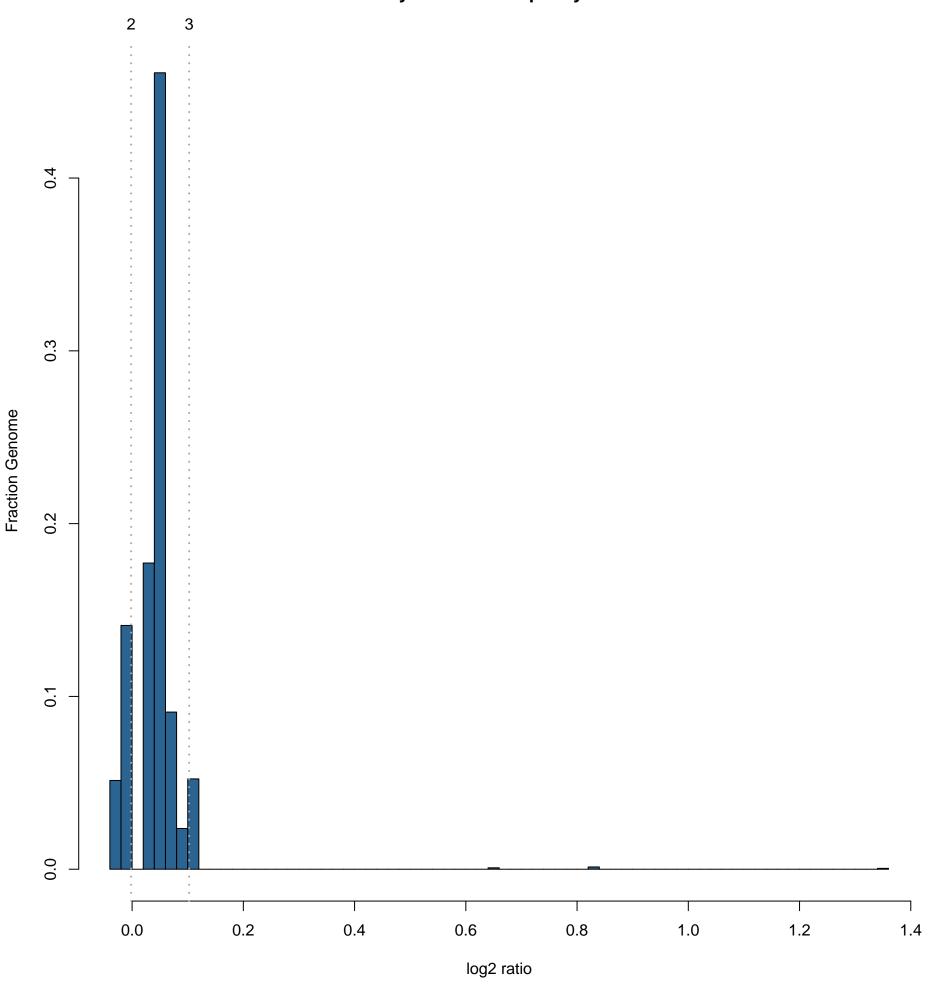
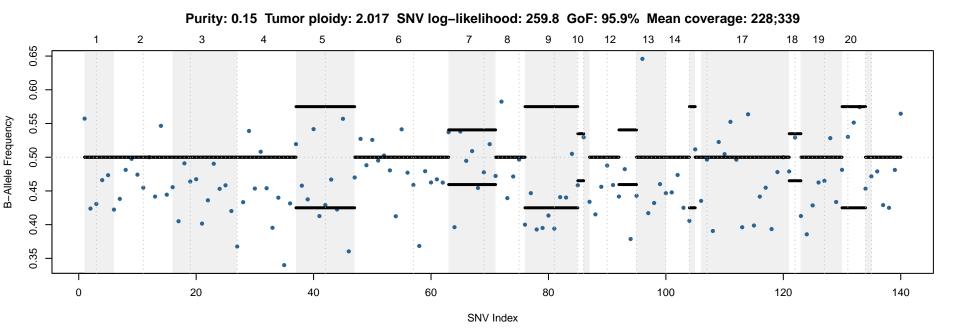
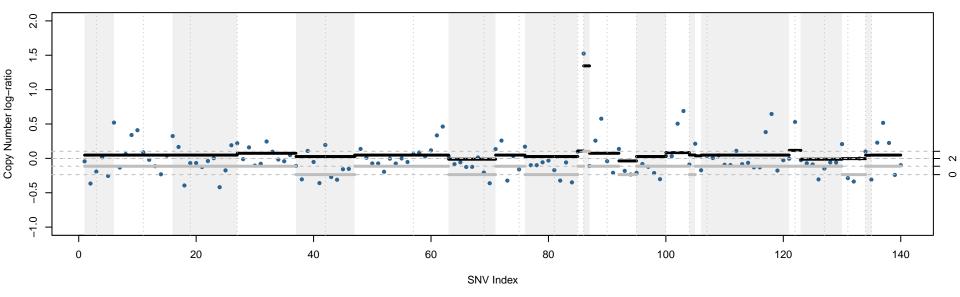
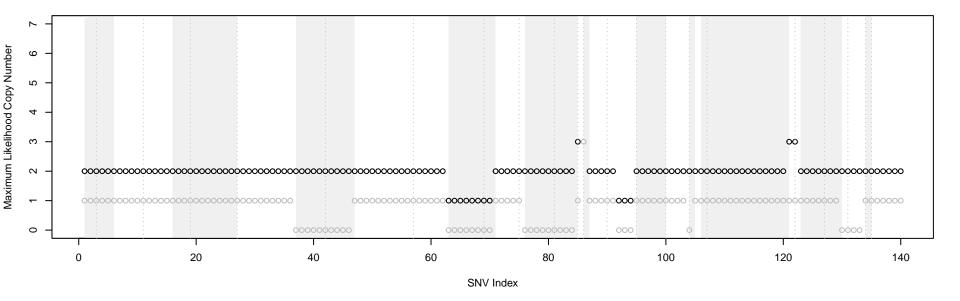
Purity: 0.15 Tumor ploidy: 2.017

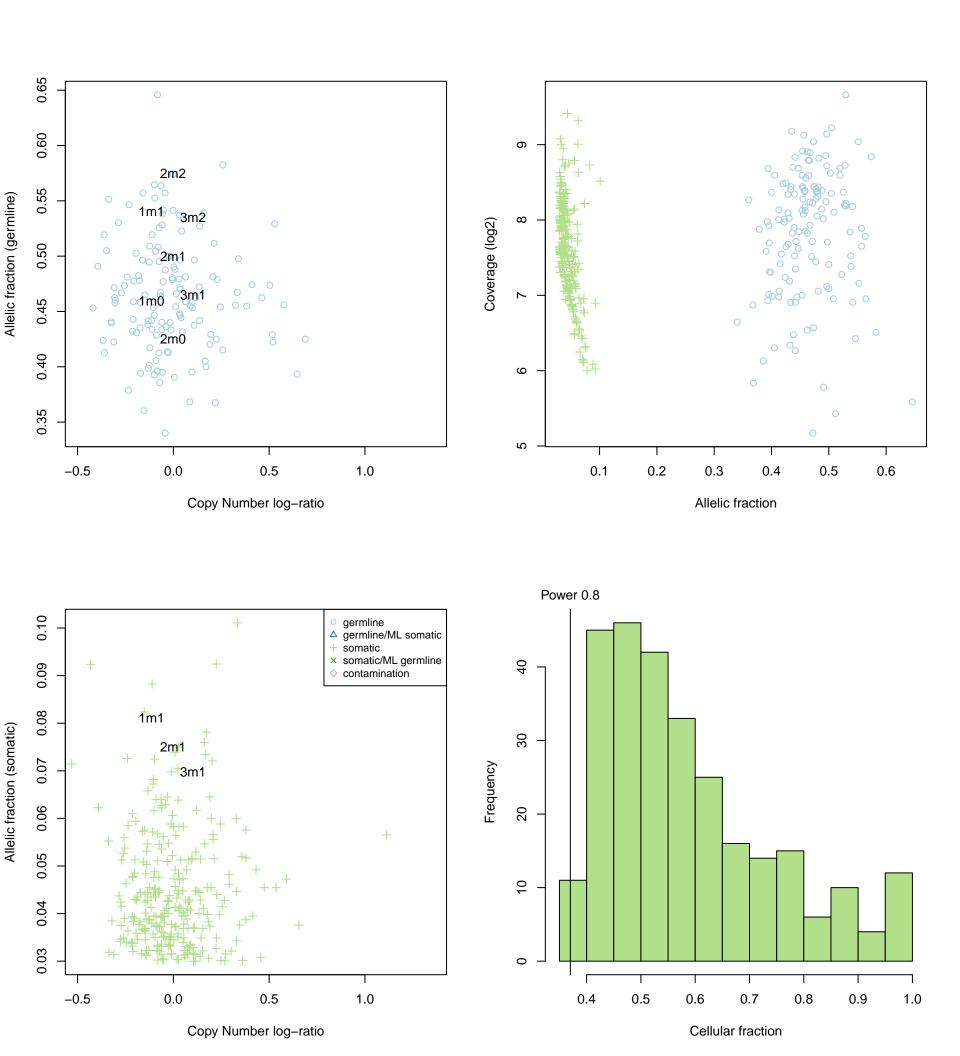




SCNA-fit log-likelihood: -4010.23

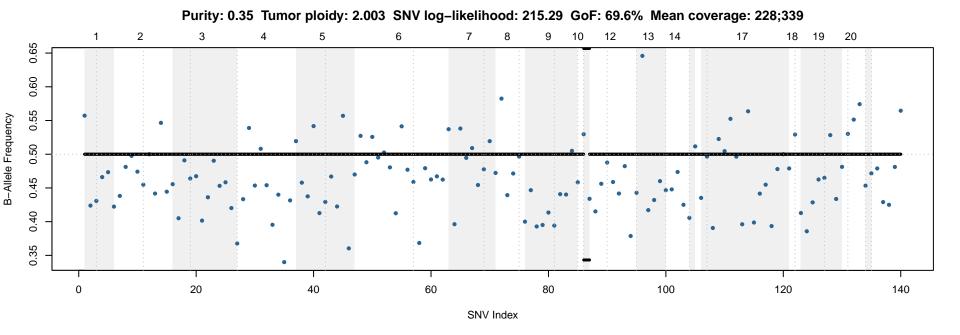




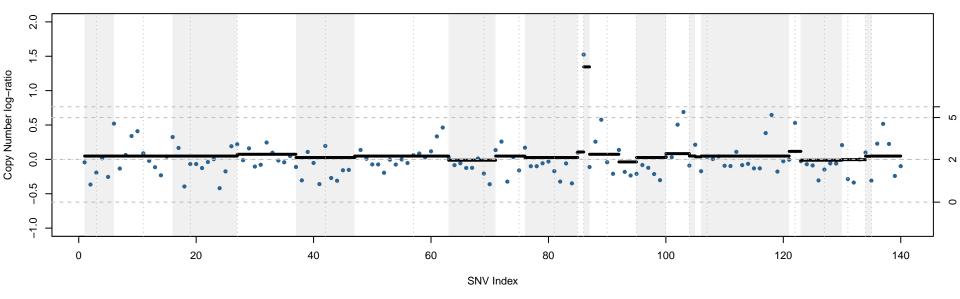


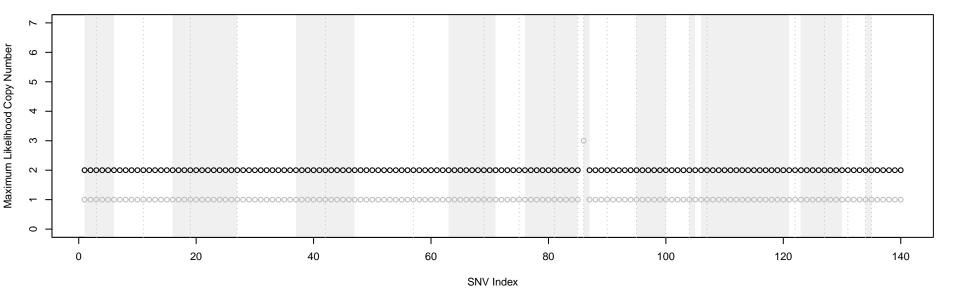
Purity: 0.35 Tumor ploidy: 2.003 0 2 6 Fraction Genome 0.2 0.1 0.0 -0.5 0.0 0.5 1.0

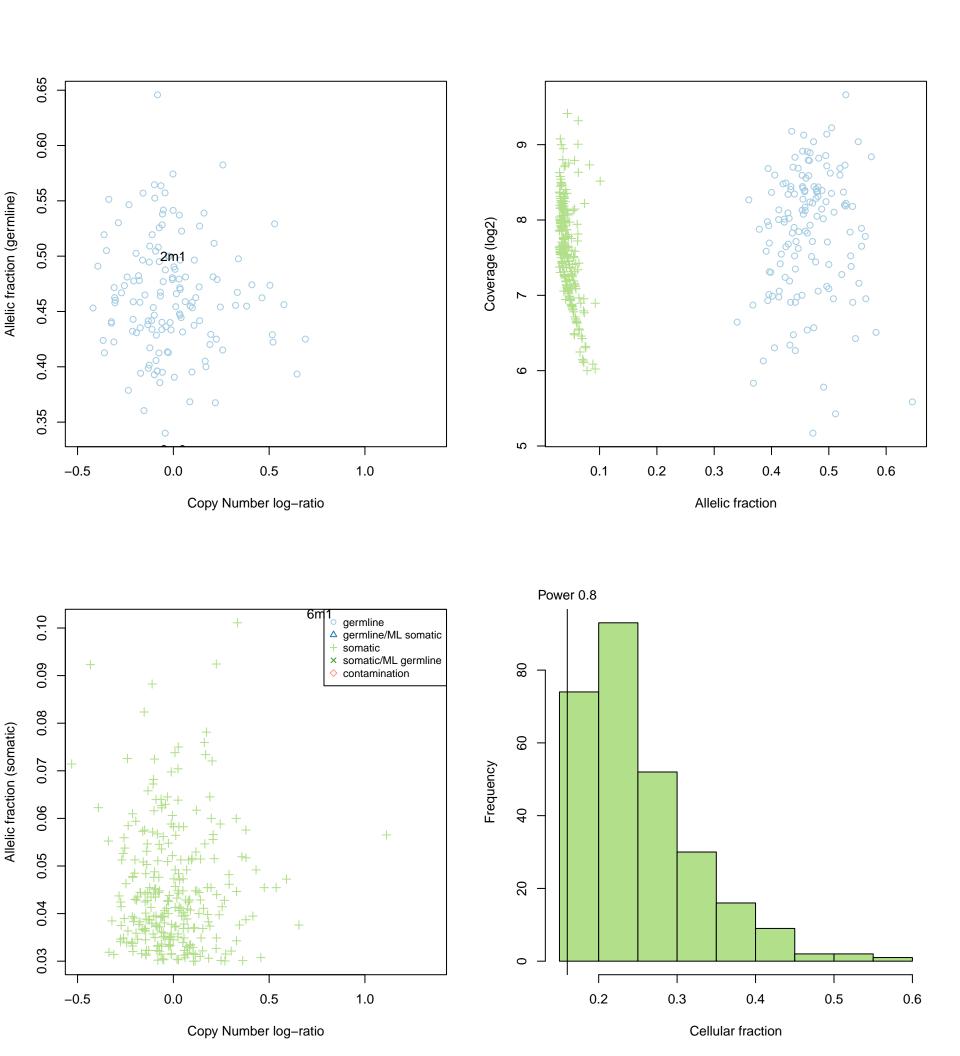
log2 ratio



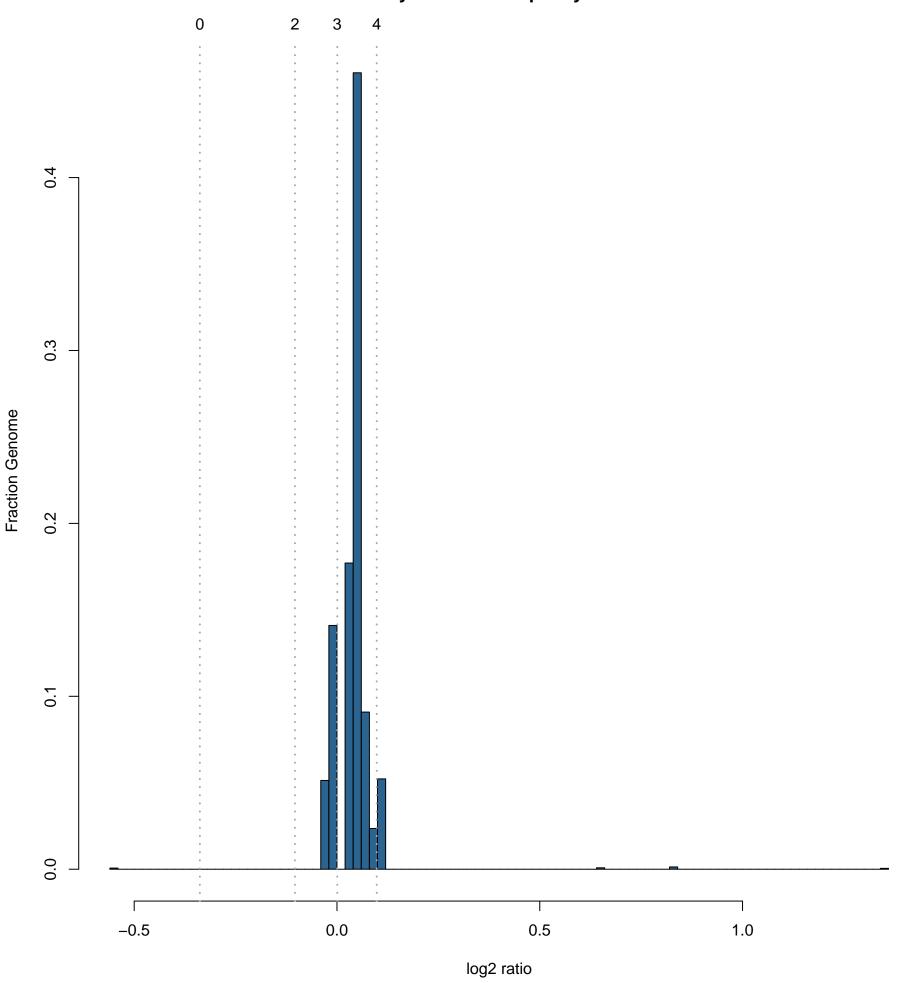
SCNA-fit log-likelihood: -3998.97

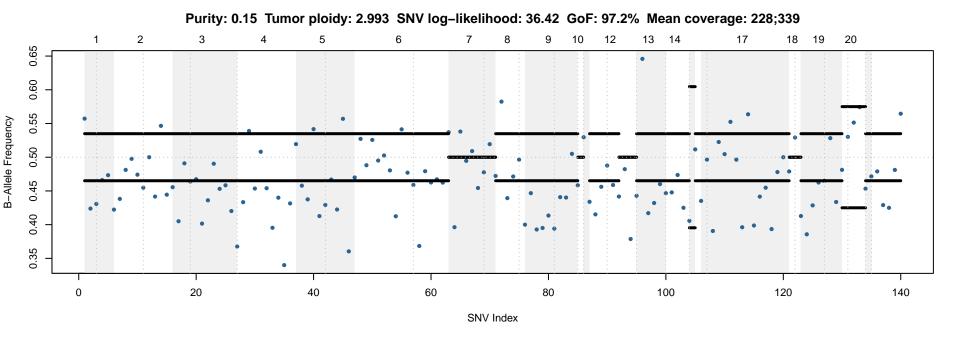




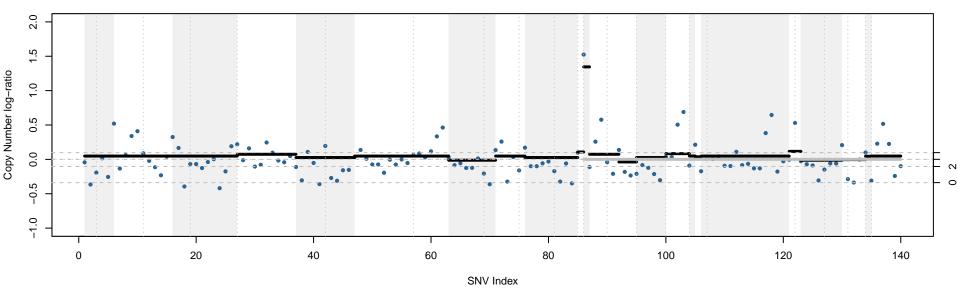


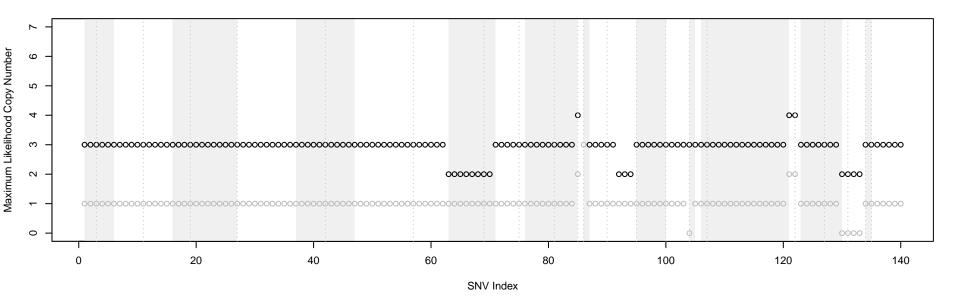
Purity: 0.15 Tumor ploidy: 2.993

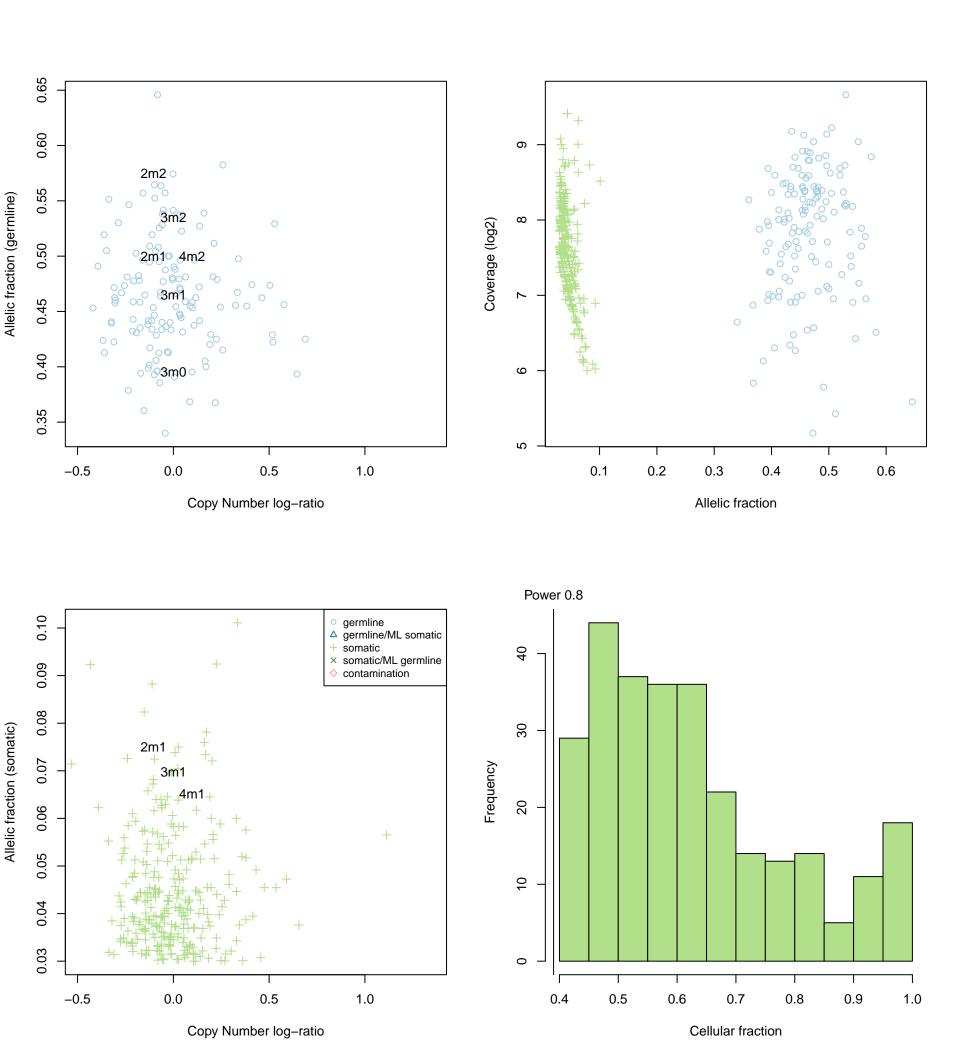




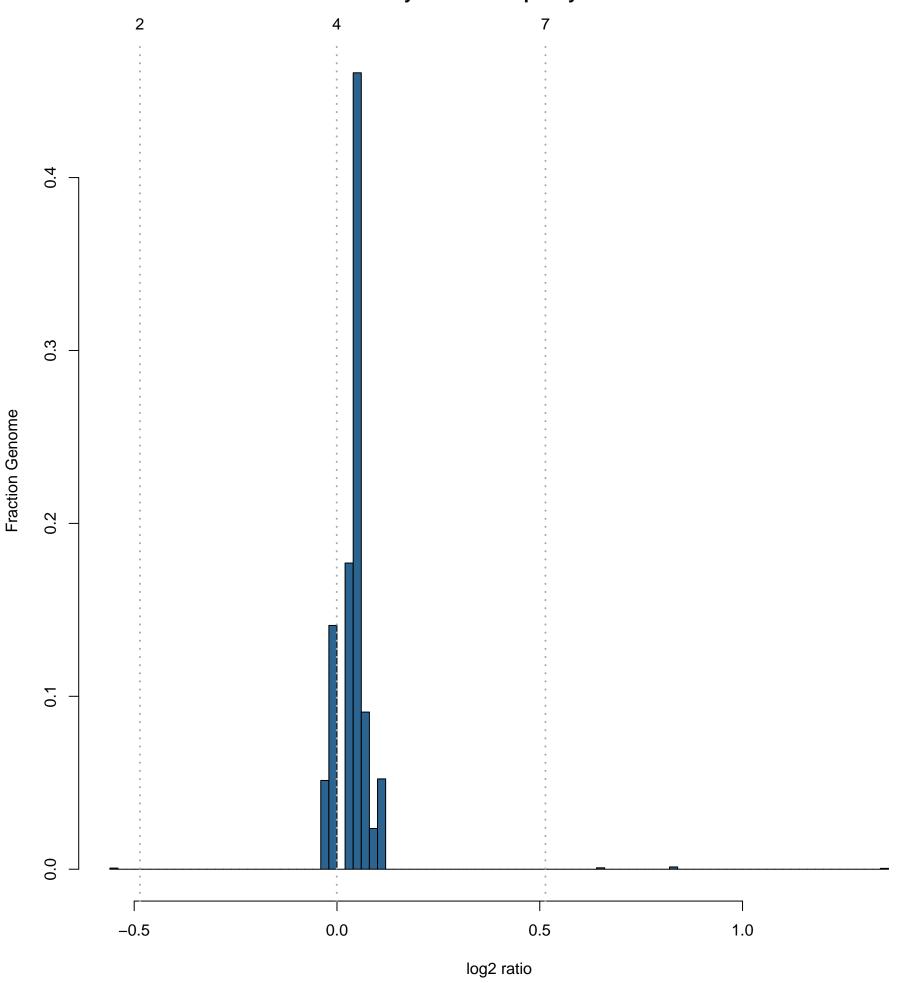
SCNA-fit log-likelihood: -4003.16

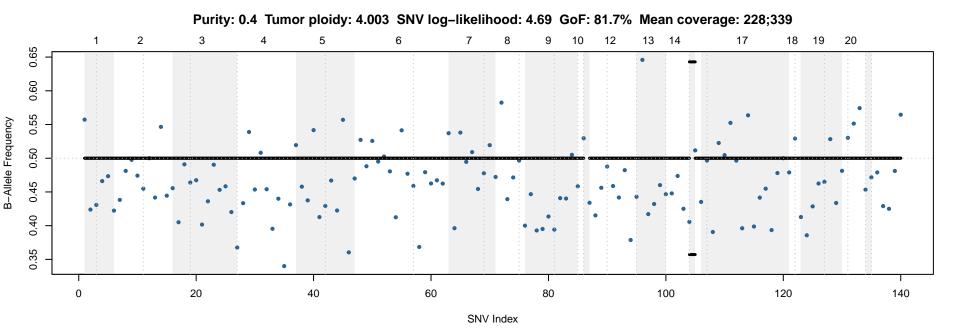




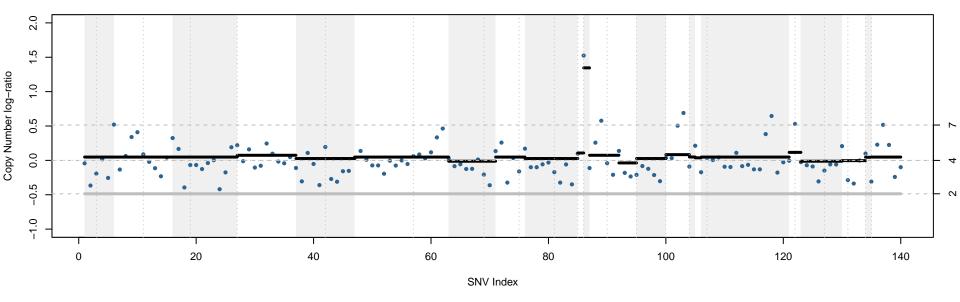


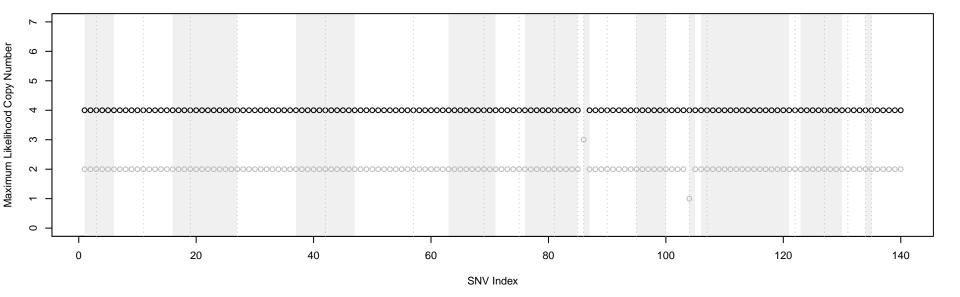
Purity: 0.4 Tumor ploidy: 4.003

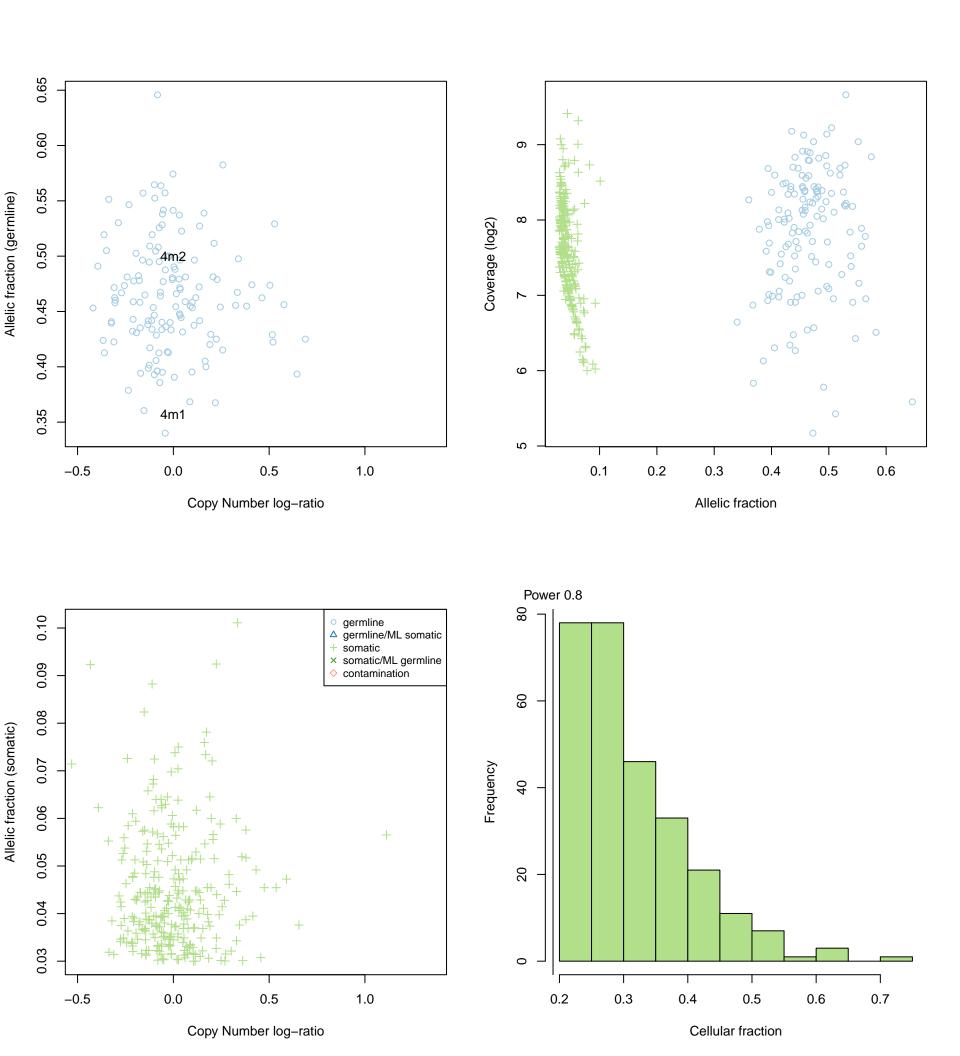




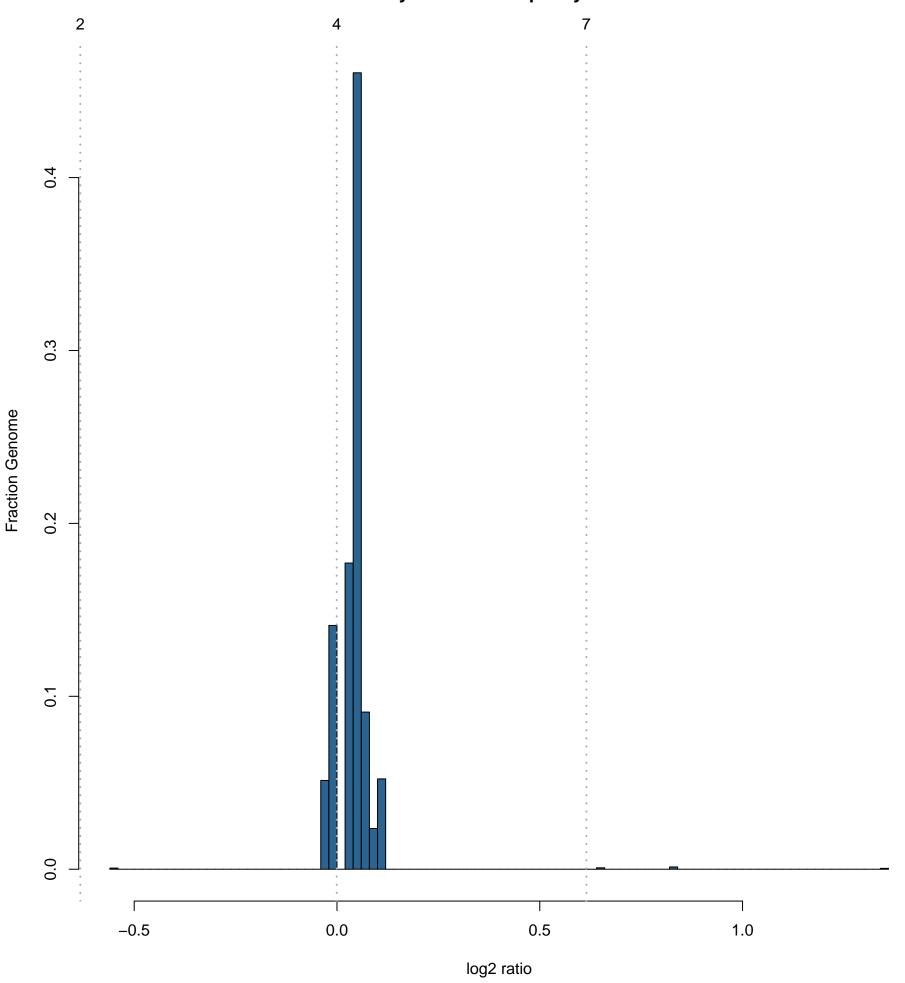
SCNA-fit log-likelihood: -4022.49

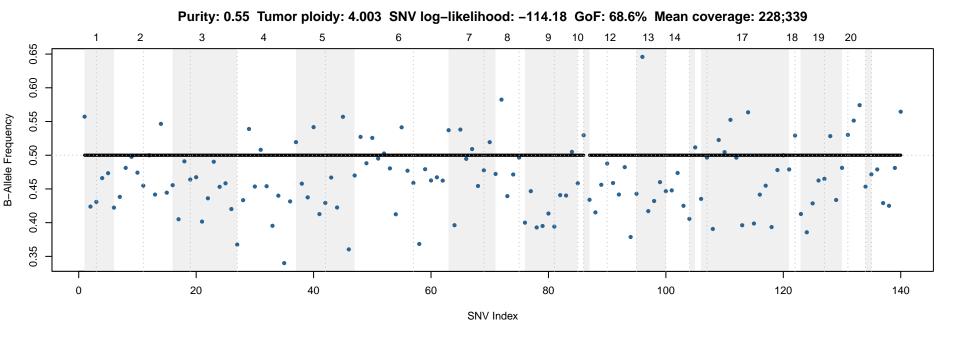




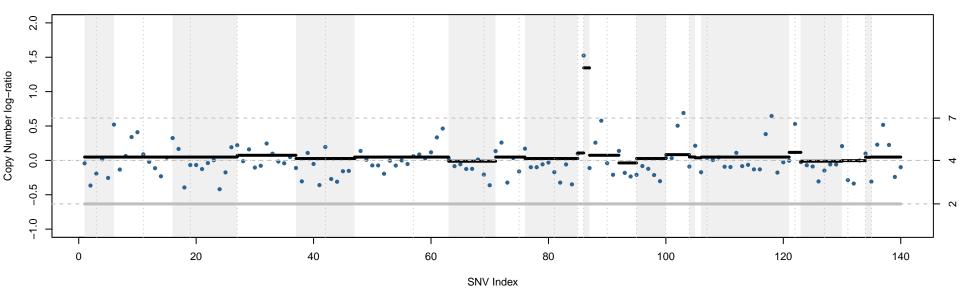


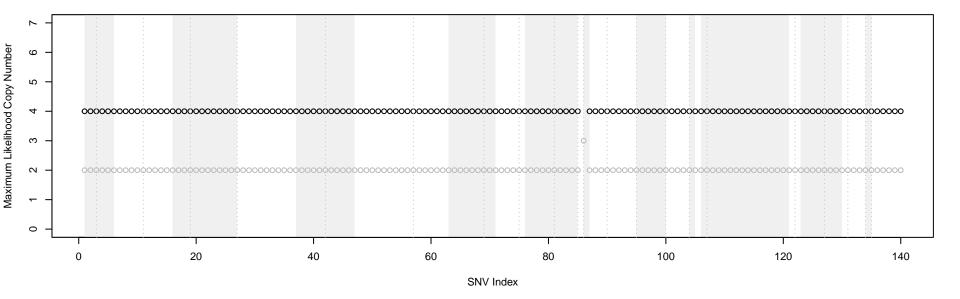
Purity: 0.55 Tumor ploidy: 4.003

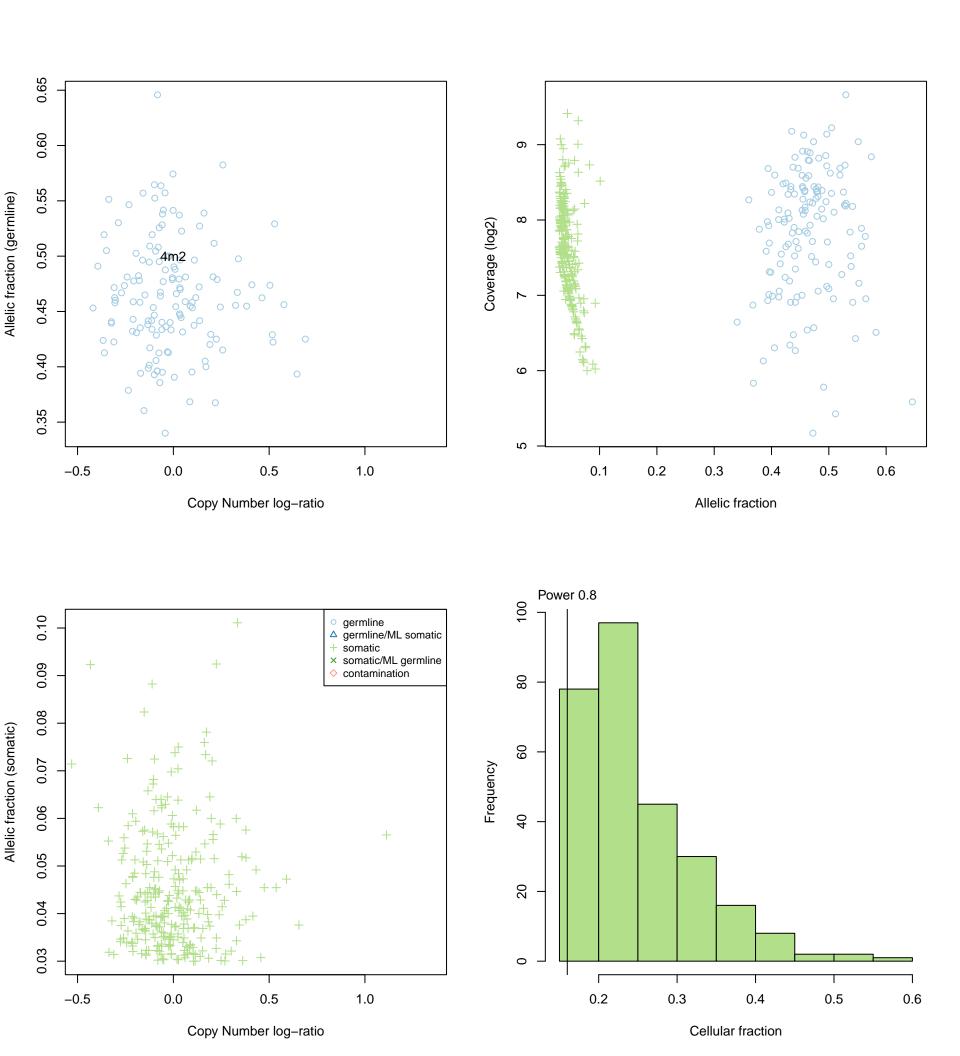




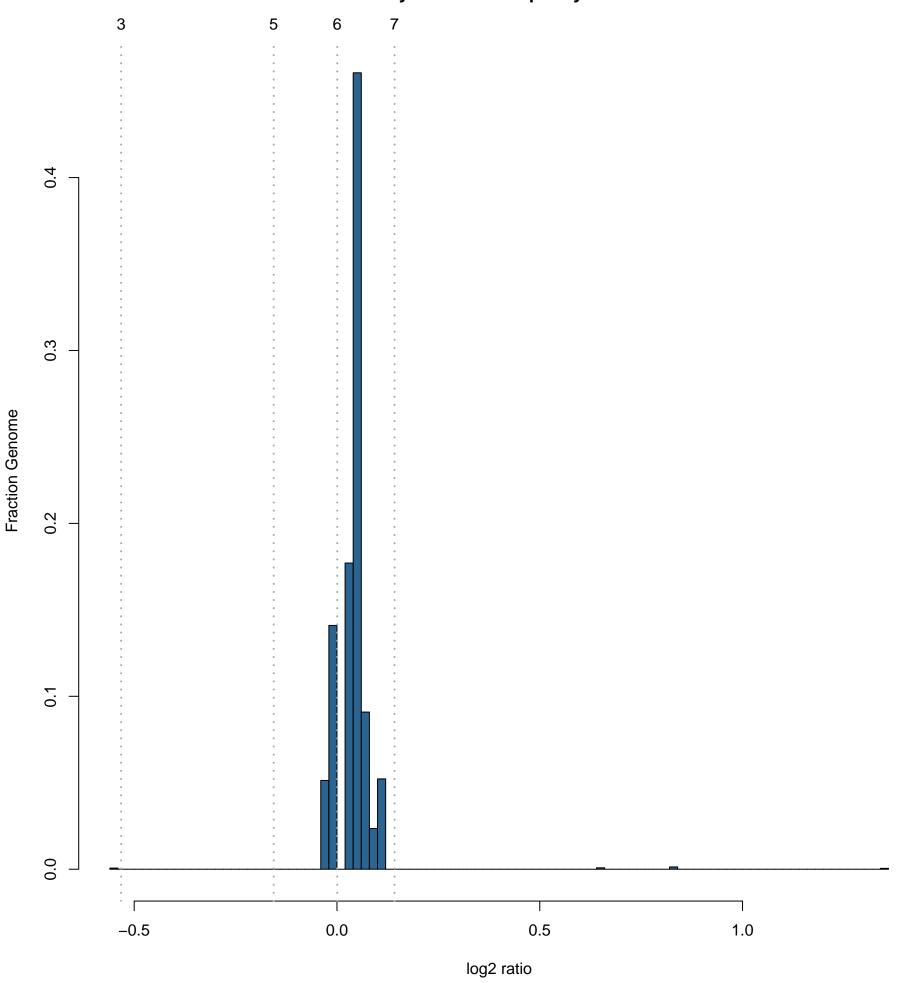


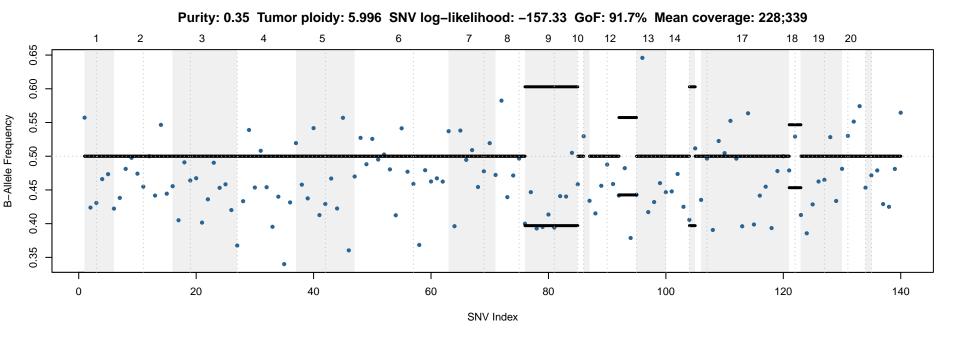




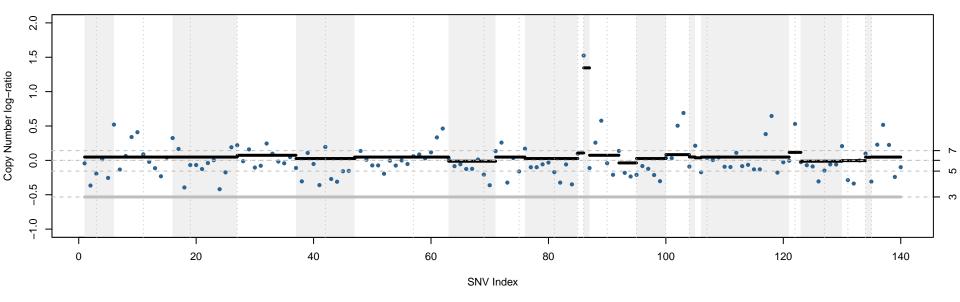


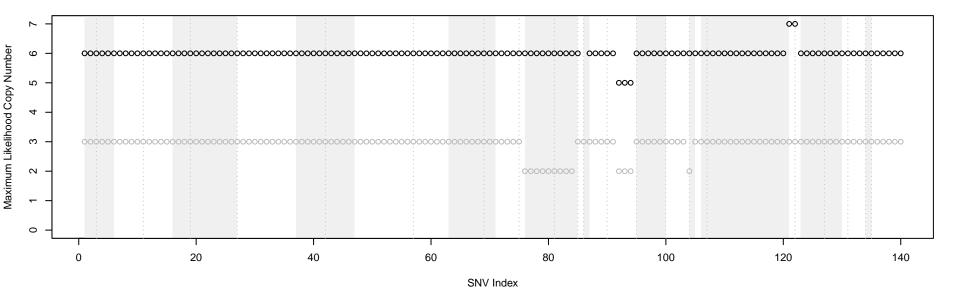
Purity: 0.35 Tumor ploidy: 5.996

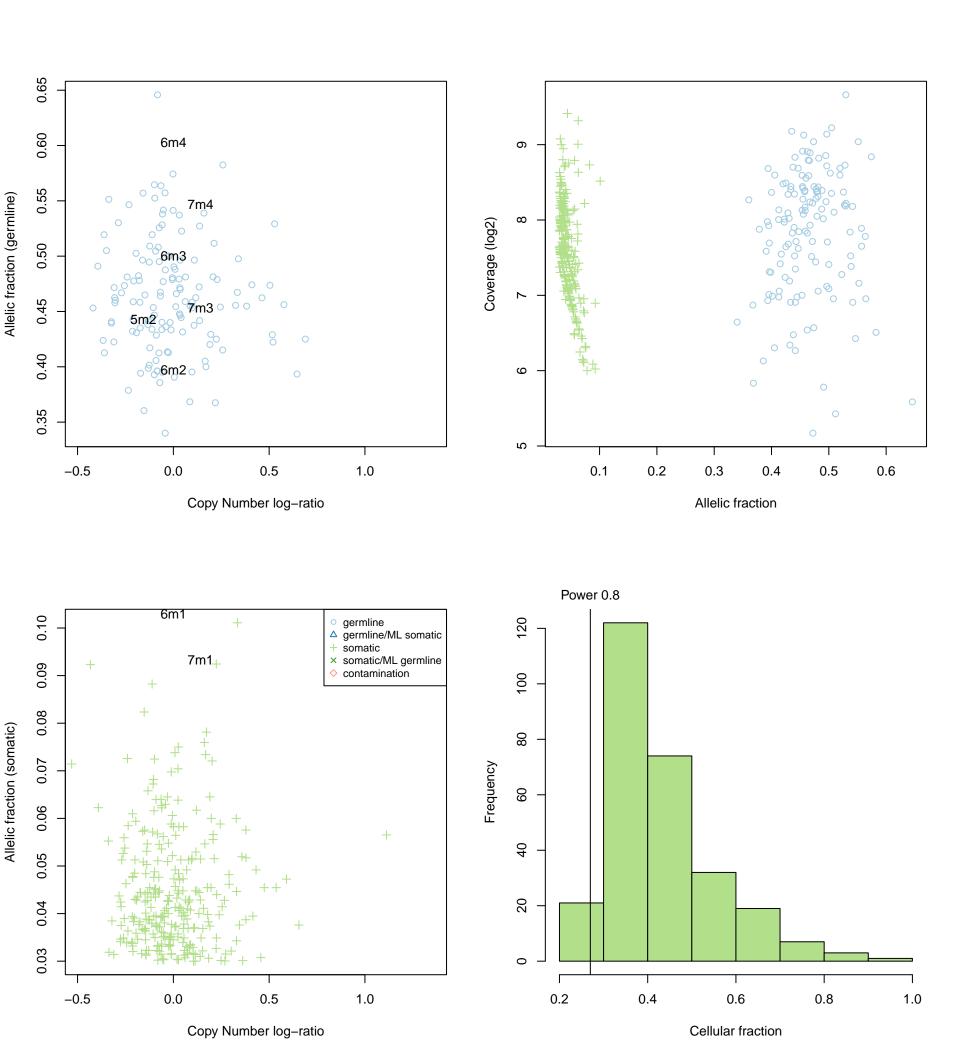




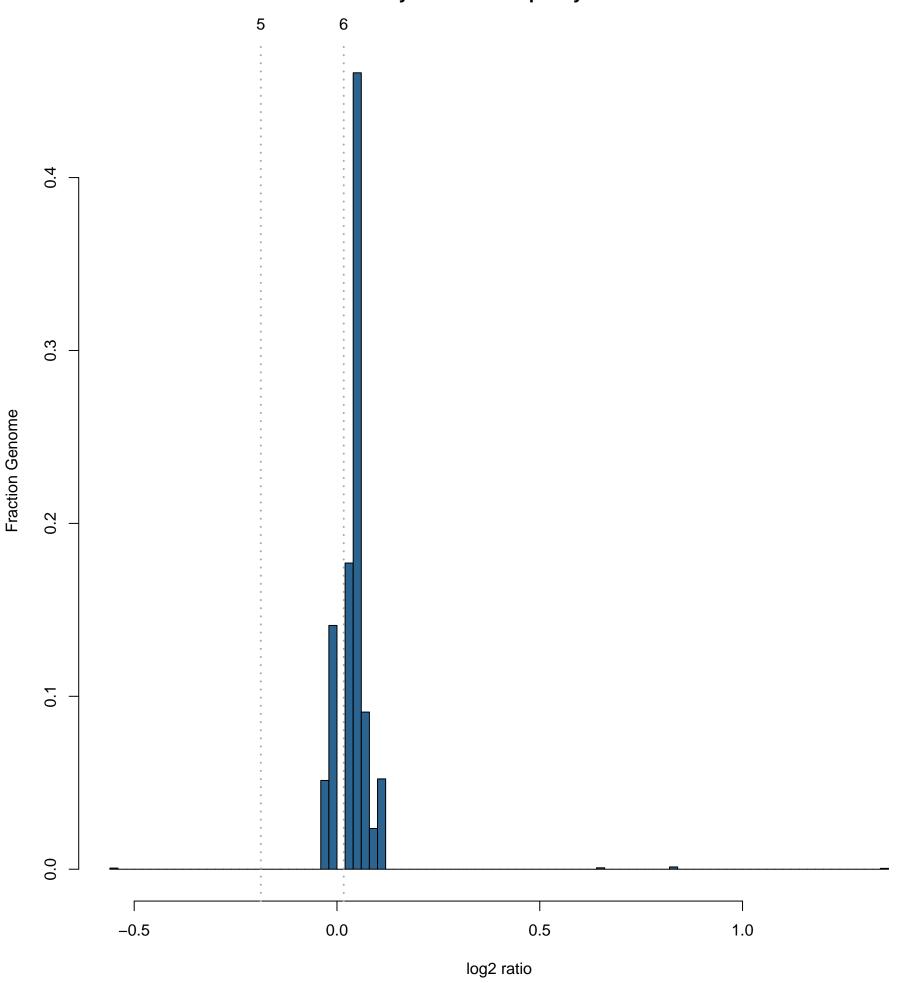
SCNA-fit log-likelihood: -4041.38

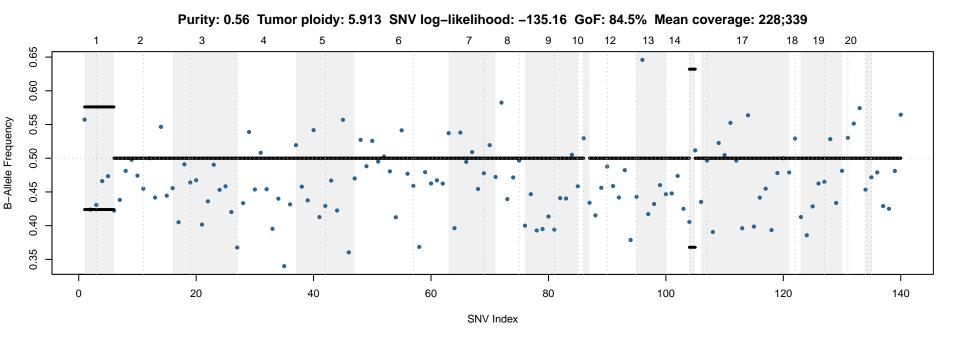




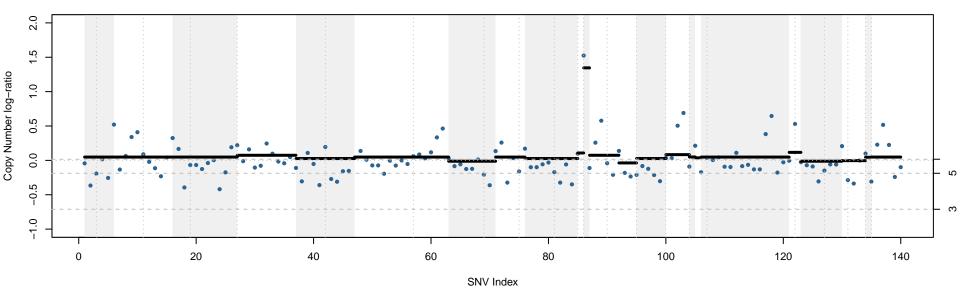


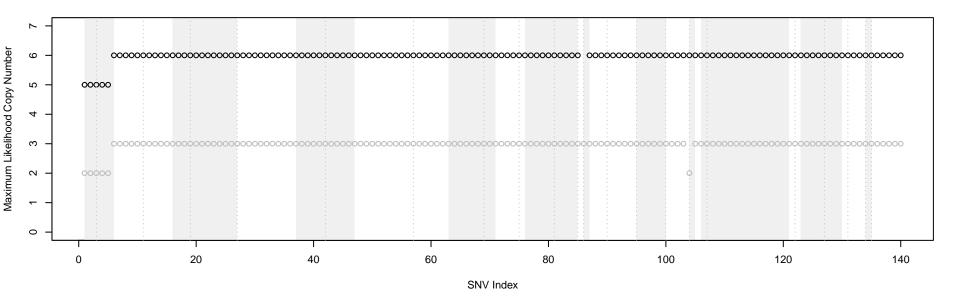
Purity: 0.56 Tumor ploidy: 5.913

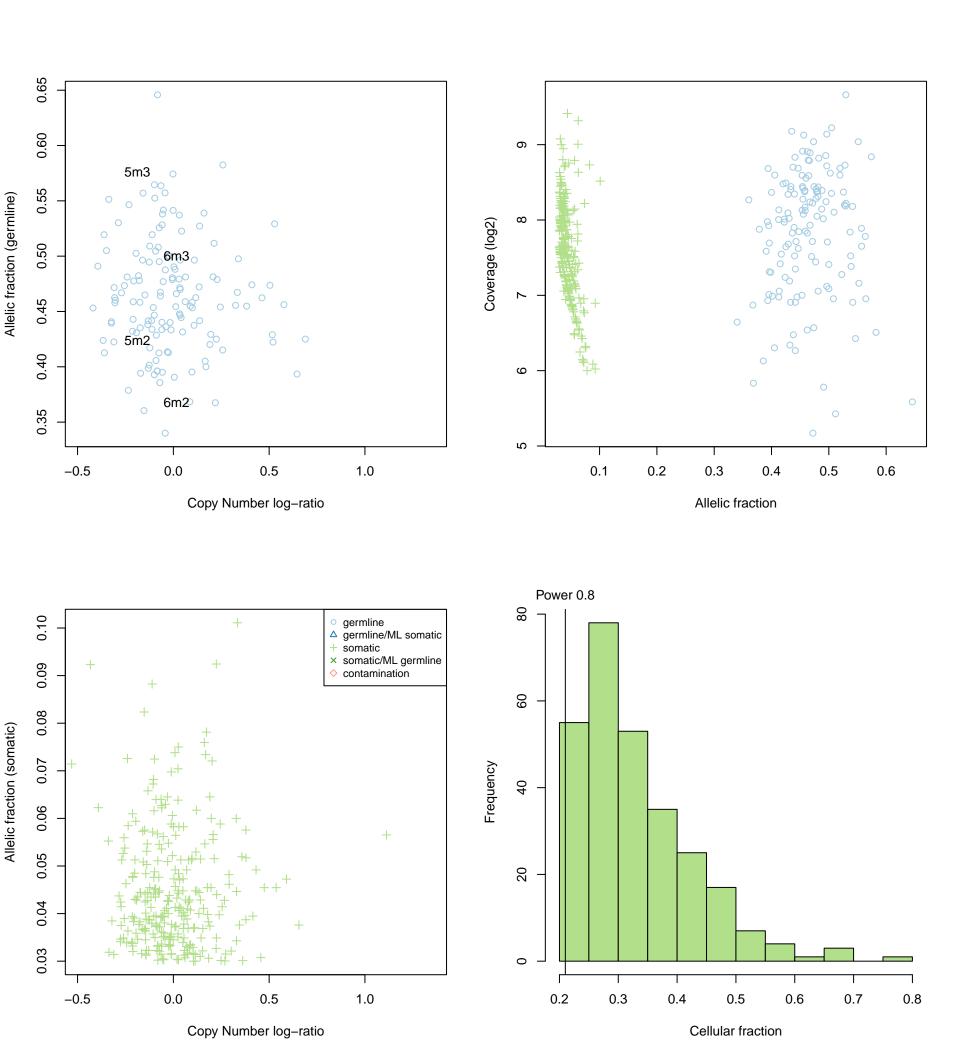




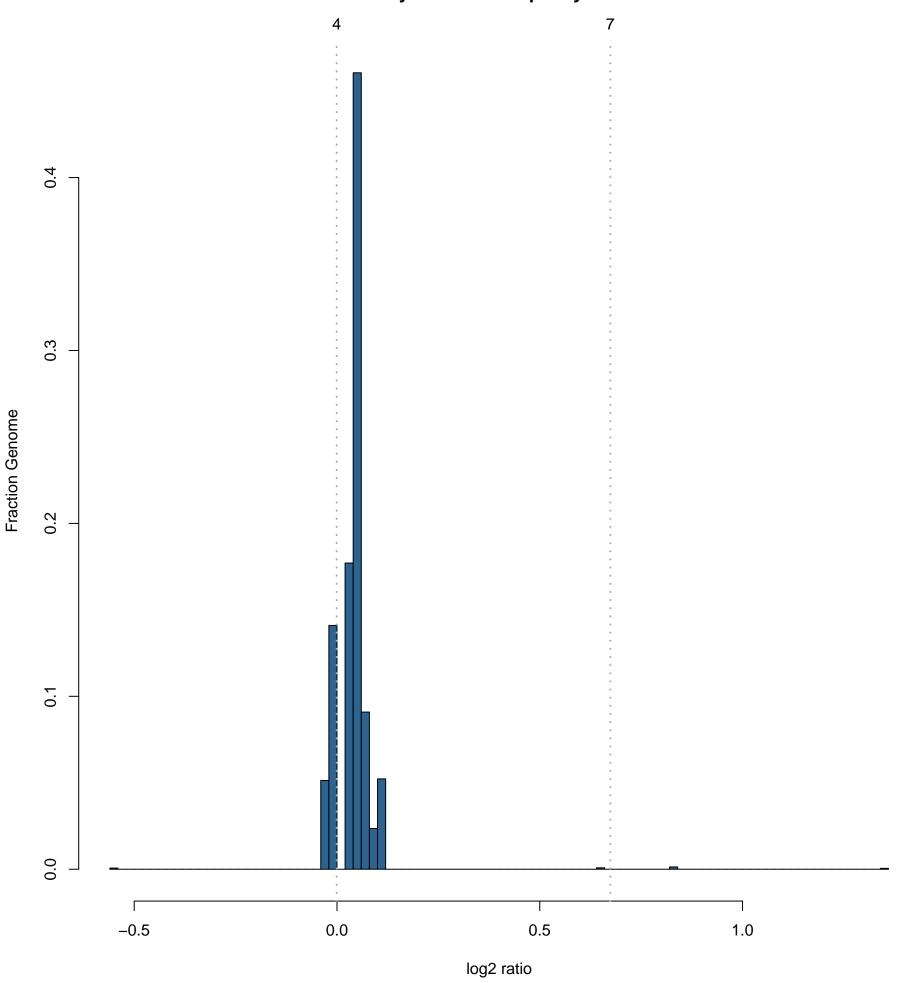
SCNA-fit log-likelihood: -4176.5

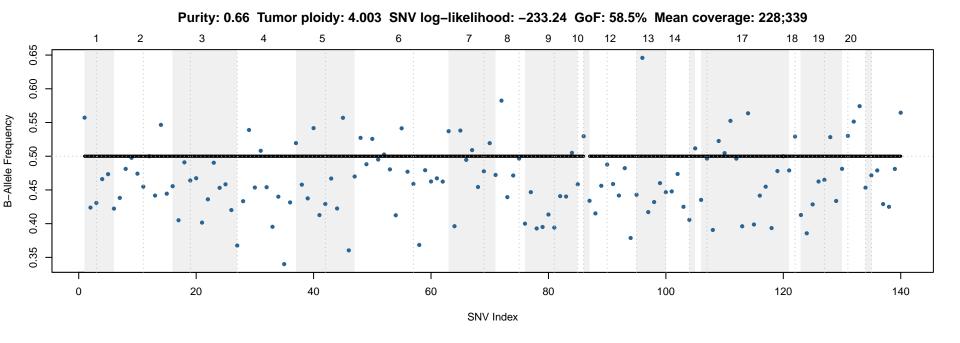




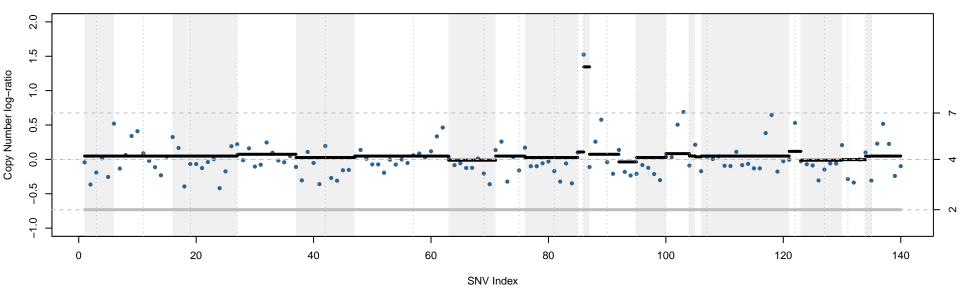


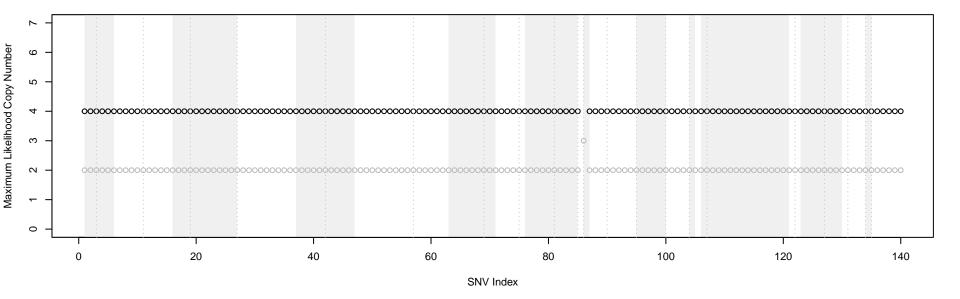
Purity: 0.66 Tumor ploidy: 4.003

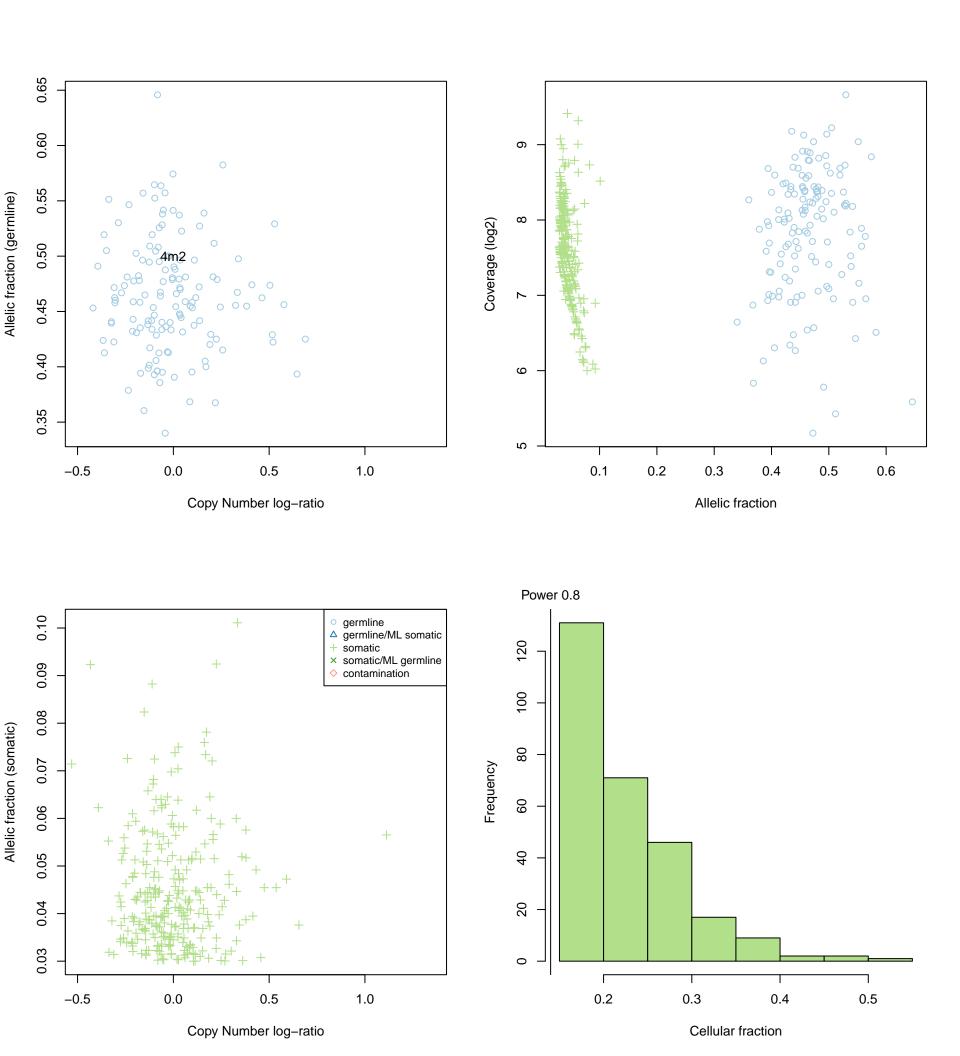




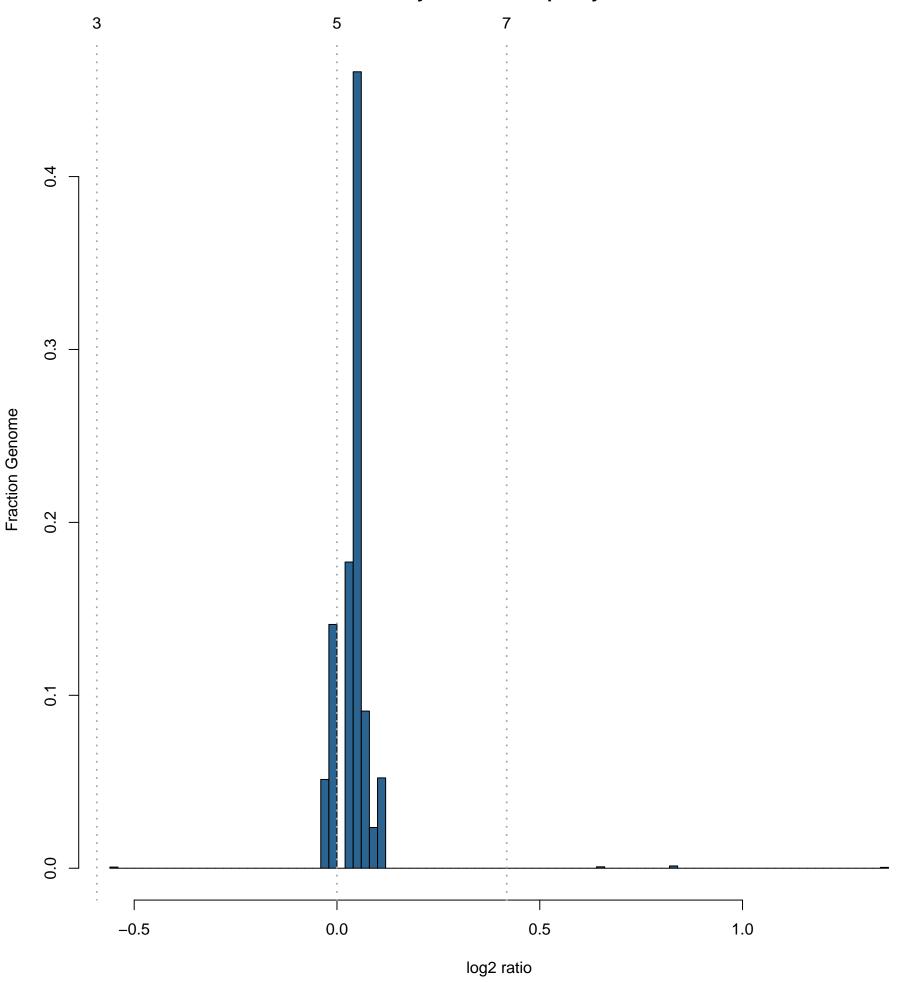
SCNA-fit log-likelihood: -4001.05

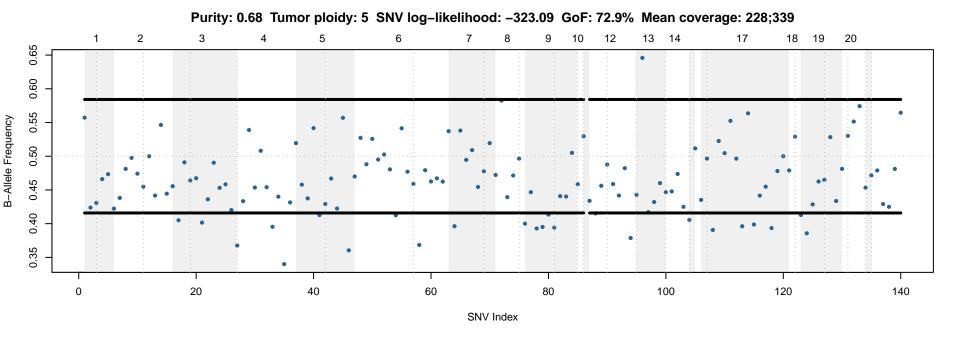




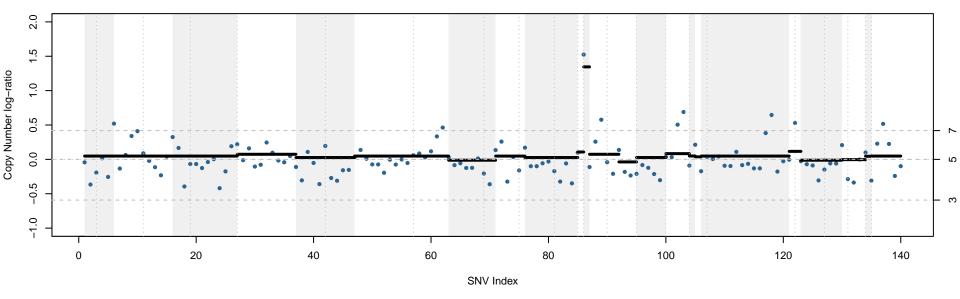


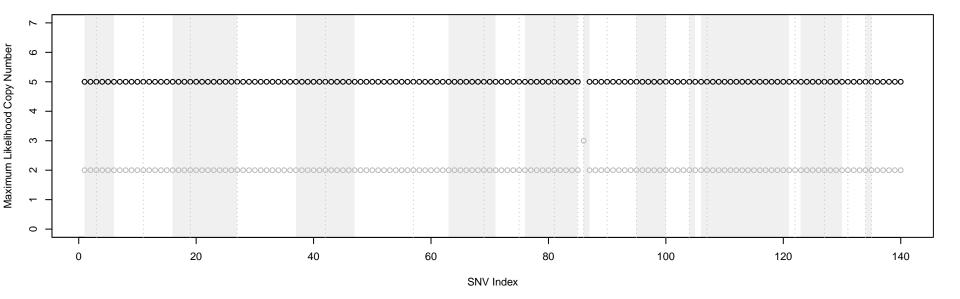
Purity: 0.68 Tumor ploidy: 5

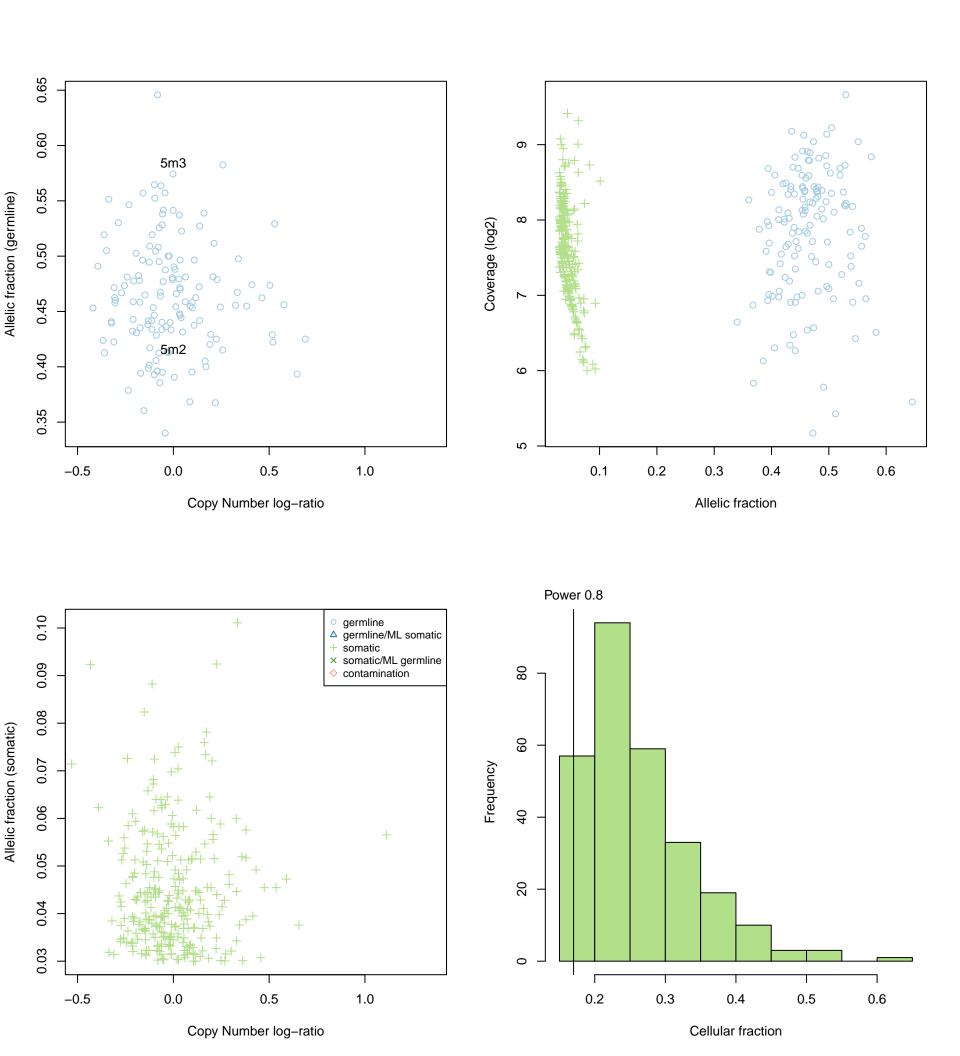




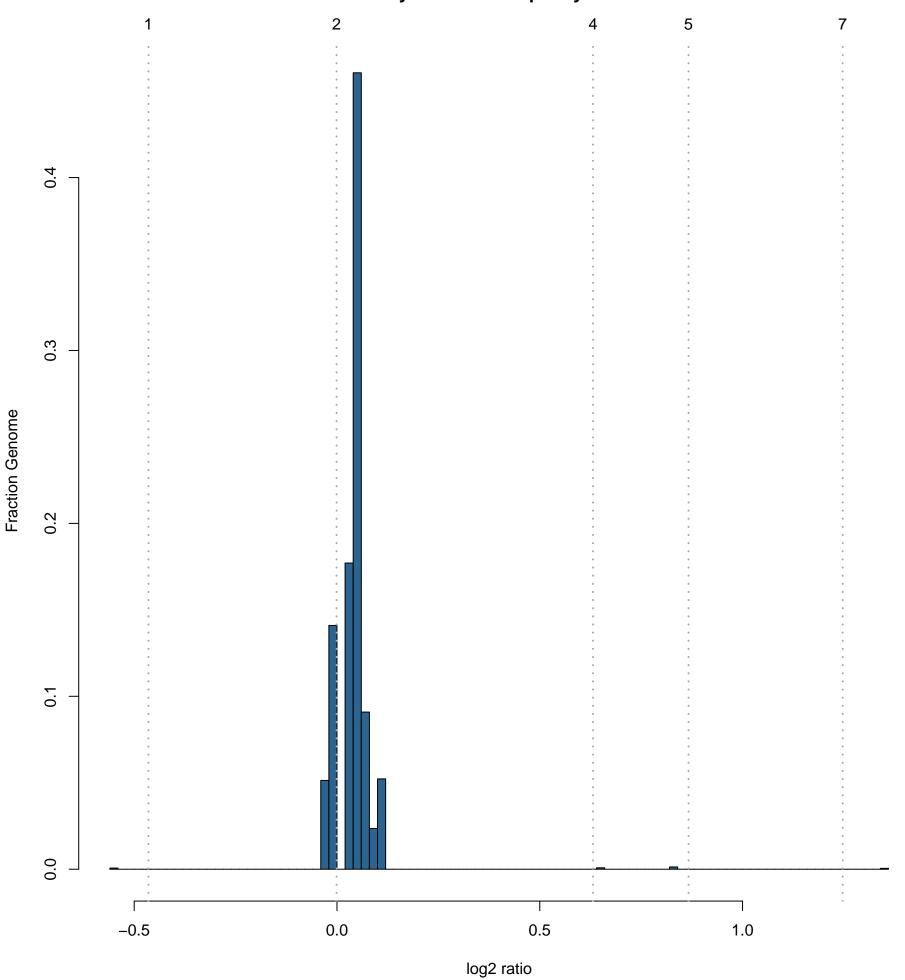
SCNA-fit log-likelihood: -4023.17

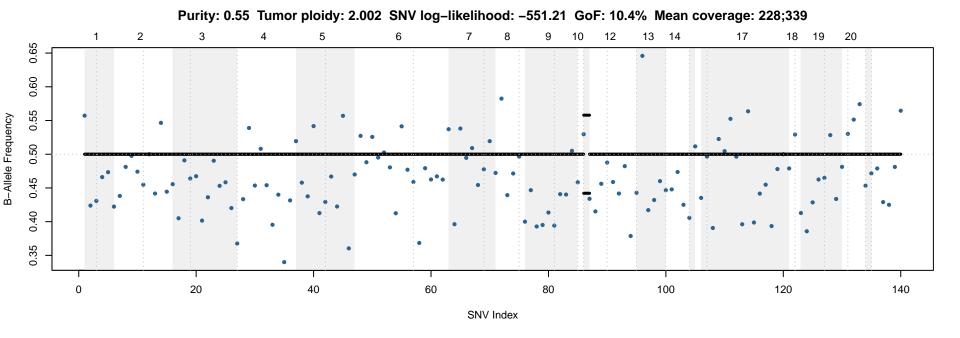




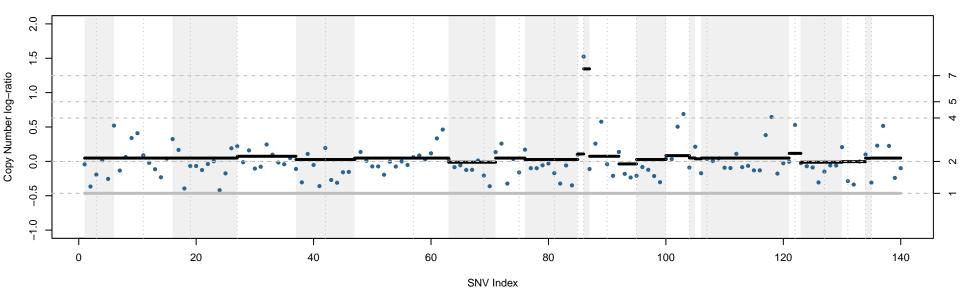


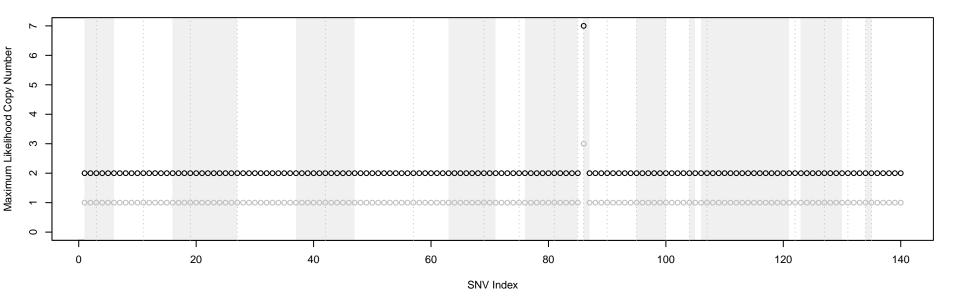
Purity: 0.55 Tumor ploidy: 2.002

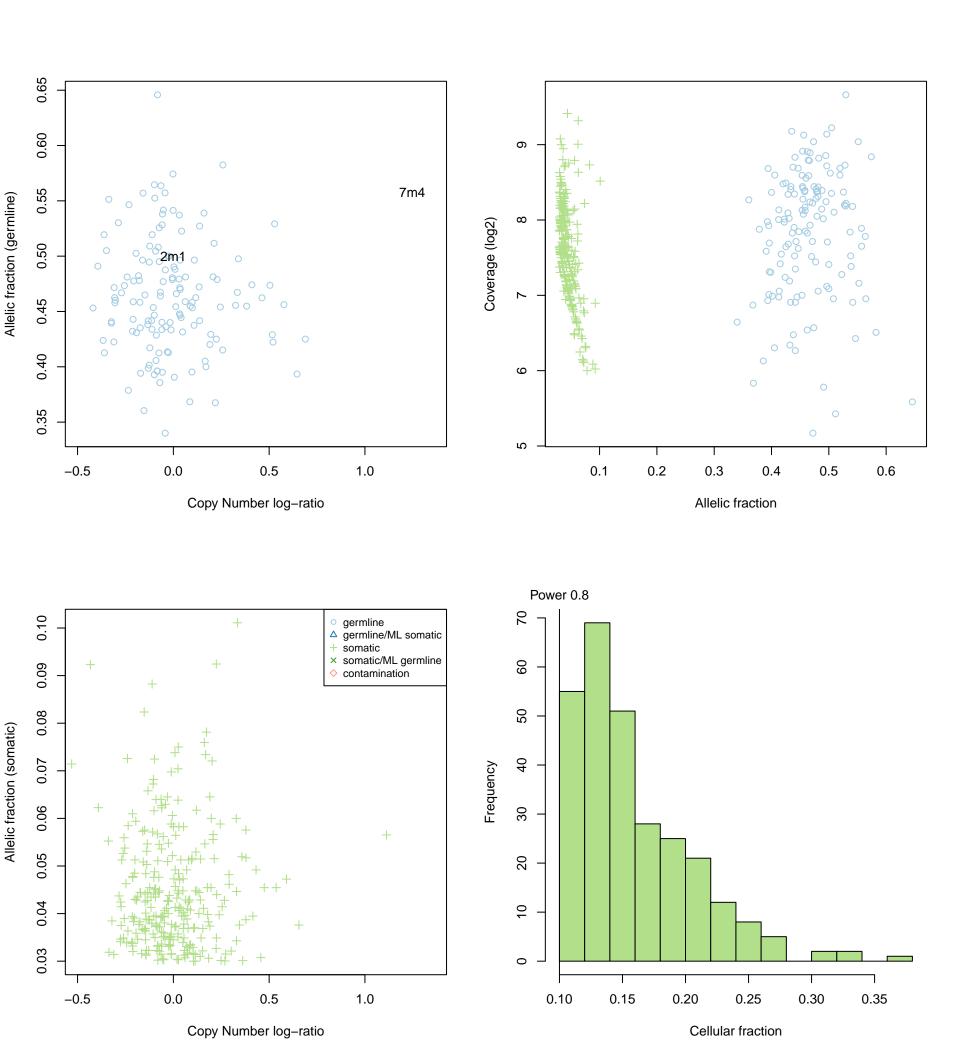




SCNA-fit log-likelihood: -3991.28

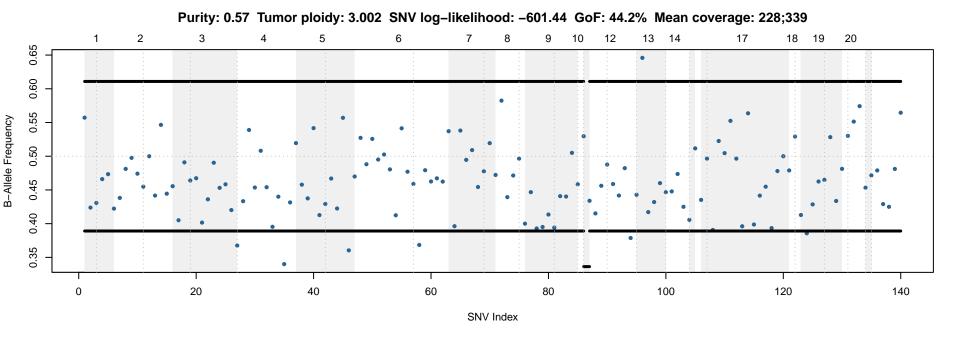




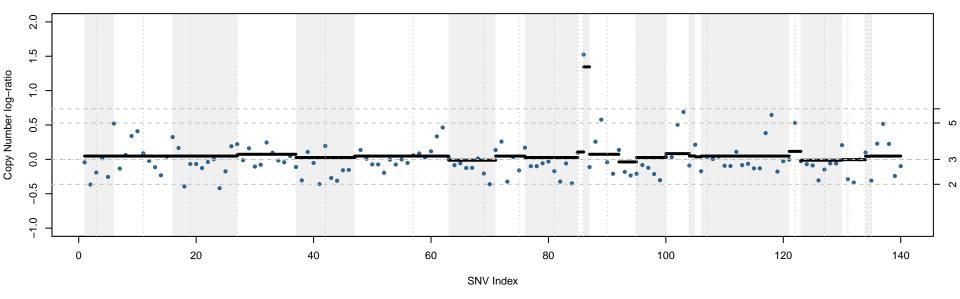


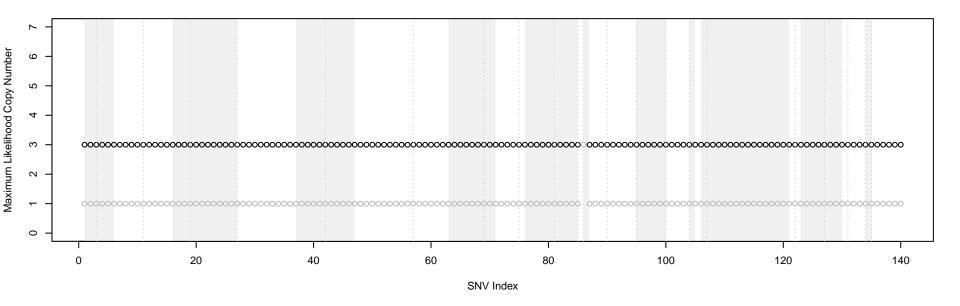
Purity: 0.57 Tumor ploidy: 3.002 3 2 Fraction Genome 0.2 0.1 0.0 -0.5 0.0 0.5 1.0

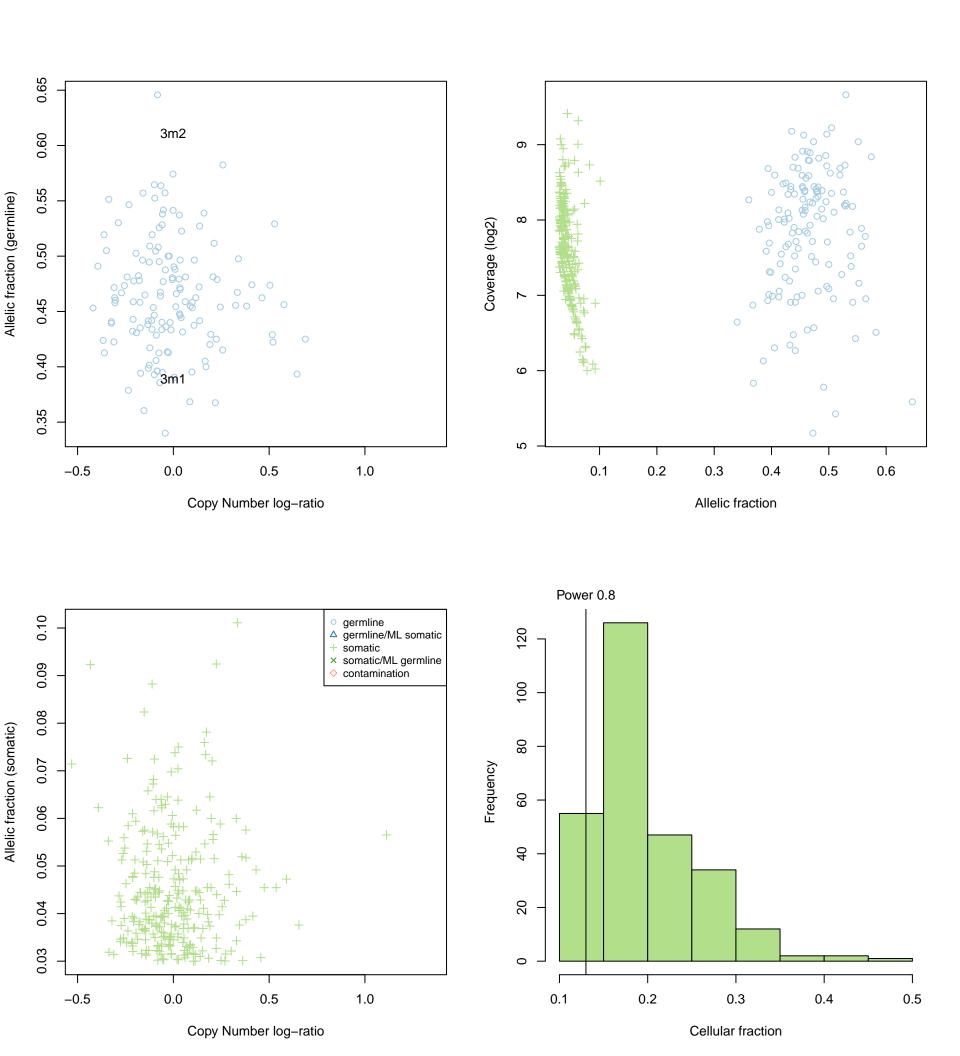
log2 ratio



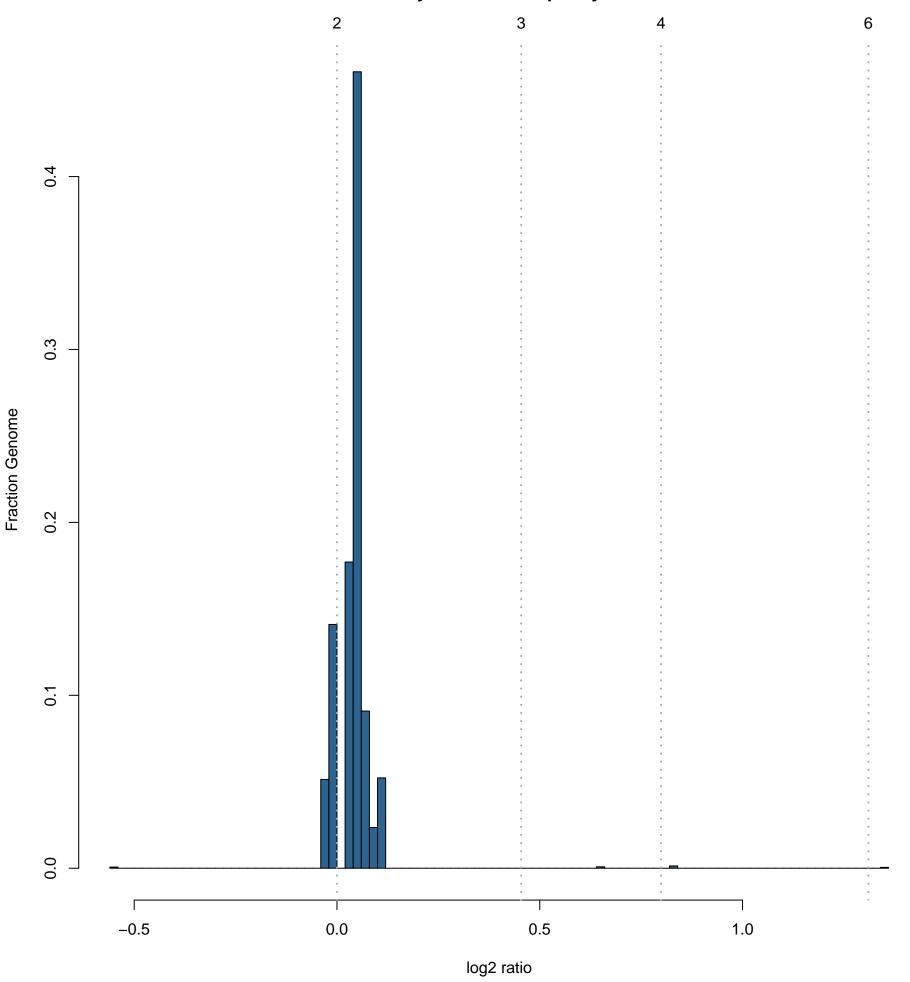
SCNA-fit log-likelihood: -4000.97

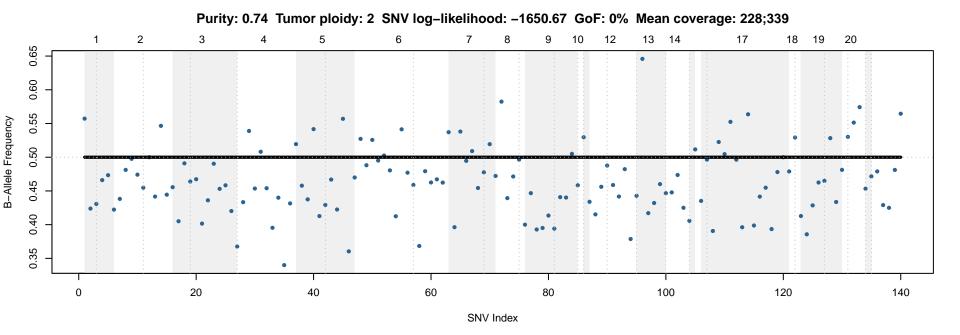




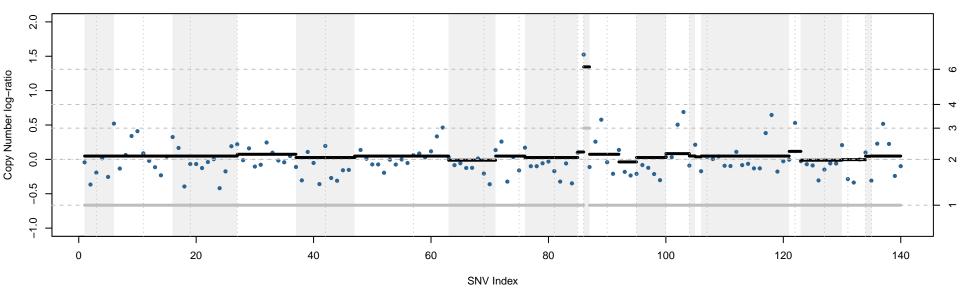


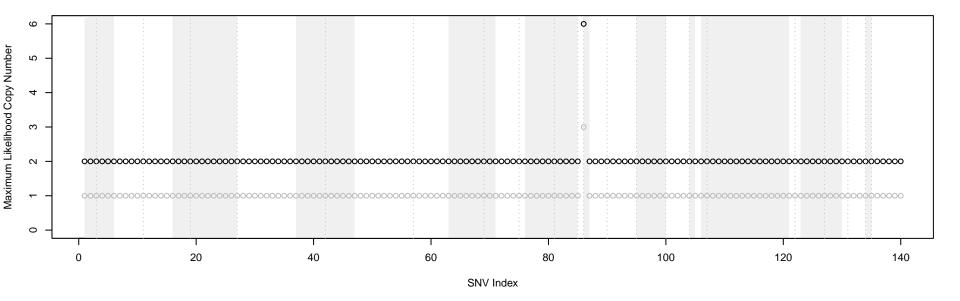
Purity: 0.74 Tumor ploidy: 2

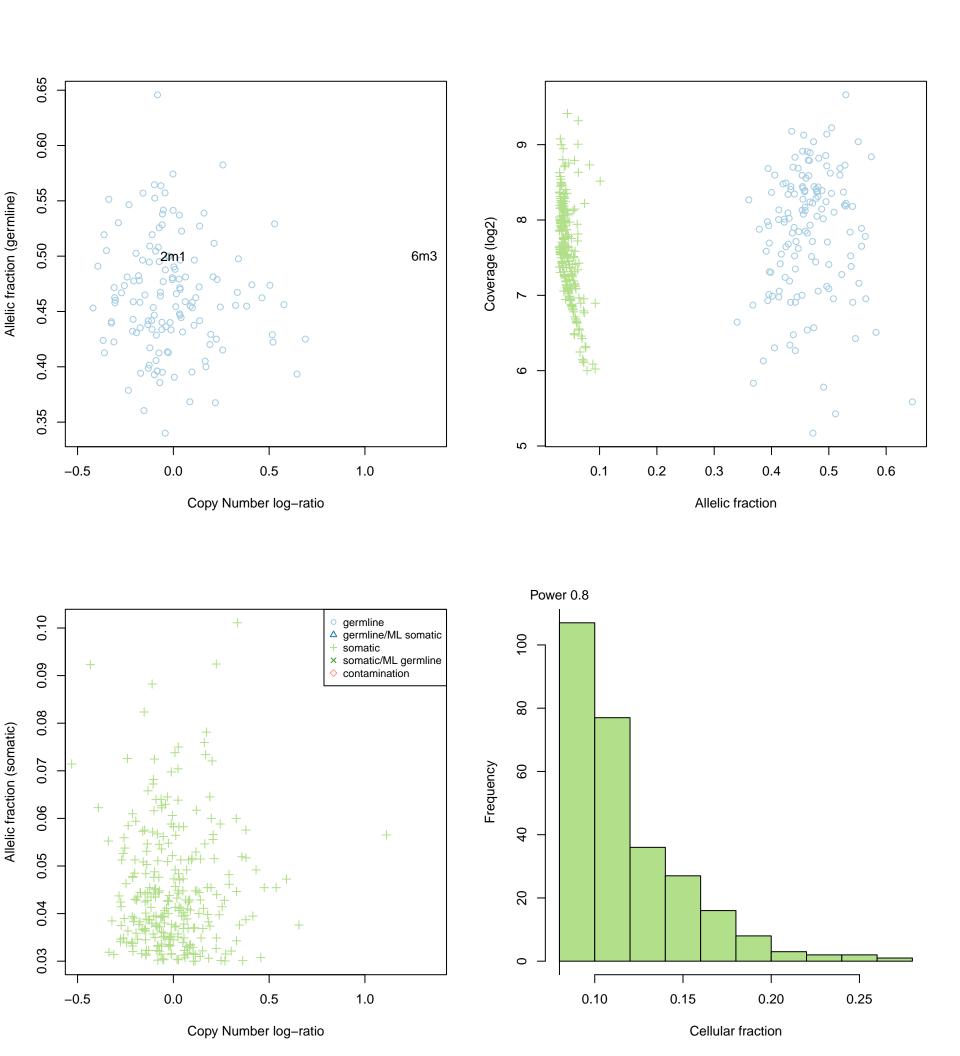




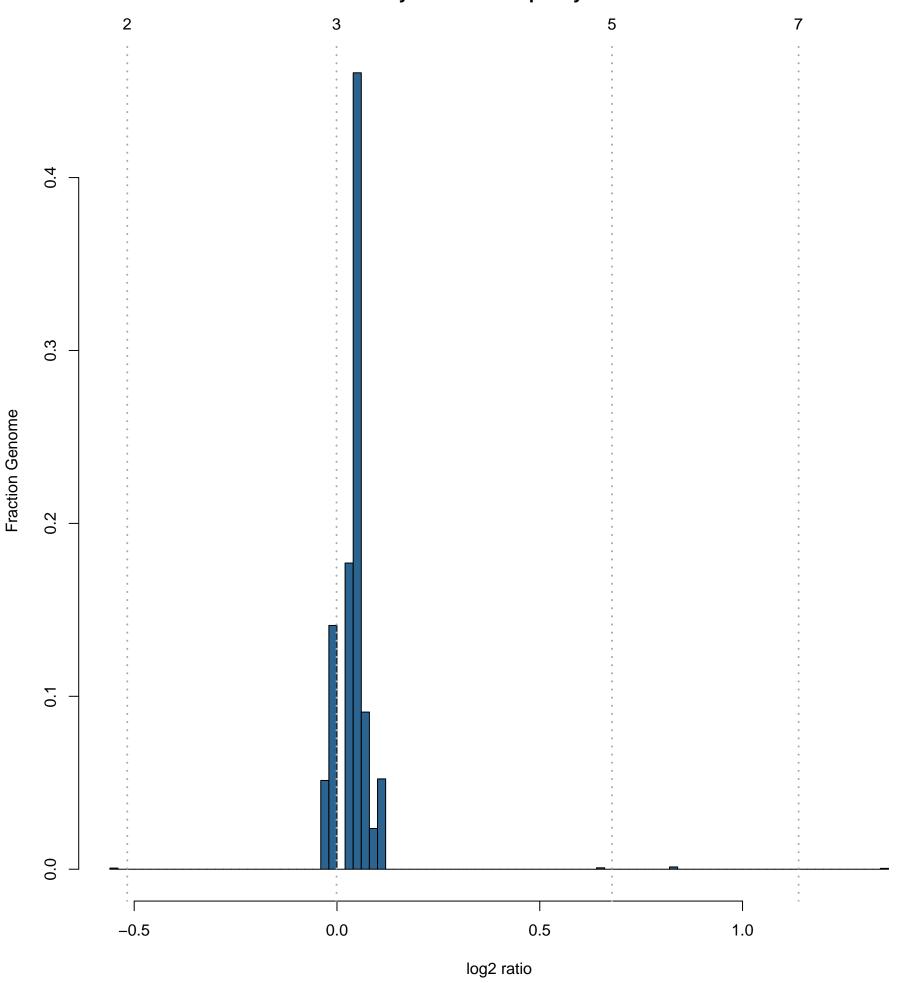
SCNA-fit log-likelihood: -3991.33

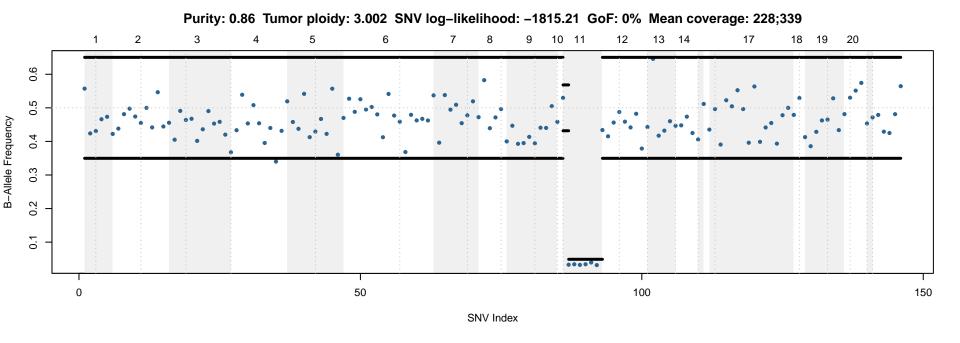






Purity: 0.86 Tumor ploidy: 3.002





SCNA-fit log-likelihood: -3992.15

