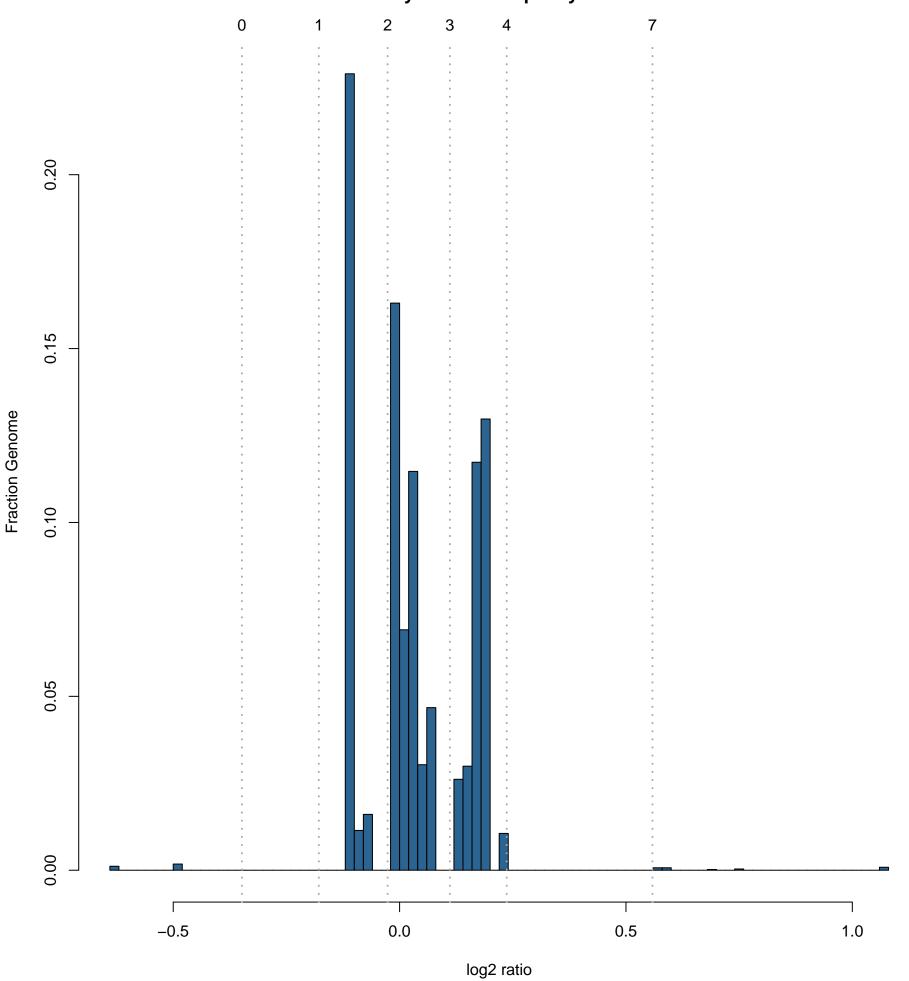
Purity: 0.2 Tumor ploidy: 2.185



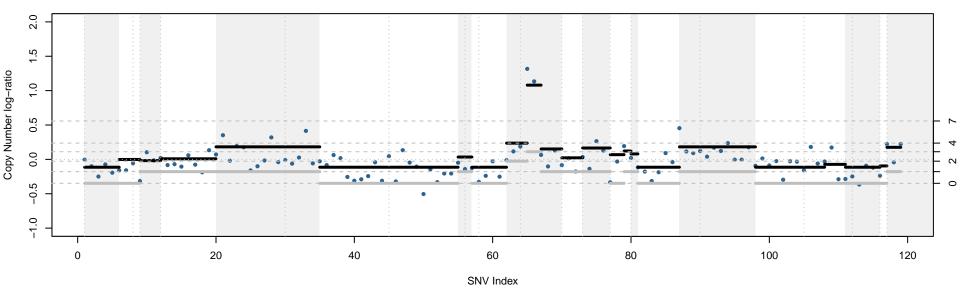
Purity: 0.2 Tumor ploidy: 2.185 SNV log-likelihood: 88.91 GoF: 94.9% Mean coverage: 597;603

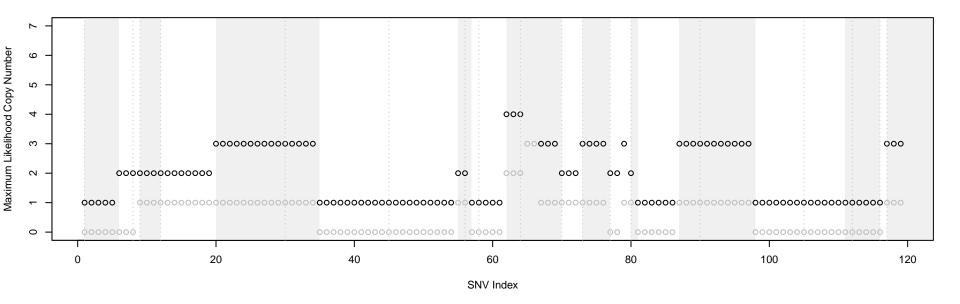
1 3 4 5 6 7 8 9 11 12 13 14 16 17 19 20 21

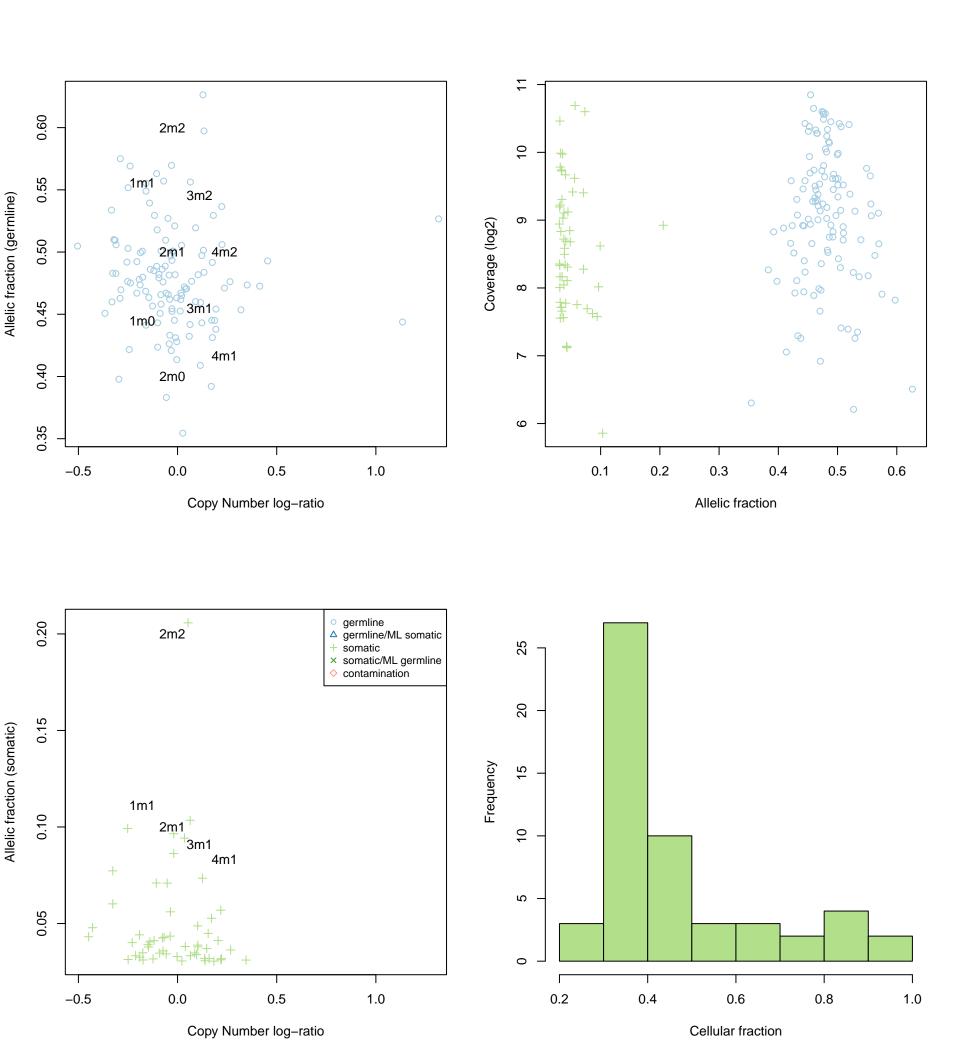
0.35

SCNA-fit log-likelihood: -5250.21

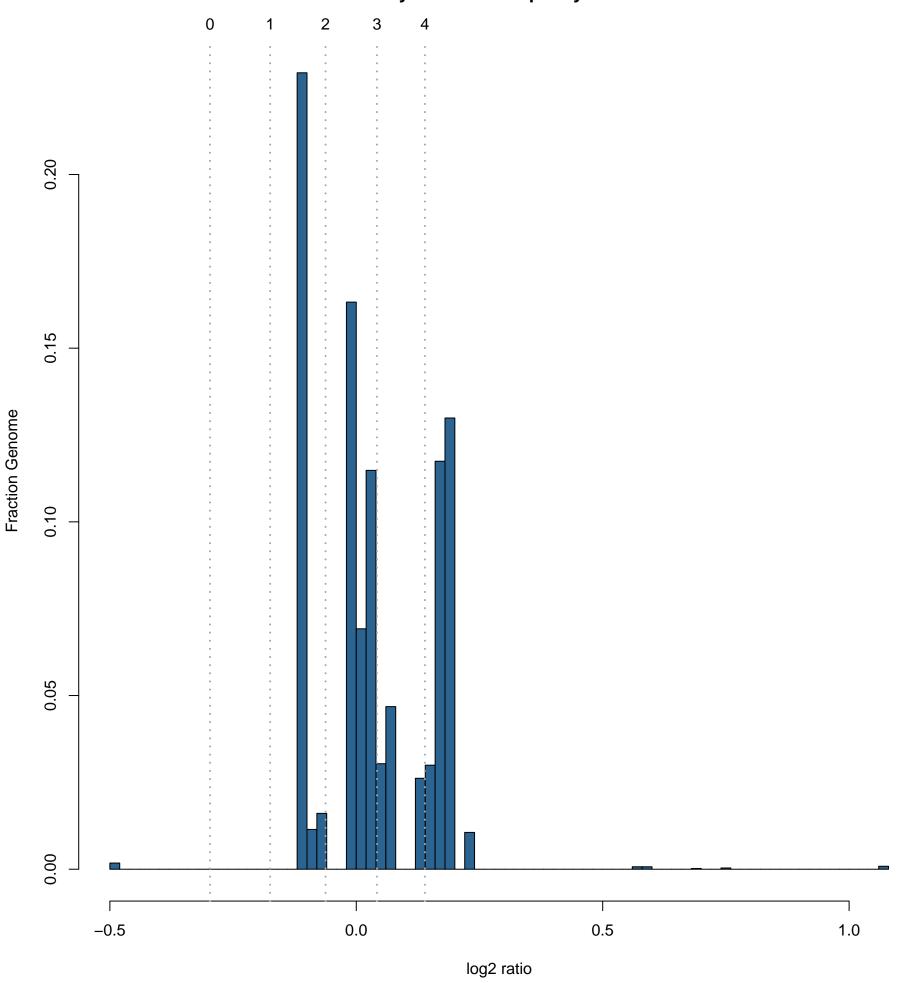
SNV Index



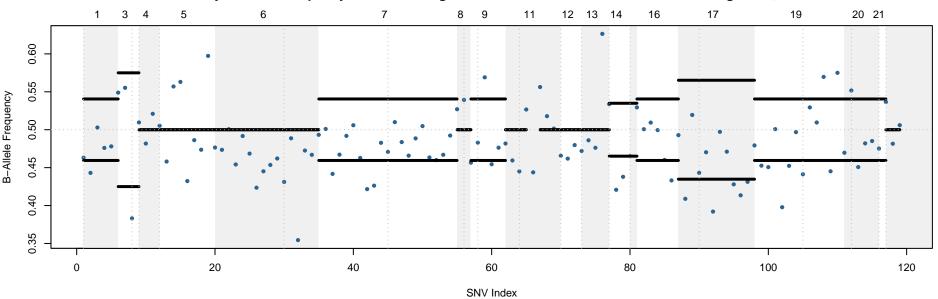




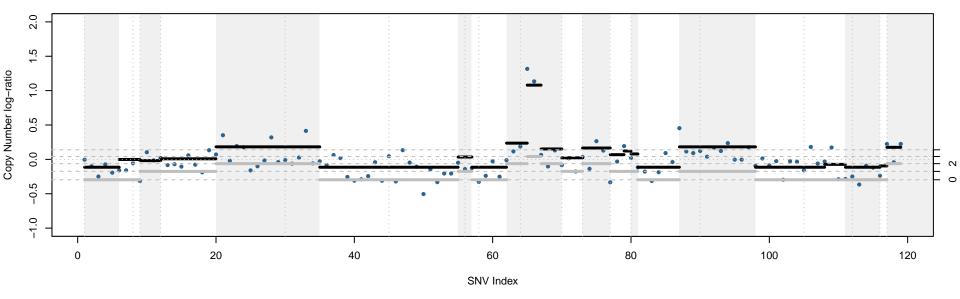
Purity: 0.15 Tumor ploidy: 2.589

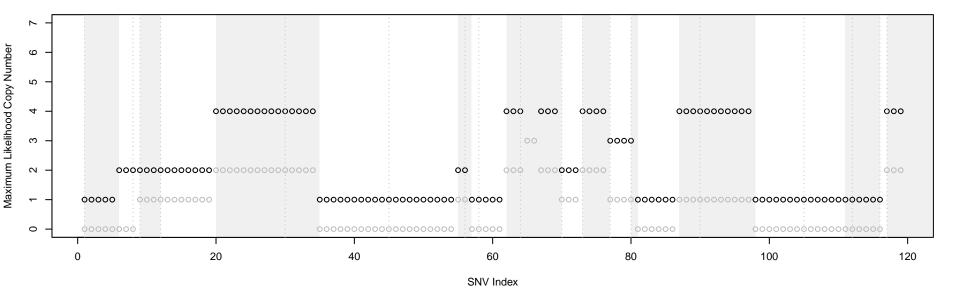


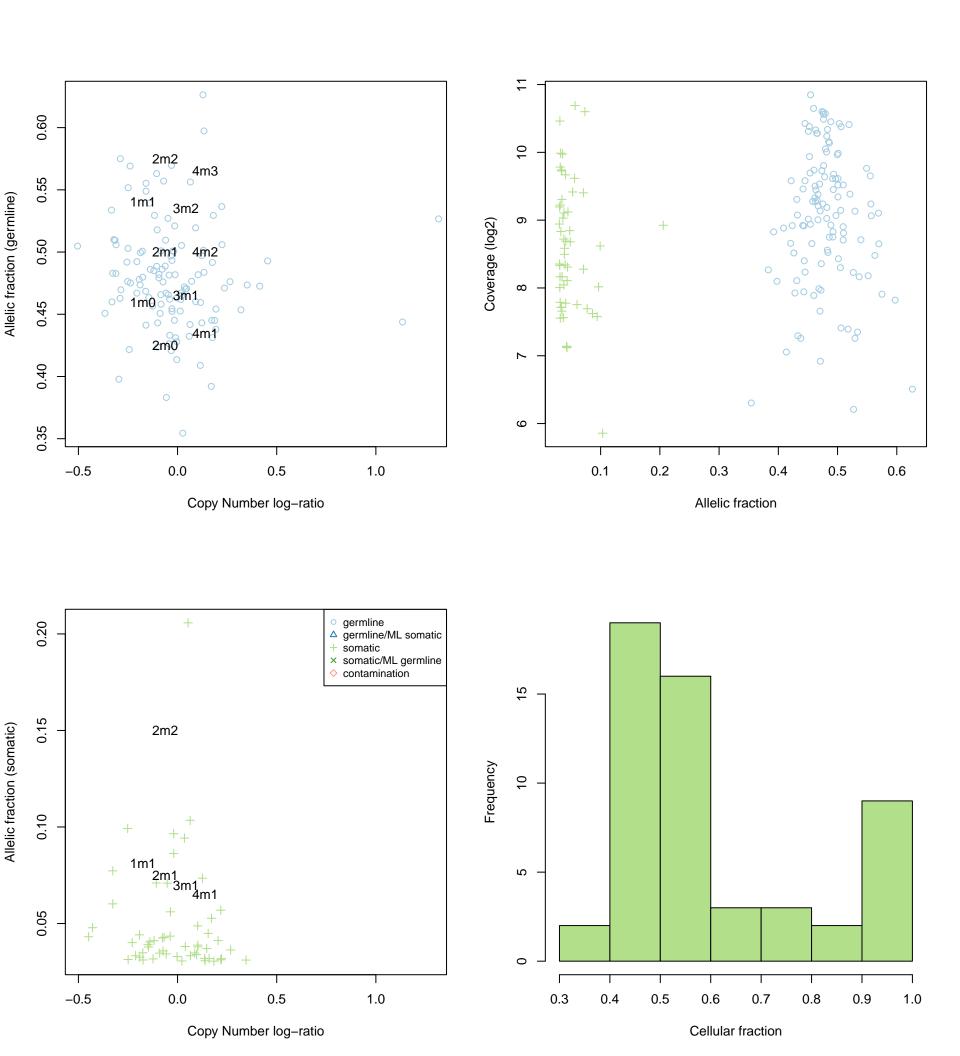
Purity: 0.15 Tumor ploidy: 2.589 SNV log-likelihood: 79.98 GoF: 96.4% Mean coverage: 597;603



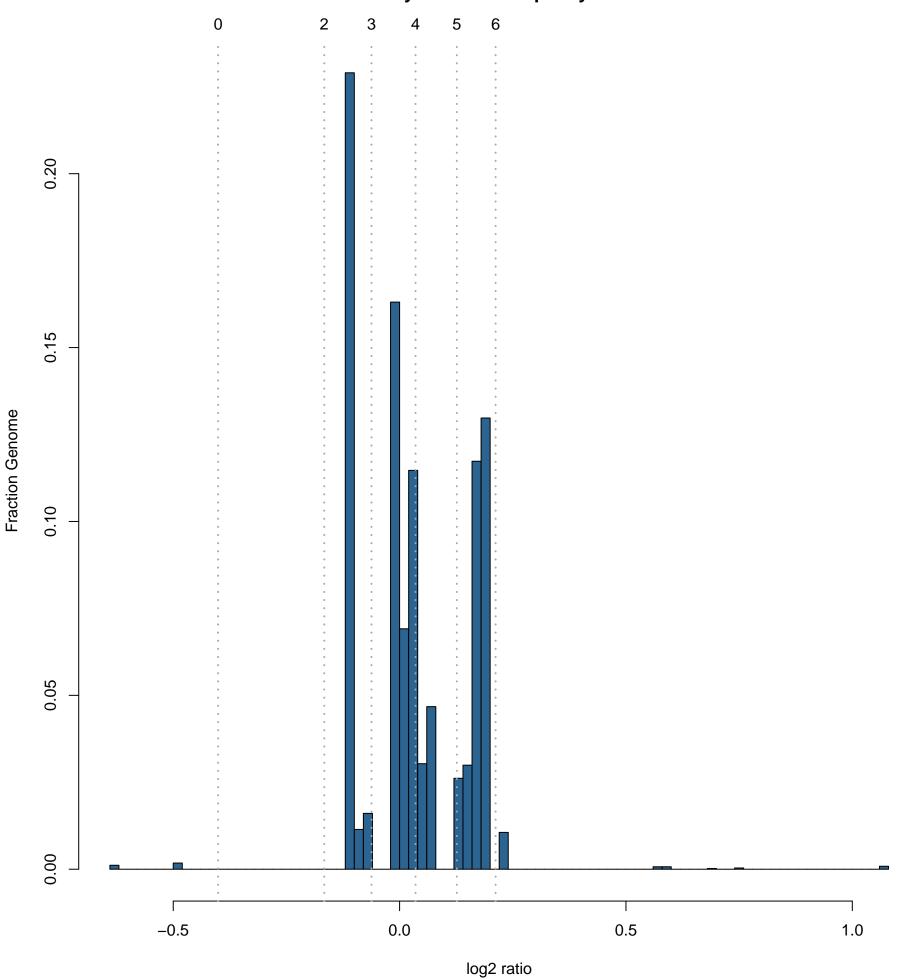
SCNA-fit log-likelihood: -5274.74

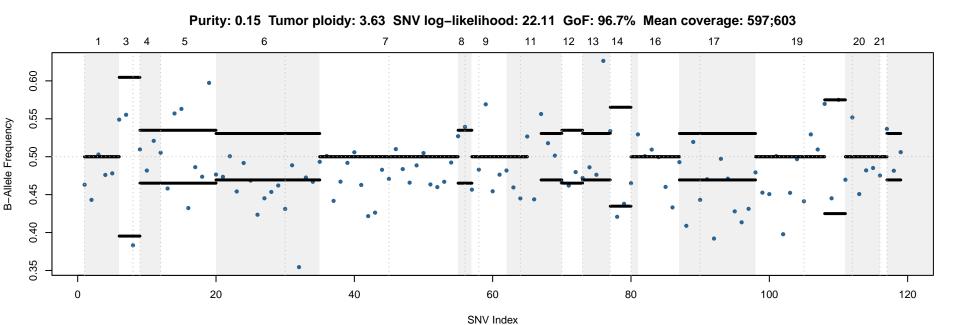




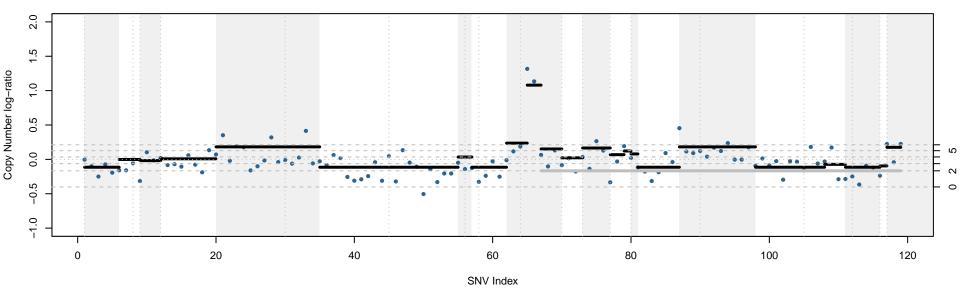


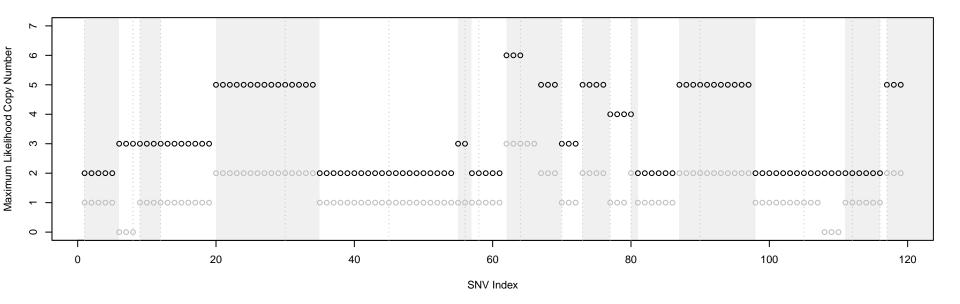
Purity: 0.15 Tumor ploidy: 3.63

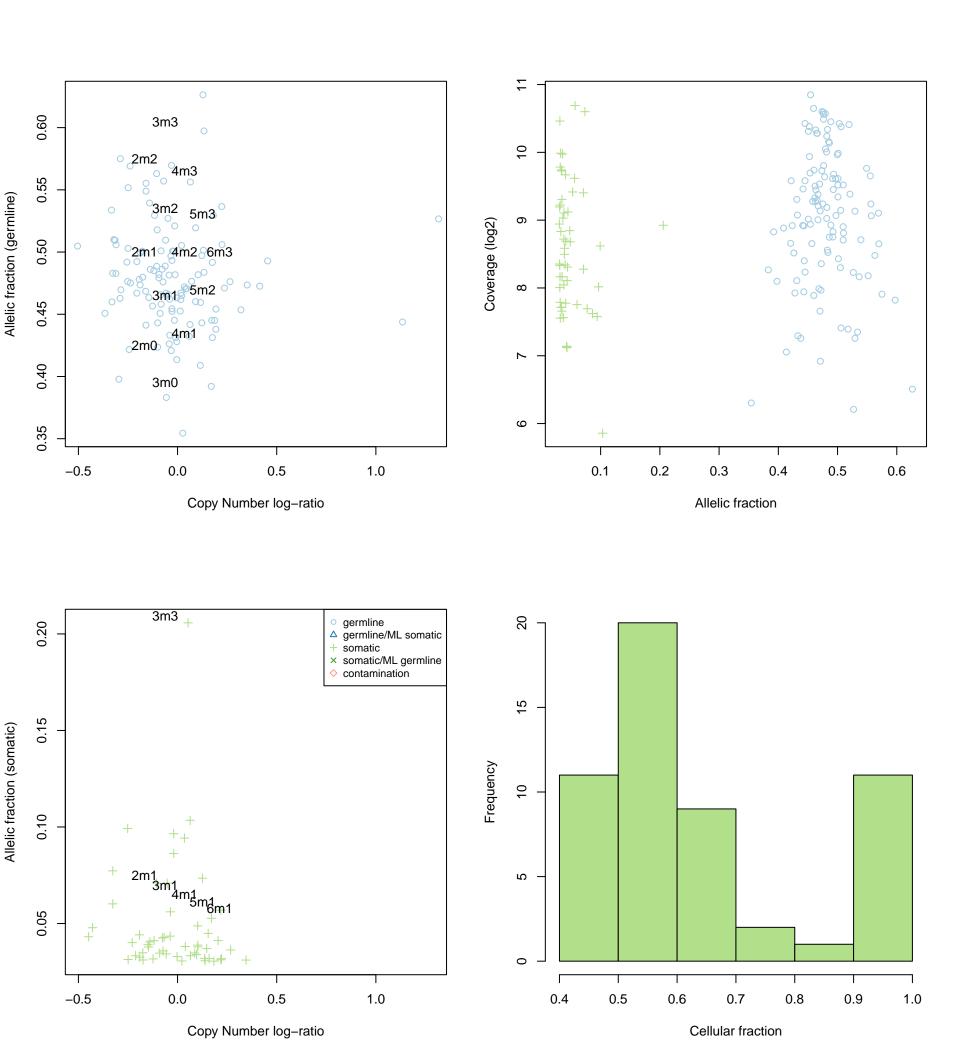




SCNA-fit log-likelihood: -5259.41







Purity: 0.34 Tumor ploidy: 2.454 2 3 0 5 6 7 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0

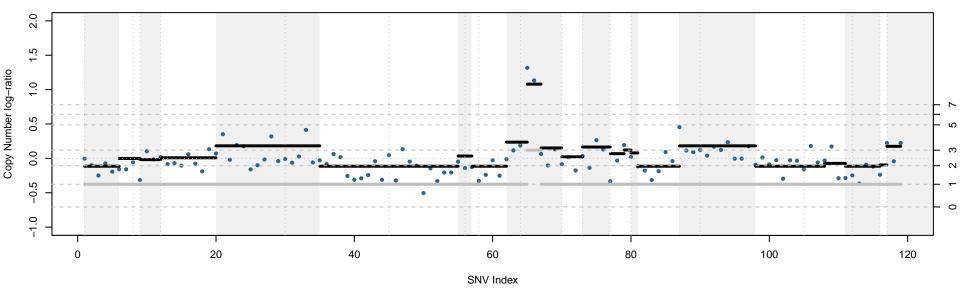
Purity: 0.34 Tumor ploidy: 2.454 SNV log-likelihood: 29.48 GoF: 86.3% Mean coverage: 597;603

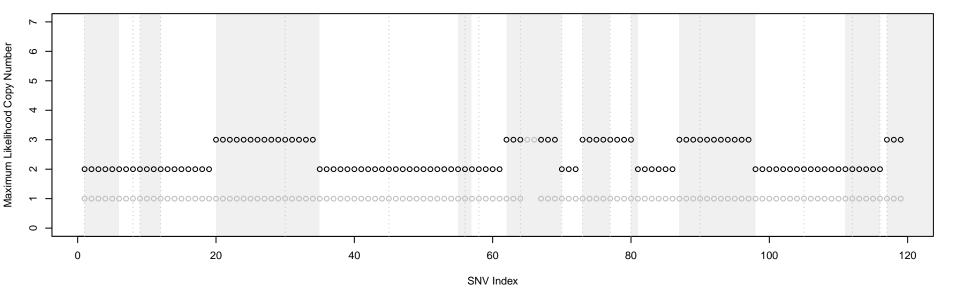
1 3 4 5 6 7 8 9 11 12 13 14 16 17 19 20 21

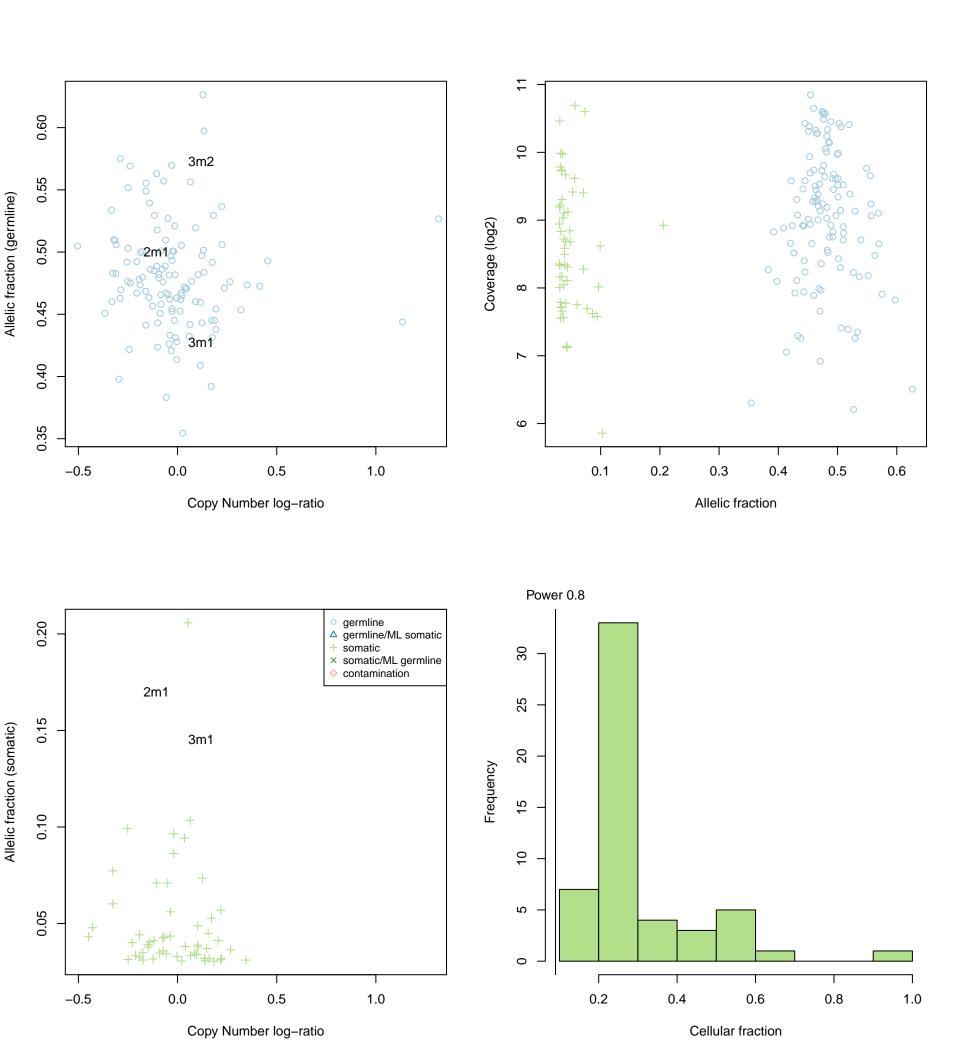
0.35

SCNA-fit log-likelihood: -5406.32

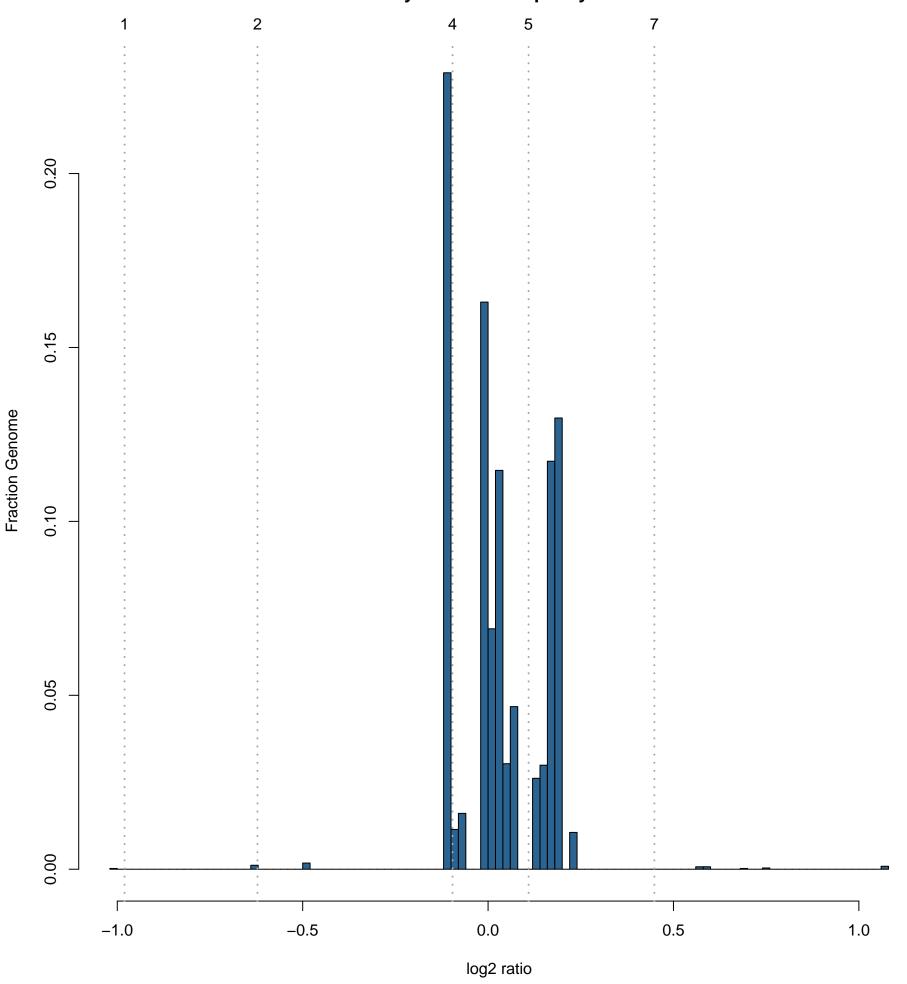
SNV Index

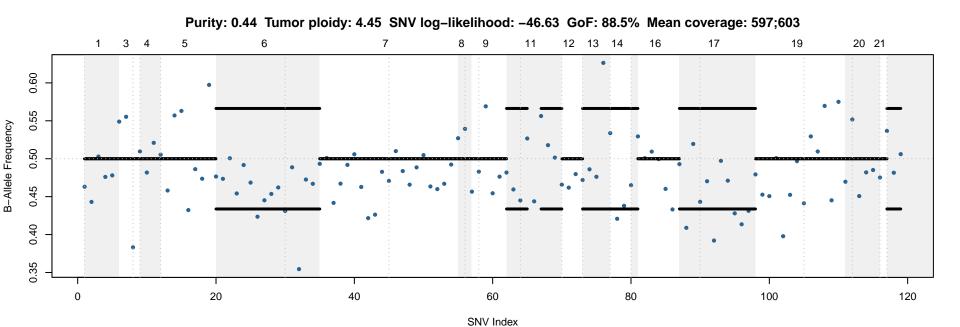




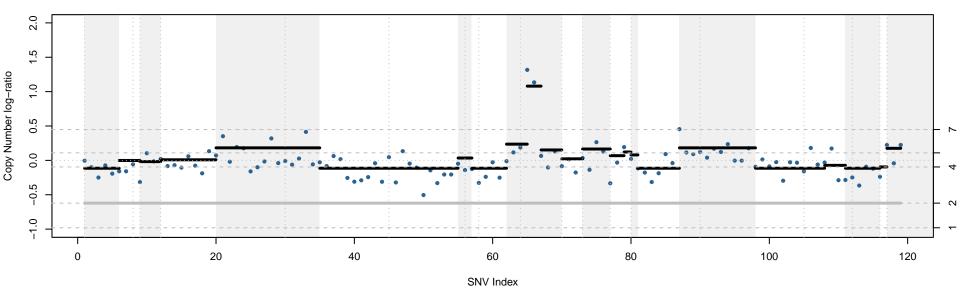


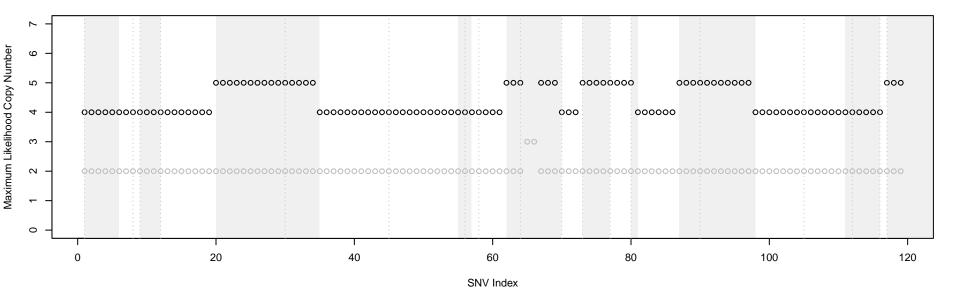
Purity: 0.44 Tumor ploidy: 4.45

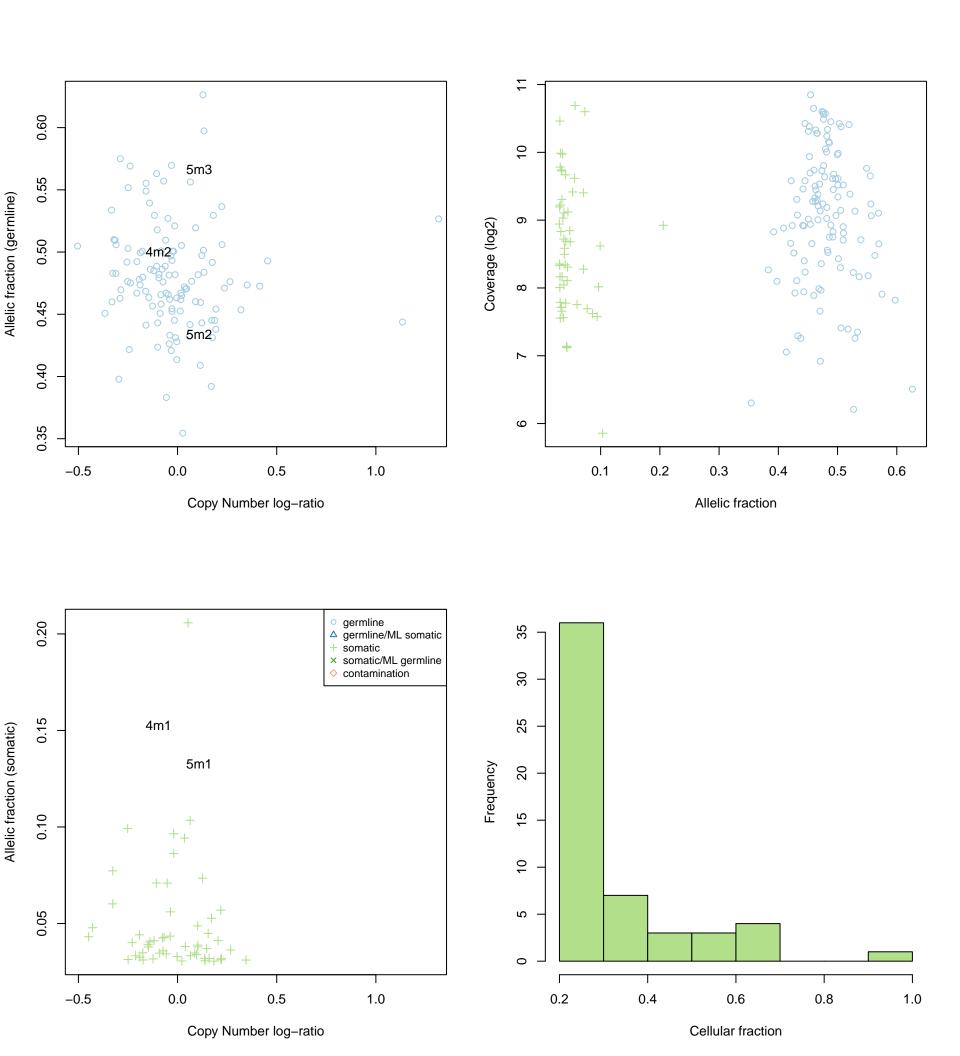




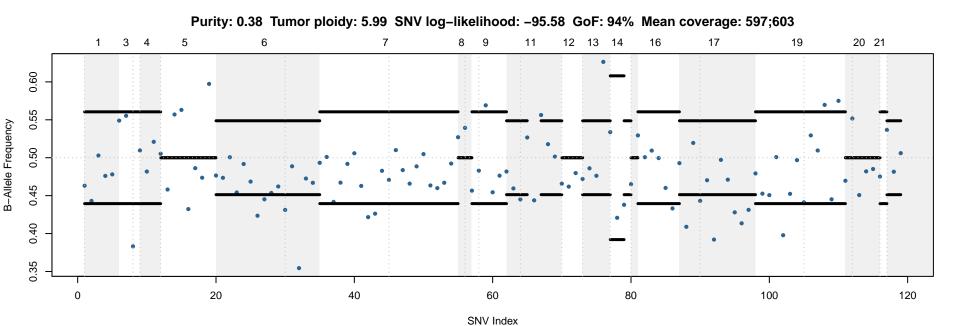
SCNA-fit log-likelihood: -5383.18



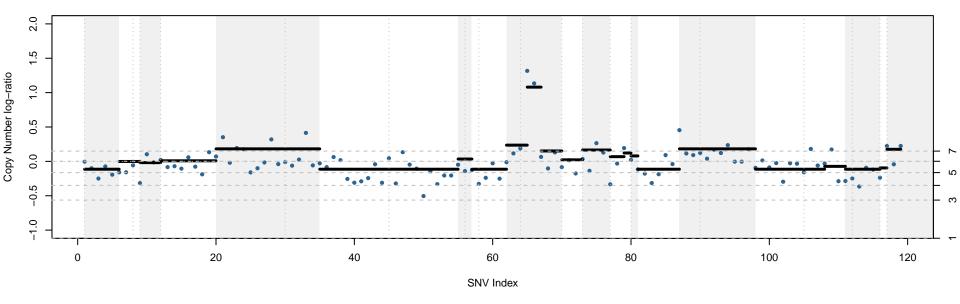


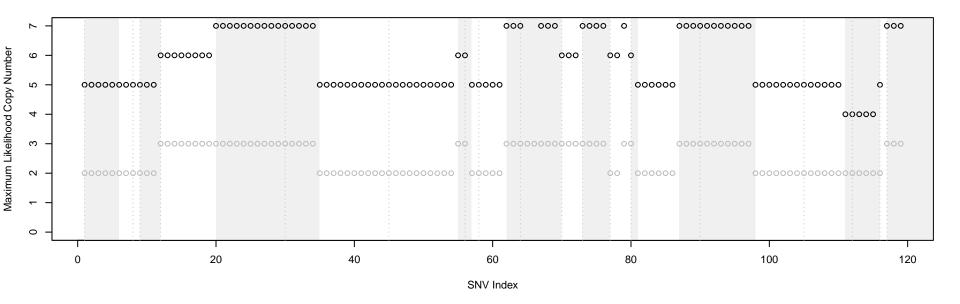


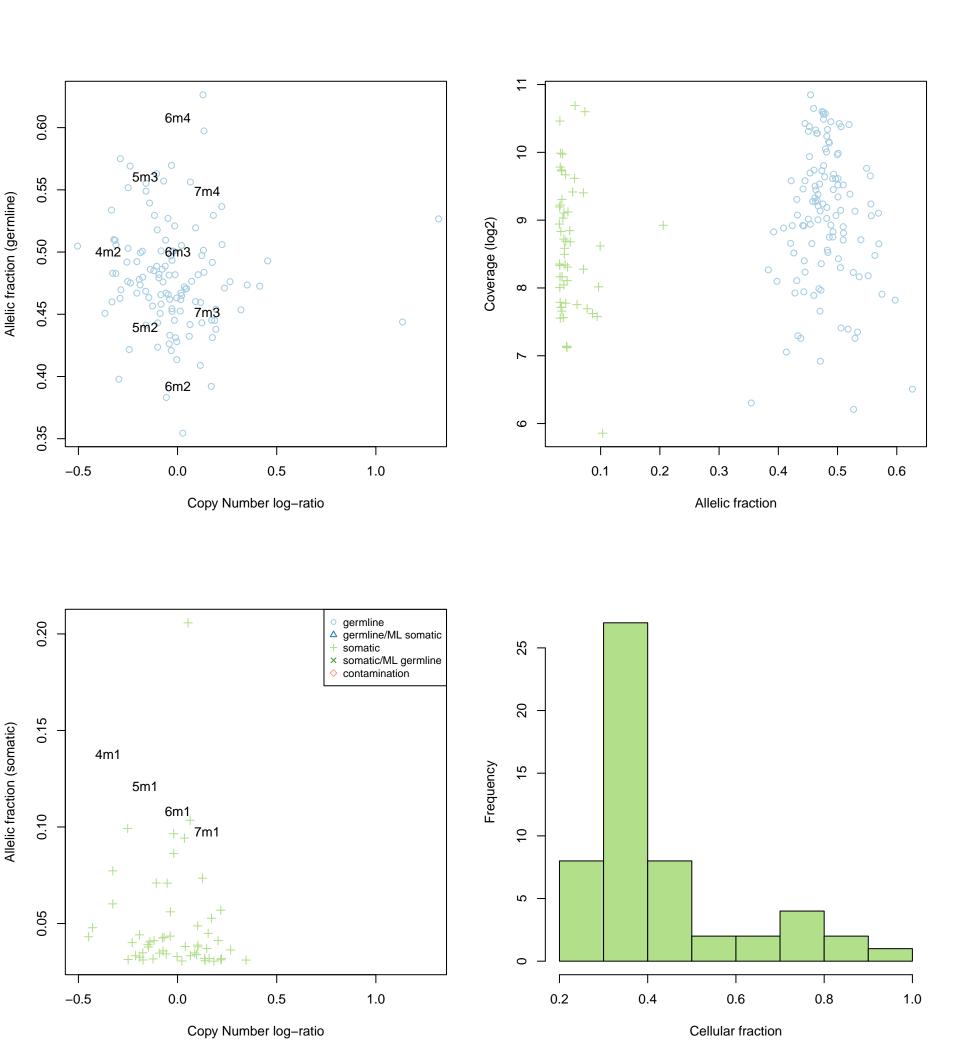
Purity: 0.38 Tumor ploidy: 5.99 6 3 5 7 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0



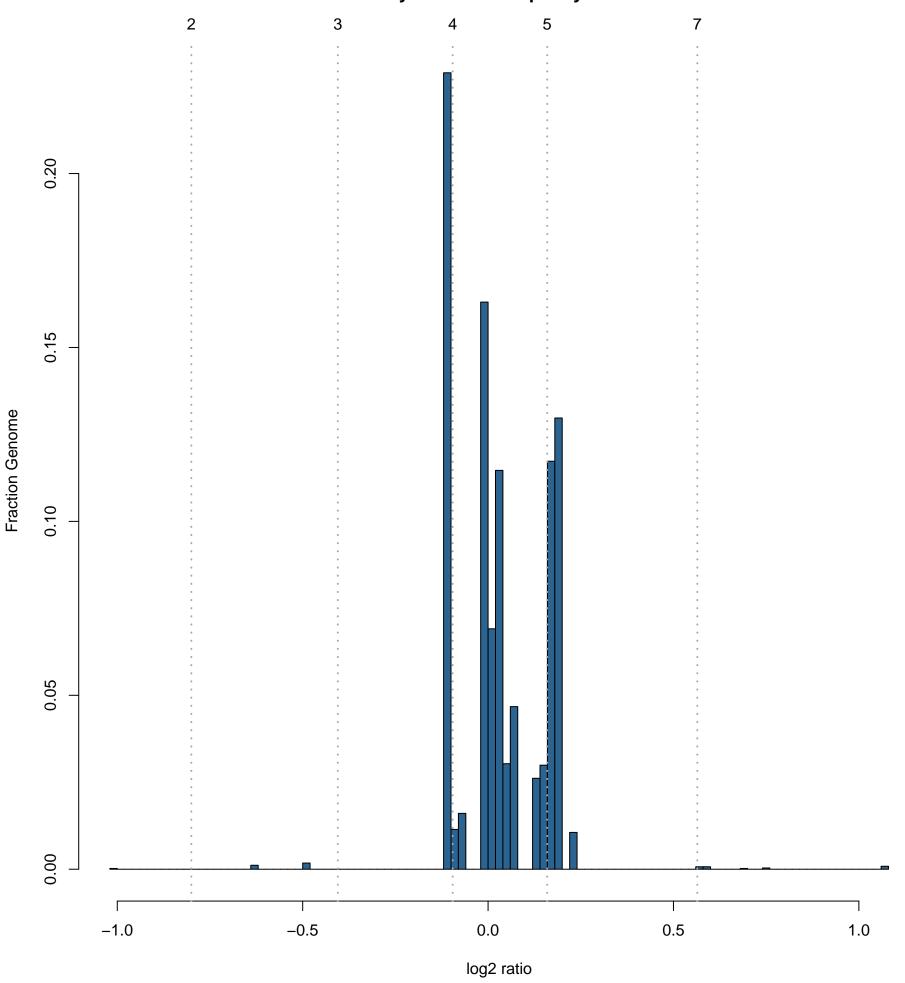
SCNA-fit log-likelihood: -5387.77

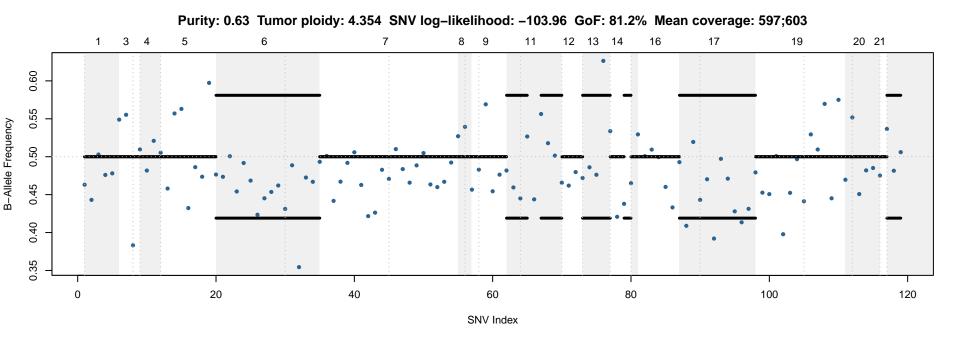




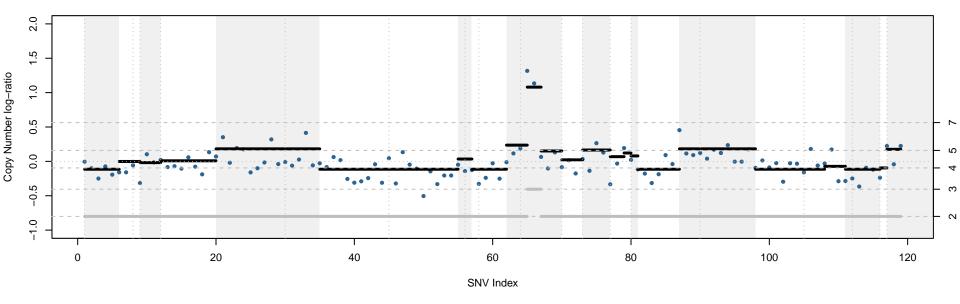


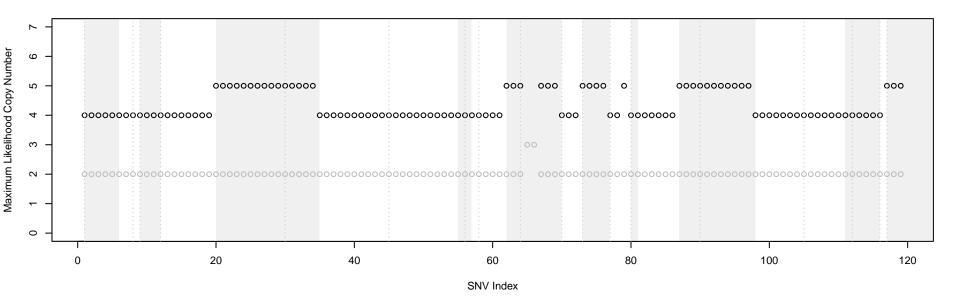
Purity: 0.63 Tumor ploidy: 4.354

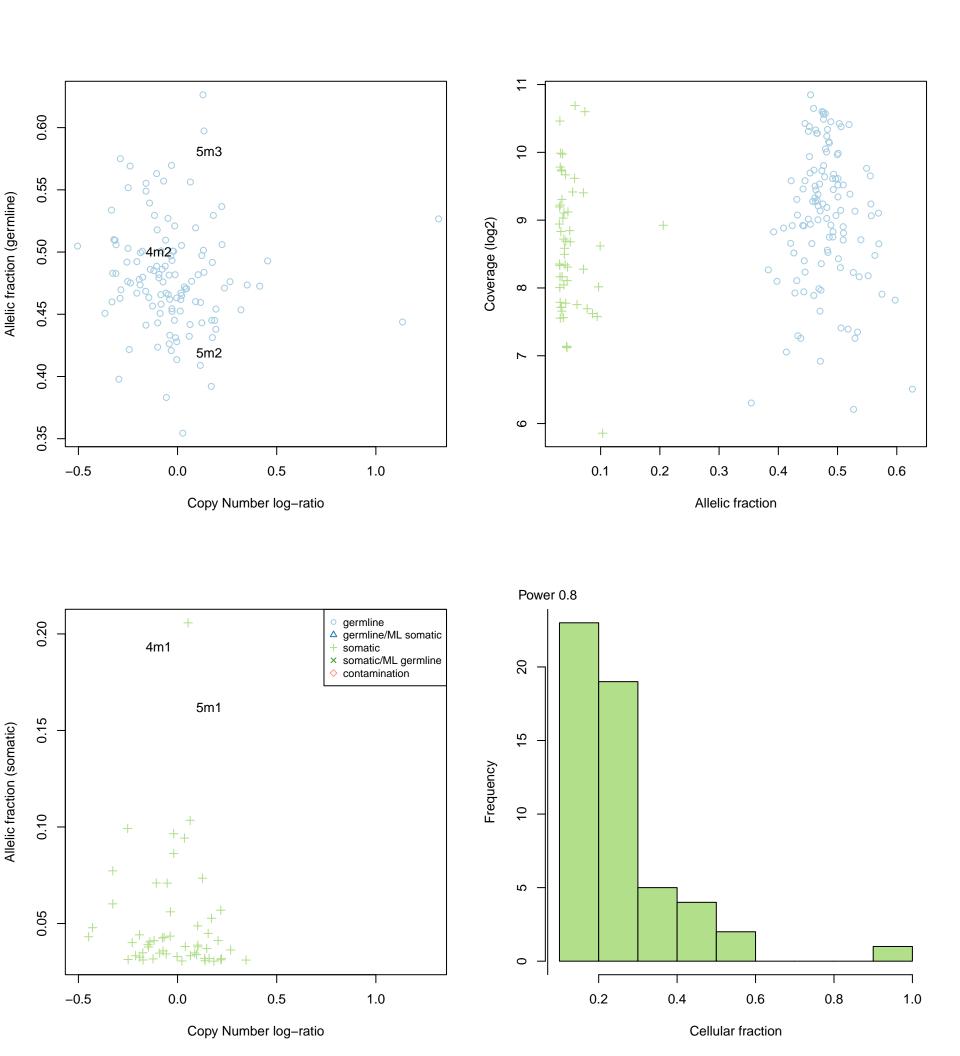




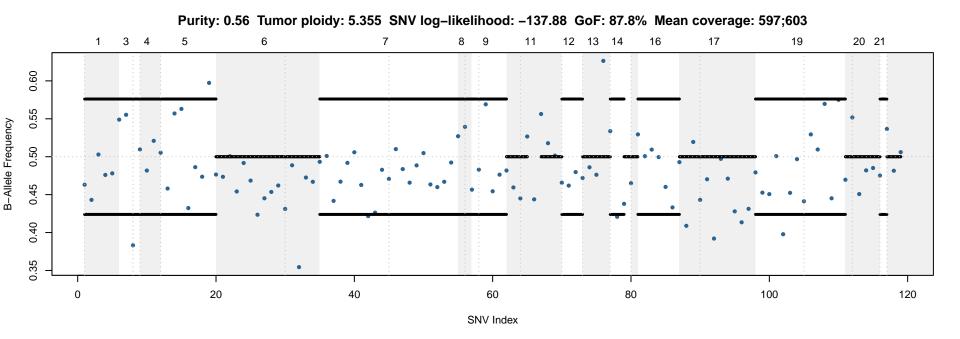
SCNA-fit log-likelihood: -5416.85



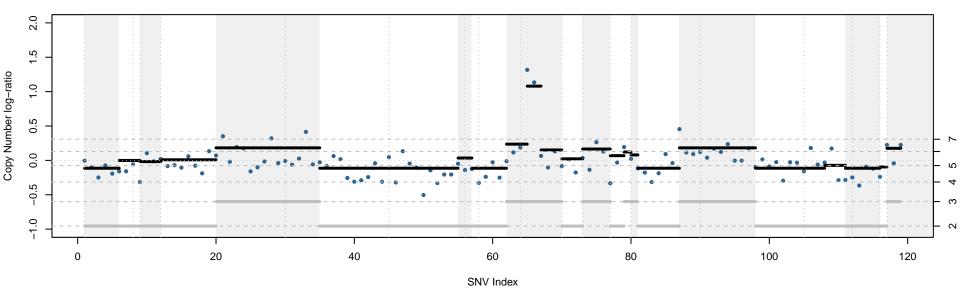


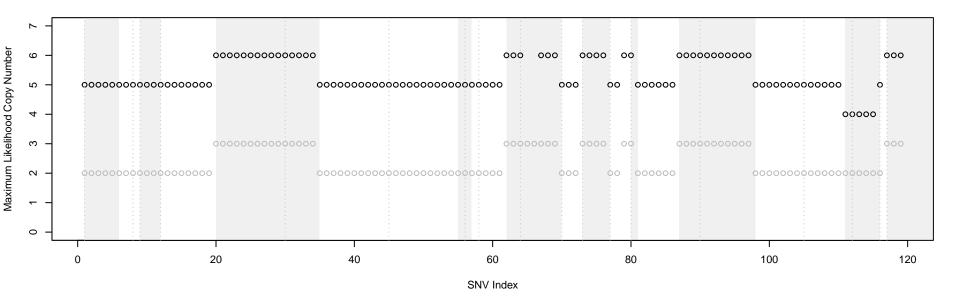


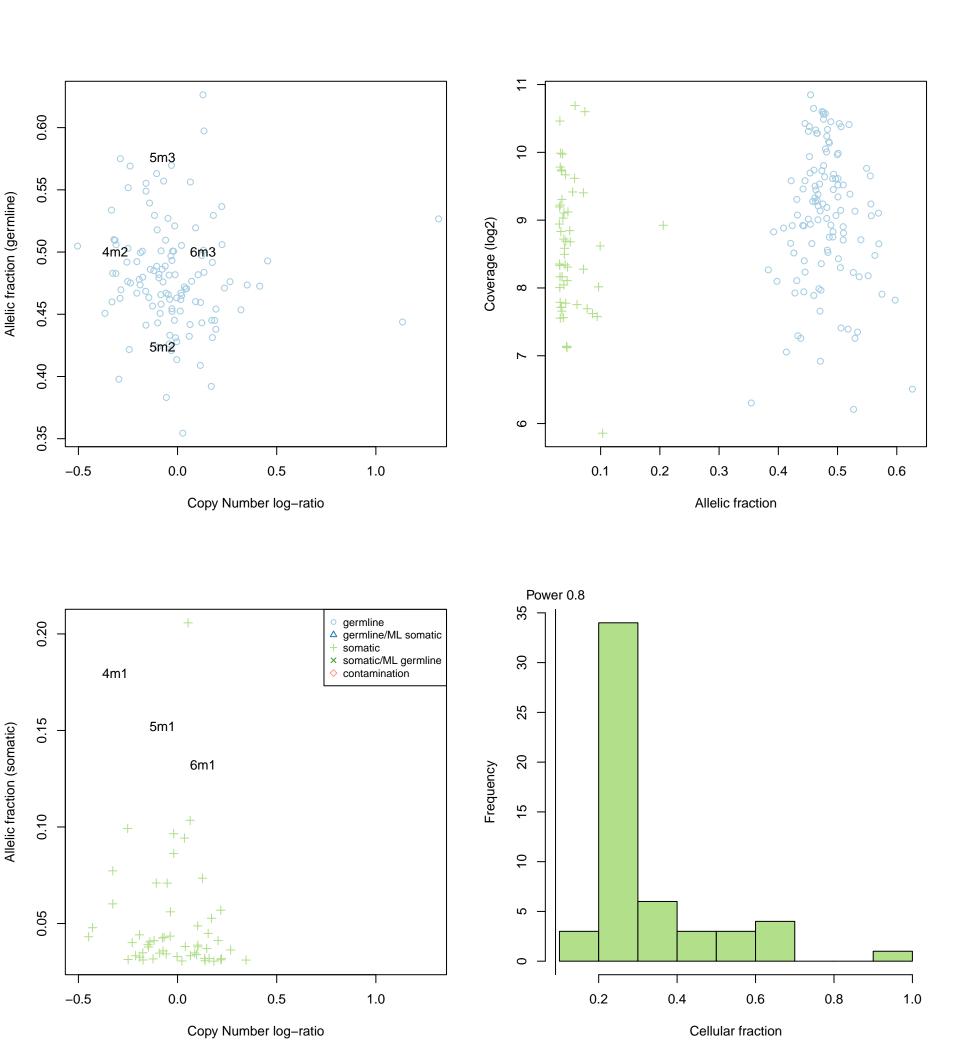
Purity: 0.56 Tumor ploidy: 5.355 2 3 6 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



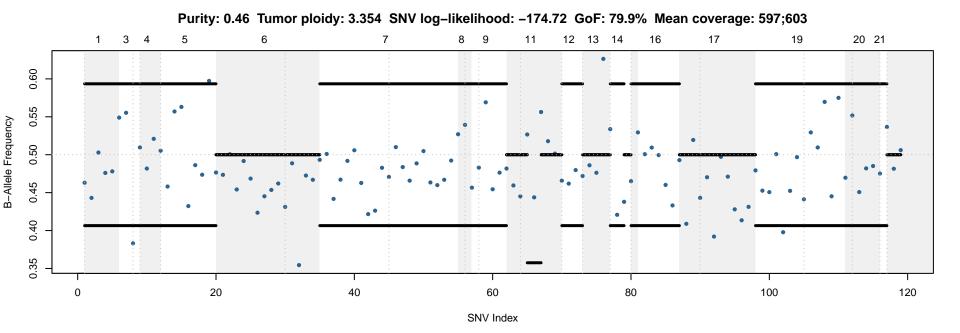
SCNA-fit log-likelihood: -5381.2



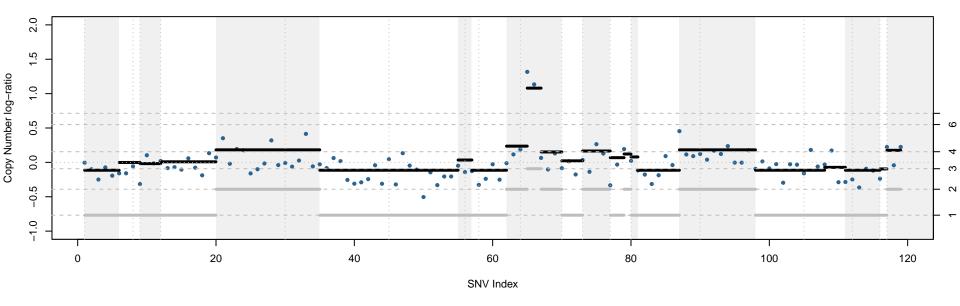


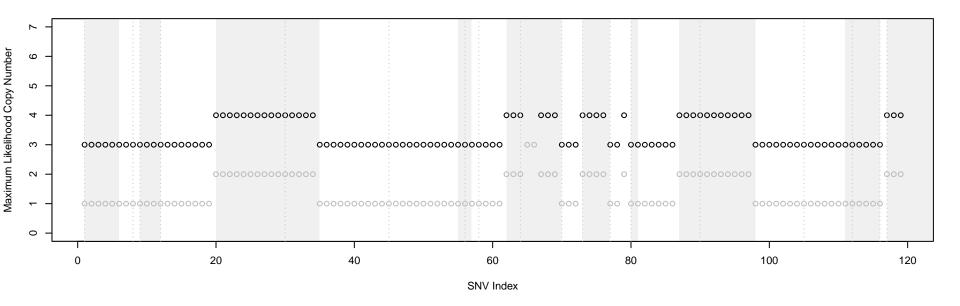


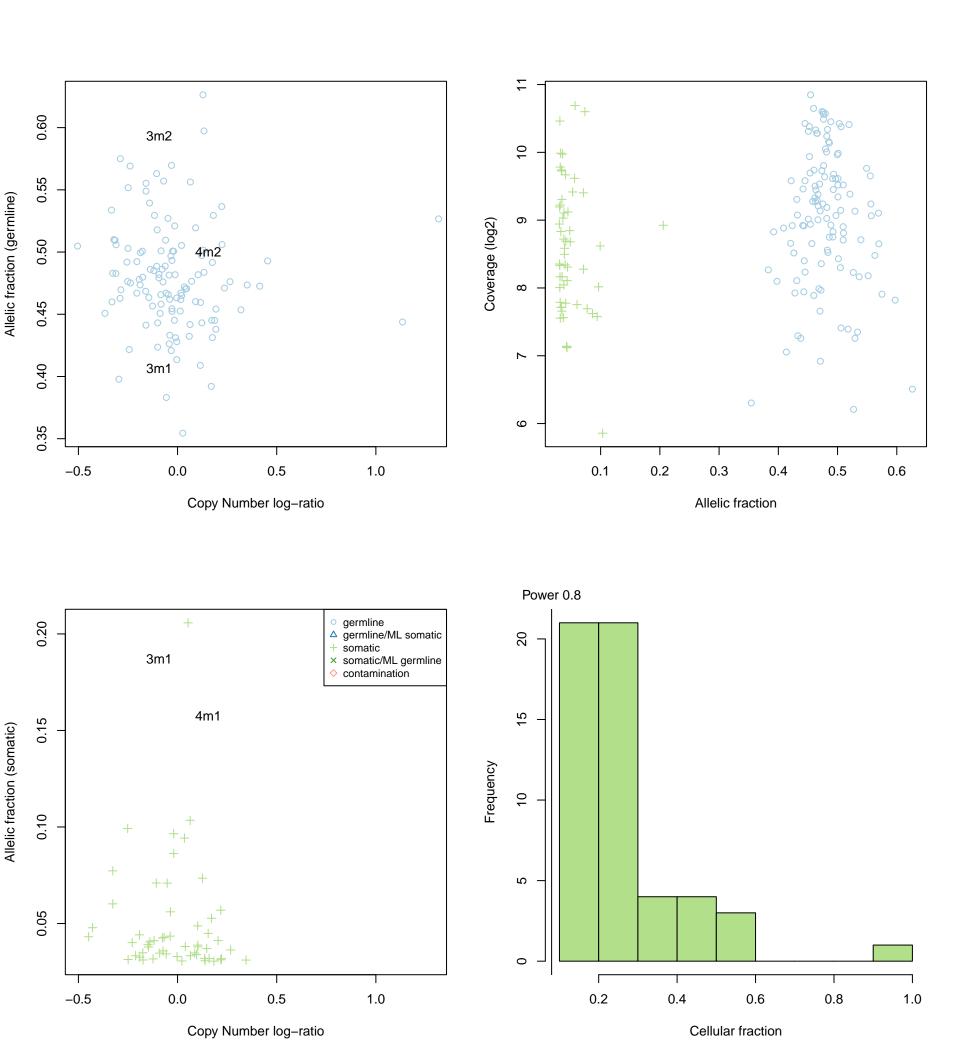
Purity: 0.46 Tumor ploidy: 3.354 3 2 6 7 Fraction Genome 0.05 0.00 0.0 -1.0 -0.5 0.5 1.0



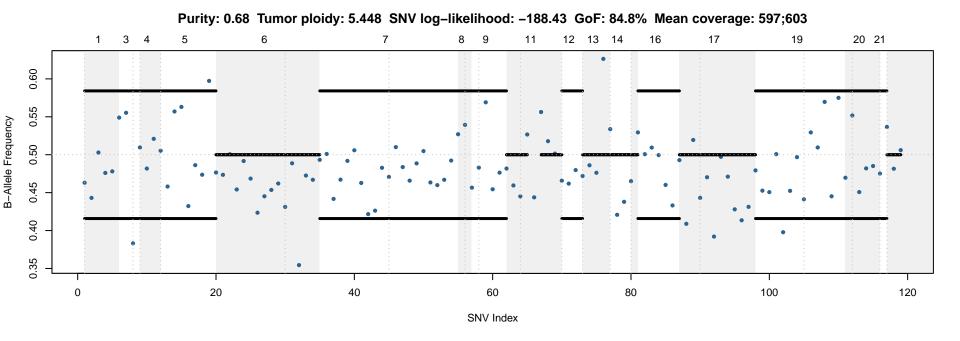
SCNA-fit log-likelihood: -5407.7



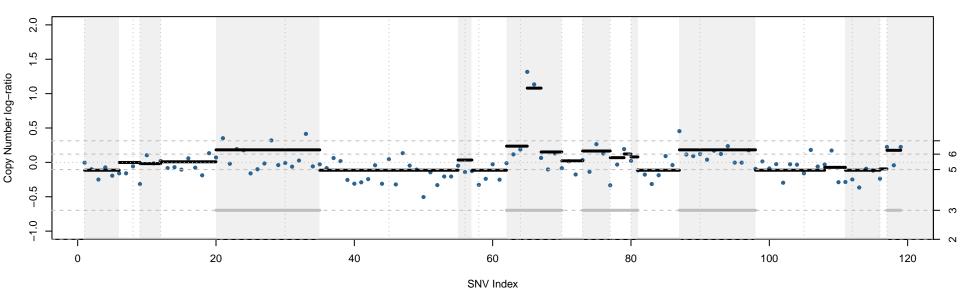


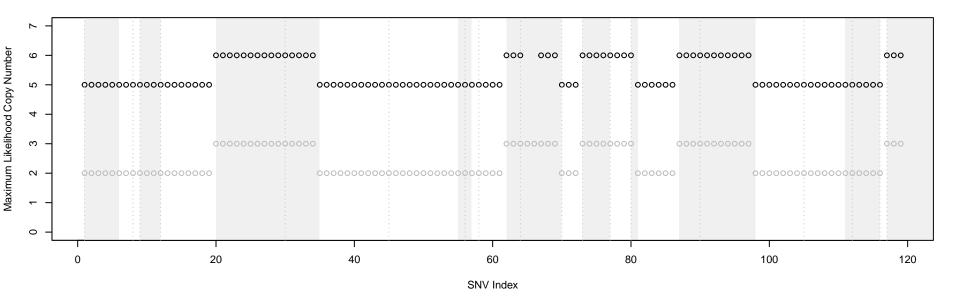


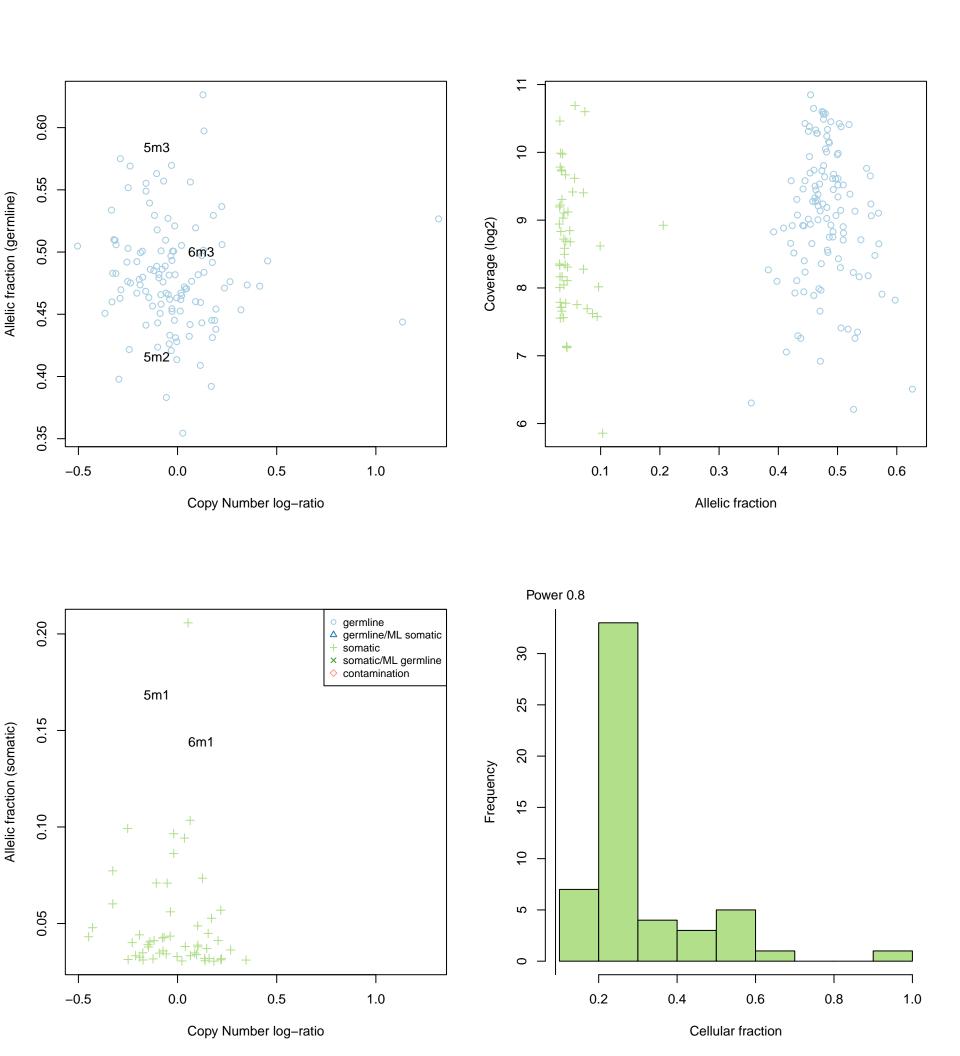
Purity: 0.68 Tumor ploidy: 5.448 3 5 6 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



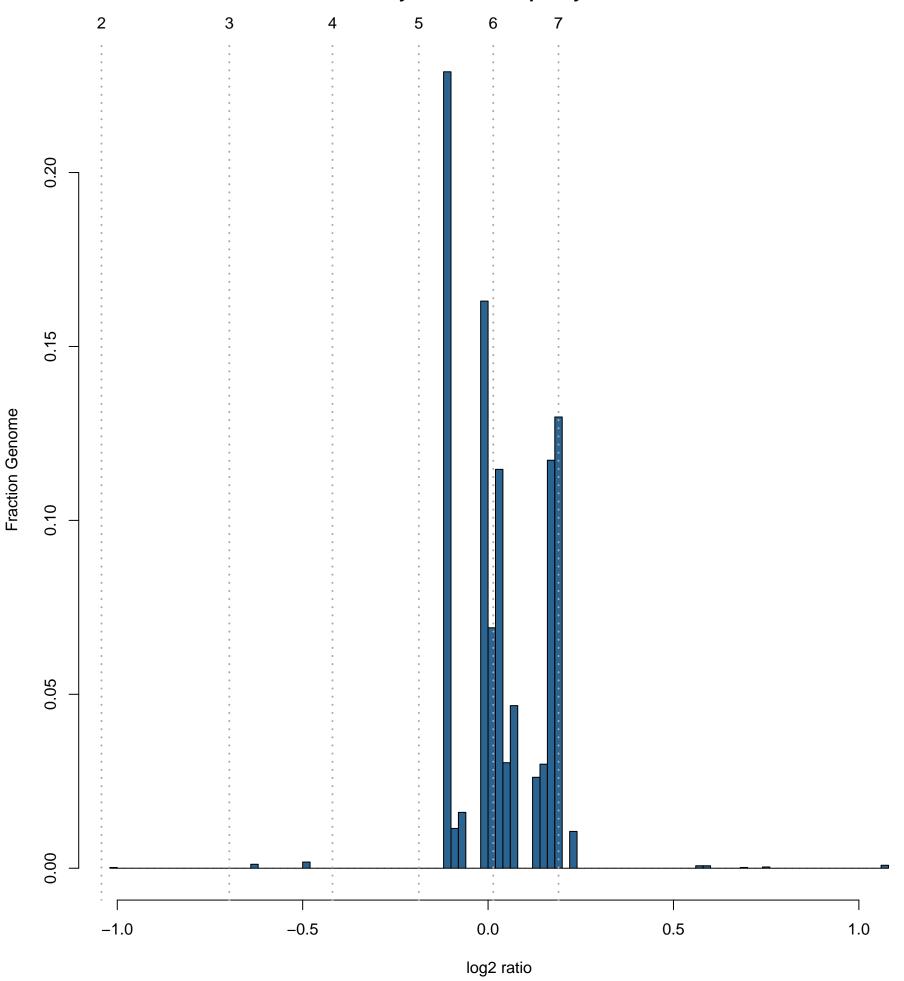
SCNA-fit log-likelihood: -5399.7

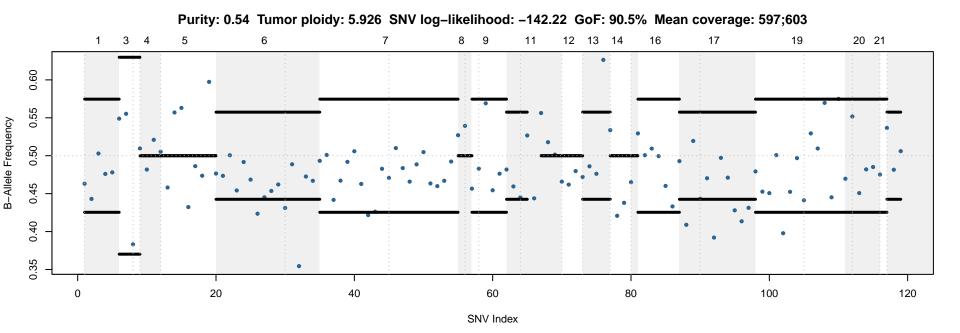




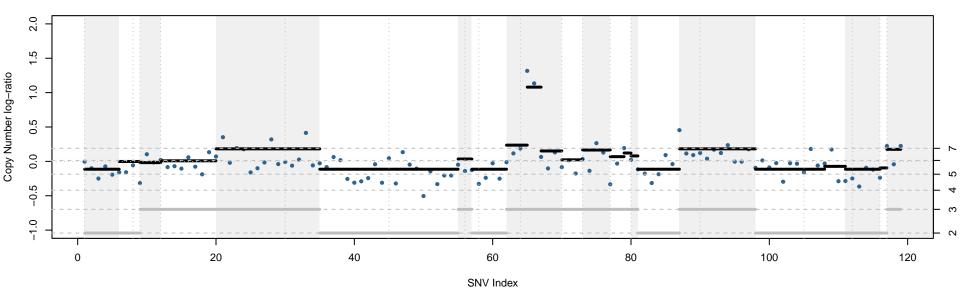


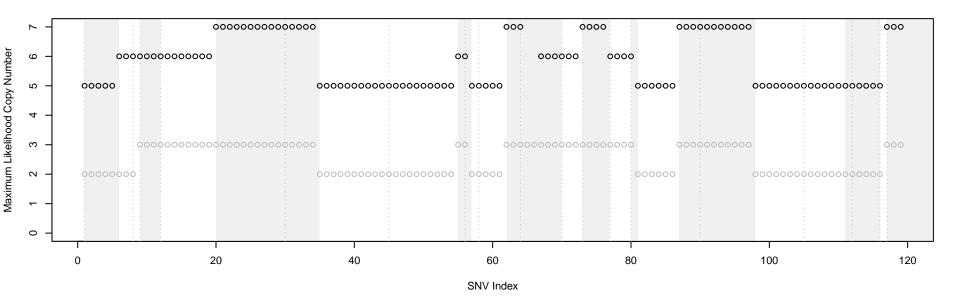
Purity: 0.54 Tumor ploidy: 5.926

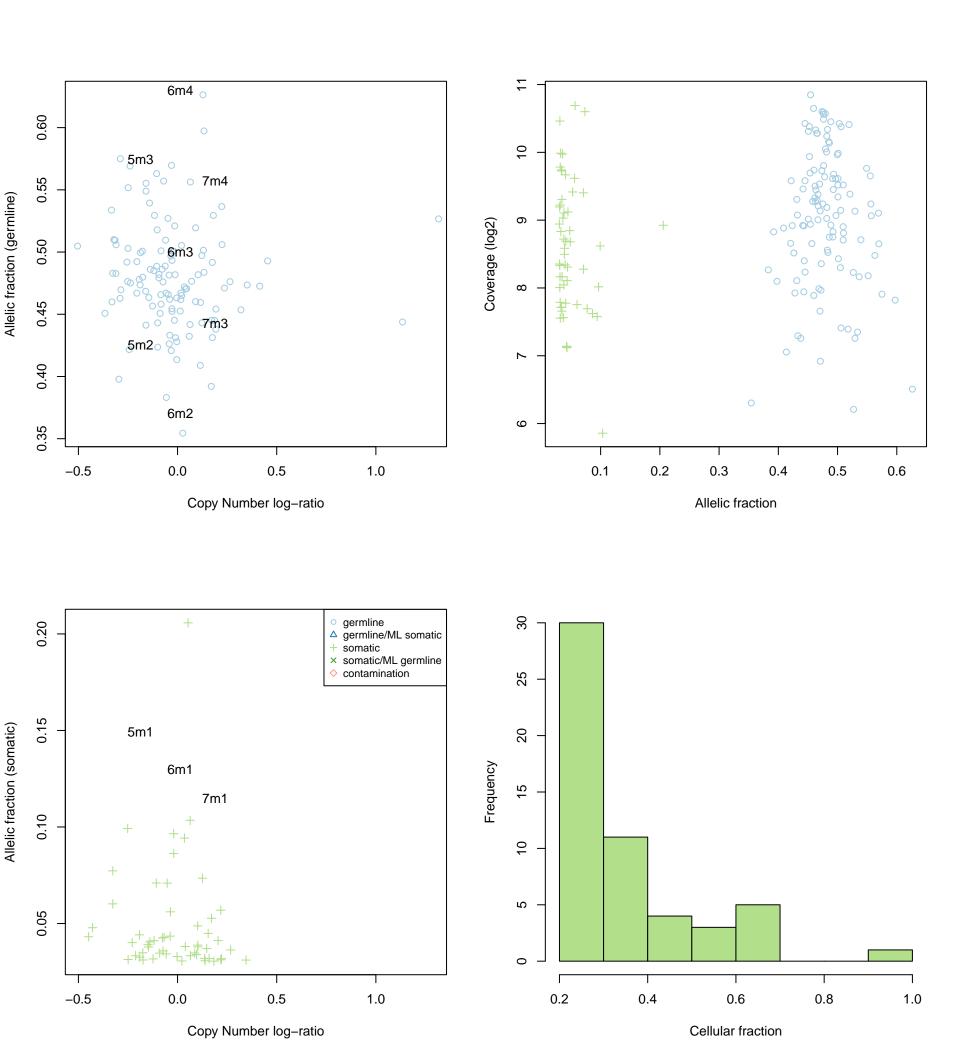




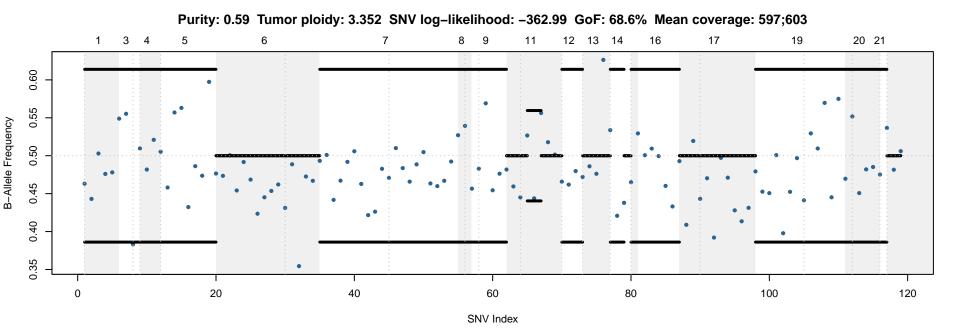
SCNA-fit log-likelihood: -5741.03



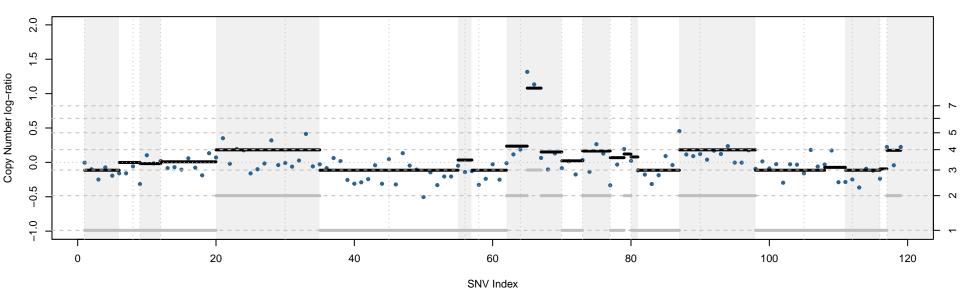


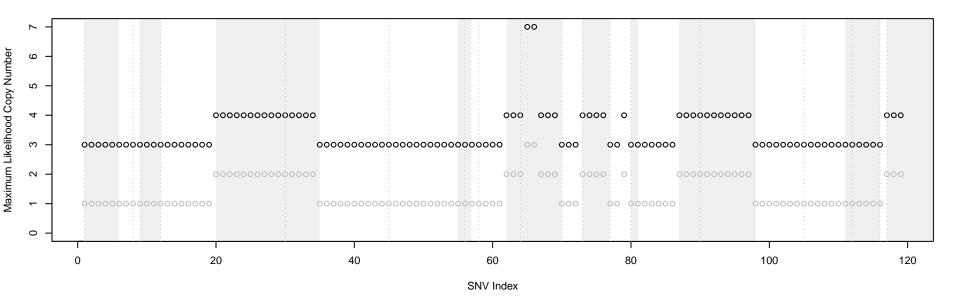


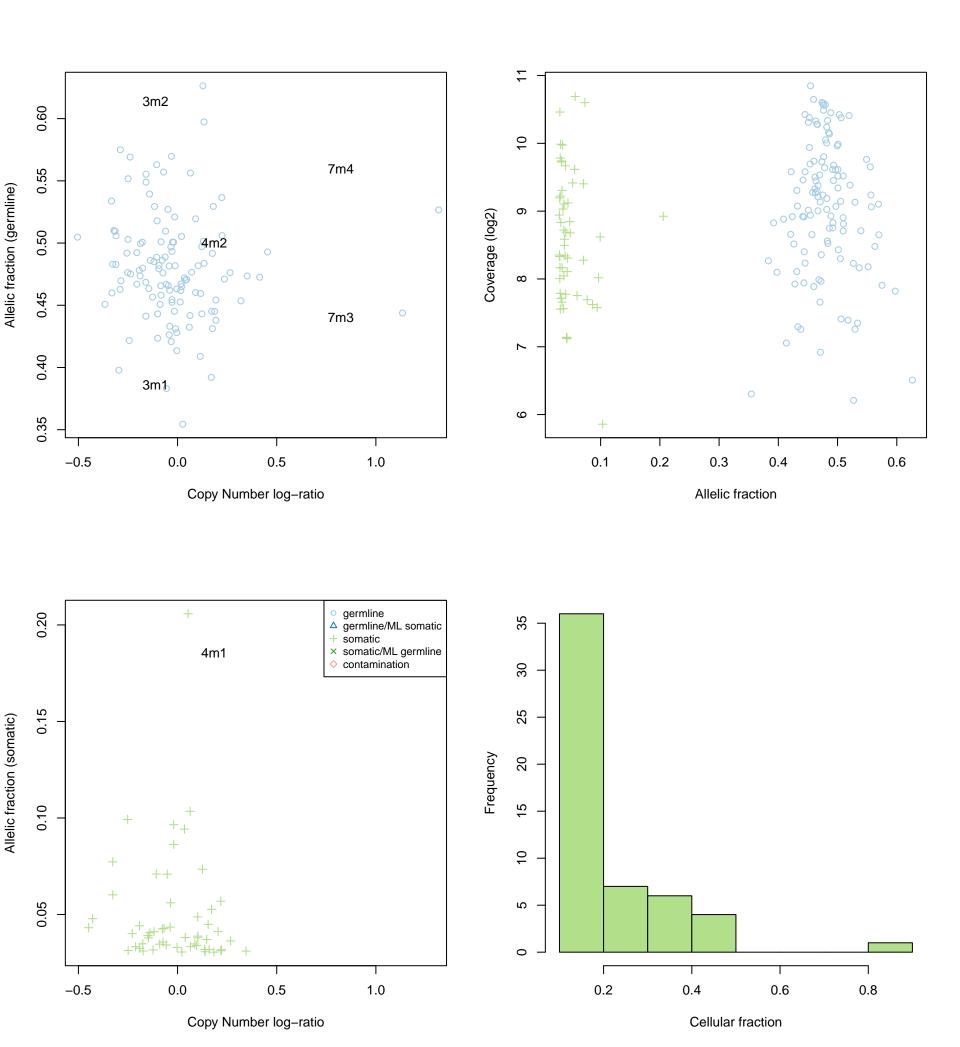
Purity: 0.59 Tumor ploidy: 3.352 2 6 5 1 Fraction Genome 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0



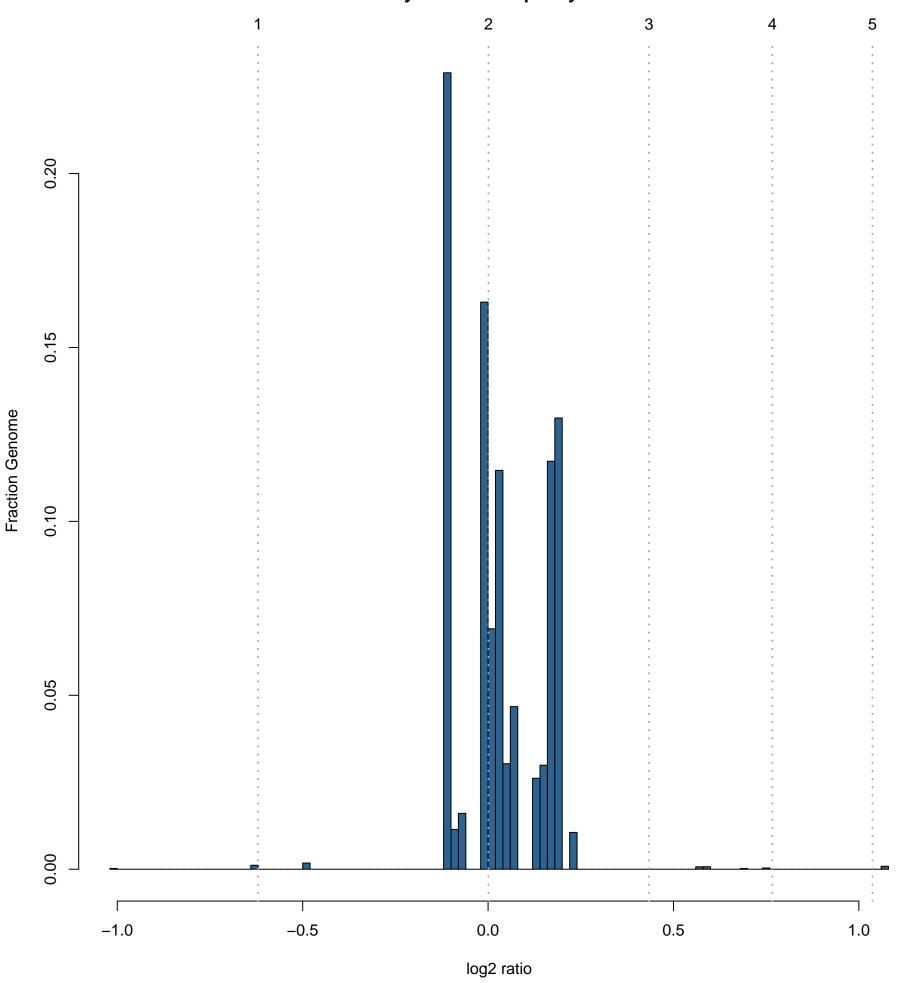
SCNA-fit log-likelihood: -5472.61

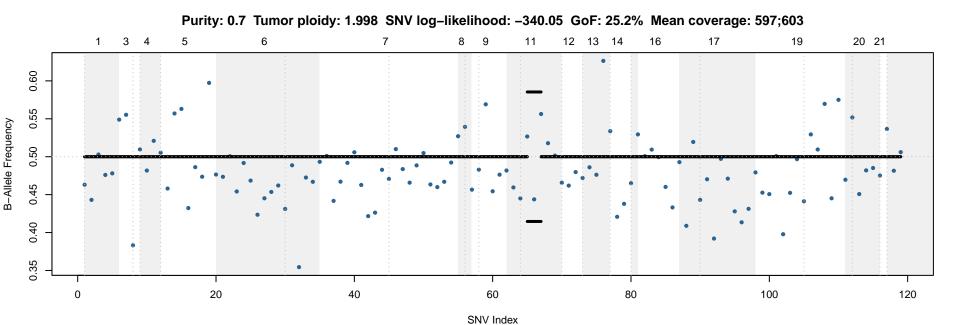




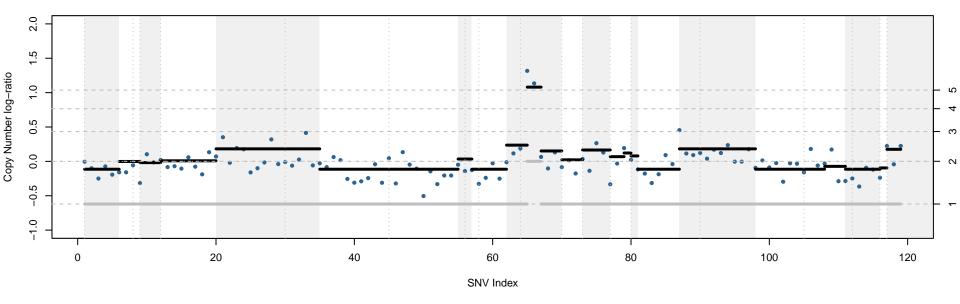


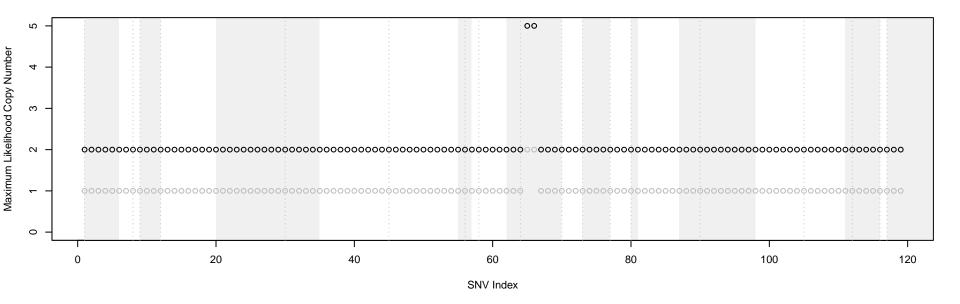
Purity: 0.7 Tumor ploidy: 1.998

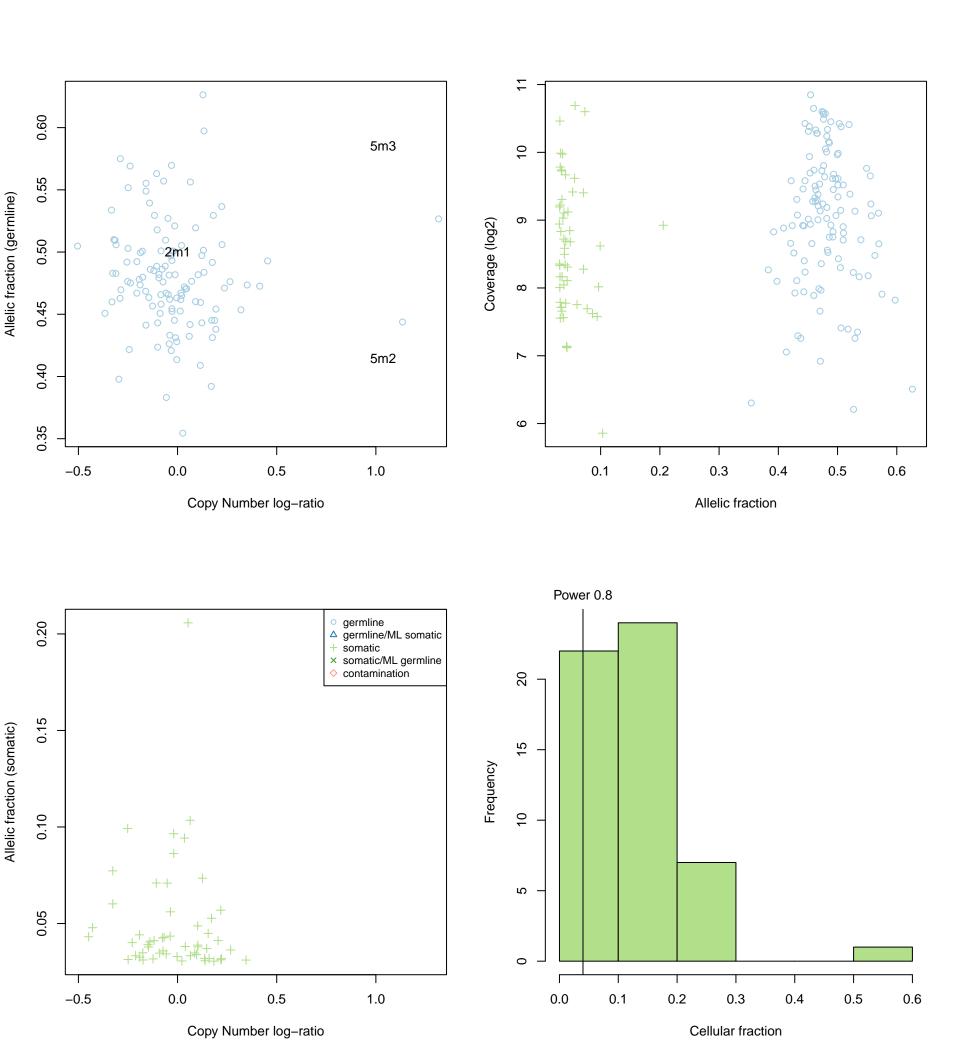




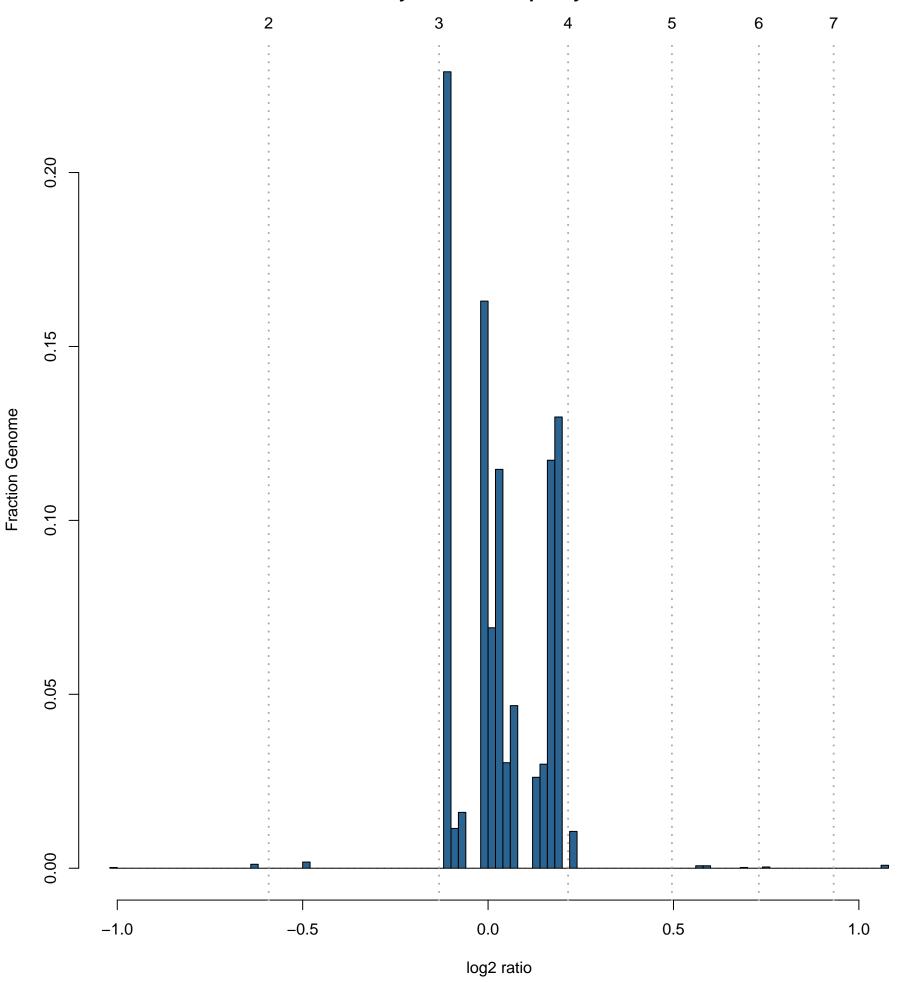
SCNA-fit log-likelihood: -5851.23

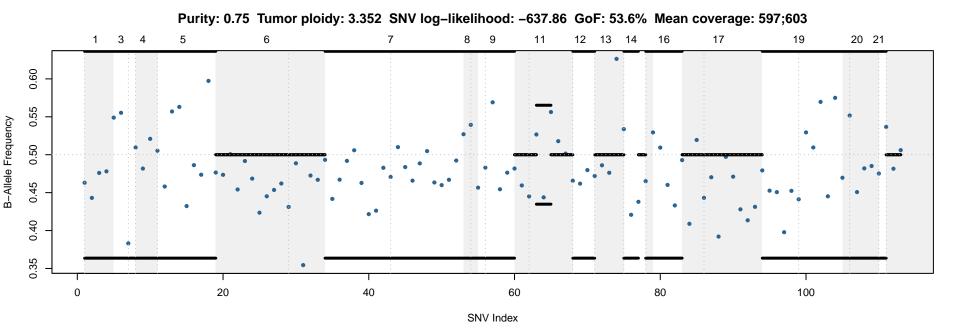






Purity: 0.75 Tumor ploidy: 3.352





SCNA-fit log-likelihood: -5618.02

