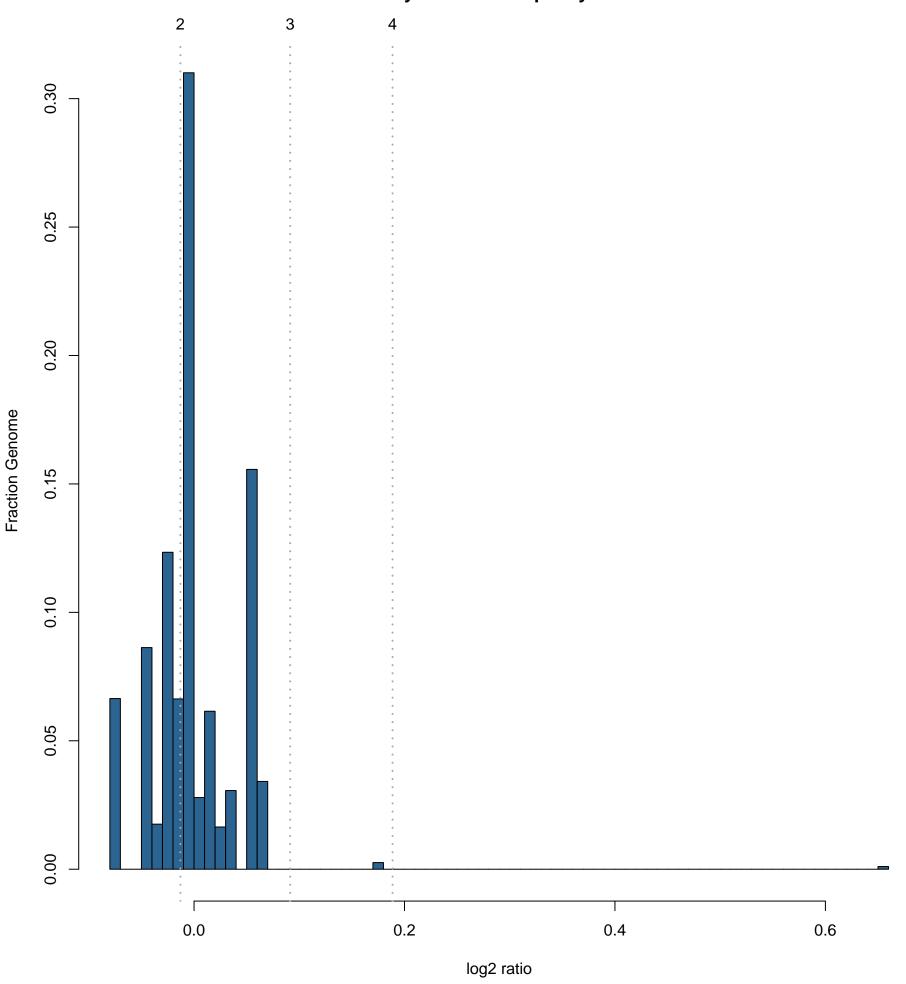
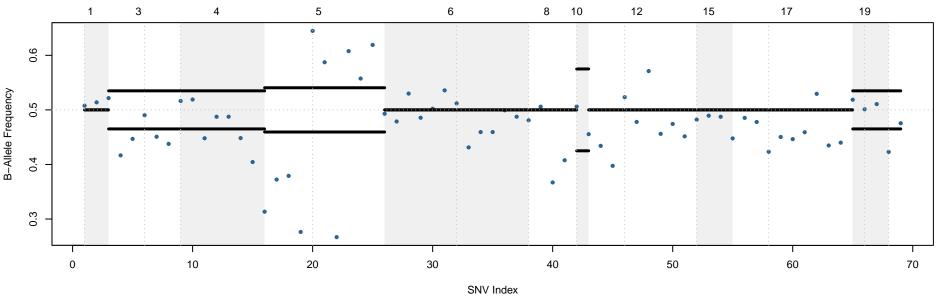
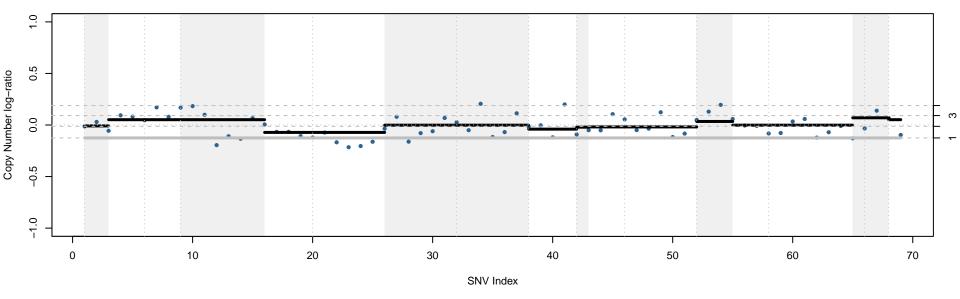
Purity: 0.15 Tumor ploidy: 2.12

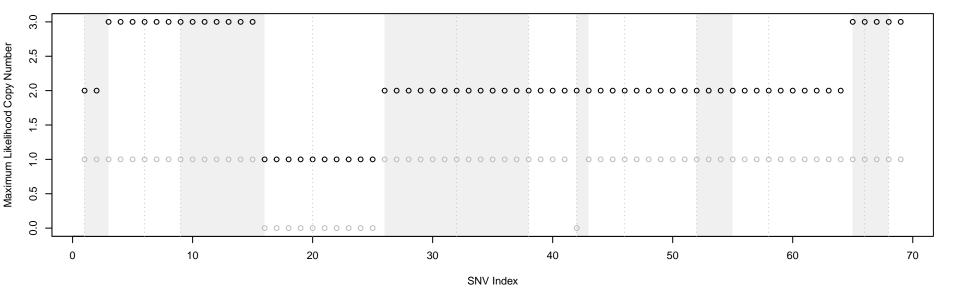


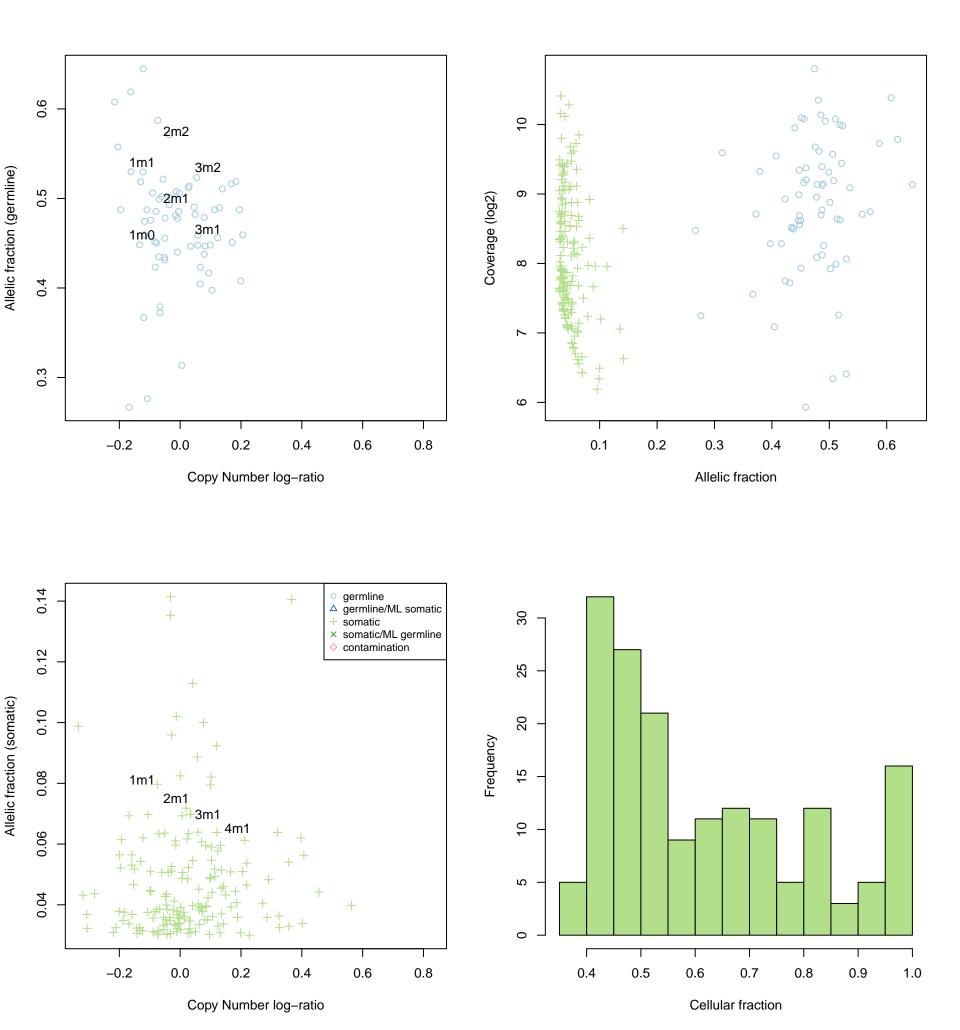




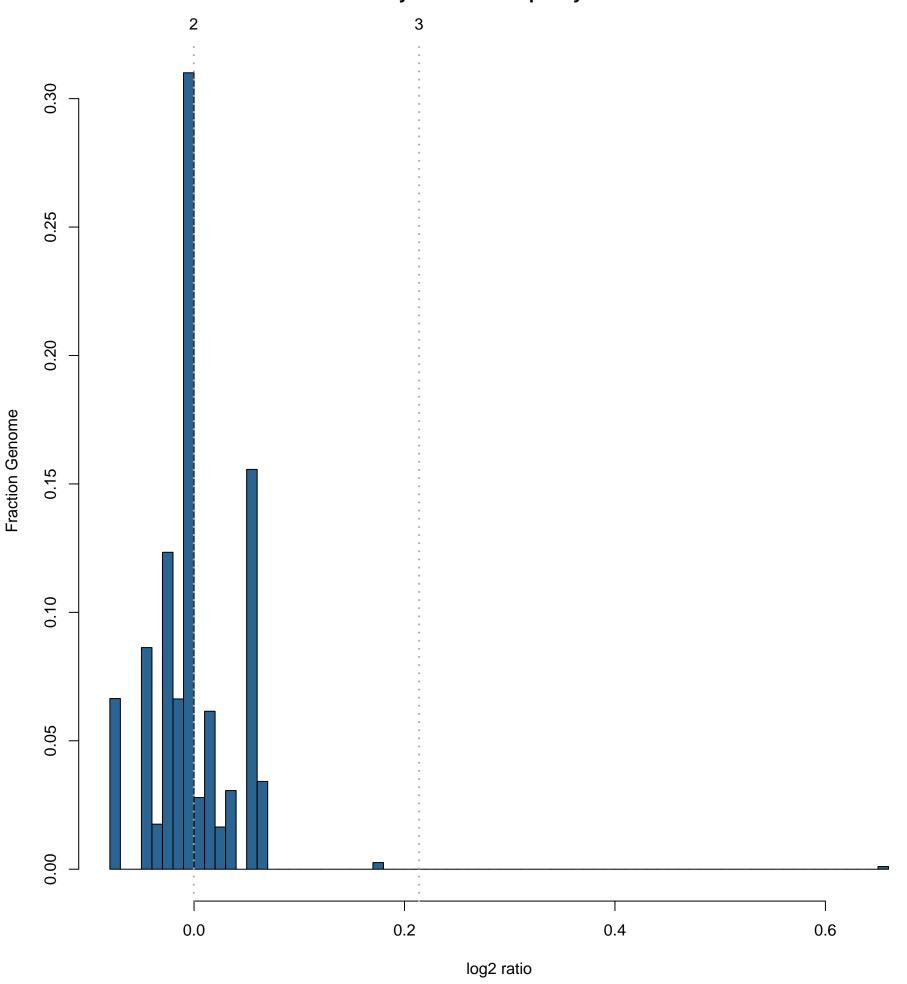
## SCNA-fit log-likelihood: -1083.38

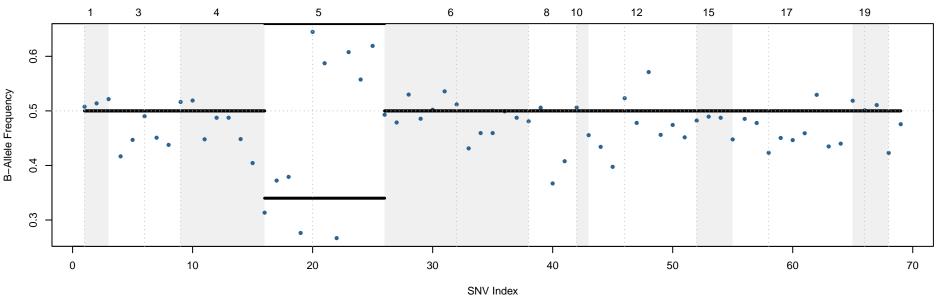




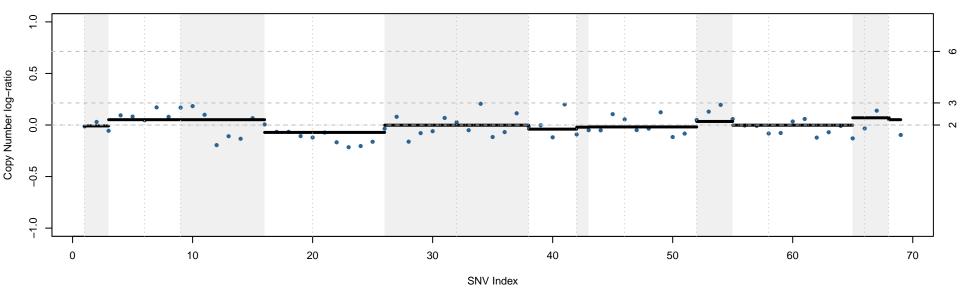


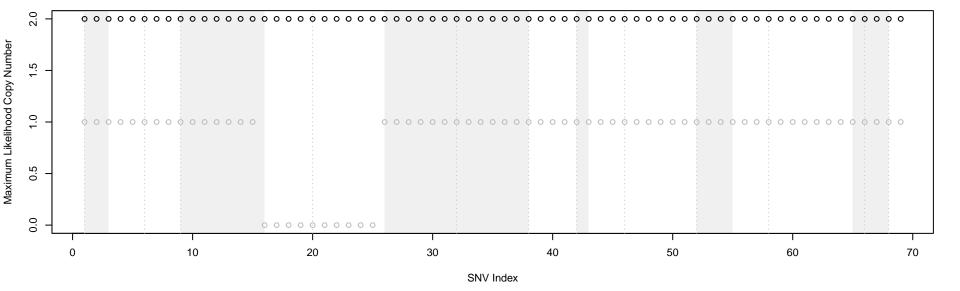
Purity: 0.32 Tumor ploidy: 2.001

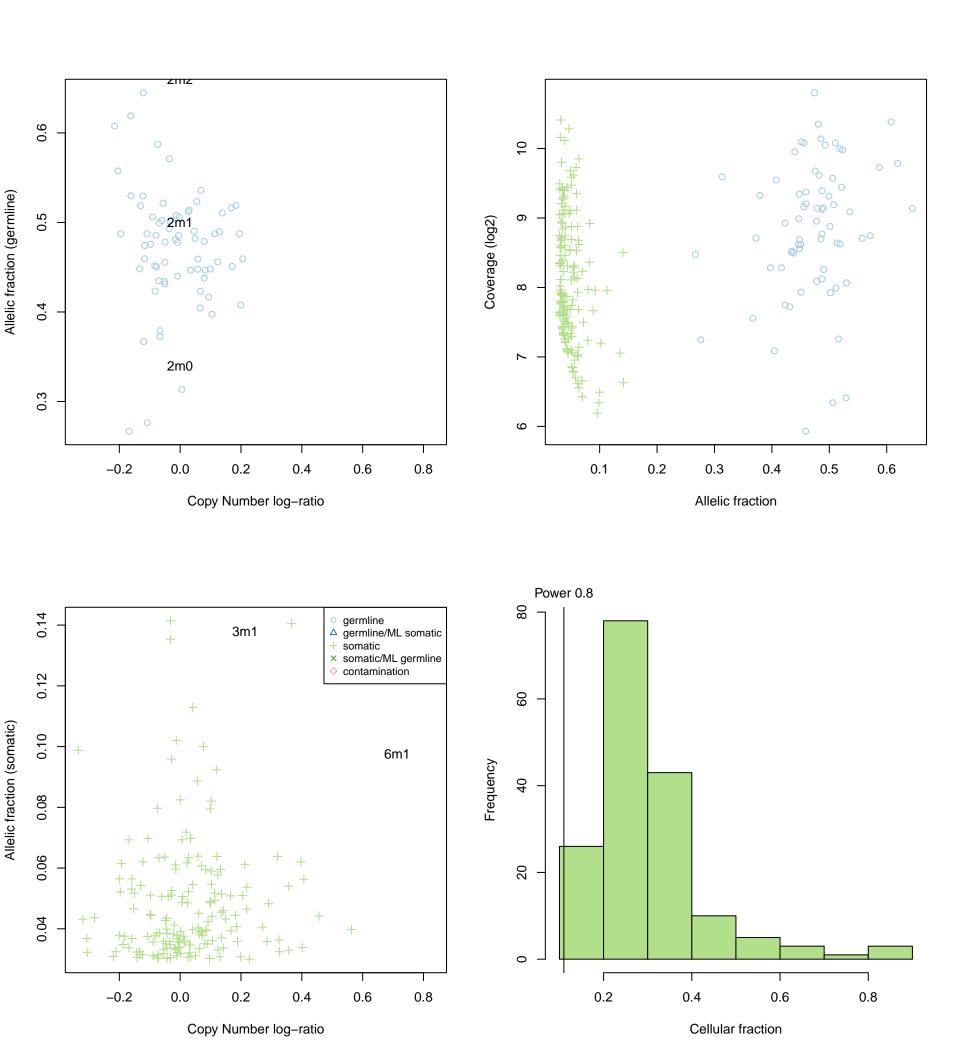




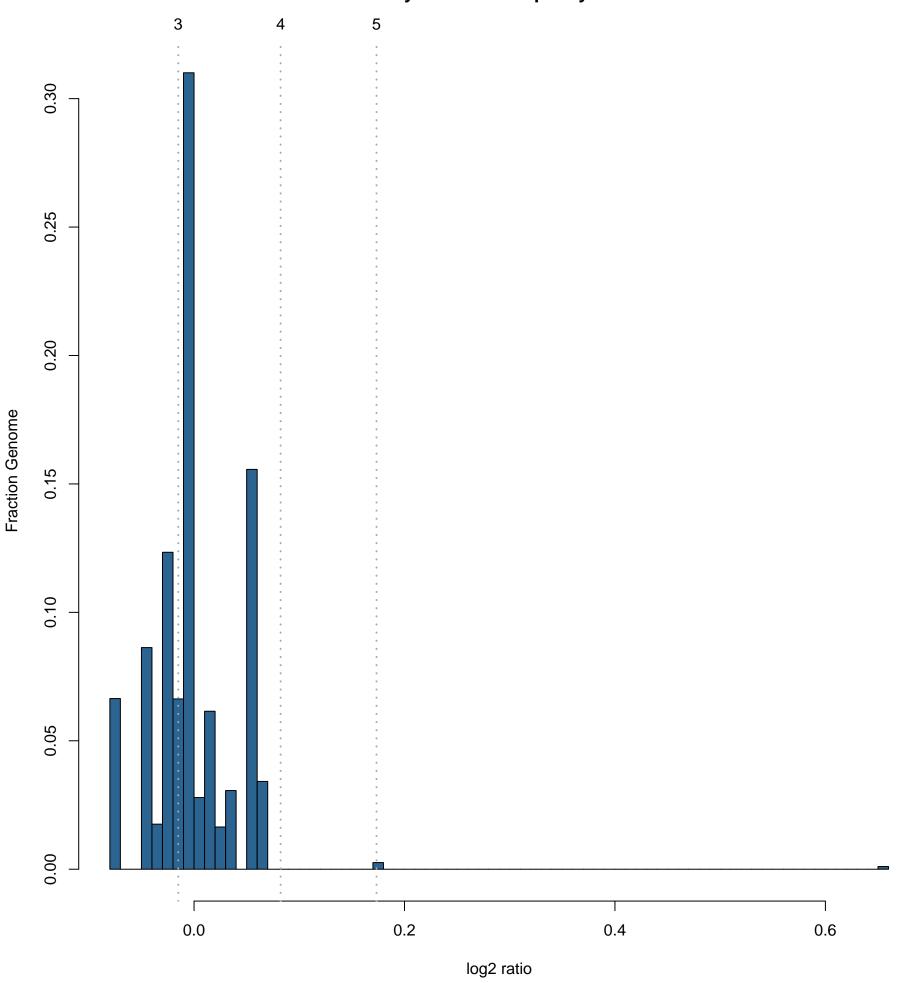
# SCNA-fit log-likelihood: -1131.67

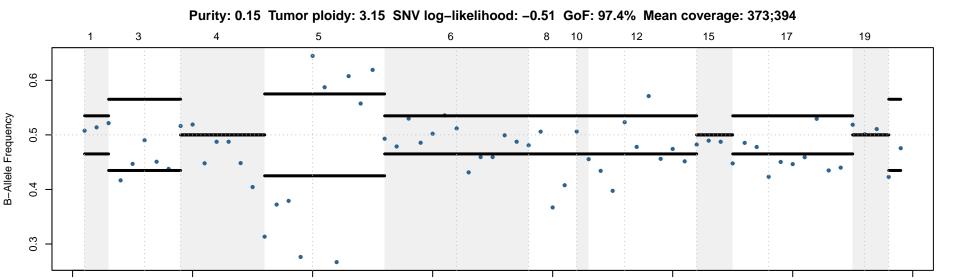






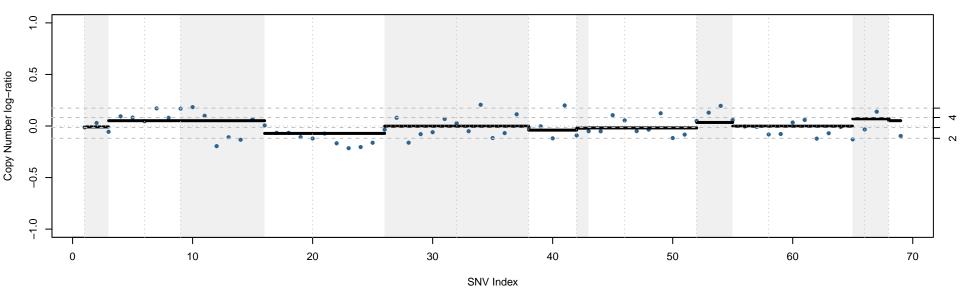
Purity: 0.15 Tumor ploidy: 3.15

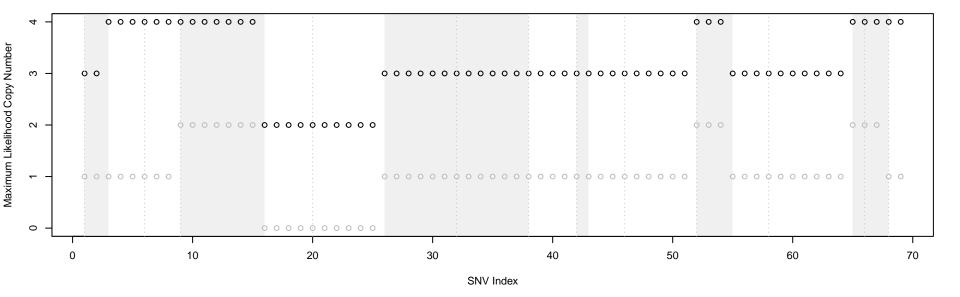


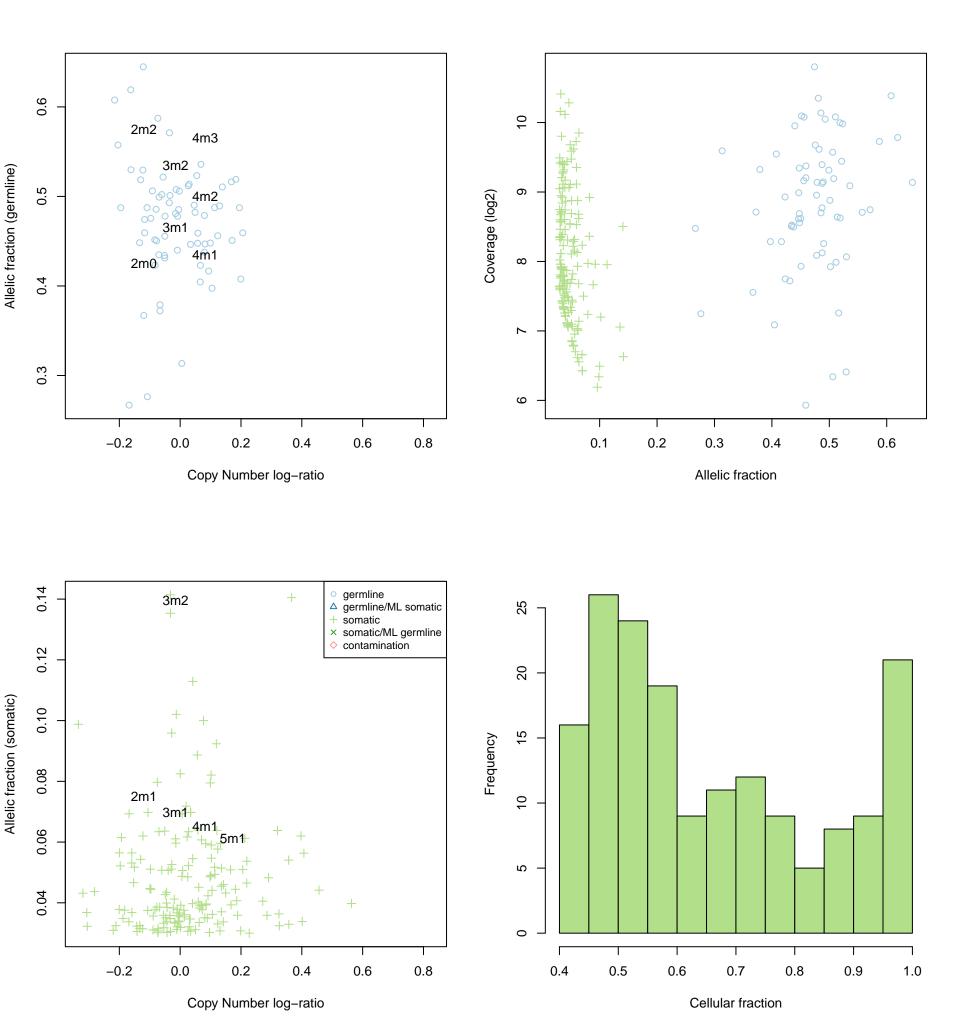


## SCNA-fit log-likelihood: -1059.32

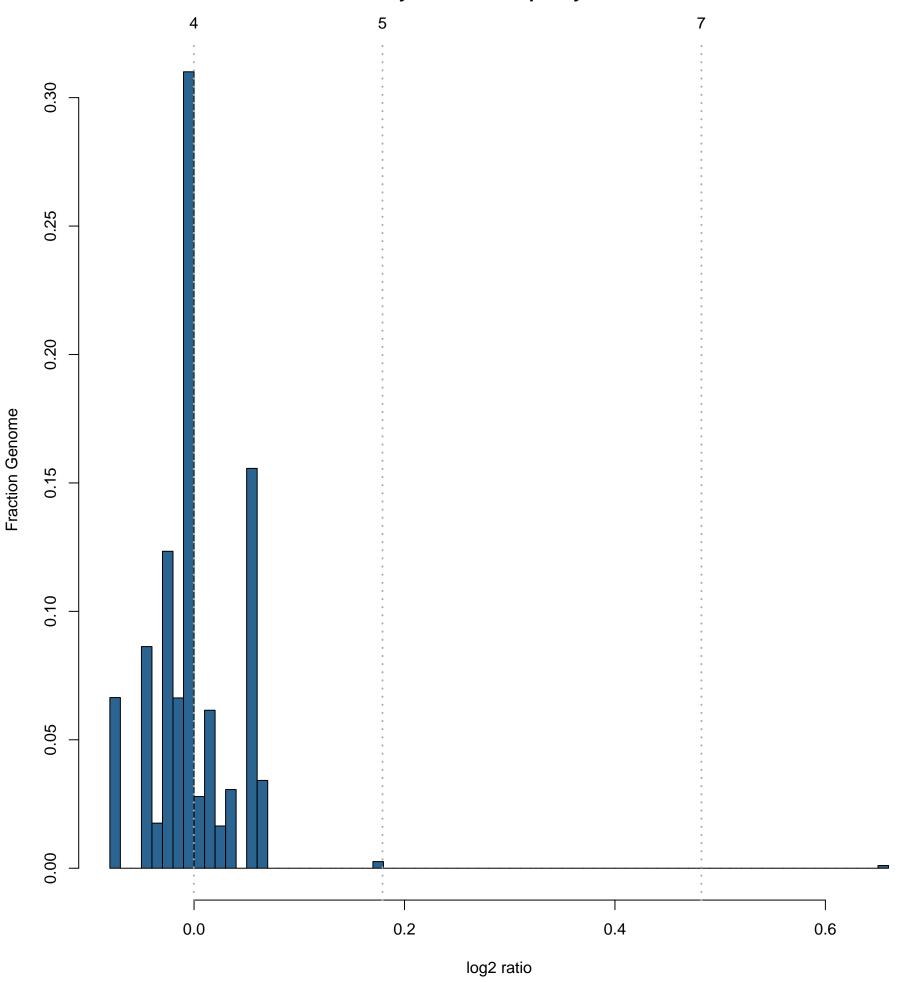
SNV Index



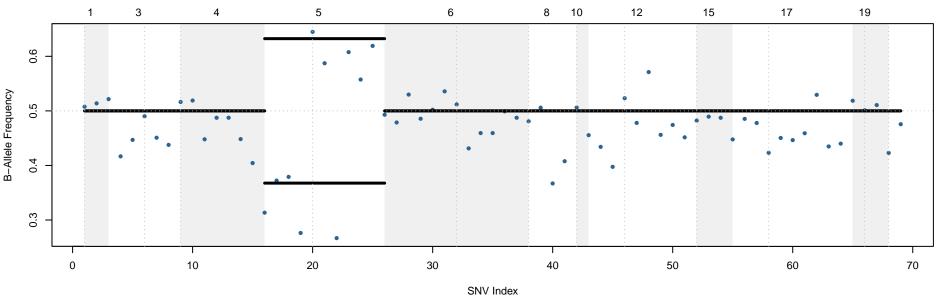




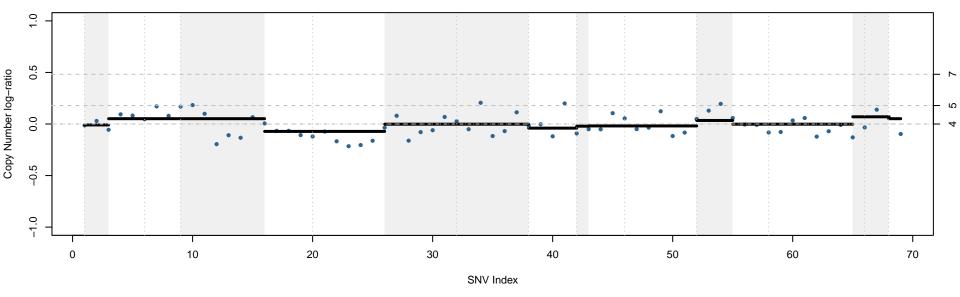
Purity: 0.36 Tumor ploidy: 4.001

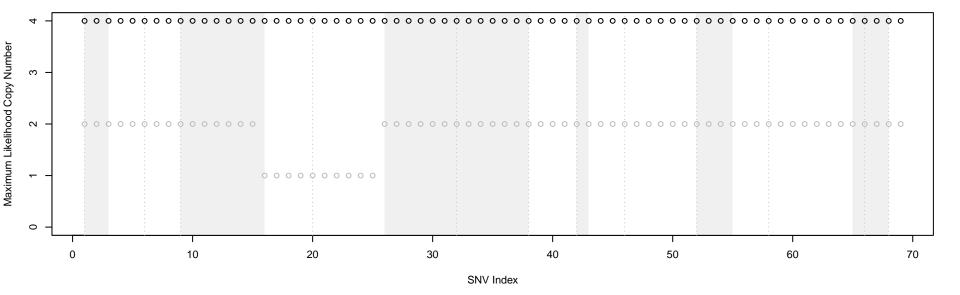


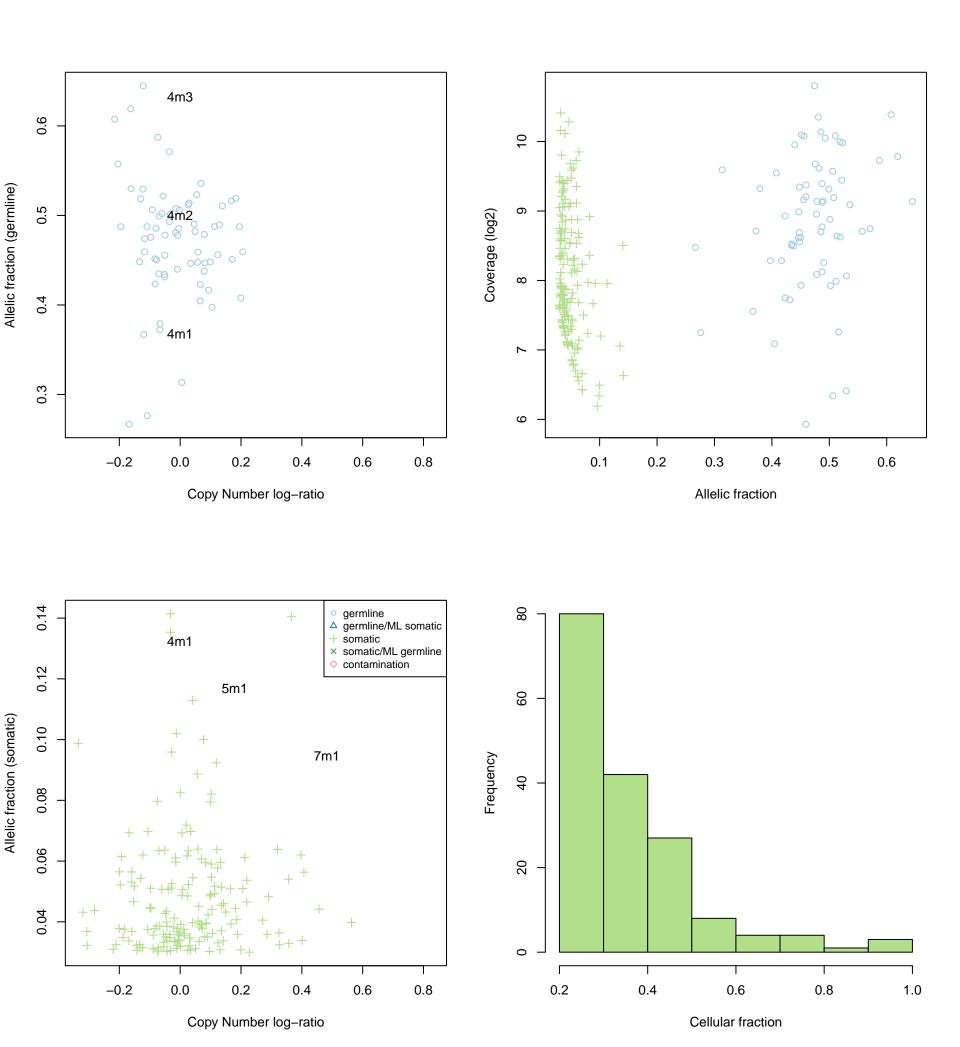




# SCNA-fit log-likelihood: -1136.17

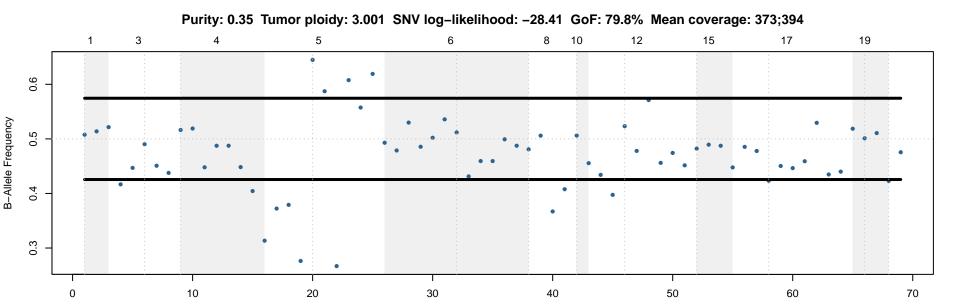






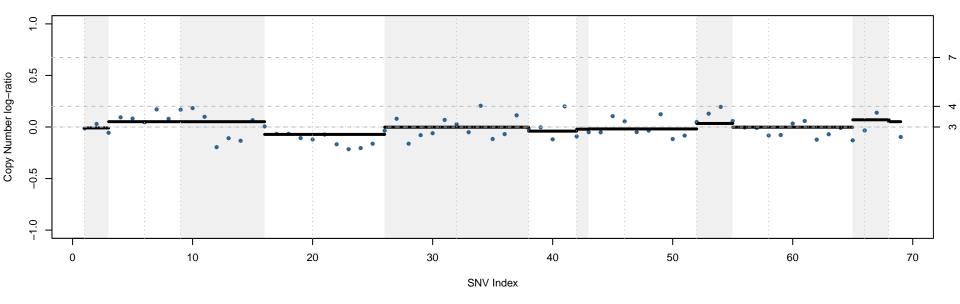
Purity: 0.35 Tumor ploidy: 3.001 3 7 0.30 0.20 Fraction Genome 0.15 0.10 0.05 0.00 0.0 0.2 0.4 0.6

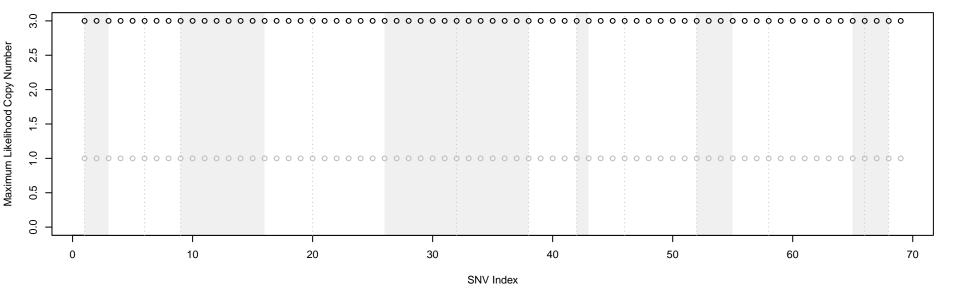
log2 ratio

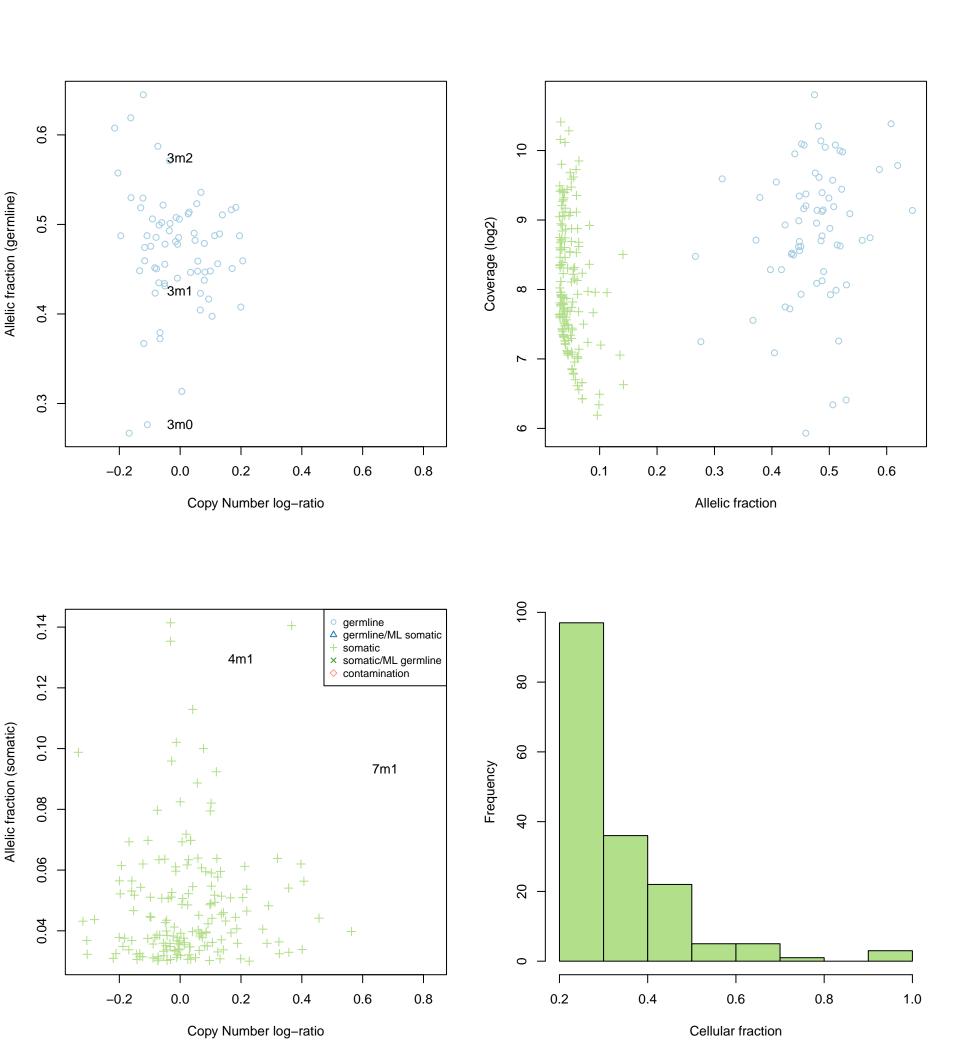


# SCNA-fit log-likelihood: -1131.06

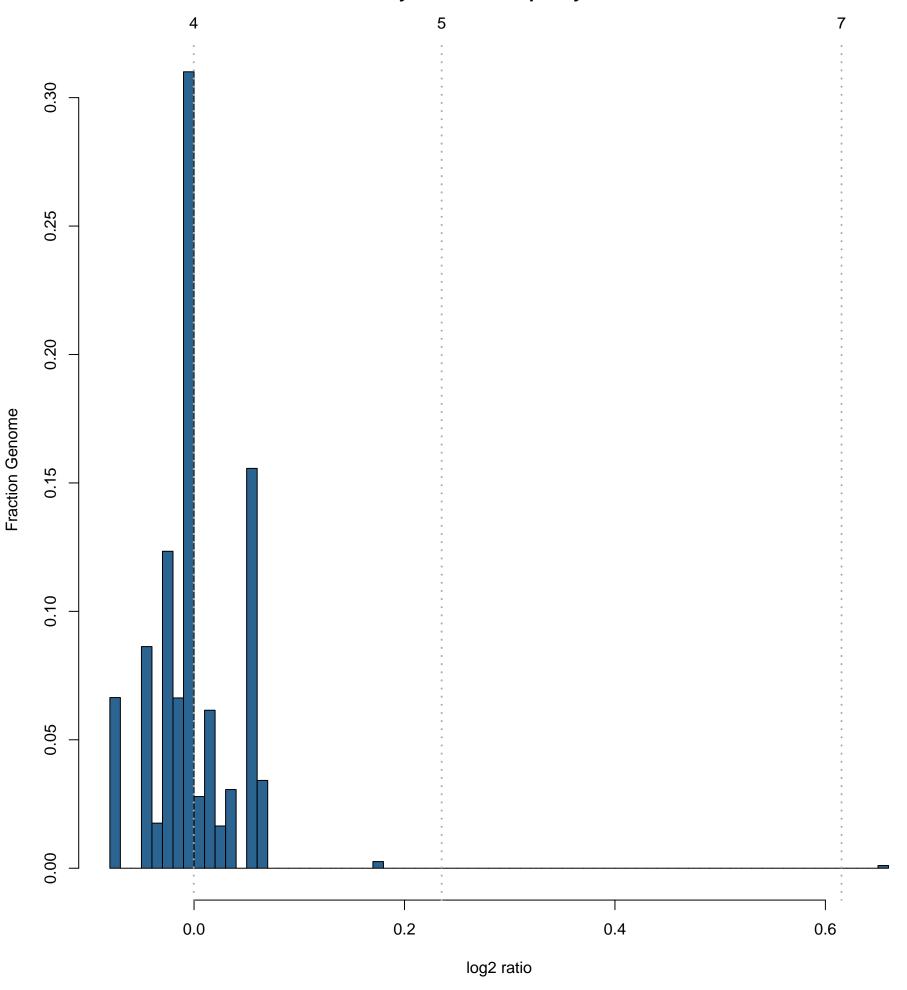
SNV Index

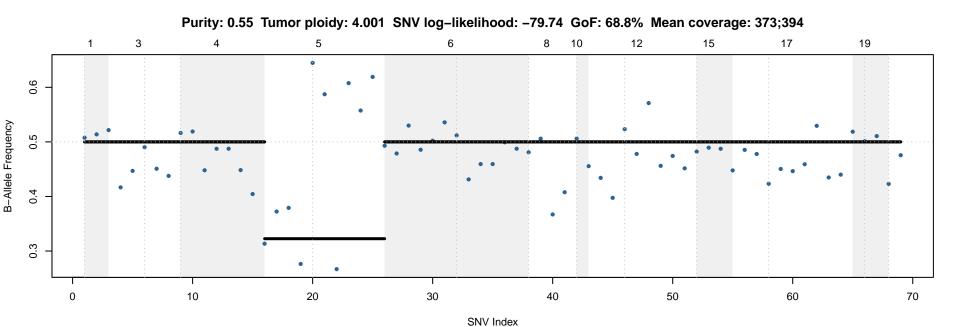




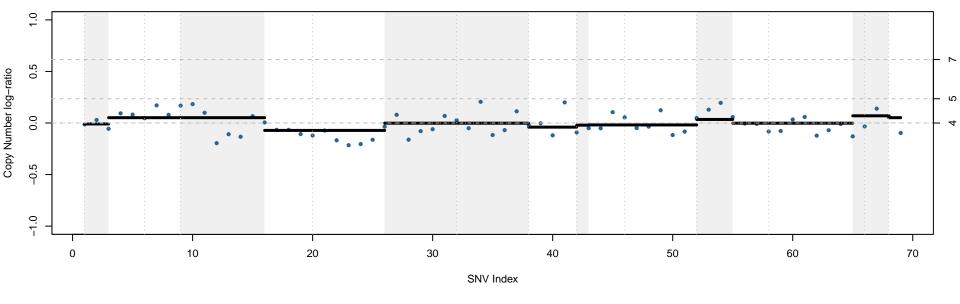


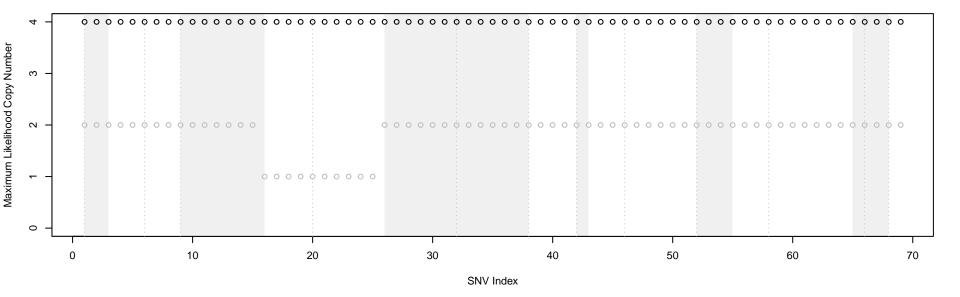
Purity: 0.55 Tumor ploidy: 4.001

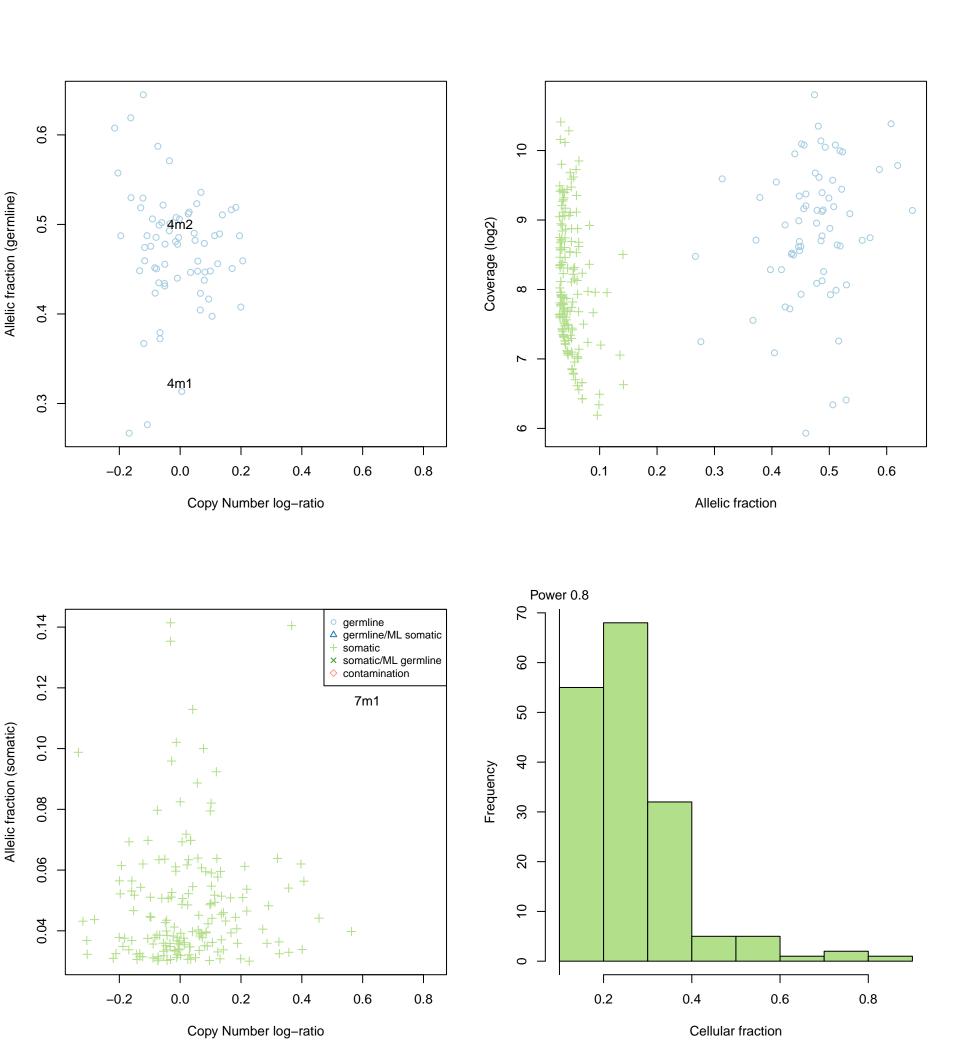




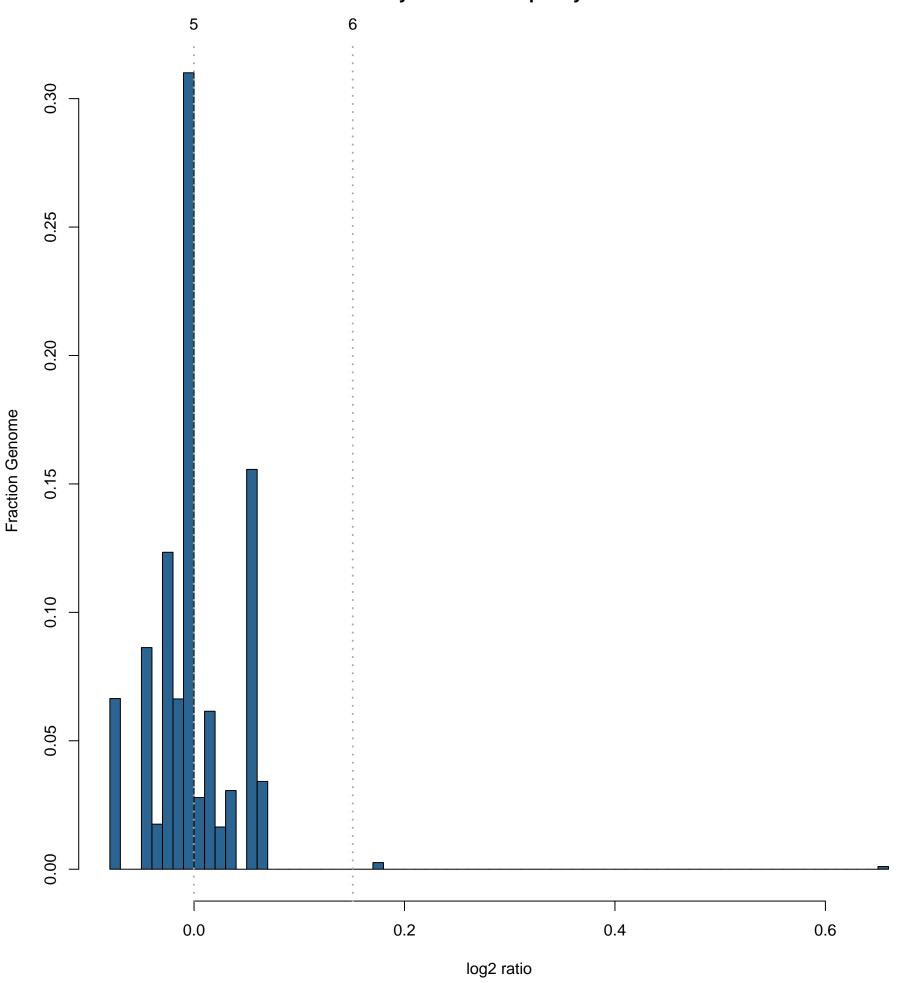
# SCNA-fit log-likelihood: -1132.74



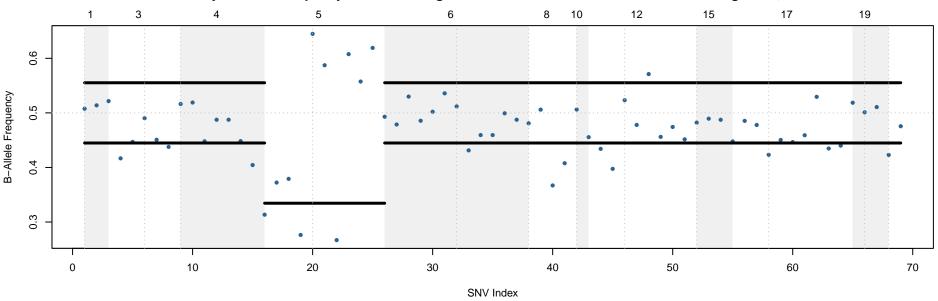




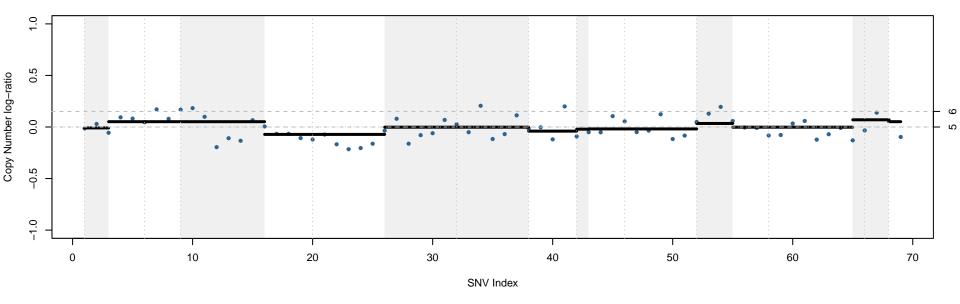
Purity: 0.33 Tumor ploidy: 5.001

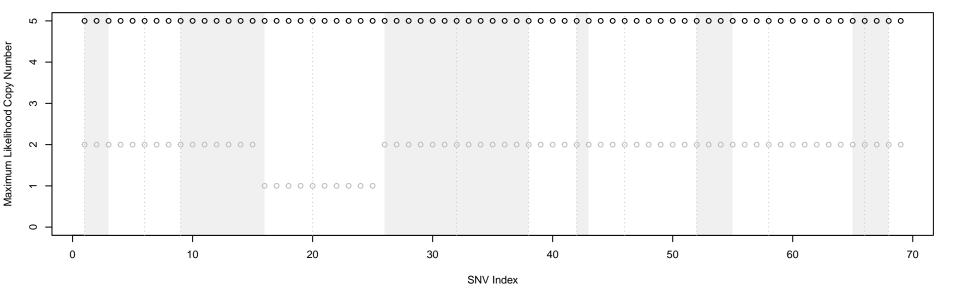


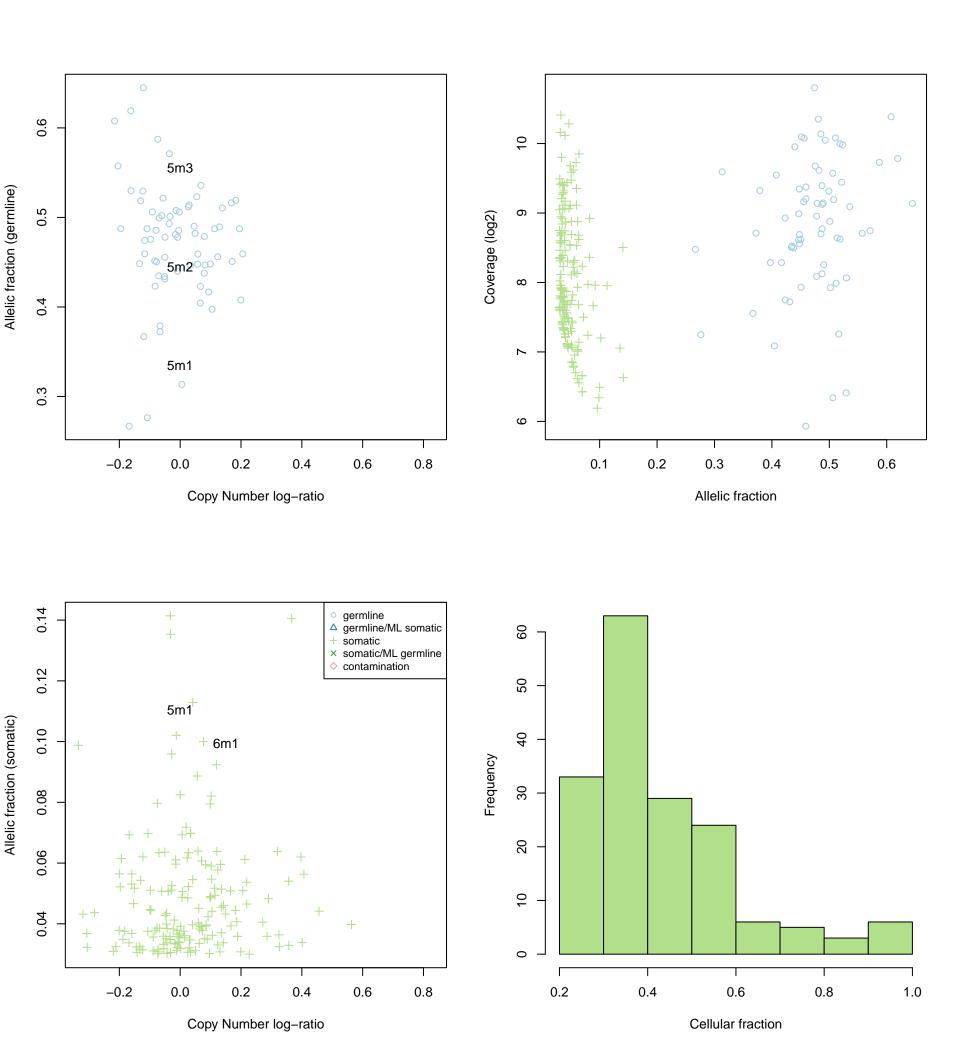




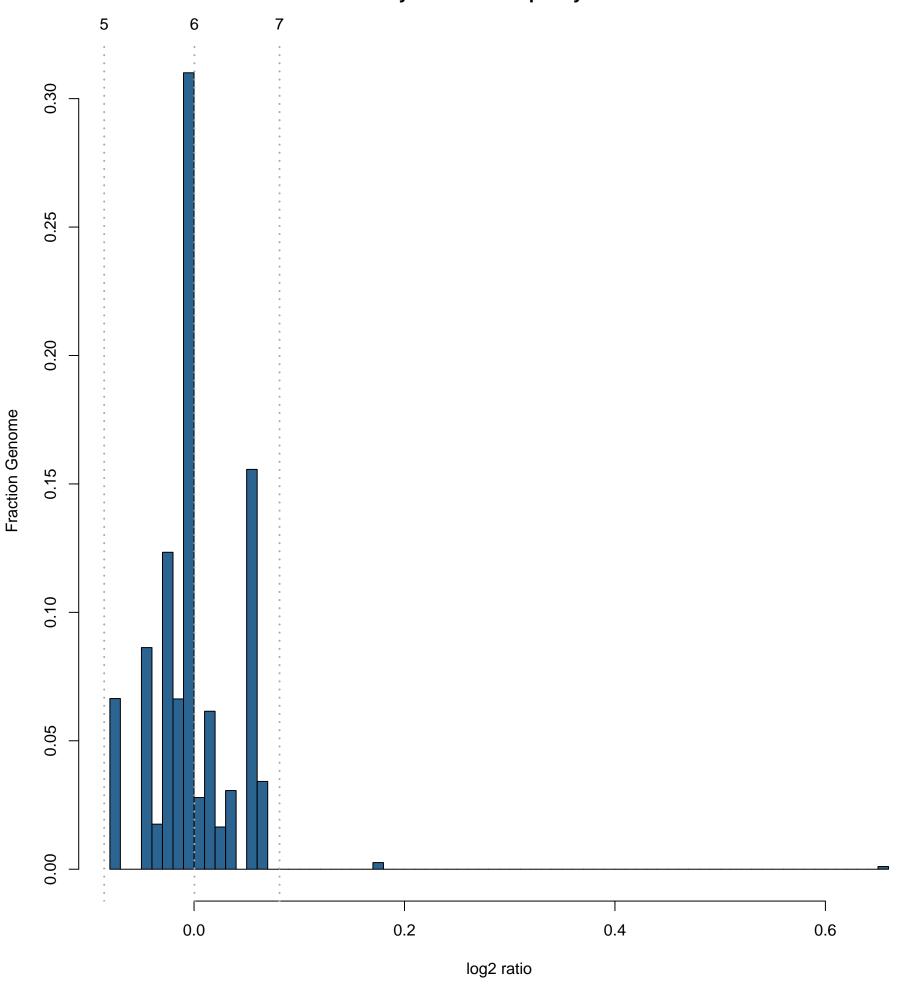
# SCNA-fit log-likelihood: -1169.6



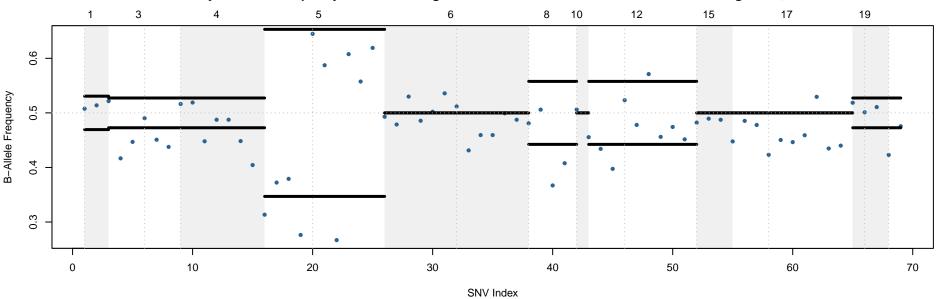




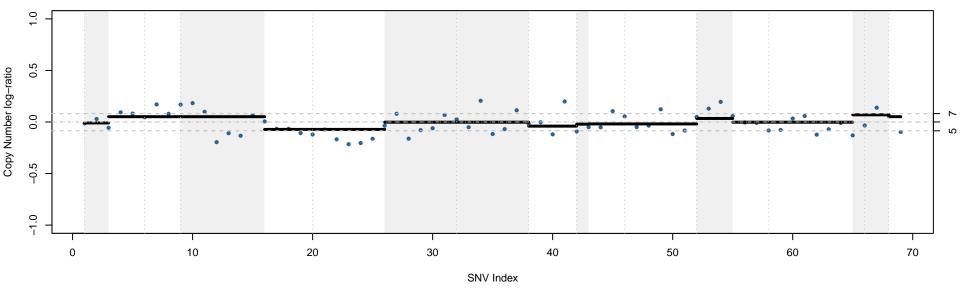
Purity: 0.15 Tumor ploidy: 5.996

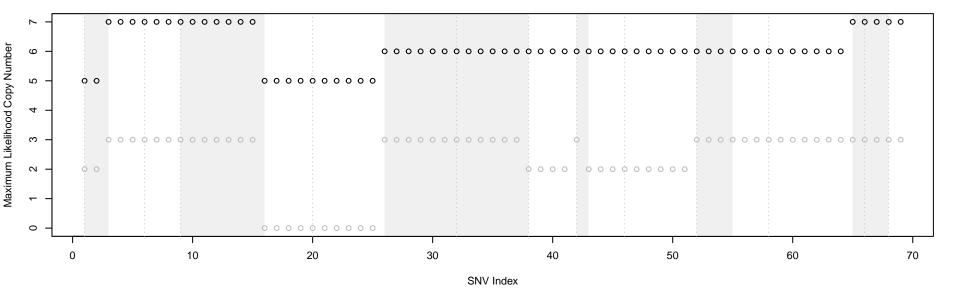


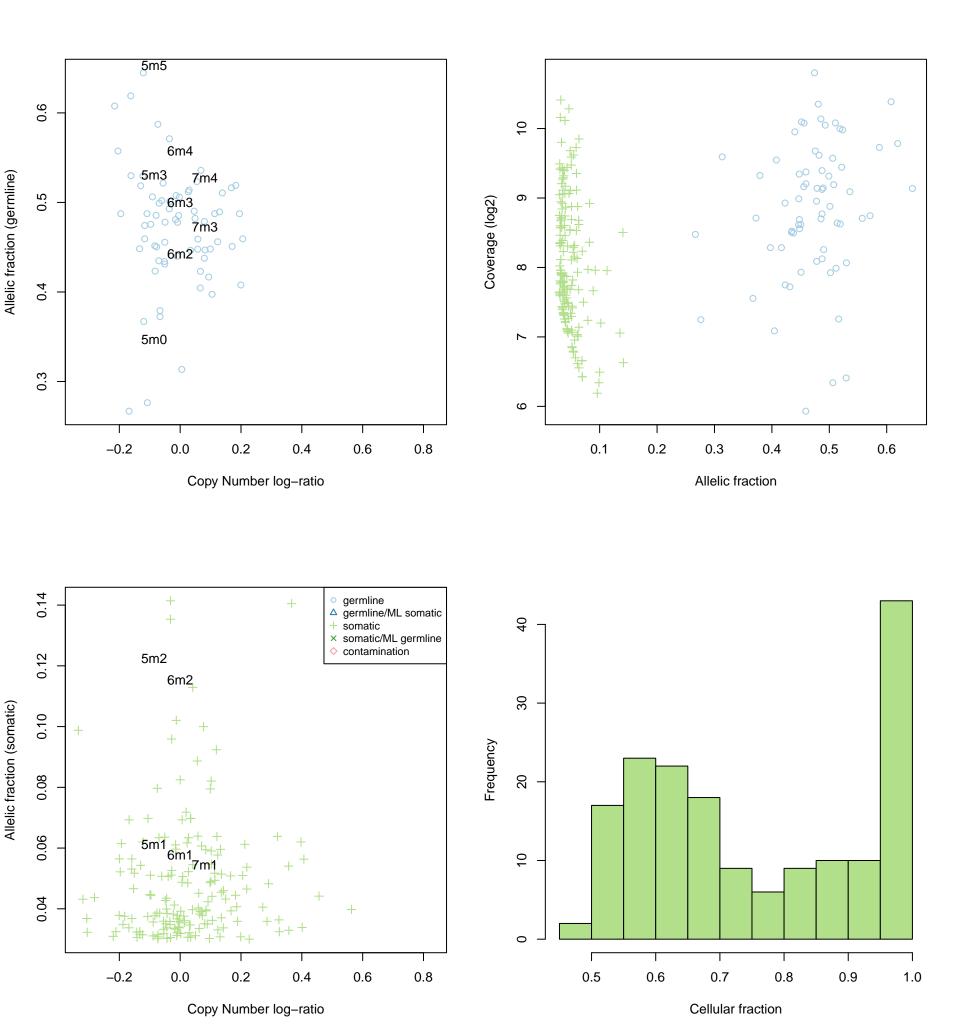
Purity: 0.15 Tumor ploidy: 5.996 SNV log-likelihood: -114.66 GoF: 98.5% Mean coverage: 373;394



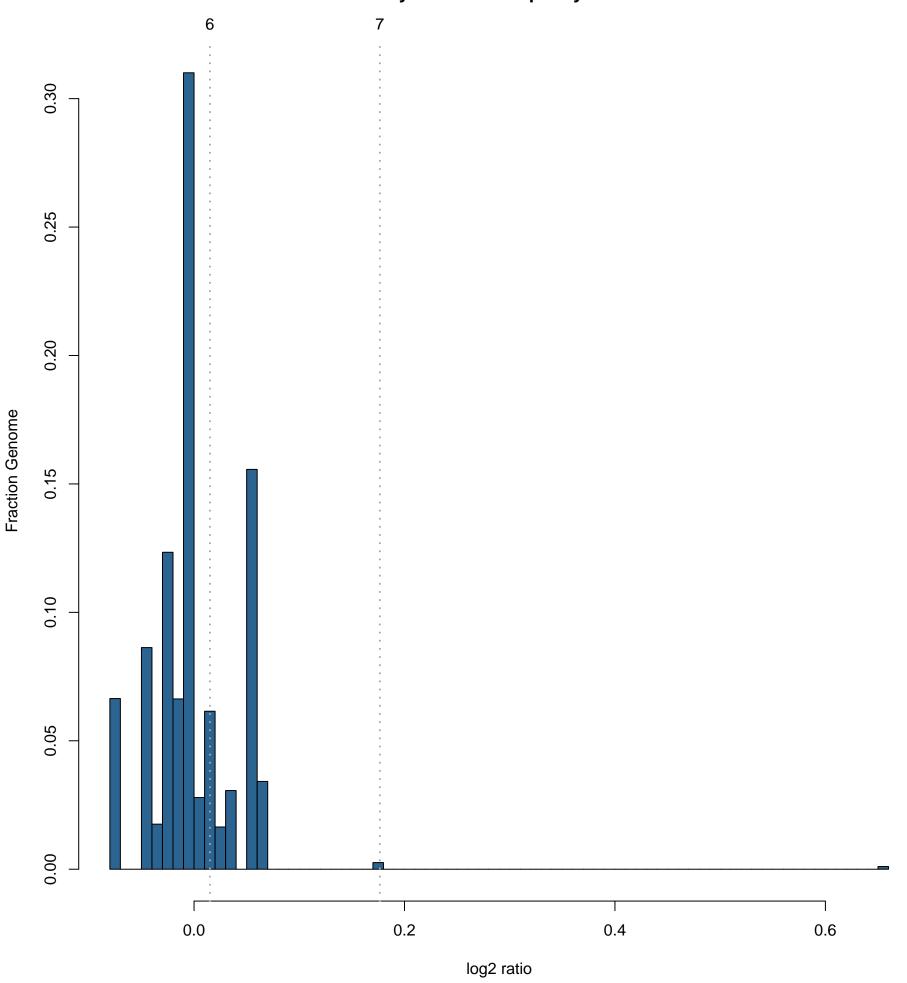
## SCNA-fit log-likelihood: -1121.14

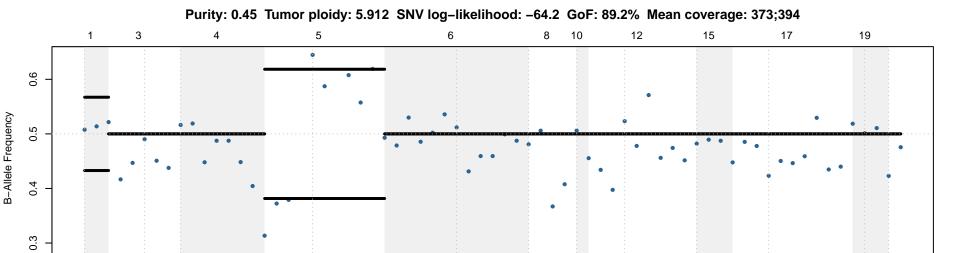






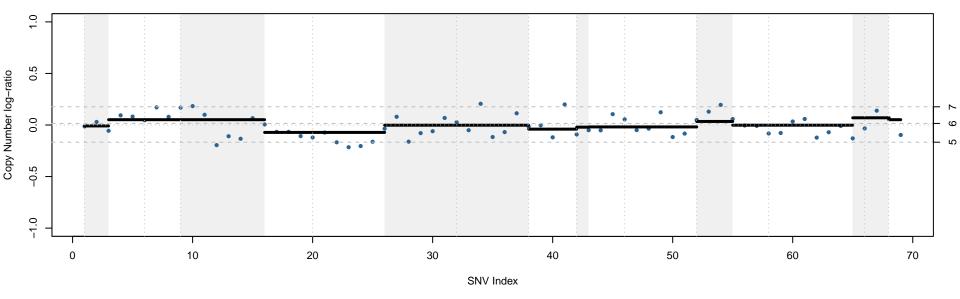
Purity: 0.45 Tumor ploidy: 5.912

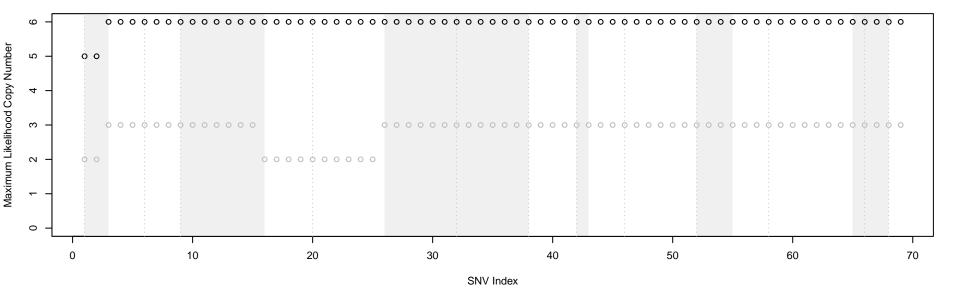


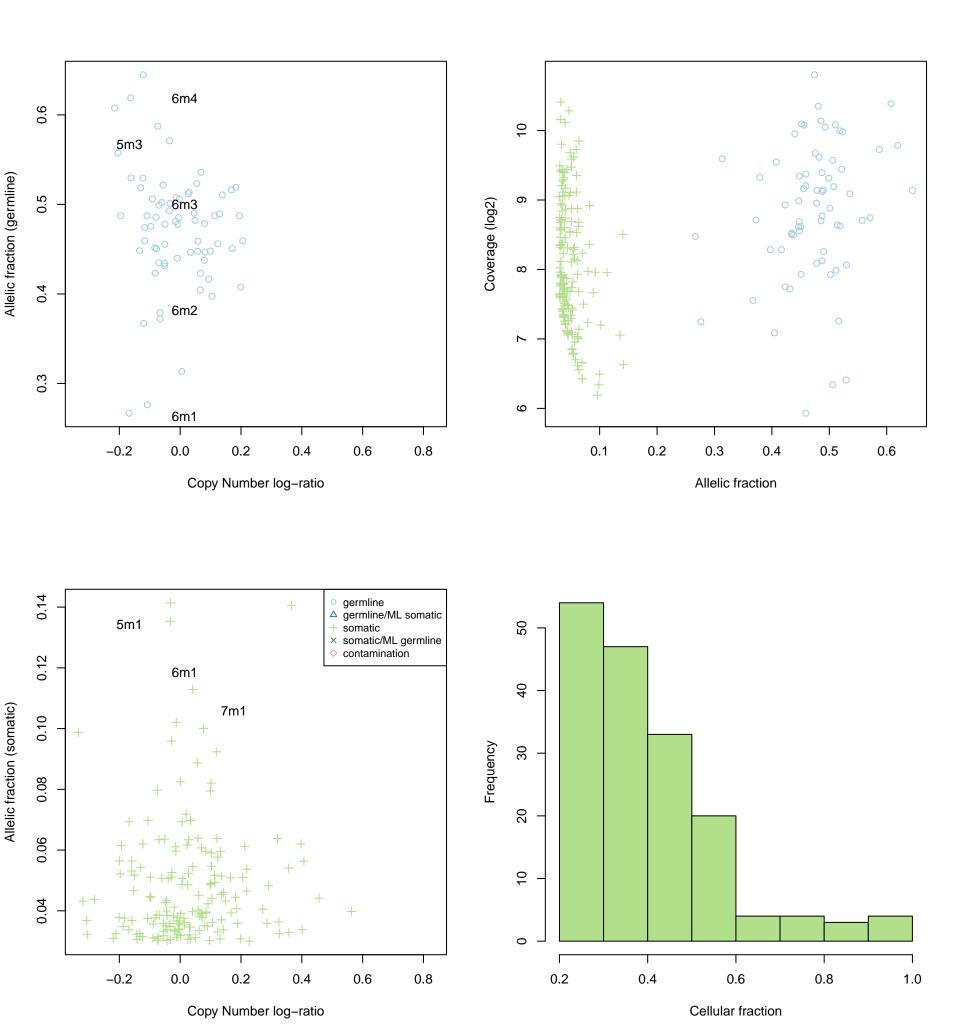


## SCNA-fit log-likelihood: -1530.99

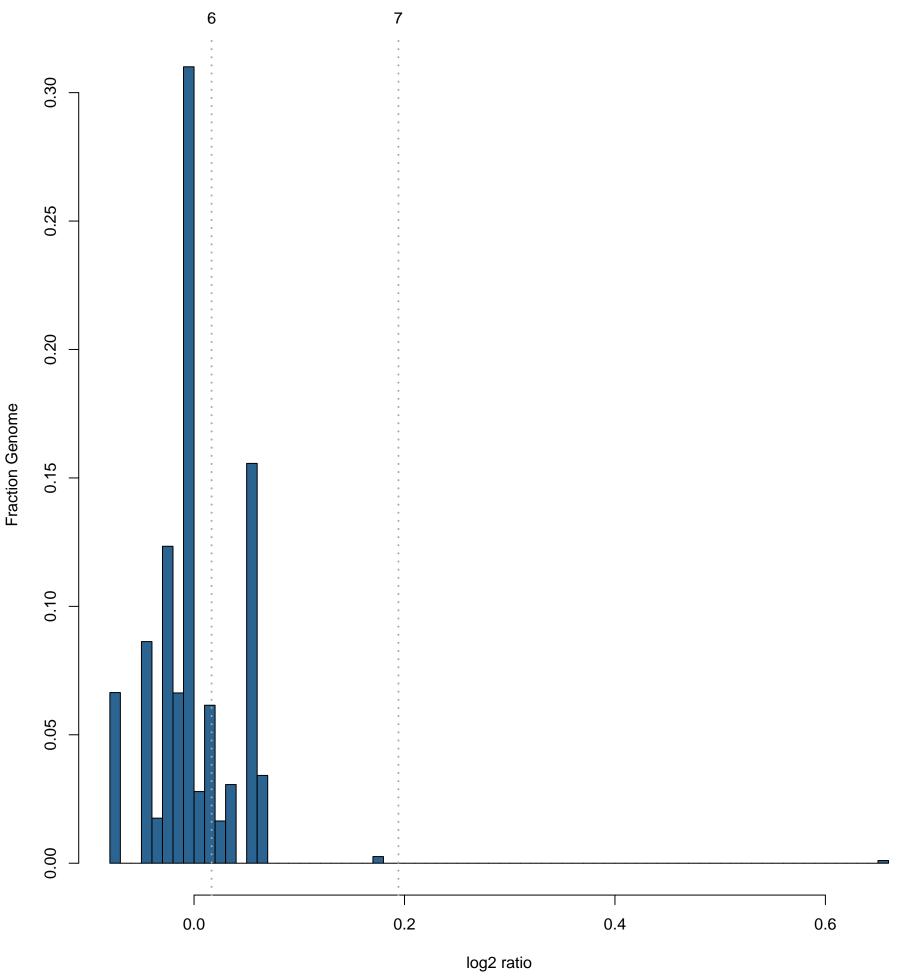
SNV Index

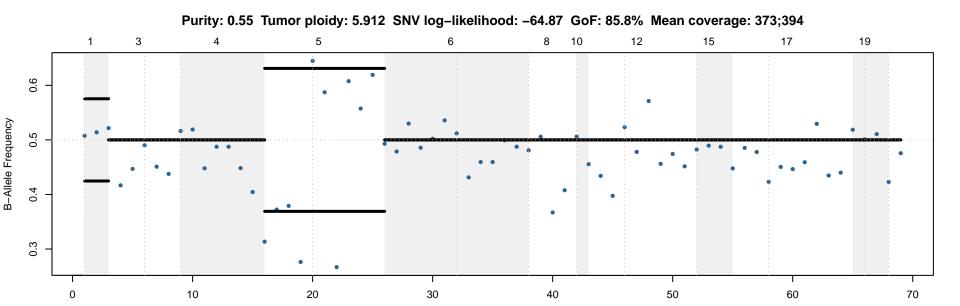






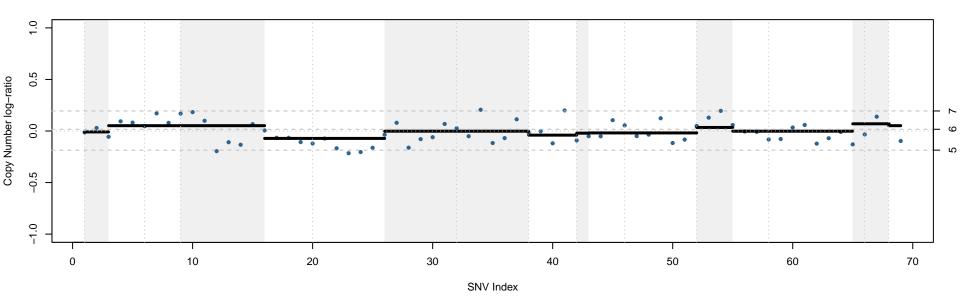
Purity: 0.55 Tumor ploidy: 5.912

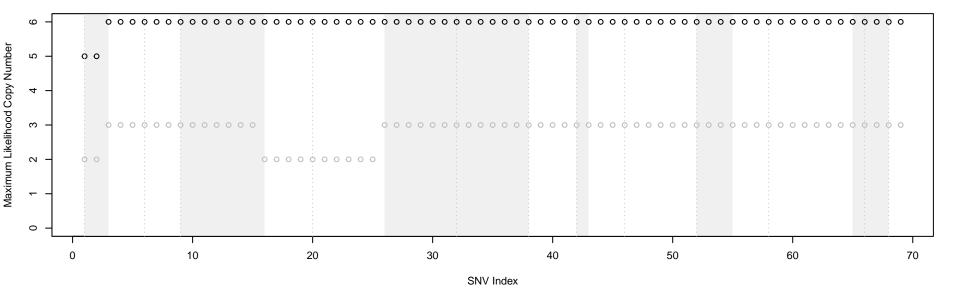


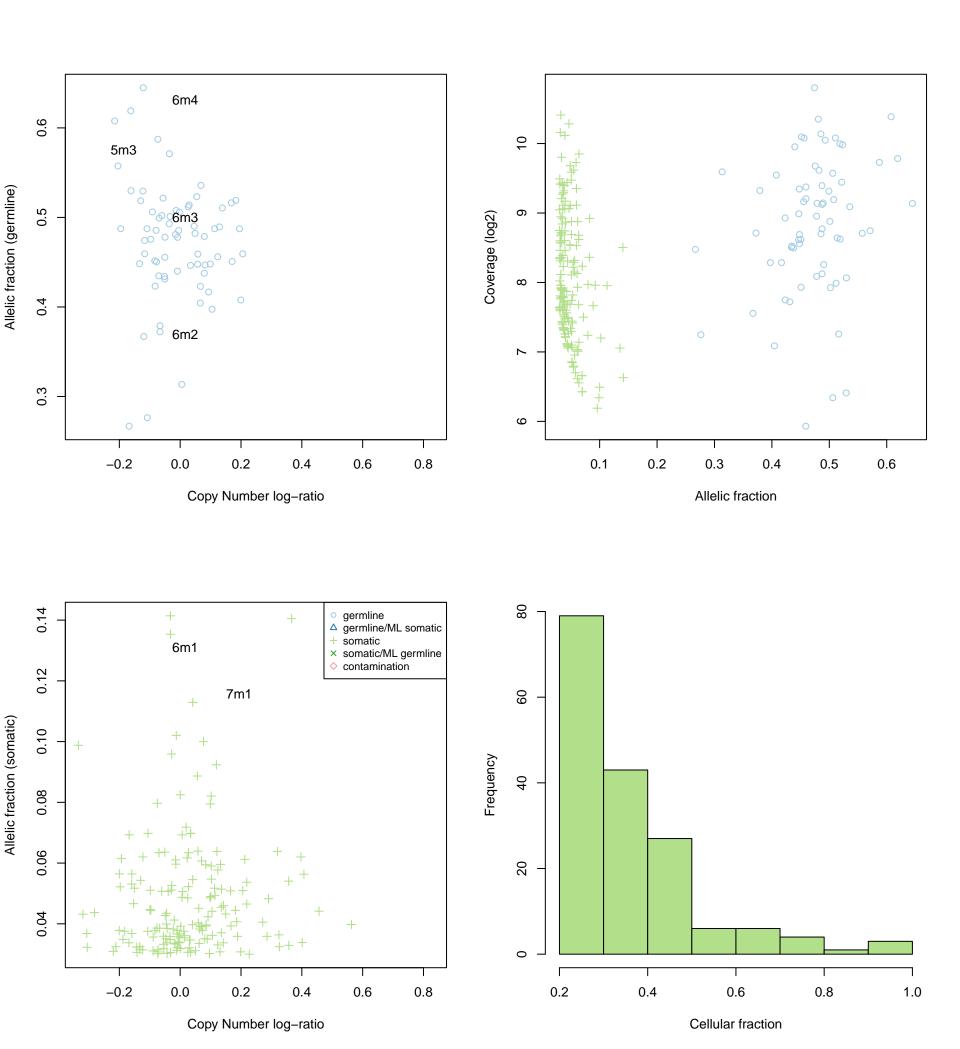


# SCNA-fit log-likelihood: -1615.2

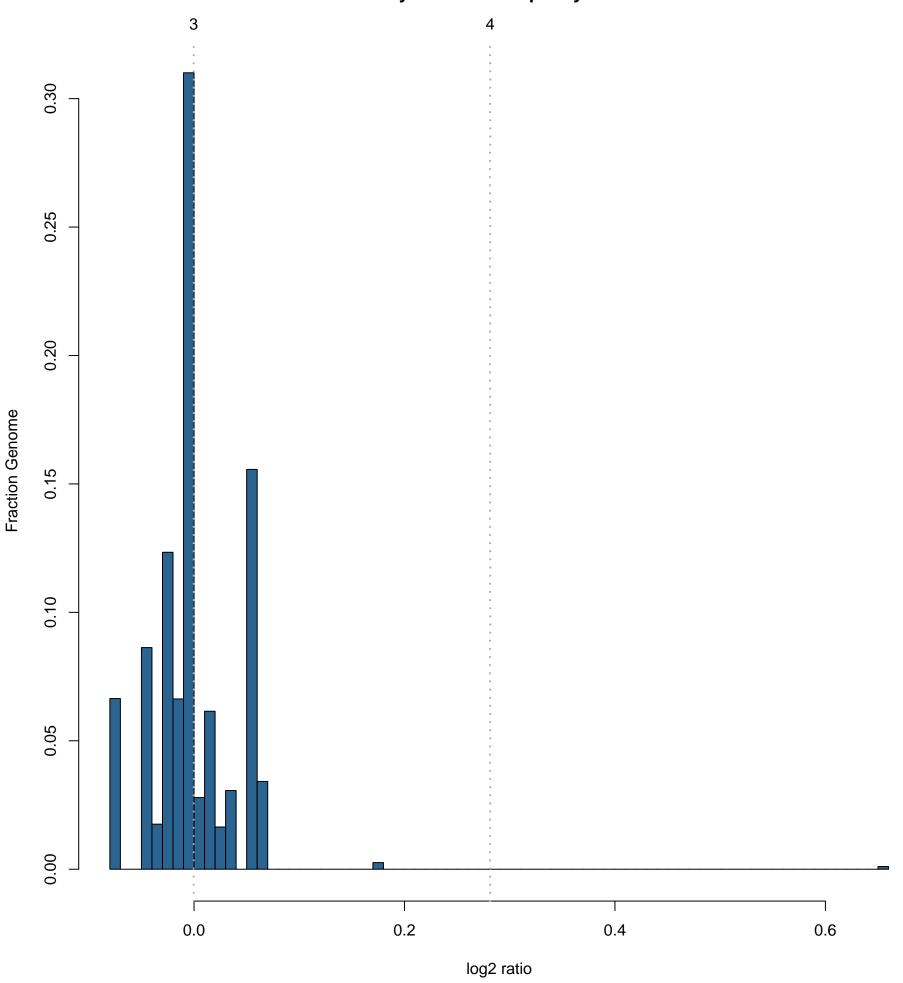
SNV Index



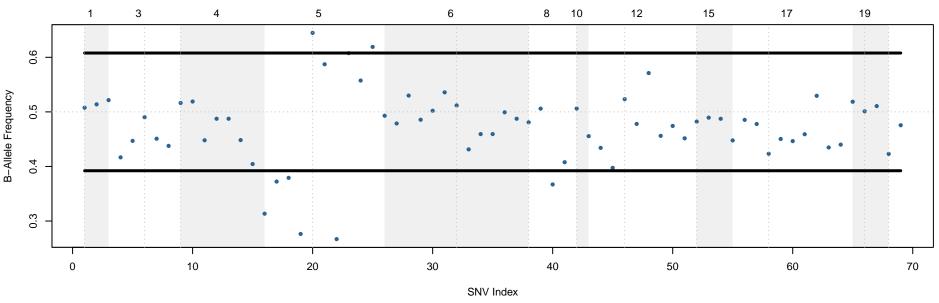




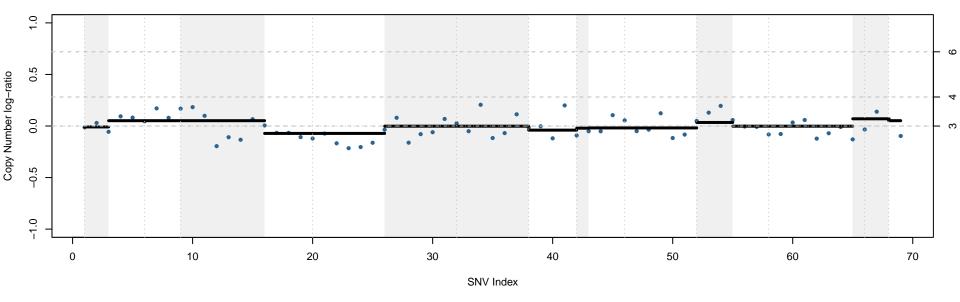
Purity: 0.55 Tumor ploidy: 3.001

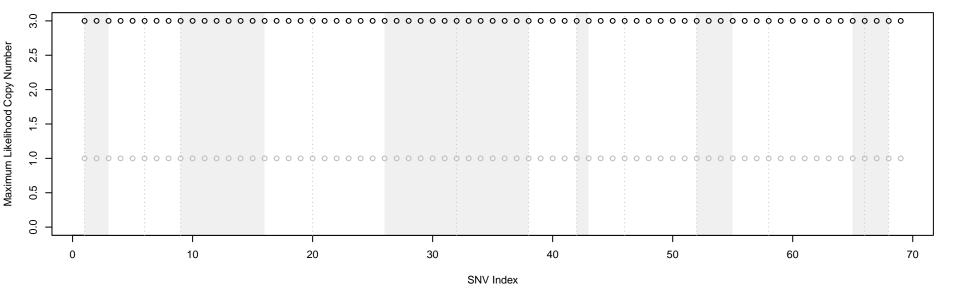


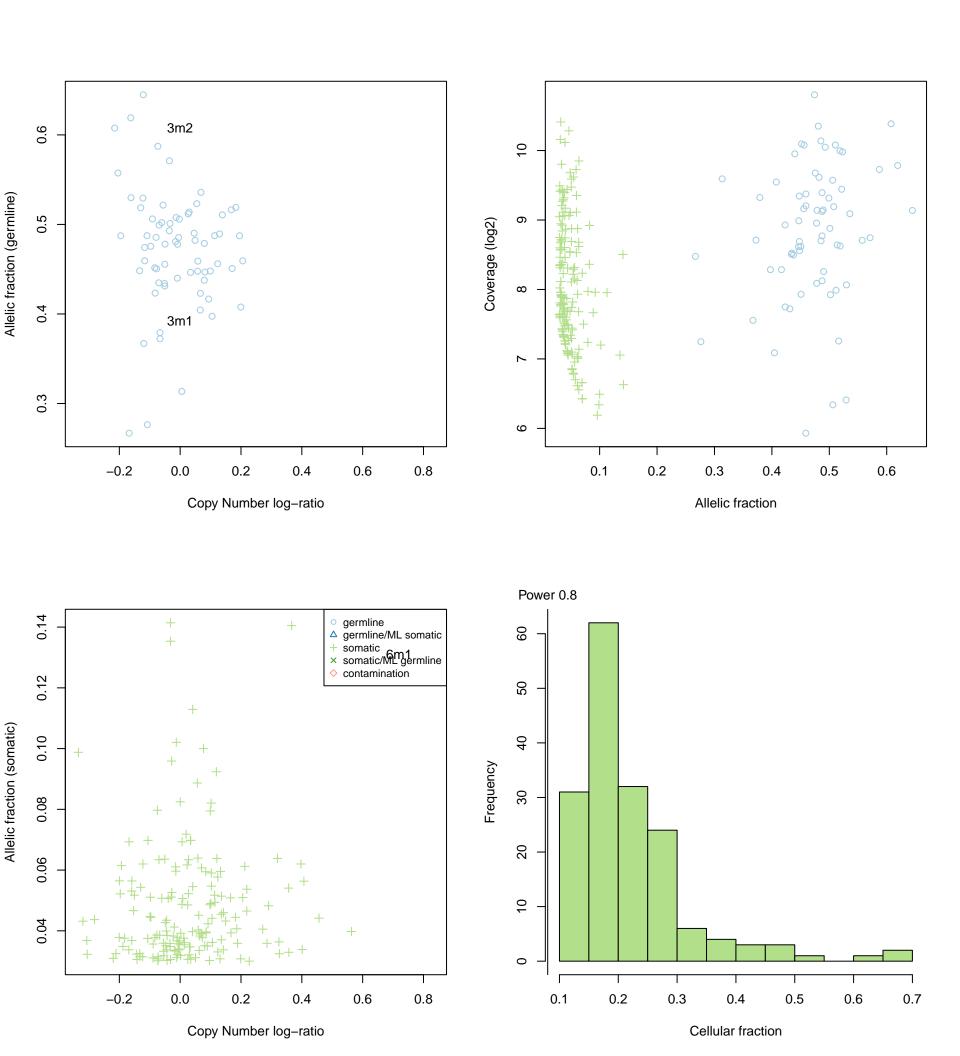




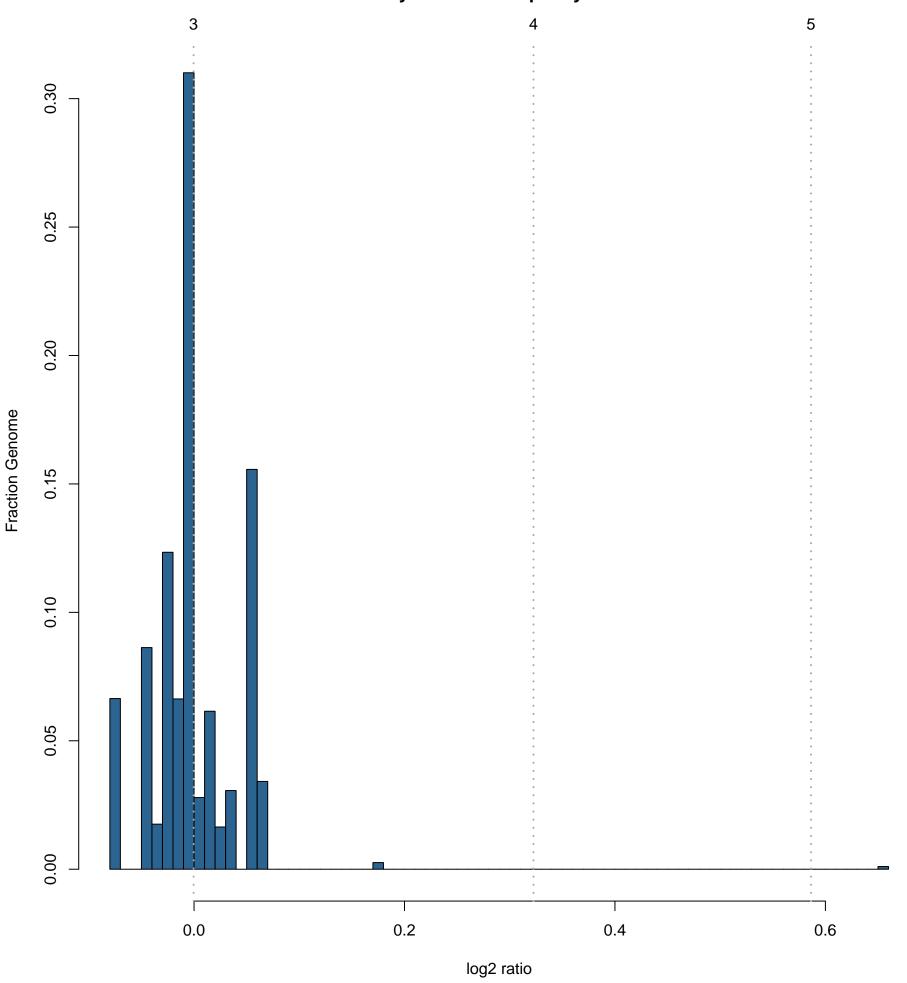
# SCNA-fit log-likelihood: -1136.19



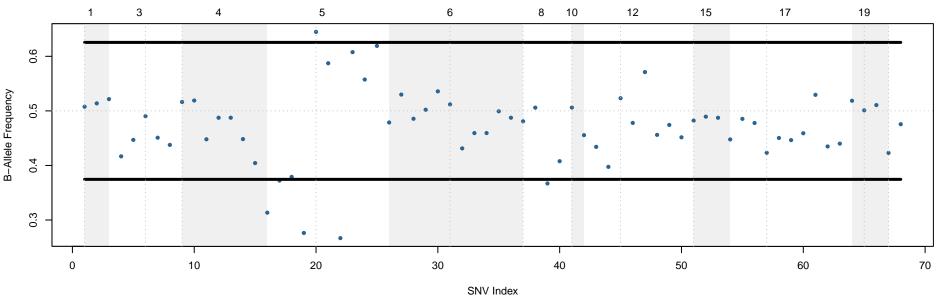




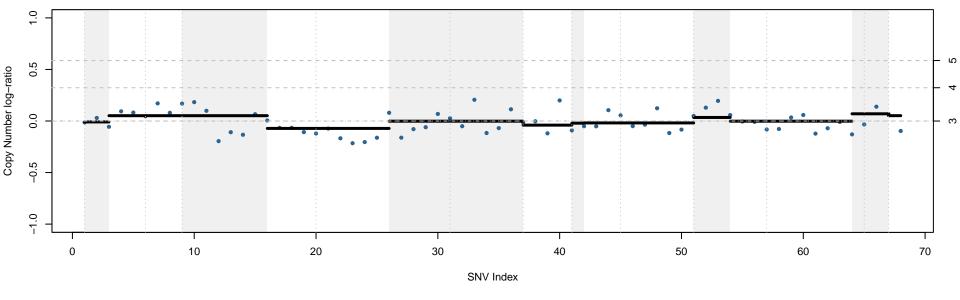
Purity: 0.67 Tumor ploidy: 3.001

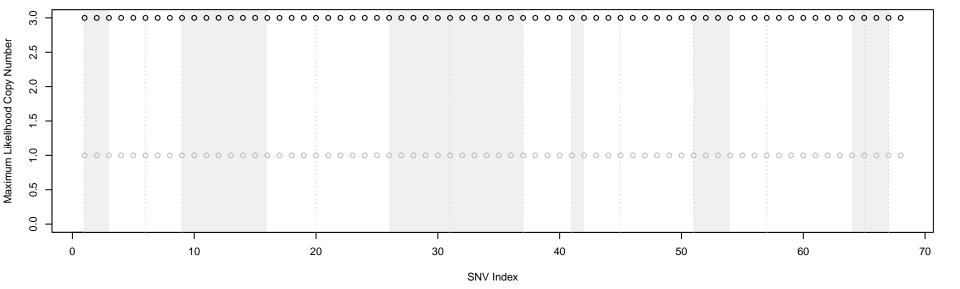


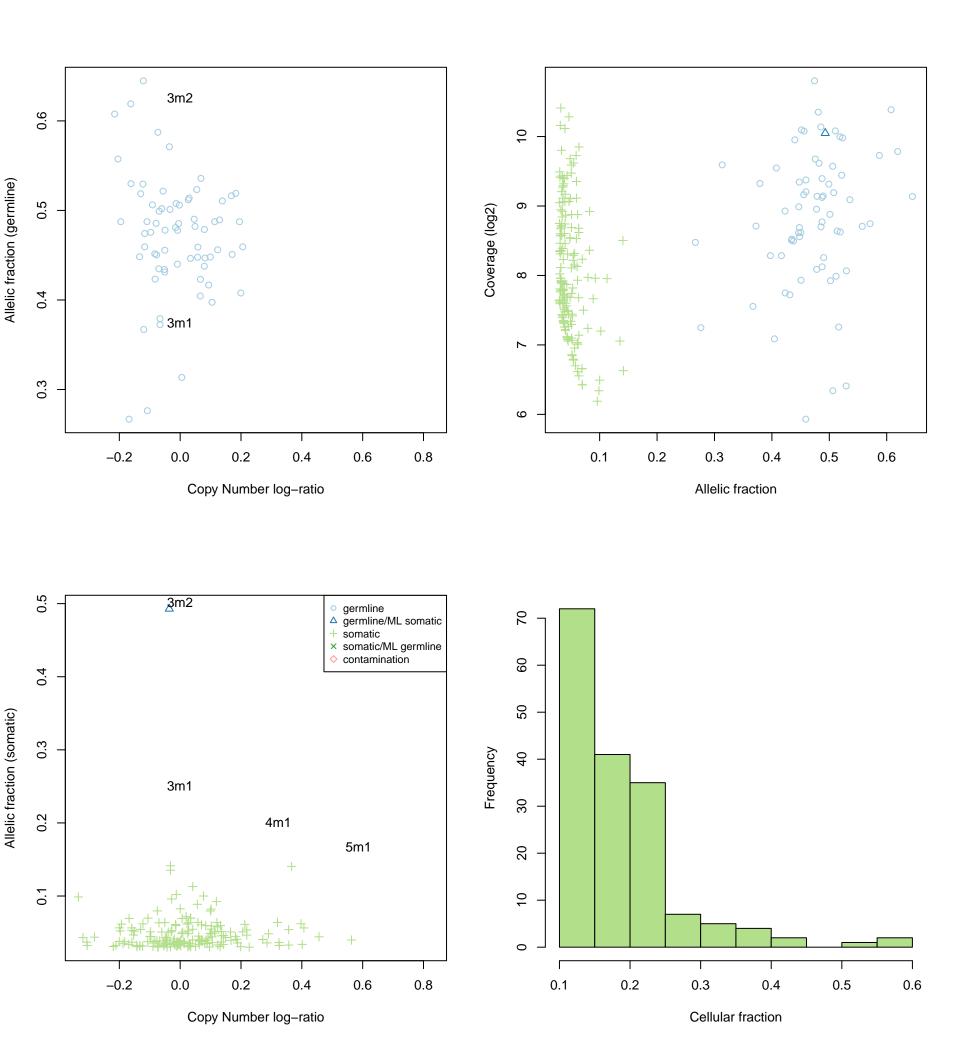




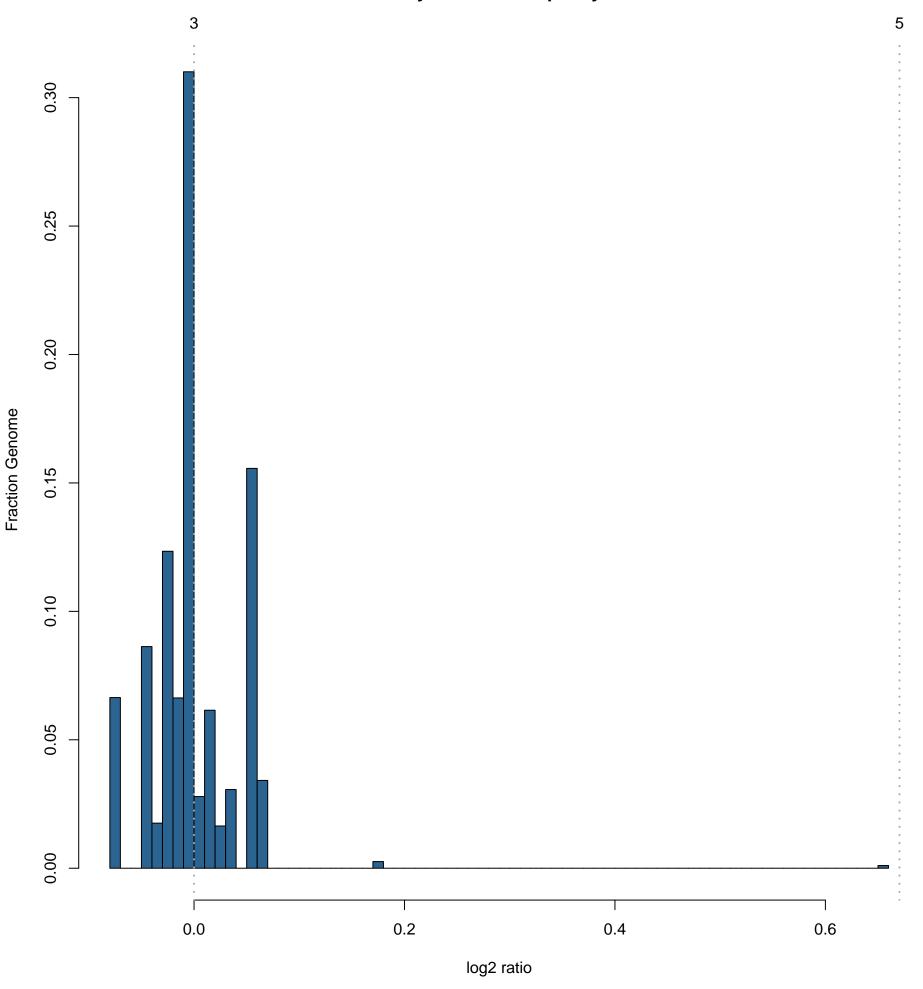
# SCNA-fit log-likelihood: -1140.88



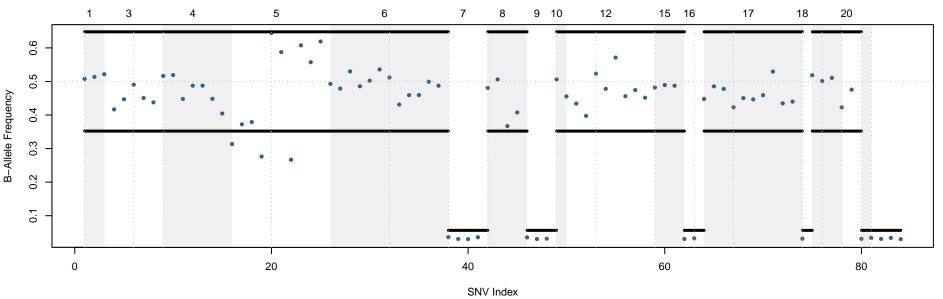




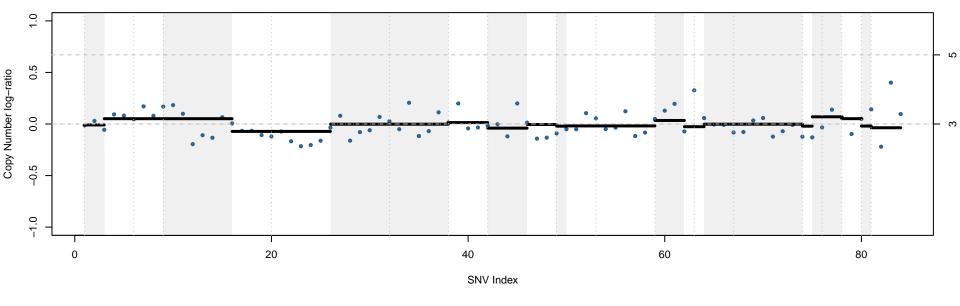
Purity: 0.84 Tumor ploidy: 3

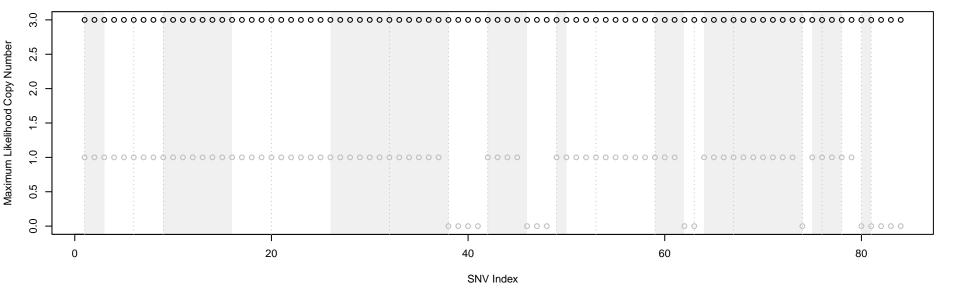


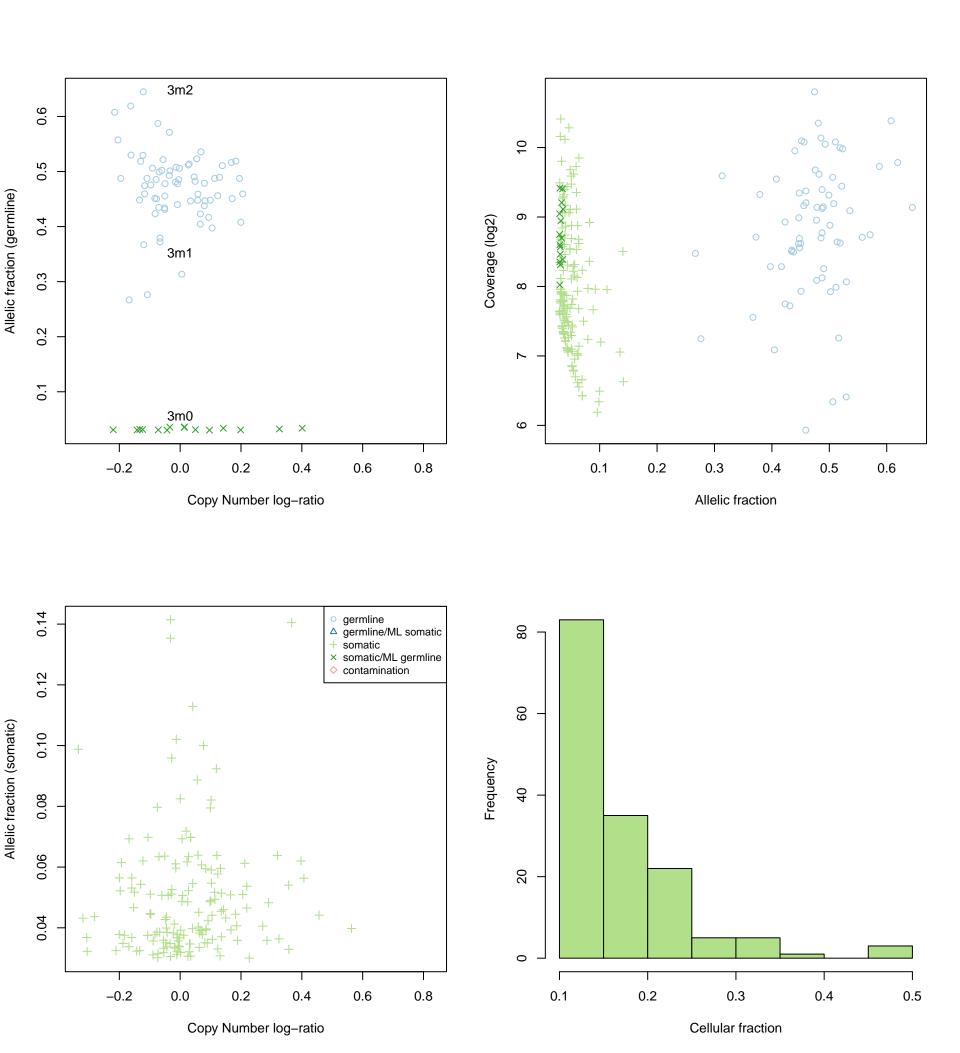
Purity: 0.84 Tumor ploidy: 3 SNV log-likelihood: -1094.19 GoF: 0% Mean coverage: 373;394



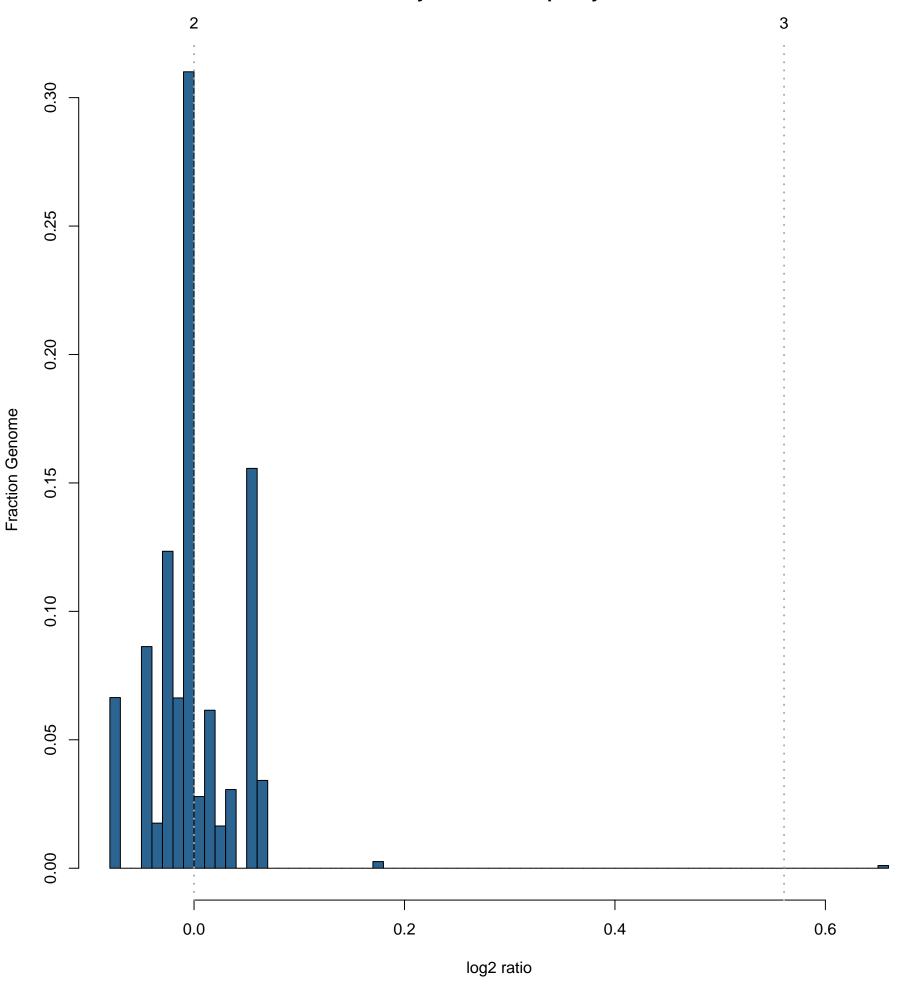
## SCNA-fit log-likelihood: -1144.94

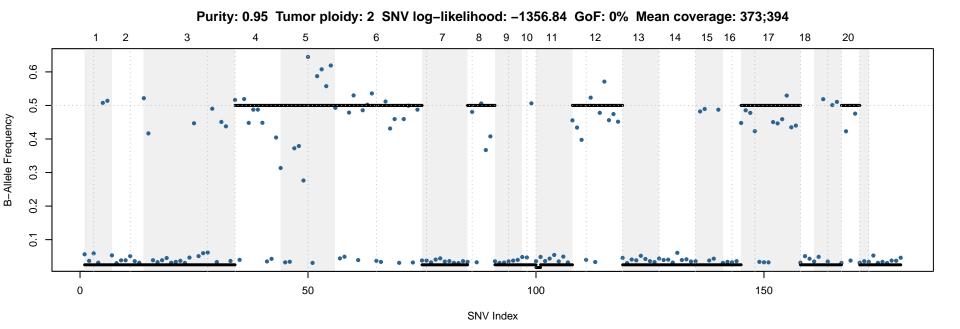






Purity: 0.95 Tumor ploidy: 2





## SCNA-fit log-likelihood: -1146.68

