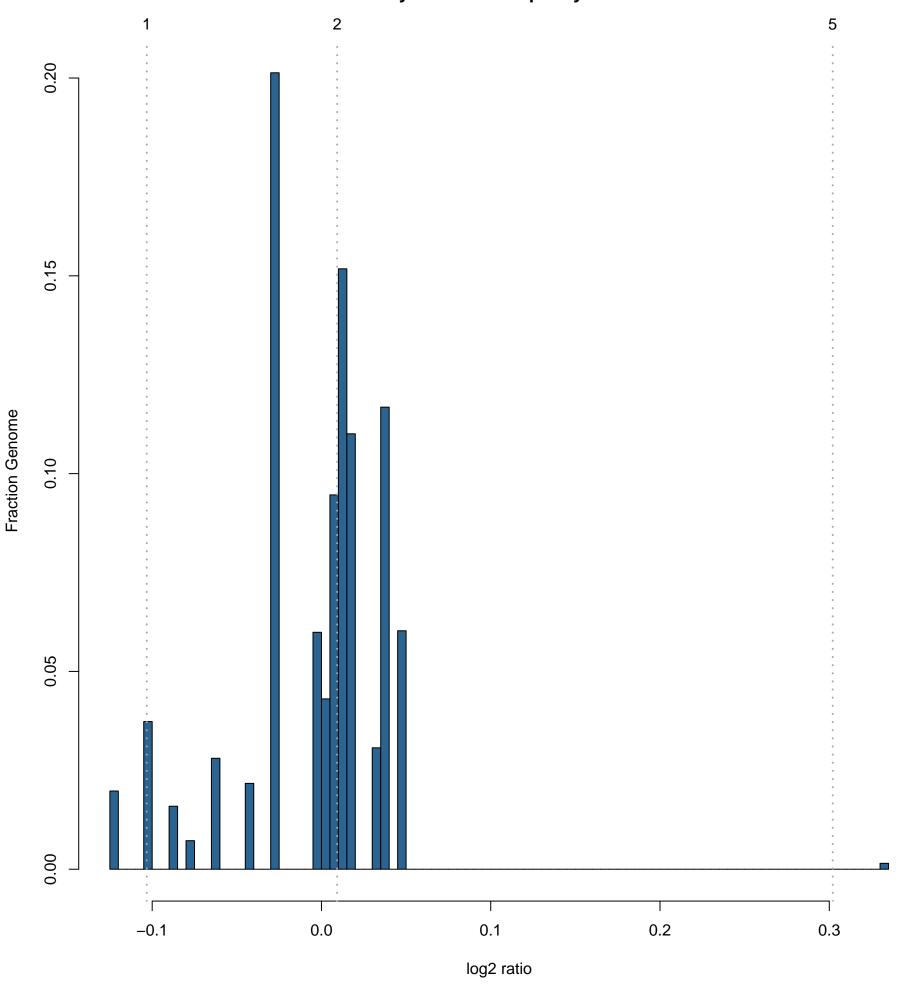
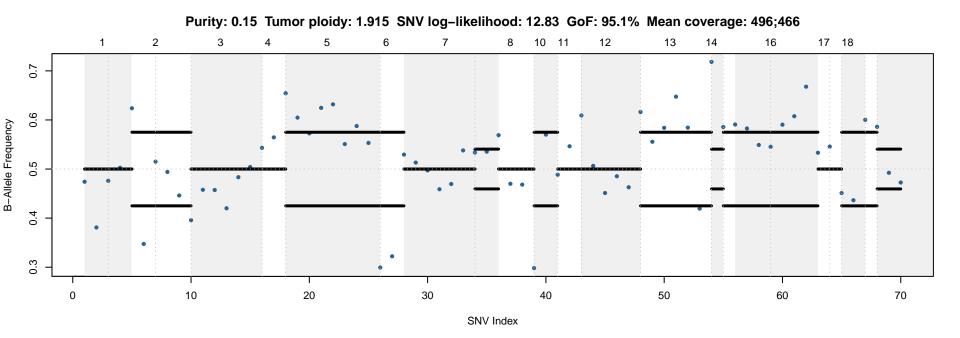
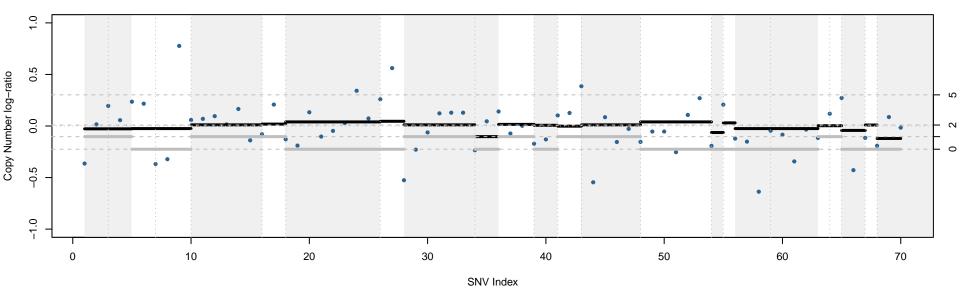
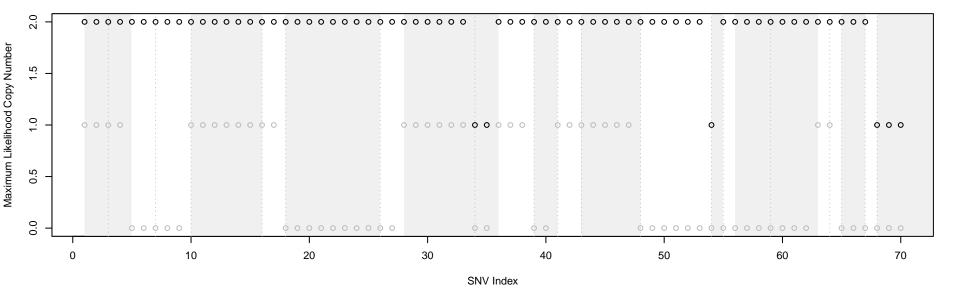
Purity: 0.15 Tumor ploidy: 1.915

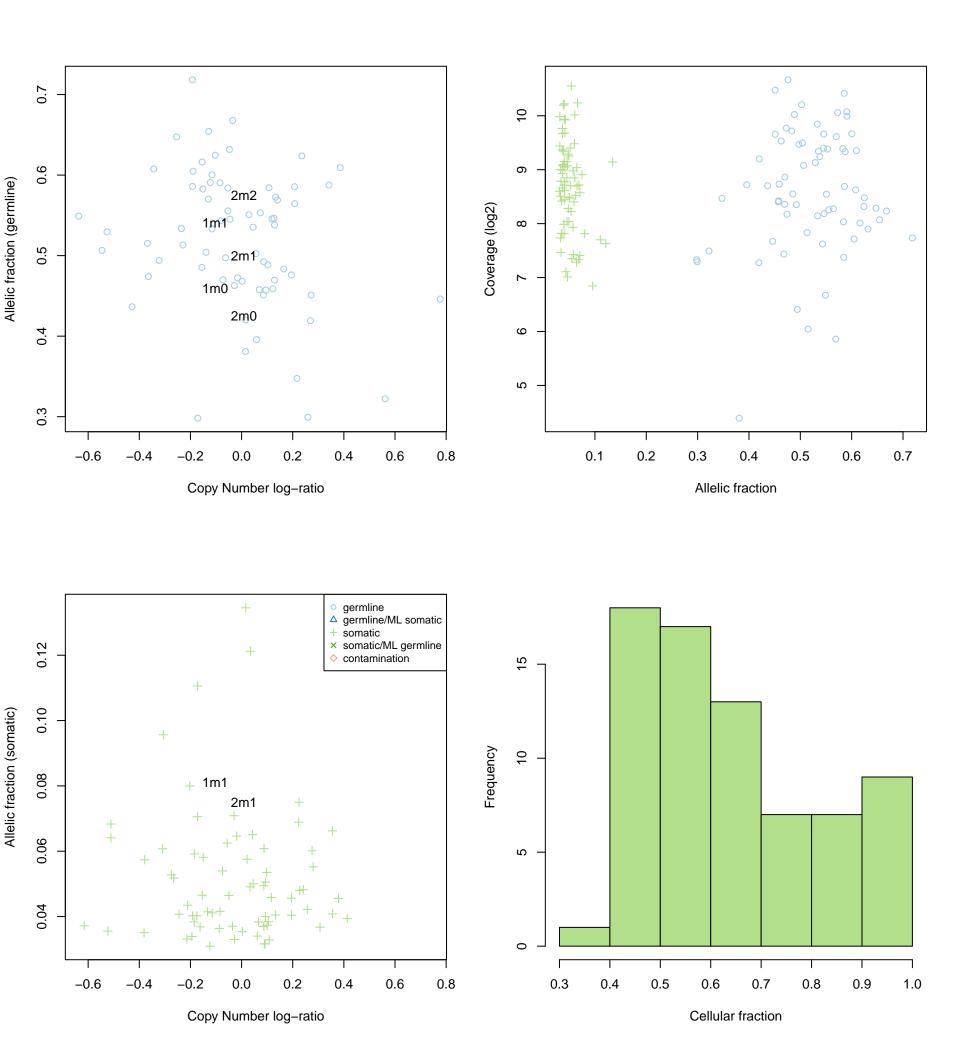




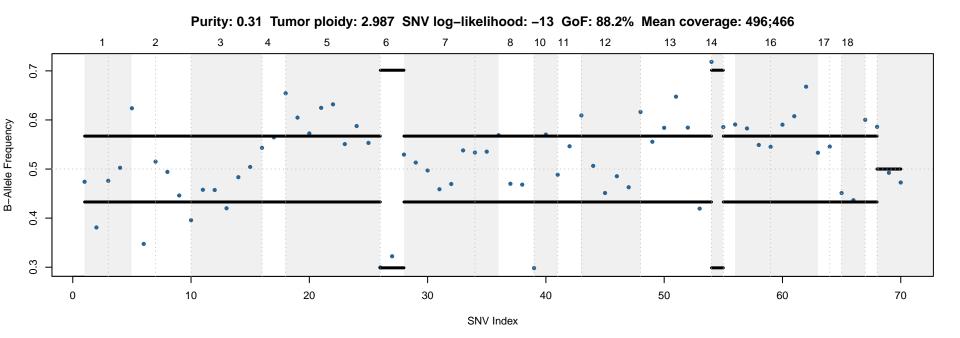
SCNA-fit log-likelihood: -9281.51



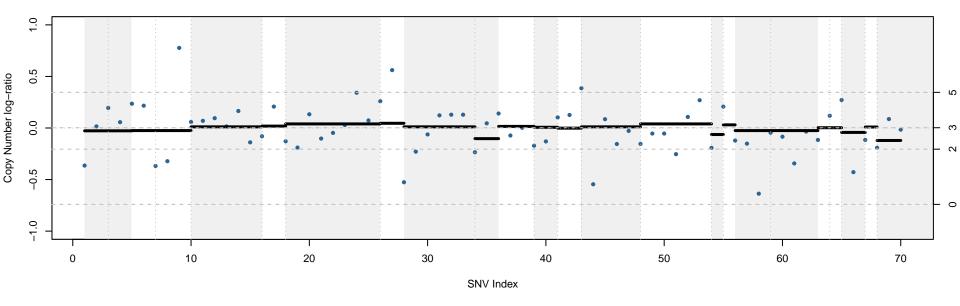


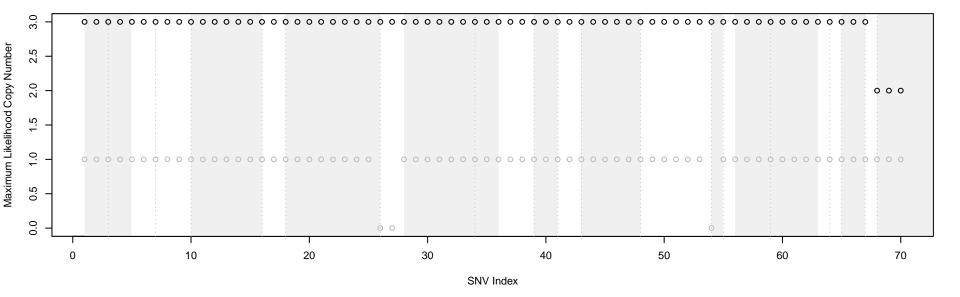


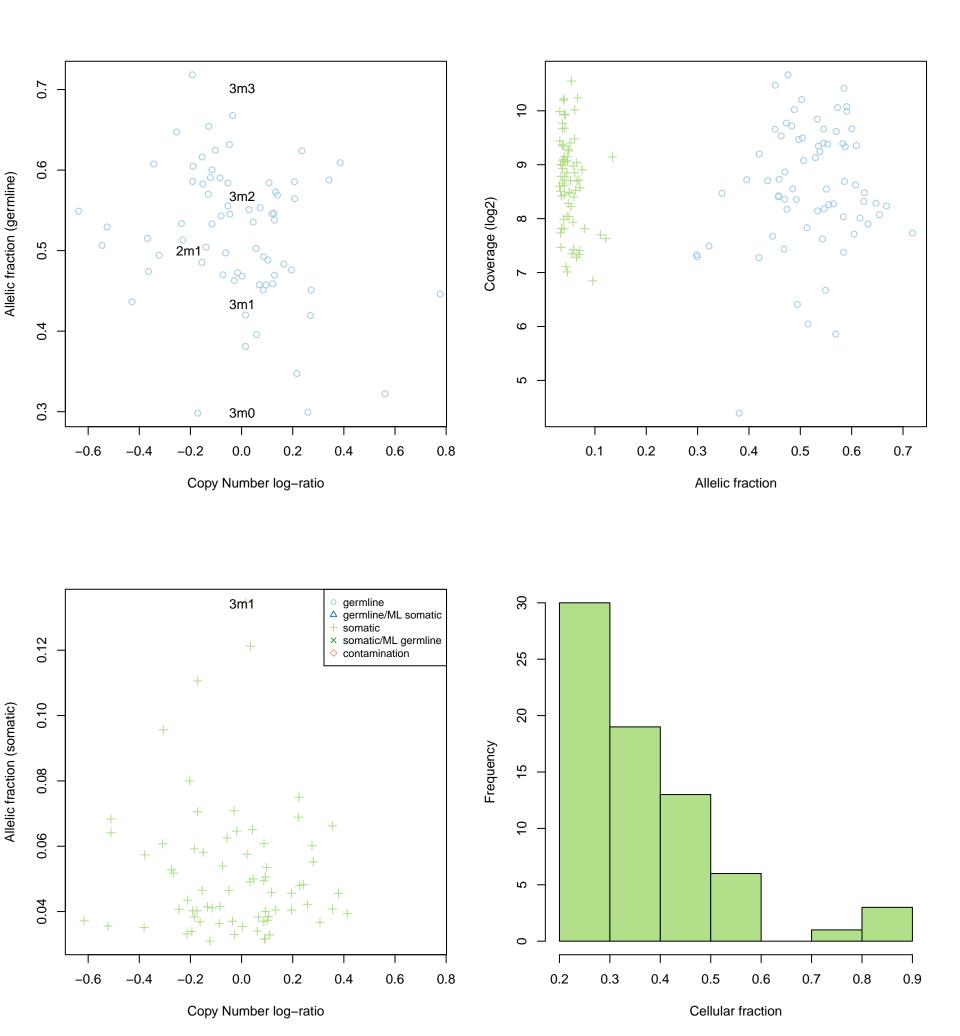
Purity: 0.31 Tumor ploidy: 2.987 5 3 Fraction Genome 0.1 0.0 -1.0 -0.5 0.0 log2 ratio



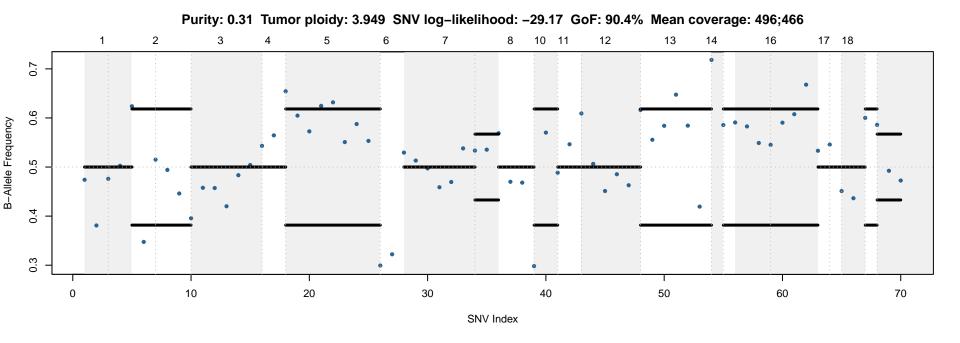
SCNA-fit log-likelihood: -9337.45



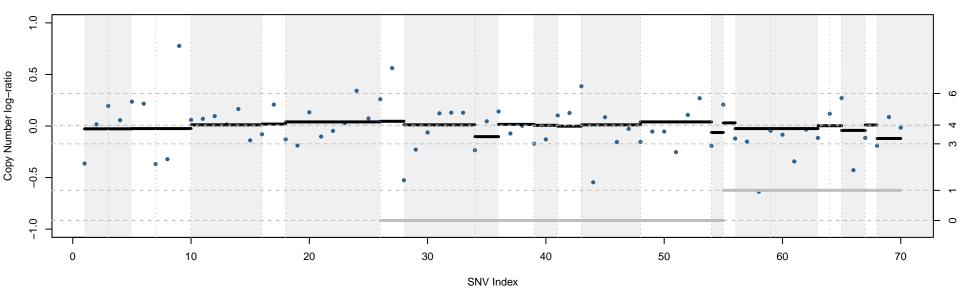


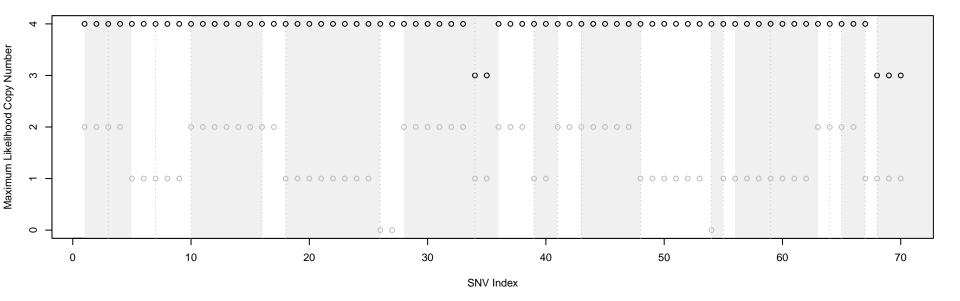


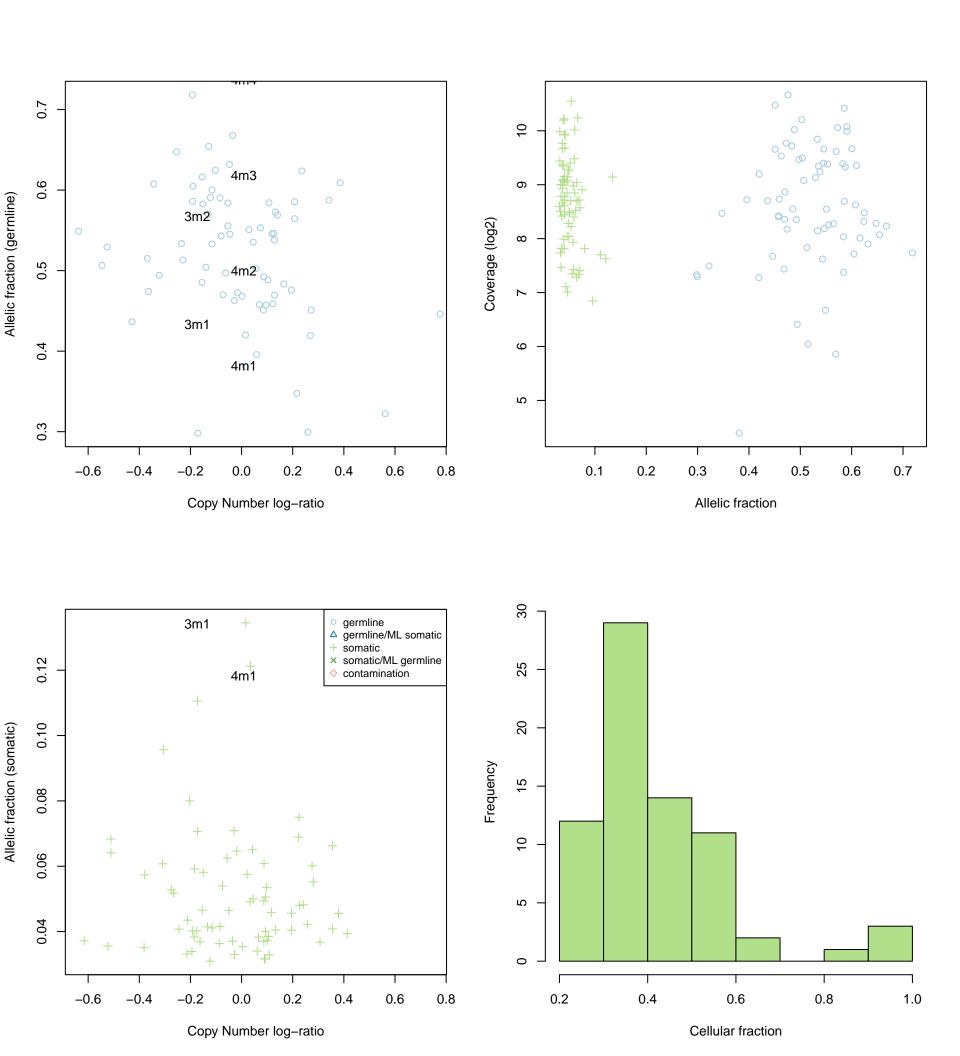
Purity: 0.31 Tumor ploidy: 3.949 3 0 6 Fraction Genome 0.1 0.0 -1.0 -0.5 0.0 log2 ratio



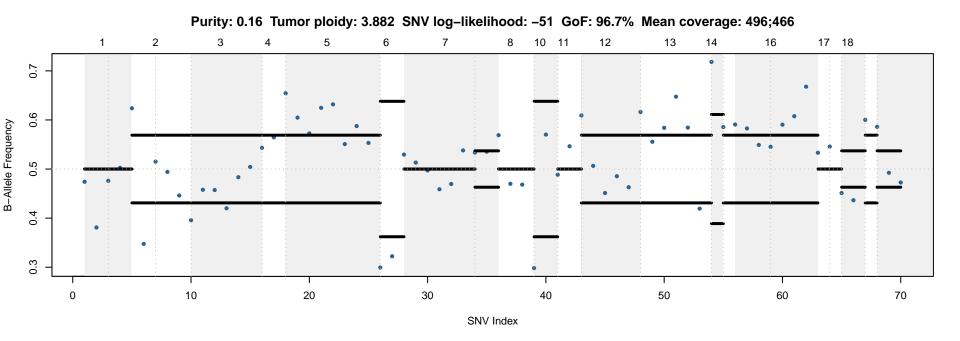
SCNA-fit log-likelihood: -9313.16



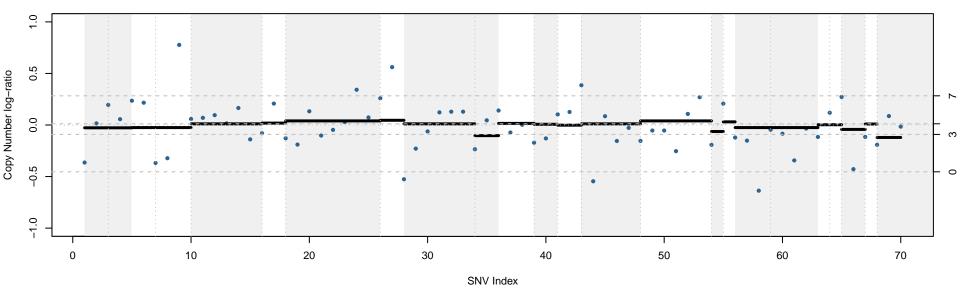


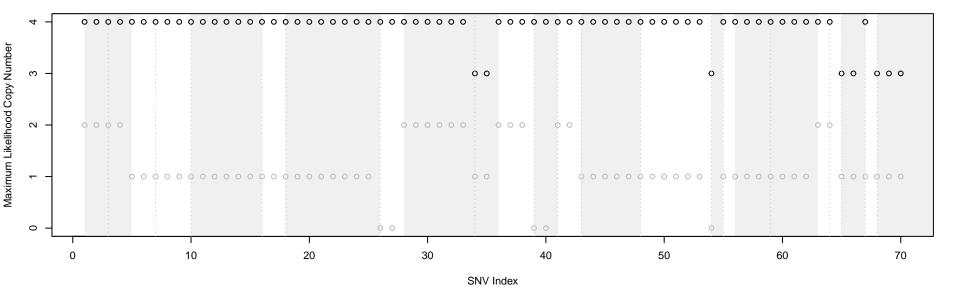


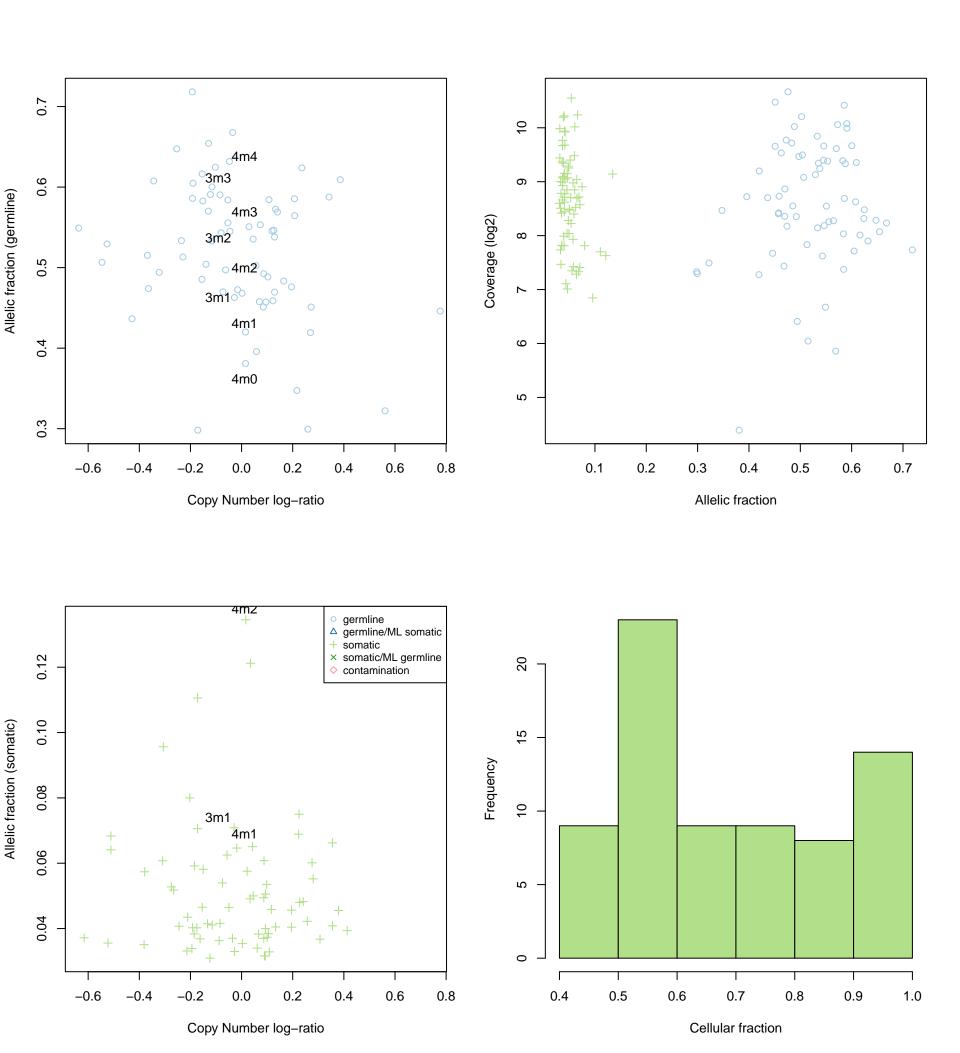
Purity: 0.16 Tumor ploidy: 3.882 3 7 0.3 Fraction Genome 0.1 0.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



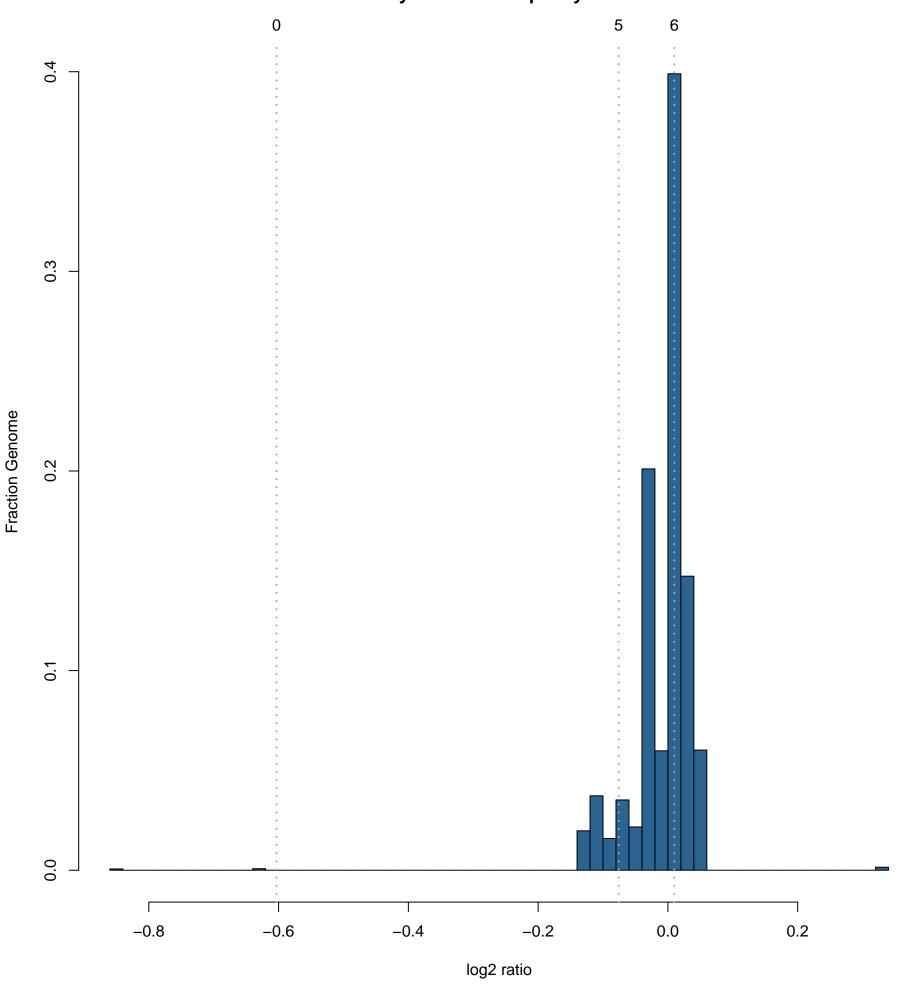
SCNA-fit log-likelihood: -9280.53

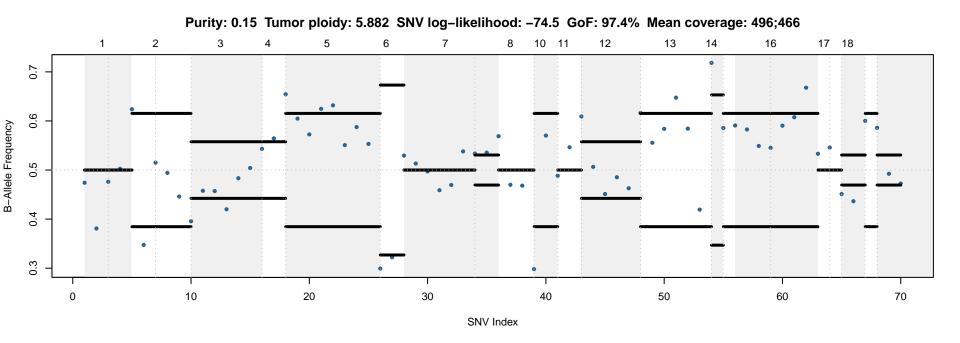




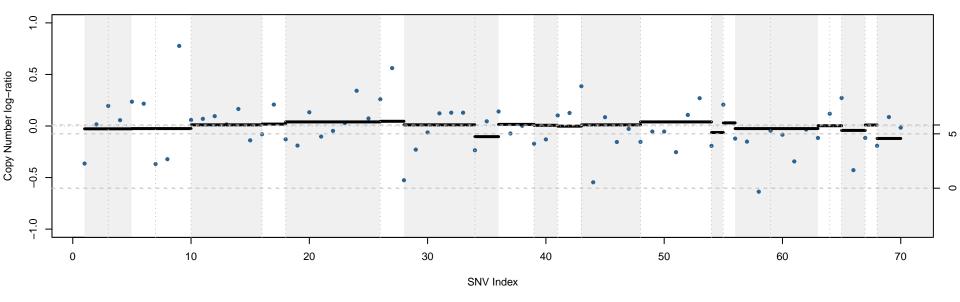


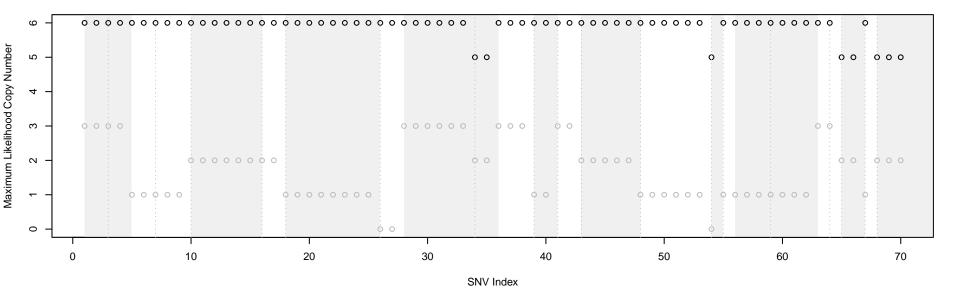
Purity: 0.15 Tumor ploidy: 5.882

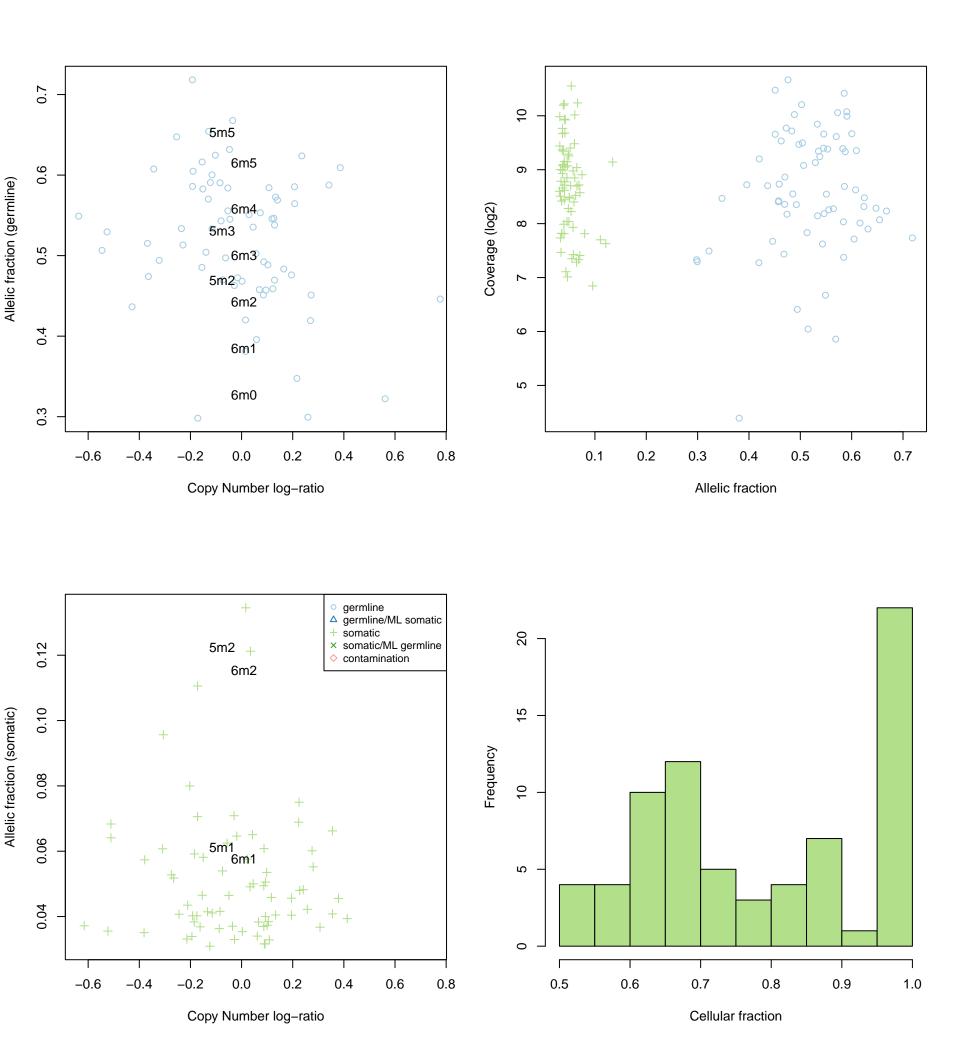




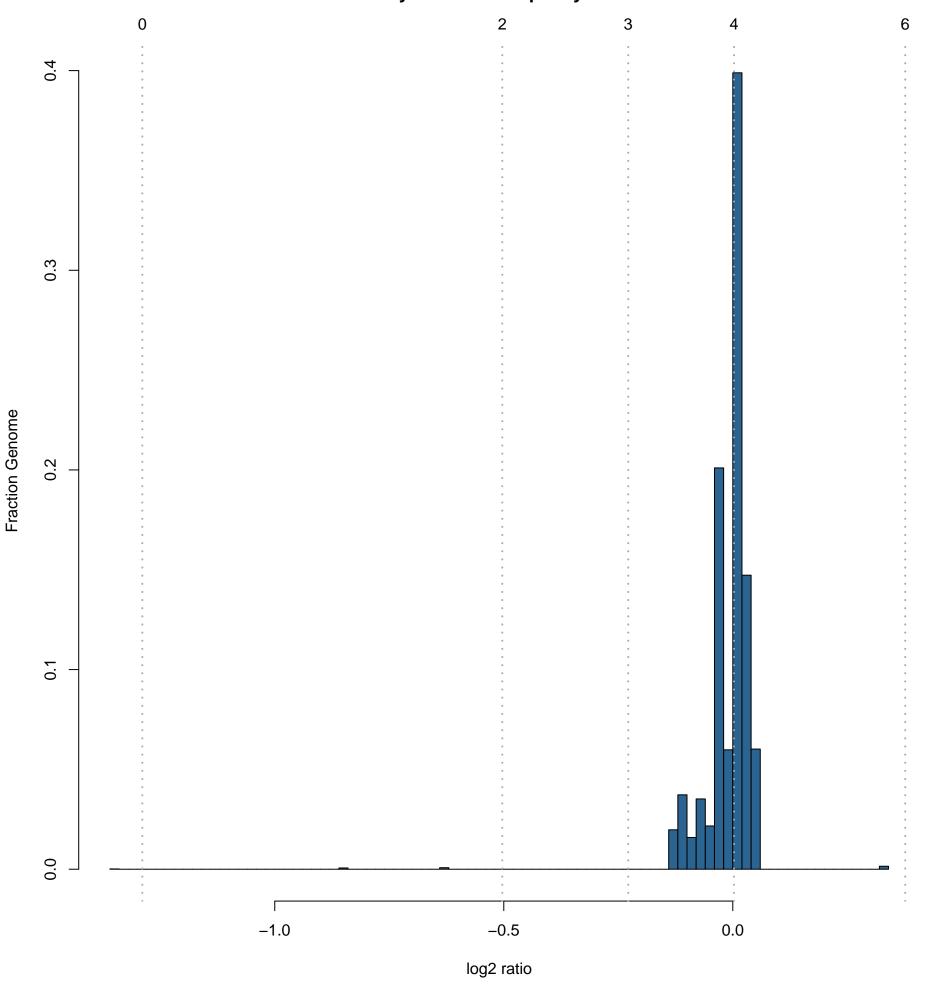
SCNA-fit log-likelihood: -9310.61

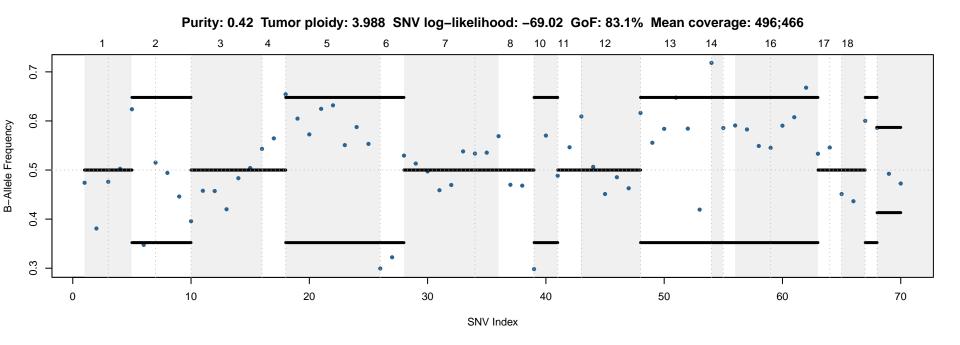




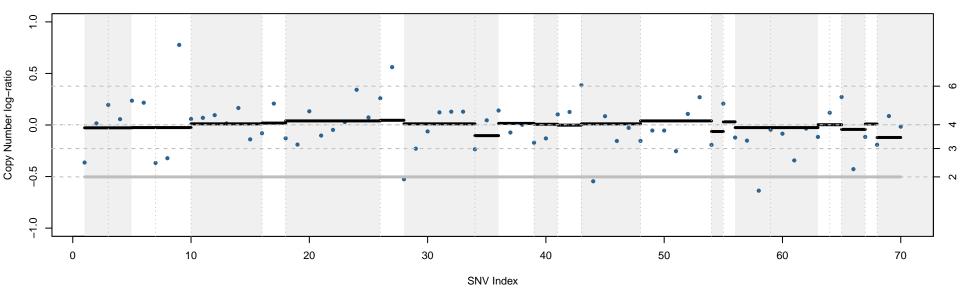


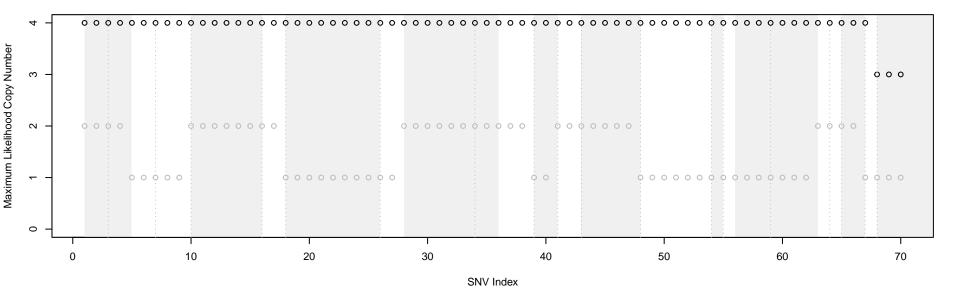
Purity: 0.42 Tumor ploidy: 3.988

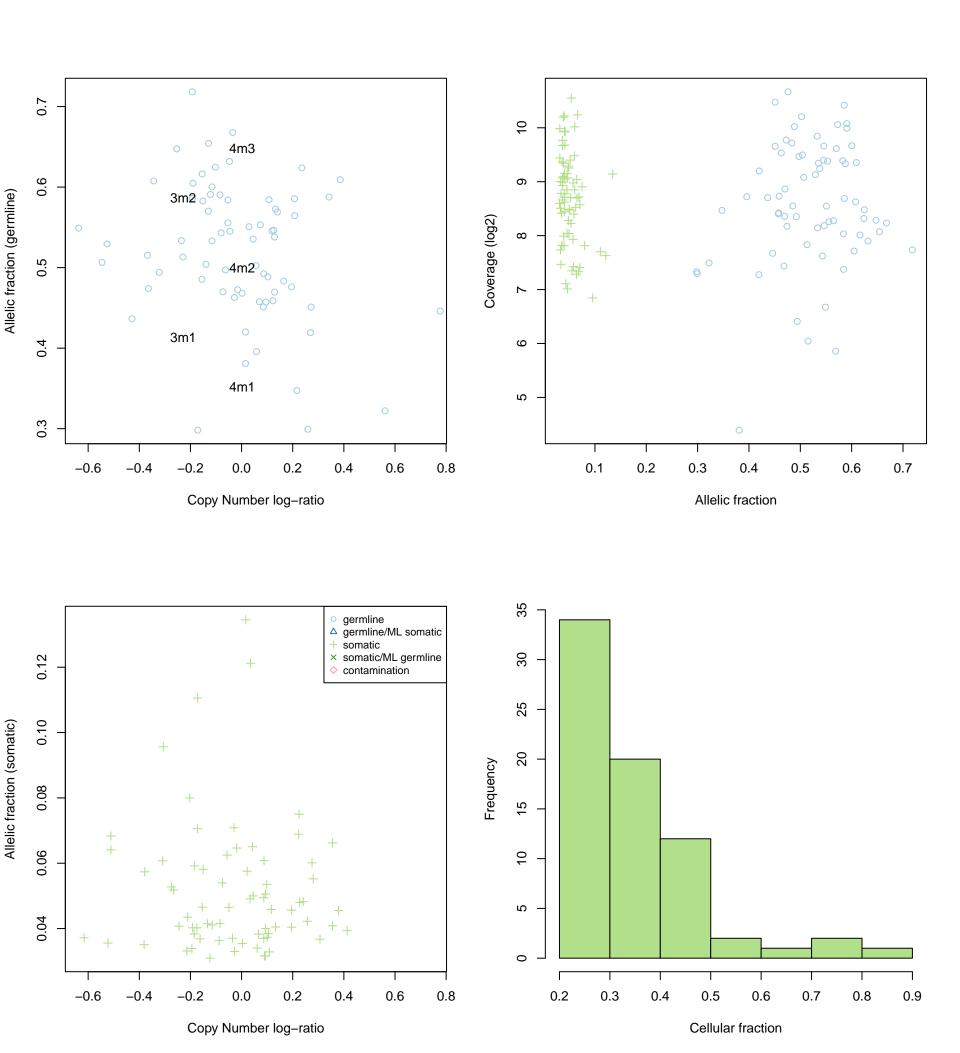




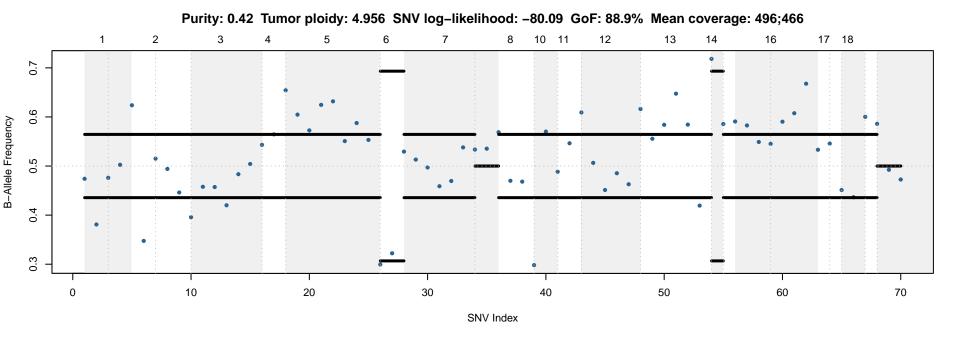
SCNA-fit log-likelihood: -9341.1



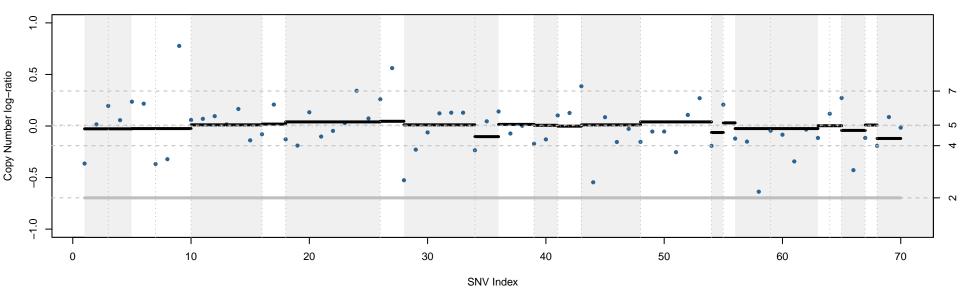


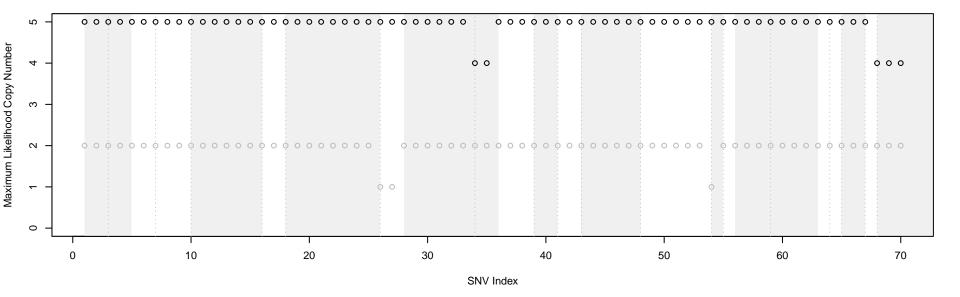


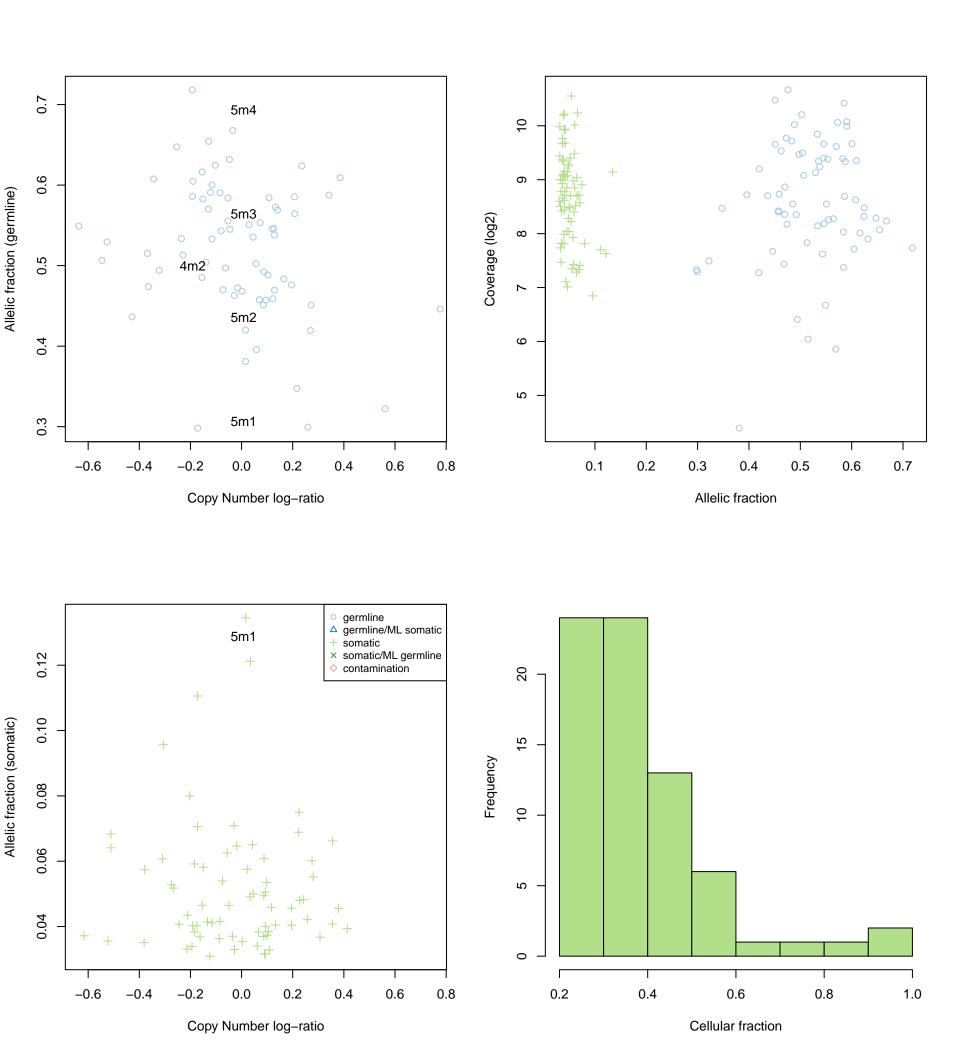
Purity: 0.42 Tumor ploidy: 4.956 5 7 Fraction Genome 0.1 0.0 -1.0 -0.5 0.0 log2 ratio



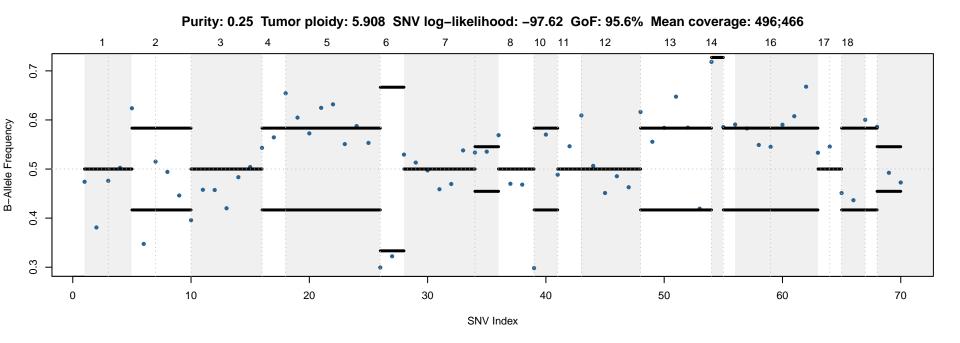
SCNA-fit log-likelihood: -9323.28



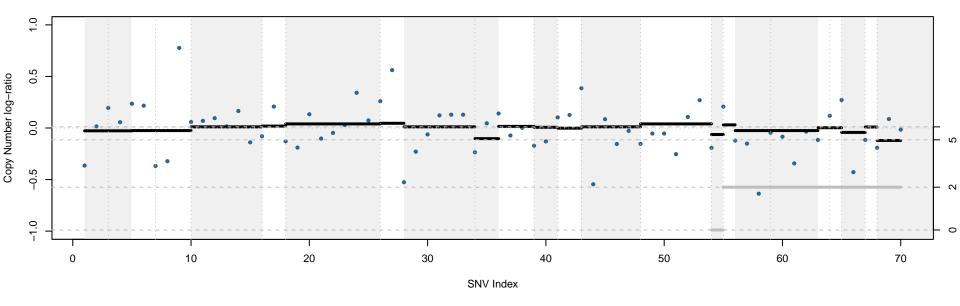


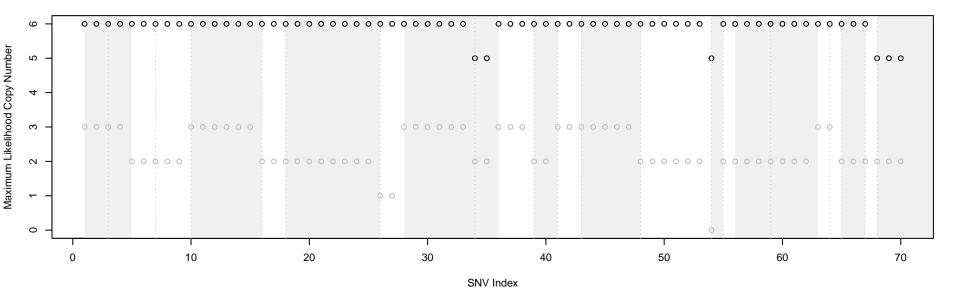


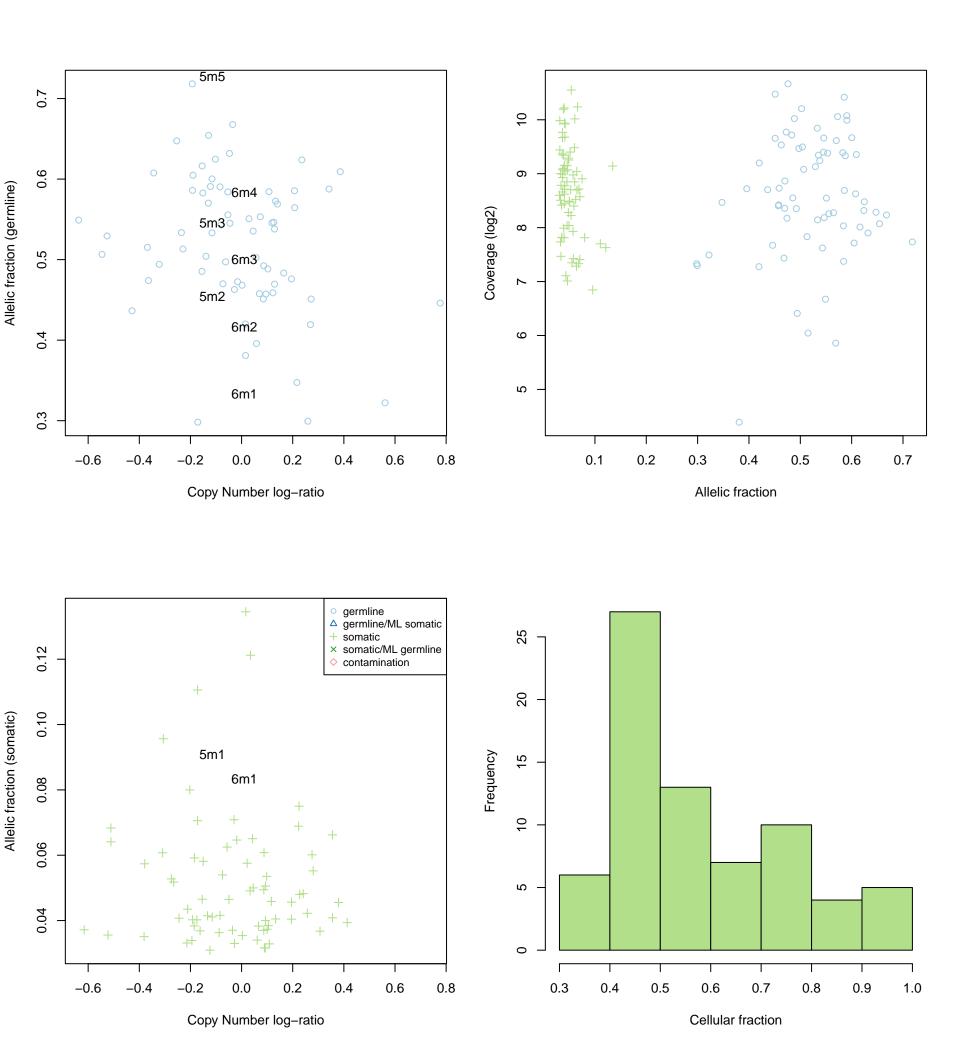
Purity: 0.25 Tumor ploidy: 5.908 6 0 5 0.3 Fraction Genome 0.1 0.0 -1.0 -0.5 0.0 log2 ratio



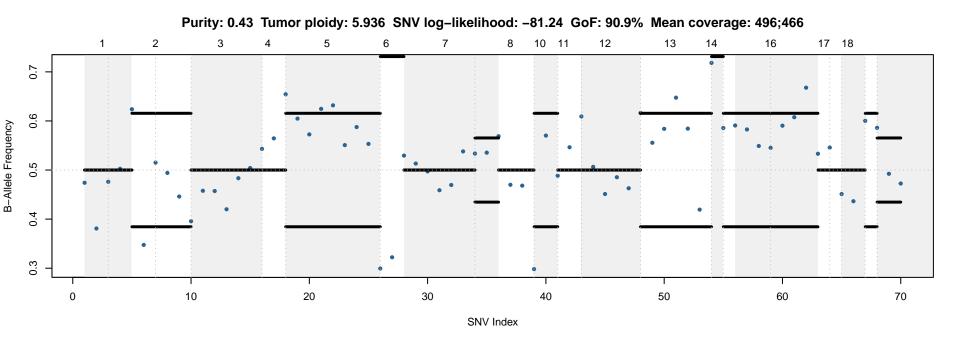
SCNA-fit log-likelihood: -9314.29



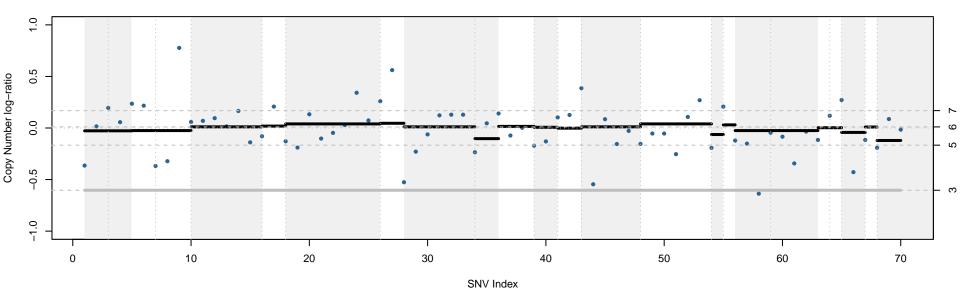


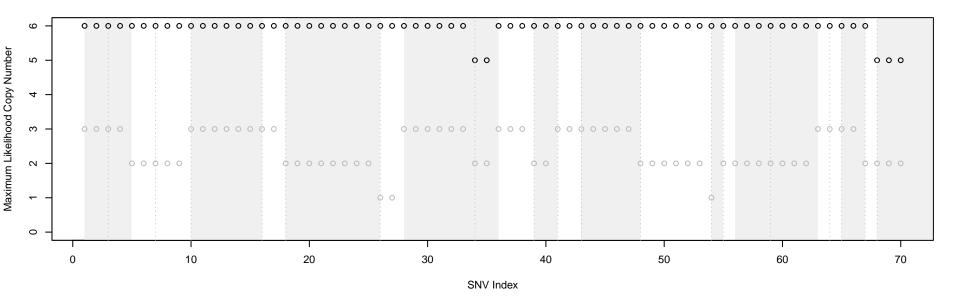


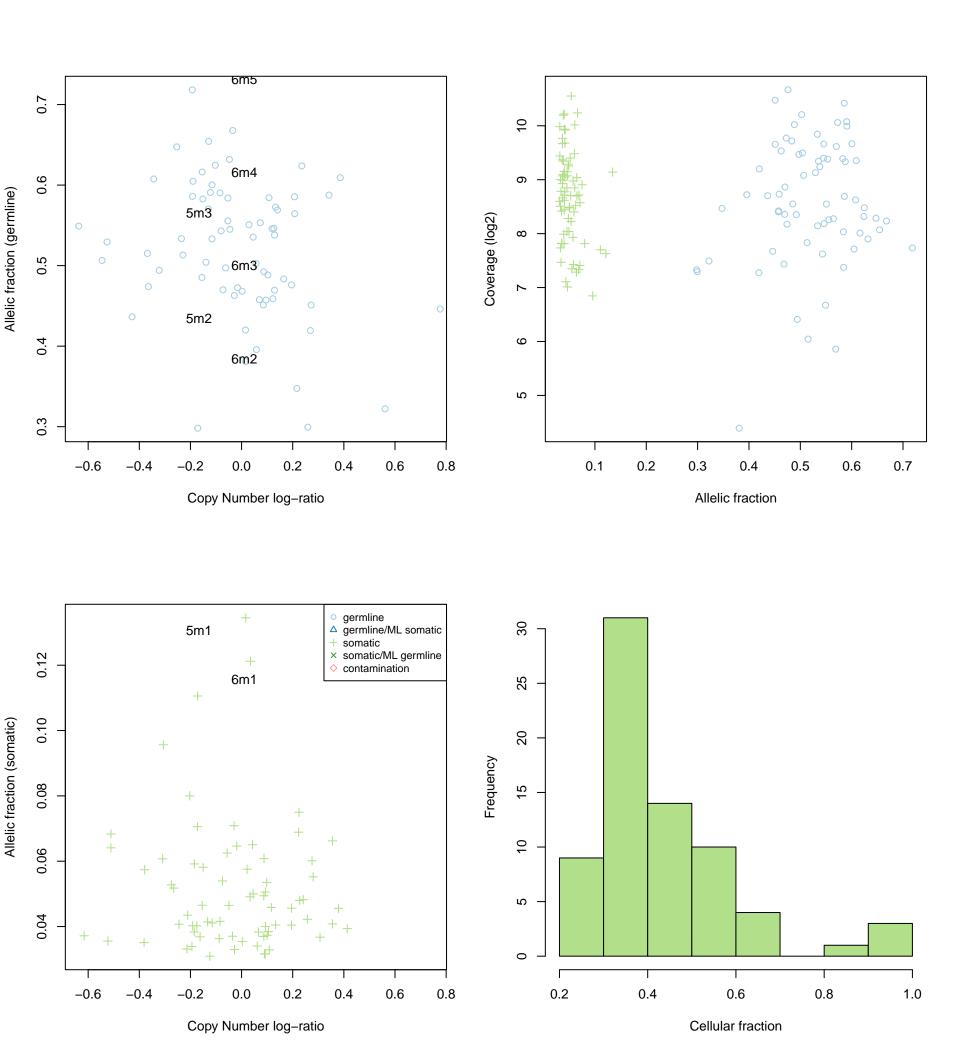
Purity: 0.43 Tumor ploidy: 5.936 6 5 3 7 Fraction Genome 0.1 0.0 -1.0 -0.5 0.0 log2 ratio



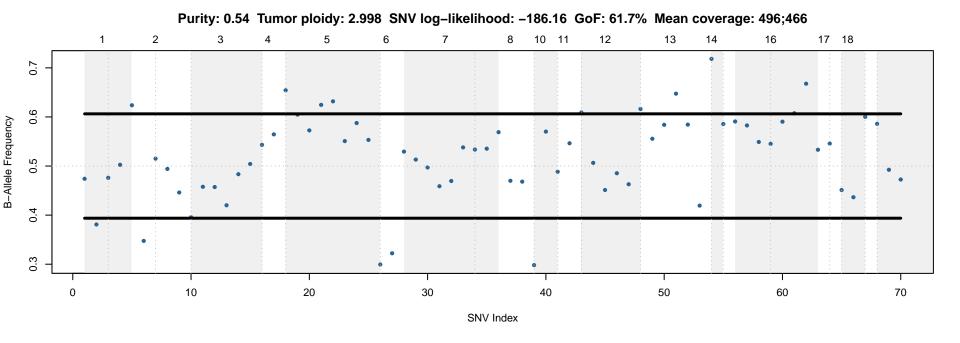
SCNA-fit log-likelihood: -9310.78



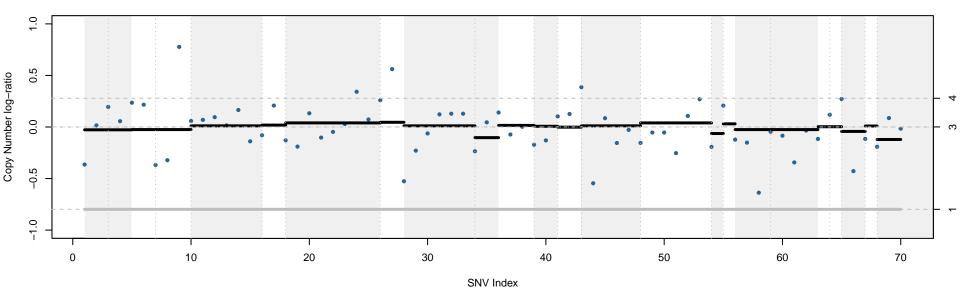


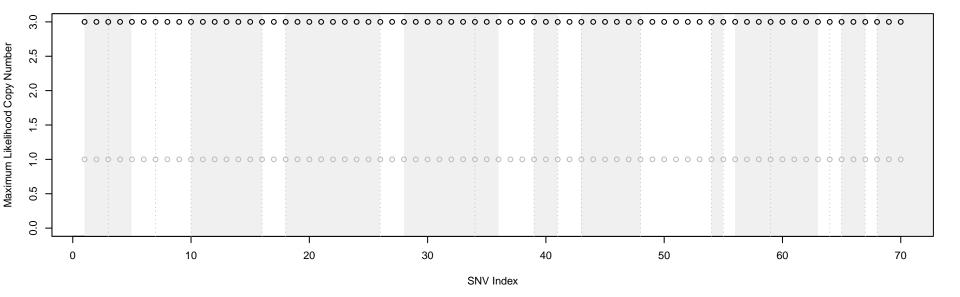


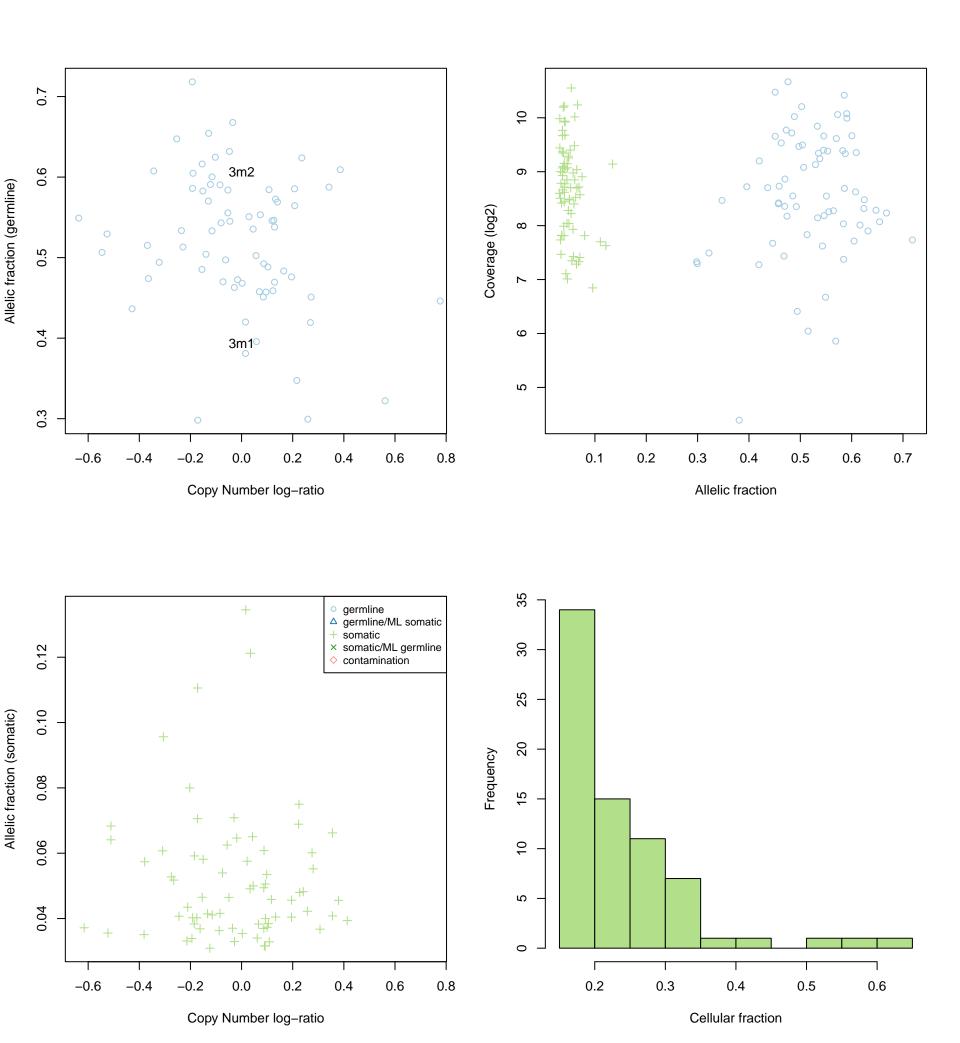
Purity: 0.54 Tumor ploidy: 2.998 3 Fraction Genome 0.1 0.0 -1.0 -0.5 0.0 log2 ratio



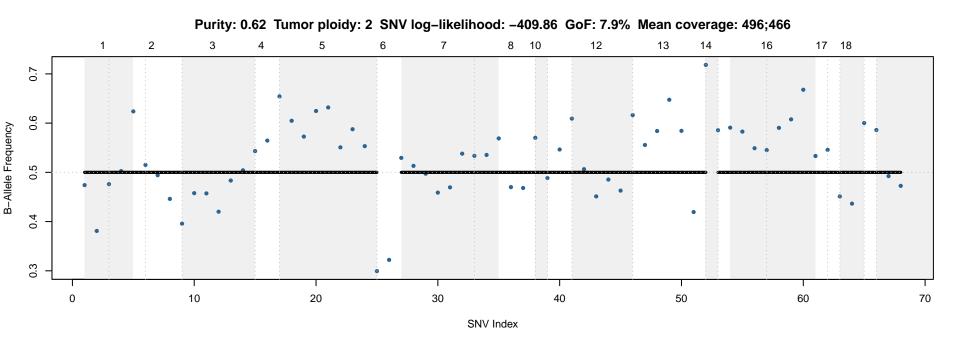
SCNA-fit log-likelihood: -9343.79



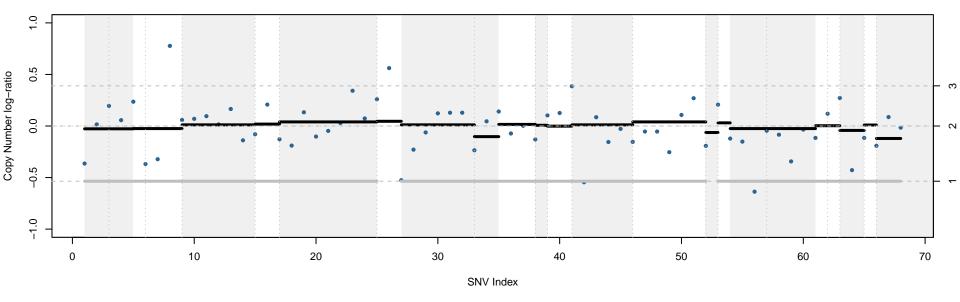


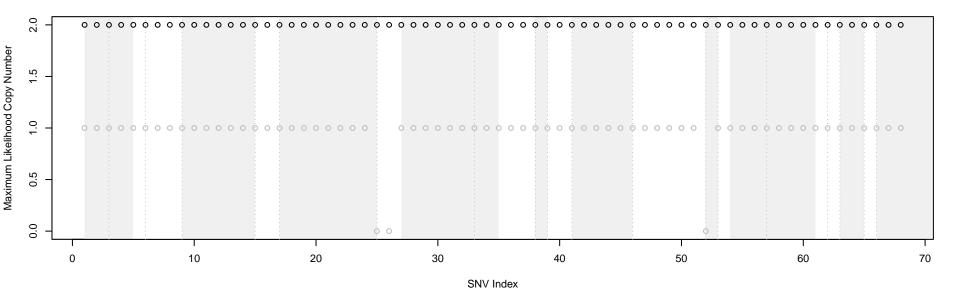


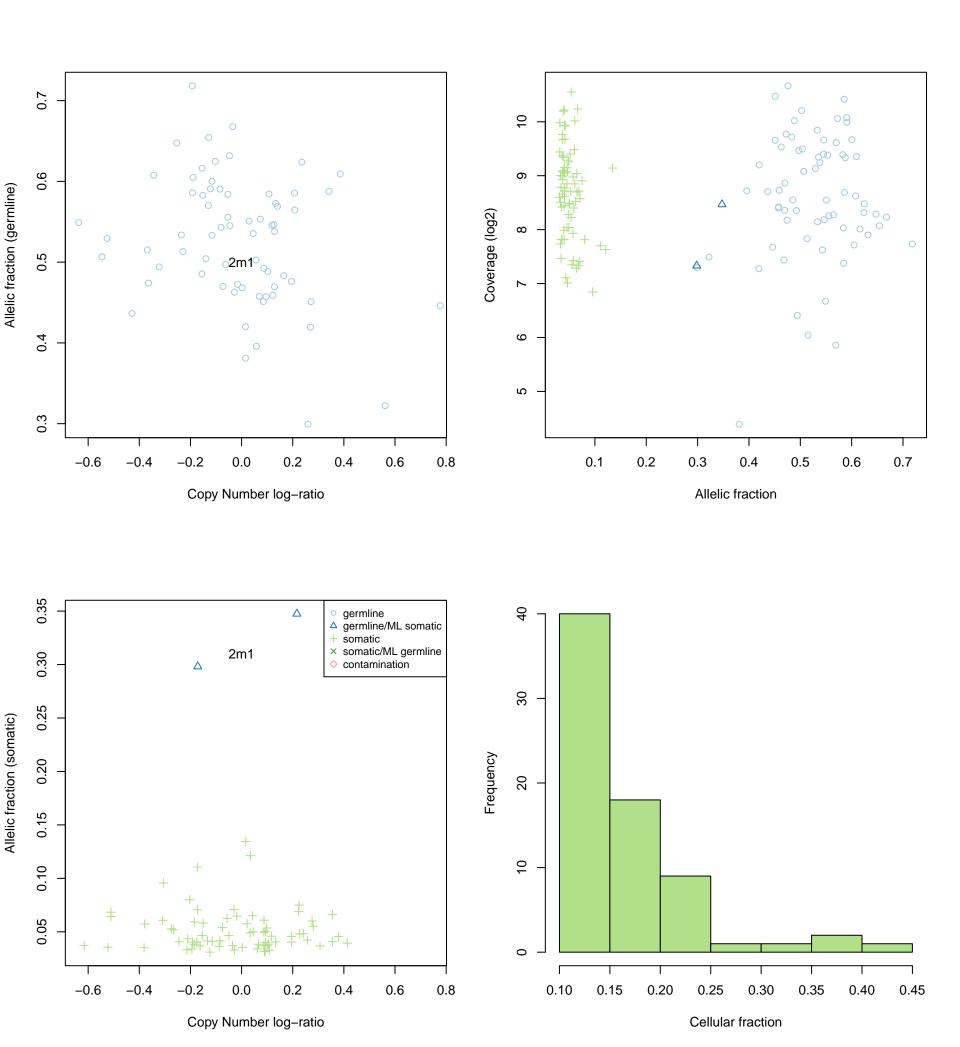
Purity: 0.62 Tumor ploidy: 2 2 0 Fraction Genome 0.1 0.0 -1.0 -0.5 0.0 log2 ratio



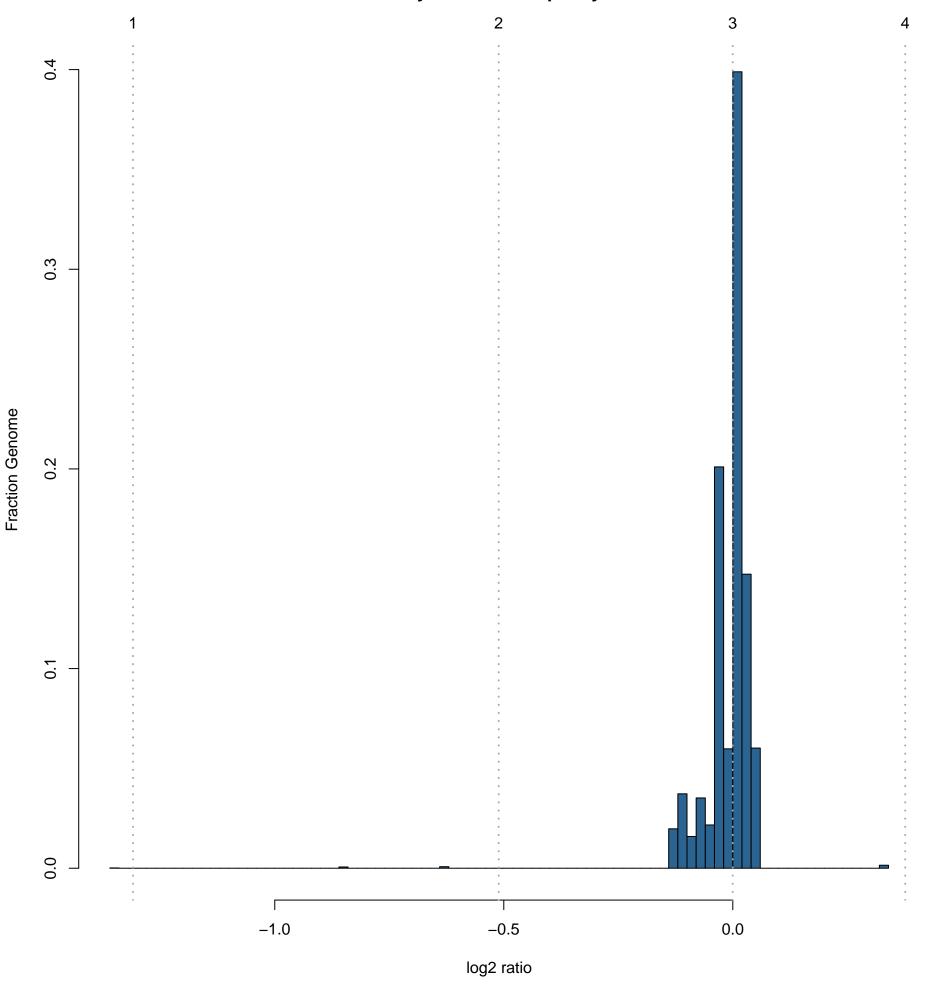
SCNA-fit log-likelihood: -9342.84

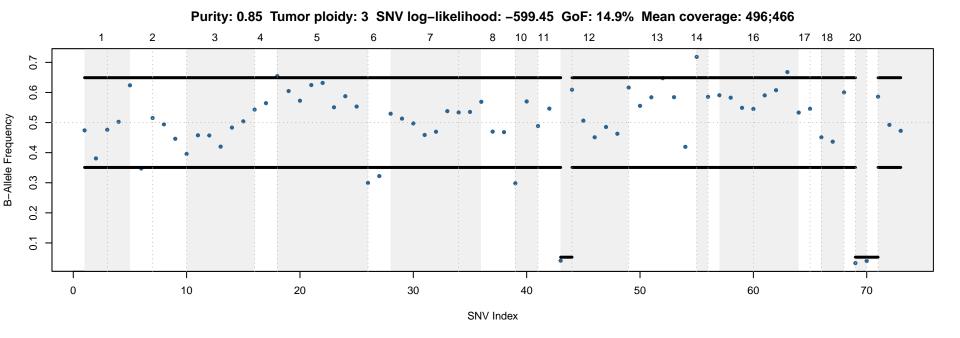






Purity: 0.85 Tumor ploidy: 3





SCNA-fit log-likelihood: -9344.01

