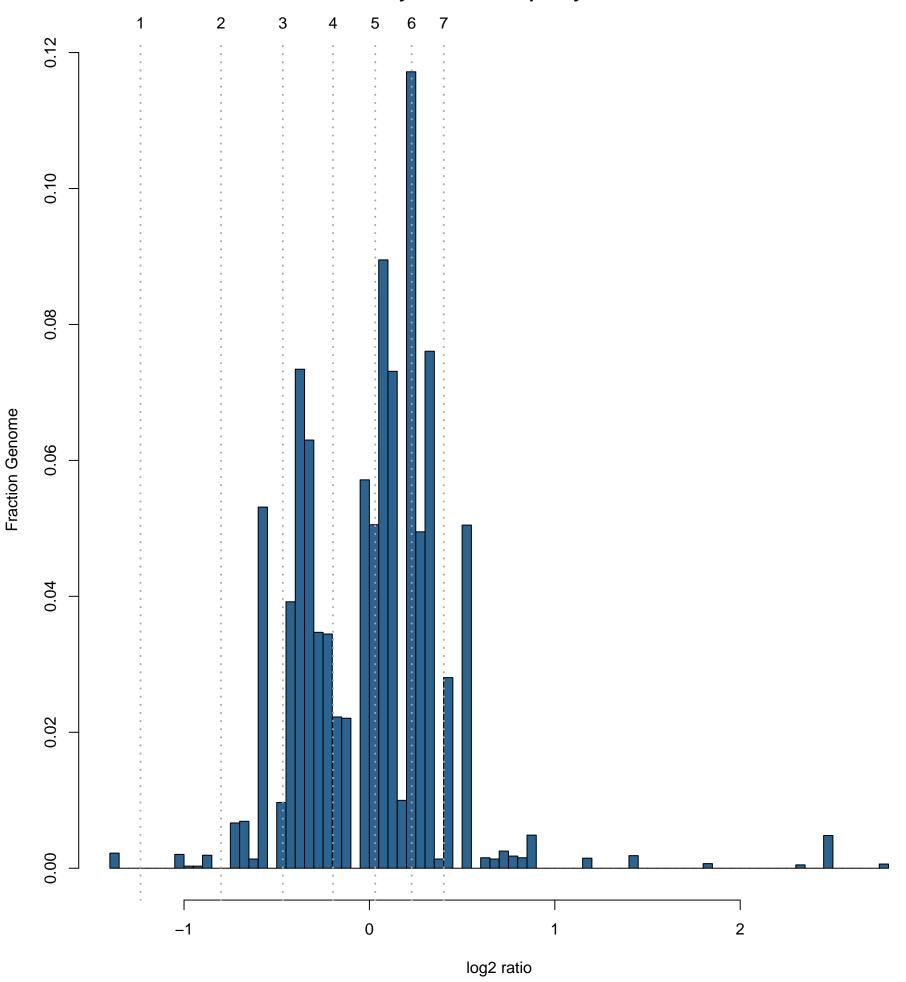
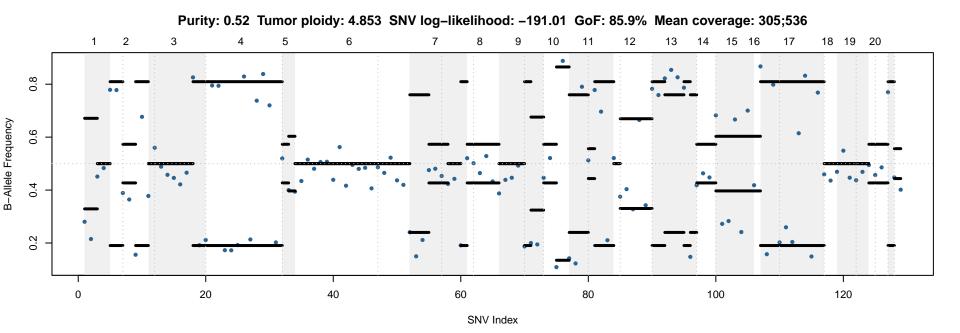
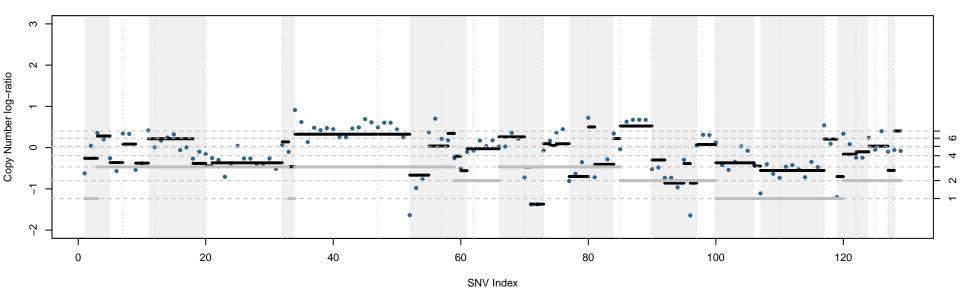
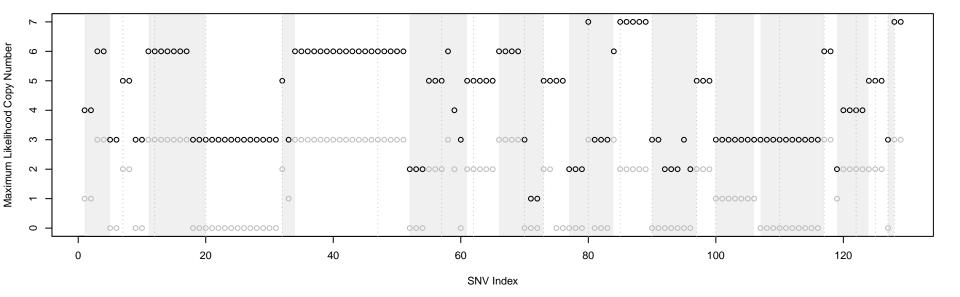
Purity: 0.52 Tumor ploidy: 4.853

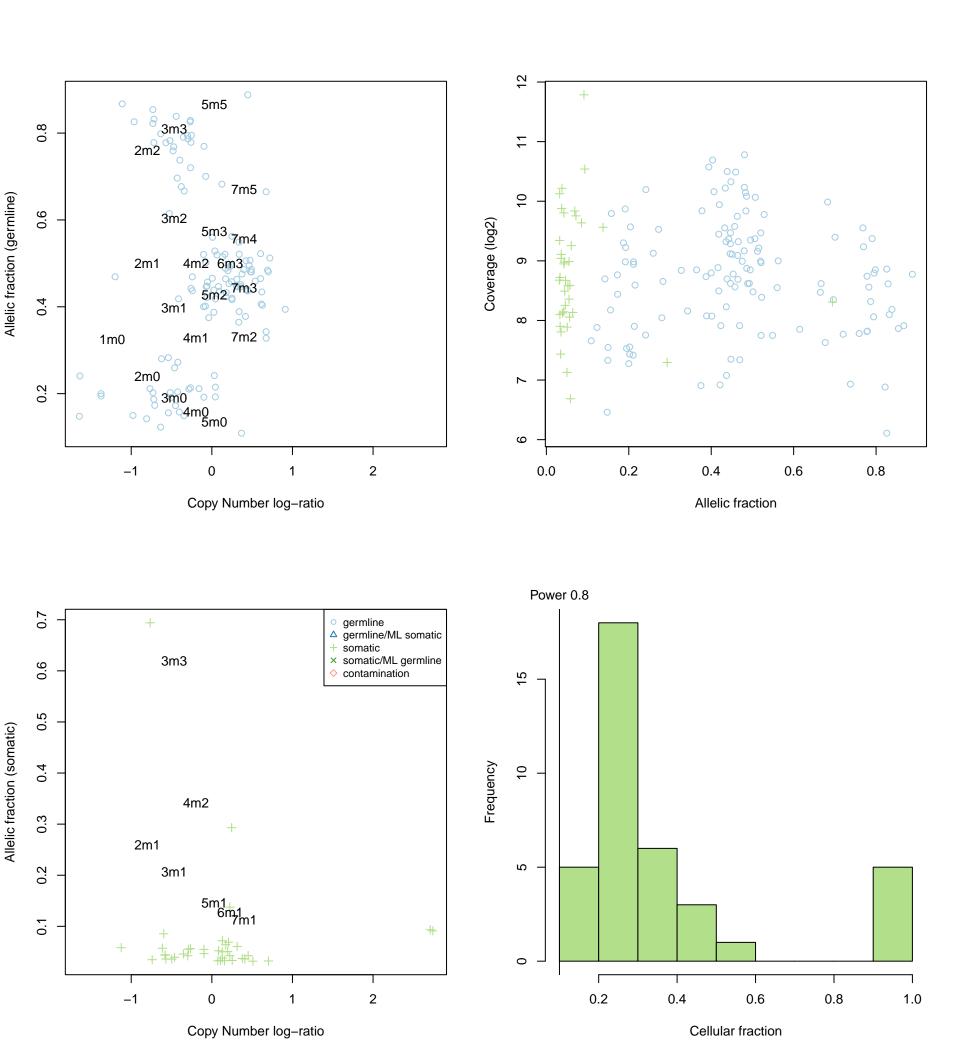




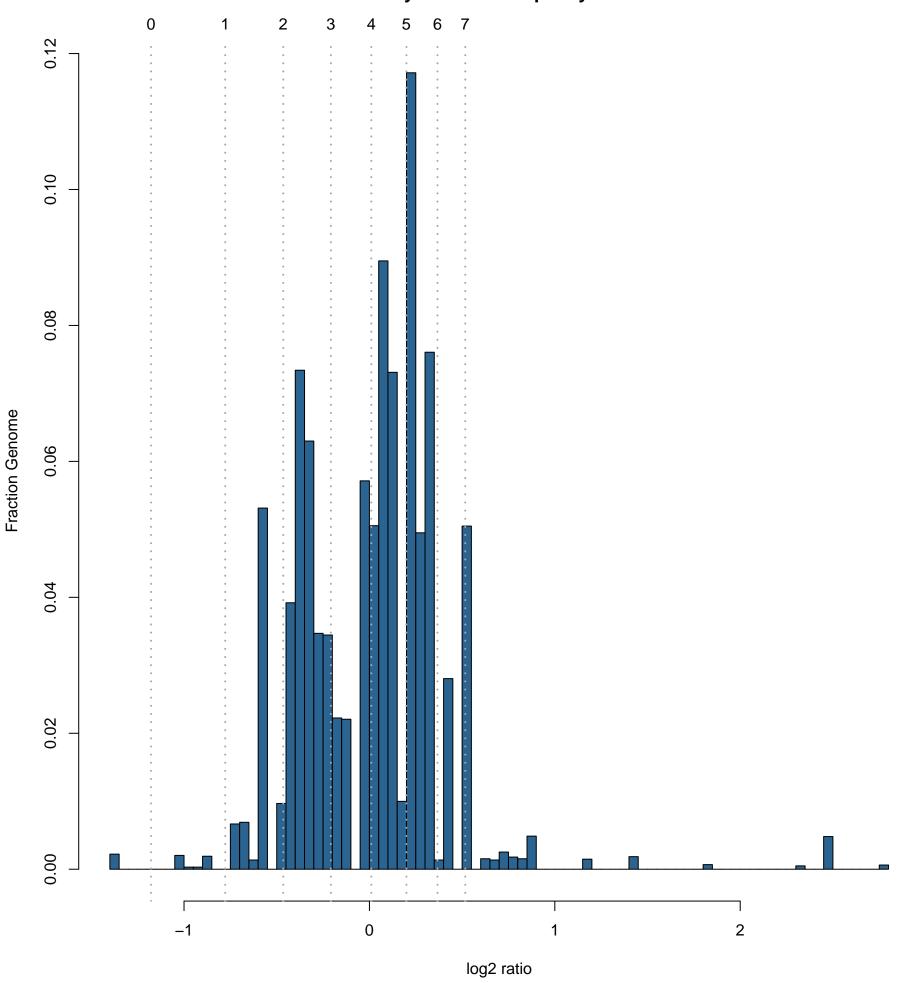
SCNA-fit log-likelihood: -7409.2

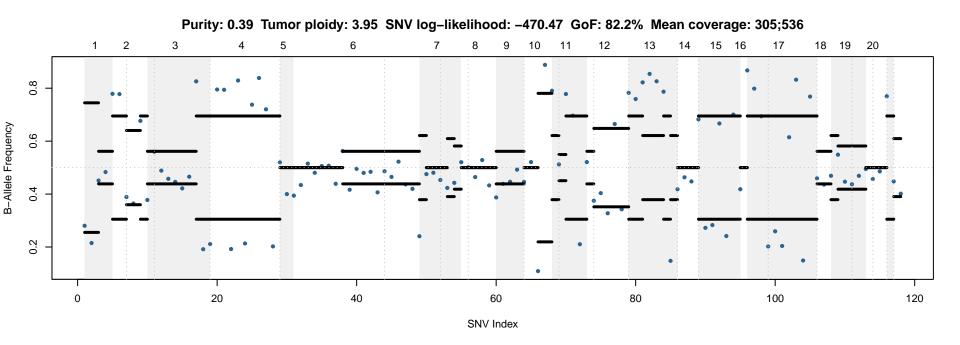




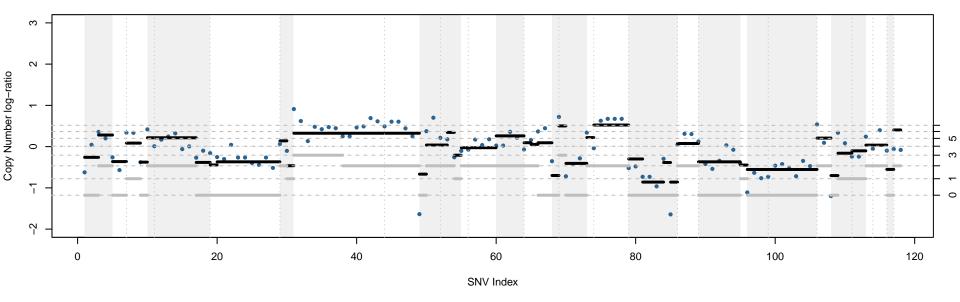


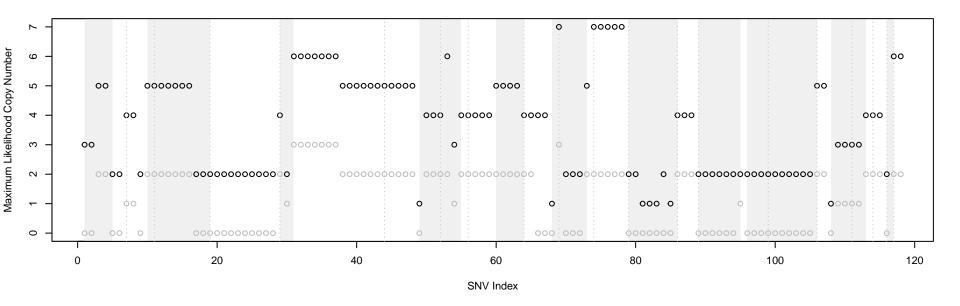
Purity: 0.39 Tumor ploidy: 3.95

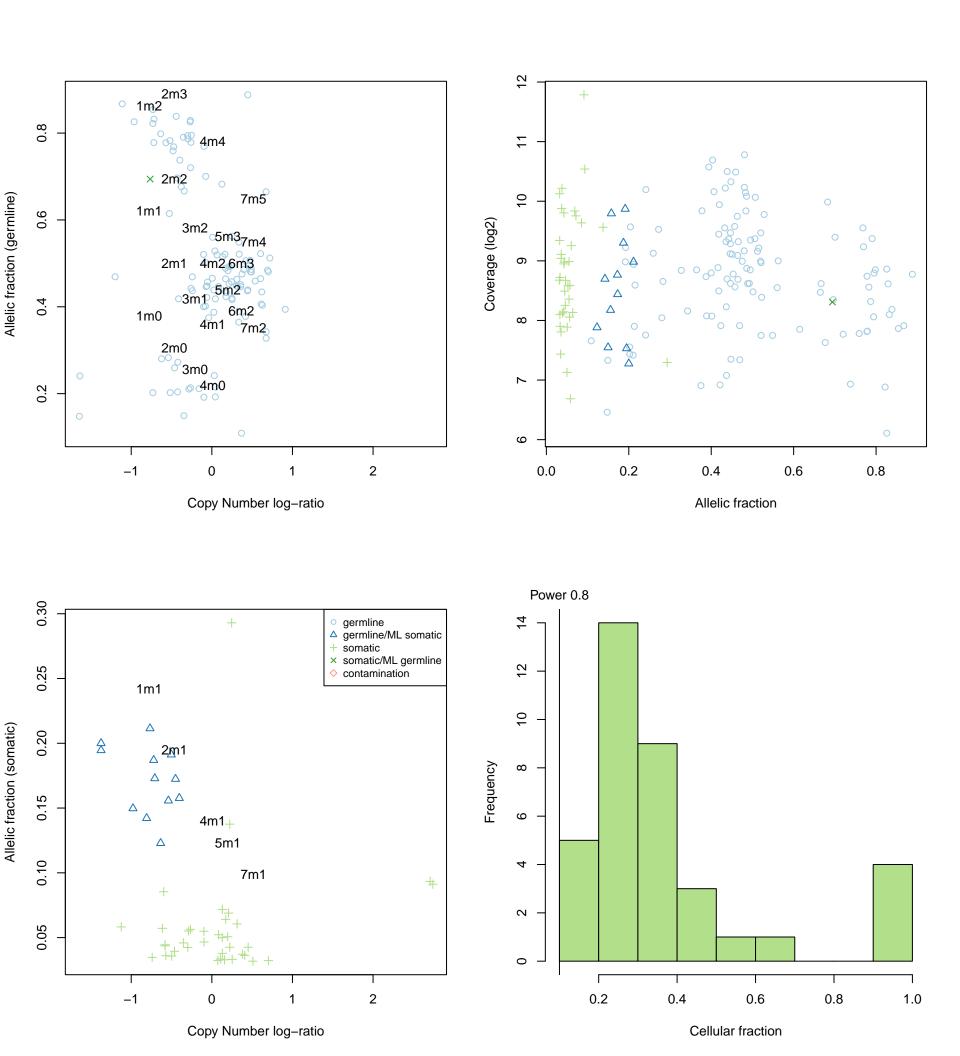




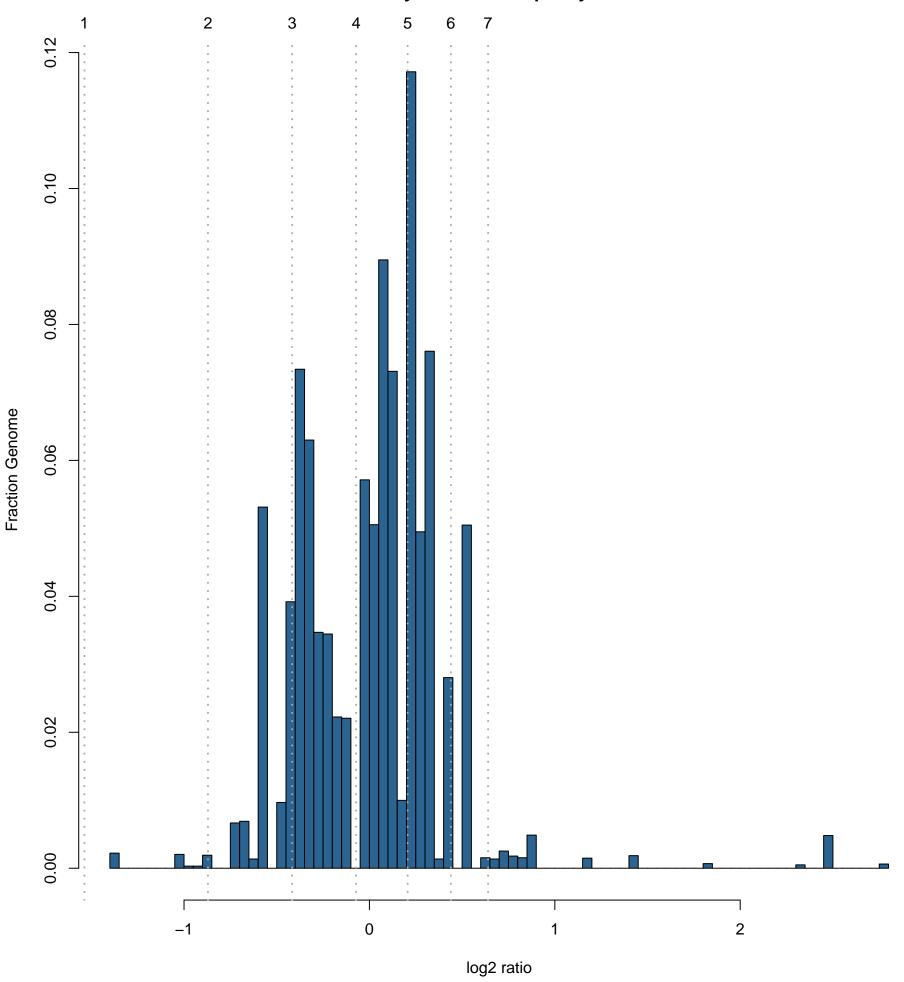
SCNA-fit log-likelihood: -7363.02



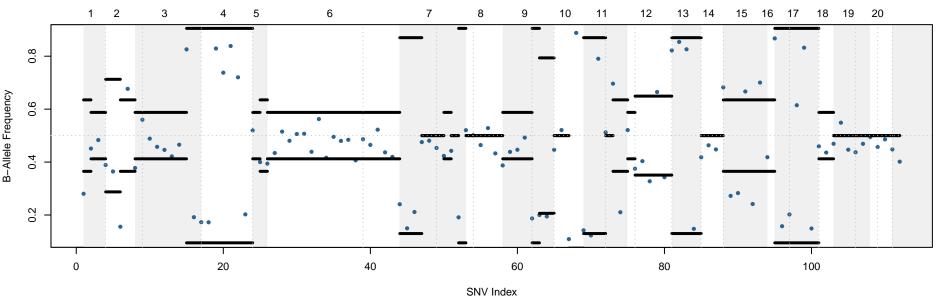




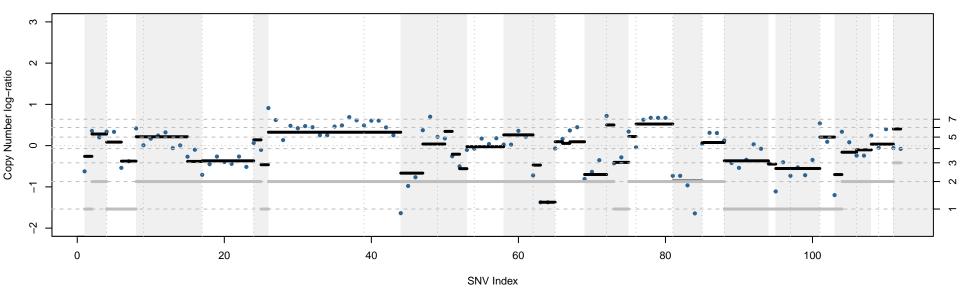
Purity: 0.74 Tumor ploidy: 4.24

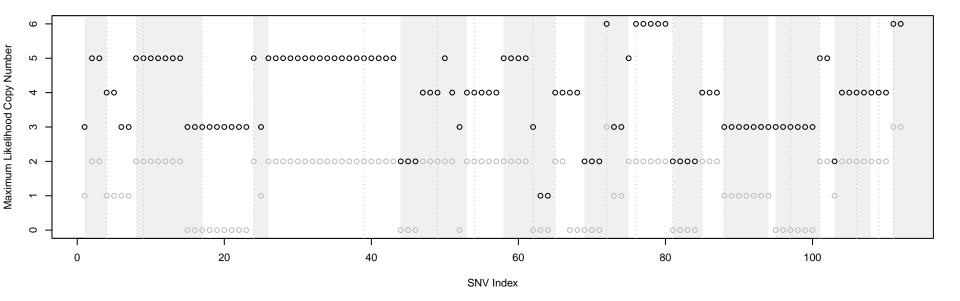


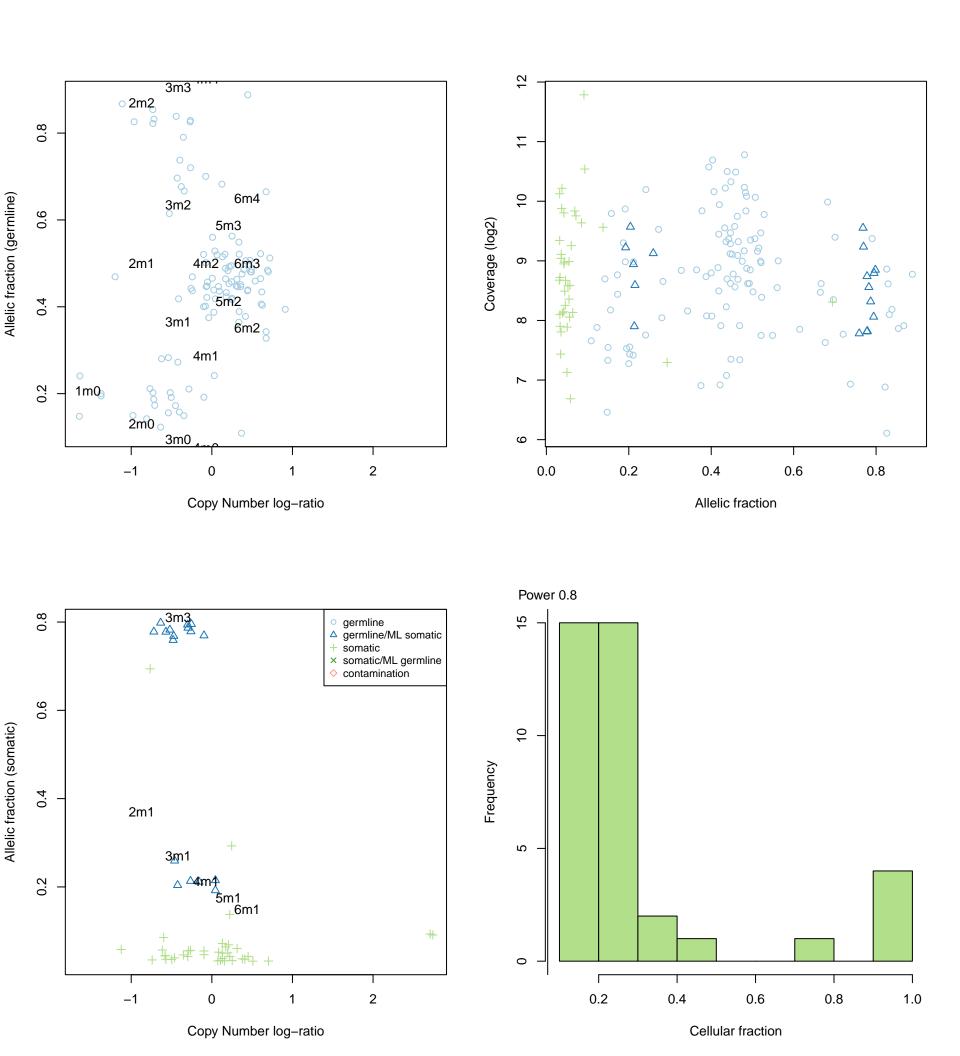
Purity: 0.74 Tumor ploidy: 4.24 SNV log-likelihood: -488.35 GoF: 75.9% Mean coverage: 305;536



SCNA-fit log-likelihood: -7408.02



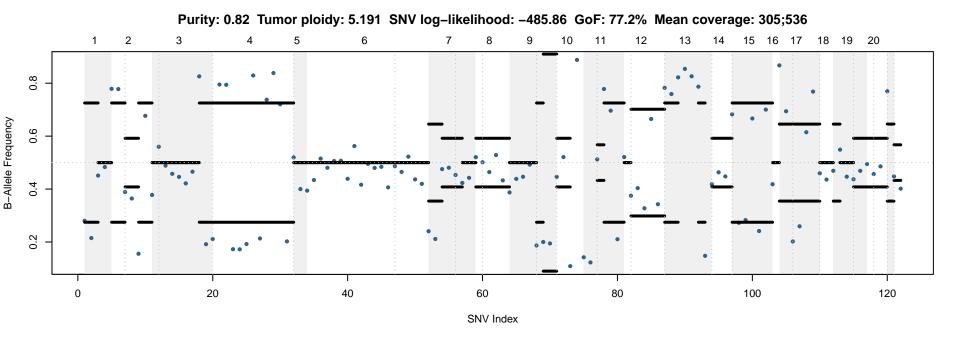




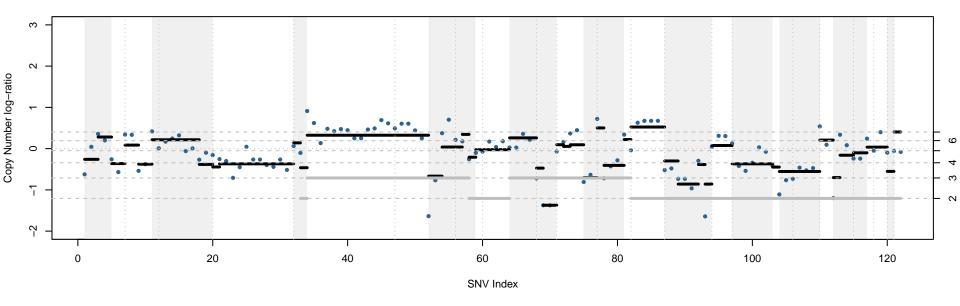
Purity: 0.82 Tumor ploidy: 5.191 2 3 5 6 4 0.10 0.08 90.0 0.04 0.02 0.00 -1 0 2 1

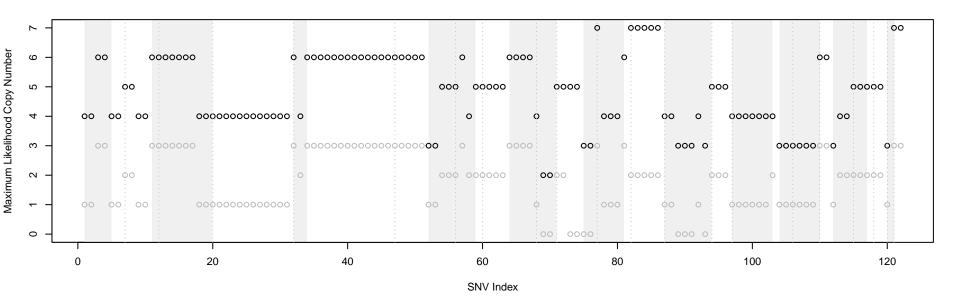
log2 ratio

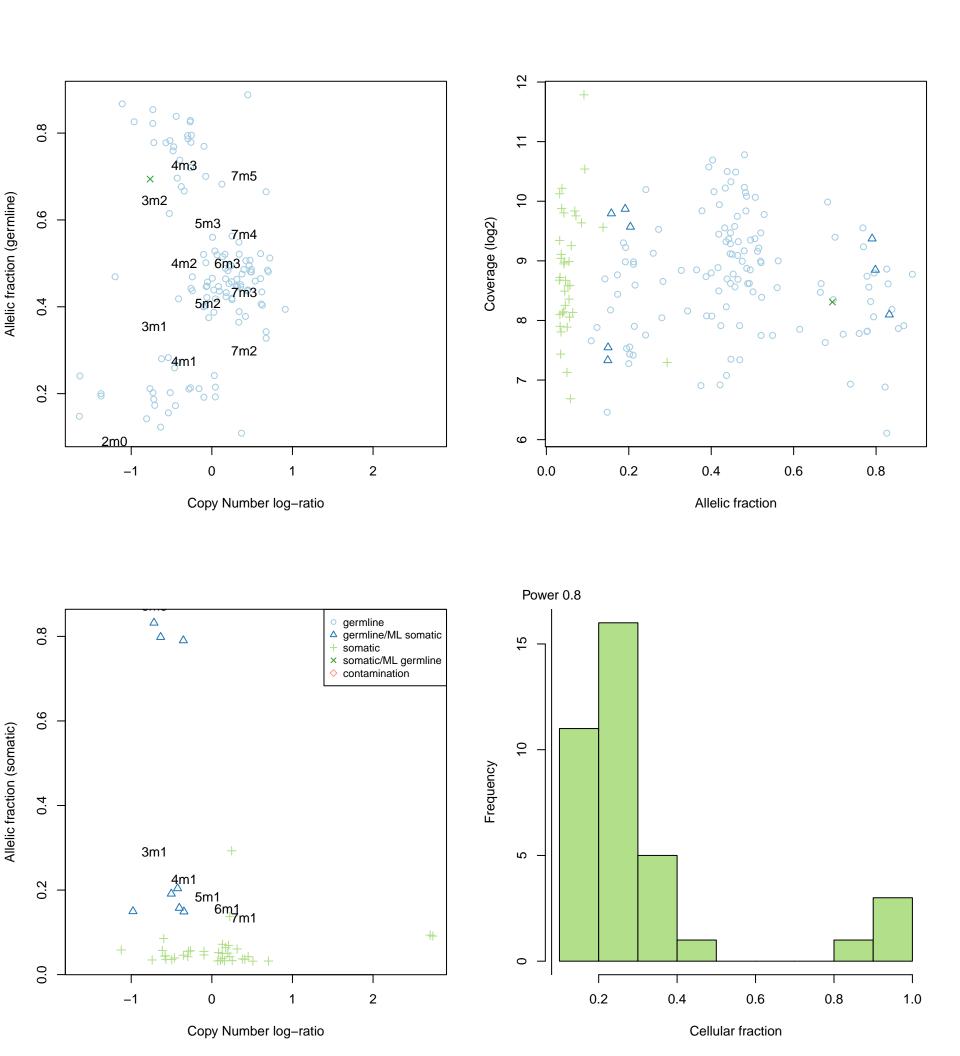
Fraction Genome

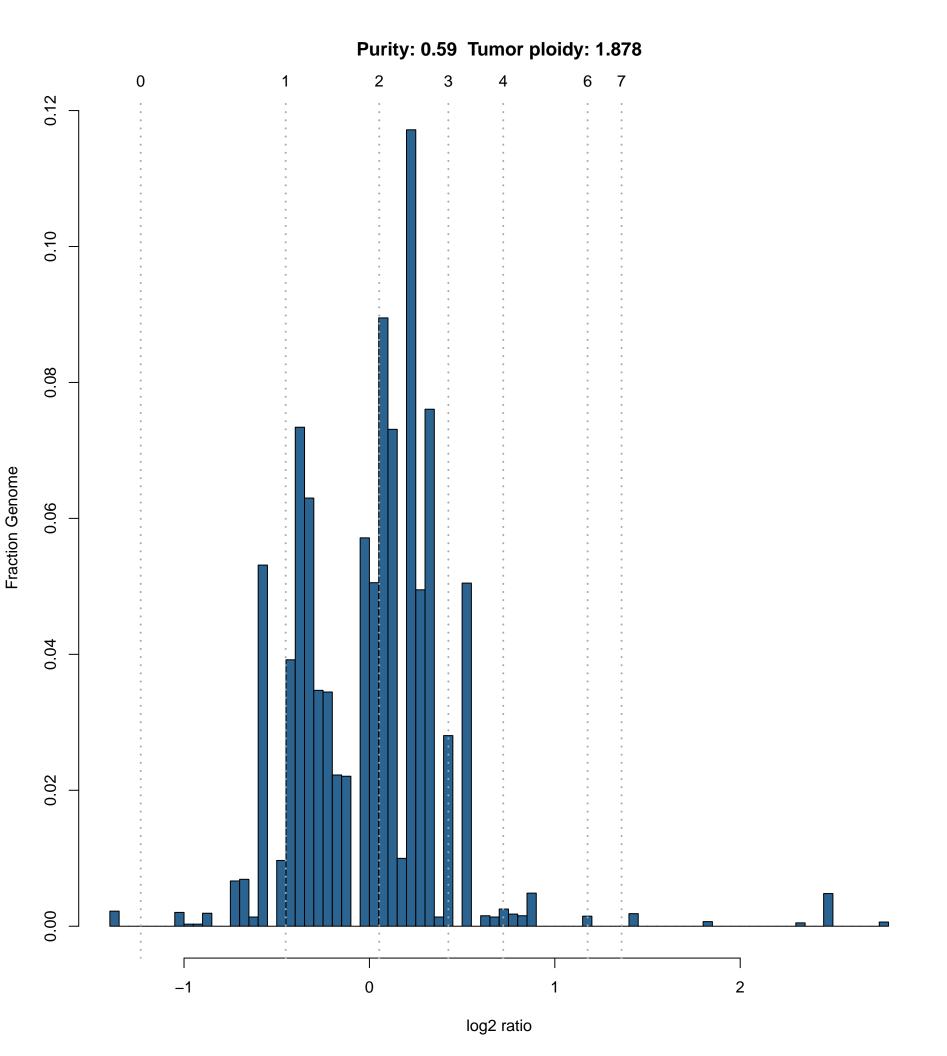


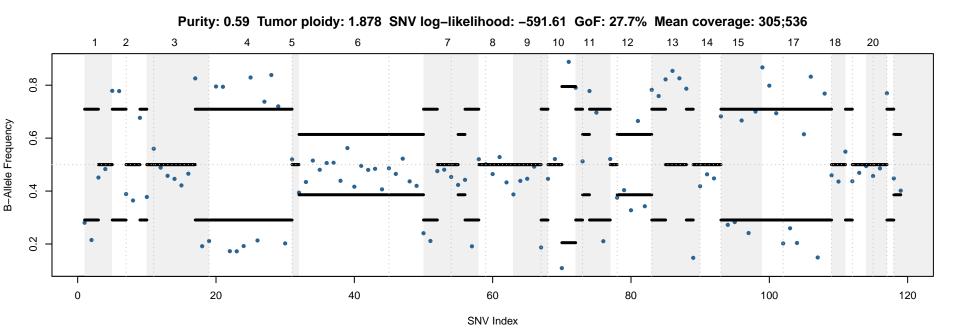
SCNA-fit log-likelihood: -7436.13











SCNA-fit log-likelihood: -7693.97

