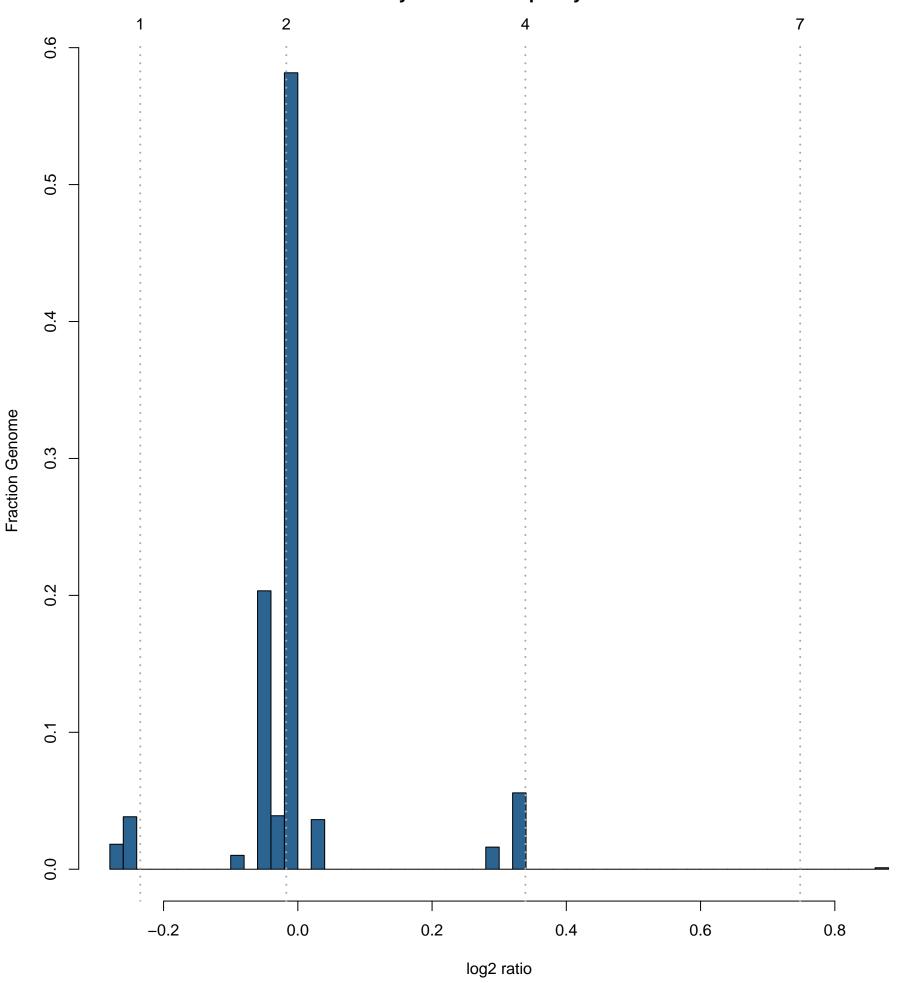
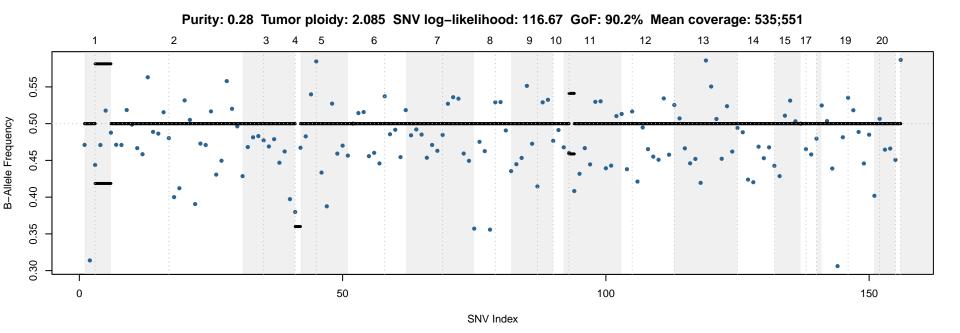
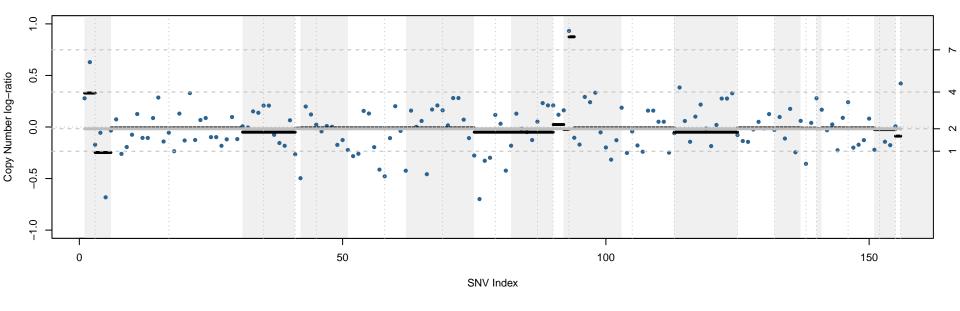
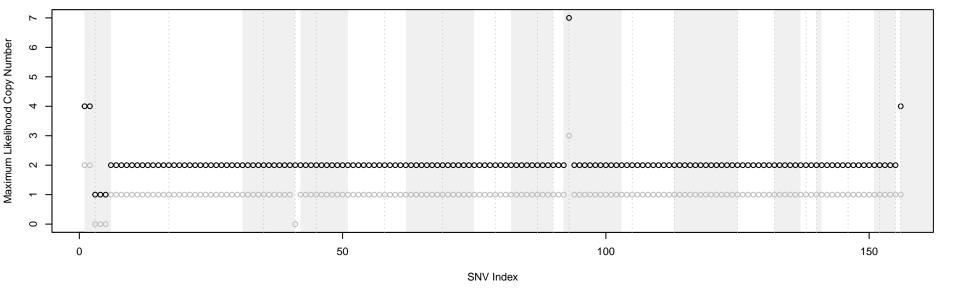
Purity: 0.28 Tumor ploidy: 2.085

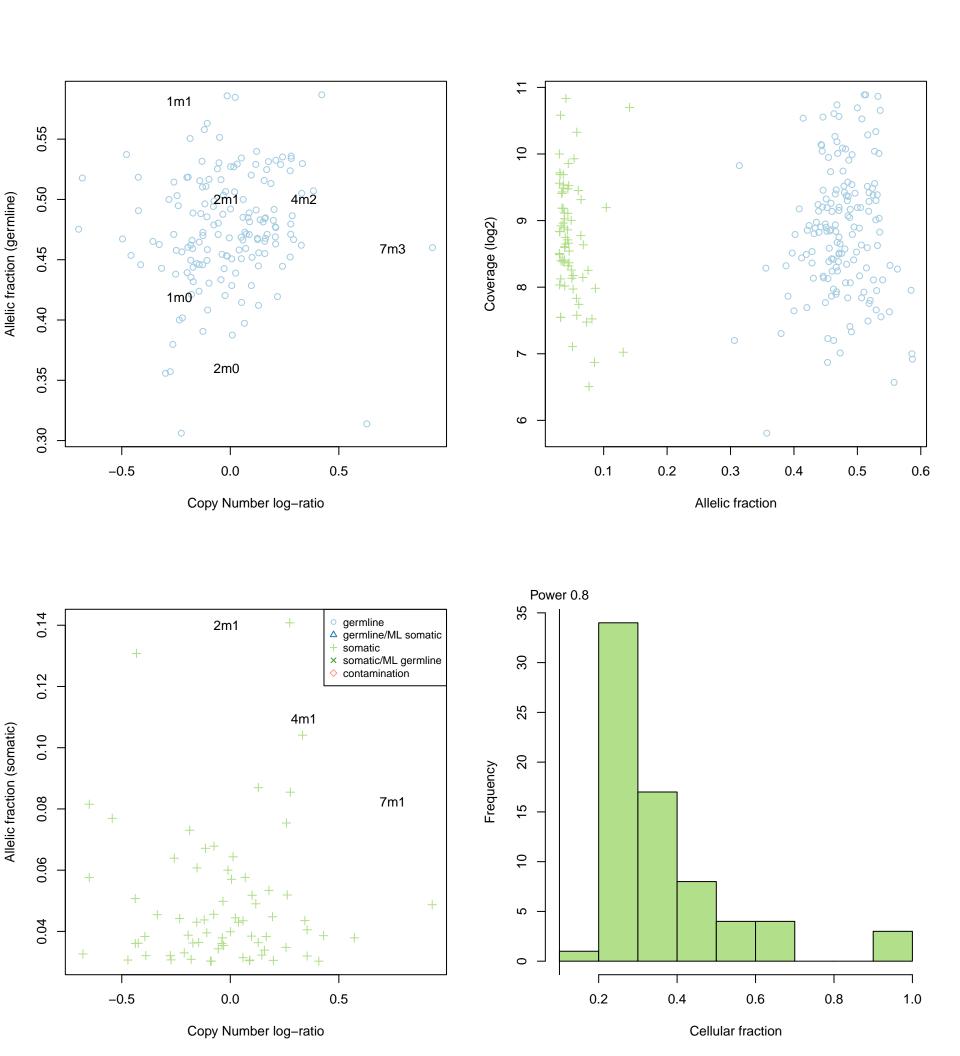




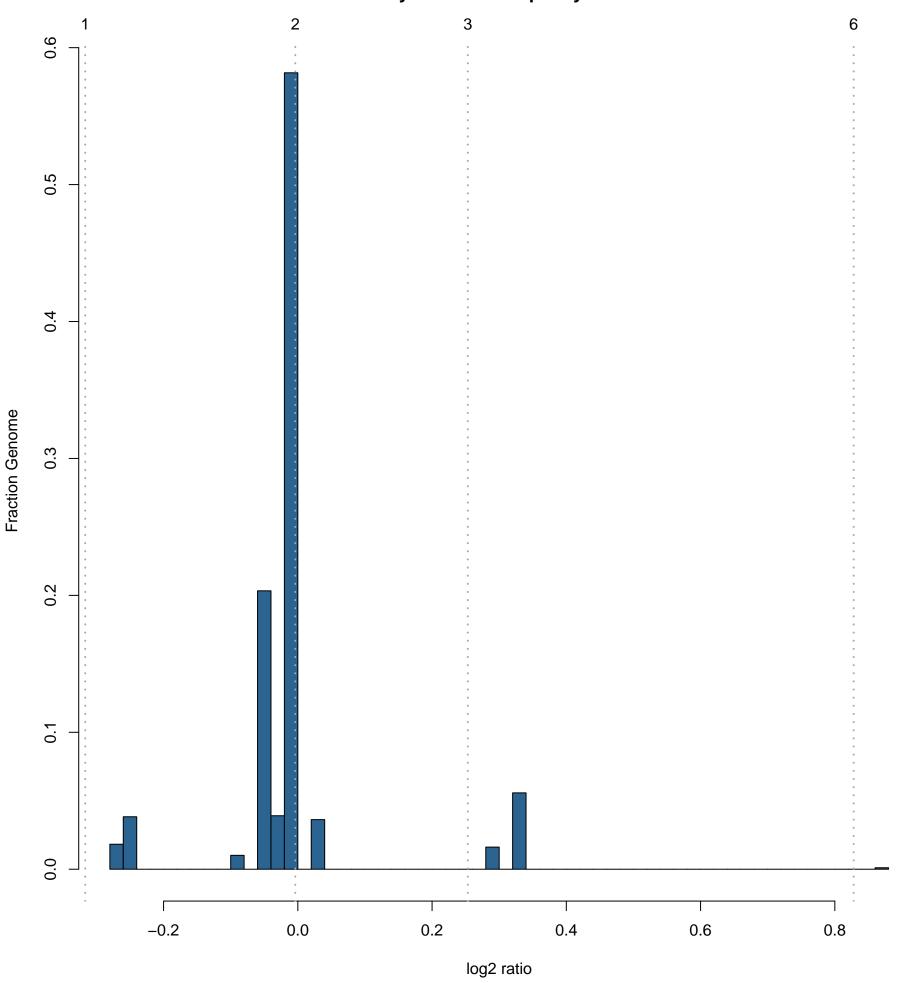
SCNA-fit log-likelihood: -10740.66

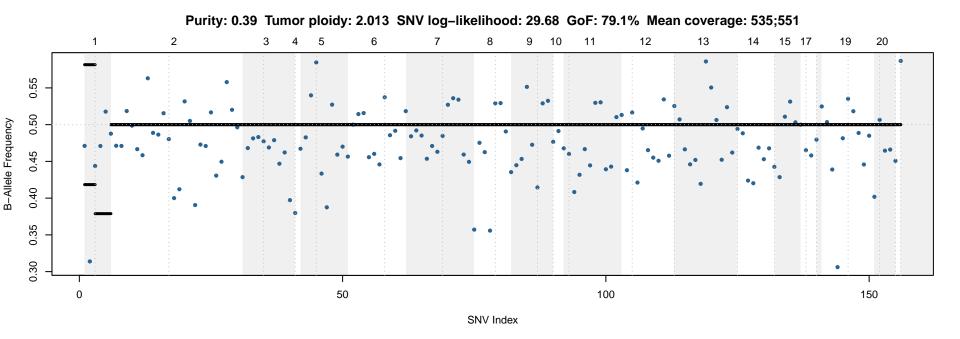




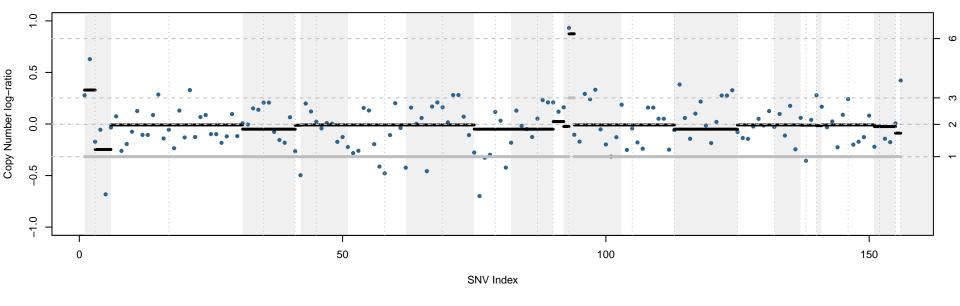


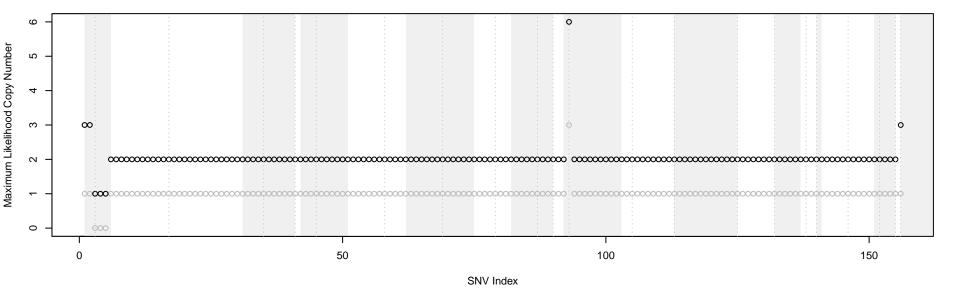
Purity: 0.39 Tumor ploidy: 2.013

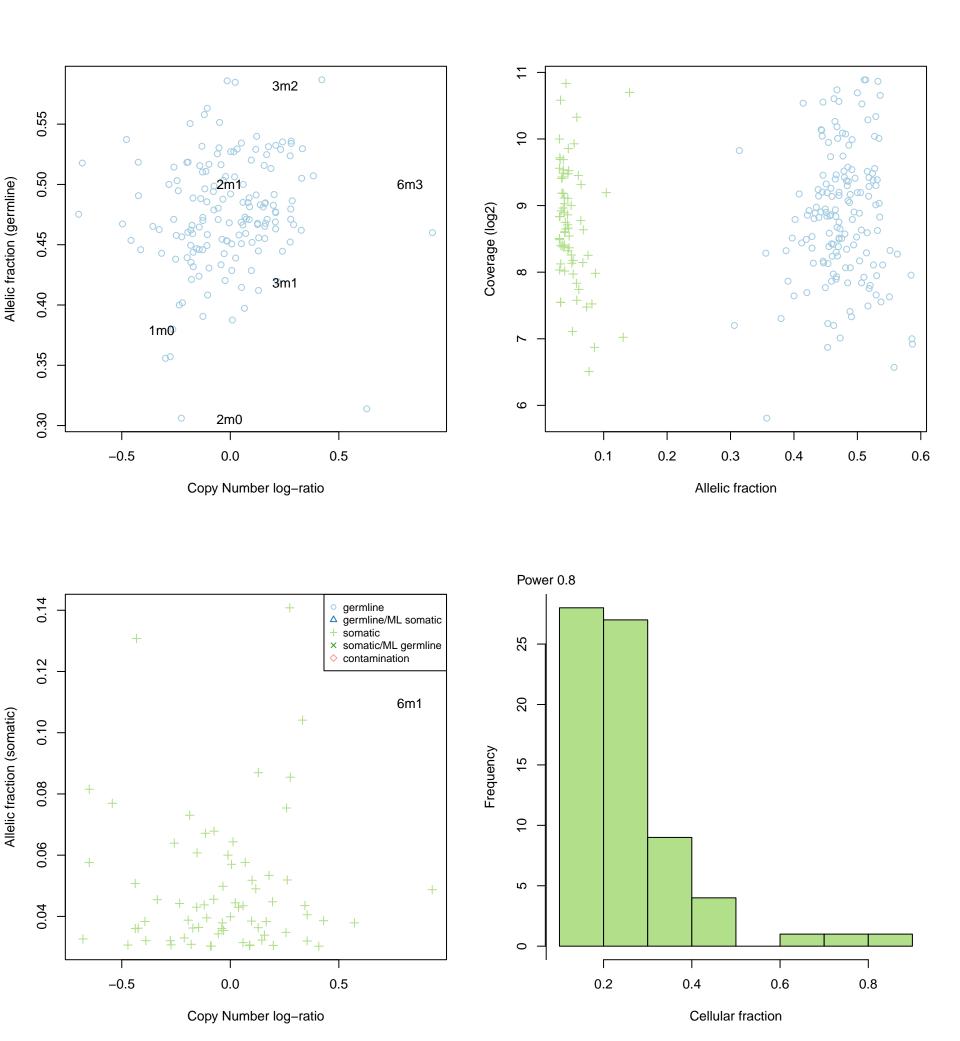




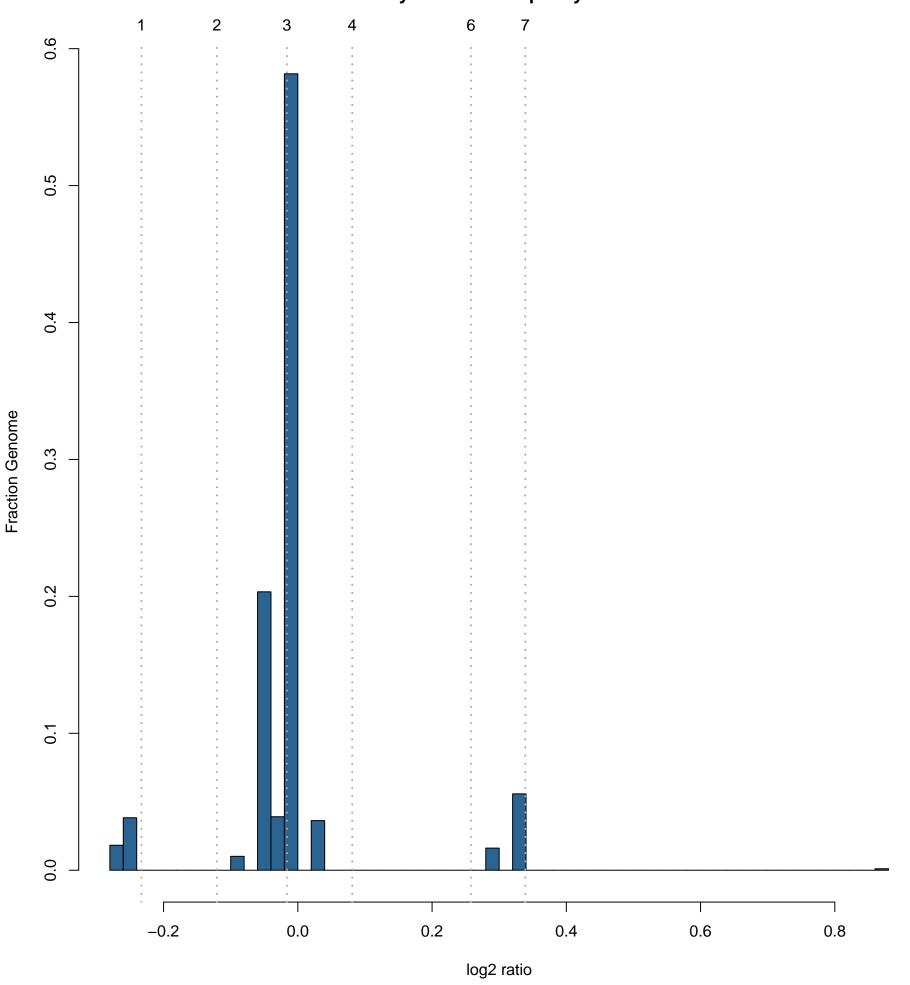
SCNA-fit log-likelihood: -10780.04

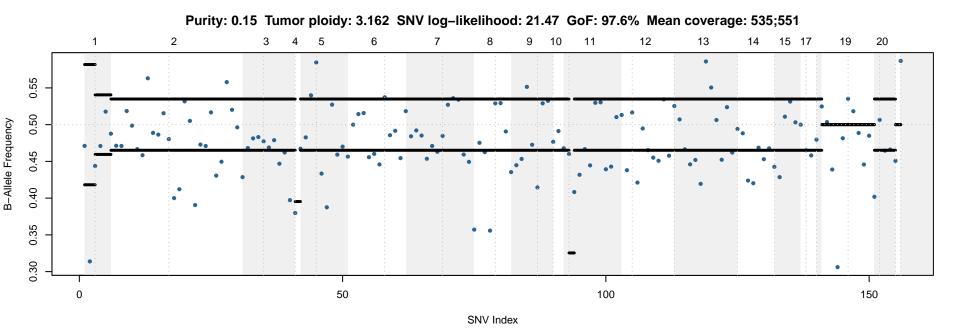




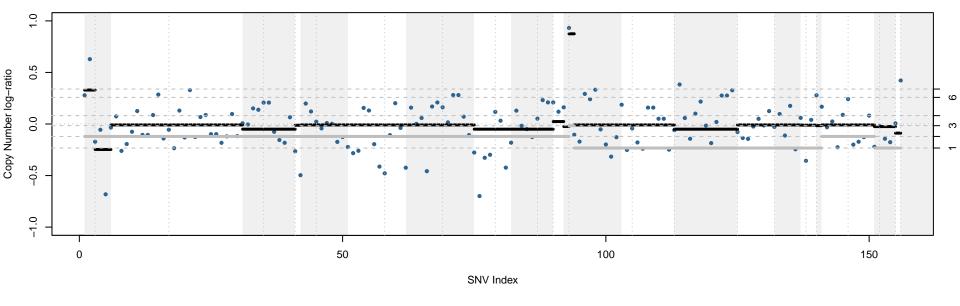


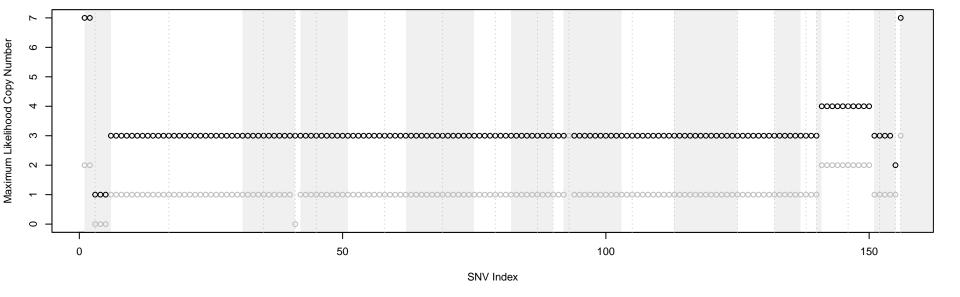
Purity: 0.15 Tumor ploidy: 3.162

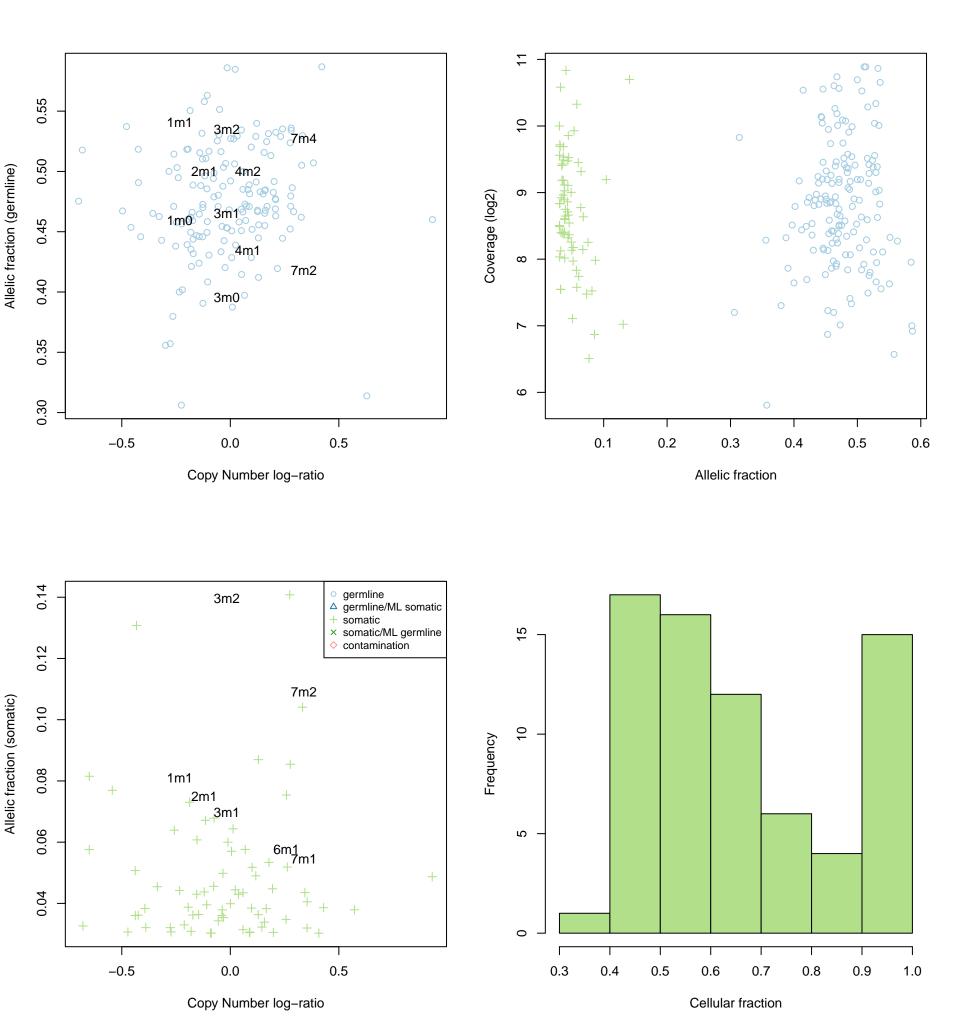




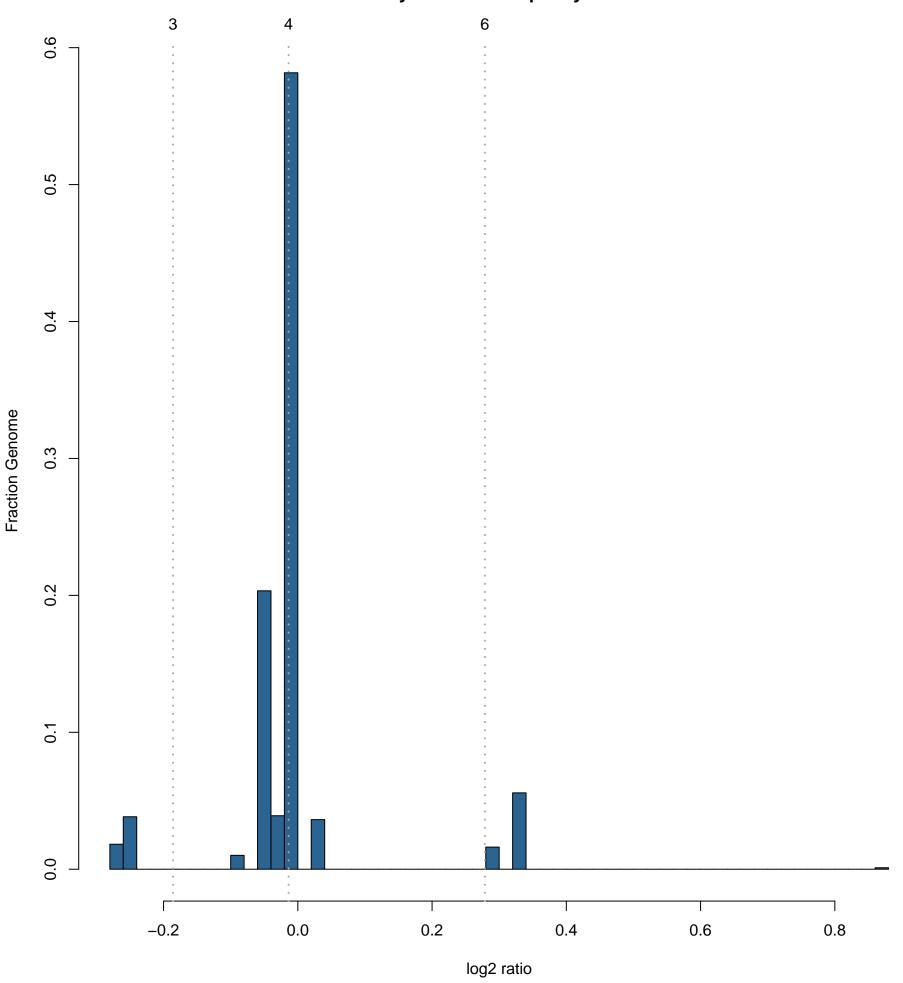
SCNA-fit log-likelihood: -10762.96

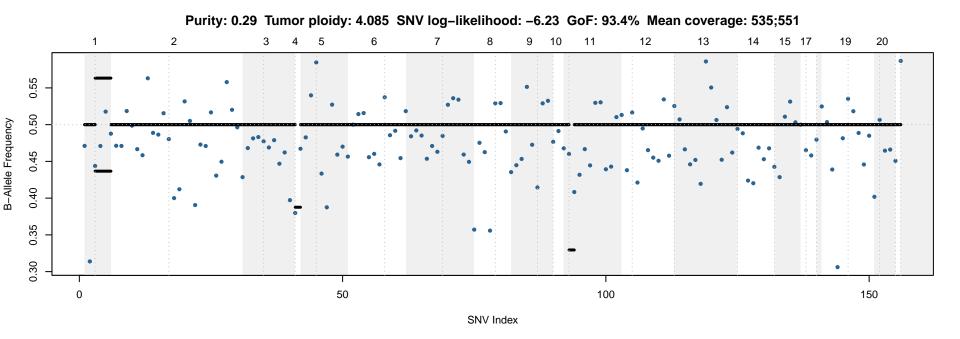




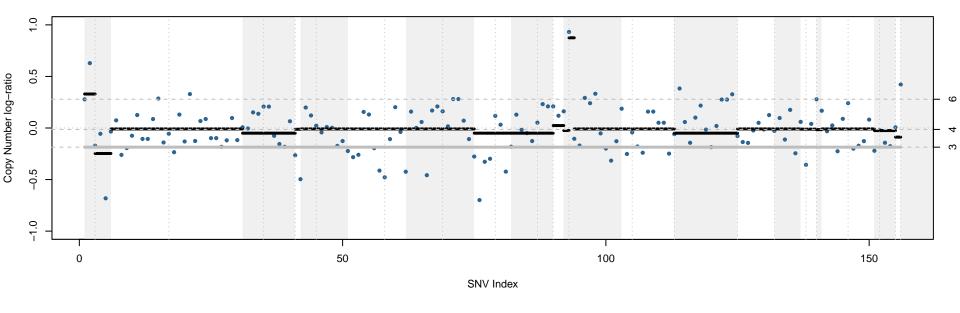


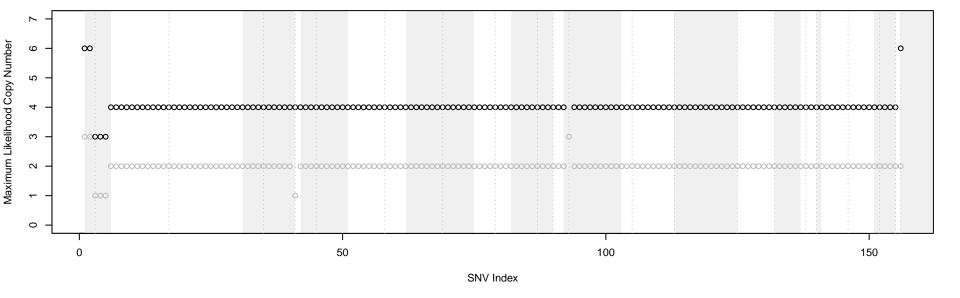
Purity: 0.29 Tumor ploidy: 4.085

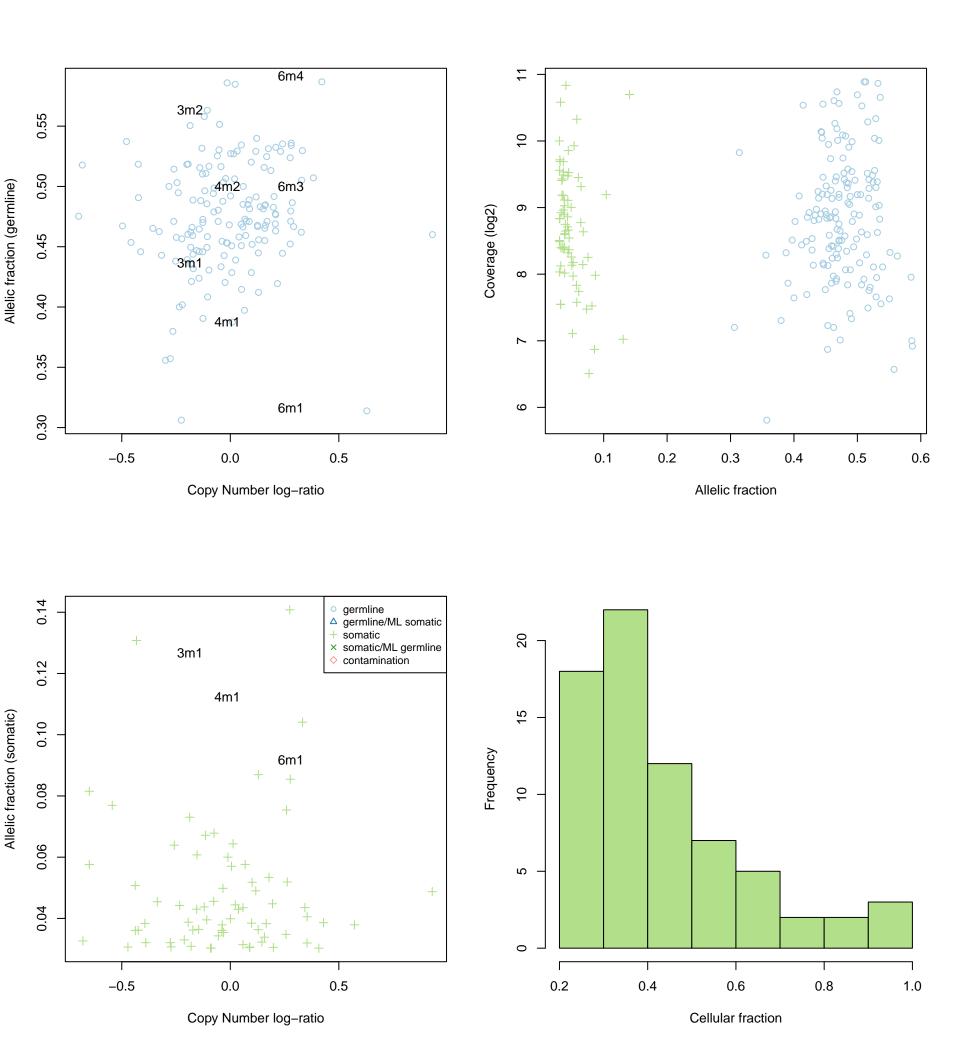




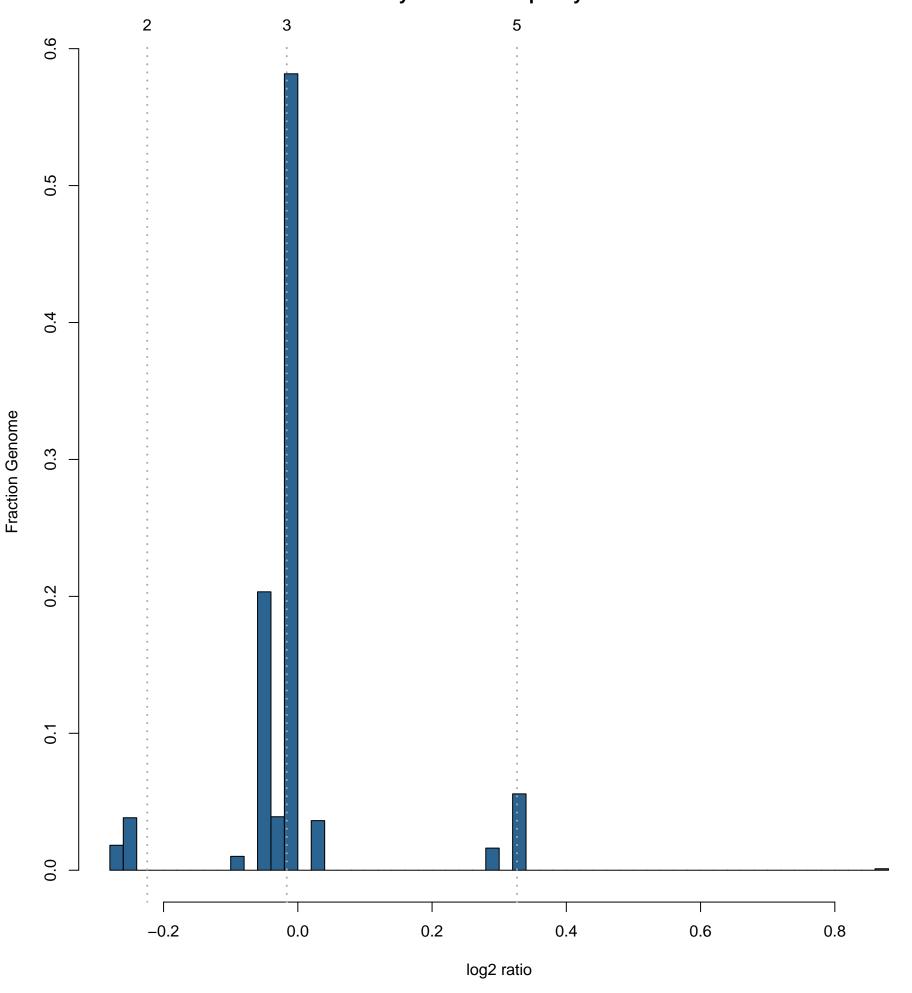
SCNA-fit log-likelihood: -10789.2

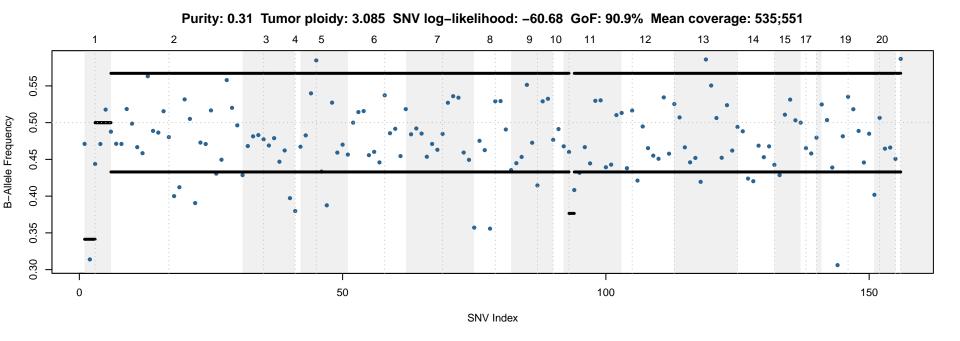




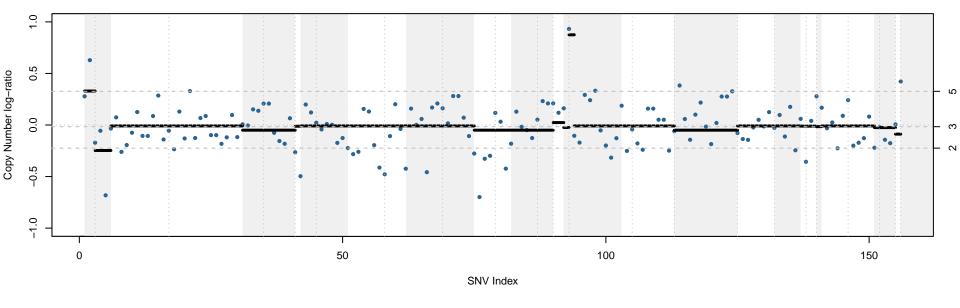


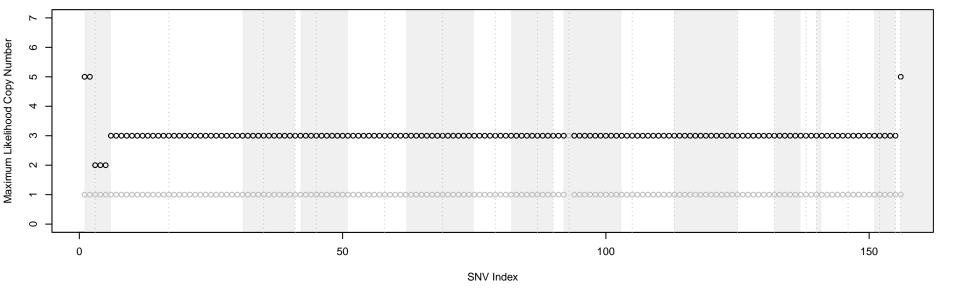
Purity: 0.31 Tumor ploidy: 3.085

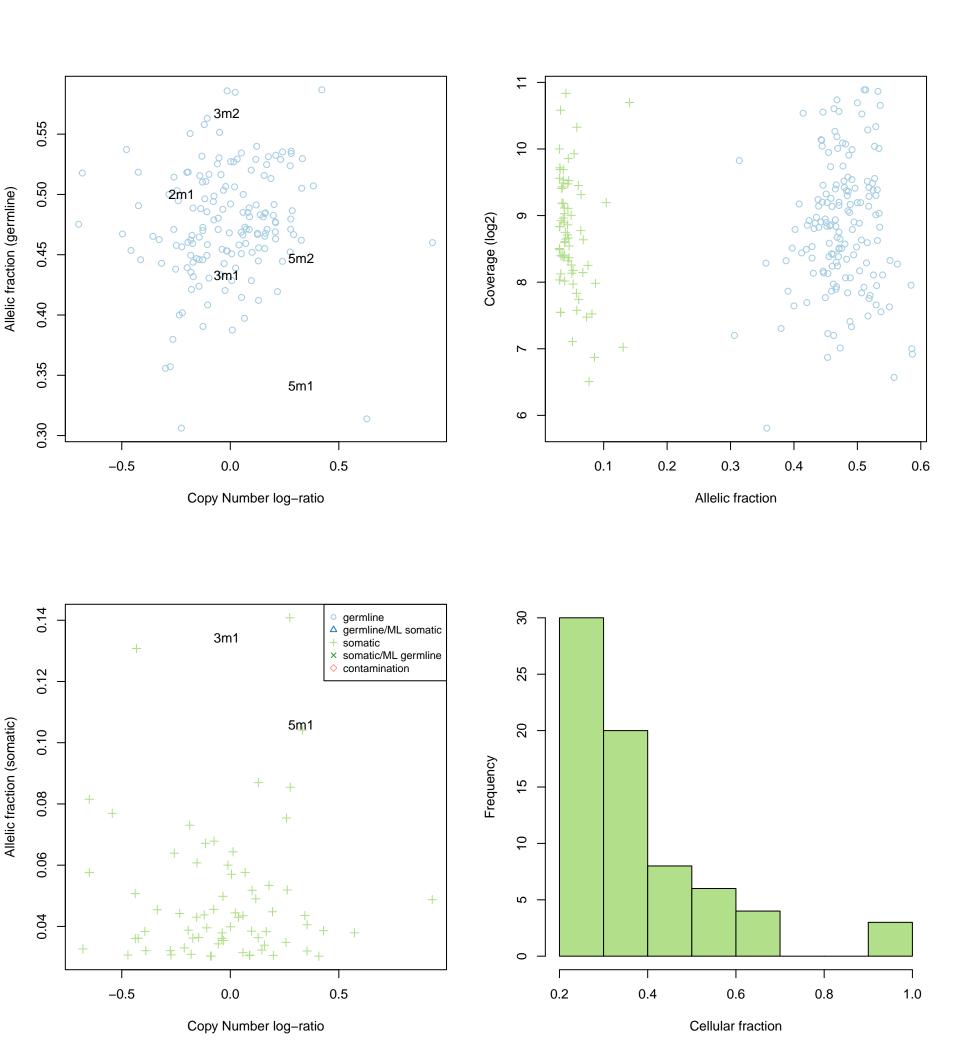




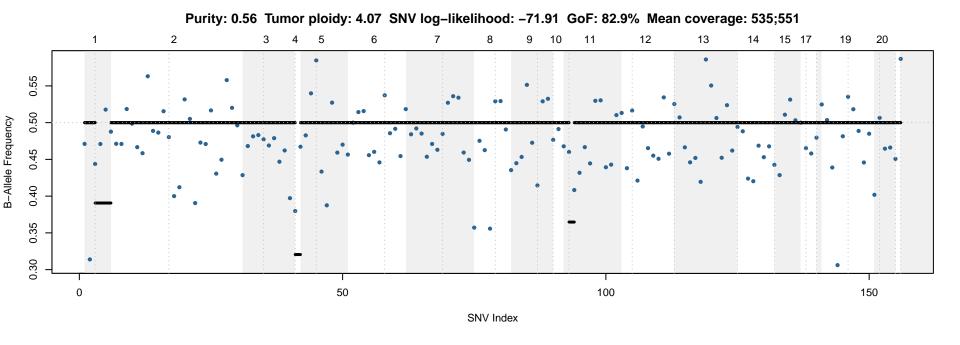
SCNA-fit log-likelihood: -10768.88



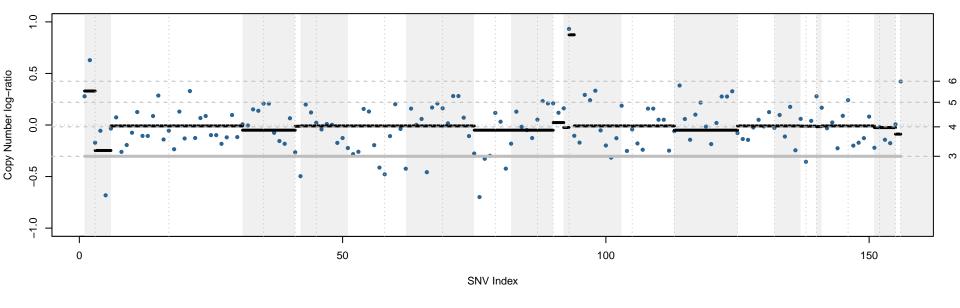


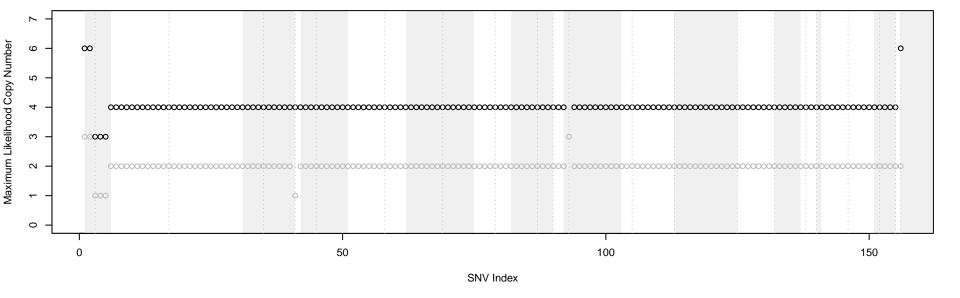


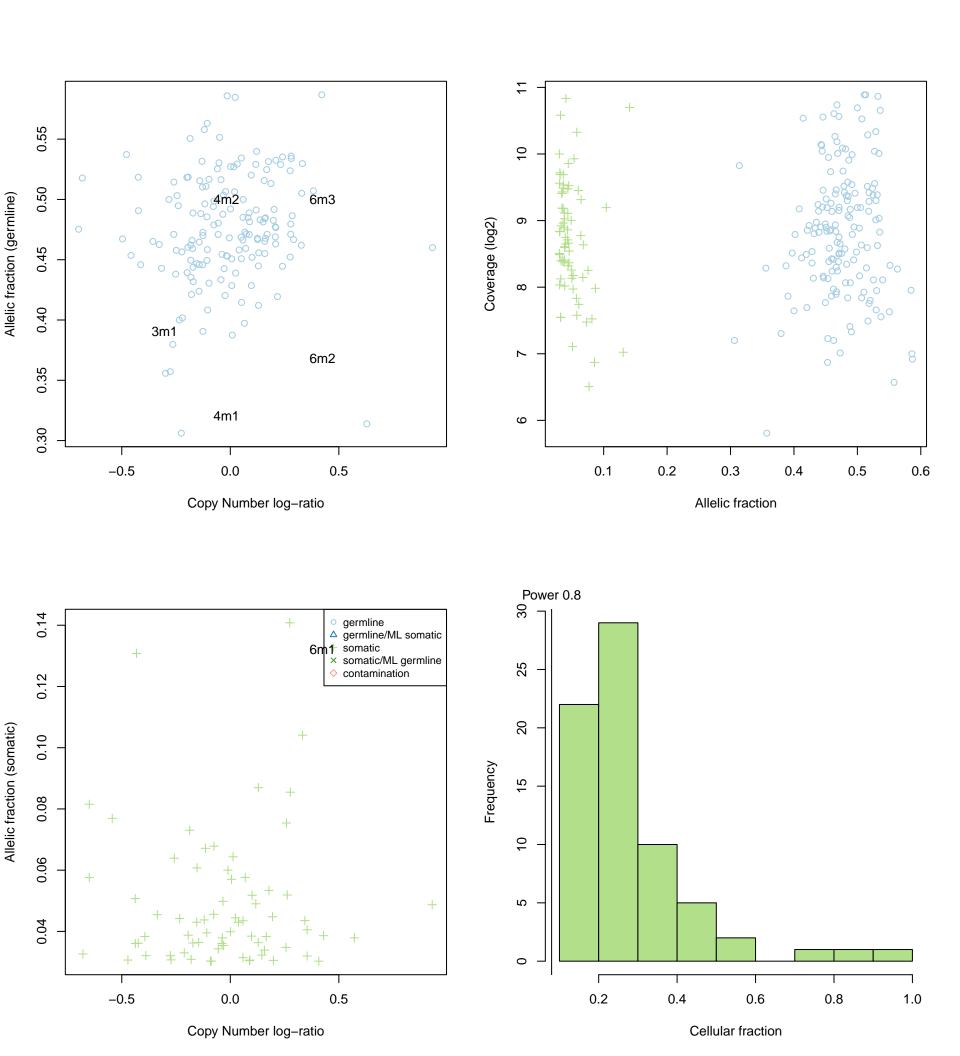
Purity: 0.56 Tumor ploidy: 4.07 6 3 9.0 0.5 Fraction Genome 0.3 0.2 0.1 0.0 -0.2 0.0 0.2 0.4 0.6 8.0 log2 ratio



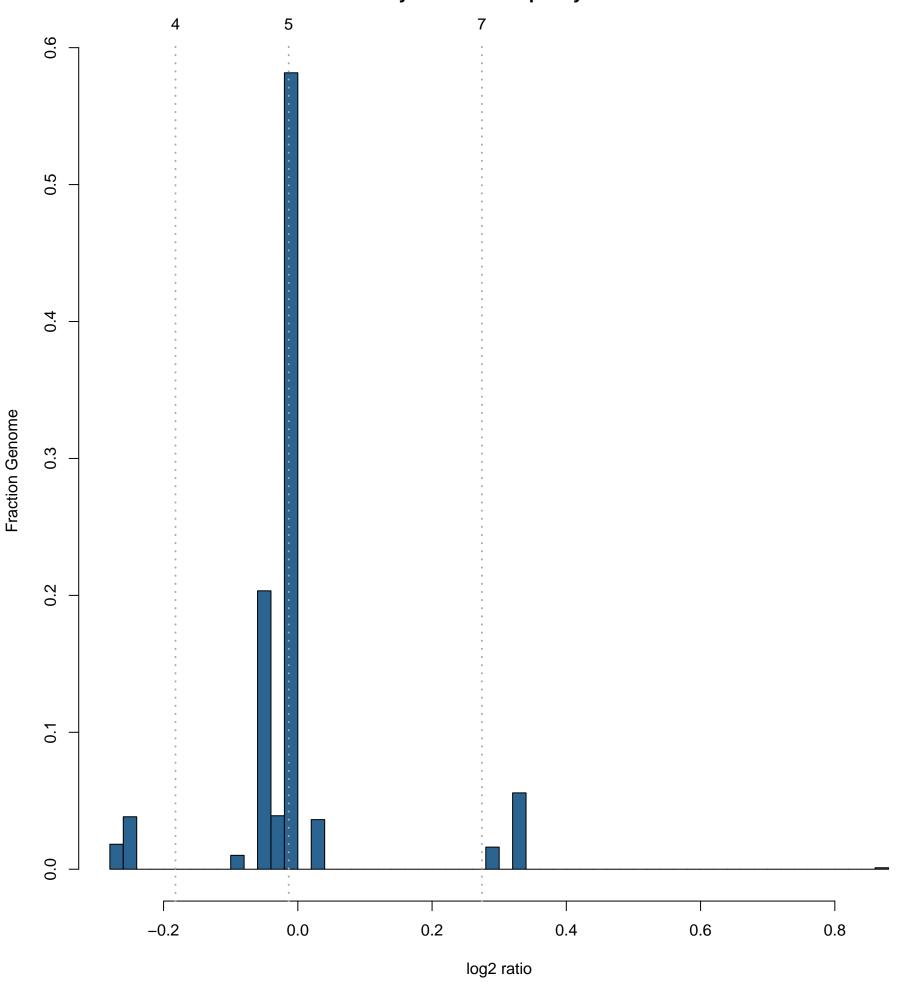
SCNA-fit log-likelihood: -10803.53

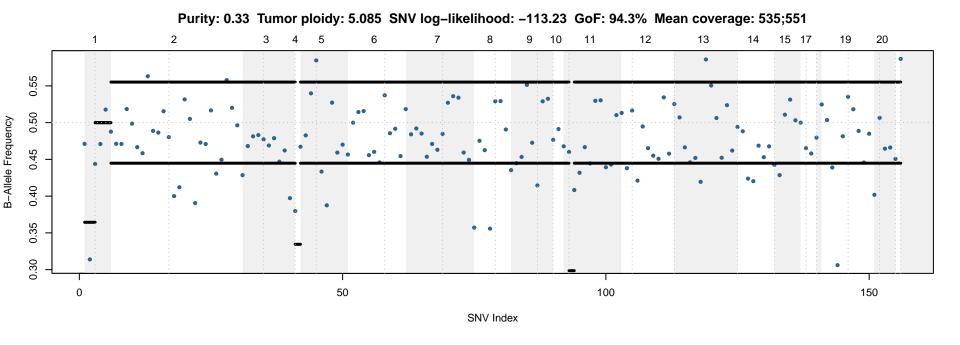




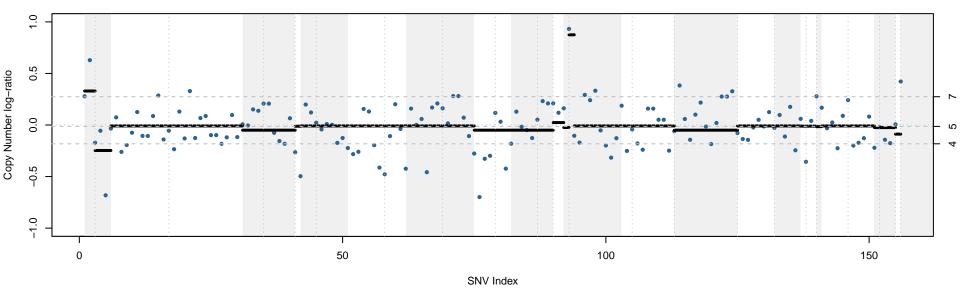


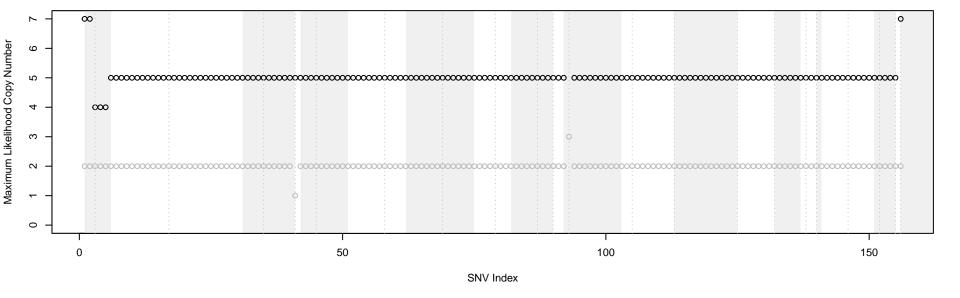
Purity: 0.33 Tumor ploidy: 5.085

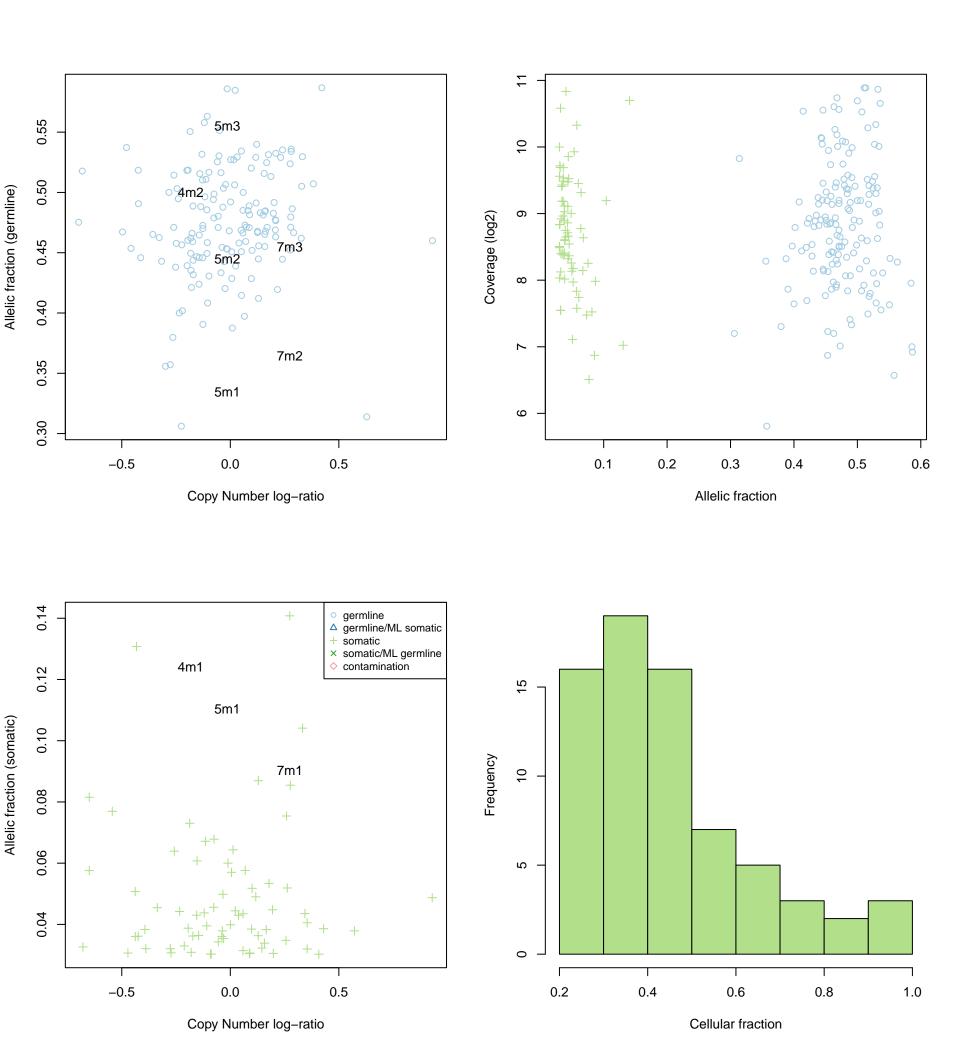




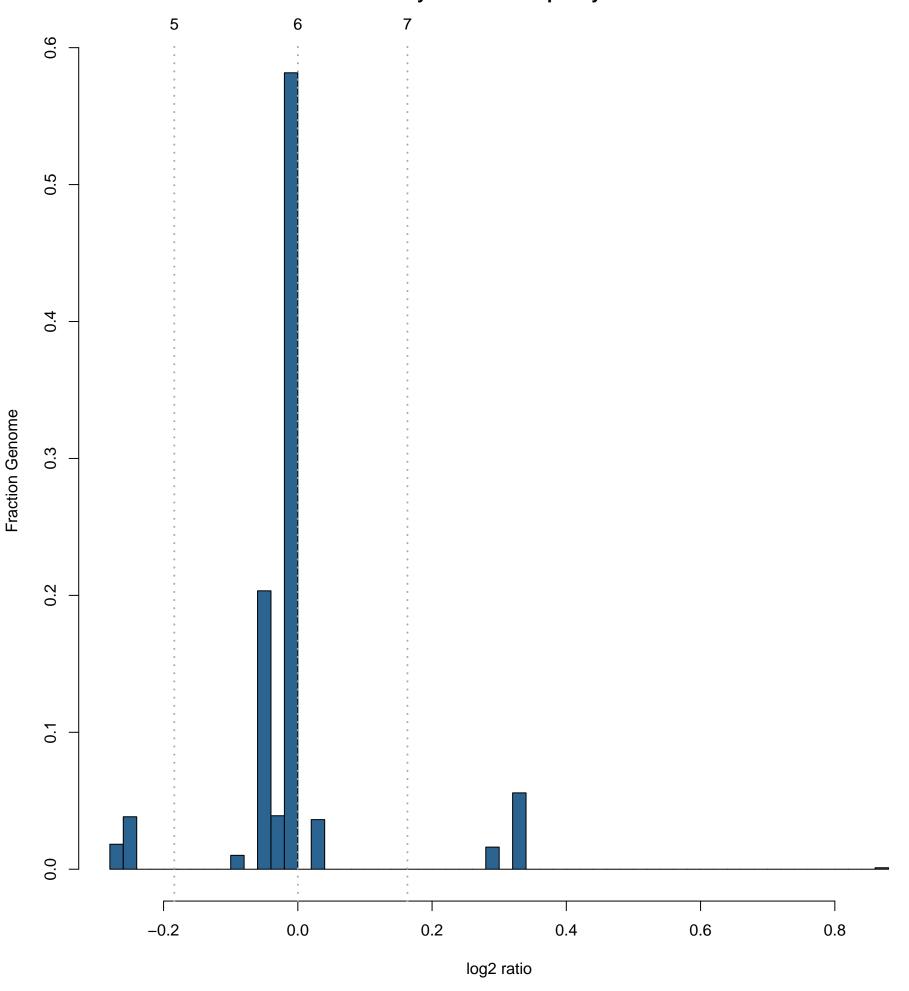
SCNA-fit log-likelihood: -10792.69

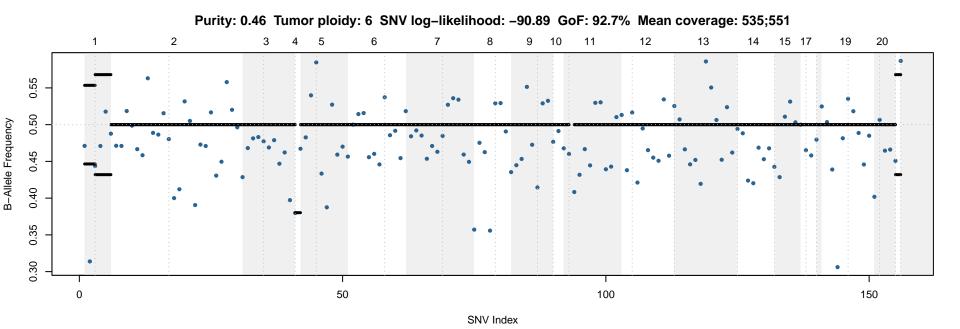




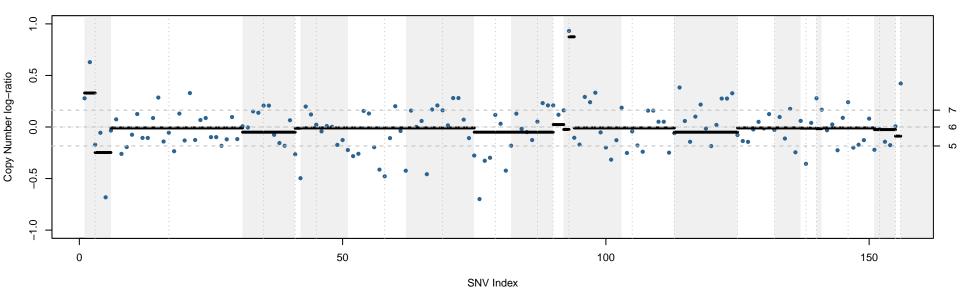


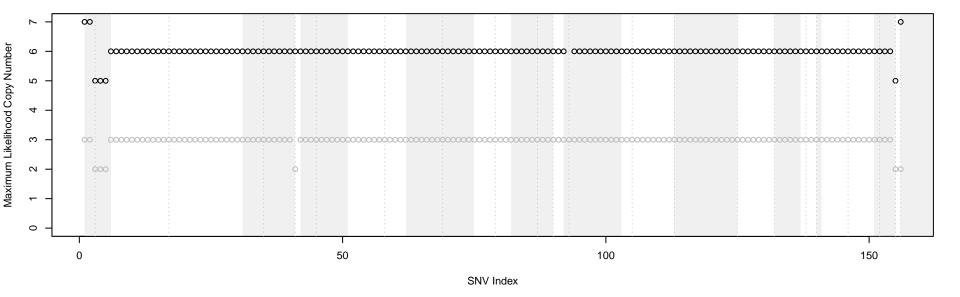
Purity: 0.46 Tumor ploidy: 6

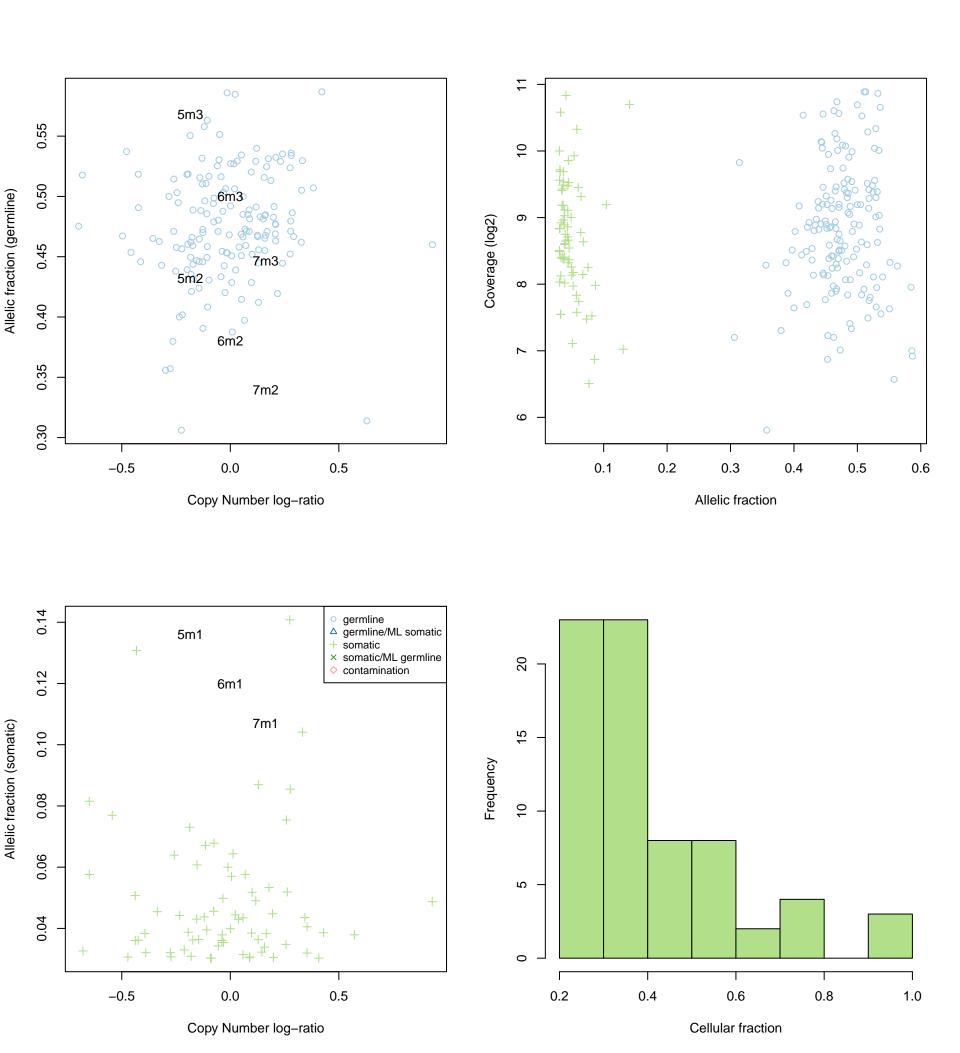




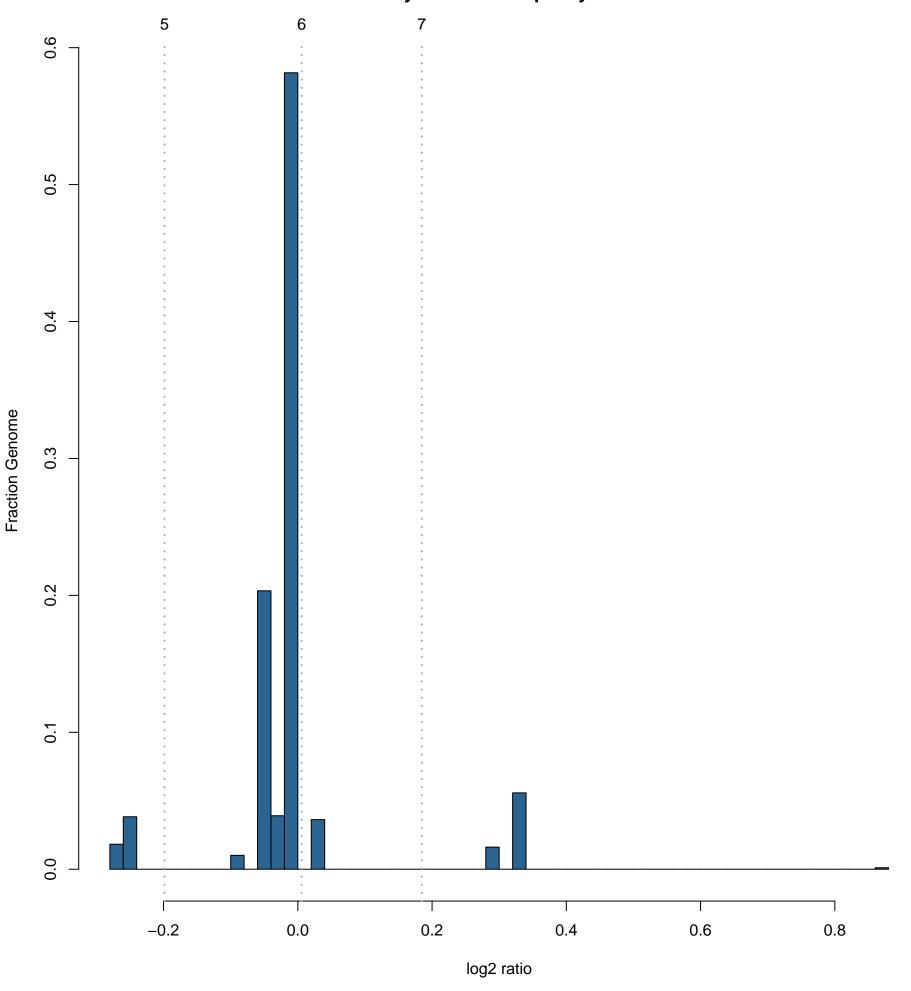
SCNA-fit log-likelihood: -10904.09

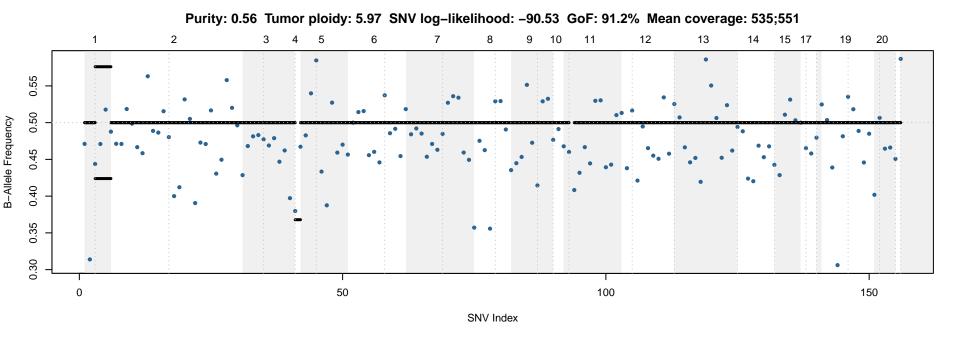




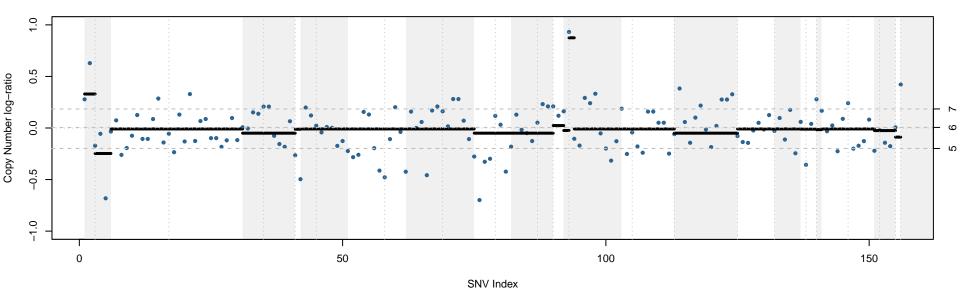


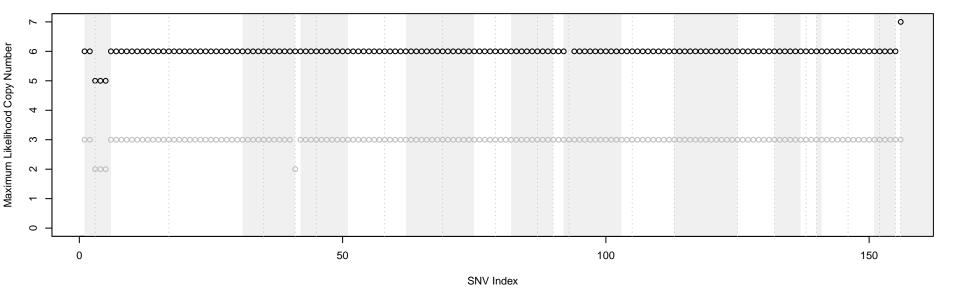
Purity: 0.56 Tumor ploidy: 5.97

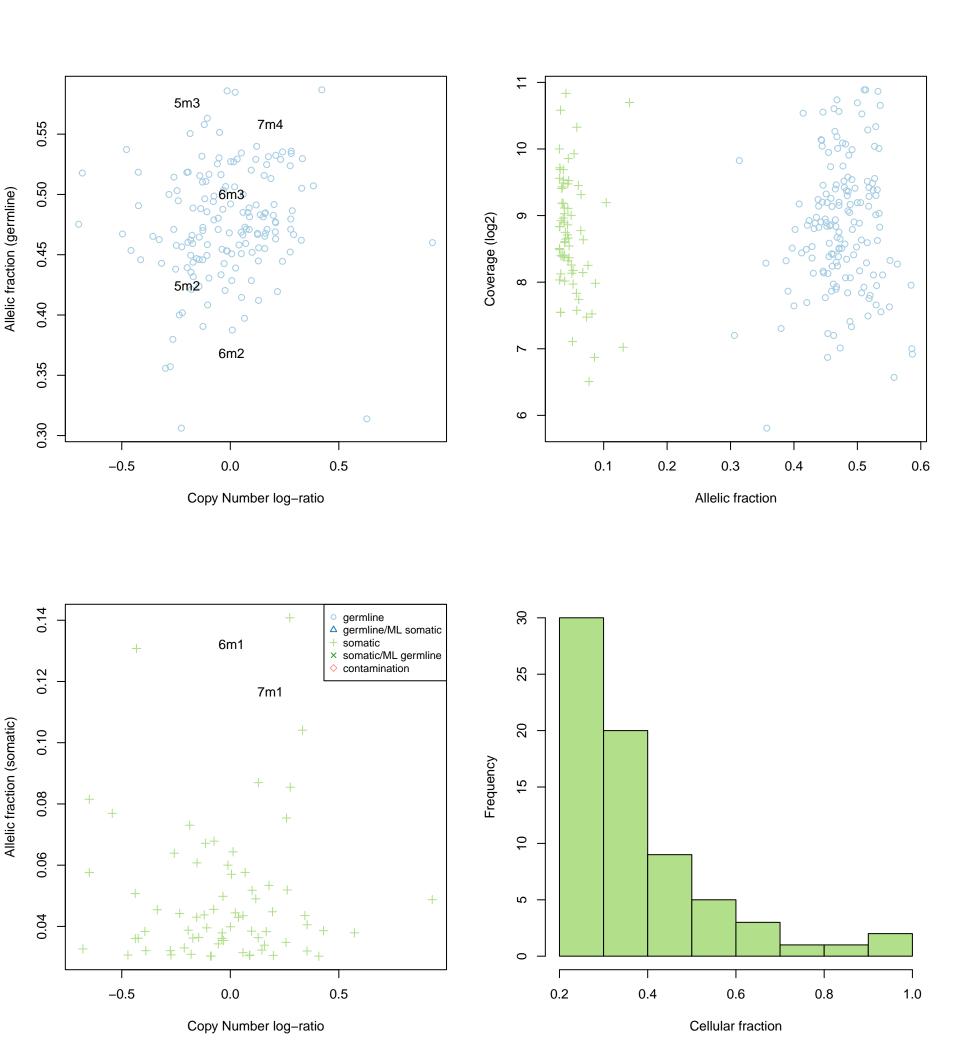




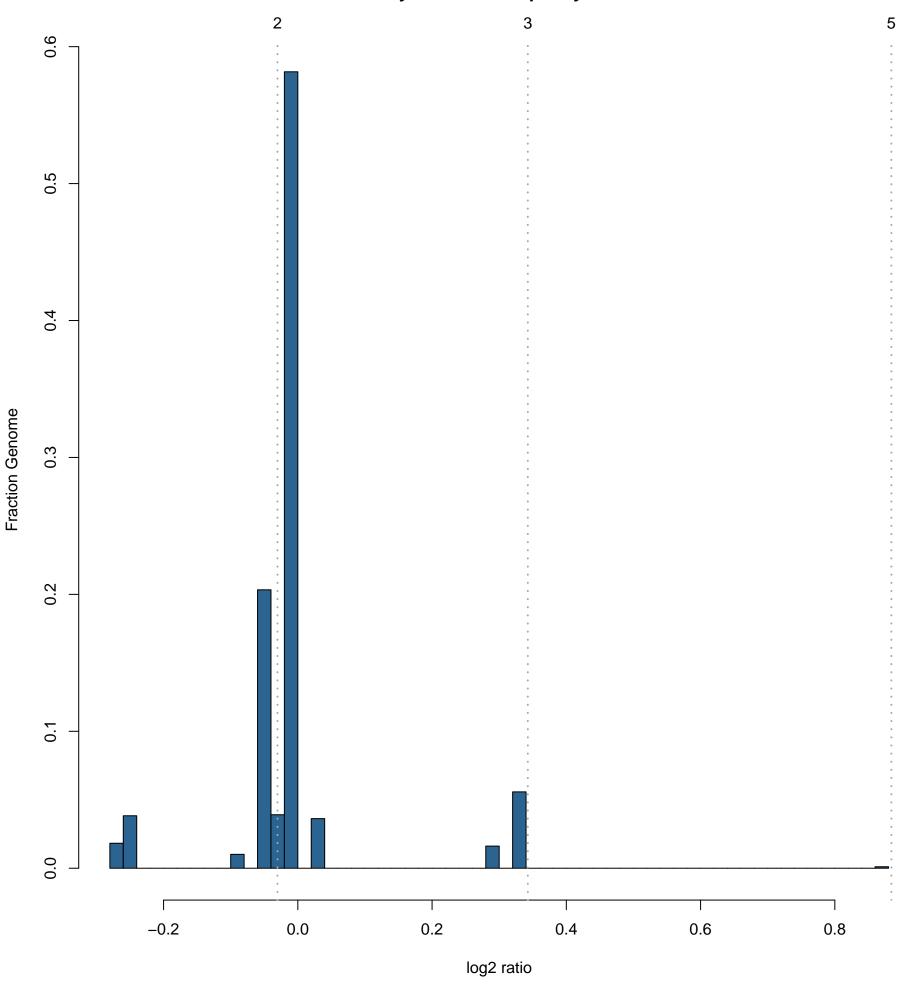
SCNA-fit log-likelihood: -11080.37

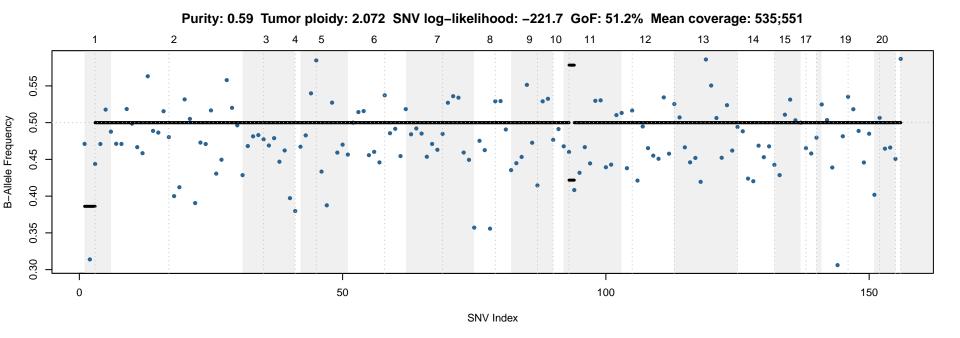




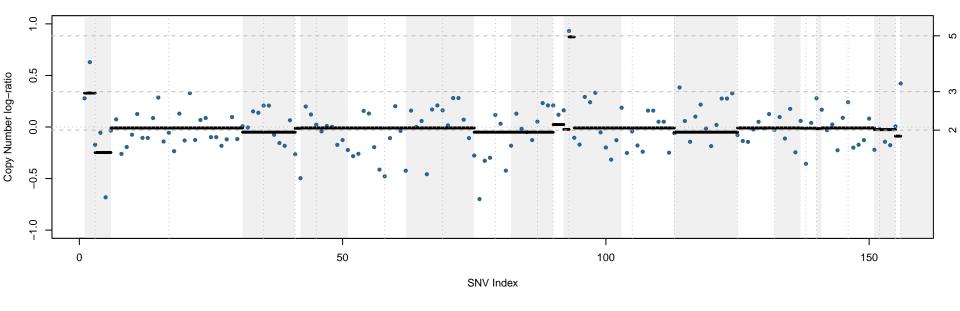


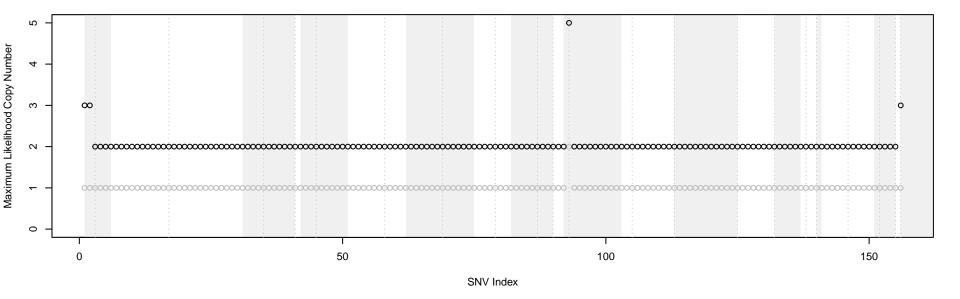
Purity: 0.59 Tumor ploidy: 2.072

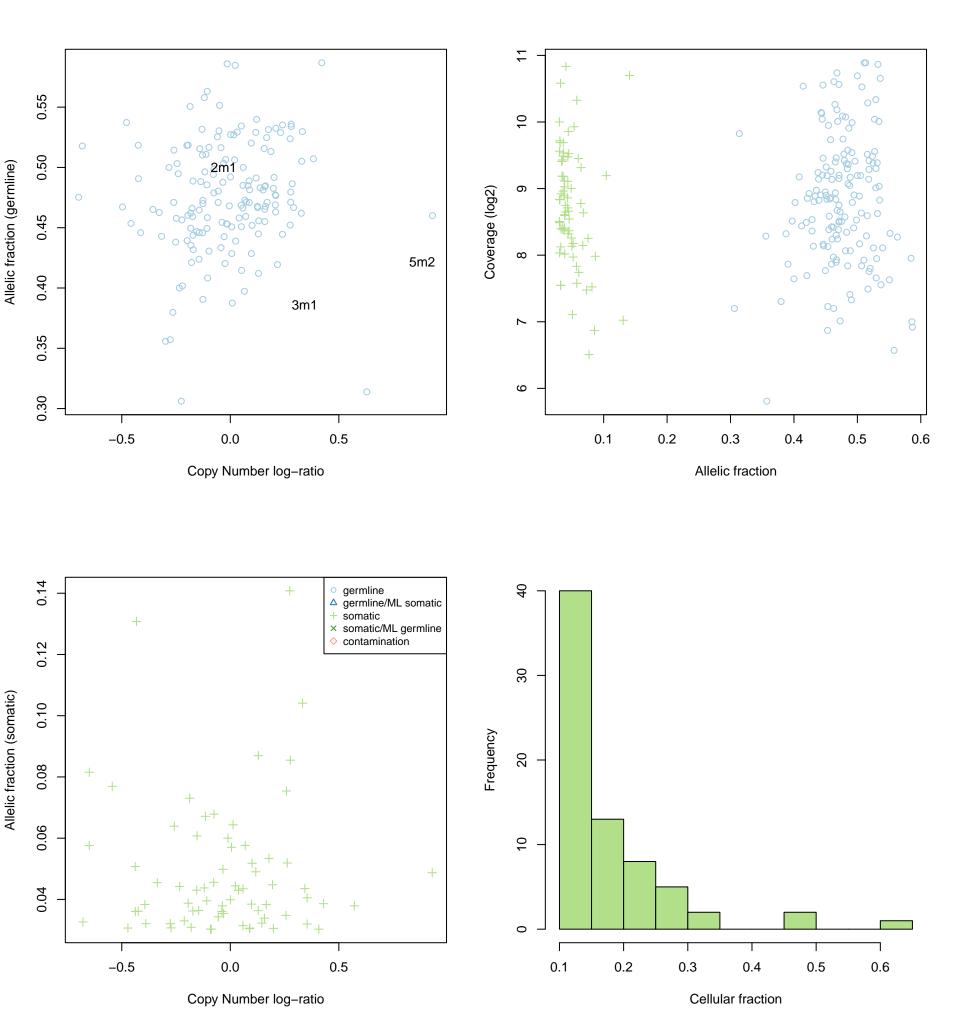




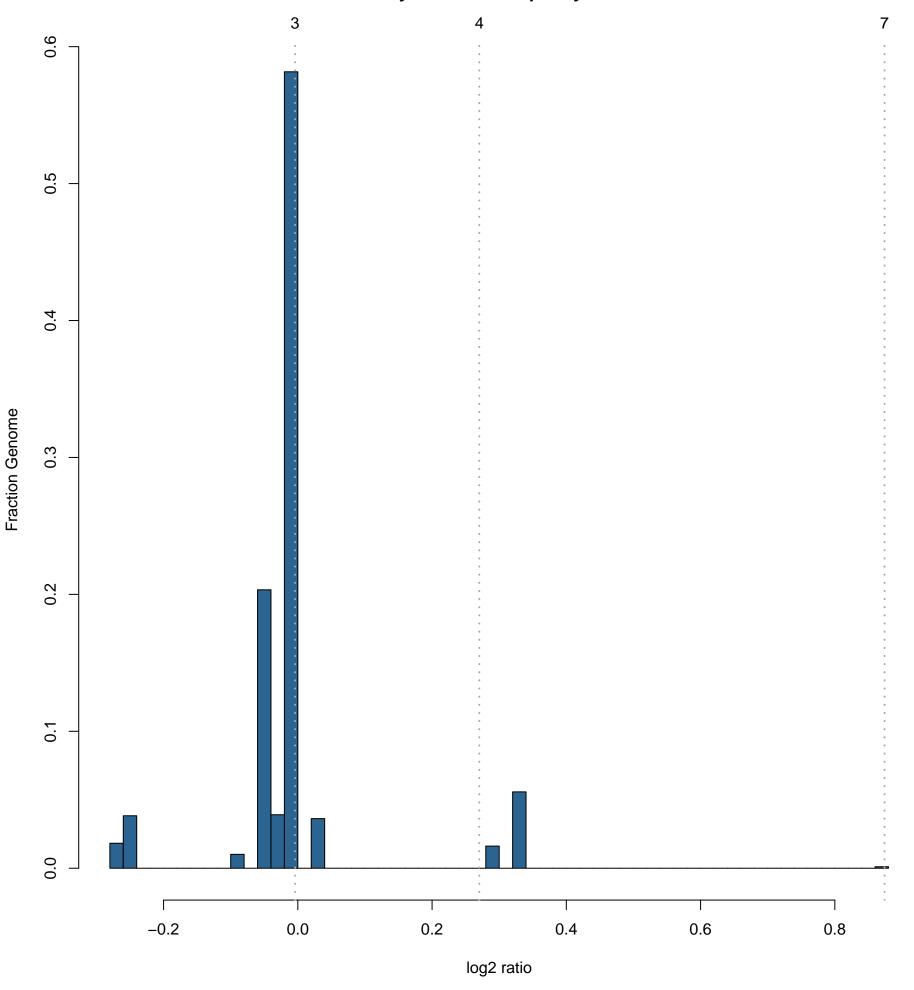
SCNA-fit log-likelihood: -10913.36

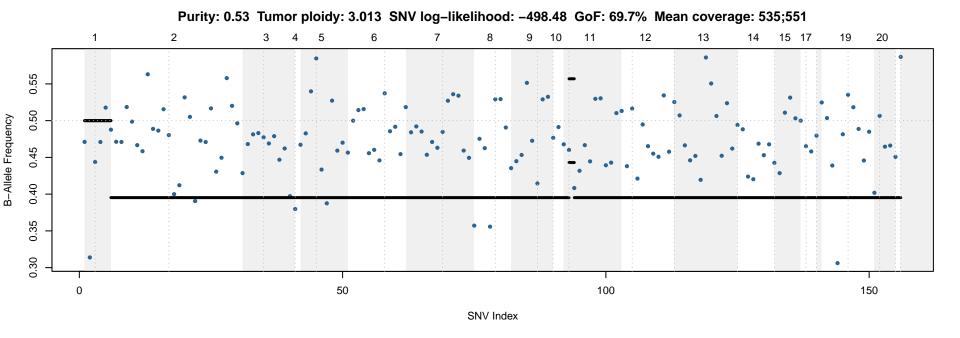




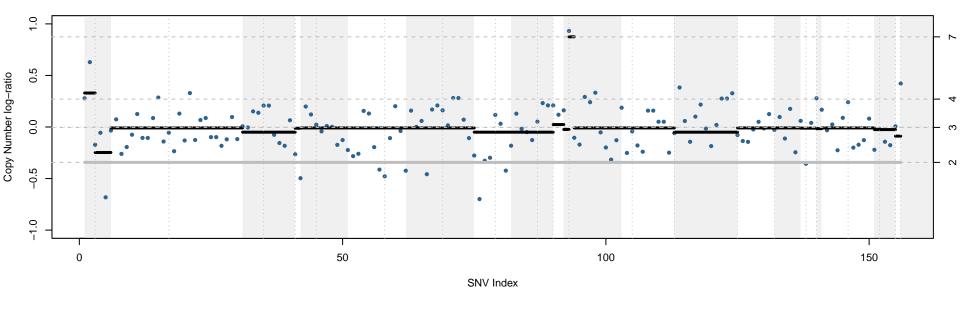


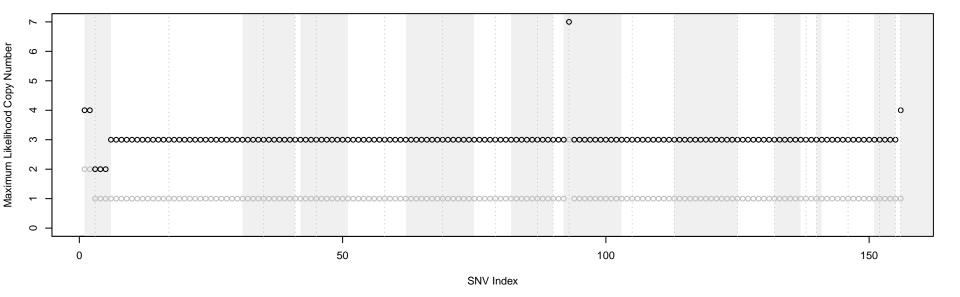
Purity: 0.53 Tumor ploidy: 3.013

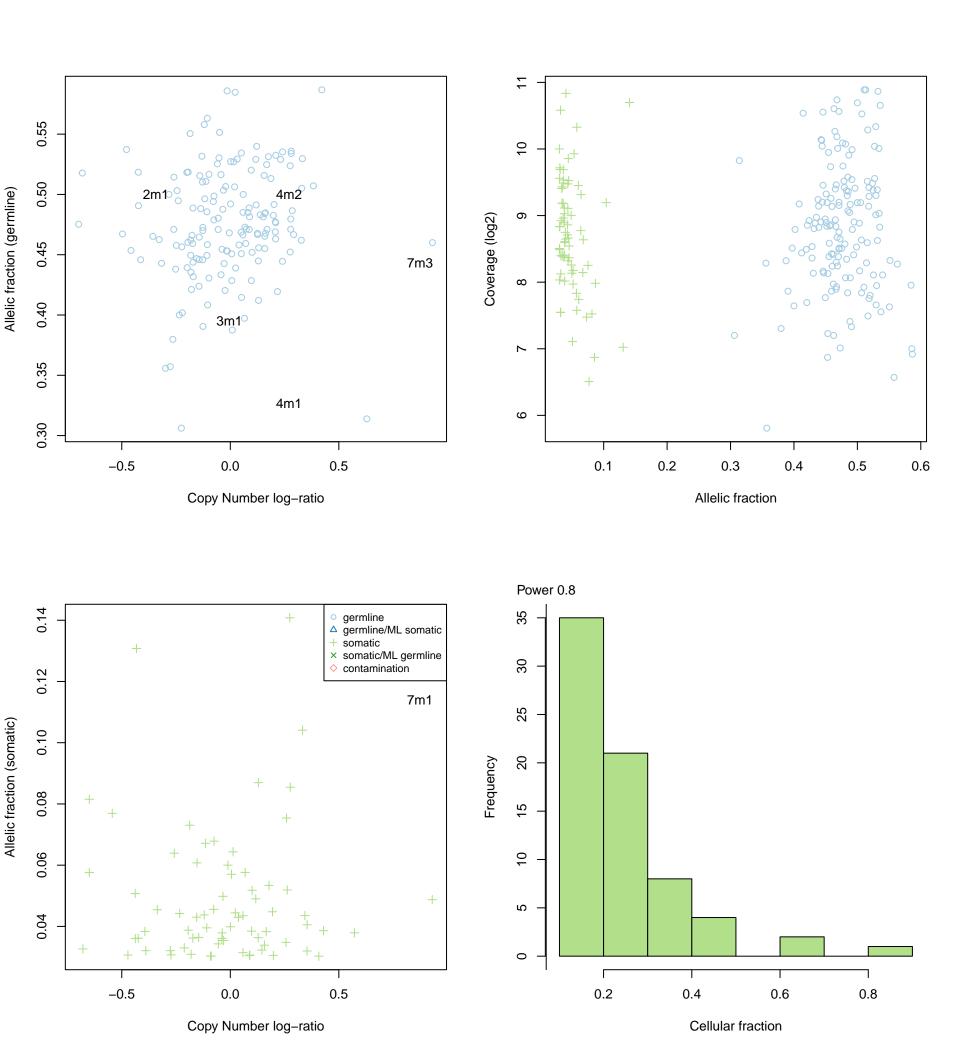




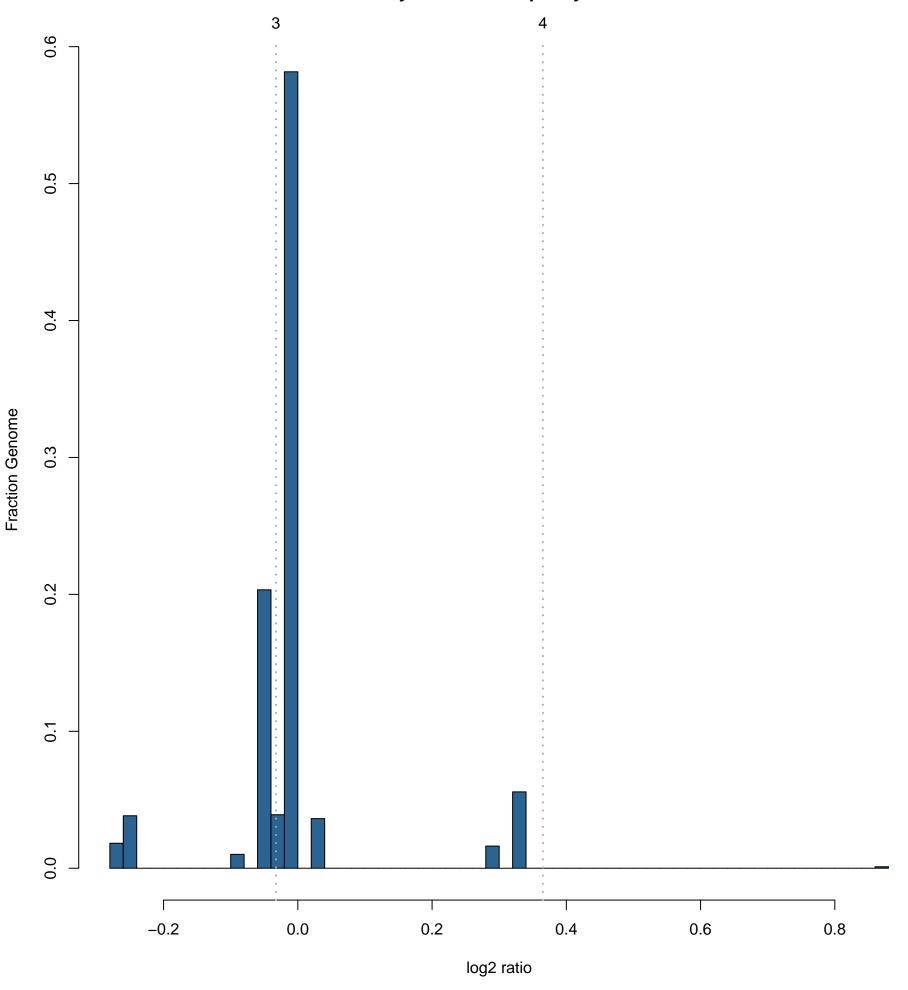
SCNA-fit log-likelihood: -10784.3

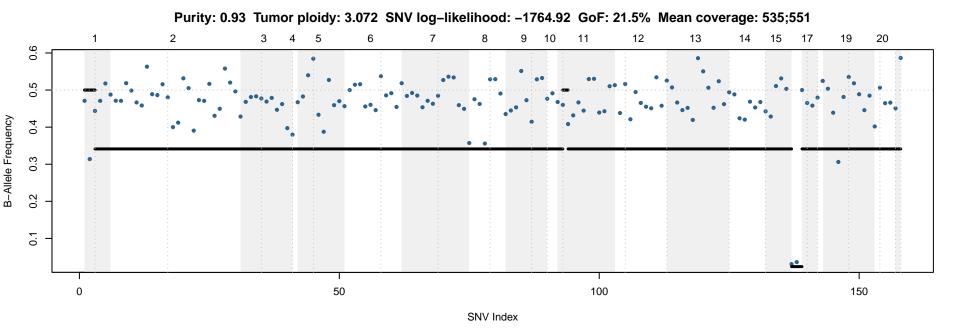






Purity: 0.93 Tumor ploidy: 3.072





SCNA-fit log-likelihood: -10920.67

