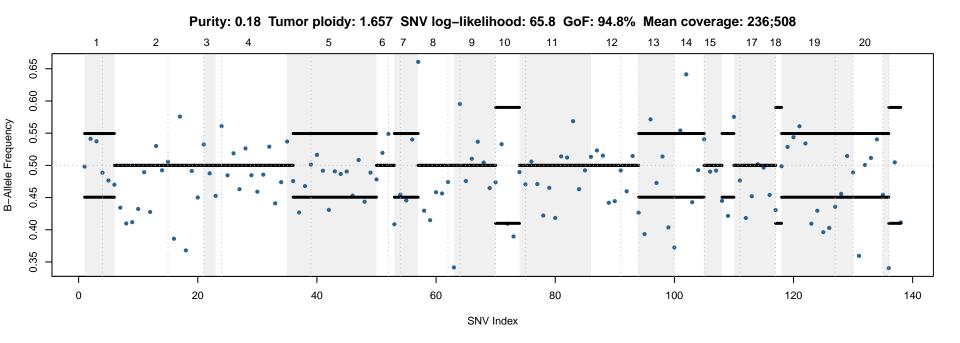
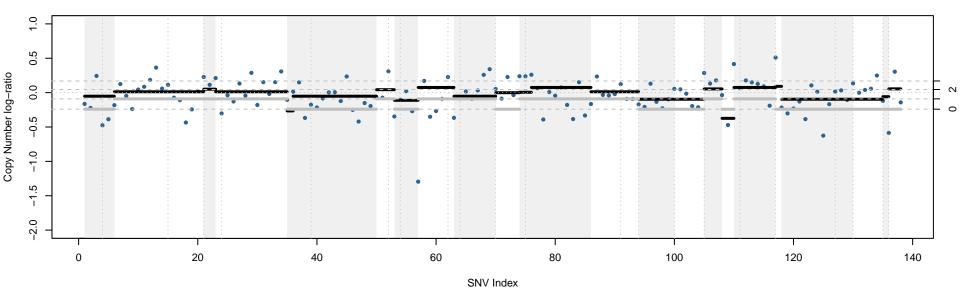
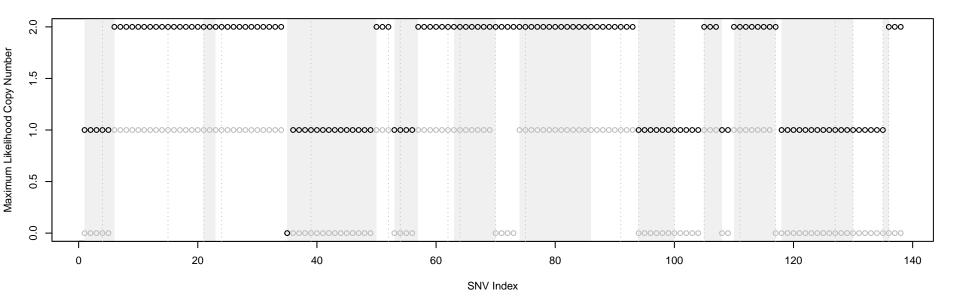
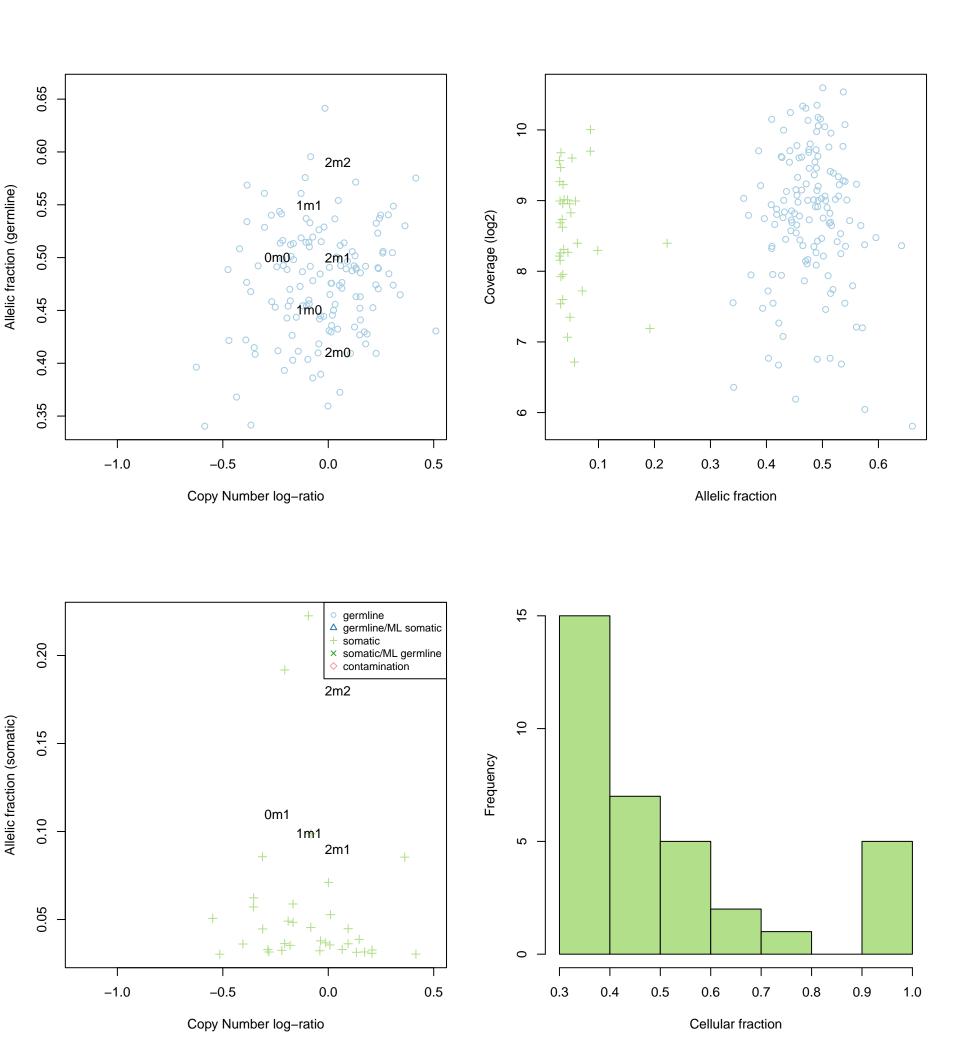
Purity: 0.18 Tumor ploidy: 1.657 3 0 2 1 0.20 Fraction Genome 0.05 0.00 -0.4 -0.2 0.0 0.2 0.4 0.6 8.0



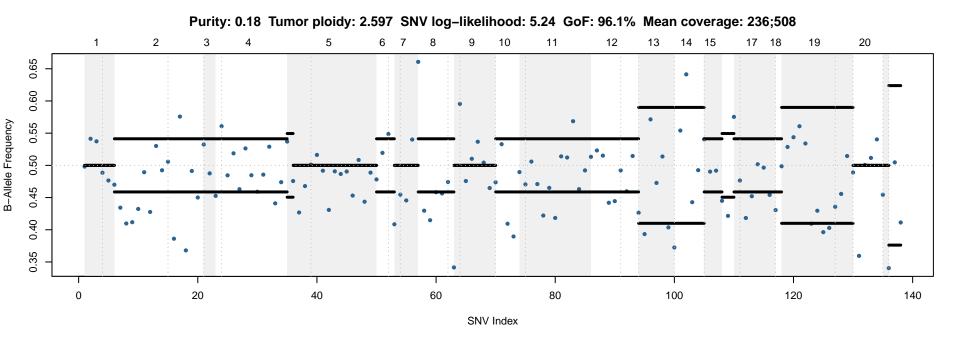
SCNA-fit log-likelihood: -10337.86



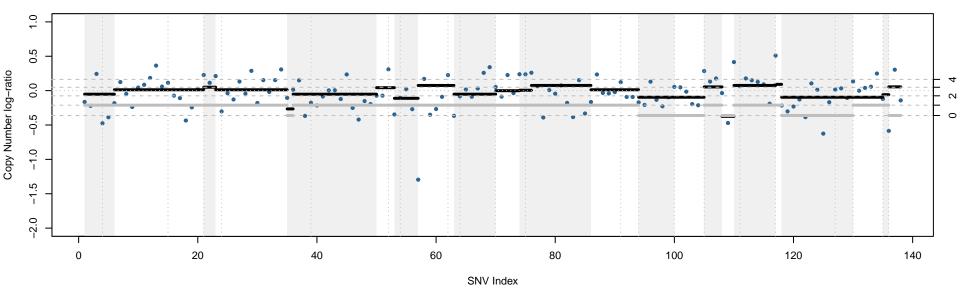


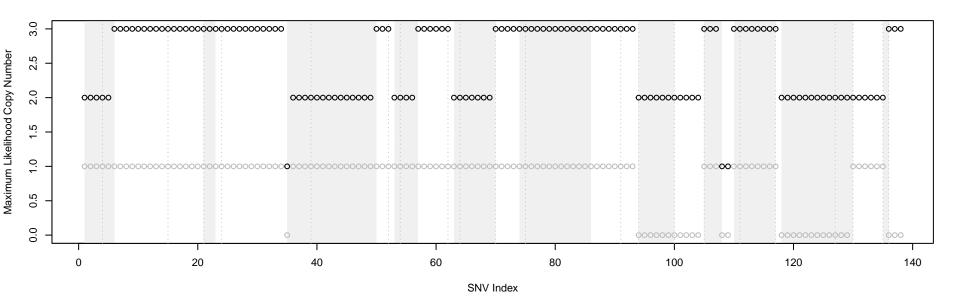


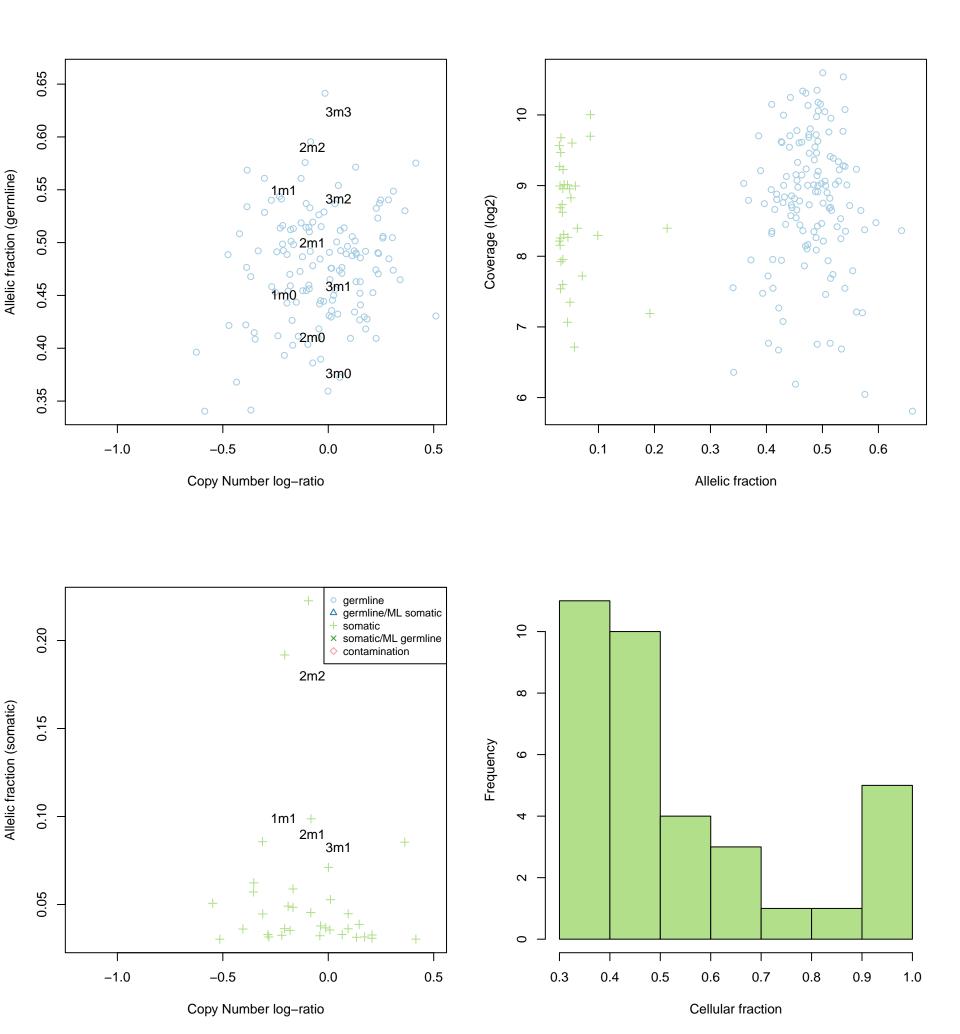
Purity: 0.18 Tumor ploidy: 2.597 2 0 3 0.20 Fraction Genome 0.05 0.00 -0.4 -0.2 0.0 0.2 0.4 0.6 8.0



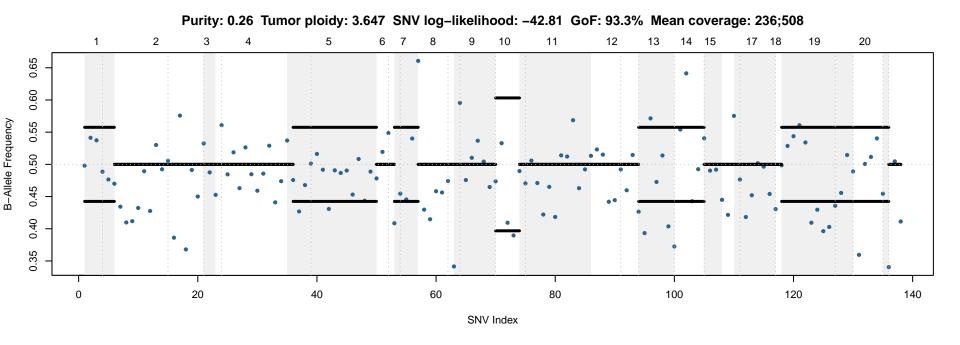
SCNA-fit log-likelihood: -10290.17



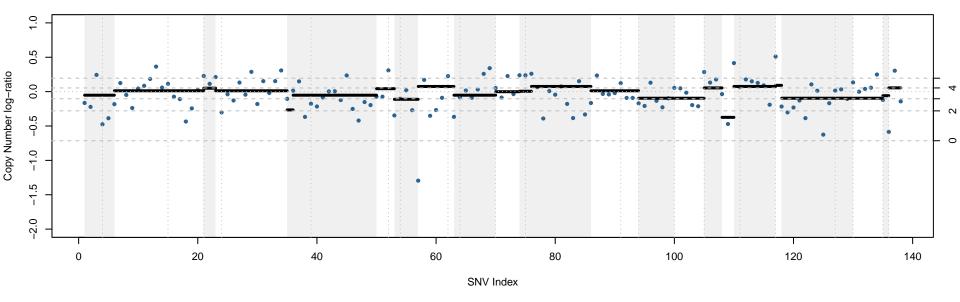


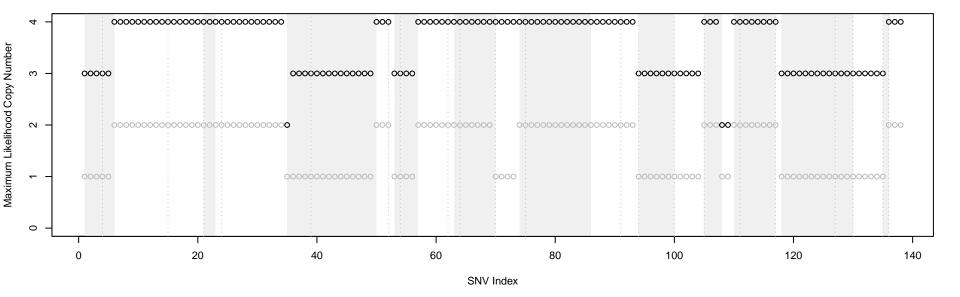


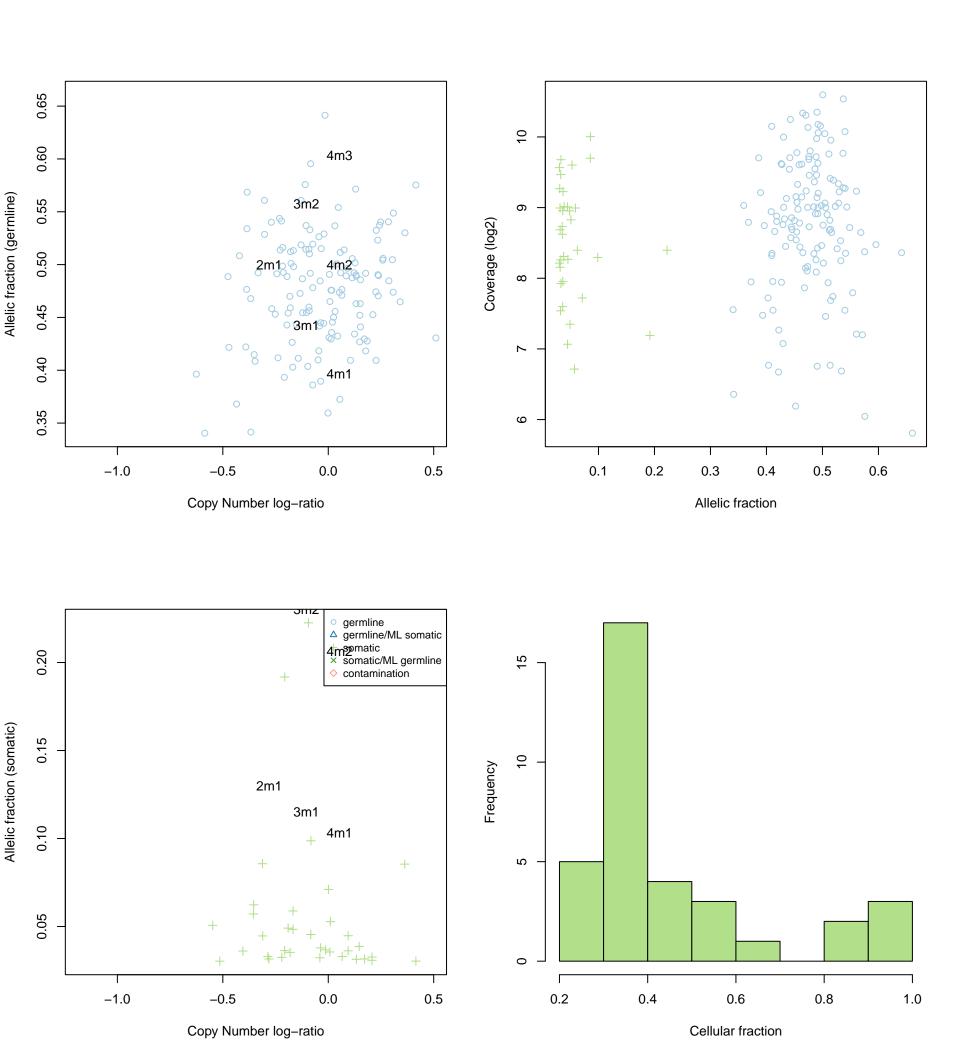
Purity: 0.26 Tumor ploidy: 3.647 2 3 5 4 0.20 Fraction Genome 0.05 0.00 -0.4 -0.2 0.0 0.2 0.4 0.6 8.0 log2 ratio



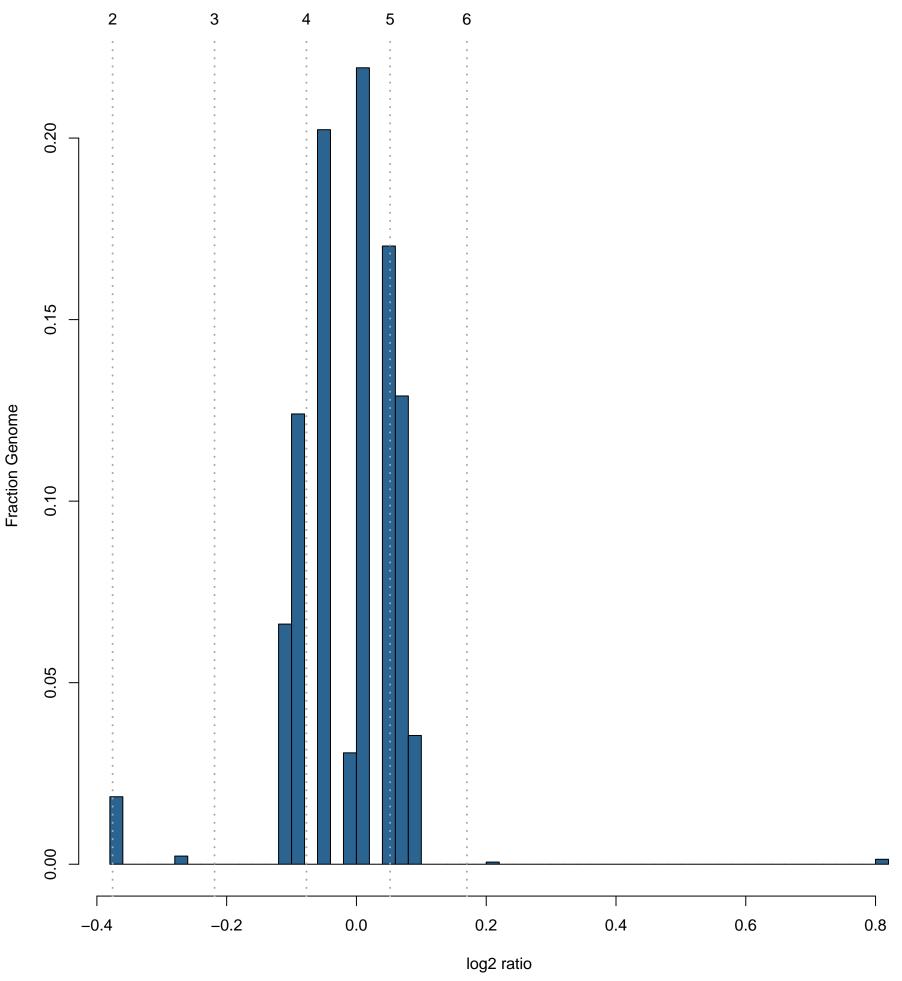
SCNA-fit log-likelihood: -10292.32

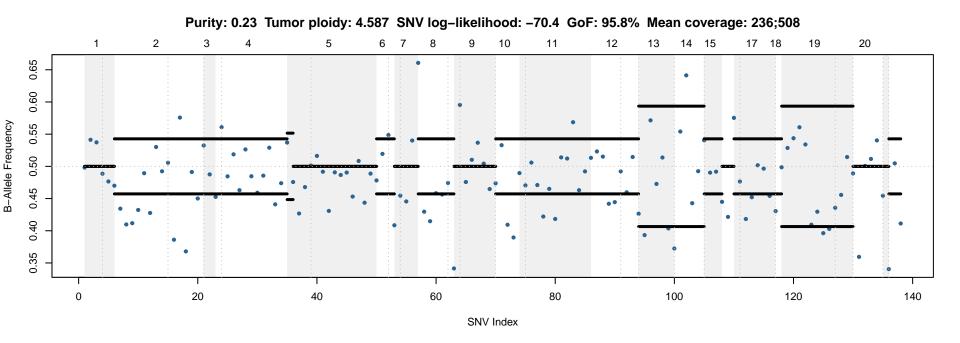




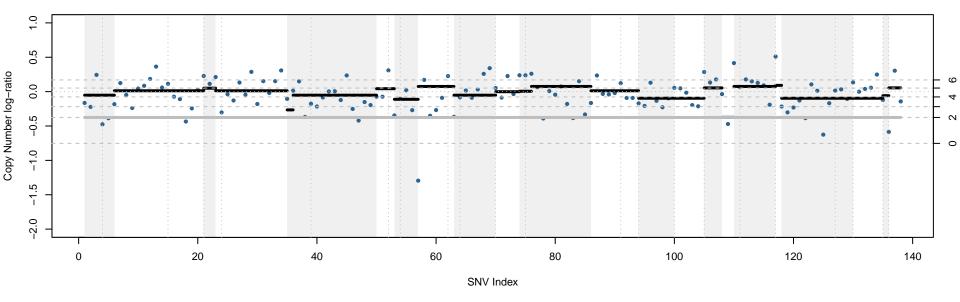


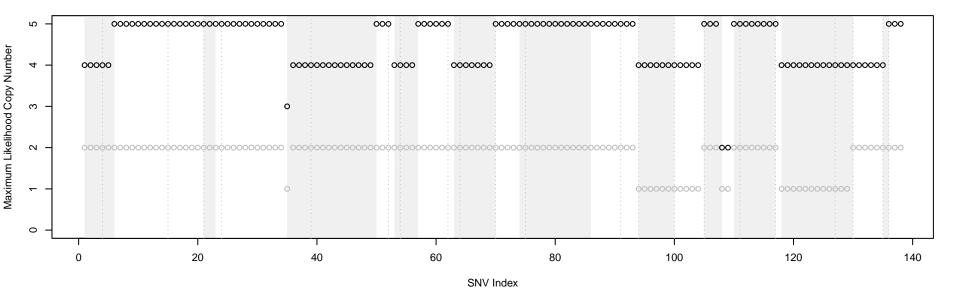
Purity: 0.23 Tumor ploidy: 4.587

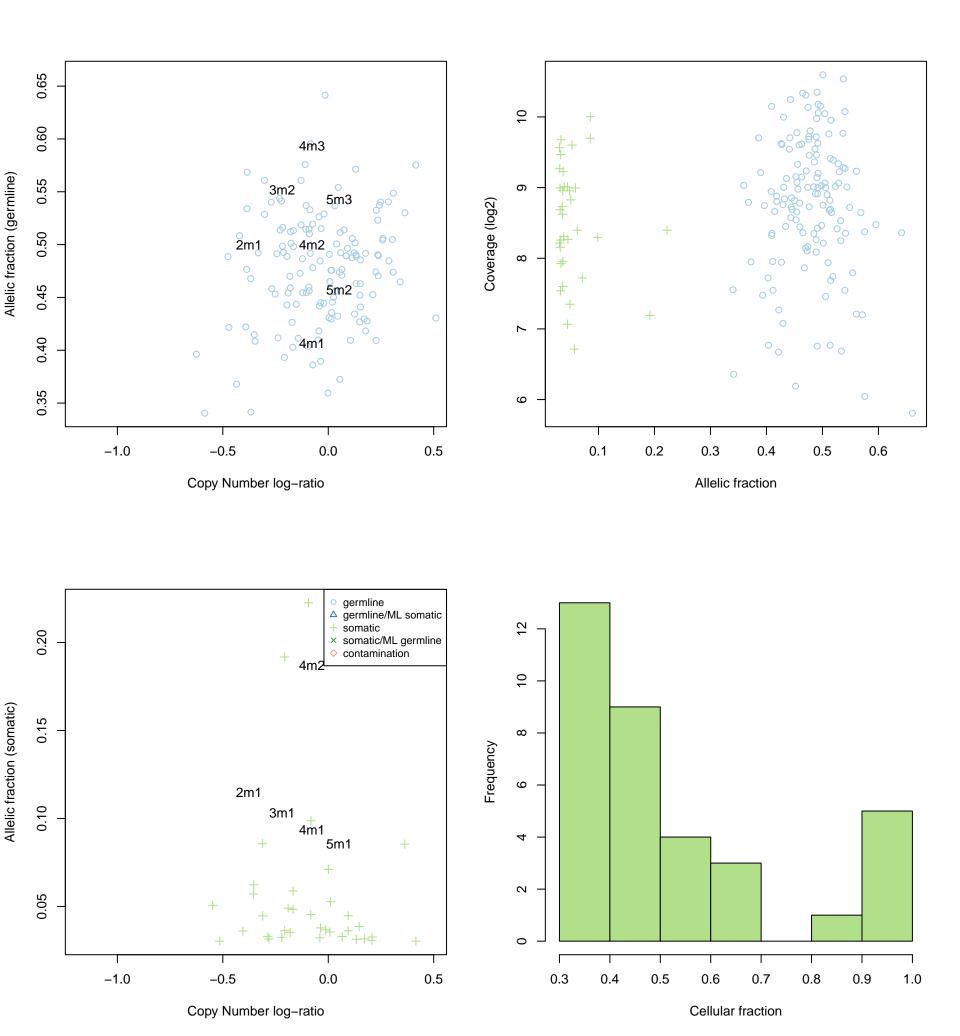




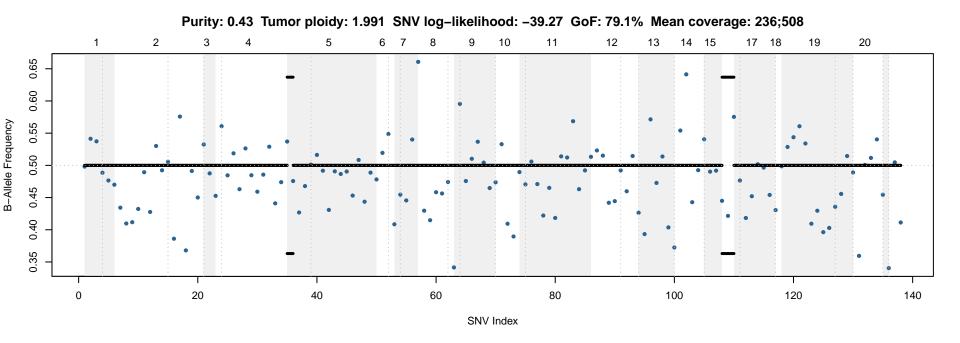
SCNA-fit log-likelihood: -10270.46



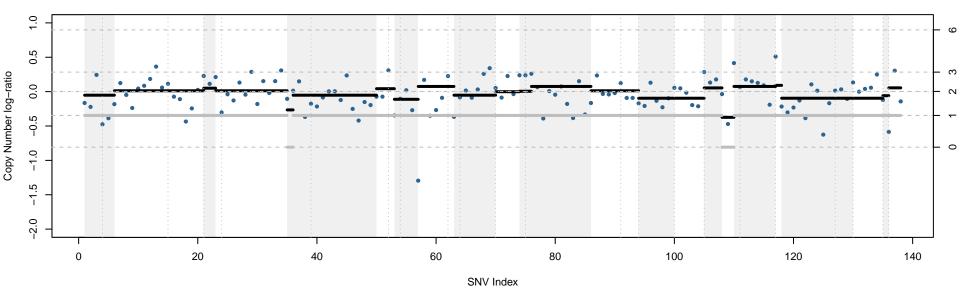


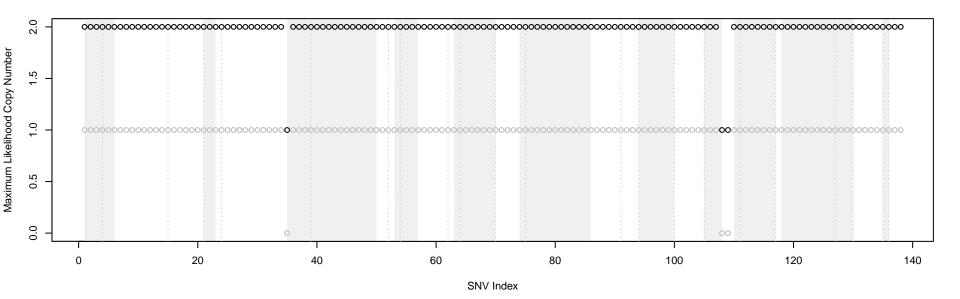


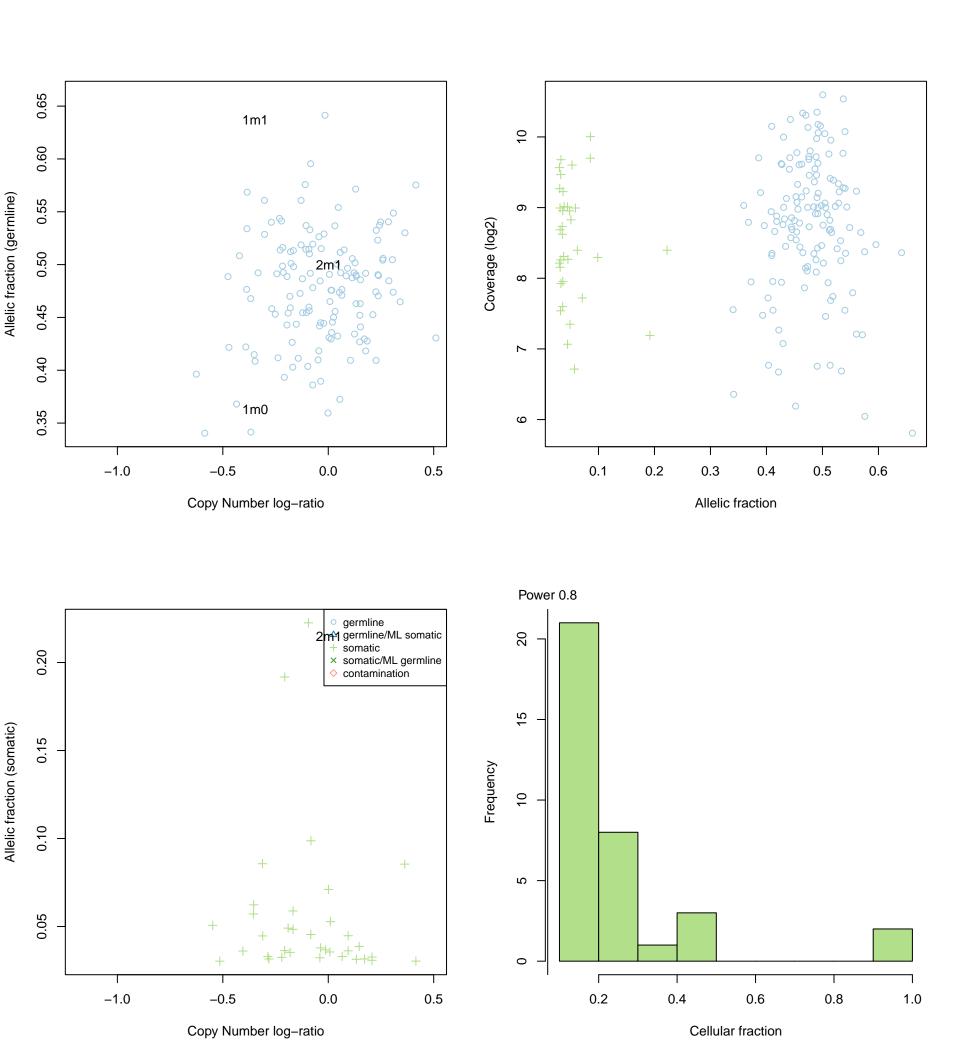
Purity: 0.43 Tumor ploidy: 1.991 2 1 0.20 Fraction Genome 0.05 0.00 -0.4 -0.2 0.0 0.2 0.4 0.6 8.0 log2 ratio



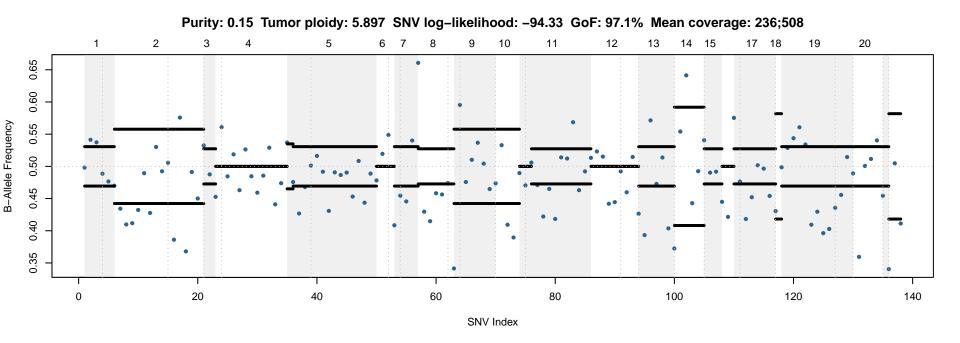
SCNA-fit log-likelihood: -10381.76



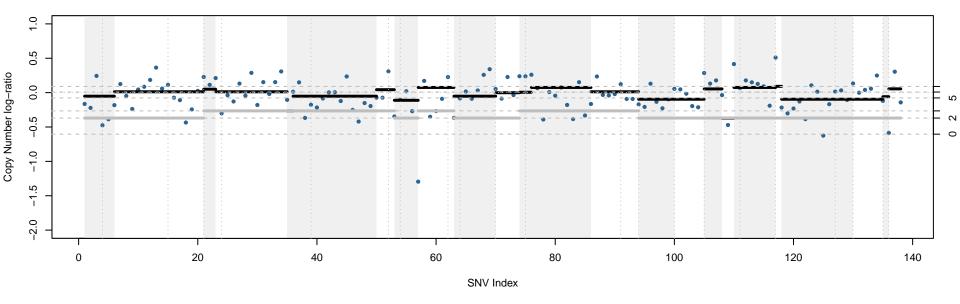


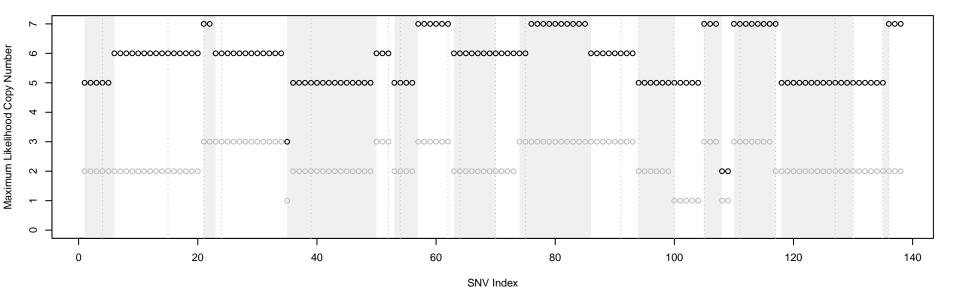


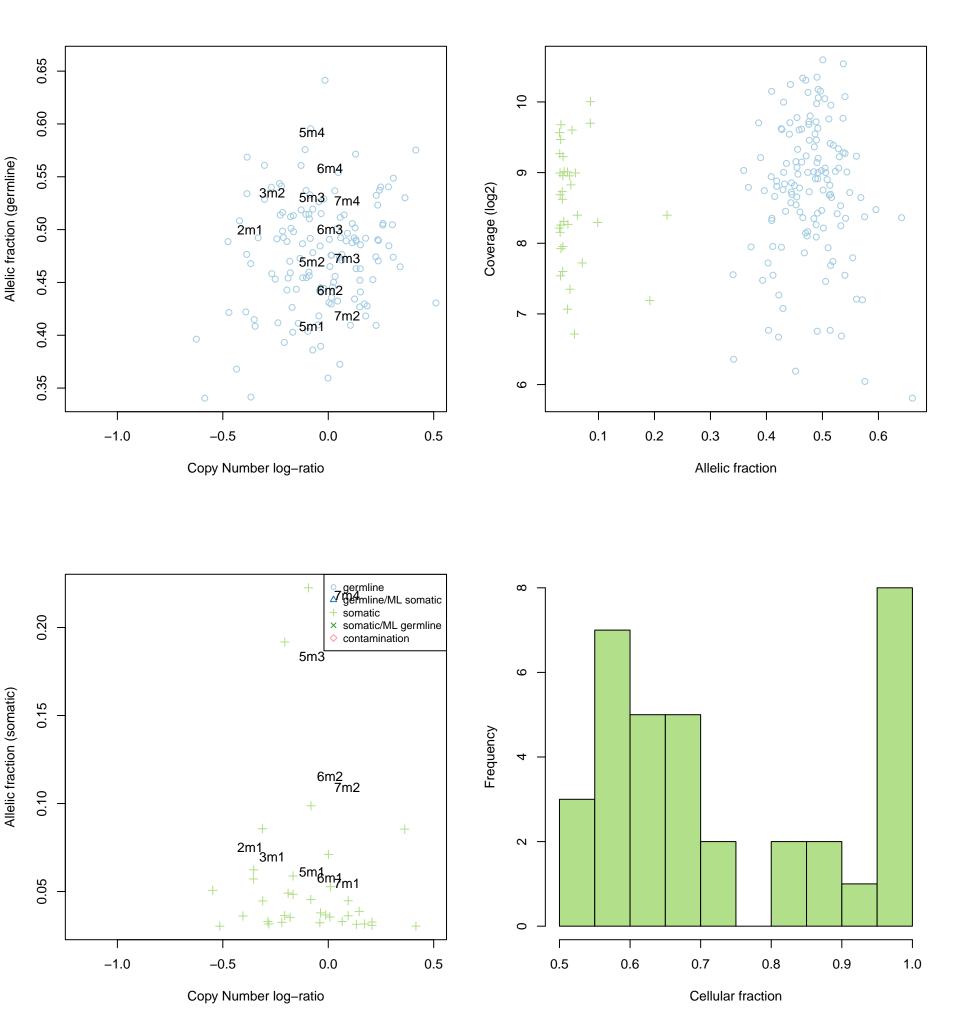
Purity: 0.15 Tumor ploidy: 5.897 2 3 5 6 7 0.20 Fraction Genome 0.05 0.00 -0.4 -0.2 0.0 0.2 0.4 0.6 8.0 log2 ratio



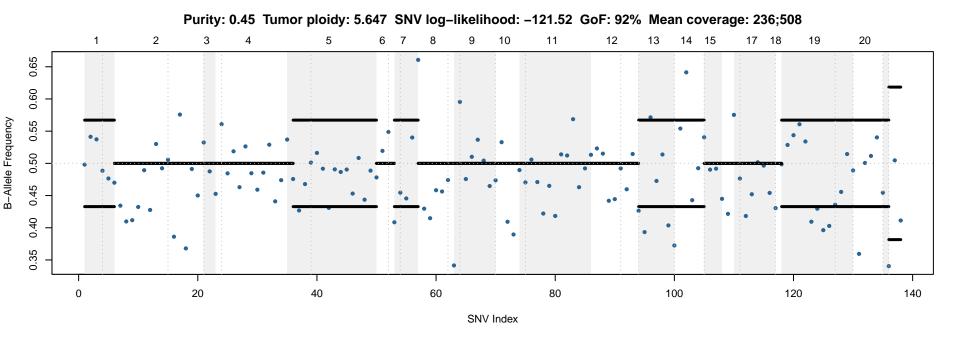
SCNA-fit log-likelihood: -10259.37



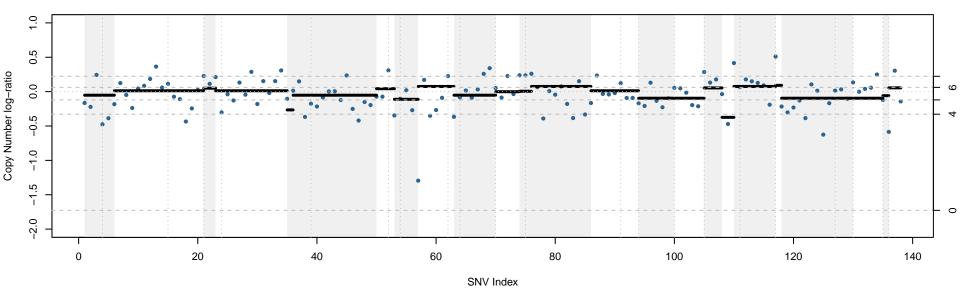


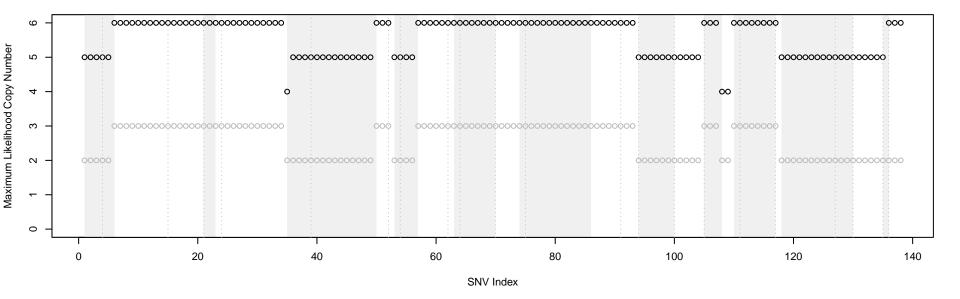


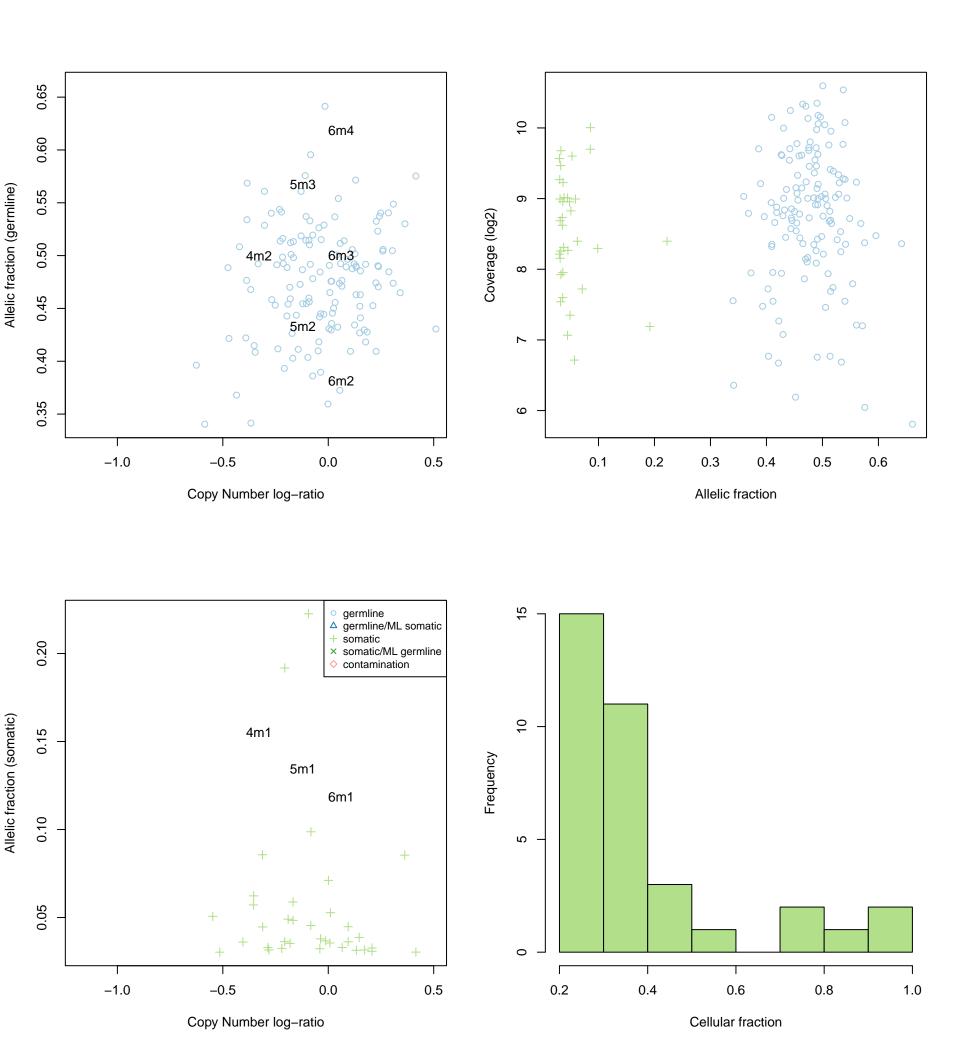
Purity: 0.45 Tumor ploidy: 5.647 0 6 7 5 0.30 0.20 Fraction Genome 0.15 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio



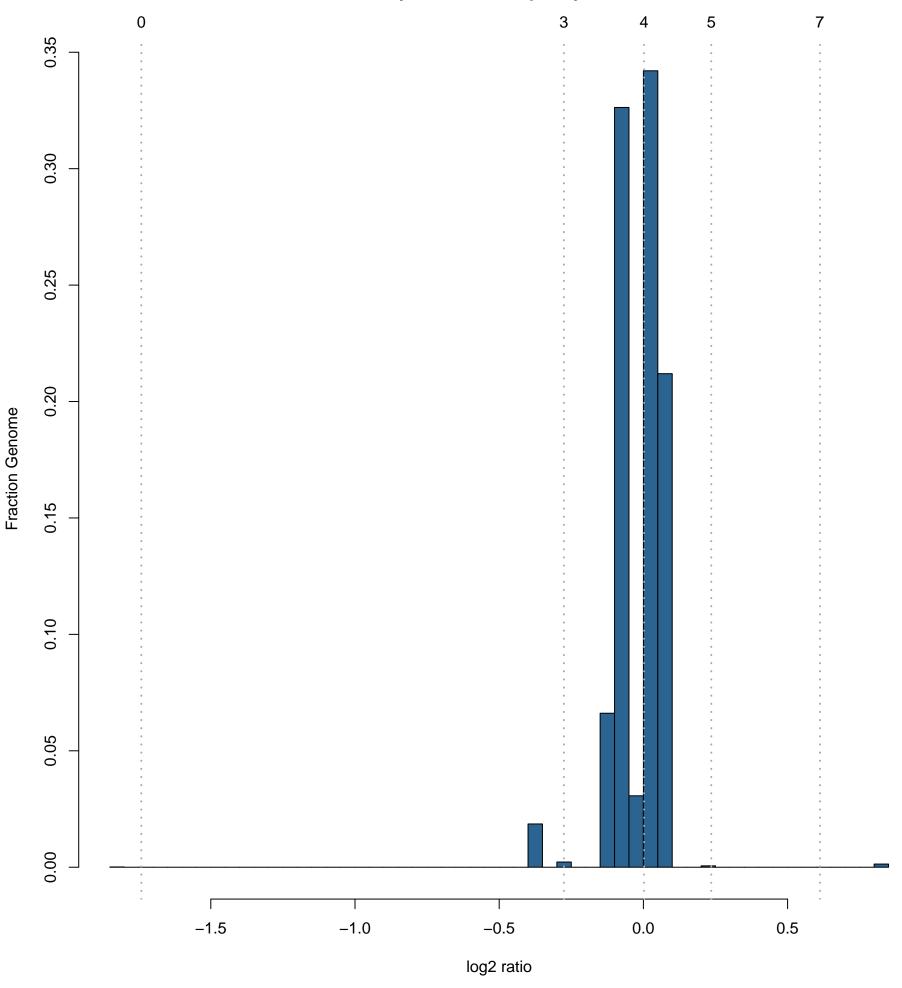
SCNA-fit log-likelihood: -10310.51

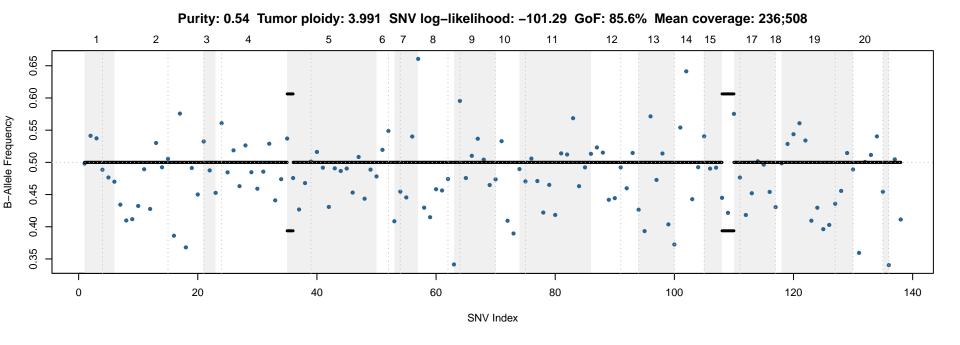




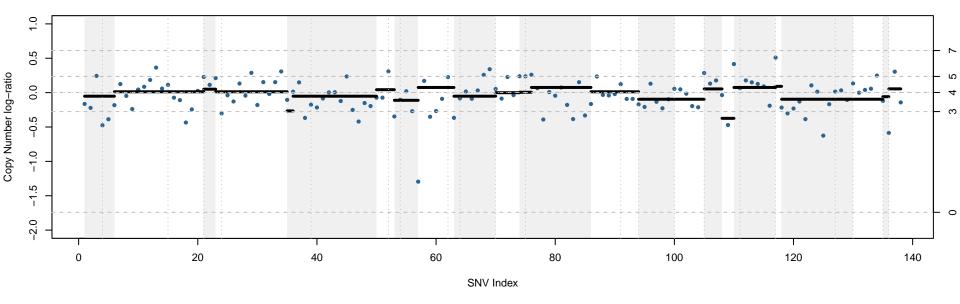


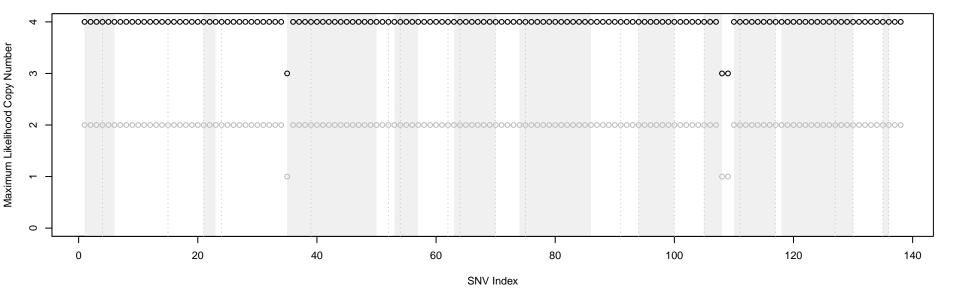
Purity: 0.54 Tumor ploidy: 3.991

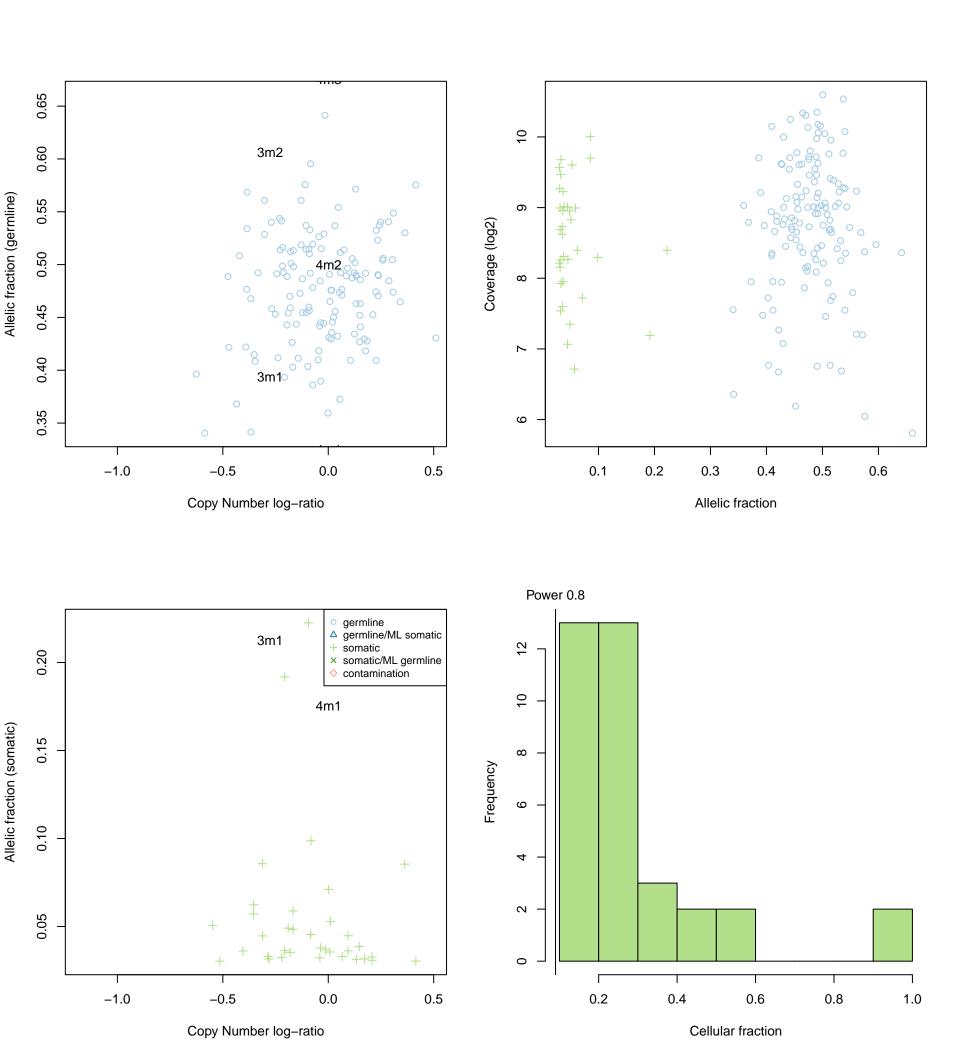




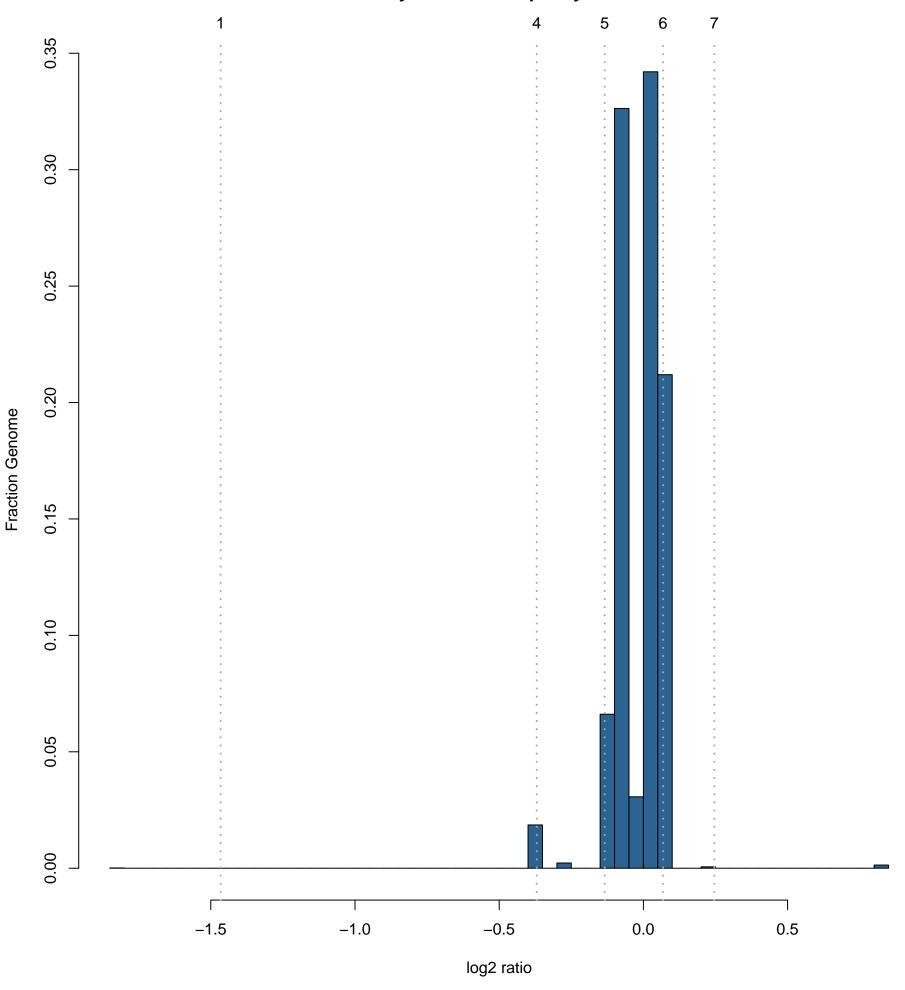
SCNA-fit log-likelihood: -10387.17

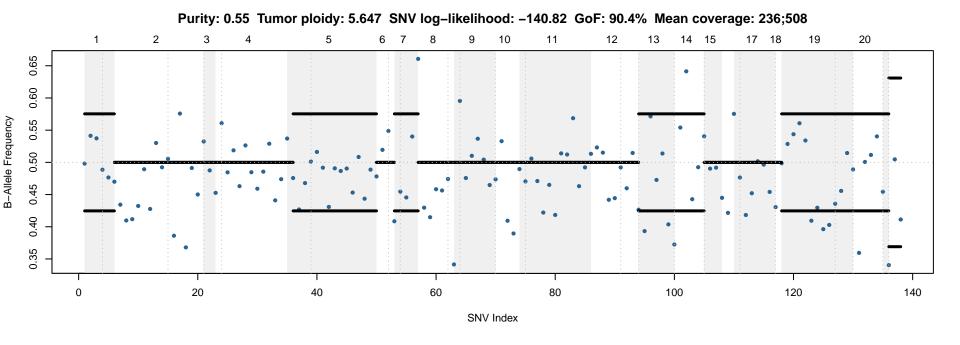




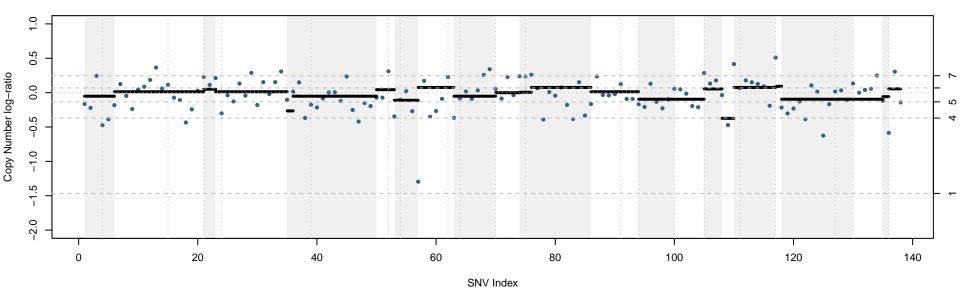


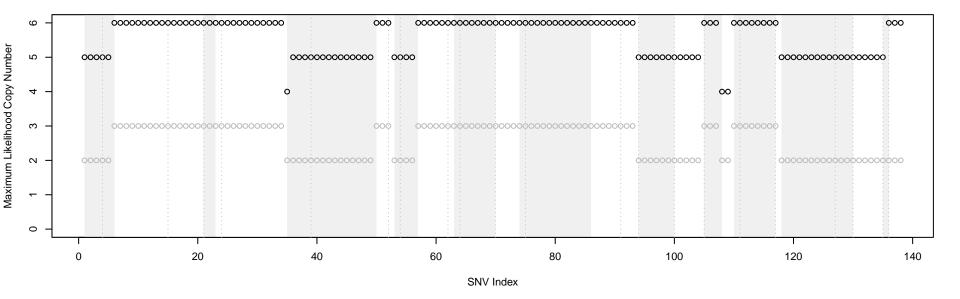
Purity: 0.55 Tumor ploidy: 5.647

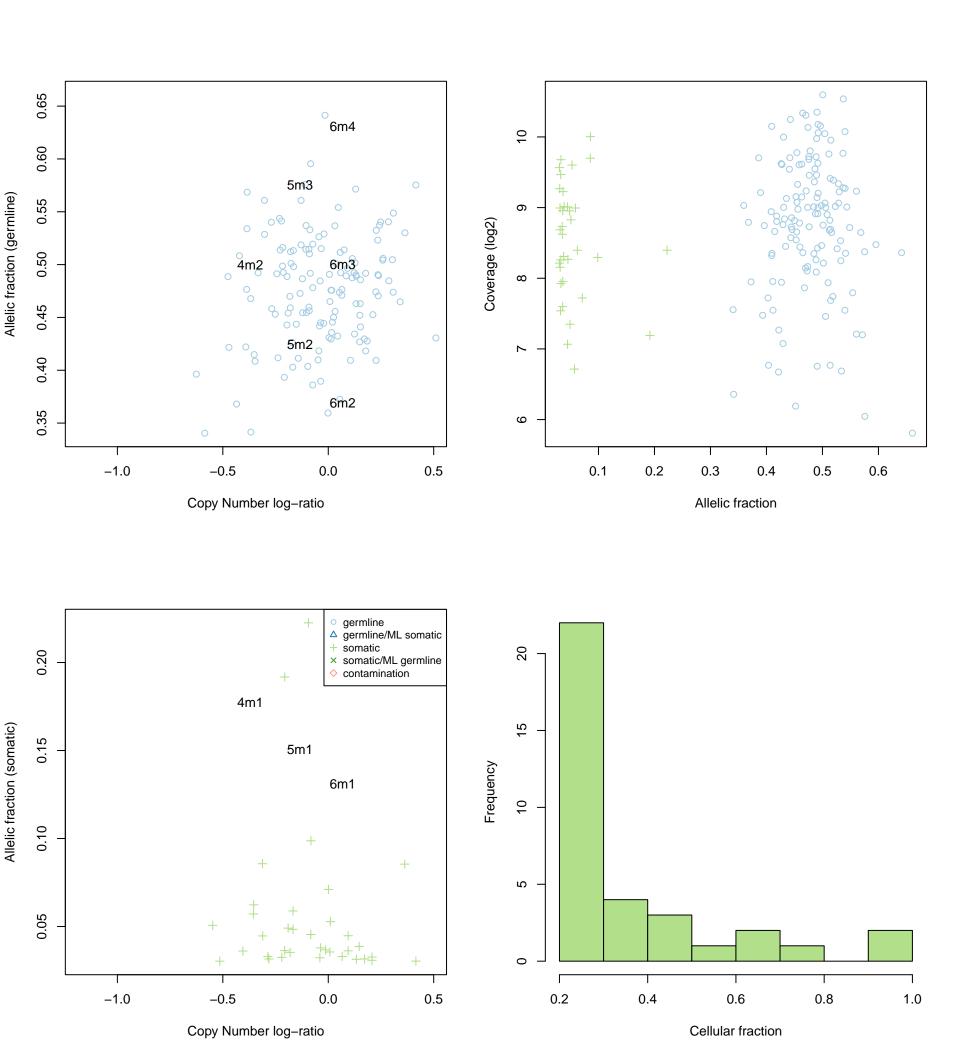




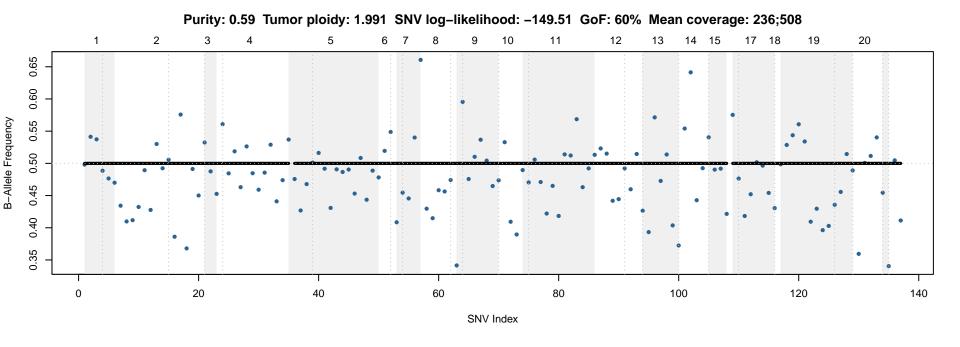
SCNA-fit log-likelihood: -10340.88



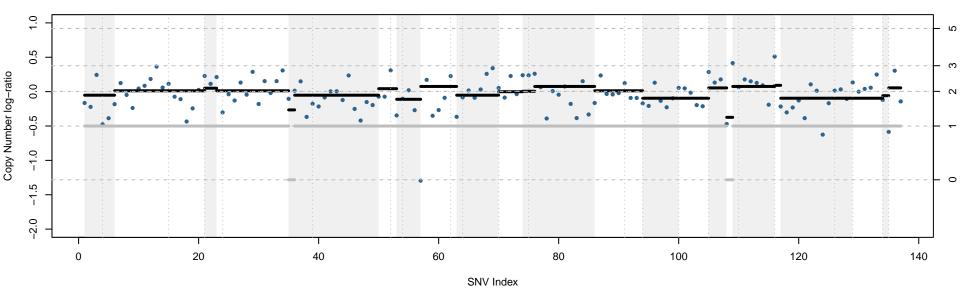


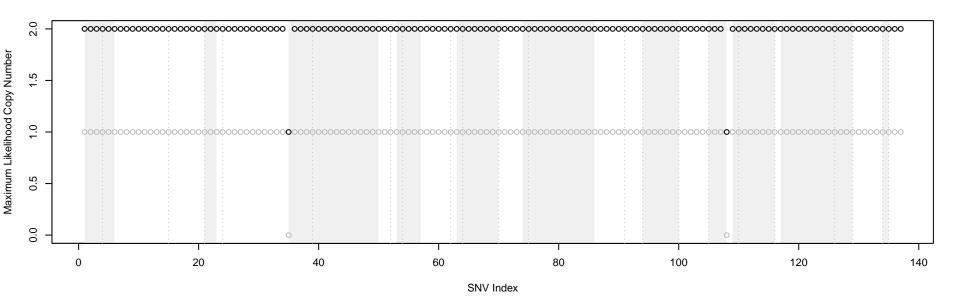


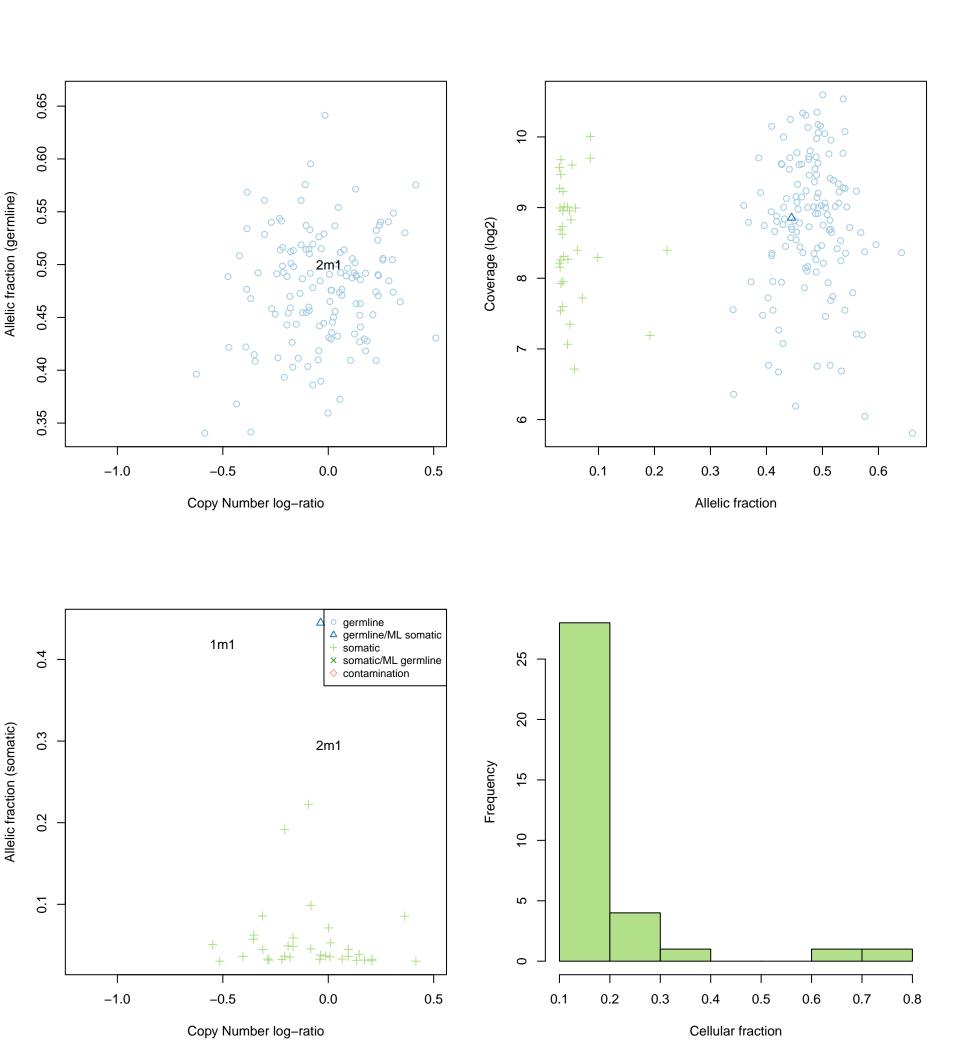
Purity: 0.59 Tumor ploidy: 1.991 3 0 2 5 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5



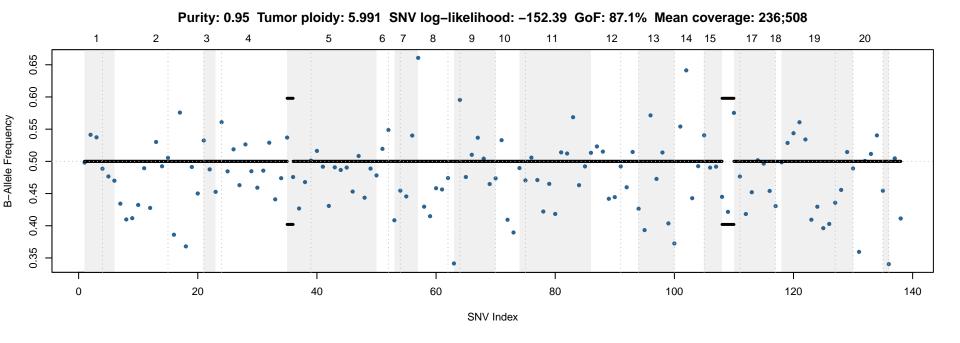
SCNA-fit log-likelihood: -10401



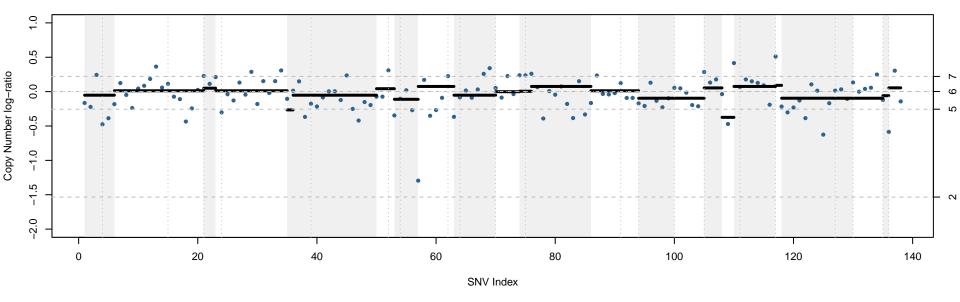


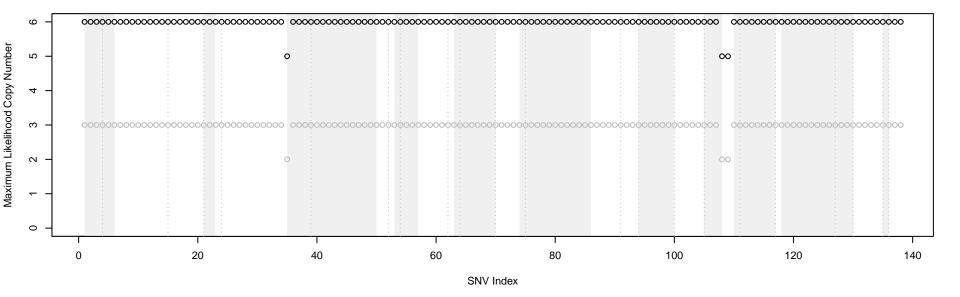


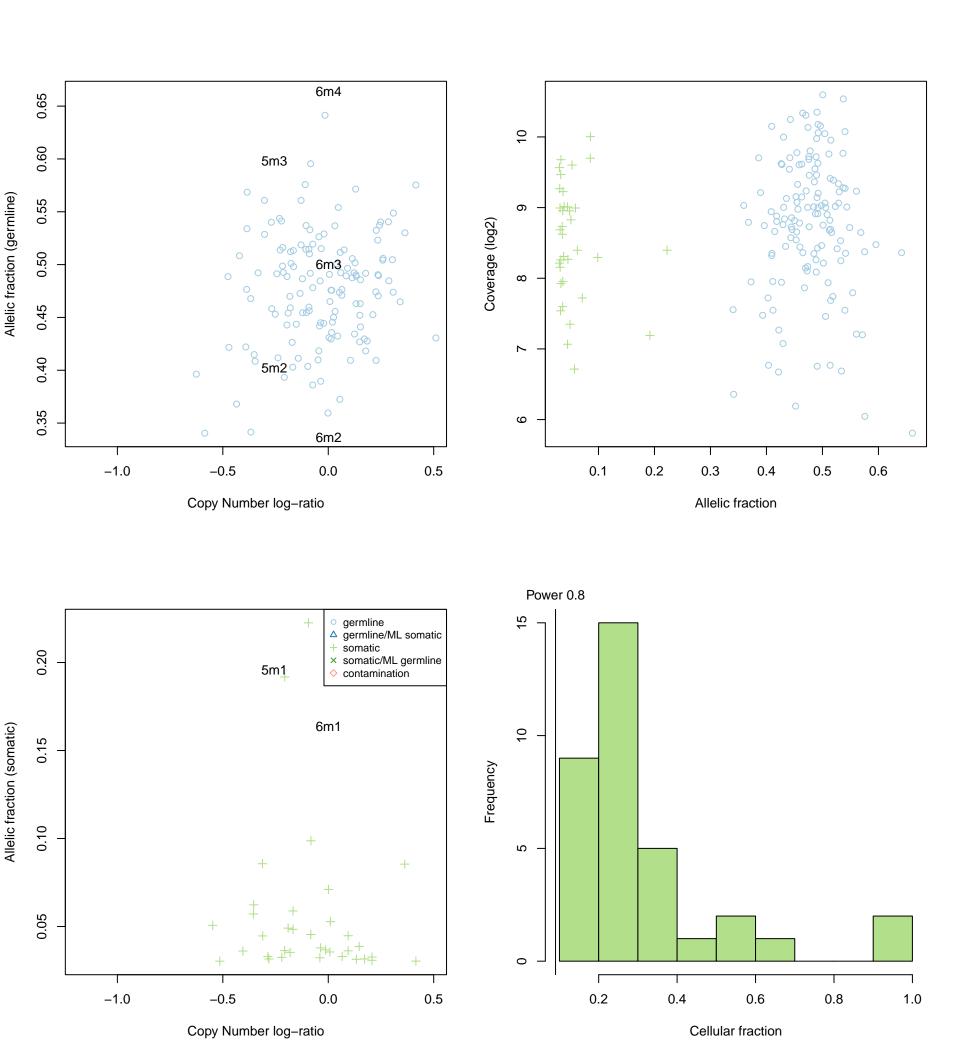
Purity: 0.95 Tumor ploidy: 5.991 2 7 6 0.30 0.20 Fraction Genome 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio



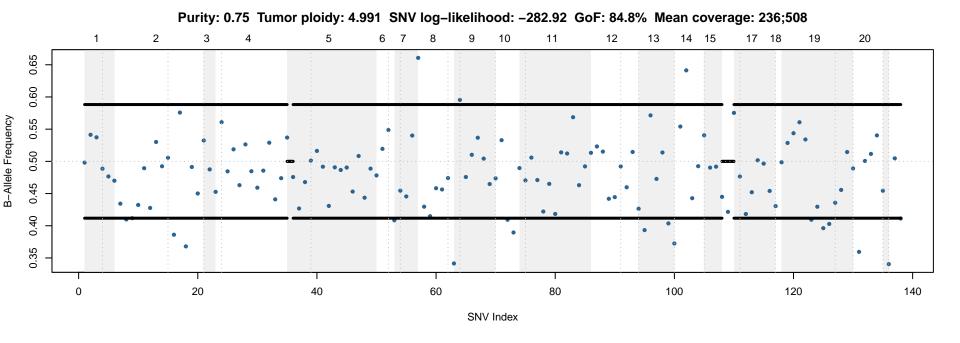
SCNA-fit log-likelihood: -10416.13



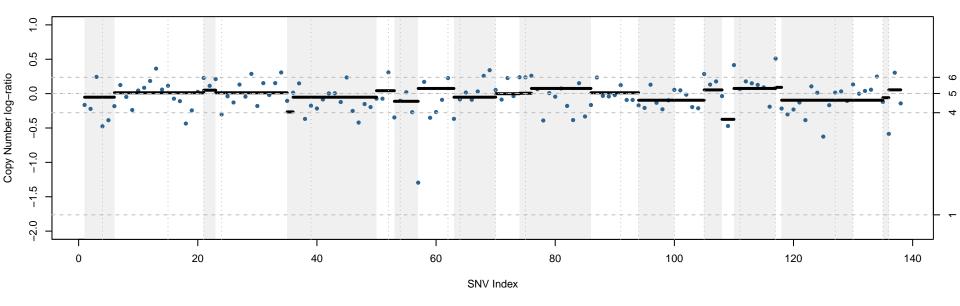


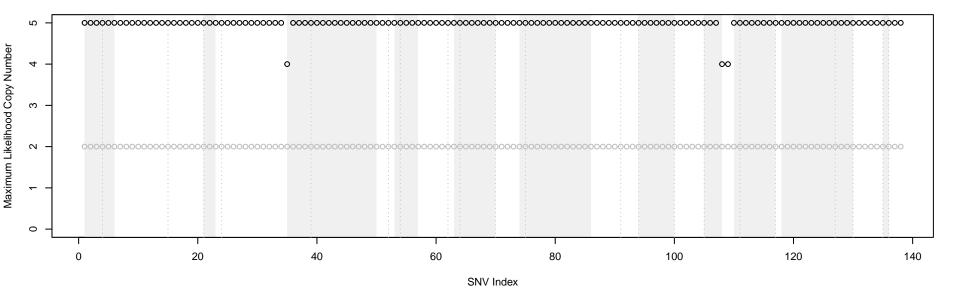


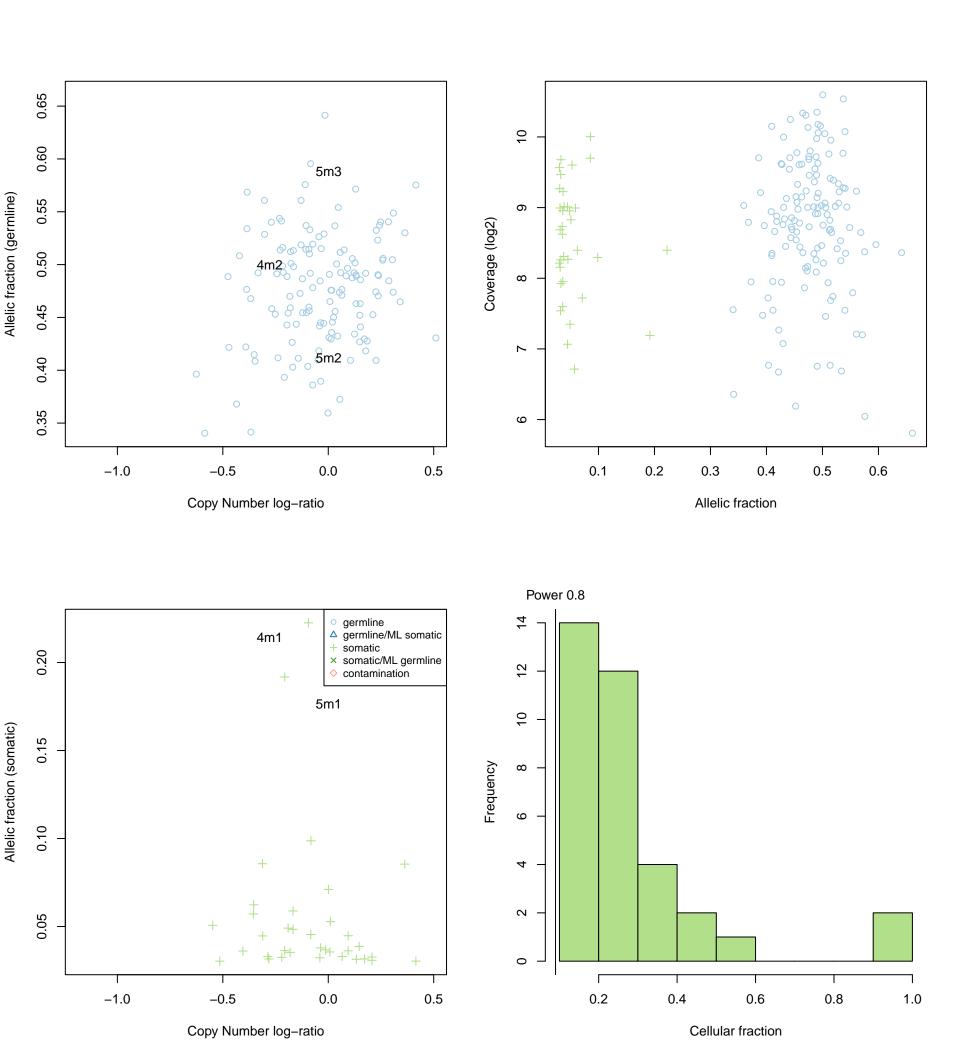
Purity: 0.75 Tumor ploidy: 4.991 5 6 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -0.5 -1.5 -1.0 0.0 0.5



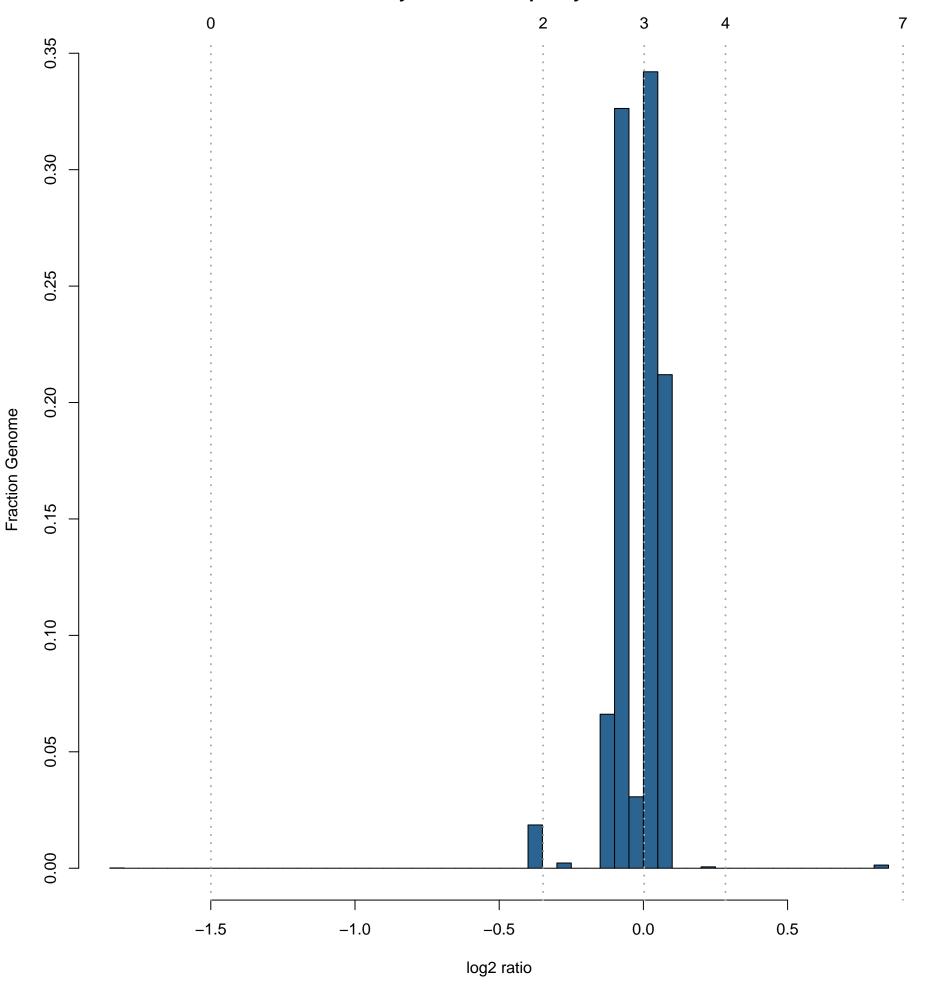
SCNA-fit log-likelihood: -10412.6

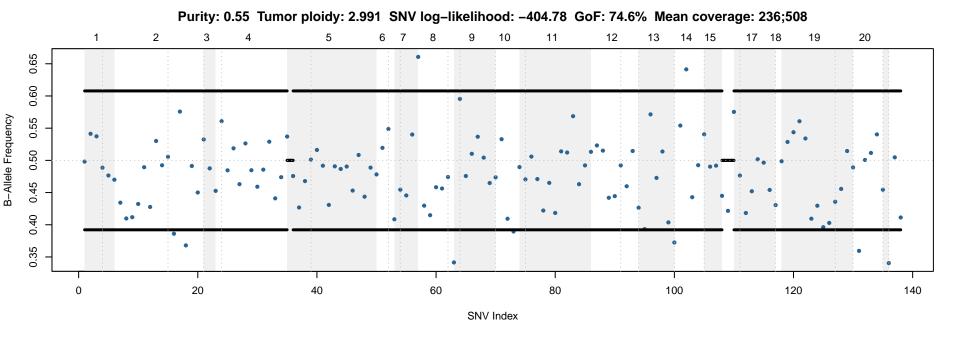




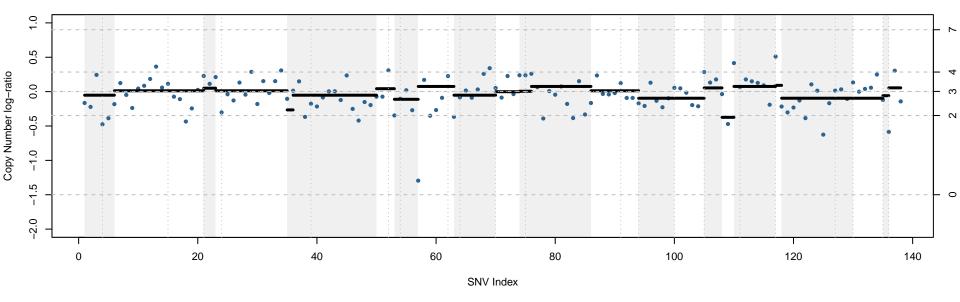


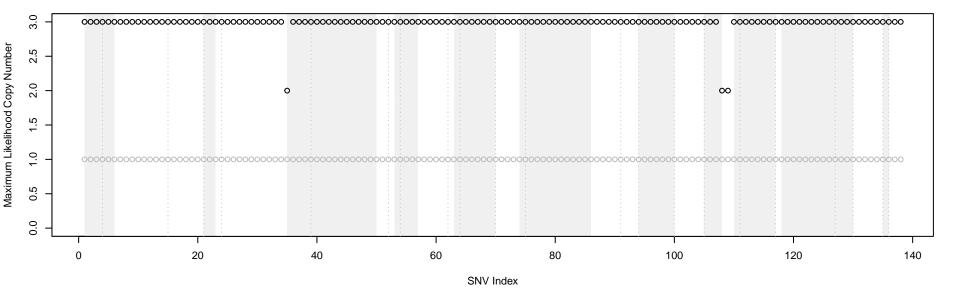
Purity: 0.55 Tumor ploidy: 2.991

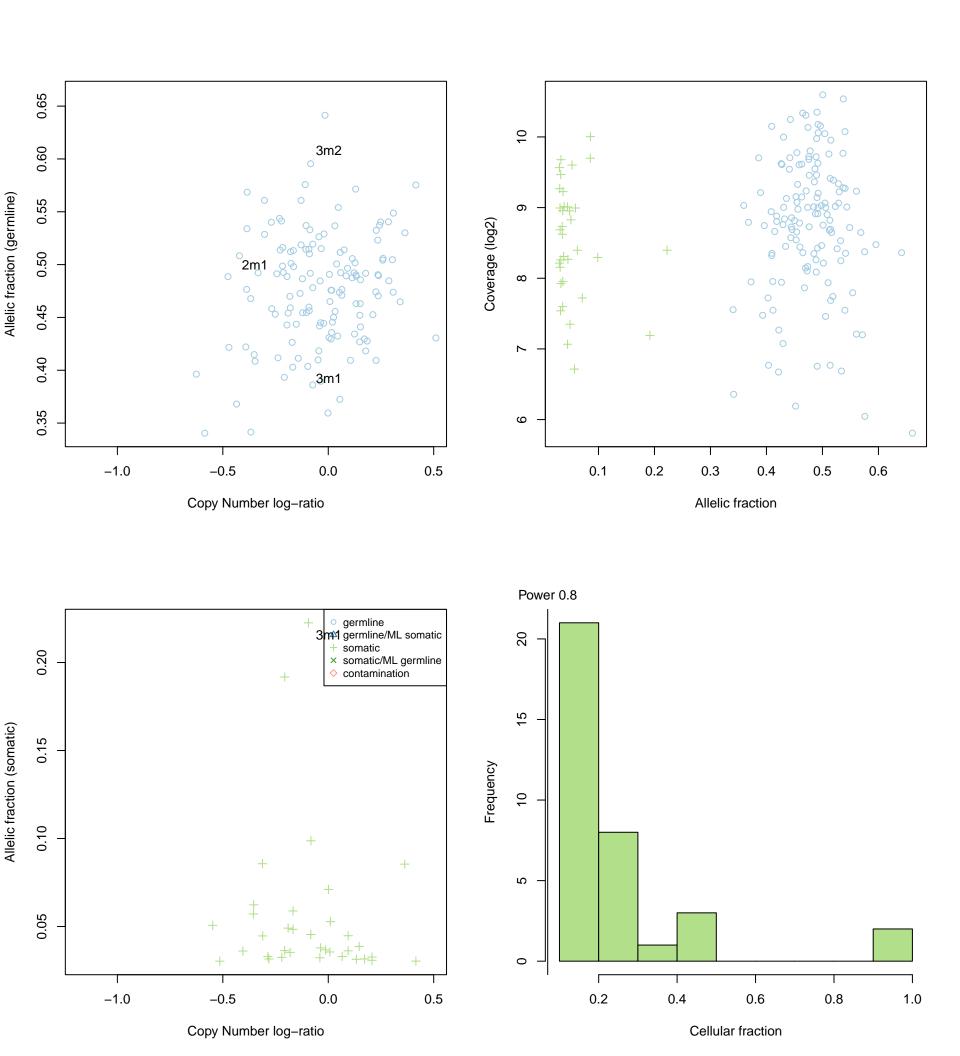




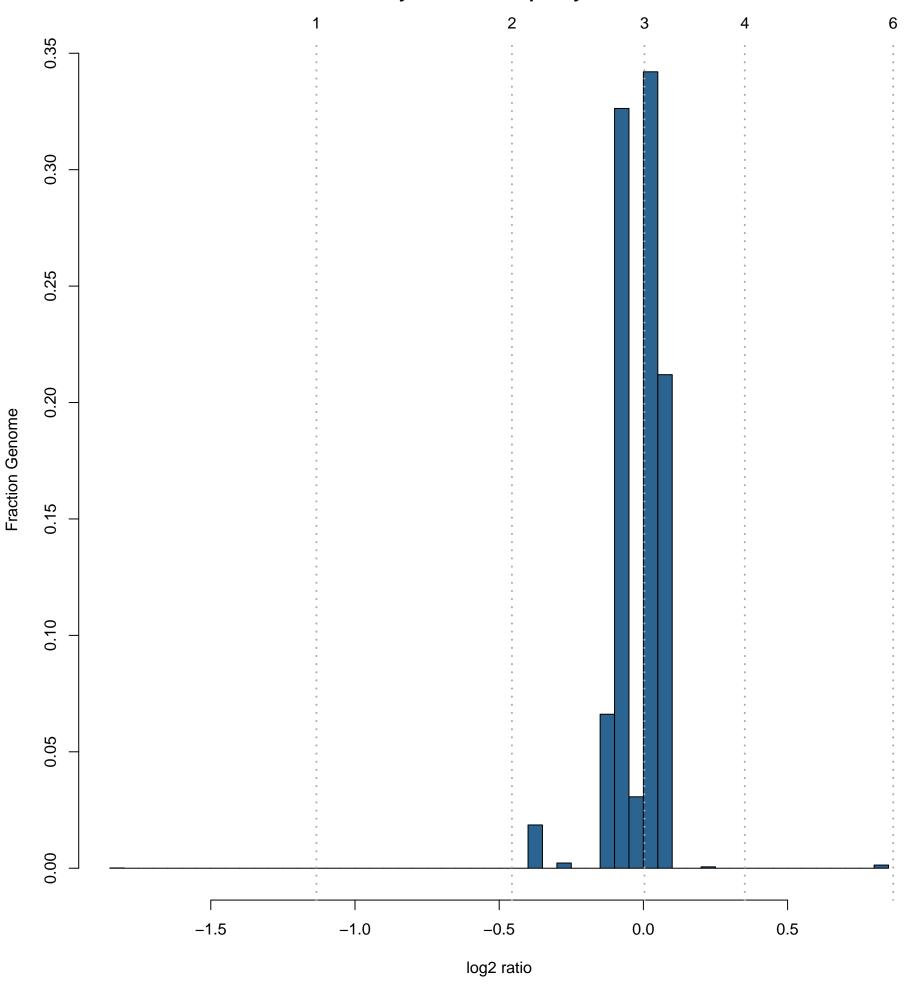
SCNA-fit log-likelihood: -10379.83

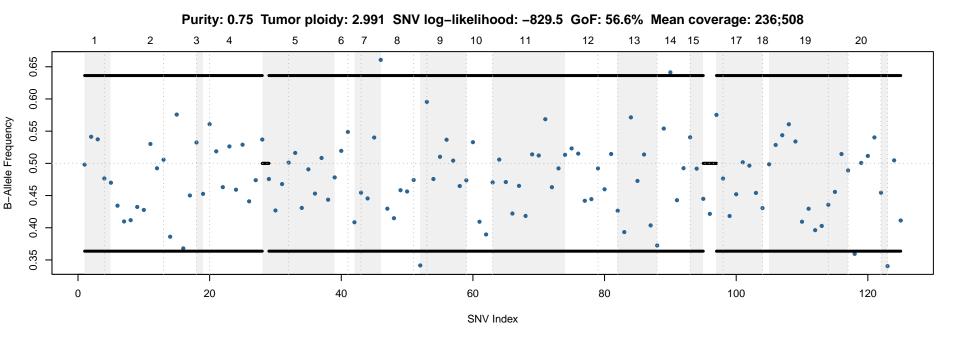






Purity: 0.75 Tumor ploidy: 2.991





SCNA-fit log-likelihood: -10391.05

