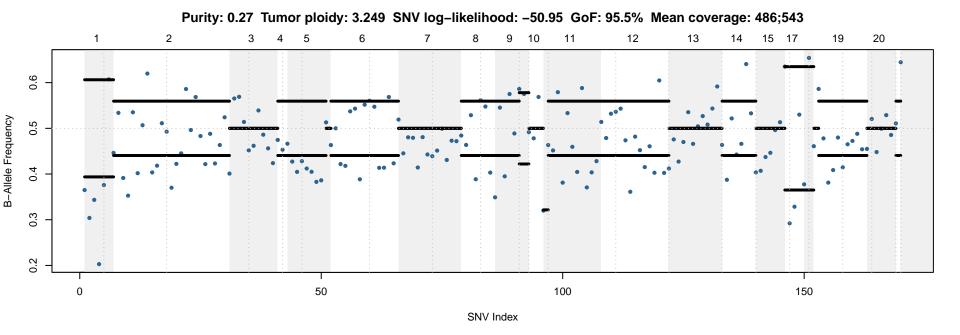
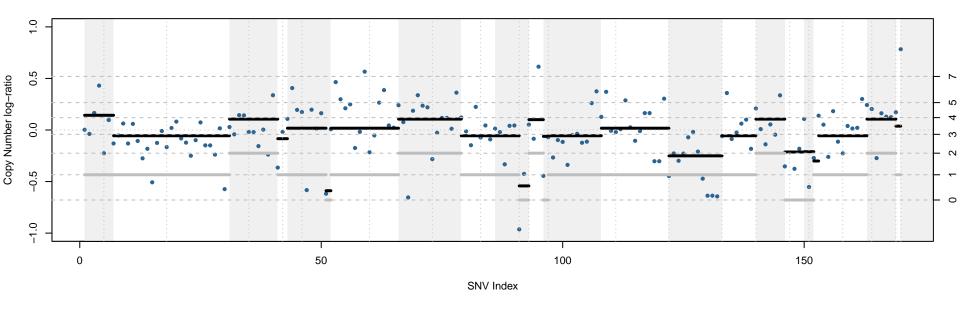
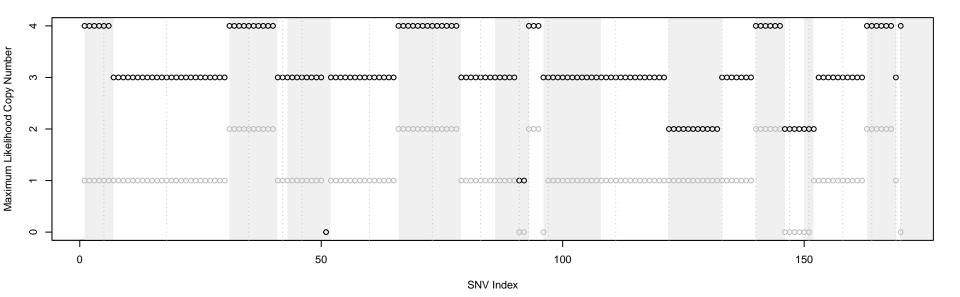
Purity: 0.27 Tumor ploidy: 3.249 5 2 3 7 0 0.25 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0

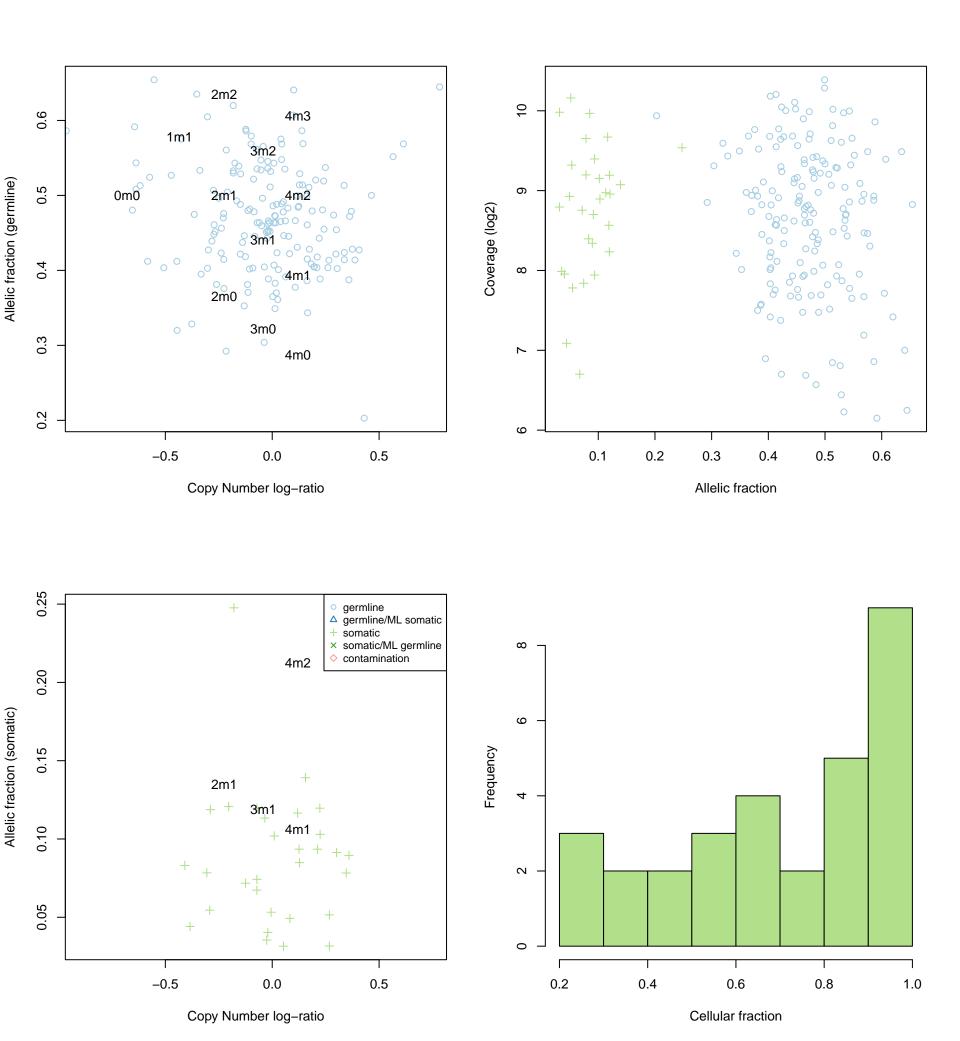
log2 ratio

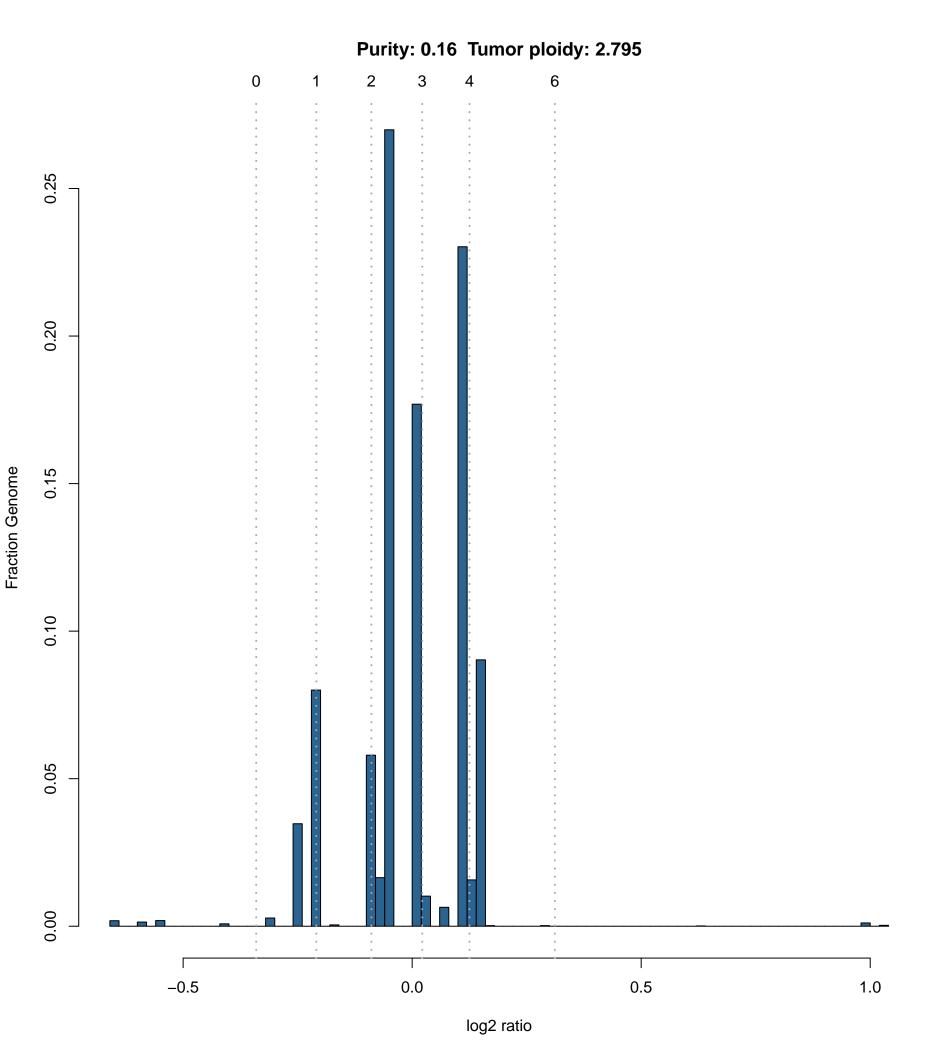


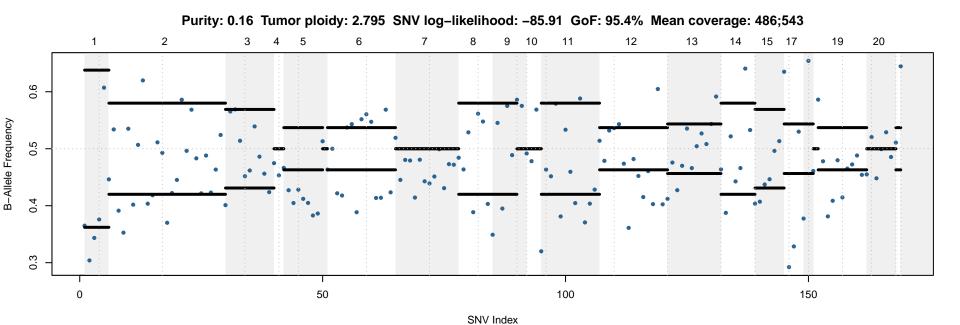
### SCNA-fit log-likelihood: -10208.97



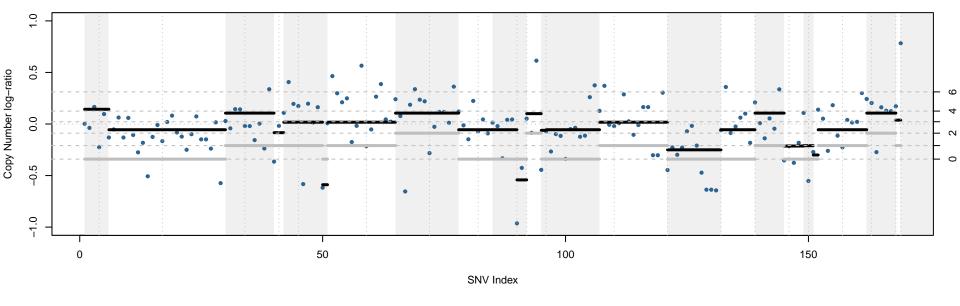


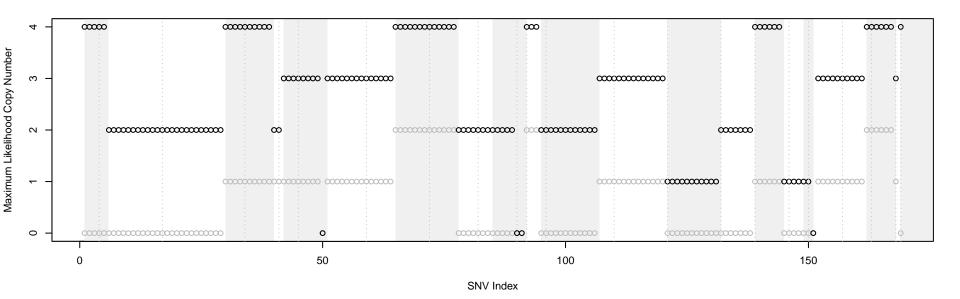


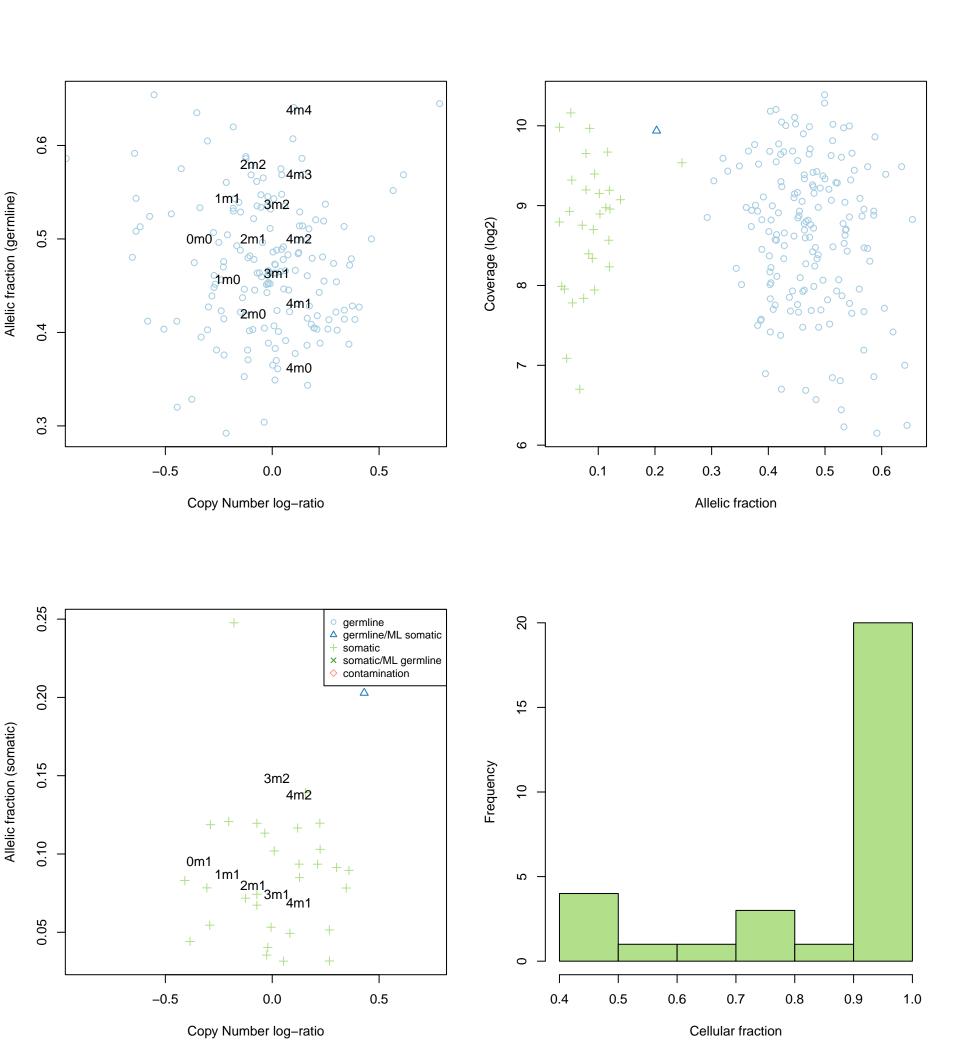




#### SCNA-fit log-likelihood: -10206.17

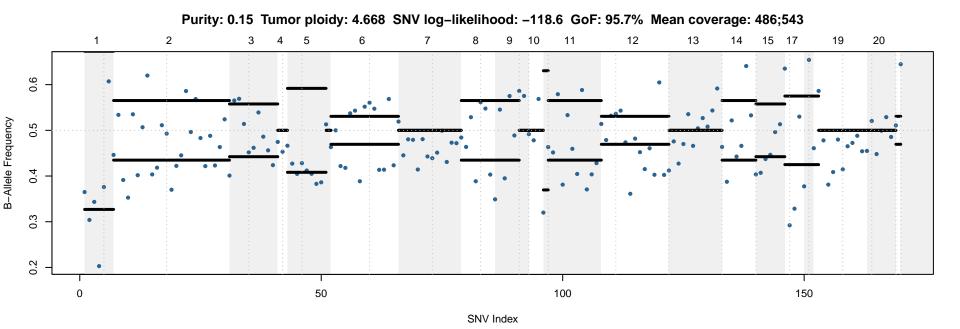




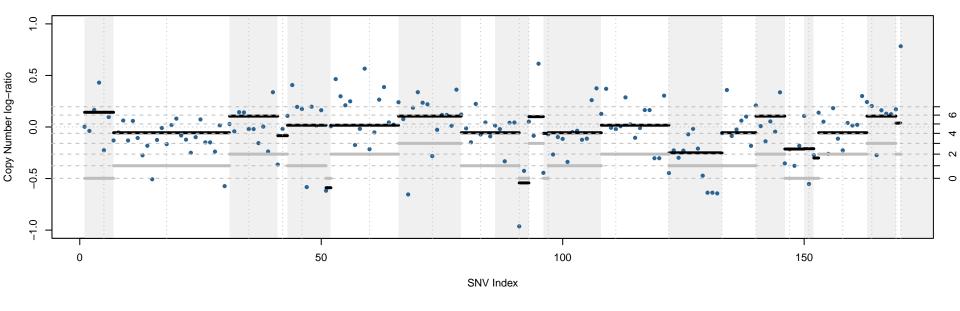


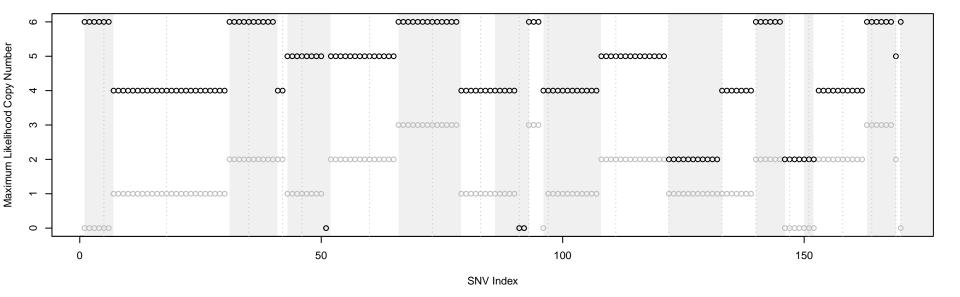
Purity: 0.15 Tumor ploidy: 4.668 0 2 3 5 6 0.25 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0

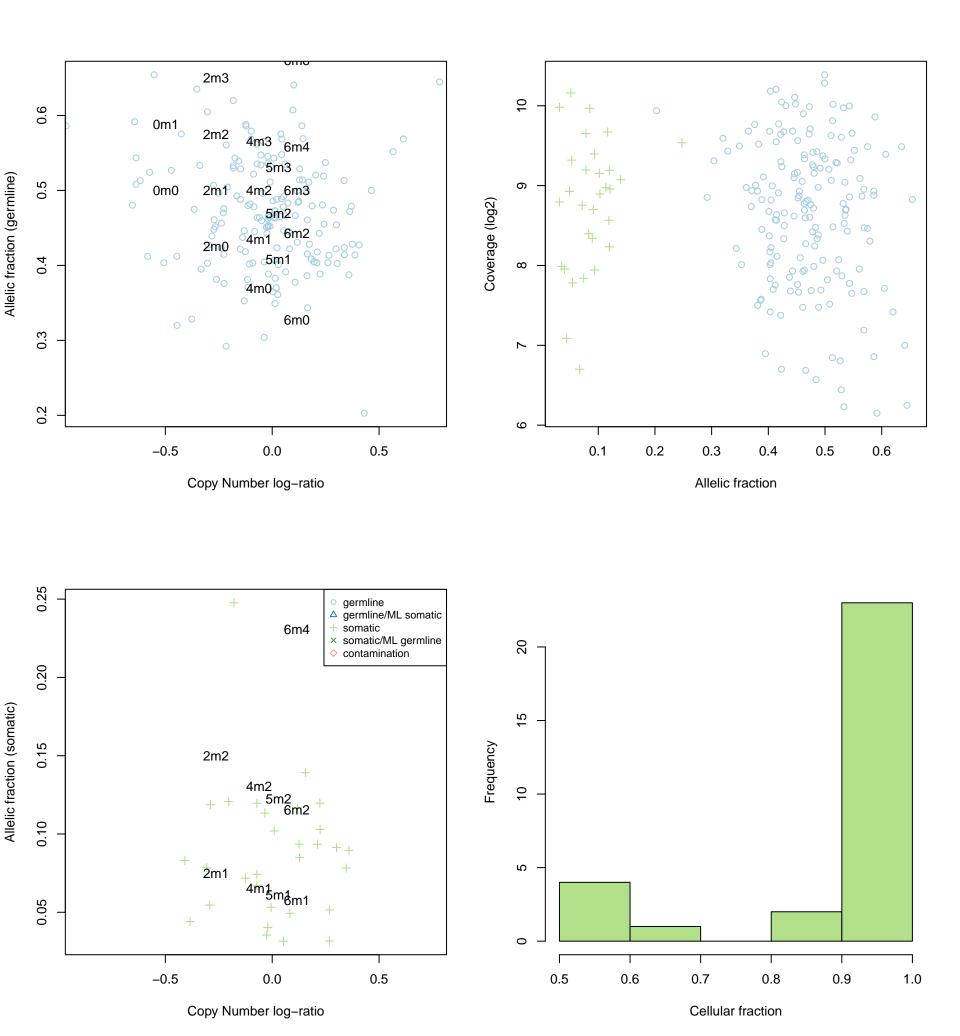
log2 ratio



### SCNA-fit log-likelihood: -10177.51

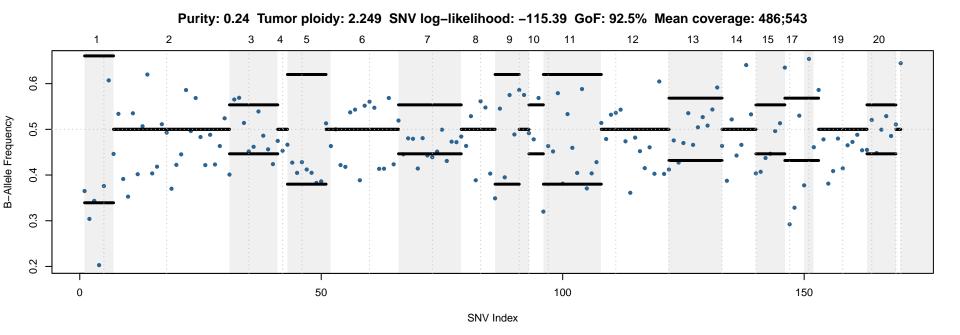




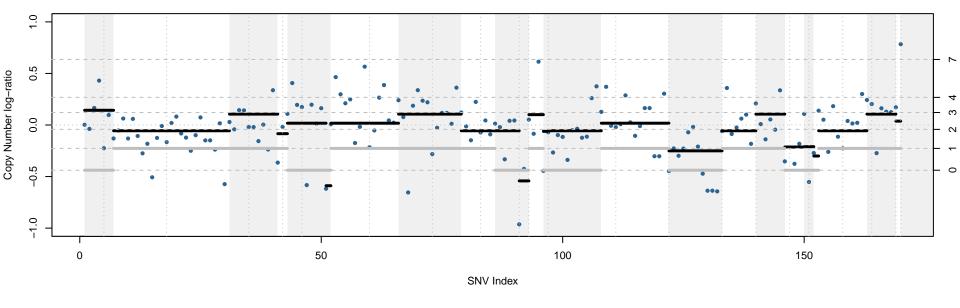


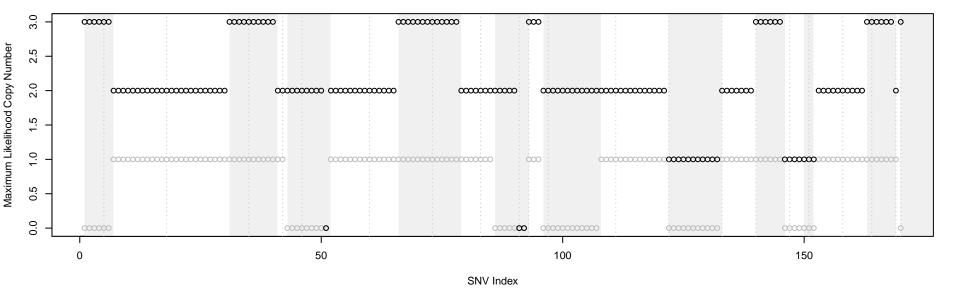
Purity: 0.24 Tumor ploidy: 2.249 2 0 3 7 0.25 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0

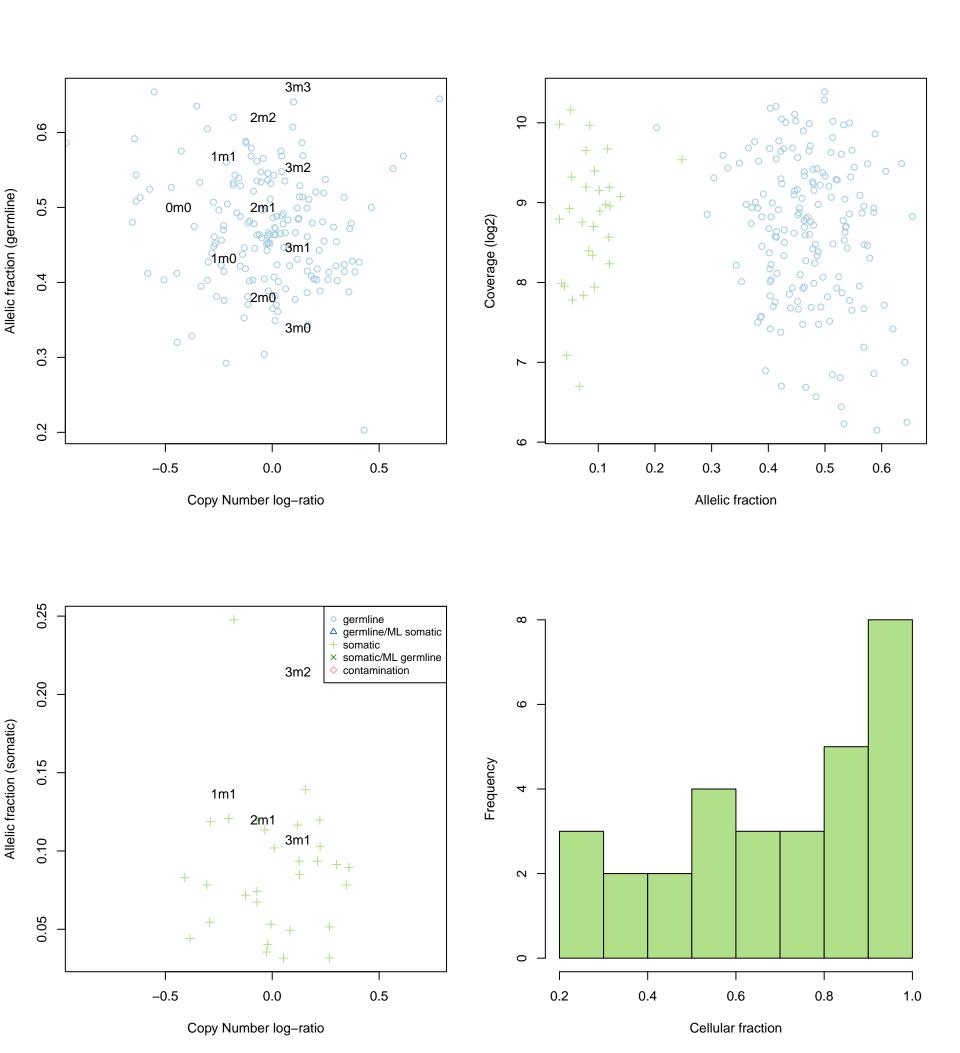
log2 ratio

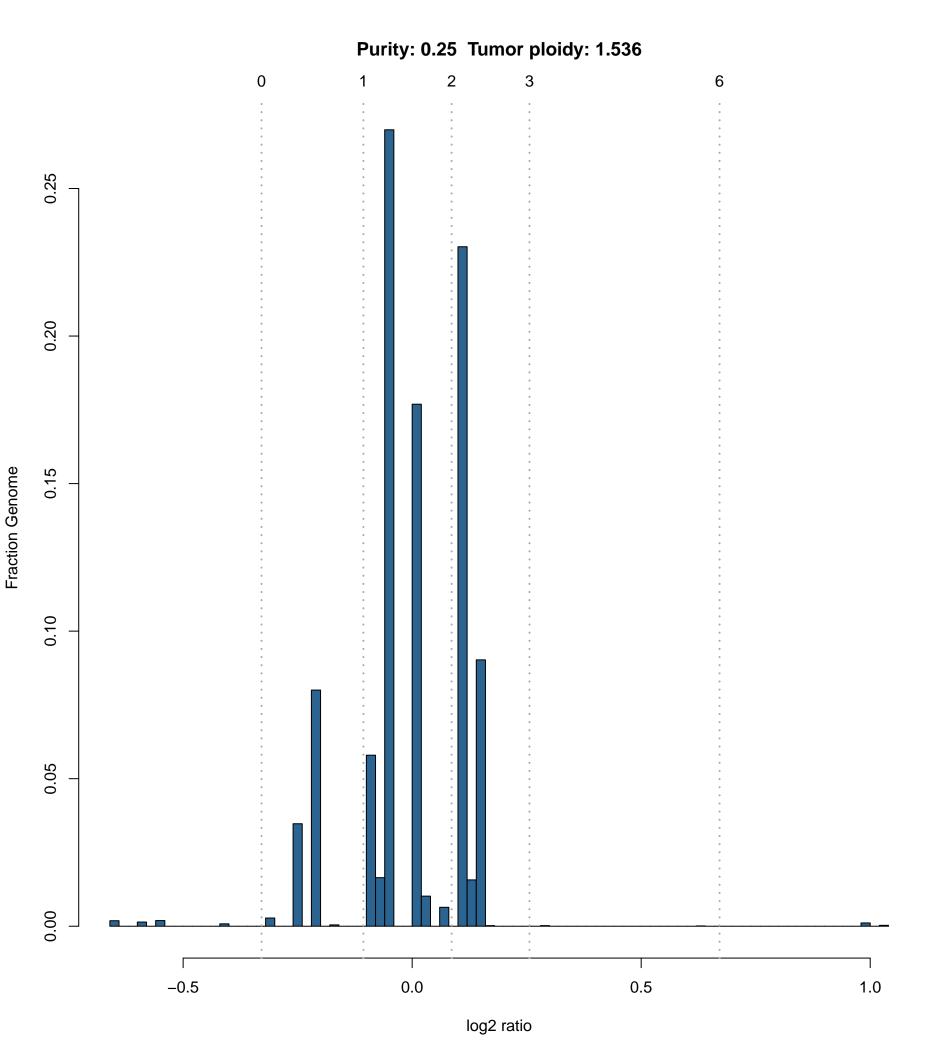


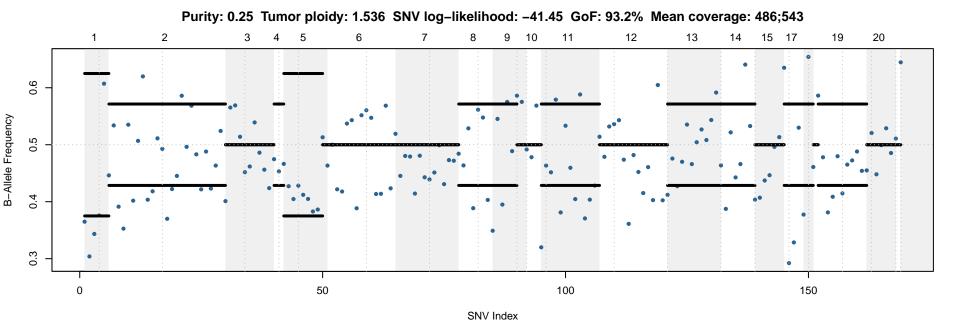
### SCNA-fit log-likelihood: -10222.33



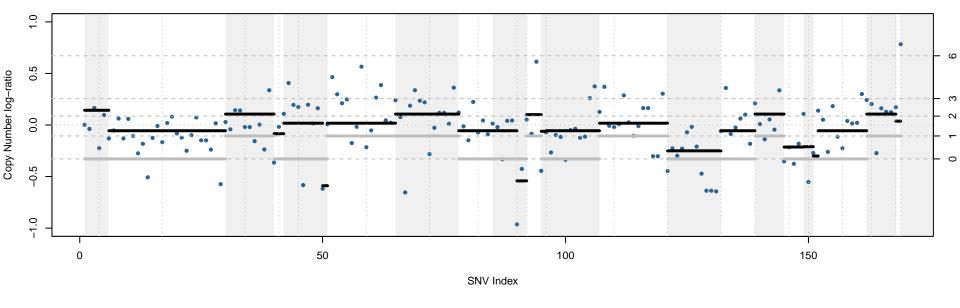


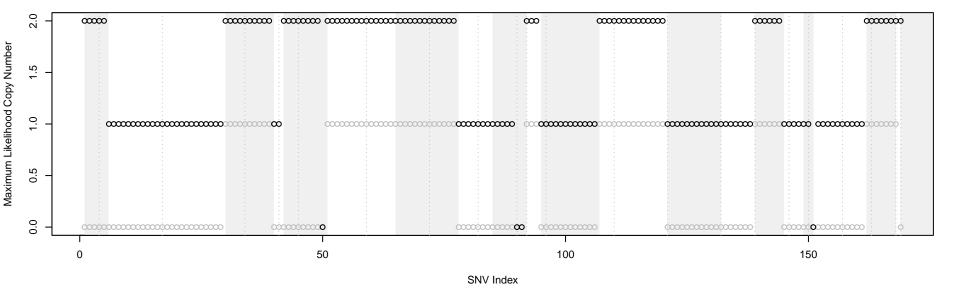


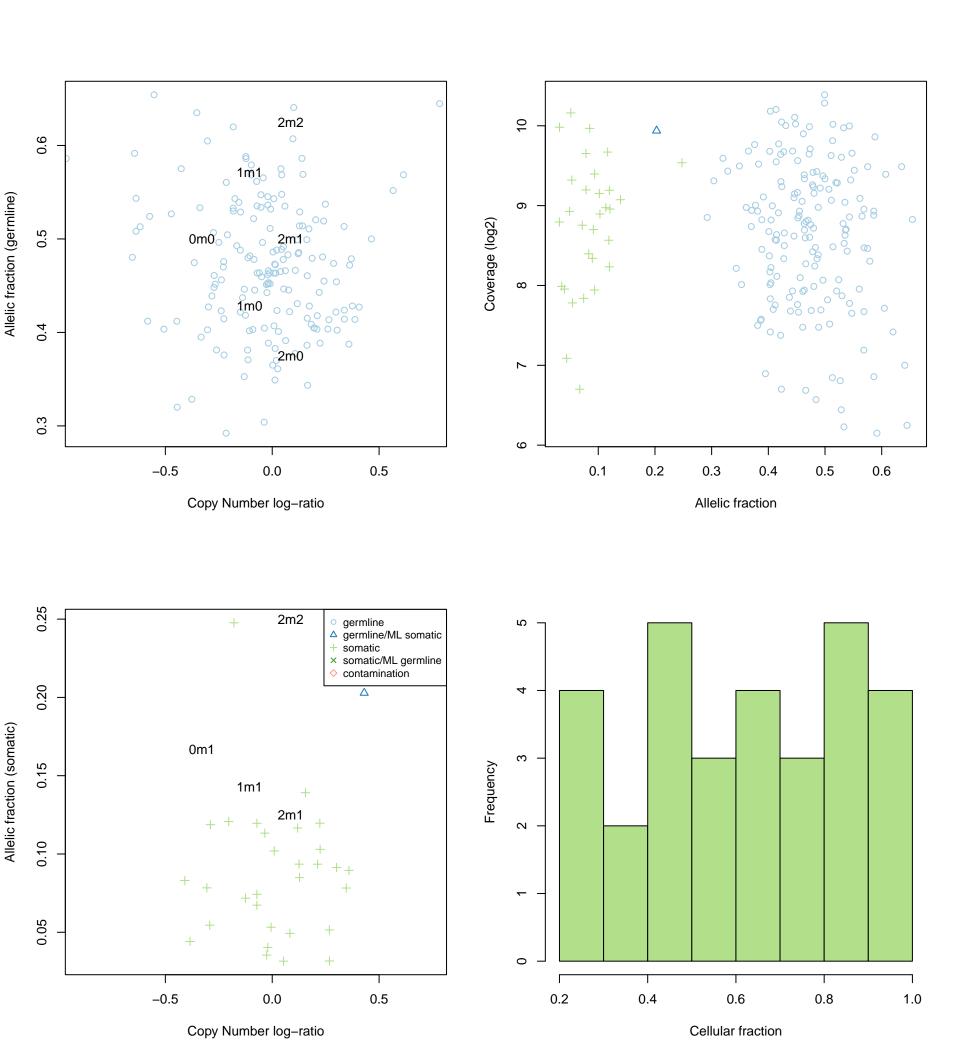




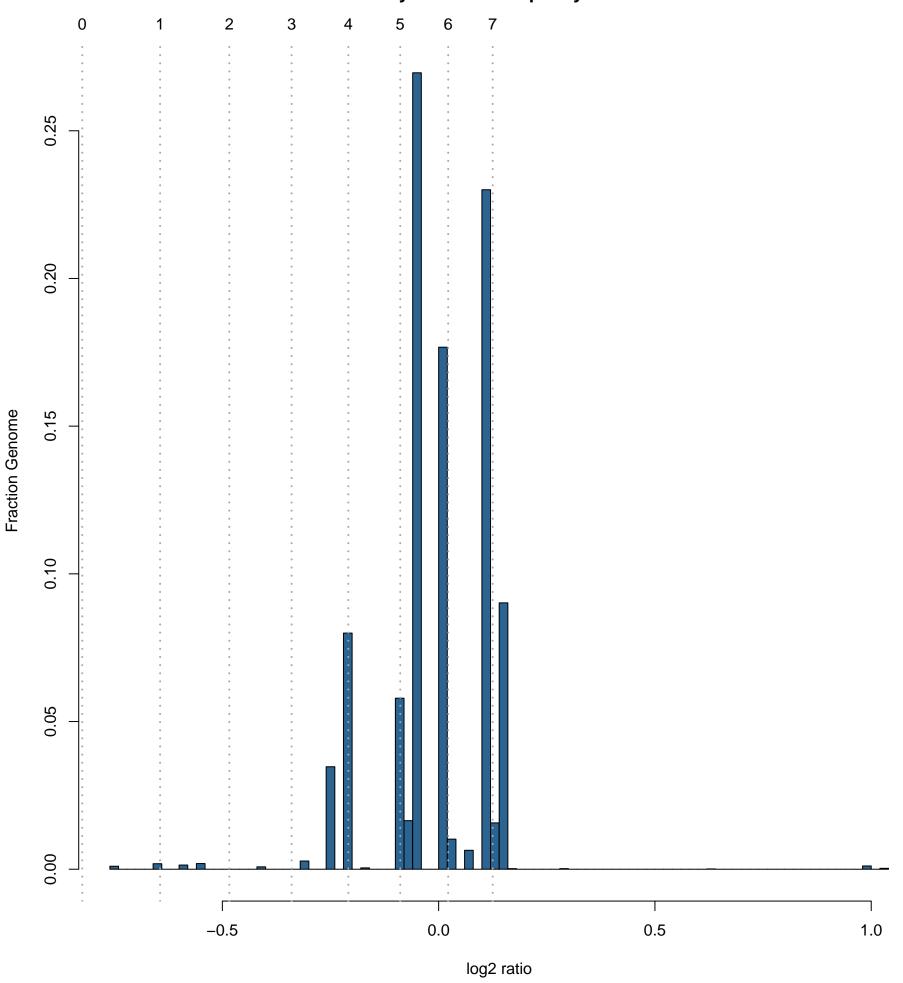
#### SCNA-fit log-likelihood: -10396.81

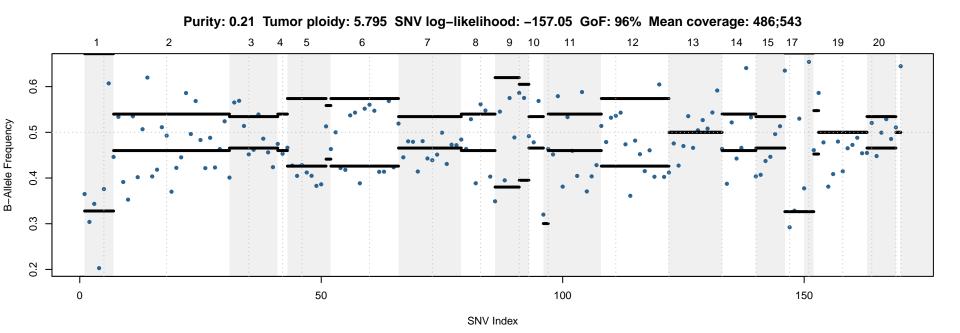




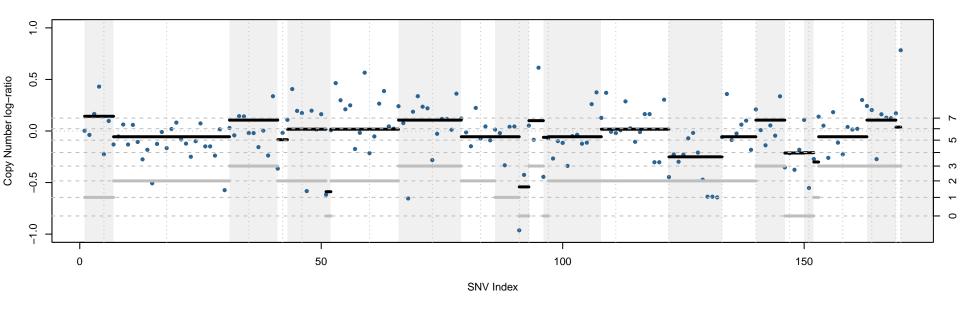


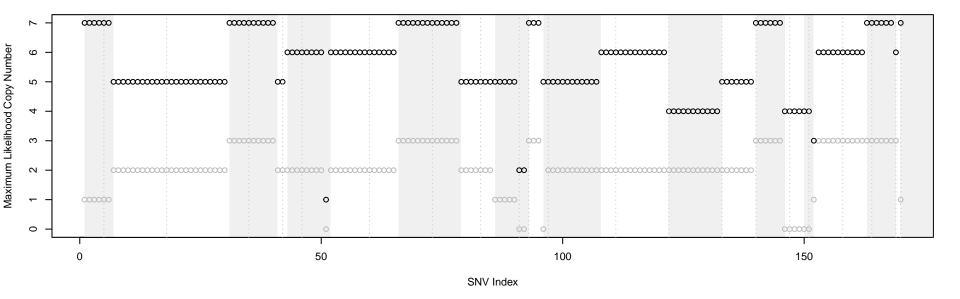
Purity: 0.21 Tumor ploidy: 5.795

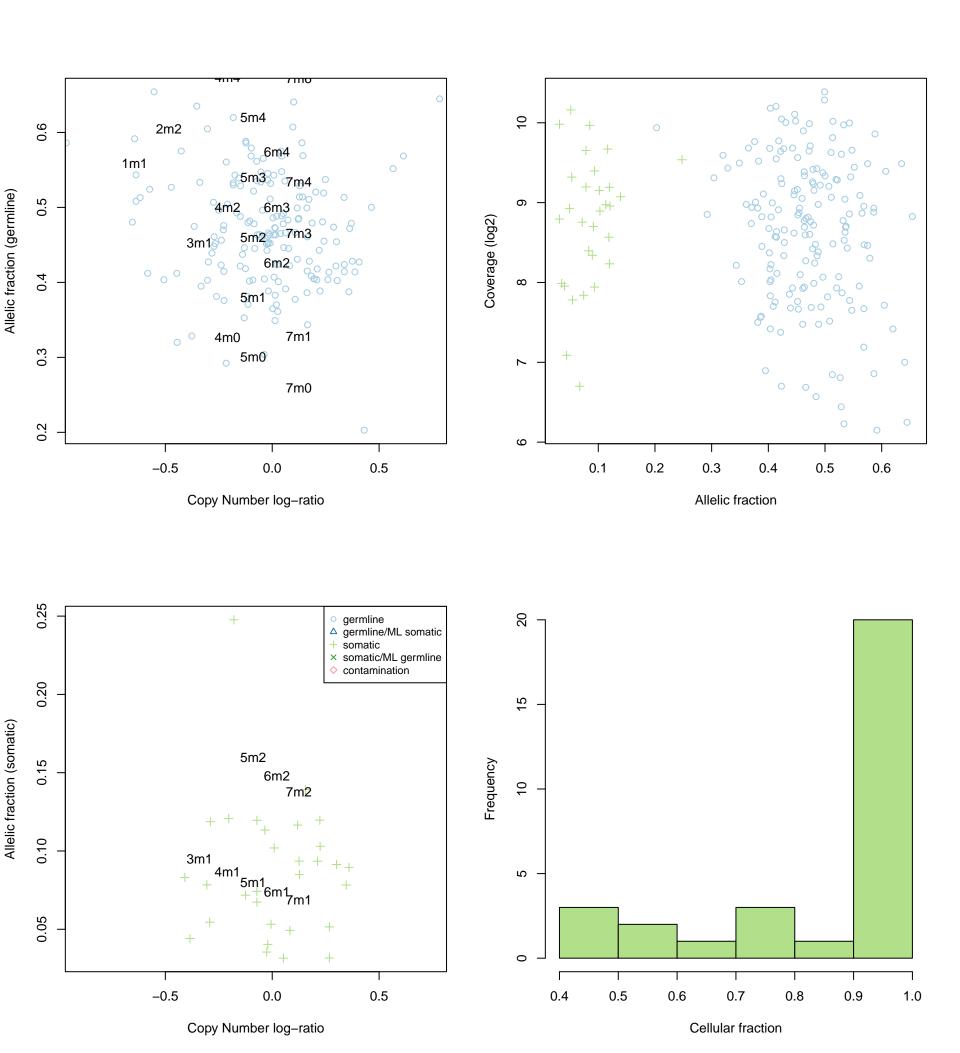




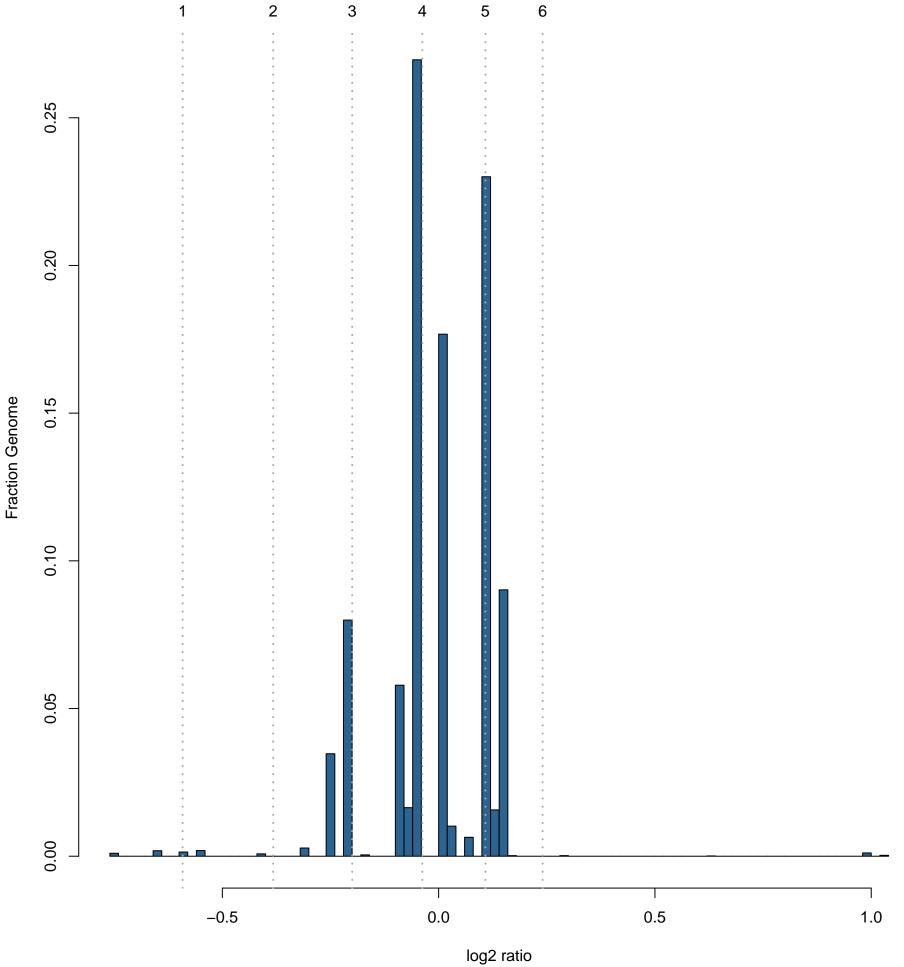
### SCNA-fit log-likelihood: -10178.53

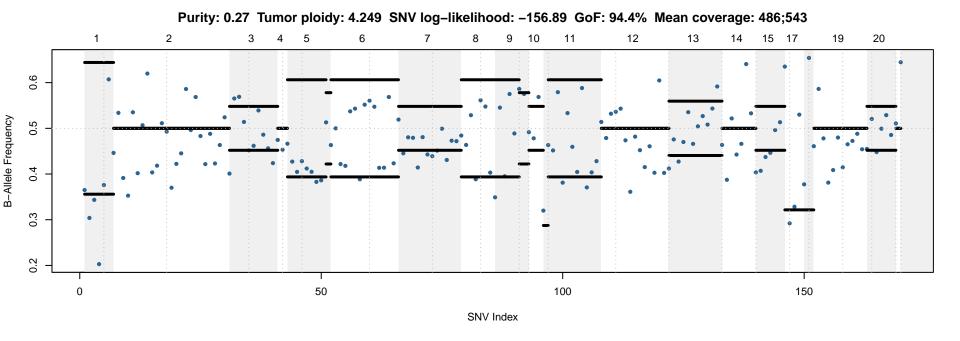




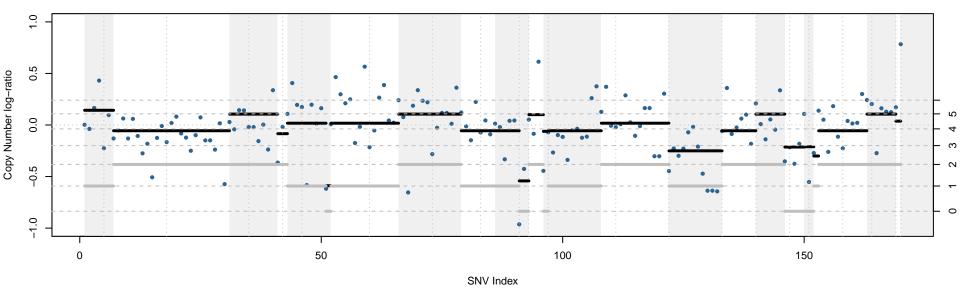


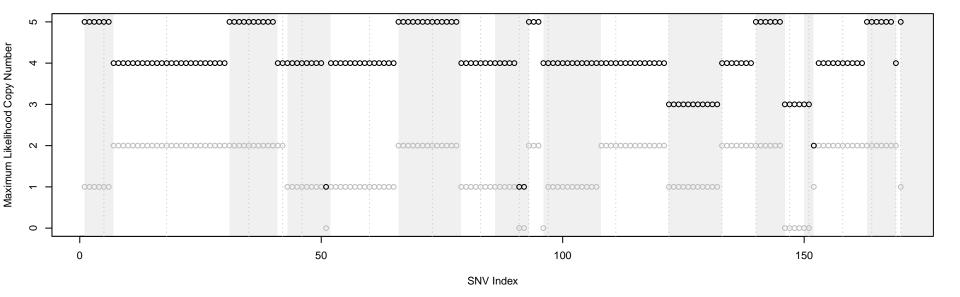
**Purity: 0.27 Tumor ploidy: 4.249**3 4 5 6

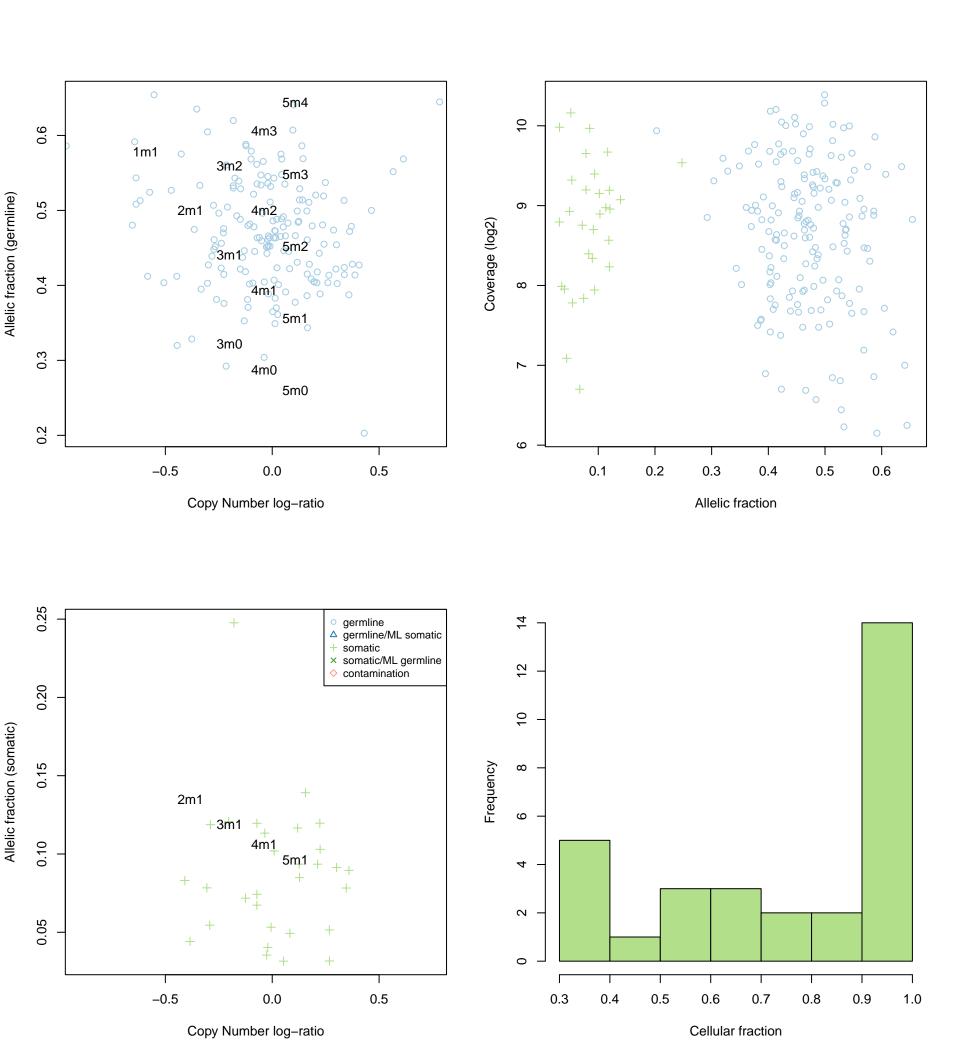




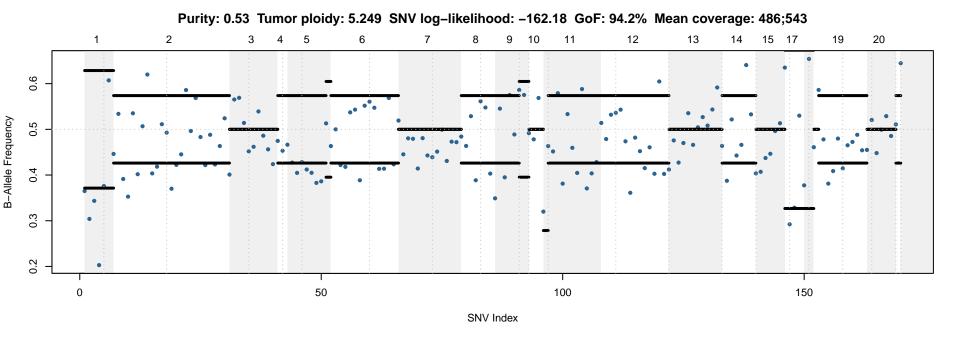
### SCNA-fit log-likelihood: -10213.17



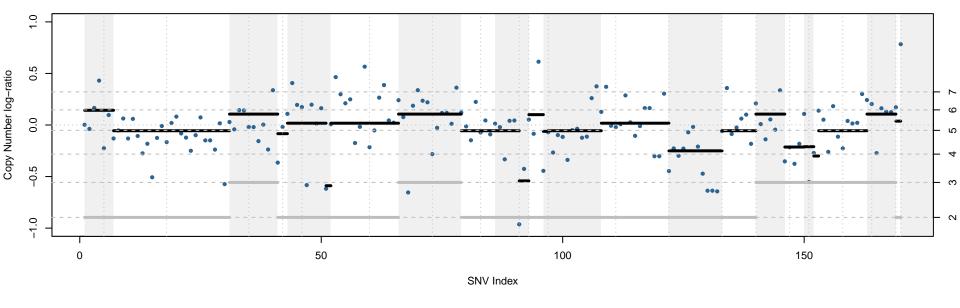


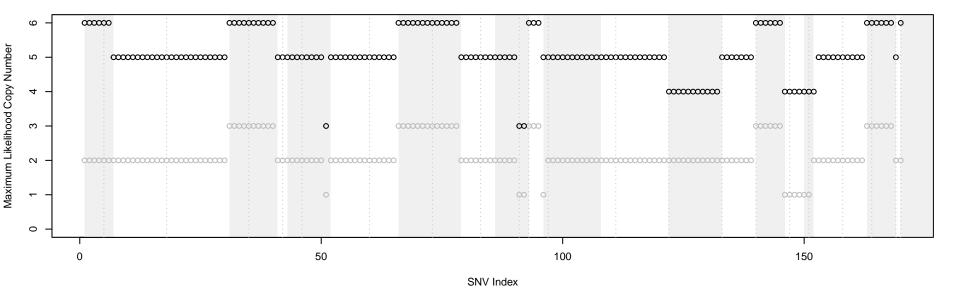


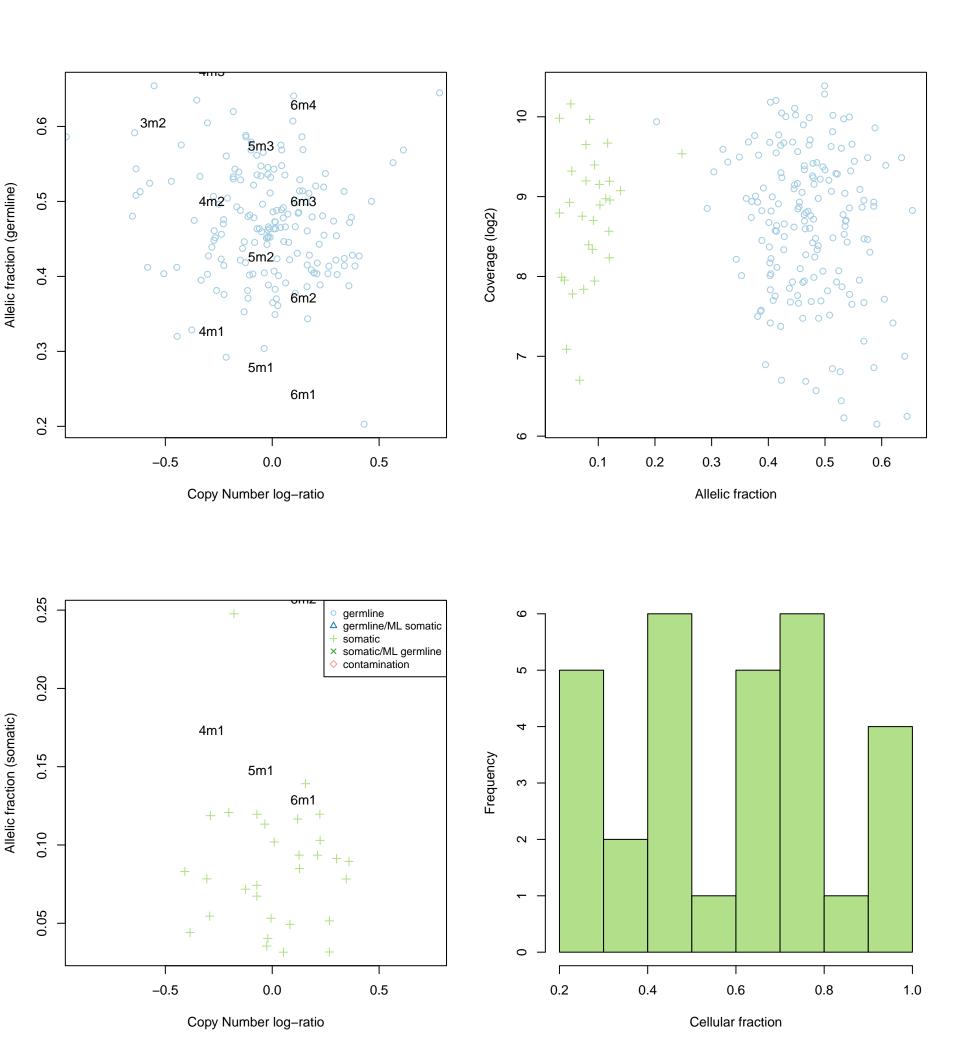
Purity: 0.53 Tumor ploidy: 5.249 6 3 5 4 0.25 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio



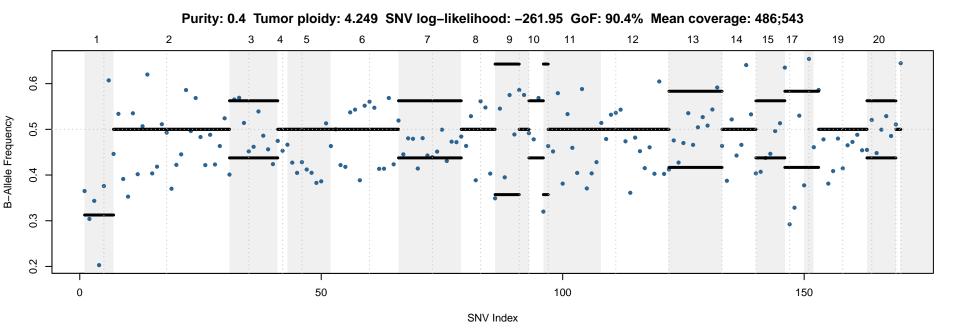
### SCNA-fit log-likelihood: -10265.74



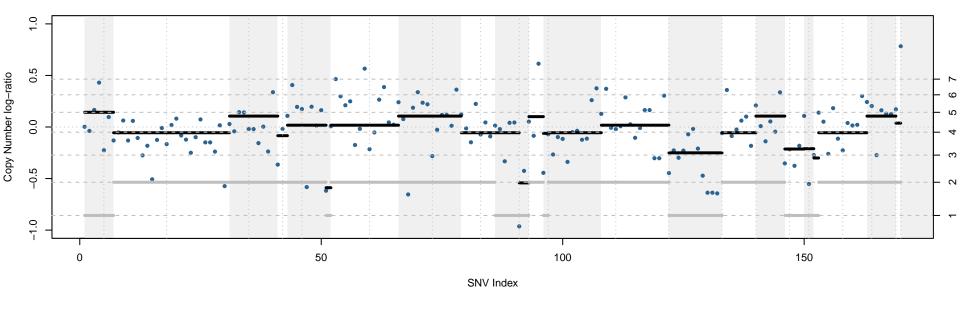


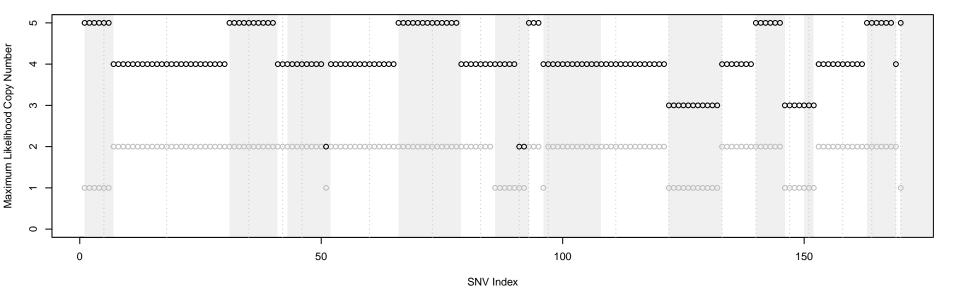


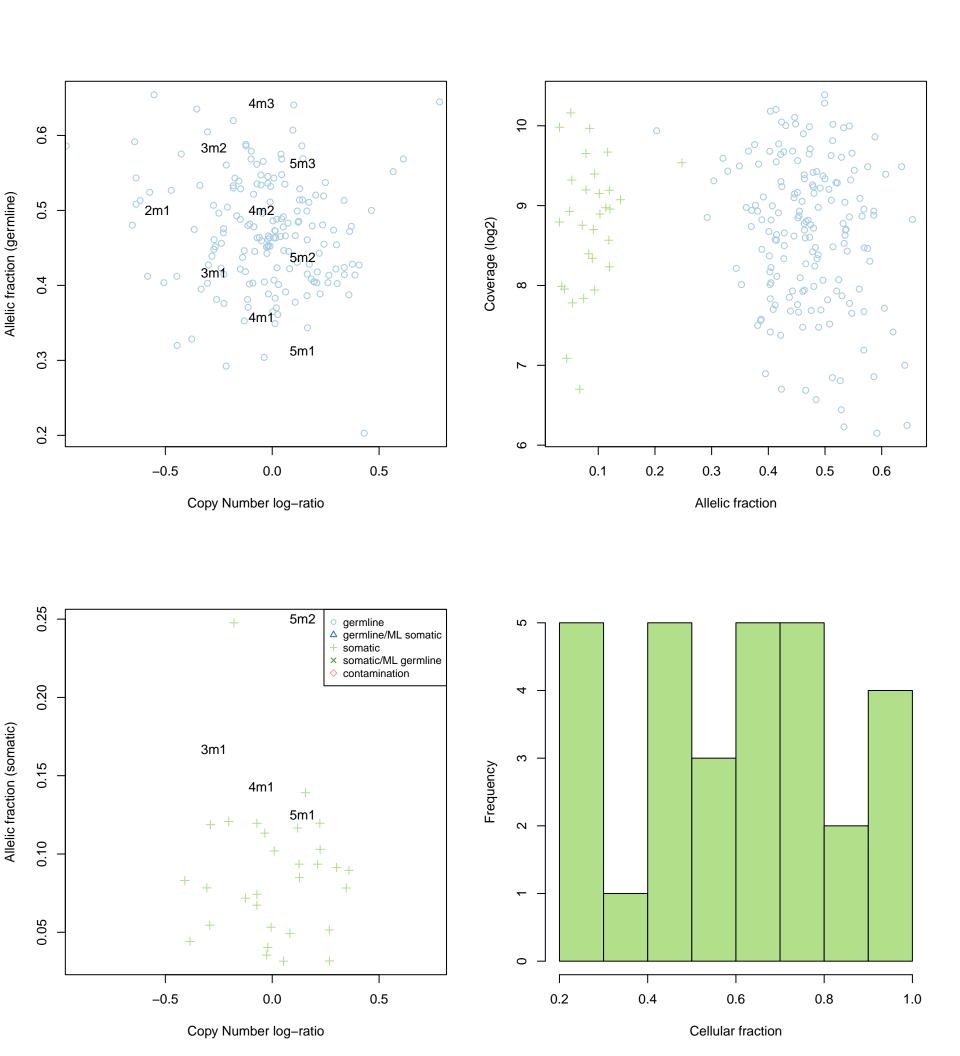
Purity: 0.4 Tumor ploidy: 4.249 2 3 6 5 0.25 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio



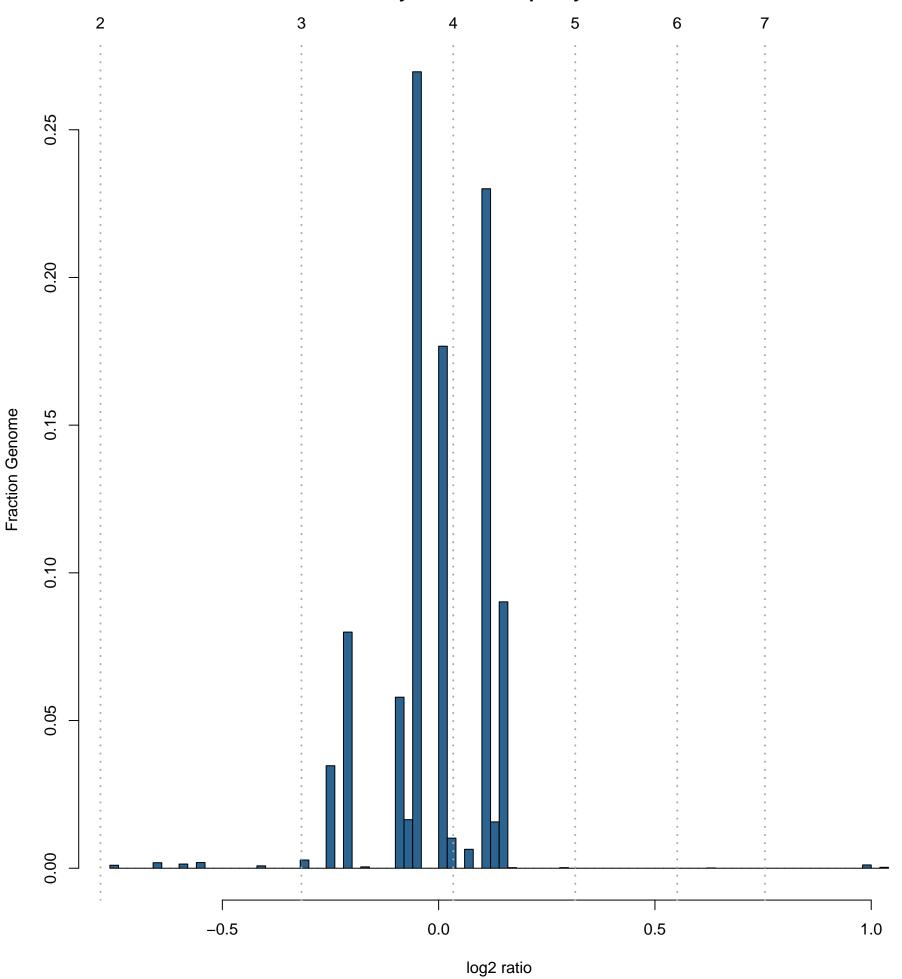
## SCNA-fit log-likelihood: -10248.31

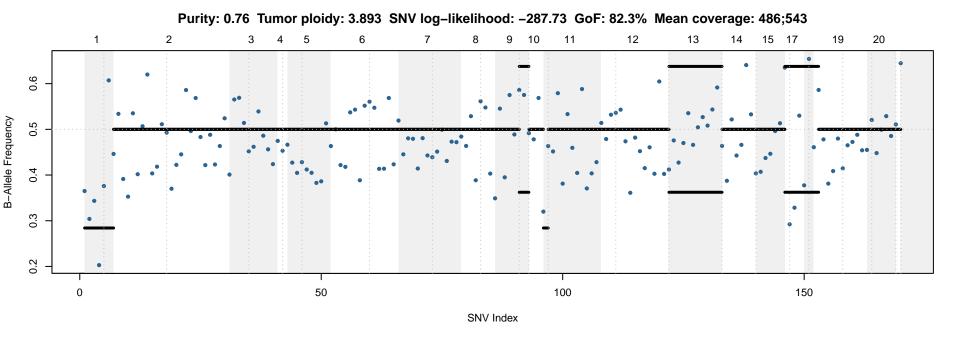




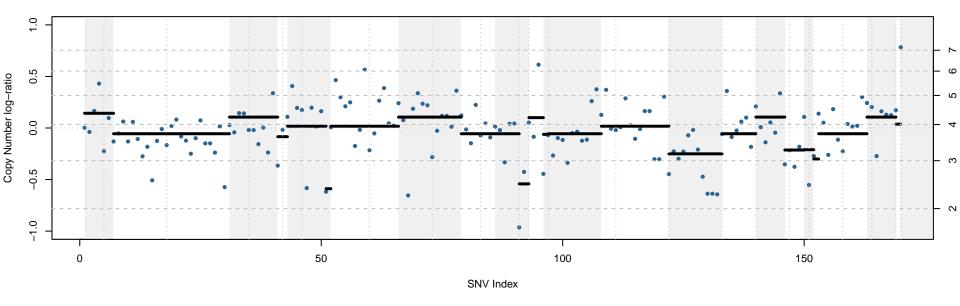


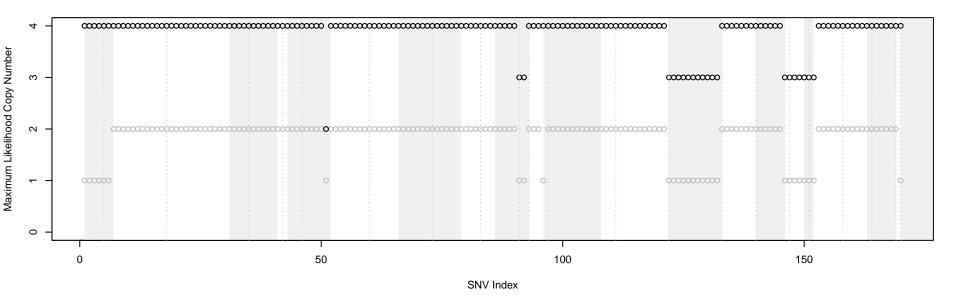
Purity: 0.76 Tumor ploidy: 3.893

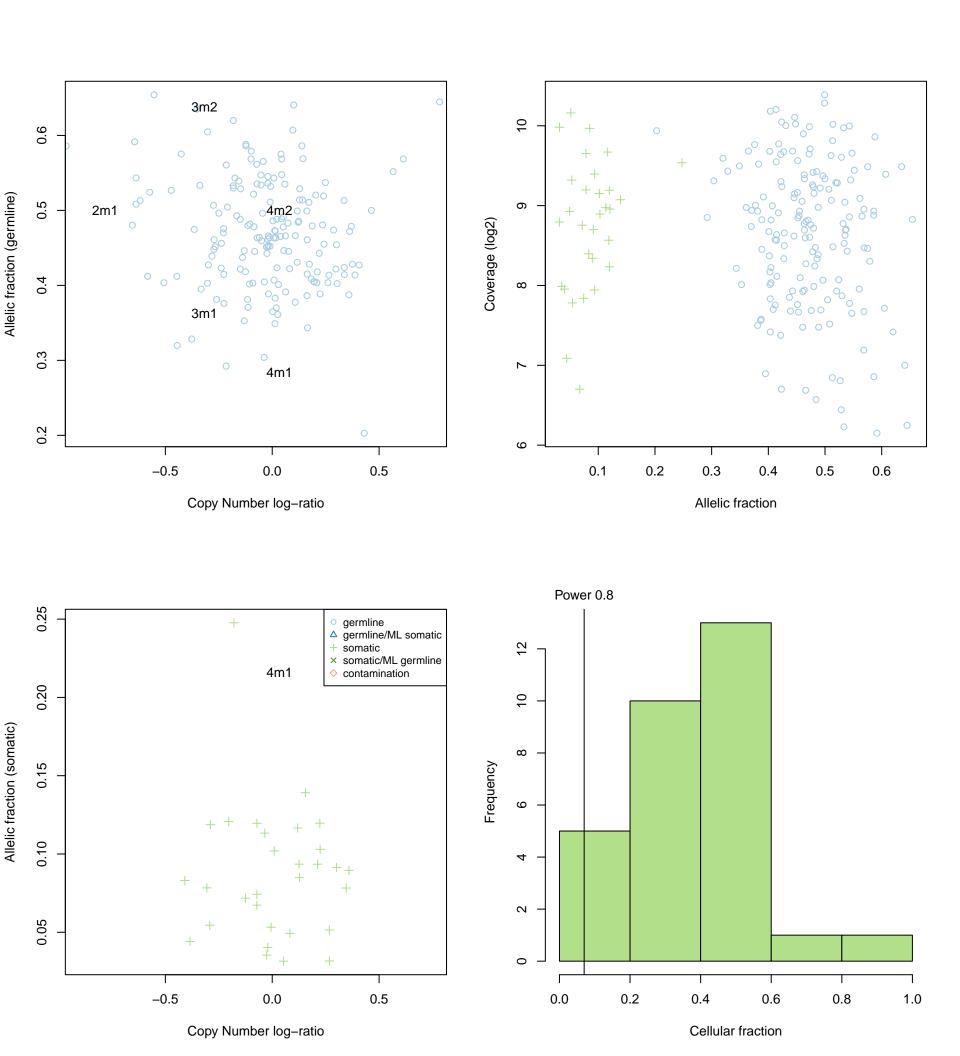




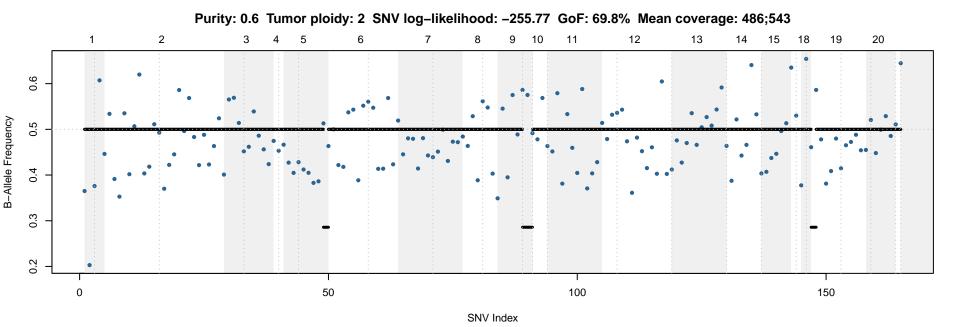
## SCNA-fit log-likelihood: -10516.67



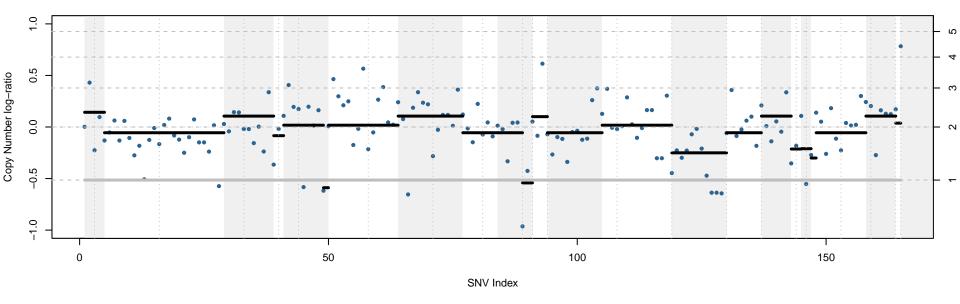


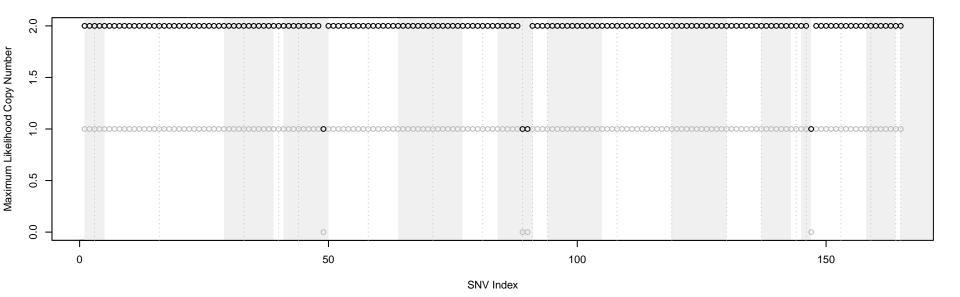


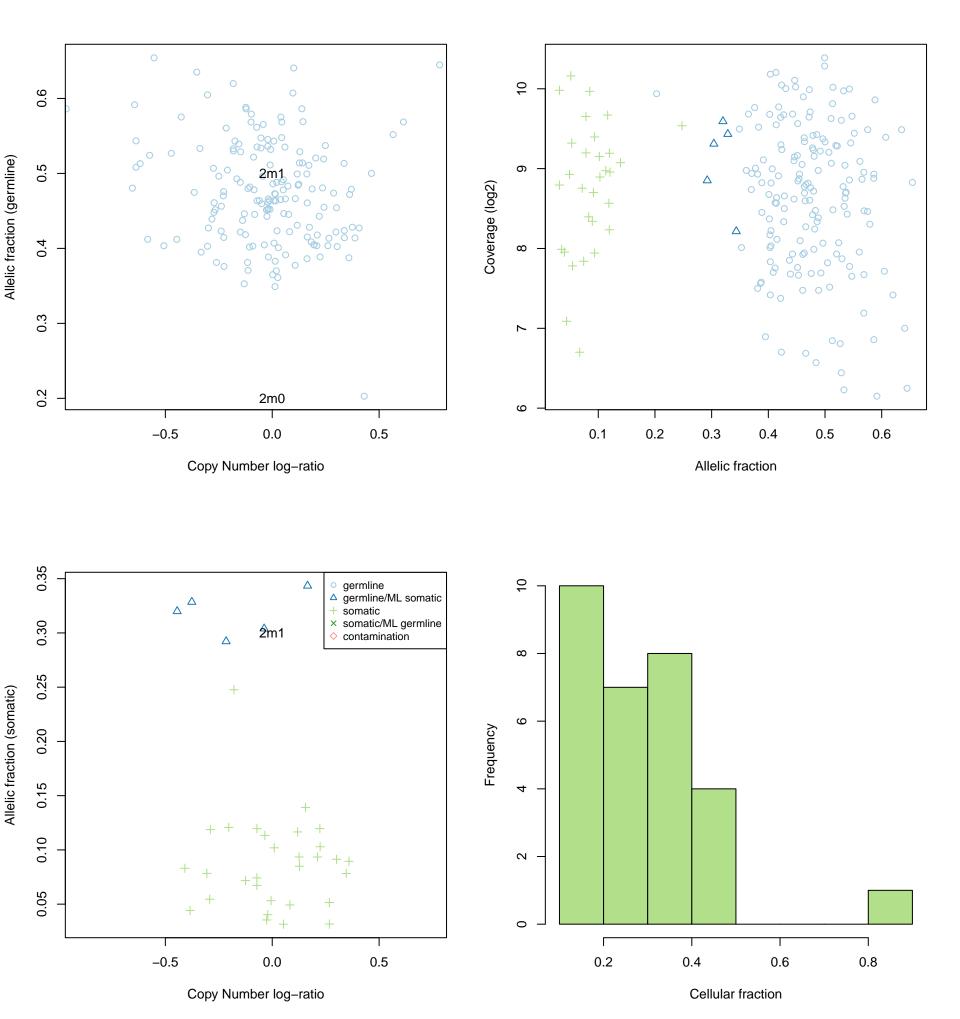
Purity: 0.6 Tumor ploidy: 2 5 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio



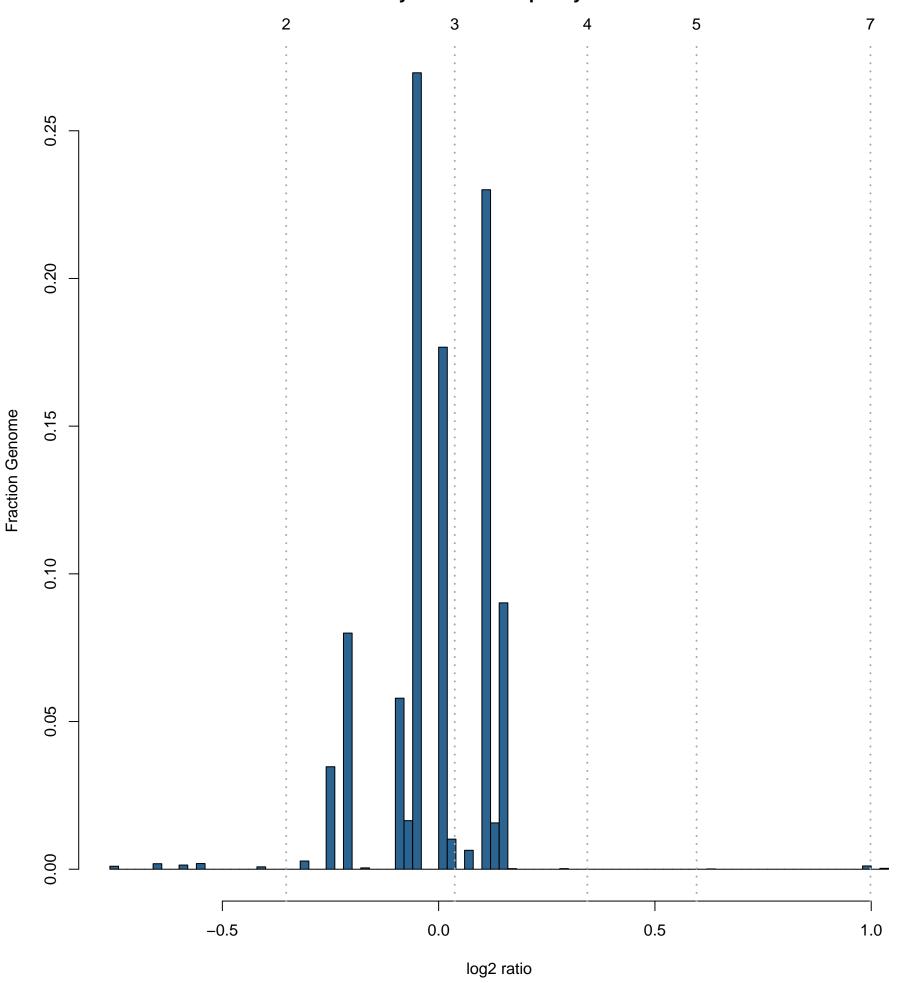
# SCNA-fit log-likelihood: -10810.51

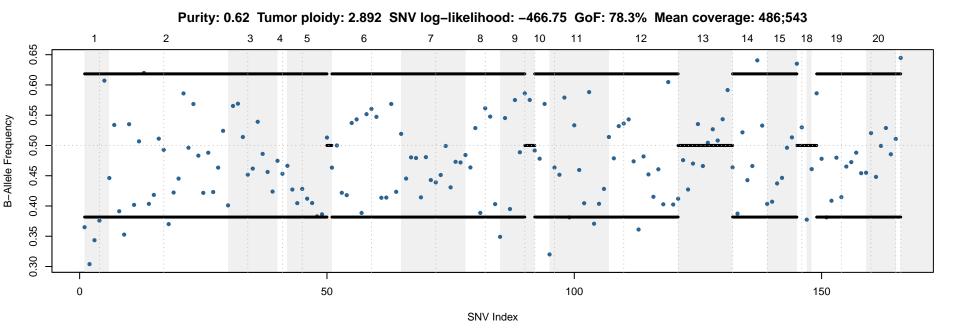




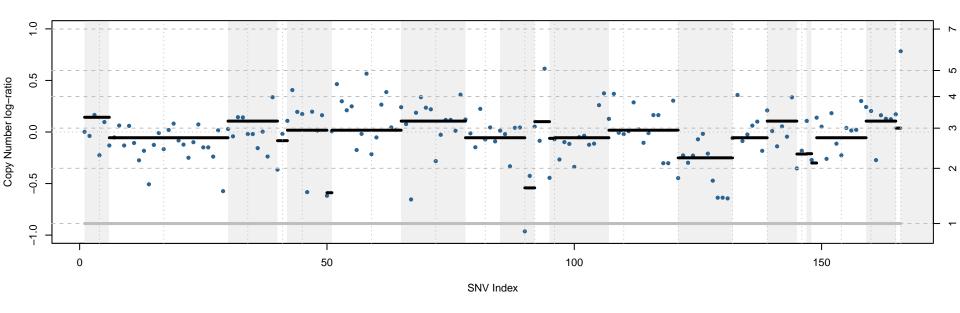


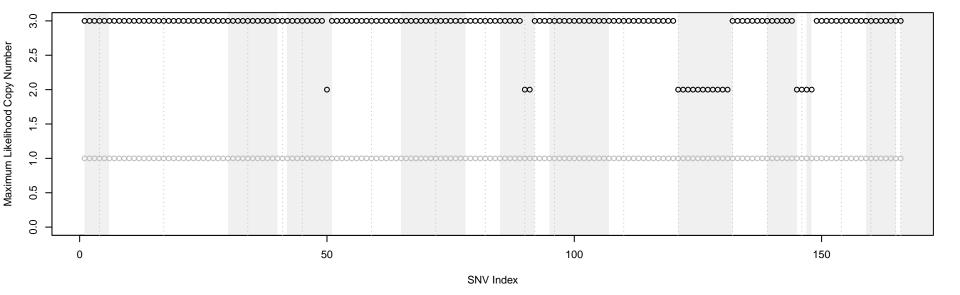
Purity: 0.62 Tumor ploidy: 2.892

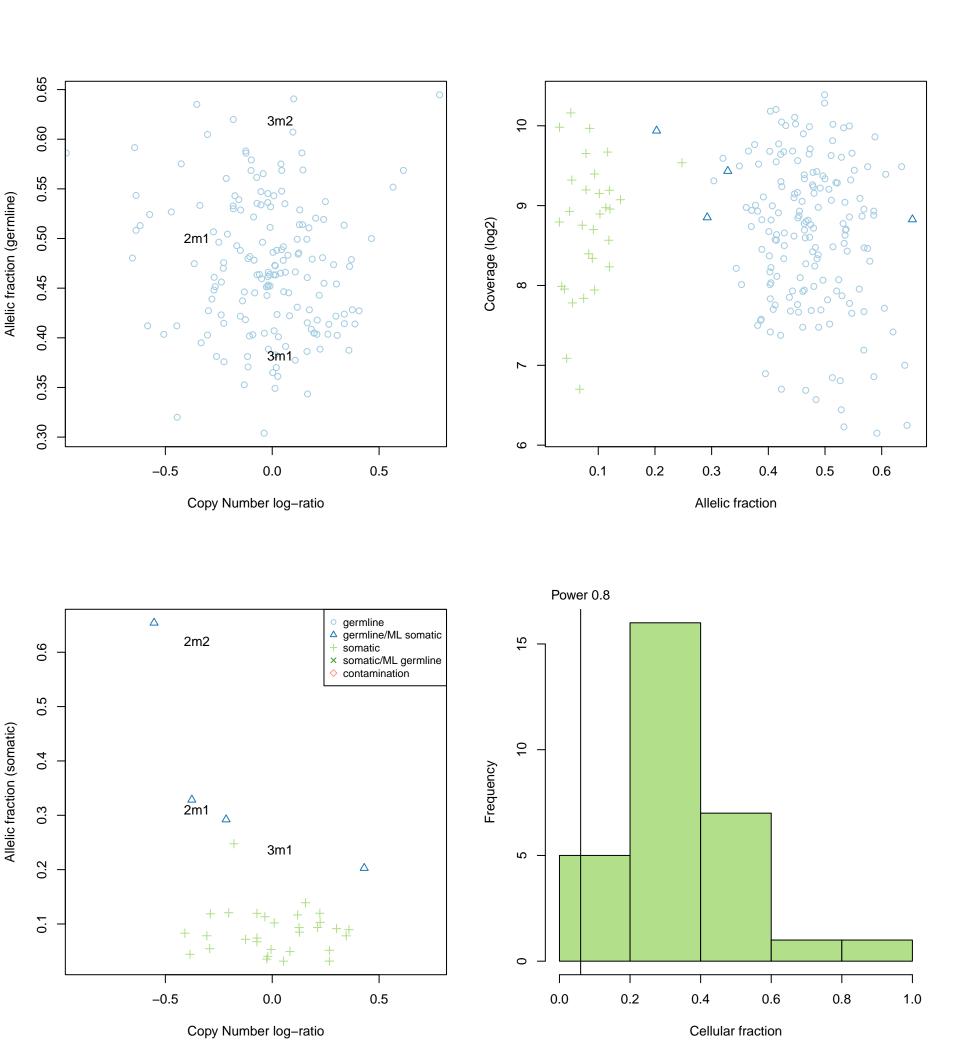




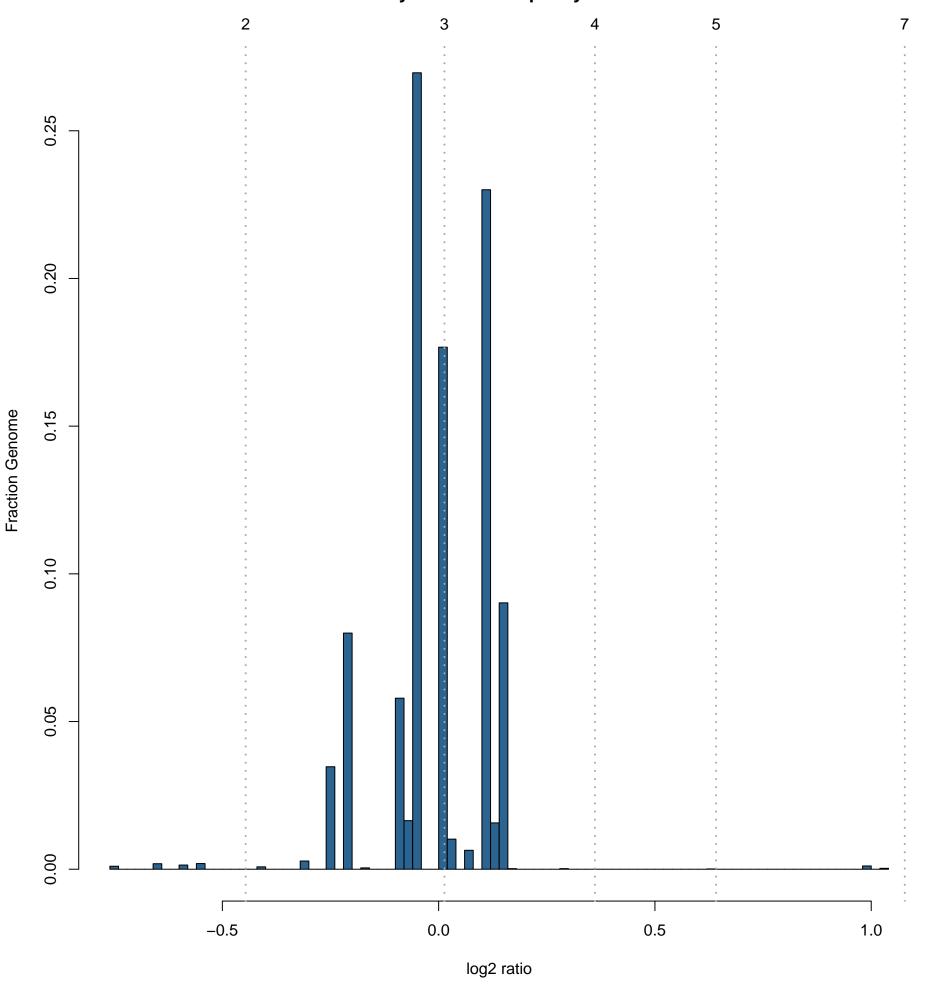
## SCNA-fit log-likelihood: -10566.2

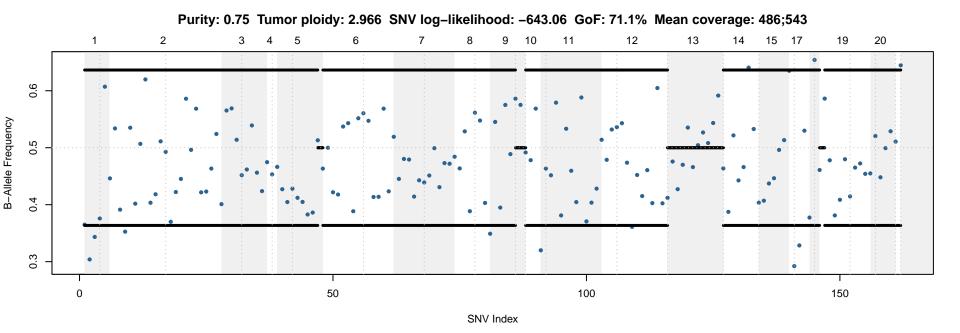






Purity: 0.75 Tumor ploidy: 2.966





## SCNA-fit log-likelihood: -10765.68

