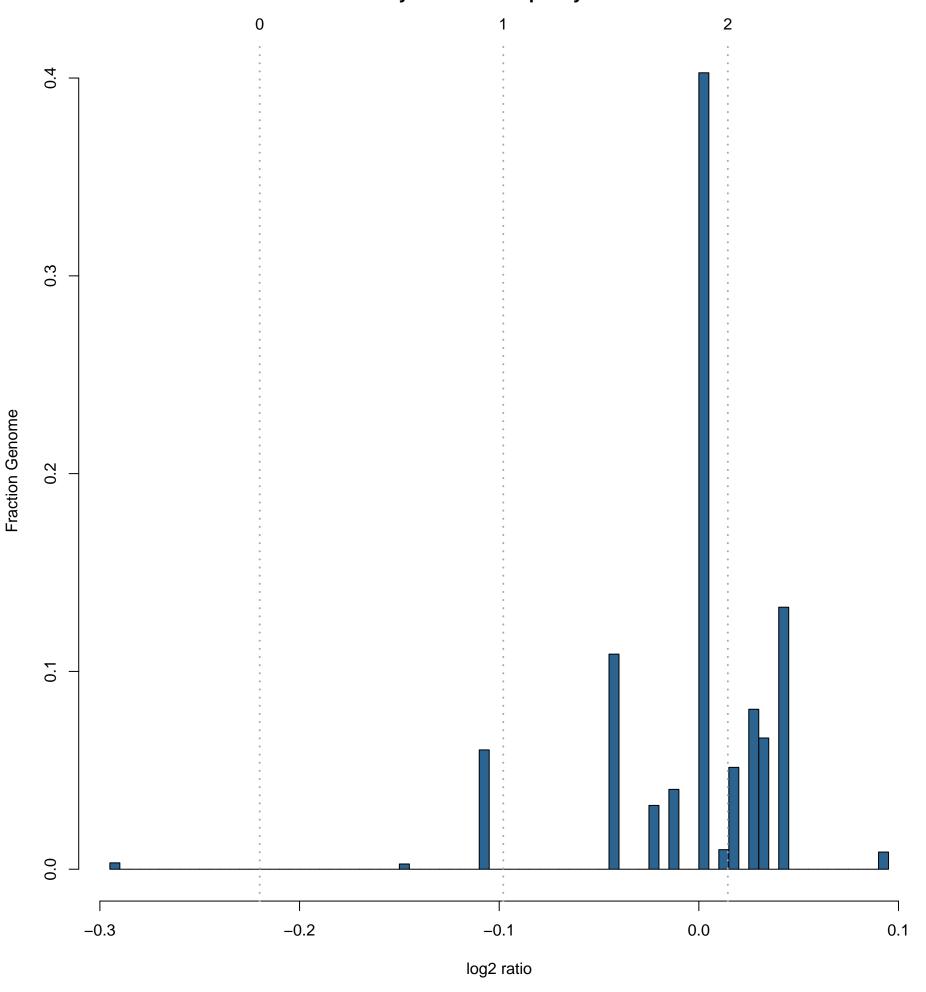
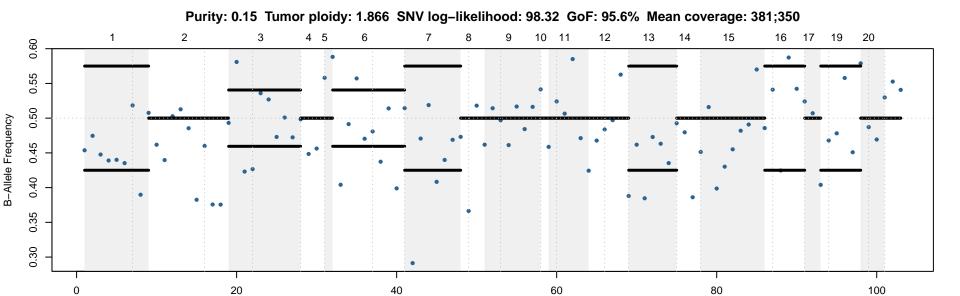
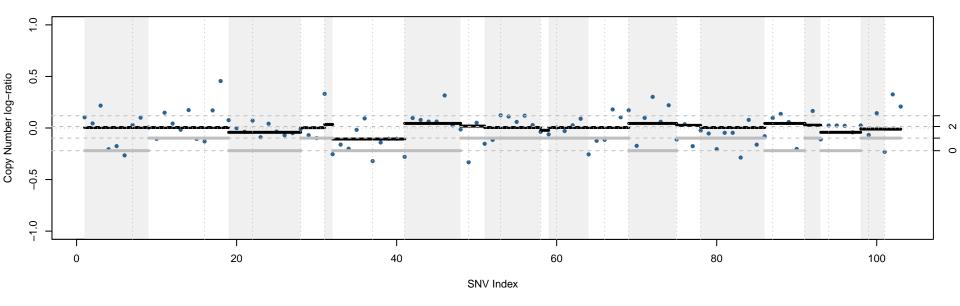
Purity: 0.15 Tumor ploidy: 1.866

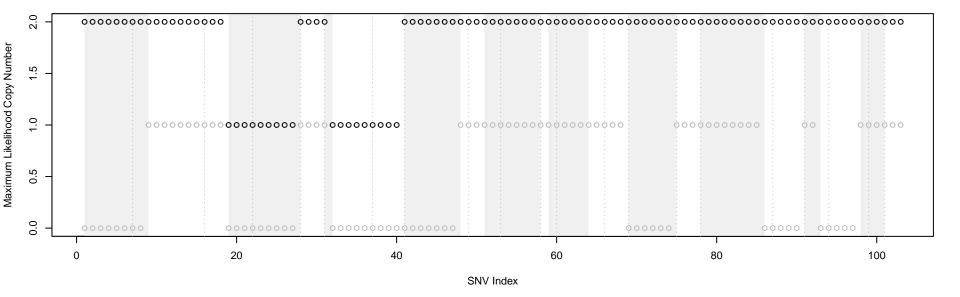


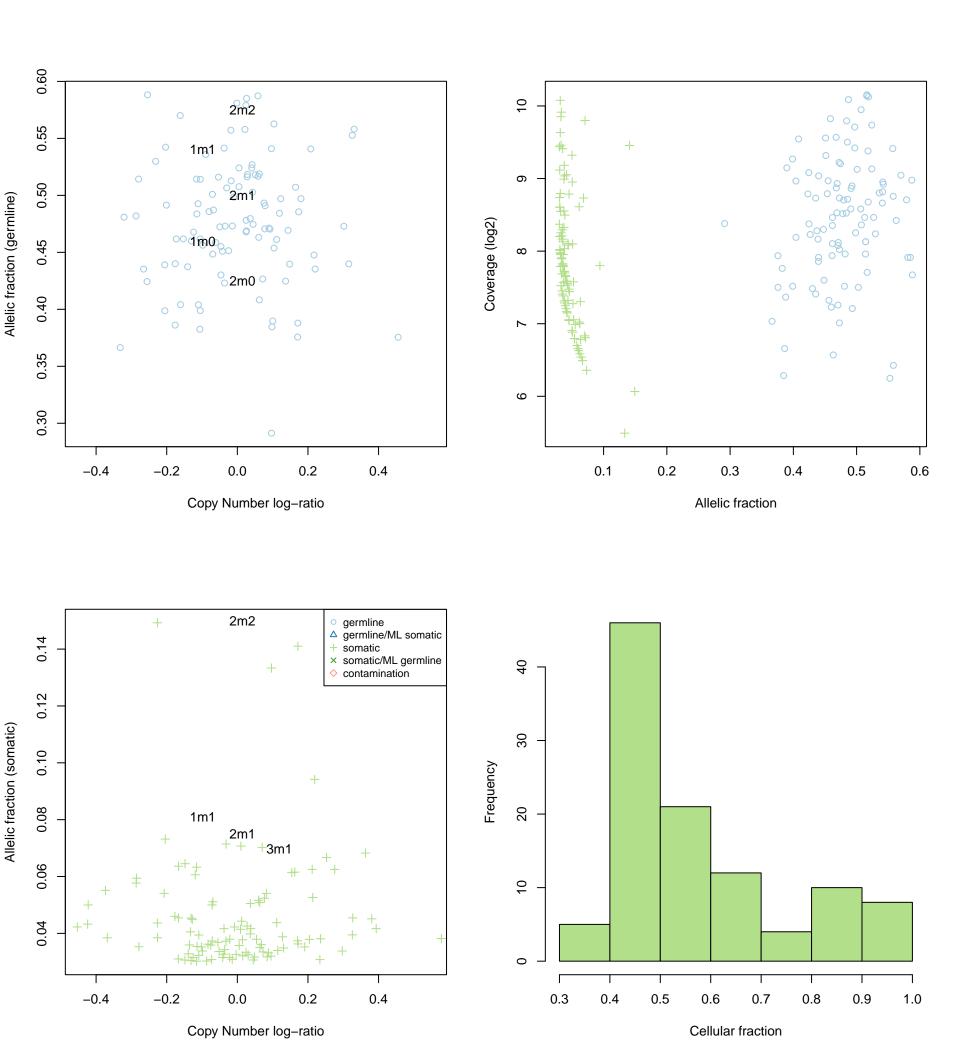


SCNA-fit log-likelihood: -9219.39

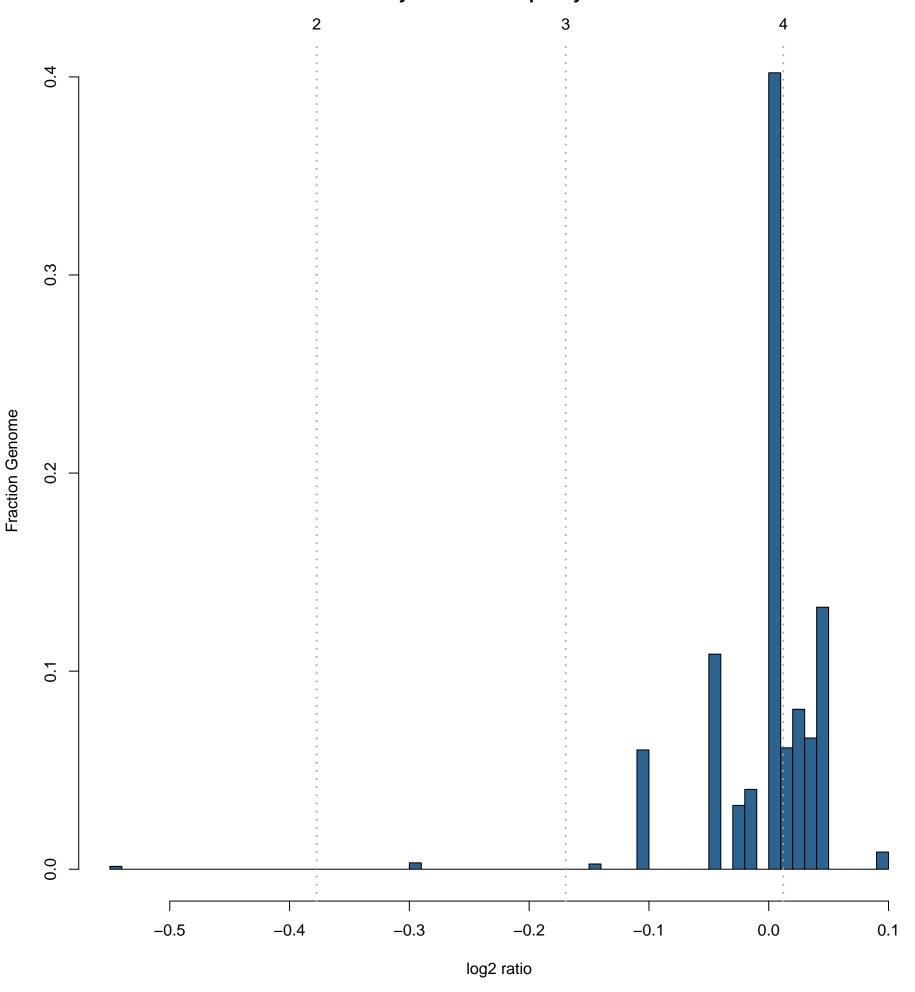
SNV Index

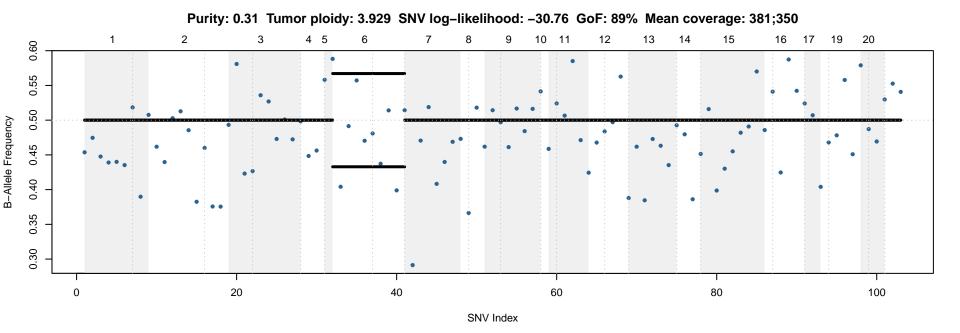




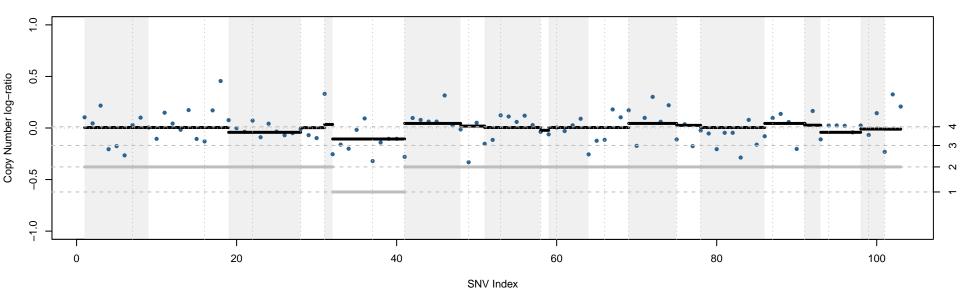


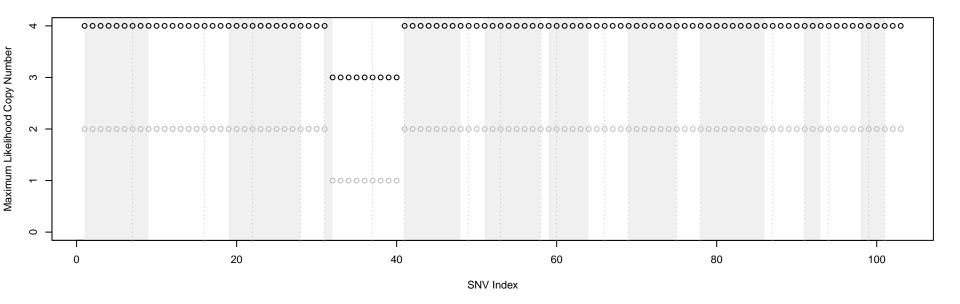
Purity: 0.31 Tumor ploidy: 3.929

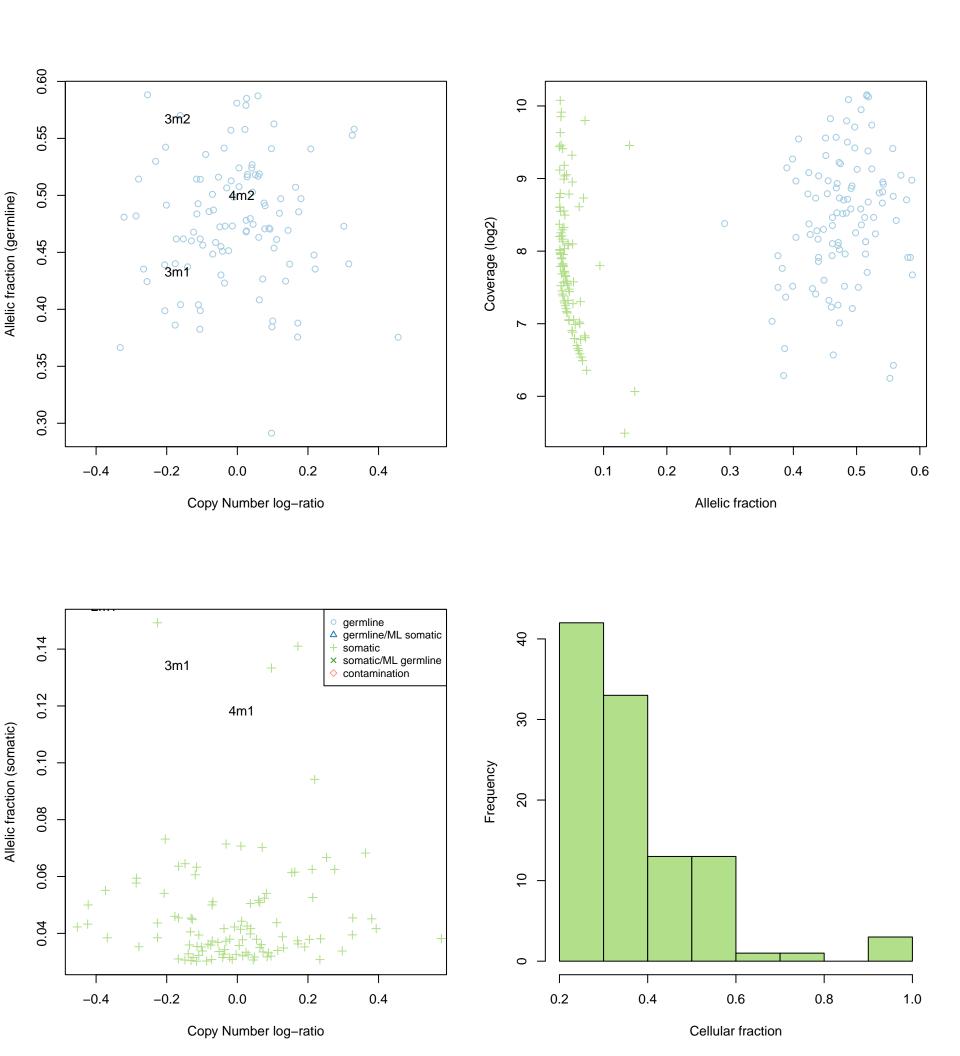




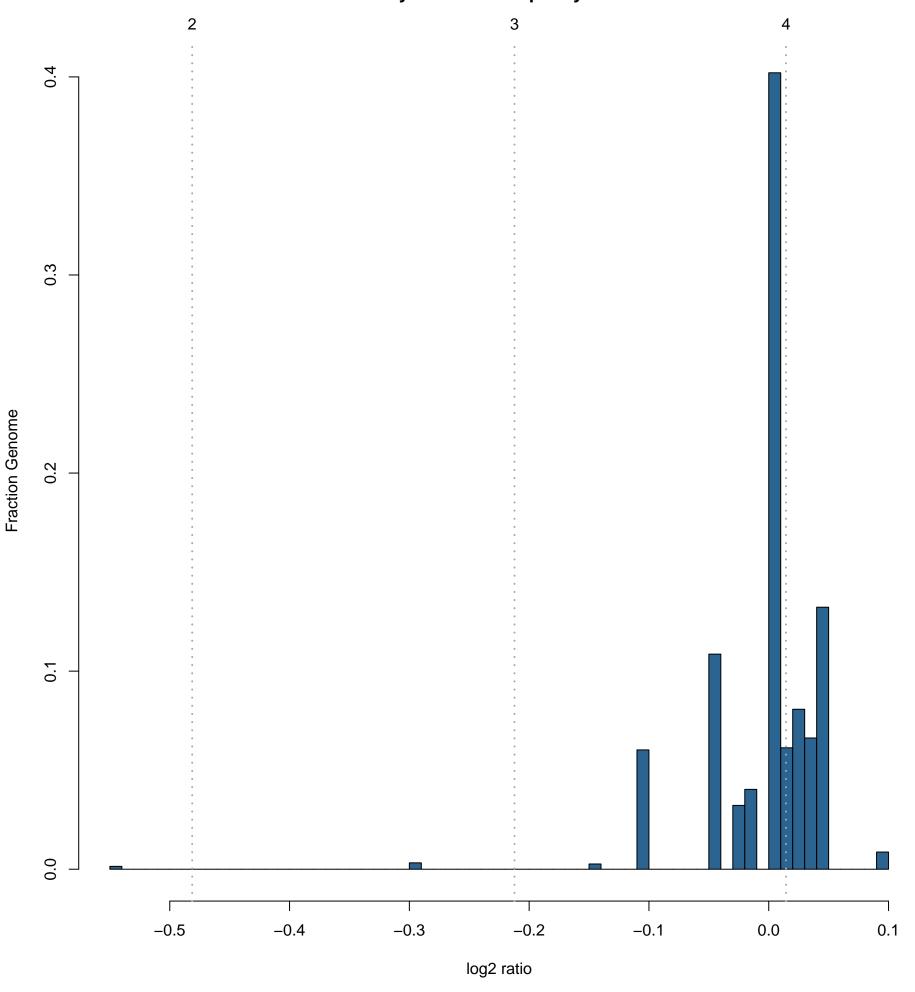
SCNA-fit log-likelihood: -9233.18

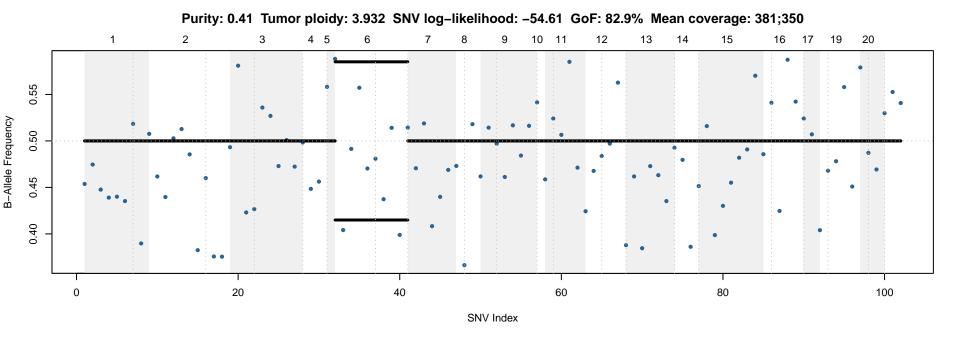




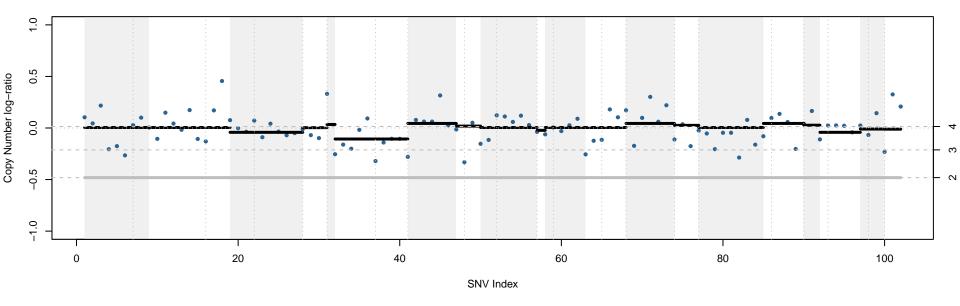


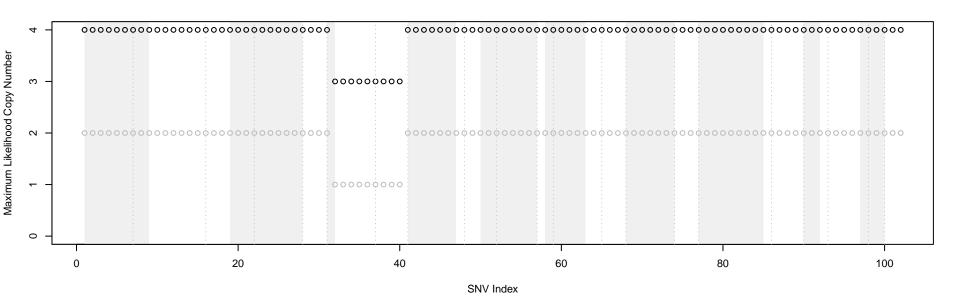
Purity: 0.41 Tumor ploidy: 3.932

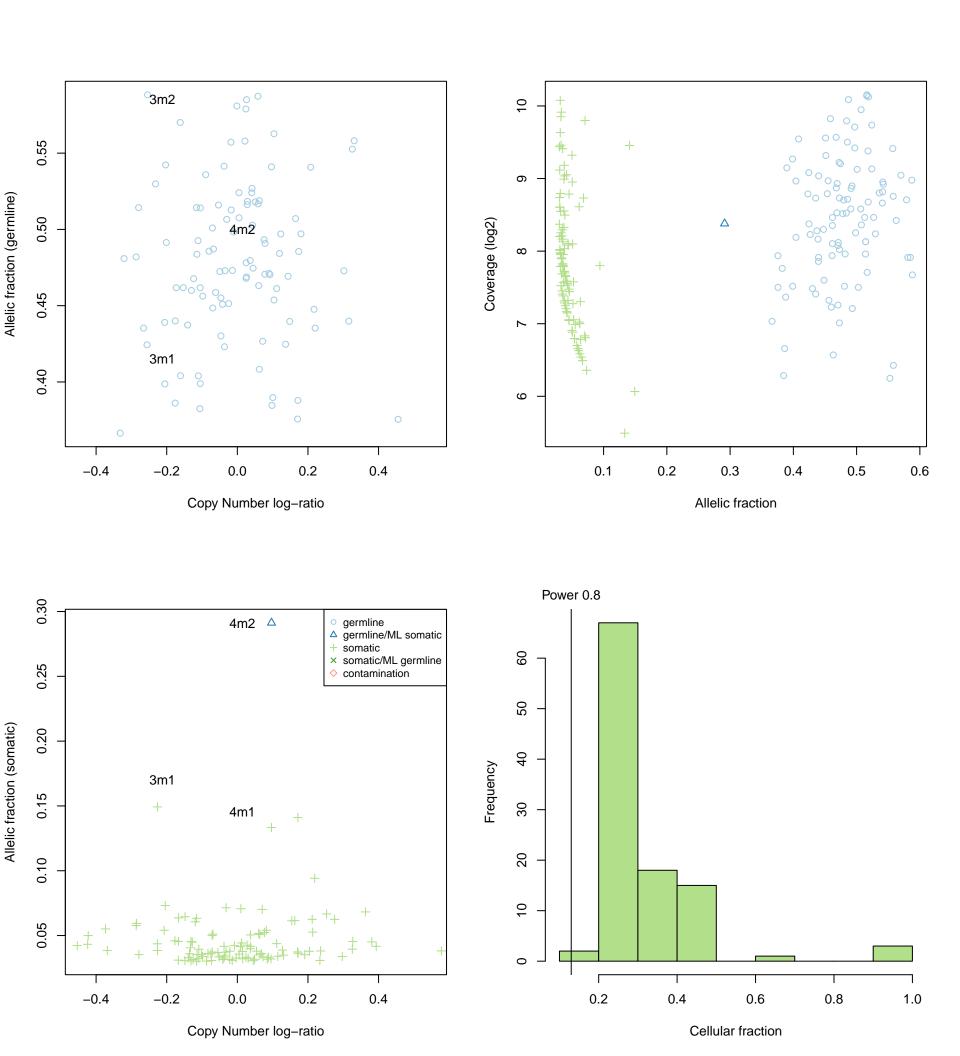




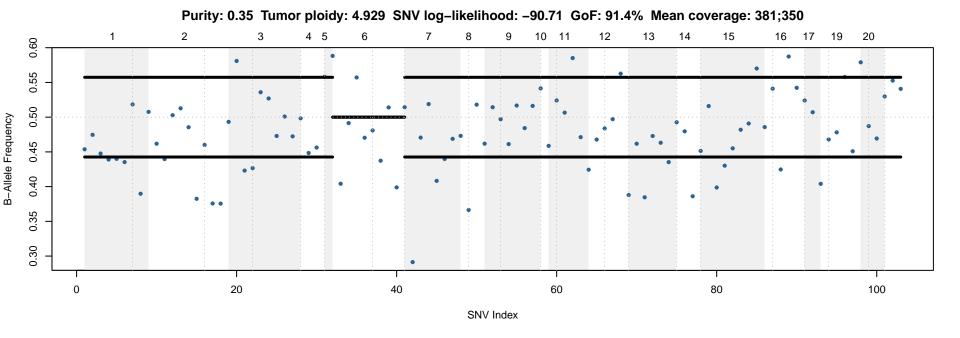
SCNA-fit log-likelihood: -9265.9



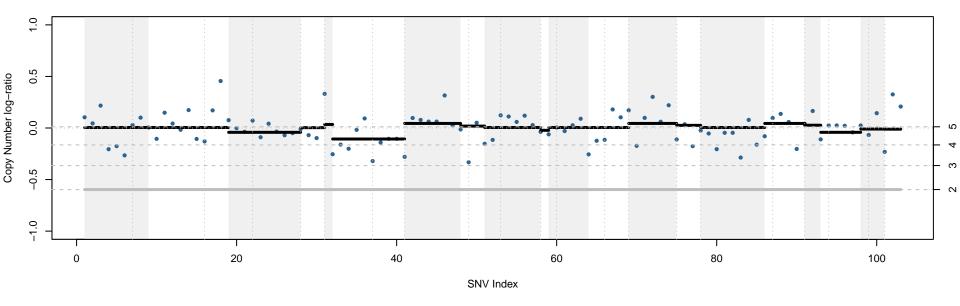


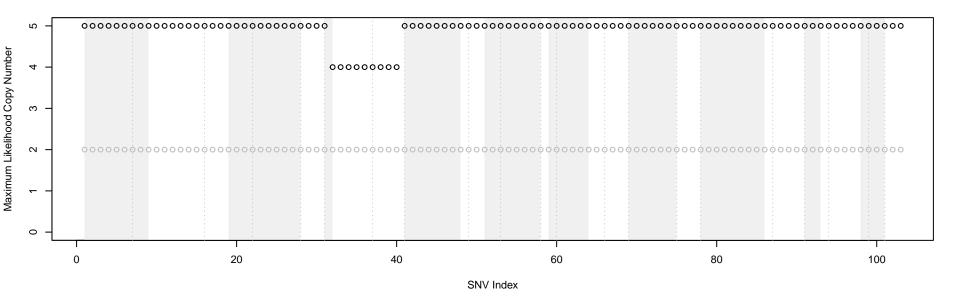


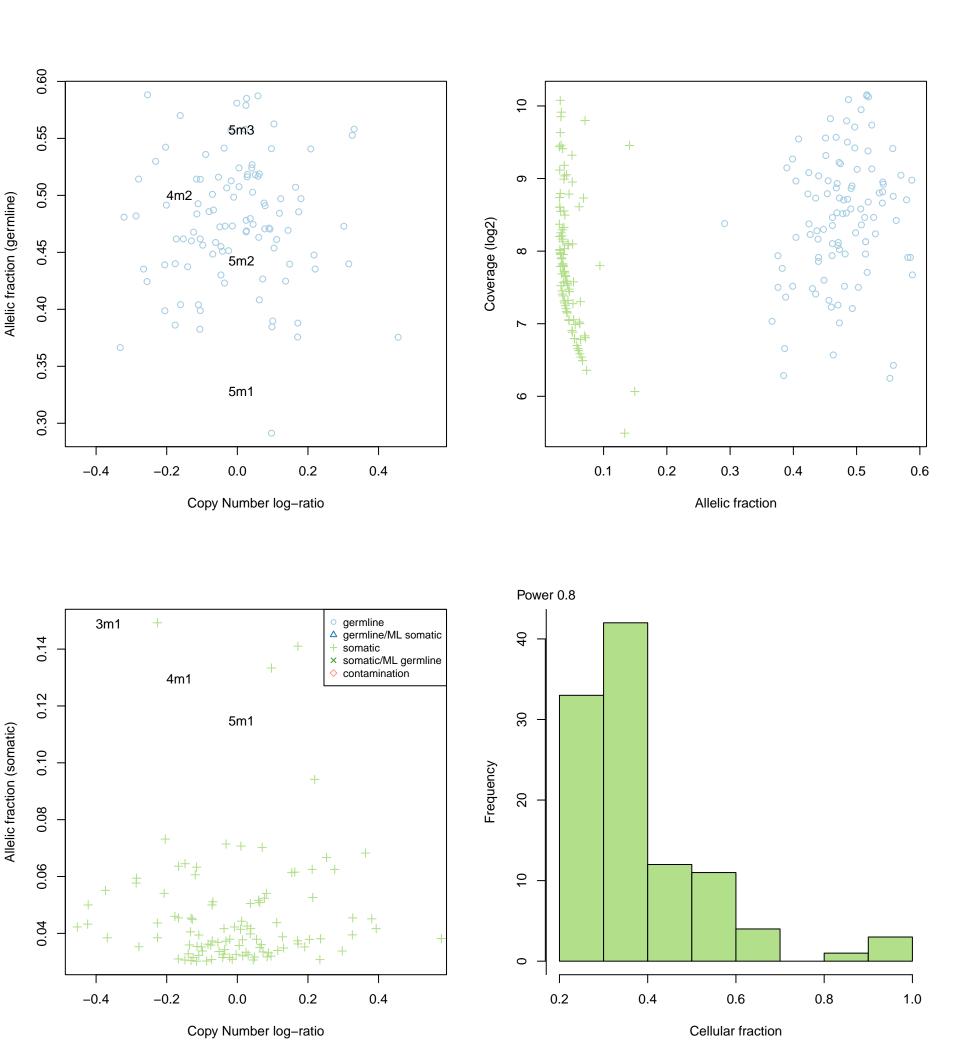
Purity: 0.35 Tumor ploidy: 4.929 3 5 0.4 0.3 Fraction Genome 0.1 0.0 -0.5 -0.4 -0.3 -0.2 -0.1 0.0 0.1 log2 ratio



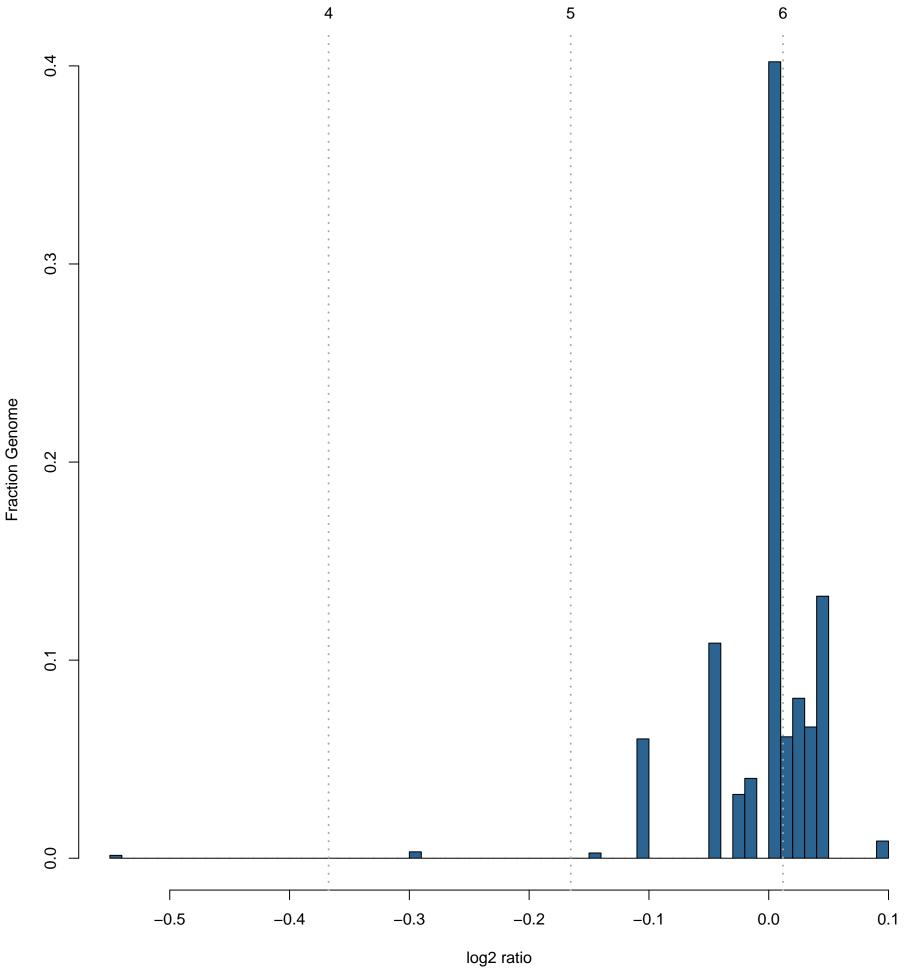
SCNA-fit log-likelihood: -9229.37

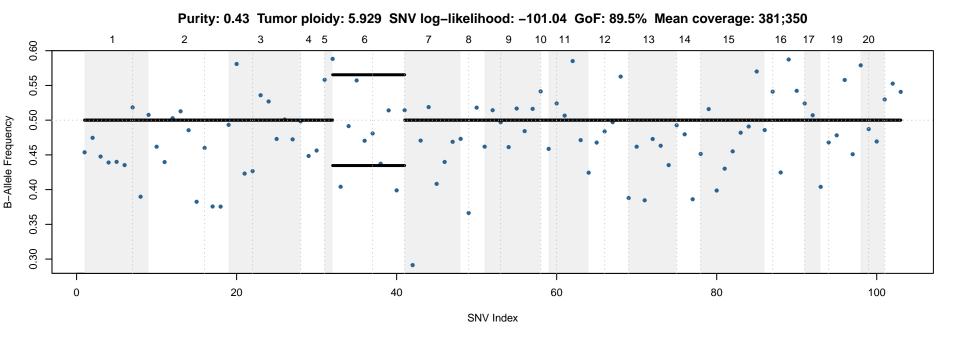




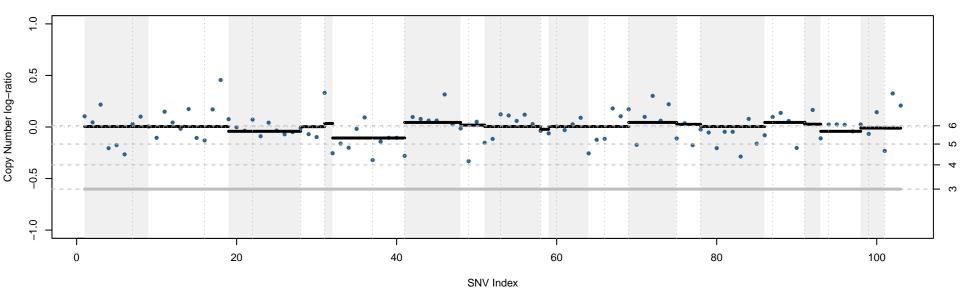


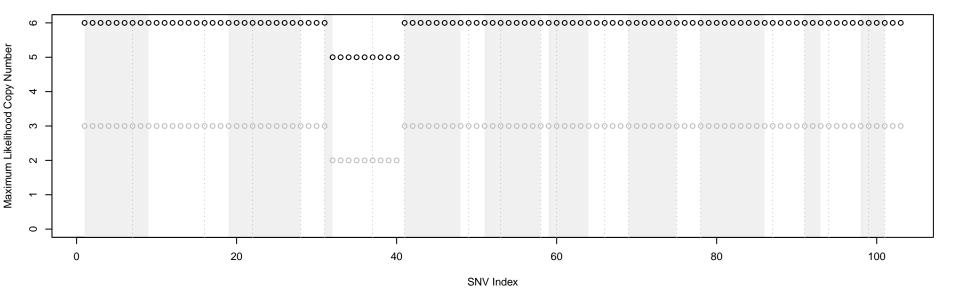
Purity: 0.43 Tumor ploidy: 5.929

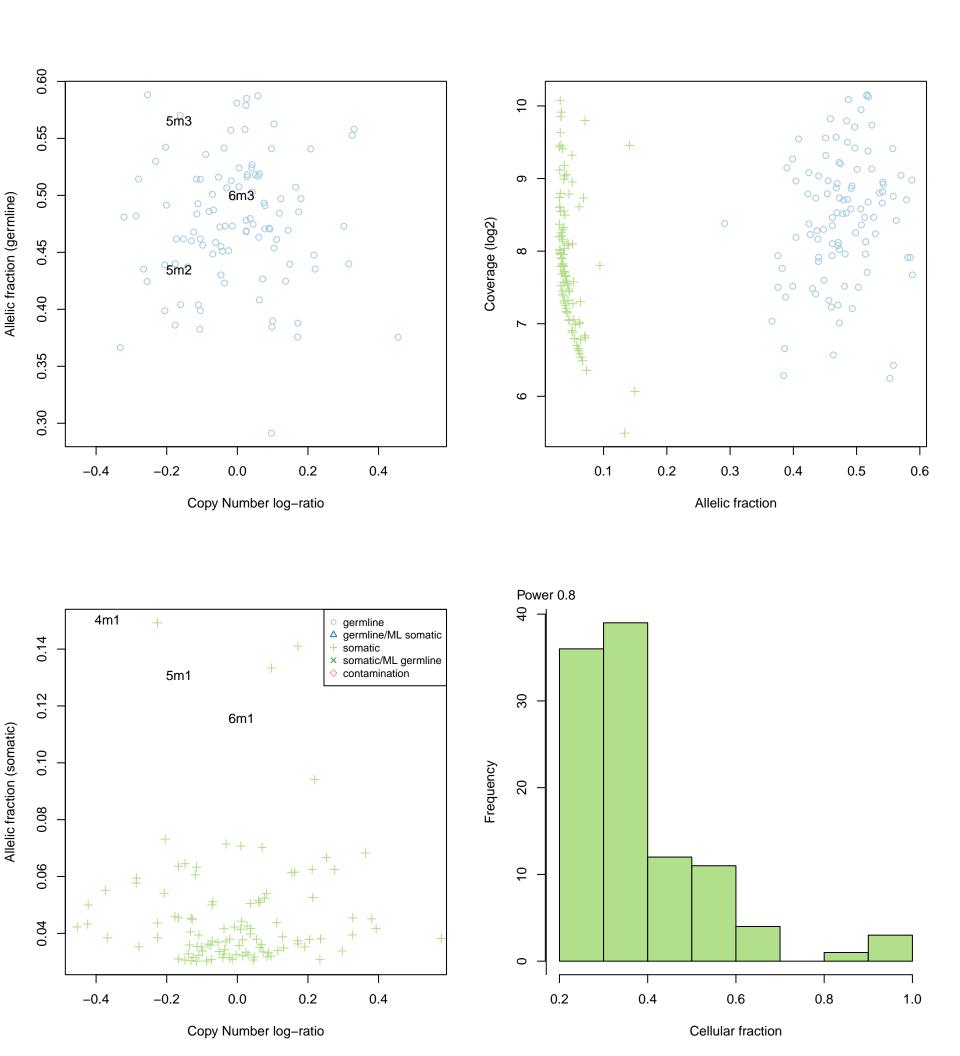




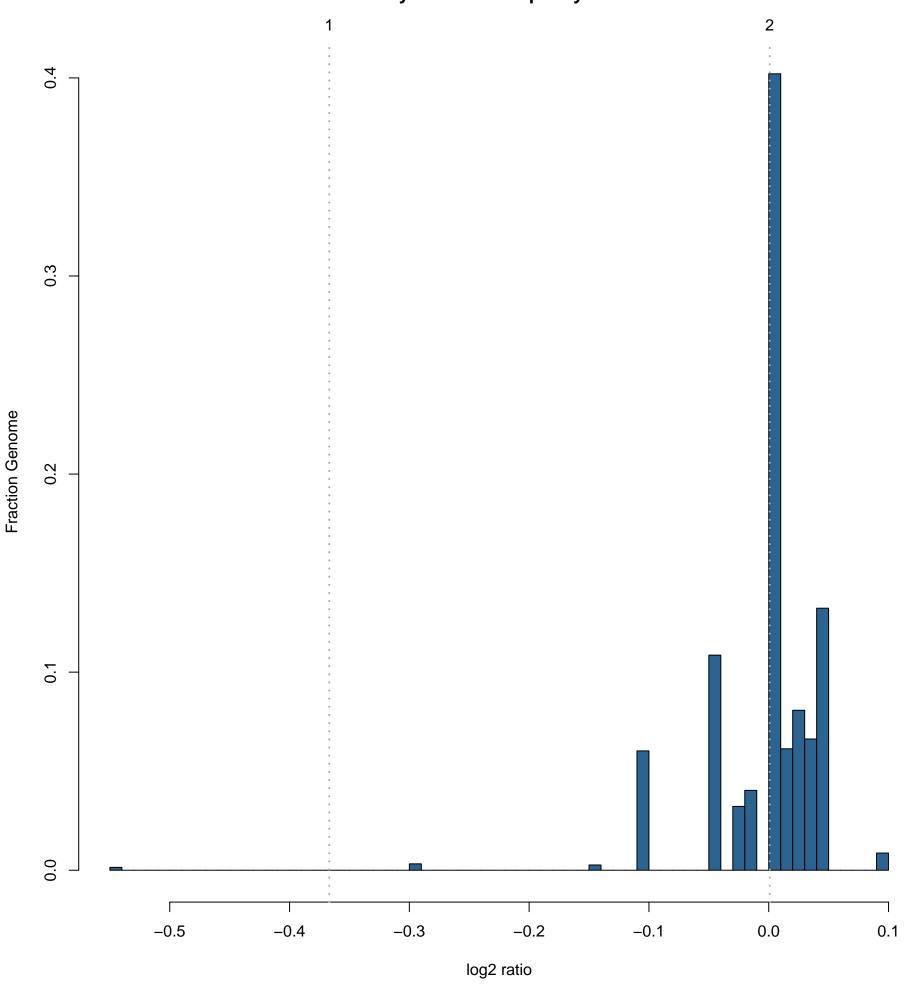
SCNA-fit log-likelihood: -9230.2

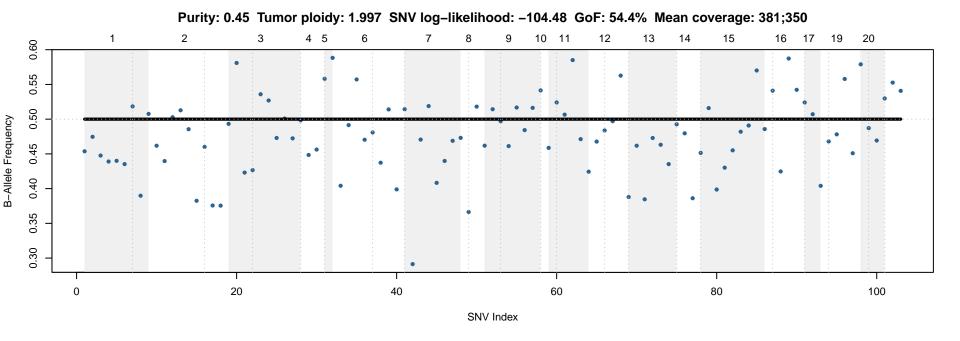




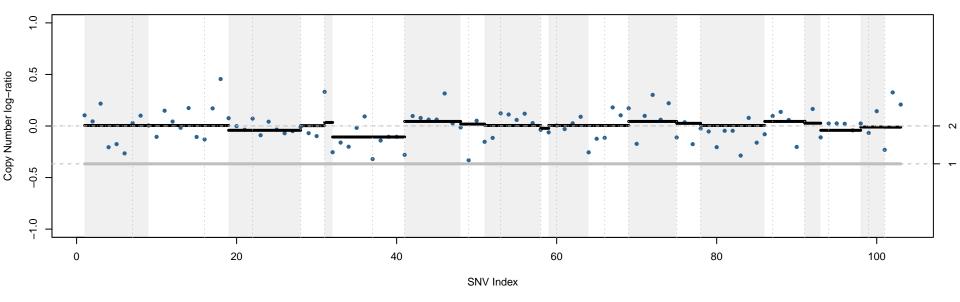


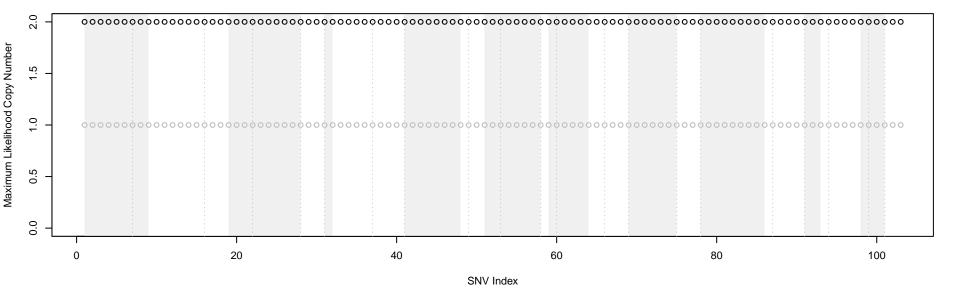
Purity: 0.45 Tumor ploidy: 1.997

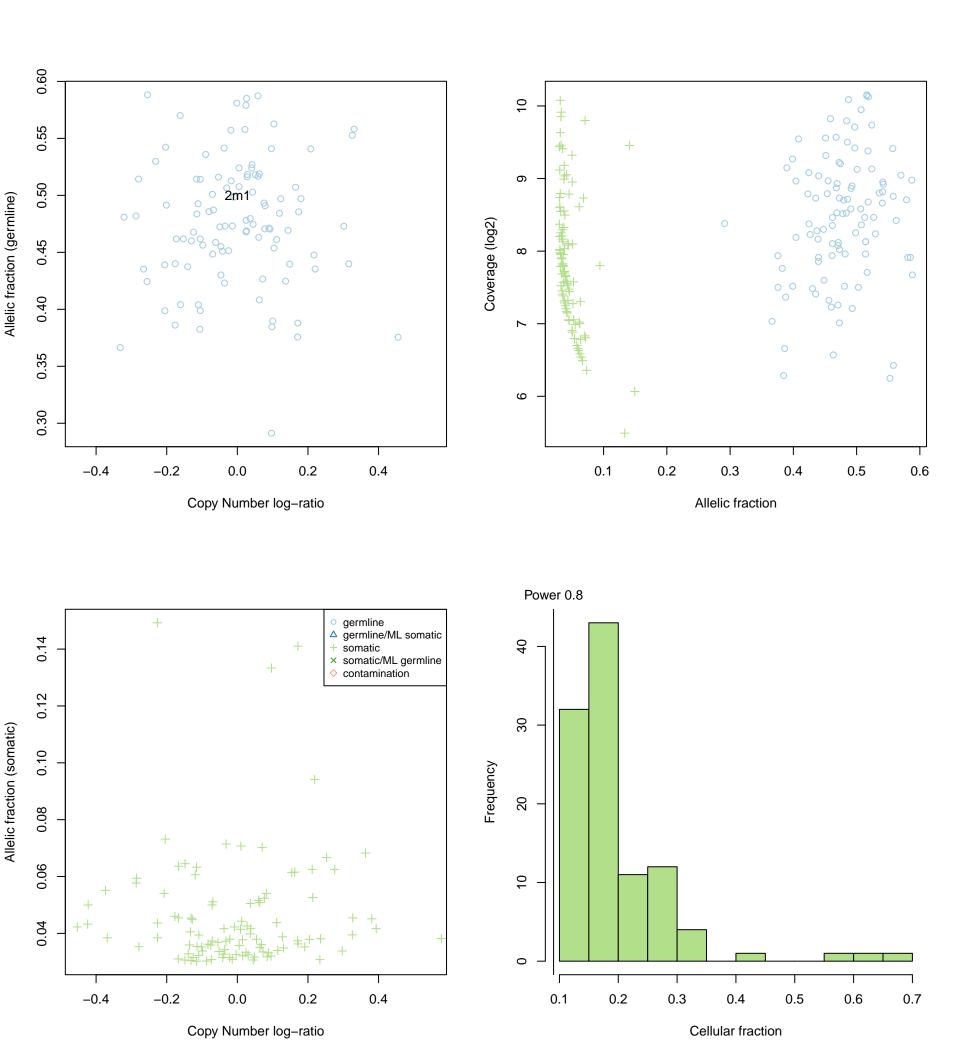




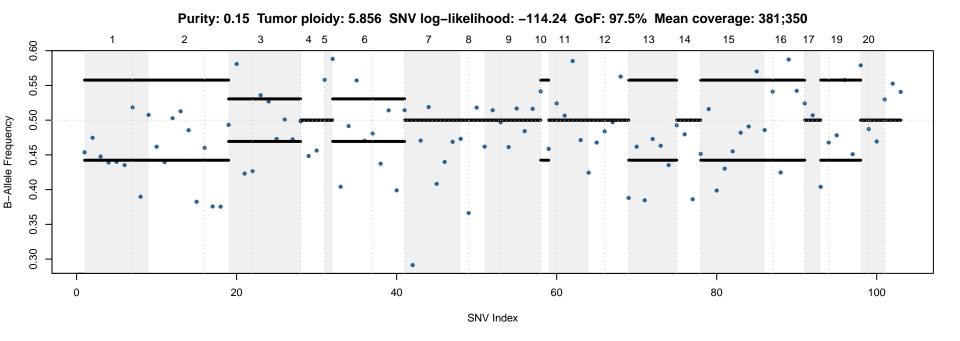
SCNA-fit log-likelihood: -9277.34



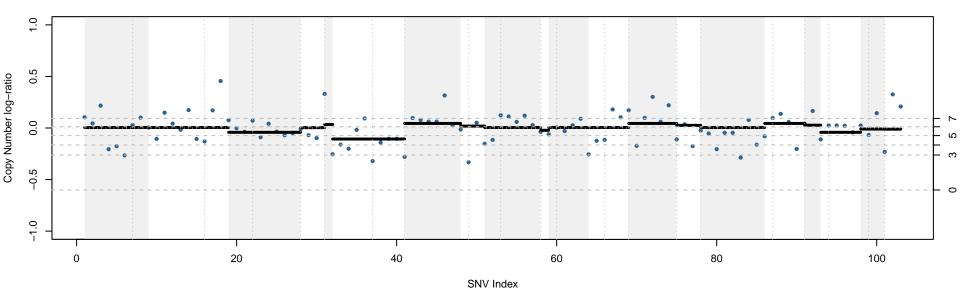


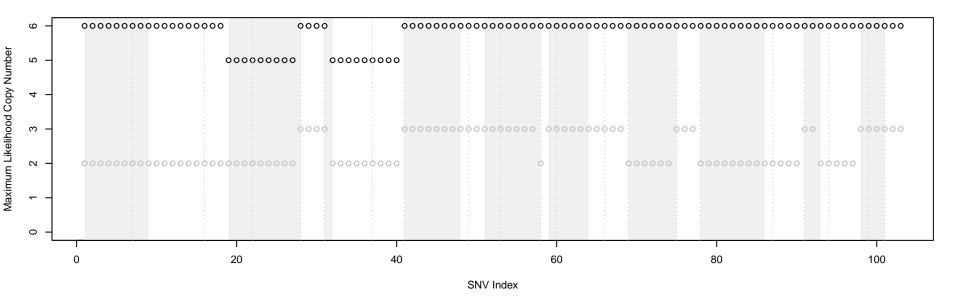


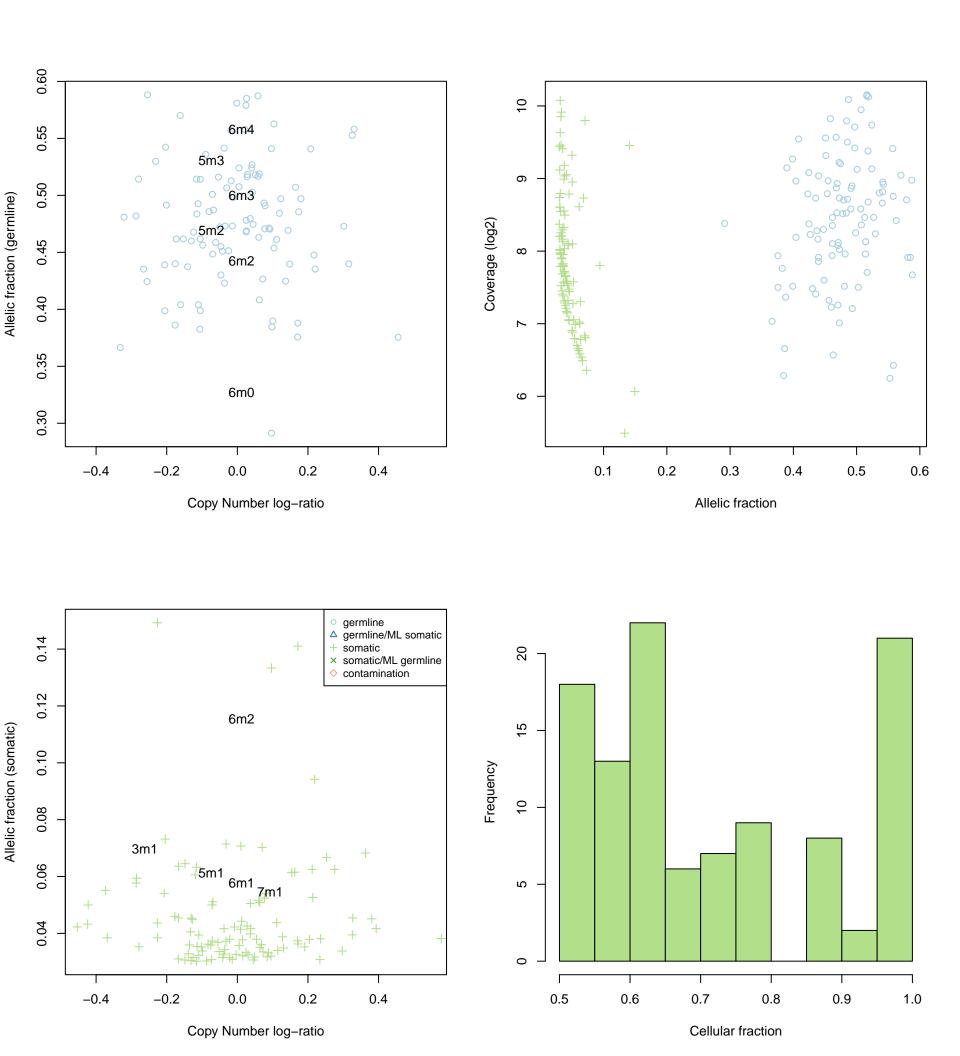
Purity: 0.15 Tumor ploidy: 5.856 3 5 6 7 0.4 0.3 Fraction Genome 0.1 0.0 -0.5 -0.4 -0.3 -0.2 -0.1 0.0 0.1 log2 ratio



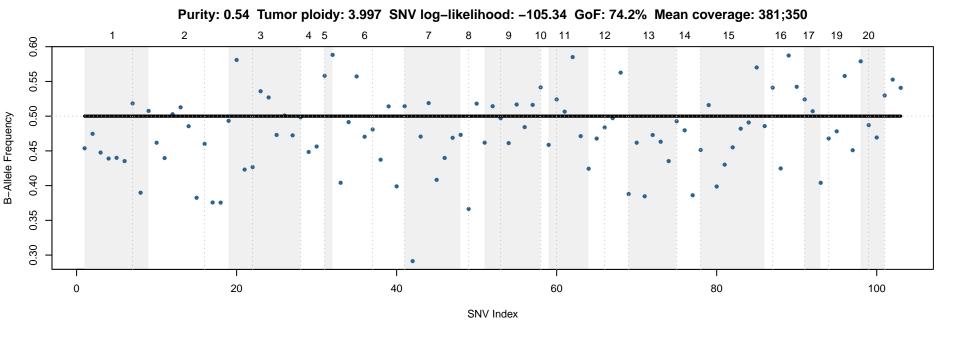
SCNA-fit log-likelihood: -9195.45



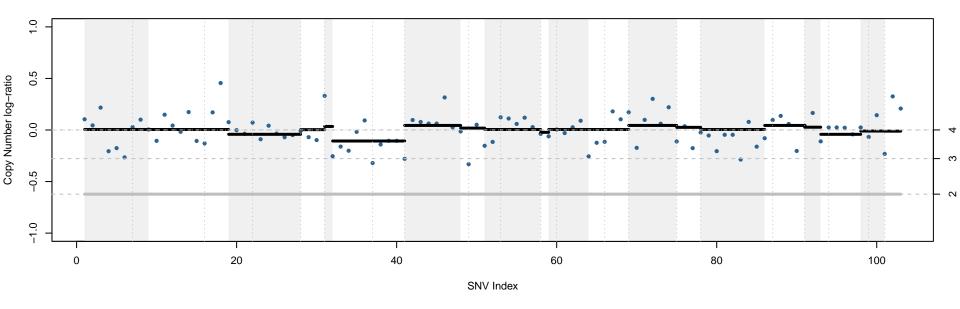


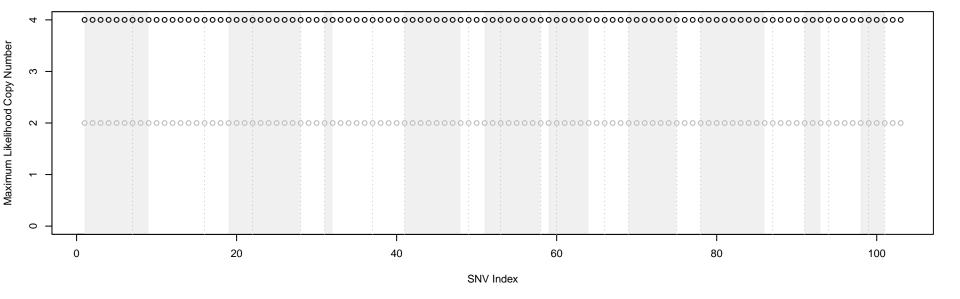


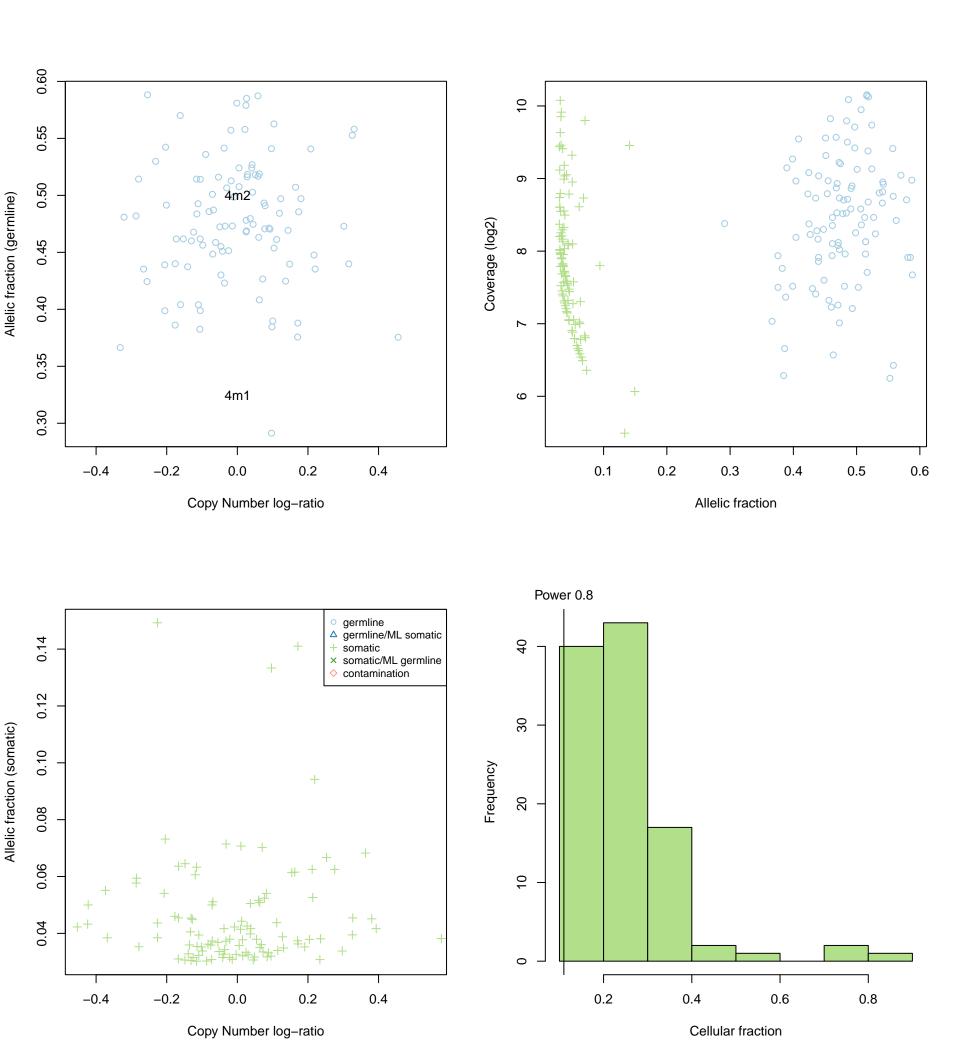
Purity: 0.54 Tumor ploidy: 3.997 0.4 0.3 Fraction Genome 0.1 0.0 -0.5 -0.4 -0.3 -0.2 -0.1 0.0 0.1 log2 ratio



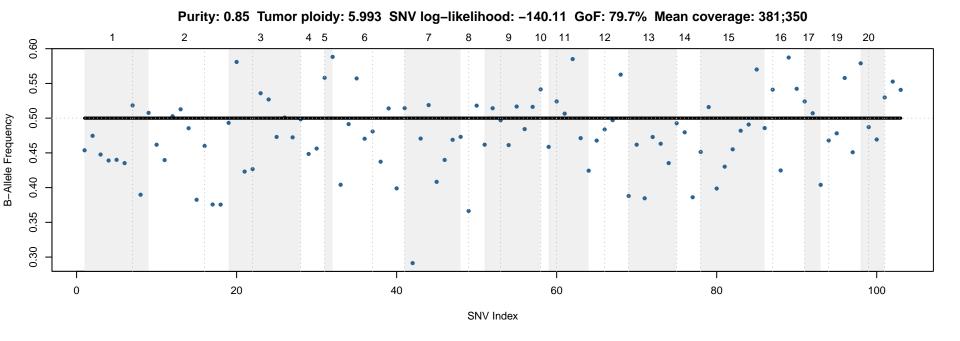
SCNA-fit log-likelihood: -9272.96



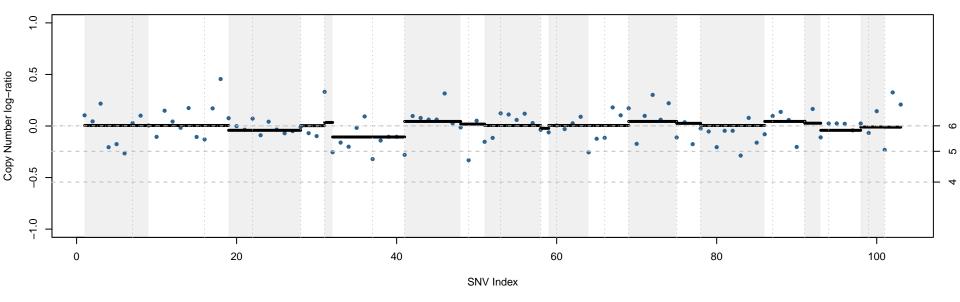


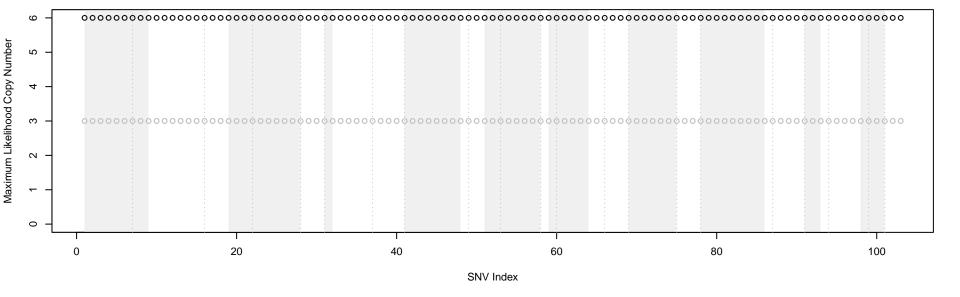


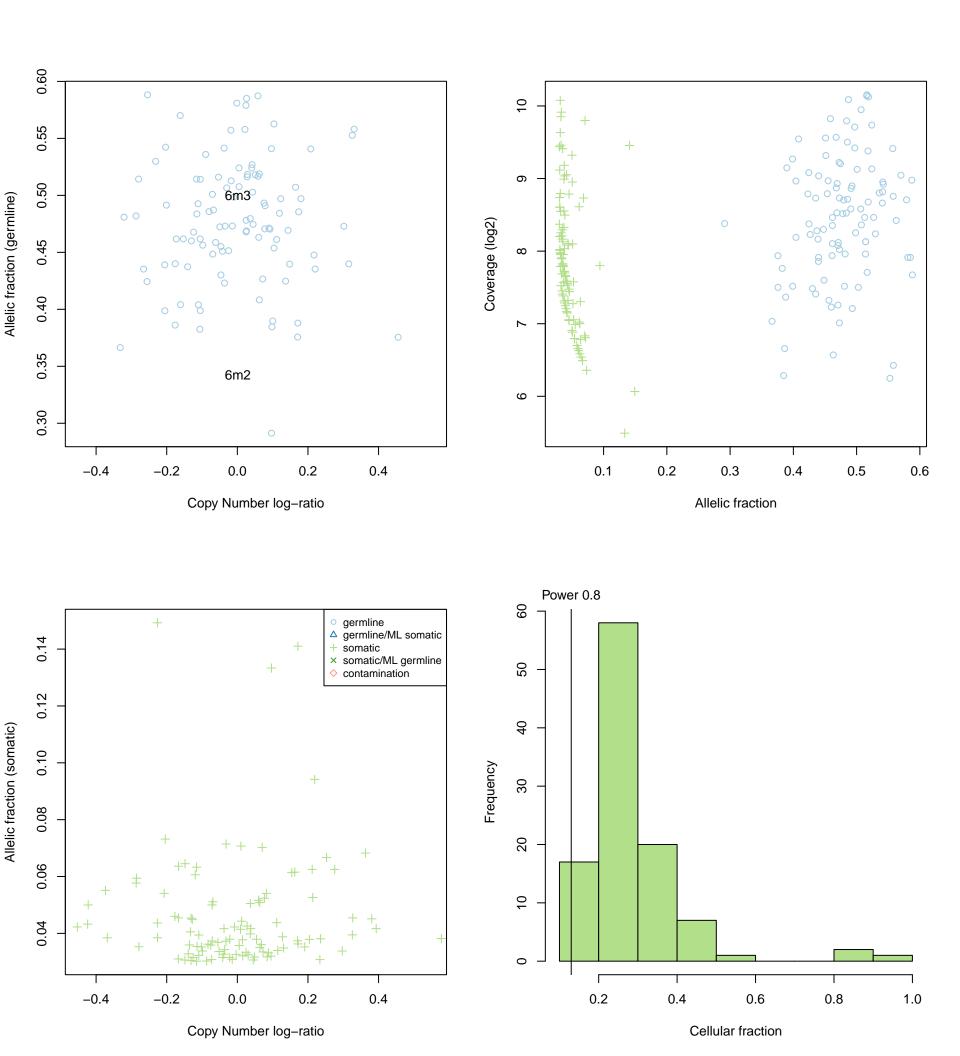
Purity: 0.85 Tumor ploidy: 5.993 6 4 5 0.4 0.3 Fraction Genome 0.2 0.1 0.0 -0.5 -0.4 -0.3 -0.2 -0.1 0.0 0.1 log2 ratio



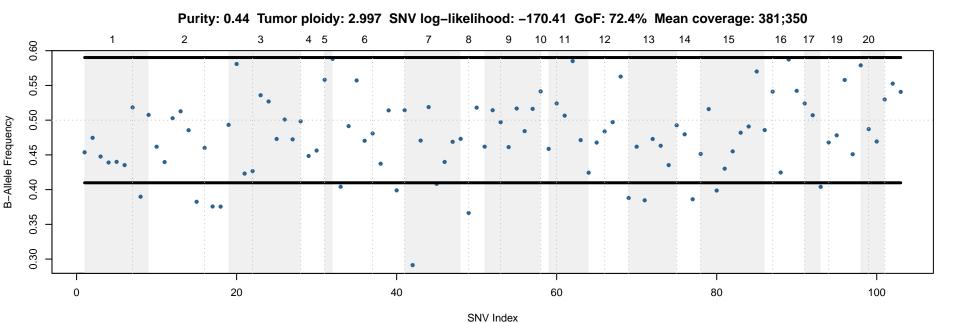
SCNA-fit log-likelihood: -9271.47



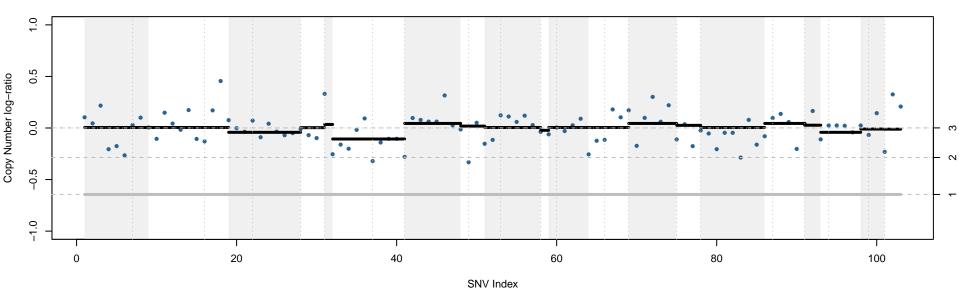


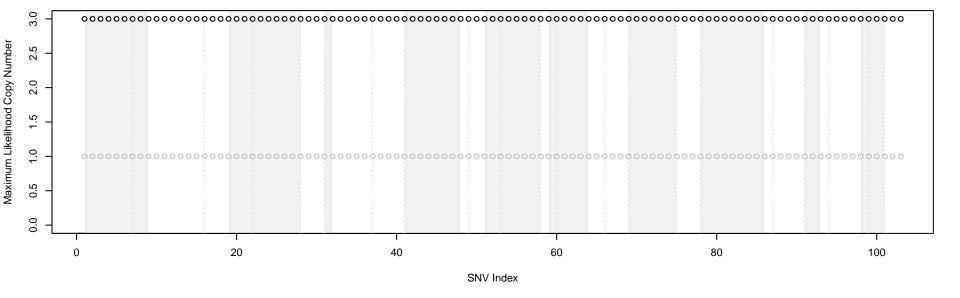


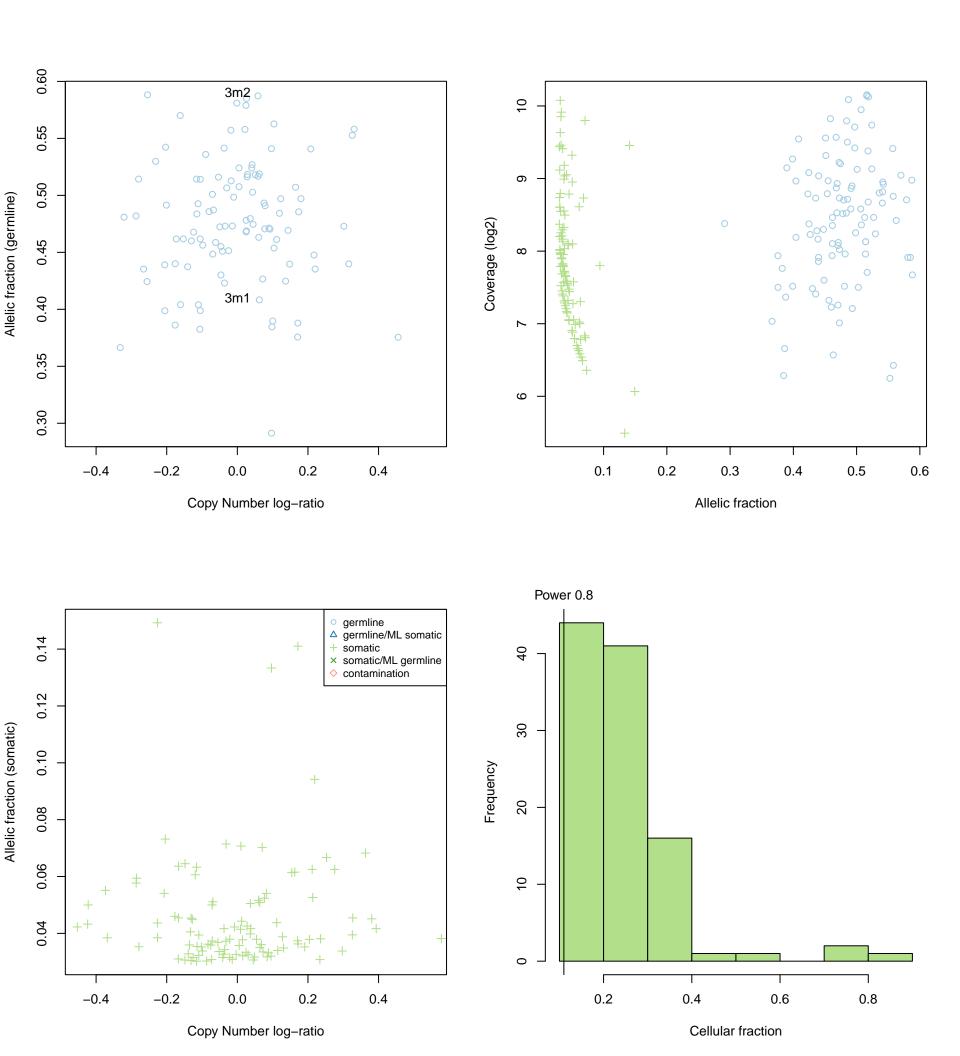
Purity: 0.44 Tumor ploidy: 2.997 3 2 0.4 0.3 Fraction Genome 0.1 0.0 -0.5 -0.4 -0.3 -0.2 -0.1 0.0 0.1 log2 ratio



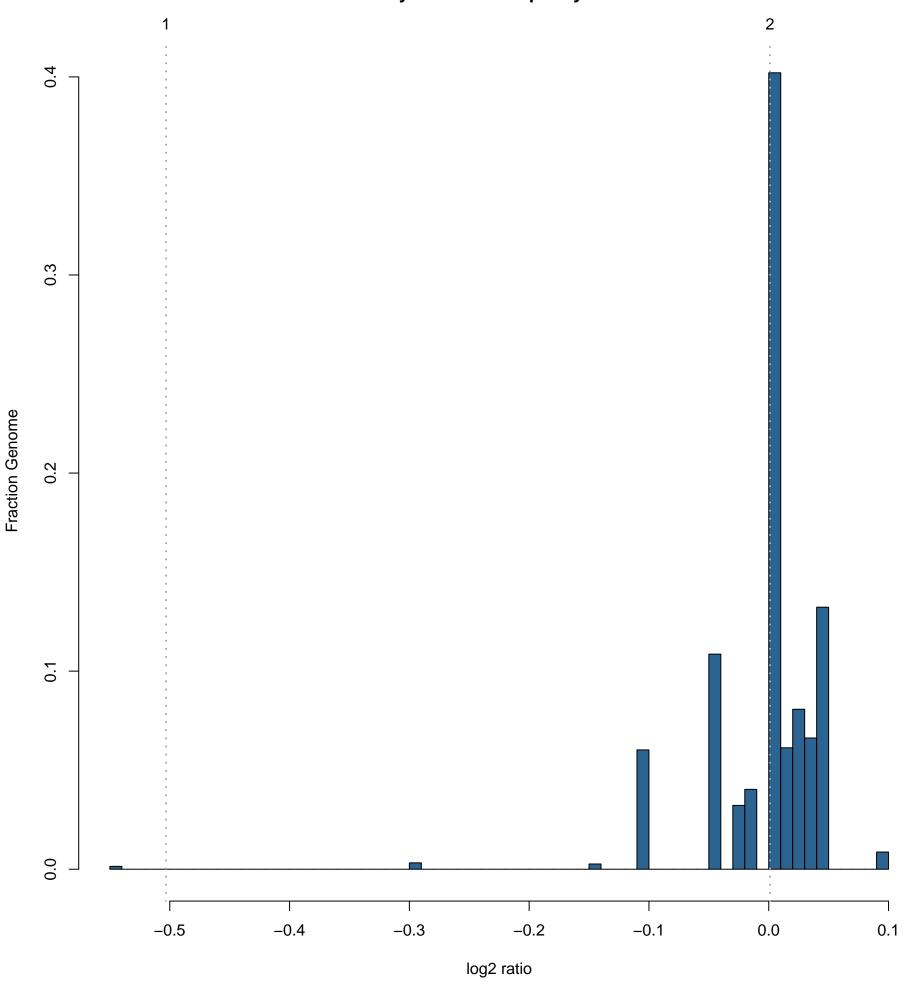
SCNA-fit log-likelihood: -9273.73

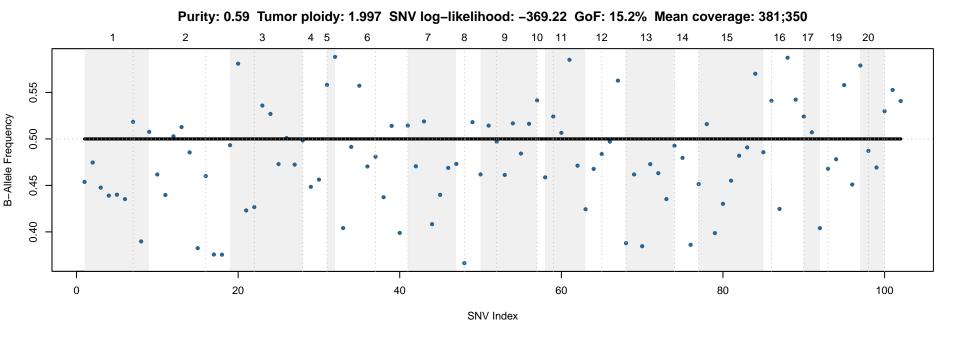




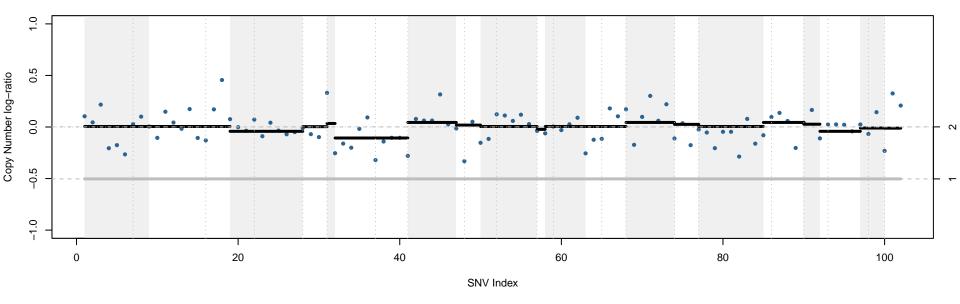


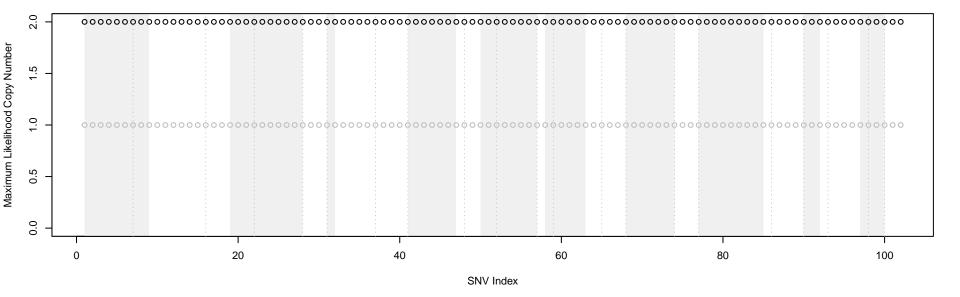
Purity: 0.59 Tumor ploidy: 1.997

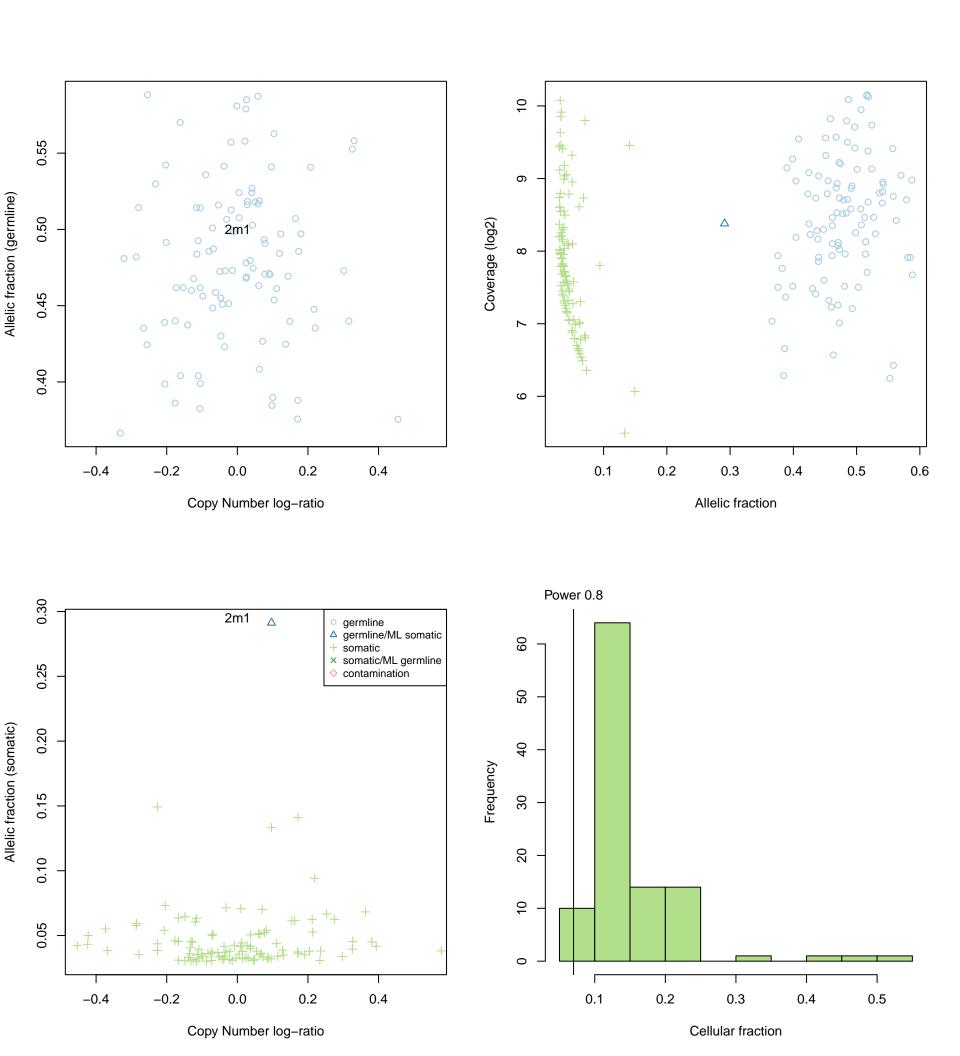




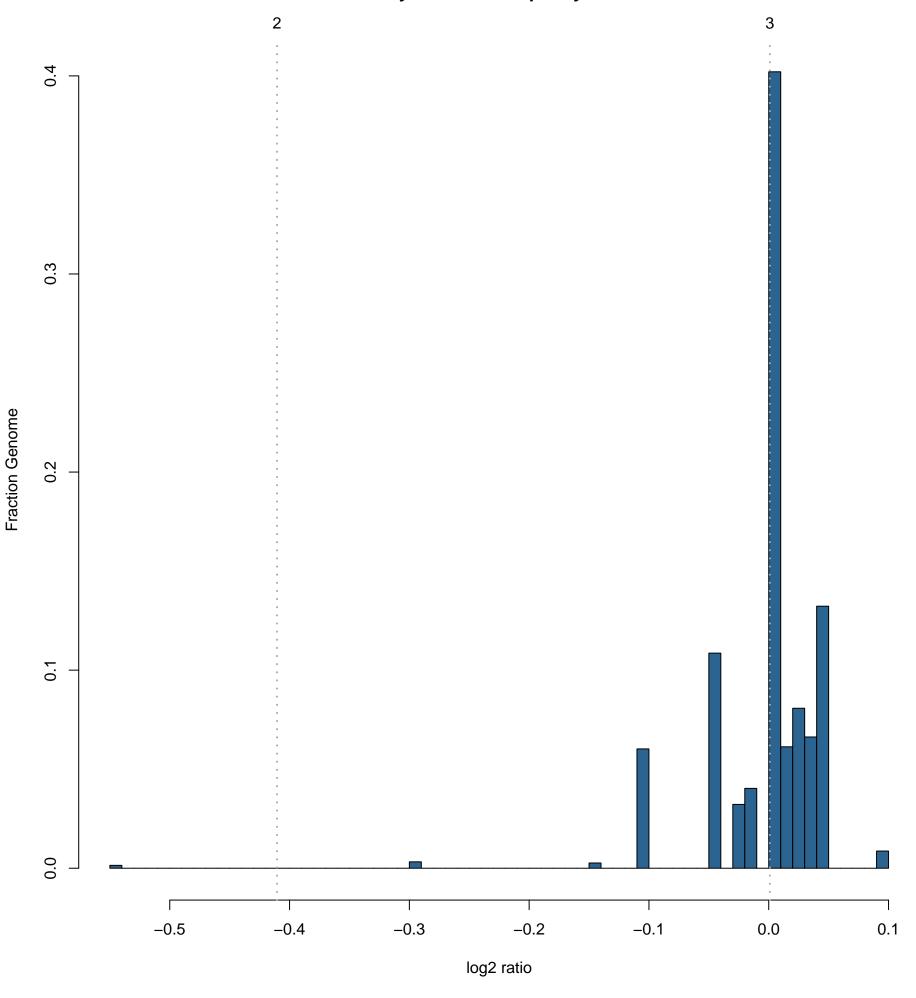
SCNA-fit log-likelihood: -9283.26

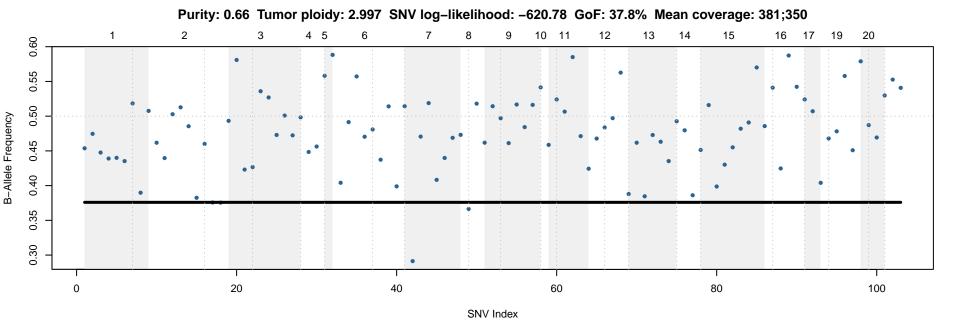




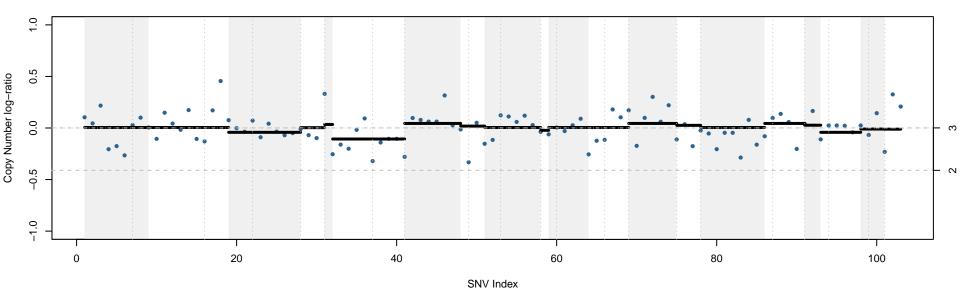


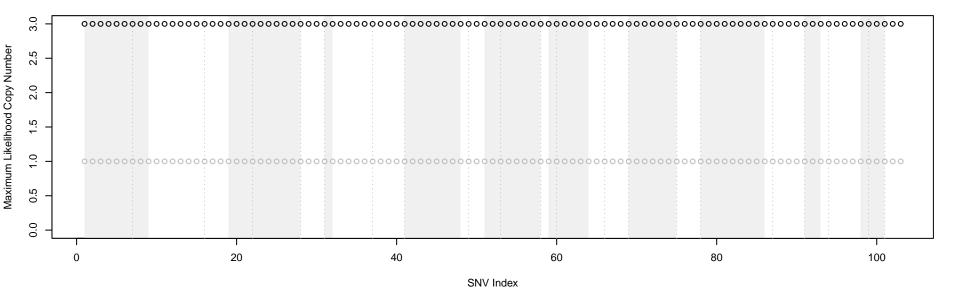
Purity: 0.66 Tumor ploidy: 2.997

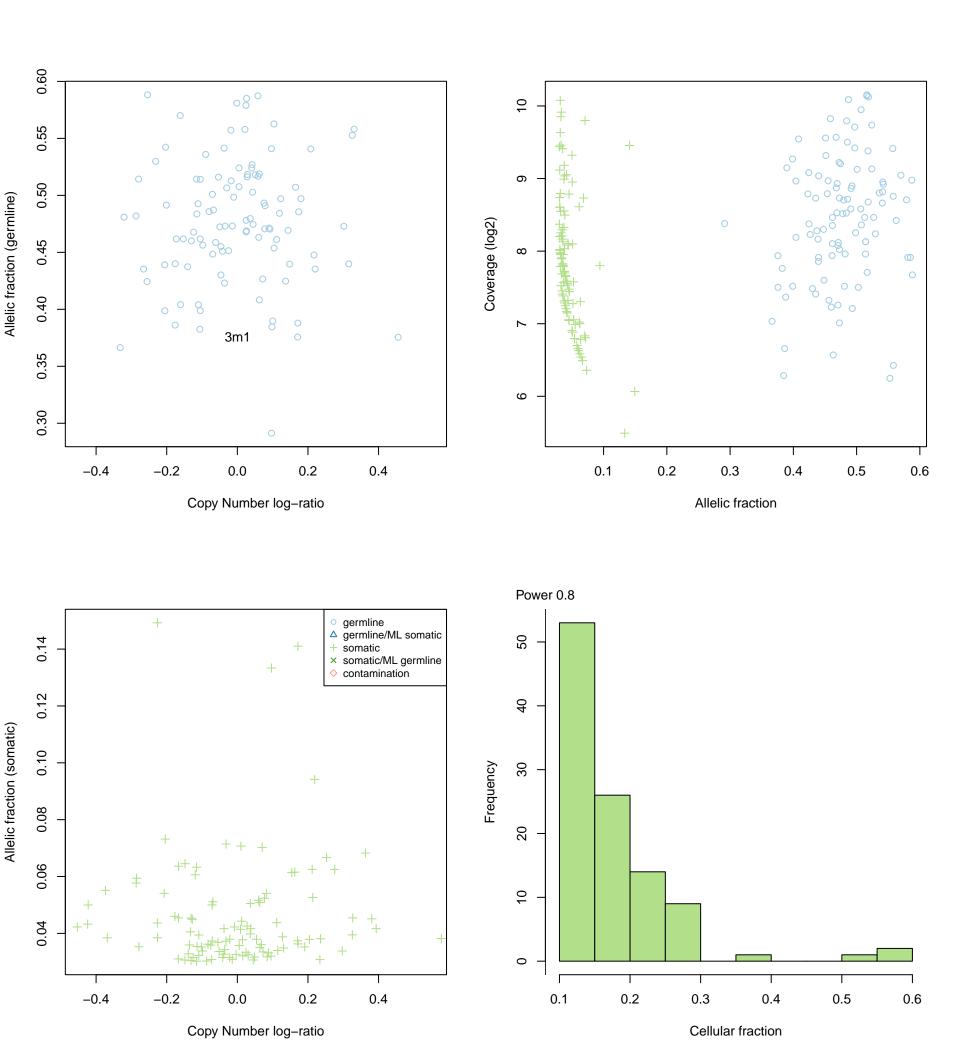




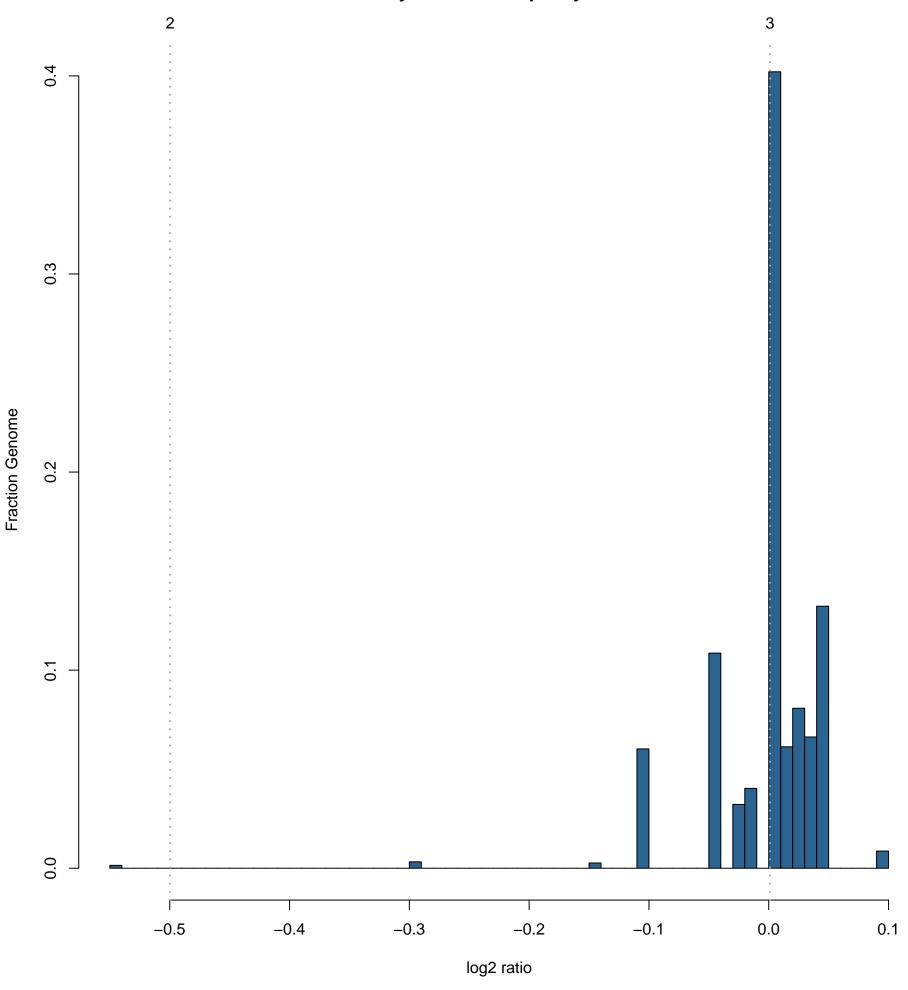
SCNA-fit log-likelihood: -9277.88

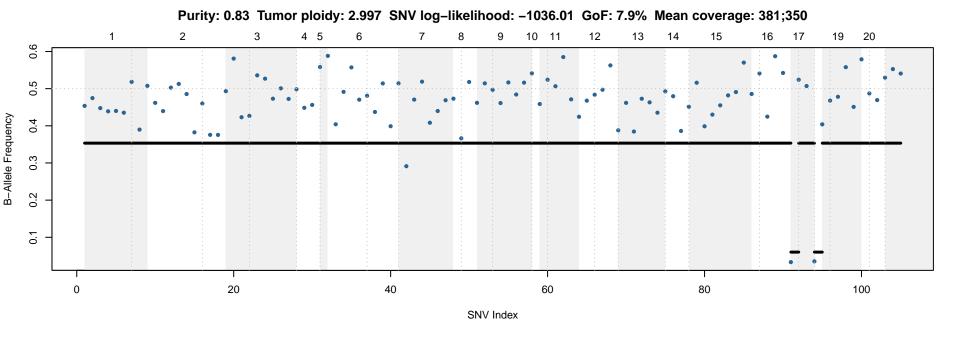






Purity: 0.83 Tumor ploidy: 2.997





SCNA-fit log-likelihood: -9282.97

