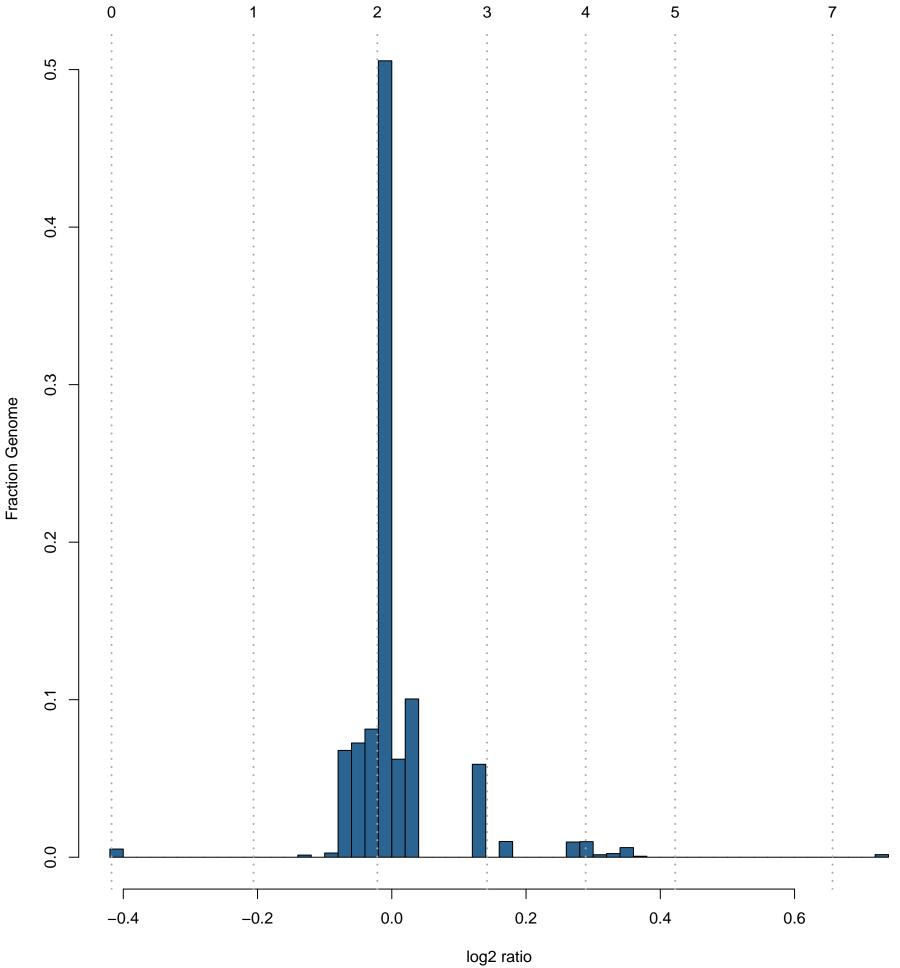
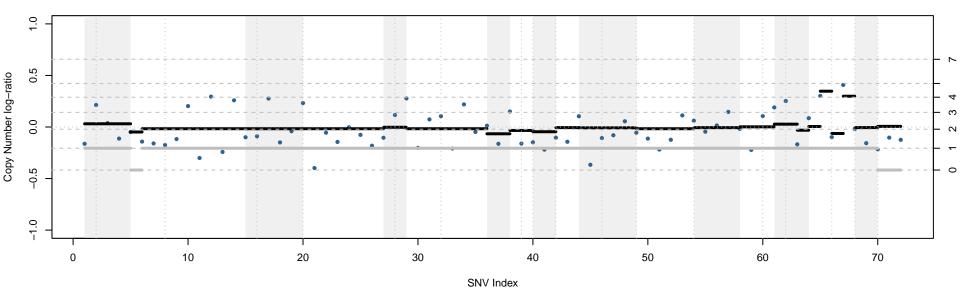
Purity: 0.24 Tumor ploidy: 2.125

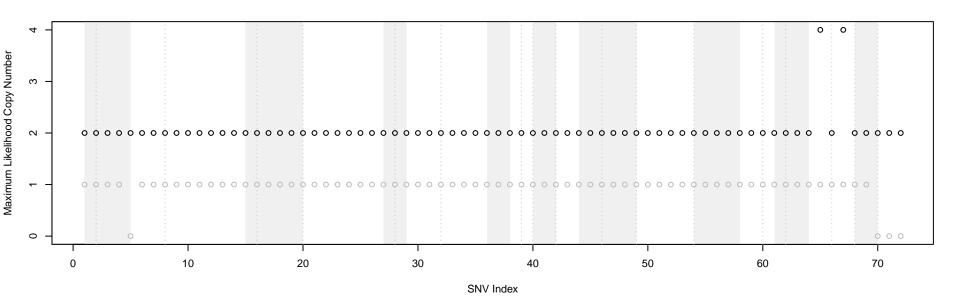


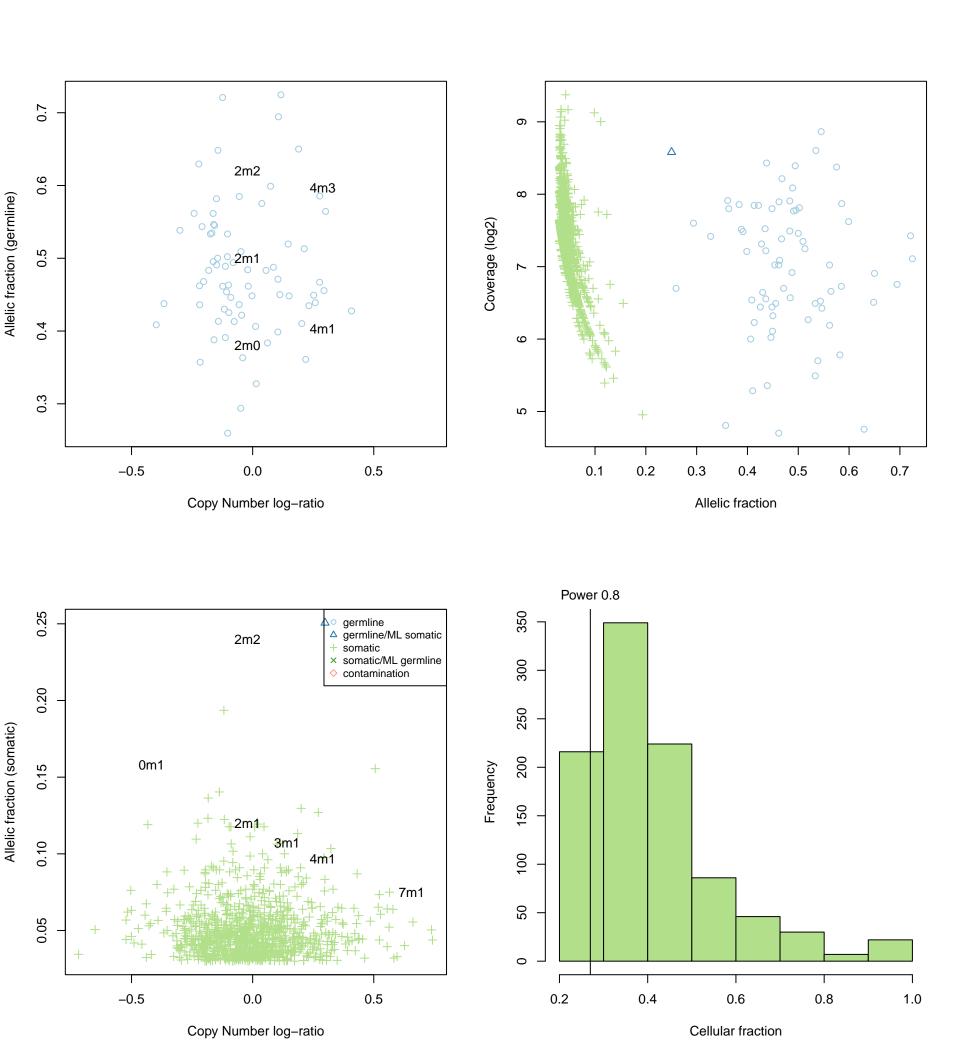
Purity: 0.24 Tumor ploidy: 2.125 SNV log-likelihood: 921.8 GoF: 87.3% Mean coverage: 149;174 5 10 11 19 20 0.7 9.0 B-Allele Frequency 0.5 9.0 0.3 0 10 20 30 40 50 60 70

## SCNA-fit log-likelihood: -4177.71

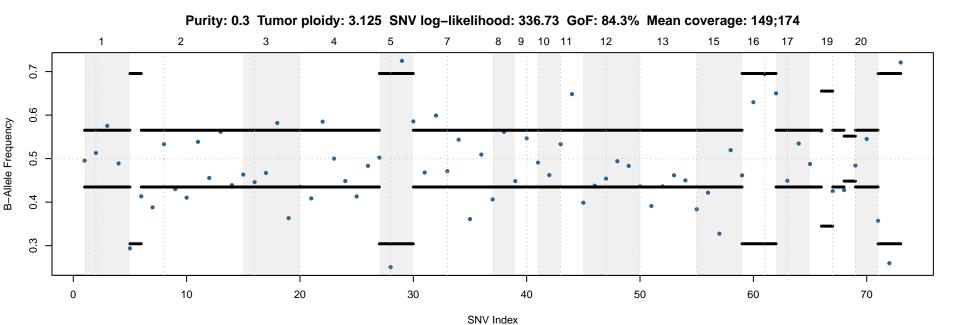
SNV Index



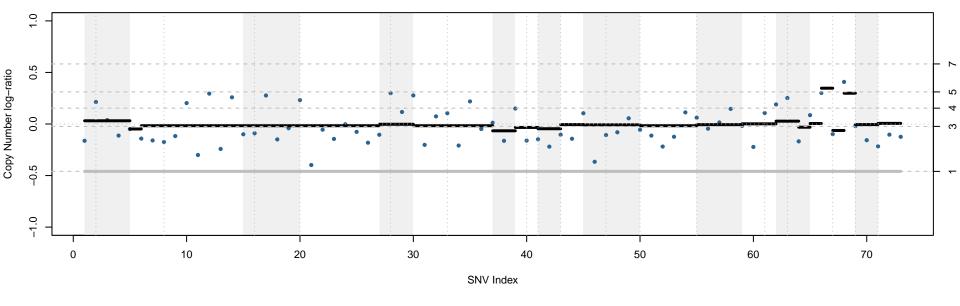


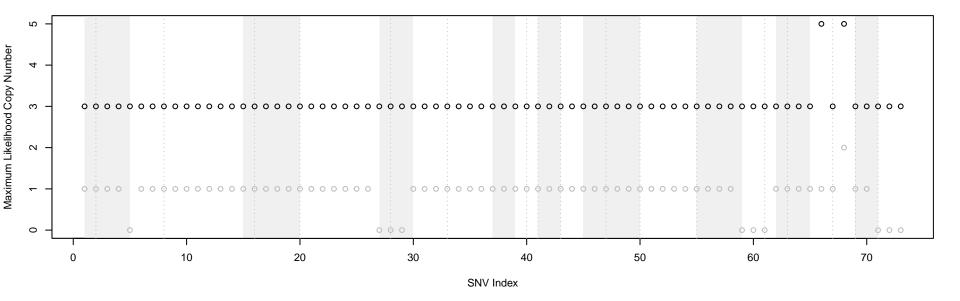


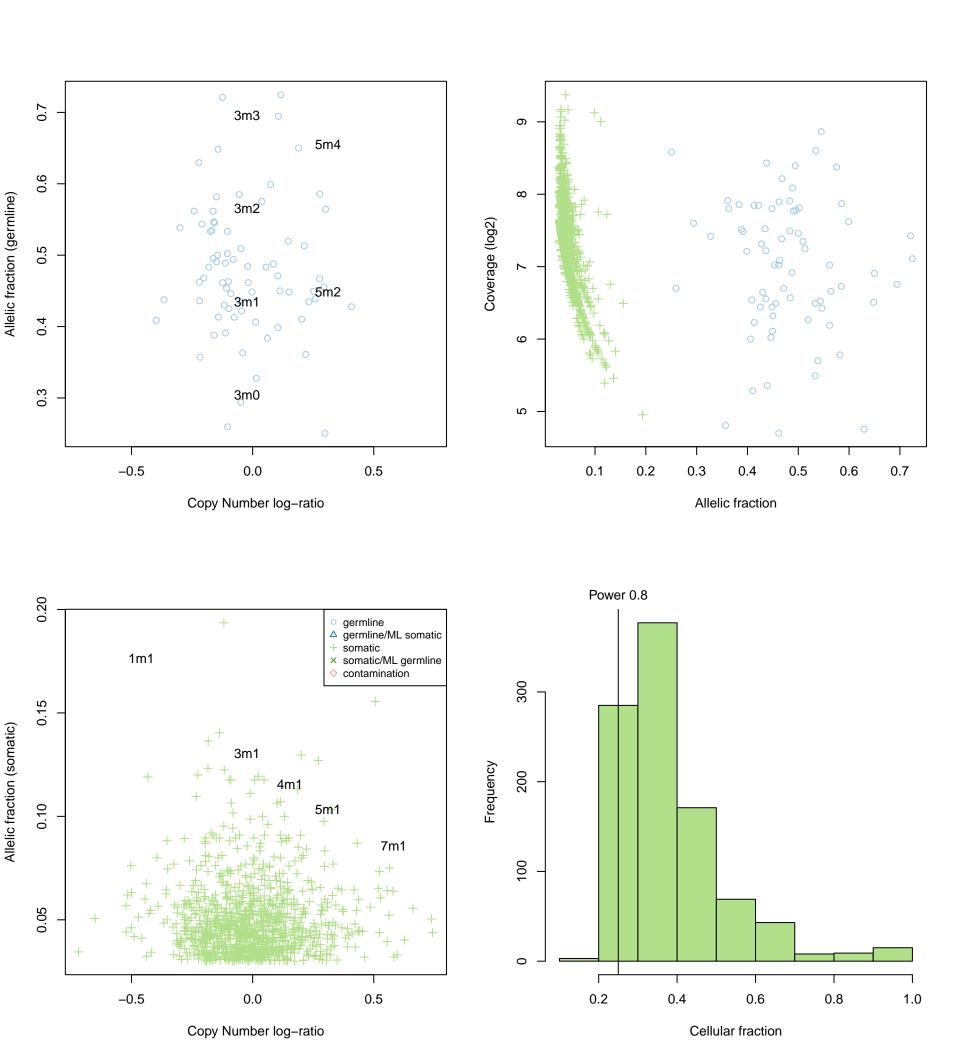
Purity: 0.3 Tumor ploidy: 3.125 3 7 0.5 0.3 Fraction Genome 0.2 0.1 0.0 -0.4 -0.2 0.0 0.2 0.4 0.6 log2 ratio



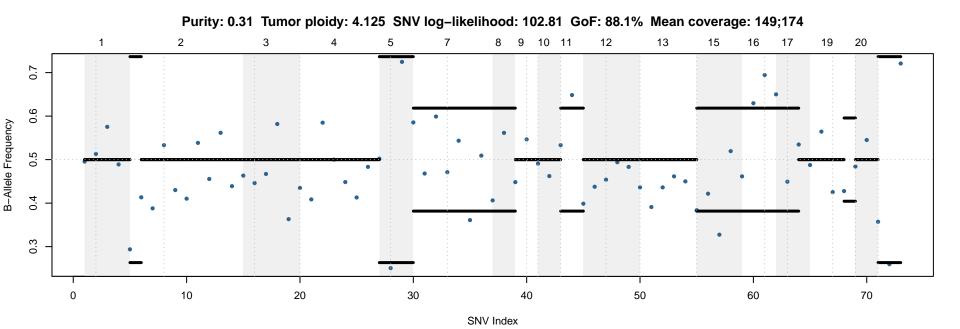
### SCNA-fit log-likelihood: -4186.52



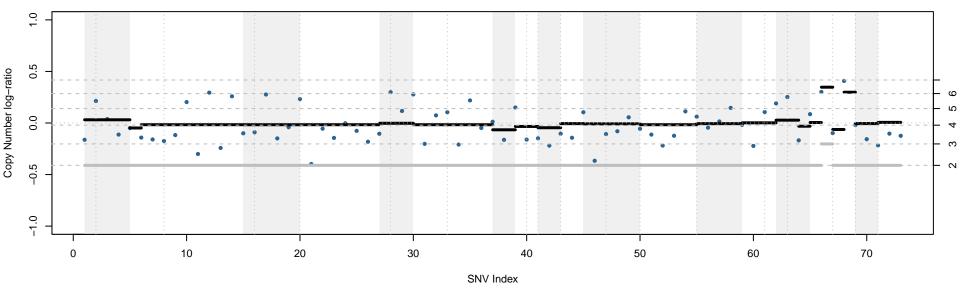


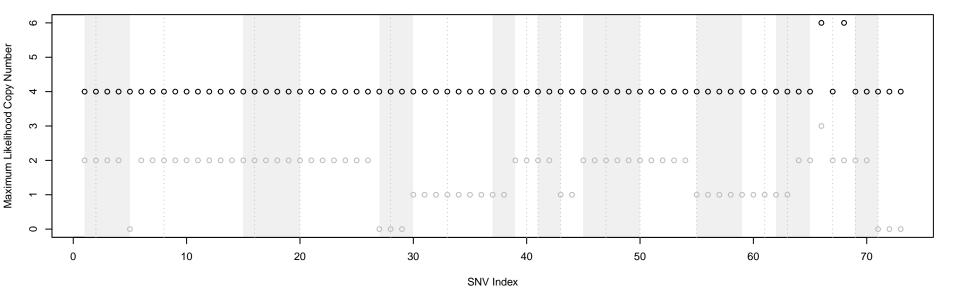


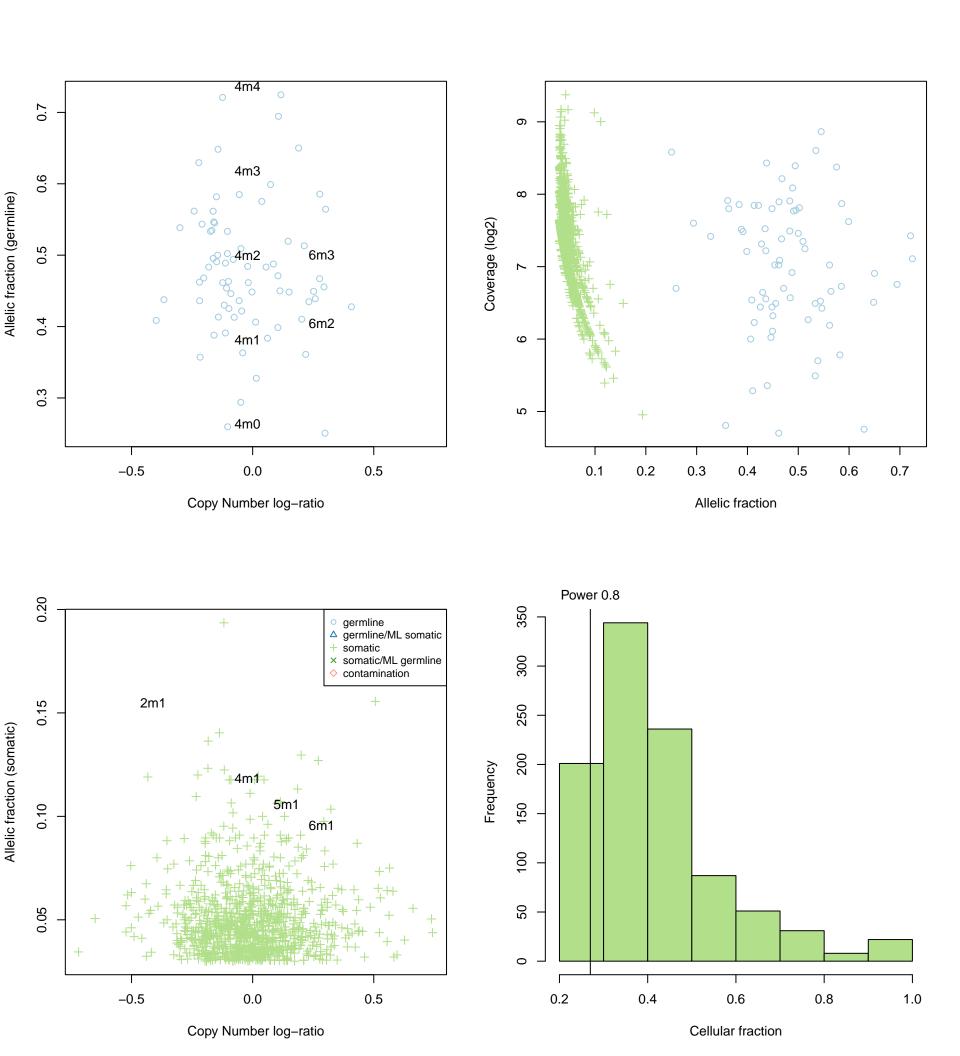
Purity: 0.31 Tumor ploidy: 4.125 2 3 6 7 5 0.5 Fraction Genome 0.2 0.1 0.0 -0.4 -0.2 0.0 0.2 0.4 0.6 log2 ratio



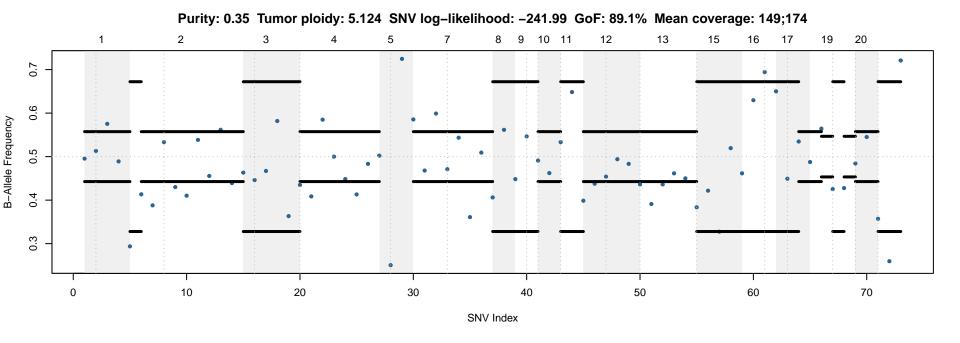
## SCNA-fit log-likelihood: -4230.73



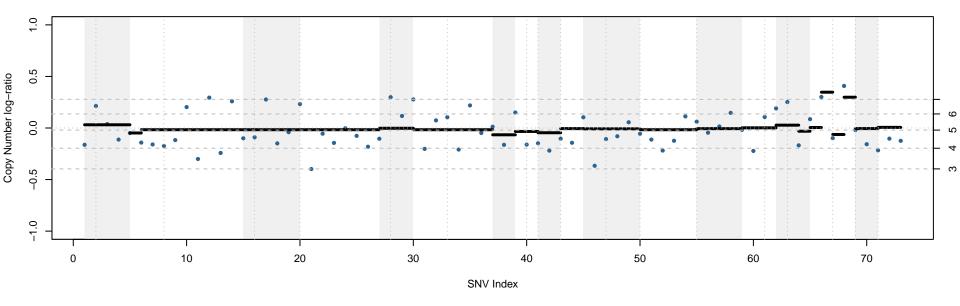


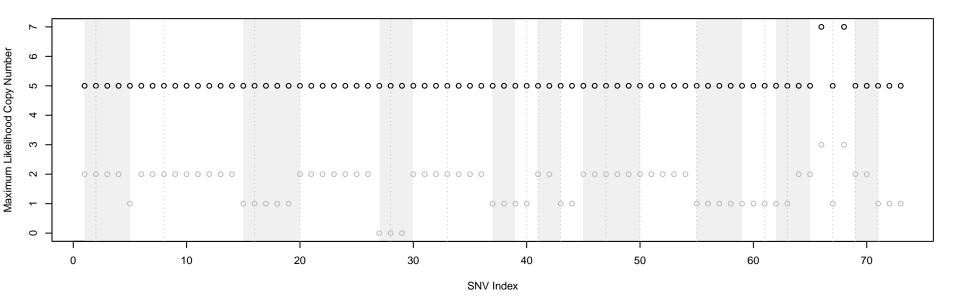


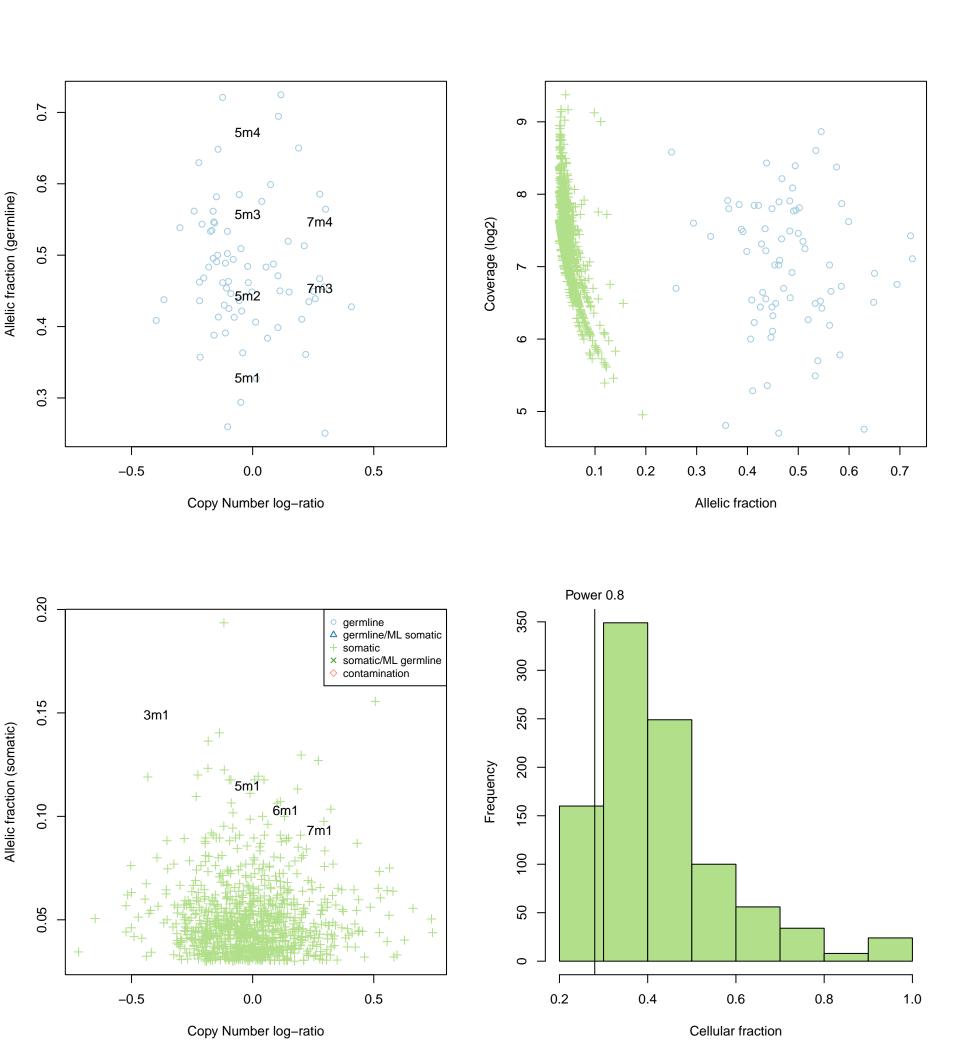
Purity: 0.35 Tumor ploidy: 5.124 3 5 6 0.5 0.3 Fraction Genome 0.2 0.1 0.0 -0.4 -0.2 0.0 0.2 0.4 0.6 log2 ratio



# SCNA-fit log-likelihood: -4231.23

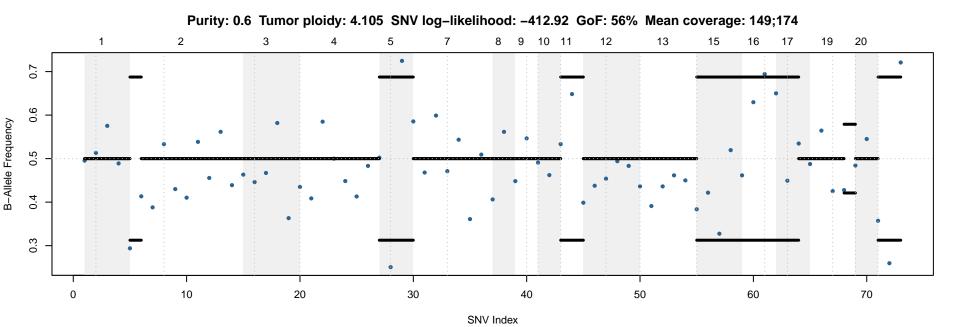




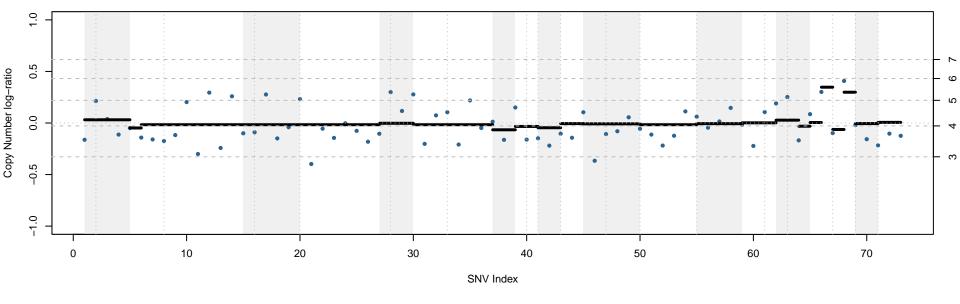


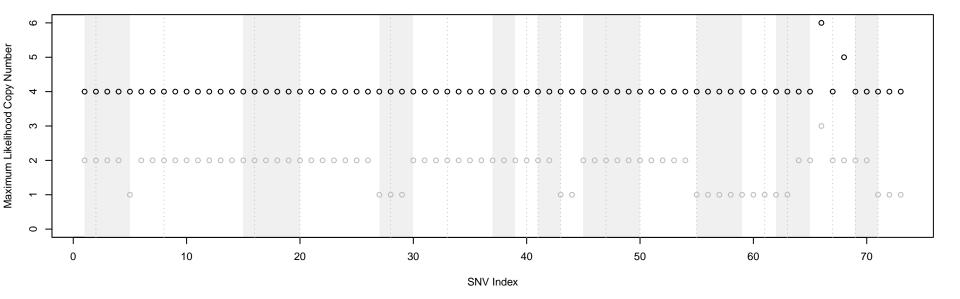
Purity: 0.6 Tumor ploidy: 4.105 3 6 7 Fraction Genome 0.1 0.0 -0.4 -0.2 0.0 0.2 0.4 0.6

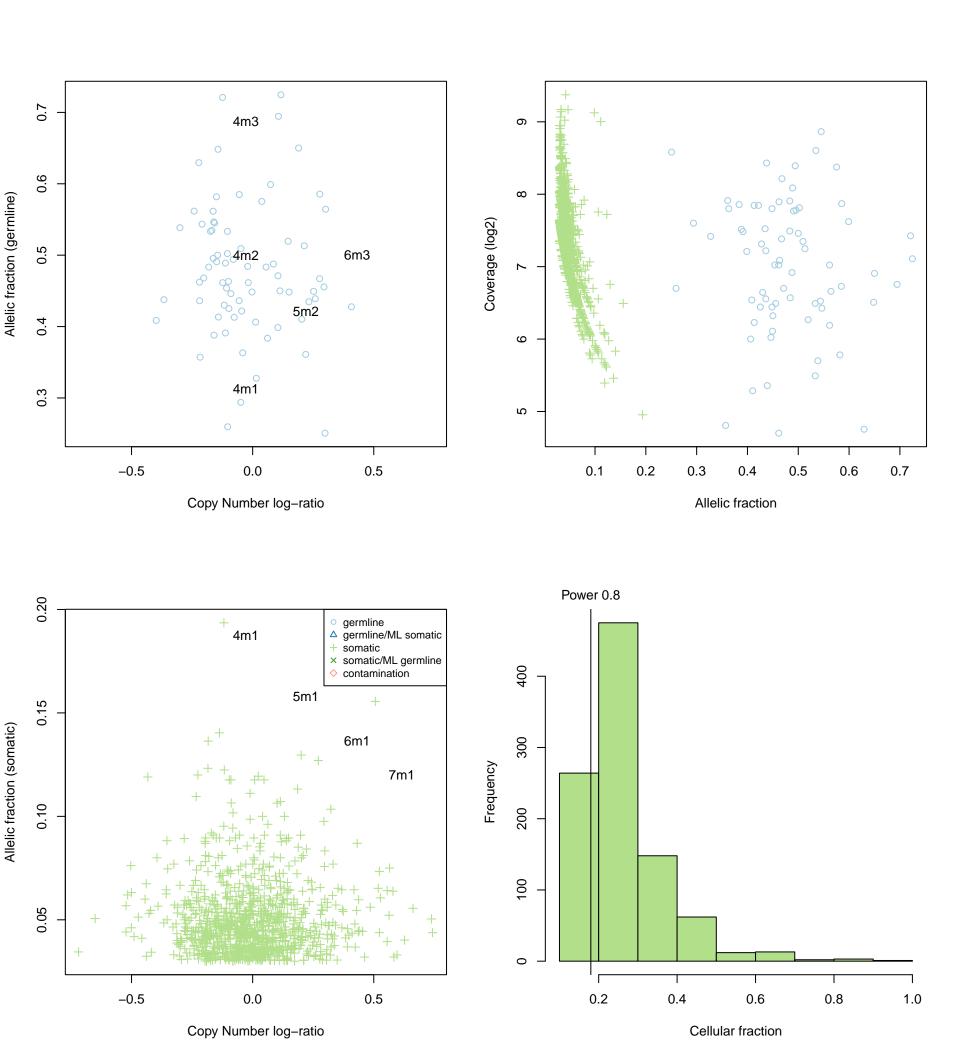
log2 ratio



SCNA-fit log-likelihood: -4264.17

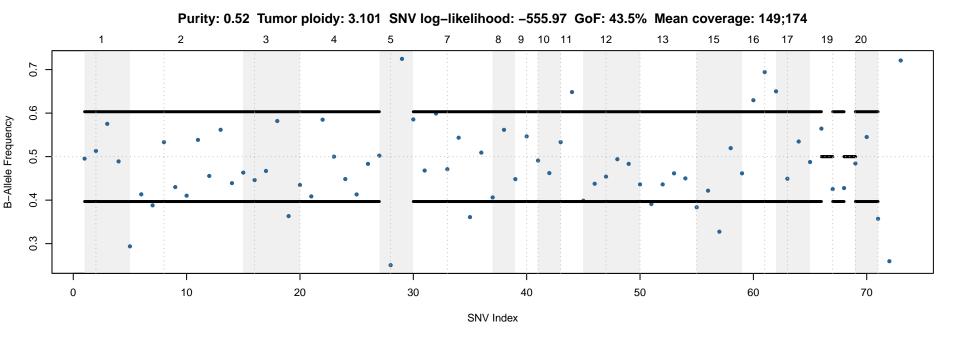




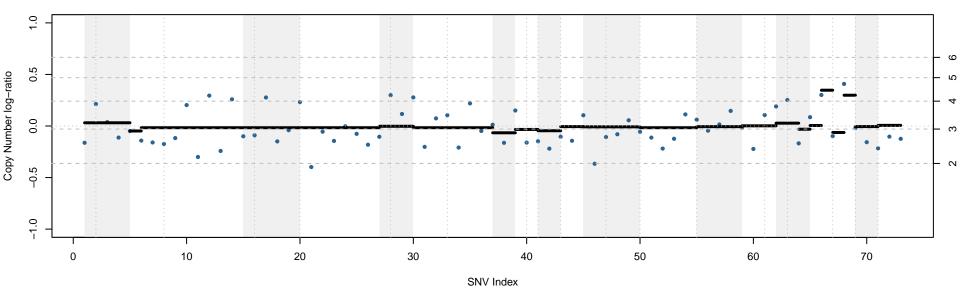


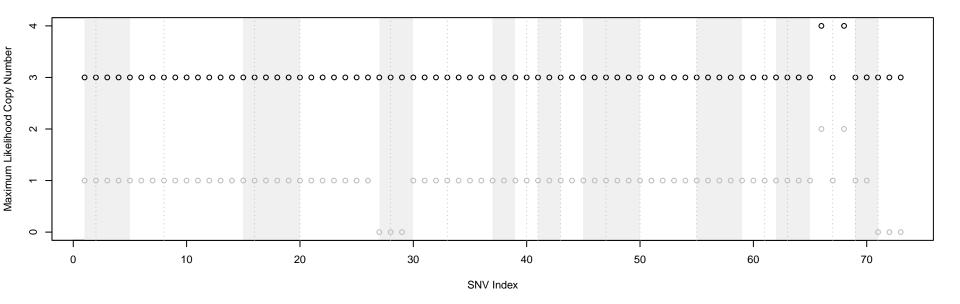
Purity: 0.52 Tumor ploidy: 3.101 2 3 5 6 0.3 Fraction Genome 0.2 0.1 0.0 -0.4 -0.2 0.0 0.2 0.4 0.6

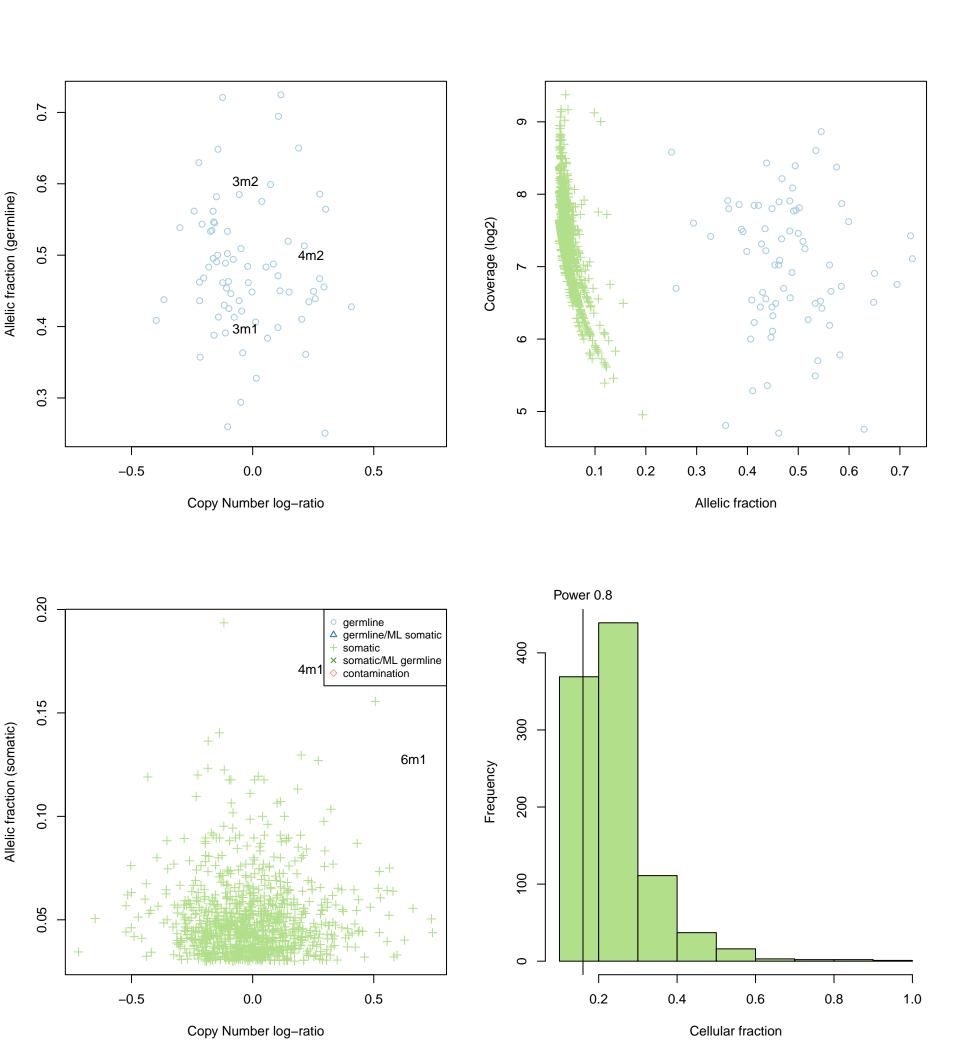
log2 ratio



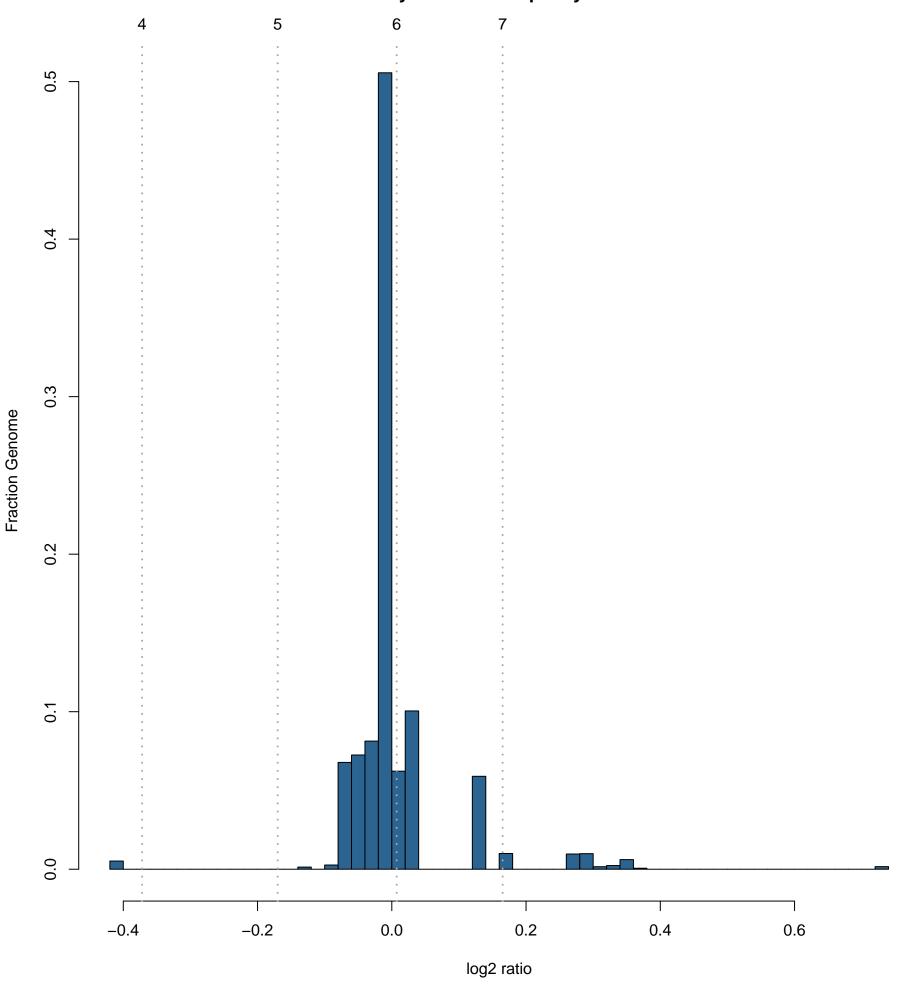
### SCNA-fit log-likelihood: -4292.03

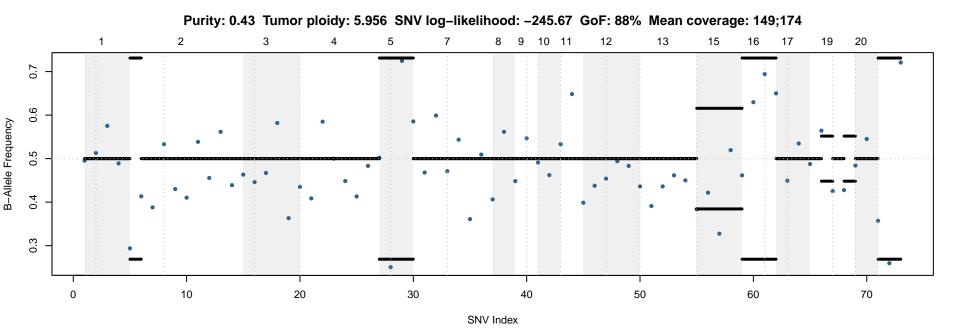




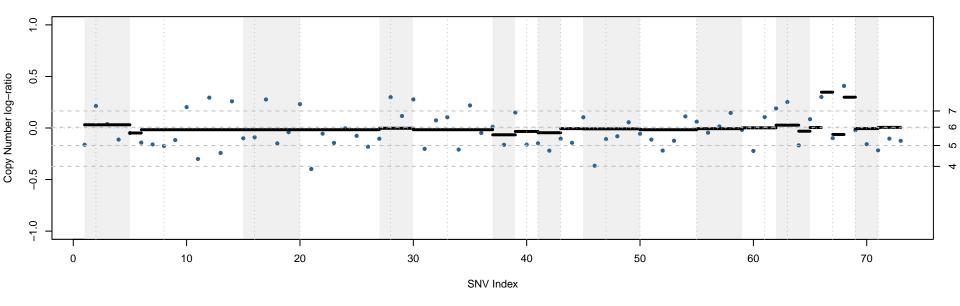


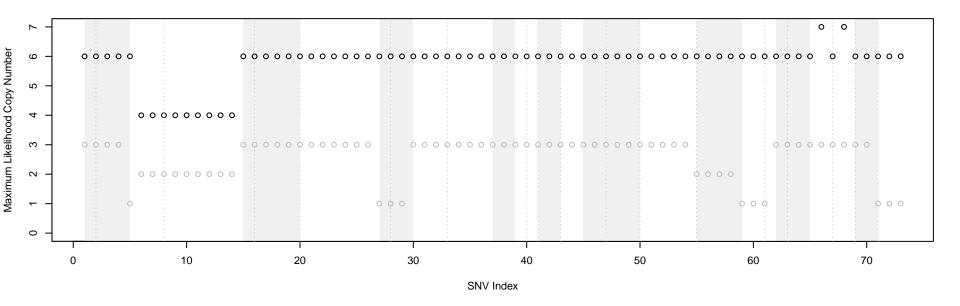
Purity: 0.43 Tumor ploidy: 5.956

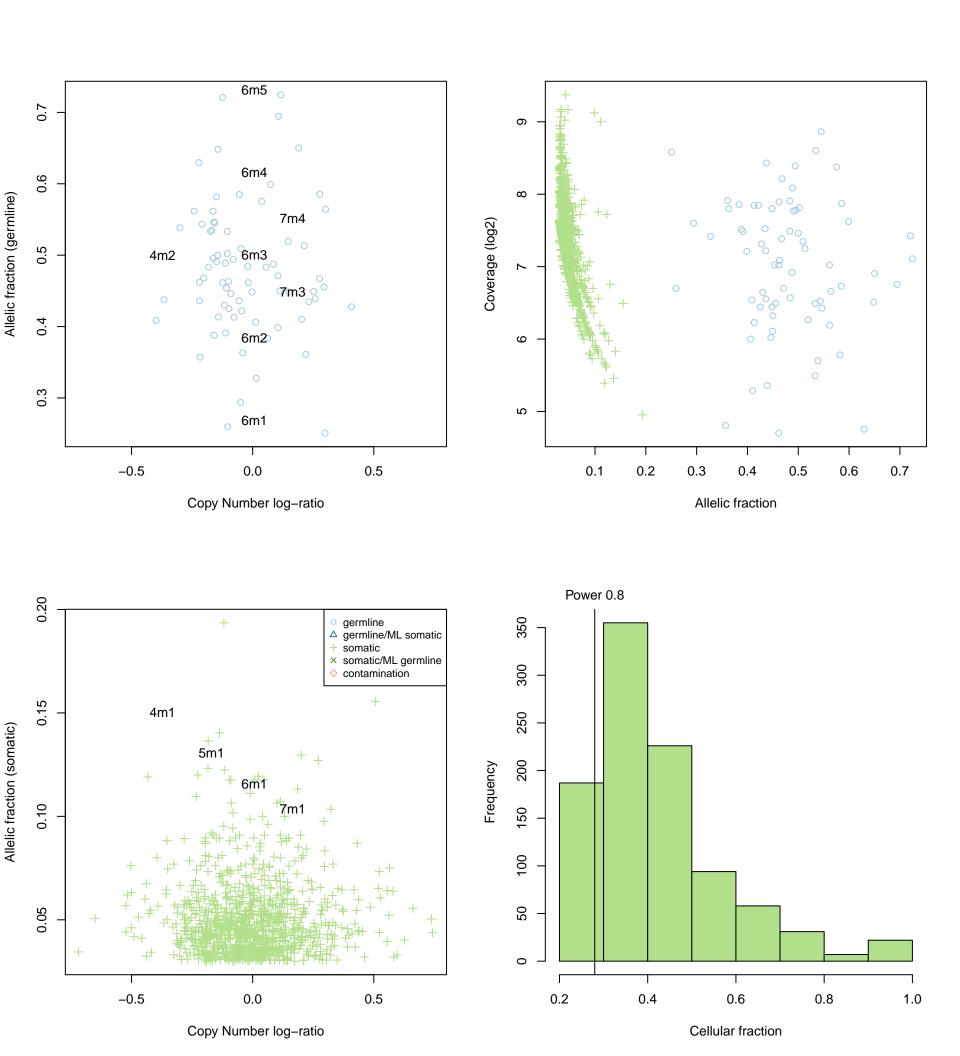




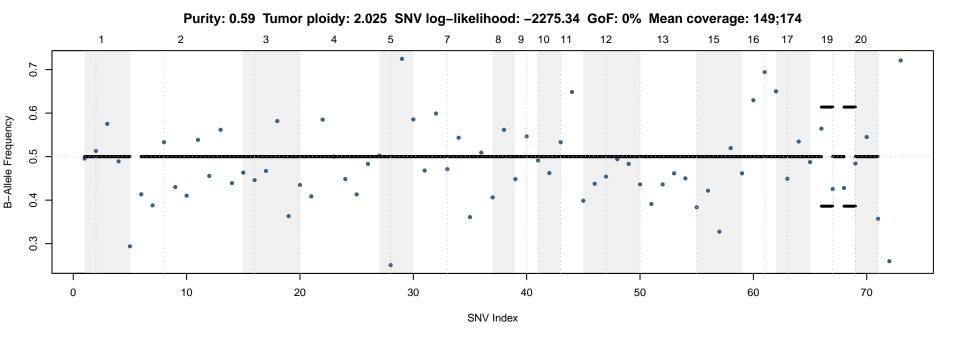
### SCNA-fit log-likelihood: -5258.62



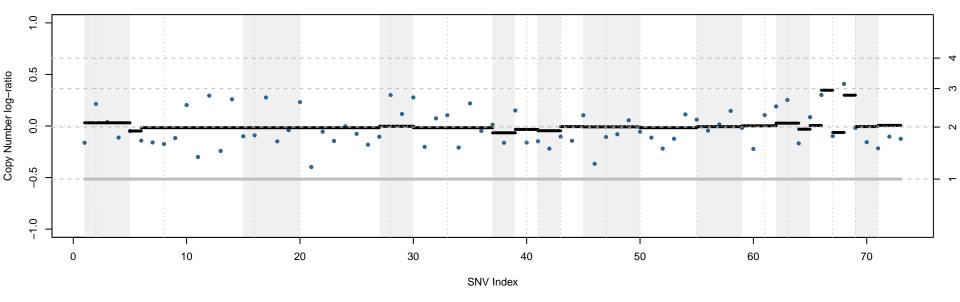


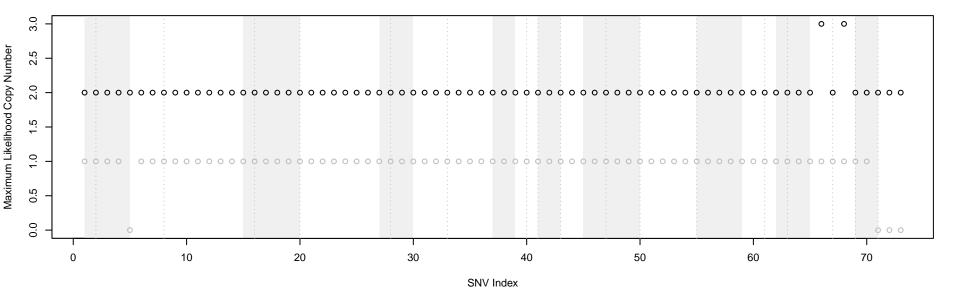


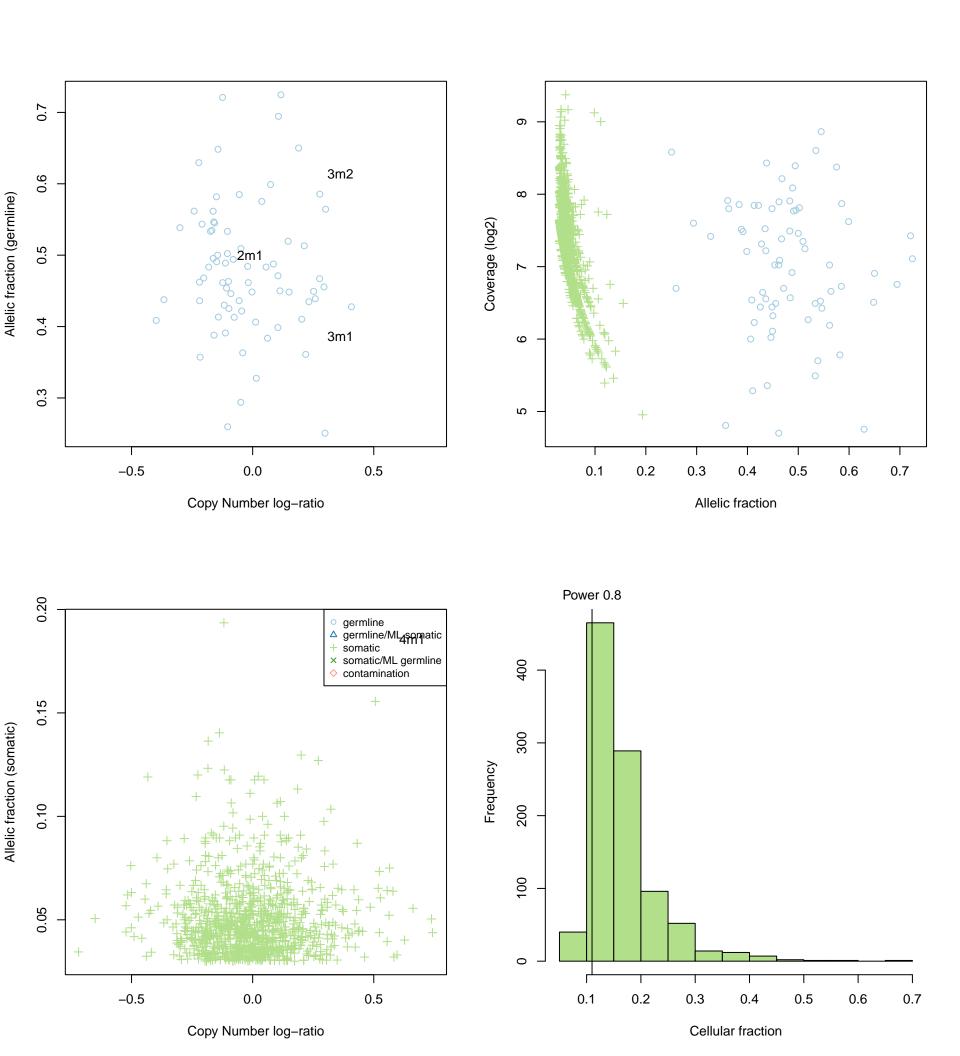
Purity: 0.59 Tumor ploidy: 2.025 3 Fraction Genome 0.1 0.0 -0.4 -0.2 0.0 0.2 0.4 0.6 log2 ratio



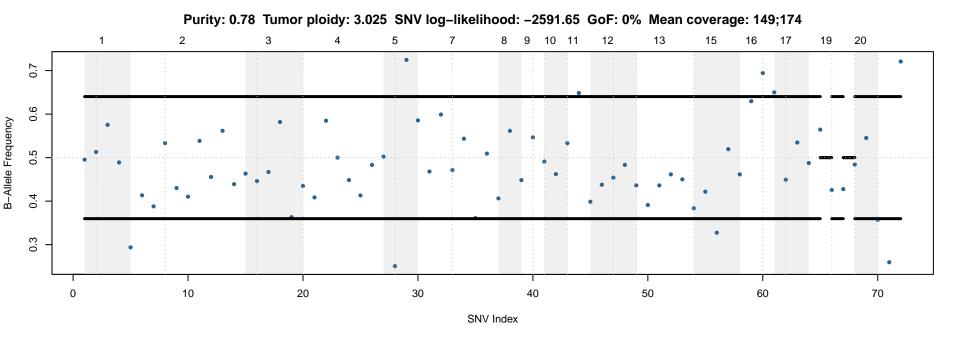
# SCNA-fit log-likelihood: -4381.9







Purity: 0.78 Tumor ploidy: 3.025 5 Fraction Genome 0.1 0.0 -0.4 -0.2 0.0 0.2 0.4 0.6 log2 ratio



## SCNA-fit log-likelihood: -4373.33

