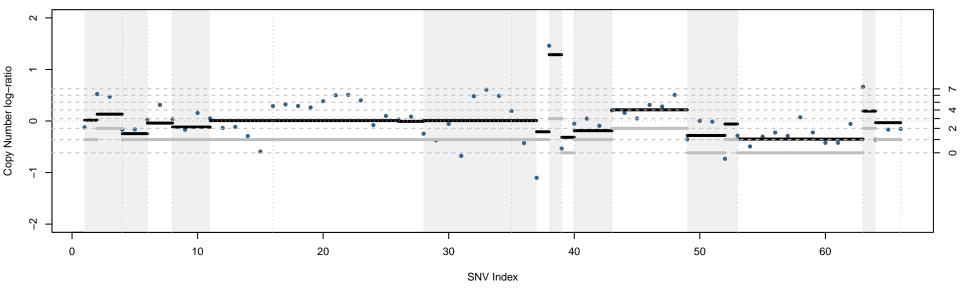
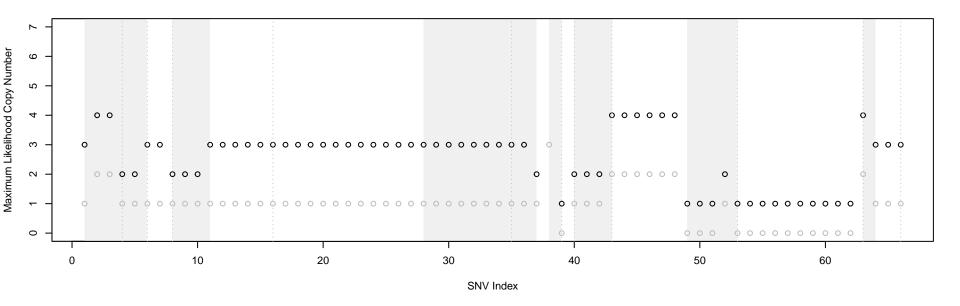
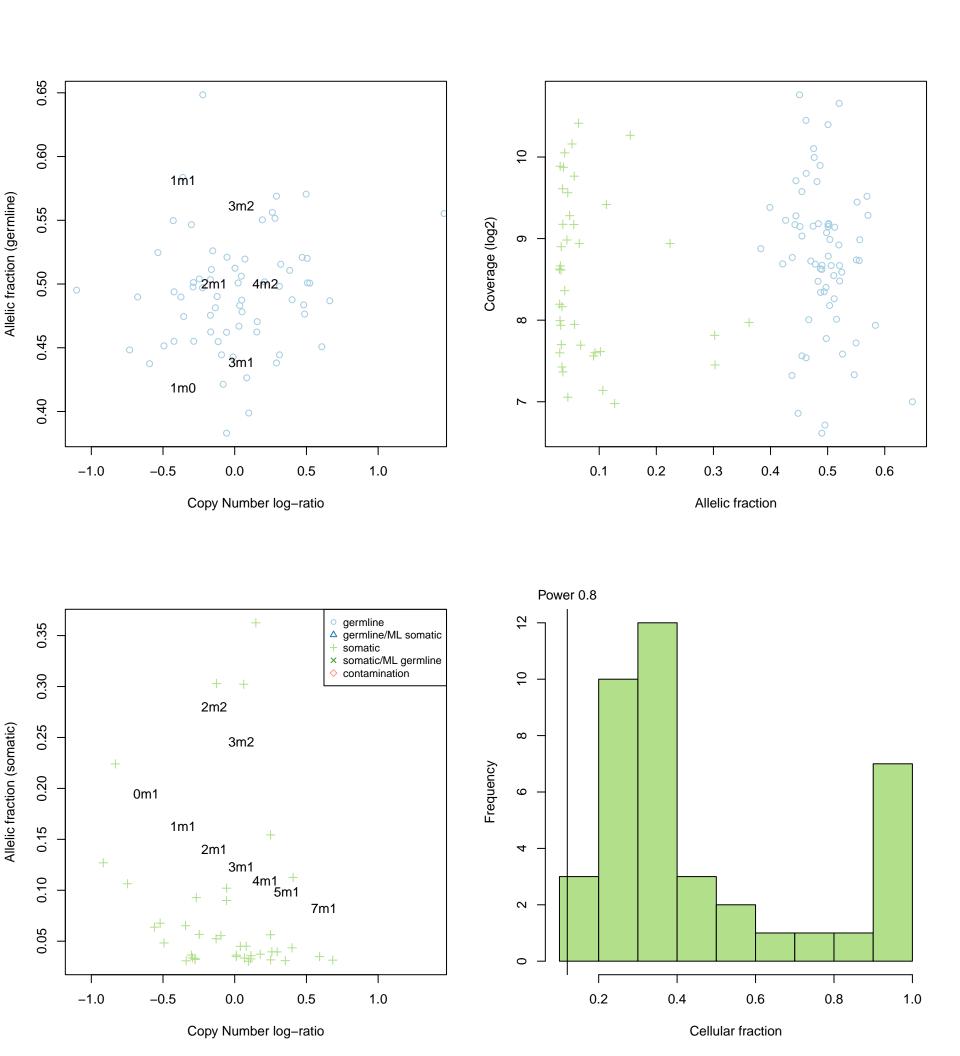


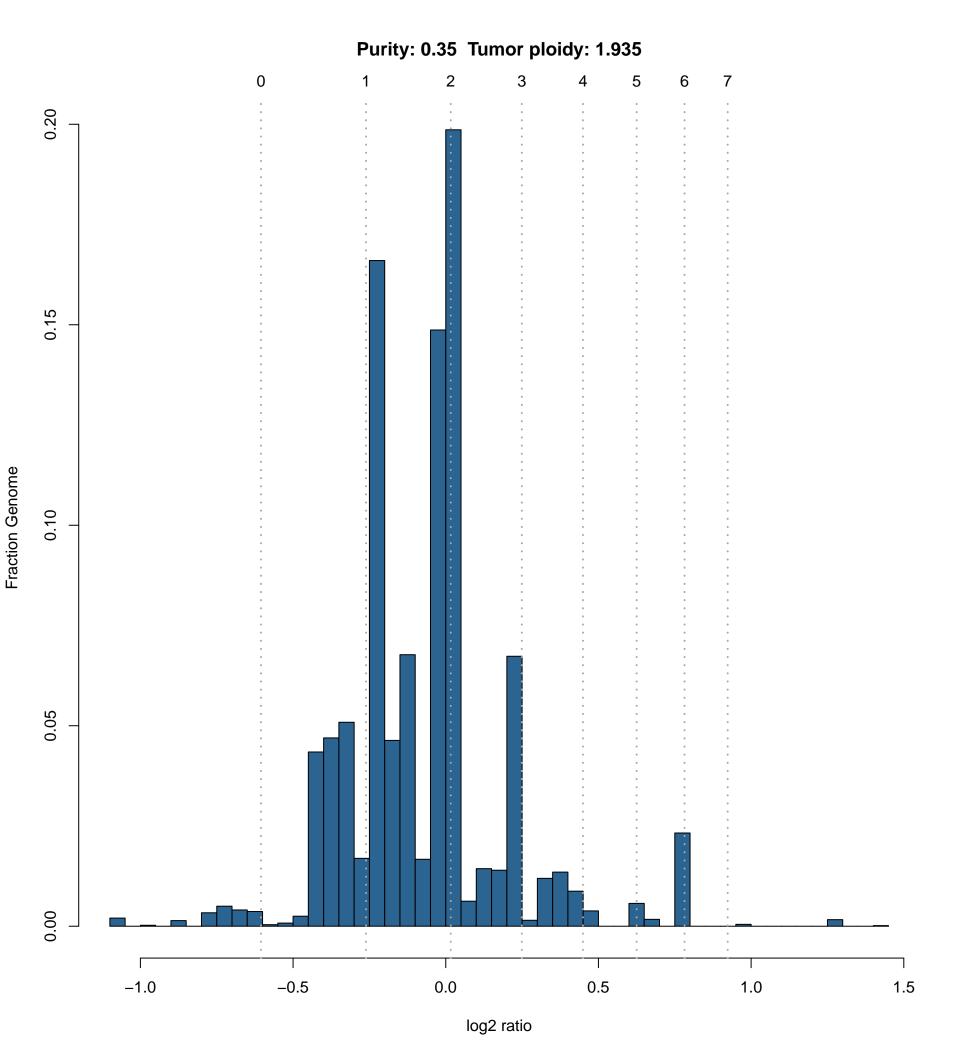
# SCNA-fit log-likelihood: -5324.84

SNV Index

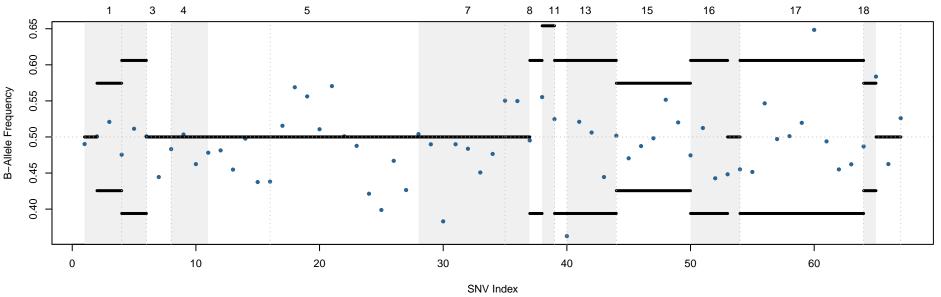




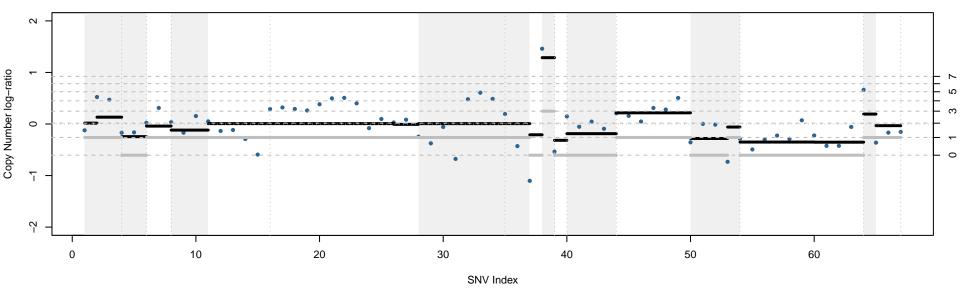


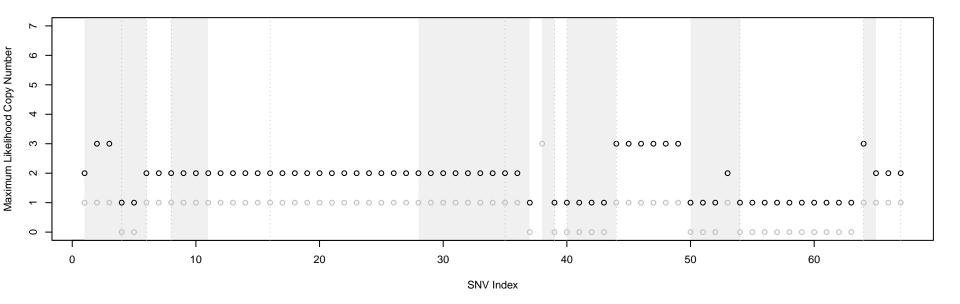


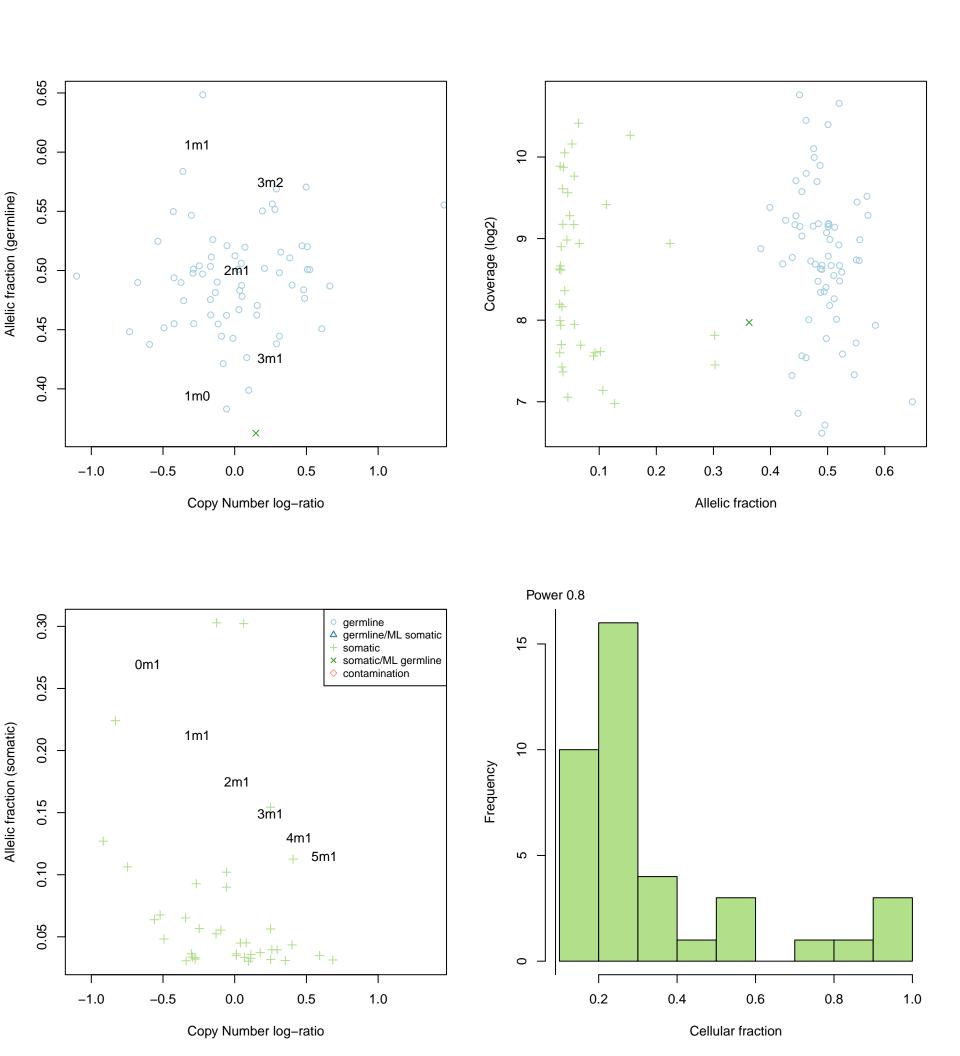
Purity: 0.35 Tumor ploidy: 1.935 SNV log-likelihood: -96.92 GoF: 78% Mean coverage: 290;505

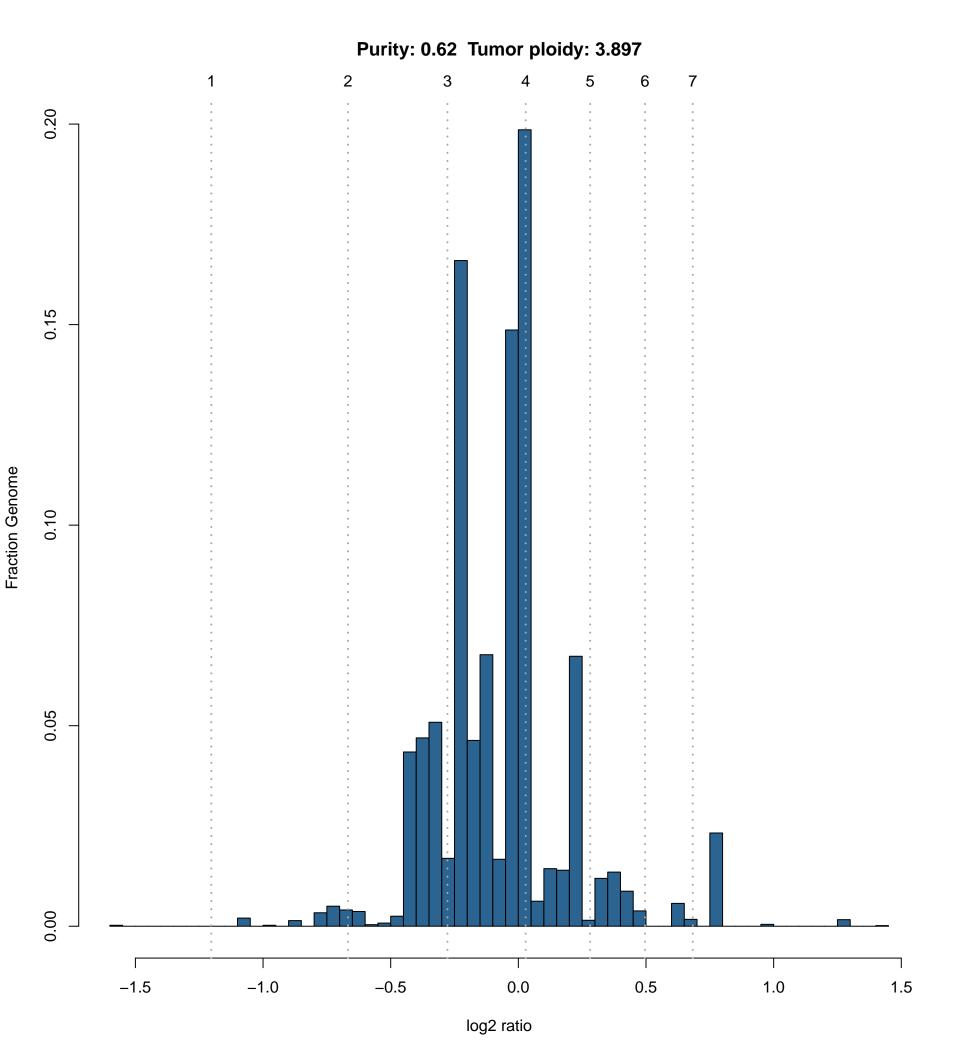


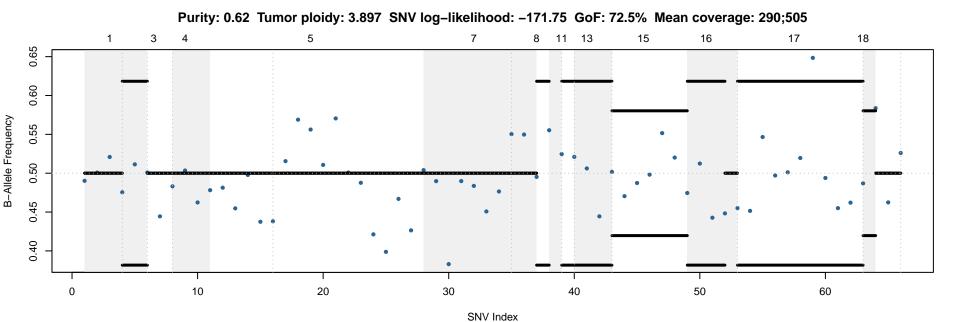
# SCNA-fit log-likelihood: -5325.6



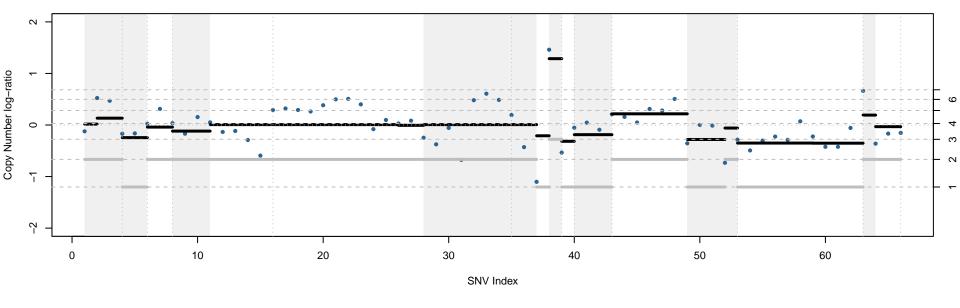


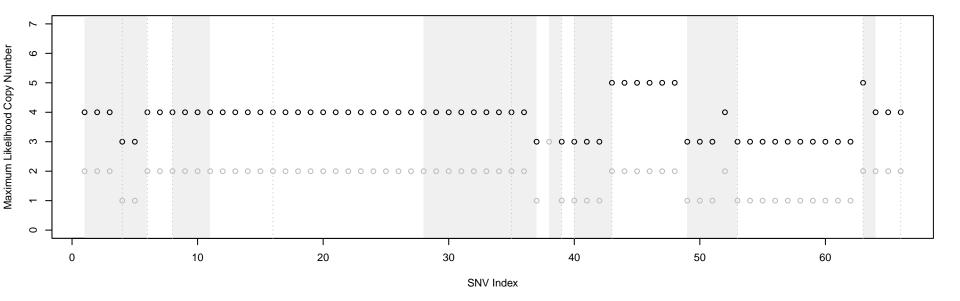


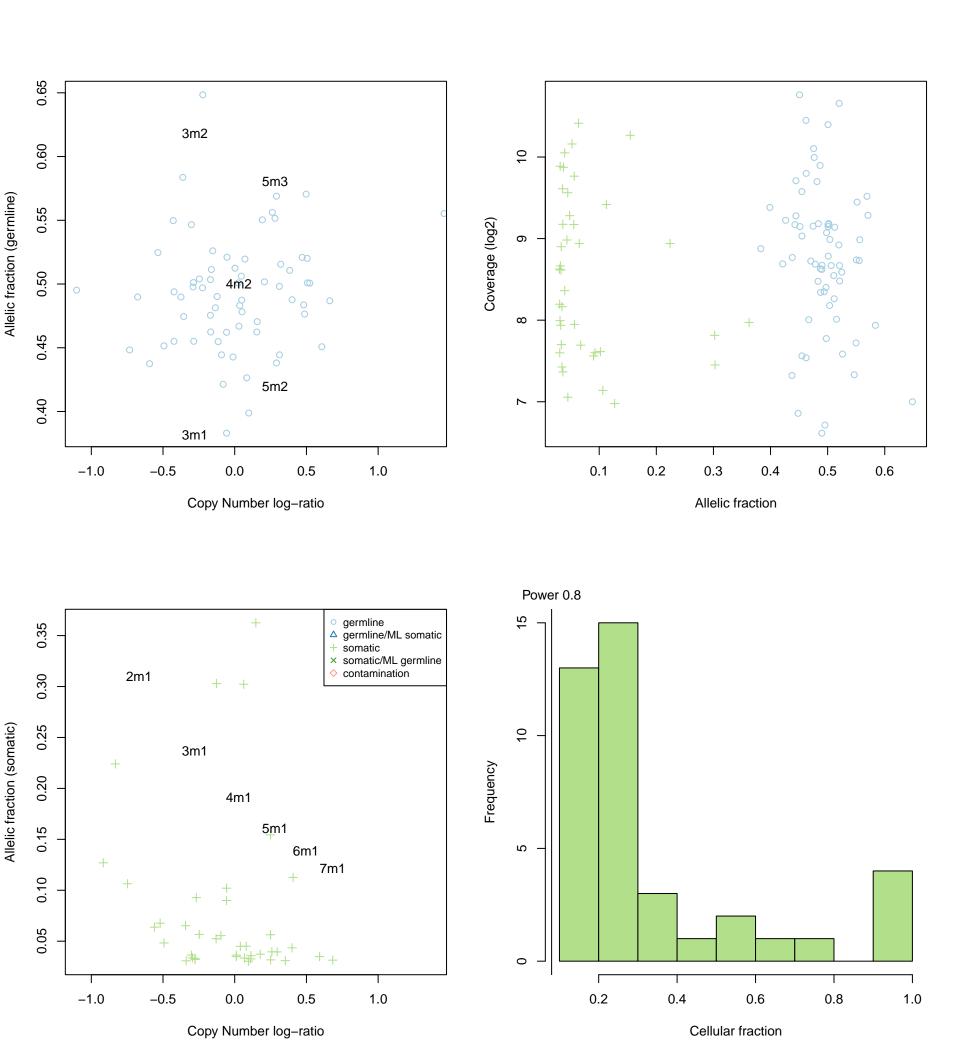


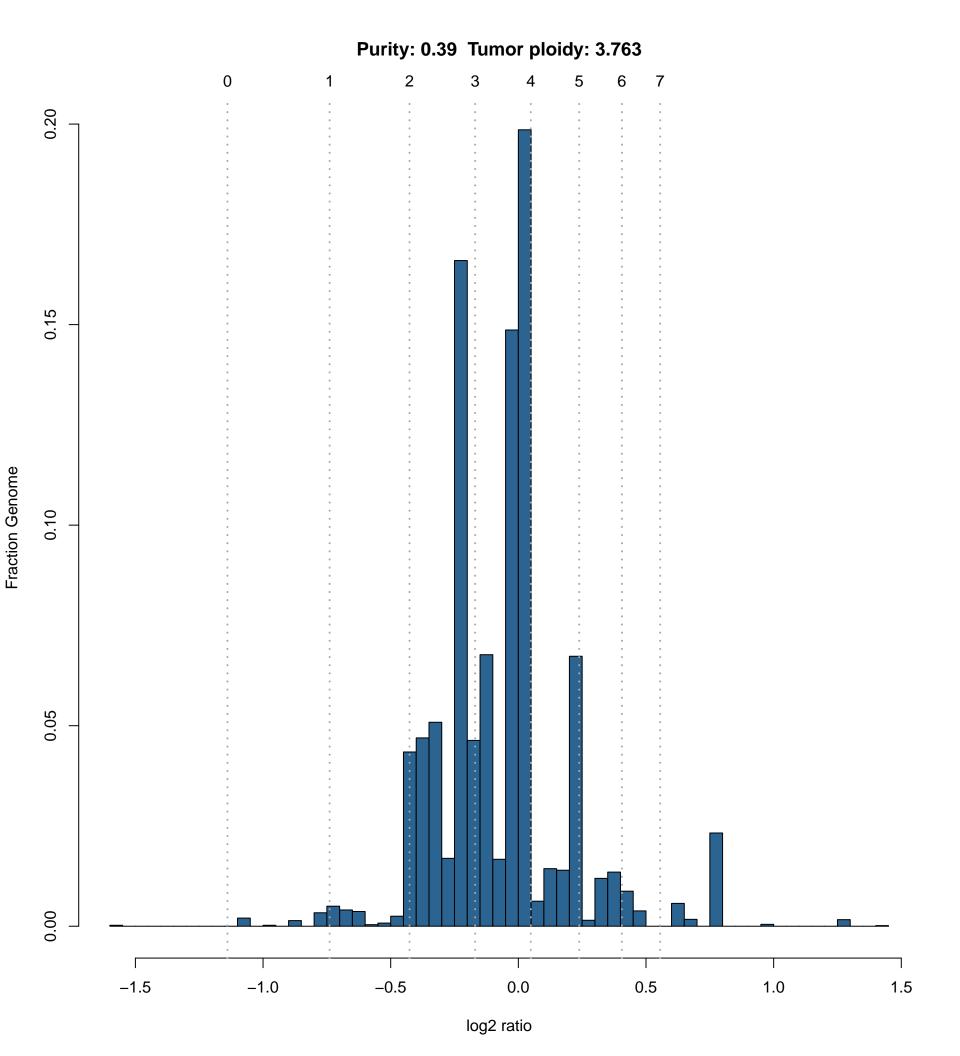


SCNA-fit log-likelihood: -5374.06





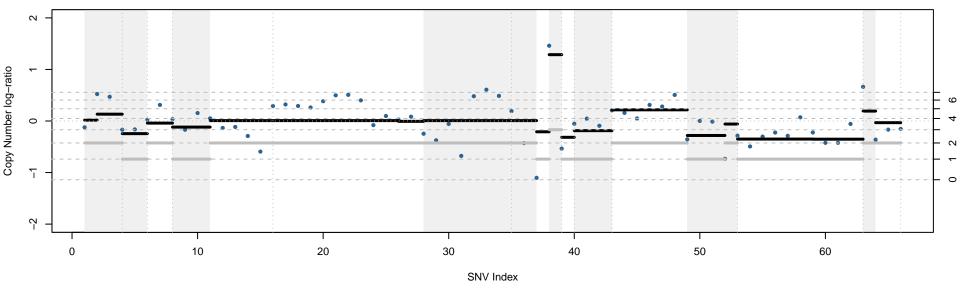


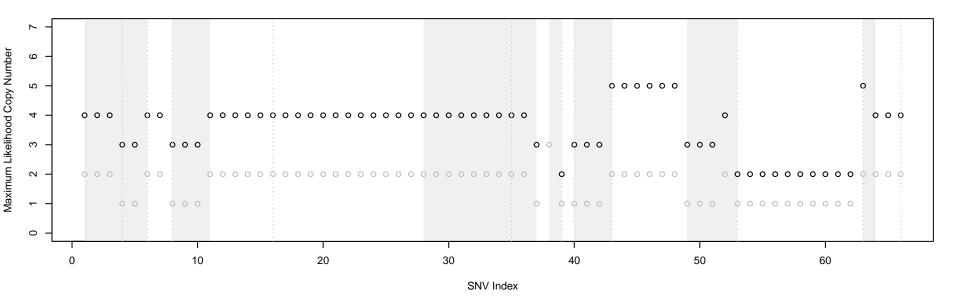


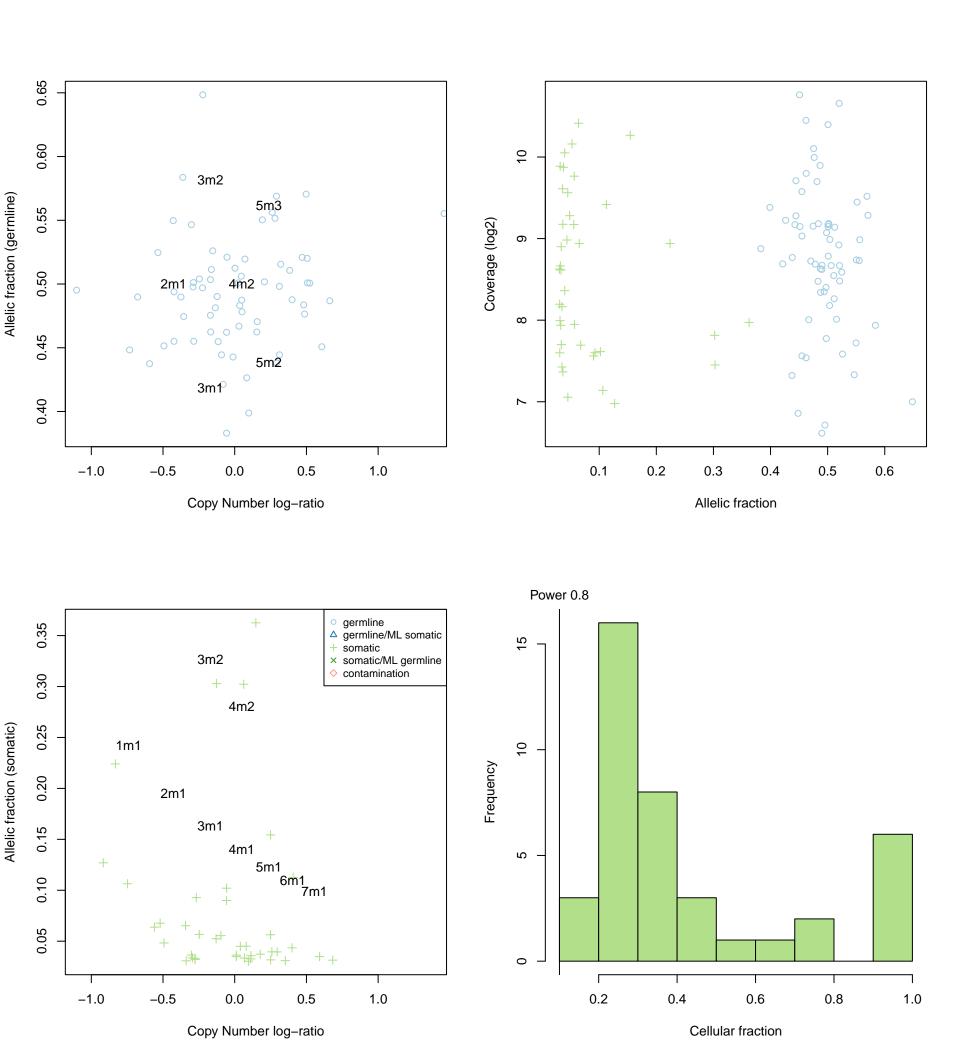
Purity: 0.39 Tumor ploidy: 3.763 SNV log-likelihood: -45.31 GoF: 87% Mean coverage: 290;505

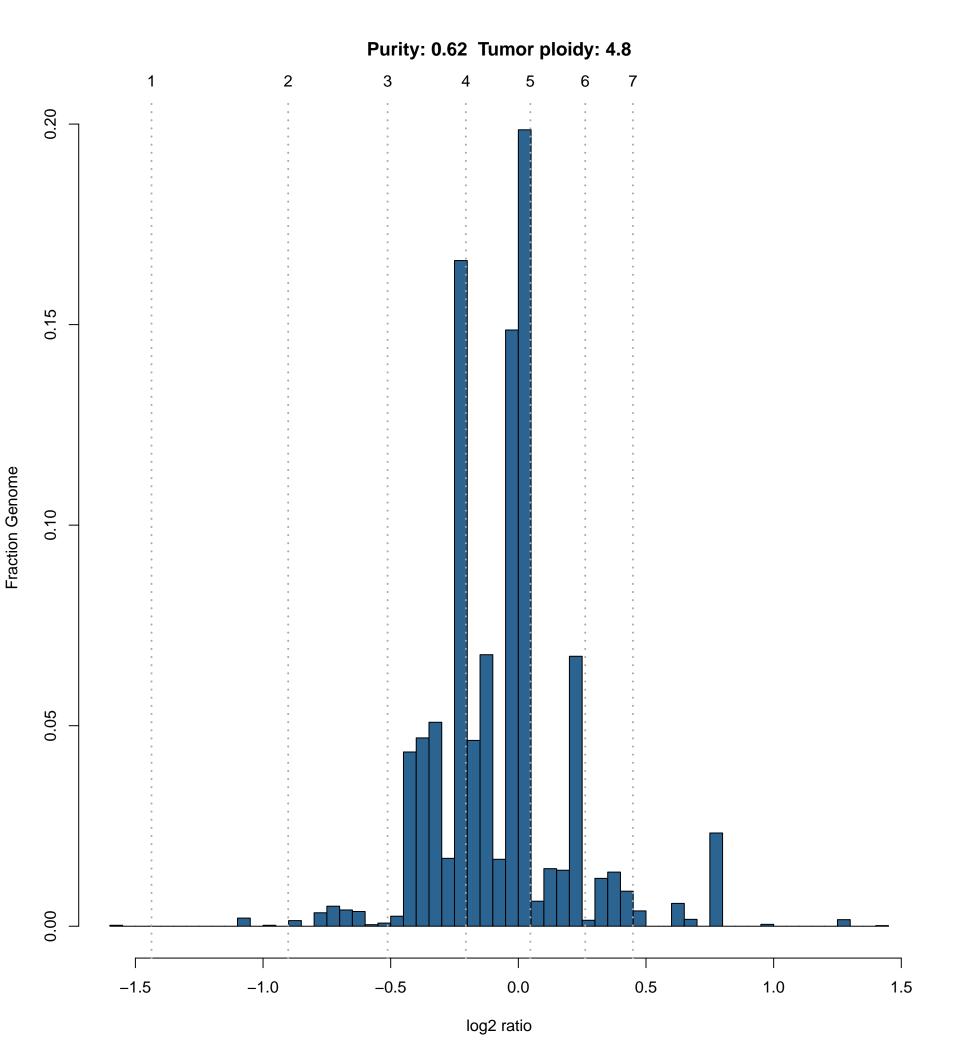
# SCNA-fit log-likelihood: -5645.33

SNV Index

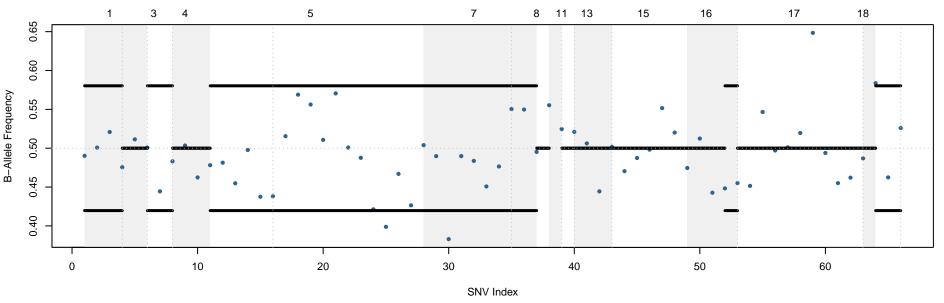




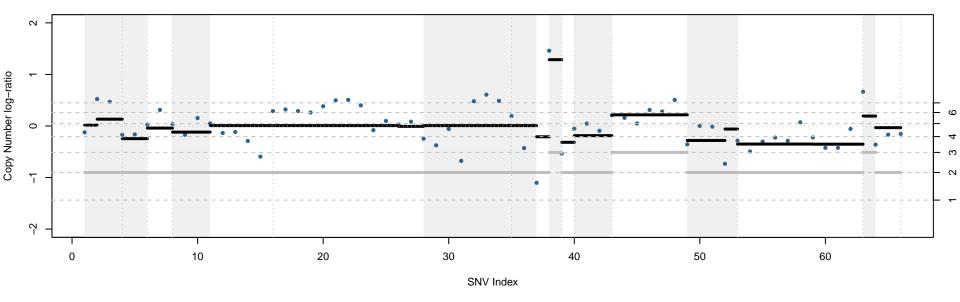


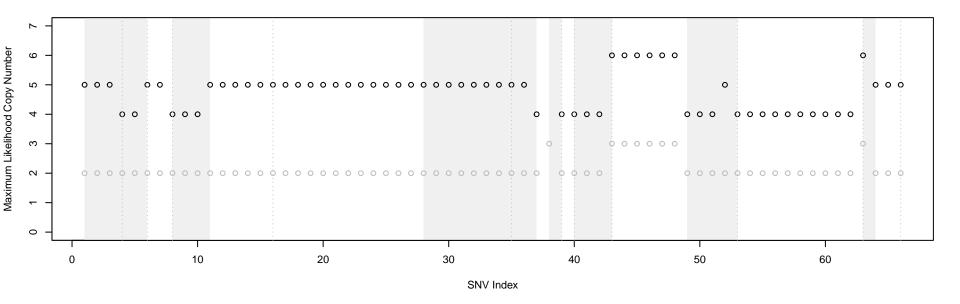


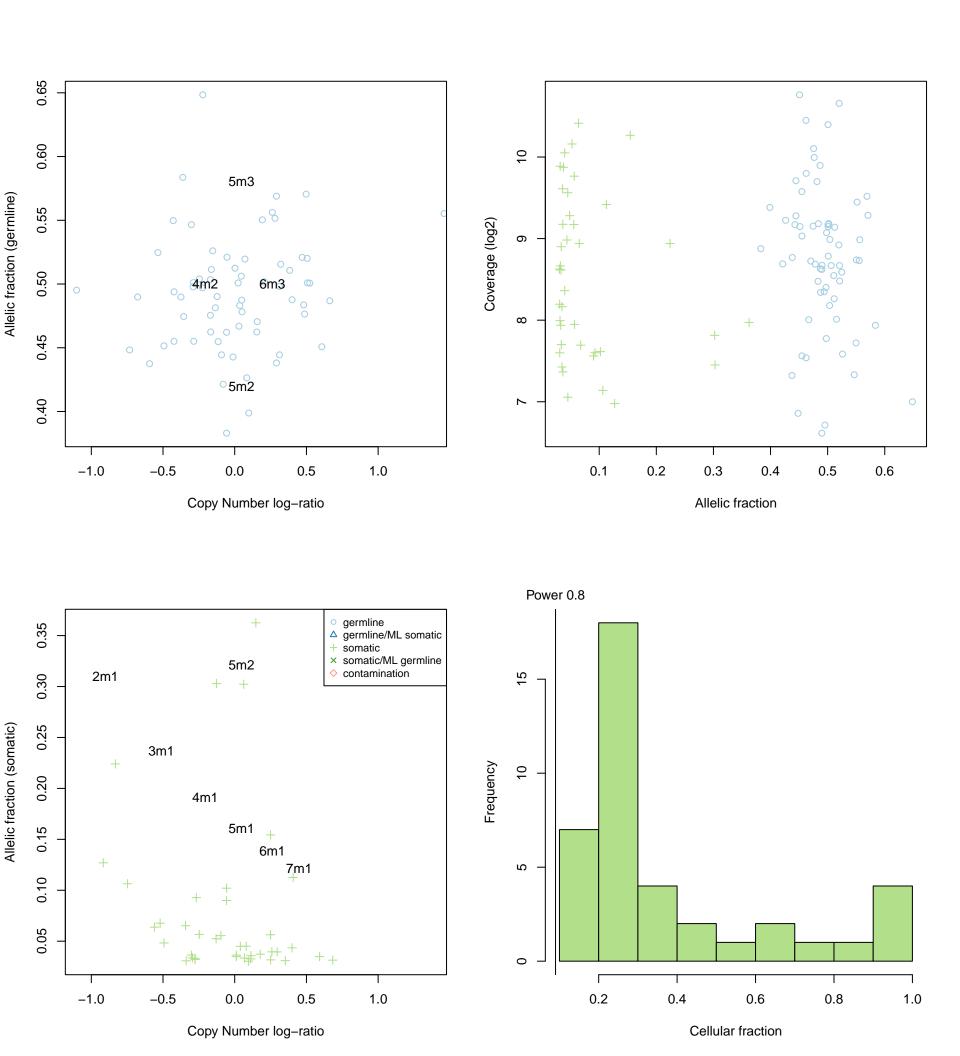
Purity: 0.62 Tumor ploidy: 4.8 SNV log-likelihood: -78.52 GoF: 83.1% Mean coverage: 290;505



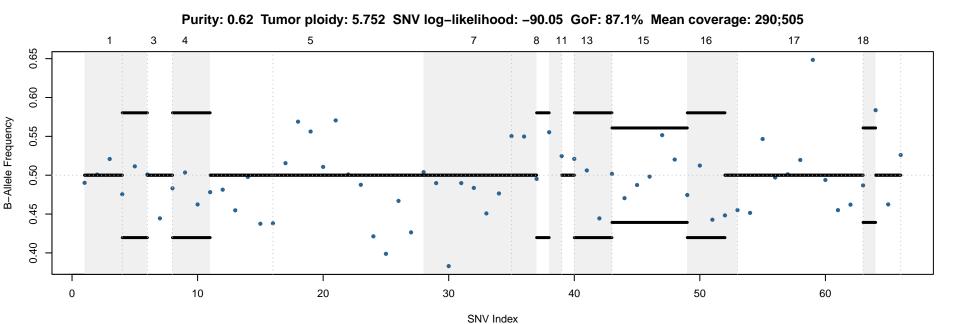
# SCNA-fit log-likelihood: -5705.96



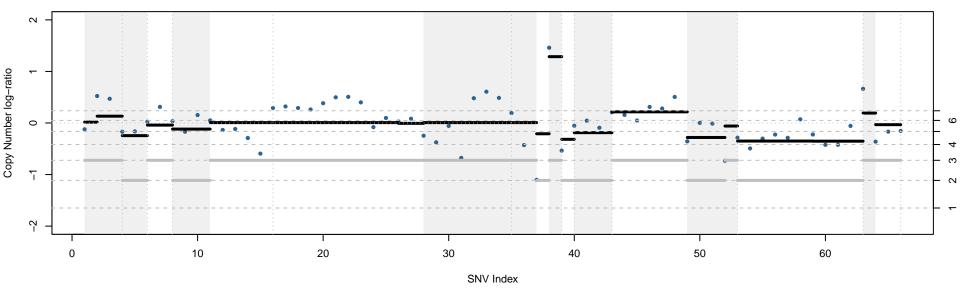


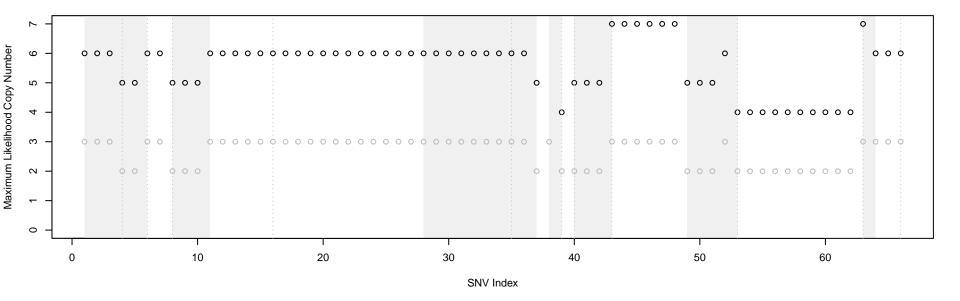


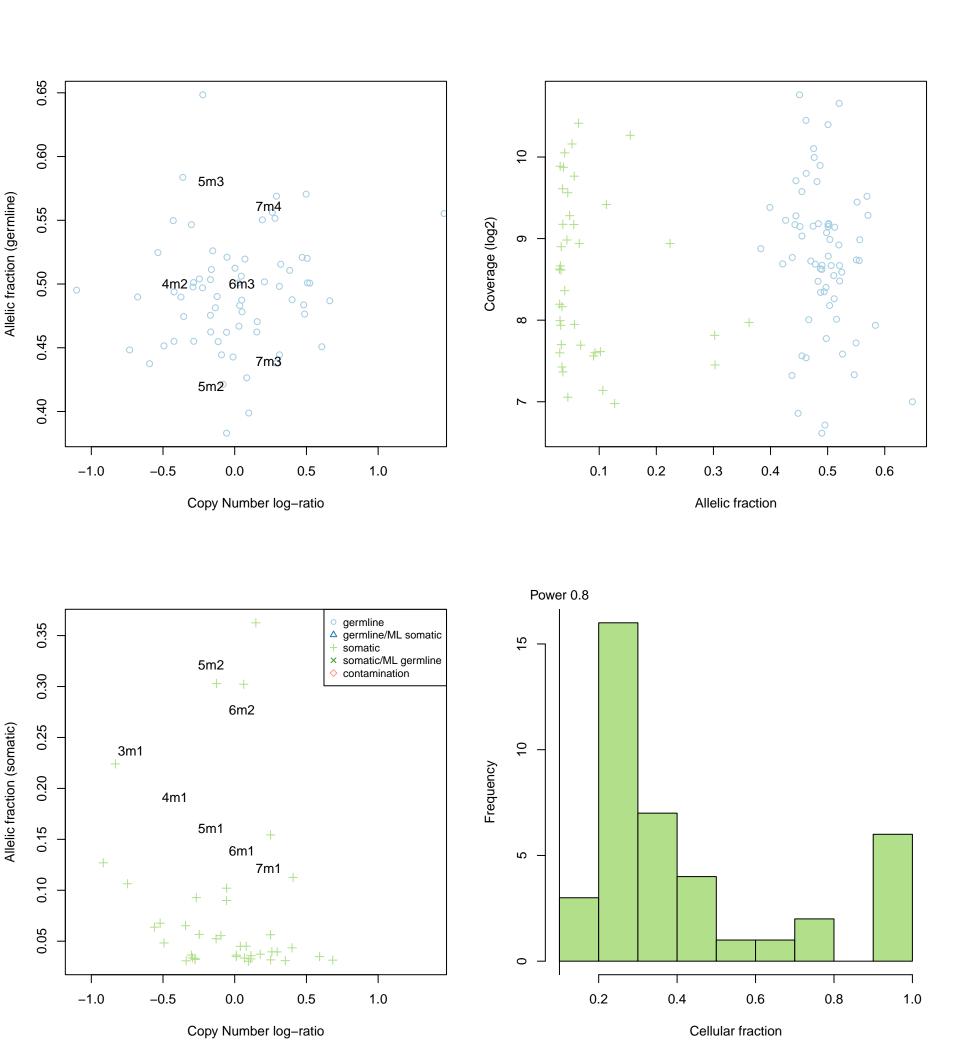
Purity: 0.62 Tumor ploidy: 5.752 5 2 3 6 0.20 0.15 Fraction Genome 0.10 0.05 0.00 -1.0 -1.5 -0.5 0.0 0.5 1.0 1.5 log2 ratio

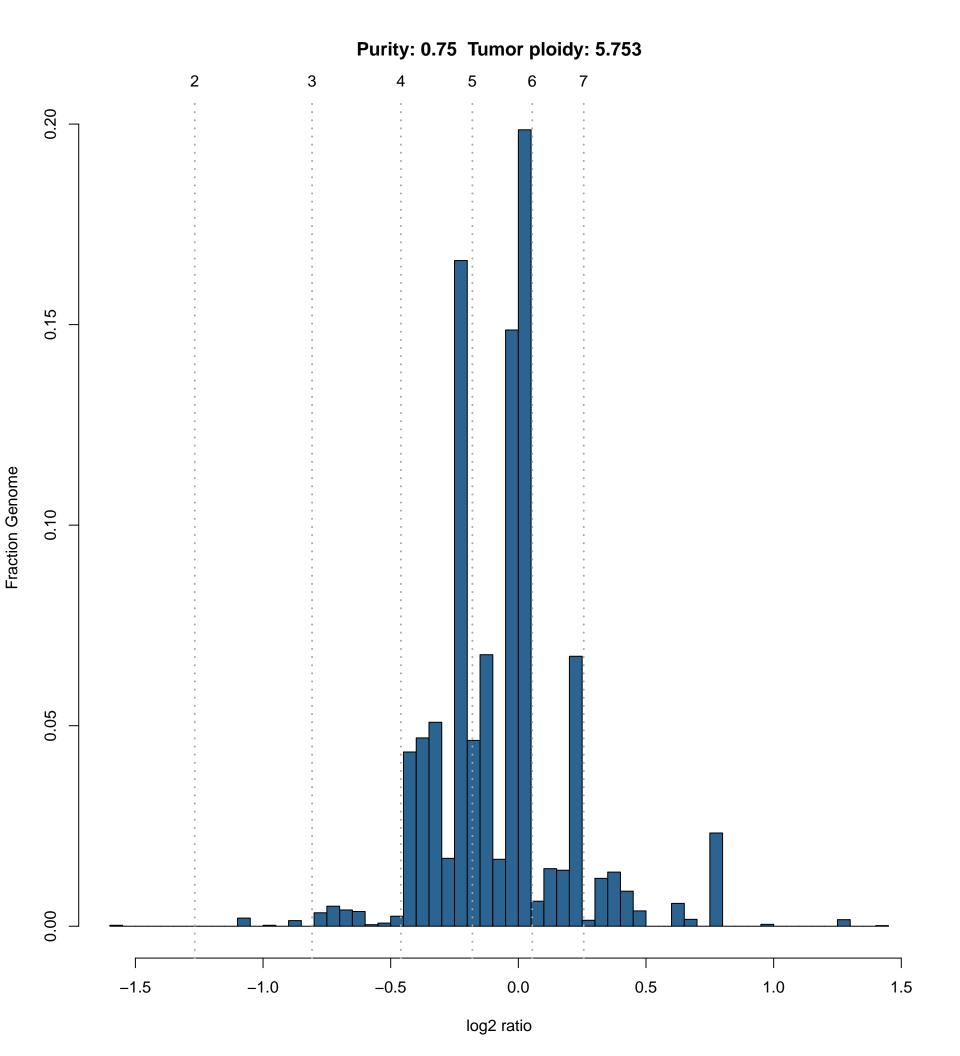


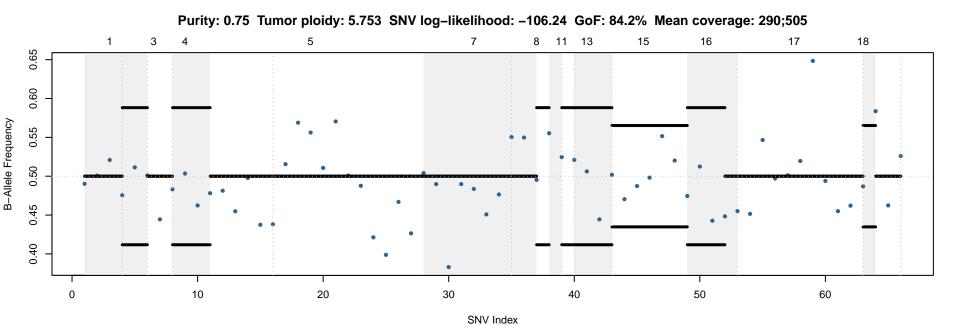
# SCNA-fit log-likelihood: -5769.58



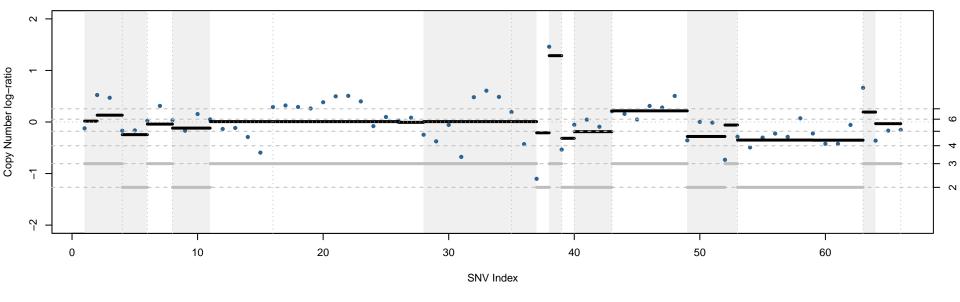


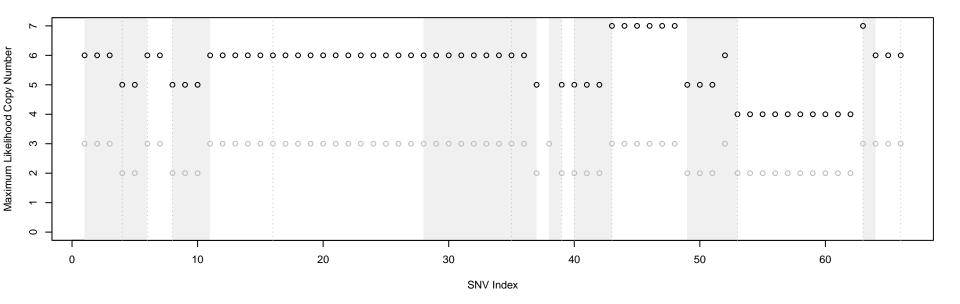


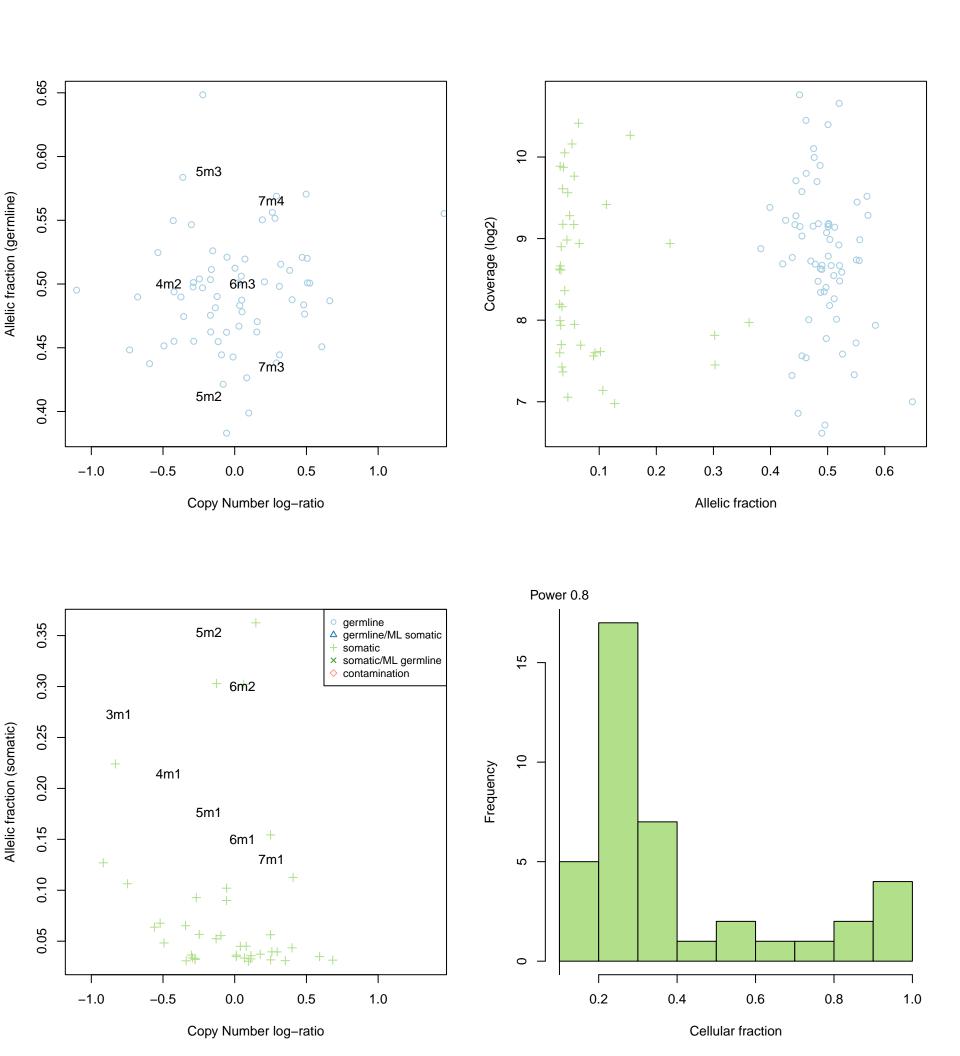




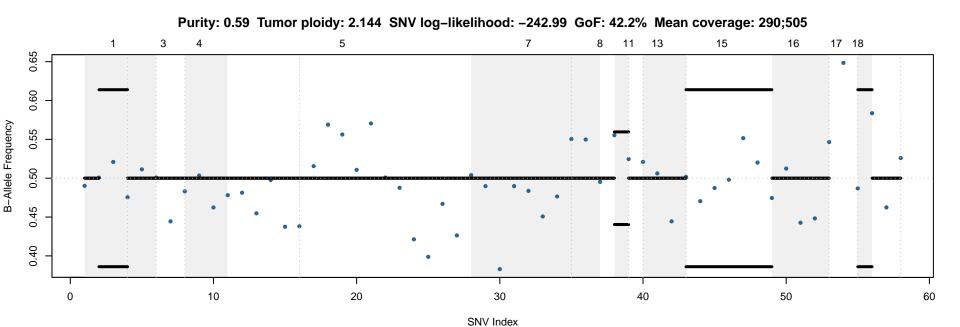
# SCNA-fit log-likelihood: -5799.81







Purity: 0.59 Tumor ploidy: 2.144 2 3 0 5 6 7 Fraction Genome 0.10 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



## SCNA-fit log-likelihood: -5803.64

