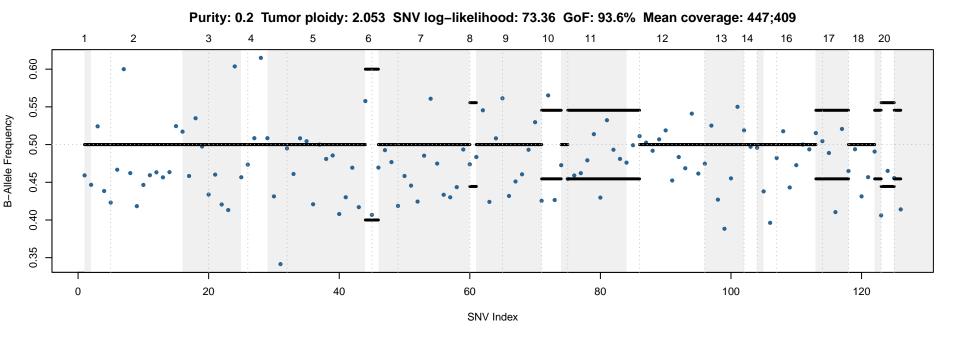
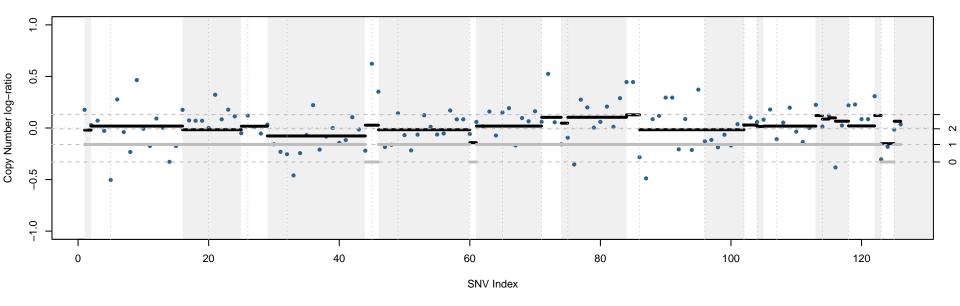
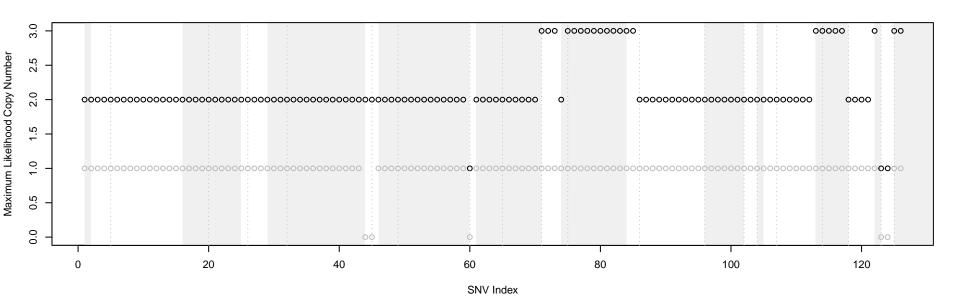
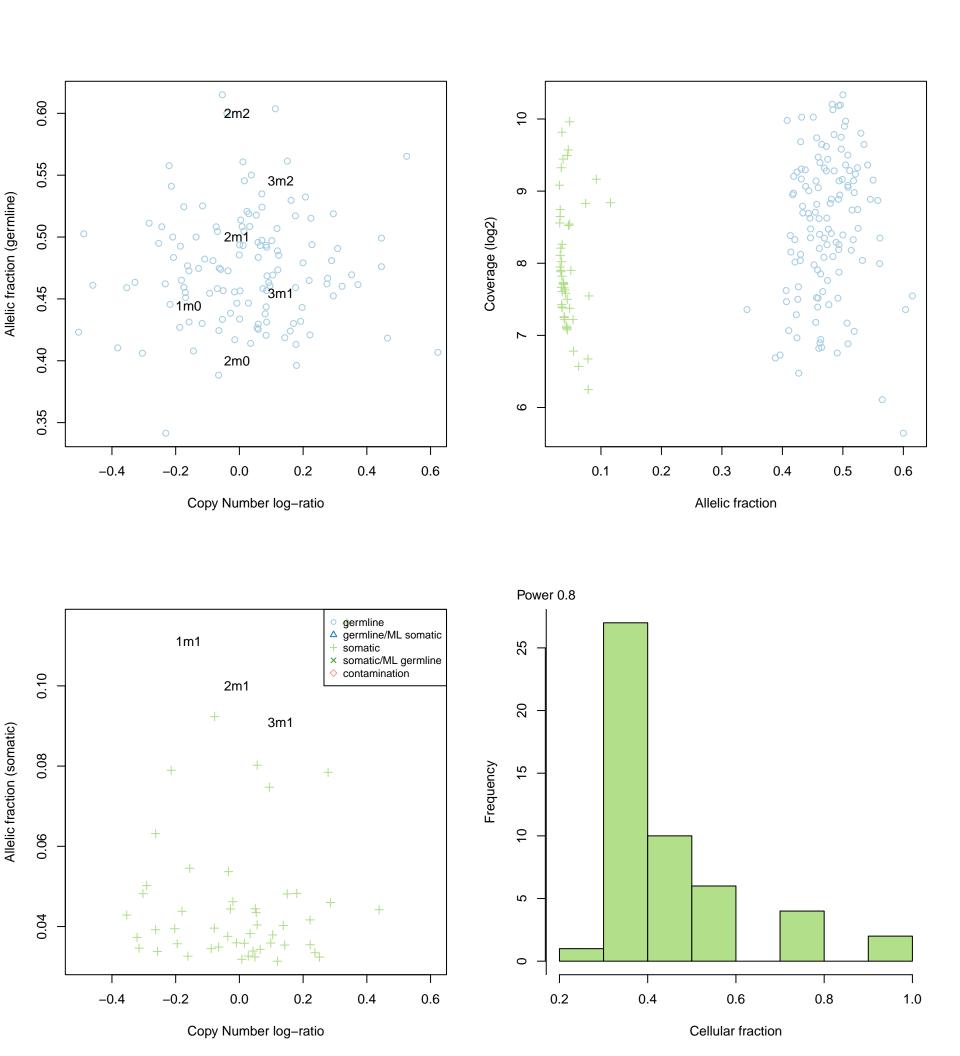
Purity: 0.2 Tumor ploidy: 2.053 2 3 0.20 Fraction Genome 0.05 0.00 -0.2 -0.6 -0.4 0.0 0.2 log2 ratio



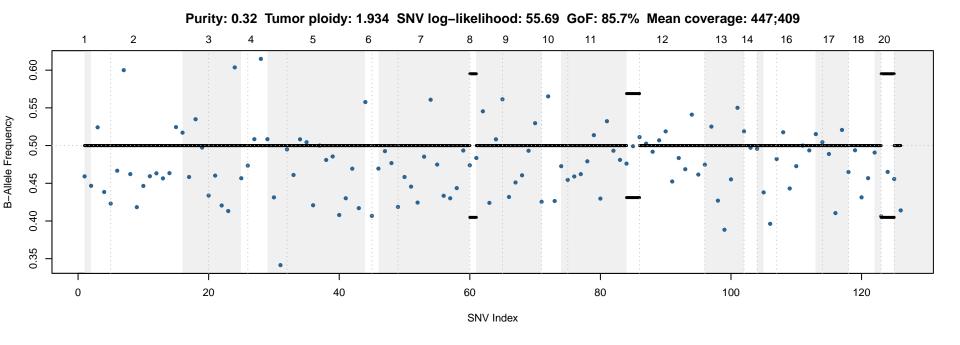
SCNA-fit log-likelihood: -7201.23



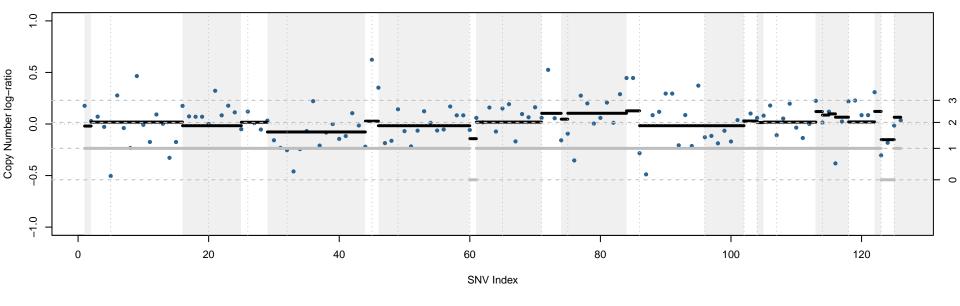


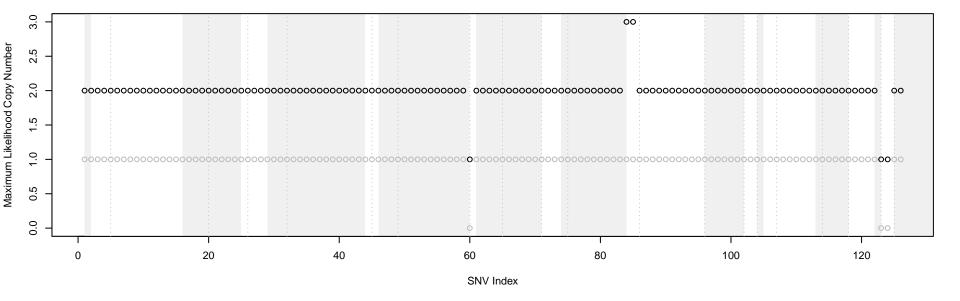


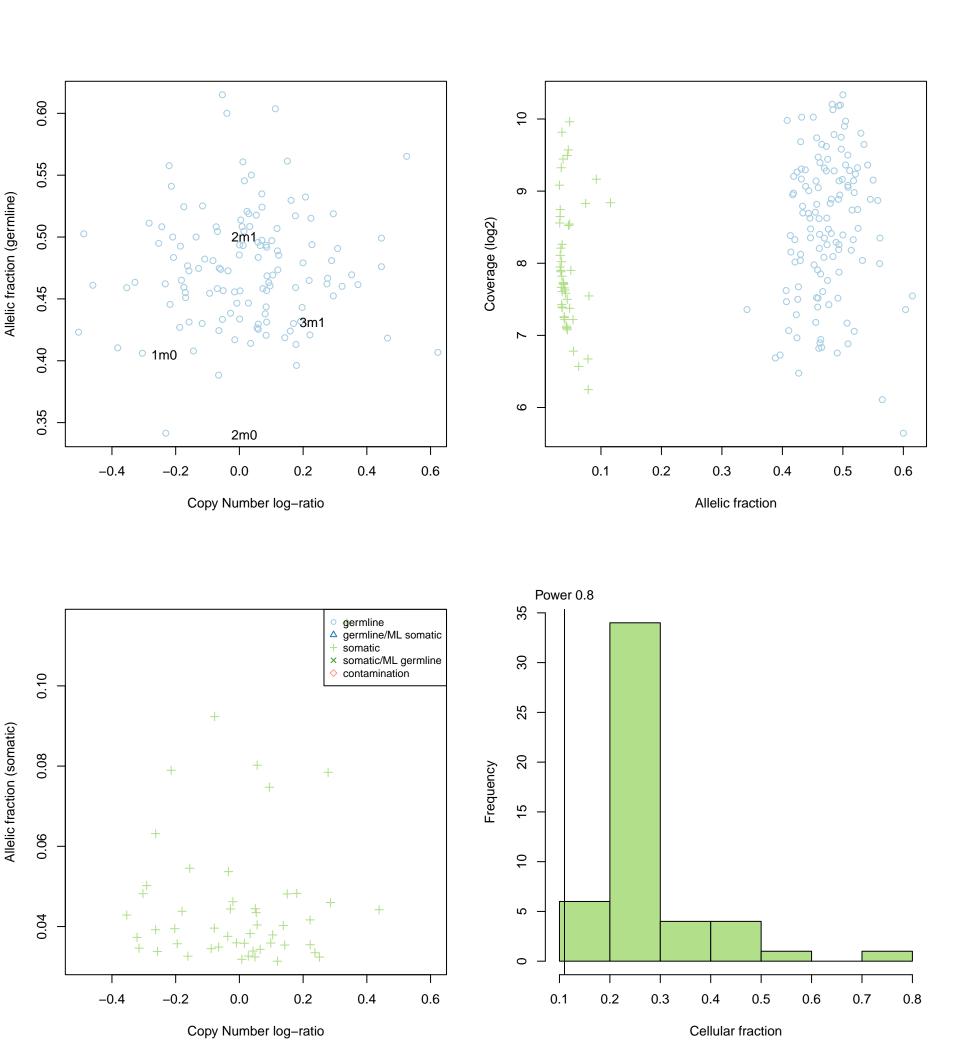
Purity: 0.32 Tumor ploidy: 1.934 2 3 0.20 Fraction Genome 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



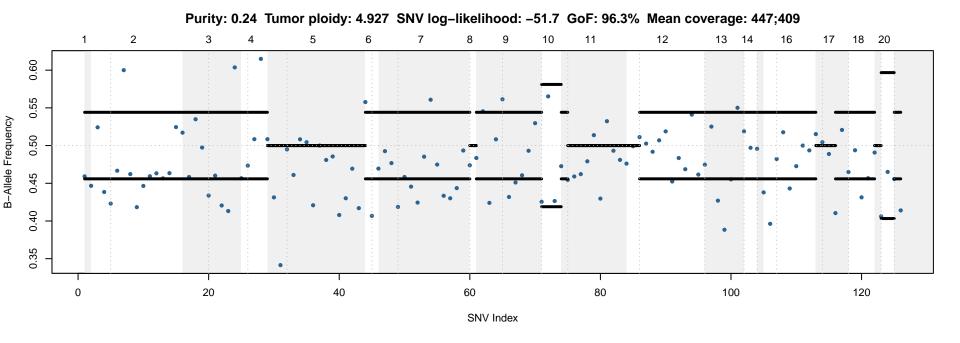
SCNA-fit log-likelihood: -7280.14



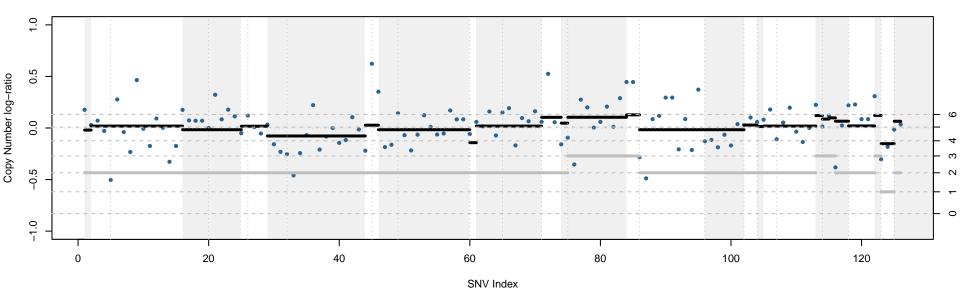


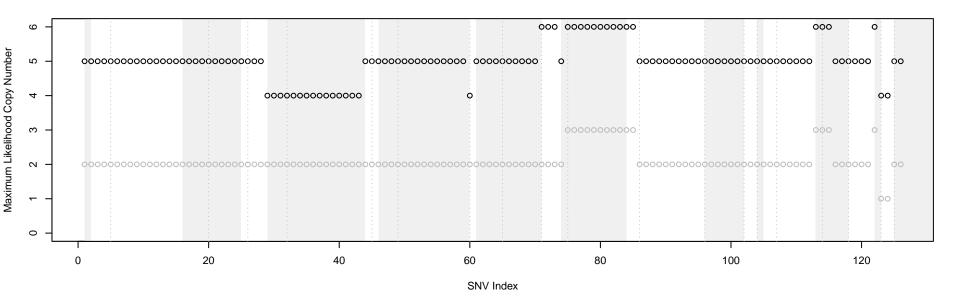


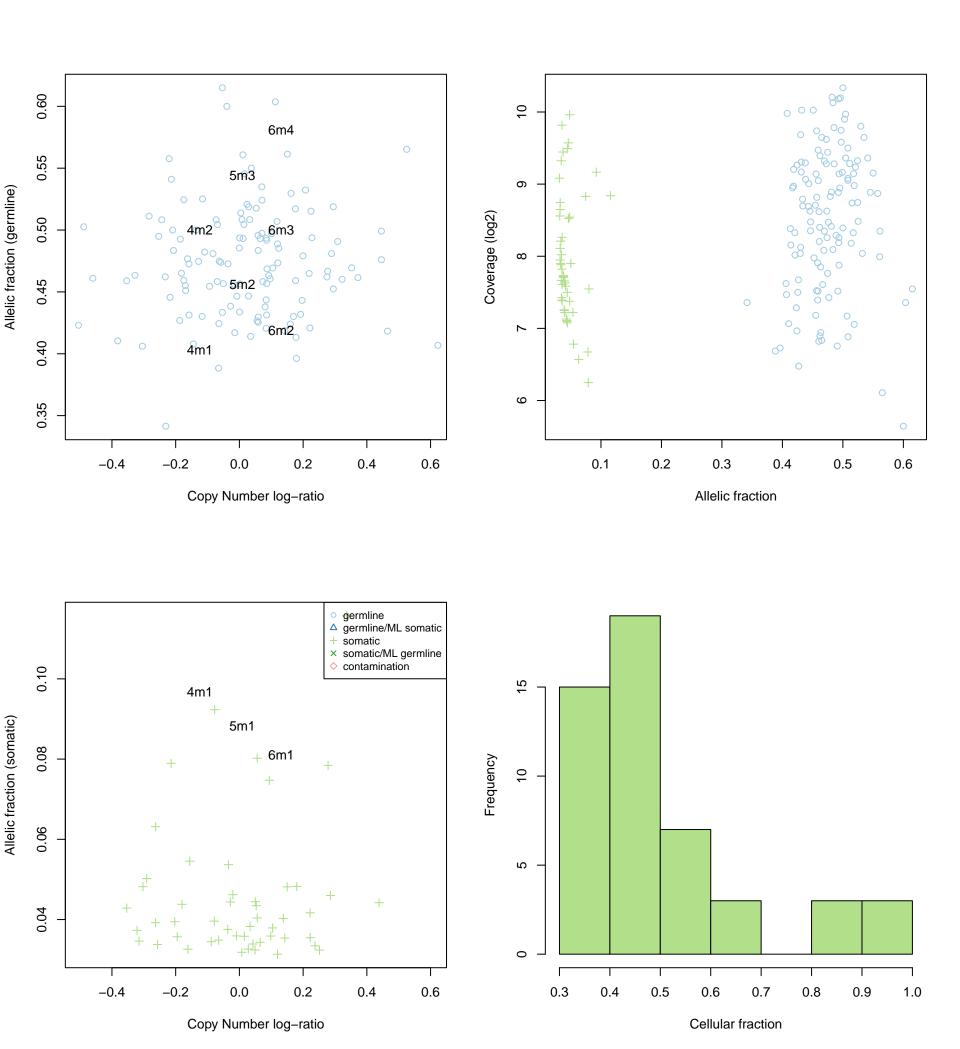
Purity: 0.24 Tumor ploidy: 4.927 2 3 5 6 0 0.20 0.15 Fraction Genome 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



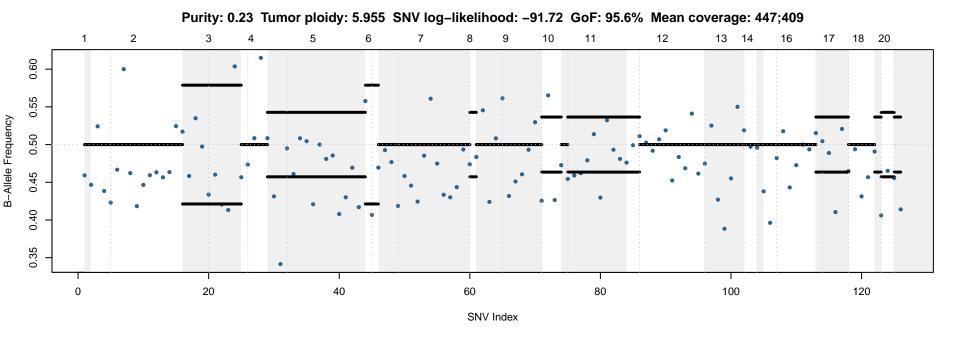
SCNA-fit log-likelihood: -7160.44



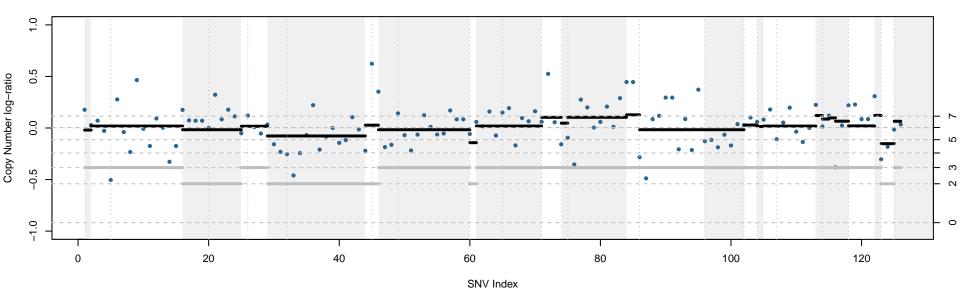


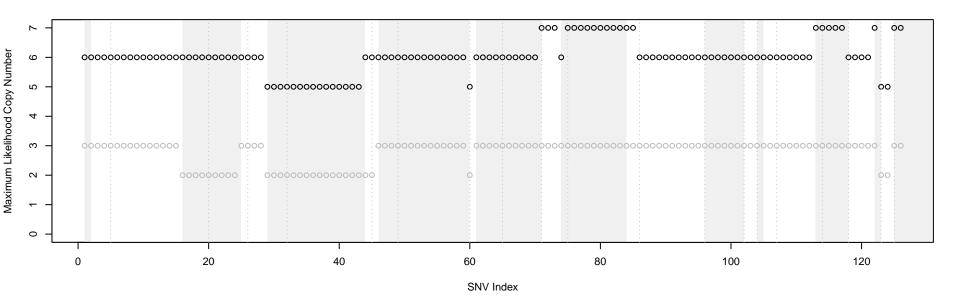


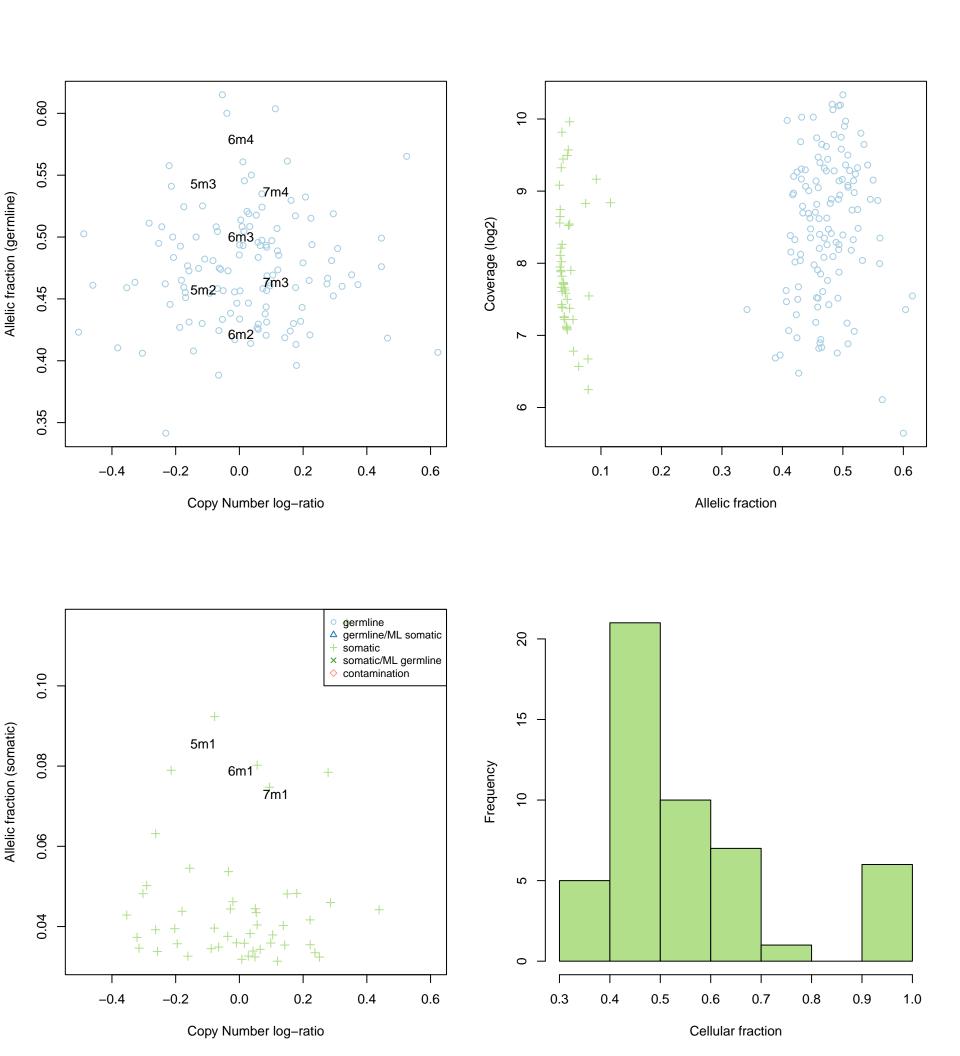
Purity: 0.23 Tumor ploidy: 5.955 3 0 5 6 7 0.20 Fraction Genome 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



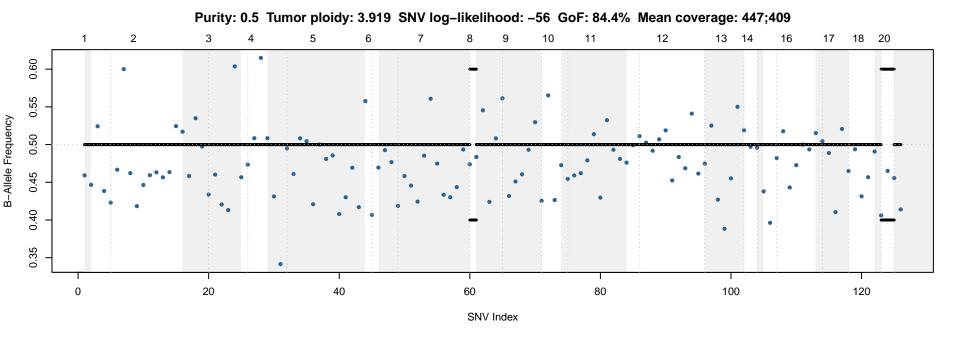
SCNA-fit log-likelihood: -7151



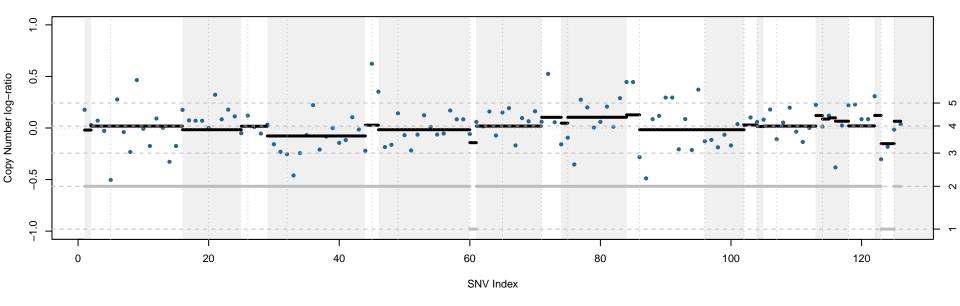


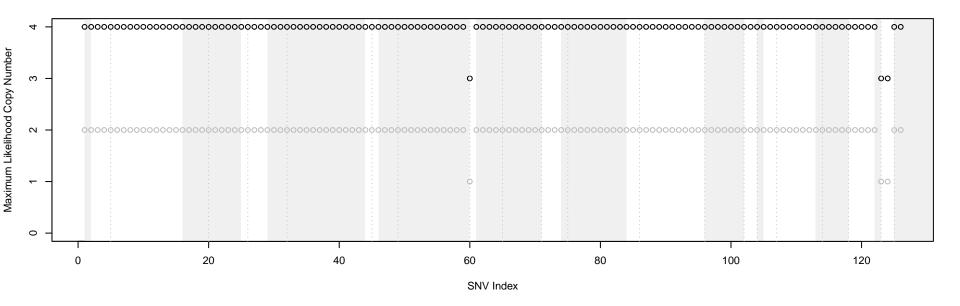


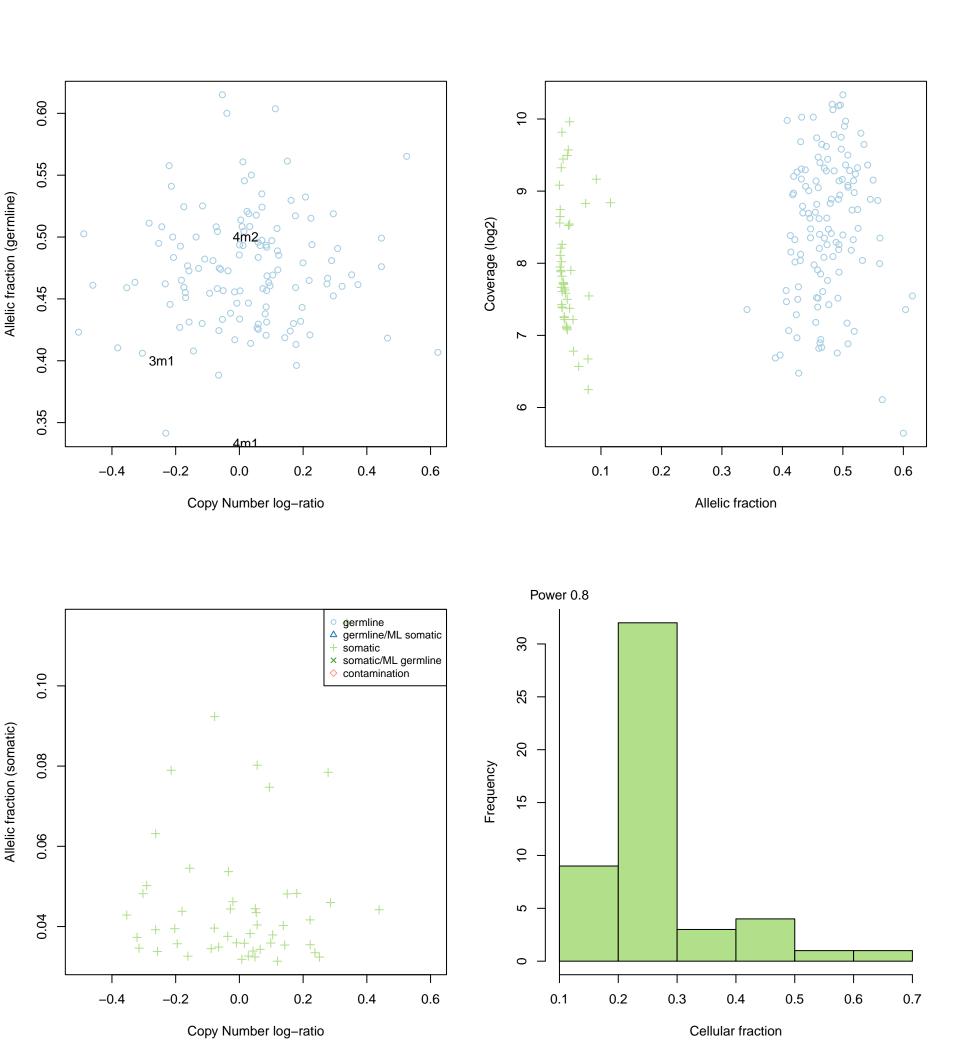
Purity: 0.5 Tumor ploidy: 3.919 3 5 2 1 0.20 0.15 Fraction Genome 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



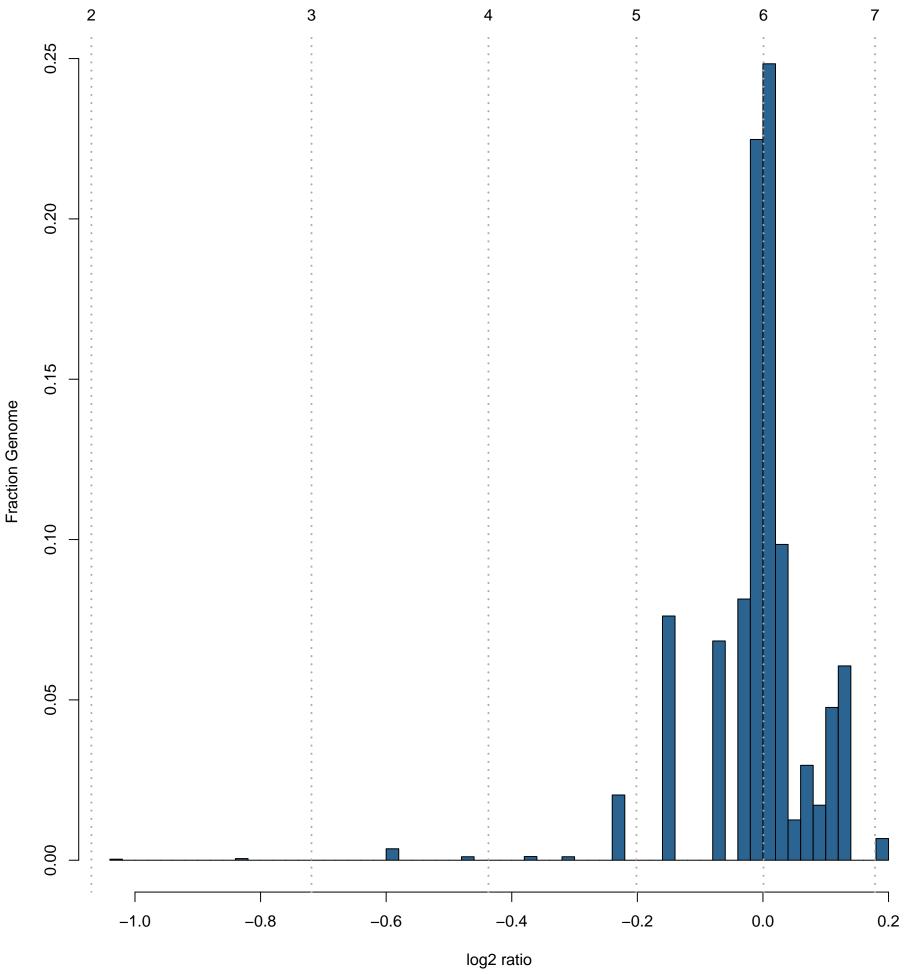
SCNA-fit log-likelihood: -7283.4

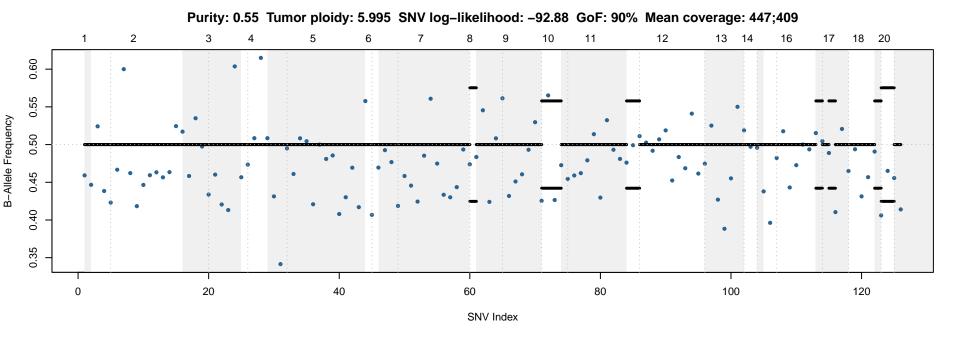




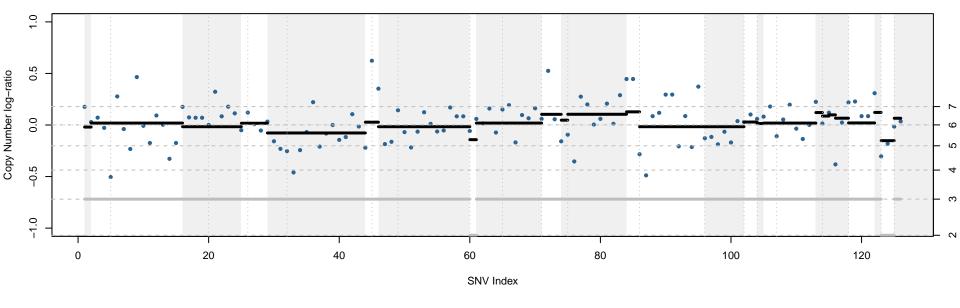


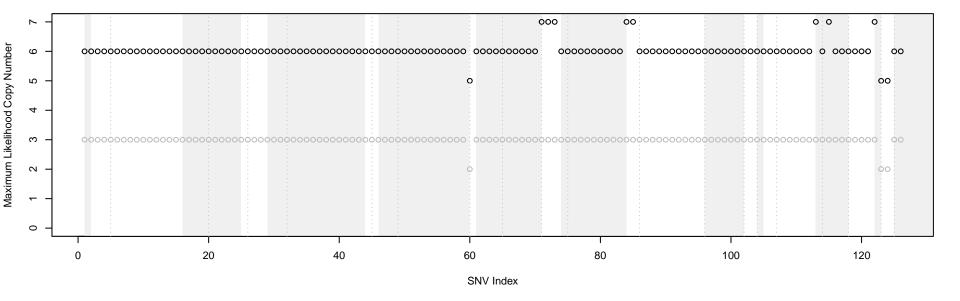
Purity: 0.55 Tumor ploidy: 5.995

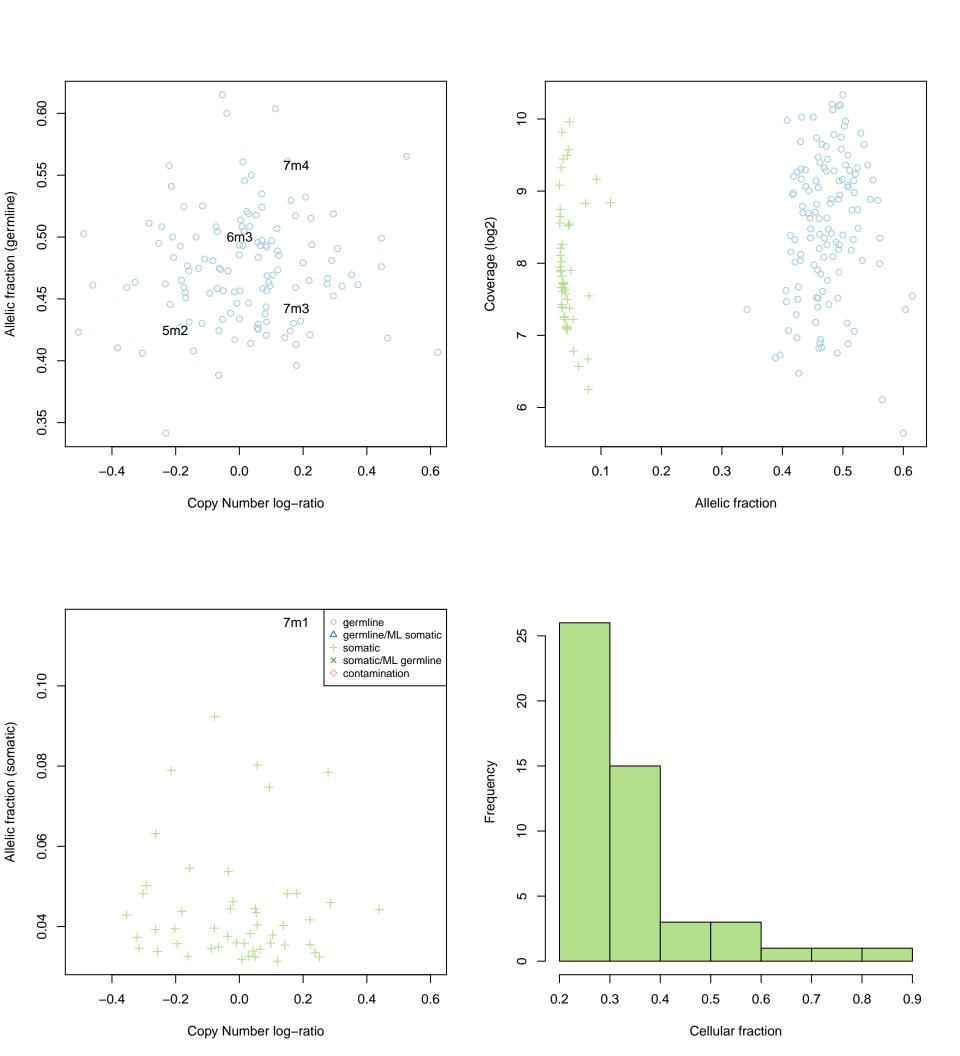




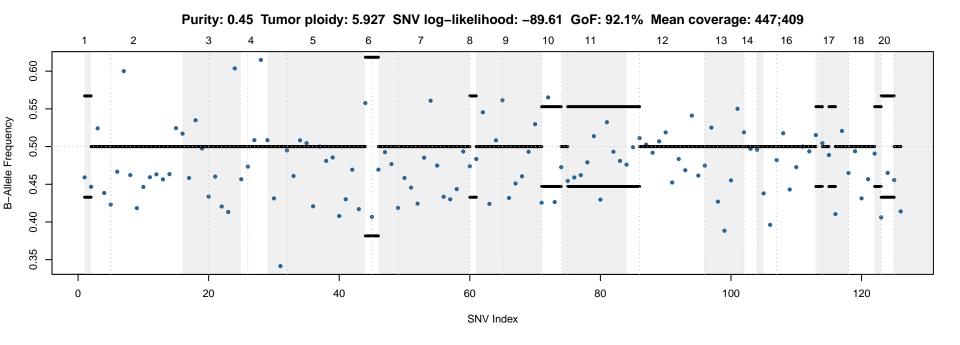
SCNA-fit log-likelihood: -7222.79



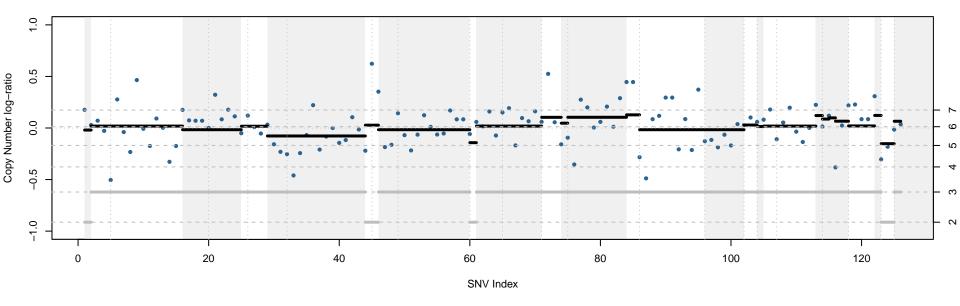


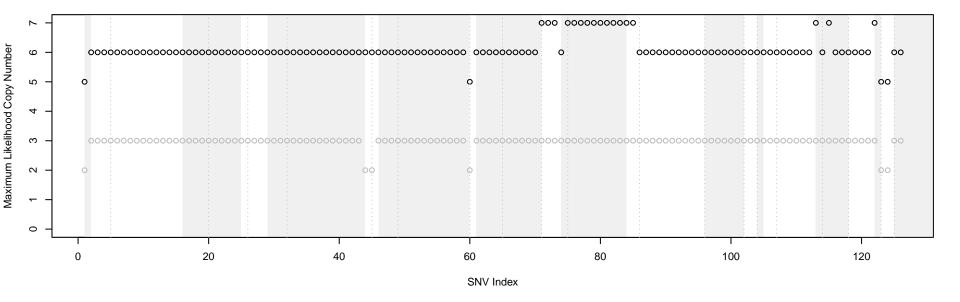


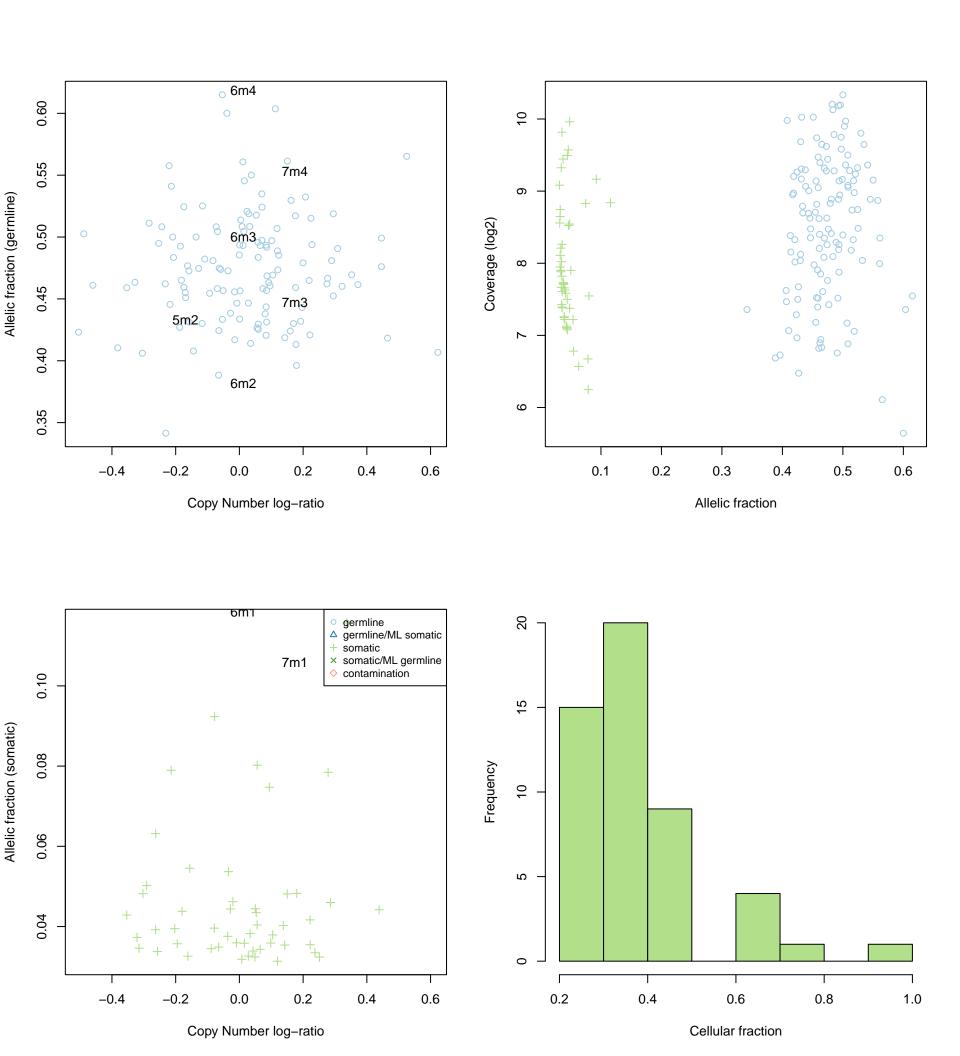
Purity: 0.45 Tumor ploidy: 5.927 6 2 3 7 5 0.20 Fraction Genome 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



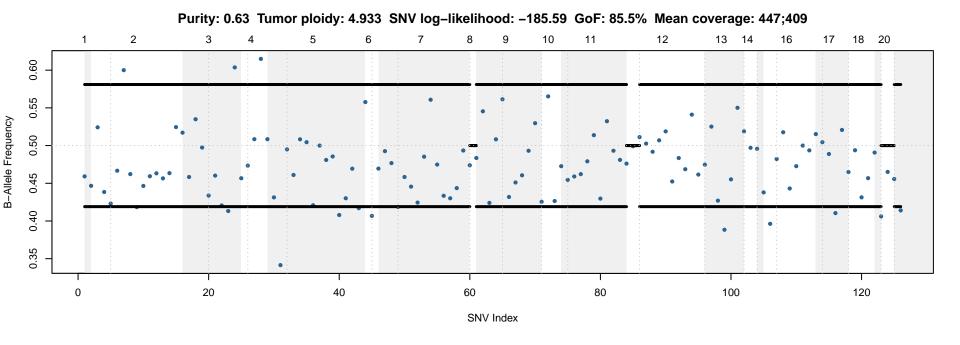
SCNA-fit log-likelihood: -7302.33



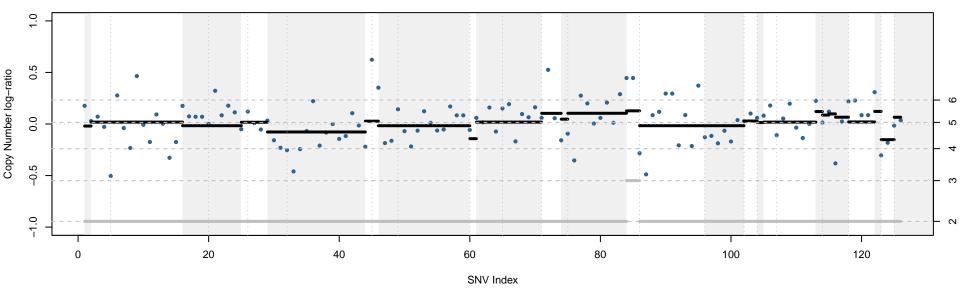


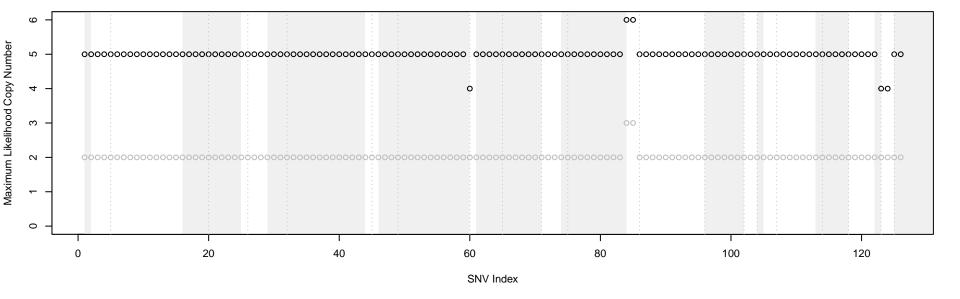


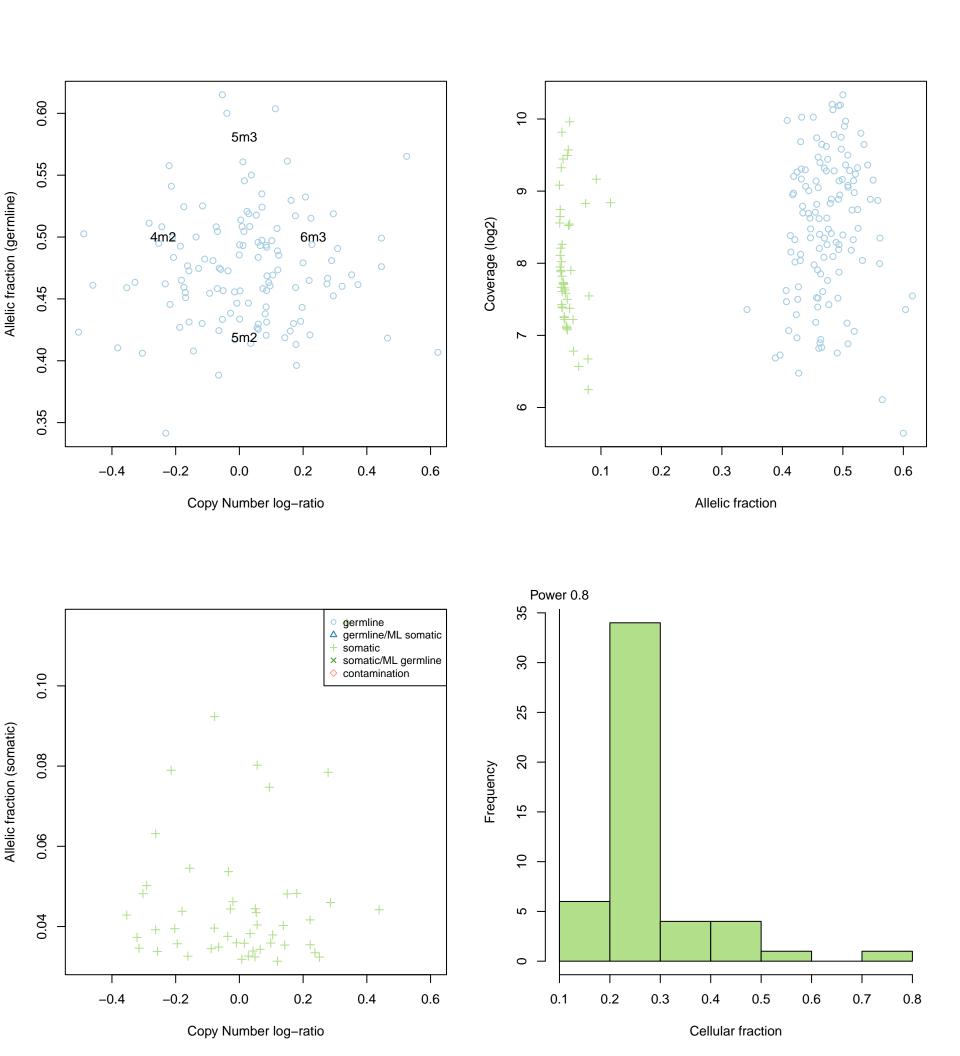
Purity: 0.63 Tumor ploidy: 4.933 2 3 6 5 0.20 Fraction Genome 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



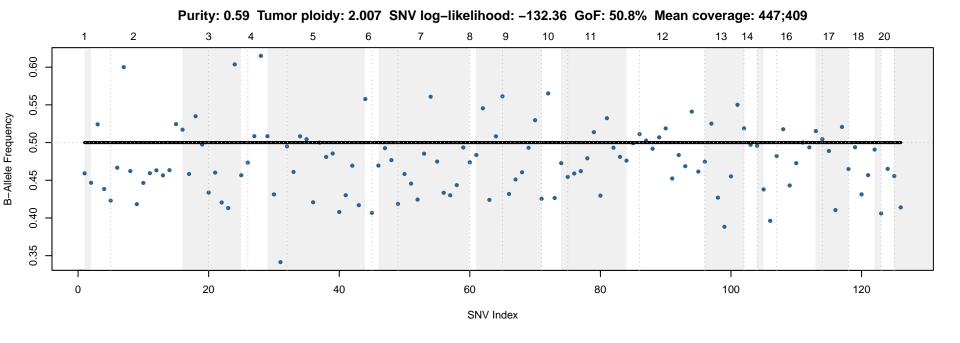
SCNA-fit log-likelihood: -7276.79



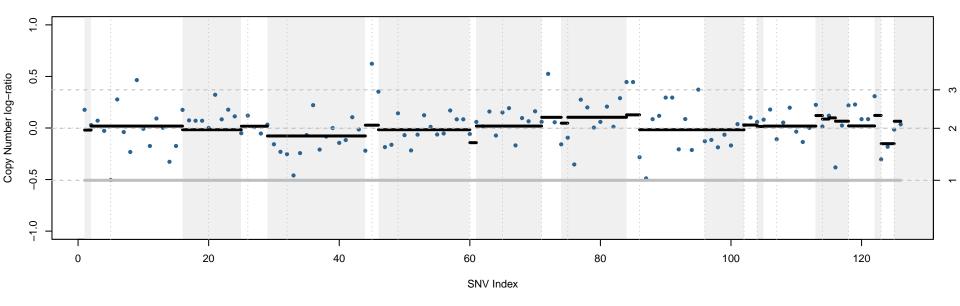


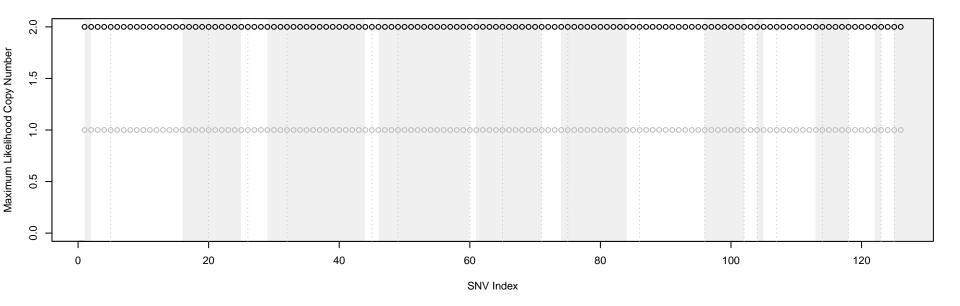


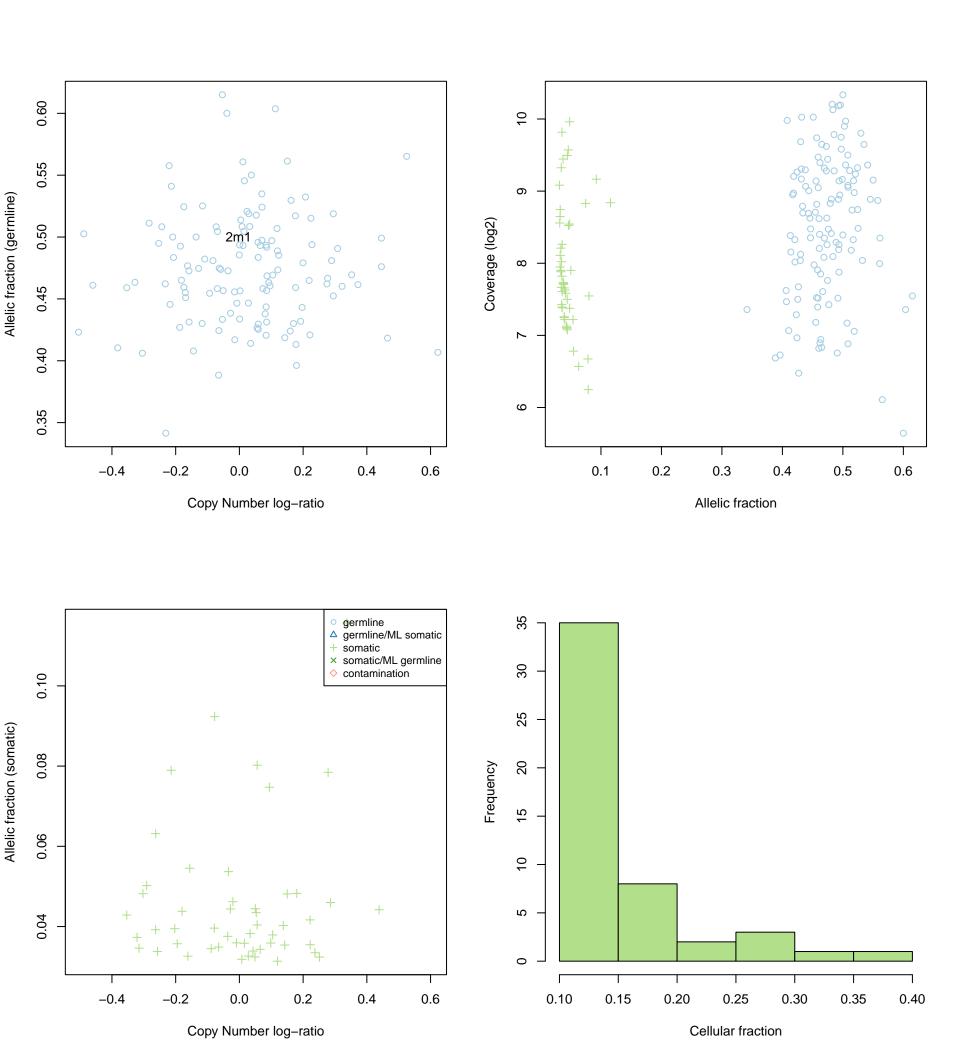
Purity: 0.59 Tumor ploidy: 2.007 2 0.25 0.20 0.15 Fraction Genome 0.10 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



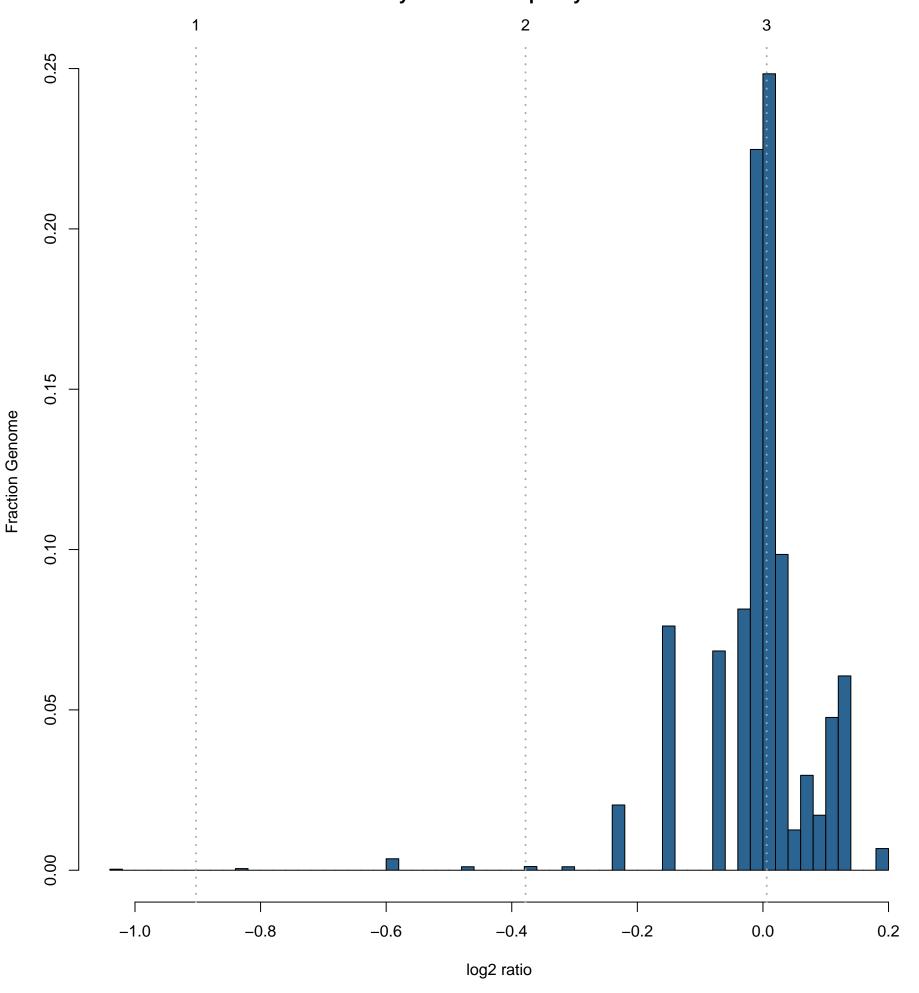
SCNA-fit log-likelihood: -7412.81

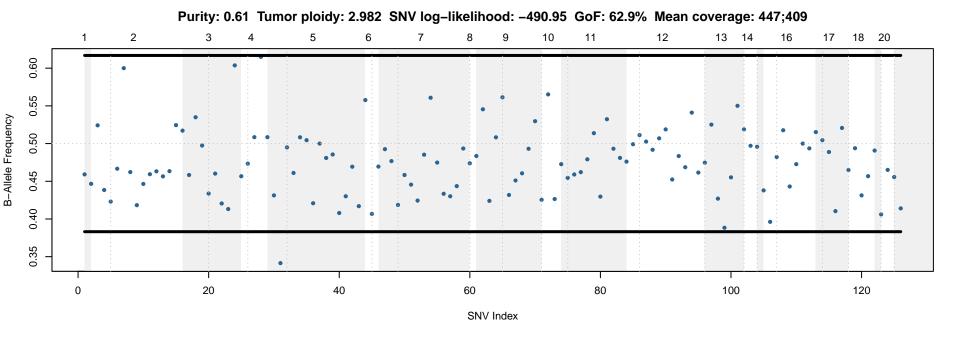




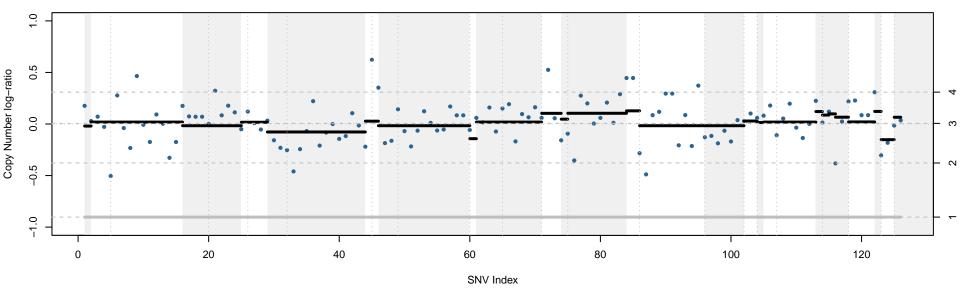


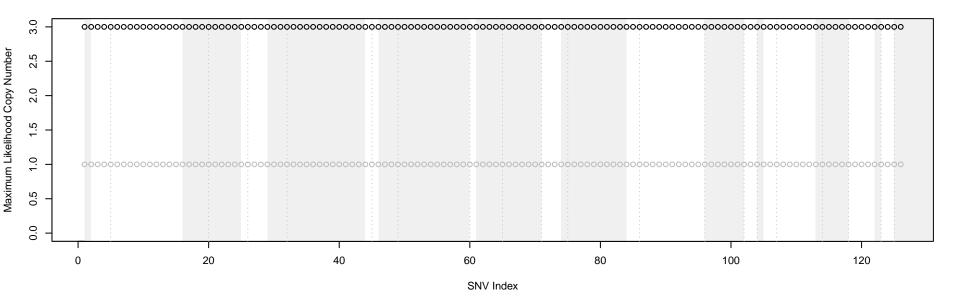
Purity: 0.61 Tumor ploidy: 2.982

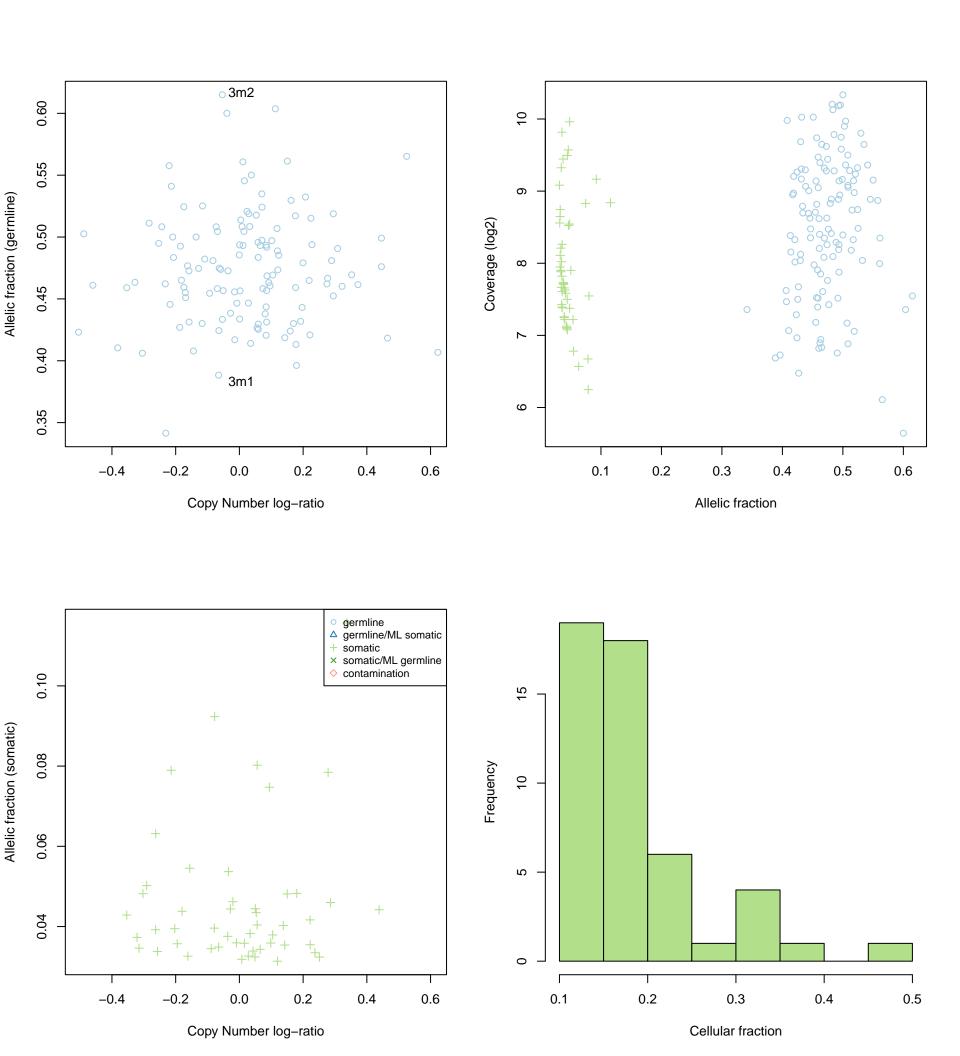




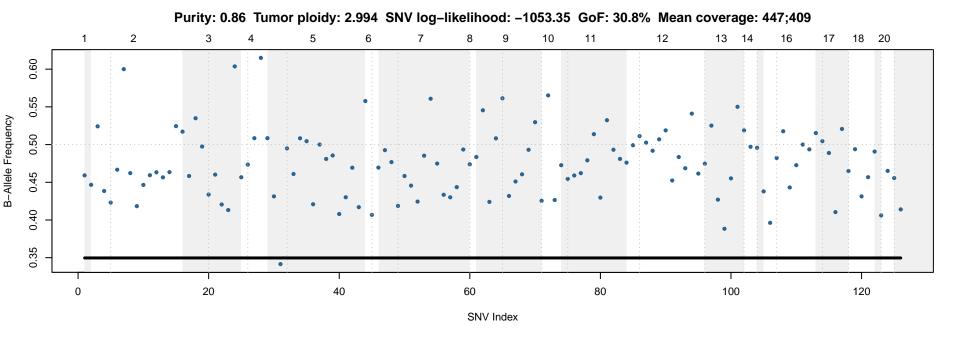
SCNA-fit log-likelihood: -7377.58







Purity: 0.86 Tumor ploidy: 2.994 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 log2 ratio



SCNA-fit log-likelihood: -7414.18

