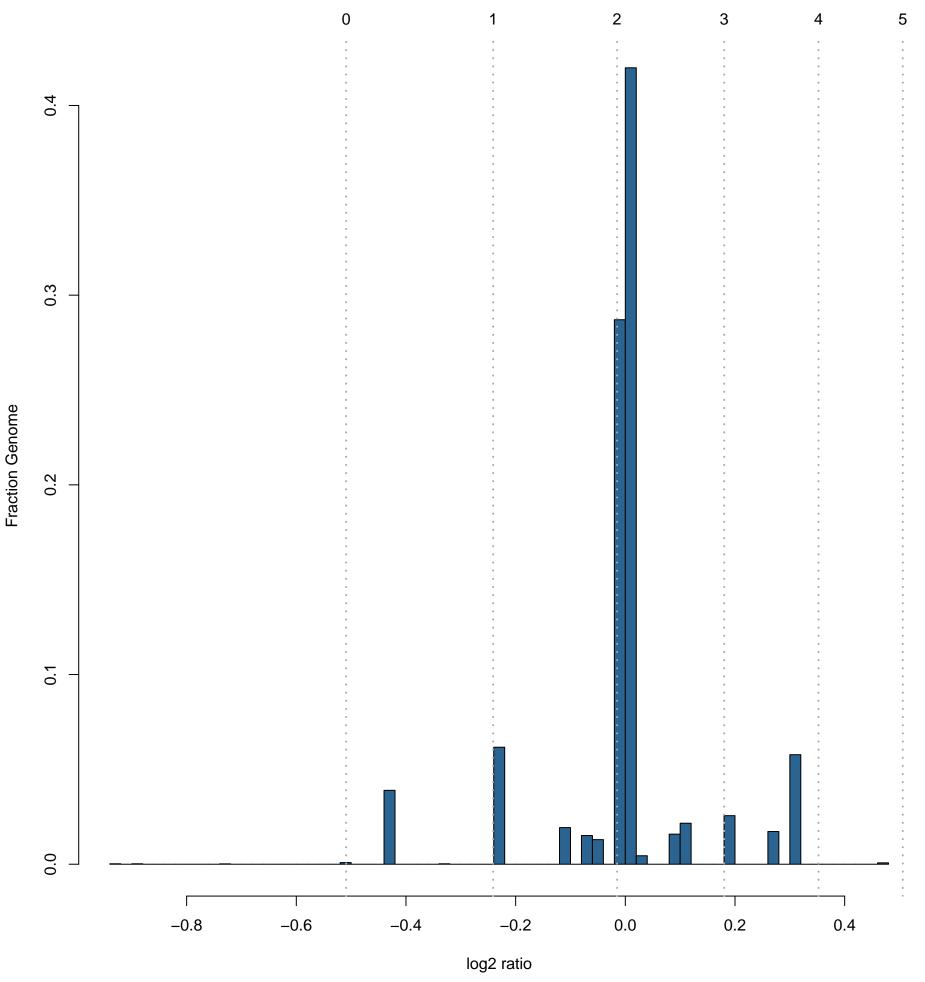
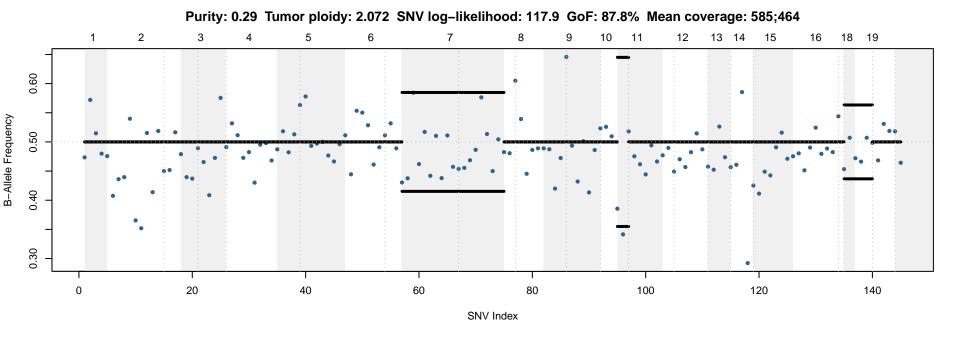
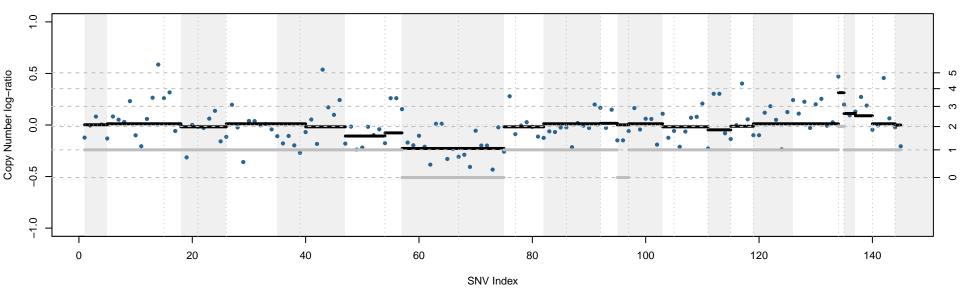
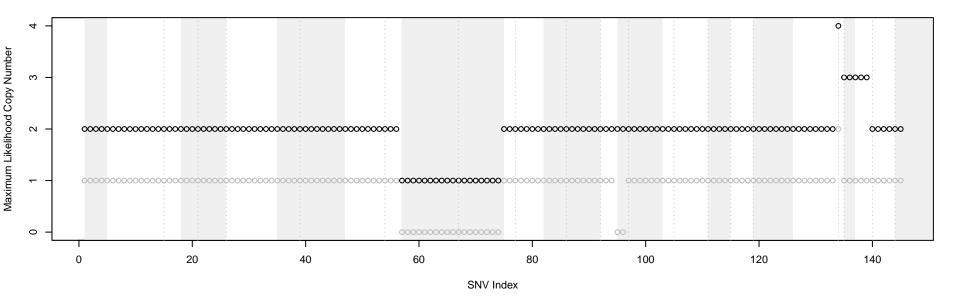
Purity: 0.29 Tumor ploidy: 2.072

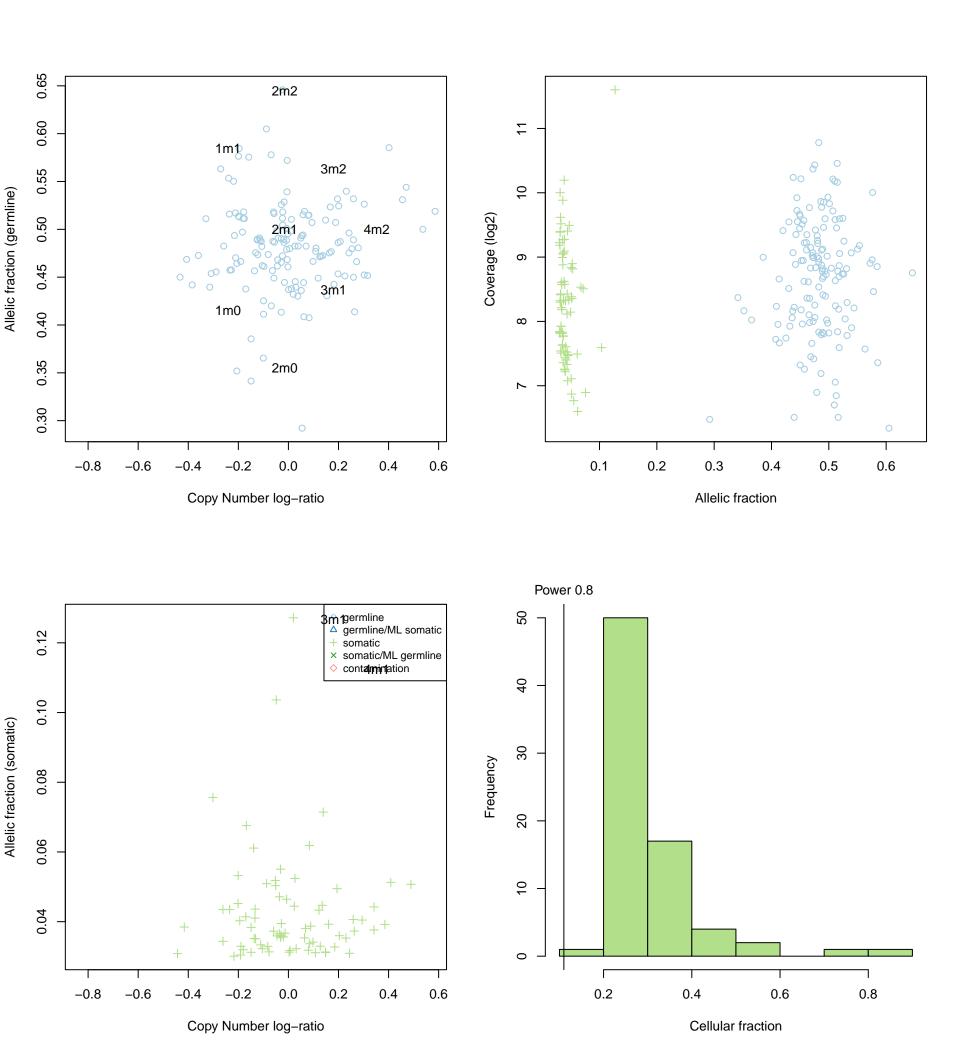




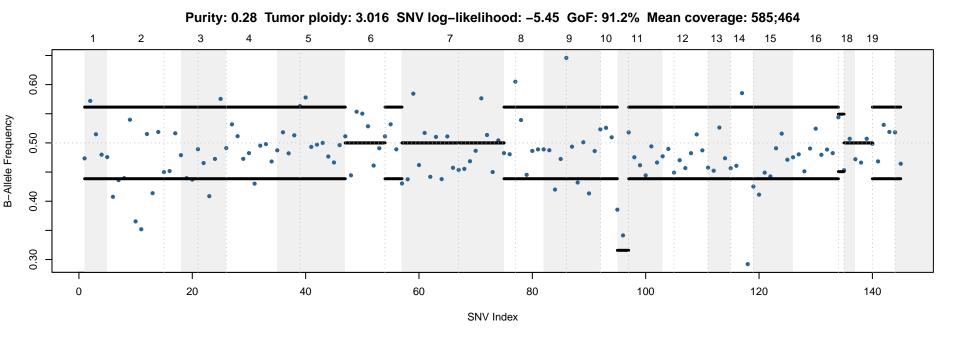
## SCNA-fit log-likelihood: -5786.71



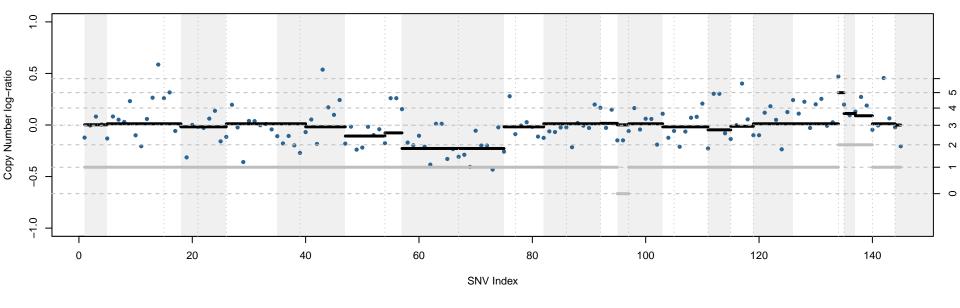


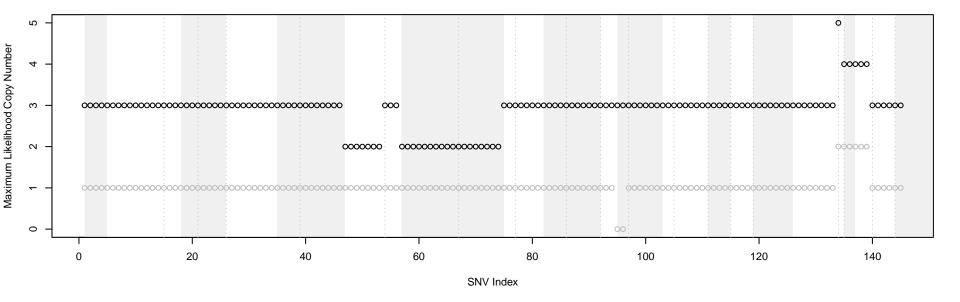


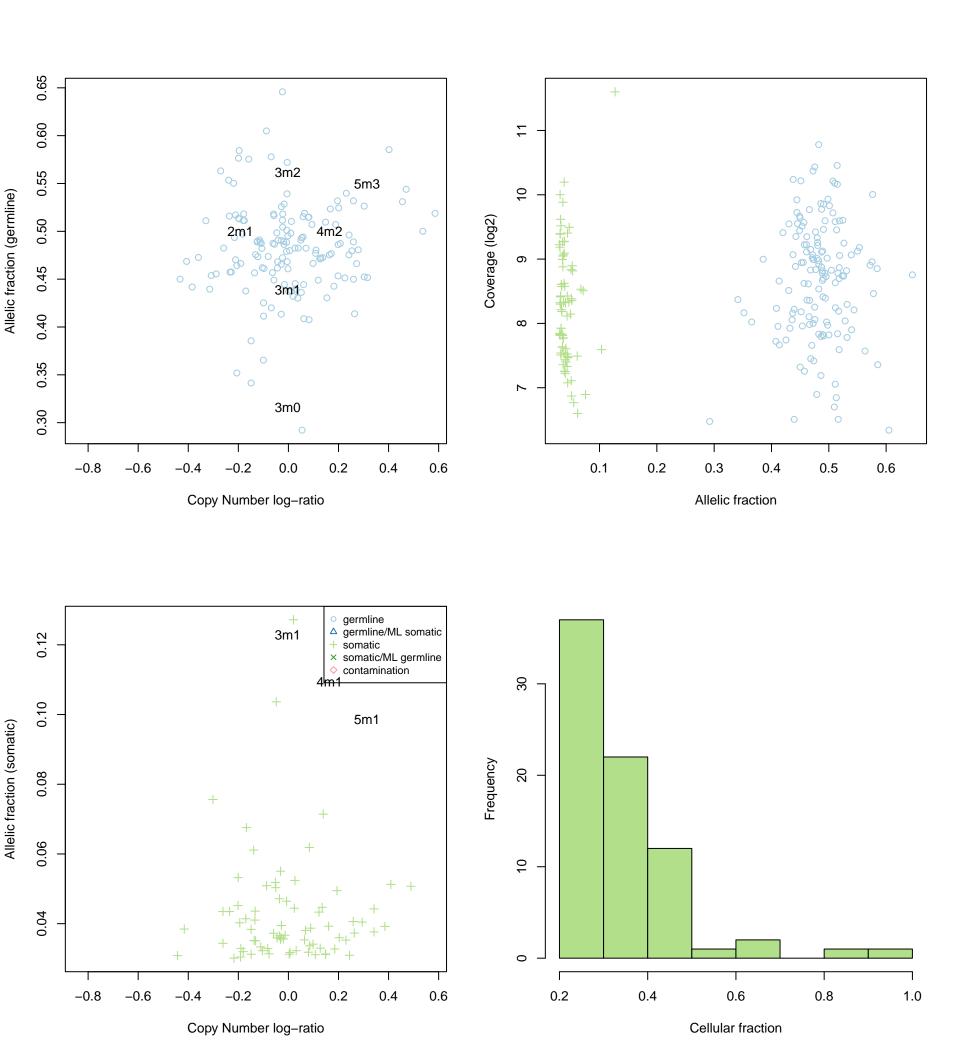
Purity: 0.28 Tumor ploidy: 3.016 2 6 0 5 0.3 Fraction Genome 0.2 0.1 0.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 0.4 log2 ratio

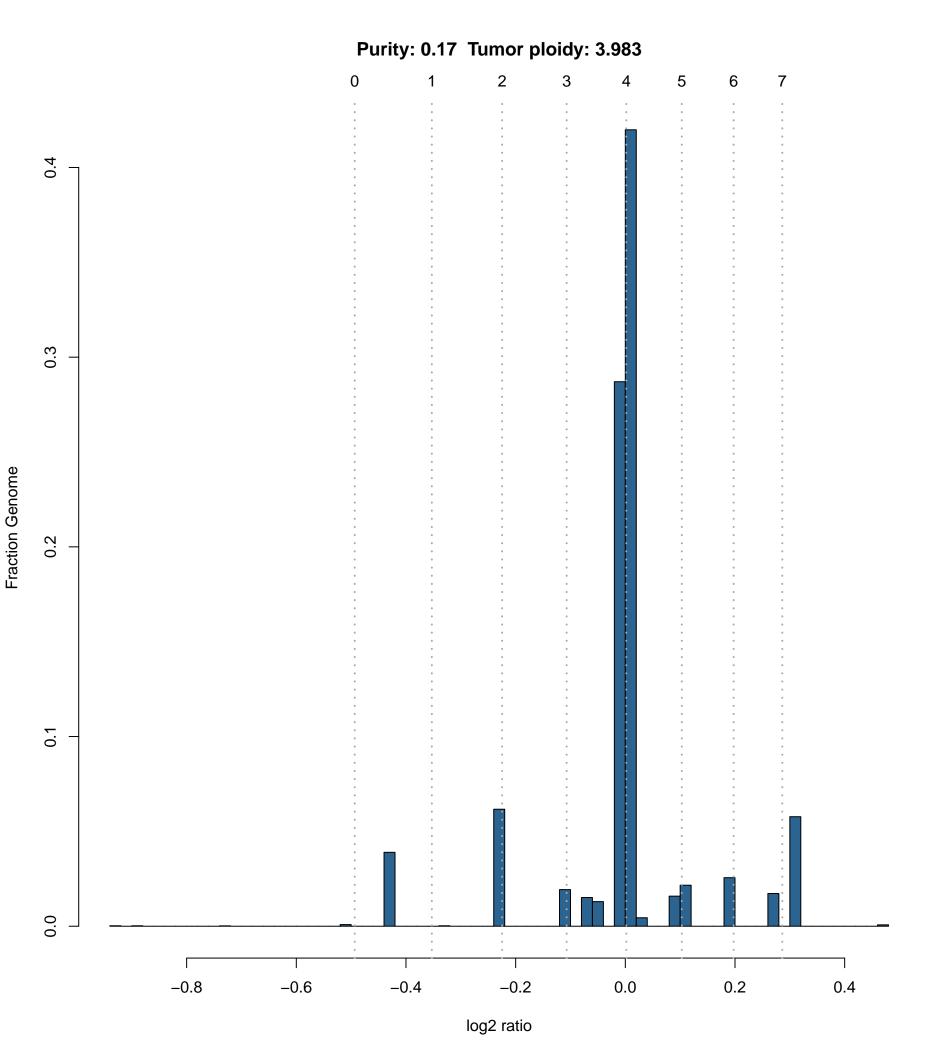


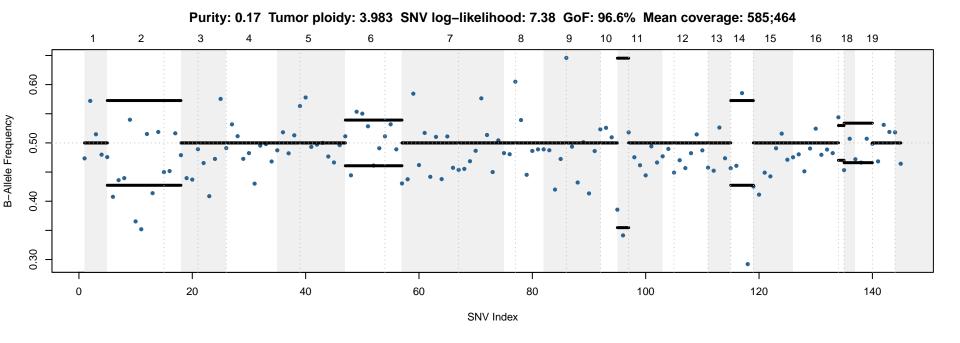
## SCNA-fit log-likelihood: -5610.11



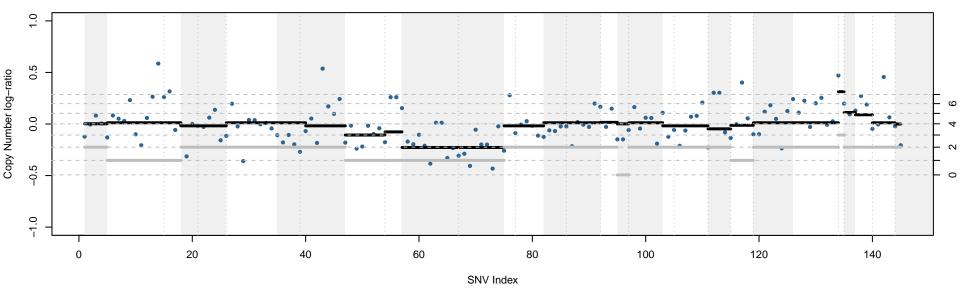


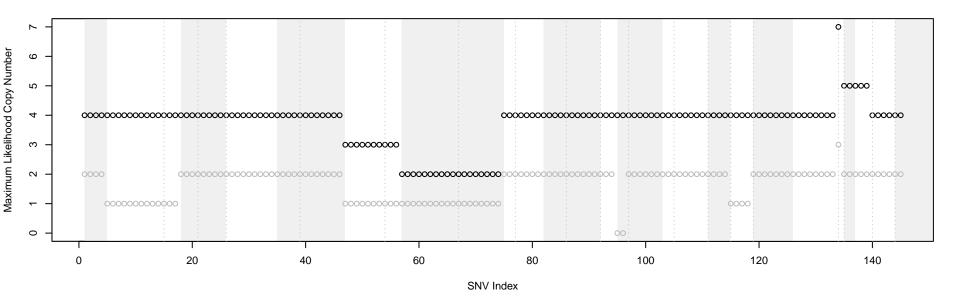


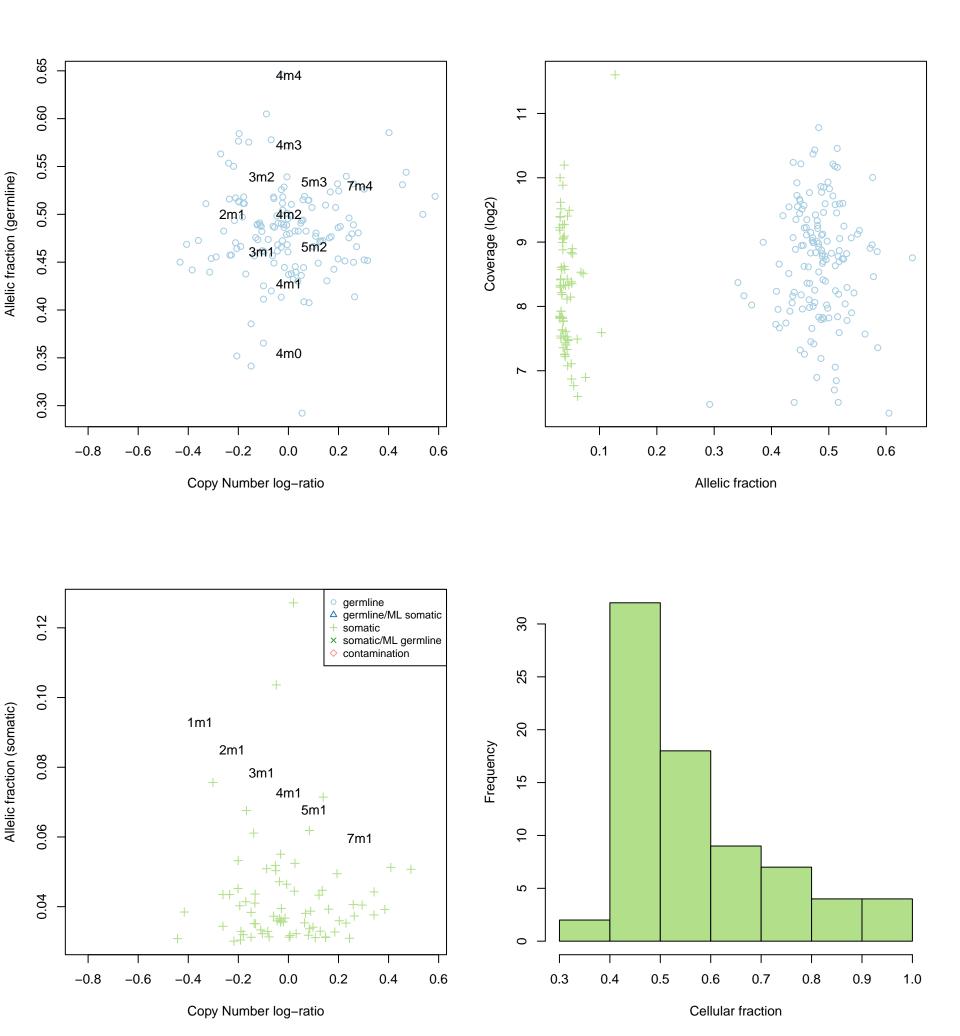




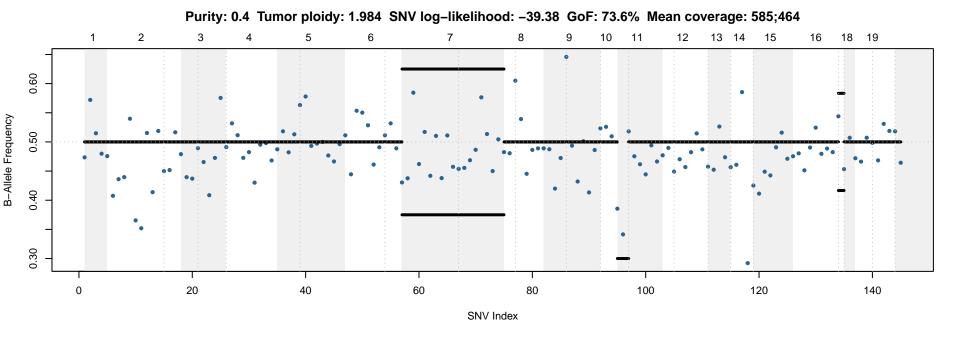
### SCNA-fit log-likelihood: -5613.59



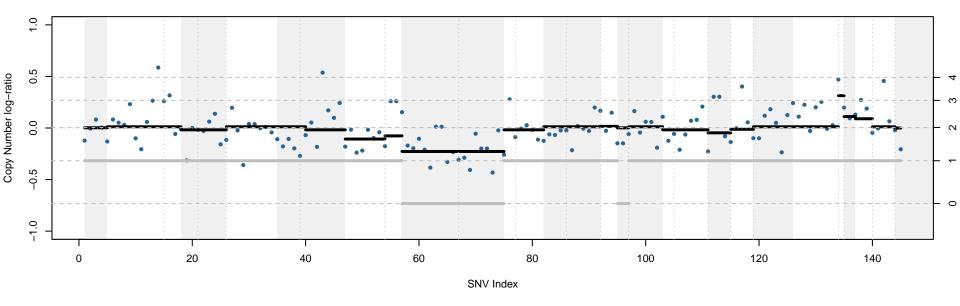


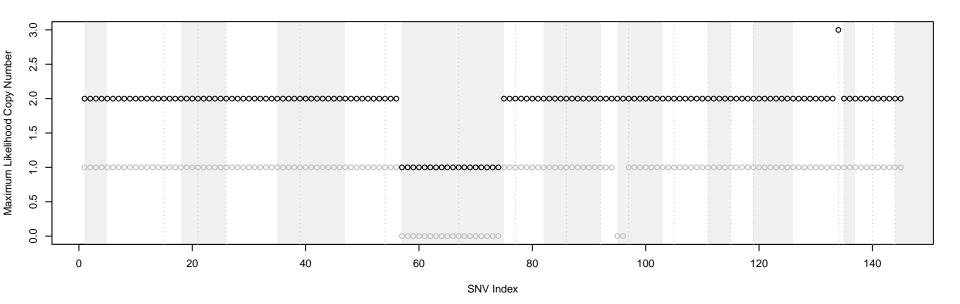


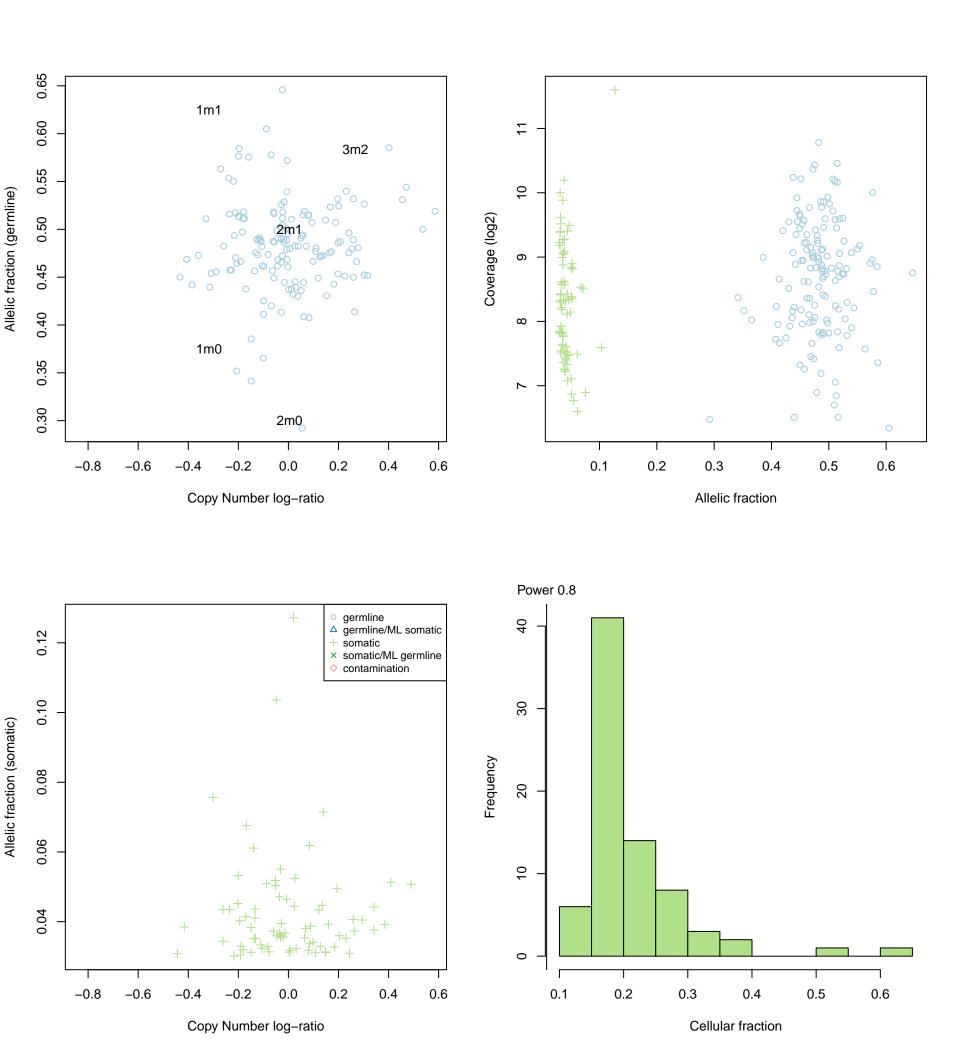
Purity: 0.4 Tumor ploidy: 1.984 0 3 0.3 Fraction Genome 0.2 0.1 0.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 0.4 log2 ratio



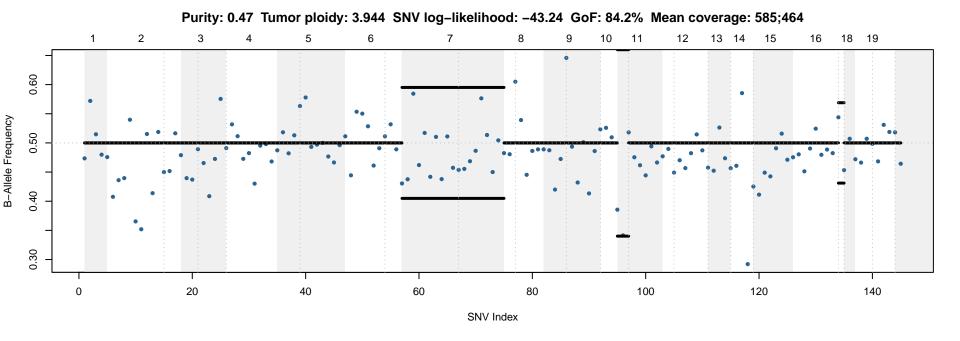
# SCNA-fit log-likelihood: -5760.17



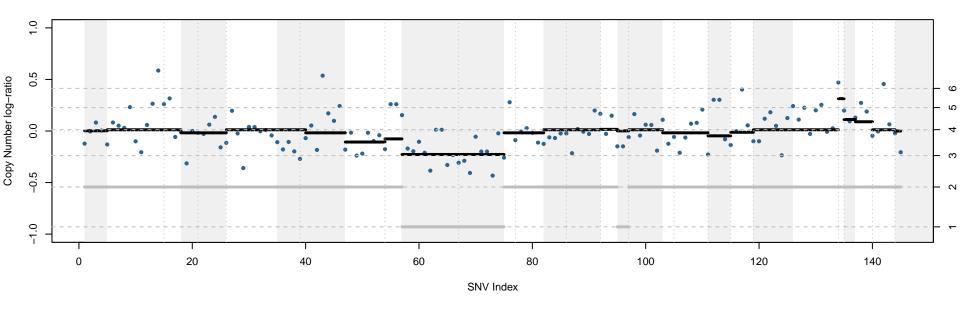


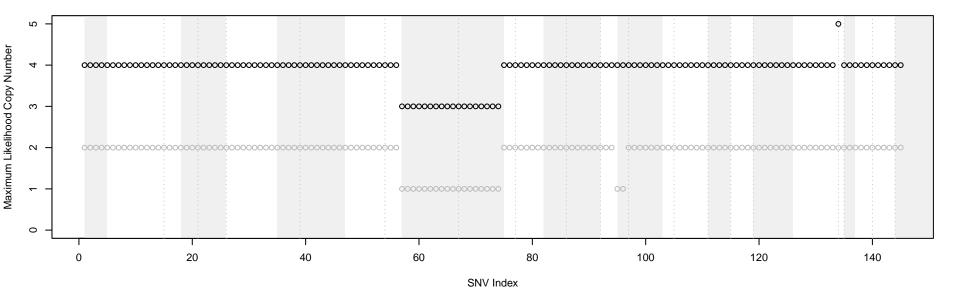


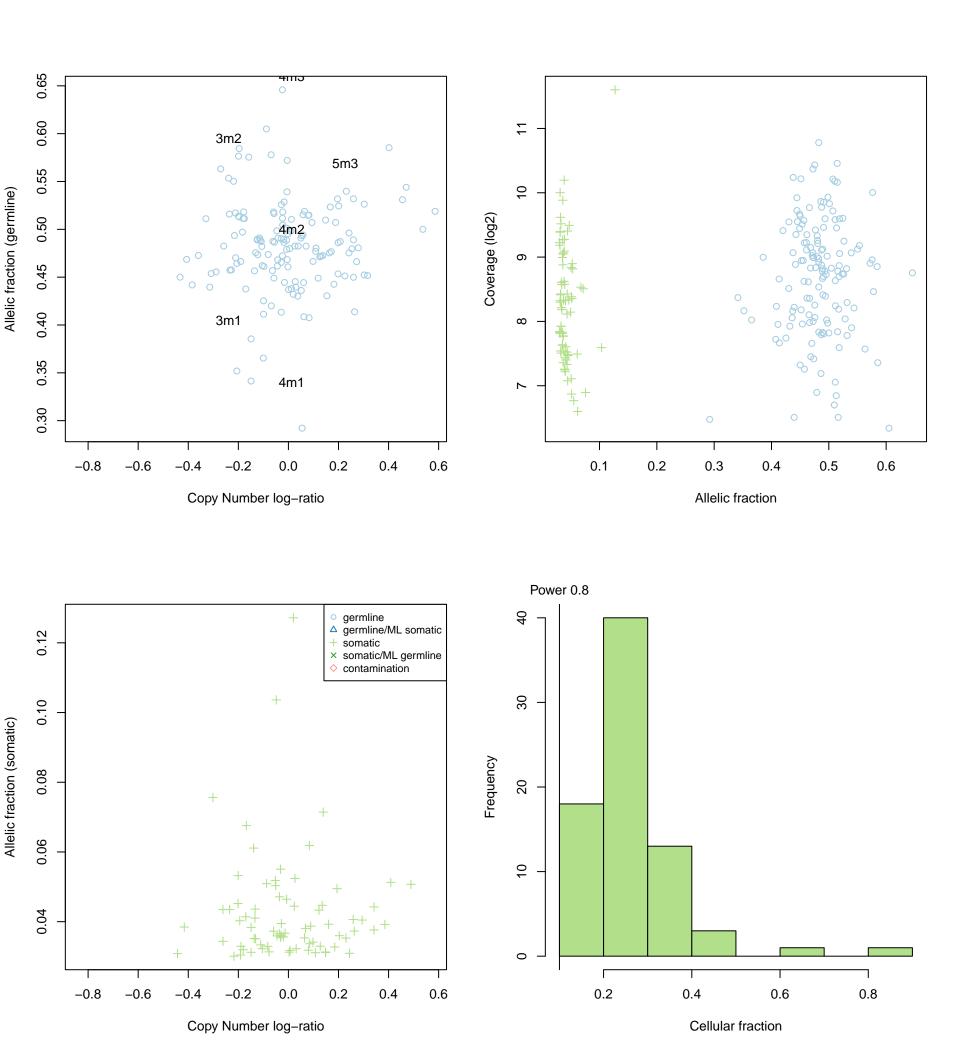
Purity: 0.47 Tumor ploidy: 3.944 0 6 5 0.3 Fraction Genome 0.2 0.1 0.0 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio

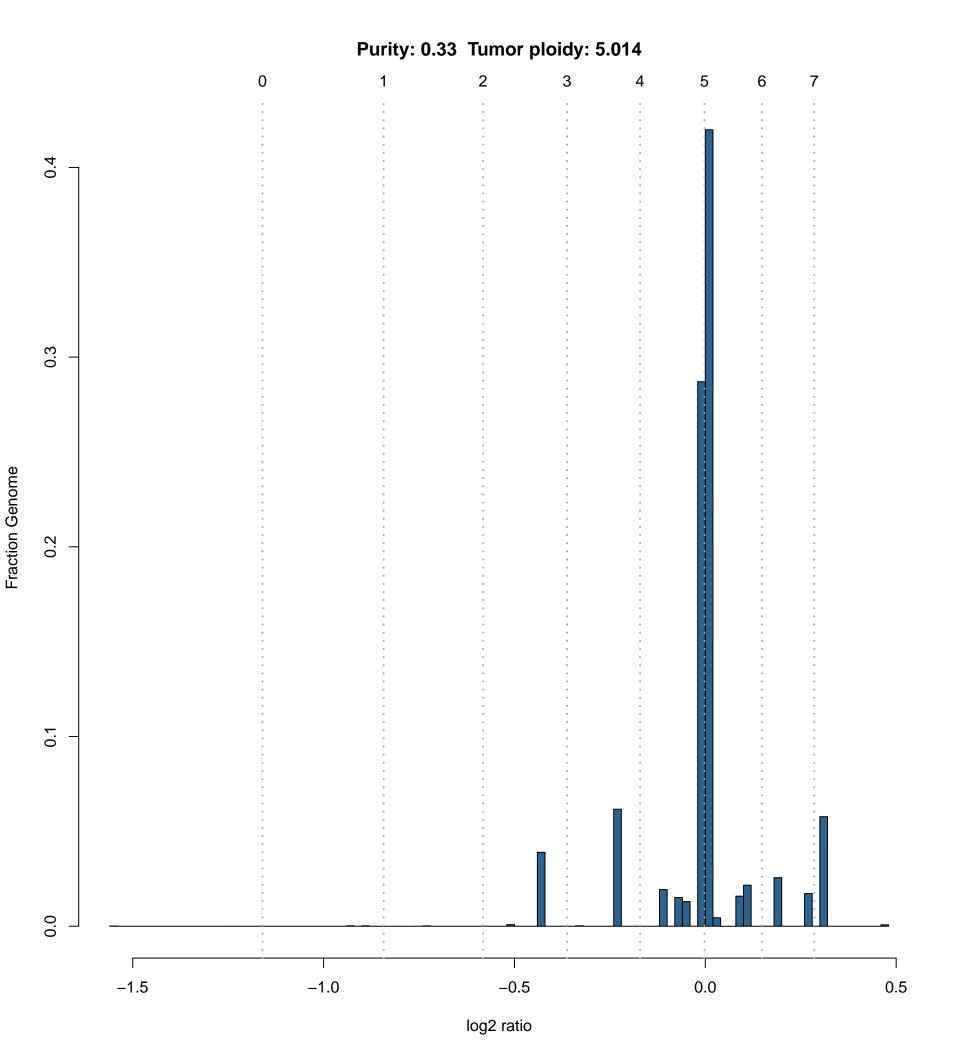


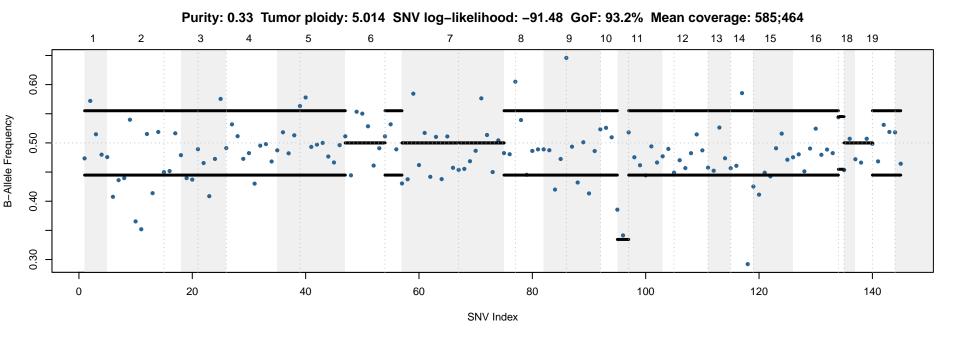
## SCNA-fit log-likelihood: -5736.06



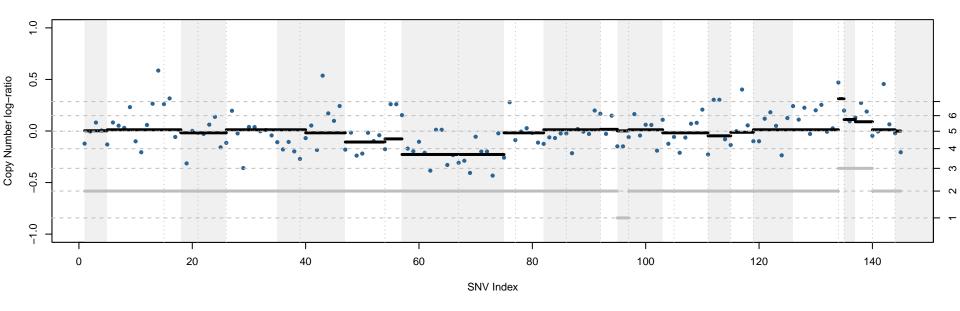


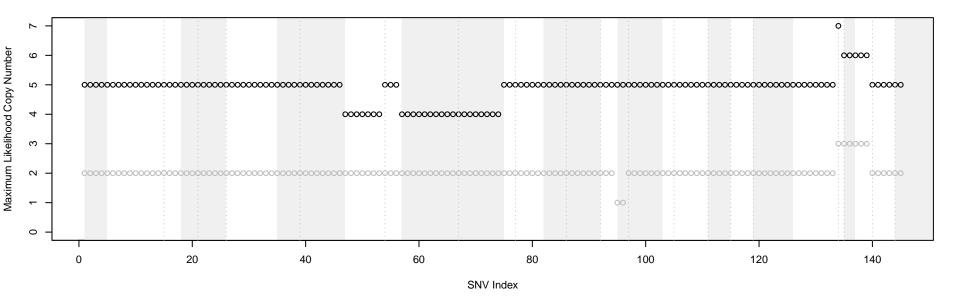


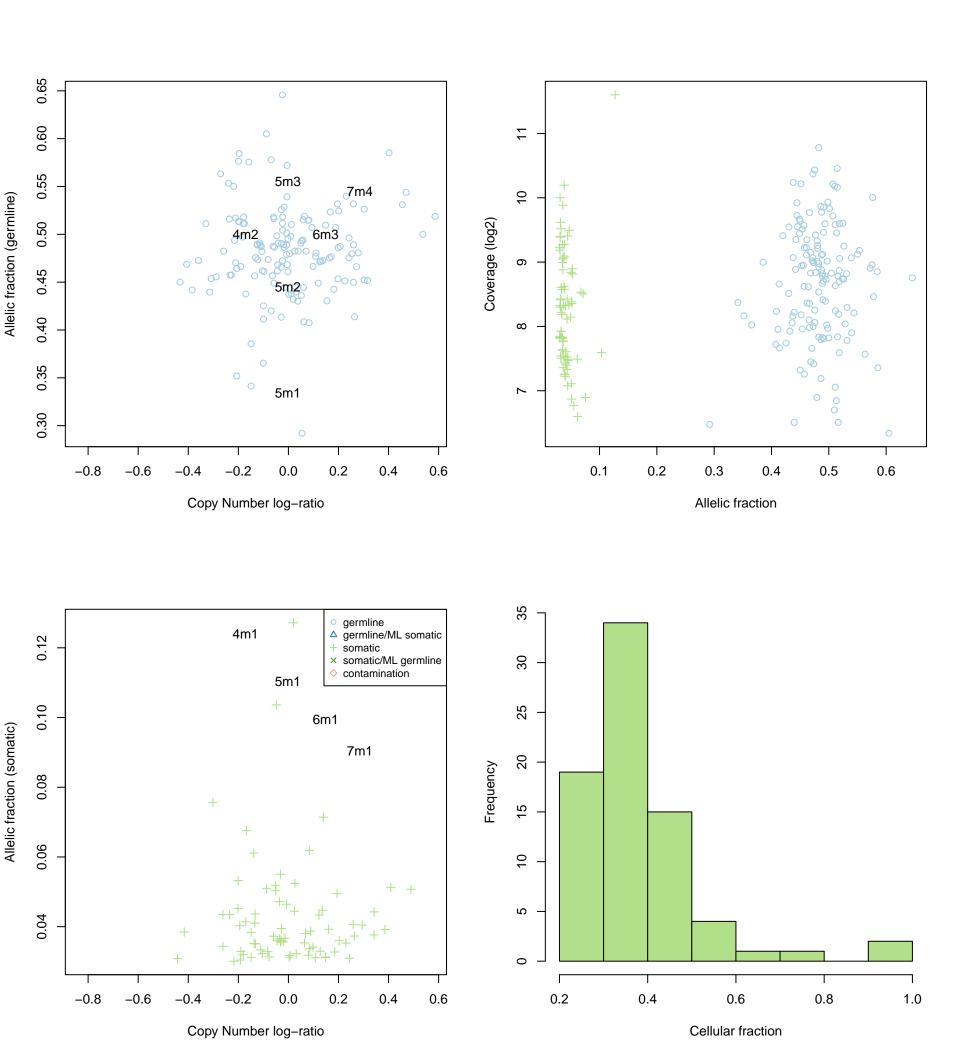




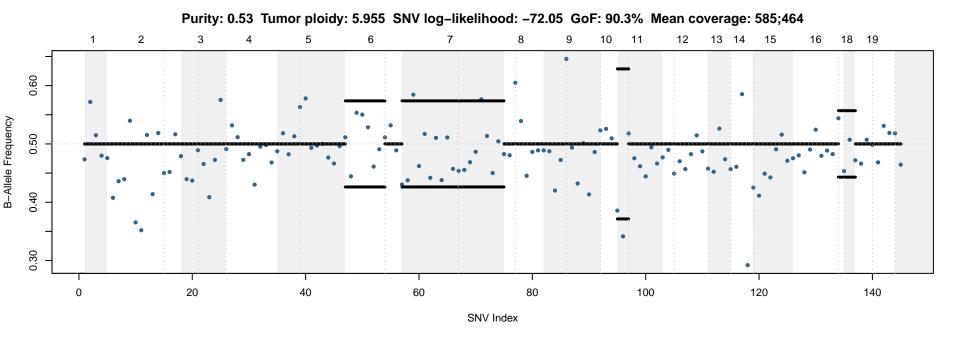
### SCNA-fit log-likelihood: -5627.38



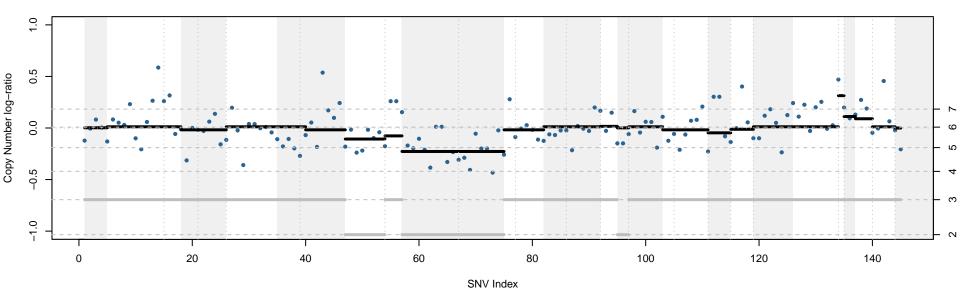


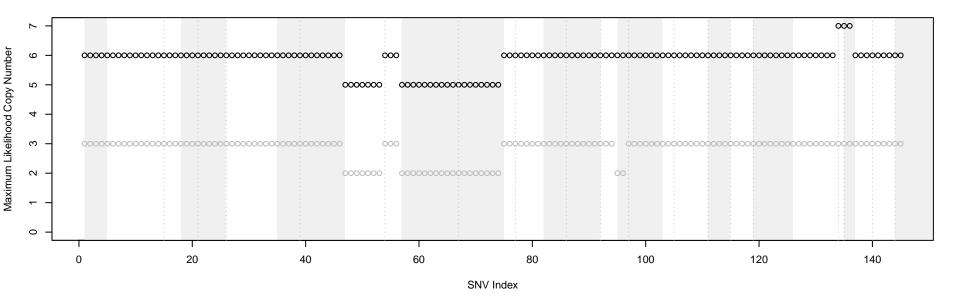


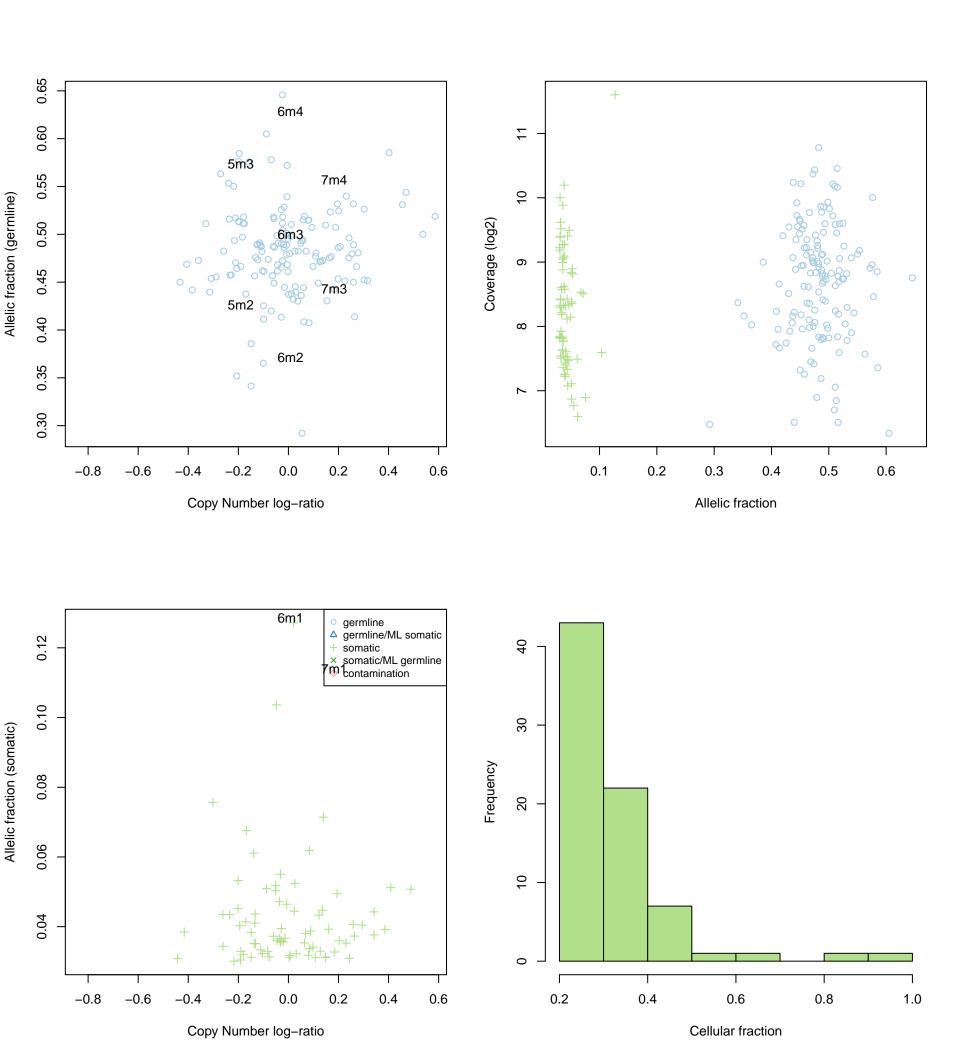
Purity: 0.53 Tumor ploidy: 5.955 2 3 6 7 0.3 Fraction Genome 0.2 0.1 0.0 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio



### SCNA-fit log-likelihood: -5745.1







Purity: 0.5 Tumor ploidy: 2.984 5 0 3 2 0.3 Fraction Genome 0.2 0.1 0.0

-0.5

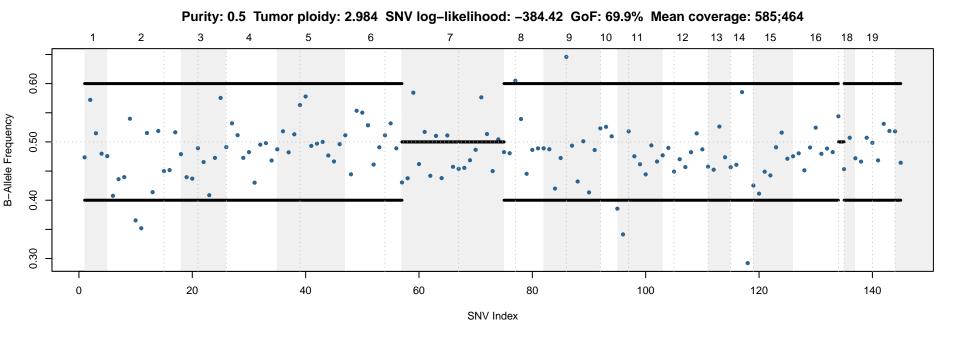
log2 ratio

0.0

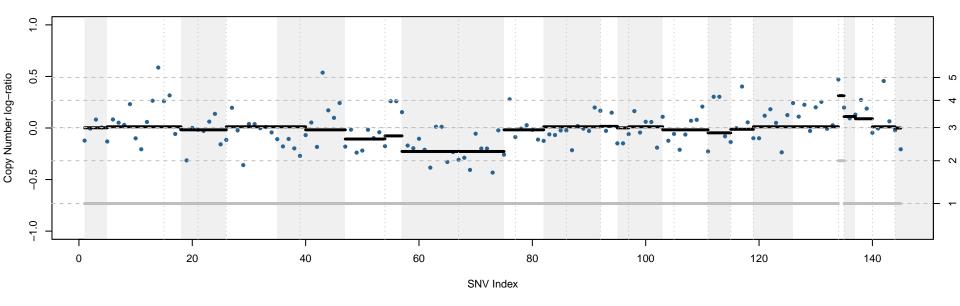
0.5

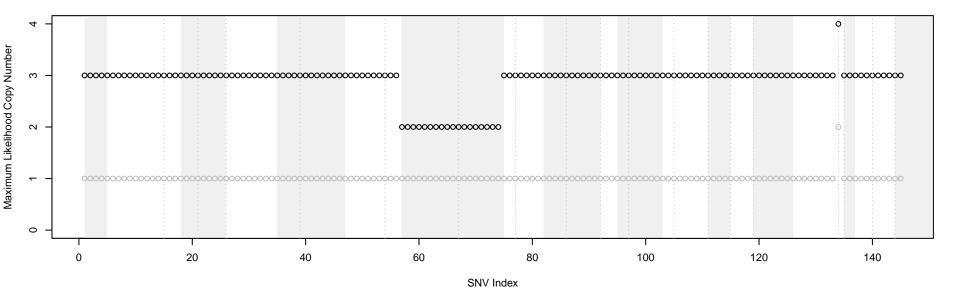
-1.5

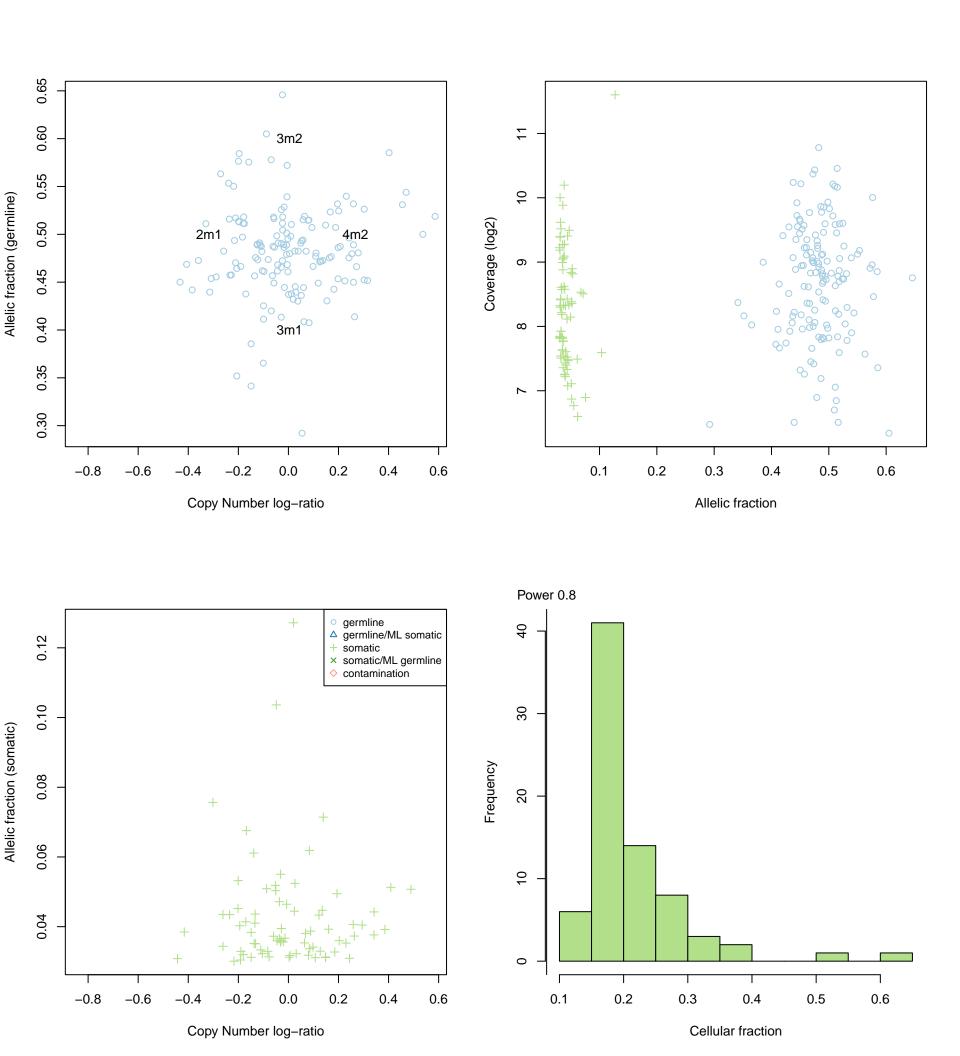
-1.0



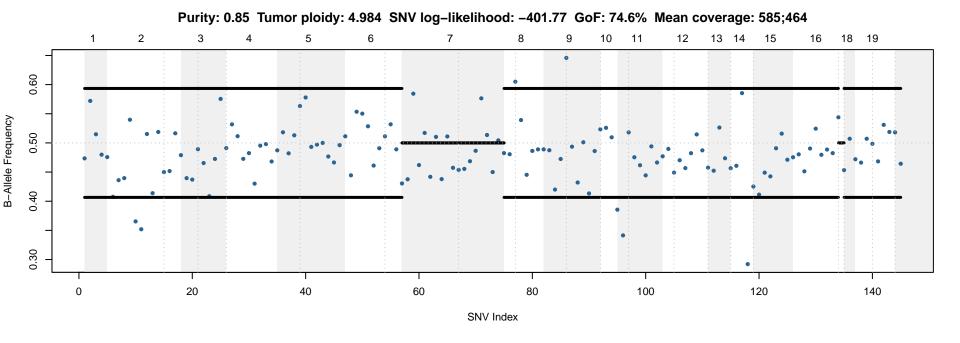
## SCNA-fit log-likelihood: -5758.1



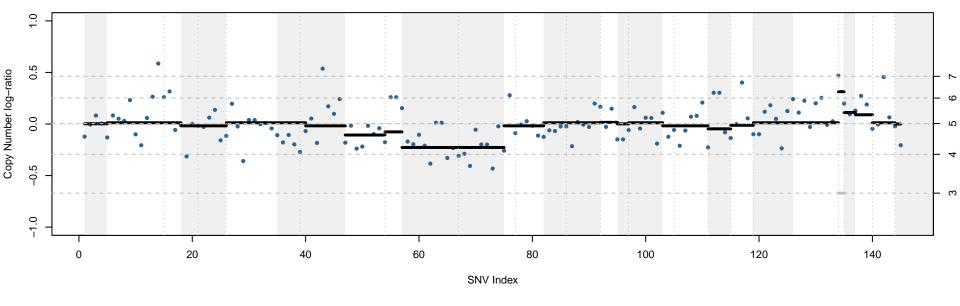


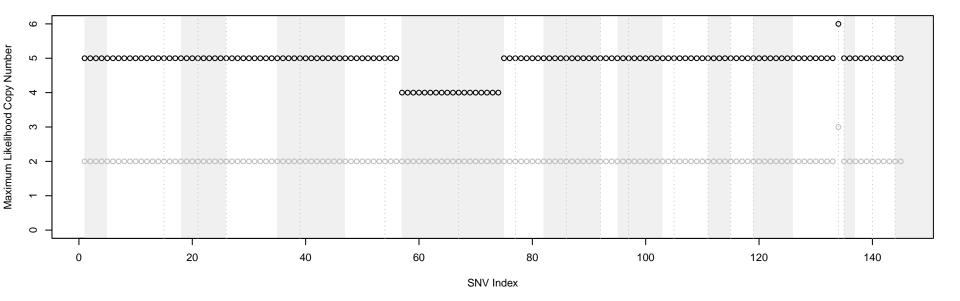


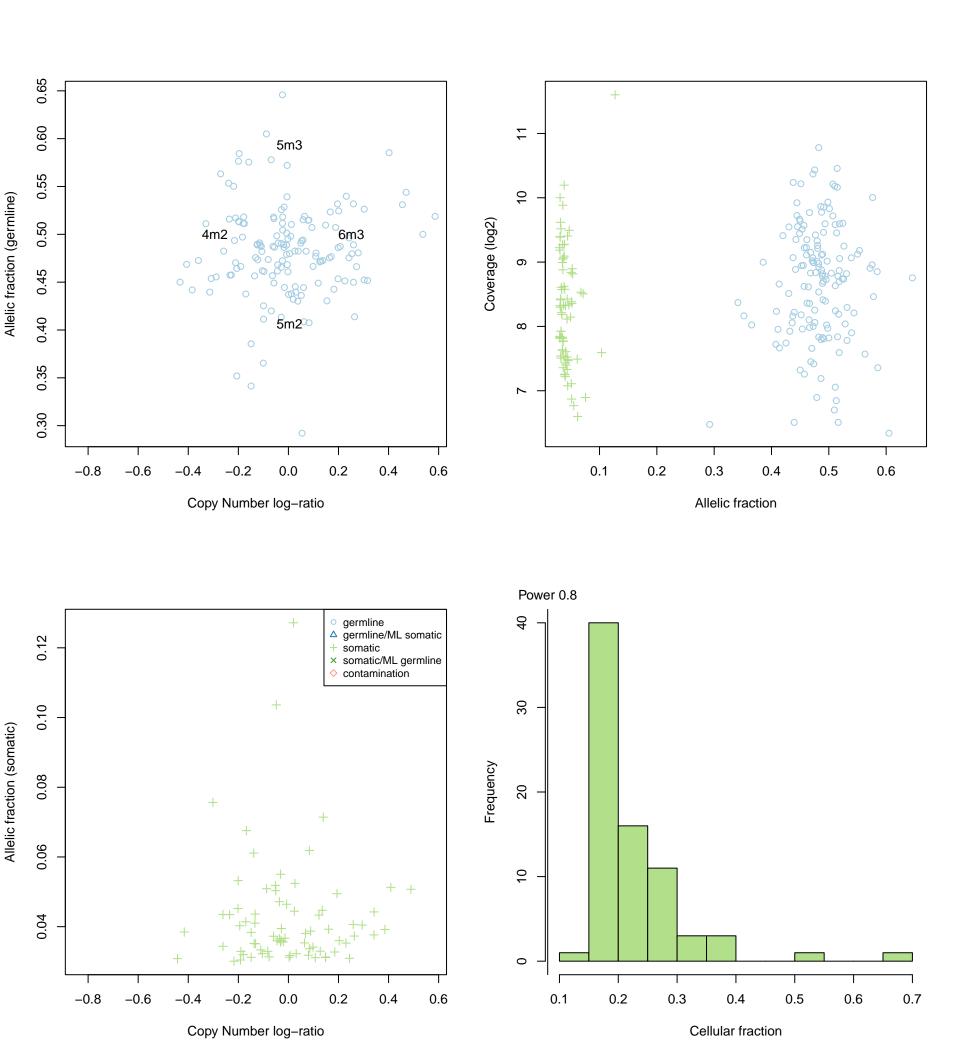
Purity: 0.85 Tumor ploidy: 4.984 2 5 6 7 0.3 Fraction Genome 0.2 0.1 0.0 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio



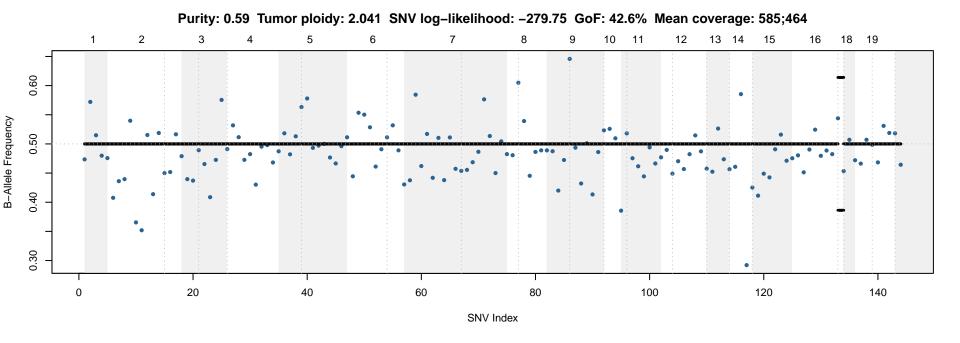
### SCNA-fit log-likelihood: -5764.26



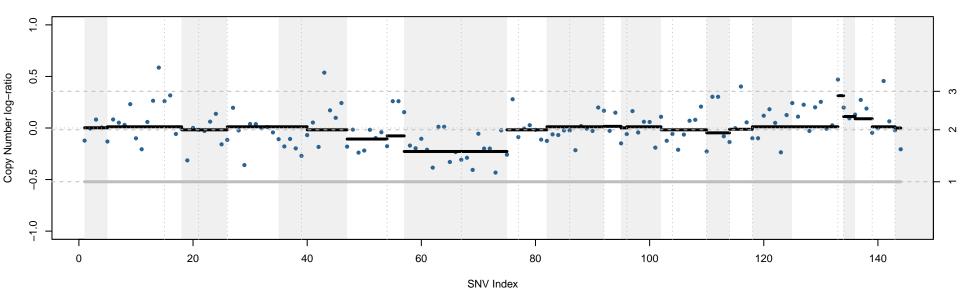


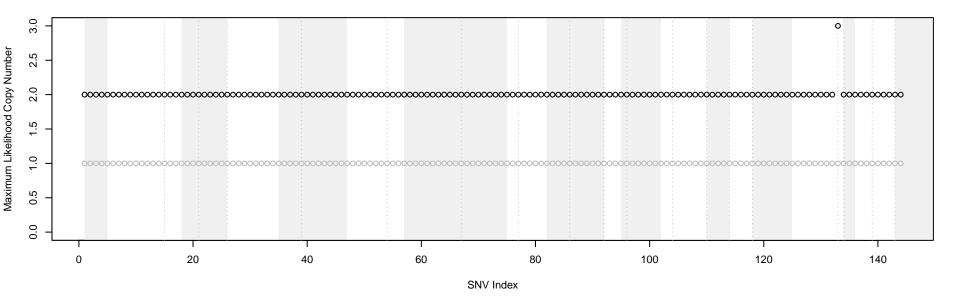


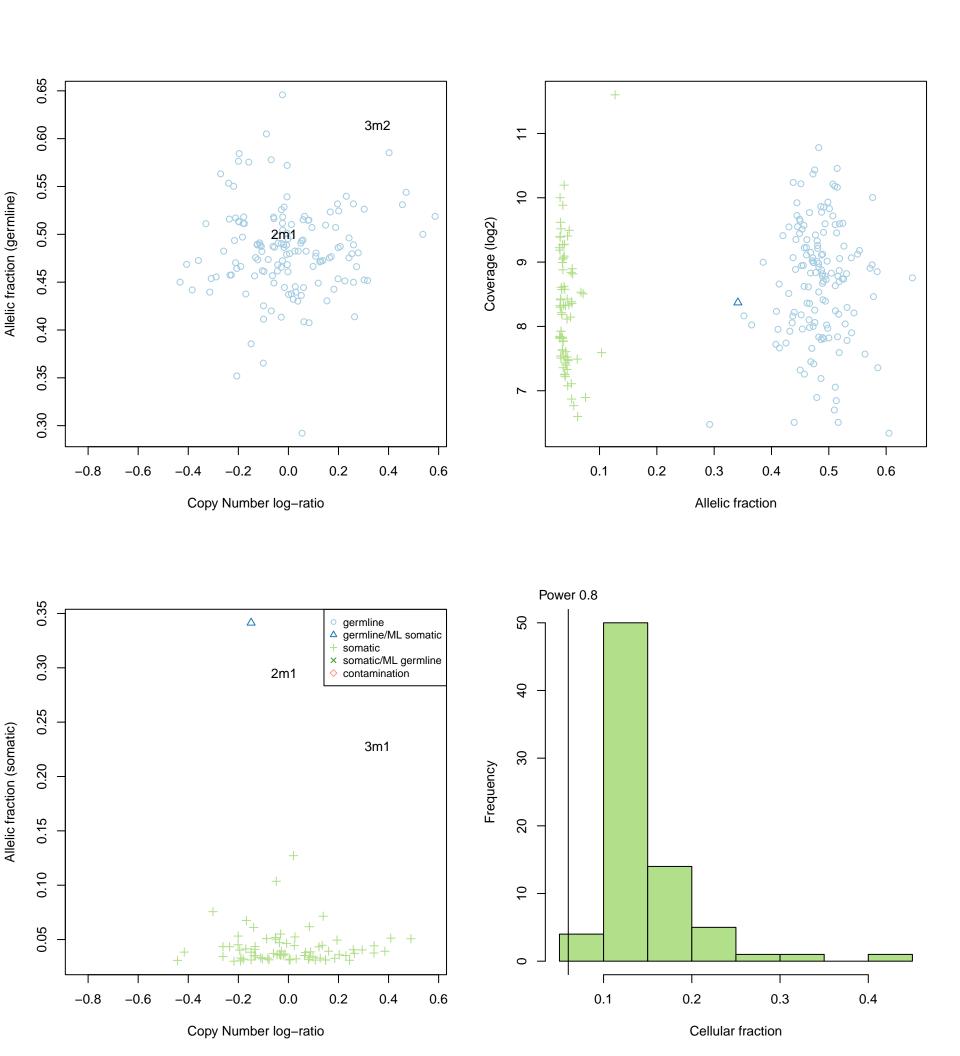
Purity: 0.59 Tumor ploidy: 2.041 0 2 3 0.3 Fraction Genome 0.2 0.1 0.0 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio



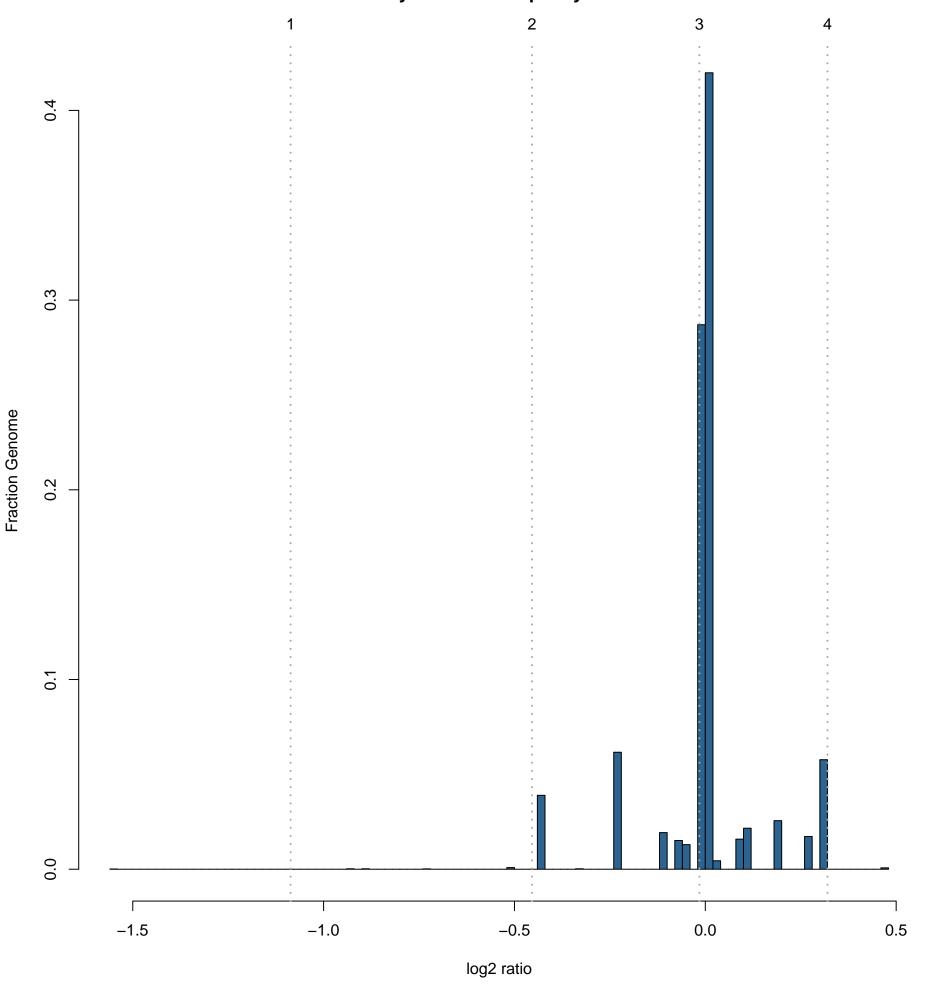
# SCNA-fit log-likelihood: -6059.19

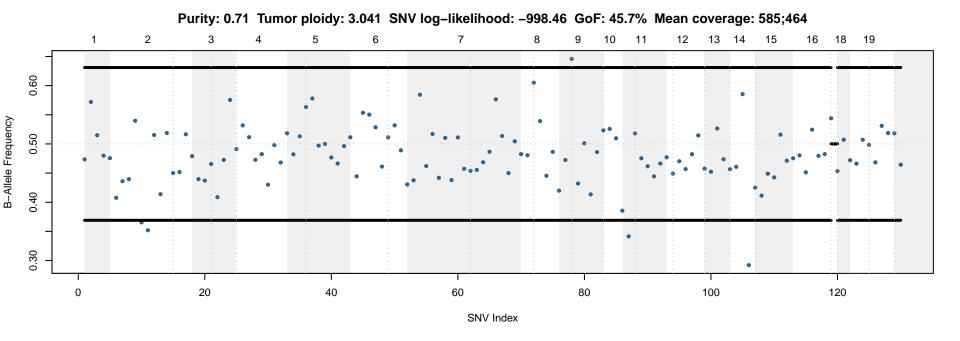






Purity: 0.71 Tumor ploidy: 3.041





## SCNA-fit log-likelihood: -5983.56

