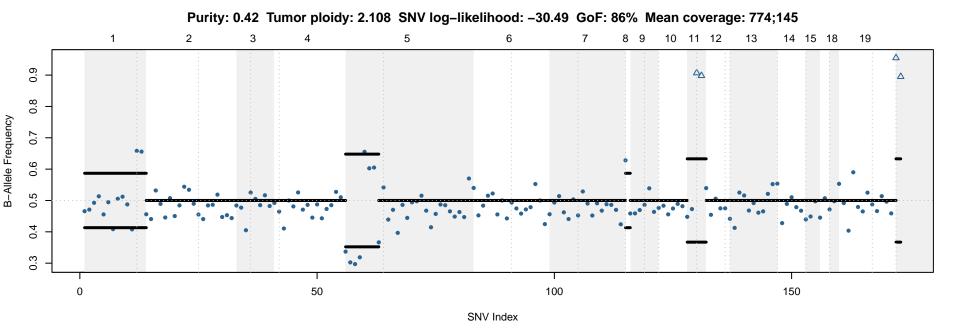
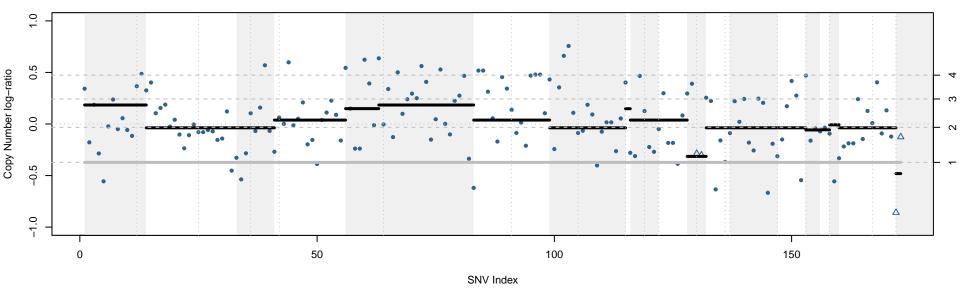
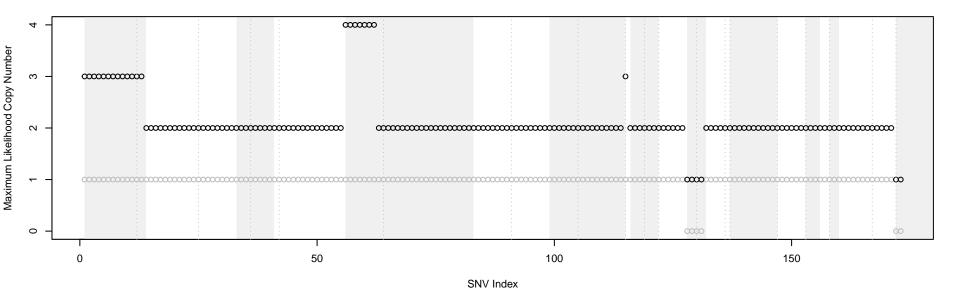
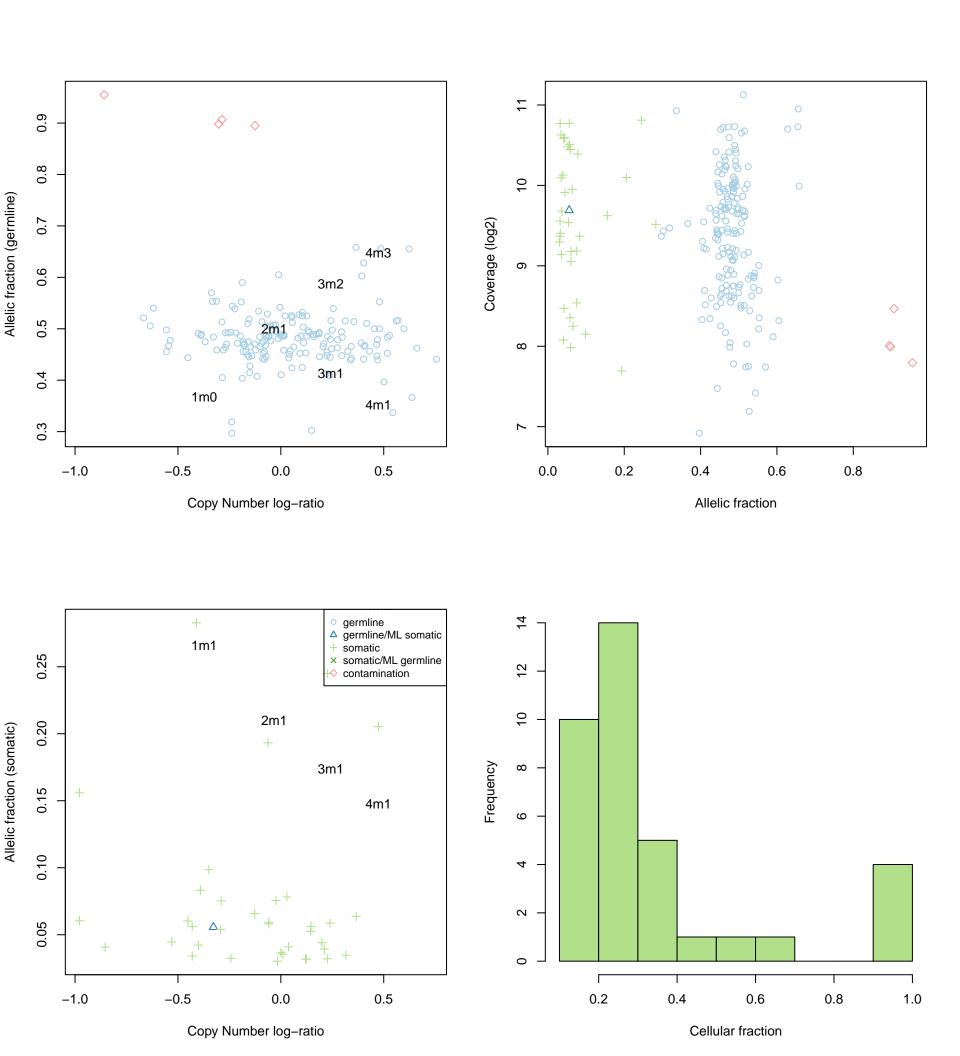
Purity: 0.42 Tumor ploidy: 2.108 2 3 Fraction Genome 0.2 0.1 0.0 -0.5 0.0 0.5 1.0 1.5 2.0 log2 ratio



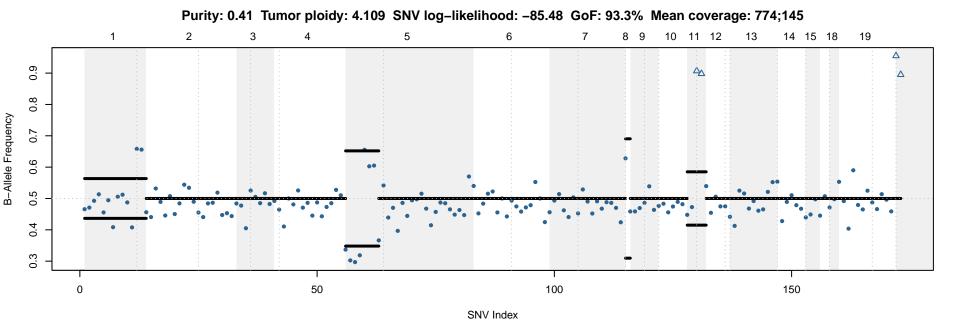
### SCNA-fit log-likelihood: -23906.62



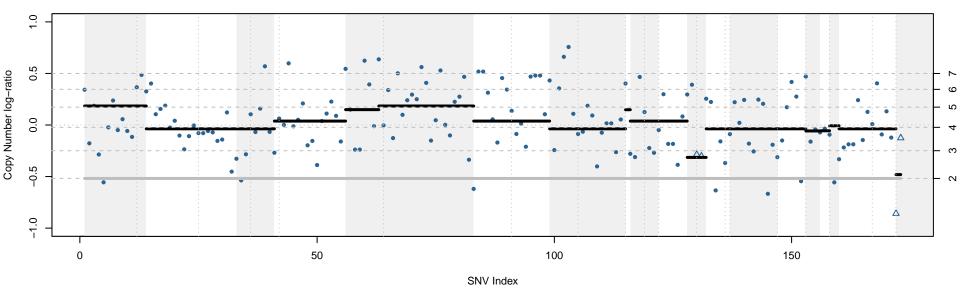


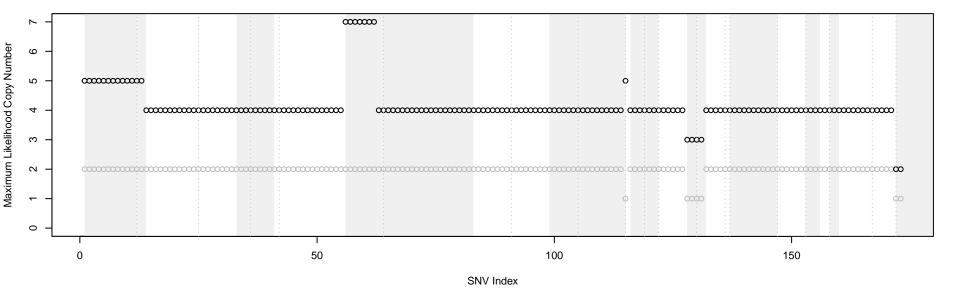


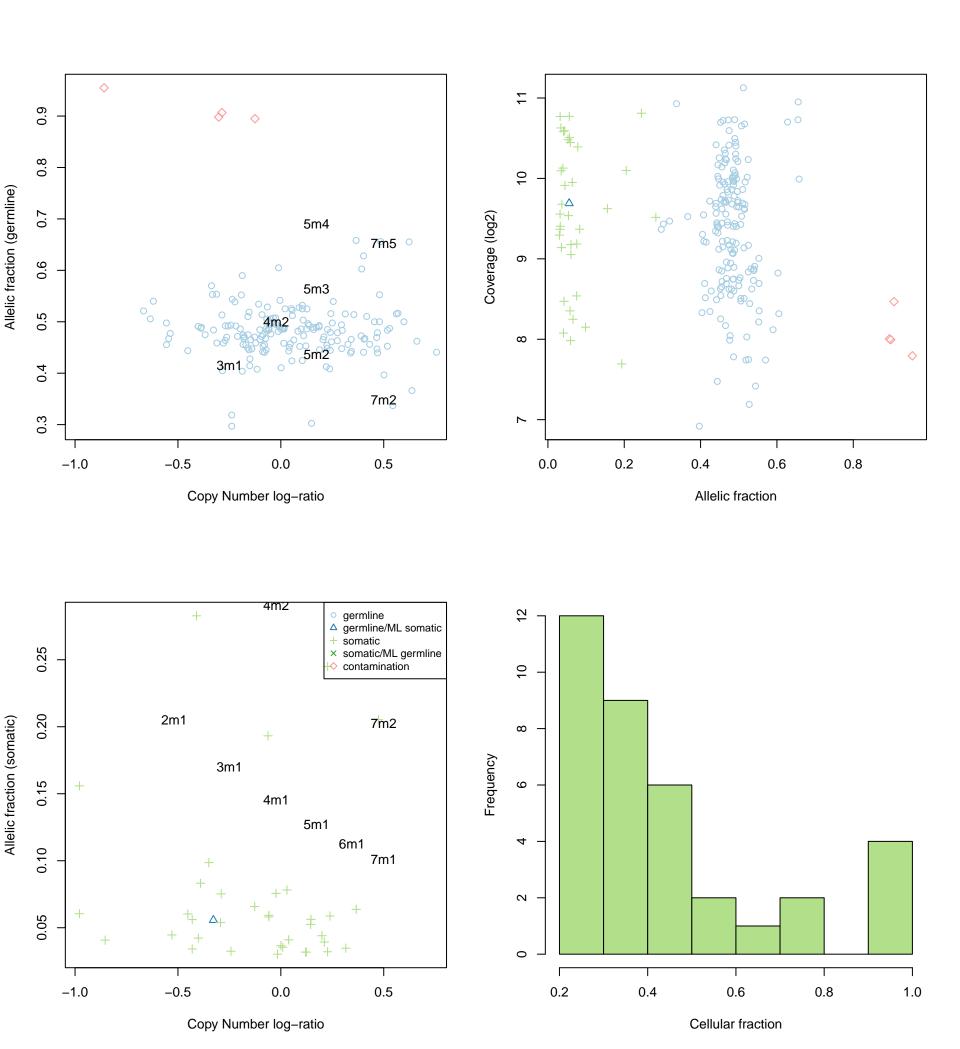
Purity: 0.41 Tumor ploidy: 4.109 7 3 6 2 5 Fraction Genome 0.2 0.1 0.0 -0.5 0.0 0.5 1.0 1.5 2.0 log2 ratio



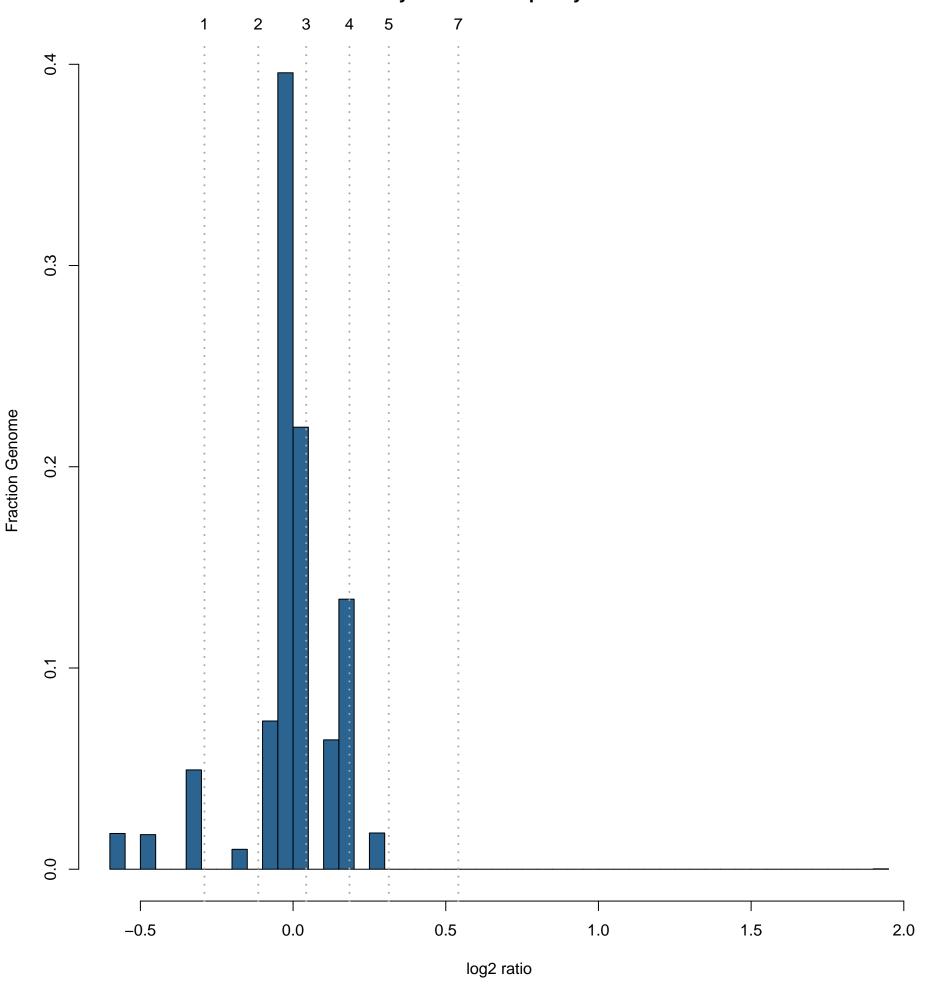
### SCNA-fit log-likelihood: -23884.61

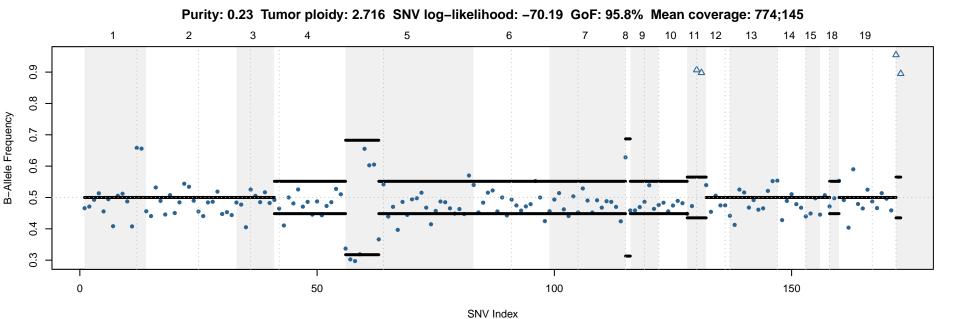




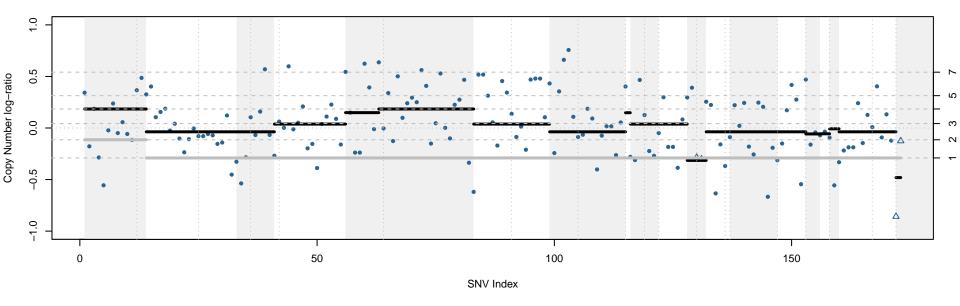


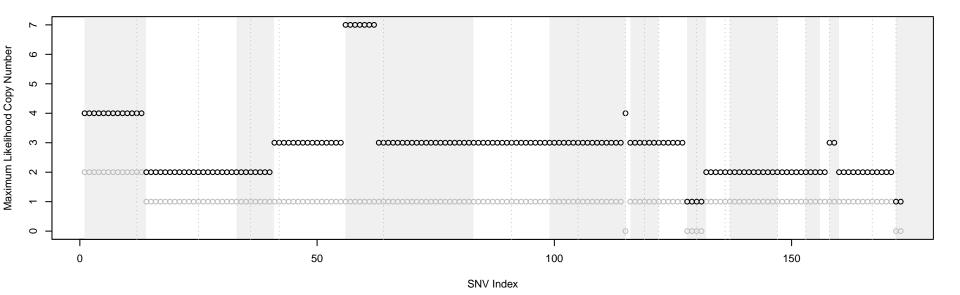
Purity: 0.23 Tumor ploidy: 2.716

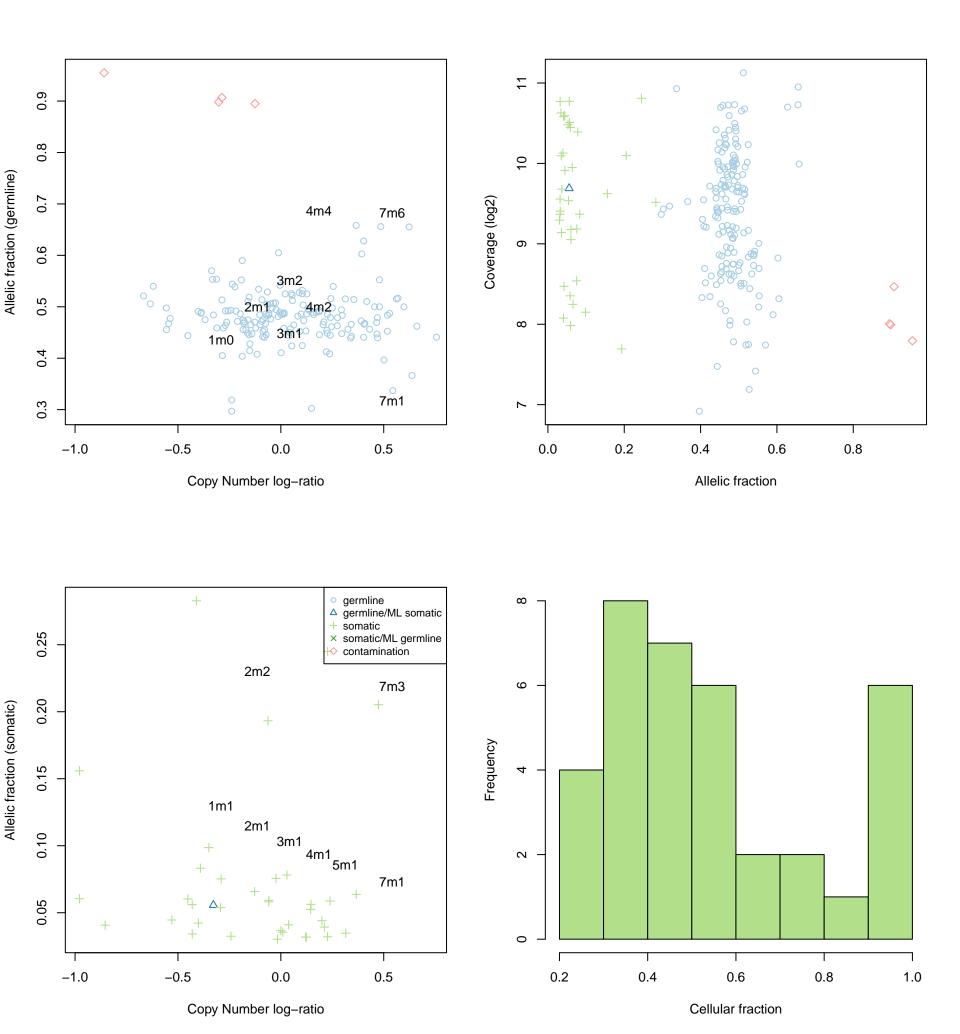




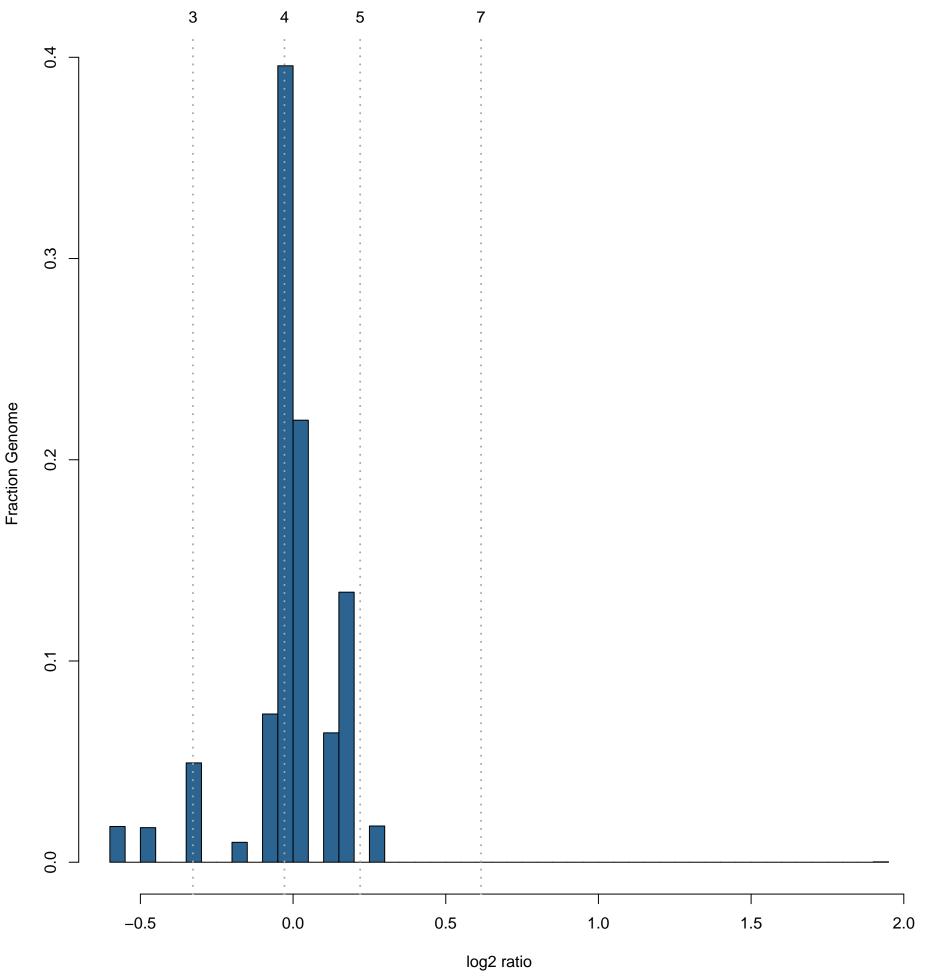
SCNA-fit log-likelihood: -23923.77

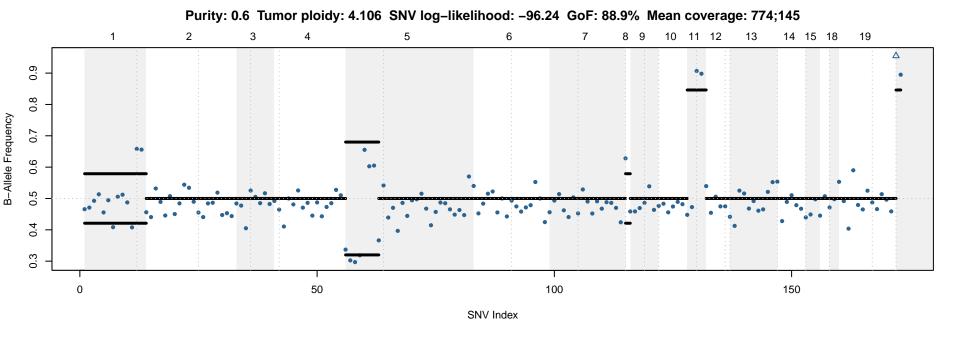




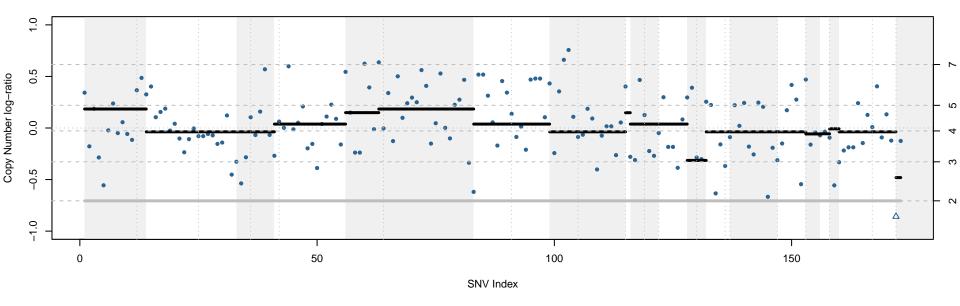


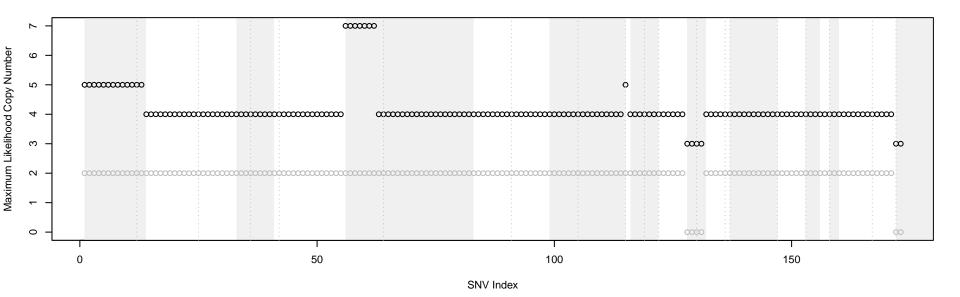
Purity: 0.6 Tumor ploidy: 4.106

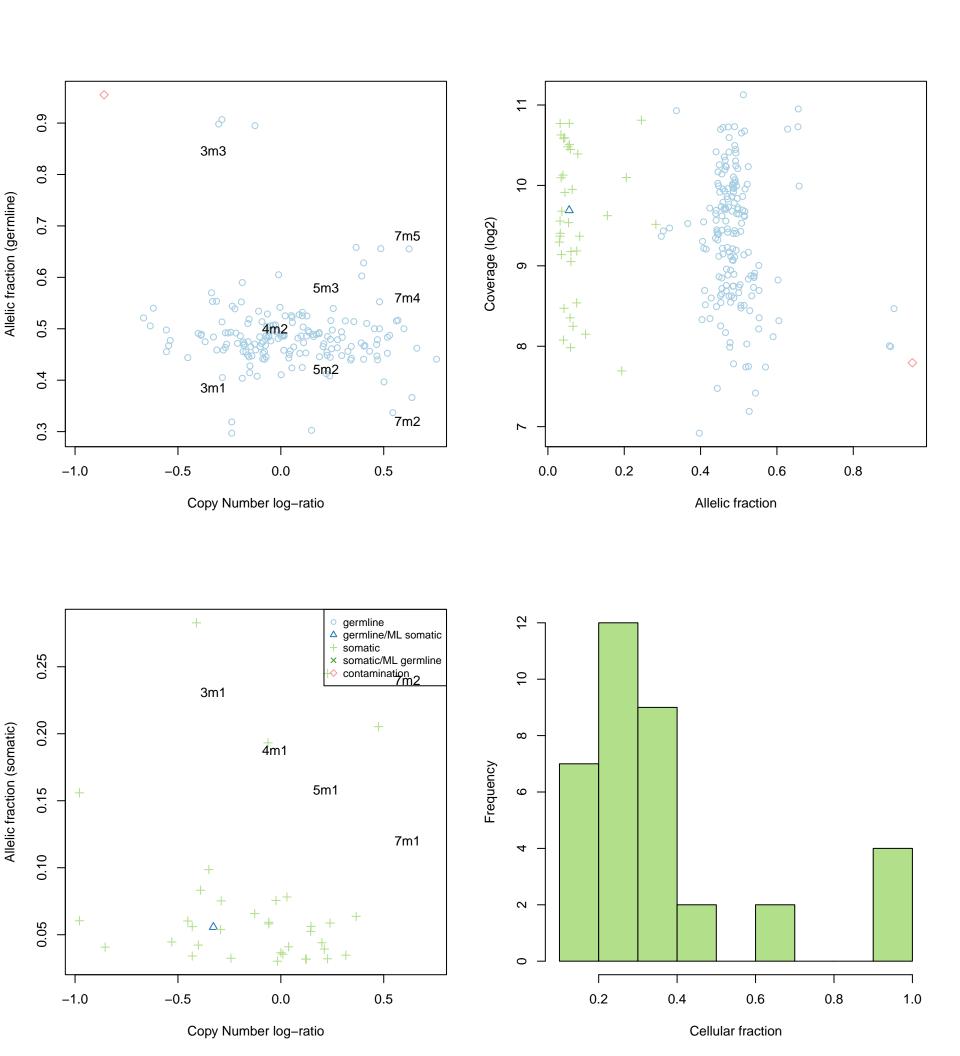




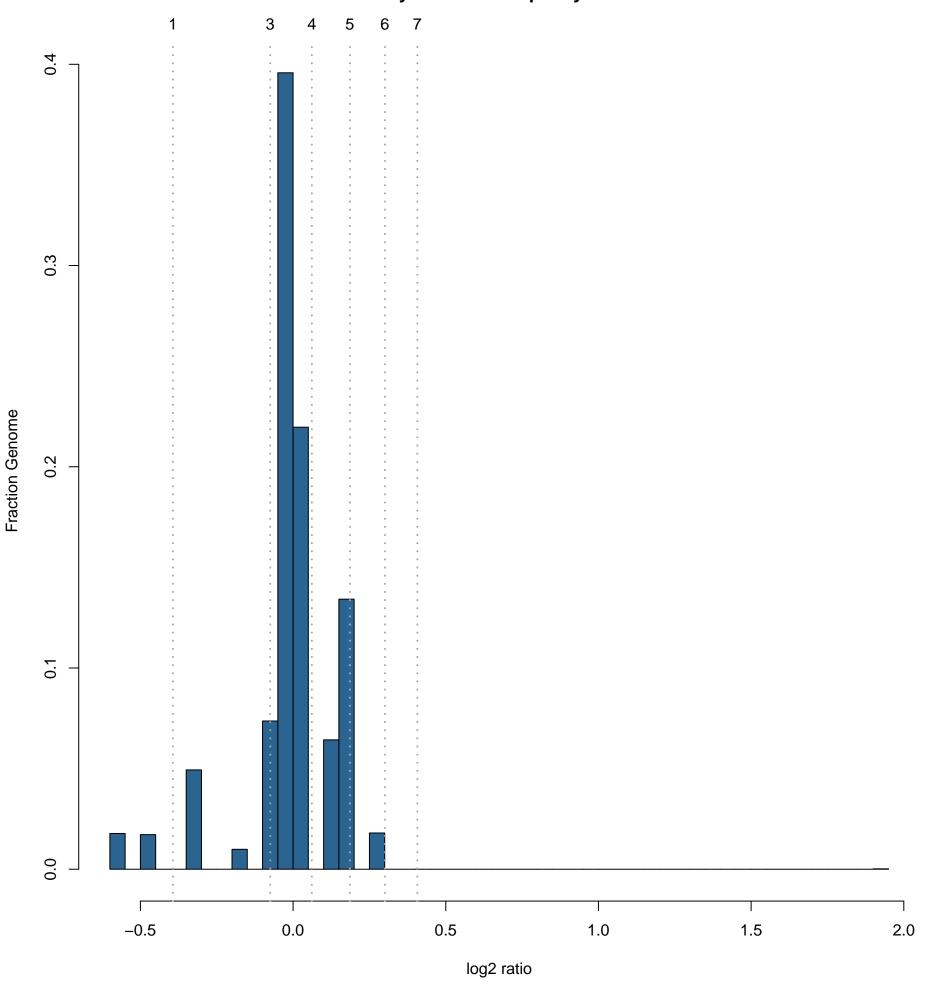
### SCNA-fit log-likelihood: -23896.68

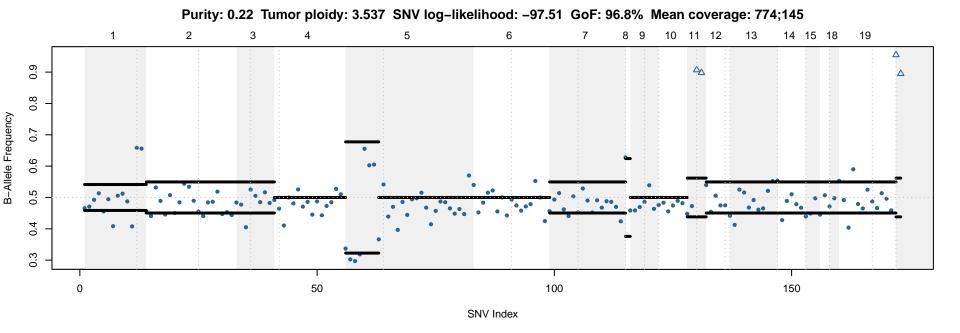




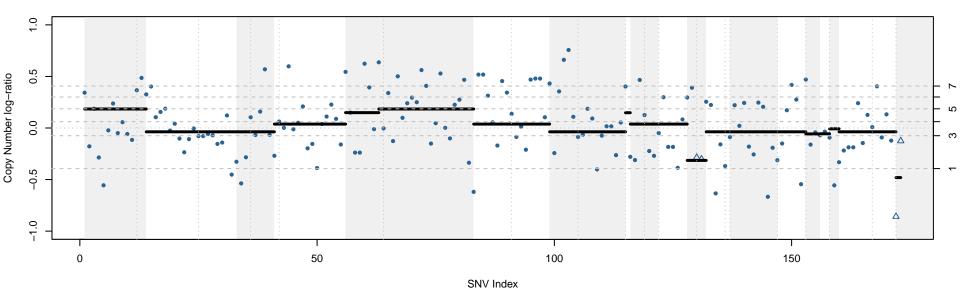


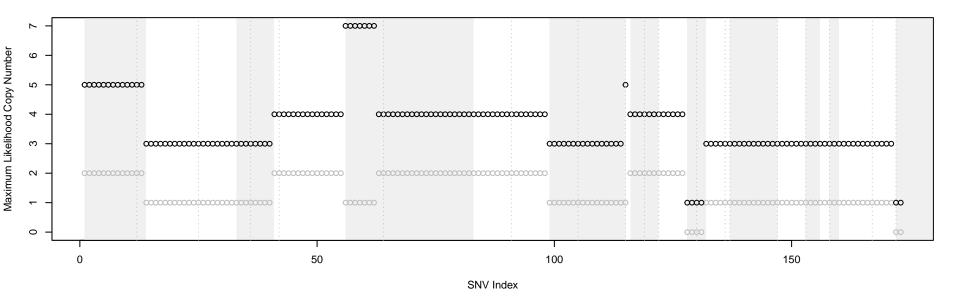
Purity: 0.22 Tumor ploidy: 3.537

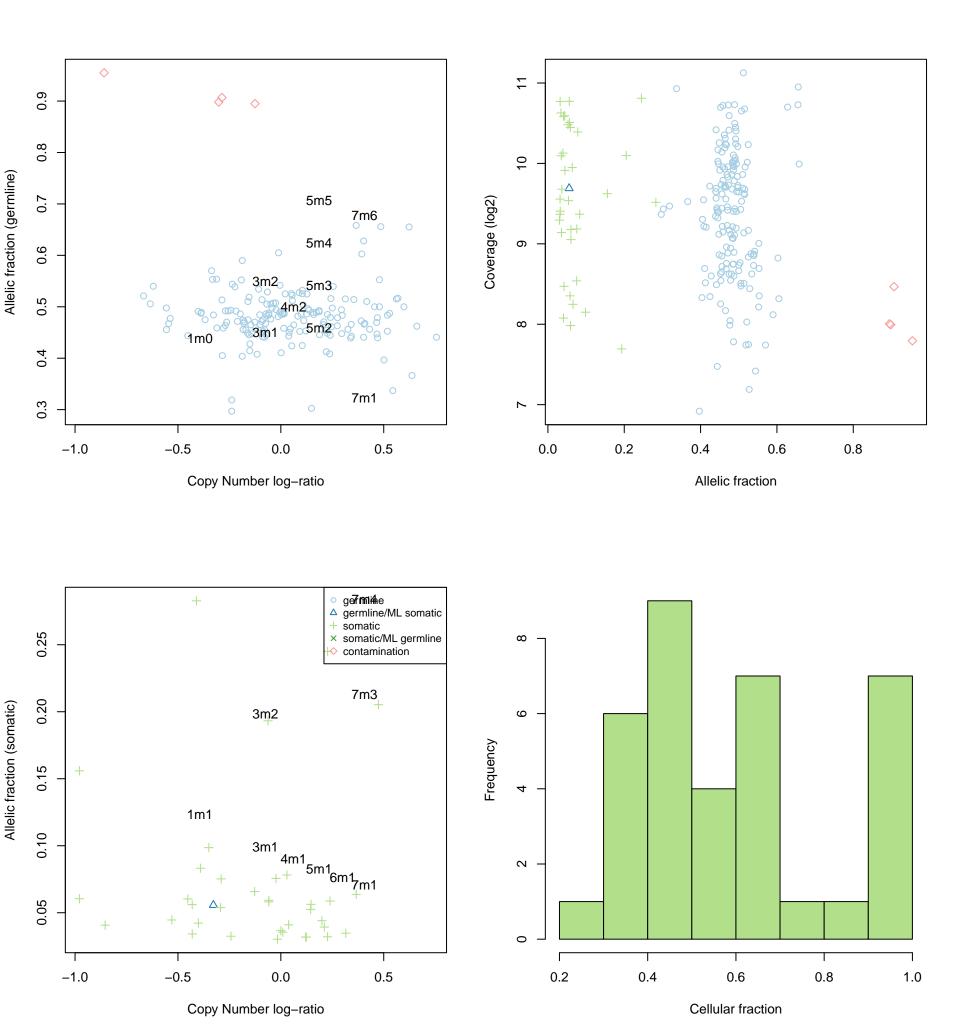




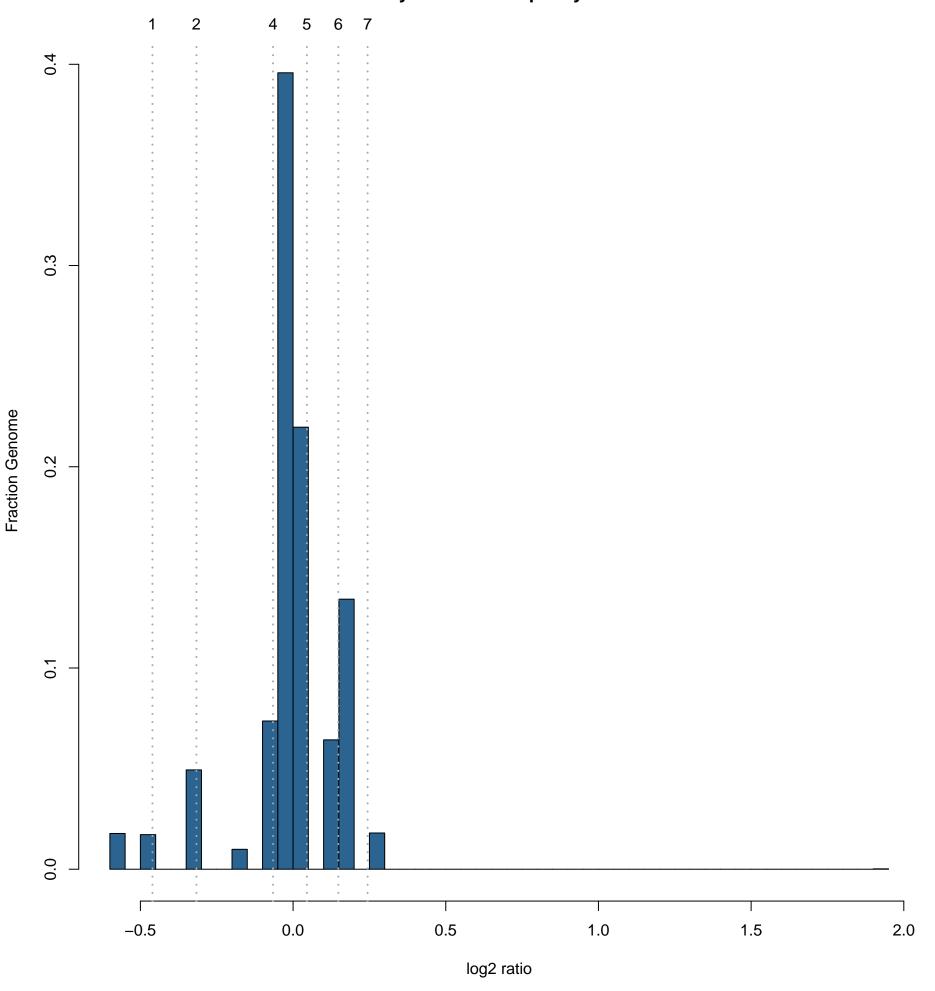
### SCNA-fit log-likelihood: -23888.23

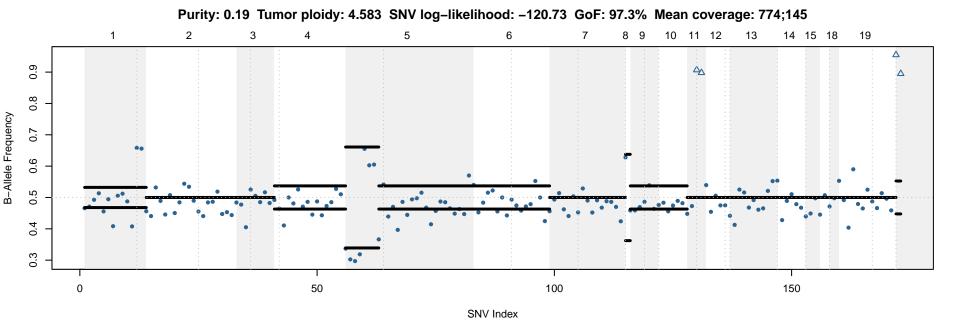




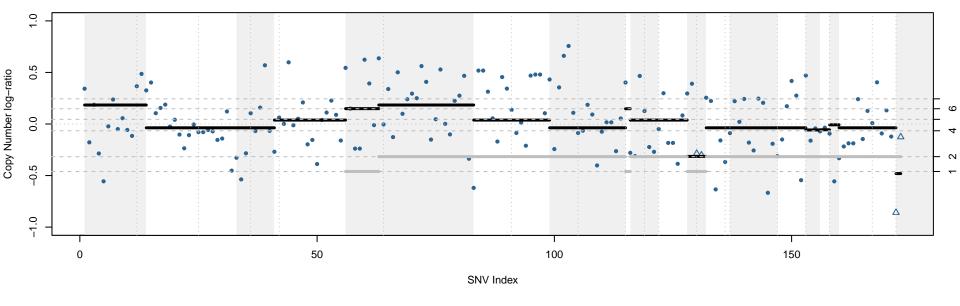


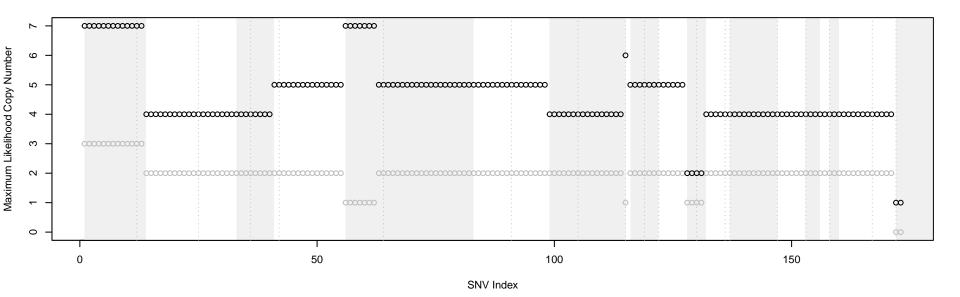
Purity: 0.19 Tumor ploidy: 4.583

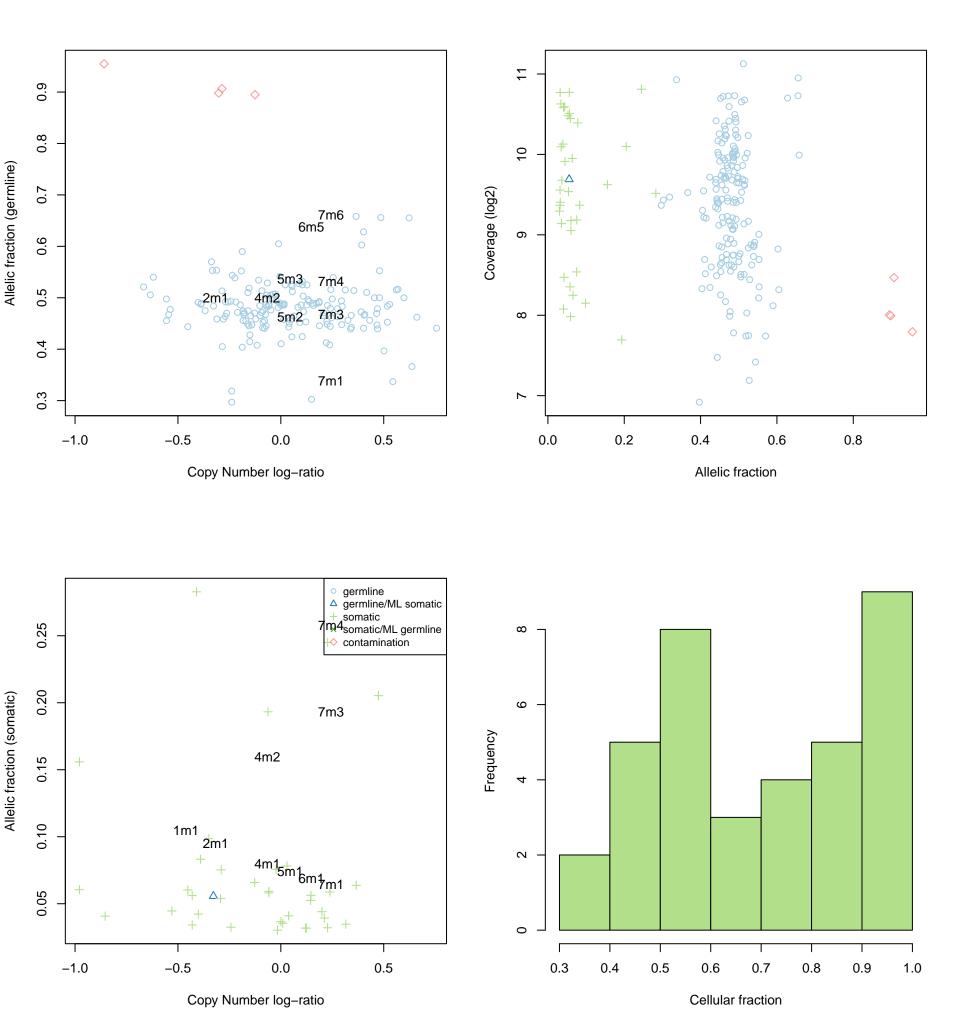




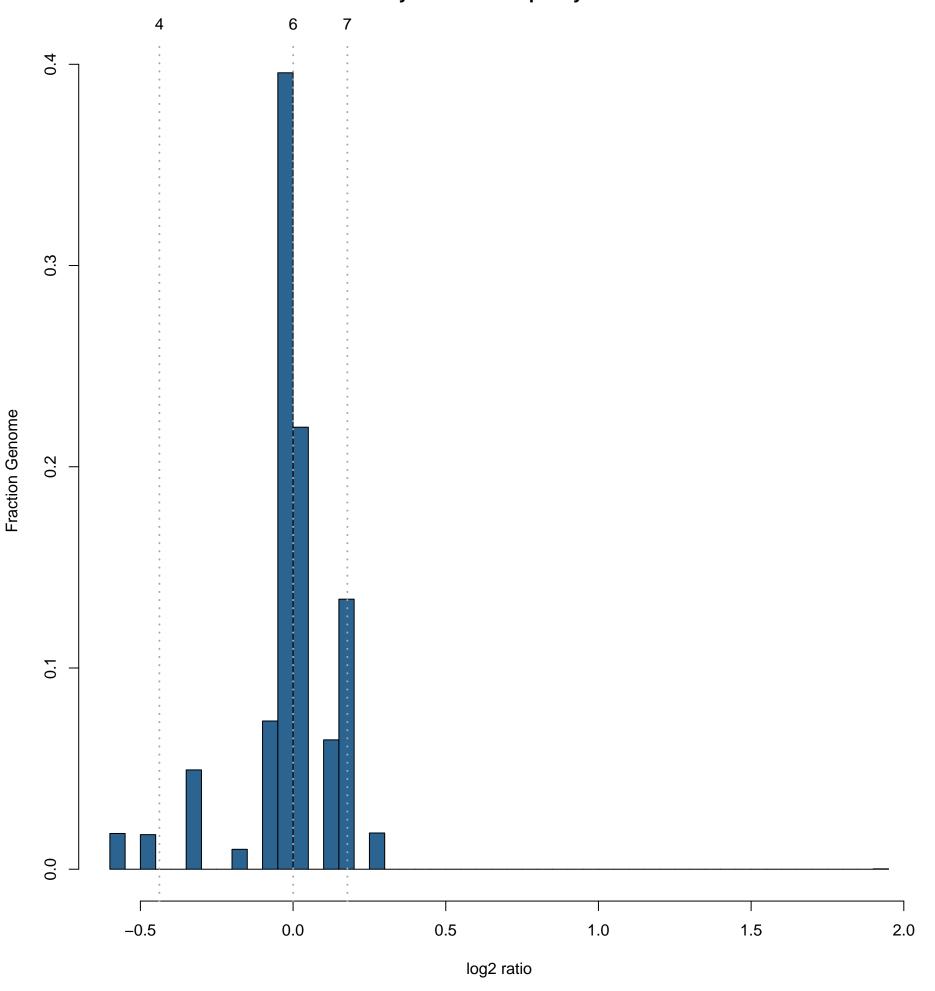
## SCNA-fit log-likelihood: -23885.38

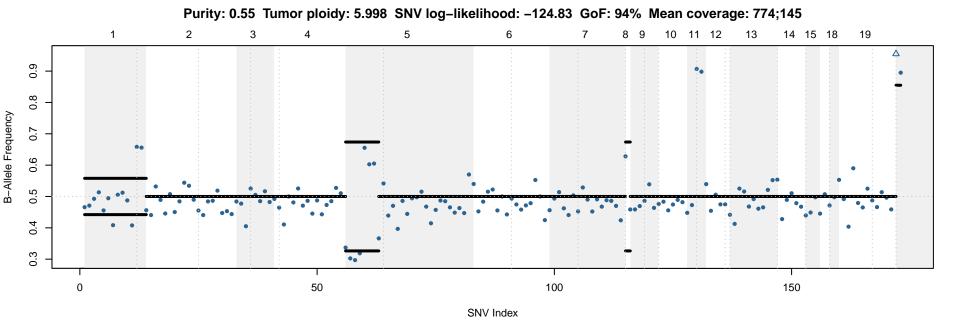




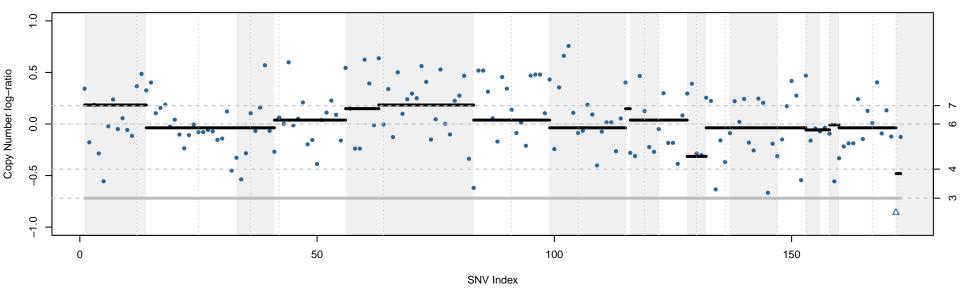


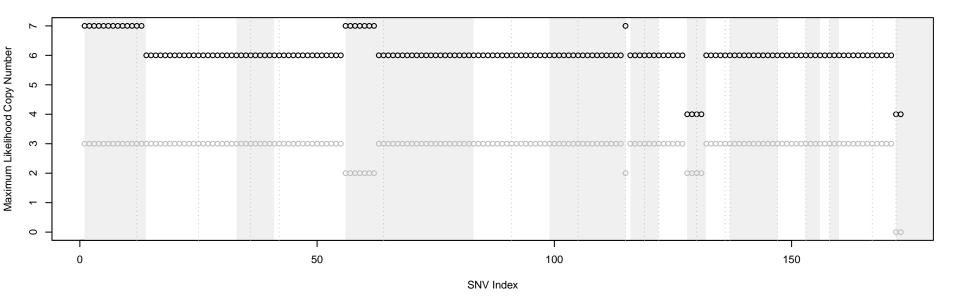
Purity: 0.55 Tumor ploidy: 5.998

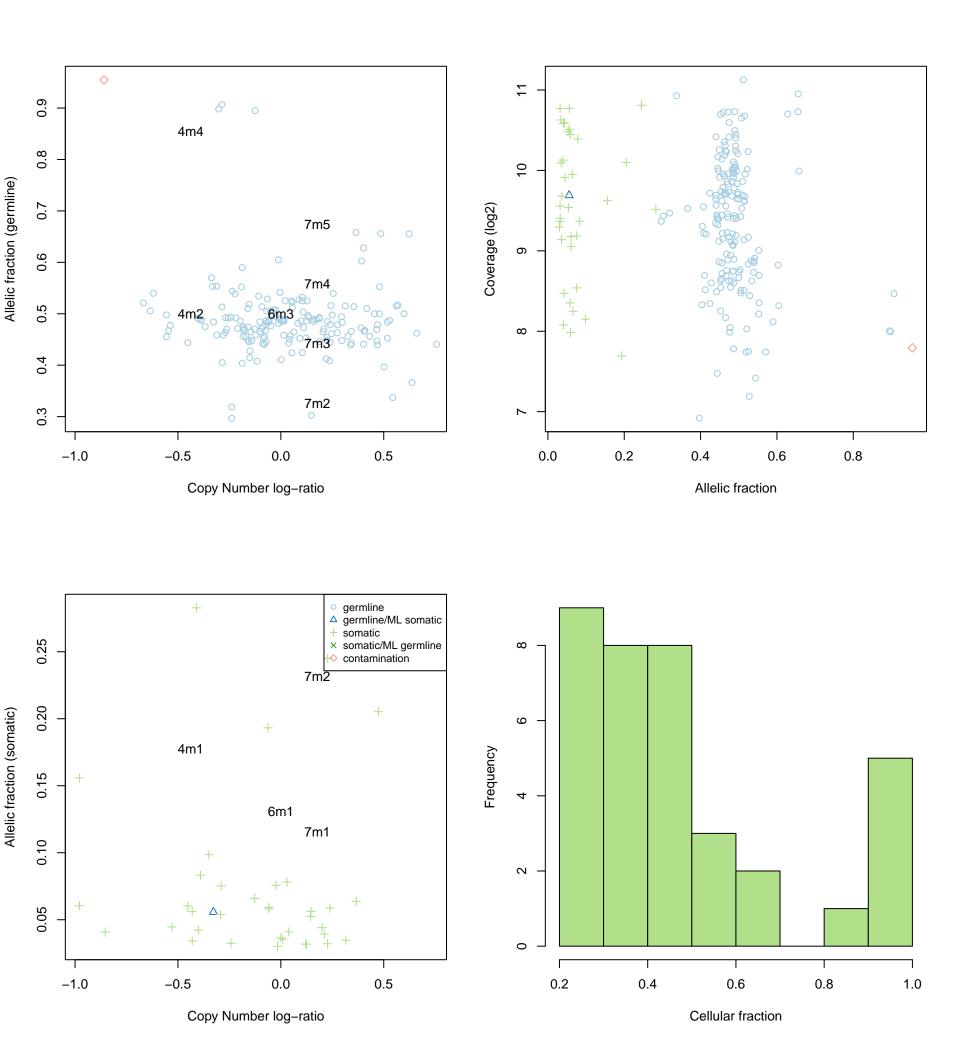




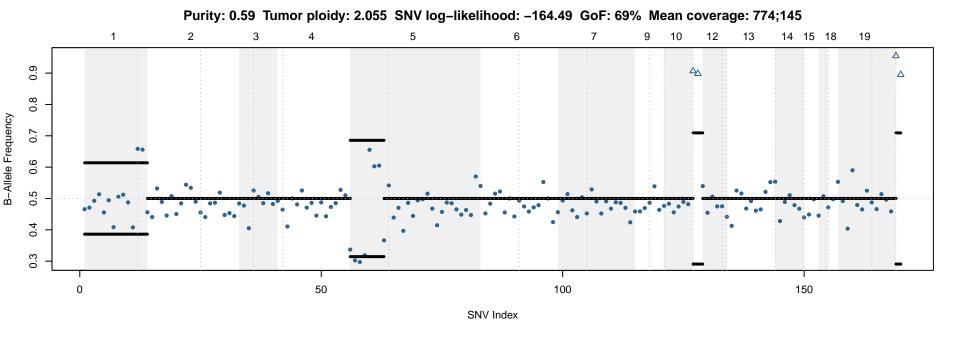
### SCNA-fit log-likelihood: -23930.52



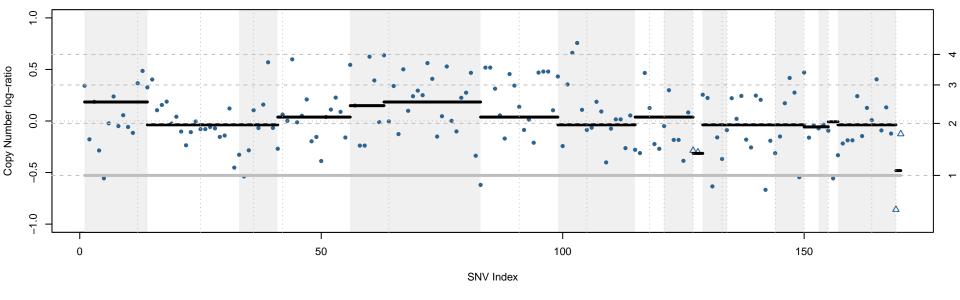


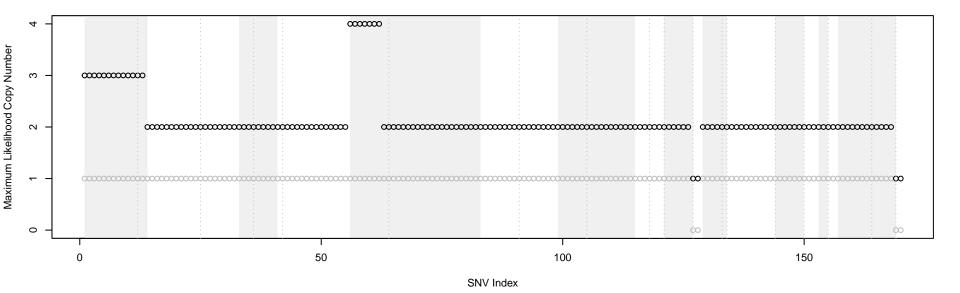


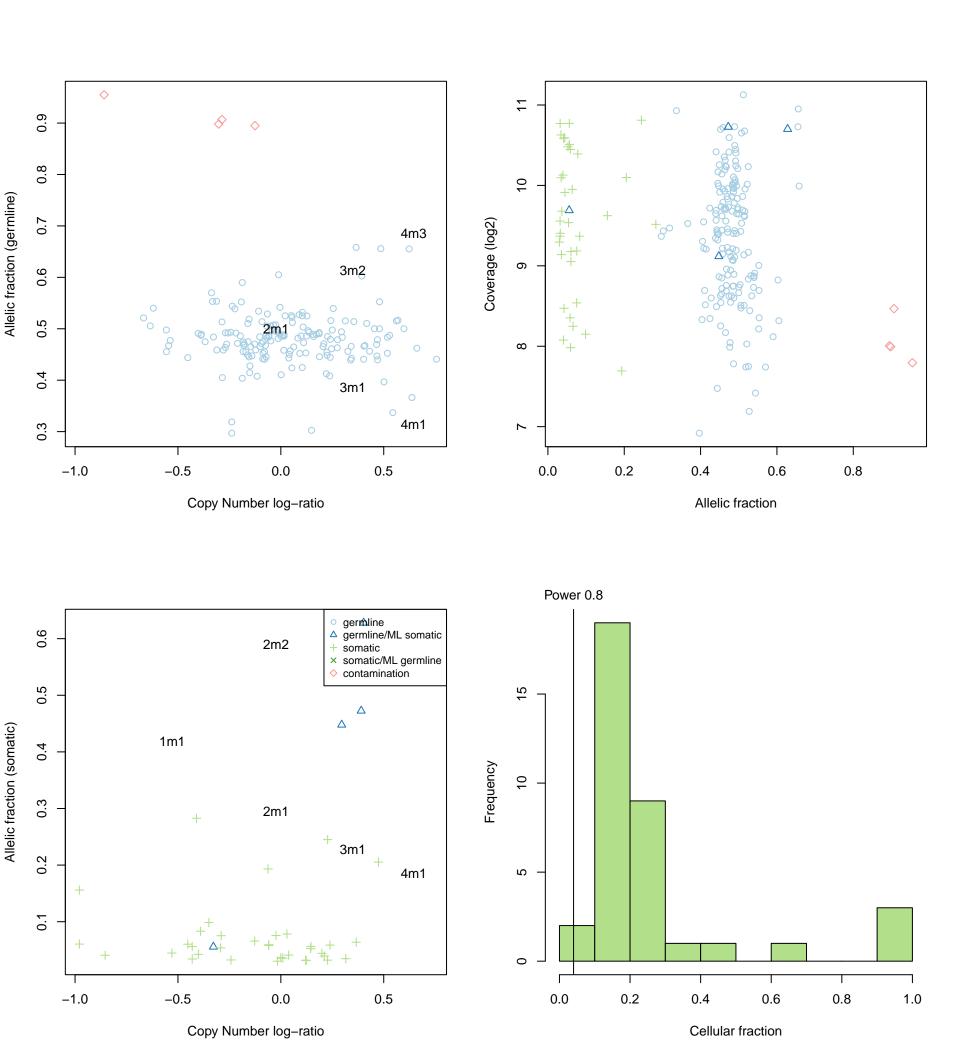
Purity: 0.59 Tumor ploidy: 2.055 3 2 Fraction Genome 0.2 0.1 0.0 -0.5 0.0 0.5 1.0 1.5 2.0 log2 ratio



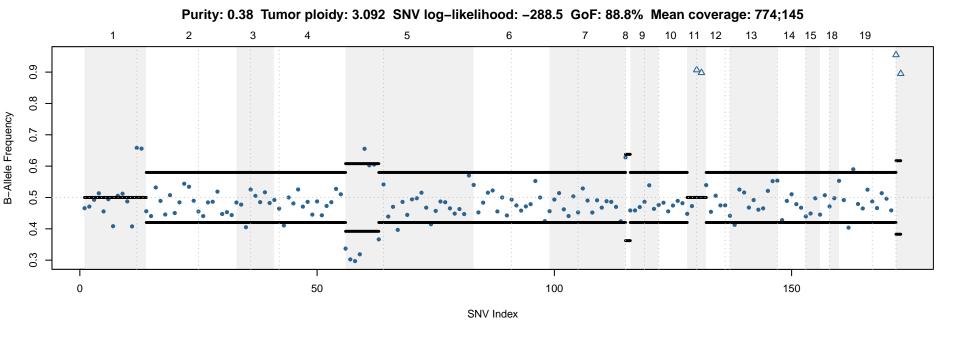
# SCNA-fit log-likelihood: -23968.28



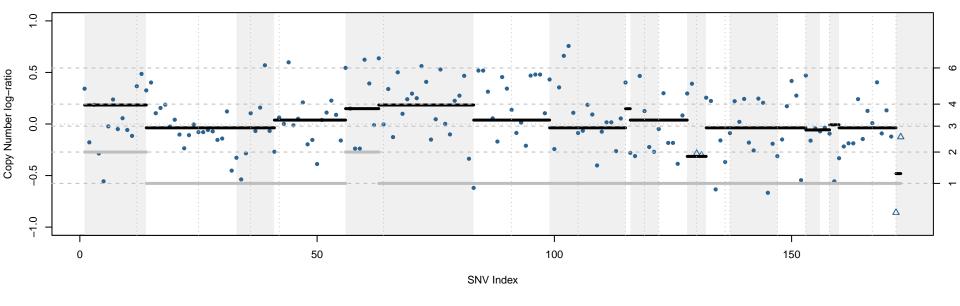


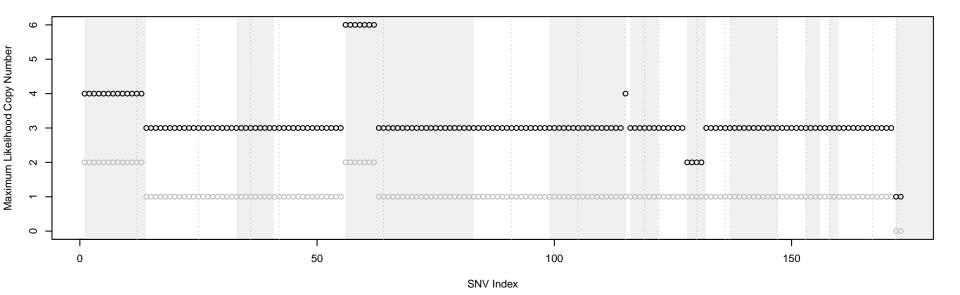


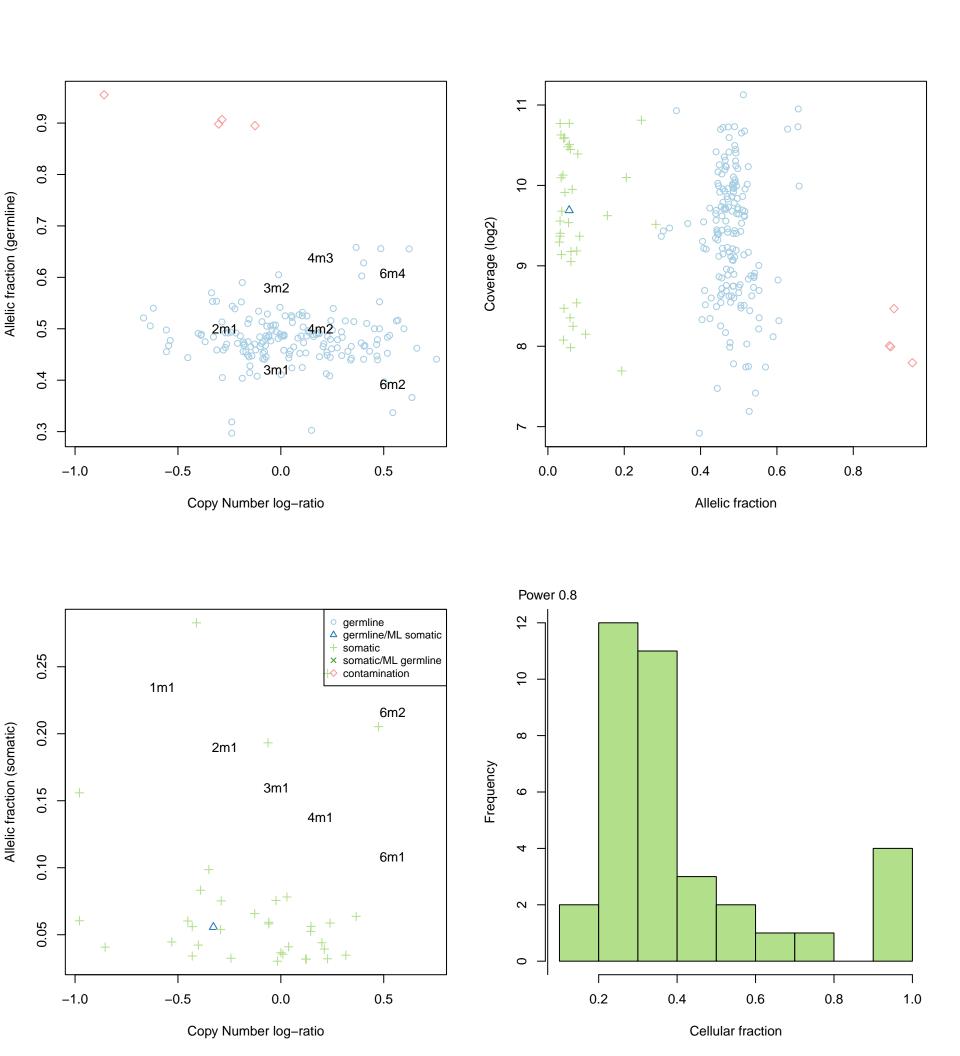
Purity: 0.38 Tumor ploidy: 3.092 2 3 6 Fraction Genome 0.2 0.1 0.0 -0.5 0.0 0.5 1.0 1.5 2.0 log2 ratio



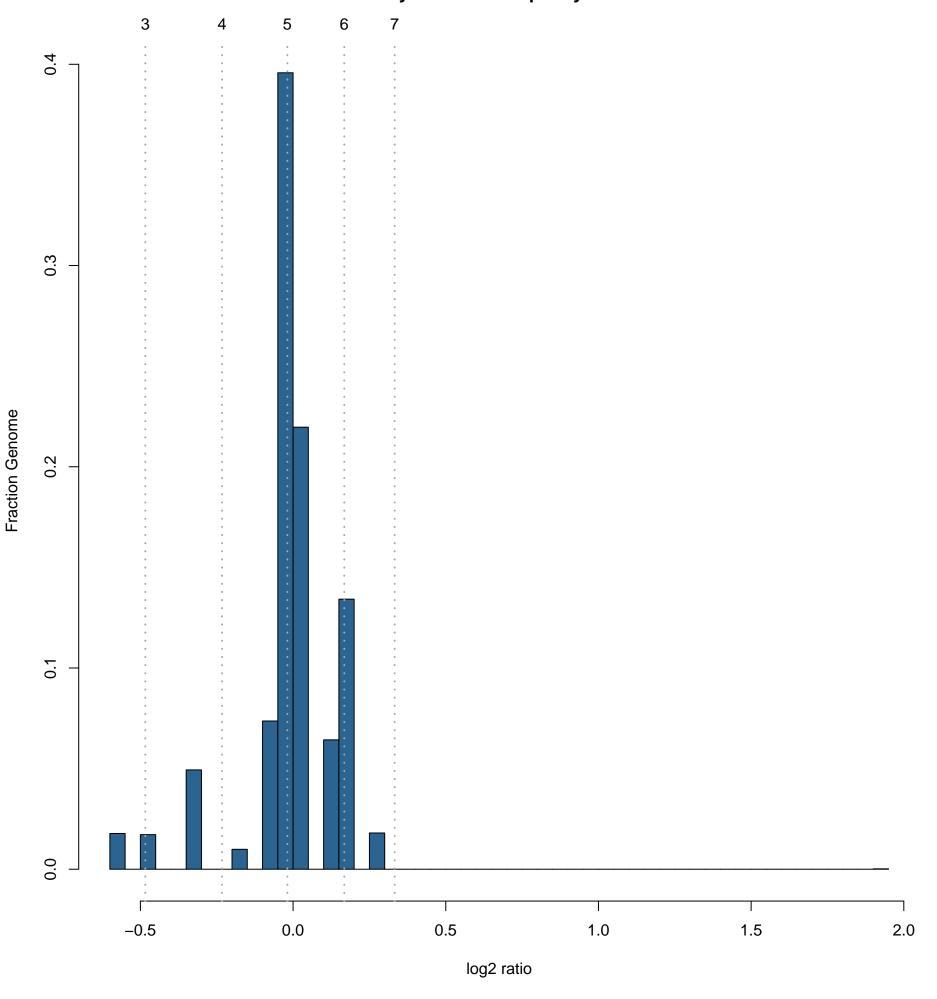
### SCNA-fit log-likelihood: -23883.17

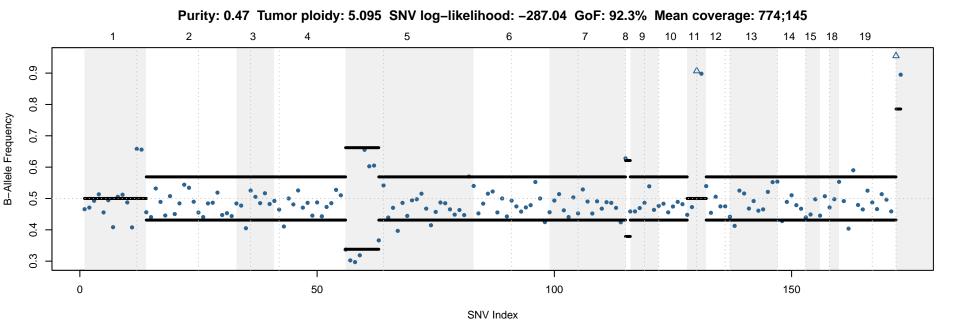




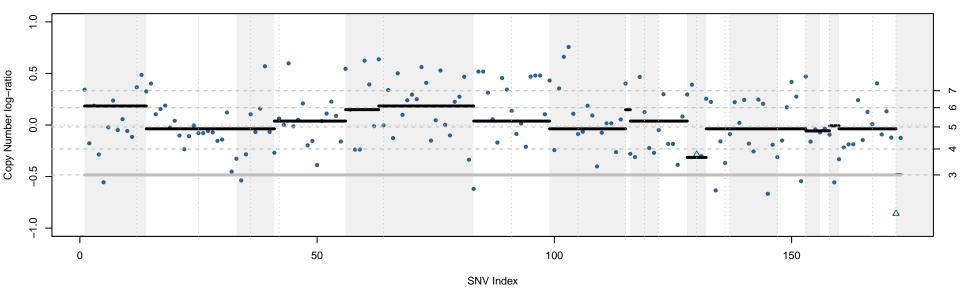


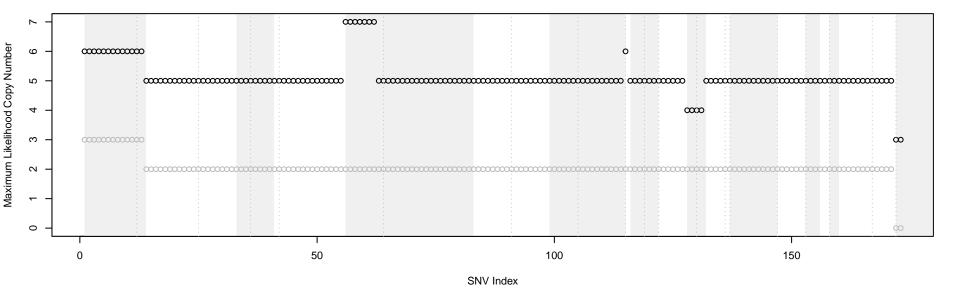
Purity: 0.47 Tumor ploidy: 5.095

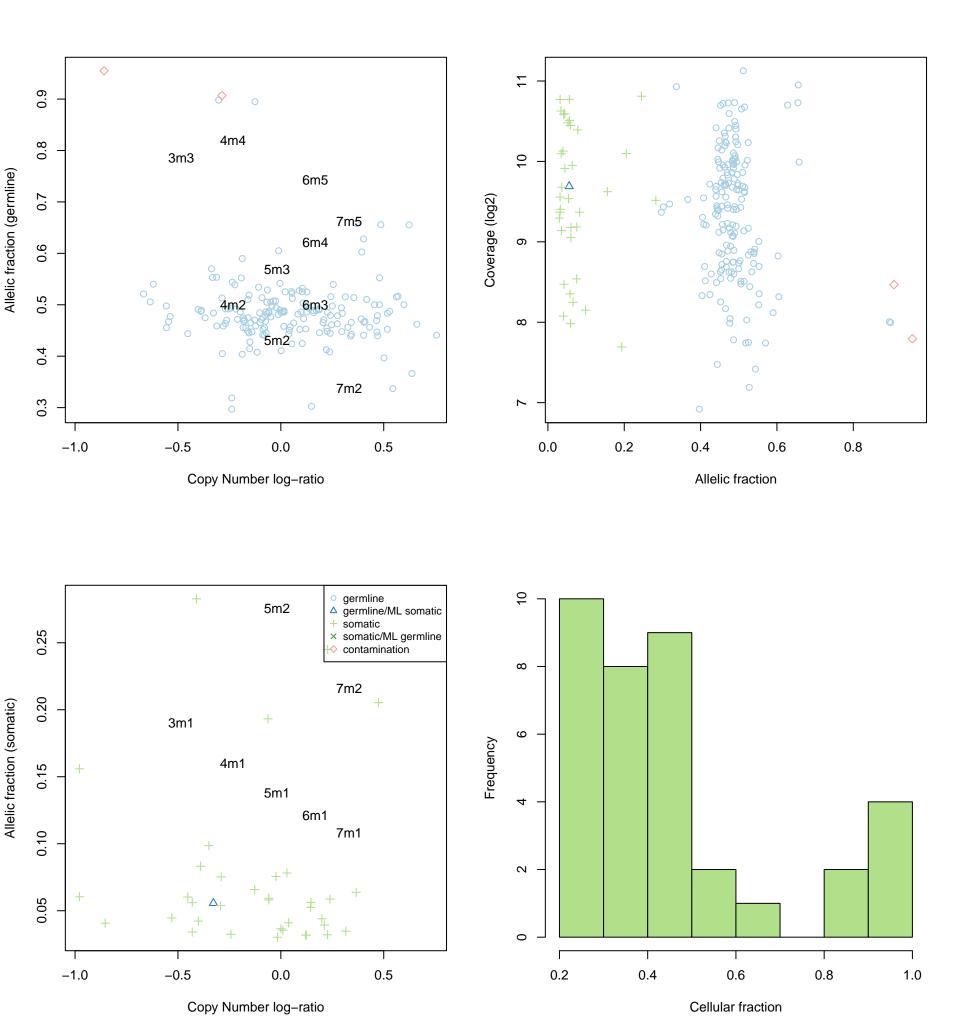


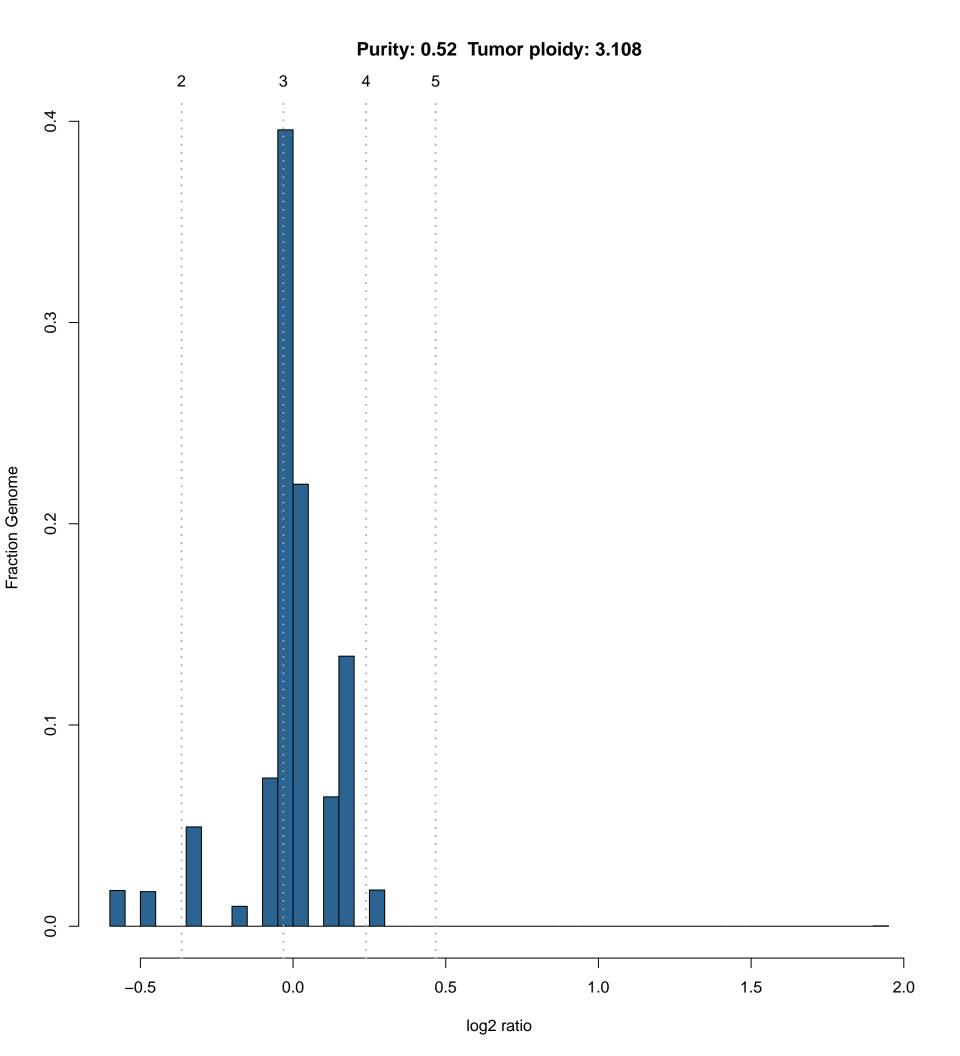


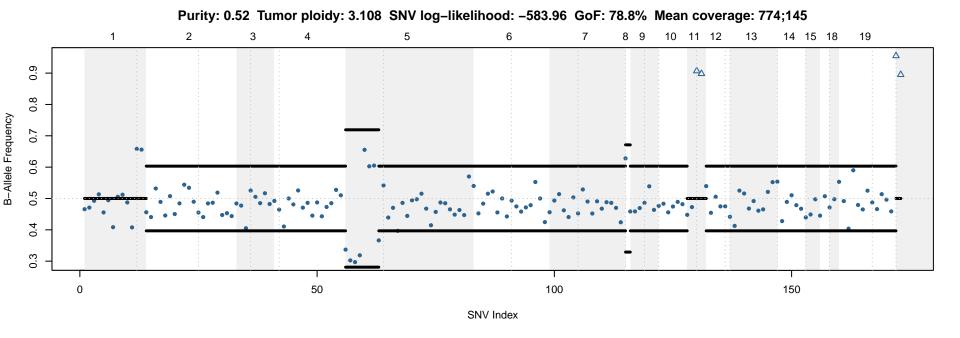
### SCNA-fit log-likelihood: -23896.88











### SCNA-fit log-likelihood: -23906.51

