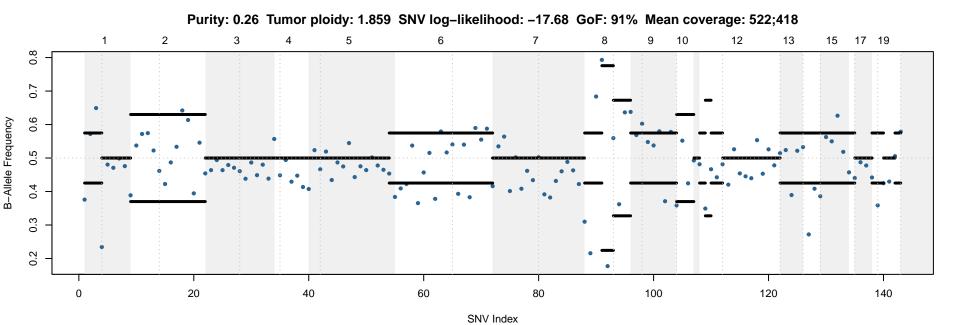
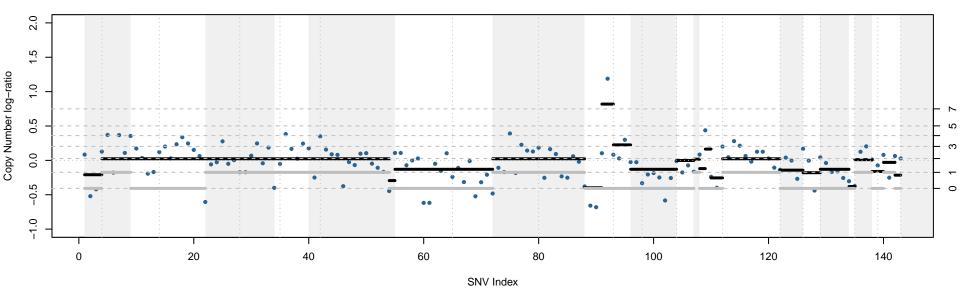
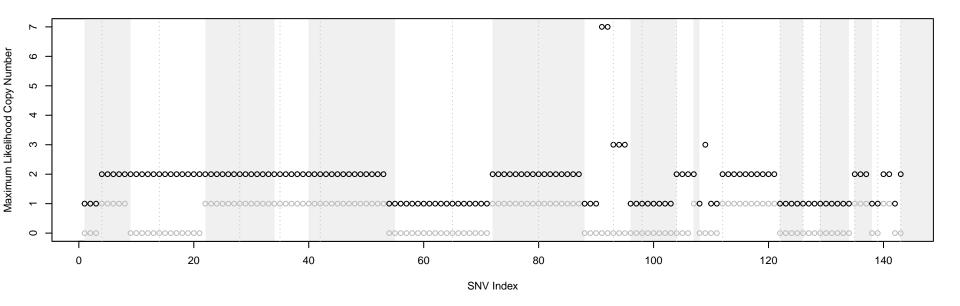
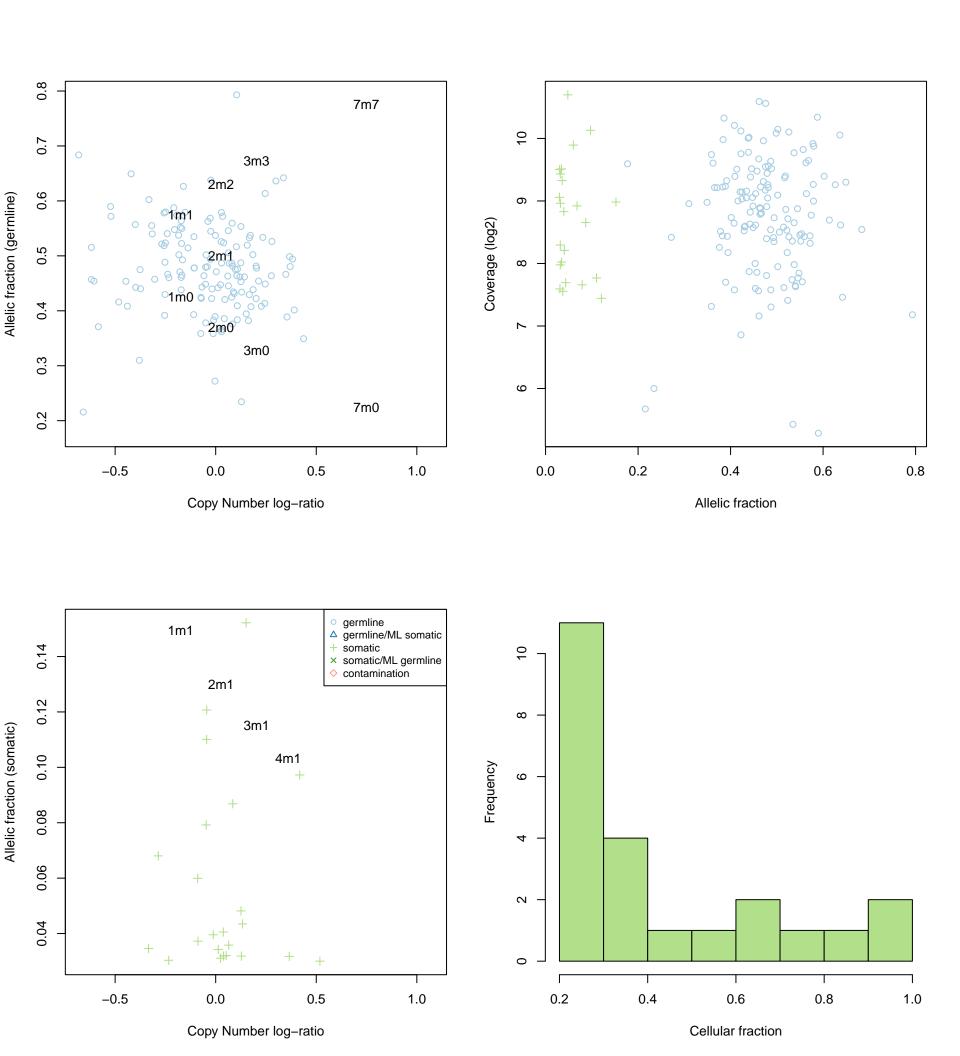
Purity: 0.26 Tumor ploidy: 1.859 2 3 0 5 Fraction Genome 0.1 0.0 0.0 0.5 1.0 log2 ratio

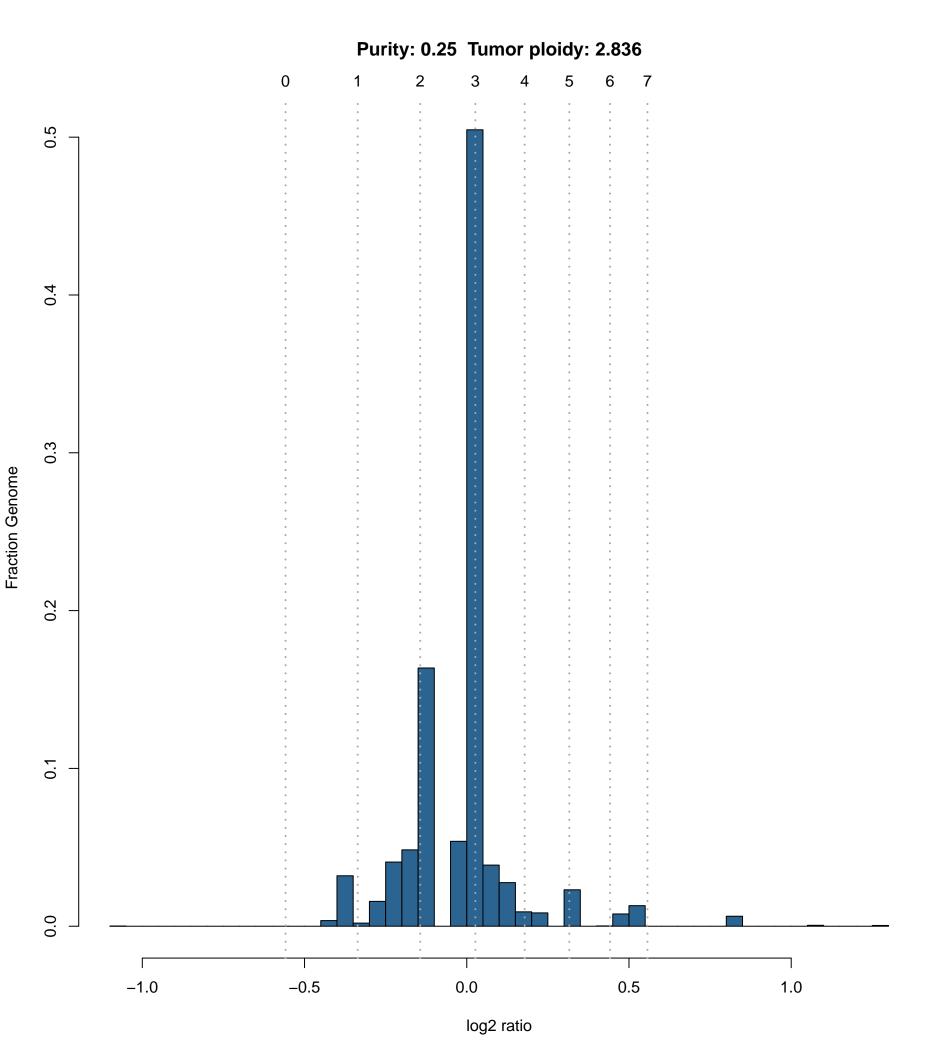


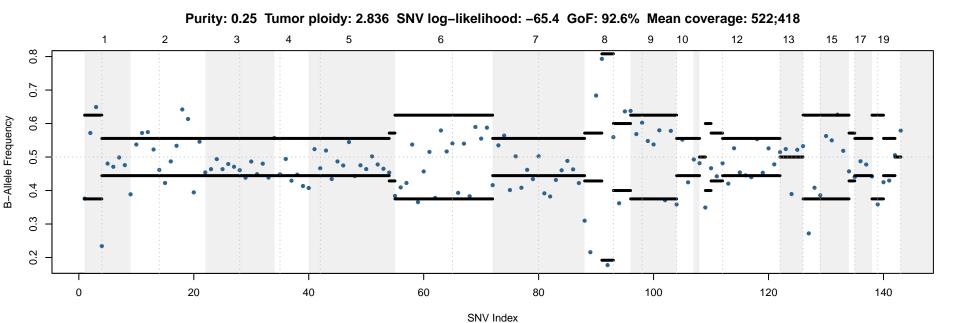
SCNA-fit log-likelihood: -5528.43



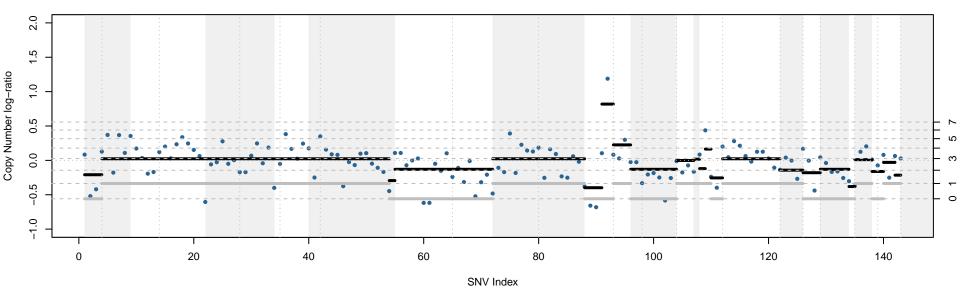


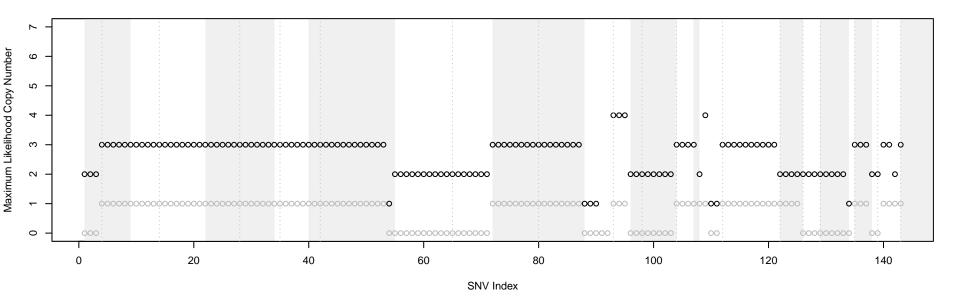


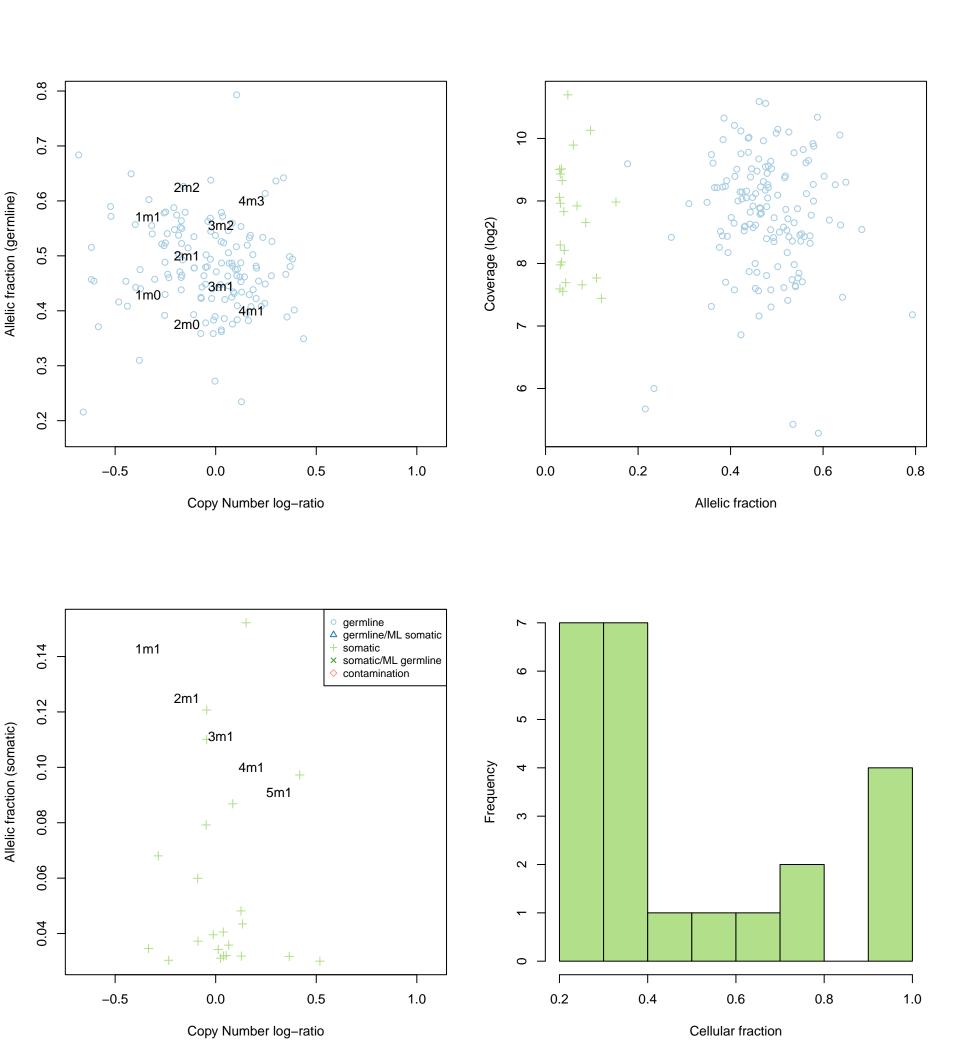


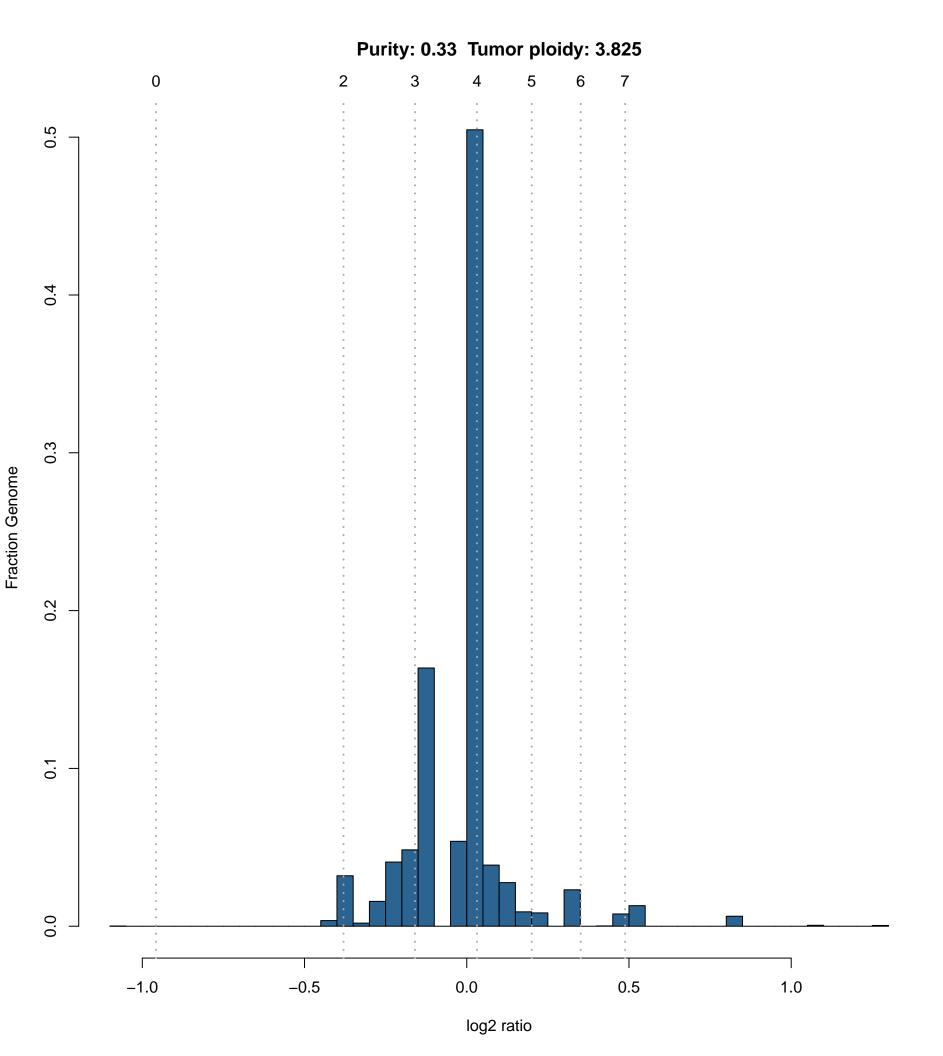


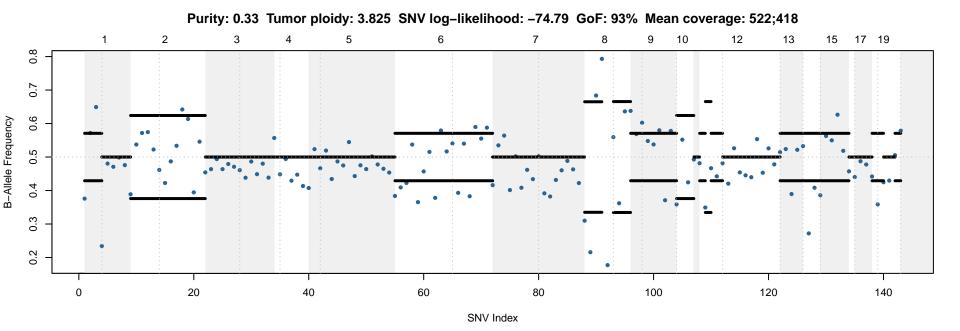
SCNA-fit log-likelihood: -5517.5



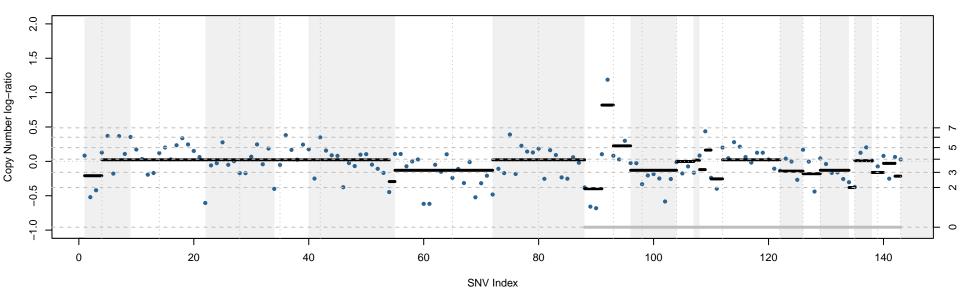


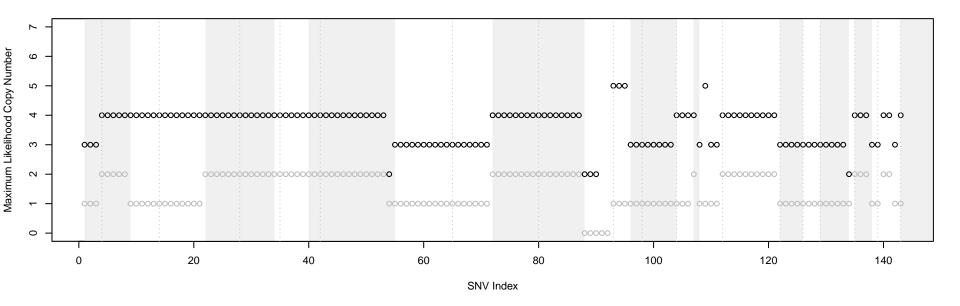


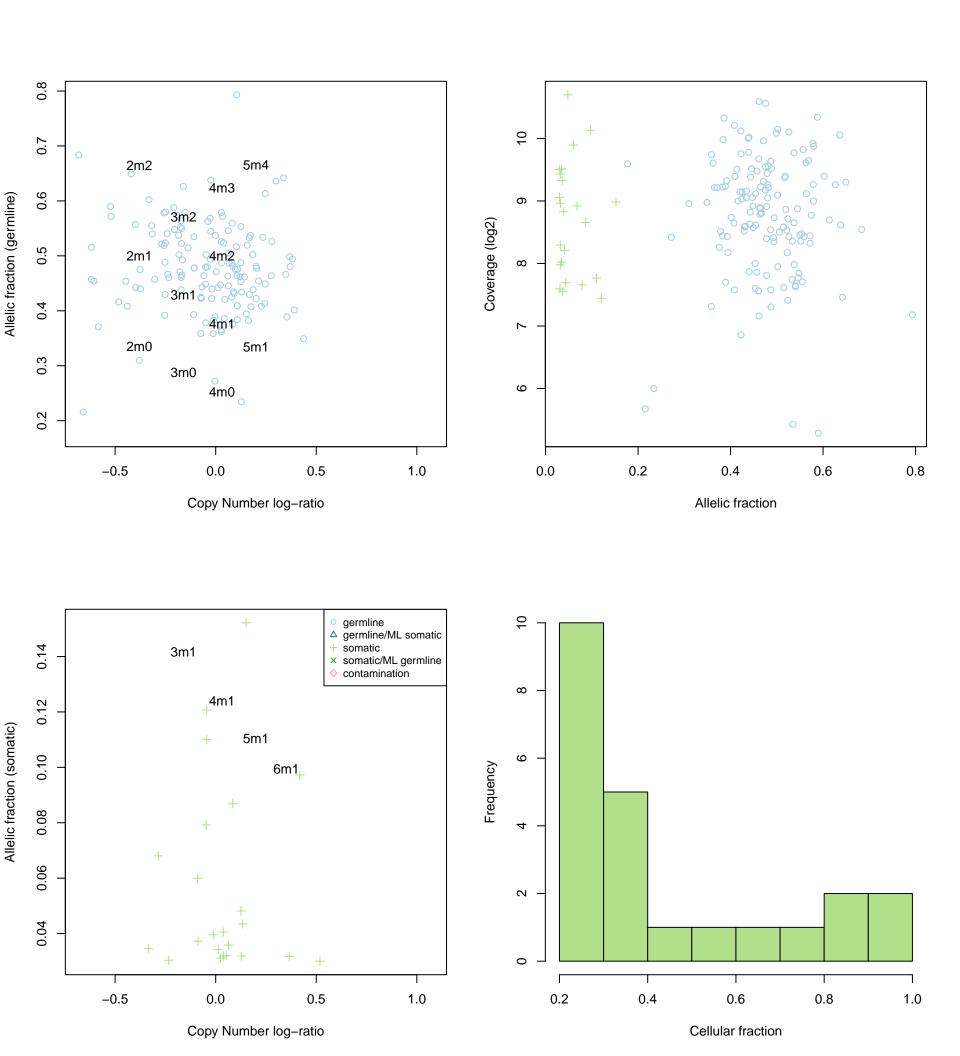


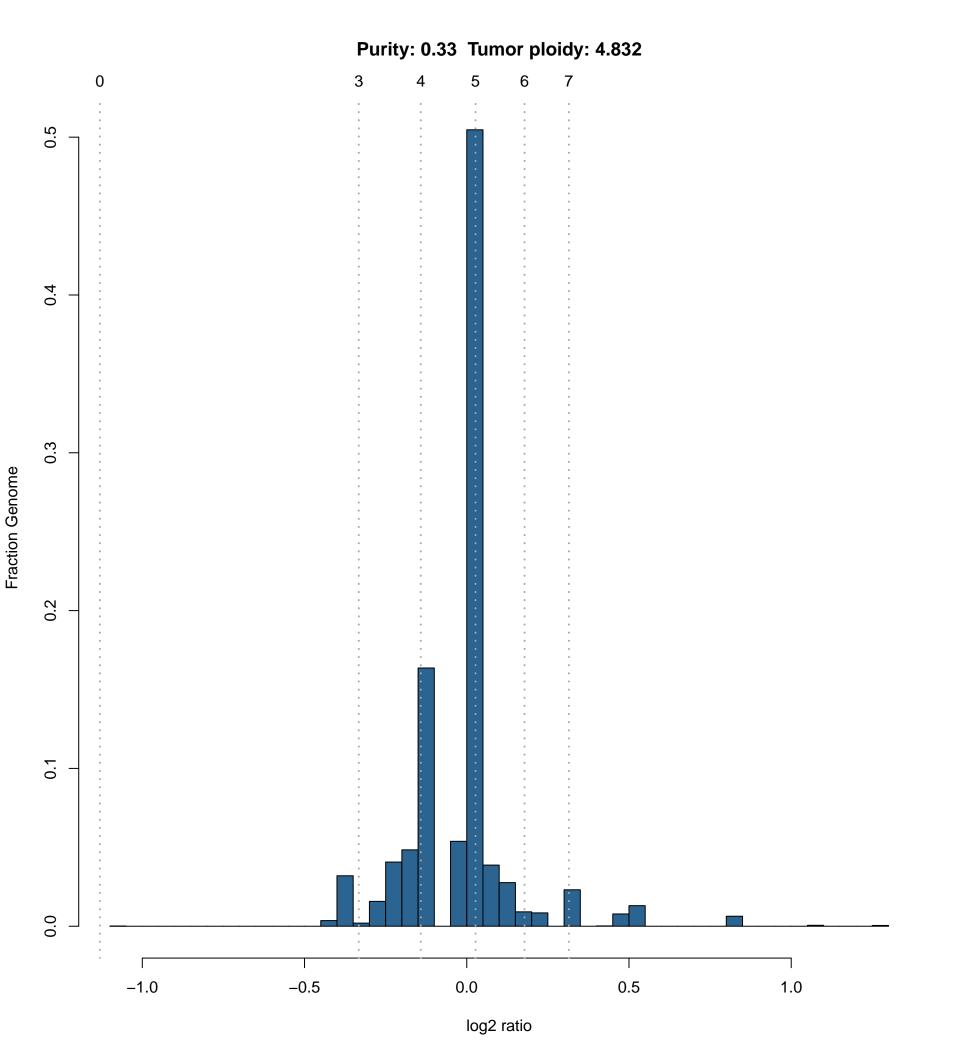


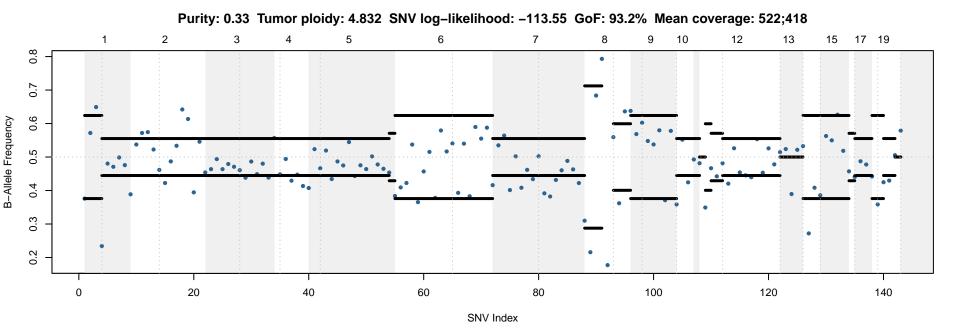
SCNA-fit log-likelihood: -5527.83



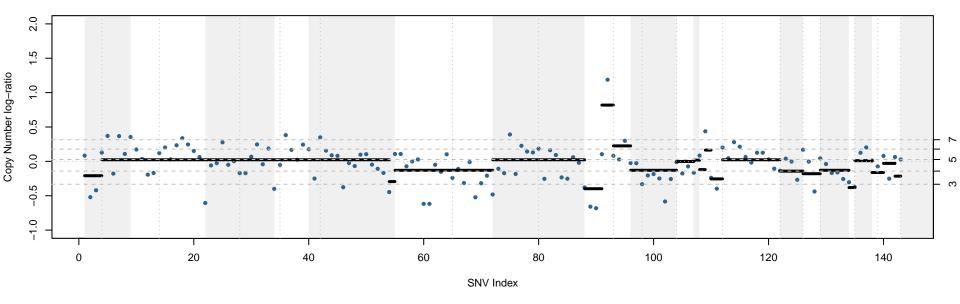


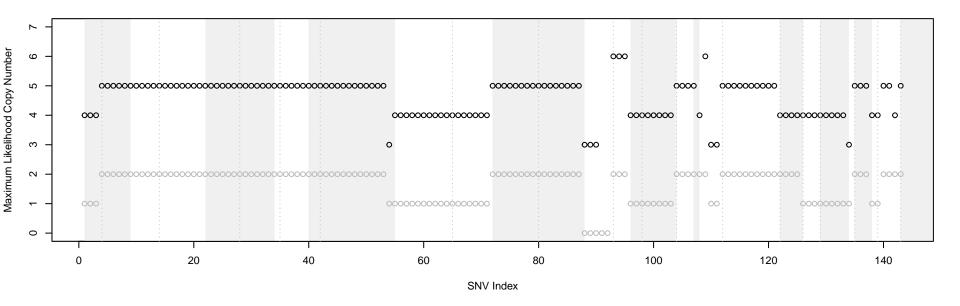


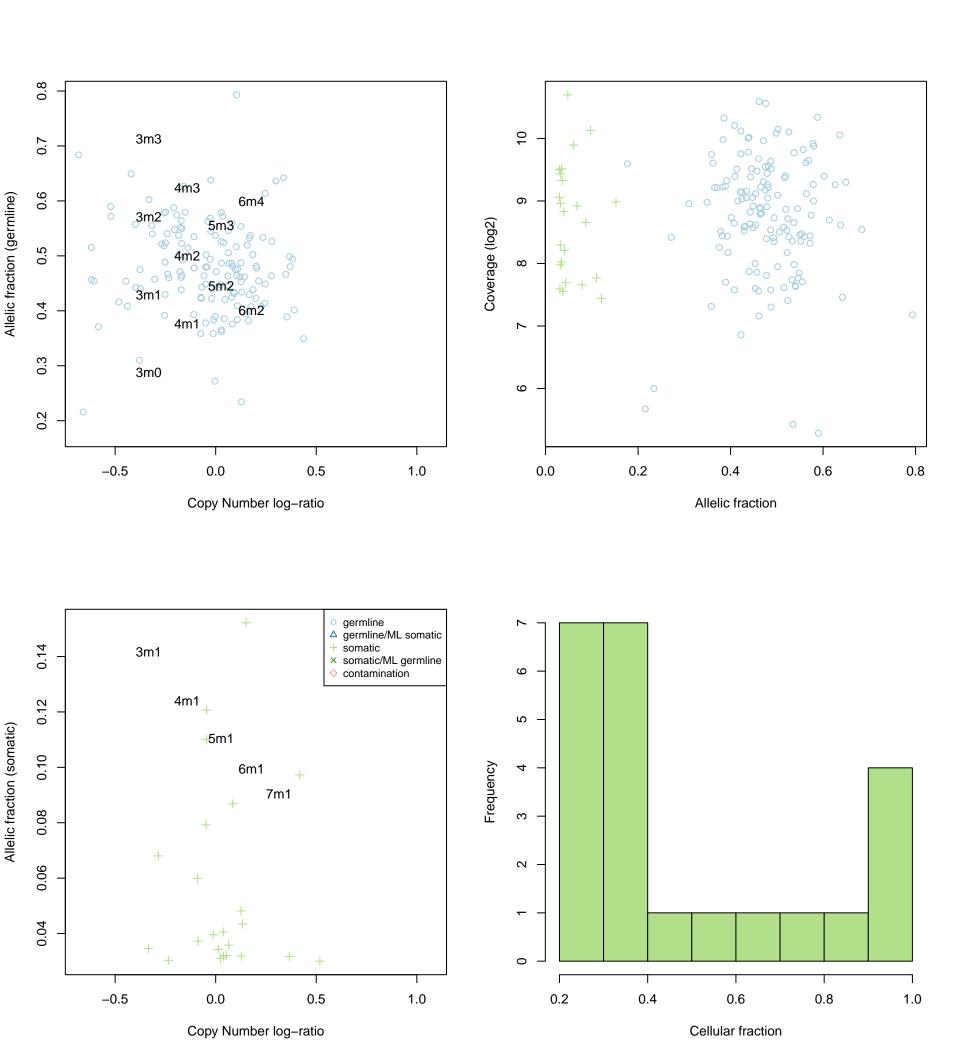


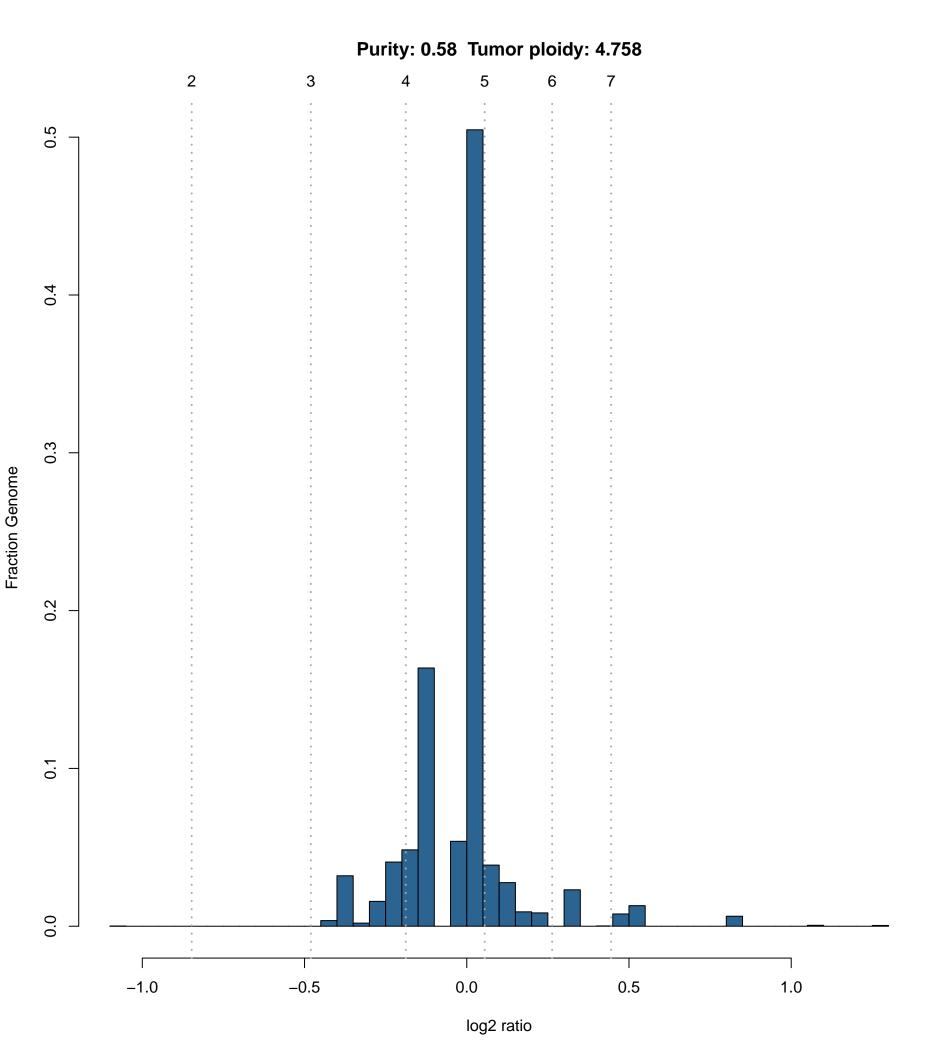


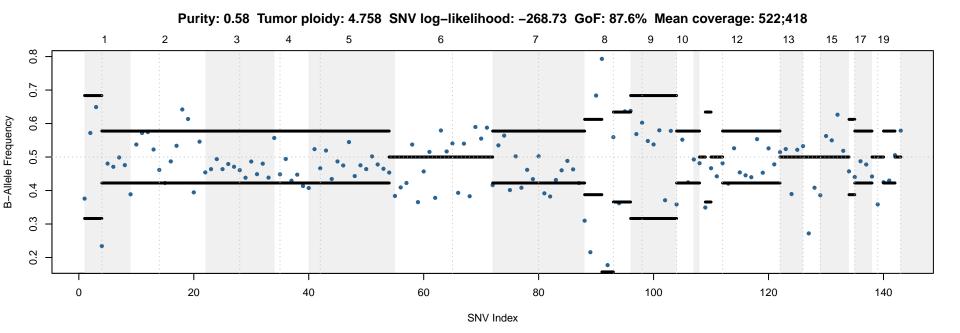
SCNA-fit log-likelihood: -5926.05



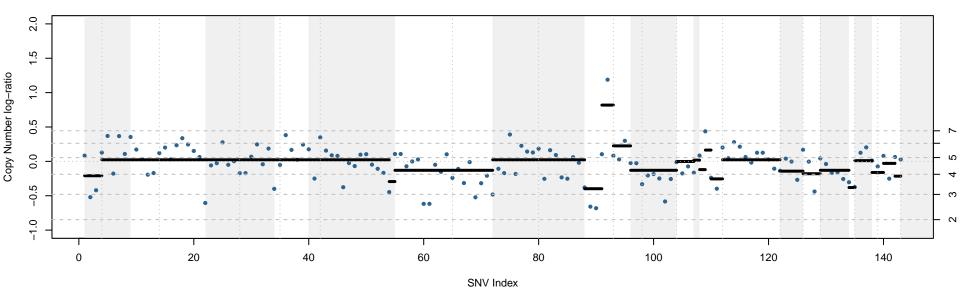


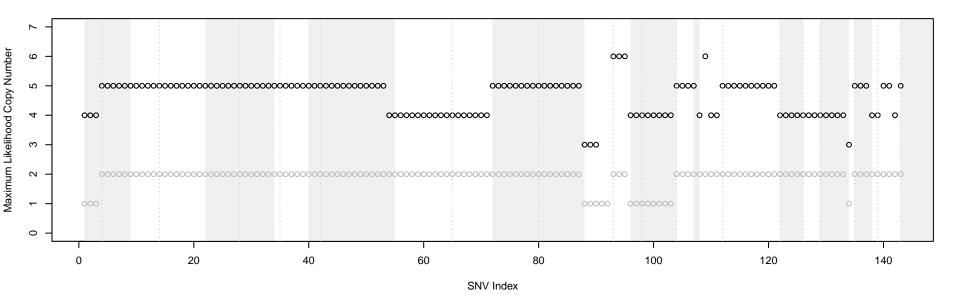


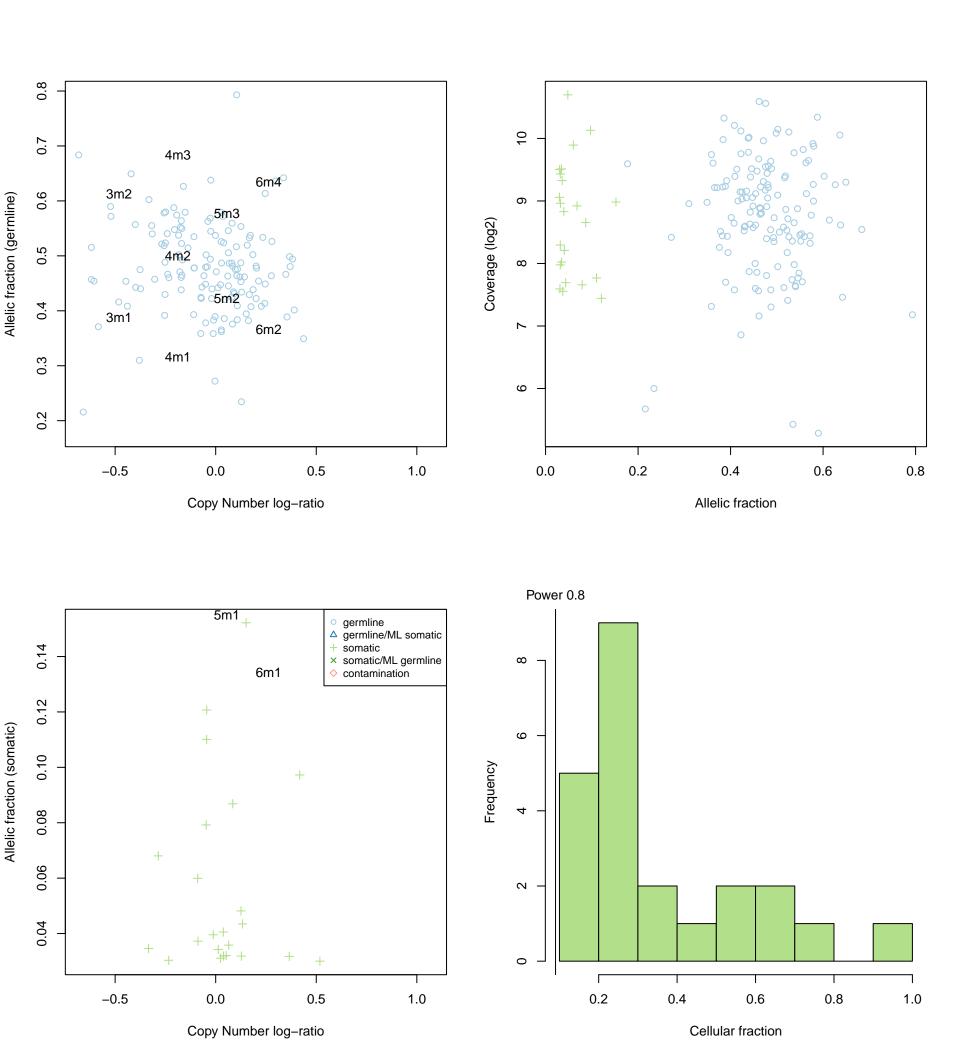




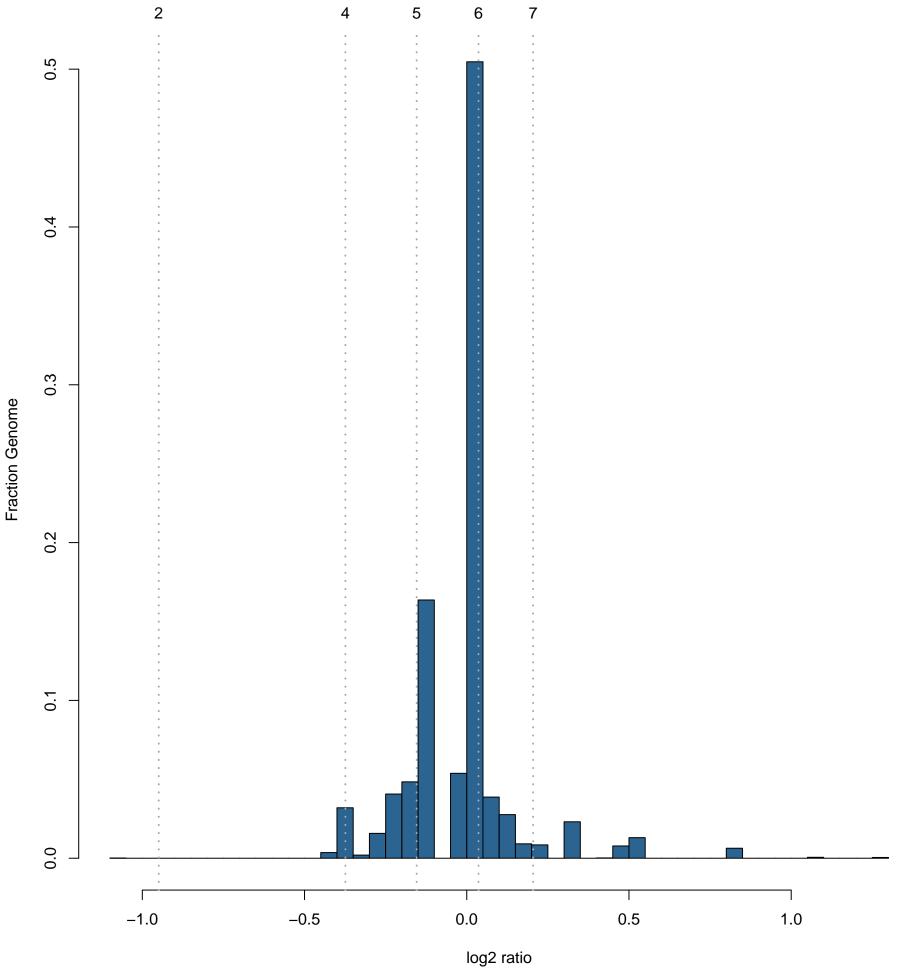
SCNA-fit log-likelihood: -5690.51

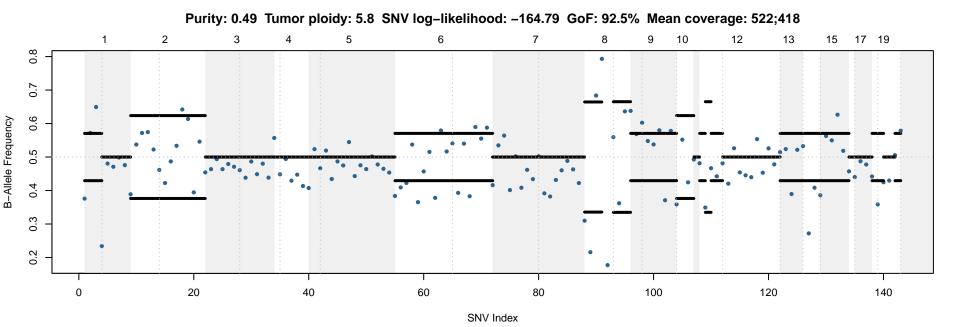




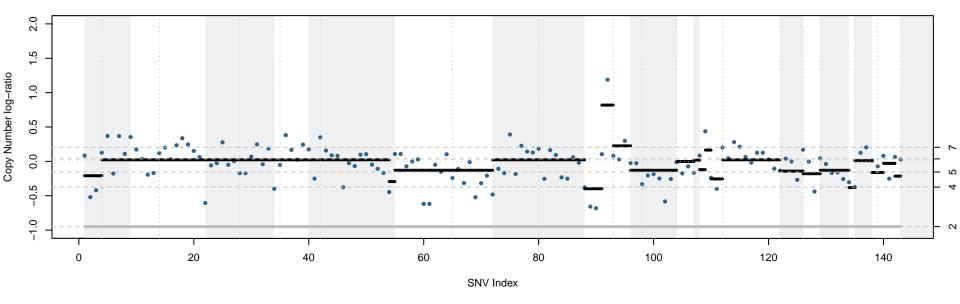


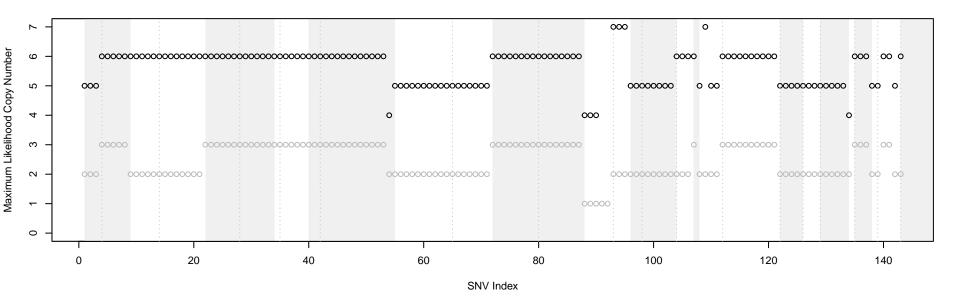
Purity: 0.49 Tumor ploidy: 5.8

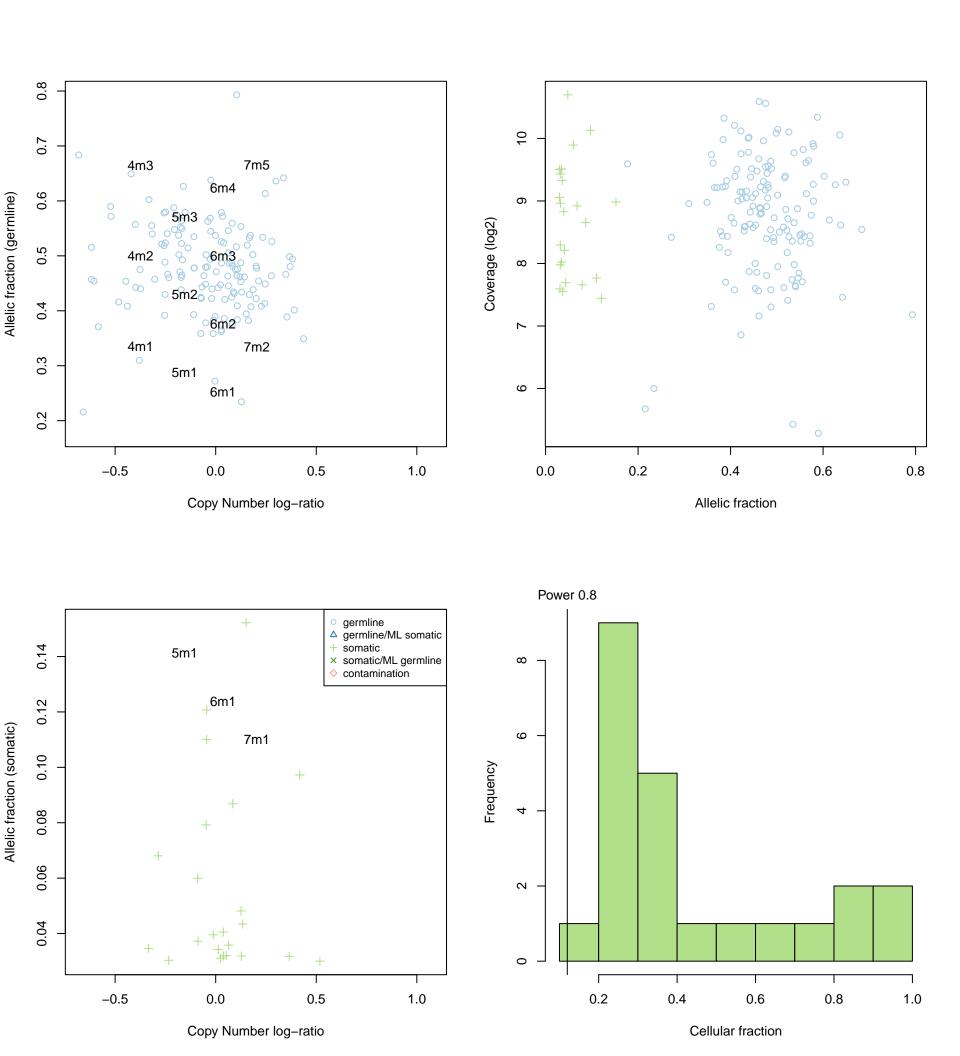


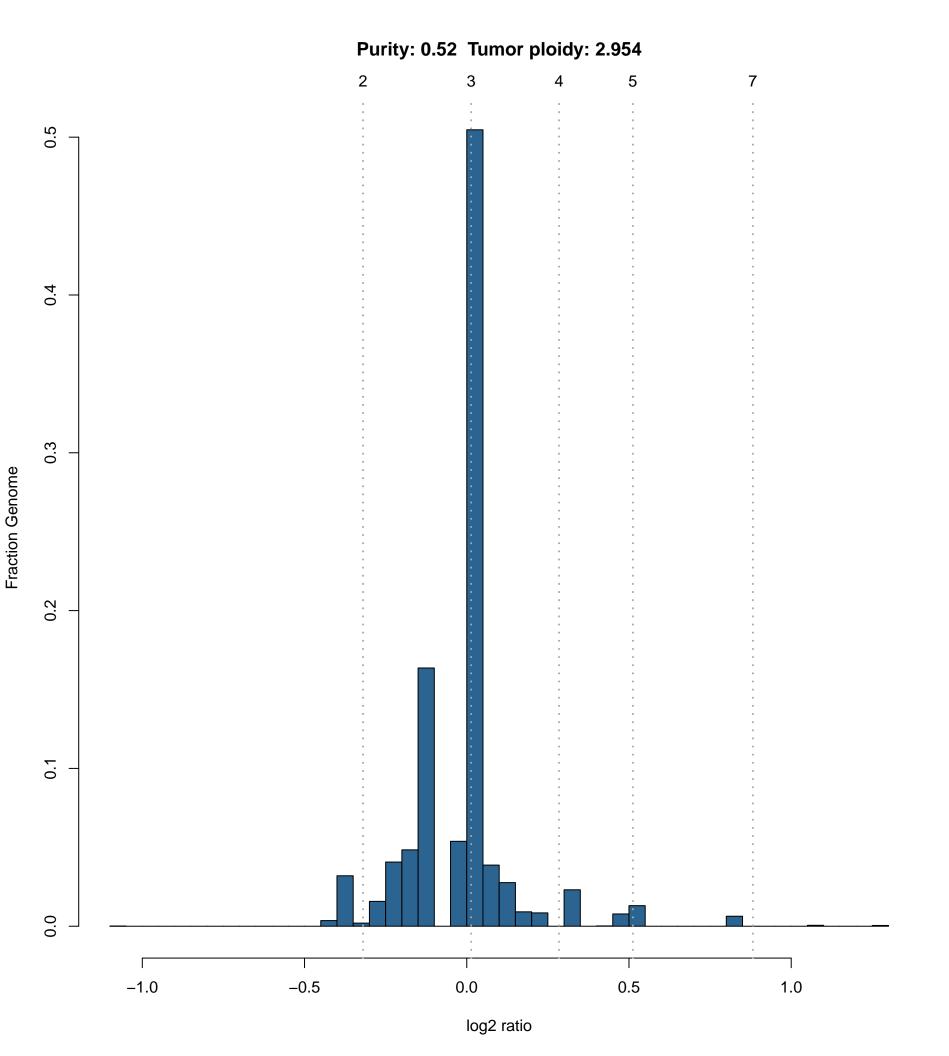


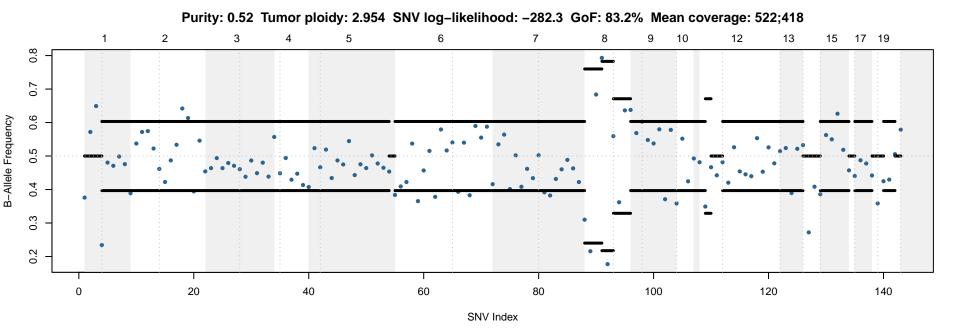
SCNA-fit log-likelihood: -5979.83



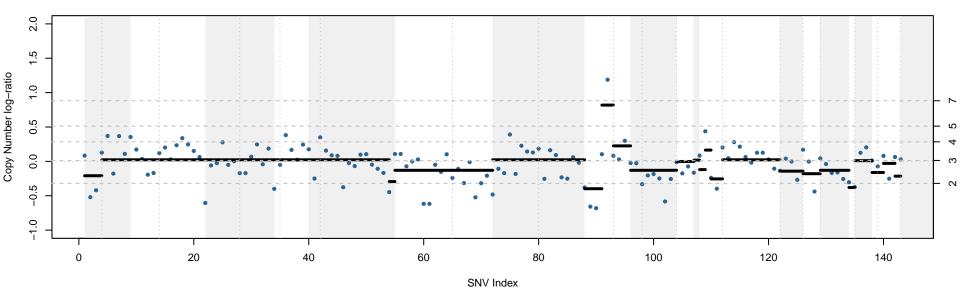


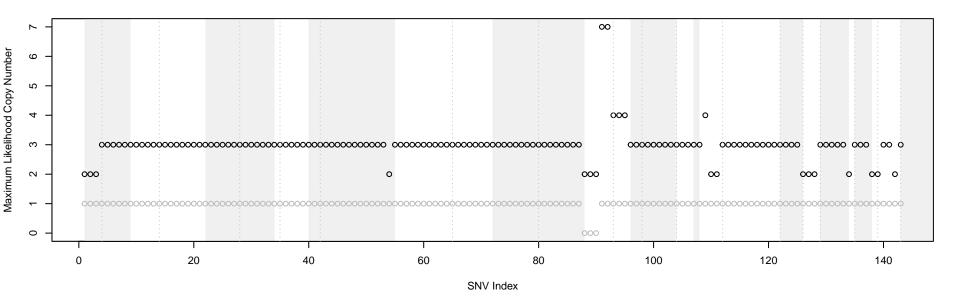


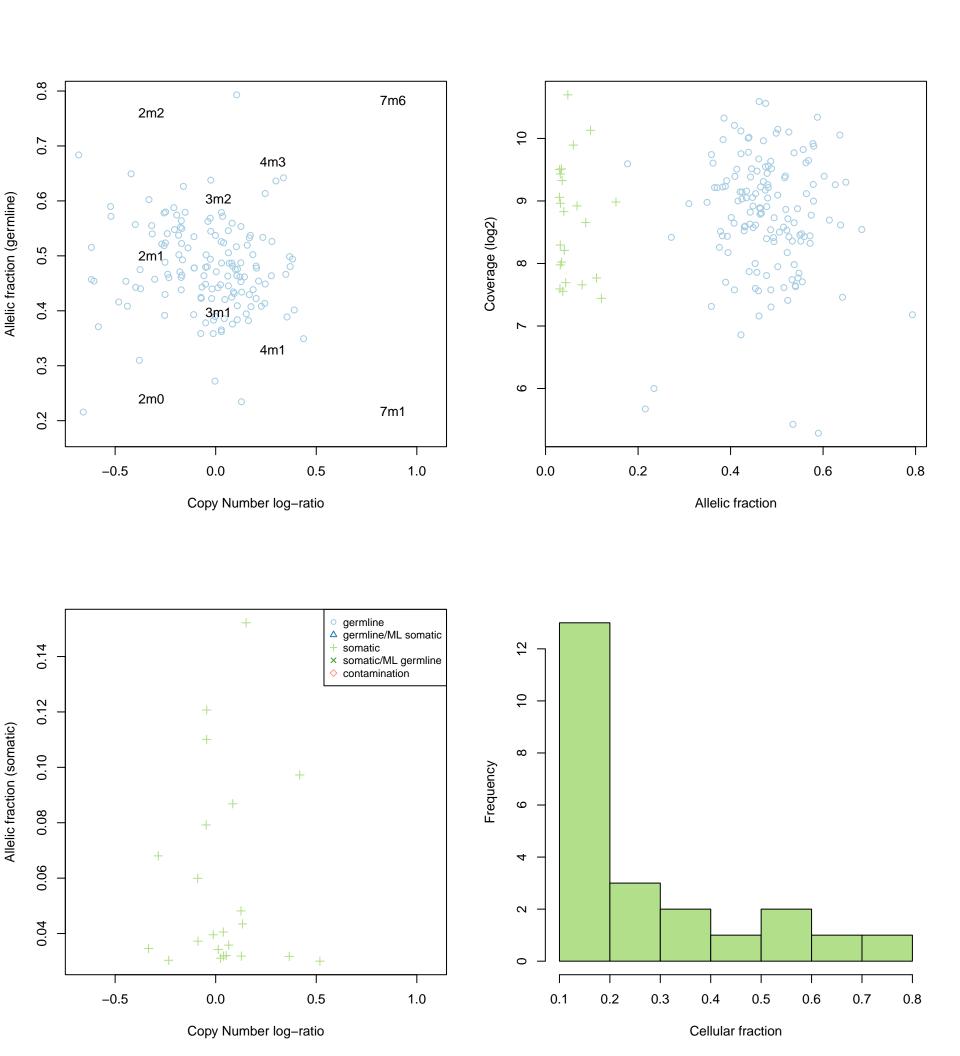




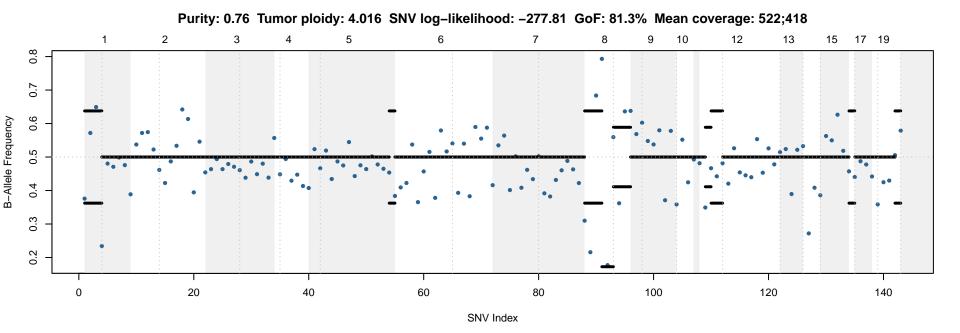
SCNA-fit log-likelihood: -5879.25



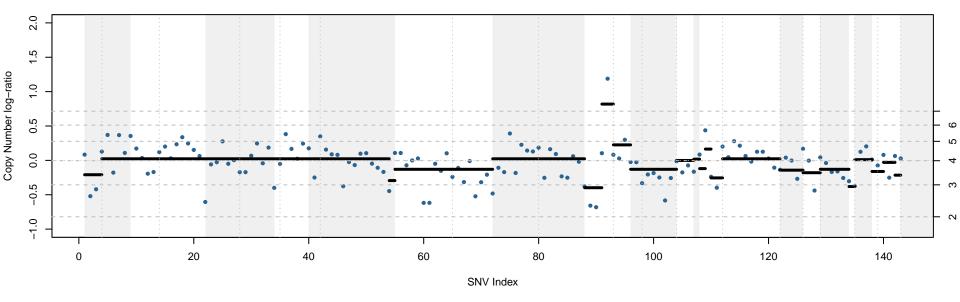


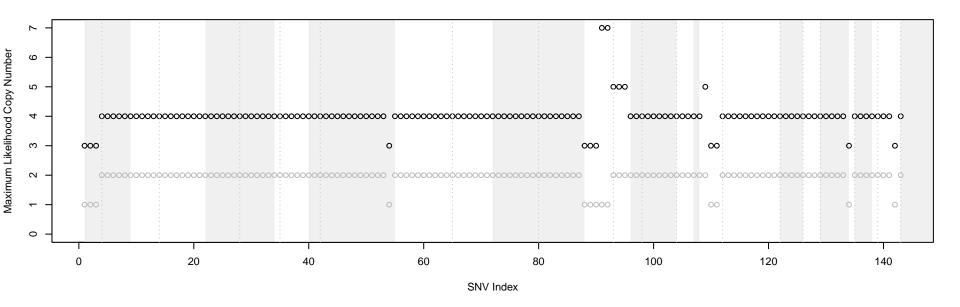


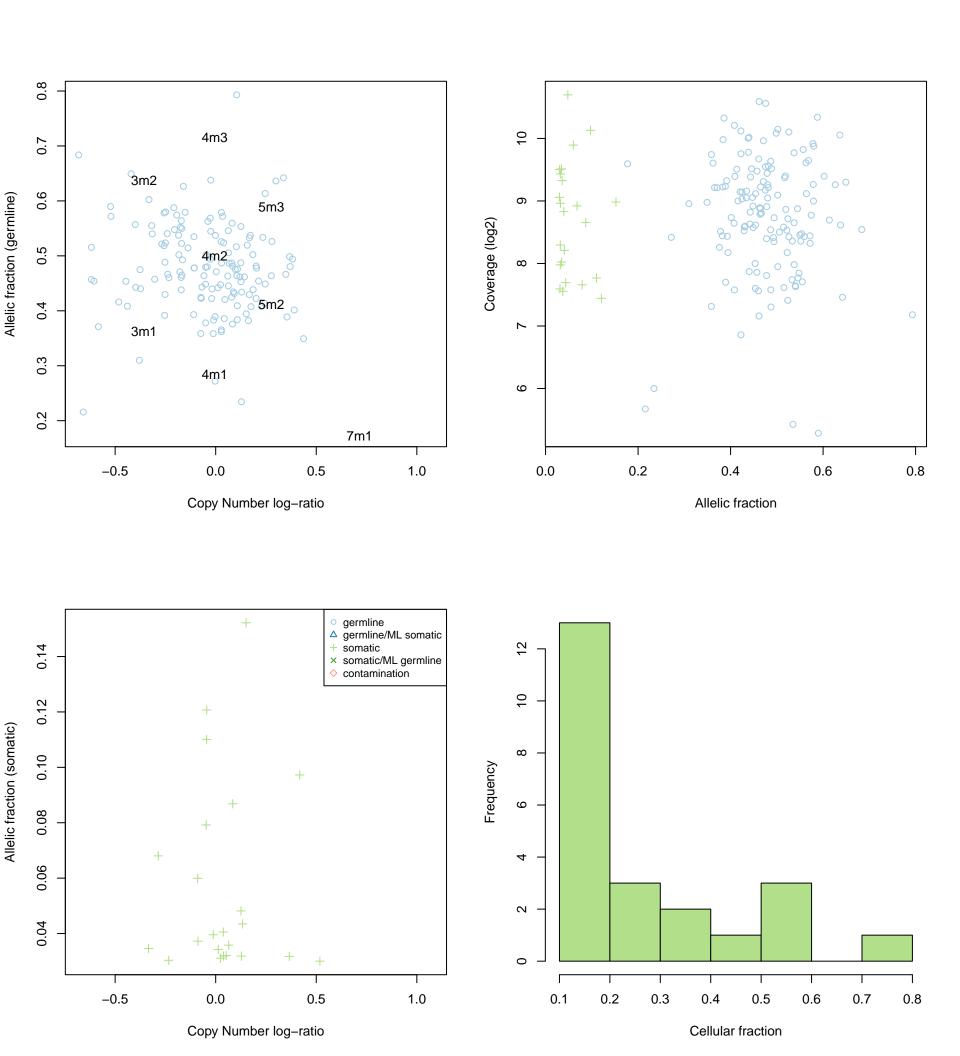
Purity: 0.76 Tumor ploidy: 4.016 2 5 6 3 7 Fraction Genome 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



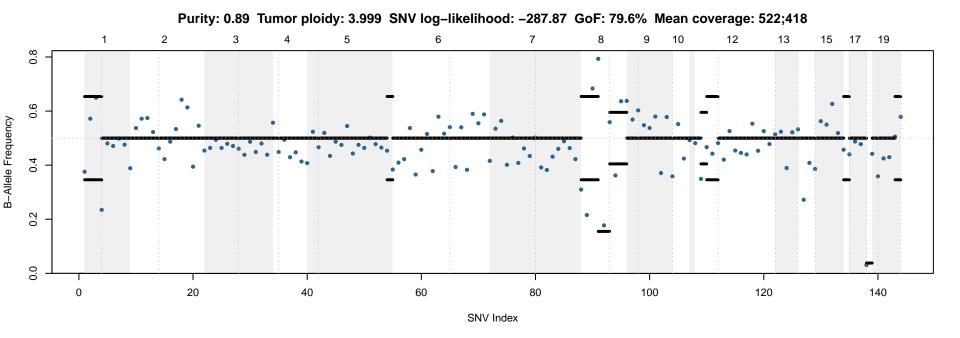
SCNA-fit log-likelihood: -5924.98



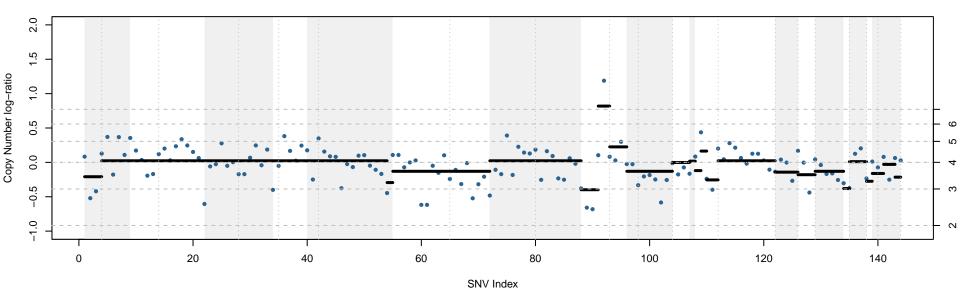


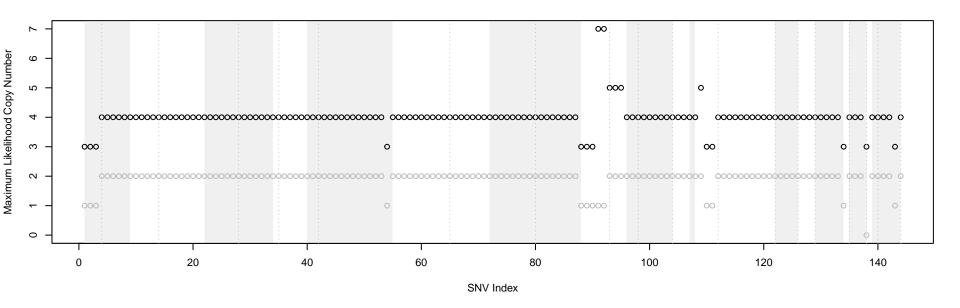


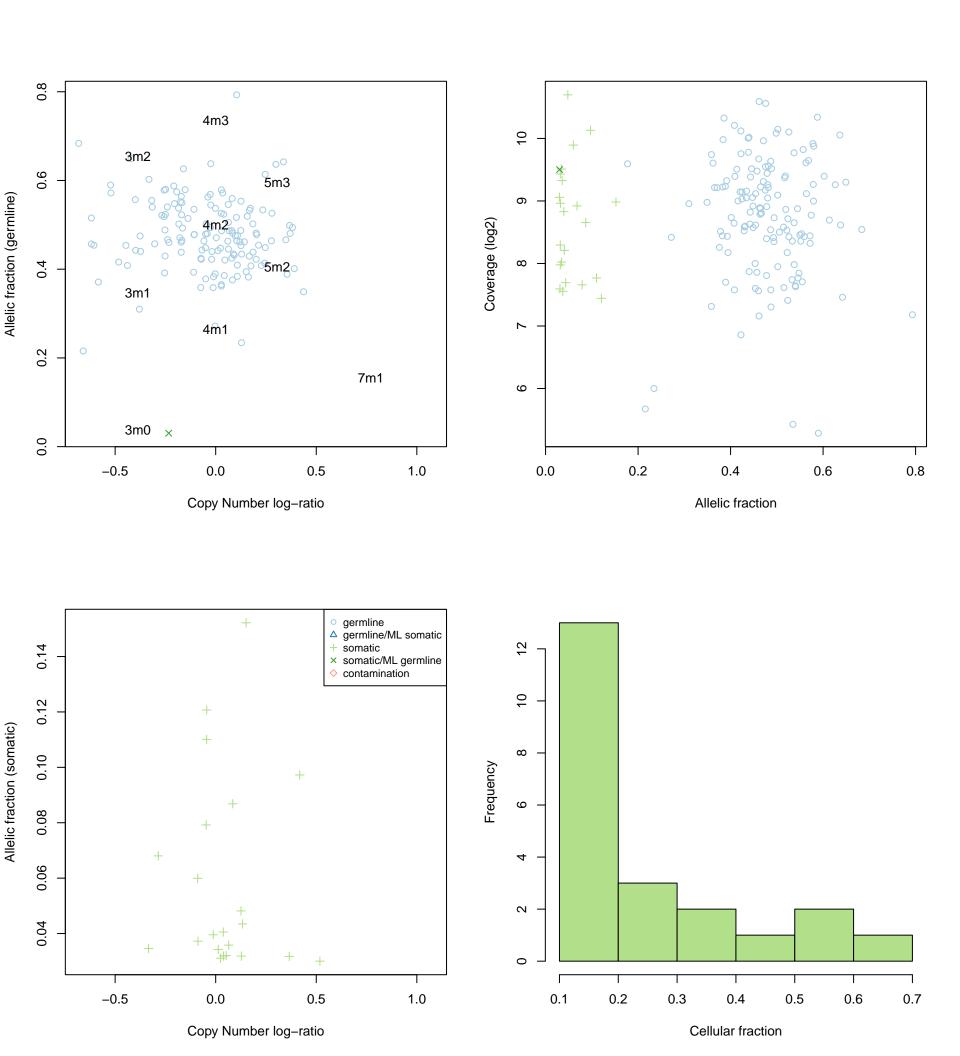
Purity: 0.89 Tumor ploidy: 3.999 2 5 3 6 Fraction Genome 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



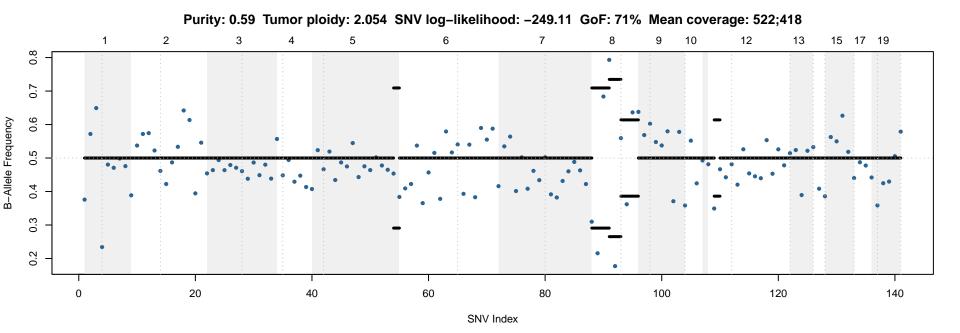
SCNA-fit log-likelihood: -5994.23



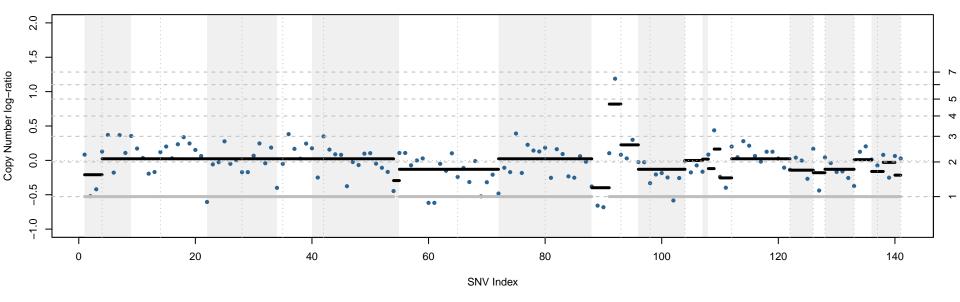


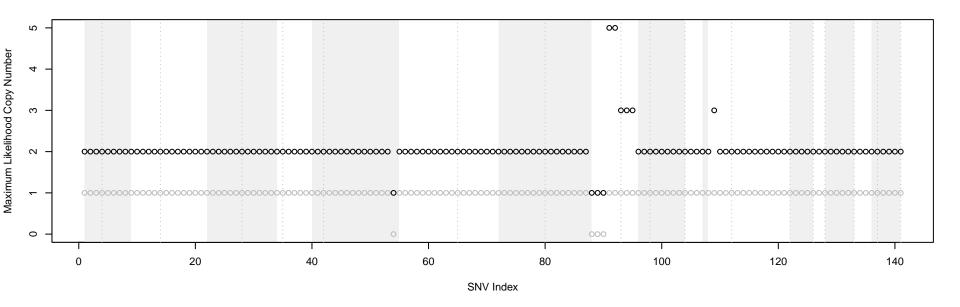


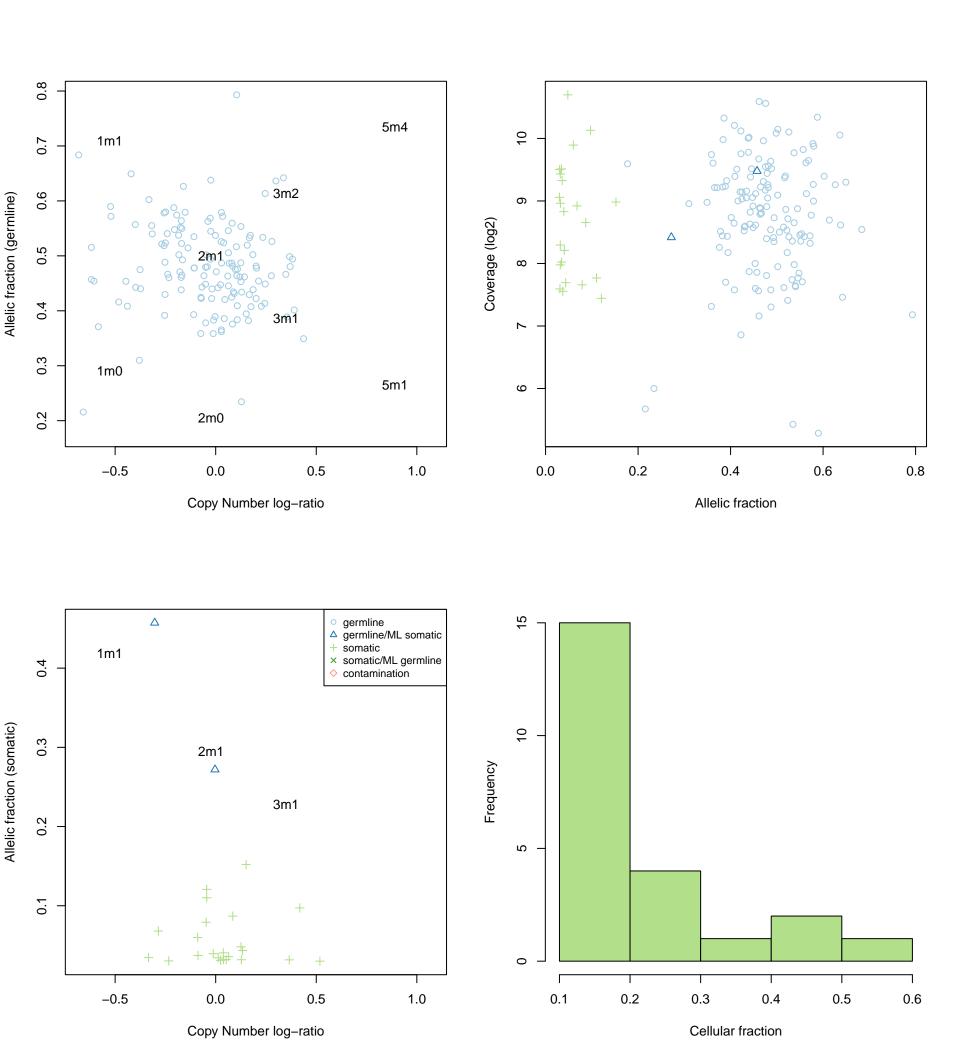
Purity: 0.59 Tumor ploidy: 2.054 2 3 6 5 Fraction Genome 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



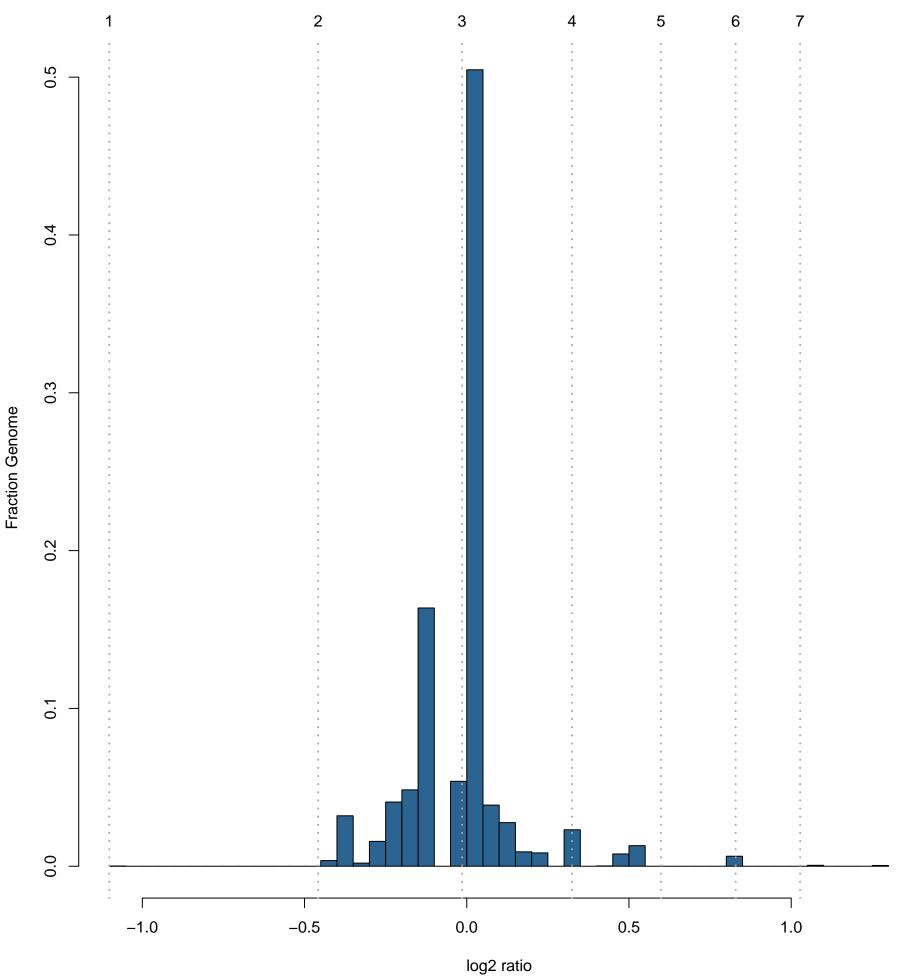
SCNA-fit log-likelihood: -6147.63

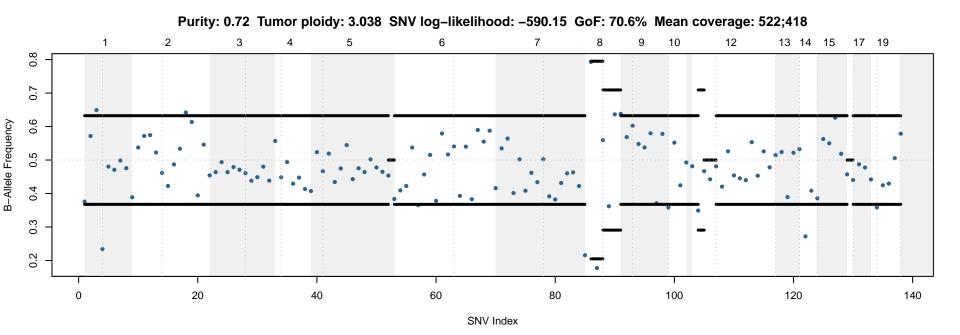






Purity: 0.72 Tumor ploidy: 3.038





SCNA-fit log-likelihood: -6028.73

