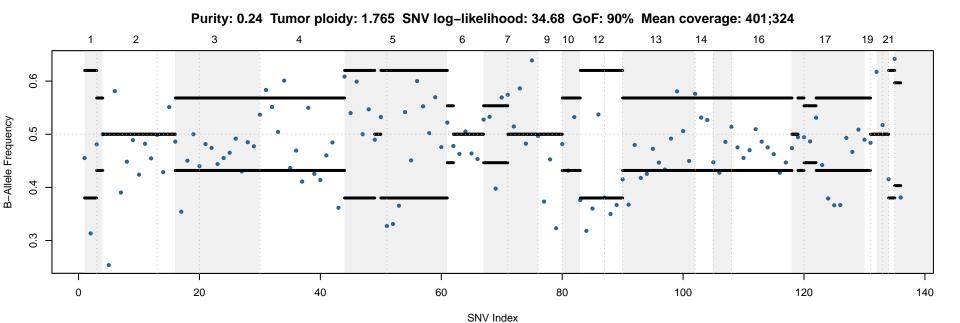
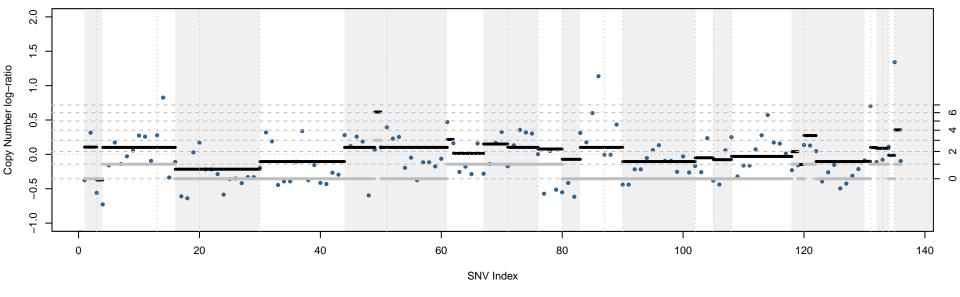
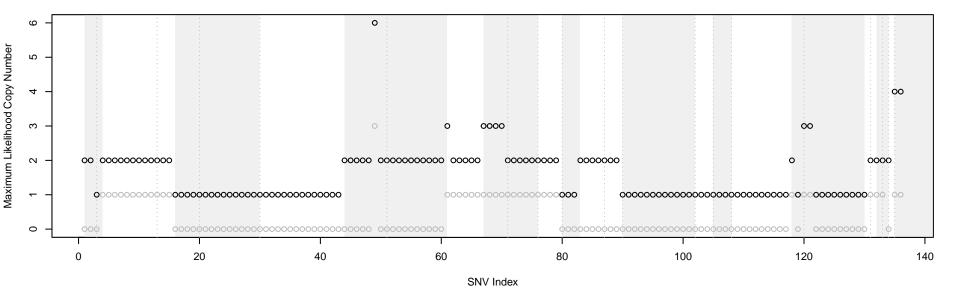
Purity: 0.24 Tumor ploidy: 1.765 2 6 0 3 5 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -0.5 0.0 0.5 1.0

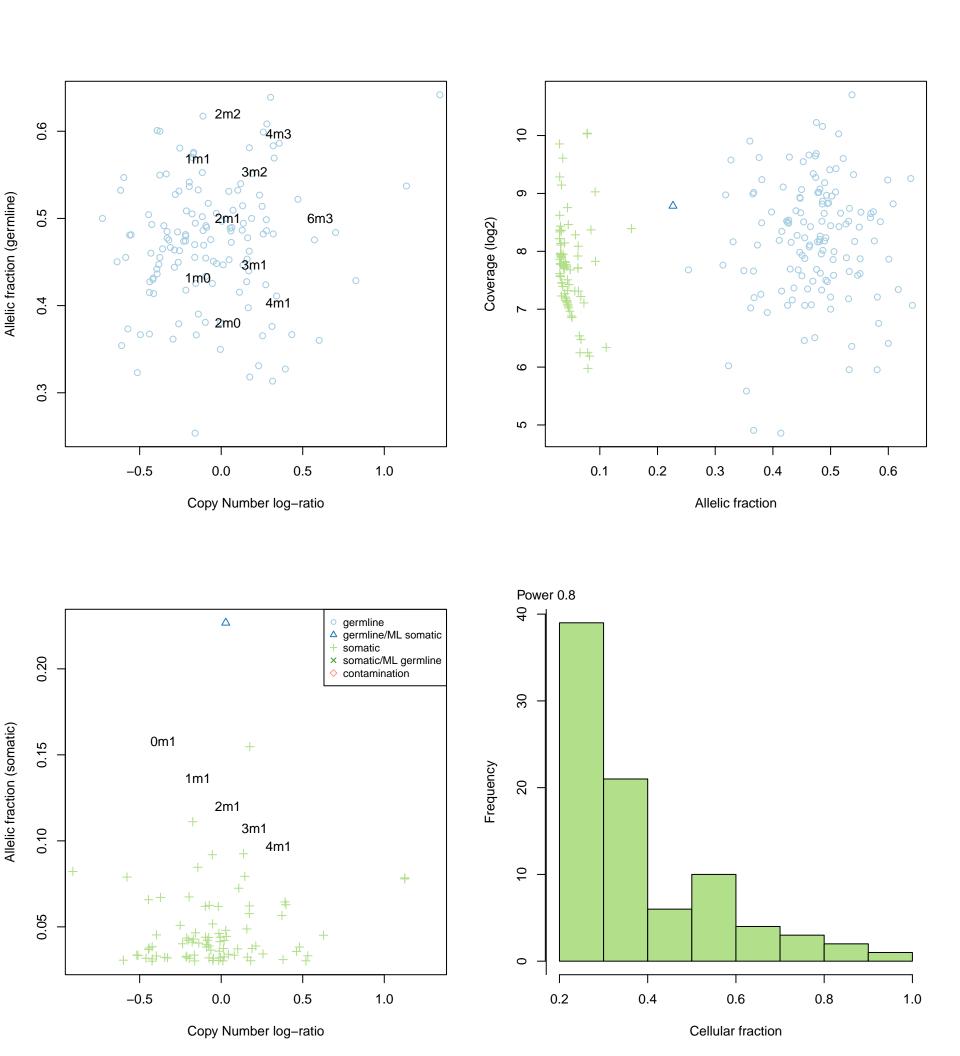
log2 ratio

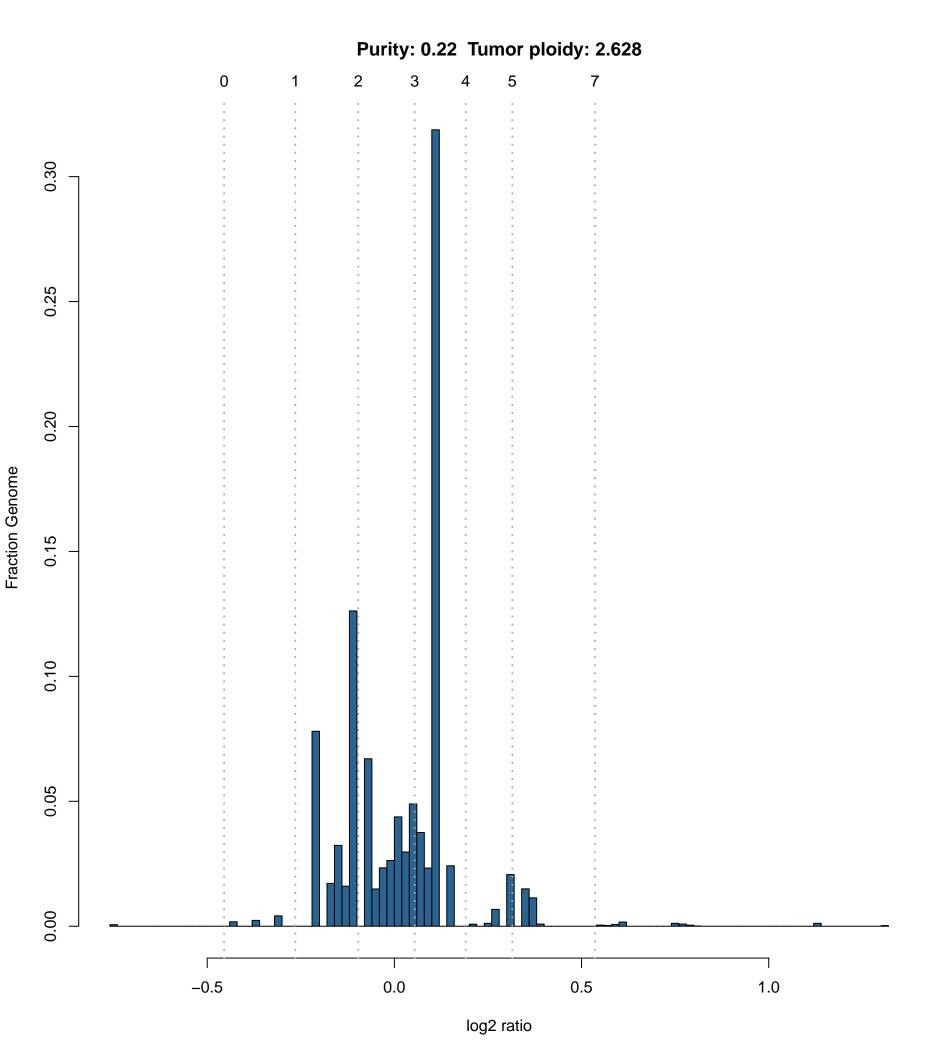


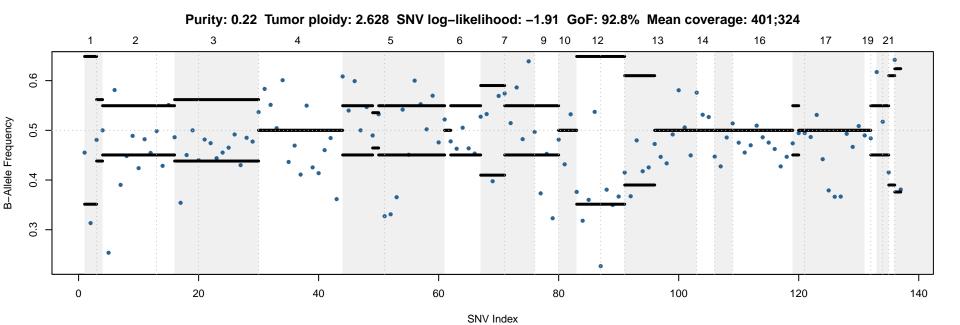
SCNA-fit log-likelihood: -12961.65



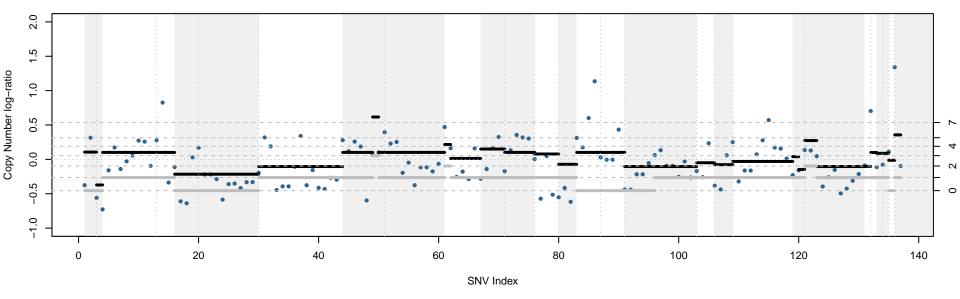


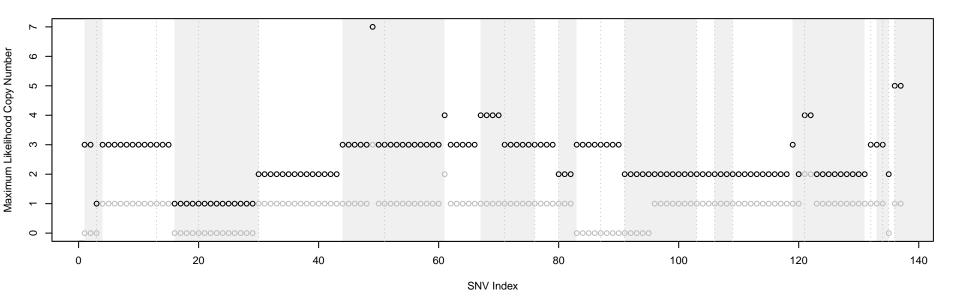


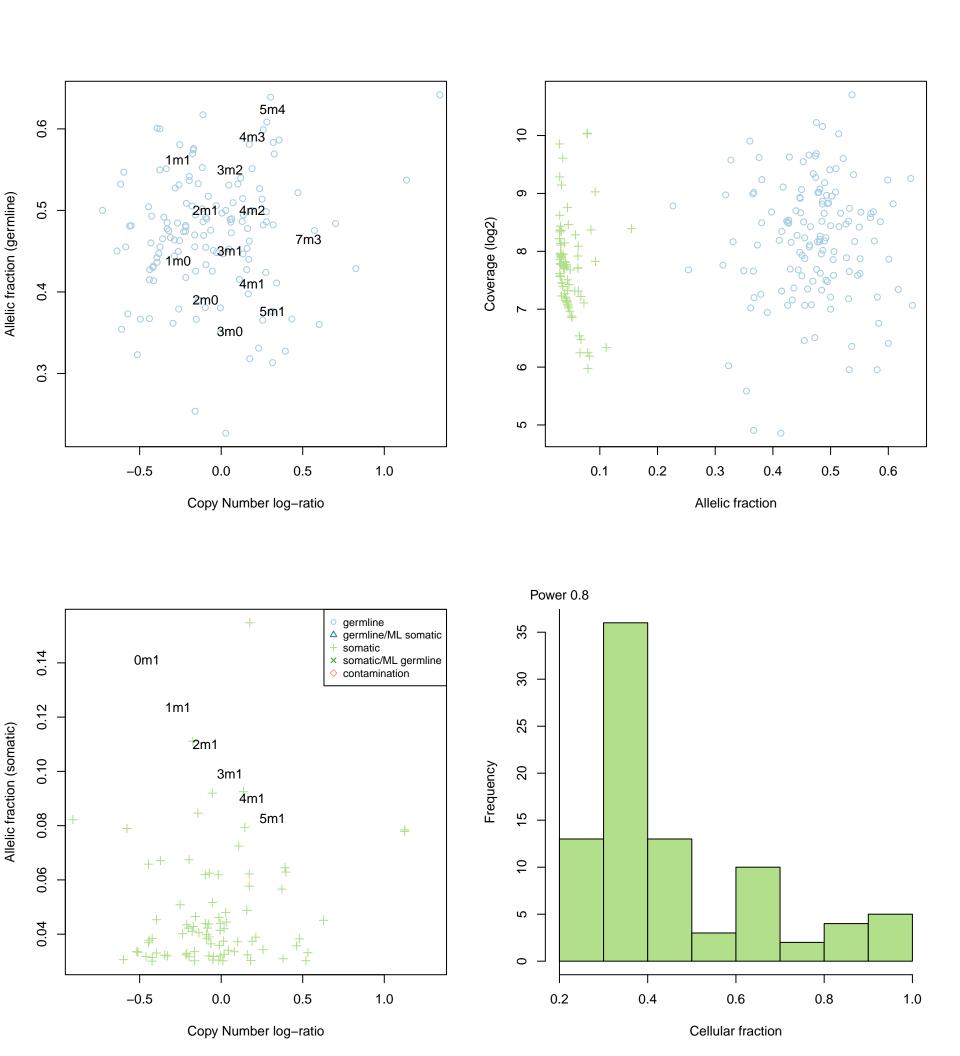


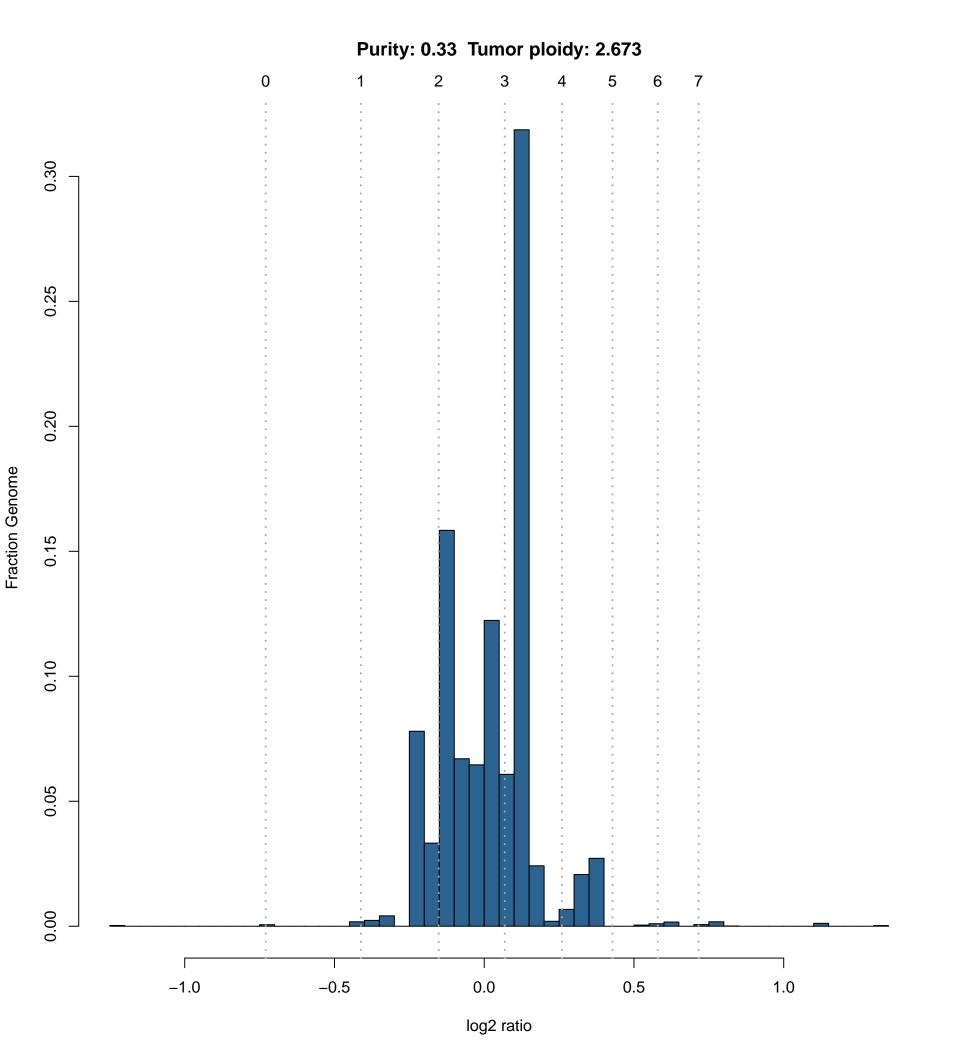


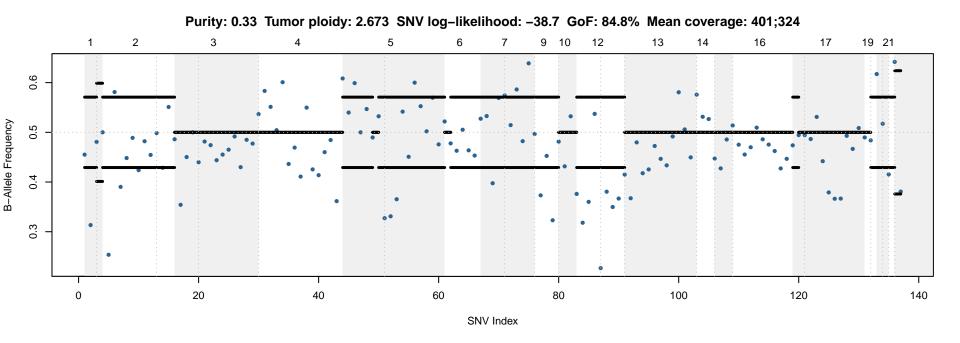
SCNA-fit log-likelihood: -12944.13



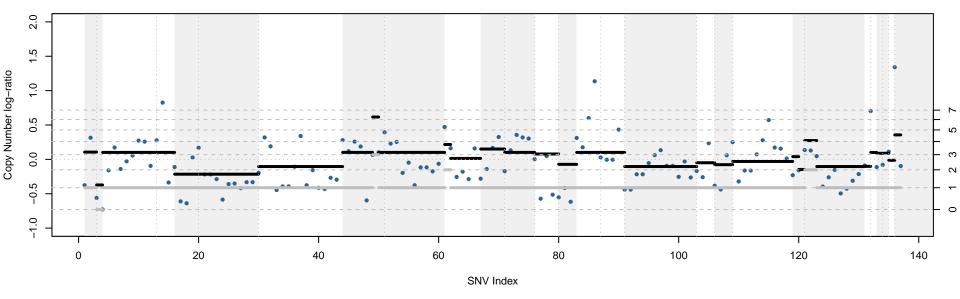


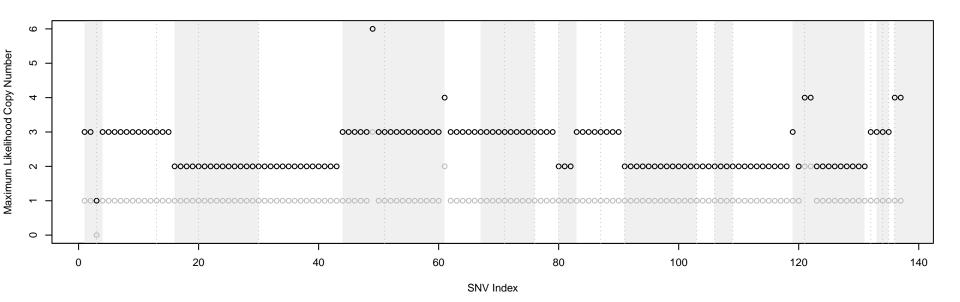


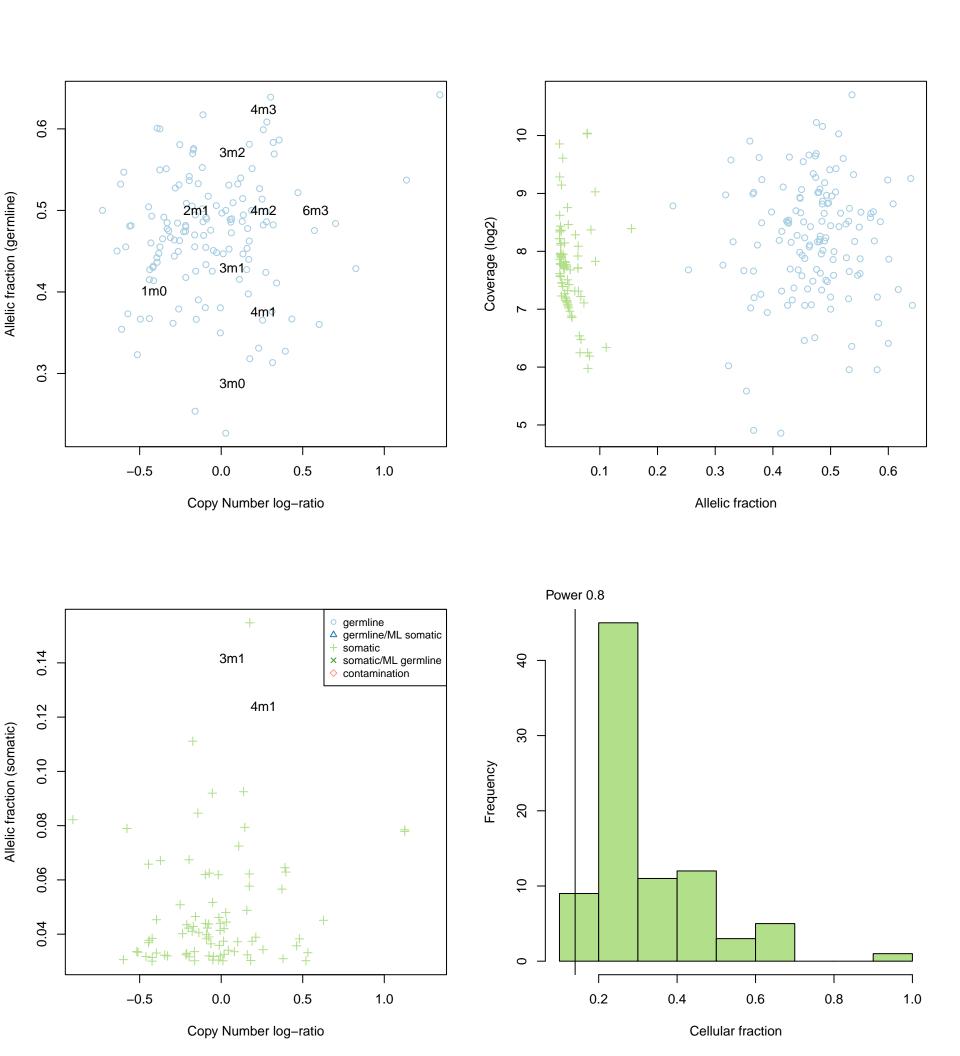


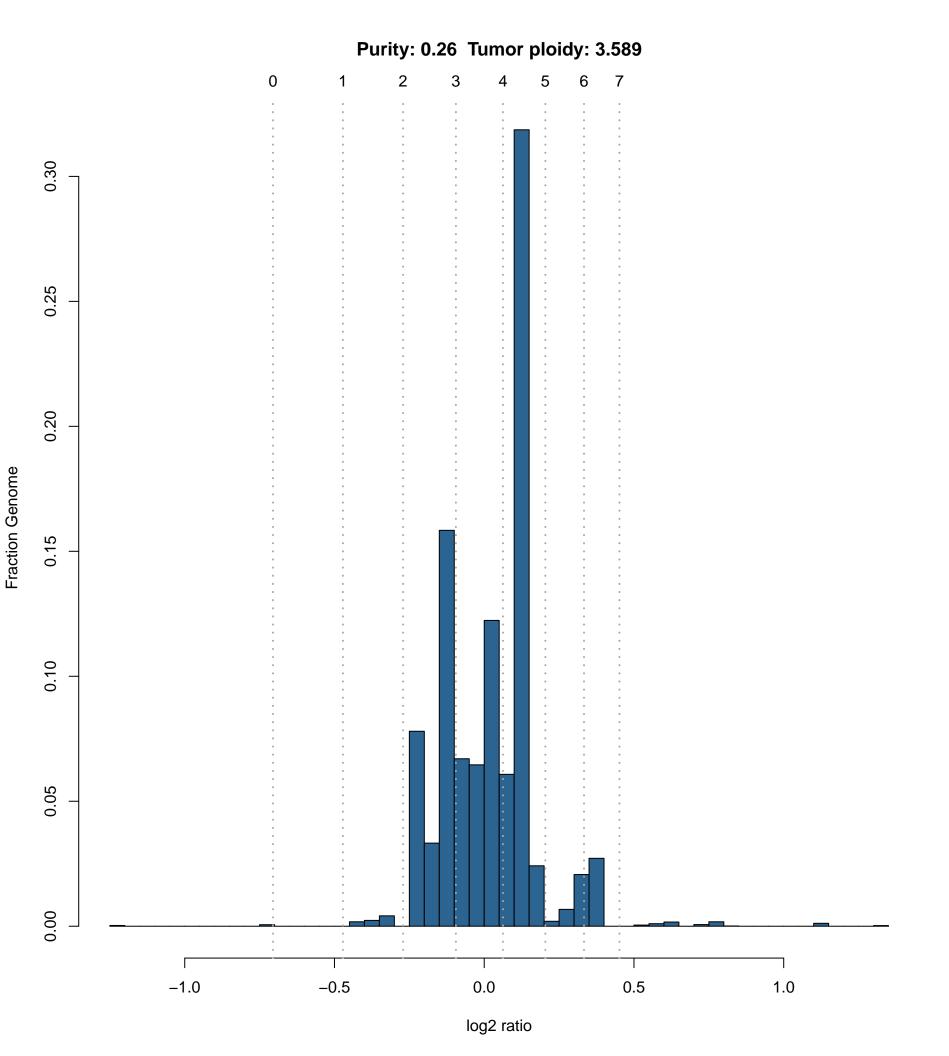


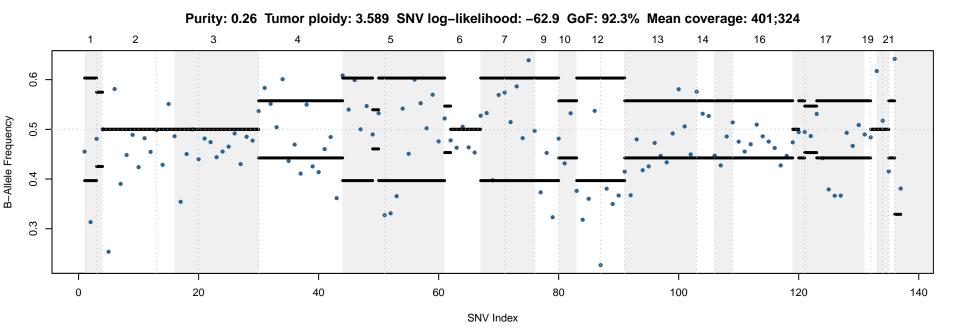
SCNA-fit log-likelihood: -12941.4



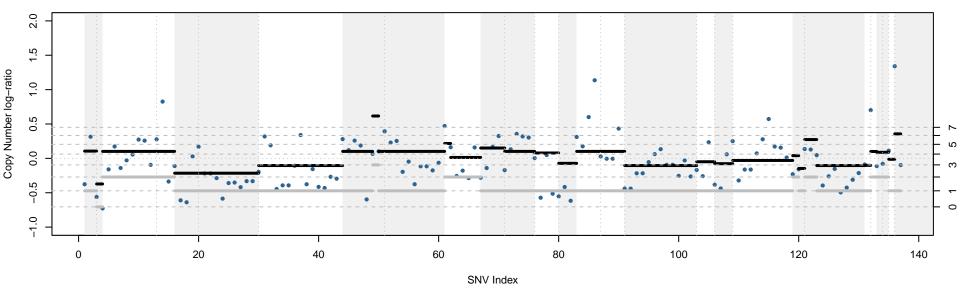


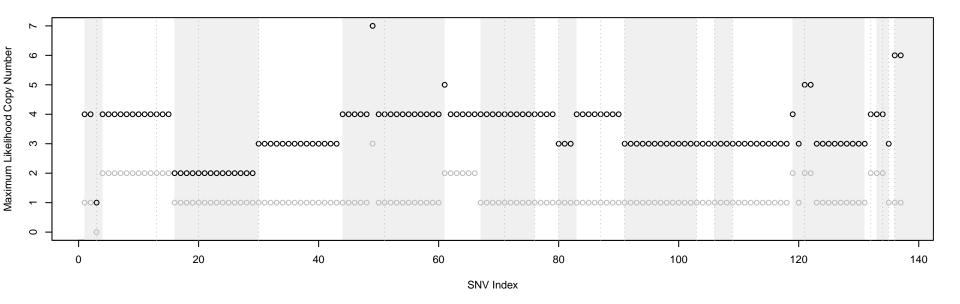


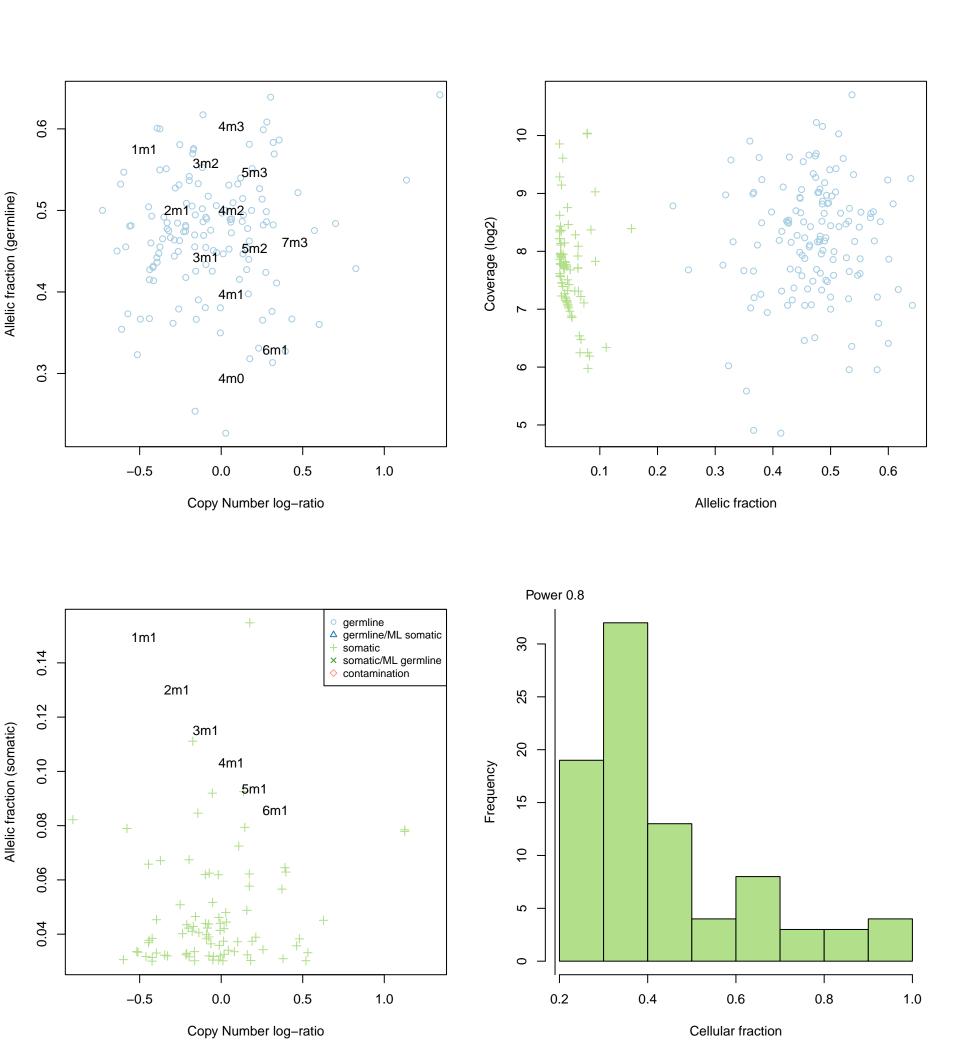




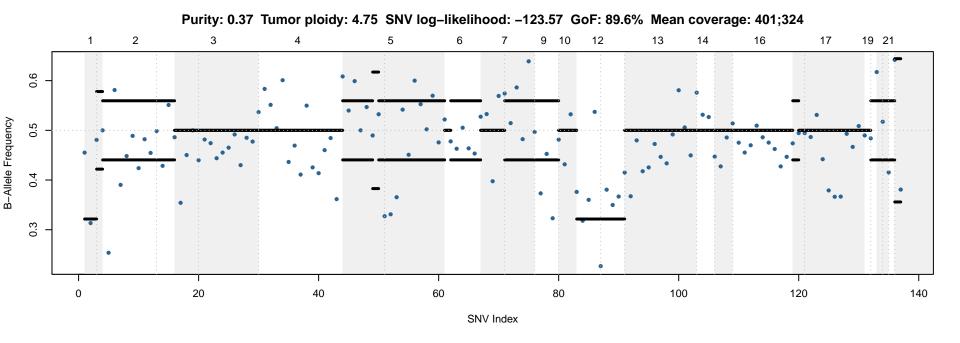
SCNA-fit log-likelihood: -12942.76



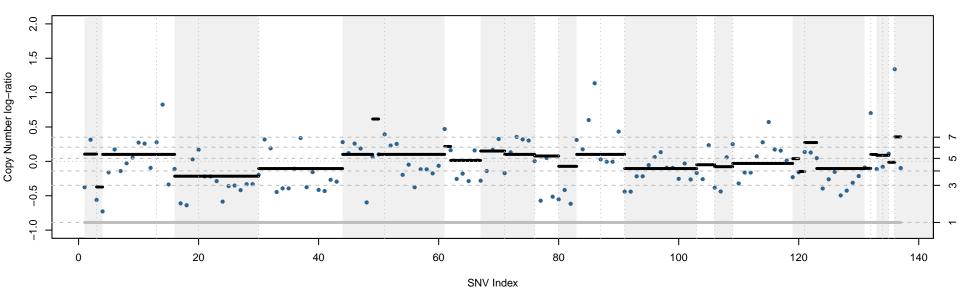


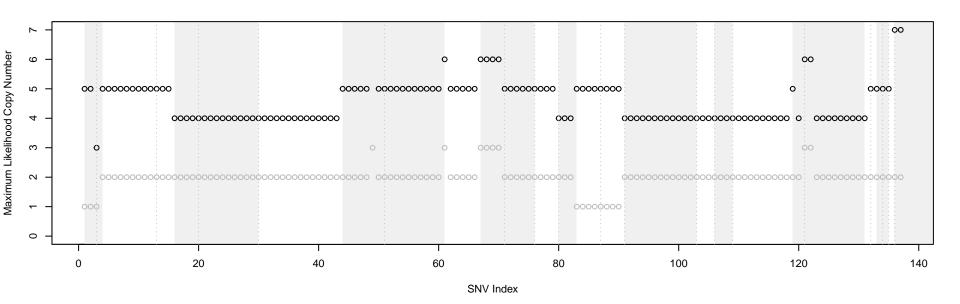


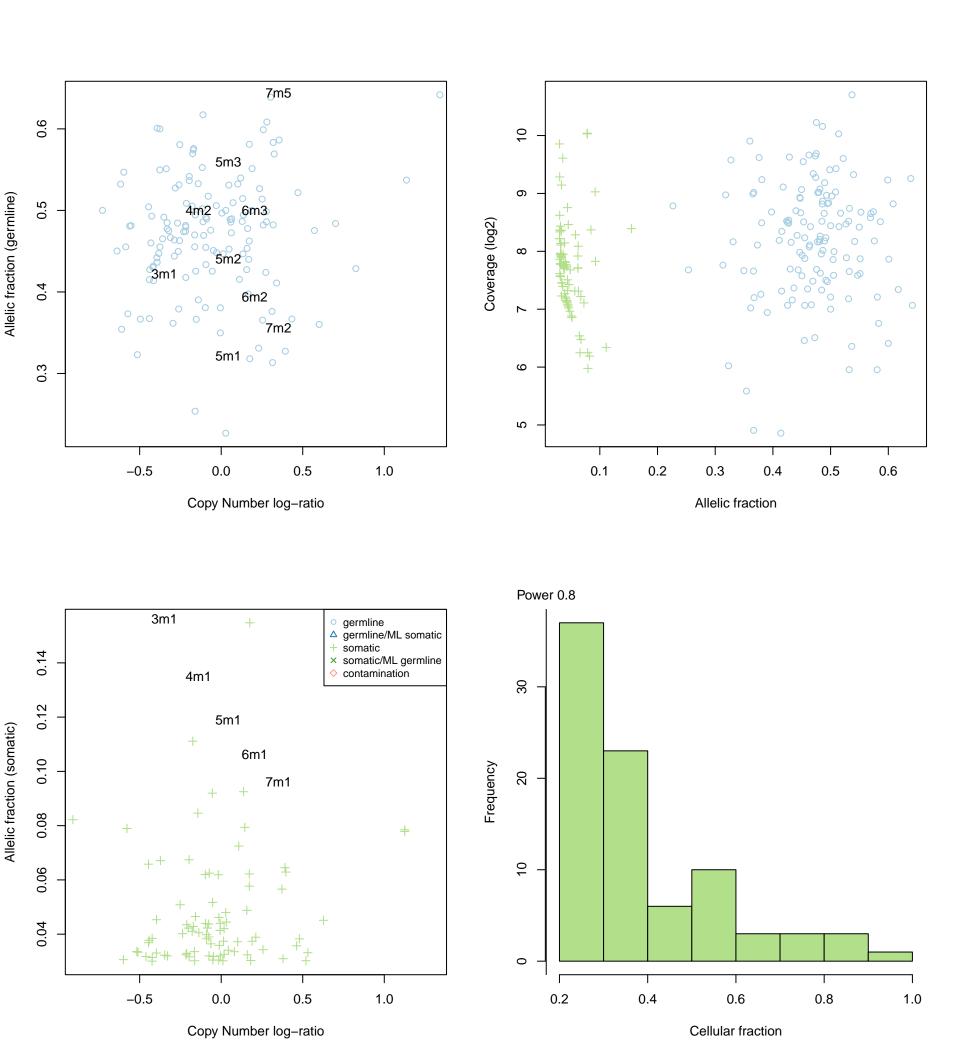
Purity: 0.37 Tumor ploidy: 4.75 3 5 6 0 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio

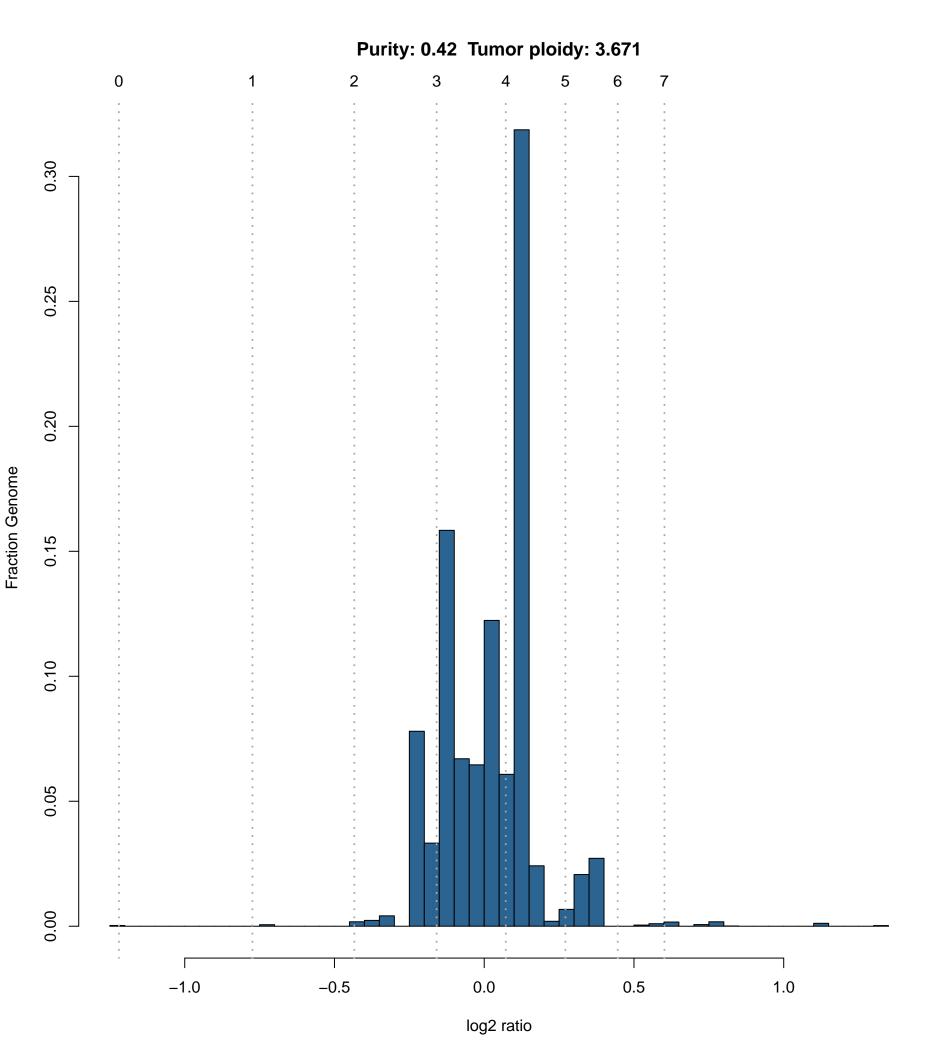


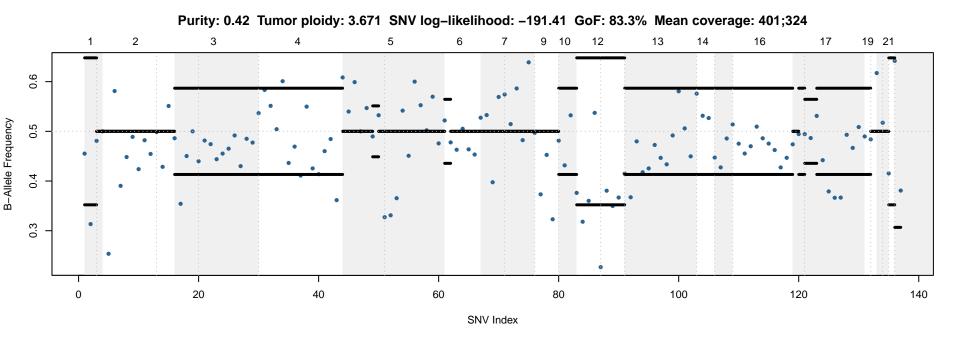
SCNA-fit log-likelihood: -13027.25



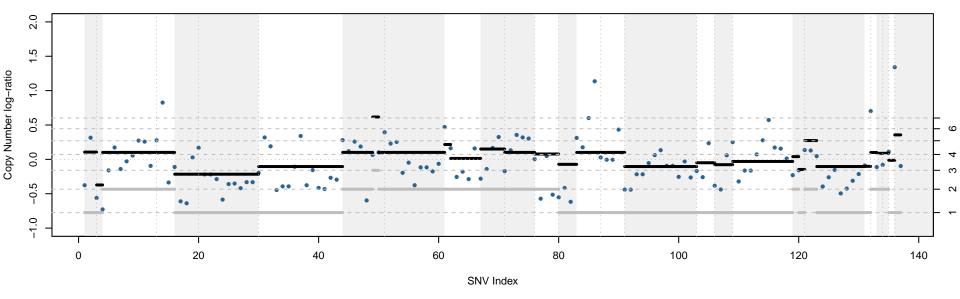


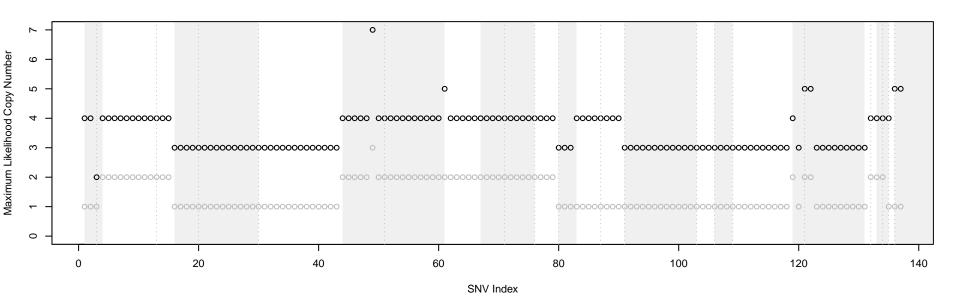


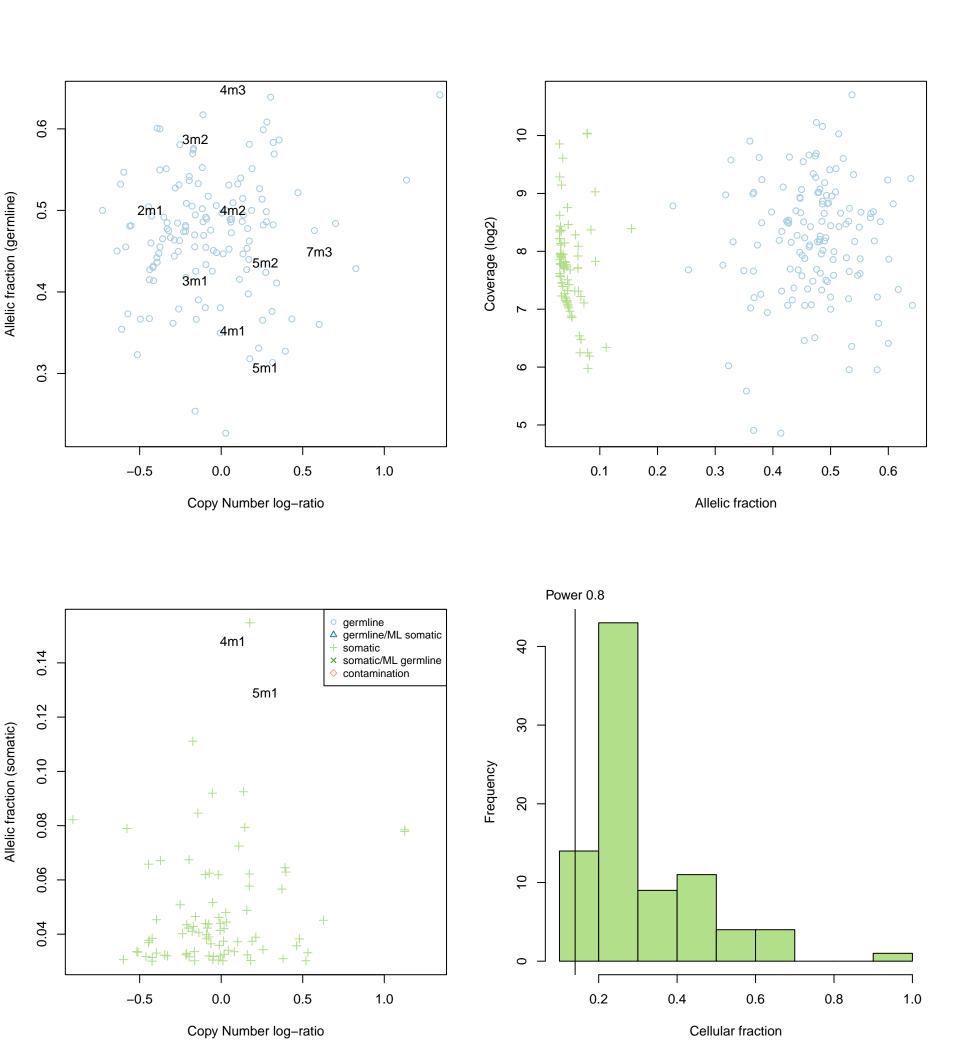


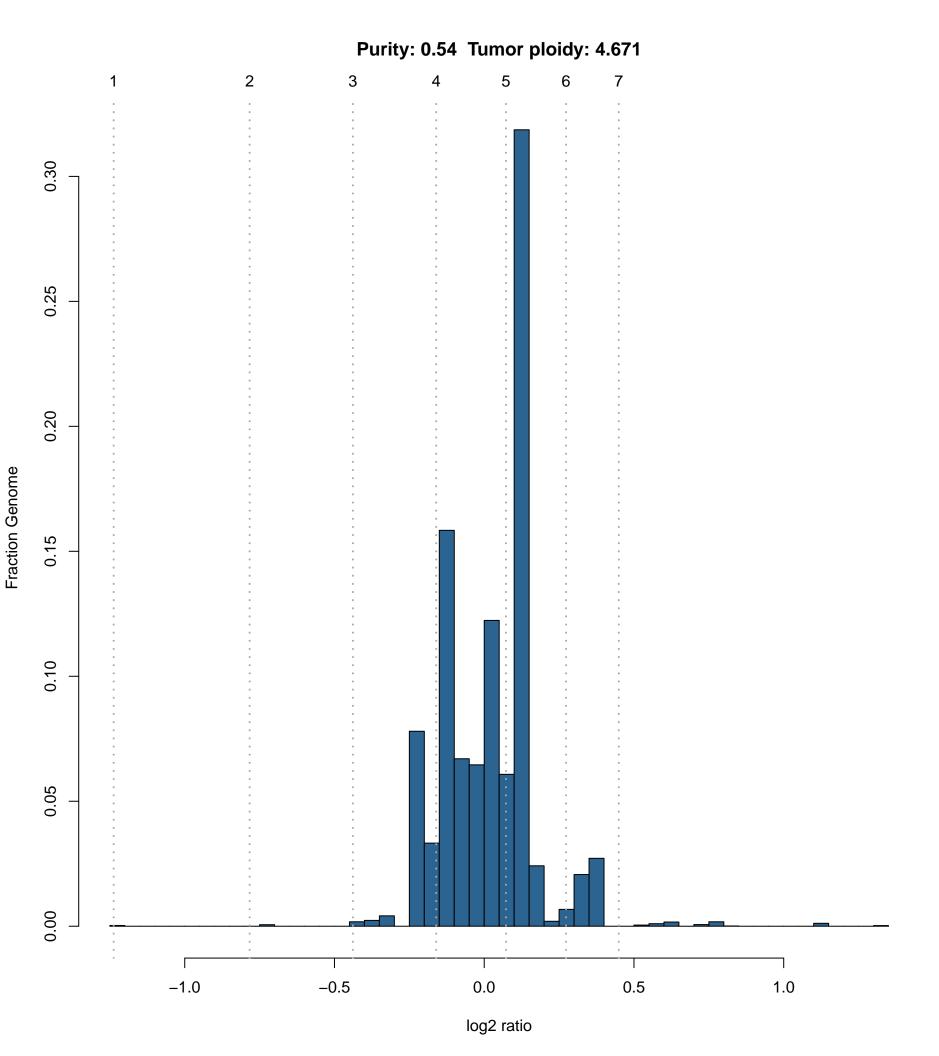


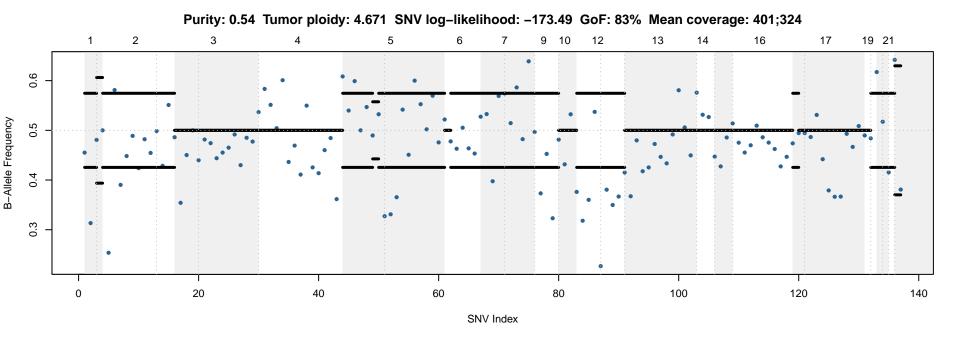
SCNA-fit log-likelihood: -12942.57



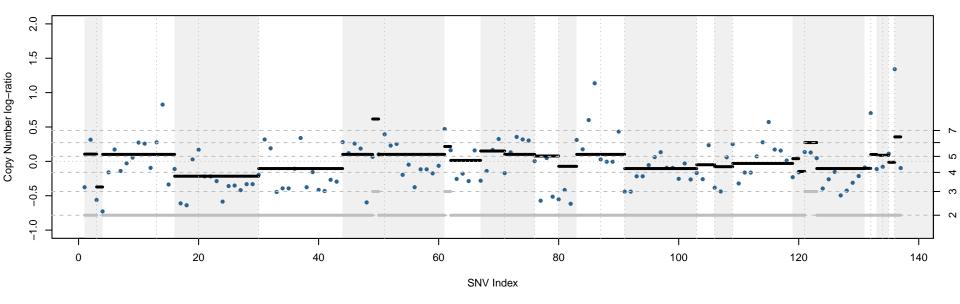


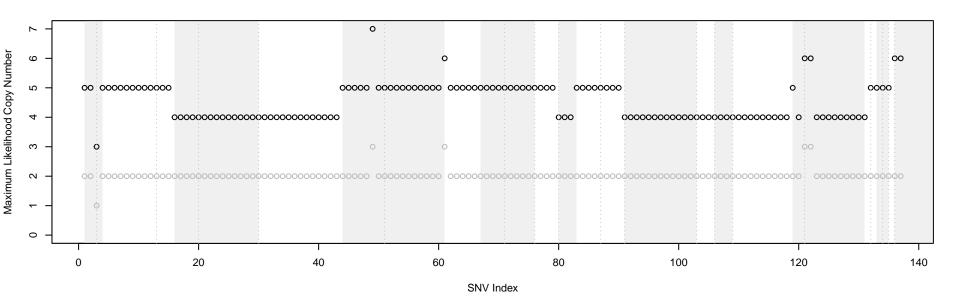


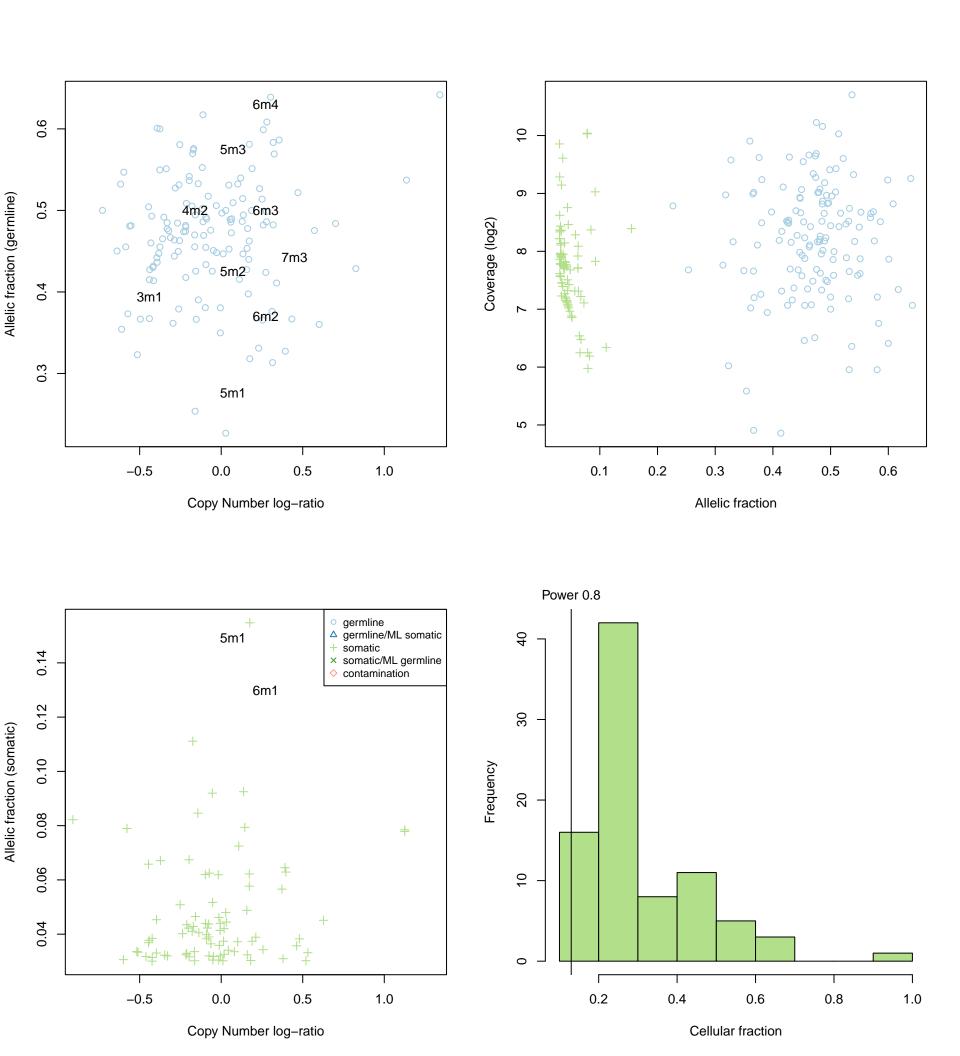


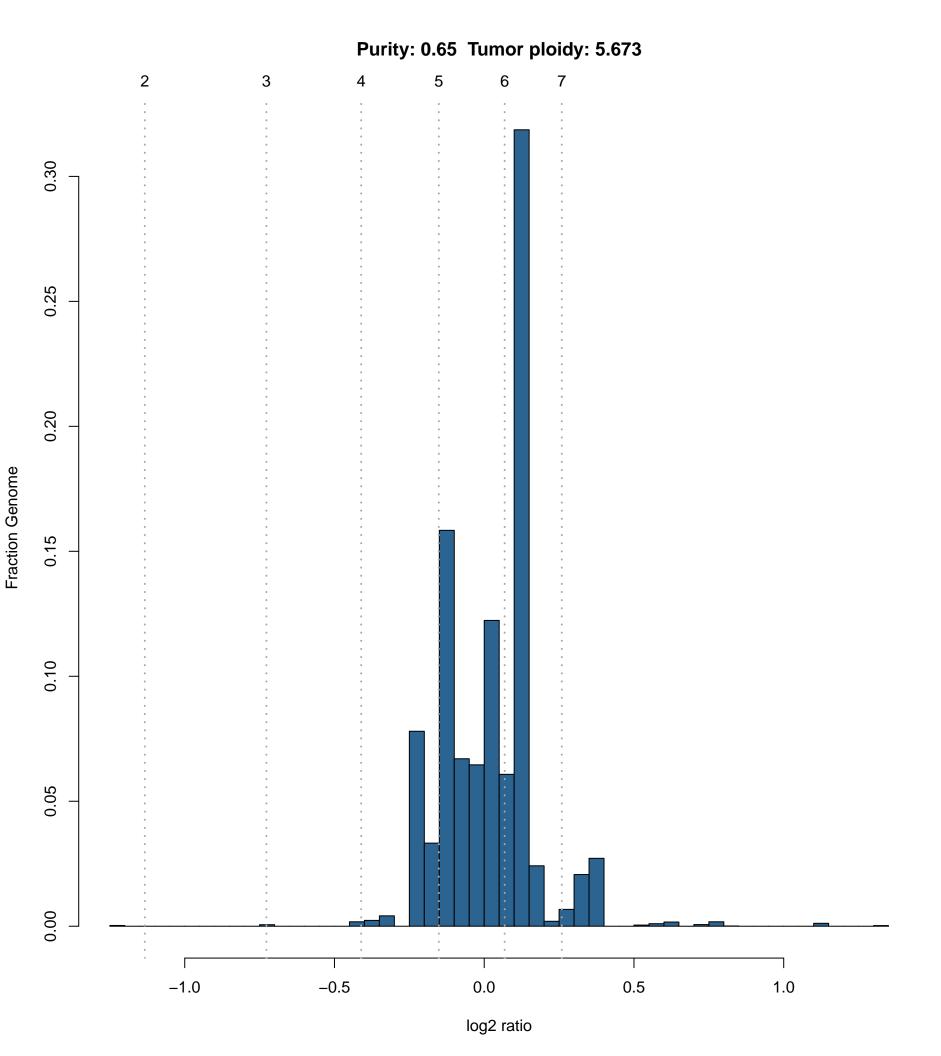


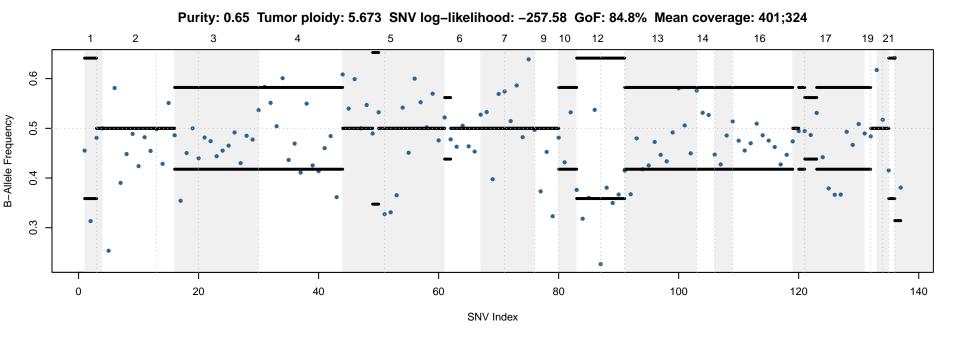
SCNA-fit log-likelihood: -12985.83



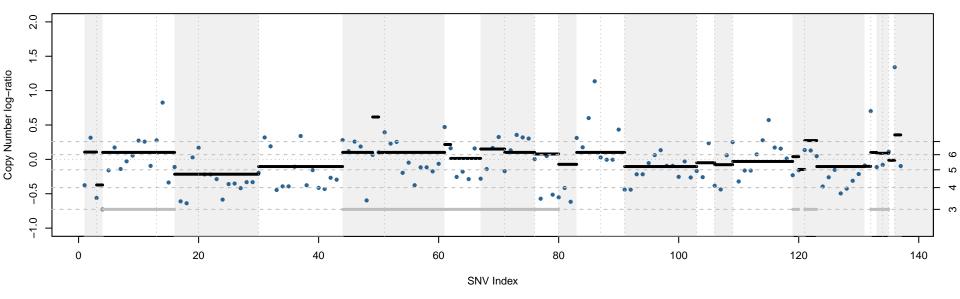


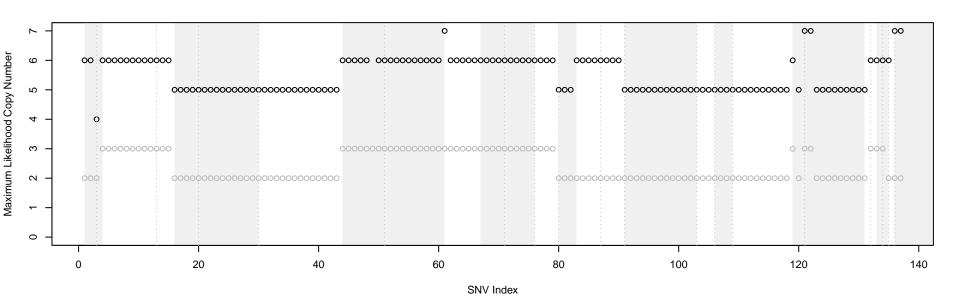


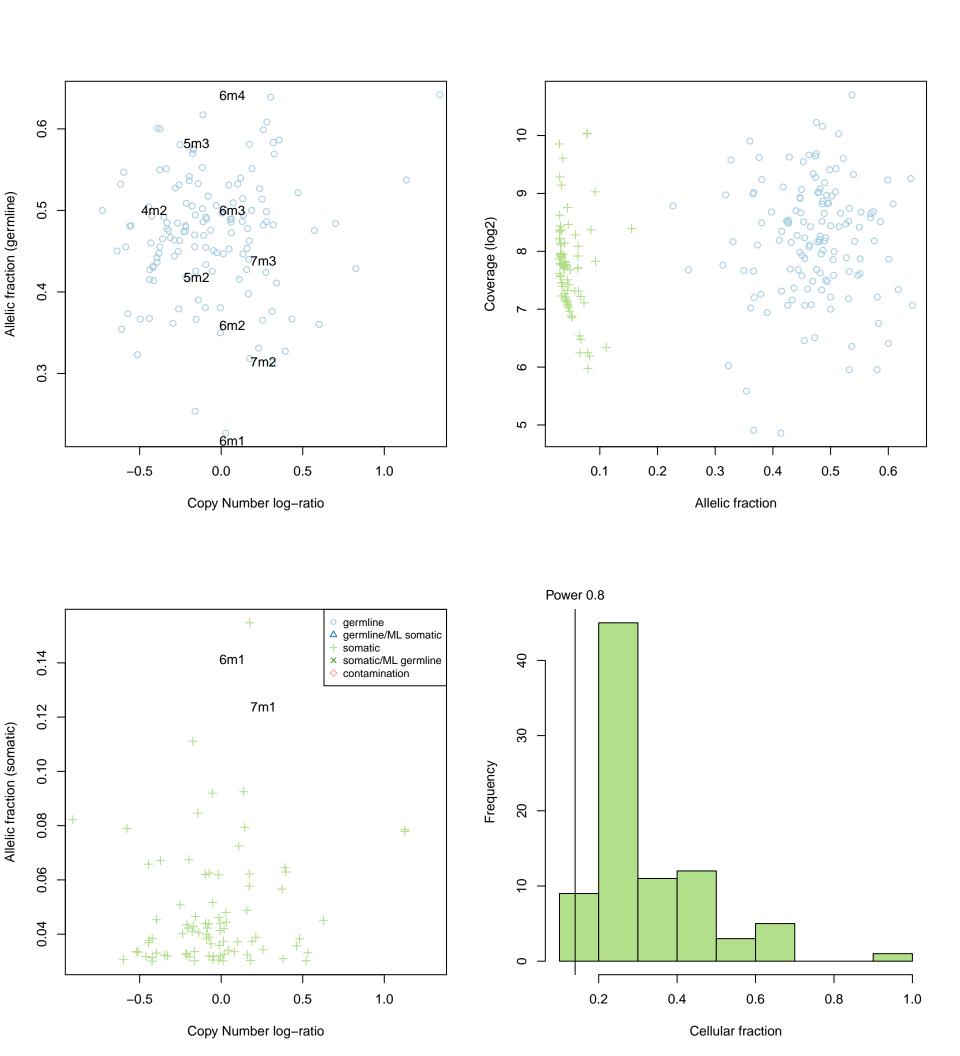


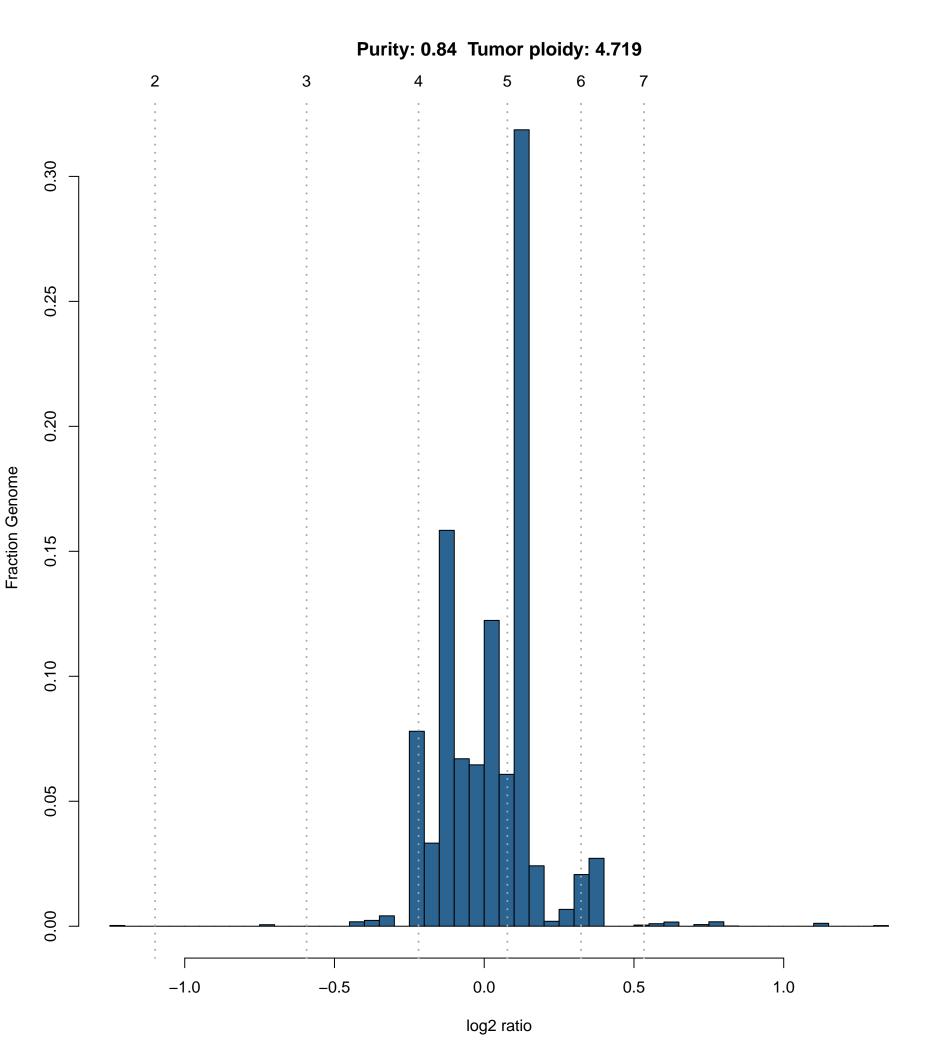


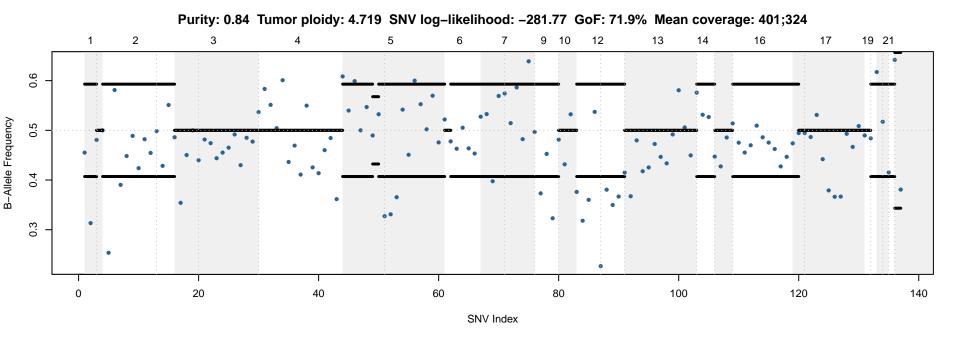
SCNA-fit log-likelihood: -13045.04



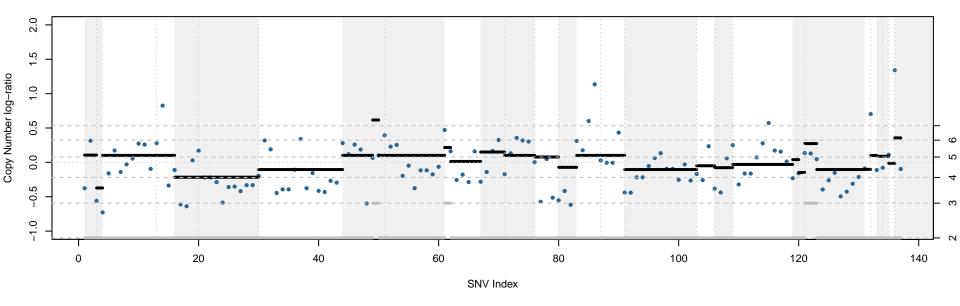


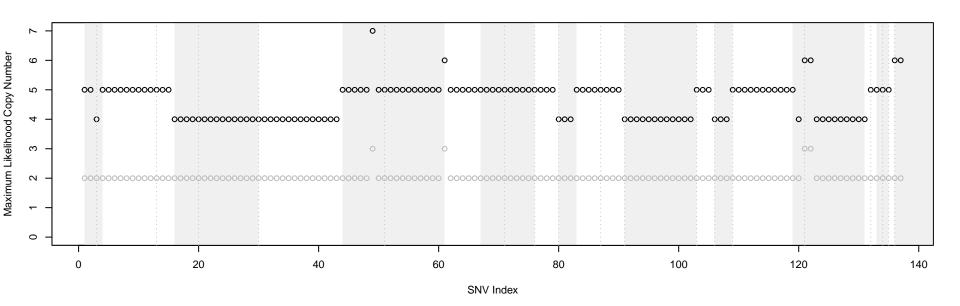


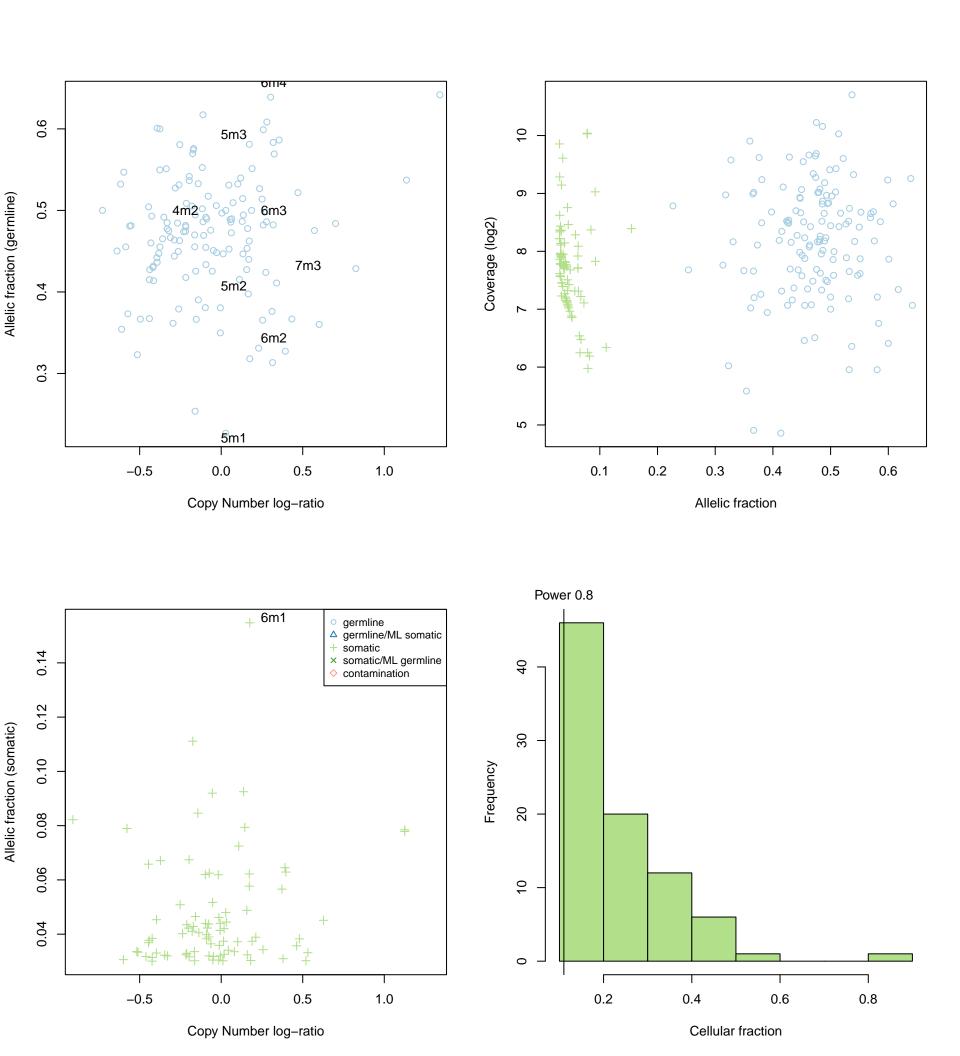




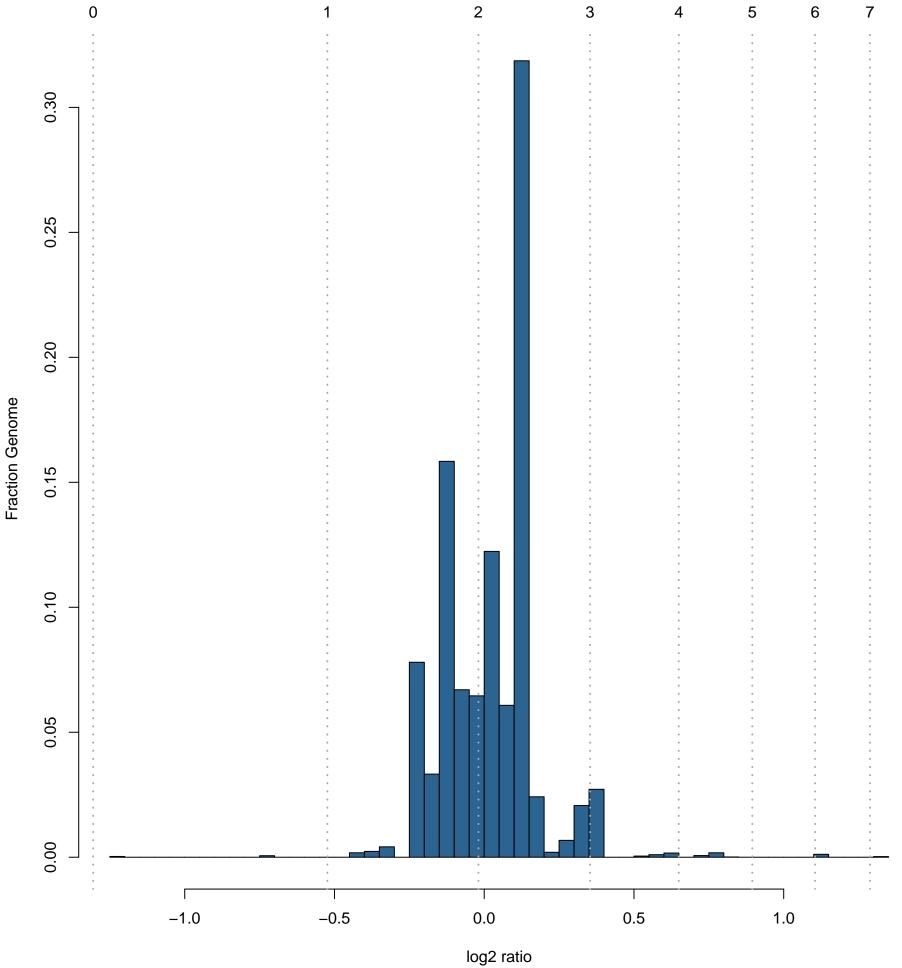
SCNA-fit log-likelihood: -13045.13

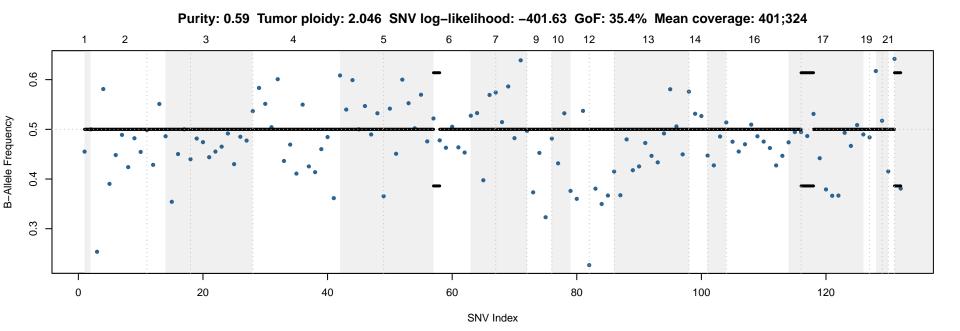




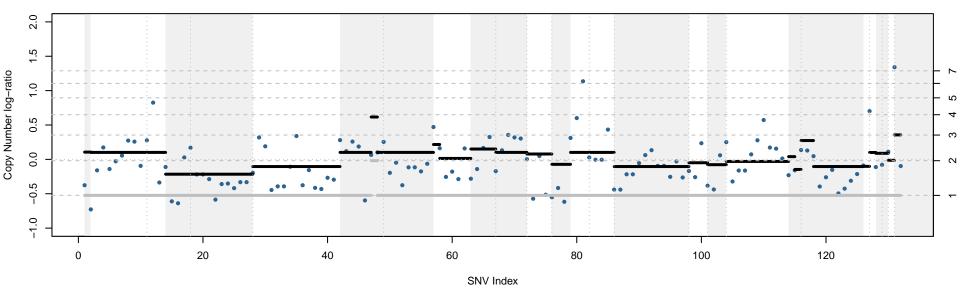


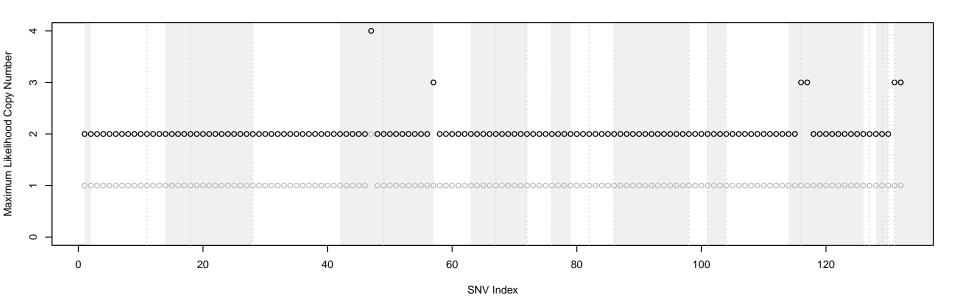
Purity: 0.59 Tumor ploidy: 2.046
2 3

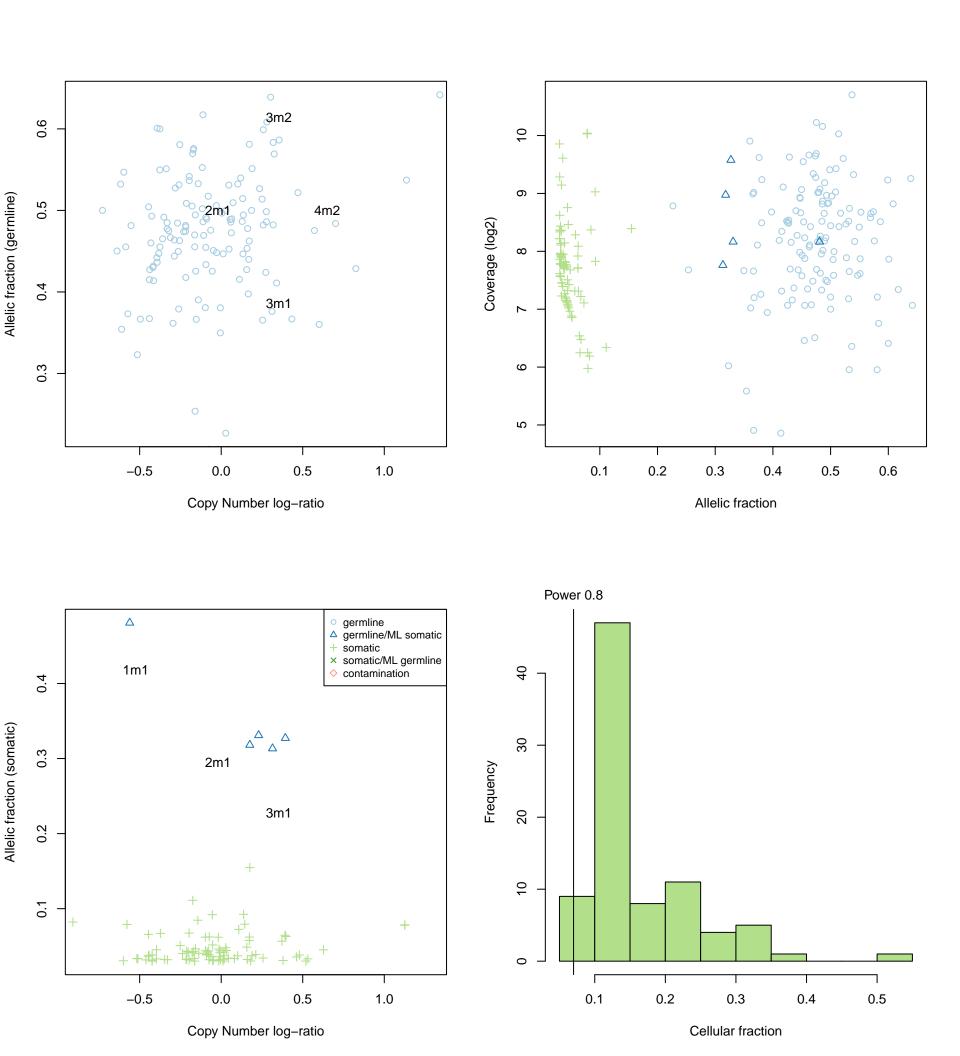




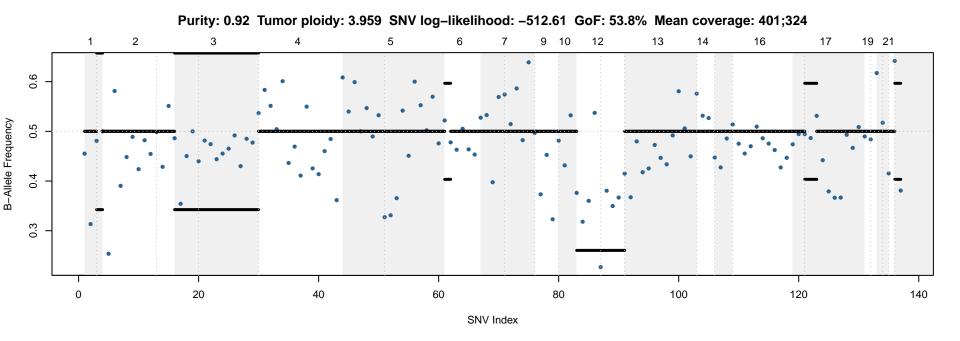
SCNA-fit log-likelihood: -13326.18



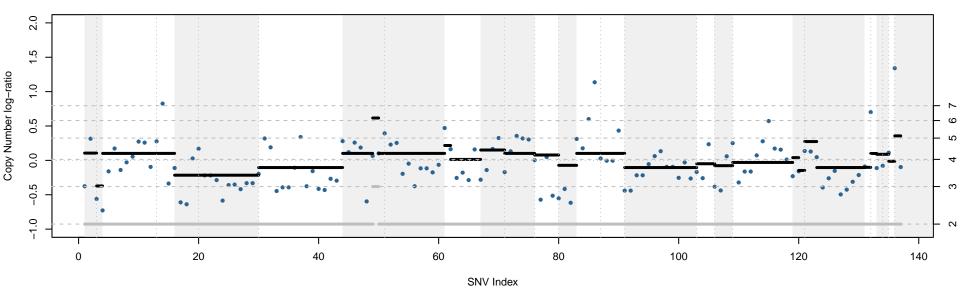


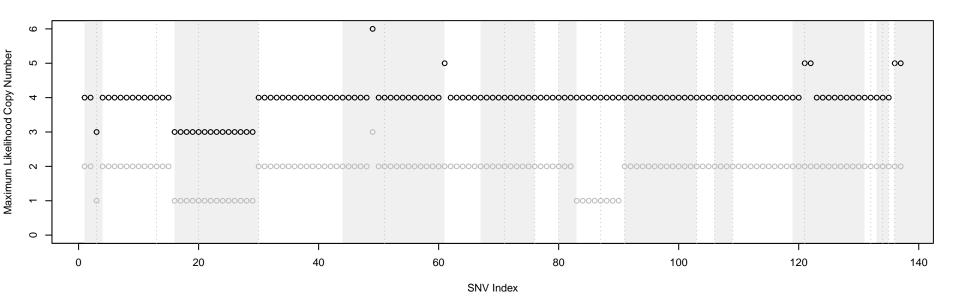


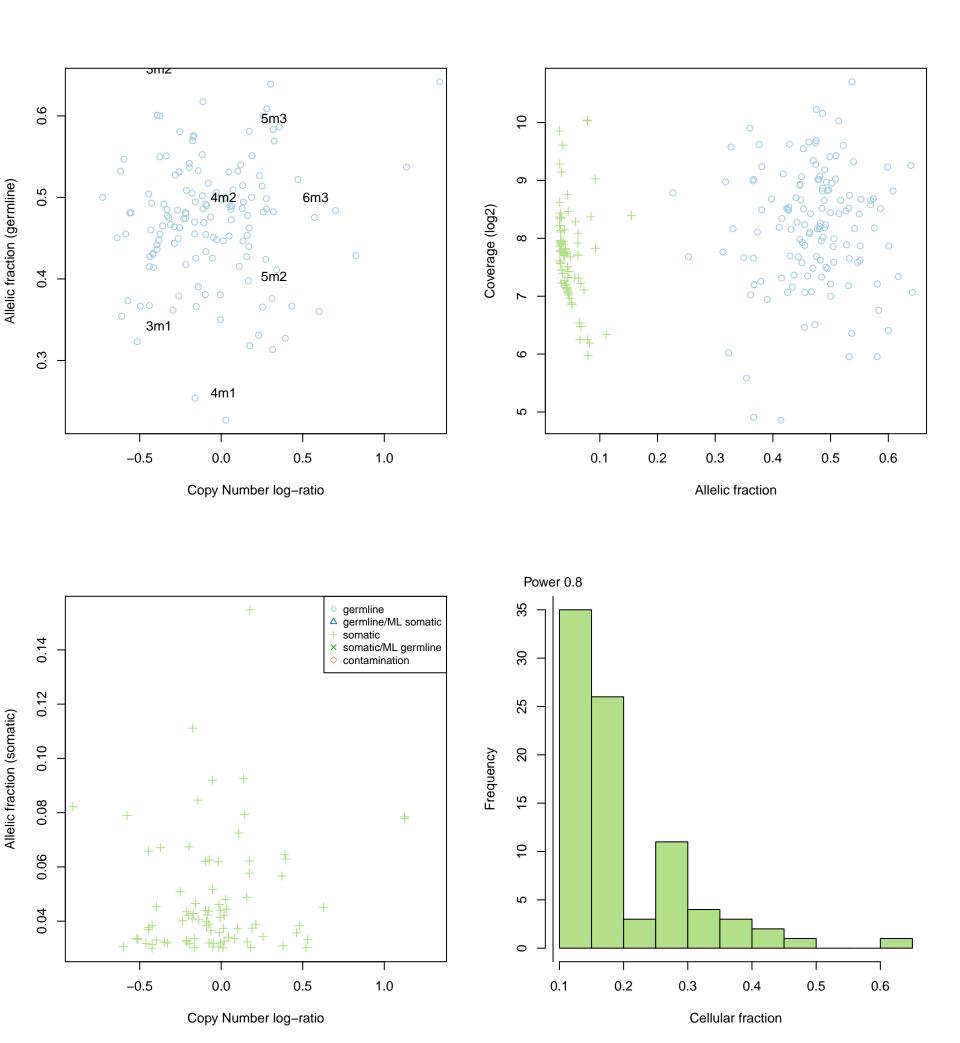
Purity: 0.92 Tumor ploidy: 3.959 2 5 7 6 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



SCNA-fit log-likelihood: -13251.63

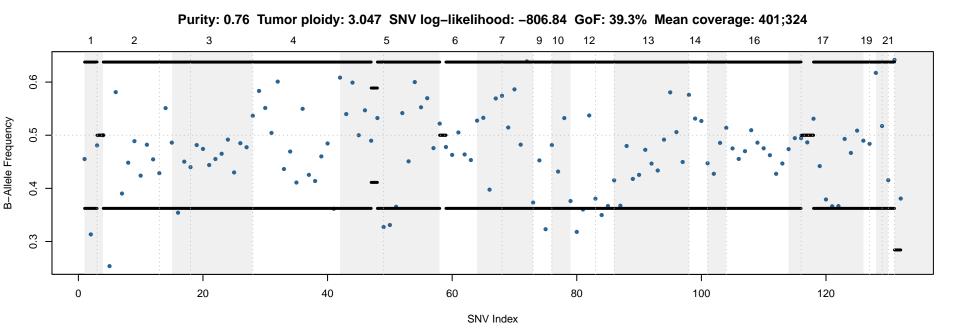






Purity: 0.76 Tumor ploidy: 3.047 3 2 6 7 5 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0

log2 ratio



SCNA-fit log-likelihood: -13320.28

