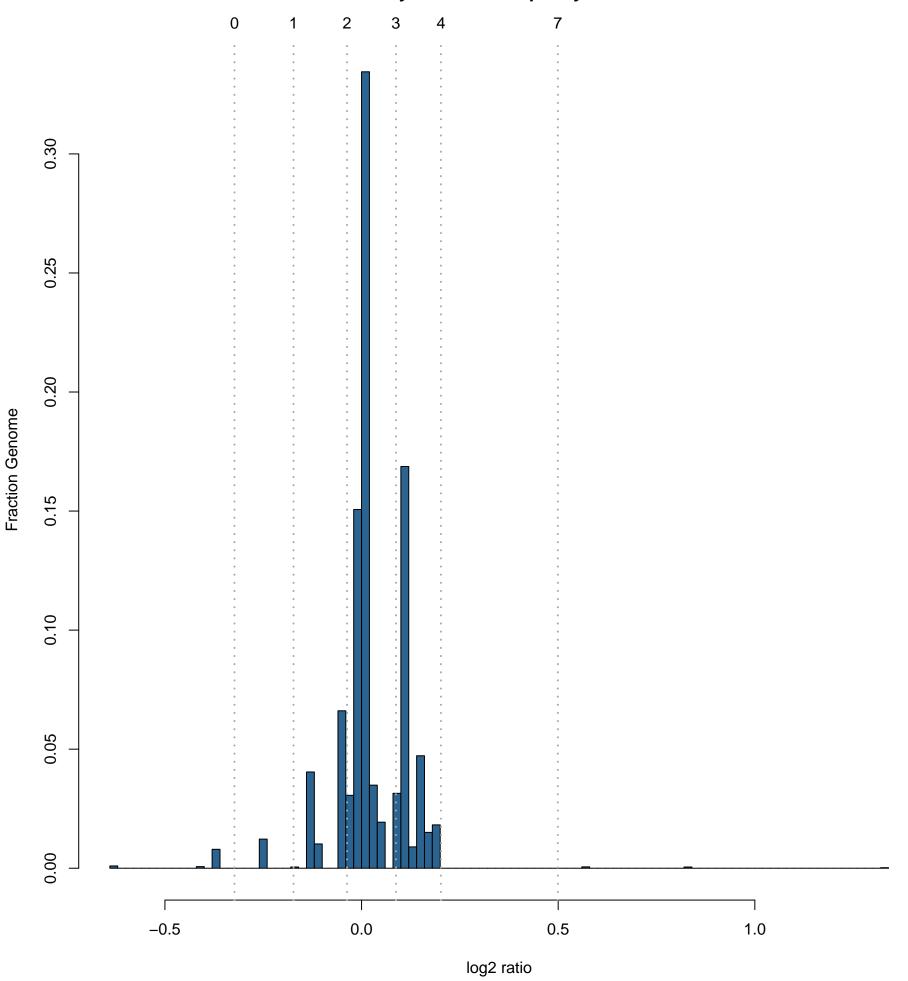
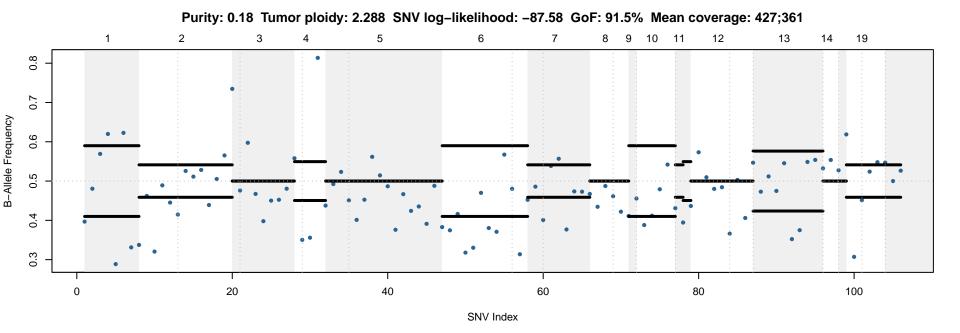
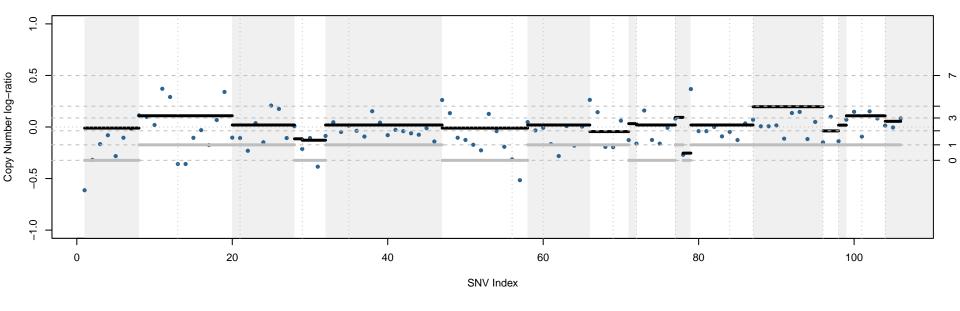
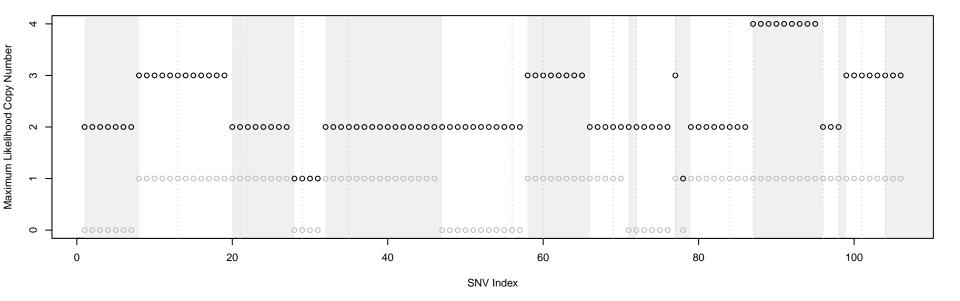
Purity: 0.18 Tumor ploidy: 2.288

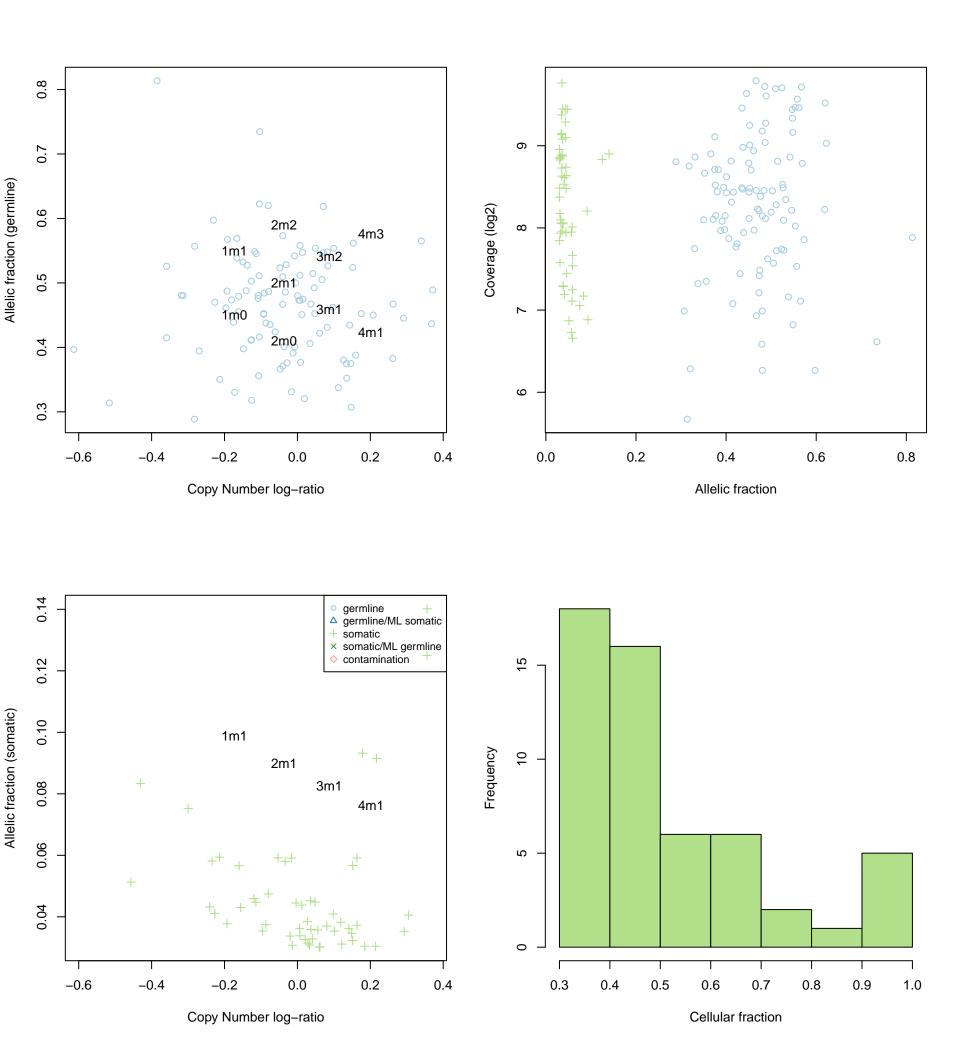




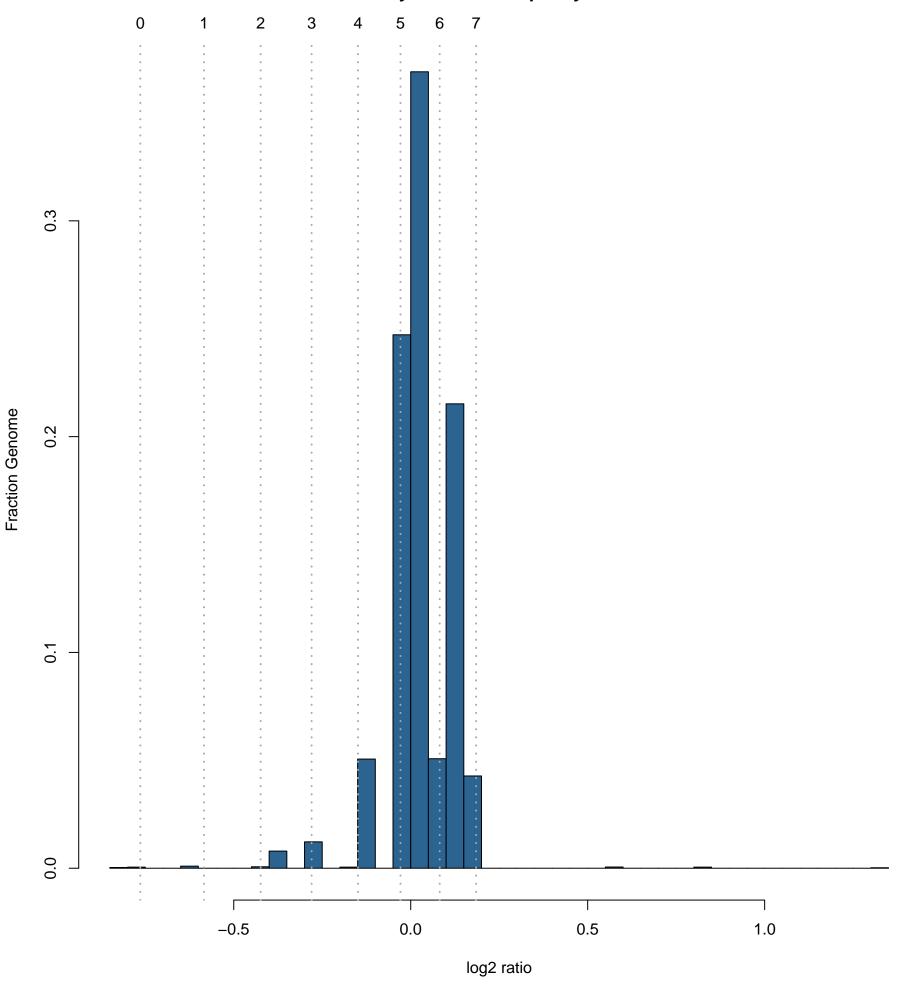
SCNA-fit log-likelihood: -5812.27

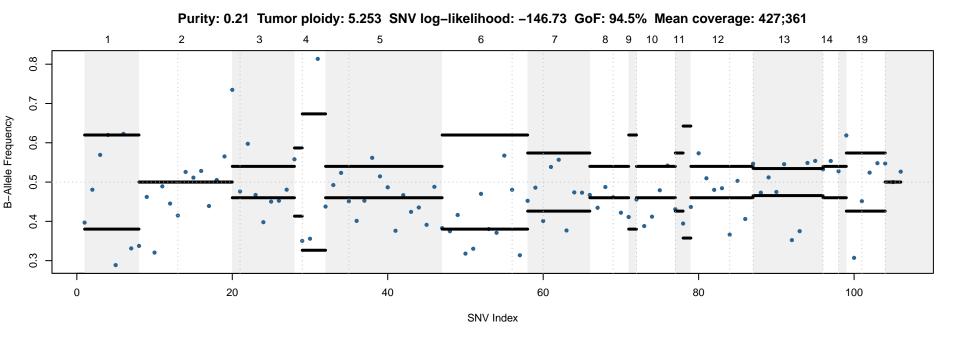




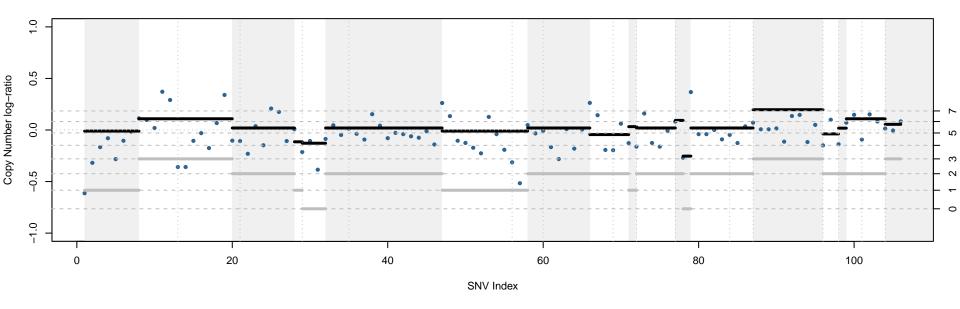


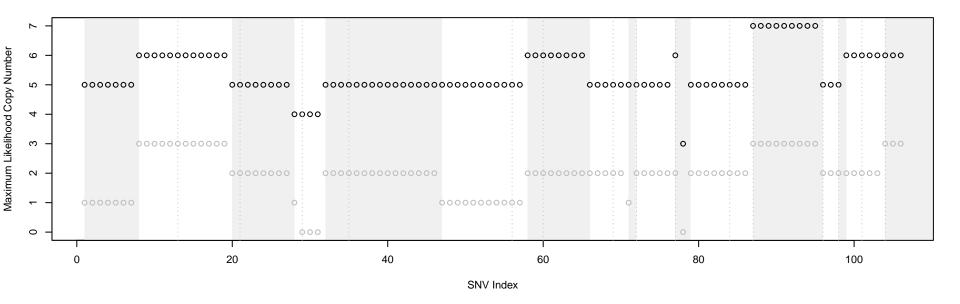
Purity: 0.21 Tumor ploidy: 5.253

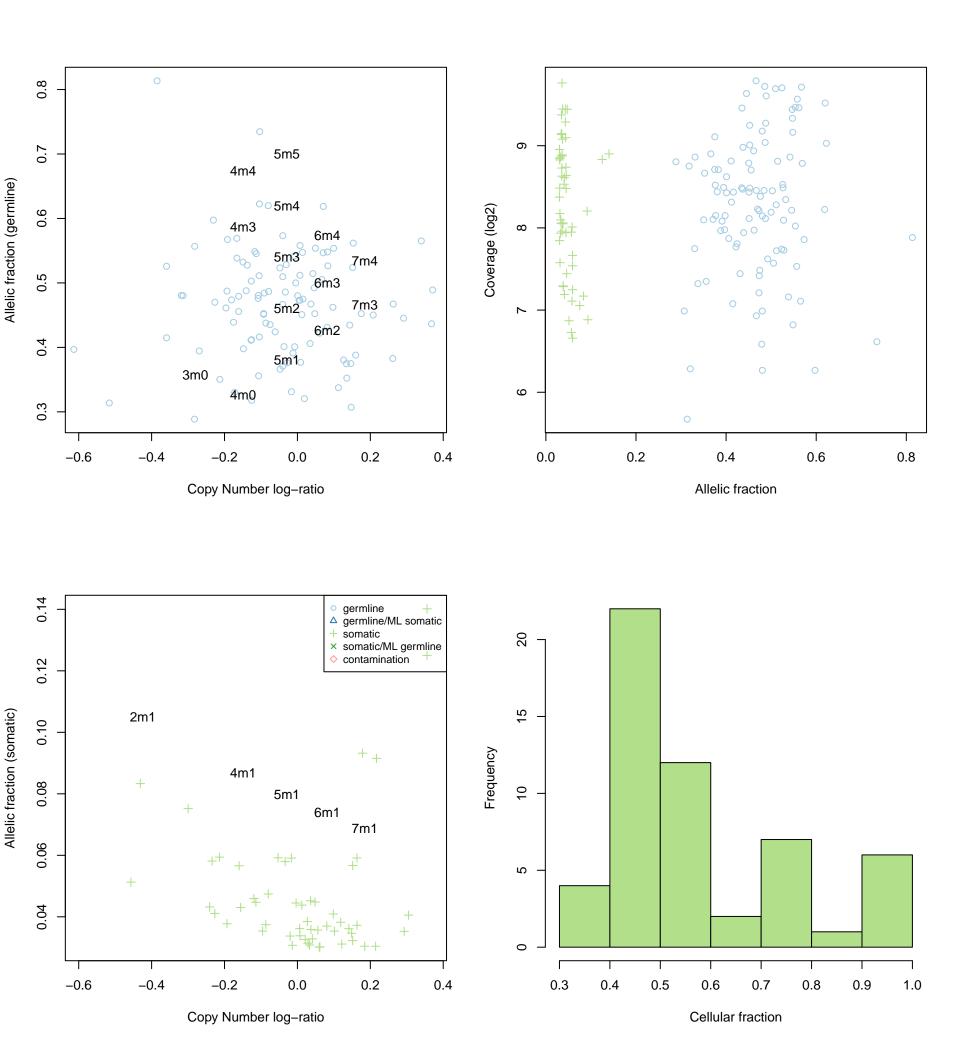




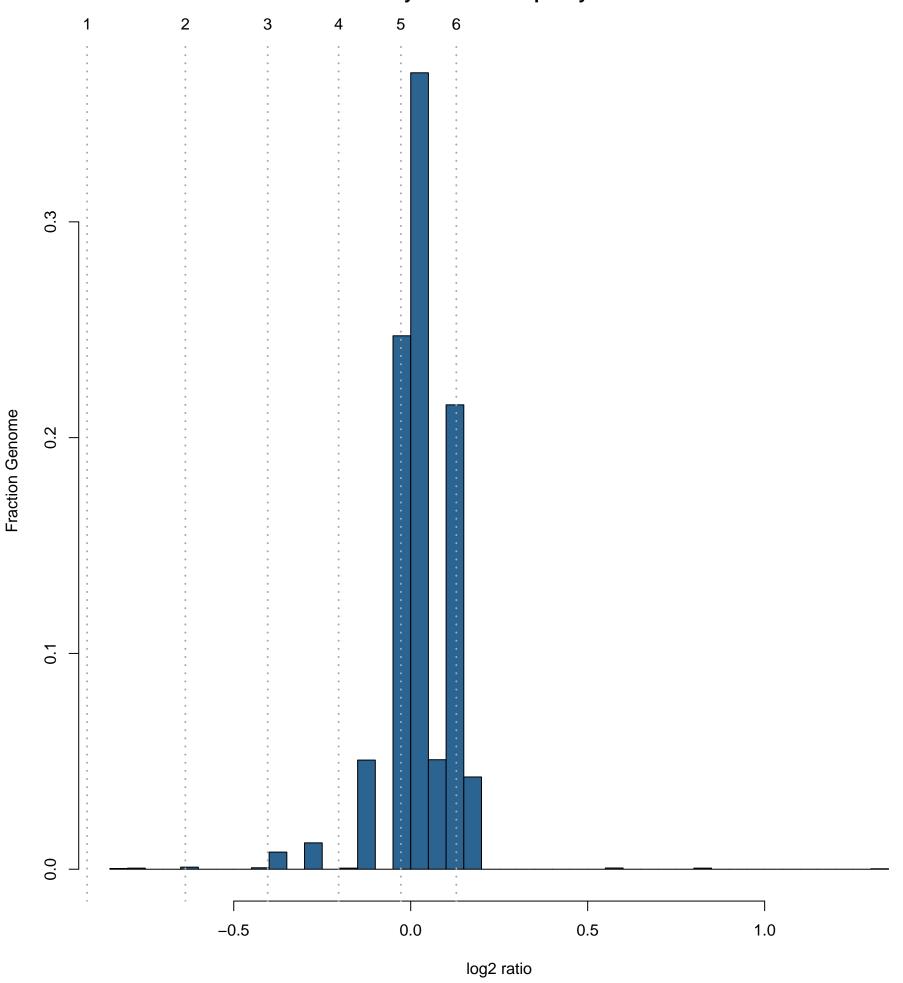
SCNA-fit log-likelihood: -5746.36

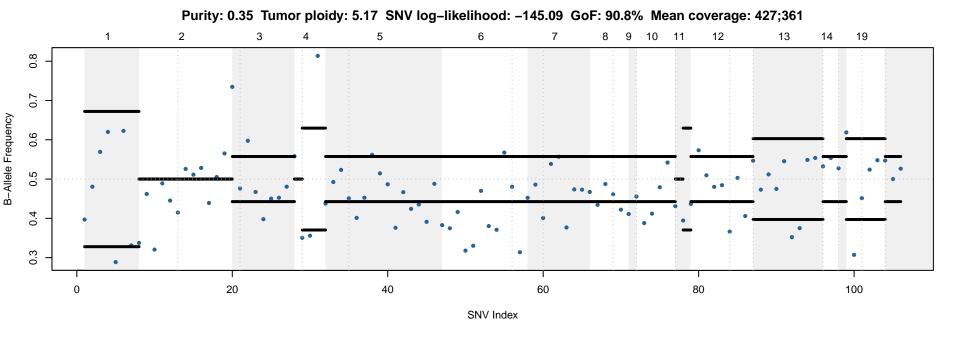




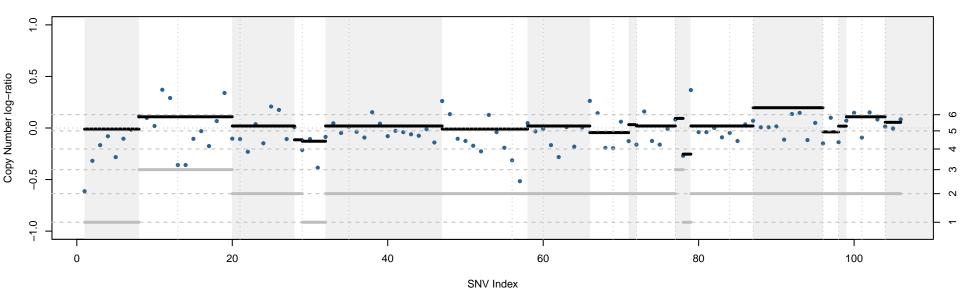


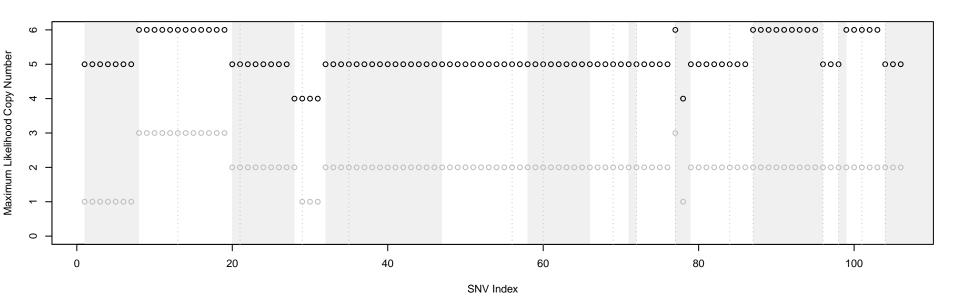
Purity: 0.35 Tumor ploidy: 5.17

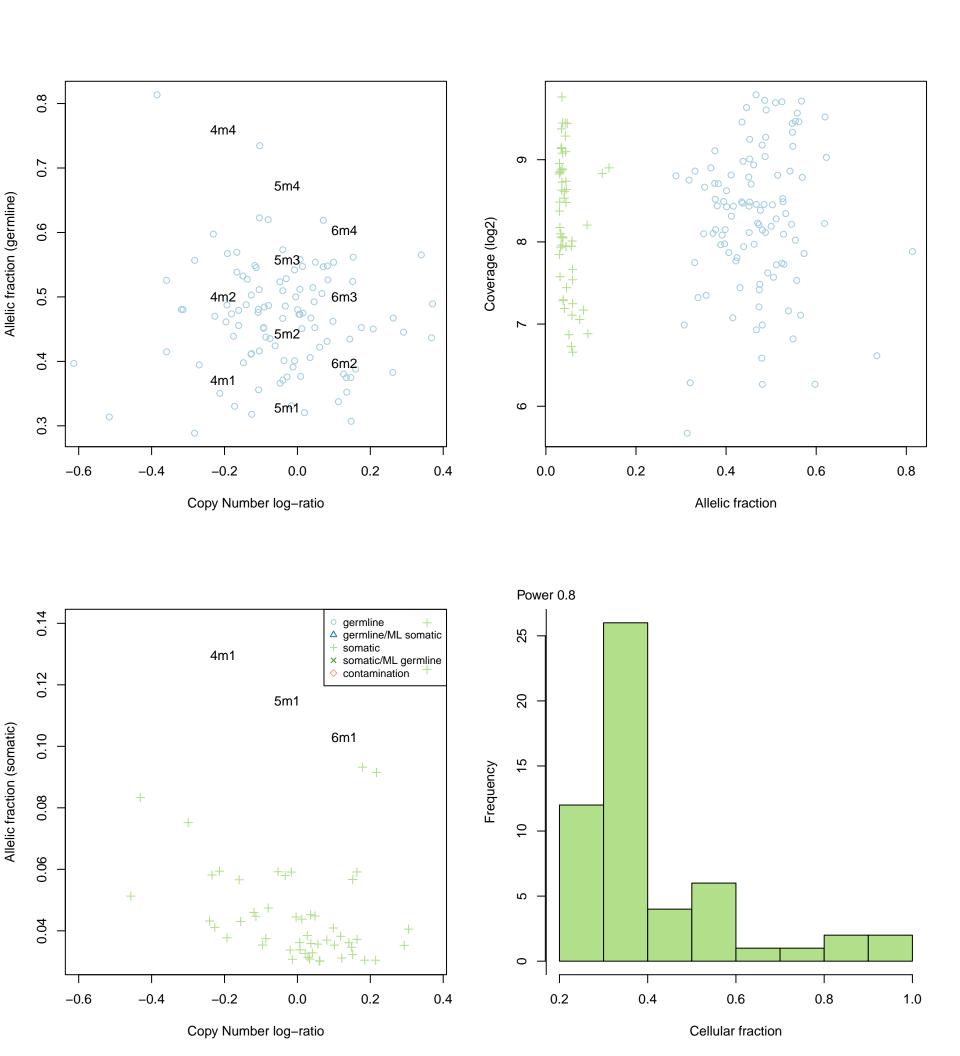




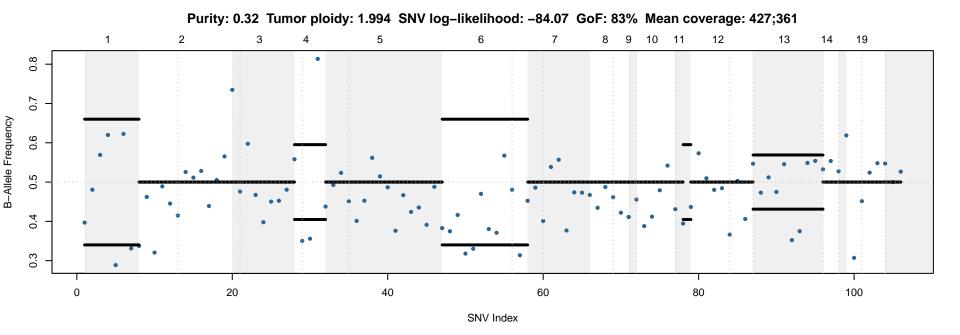
SCNA-fit log-likelihood: -5791.83



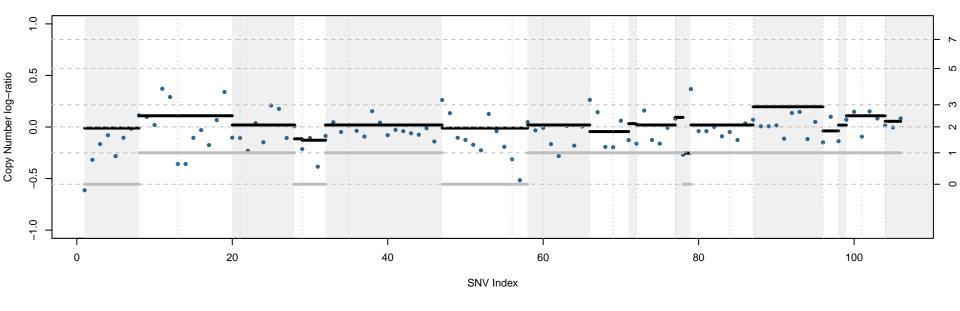


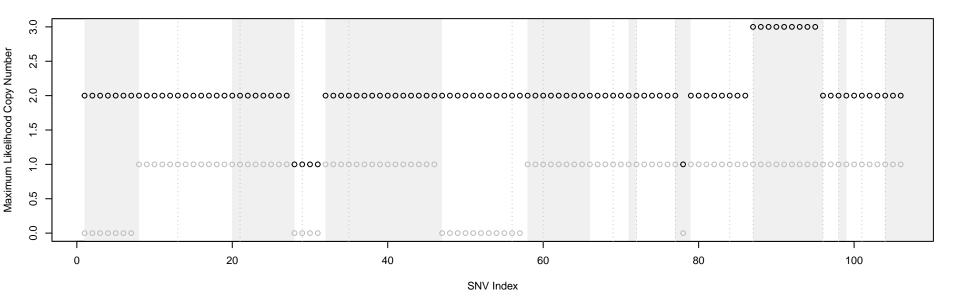


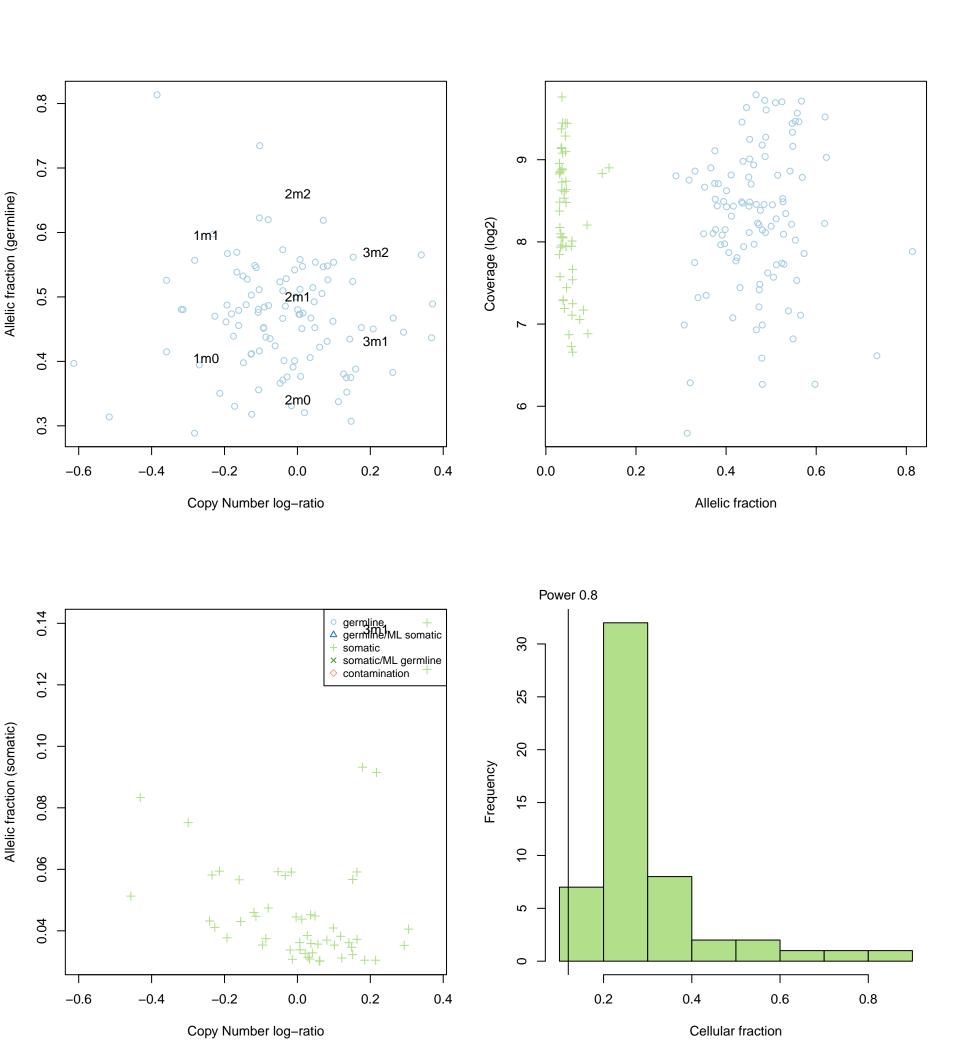
Purity: 0.32 Tumor ploidy: 1.994 3 7 0 Fraction Genome 0.0 -0.5 0.0 0.5 1.0 log2 ratio



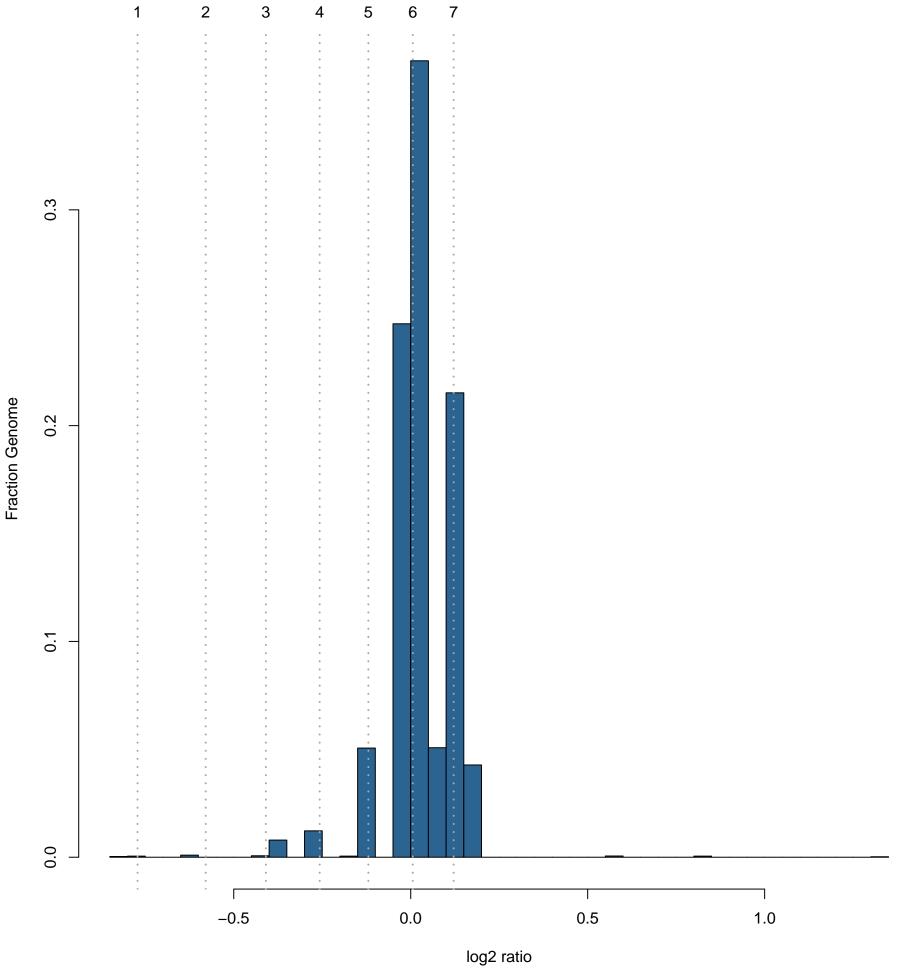
SCNA-fit log-likelihood: -5954.85

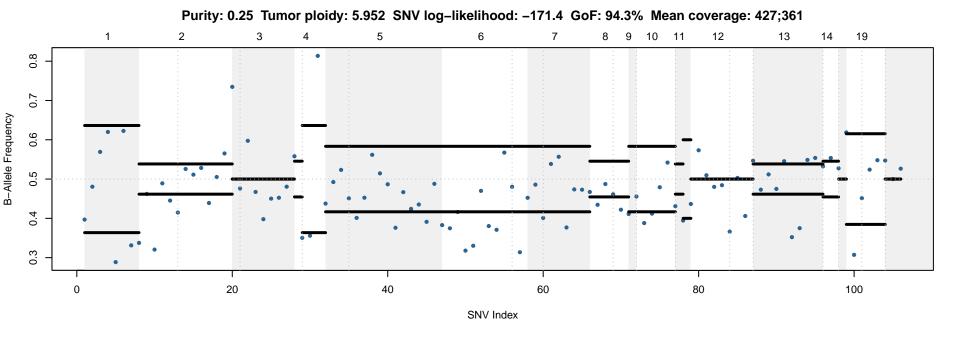




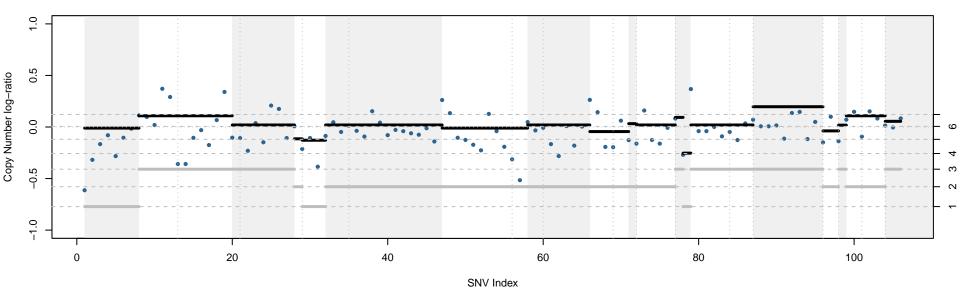


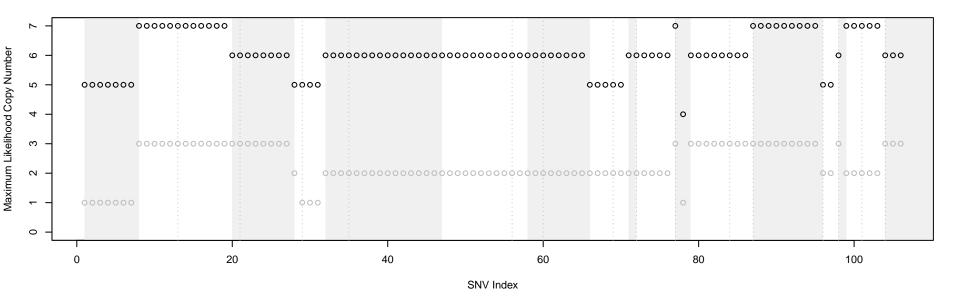
Purity: 0.25 Tumor ploidy: 5.952

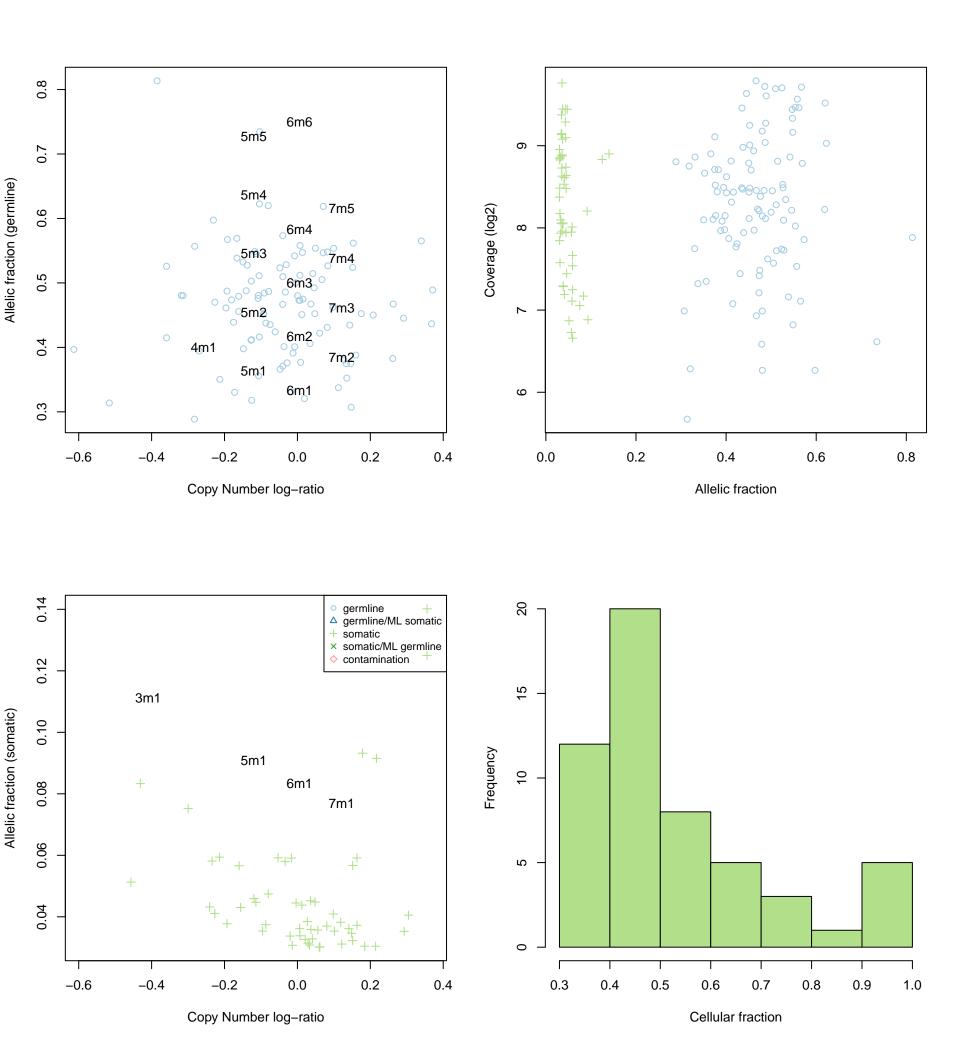




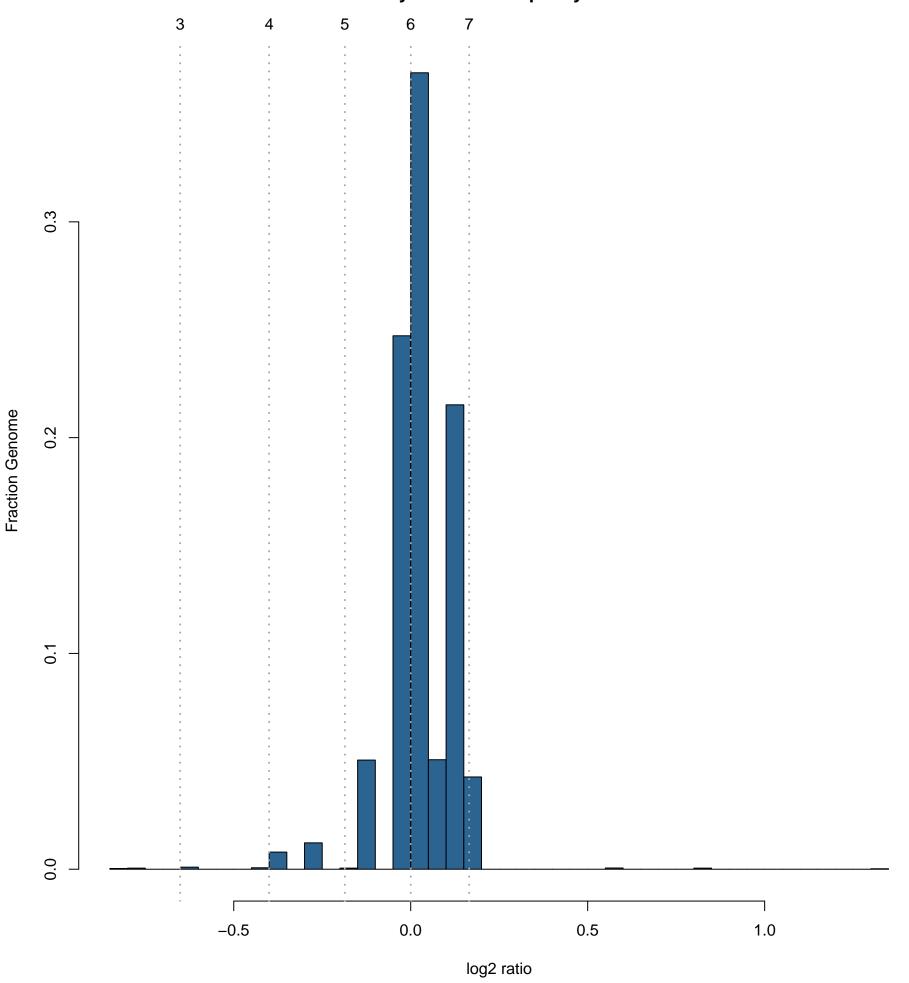
SCNA-fit log-likelihood: -5809.71

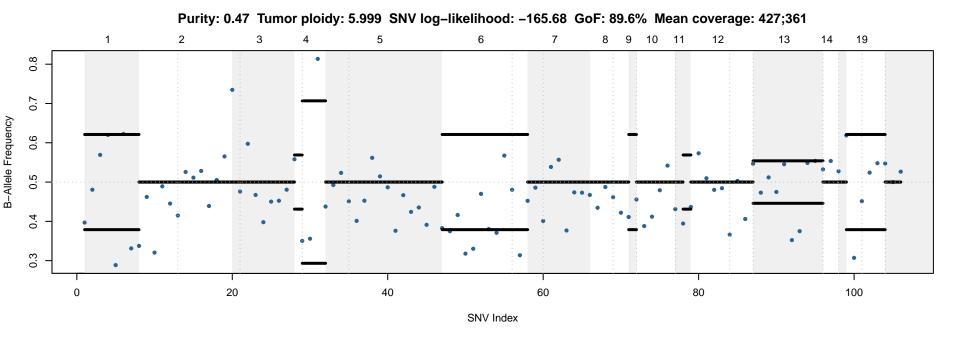




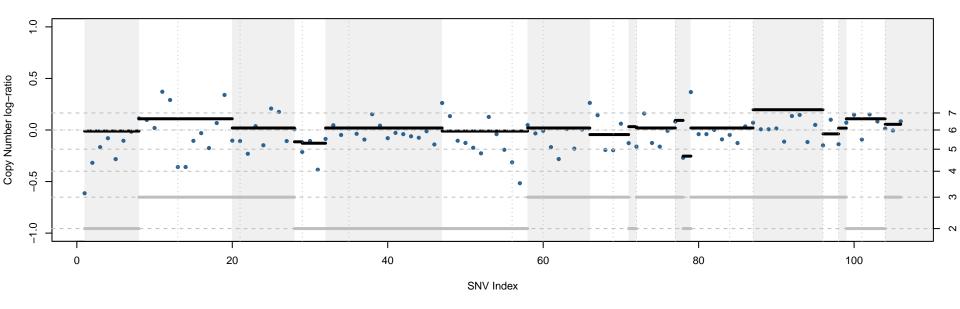


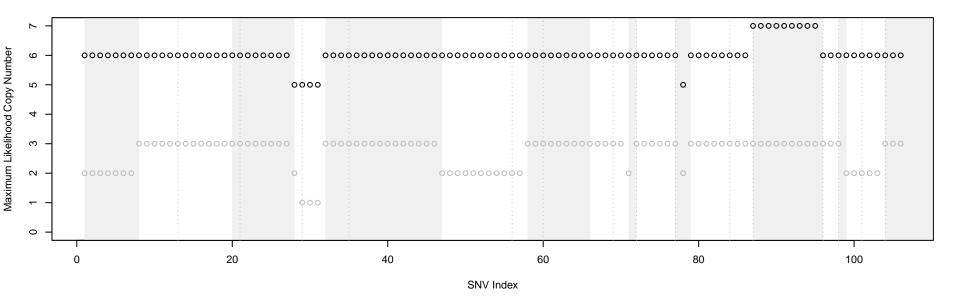
Purity: 0.47 Tumor ploidy: 5.999

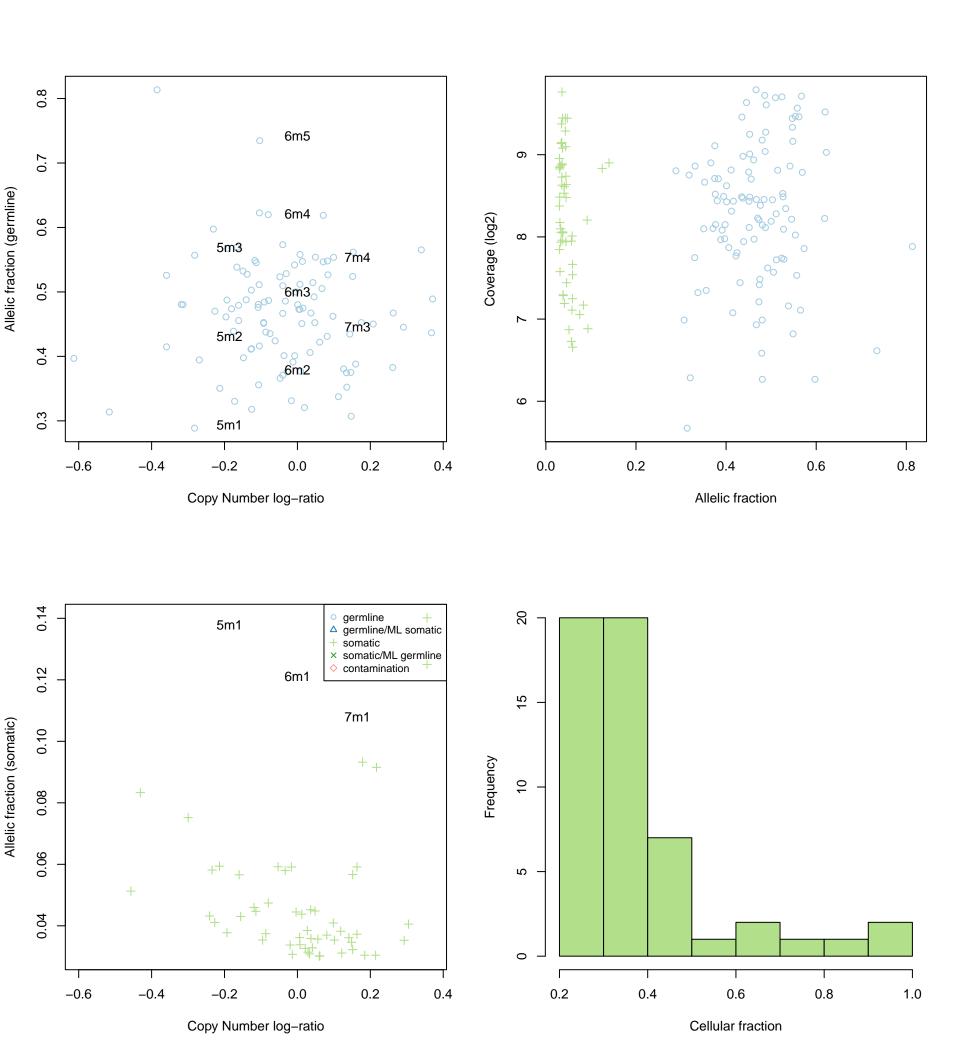






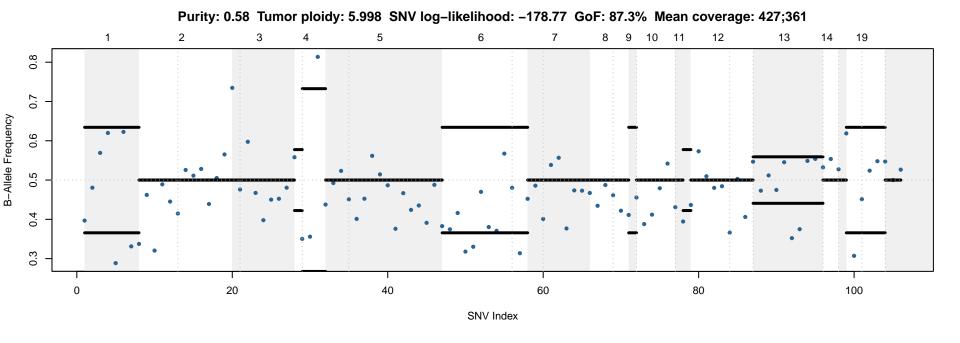




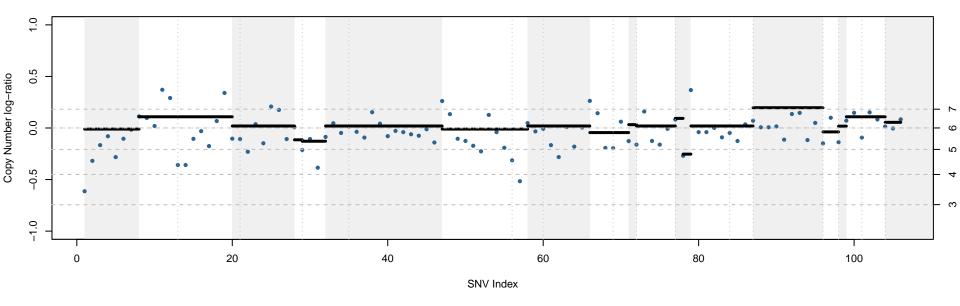


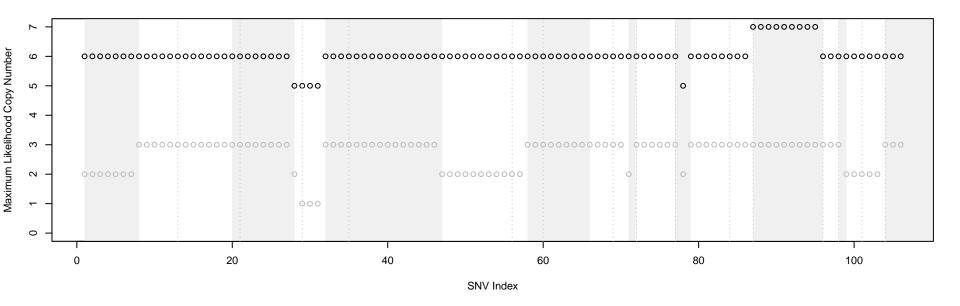
Purity: 0.58 Tumor ploidy: 5.998 3 5 Fraction Genome 0.2 0.0 -0.5 0.0 0.5 1.0

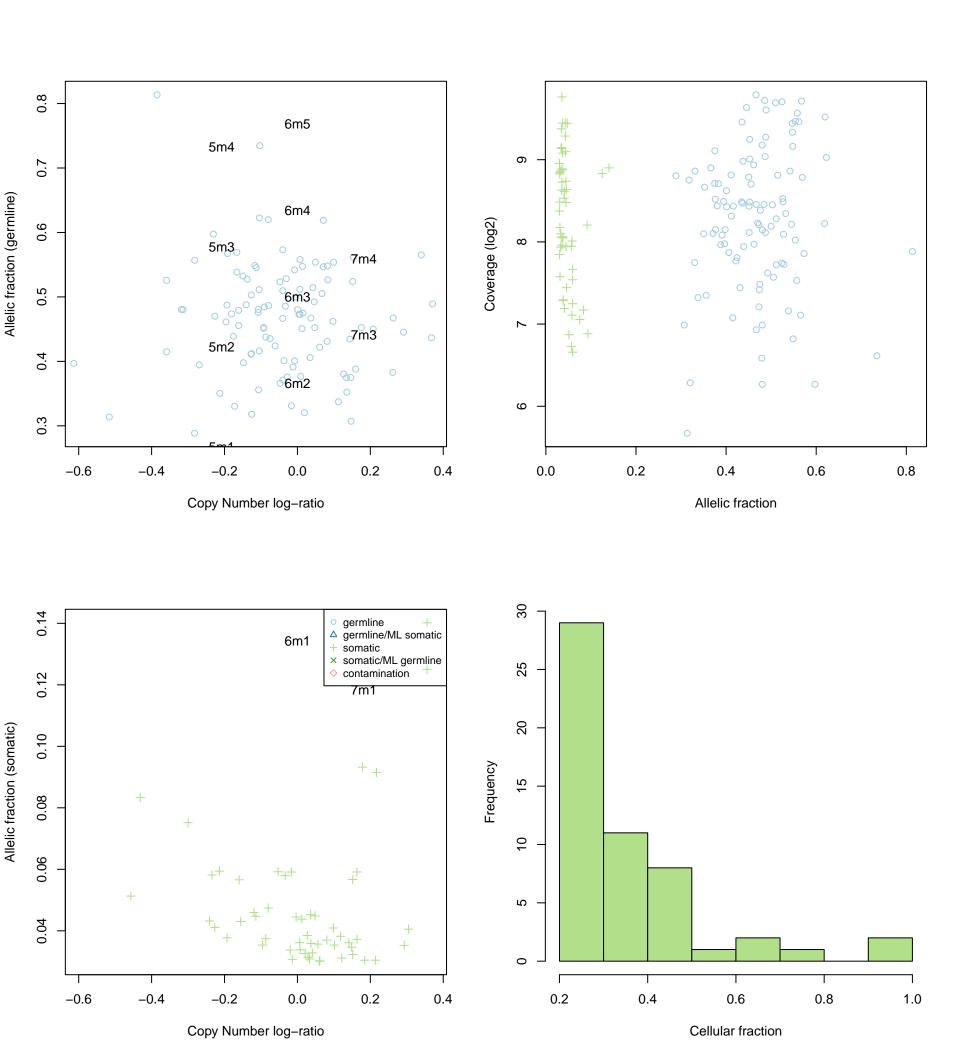
log2 ratio



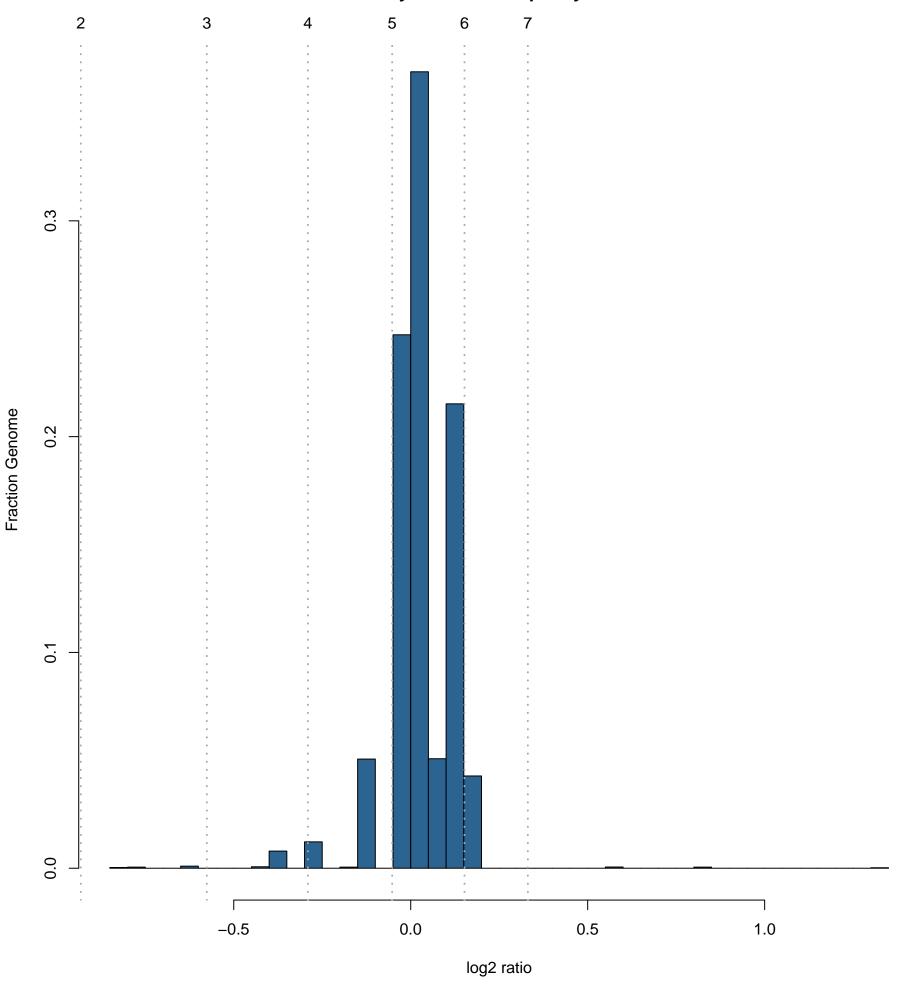
SCNA-fit log-likelihood: -5906.59

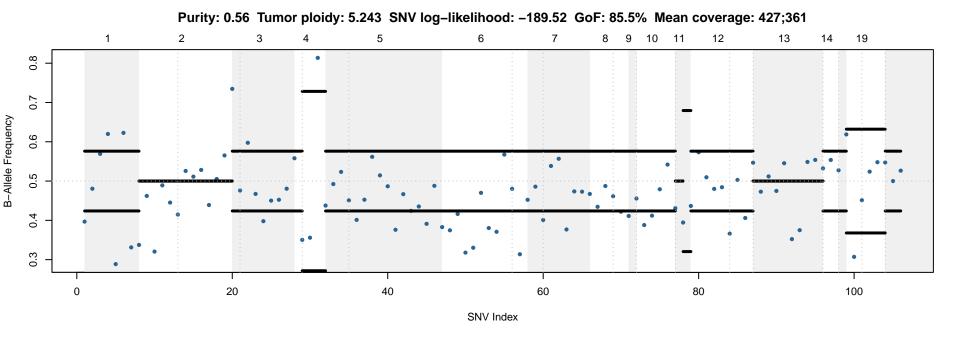




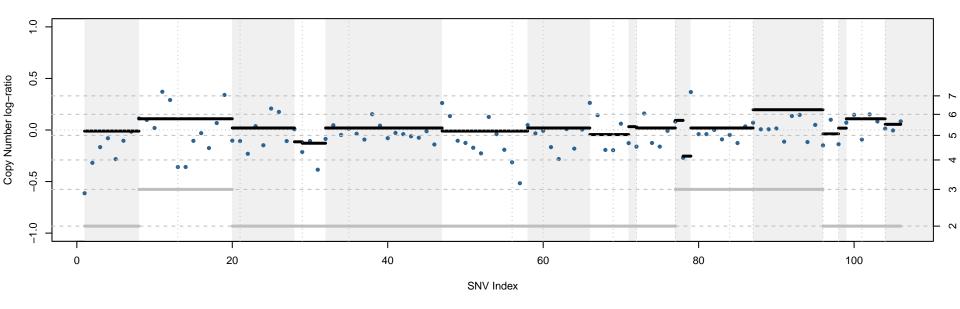


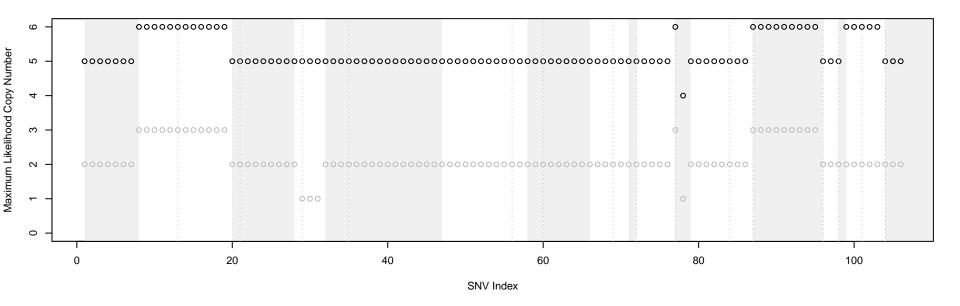
Purity: 0.56 Tumor ploidy: 5.243

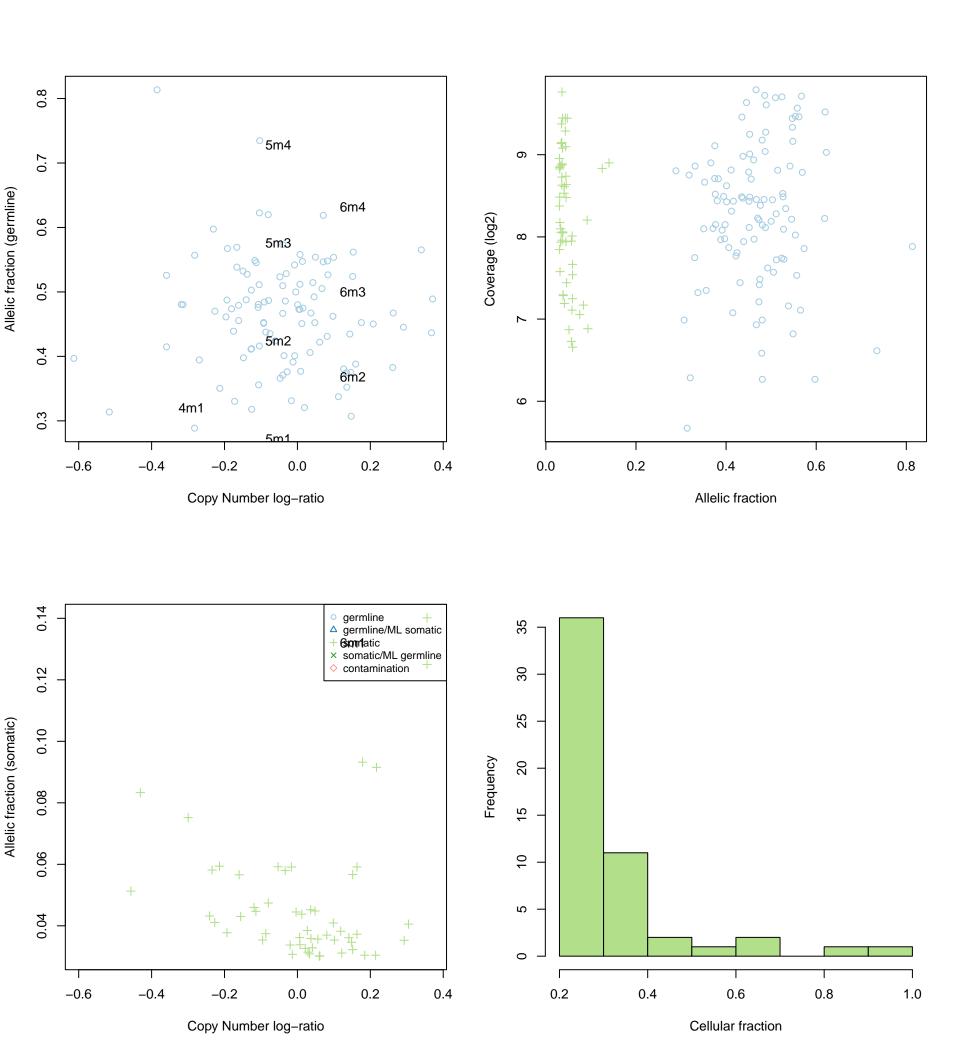


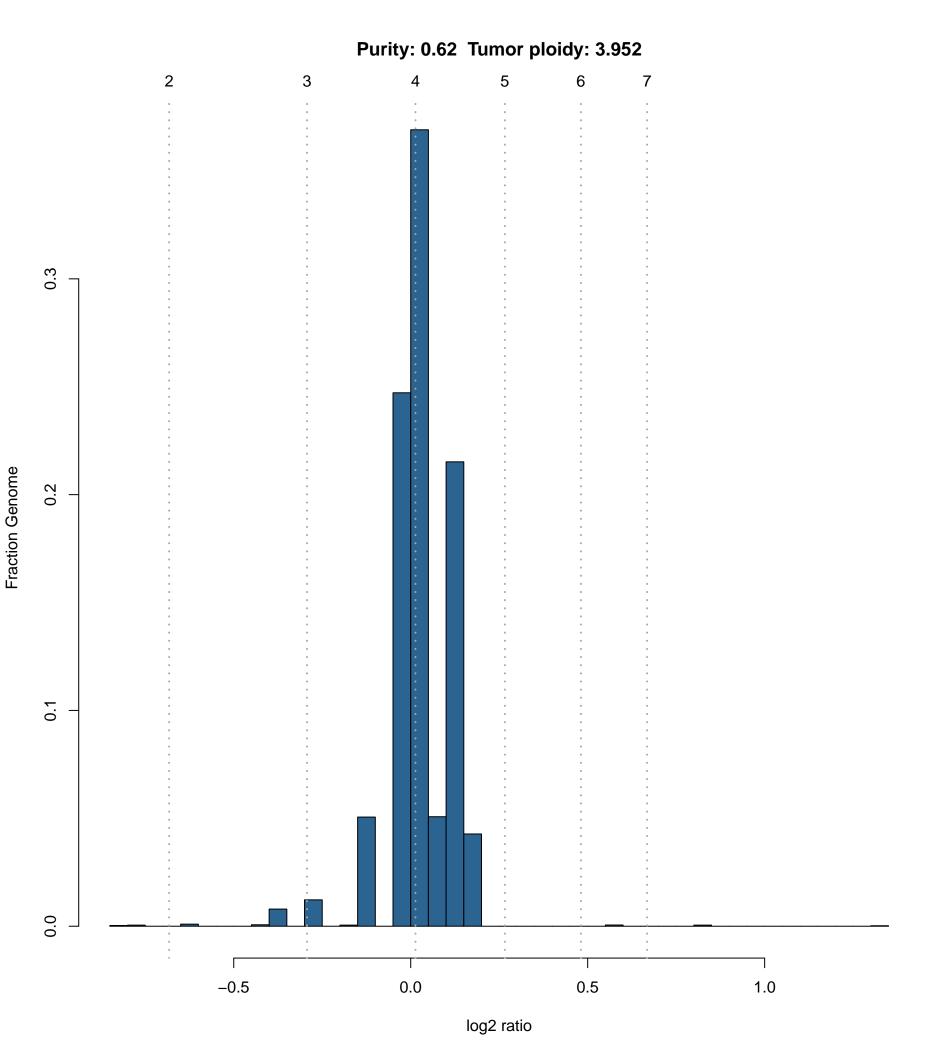


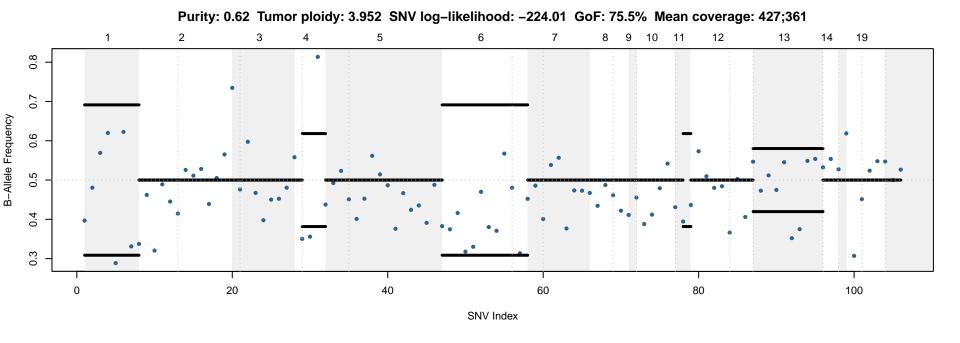
SCNA-fit log-likelihood: -5905.43



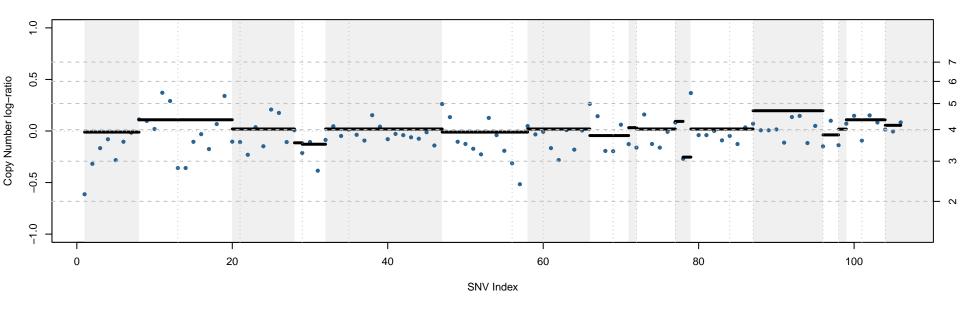


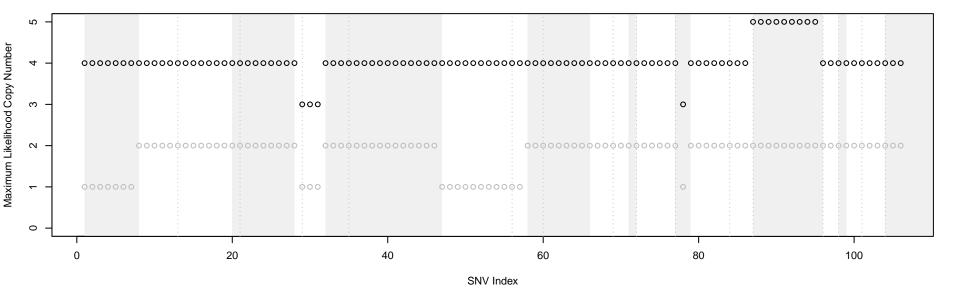


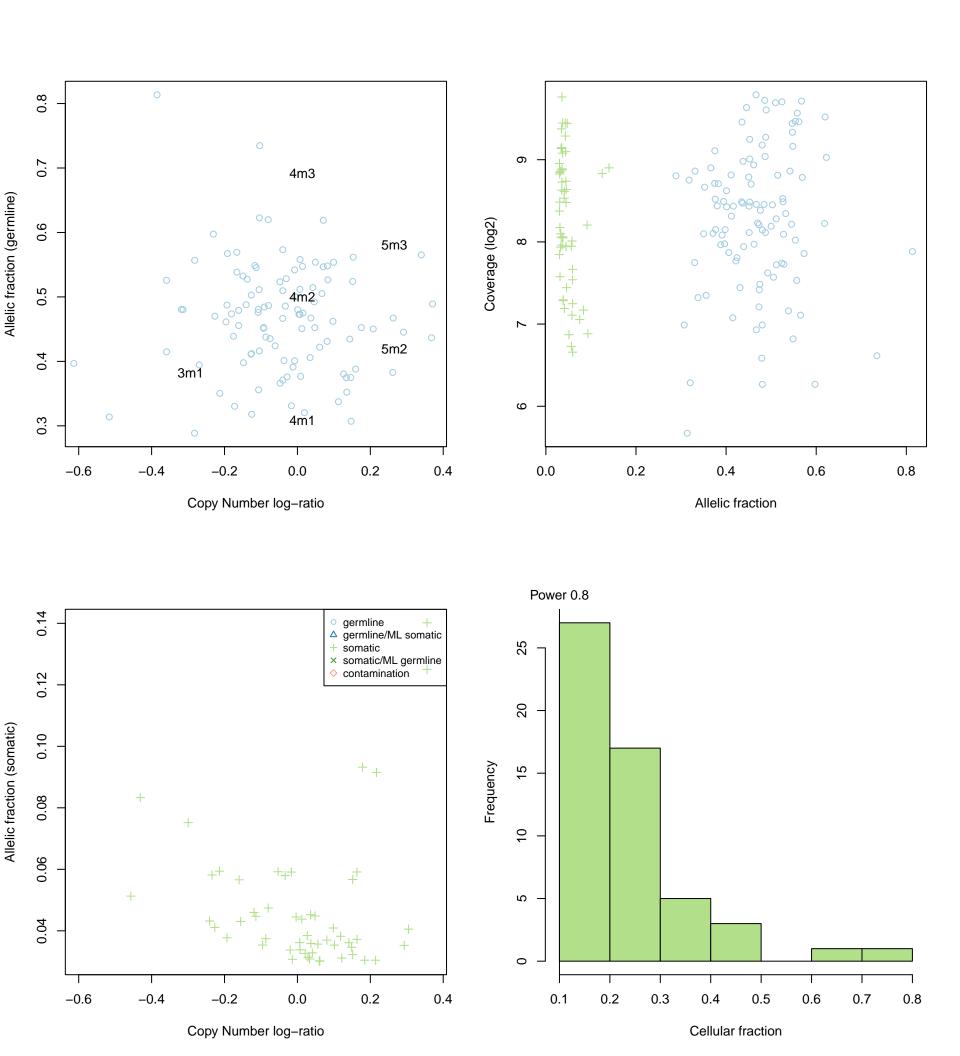




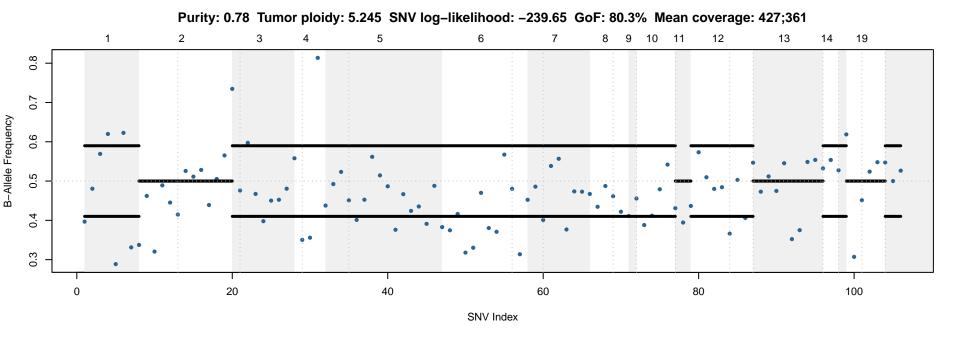
SCNA-fit log-likelihood: -6024.02



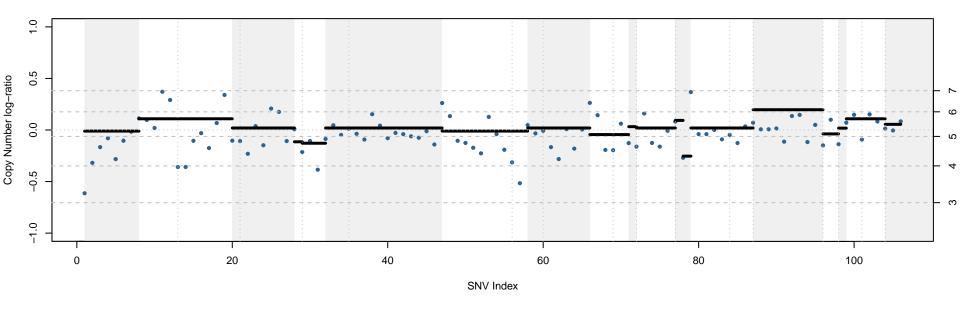


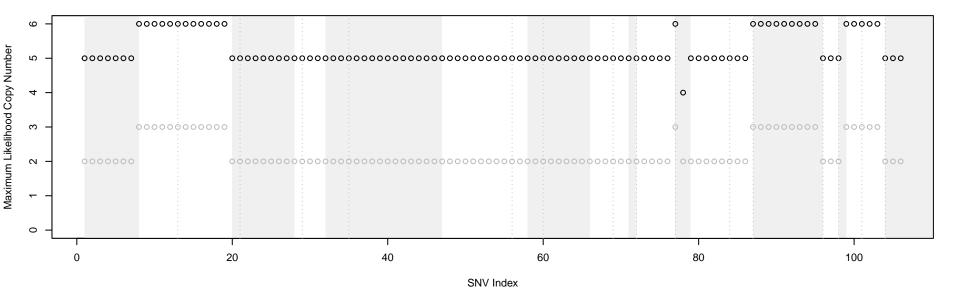


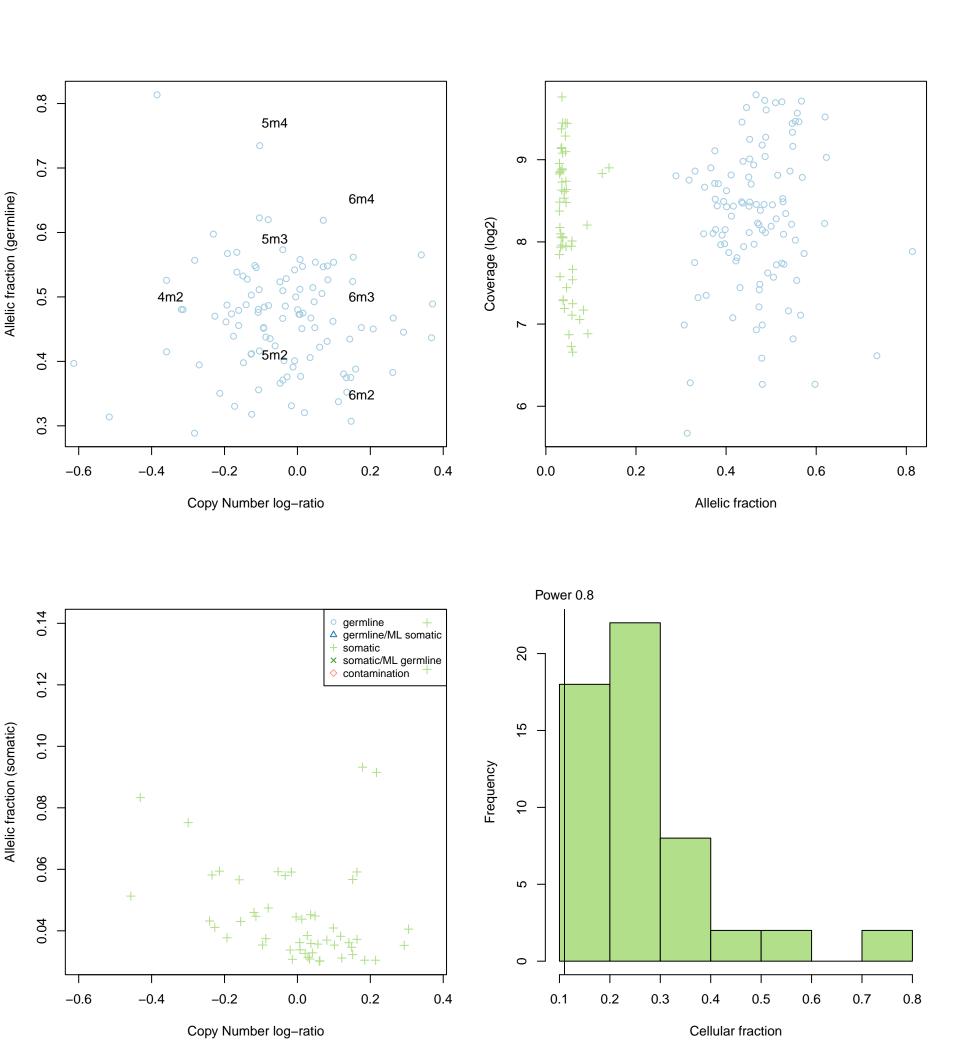
Purity: 0.78 Tumor ploidy: 5.245 6 3 5 7 Fraction Genome 0.2 0.0 -0.5 0.0 0.5 1.0 log2 ratio



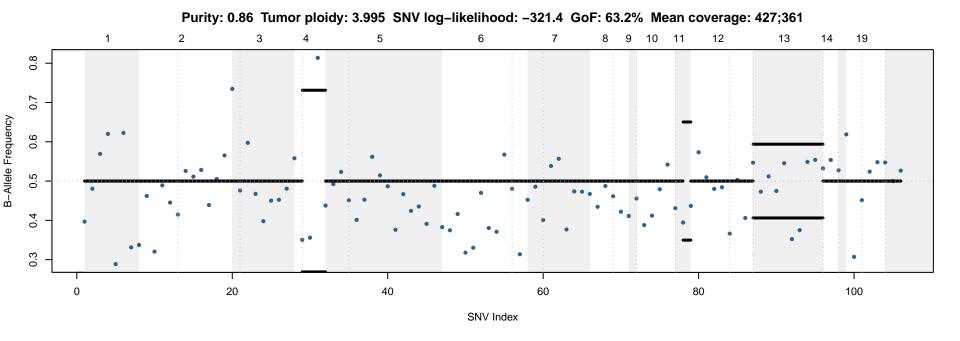




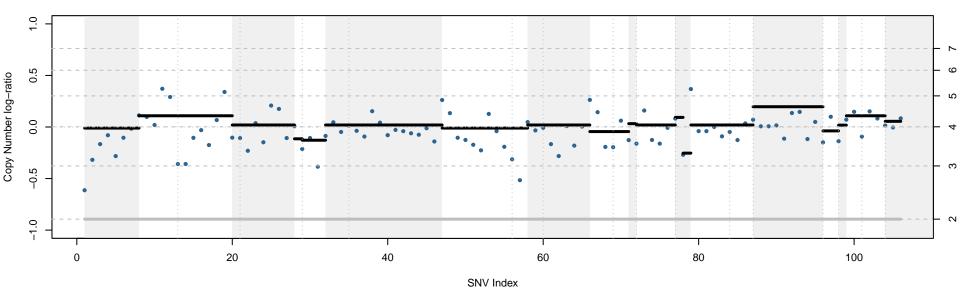


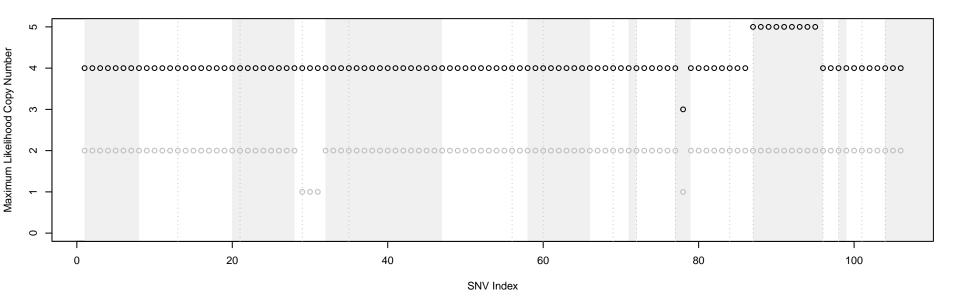


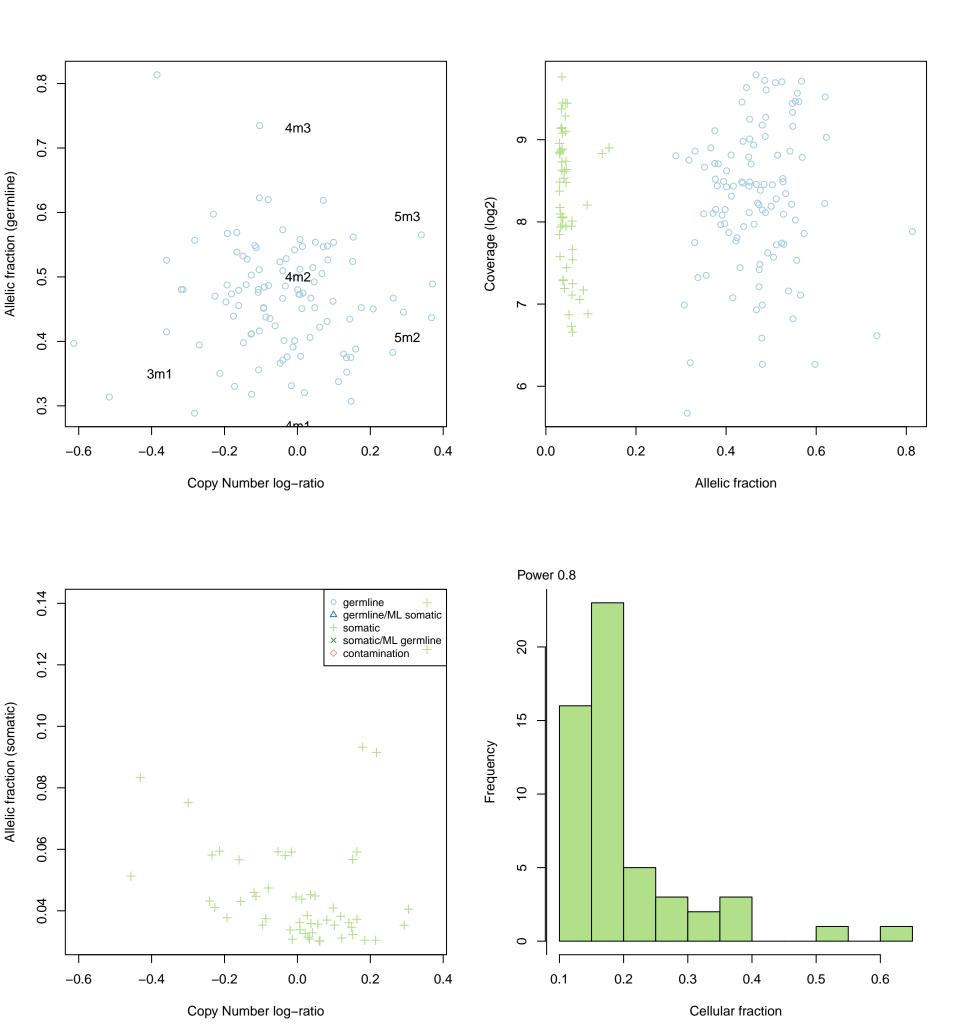
Purity: 0.86 Tumor ploidy: 3.995 2 6 3 5 Fraction Genome 0.2 0.1 0.0 -0.5 0.0 0.5 1.0 log2 ratio



SCNA-fit log-likelihood: -6070.21

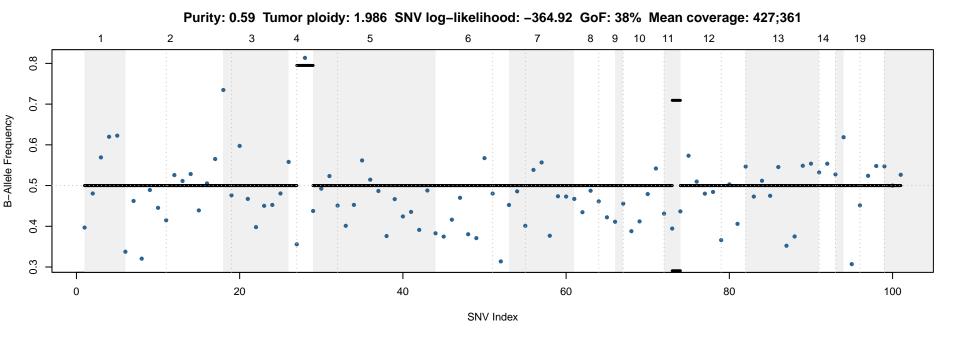




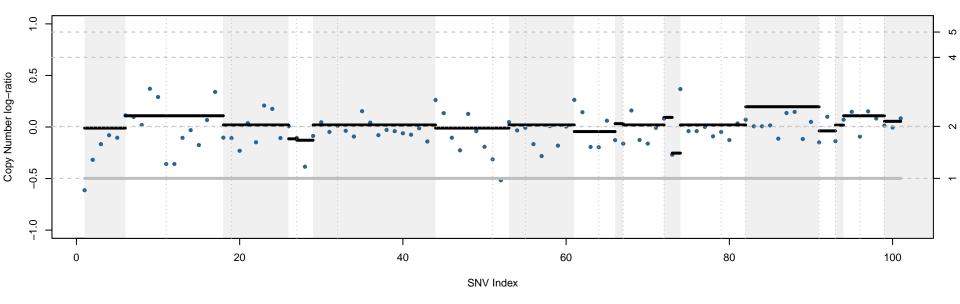


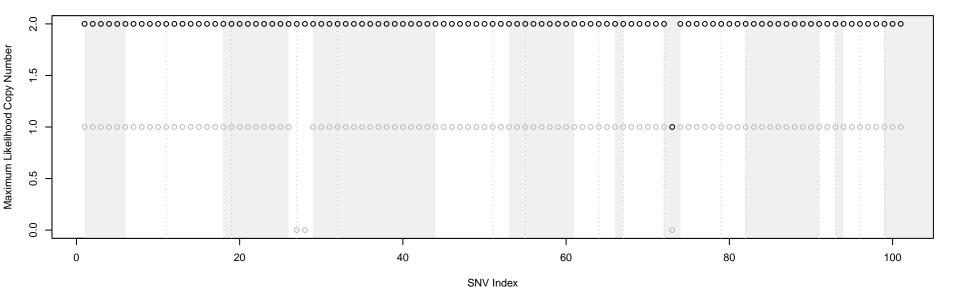
Purity: 0.59 Tumor ploidy: 1.986 5 7 Fraction Genome 0.0 -0.5 0.0 0.5 1.0

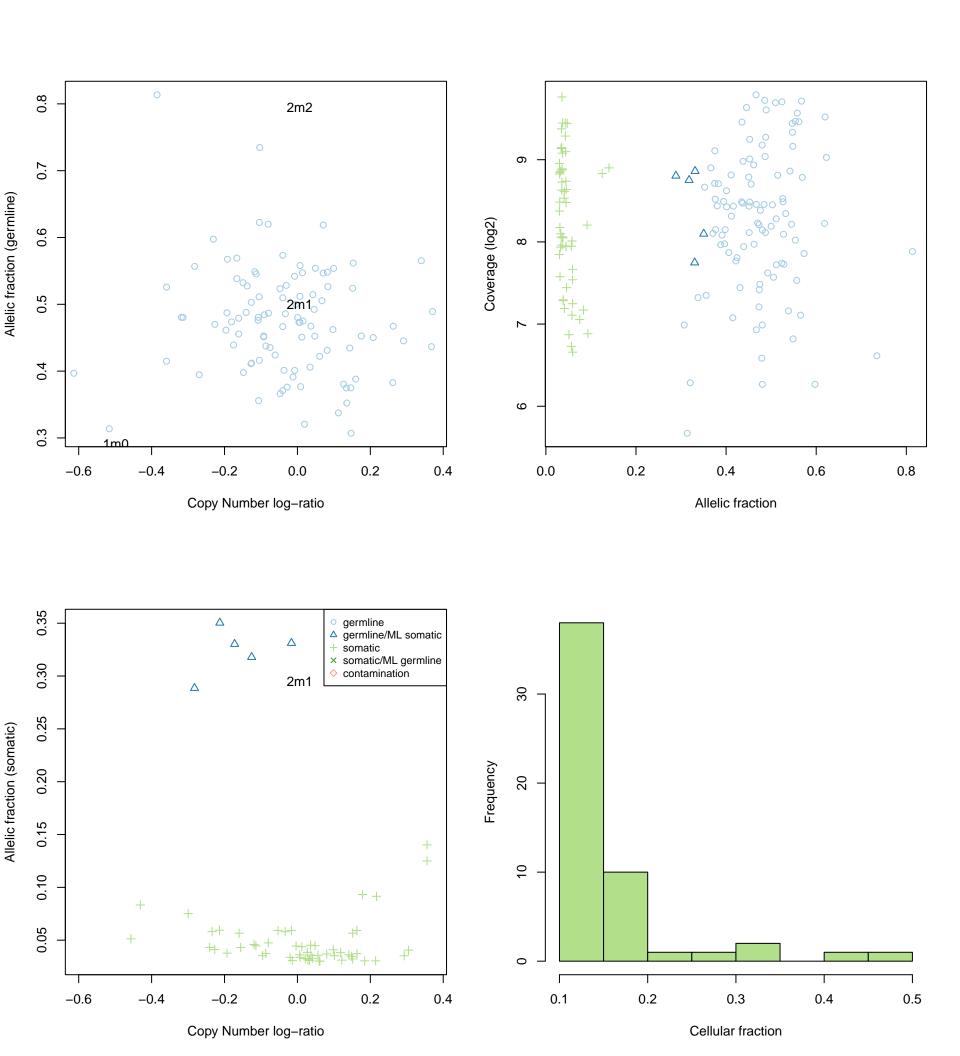
log2 ratio



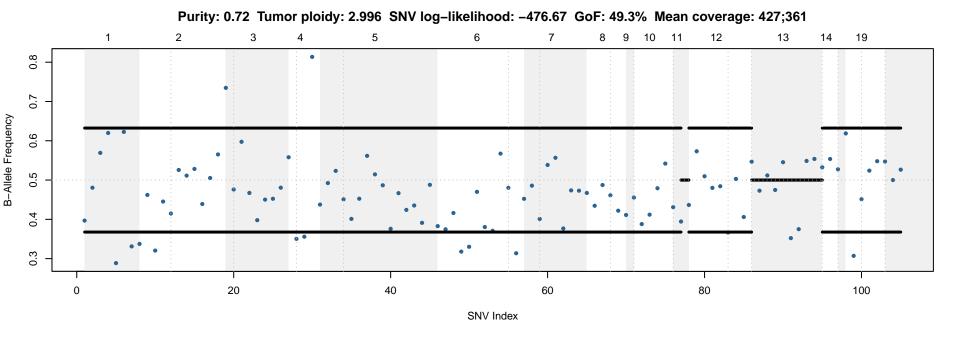
SCNA-fit log-likelihood: -6126.76



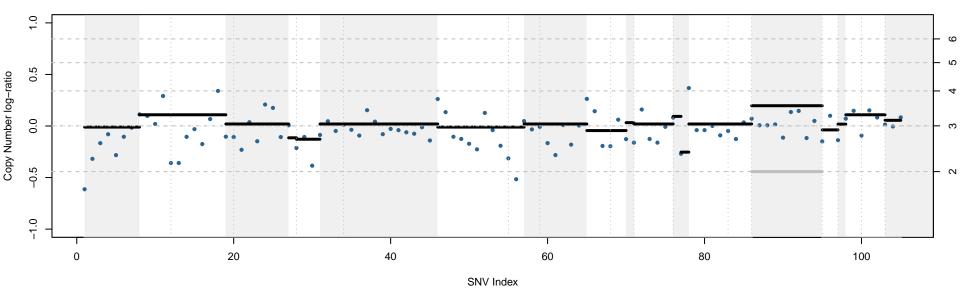


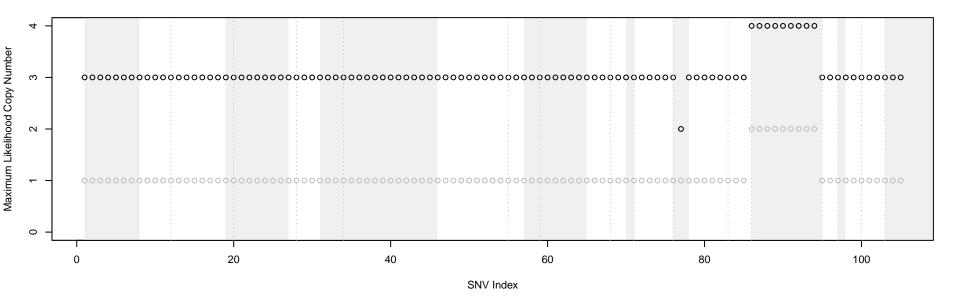


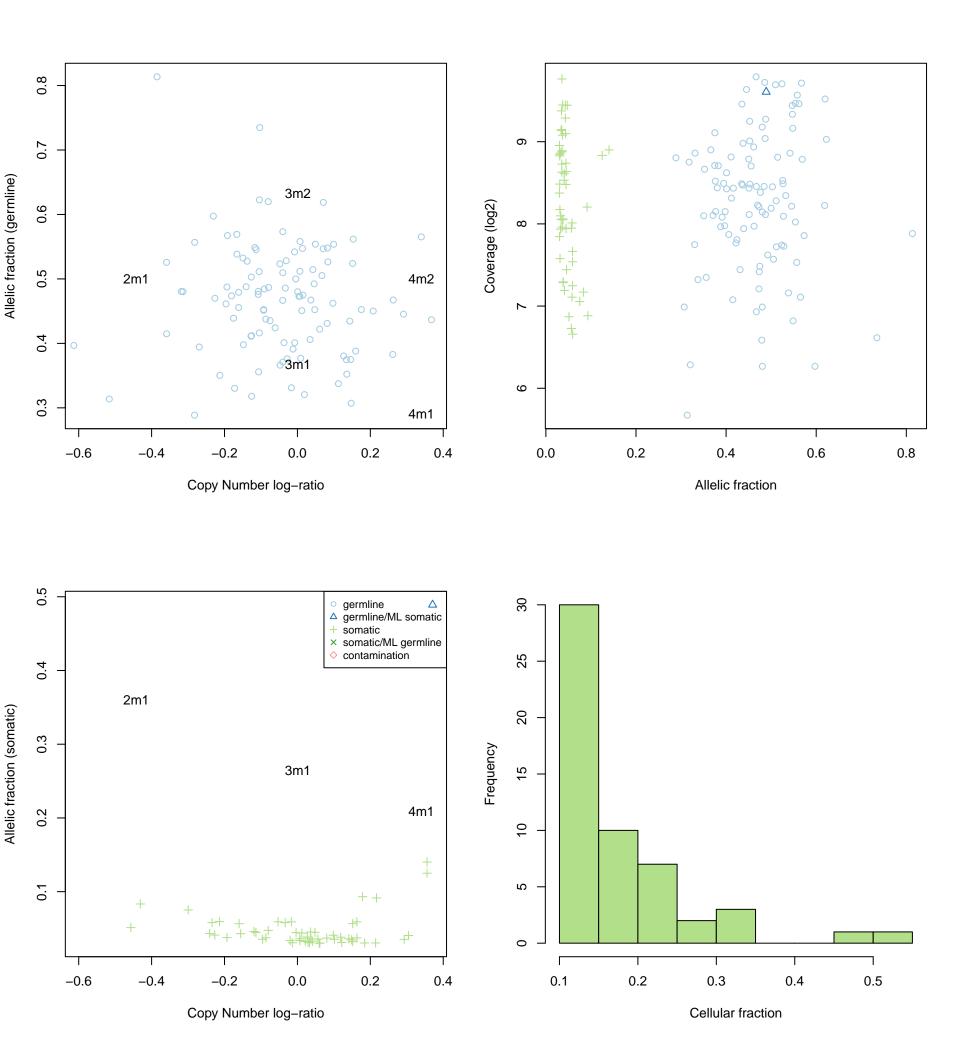
Purity: 0.72 Tumor ploidy: 2.996 2 6 Fraction Genome 0.0 -0.5 0.0 0.5 1.0 log2 ratio



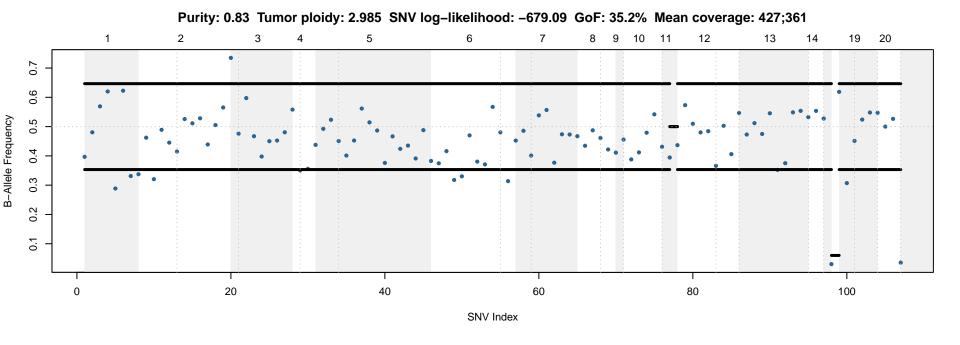
SCNA-fit log-likelihood: -6108.15







Purity: 0.83 Tumor ploidy: 2.985 2 5 6 7 Fraction Genome 0.0 -0.5 0.0 0.5 1.0 log2 ratio



SCNA-fit log-likelihood: -6124.96

