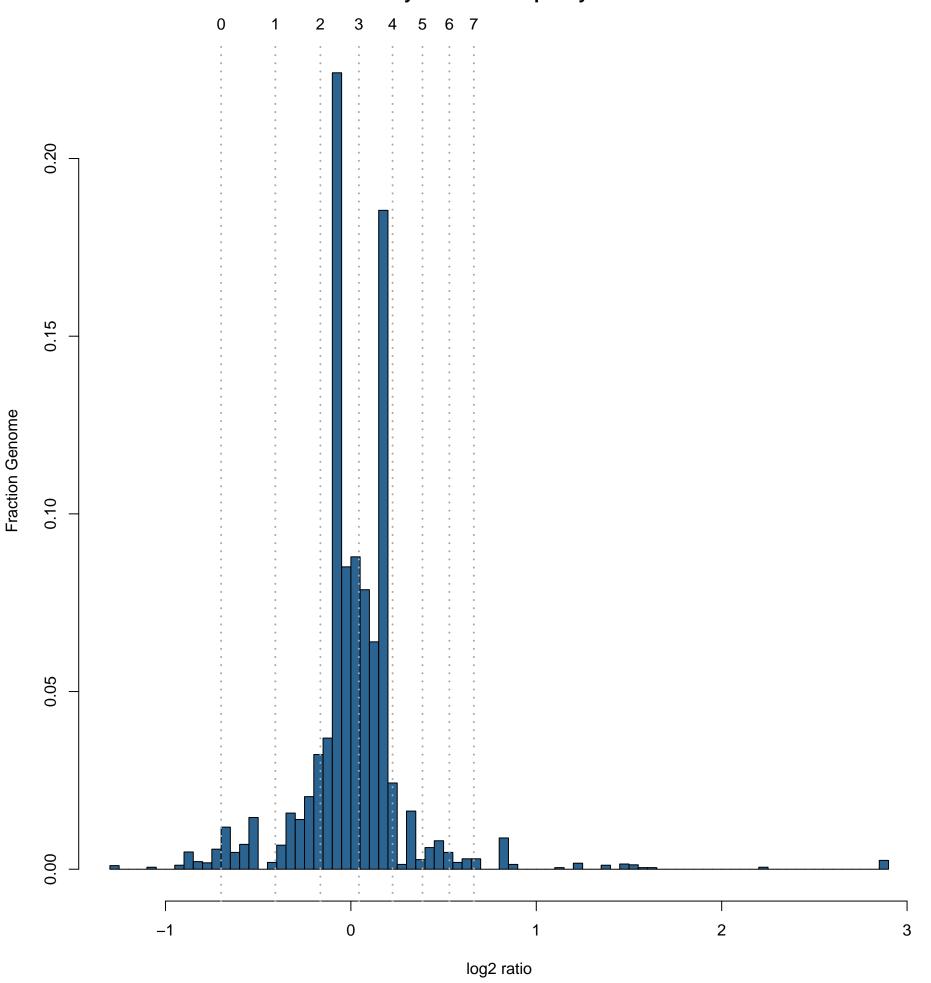
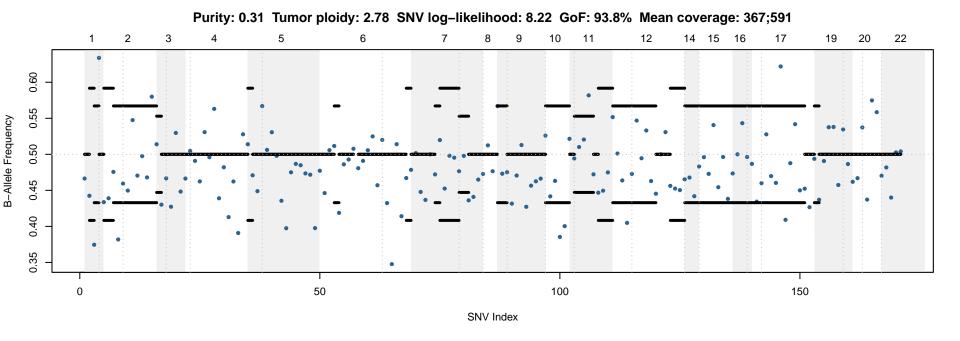
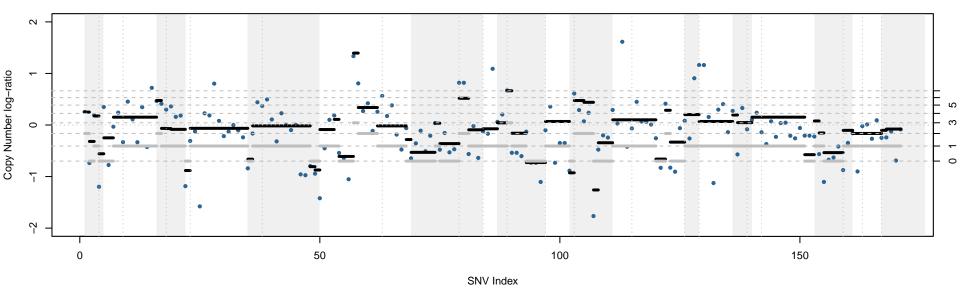
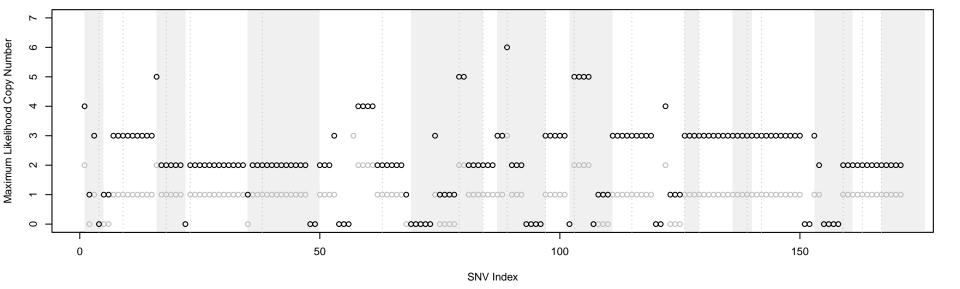
Purity: 0.31 Tumor ploidy: 2.78

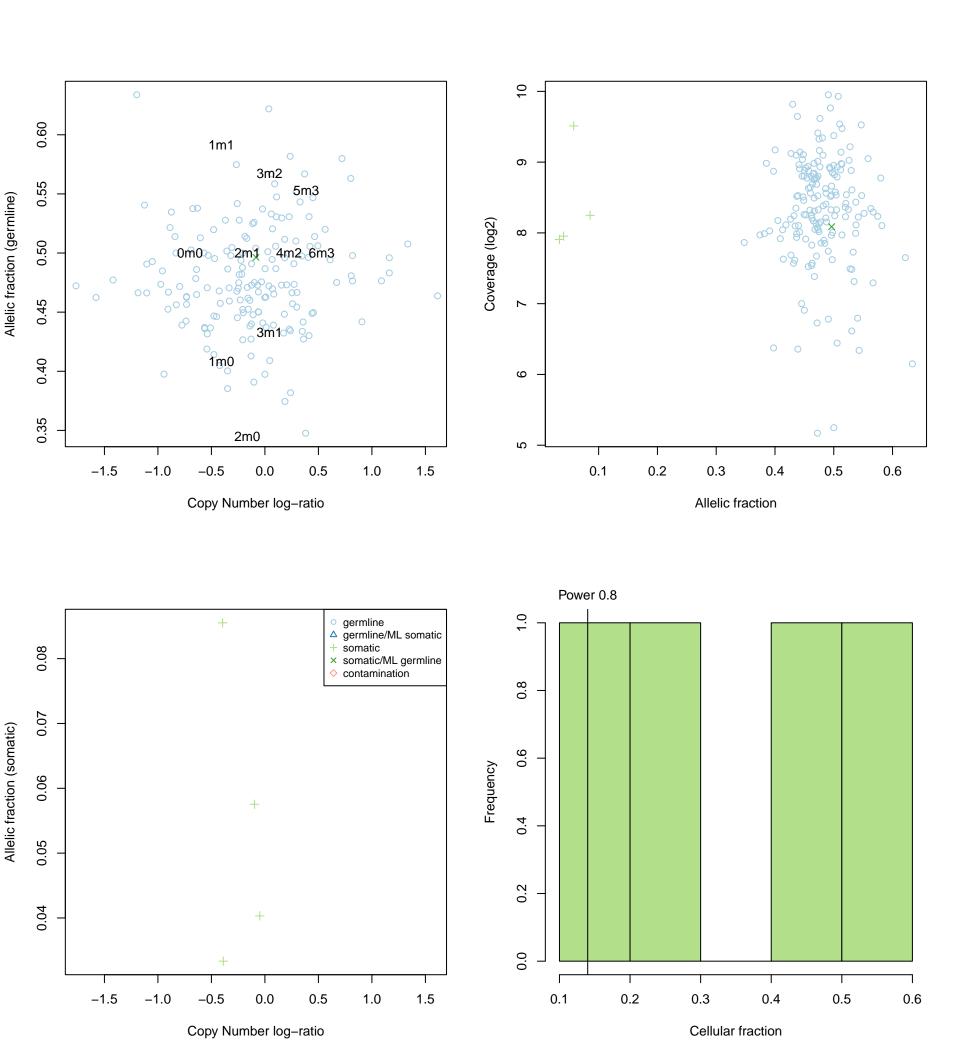




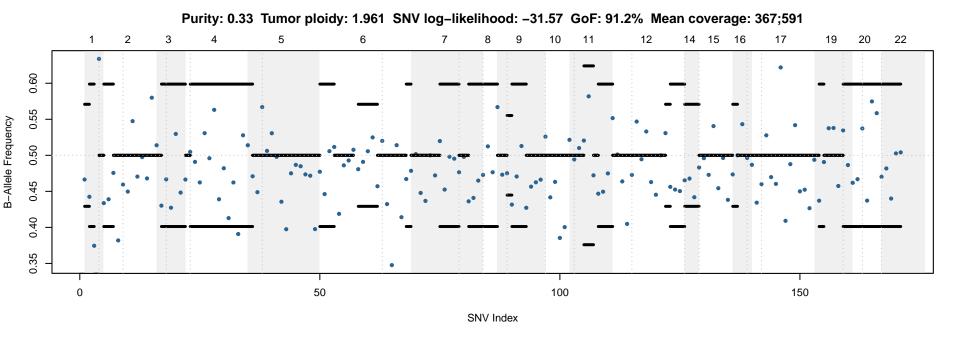
# SCNA-fit log-likelihood: -5730.01



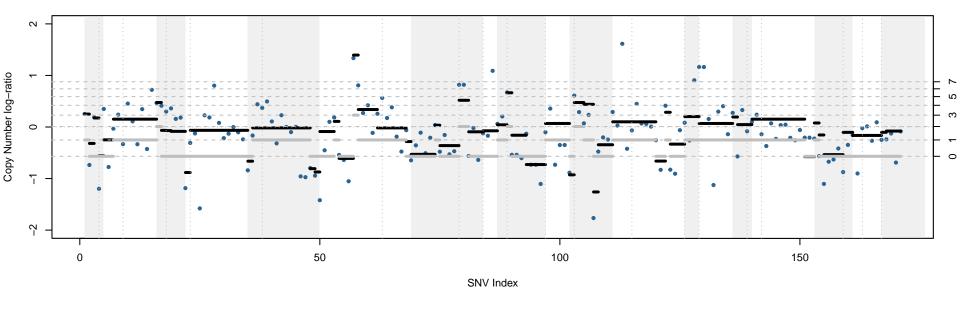


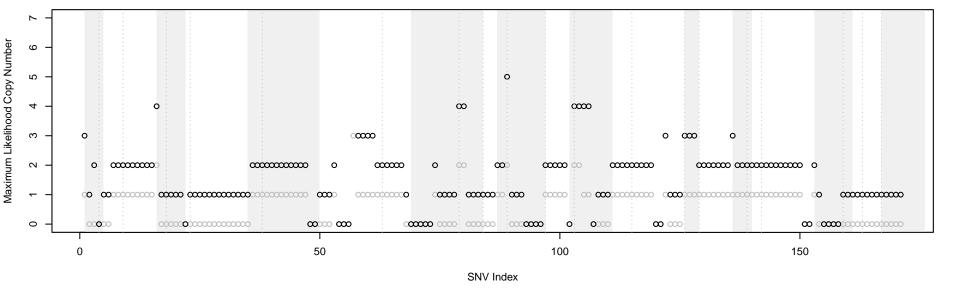


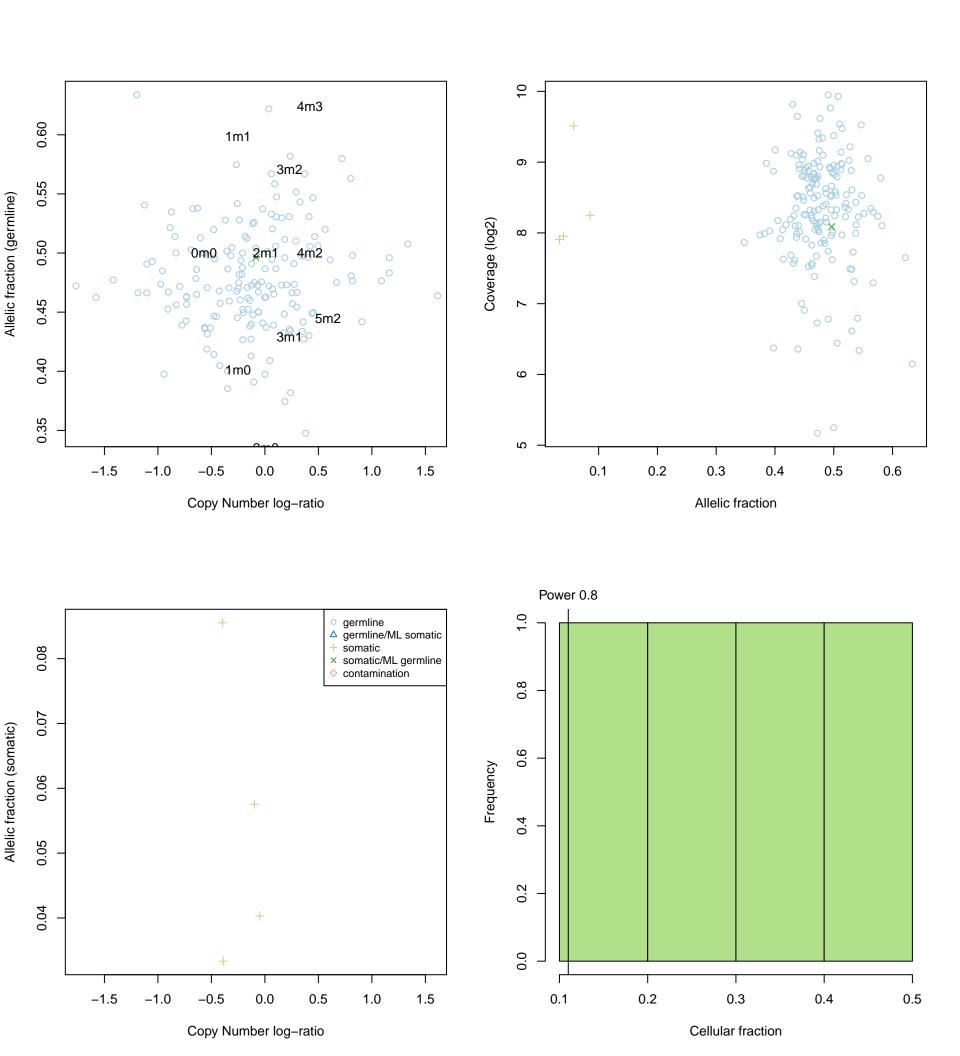
Purity: 0.33 Tumor ploidy: 1.961 0 2 1 0.20 Fraction Genome 0.10 0.05 0.00 -1 0 2 3 1 log2 ratio



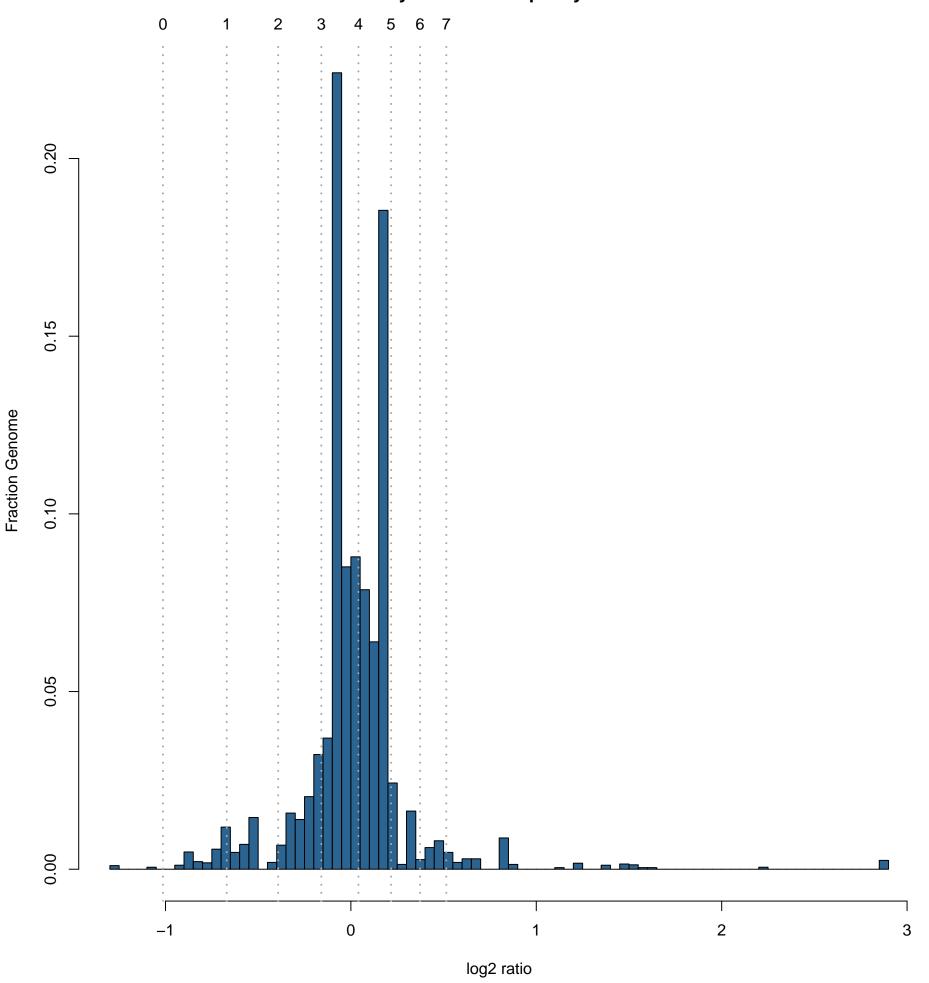
# SCNA-fit log-likelihood: -5839.51

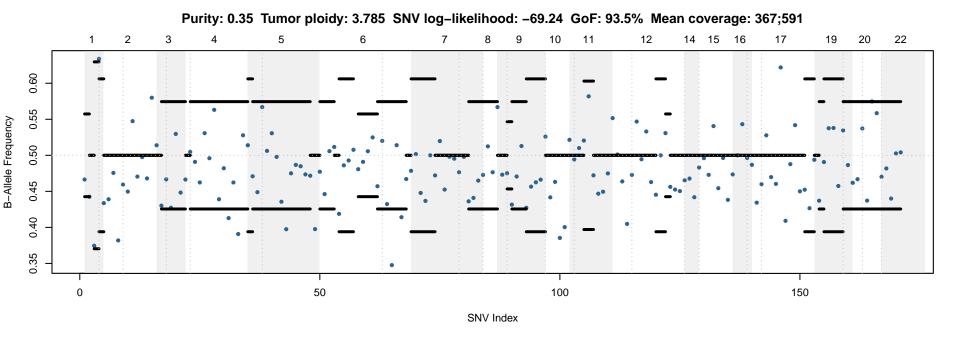




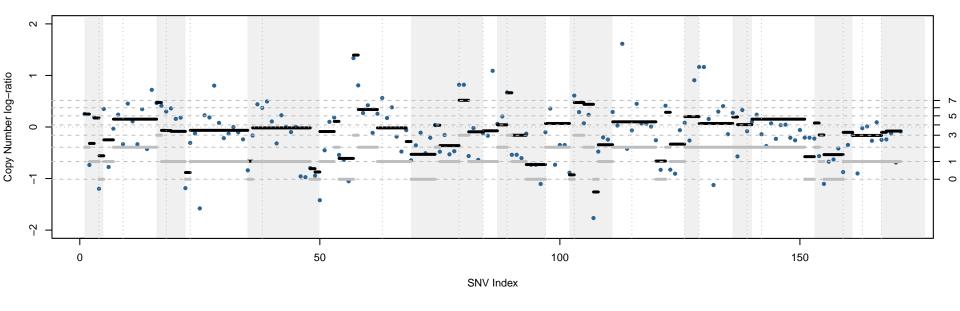


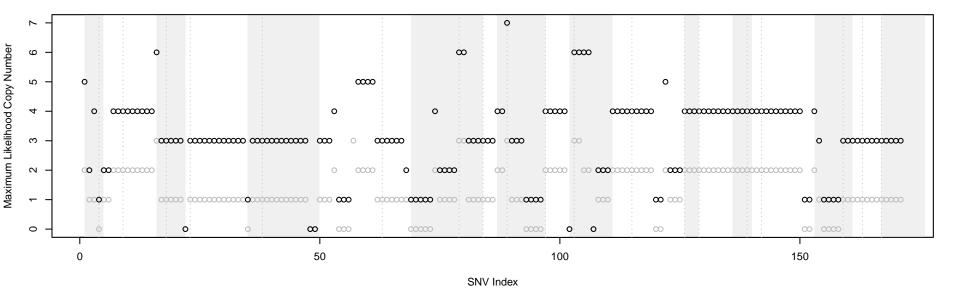
Purity: 0.35 Tumor ploidy: 3.785

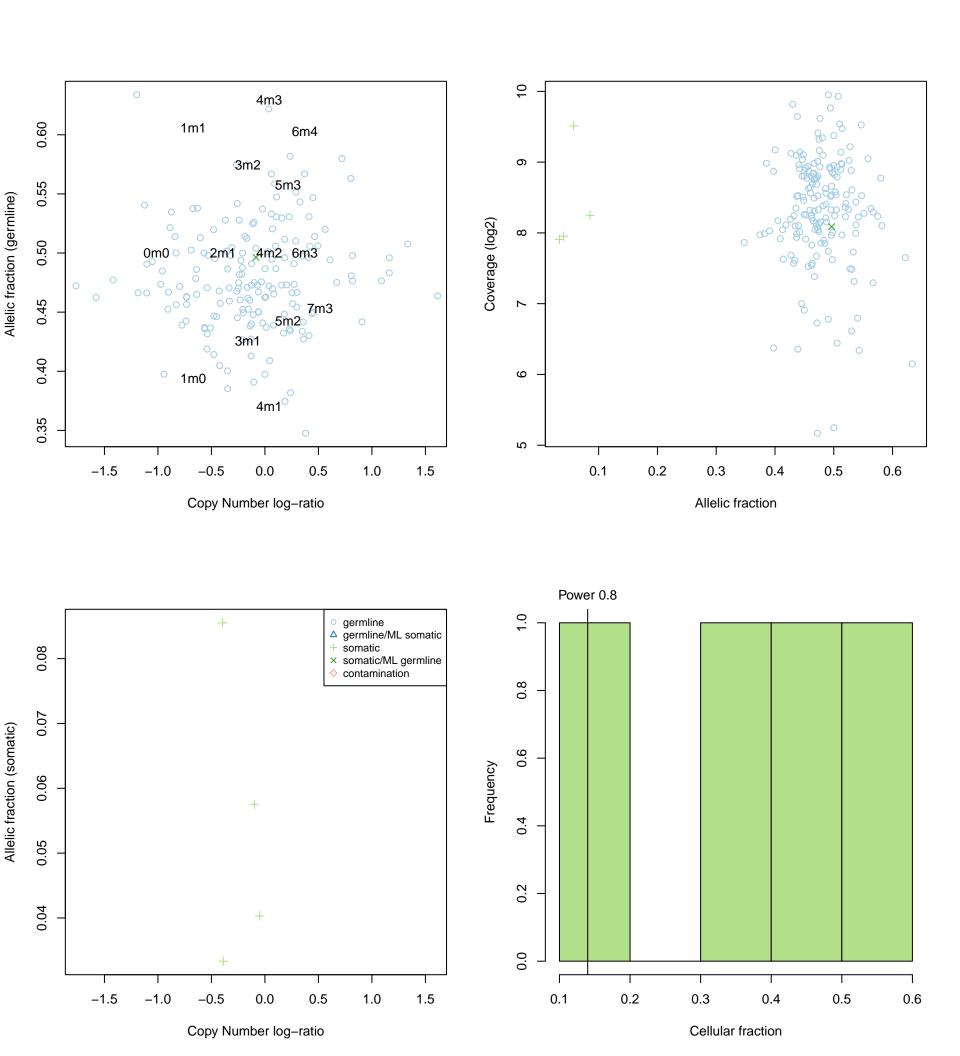




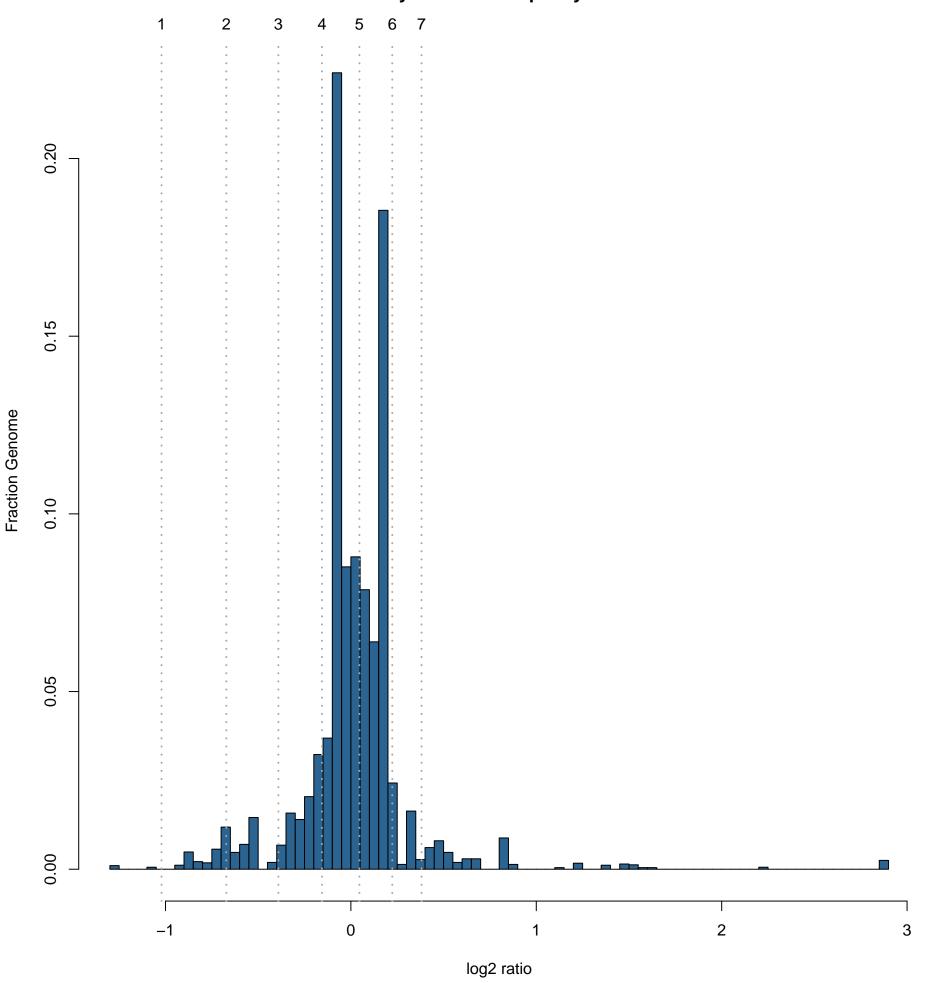
# SCNA-fit log-likelihood: -5772.98

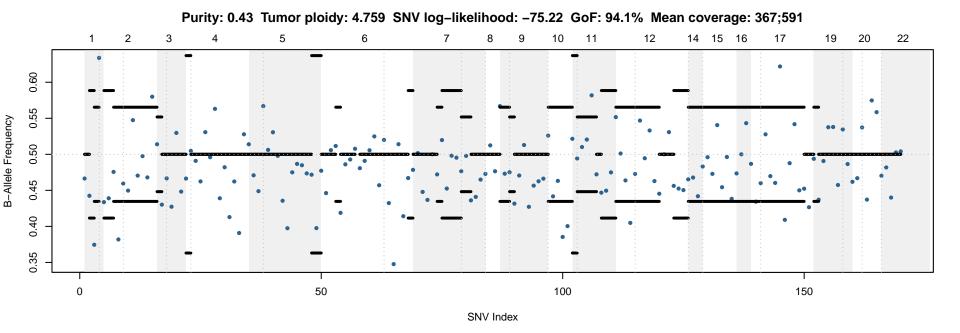




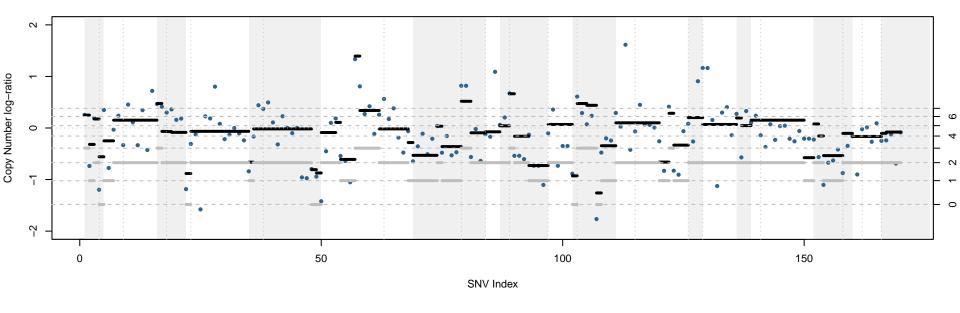


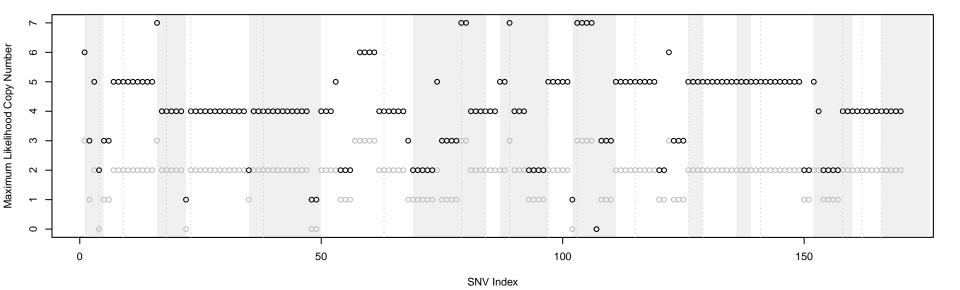
Purity: 0.43 Tumor ploidy: 4.759

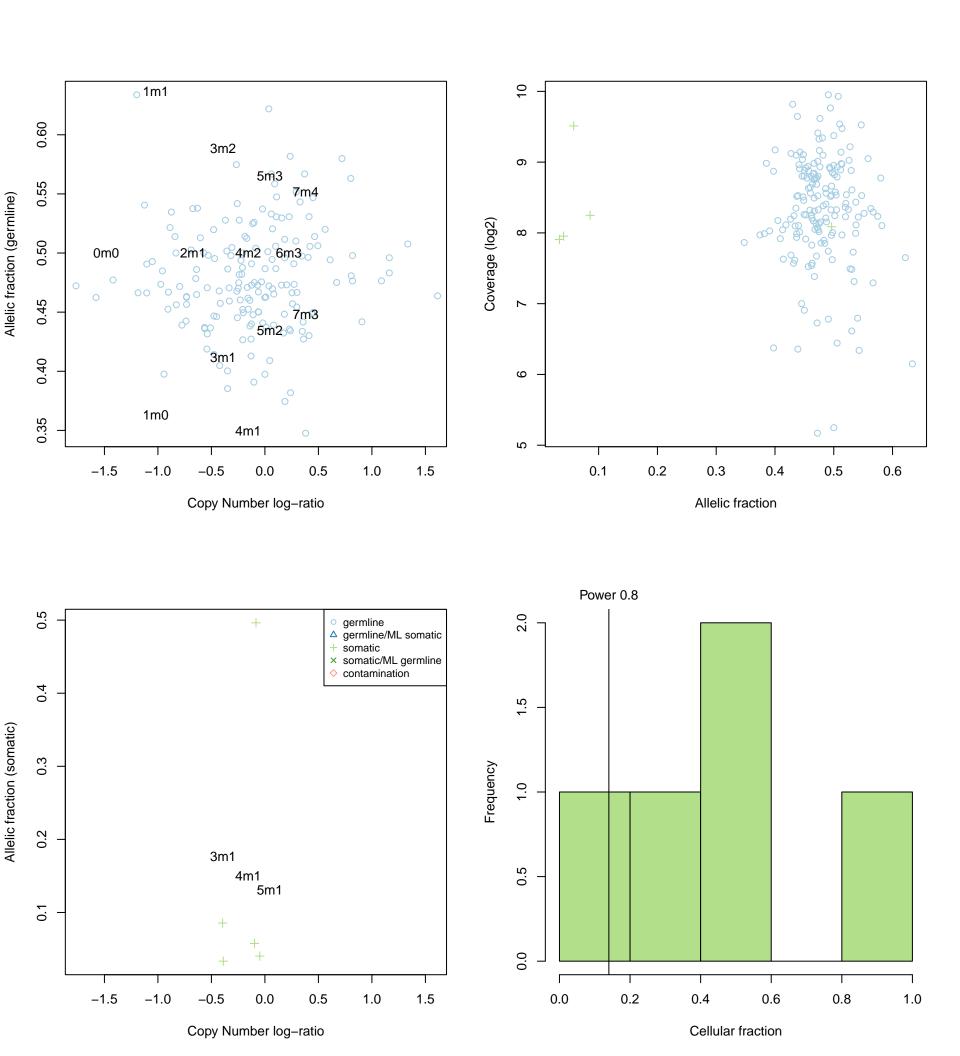




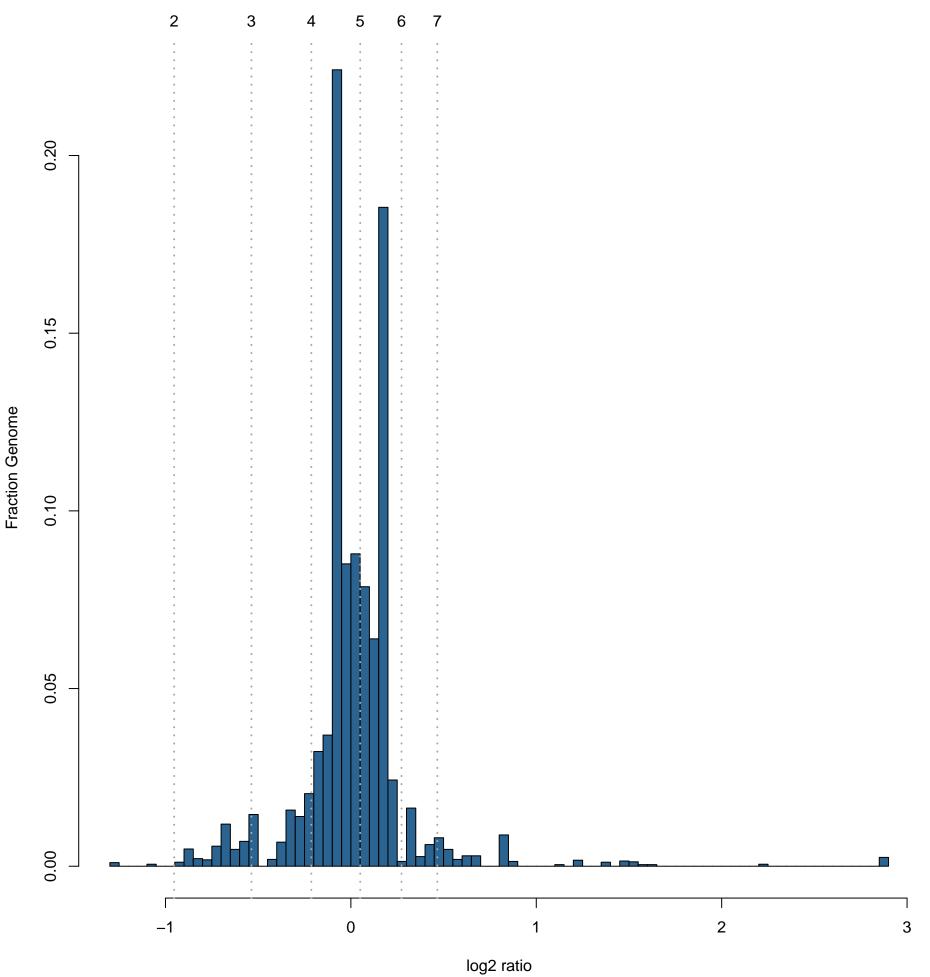
# SCNA-fit log-likelihood: -5780.66

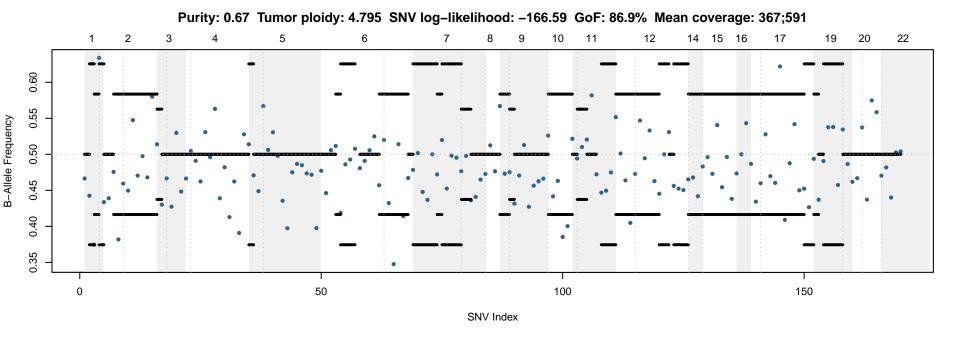




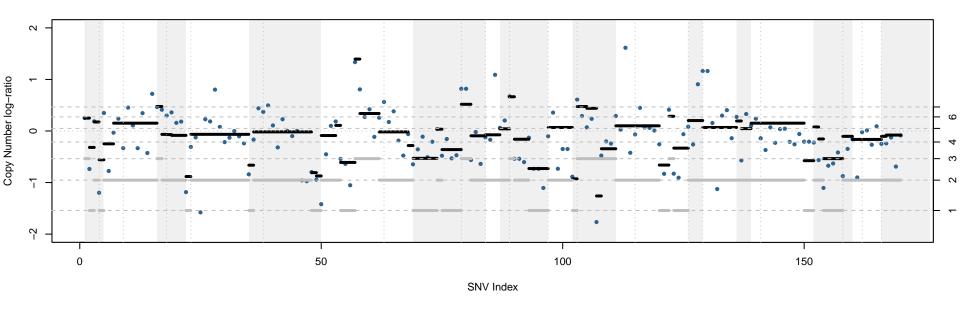


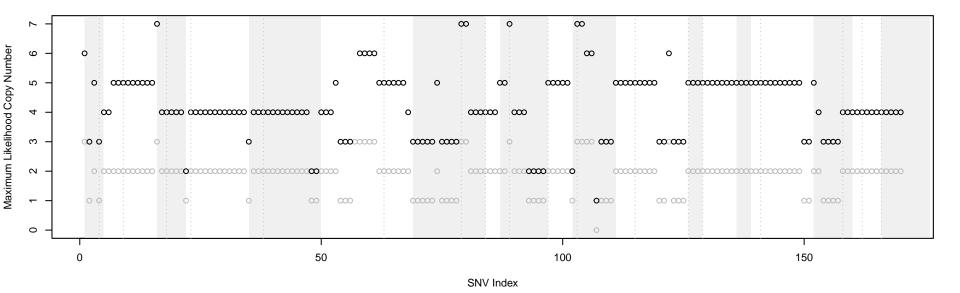
Purity: 0.67 Tumor ploidy: 4.795

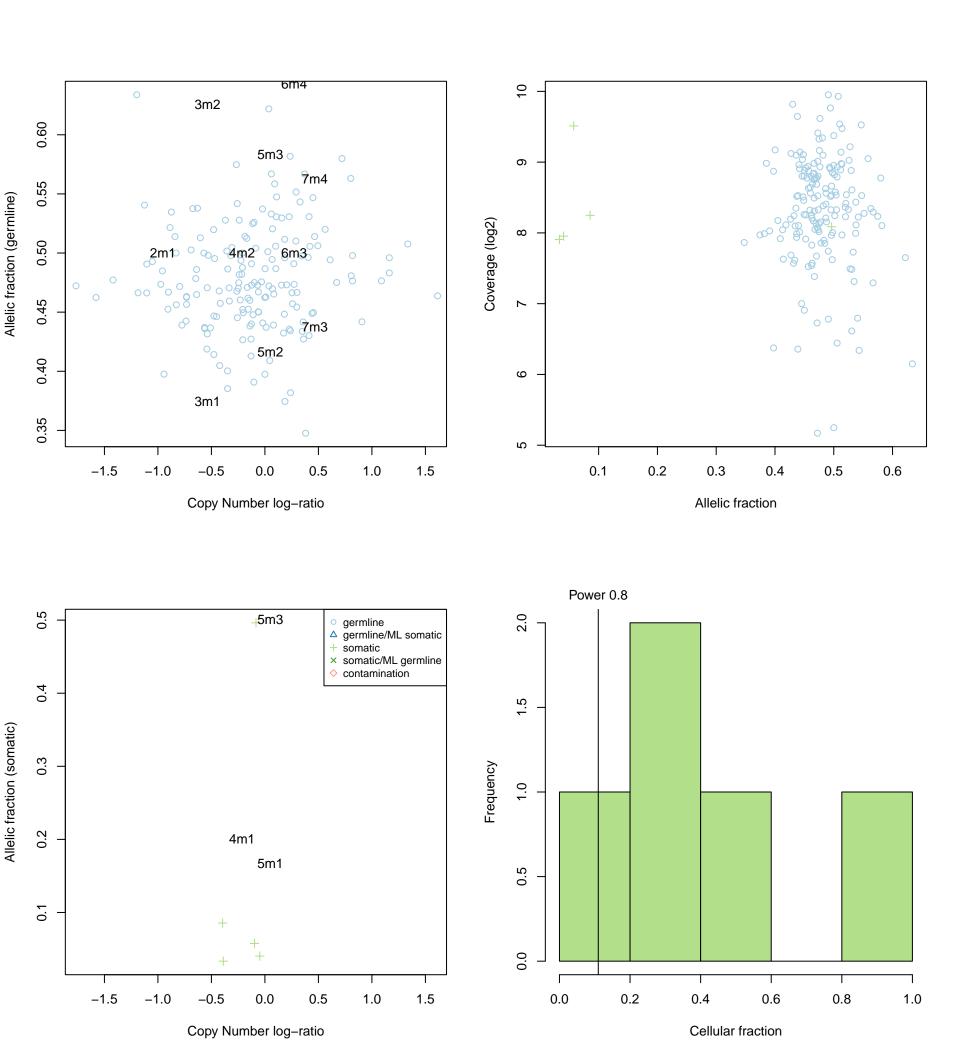




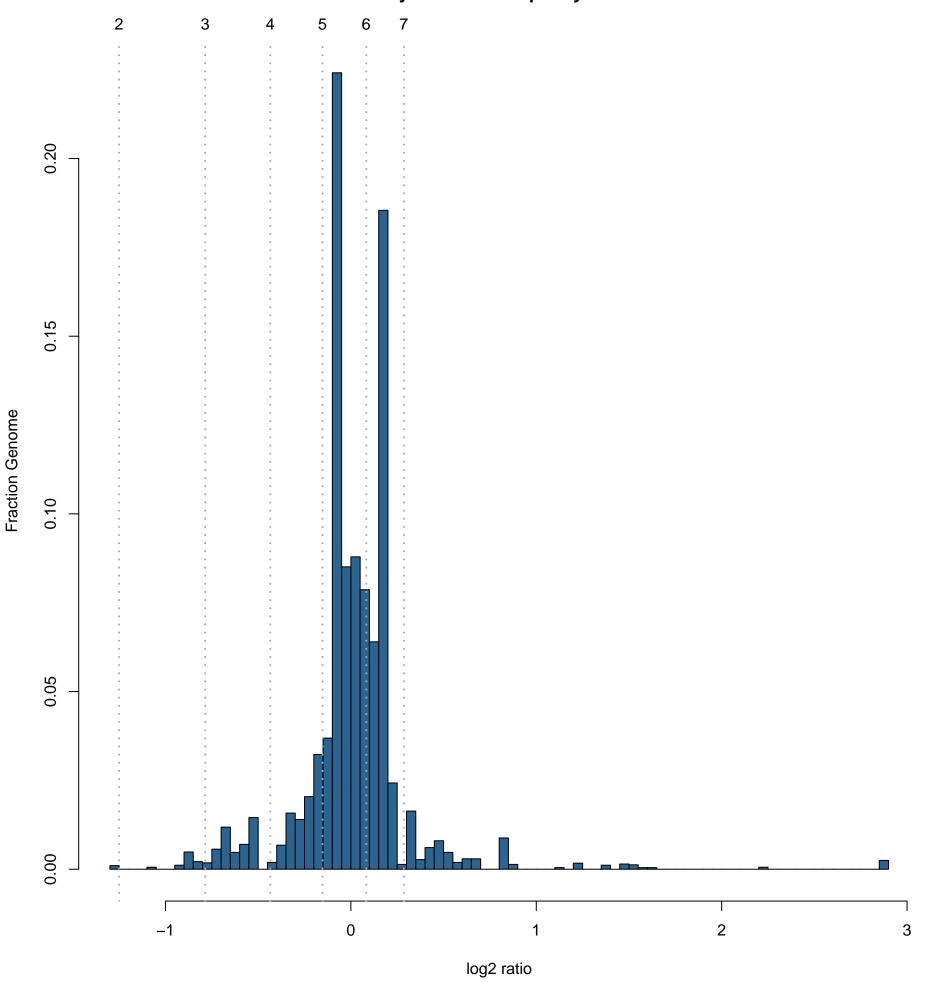
# SCNA-fit log-likelihood: -5836.69

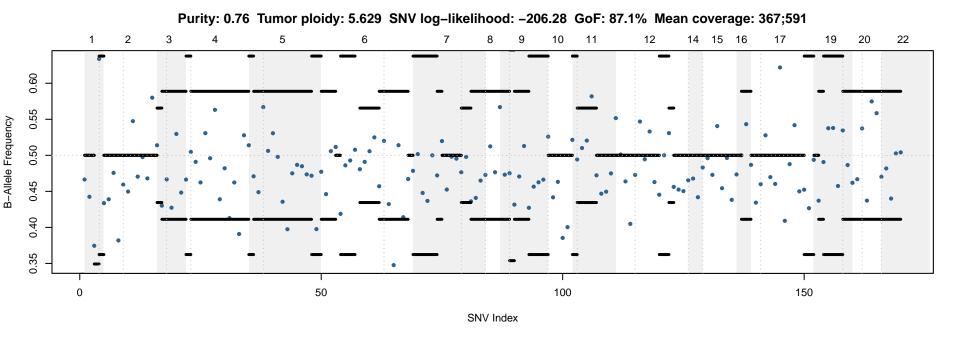




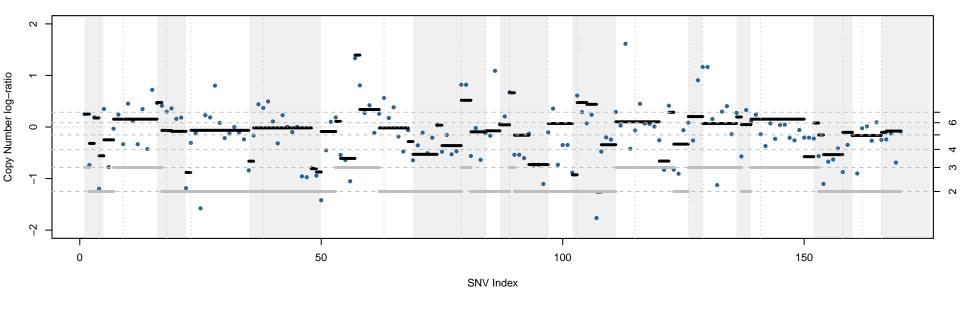


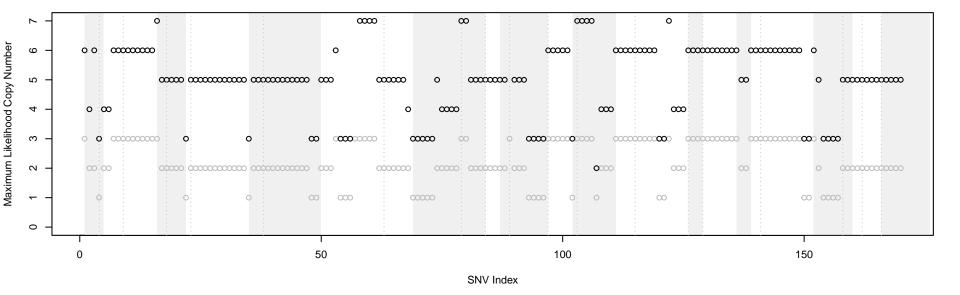
Purity: 0.76 Tumor ploidy: 5.629

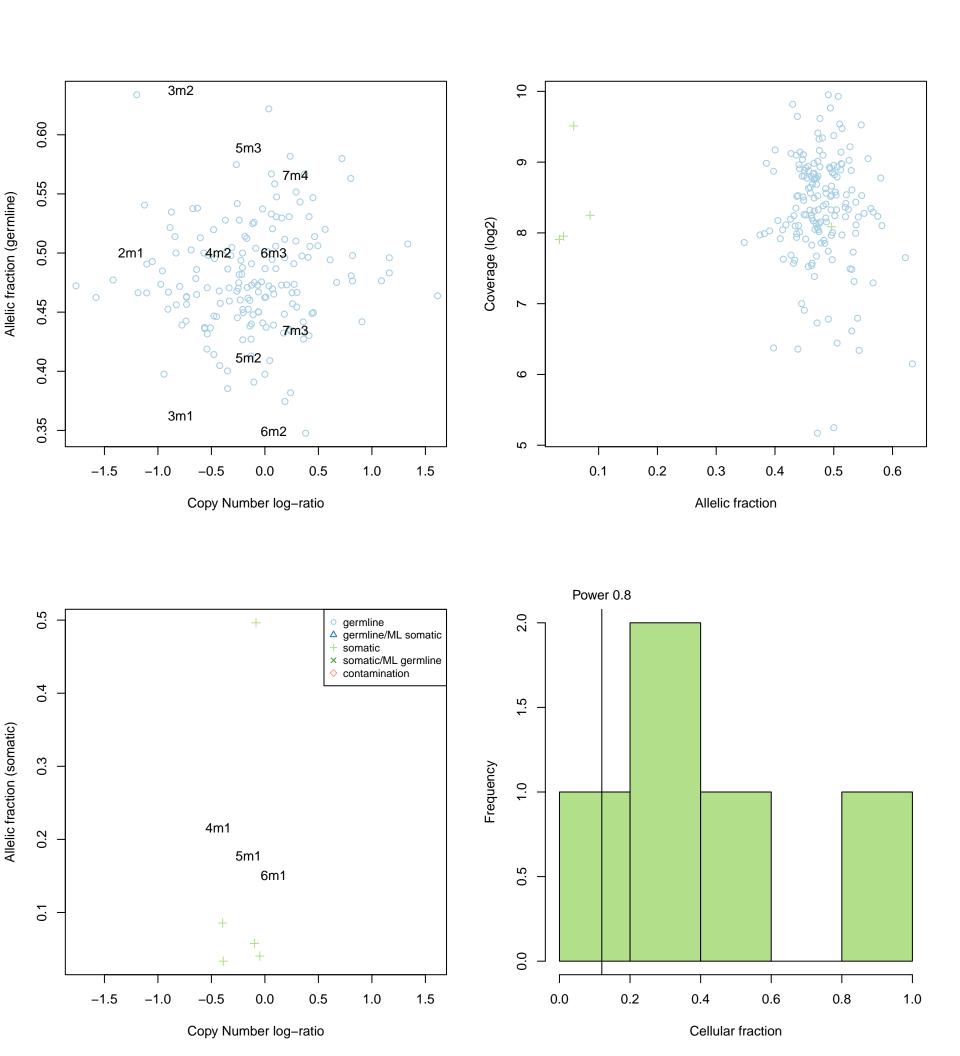


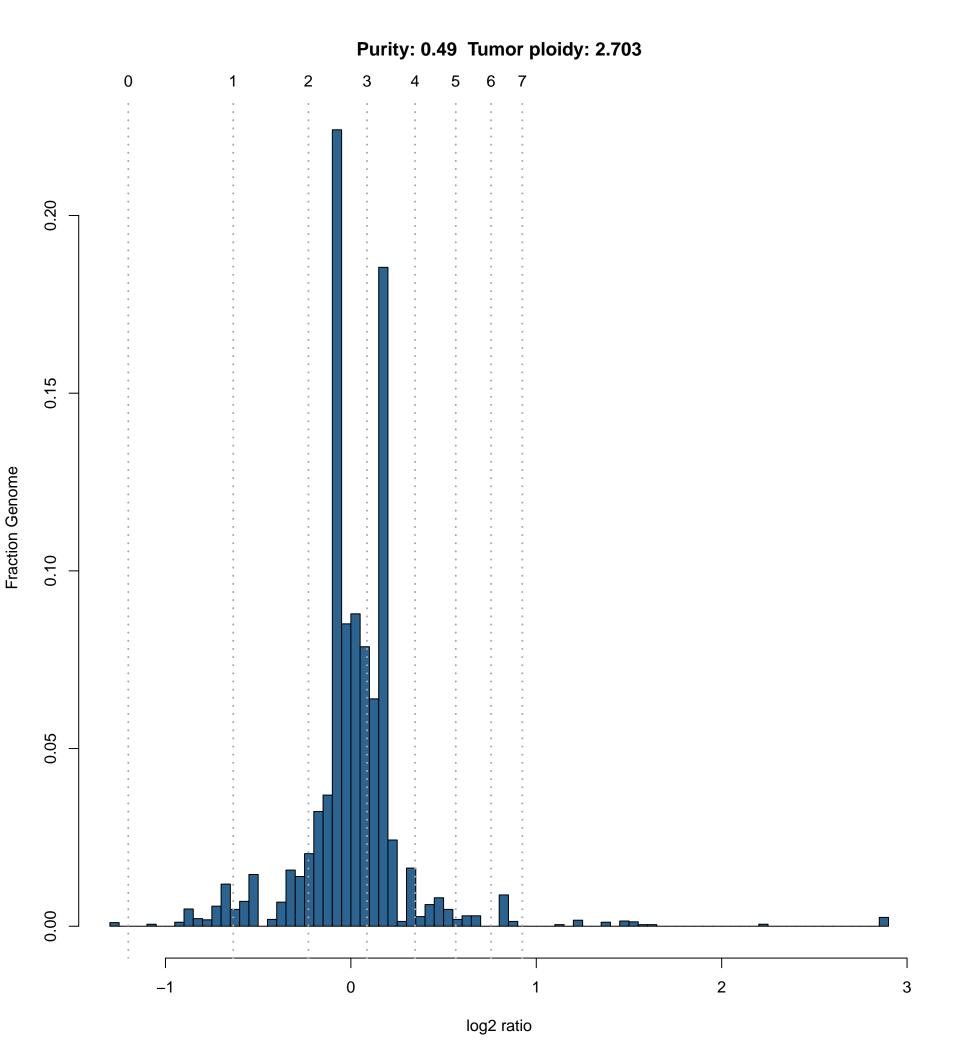


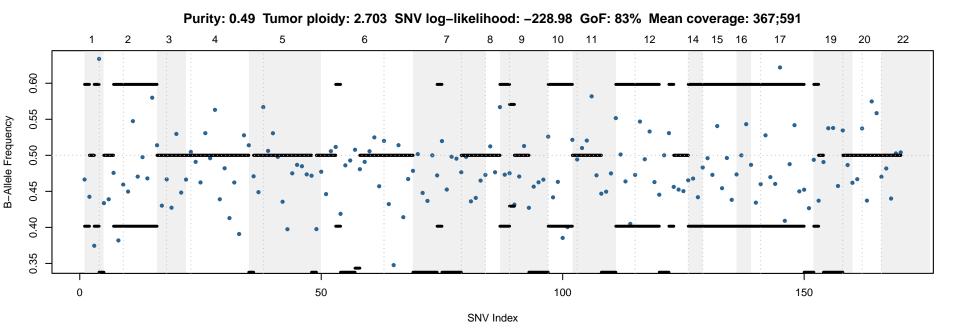
# SCNA-fit log-likelihood: -5837.33











# SCNA-fit log-likelihood: -5803.26

