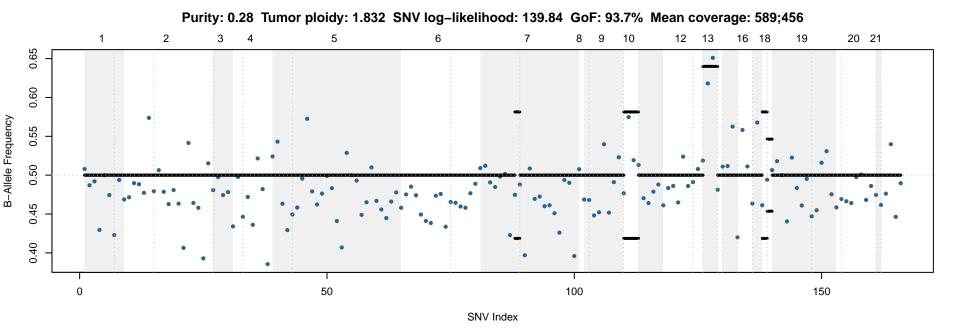
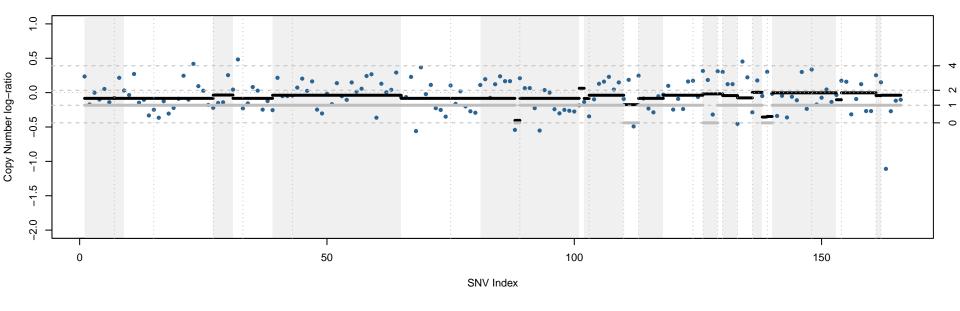
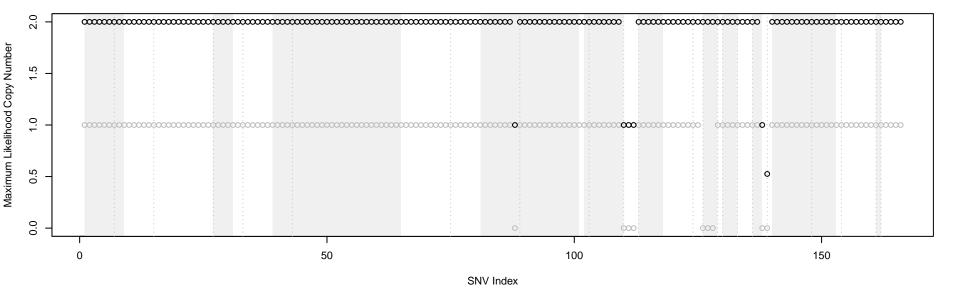
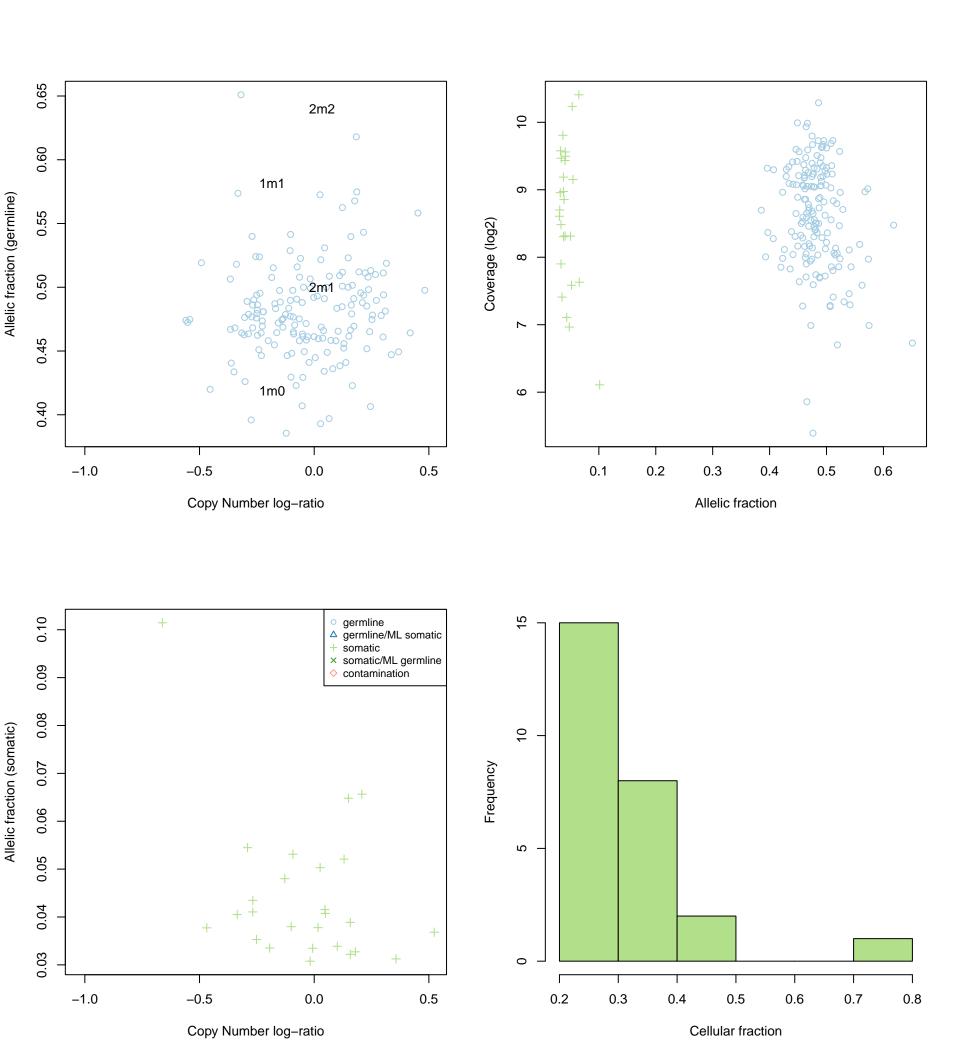
Purity: 0.28 Tumor ploidy: 1.832 0 Fraction Genome 0.1 0.0 -0.5 0.0 0.5 1.0 log2 ratio

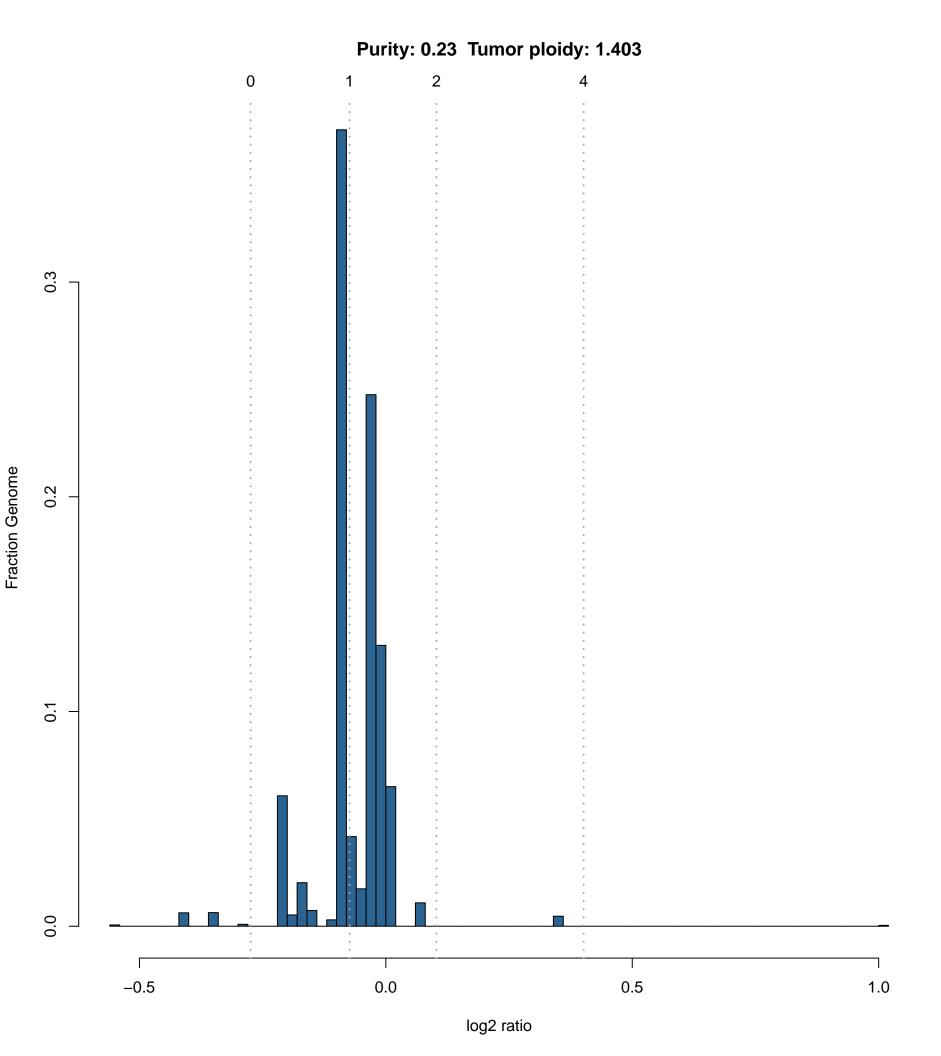


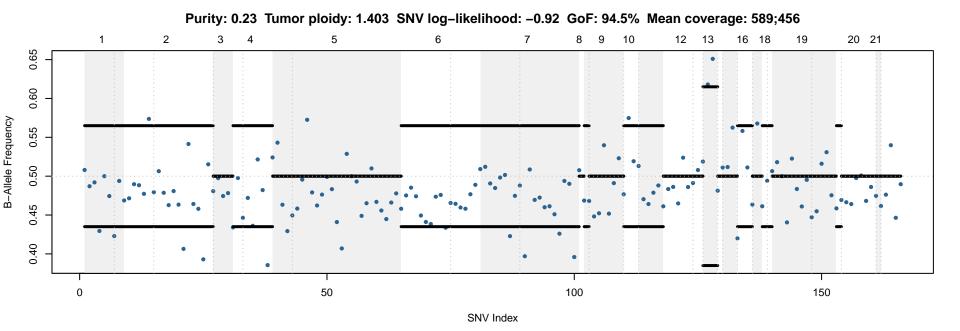
SCNA-fit log-likelihood: -4342.67



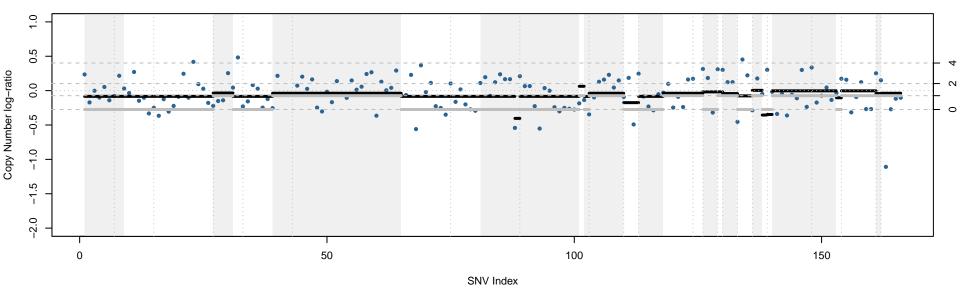


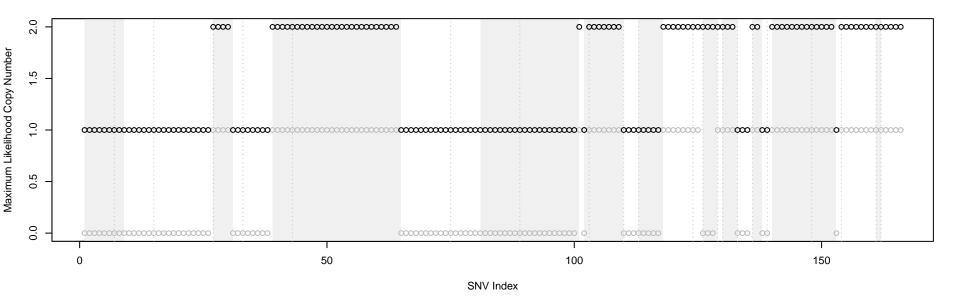


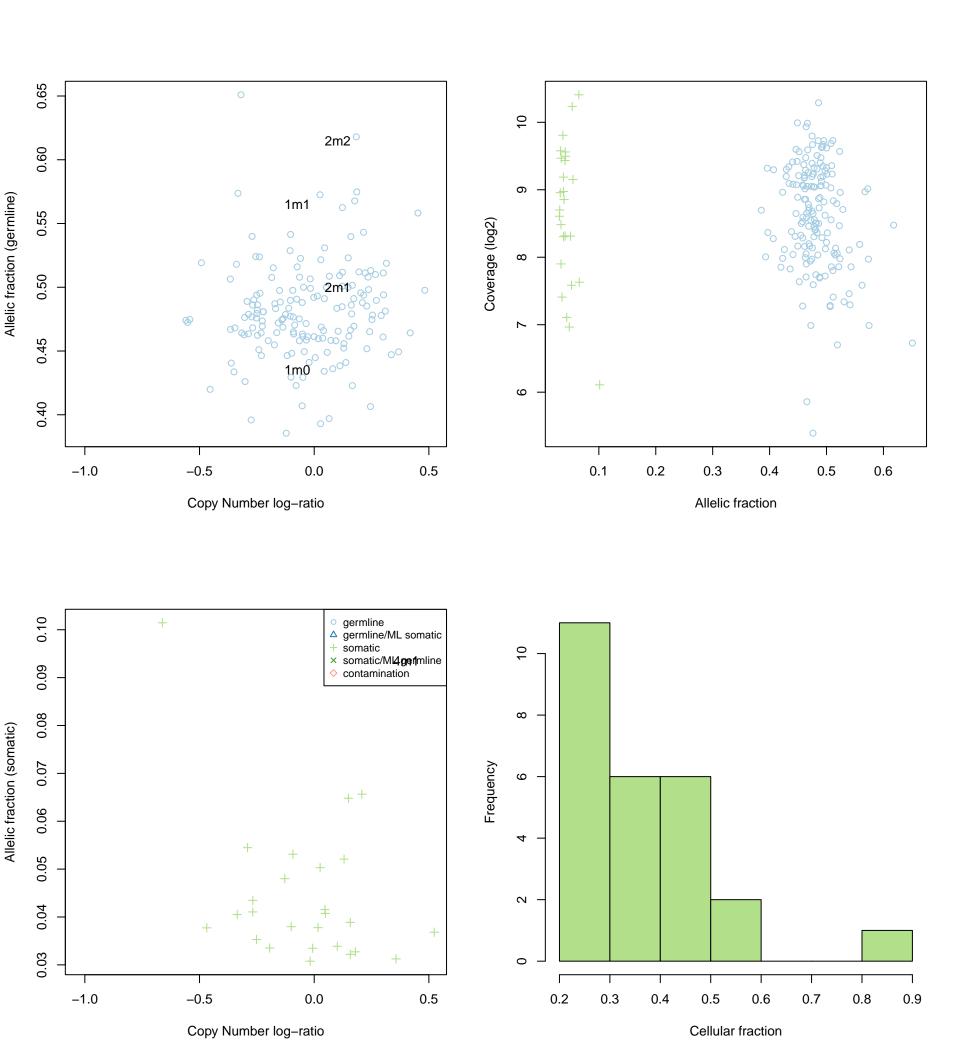




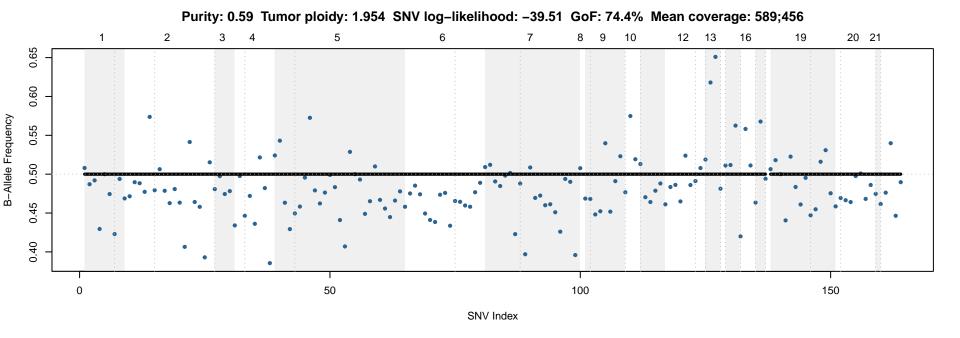
SCNA-fit log-likelihood: -4453.44



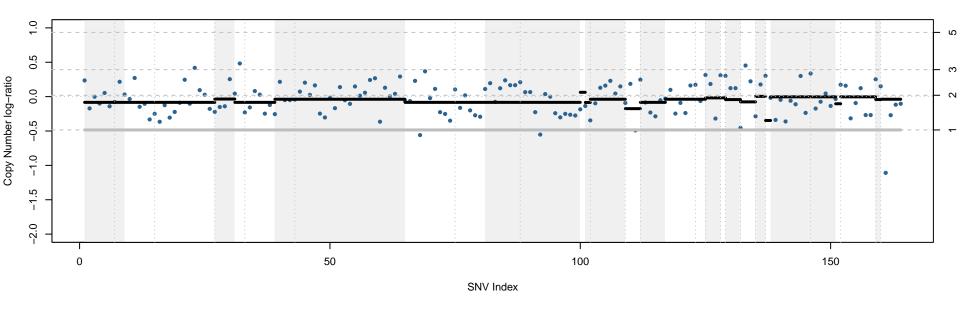


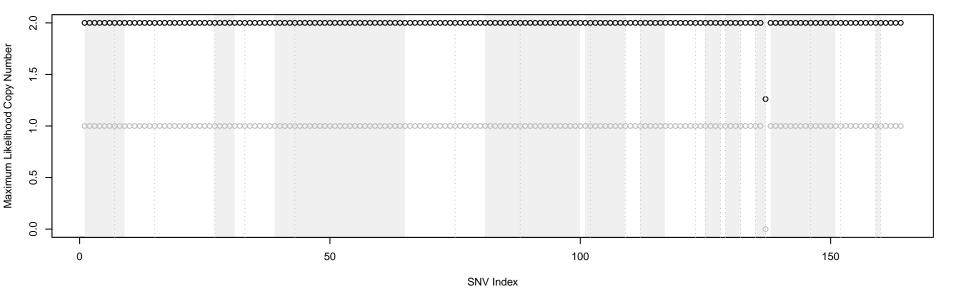


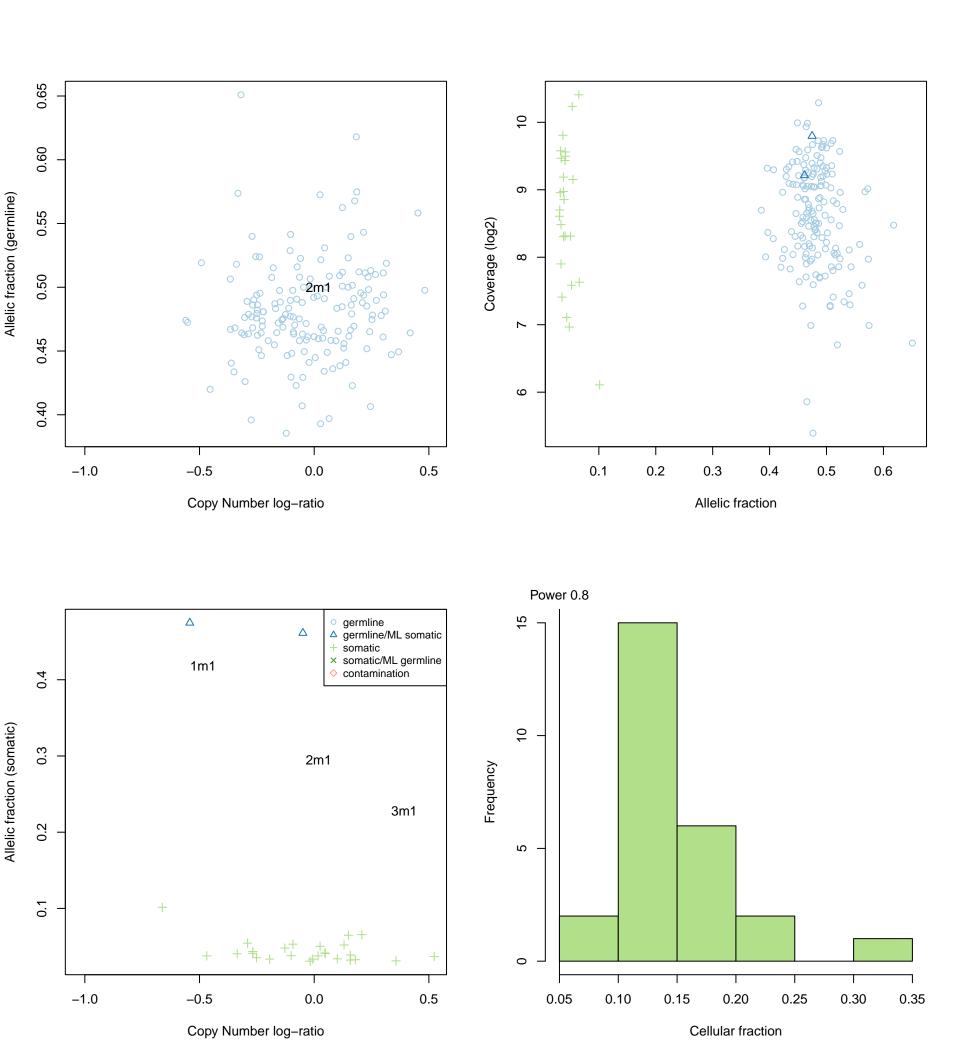
Purity: 0.59 Tumor ploidy: 1.954 2 5 Fraction Genome 0.1 0.0 -0.5 0.0 0.5 1.0 log2 ratio



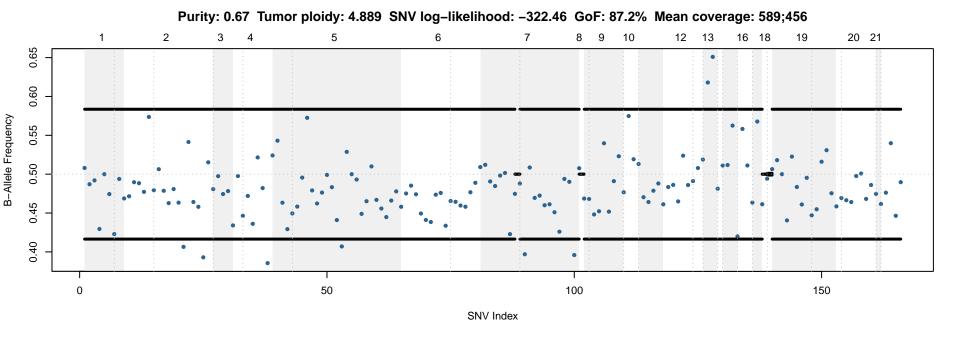
SCNA-fit log-likelihood: -4497.07



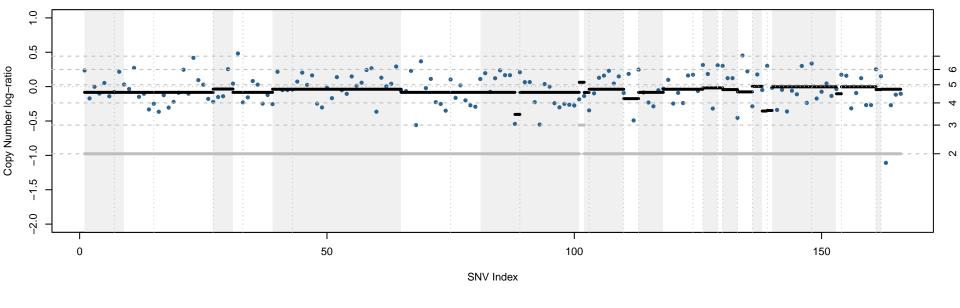


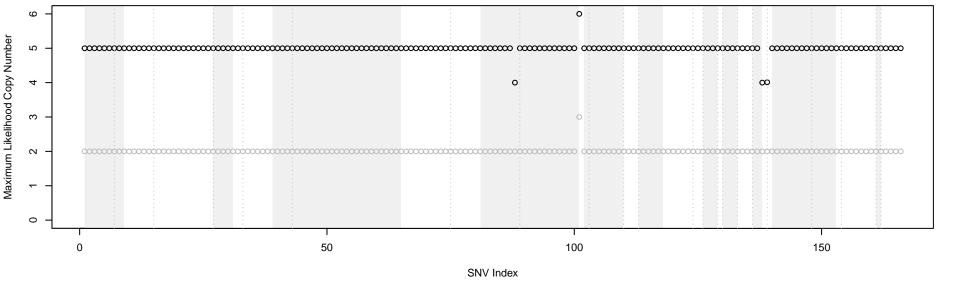


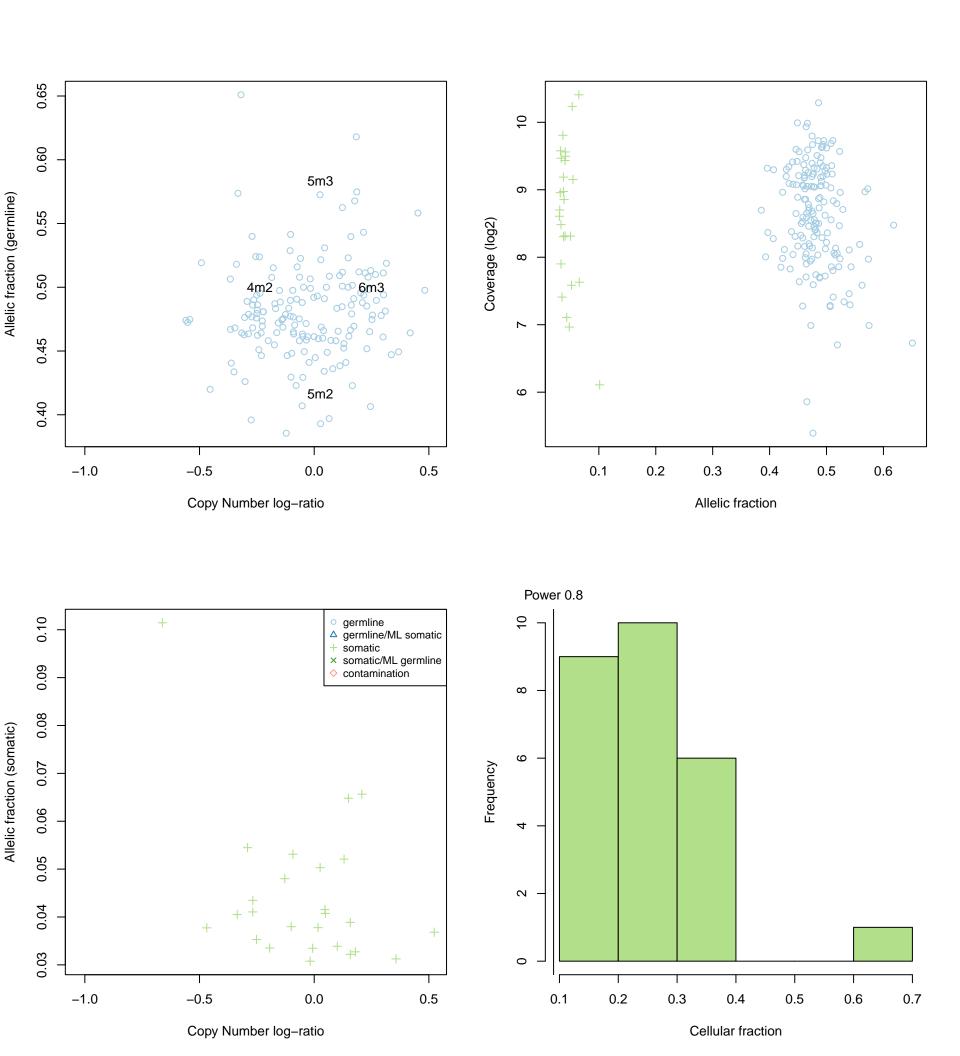
Purity: 0.67 Tumor ploidy: 4.889 6 2 3 7 Fraction Genome 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



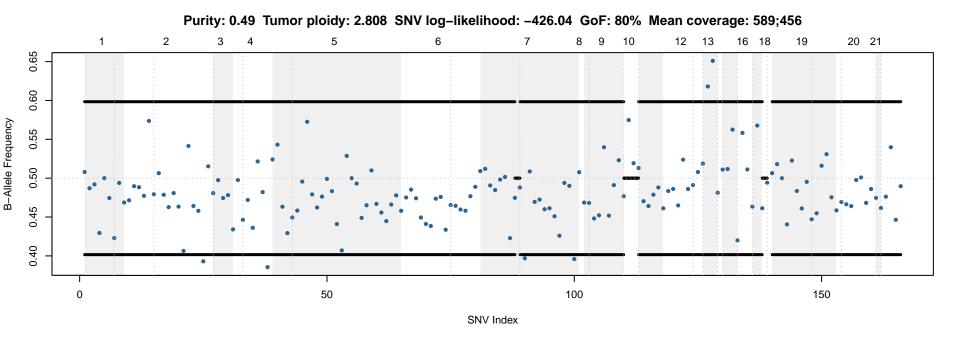
SCNA-fit log-likelihood: -4302.43



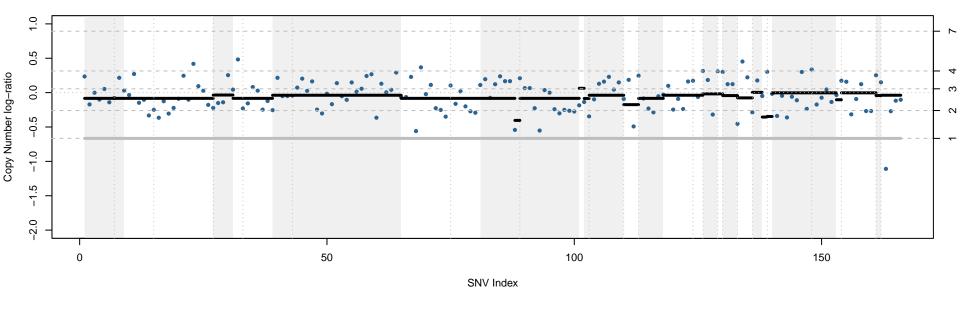


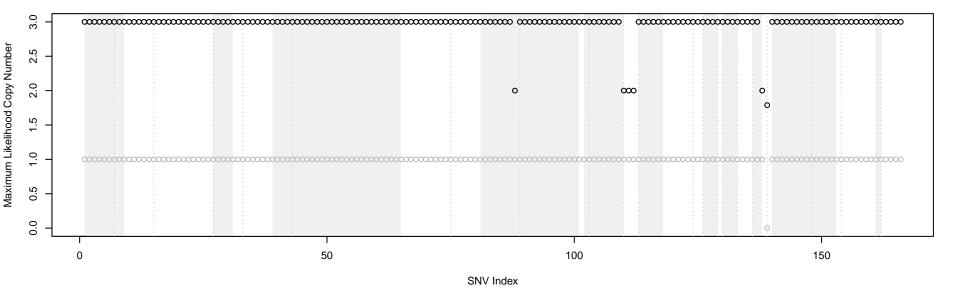


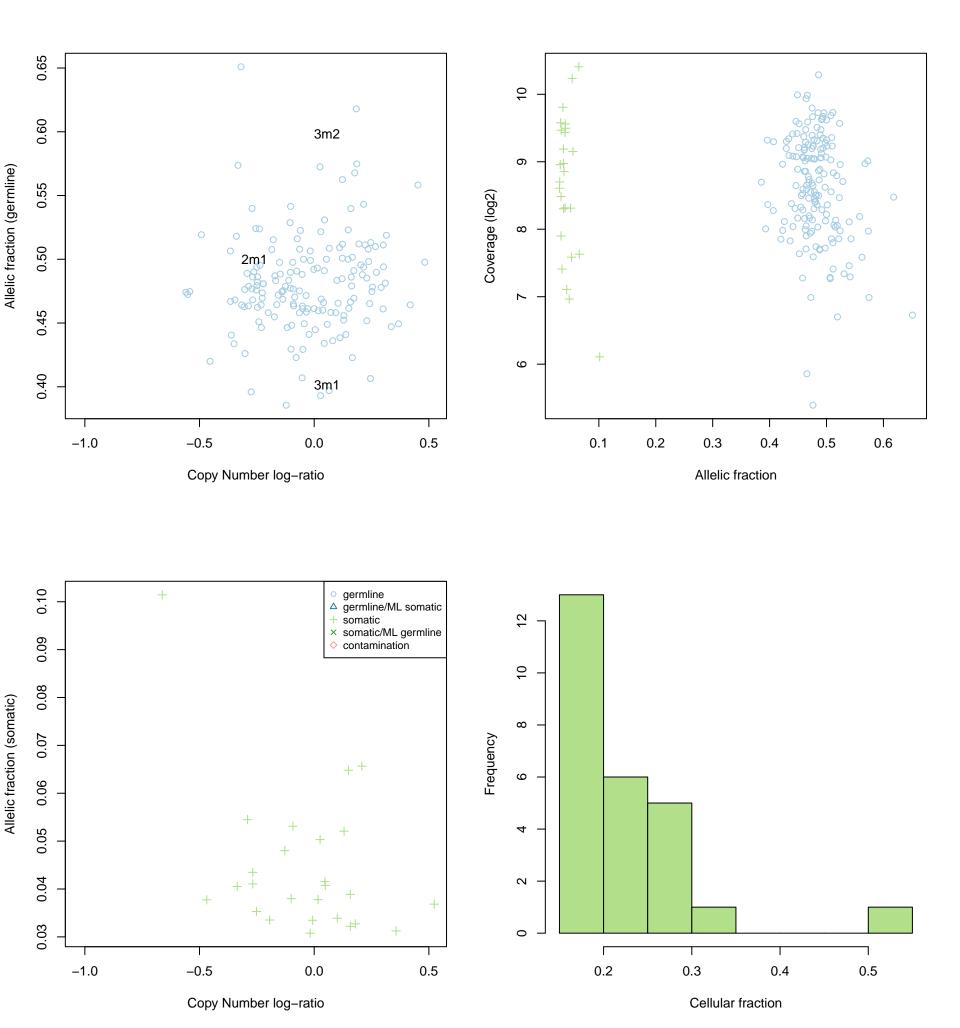
Purity: 0.49 Tumor ploidy: 2.808 3 2 7 Fraction Genome 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



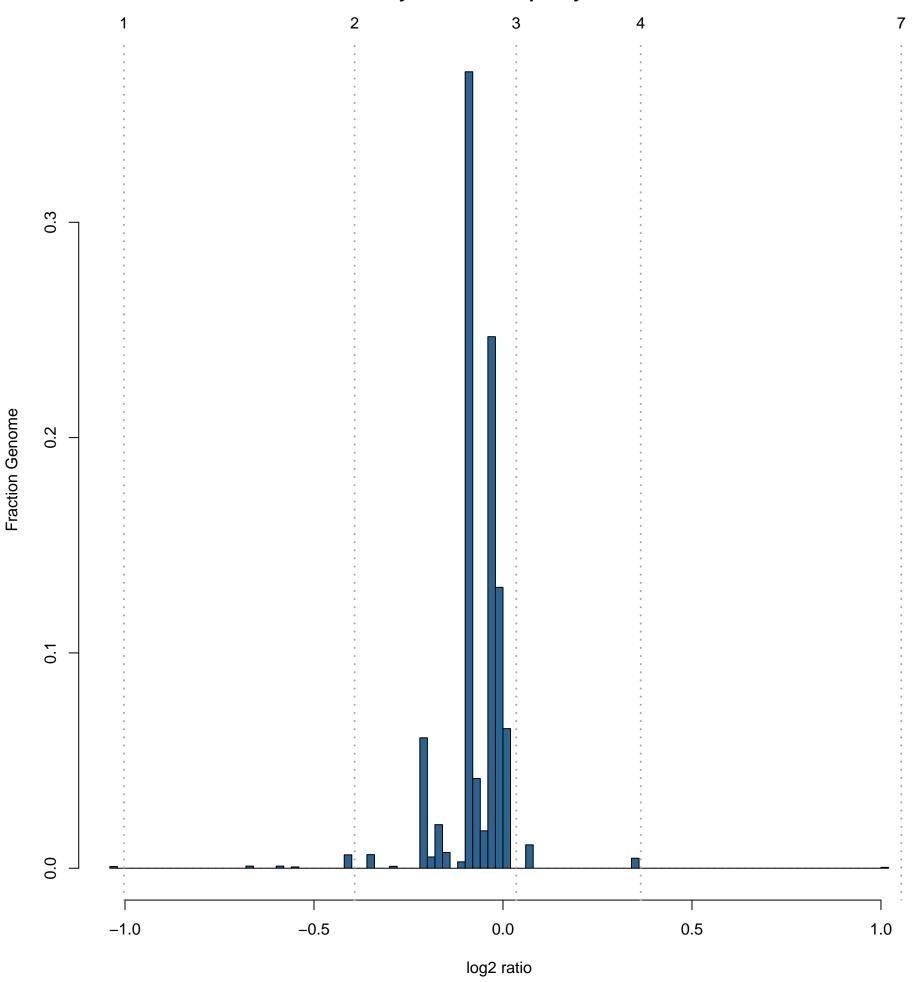
SCNA-fit log-likelihood: -4555.63

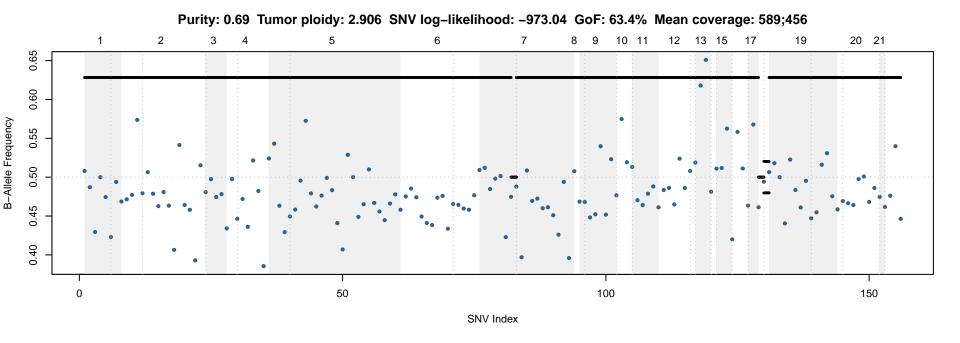






Purity: 0.69 Tumor ploidy: 2.906





SCNA-fit log-likelihood: -4526.77

