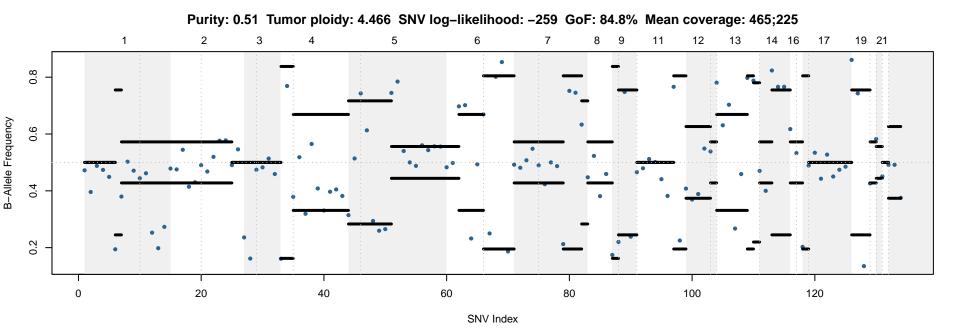
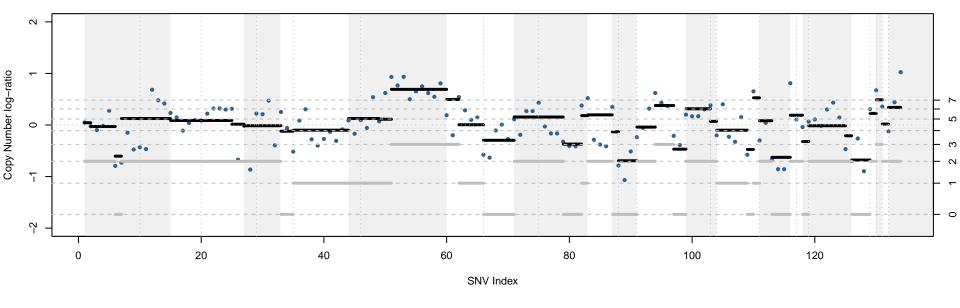
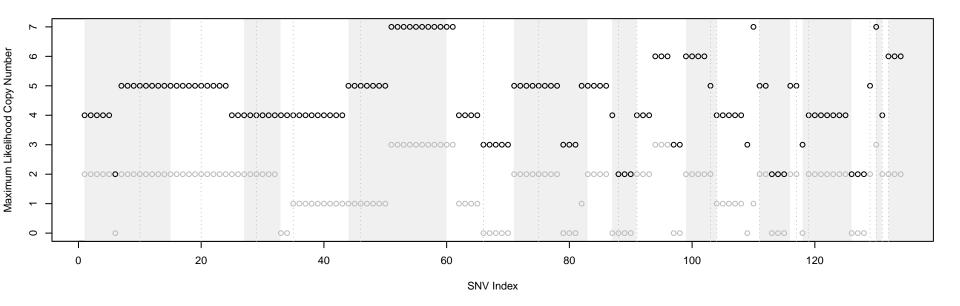
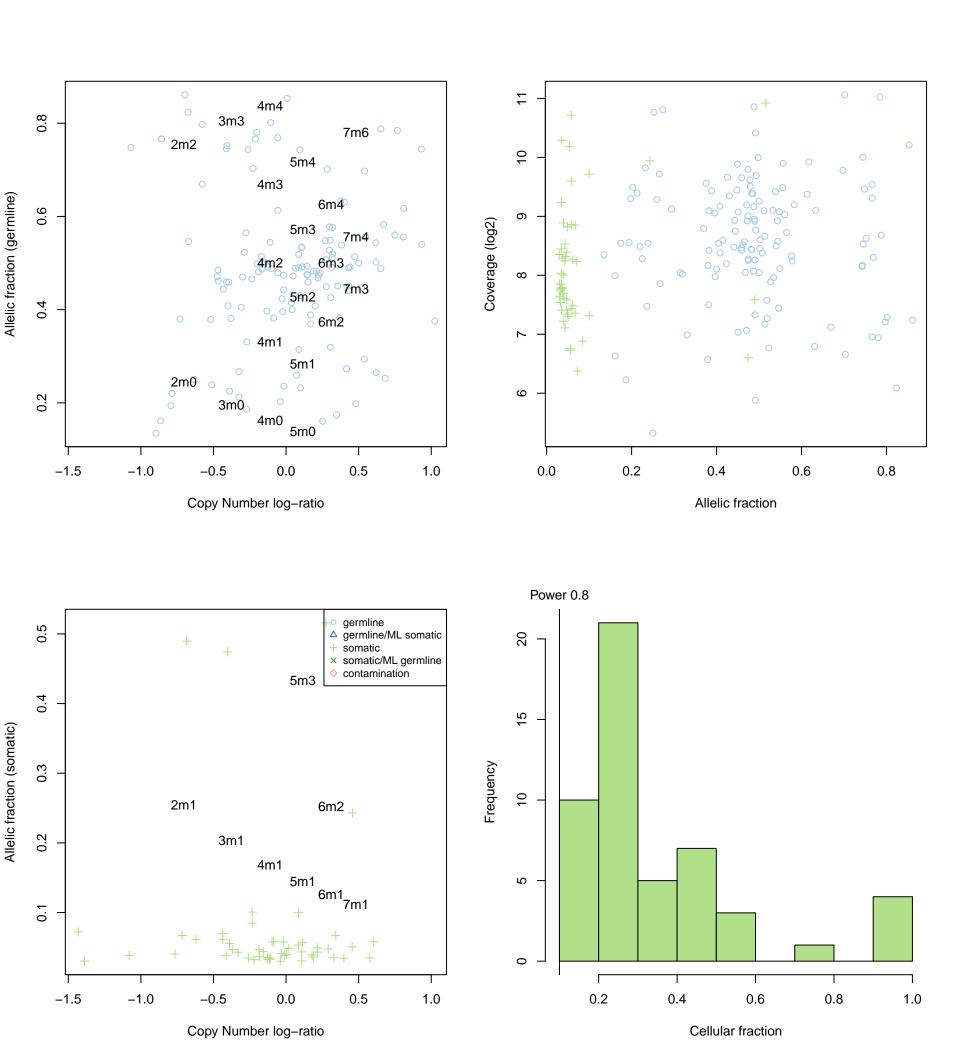
Purity: 0.51 Tumor ploidy: 4.466 2 3 6 7 0.08 Fraction Genome 90.0 0.04 0.02 0.00 -1.0 -1.5 -0.5 0.0 0.5 1.0 log2 ratio



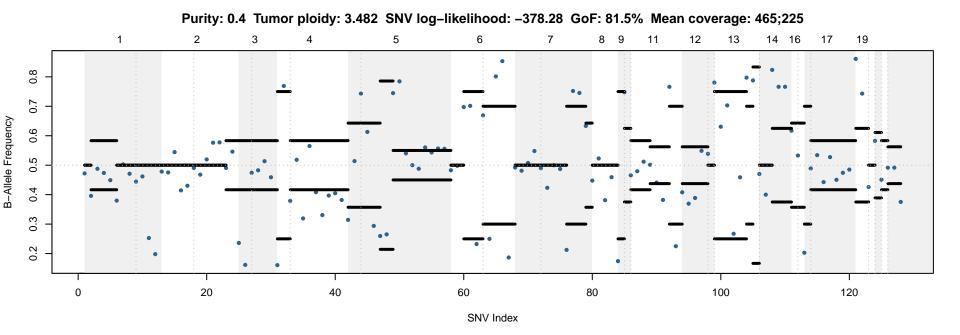
SCNA-fit log-likelihood: -14959.12



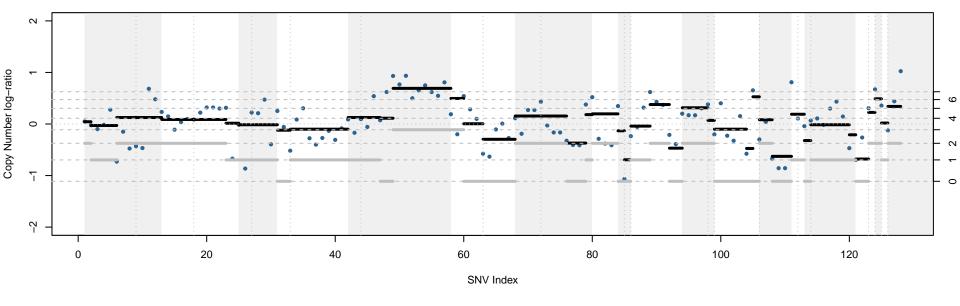


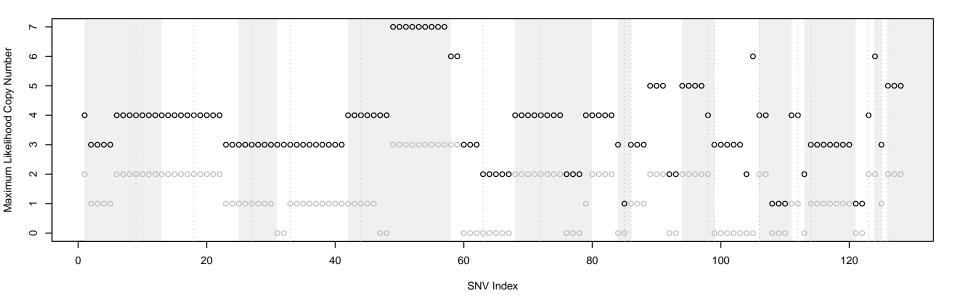


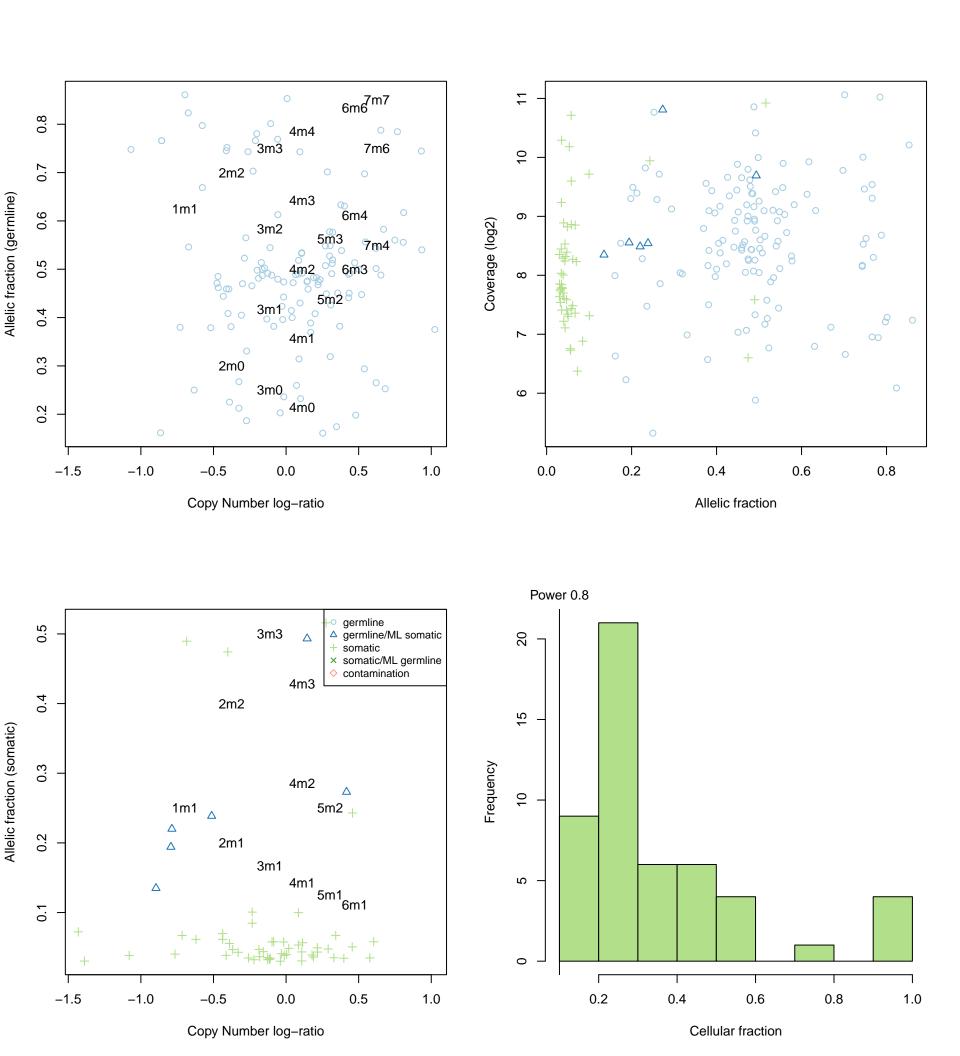
Purity: 0.4 Tumor ploidy: 3.482 0 2 3 5 6 7 0.08 Fraction Genome 90.0 0.04 0.02 0.00 -1.0 -1.5 -0.5 0.0 0.5 1.0 log2 ratio



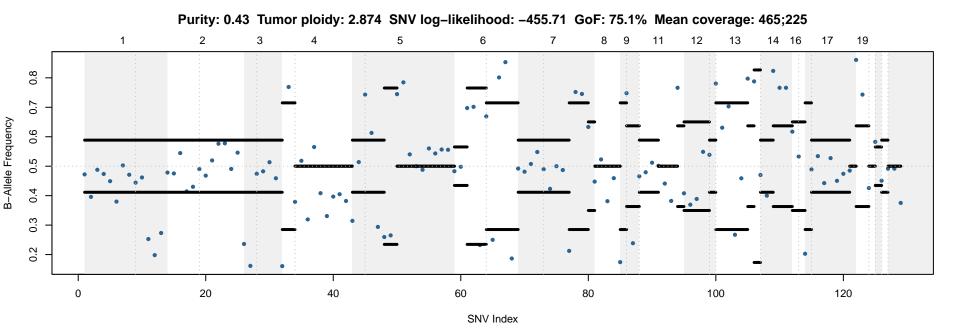
SCNA-fit log-likelihood: -14801.45



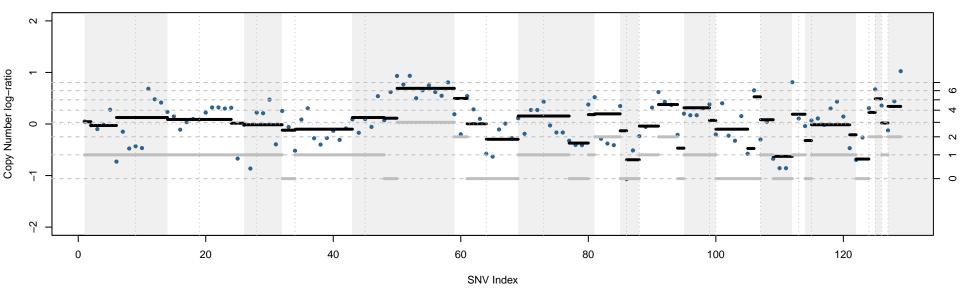


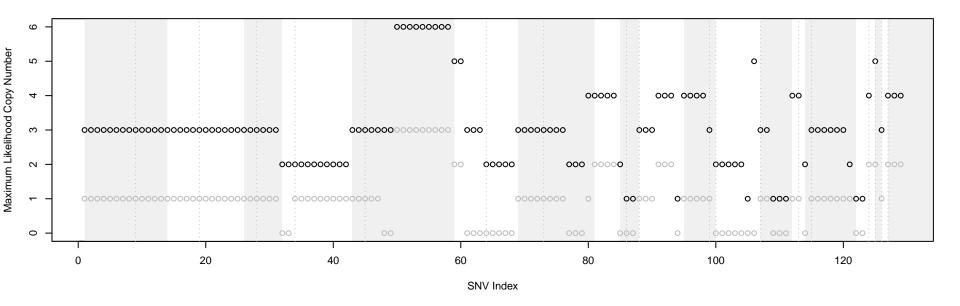


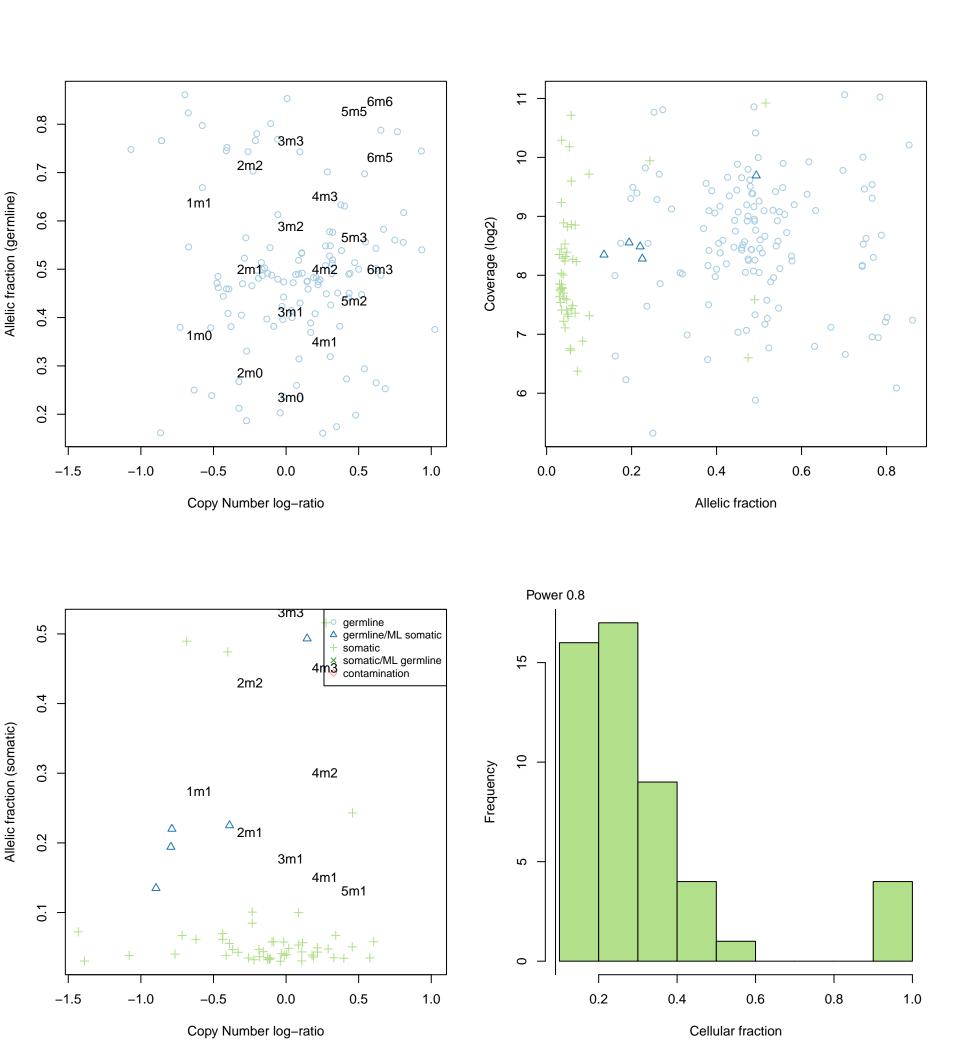
Purity: 0.43 Tumor ploidy: 2.874 3 0 2 6 5 7 0.08 Fraction Genome 90.0 0.04 0.02 0.00 -1.5 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



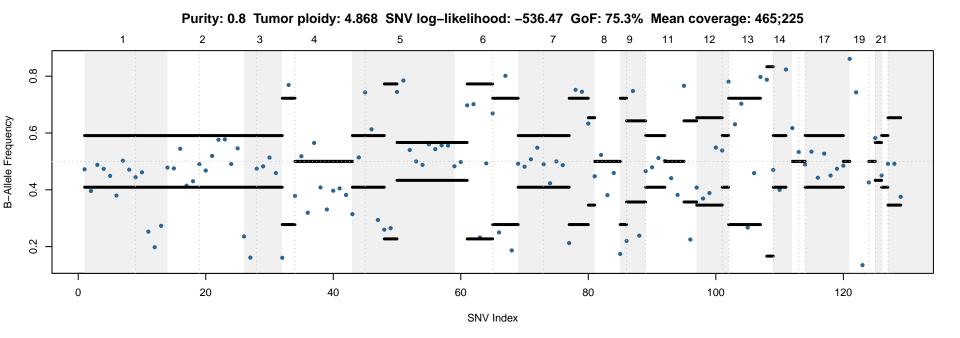
SCNA-fit log-likelihood: -14920.04



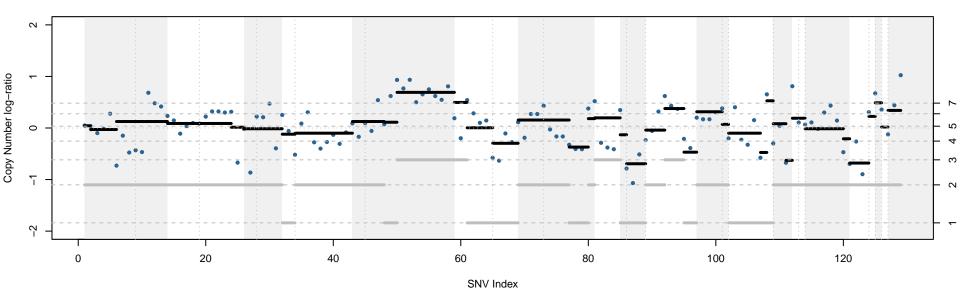


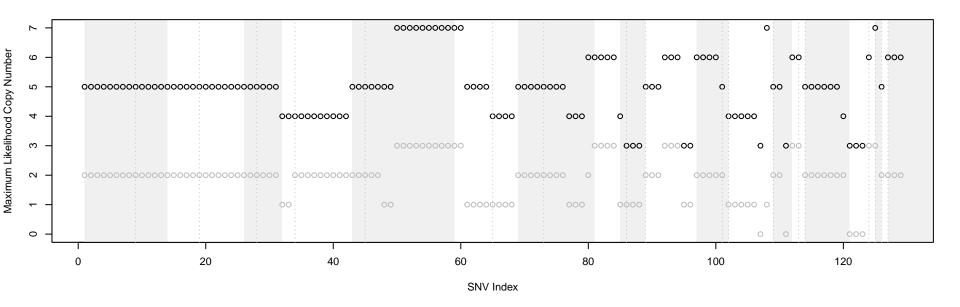


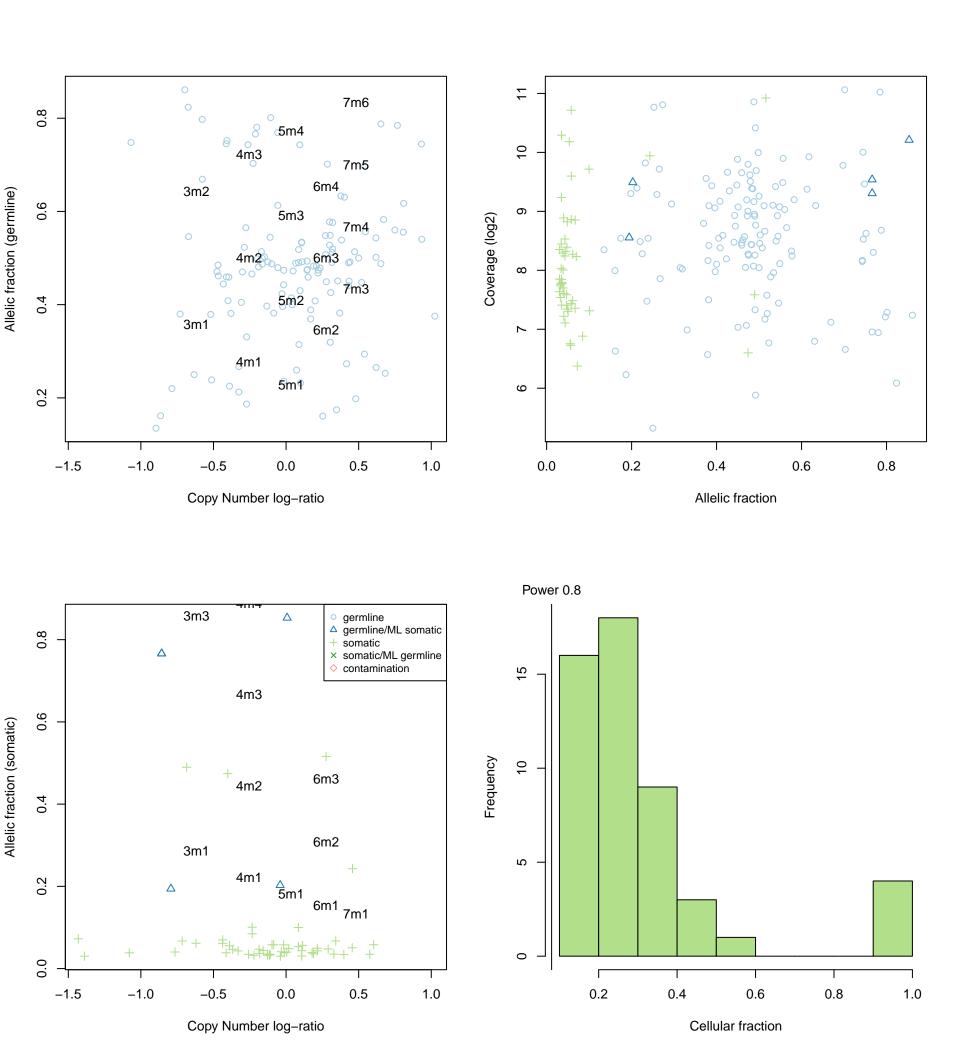
Purity: 0.8 Tumor ploidy: 4.868 2 6 7 0.08 Fraction Genome 90.0 0.04 0.02 0.00 -1.0 -1.5 -0.5 0.0 0.5 1.0 log2 ratio



SCNA-fit log-likelihood: -15091.06

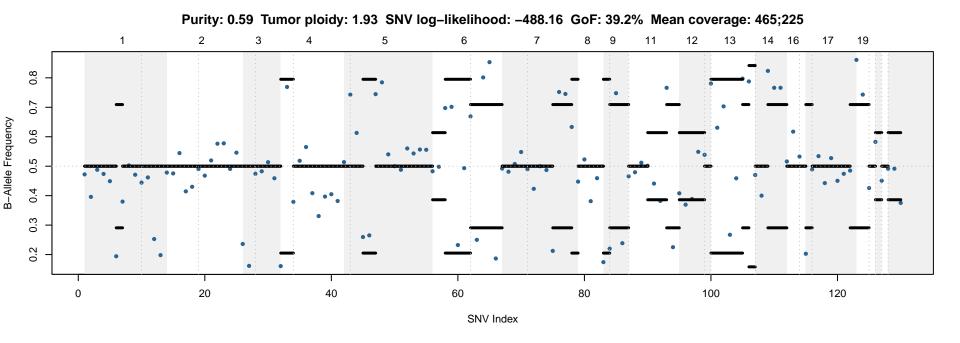




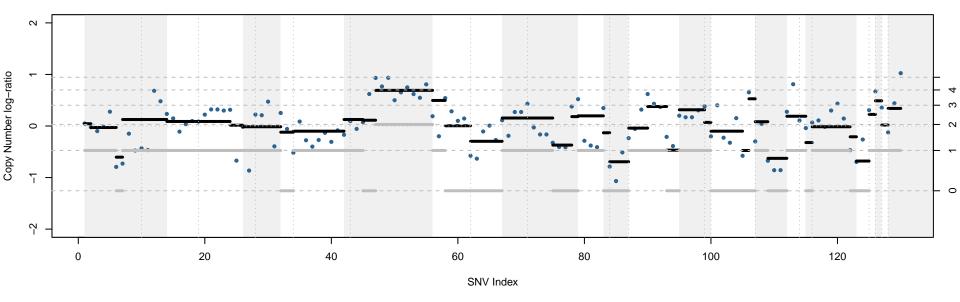


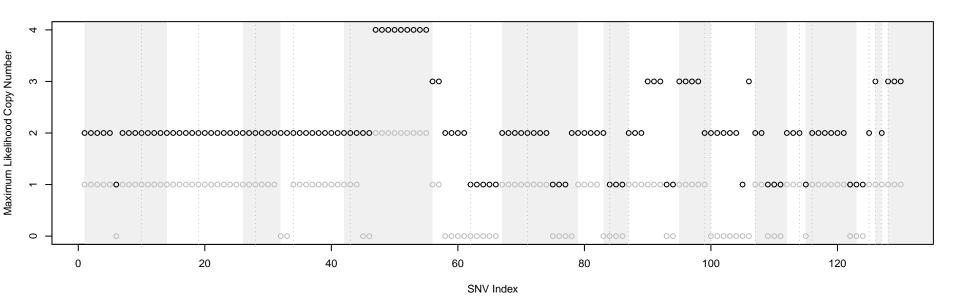
Purity: 0.59 Tumor ploidy: 1.93 2 0 3 5 0.08 Fraction Genome 90.0 0.04 0.02 0.00 -1.5 -1.0 -0.5 0.0 0.5 1.0

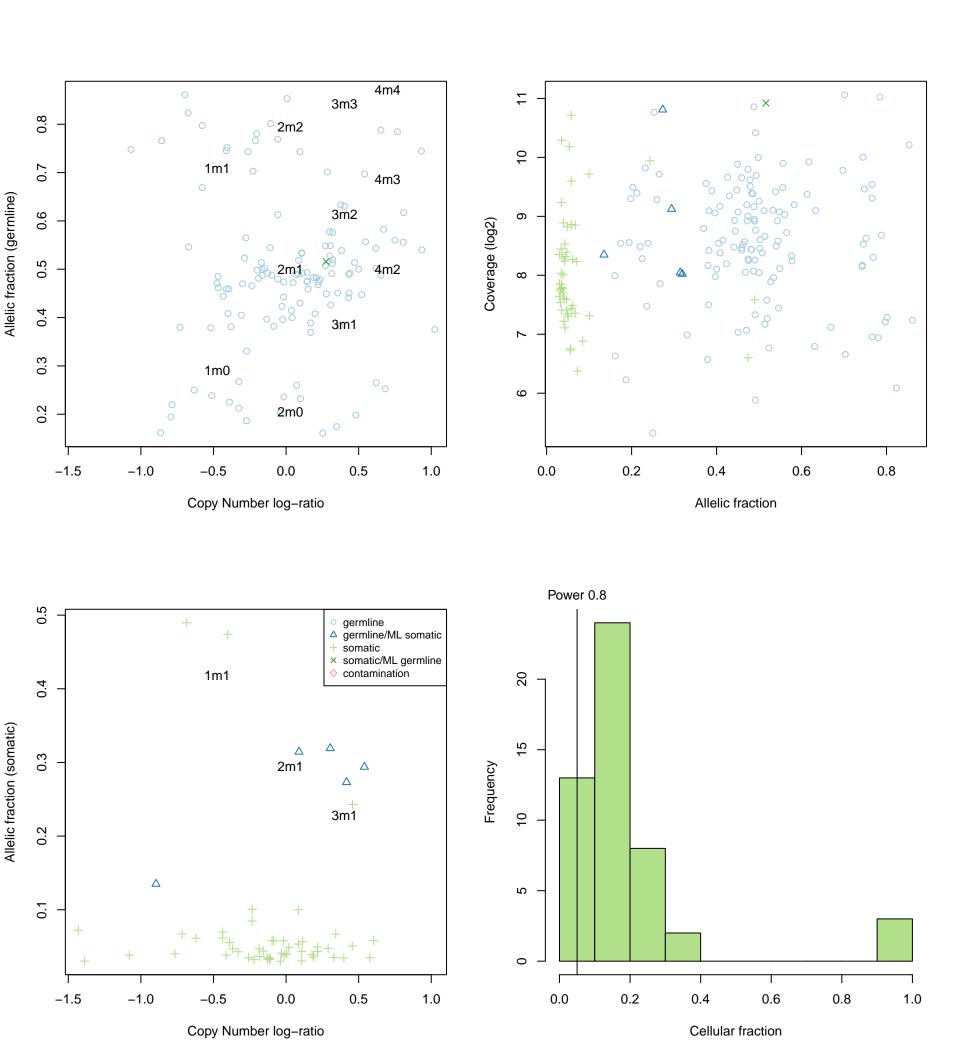
log2 ratio

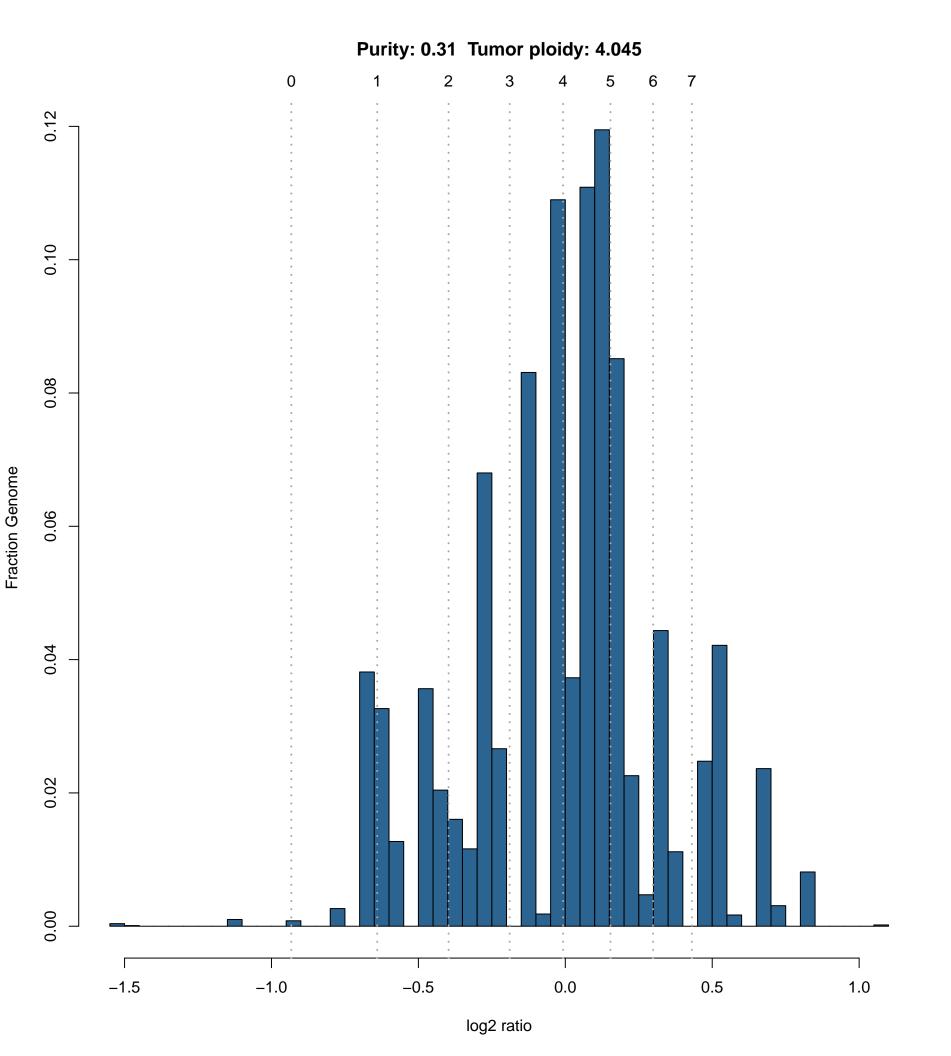


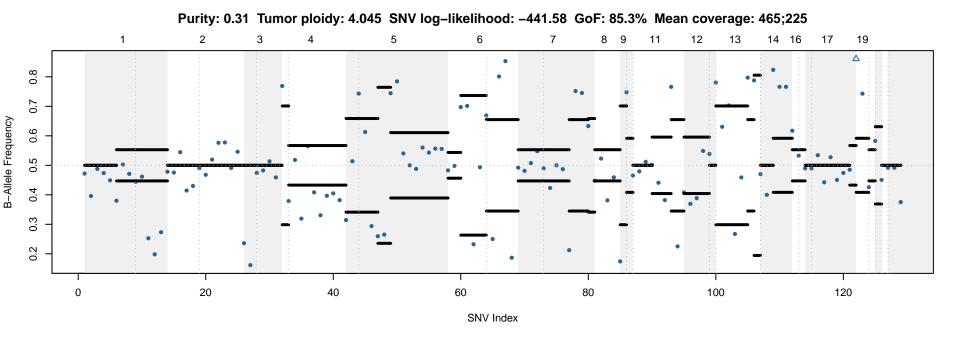
SCNA-fit log-likelihood: -15246.03



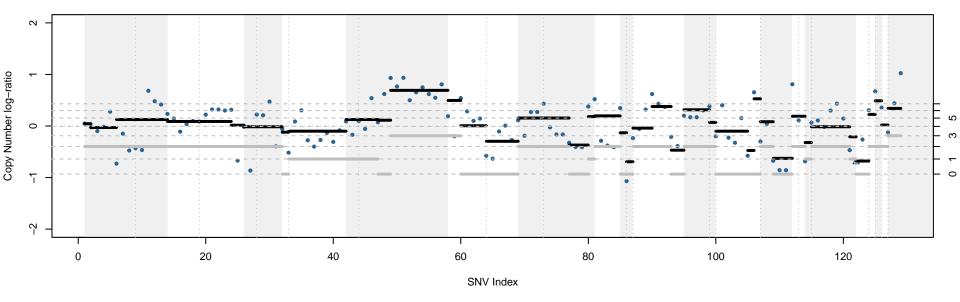


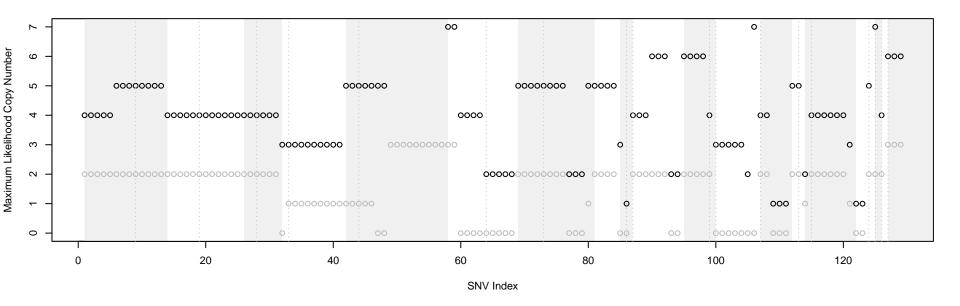


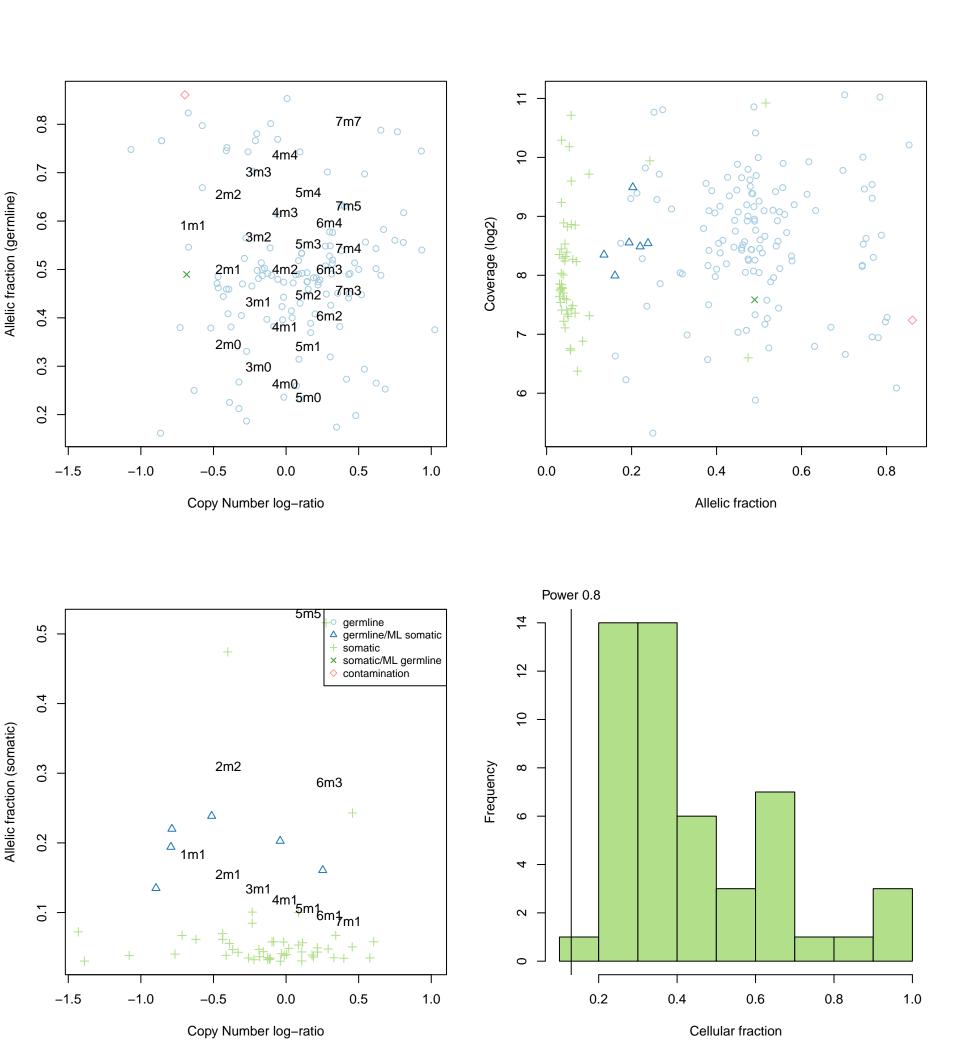




SCNA-fit log-likelihood: -15398.12

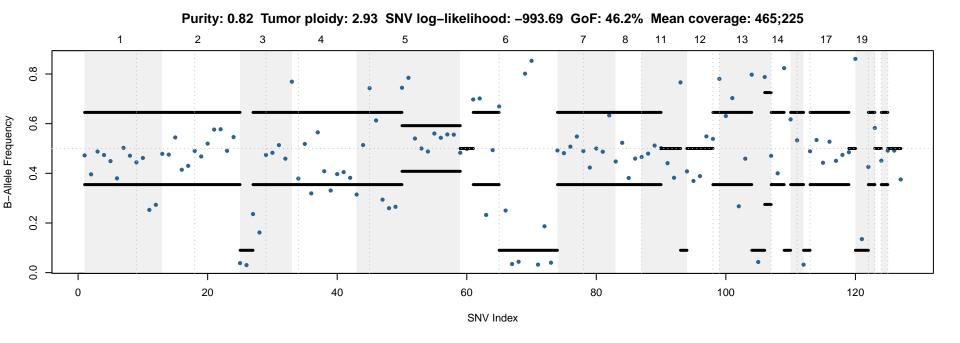






Purity: 0.82 Tumor ploidy: 2.93 6 2 3 5 0.08 Fraction Genome 90.0 0.04 0.02 0.00 -1.5 -1.0 -0.5 0.0 0.5 1.0

log2 ratio



SCNA-fit log-likelihood: -15244.76

