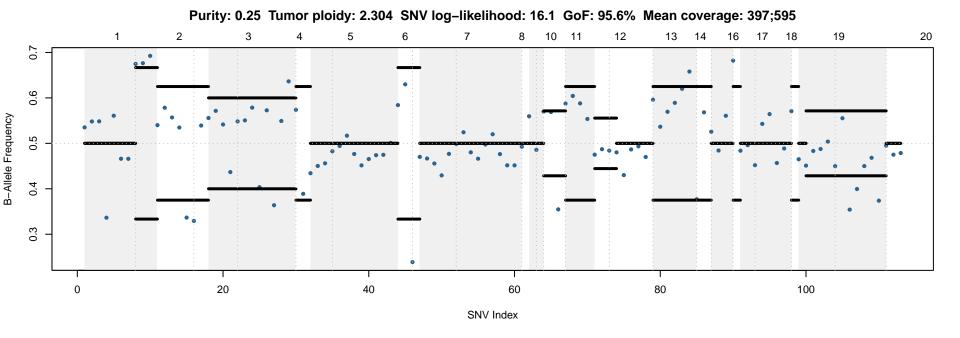
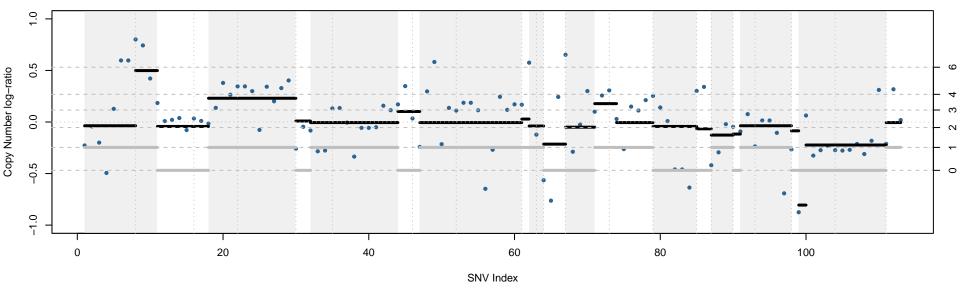
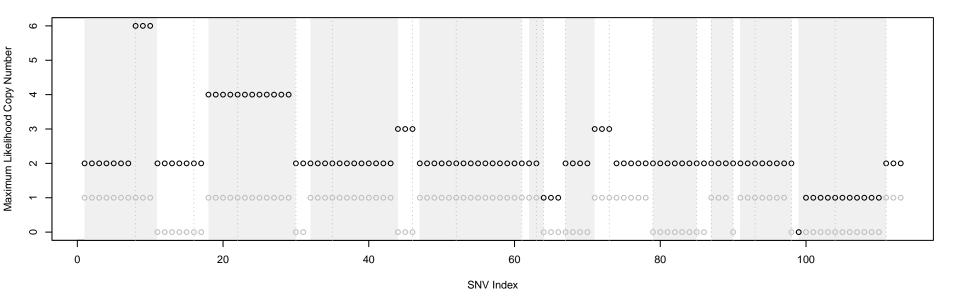
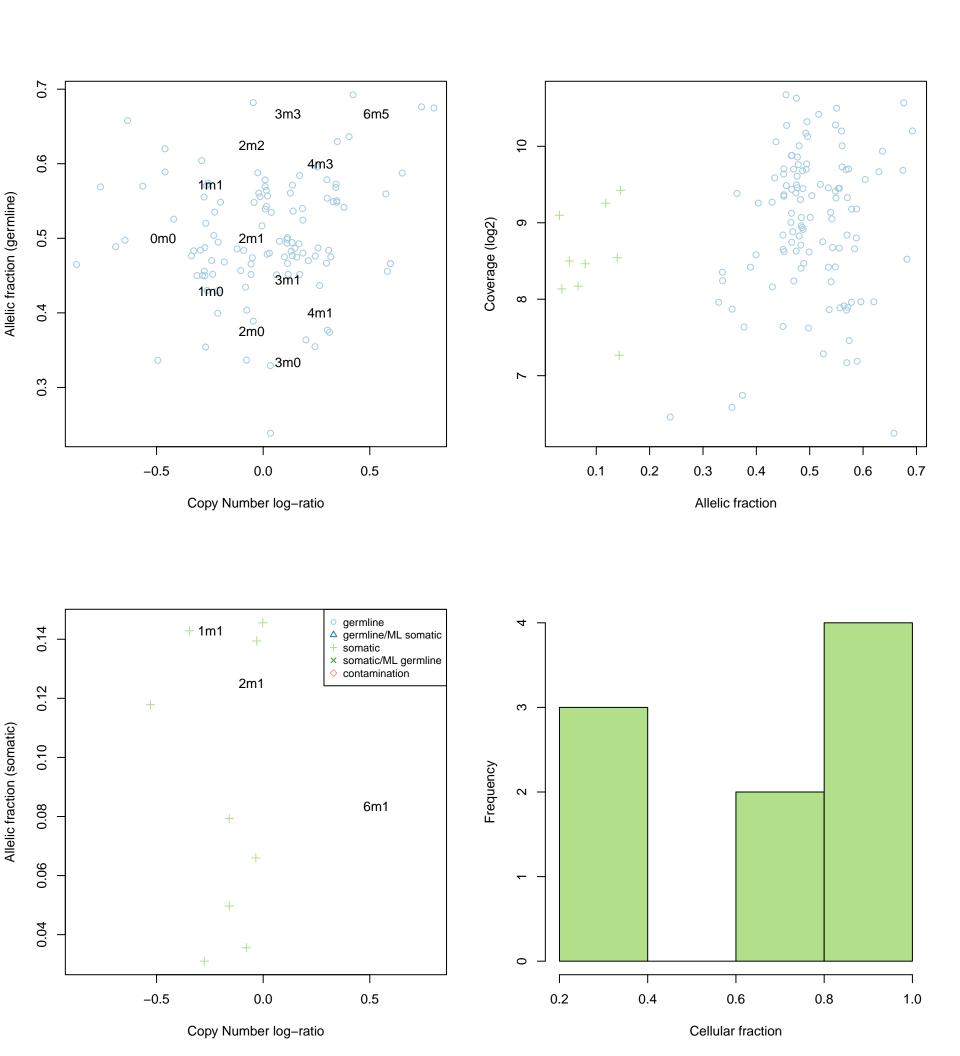
Purity: 0.25 Tumor ploidy: 2.304 2 3 6 Fraction Genome 0.05 0.00 -0.8 -0.6 -0.4 -0.2 0.0 0.2 0.4 log2 ratio



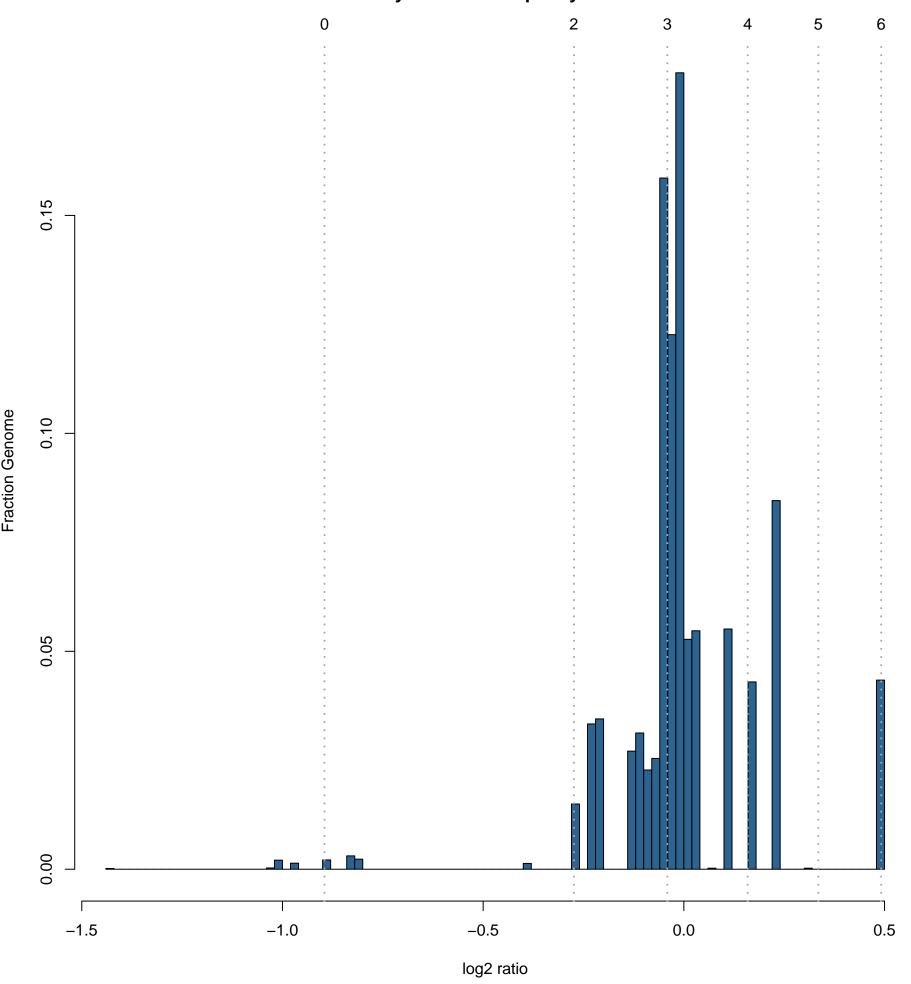
SCNA-fit log-likelihood: -12119.2

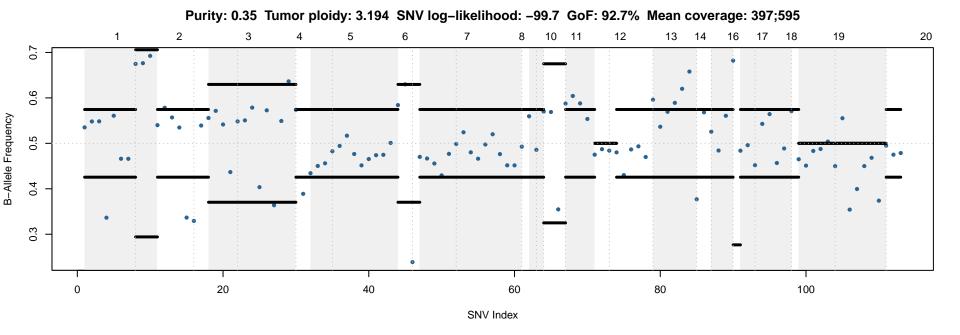




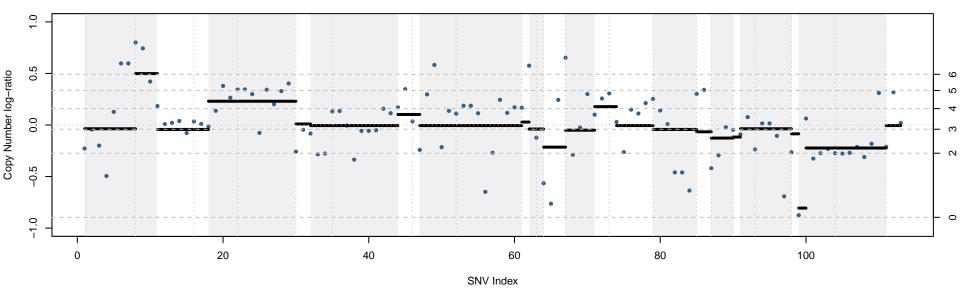


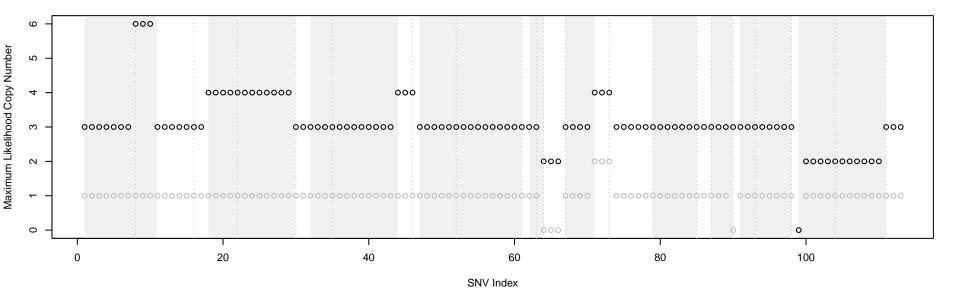
Purity: 0.35 Tumor ploidy: 3.194

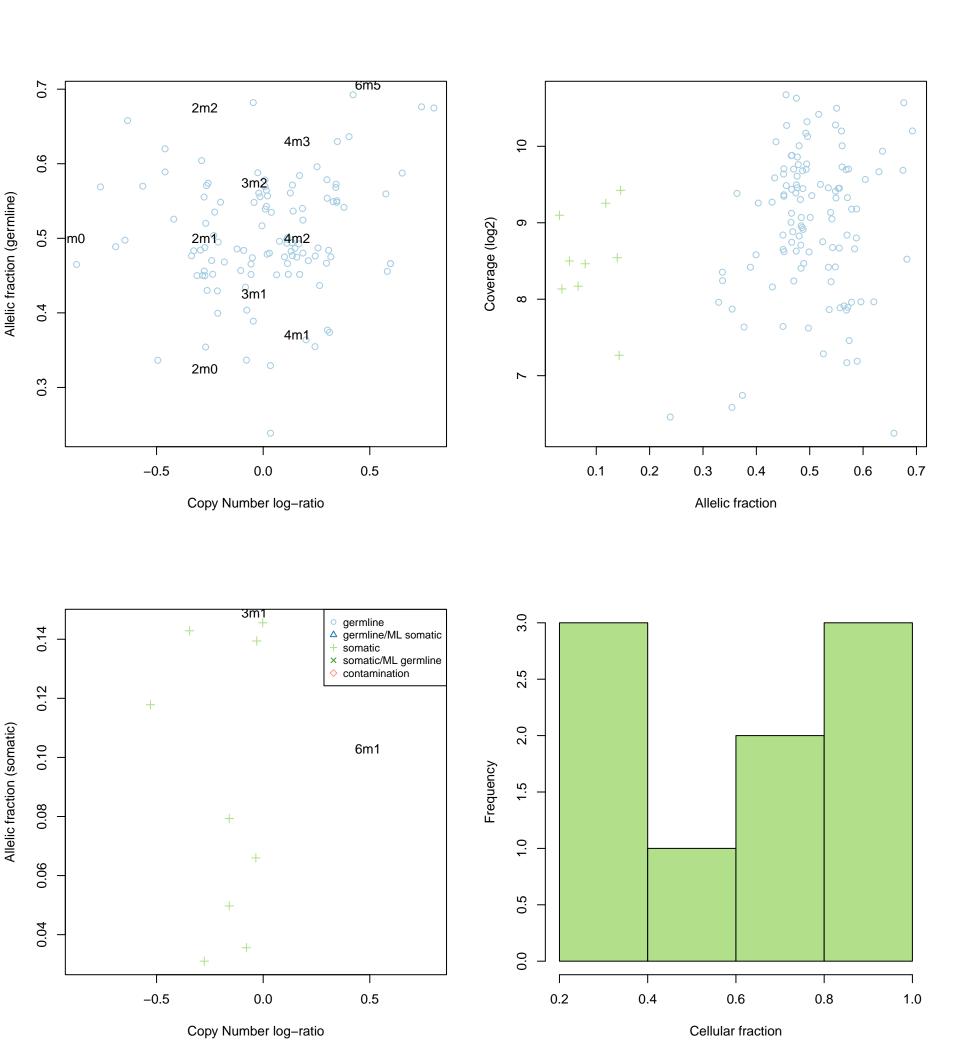




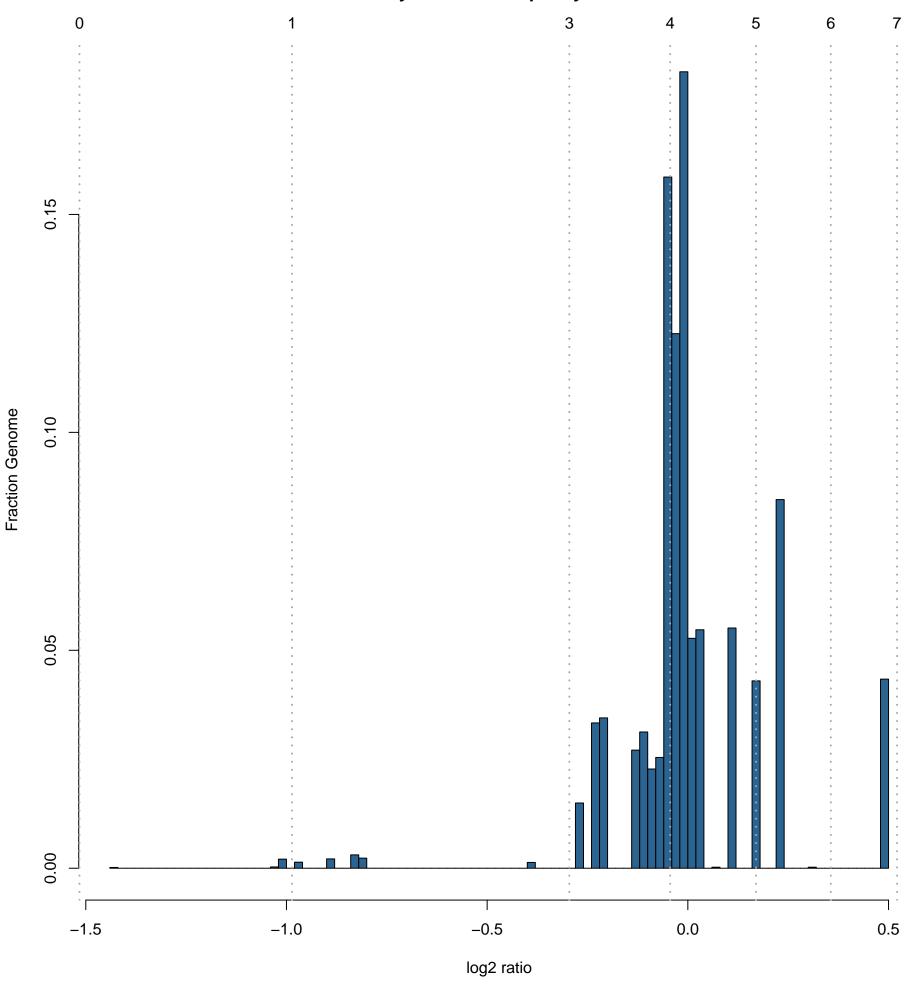
SCNA-fit log-likelihood: -12048.14

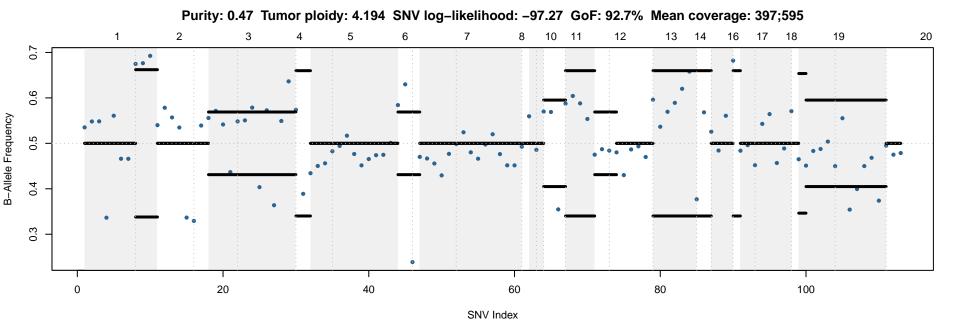




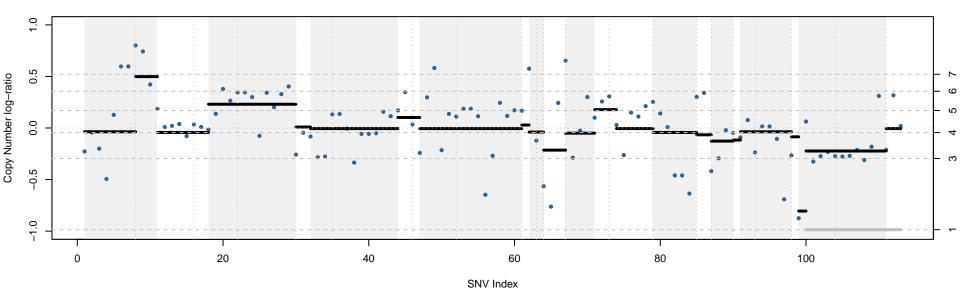


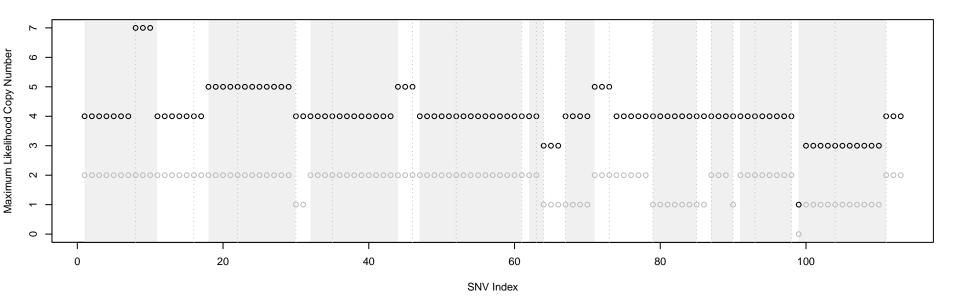
Purity: 0.47 Tumor ploidy: 4.194

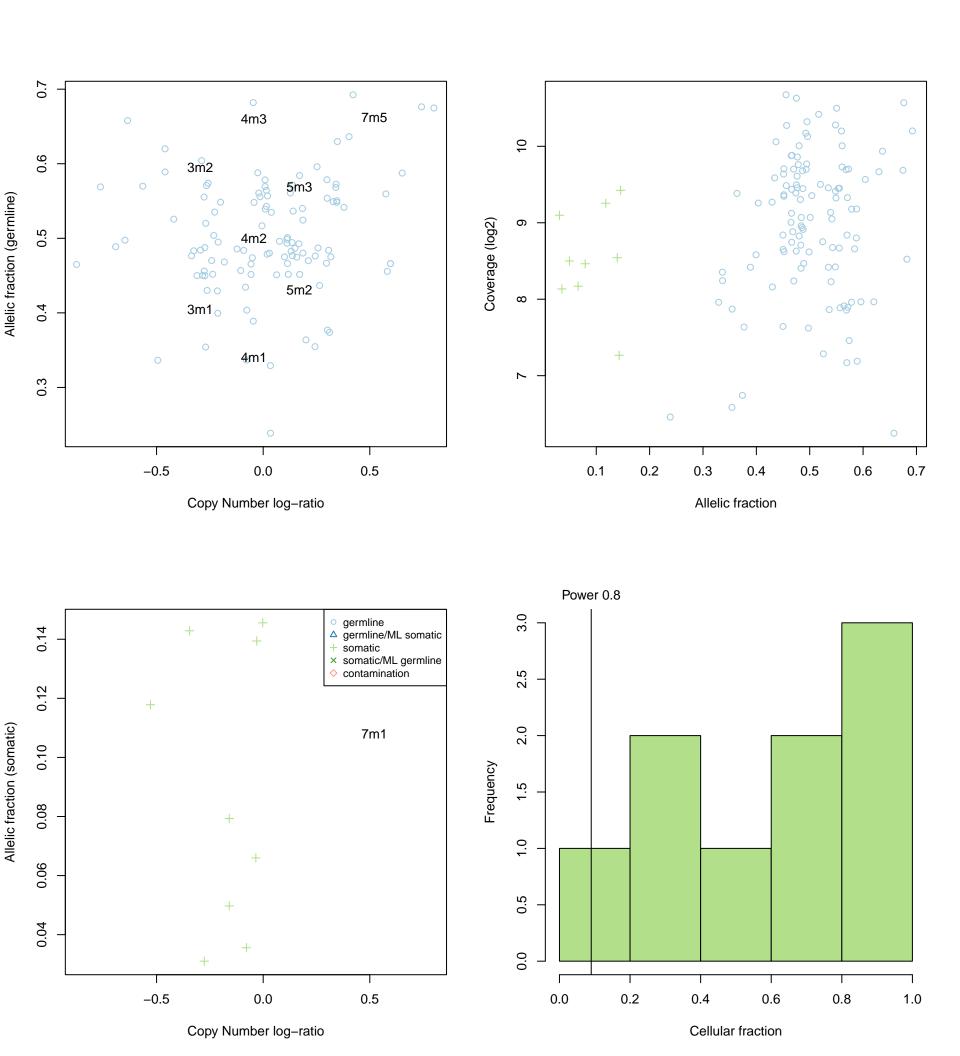




SCNA-fit log-likelihood: -12055.73

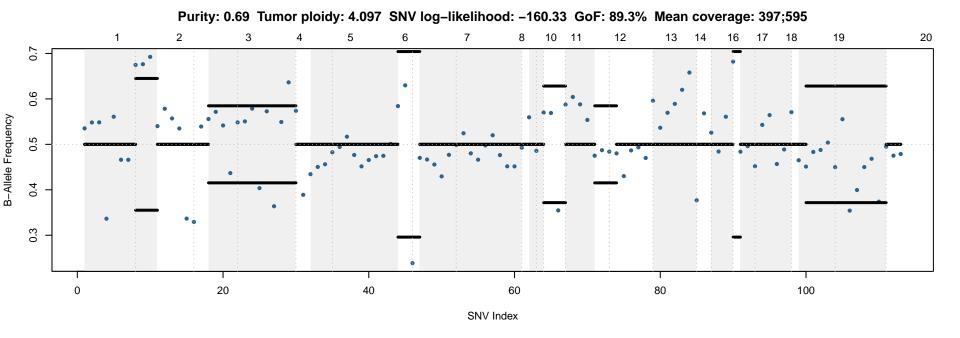




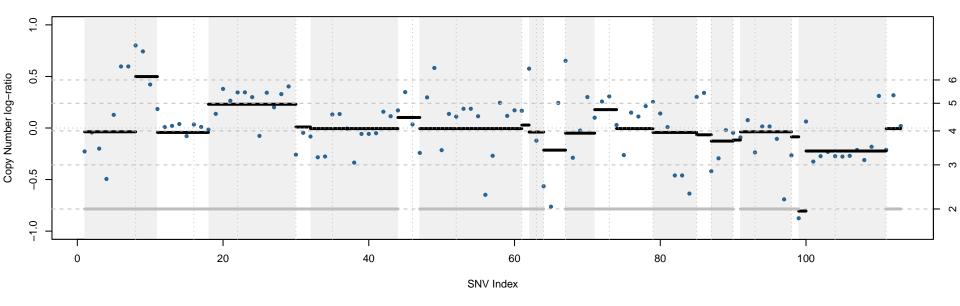


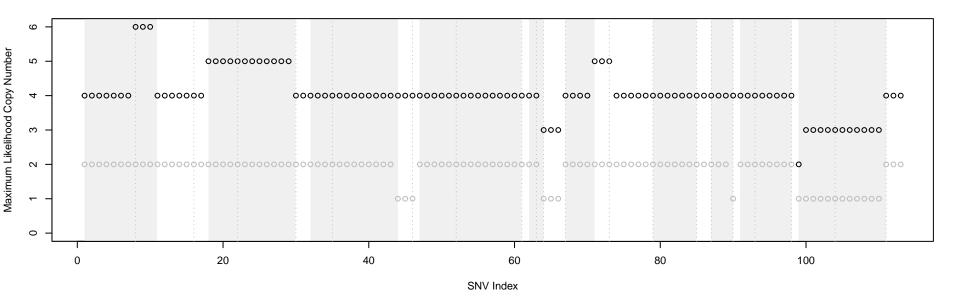
Purity: 0.69 Tumor ploidy: 4.097 5 6 Fraction Genome 0.00 -1.5 -1.0 -0.5 0.0 0.5

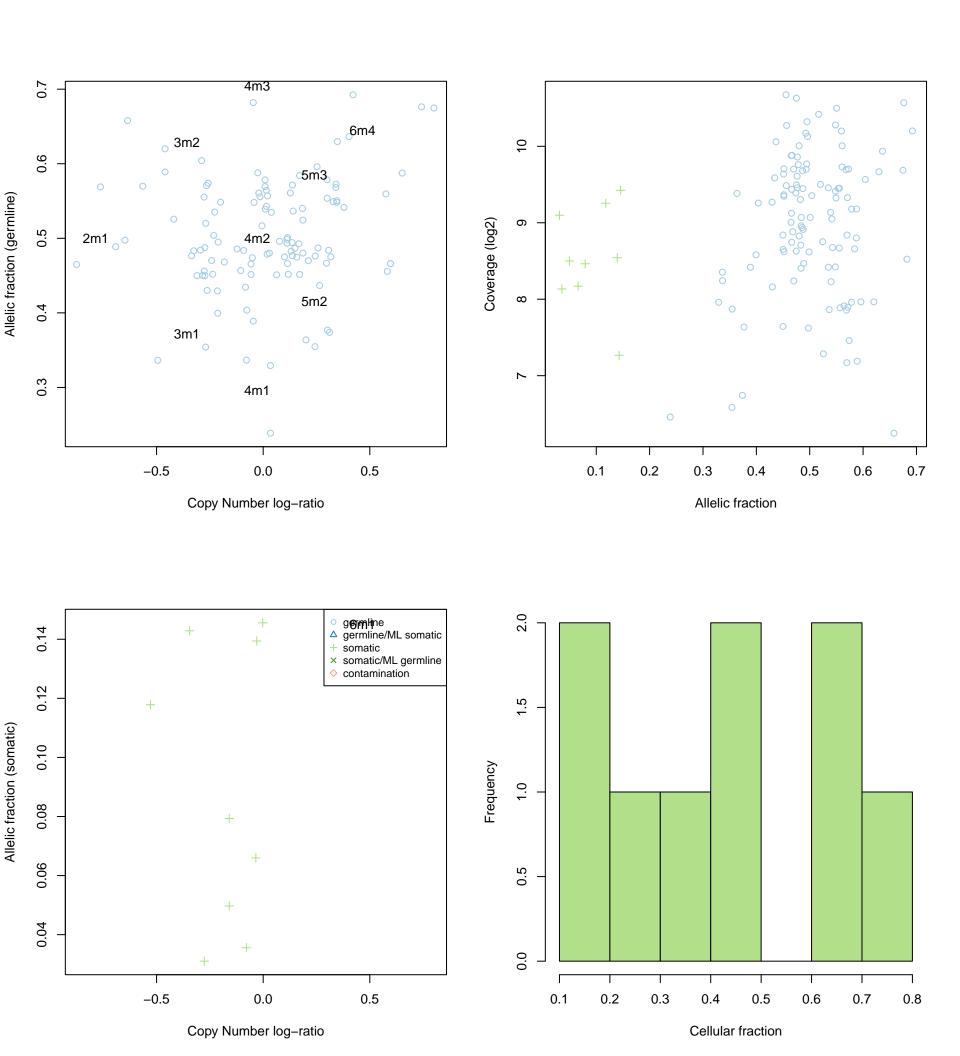
log2 ratio

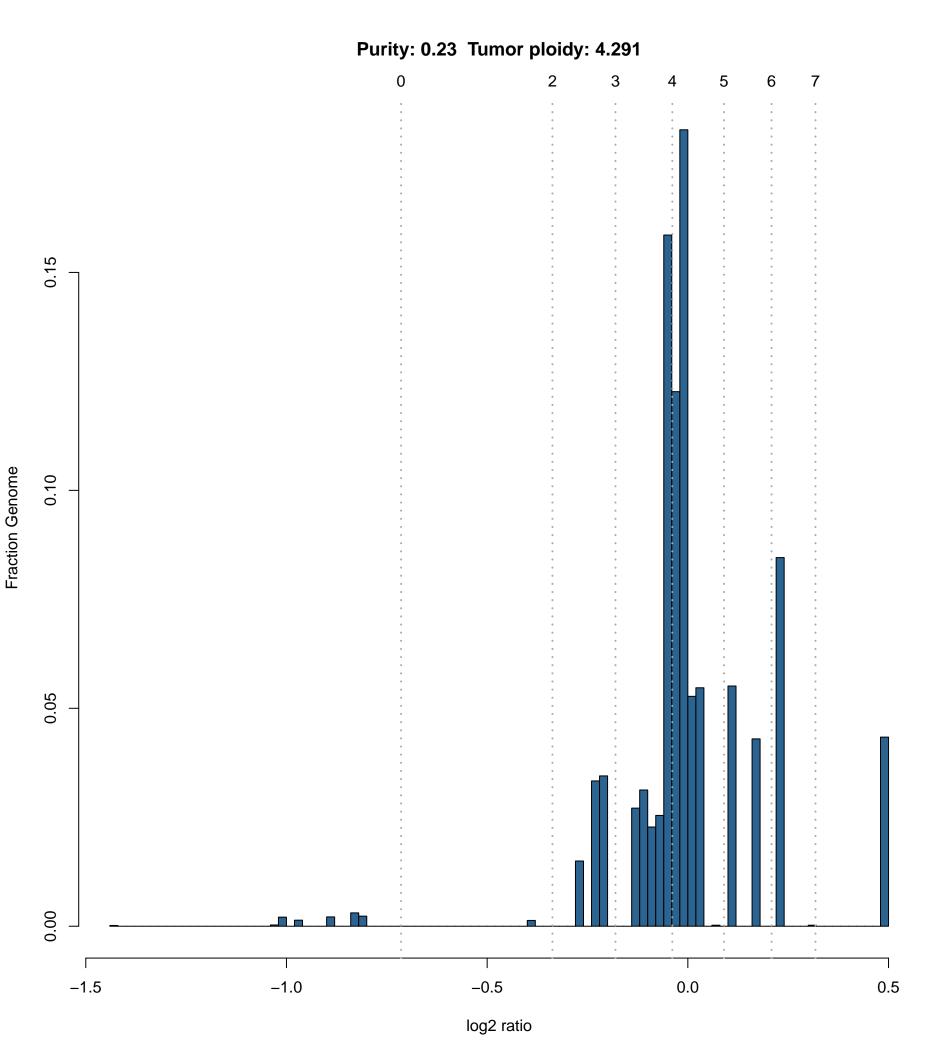


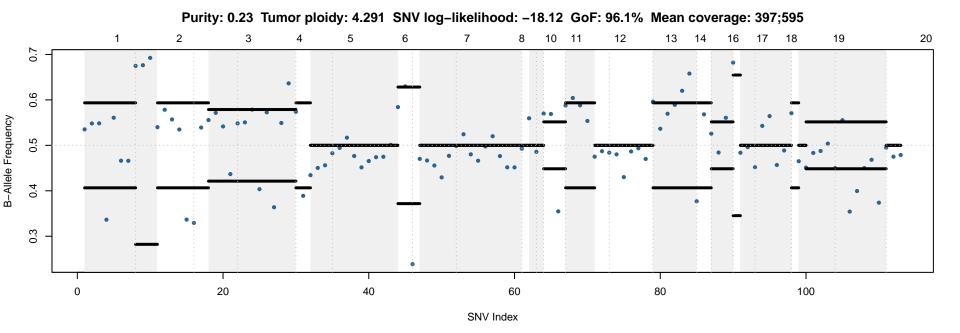
SCNA-fit log-likelihood: -12110.79



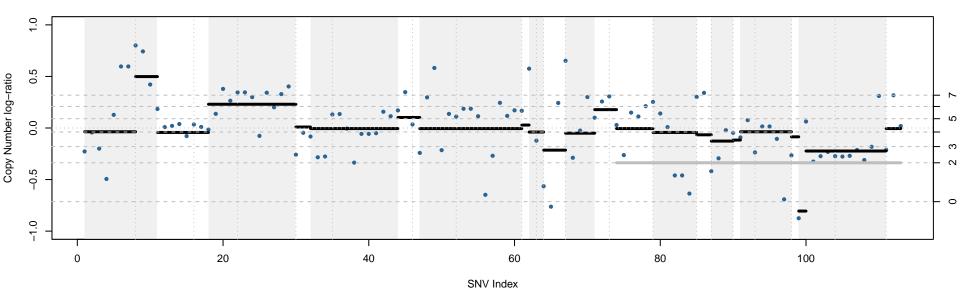


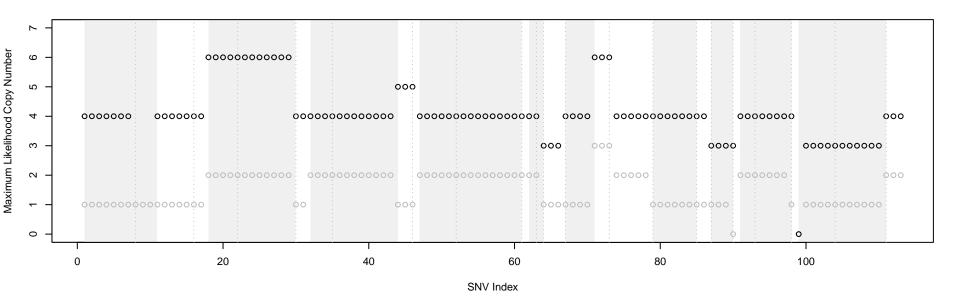


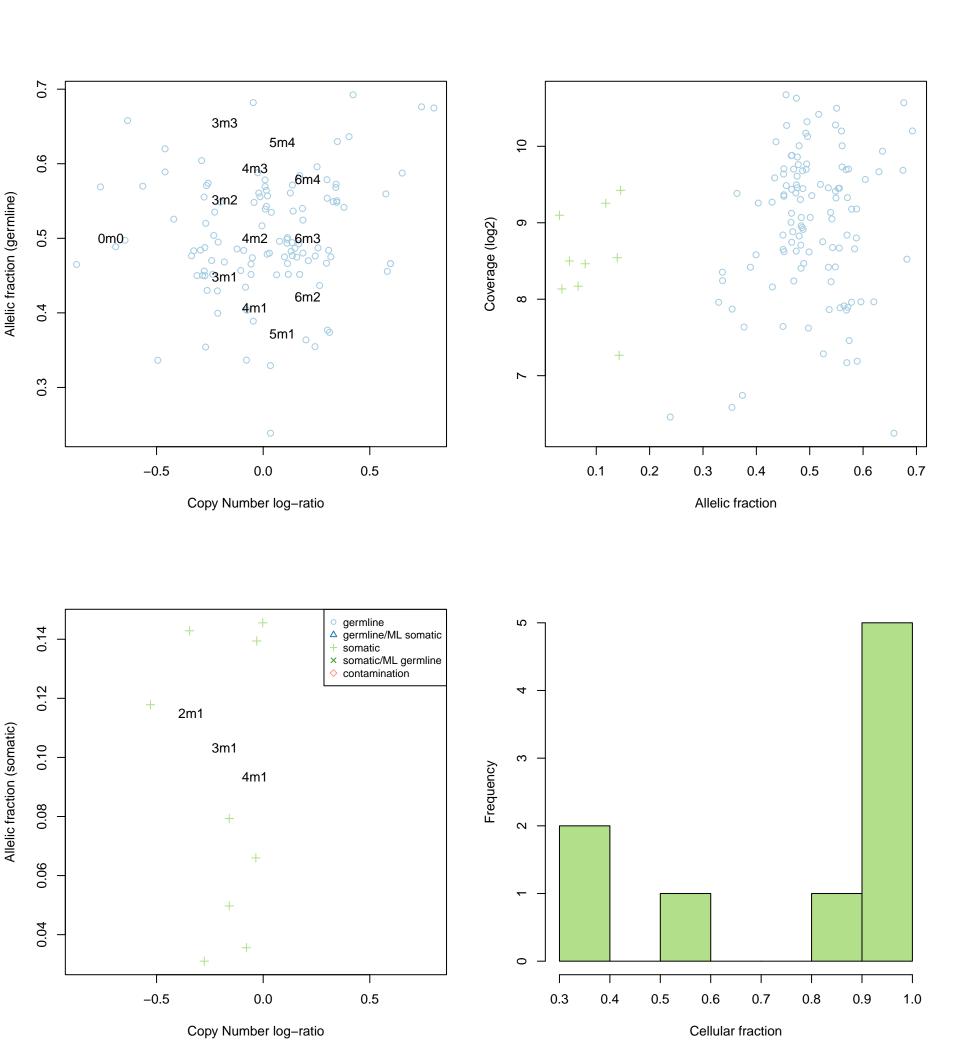




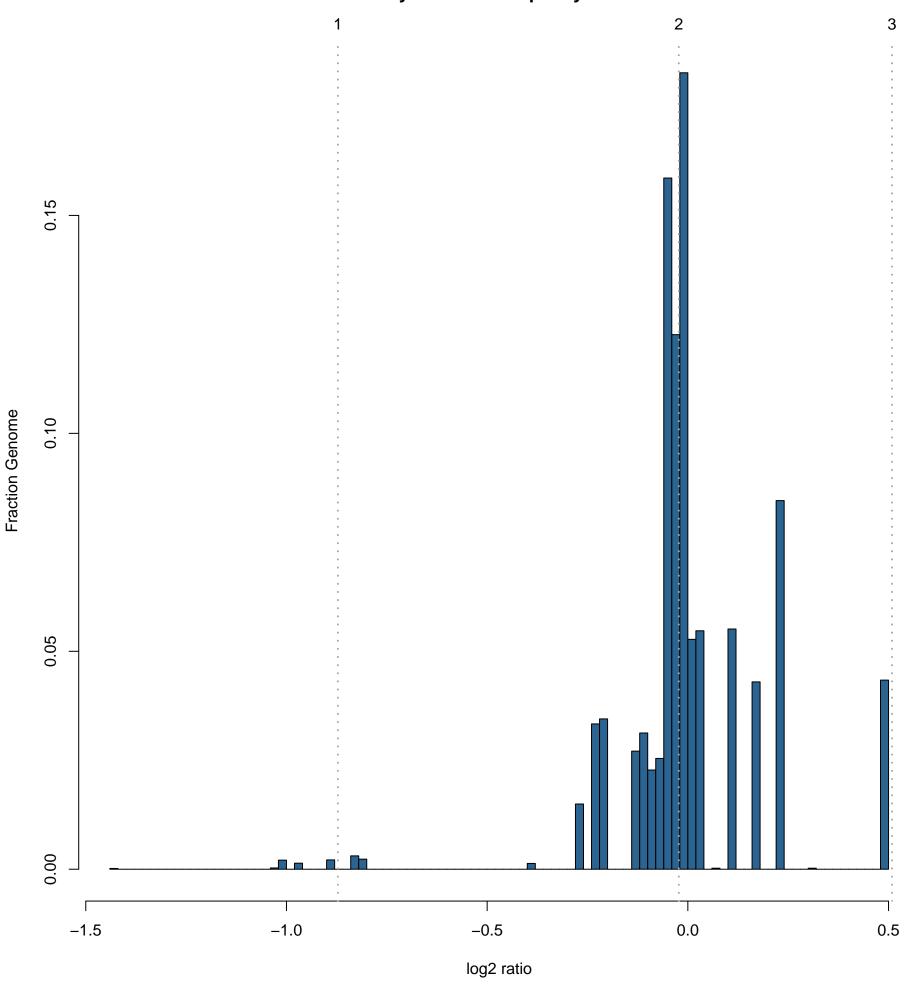
SCNA-fit log-likelihood: -12597.76

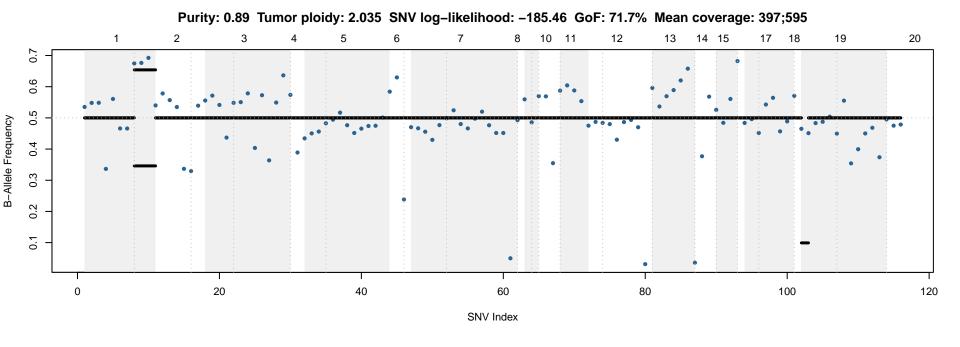




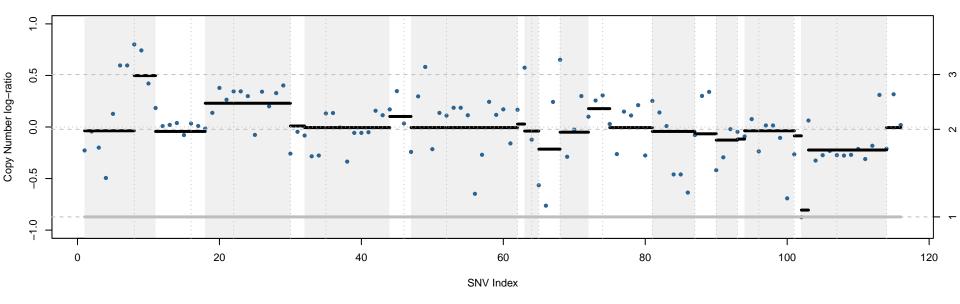


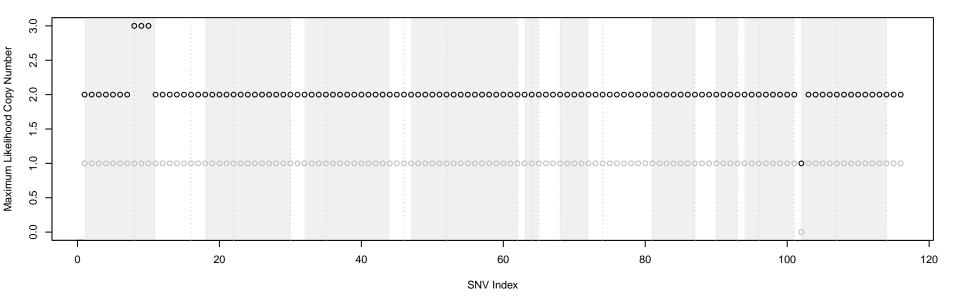
Purity: 0.89 Tumor ploidy: 2.035

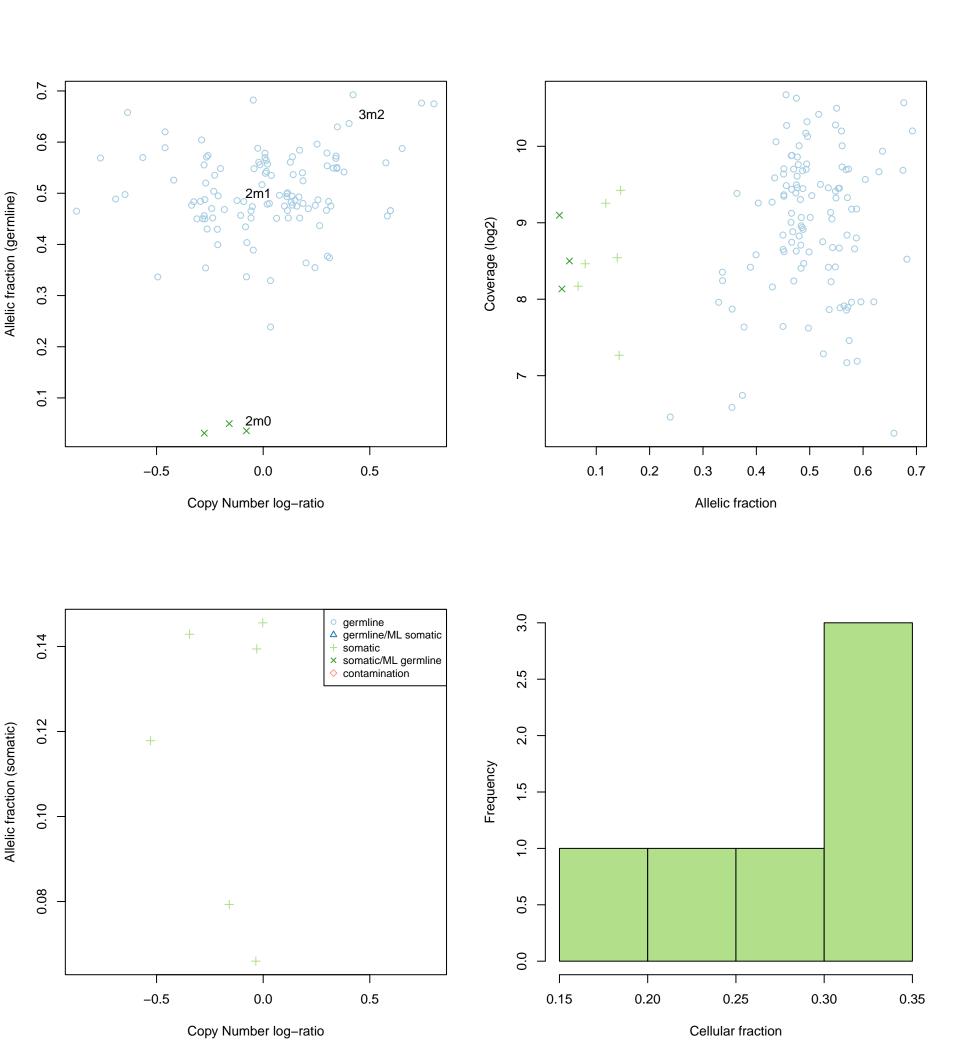




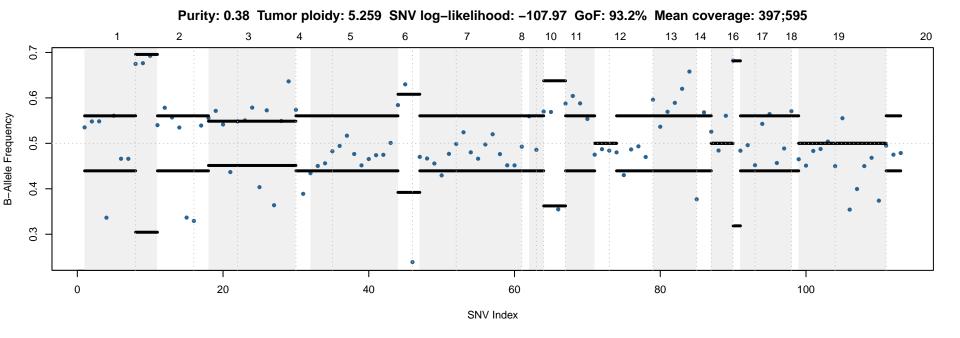
SCNA-fit log-likelihood: -12430.55



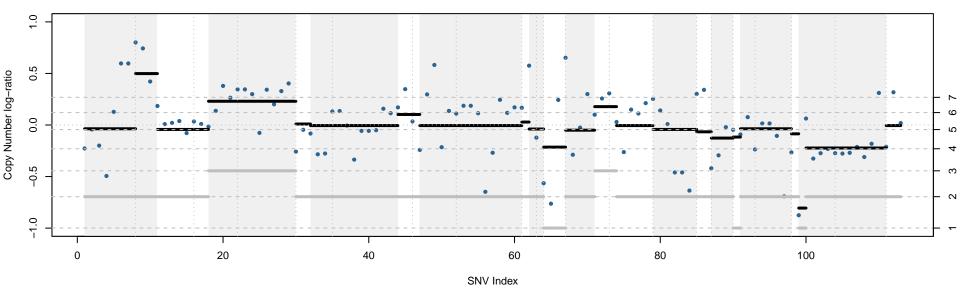


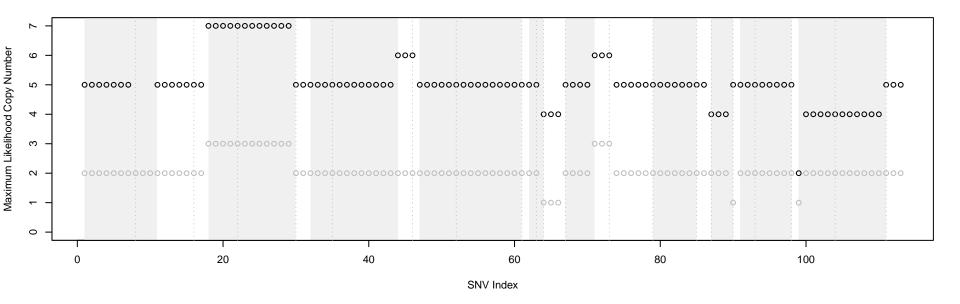


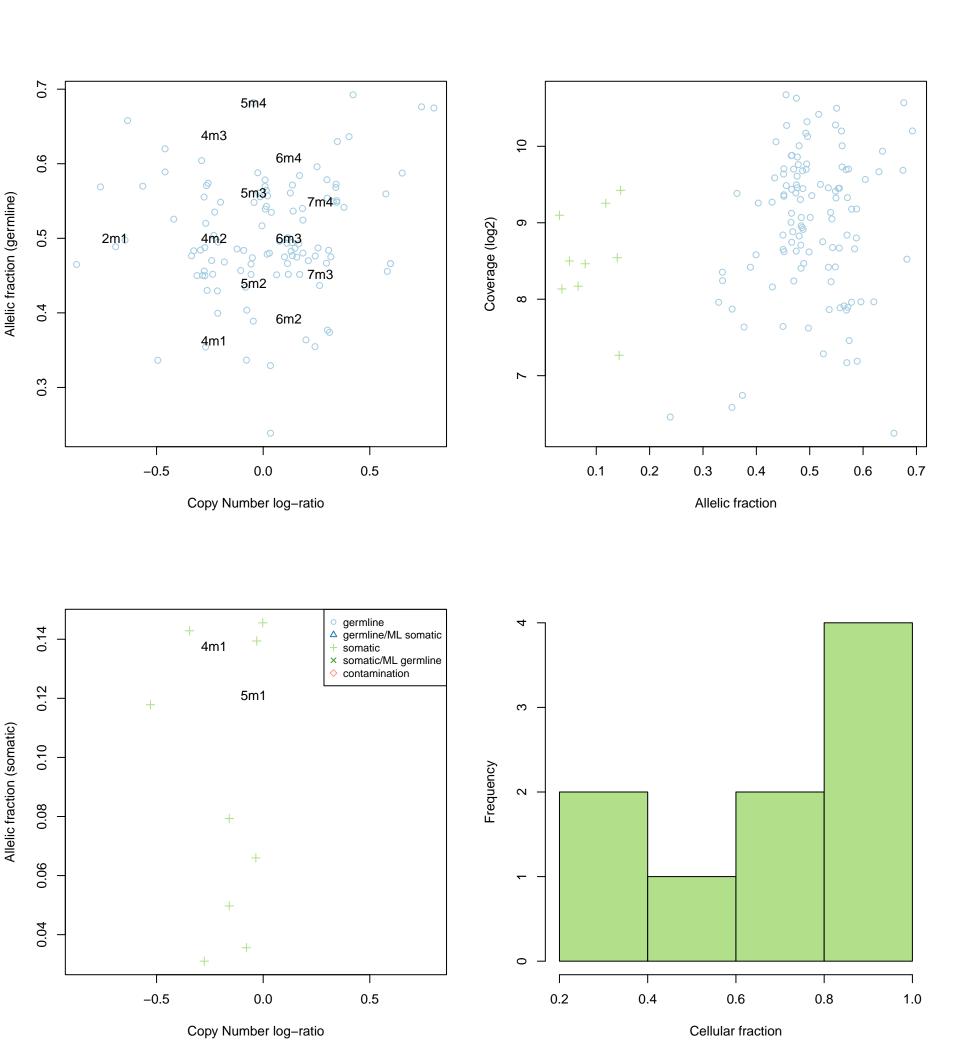
Purity: 0.38 Tumor ploidy: 5.259 3 0 5 6 Fraction Genome 0.05 0.00 -1.0 -1.5 -0.5 0.0 0.5 log2 ratio



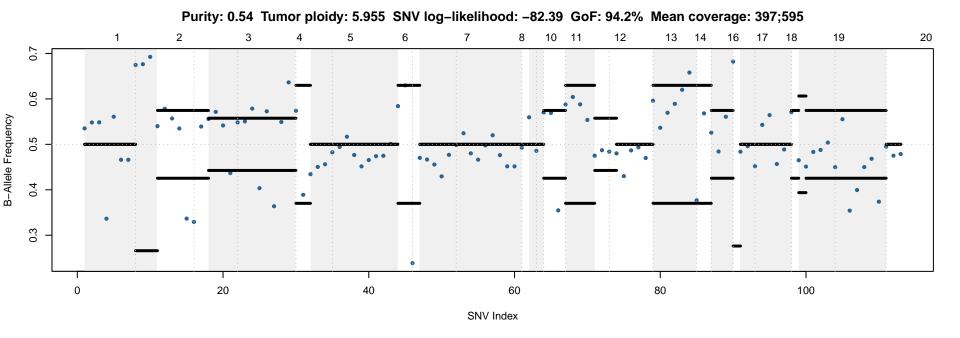
SCNA-fit log-likelihood: -12598.42



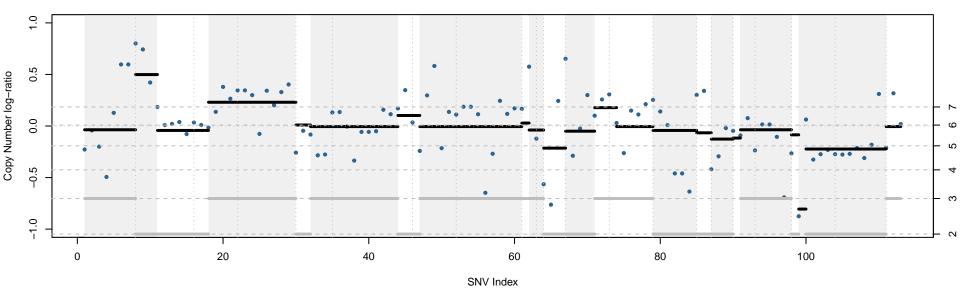


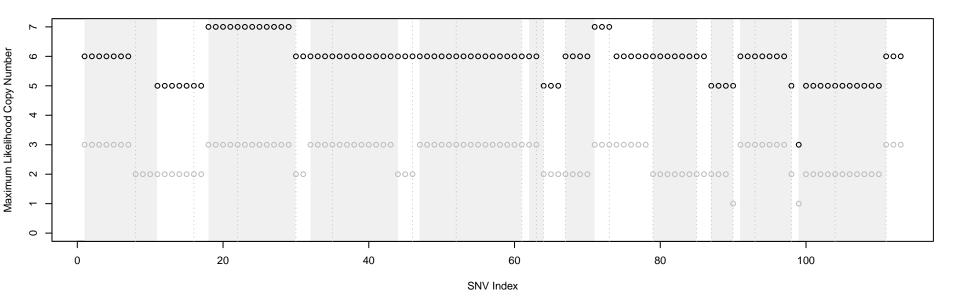


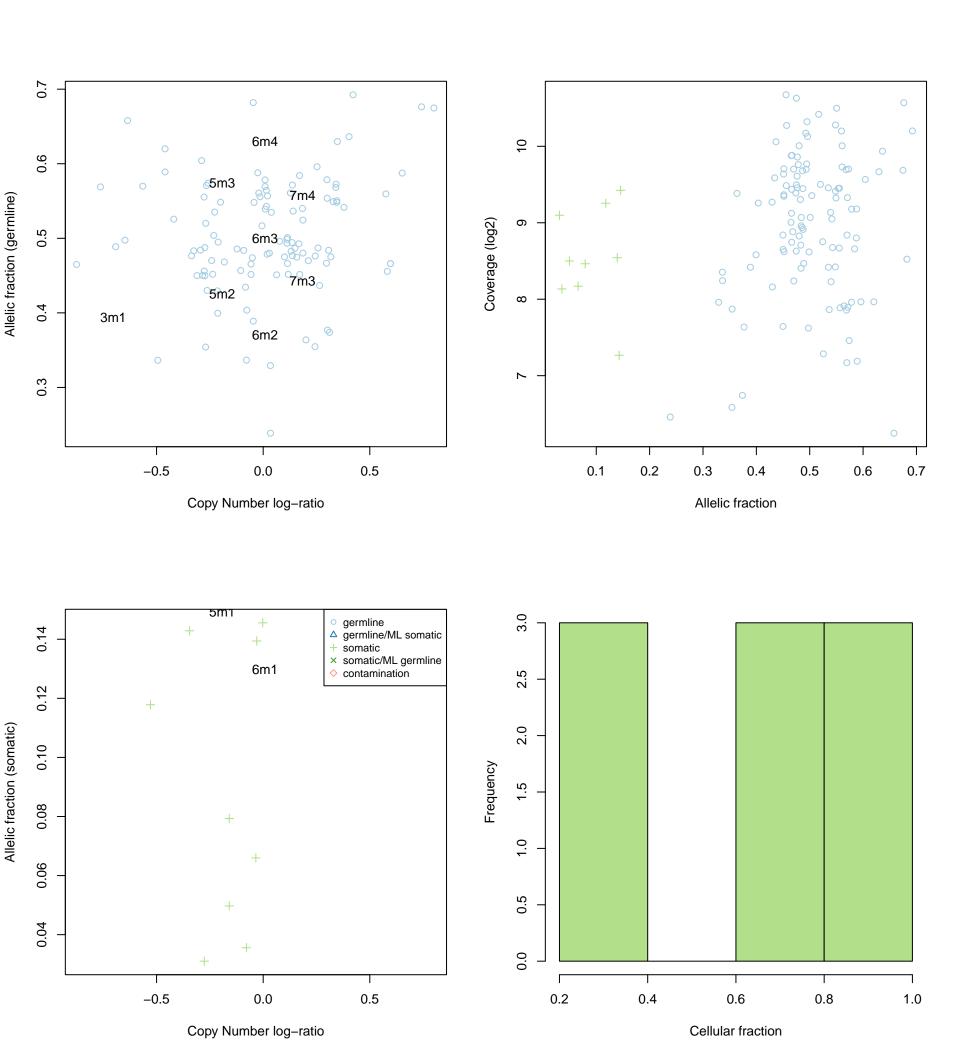
Purity: 0.54 Tumor ploidy: 5.955 2 5 7 Fraction Genome 0.10 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio



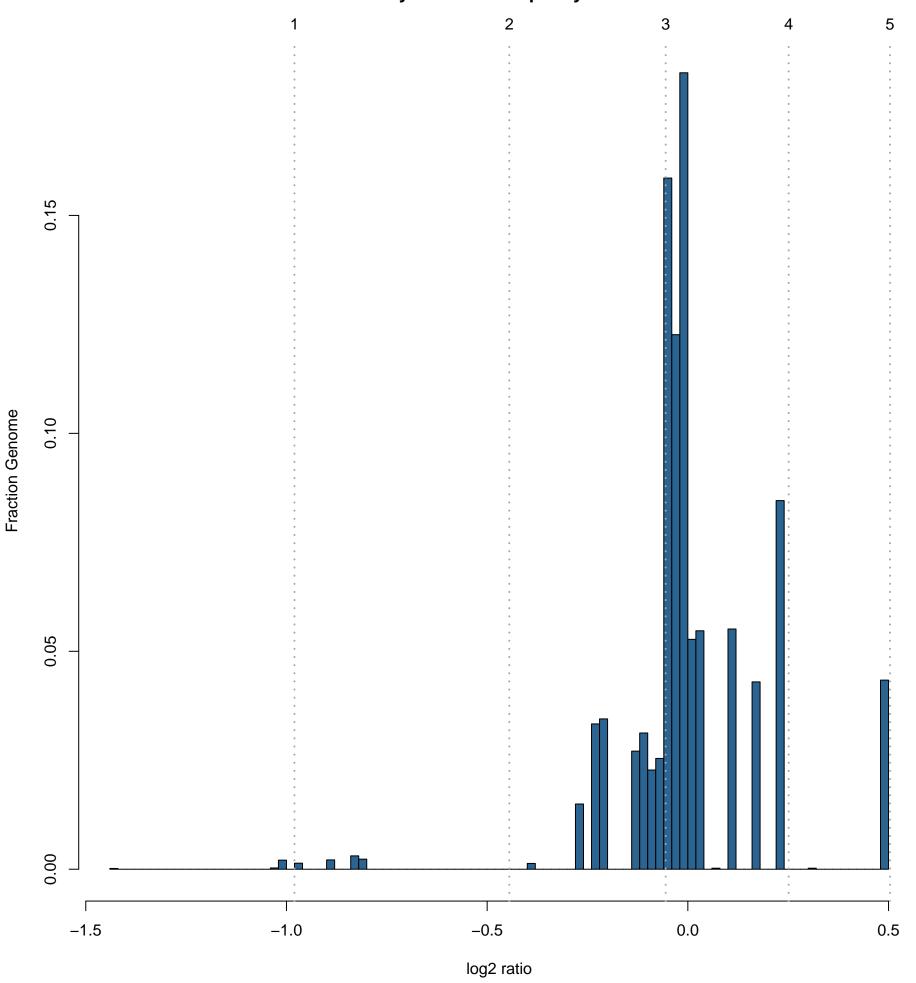
SCNA-fit log-likelihood: -12688.83

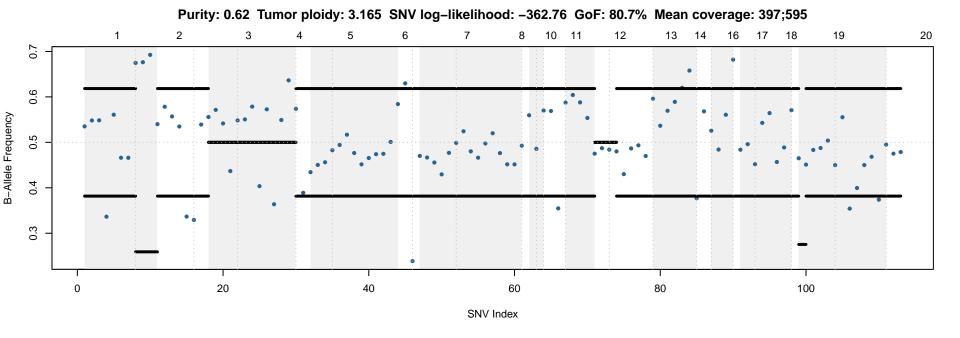






Purity: 0.62 Tumor ploidy: 3.165





SCNA-fit log-likelihood: -12172.35

