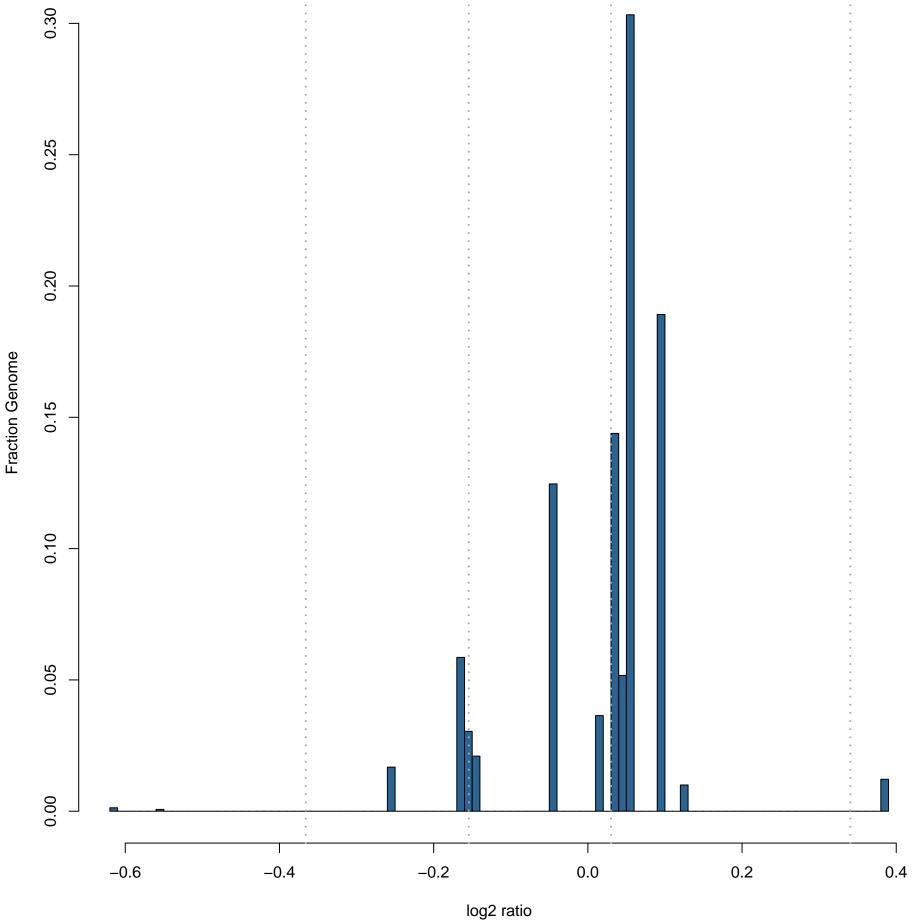
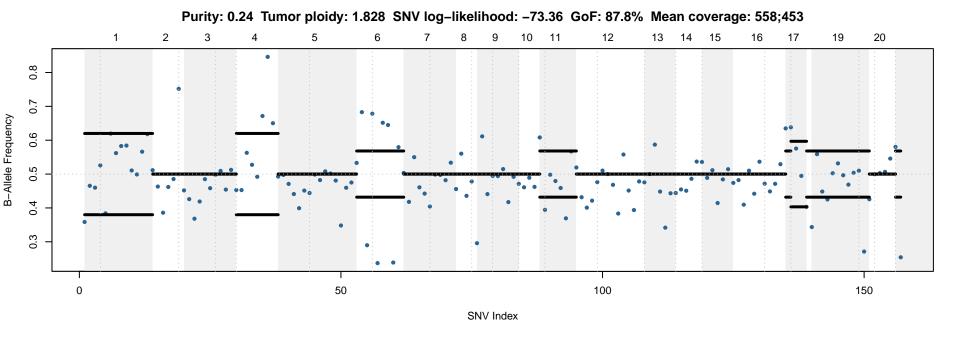
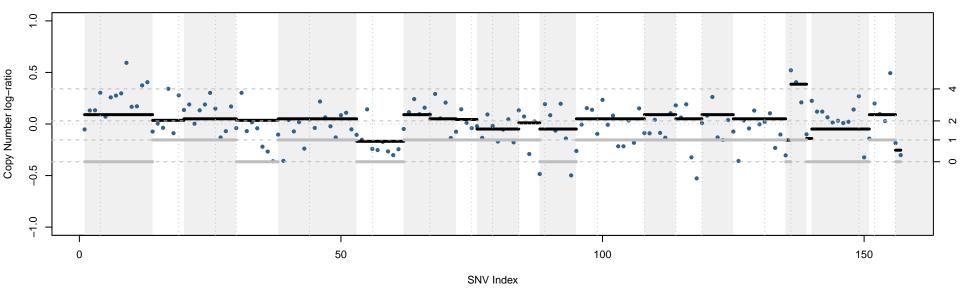
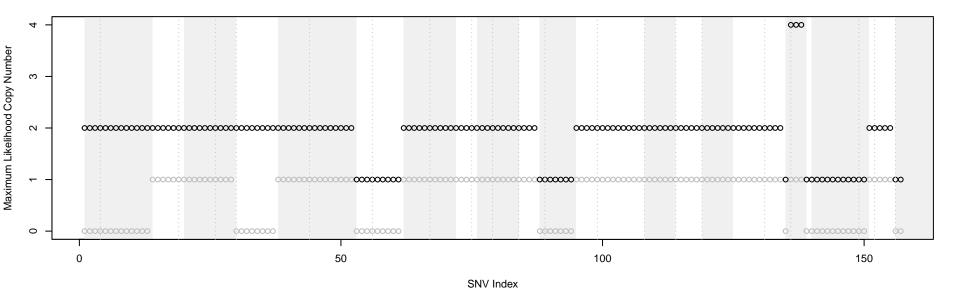
Purity: 0.24 Tumor ploidy: 1.828

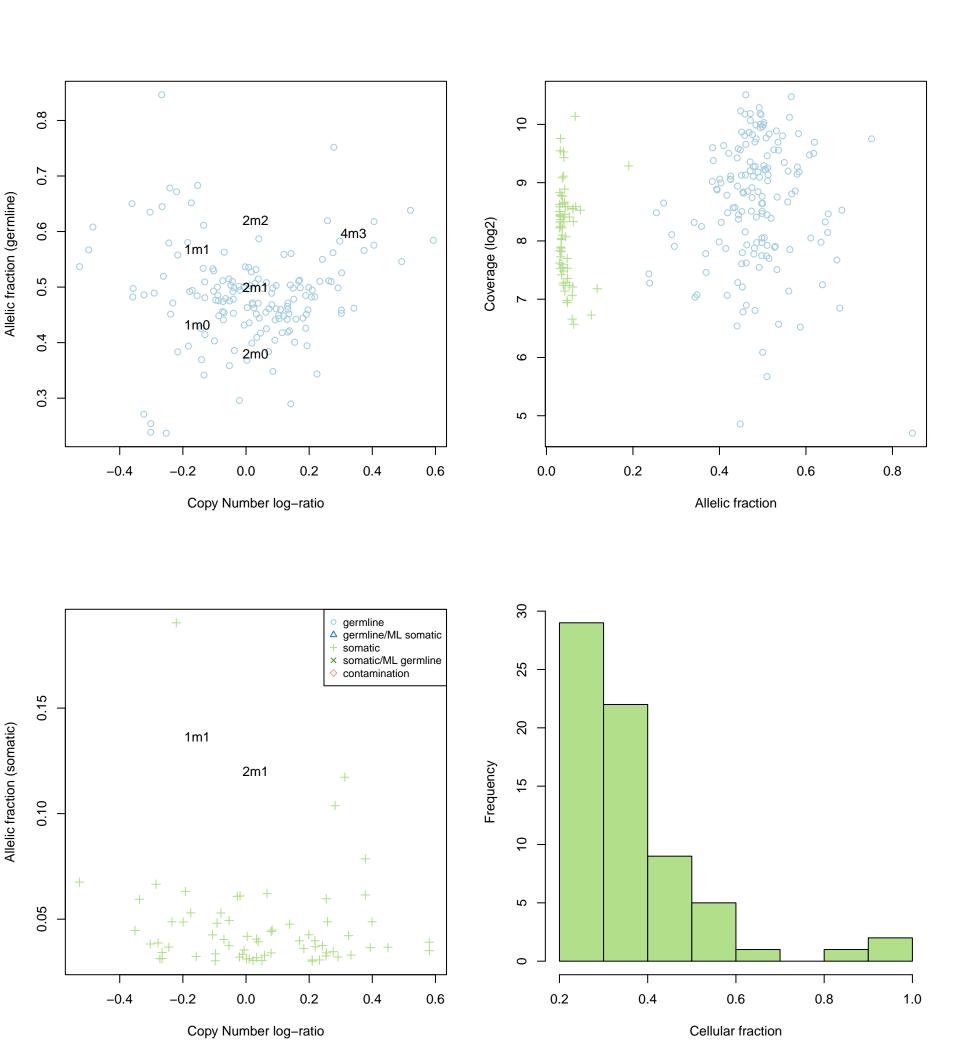




SCNA-fit log-likelihood: -13122.27

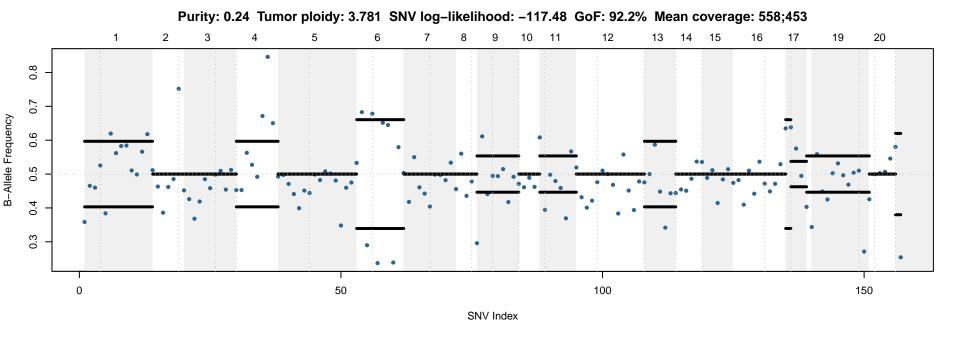




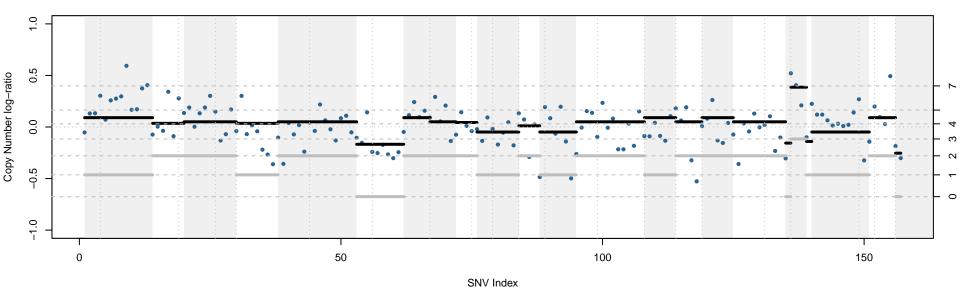


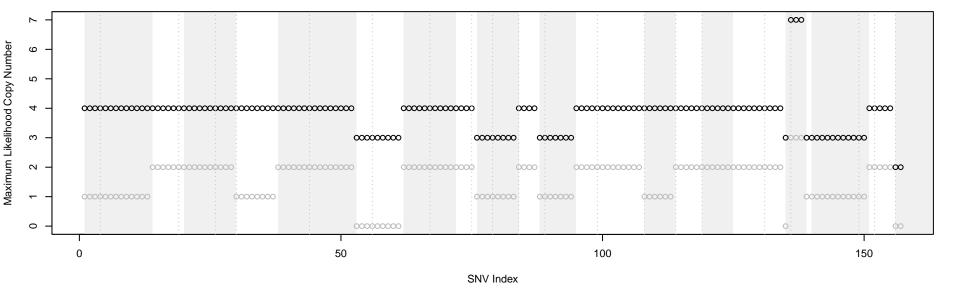
Purity: 0.24 Tumor ploidy: 3.781 3 0 5 7 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -0.2 -0.8 -0.6 -0.4 0.0 0.2 0.4

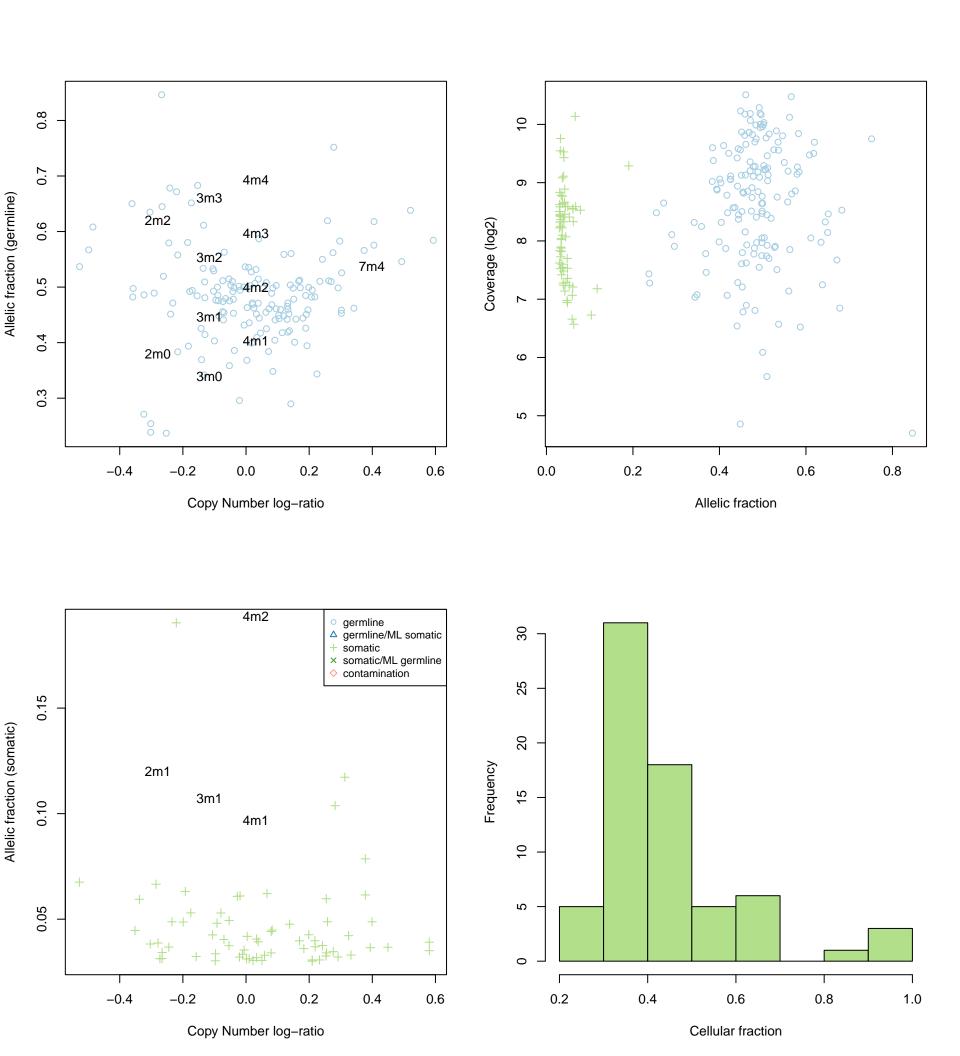
log2 ratio



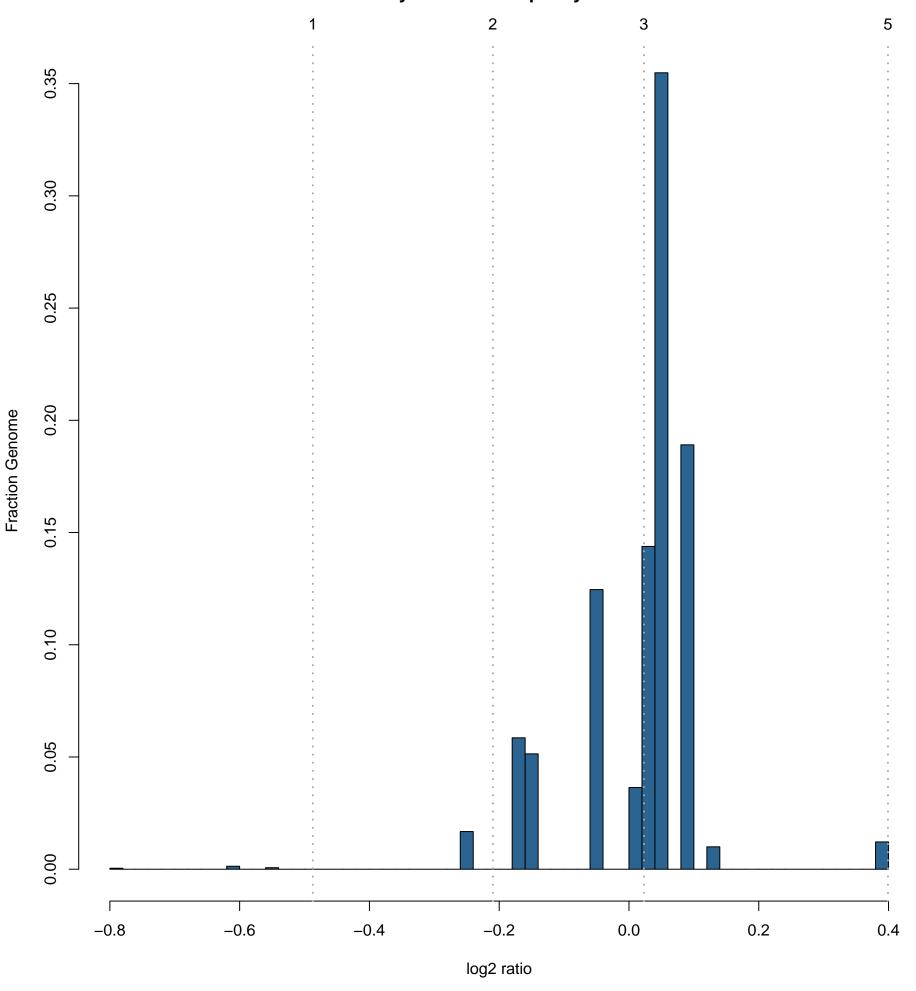
SCNA-fit log-likelihood: -13094.93

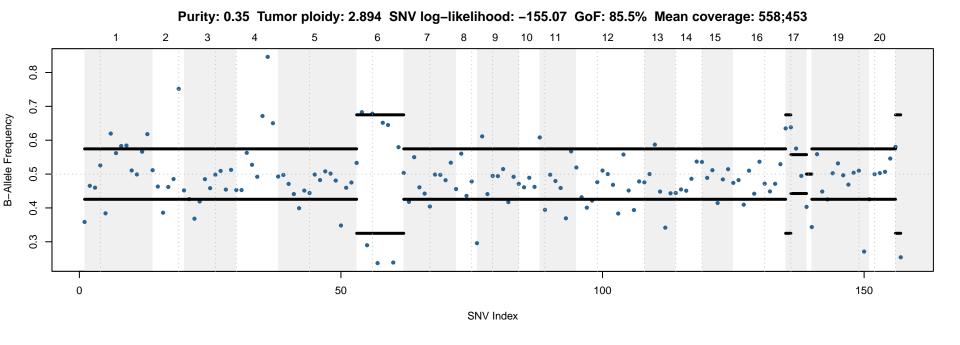




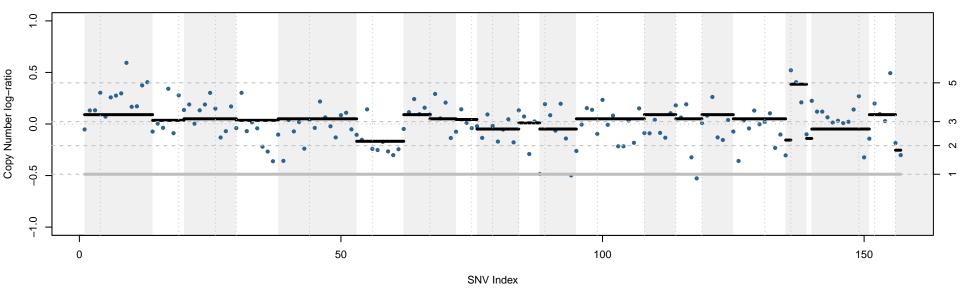


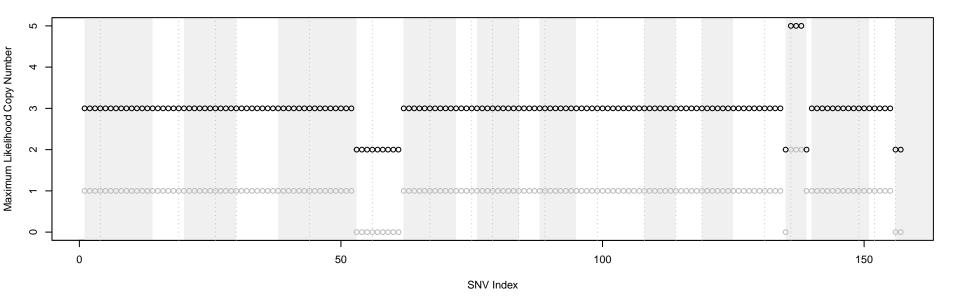
Purity: 0.35 Tumor ploidy: 2.894

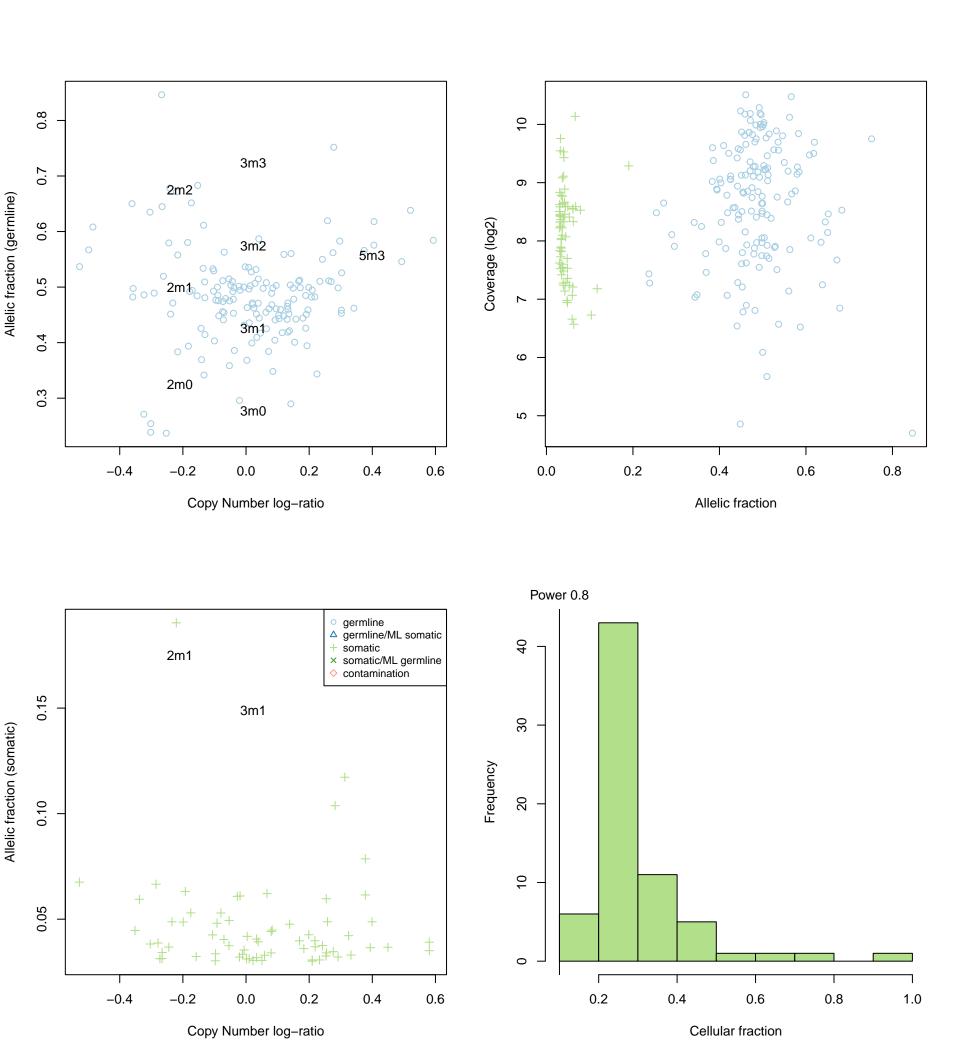




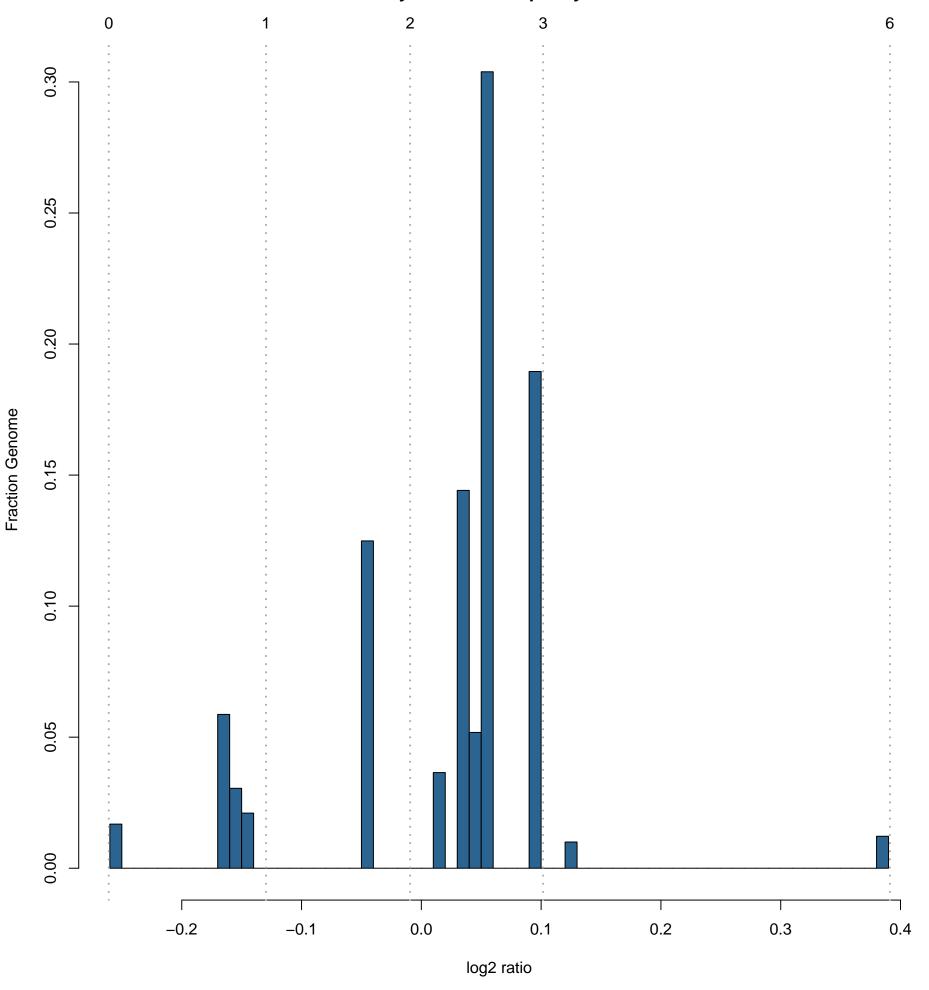
SCNA-fit log-likelihood: -13122.43

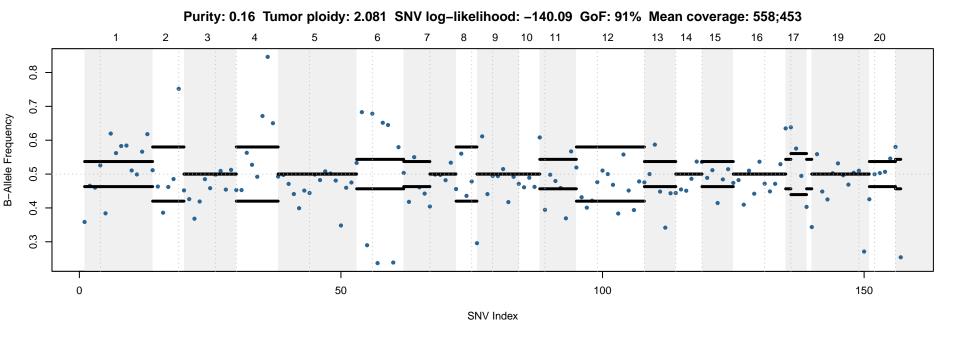




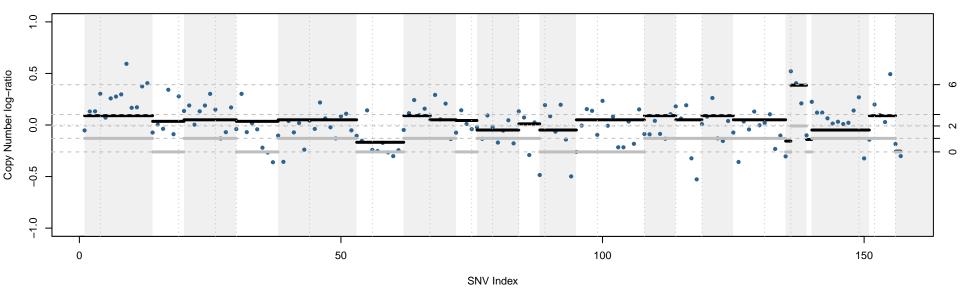


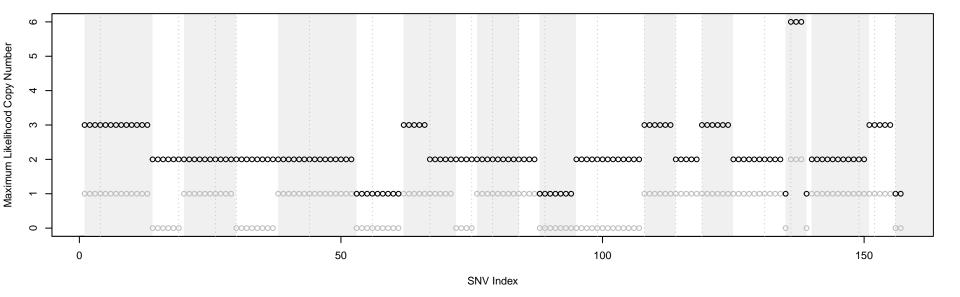
Purity: 0.16 Tumor ploidy: 2.081

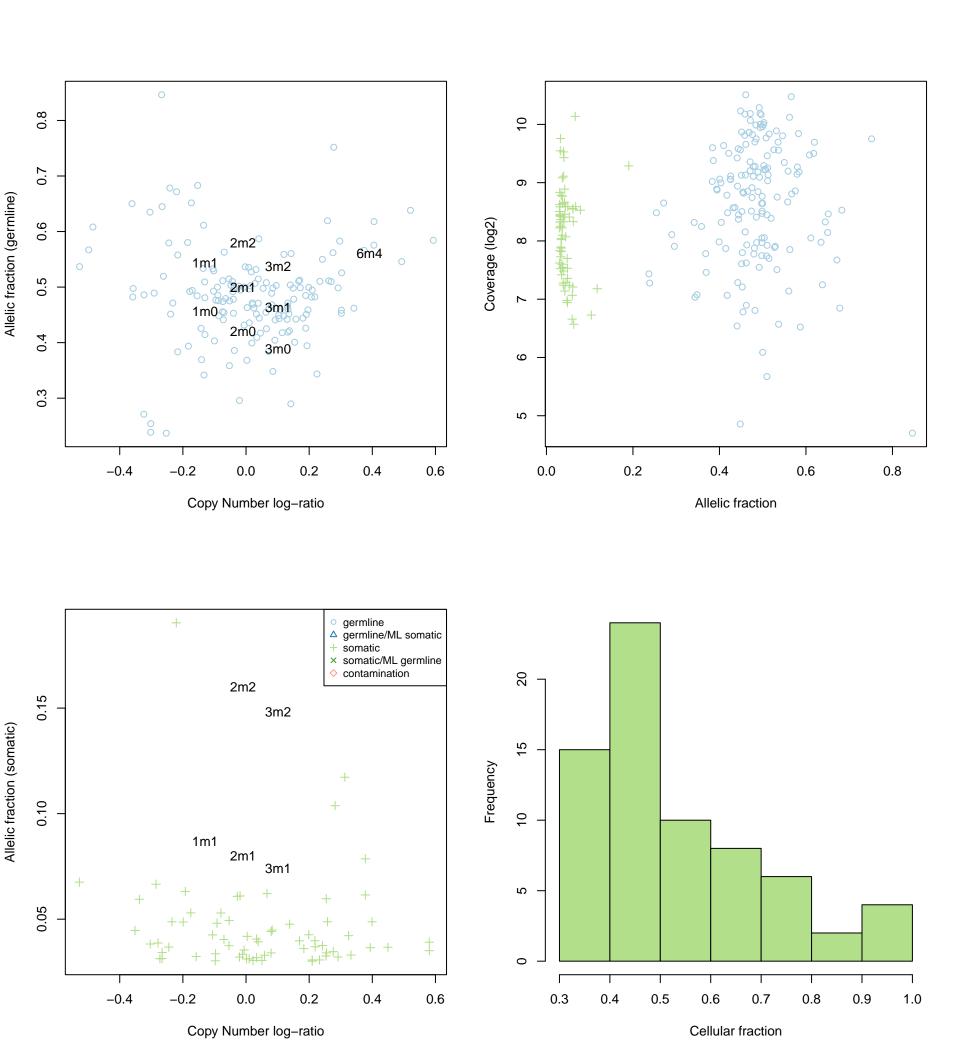




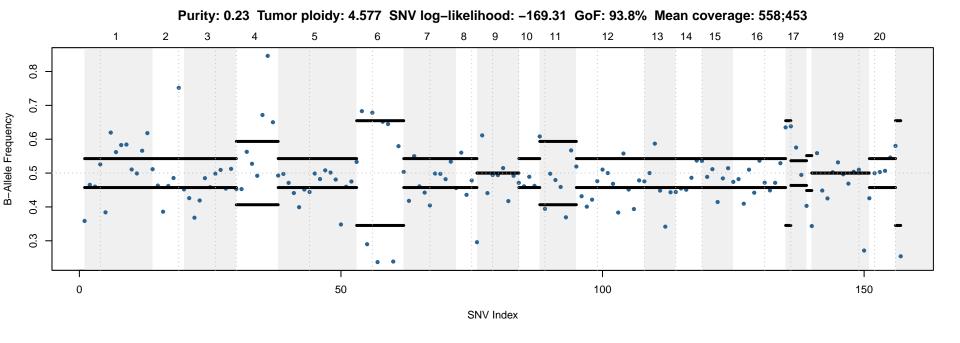
SCNA-fit log-likelihood: -13136.22



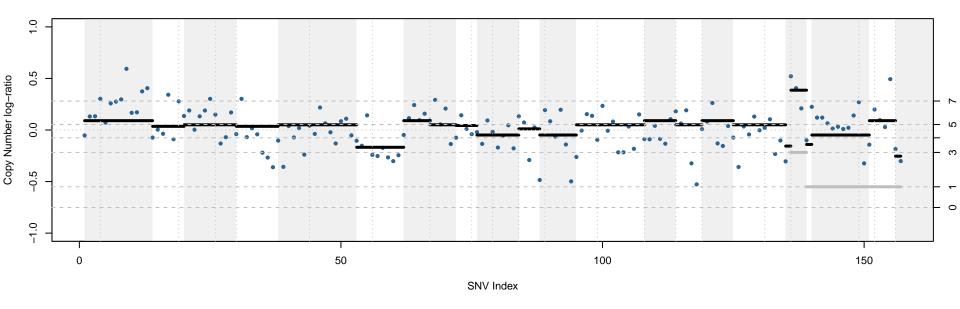


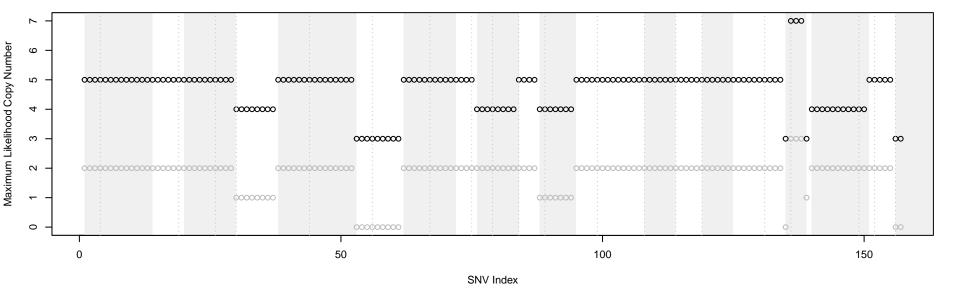


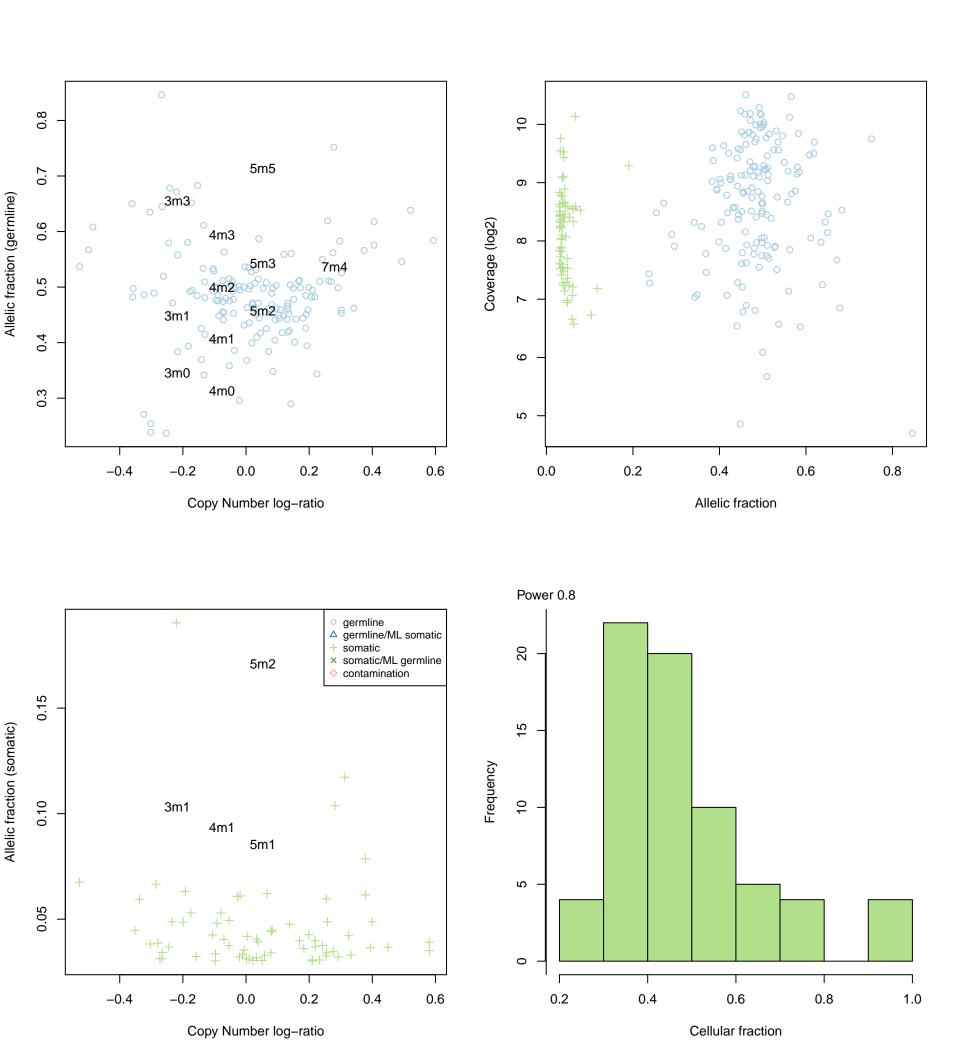
Purity: 0.23 Tumor ploidy: 4.577 0 7 3 5 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -0.8 -0.6 -0.4 -0.2 0.0 0.2 0.4 log2 ratio



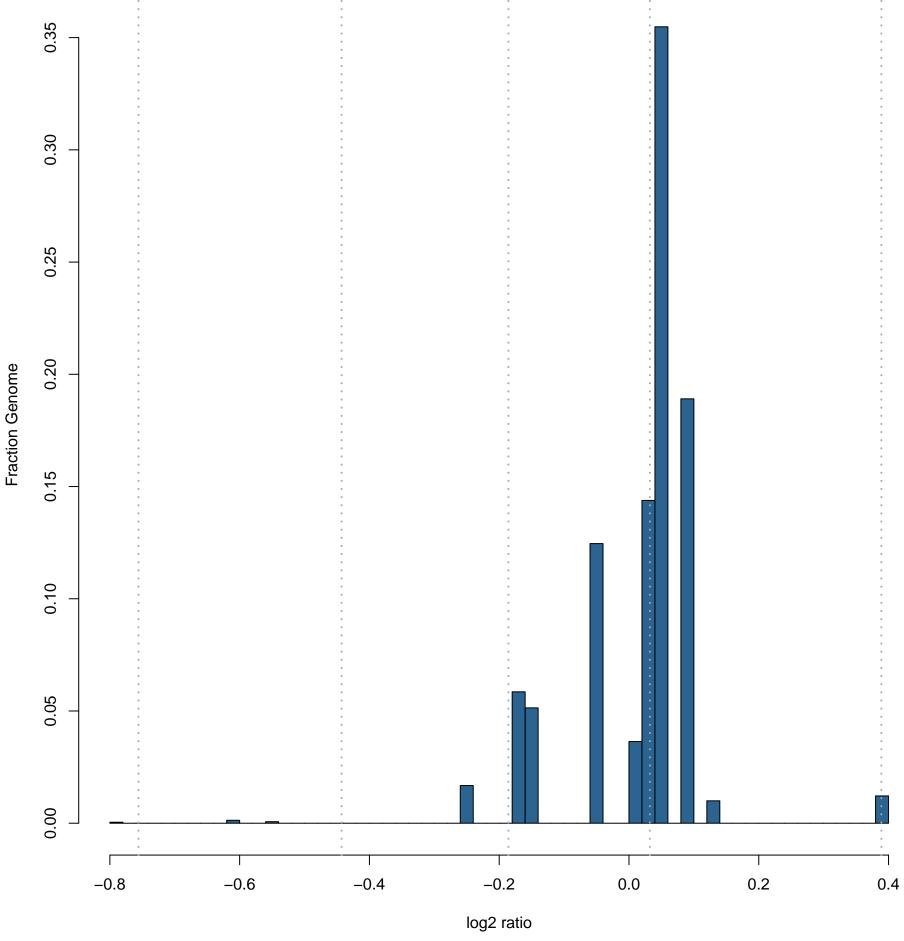
SCNA-fit log-likelihood: -13078.37

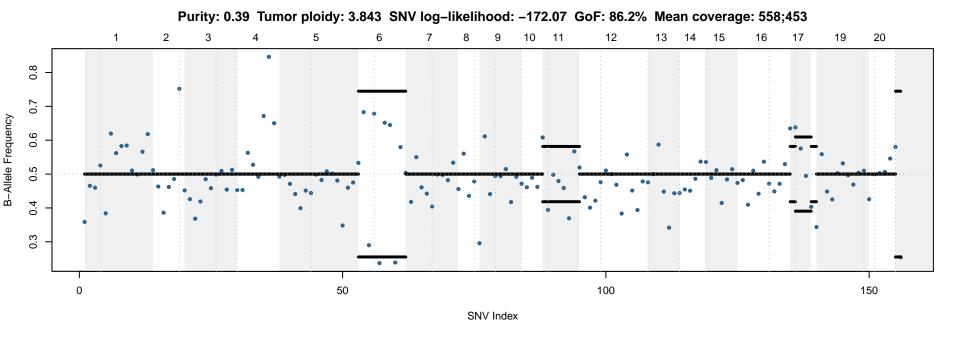




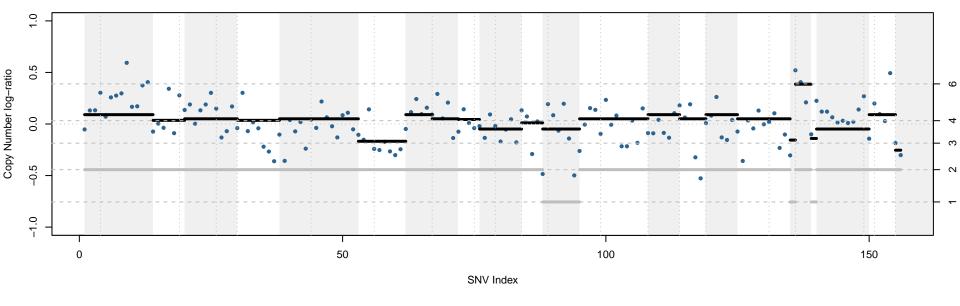


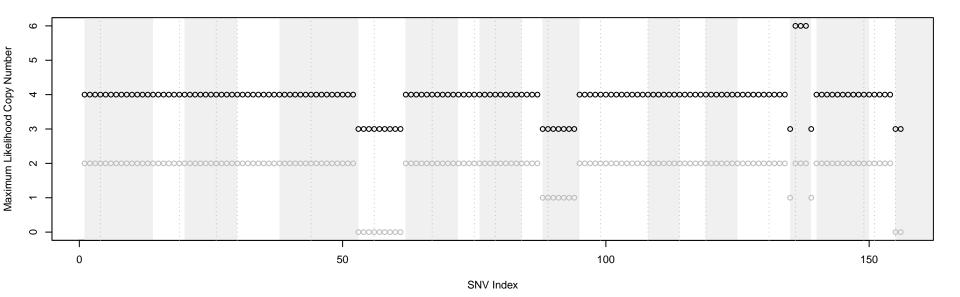
Purity: 0.39 Tumor ploidy: 3.843

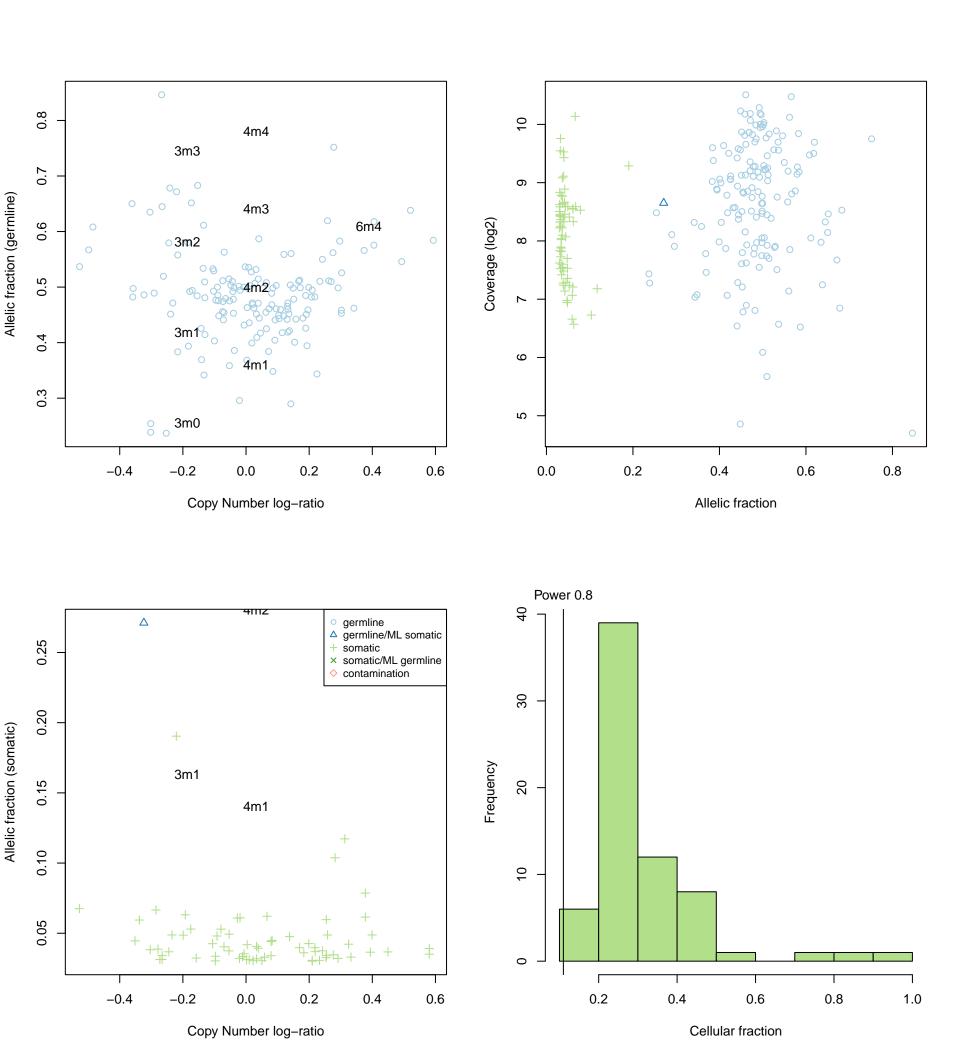




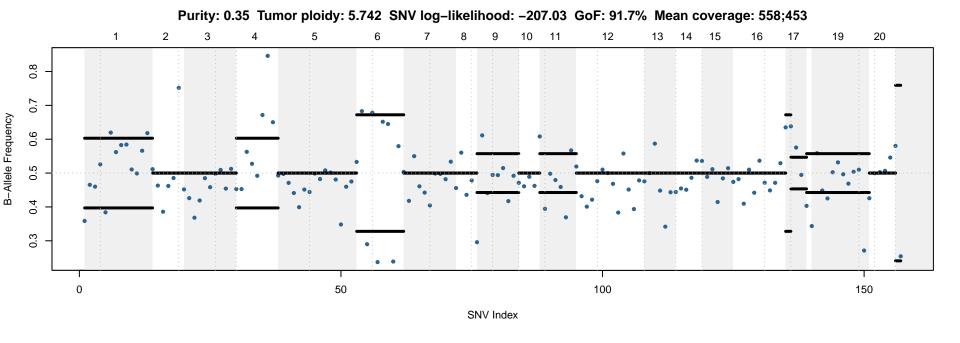
SCNA-fit log-likelihood: -13116.32



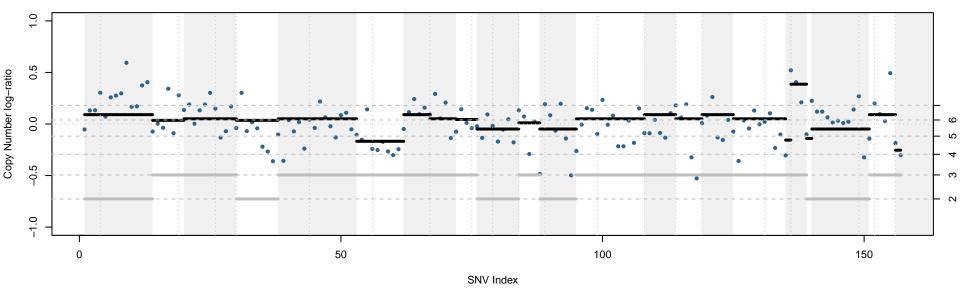


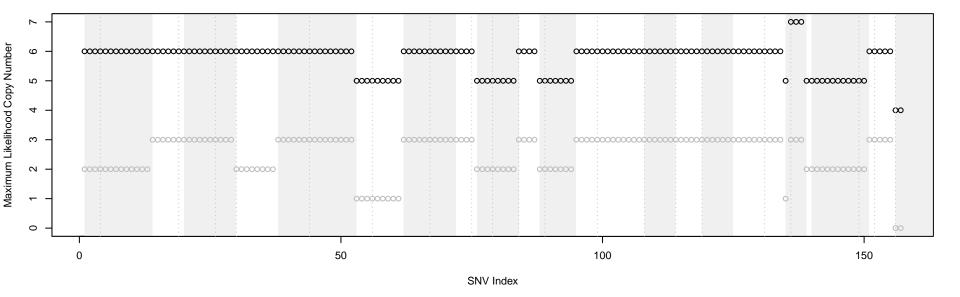


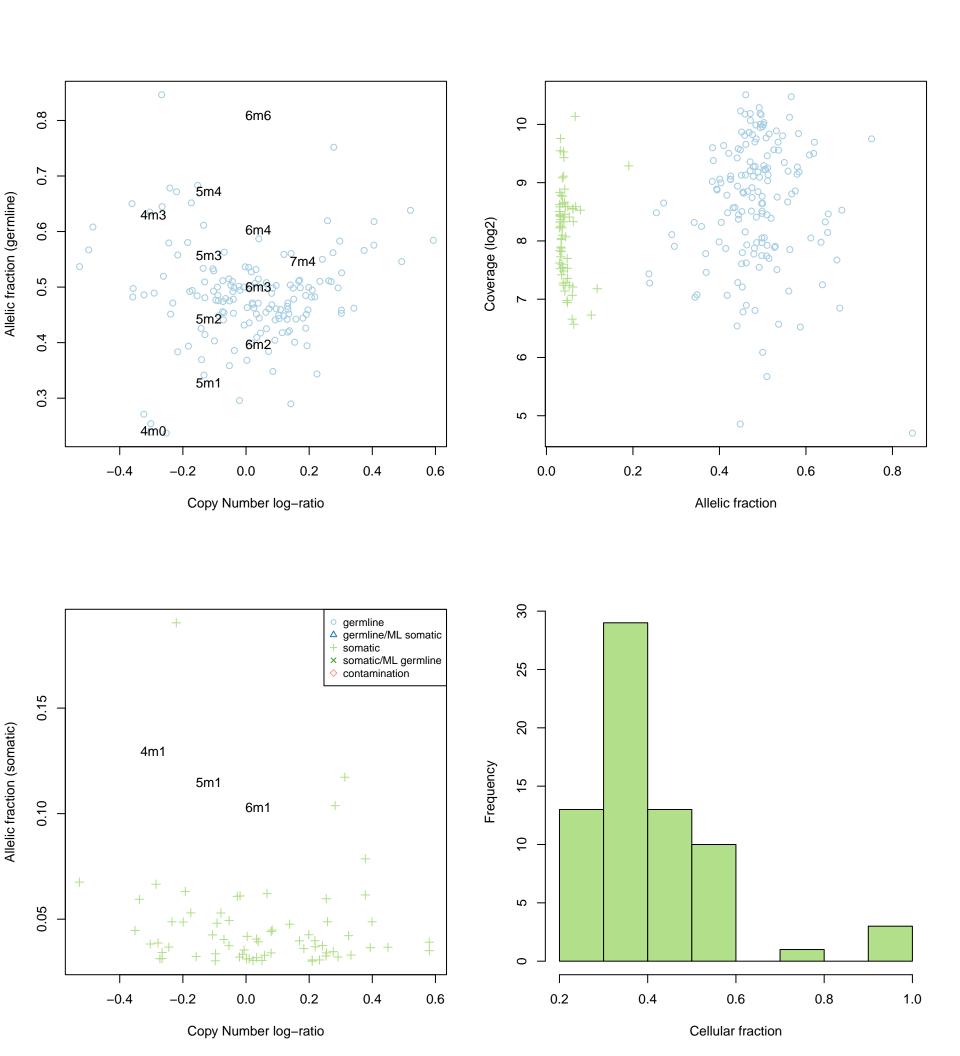
Purity: 0.35 Tumor ploidy: 5.742 2 5 6 7 3 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -0.2 -0.8 -0.6 -0.4 0.0 0.2 0.4 log2 ratio



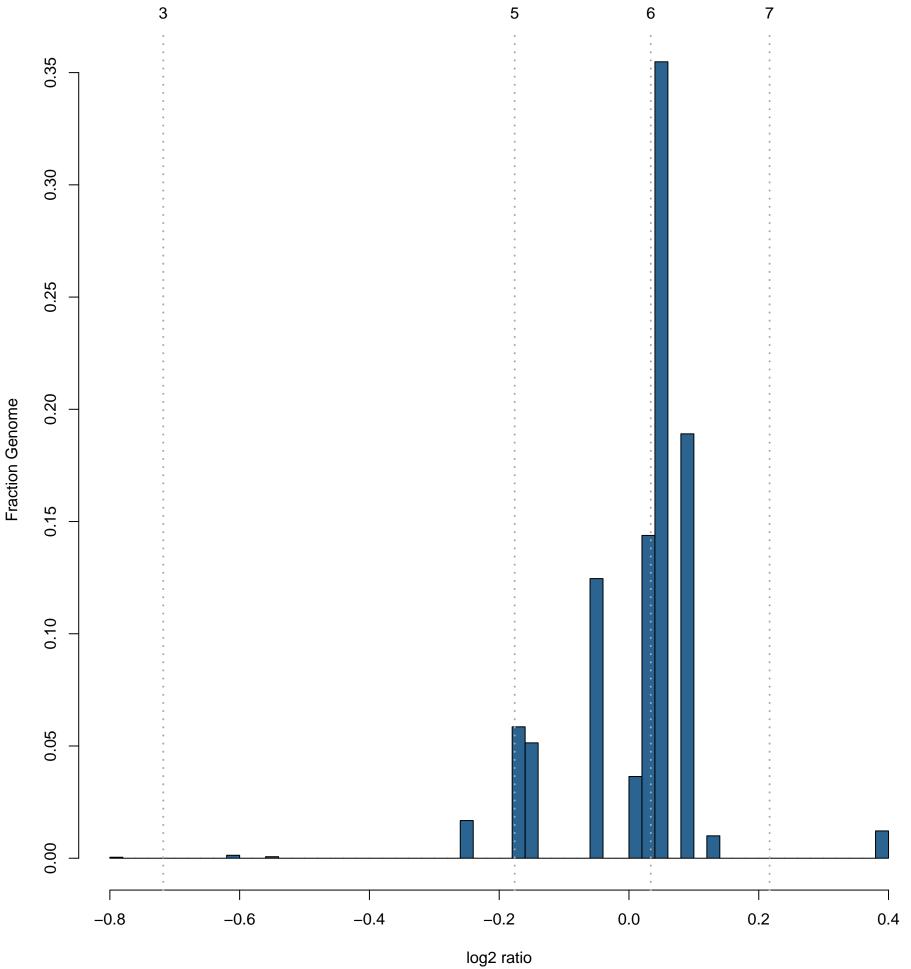
SCNA-fit log-likelihood: -13111.54

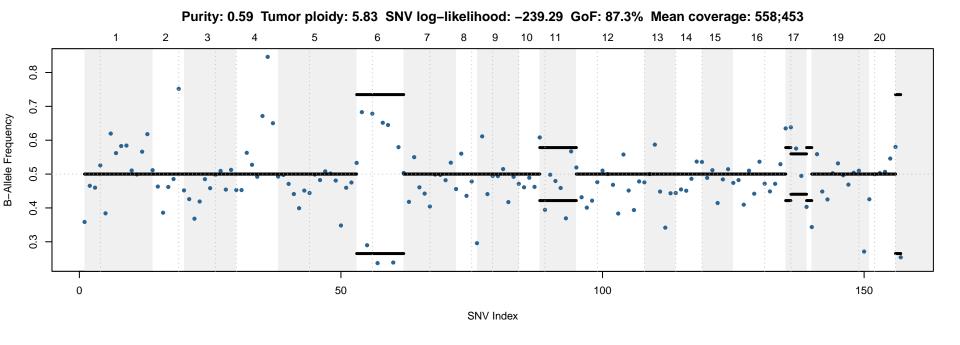




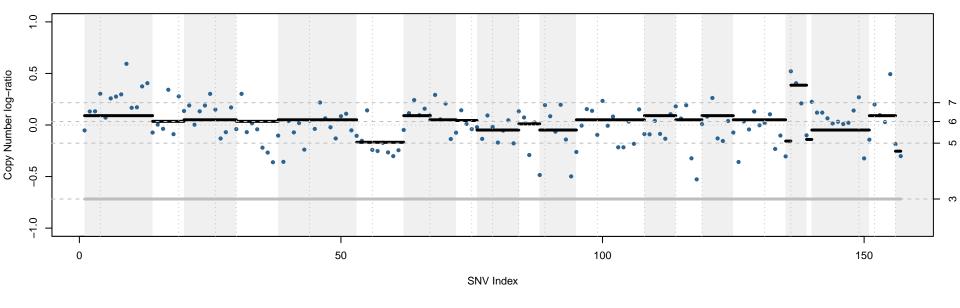


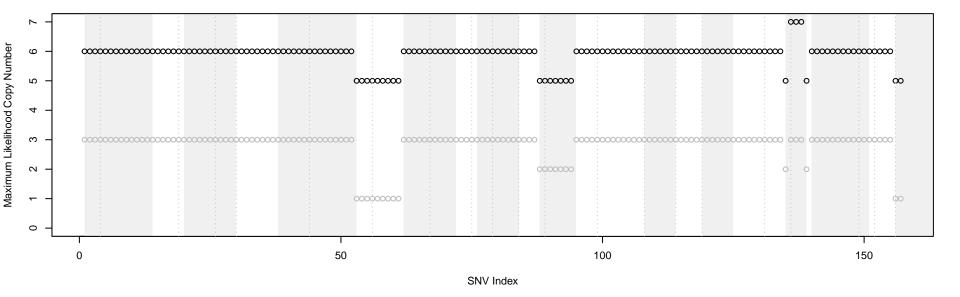
Purity: 0.59 Tumor ploidy: 5.83

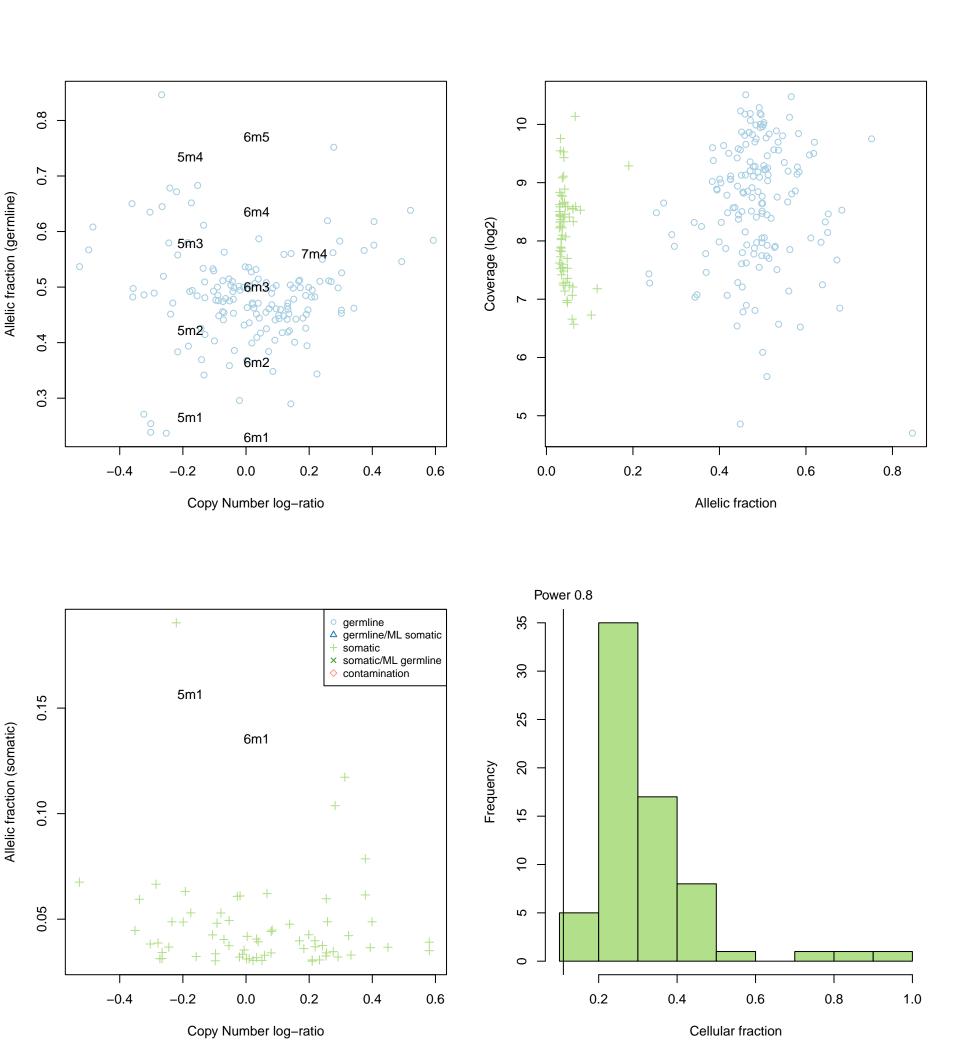




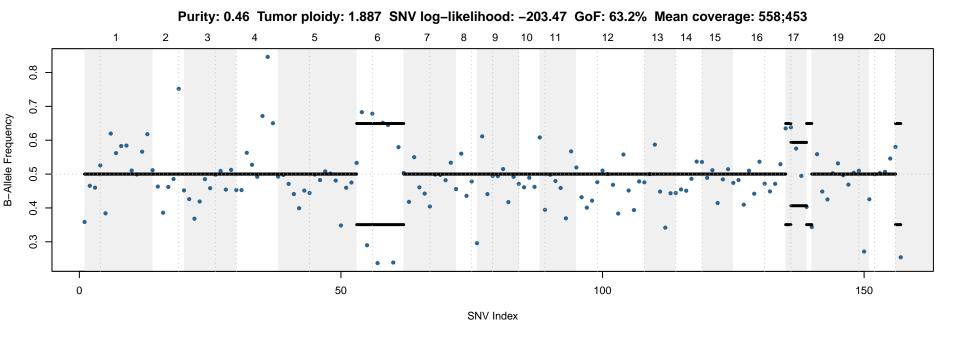
SCNA-fit log-likelihood: -13125.68



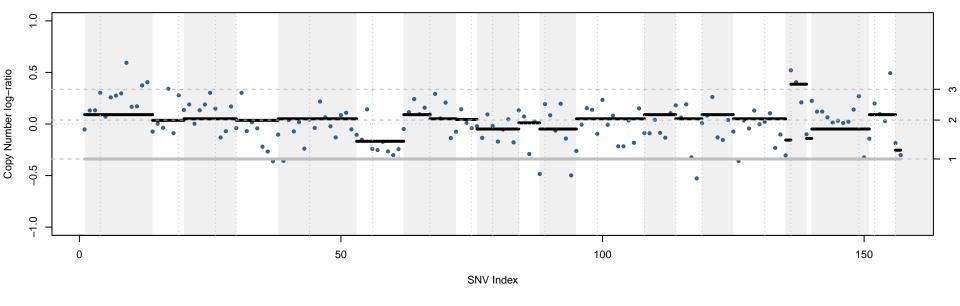


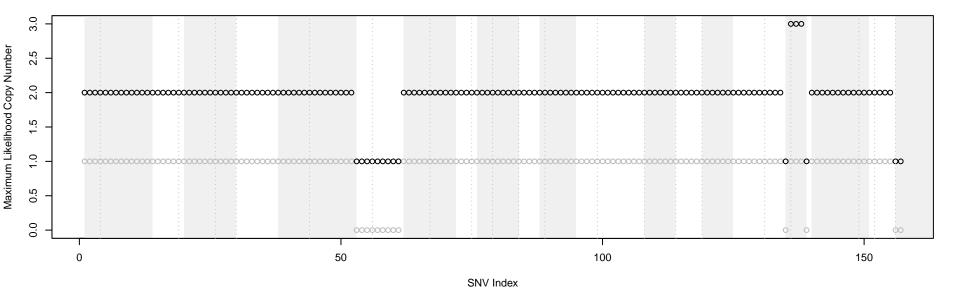


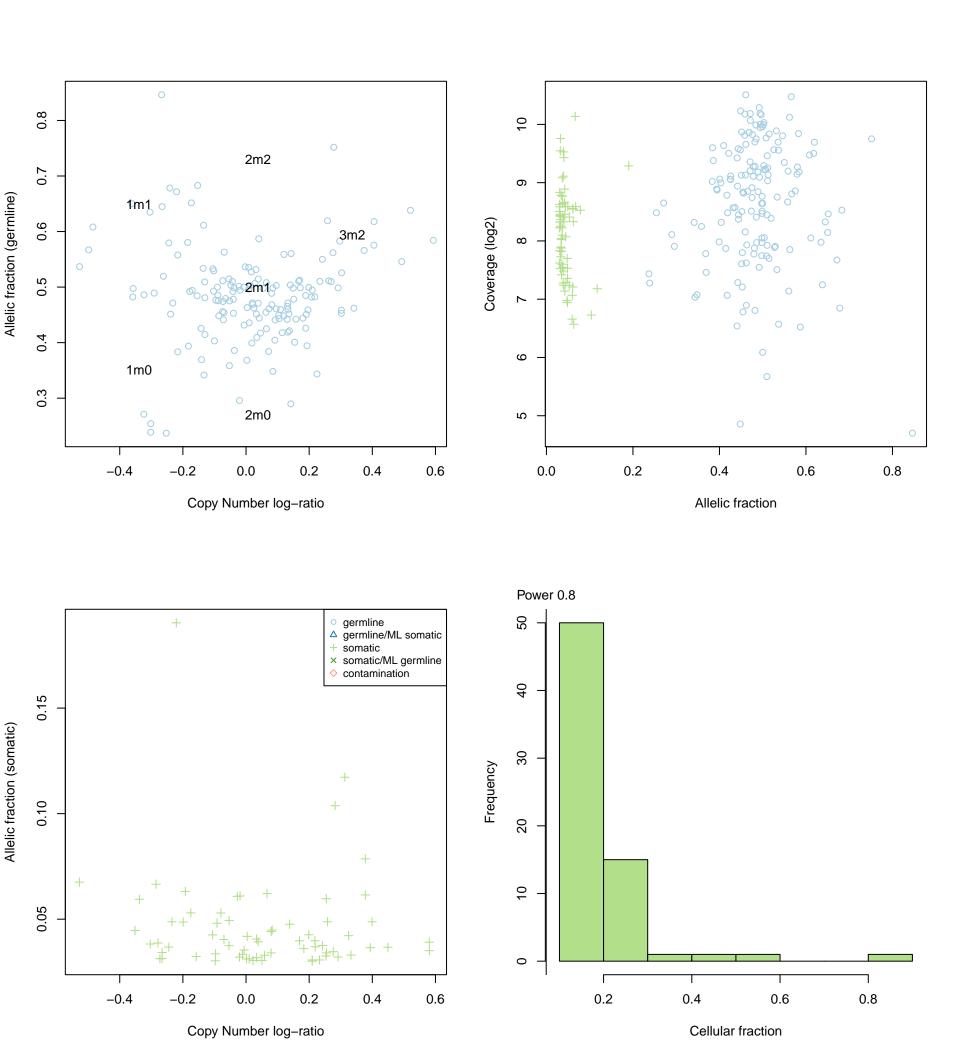
Purity: 0.46 Tumor ploidy: 1.887 3 1 0.30 0.25 0.20 Fraction Genome 0.05 0.00 -0.2 -0.6 -0.4 0.0 0.2 0.4 log2 ratio



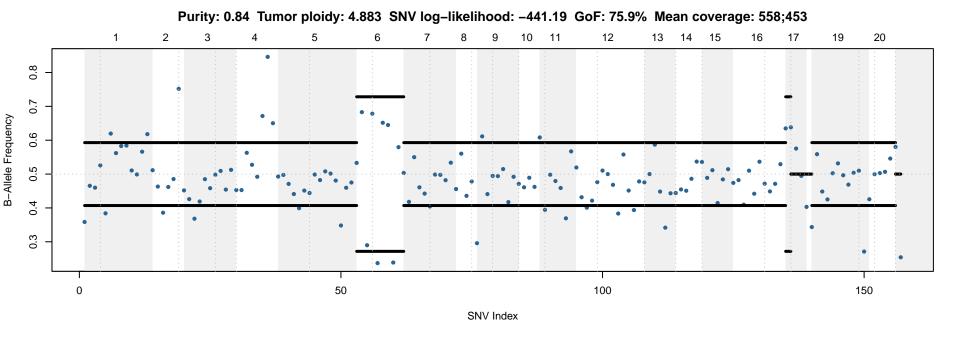
SCNA-fit log-likelihood: -13267.23



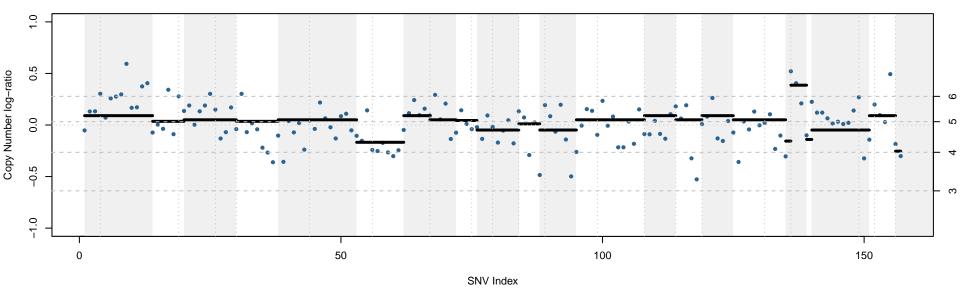


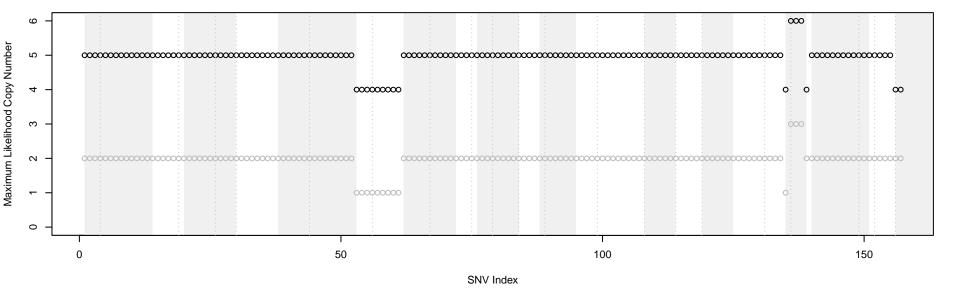


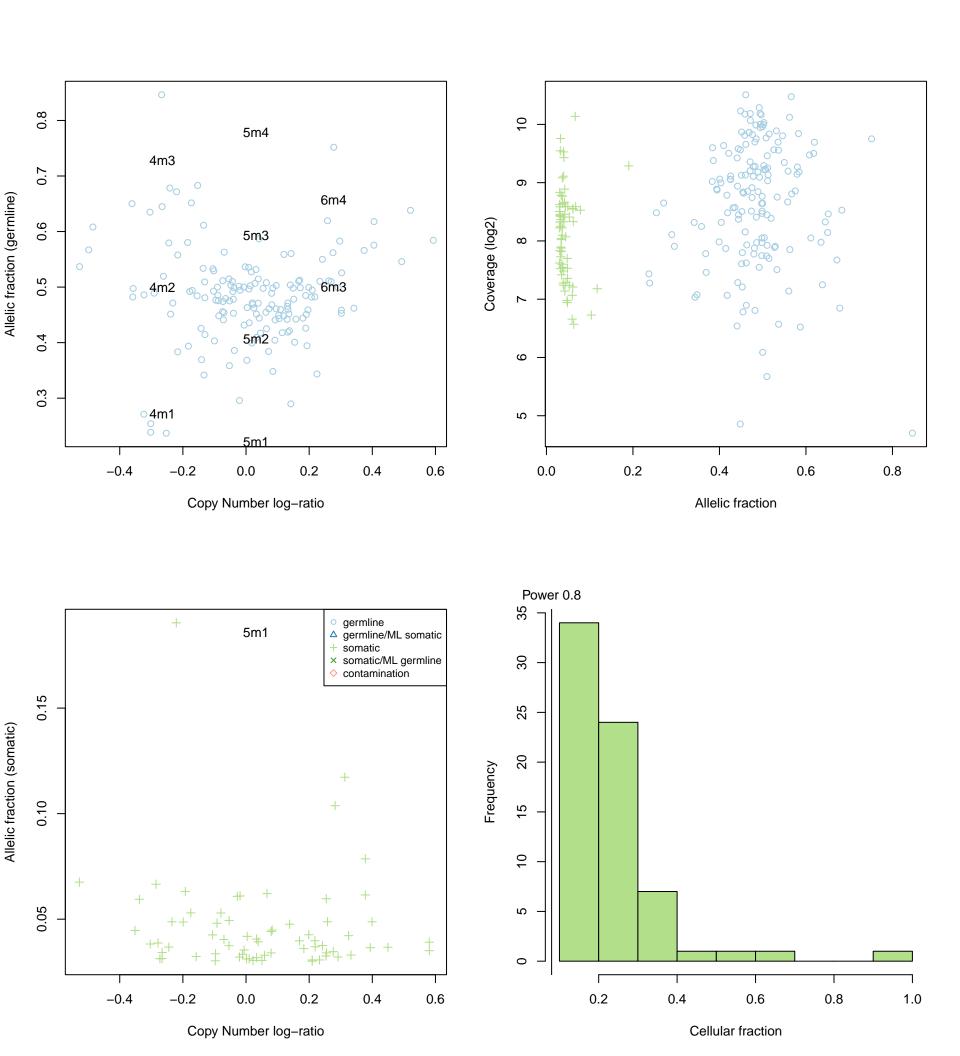
Purity: 0.84 Tumor ploidy: 4.883 5 3 6 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -0.2 -0.8 -0.6 -0.4 0.0 0.2 0.4 log2 ratio



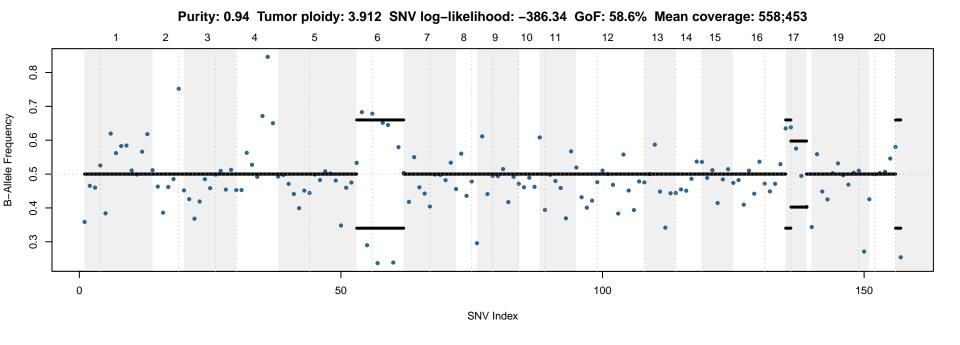
SCNA-fit log-likelihood: -13162.22



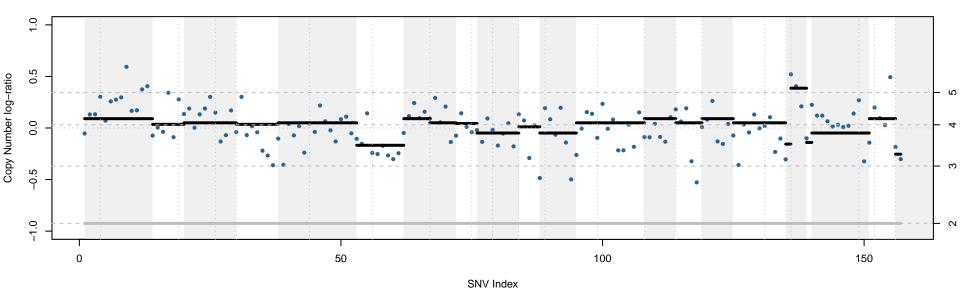


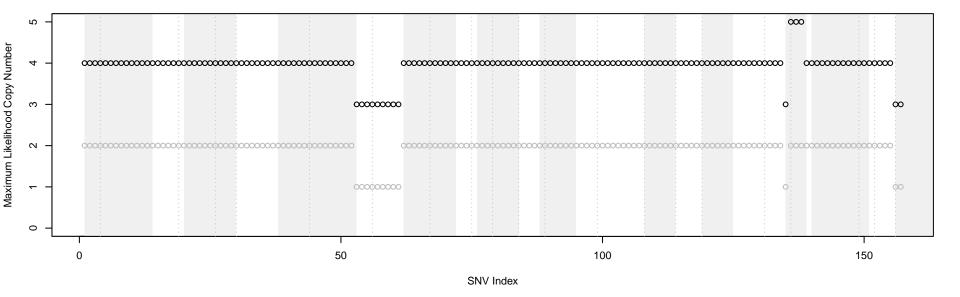


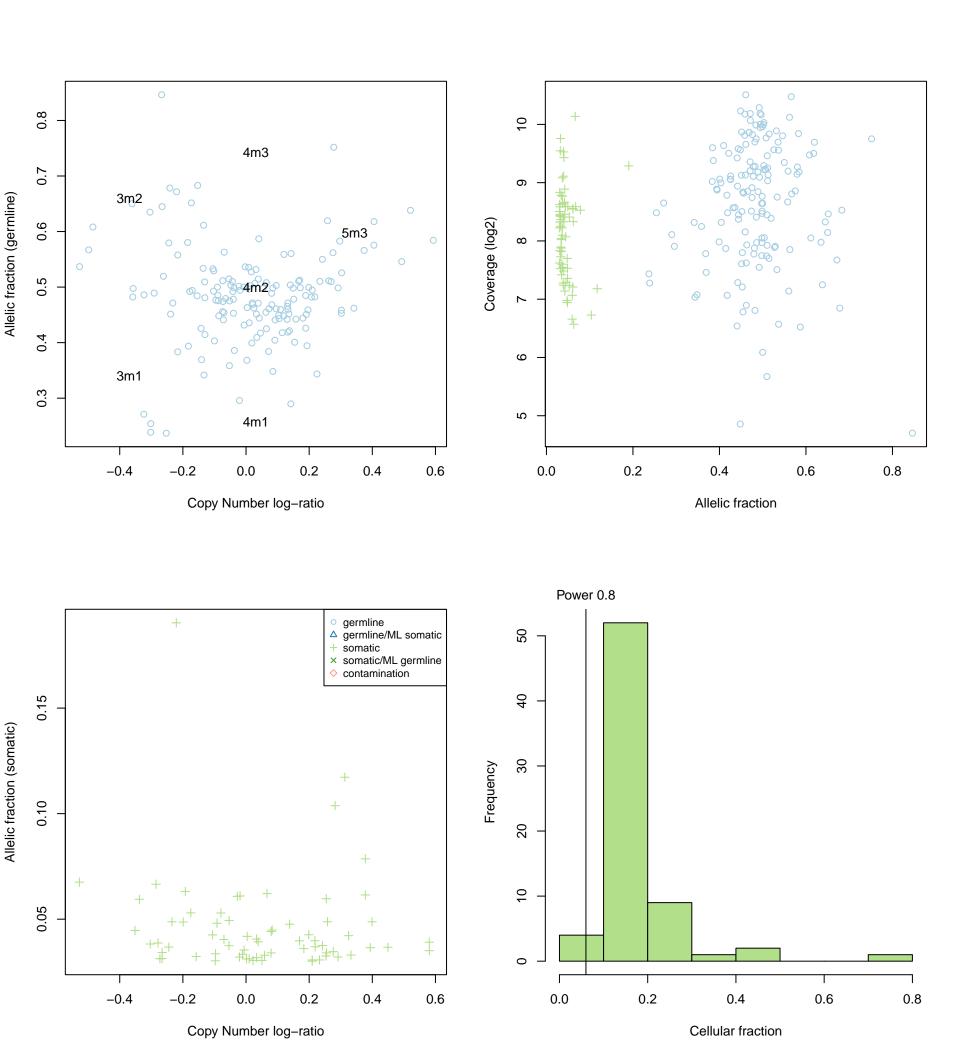
Purity: 0.94 Tumor ploidy: 3.912 3 5 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -0.8 -0.6 -0.4 -0.2 0.0 0.2 0.4 log2 ratio



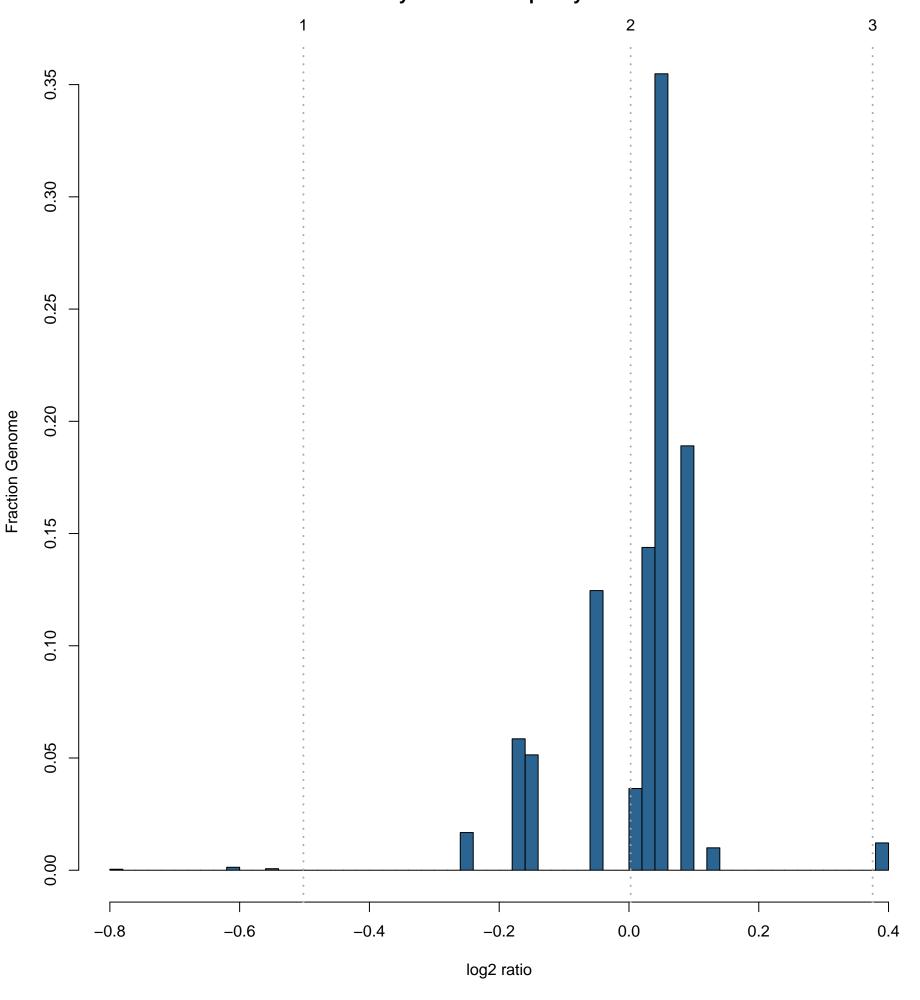
SCNA-fit log-likelihood: -13310.01

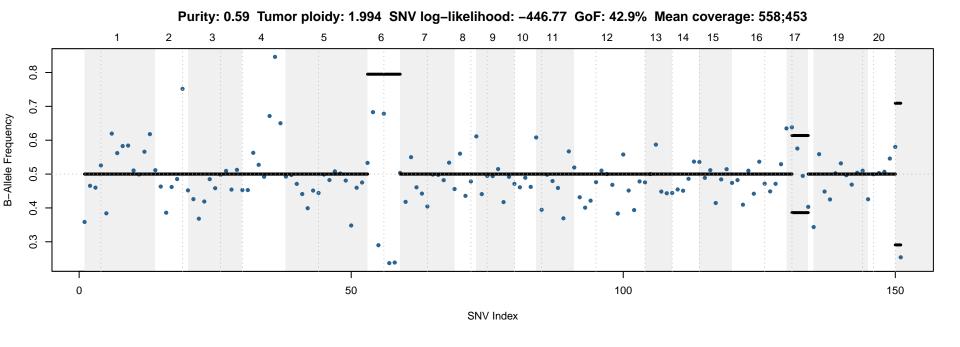




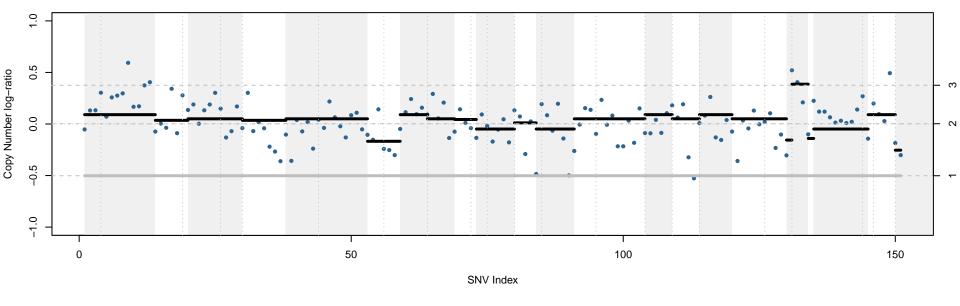


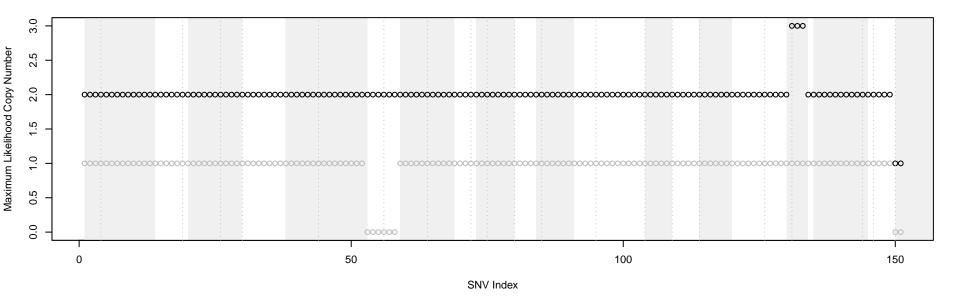
Purity: 0.59 Tumor ploidy: 1.994

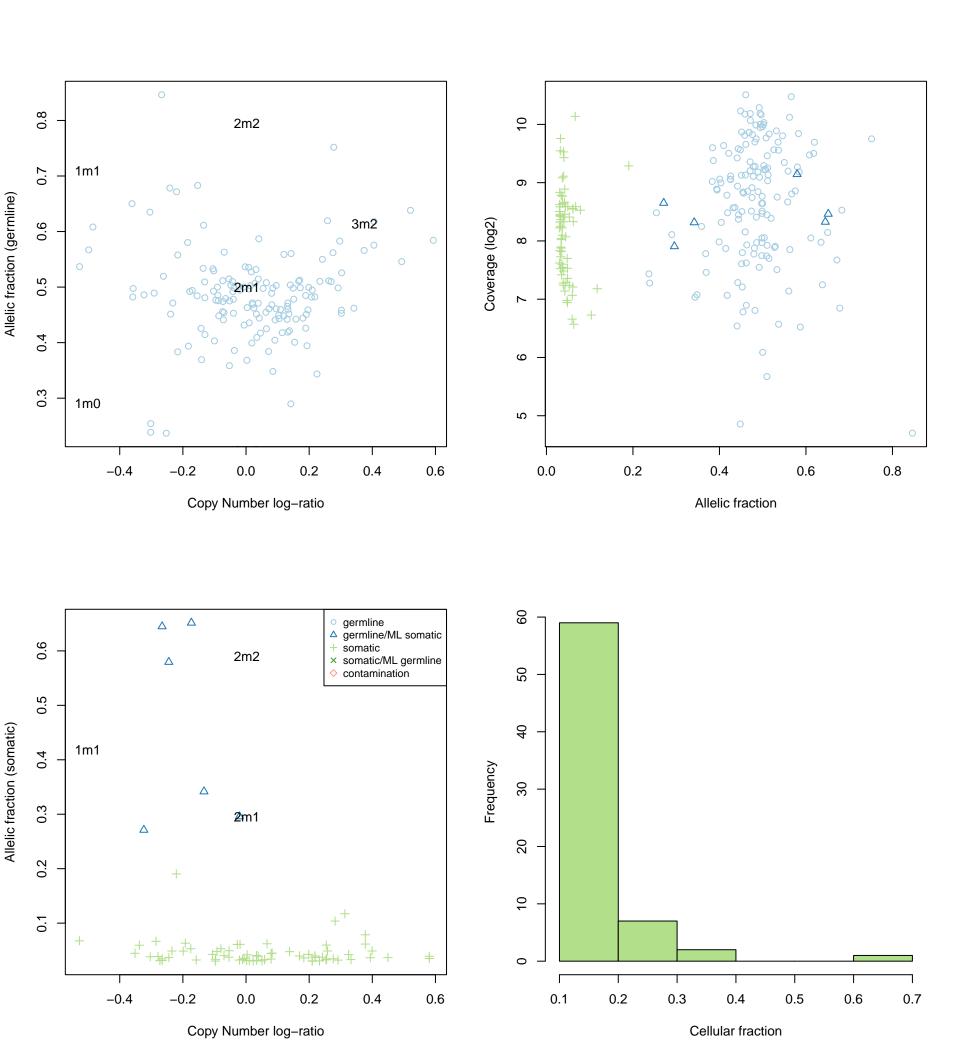




SCNA-fit log-likelihood: -13339.88

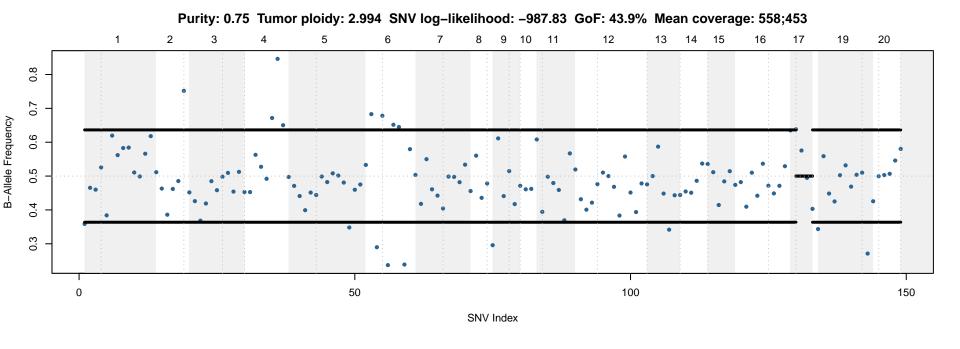




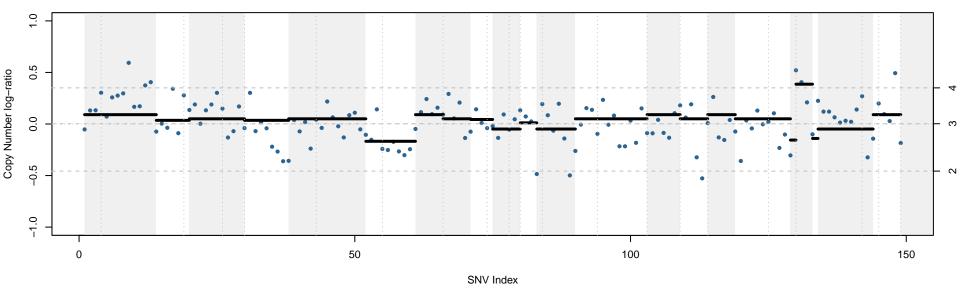


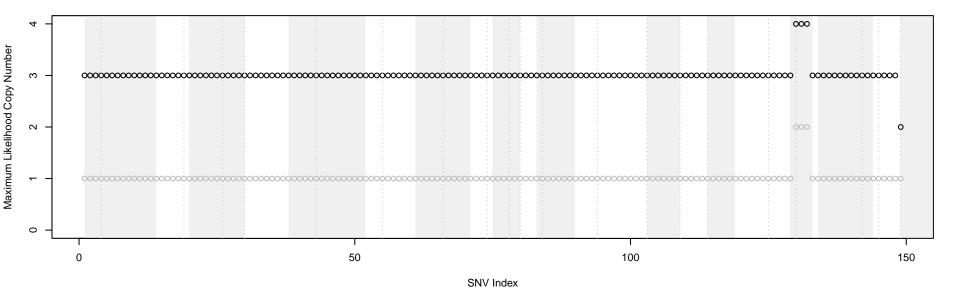
Purity: 0.75 Tumor ploidy: 2.994 2 3 4 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -0.8 -0.6 -0.4 -0.2 0.0 0.2 0.4

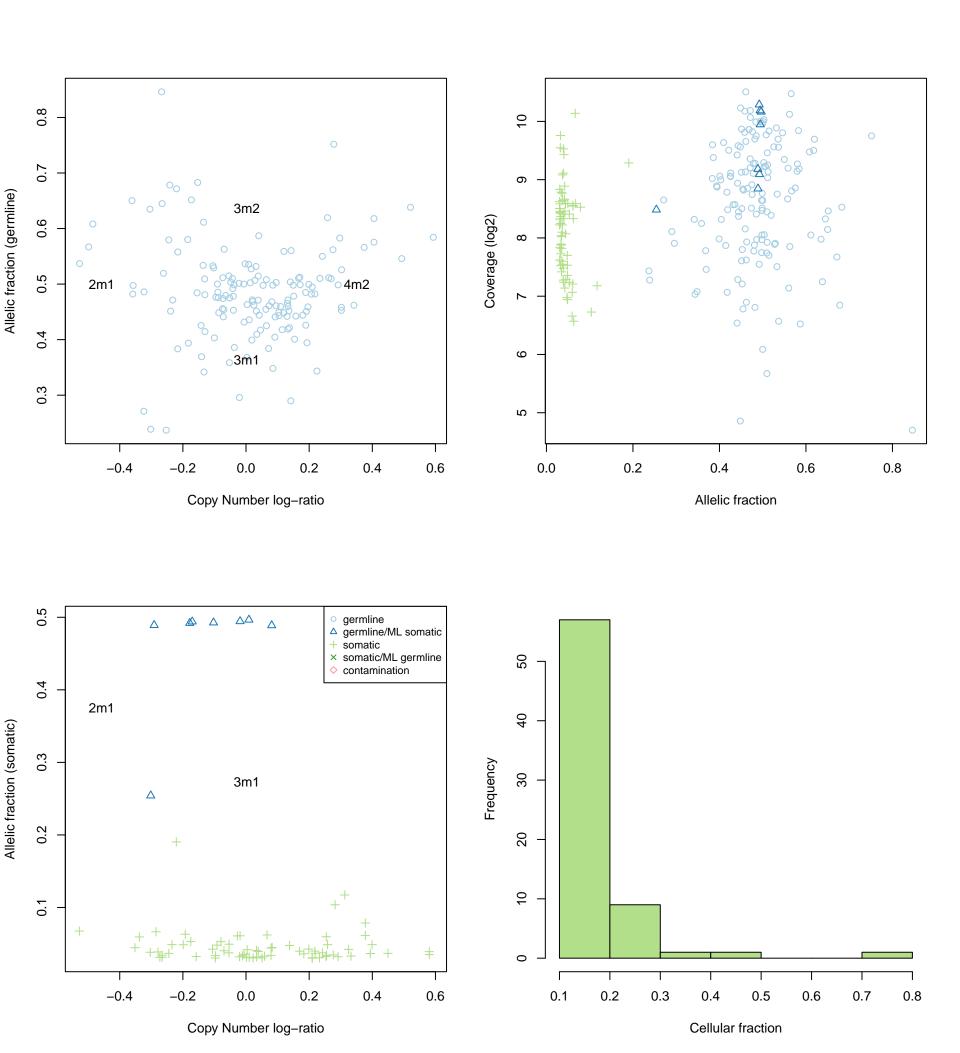
log2 ratio



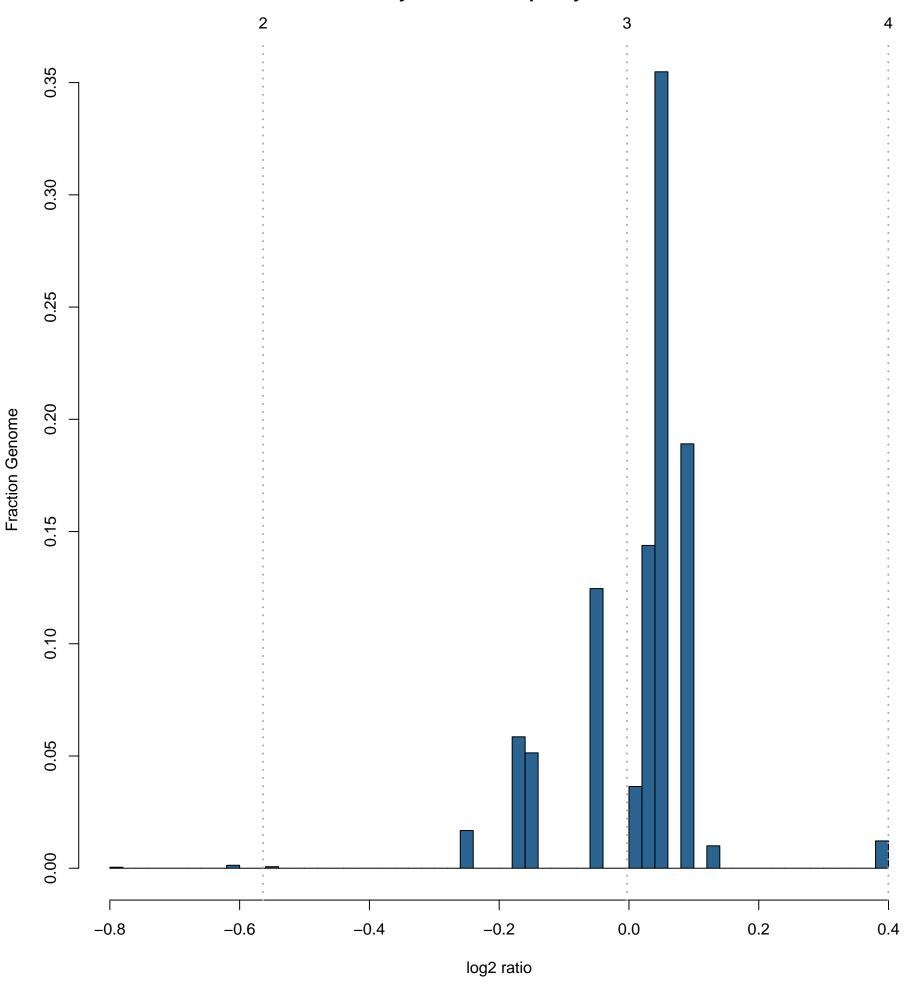
SCNA-fit log-likelihood: -13326.38

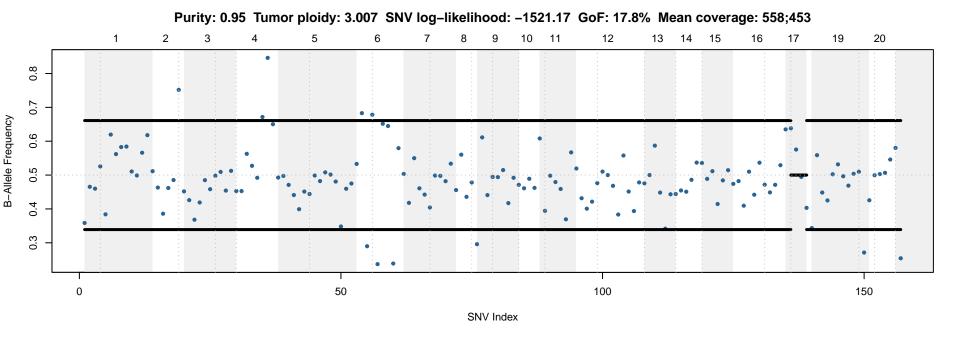






Purity: 0.95 Tumor ploidy: 3.007





SCNA-fit log-likelihood: -13354.4

