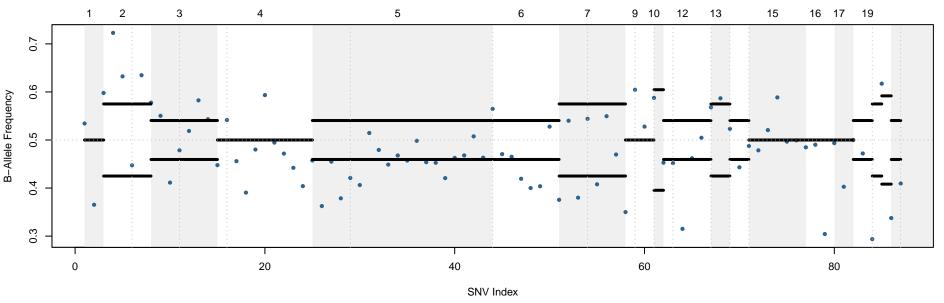
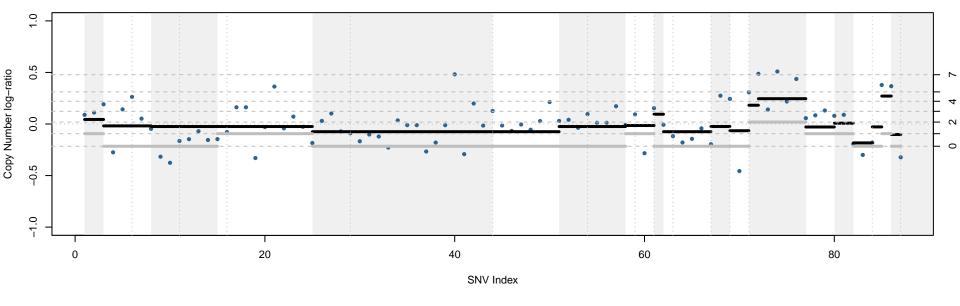
Purity: 0.15 Tumor ploidy: 1.829 7 0 1 2 3 5 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 0.0 0.5 1.0

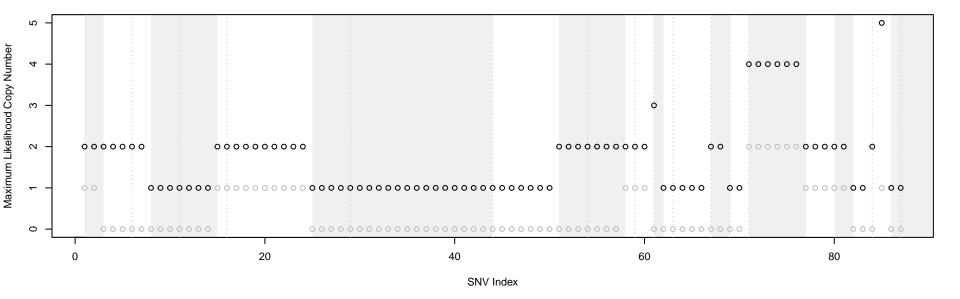
log2 ratio

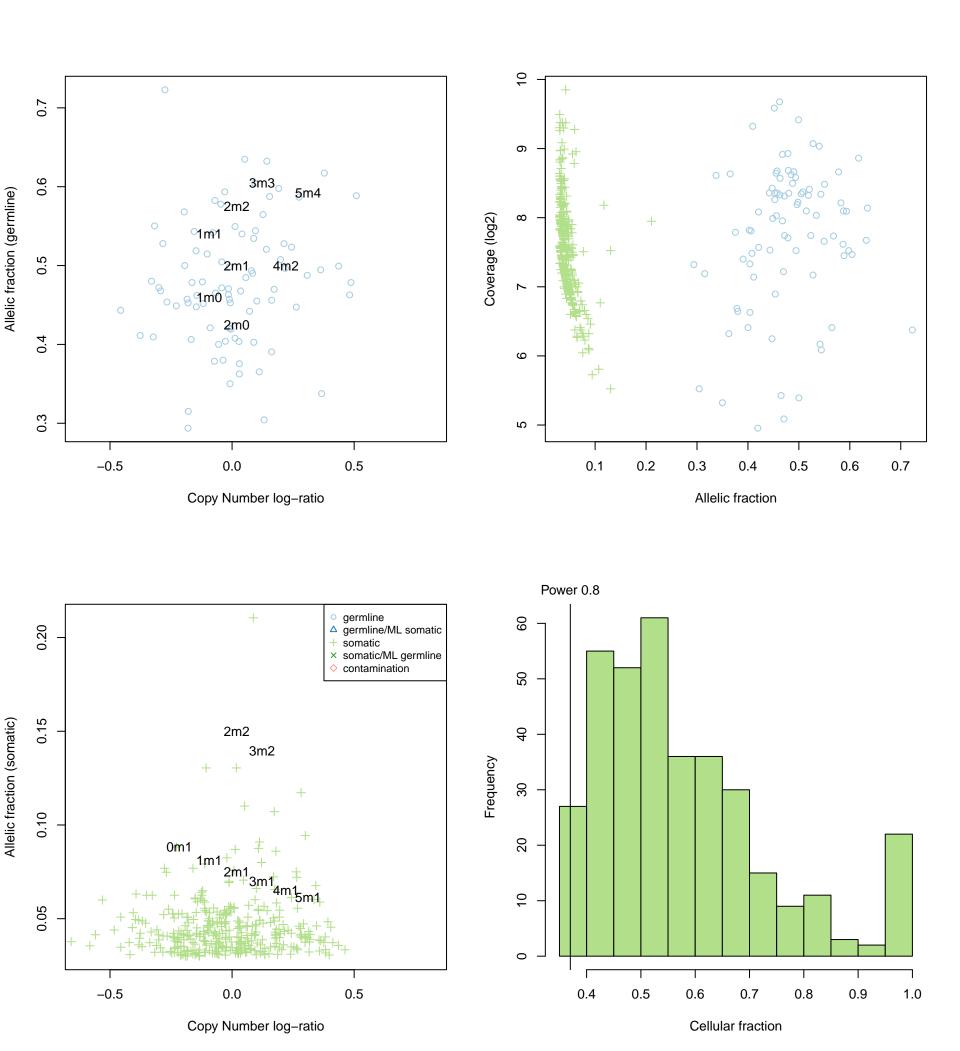
Purity: 0.15 Tumor ploidy: 1.829 SNV log-likelihood: 310.32 GoF: 96% Mean coverage: 219;199



### SCNA-fit log-likelihood: -9002.84

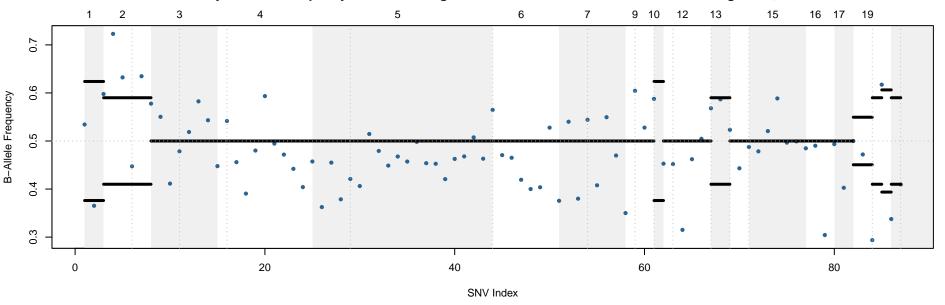




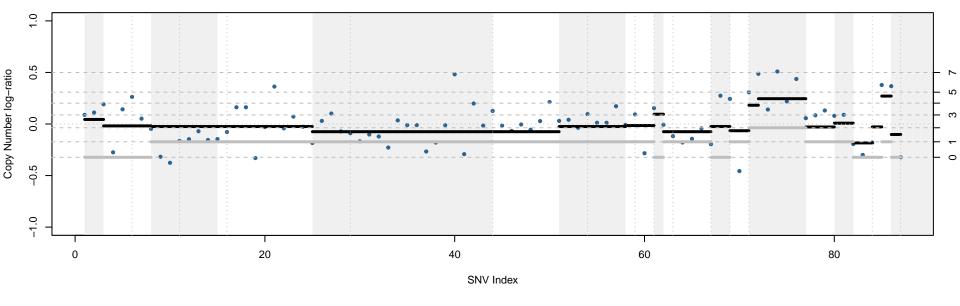


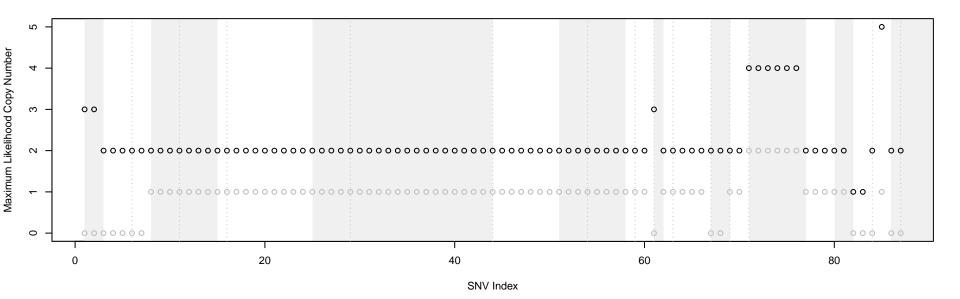
Purity: 0.18 Tumor ploidy: 2.285 0 2 3 5 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 0.0 0.5 1.0 log2 ratio

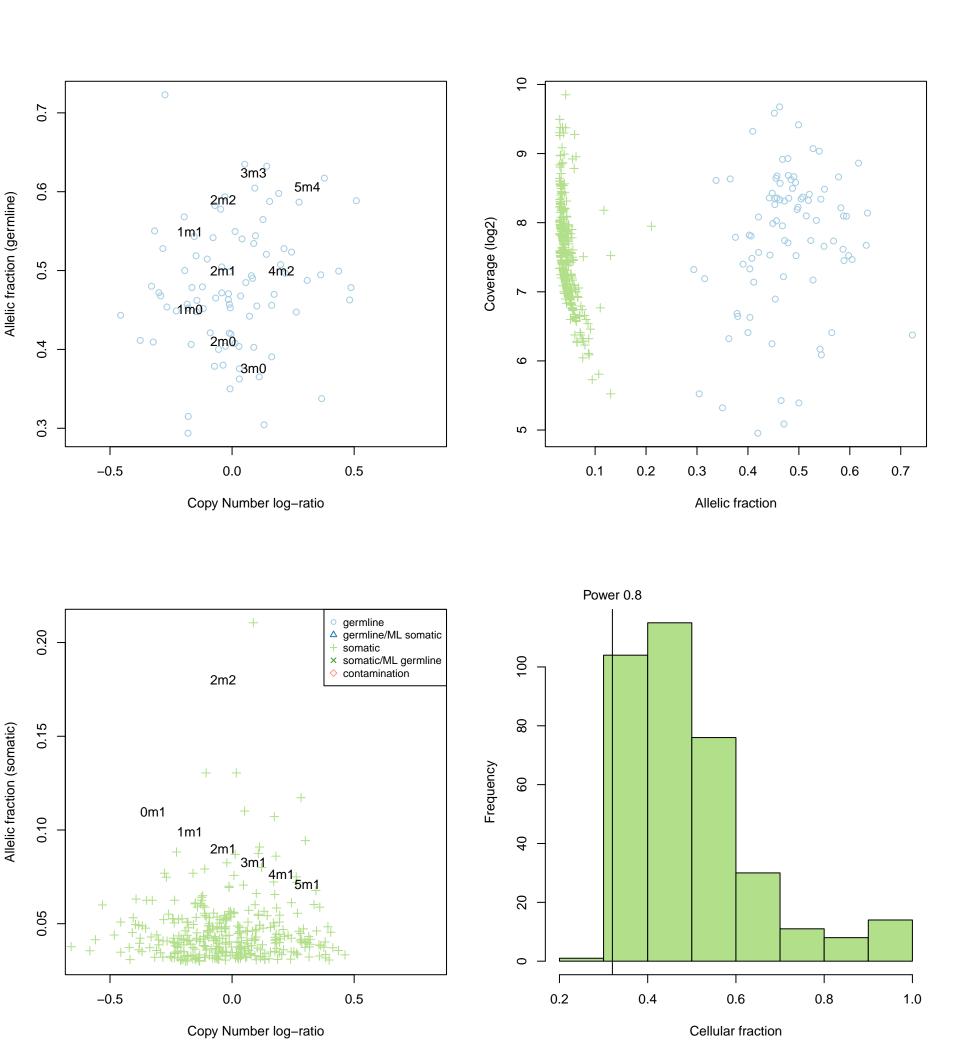
Purity: 0.18 Tumor ploidy: 2.285 SNV log-likelihood: 273.3 GoF: 93.4% Mean coverage: 219;199

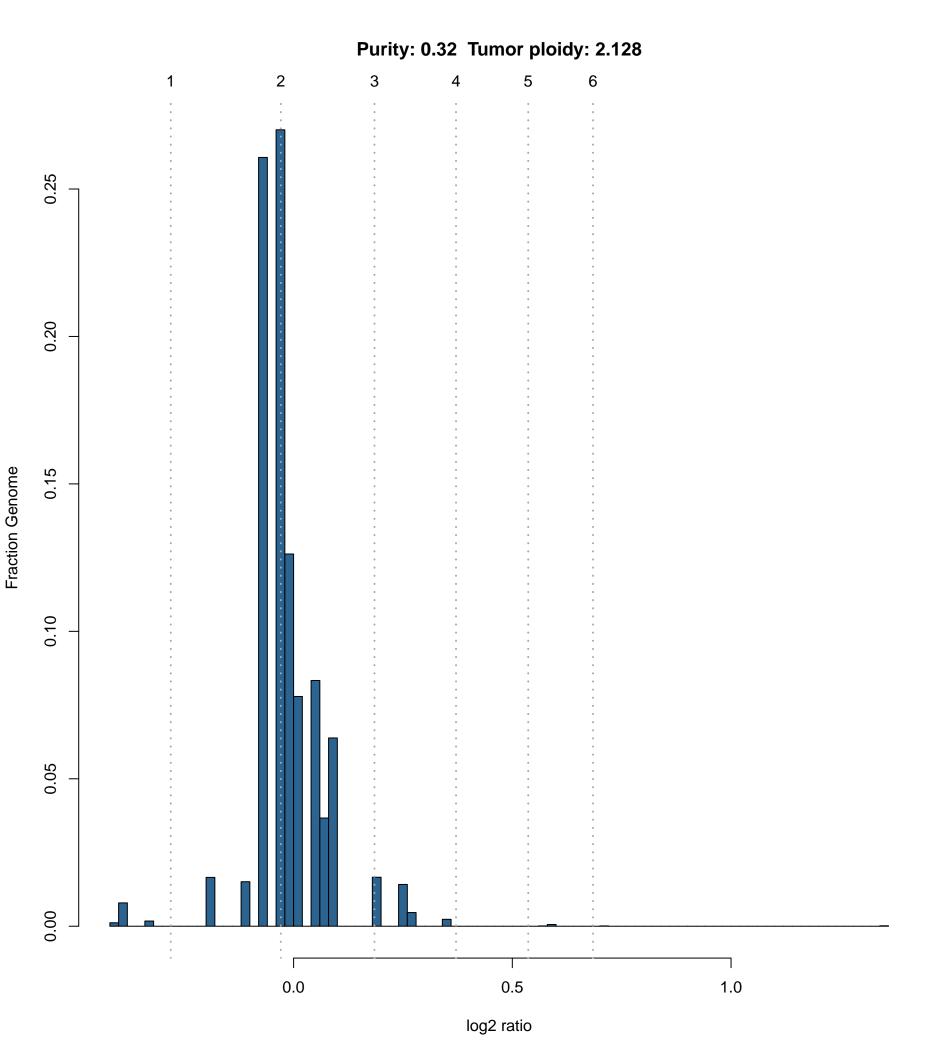


# SCNA-fit log-likelihood: -8951.6

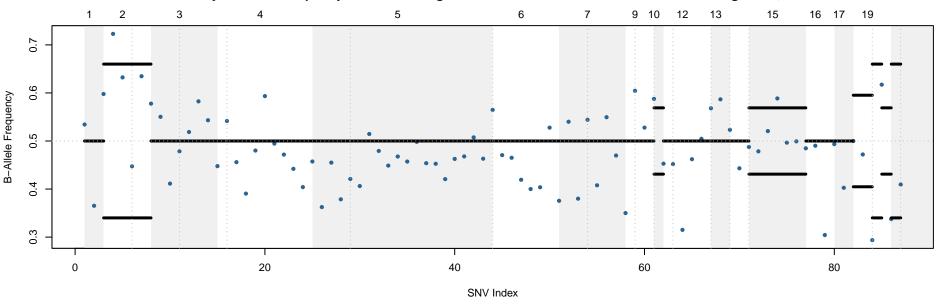




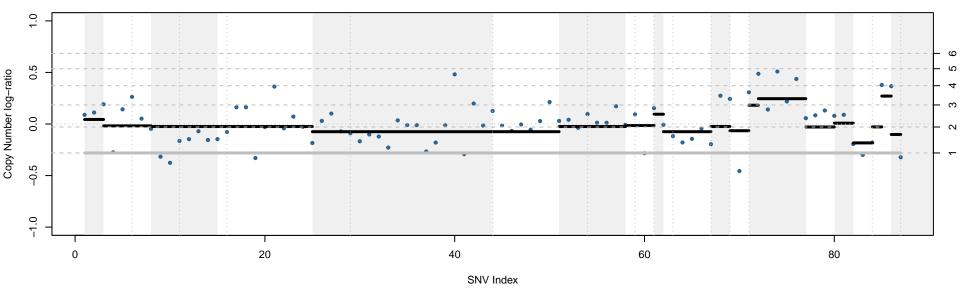


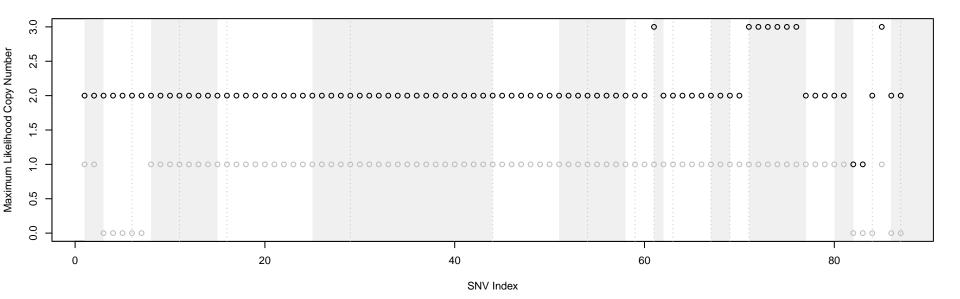


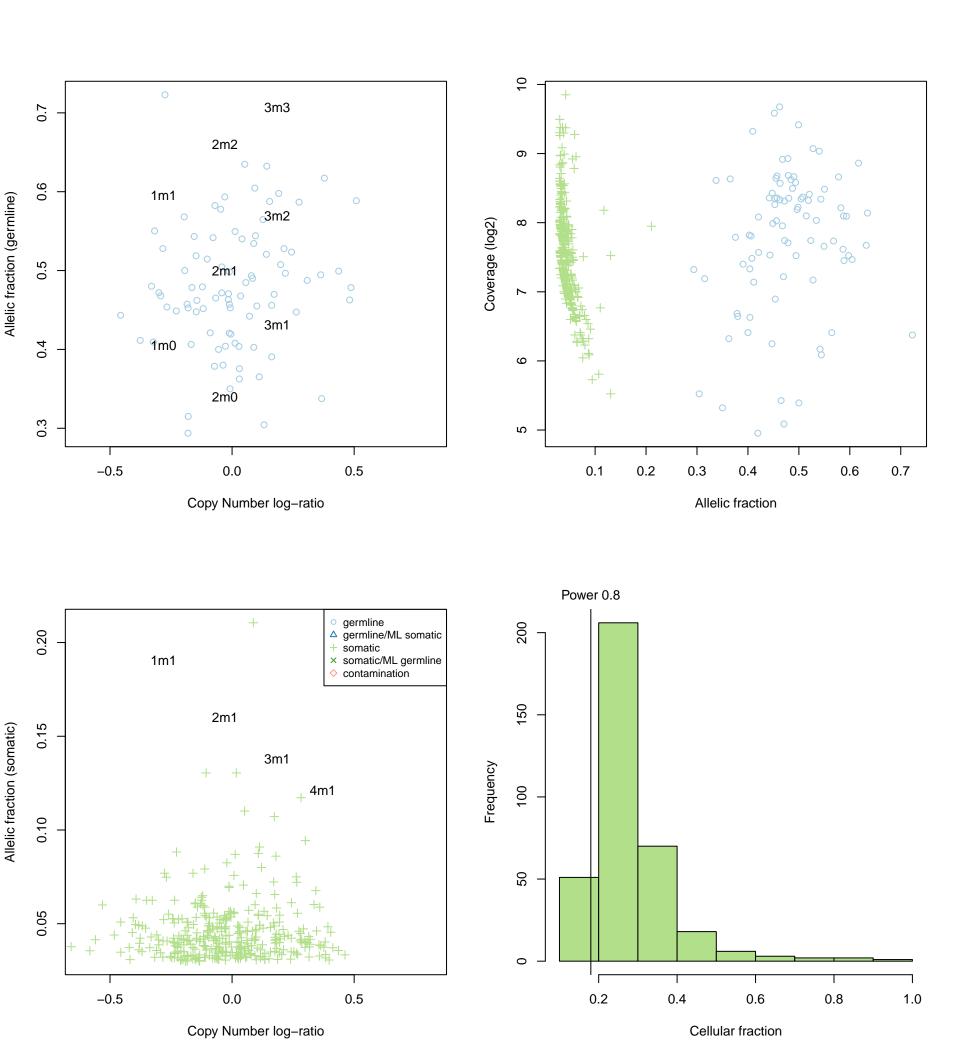
Purity: 0.32 Tumor ploidy: 2.128 SNV log-likelihood: 242.29 GoF: 71.2% Mean coverage: 219;199



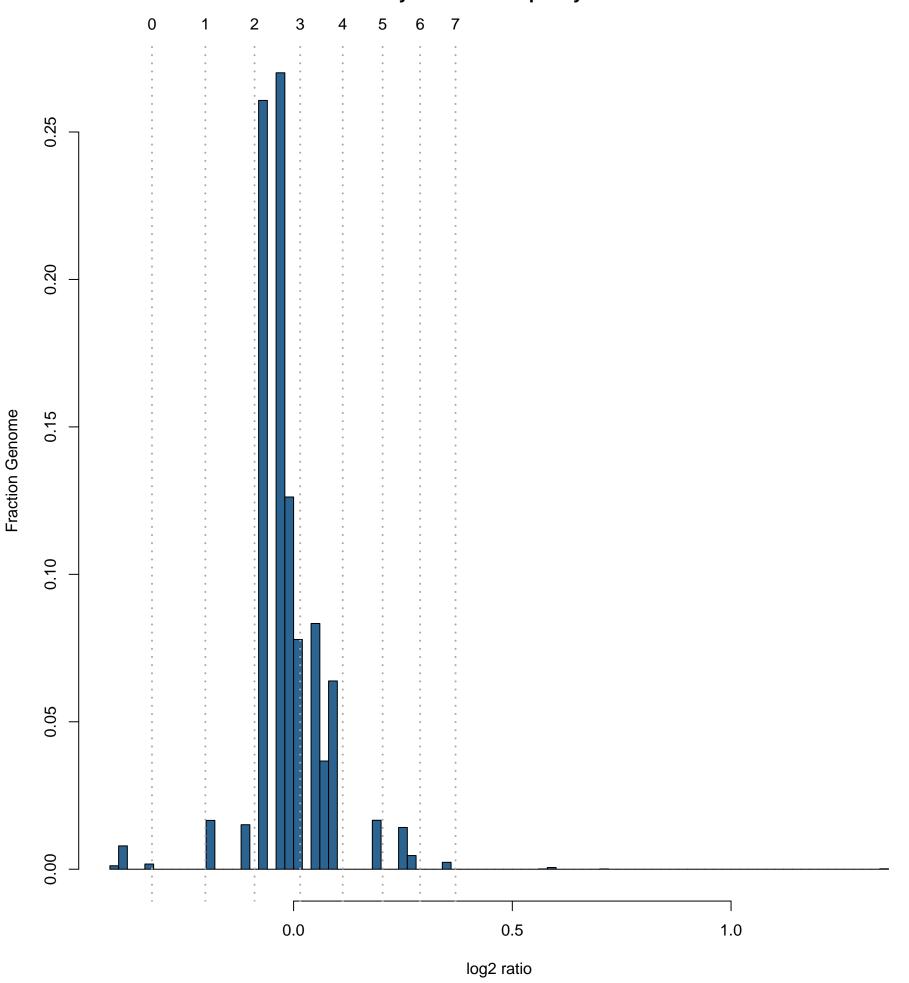
### SCNA-fit log-likelihood: -9038.58



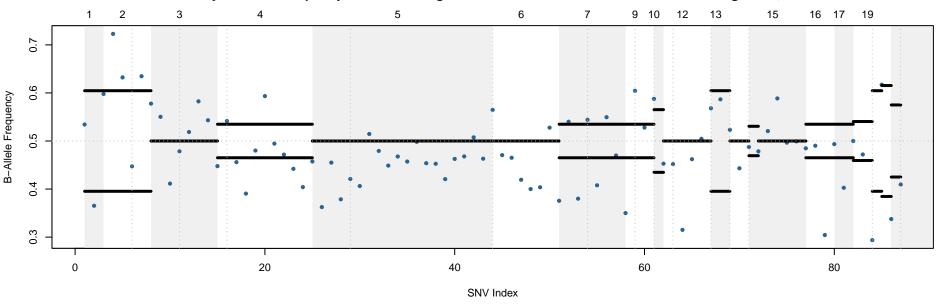




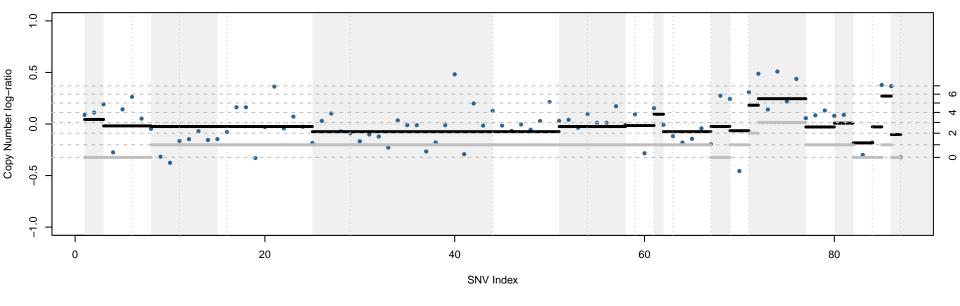
Purity: 0.15 Tumor ploidy: 2.851

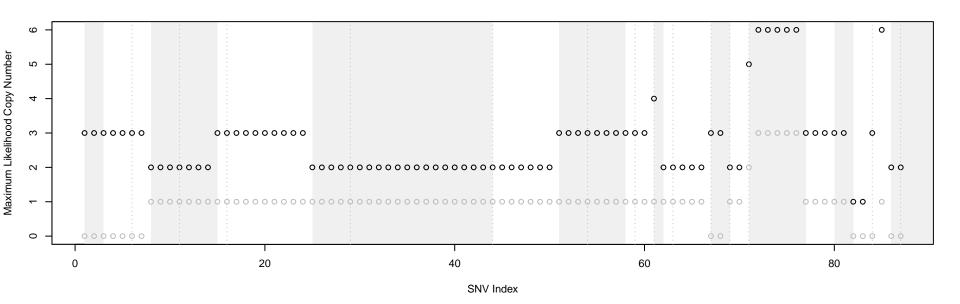


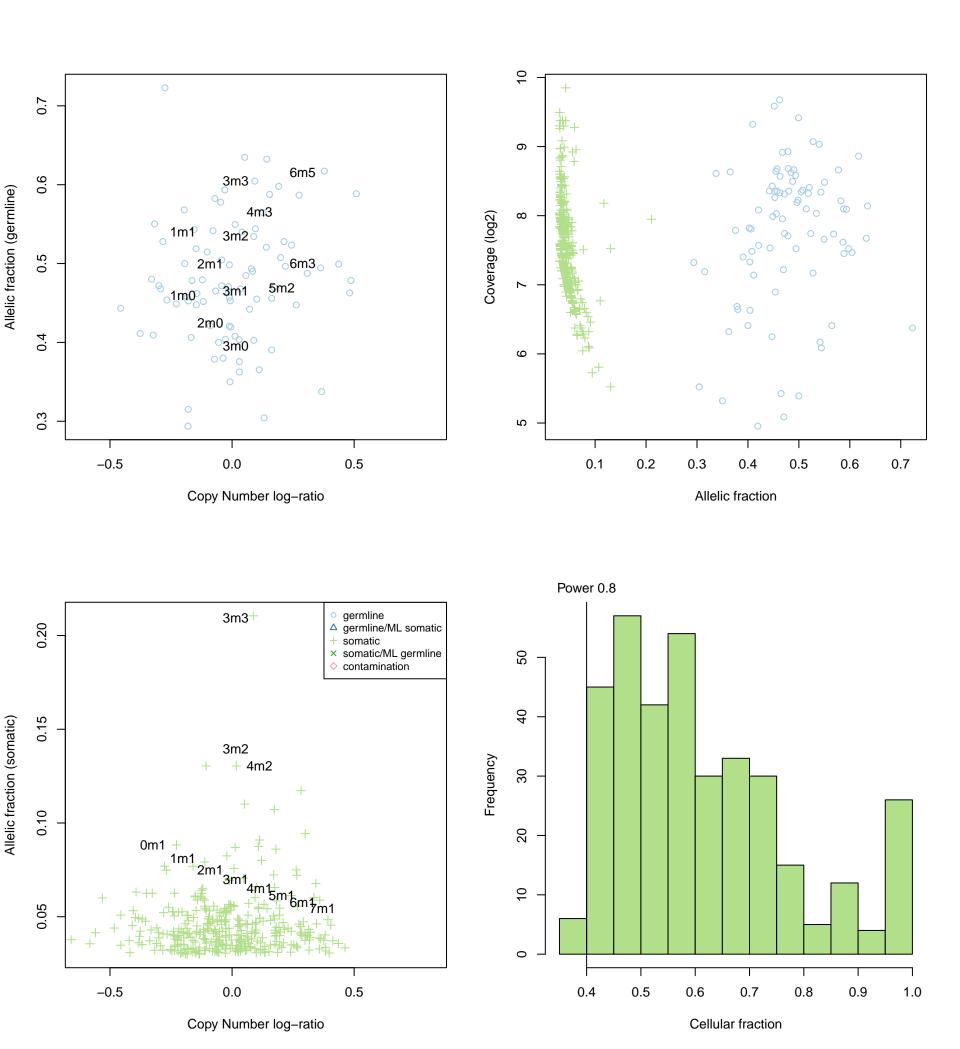
Purity: 0.15 Tumor ploidy: 2.851 SNV log-likelihood: 128.61 GoF: 96.4% Mean coverage: 219;199



## SCNA-fit log-likelihood: -8945.12



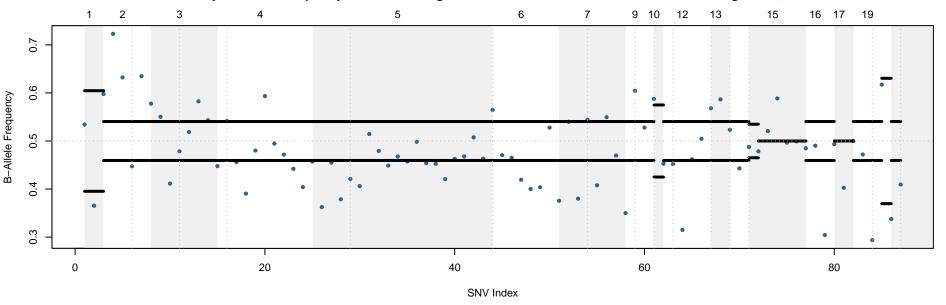




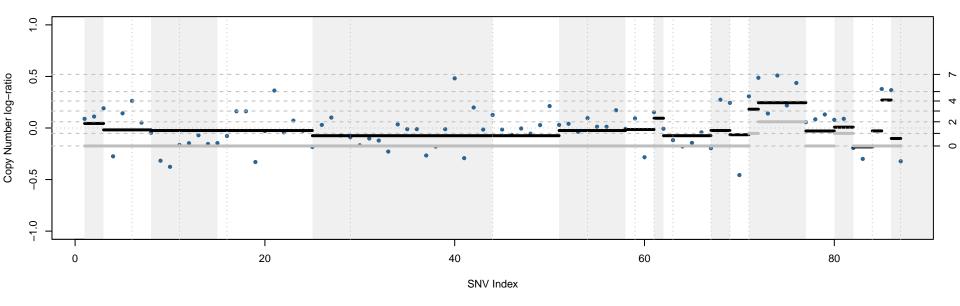
Purity: 0.15 Tumor ploidy: 1.455 0 2 3 5 7 0.20 Fraction Genome 0.10 0.05 0.00 0.0 0.5 1.0

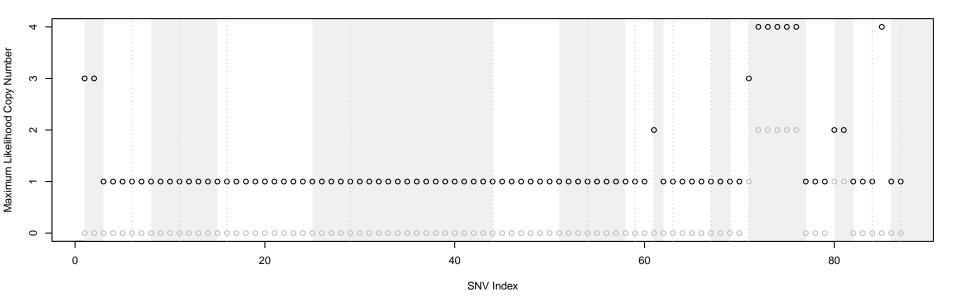
log2 ratio

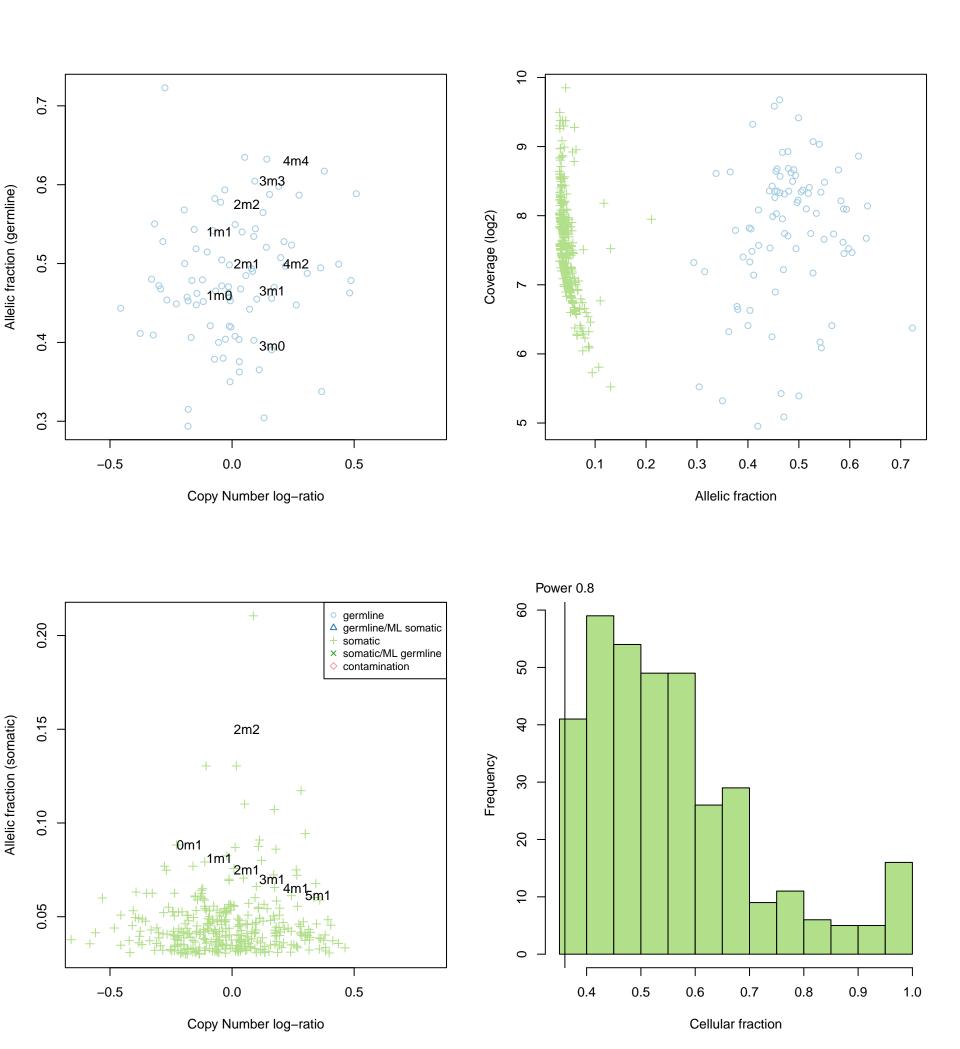
Purity: 0.15 Tumor ploidy: 1.455 SNV log-likelihood: 122.76 GoF: 95.8% Mean coverage: 219;199



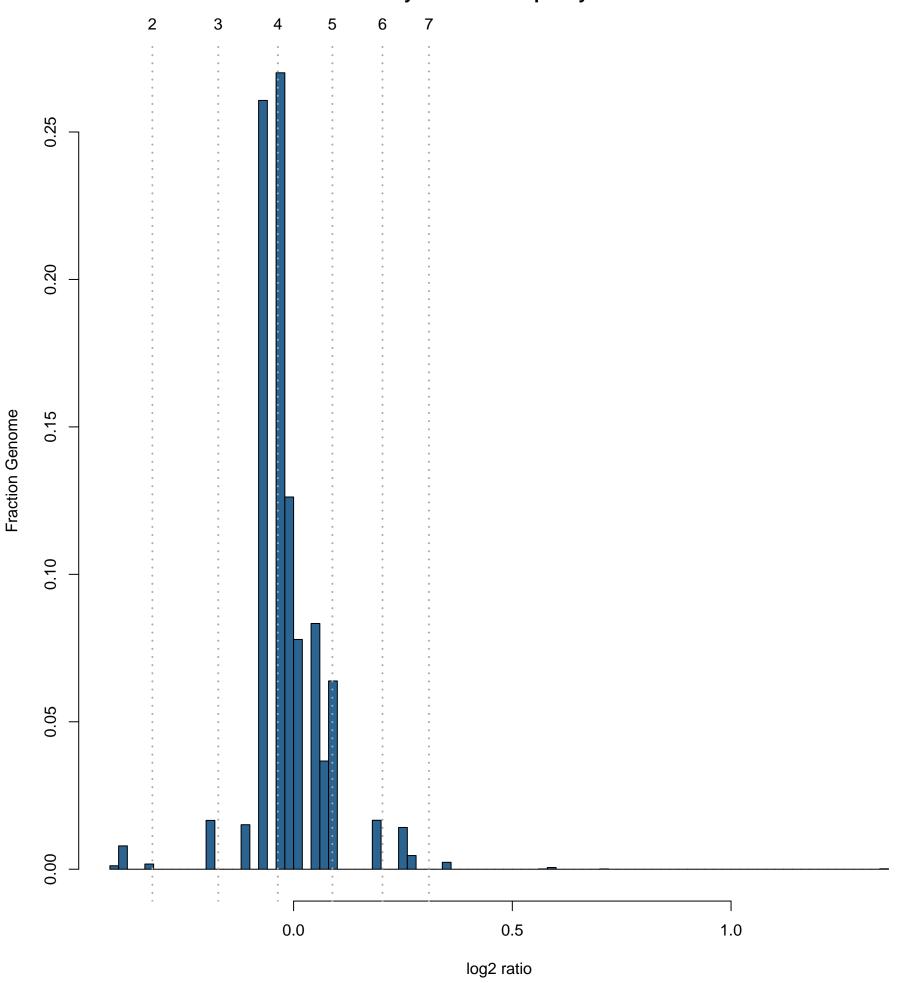
## SCNA-fit log-likelihood: -9104.18



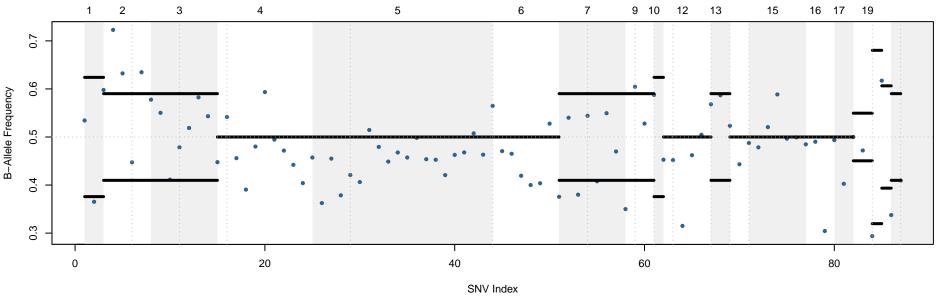




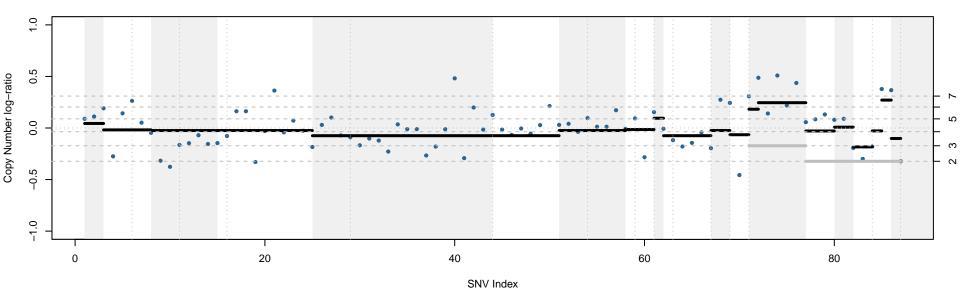
Purity: 0.22 Tumor ploidy: 4.28

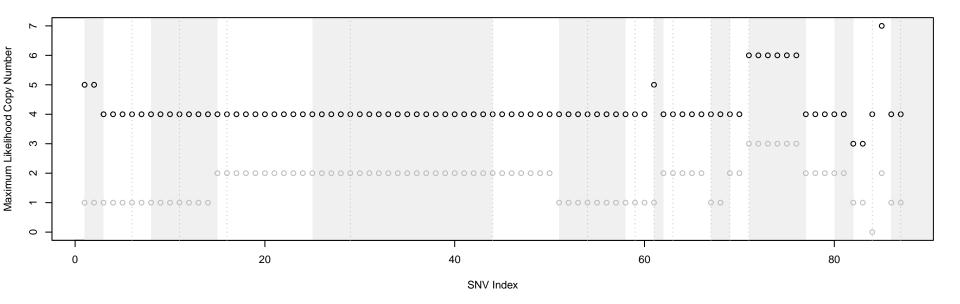


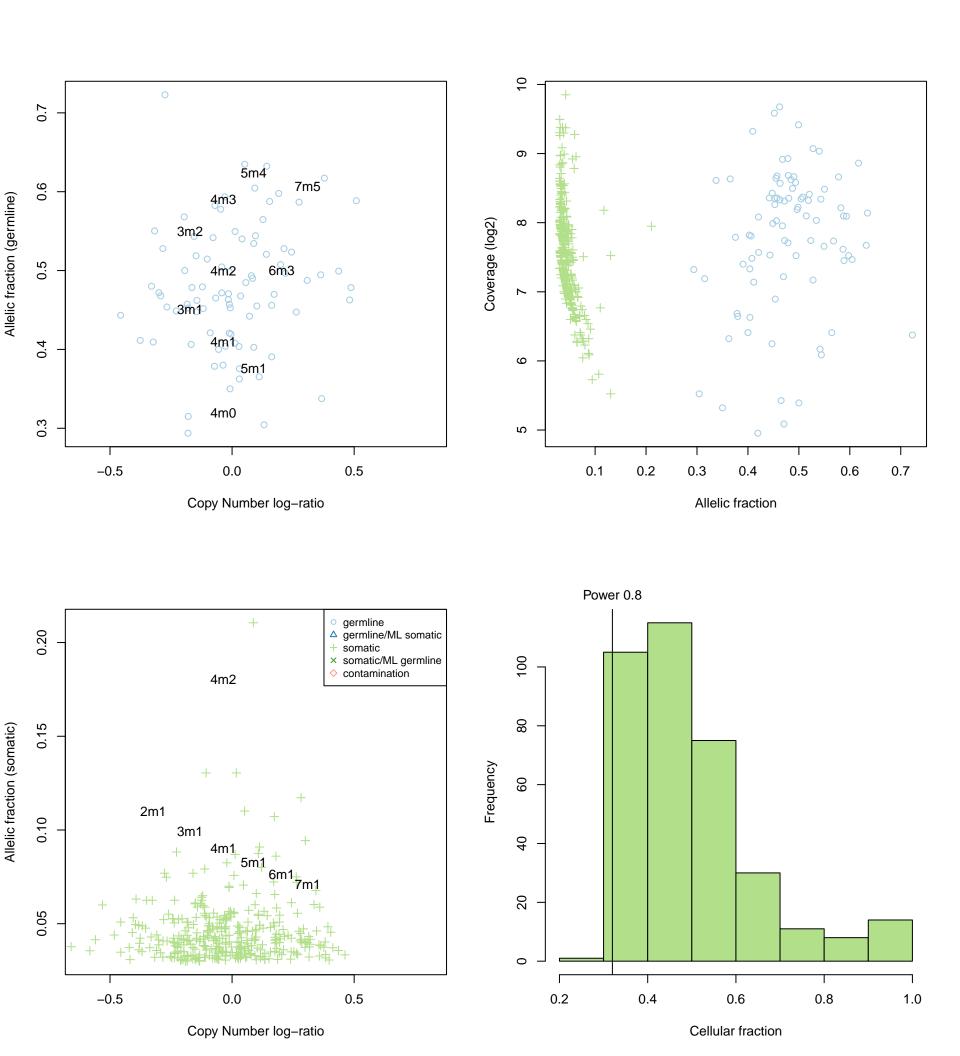
Purity: 0.22 Tumor ploidy: 4.28 SNV log-likelihood: -20.18 GoF: 94.1% Mean coverage: 219;199

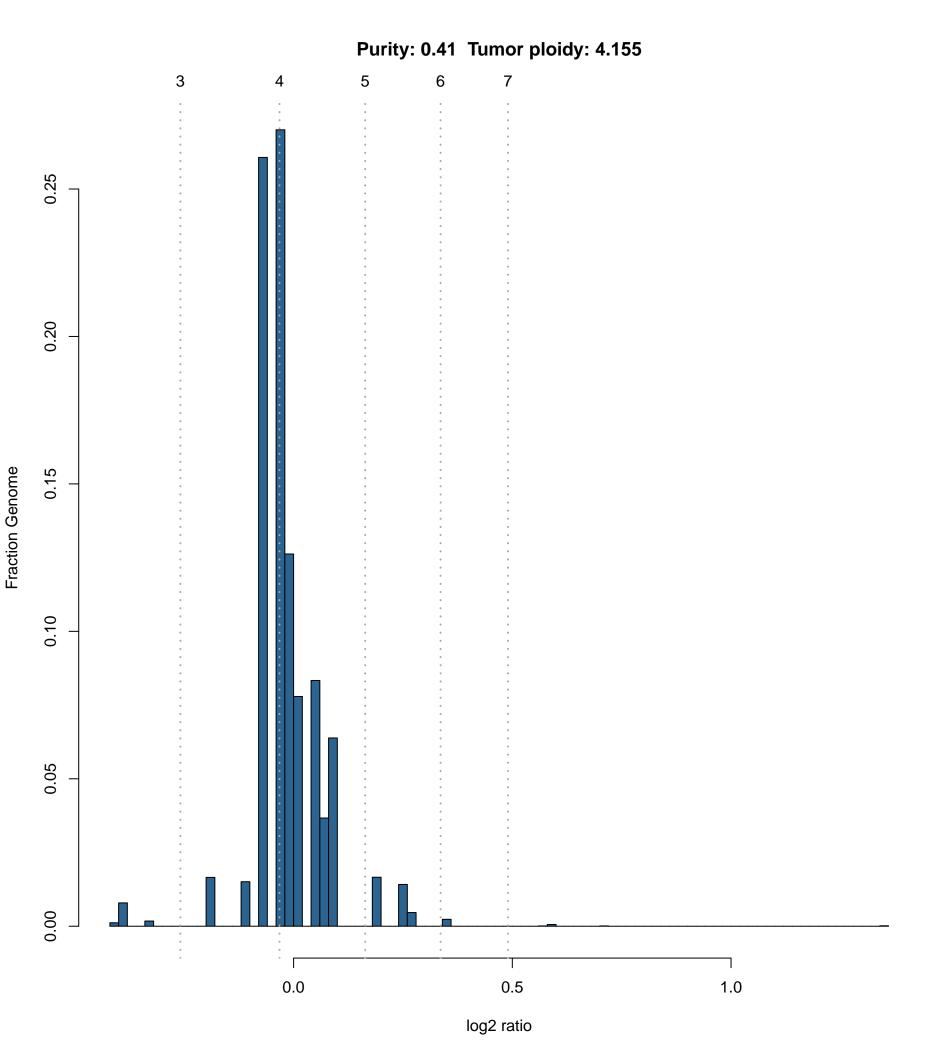


# SCNA-fit log-likelihood: -8938.9

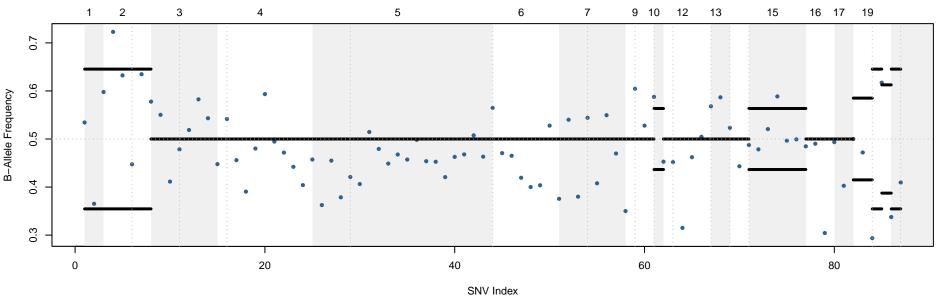




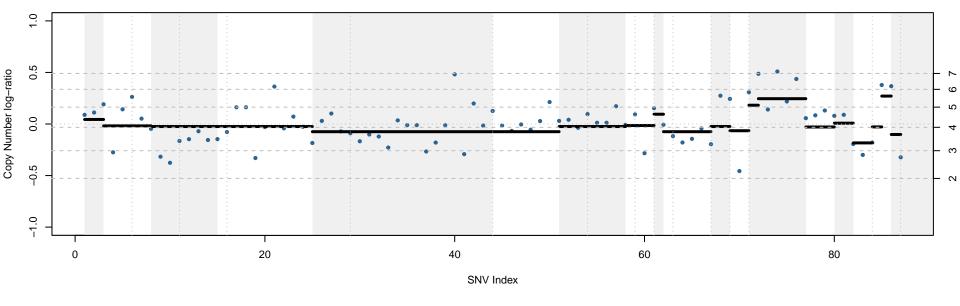


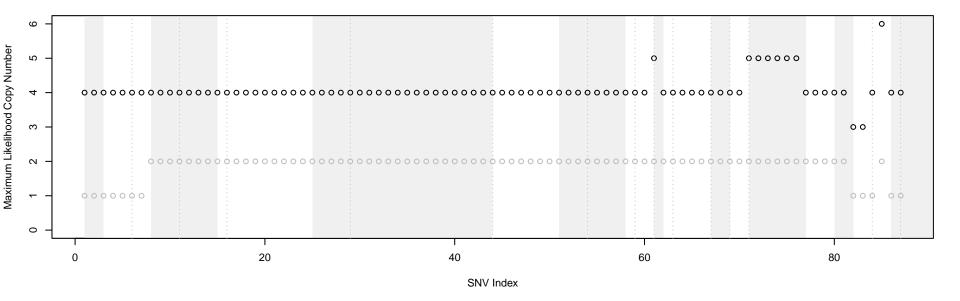


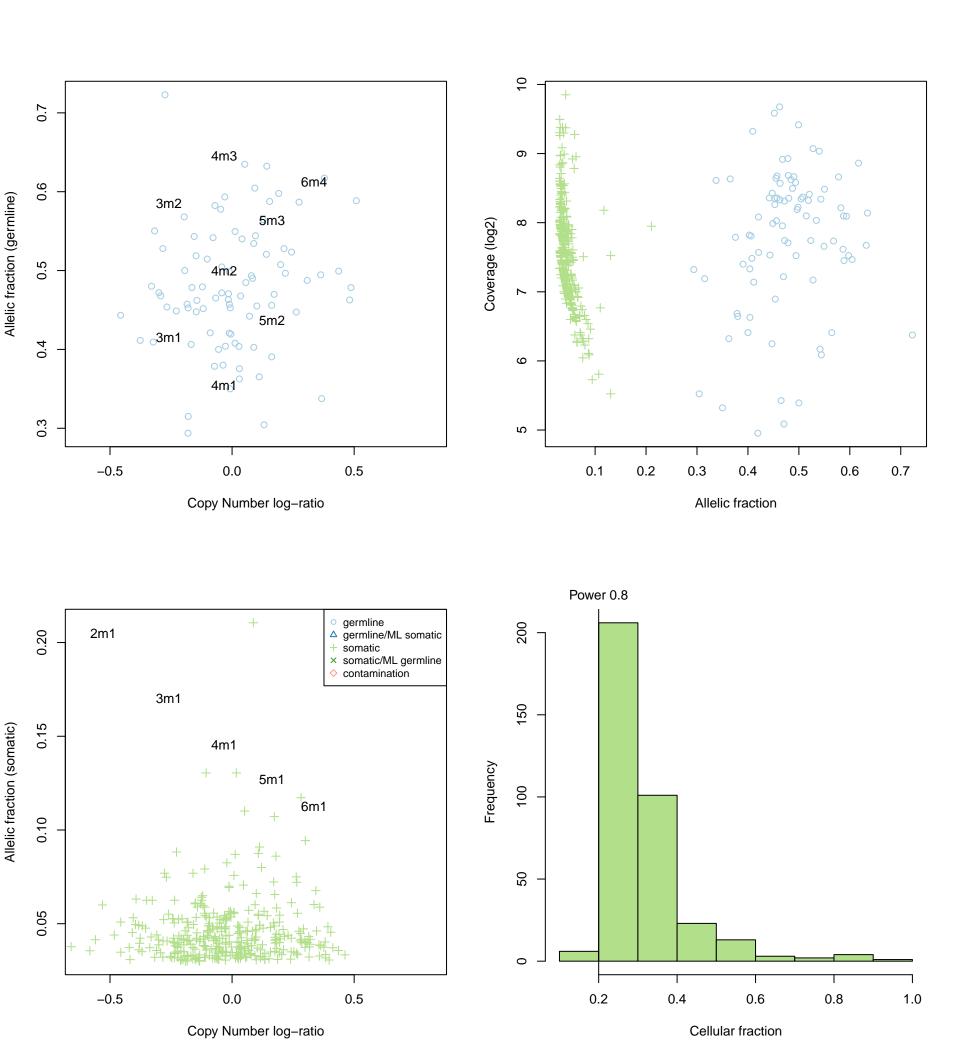
Purity: 0.41 Tumor ploidy: 4.155 SNV log-likelihood: -15.2 GoF: 77.4% Mean coverage: 219;199



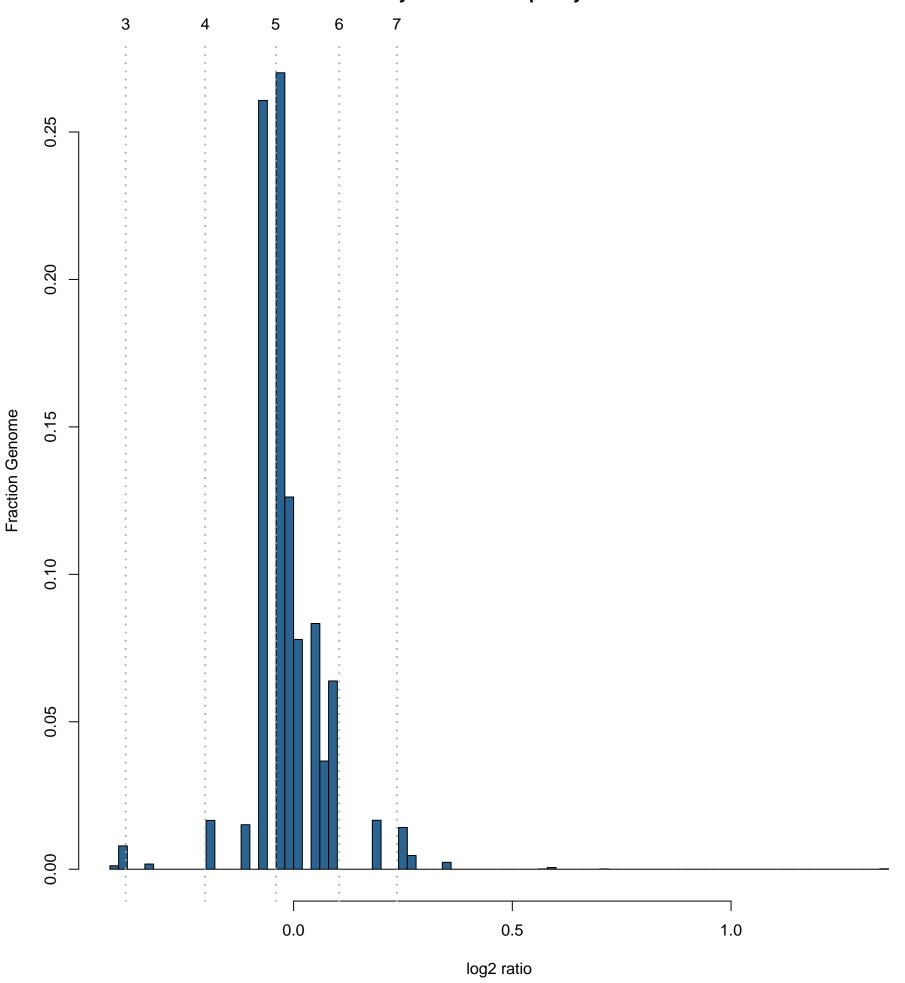
# SCNA-fit log-likelihood: -9020.95

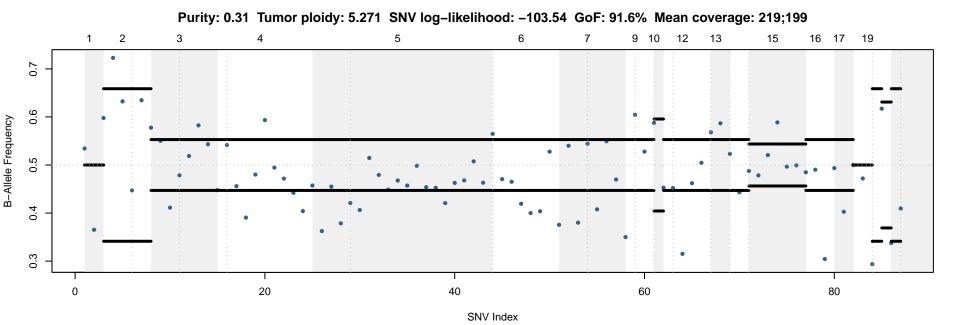




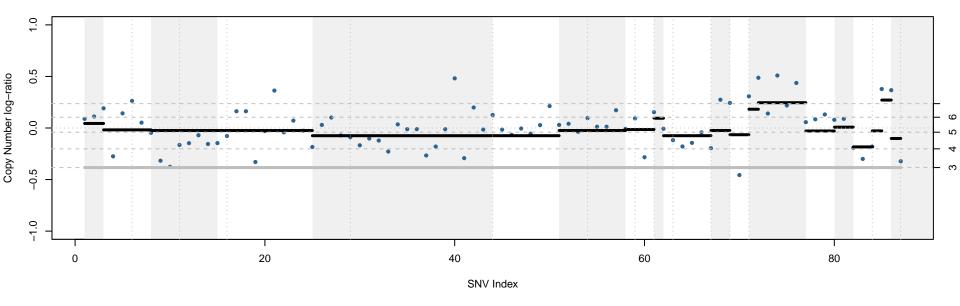


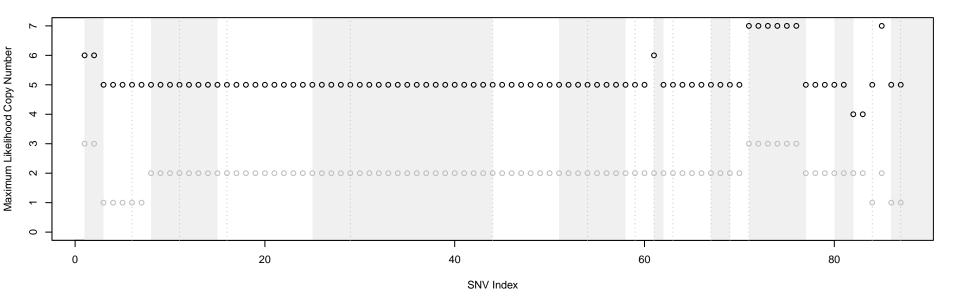
Purity: 0.31 Tumor ploidy: 5.271

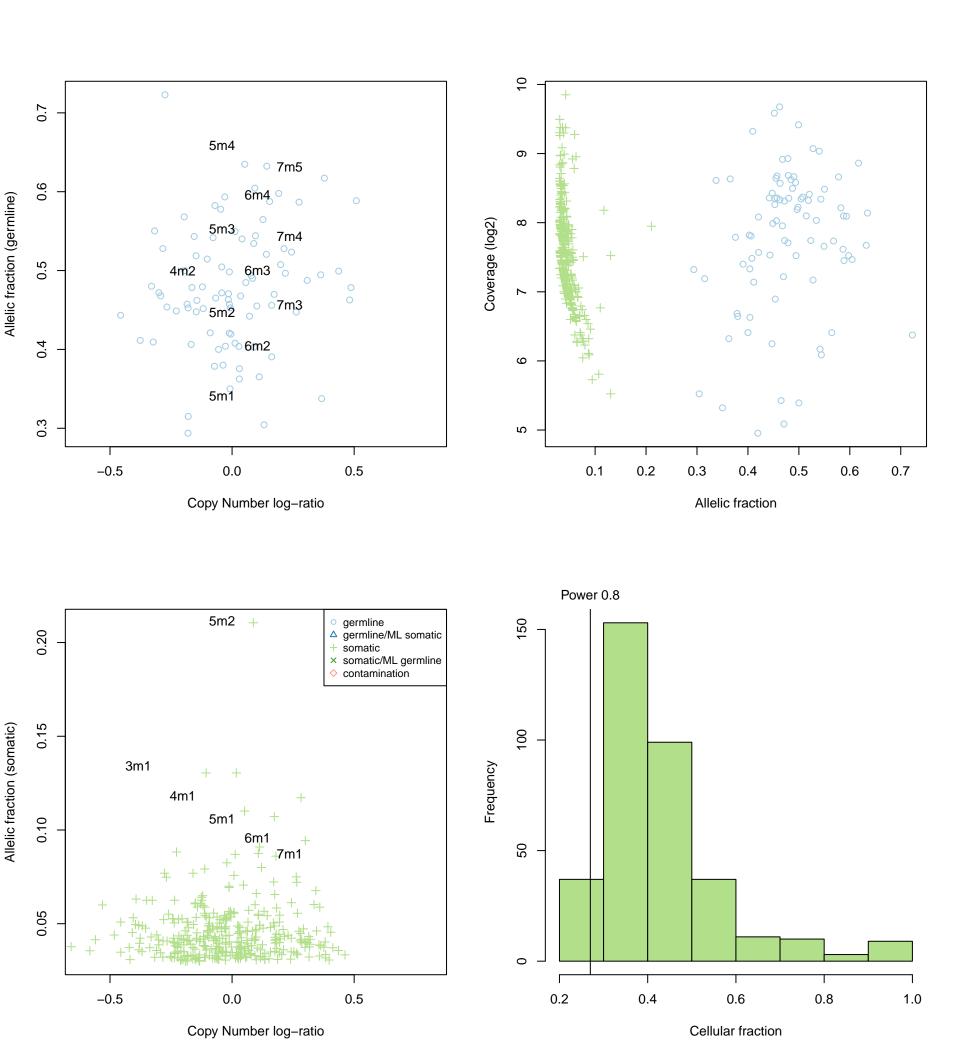




## SCNA-fit log-likelihood: -8953.02





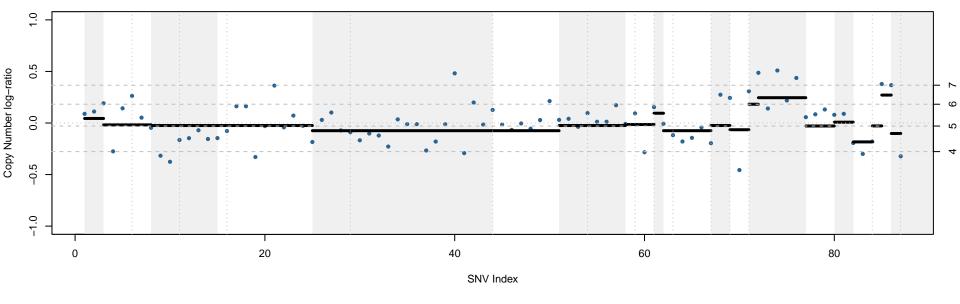


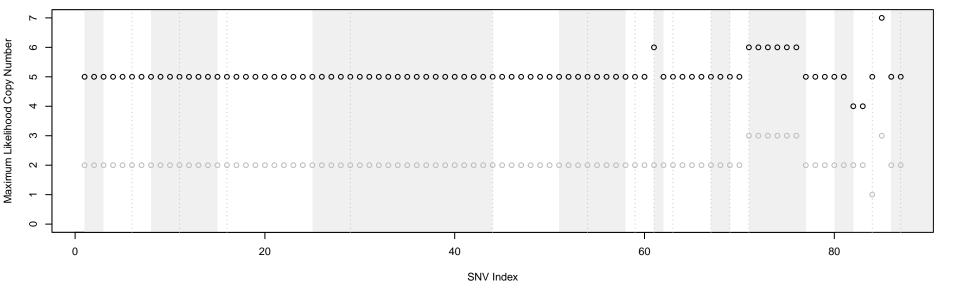
Purity: 0.6 Tumor ploidy: 5.131 4 6 5 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 0.0 0.5 1.0 log2 ratio

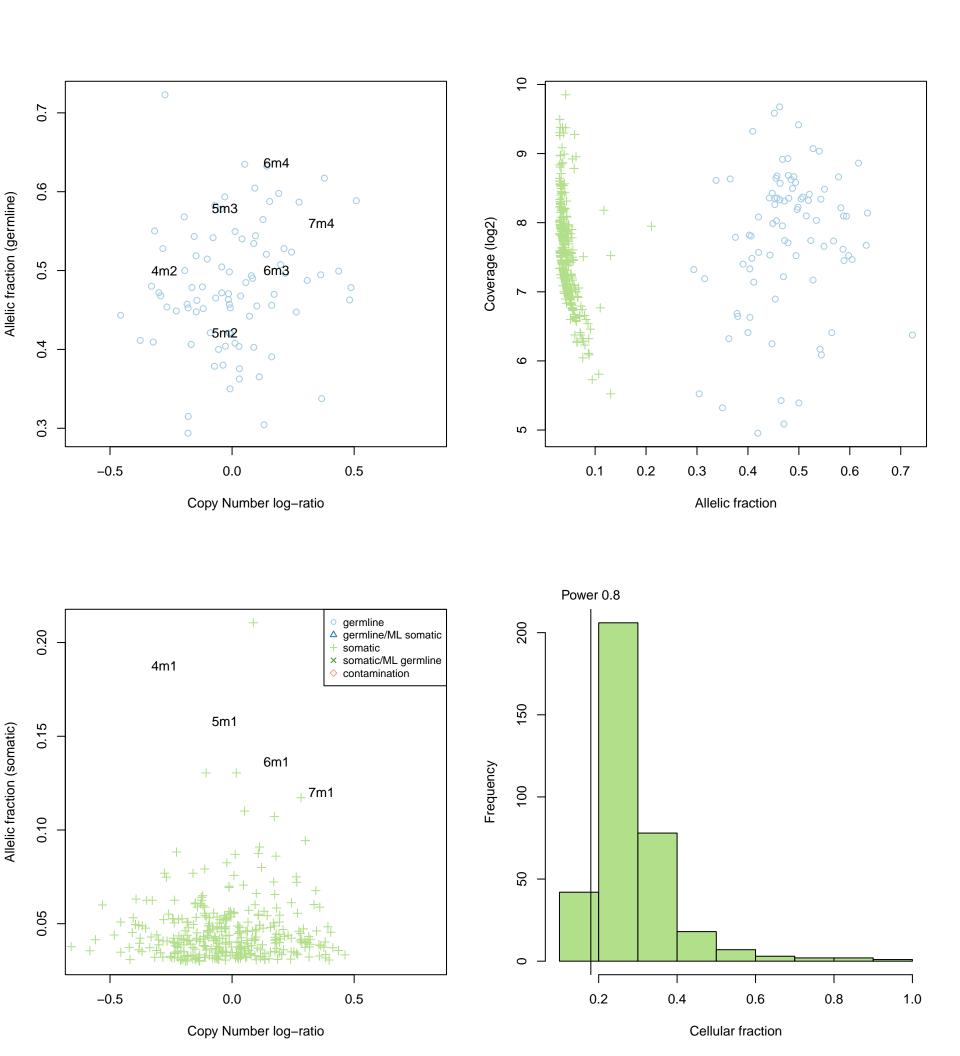
Purity: 0.6 Tumor ploidy: 5.131 SNV log-likelihood: -219.79 GoF: 73.2% Mean coverage: 219;199

# SCNA-fit log-likelihood: -9040.25

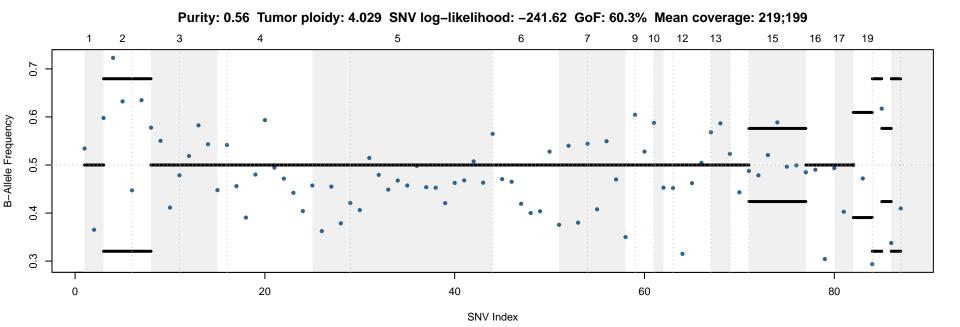
SNV Index



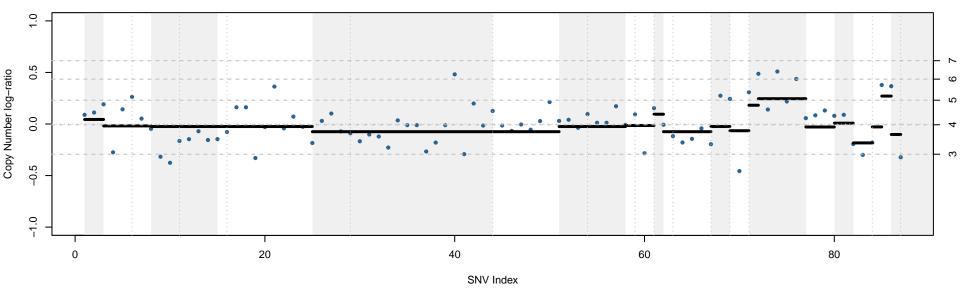


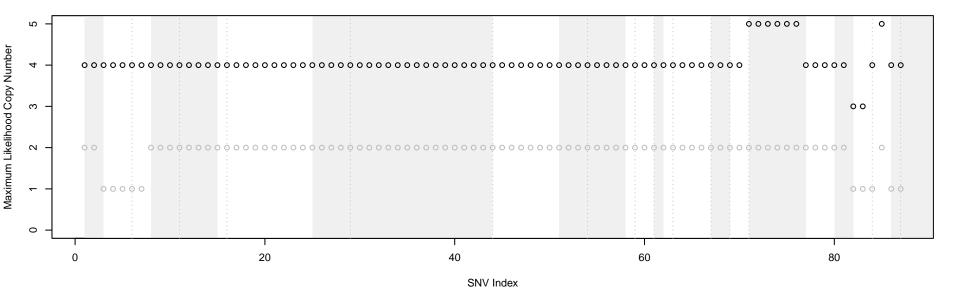


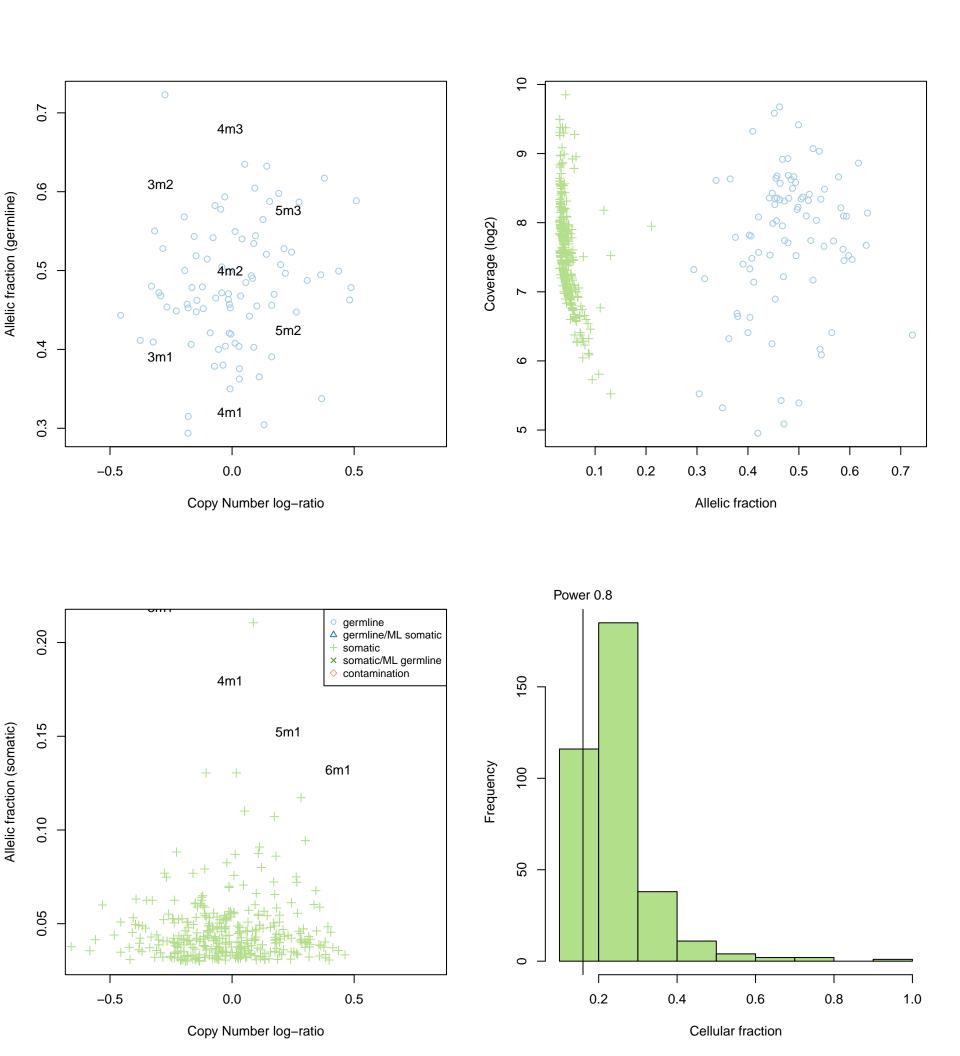
Purity: 0.56 Tumor ploidy: 4.029 3 6 5 0.25 0.20 0.15 Fraction Genome 0.10 0.05 0.00 0.0 0.5 1.0 log2 ratio



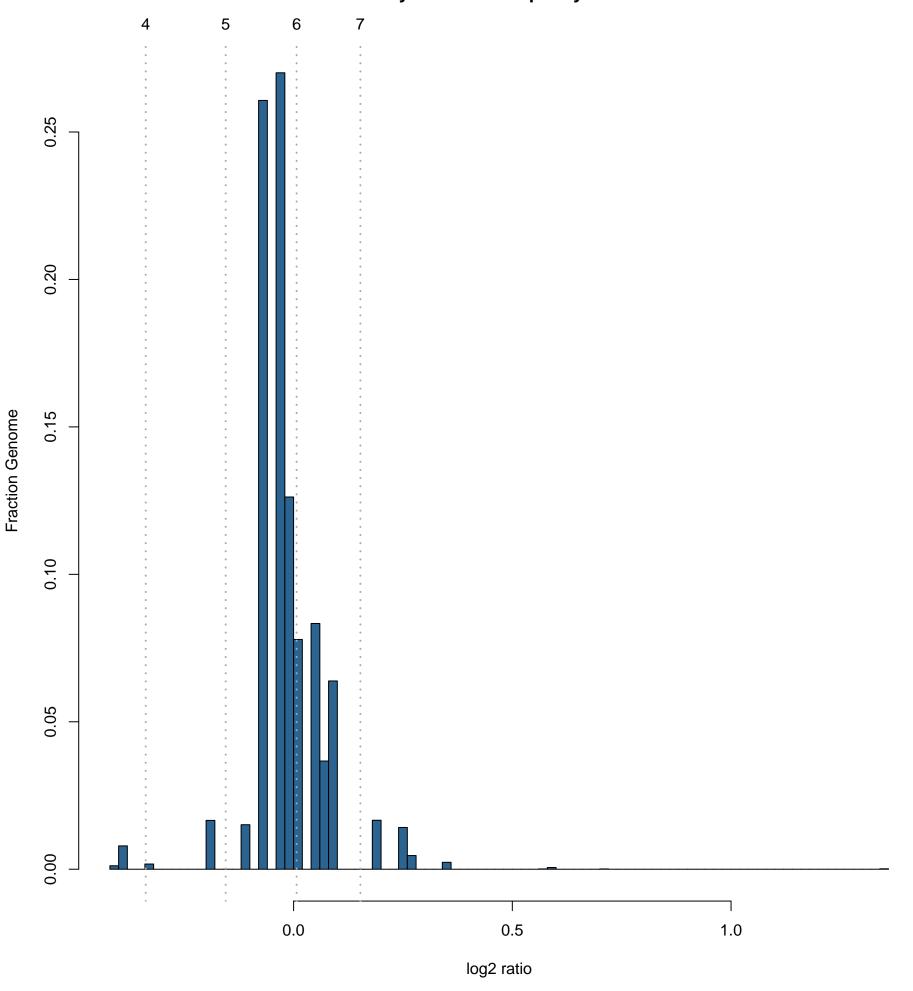
SCNA-fit log-likelihood: -9066.54

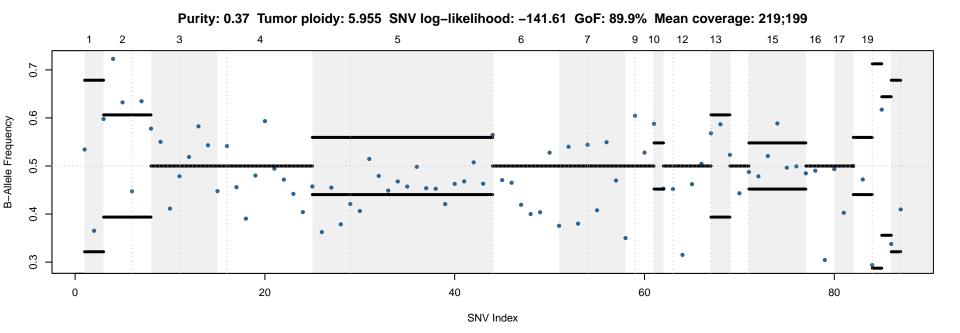




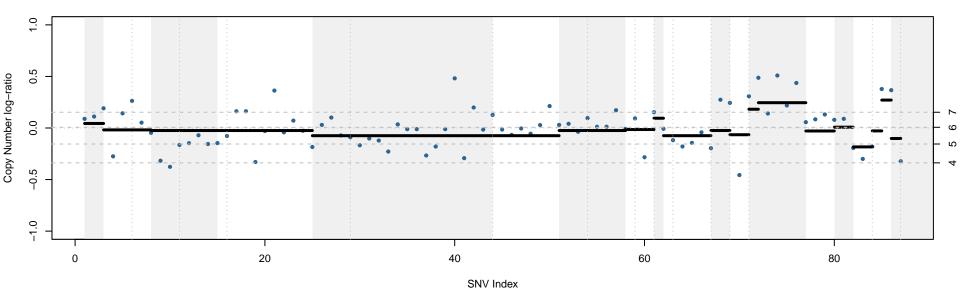


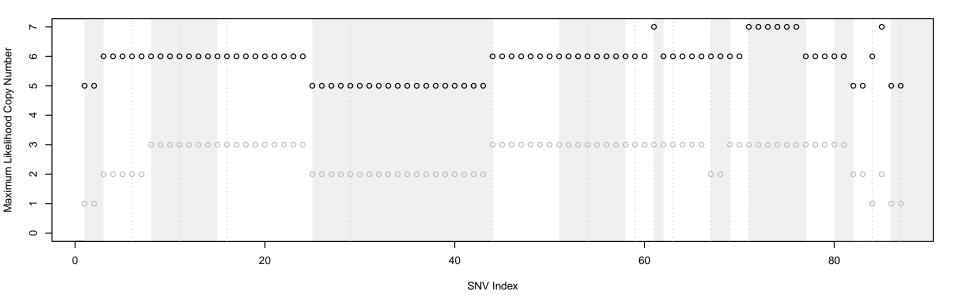
Purity: 0.37 Tumor ploidy: 5.955

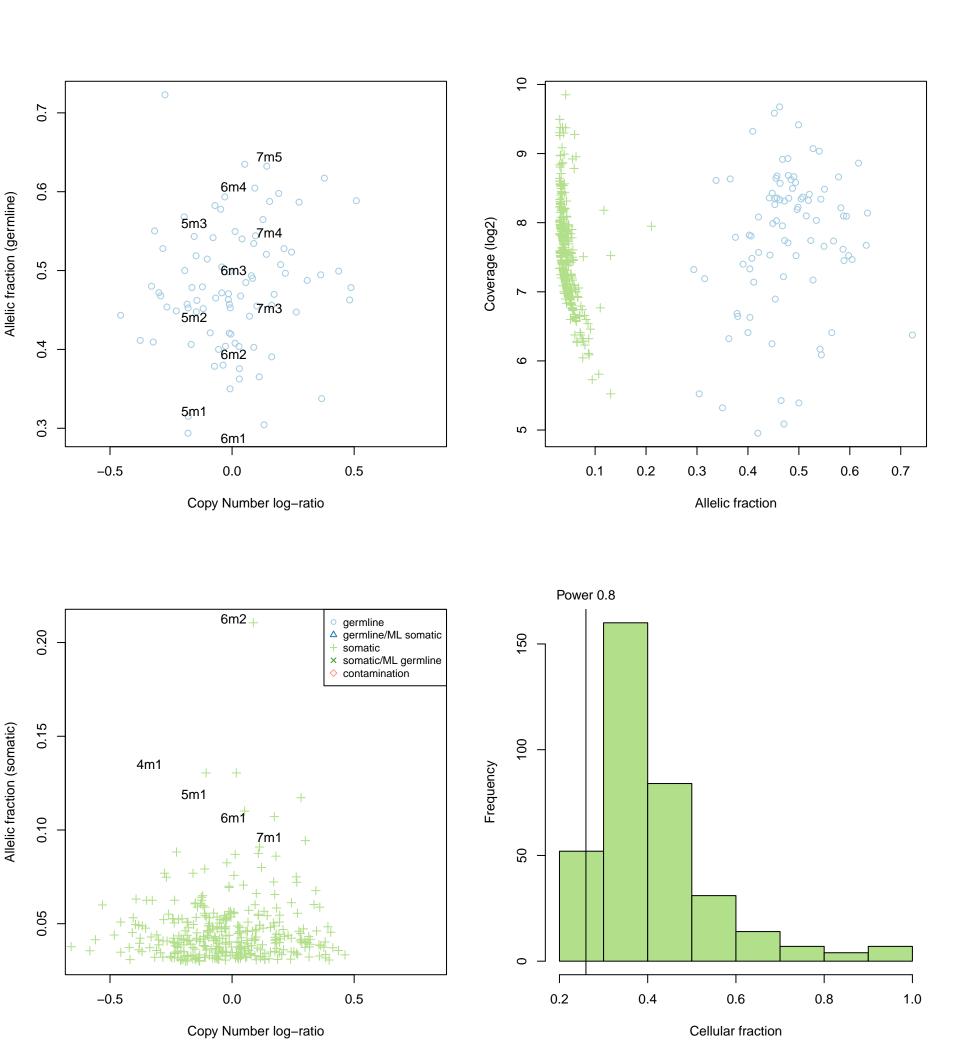


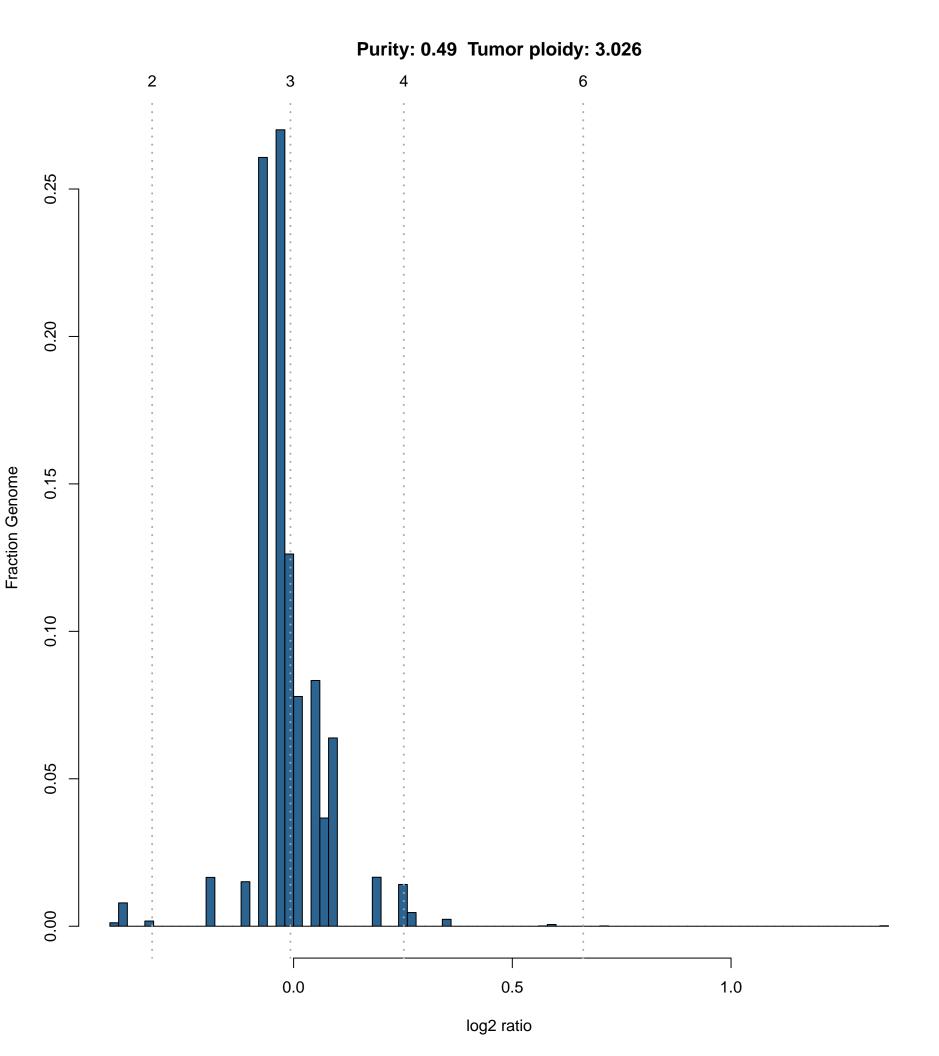


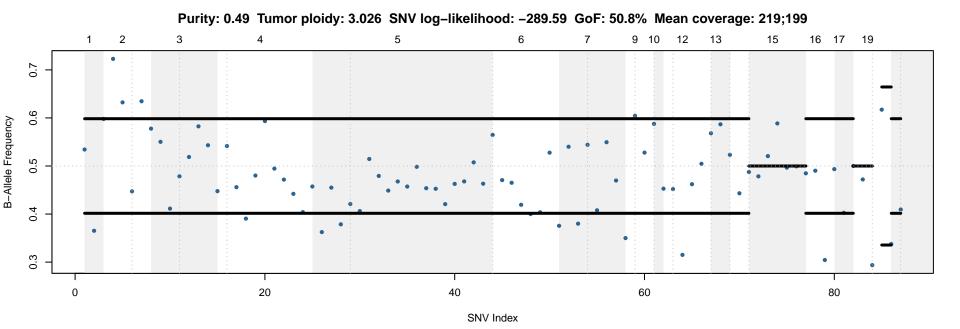
### SCNA-fit log-likelihood: -9323.64



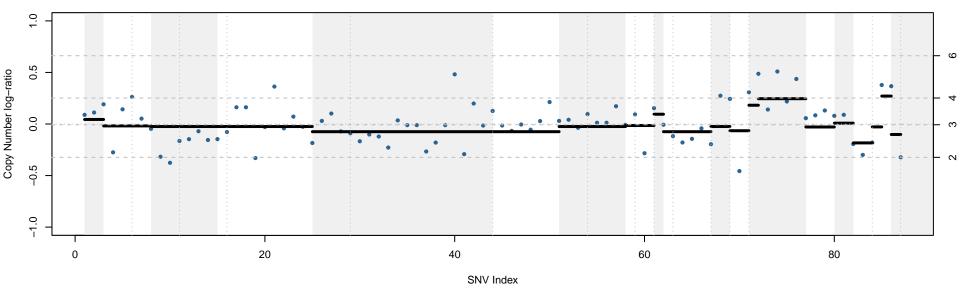


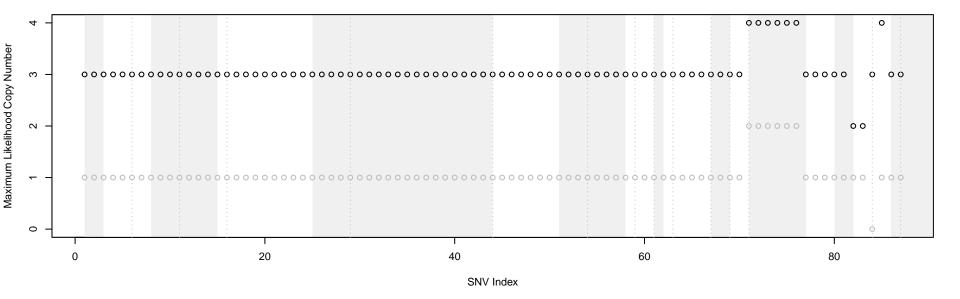


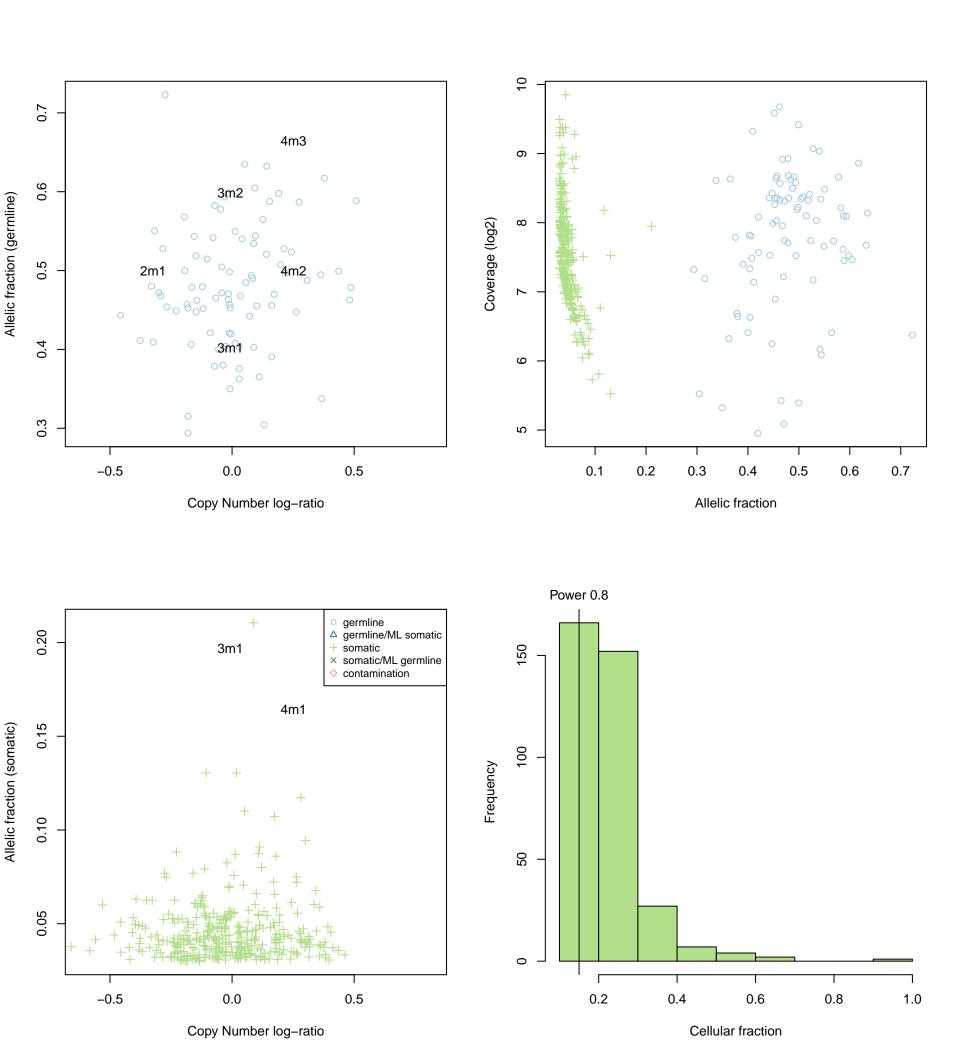


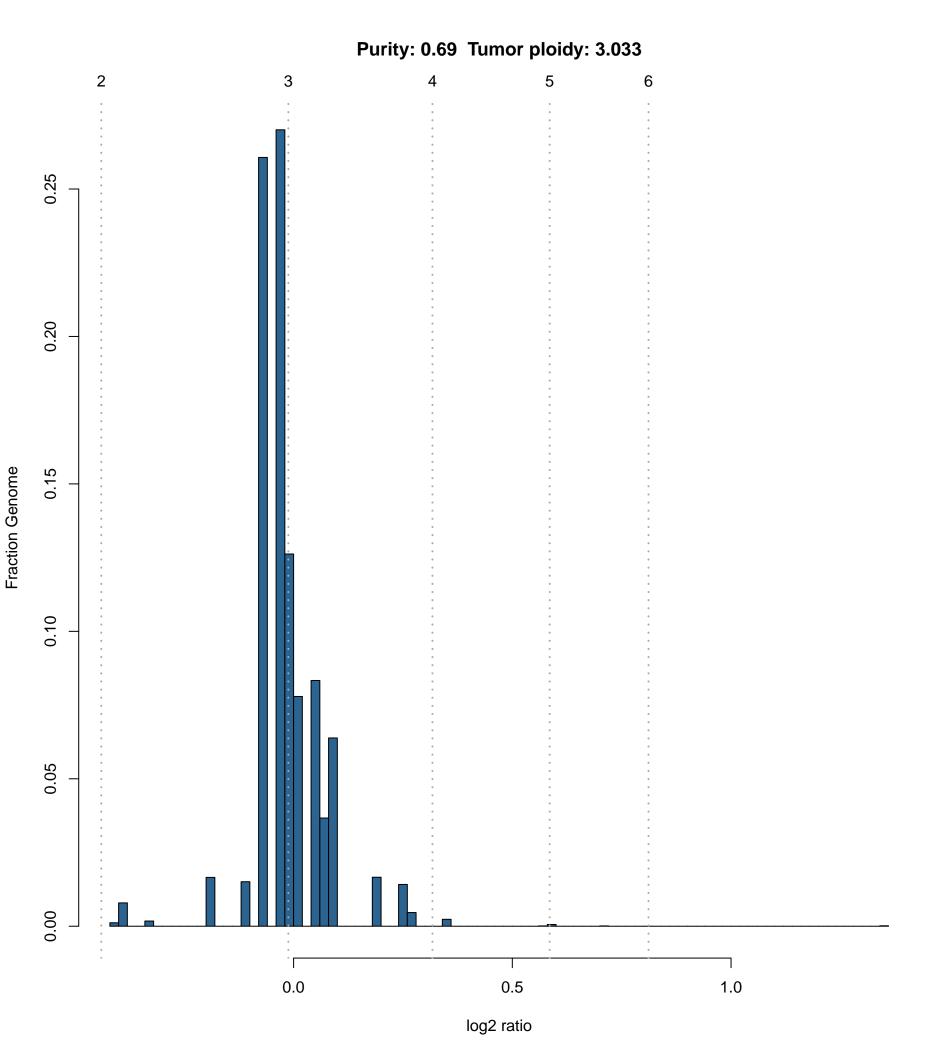


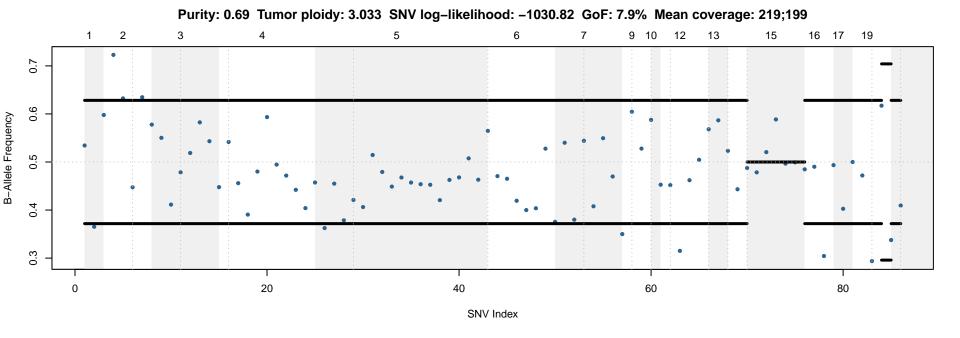
### SCNA-fit log-likelihood: -9076.08



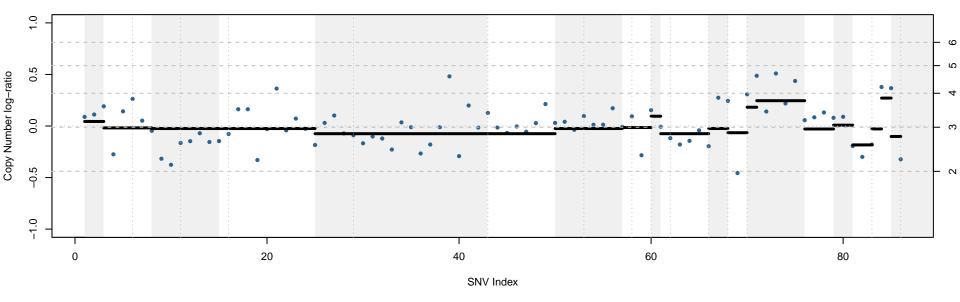


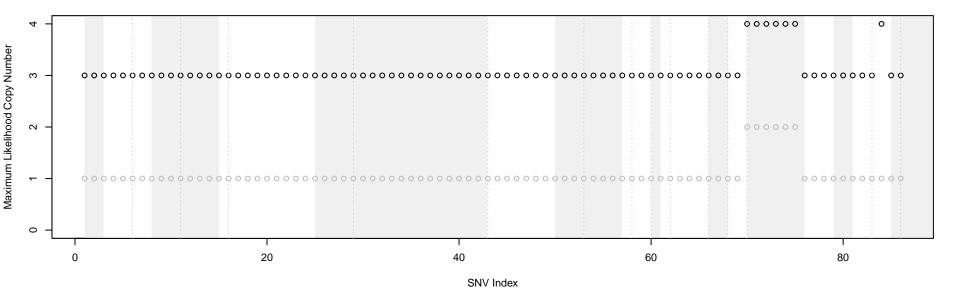


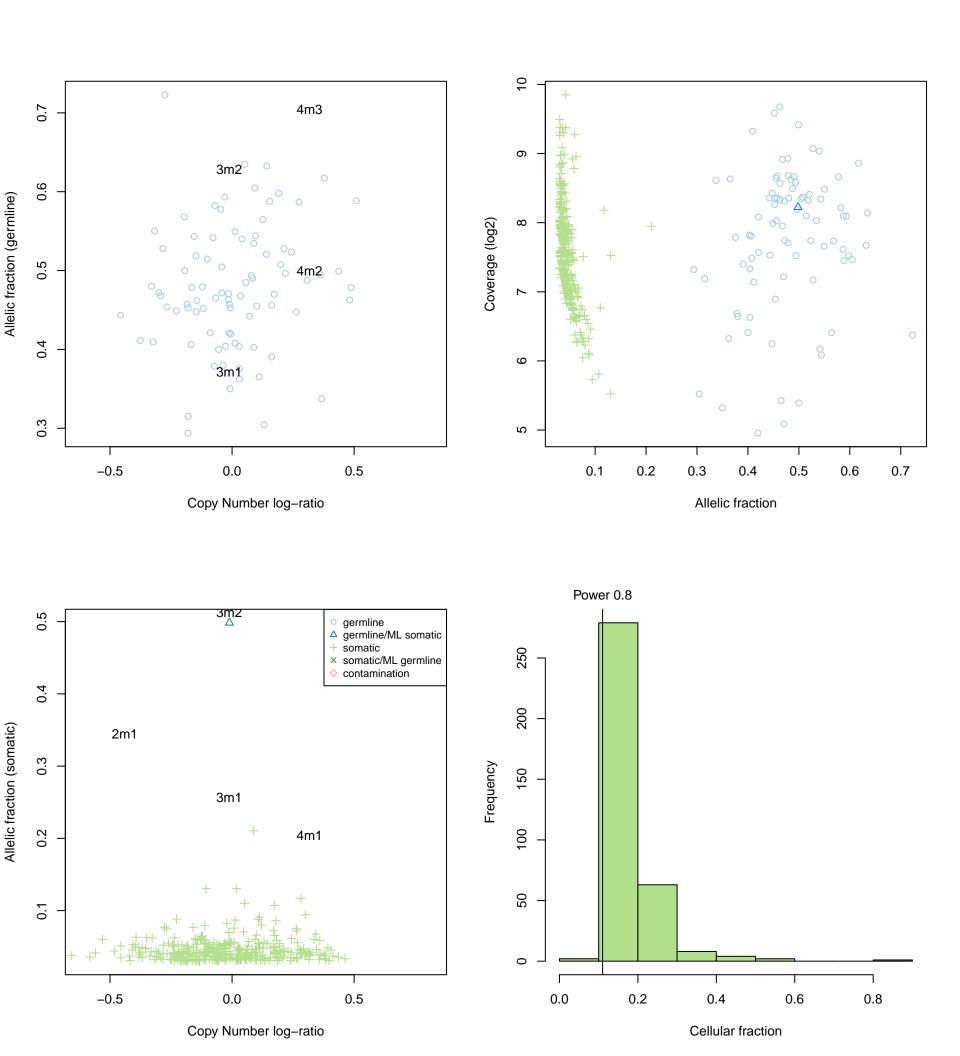




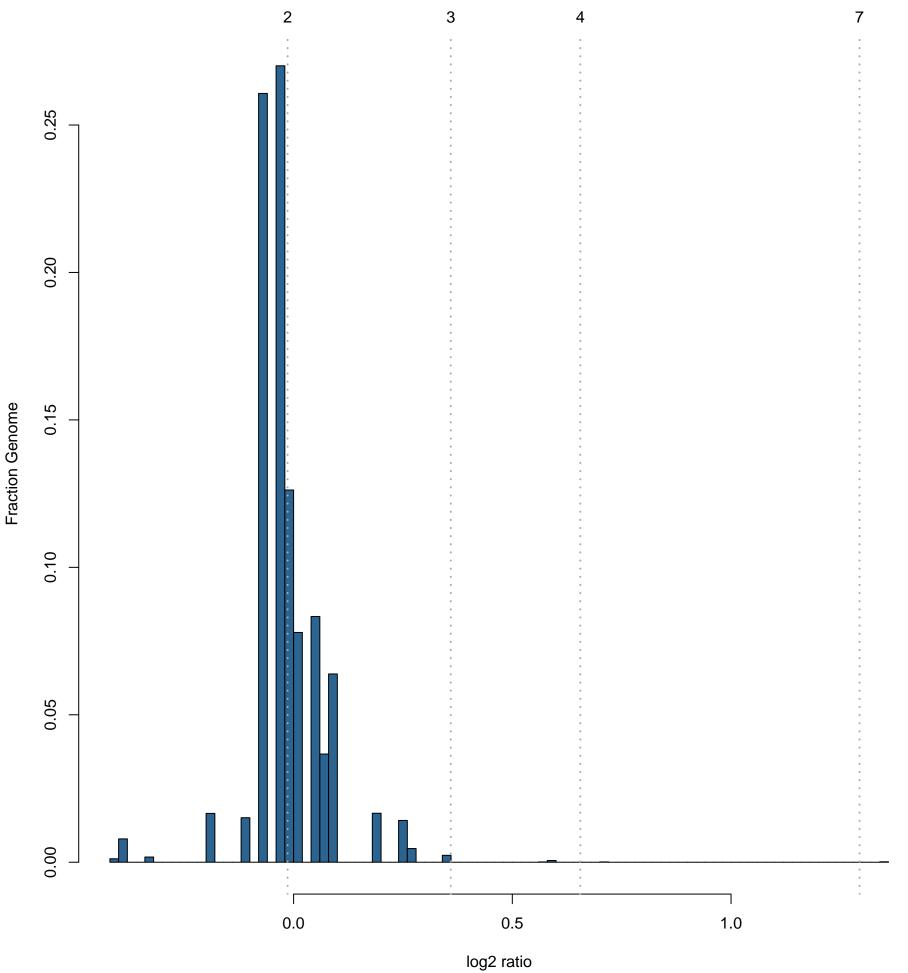
# SCNA-fit log-likelihood: -9098.76

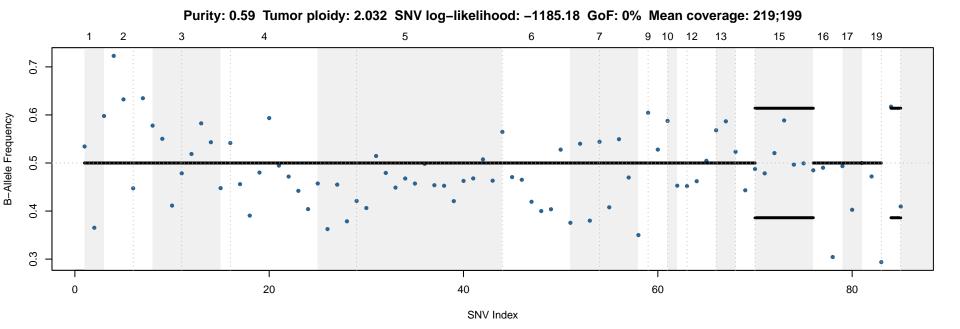






Purity: **0.59** Tumor ploidy: **2.032** 





# SCNA-fit log-likelihood: -9129.34

