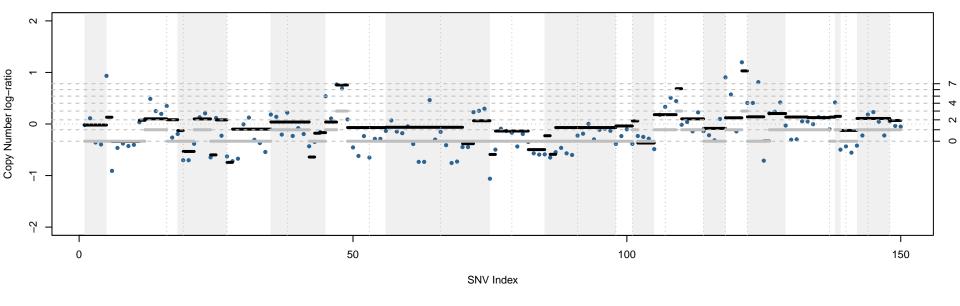
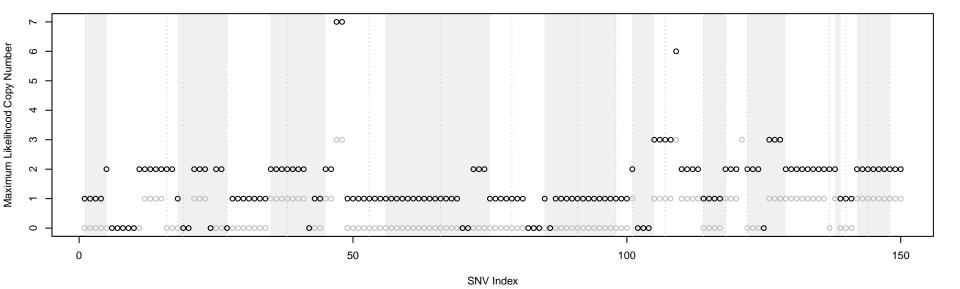
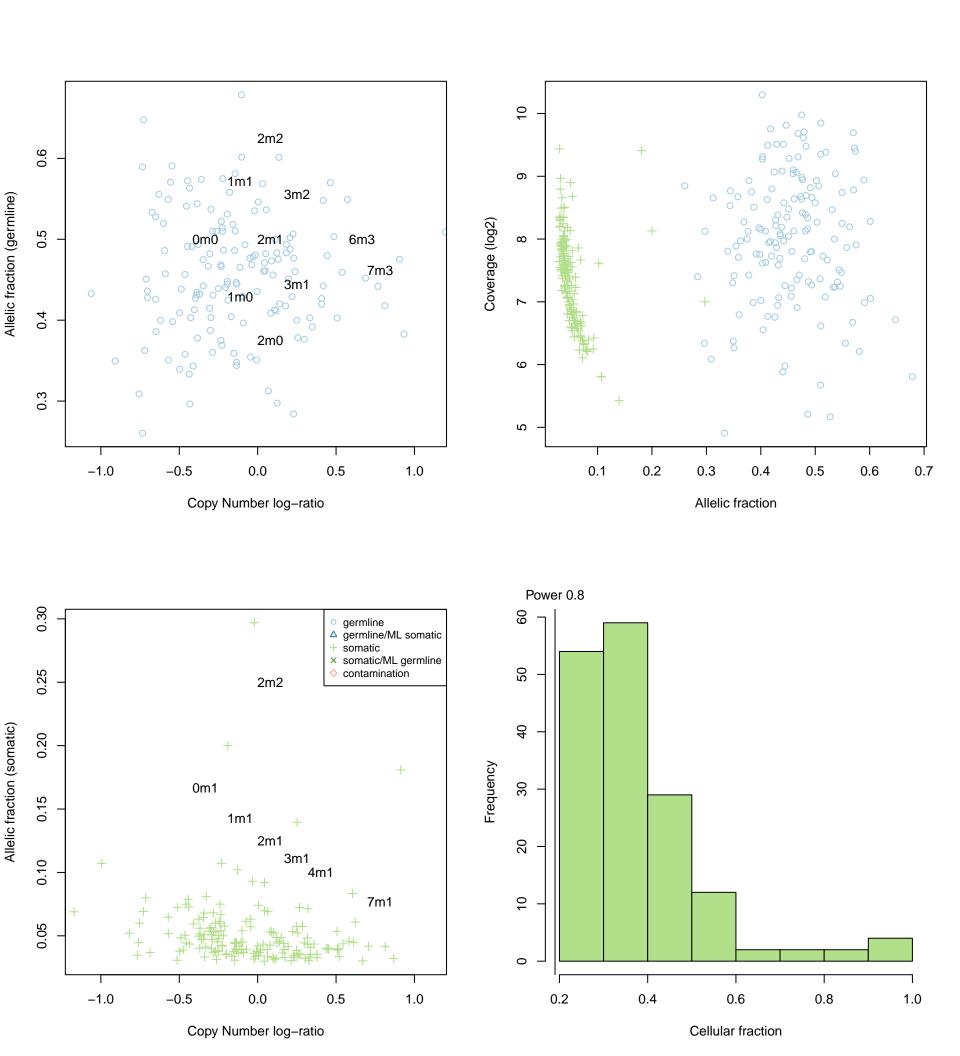
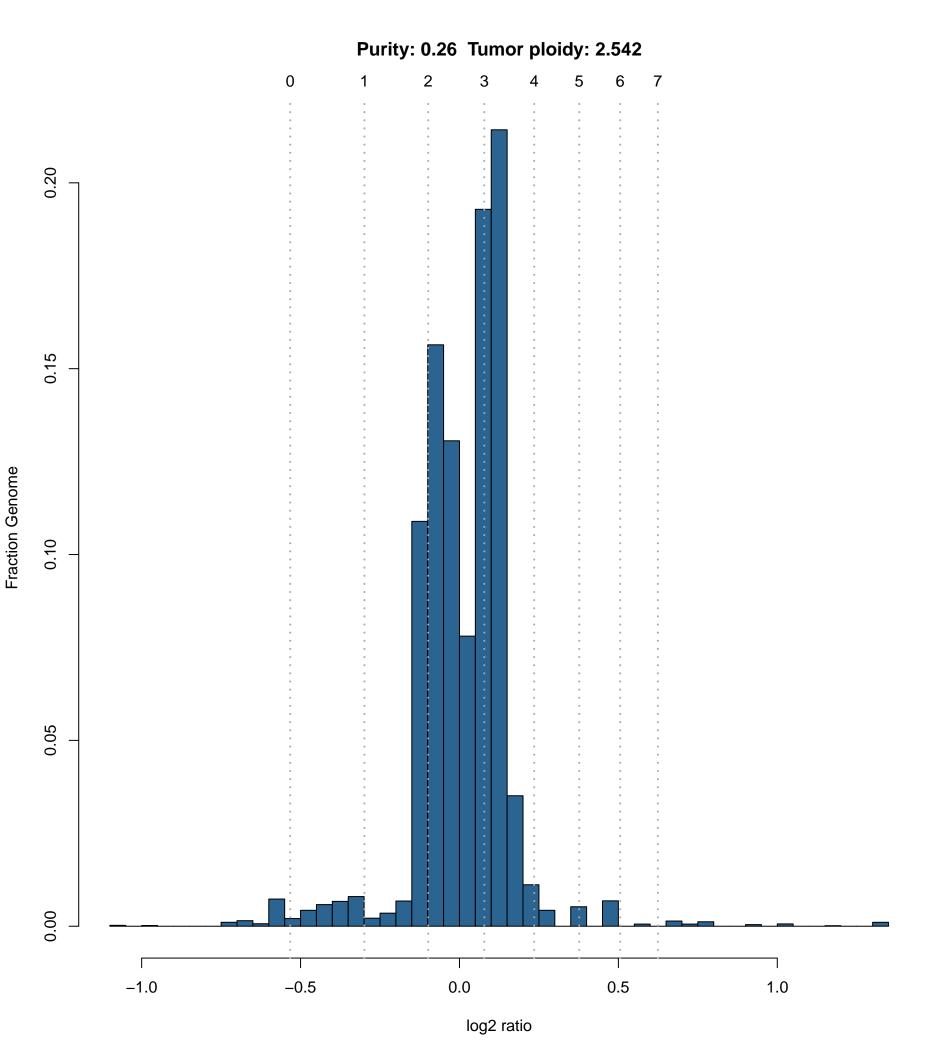


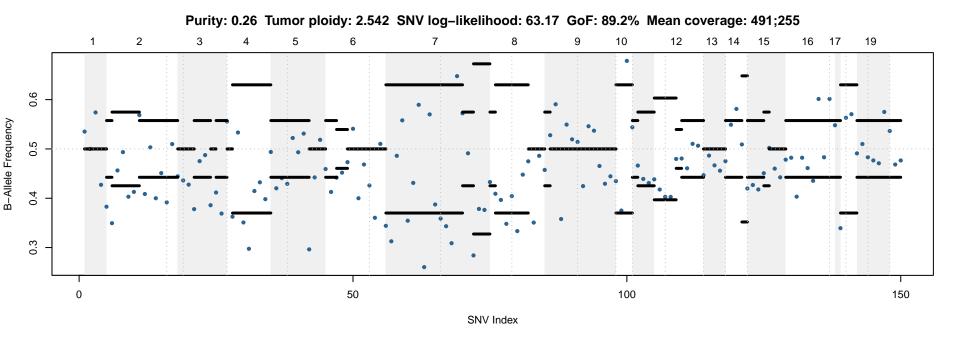
SCNA-fit log-likelihood: -10646.32



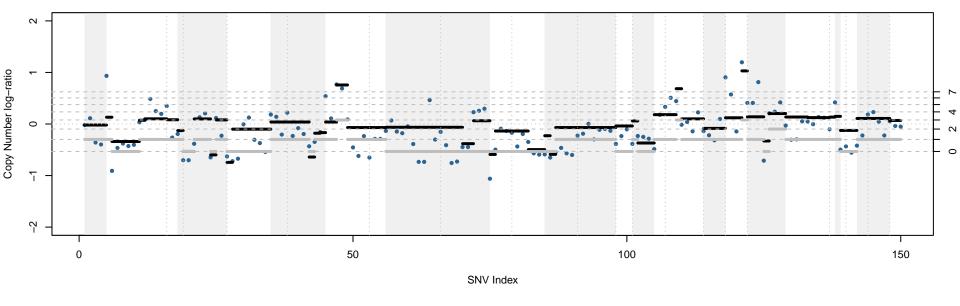


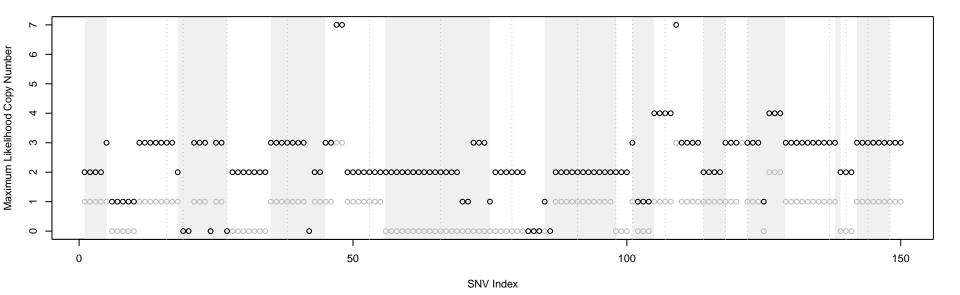


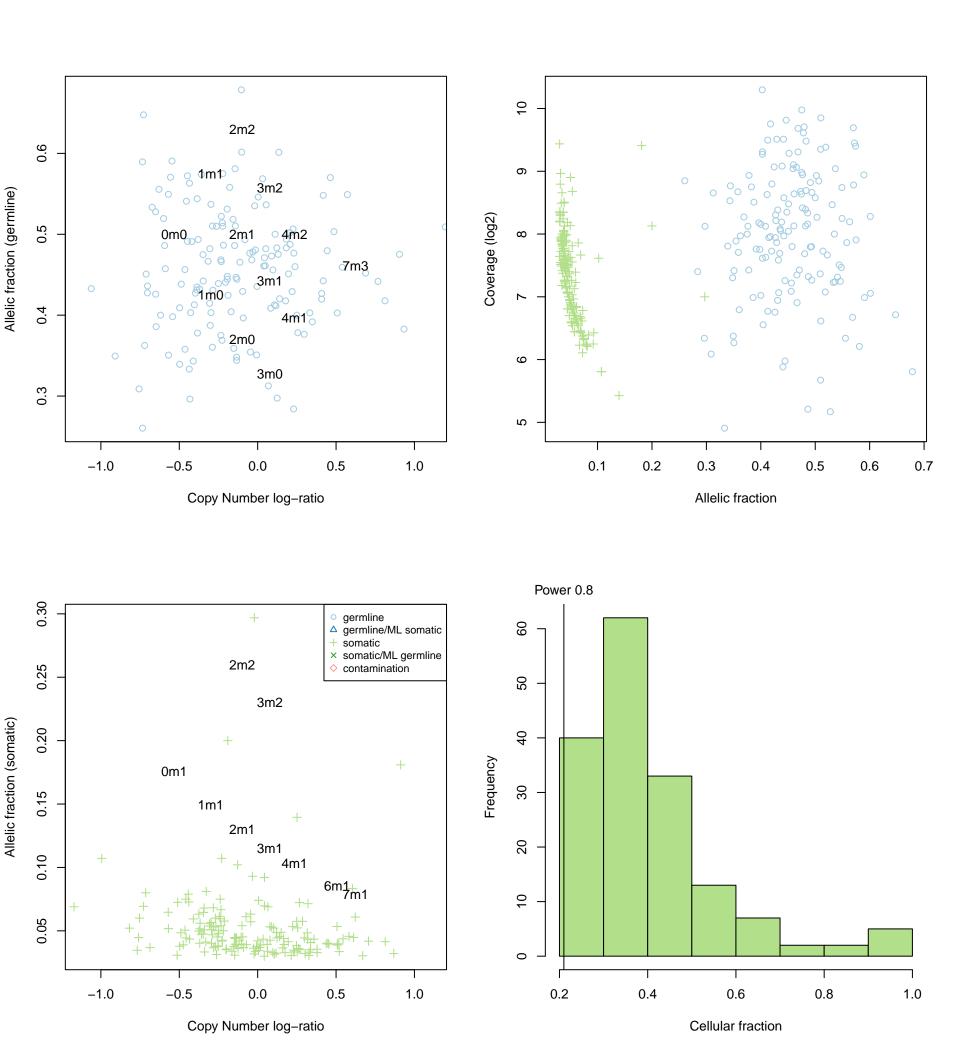


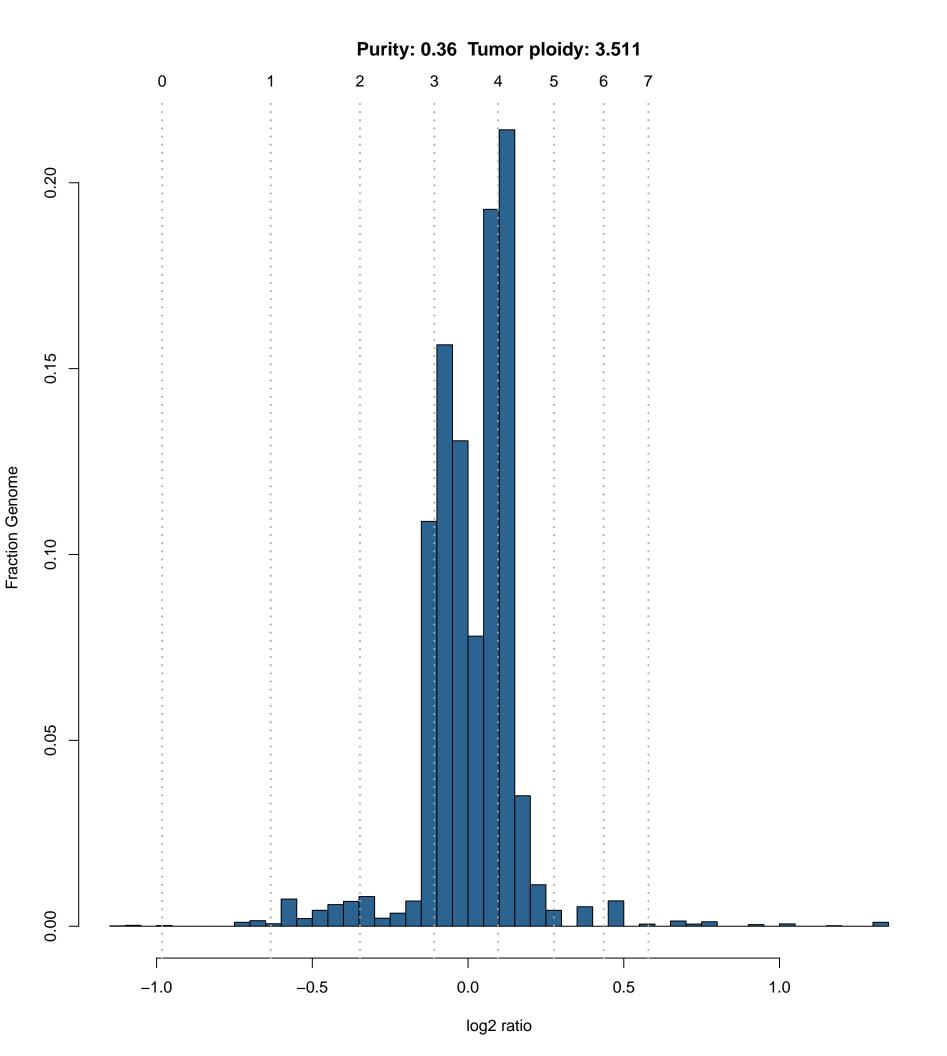


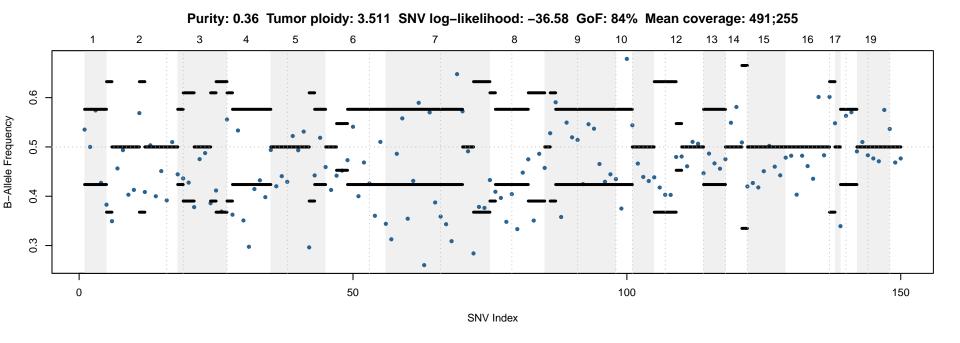
SCNA-fit log-likelihood: -10534.02



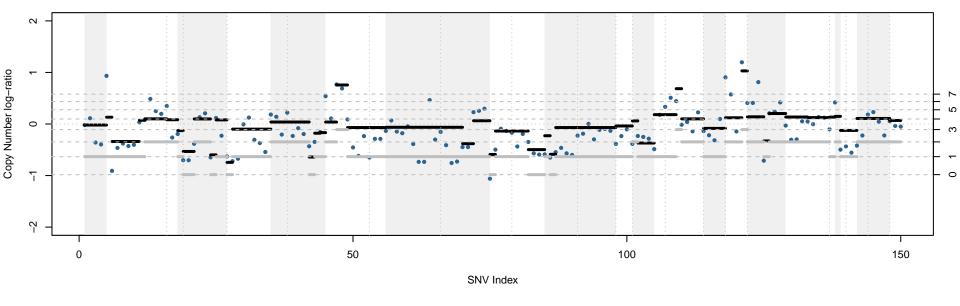


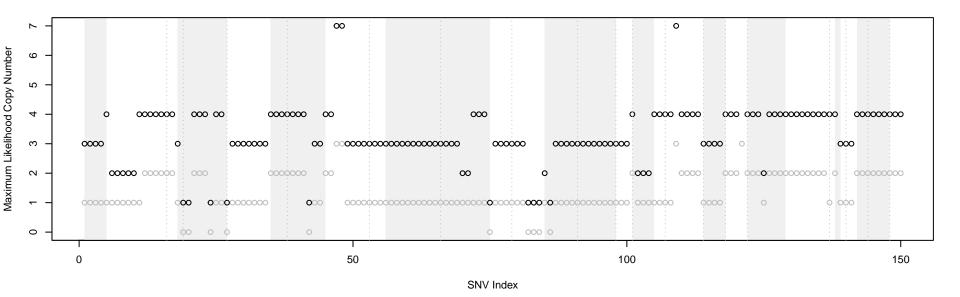


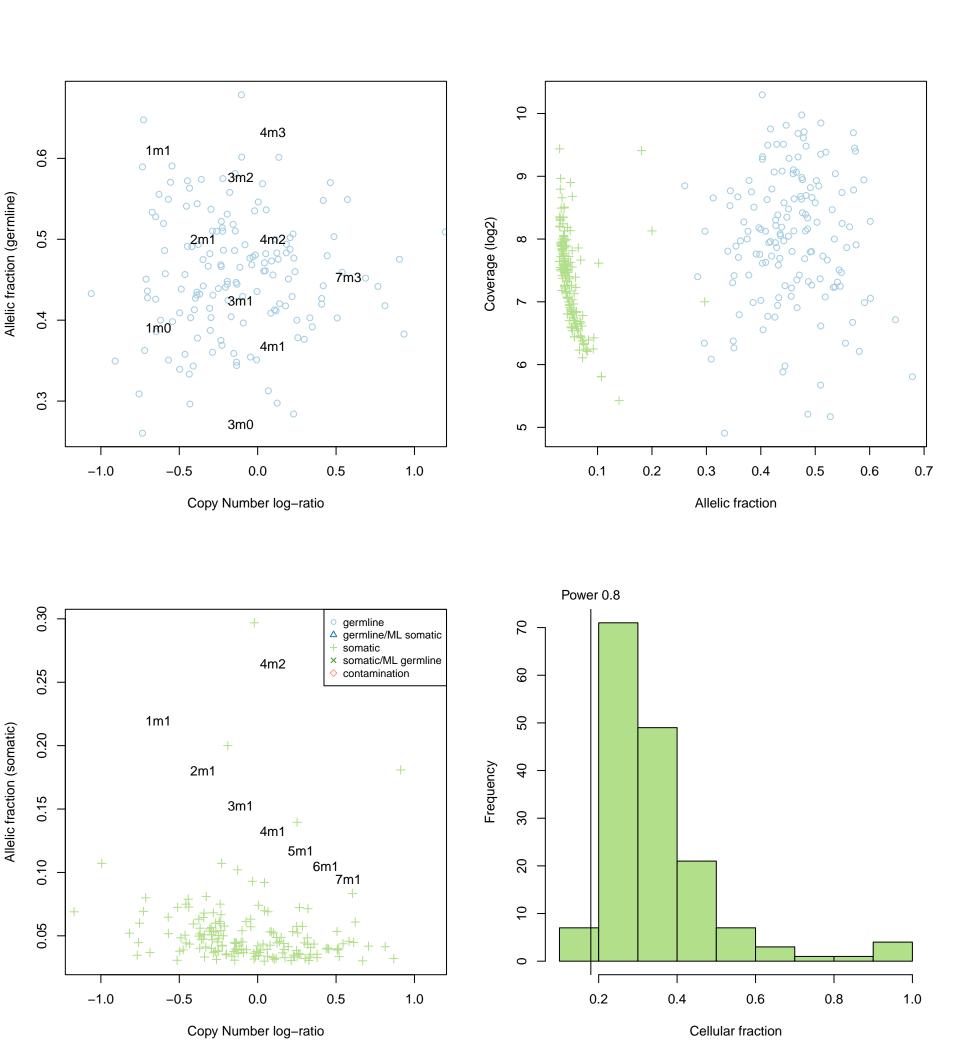


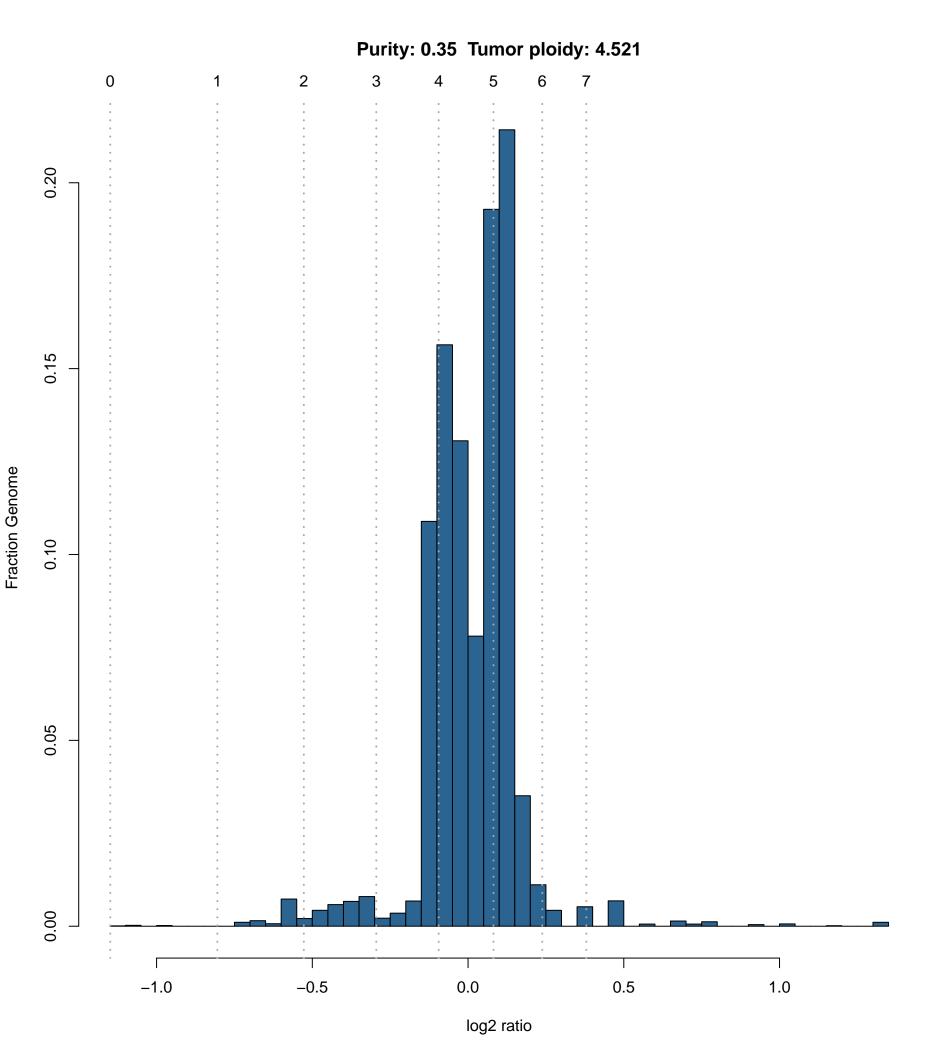


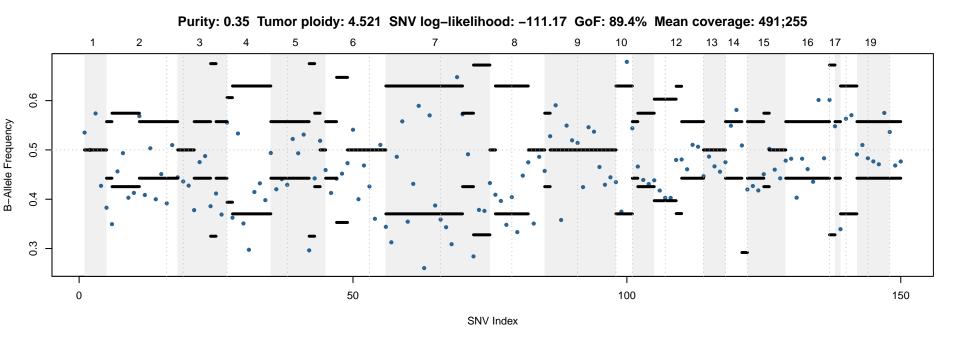
SCNA-fit log-likelihood: -10538.42



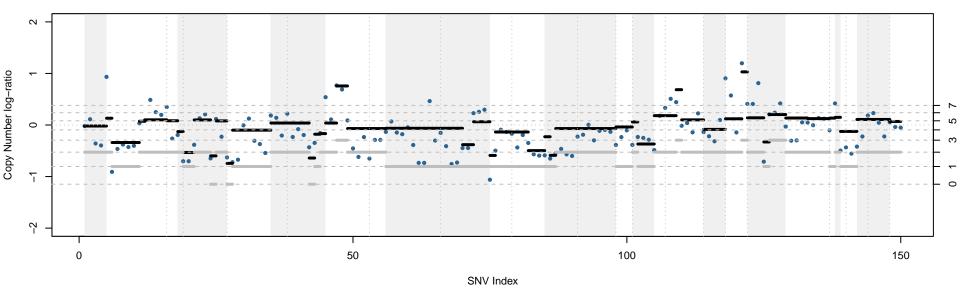


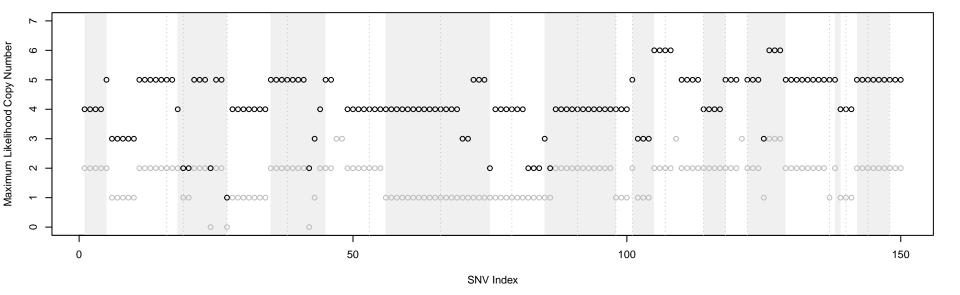


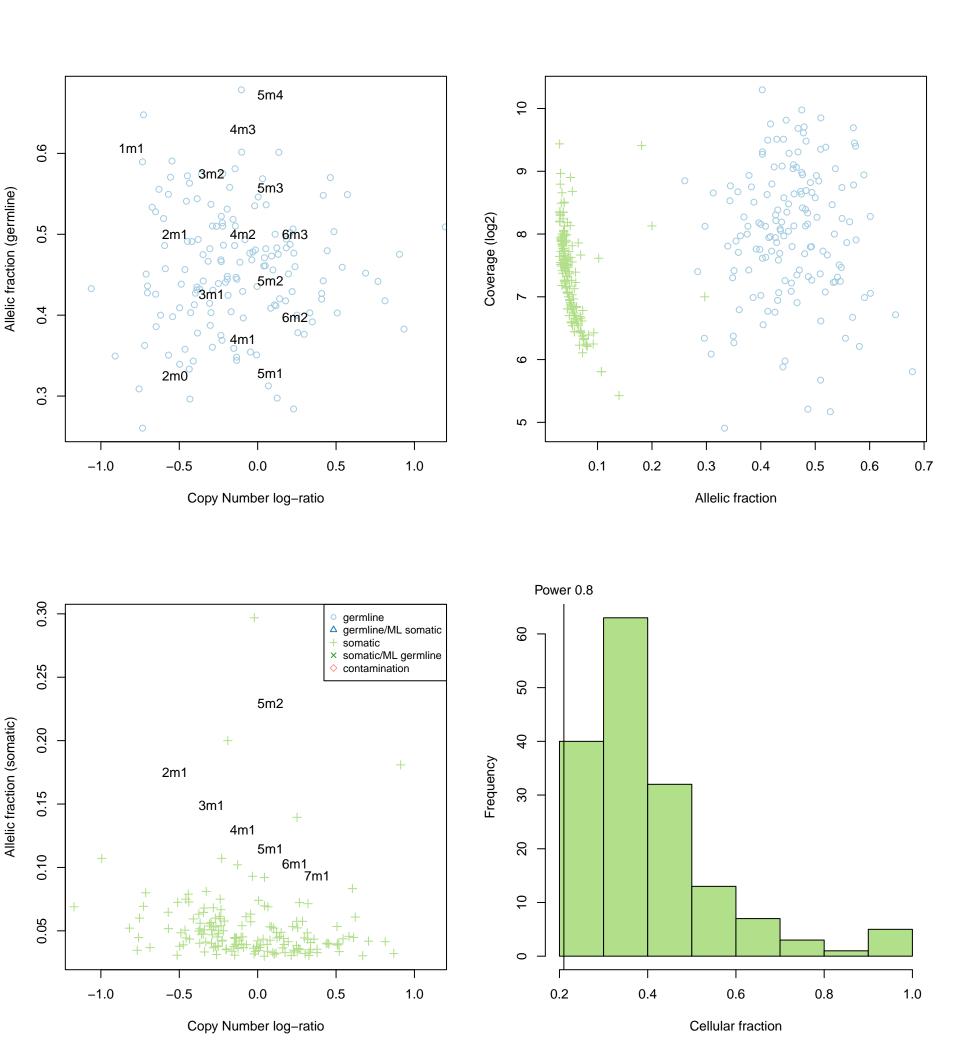


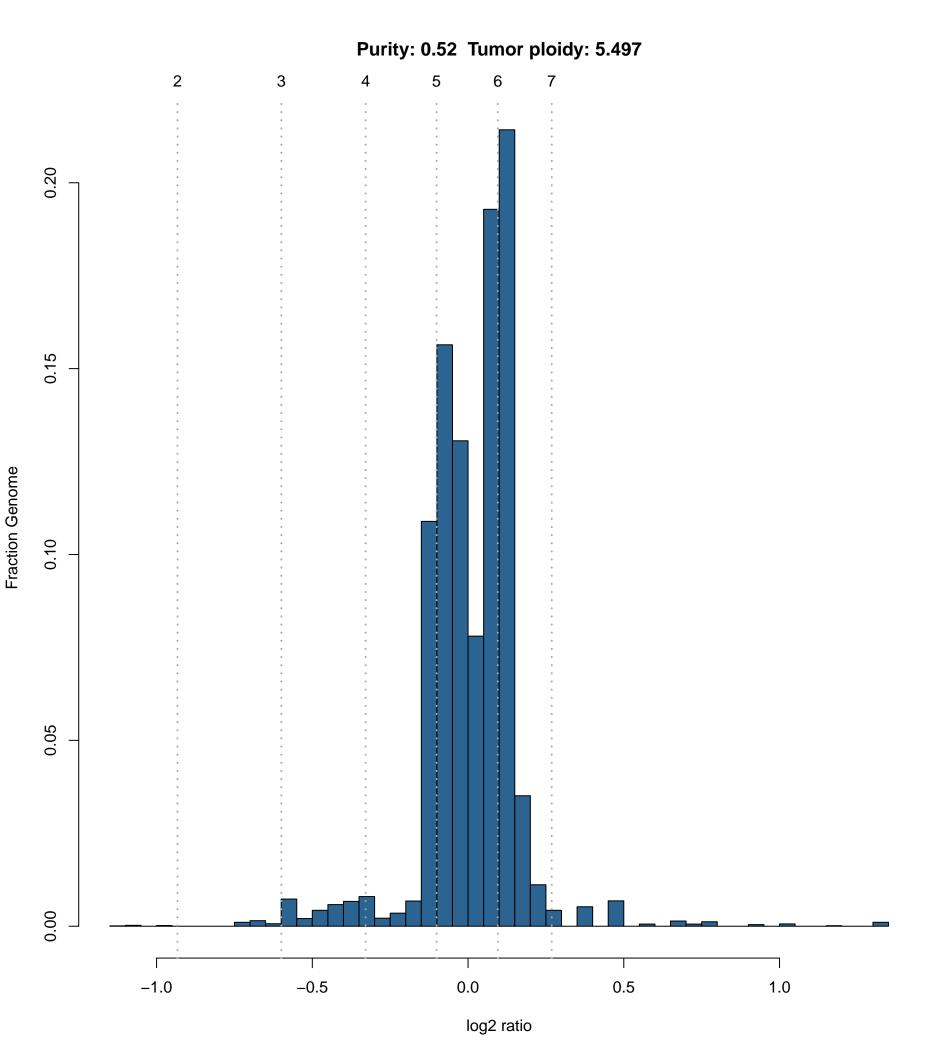


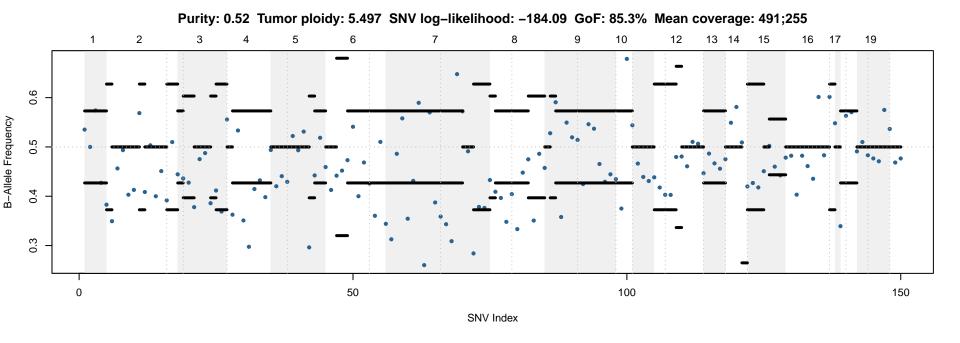
SCNA-fit log-likelihood: -10594.91



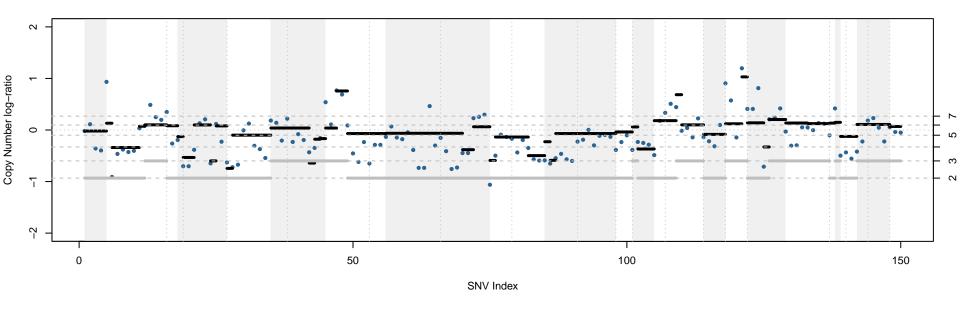


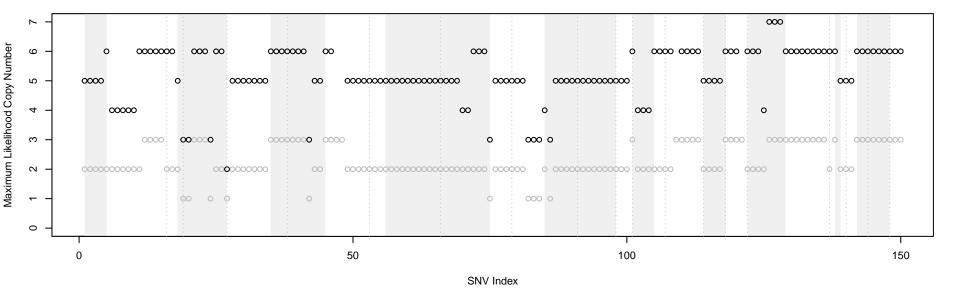


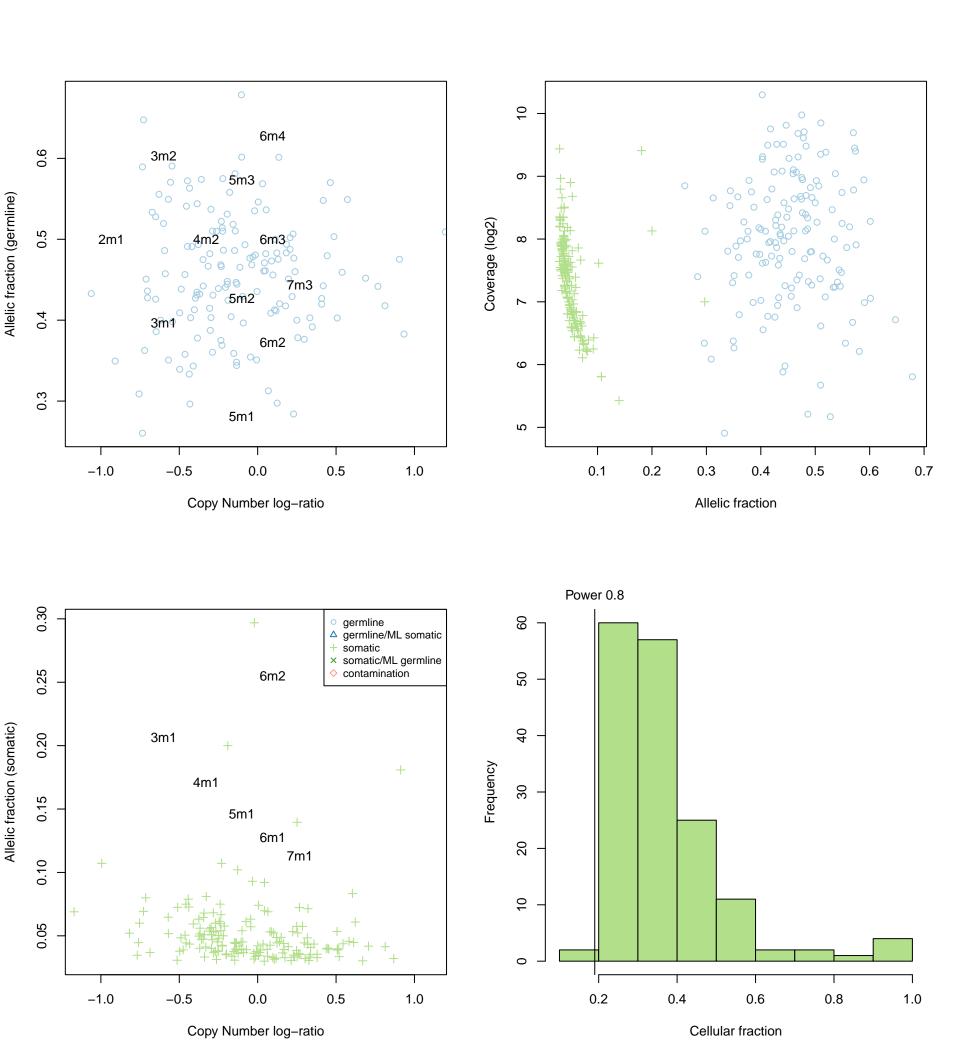




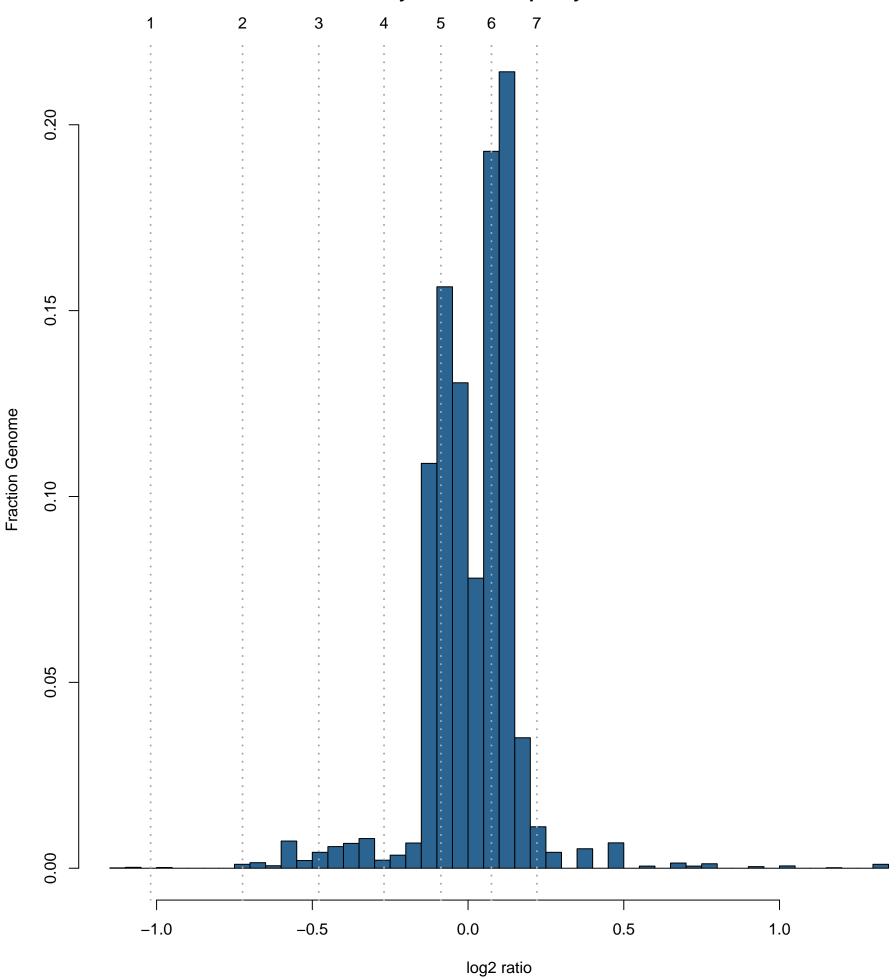
SCNA-fit log-likelihood: -10644.58

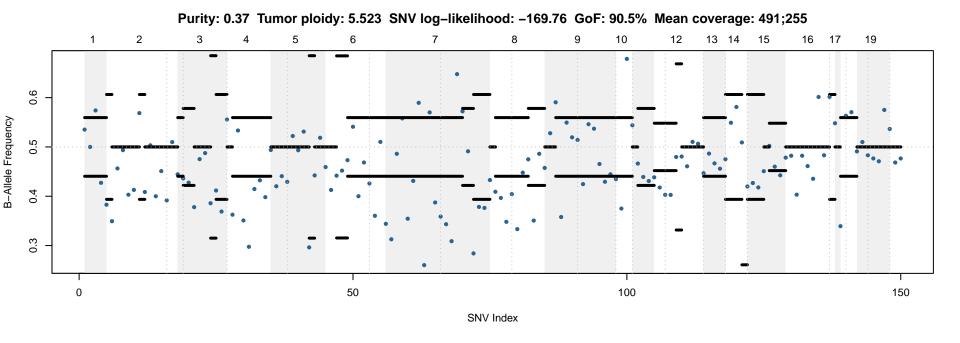




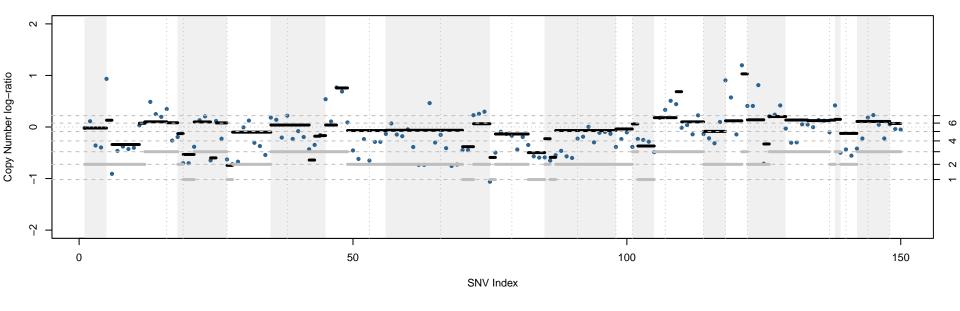


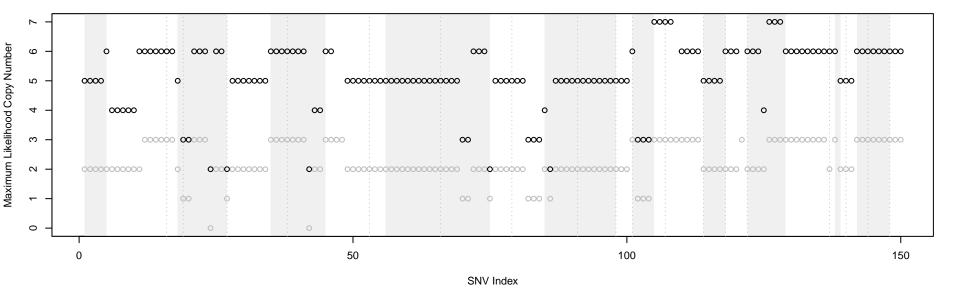
Purity: 0.37 Tumor ploidy: 5.523

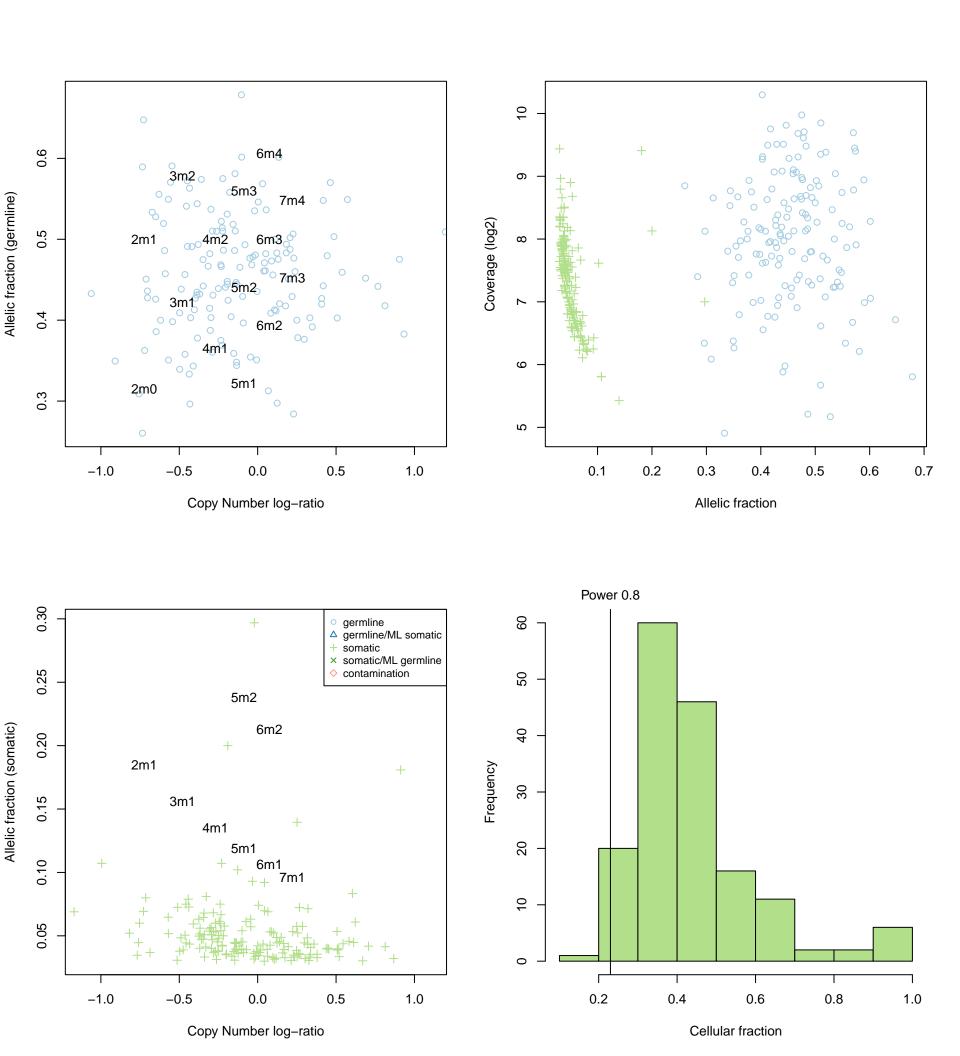


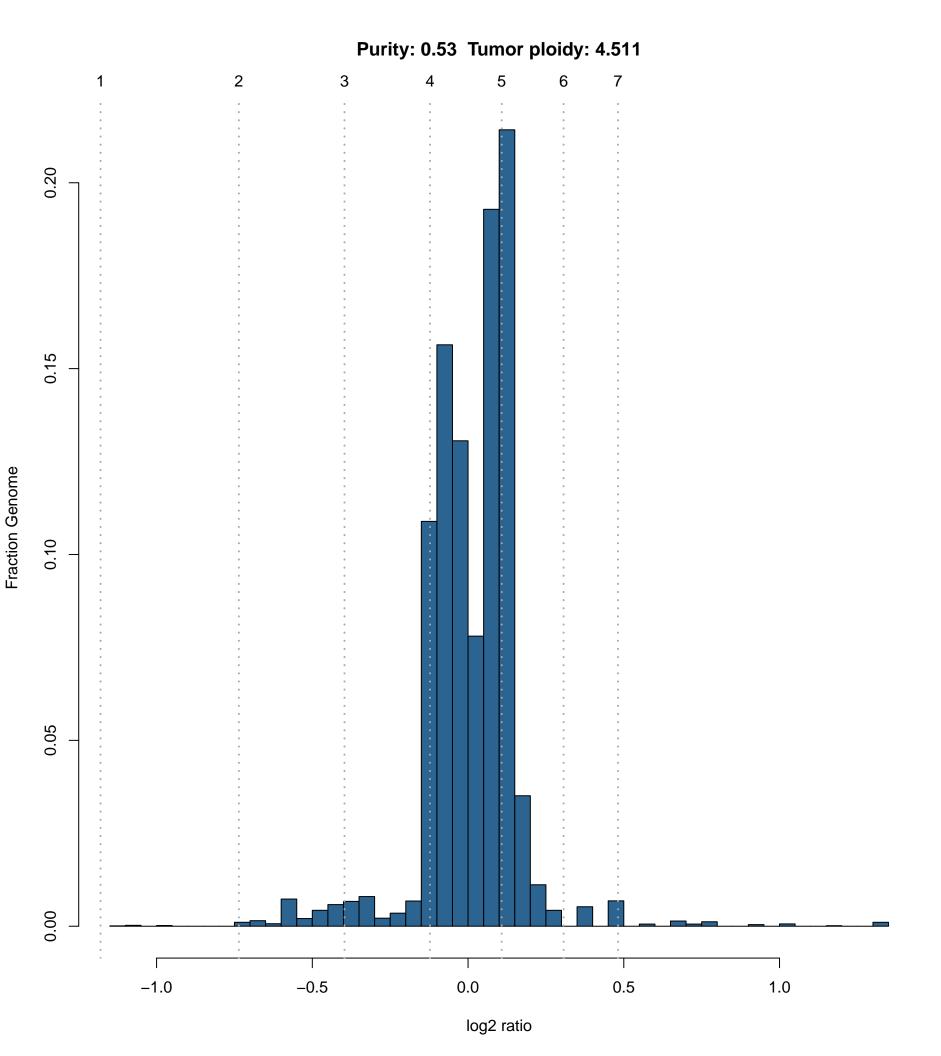


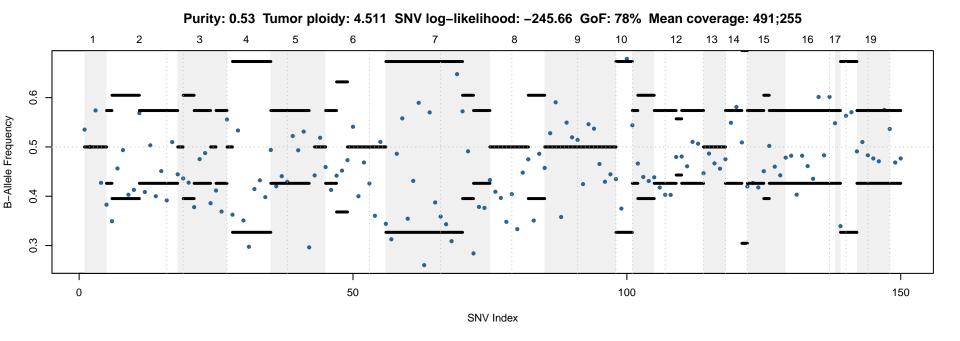
SCNA-fit log-likelihood: -10736.1



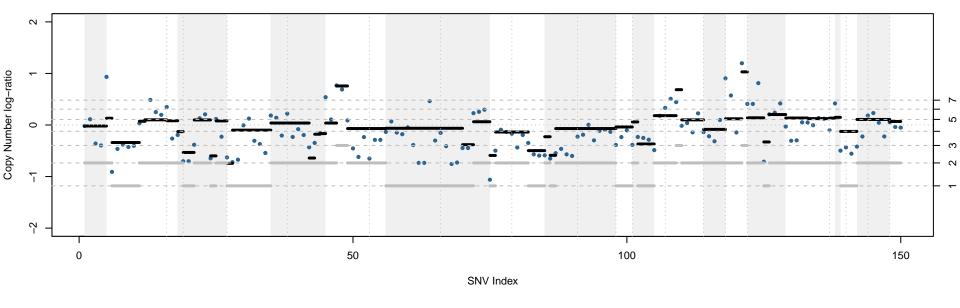


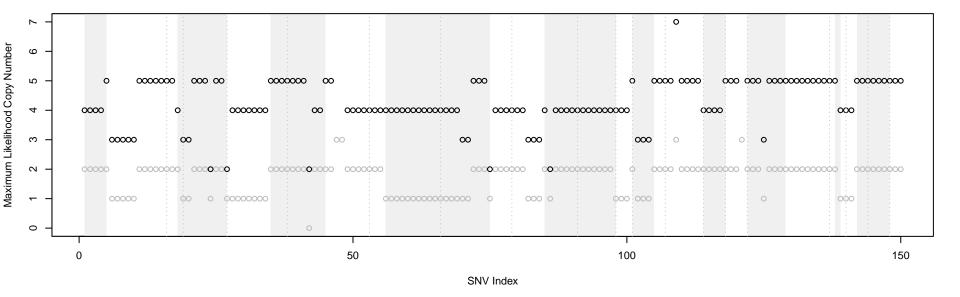


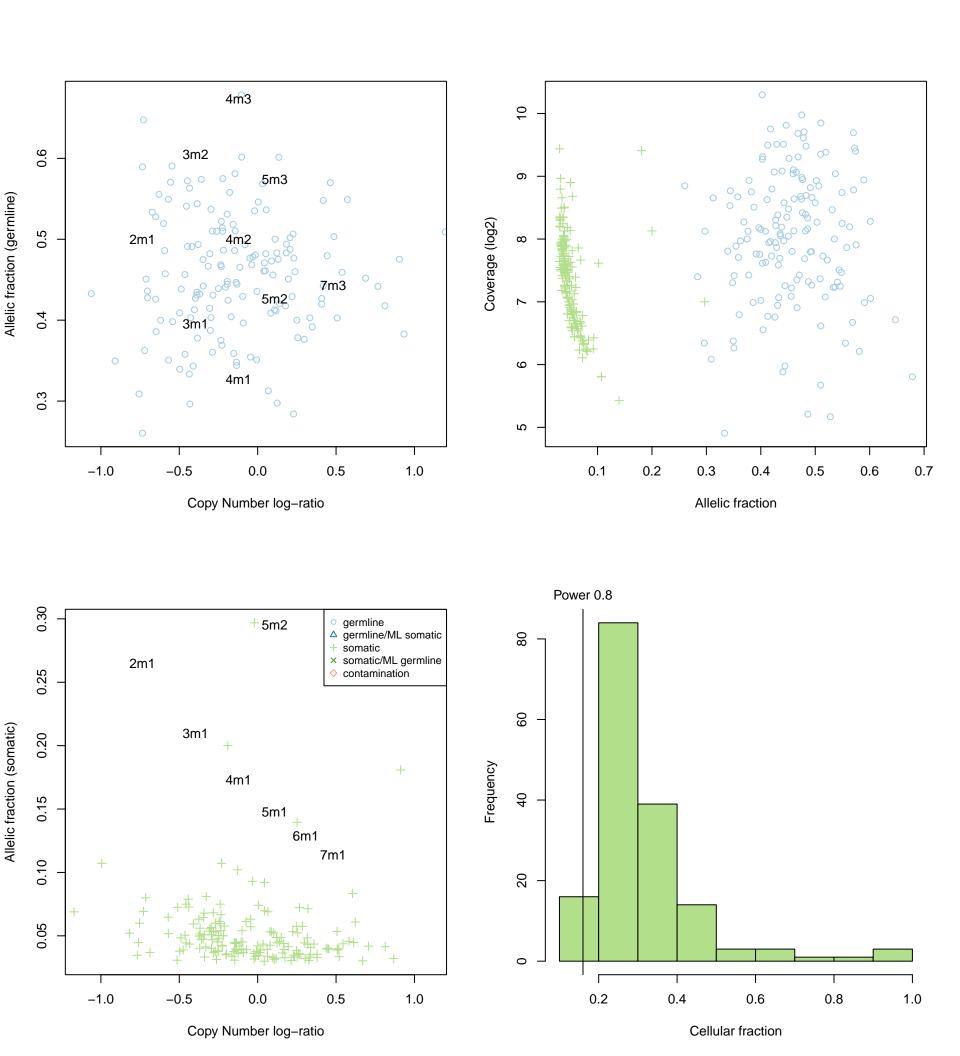




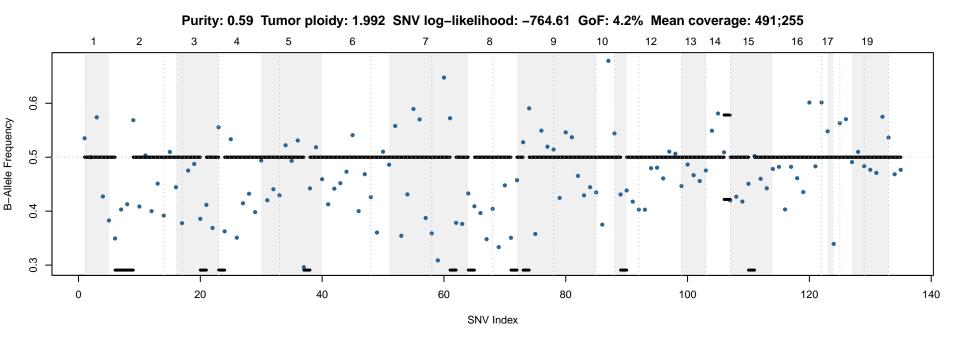
SCNA-fit log-likelihood: -10621.19



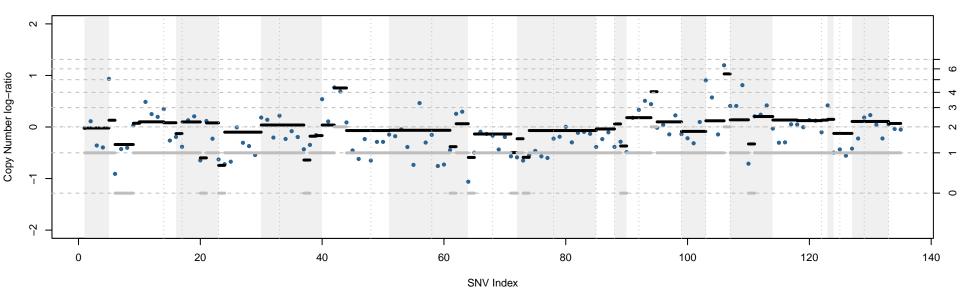


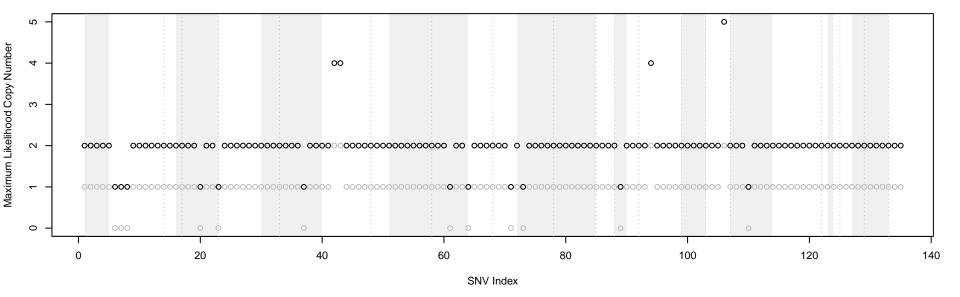


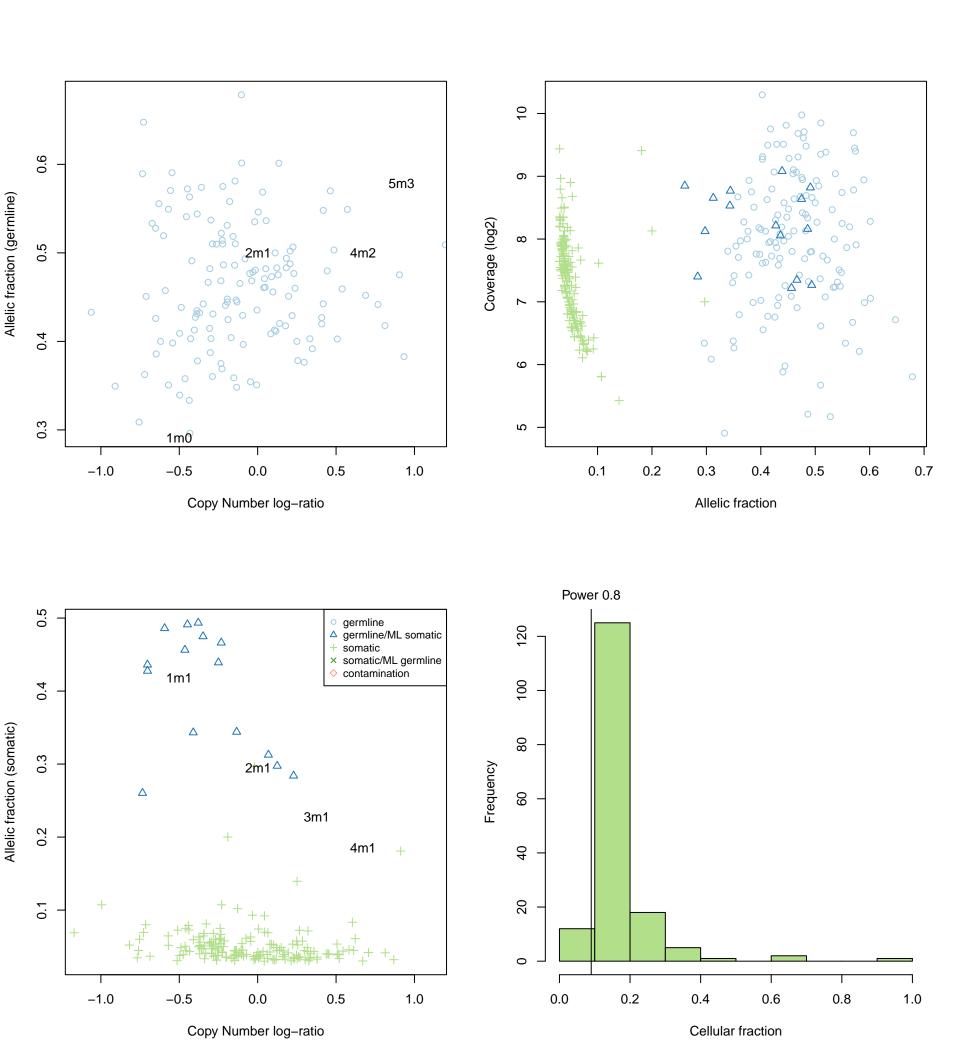
Purity: 0.59 Tumor ploidy: 1.992 2 6 7 5 Fraction Genome 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



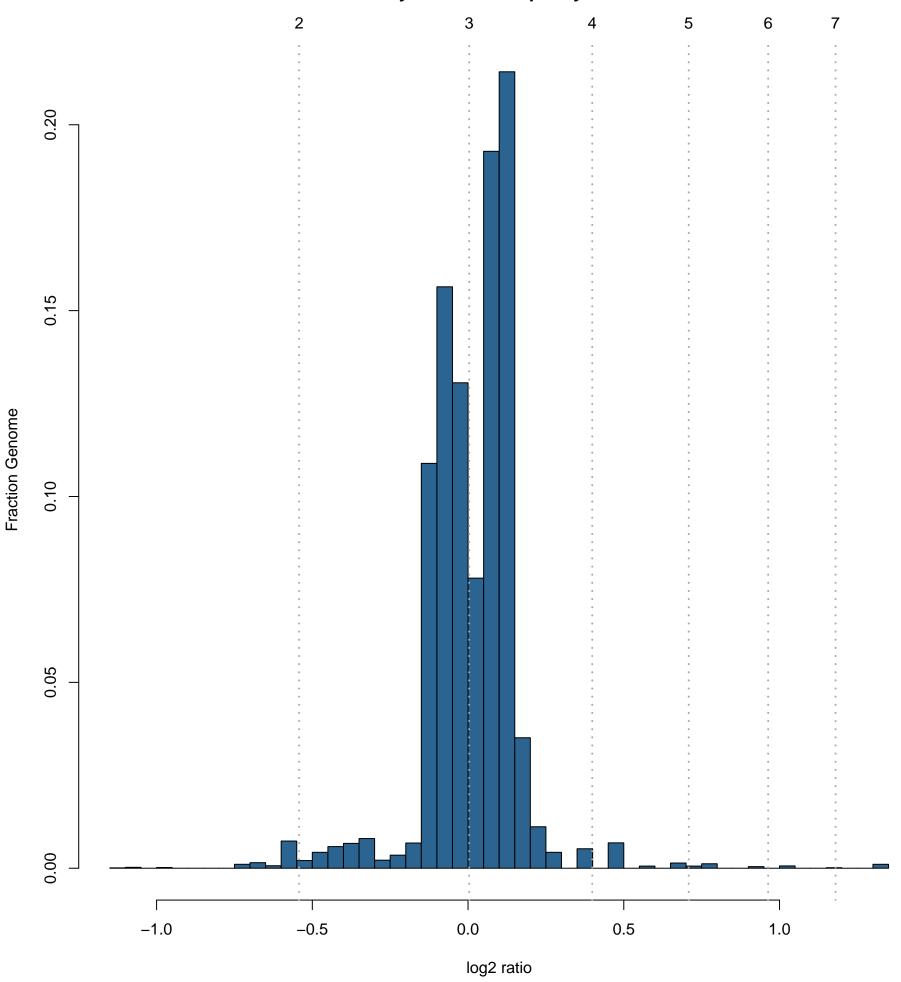
SCNA-fit log-likelihood: -10913.7

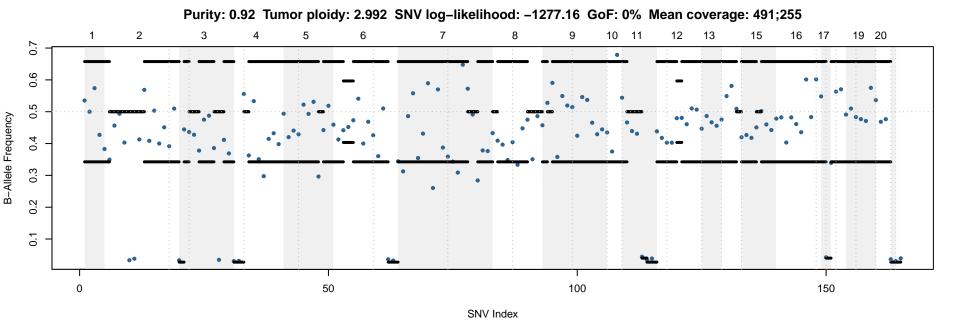






Purity: 0.92 Tumor ploidy: 2.992





SCNA-fit log-likelihood: -10928.01

