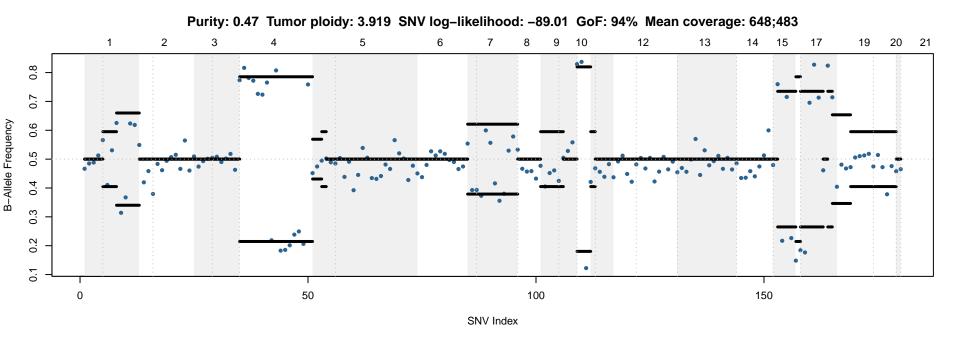
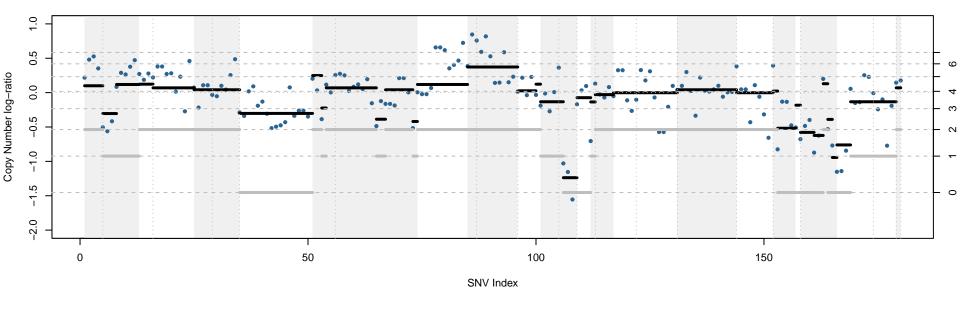
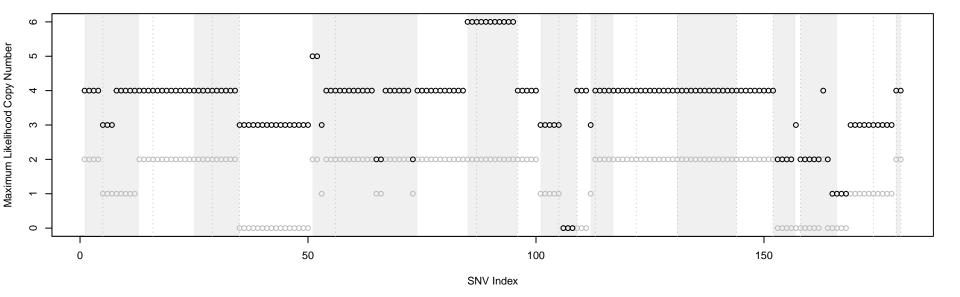
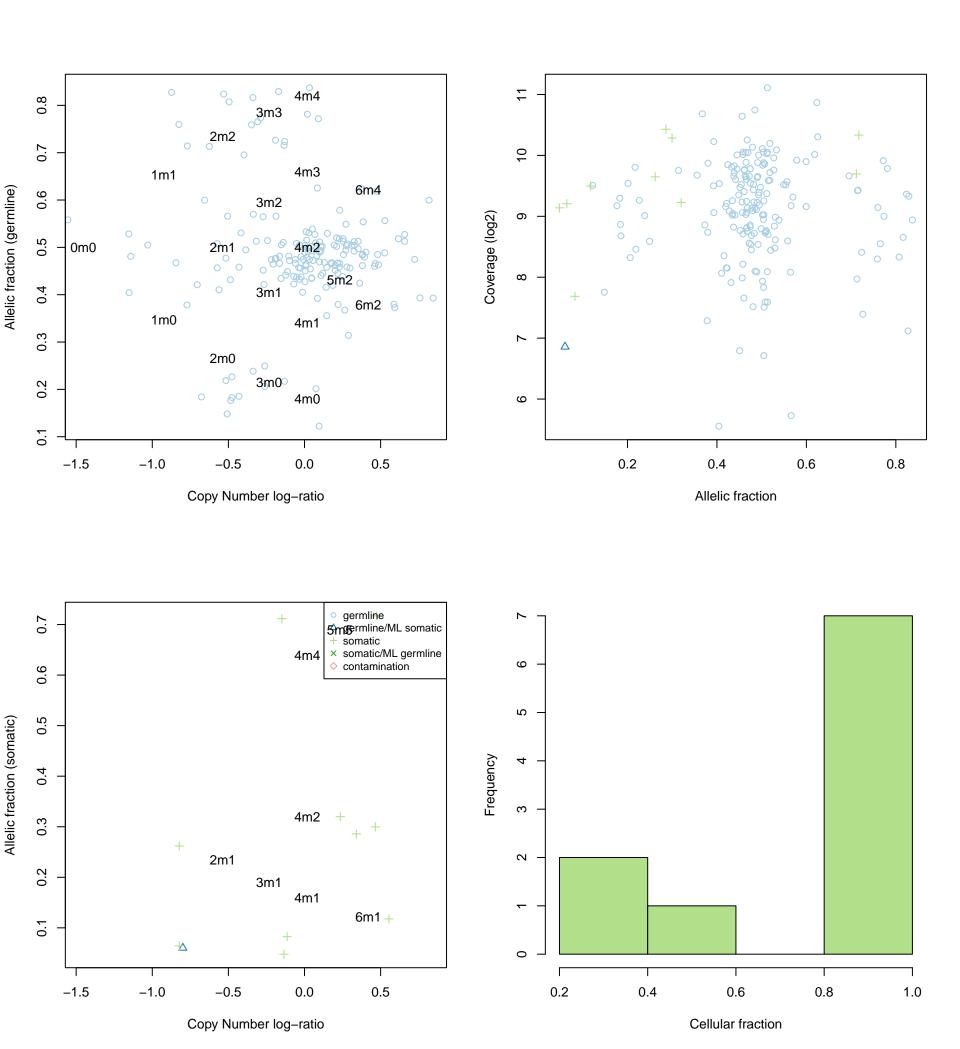
Purity: 0.47 Tumor ploidy: 3.919 3 0 2 5 6 7 Fraction Genome 0.10 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio



#### SCNA-fit log-likelihood: -4753.89

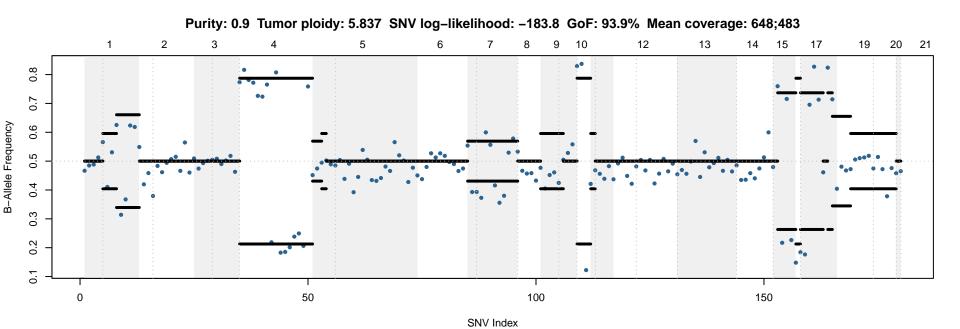




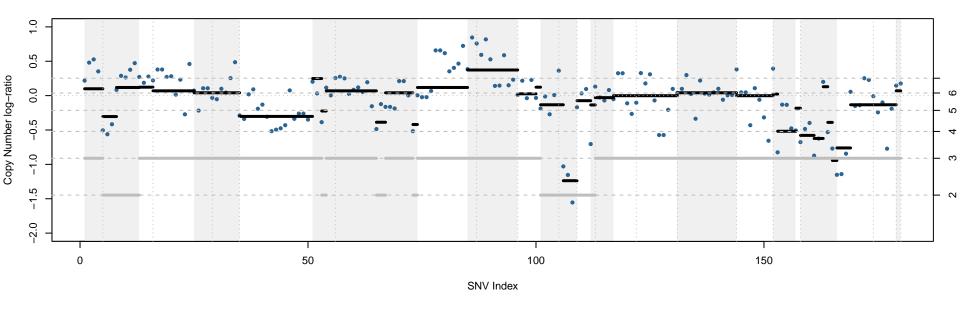


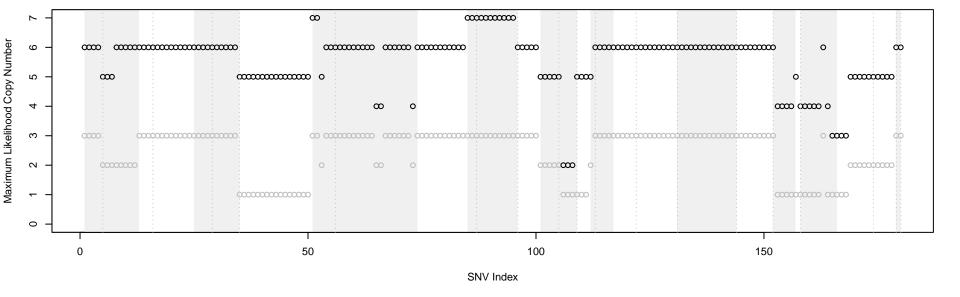
Purity: 0.9 Tumor ploidy: 5.837 2 3 6 Fraction Genome 0.10 0.05 0.00 -0.5 -1.5 -1.0 0.0 0.5

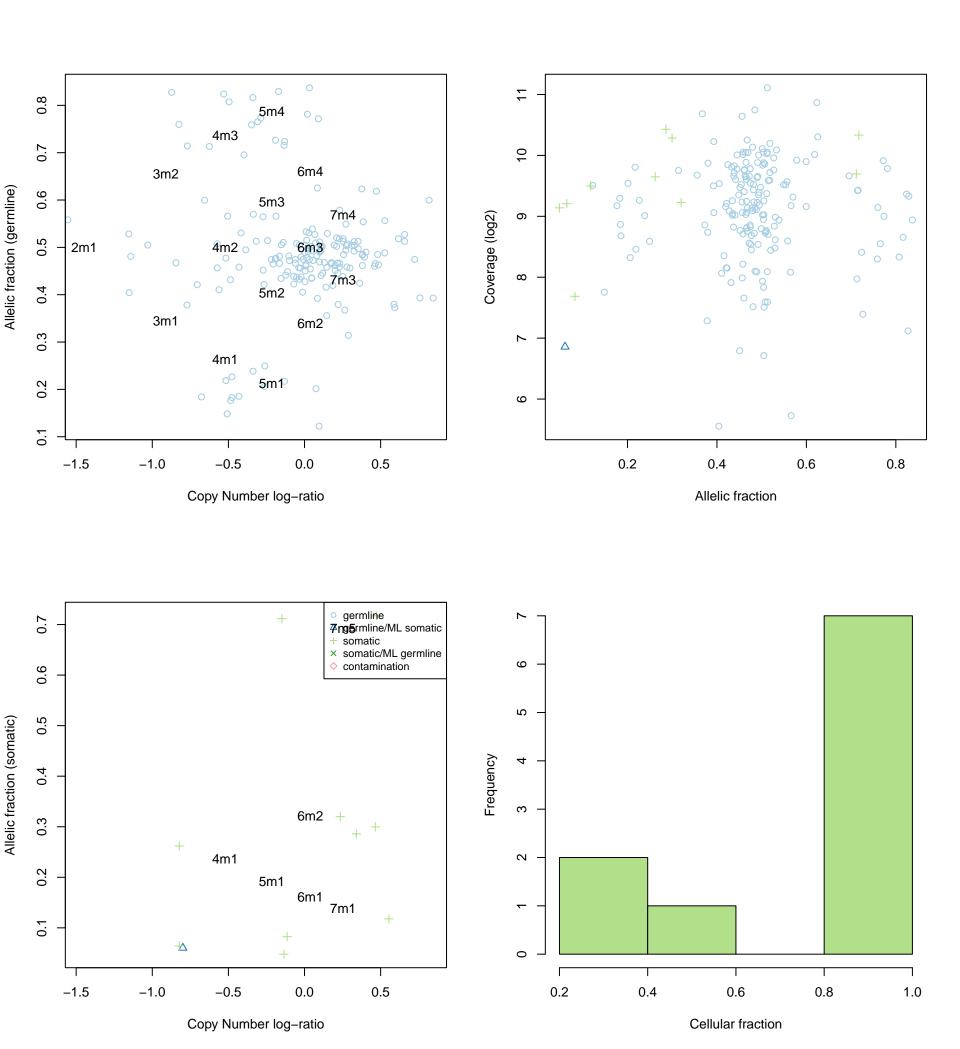
log2 ratio



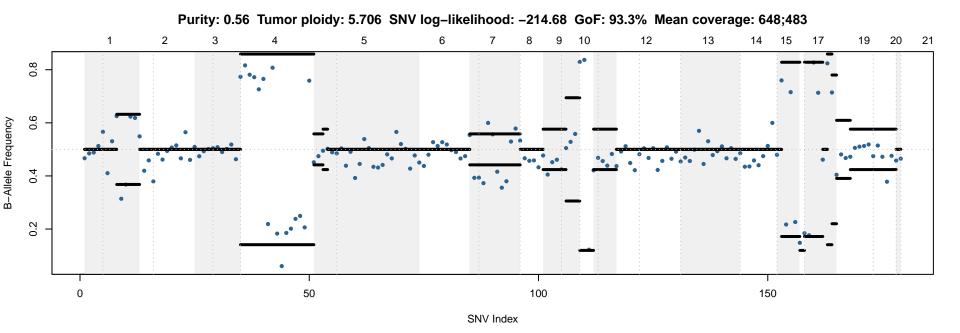
#### SCNA-fit log-likelihood: -4819.9



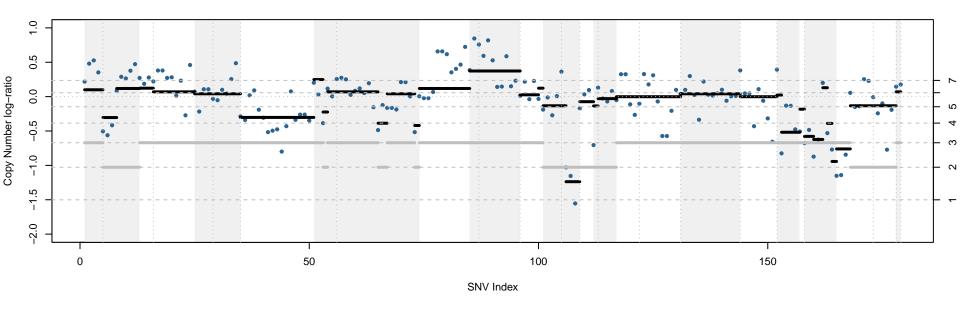


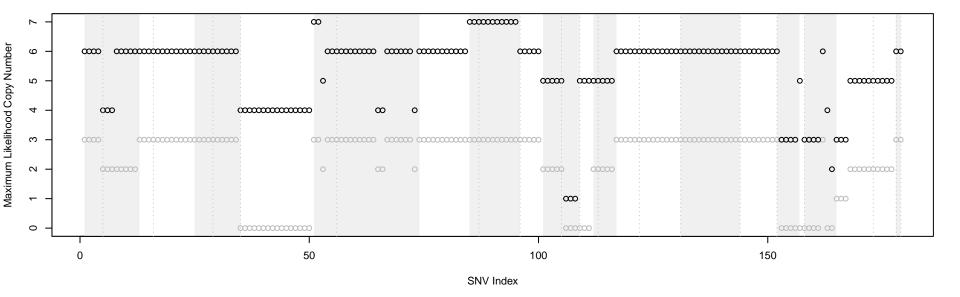


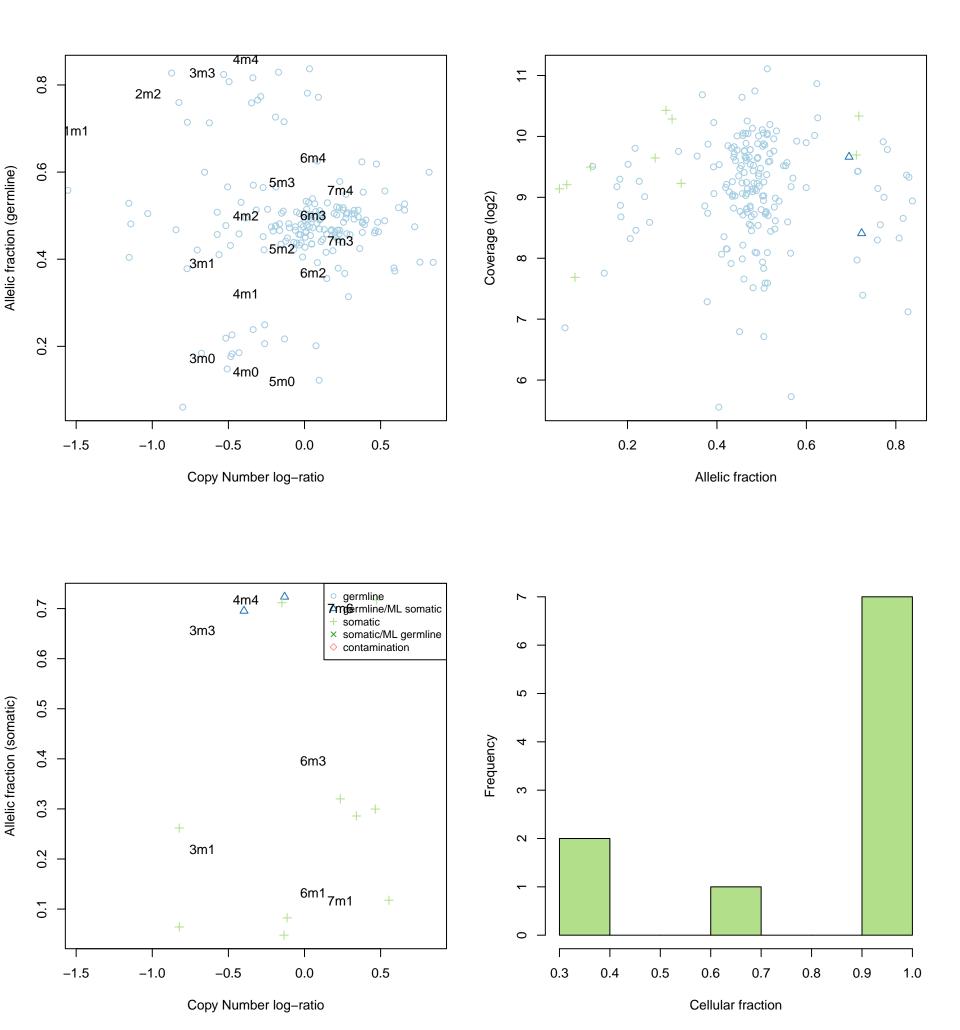
Purity: 0.56 Tumor ploidy: 5.706 2 5 7 6 Fraction Genome 0.10 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio

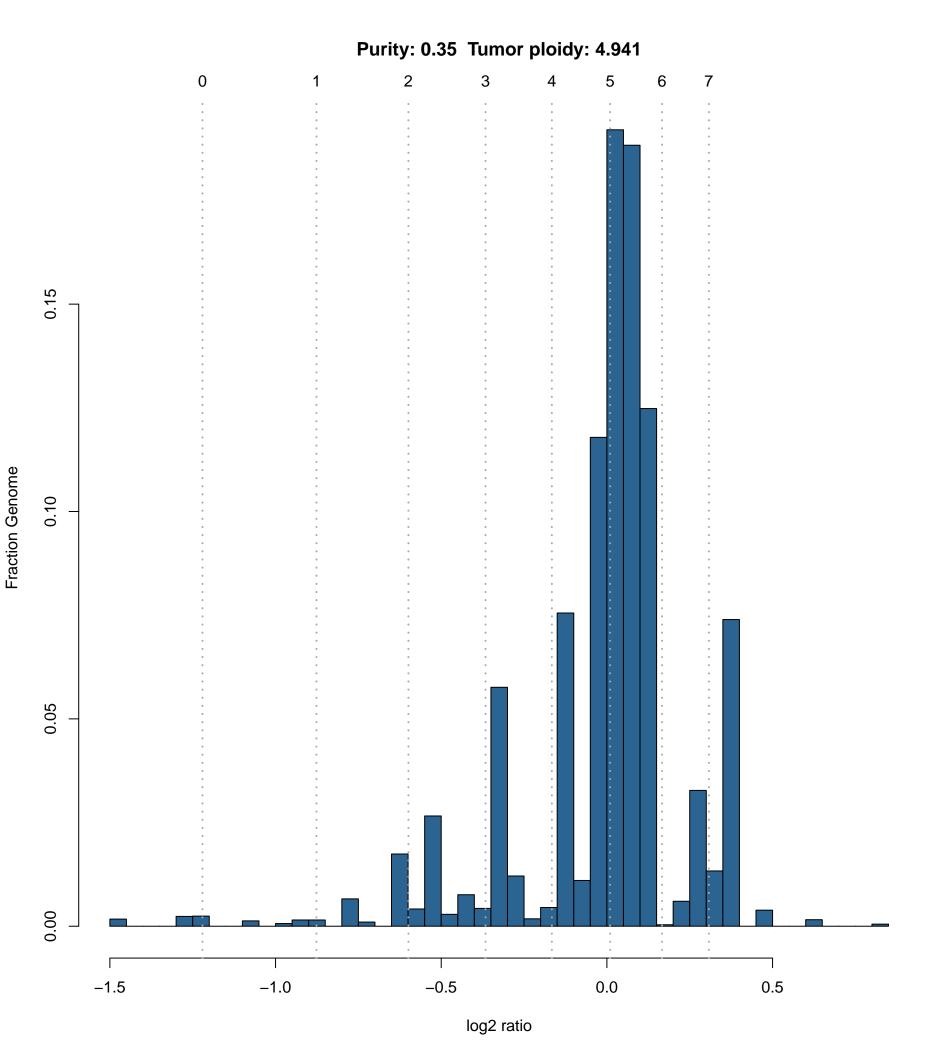


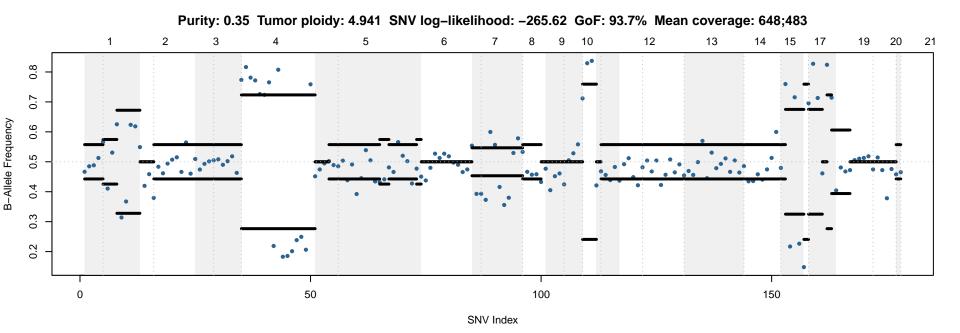
#### SCNA-fit log-likelihood: -4808.54



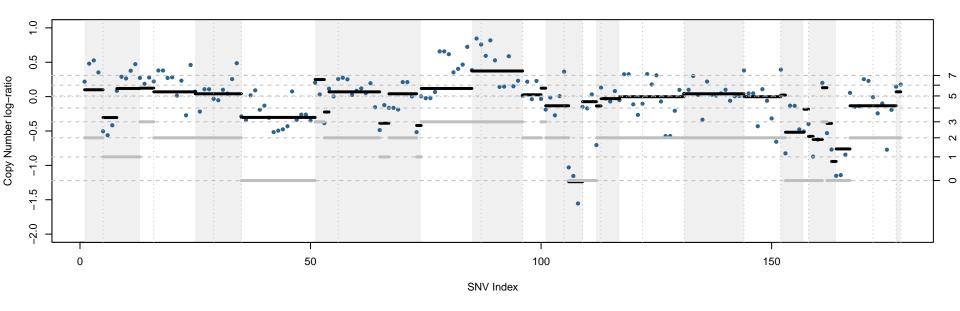


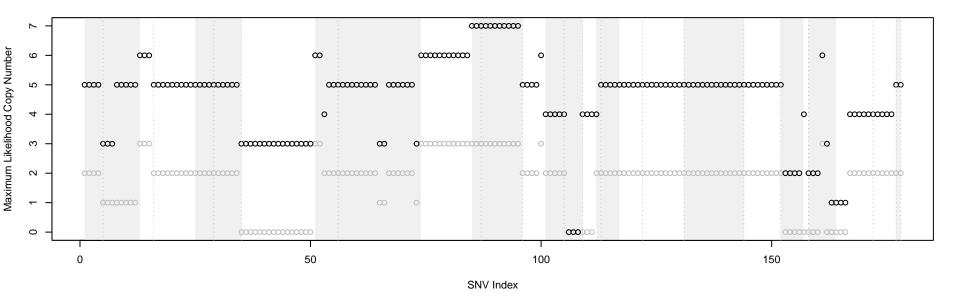


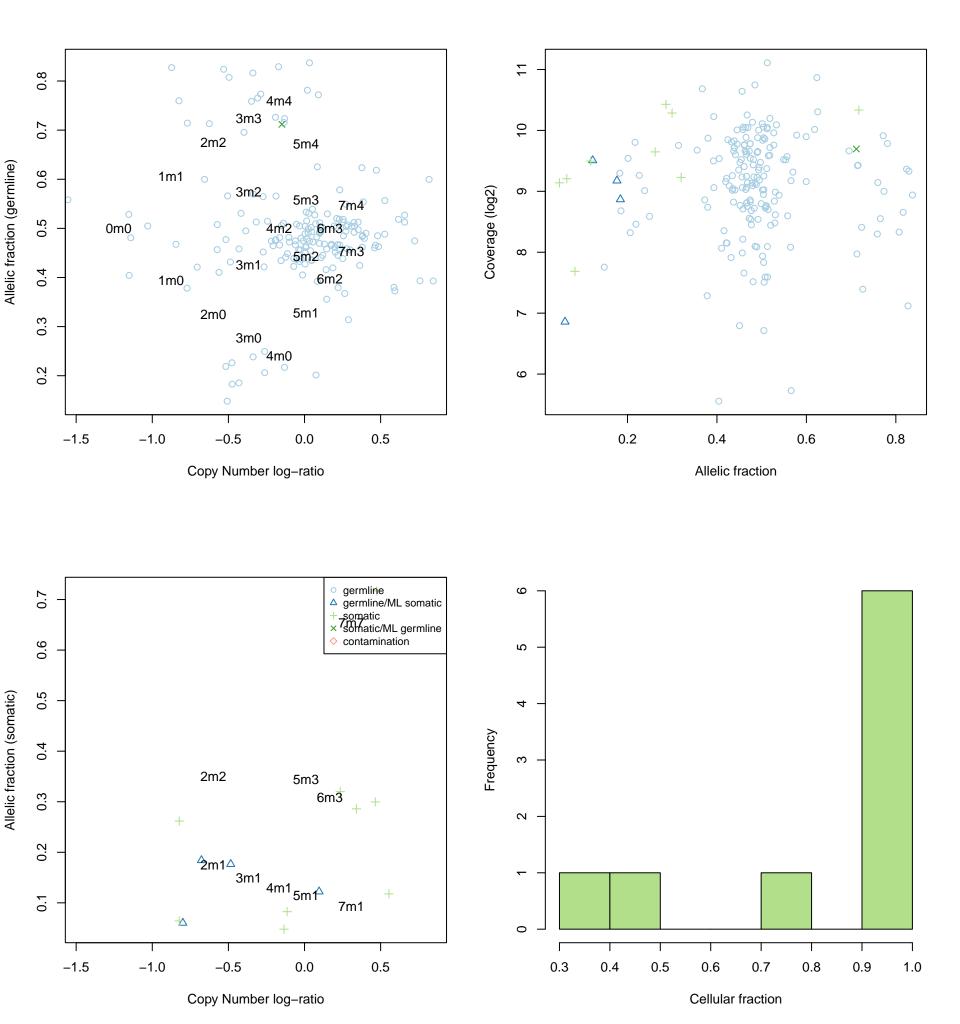




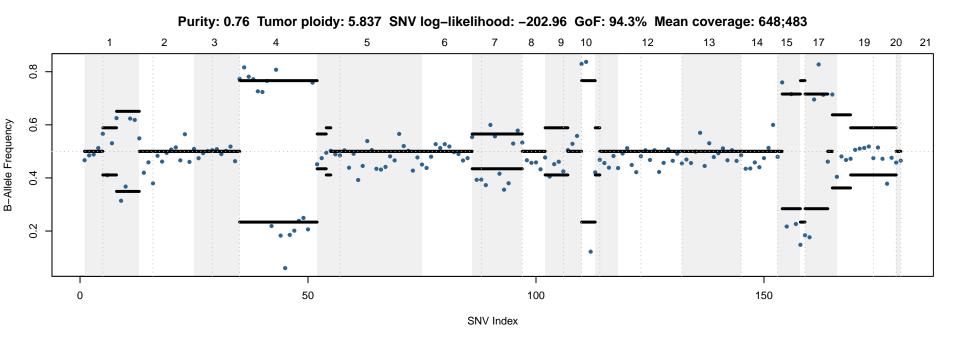
#### SCNA-fit log-likelihood: -4698.07



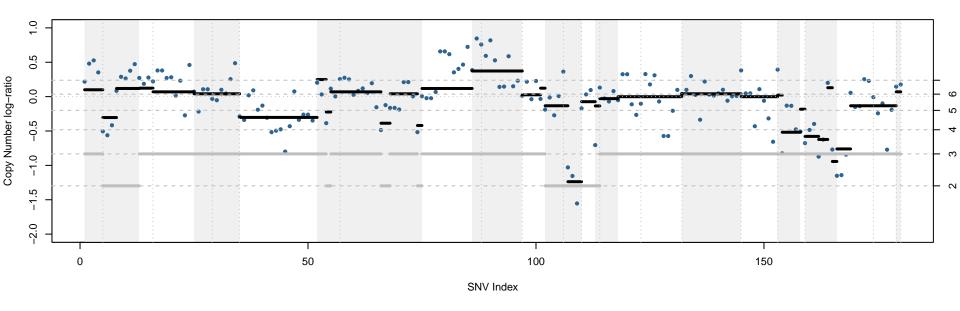


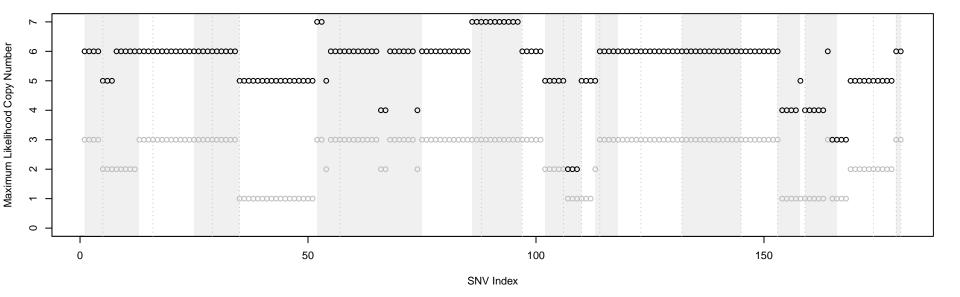


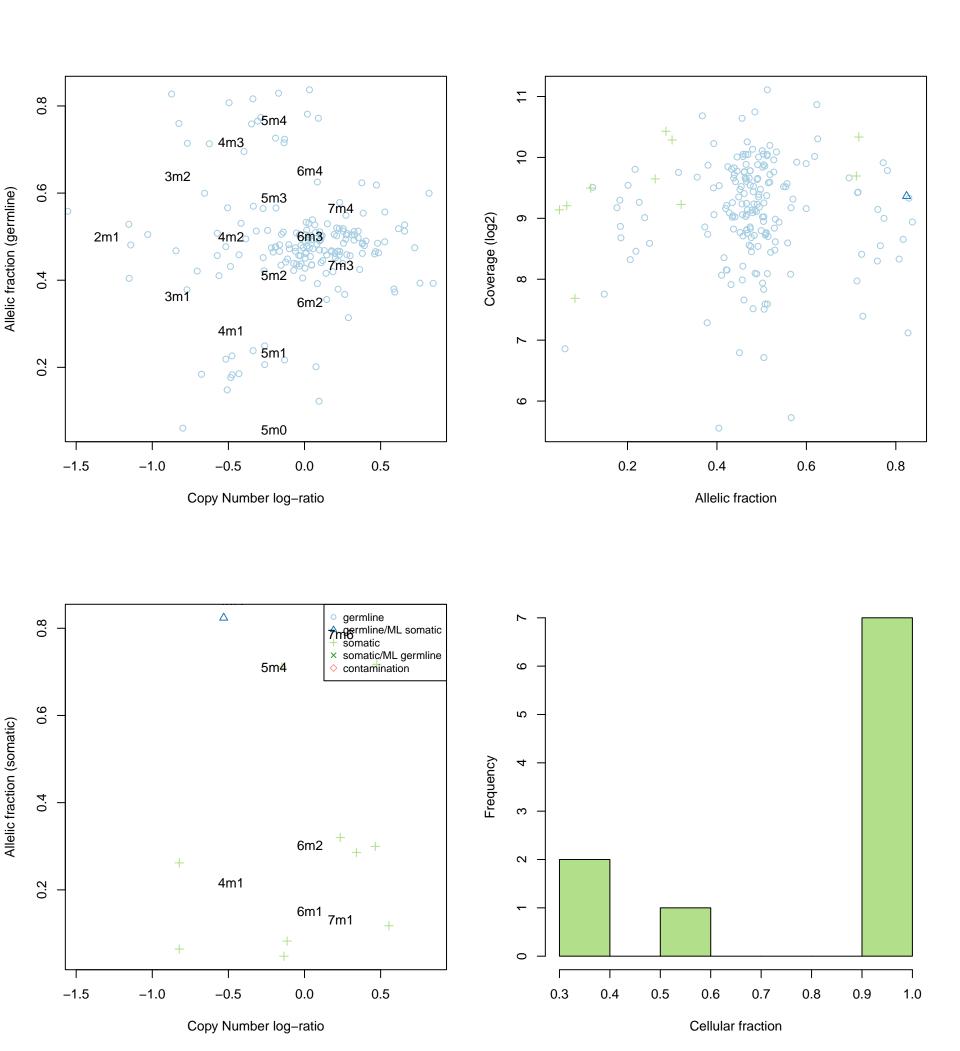
Purity: 0.76 Tumor ploidy: 5.837 2 3 6 7 Fraction Genome 0.10 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio



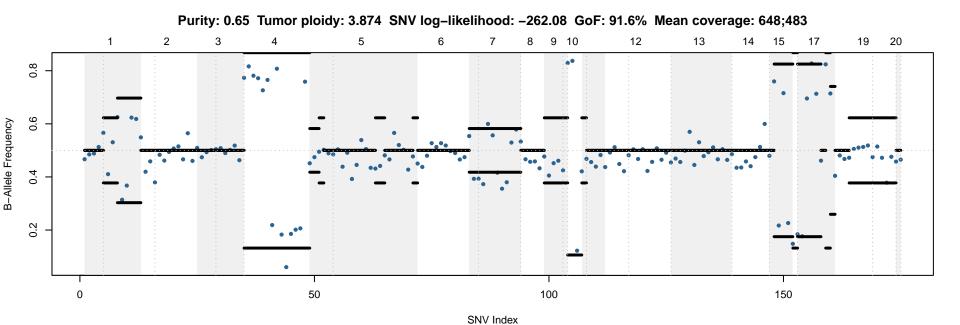
#### SCNA-fit log-likelihood: -4844.52



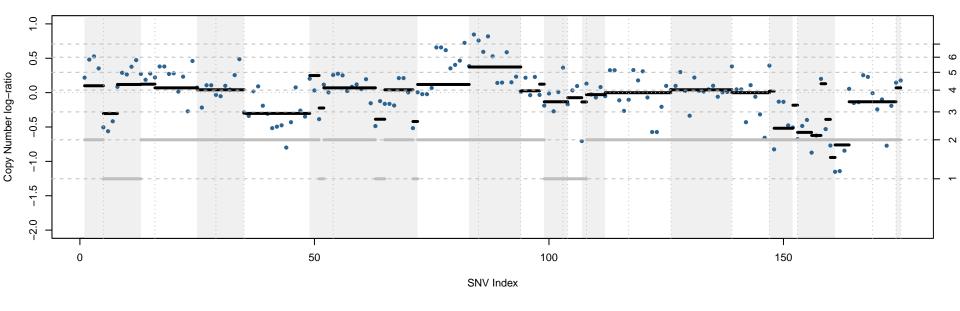


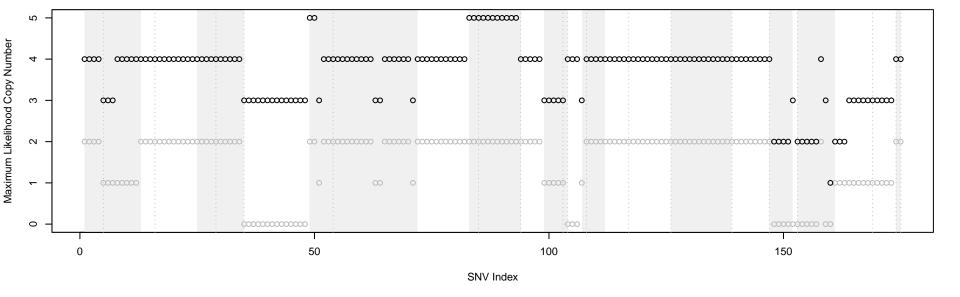


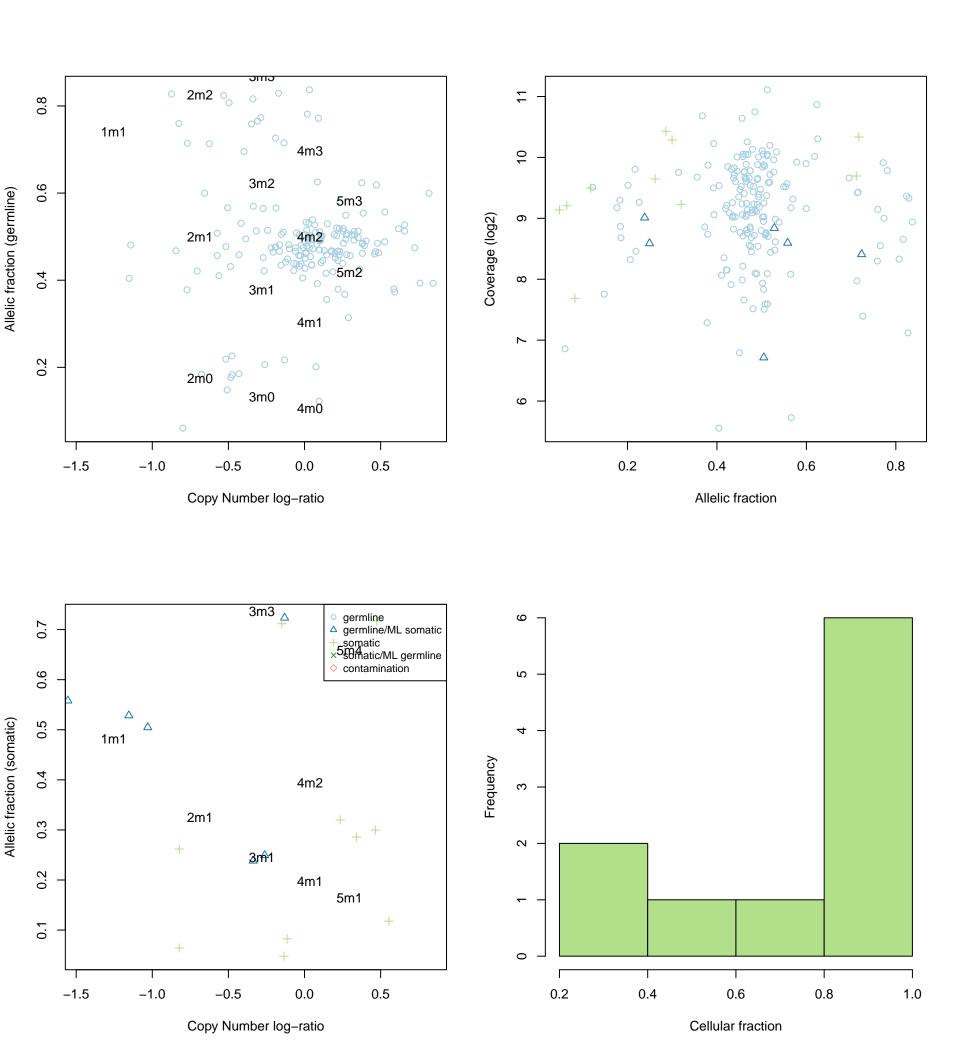
Purity: 0.65 Tumor ploidy: 3.874 3 5 6 7 2 Fraction Genome 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio



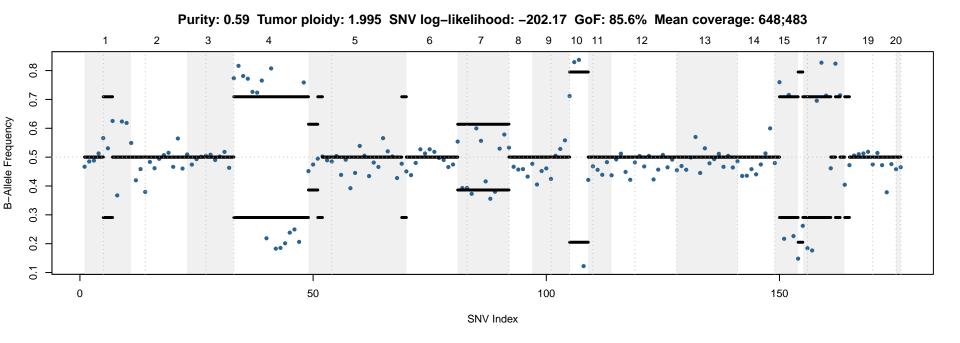
### SCNA-fit log-likelihood: -4794.96



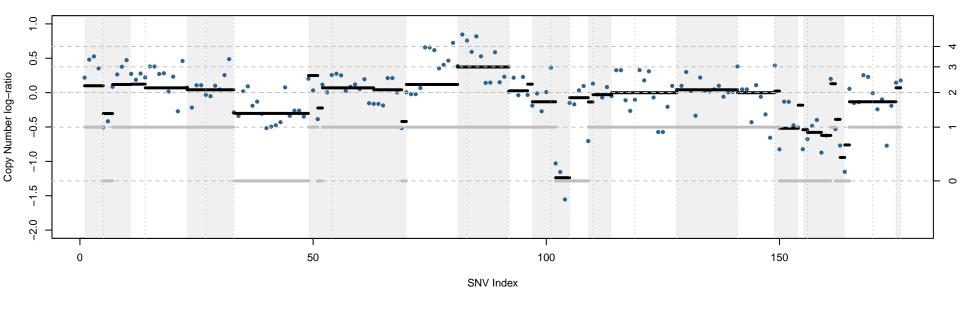


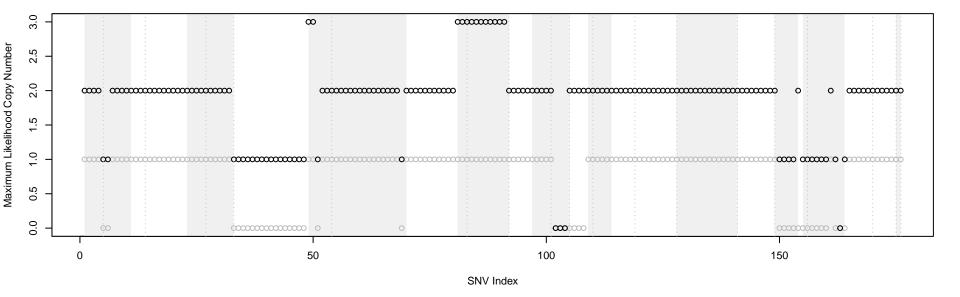


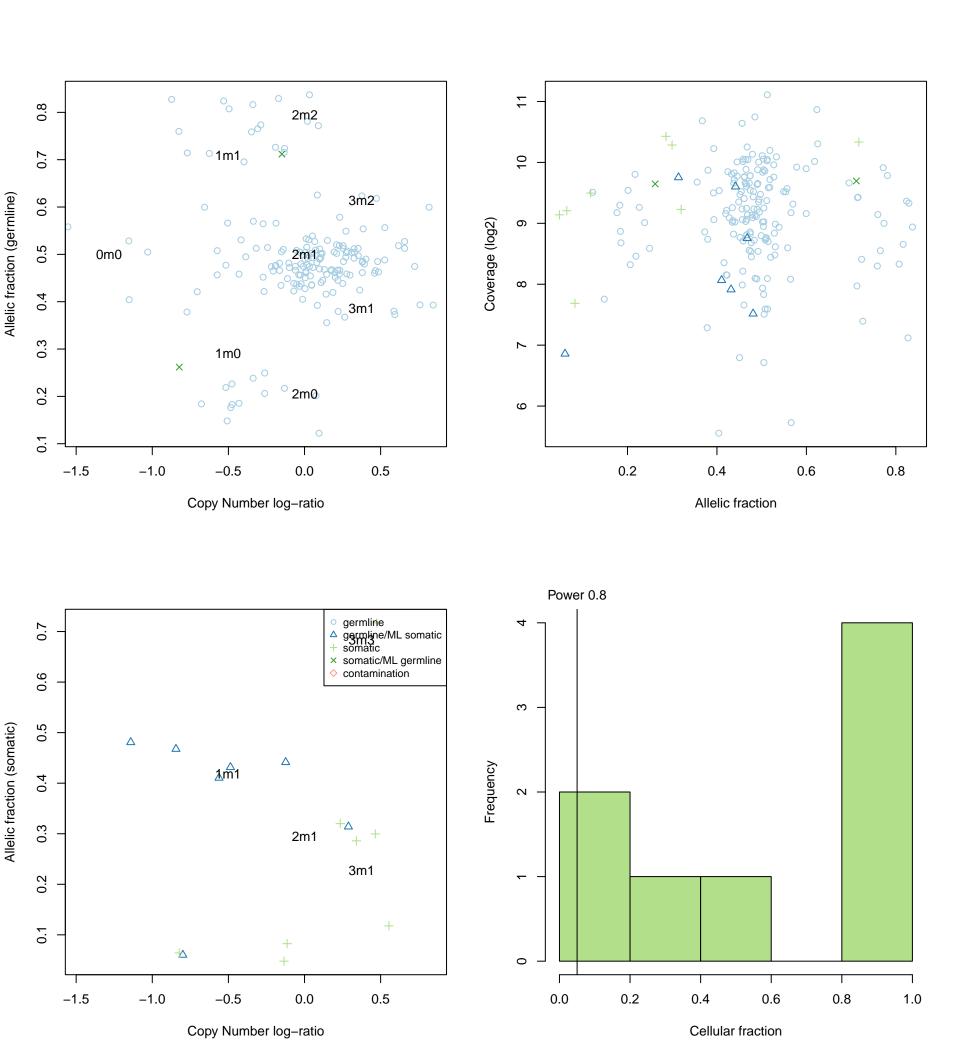
Purity: 0.59 Tumor ploidy: 1.995 2 0 3 Fraction Genome 0.10 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio



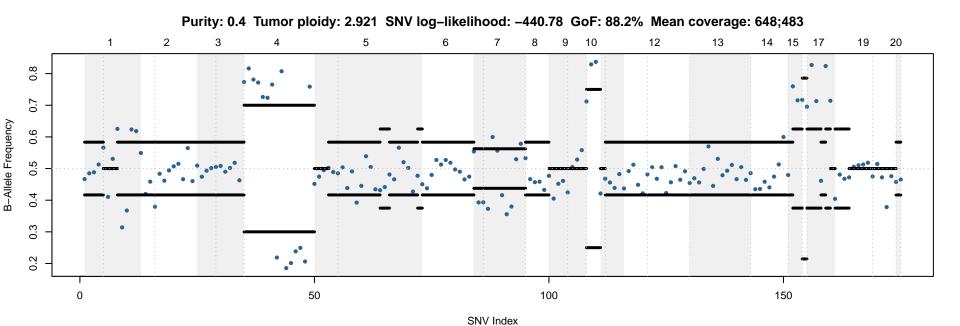
## SCNA-fit log-likelihood: -5059.95



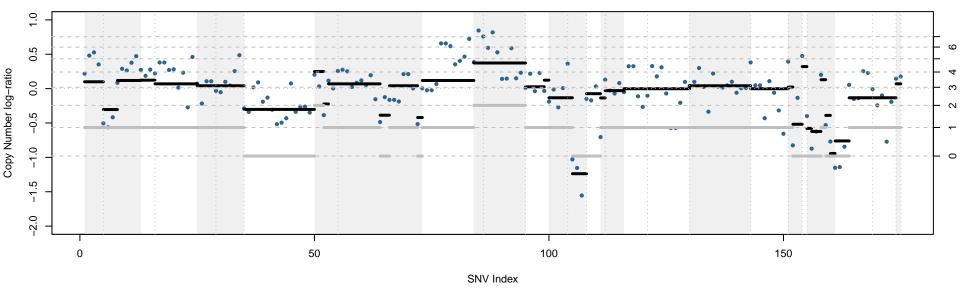


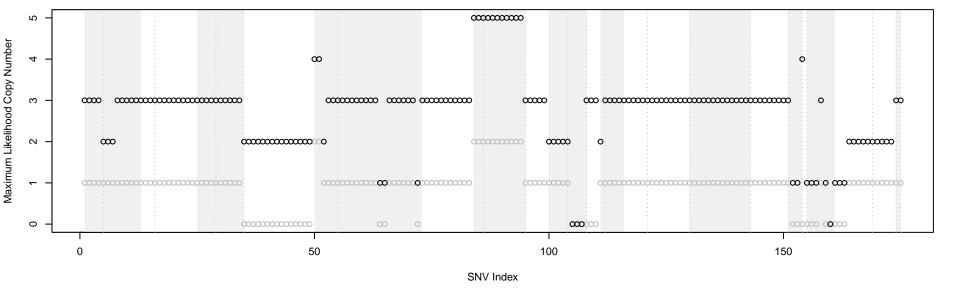


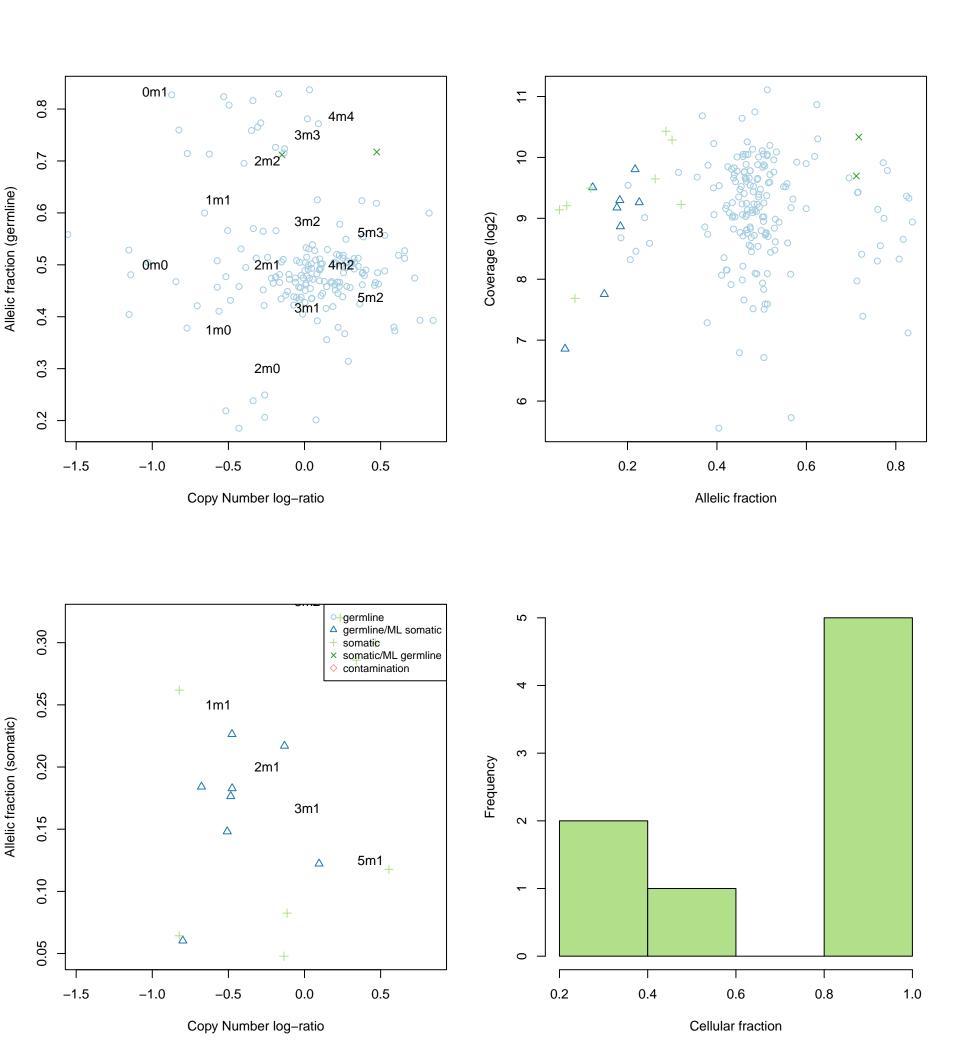
Purity: 0.4 Tumor ploidy: 2.921 0 2 5 6 4 Fraction Genome 0.10 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio



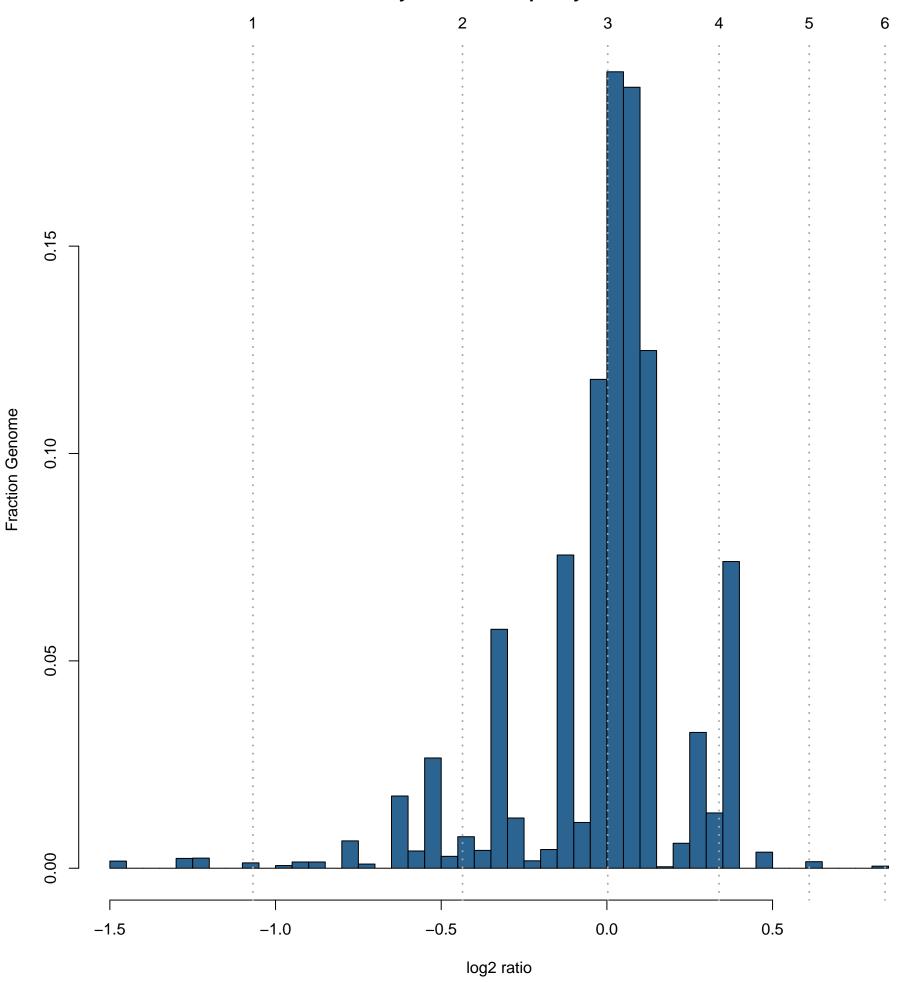
#### SCNA-fit log-likelihood: -4809.3

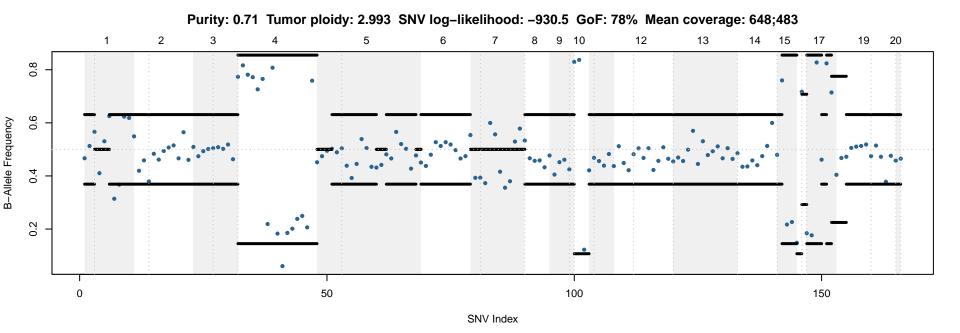






Purity: 0.71 Tumor ploidy: 2.993





# SCNA-fit log-likelihood: -4997.96

