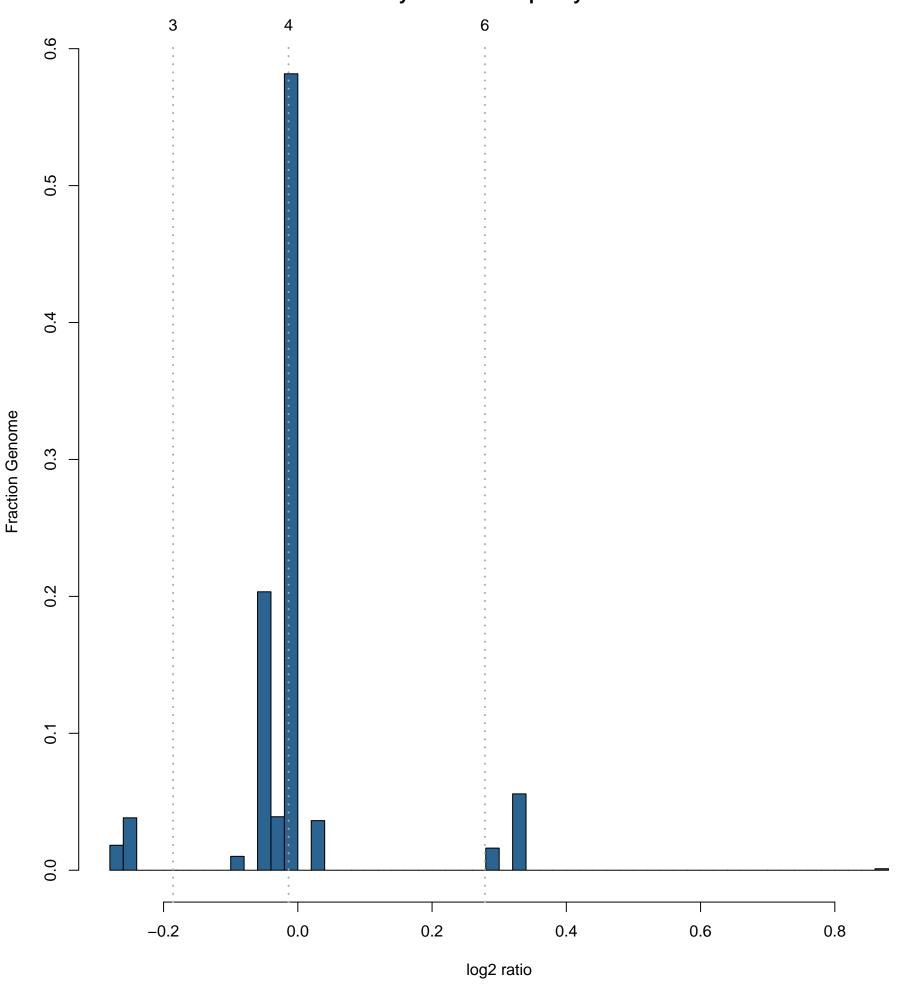
SCNA-fit log-likelihood: -10762.61

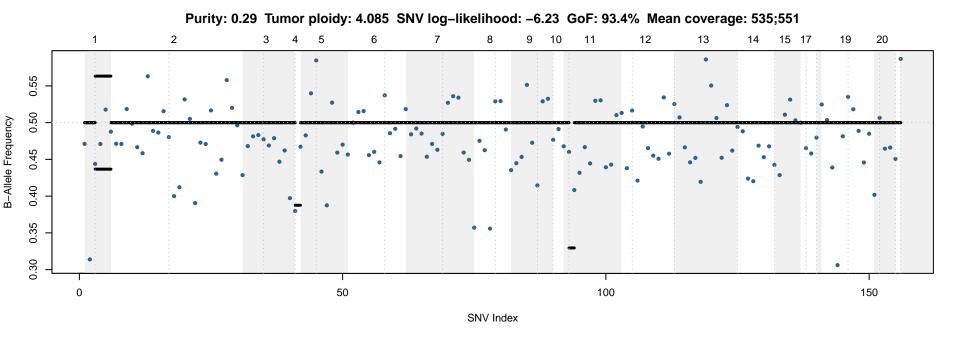




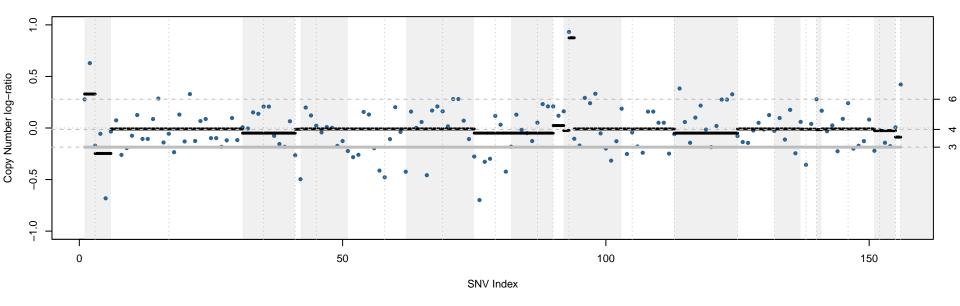


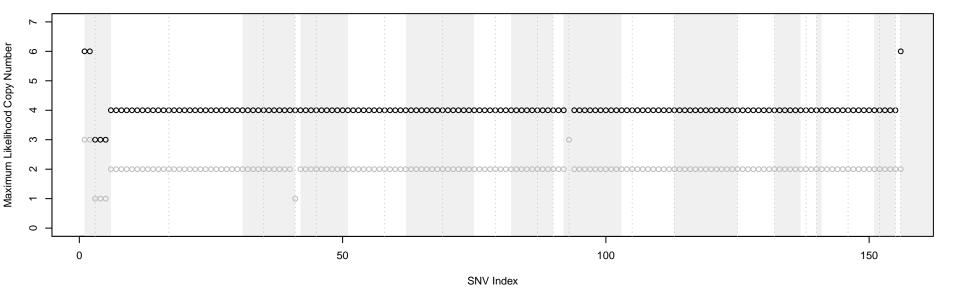
Purity: 0.29 Tumor ploidy: 4.085

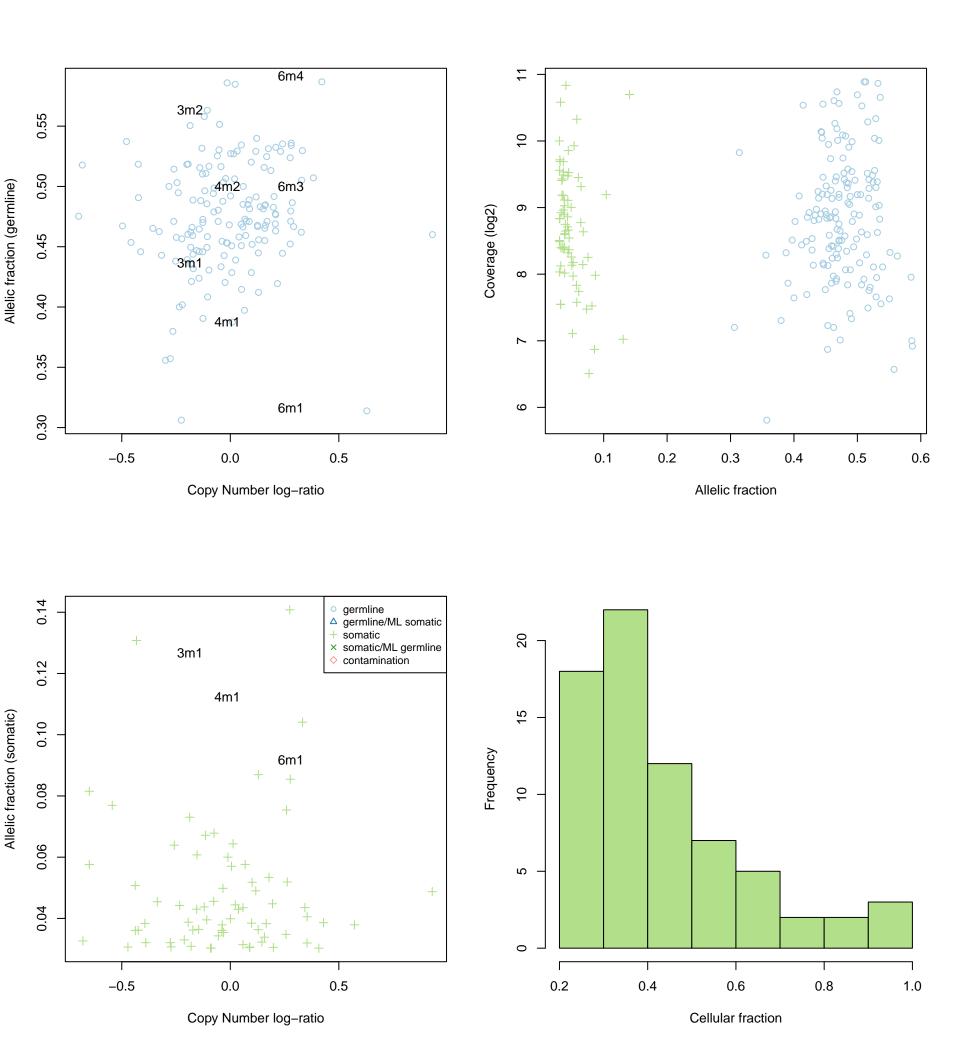




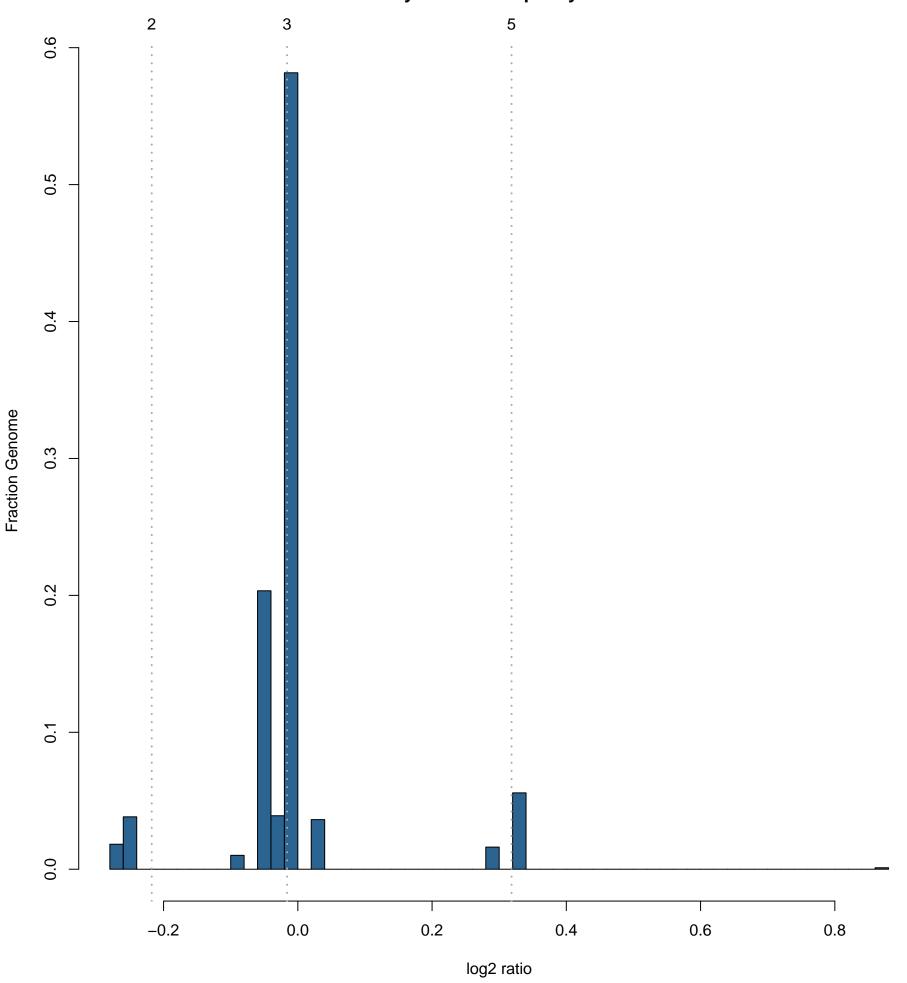
SCNA-fit log-likelihood: -10788.76

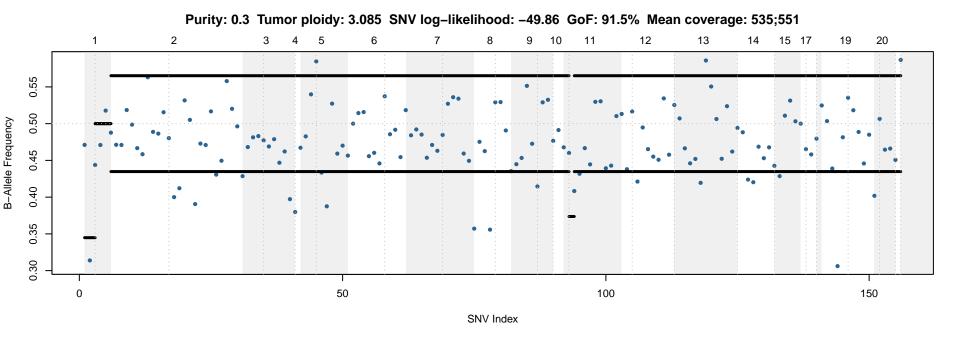




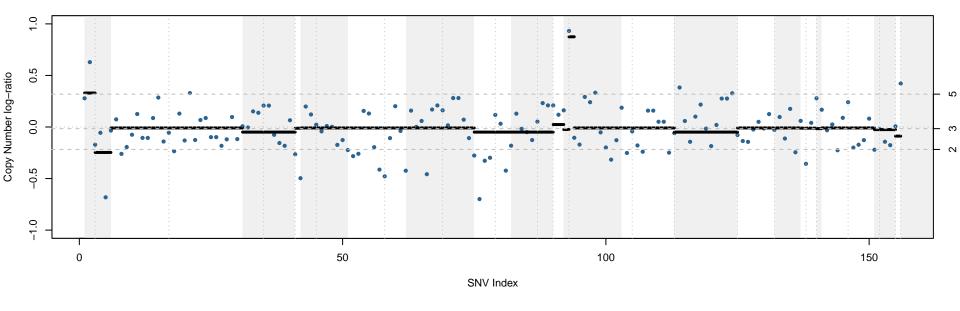


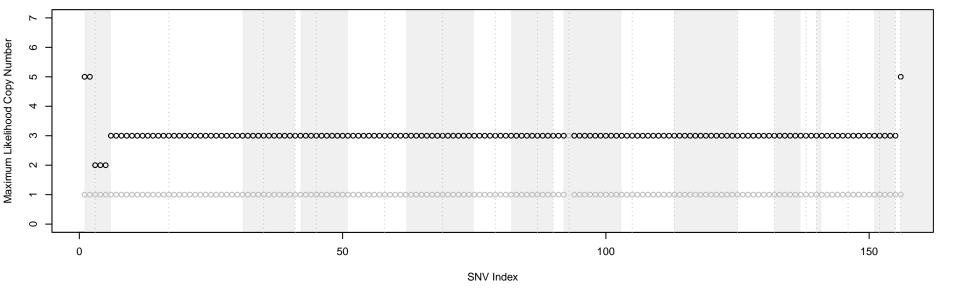
Purity: 0.3 Tumor ploidy: 3.085

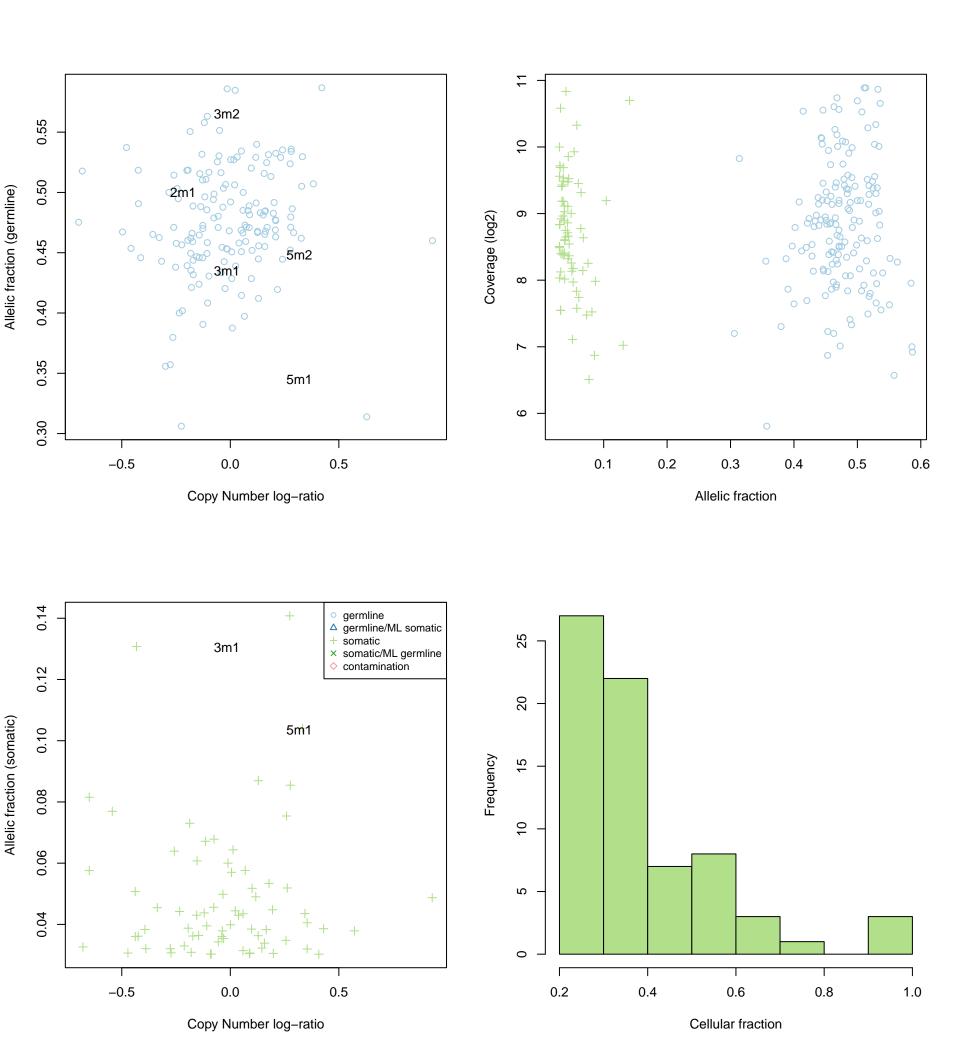




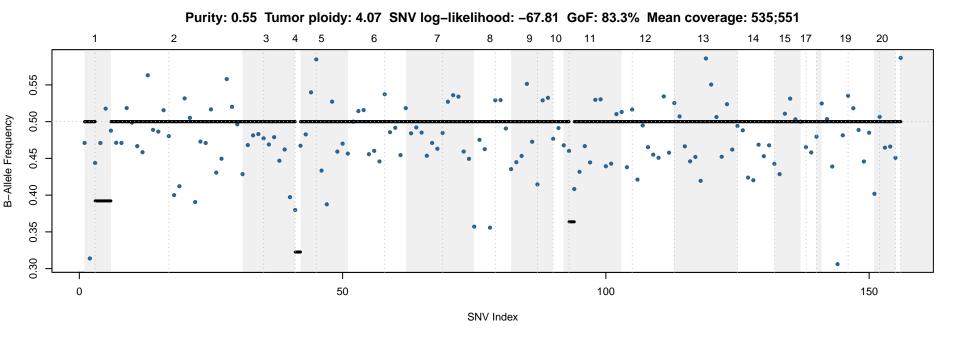
SCNA-fit log-likelihood: -10769.85



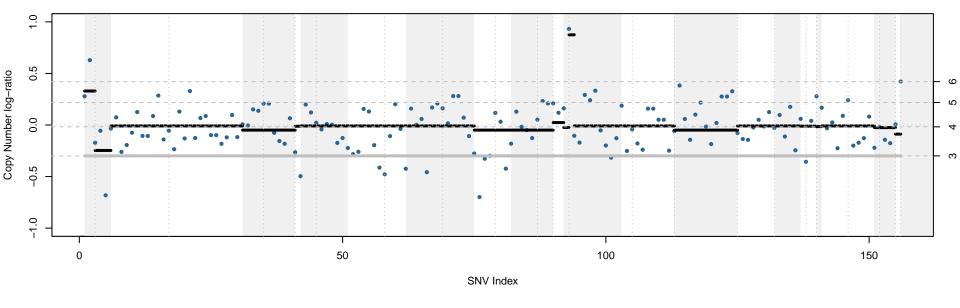


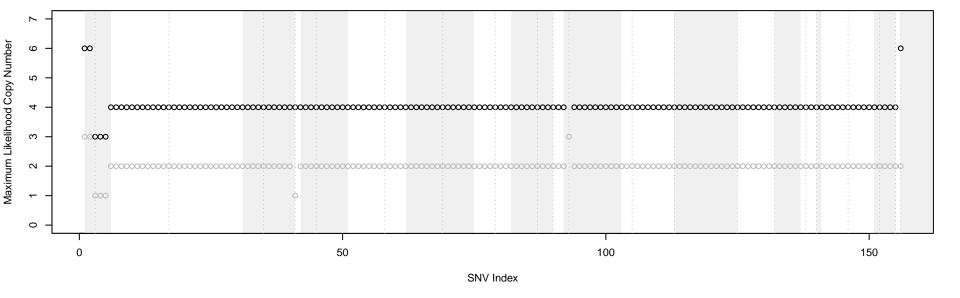


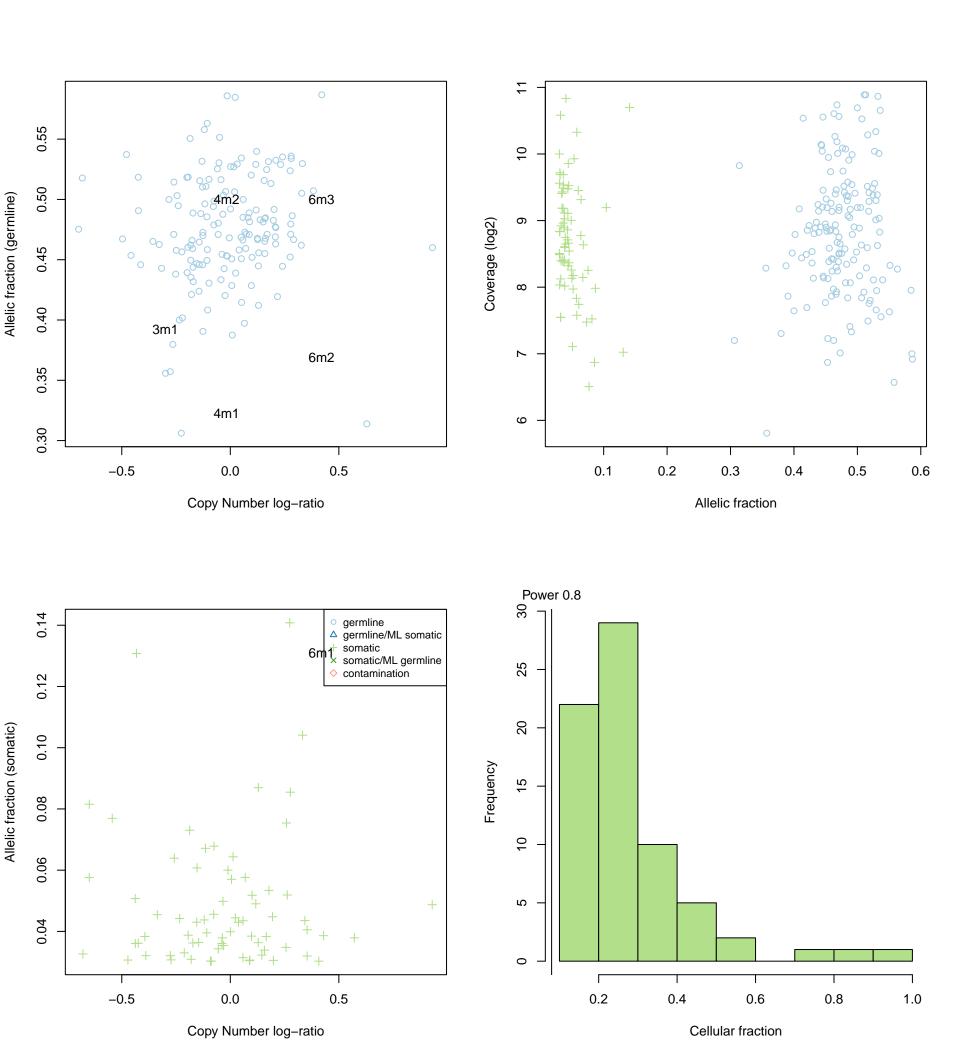
Purity: 0.55 Tumor ploidy: 4.07 3 6 9.0 0.5 Fraction Genome 0.3 0.2 0.1 0.0 -0.2 0.0 0.2 0.4 0.6 8.0 log2 ratio



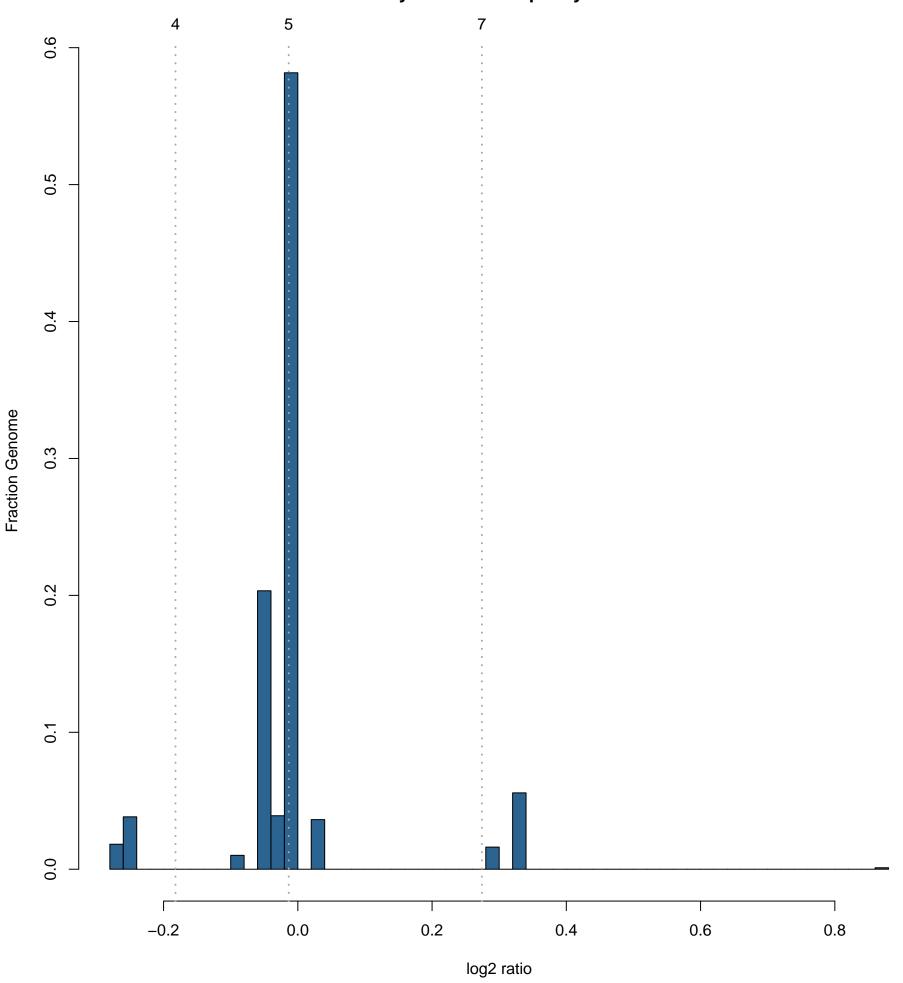
SCNA-fit log-likelihood: -10799.79

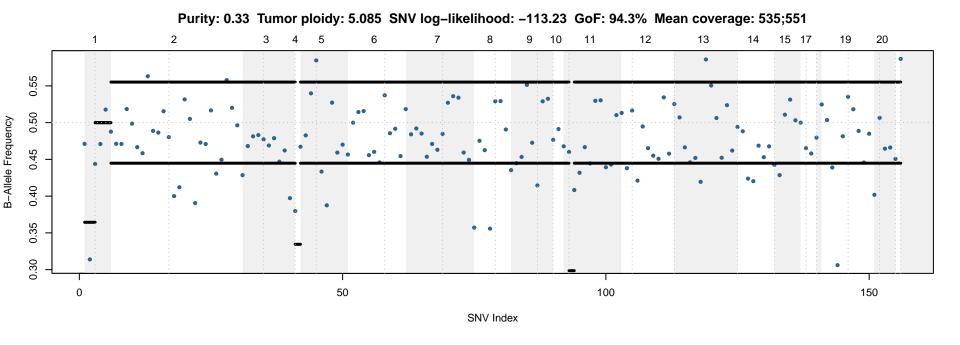




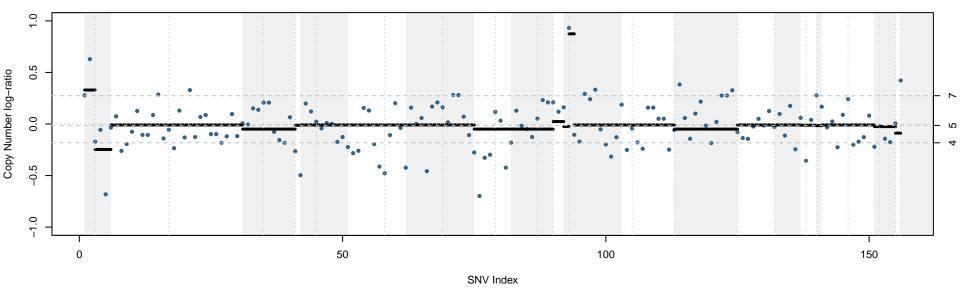


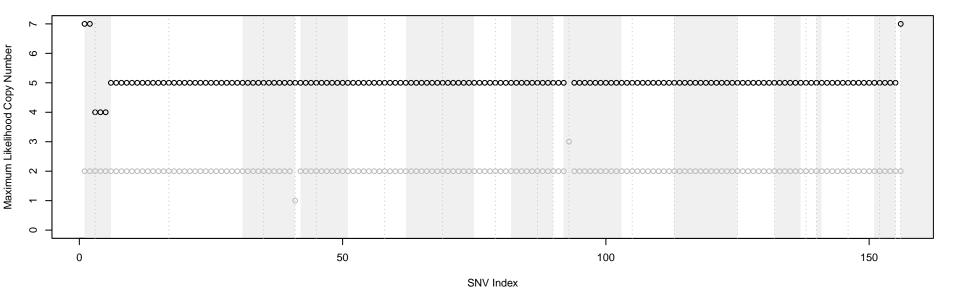
Purity: 0.33 Tumor ploidy: 5.085

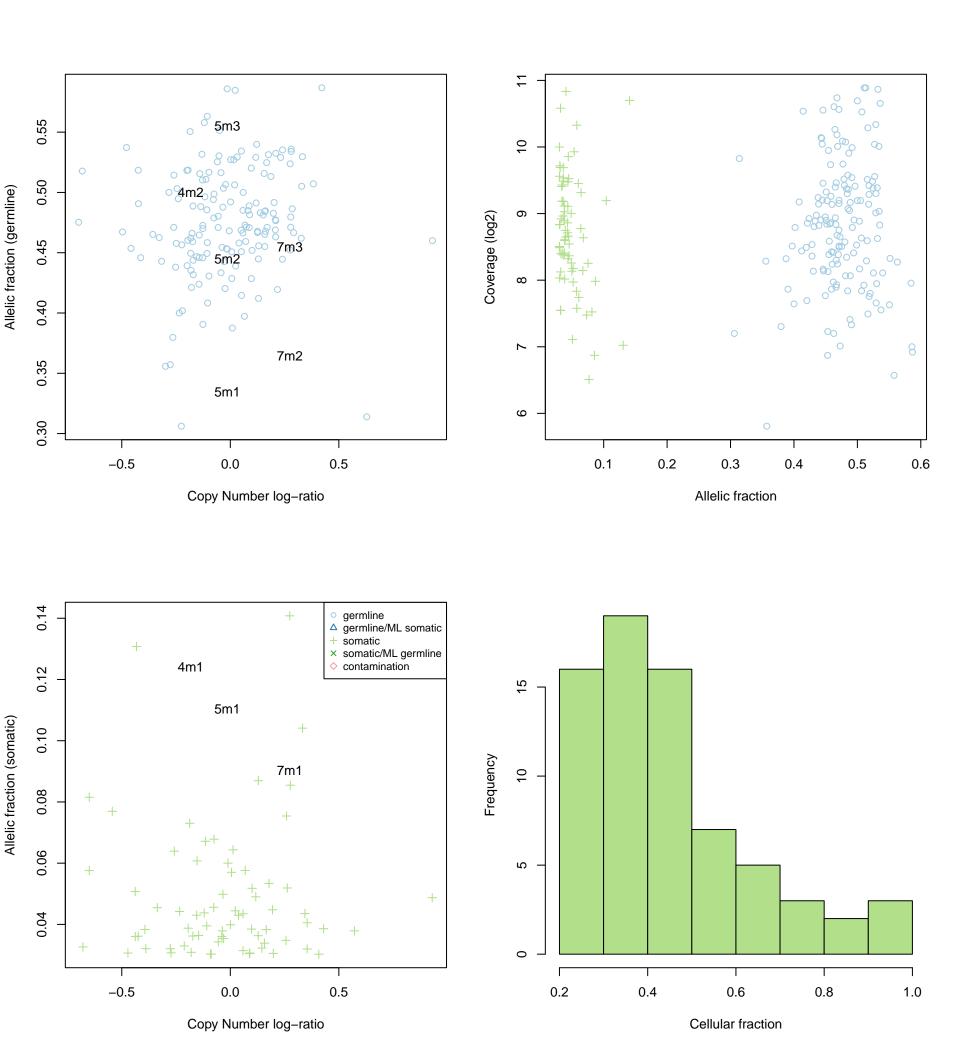




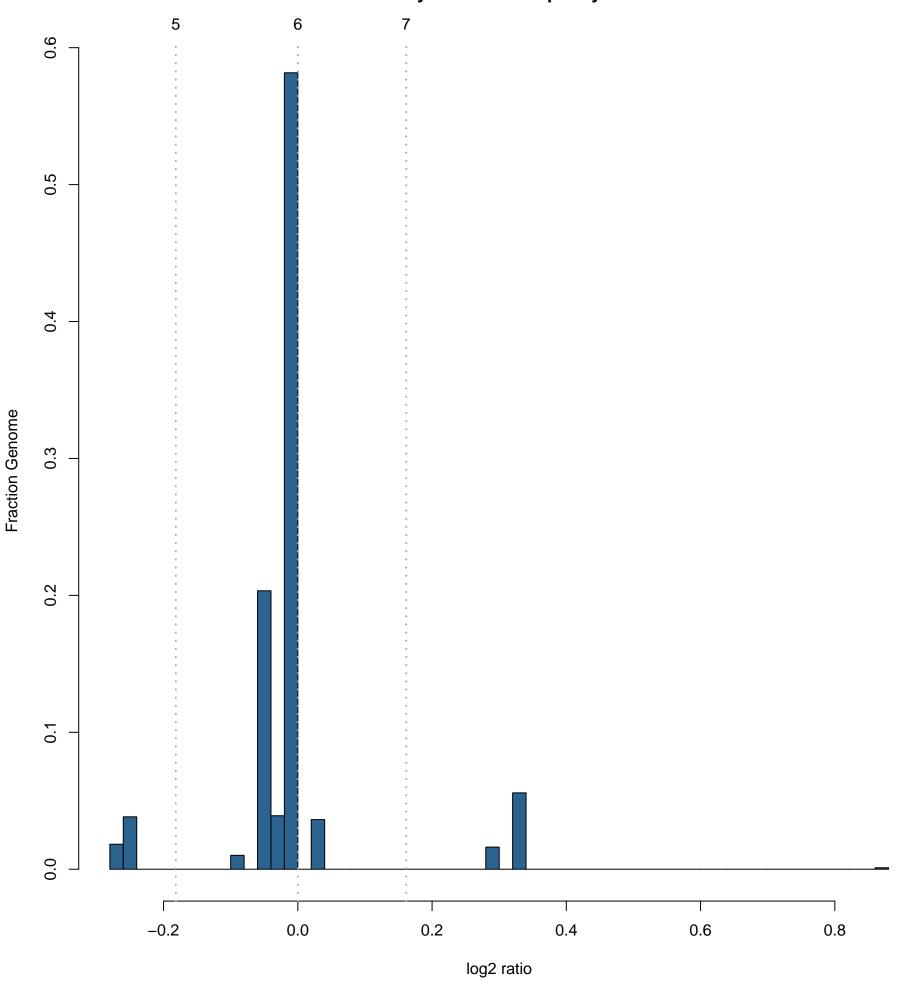
SCNA-fit log-likelihood: -10792.24

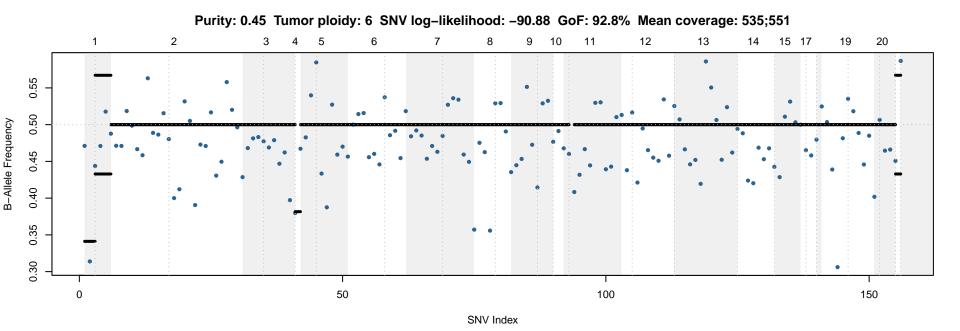




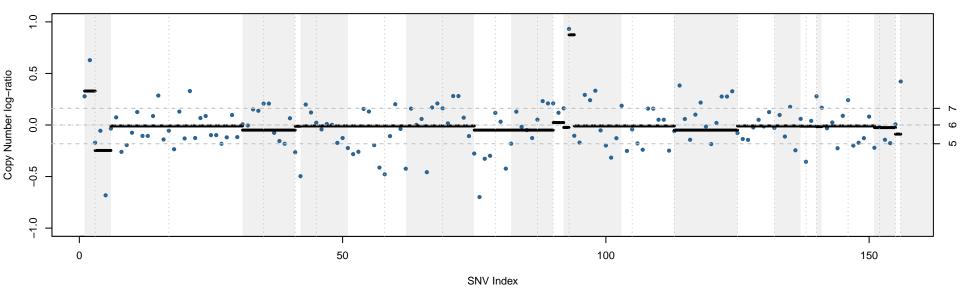


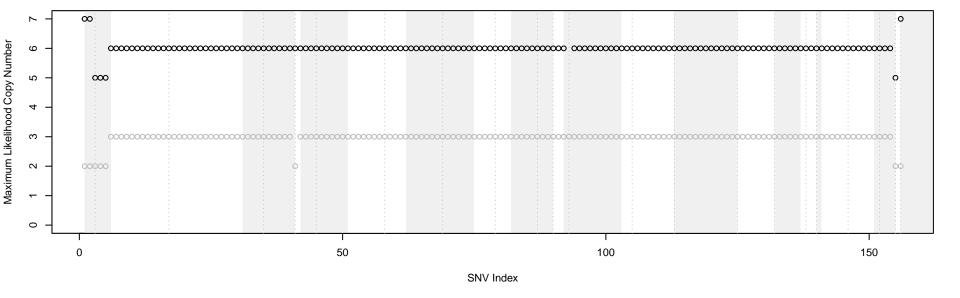
Purity: 0.45 Tumor ploidy: 6

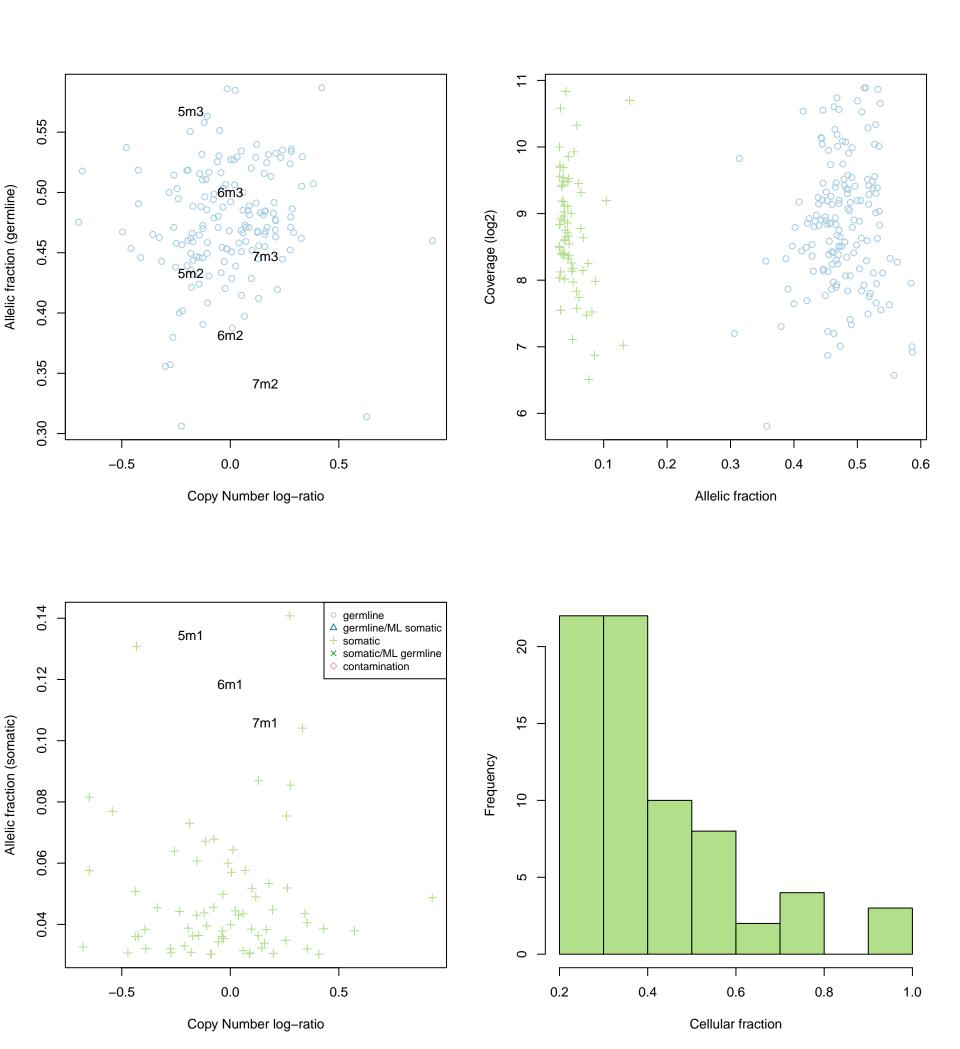




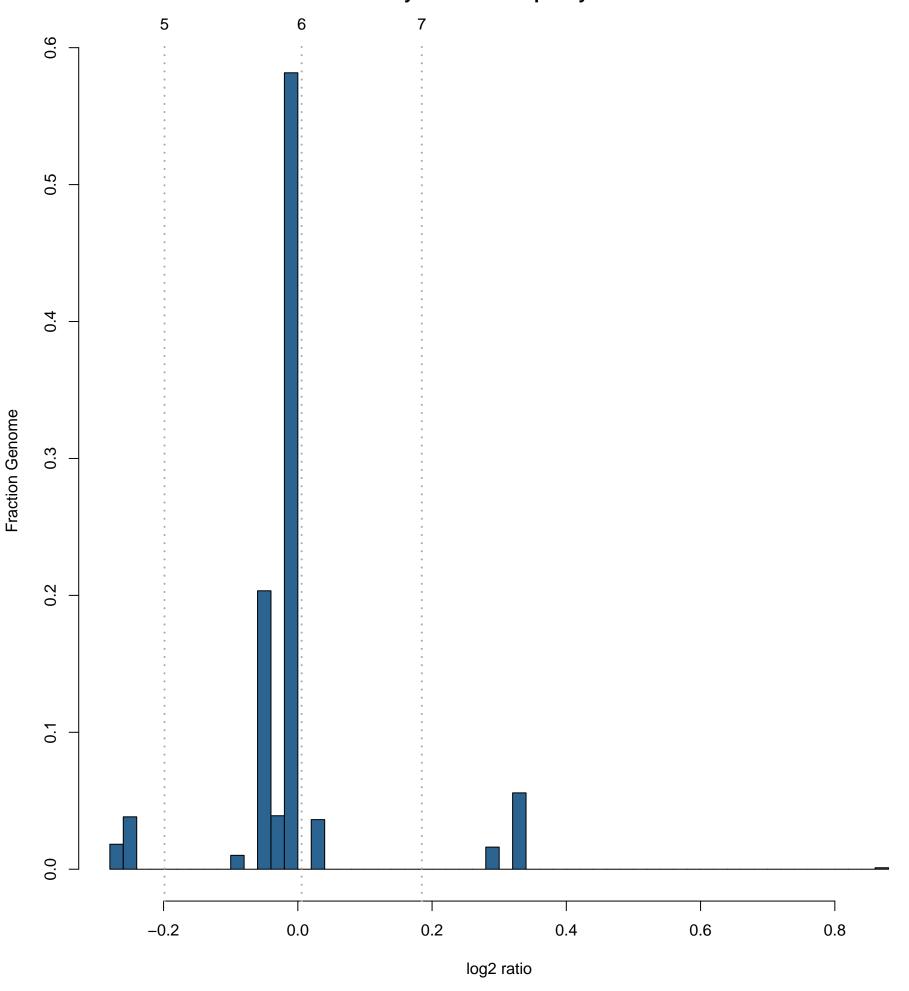
SCNA-fit log-likelihood: -10906.75

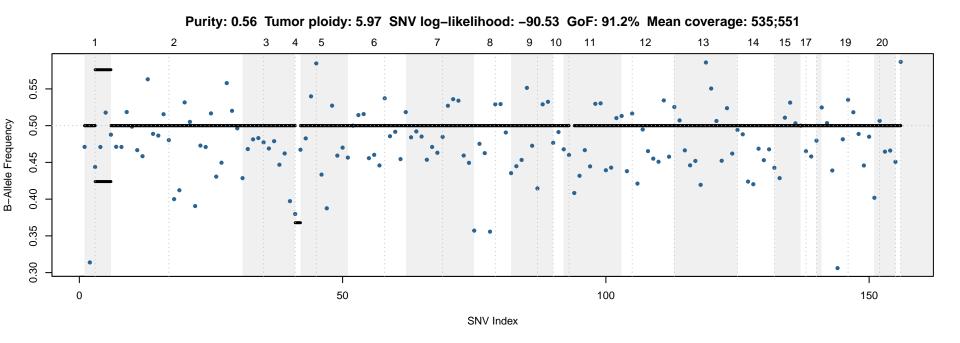




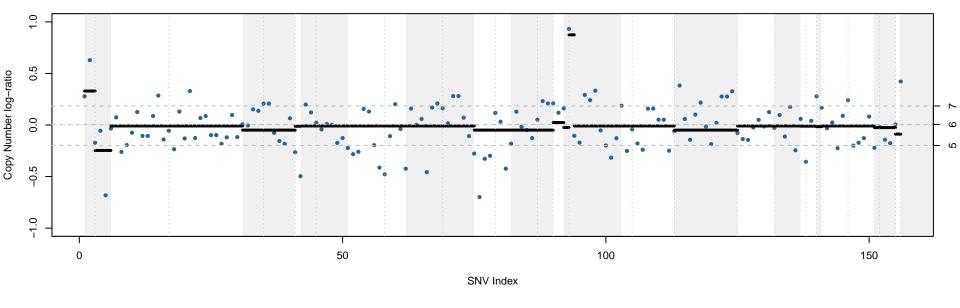


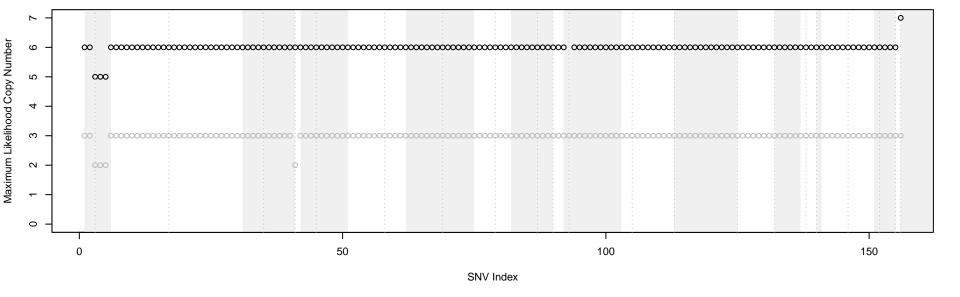
Purity: 0.56 Tumor ploidy: 5.97

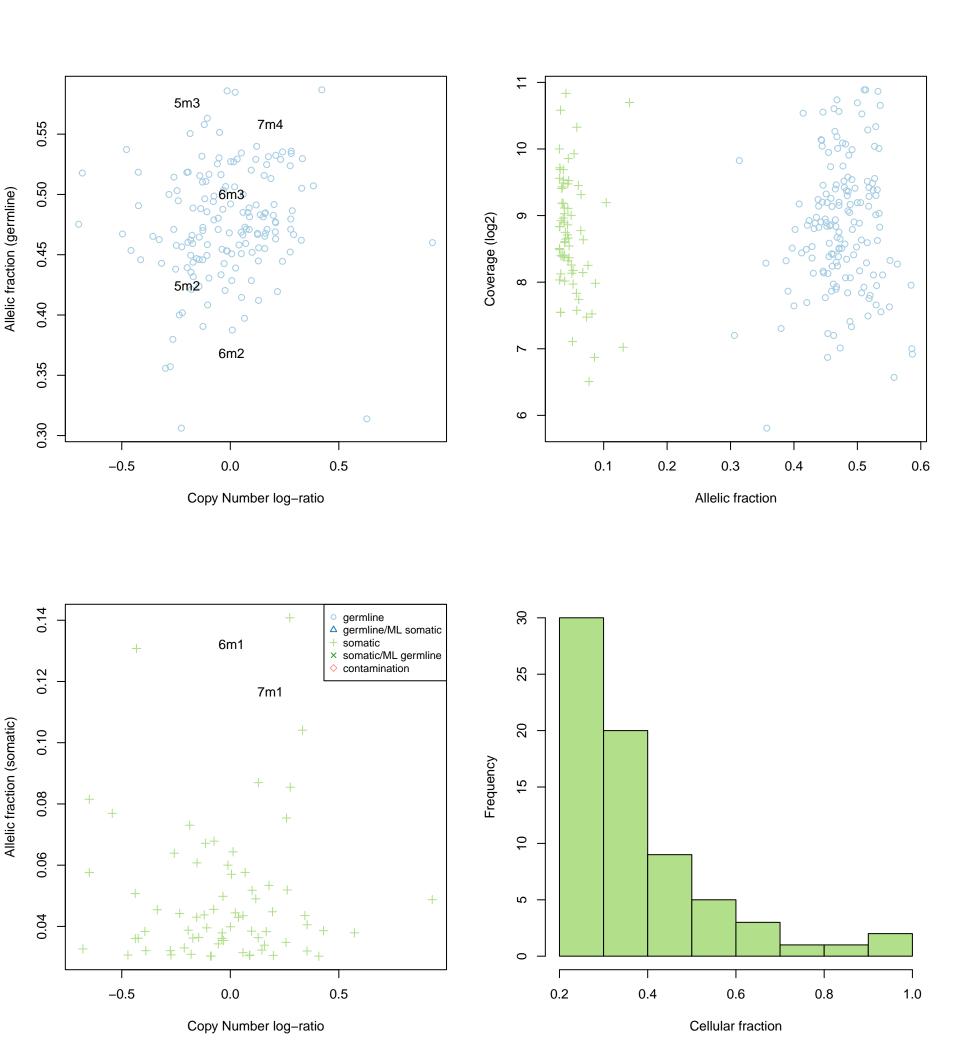




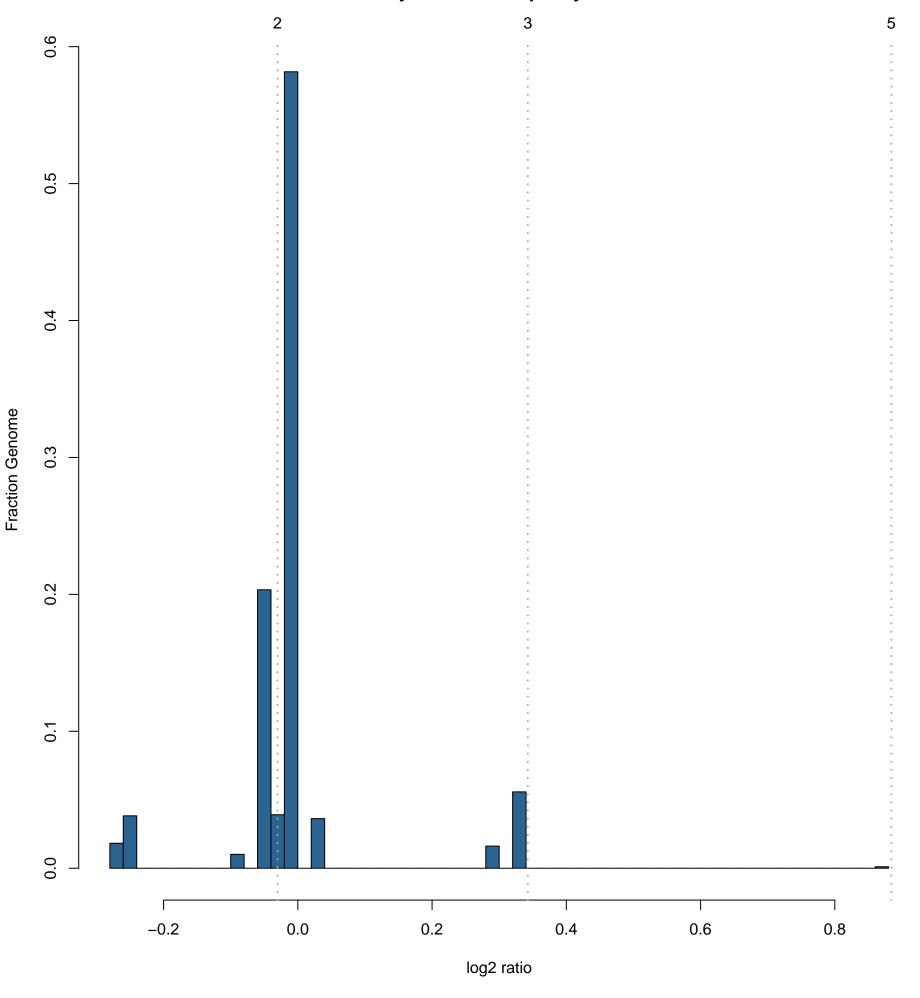
SCNA-fit log-likelihood: -11079.87

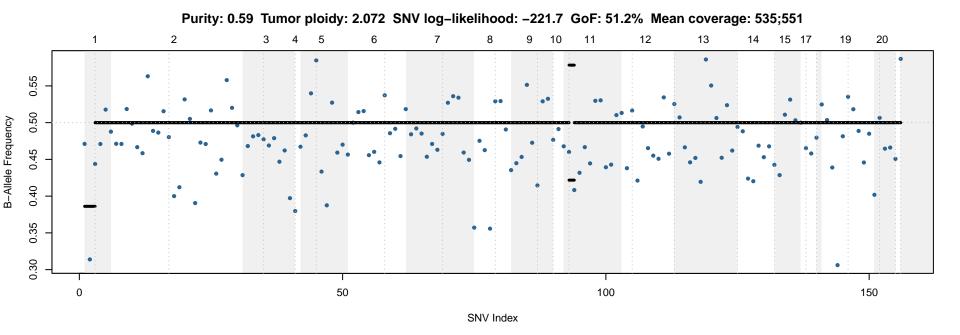




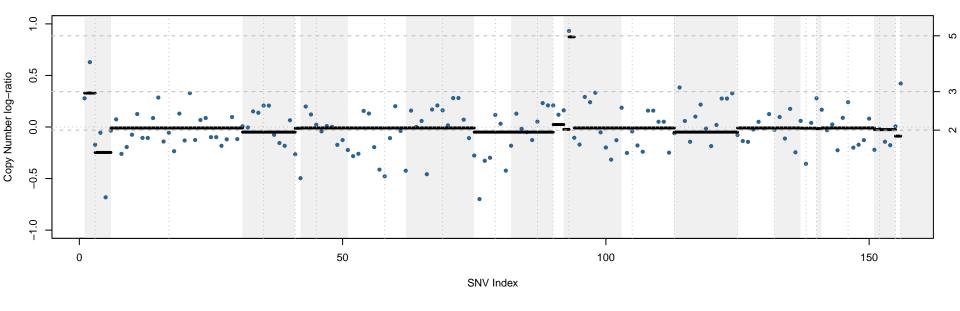


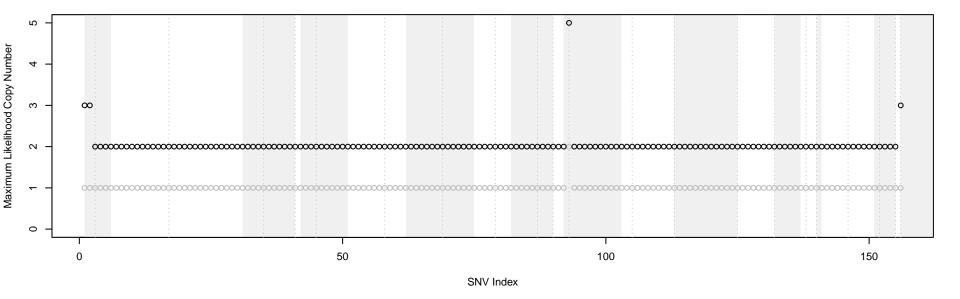
Purity: 0.59 Tumor ploidy: 2.072

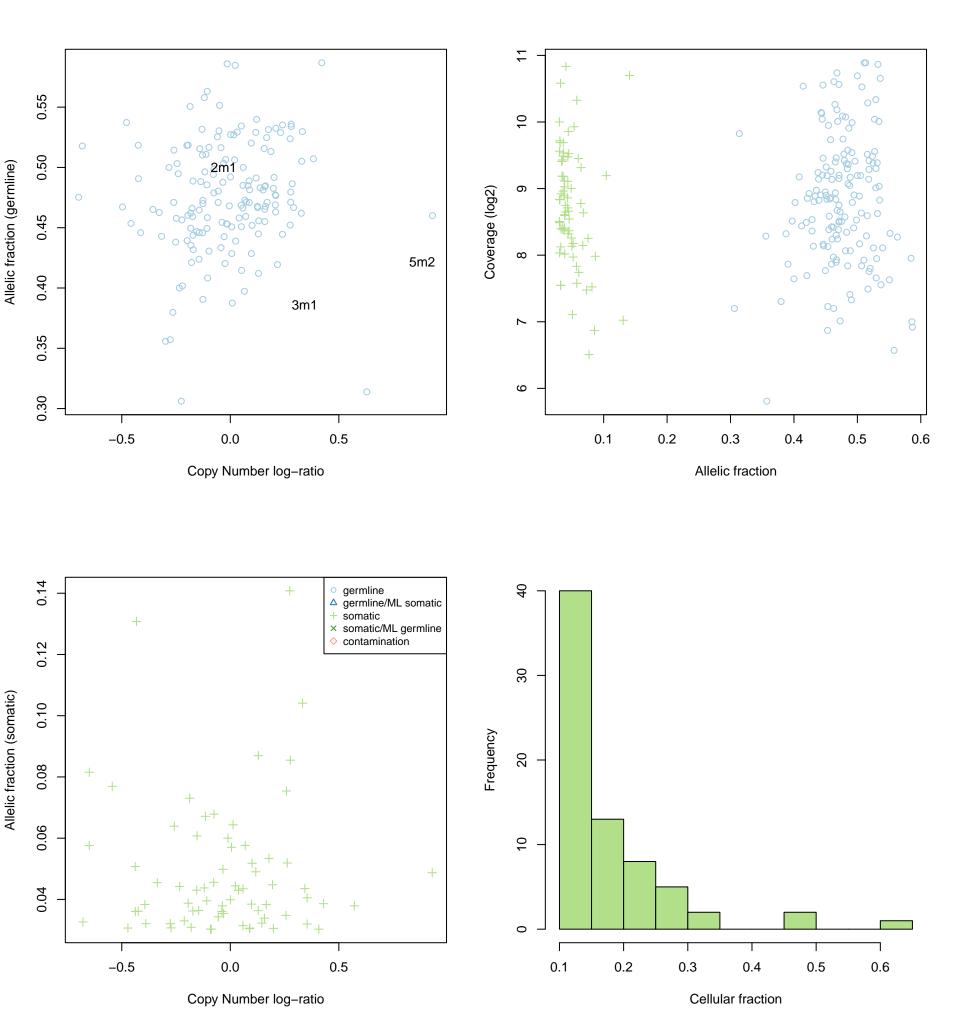




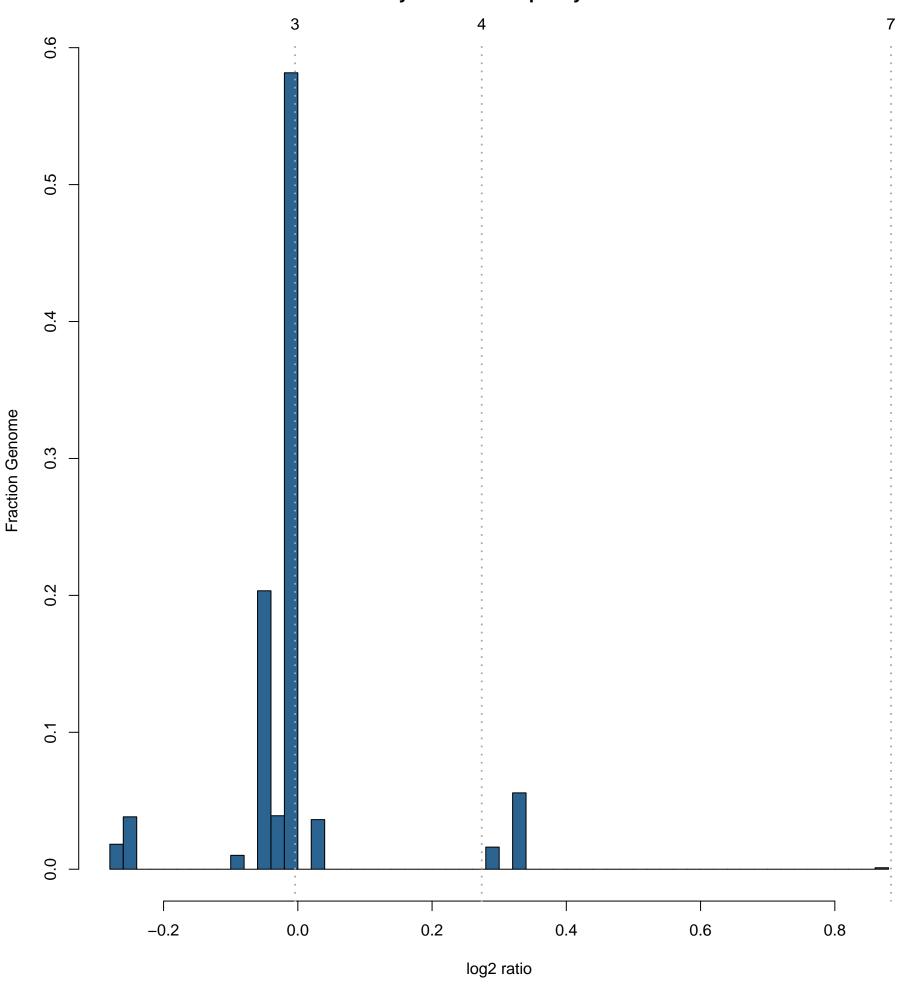
SCNA-fit log-likelihood: -10912.47

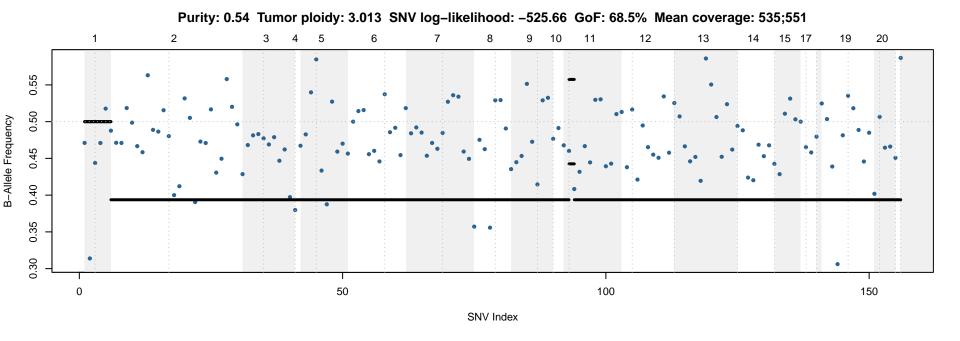




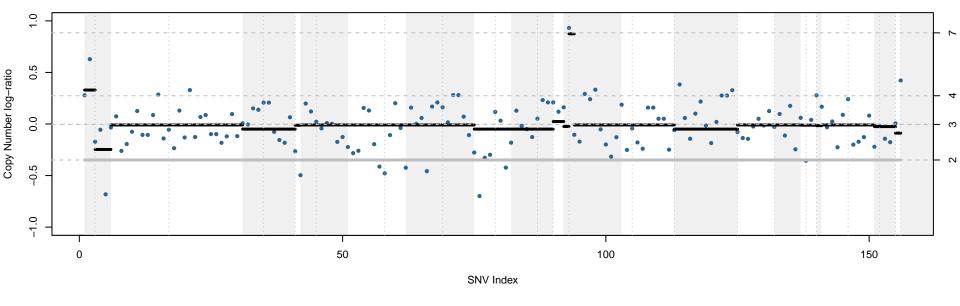


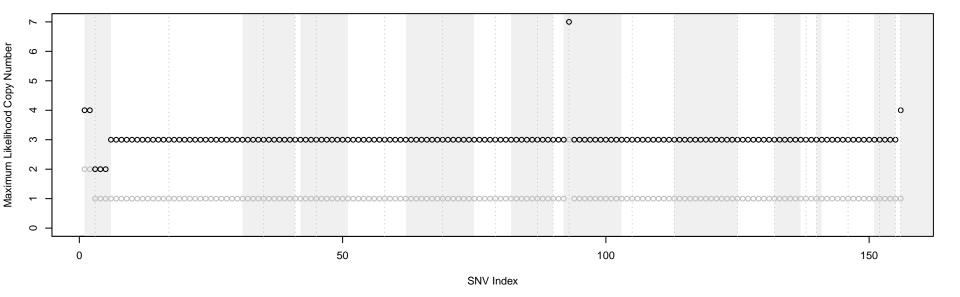
Purity: 0.54 Tumor ploidy: 3.013

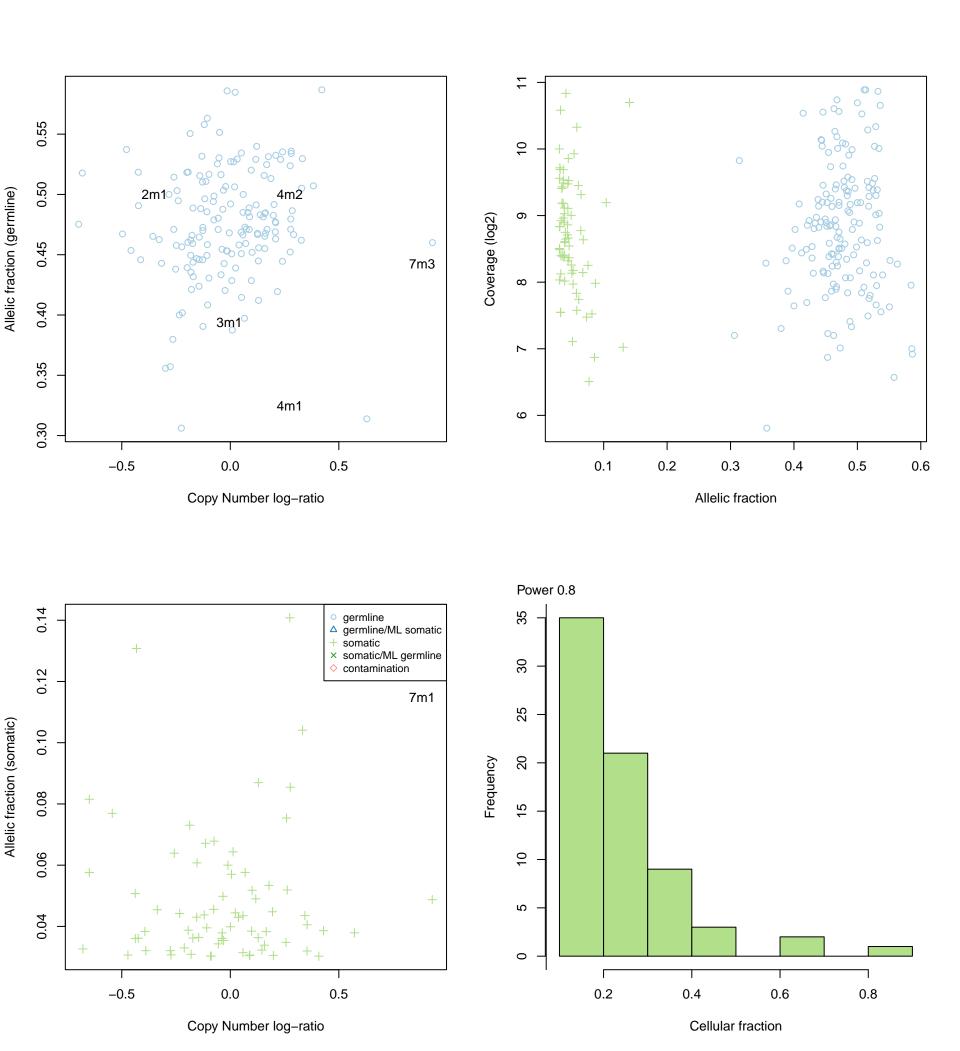




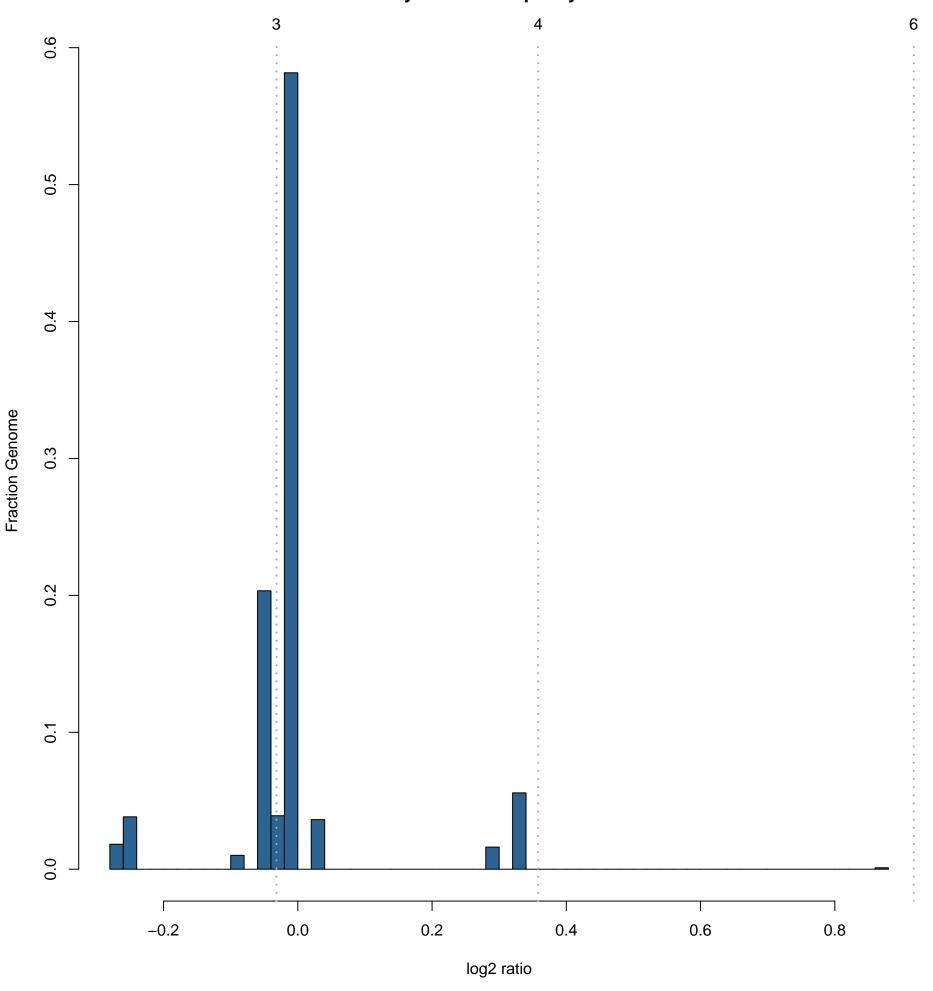
SCNA-fit log-likelihood: -10786.07

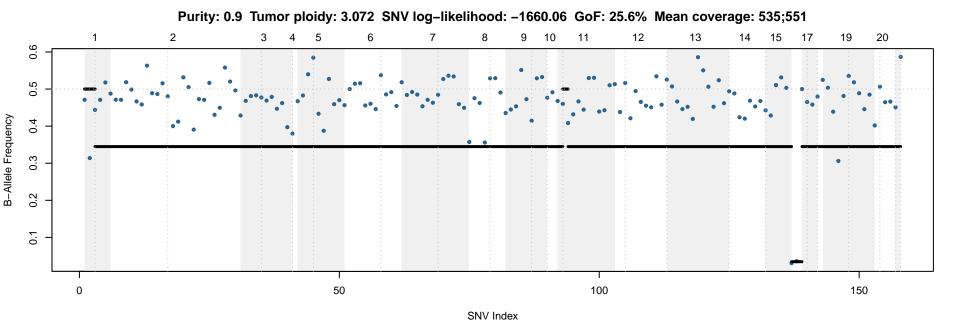






Purity: 0.9 Tumor ploidy: 3.072





SCNA-fit log-likelihood: -10917.06

