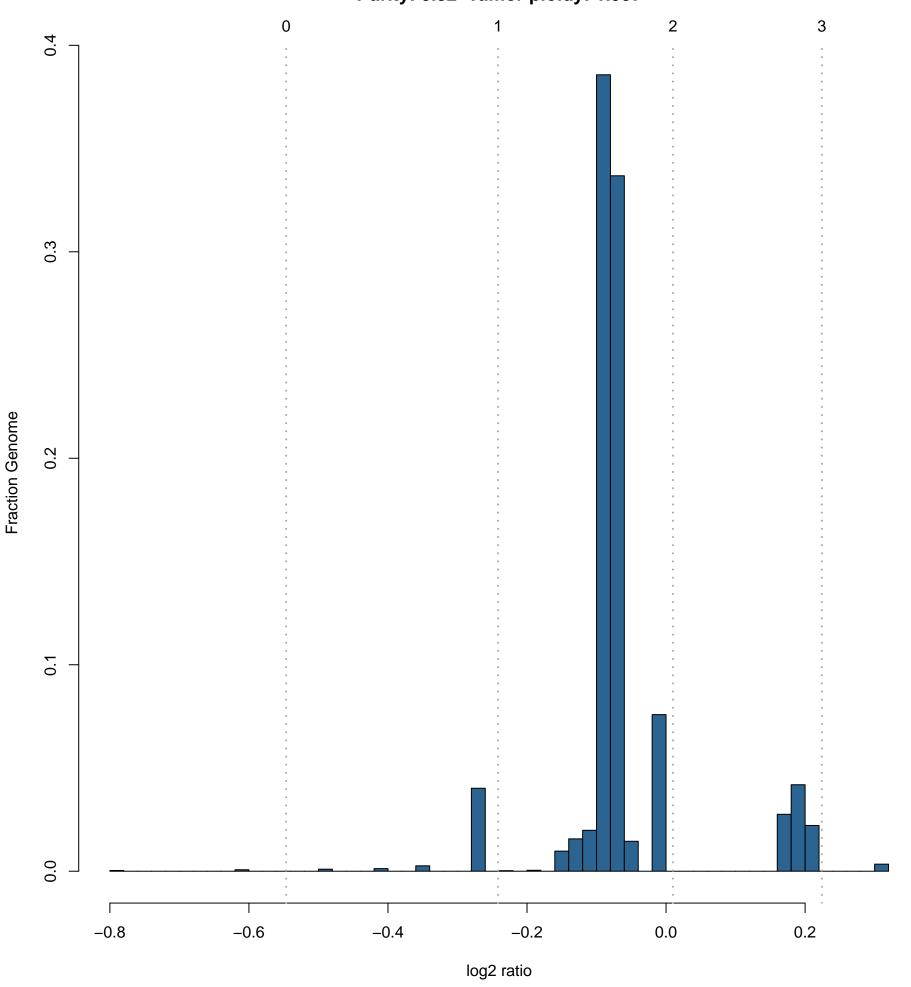
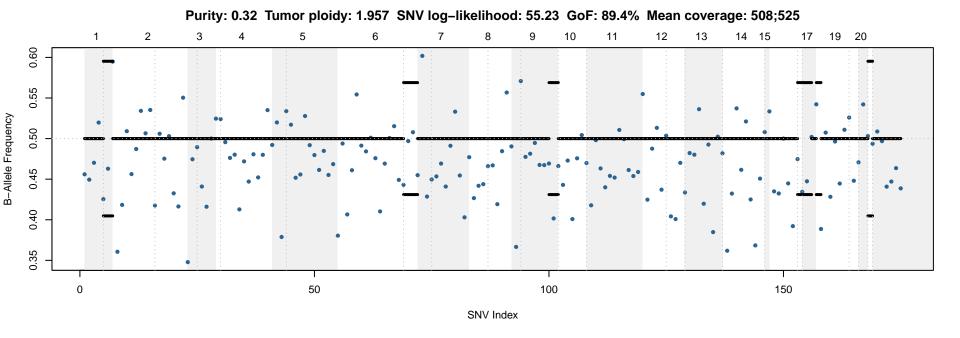
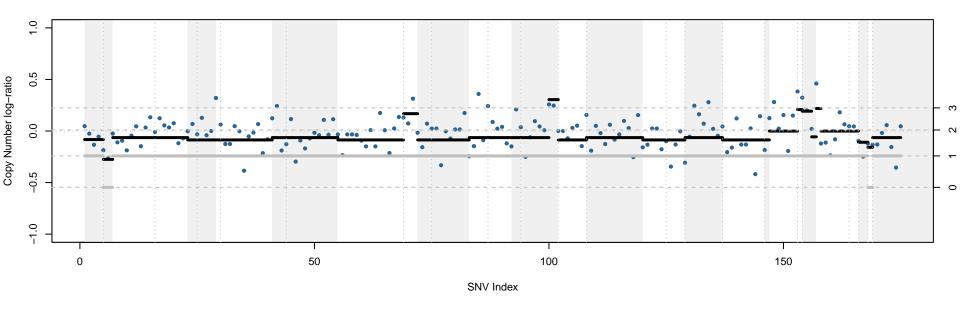
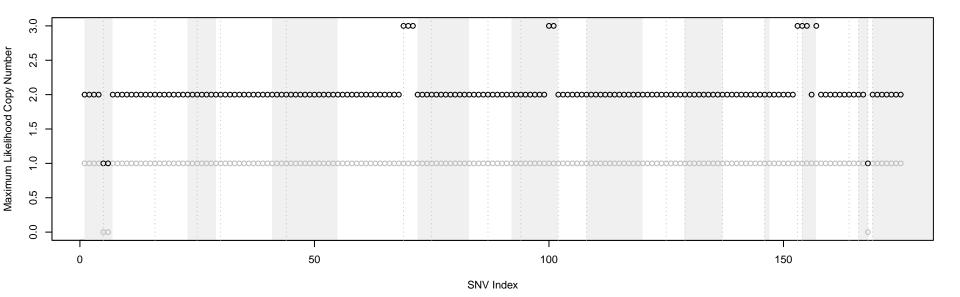
Purity: 0.32 Tumor ploidy: 1.957

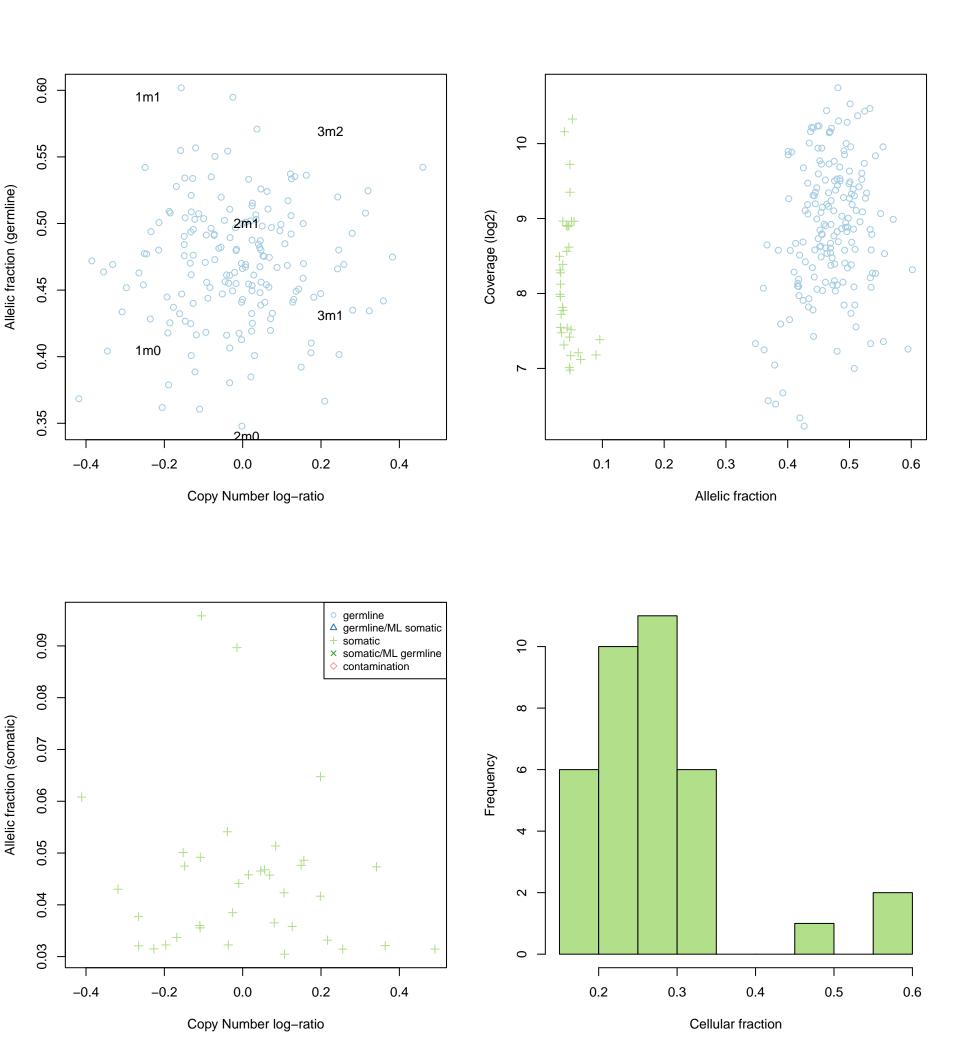




## SCNA-fit log-likelihood: -3807.21

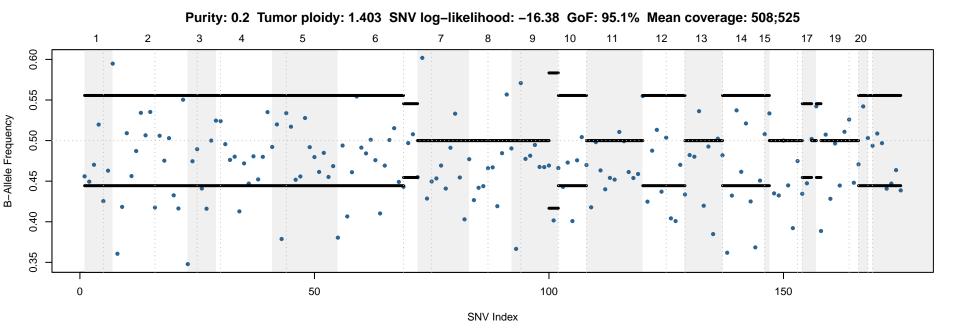




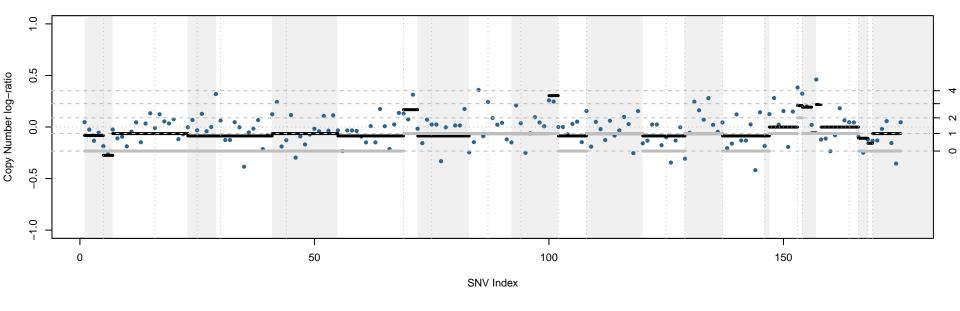


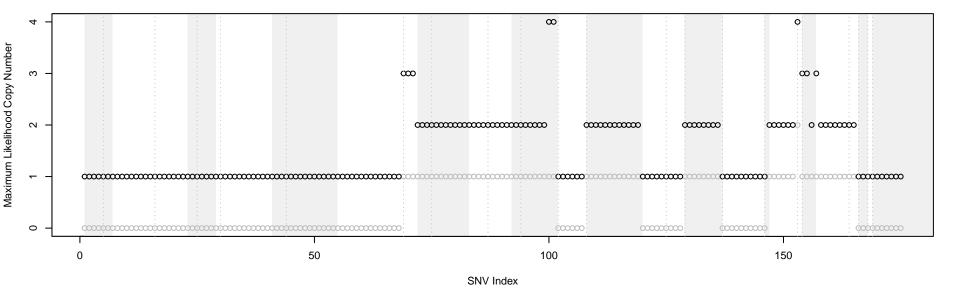
Purity: 0.2 Tumor ploidy: 1.403 0 3 0.4 0.2 0.1 0.0 -0.4 -0.2 0.0 0.2 log2 ratio

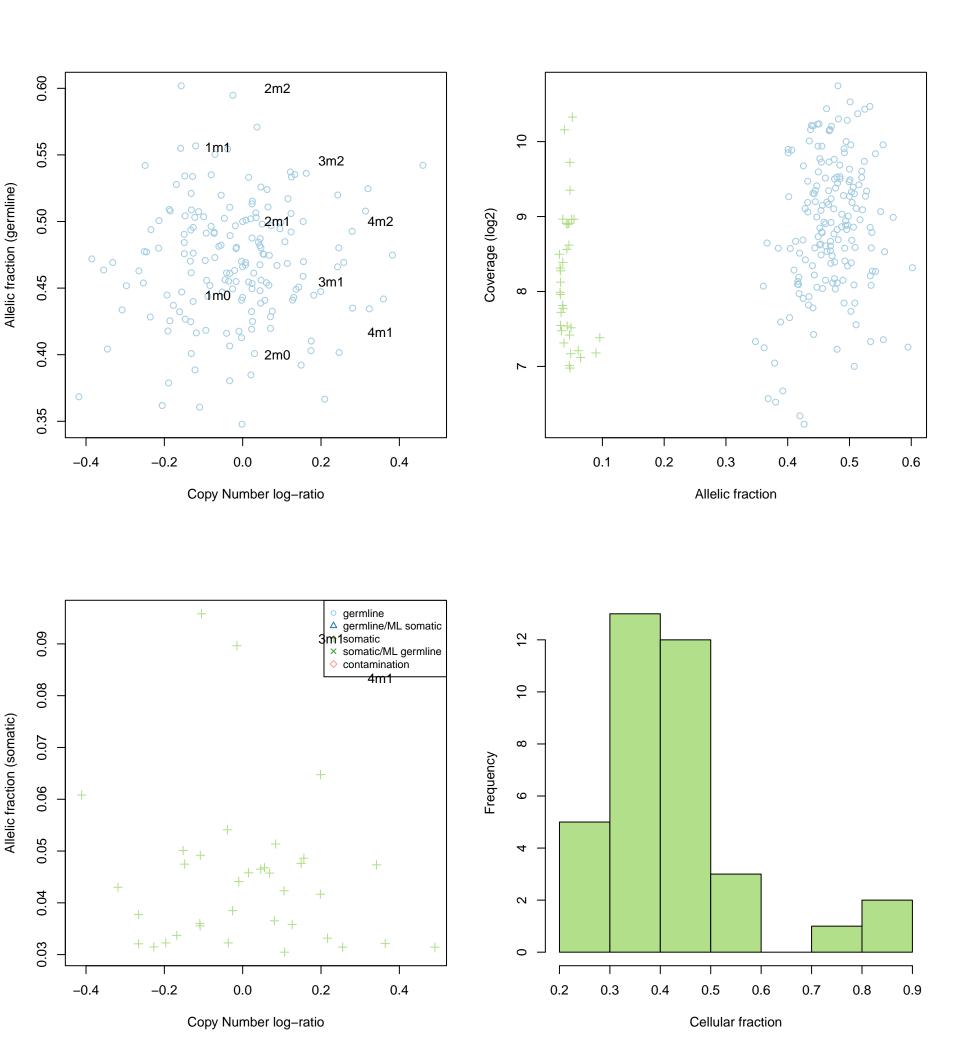
Fraction Genome



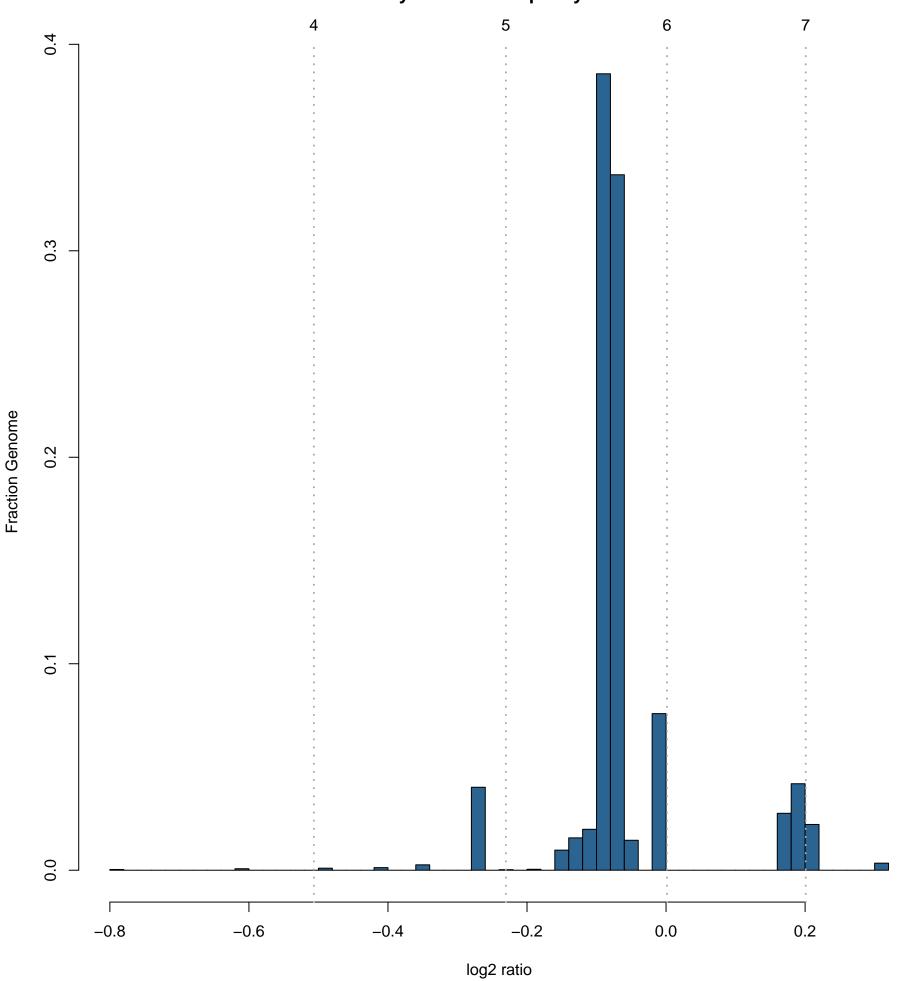
### SCNA-fit log-likelihood: -3820.69

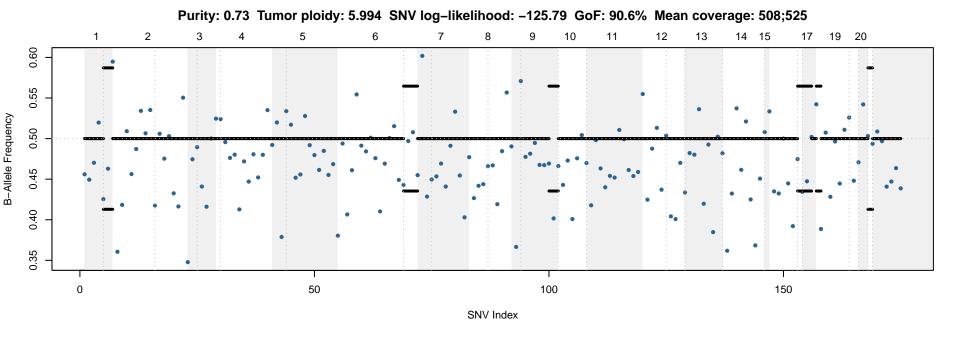




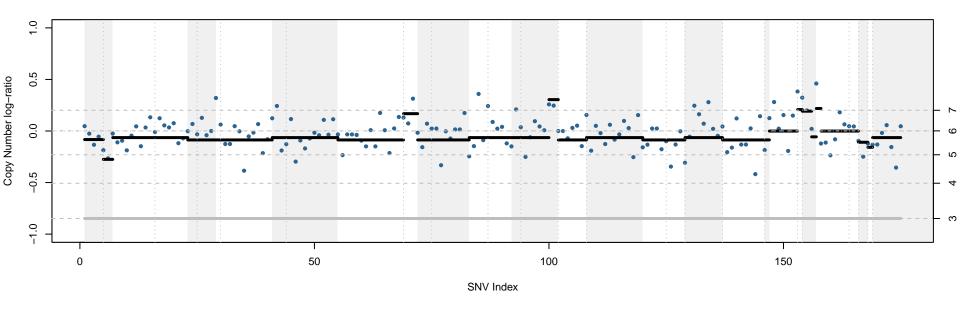


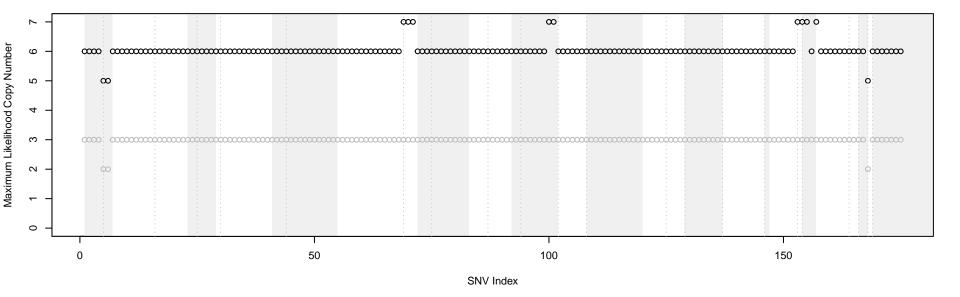
Purity: 0.73 Tumor ploidy: 5.994

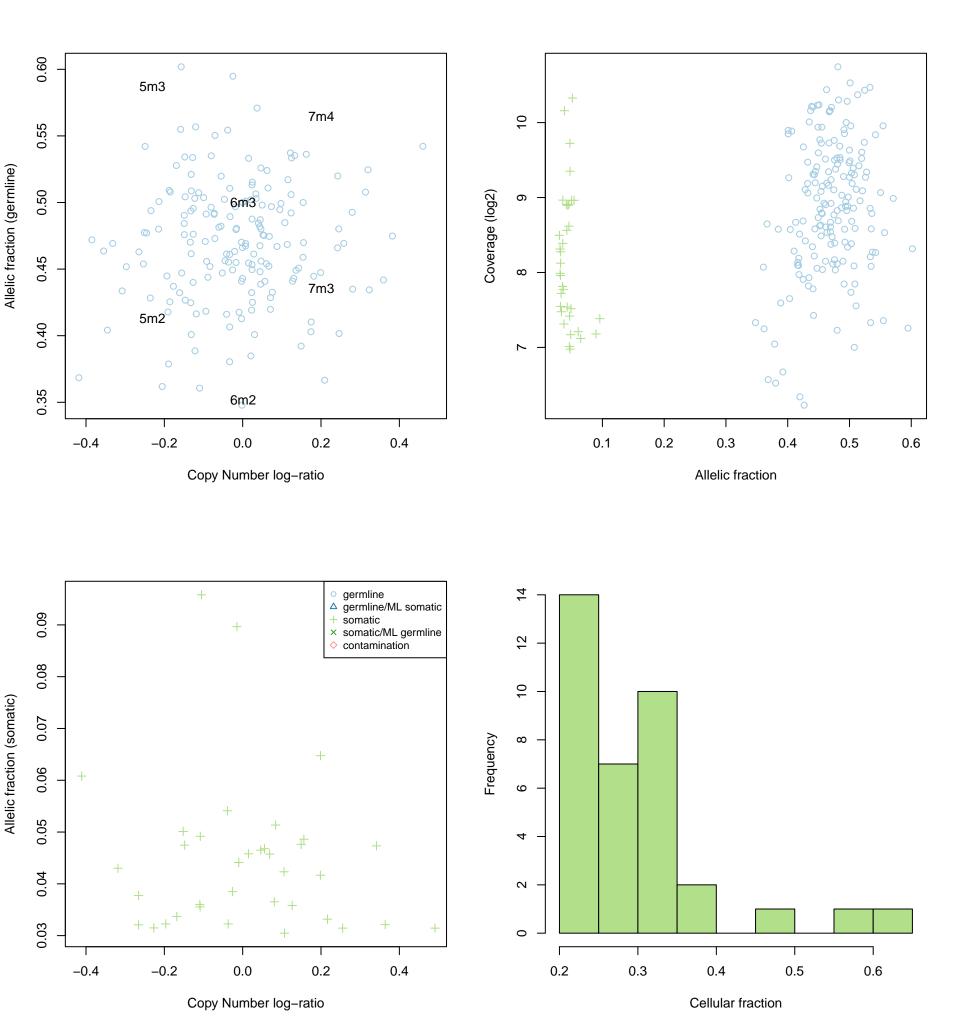




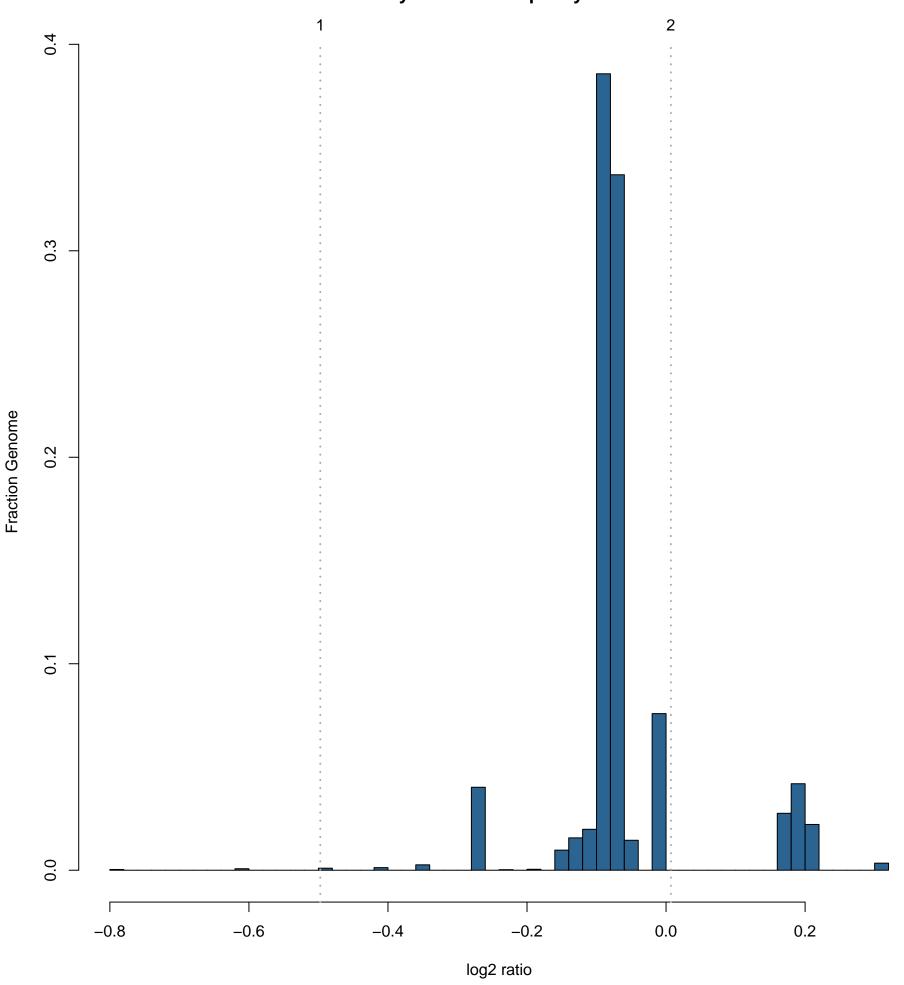
### SCNA-fit log-likelihood: -3630.52

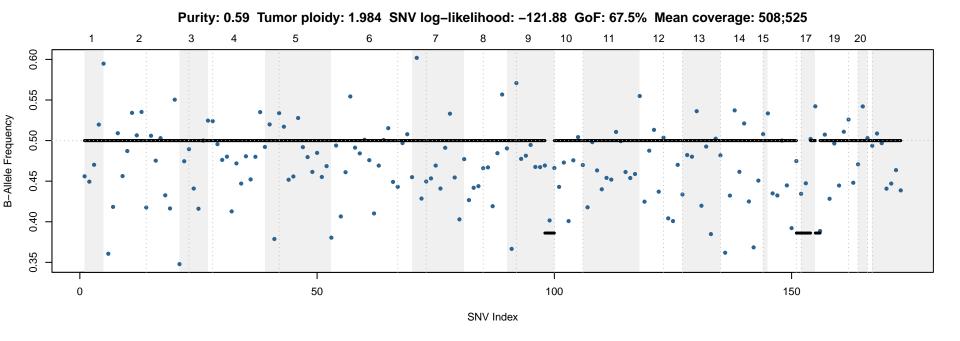




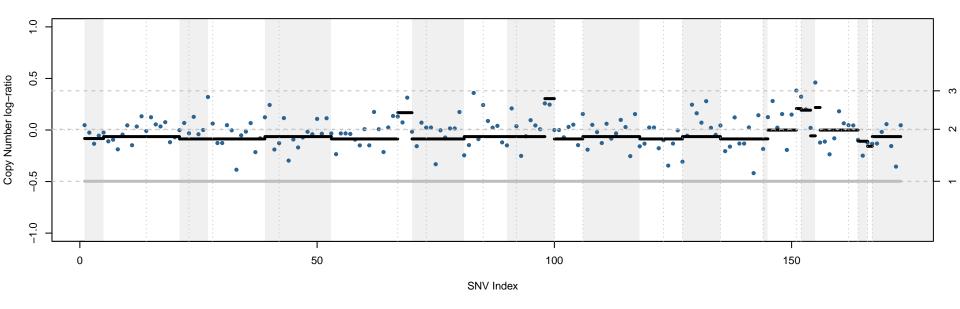


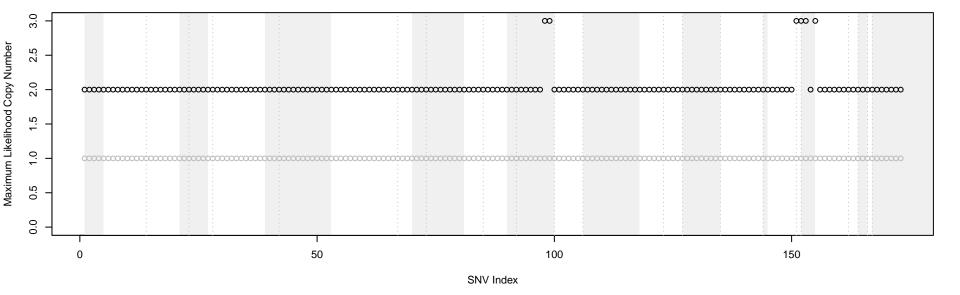
Purity: 0.59 Tumor ploidy: 1.984

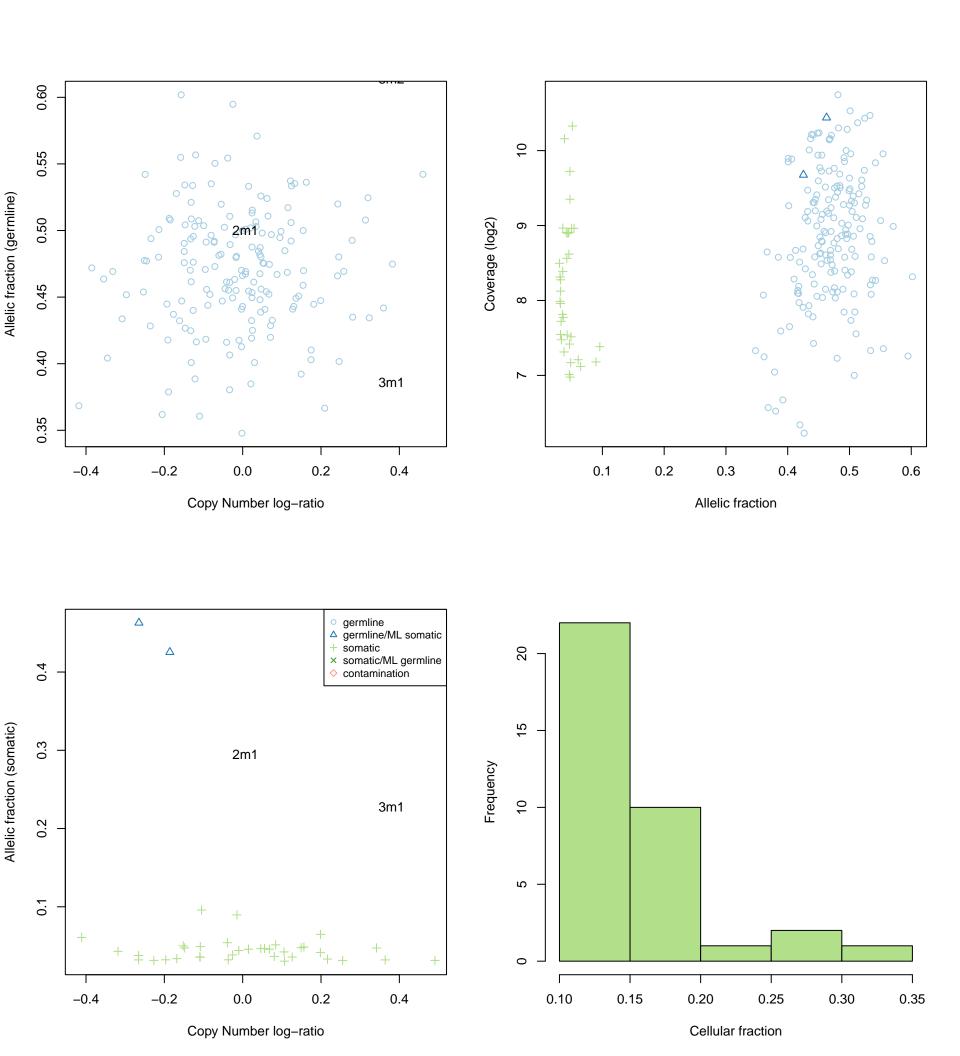




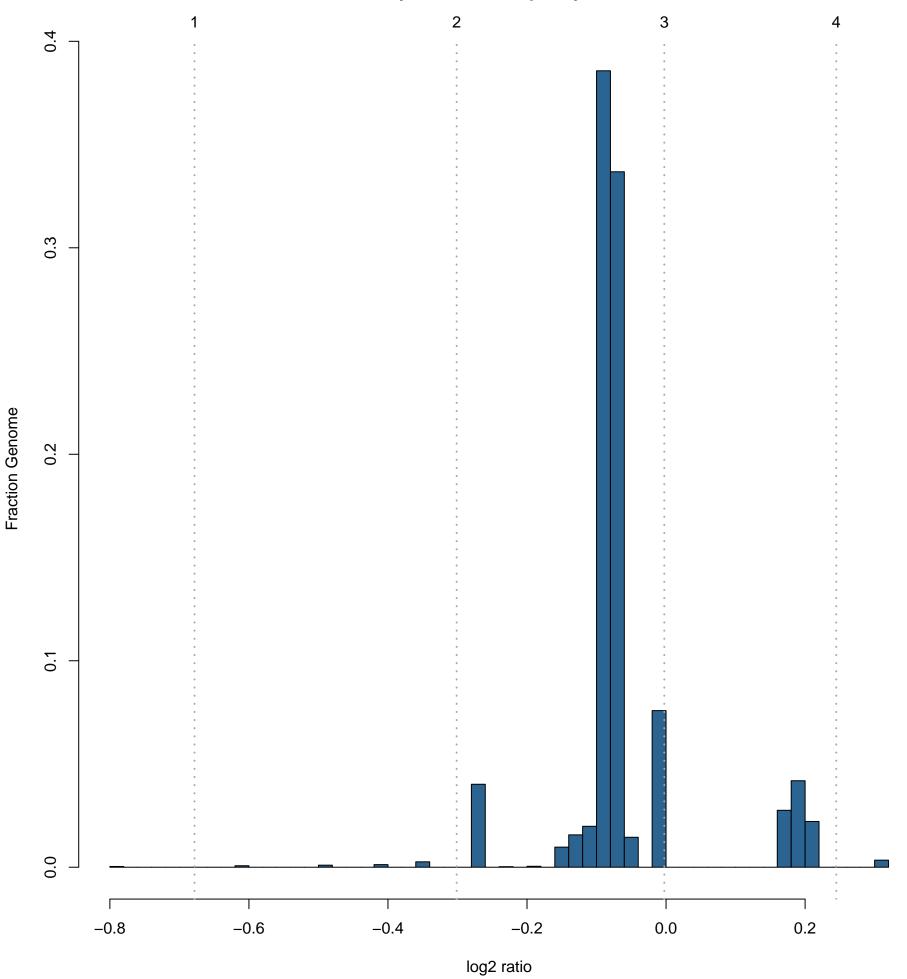
### SCNA-fit log-likelihood: -3996

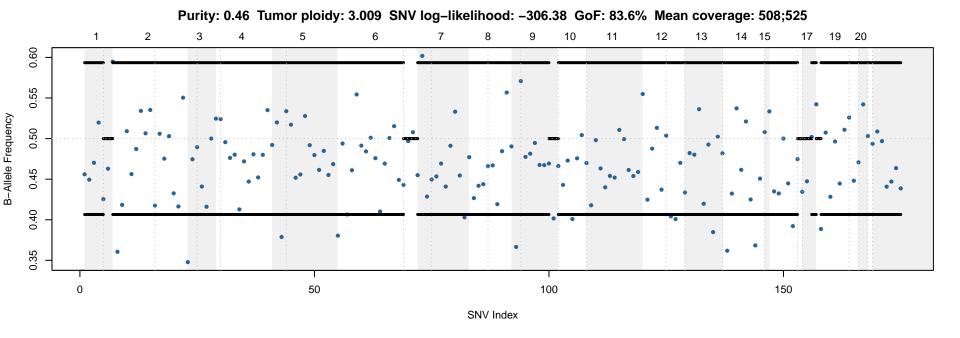




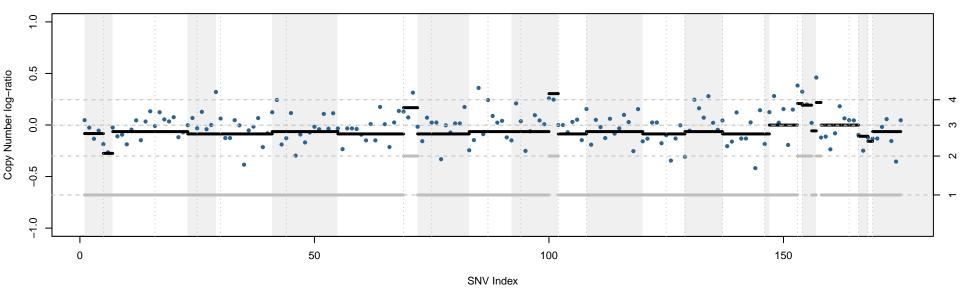


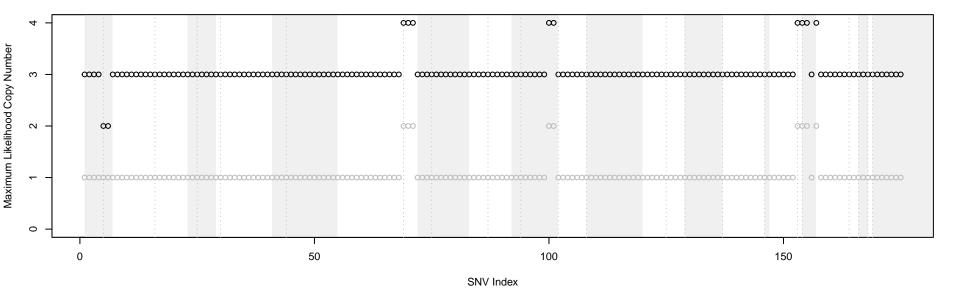
Purity: 0.46 Tumor ploidy: 3.009

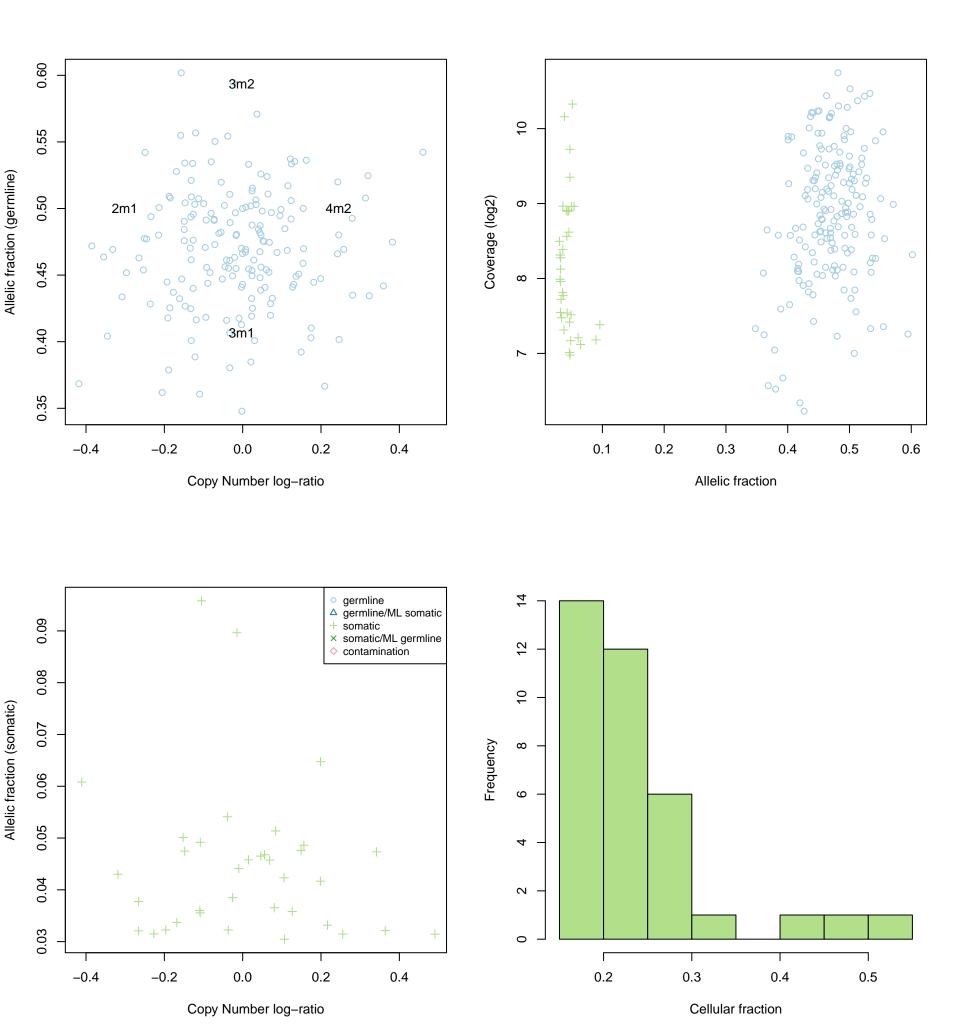




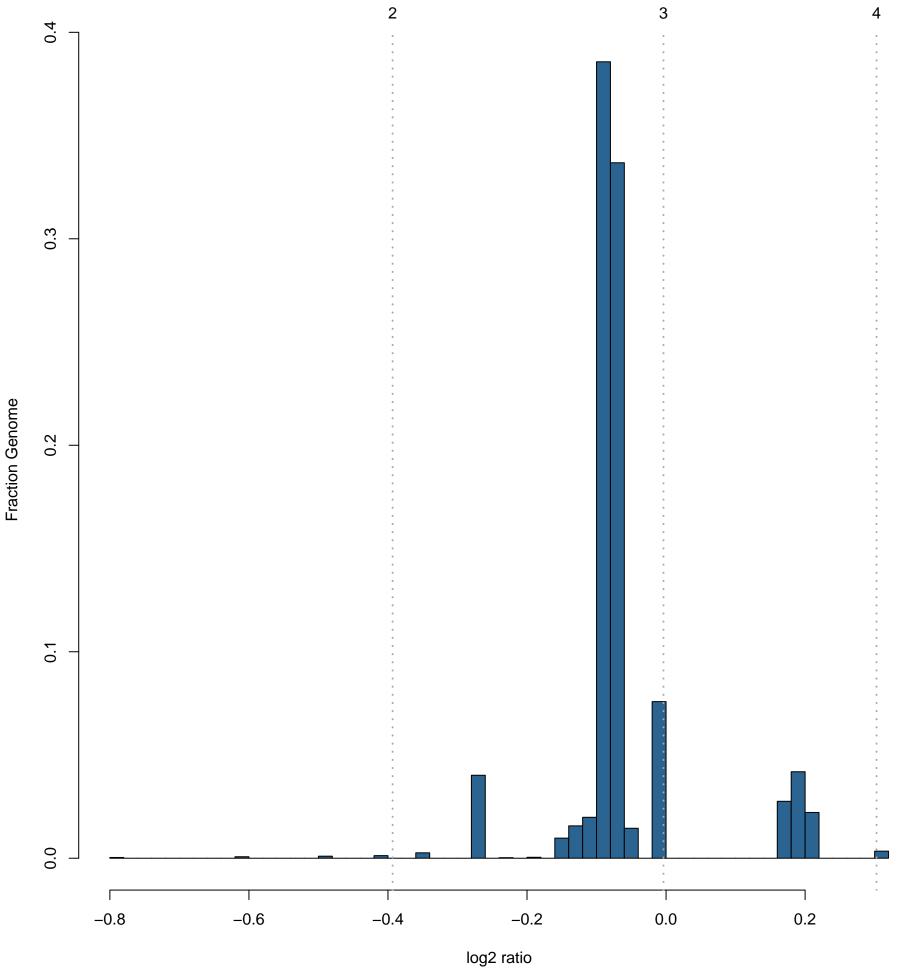
### SCNA-fit log-likelihood: -3741.61

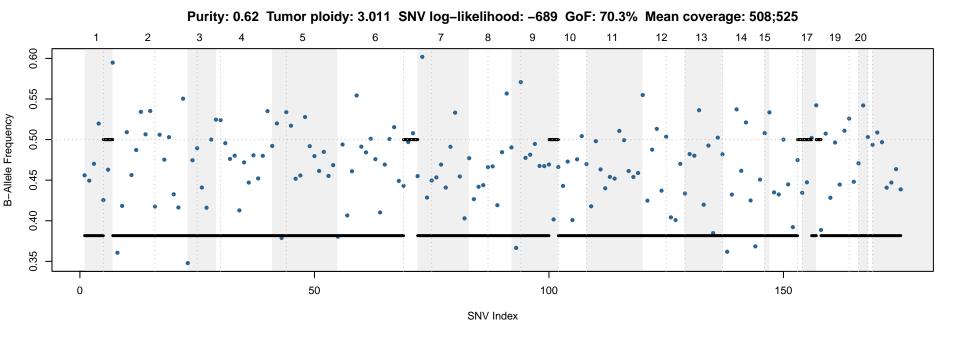




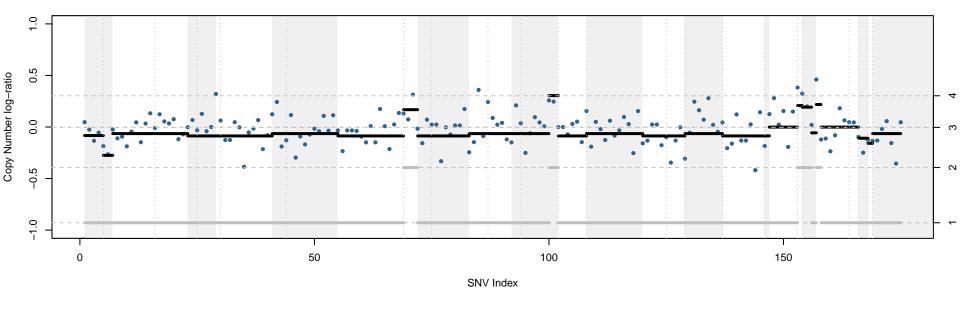


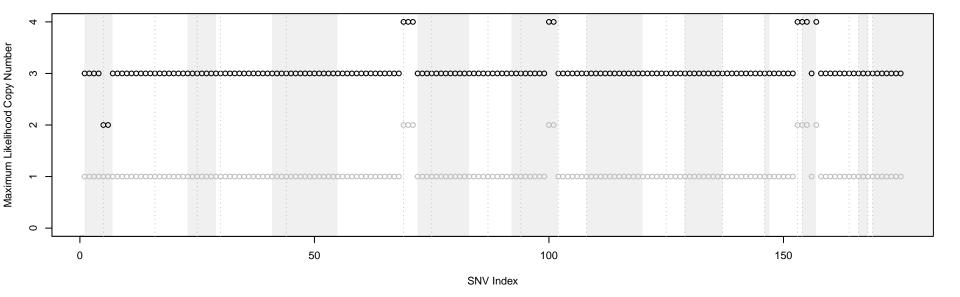
Purity: 0.62 Tumor ploidy: 3.011

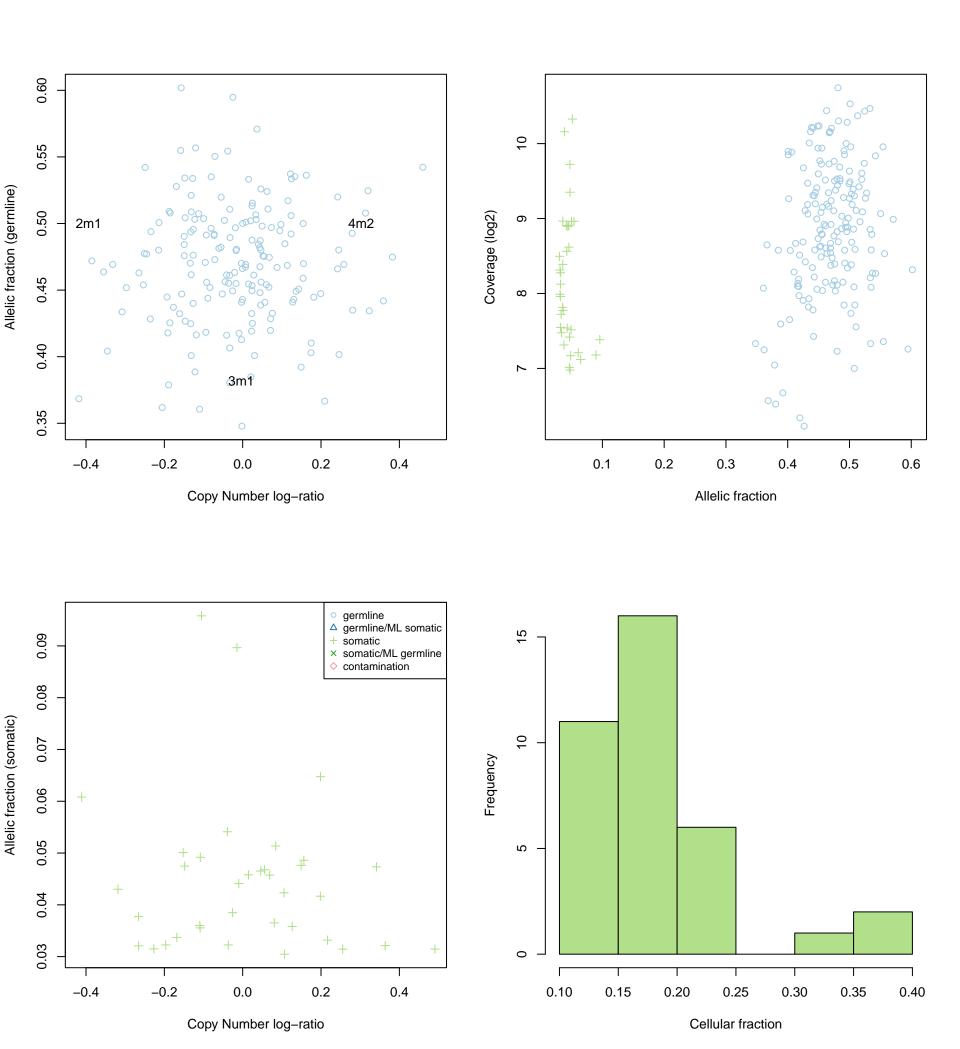




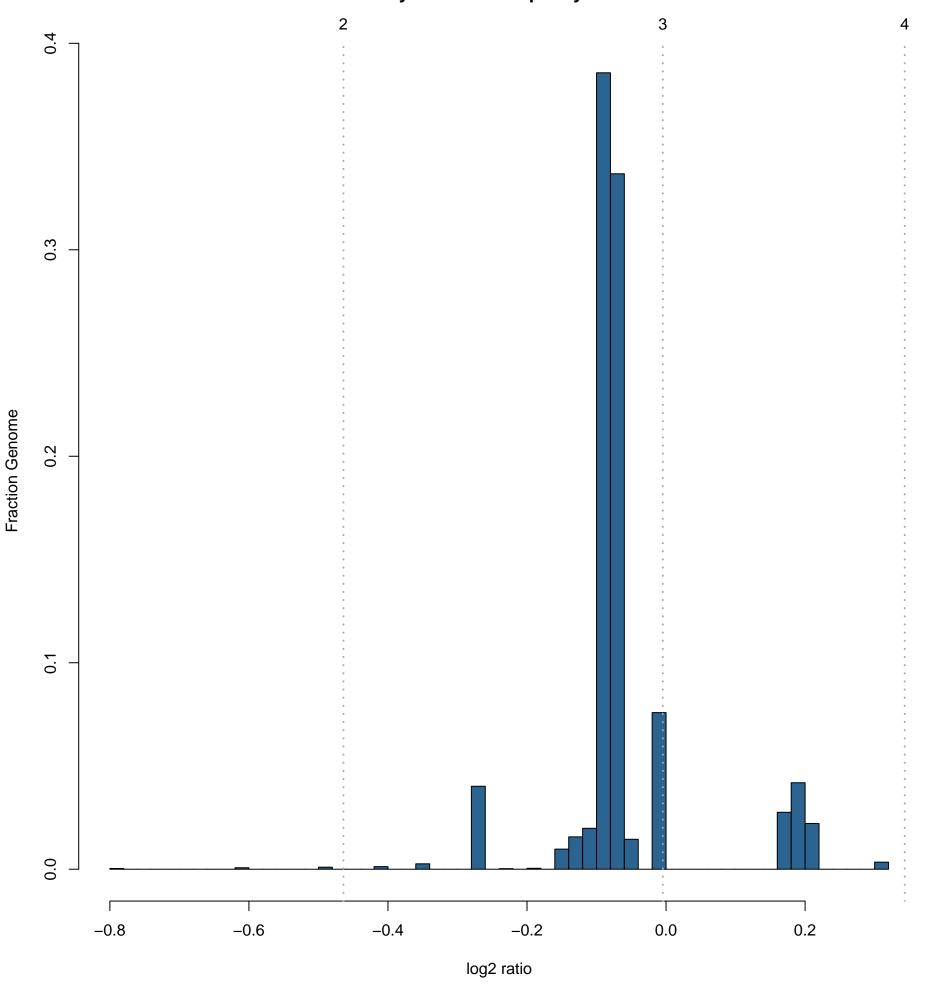
### SCNA-fit log-likelihood: -3785.79

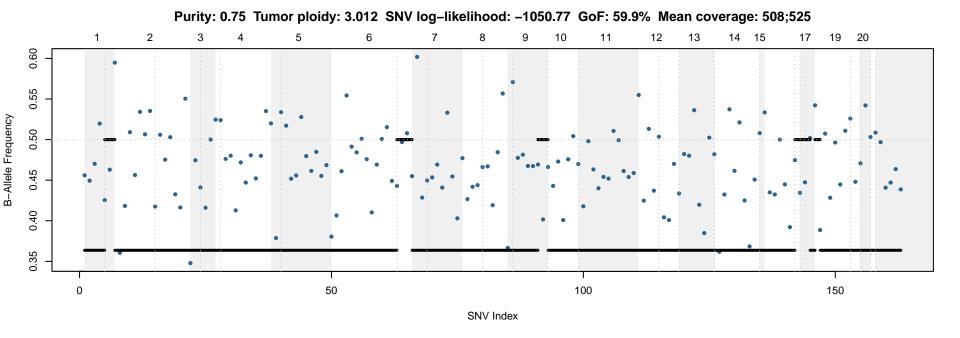






Purity: 0.75 Tumor ploidy: 3.012





# SCNA-fit log-likelihood: -3858.33

