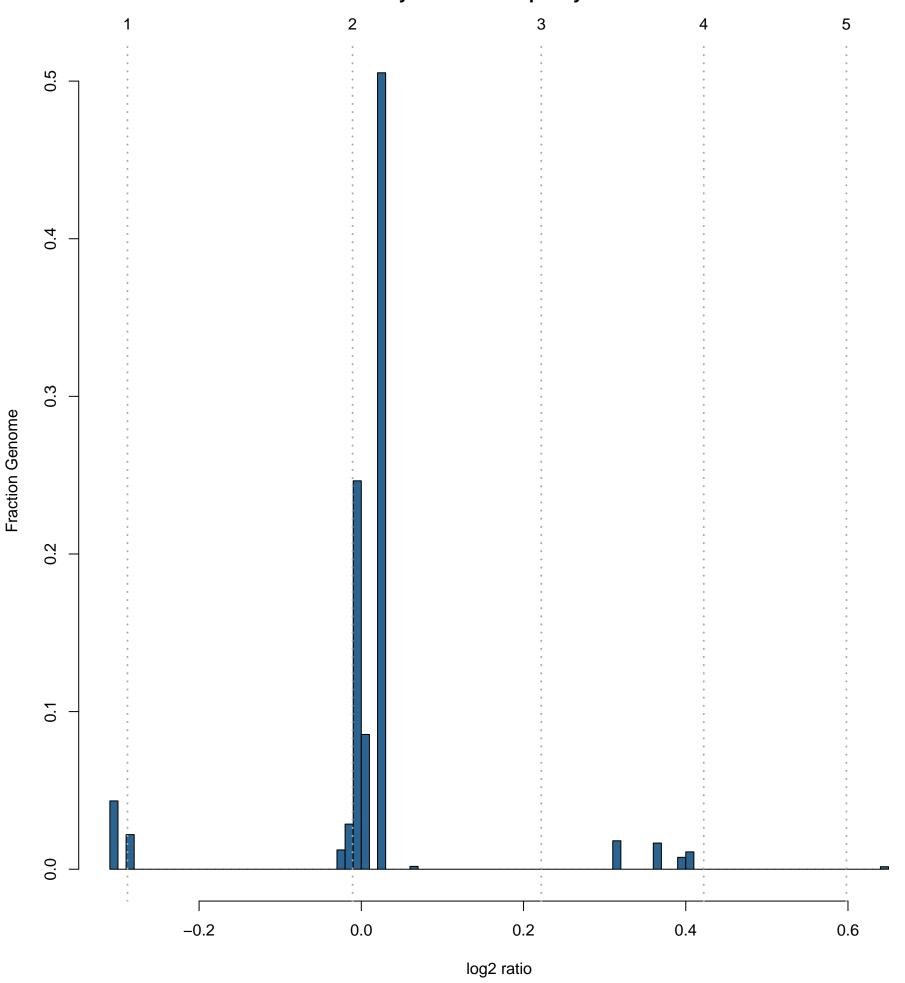
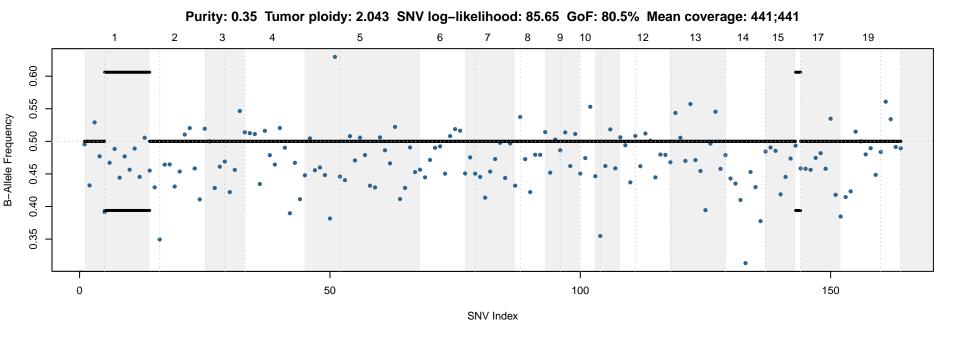
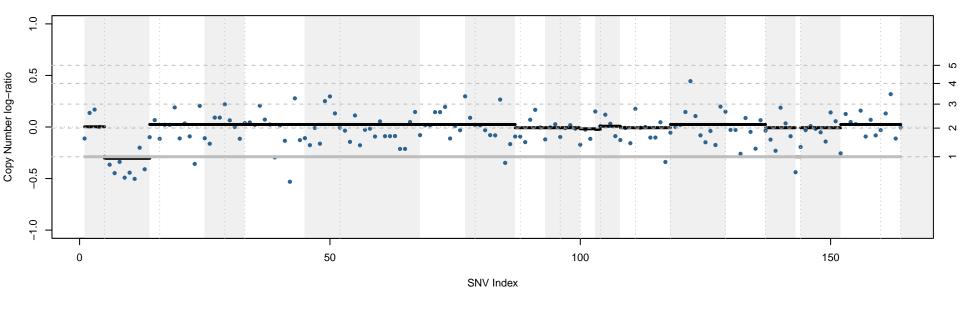
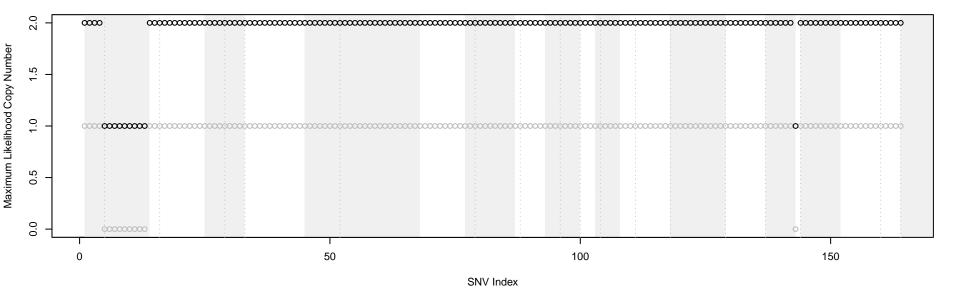
Purity: 0.35 Tumor ploidy: 2.043

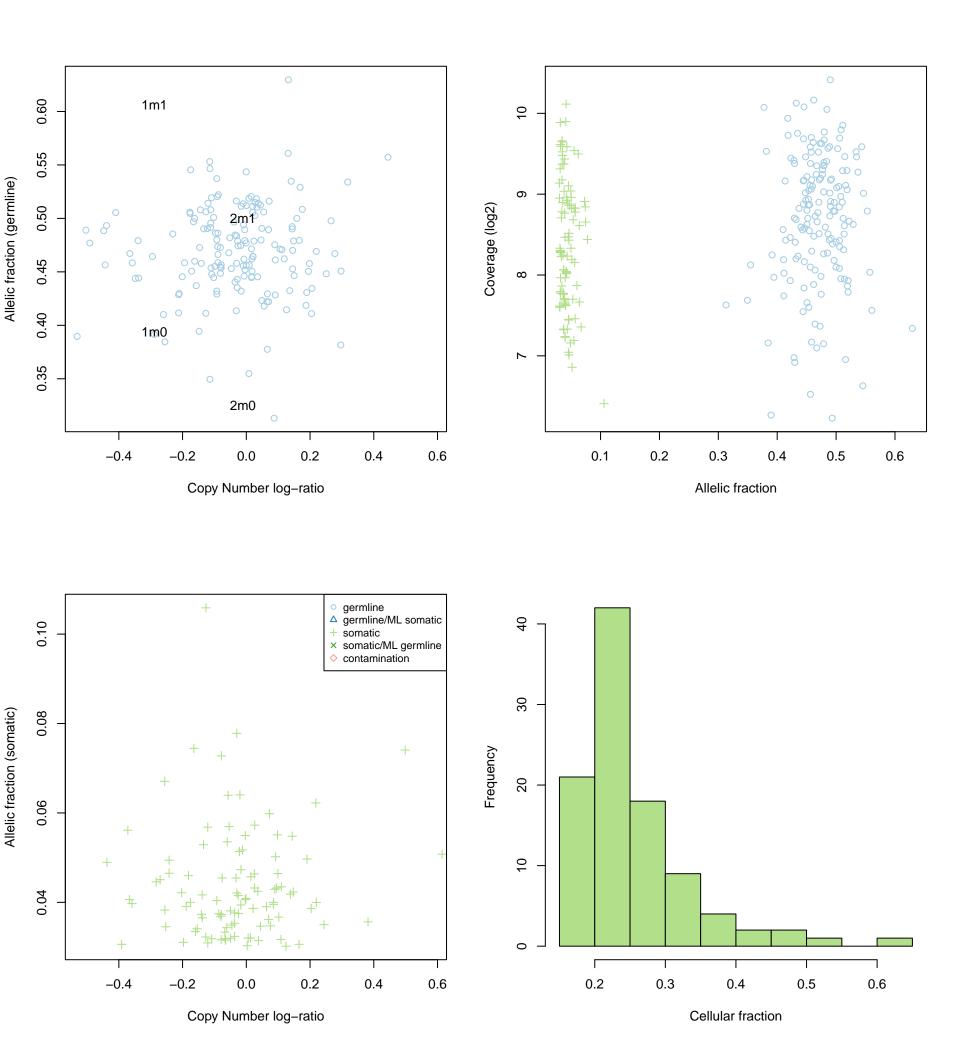




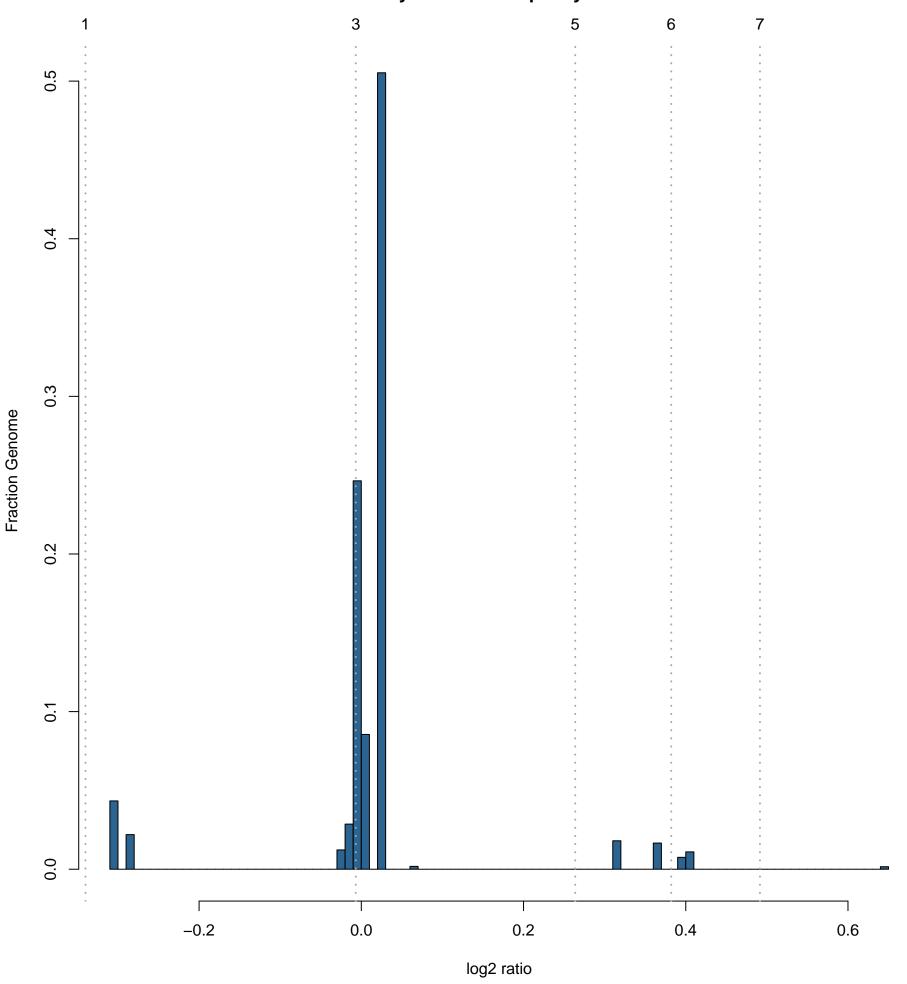
SCNA-fit log-likelihood: -3329.95

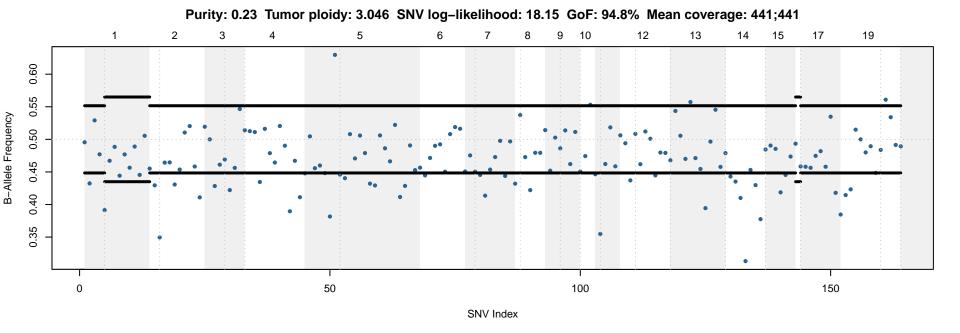




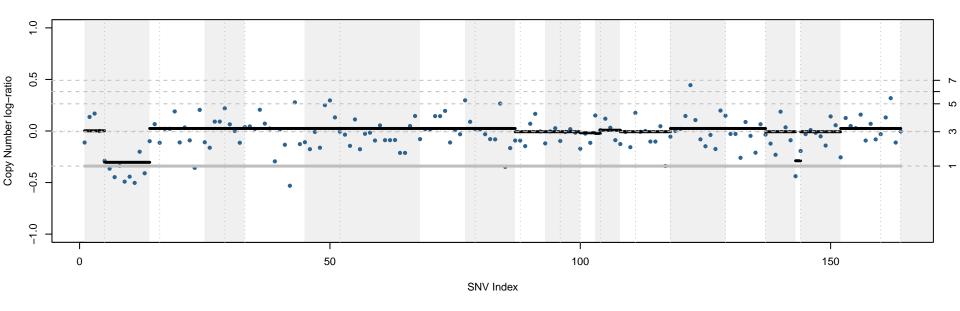


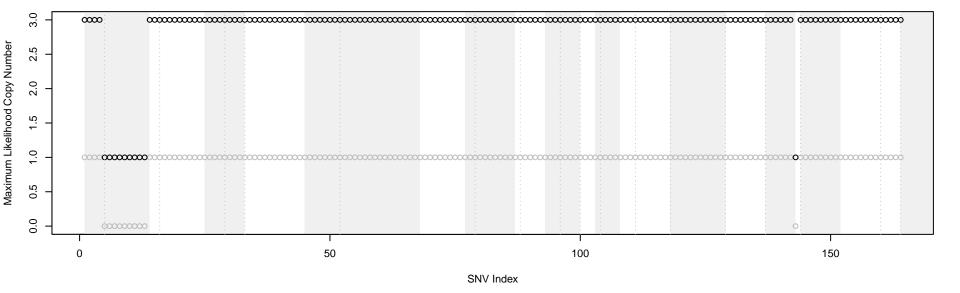
Purity: 0.23 Tumor ploidy: 3.046

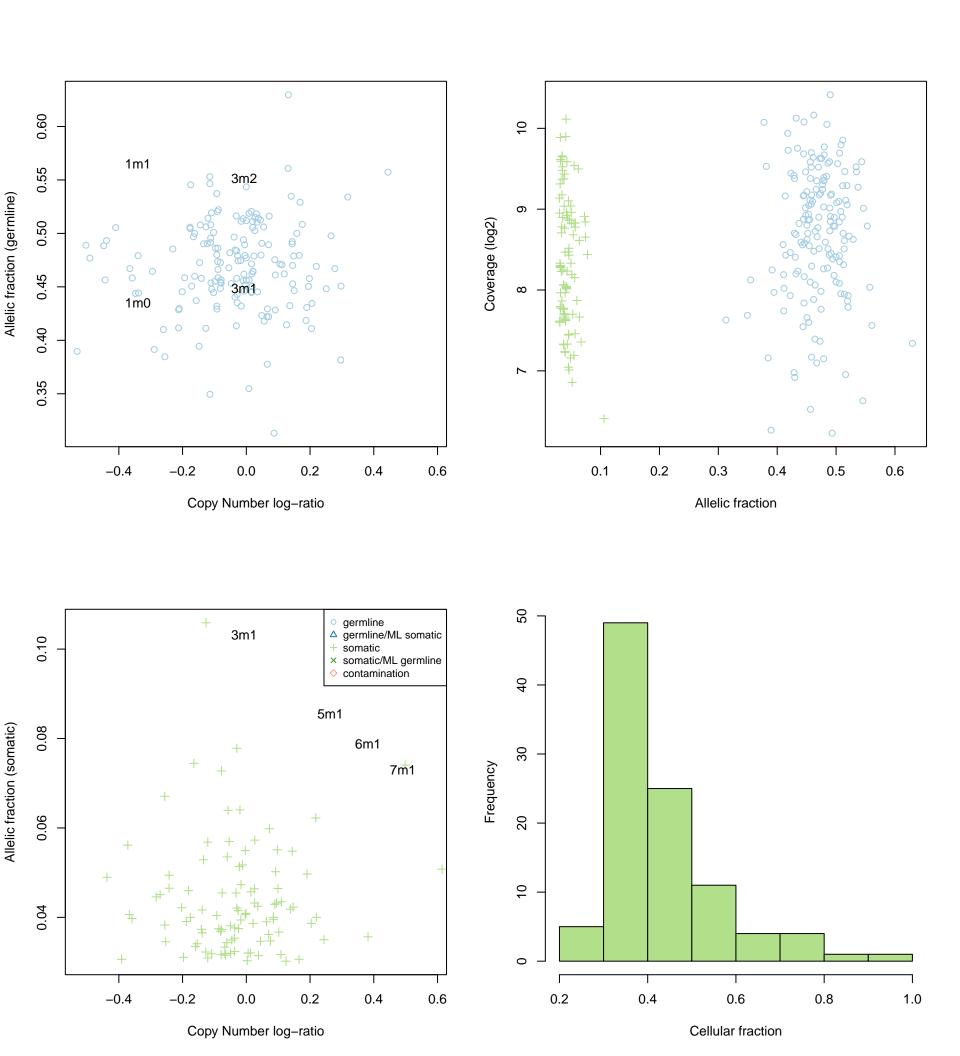




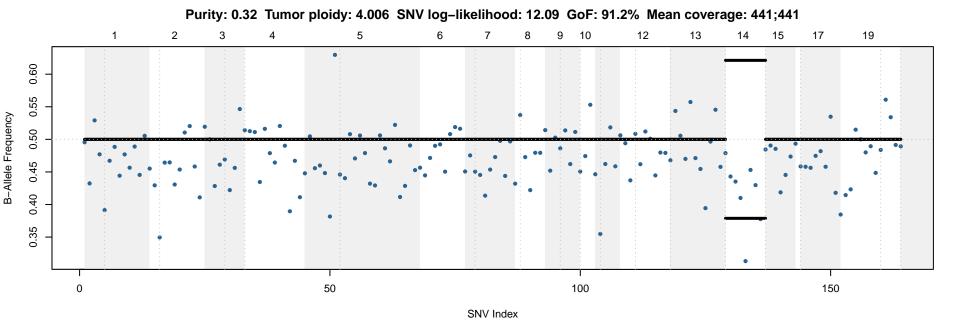
SCNA-fit log-likelihood: -3314.91



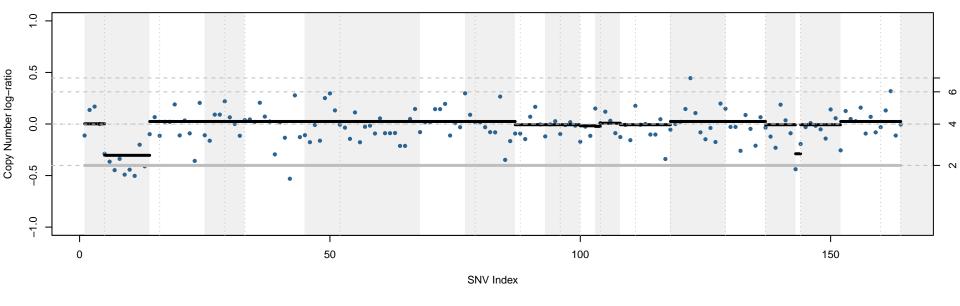


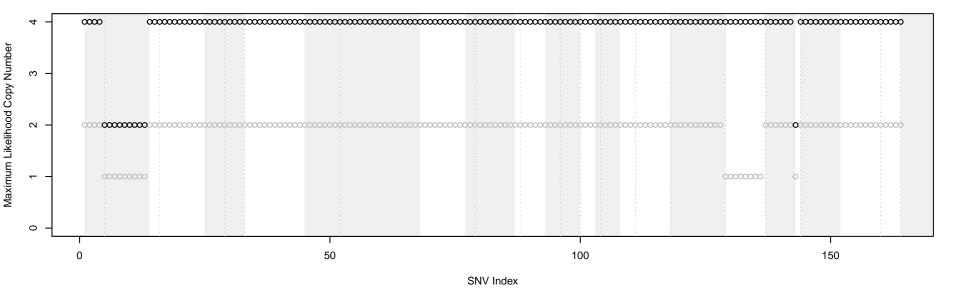


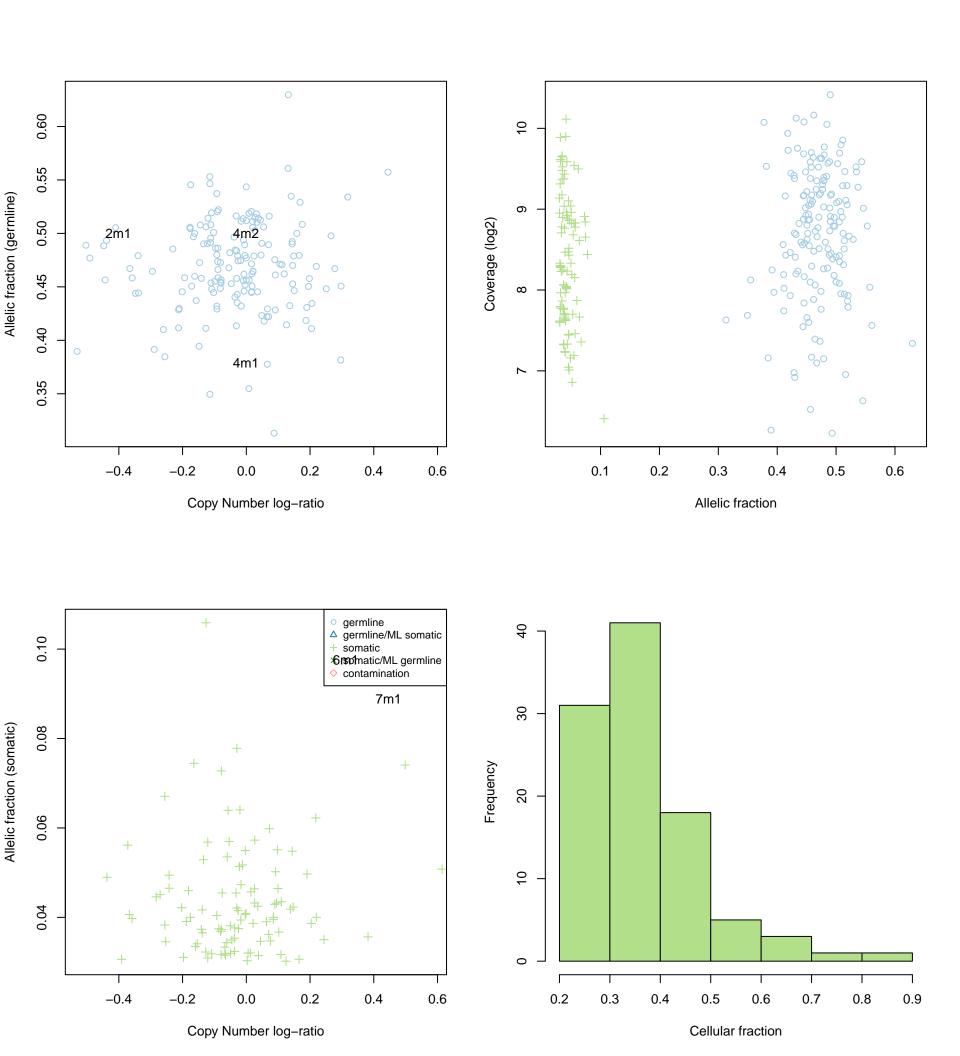
Purity: 0.32 Tumor ploidy: 4.006 7 Fraction Genome 0.1 0.0 -0.2 0.0 0.2 0.4 0.6 log2 ratio



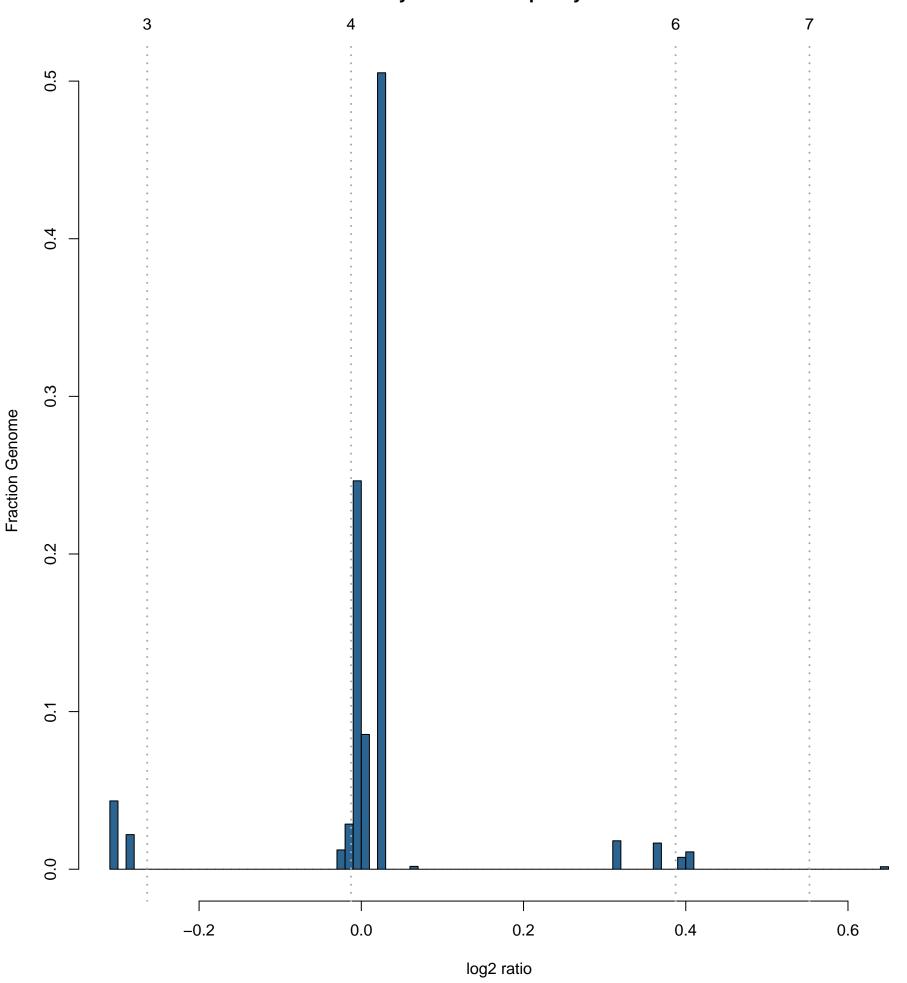
SCNA-fit log-likelihood: -3353.48

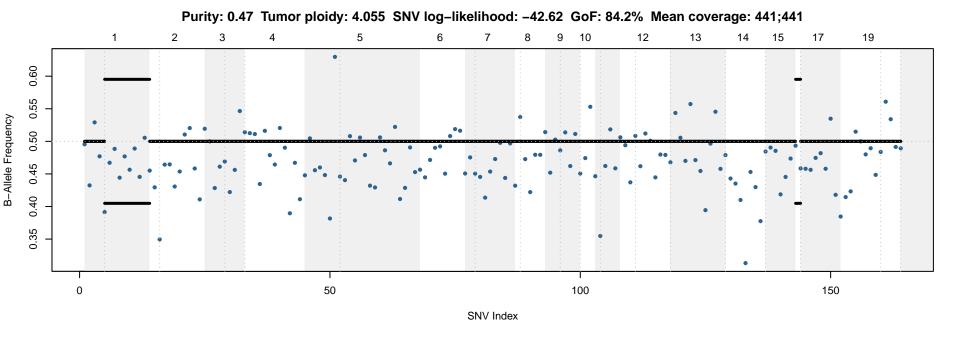




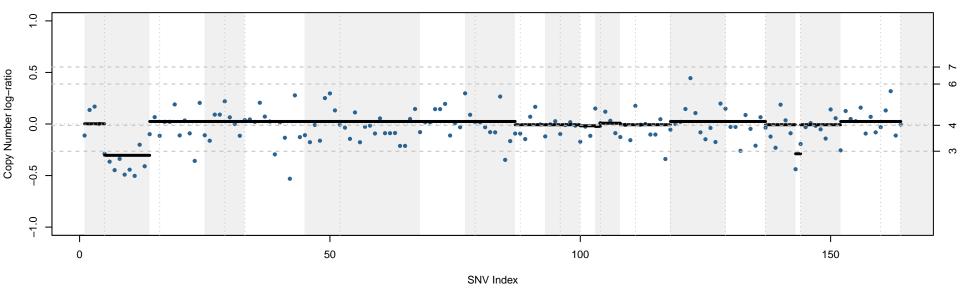


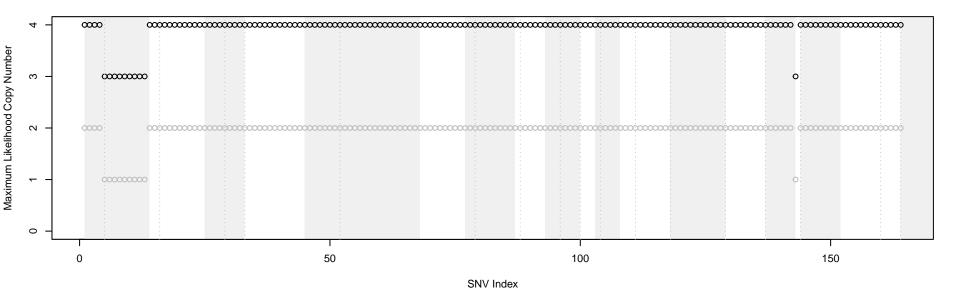
Purity: 0.47 Tumor ploidy: 4.055

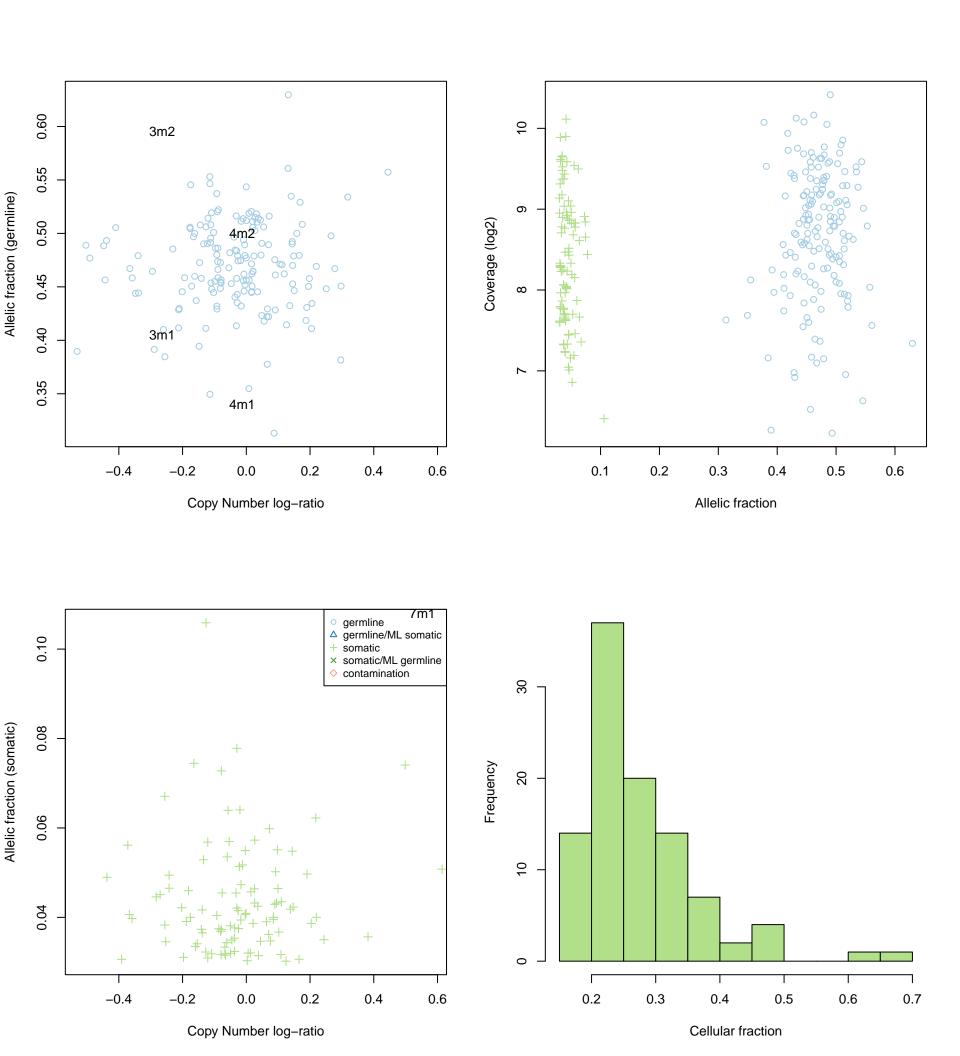




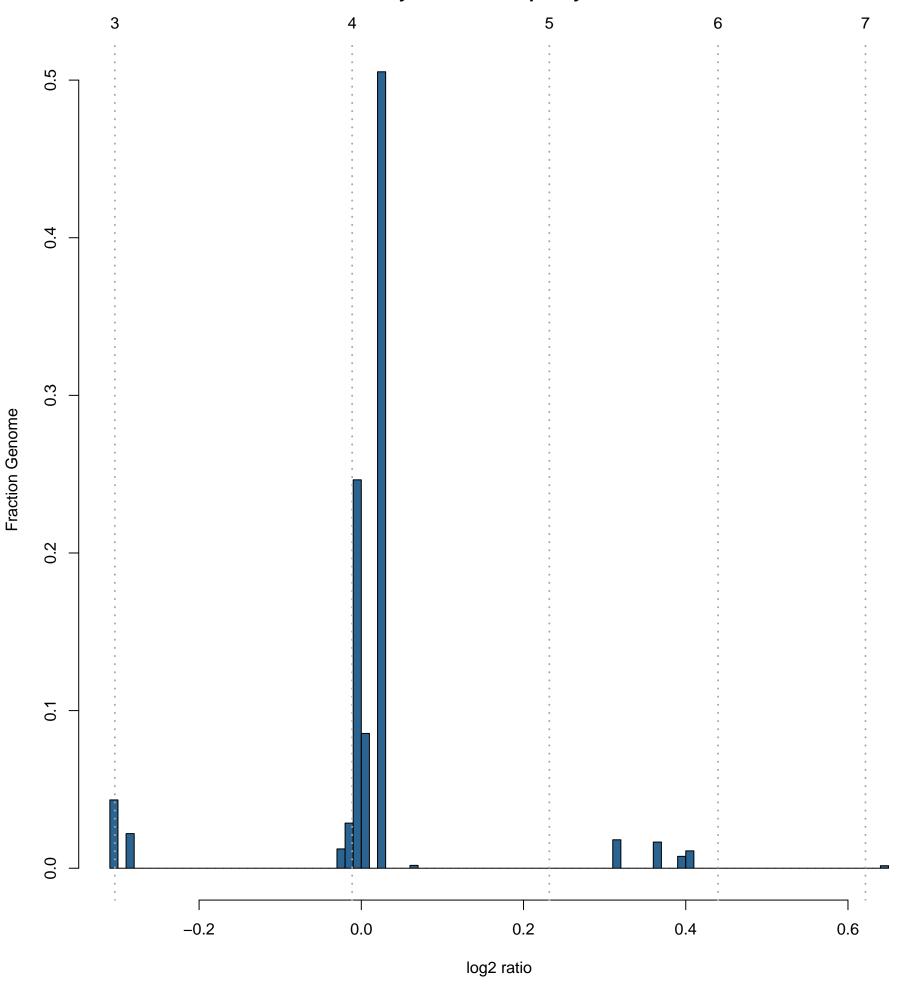
SCNA-fit log-likelihood: -3335.99

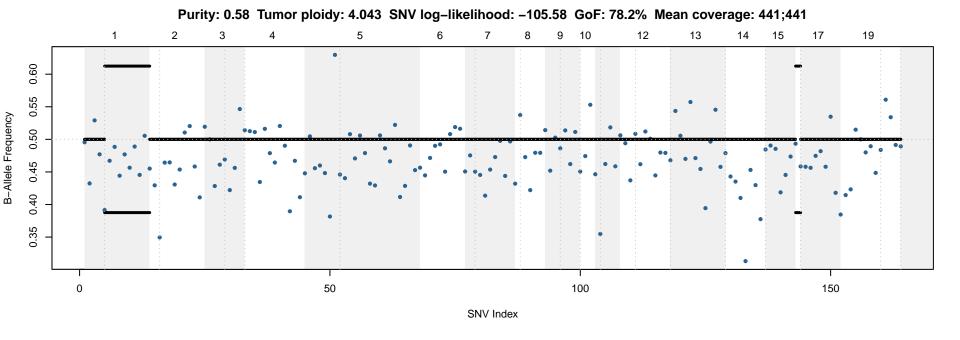




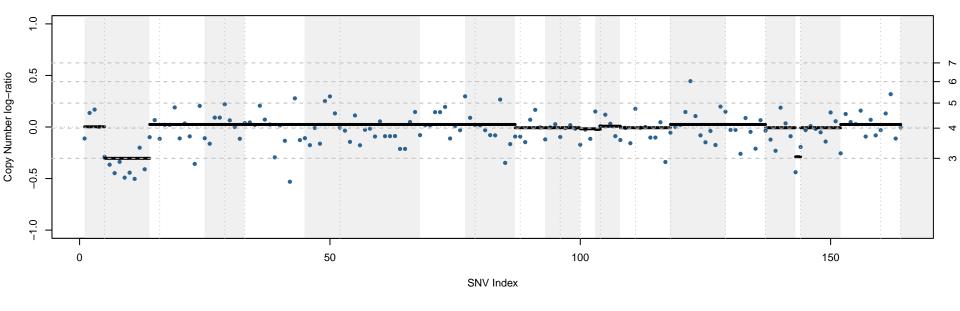


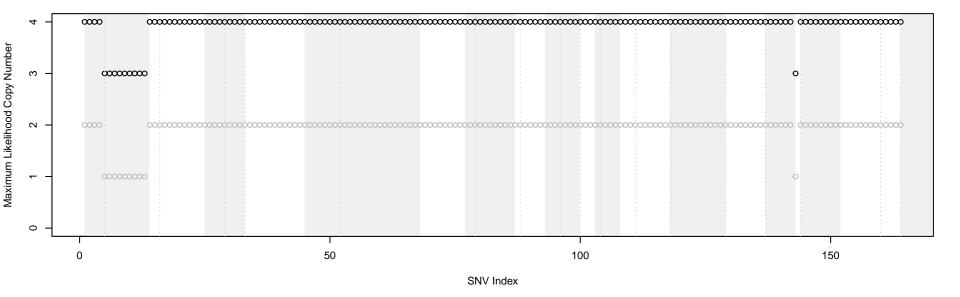
Purity: 0.58 Tumor ploidy: 4.043

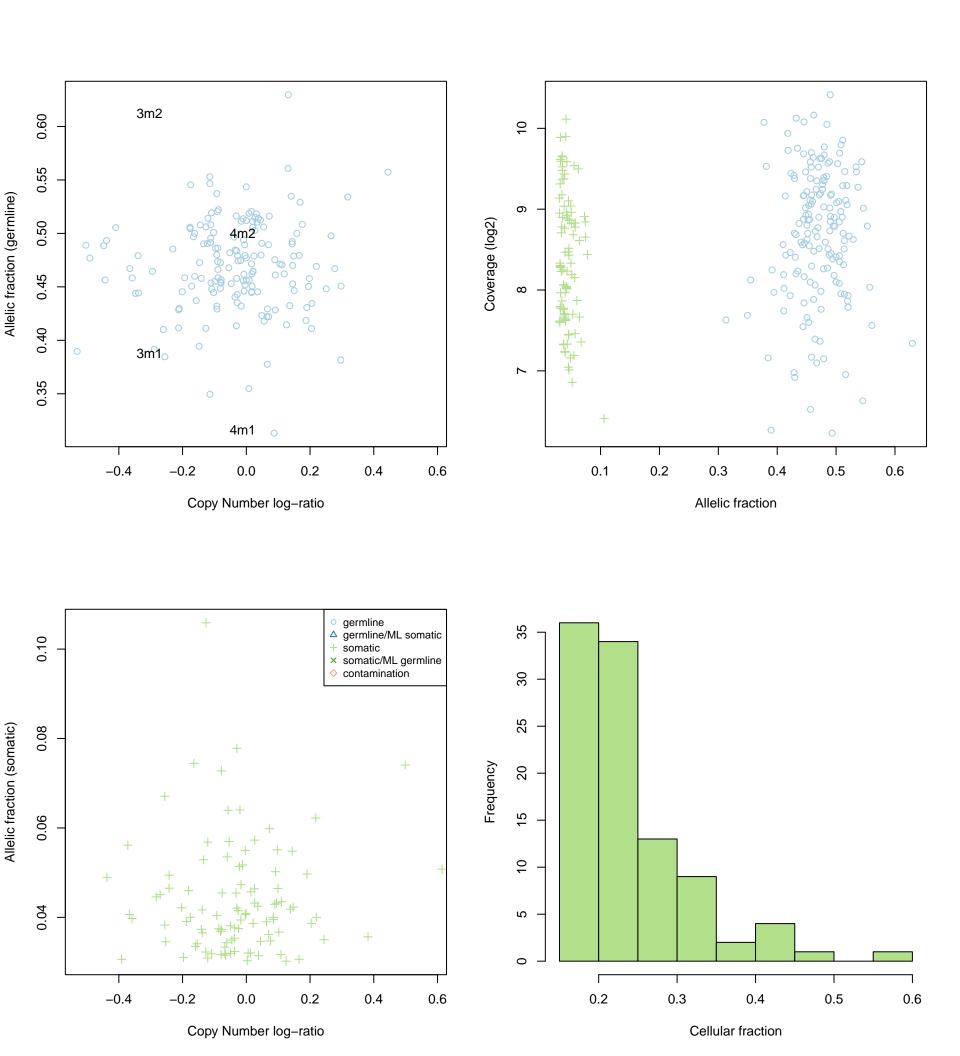




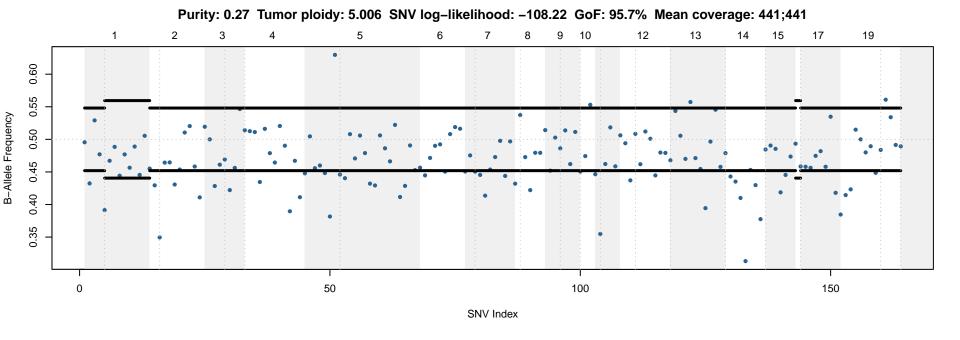
SCNA-fit log-likelihood: -3331.2



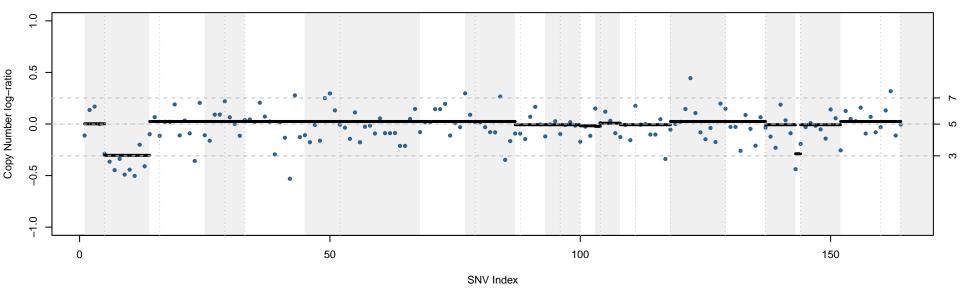


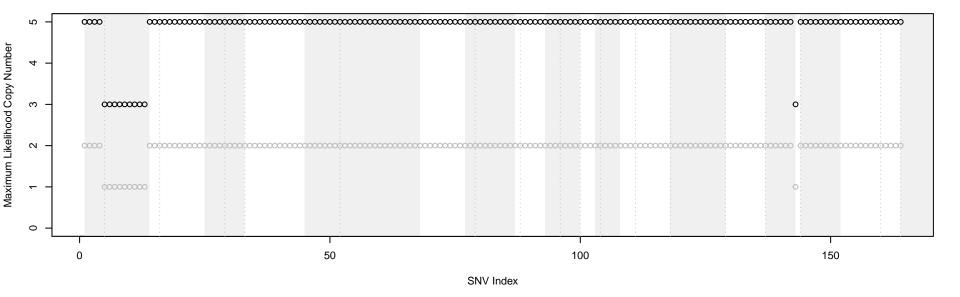


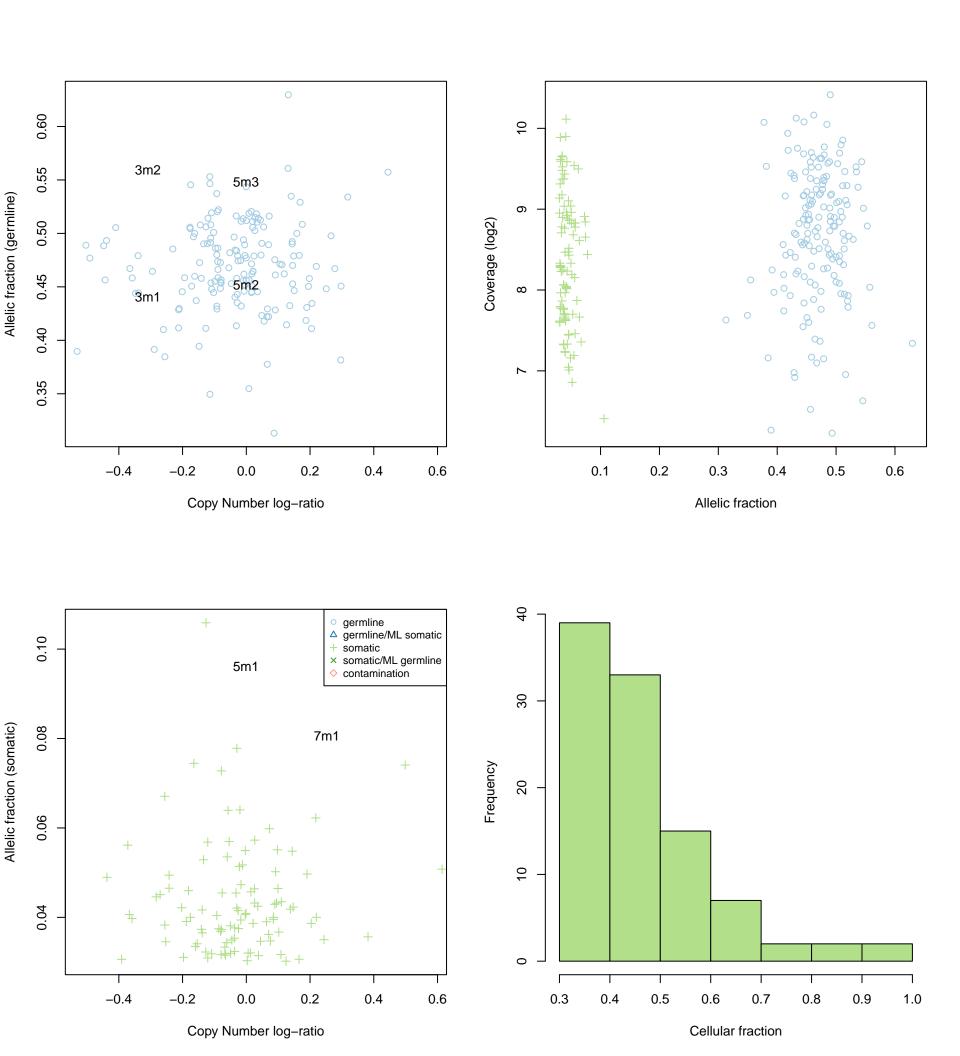
Purity: 0.27 Tumor ploidy: 5.006 5 3 Fraction Genome 0.1 0.0 -0.2 0.0 0.2 0.4 0.6 log2 ratio



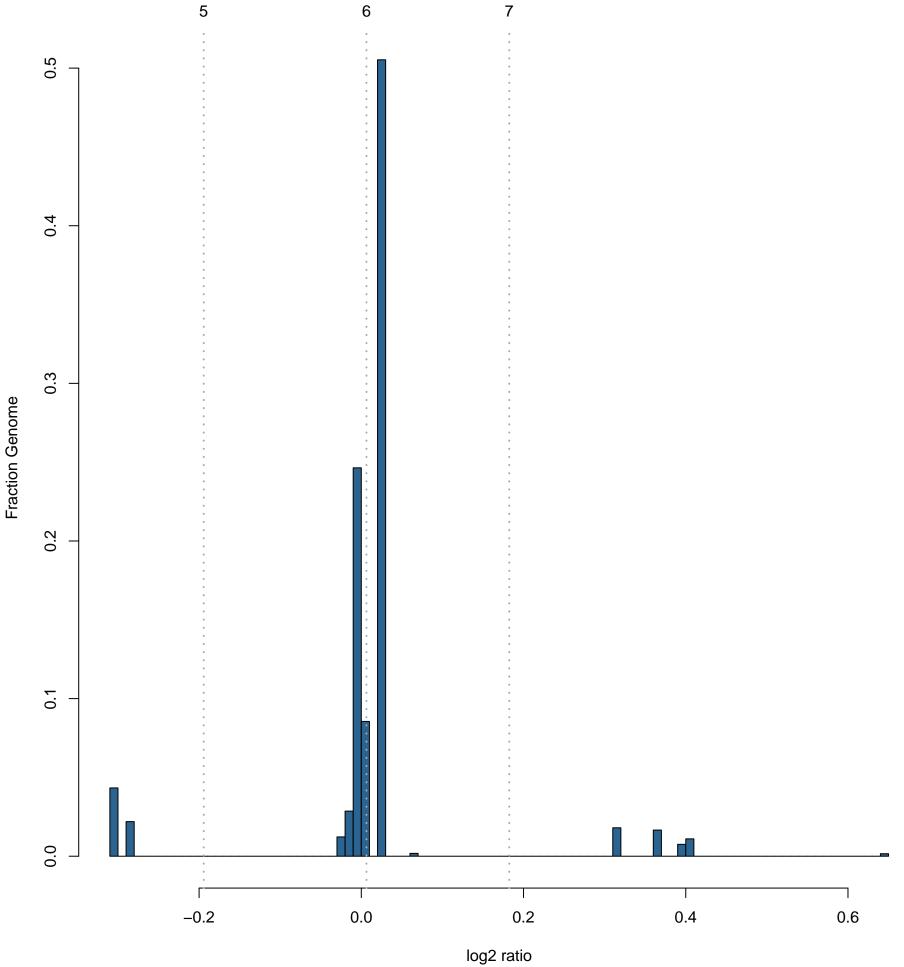
SCNA-fit log-likelihood: -3378.7

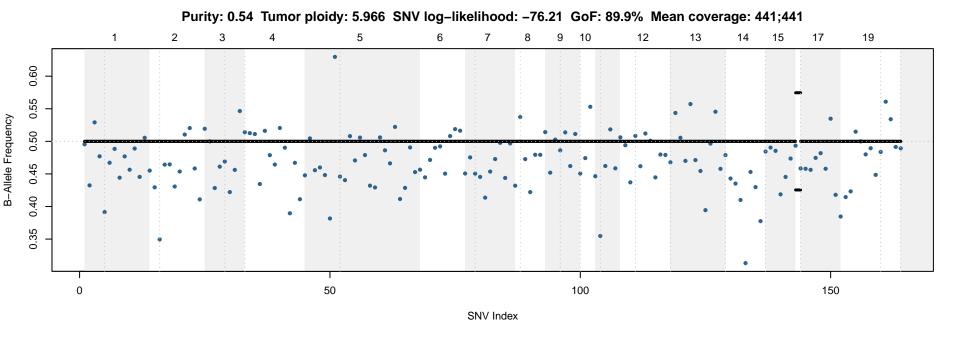




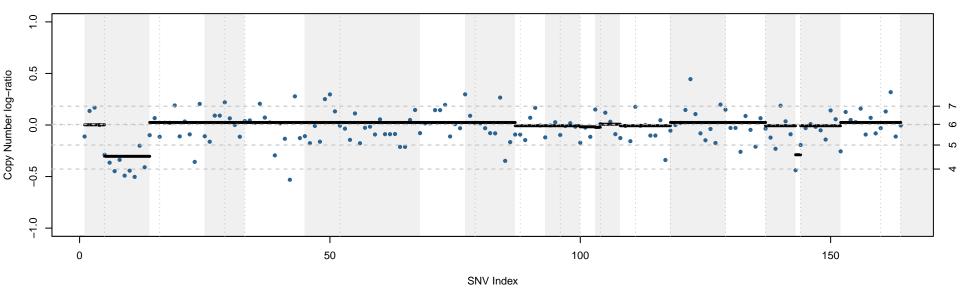


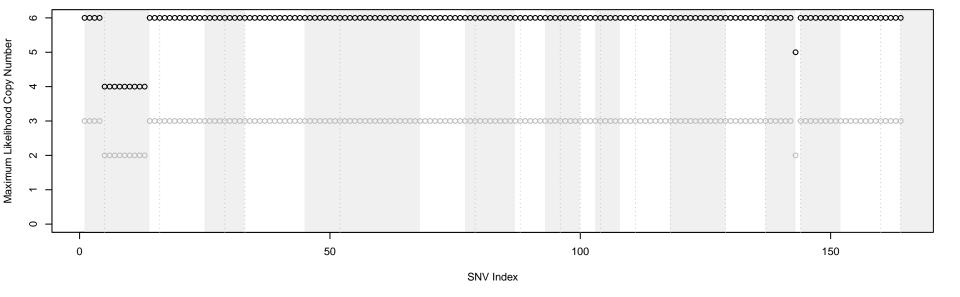
Purity: 0.54 Tumor ploidy: 5.9666 7

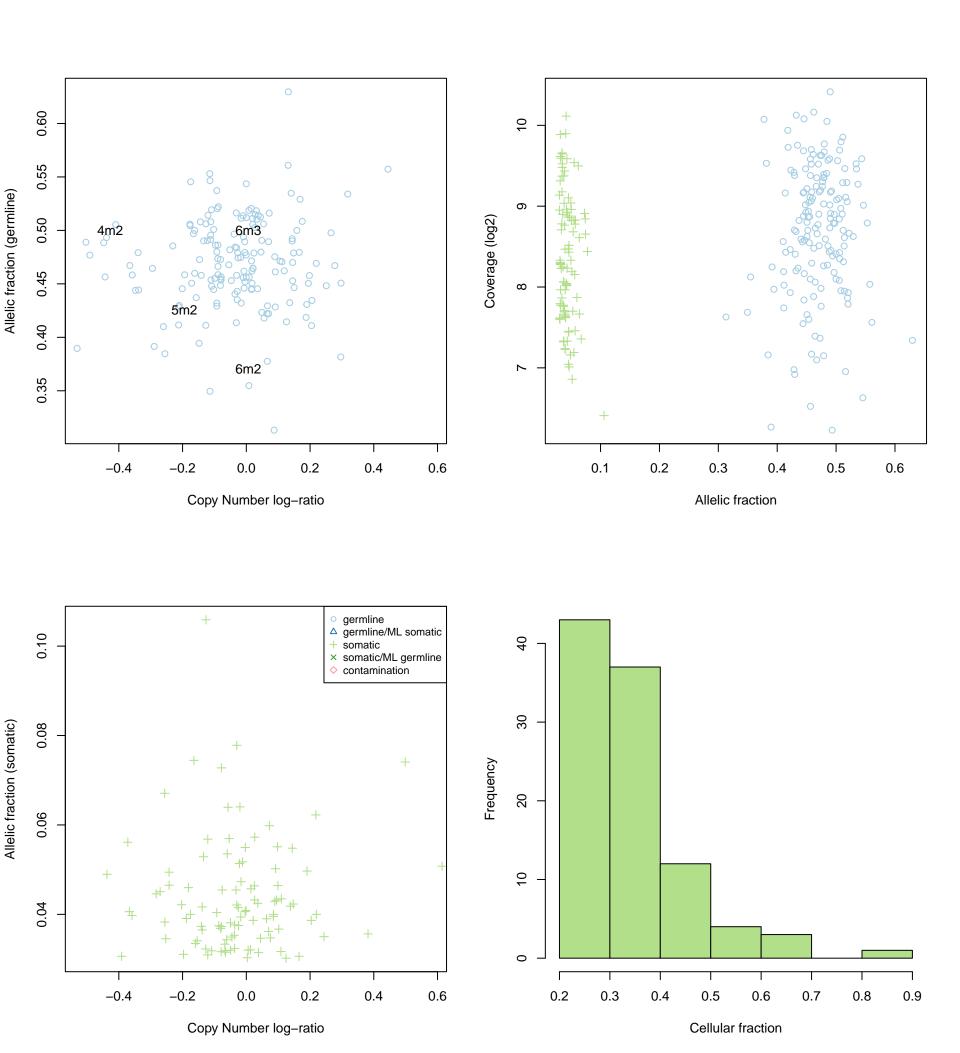




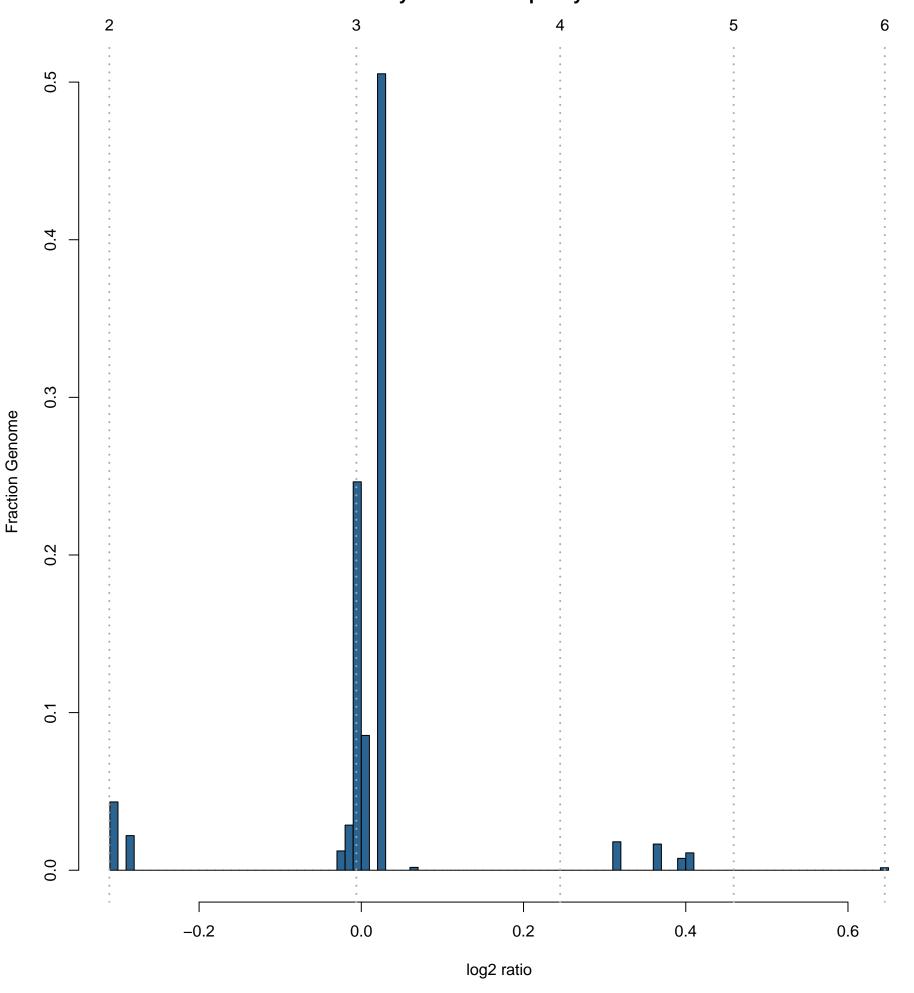
SCNA-fit log-likelihood: -3508.57

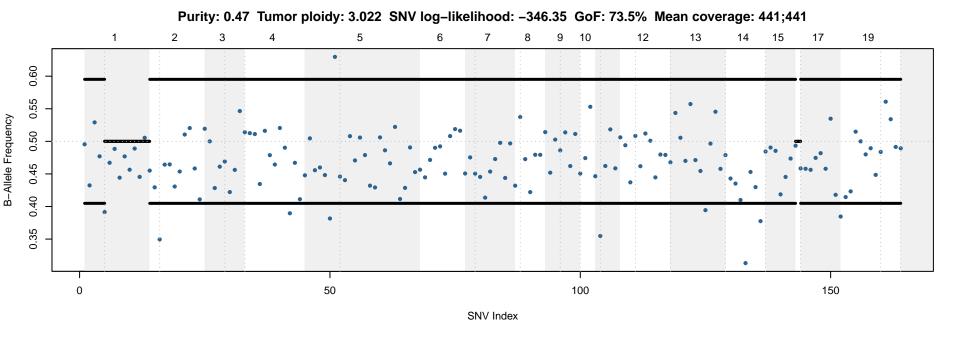




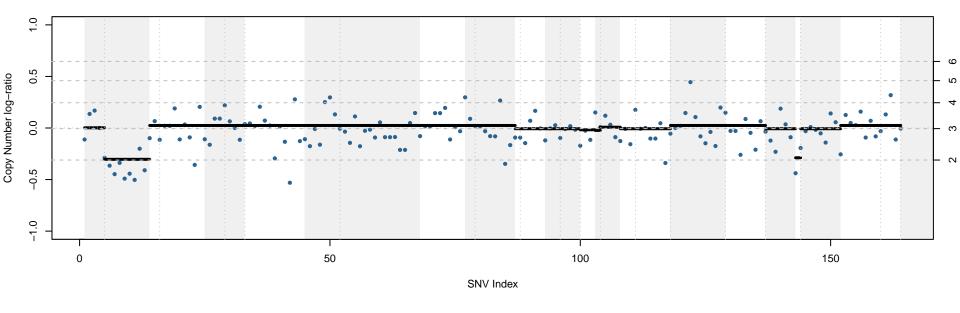


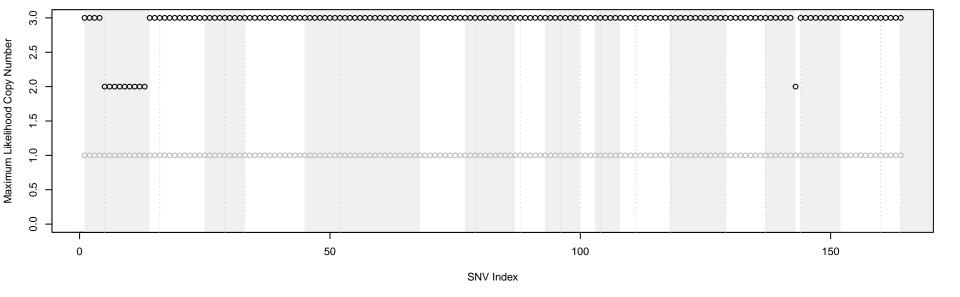
Purity: 0.47 Tumor ploidy: 3.022

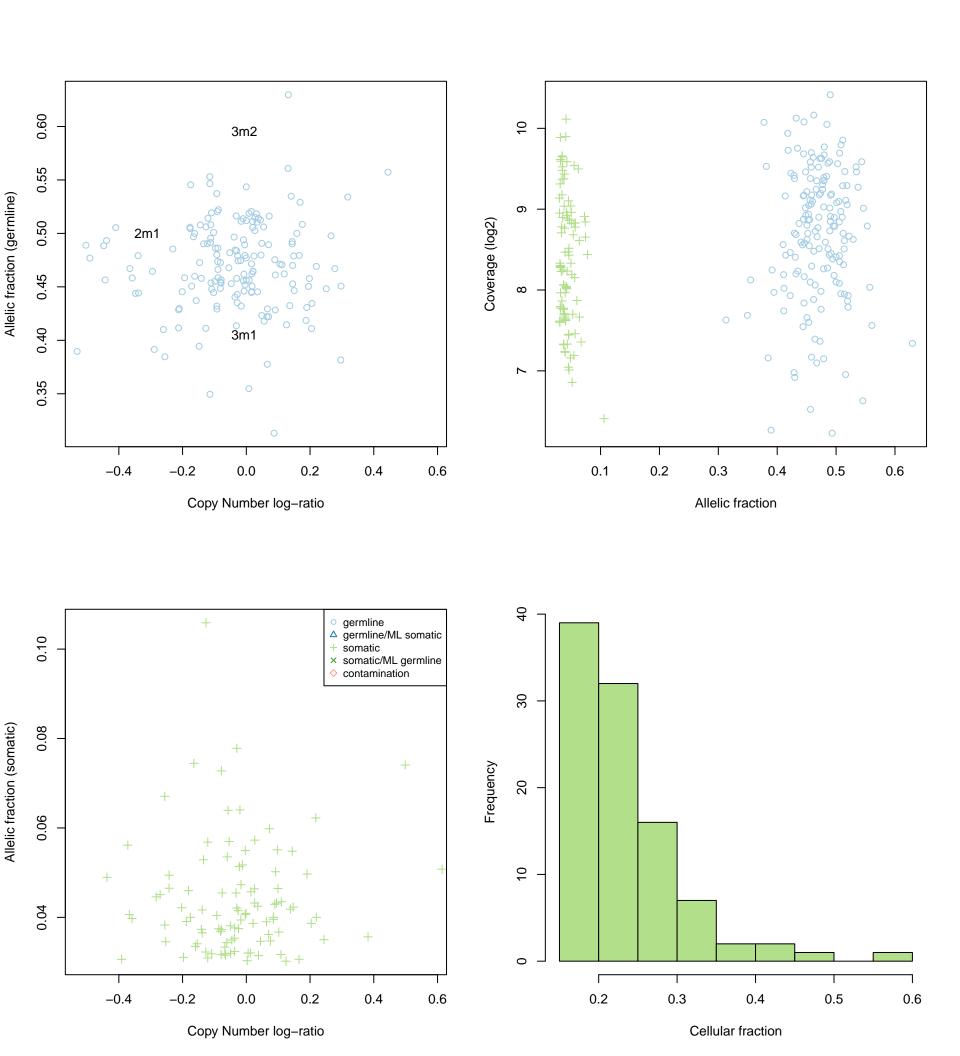




SCNA-fit log-likelihood: -3332.52

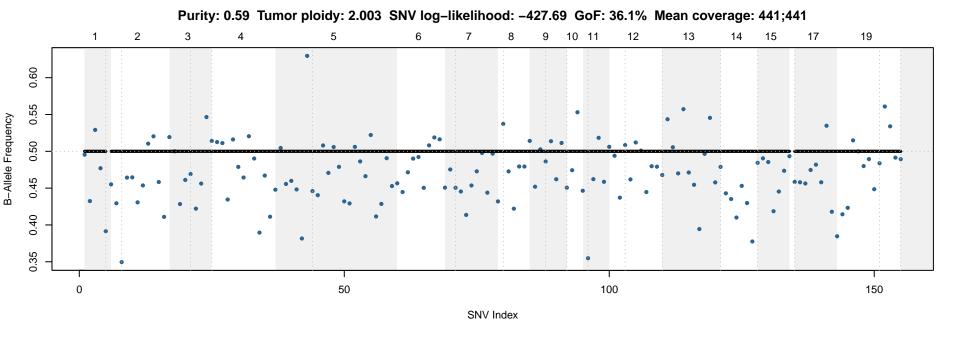




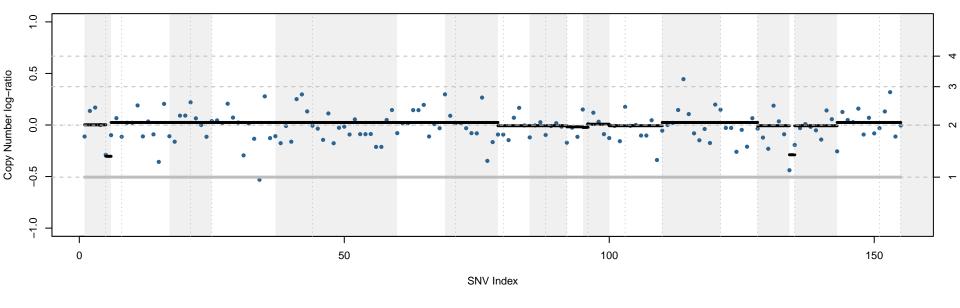


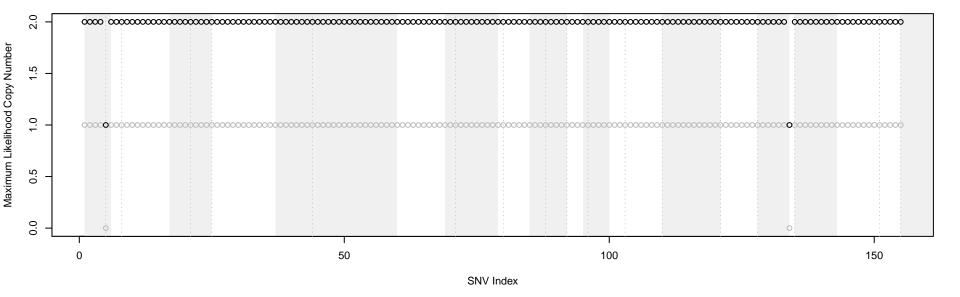
Purity: 0.59 Tumor ploidy: 2.003 2 3 Fraction Genome 0.1 -0.2 0.0 0.2 0.4 0.6

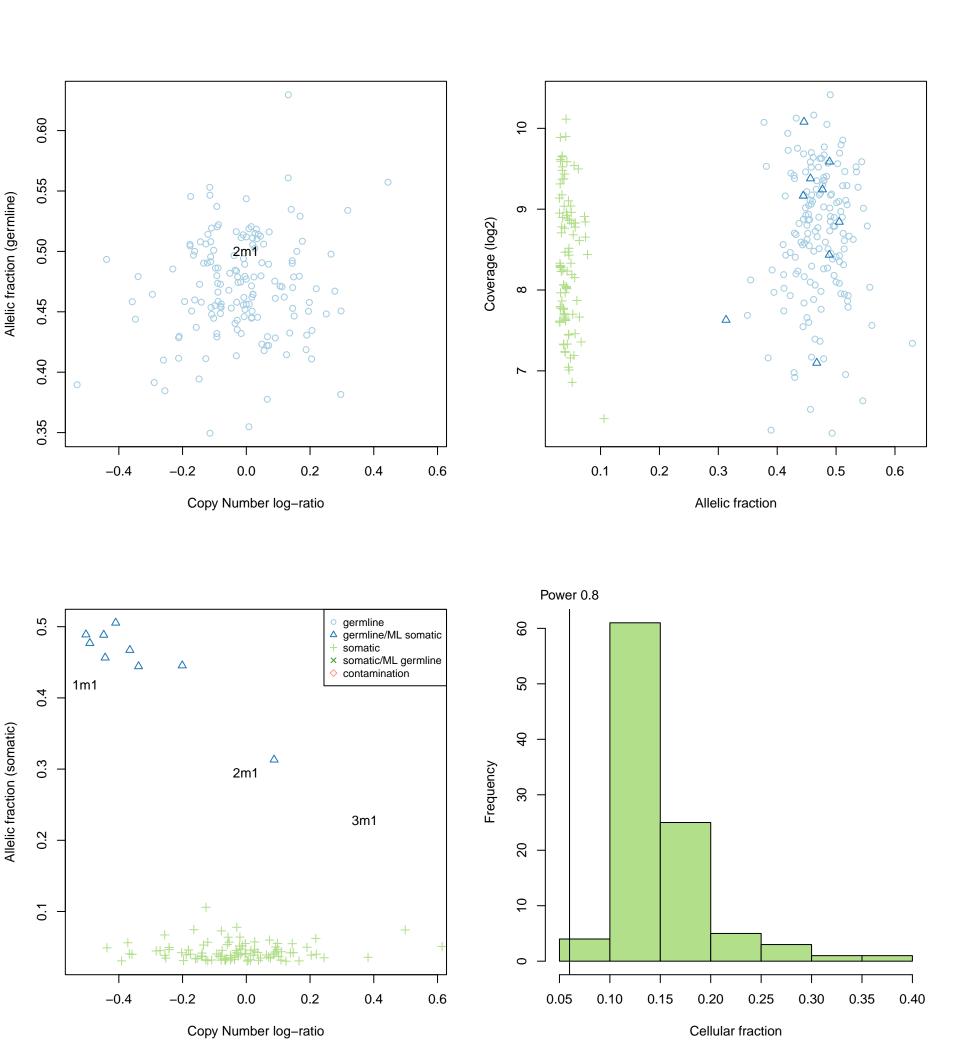
log2 ratio

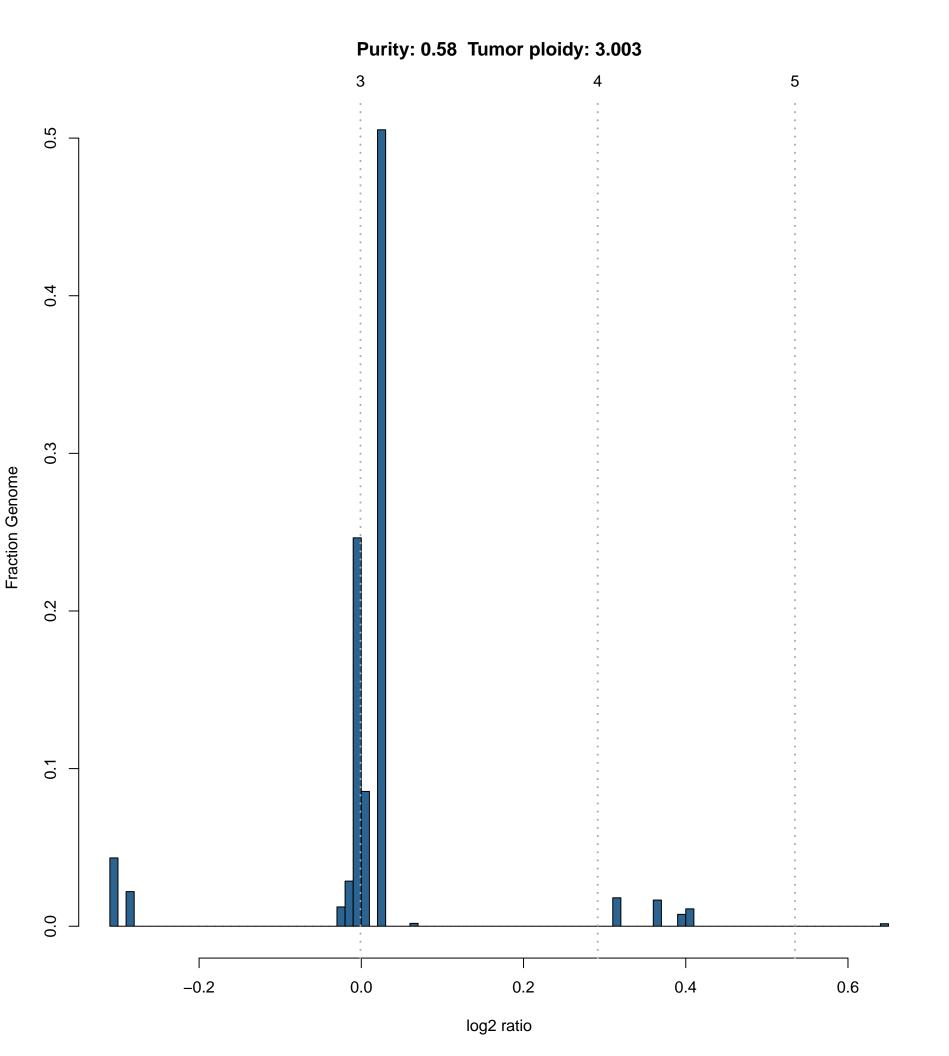


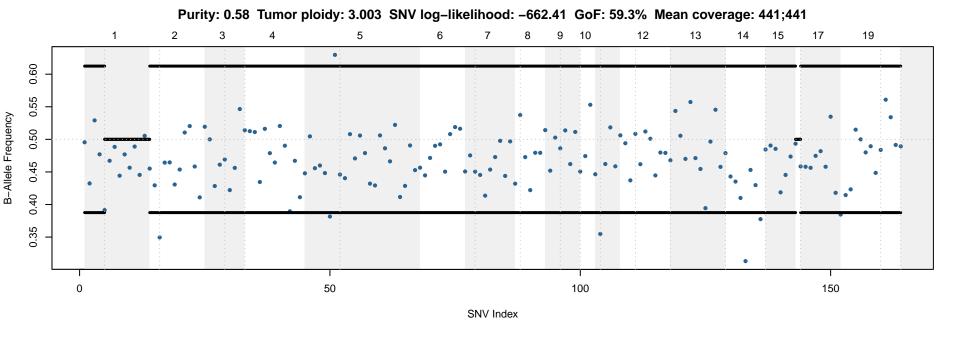
SCNA-fit log-likelihood: -3482.74











SCNA-fit log-likelihood: -3336.04

