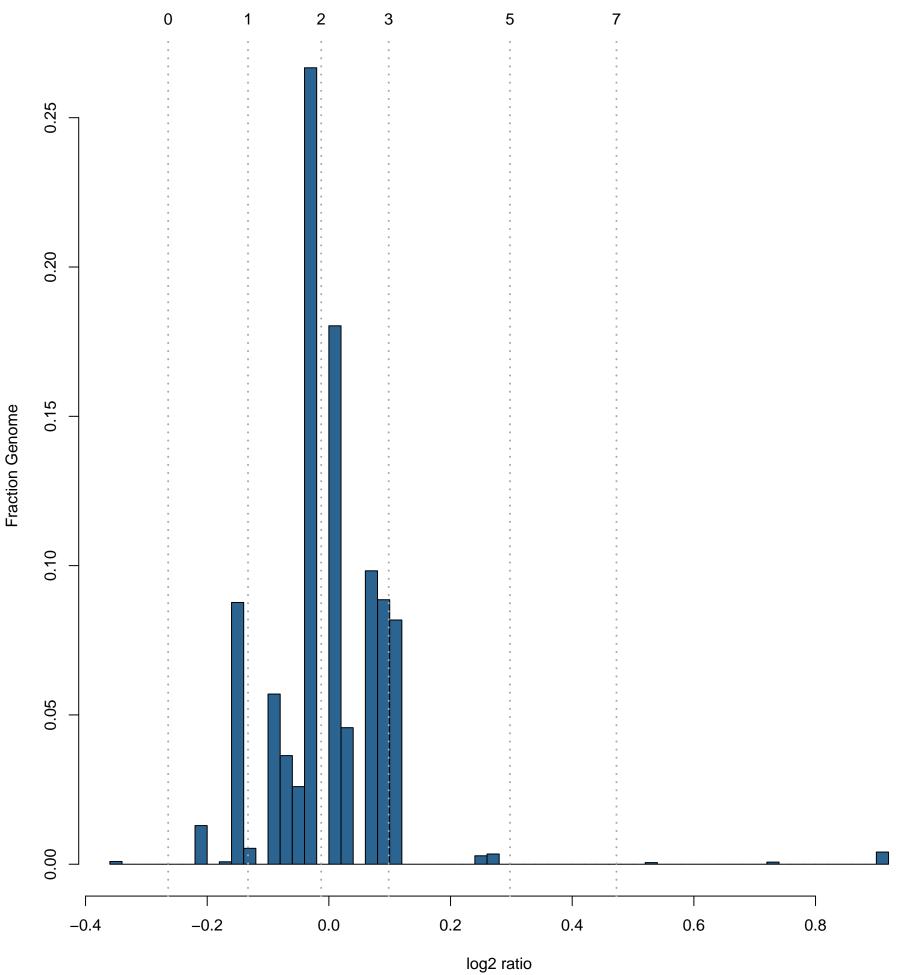
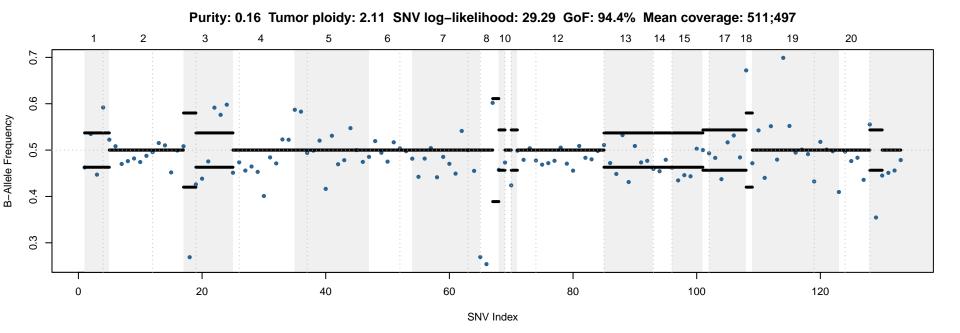
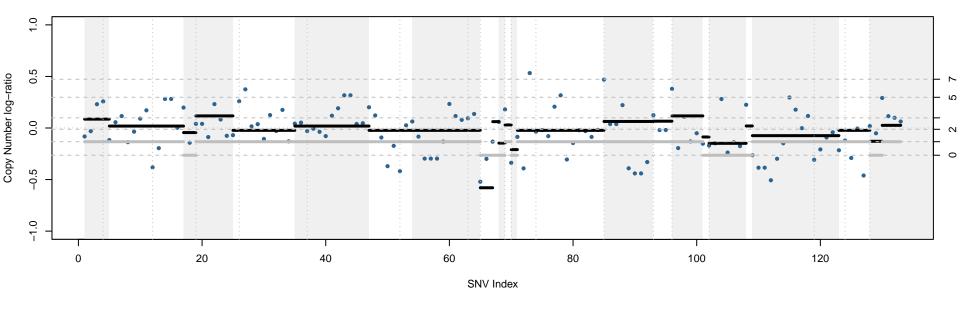
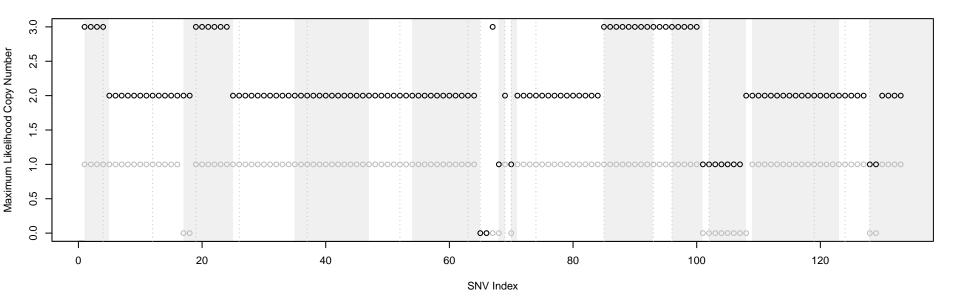
Purity: 0.16 Tumor ploidy: 2.11

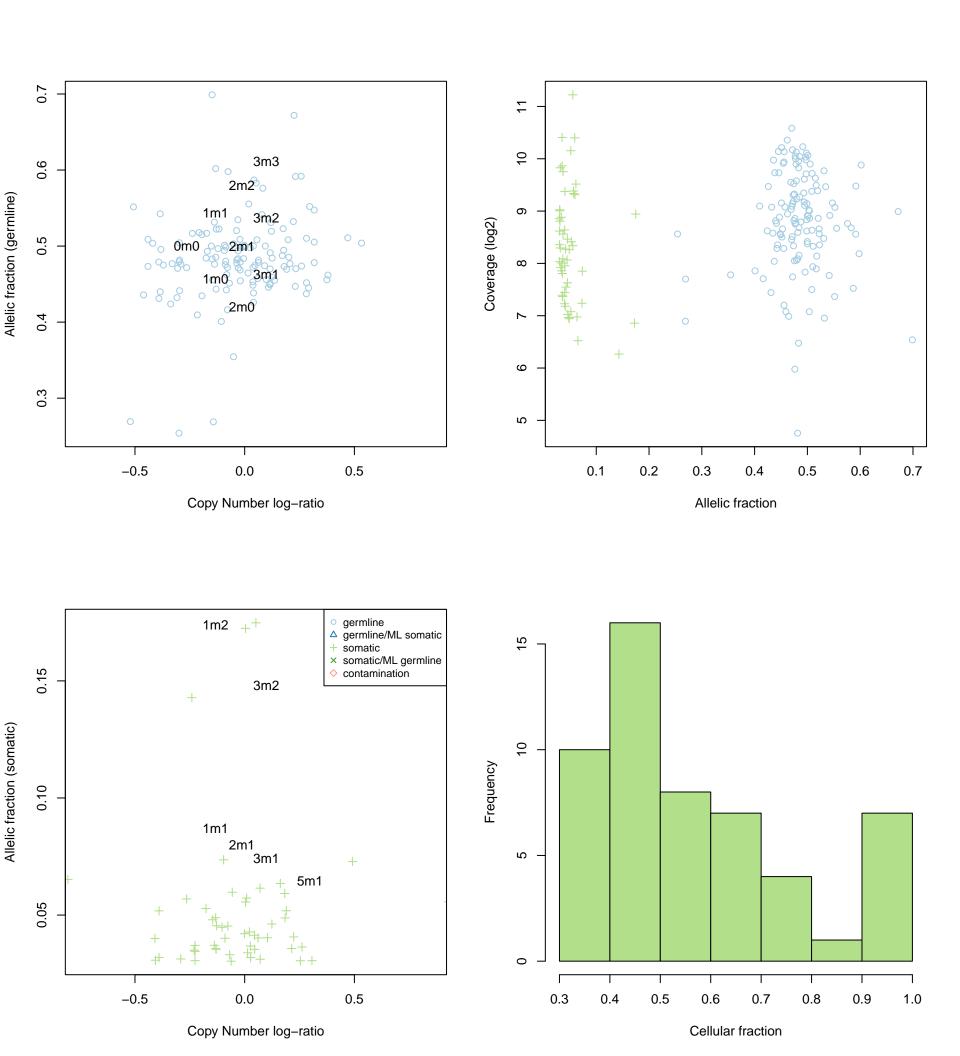


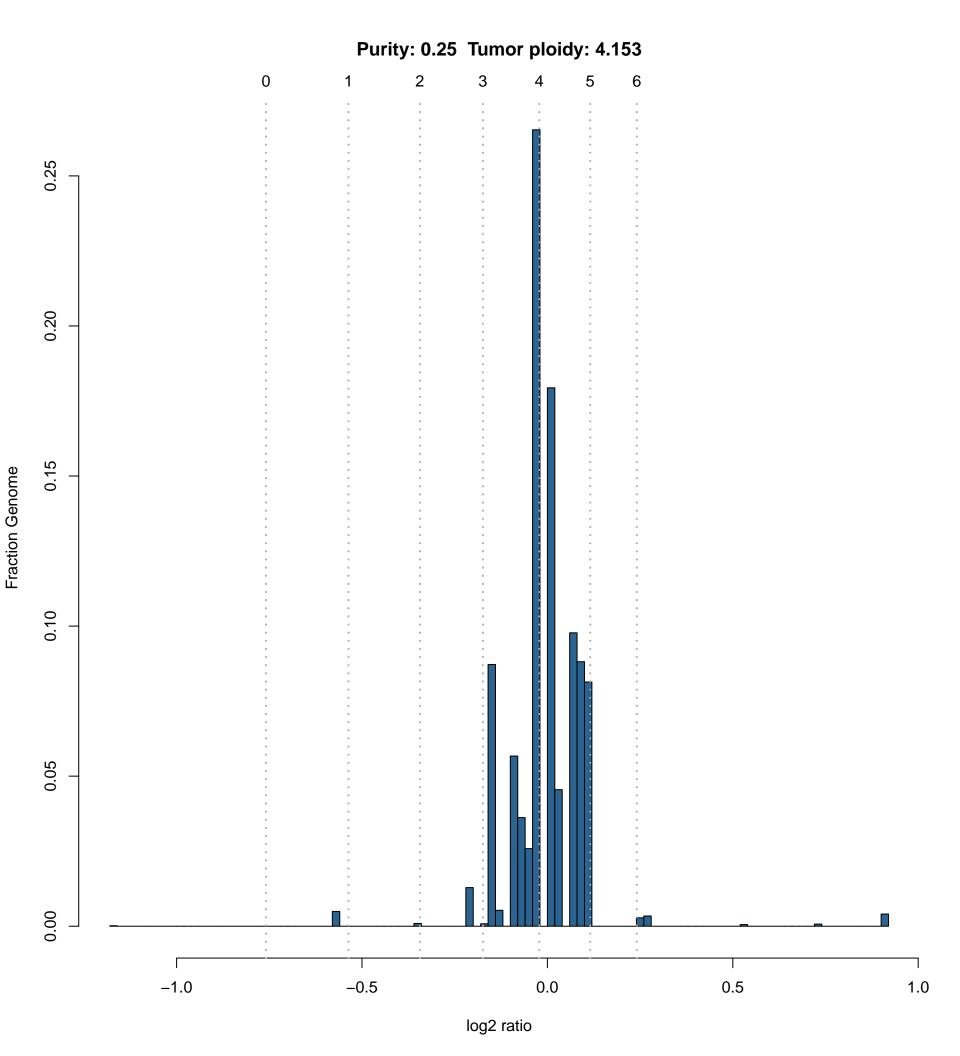


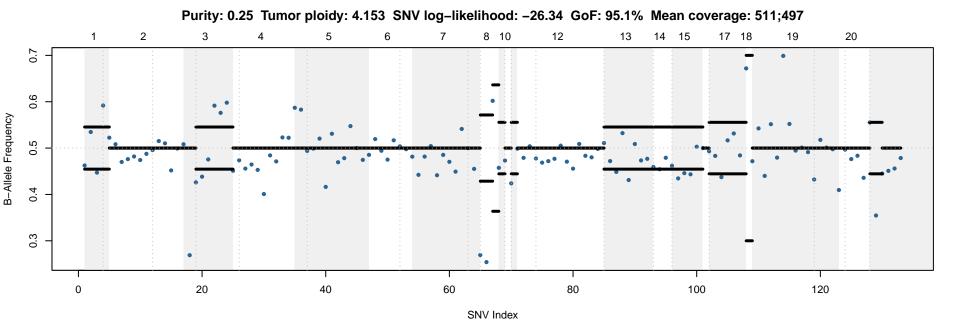
SCNA-fit log-likelihood: -8011.68



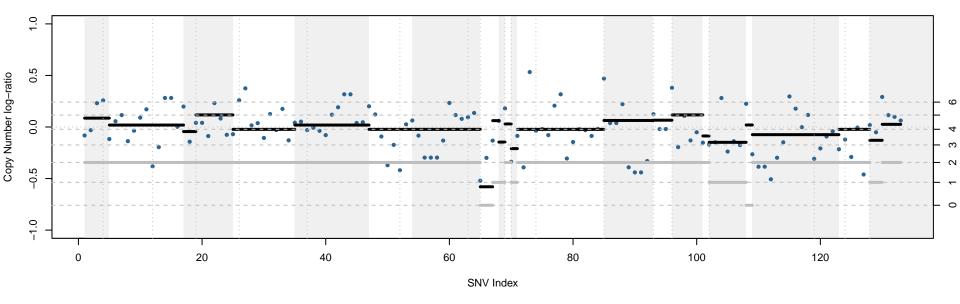


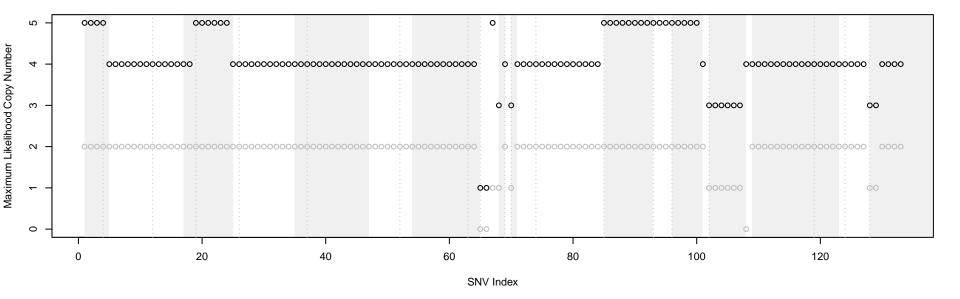


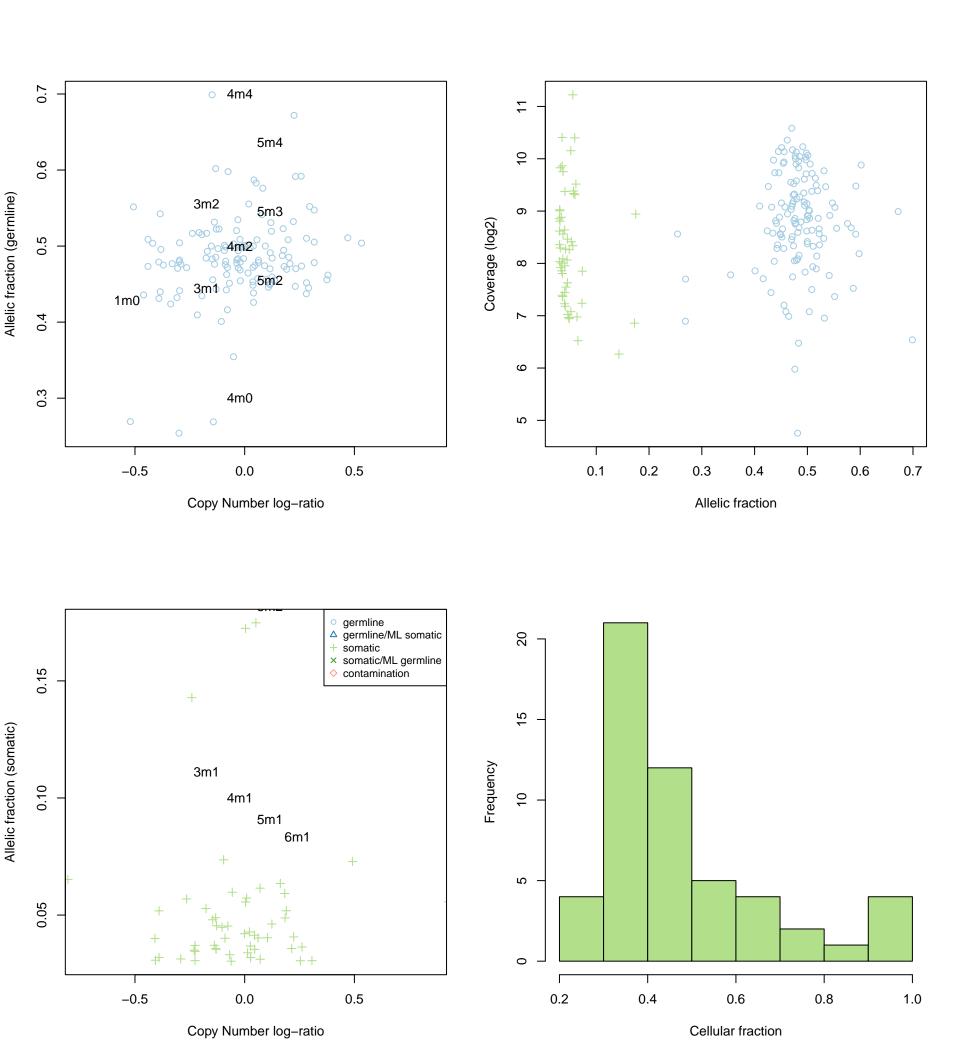




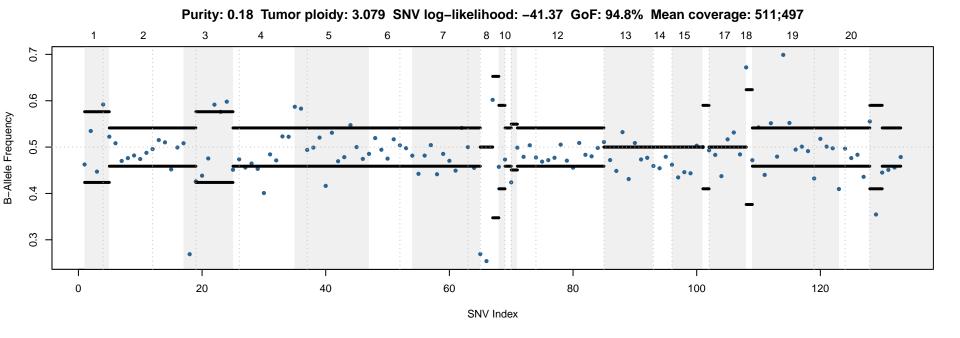
SCNA-fit log-likelihood: -8016.32



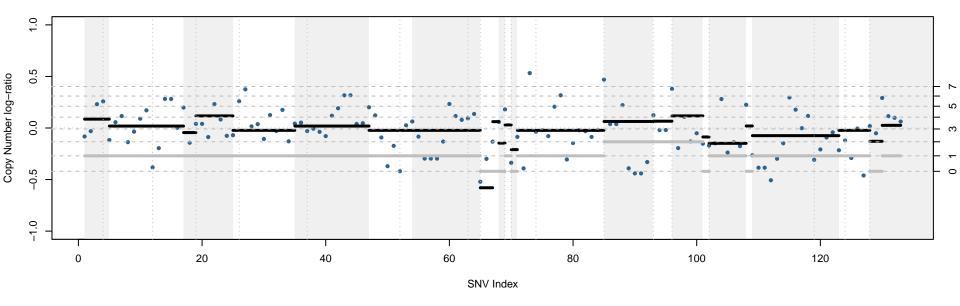


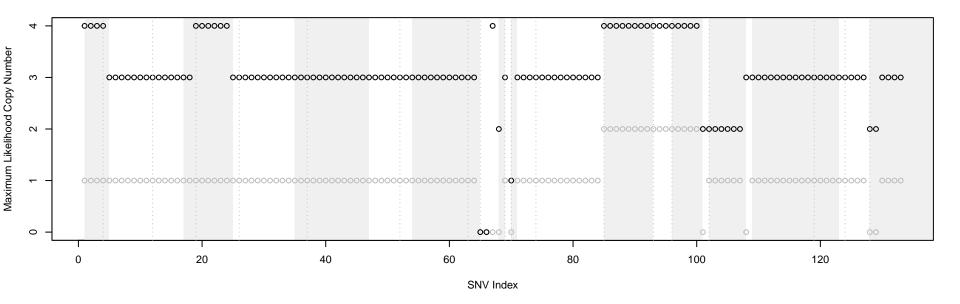


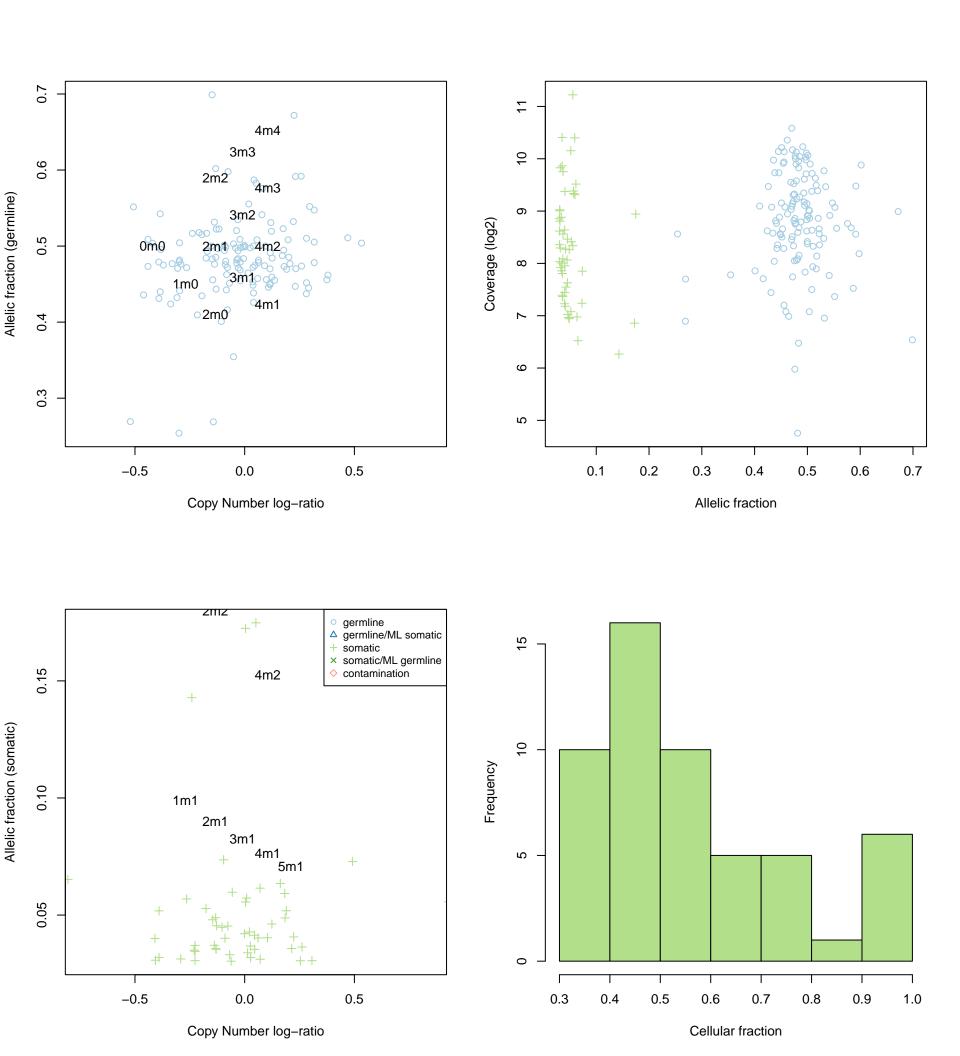
Purity: 0.18 Tumor ploidy: 3.079 3 2 0 5 6 7 0.20 Fraction Genome 0.05 0.00 0.0 -0.5 0.5 log2 ratio



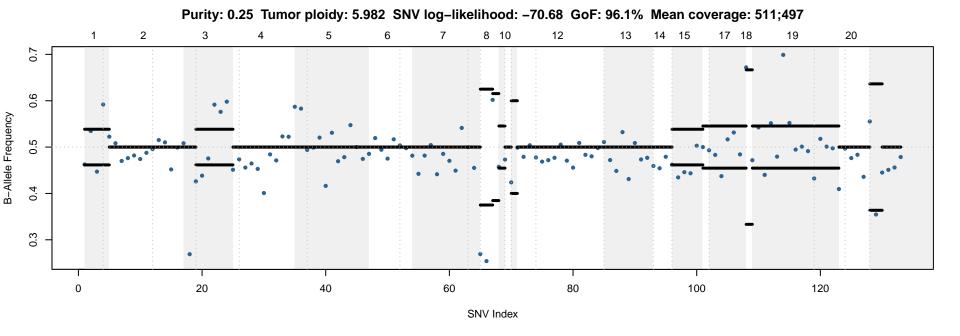
SCNA-fit log-likelihood: -7988.79



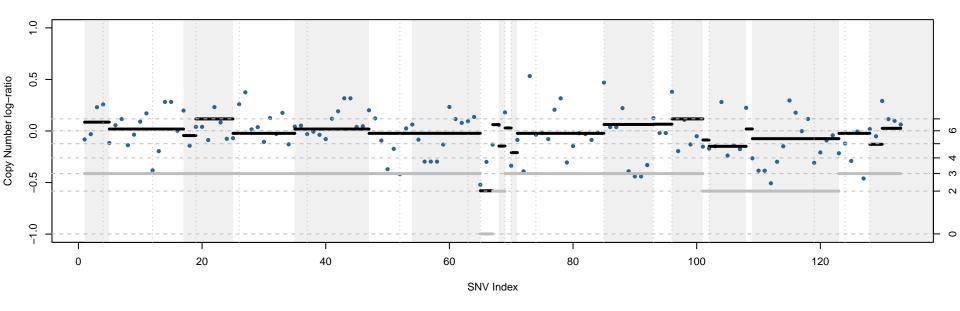


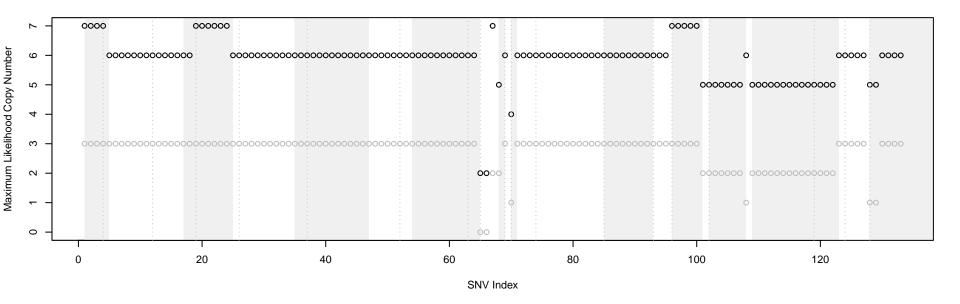


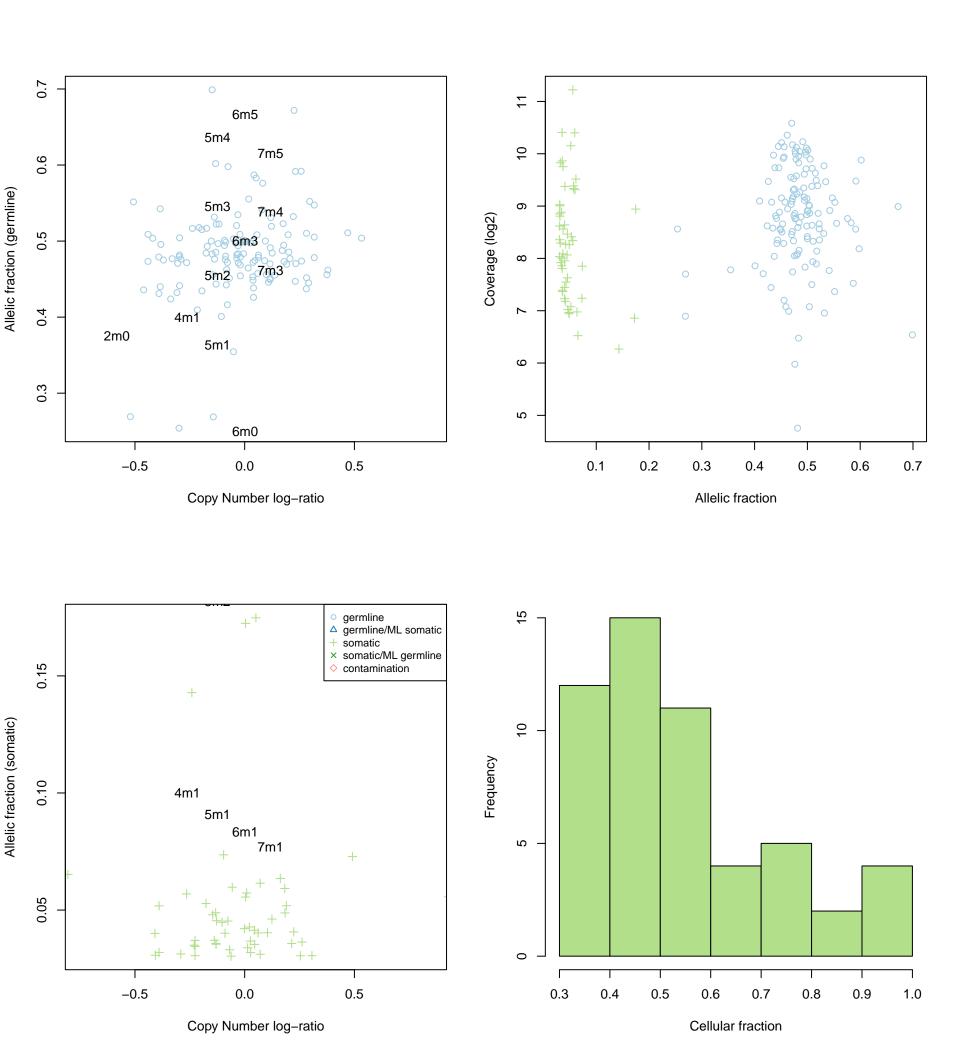
Purity: 0.25 Tumor ploidy: 5.982 0 2 3 5 6 0.20 Fraction Genome 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0



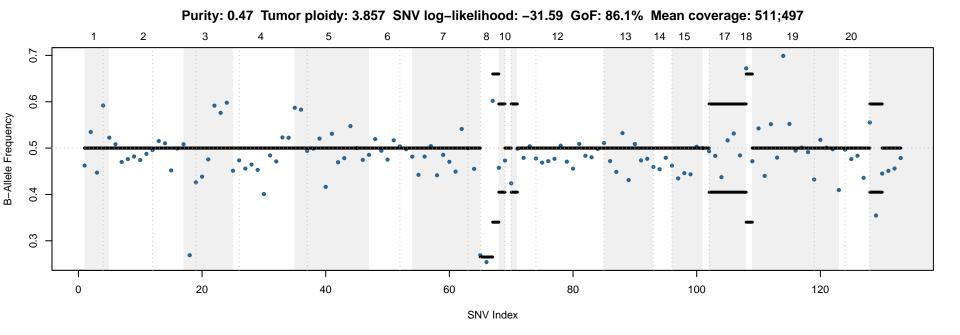
SCNA-fit log-likelihood: -8006.2



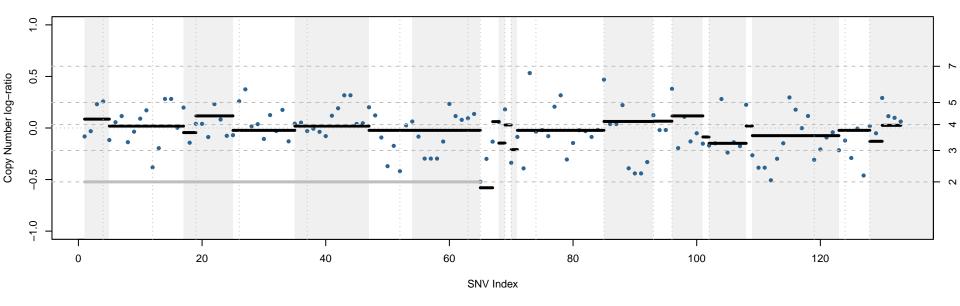


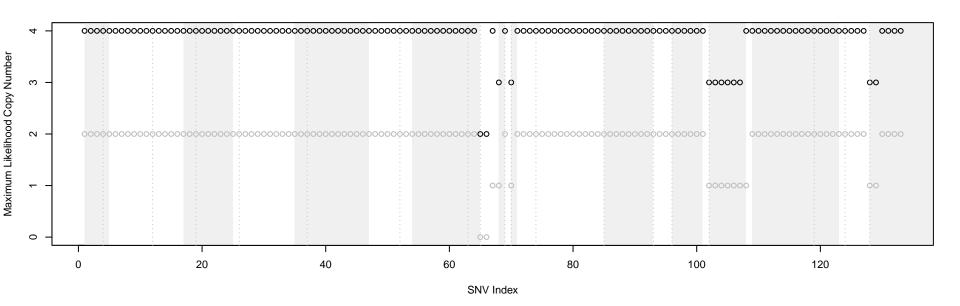


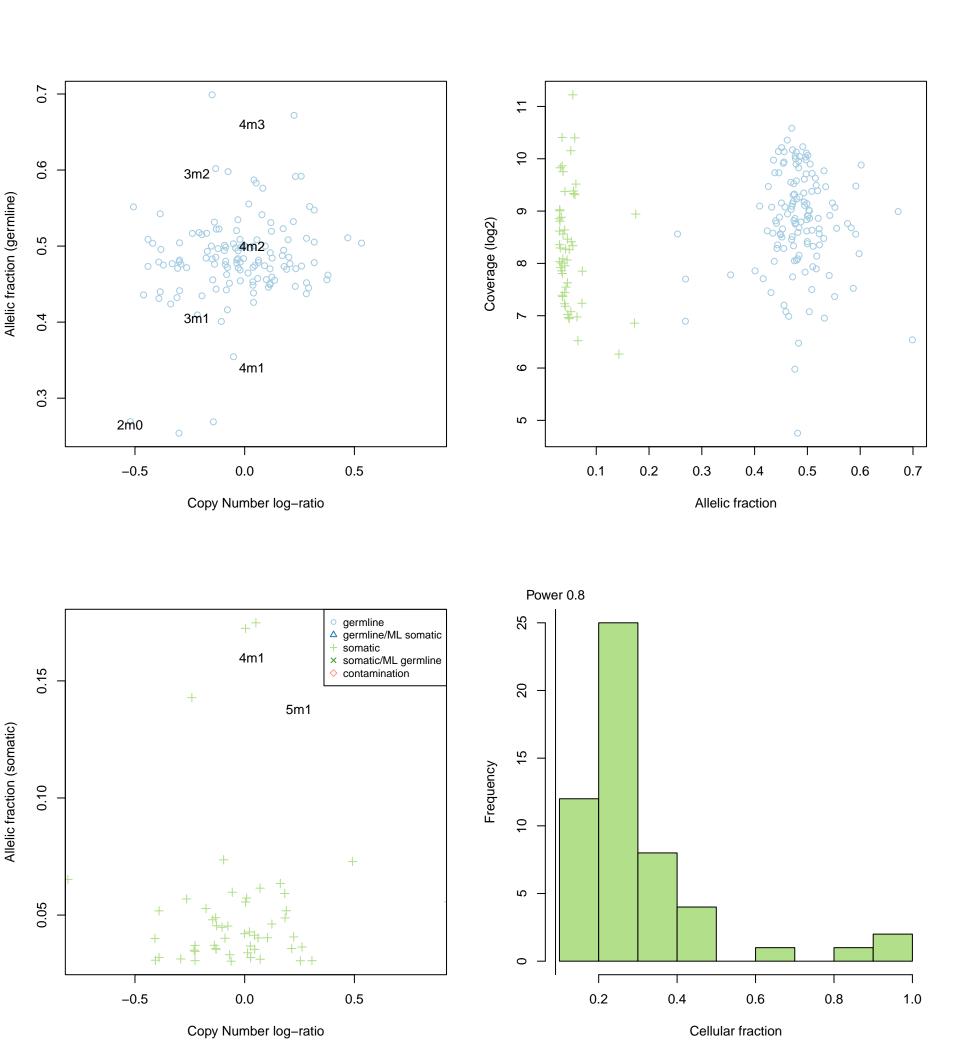
Purity: 0.47 Tumor ploidy: 3.857 2 0.20 Fraction Genome 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



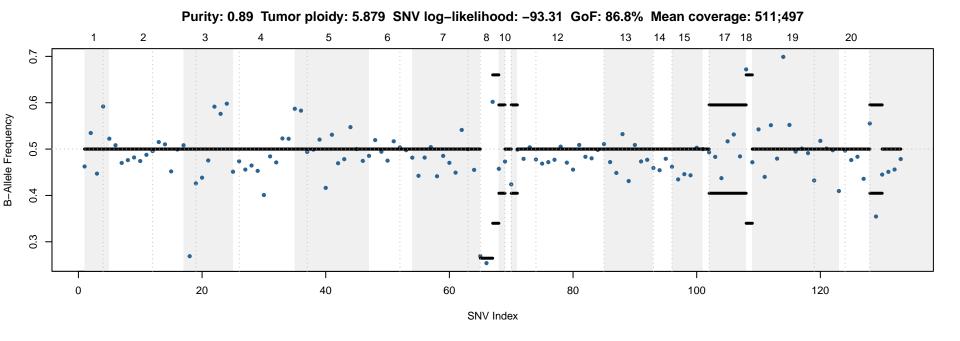
SCNA-fit log-likelihood: -8147.1



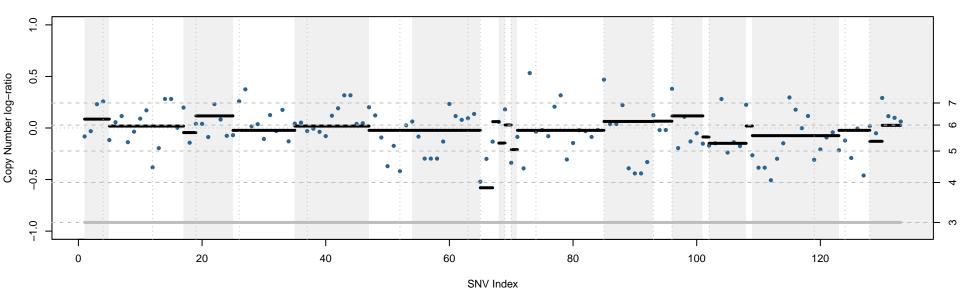


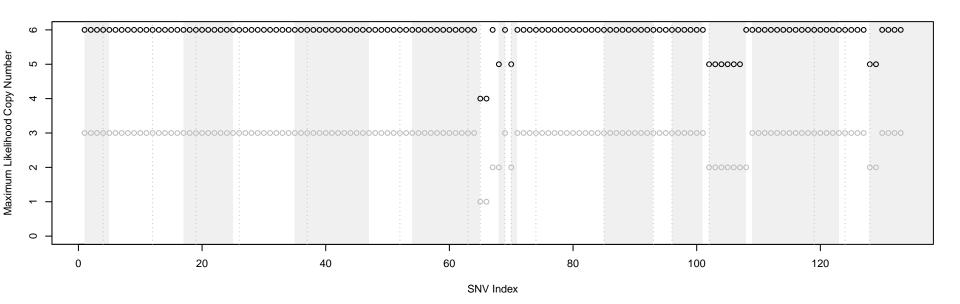


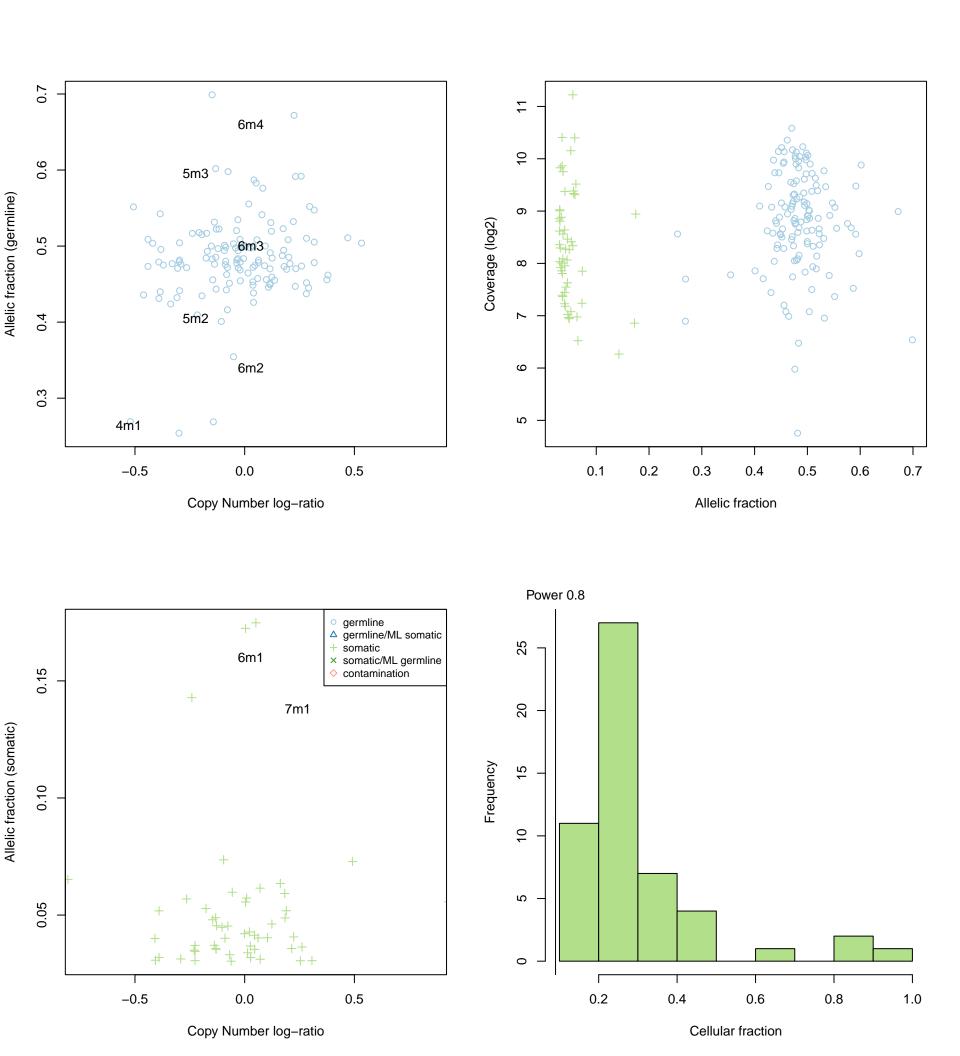
Purity: 0.89 Tumor ploidy: 5.879 3 5 6 0.20 Fraction Genome 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0



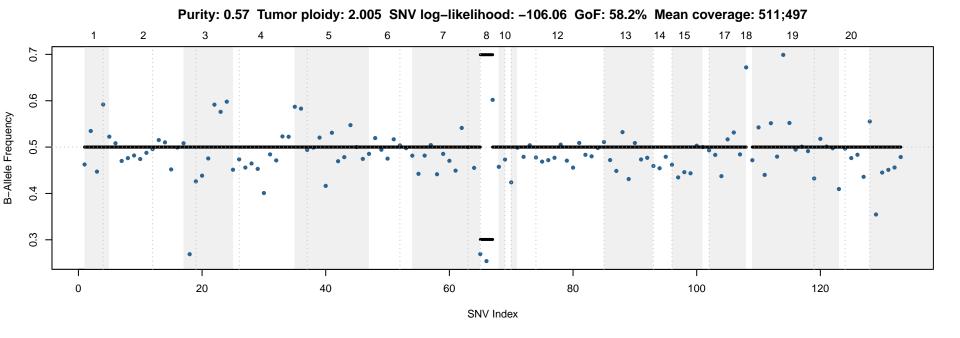
SCNA-fit log-likelihood: -8168.45



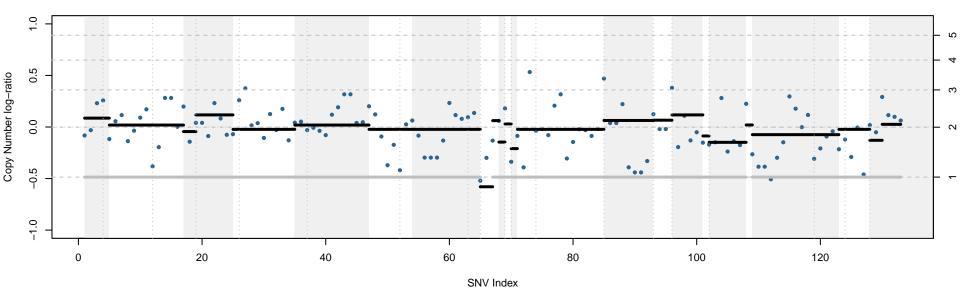


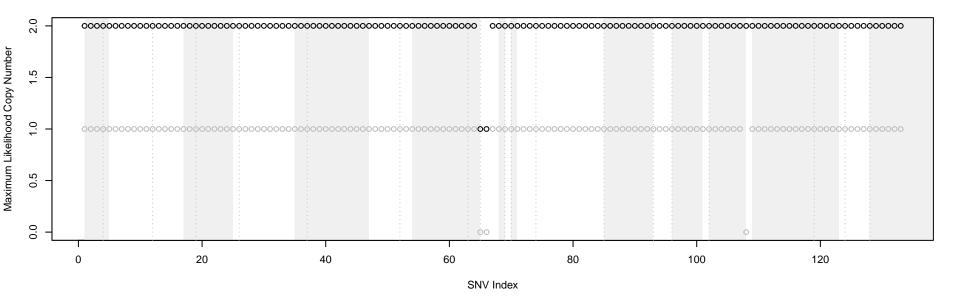


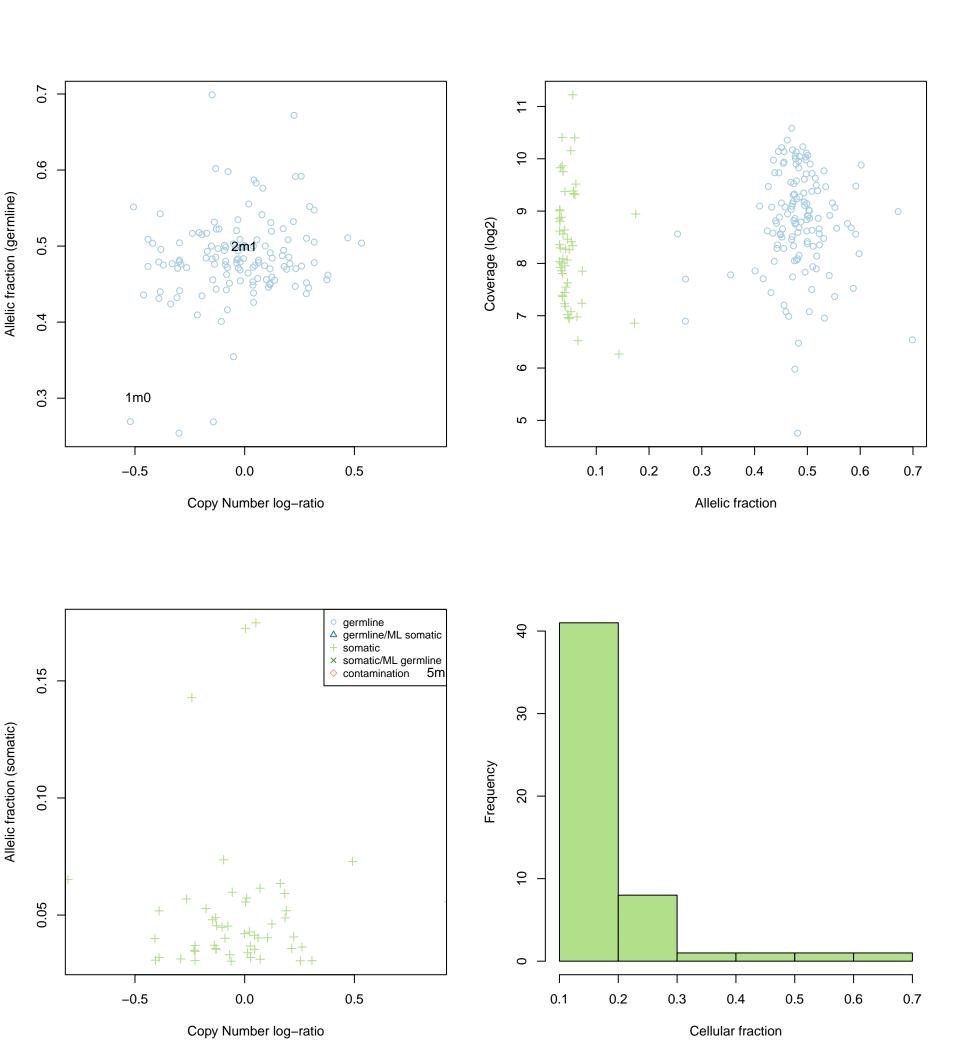
Purity: 0.57 Tumor ploidy: 2.005 0 3 5 0.20 Fraction Genome 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



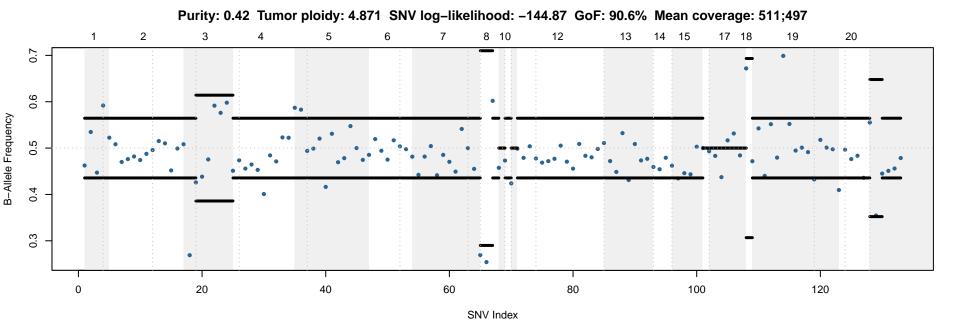
SCNA-fit log-likelihood: -8186.15



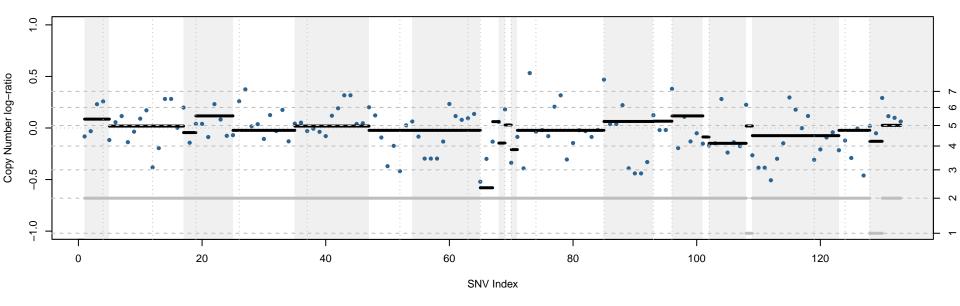


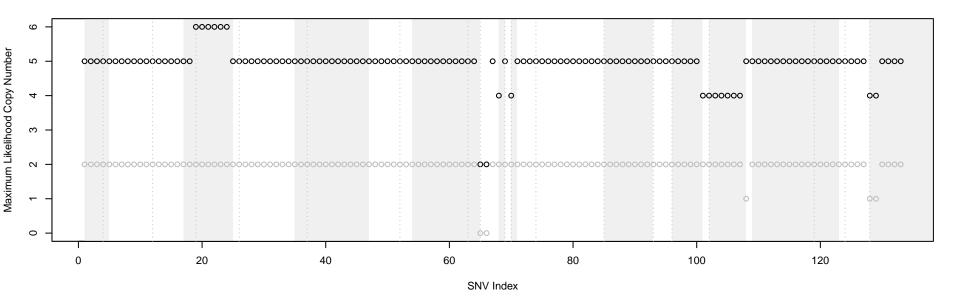


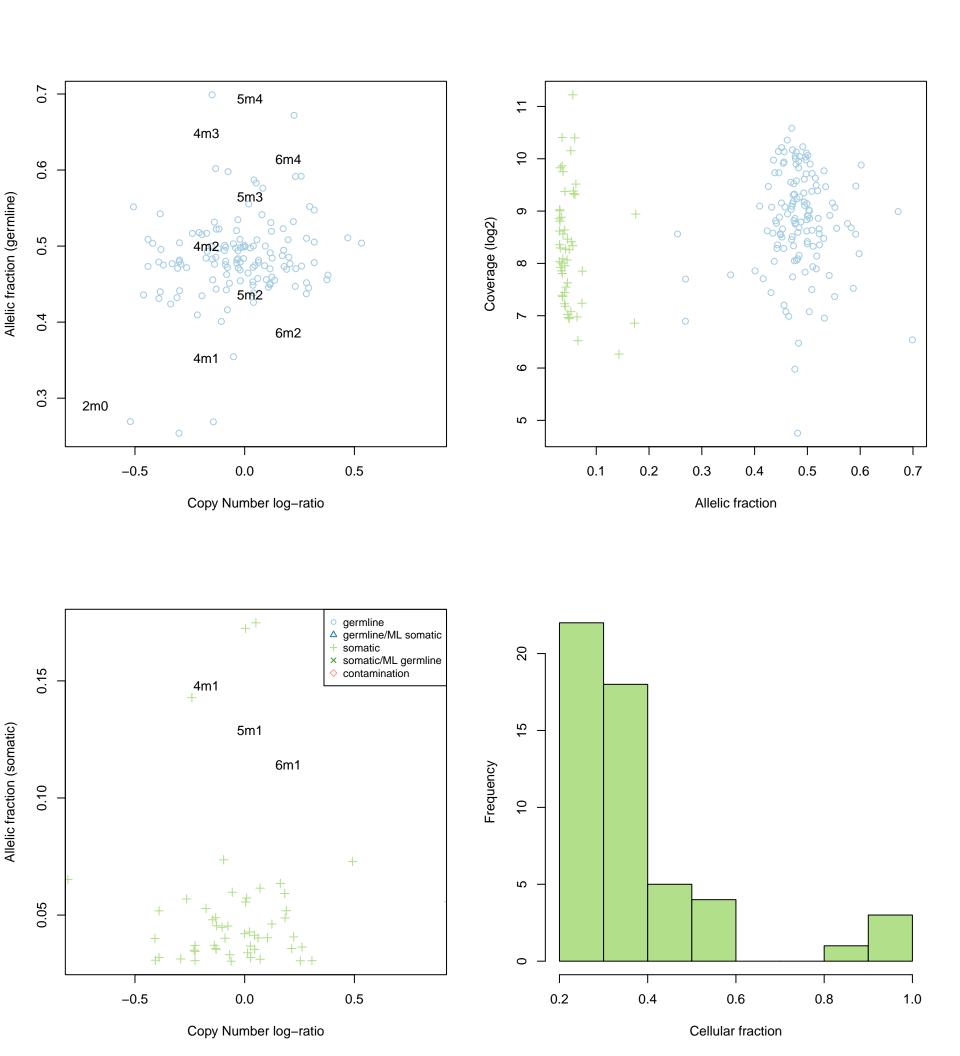
Purity: 0.42 Tumor ploidy: 4.871 2 6 5 0.20 Fraction Genome 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



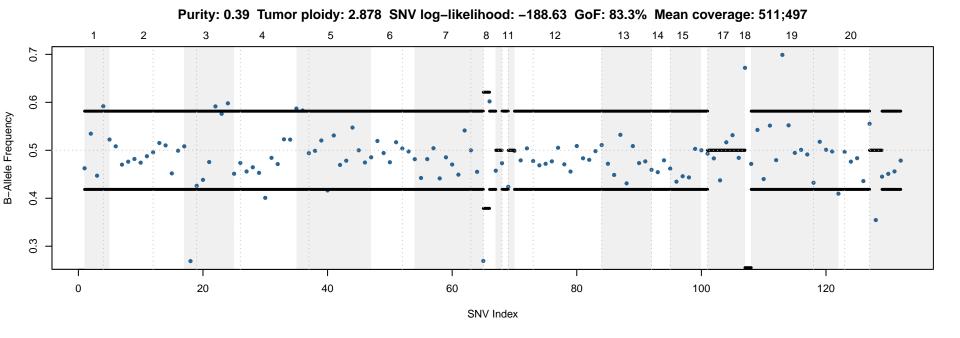
SCNA-fit log-likelihood: -8091.67



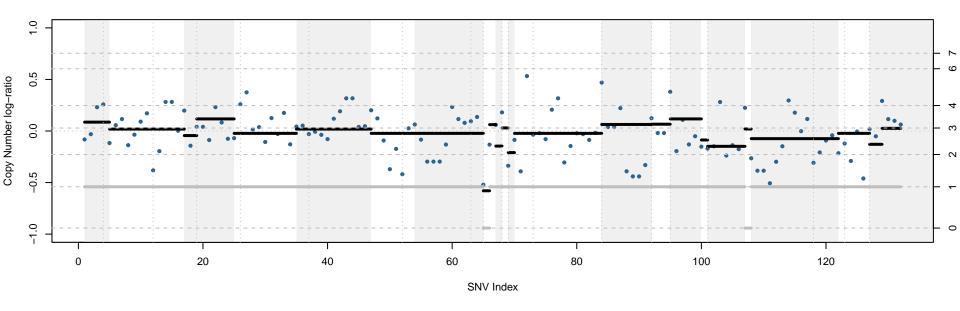


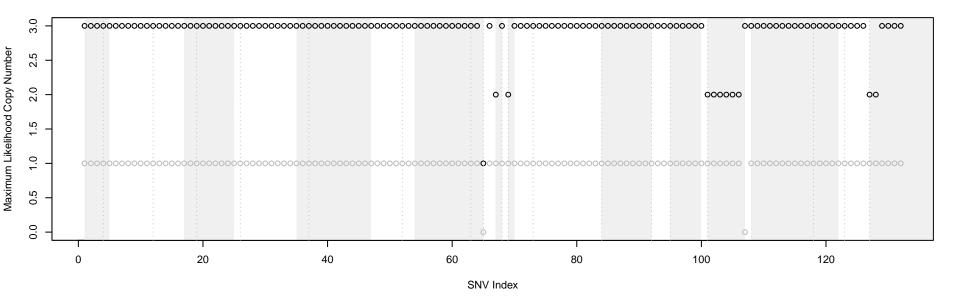


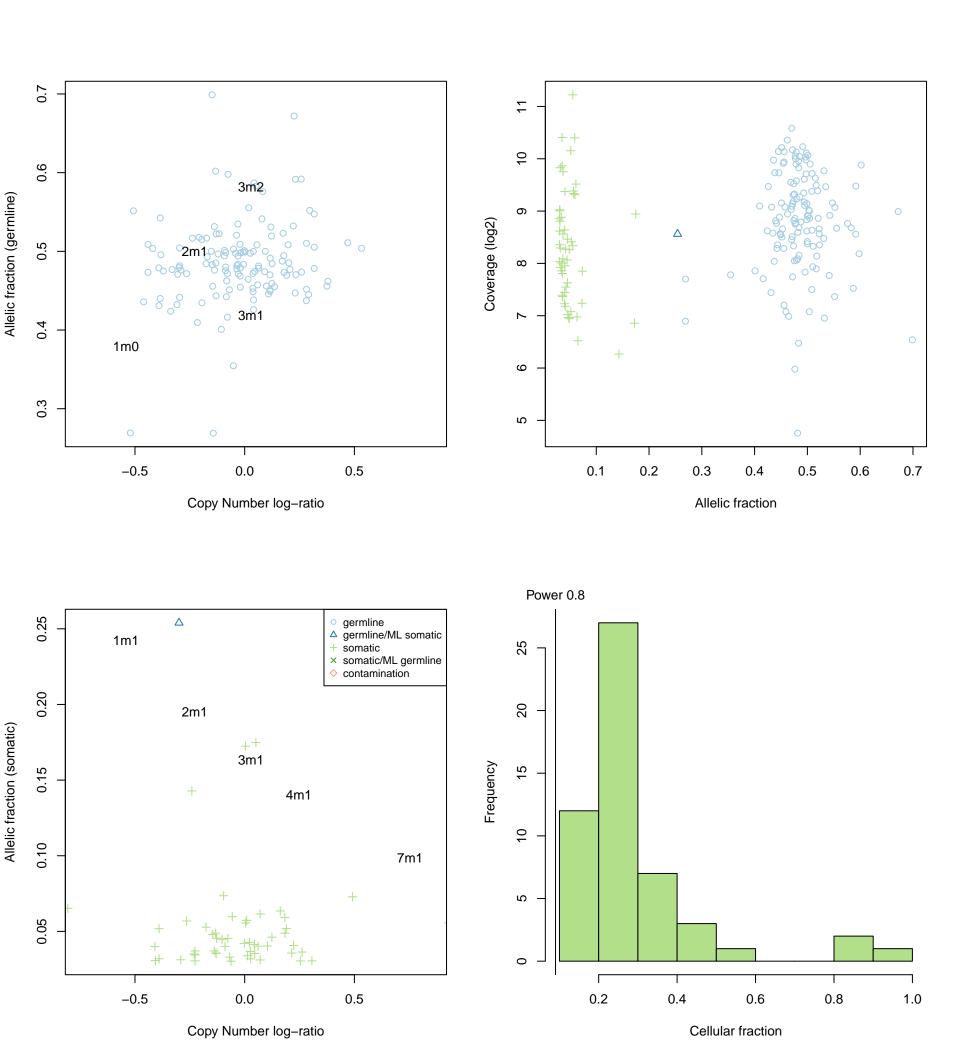
Purity: 0.39 Tumor ploidy: 2.878 3 0 6 7 0.20 Fraction Genome 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0



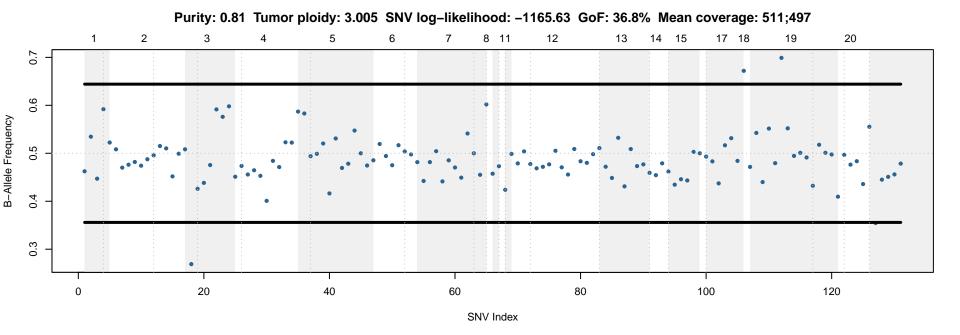
SCNA-fit log-likelihood: -8054.66







Purity: 0.81 Tumor ploidy: 3.005 2 5 6 0.20 Fraction Genome 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0



SCNA-fit log-likelihood: -8187.08

