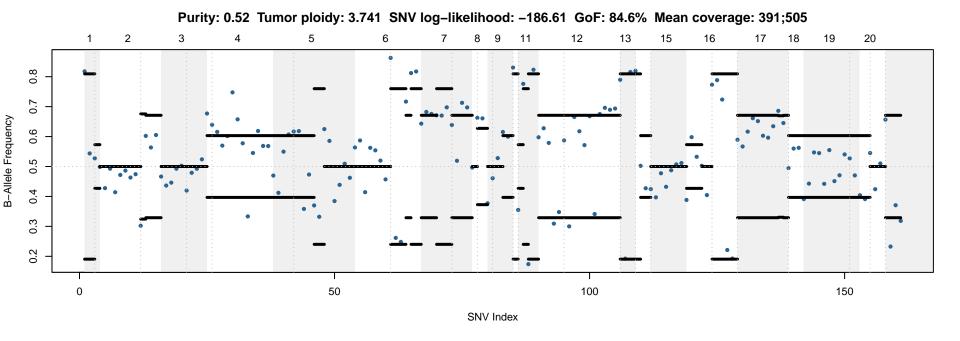
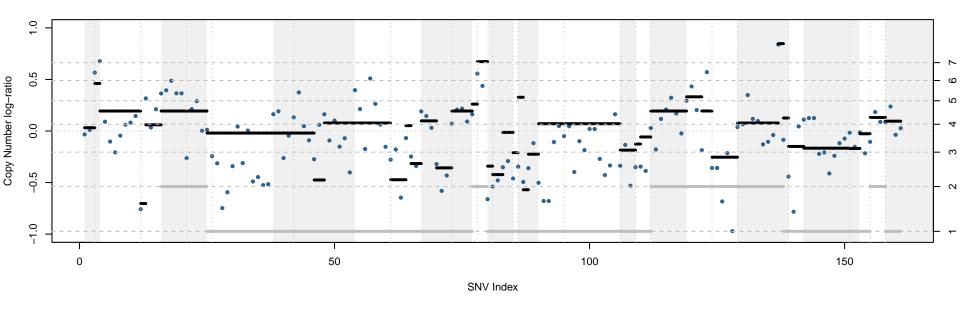
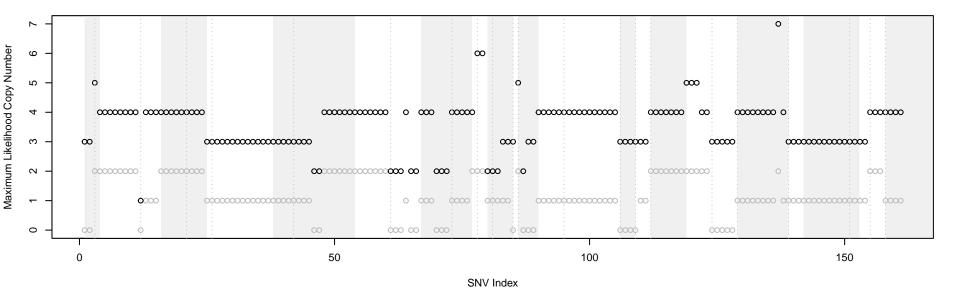
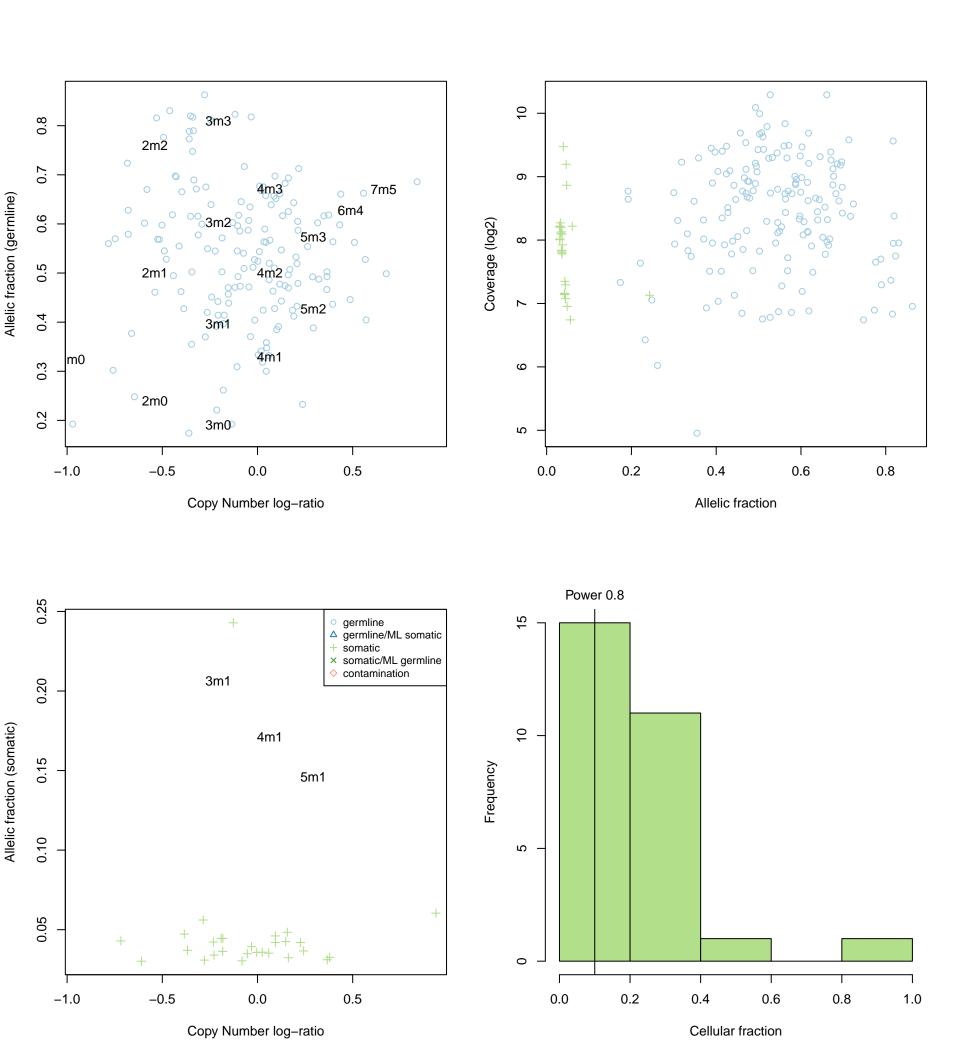
Purity: 0.52 Tumor ploidy: 3.741 2 5 6 7 3 4 1 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



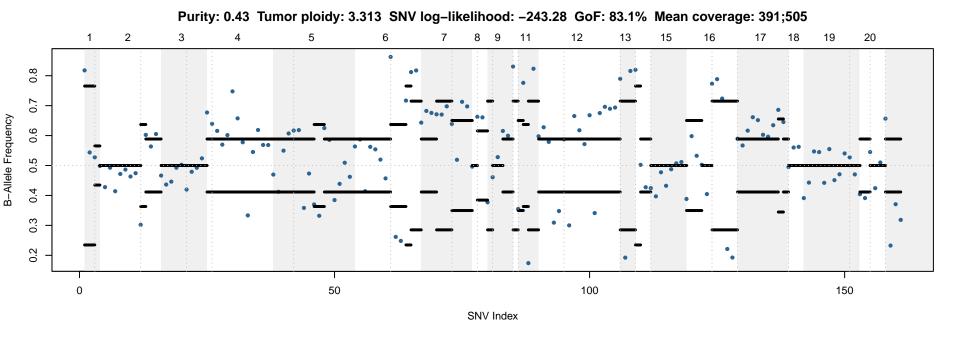
### SCNA-fit log-likelihood: -6942.1



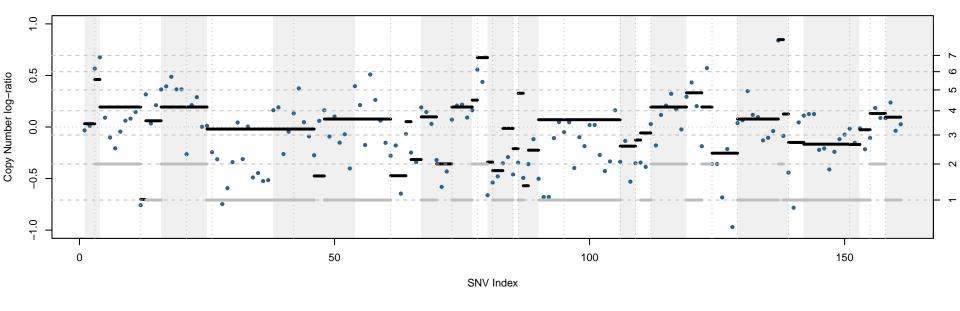


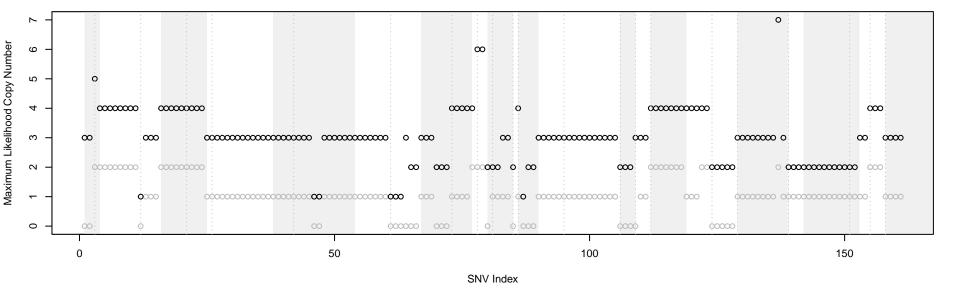


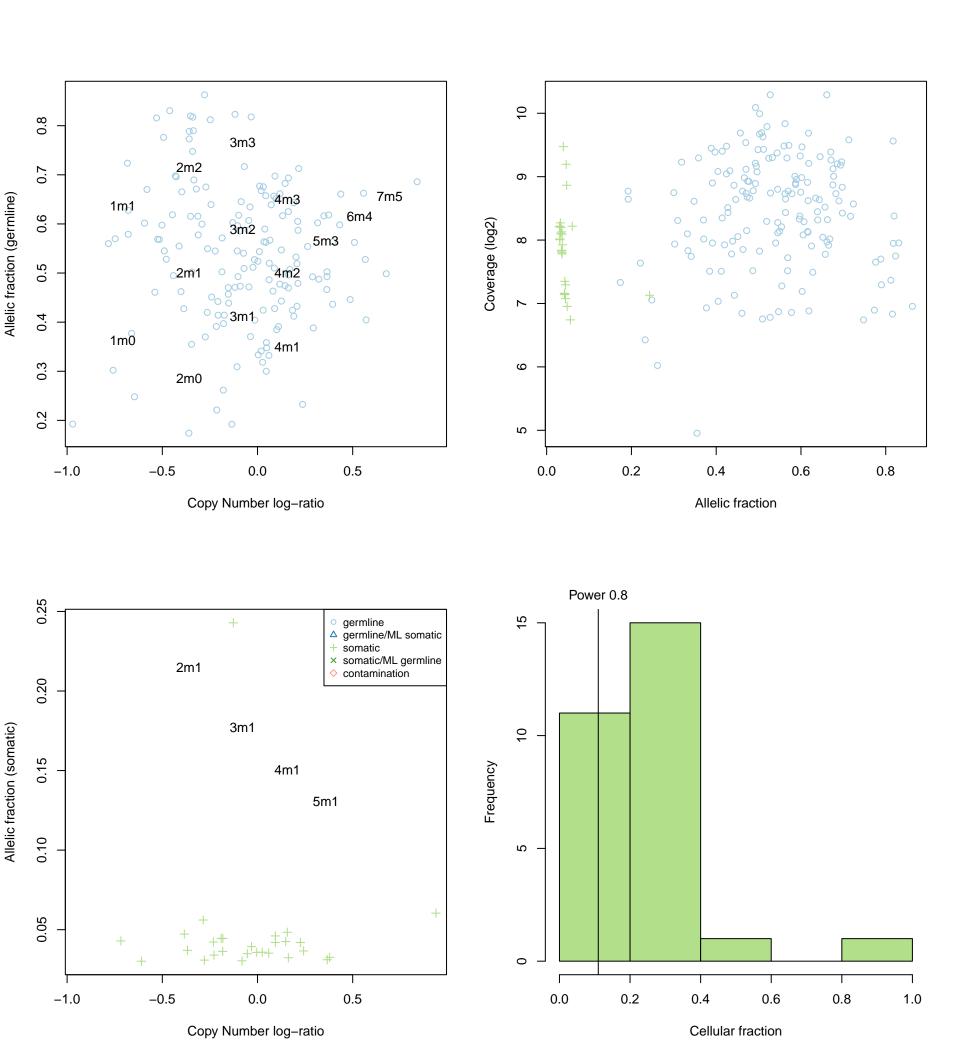
Purity: 0.43 Tumor ploidy: 3.313 3 0 2 5 6 7 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio

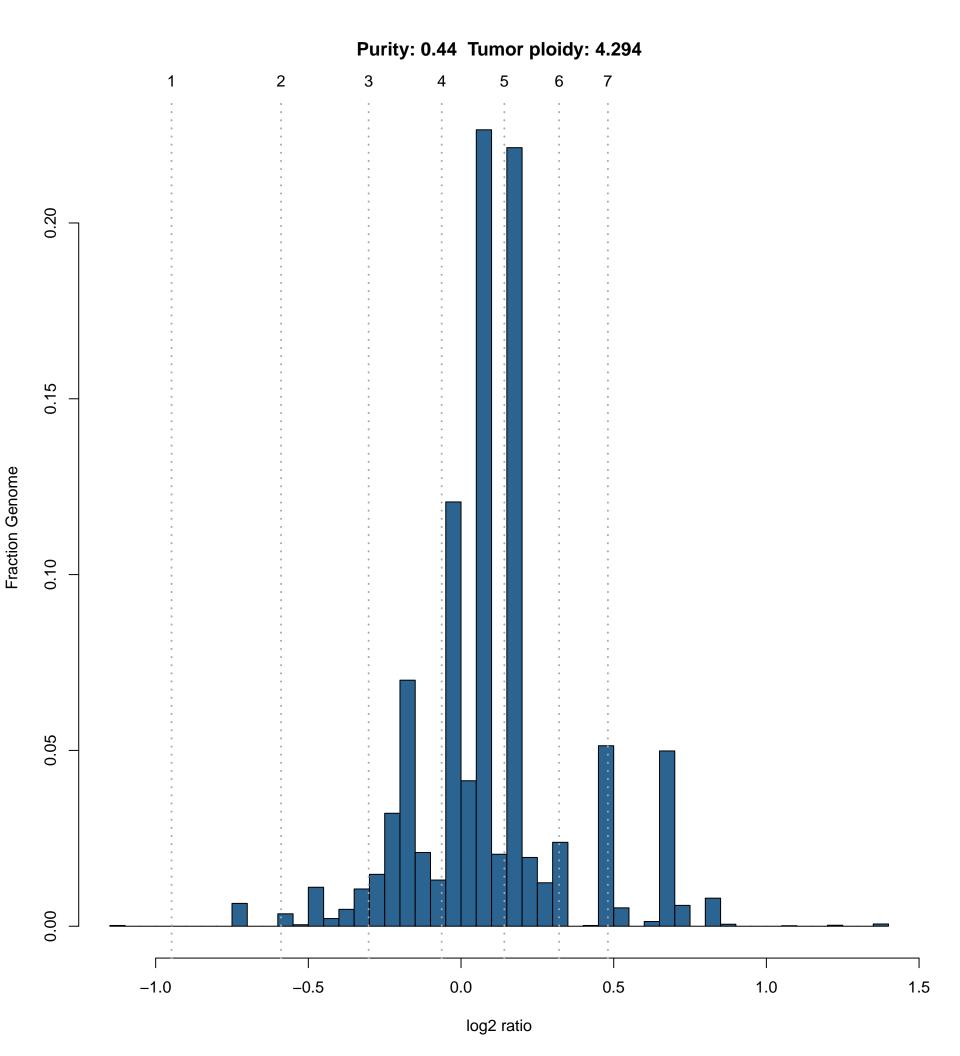


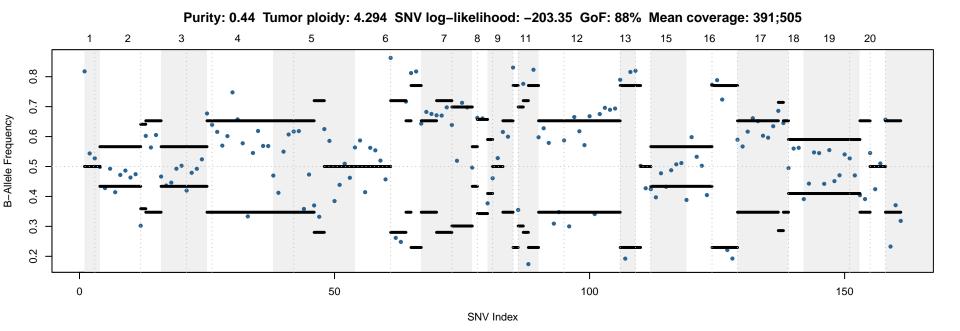
### SCNA-fit log-likelihood: -6833.87



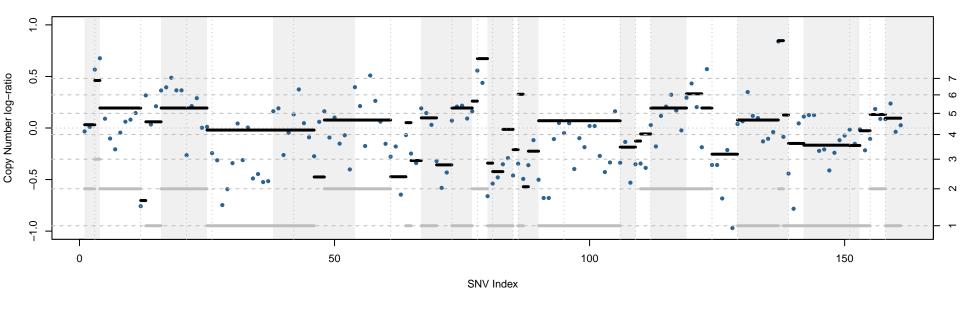


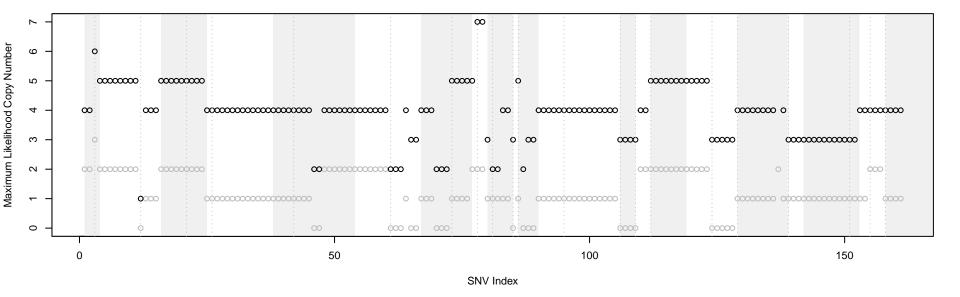


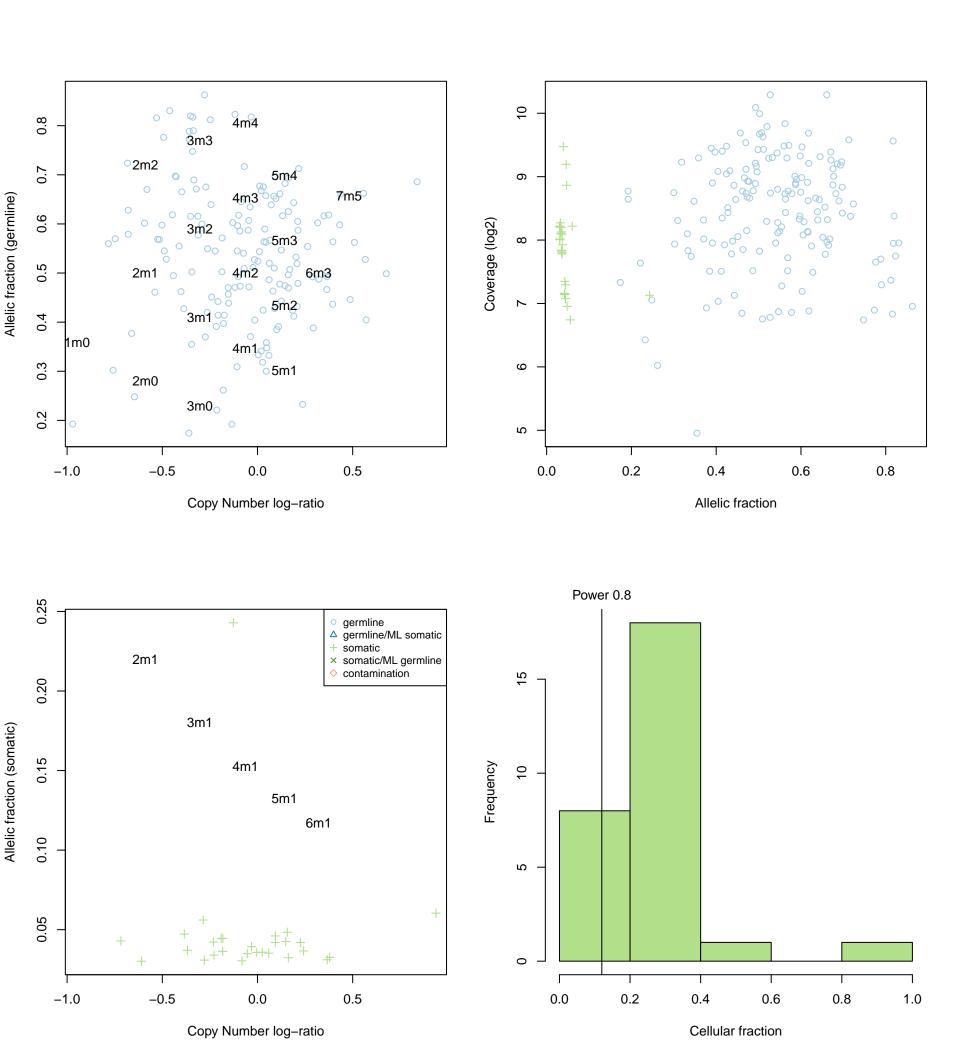


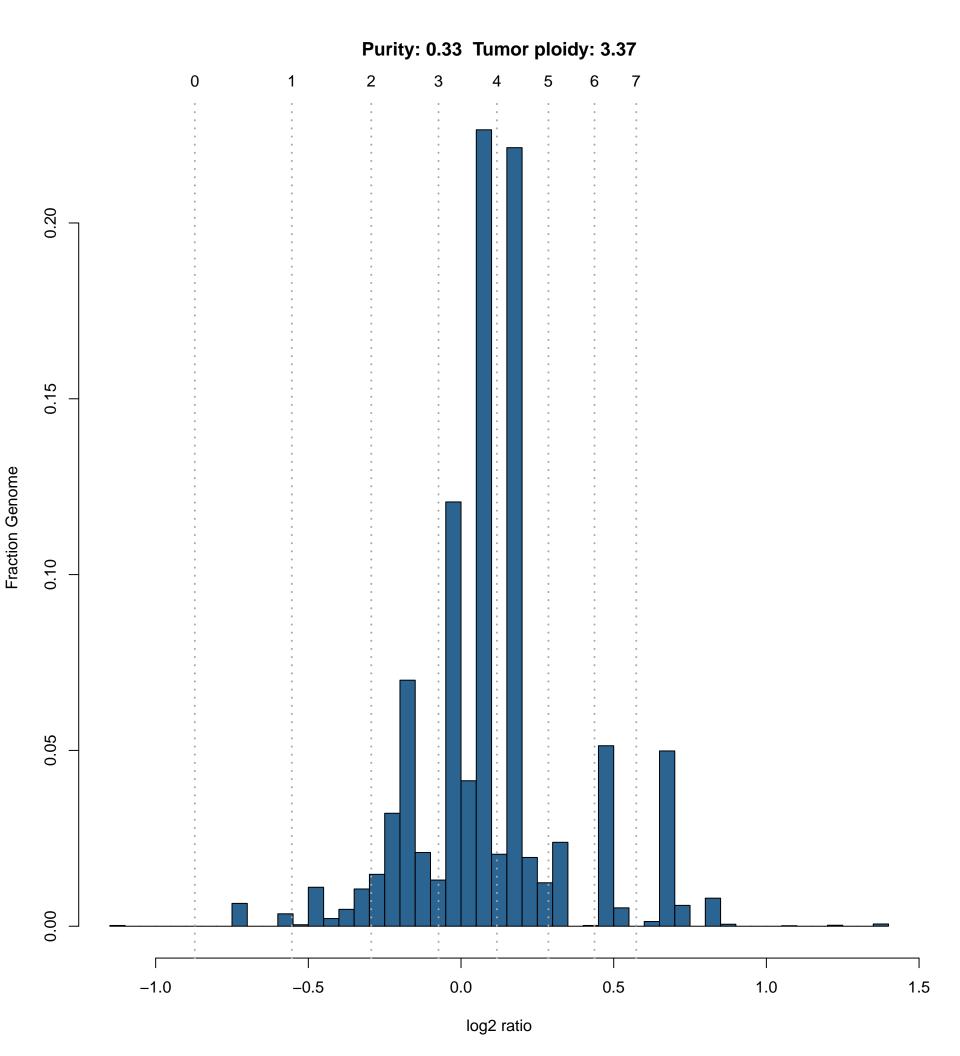


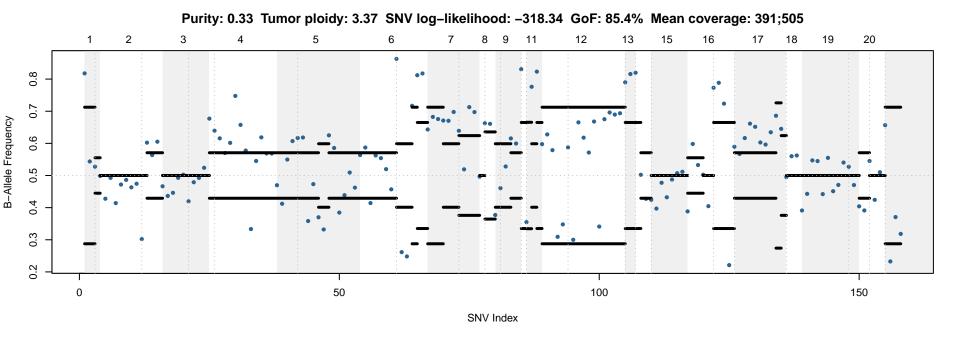
### SCNA-fit log-likelihood: -6915.49



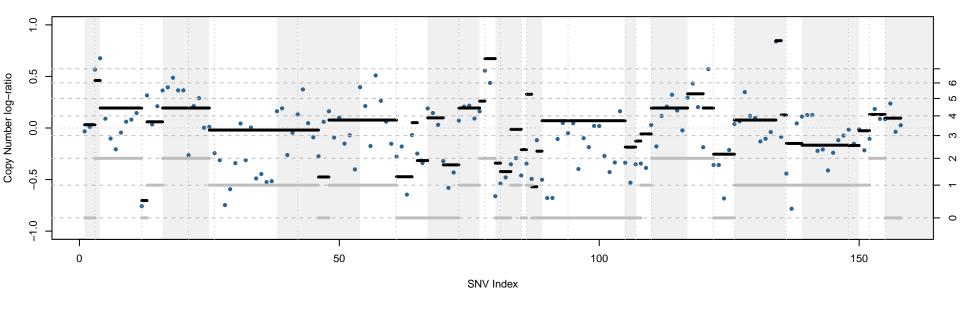


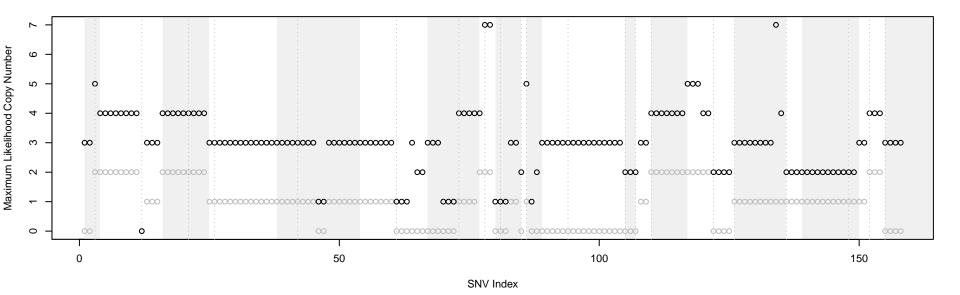


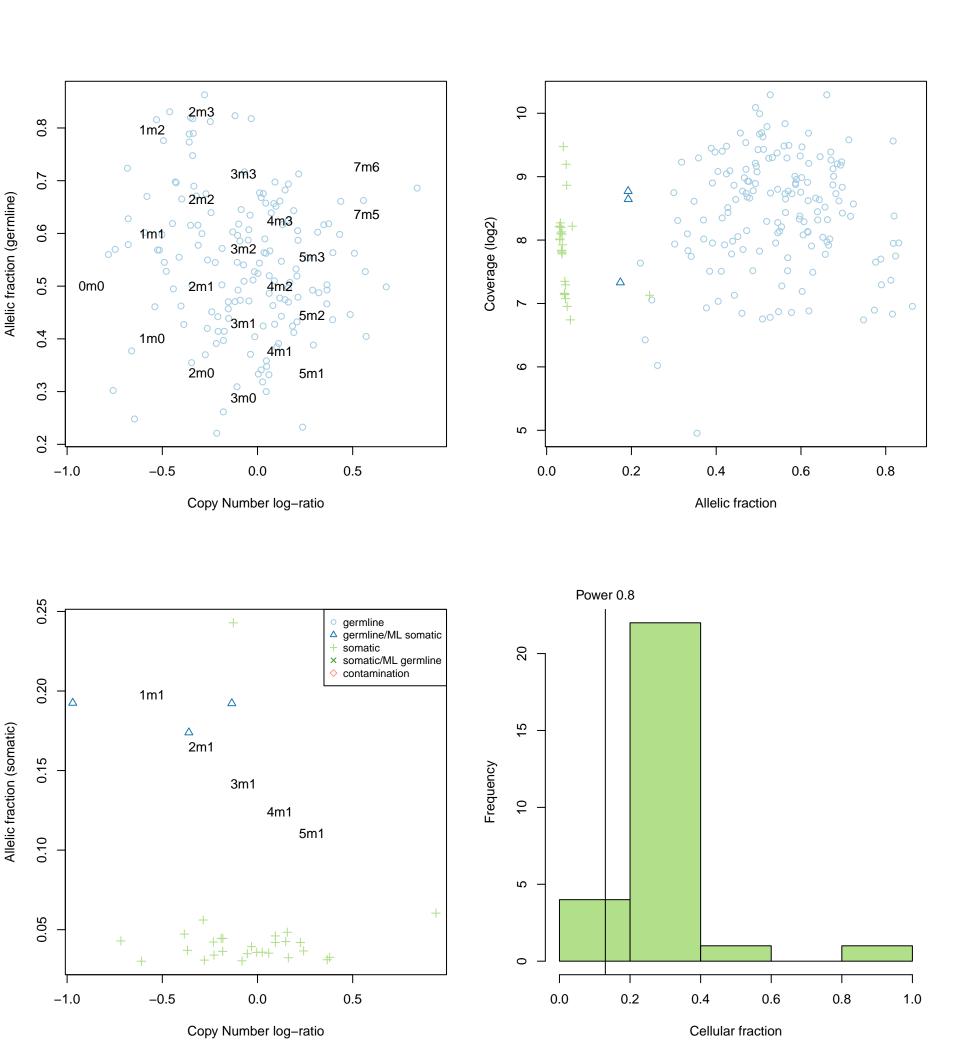




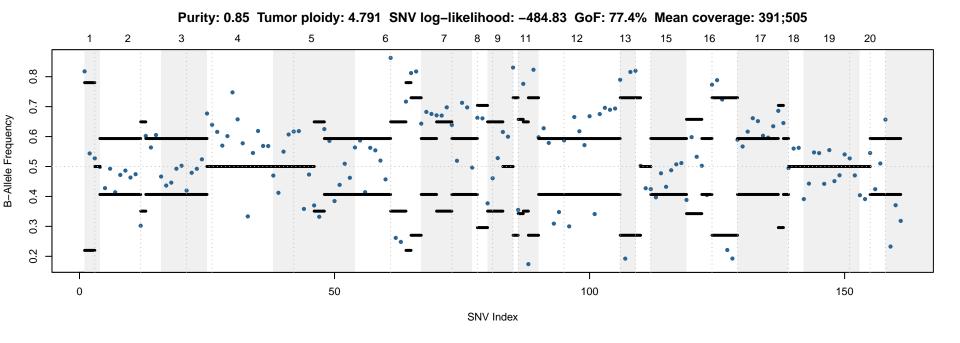
### SCNA-fit log-likelihood: -6806.56



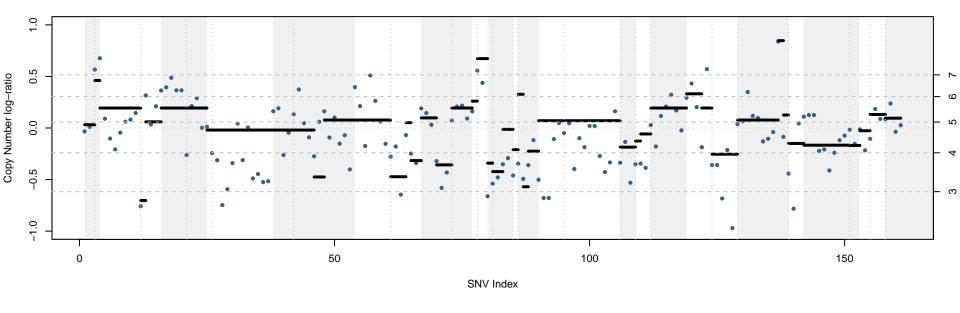


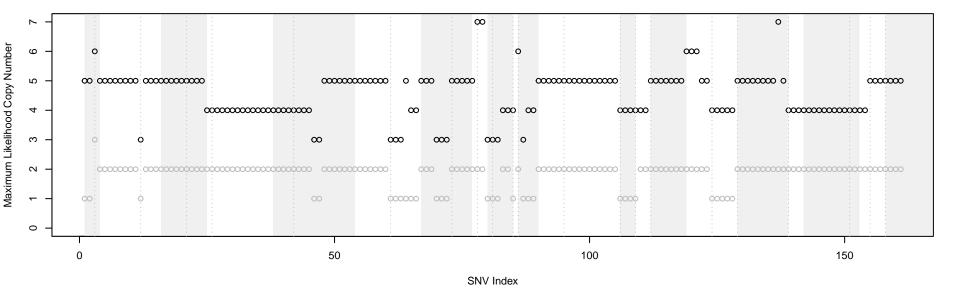


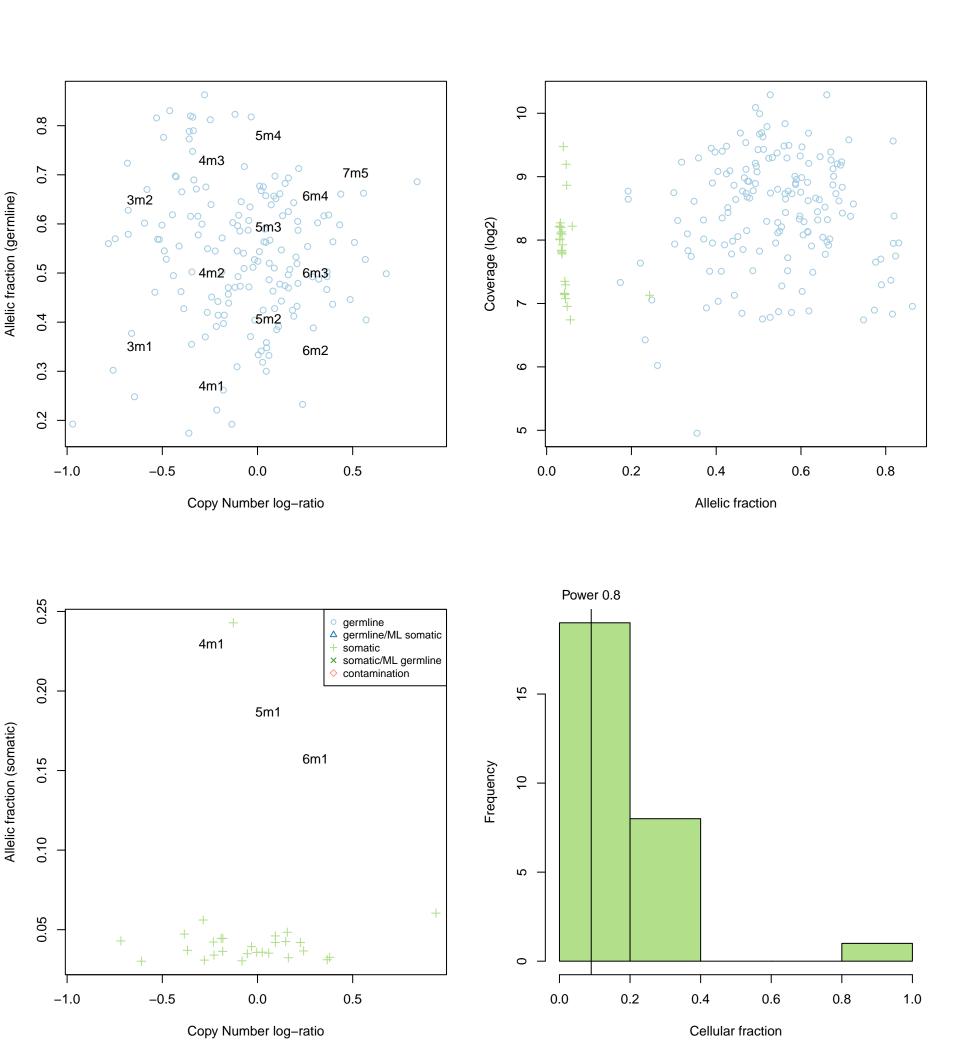
Purity: 0.85 Tumor ploidy: 4.791 2 3 6 7 5 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



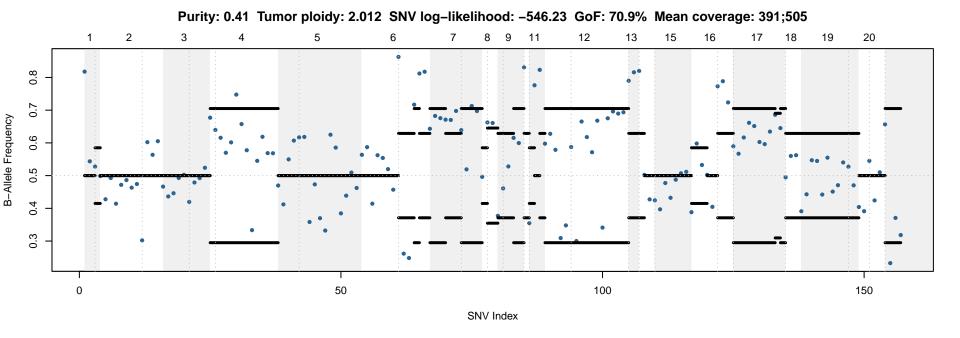
### SCNA-fit log-likelihood: -6978.51



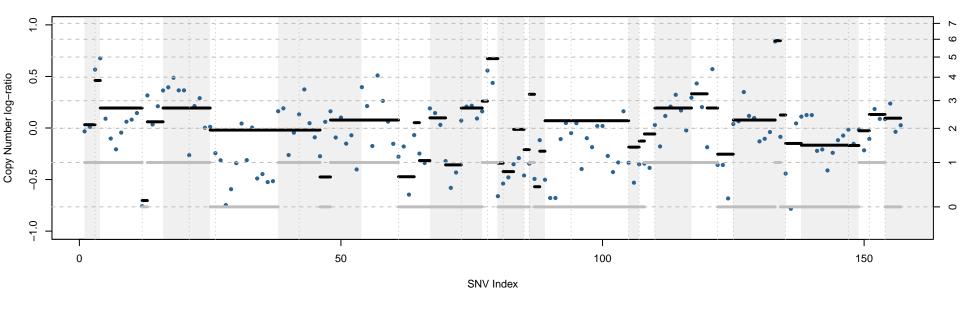


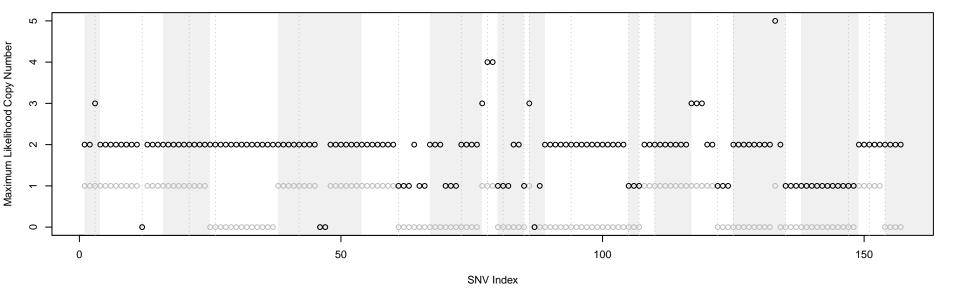


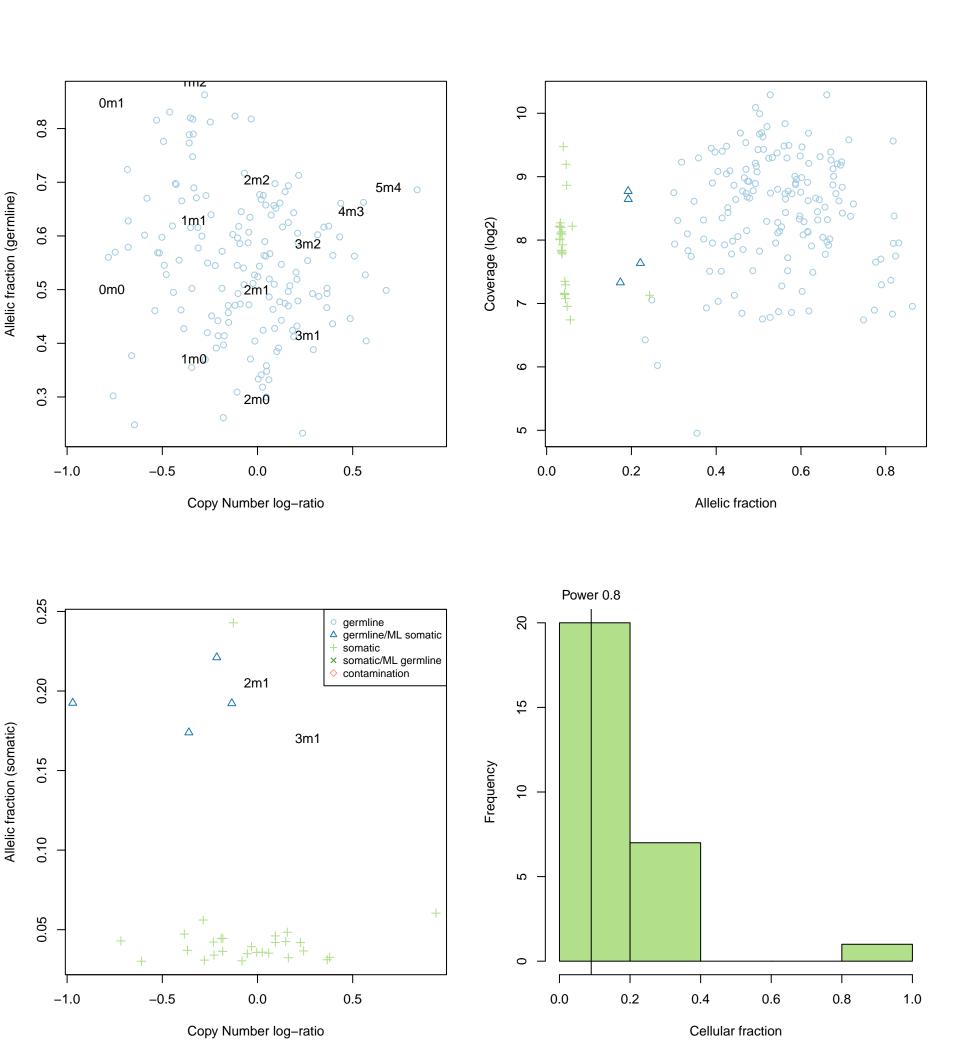
Purity: 0.41 Tumor ploidy: 2.012 0 3 5 6 7 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



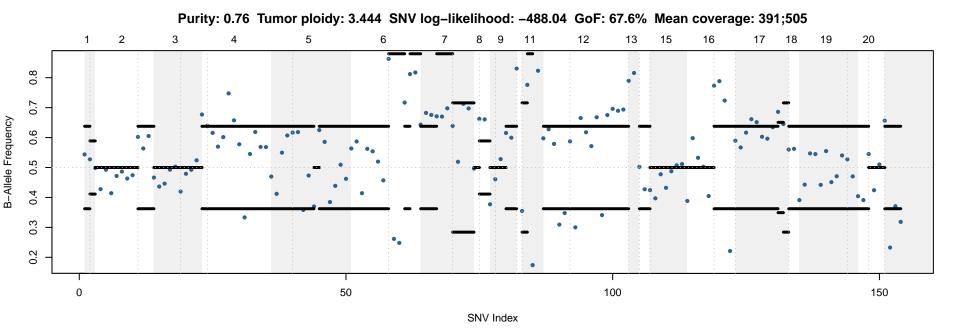
## SCNA-fit log-likelihood: -6956.62



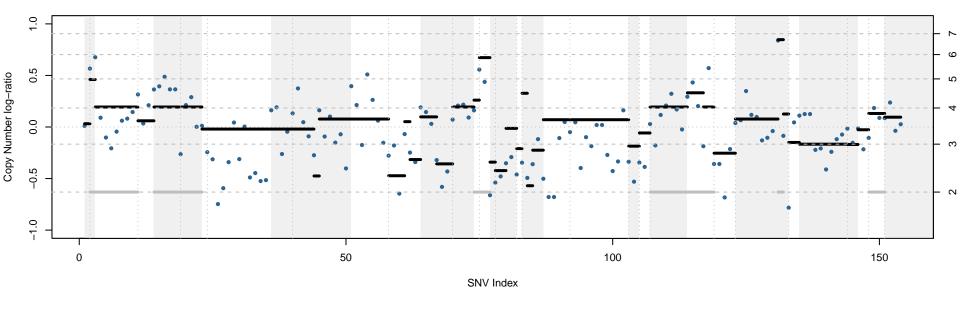


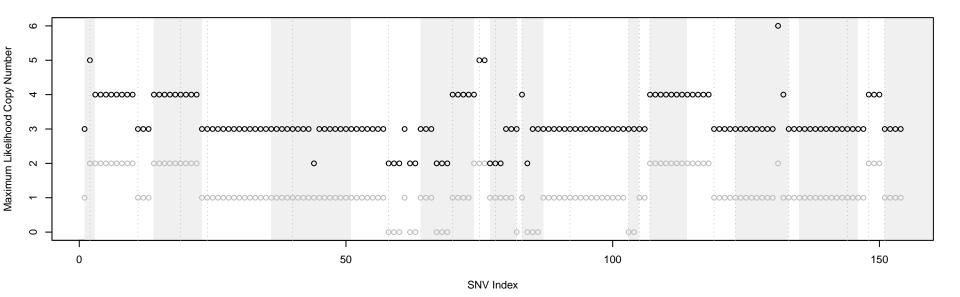


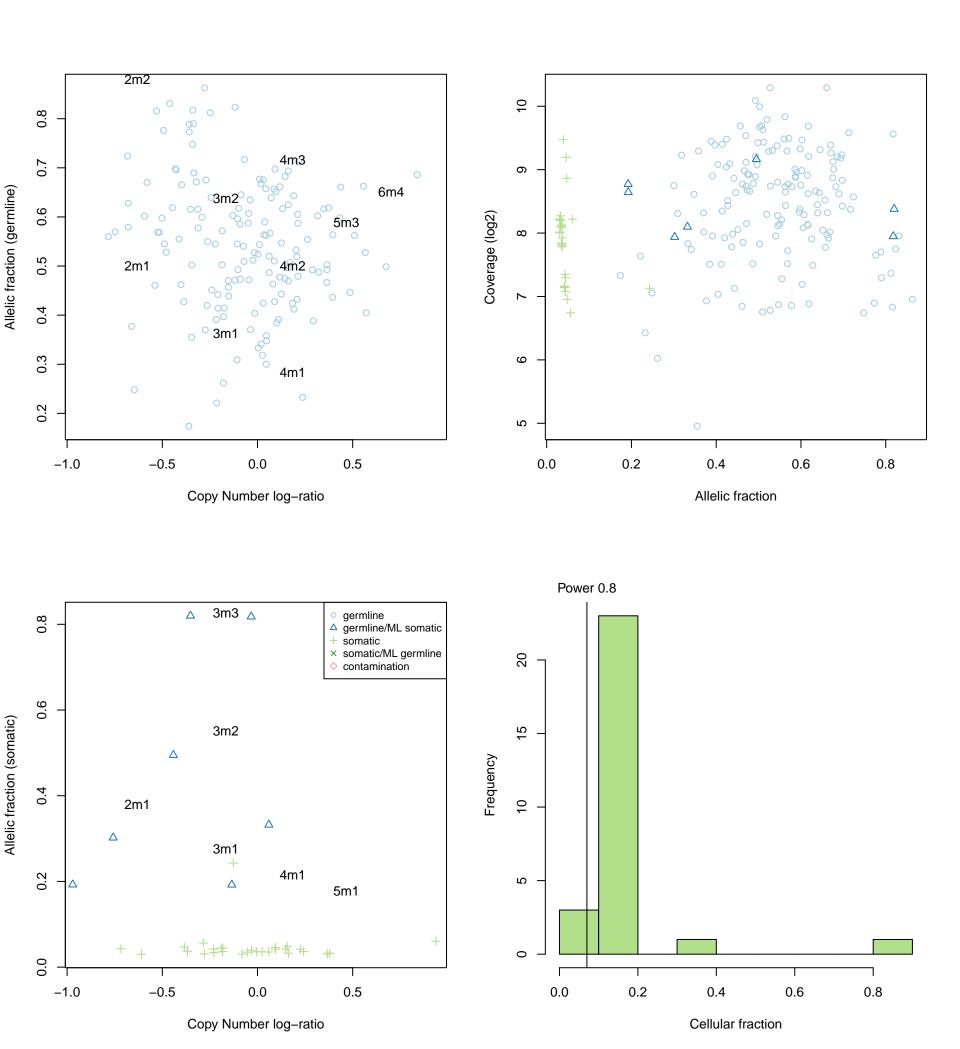
Purity: 0.76 Tumor ploidy: 3.444 2 5 6 7 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



## SCNA-fit log-likelihood: -7211.8

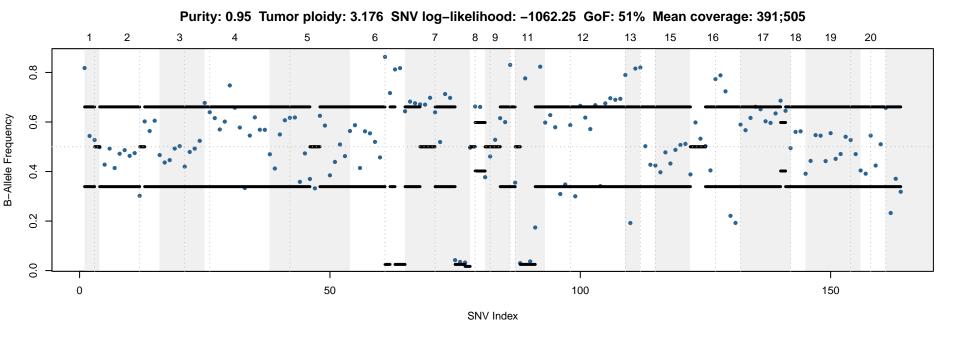






Purity: 0.95 Tumor ploidy: 3.176 2 6 3 5 7 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5

log2 ratio



# SCNA-fit log-likelihood: -7398.55

