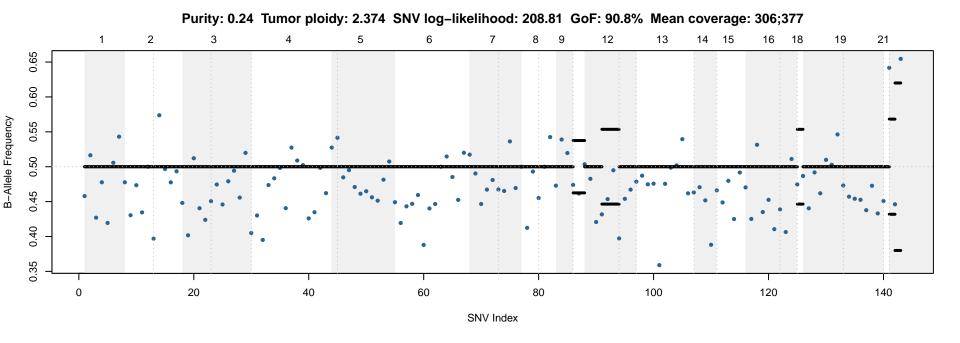
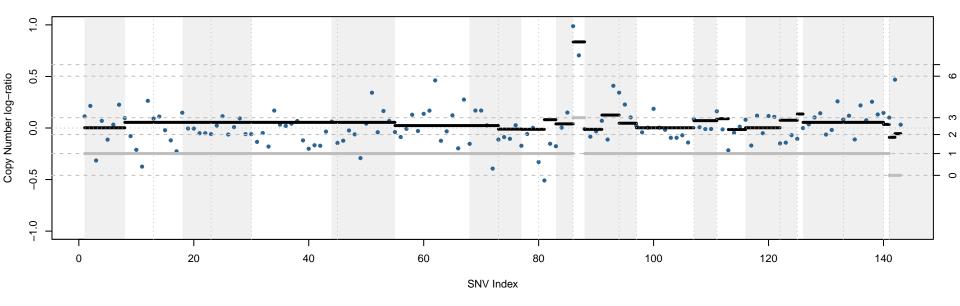
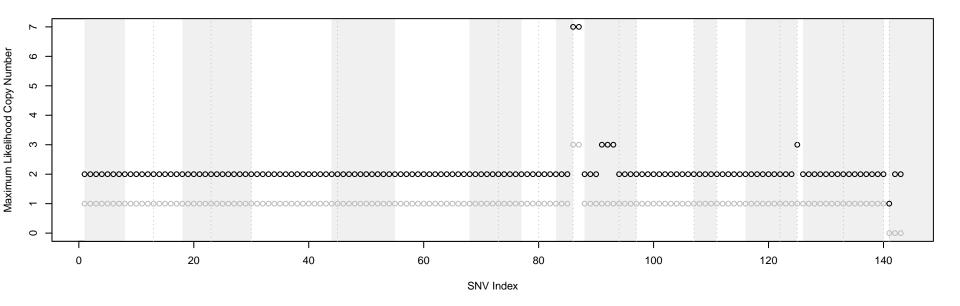
Purity: 0.24 Tumor ploidy: 2.374 0 2 0.3 Fraction Genome 0.1 0.0 -0.5 0.0 0.5 1.0

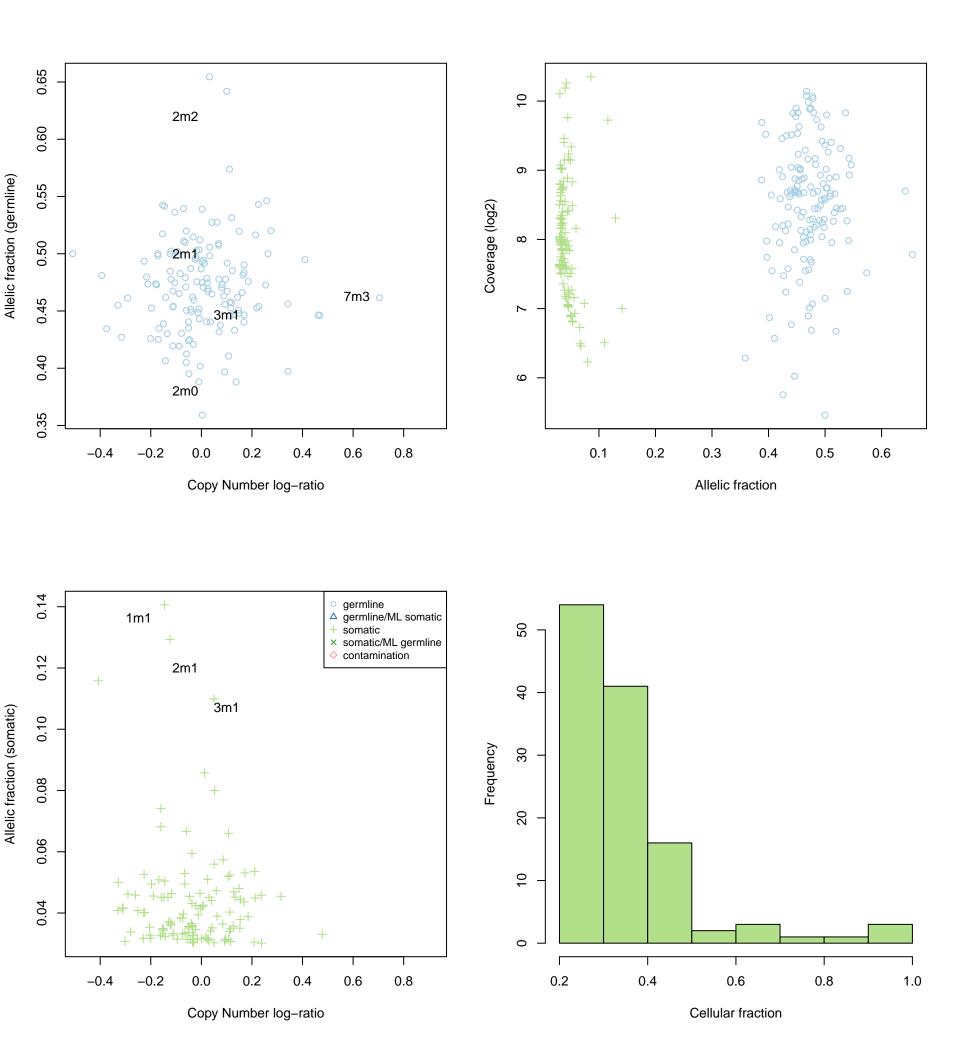
log2 ratio

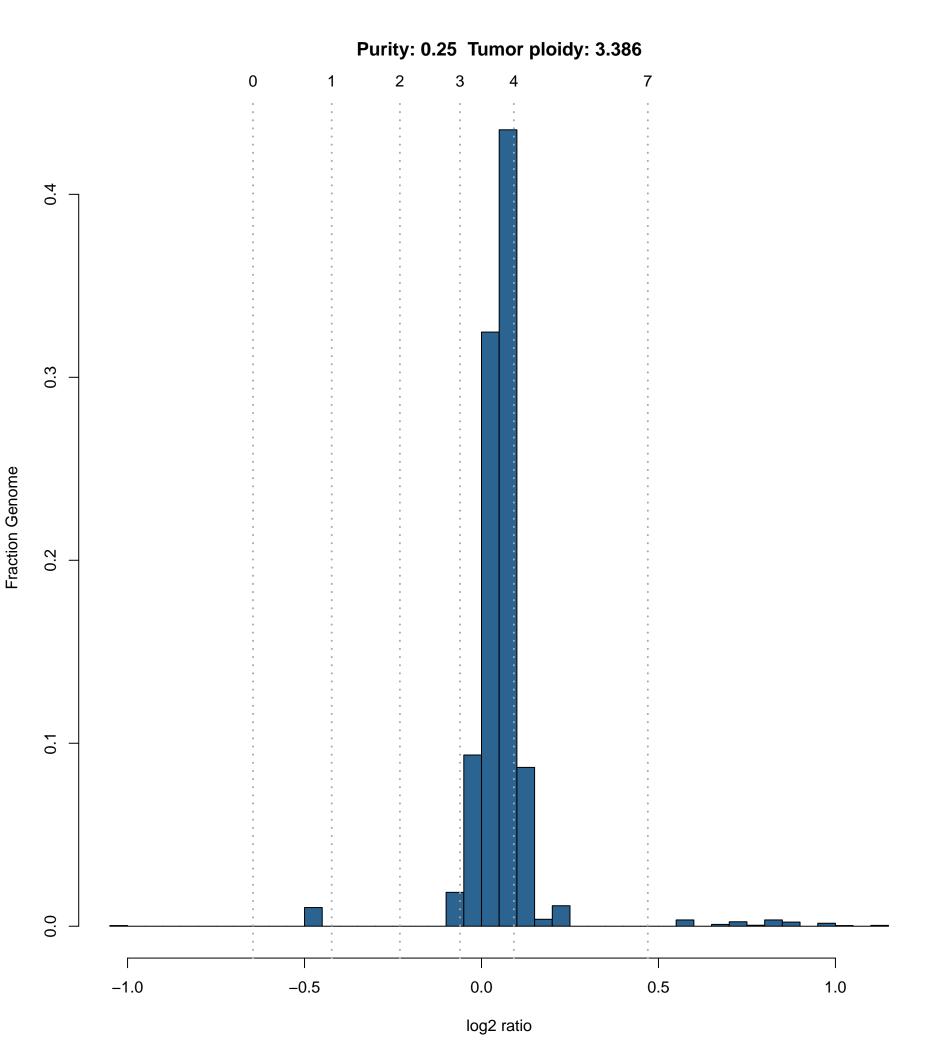


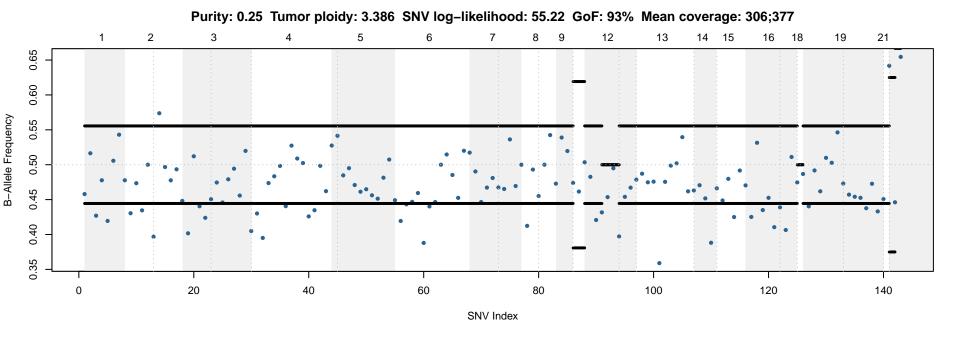
# SCNA-fit log-likelihood: -5122.39



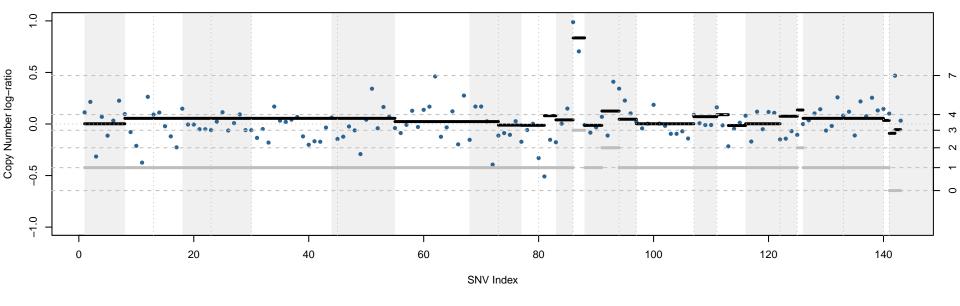


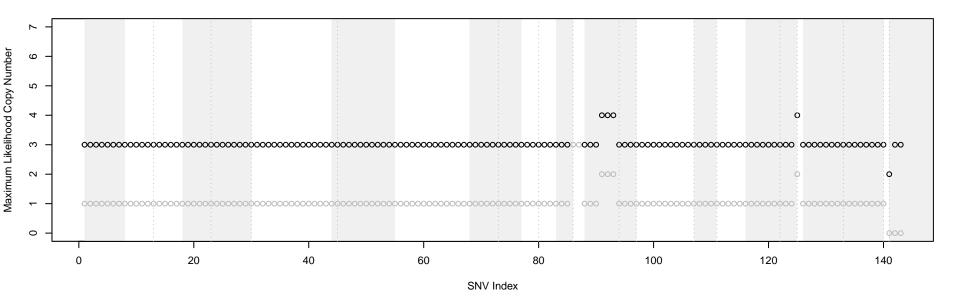


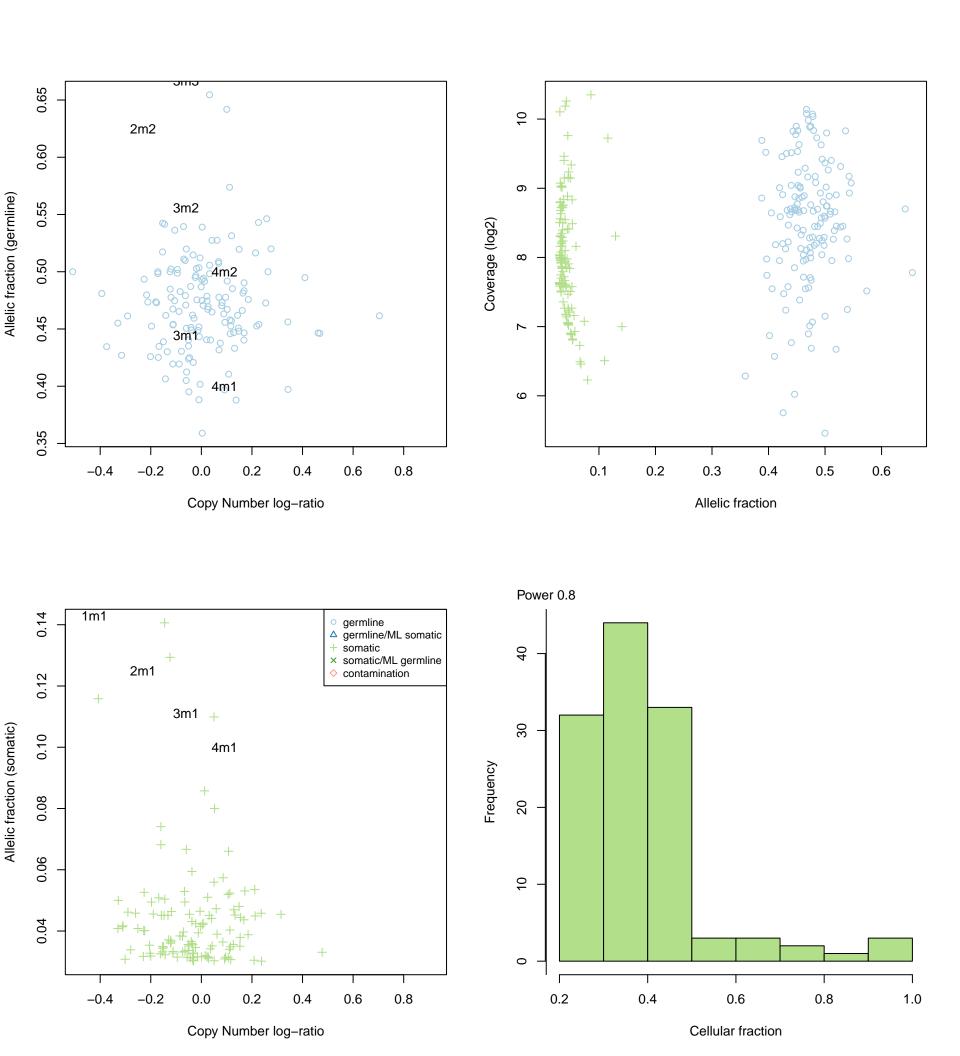




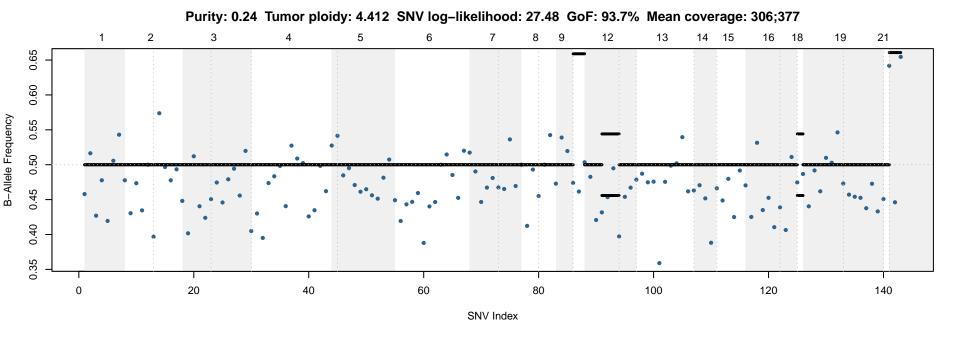
# SCNA-fit log-likelihood: -5145.17



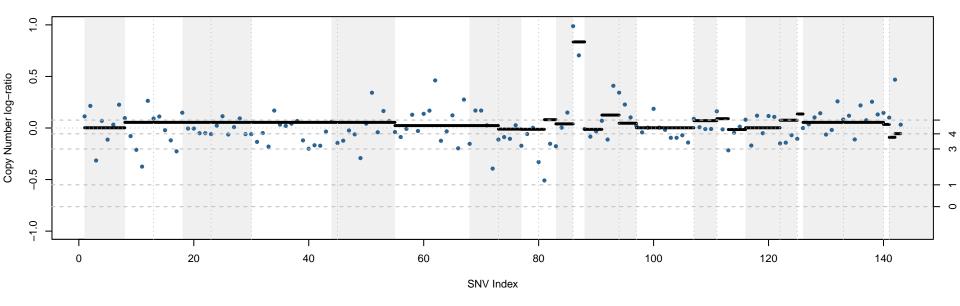


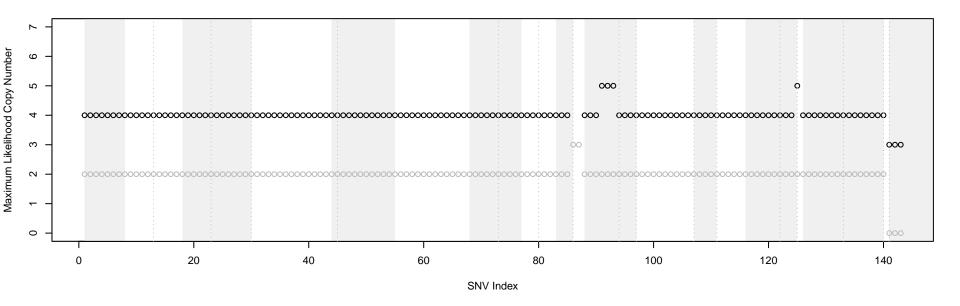


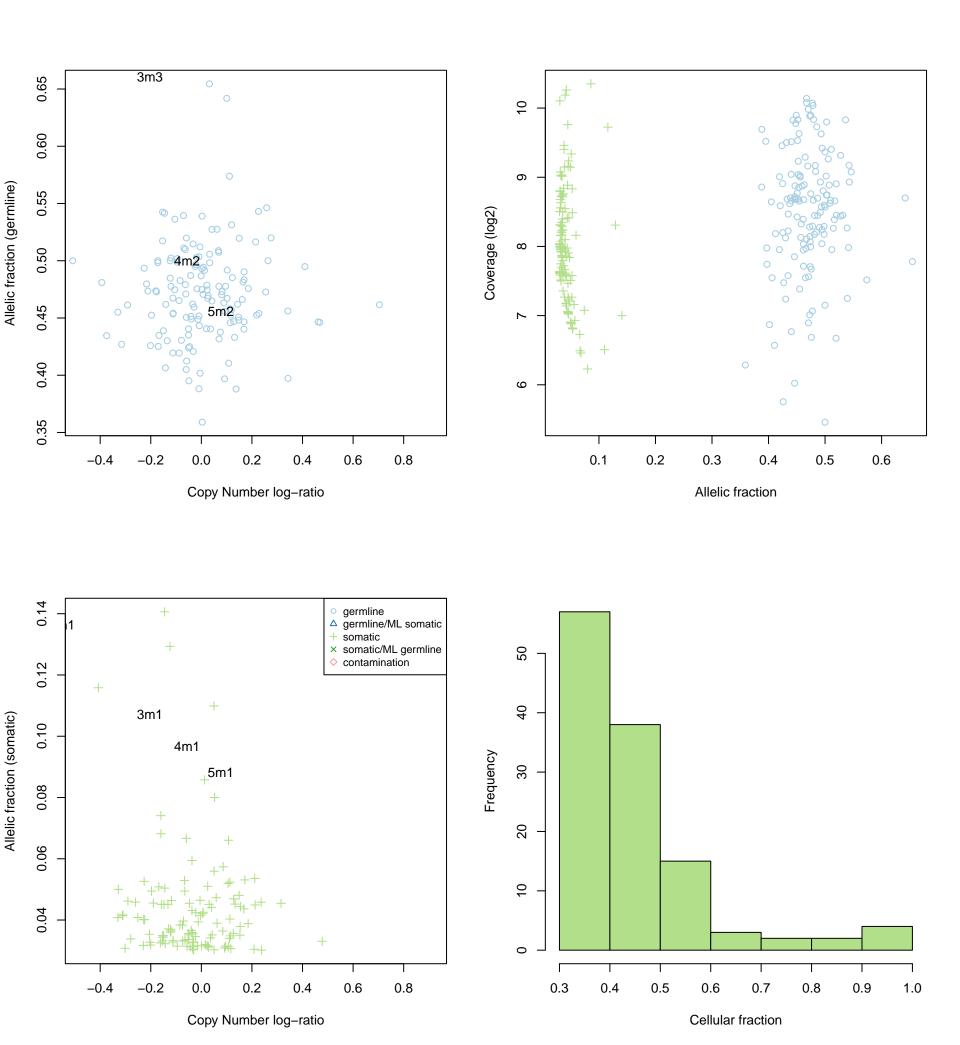
Purity: 0.24 Tumor ploidy: 4.412 0 5 0.3 Fraction Genome 0.2 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



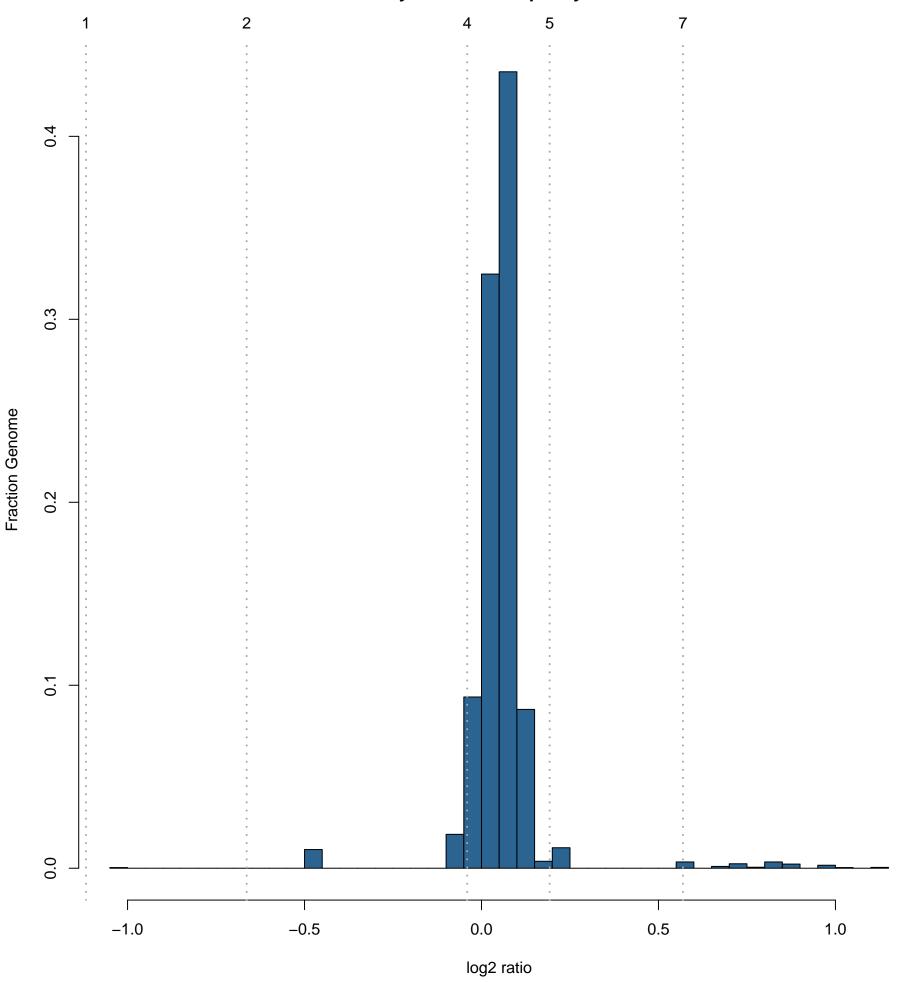
### SCNA-fit log-likelihood: -5149.08

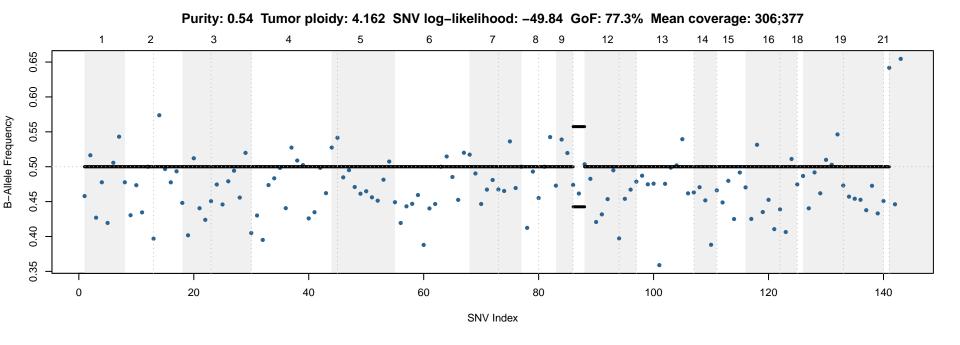




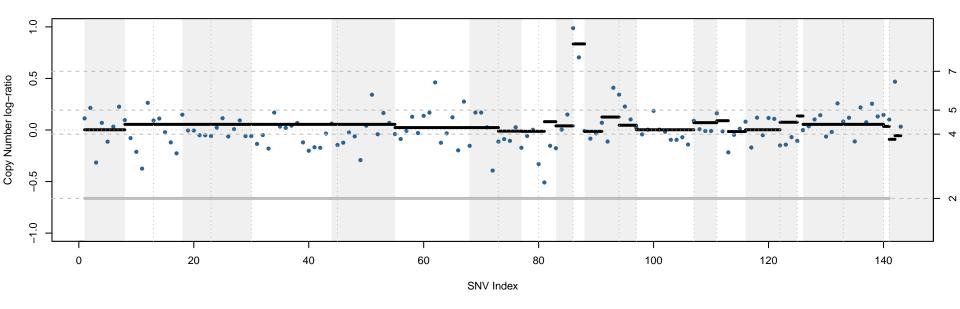


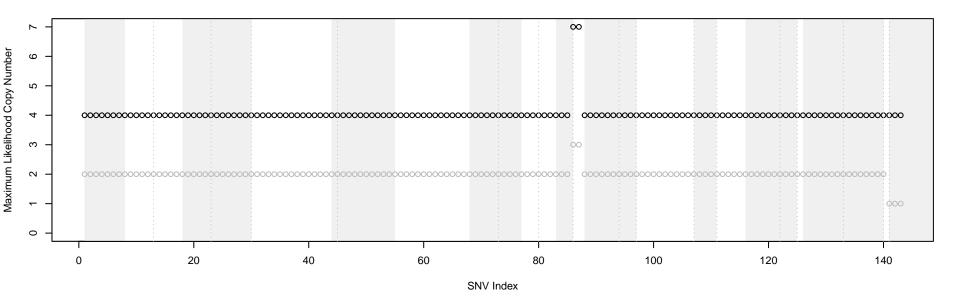
Purity: 0.54 Tumor ploidy: 4.162

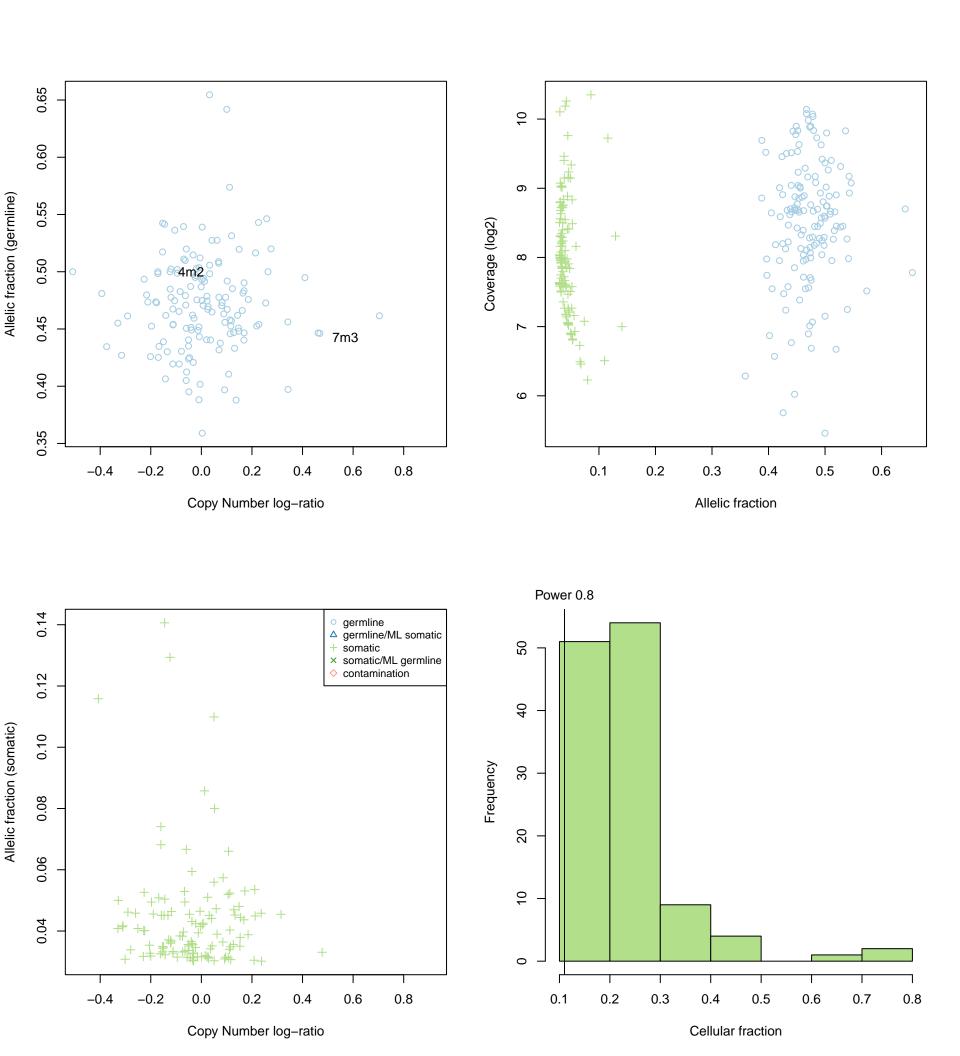




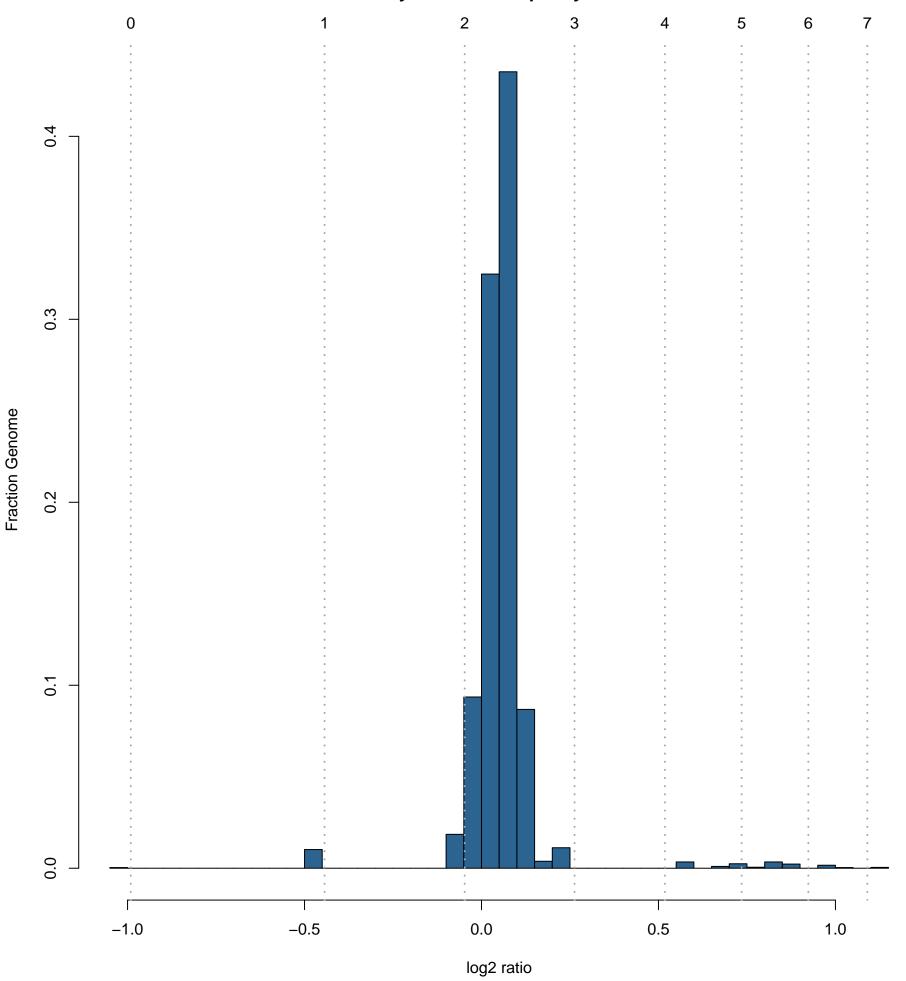
## SCNA-fit log-likelihood: -5072.43

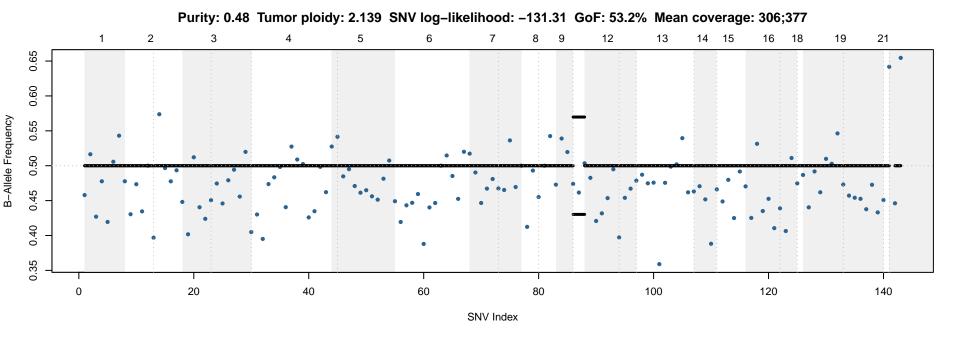




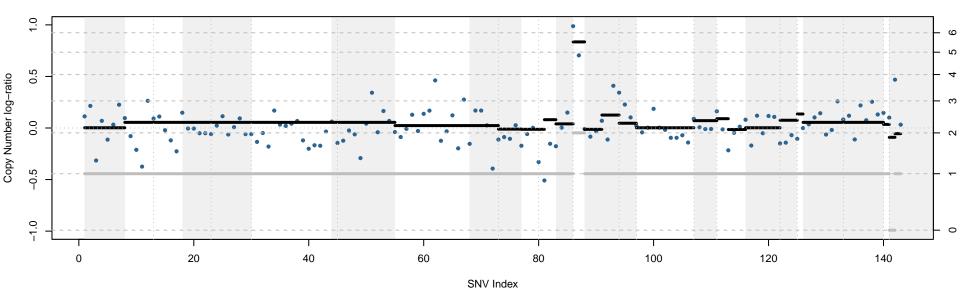


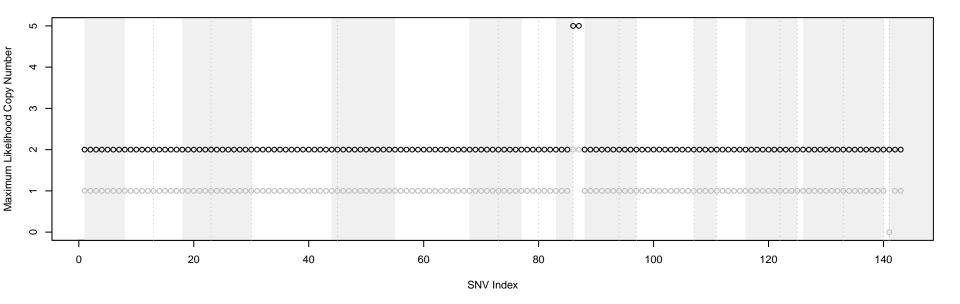
Purity: 0.48 Tumor ploidy: 2.139

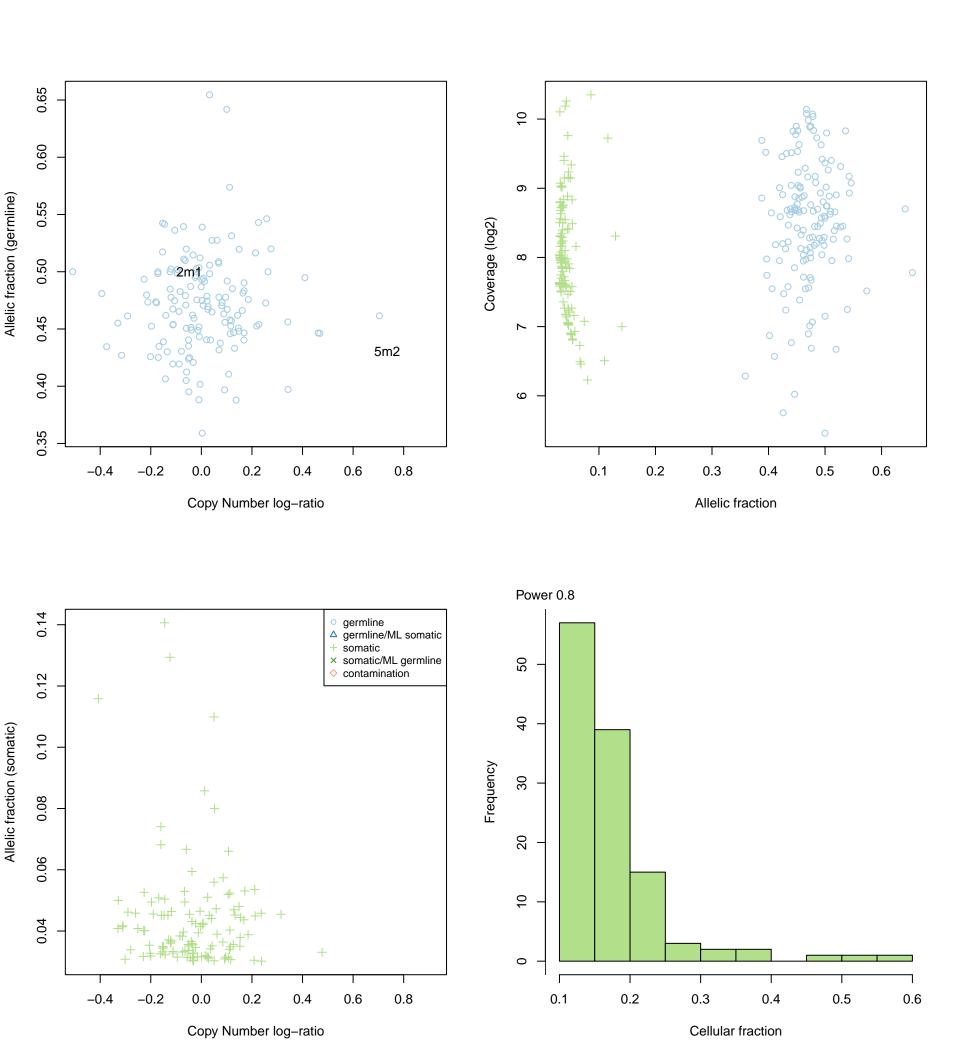




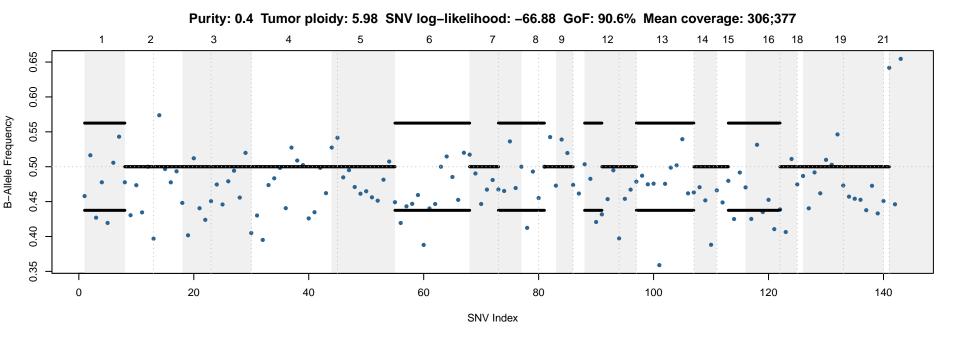
## SCNA-fit log-likelihood: -5049.04



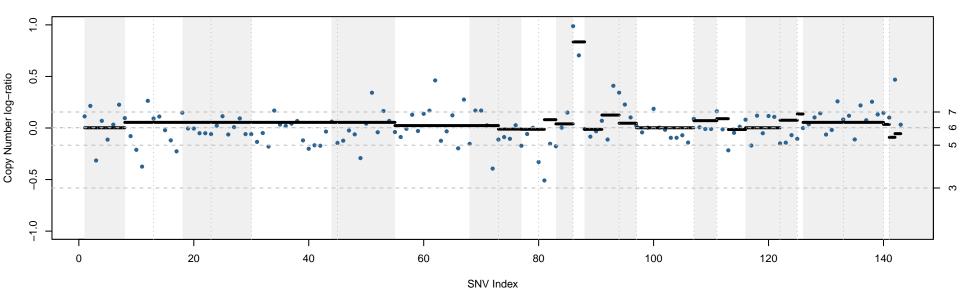


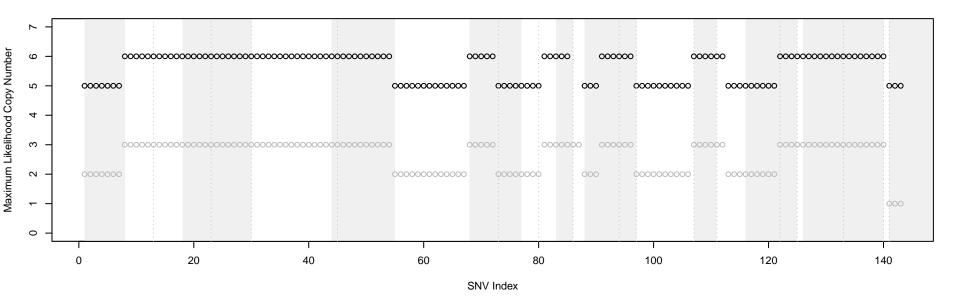


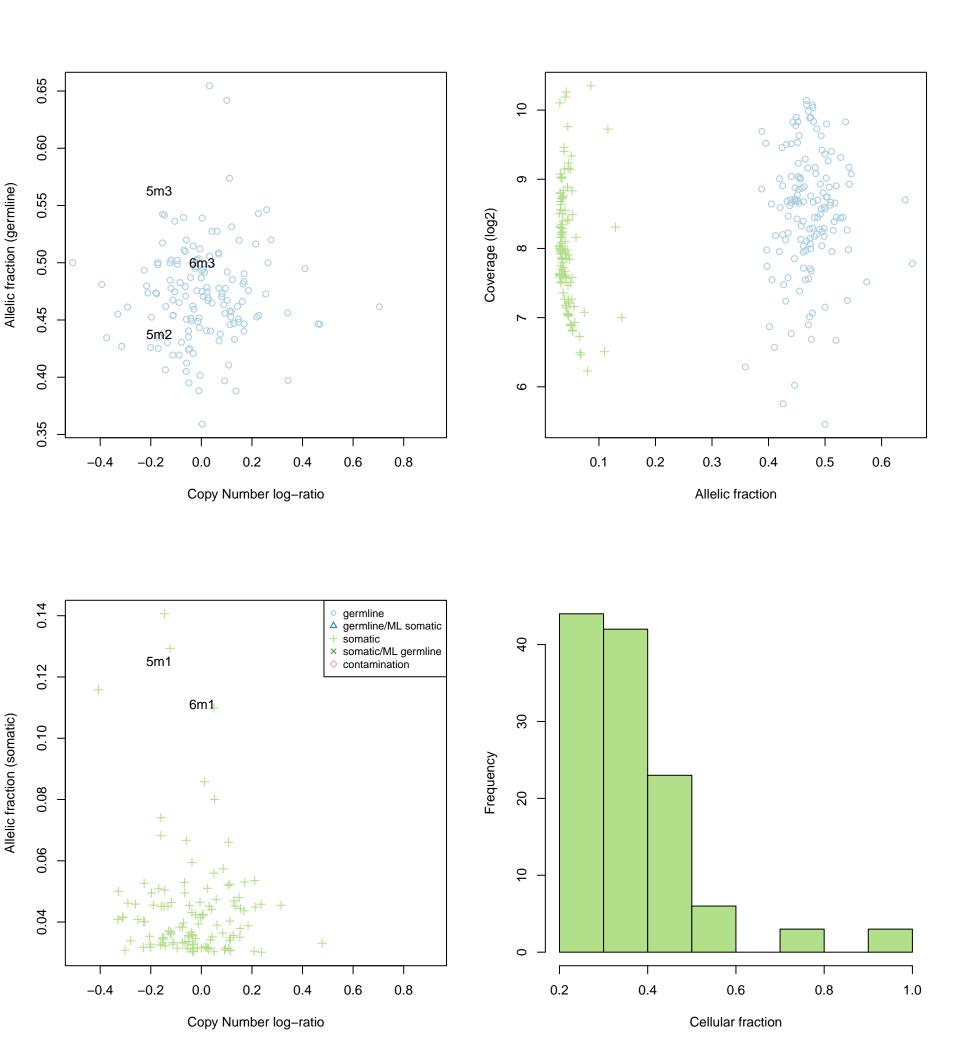
Purity: 0.4 Tumor ploidy: 5.98 6 3 7 0.3 Fraction Genome 0.2 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



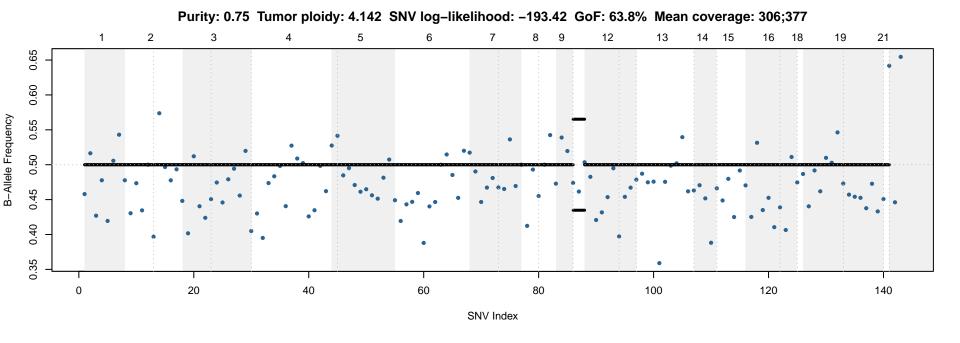
### SCNA-fit log-likelihood: -5251.31



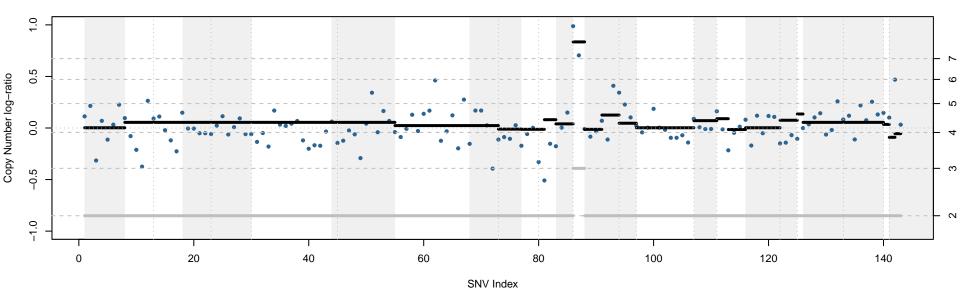


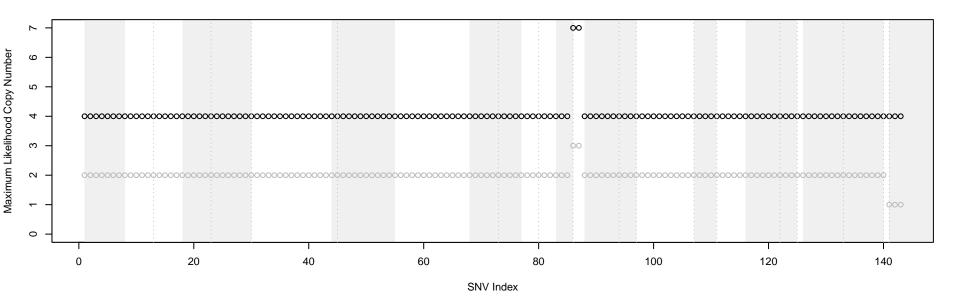


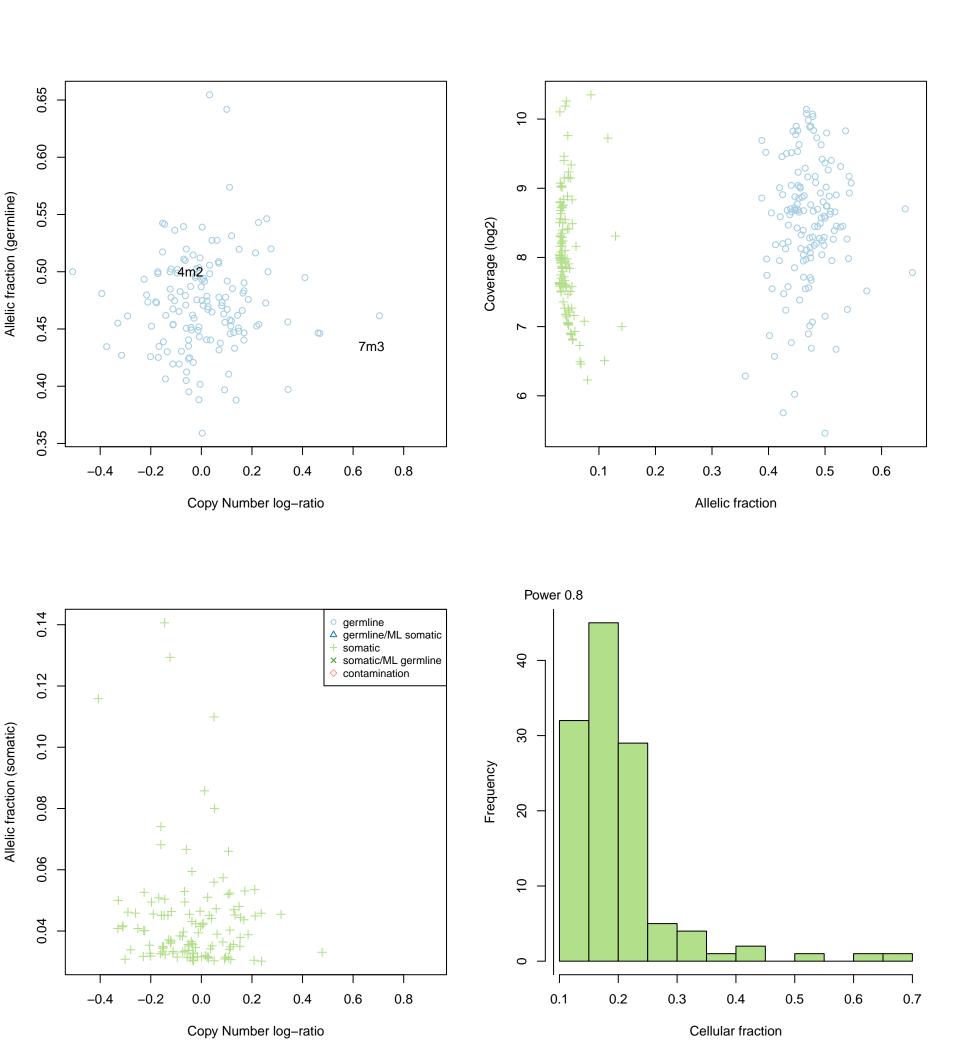
Purity: 0.75 Tumor ploidy: 4.142 2 3 6 0.3 Fraction Genome 0.2 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



### SCNA-fit log-likelihood: -5061.17







Purity: 0.59 Tumor ploidy: 2.115 5 6 0.3 Fraction Genome 0.2 0.1 0.0

0.0

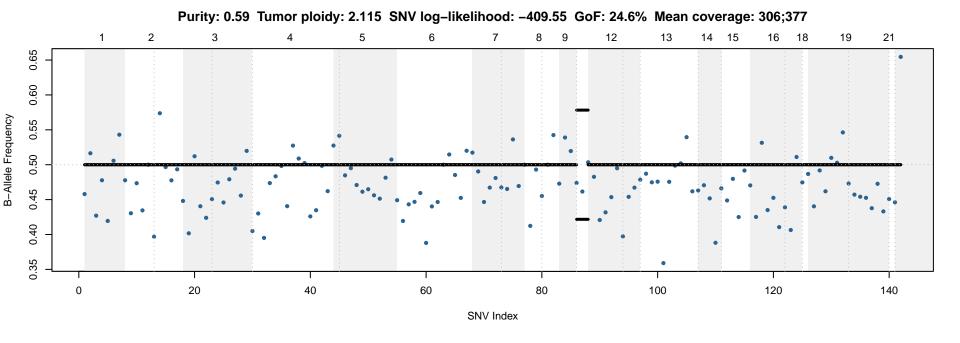
log2 ratio

0.5

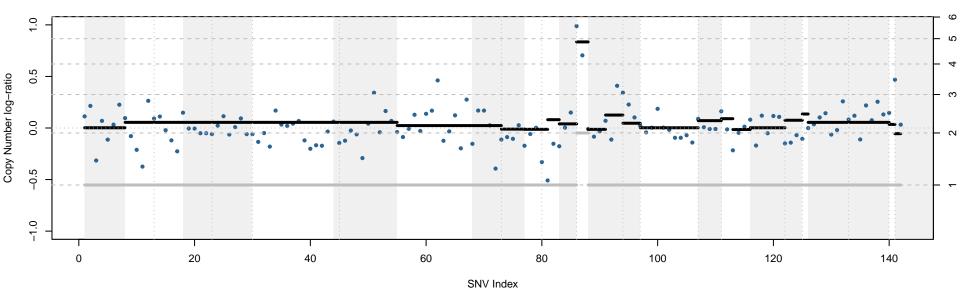
1.0

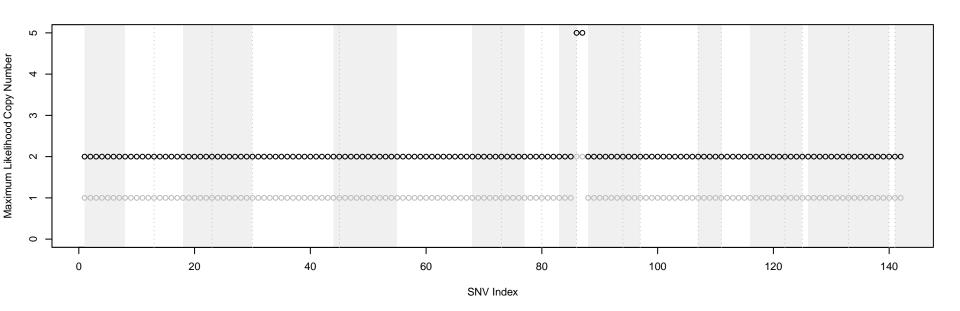
-1.0

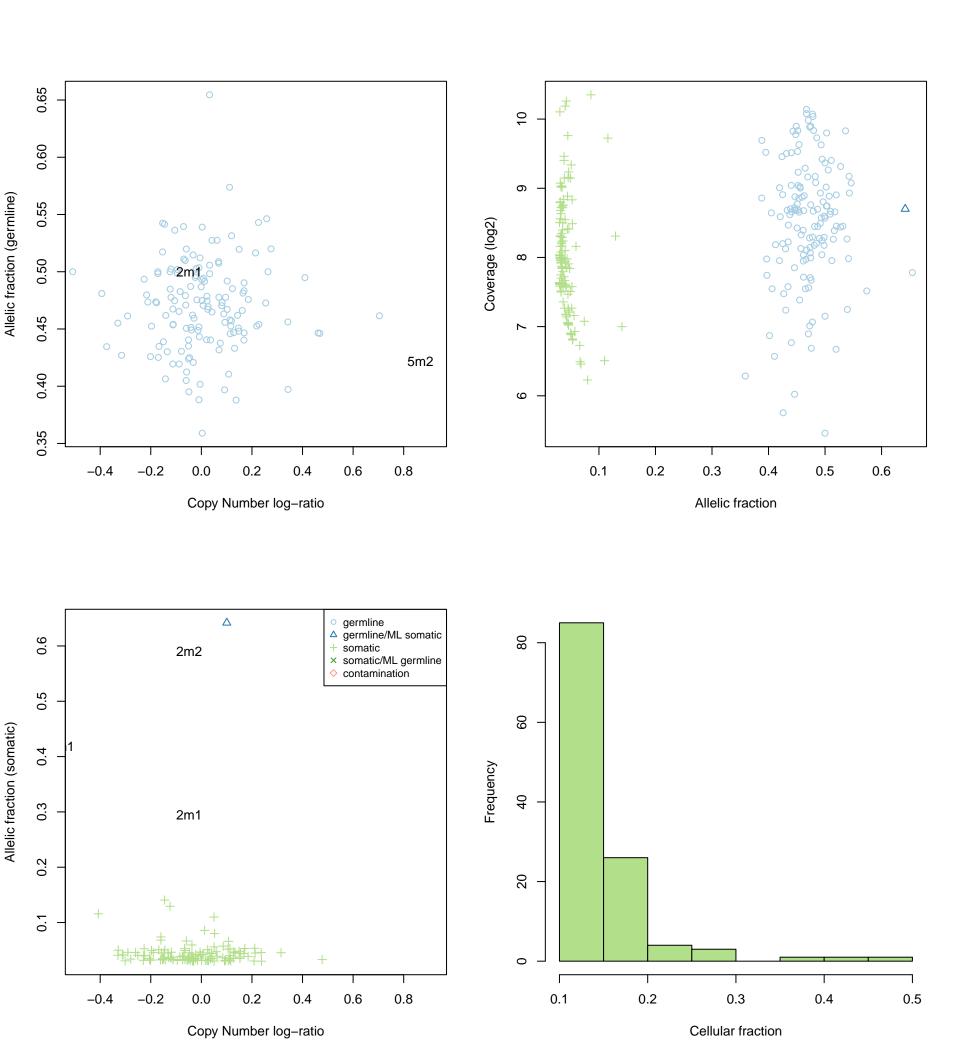
-0.5



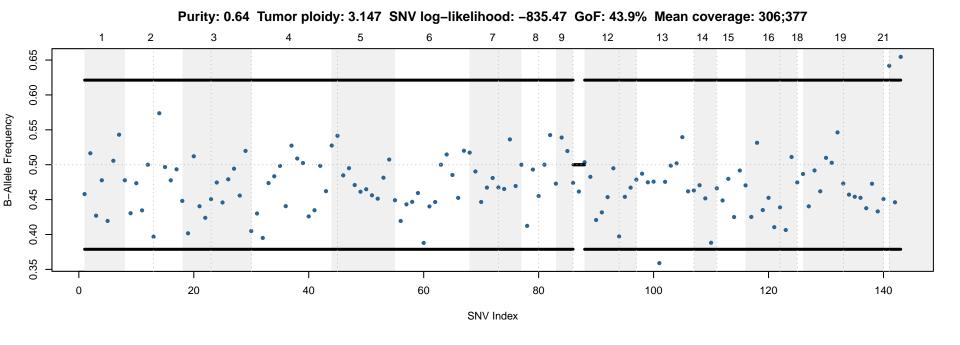
# SCNA-fit log-likelihood: -5077.53



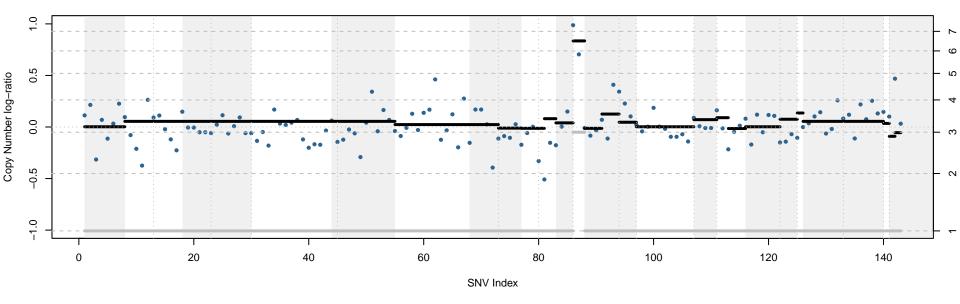


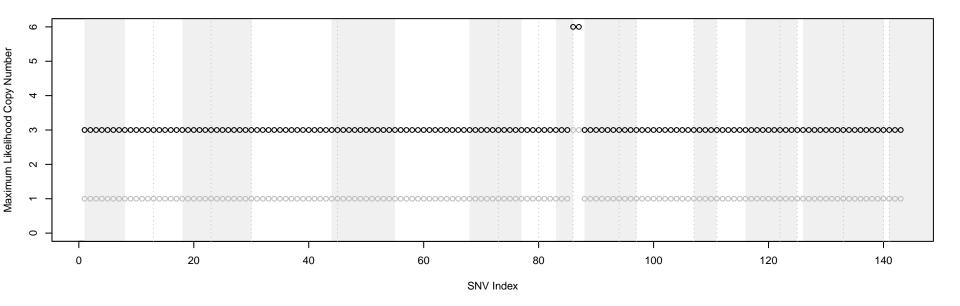


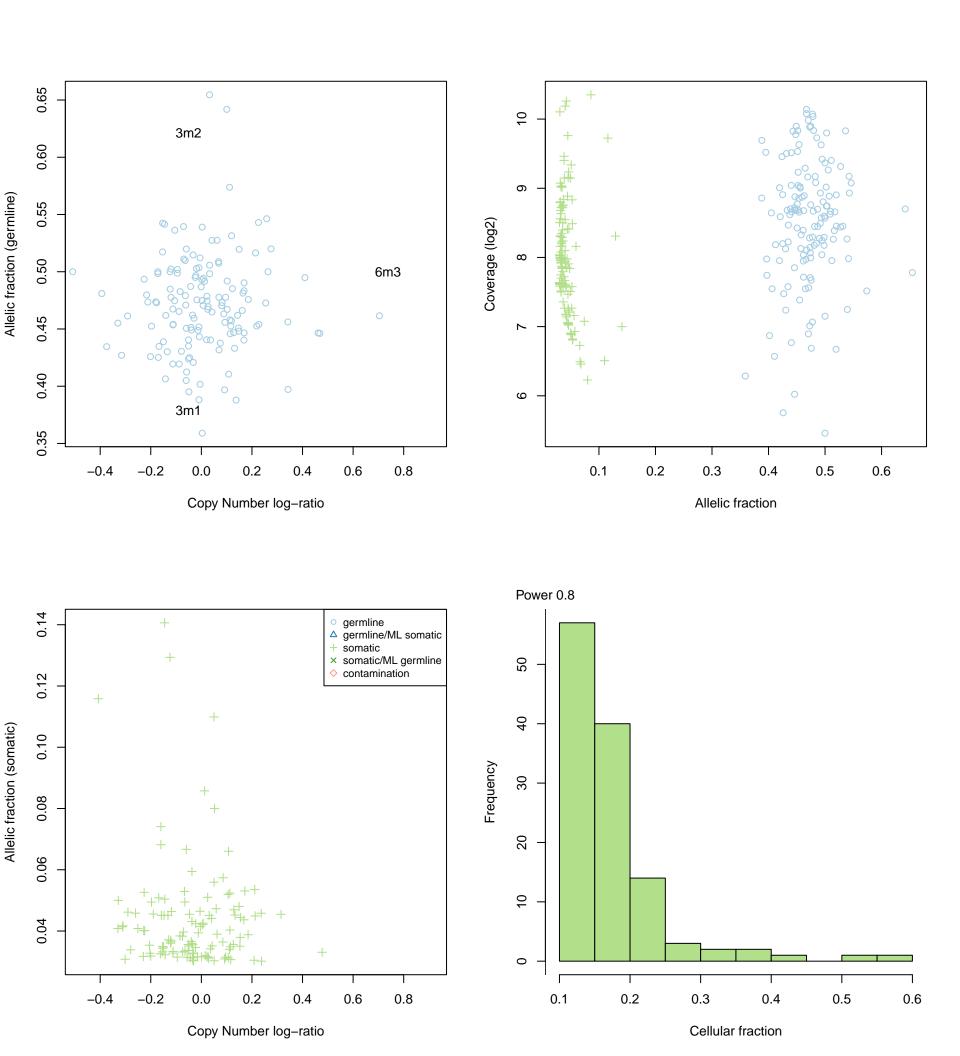
Purity: 0.64 Tumor ploidy: 3.147 2 6 7 1 0.3 Fraction Genome 0.2 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



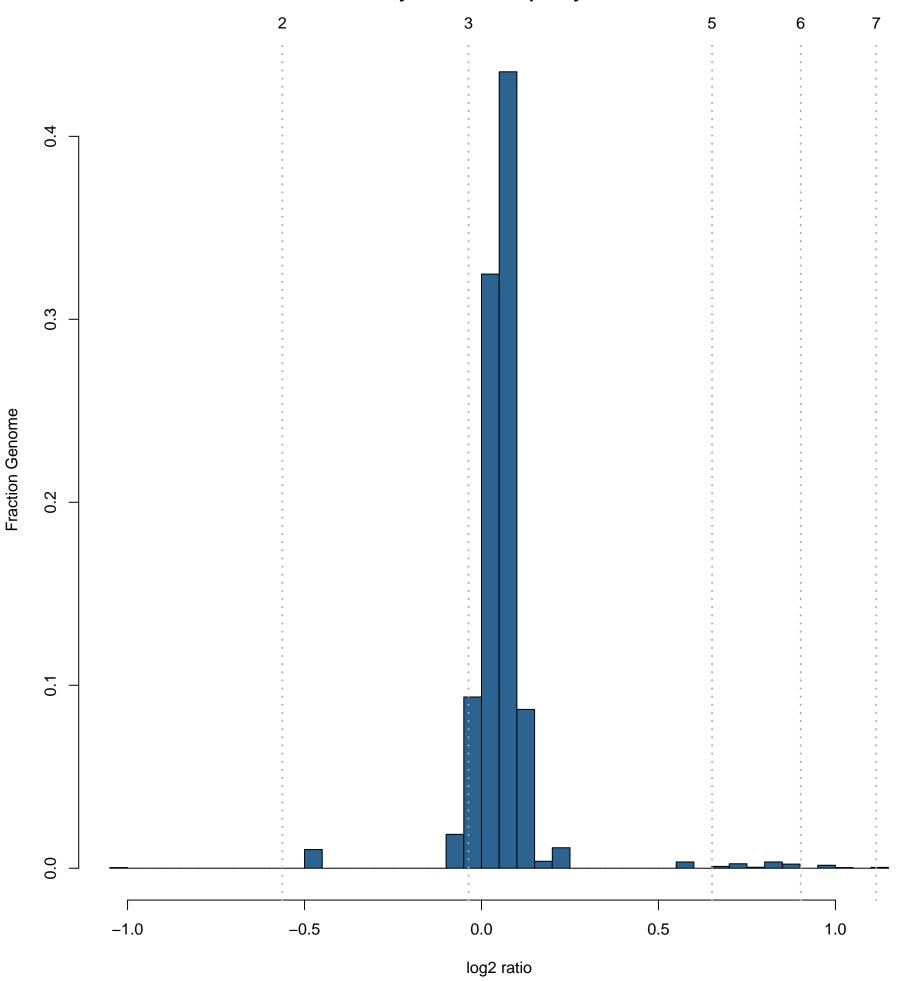
## SCNA-fit log-likelihood: -5065.96

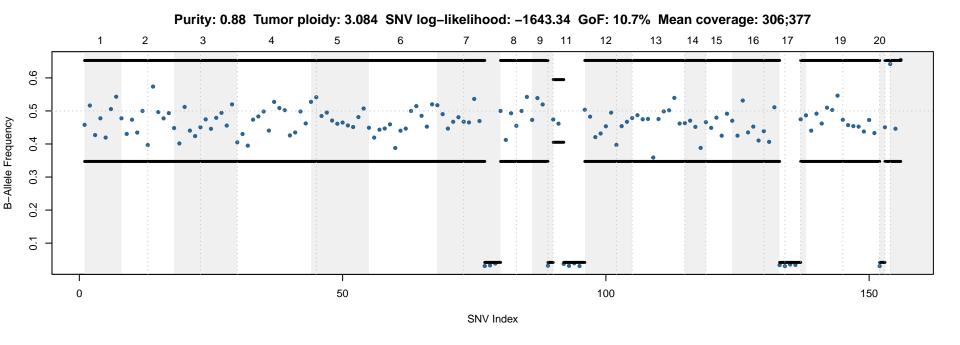






Purity: 0.88 Tumor ploidy: 3.084





## SCNA-fit log-likelihood: -5044.5

