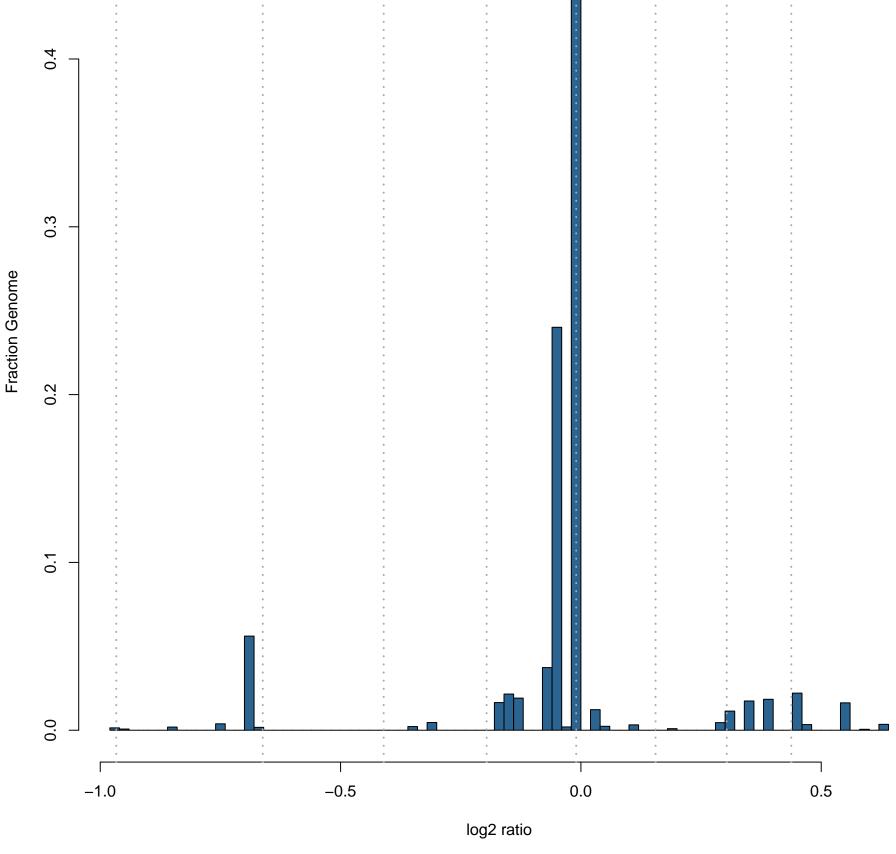
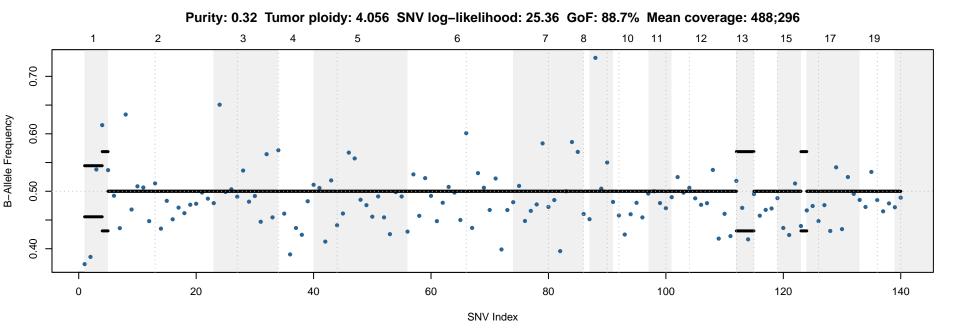
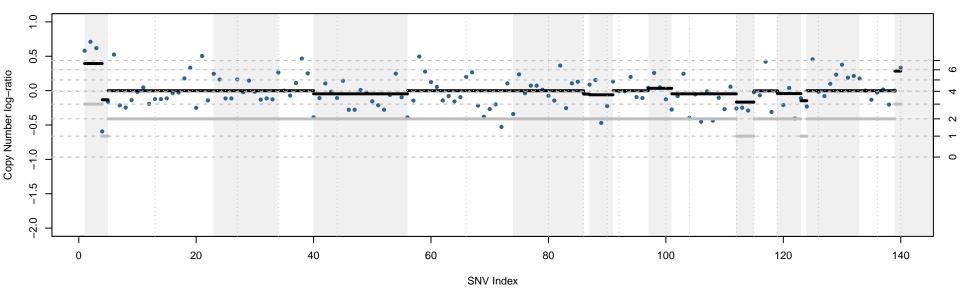
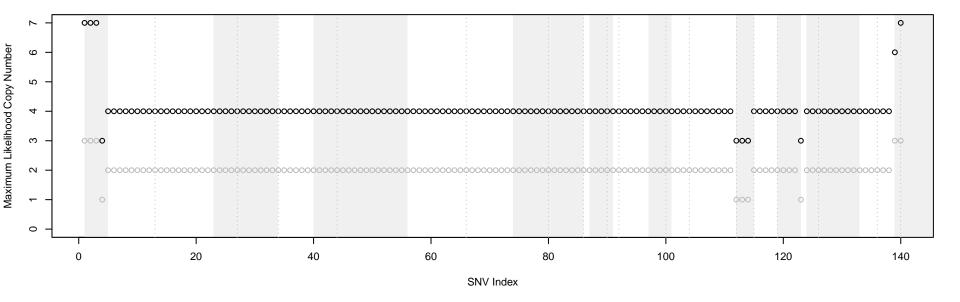
Purity: 0.32 Tumor ploidy: 4.056 

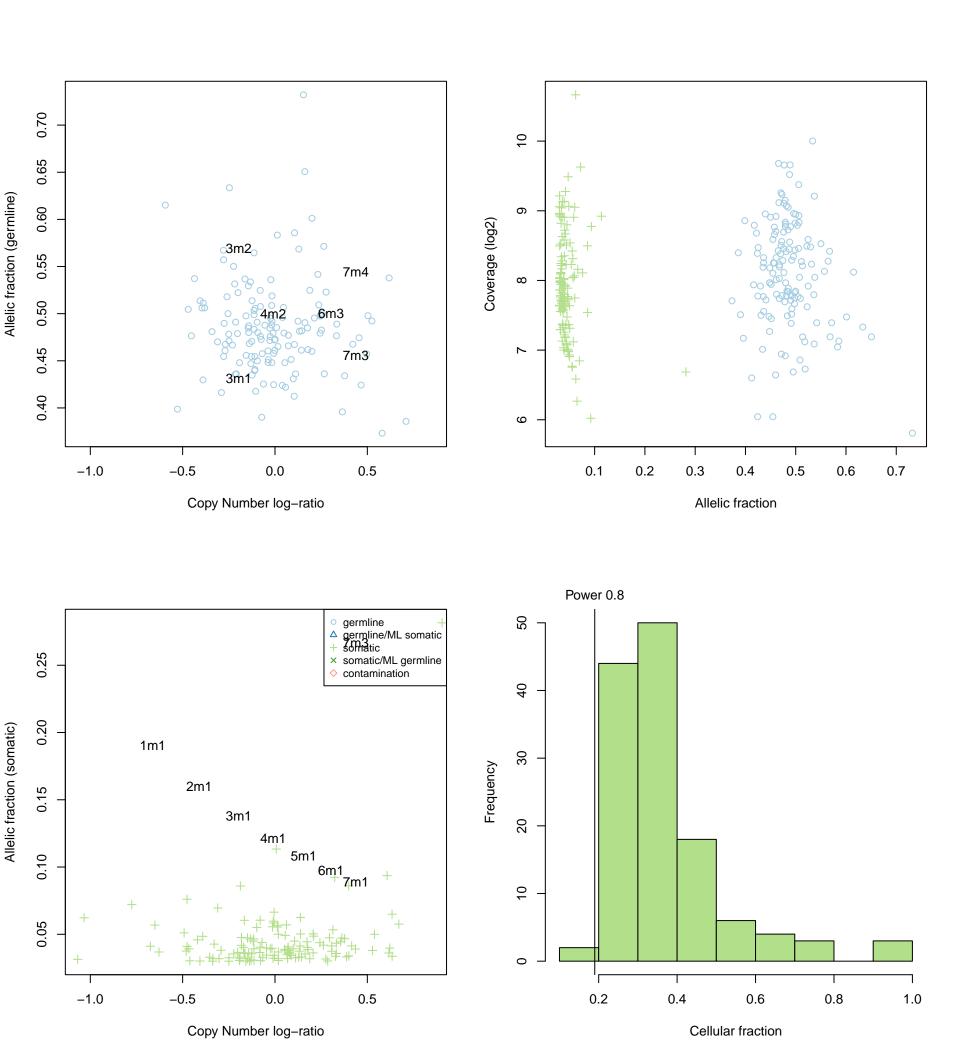




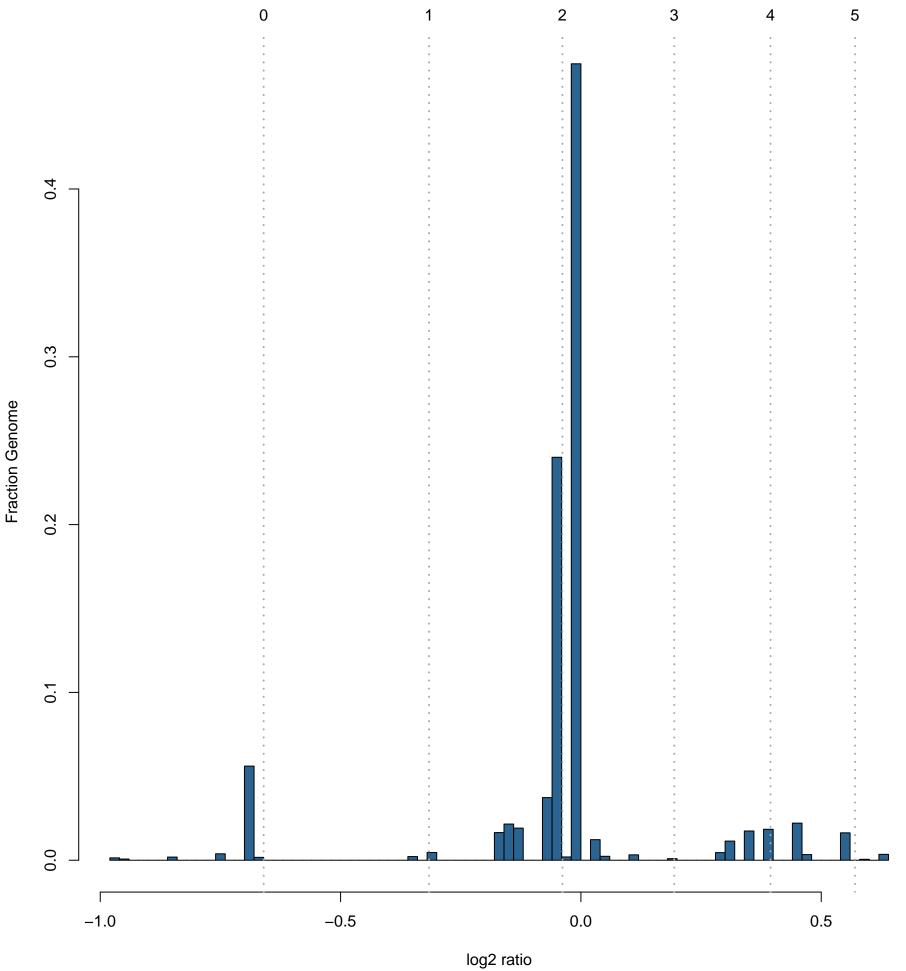
## SCNA-fit log-likelihood: -5097.23

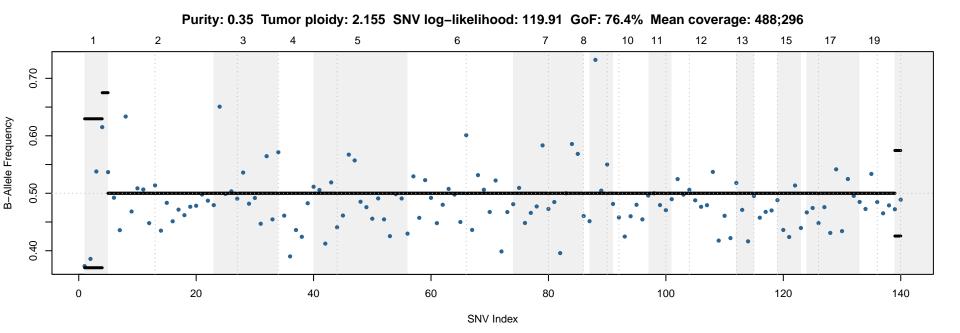




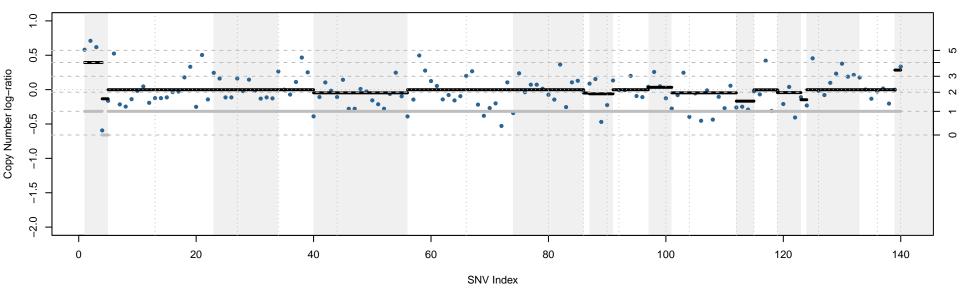


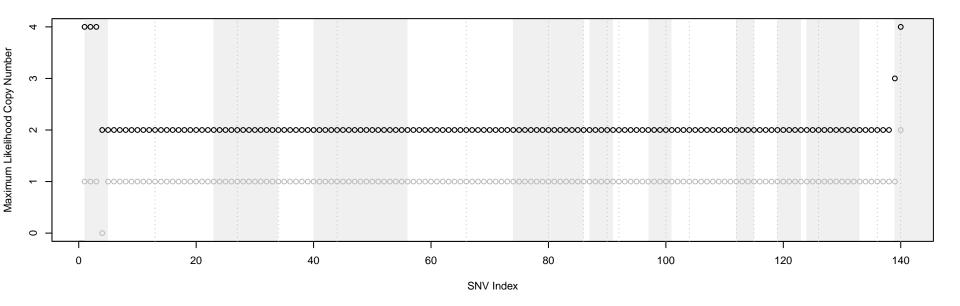
**Purity: 0.35 Tumor ploidy: 2.155** 

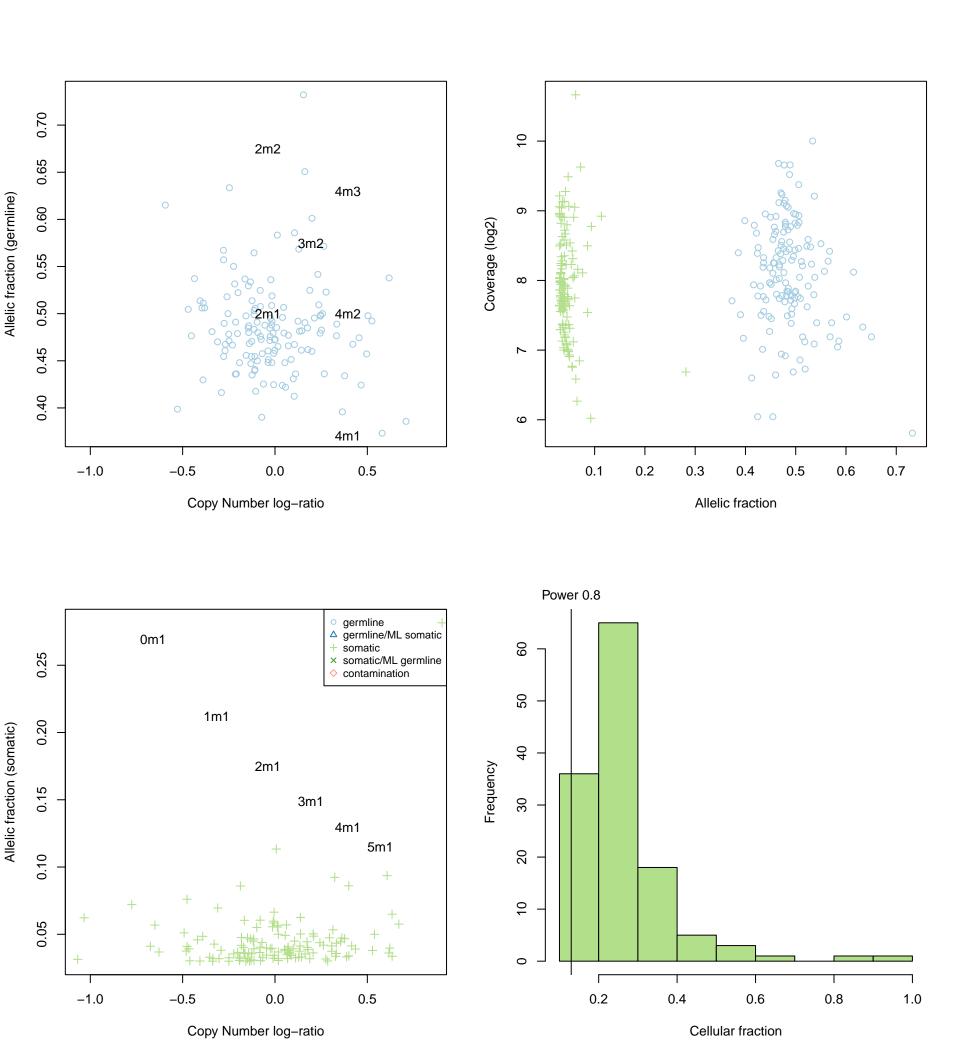




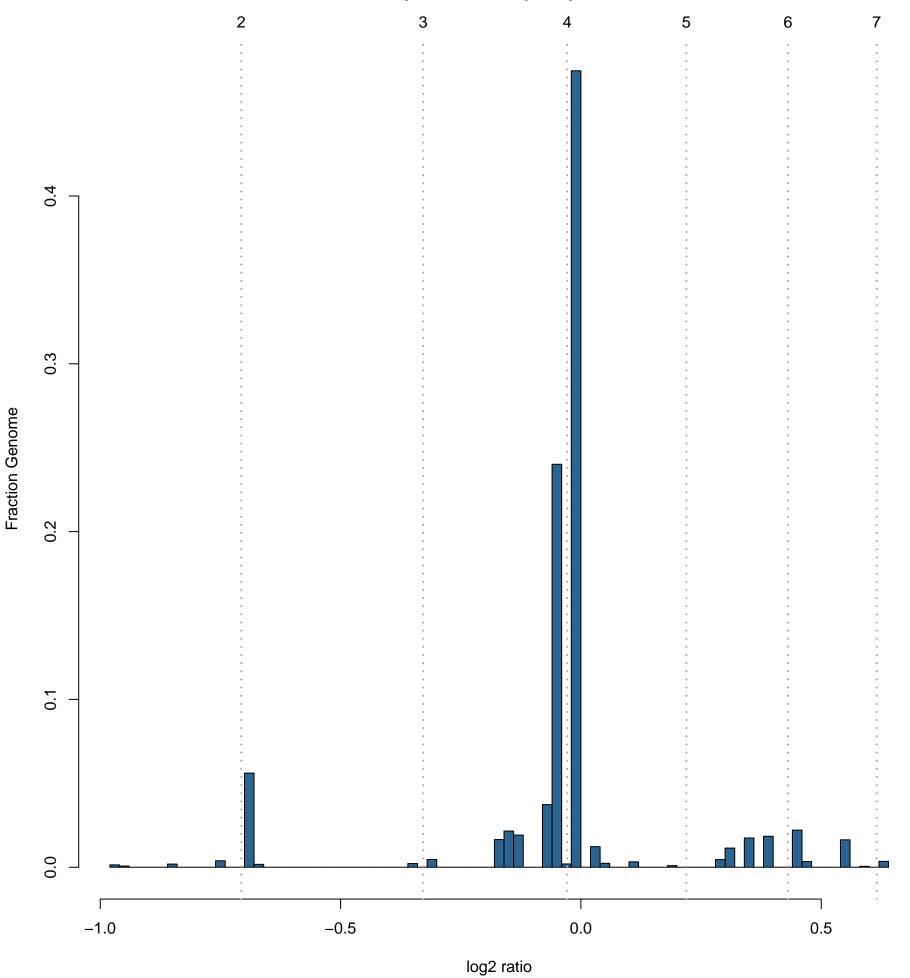
# SCNA-fit log-likelihood: -5468.36

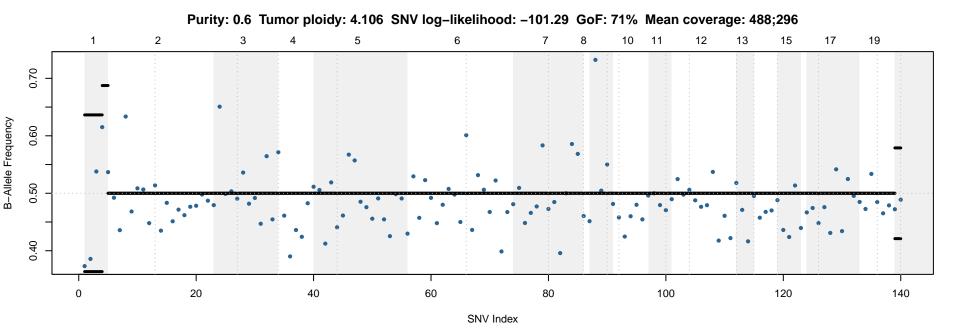




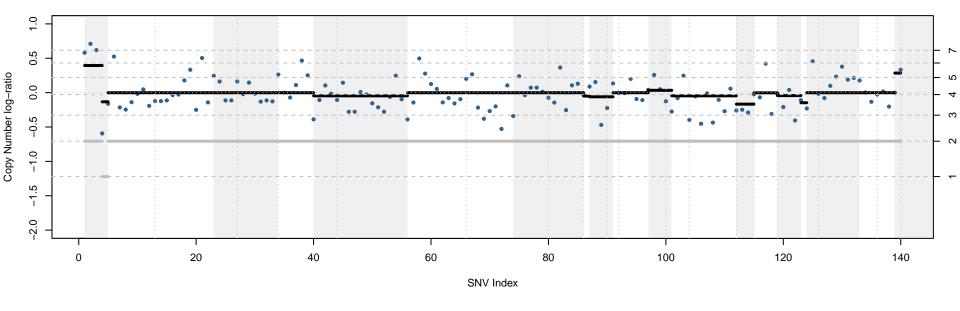


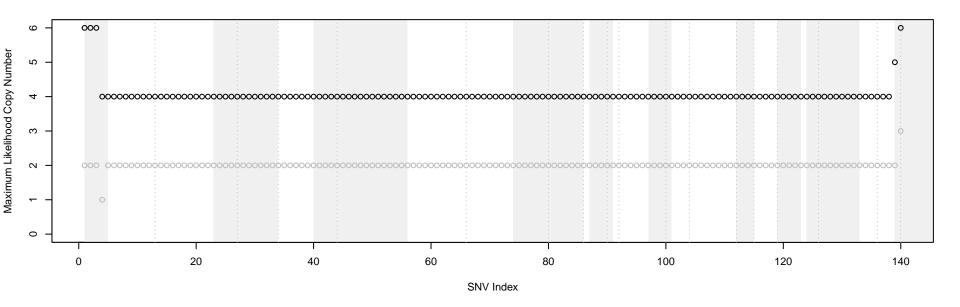
Purity: 0.6 Tumor ploidy: 4.106

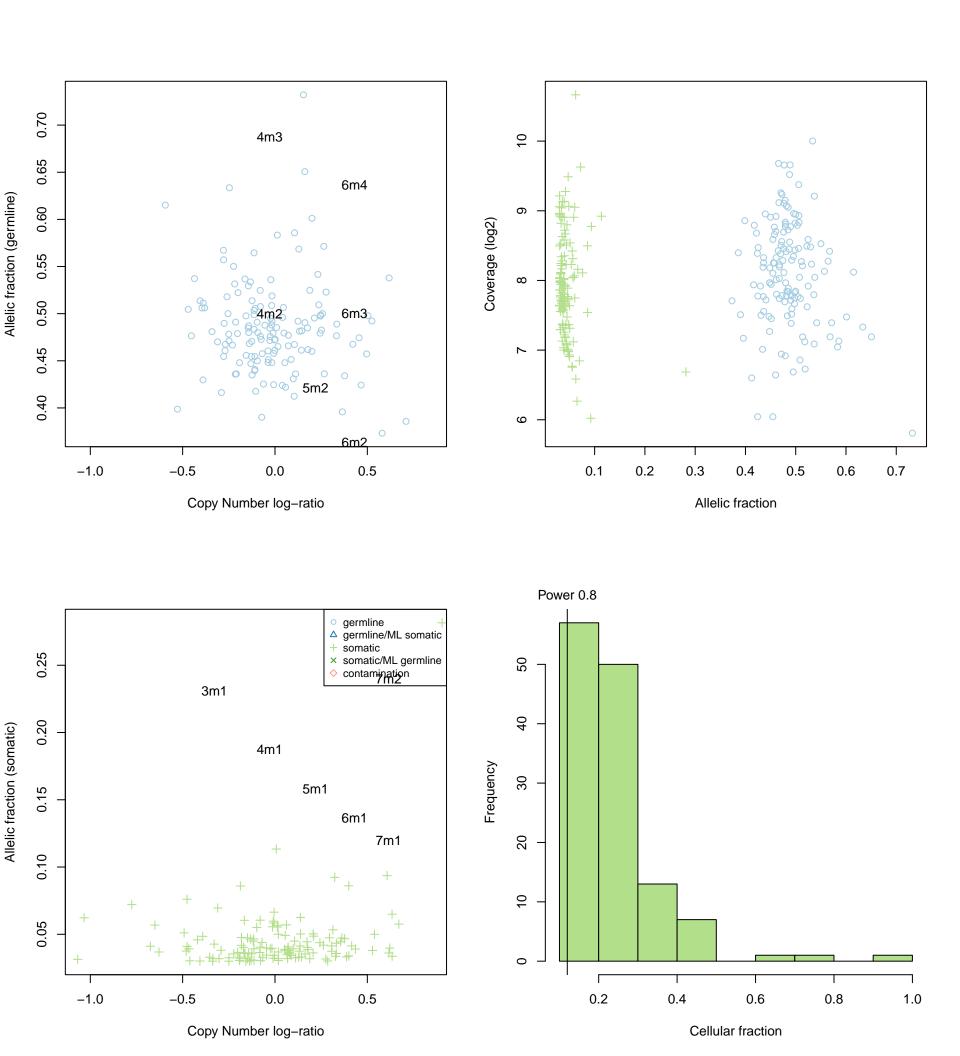




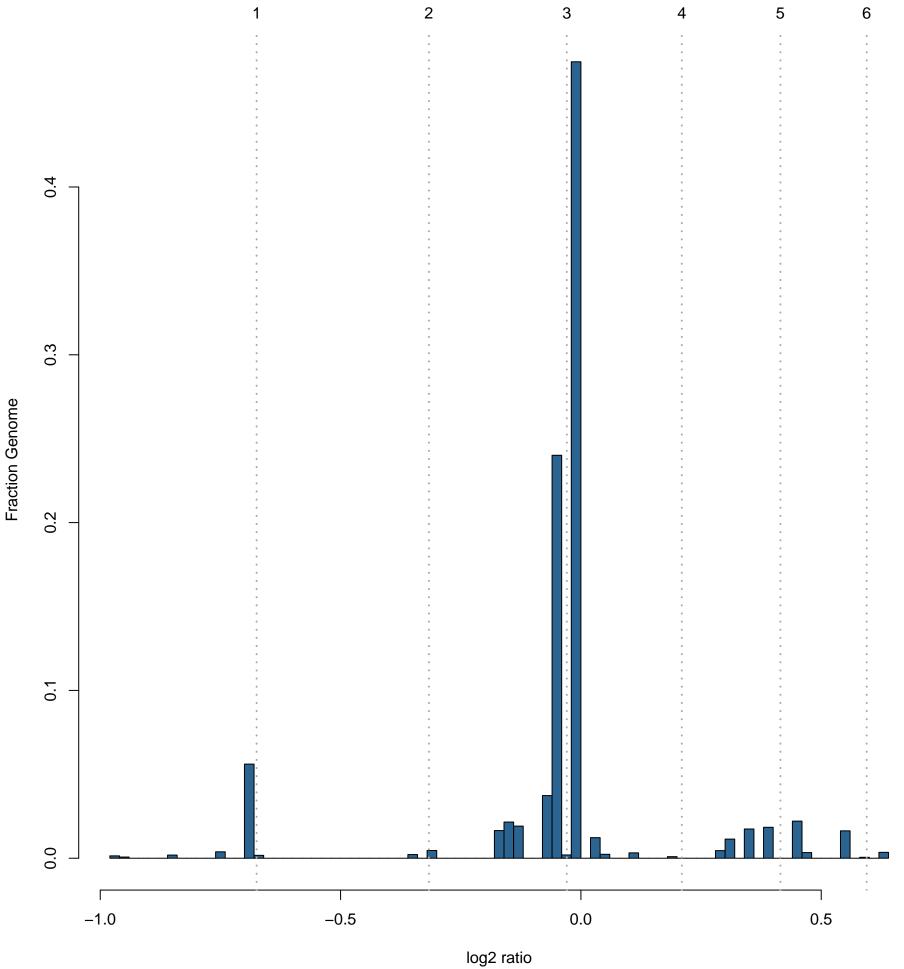
SCNA-fit log-likelihood: -5078.87

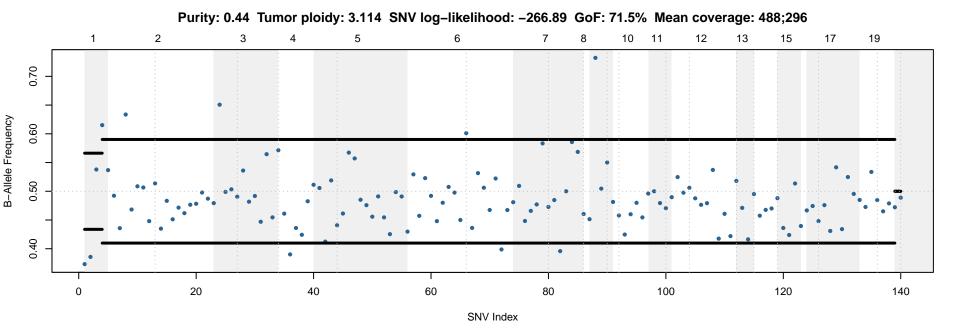




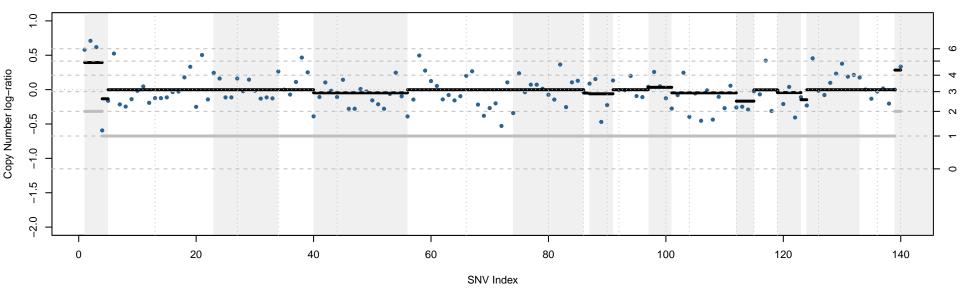


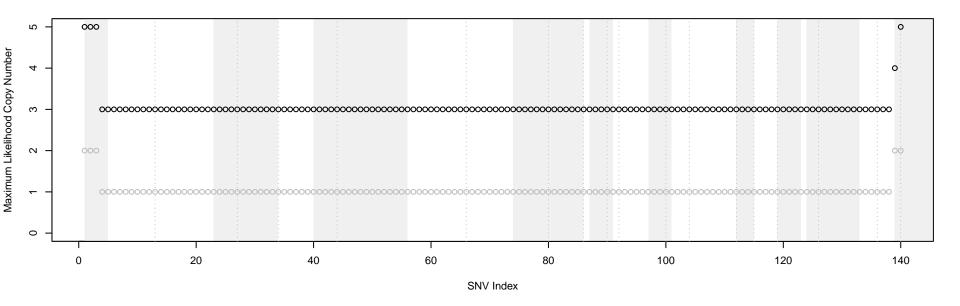
**Purity: 0.44 Tumor ploidy: 3.114**2 3

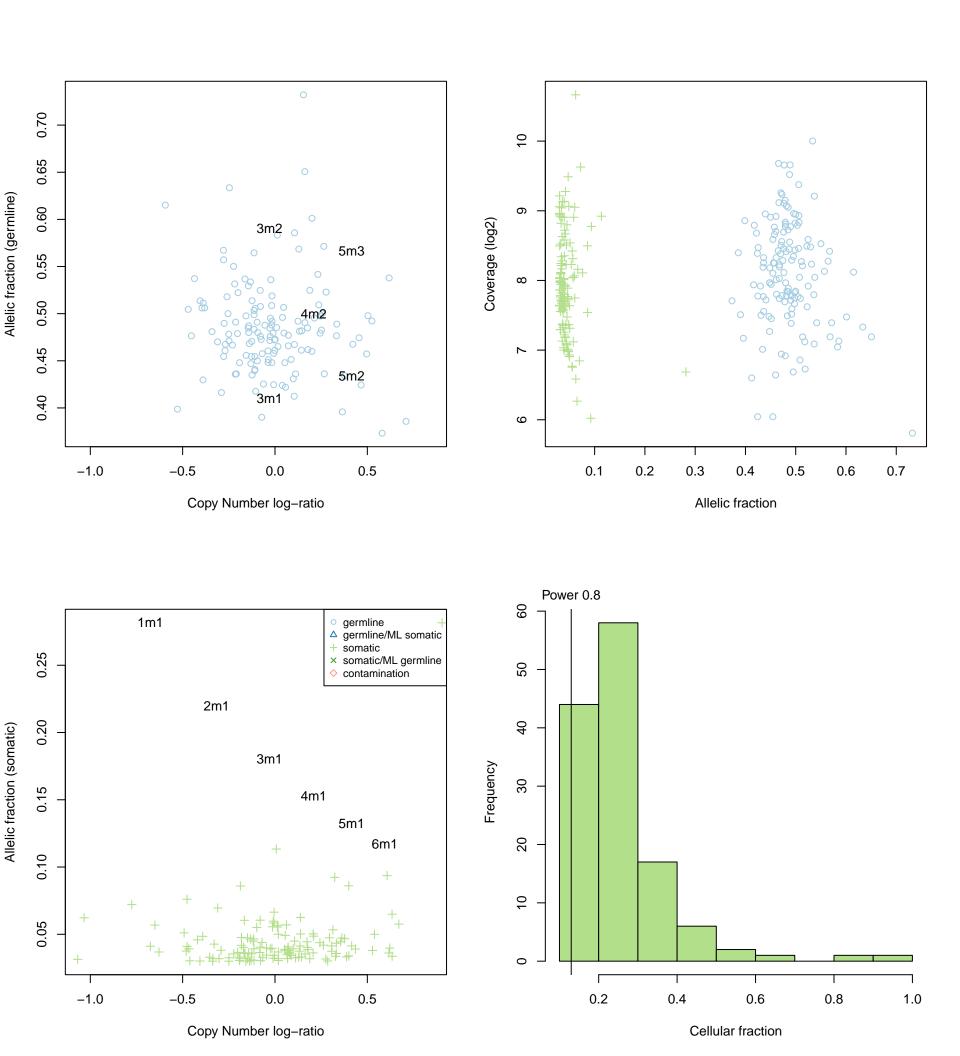




## SCNA-fit log-likelihood: -5075.4

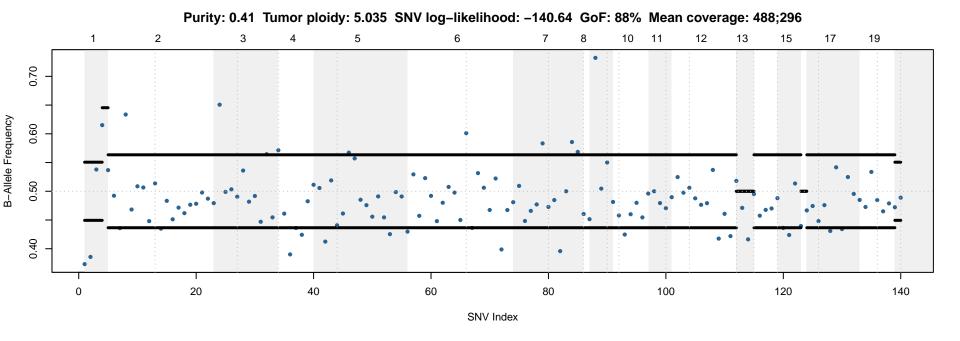




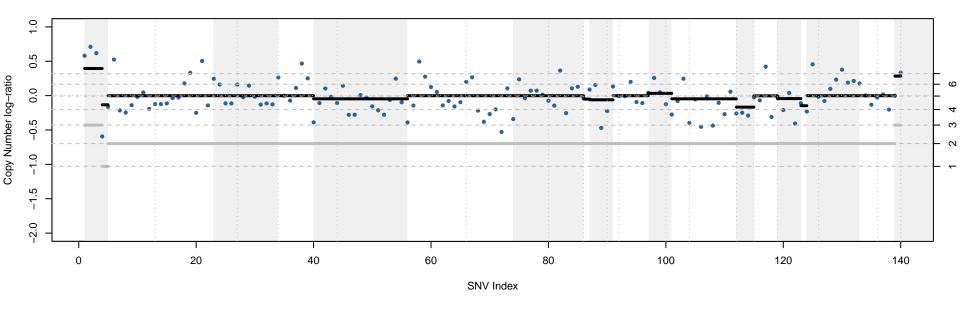


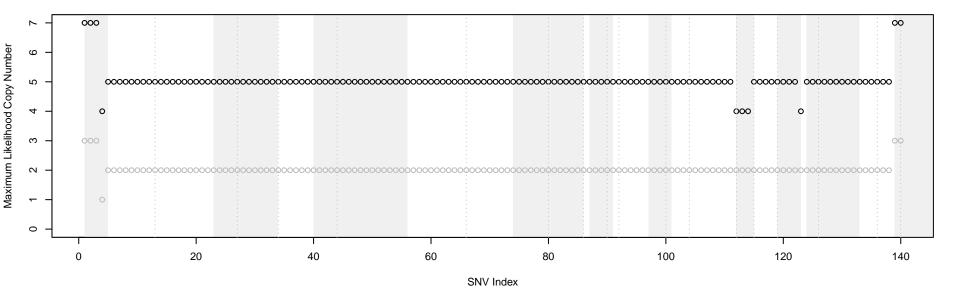
Purity: 0.41 Tumor ploidy: 5.035 2 3 5 6 7 1 0.3 Fraction Genome 0.1 0.0 -1.0 -0.5 0.0 0.5

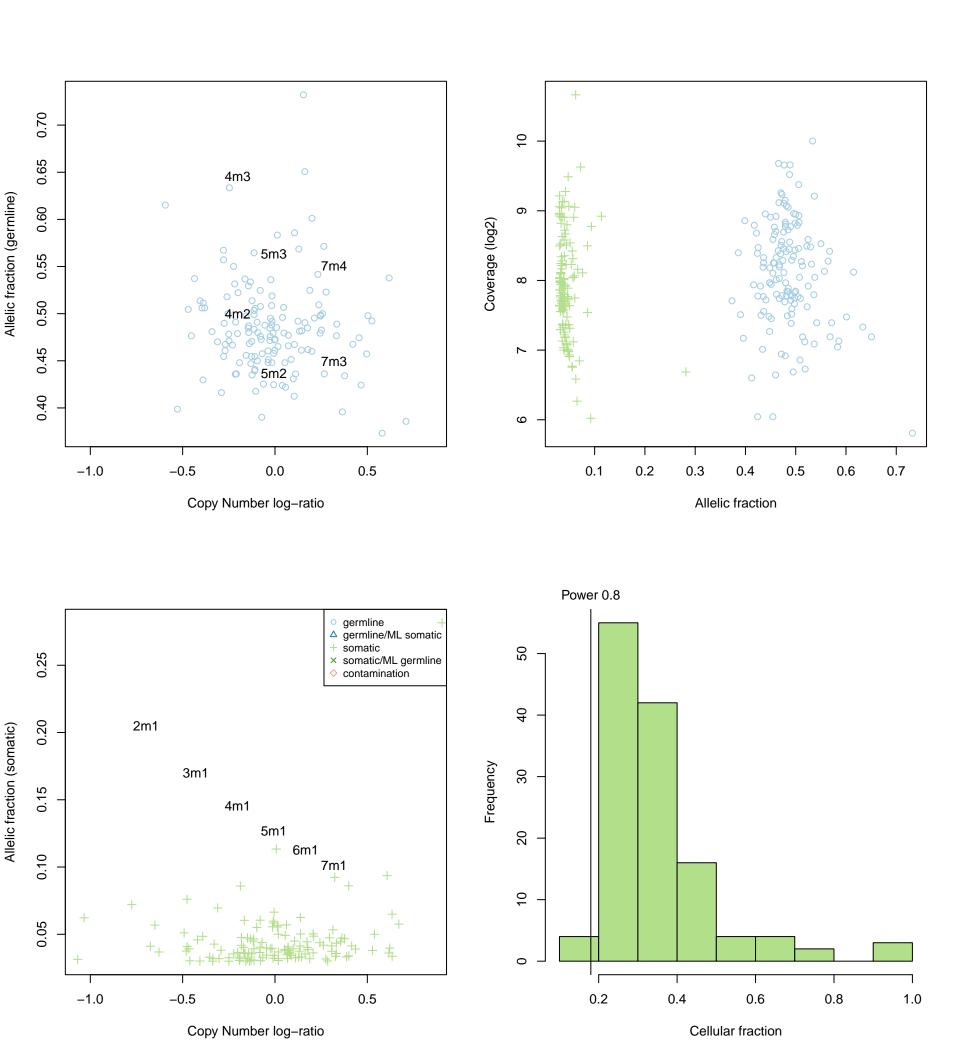
log2 ratio



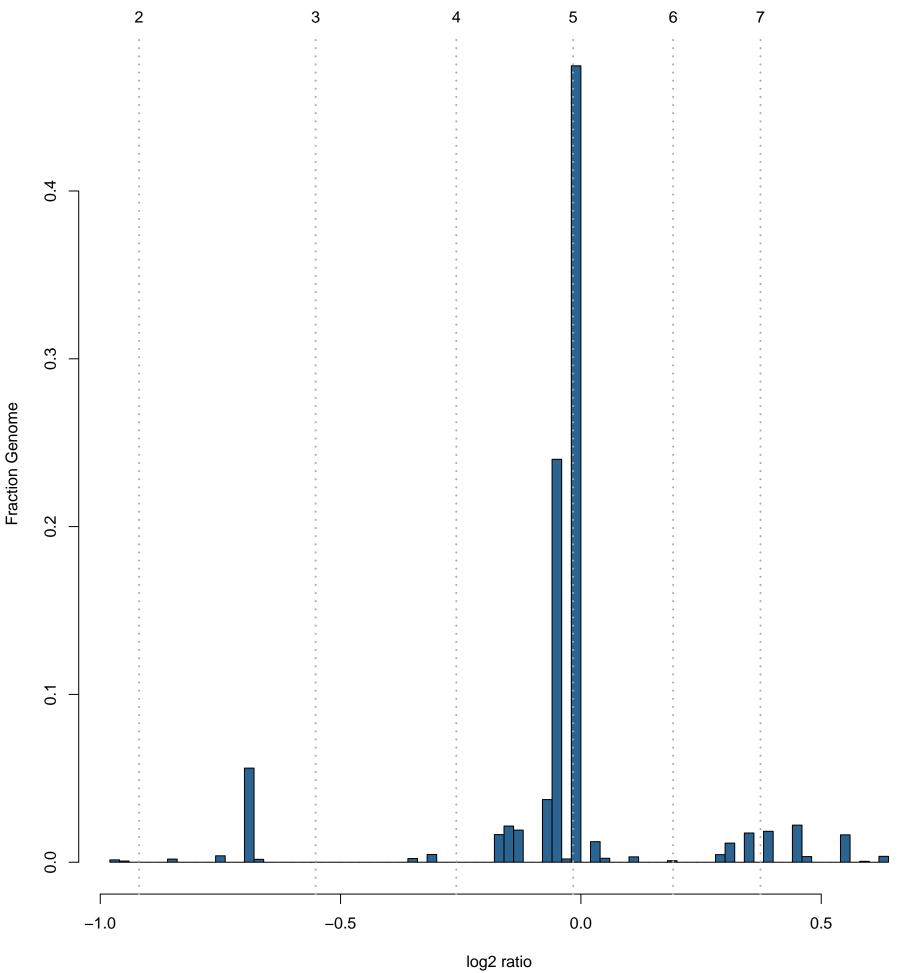
## SCNA-fit log-likelihood: -5358.8

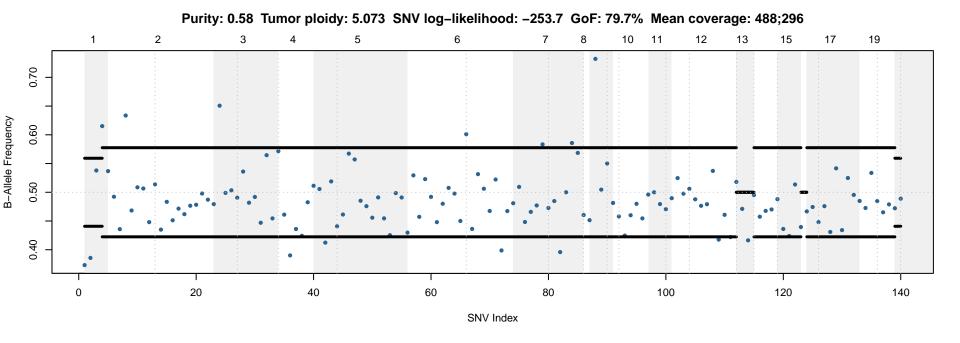




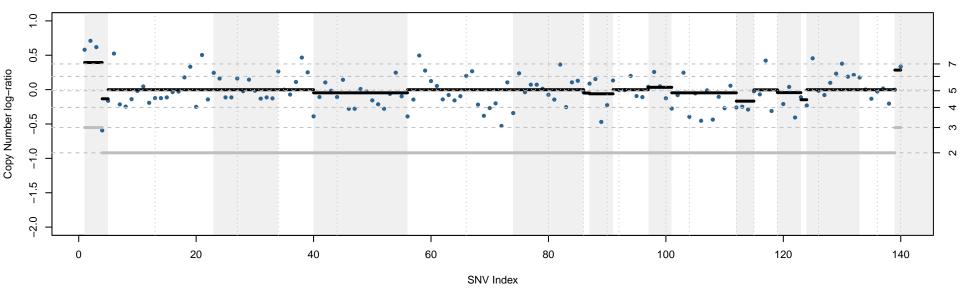


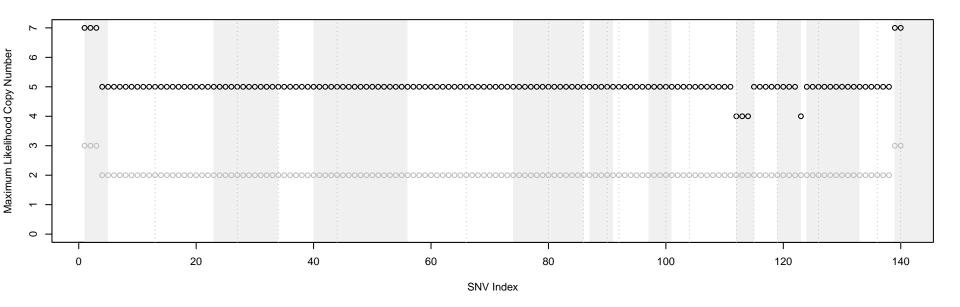
**Purity: 0.58 Tumor ploidy: 5.073**4 5

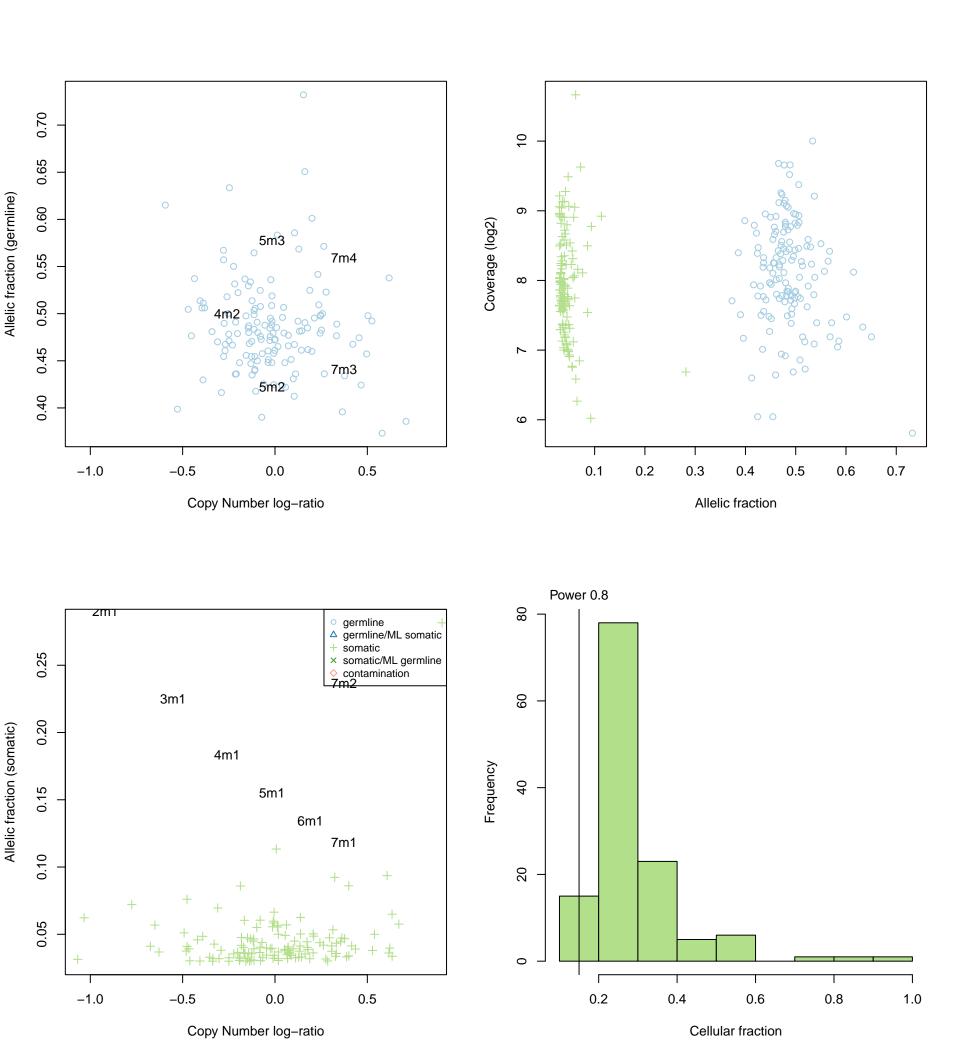




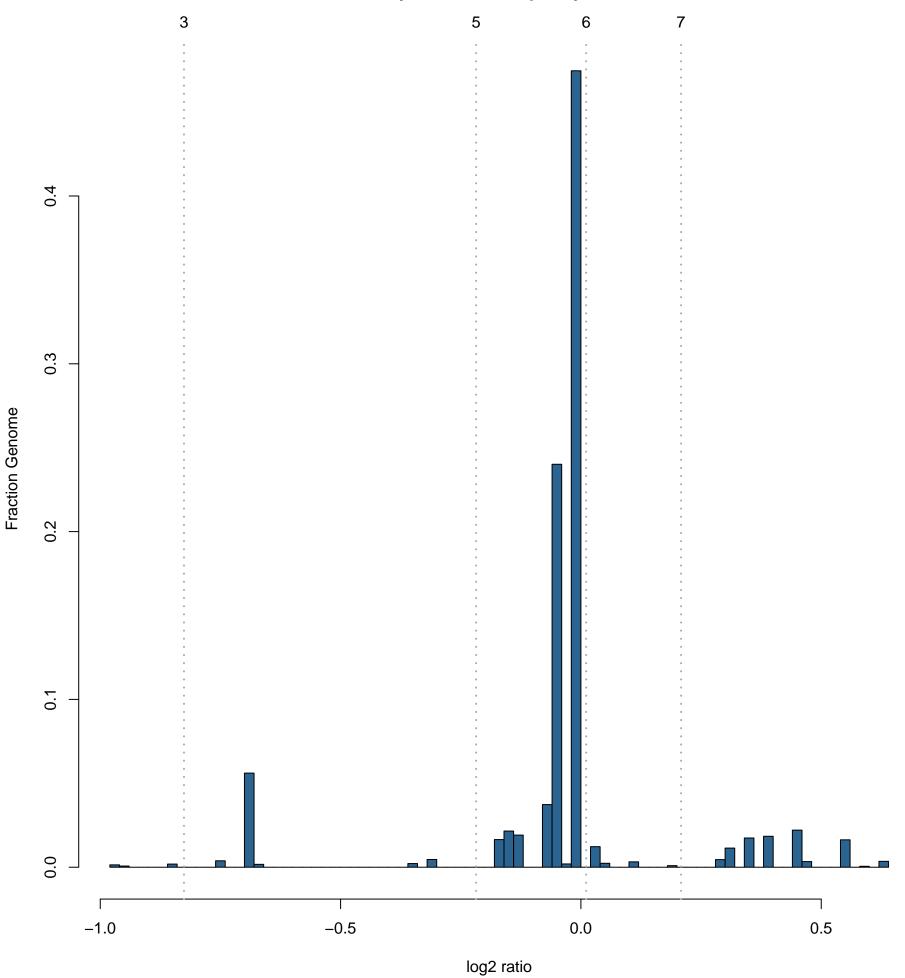
#### SCNA-fit log-likelihood: -5196.08

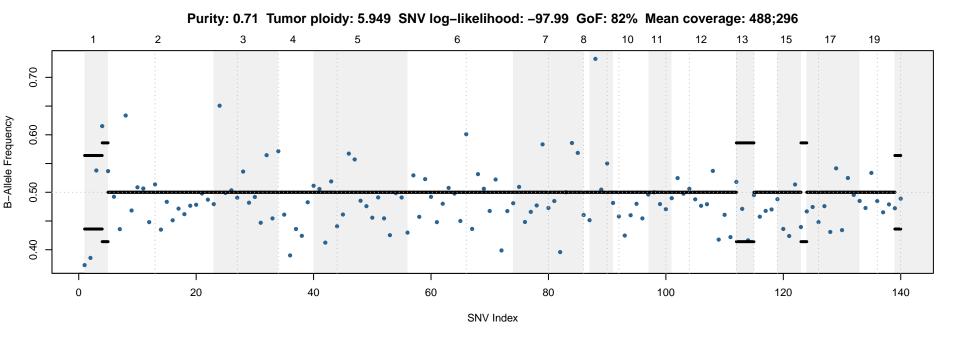




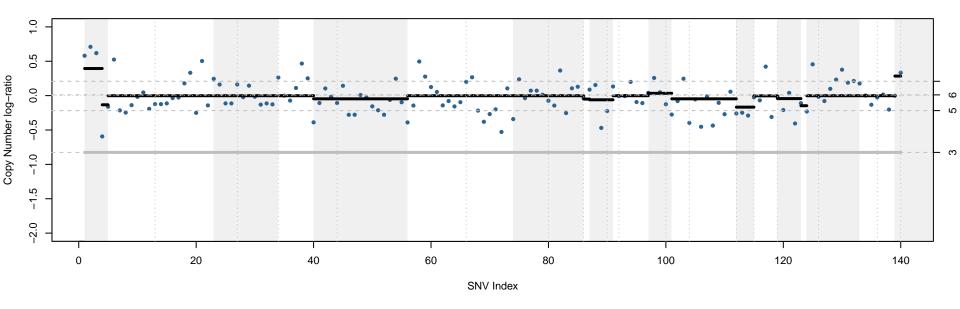


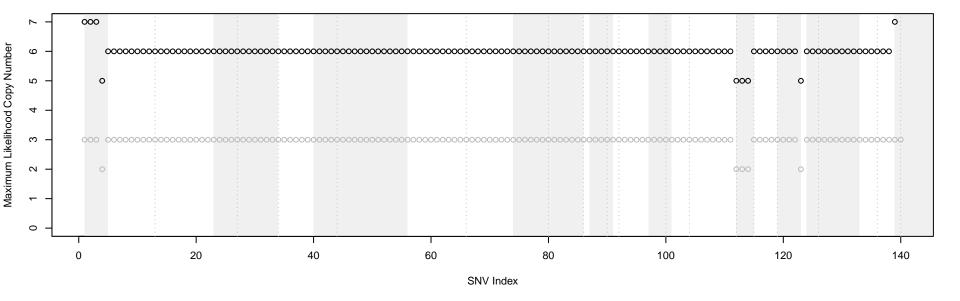
Purity: 0.71 Tumor ploidy: 5.949

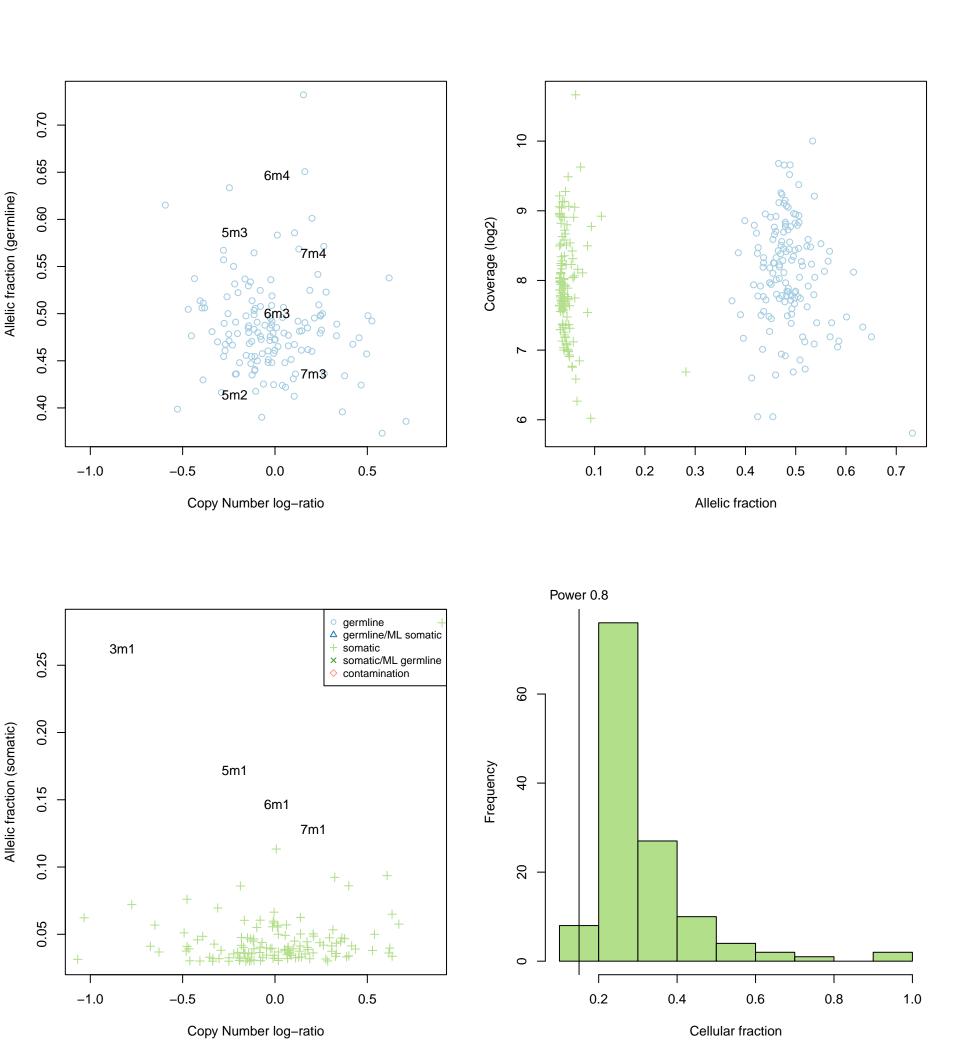




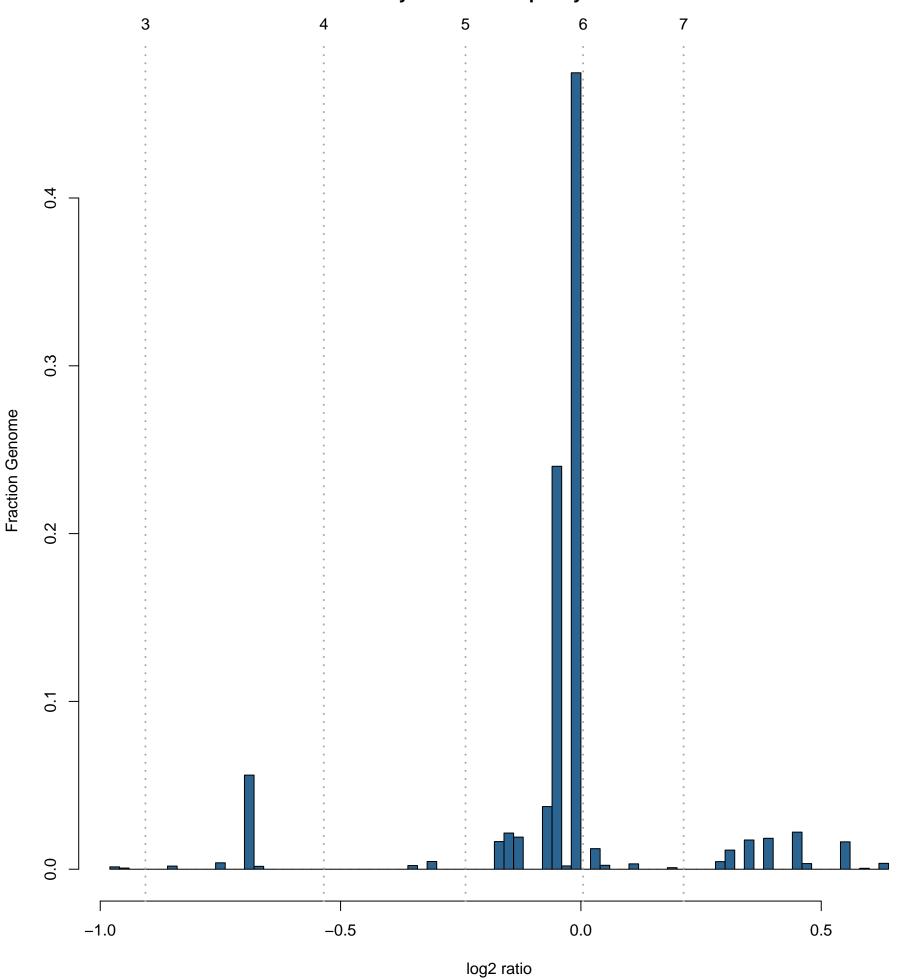
## SCNA-fit log-likelihood: -5582.48

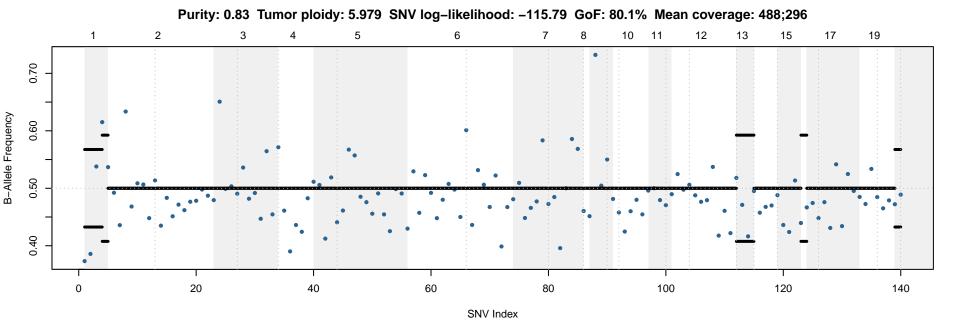




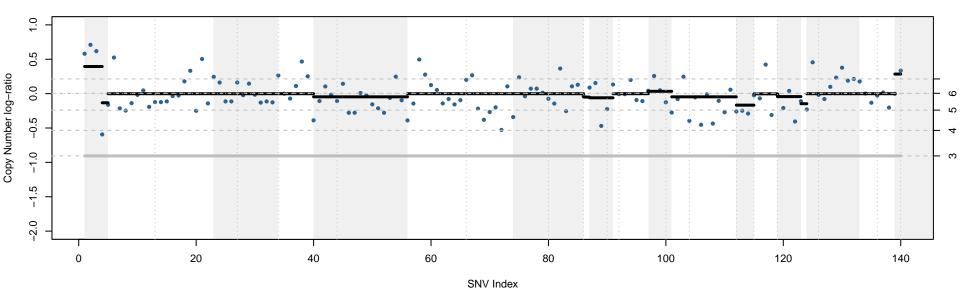


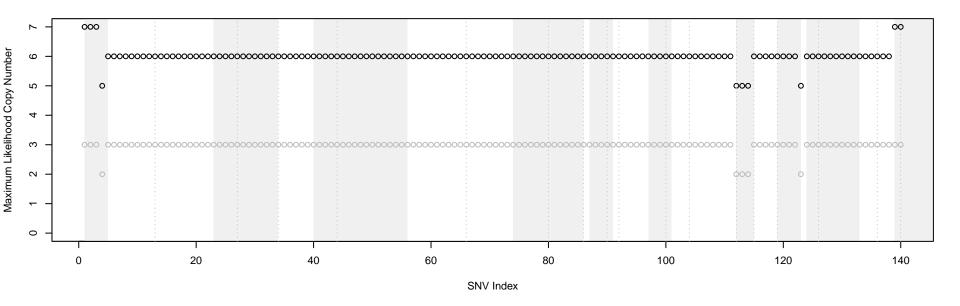
Purity: 0.83 Tumor ploidy: 5.979

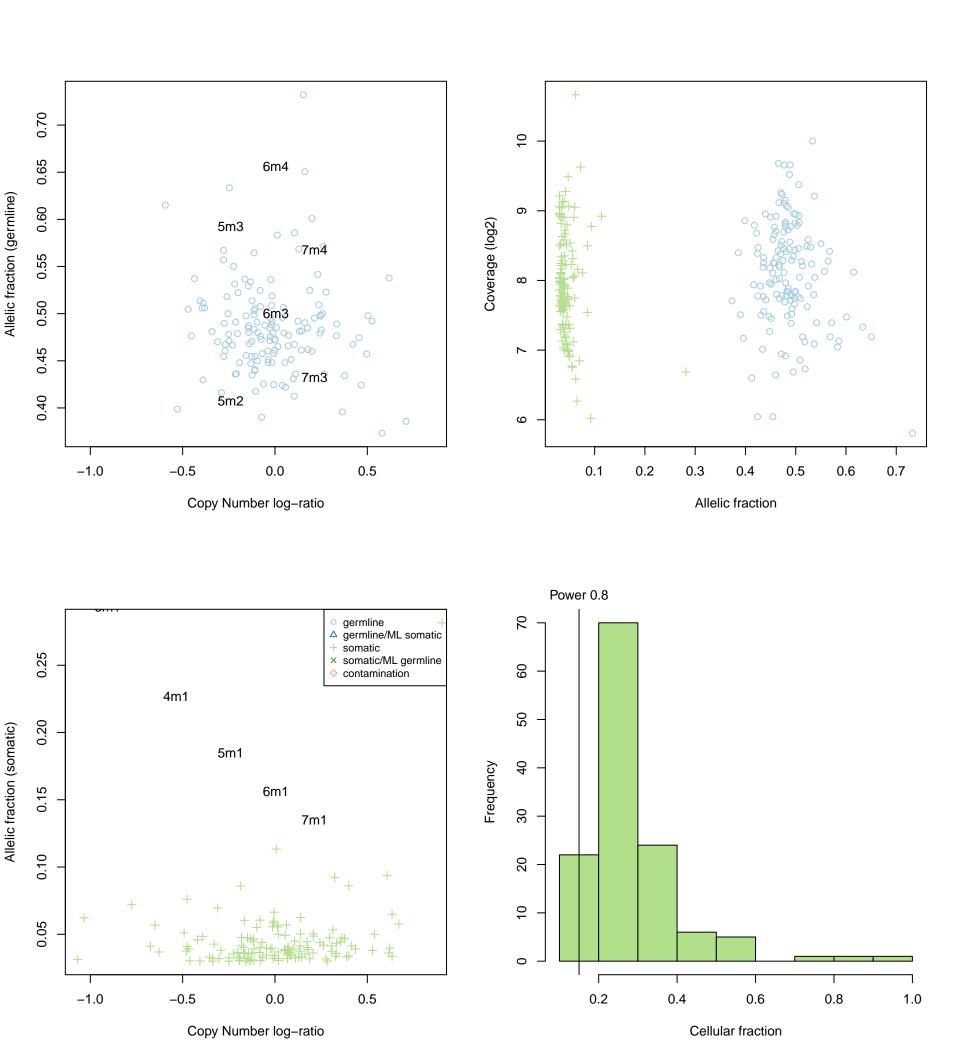




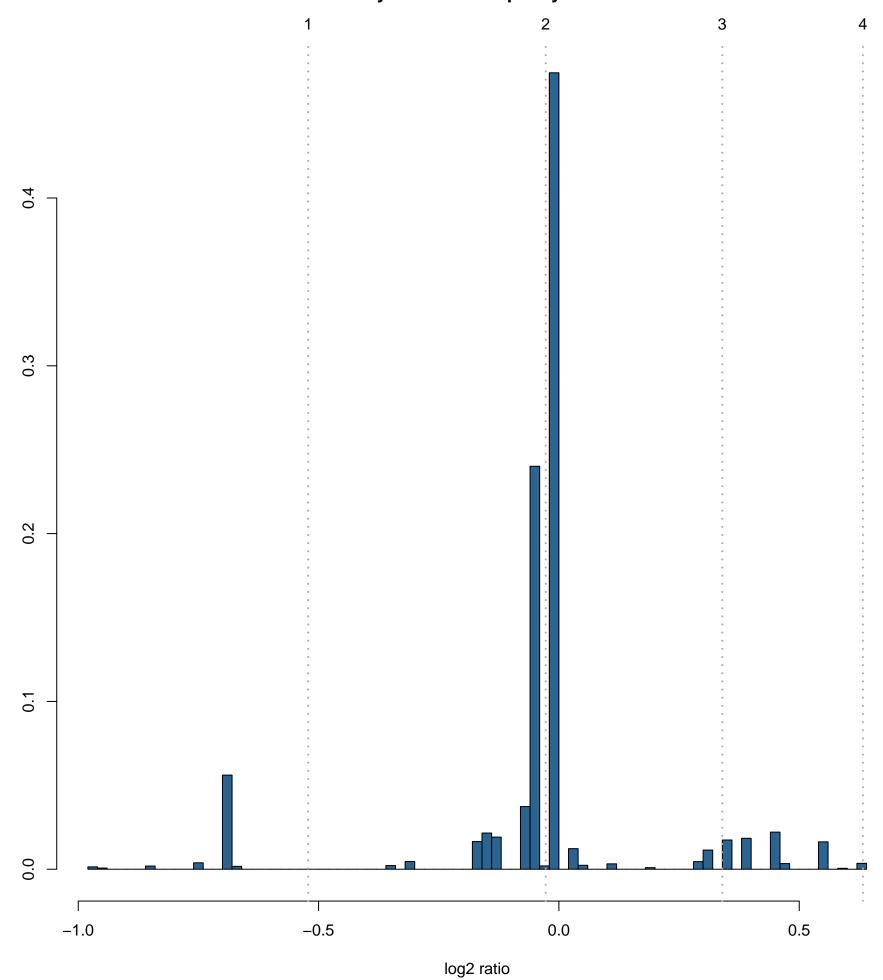
## SCNA-fit log-likelihood: -5547.1



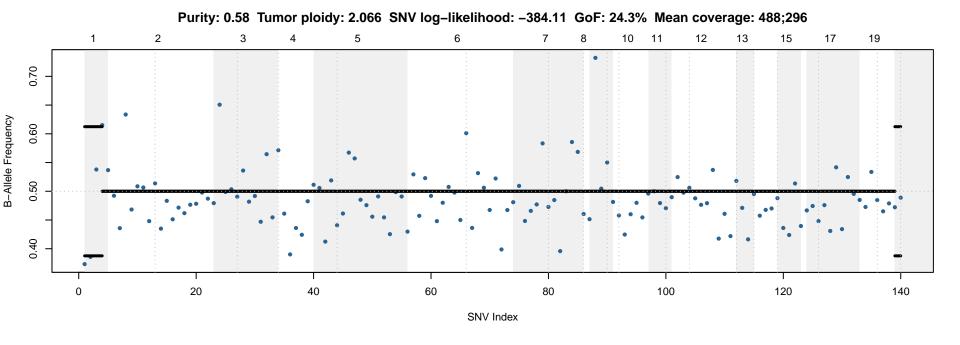




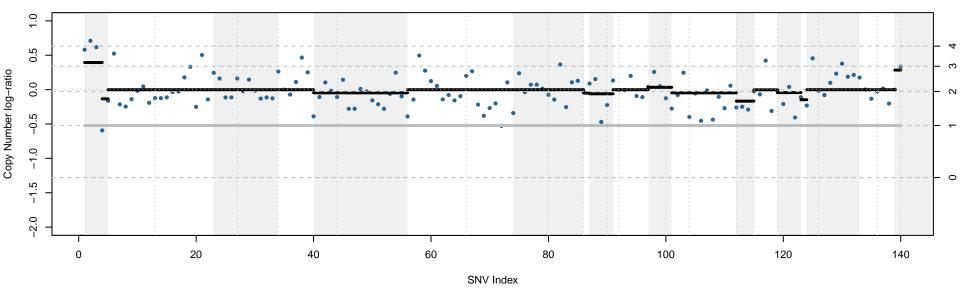
Purity: 0.58 Tumor ploidy: 2.066

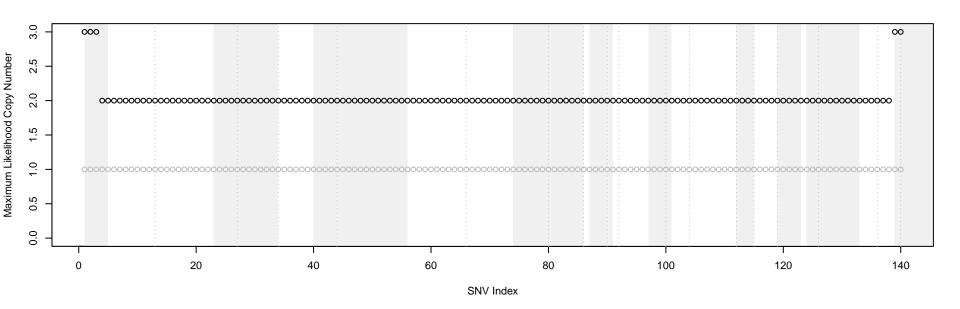


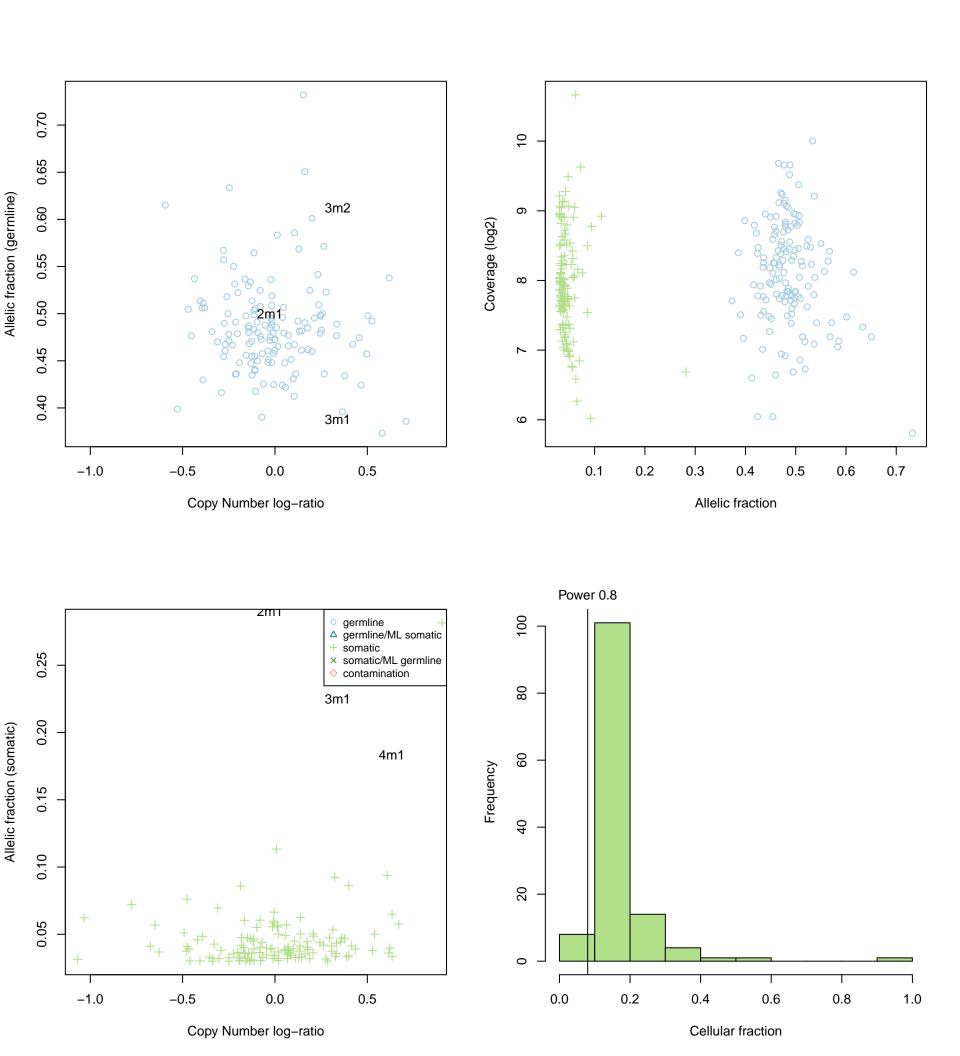
Fraction Genome



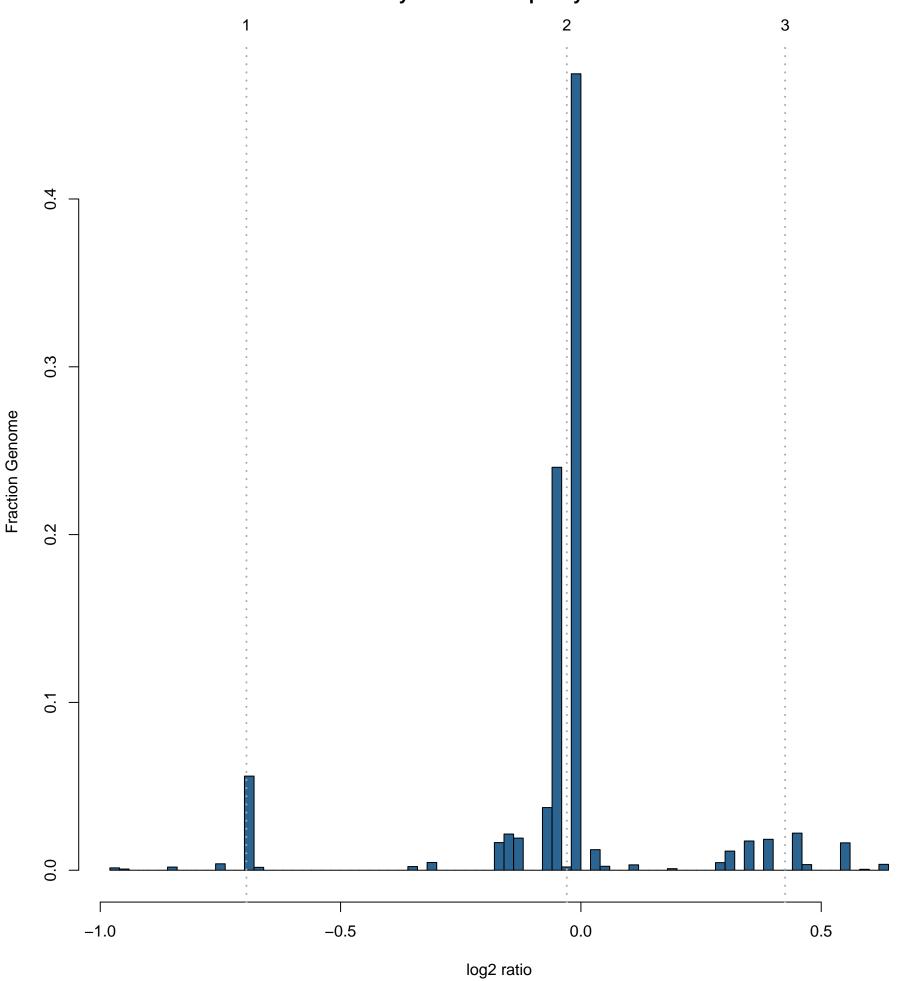
# SCNA-fit log-likelihood: -5198.42

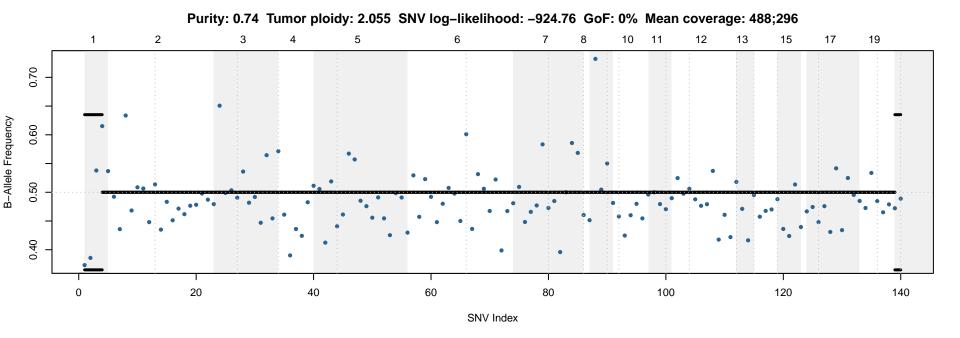




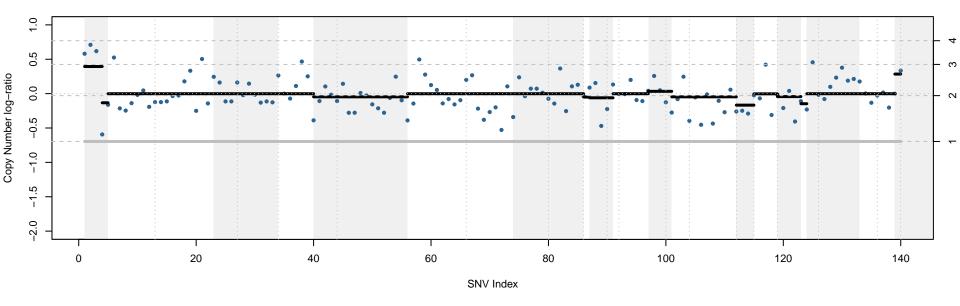


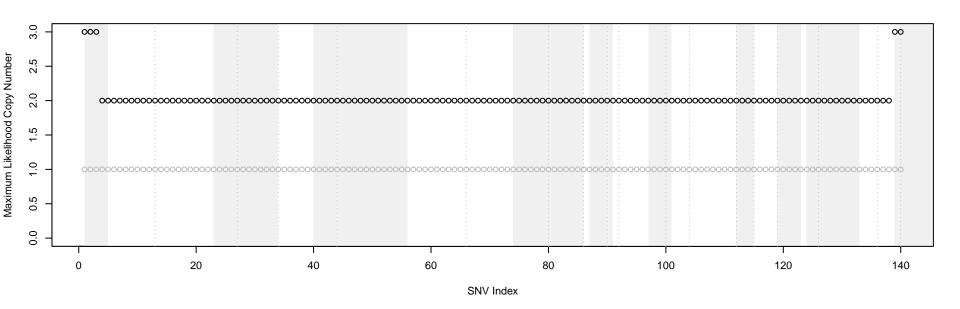
Purity: 0.74 Tumor ploidy: 2.055

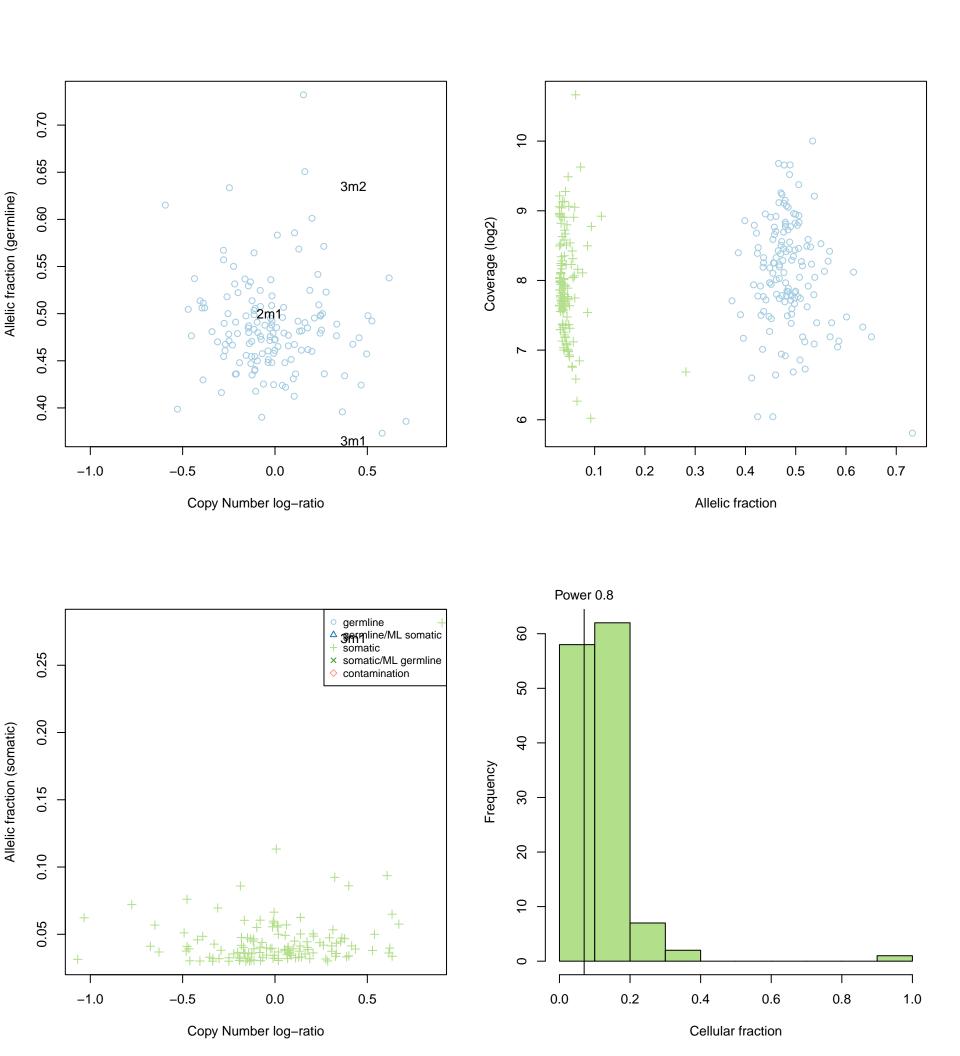




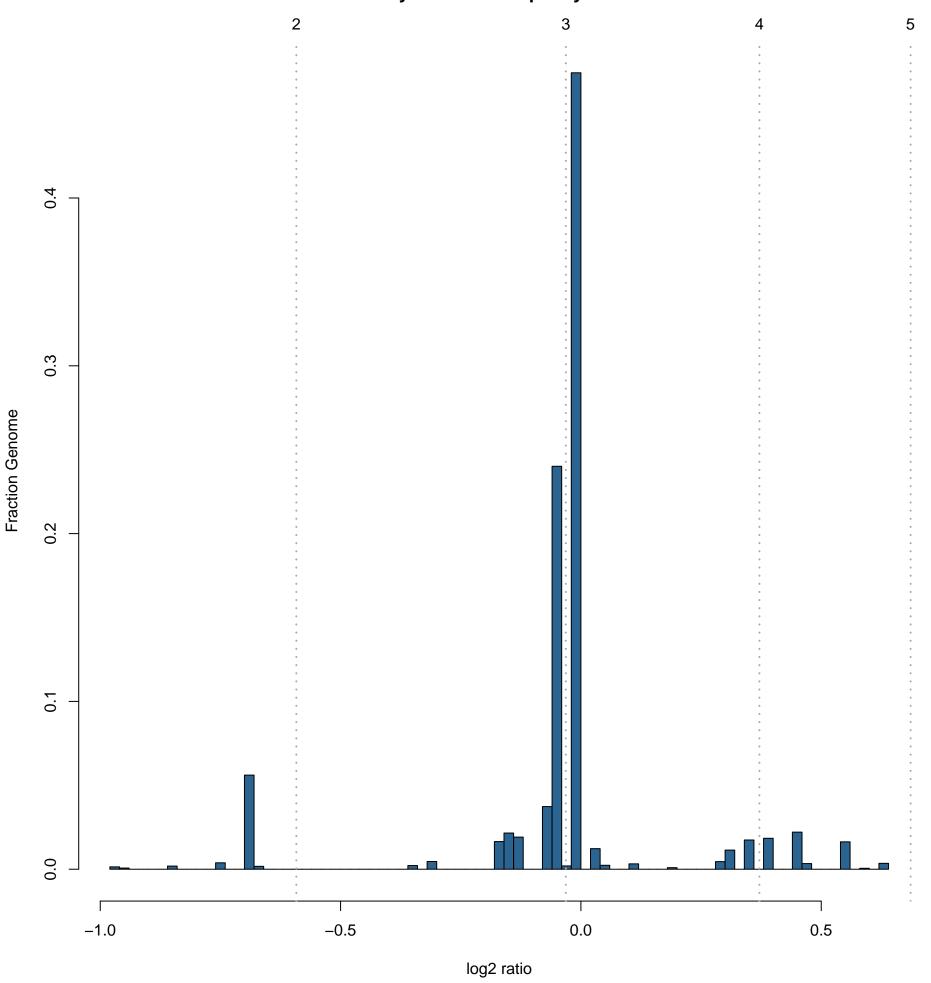
# SCNA-fit log-likelihood: -5129.07

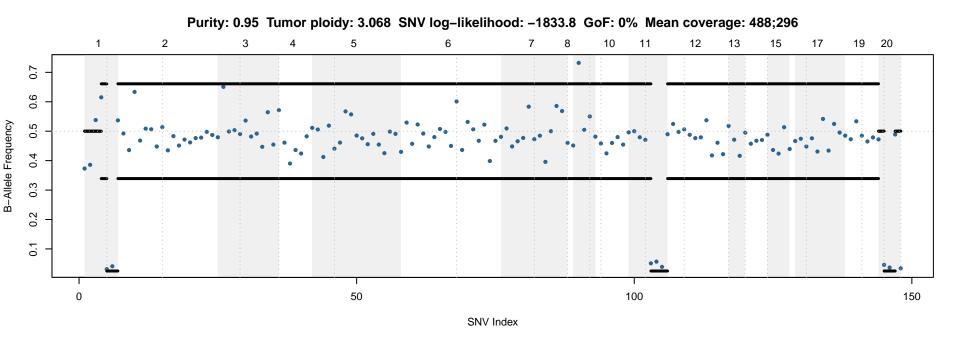






Purity: 0.95 Tumor ploidy: 3.068





#### SCNA-fit log-likelihood: -5158.43

