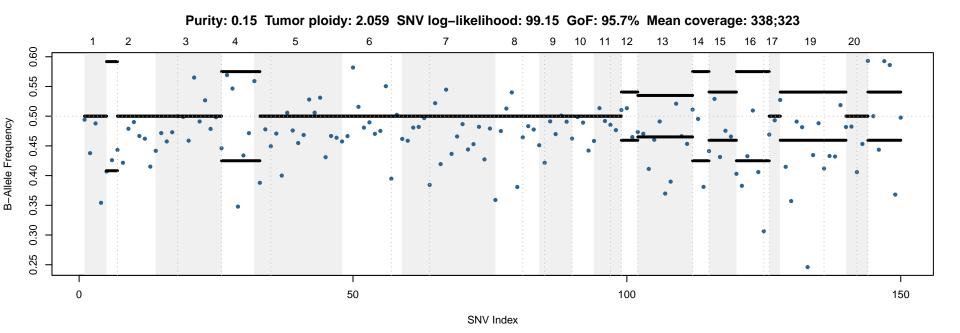
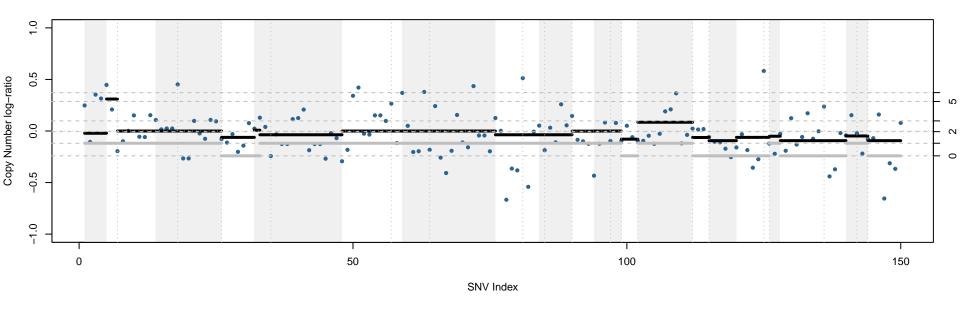
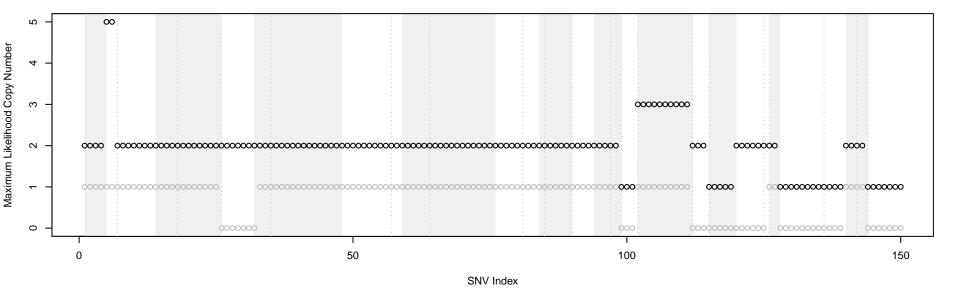
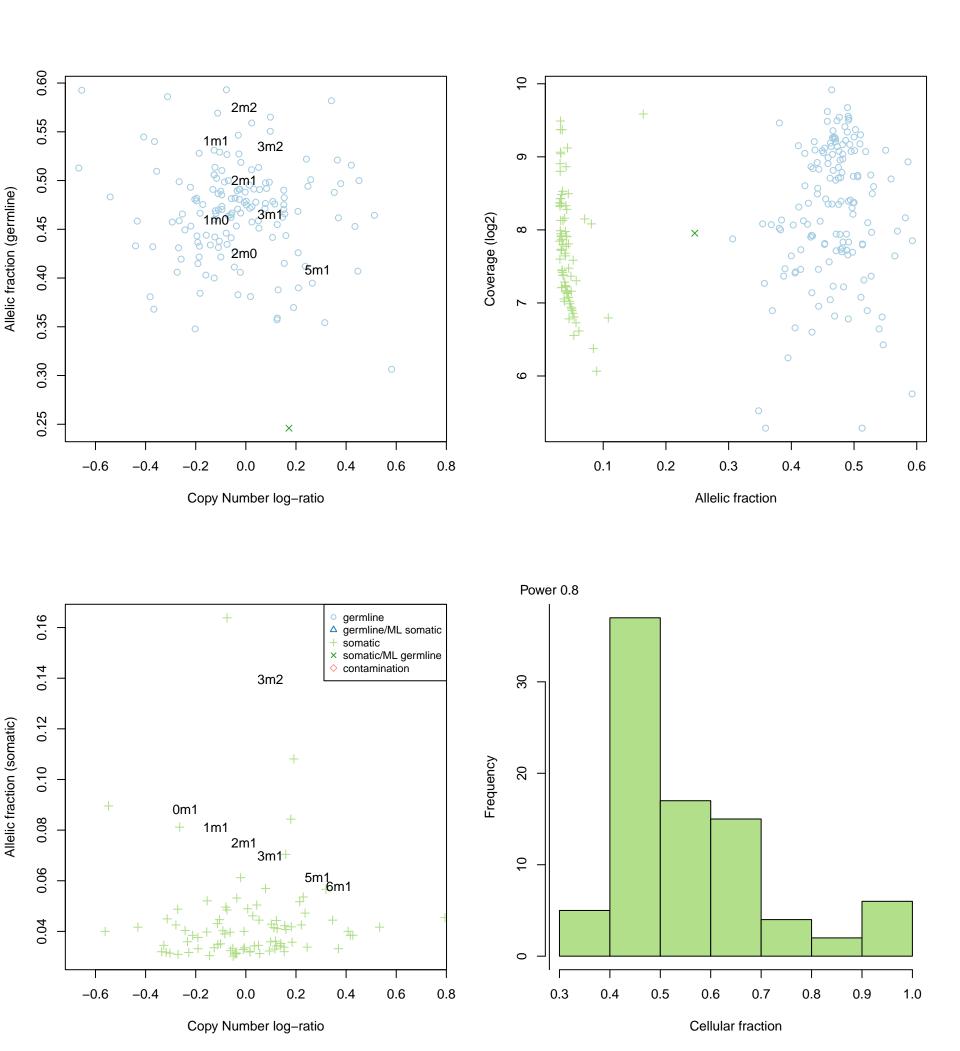
Purity: 0.15 Tumor ploidy: 2.059 0 2 3 5 6 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -0.4 -0.2 0.0 0.2 0.4 0.6 0.8 1.0 log2 ratio



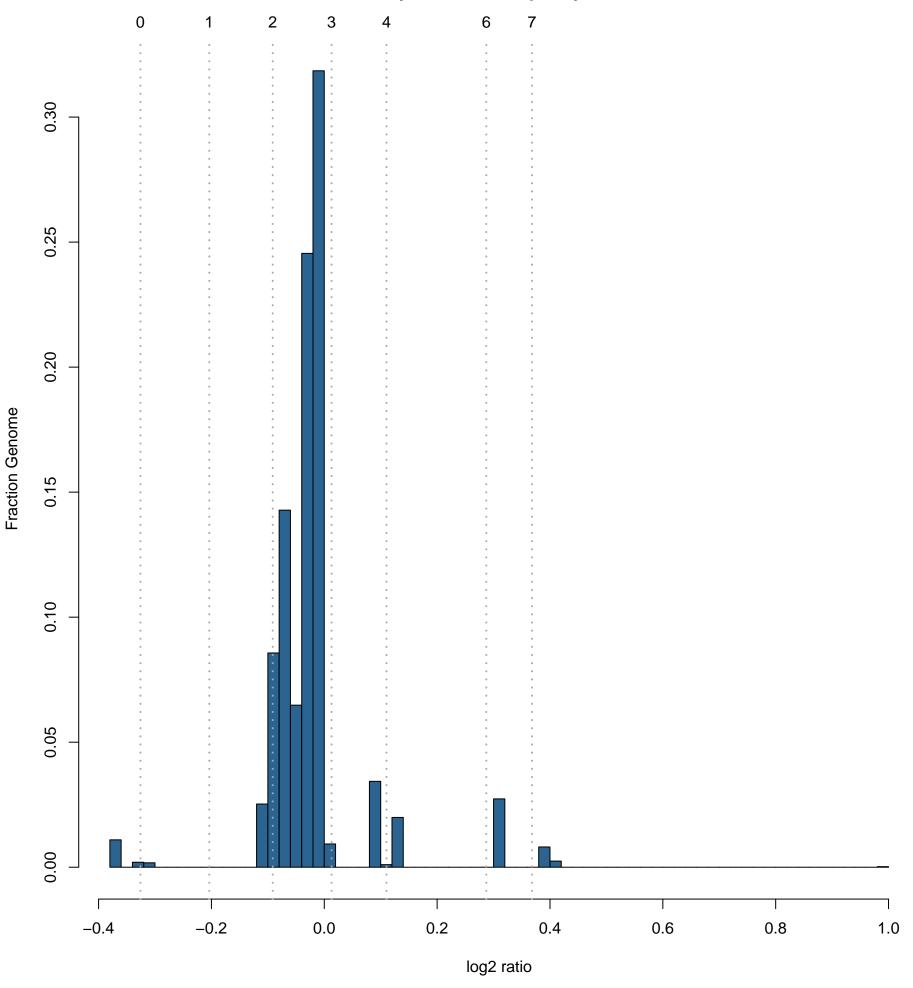
SCNA-fit log-likelihood: -6328.68

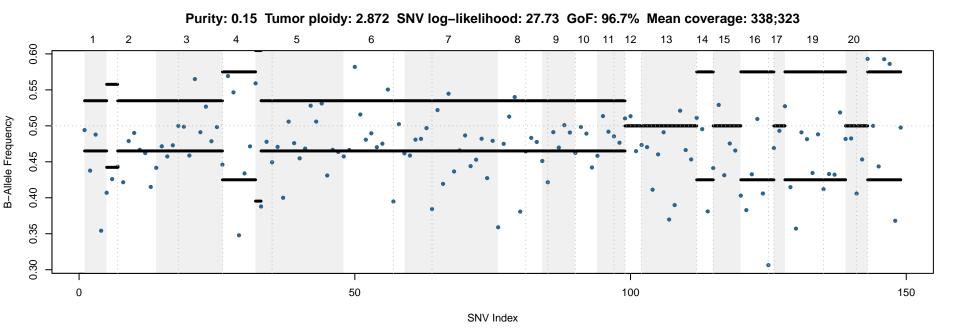




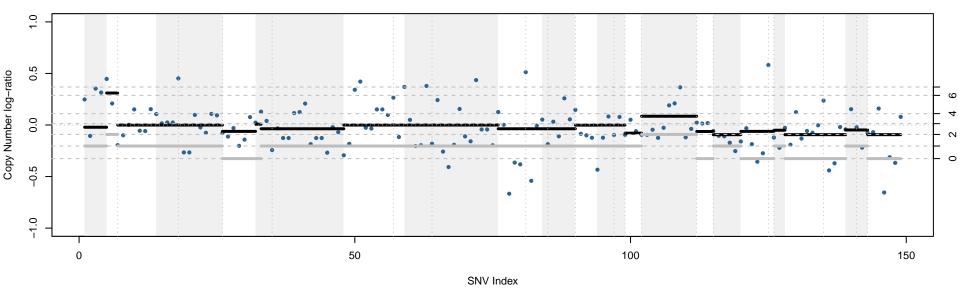


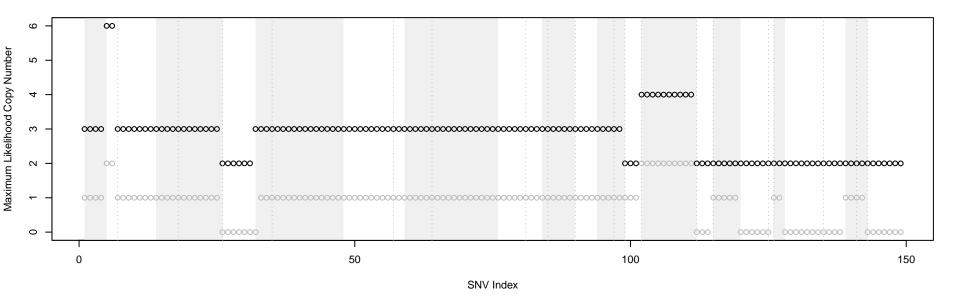
Purity: 0.15 Tumor ploidy: 2.872

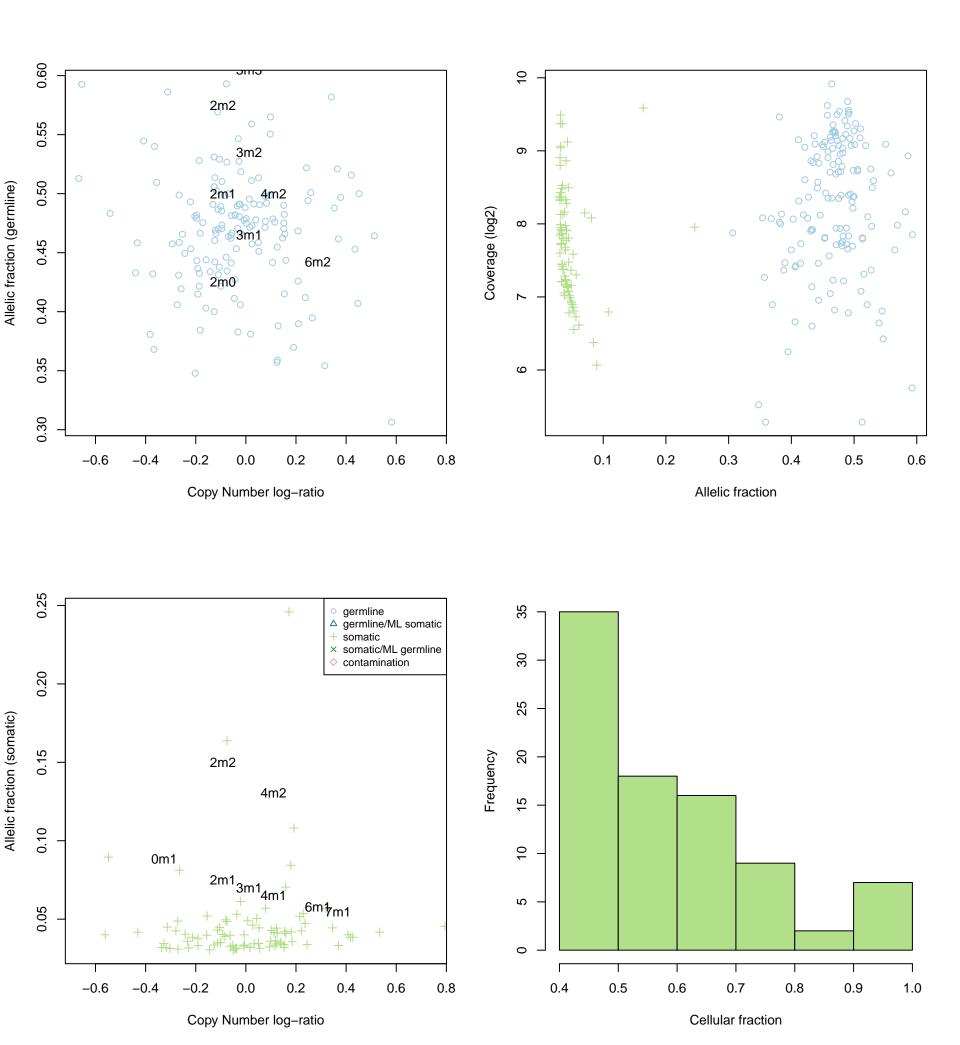


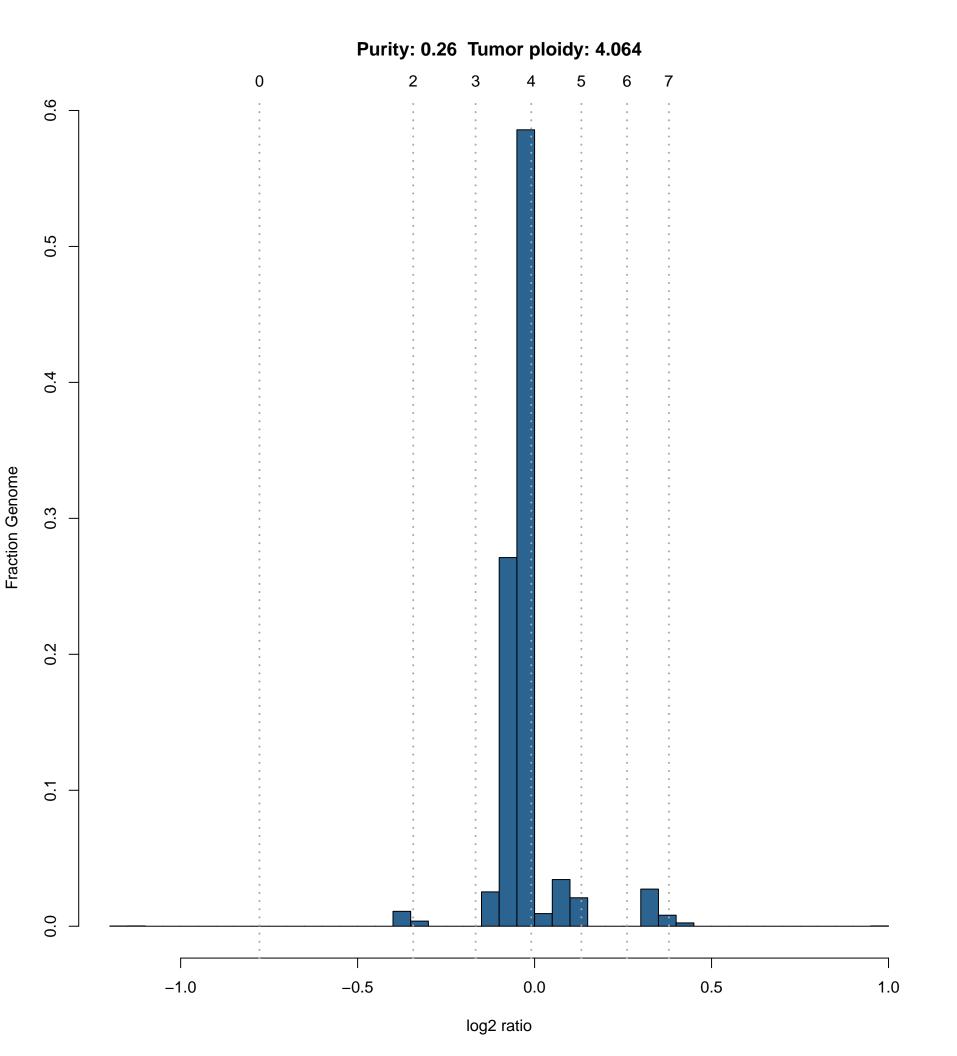


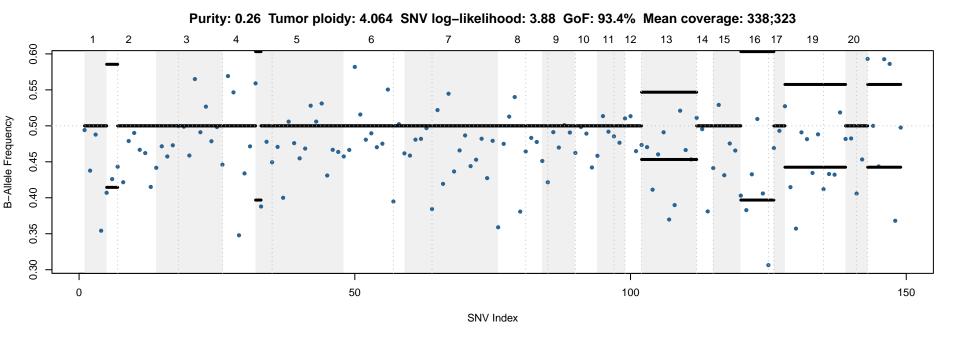
SCNA-fit log-likelihood: -6300.85



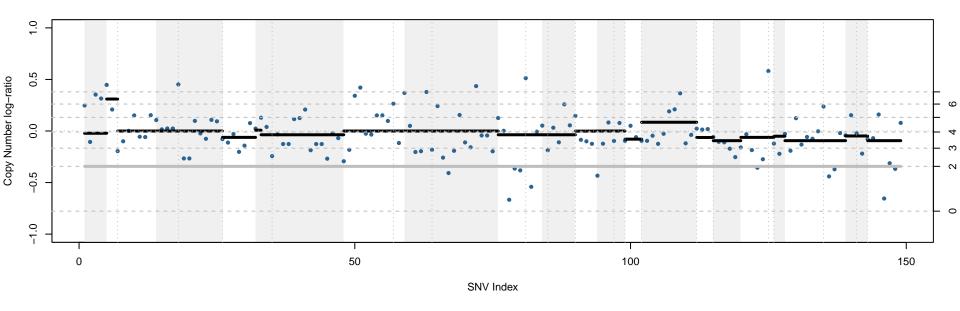


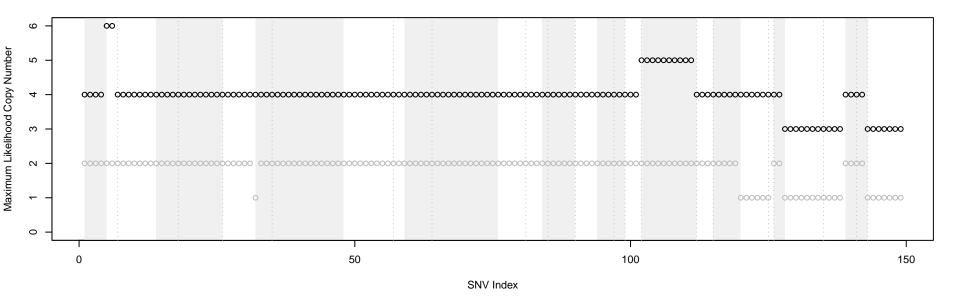


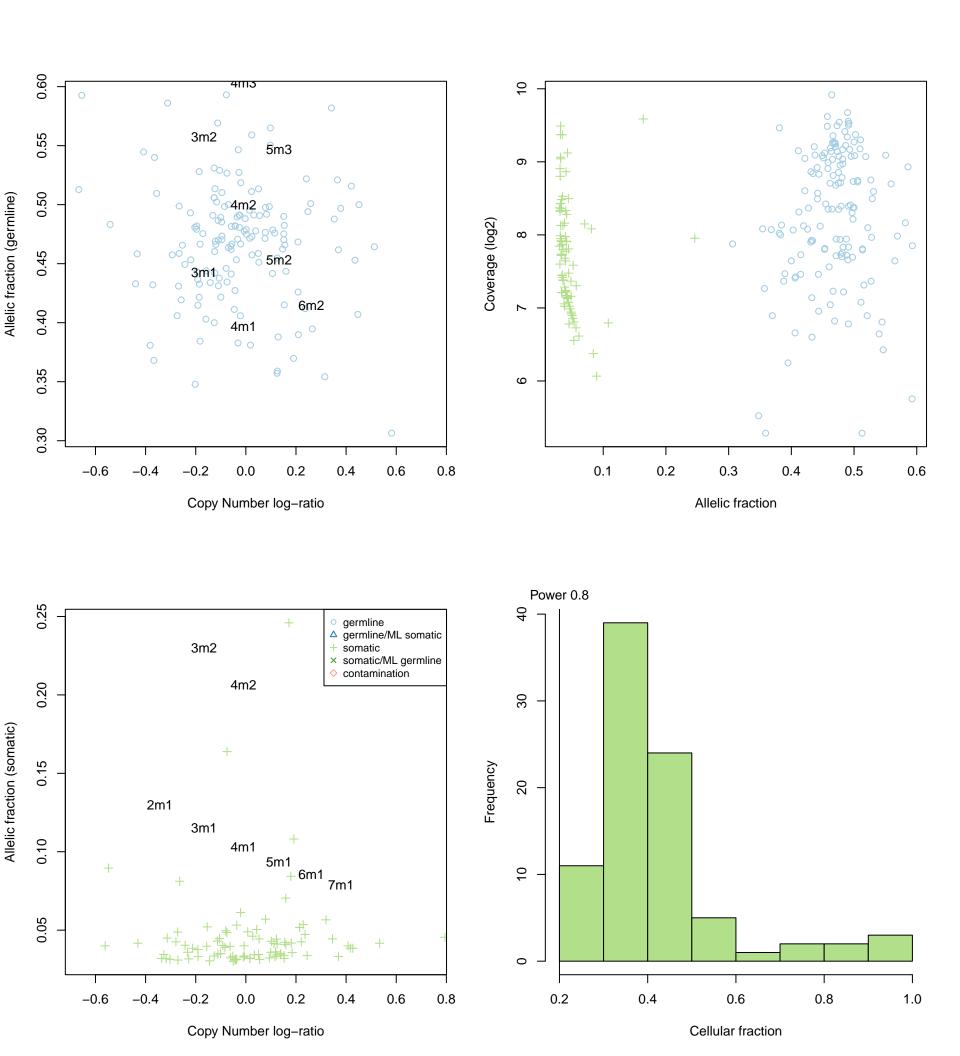


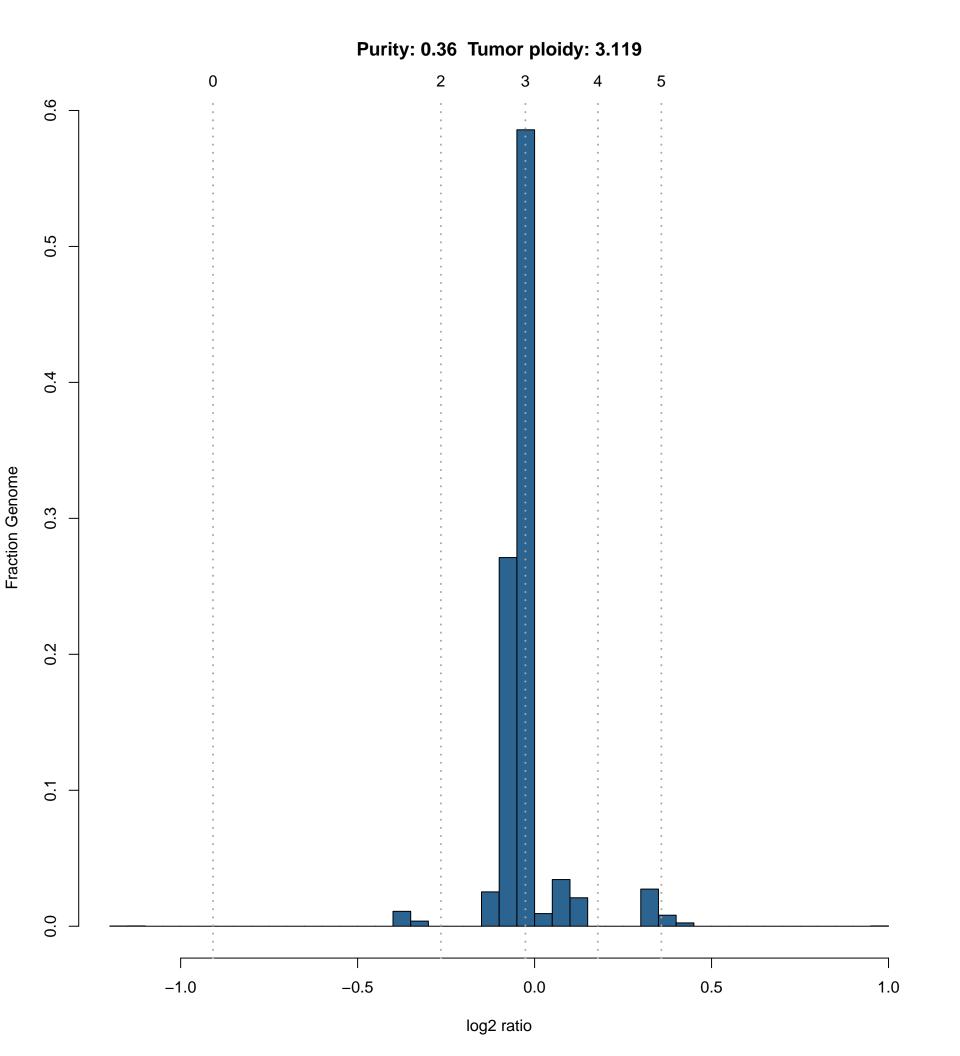


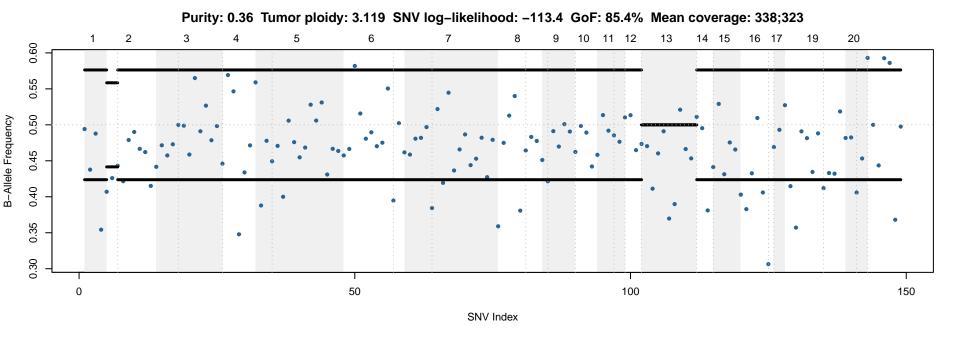
SCNA-fit log-likelihood: -6308.52



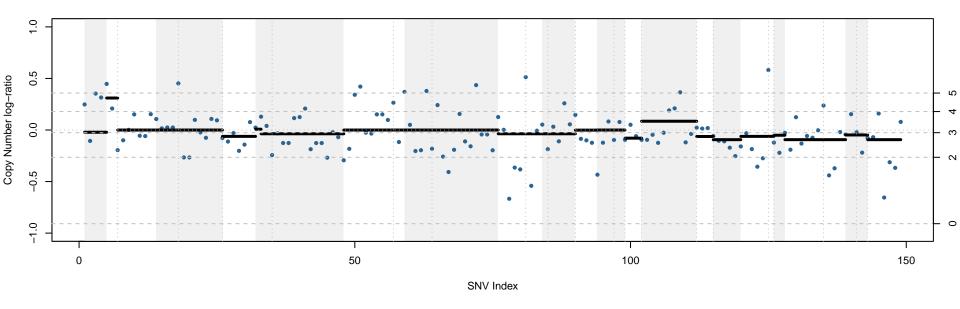


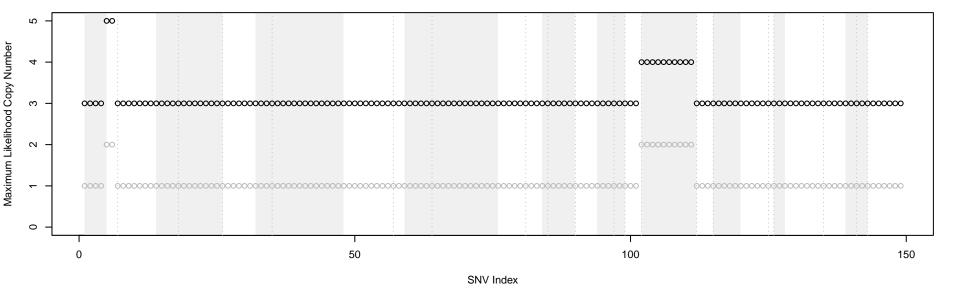


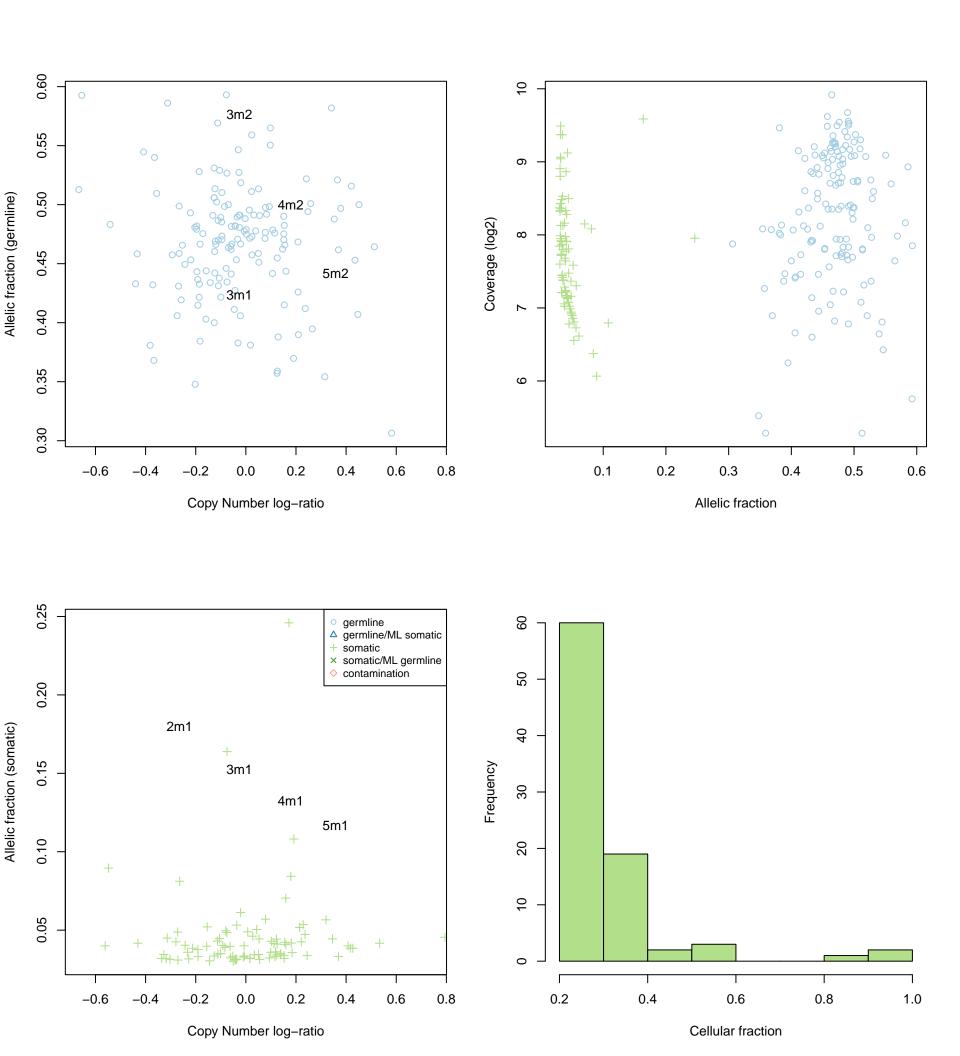


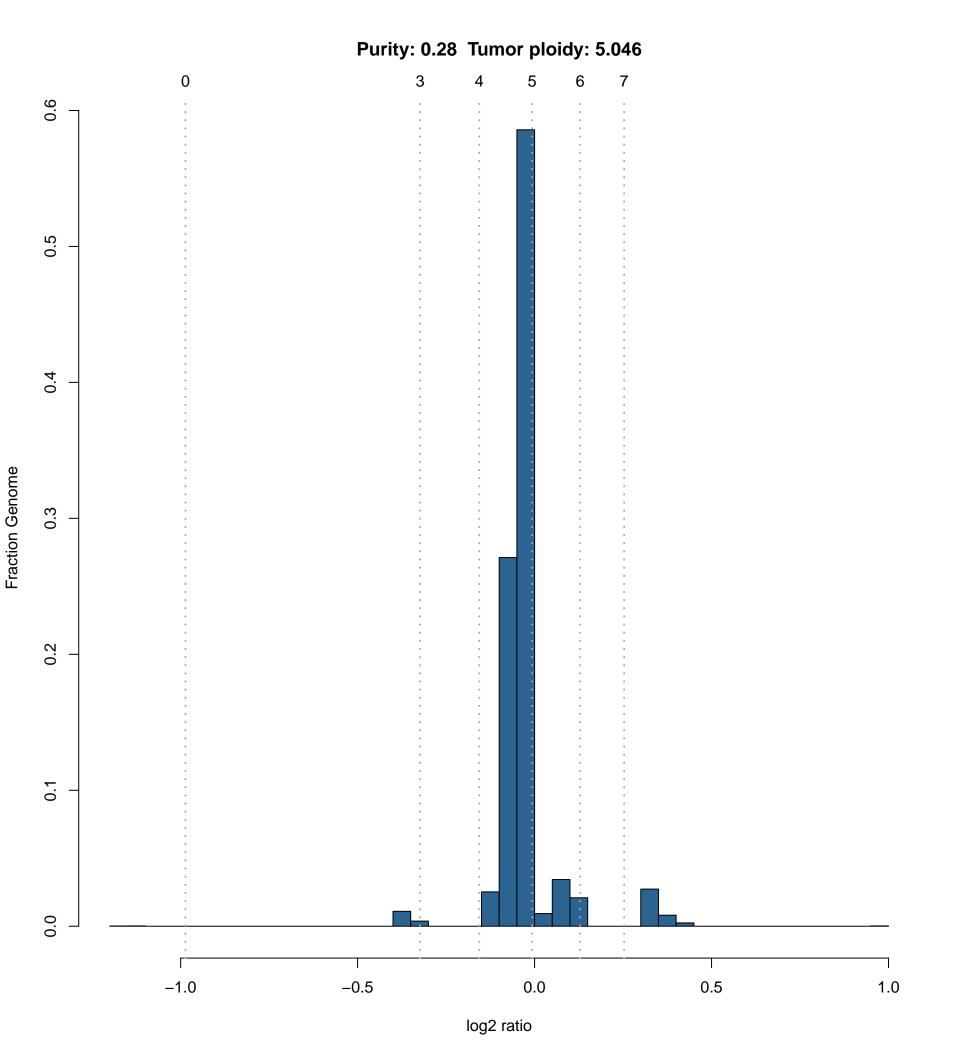


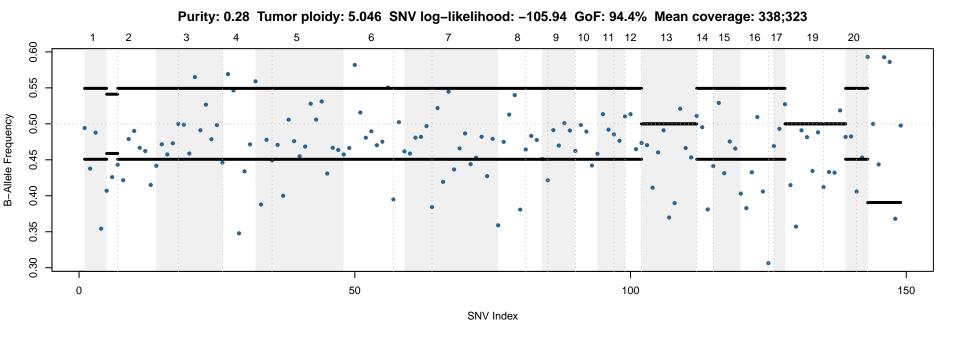
SCNA-fit log-likelihood: -6327.43



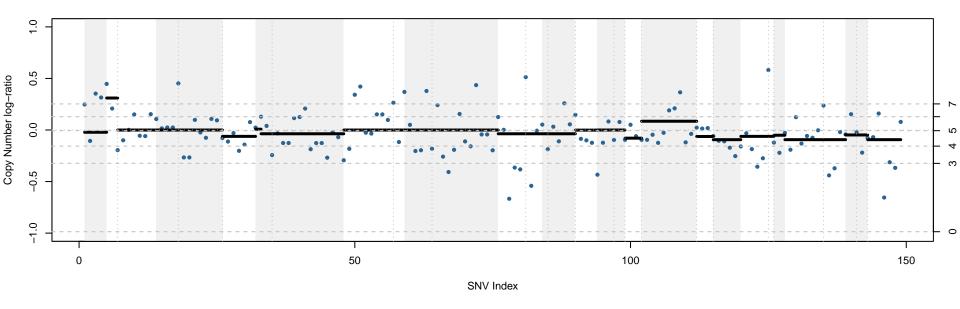


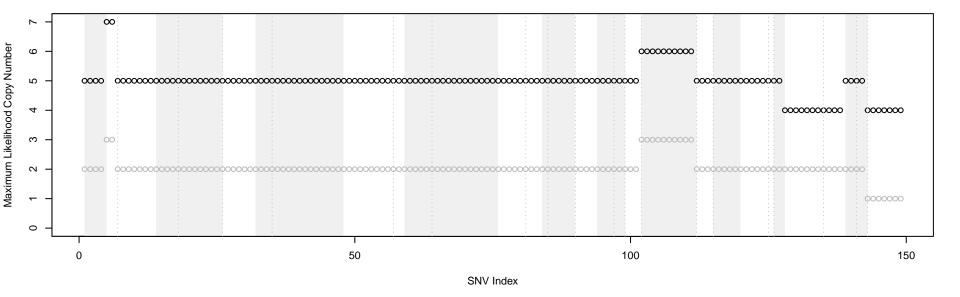


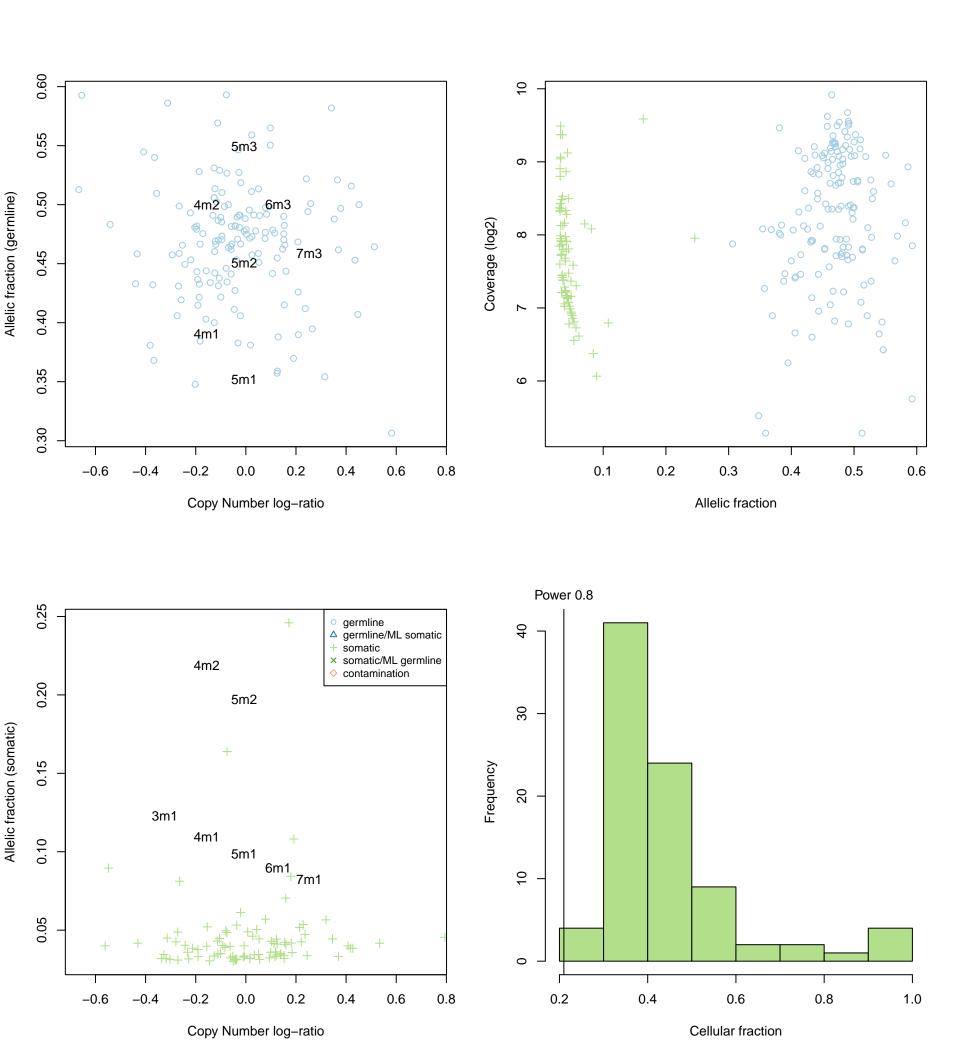




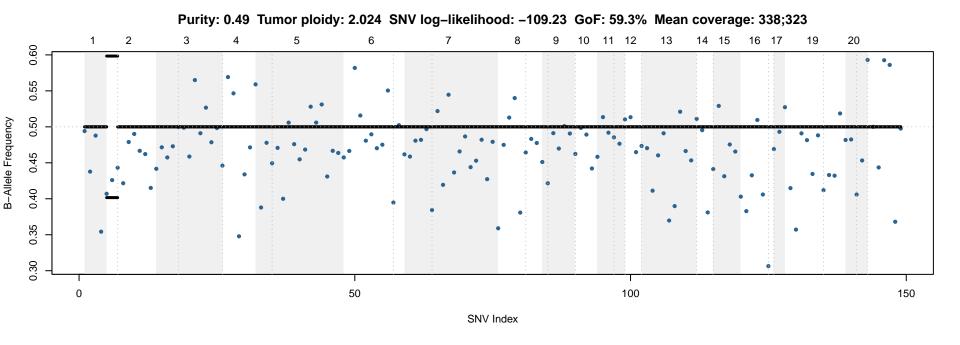
SCNA-fit log-likelihood: -6320.98



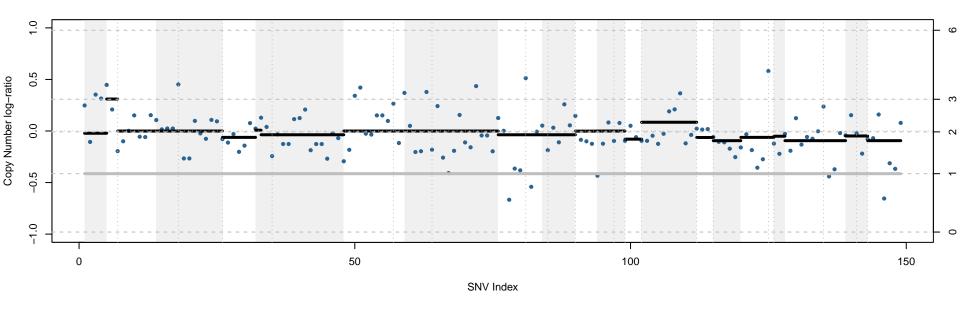


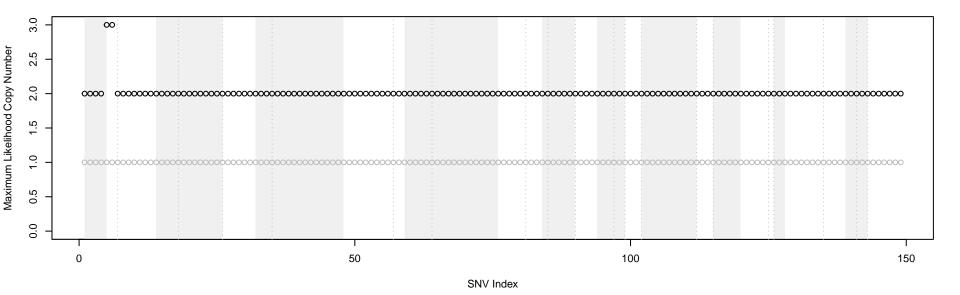


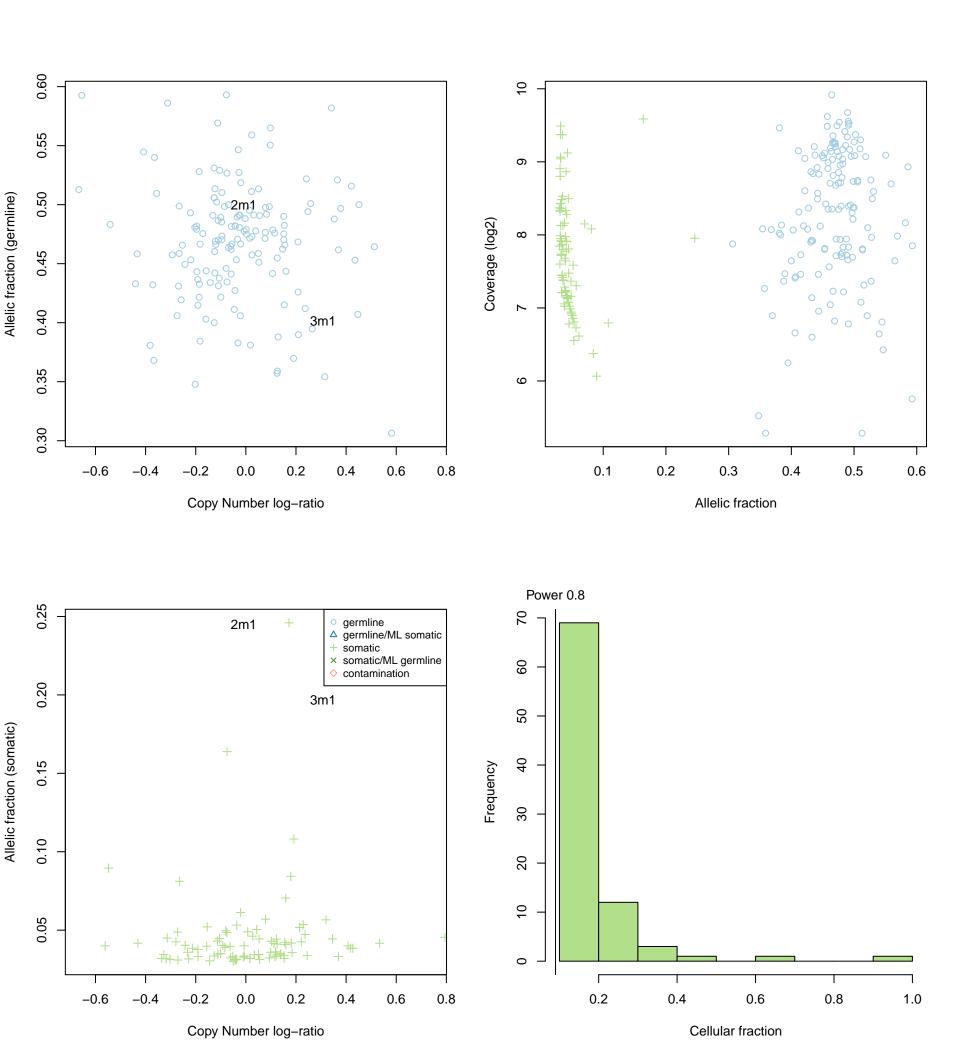
Purity: 0.49 Tumor ploidy: 2.024 2 0 6 0.5 Fraction Genome 0.3 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0 log2 ratio

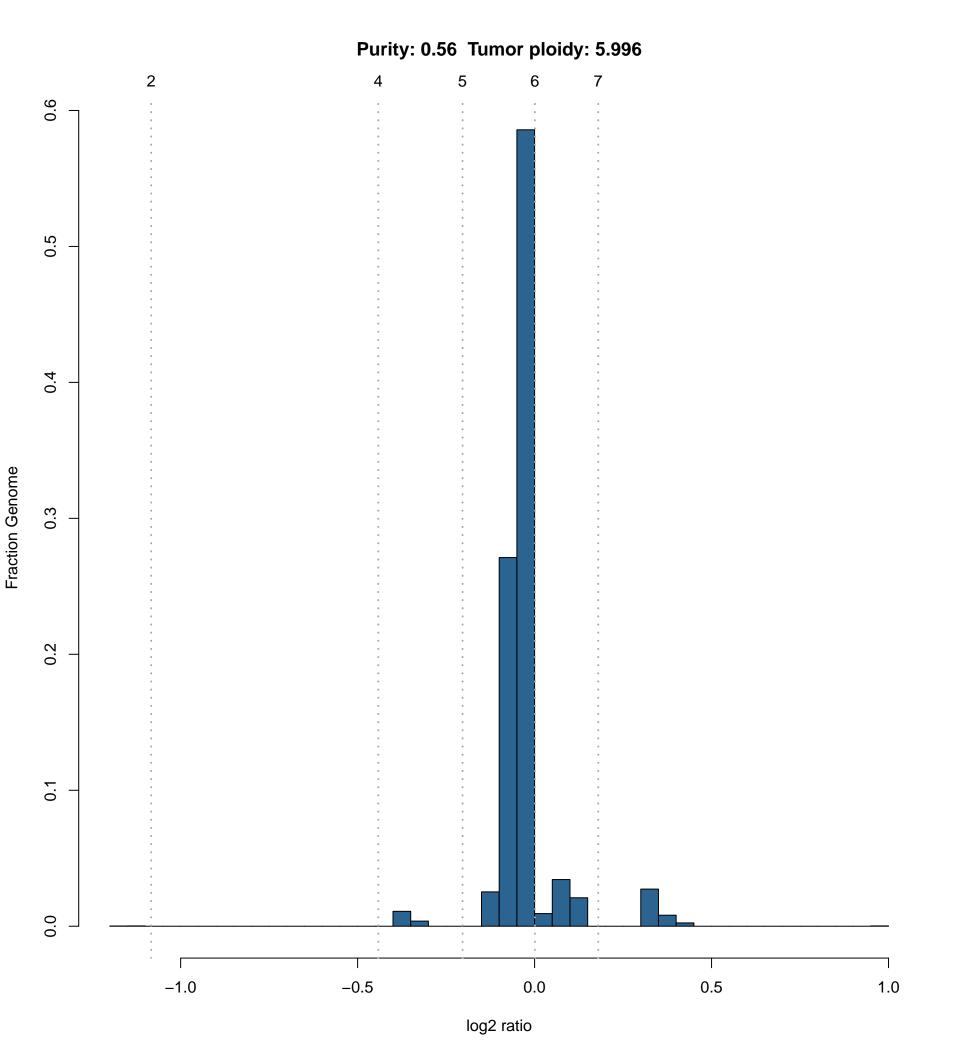


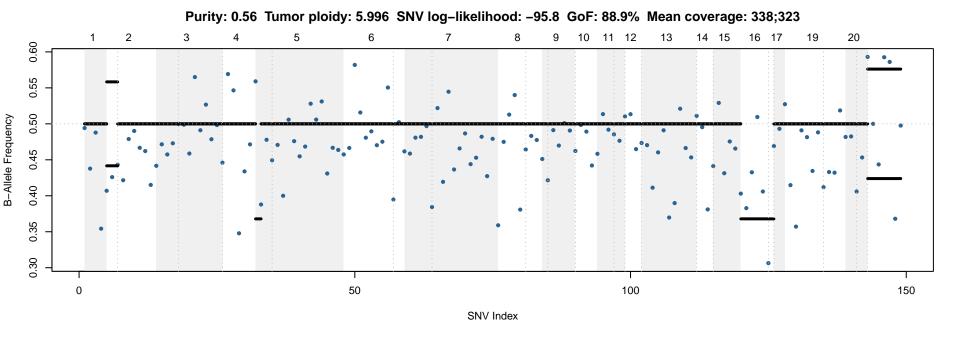
SCNA-fit log-likelihood: -6374.99



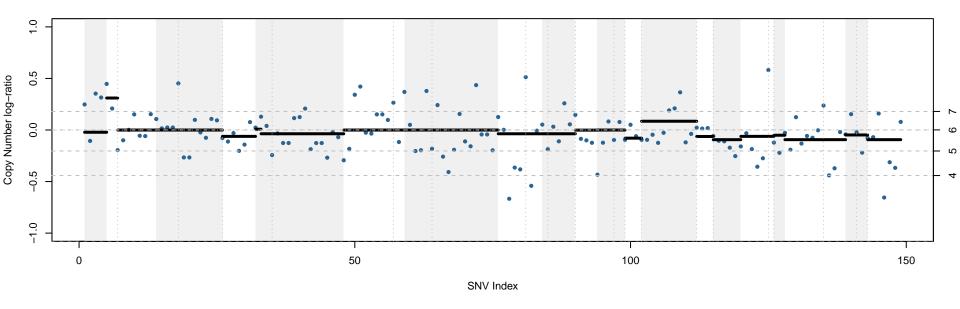


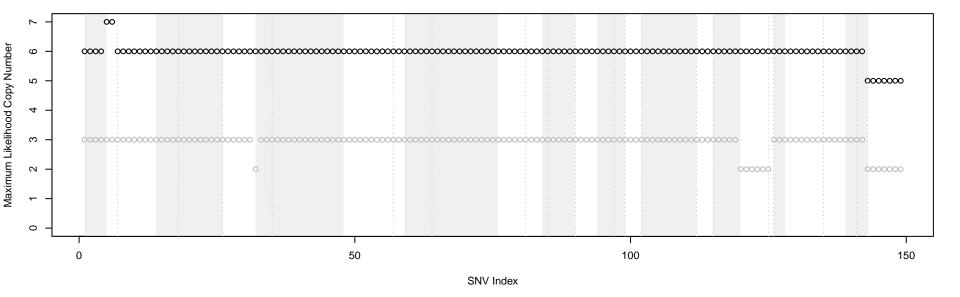


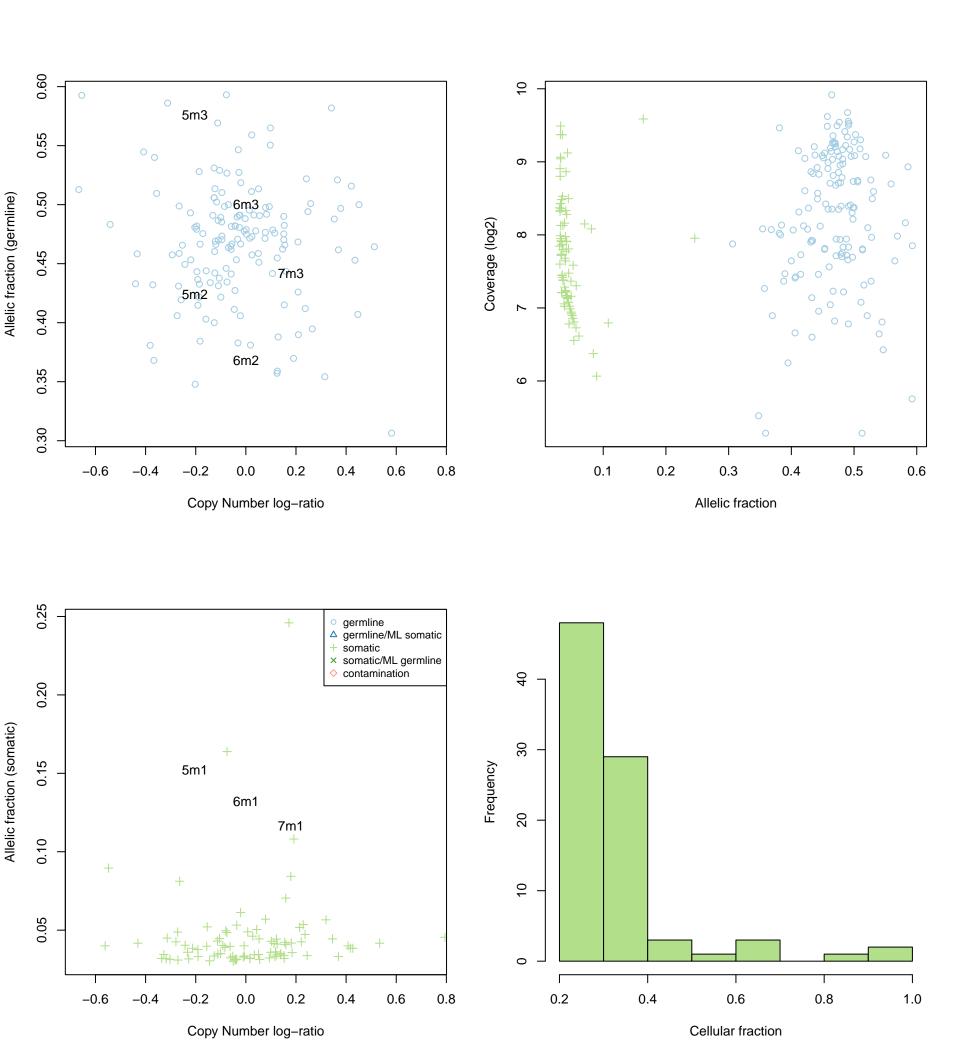


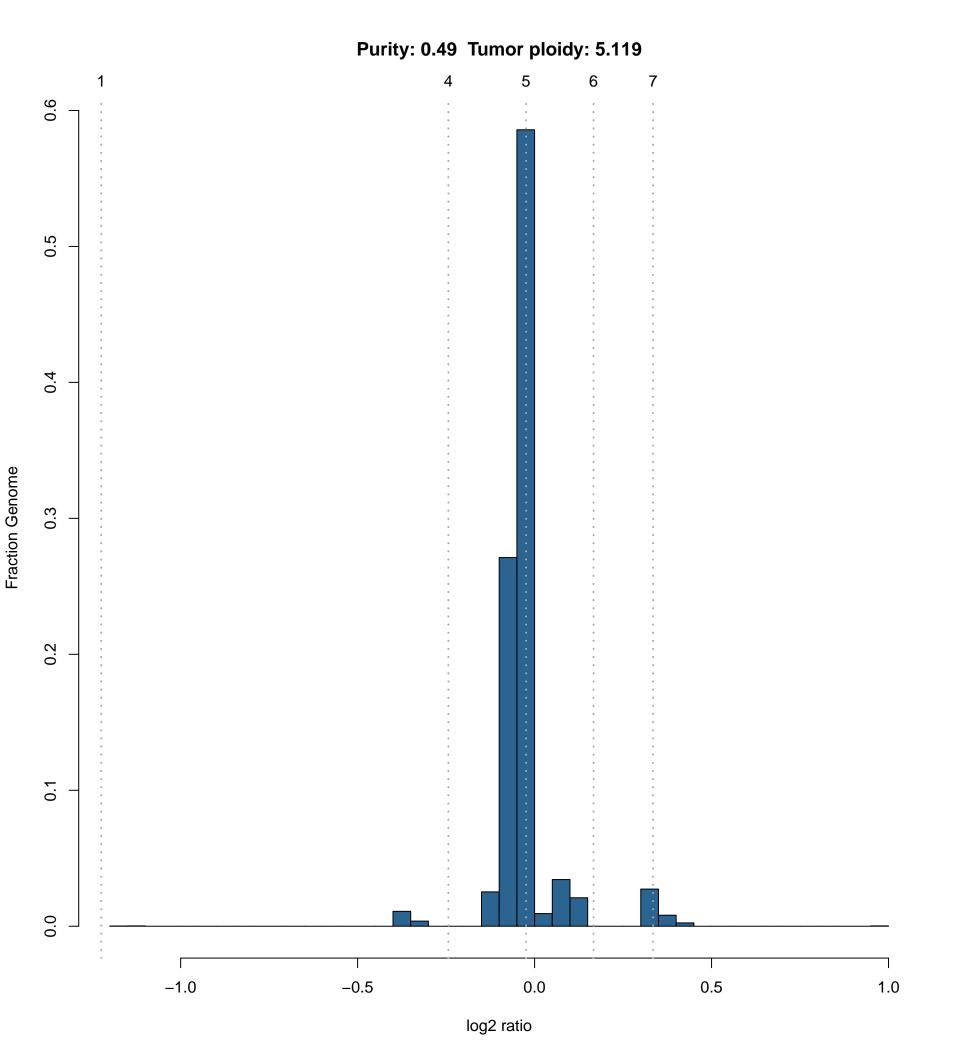


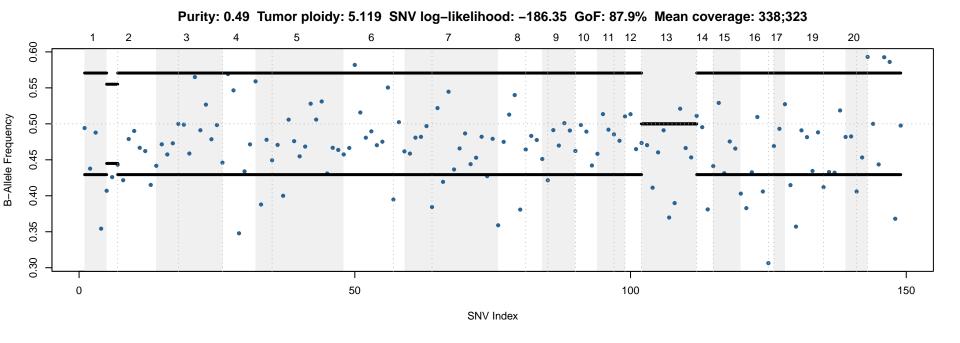
SCNA-fit log-likelihood: -6448.15



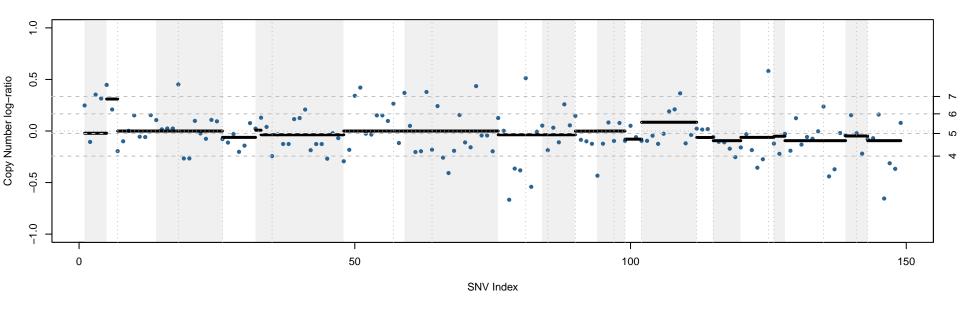


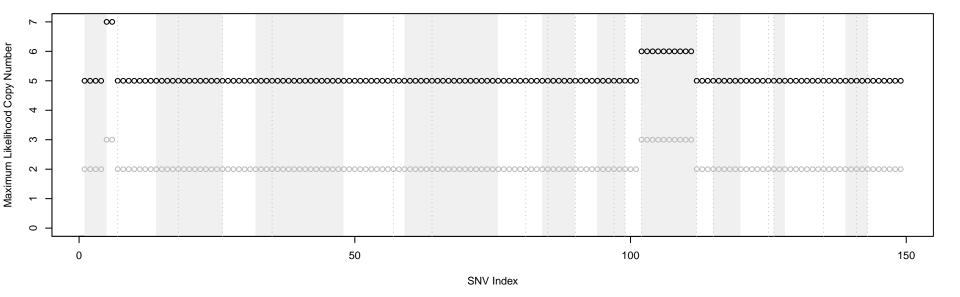


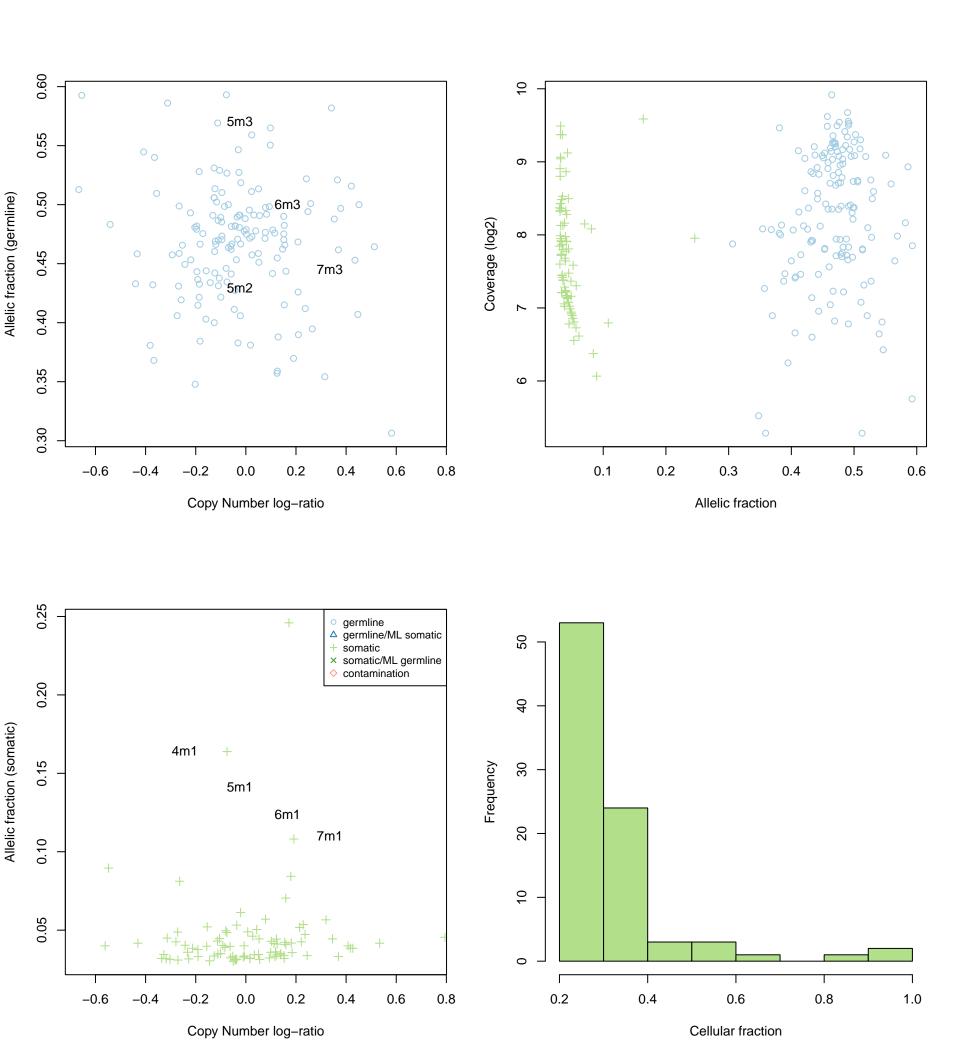




SCNA-fit log-likelihood: -6320.68

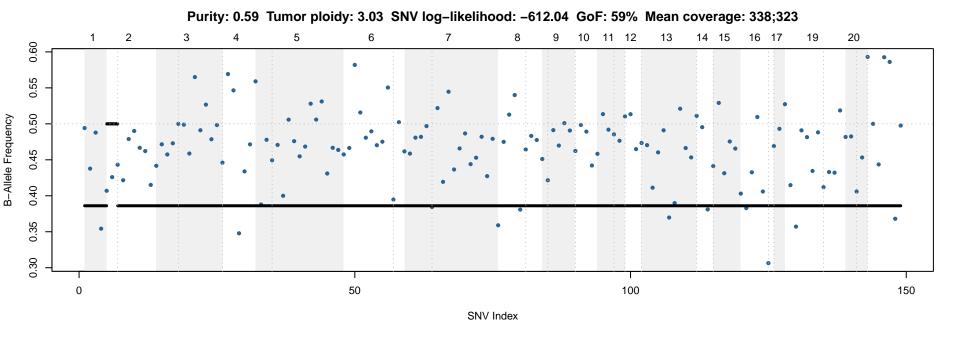




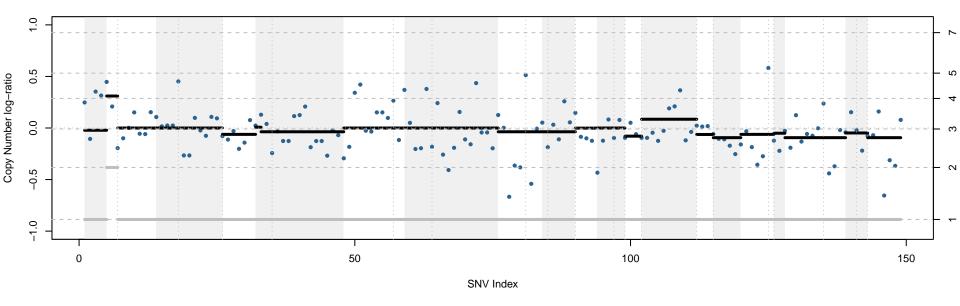


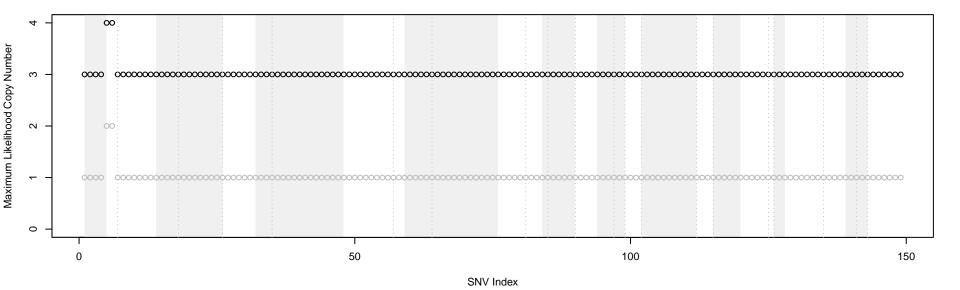
Purity: 0.59 Tumor ploidy: 3.03 3 5 7 0.5 Fraction Genome 0.3 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0

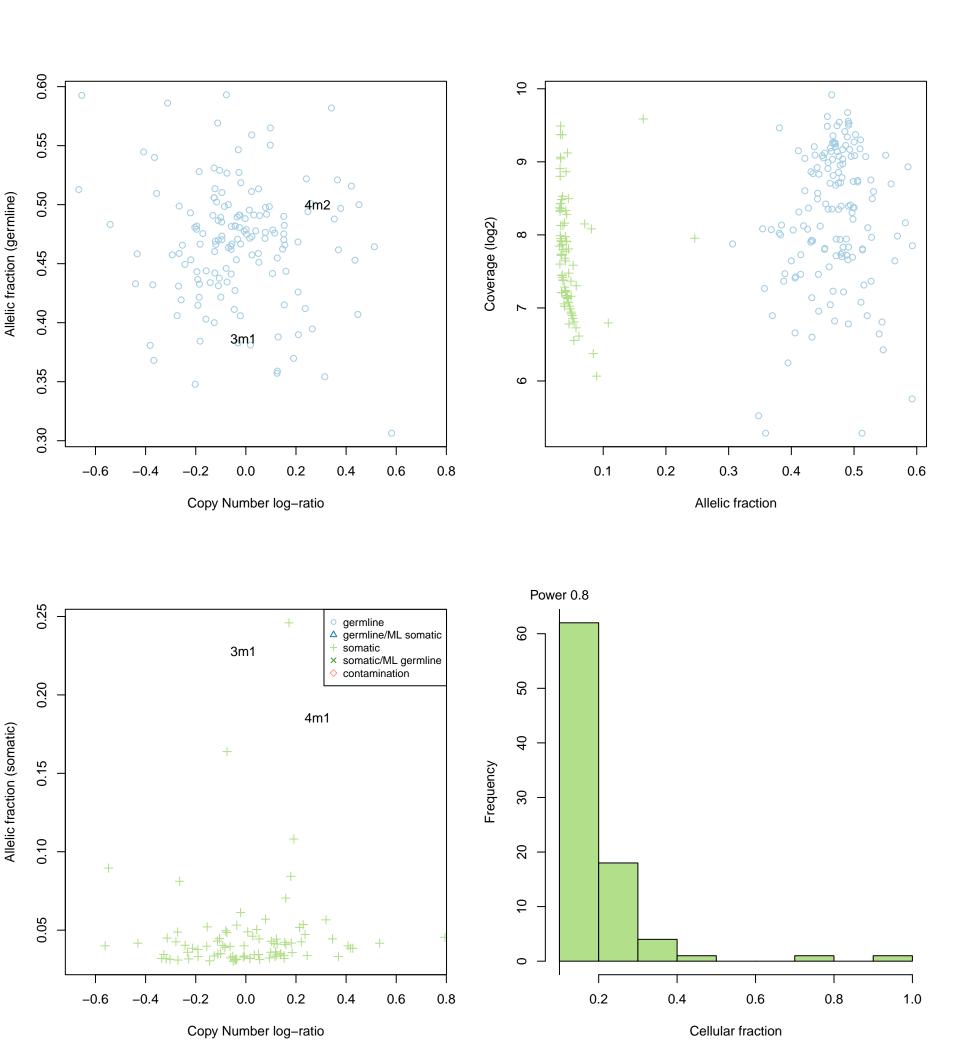
log2 ratio



SCNA-fit log-likelihood: -6374.83

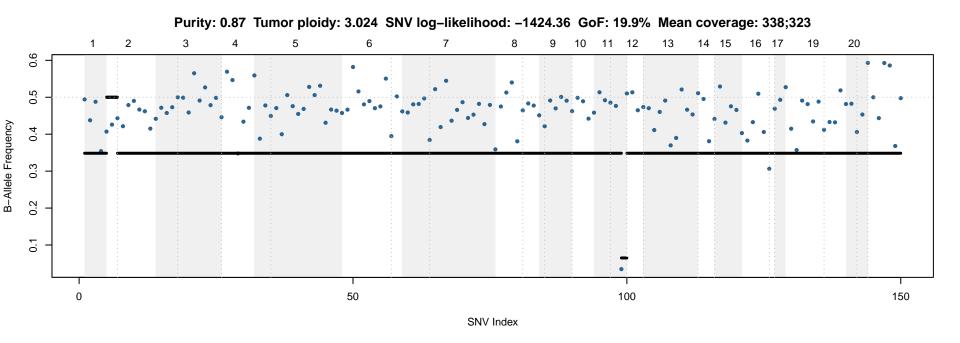






Purity: 0.87 Tumor ploidy: 3.024 3 2 6 0.5 Fraction Genome 0.3 0.1 0.0 -1.0 -0.5 0.0 0.5 1.0

log2 ratio



SCNA-fit log-likelihood: -6404.82

