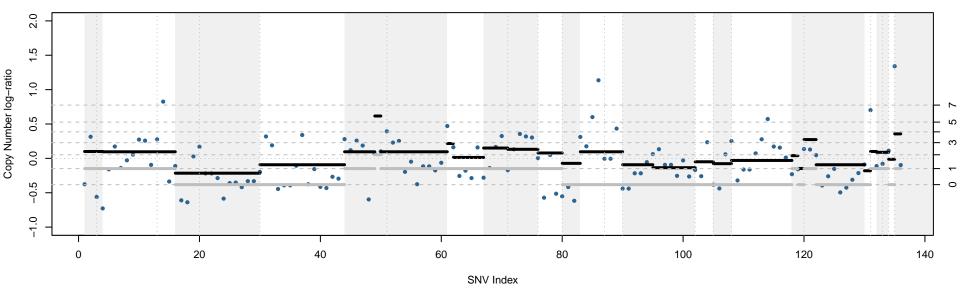
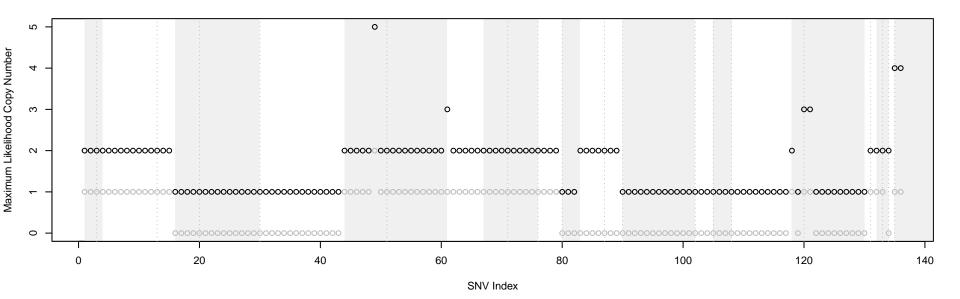
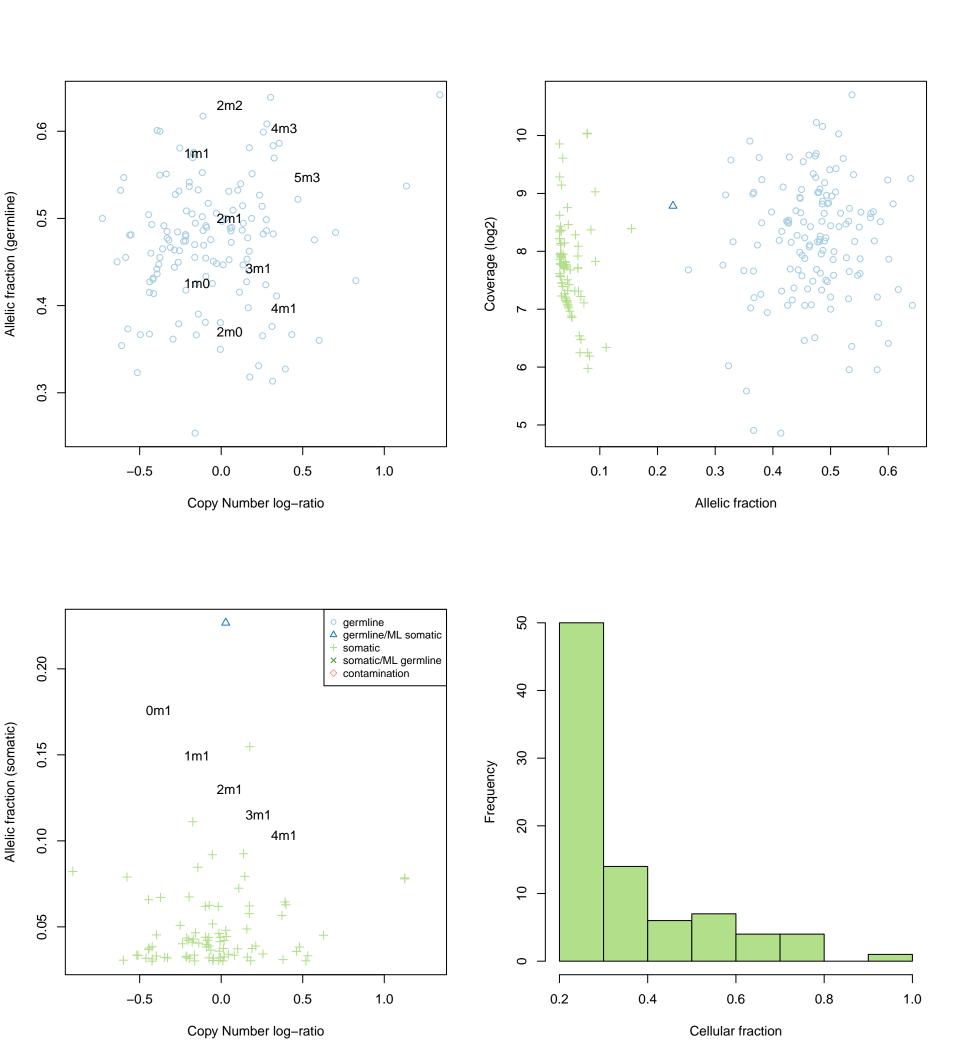
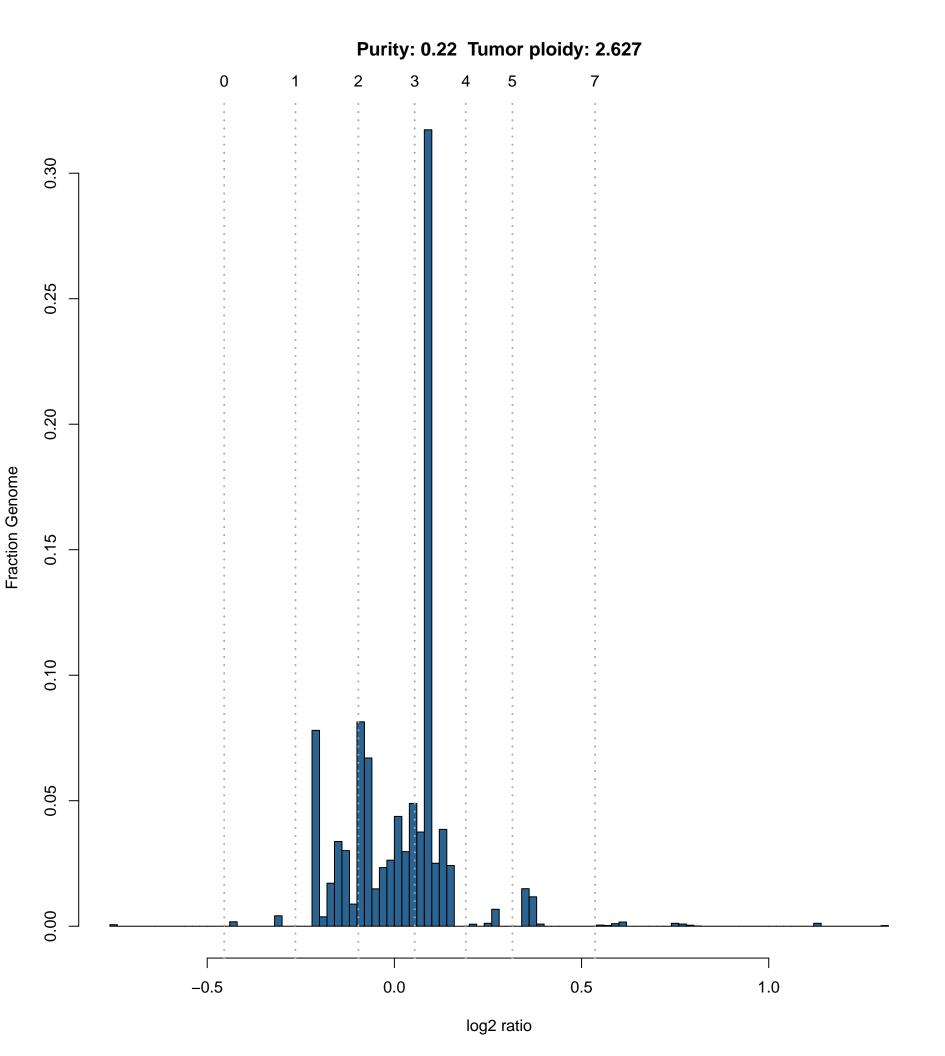


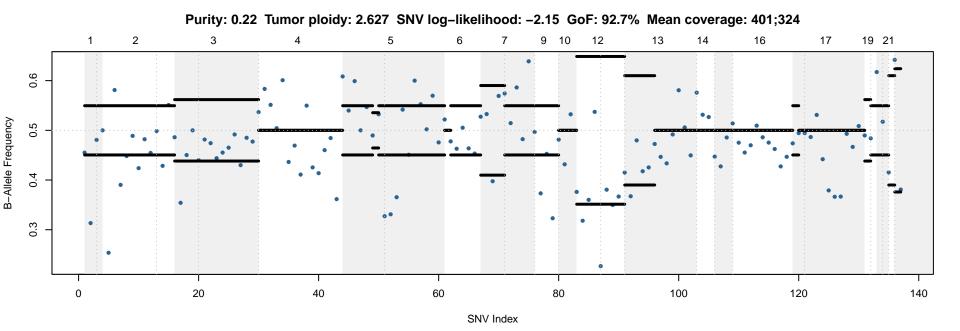
SCNA-fit log-likelihood: -13038.63



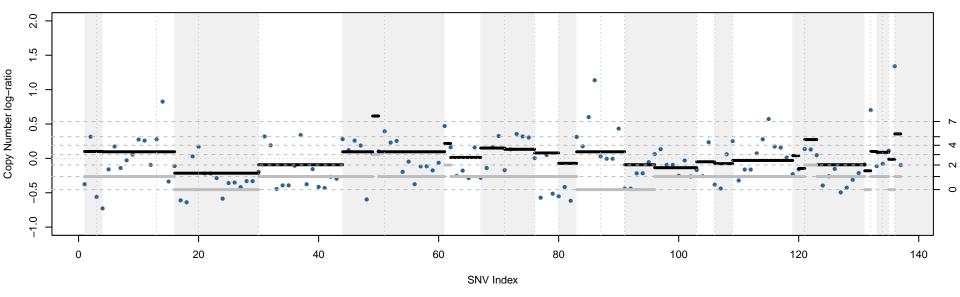


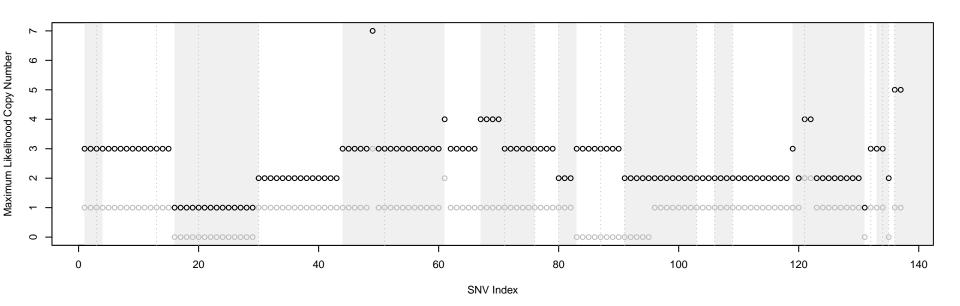


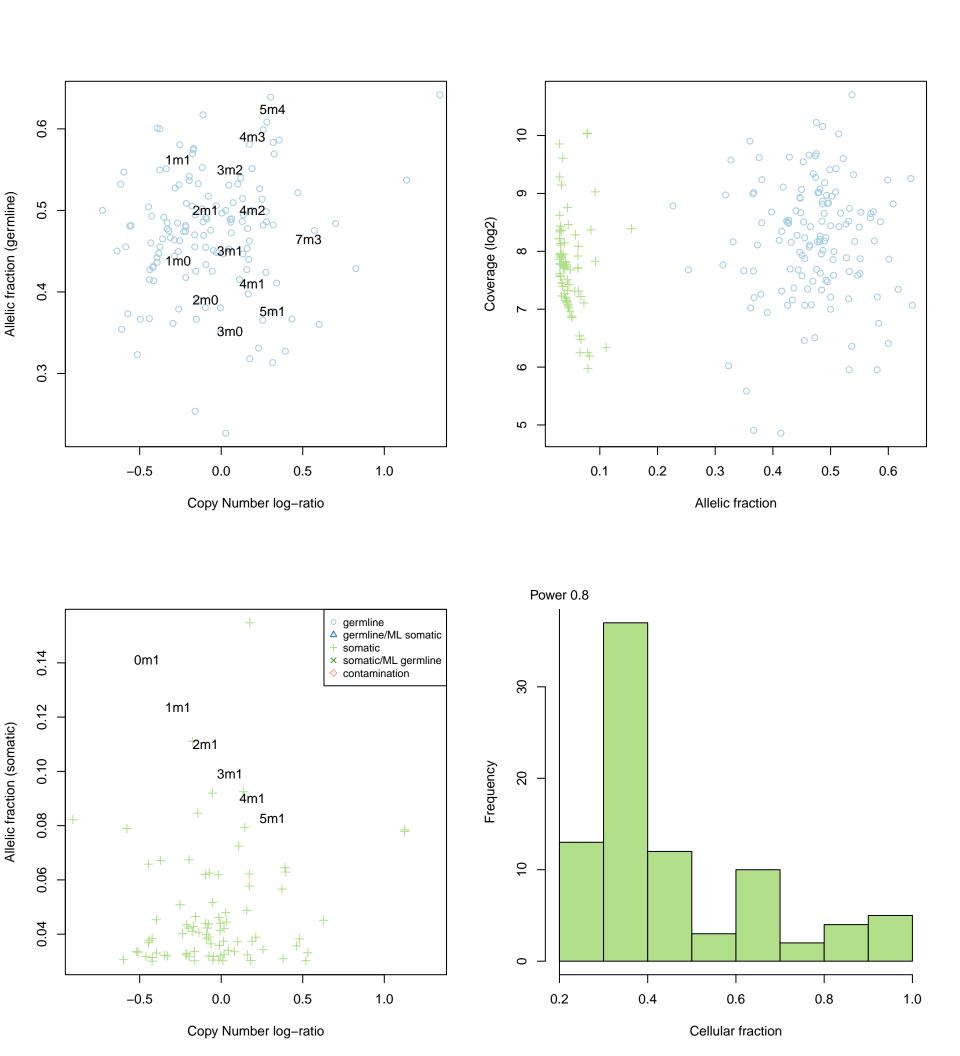


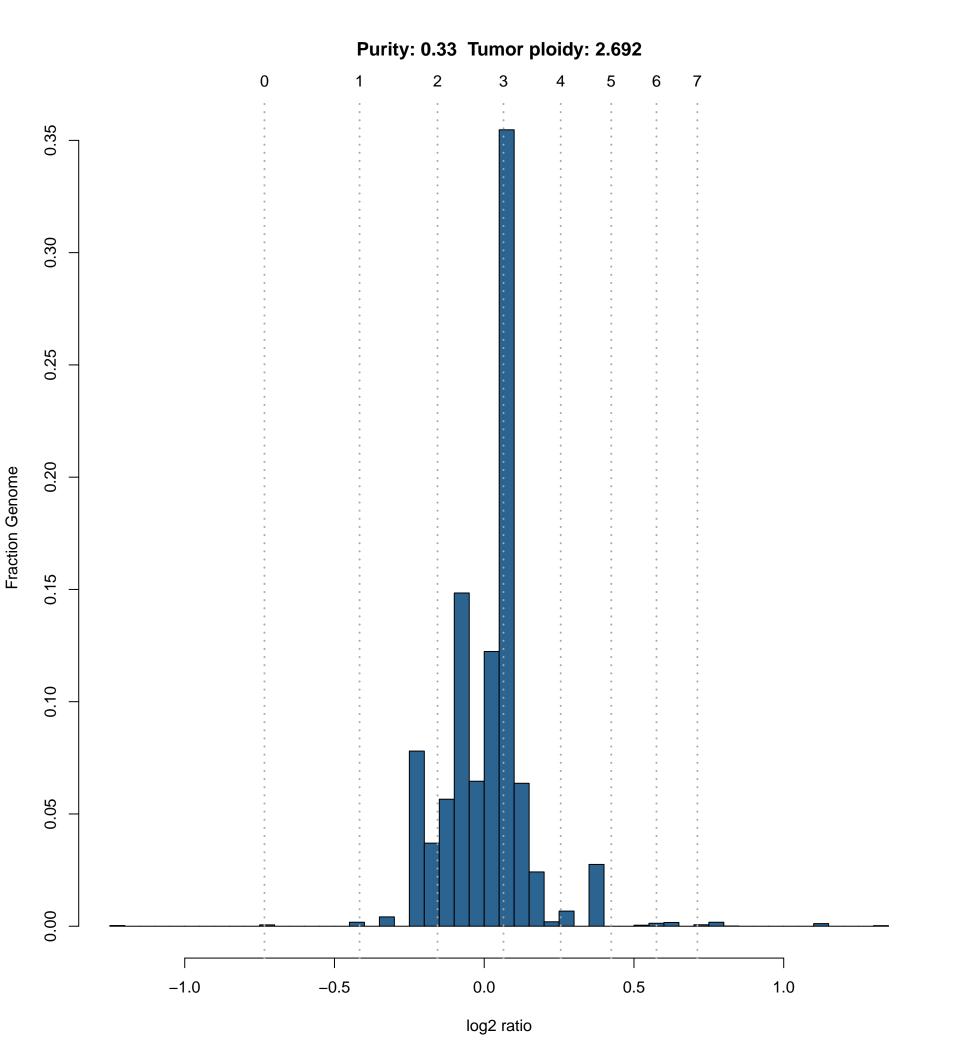


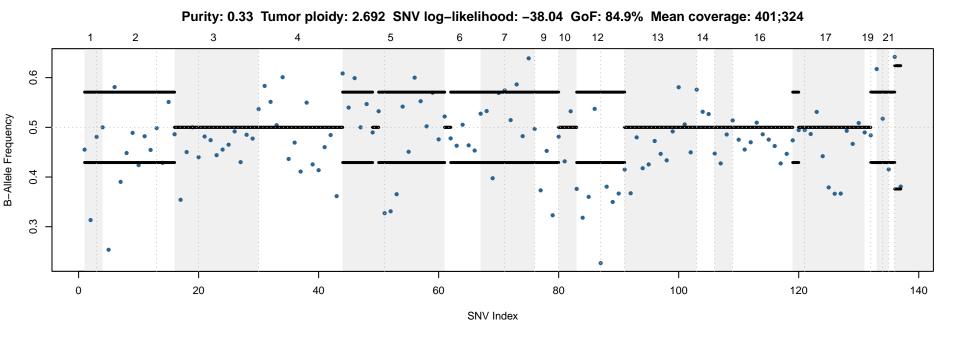
SCNA-fit log-likelihood: -13031.77



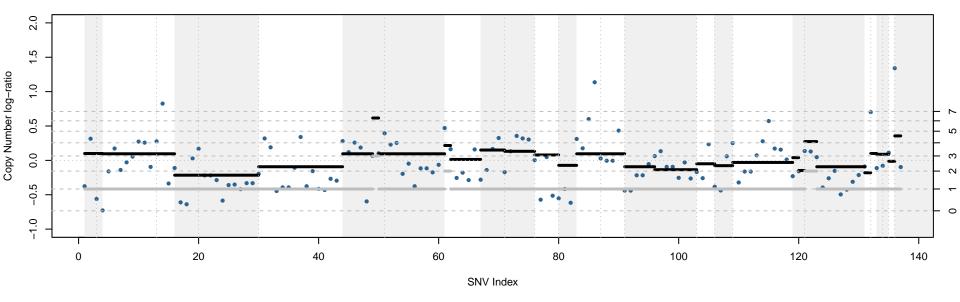


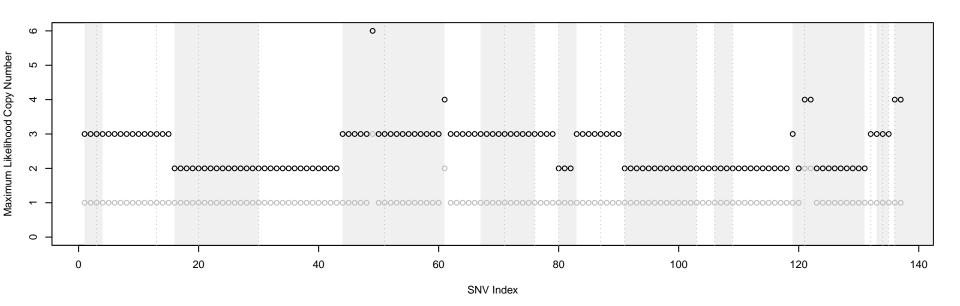


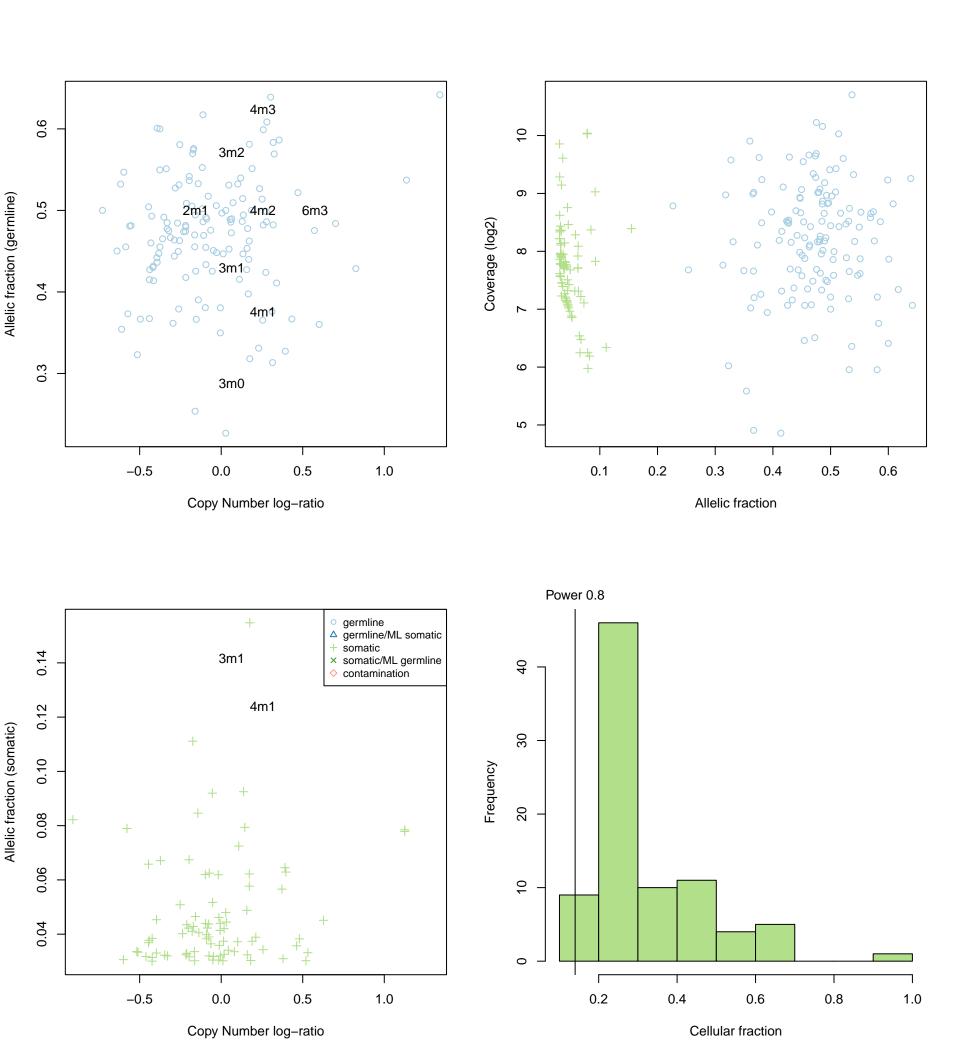


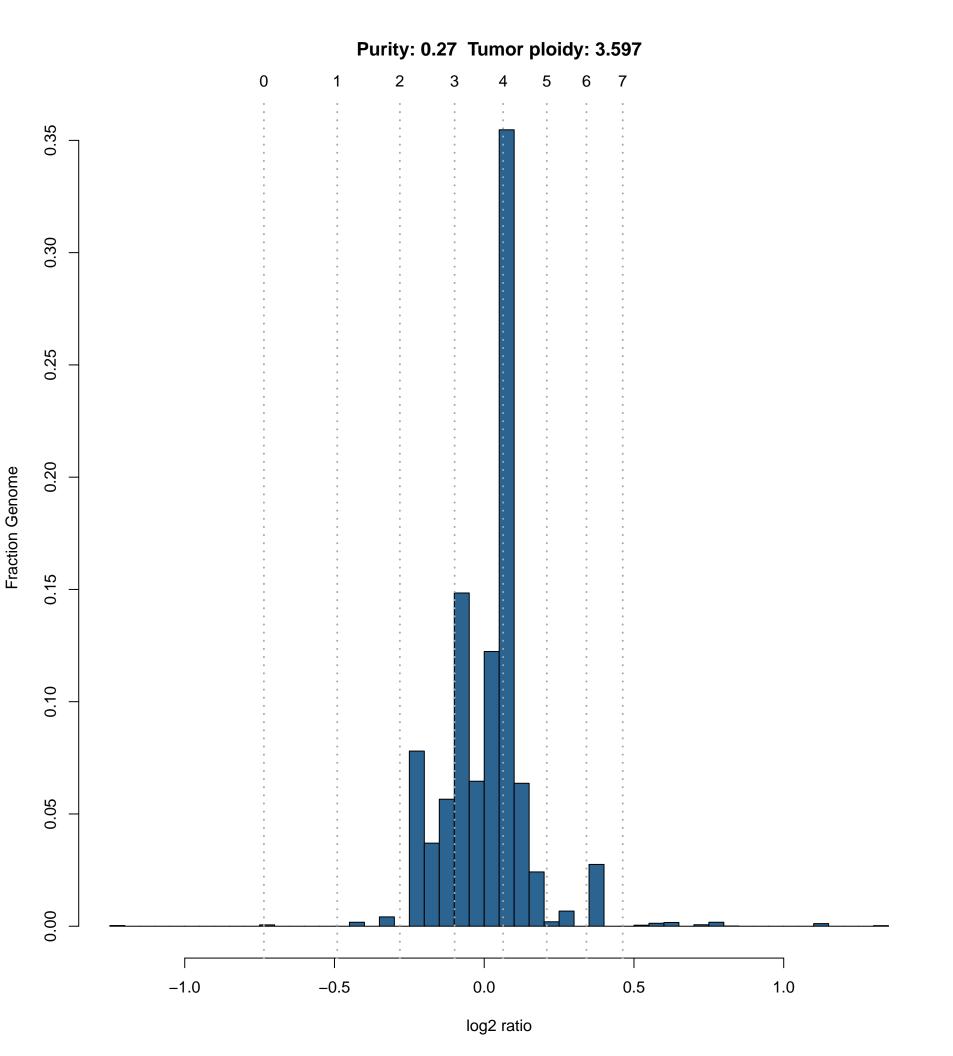


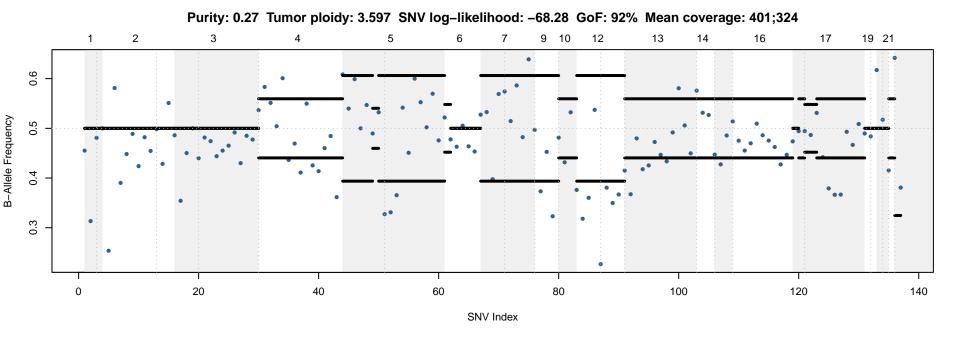
SCNA-fit log-likelihood: -13031.34



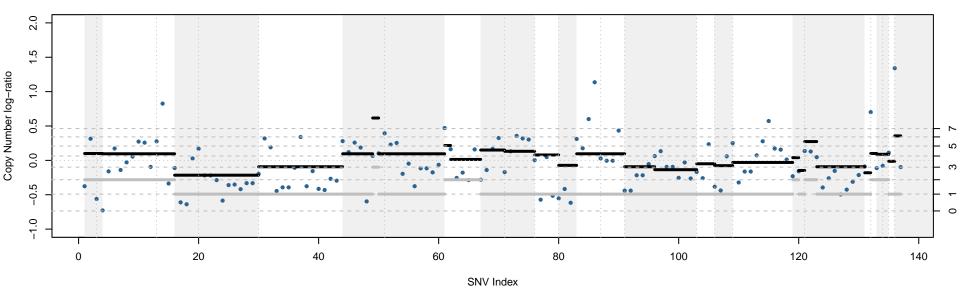


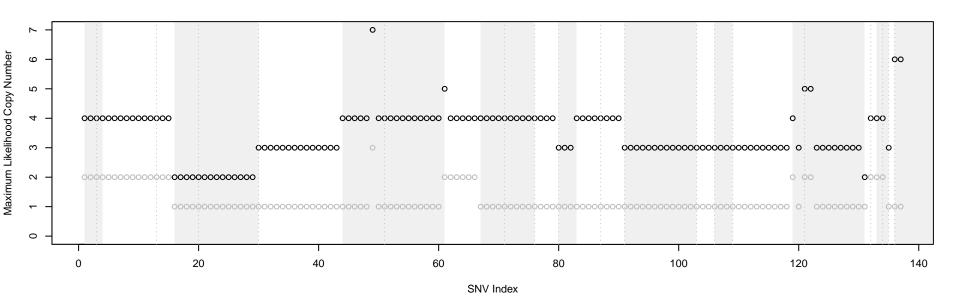


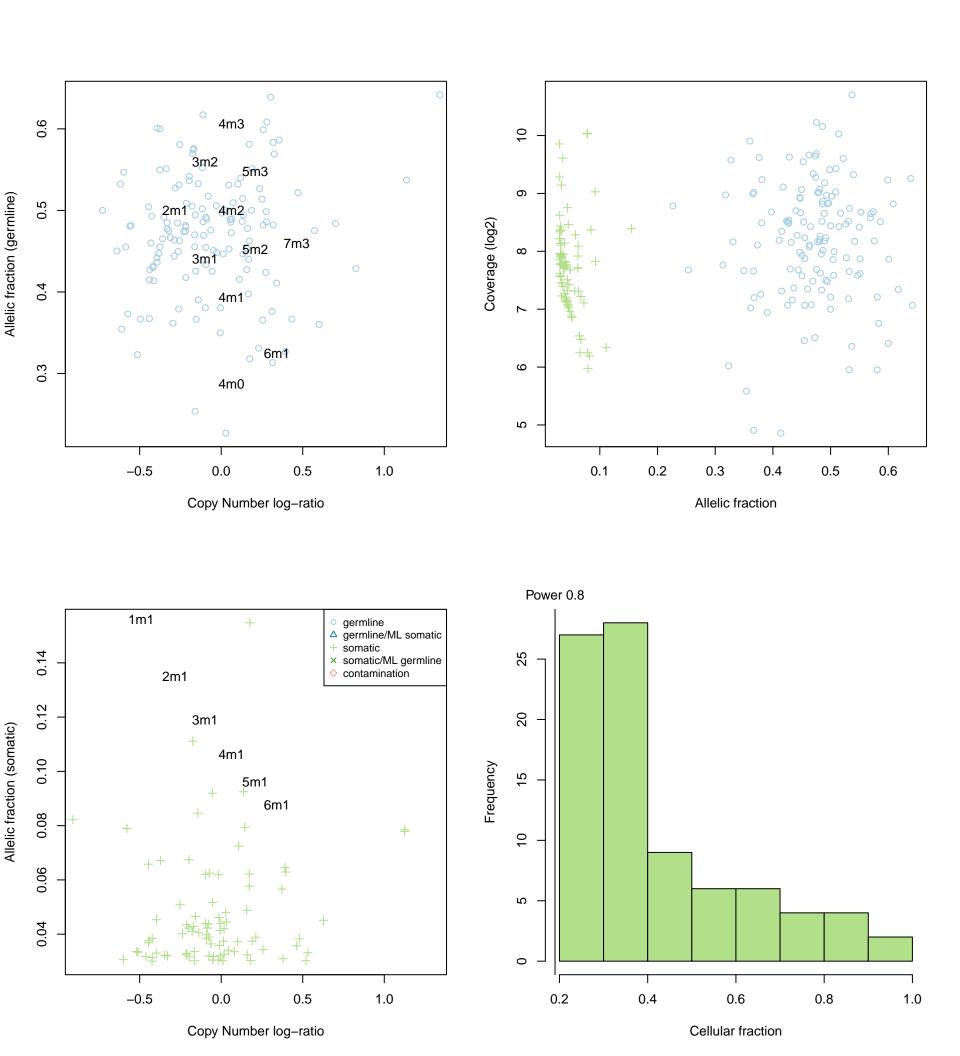


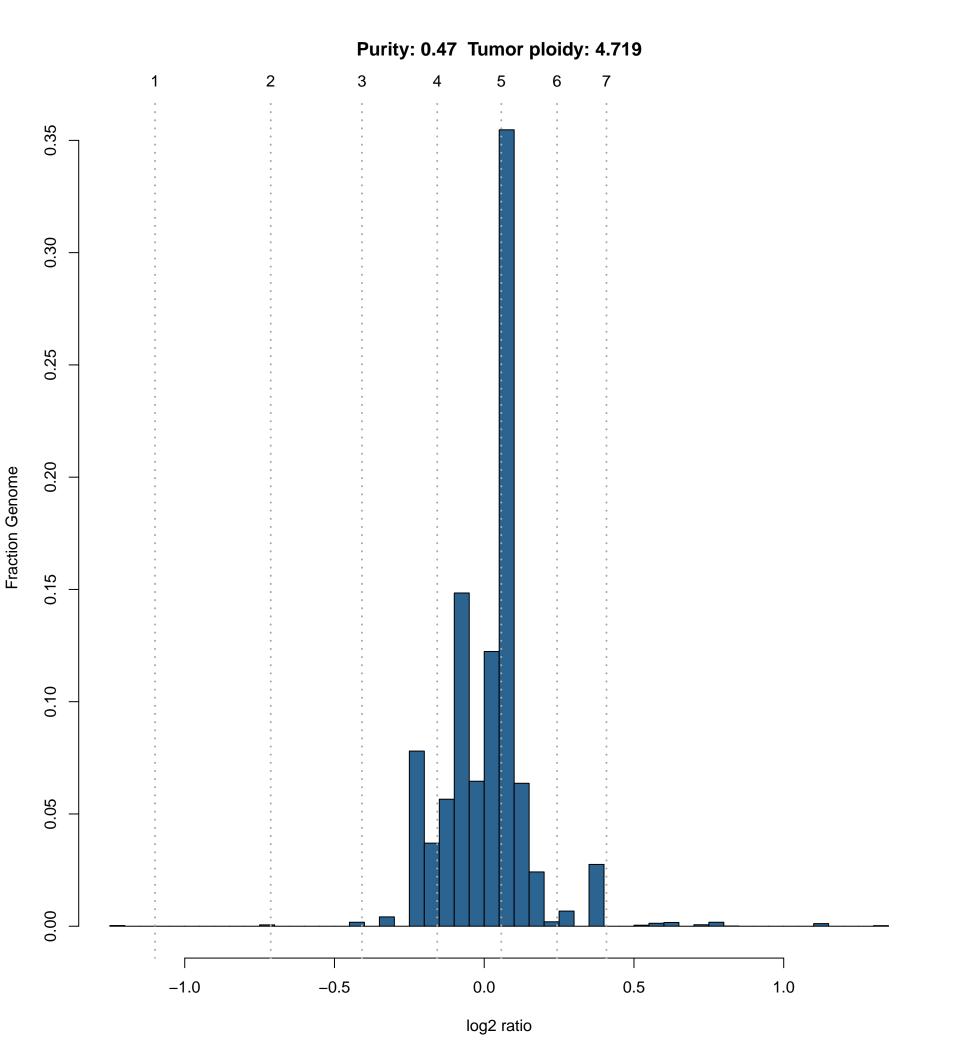


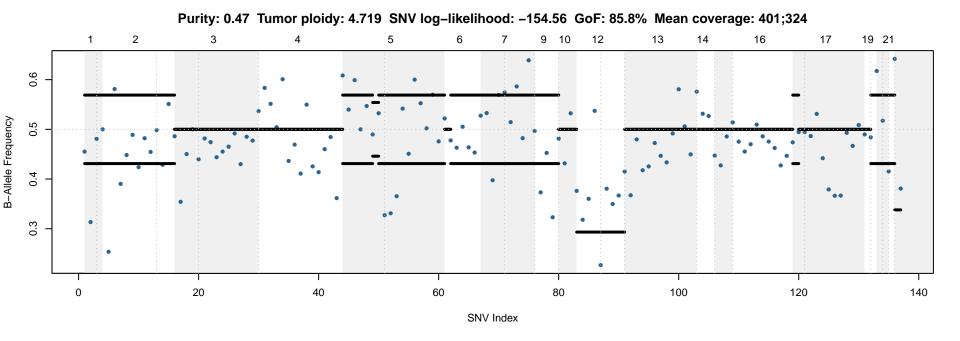
SCNA-fit log-likelihood: -13032.72



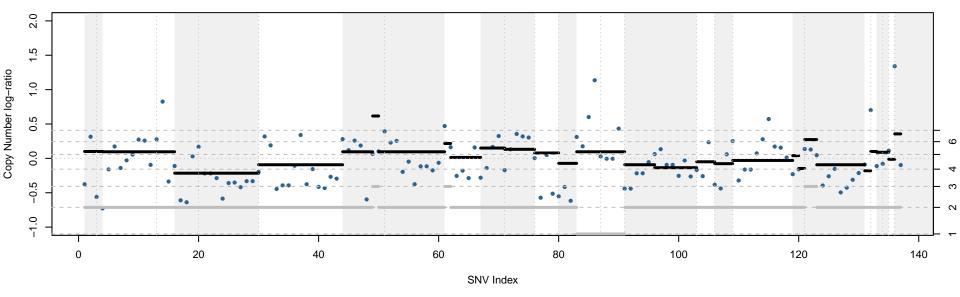


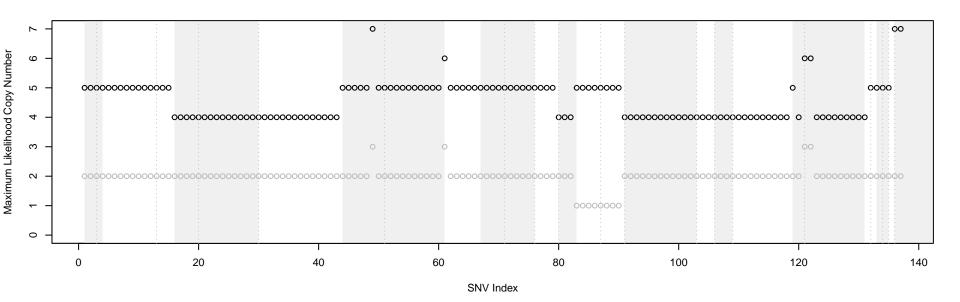


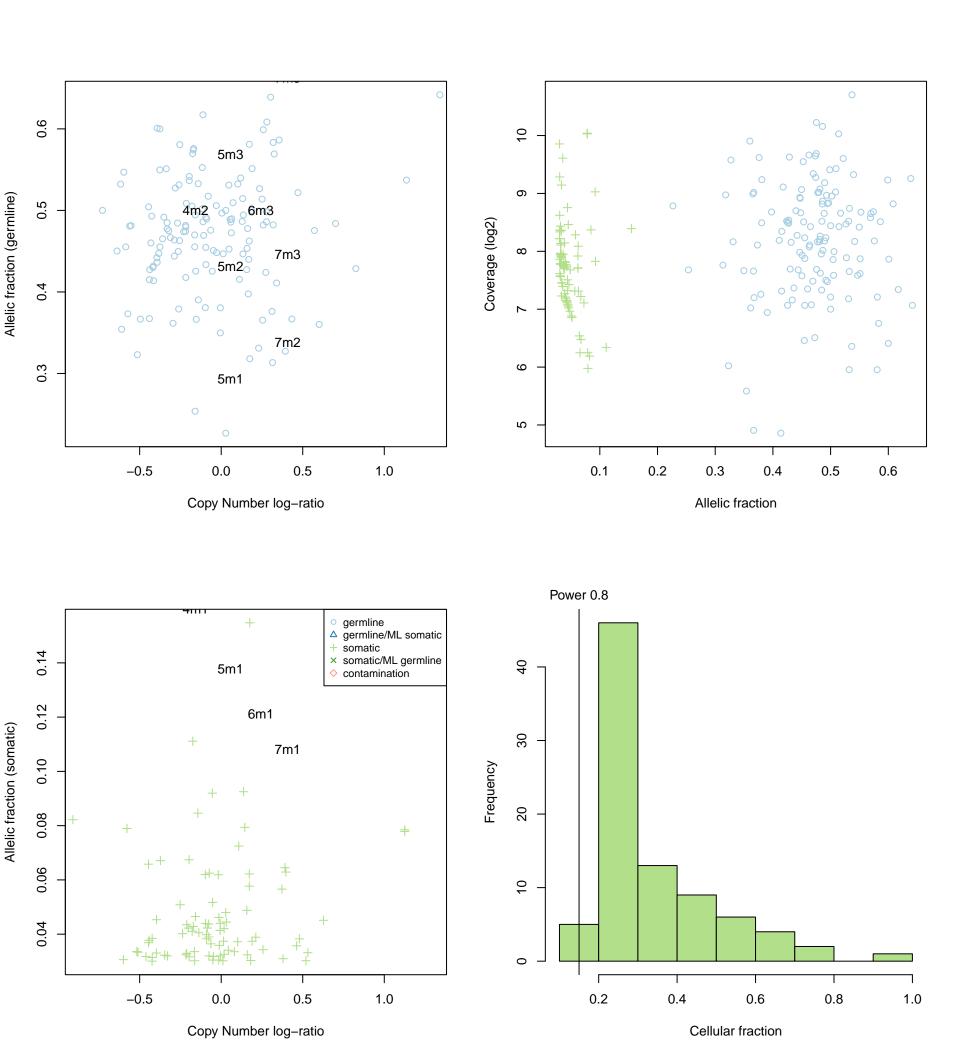


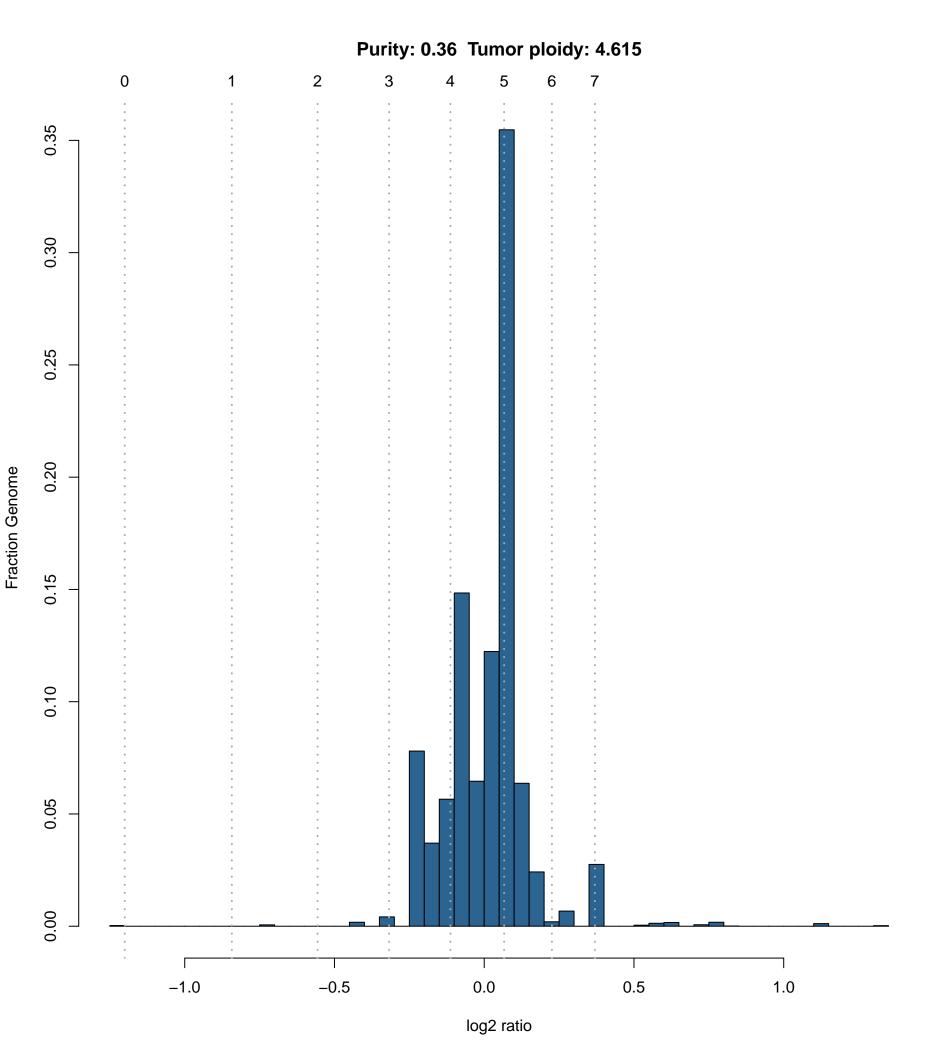


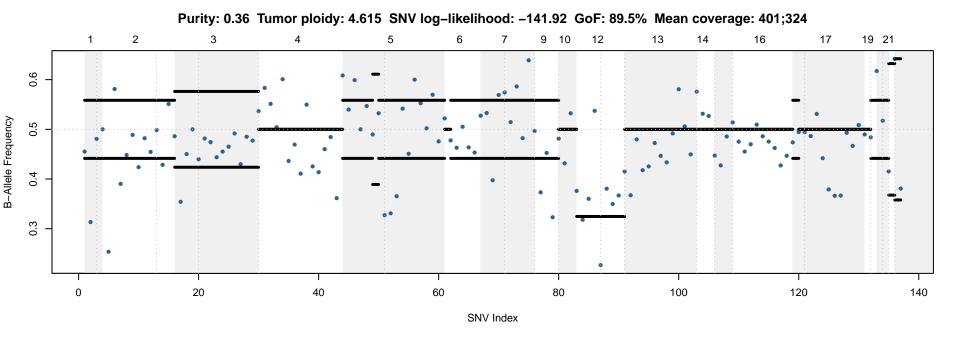
SCNA-fit log-likelihood: -13071.92



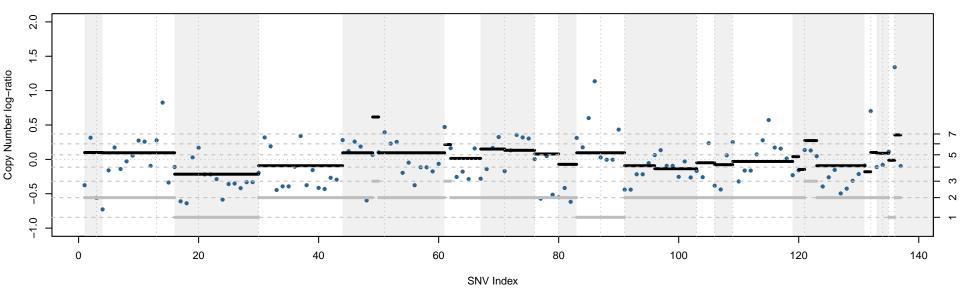


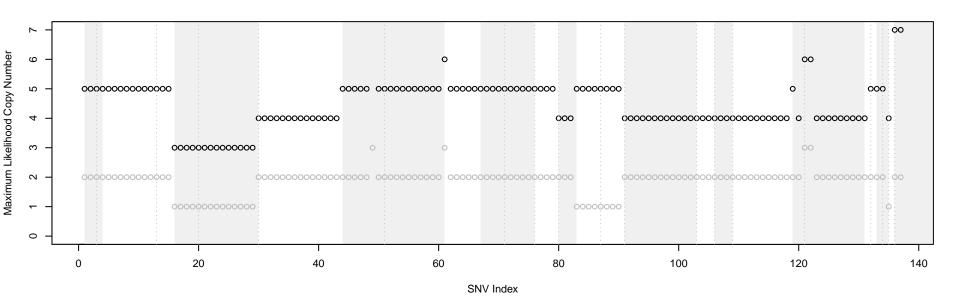


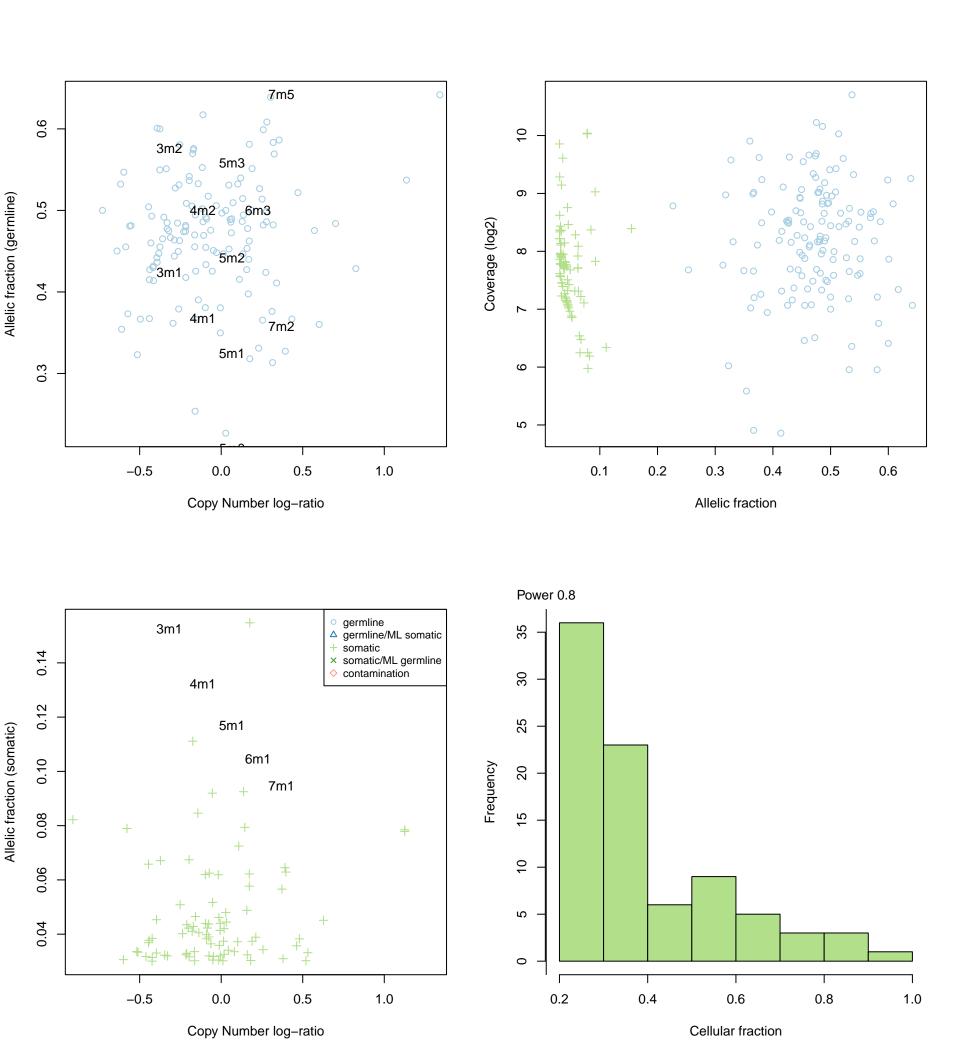




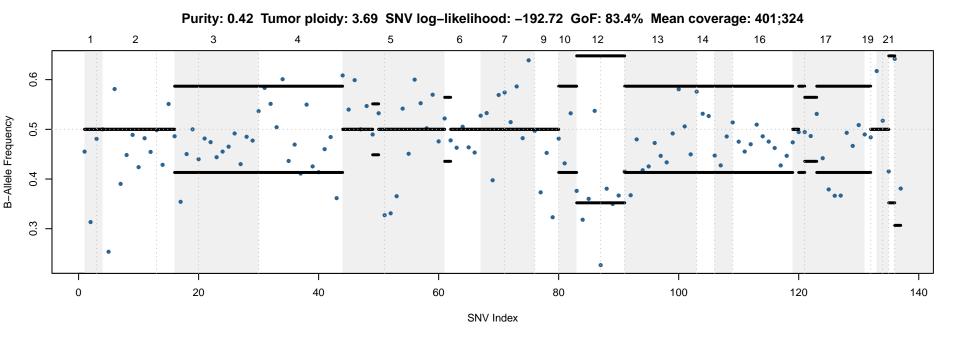
SCNA-fit log-likelihood: -13097.31



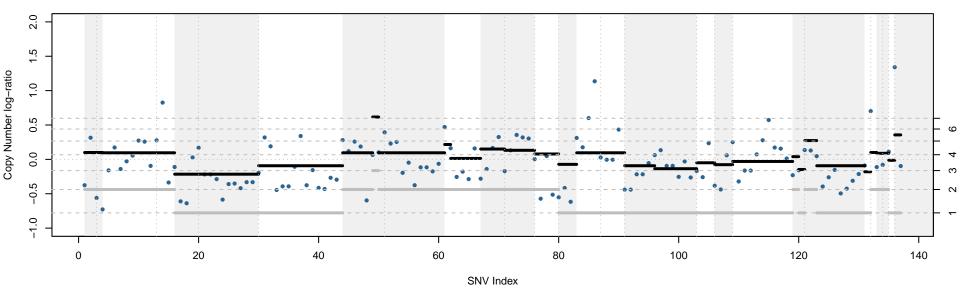


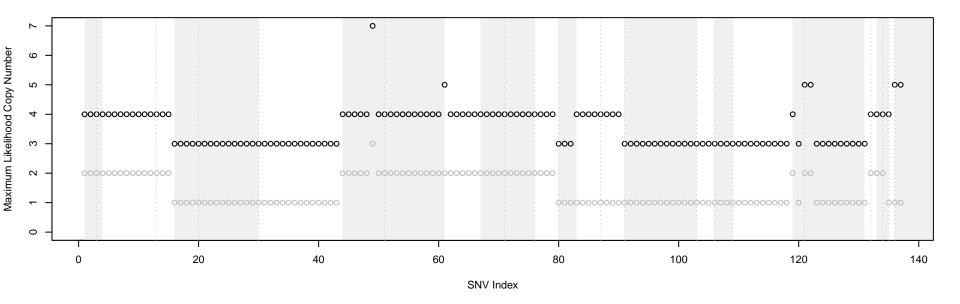


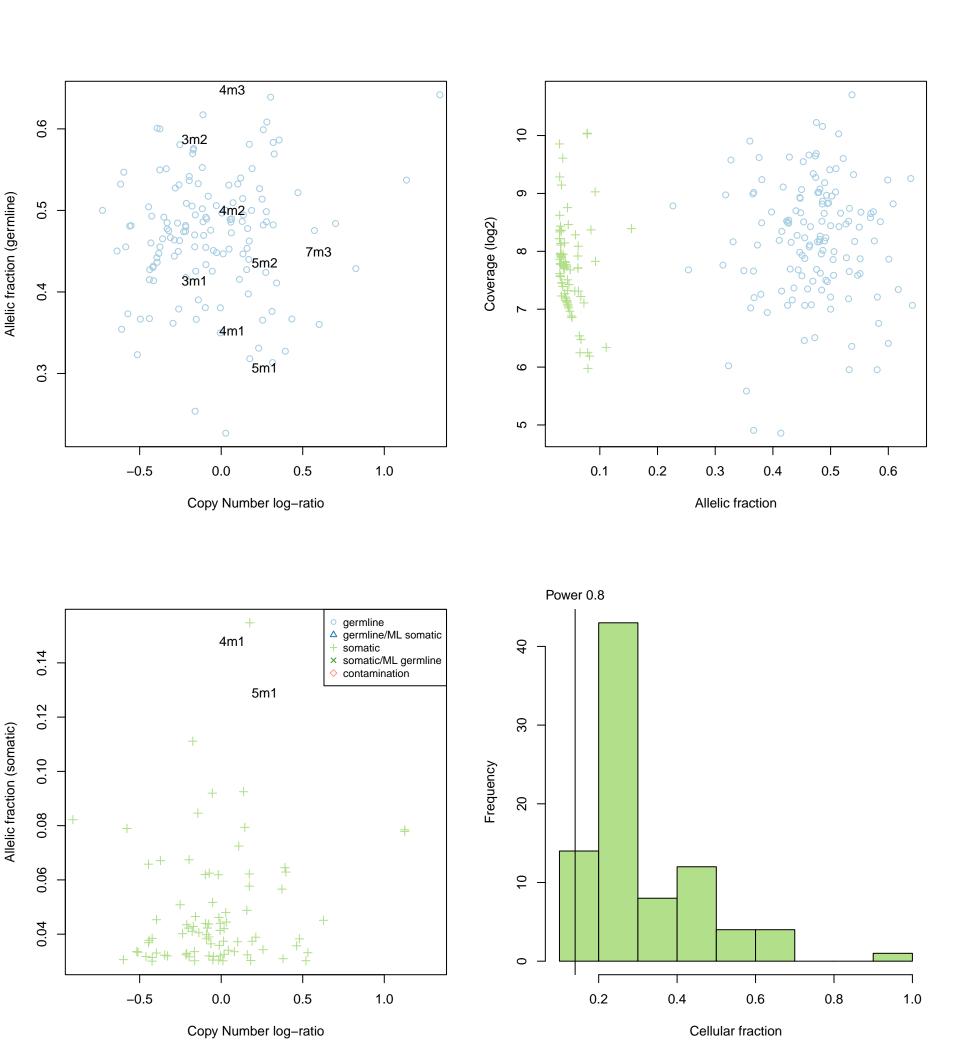
Purity: 0.42 Tumor ploidy: 3.69 2 0 6 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio

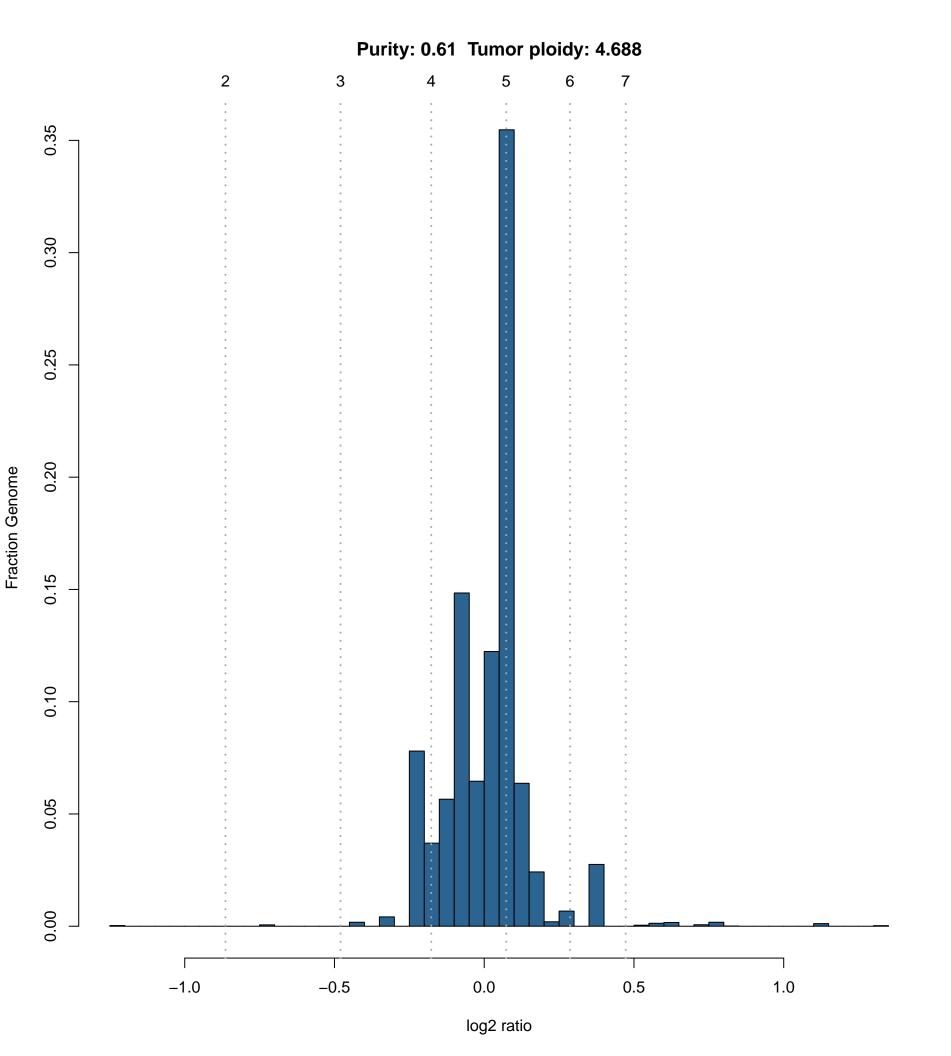


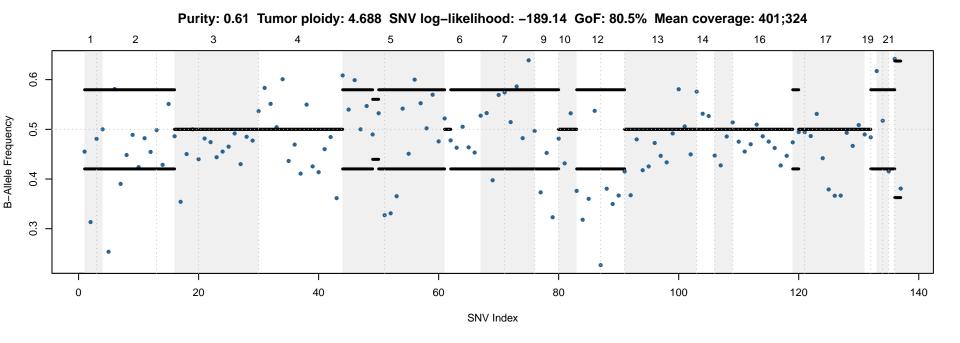
SCNA-fit log-likelihood: -13032.93



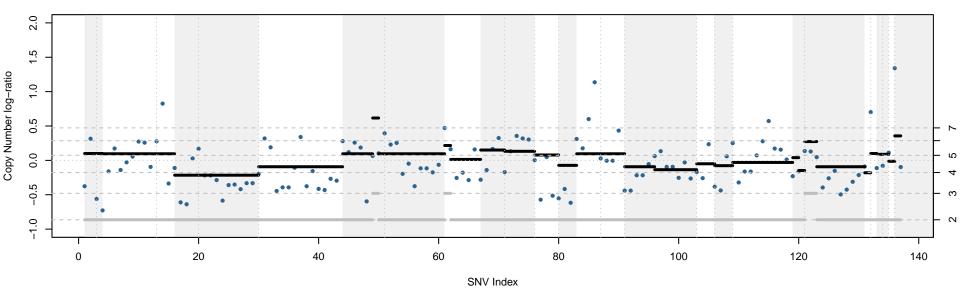


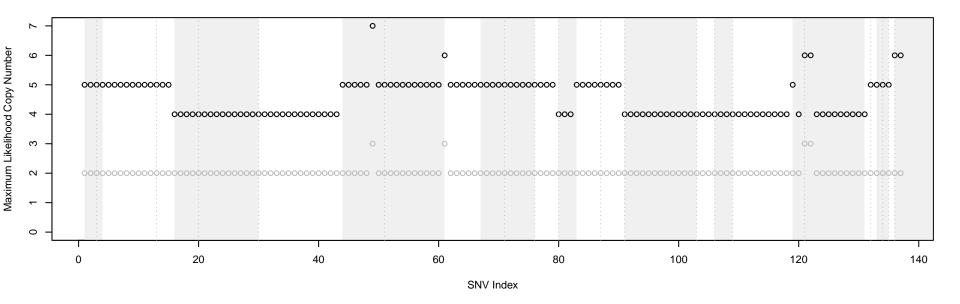


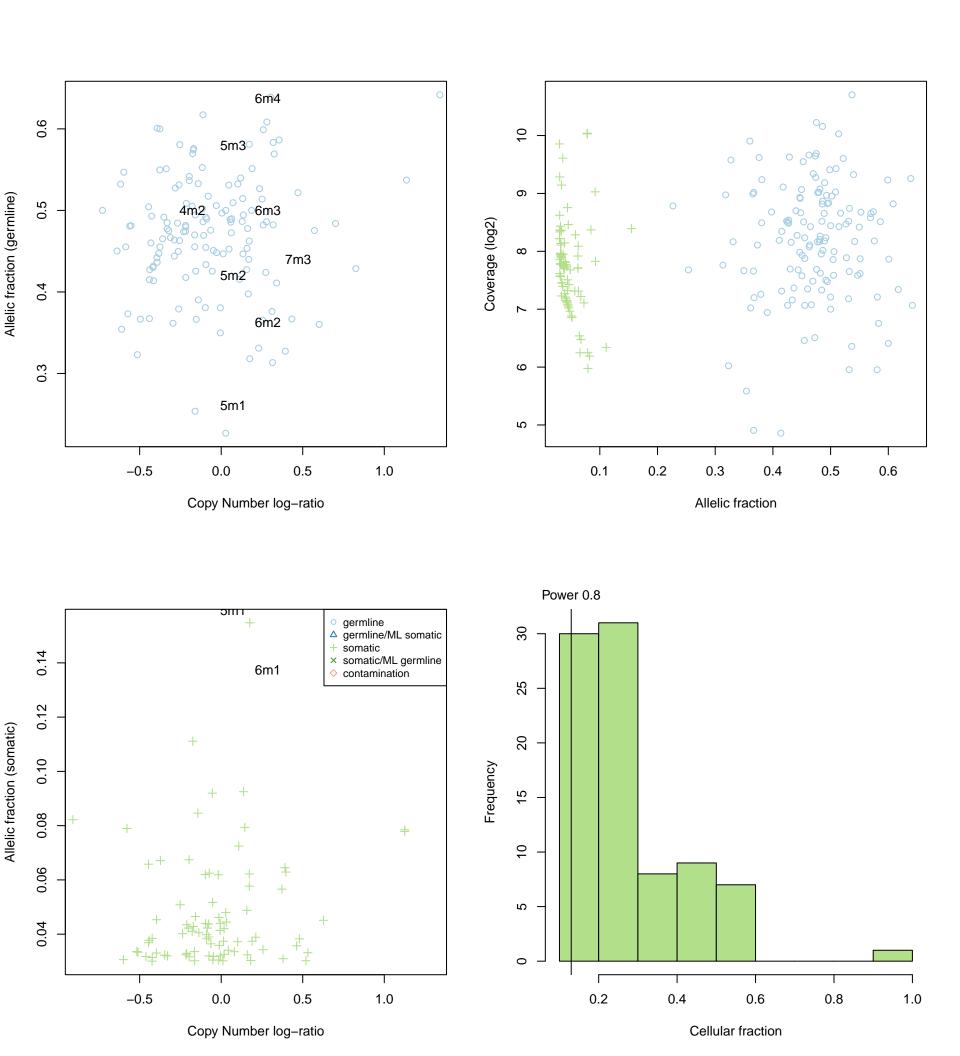


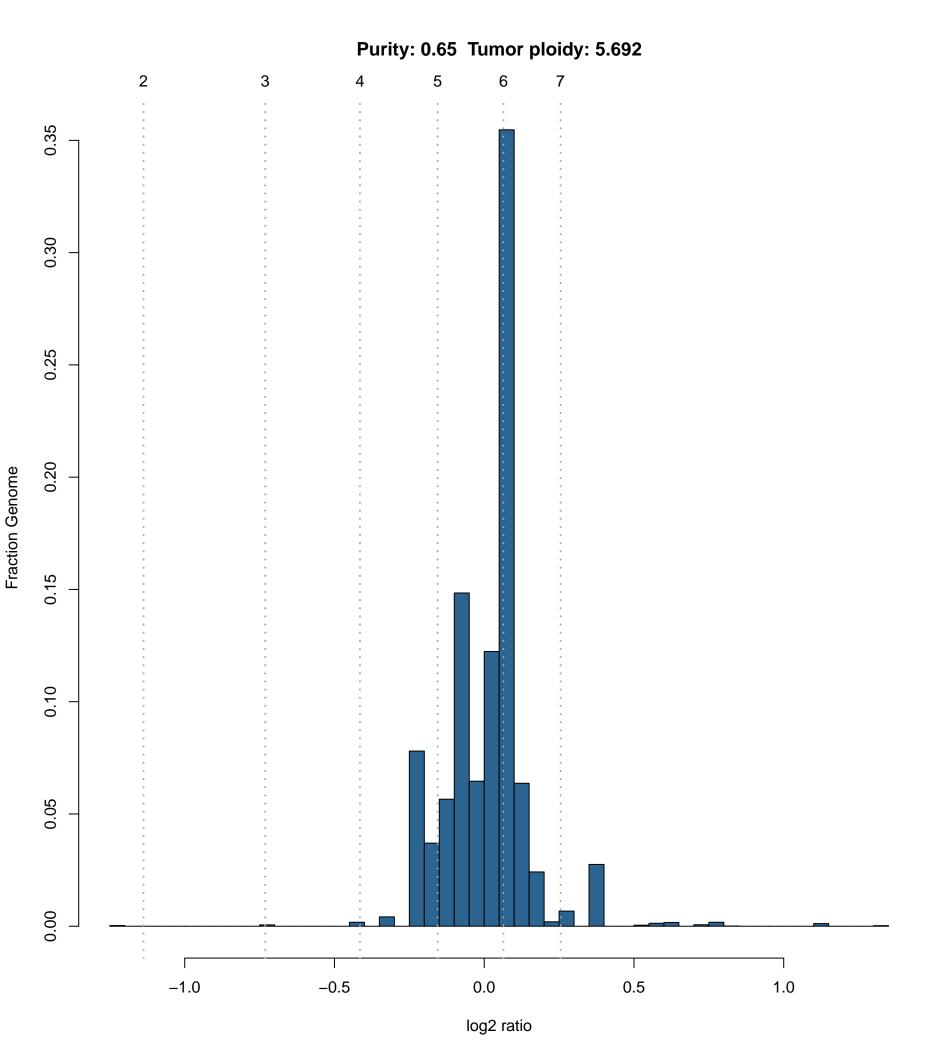


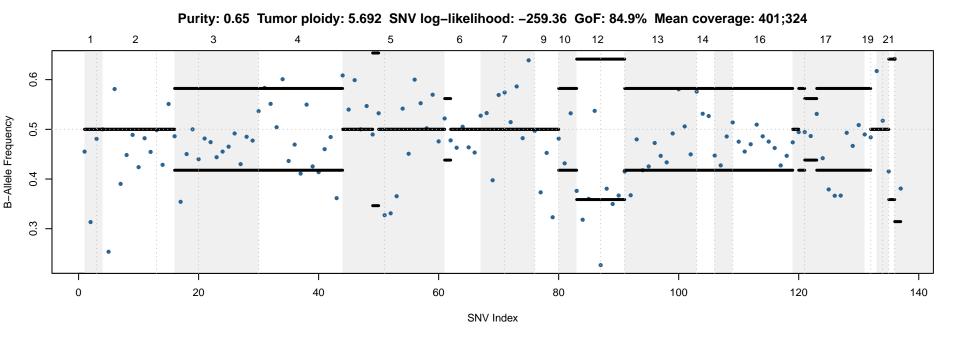
SCNA-fit log-likelihood: -13087.88



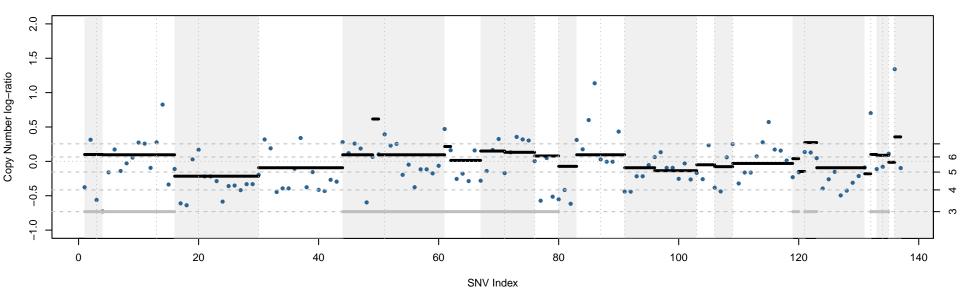


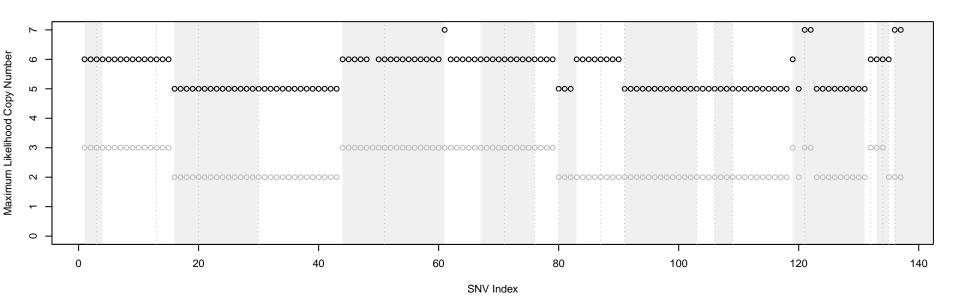


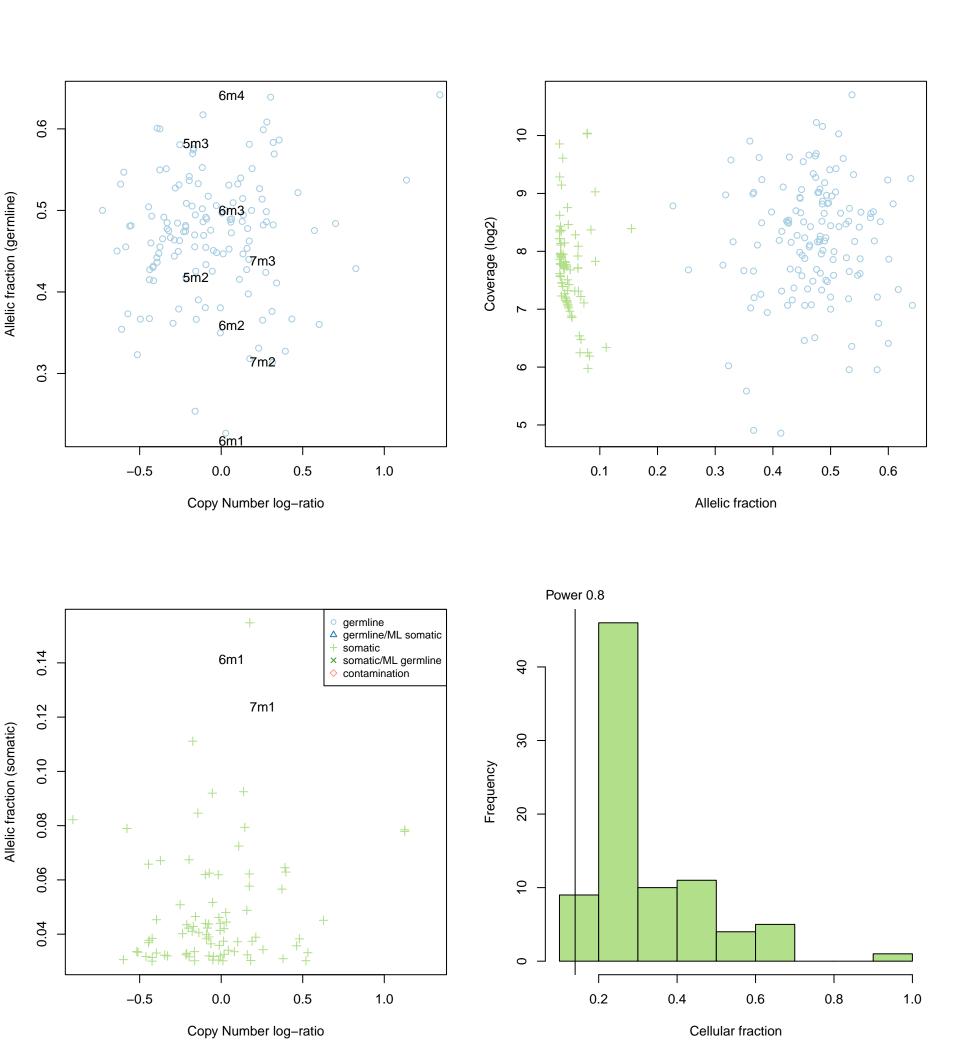


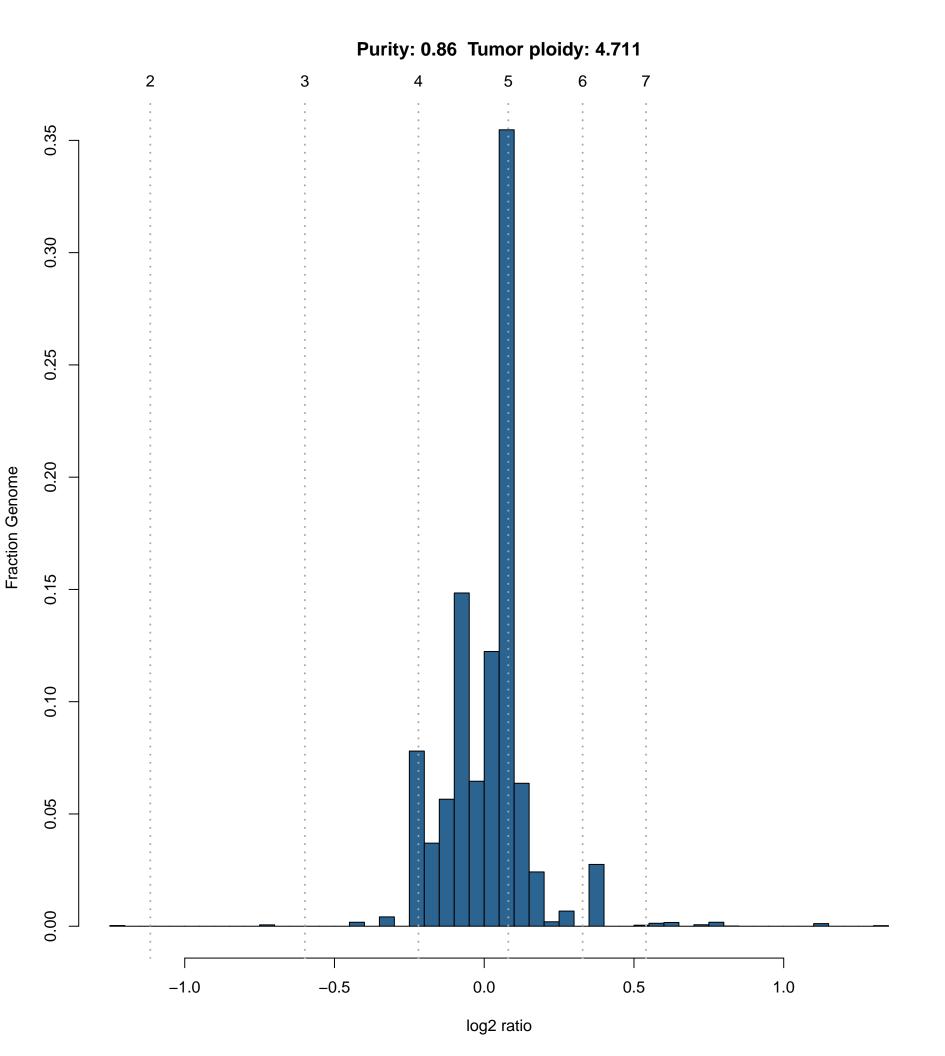


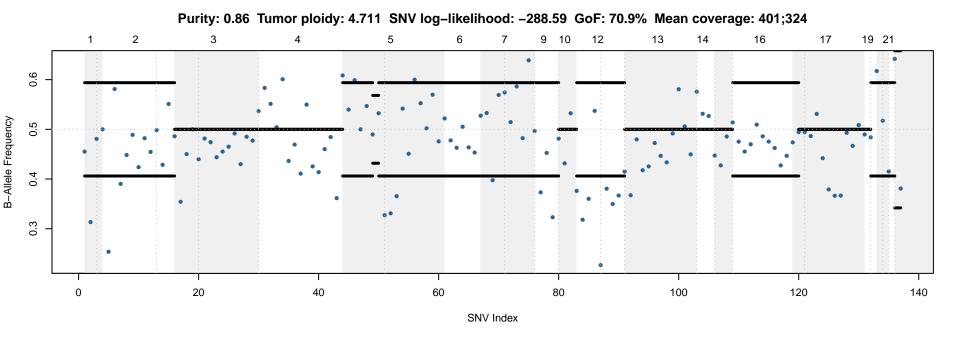
SCNA-fit log-likelihood: -13139.6



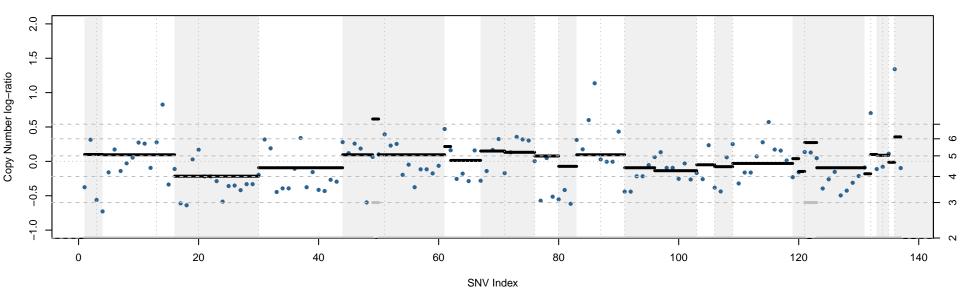


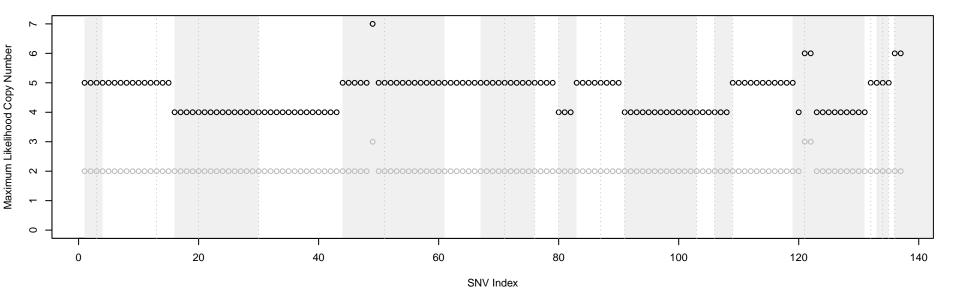


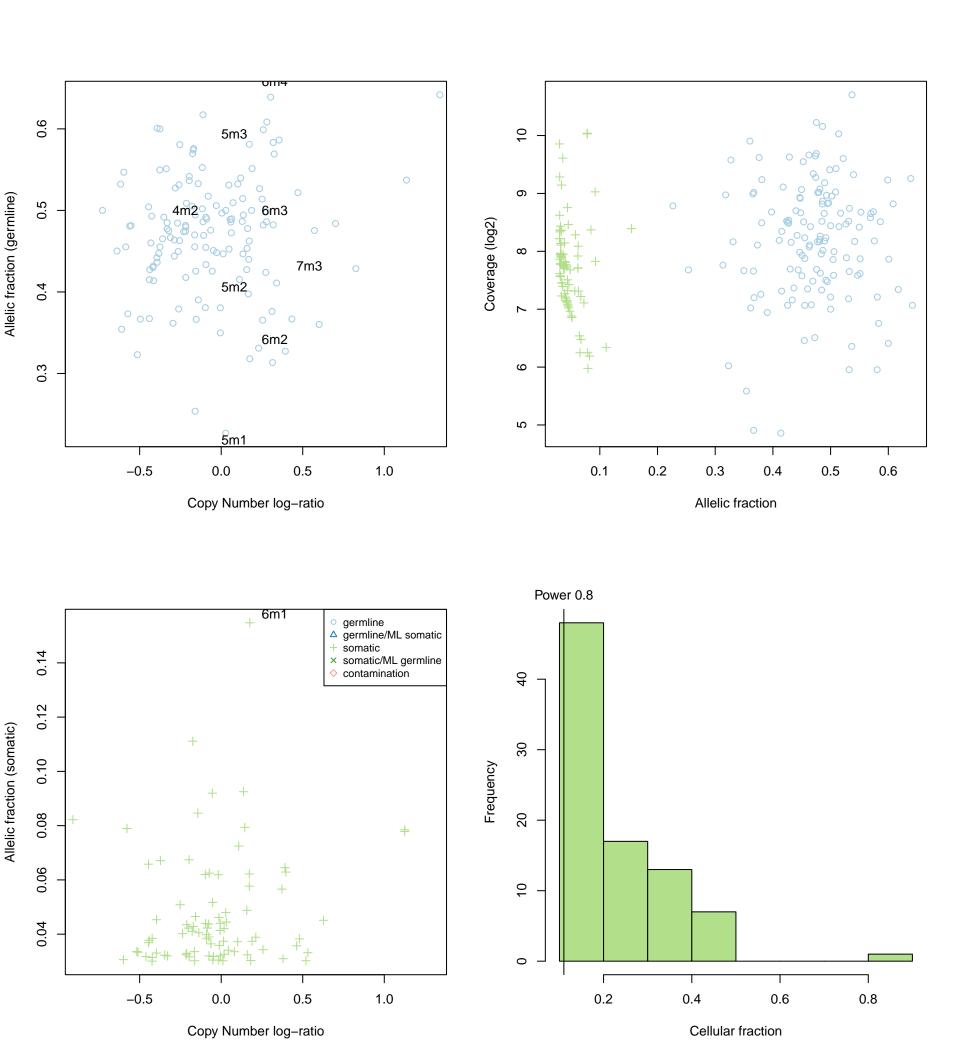




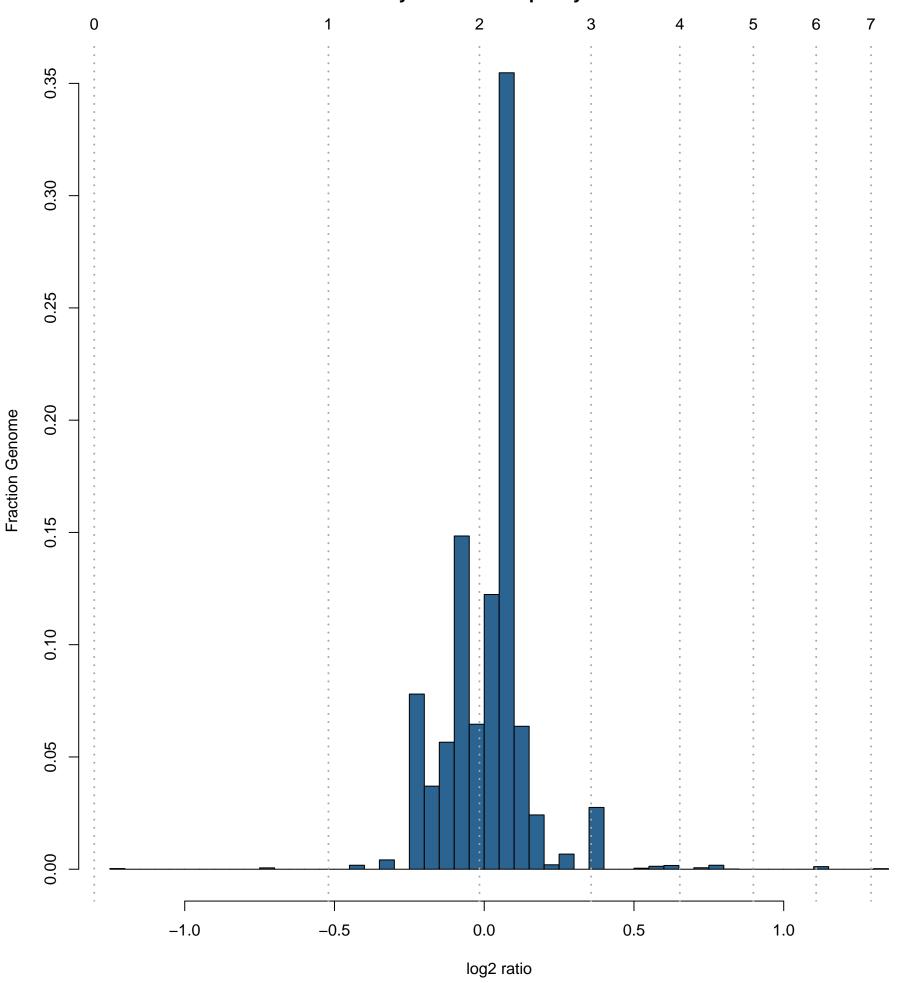
SCNA-fit log-likelihood: -13119.43

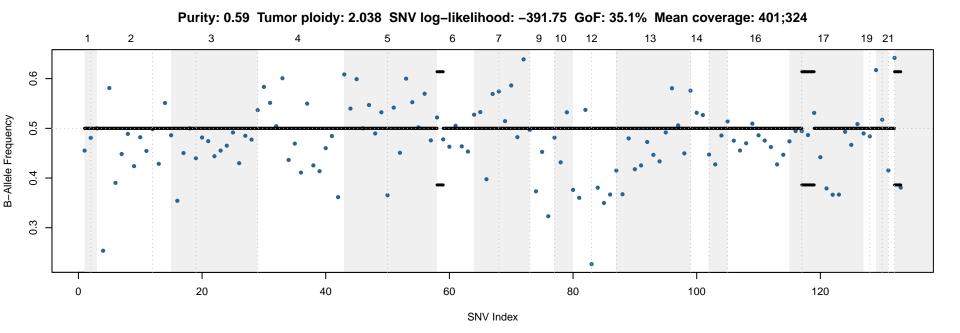




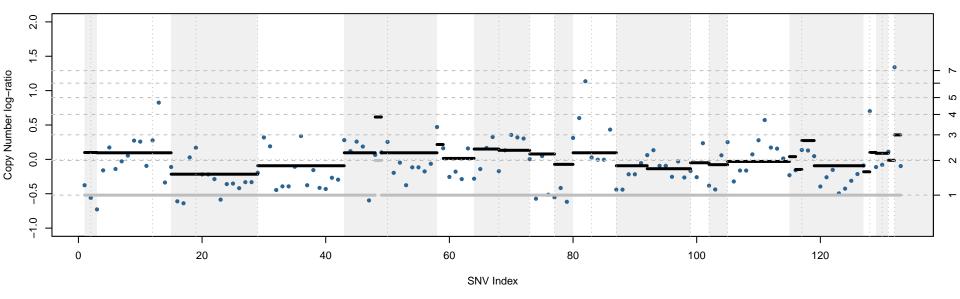


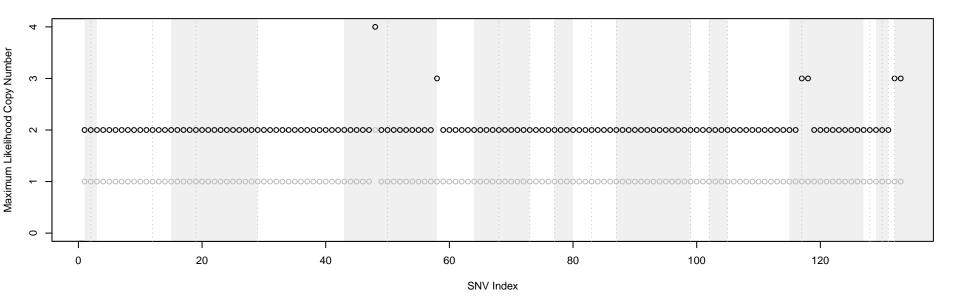
Purity: 0.59 Tumor ploidy: 2.038

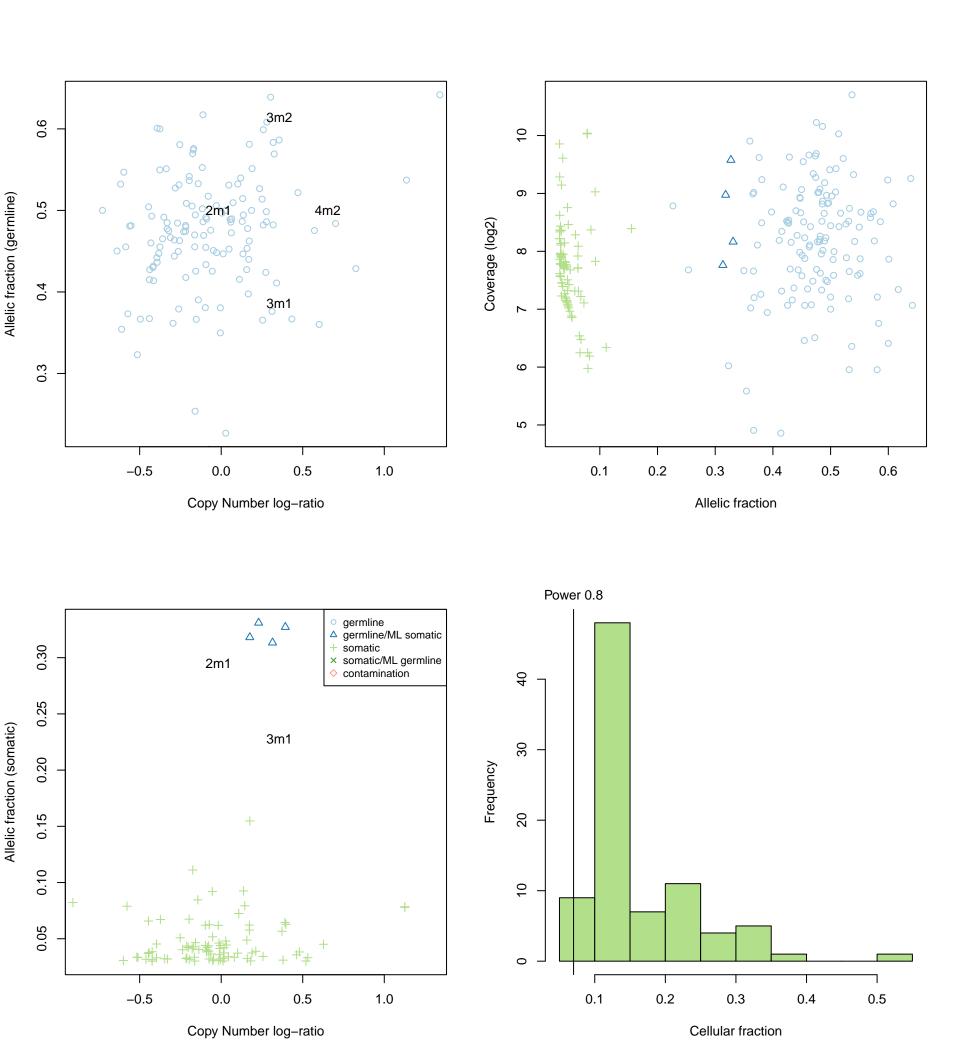




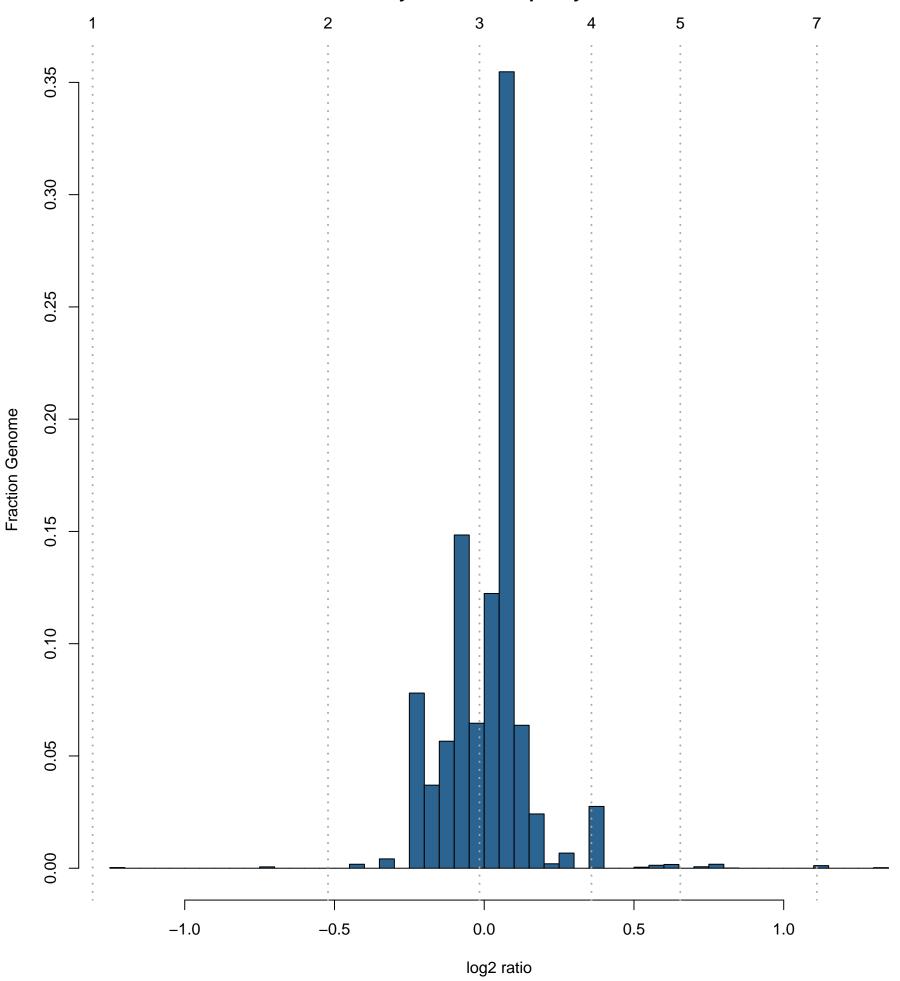
SCNA-fit log-likelihood: -13417.55

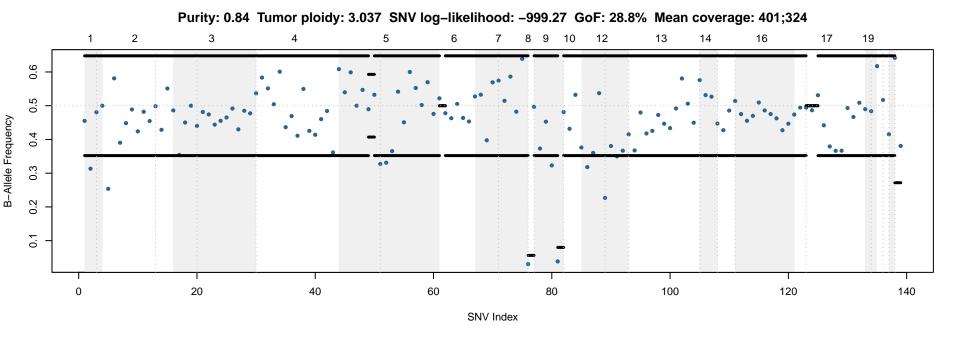






Purity: 0.84 Tumor ploidy: 3.037





SCNA-fit log-likelihood: -13418.06

