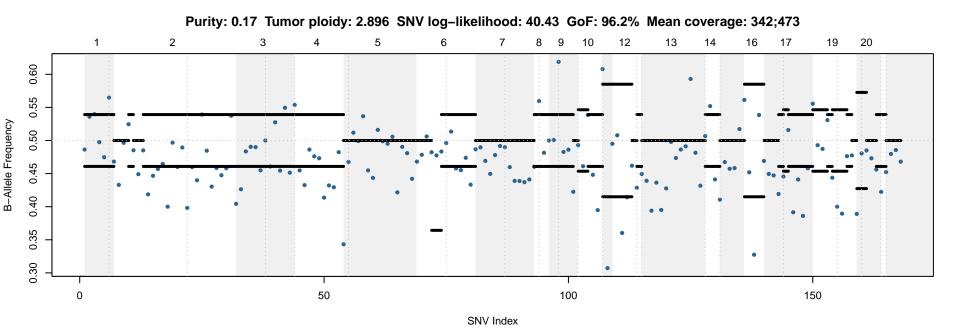
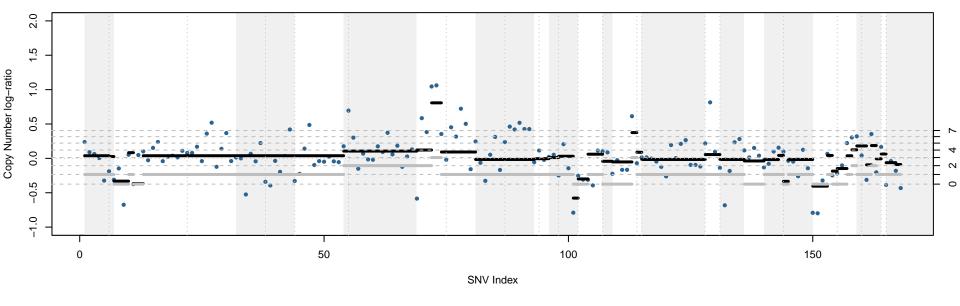
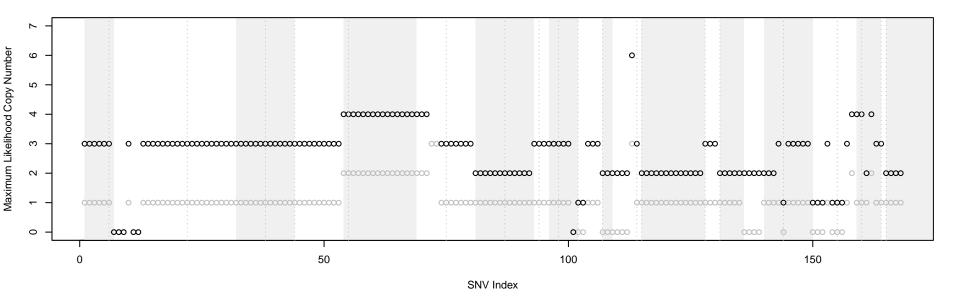
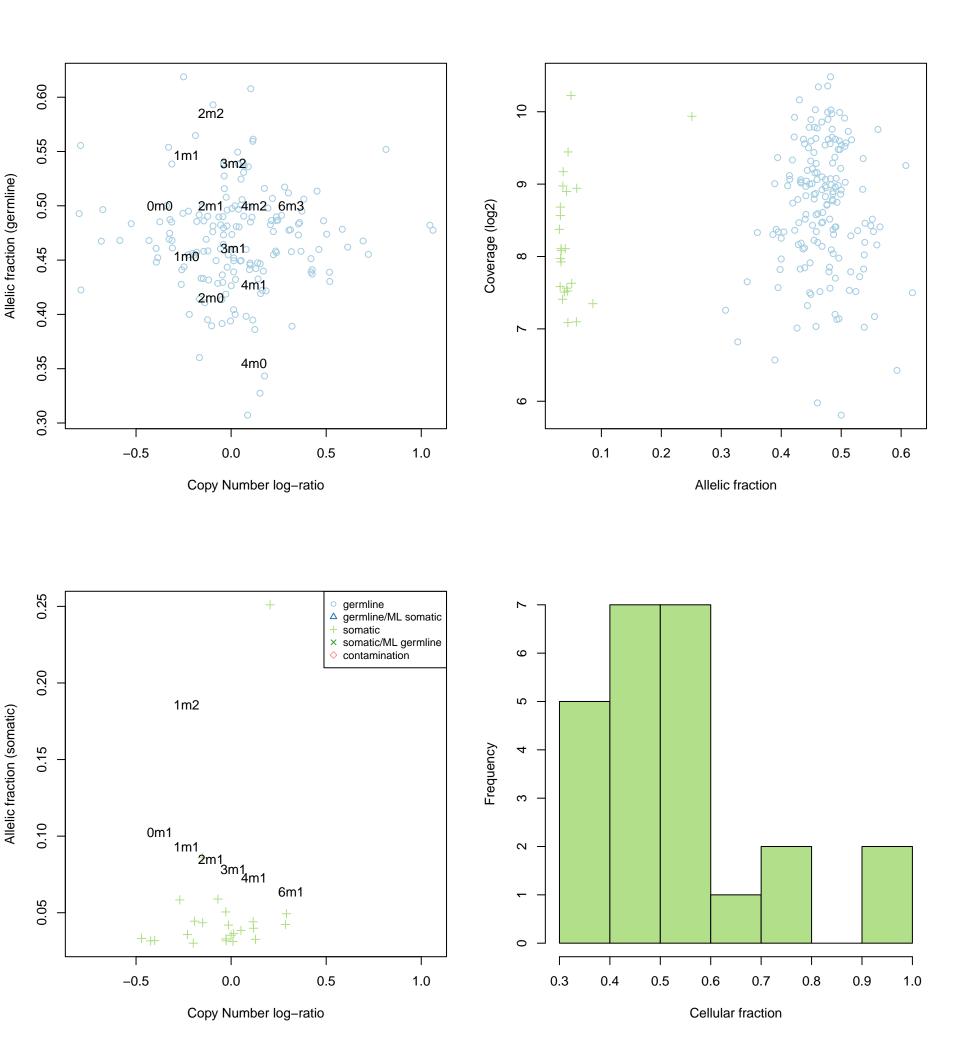
Purity: 0.17 Tumor ploidy: 2.896 0 2 3 1 5 6 0.30 0.25 0.20 Fraction Genome 0.15 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio

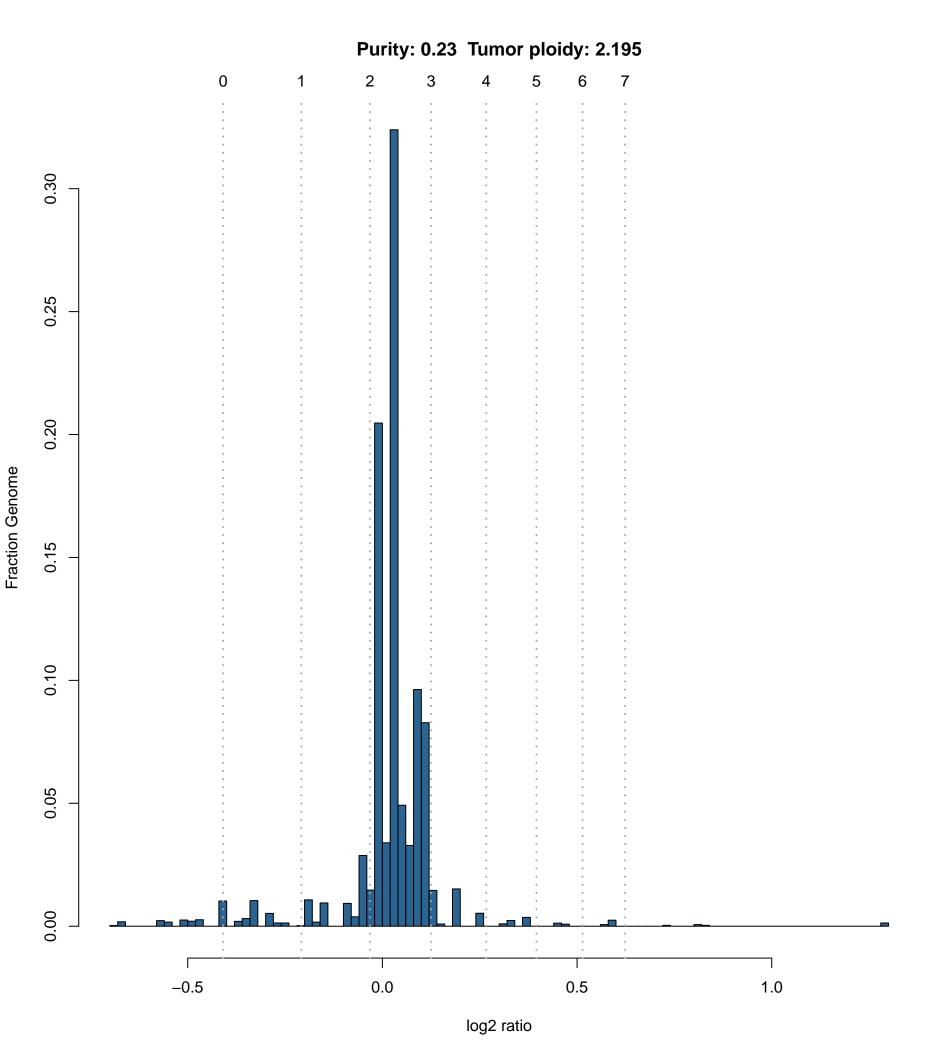


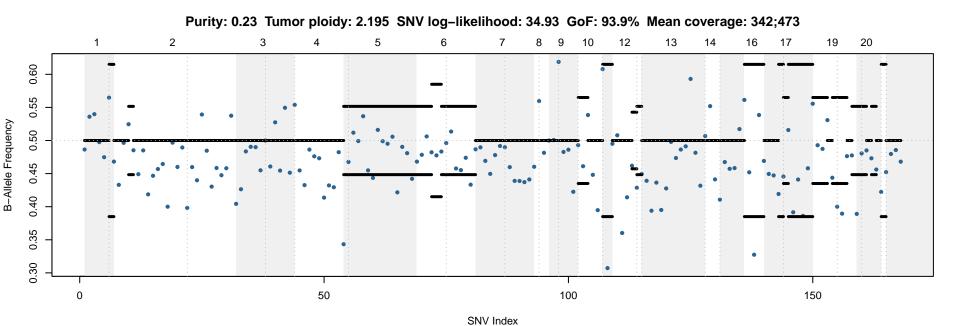
SCNA-fit log-likelihood: -7210.86



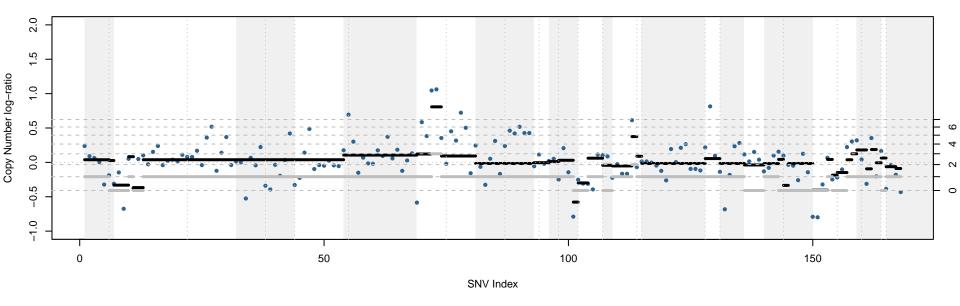


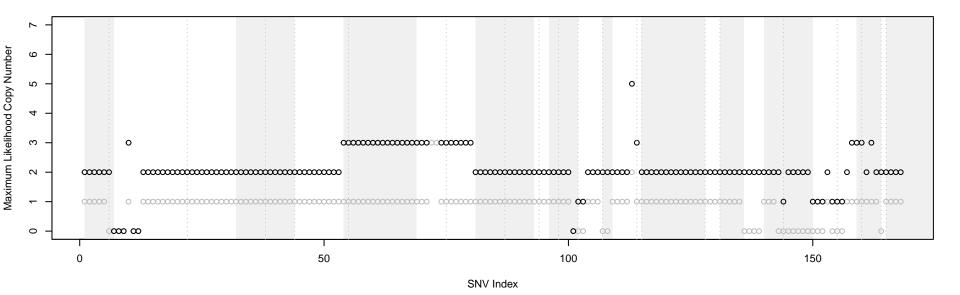


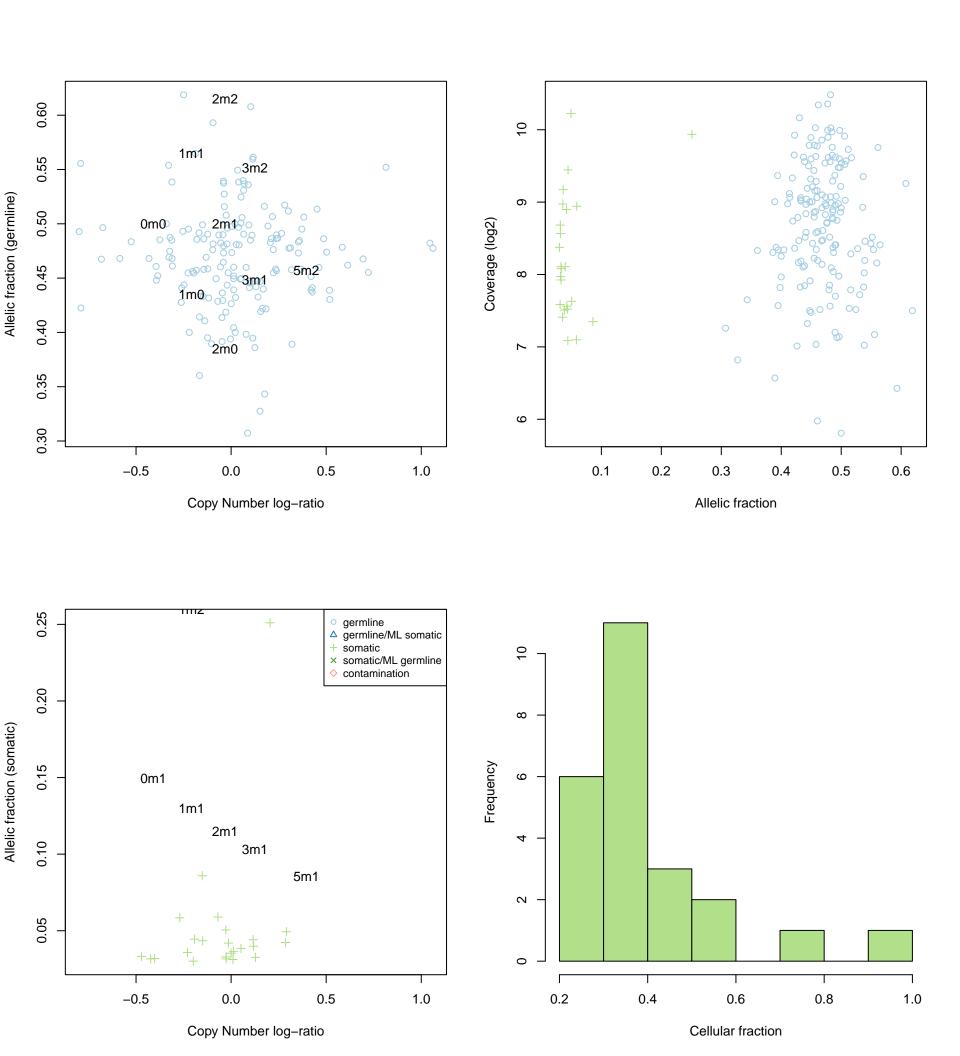


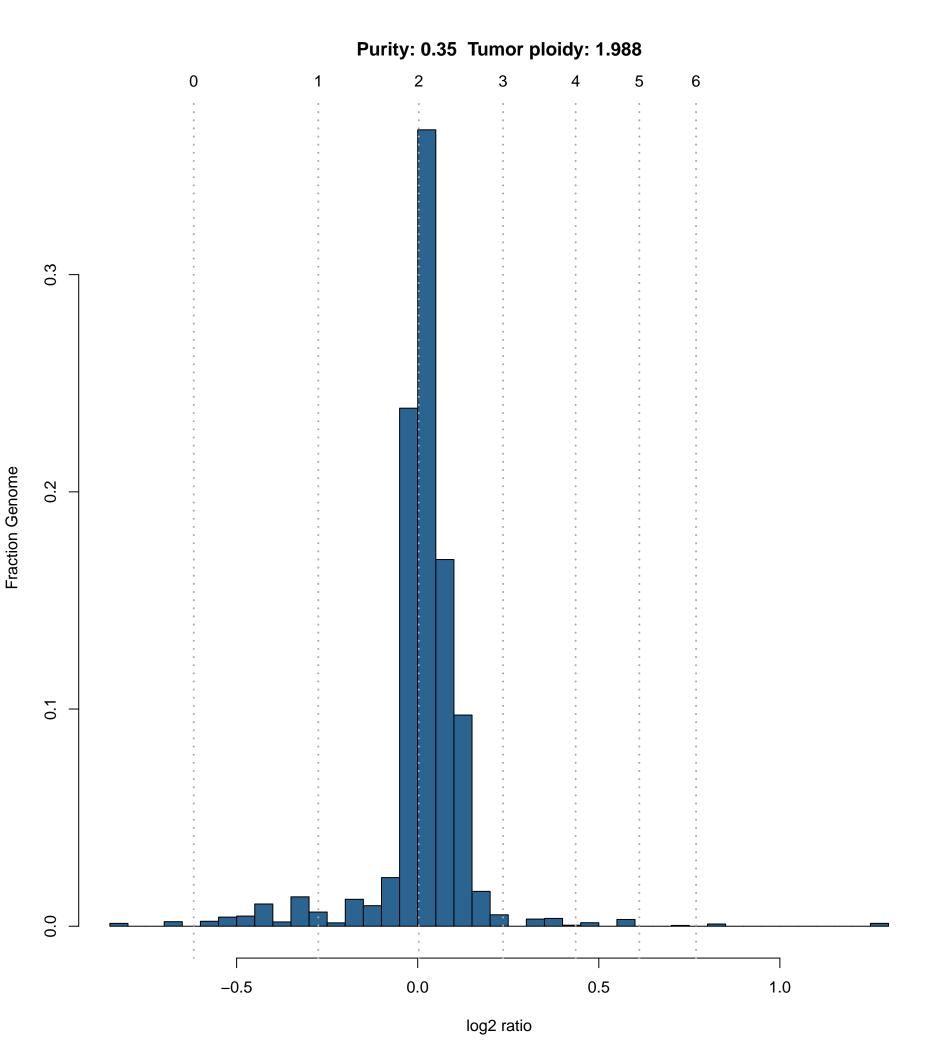


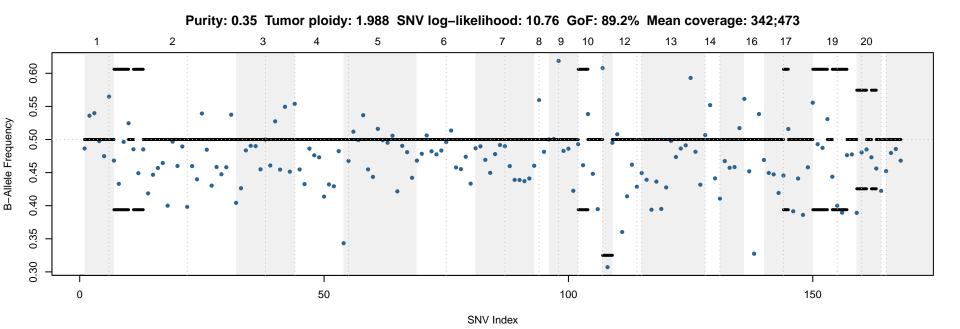
SCNA-fit log-likelihood: -7173.1



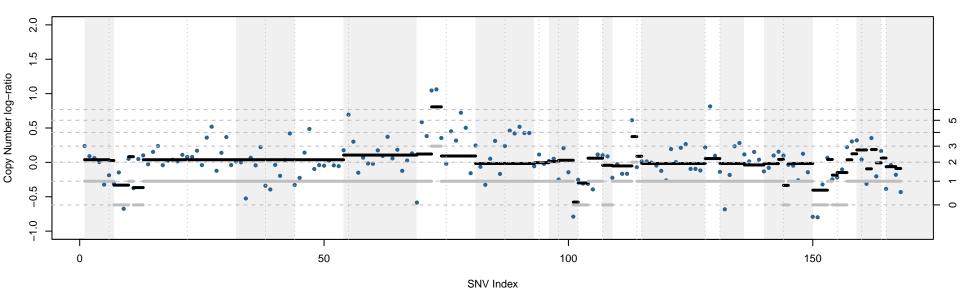


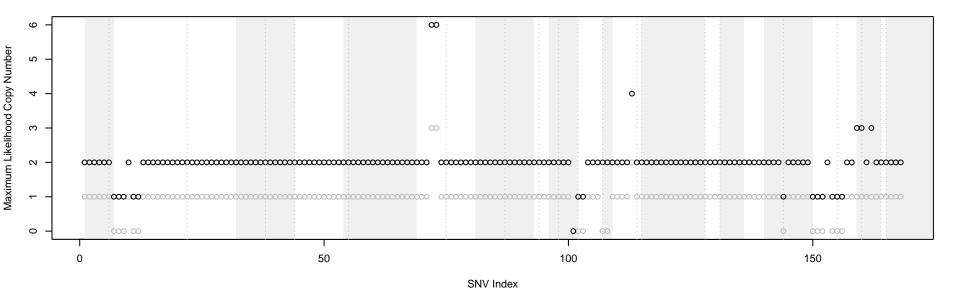


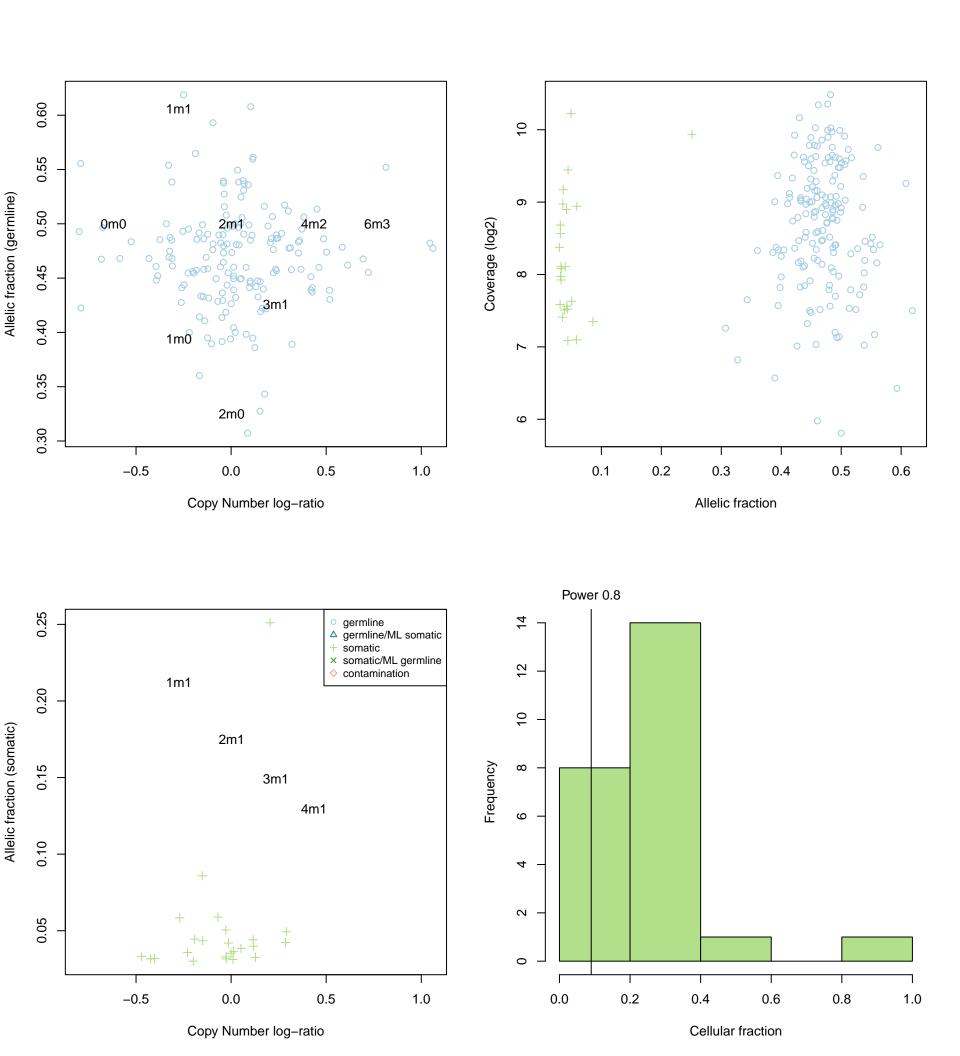


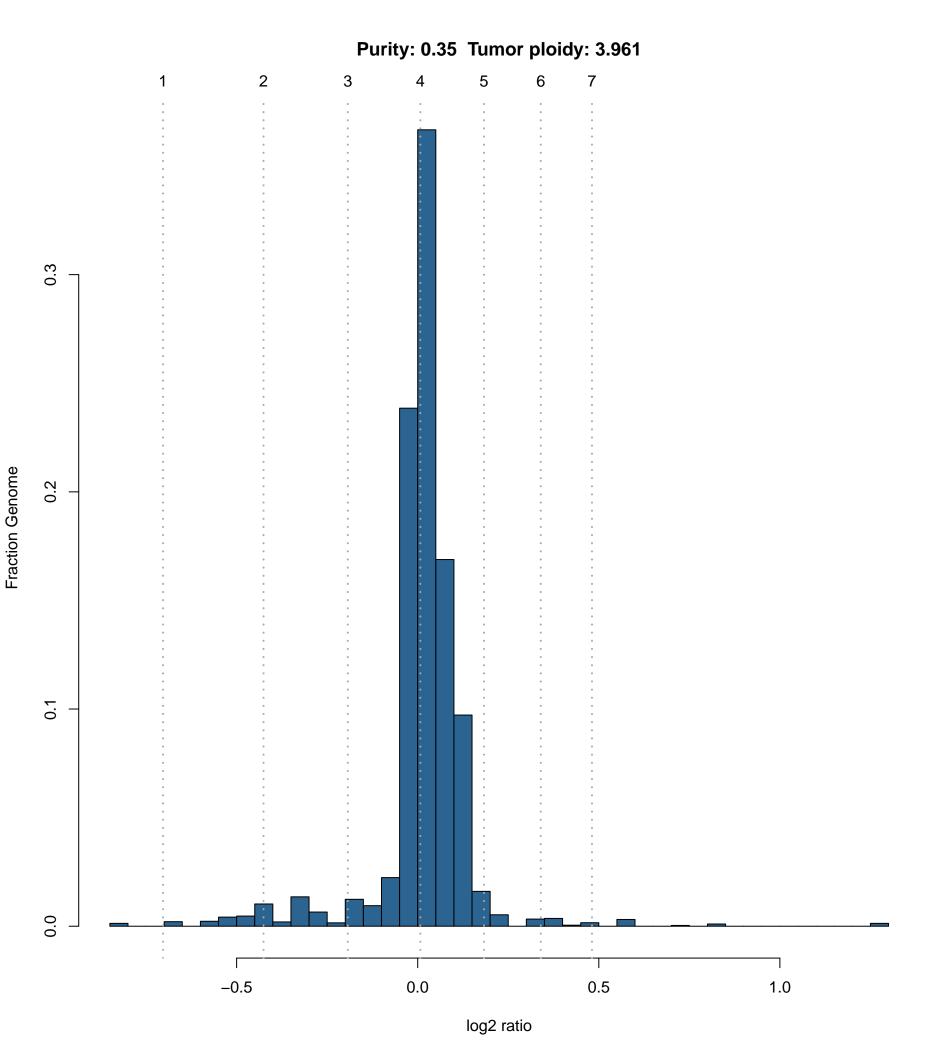


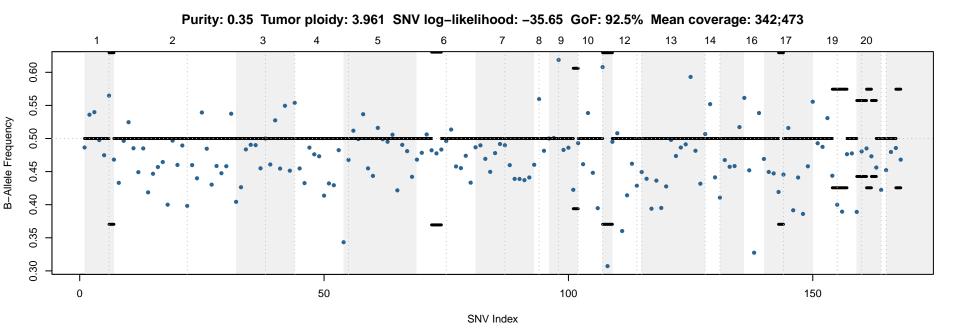
SCNA-fit log-likelihood: -7171.68



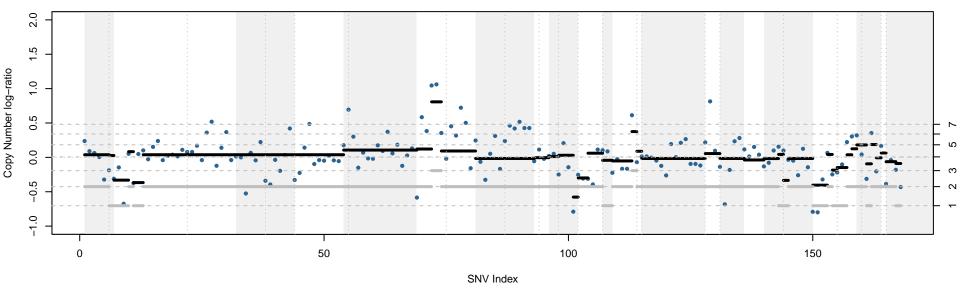


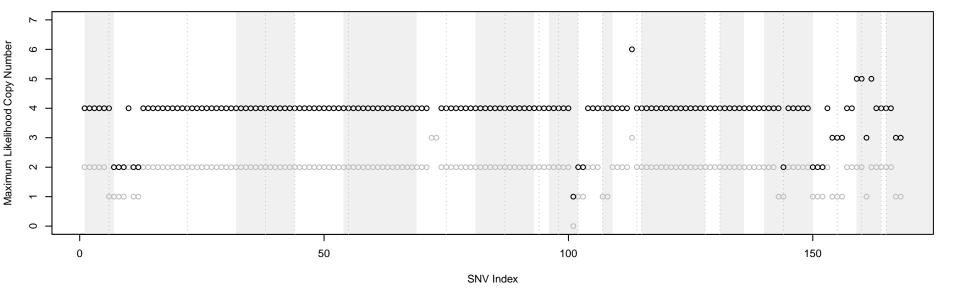


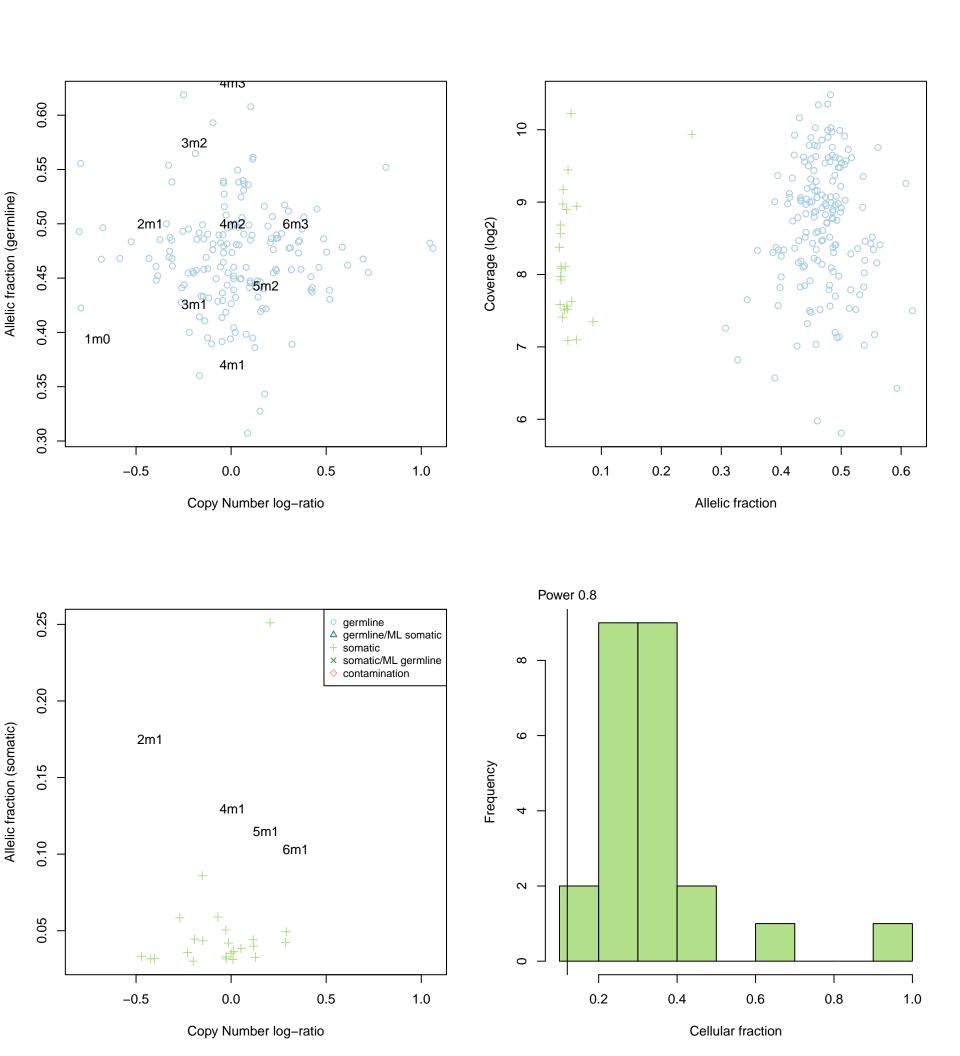




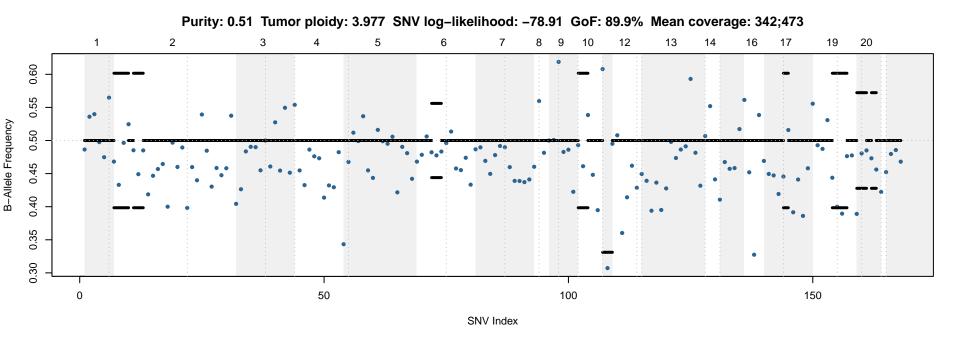
SCNA-fit log-likelihood: -7156.37



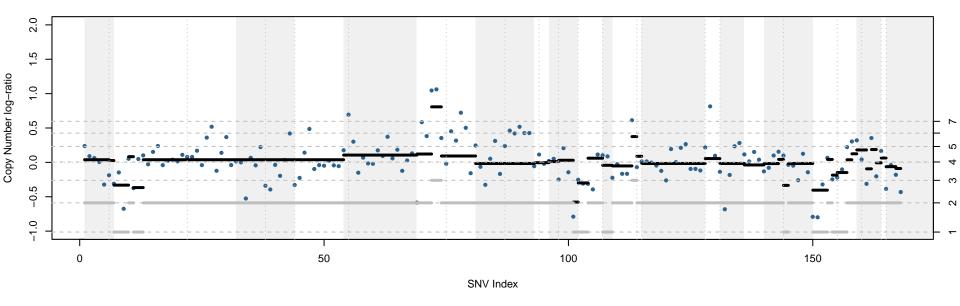


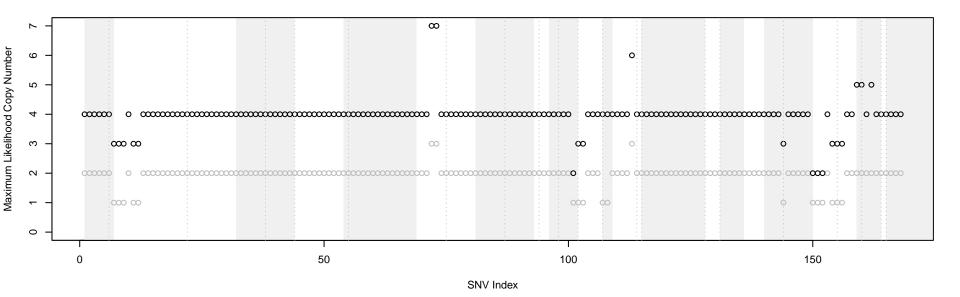


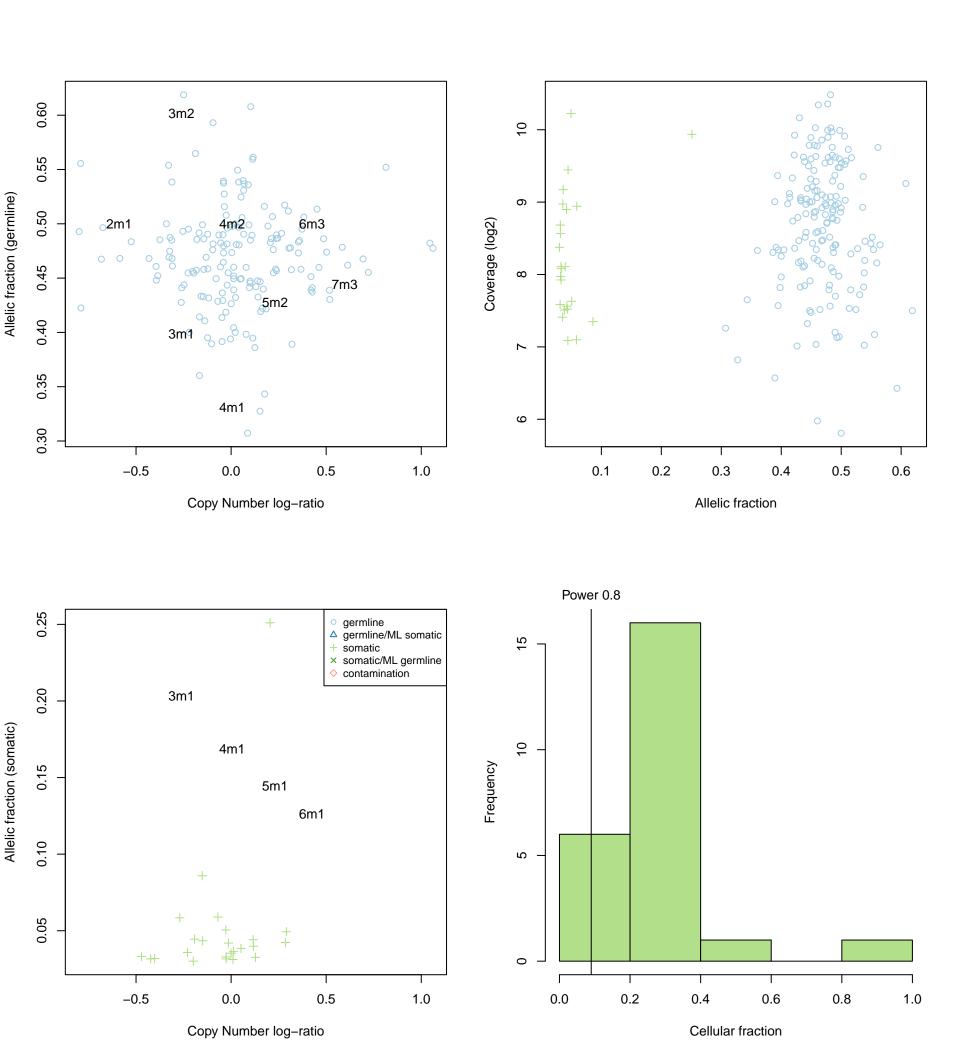
Purity: 0.51 Tumor ploidy: 3.977 5 2 3 6 0.3 Fraction Genome 0.0 -0.5 0.0 0.5 1.0 log2 ratio



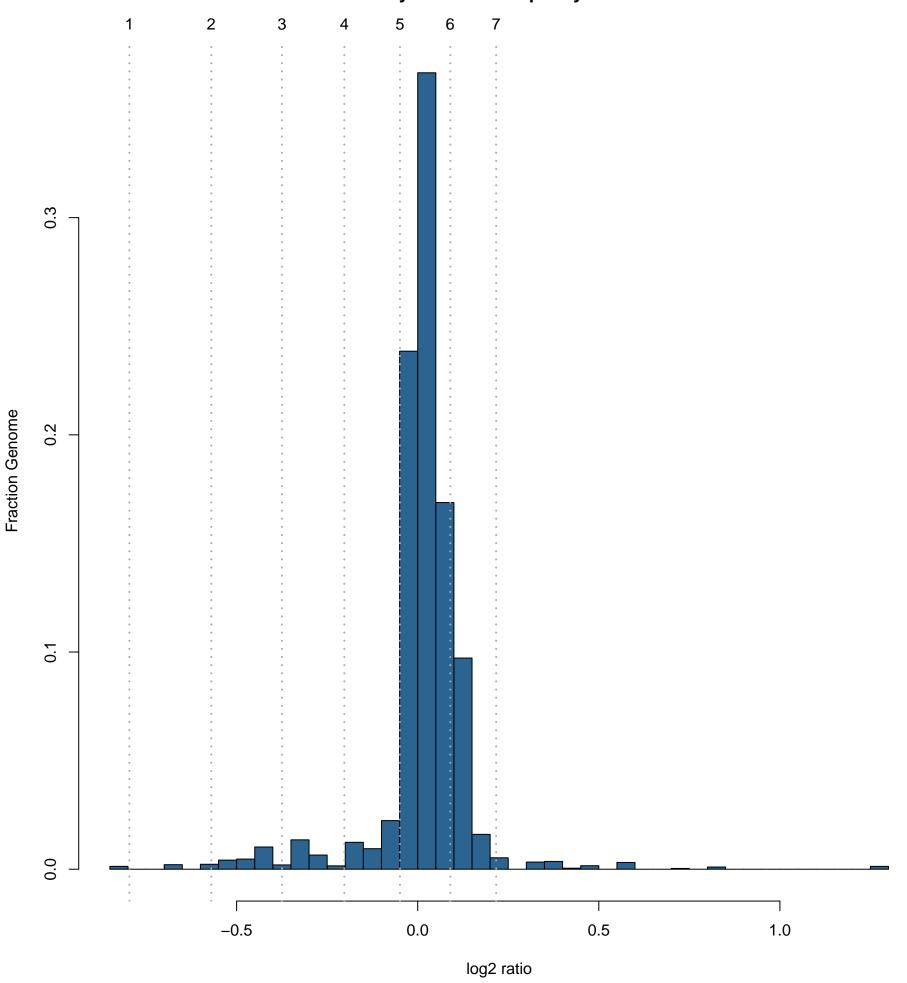
SCNA-fit log-likelihood: -7164.35

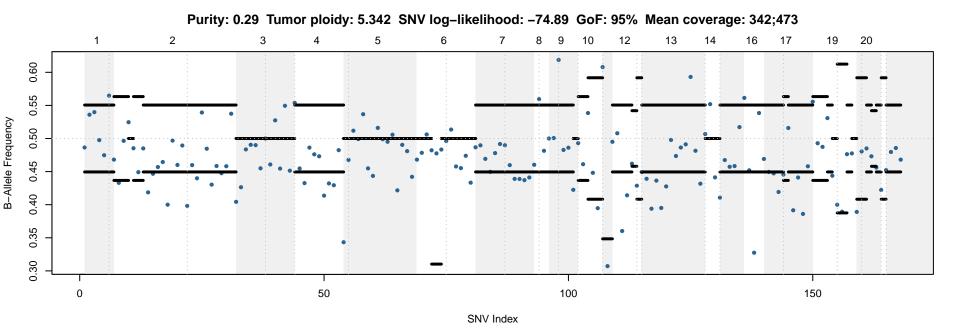




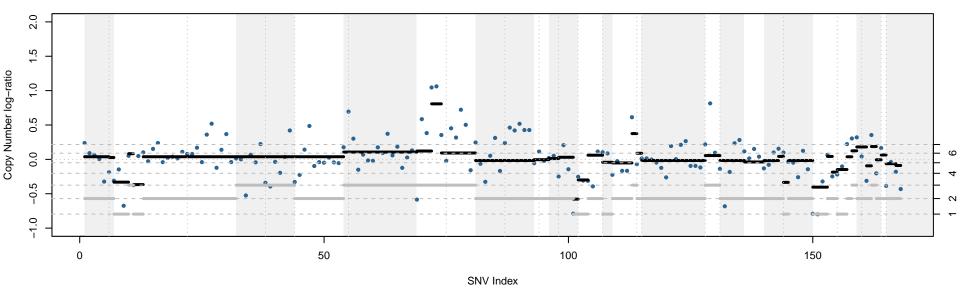


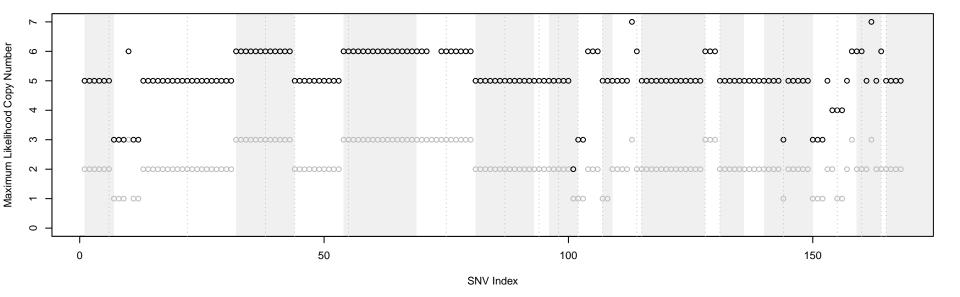
Purity: 0.29 Tumor ploidy: 5.342

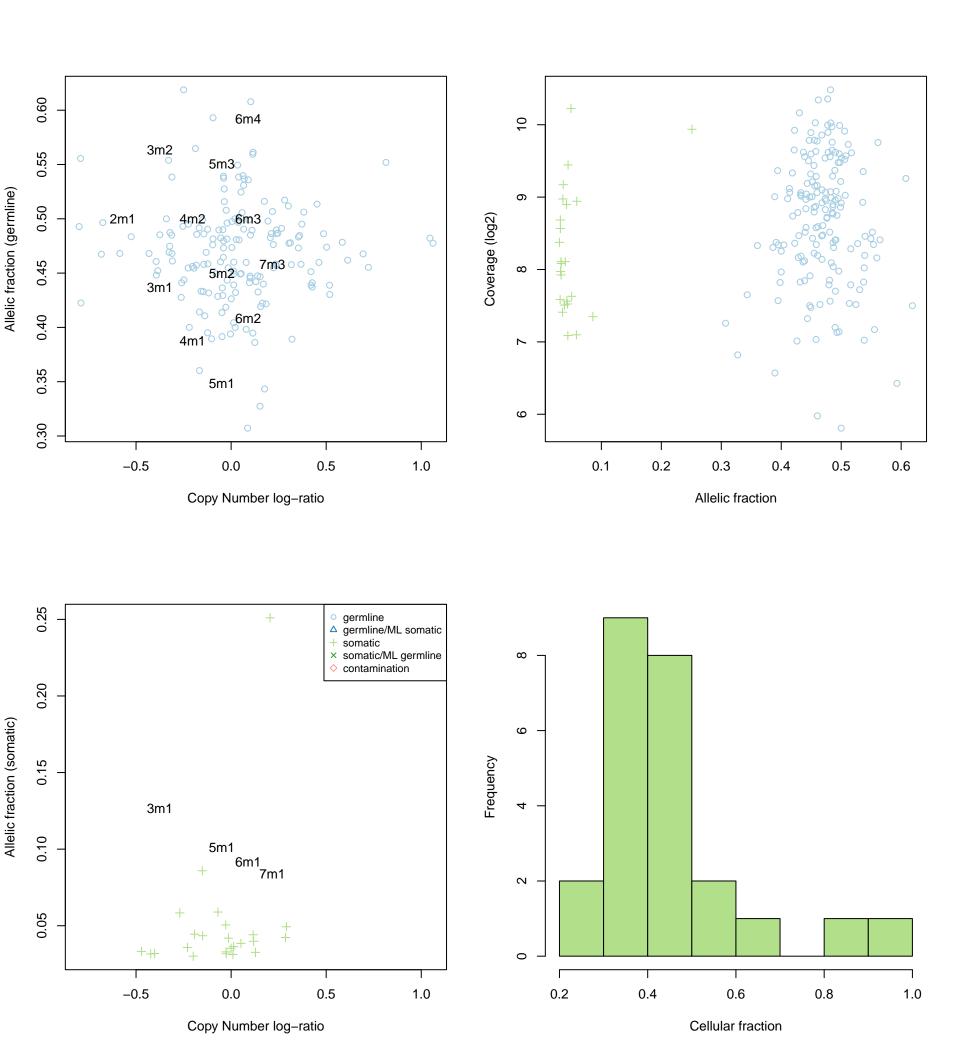




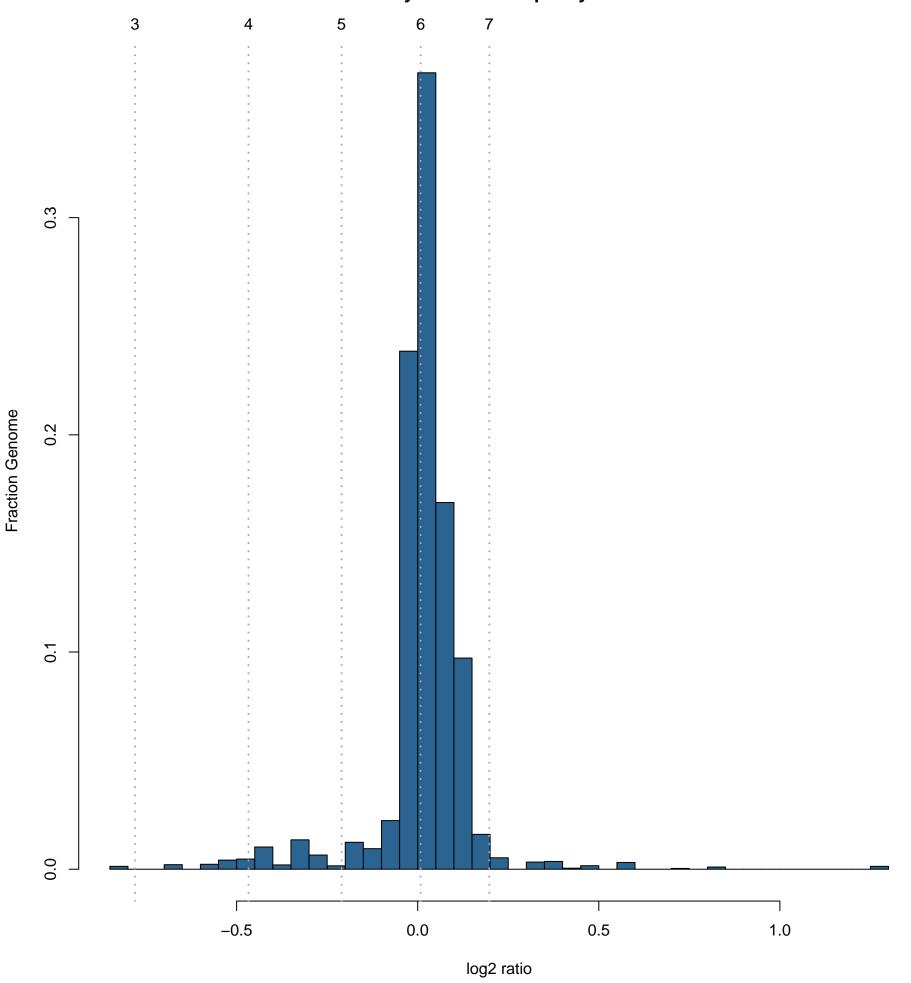
SCNA-fit log-likelihood: -7238.99

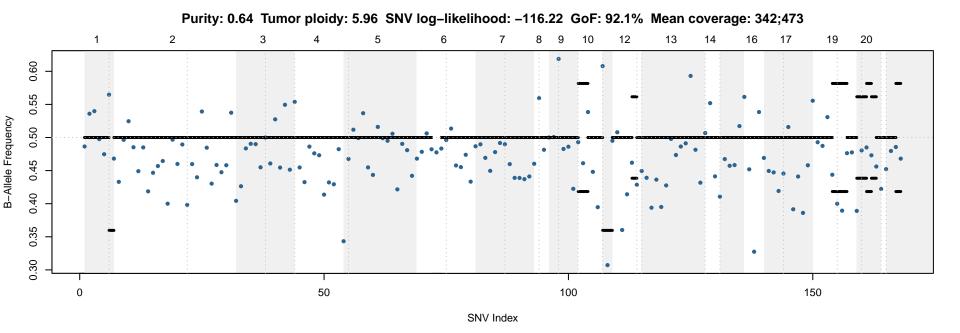




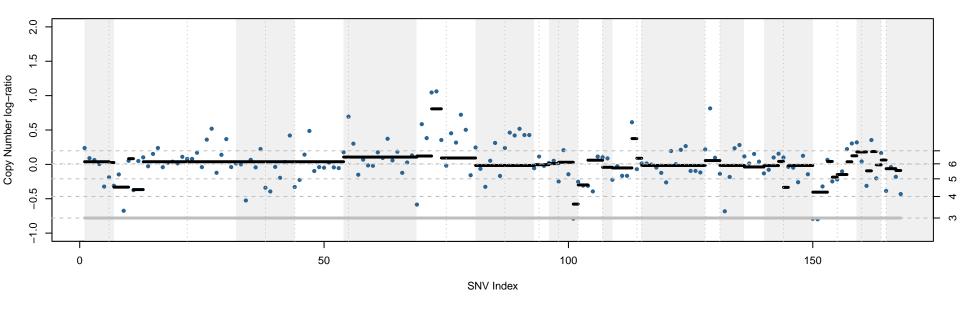


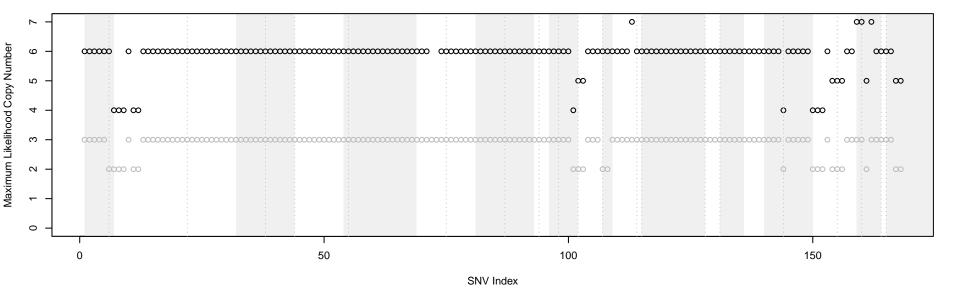
Purity: 0.64 Tumor ploidy: 5.96

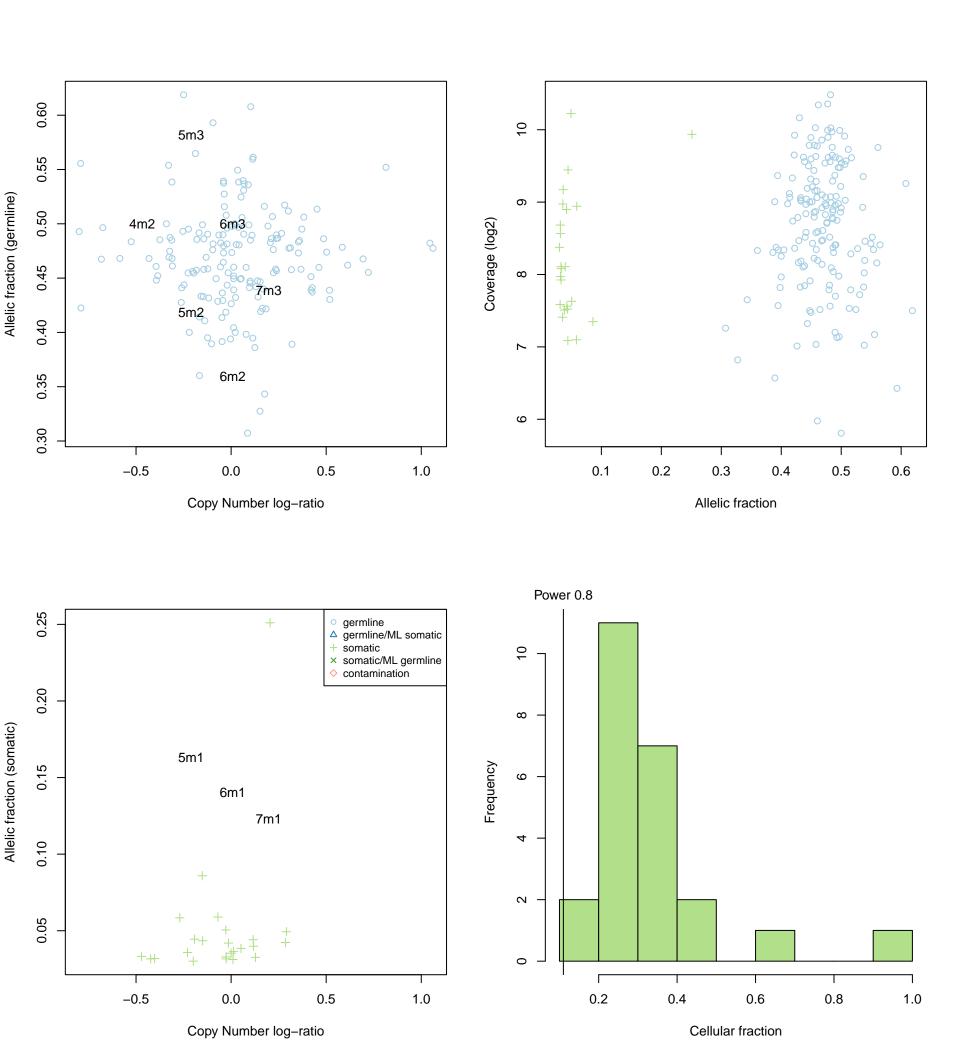




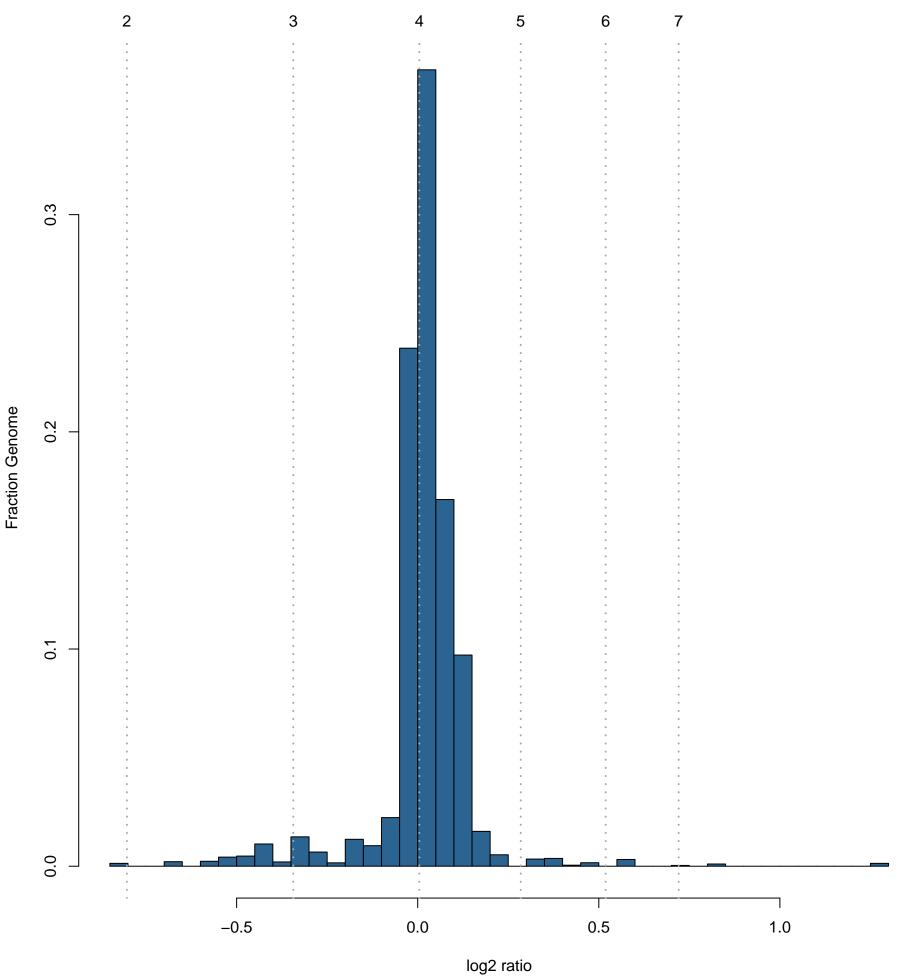
SCNA-fit log-likelihood: -7253.48

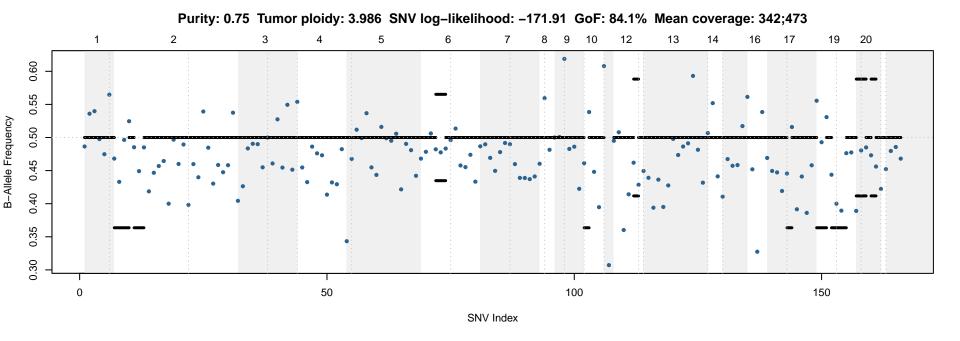




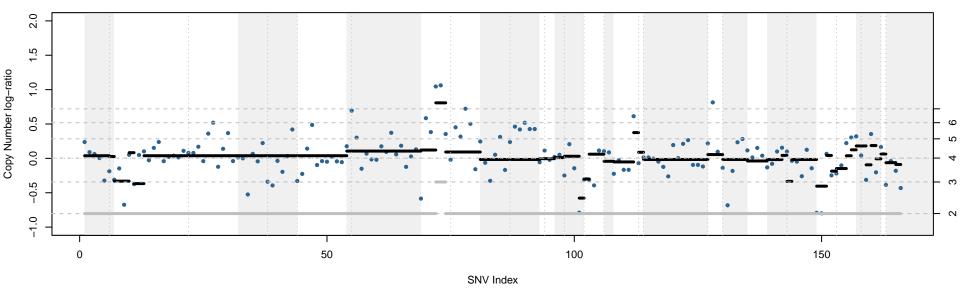


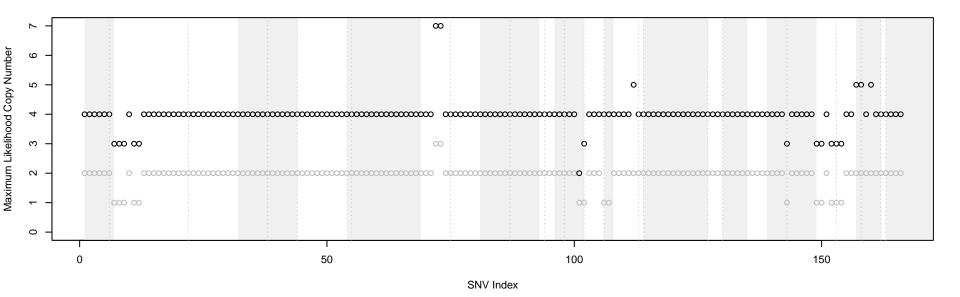
Purity: 0.75 Tumor ploidy: 3.986

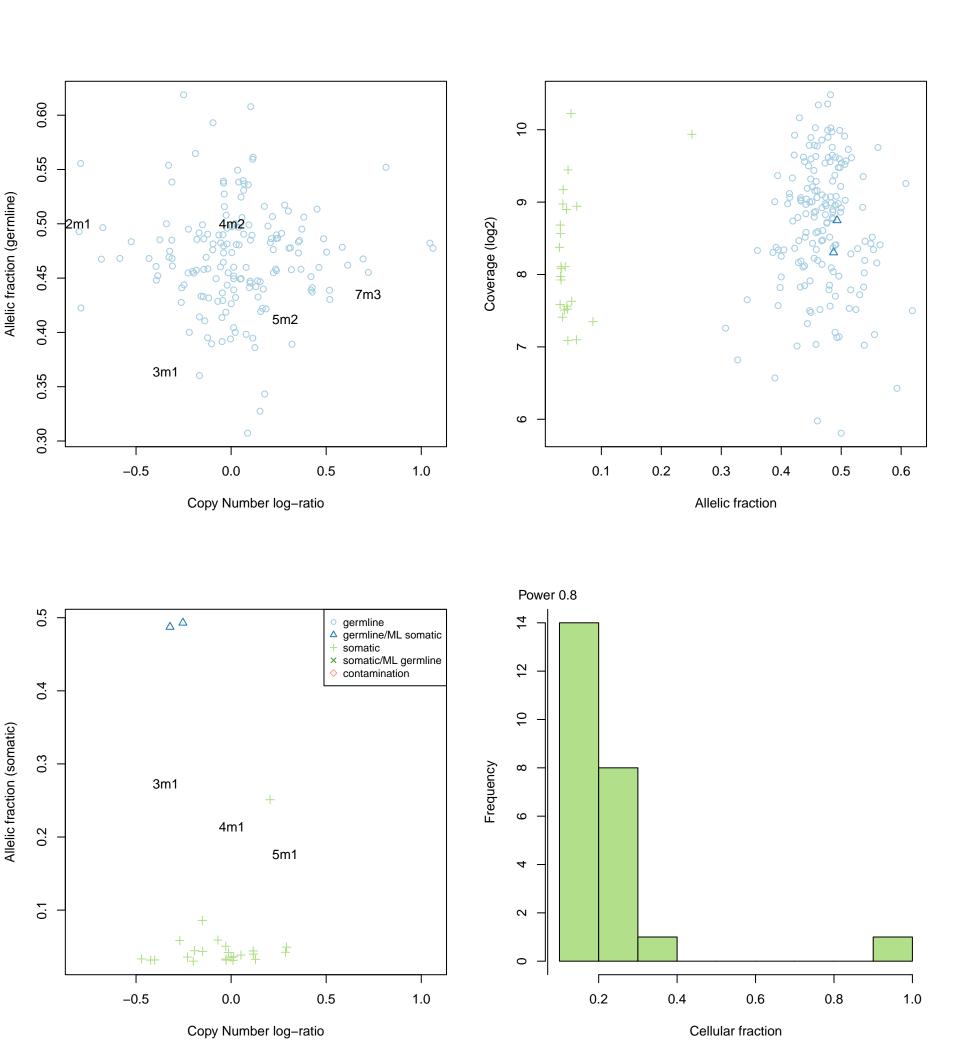




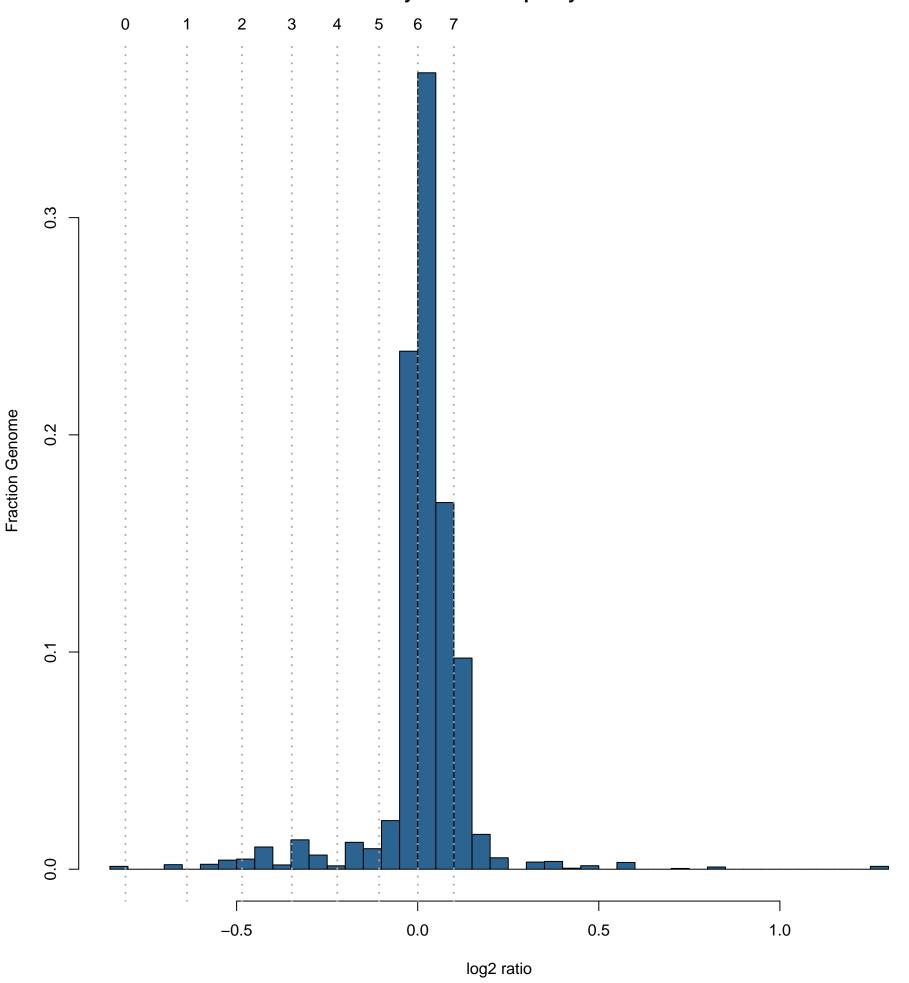
SCNA-fit log-likelihood: -7200.07

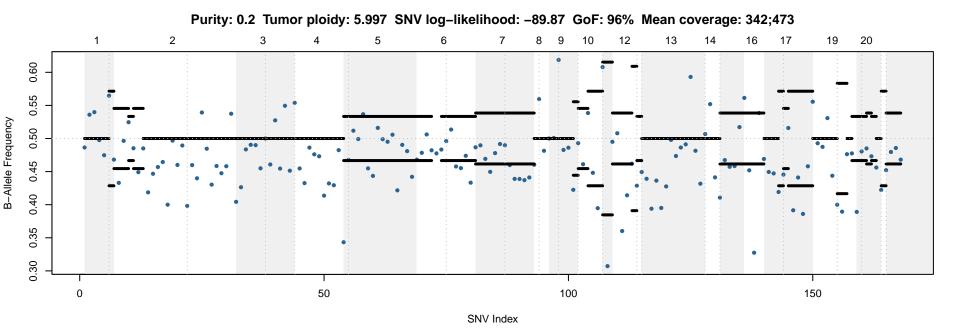




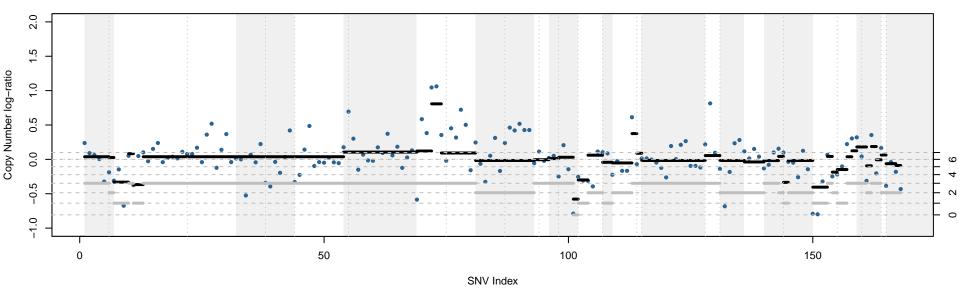


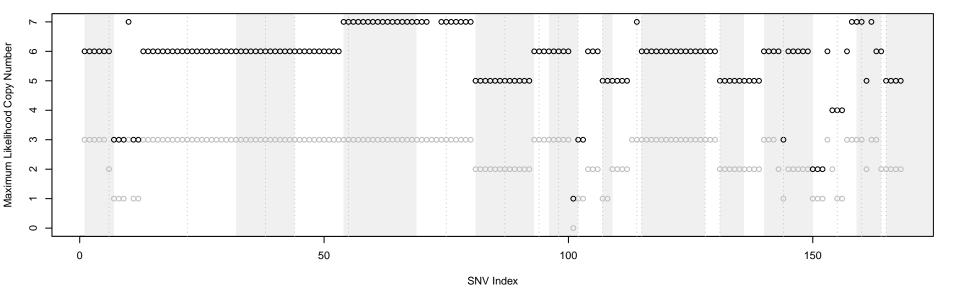
Purity: 0.2 Tumor ploidy: 5.997

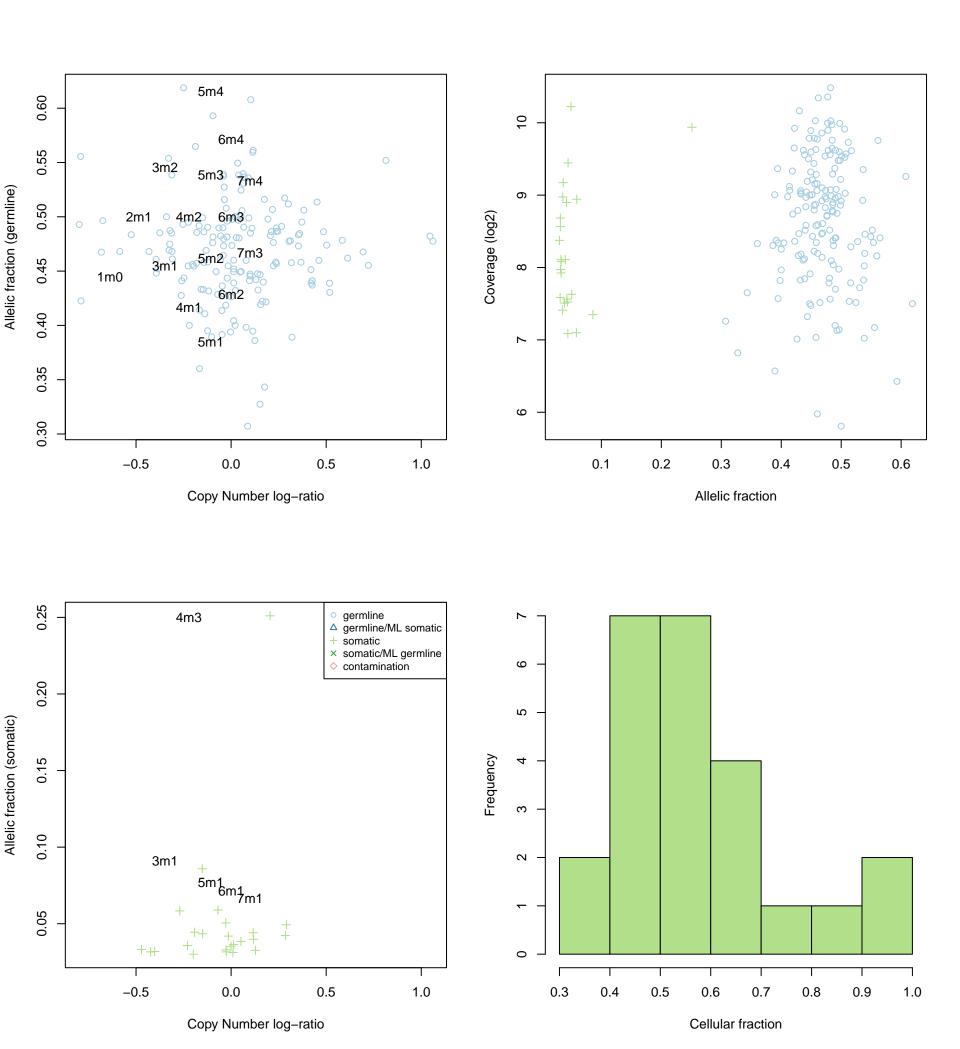




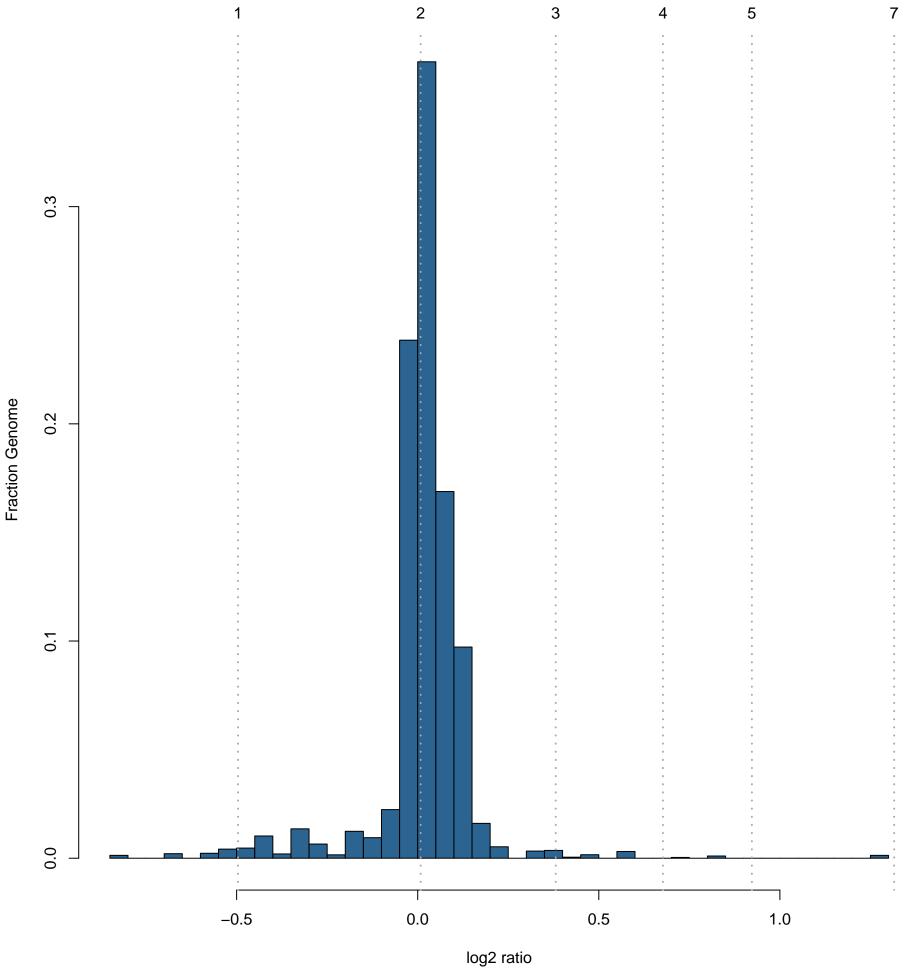
SCNA-fit log-likelihood: -7328.62

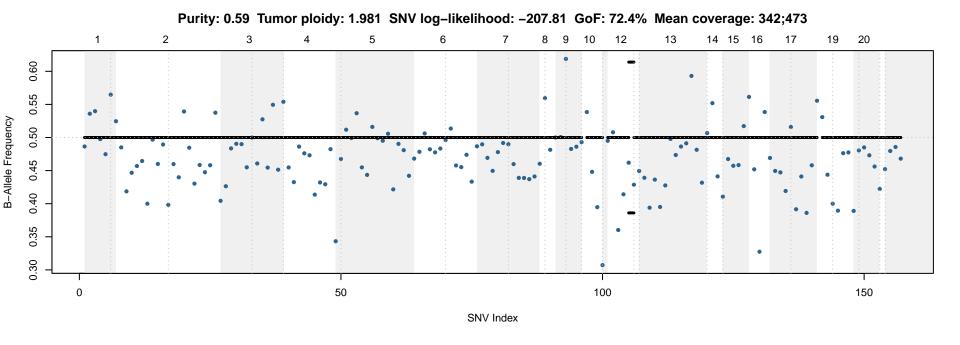




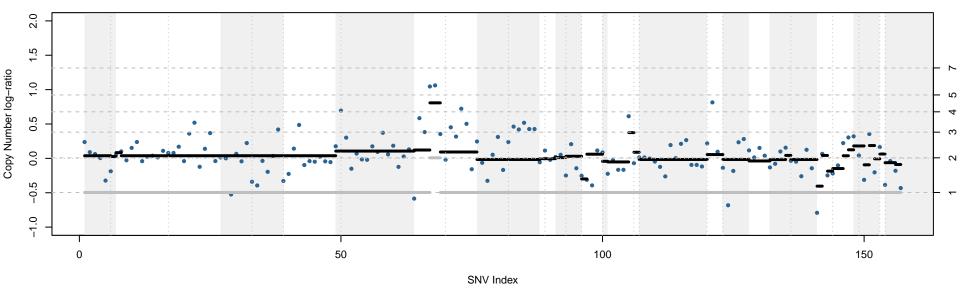


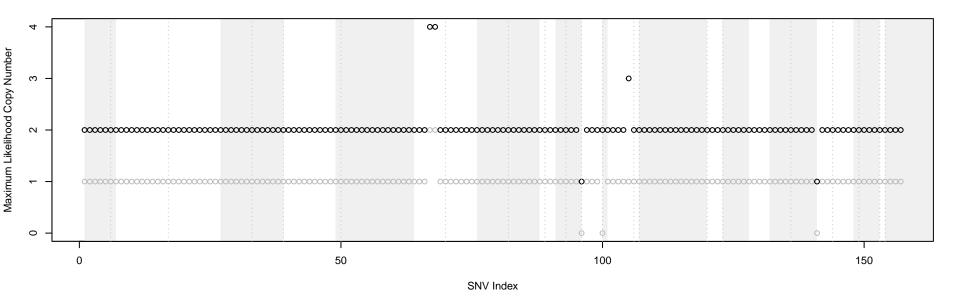
Purity: 0.59 Tumor ploidy: 1.981

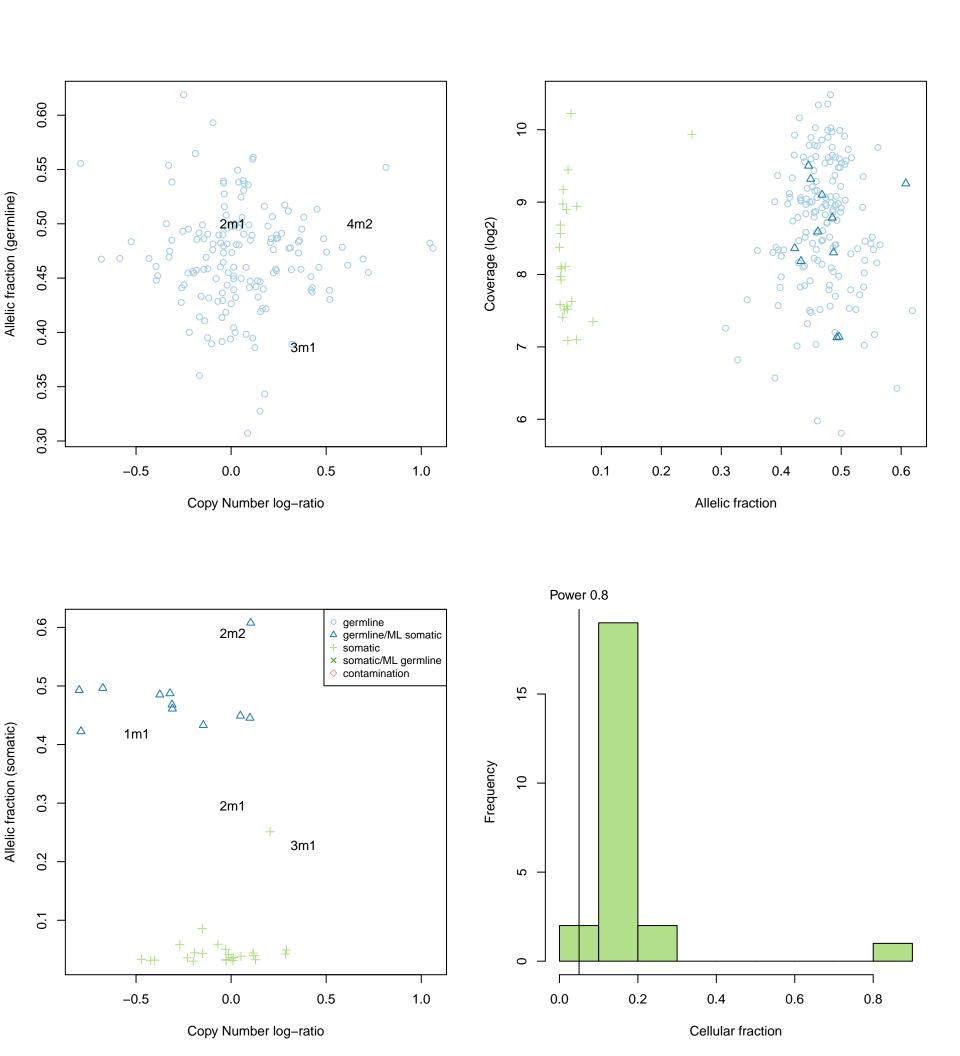




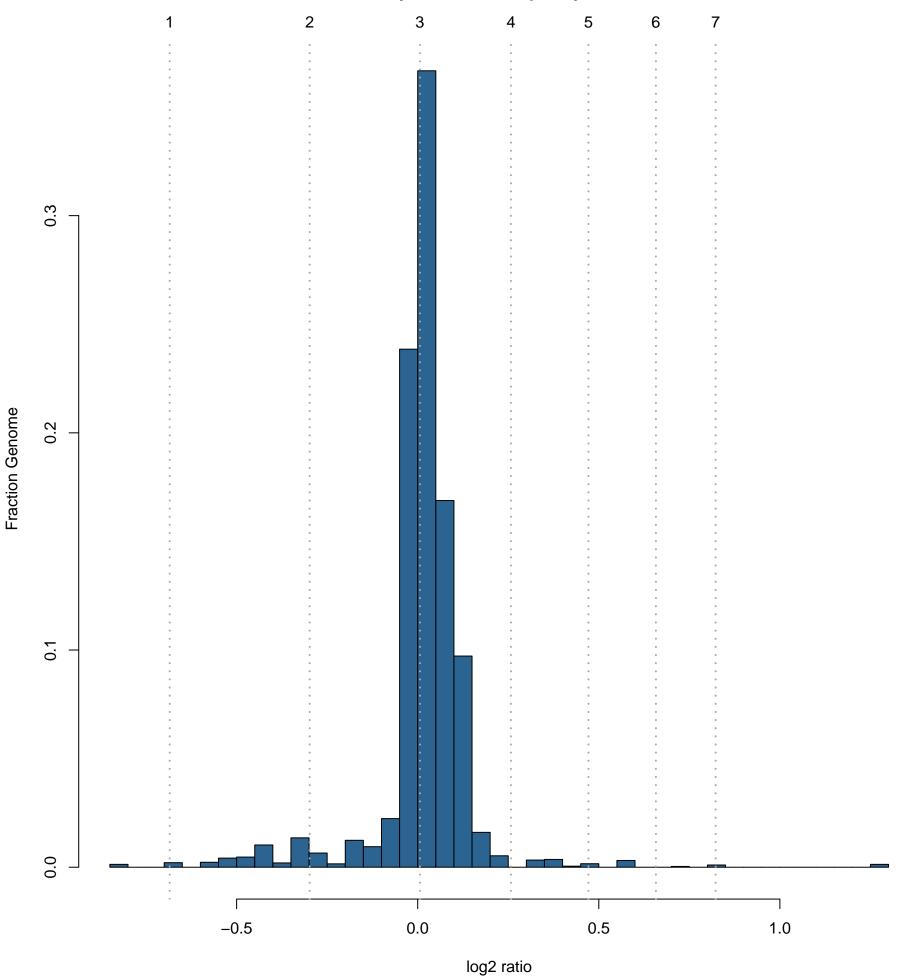
SCNA-fit log-likelihood: -7237.05

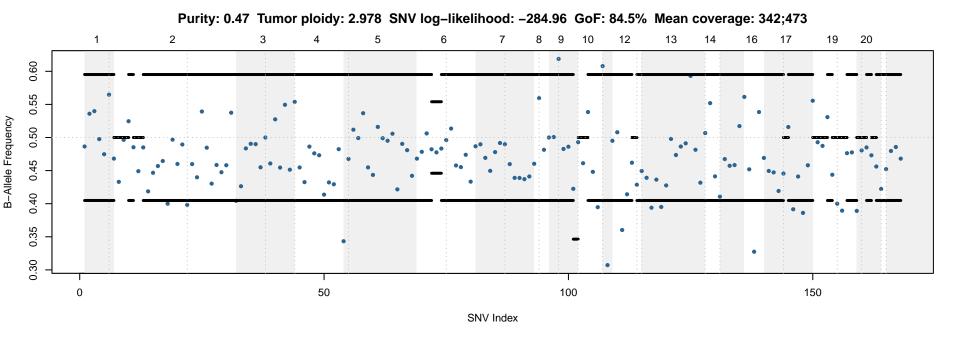




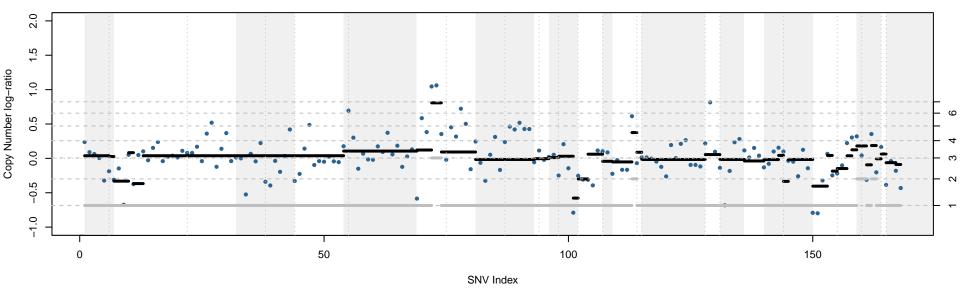


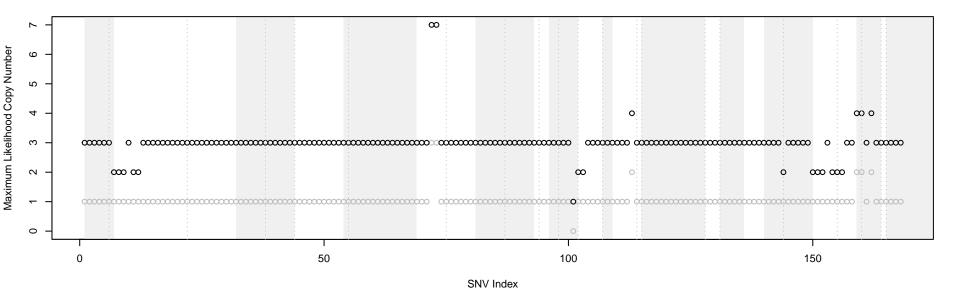
Purity: 0.47 Tumor ploidy: 2.978

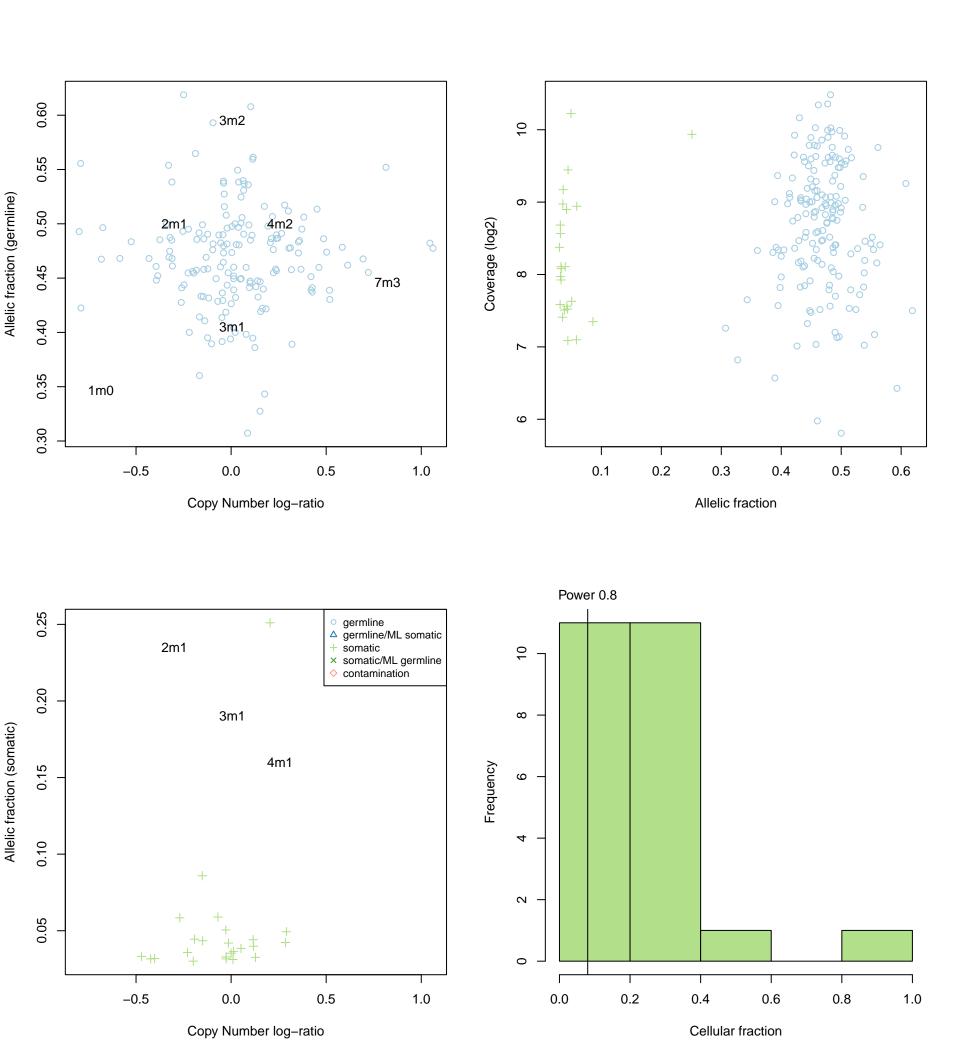




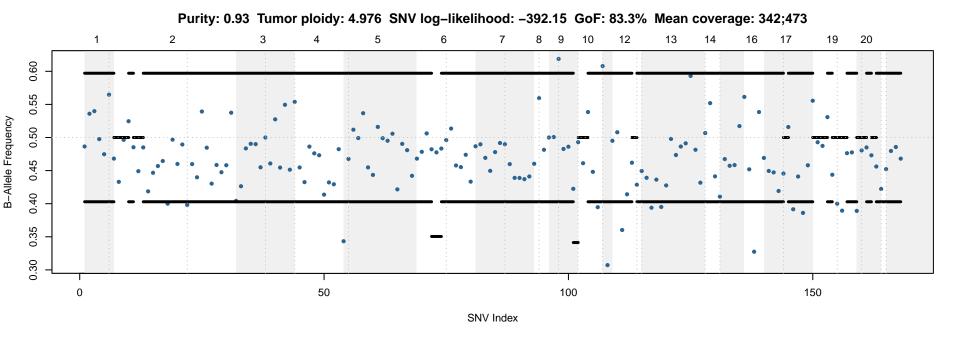
SCNA-fit log-likelihood: -7177.48



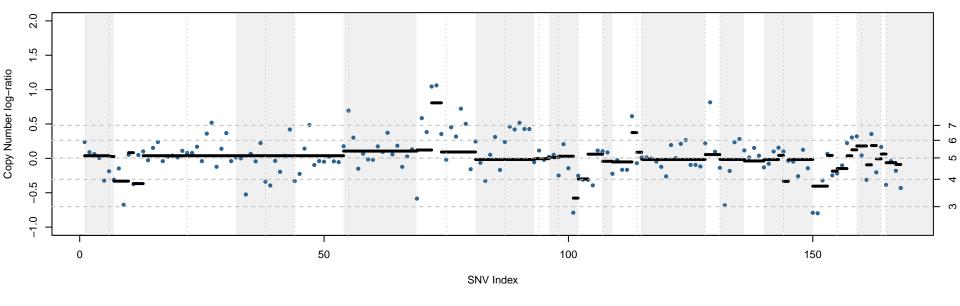


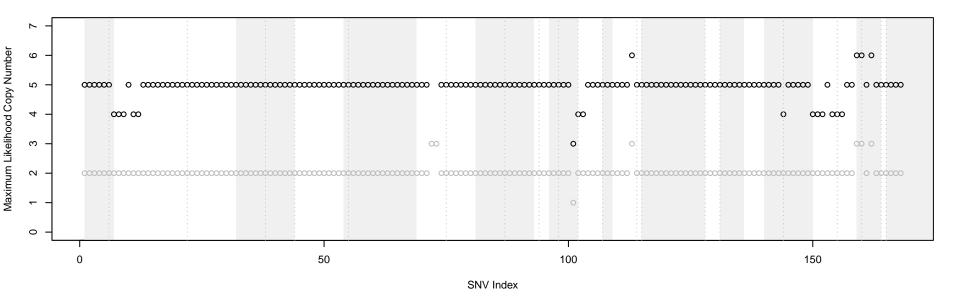


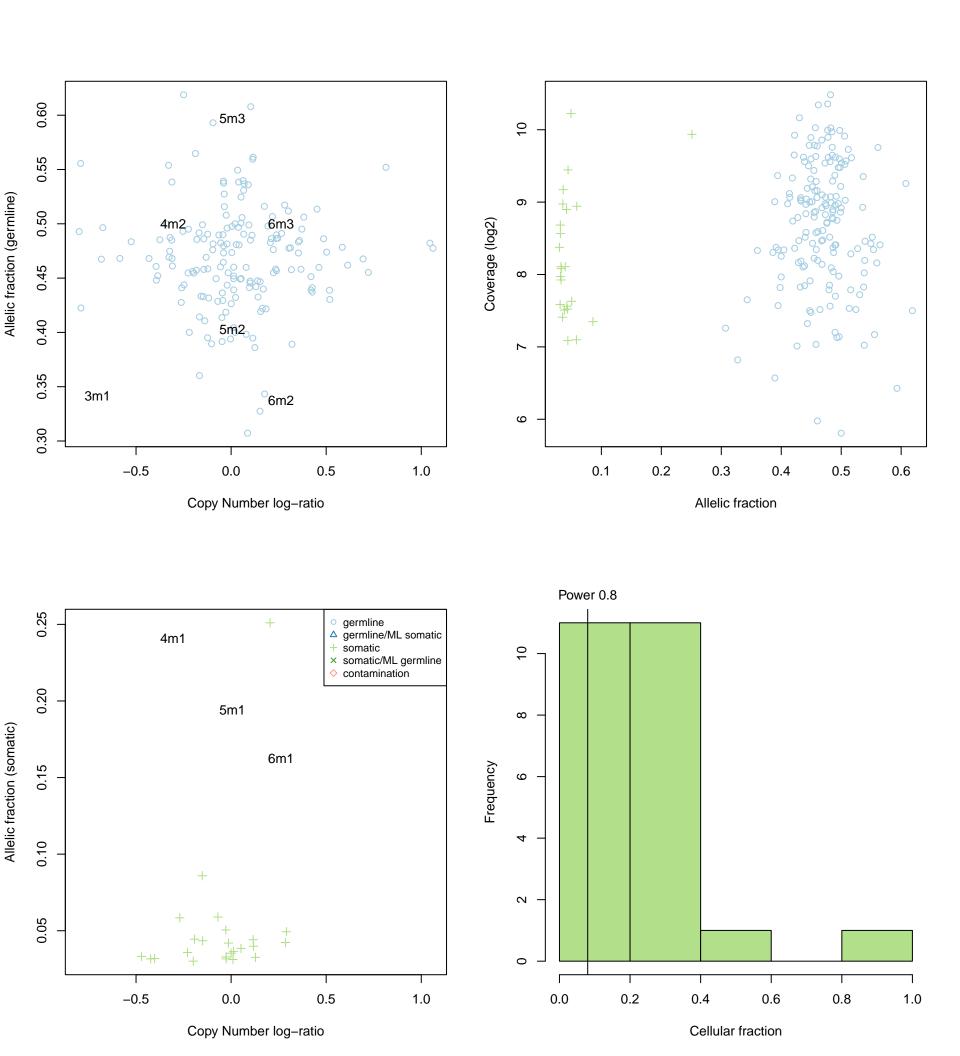
Purity: 0.93 Tumor ploidy: 4.976 6 3 5 0.3 Fraction Genome 0.1 0.0 -0.5 0.0 0.5 1.0 log2 ratio



SCNA-fit log-likelihood: -7207.25







Purity: 0.71 Tumor ploidy: 2.98 2 6 Fraction Genome 0.0

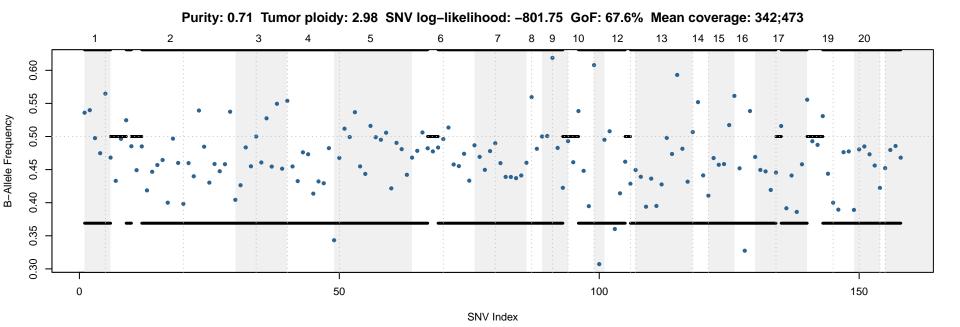
0.0

log2 ratio

0.5

1.0

-0.5



SCNA-fit log-likelihood: -7209.98

