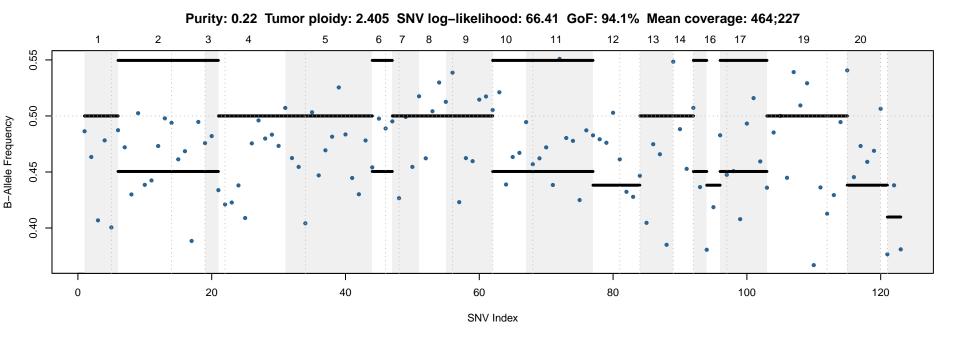
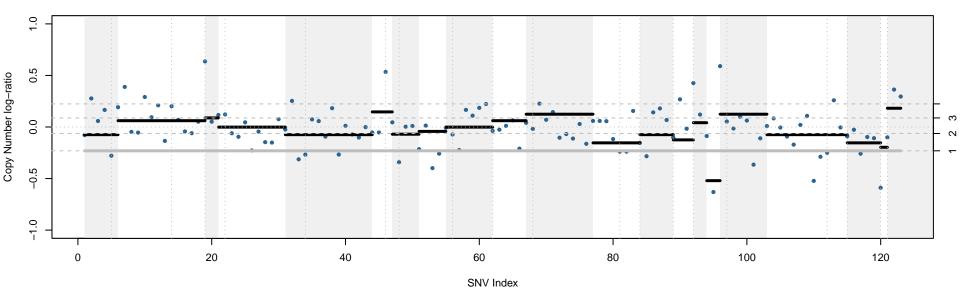
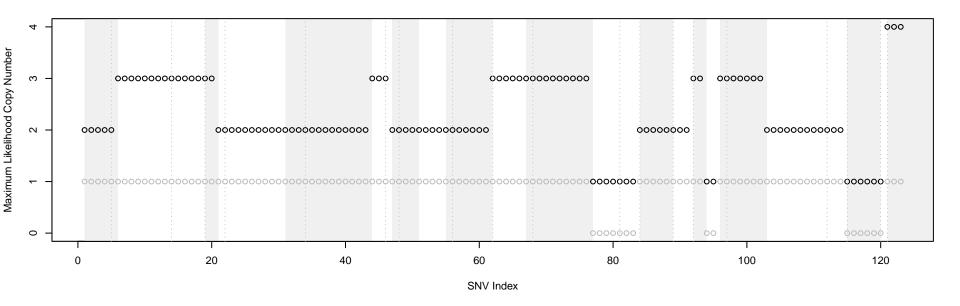
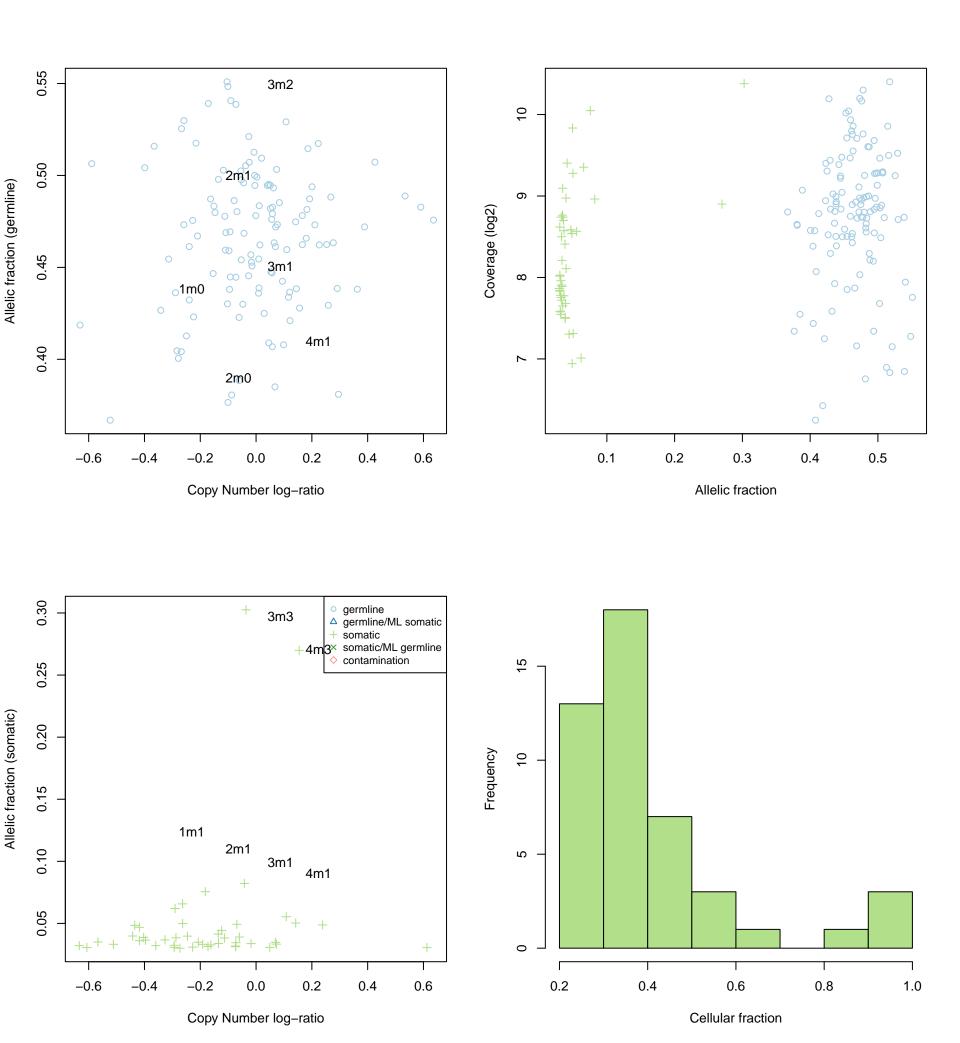
Purity: 0.22 Tumor ploidy: 2.405 2 3 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -0.2 -0.4 0.0 0.2 log2 ratio



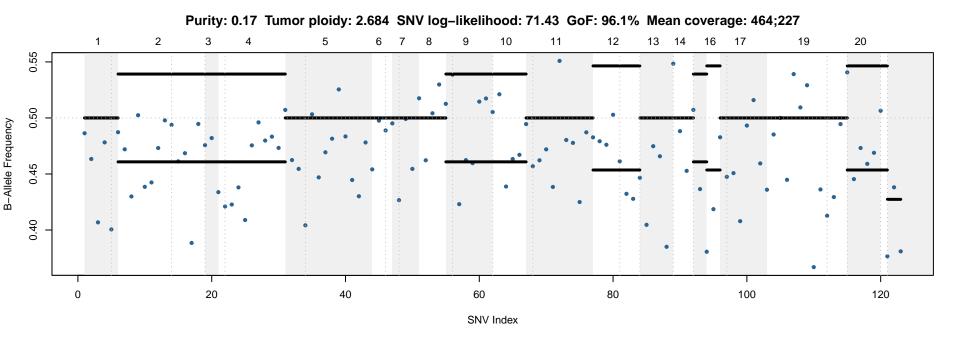
# SCNA-fit log-likelihood: -12523.51



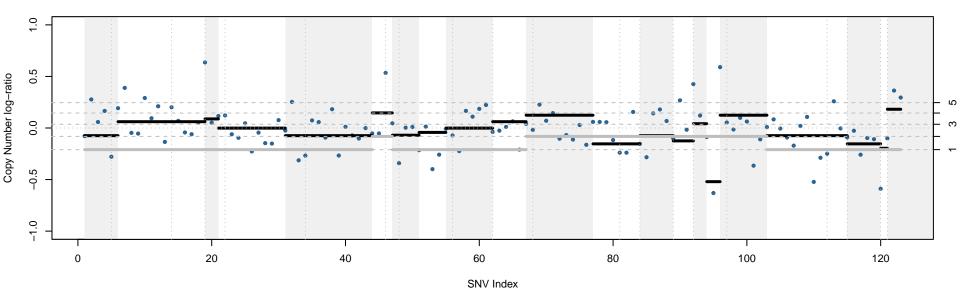


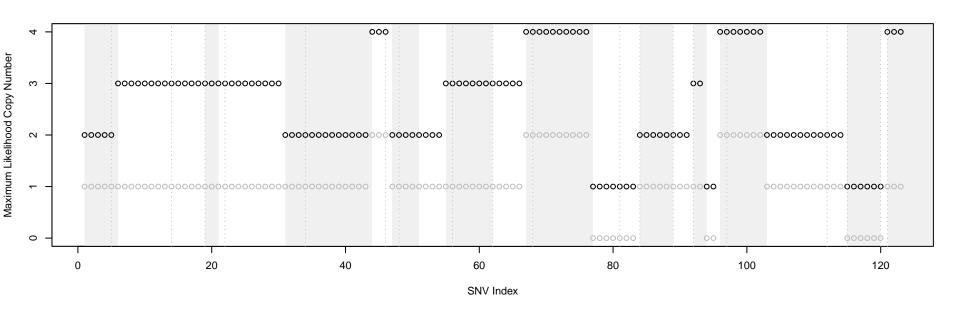


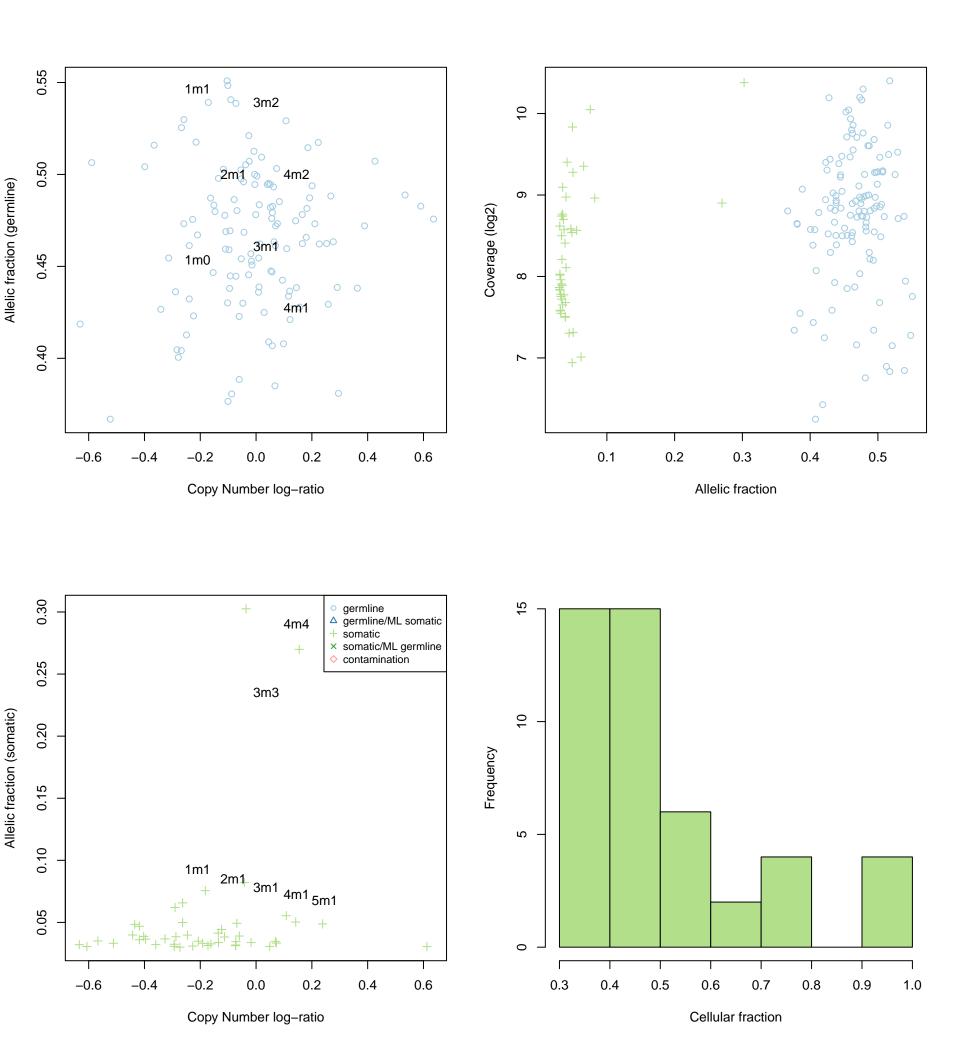
Purity: 0.17 Tumor ploidy: 2.684 5 3 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -0.4 -0.2 0.0 0.2 log2 ratio



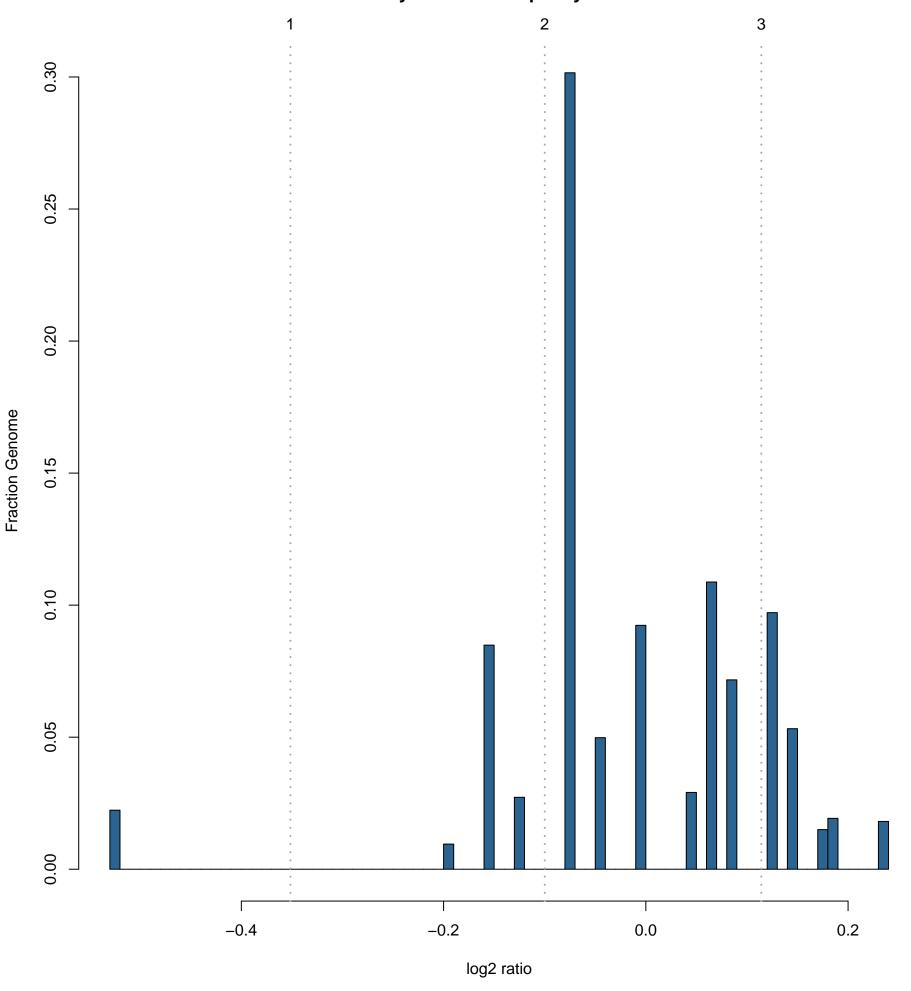
## SCNA-fit log-likelihood: -12517.49

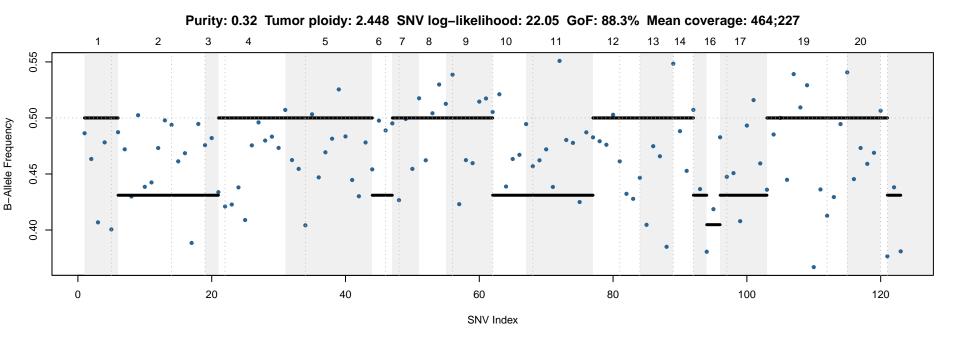




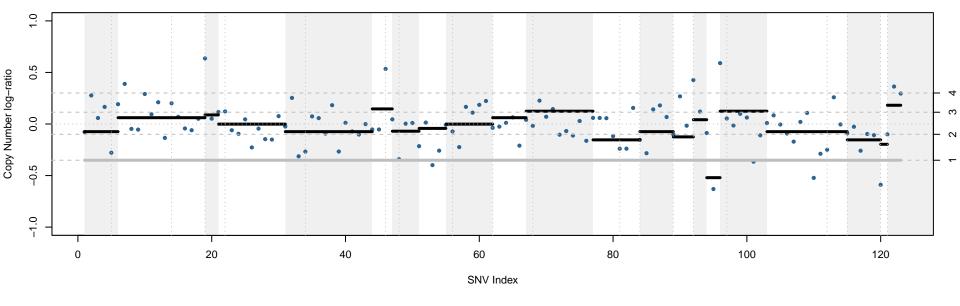


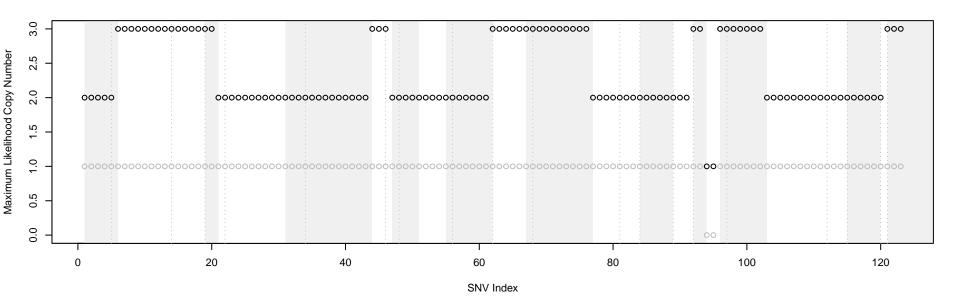
Purity: 0.32 Tumor ploidy: 2.448

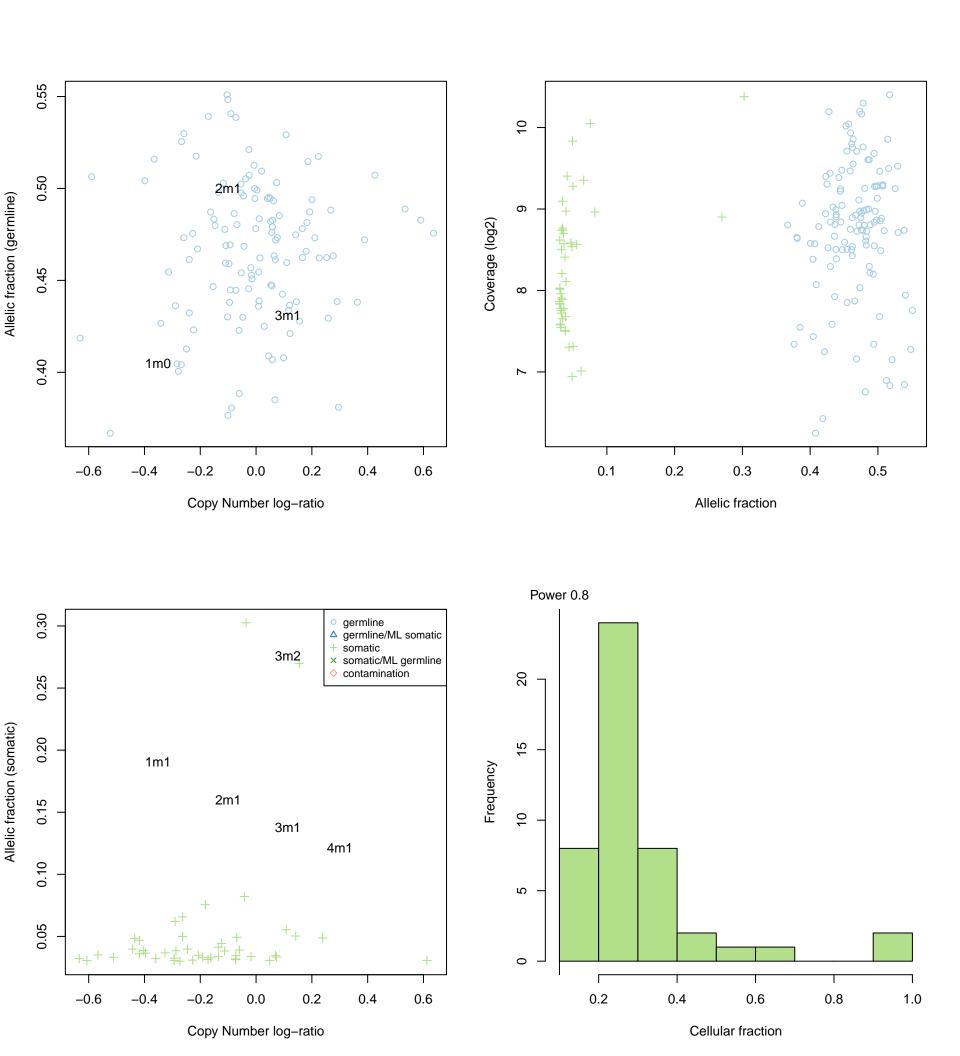




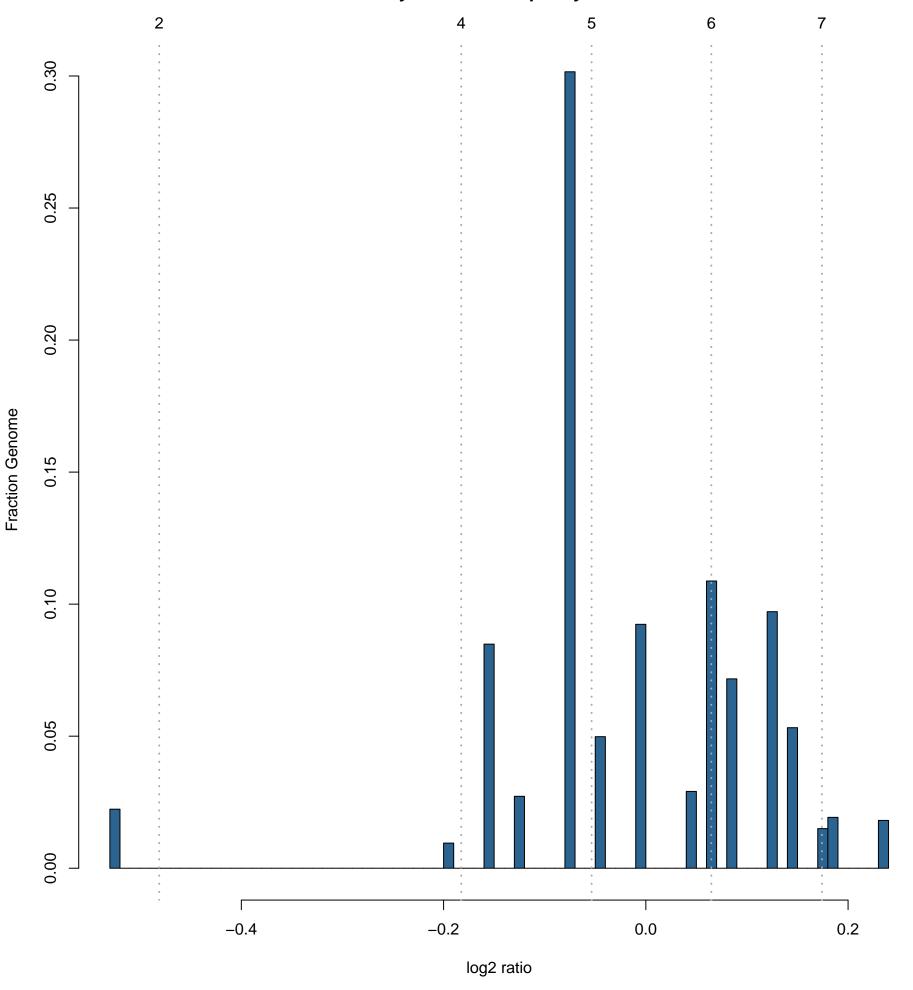
## SCNA-fit log-likelihood: -12518.77

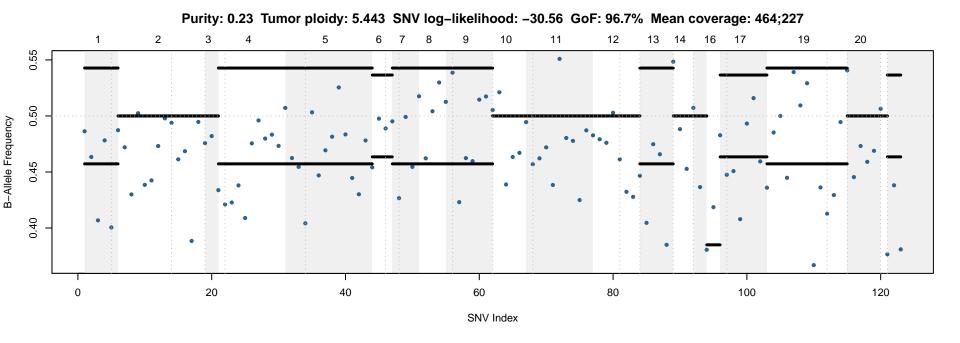




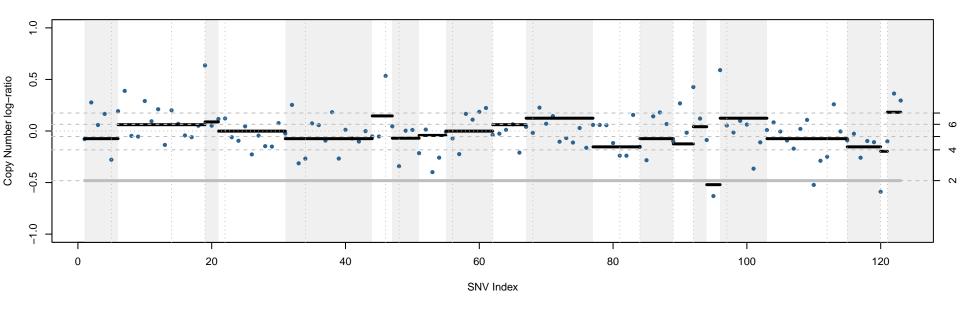


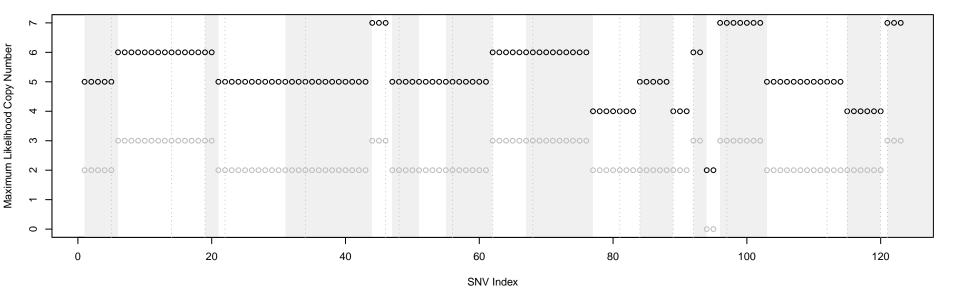
Purity: 0.23 Tumor ploidy: 5.443

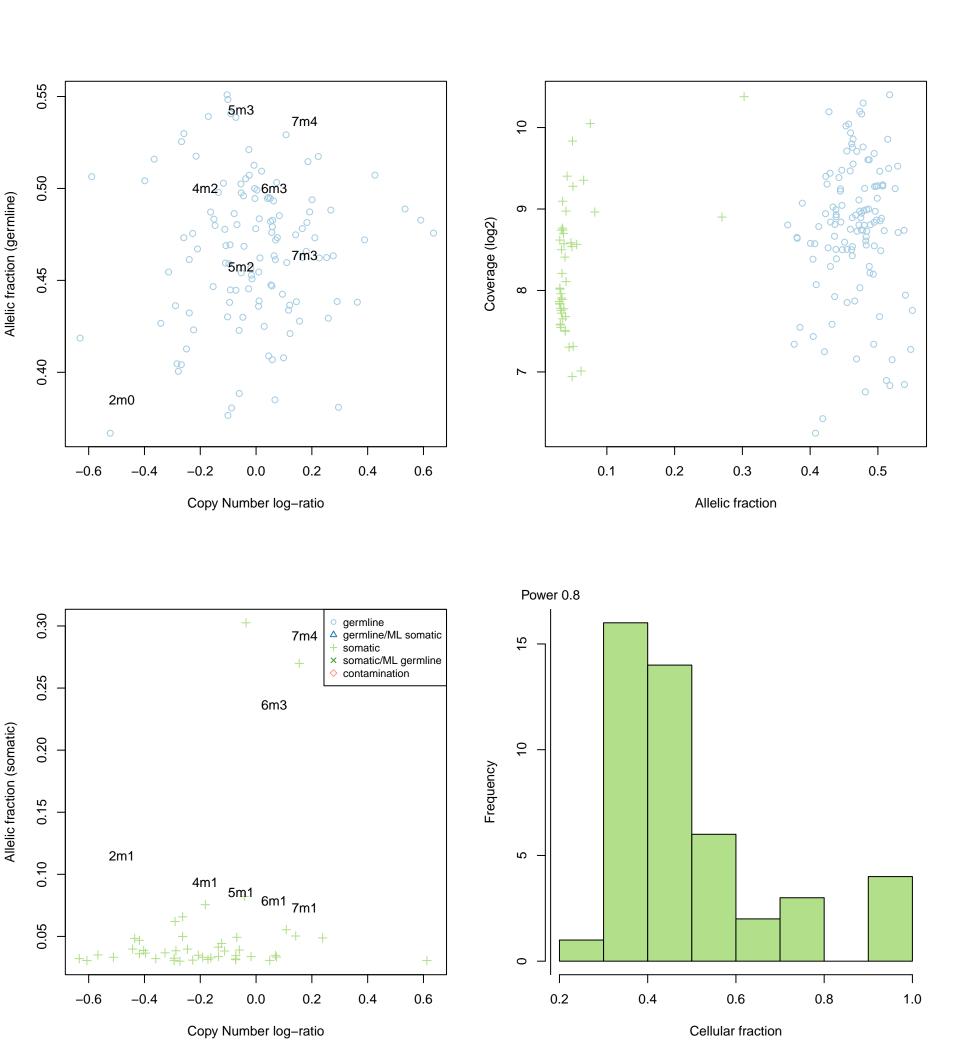




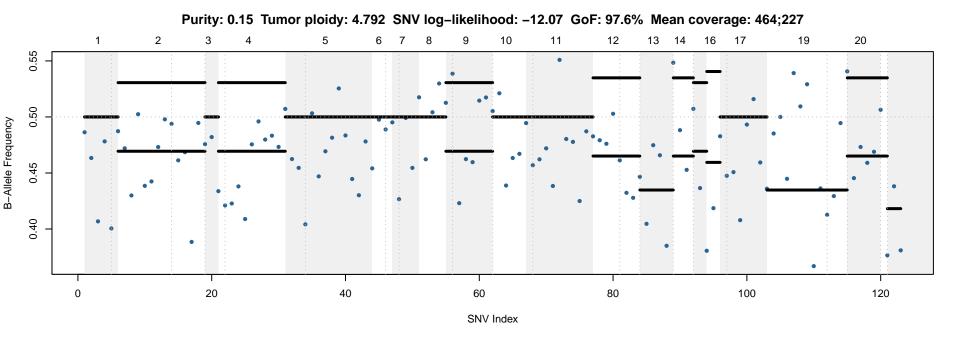
## SCNA-fit log-likelihood: -12484.9



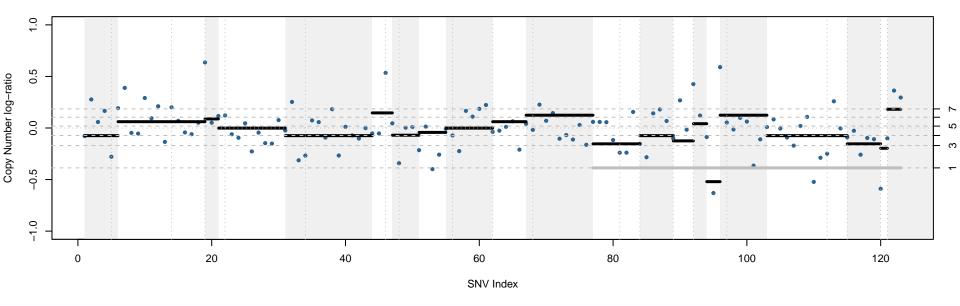


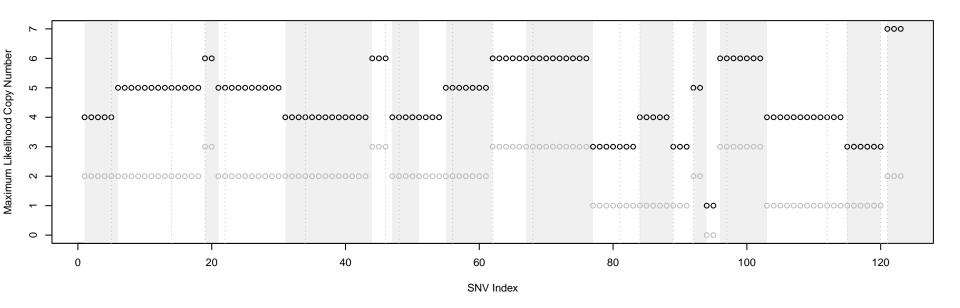


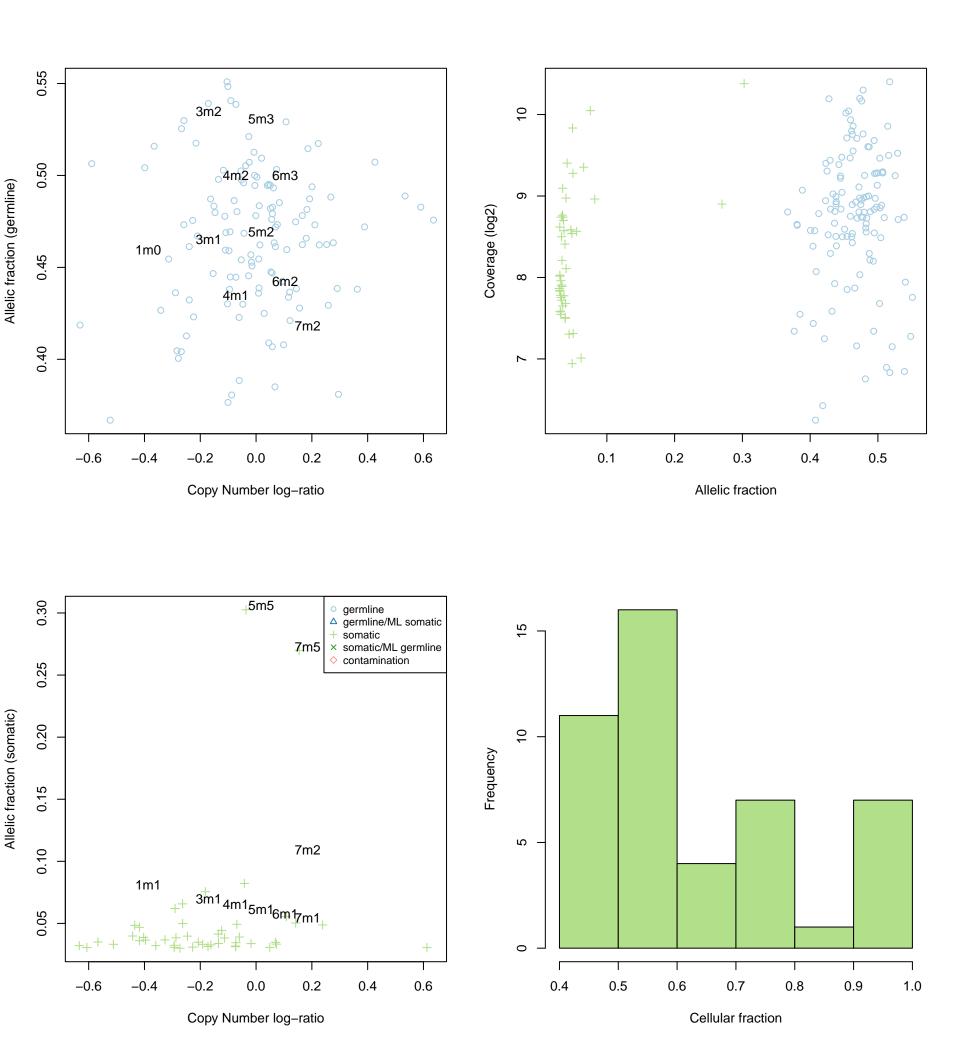
Purity: 0.15 Tumor ploidy: 4.792 3 5 6 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -0.2 -0.4 0.0 0.2 log2 ratio



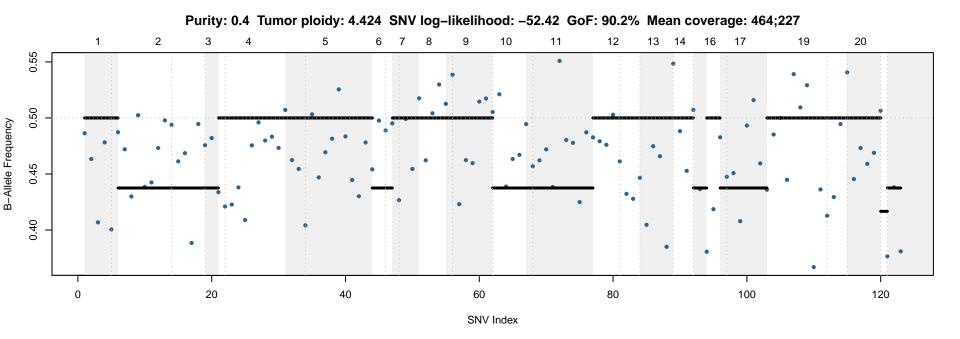
## SCNA-fit log-likelihood: -12484.49



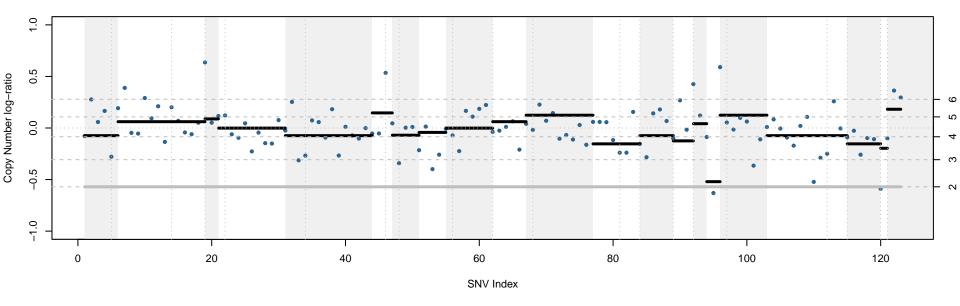


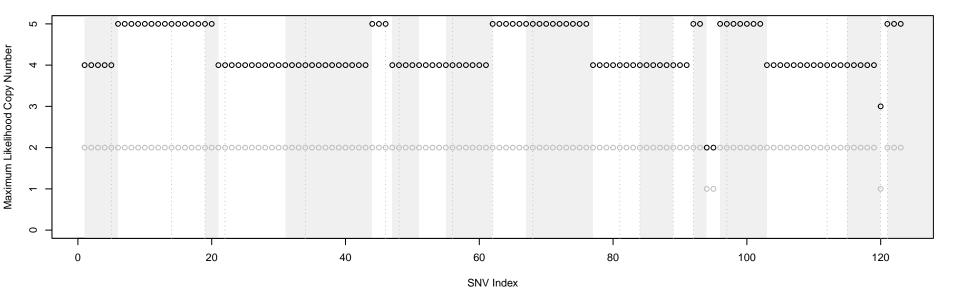


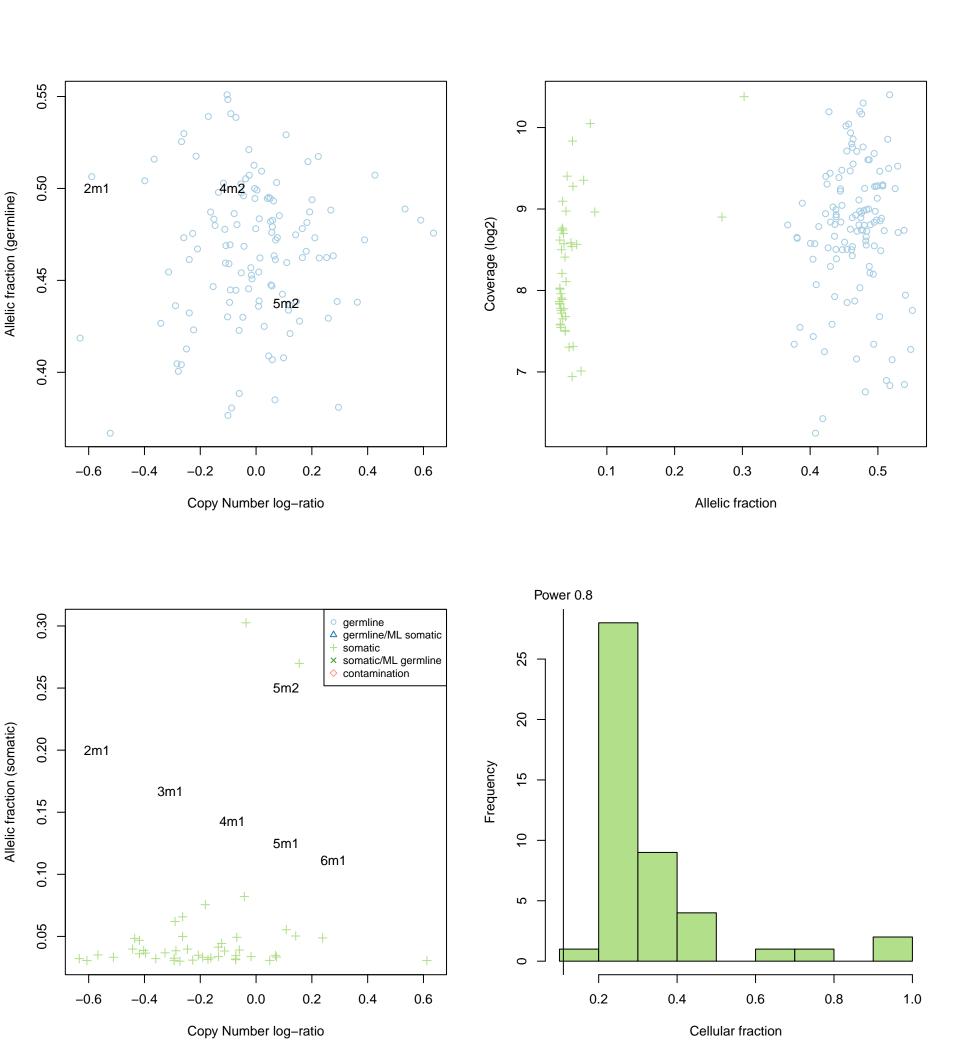
Purity: 0.4 Tumor ploidy: 4.424 3 5 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -0.4 -0.2 0.0 0.2 log2 ratio



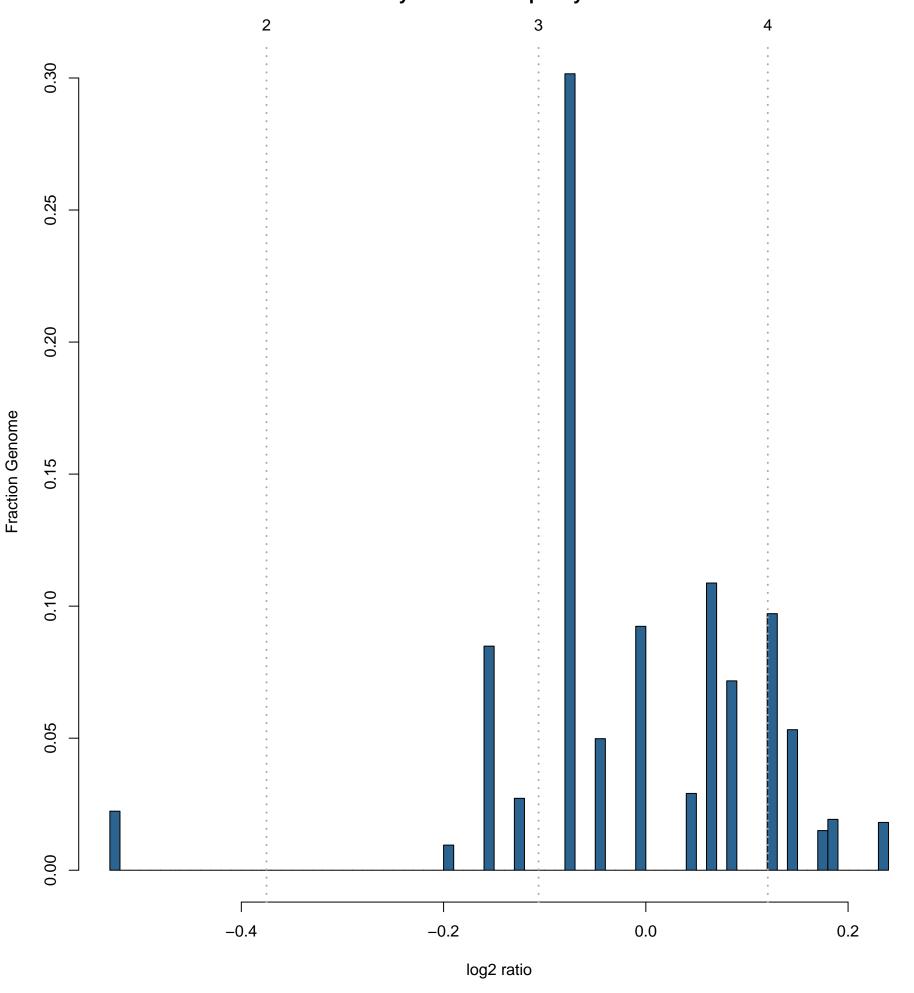
## SCNA-fit log-likelihood: -12503.88

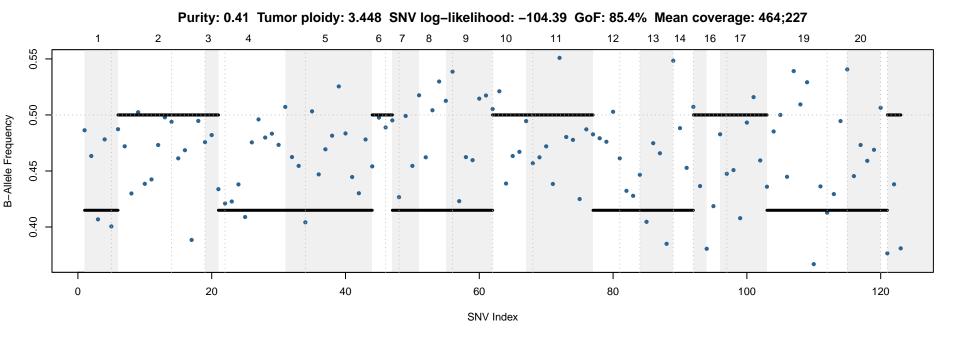




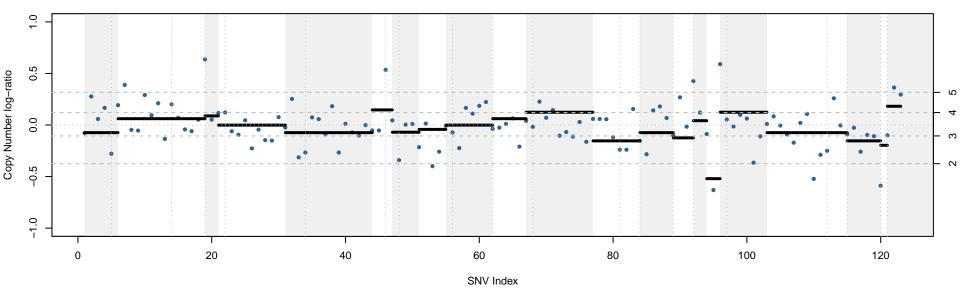


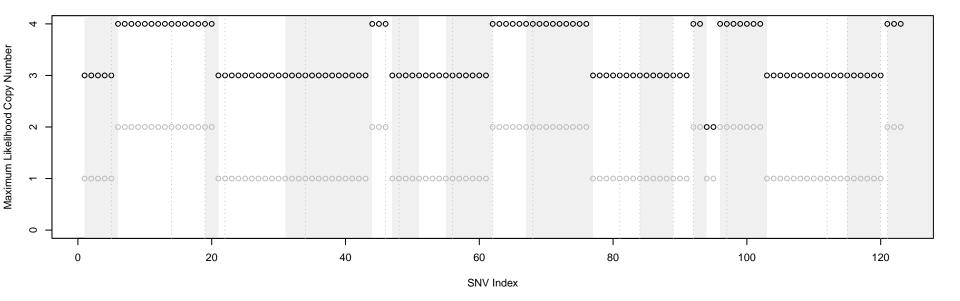
Purity: 0.41 Tumor ploidy: 3.448

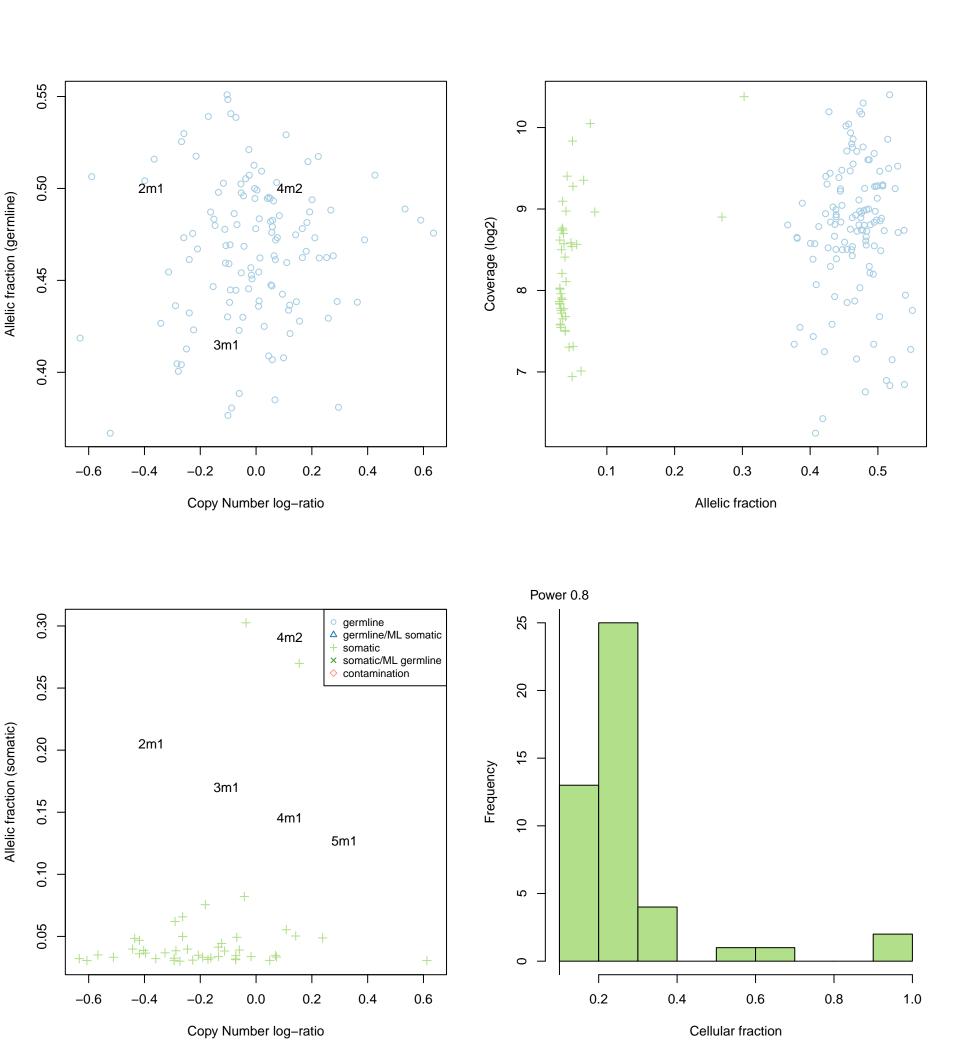




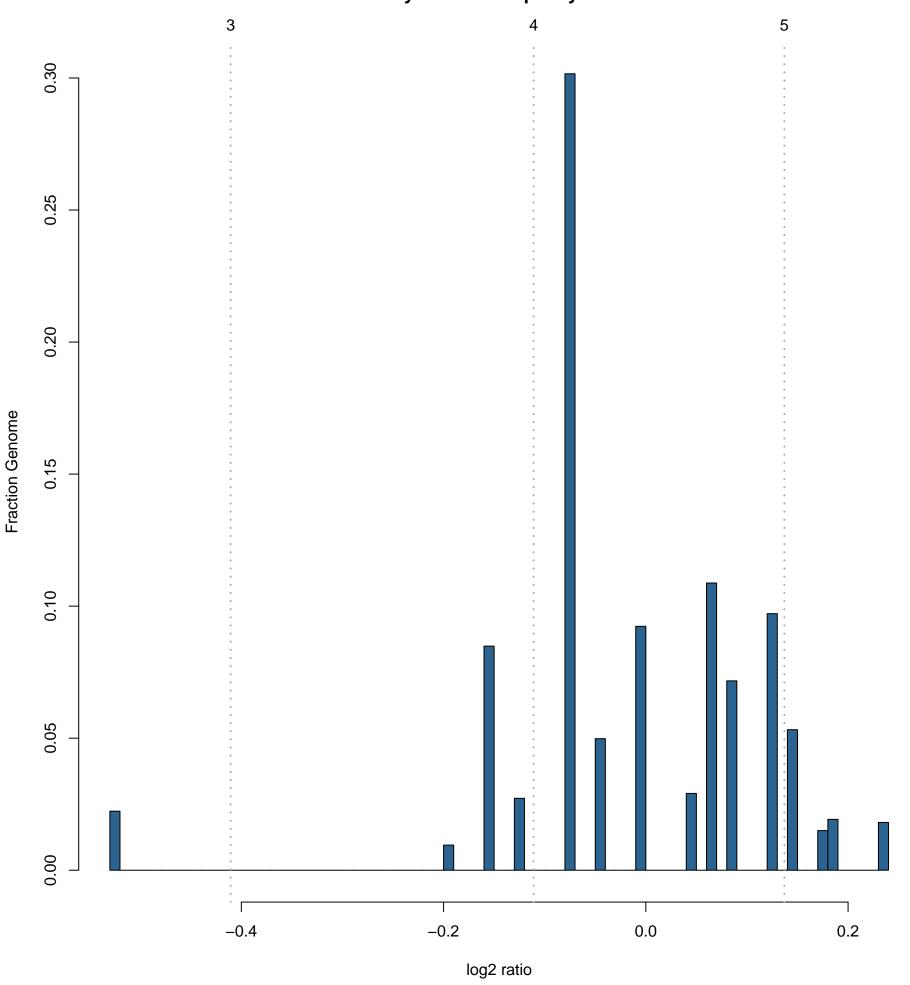
## SCNA-fit log-likelihood: -12520.86

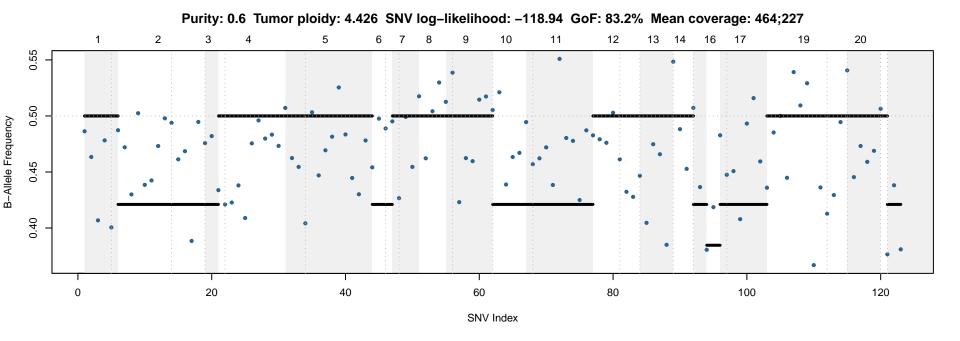




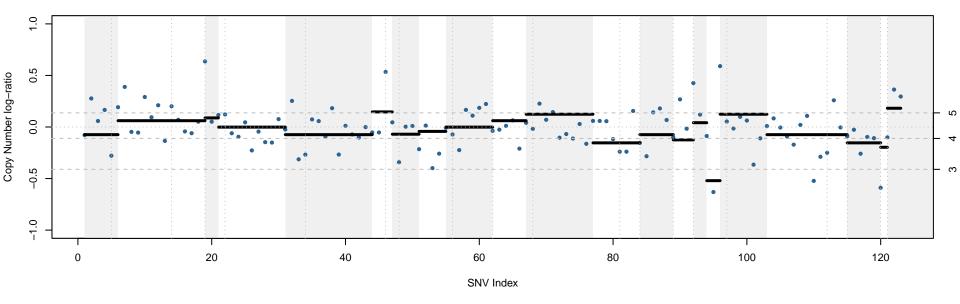


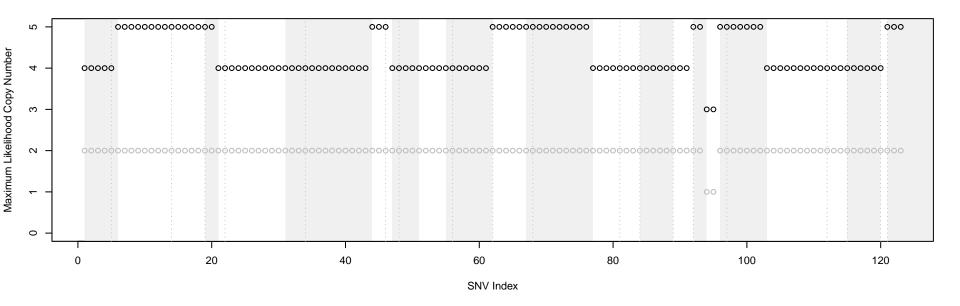
Purity: 0.6 Tumor ploidy: 4.426

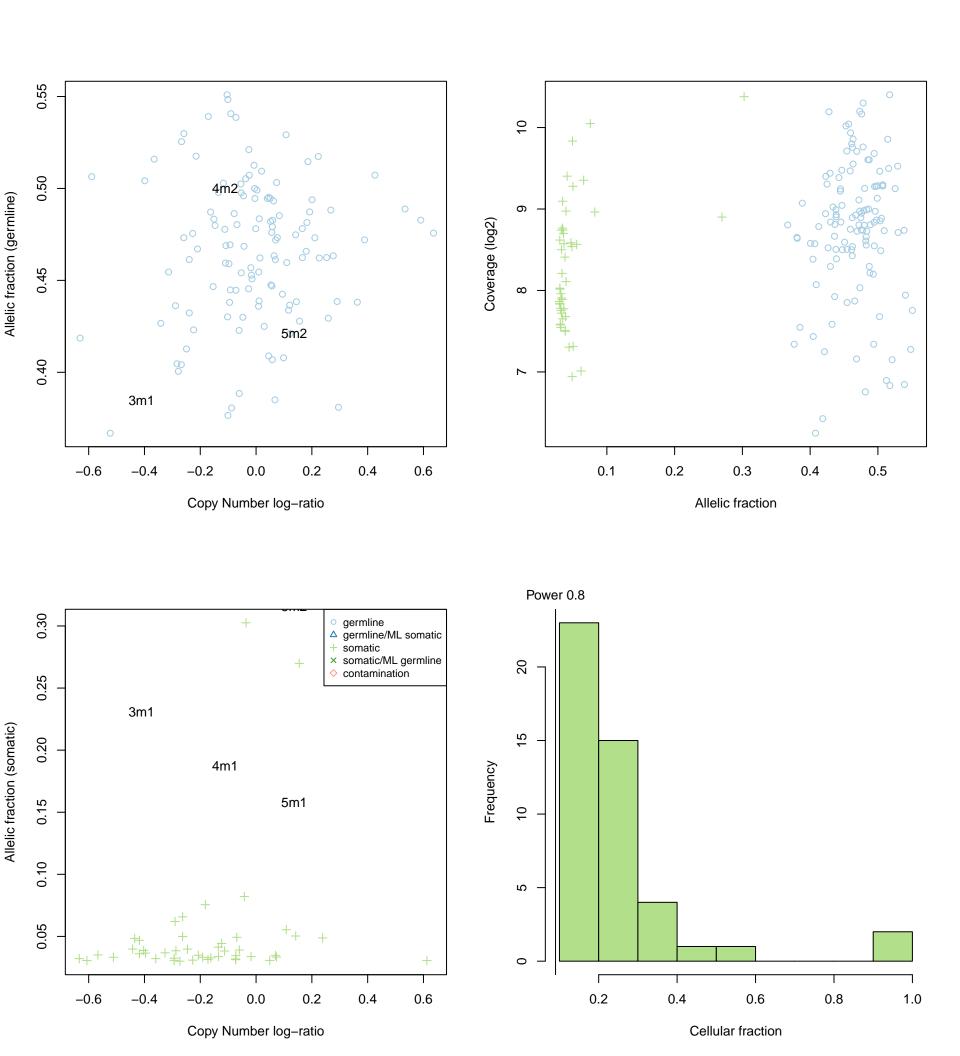




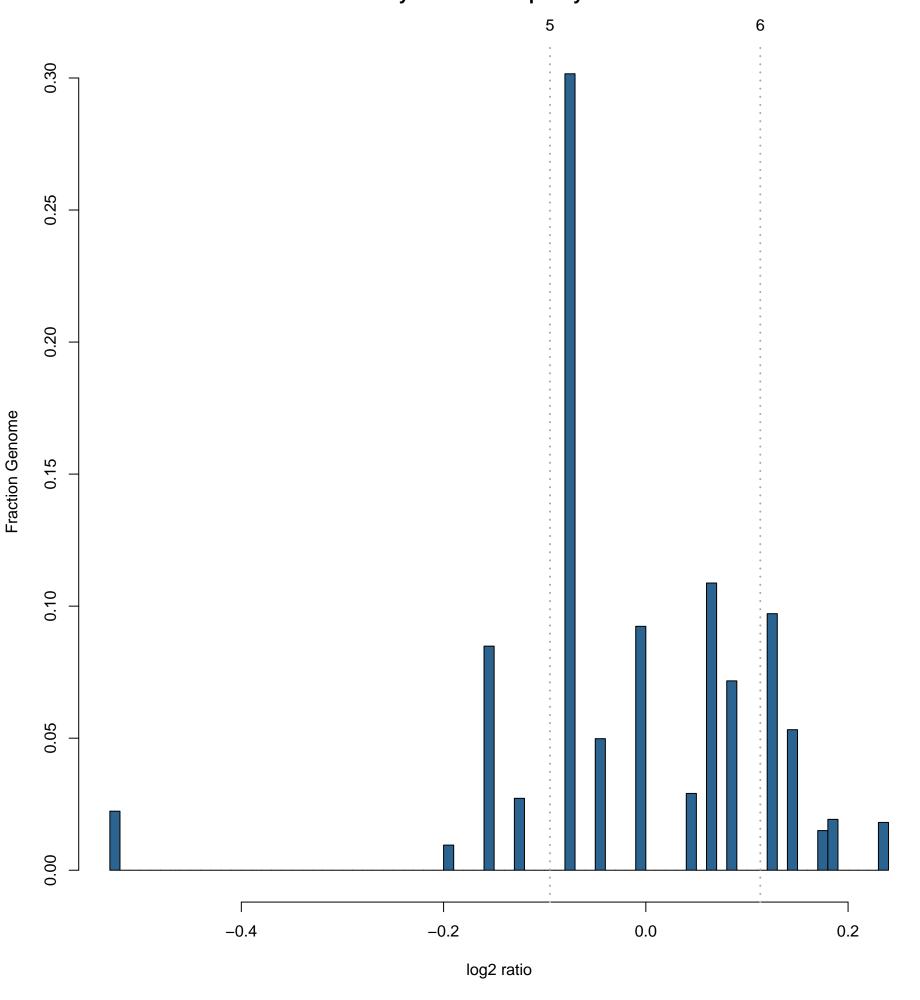
## SCNA-fit log-likelihood: -12526.69

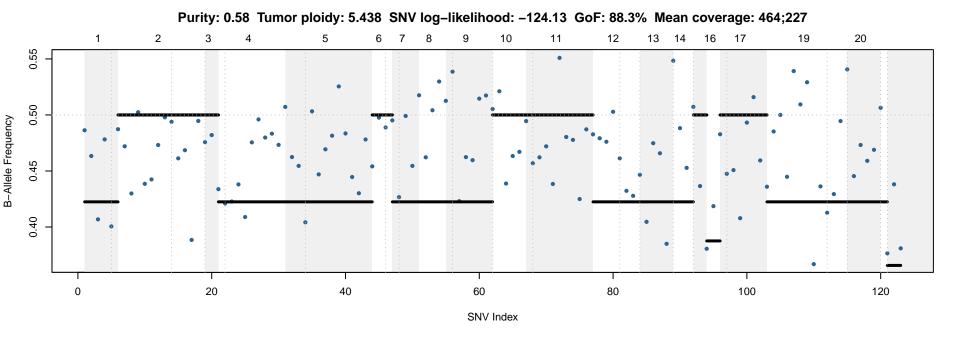




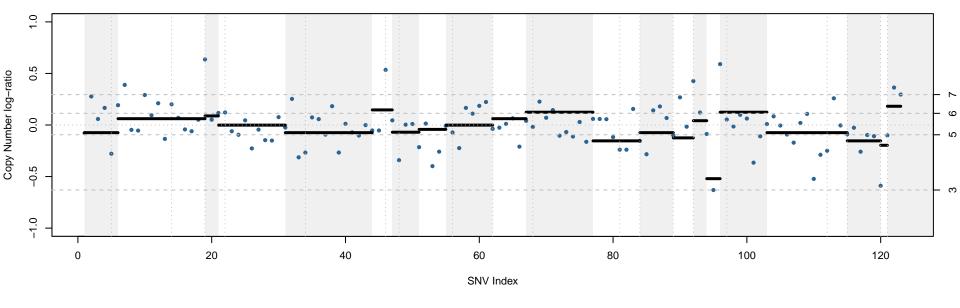


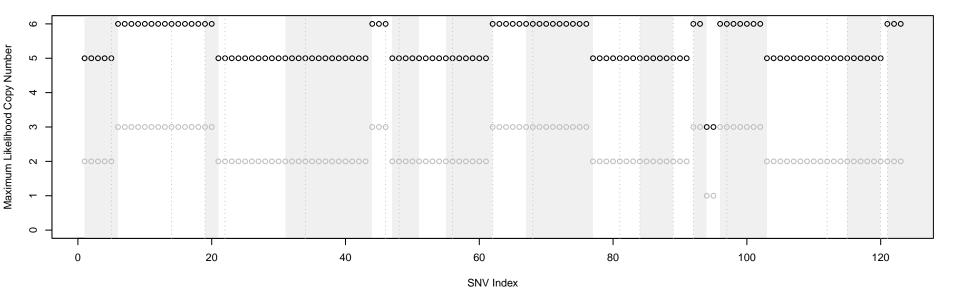
Purity: 0.58 Tumor ploidy: 5.438

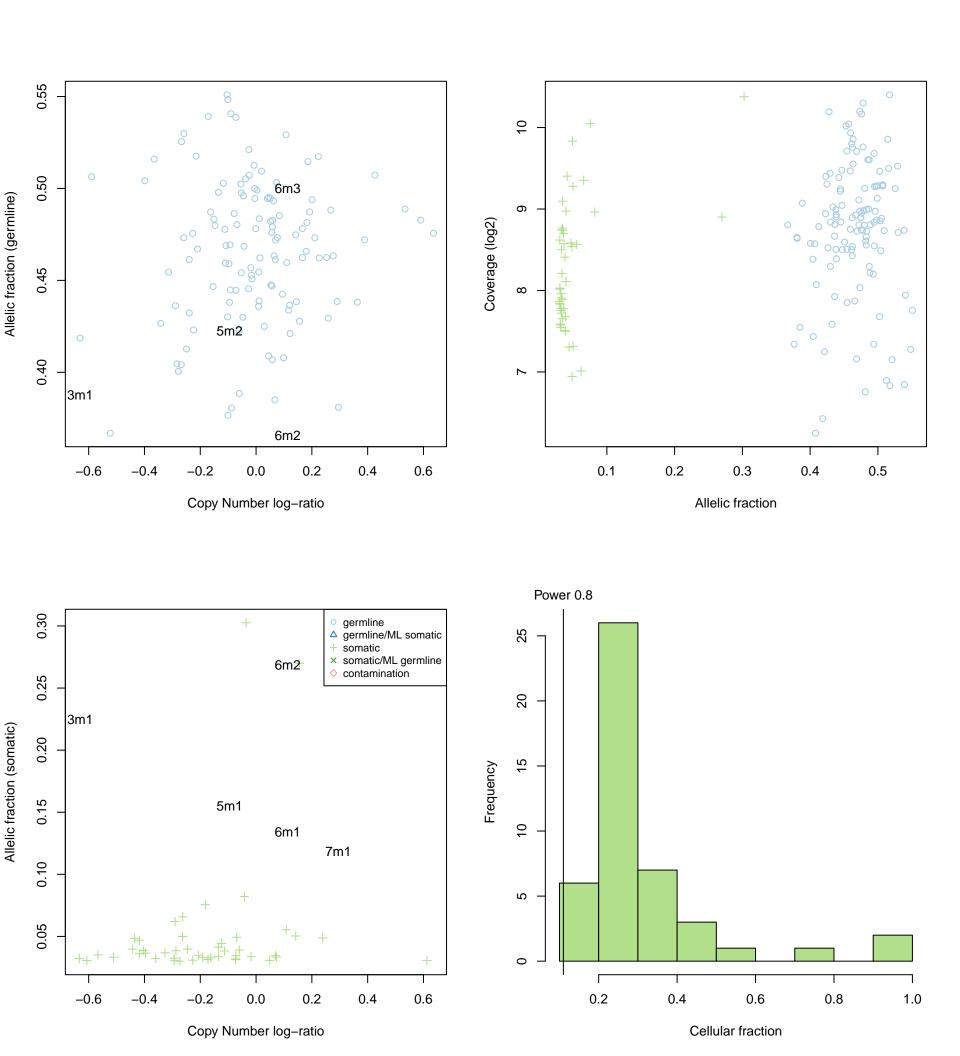




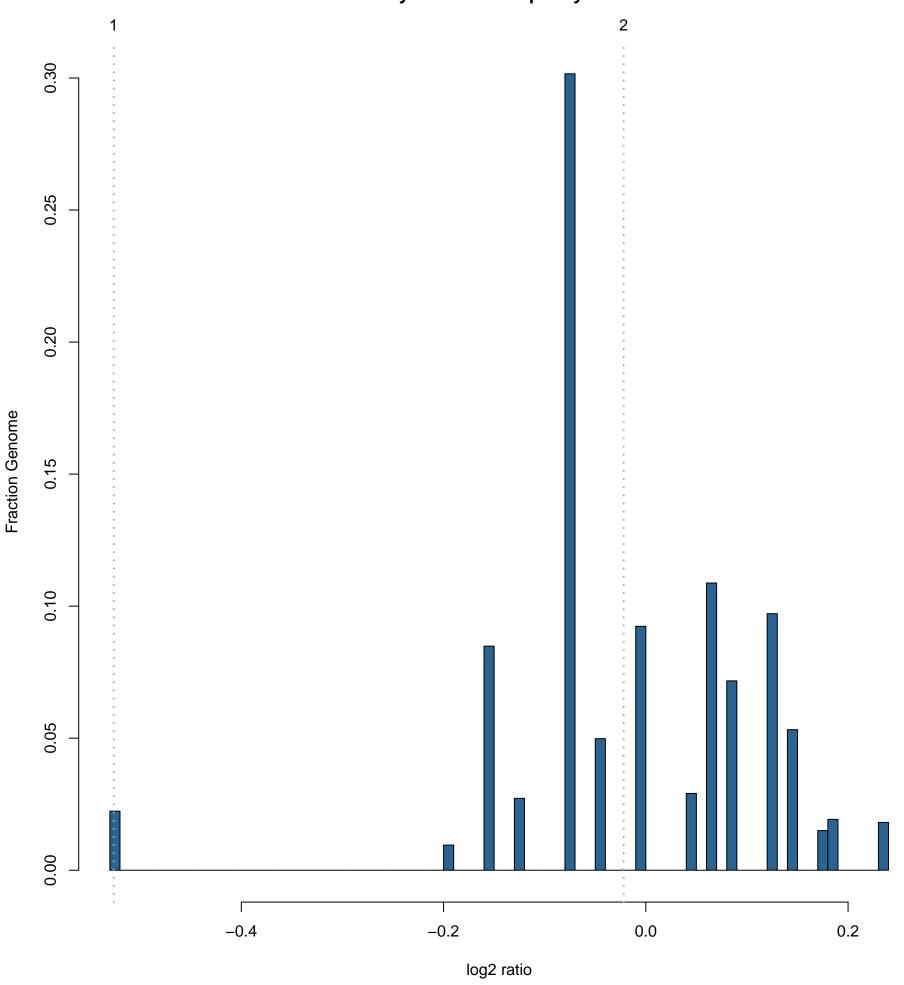


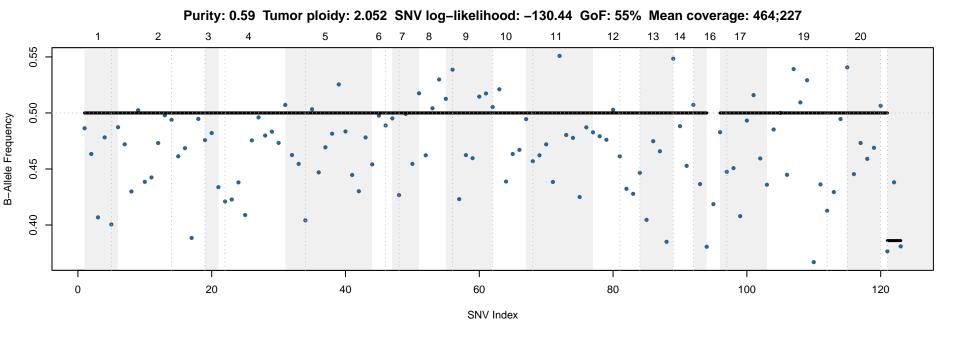




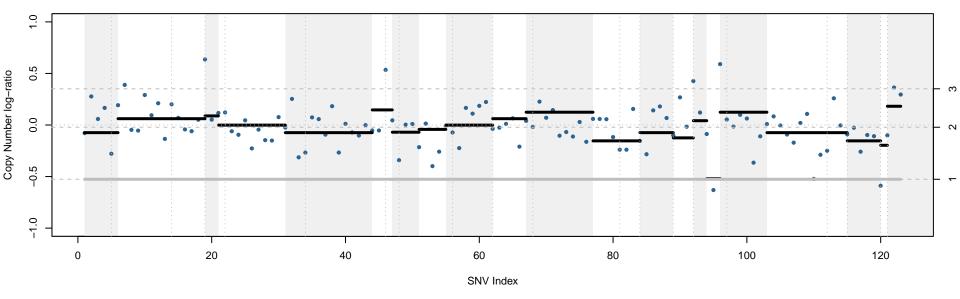


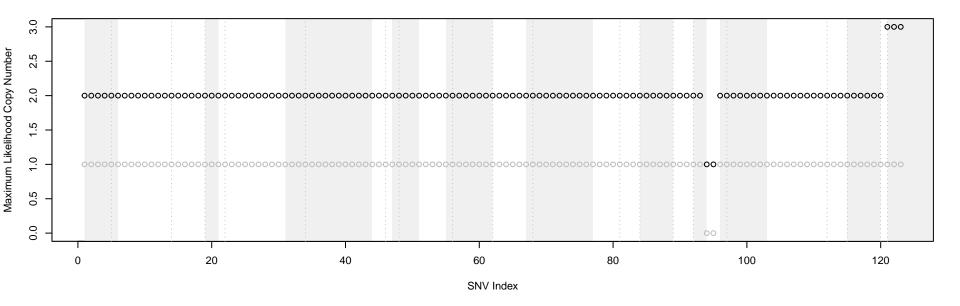
Purity: 0.59 Tumor ploidy: 2.052

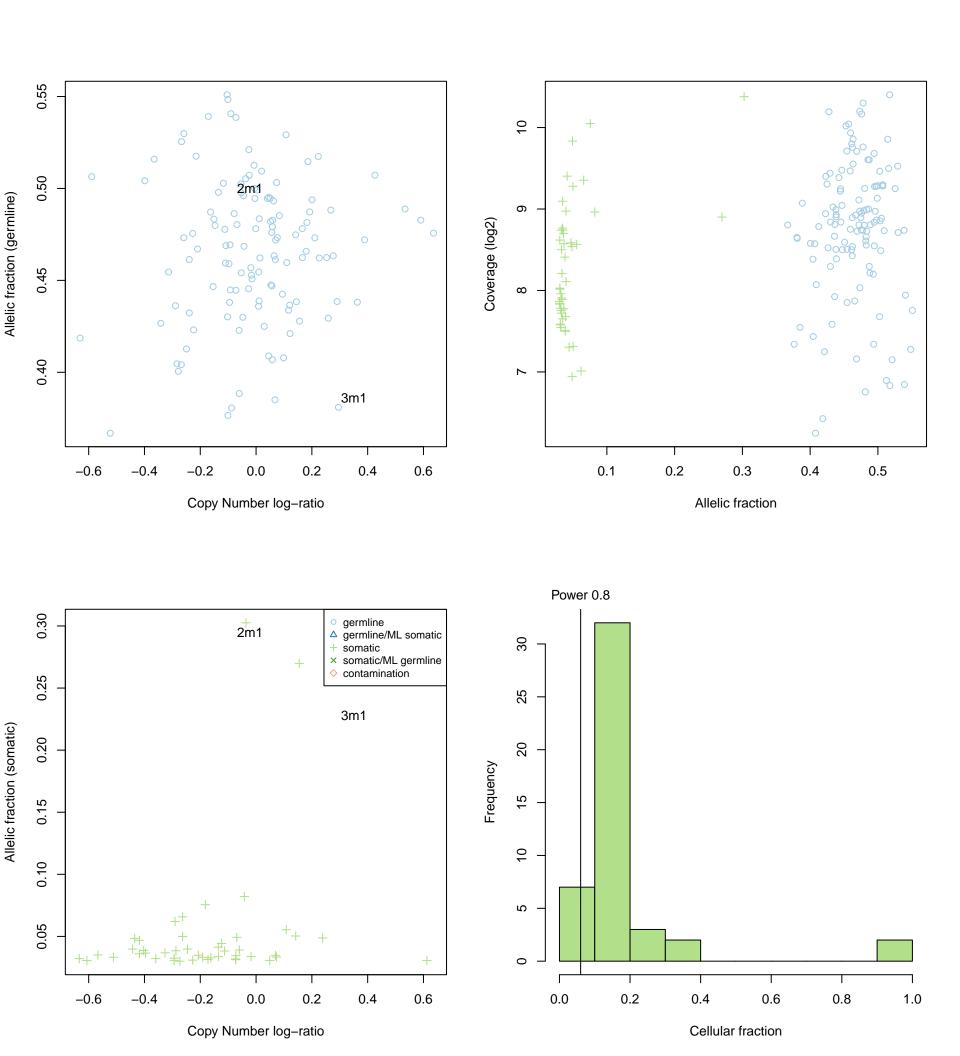




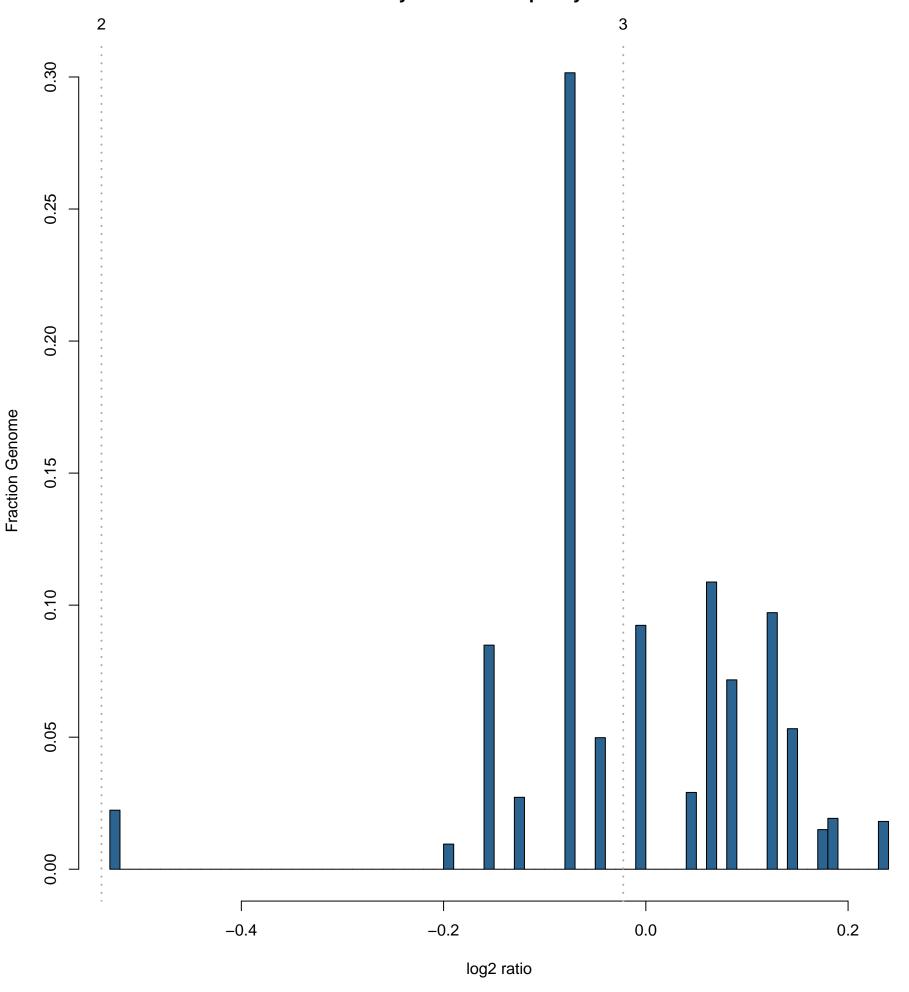
## SCNA-fit log-likelihood: -12618.91

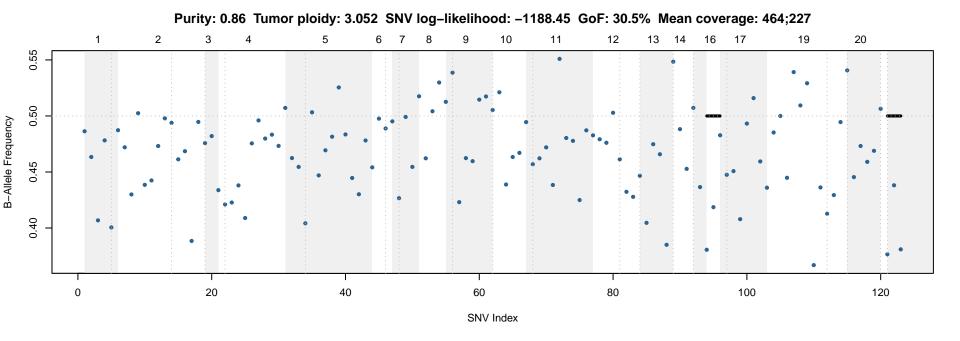






Purity: 0.86 Tumor ploidy: 3.052





## SCNA-fit log-likelihood: -12620.61

