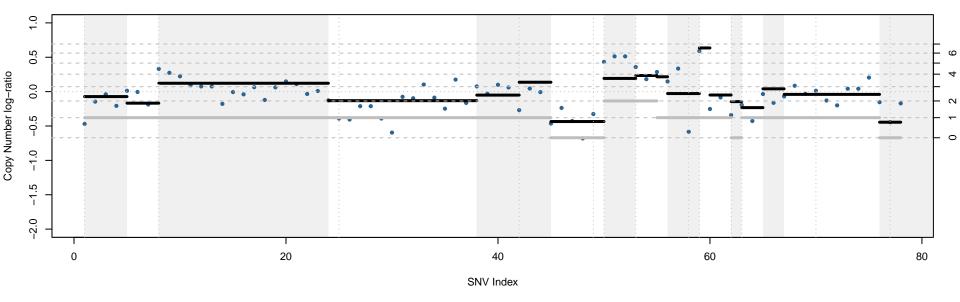
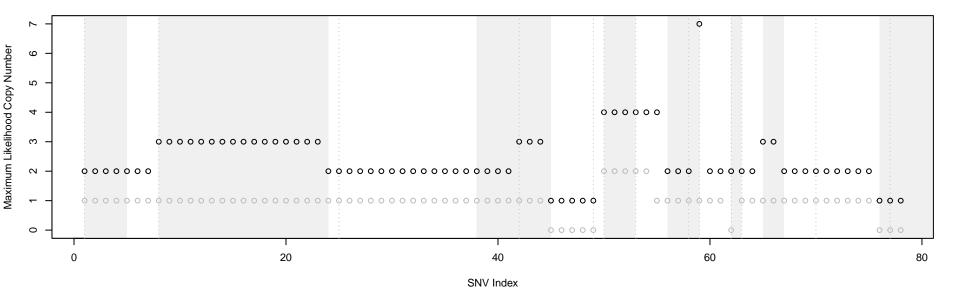
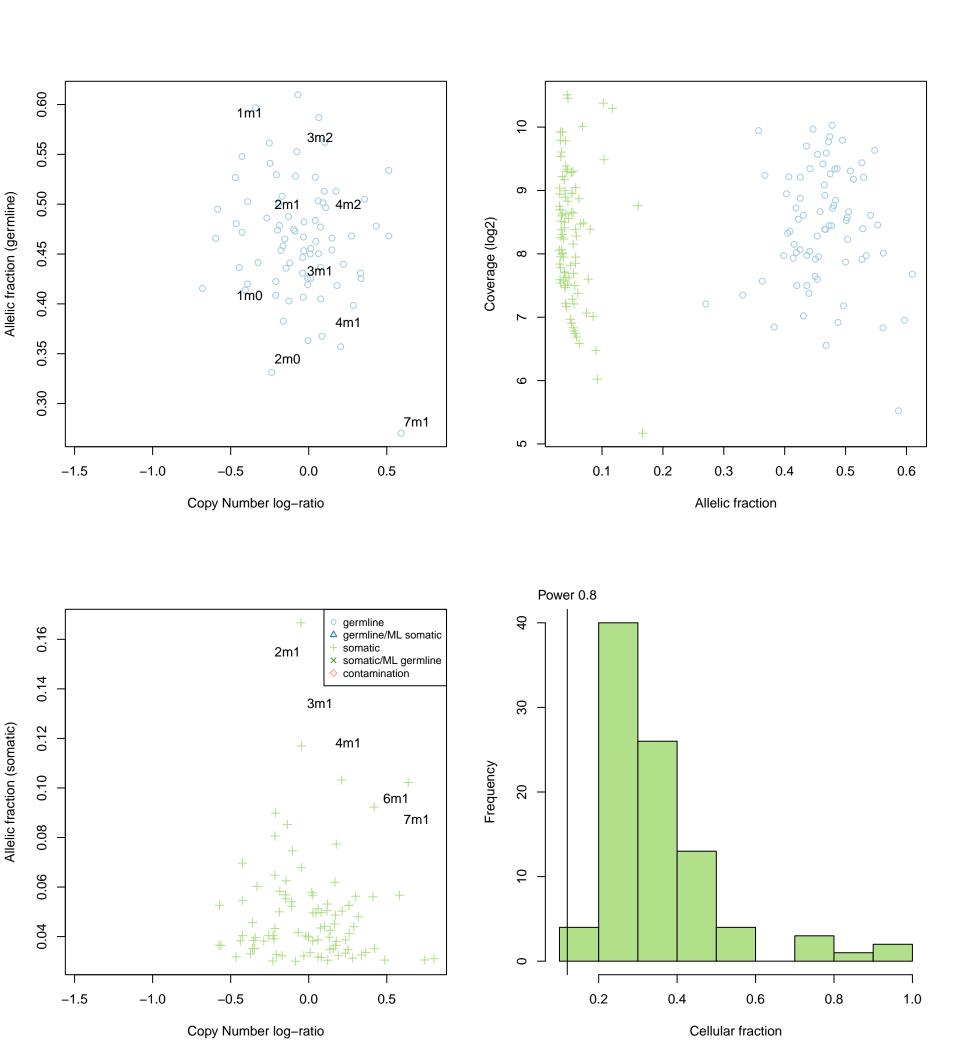
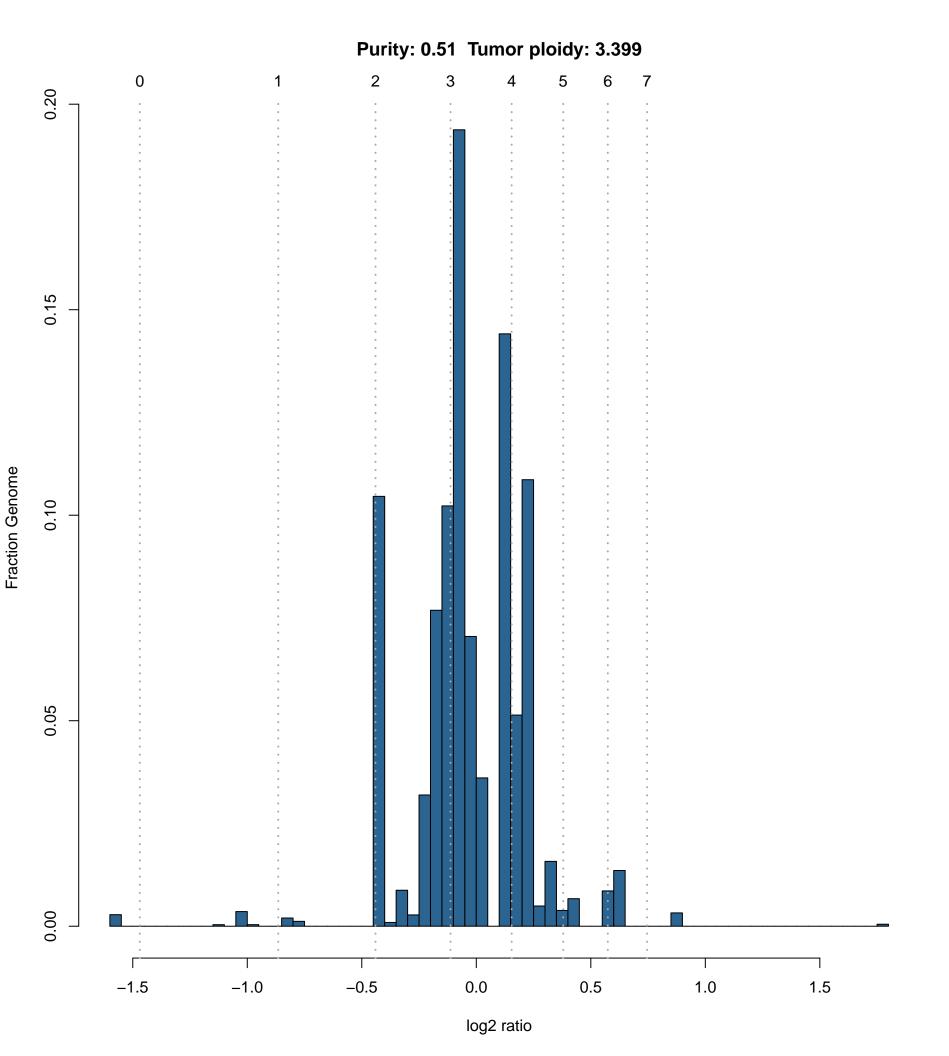


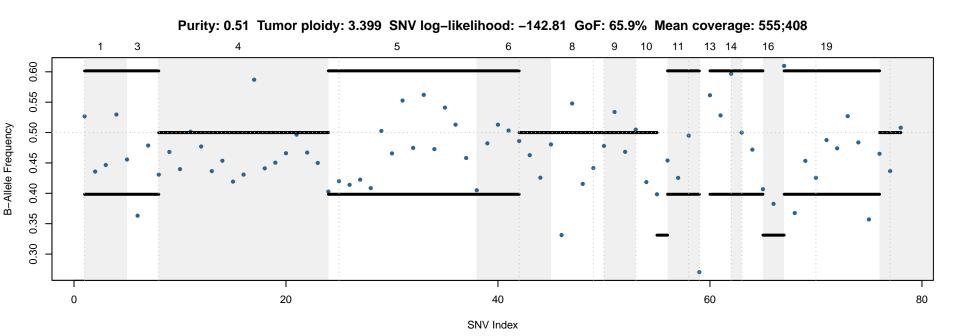
SCNA-fit log-likelihood: -8125.75



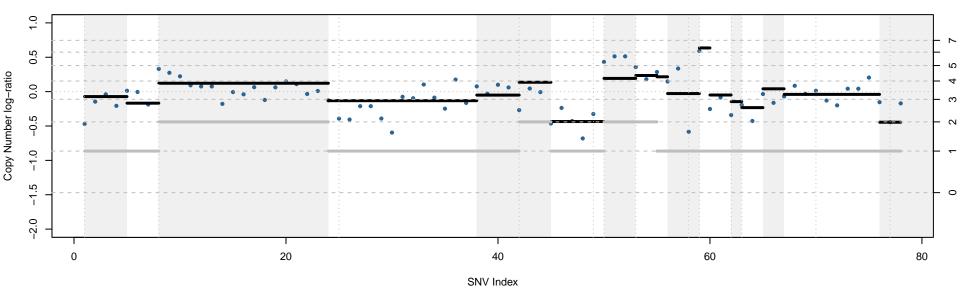


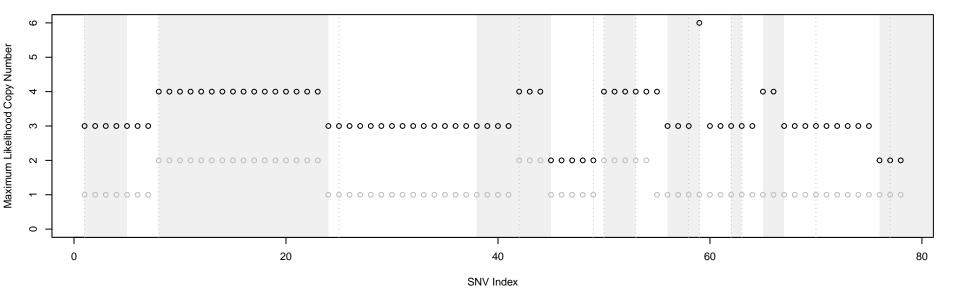


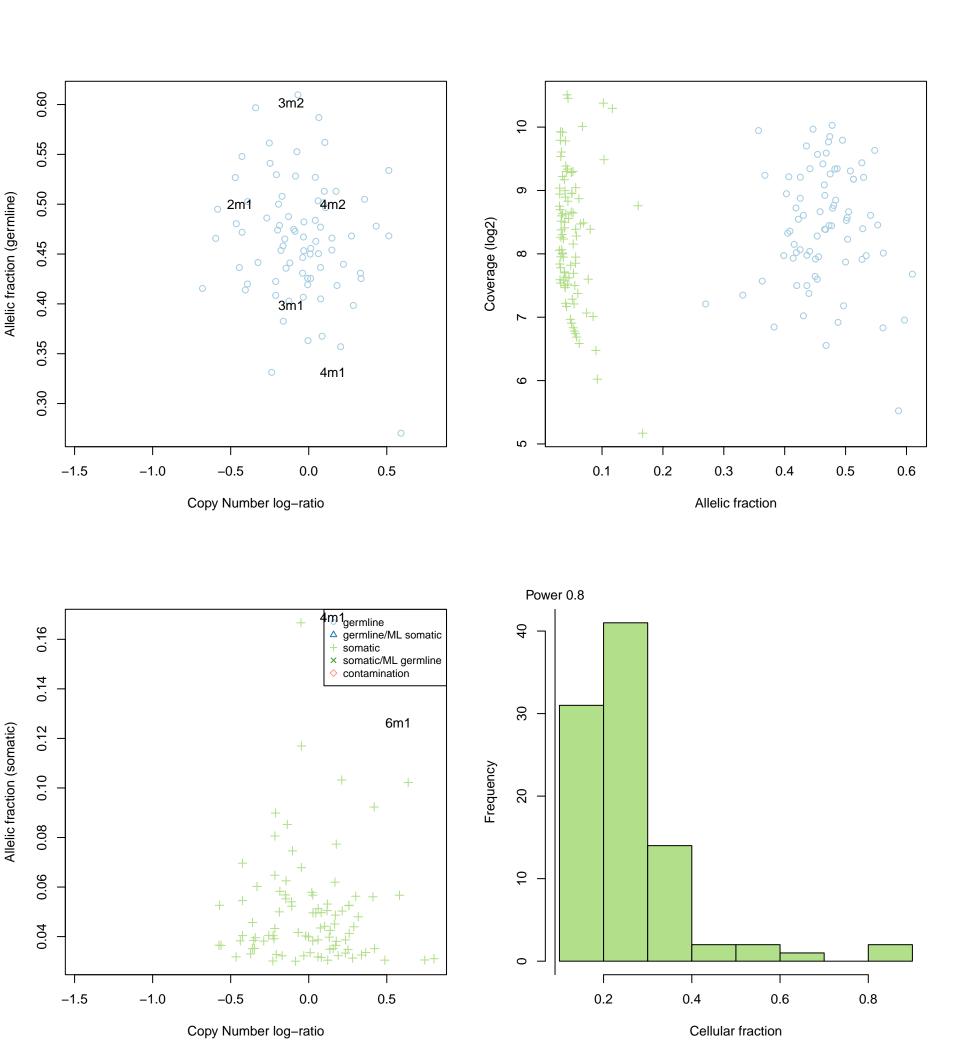


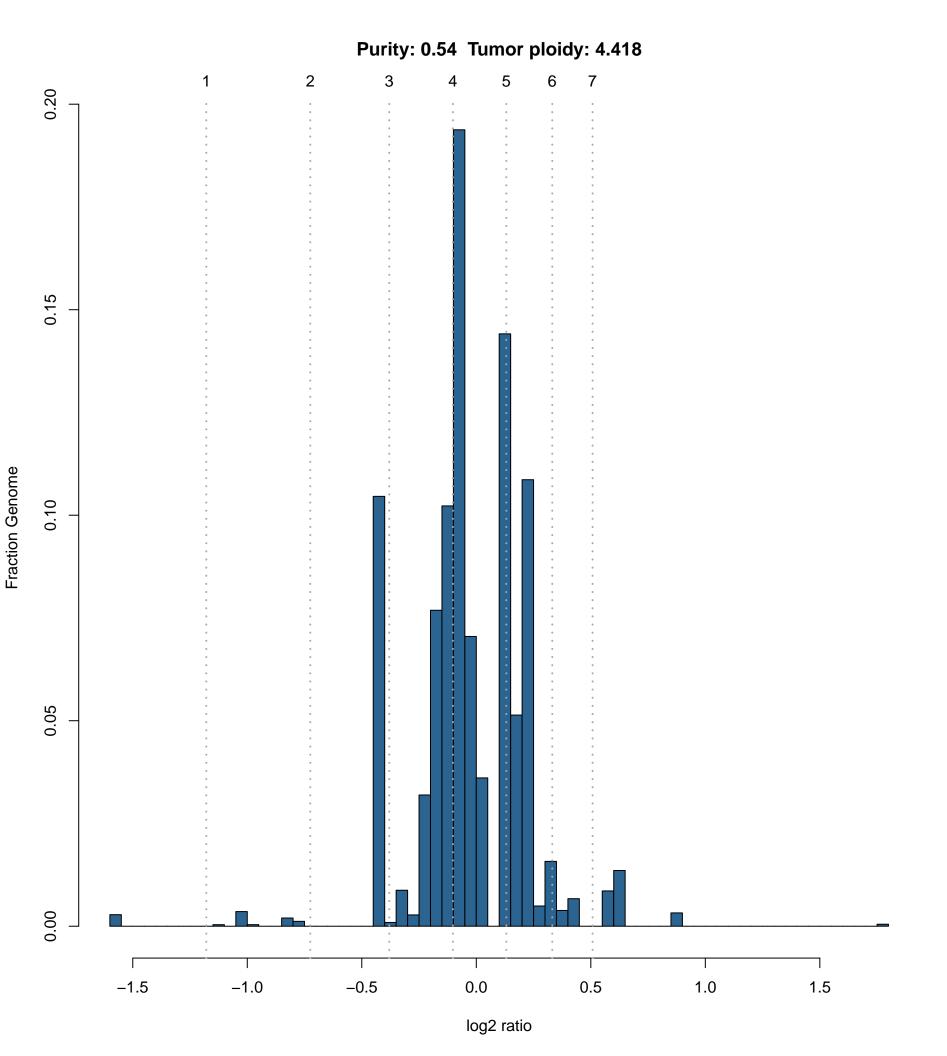


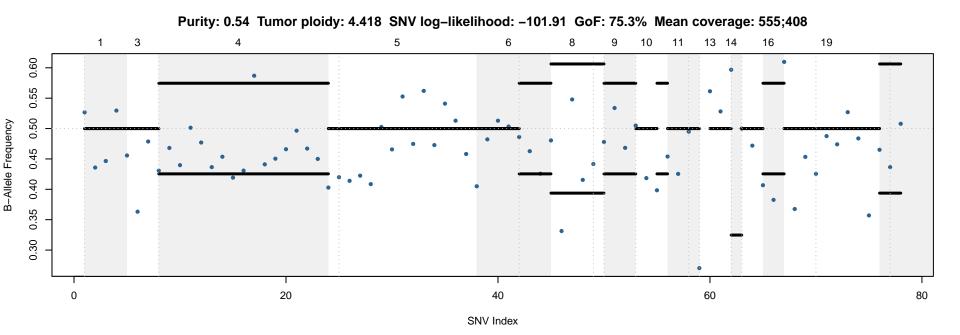
SCNA-fit log-likelihood: -8007.58



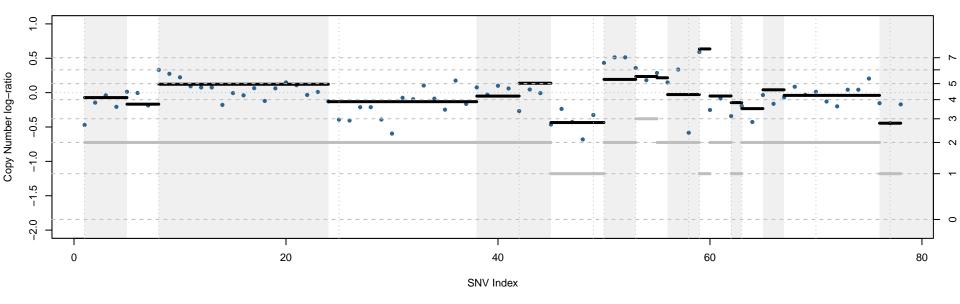


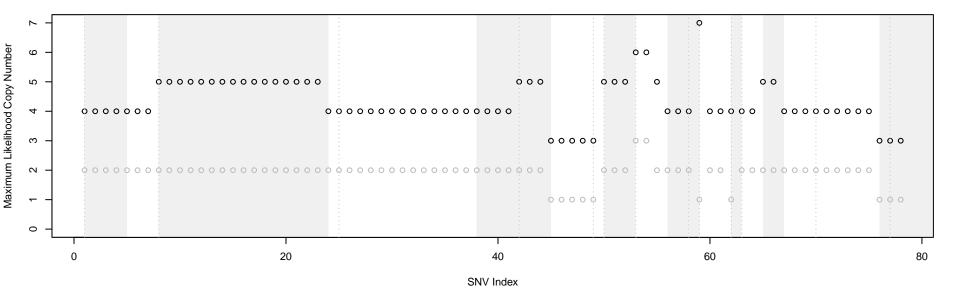


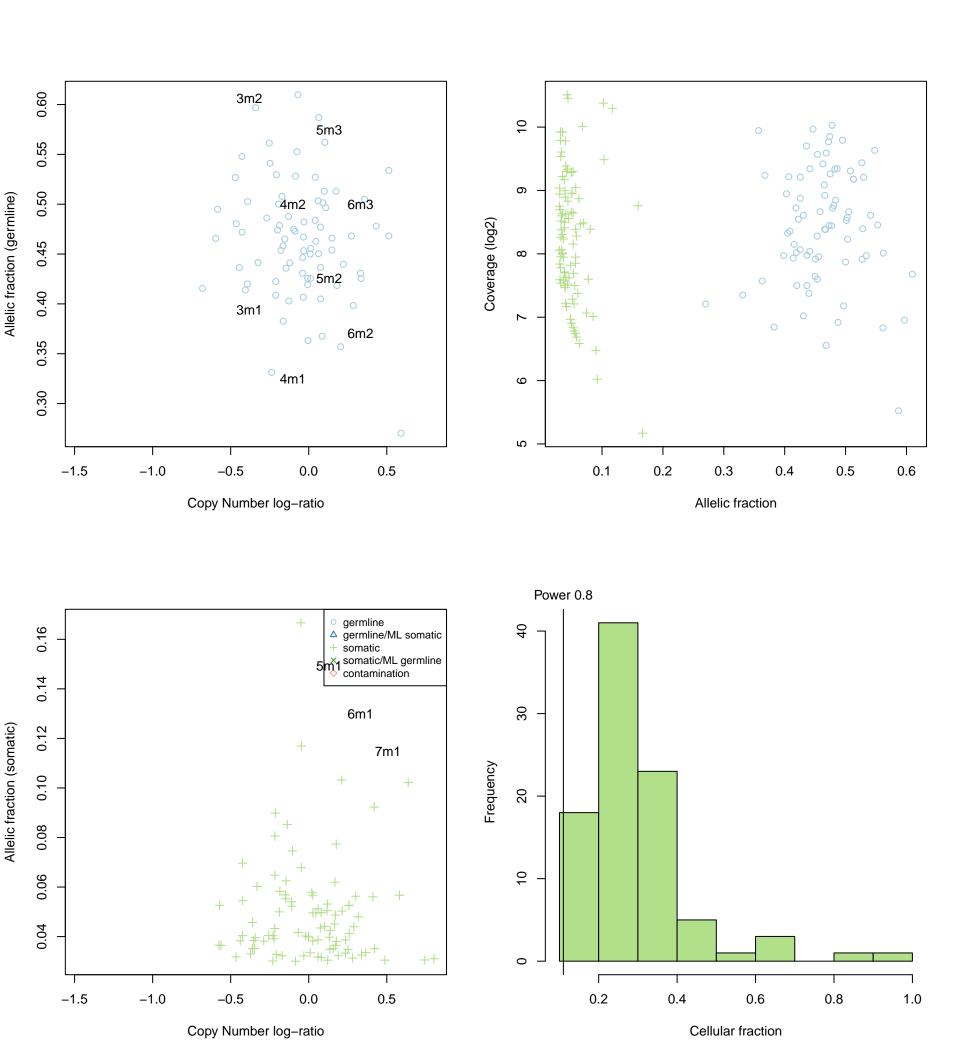




SCNA-fit log-likelihood: -8122.96

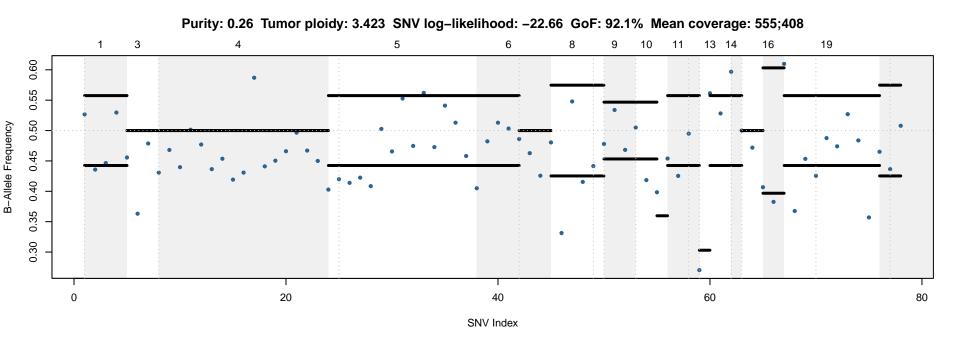




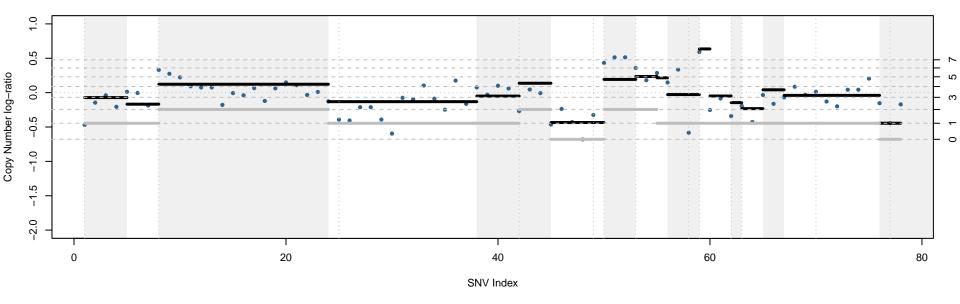


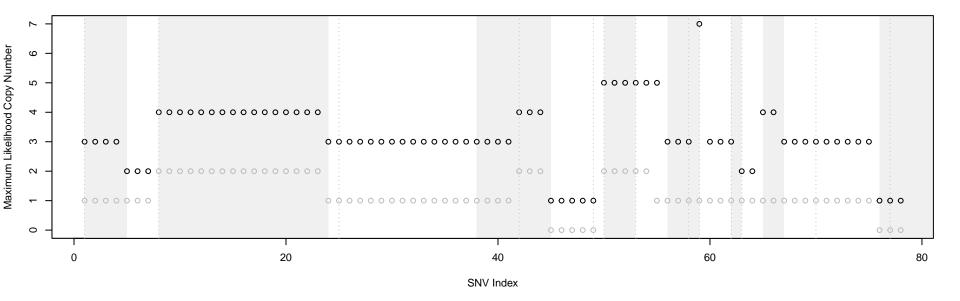
Purity: 0.26 Tumor ploidy: 3.423 0 2 3 6 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5

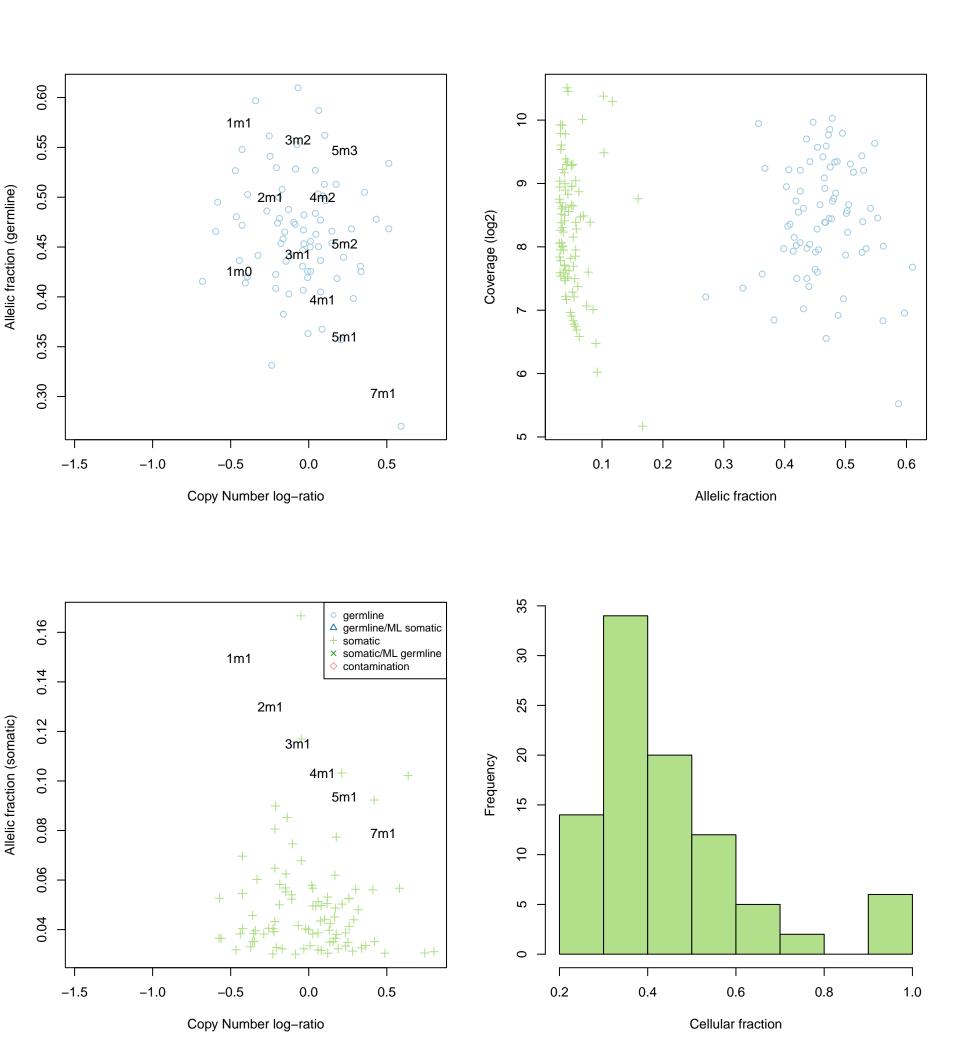
log2 ratio

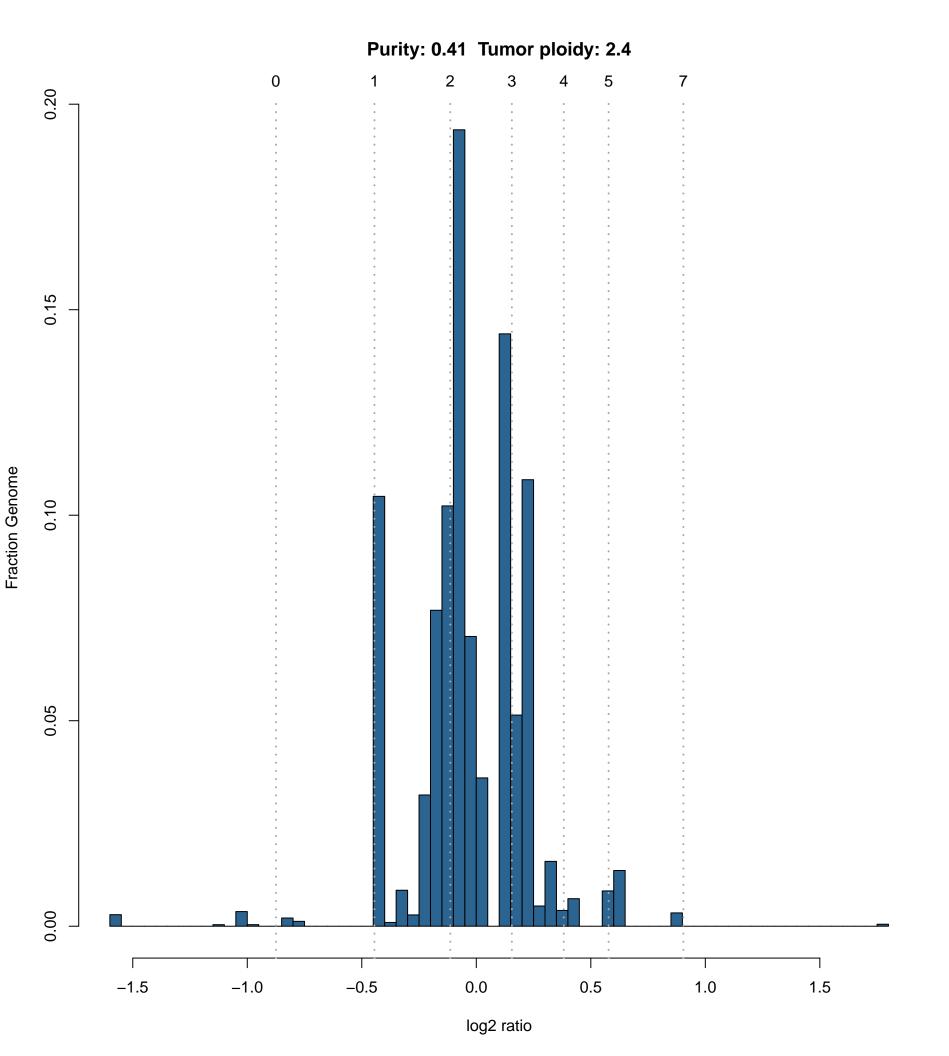


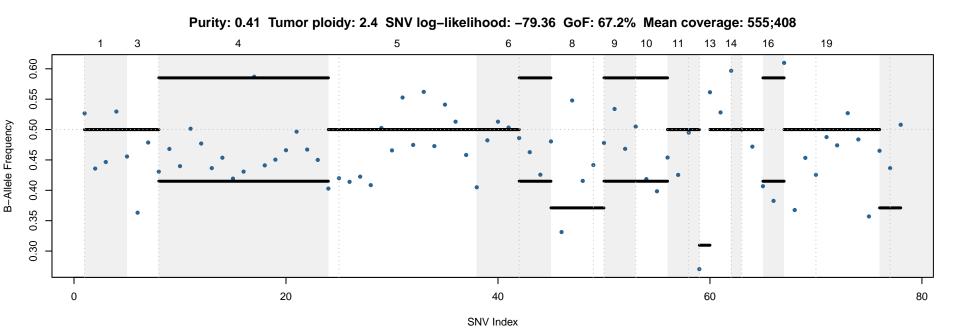
SCNA-fit log-likelihood: -8278.09



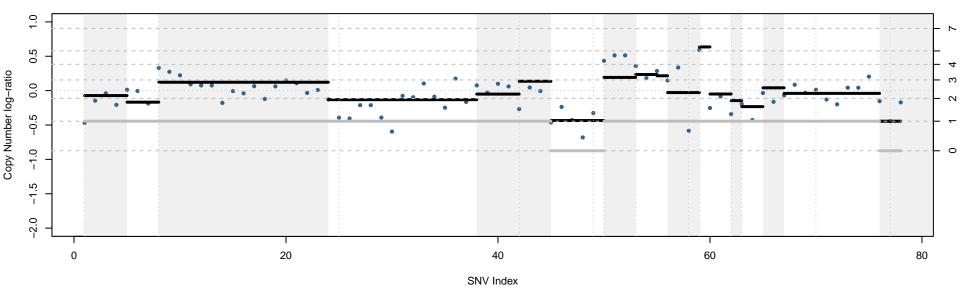


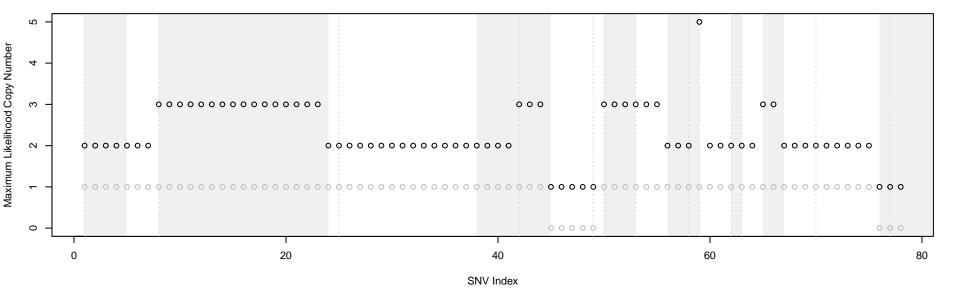


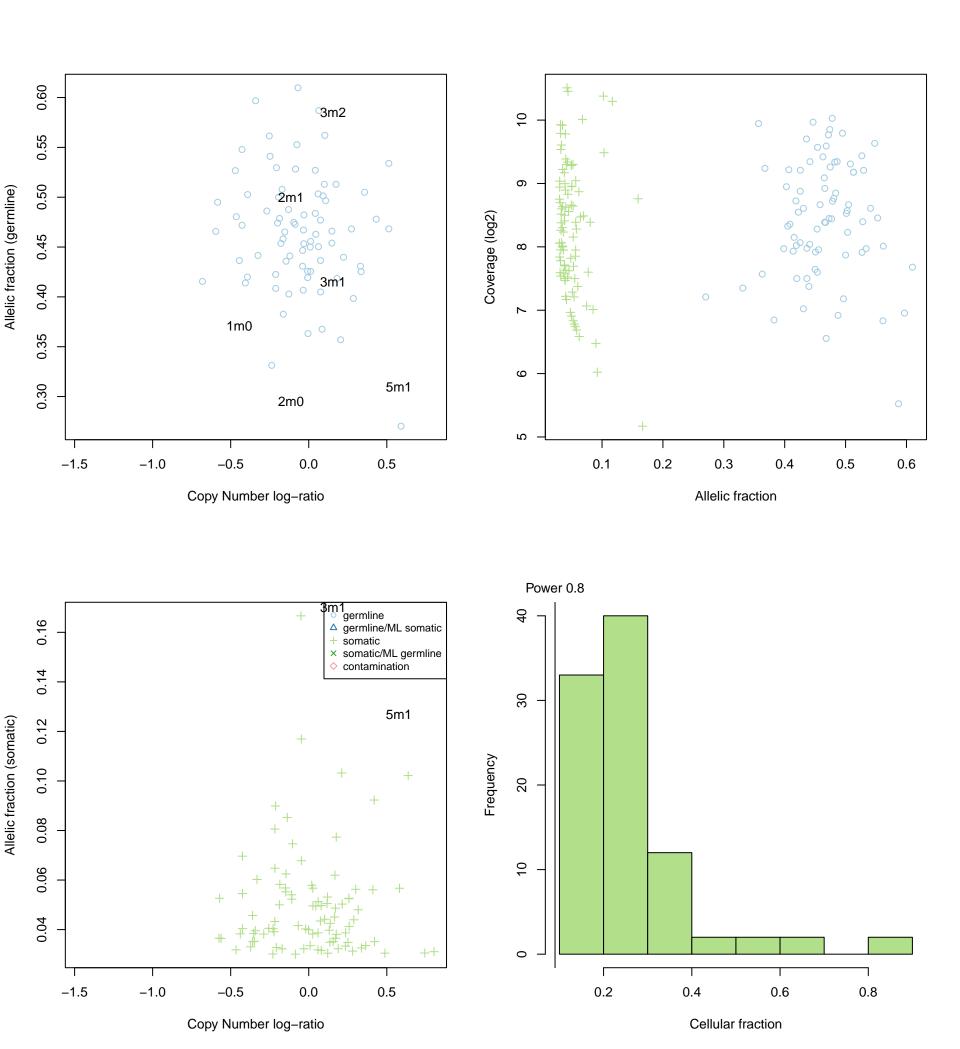




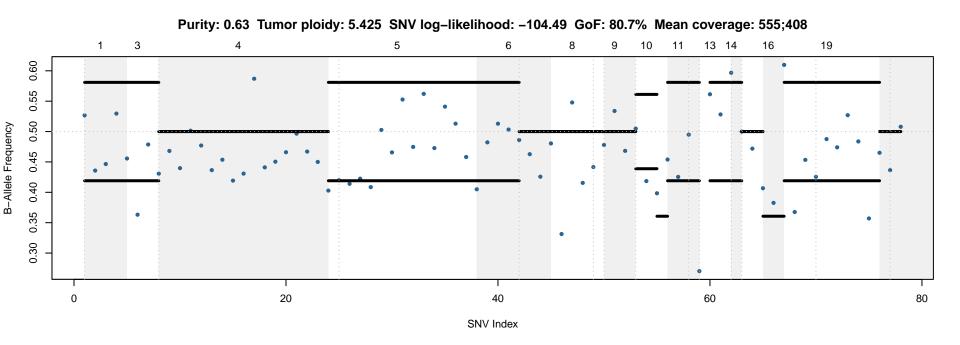
SCNA-fit log-likelihood: -8239.61



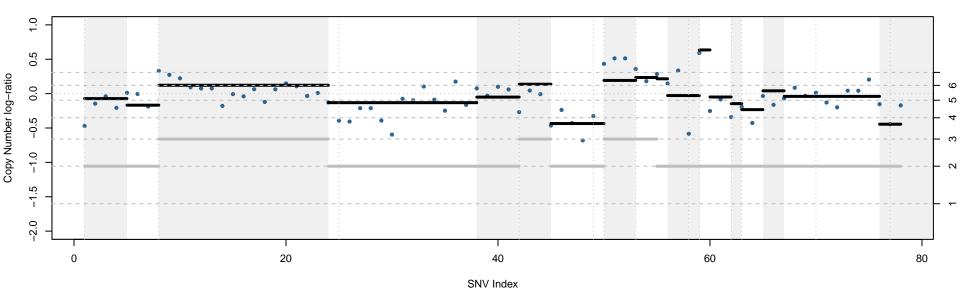


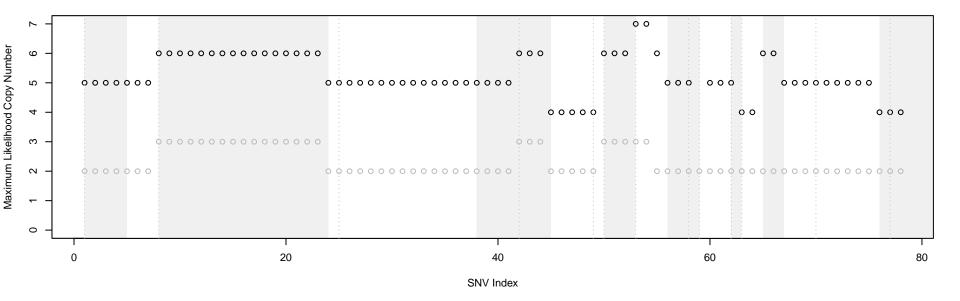


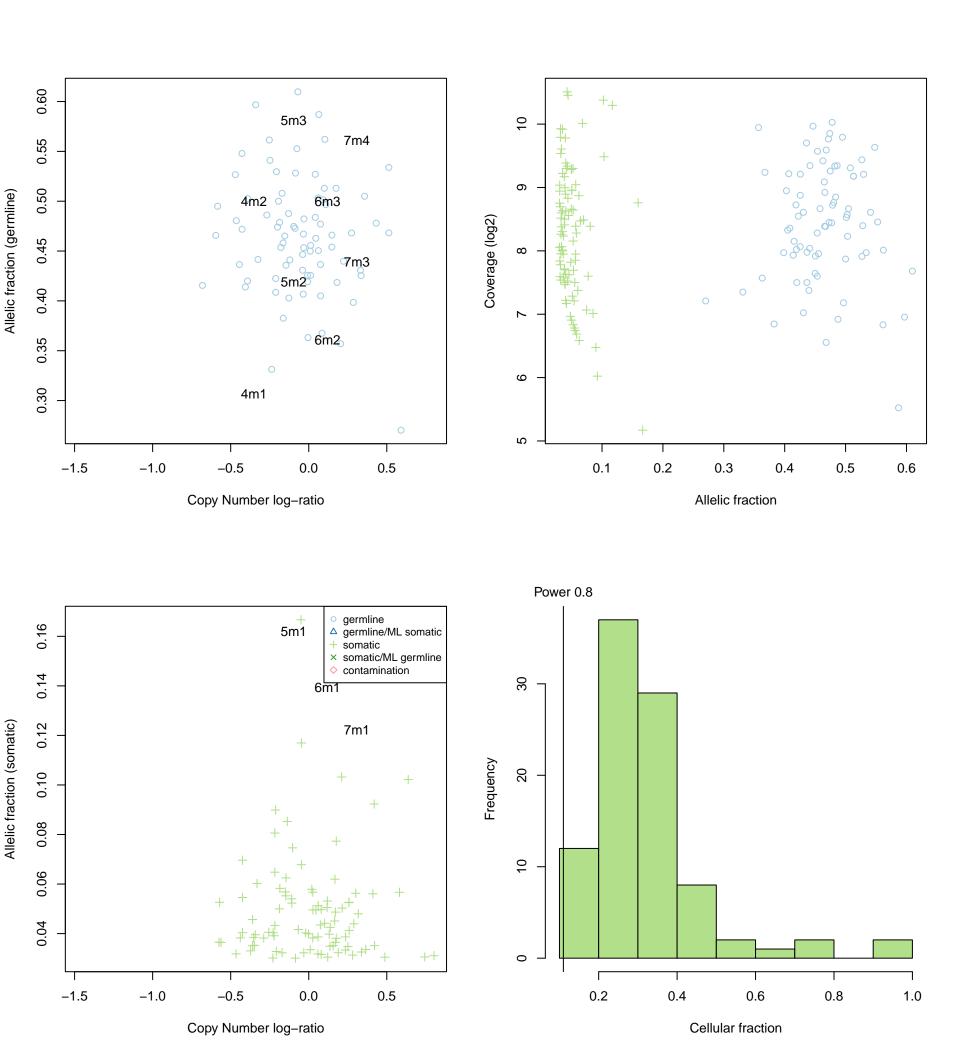
Purity: 0.63 Tumor ploidy: 5.425 5 7 2 3 6 0.20 Fraction Genome 0.10 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio

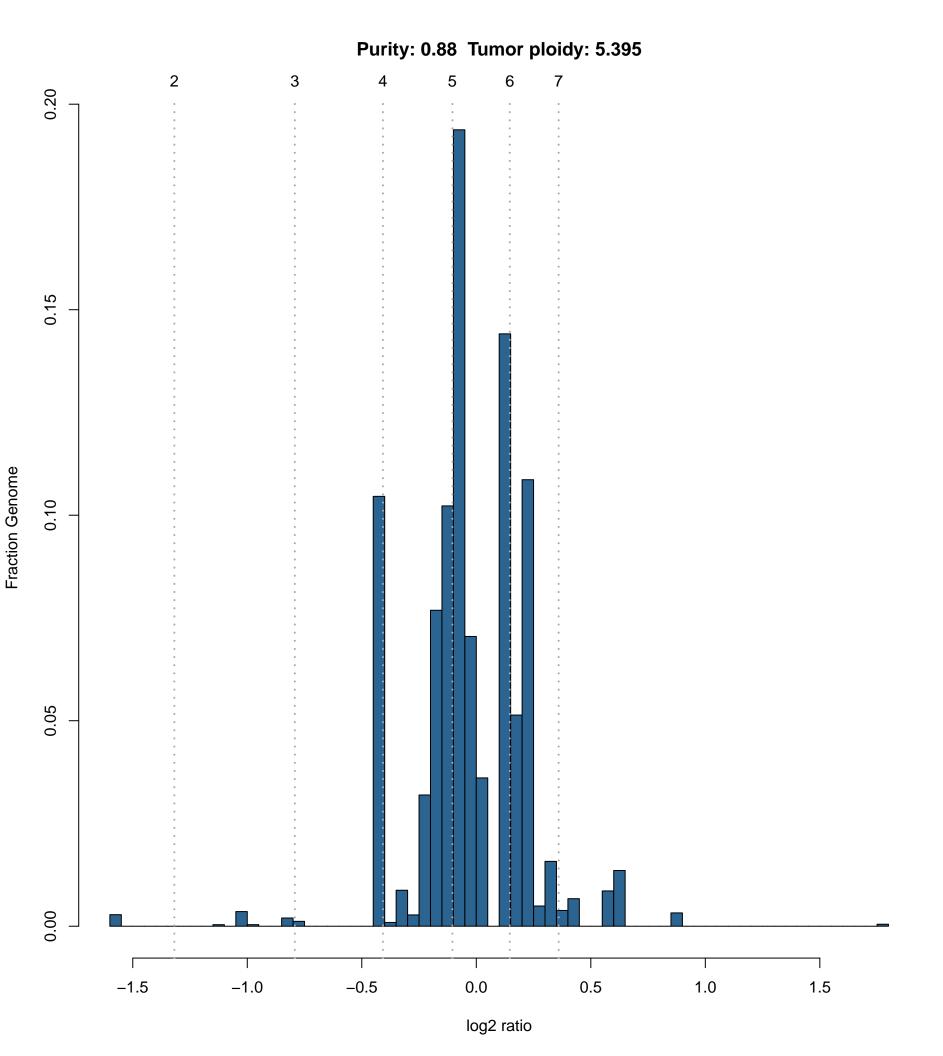


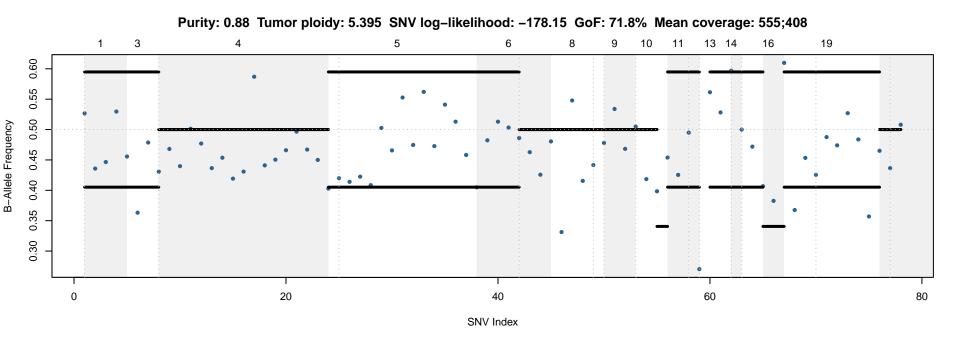
SCNA-fit log-likelihood: -8526.78



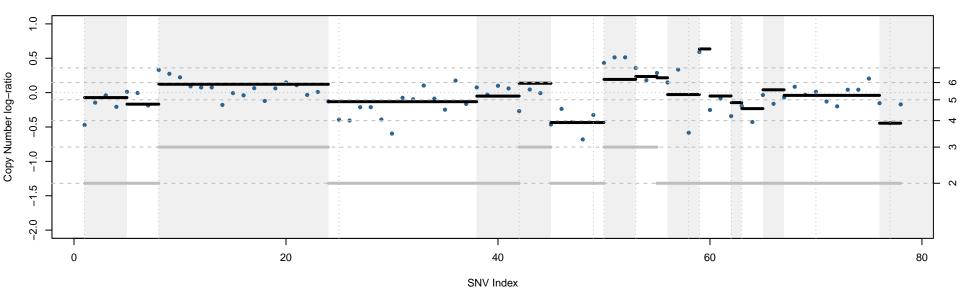


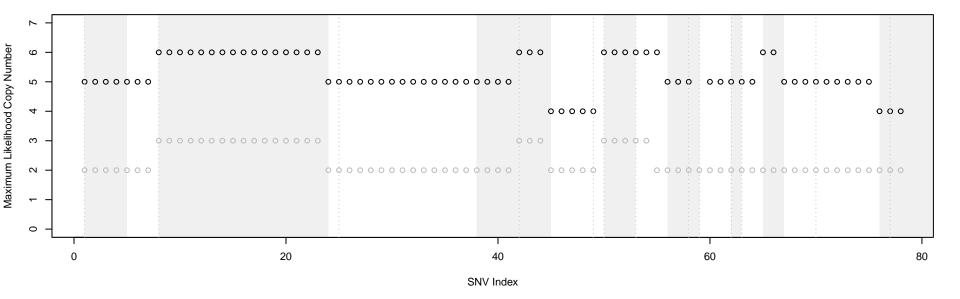


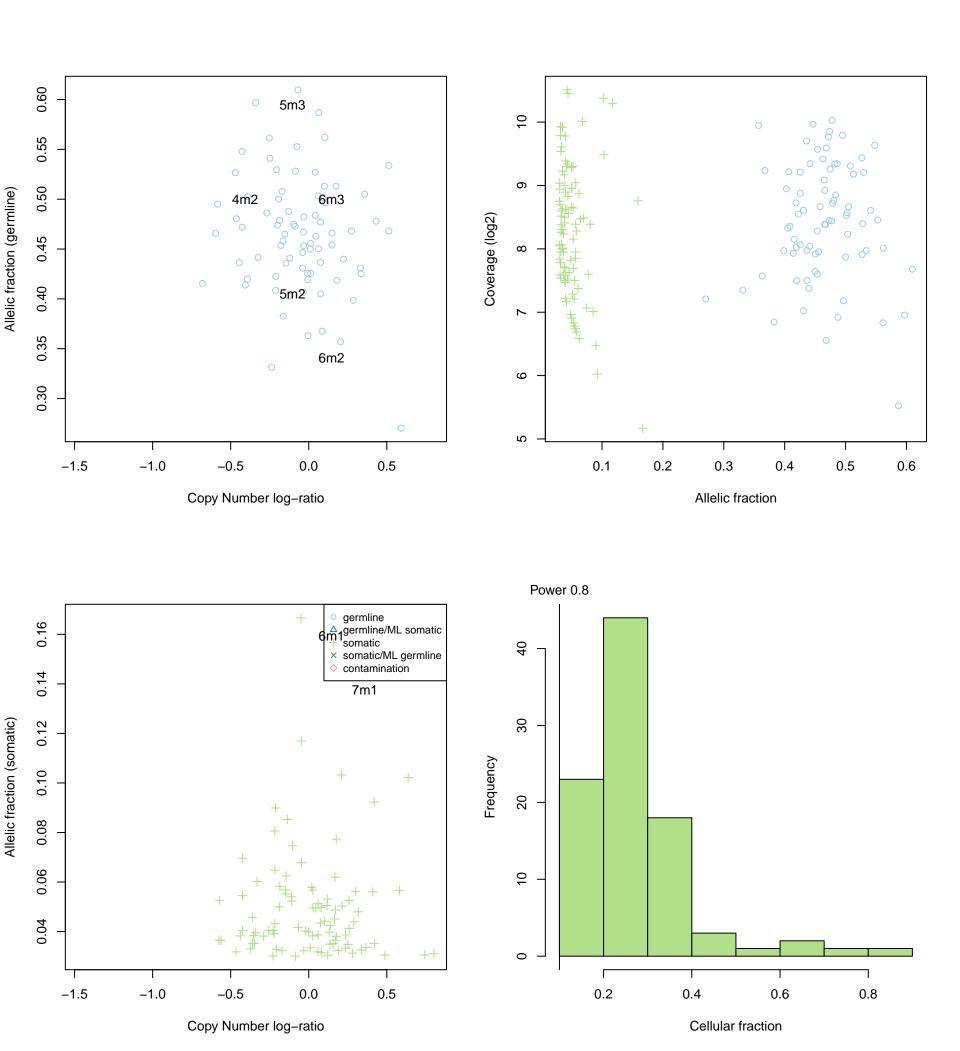


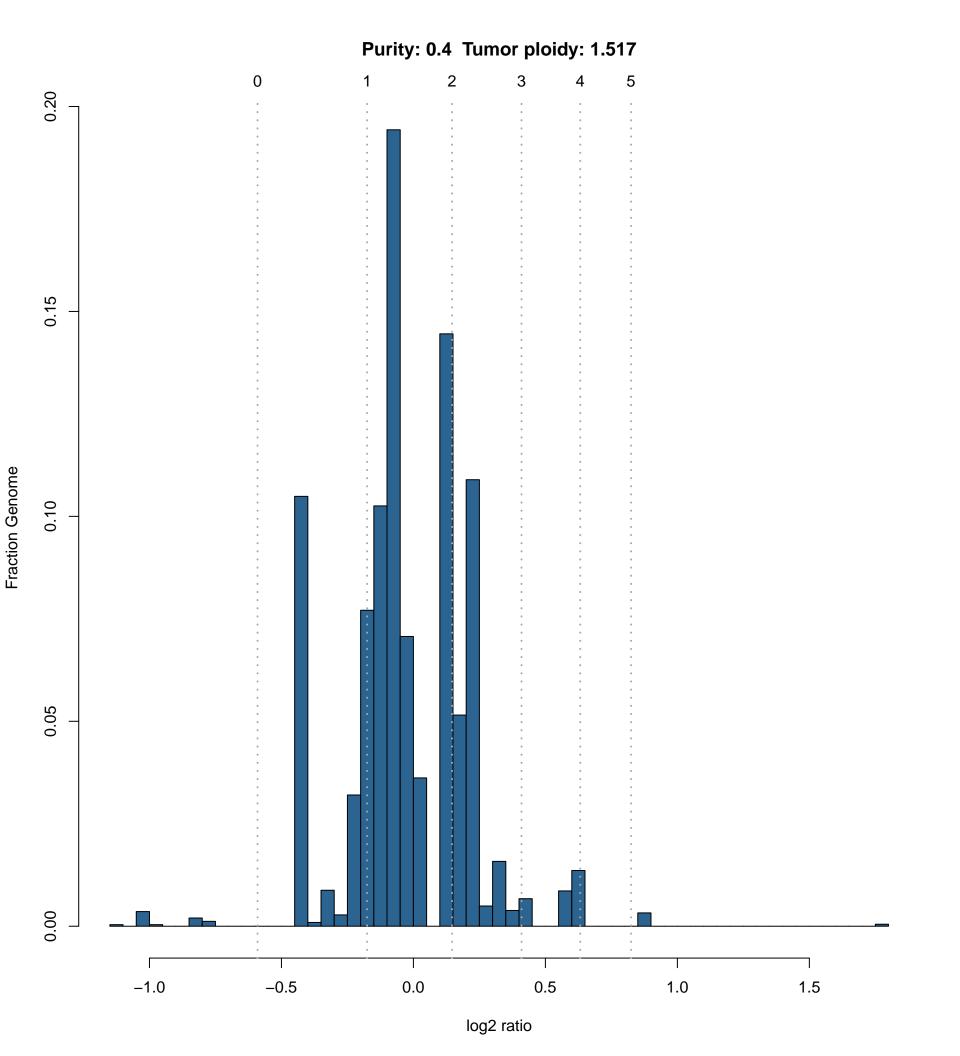


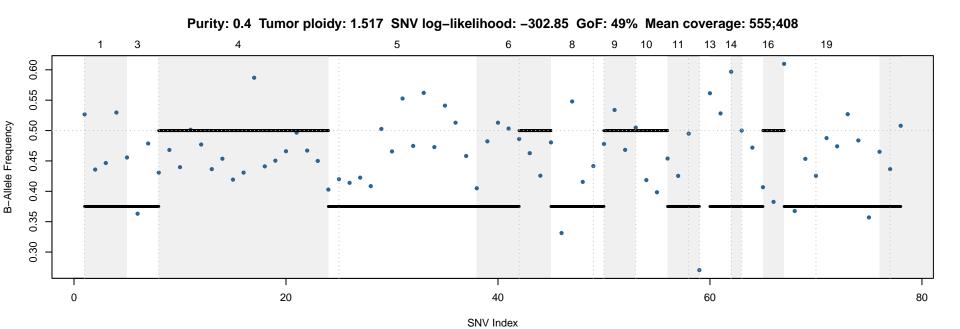
SCNA-fit log-likelihood: -8390.21



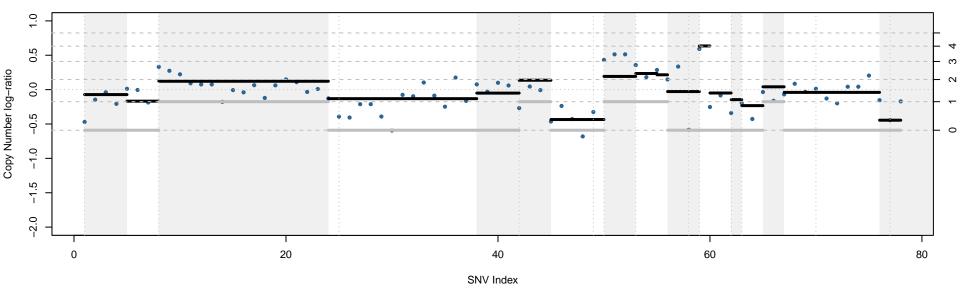


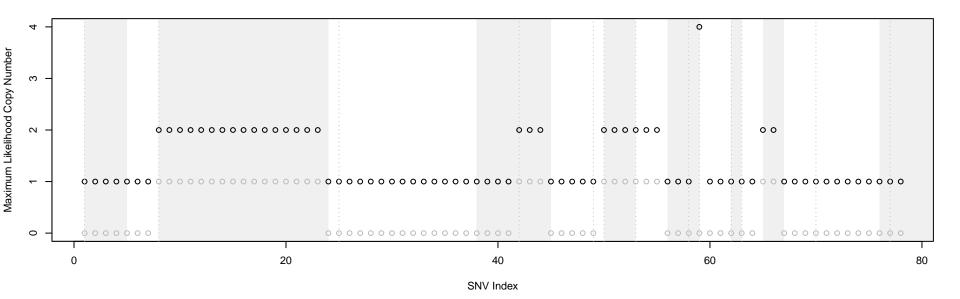


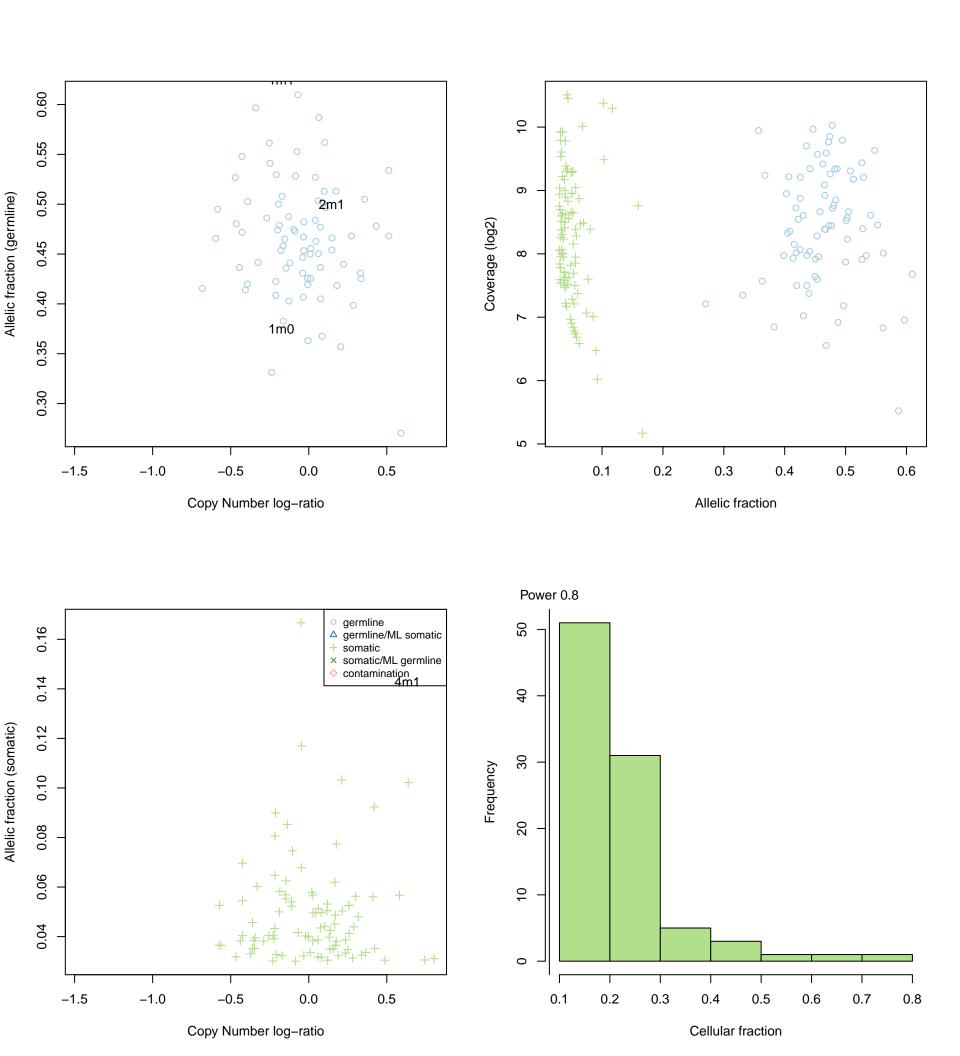




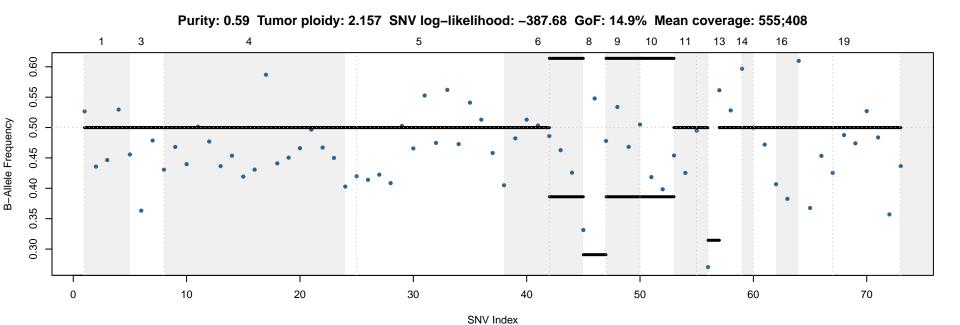
SCNA-fit log-likelihood: -8742.39







Purity: 0.59 Tumor ploidy: 2.157 3 0 5 0.20 Fraction Genome 0.10 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



SCNA-fit log-likelihood: -8614.4

