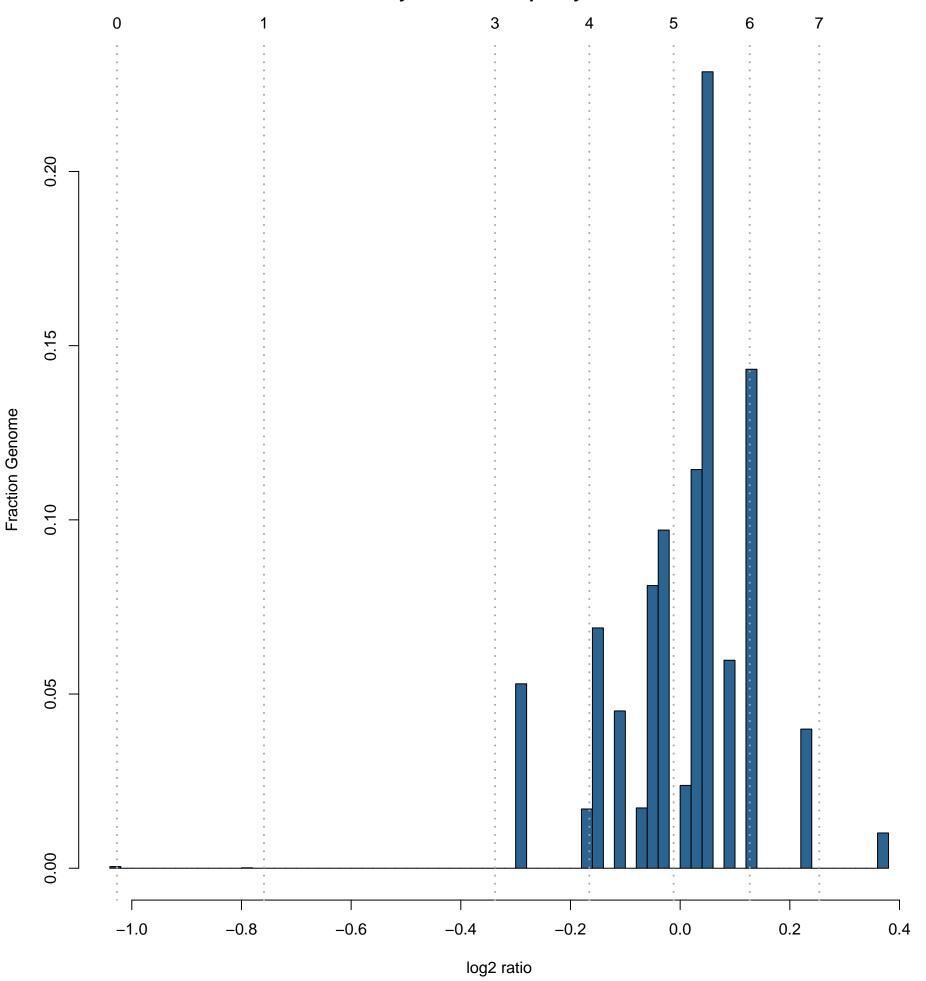
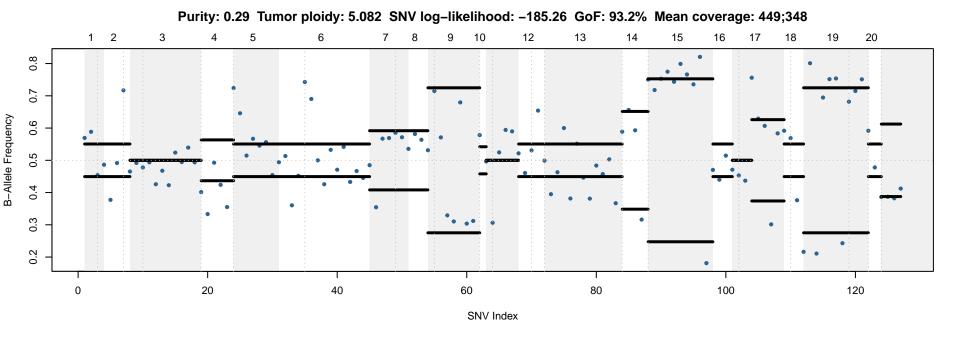
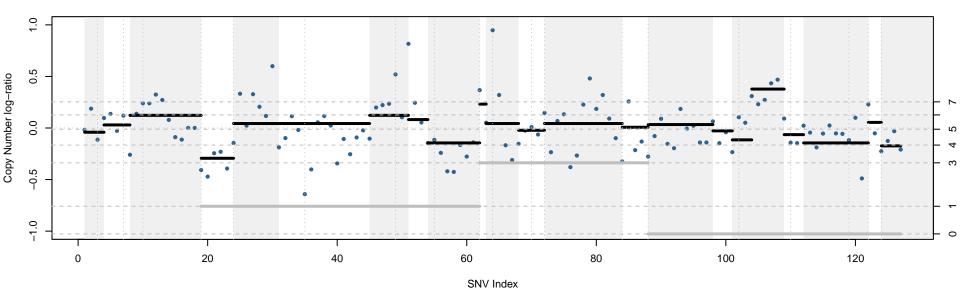
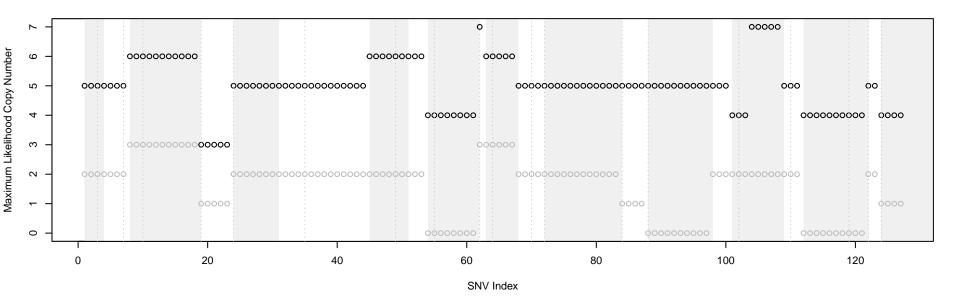
Purity: 0.29 Tumor ploidy: 5.082

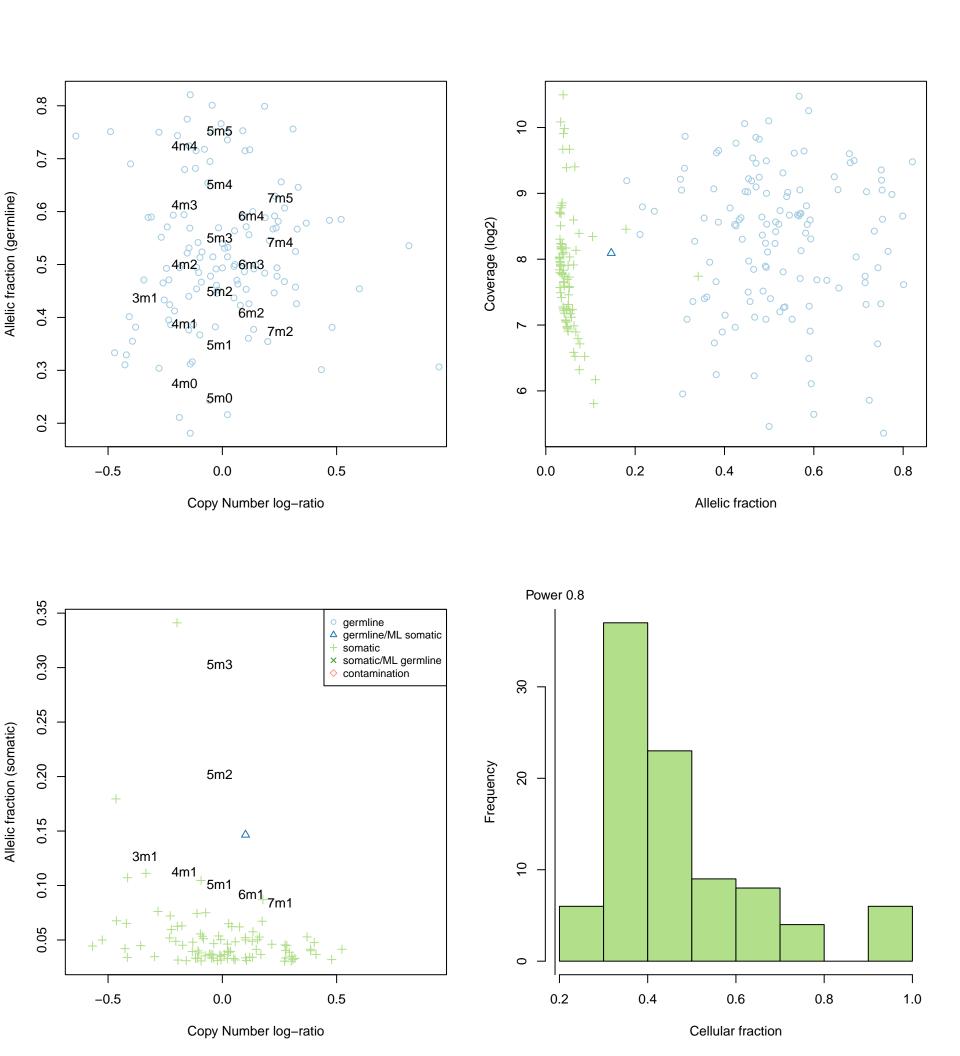




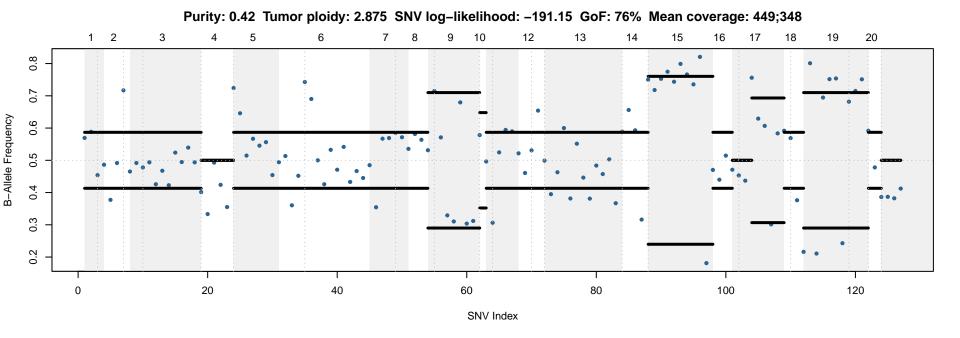
SCNA-fit log-likelihood: -11104.89



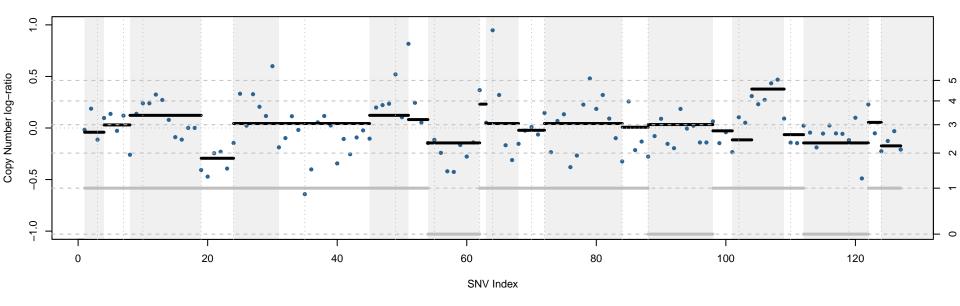


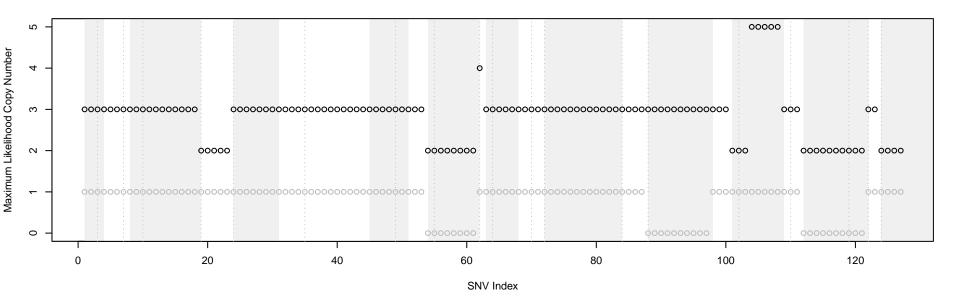


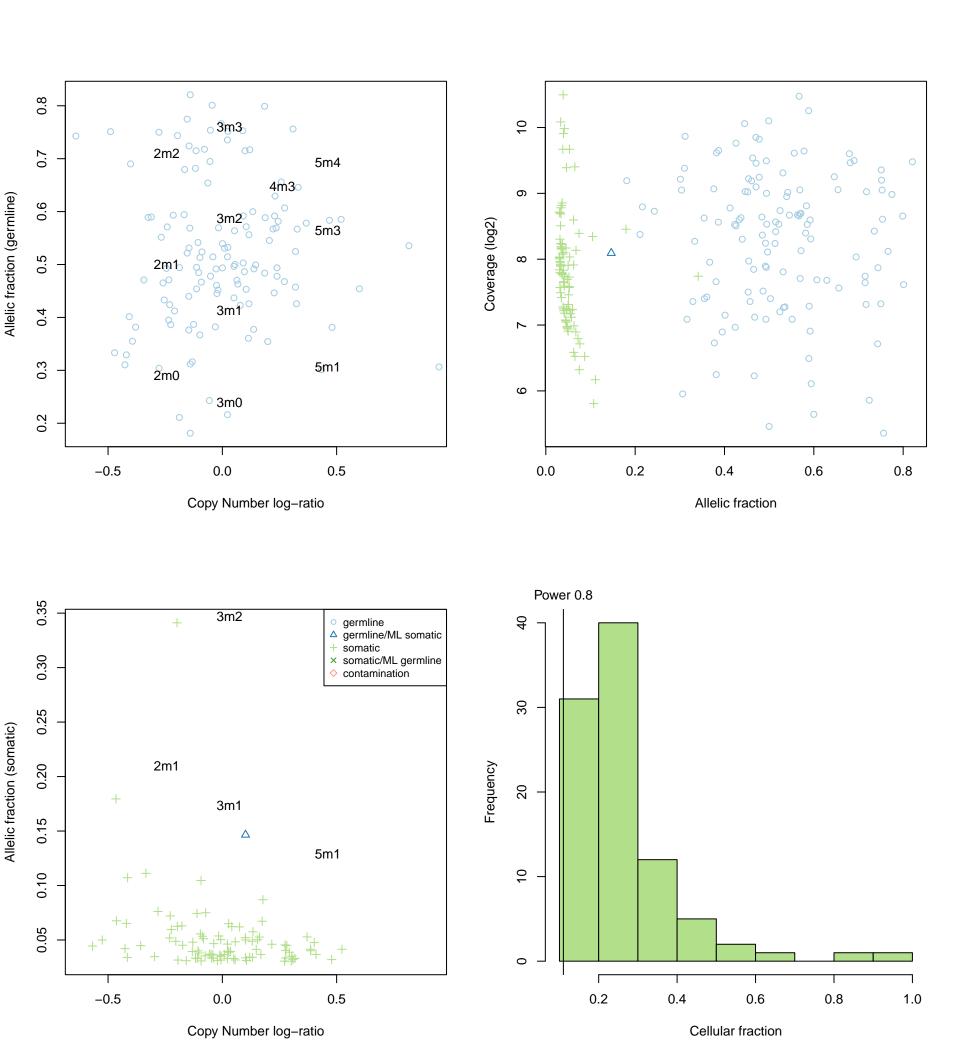
Purity: 0.42 Tumor ploidy: 2.875 3 0 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 0.4 log2 ratio



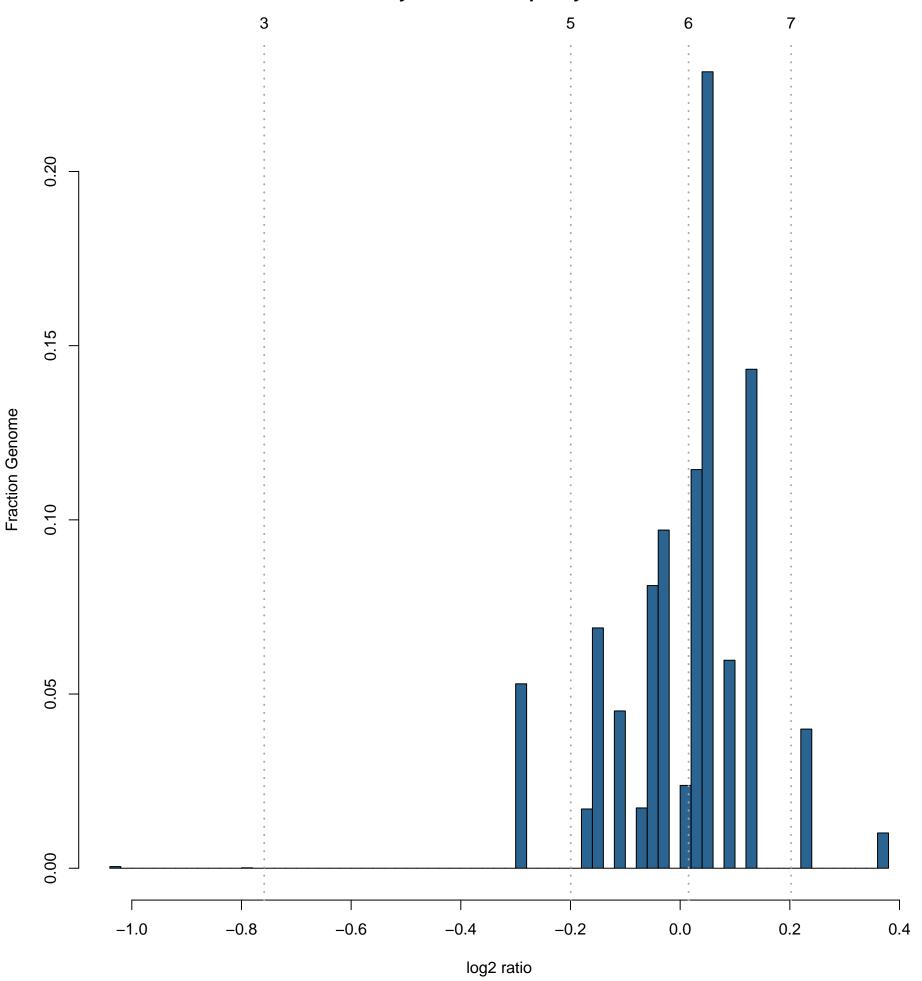
SCNA-fit log-likelihood: -11198.73

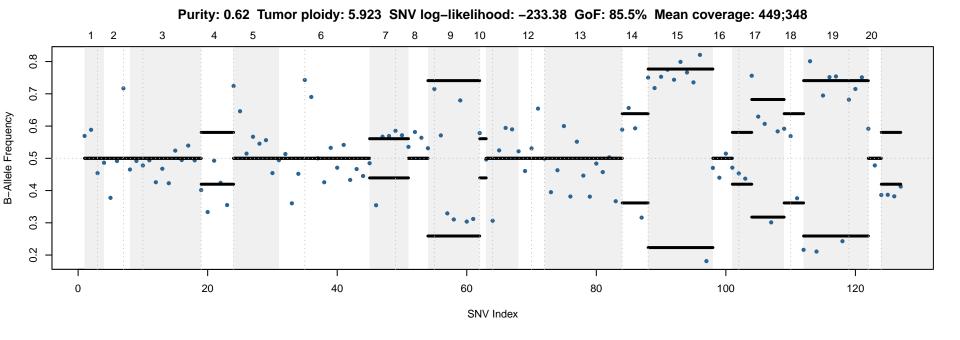




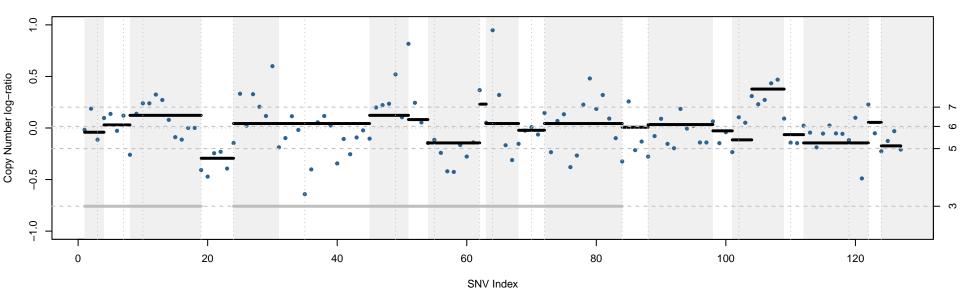


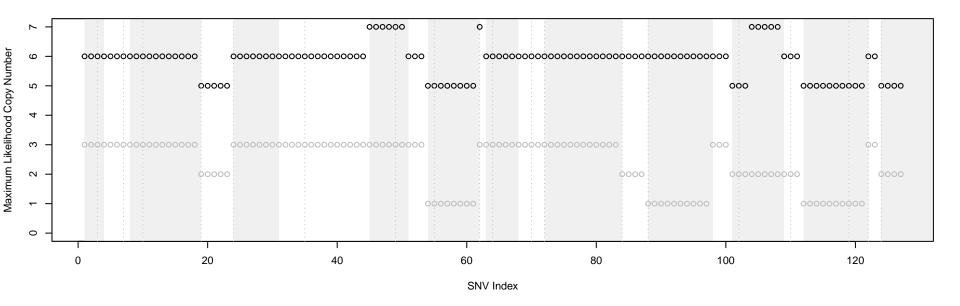
Purity: 0.62 Tumor ploidy: 5.923

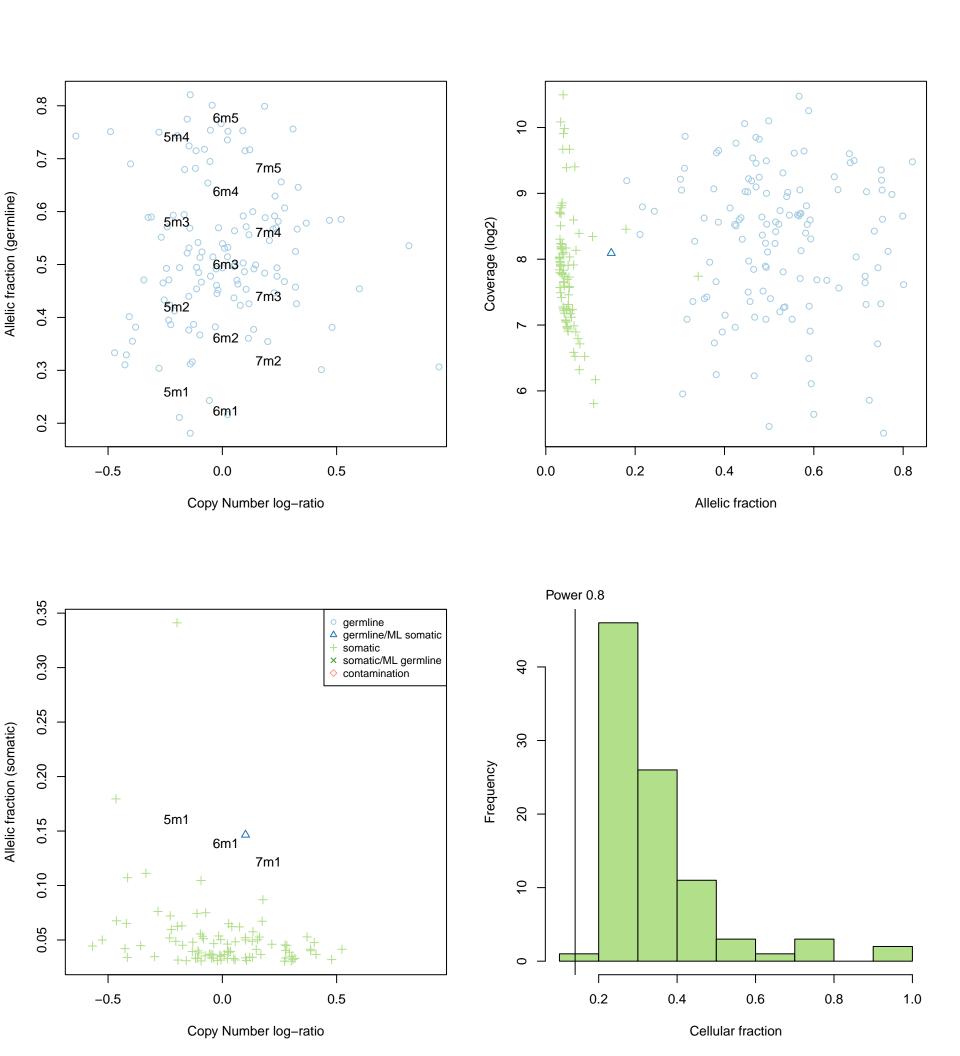




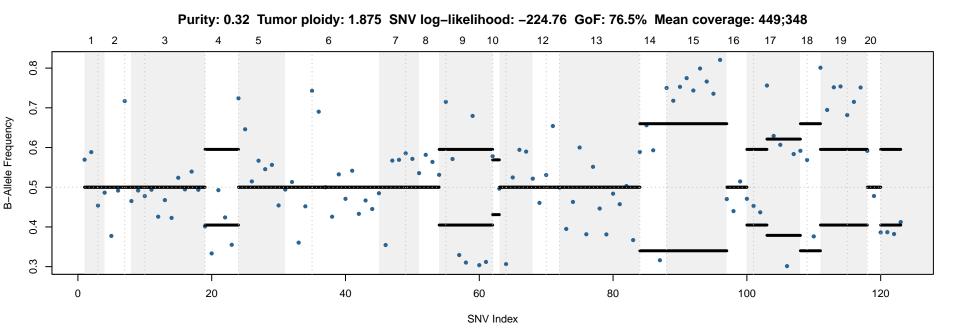
SCNA-fit log-likelihood: -11167.95



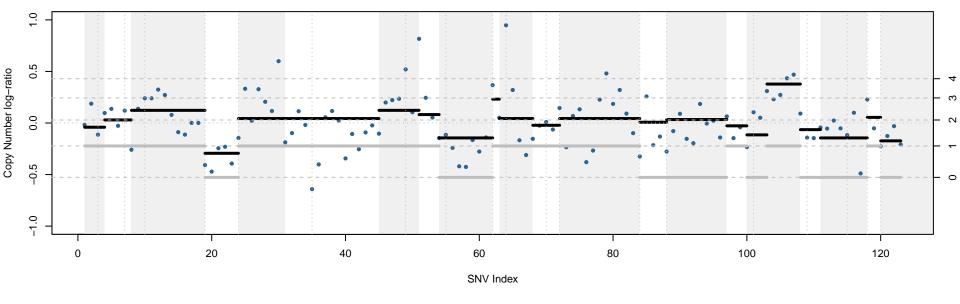


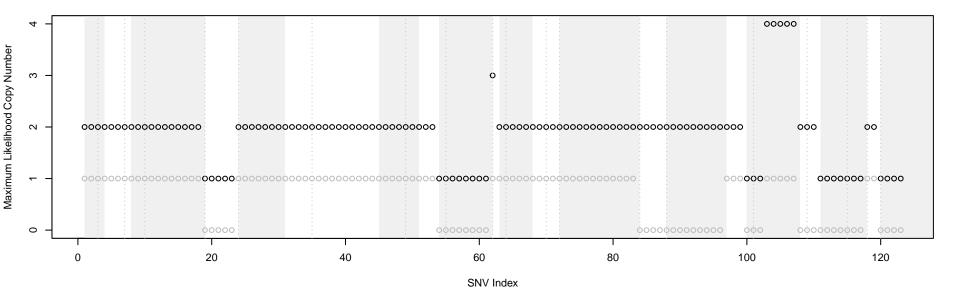


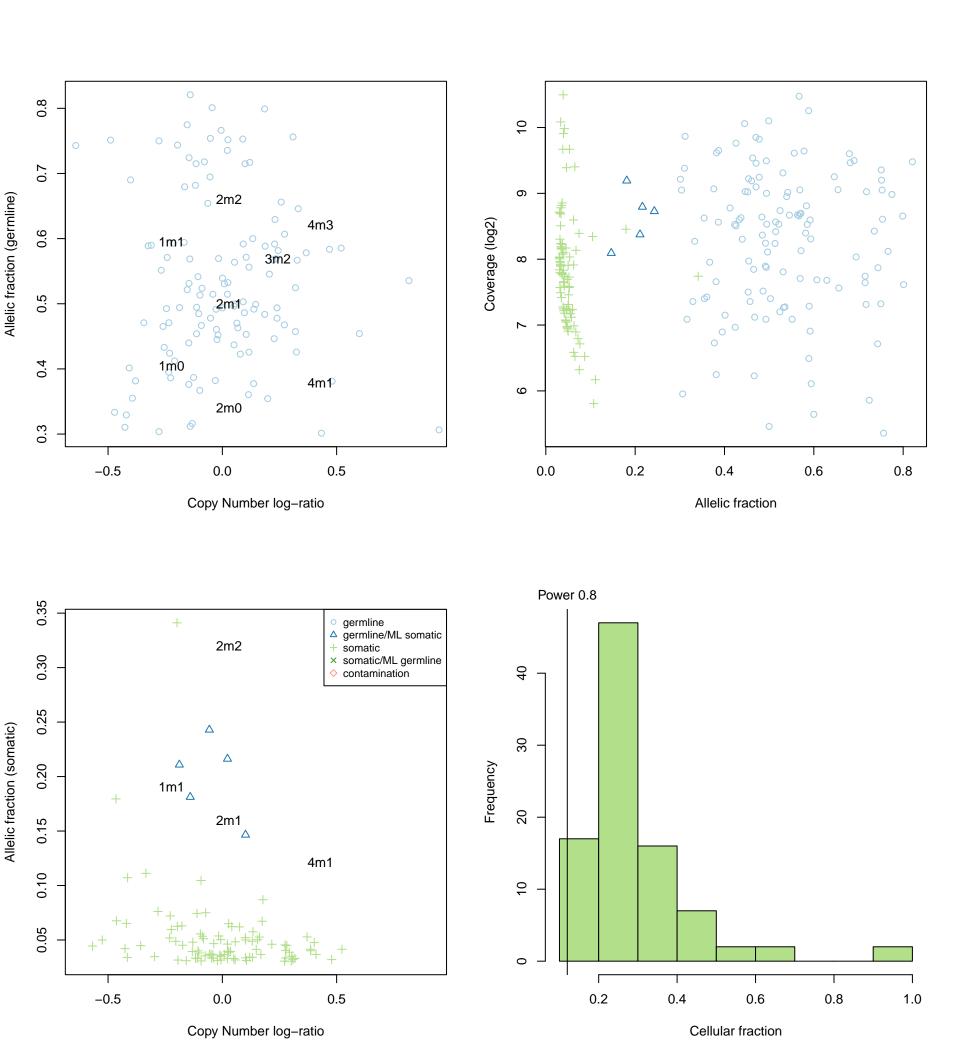
Purity: 0.32 Tumor ploidy: 1.875 2 3 Fraction Genome 0.10 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 0.4 log2 ratio



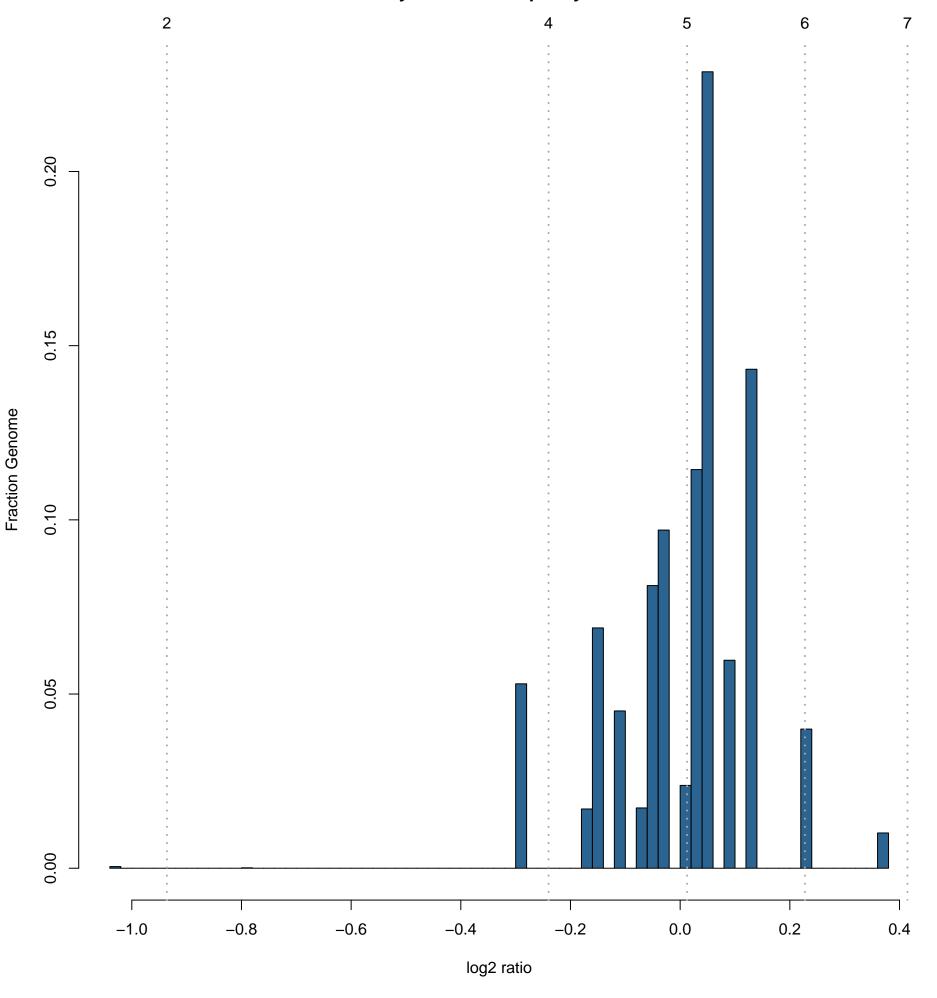
SCNA-fit log-likelihood: -11188.64

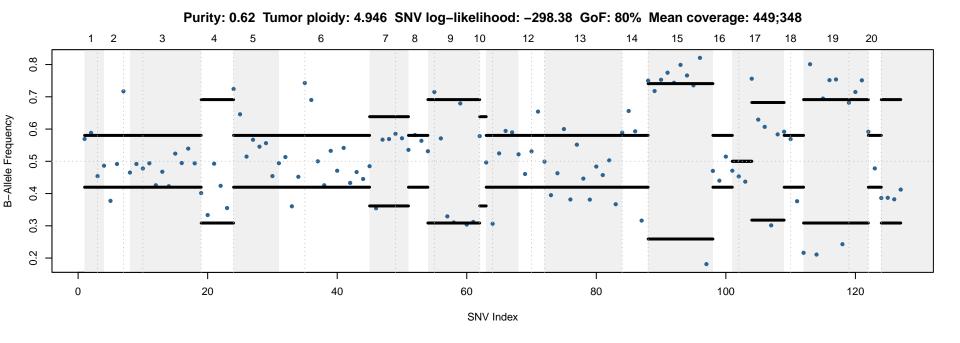




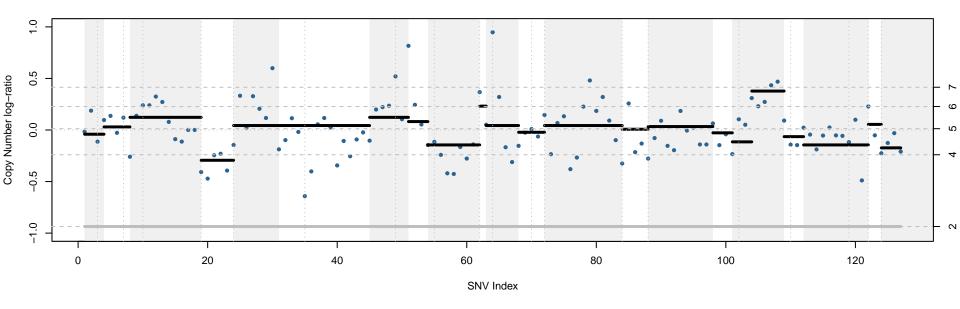


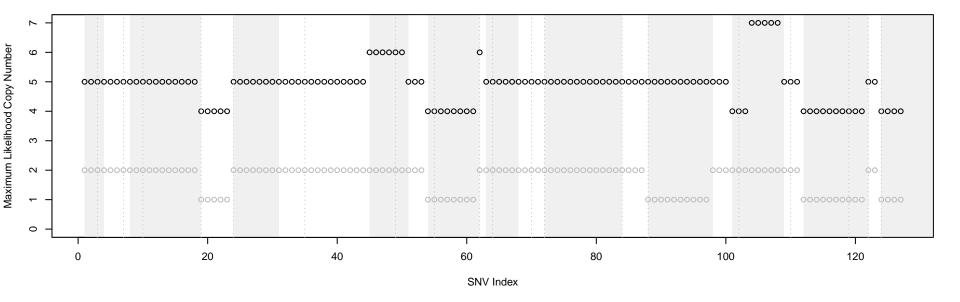
Purity: 0.62 Tumor ploidy: 4.946

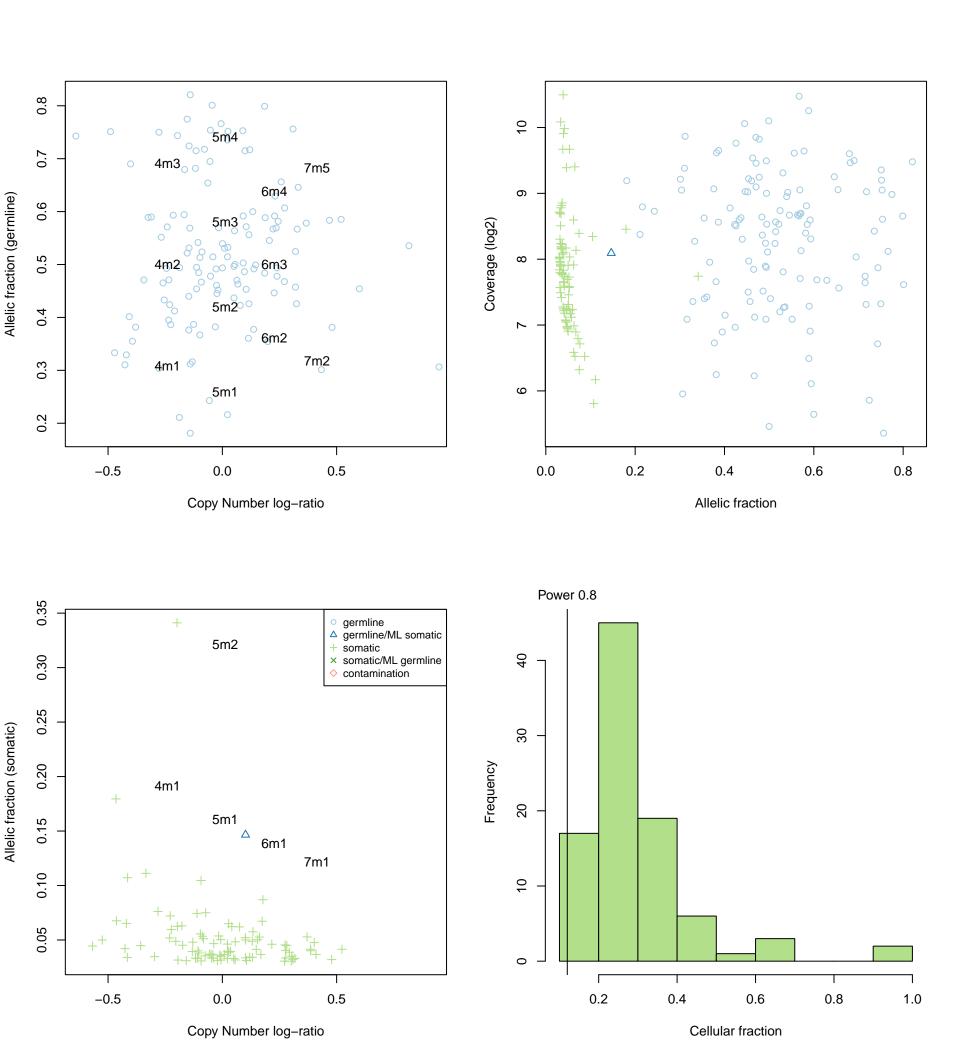




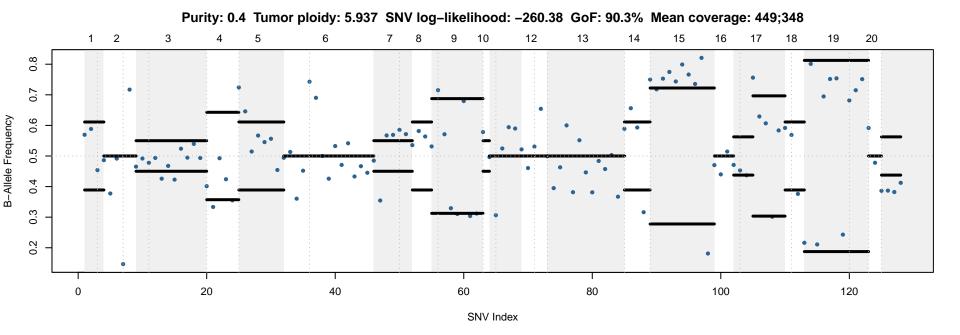
SCNA-fit log-likelihood: -11182.07



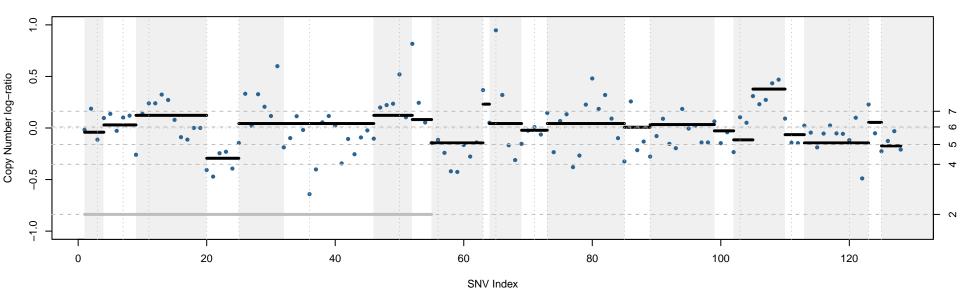


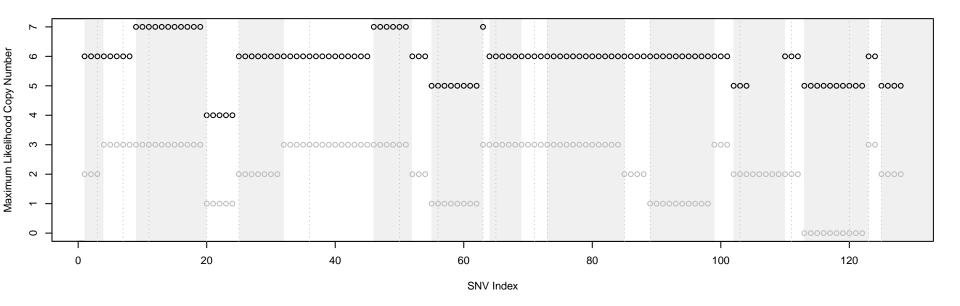


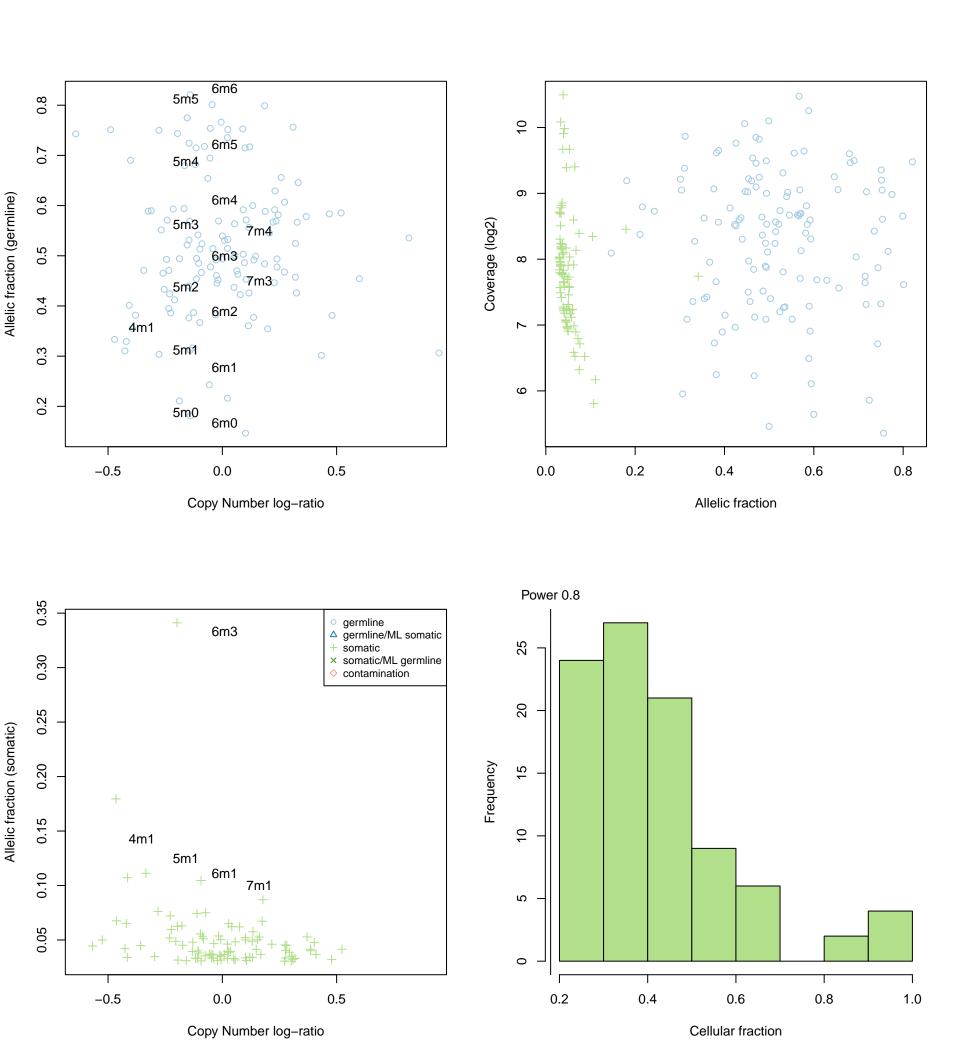
Purity: 0.4 Tumor ploidy: 5.937 2 6 7 5 0.20 0.15 Fraction Genome 0.10 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 0.4 log2 ratio



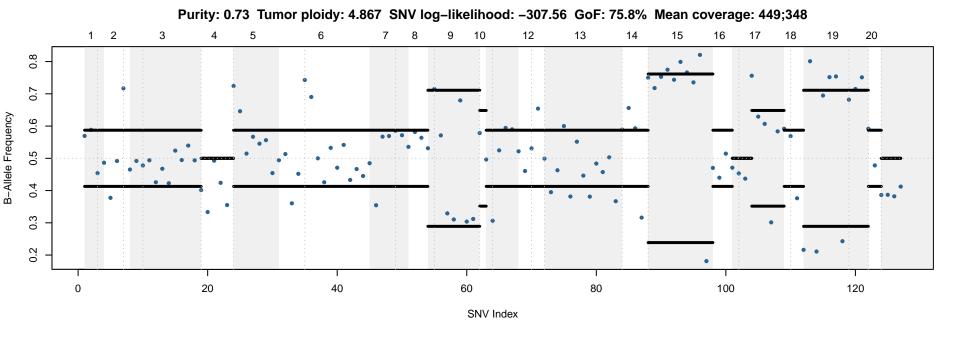
SCNA-fit log-likelihood: -11262.41



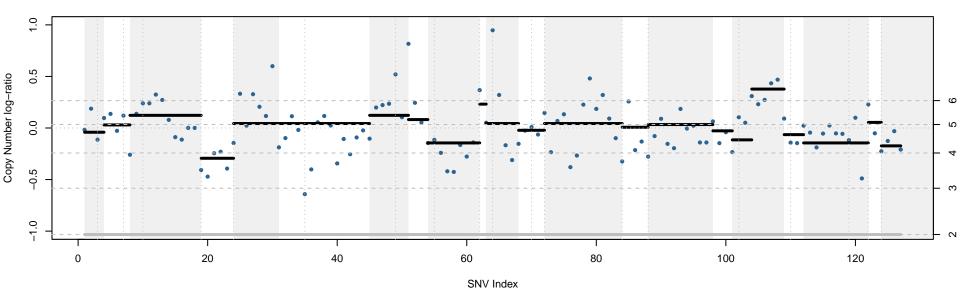


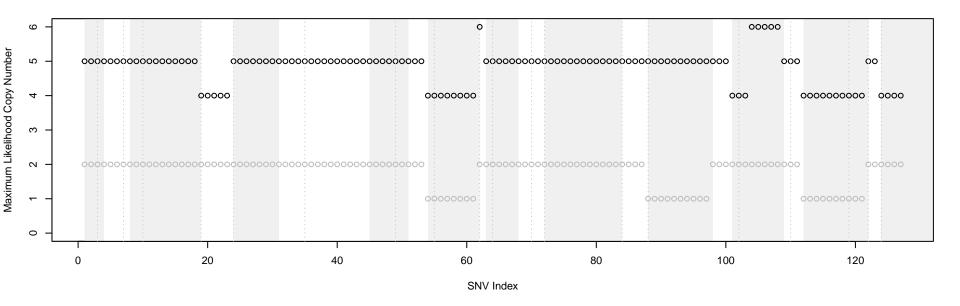


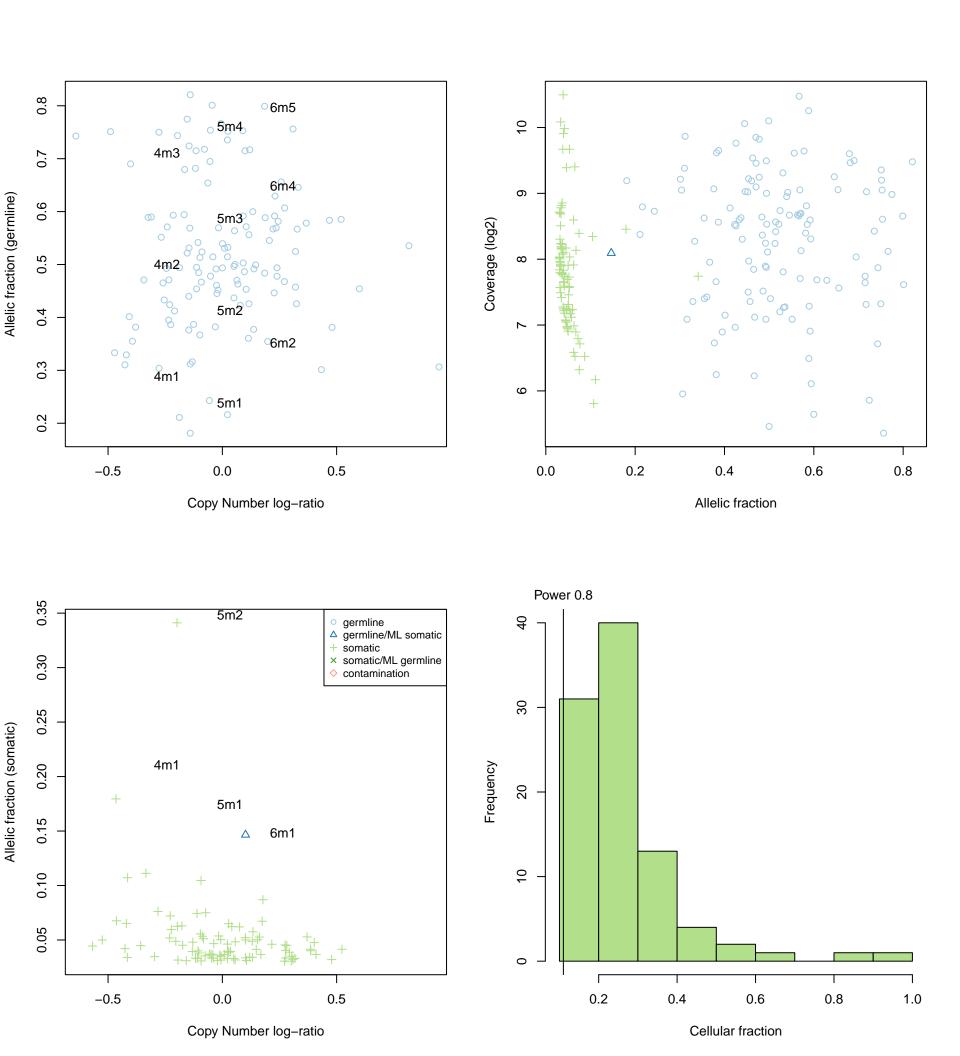
Purity: 0.73 Tumor ploidy: 4.867 2 5 6 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 0.4 log2 ratio

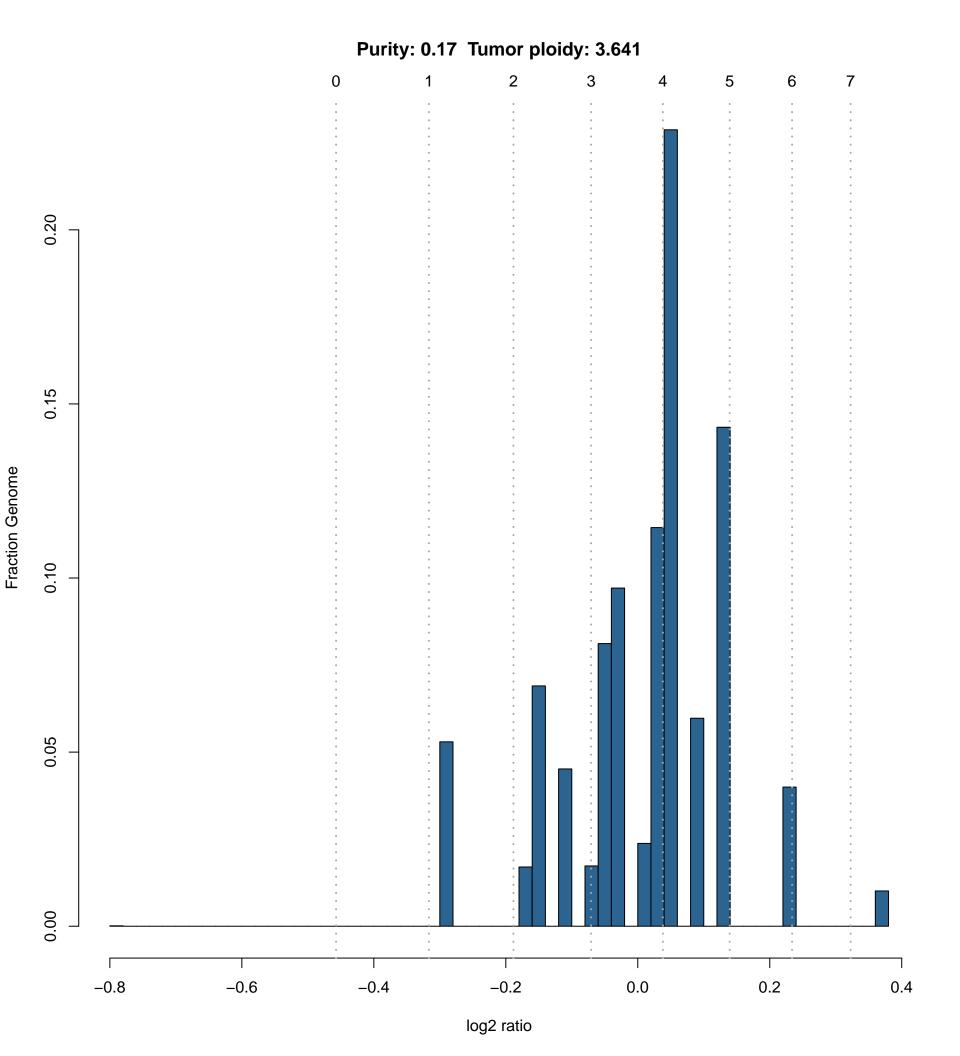


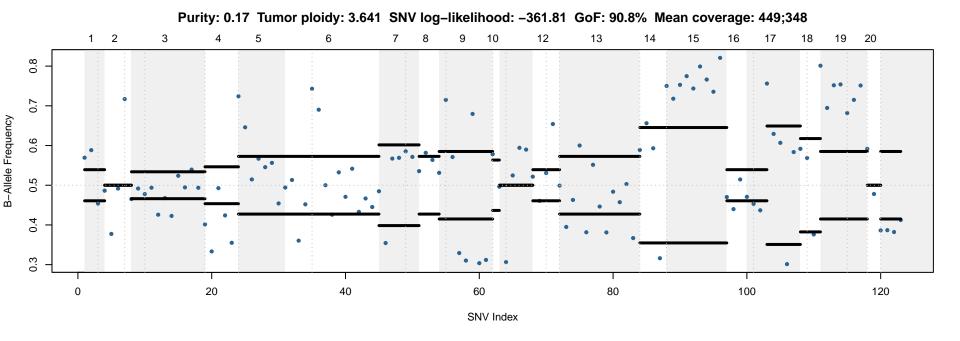
SCNA-fit log-likelihood: -11200.35



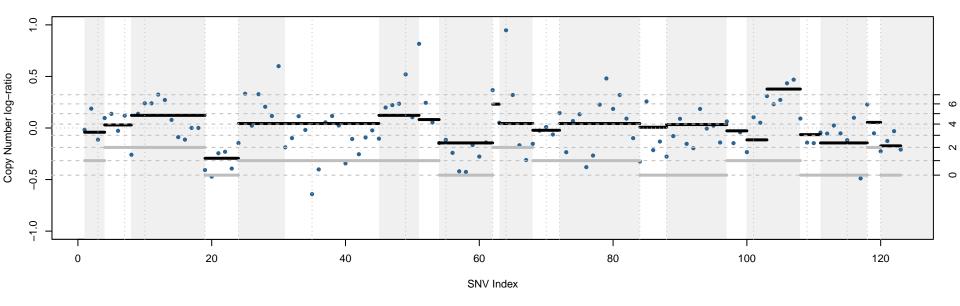


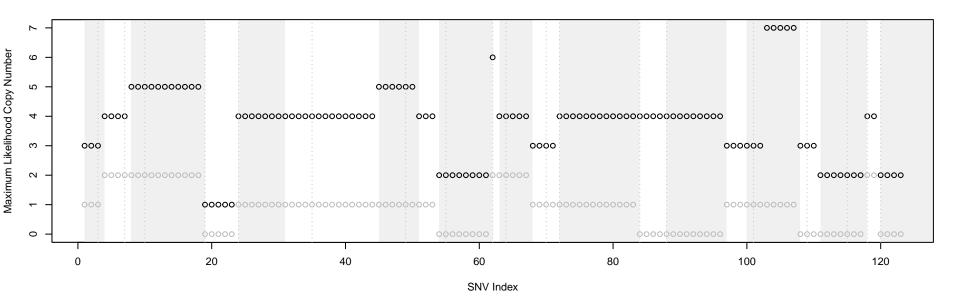


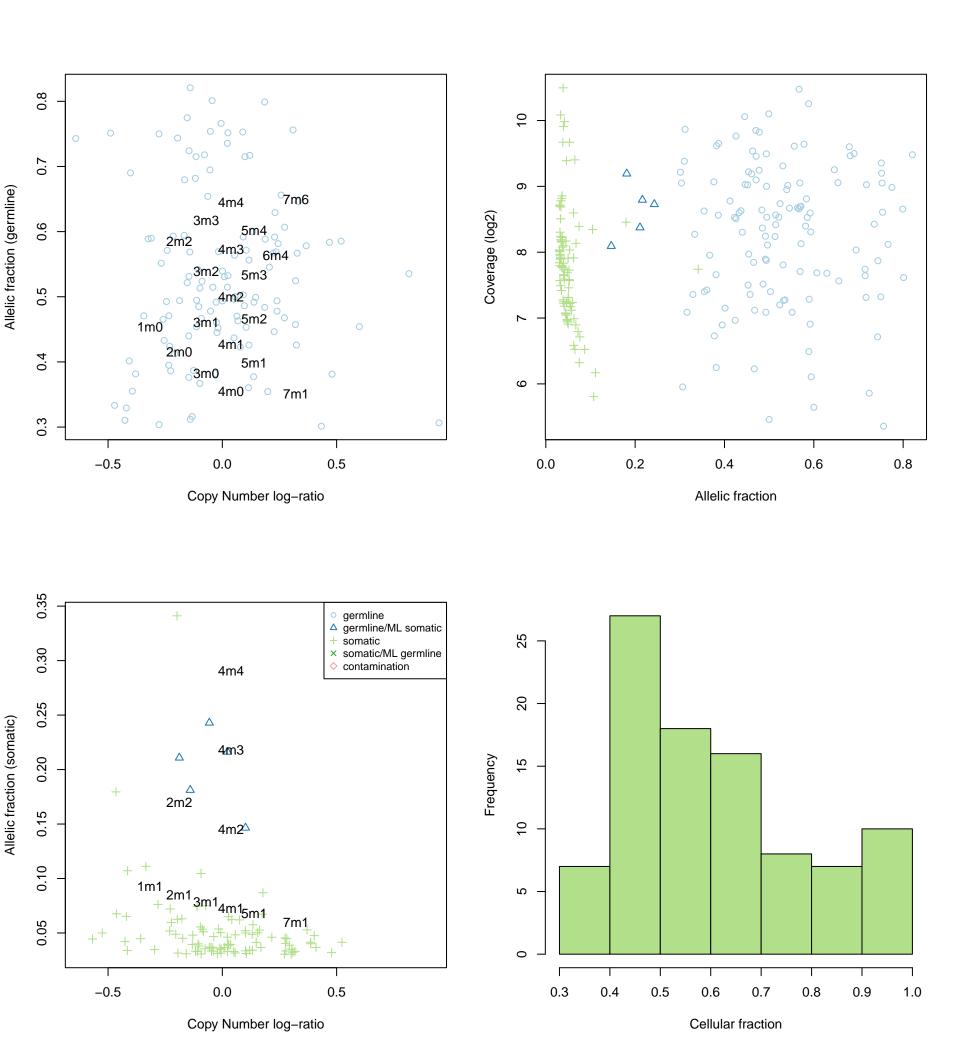




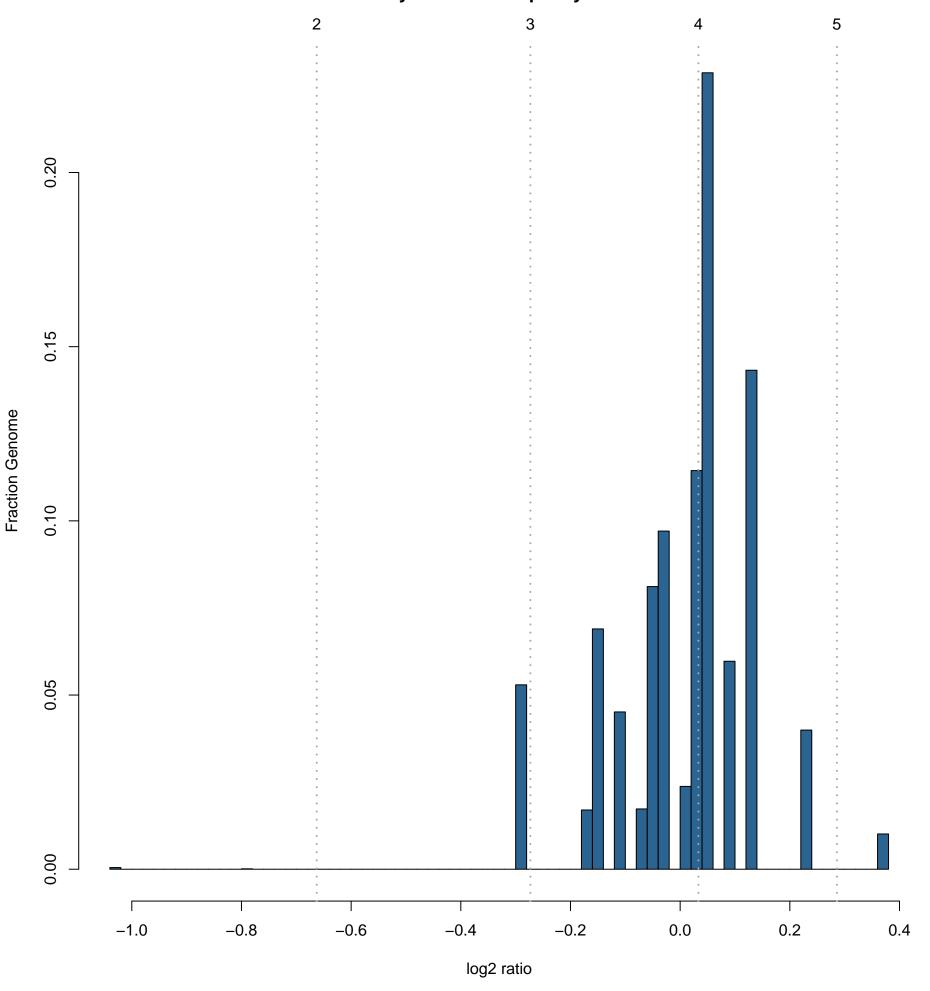
SCNA-fit log-likelihood: -11082.1

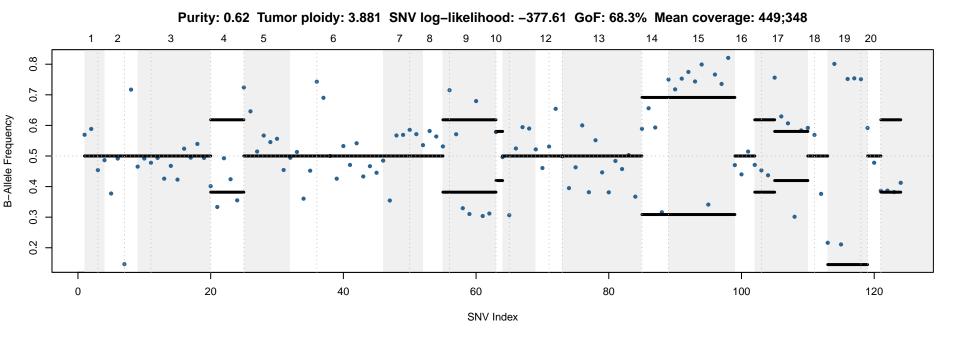




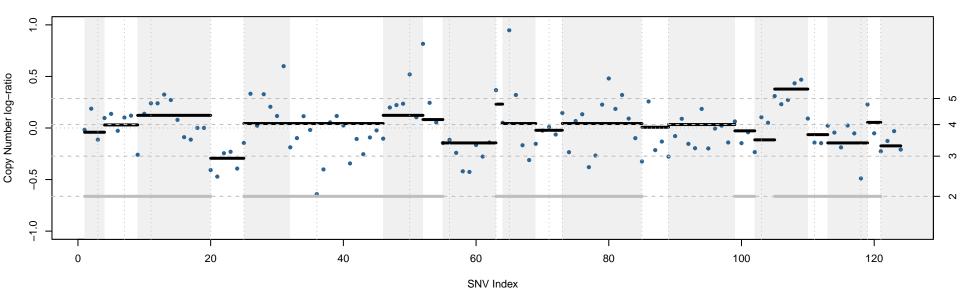


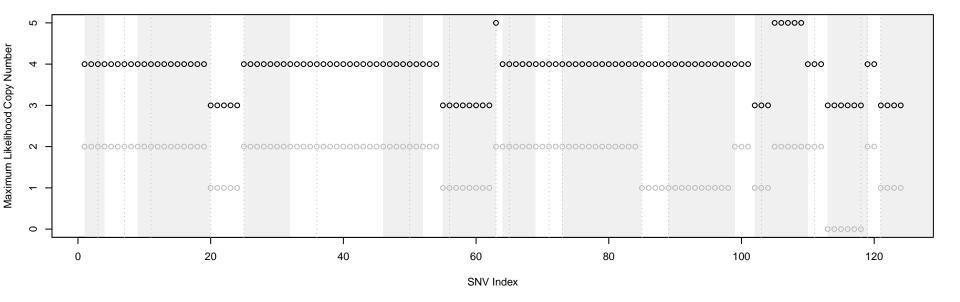
Purity: 0.62 Tumor ploidy: 3.881

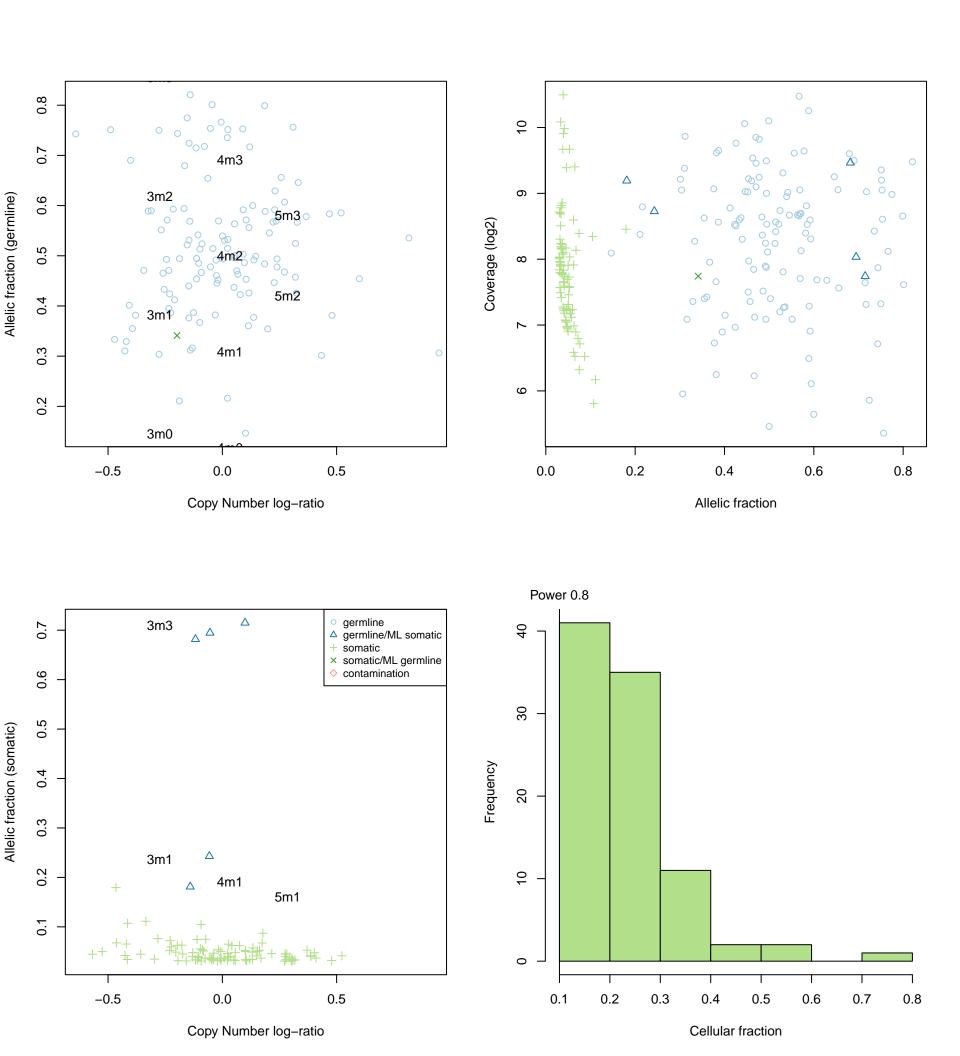






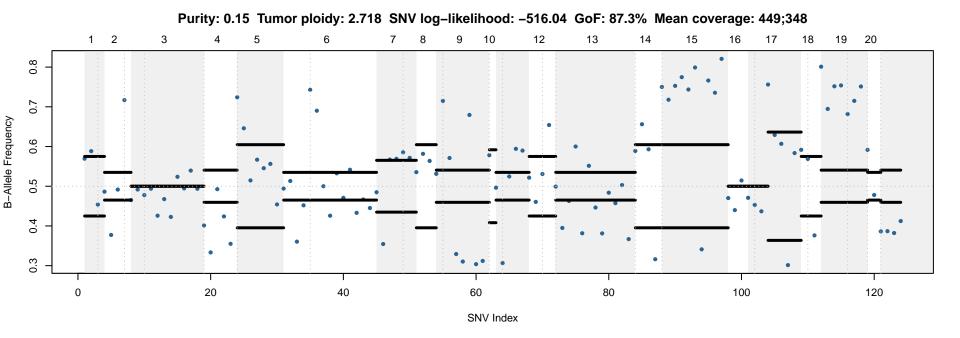




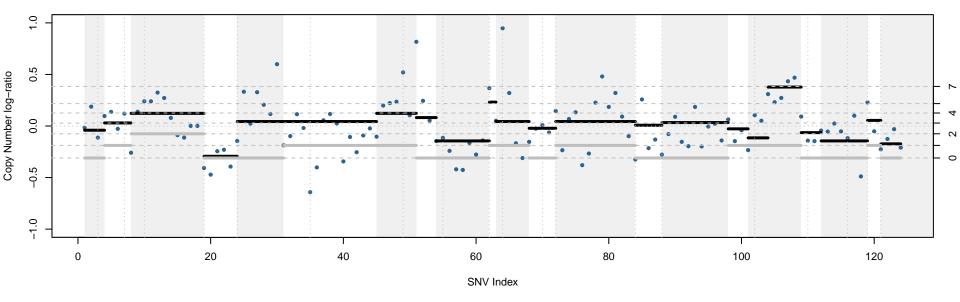


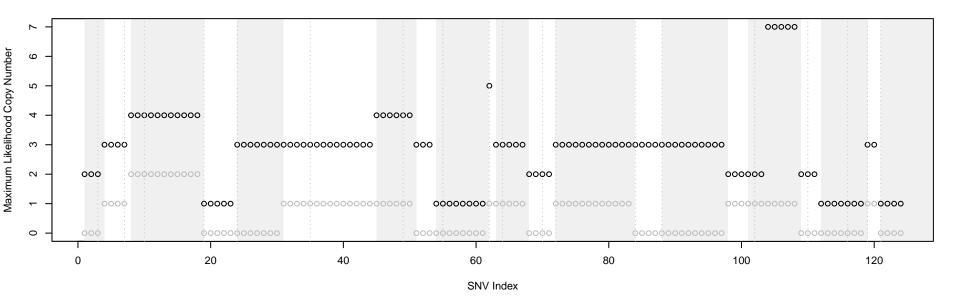
Purity: 0.15 Tumor ploidy: 2.718 2 0 3 7 5 0.20 0.15 Fraction Genome 0.10 0.05 0.00 -0.3 -0.2 -0.1 0.0 0.1 0.2 0.3 0.4

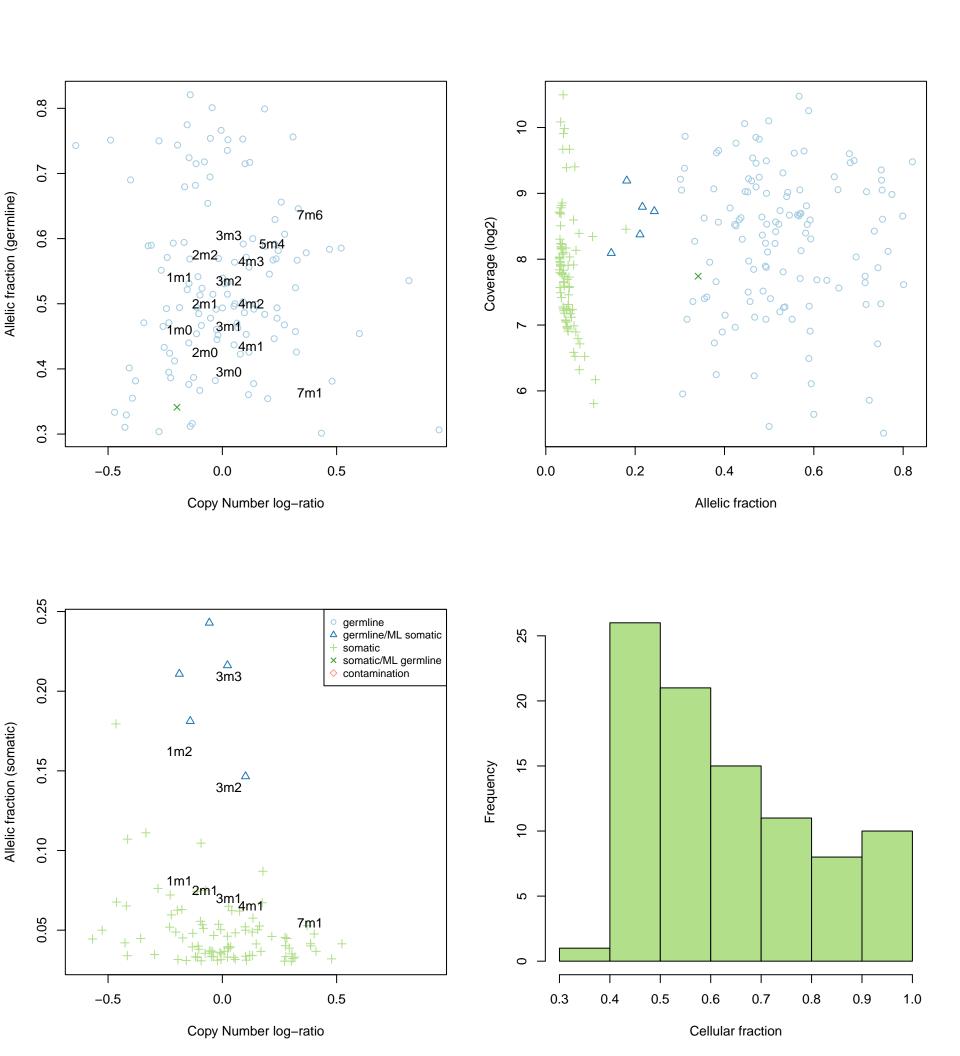
log2 ratio



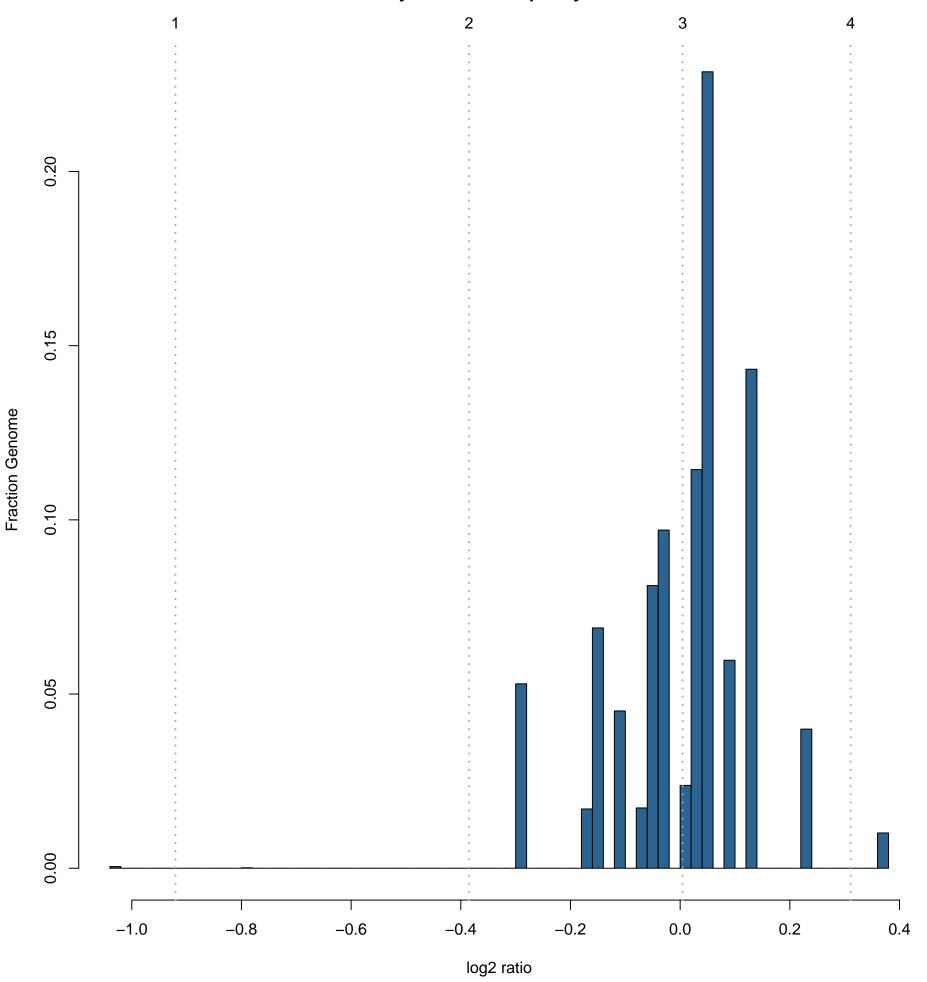
SCNA-fit log-likelihood: -11109.45

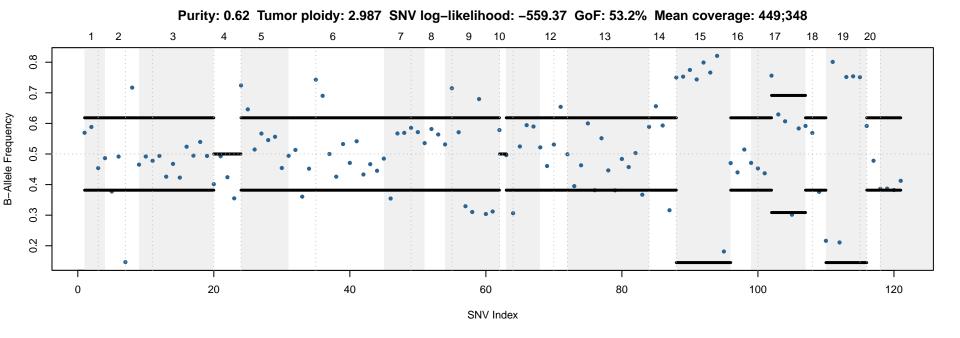




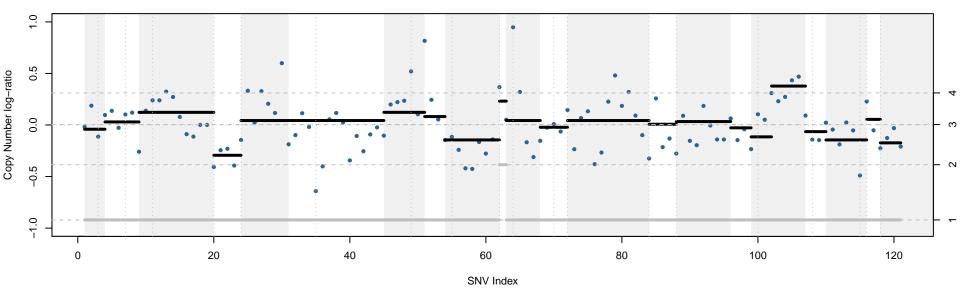


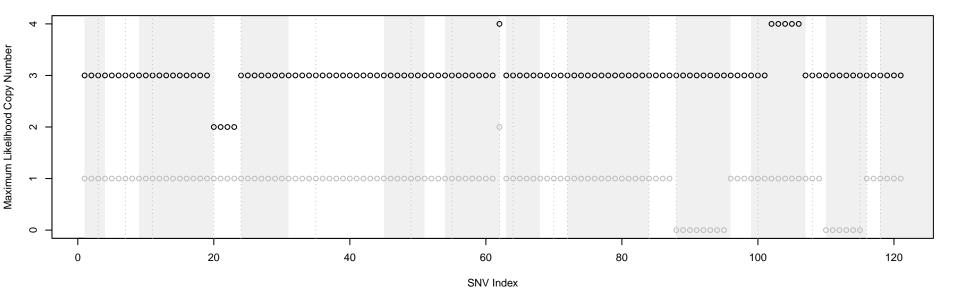
Purity: 0.62 Tumor ploidy: 2.987

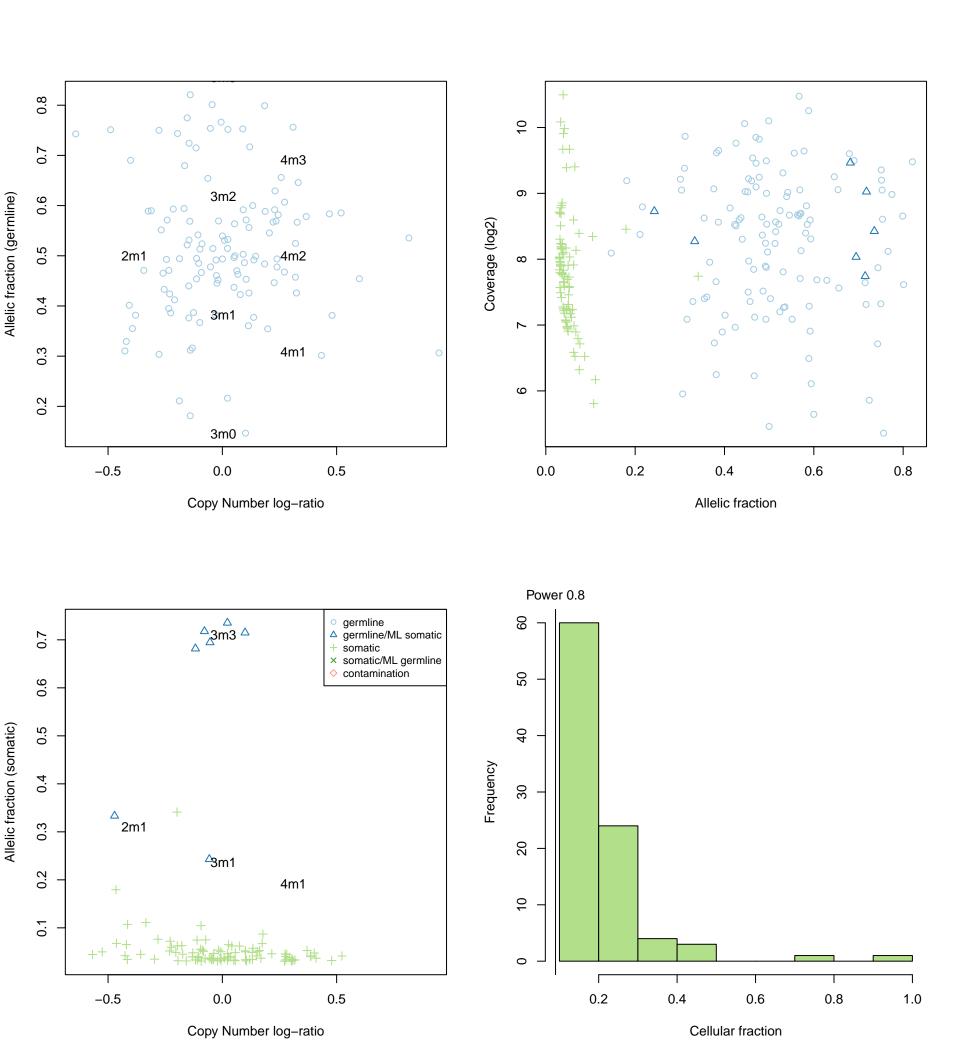




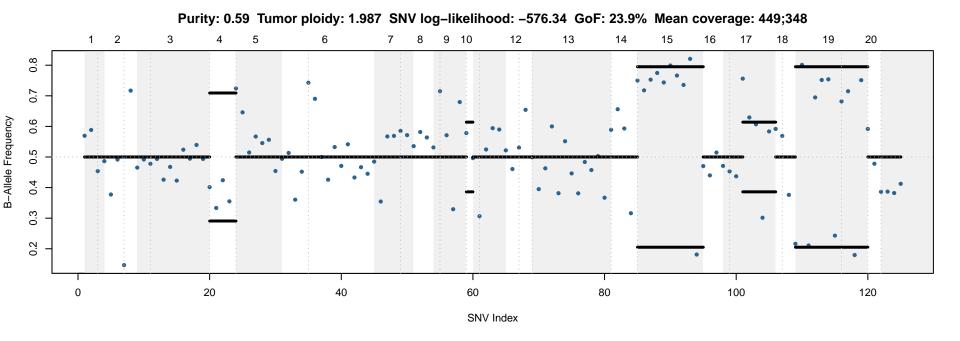
SCNA-fit log-likelihood: -11296.03







Purity: 0.59 Tumor ploidy: 1.987 2 3 0.20 0.15 Fraction Genome 0.10 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 0.4 log2 ratio



SCNA-fit log-likelihood: -11381.48

