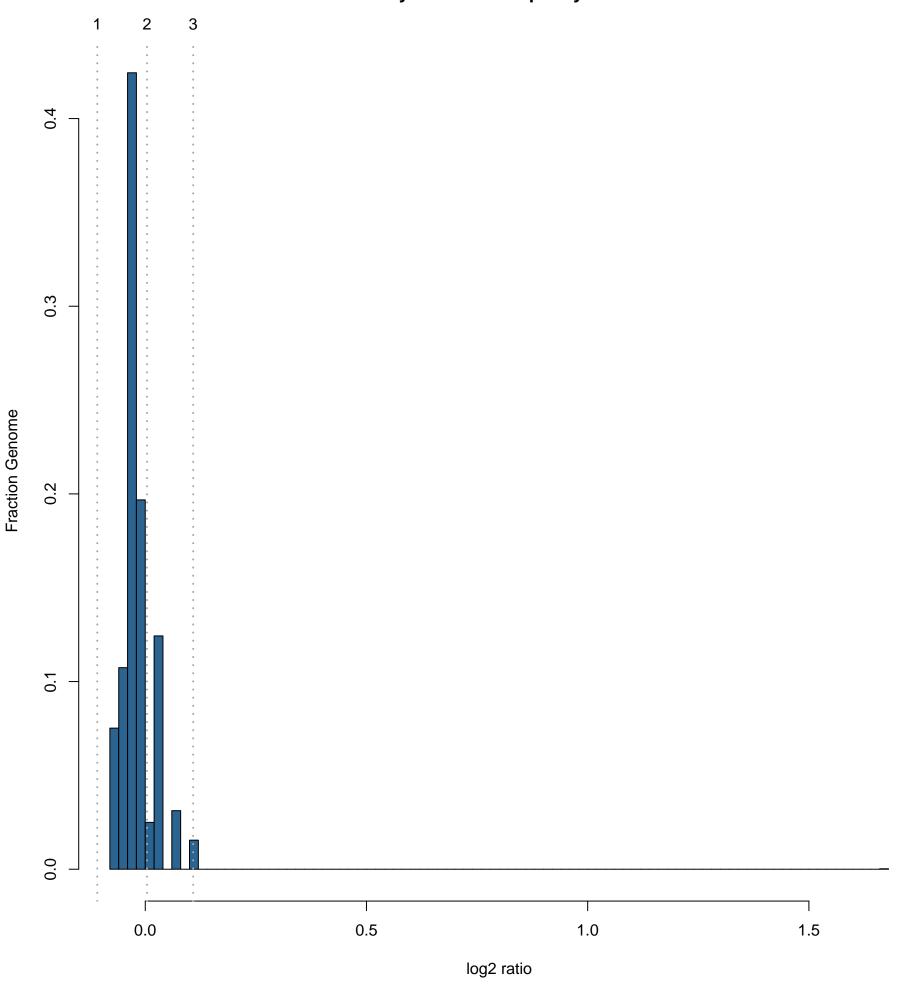
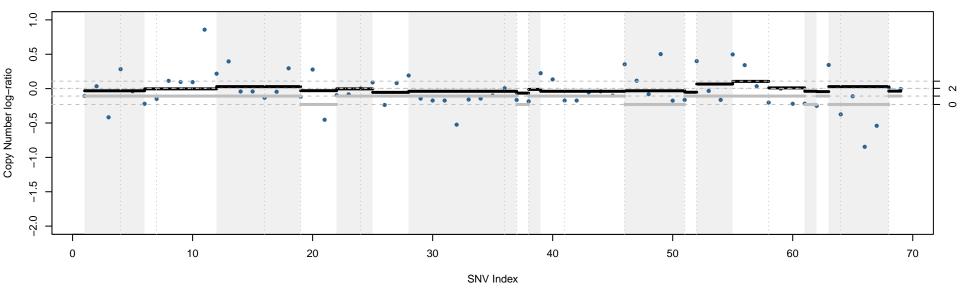
Purity: 0.15 Tumor ploidy: 1.963

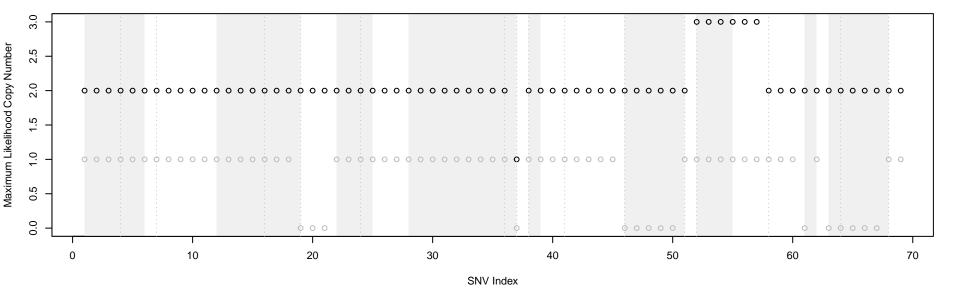


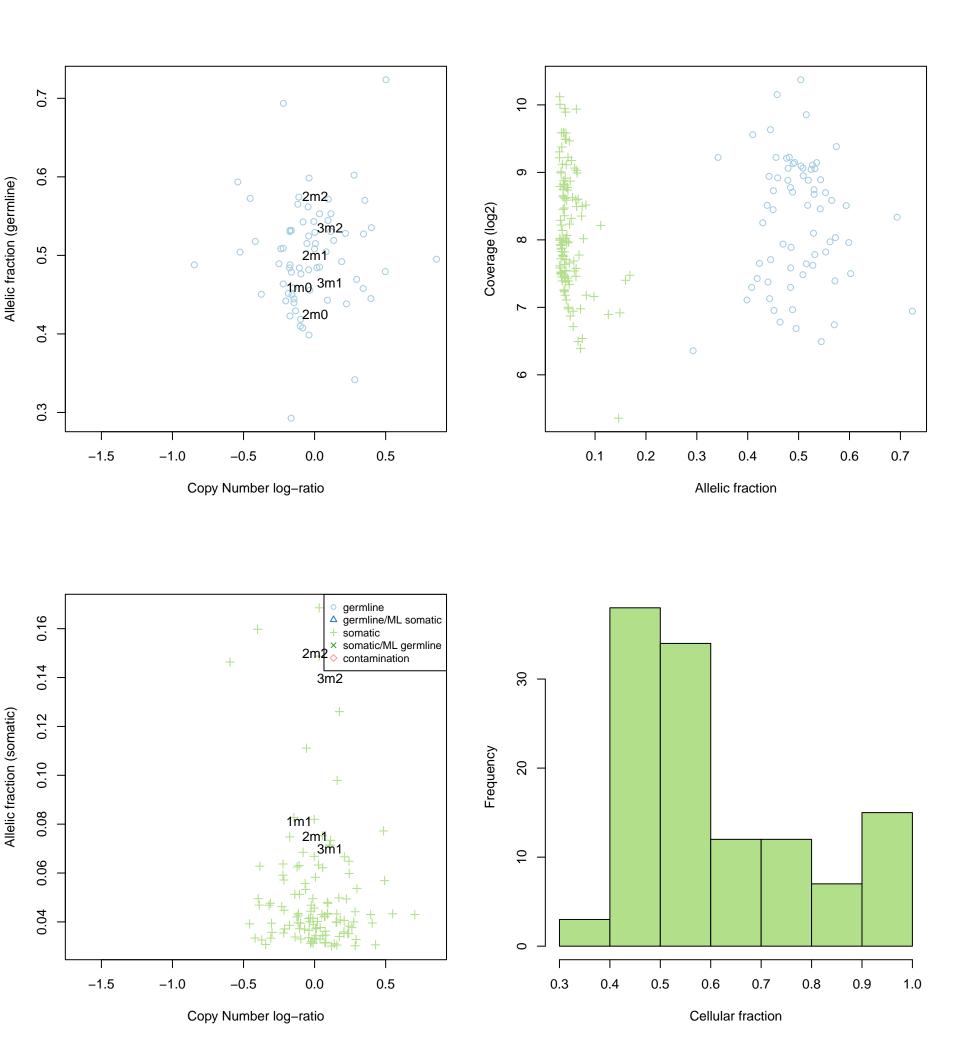
Purity: 0.15 Tumor ploidy: 1.963 SNV log-likelihood: 86.56 GoF: 95.8% Mean coverage: 355;510 2 7 13 19 0.7 9.0 B-Allele Frequency 0.5 0.4 0.3 0 10 20 30 40 50 60 70

SCNA-fit log-likelihood: -13140.83

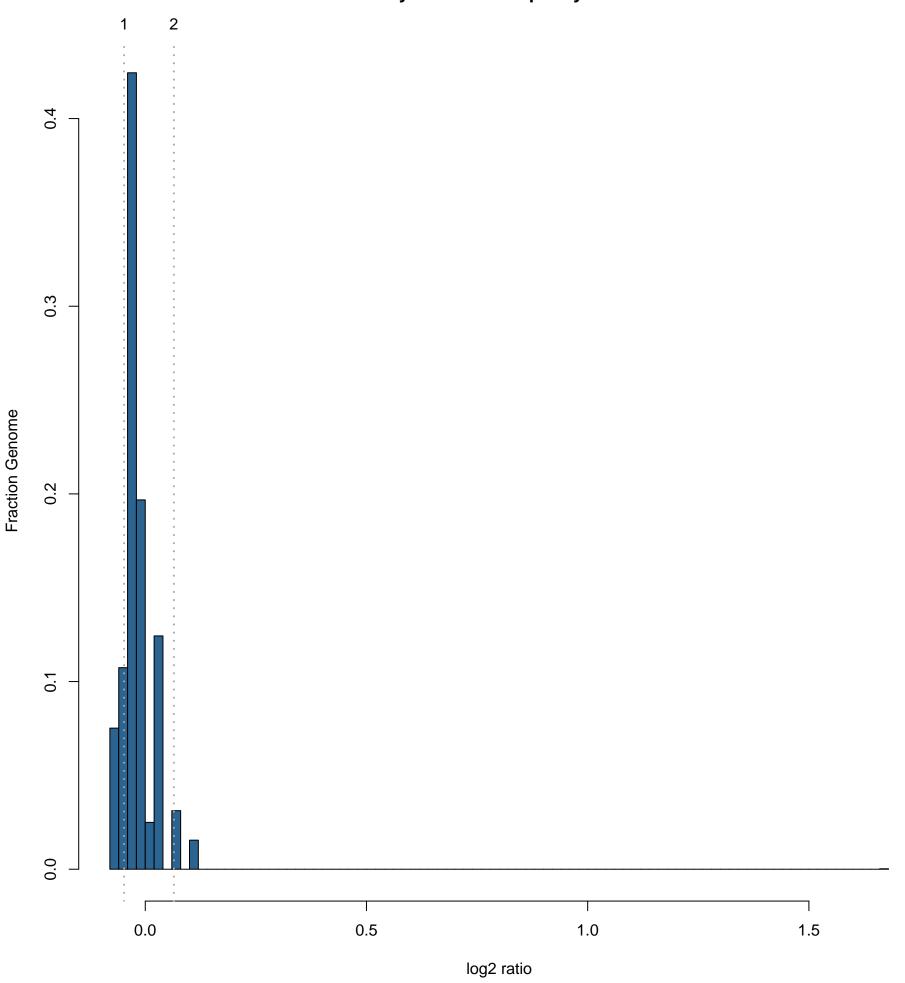
SNV Index

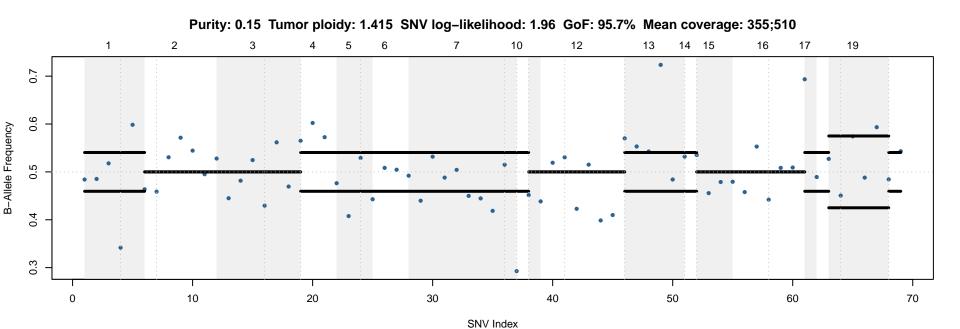




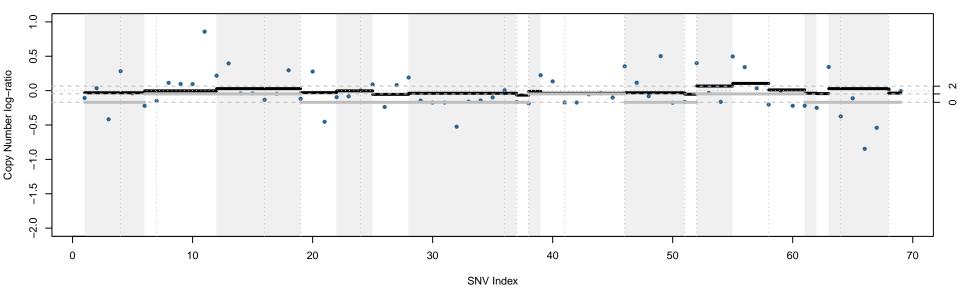


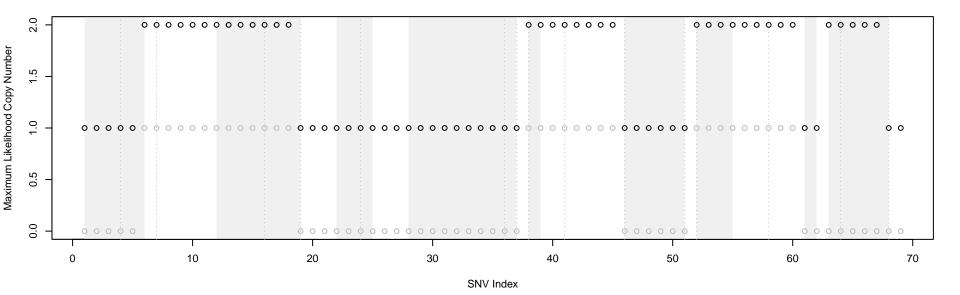
Purity: 0.15 Tumor ploidy: 1.415

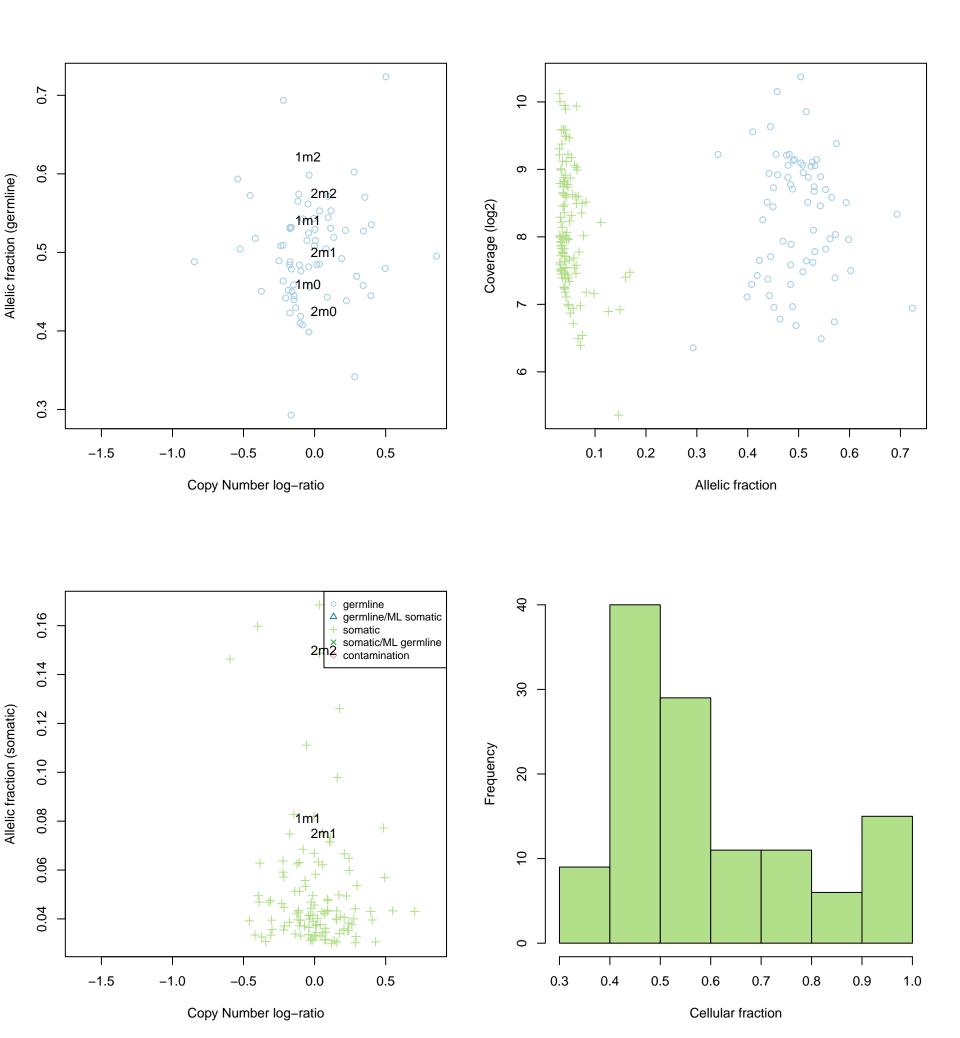




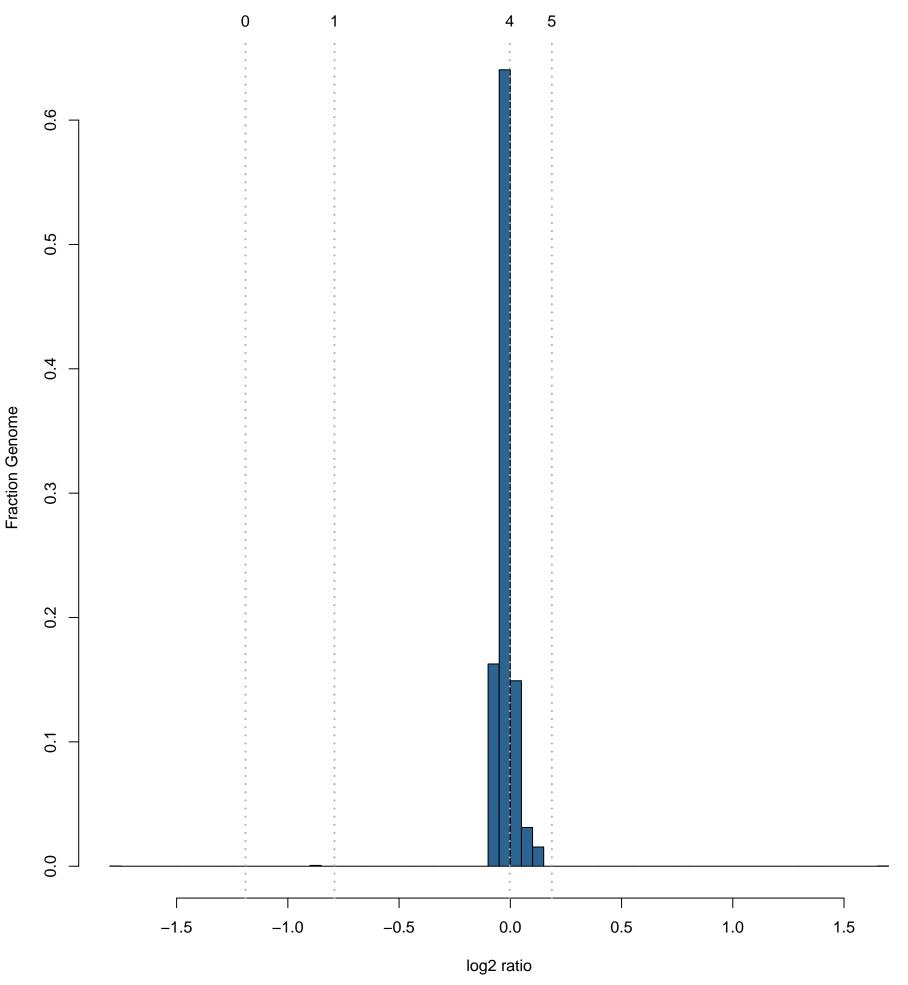
SCNA-fit log-likelihood: -13160.09

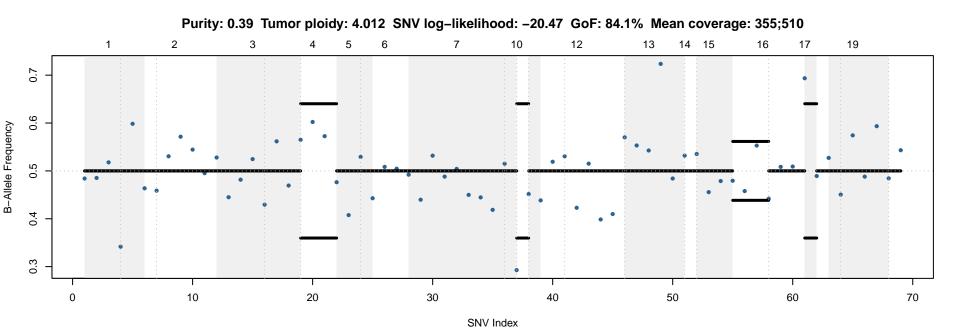




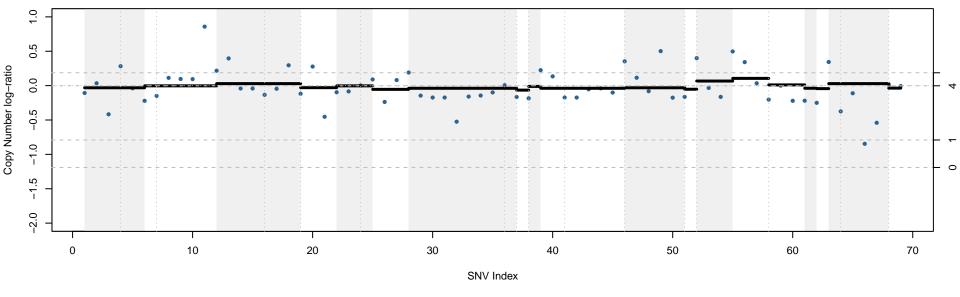


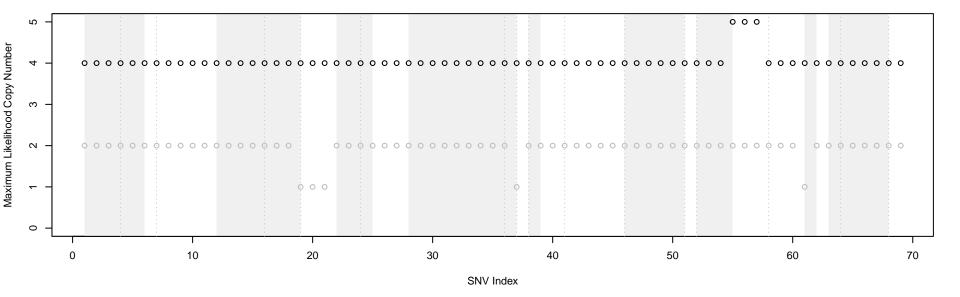
Purity: 0.39 Tumor ploidy: 4.012

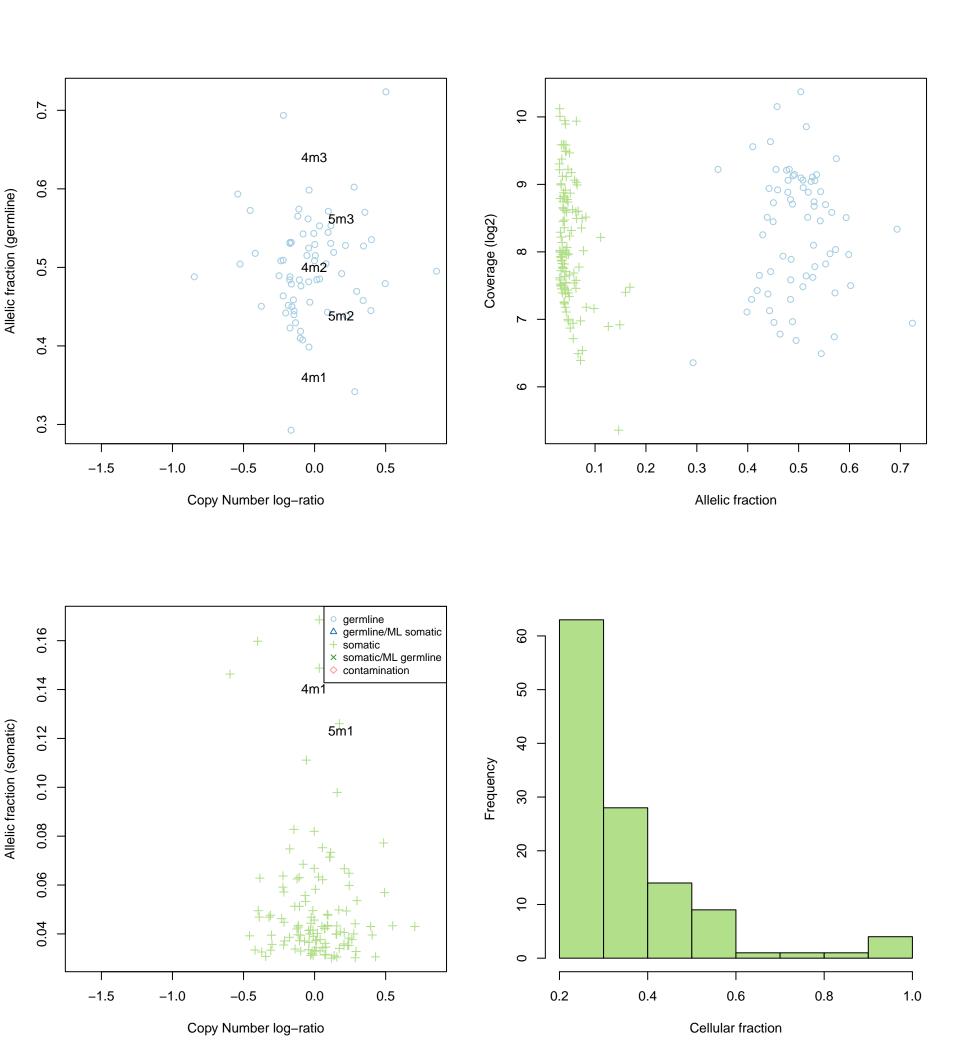




SCNA-fit log-likelihood: -13140.87

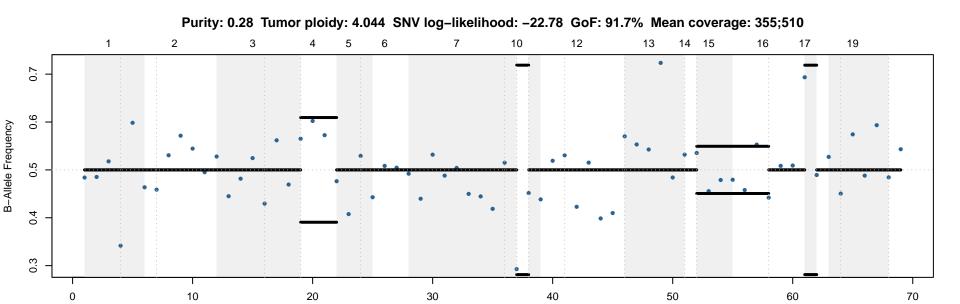






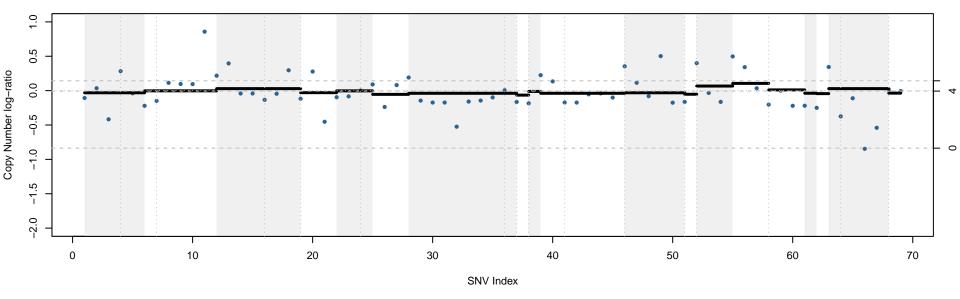
Purity: 0.28 Tumor ploidy: 4.044 0 0.5 Fraction Genome 0.3 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0 1.5

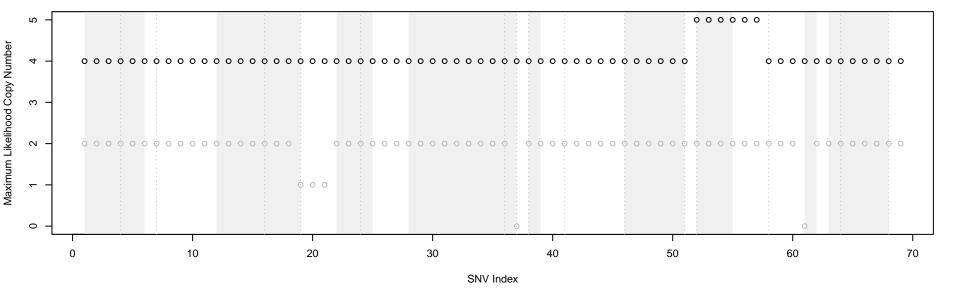
log2 ratio

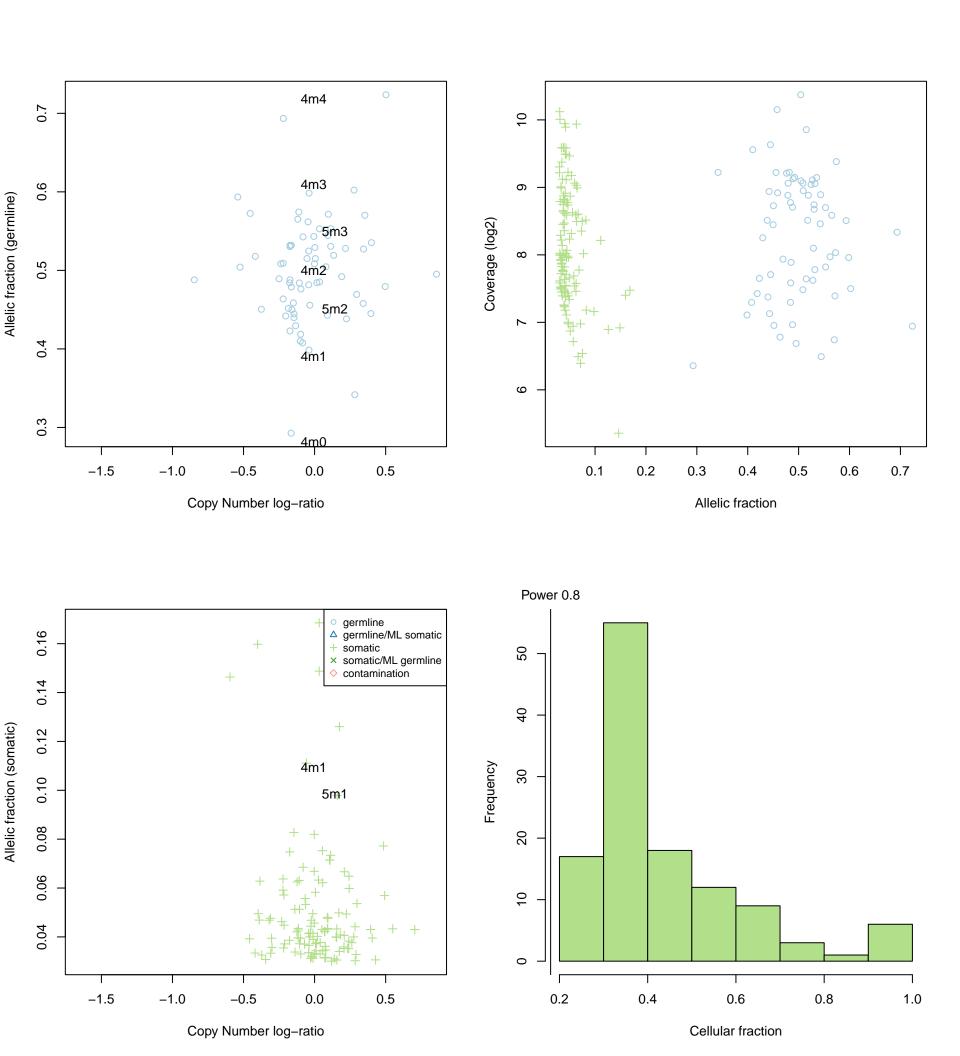


SCNA-fit log-likelihood: -13132.34

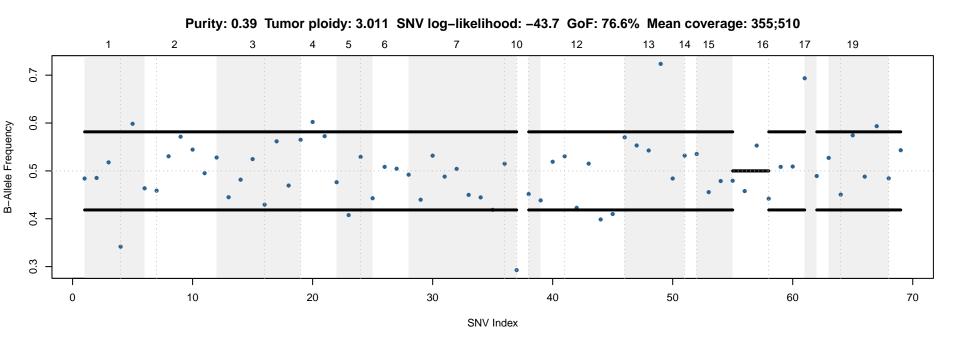
SNV Index



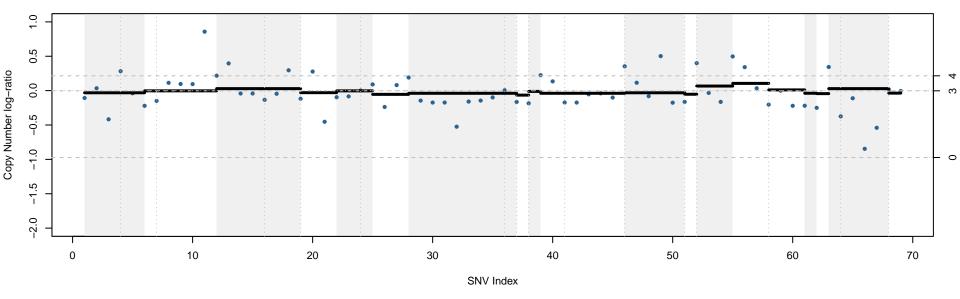


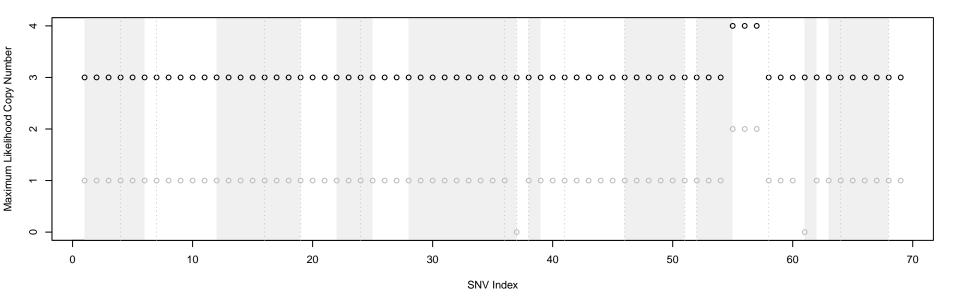


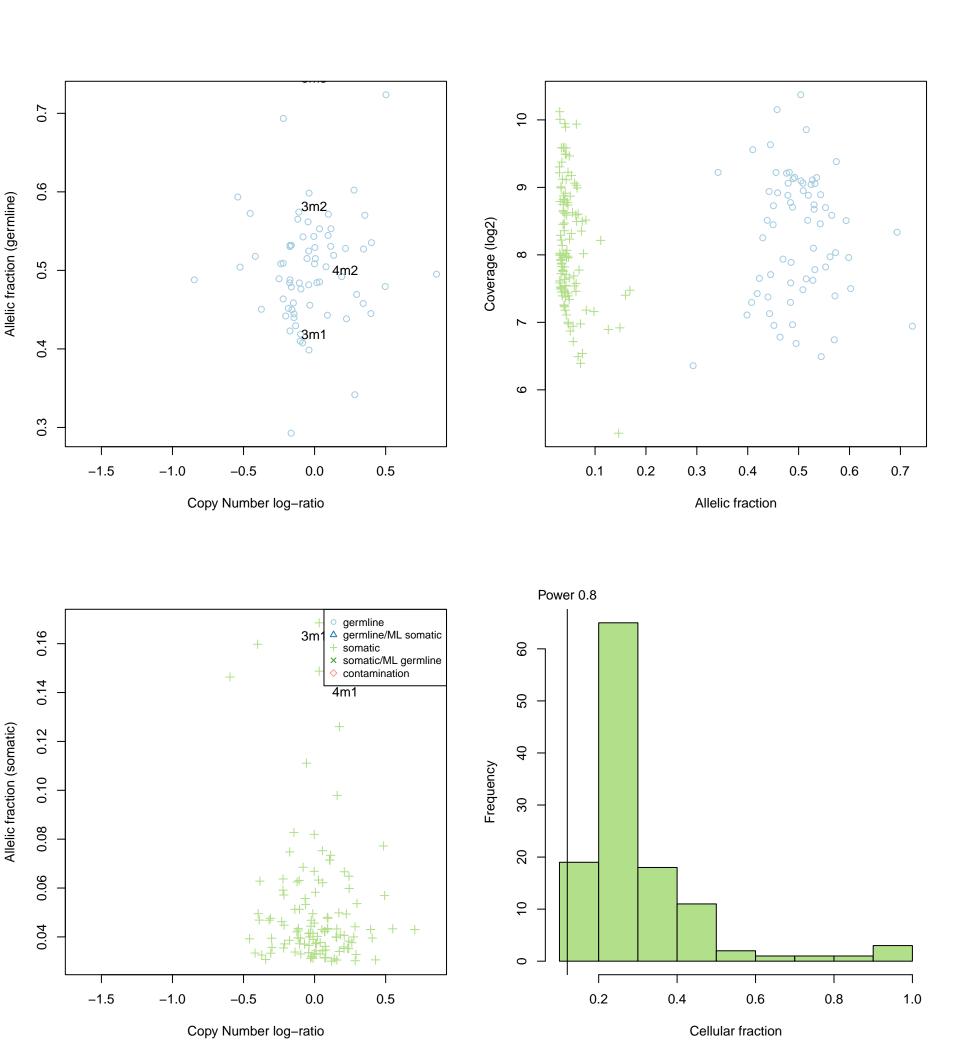
Purity: 0.39 Tumor ploidy: 3.011 0 3 0.5 Fraction Genome 0.3 0.1 0.0 -1.5 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



SCNA-fit log-likelihood: -13144.47







Purity: 0.2 Tumor ploidy: 5.153 0 5 0.5 Fraction Genome 0.3 0.1 0.0

-1.0

-0.5

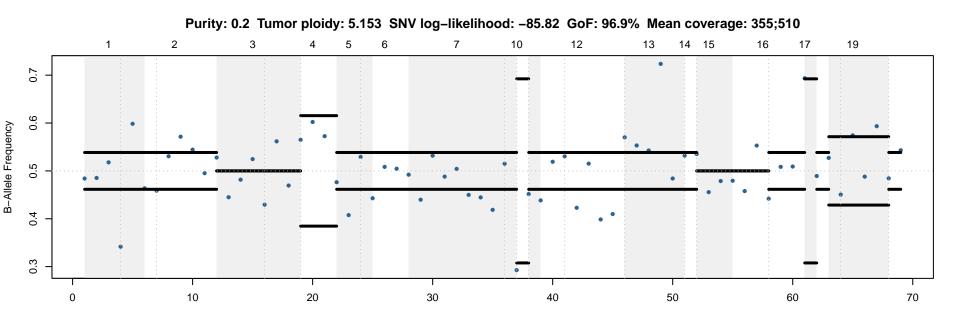
0.0

0.5

log2 ratio

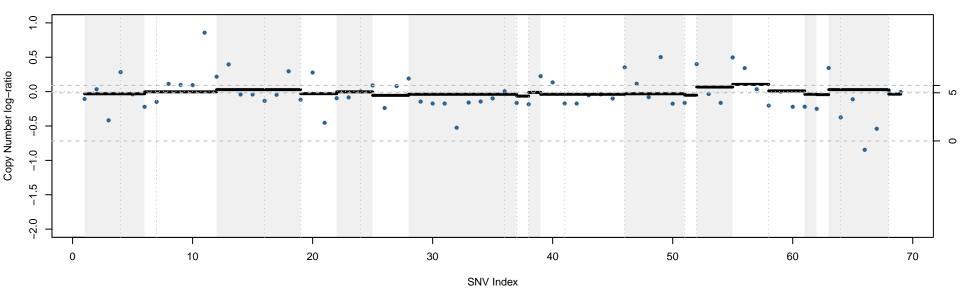
1.0

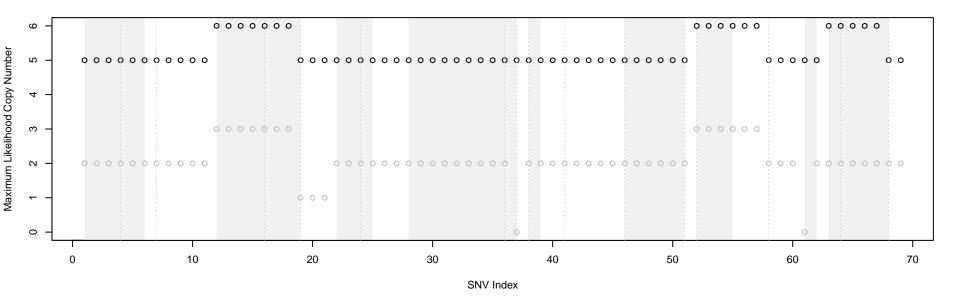
1.5

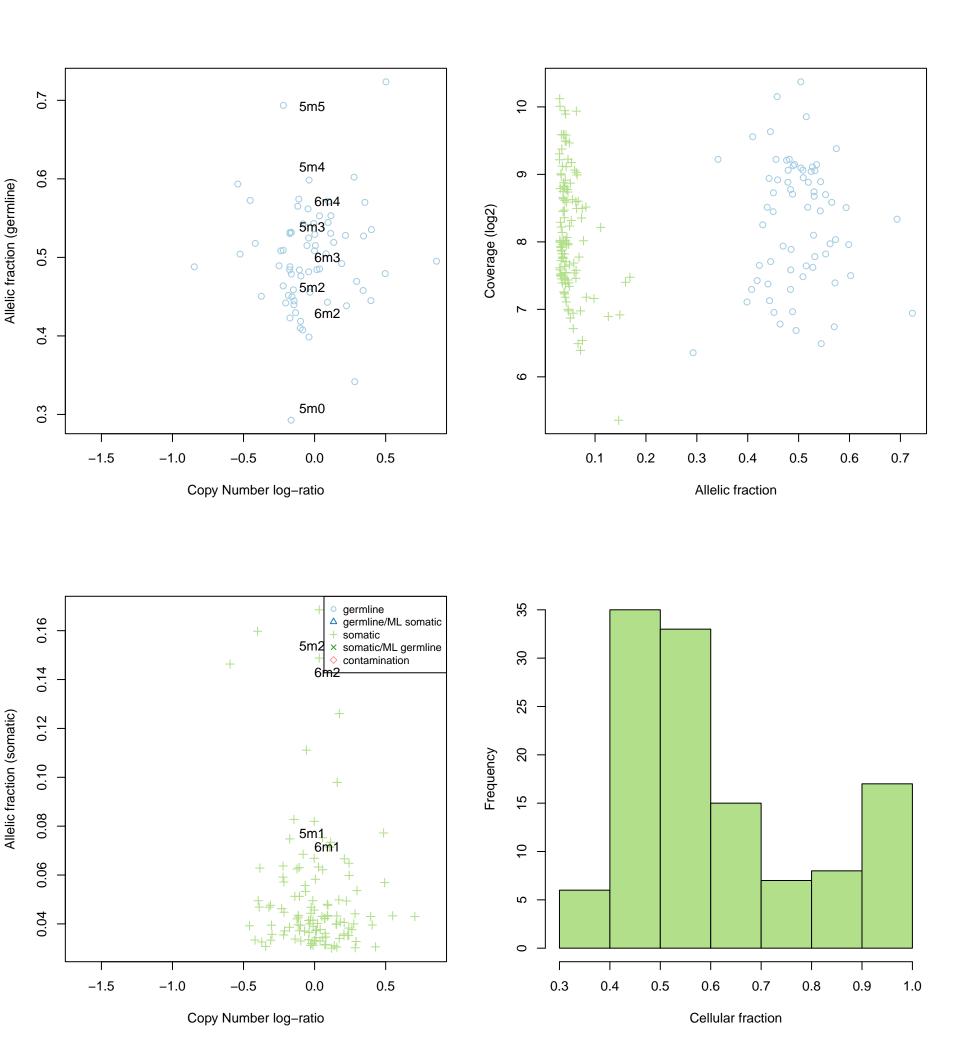


SCNA-fit log-likelihood: -13124.93

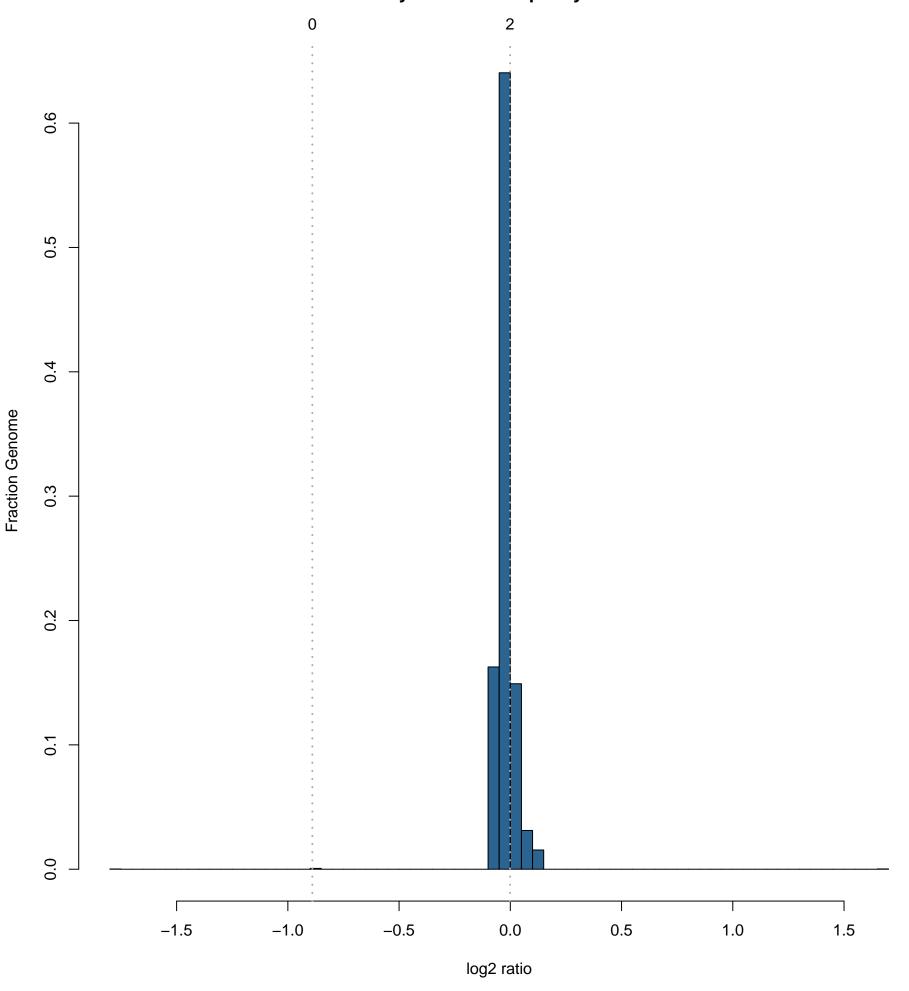
SNV Index

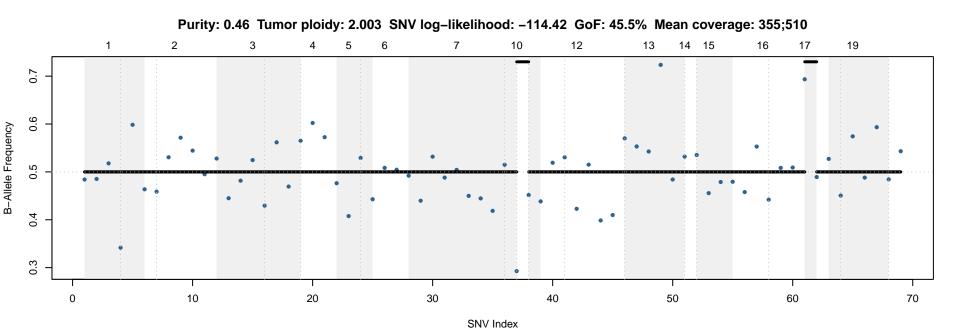




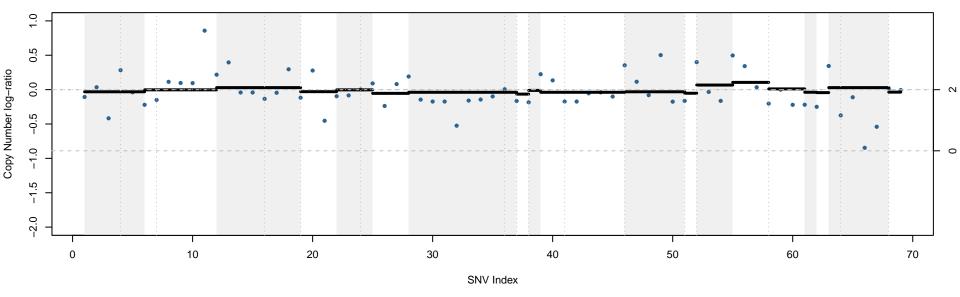


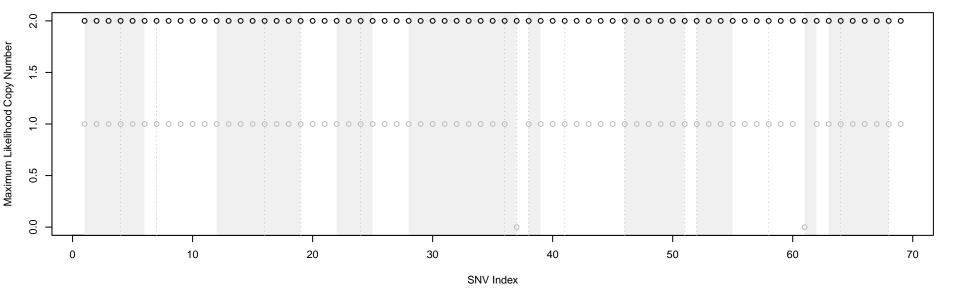
Purity: 0.46 Tumor ploidy: 2.003

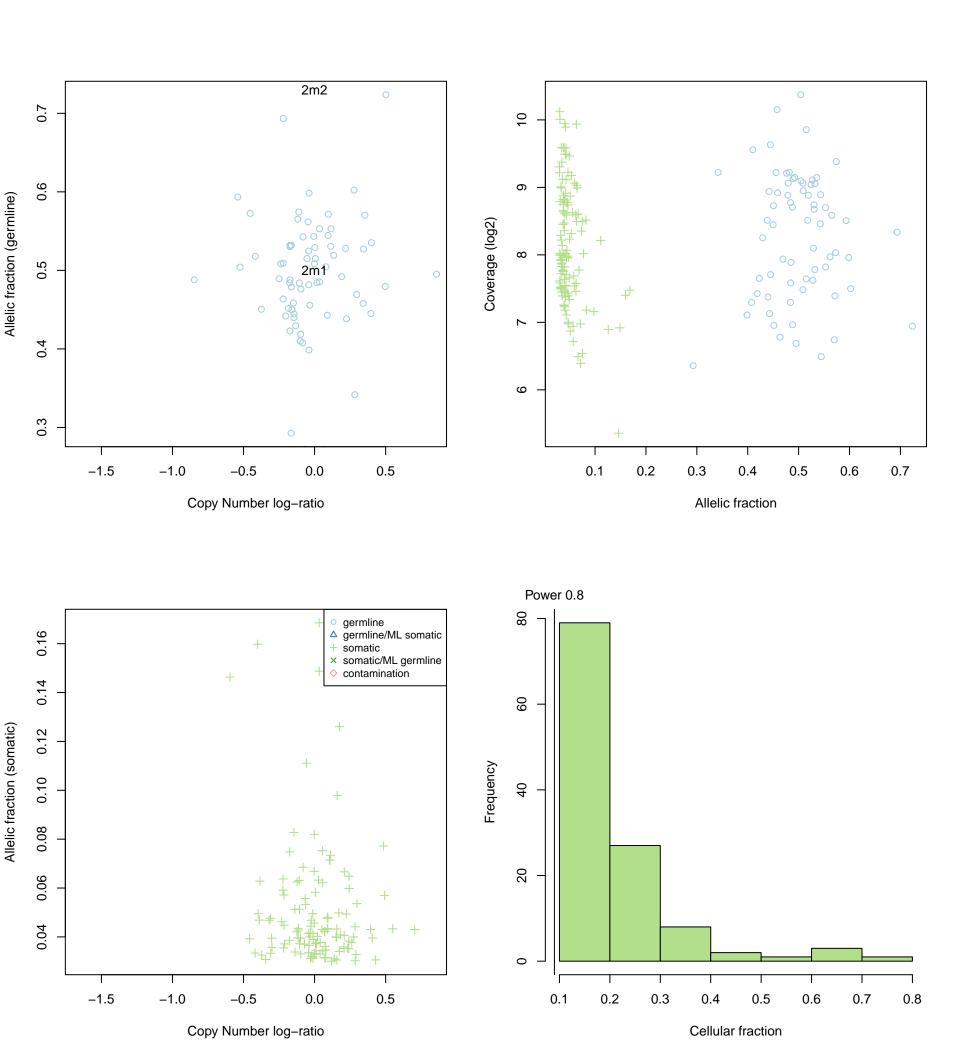




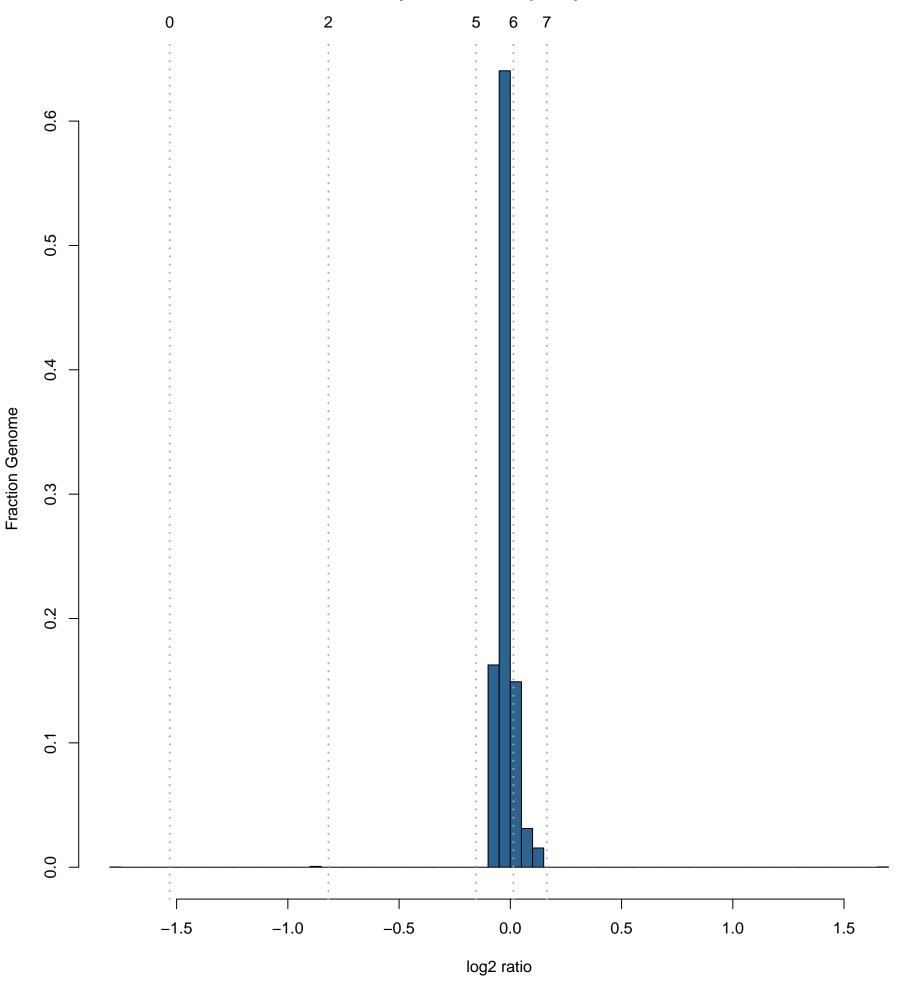
SCNA-fit log-likelihood: -13146.13

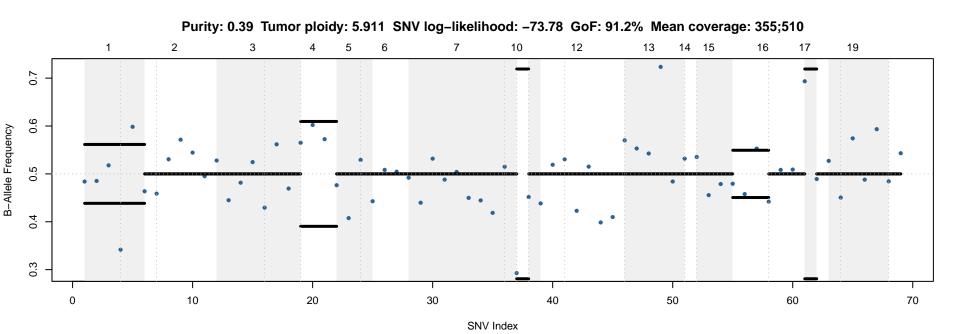




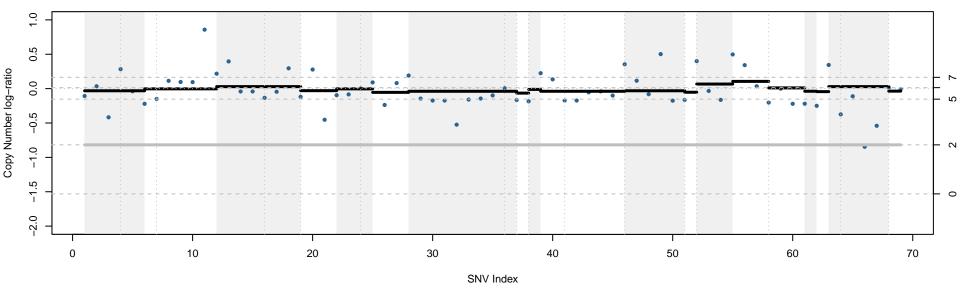


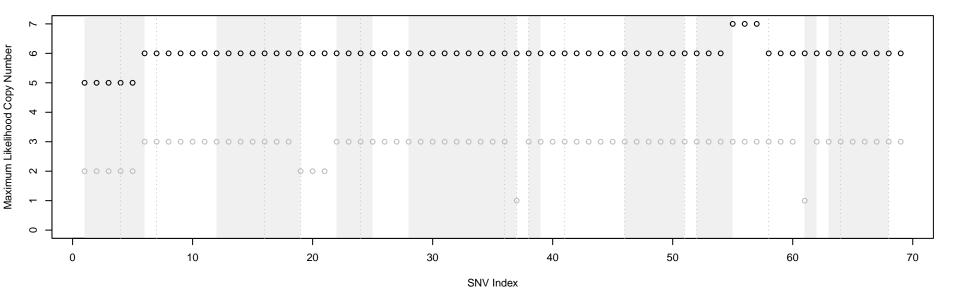
Purity: 0.39 Tumor ploidy: 5.911

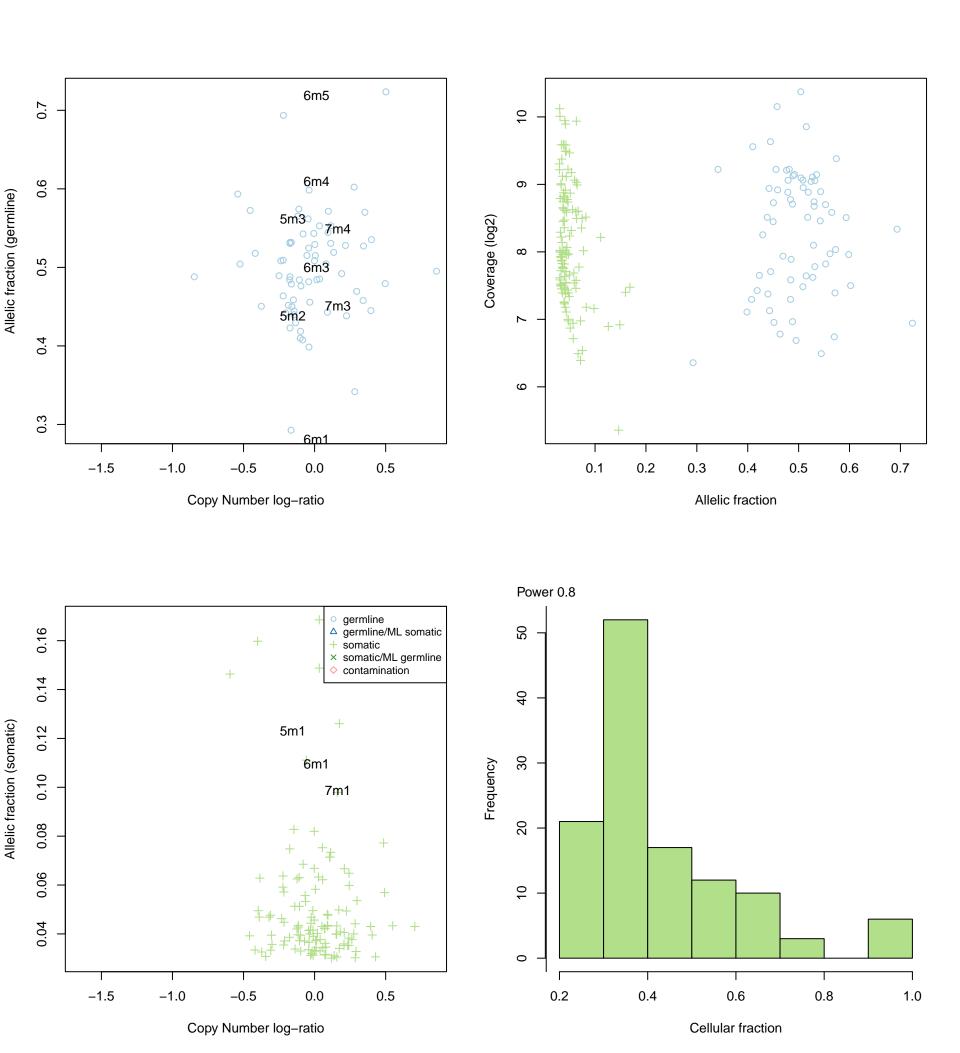




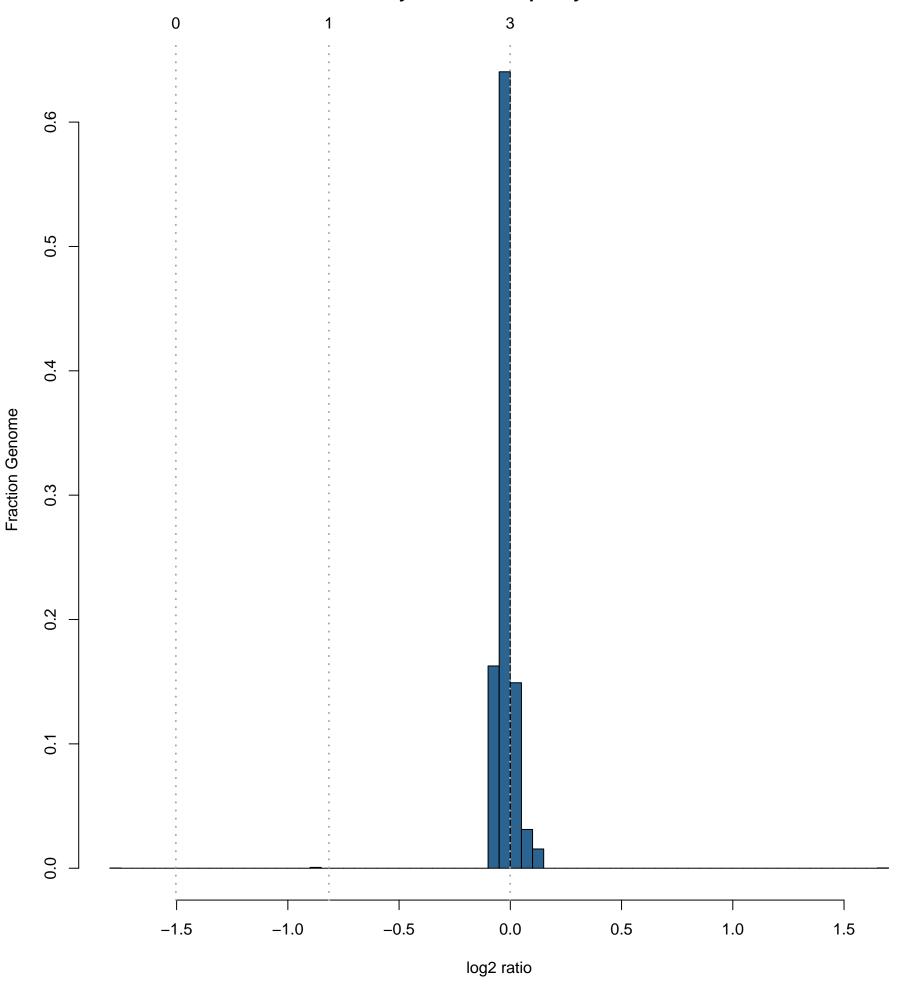
SCNA-fit log-likelihood: -13189.02

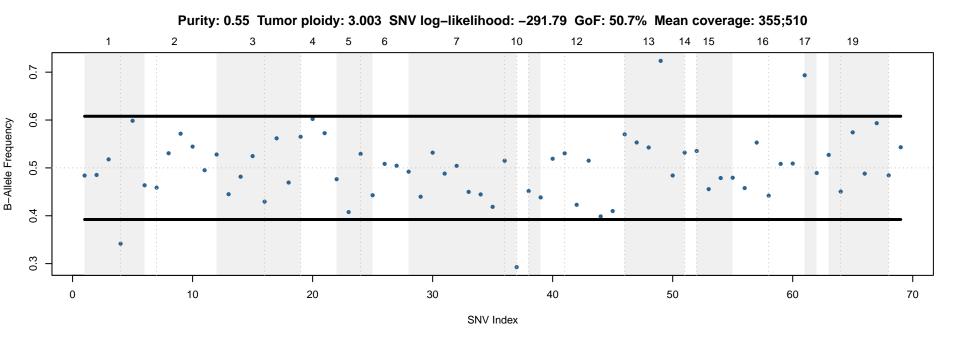




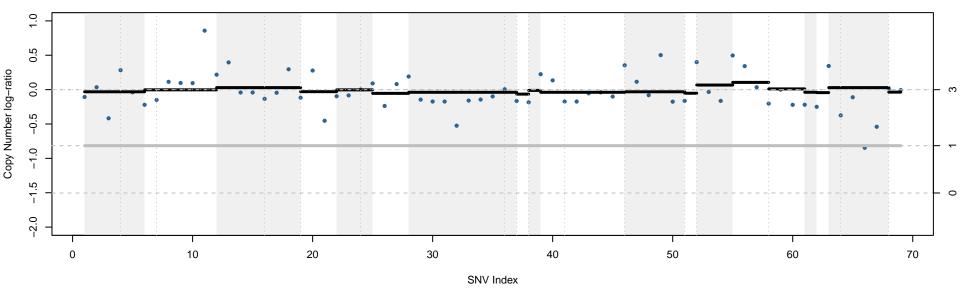


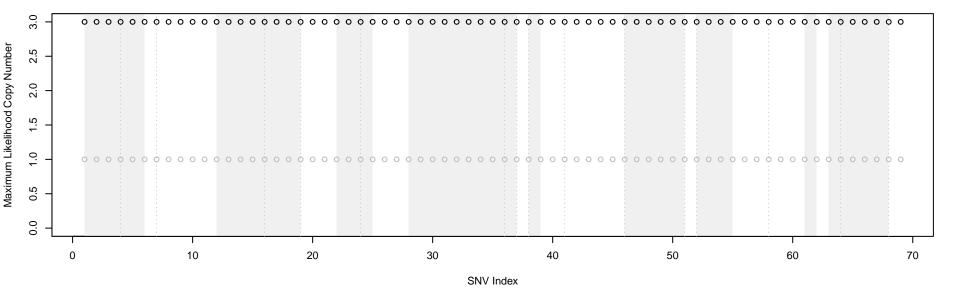
Purity: 0.55 Tumor ploidy: 3.003

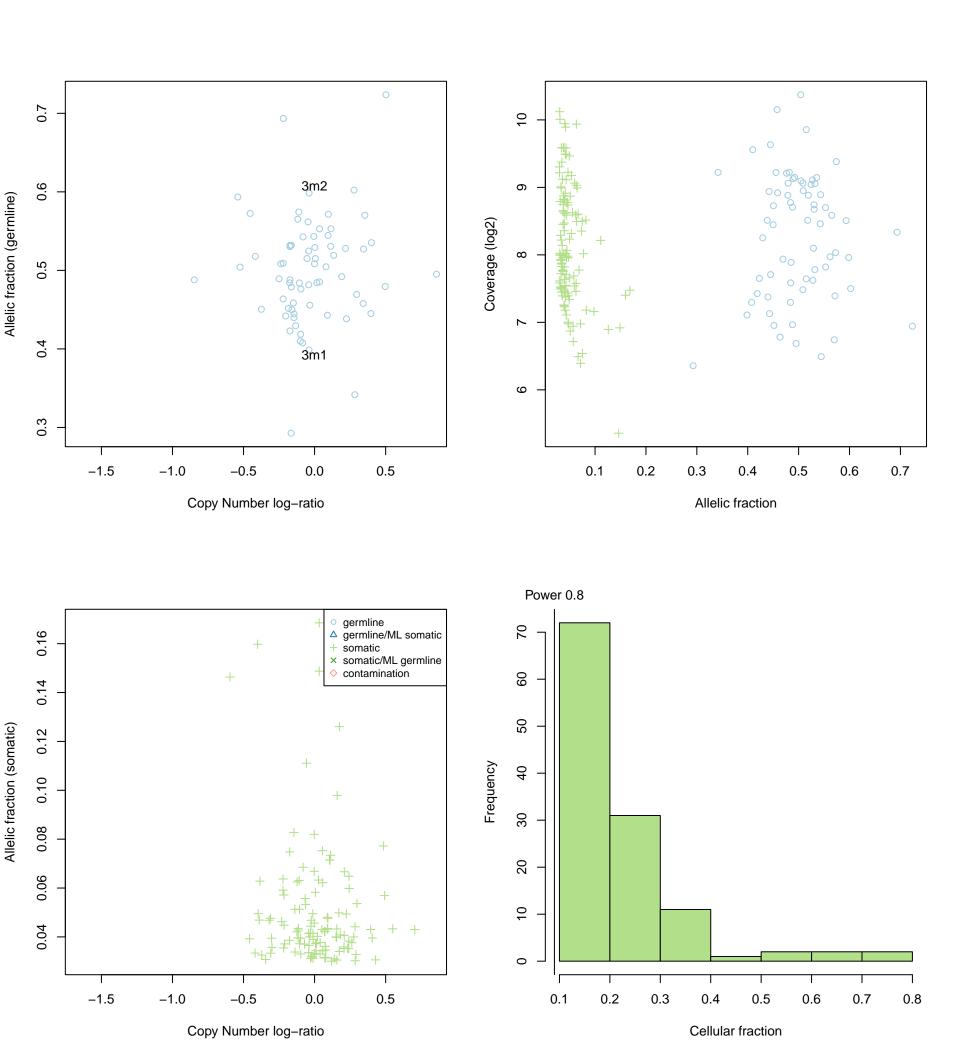


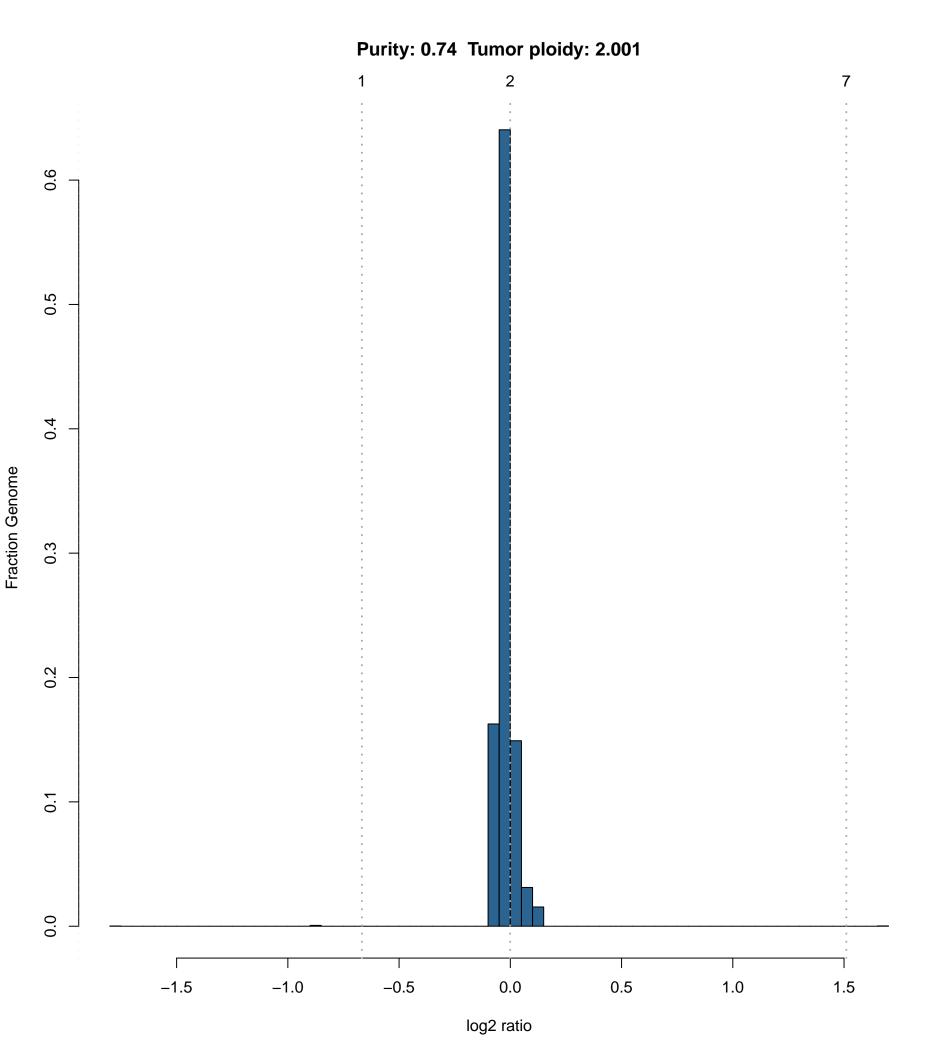


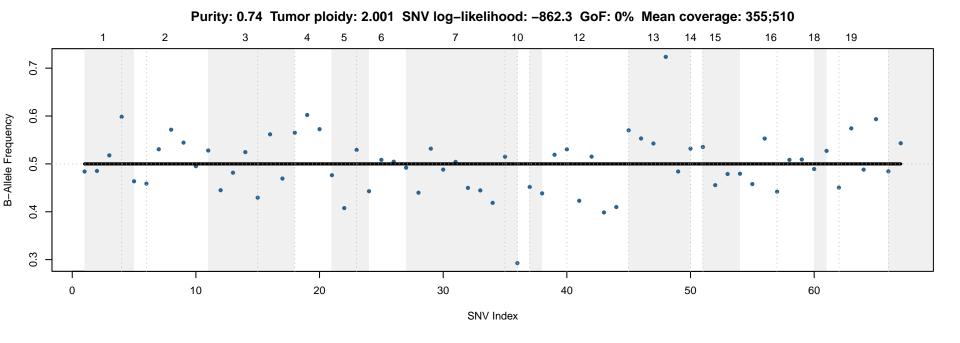
SCNA-fit log-likelihood: -13142.54



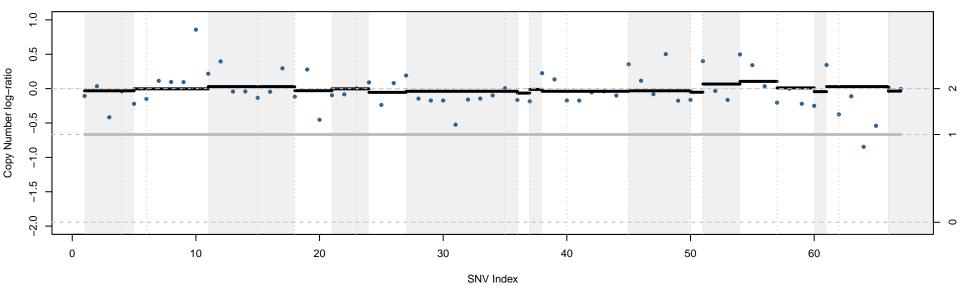


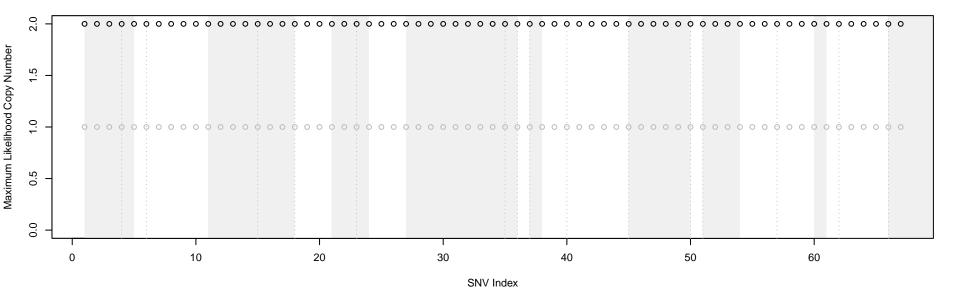


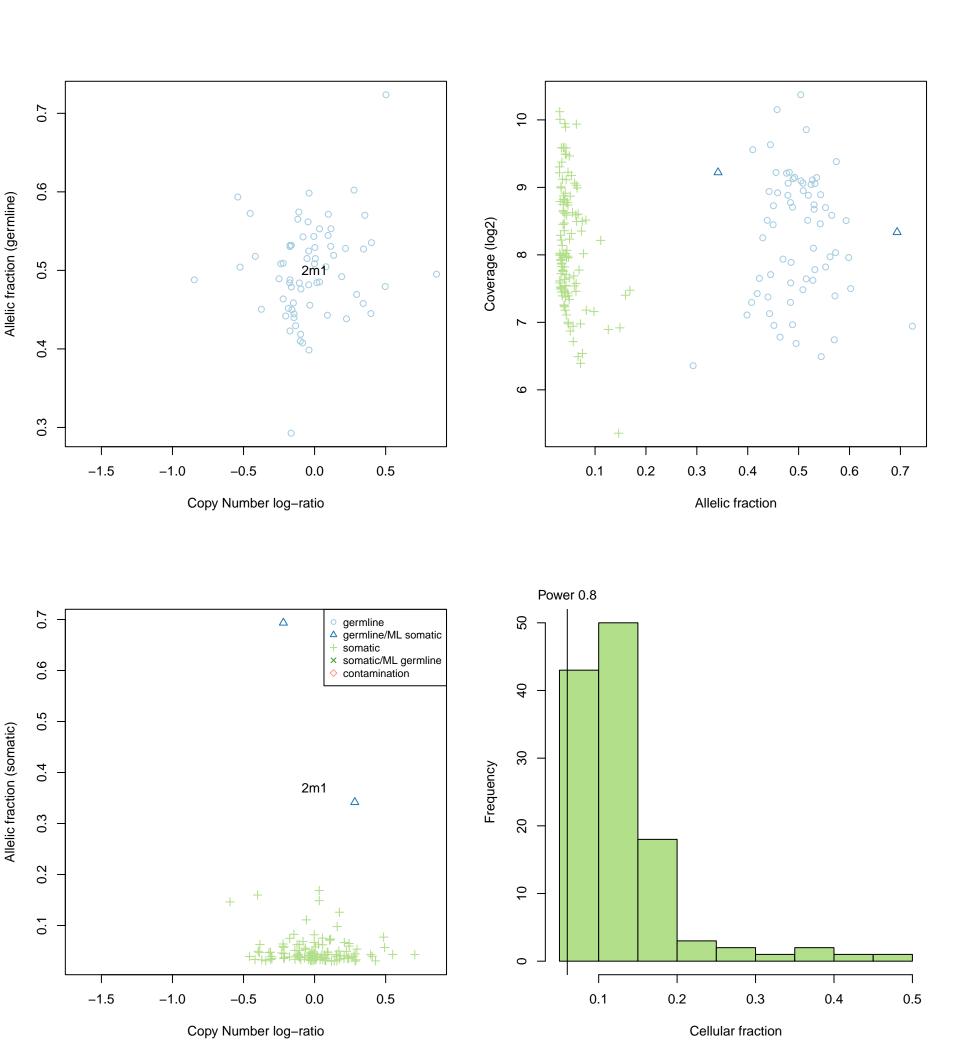




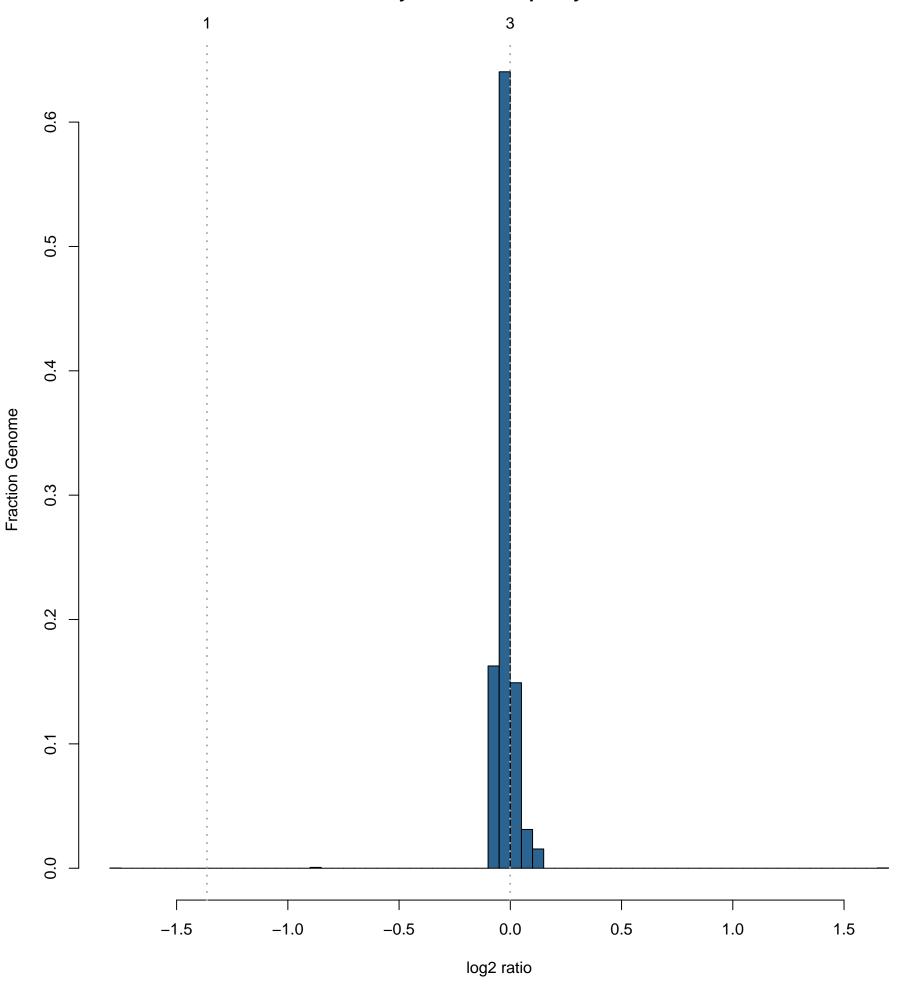
SCNA-fit log-likelihood: -13137.95

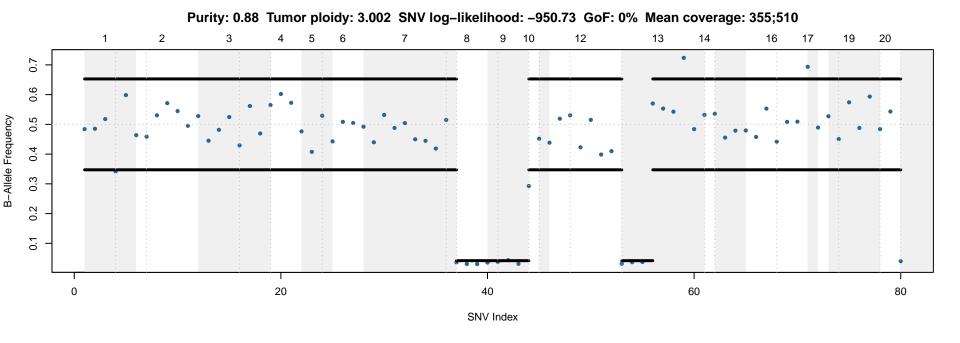






Purity: 0.88 Tumor ploidy: 3.002





SCNA-fit log-likelihood: -13143.39

