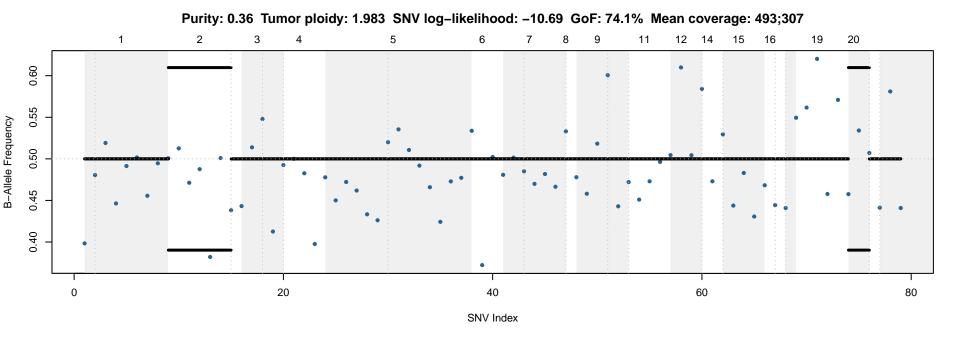
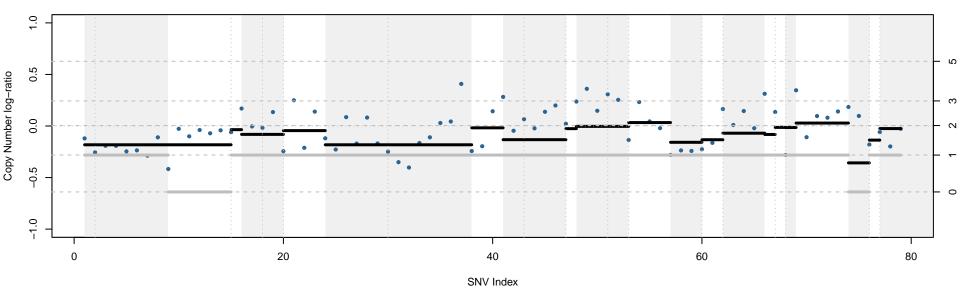
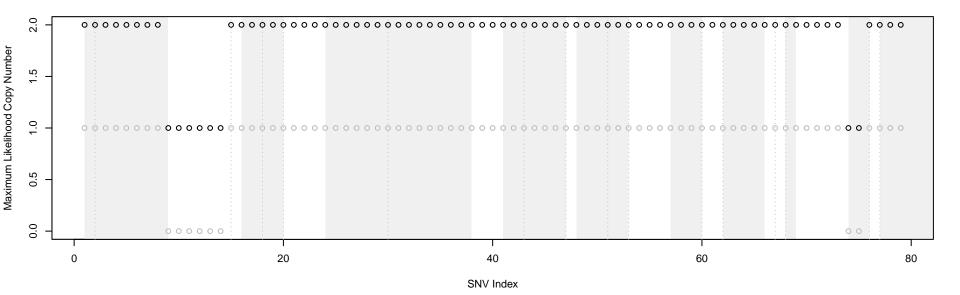
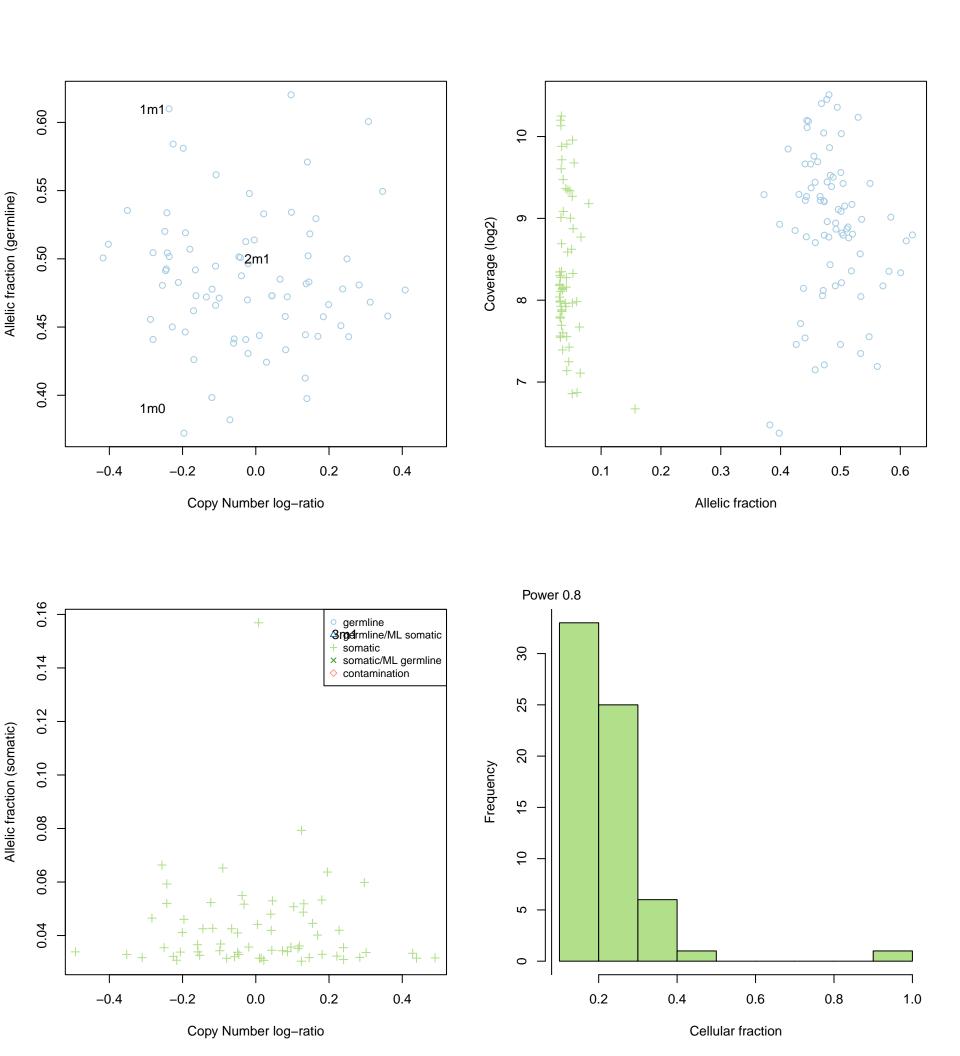
Purity: 0.36 Tumor ploidy: 1.983 2 0 3 5 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 log2 ratio



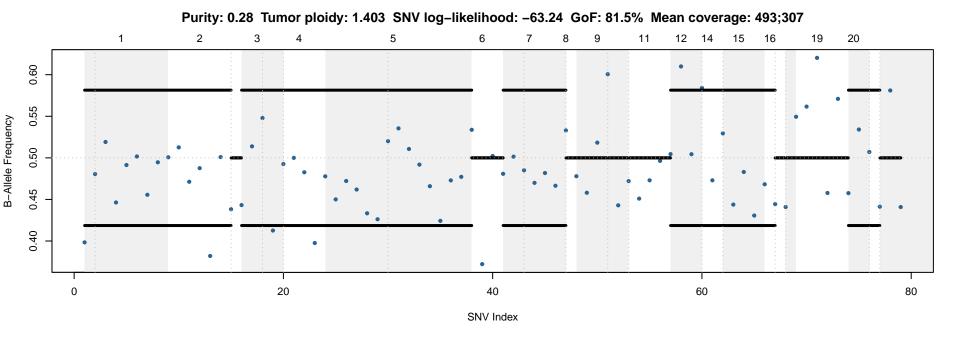
SCNA-fit log-likelihood: -13564.42



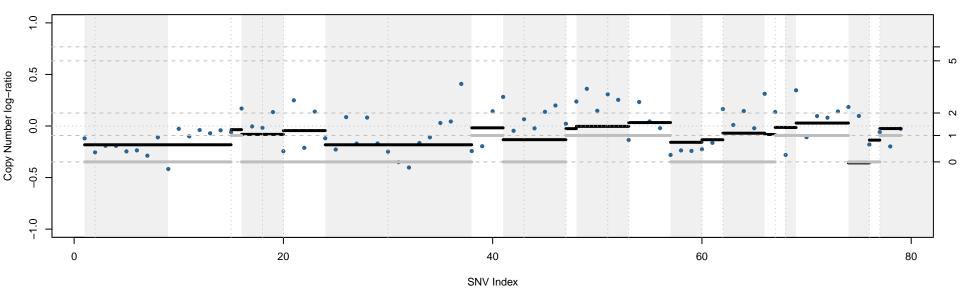


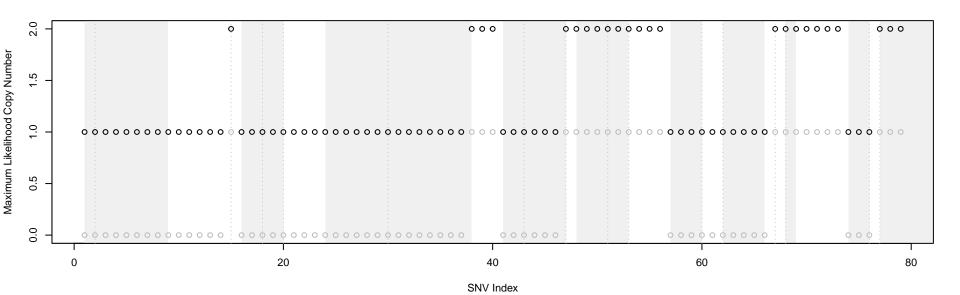


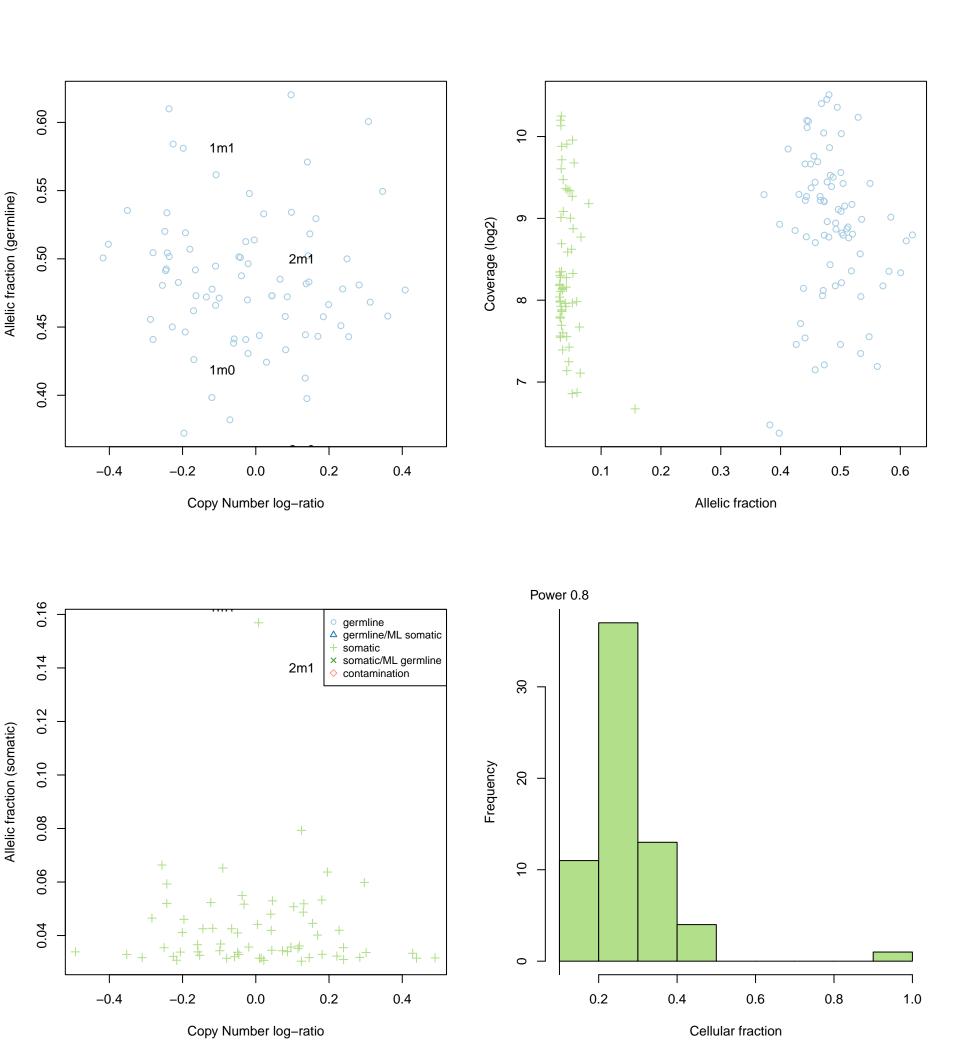
Purity: 0.28 Tumor ploidy: 1.403 0 5 Fraction Genome 0.10 0.05 0.00 -0.6 -0.4 -0.2 0.0 0.2 0.4 0.6 log2 ratio



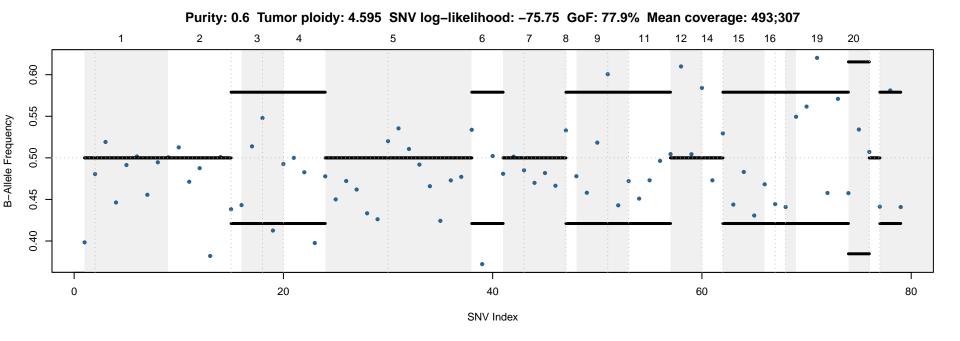
SCNA-fit log-likelihood: -13571.49



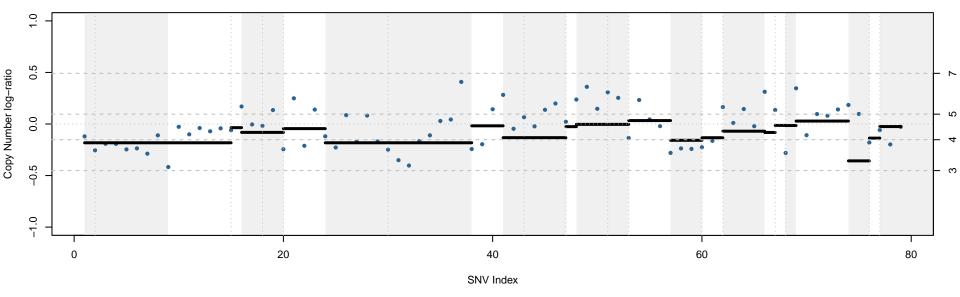


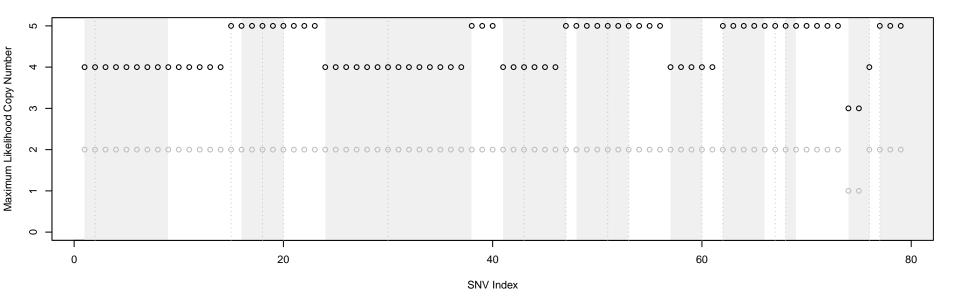


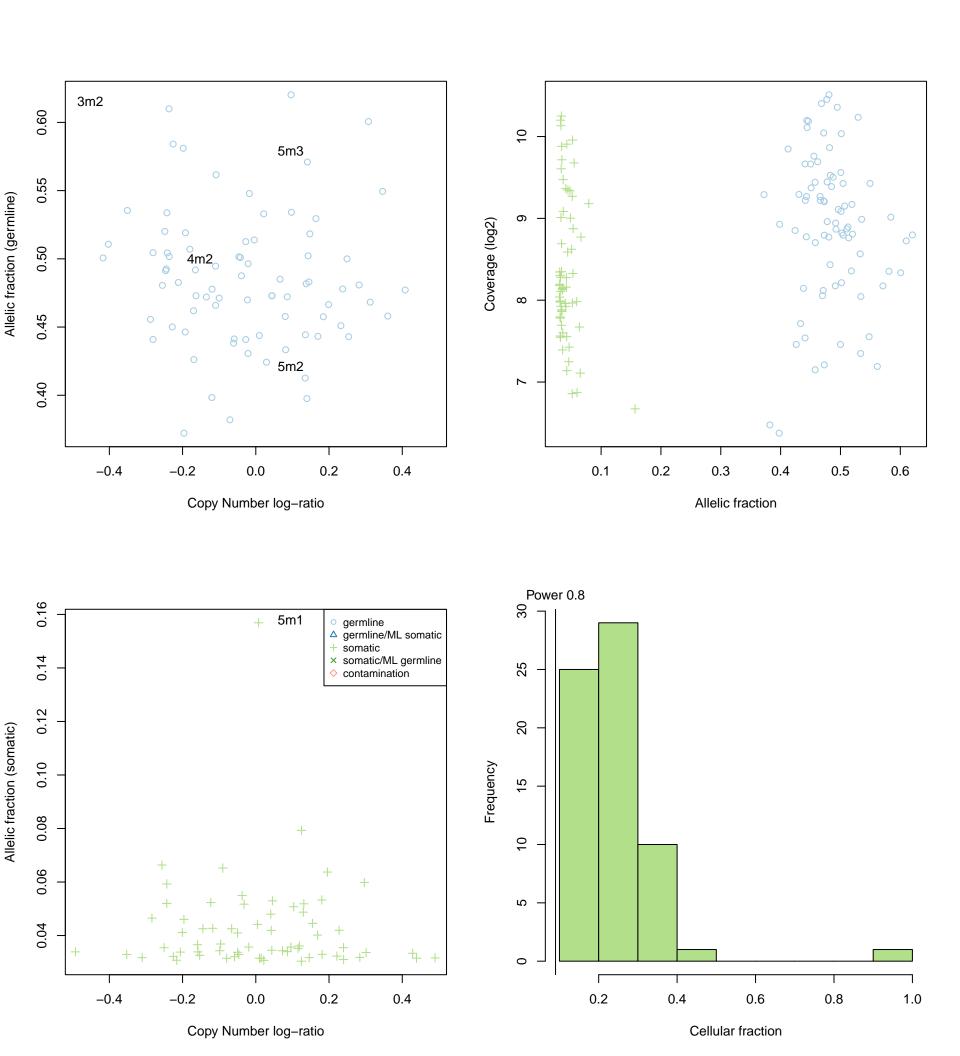
Purity: 0.6 Tumor ploidy: 4.595 5 3 7 0.30 0.25 0.20 Fraction Genome 0.15 0.05 0.00 -0.5 -1.5 -1.0 0.0 0.5 log2 ratio



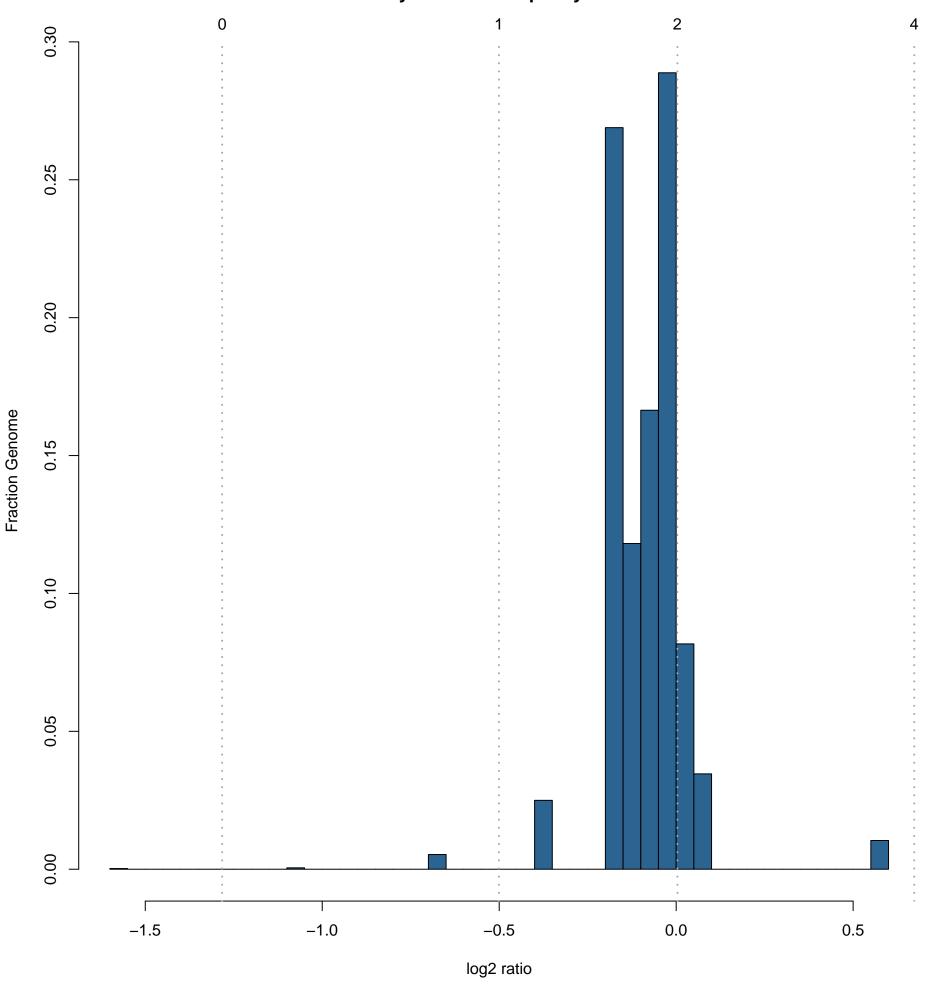
SCNA-fit log-likelihood: -13608.41

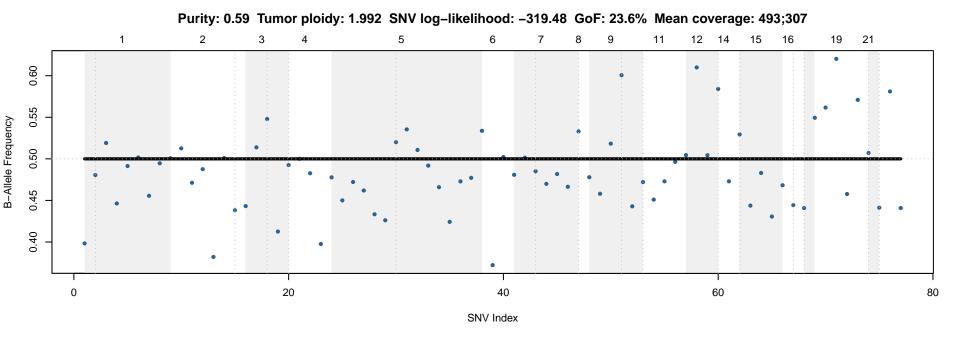




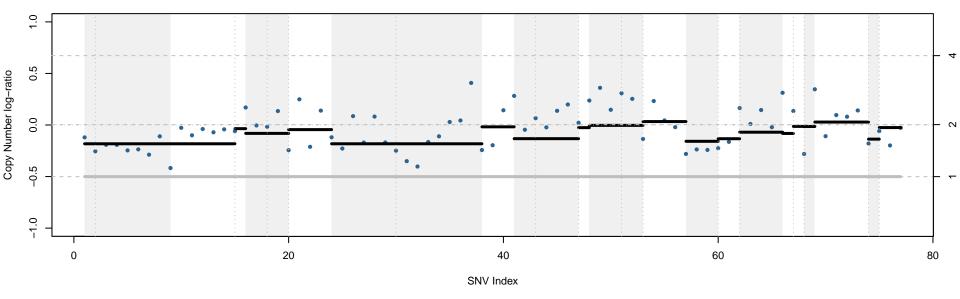


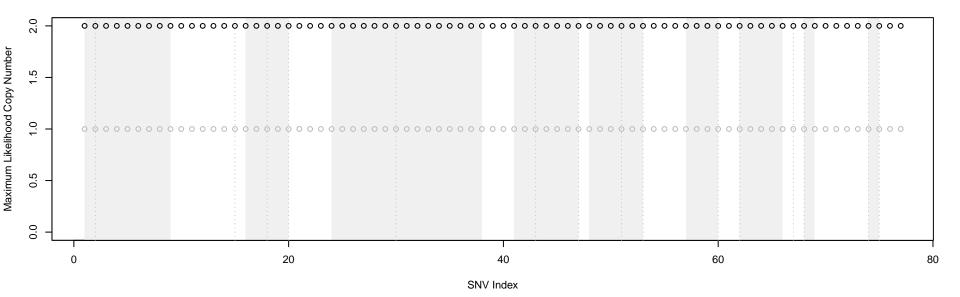
Purity: 0.59 Tumor ploidy: 1.992

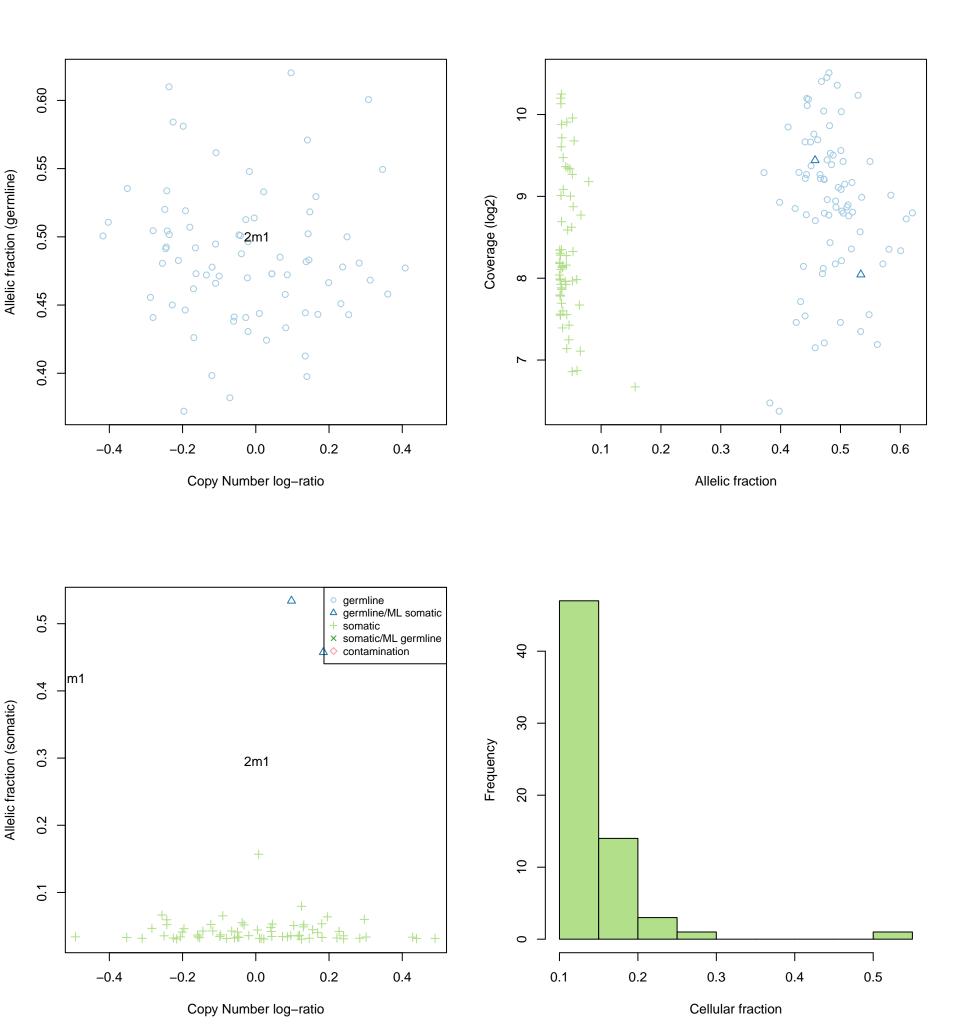




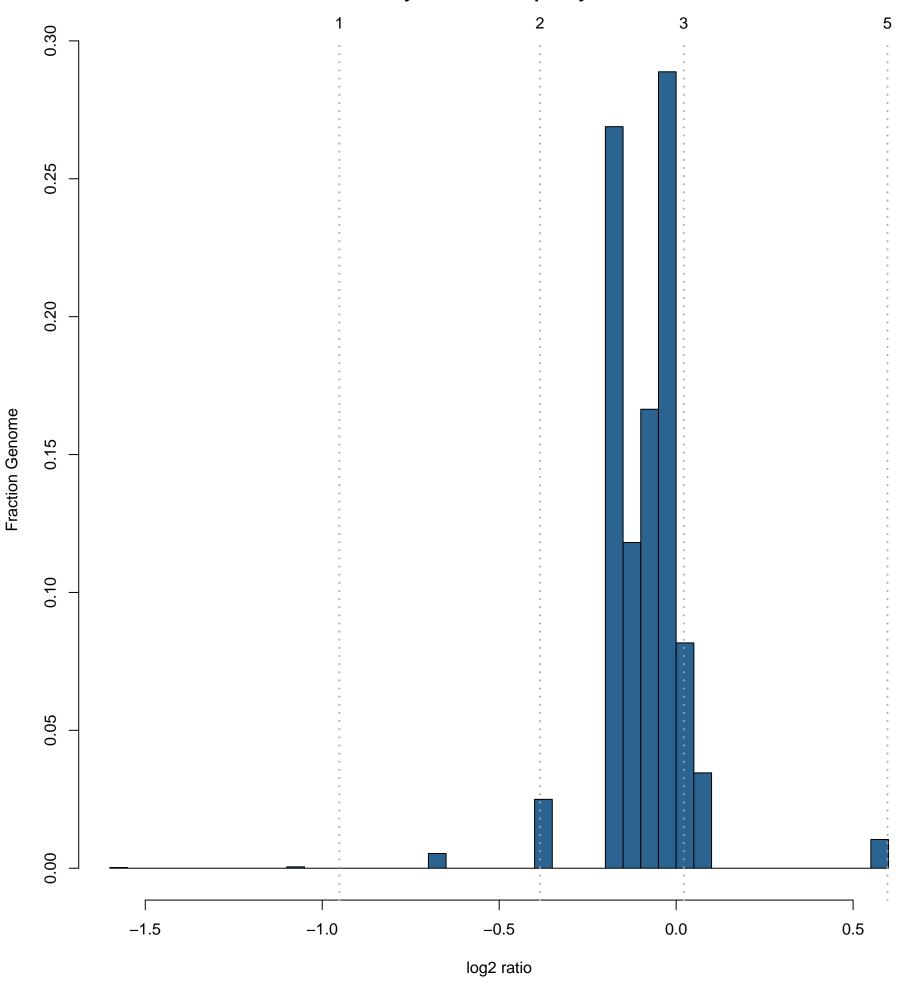
SCNA-fit log-likelihood: -13717.43

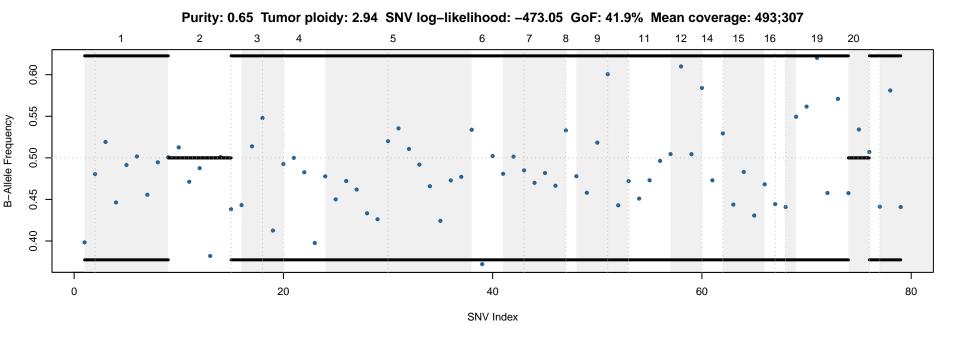






Purity: 0.65 Tumor ploidy: 2.94





SCNA-fit log-likelihood: -13749.67

