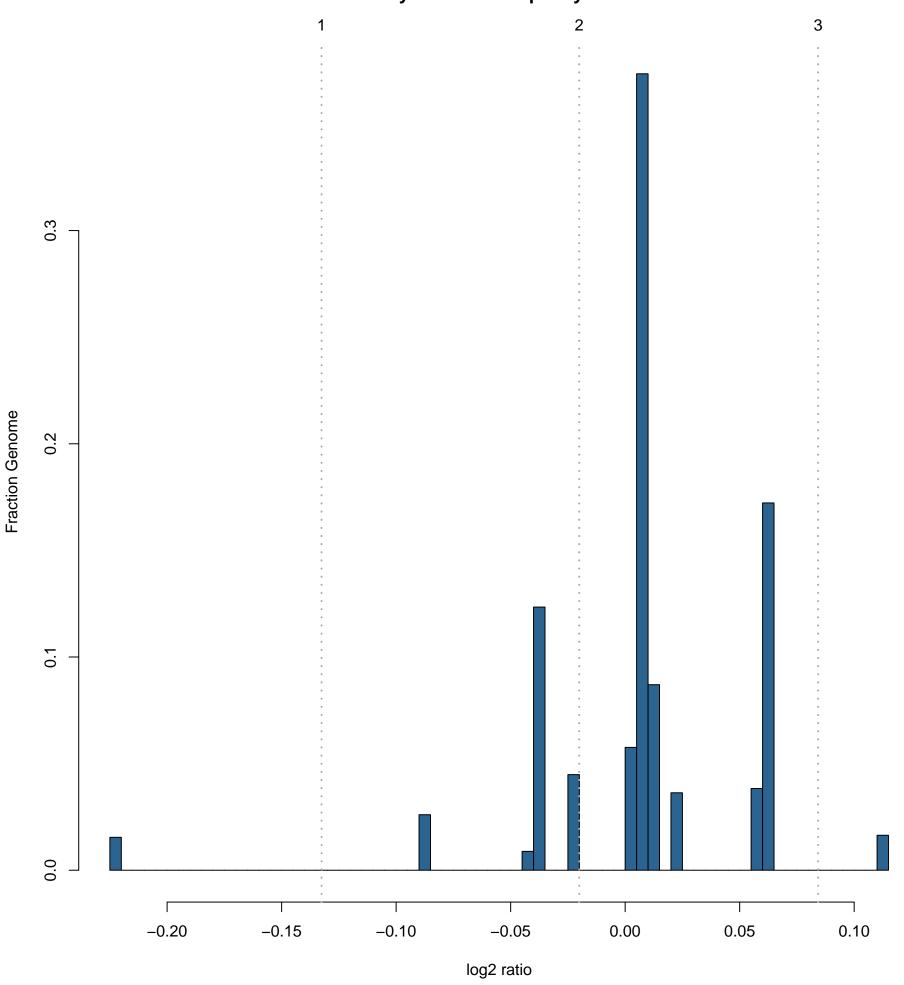
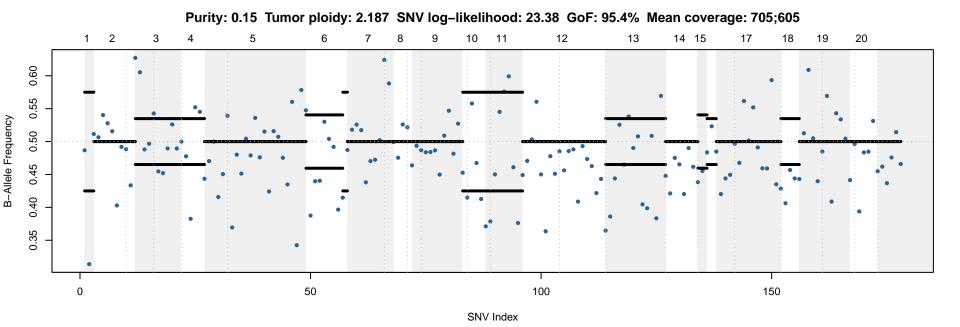
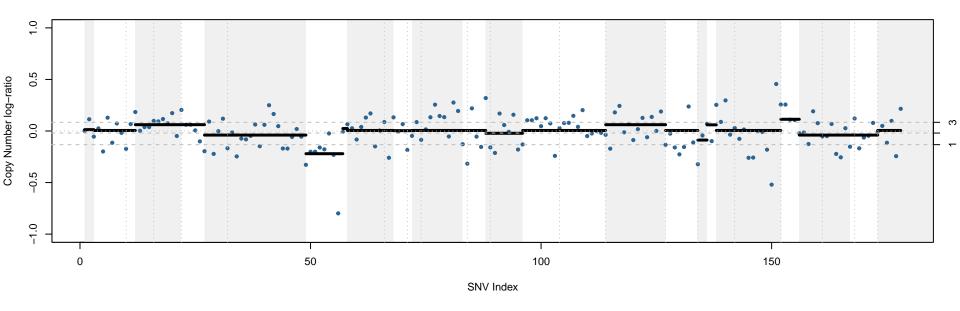
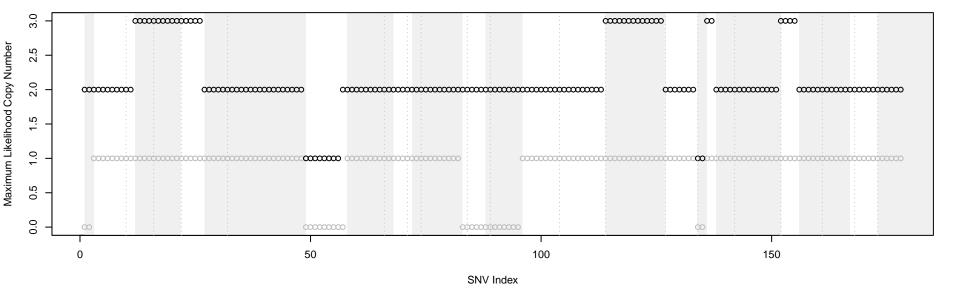
Purity: 0.15 Tumor ploidy: 2.187

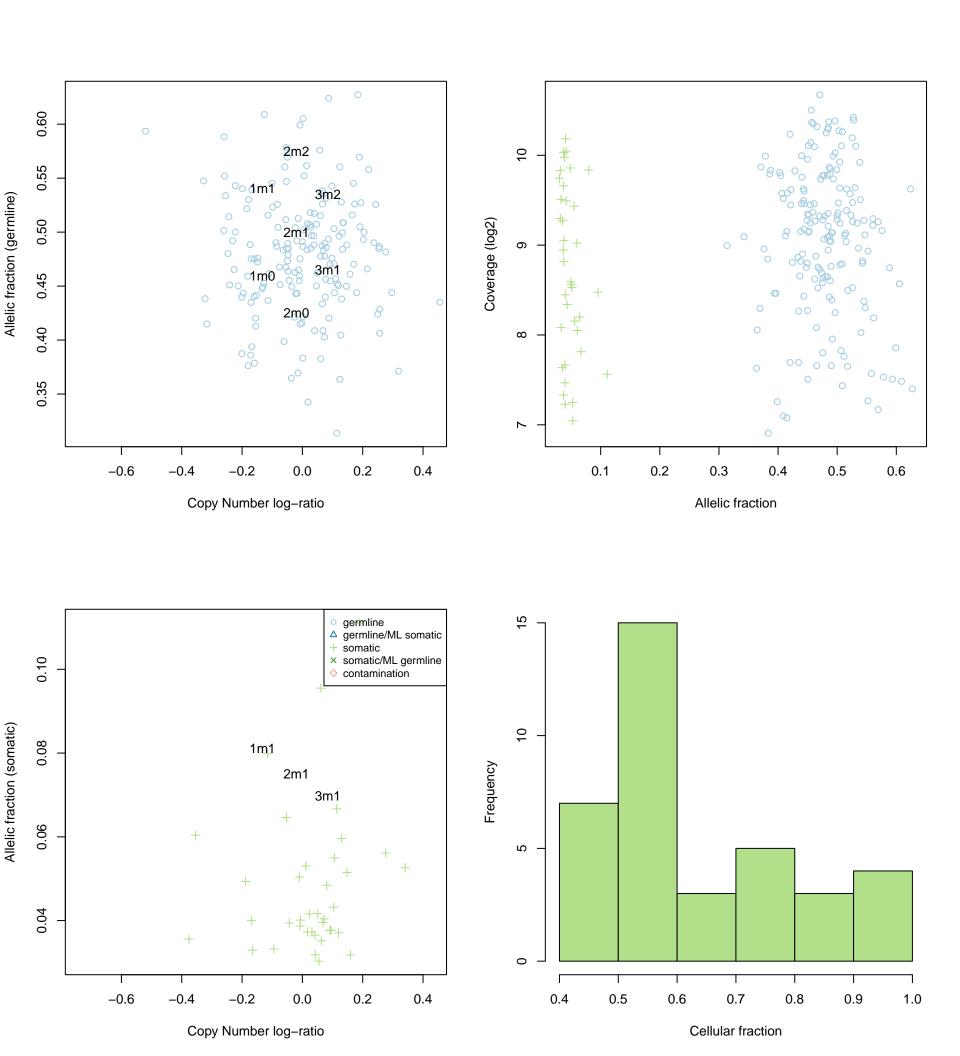




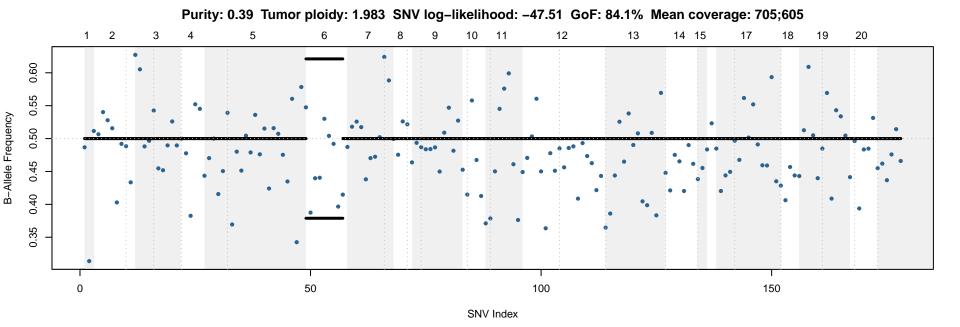
## SCNA-fit log-likelihood: -4459.91



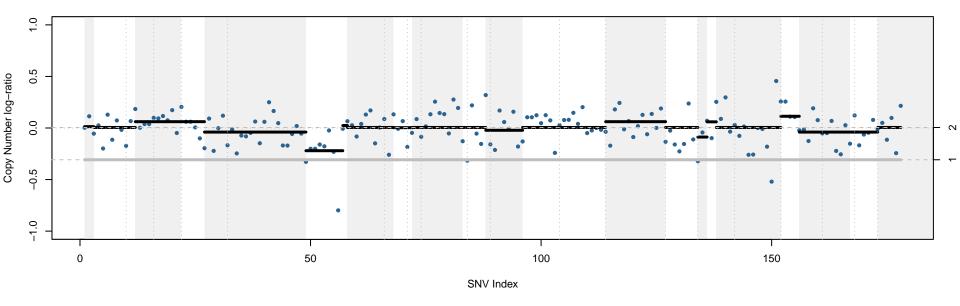


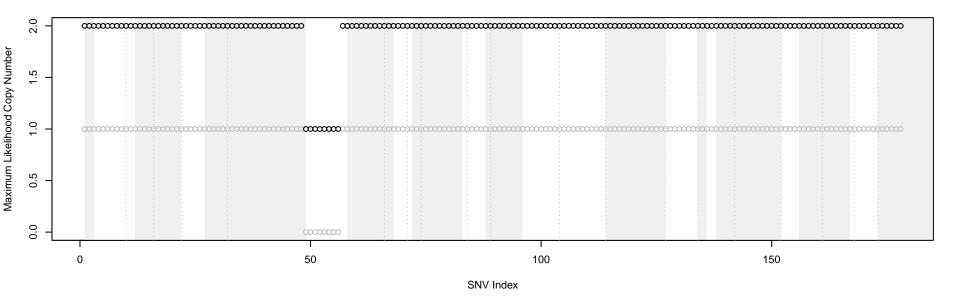


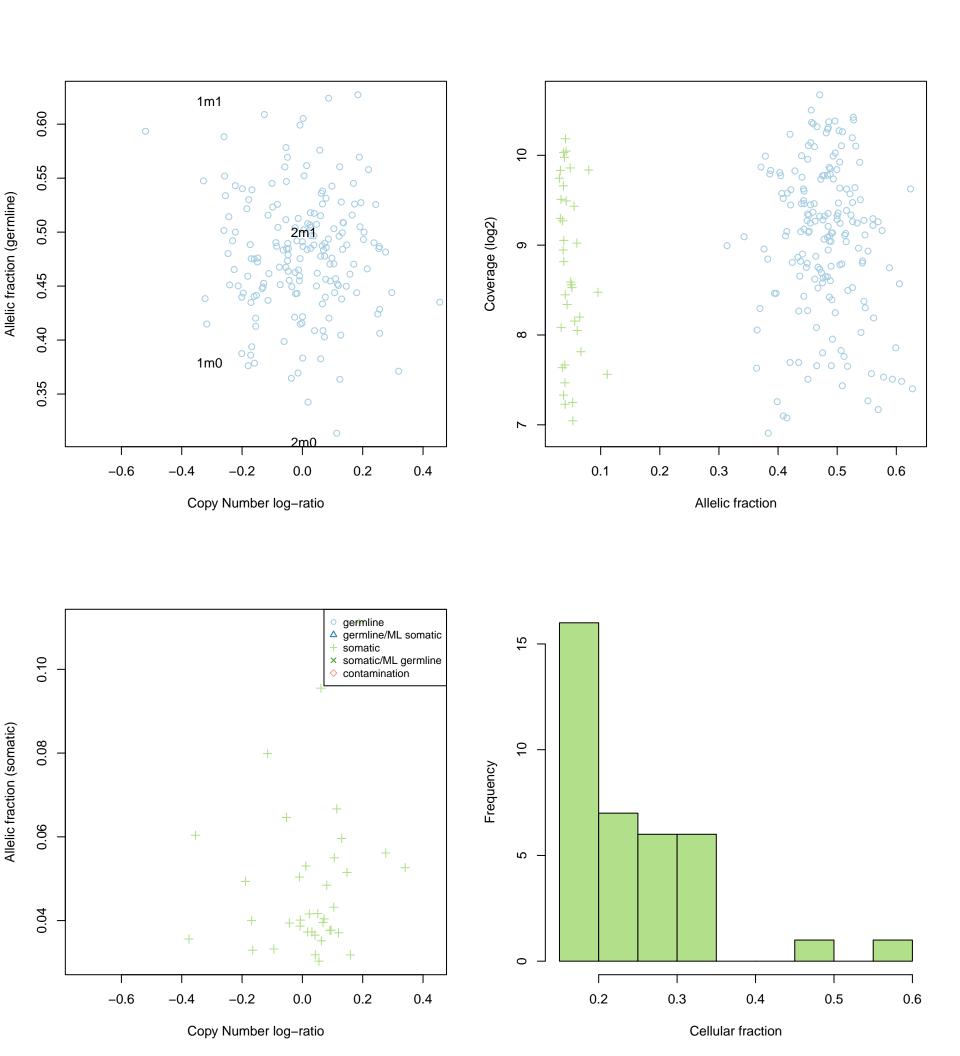
Purity: 0.39 Tumor ploidy: 1.983 2 Fraction Genome 0.2 0.1 0.0 -0.20 -0.15 -0.10 -0.05 0.00 0.05 0.10 log2 ratio



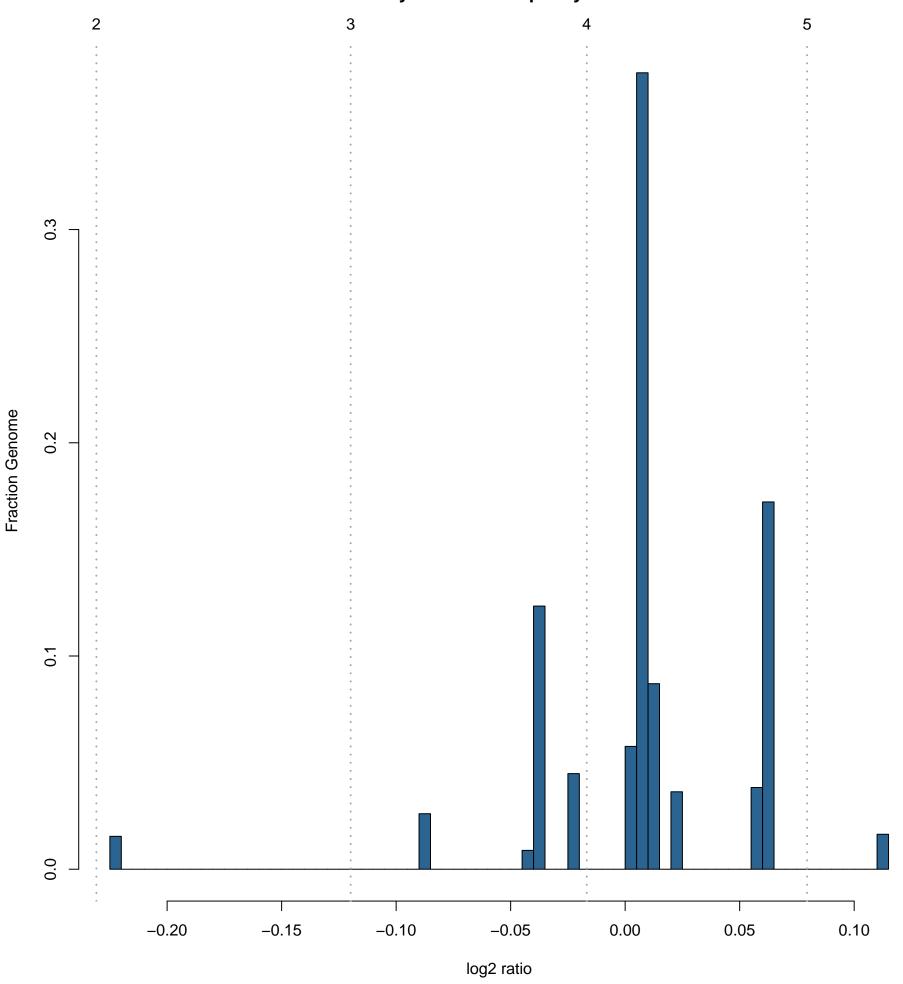
# SCNA-fit log-likelihood: -4499.97

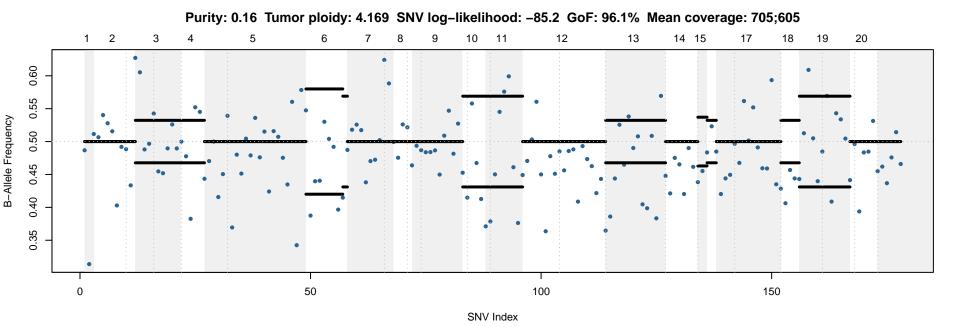




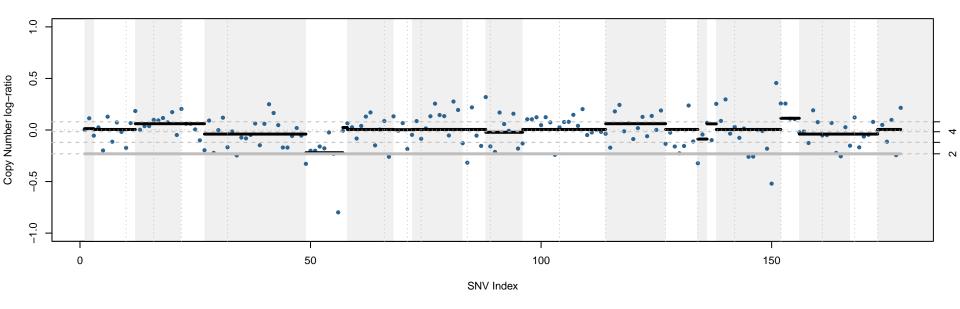


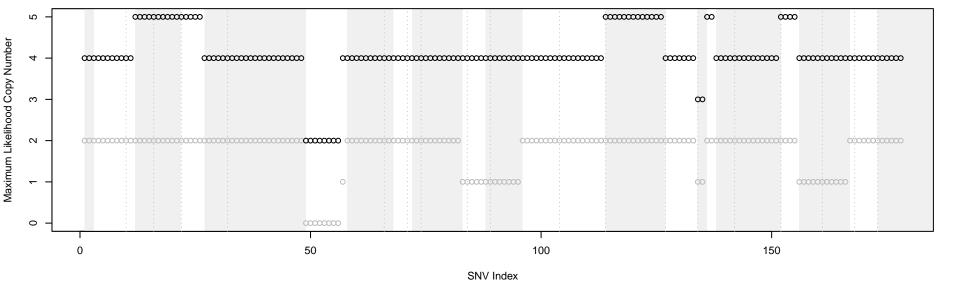
Purity: 0.16 Tumor ploidy: 4.169

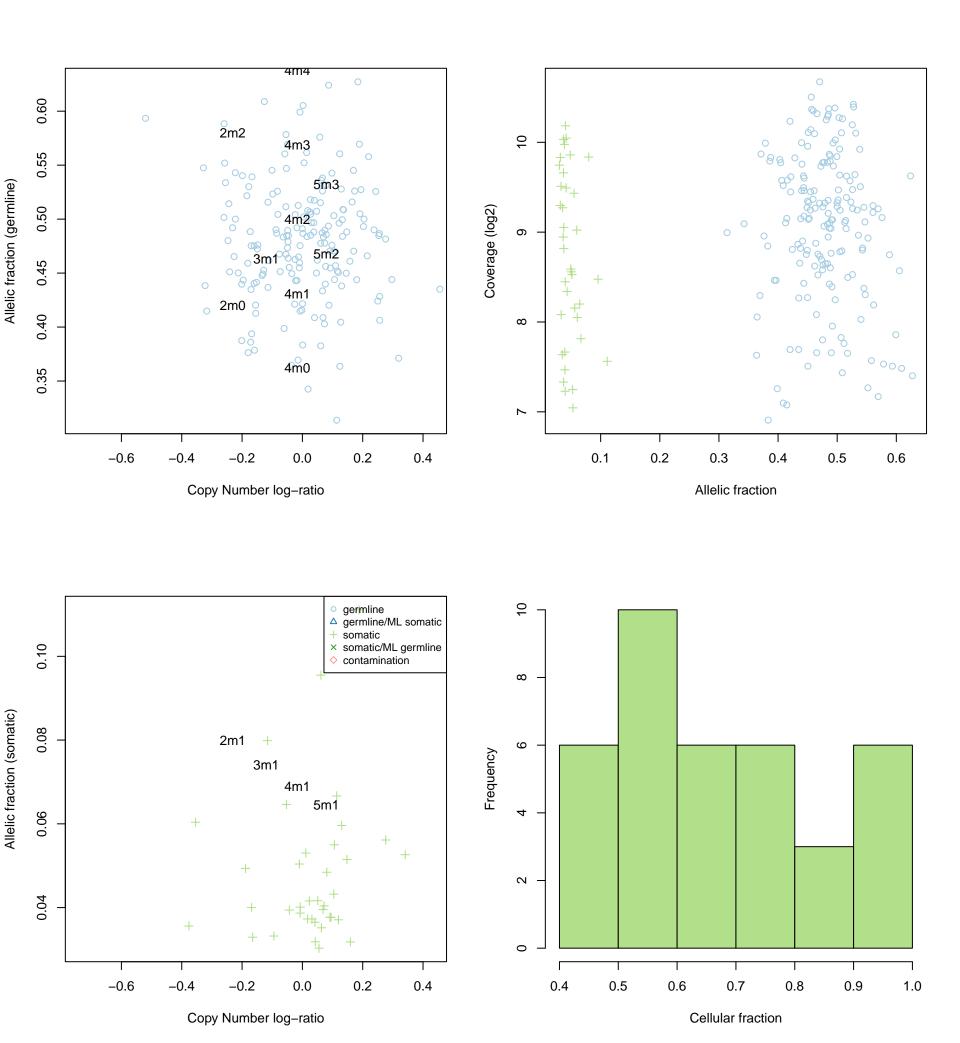




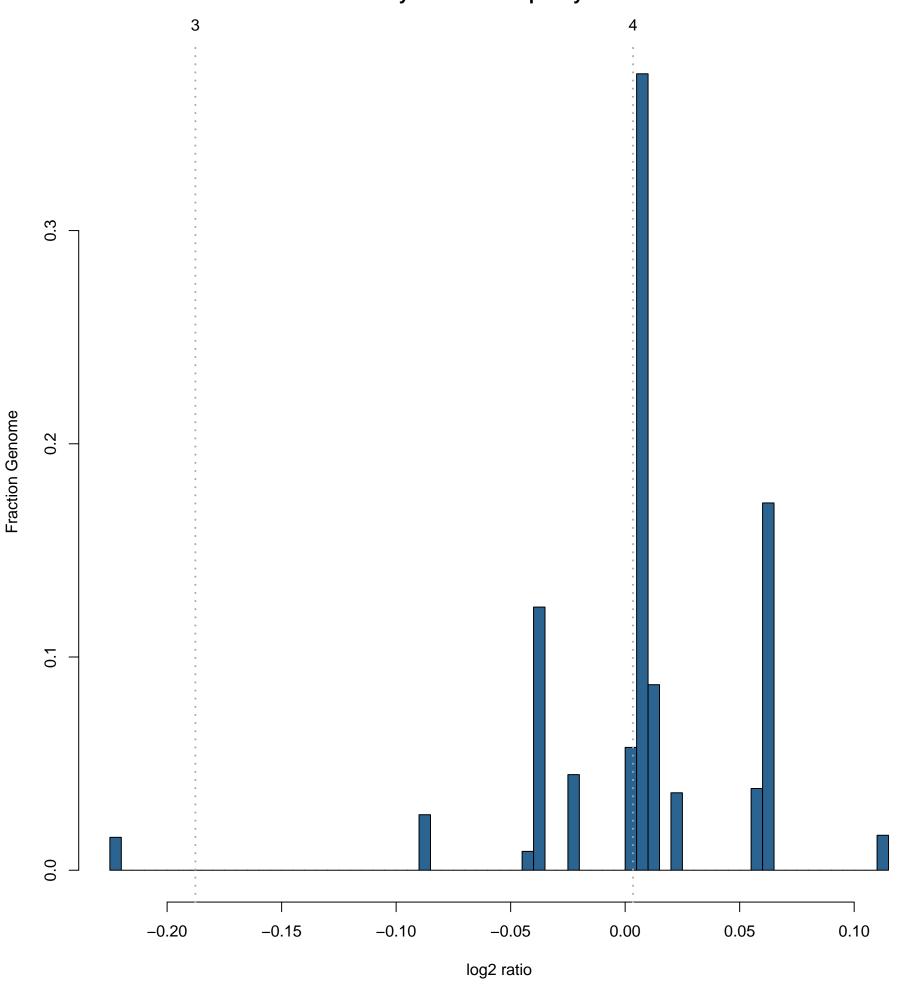
## SCNA-fit log-likelihood: -4448.21

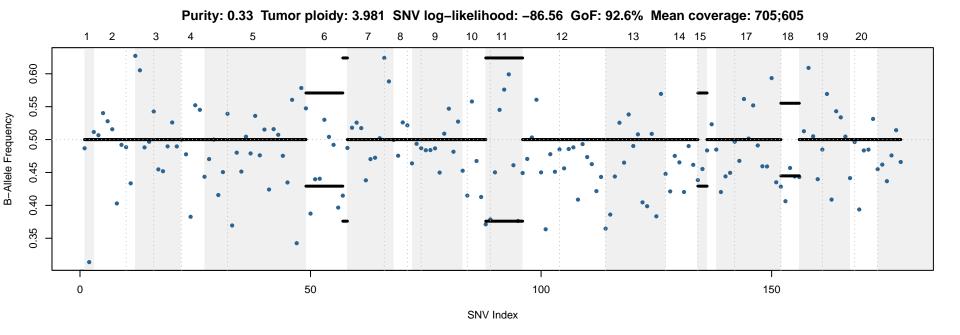




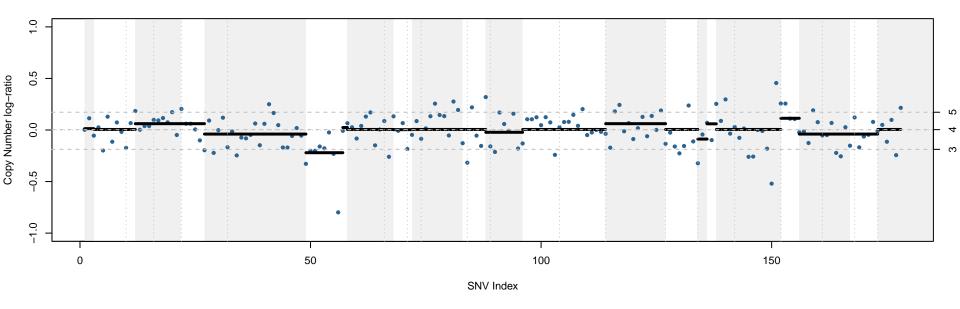


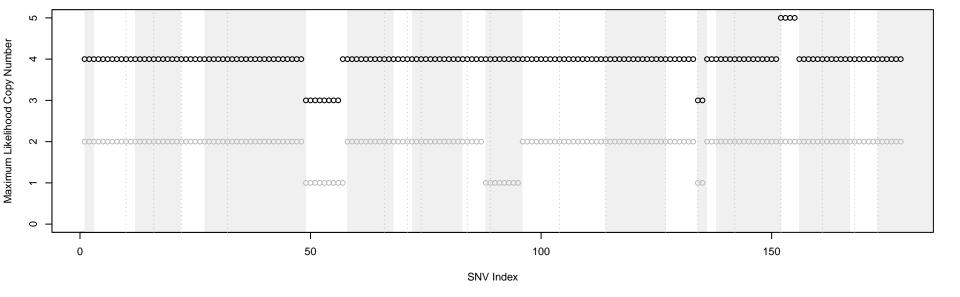
Purity: 0.33 Tumor ploidy: 3.981

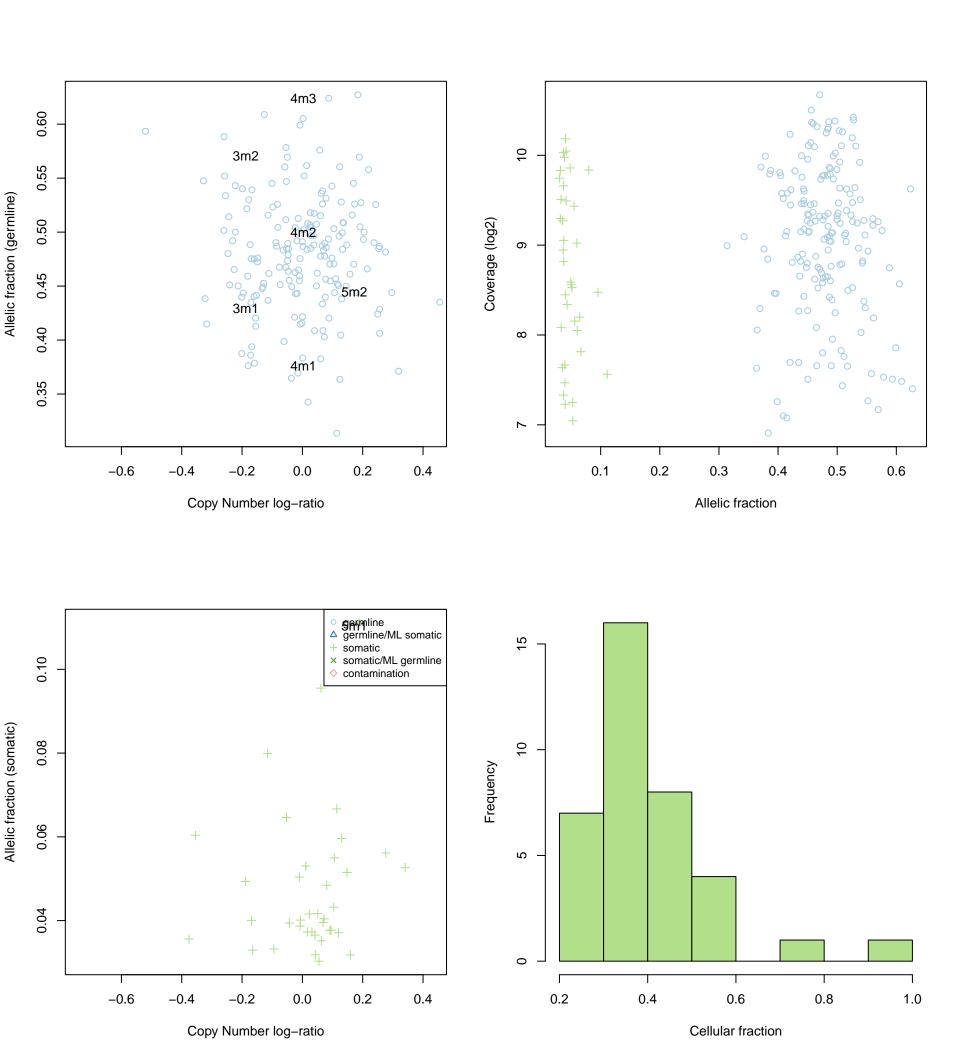




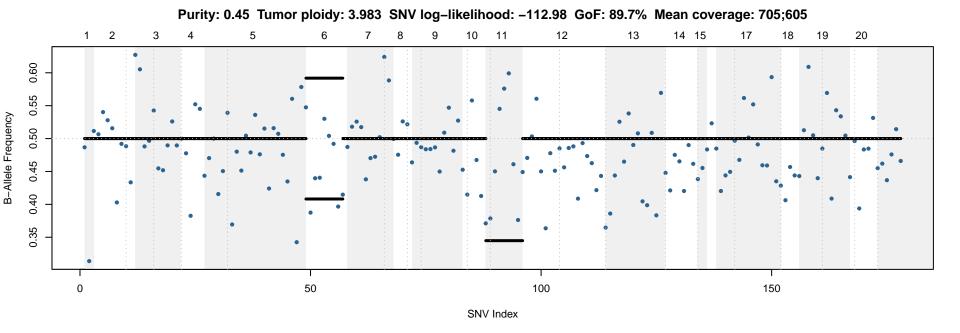
## SCNA-fit log-likelihood: -4488.94



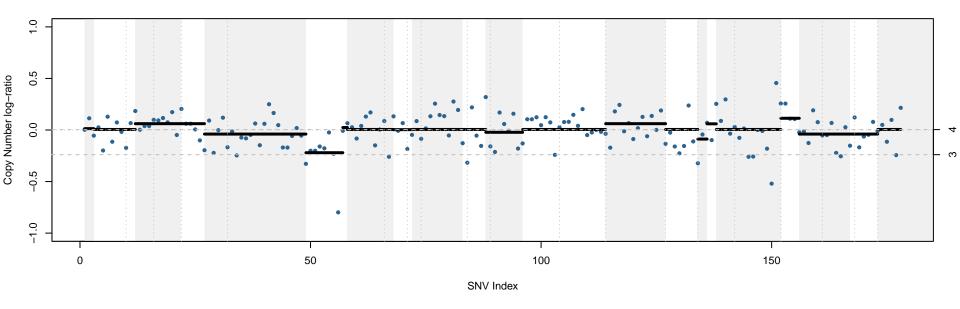


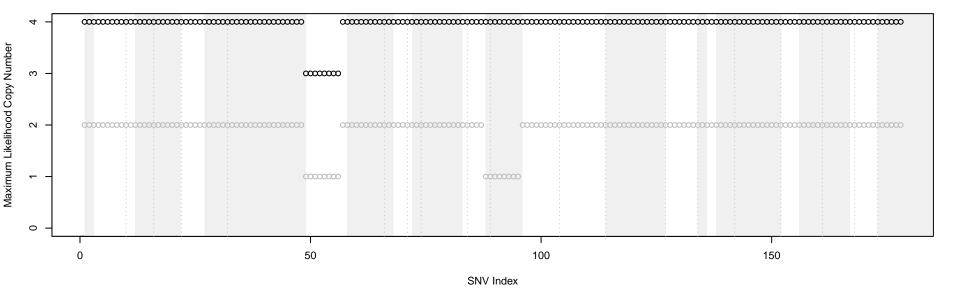


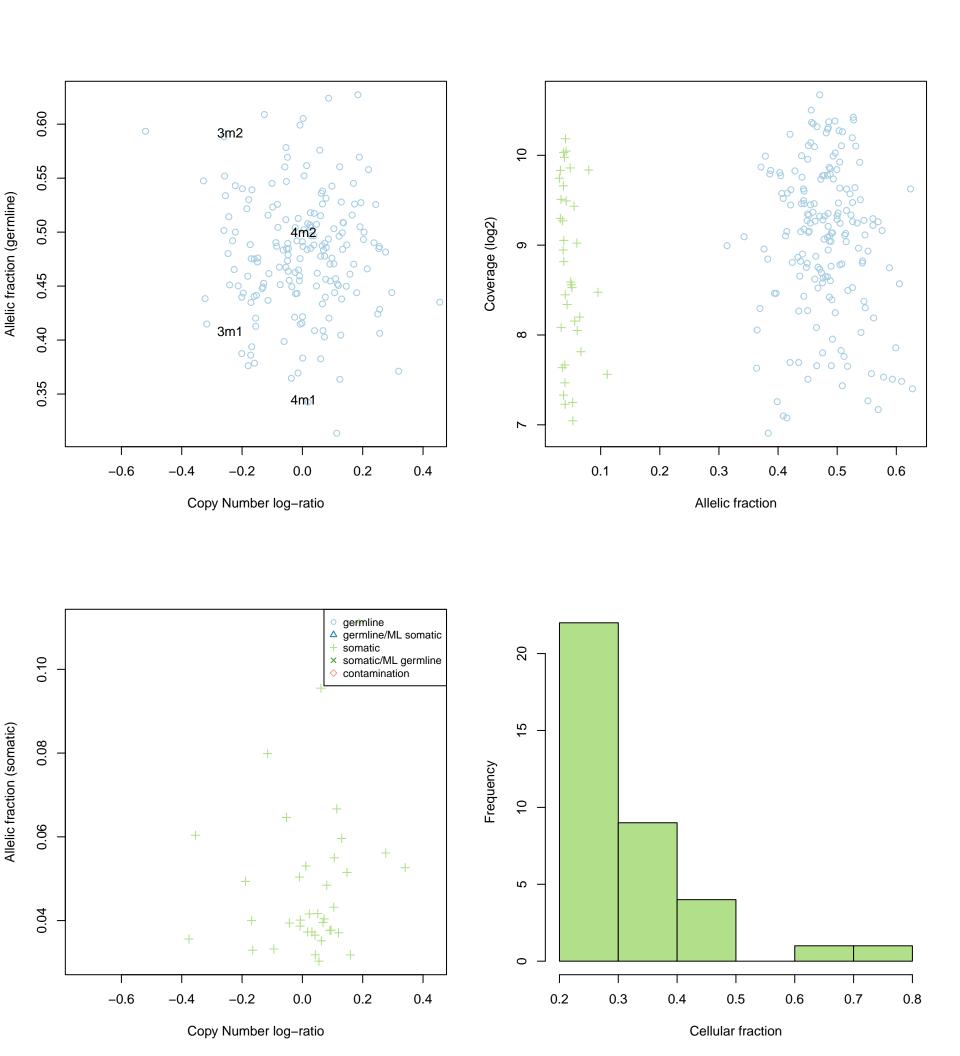
Purity: 0.45 Tumor ploidy: 3.983 Fraction Genome 0.2 0.1 0.0 -0.20 -0.15 -0.10 -0.05 0.00 0.05 0.10 log2 ratio



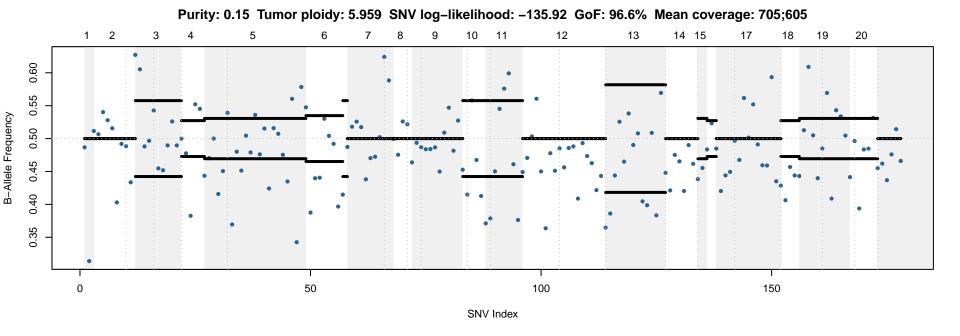
## SCNA-fit log-likelihood: -4494.53



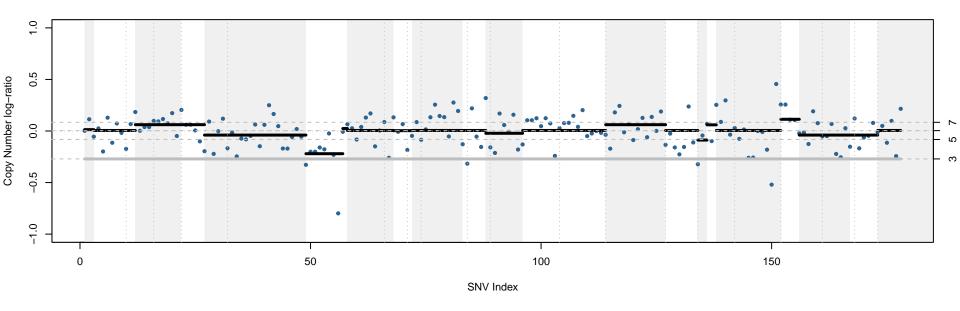


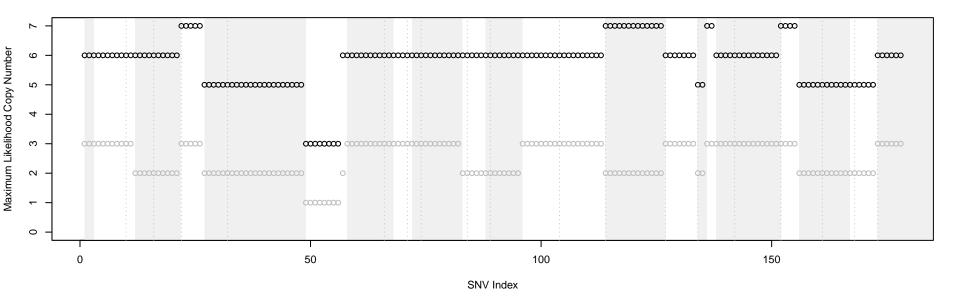


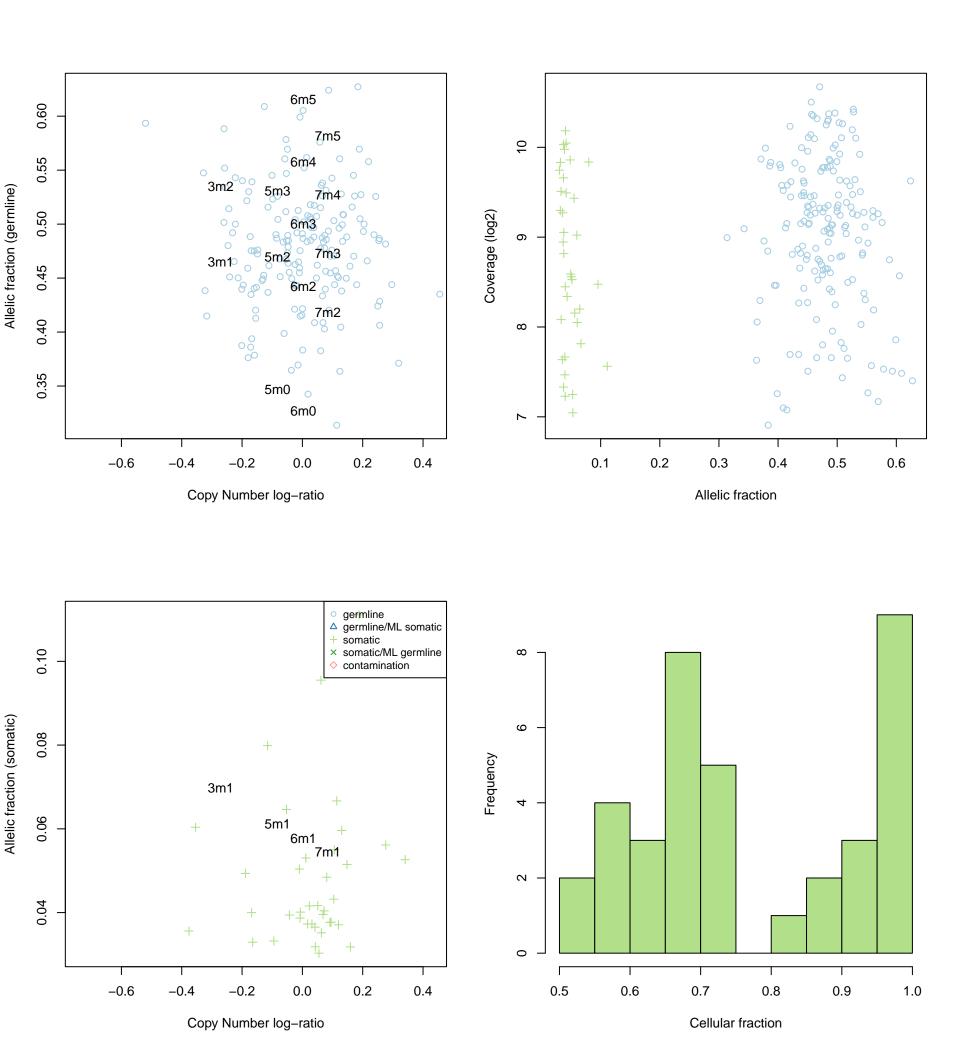
Purity: 0.15 Tumor ploidy: 5.959 6 7 Fraction Genome 0.1 0.0 -0.20 -0.15 -0.10 -0.05 0.00 0.05 0.10 log2 ratio



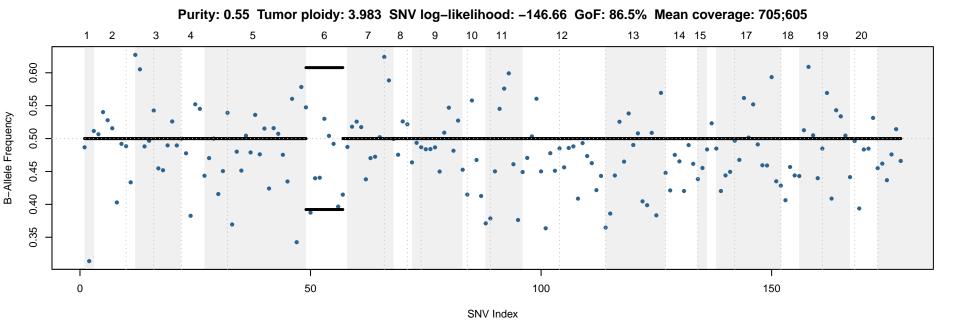
## SCNA-fit log-likelihood: -4447.29



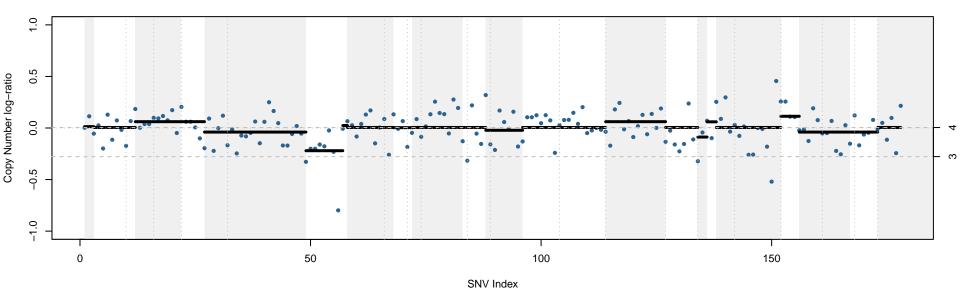


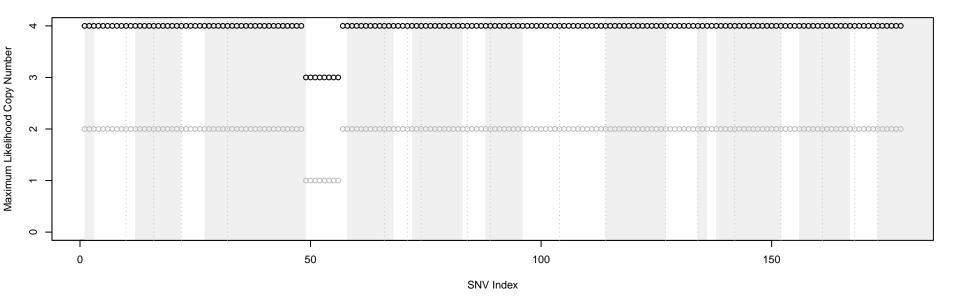


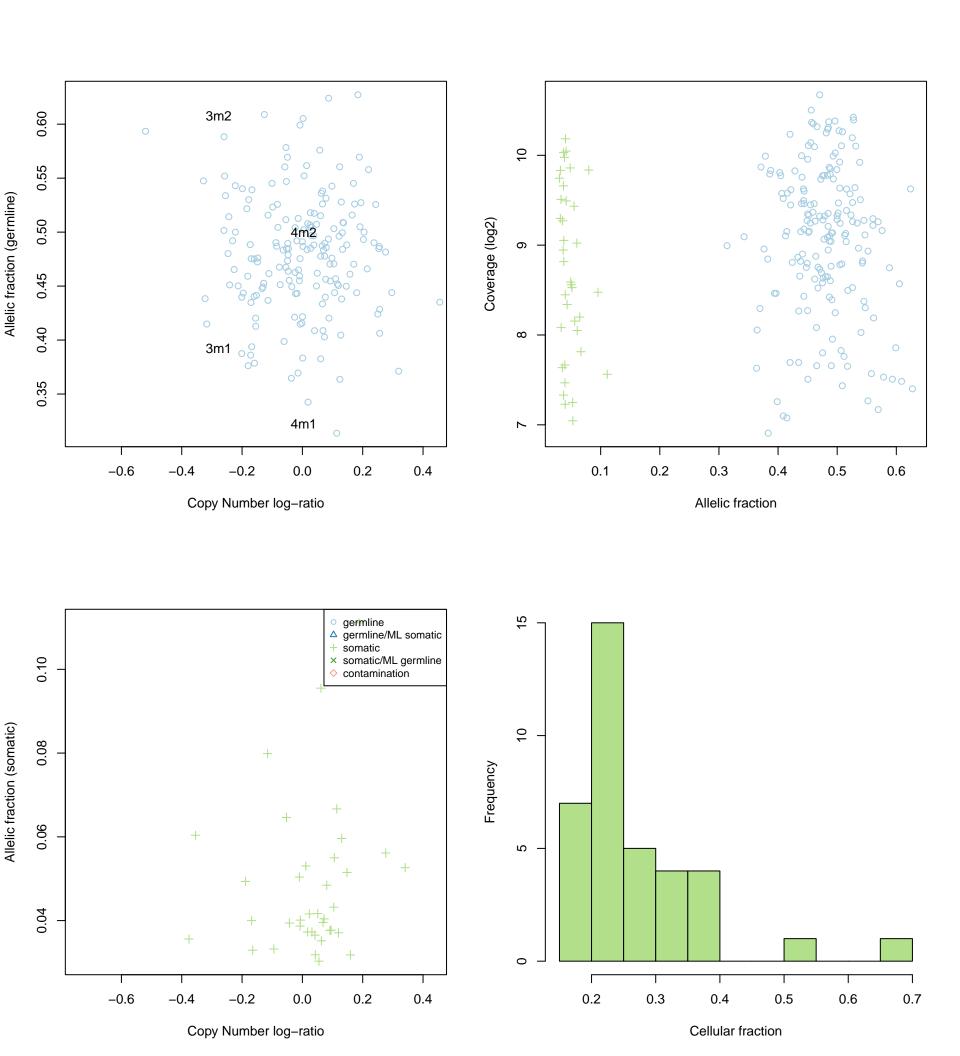
Purity: 0.55 Tumor ploidy: 3.983 Fraction Genome 0.1 0.0 -0.20 -0.15 -0.10 -0.05 0.00 0.05 0.10 log2 ratio



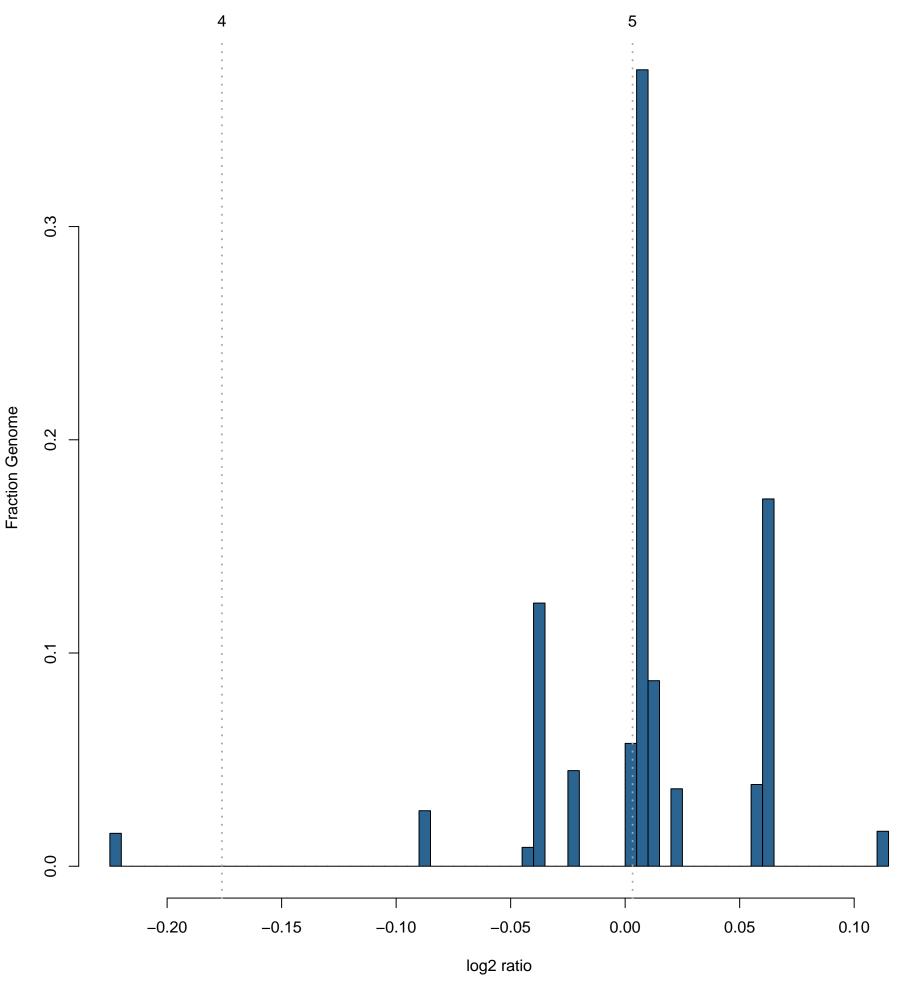
## SCNA-fit log-likelihood: -4496.52

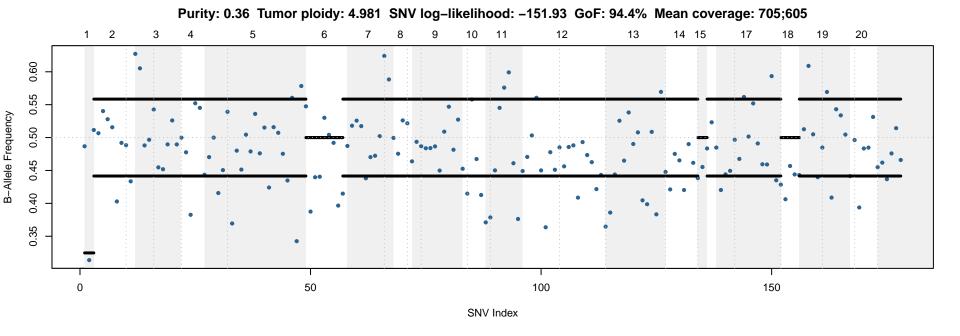




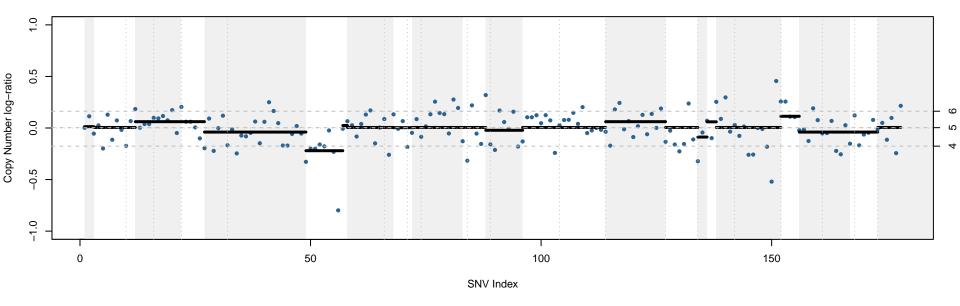


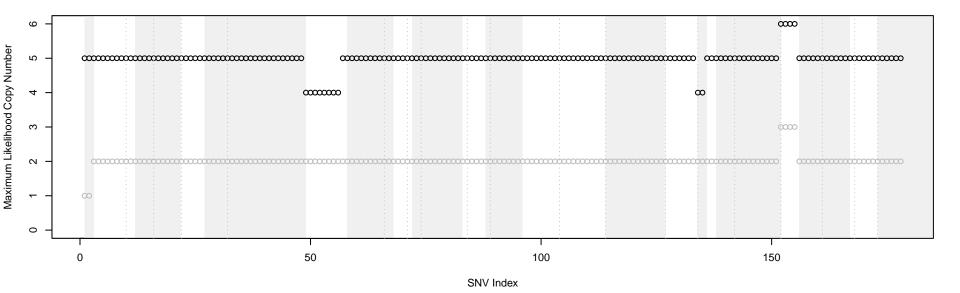
Purity: 0.36 Tumor ploidy: 4.981

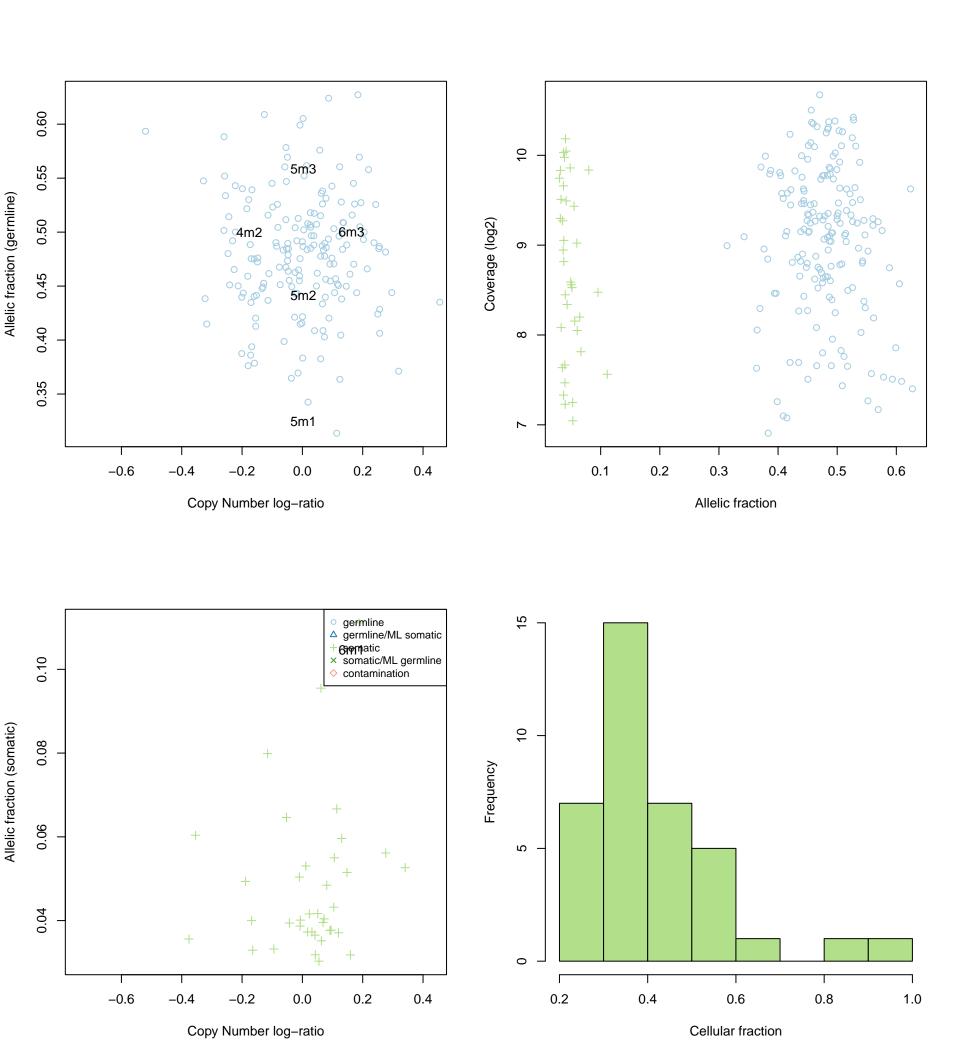




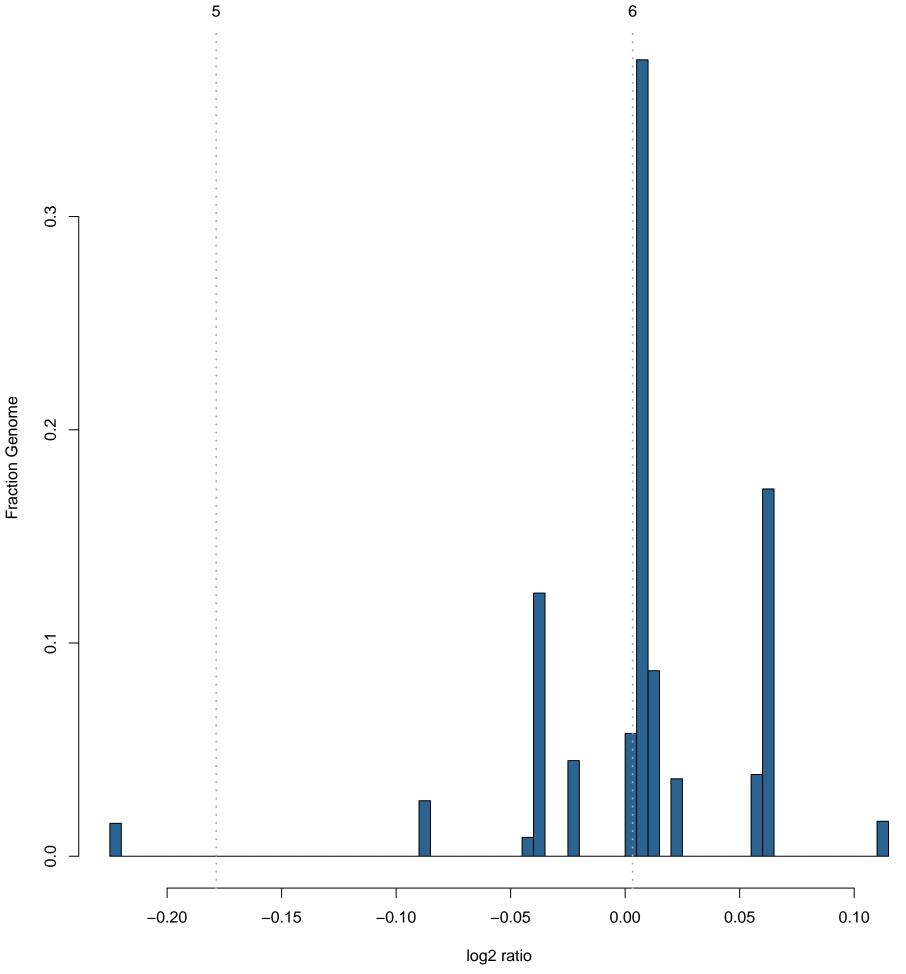
## SCNA-fit log-likelihood: -4486.41

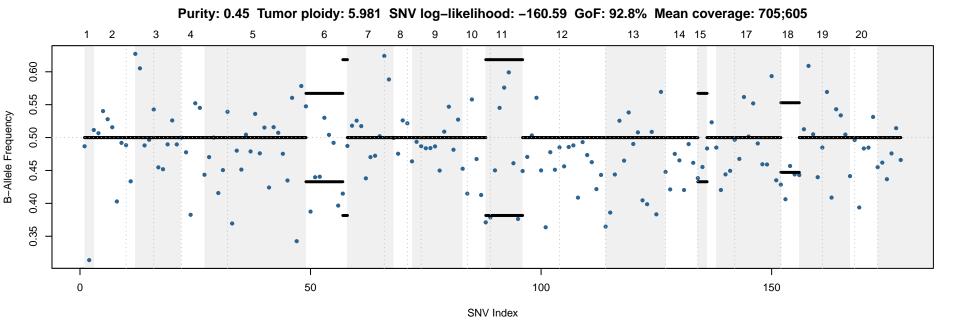




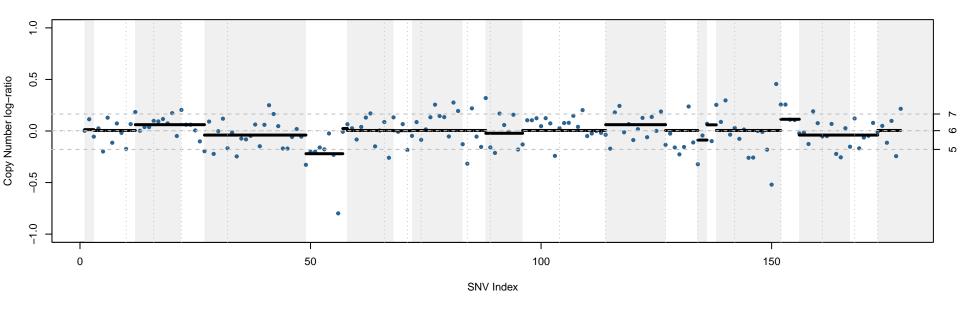


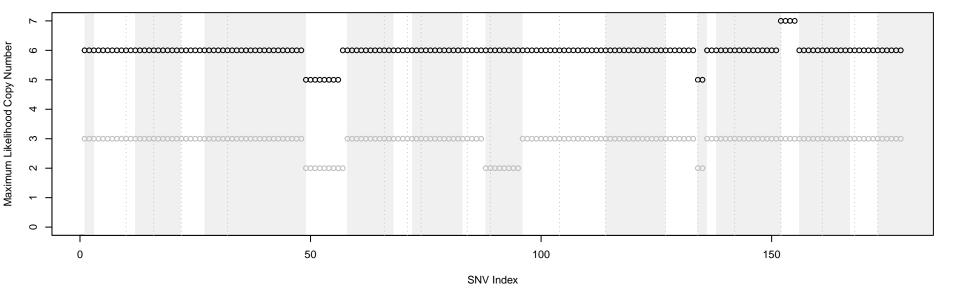
Purity: 0.45 Tumor ploidy: 5.981

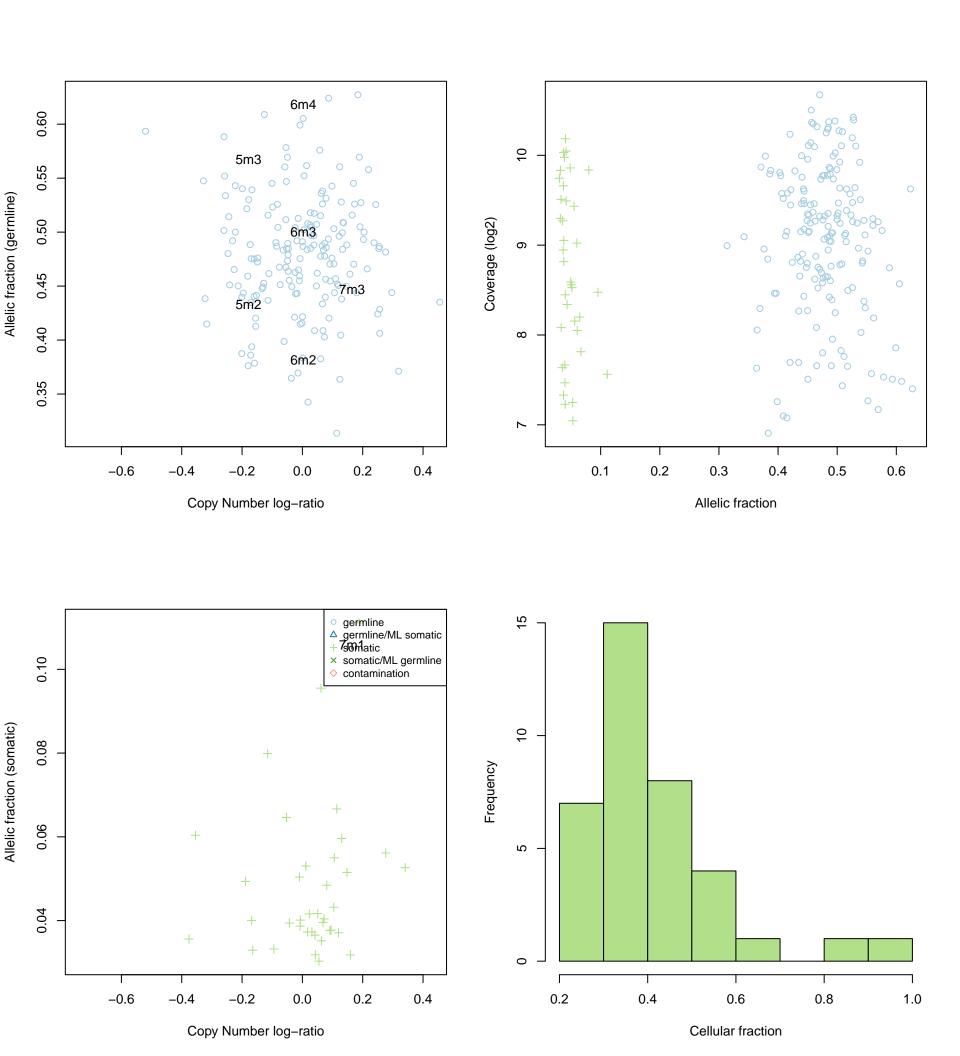




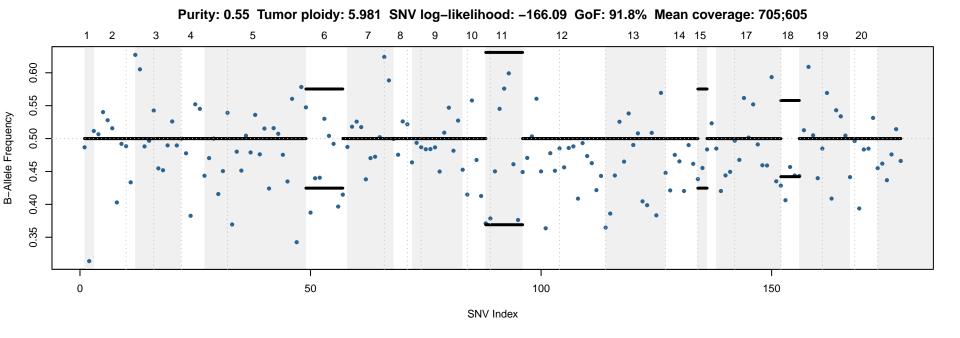
## SCNA-fit log-likelihood: -4486.93



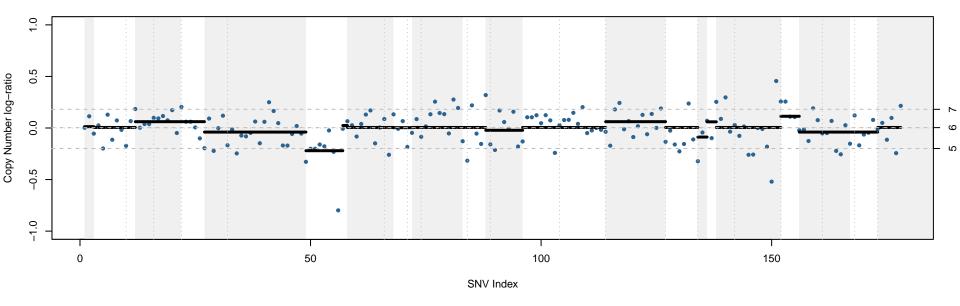


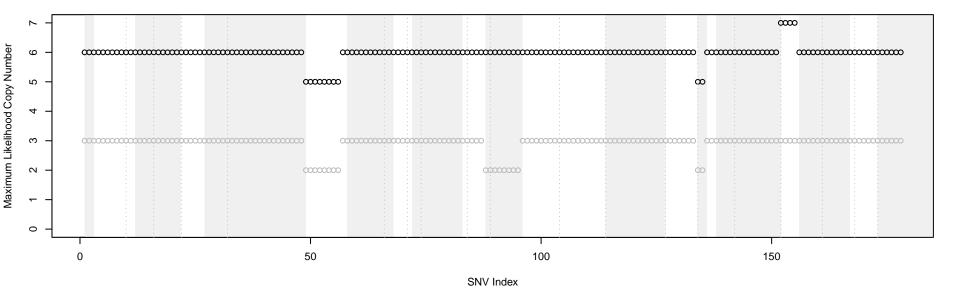


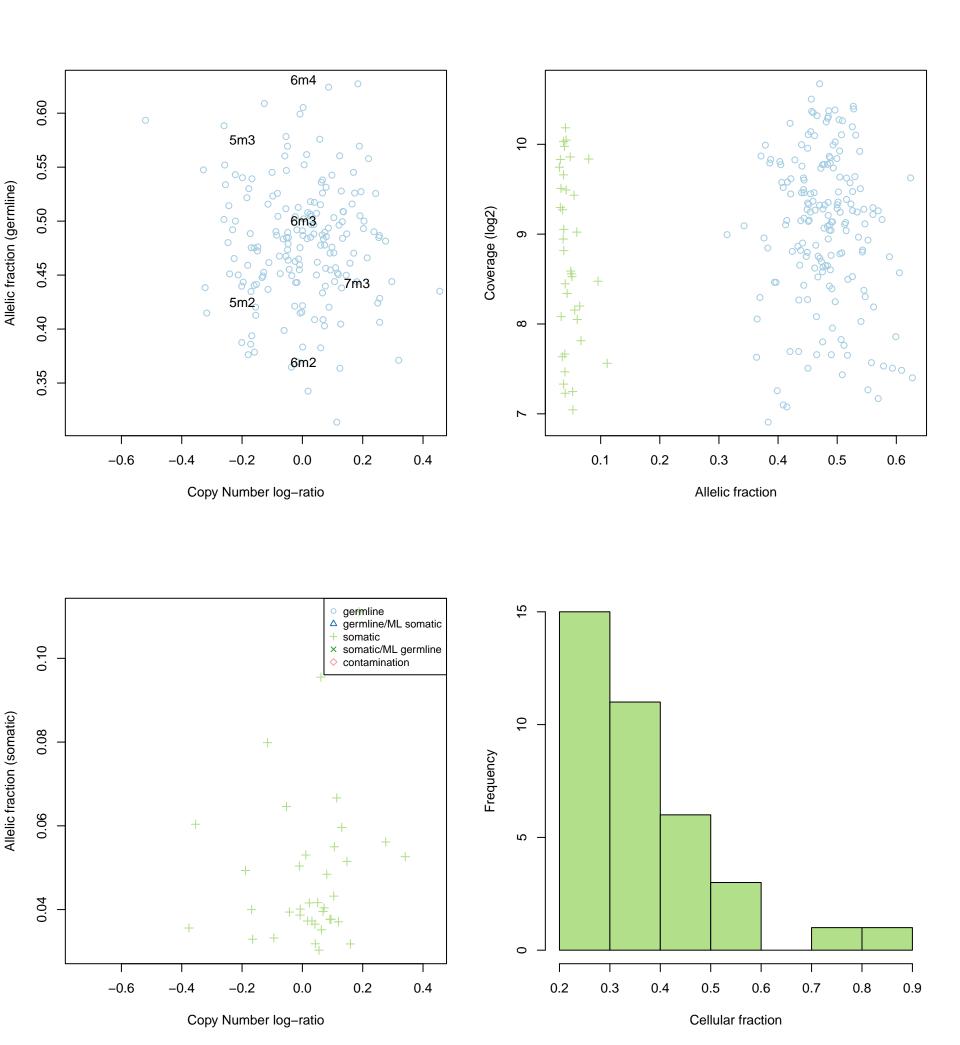
Purity: 0.55 Tumor ploidy: 5.981 6 5 Fraction Genome 0.2 0.1 0.0 -0.20 -0.15 -0.10 -0.05 0.00 0.05 0.10 log2 ratio



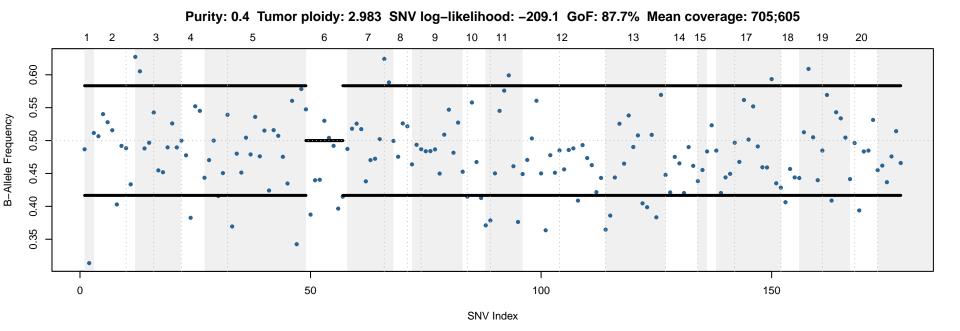
## SCNA-fit log-likelihood: -4492.5



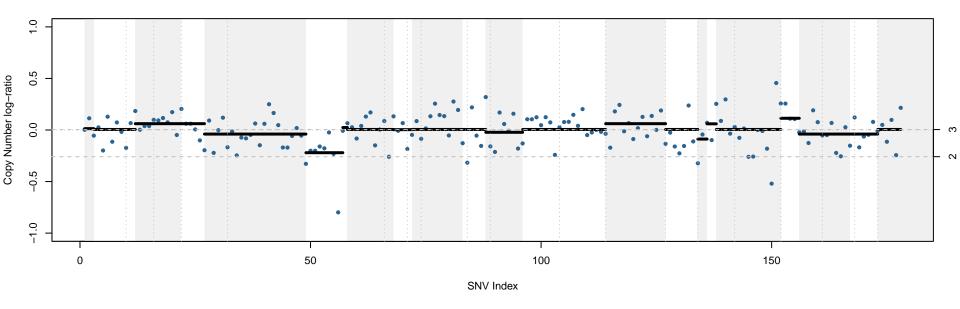


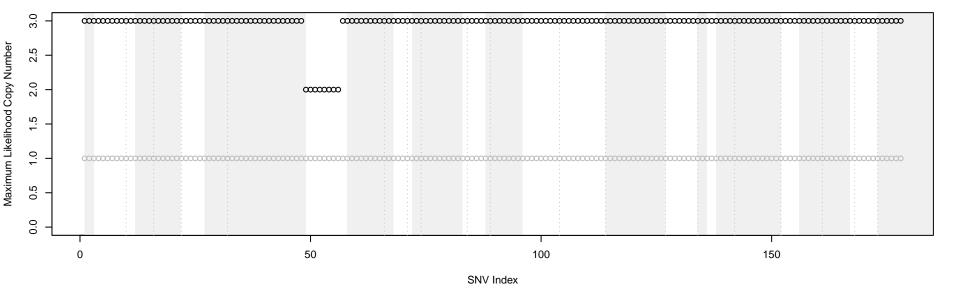


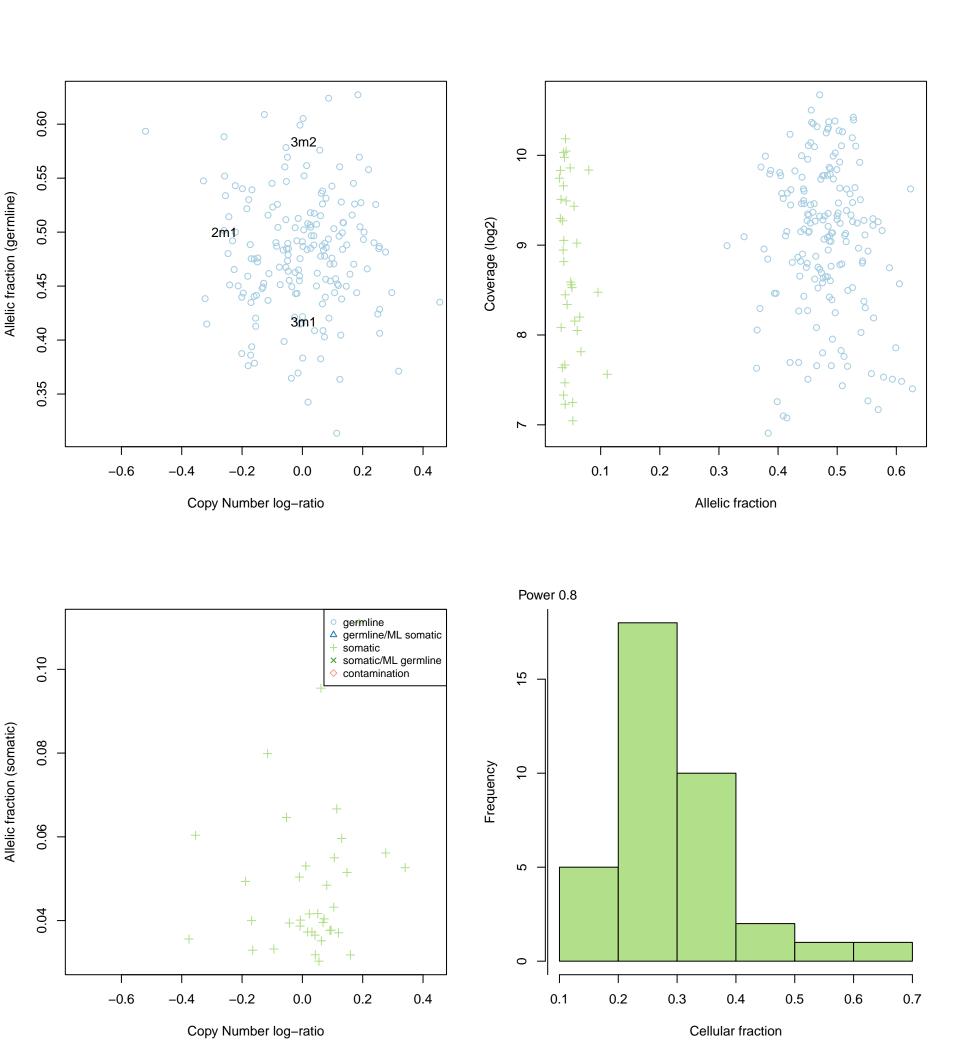
Purity: 0.4 Tumor ploidy: 2.983 3 Fraction Genome 0.2 0.1 0.0 -0.20 -0.15 -0.10 -0.05 0.00 0.05 0.10 log2 ratio

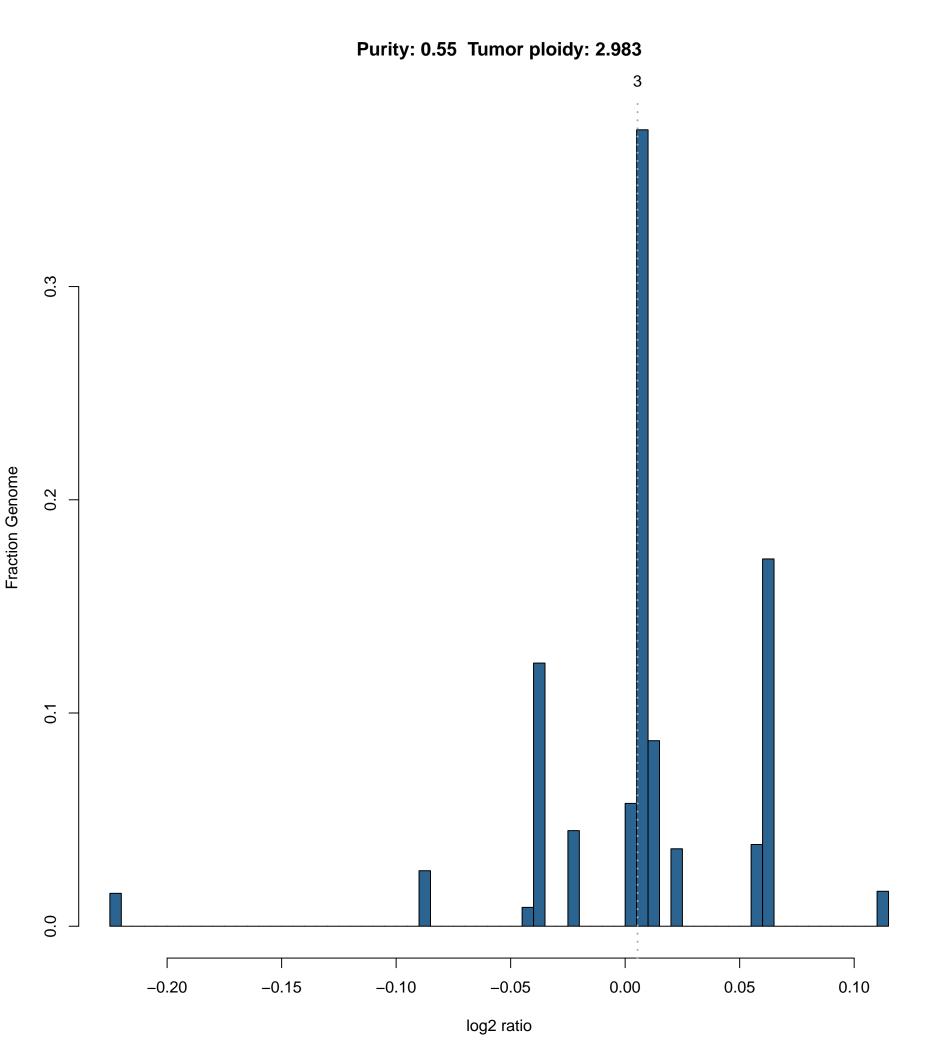


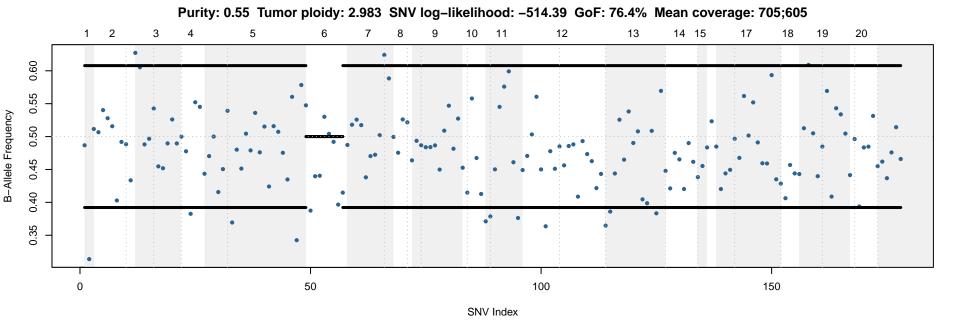
## SCNA-fit log-likelihood: -4495.33











## SCNA-fit log-likelihood: -4505.94

