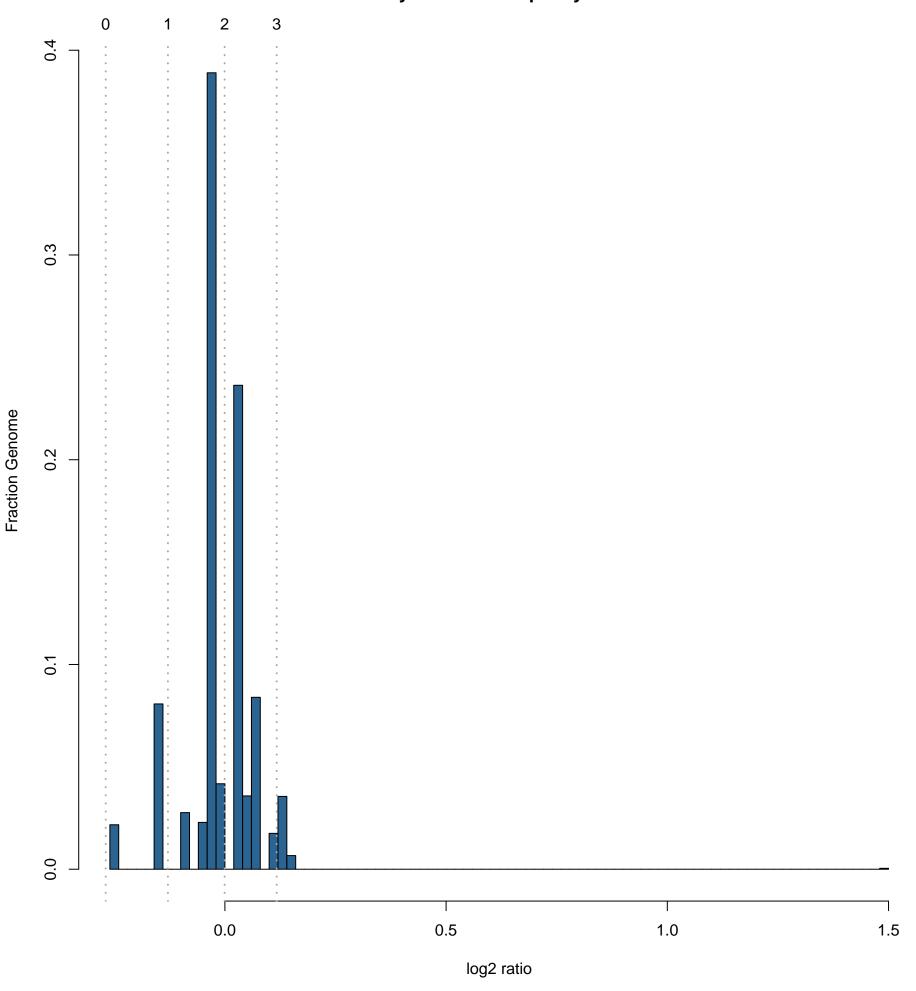
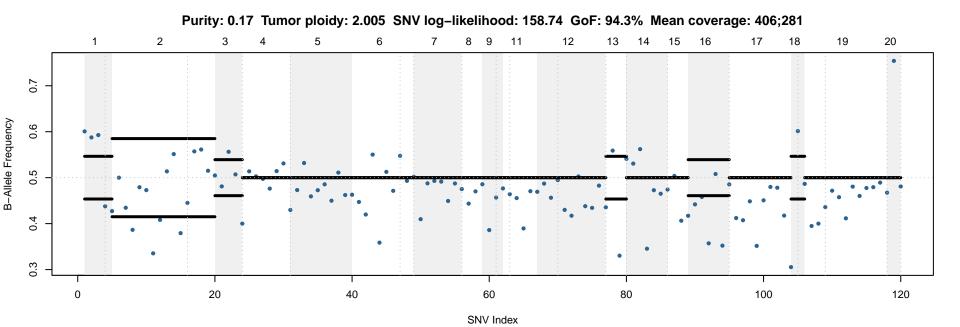
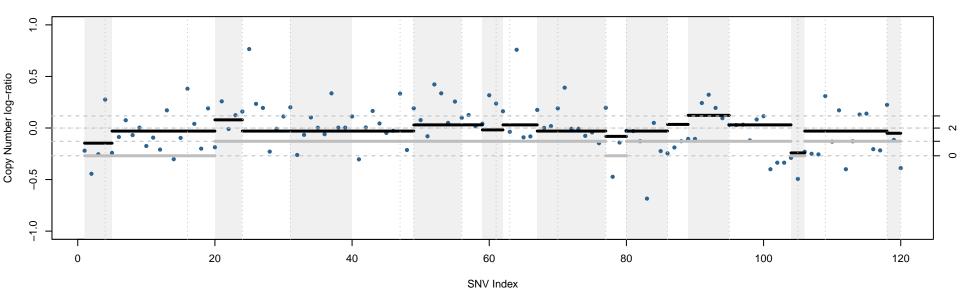
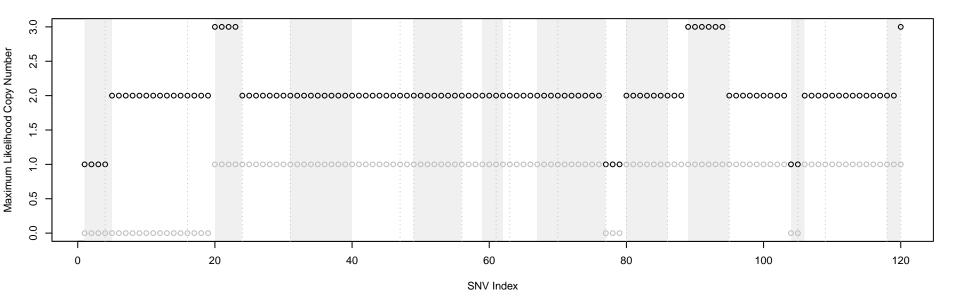
Purity: 0.17 Tumor ploidy: 2.005

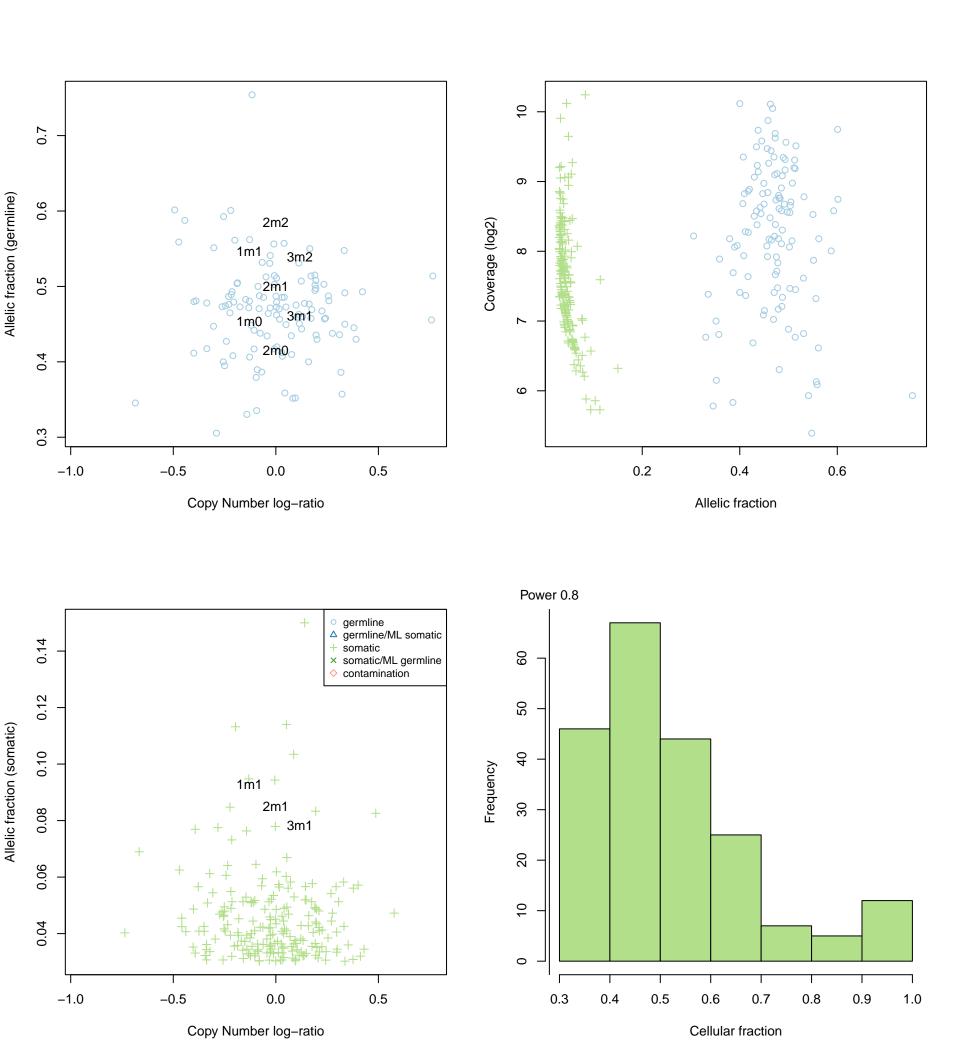




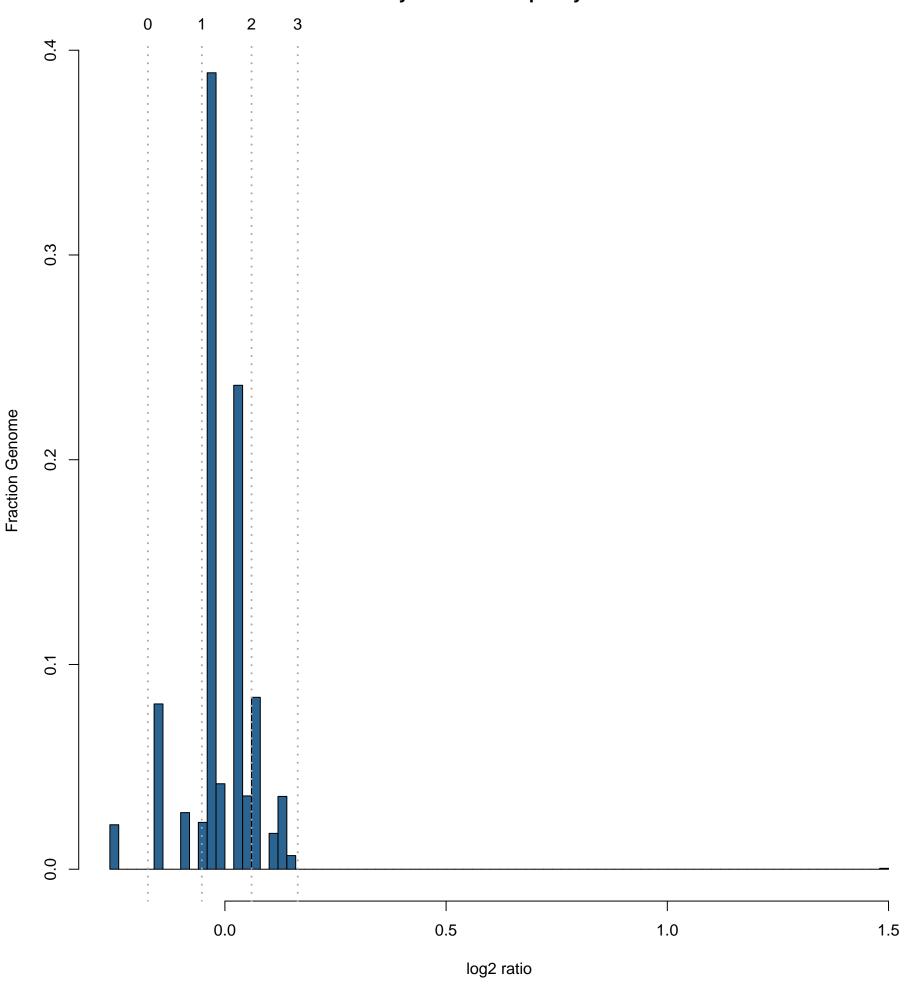
SCNA-fit log-likelihood: -15961.7

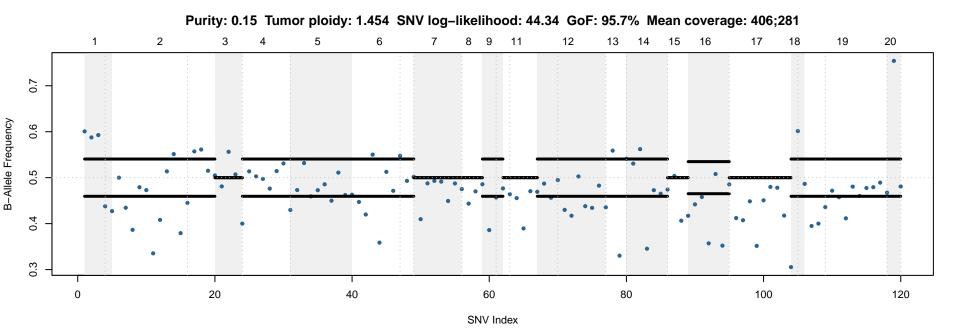




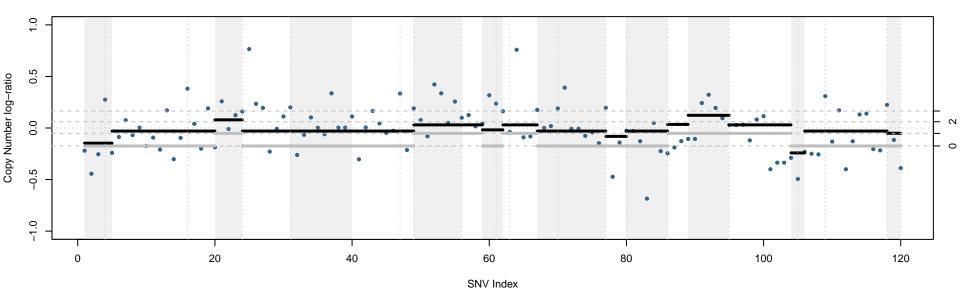


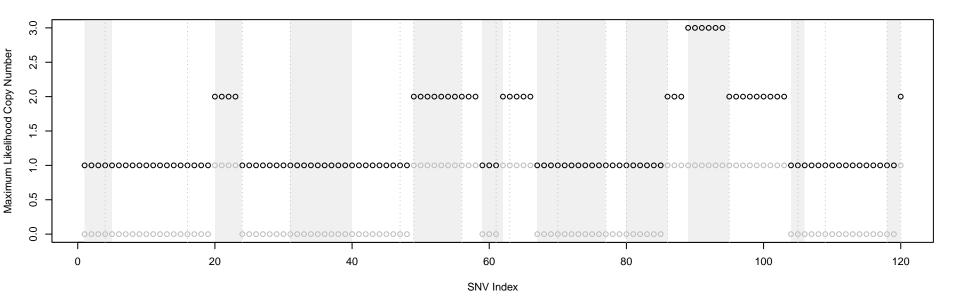
Purity: 0.15 Tumor ploidy: 1.454

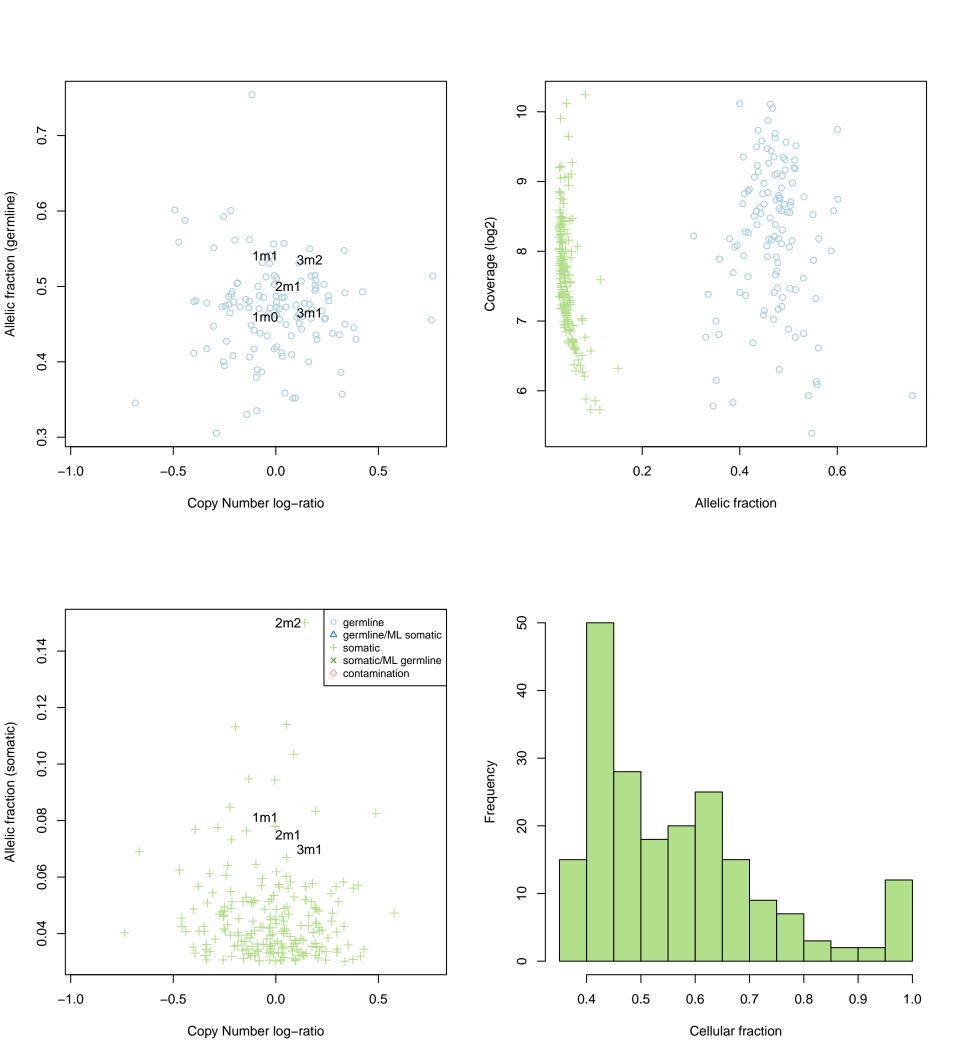




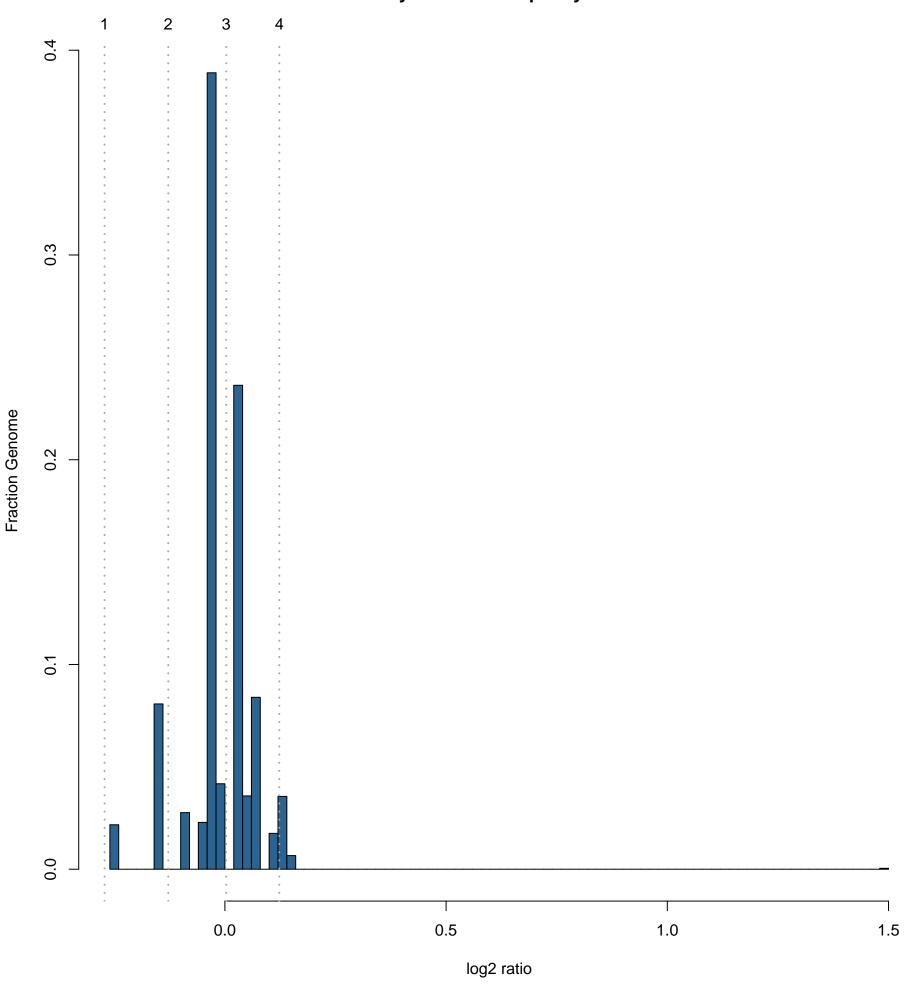


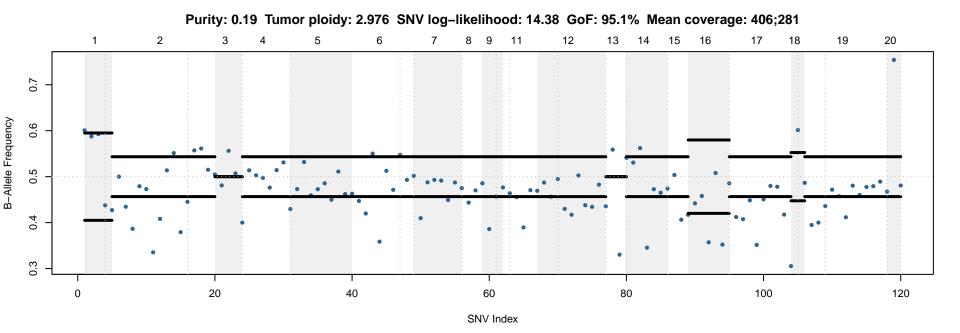




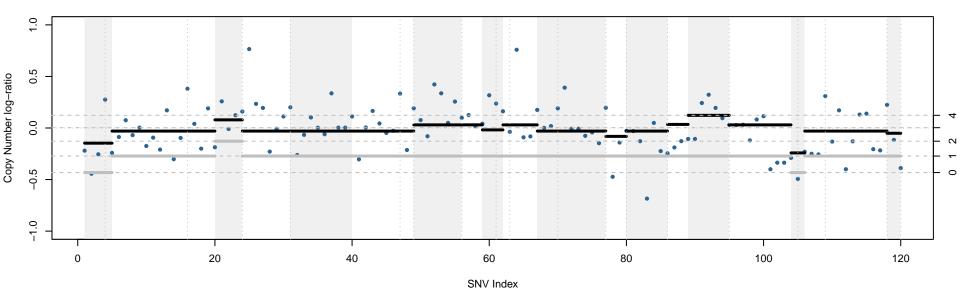


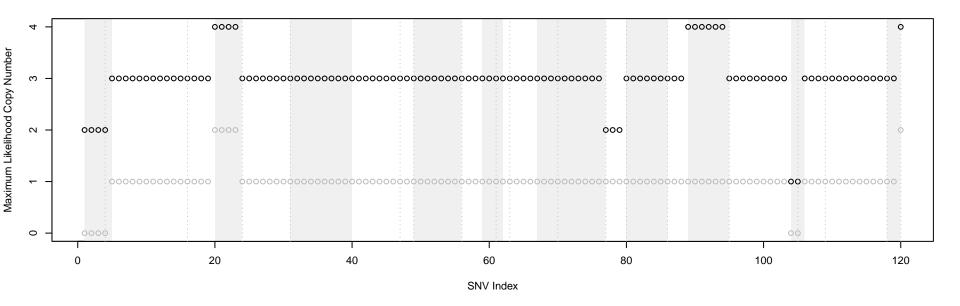
Purity: 0.19 Tumor ploidy: 2.976

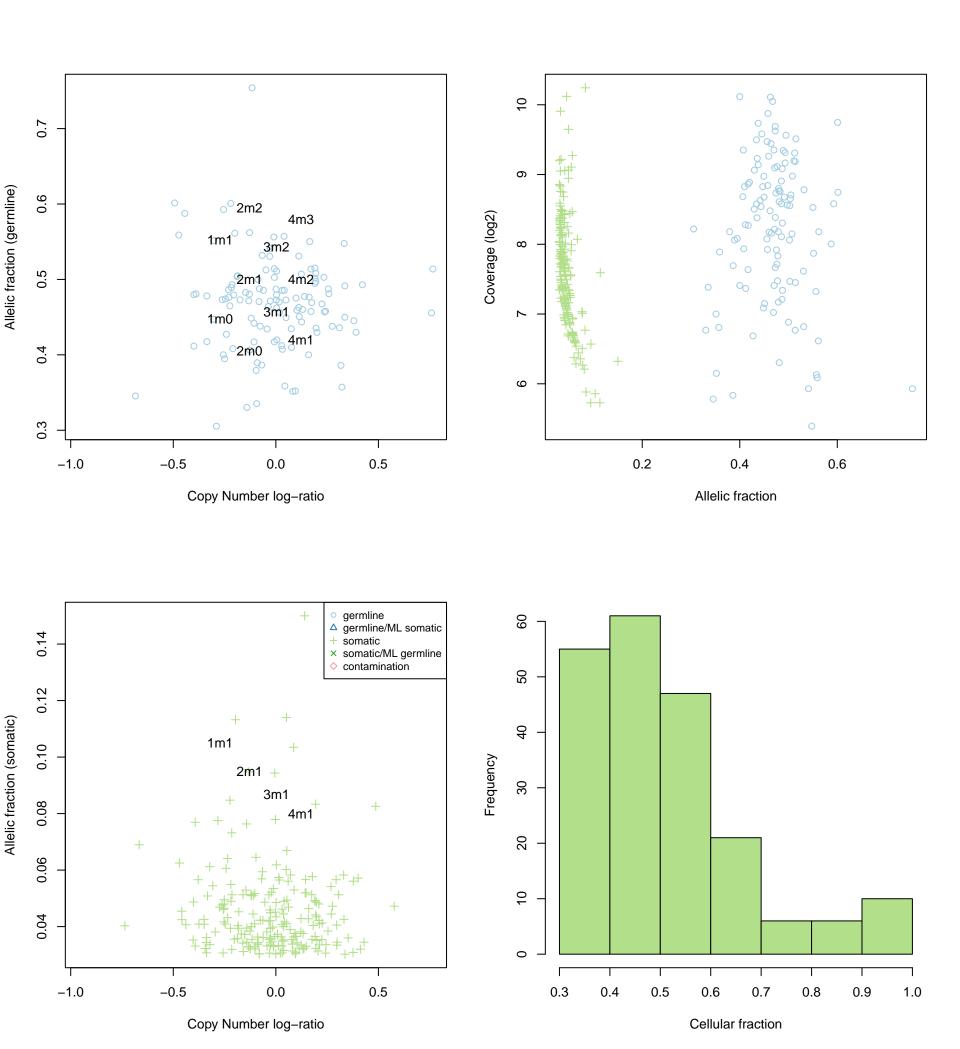




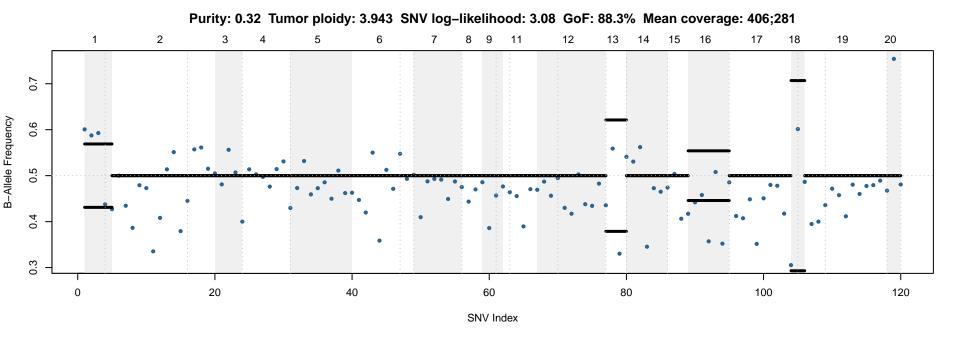




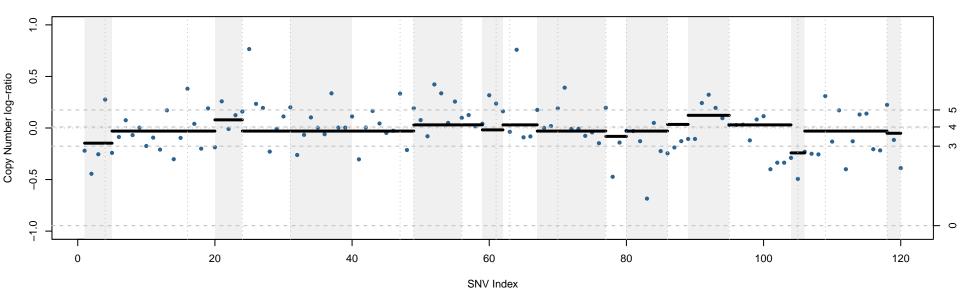


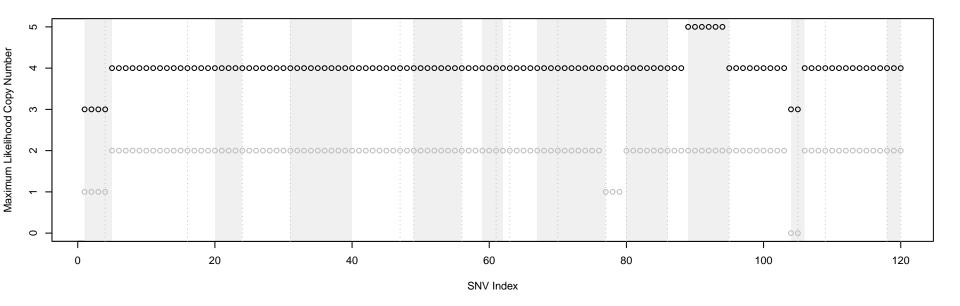


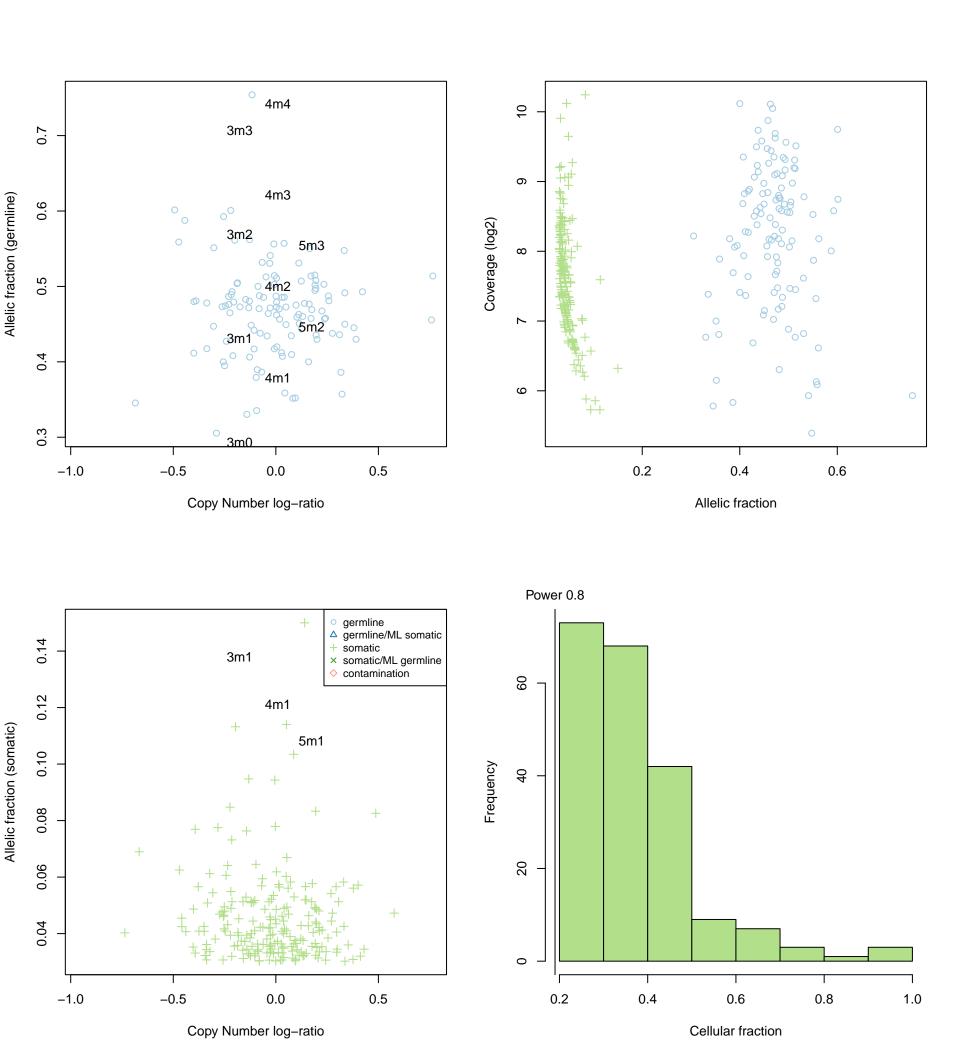
Purity: 0.32 Tumor ploidy: 3.943 3 0 5 0.3 Fraction Genome 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



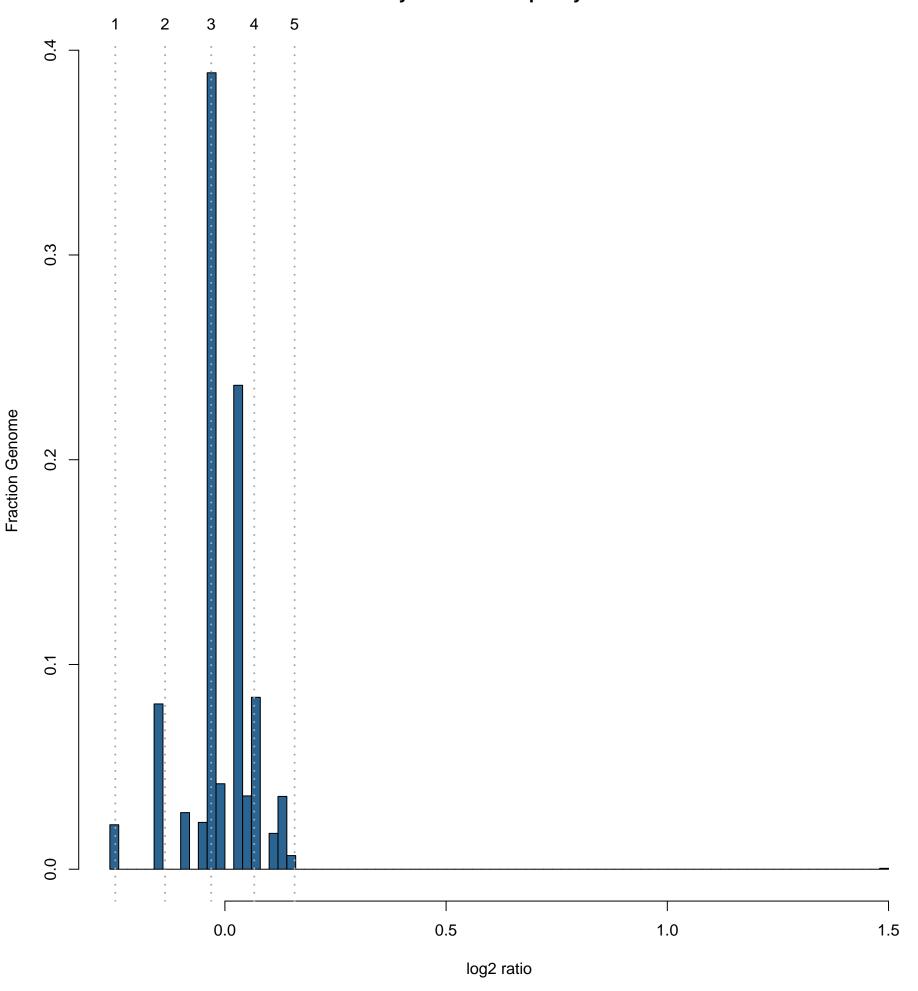
SCNA-fit log-likelihood: -15981.69

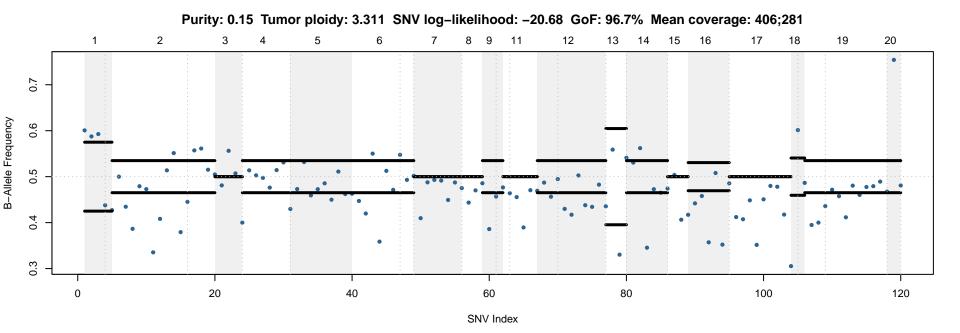




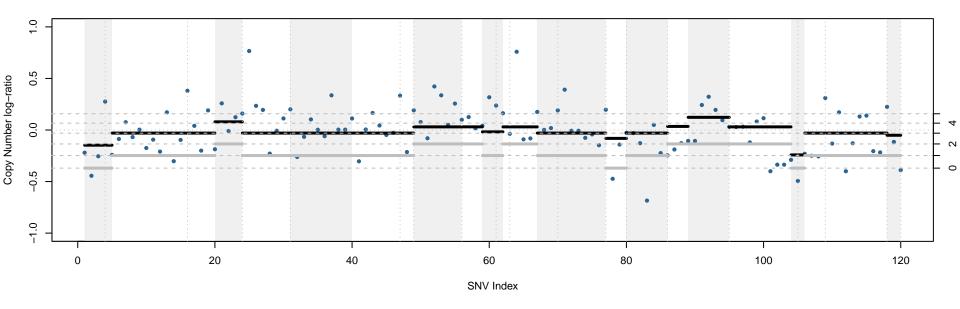


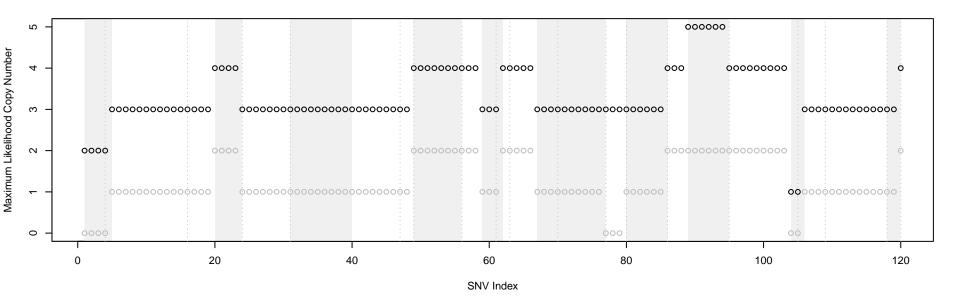
Purity: 0.15 Tumor ploidy: 3.311

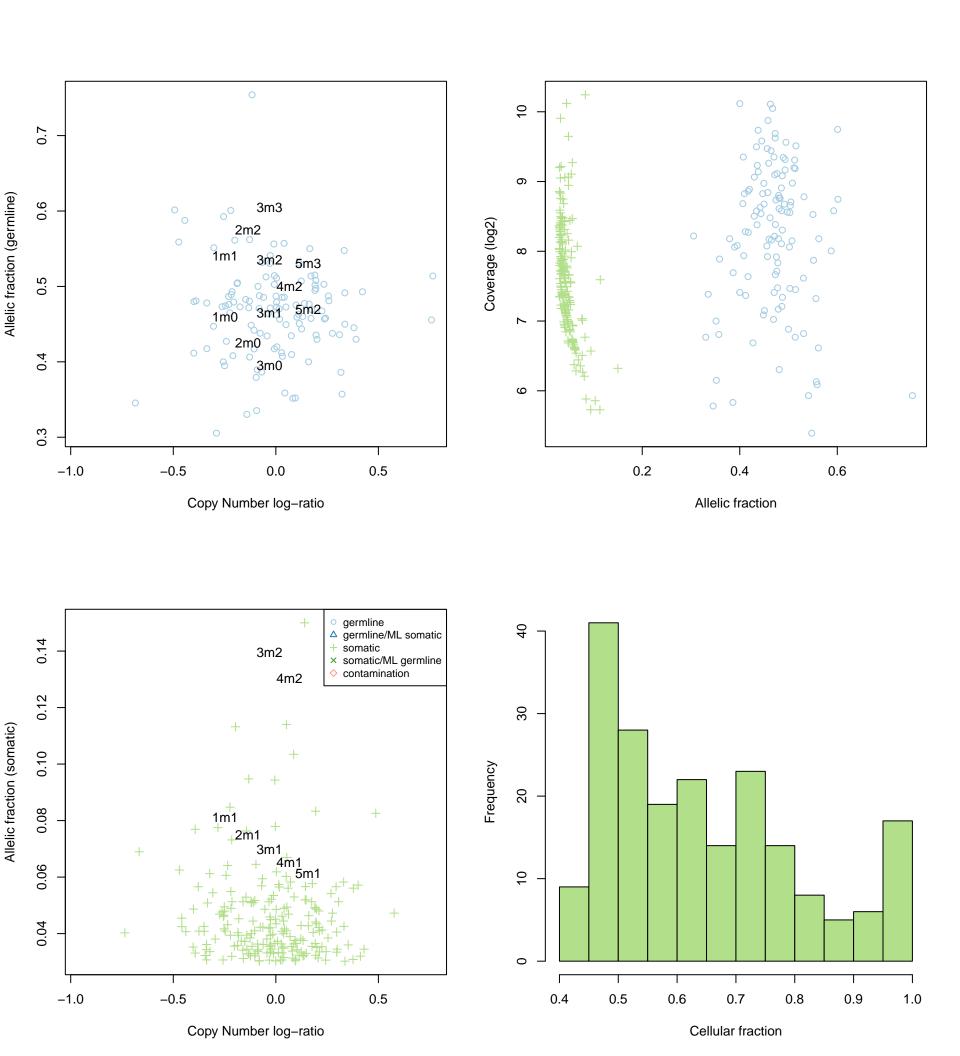




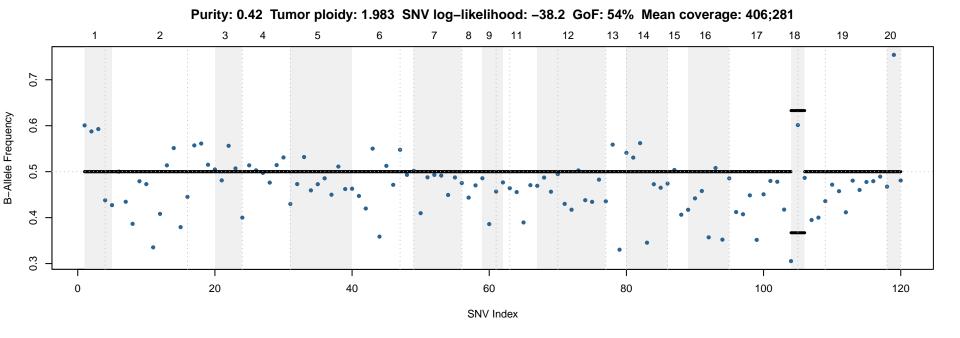
SCNA-fit log-likelihood: -15934.21



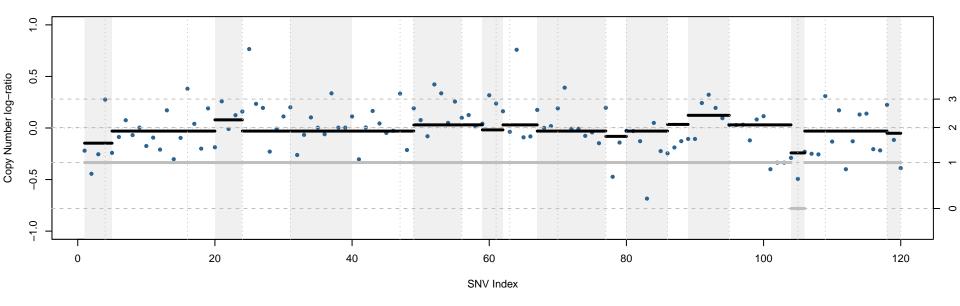


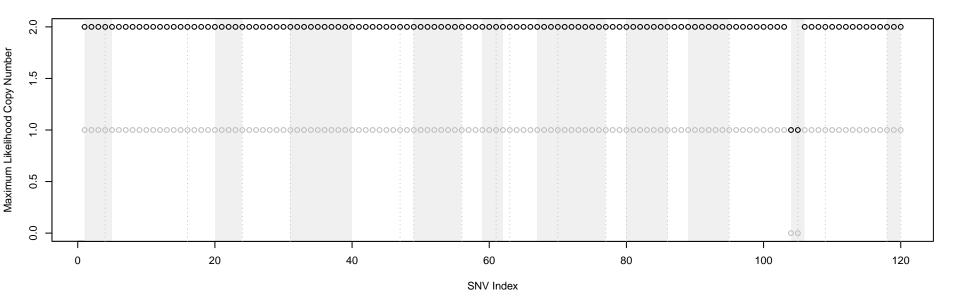


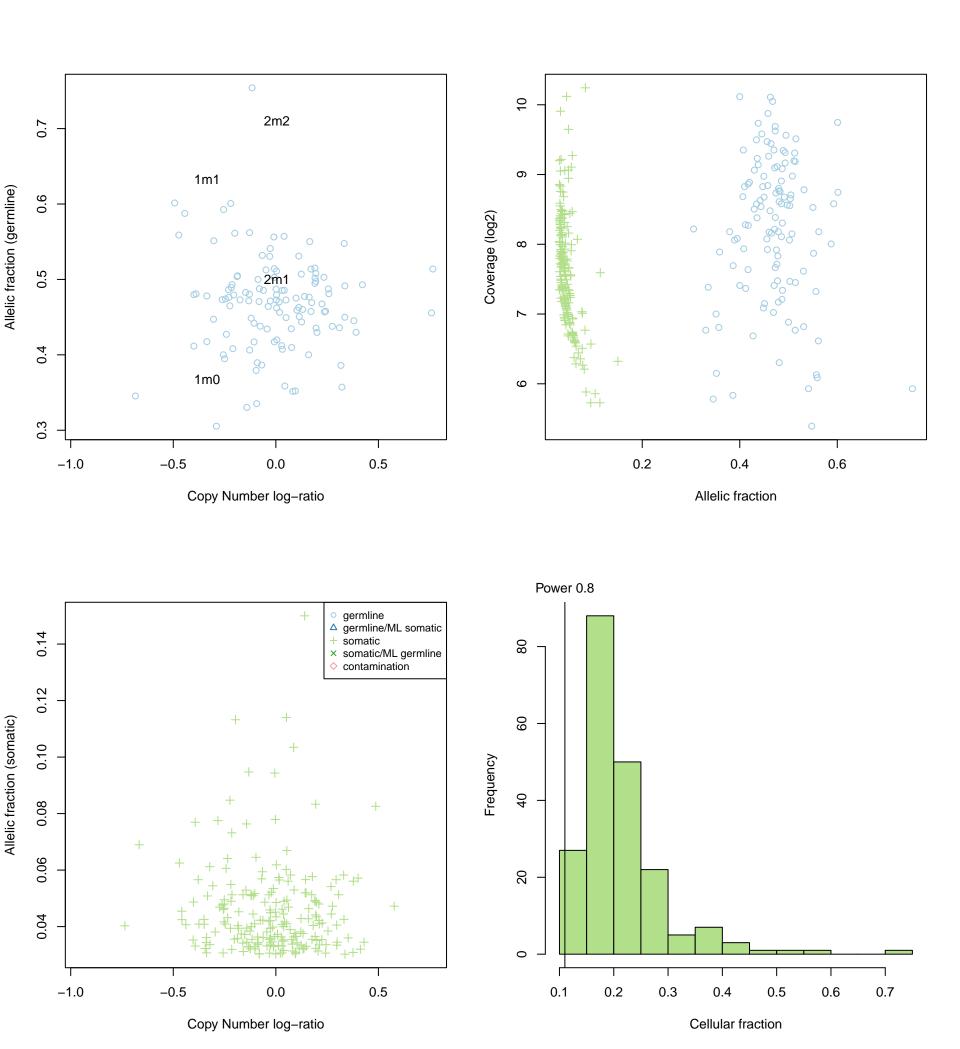
Purity: 0.42 Tumor ploidy: 1.983 0 2 3 0.3 Fraction Genome 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



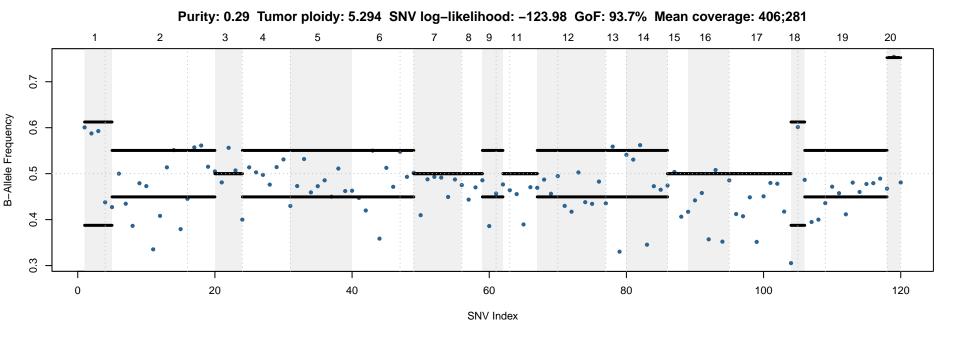
SCNA-fit log-likelihood: -16069.16



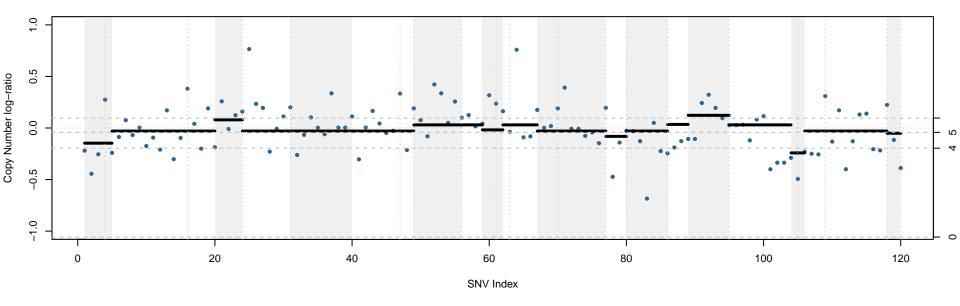


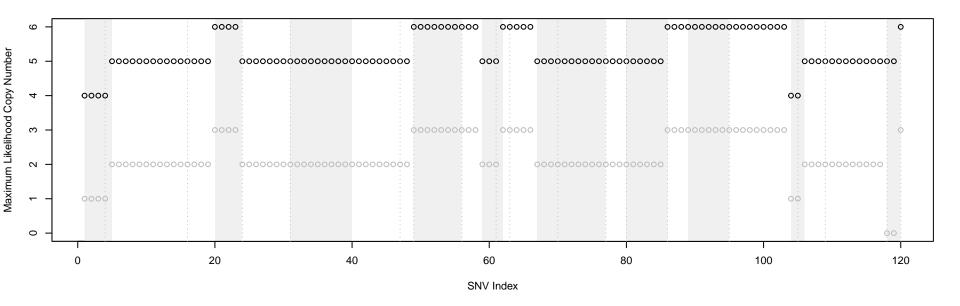


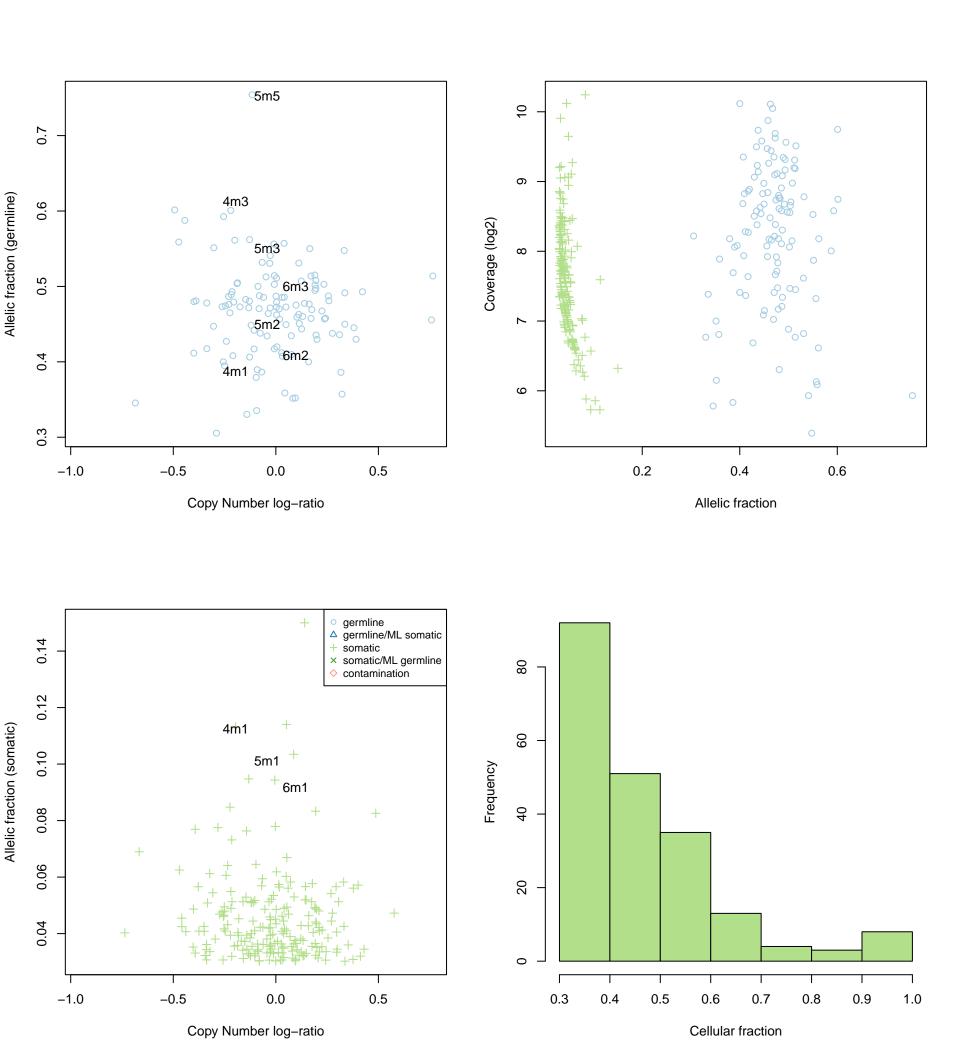
Purity: 0.29 Tumor ploidy: 5.294 0 5 6 0.3 Fraction Genome 0.2 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



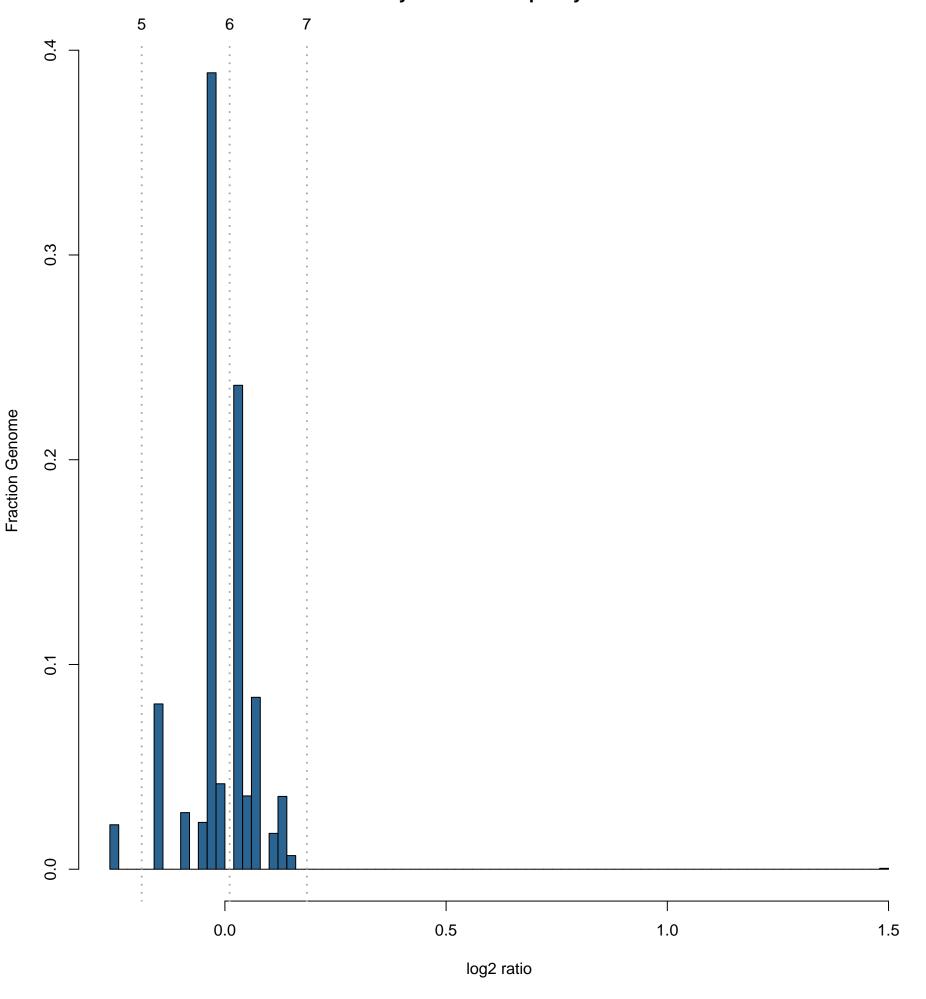
SCNA-fit log-likelihood: -15970.78

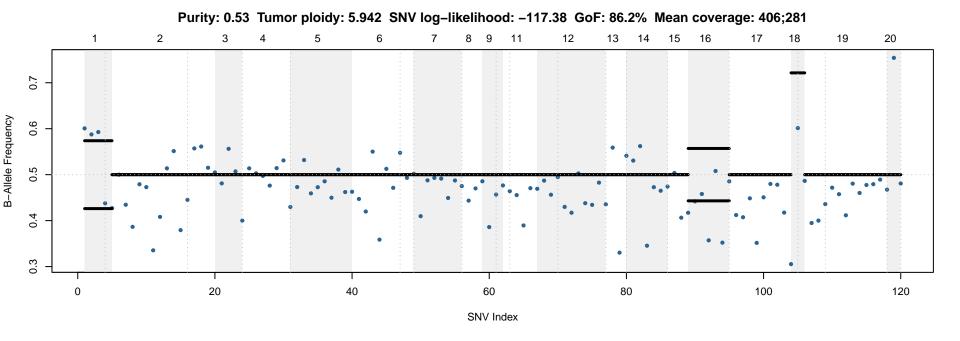




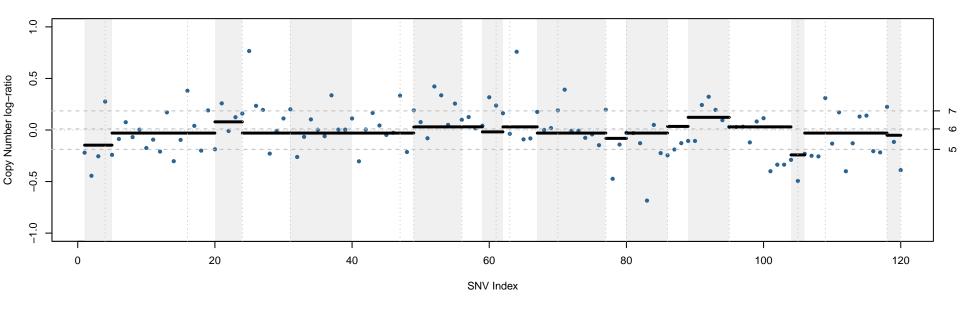


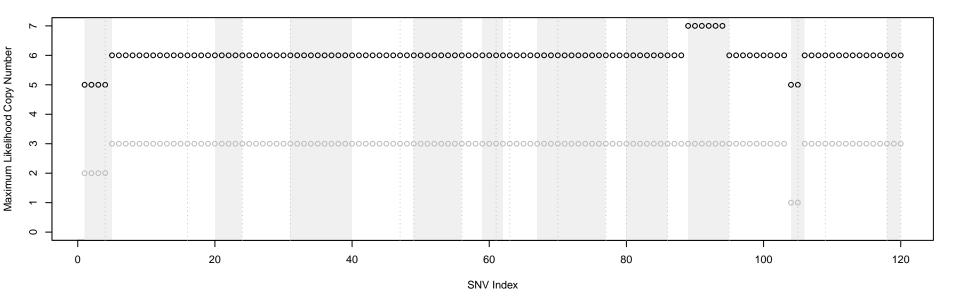
Purity: 0.53 Tumor ploidy: 5.942

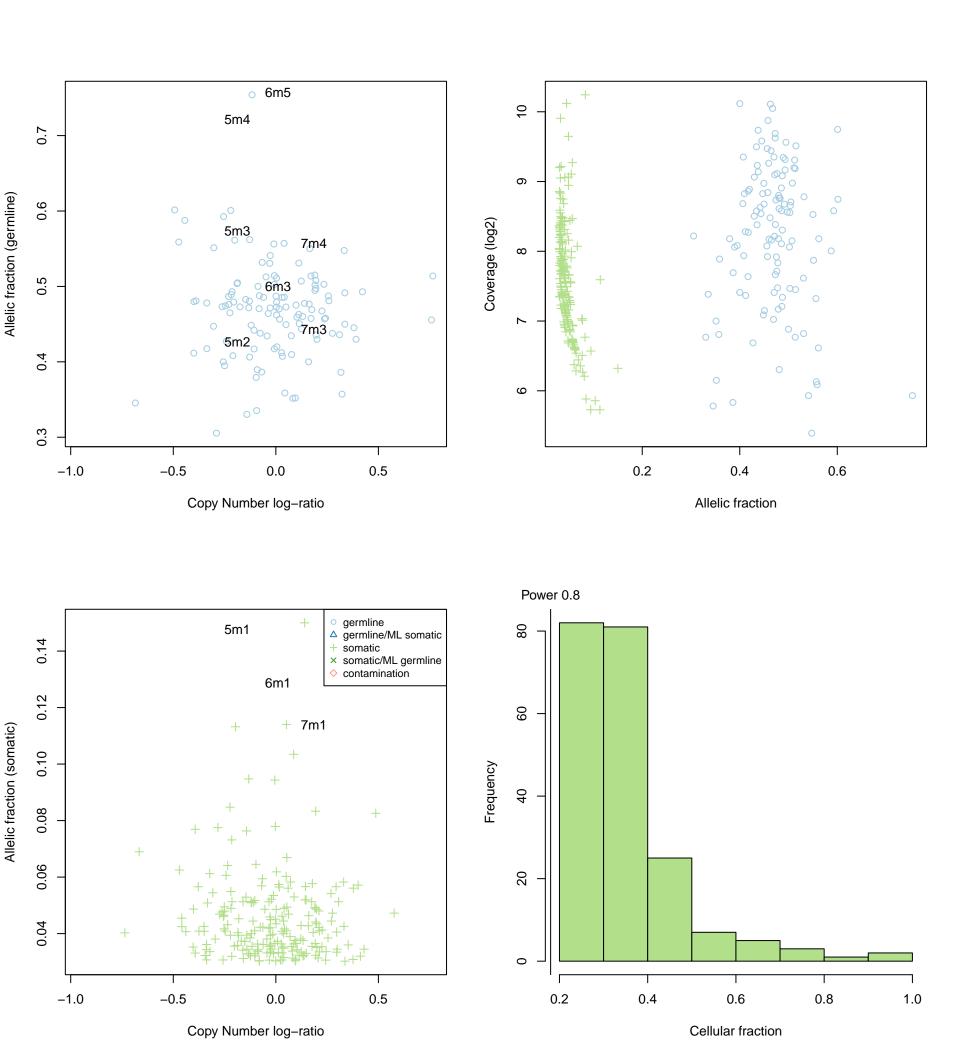




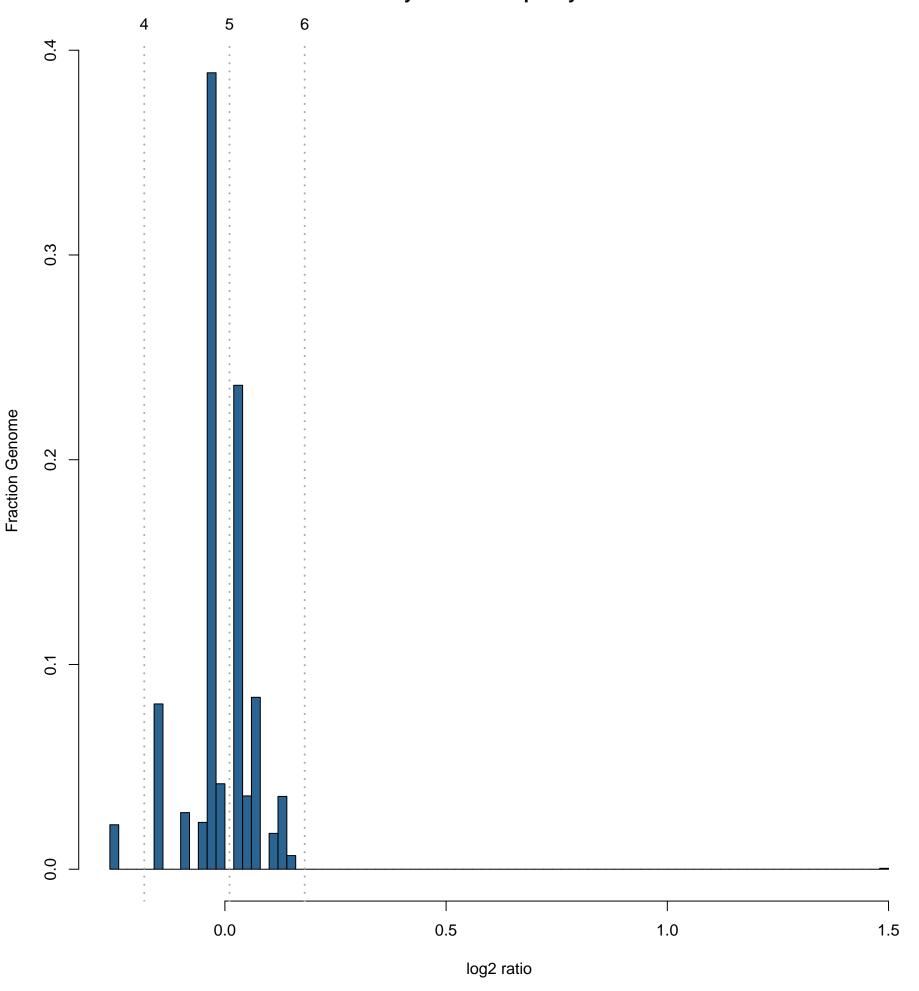
SCNA-fit log-likelihood: -15985.07

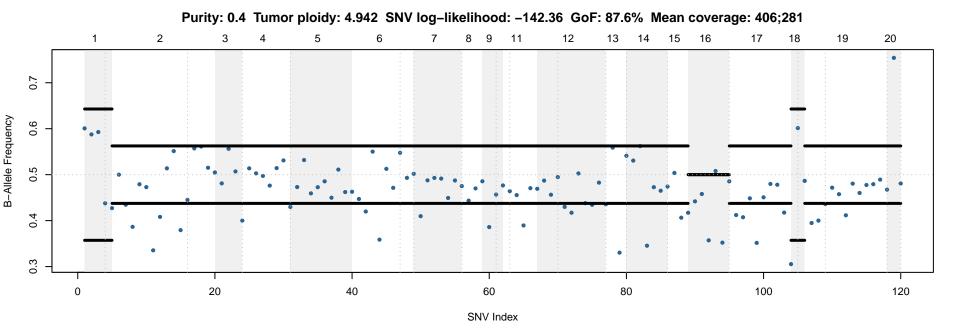




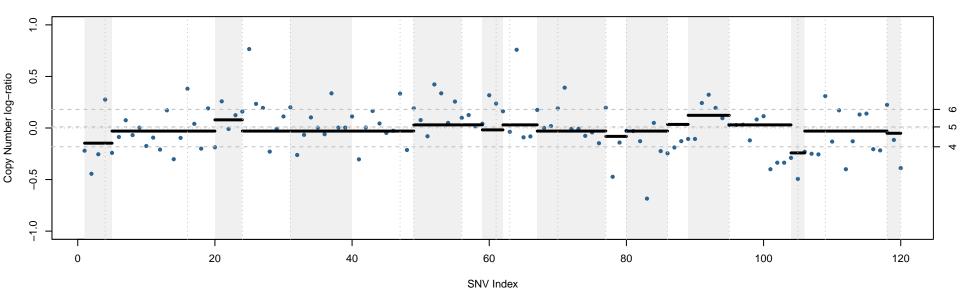


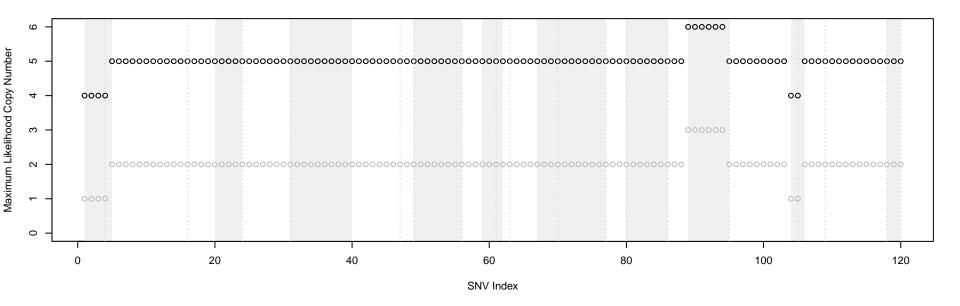
Purity: 0.4 Tumor ploidy: 4.942

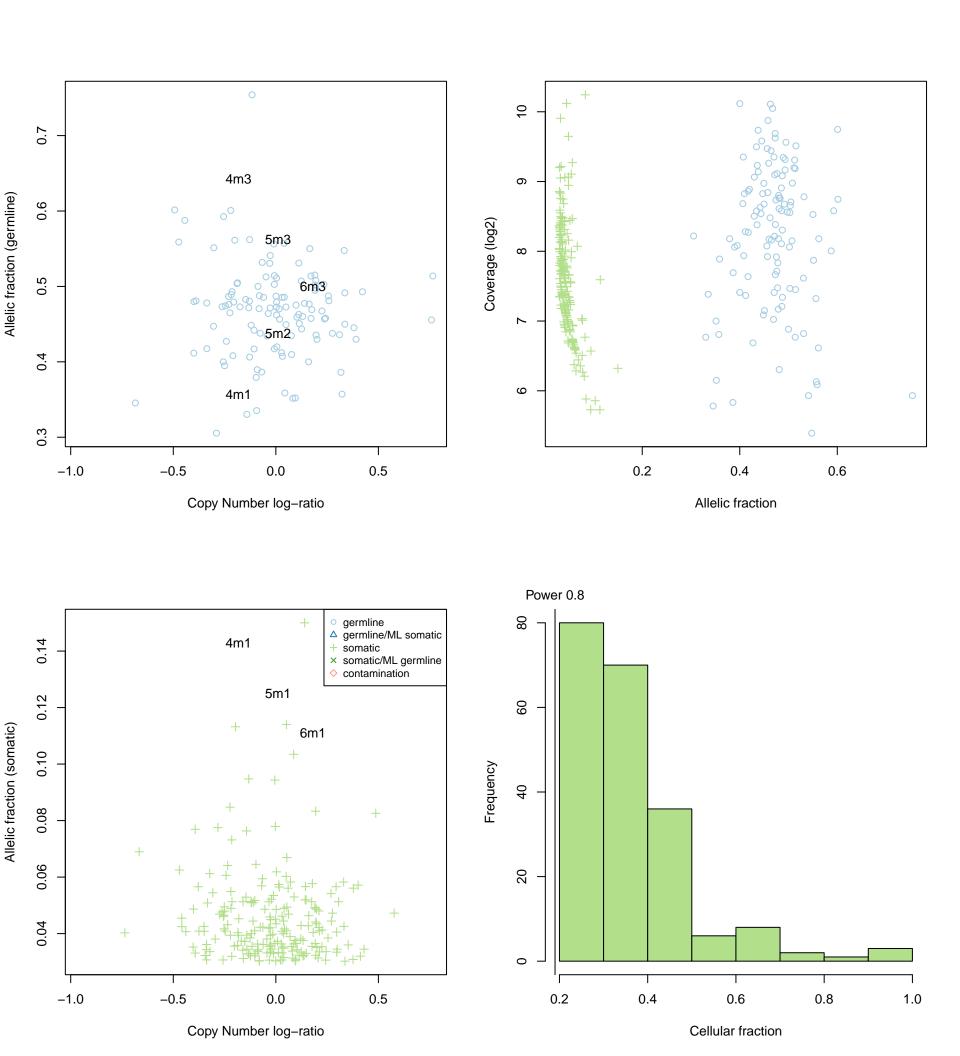




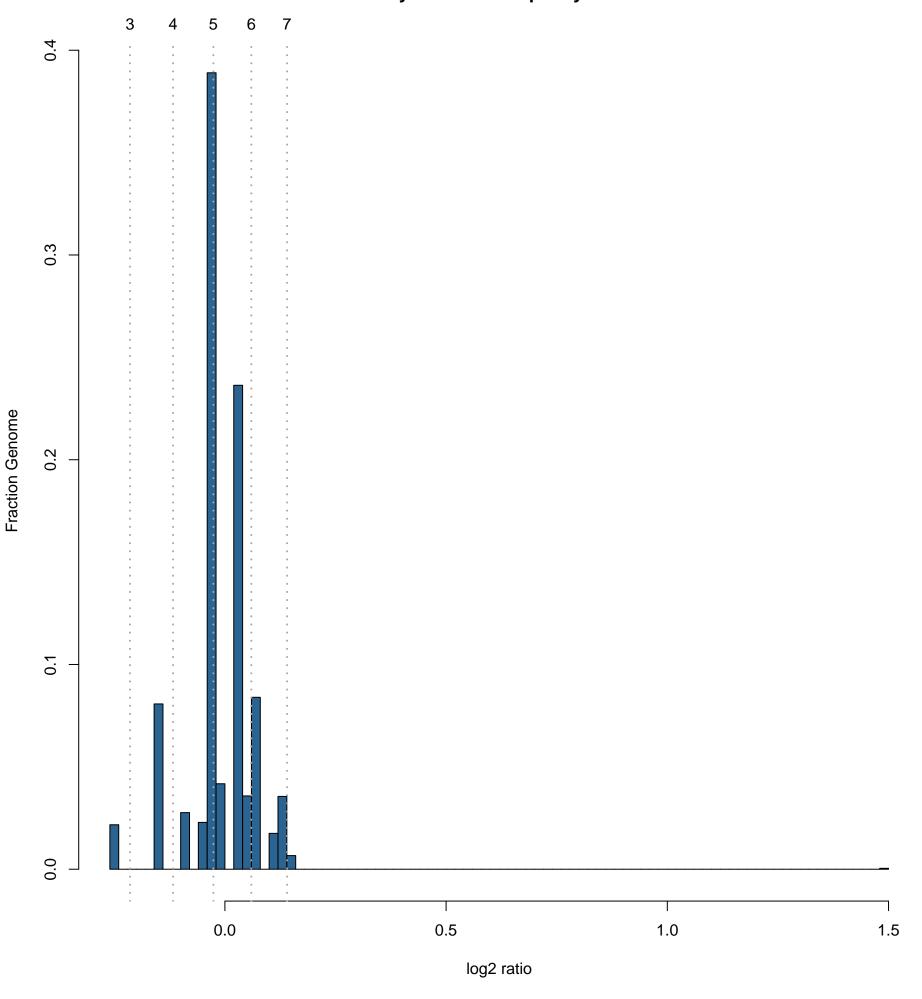
SCNA-fit log-likelihood: -15983.2

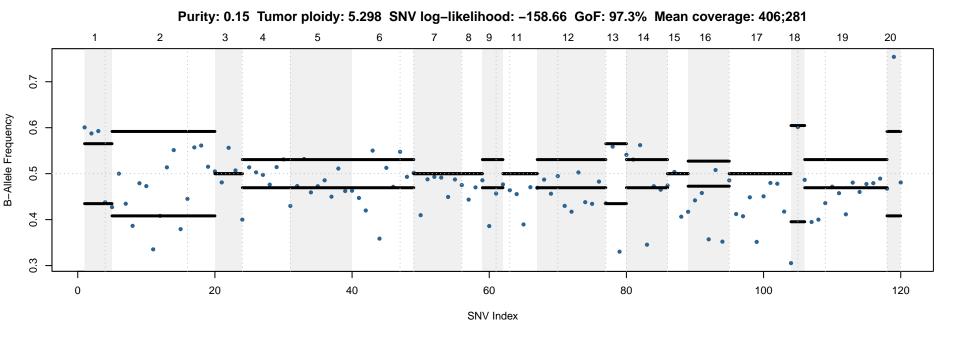




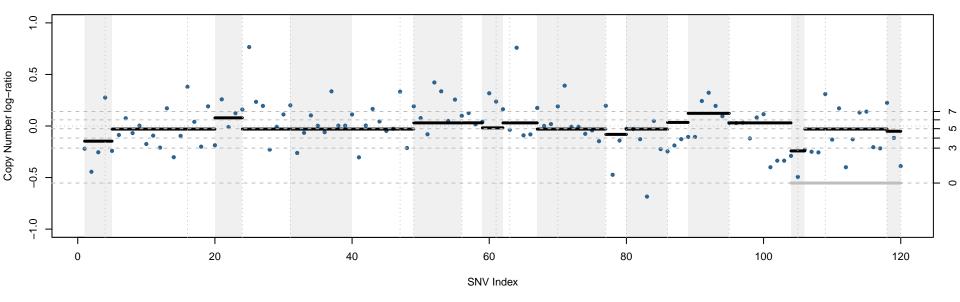


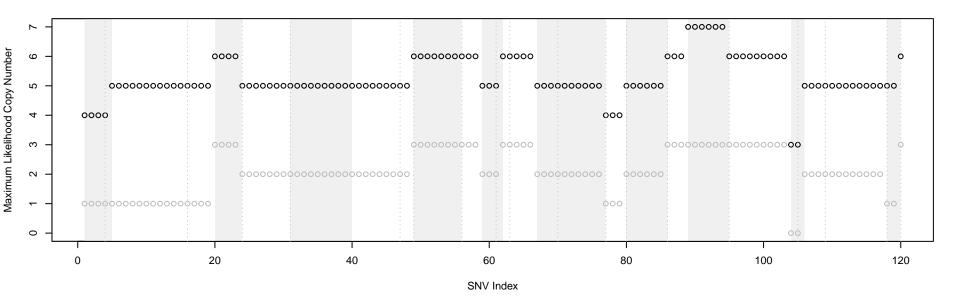
Purity: 0.15 Tumor ploidy: 5.298

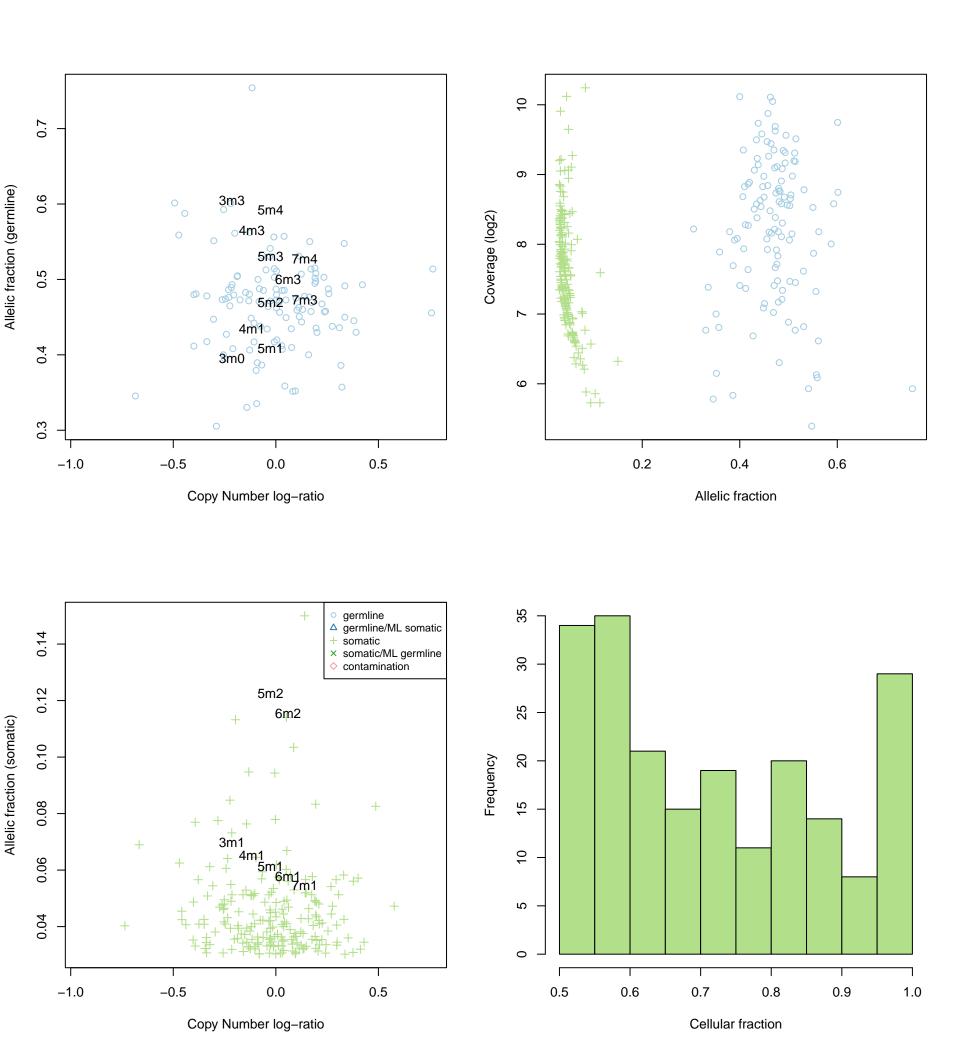




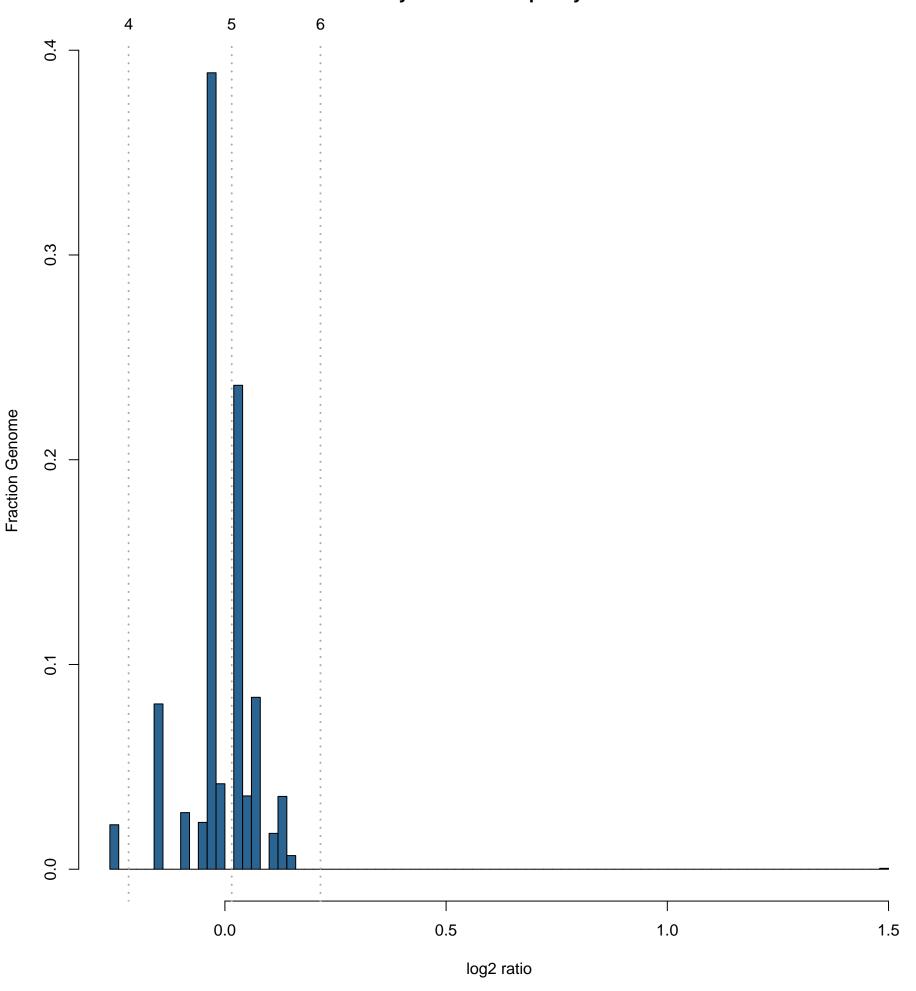
SCNA-fit log-likelihood: -15932.11

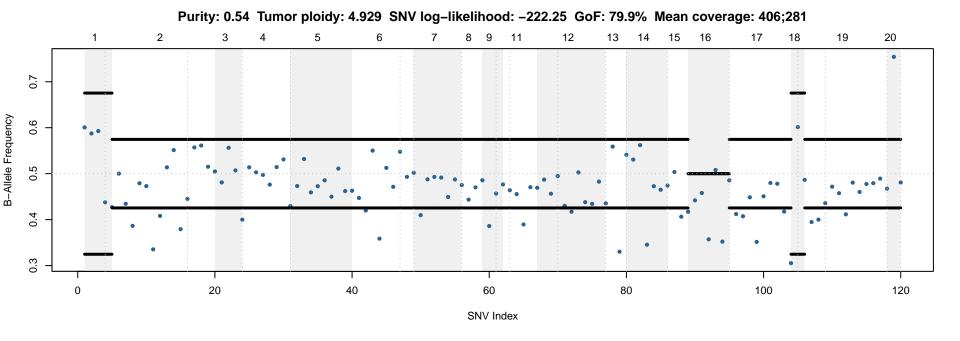




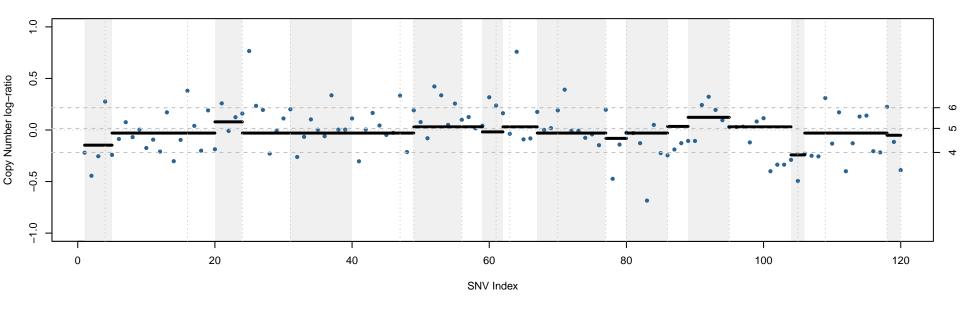


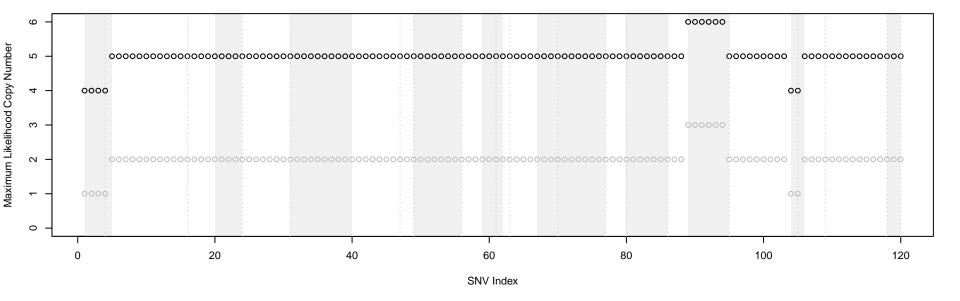
Purity: 0.54 Tumor ploidy: 4.929

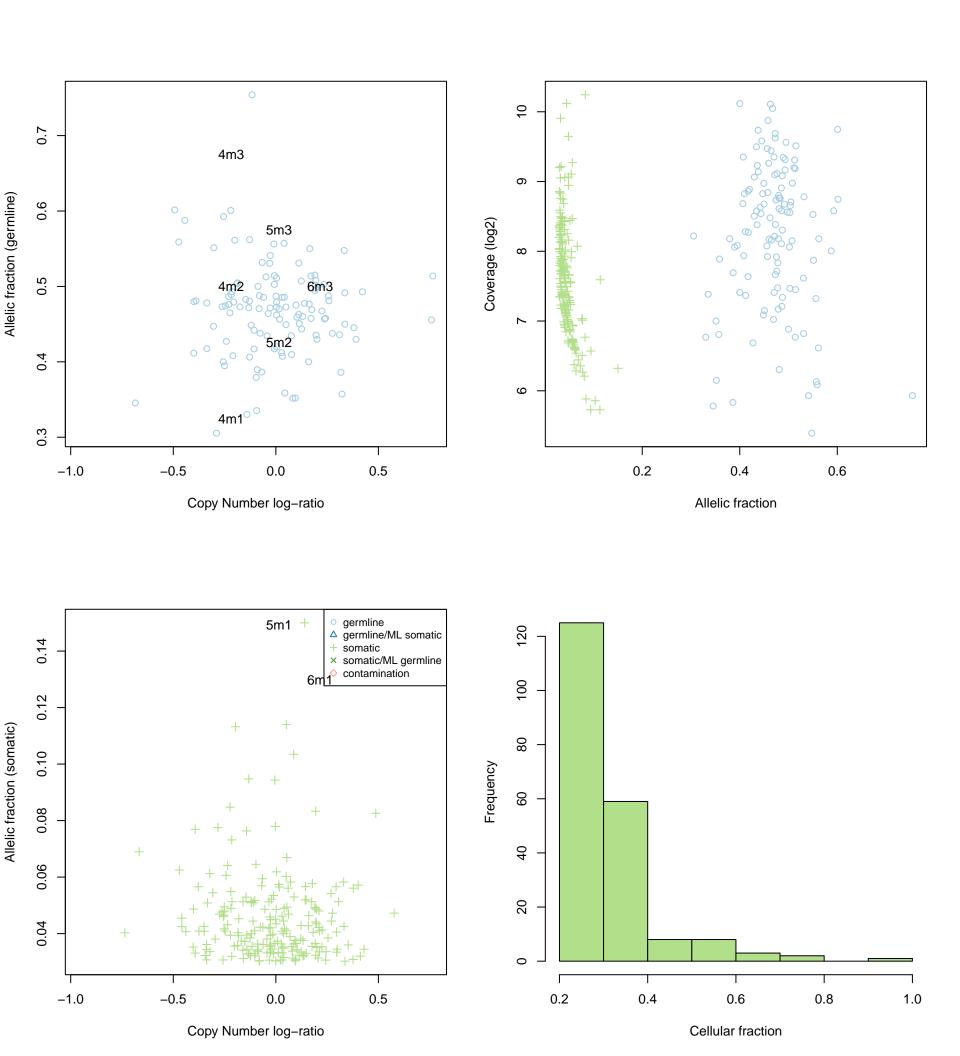




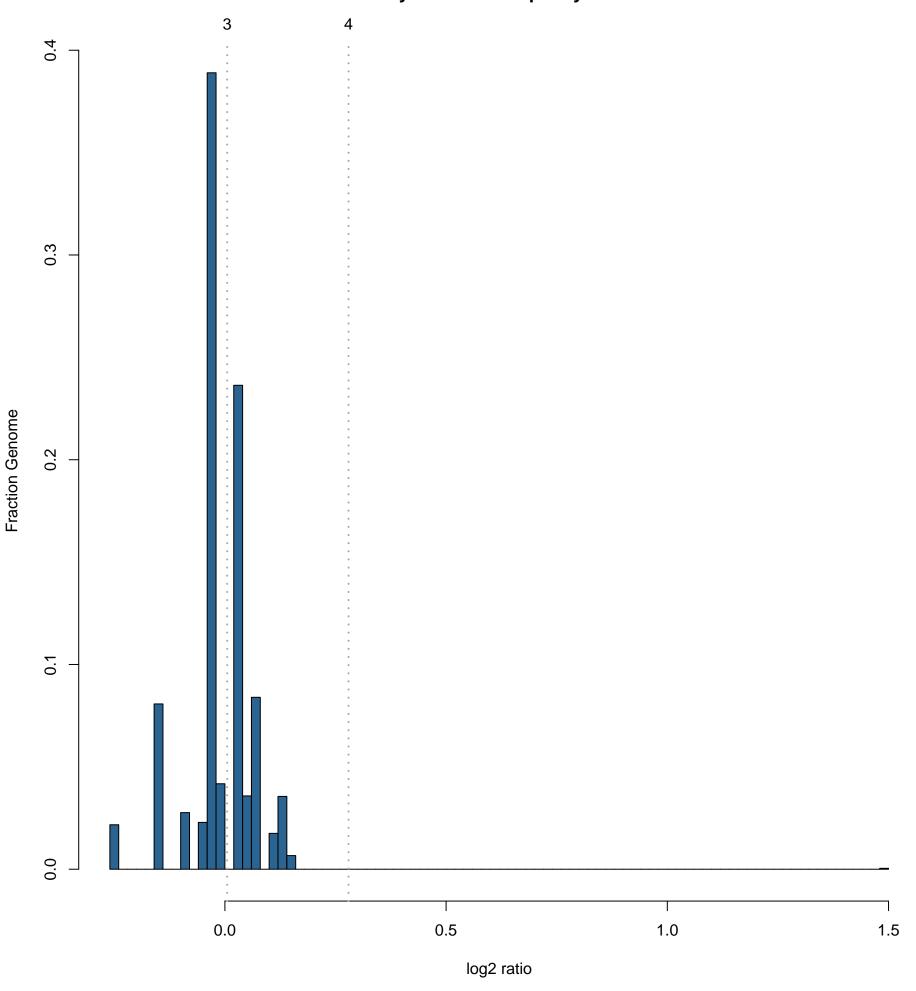
SCNA-fit log-likelihood: -16003.57

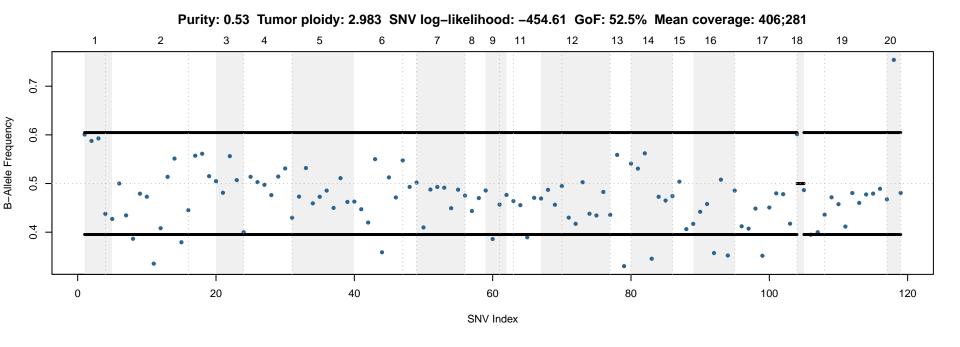




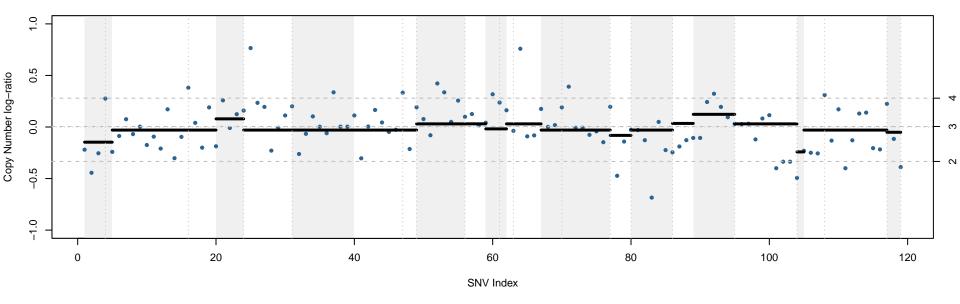


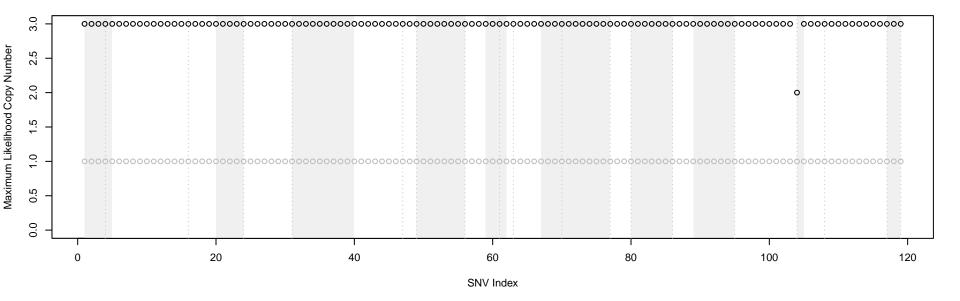
Purity: 0.53 Tumor ploidy: 2.983

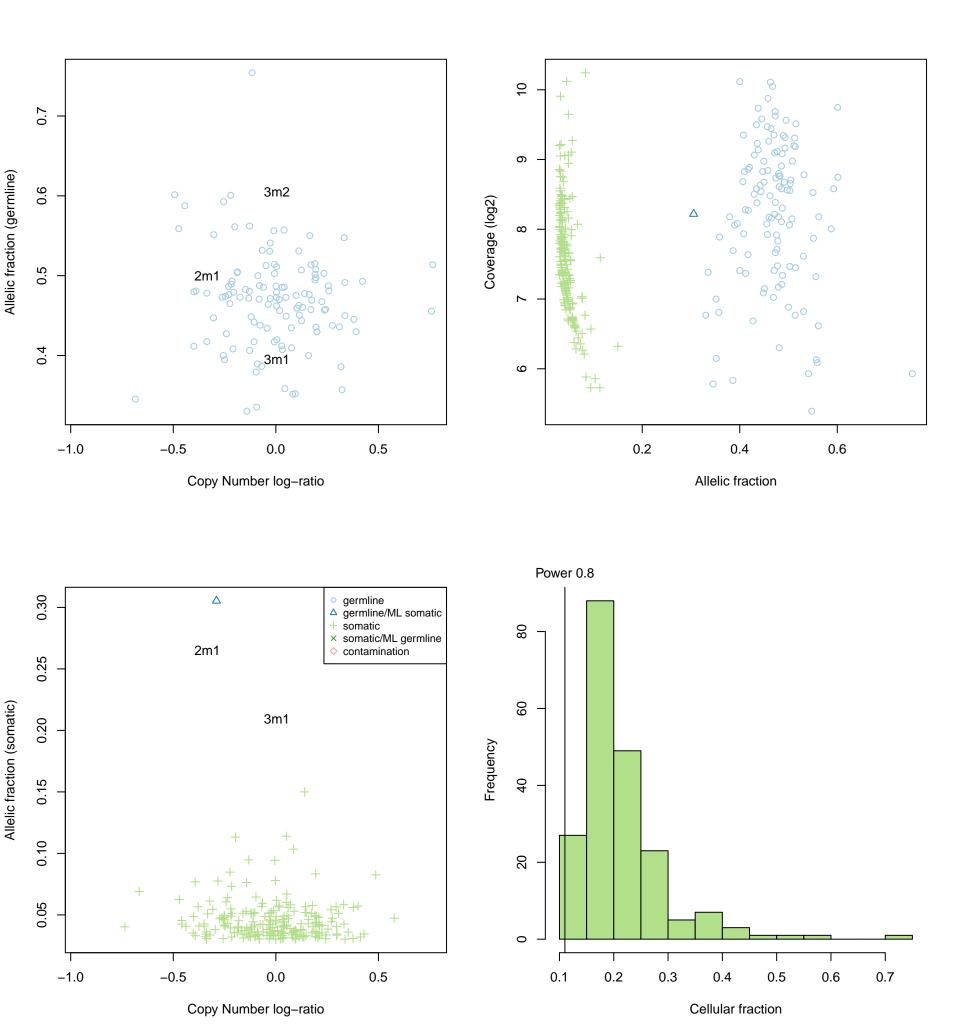




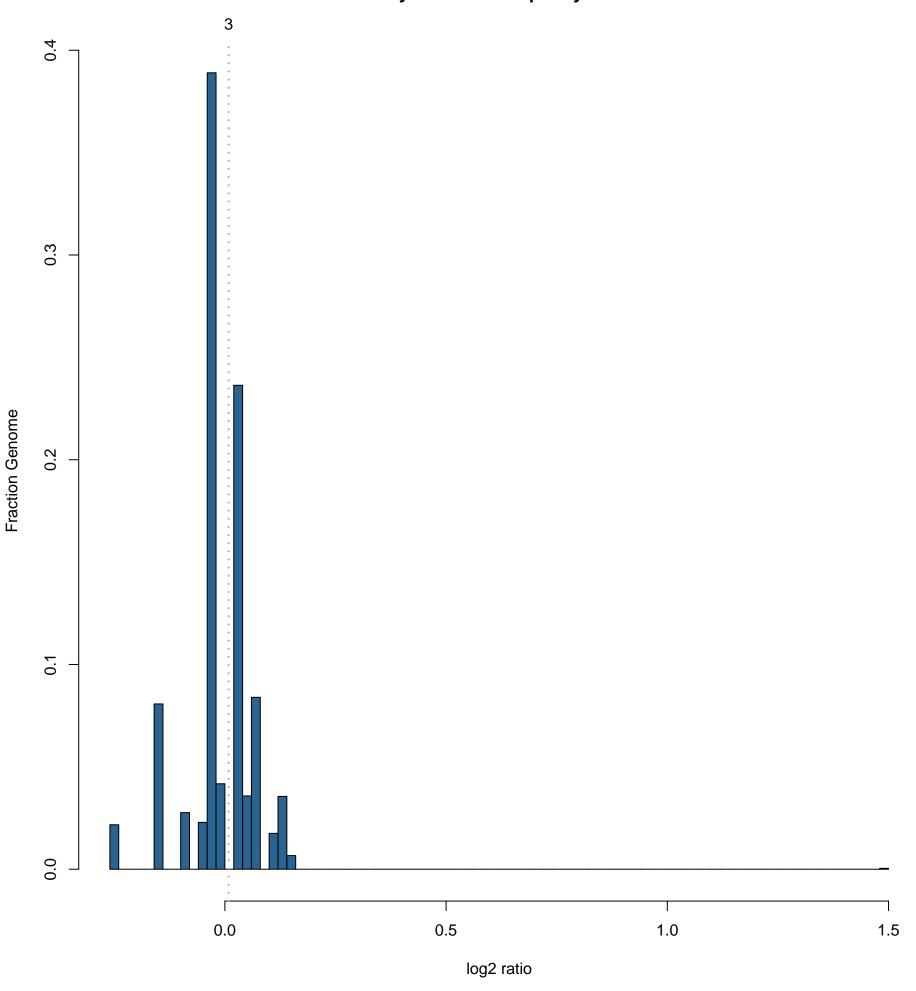
SCNA-fit log-likelihood: -16068.92

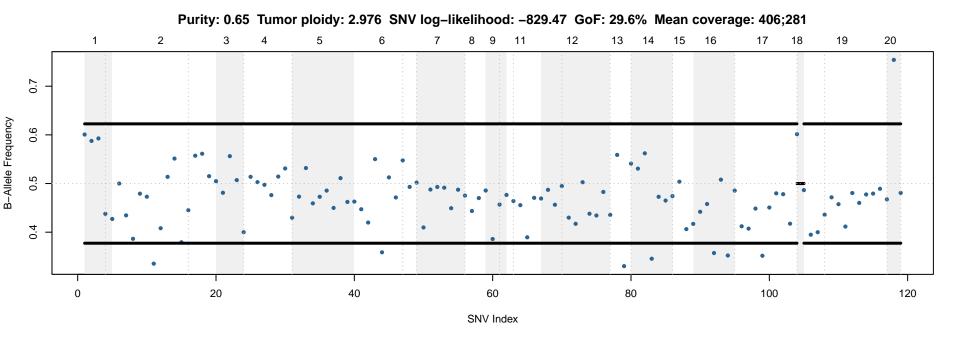






Purity: 0.65 Tumor ploidy: 2.976





SCNA-fit log-likelihood: -16085.13

