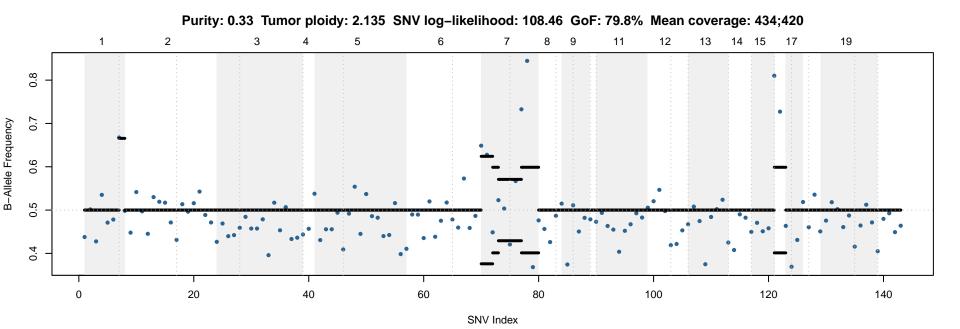
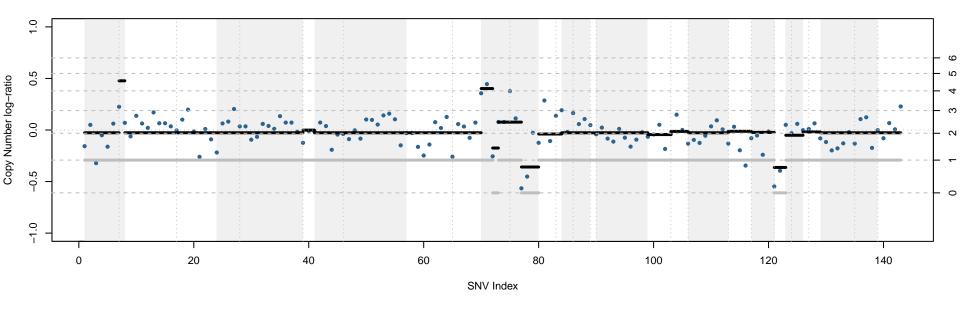
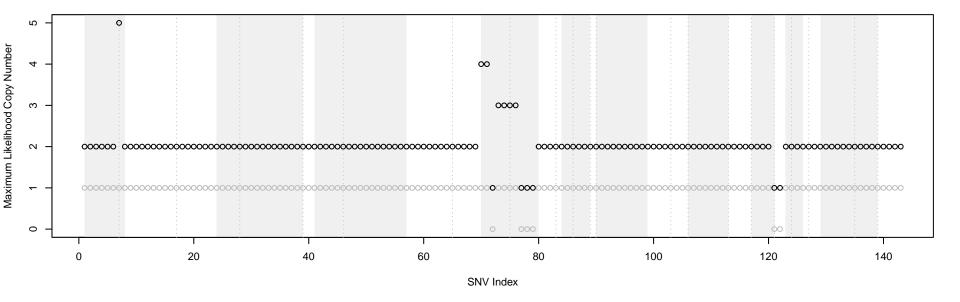
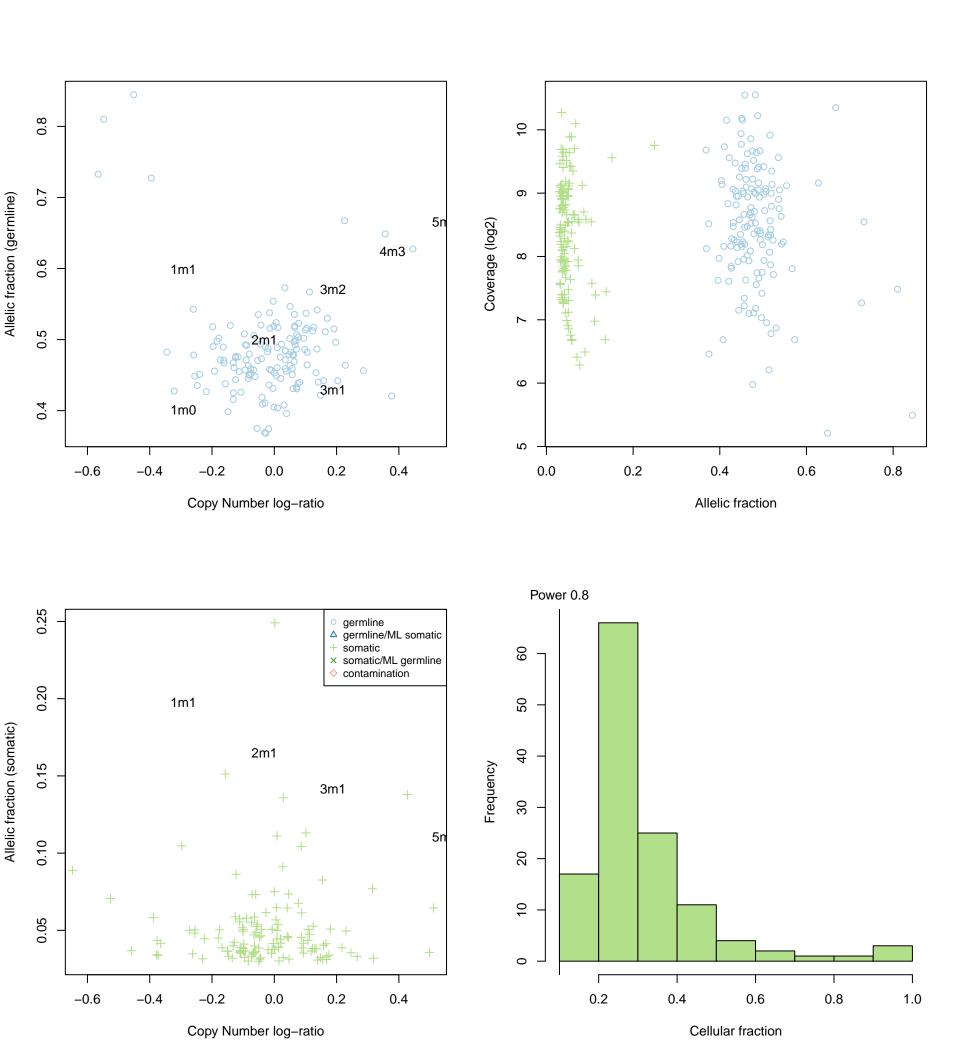
Purity: 0.33 Tumor ploidy: 2.135 3 2 5 6 0.5 Fraction Genome 0.3 0.0 -0.4 -0.2 0.0 0.2 0.4 0.6 log2 ratio



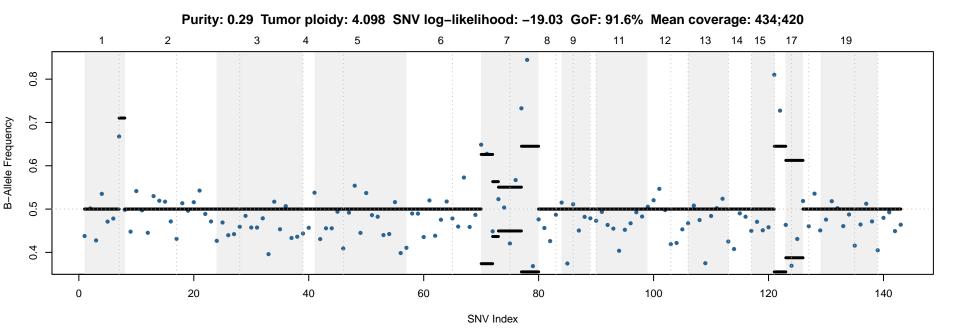
SCNA-fit log-likelihood: -3065.02



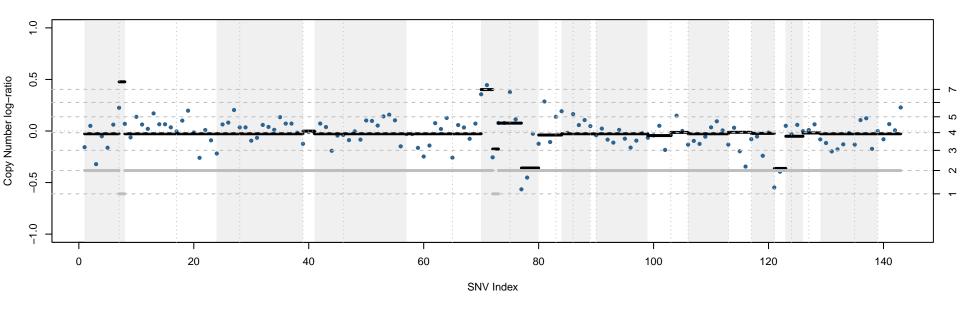


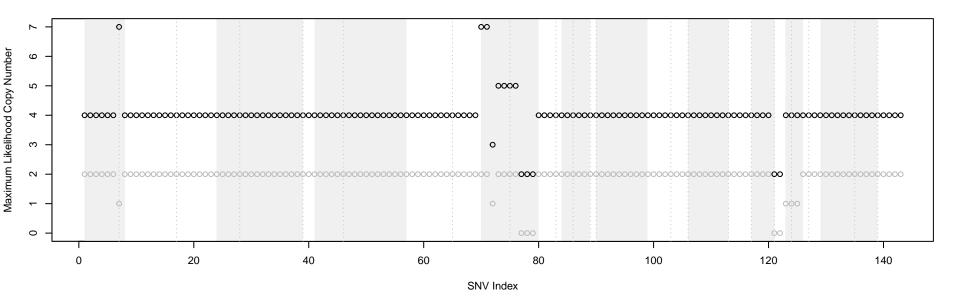


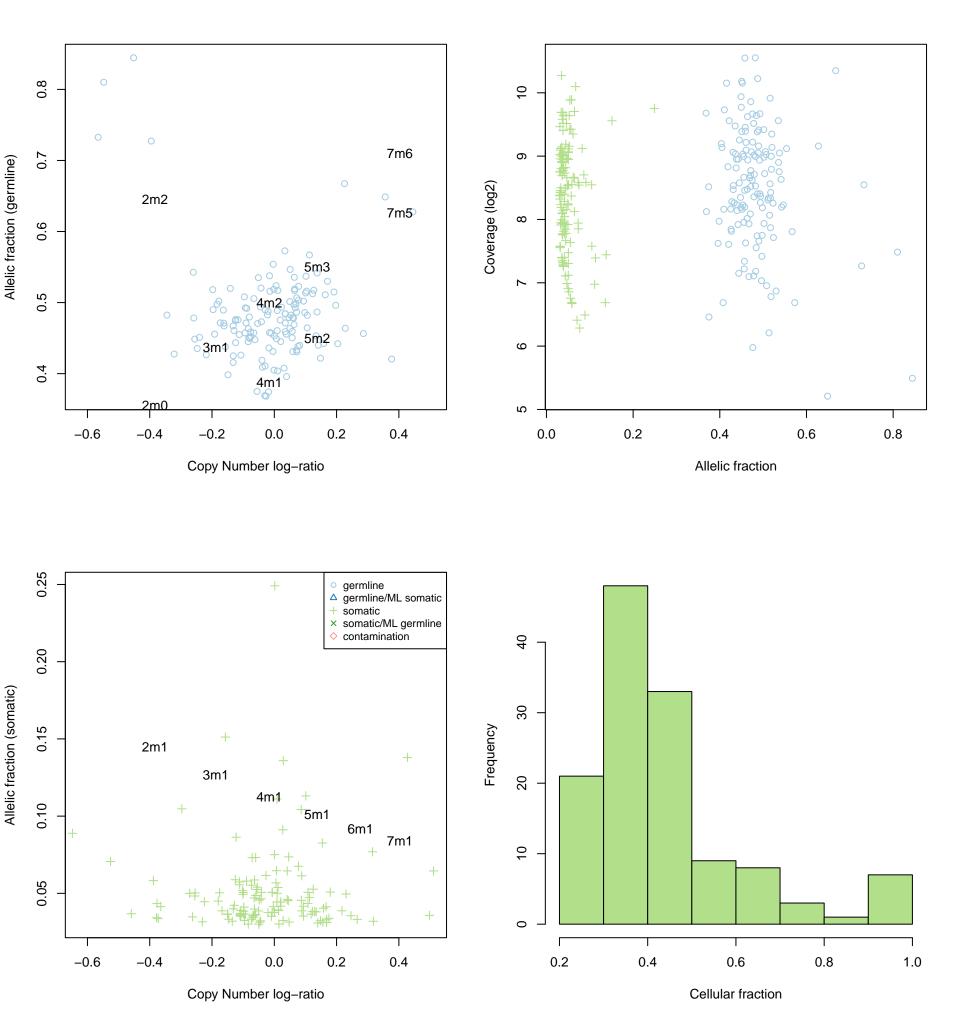
Purity: 0.29 Tumor ploidy: 4.098 2 3 7 0.5 Fraction Genome 0.3 0.2 0.1 0.0 -0.4 -0.2 0.0 0.2 0.4 0.6 log2 ratio



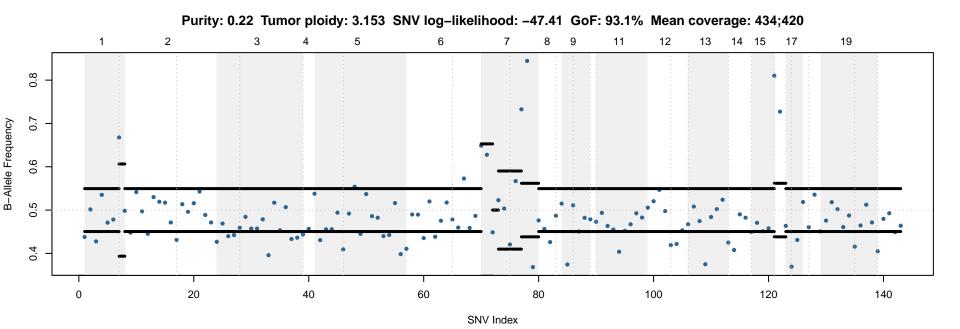
SCNA-fit log-likelihood: -3037.76



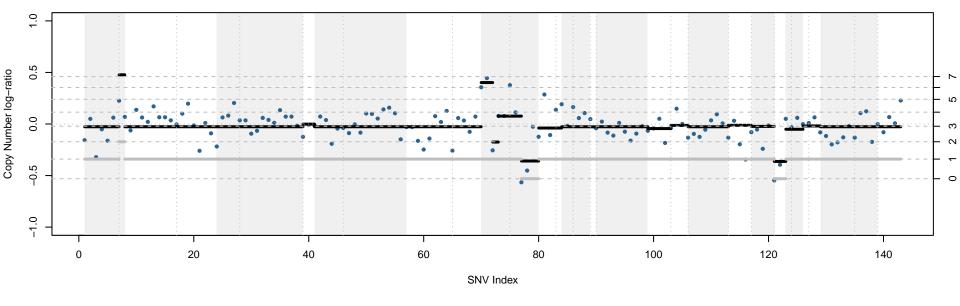


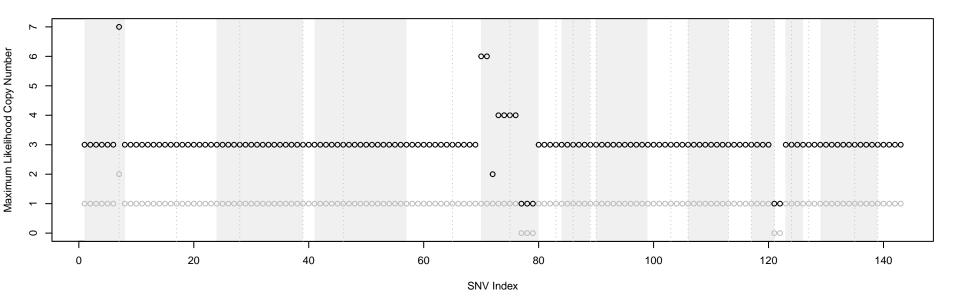


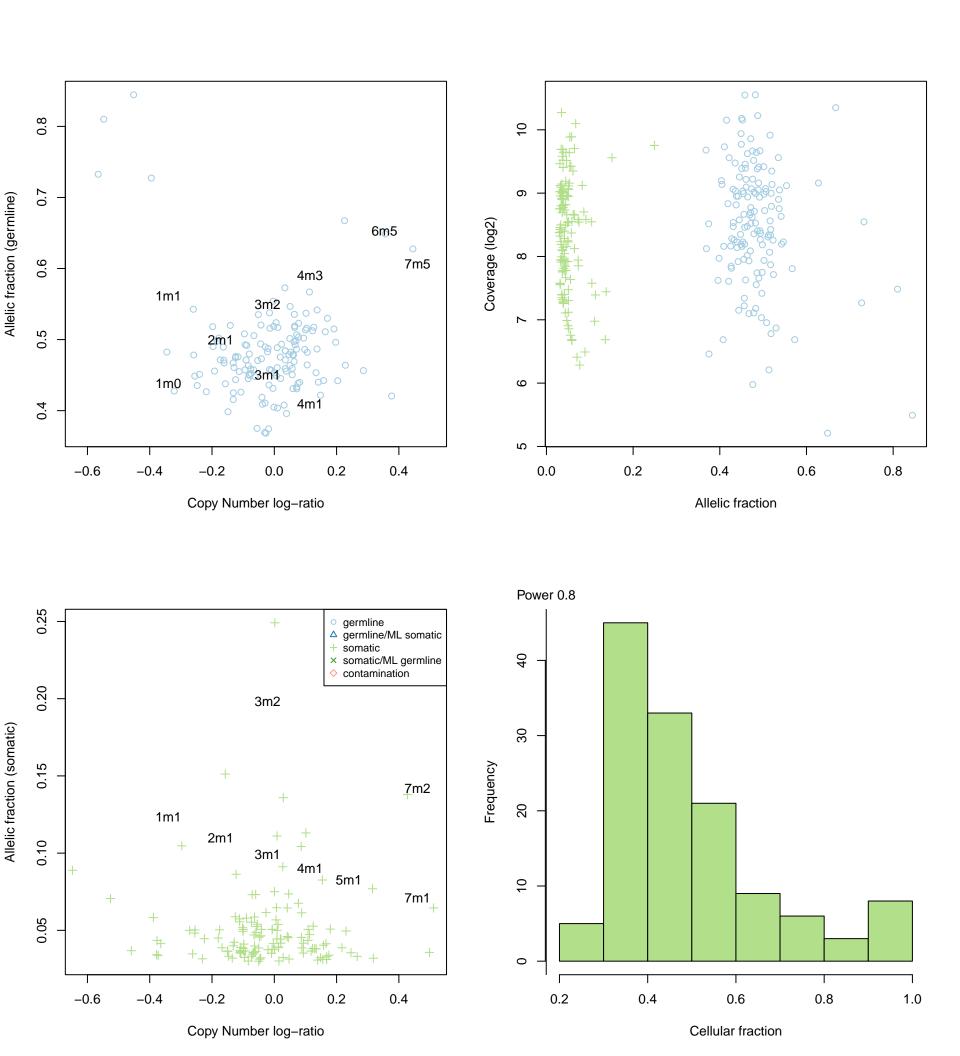
Purity: 0.22 Tumor ploidy: 3.153 2 0 3 6 7 0.5 Fraction Genome 0.3 0.1 0.0 -0.4 -0.2 0.0 0.2 0.4 0.6 log2 ratio



SCNA-fit log-likelihood: -2997.15

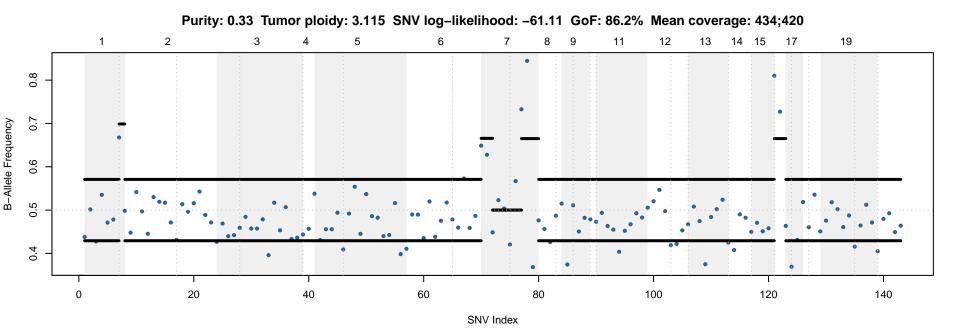




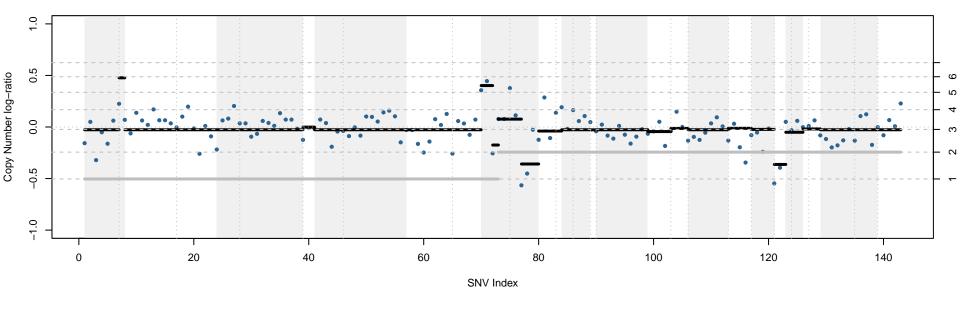


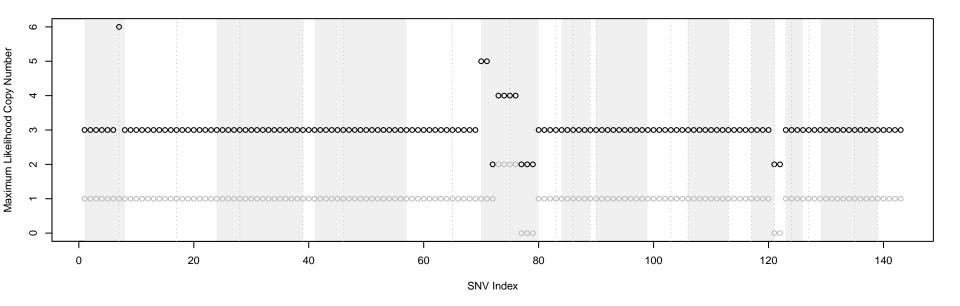
Purity: 0.33 Tumor ploidy: 3.115 3 2 5 7 6 0.5 Fraction Genome 0.3 0.2 0.1 0.0 -0.4 -0.2 0.0 0.2 0.4 0.6

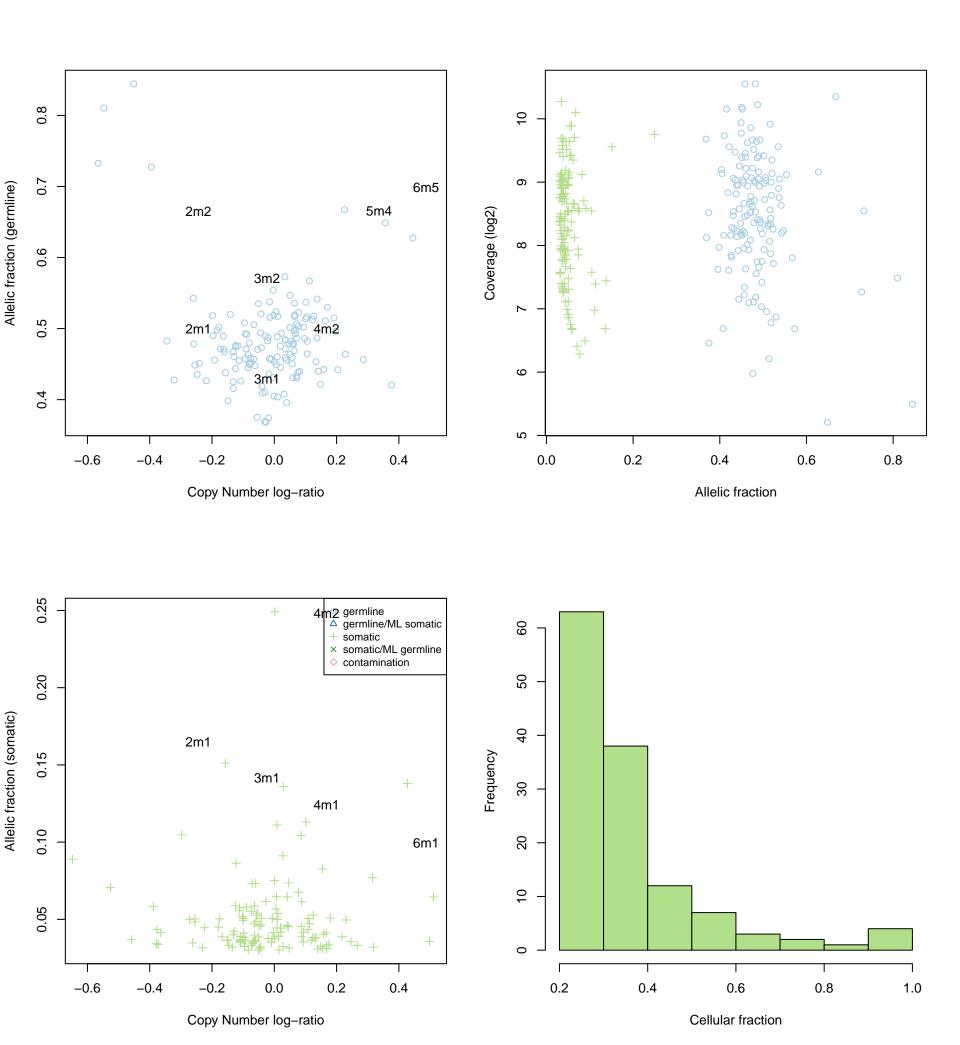
log2 ratio



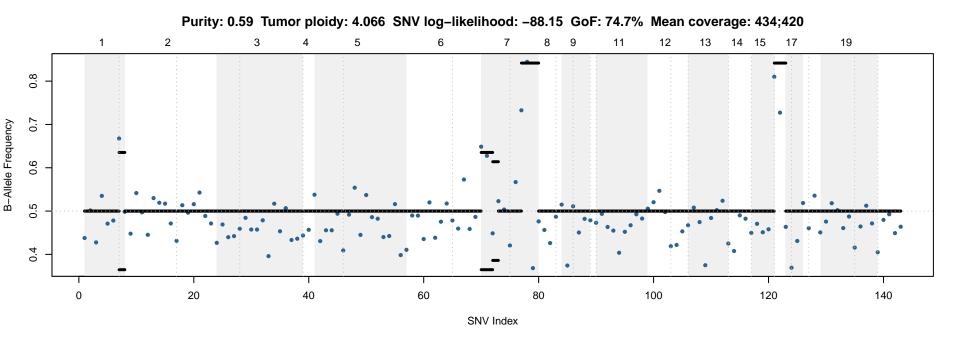
SCNA-fit log-likelihood: -3025.86



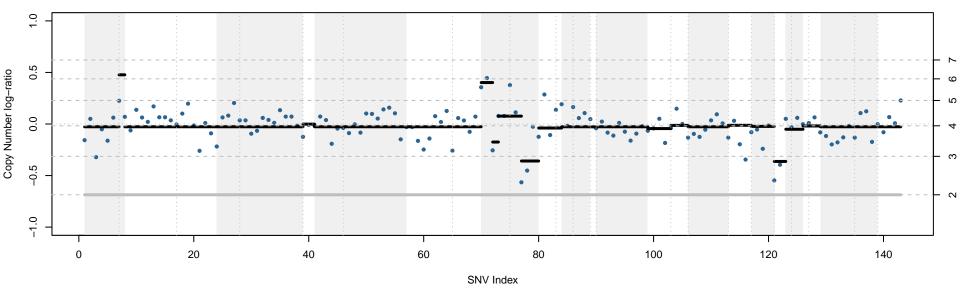


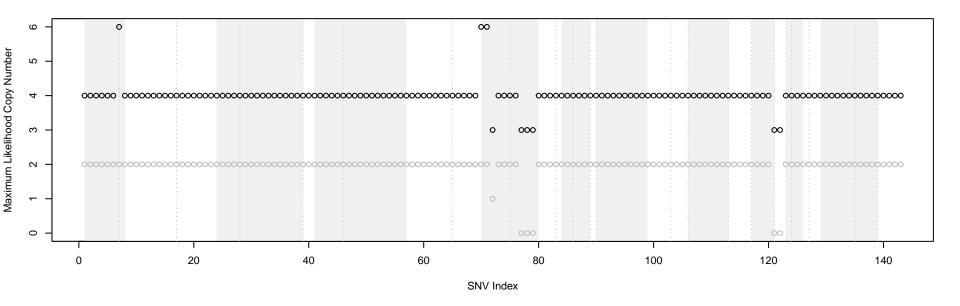


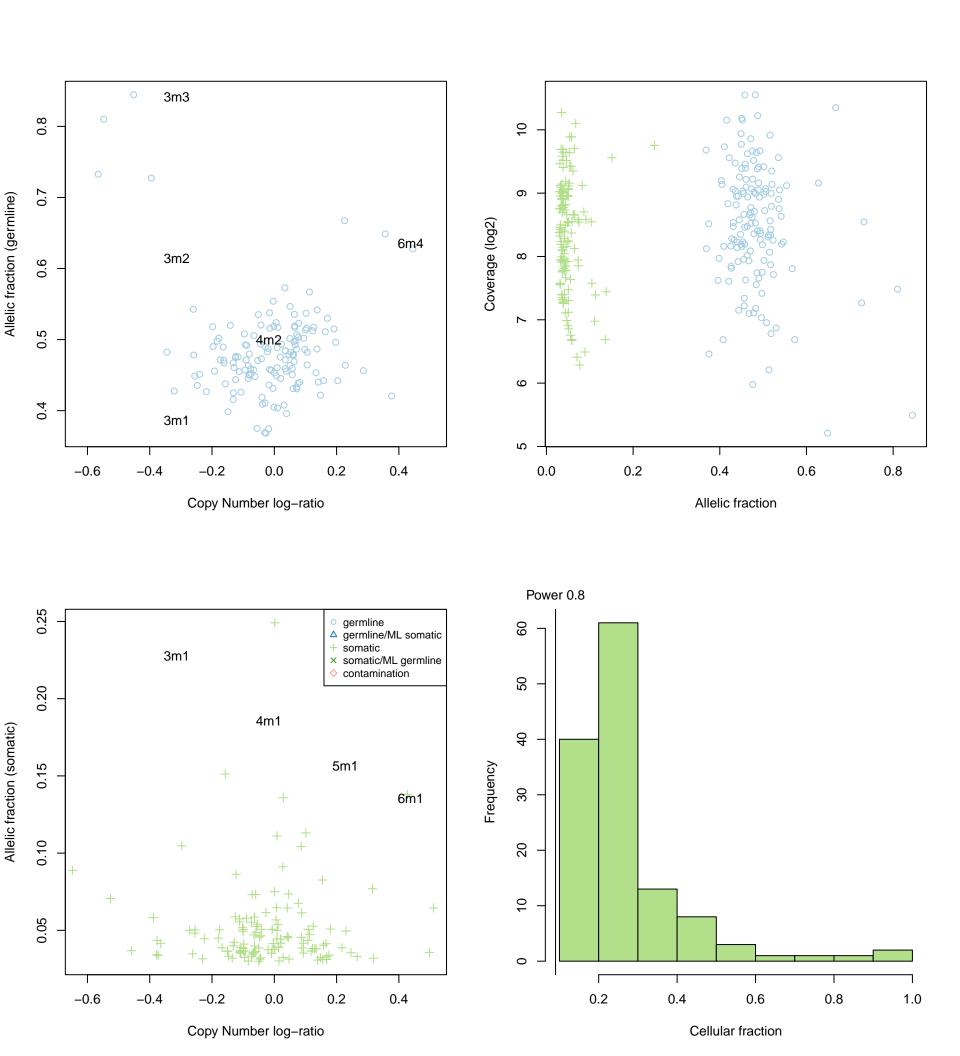
Purity: 0.59 Tumor ploidy: 4.066 3 6 7 0.5 Fraction Genome 0.3 0.2 0.1 0.0 -0.4 -0.2 0.0 0.2 0.4 0.6 log2 ratio



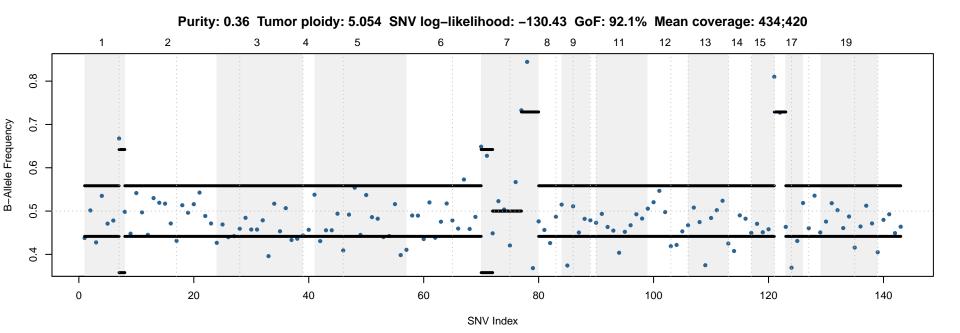
SCNA-fit log-likelihood: -3013.66



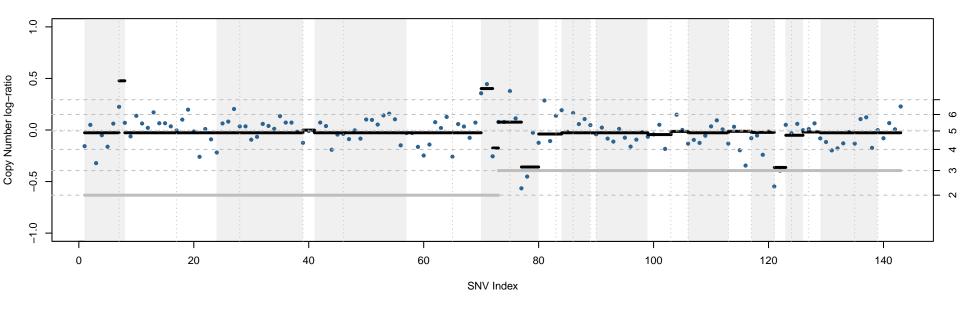


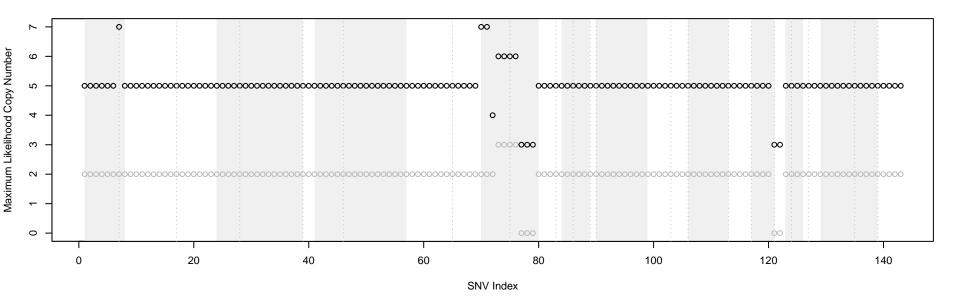


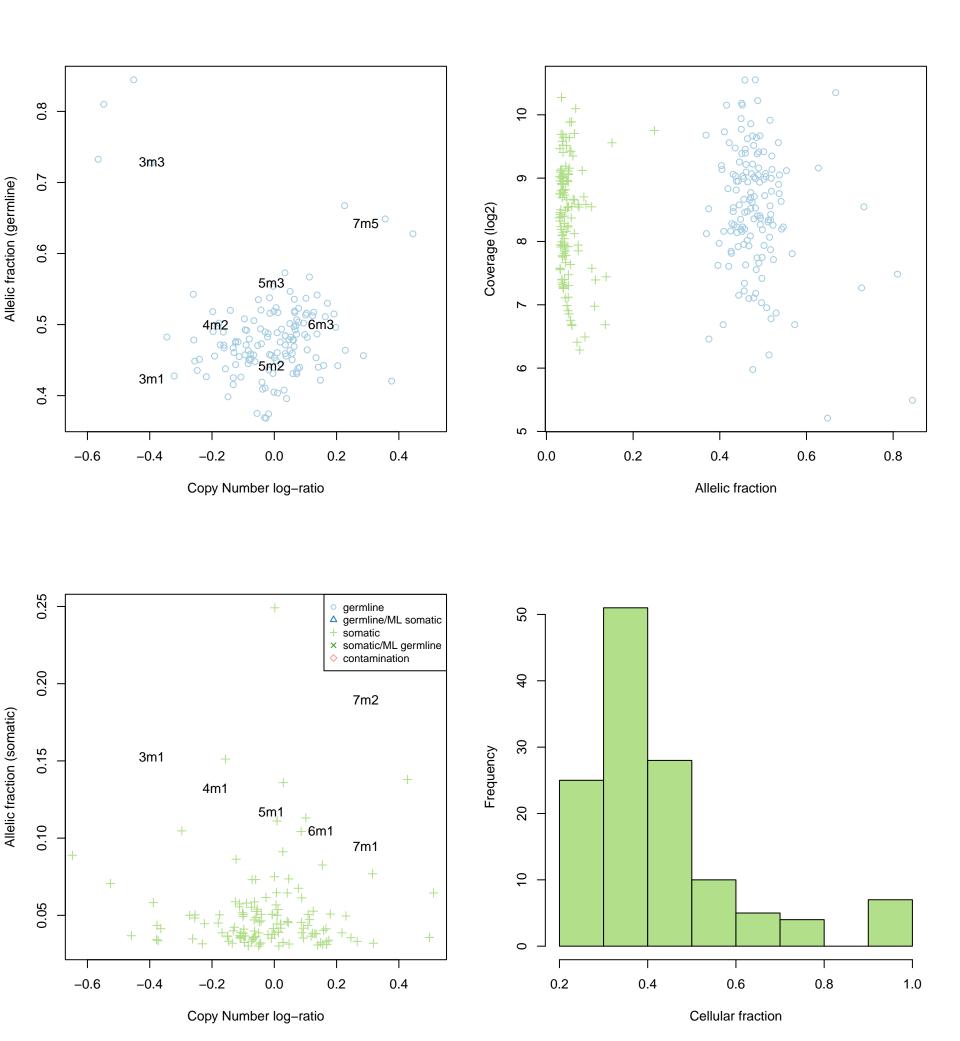
Purity: 0.36 Tumor ploidy: 5.054 5 3 6 0.5 Fraction Genome 0.3 0.2 0.1 0.0 -0.4 -0.2 0.0 0.2 0.4 0.6 log2 ratio



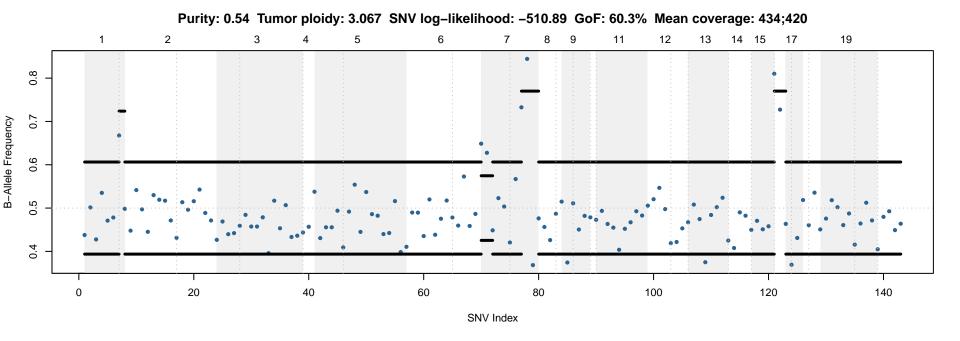
SCNA-fit log-likelihood: -3282.58



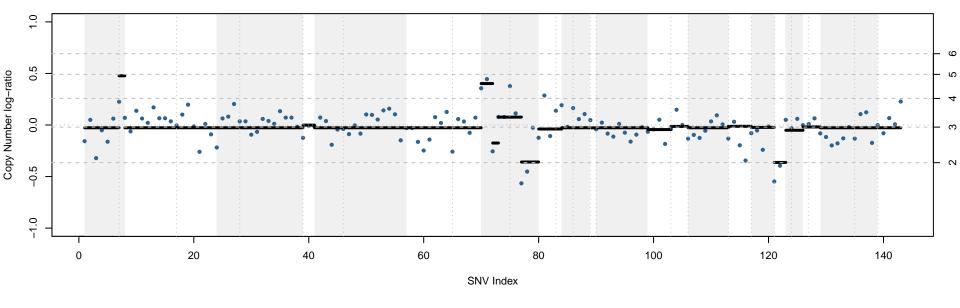


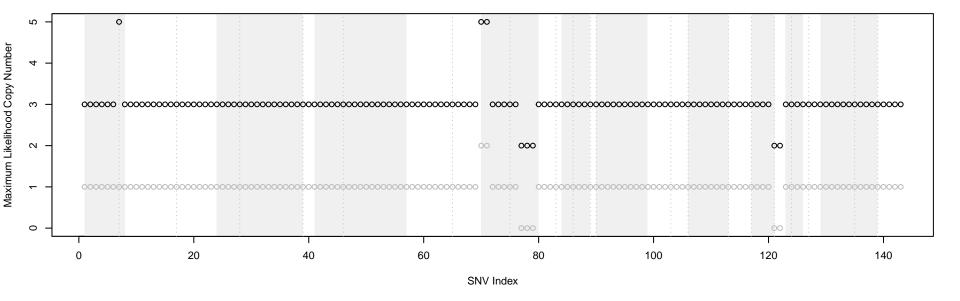


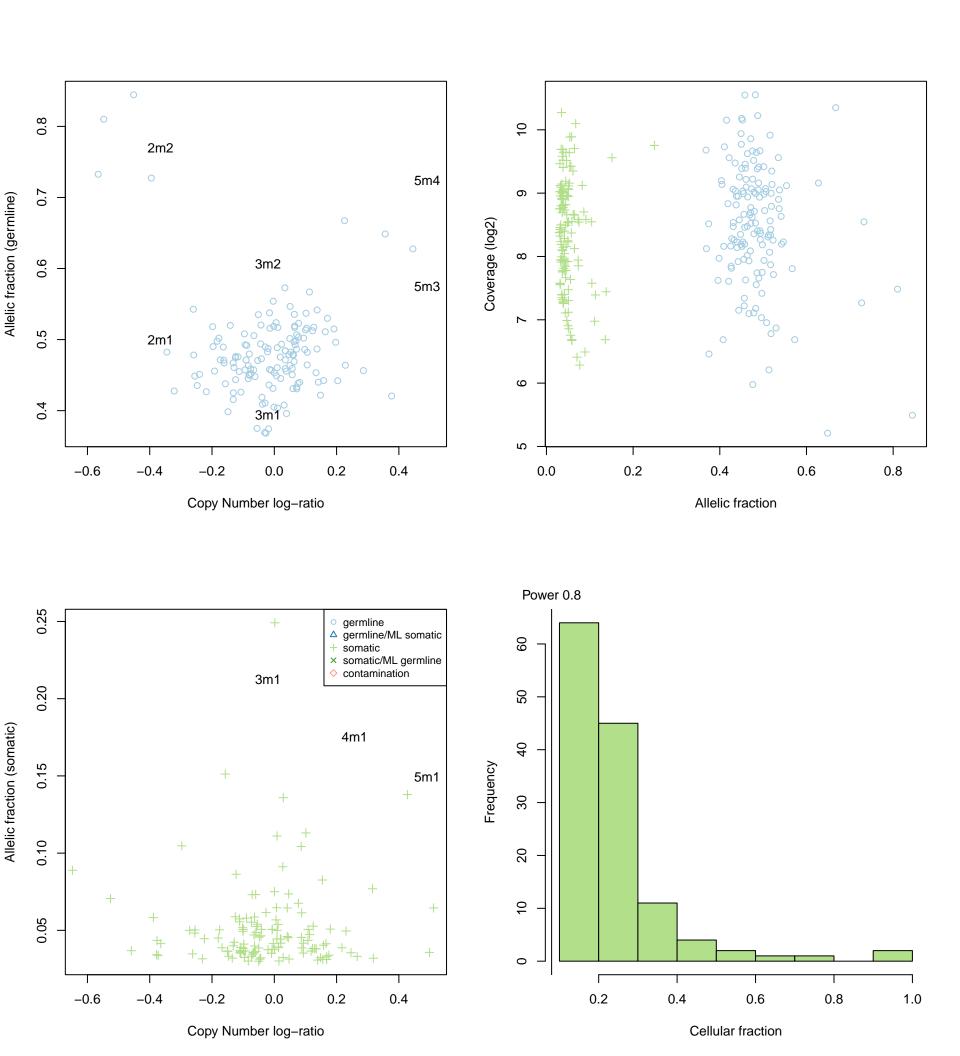
Purity: 0.54 Tumor ploidy: 3.067 2 6 5 0.5 Fraction Genome 0.3 0.2 0.1 0.0 -0.4 -0.2 0.0 0.2 0.4 0.6 log2 ratio



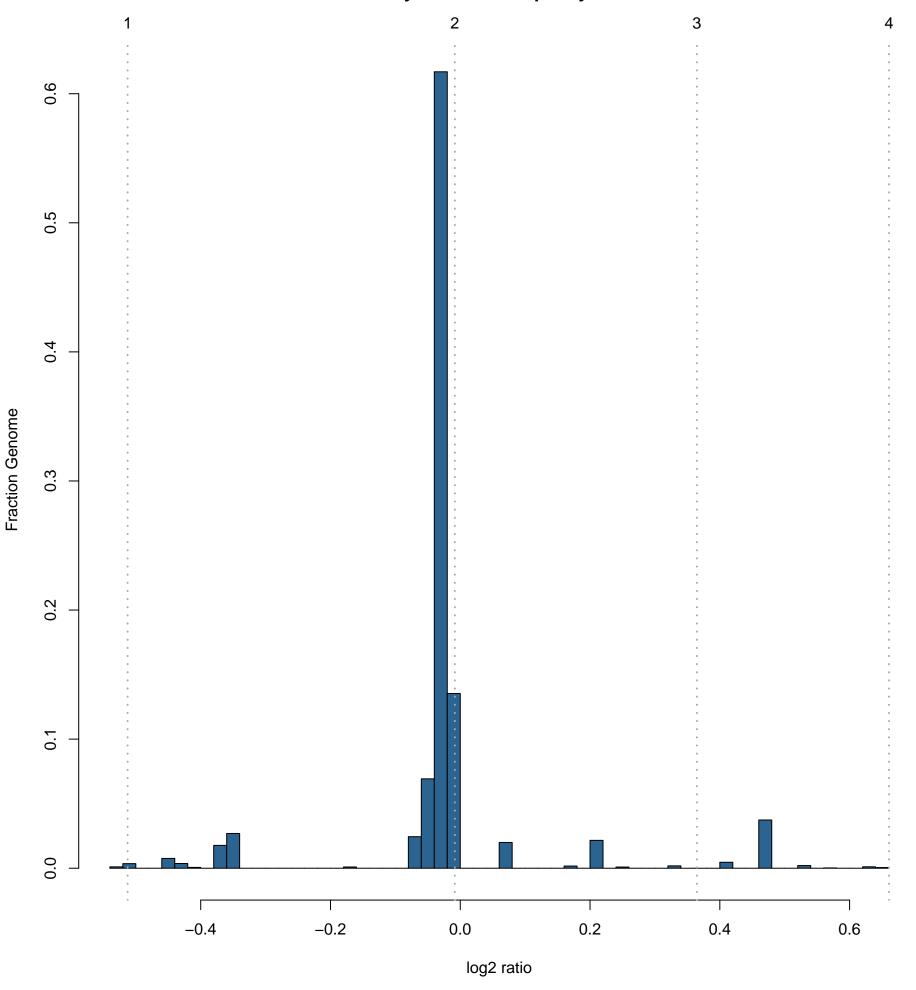
SCNA-fit log-likelihood: -2977.89

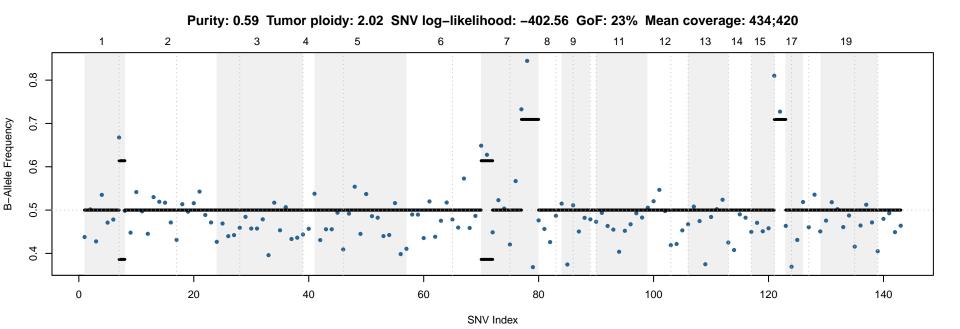




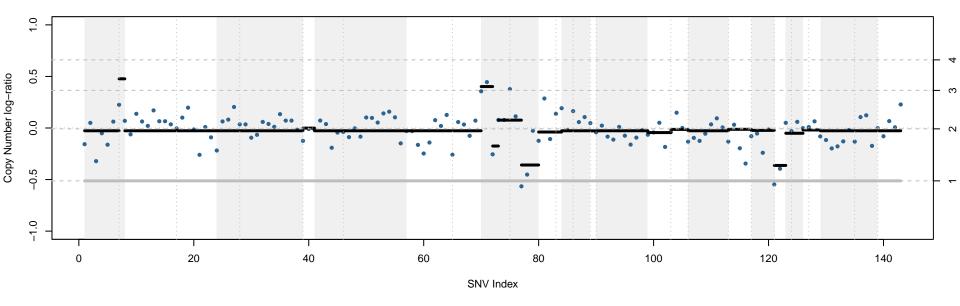


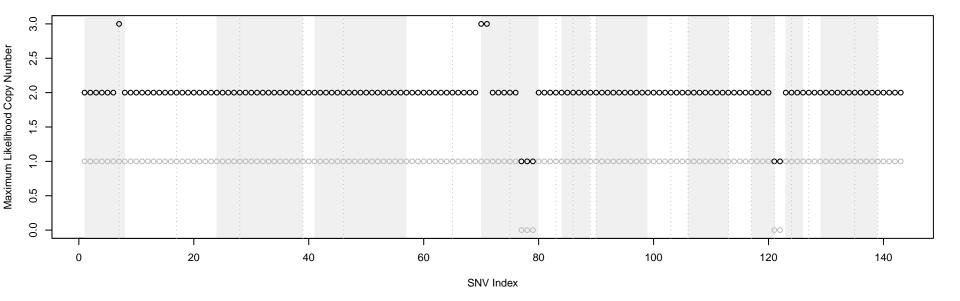
Purity: 0.59 Tumor ploidy: 2.02

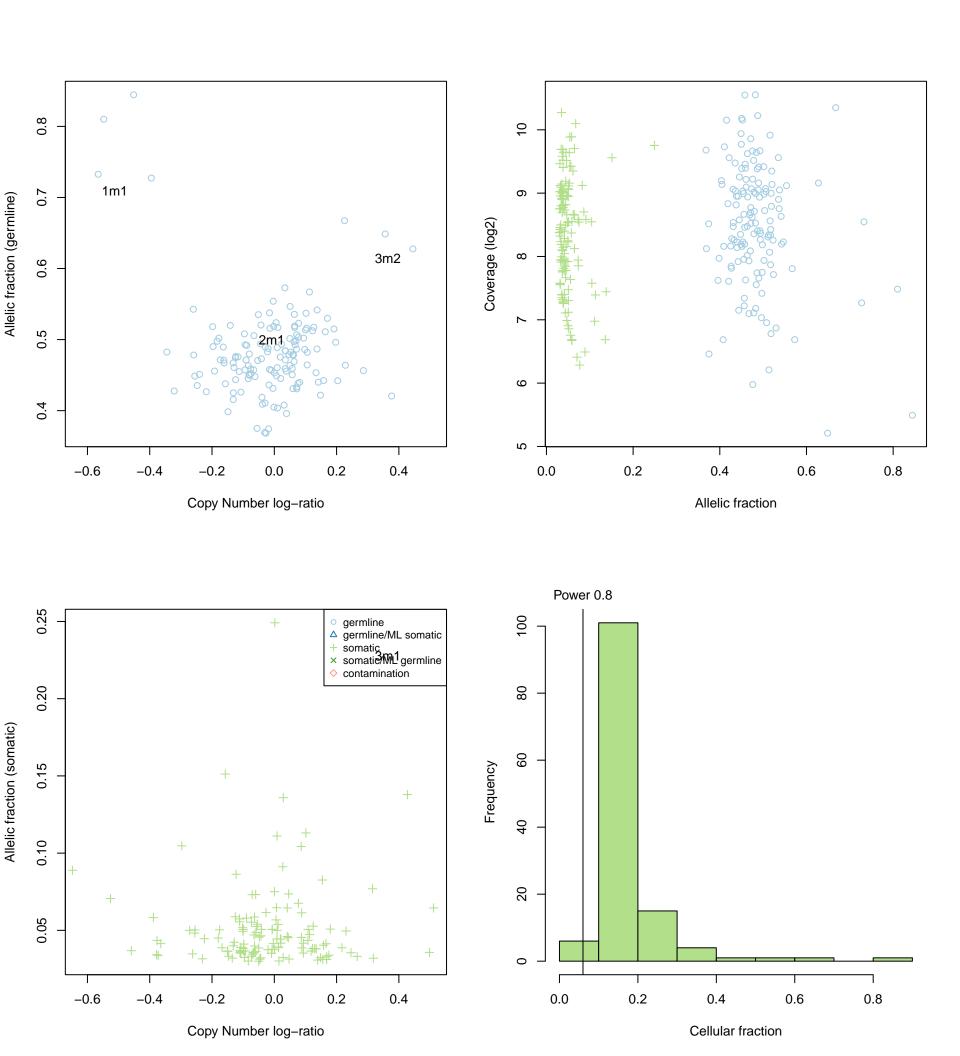




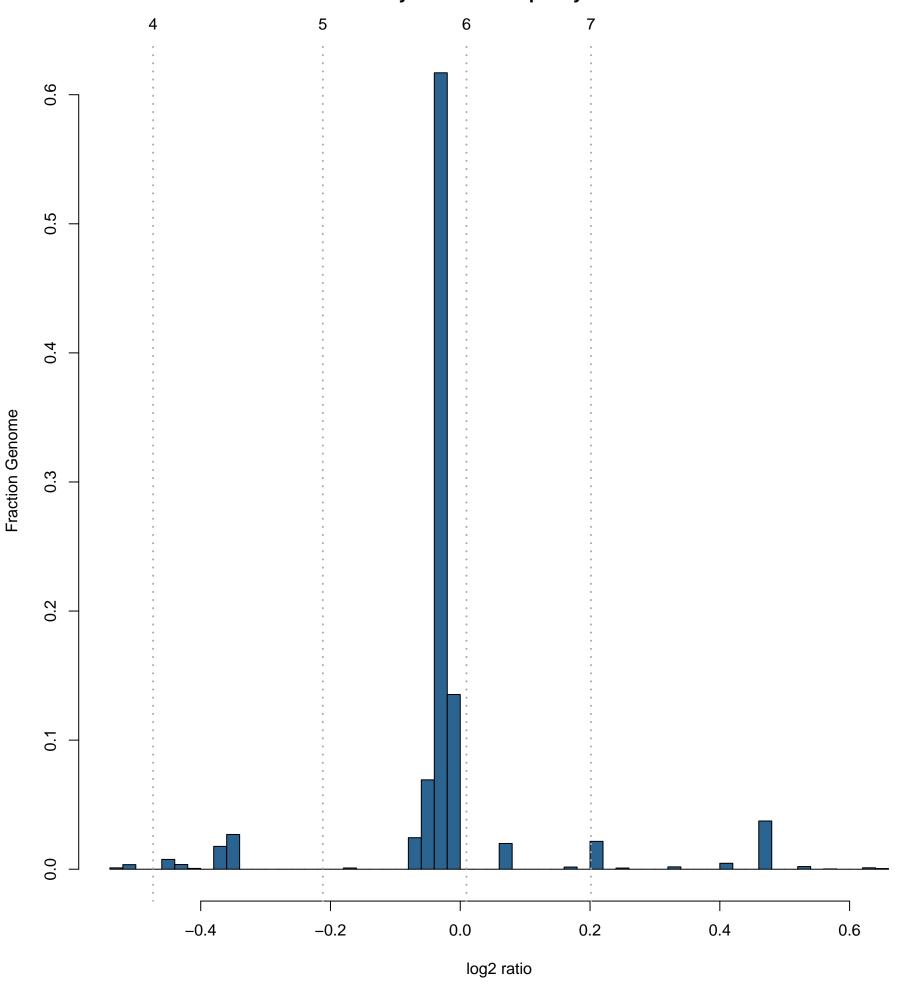
SCNA-fit log-likelihood: -3261.61

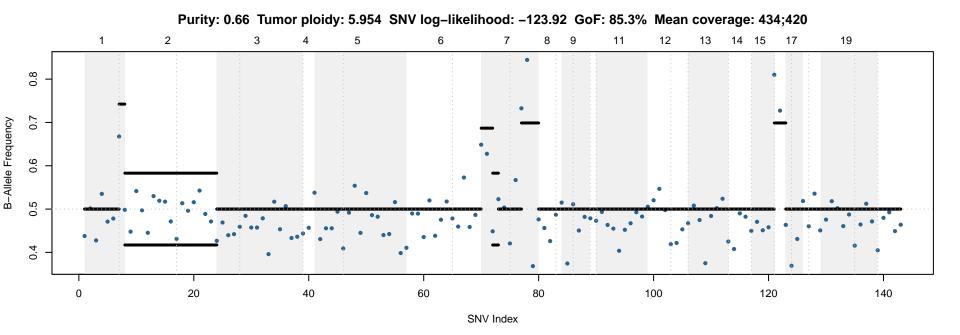




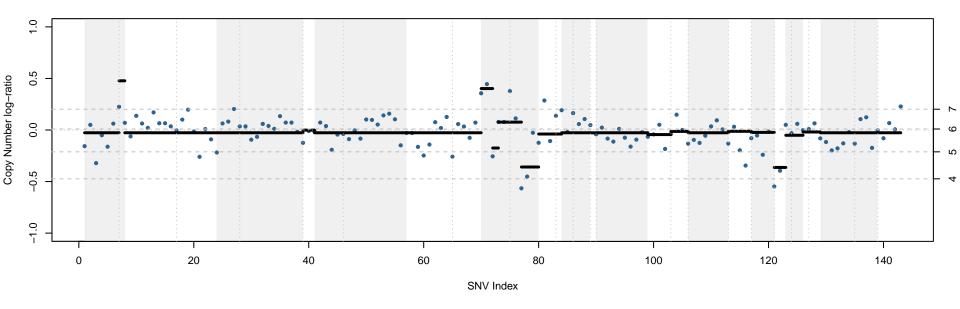


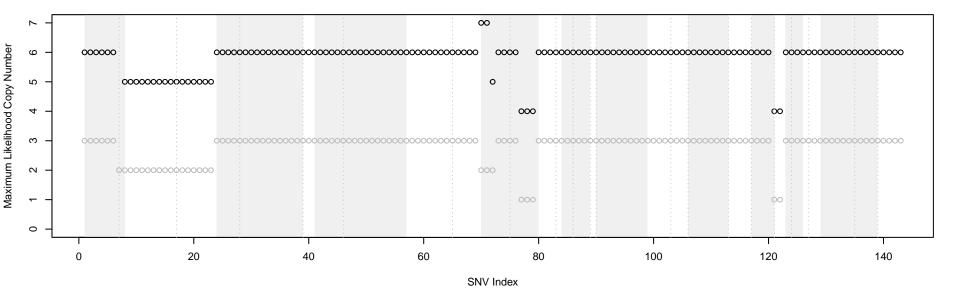
Purity: 0.66 Tumor ploidy: 5.954

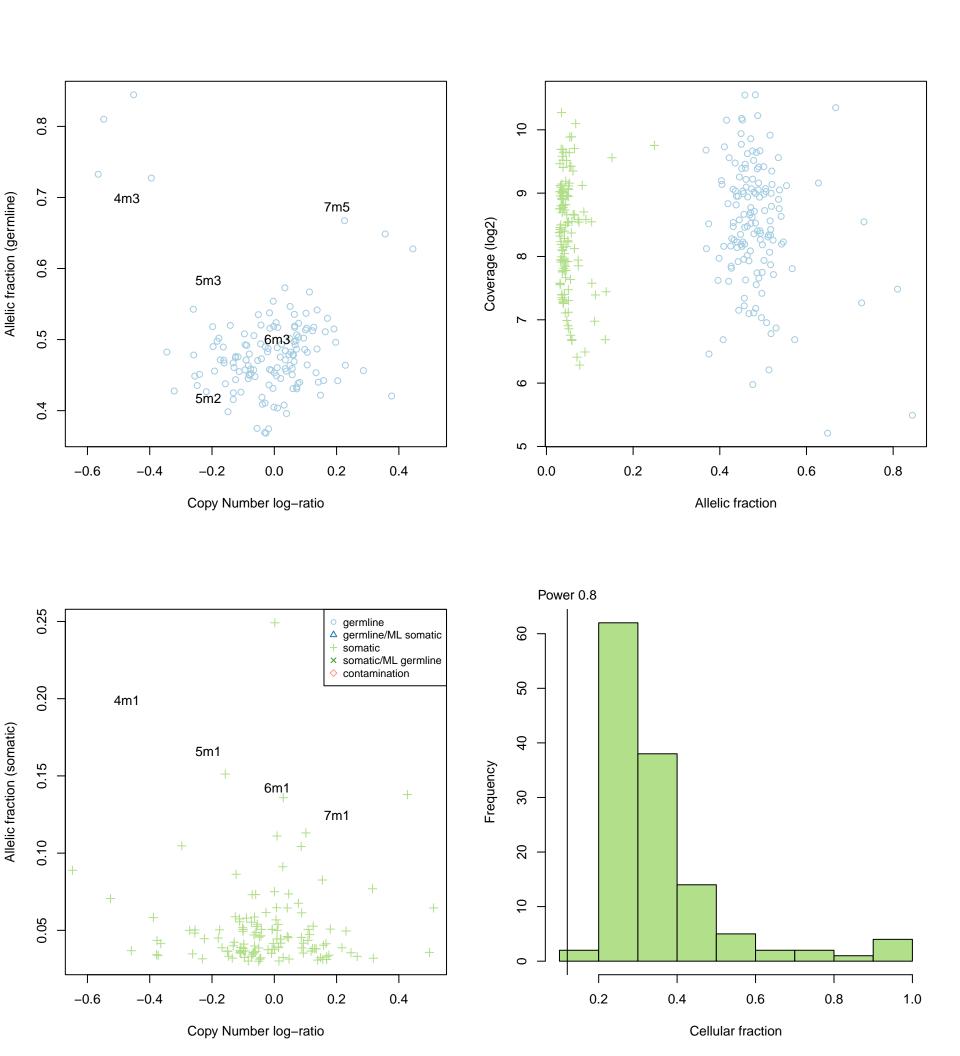




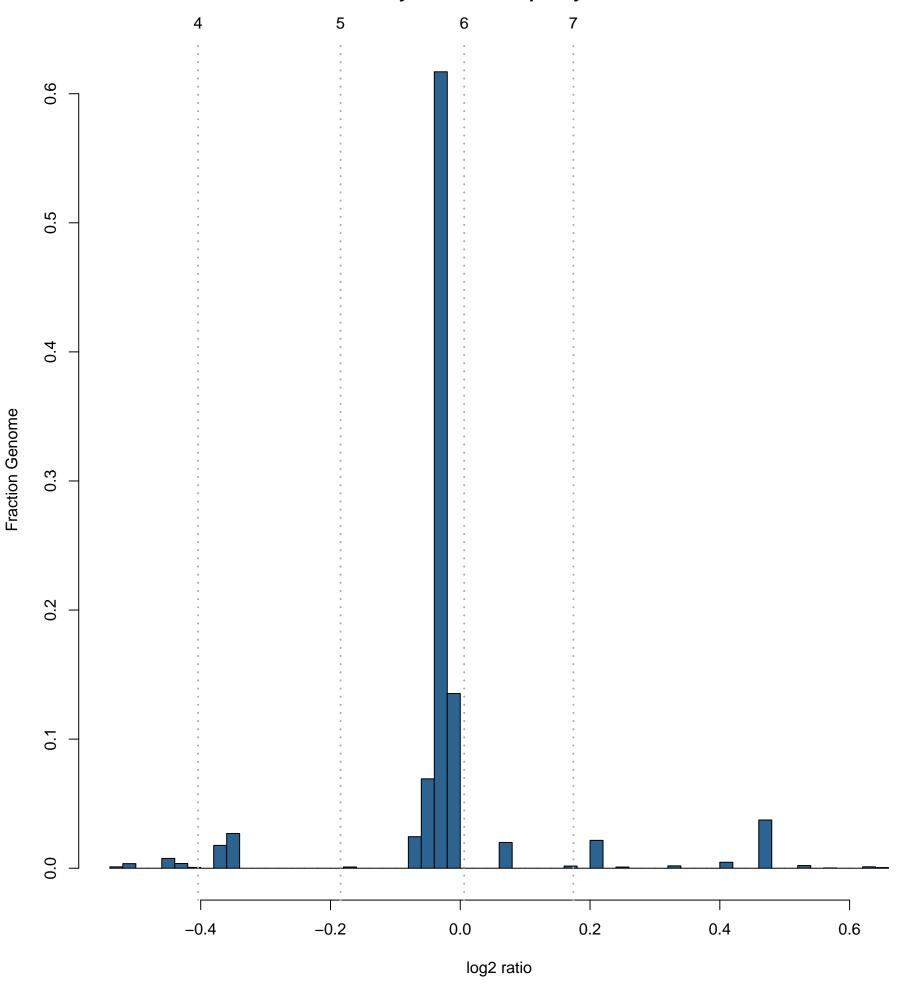
SCNA-fit log-likelihood: -4604.65

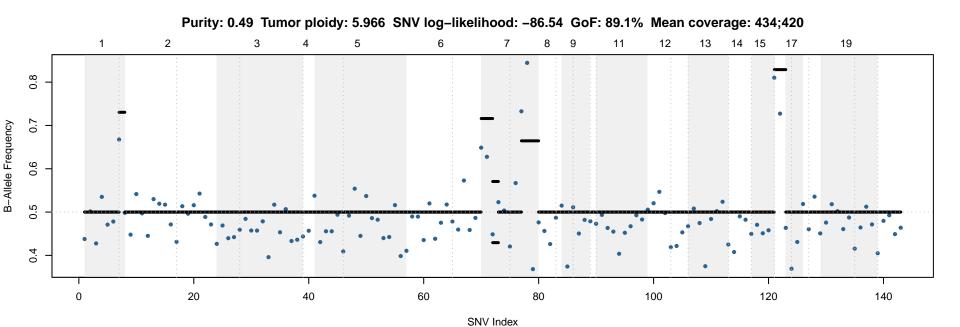




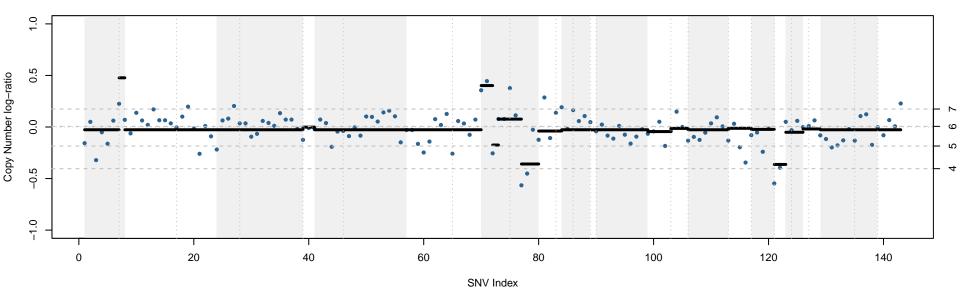


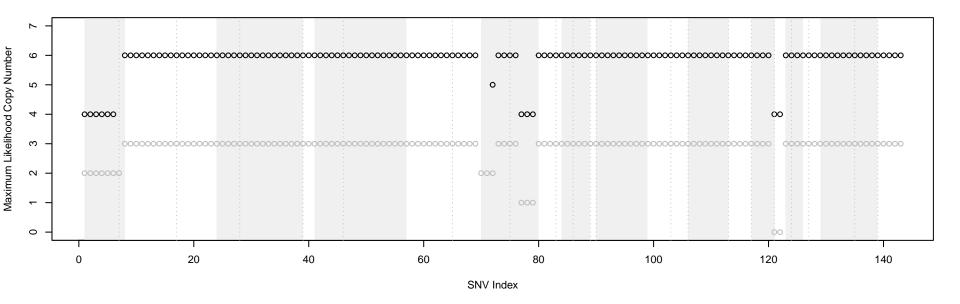
Purity: 0.49 Tumor ploidy: 5.966

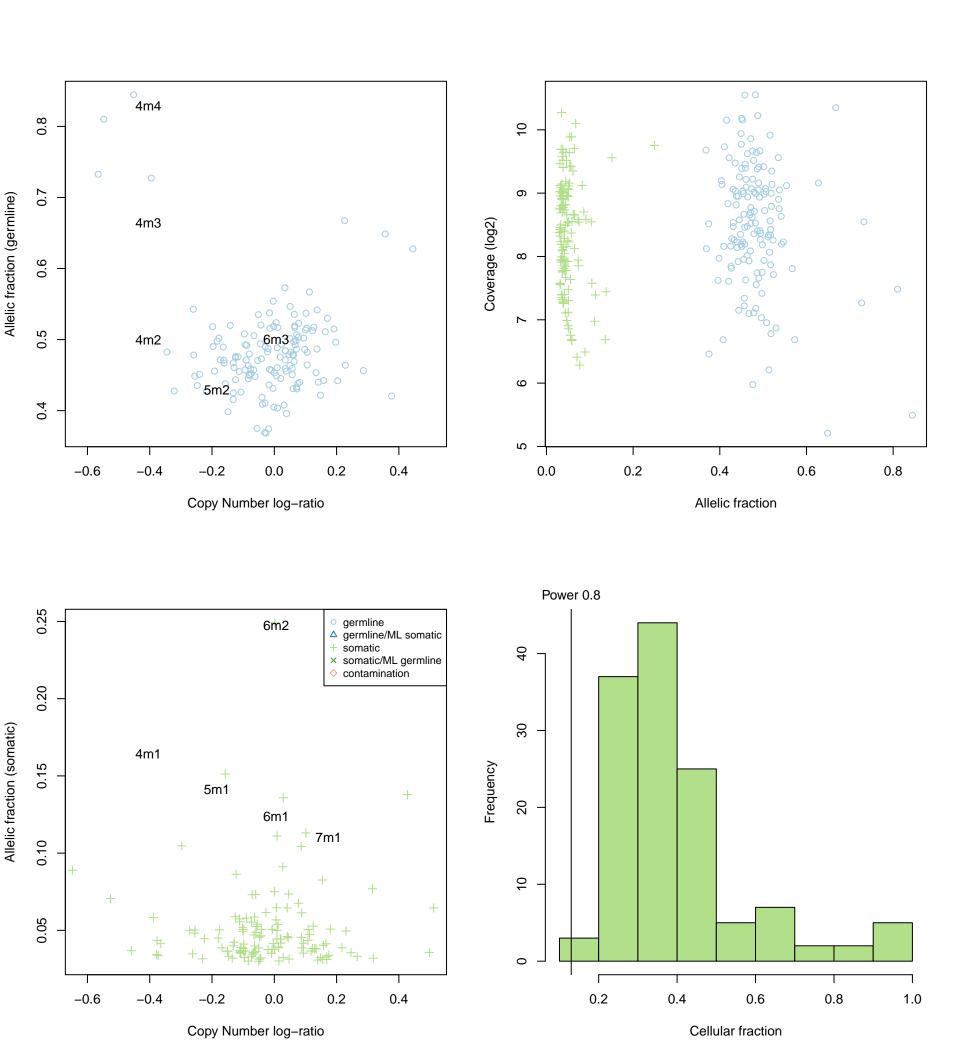




SCNA-fit log-likelihood: -5065.5

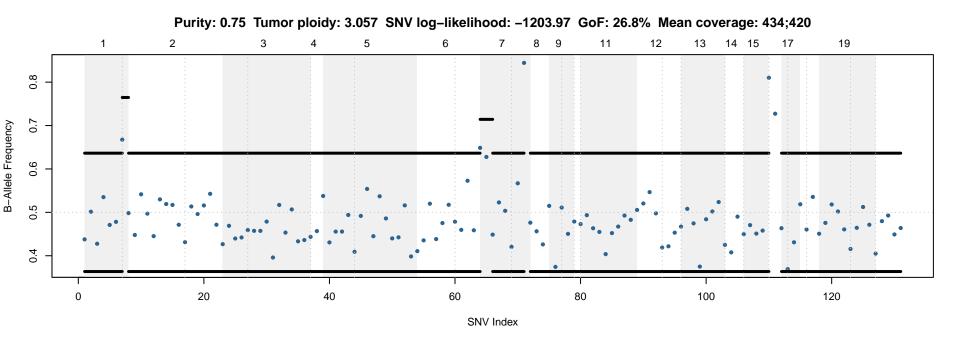






Purity: 0.75 Tumor ploidy: 3.057 2 5 0.5 Fraction Genome 0.3 0.2 0.1 0.0 -0.4 -0.2 0.0 0.2 0.4 0.6

log2 ratio



SCNA-fit log-likelihood: -3165.15

