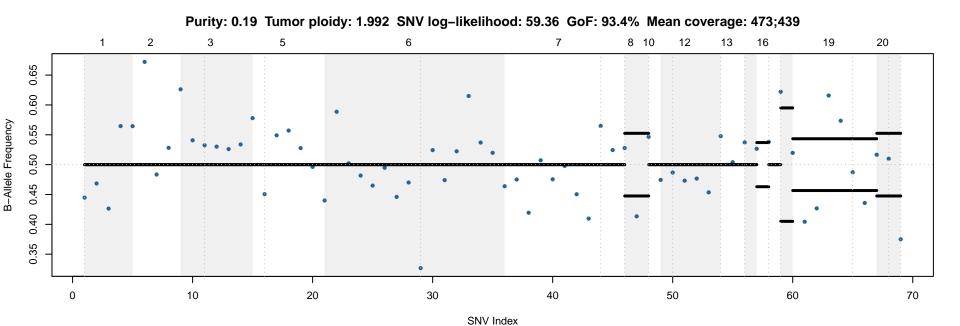
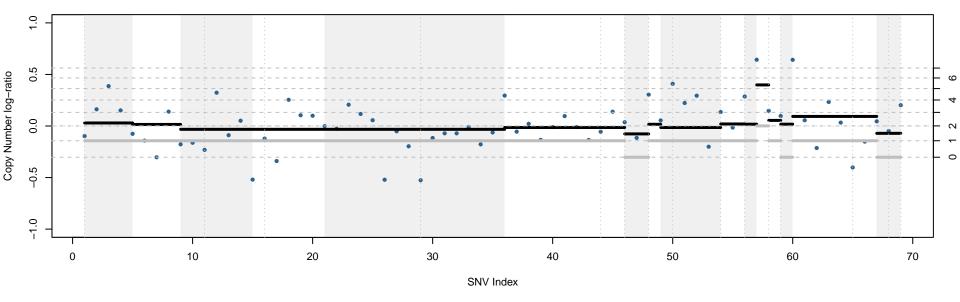
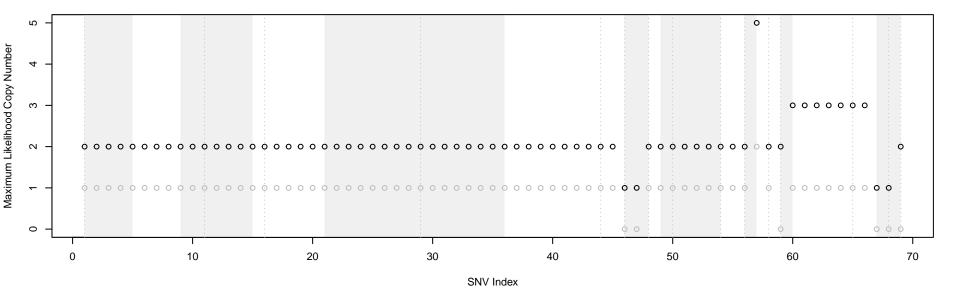
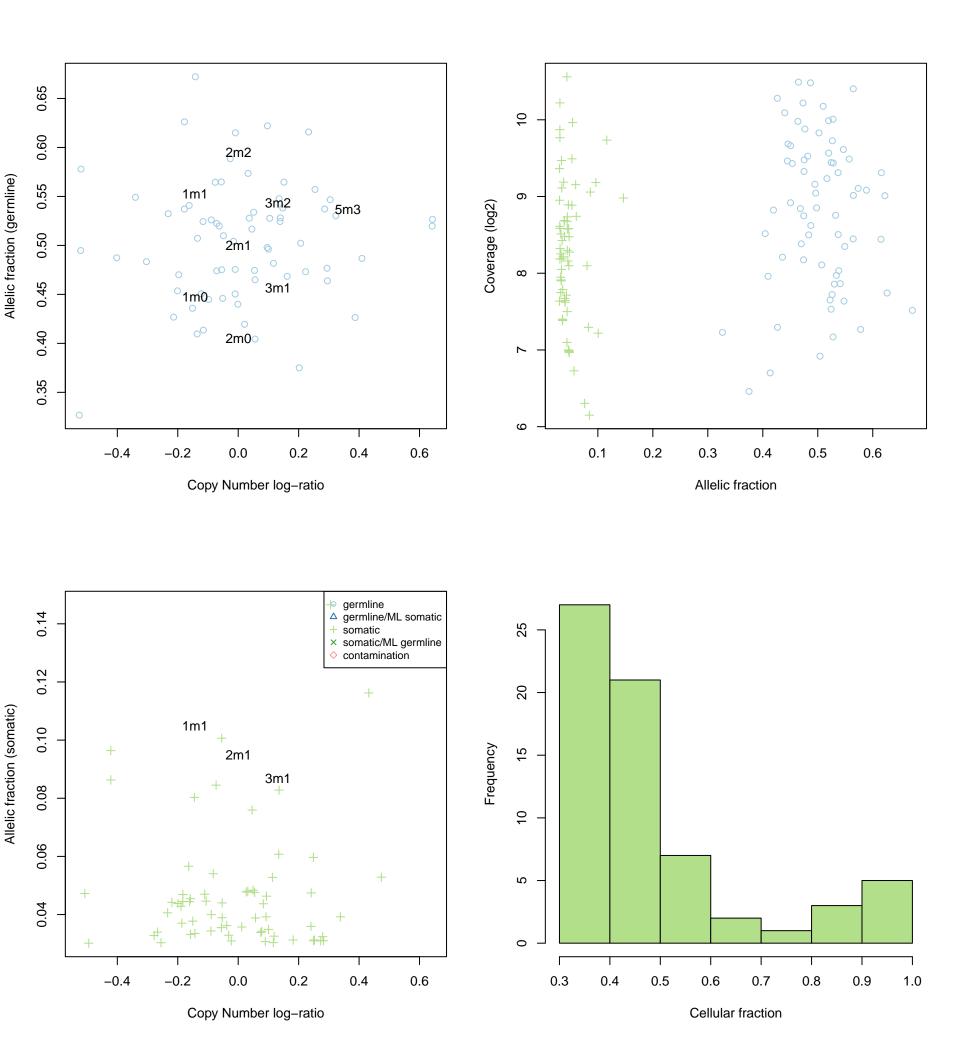
Purity: 0.19 Tumor ploidy: 1.992 3 2 5 6 0 Fraction Genome 0.10 0.05 0.00 -0.4 -0.2 0.0 0.2 0.4 0.6 8.0 log2 ratio



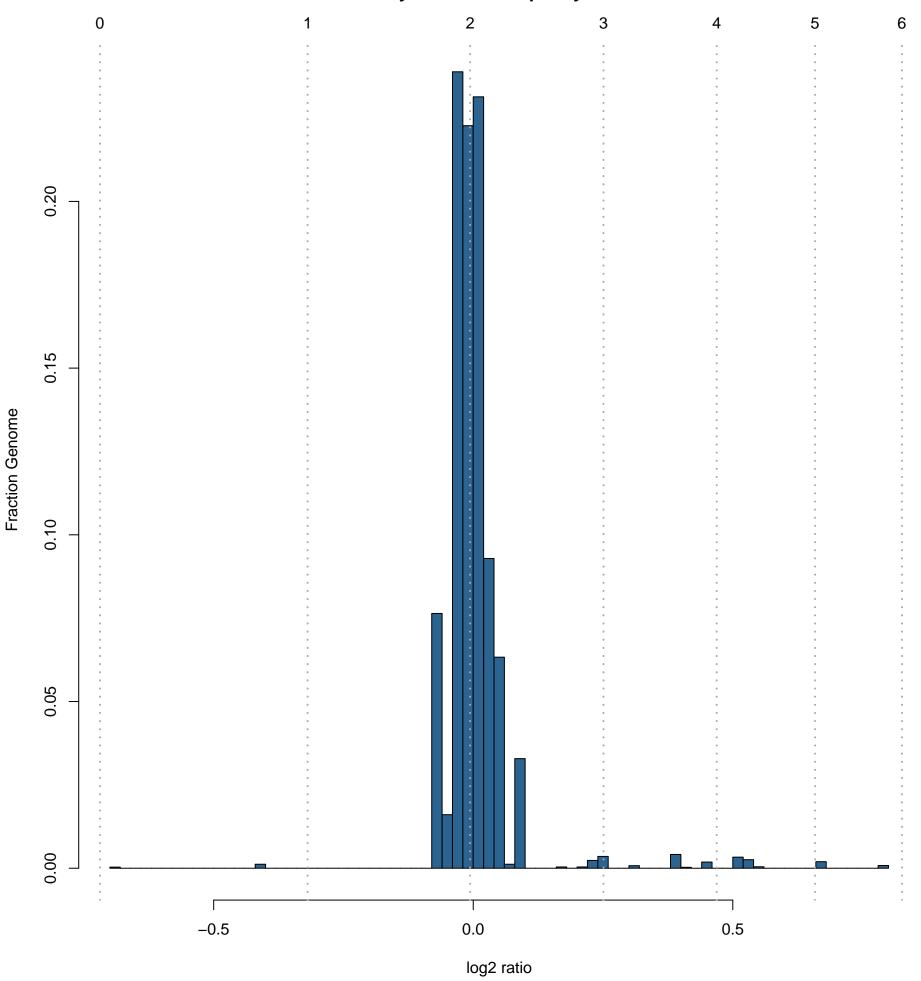
SCNA-fit log-likelihood: -6223.12

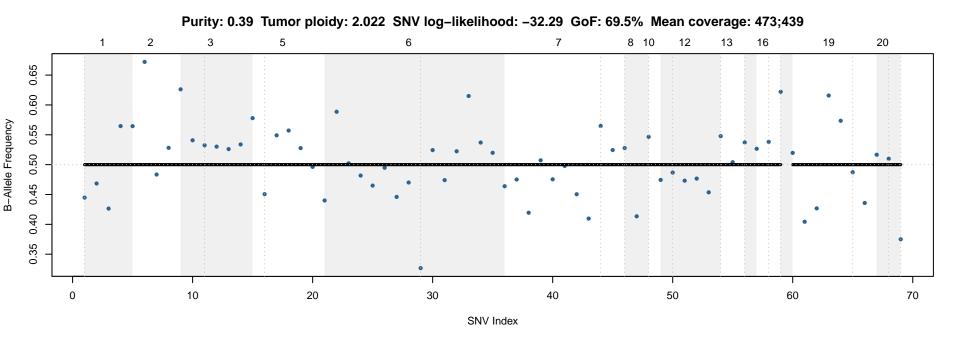




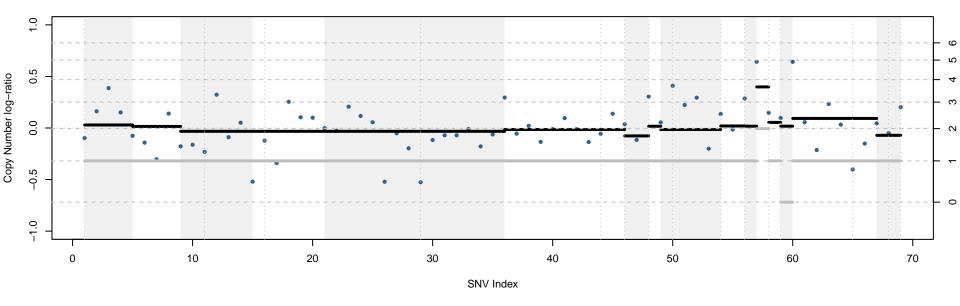


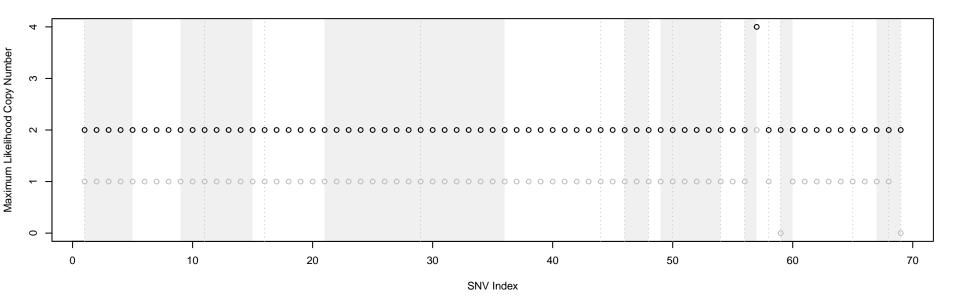
Purity: 0.39 Tumor ploidy: 2.022

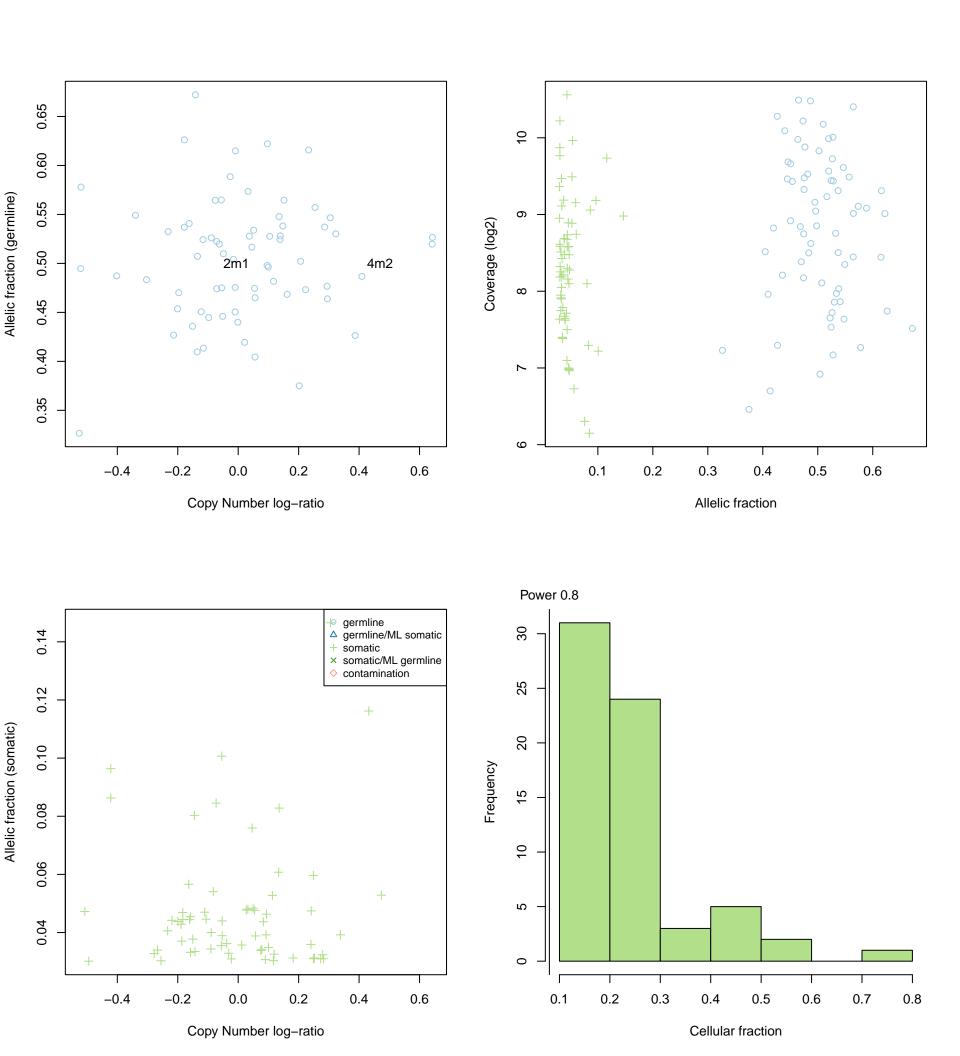




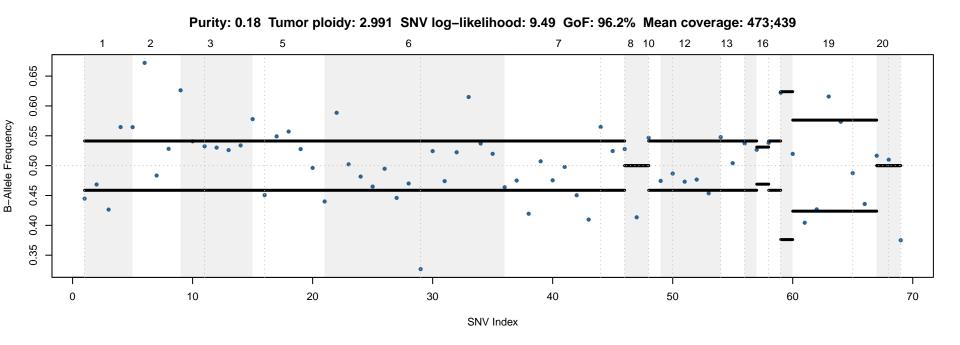
SCNA-fit log-likelihood: -6201.6



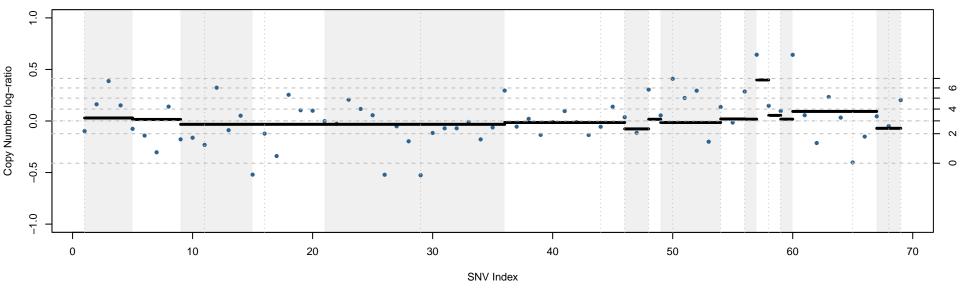


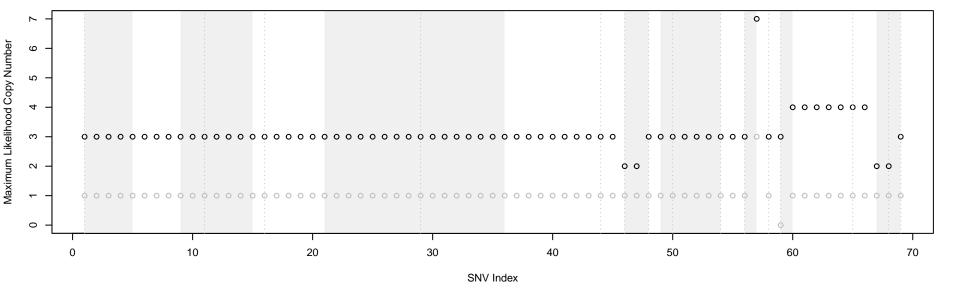


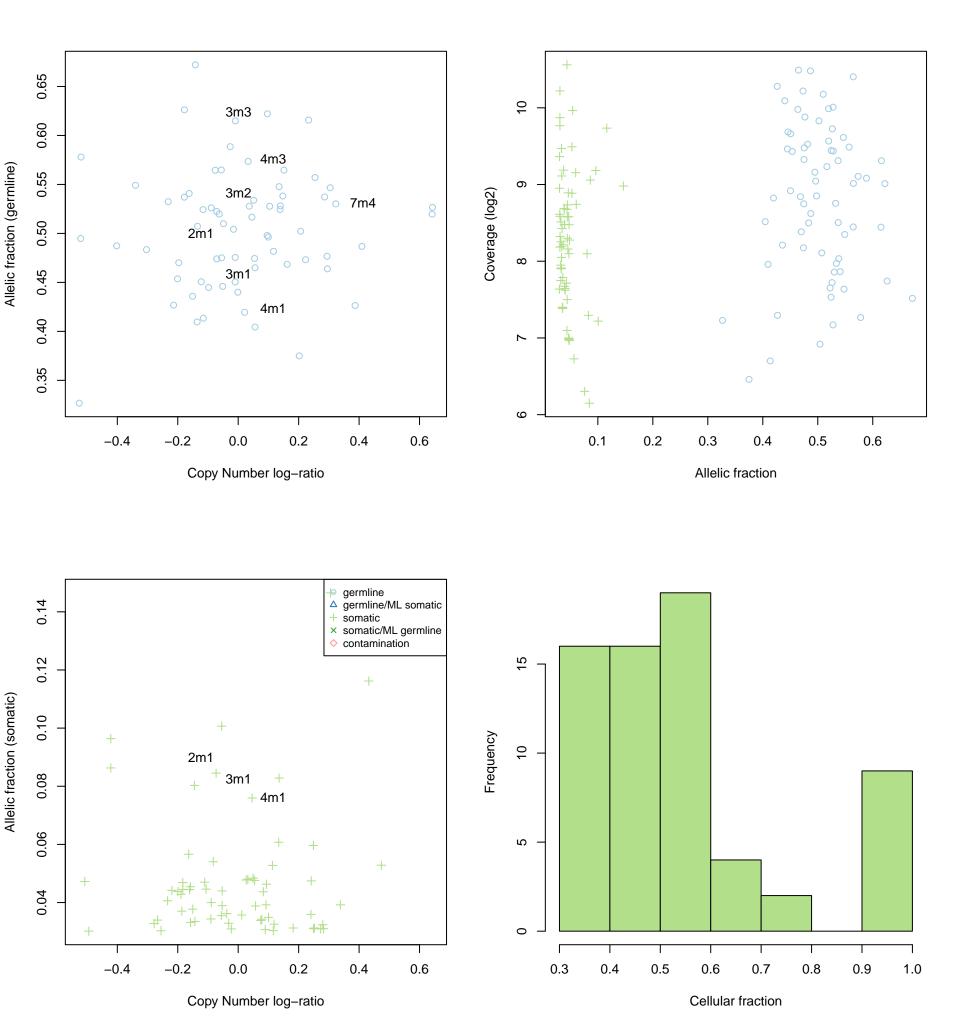
Purity: 0.18 Tumor ploidy: 2.991 3 0 7 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 log2 ratio



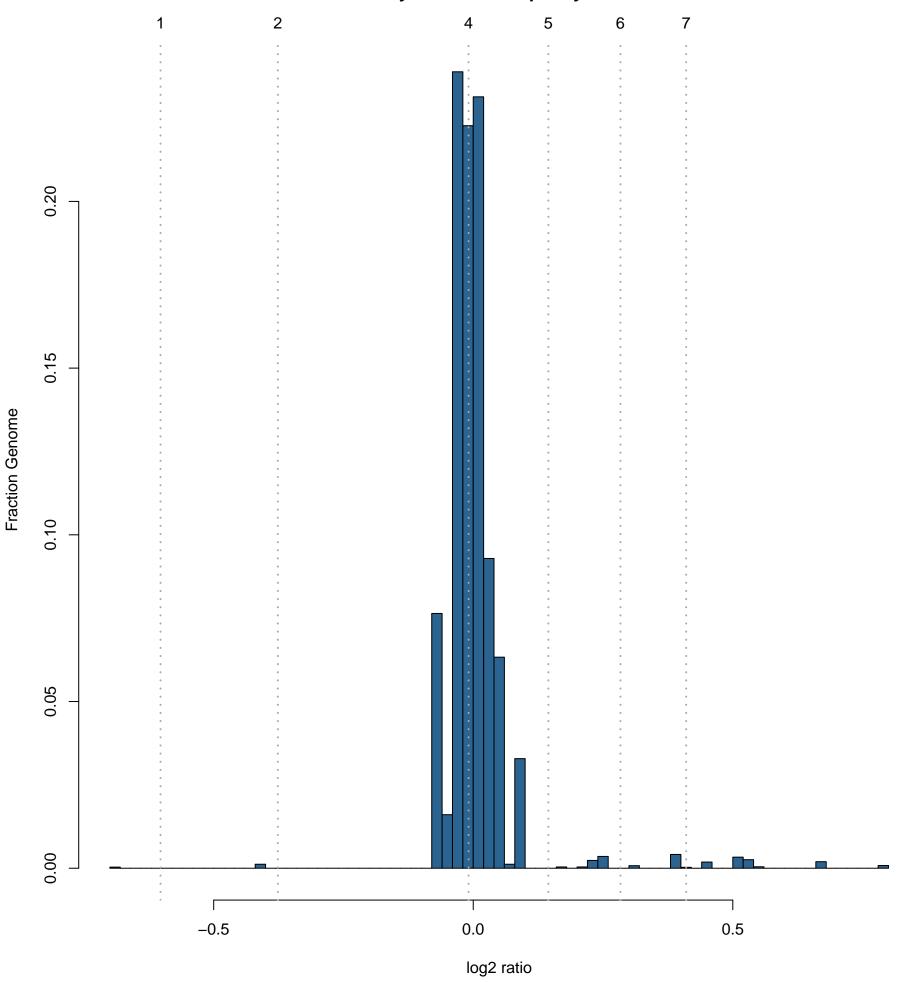
SCNA-fit log-likelihood: -6248.99

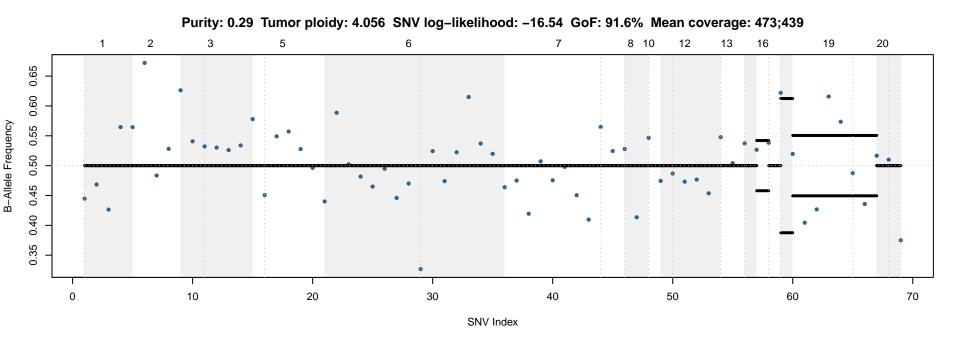




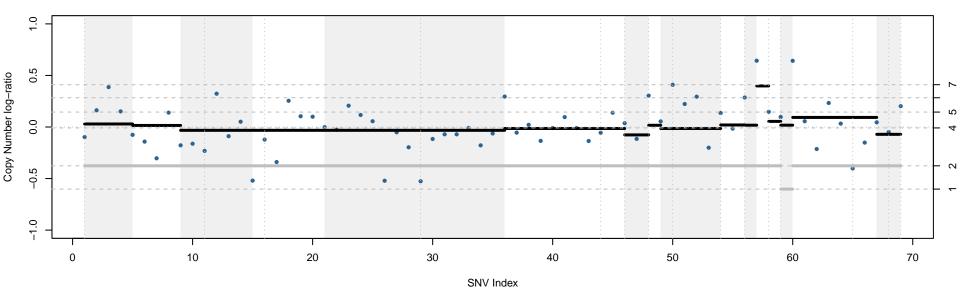


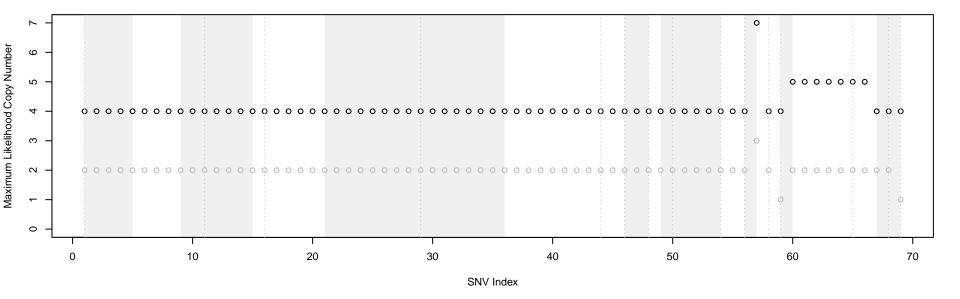
Purity: 0.29 Tumor ploidy: 4.056

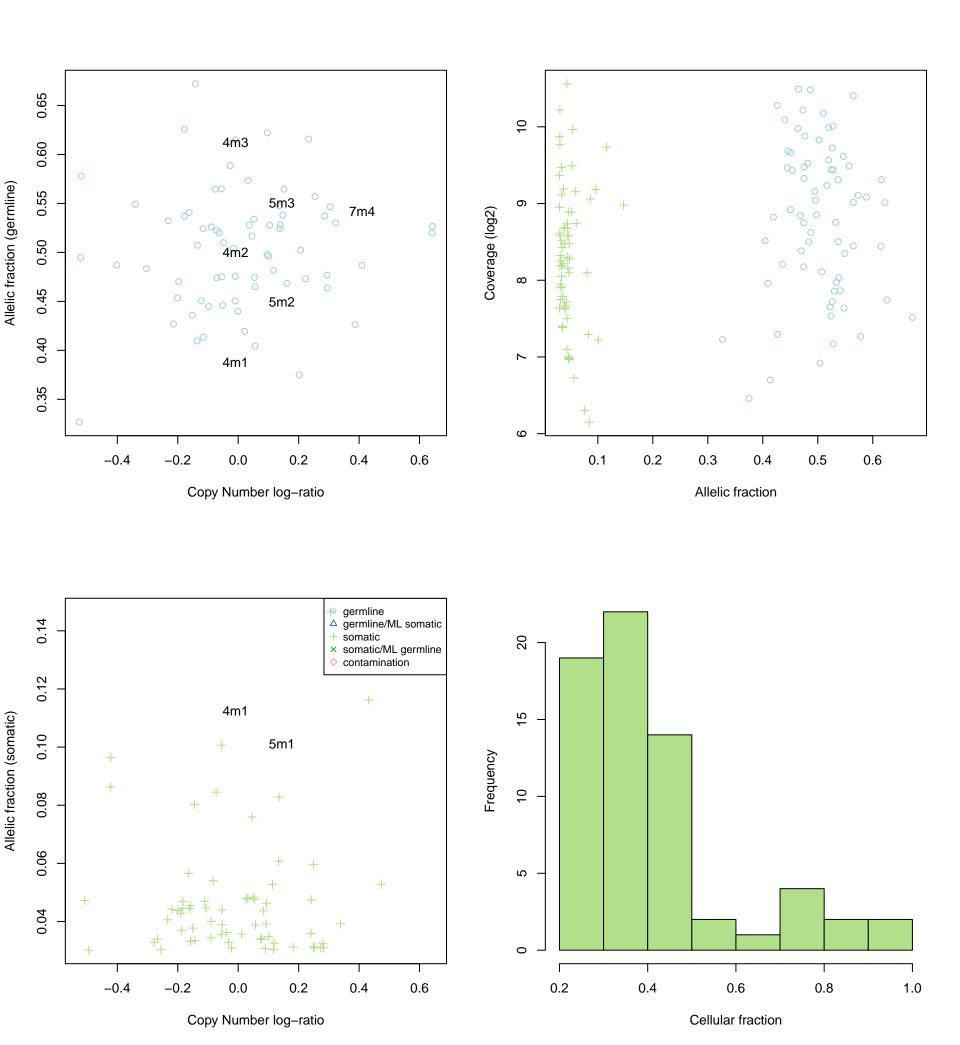




SCNA-fit log-likelihood: -6261.16

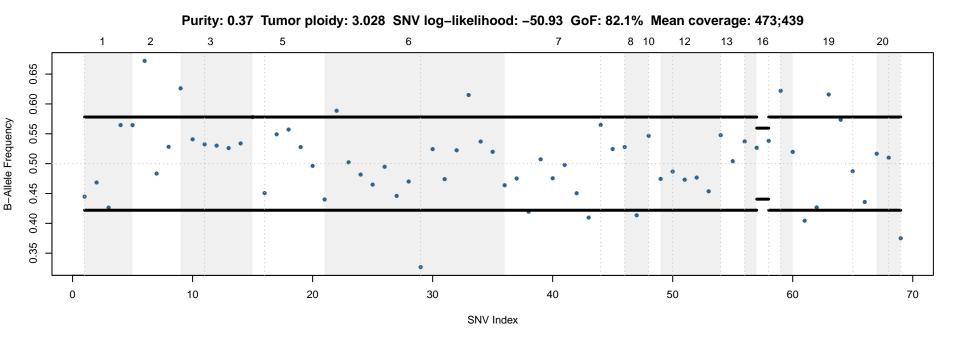




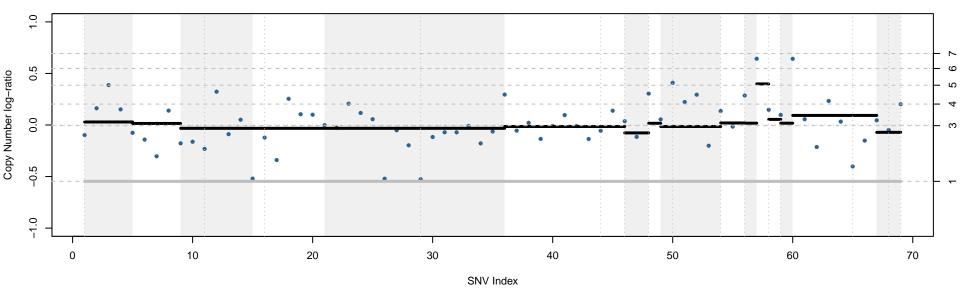


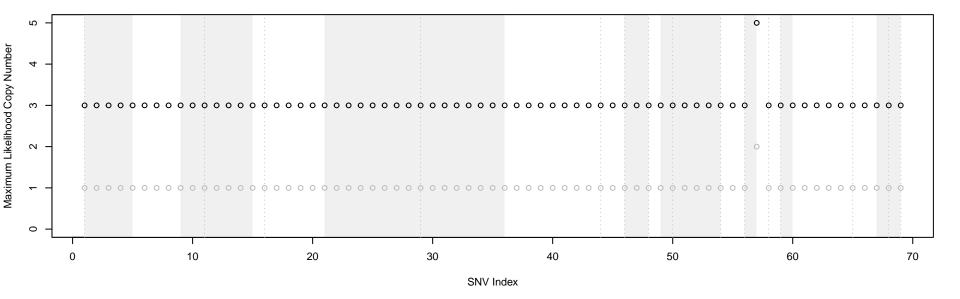
Purity: 0.37 Tumor ploidy: 3.028 3 5 6 Fraction Genome 0.05 0.00 -0.5 0.0 0.5

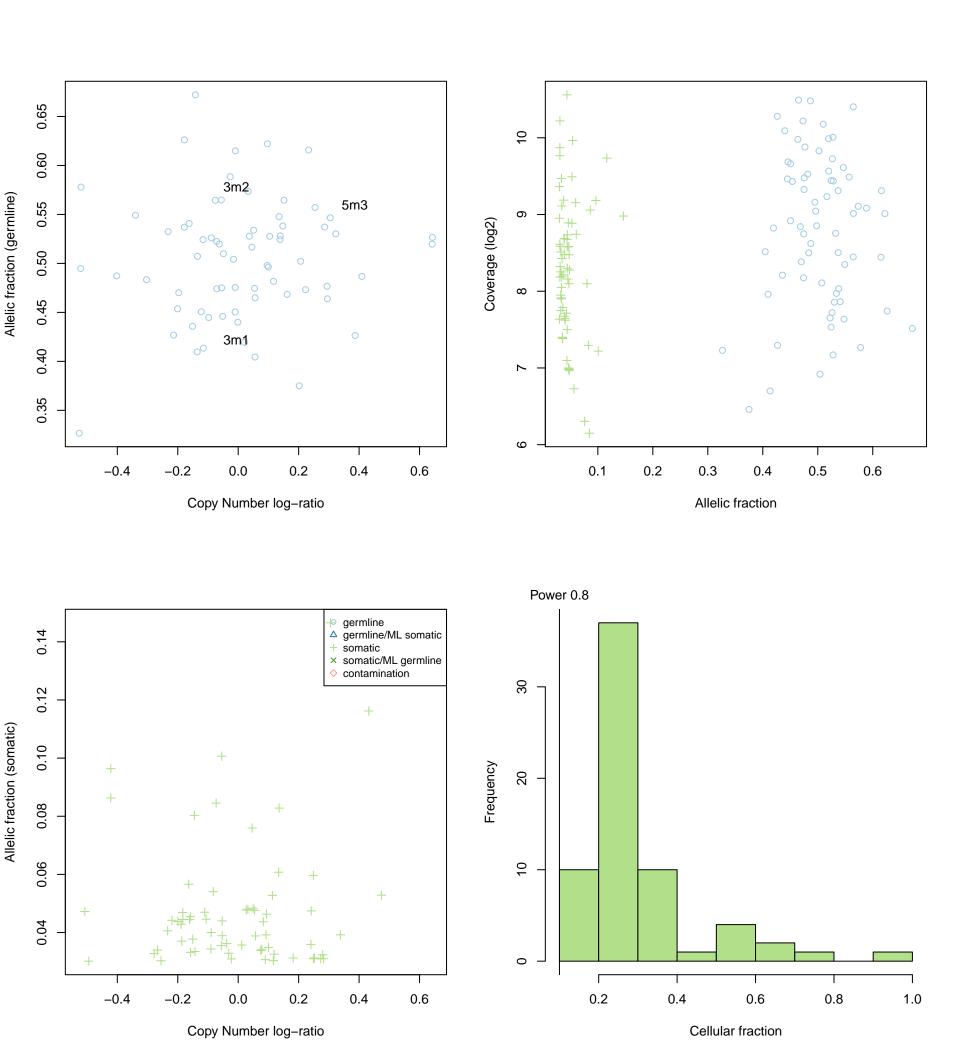
log2 ratio



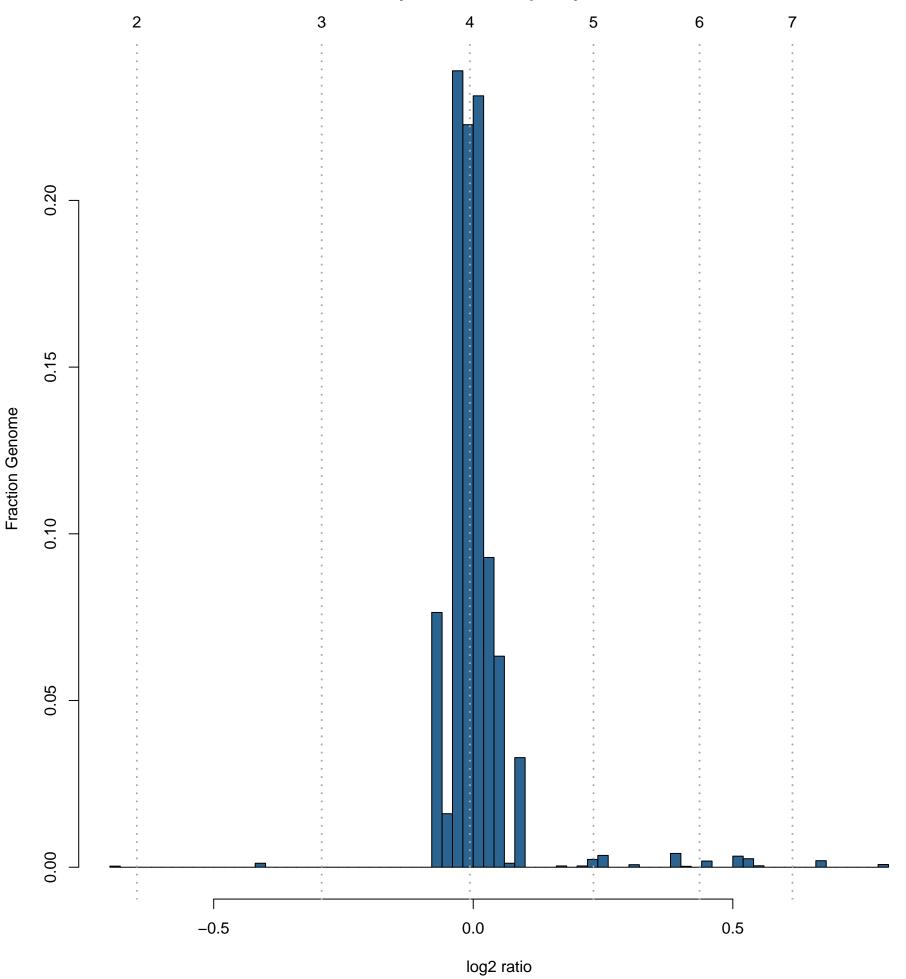
SCNA-fit log-likelihood: -6202

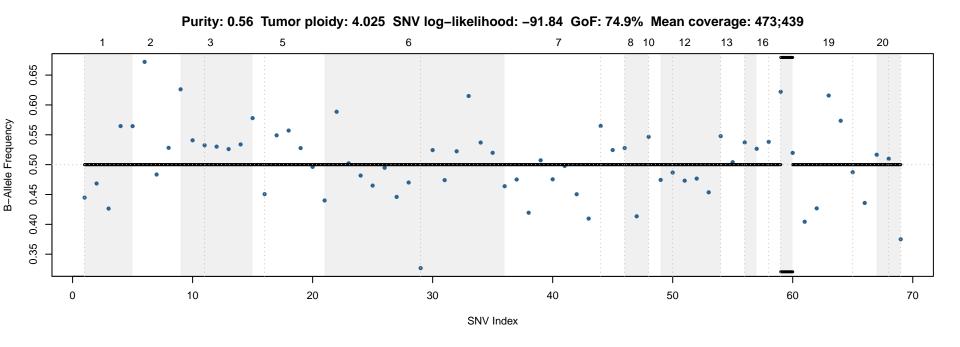




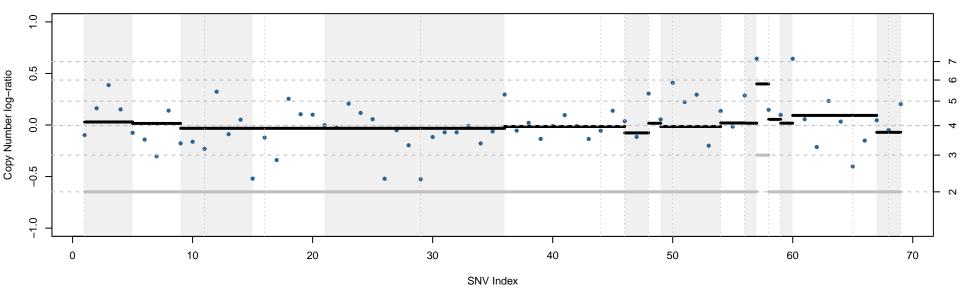


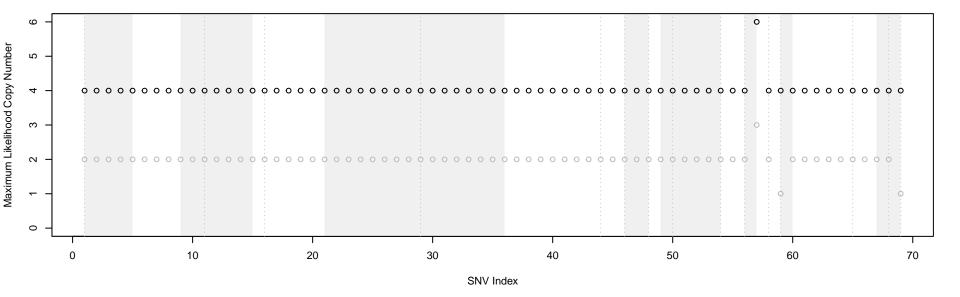
Purity: 0.56 Tumor ploidy: 4.025

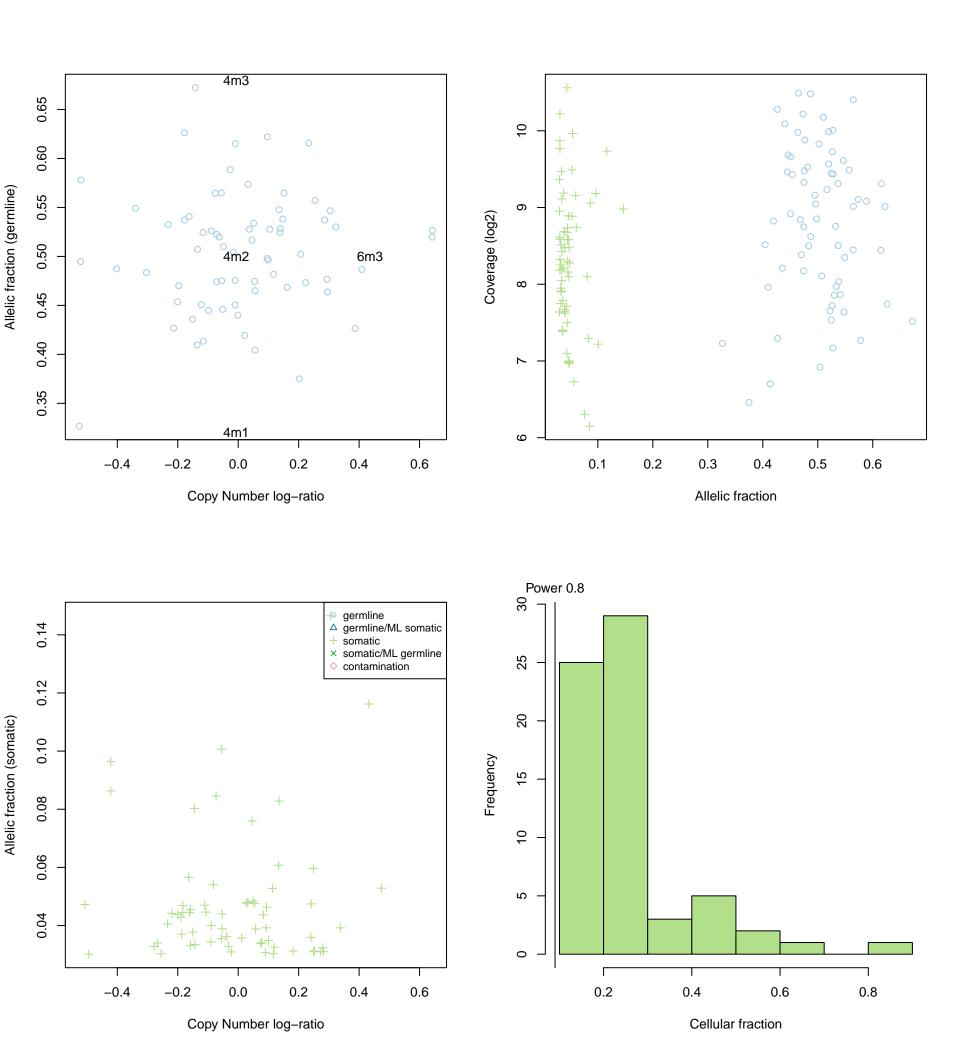




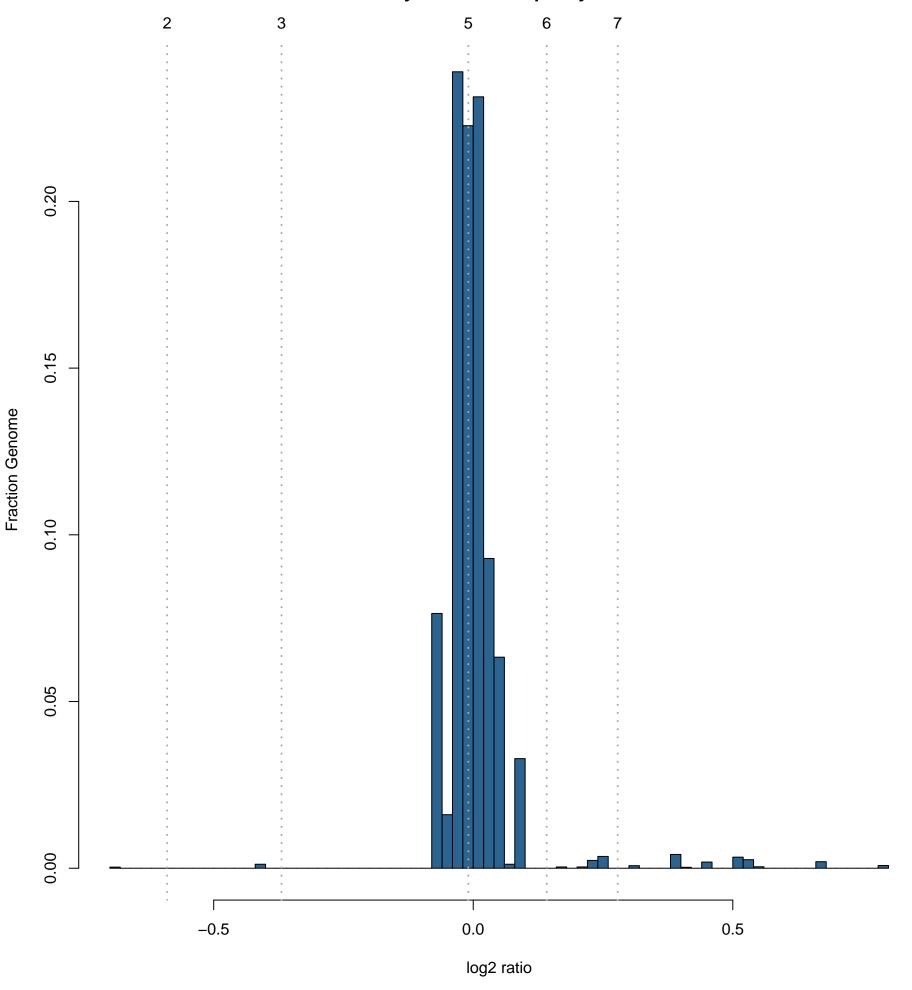
SCNA-fit log-likelihood: -6204.9

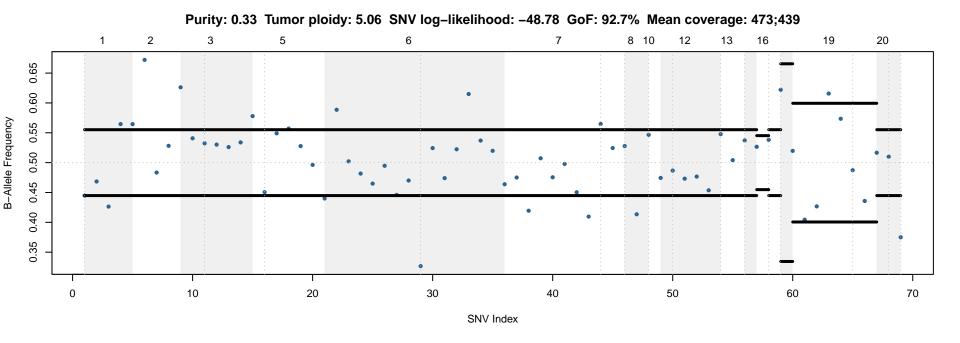




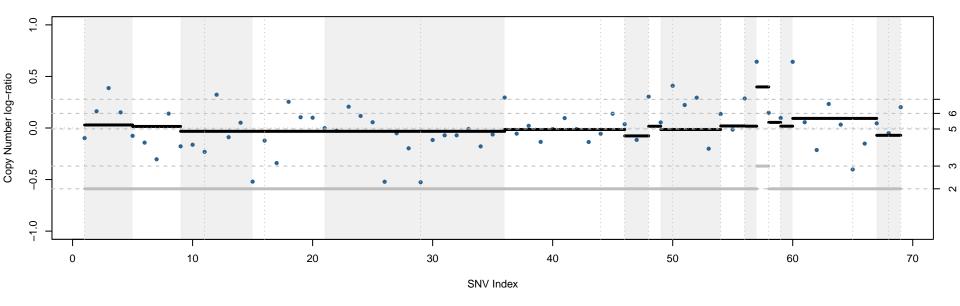


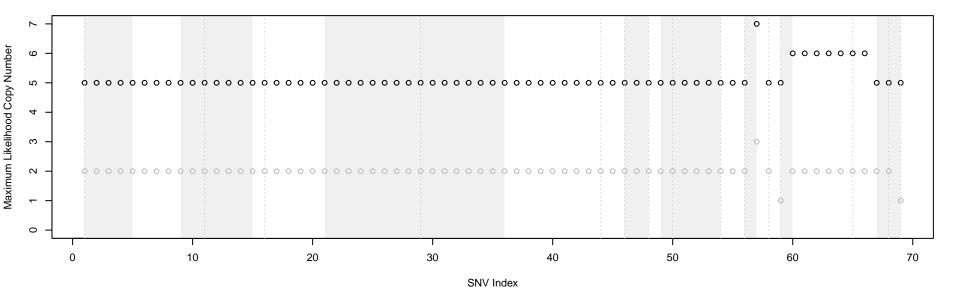
Purity: 0.33 Tumor ploidy: 5.06

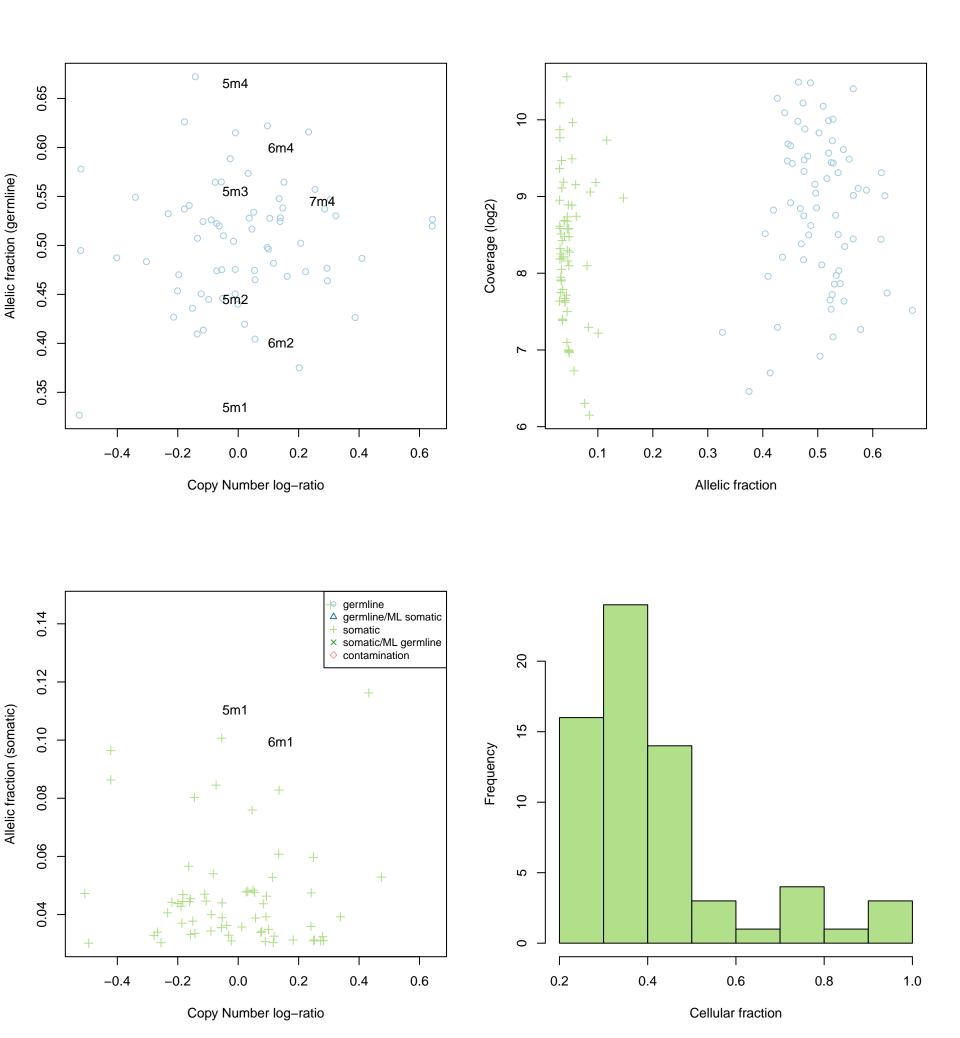




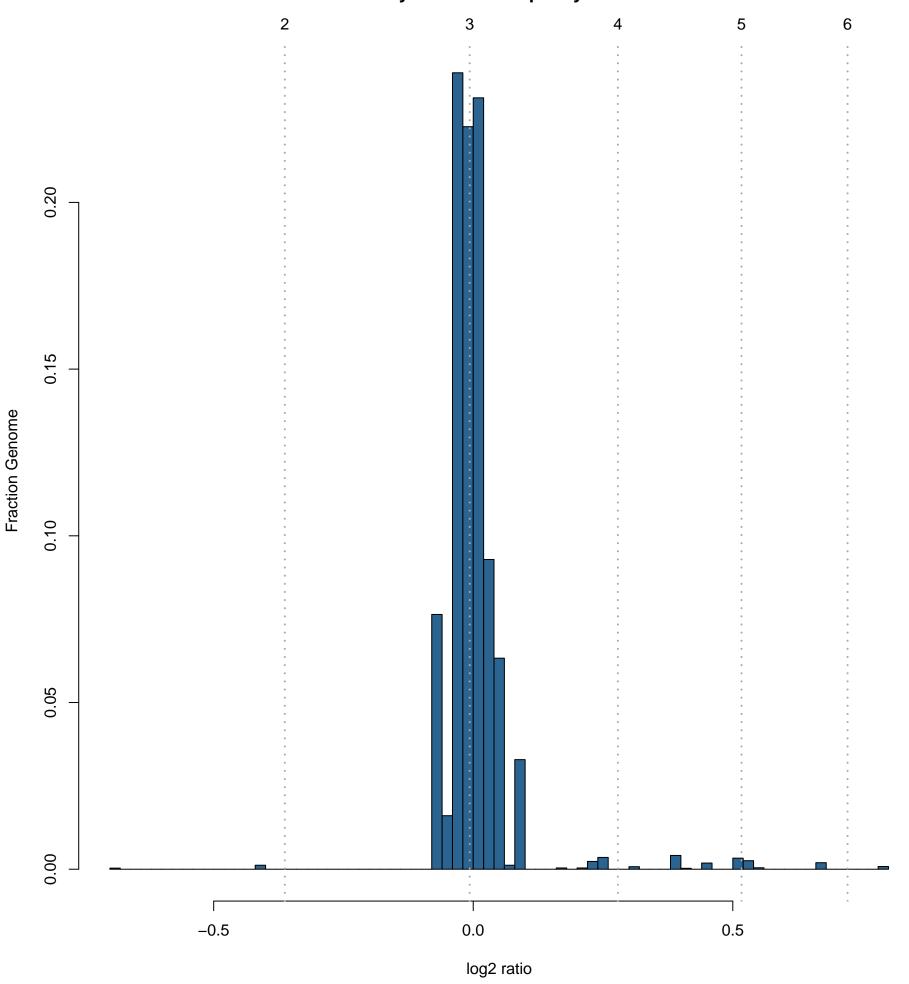
SCNA-fit log-likelihood: -6415.9

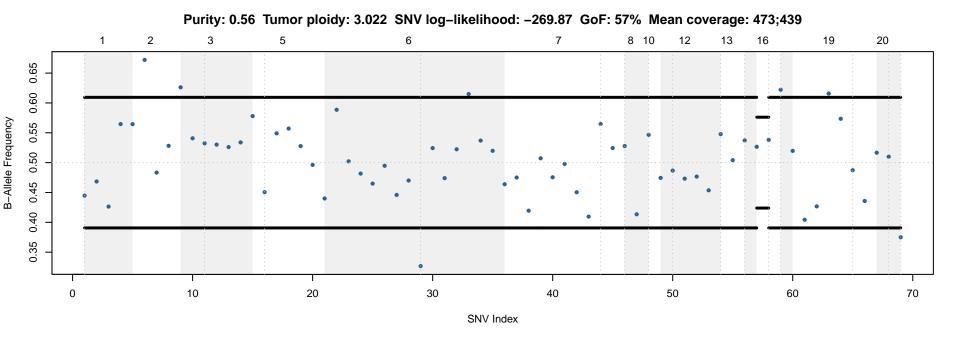




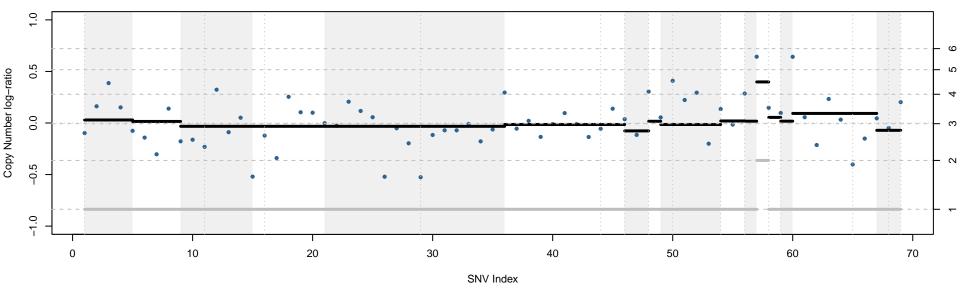


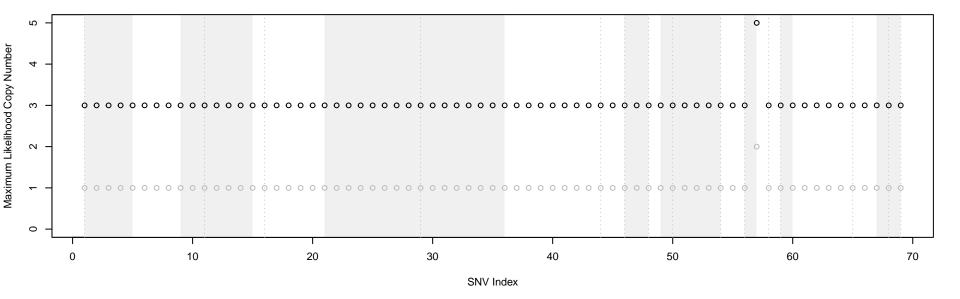
Purity: 0.56 Tumor ploidy: 3.022

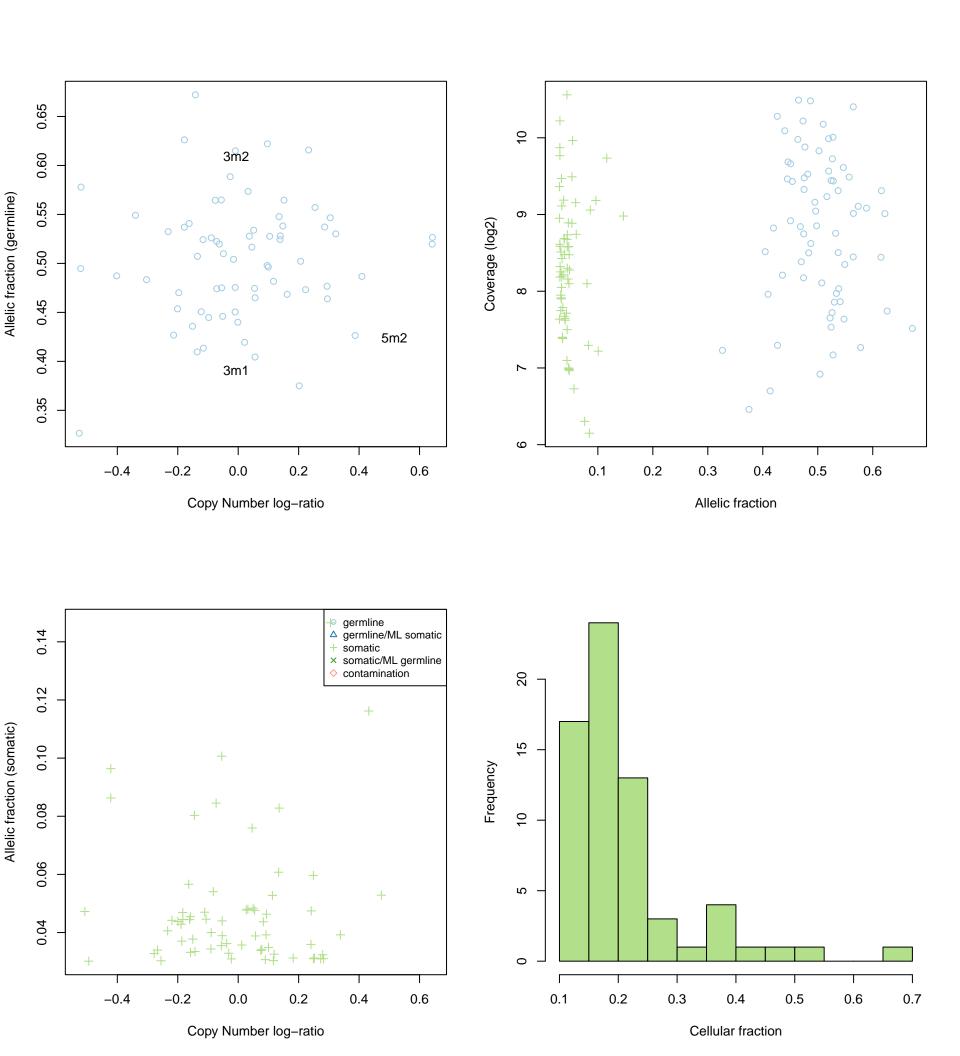




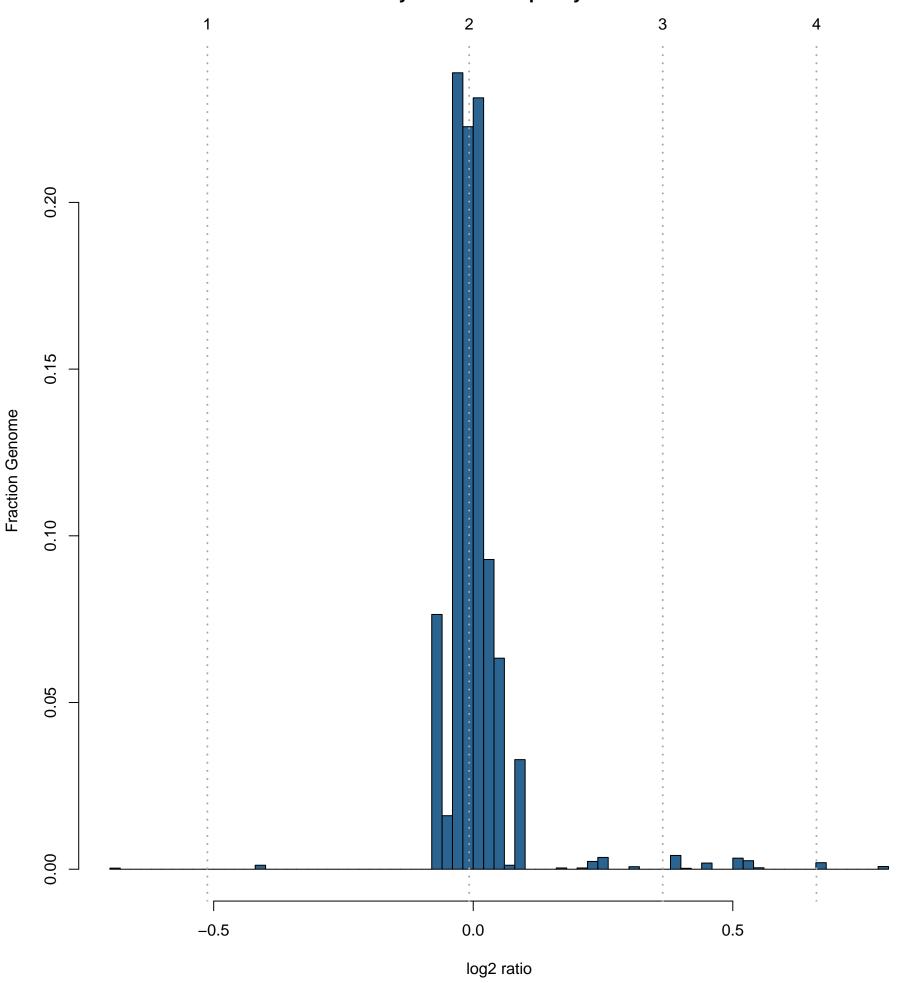
SCNA-fit log-likelihood: -6205.72

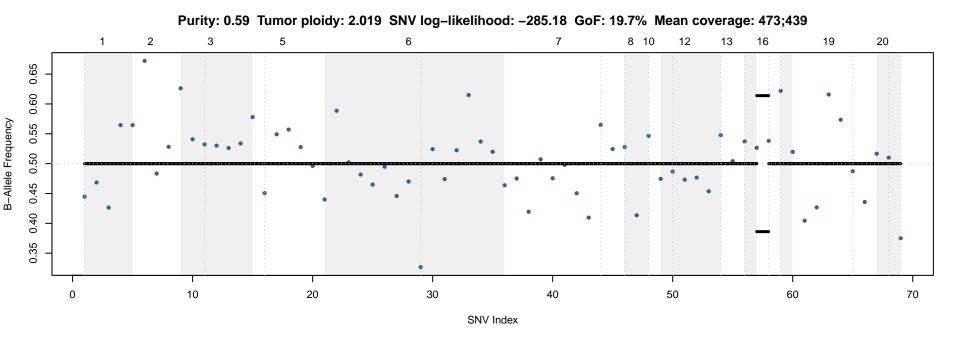




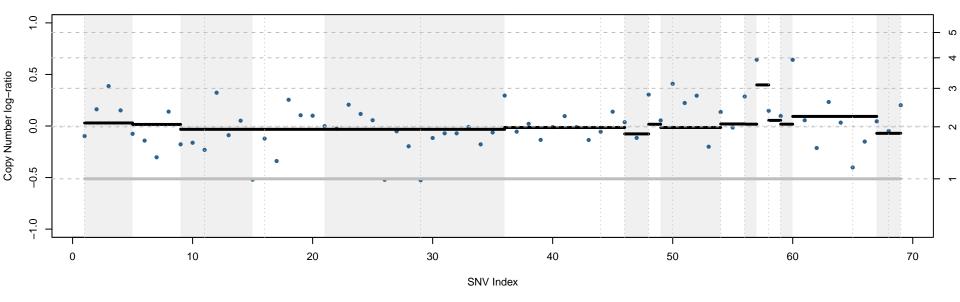


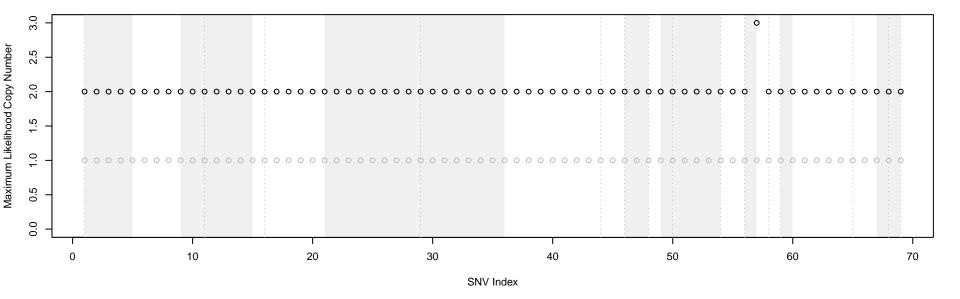
Purity: 0.59 Tumor ploidy: 2.019

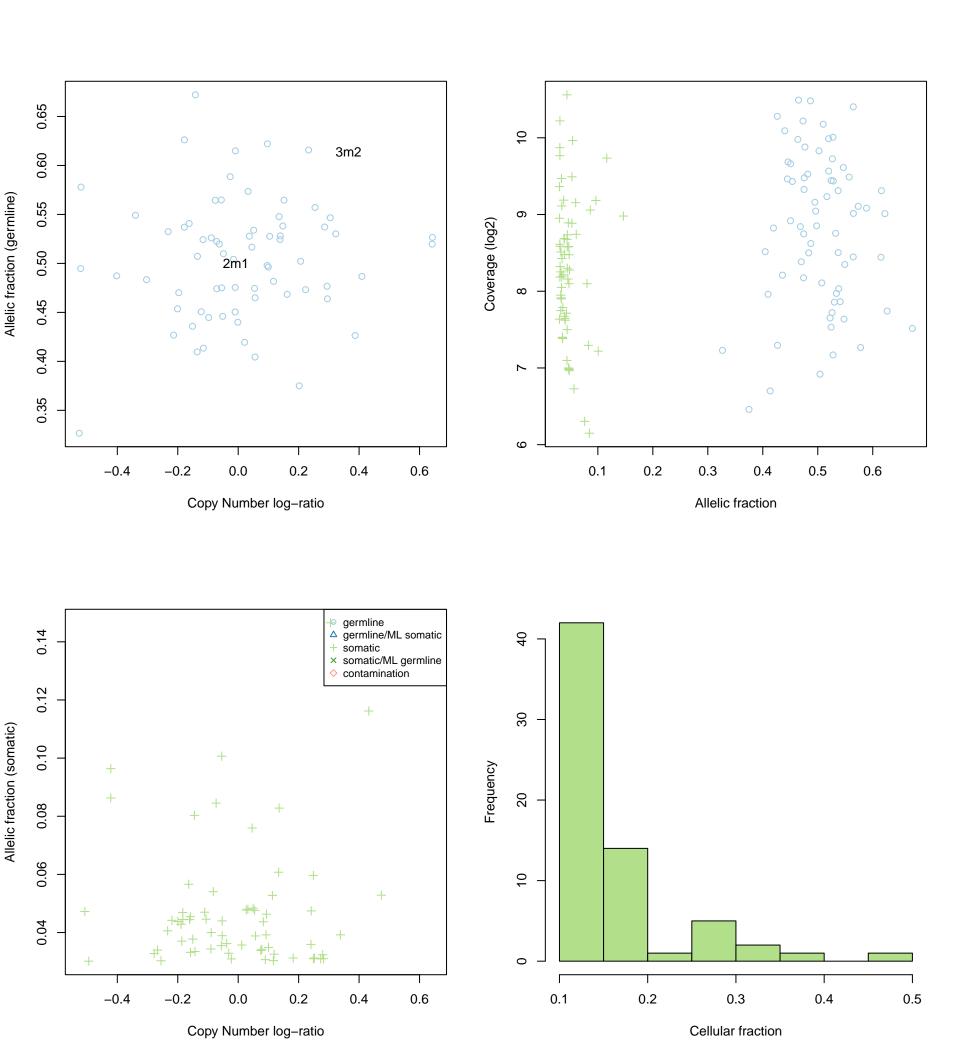




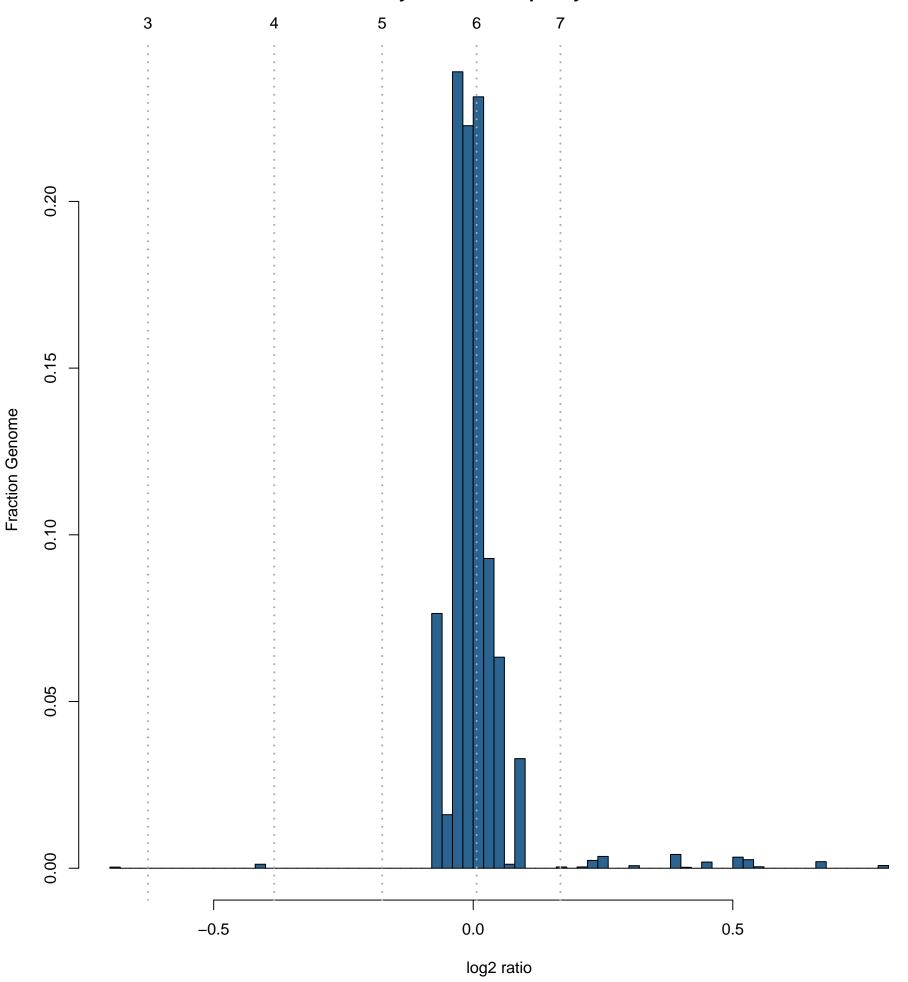
SCNA-fit log-likelihood: -6221.46

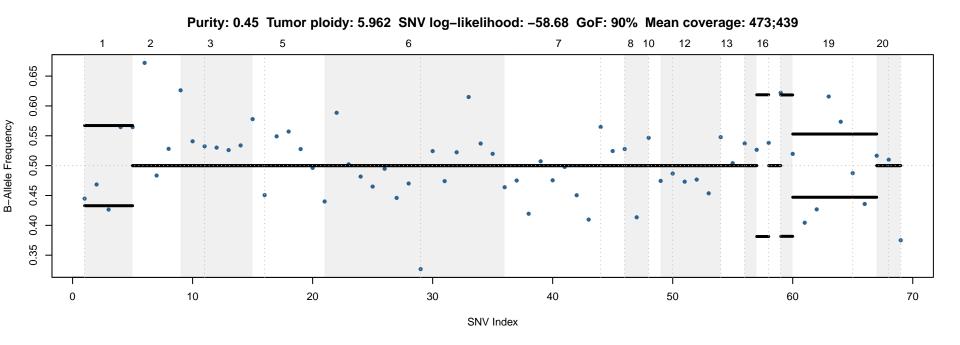




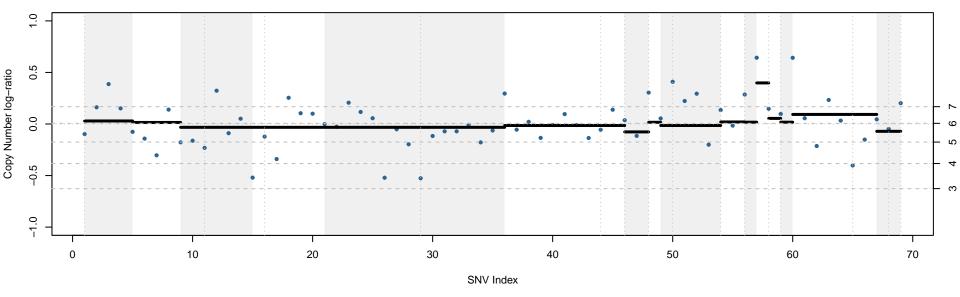


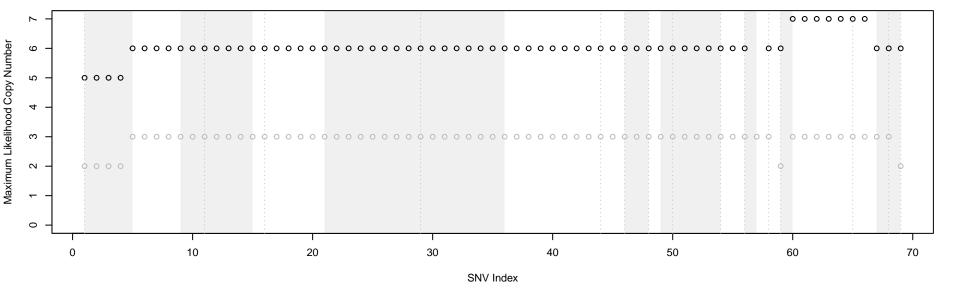
Purity: 0.45 Tumor ploidy: 5.962

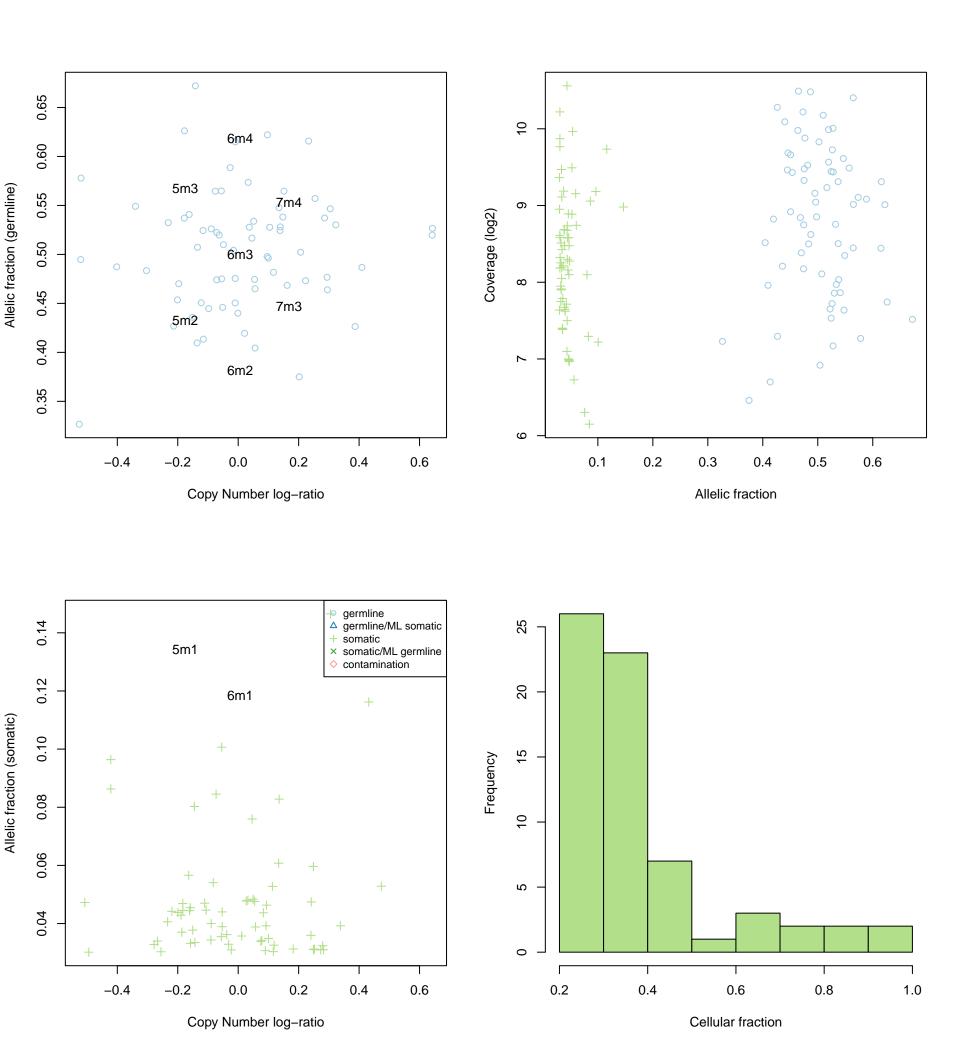




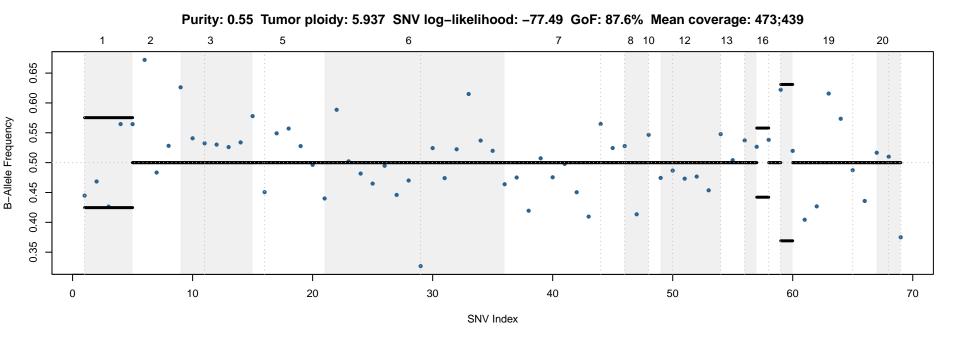
SCNA-fit log-likelihood: -6842.94



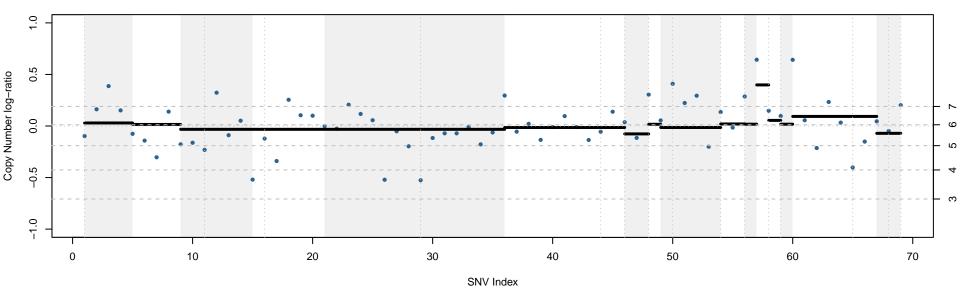


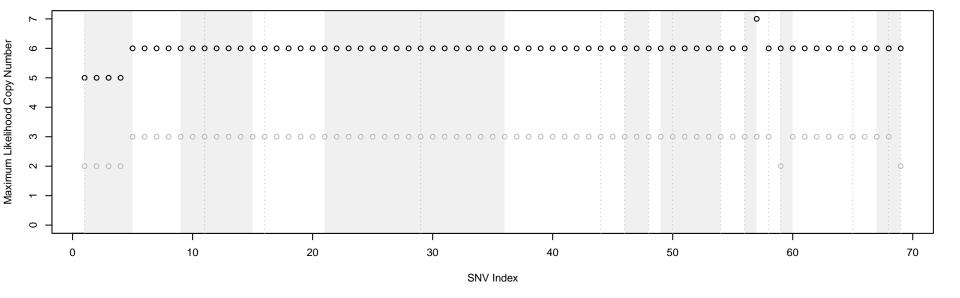


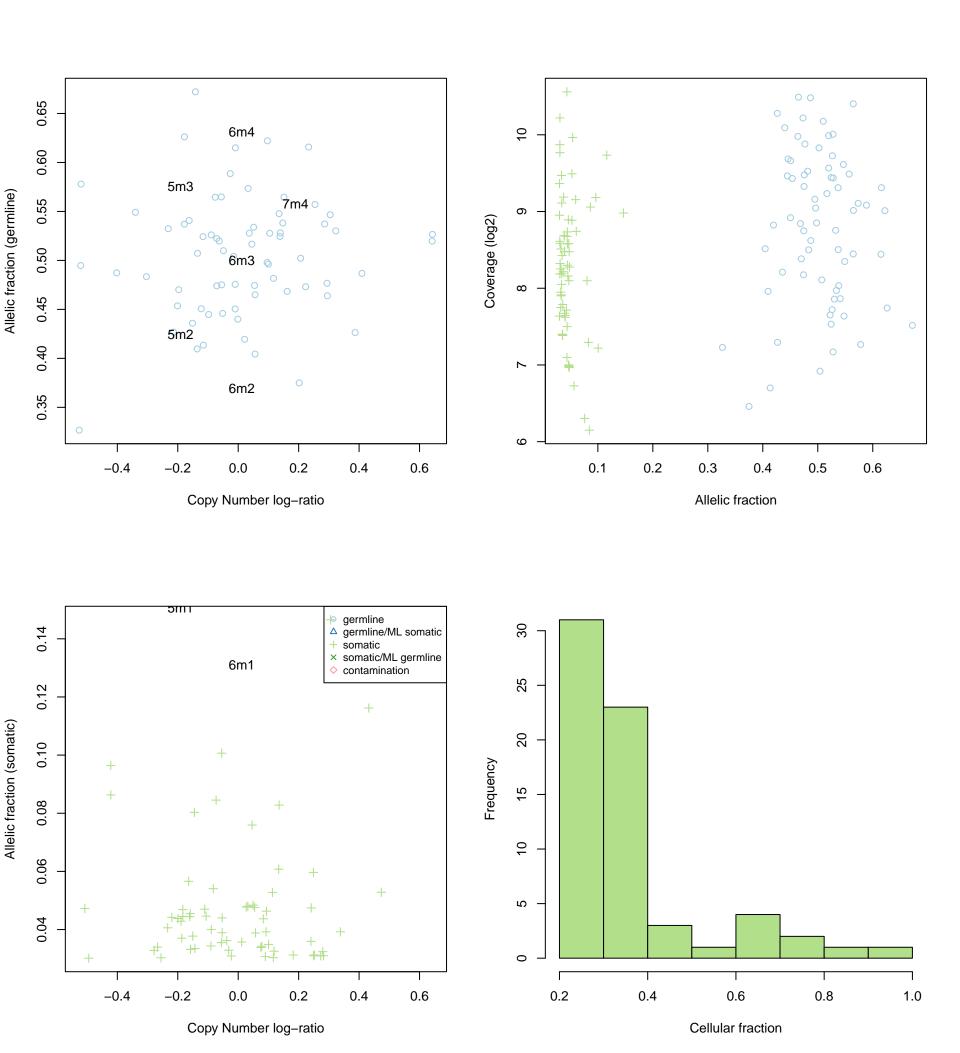
Purity: 0.55 Tumor ploidy: 5.937 3 5 6 7 Fraction Genome 0.05 0.00 -0.5 0.0 0.5 log2 ratio



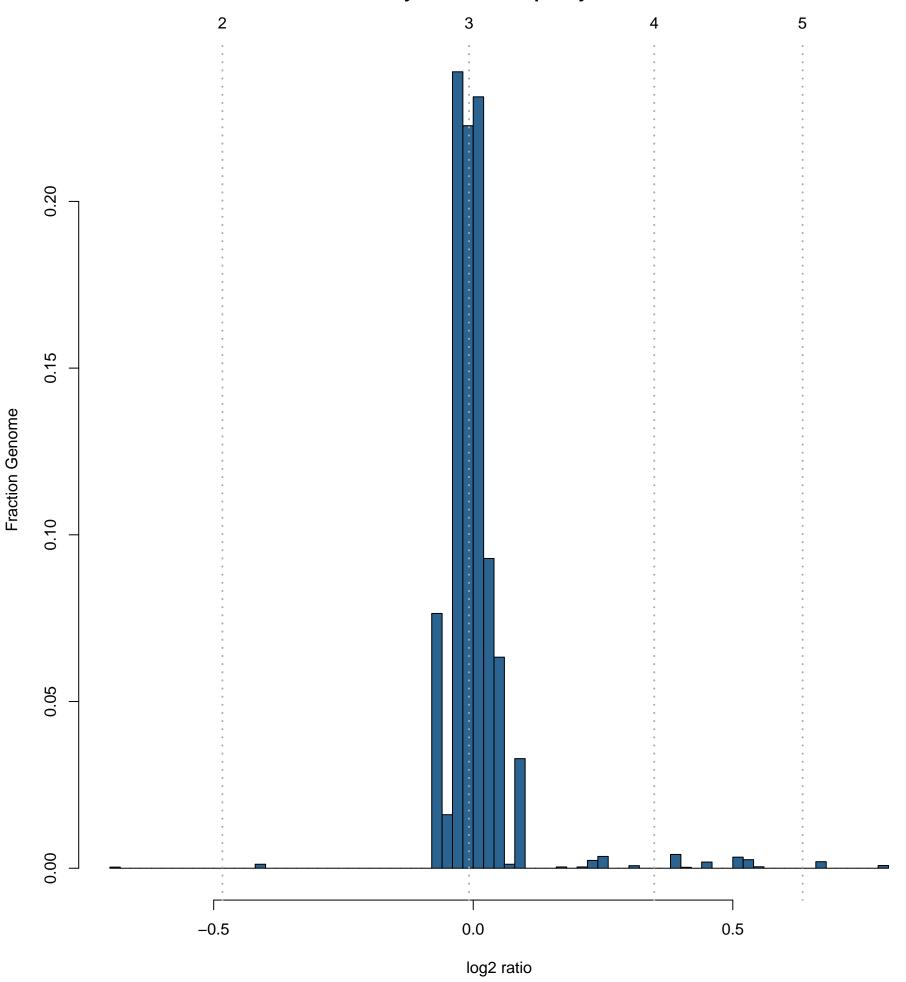
SCNA-fit log-likelihood: -6810.11

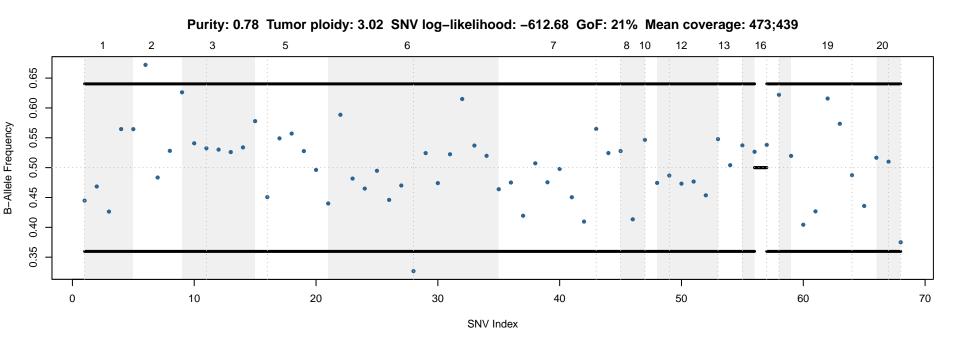






Purity: 0.78 Tumor ploidy: 3.02





SCNA-fit log-likelihood: -6216.96

