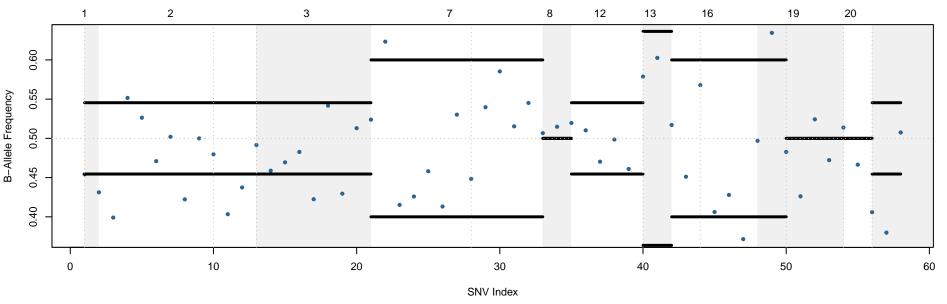
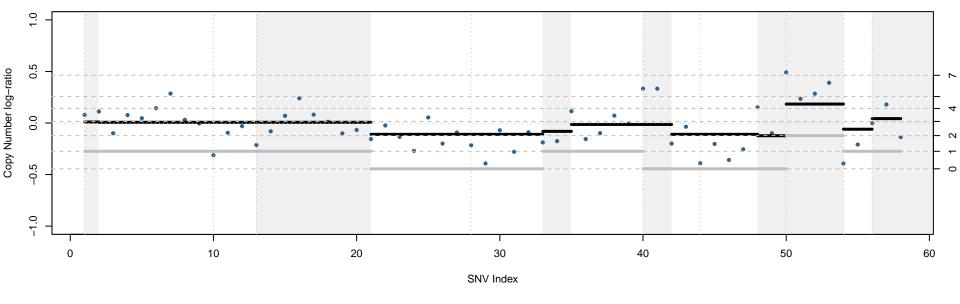
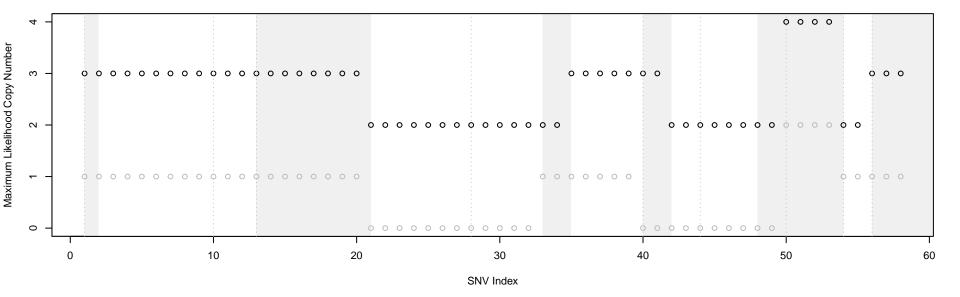
Purity: 0.2 Tumor ploidy: 2.885 2 0 3 5 Fraction Genome 0.2 0.1 0.0 -0.5 0.0 0.5 log2 ratio

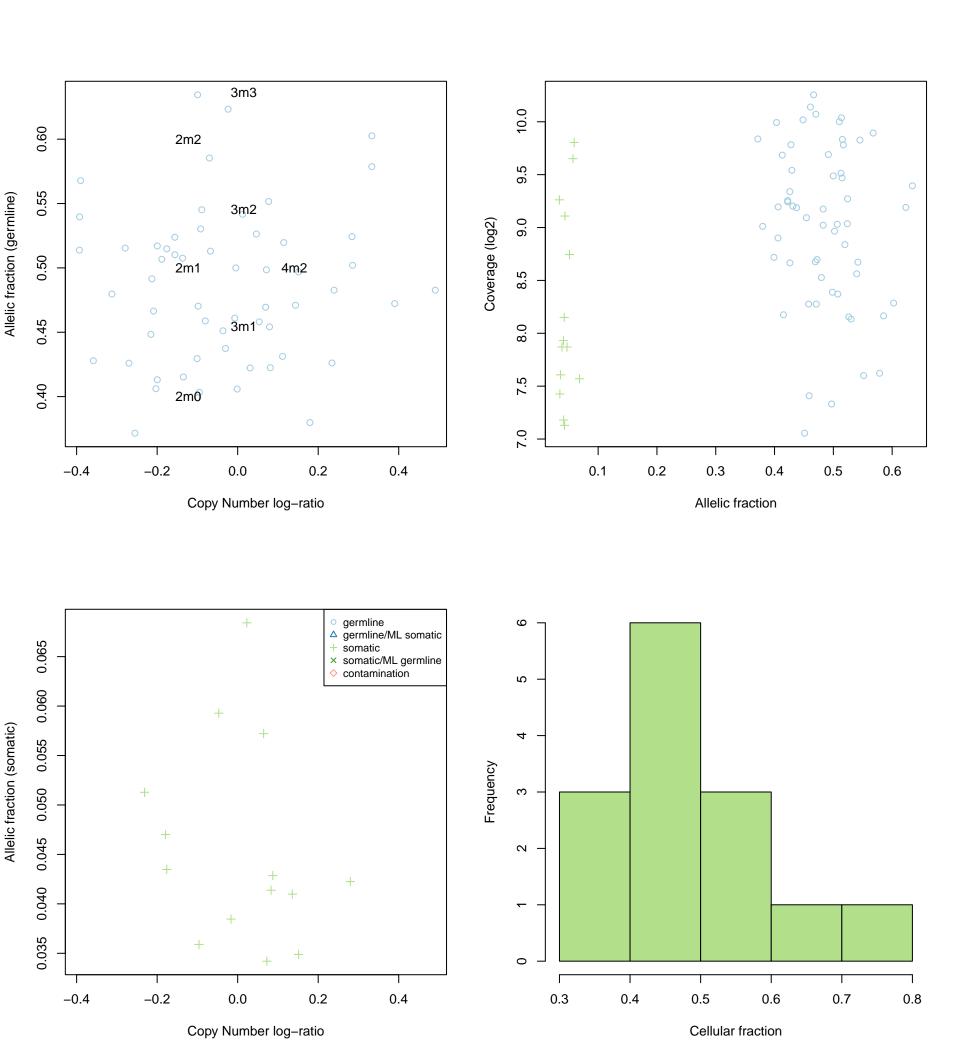
Purity: 0.2 Tumor ploidy: 2.885 SNV log-likelihood: -5.49 GoF: 95.8% Mean coverage: 545;642



SCNA-fit log-likelihood: -3375.34

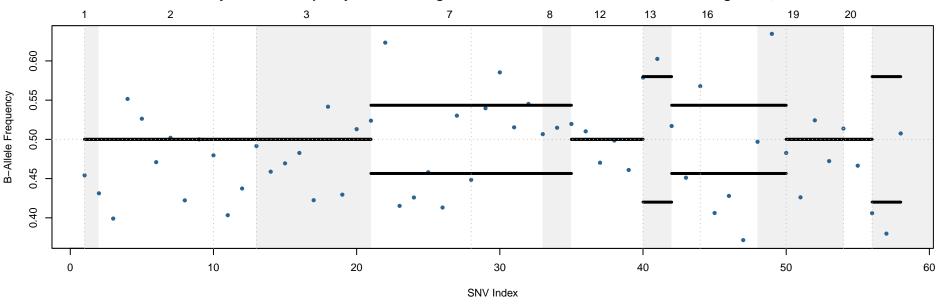




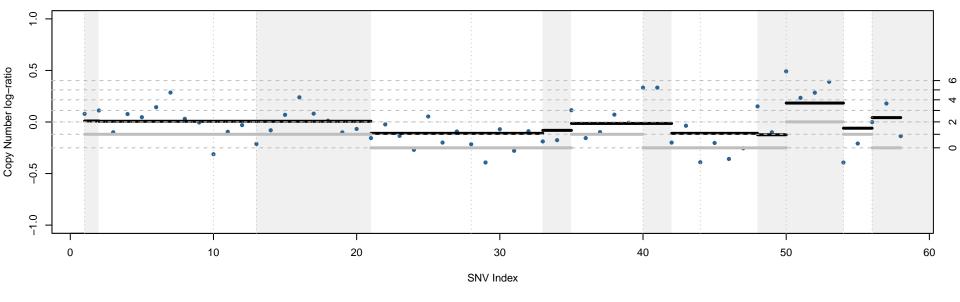


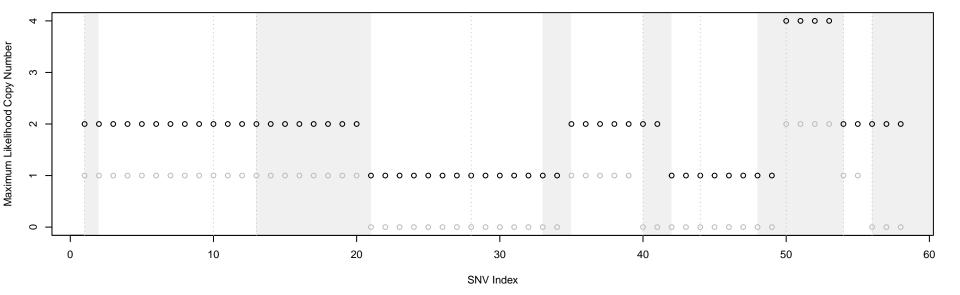
Purity: 0.16 Tumor ploidy: 1.99 2 3 0 6 4 Fraction Genome 0.2 0.1 0.0 -0.2 0.0 0.2 0.4 0.6 log2 ratio

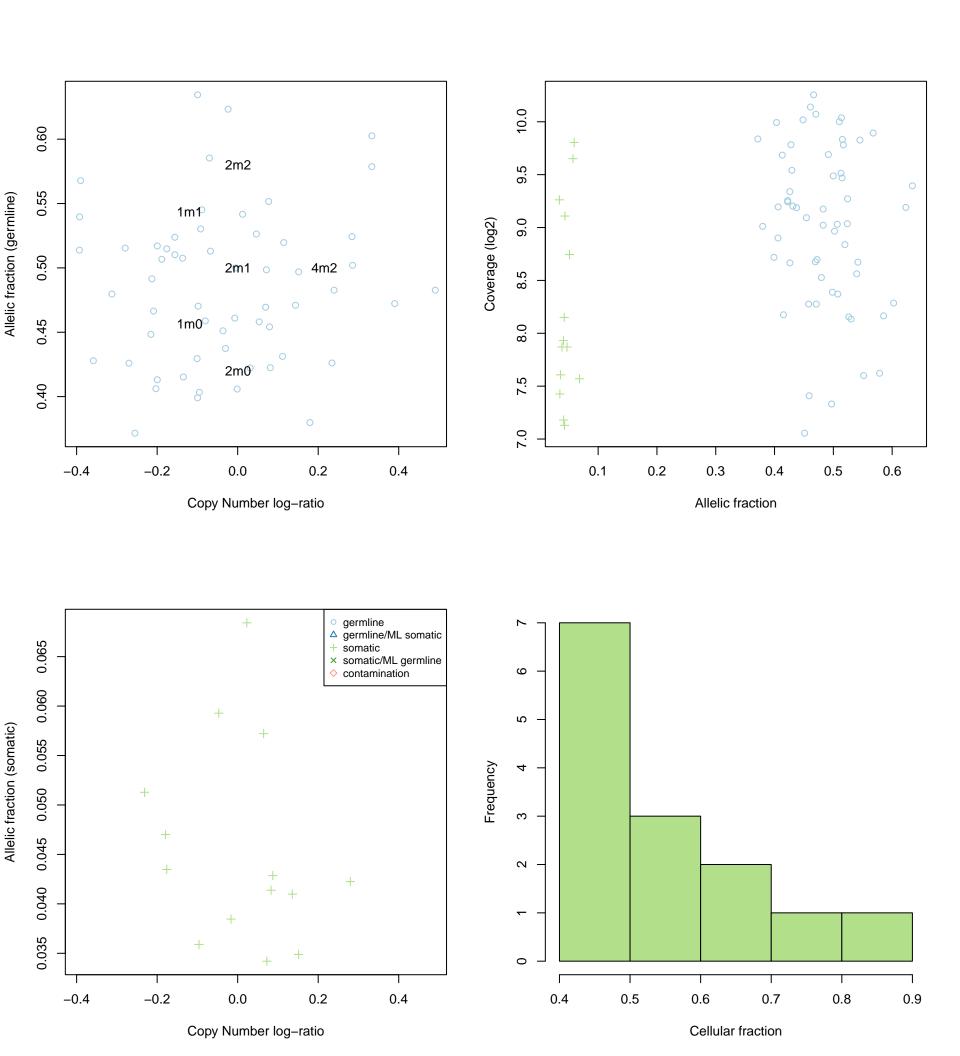
Purity: 0.16 Tumor ploidy: 1.99 SNV log-likelihood: 22.75 GoF: 95.8% Mean coverage: 545;642



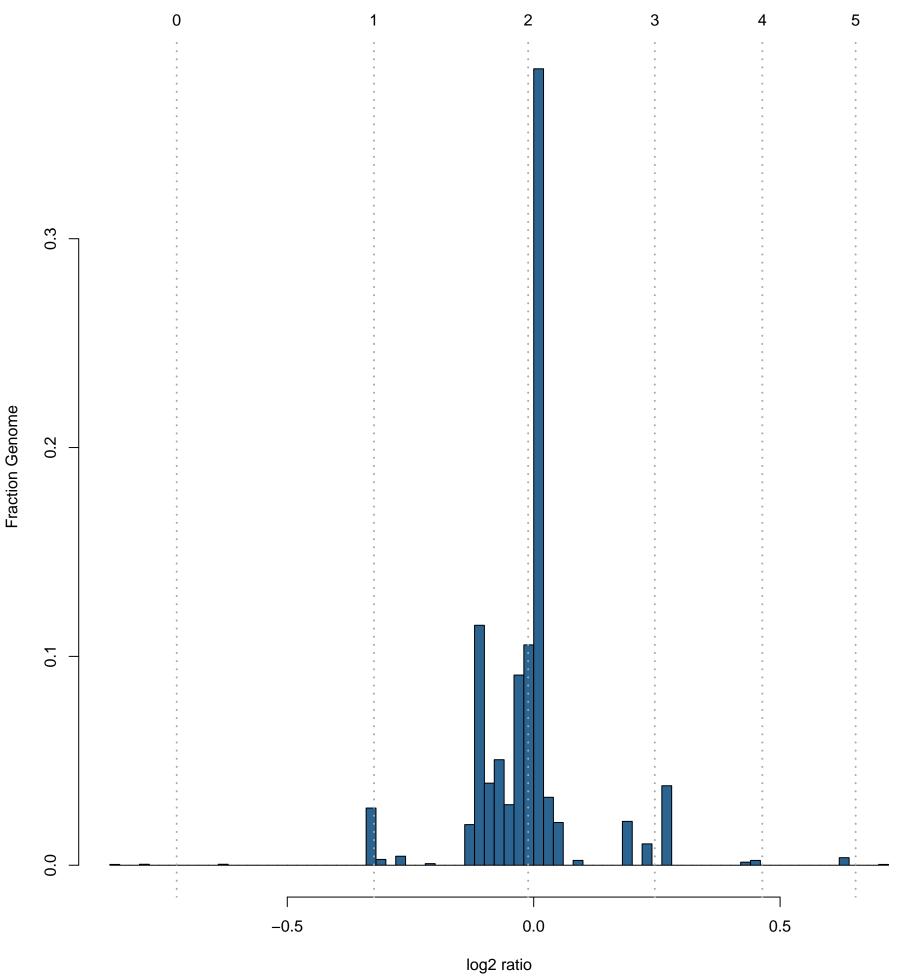
SCNA-fit log-likelihood: -3456.4



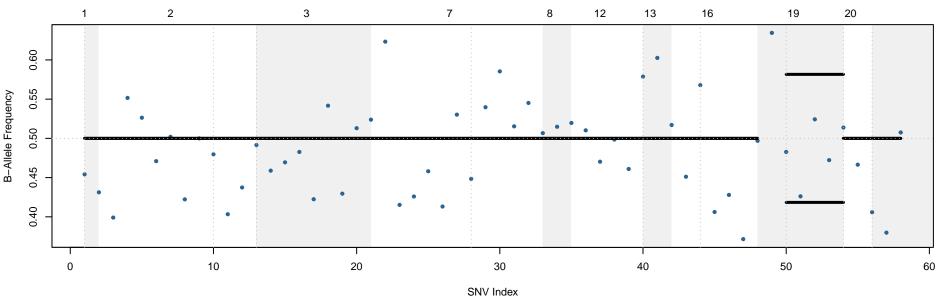




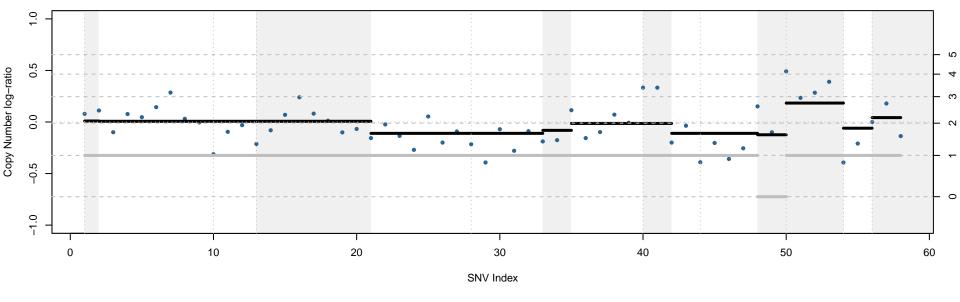
Purity: 0.39 Tumor ploidy: 2.04

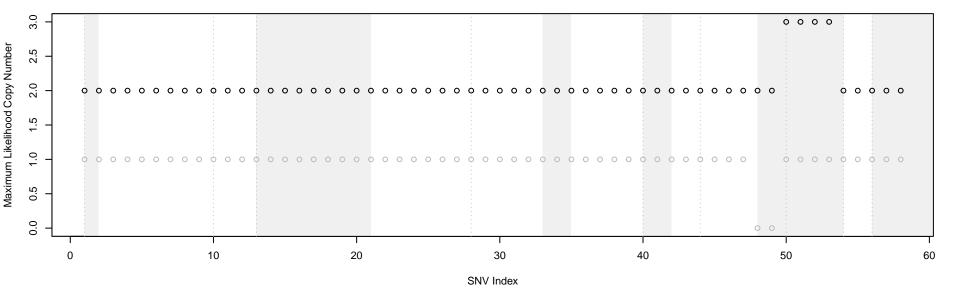


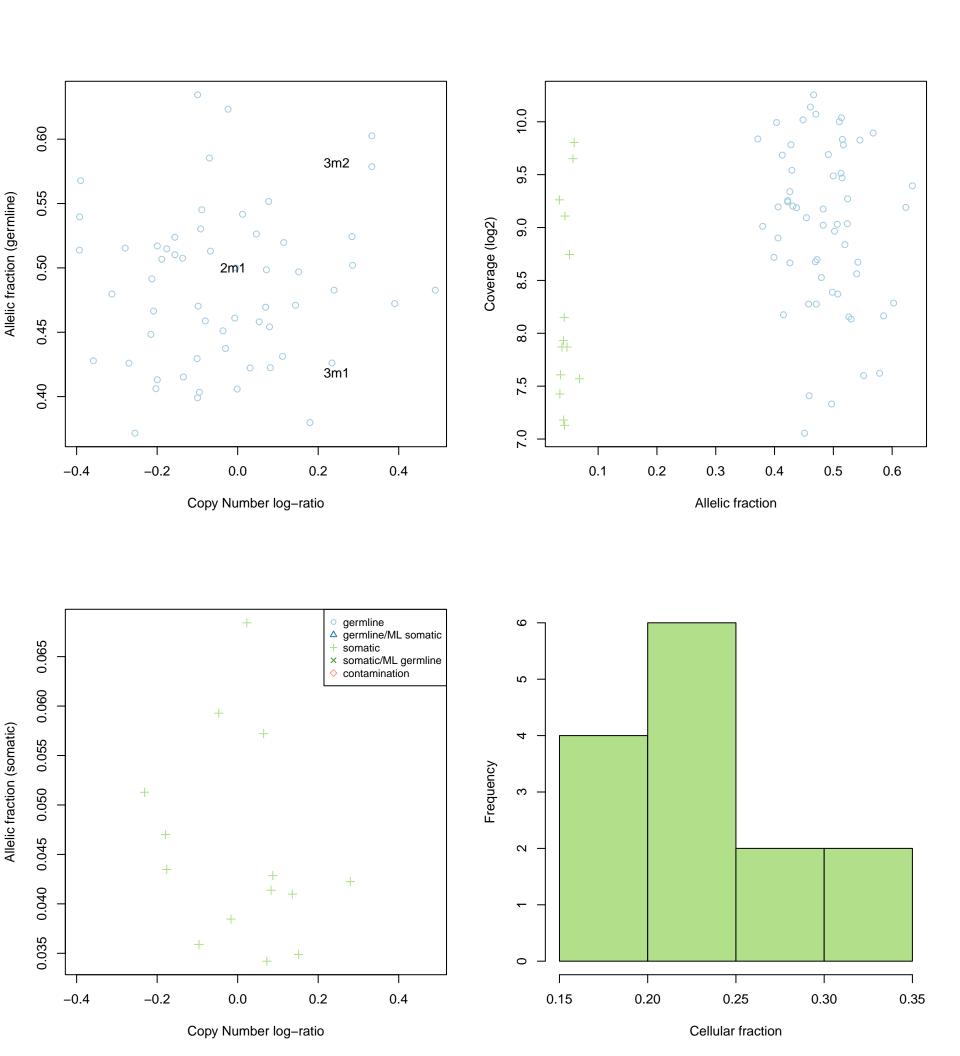
Purity: 0.39 Tumor ploidy: 2.04 SNV log-likelihood: -35.82 GoF: 82.8% Mean coverage: 545;642

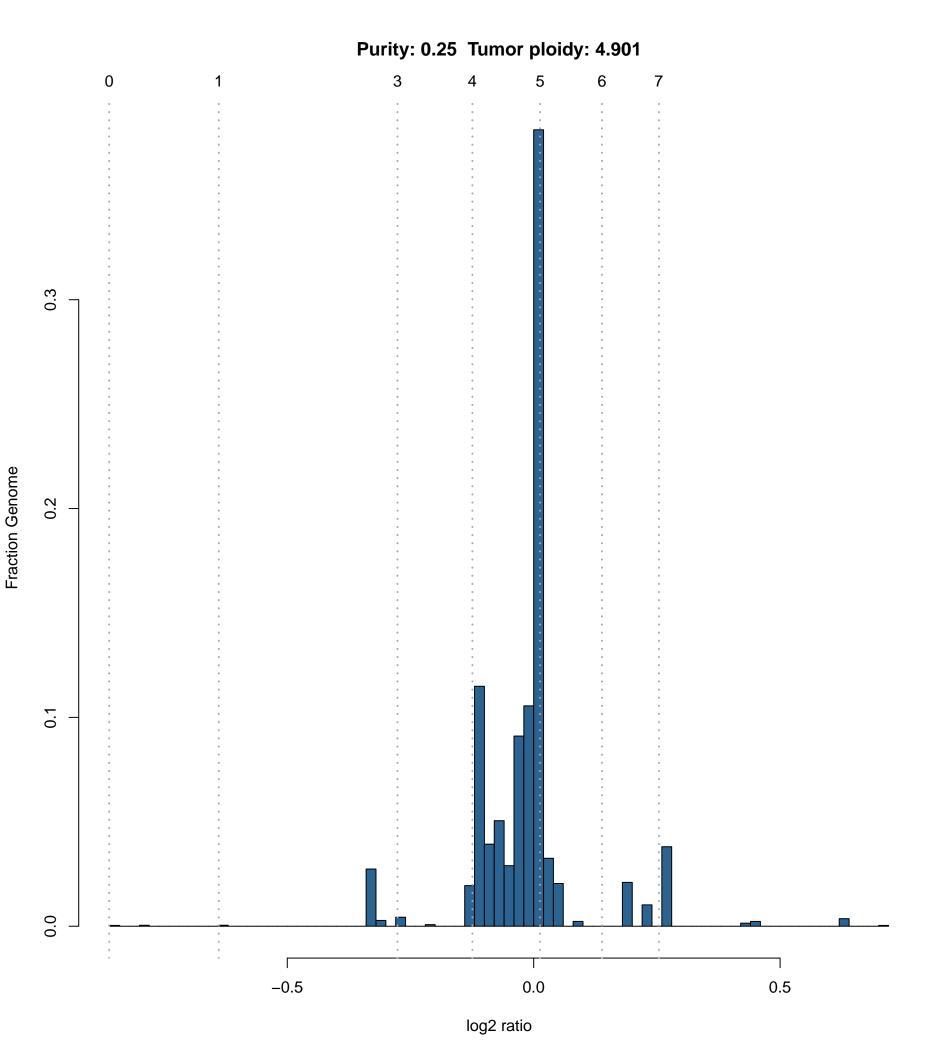


SCNA-fit log-likelihood: -3399.68

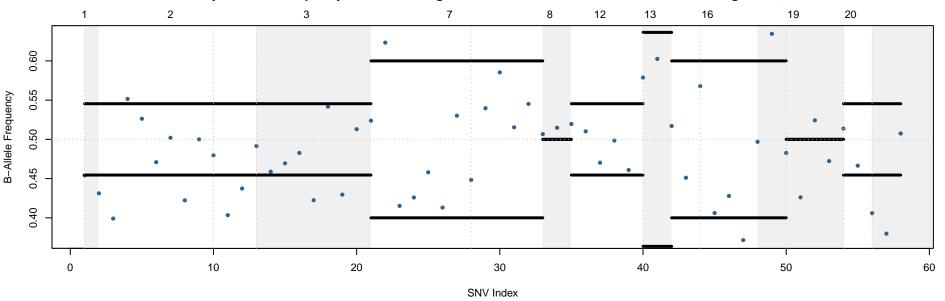




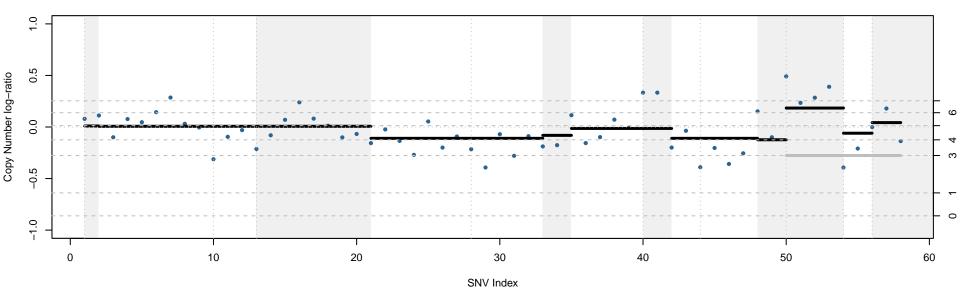


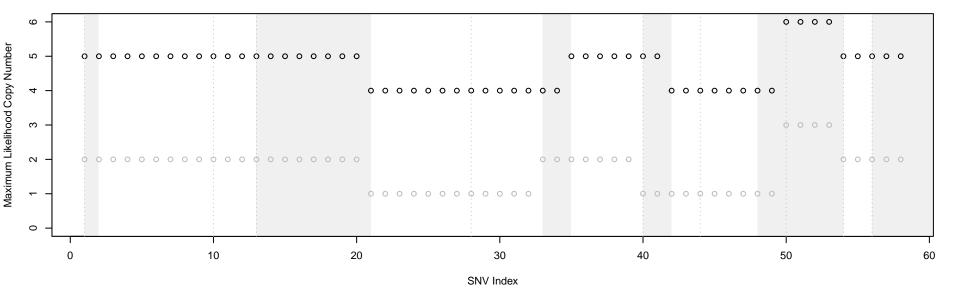


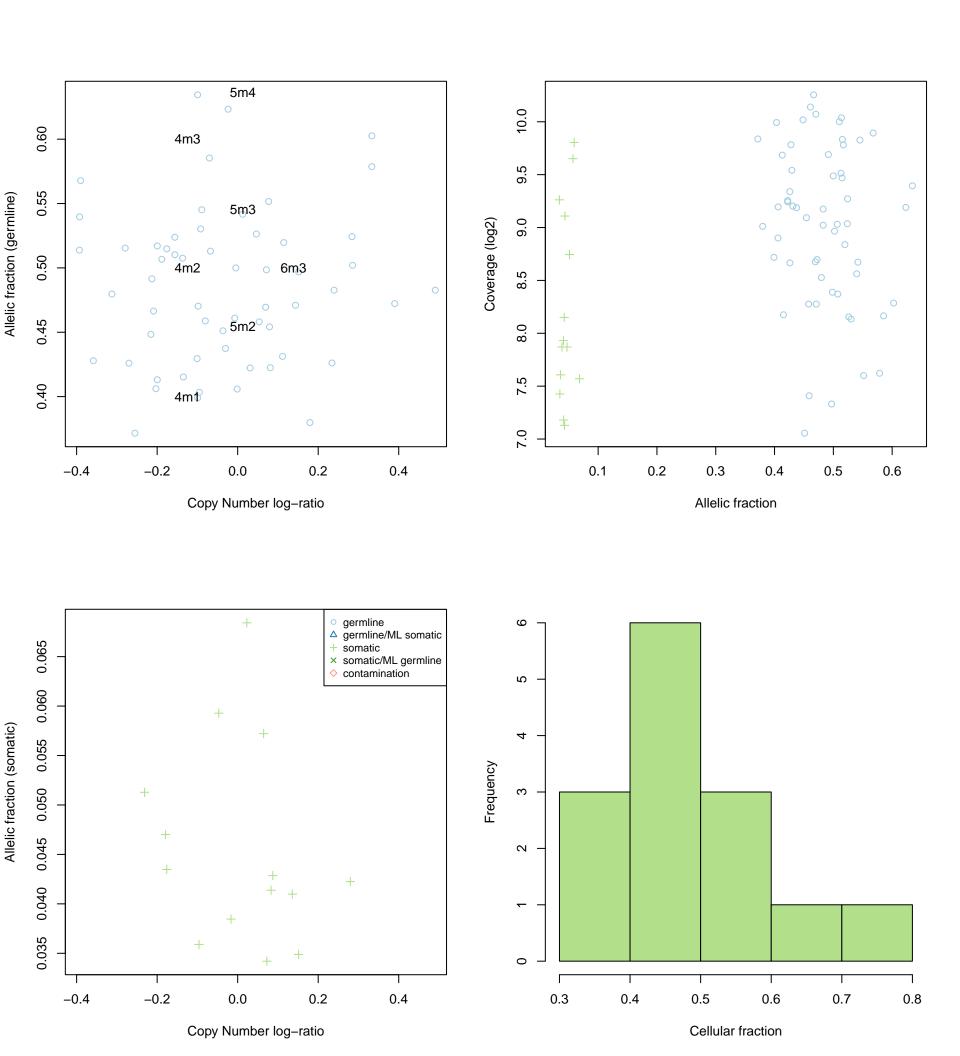
Purity: 0.25 Tumor ploidy: 4.901 SNV log-likelihood: -38.58 GoF: 95.7% Mean coverage: 545;642



SCNA-fit log-likelihood: -3417.23

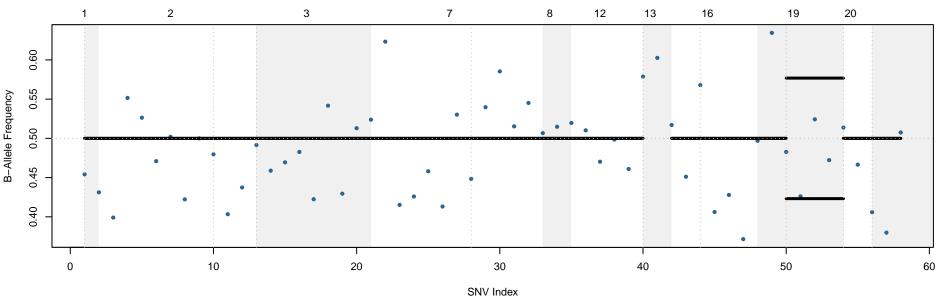




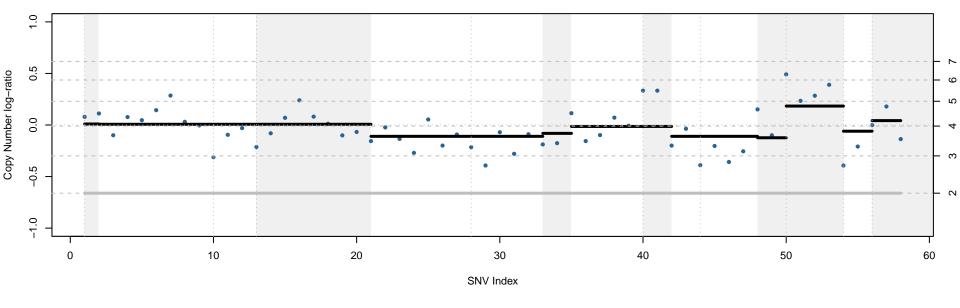


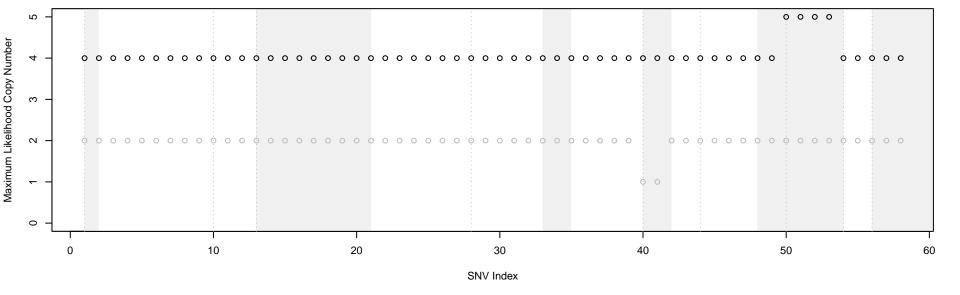
Purity: 0.57 Tumor ploidy: 4.04 2 5 6 7 Fraction Genome 0.1 0.0 -0.5 0.0 0.5 log2 ratio

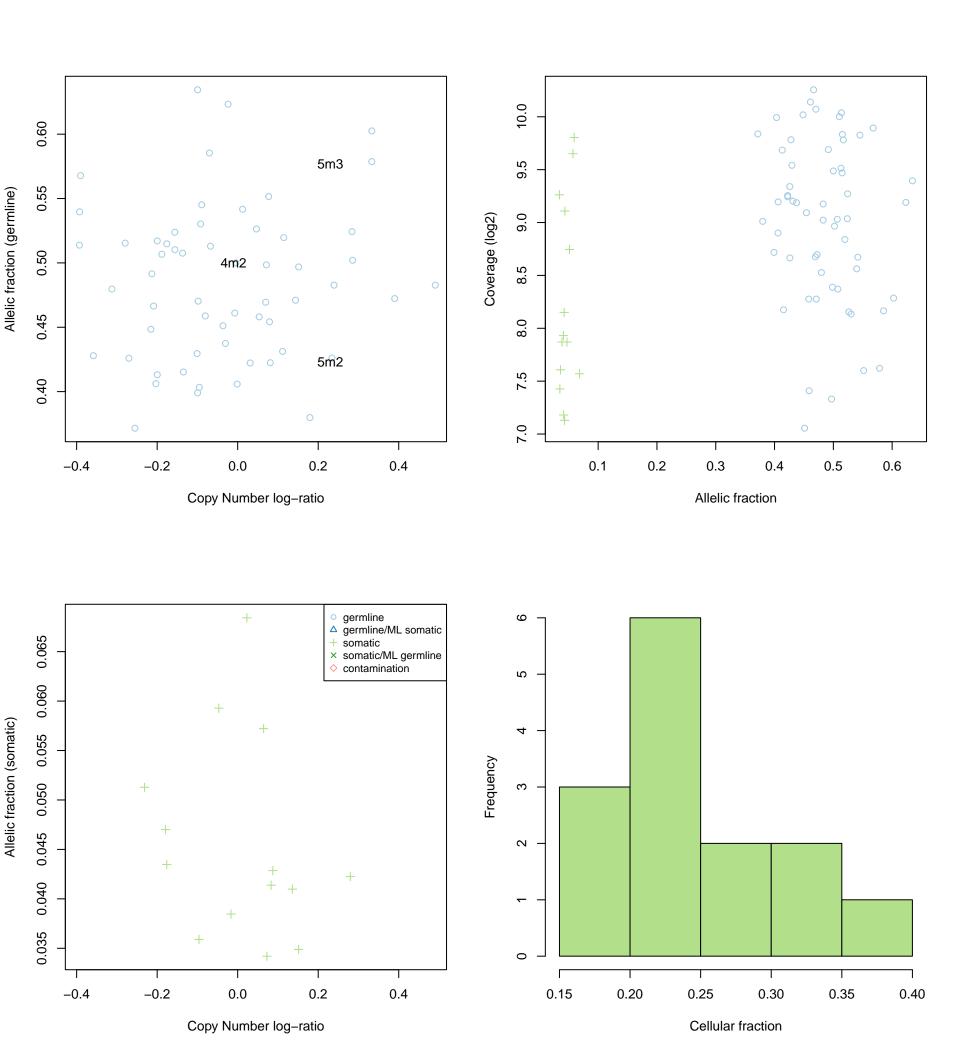
Purity: 0.57 Tumor ploidy: 4.04 SNV log-likelihood: -67.71 GoF: 85.1% Mean coverage: 545;642



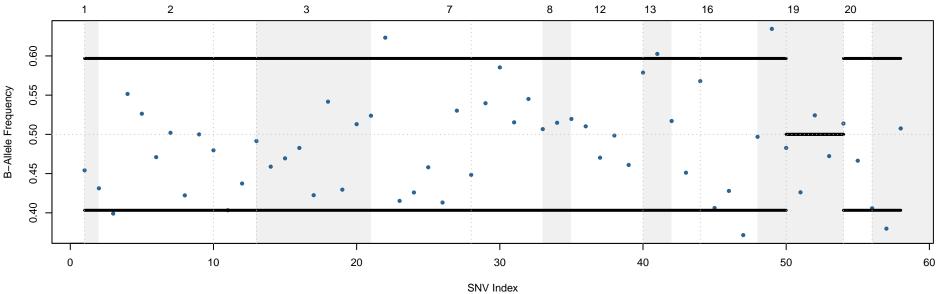
SCNA-fit log-likelihood: -3401.38



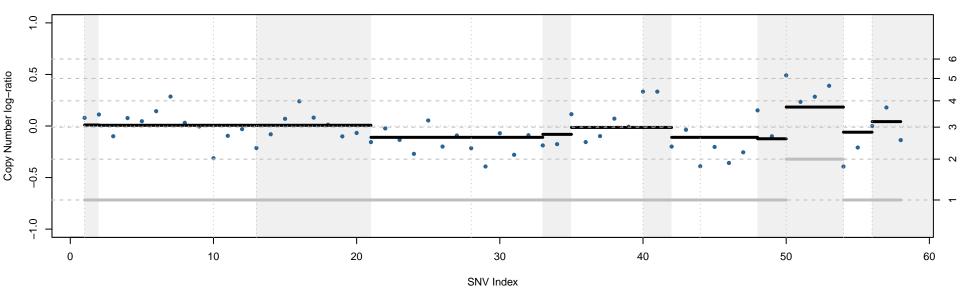


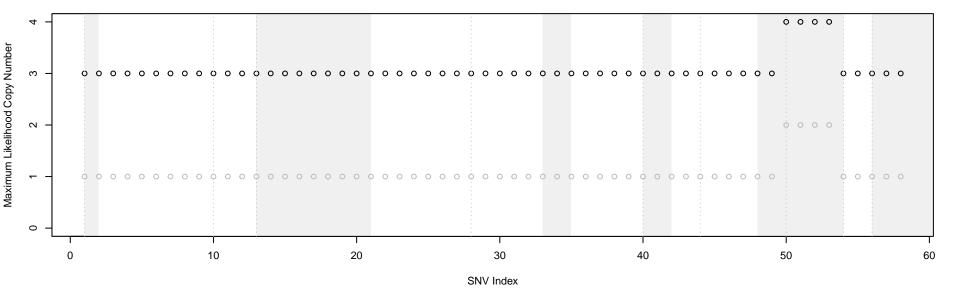


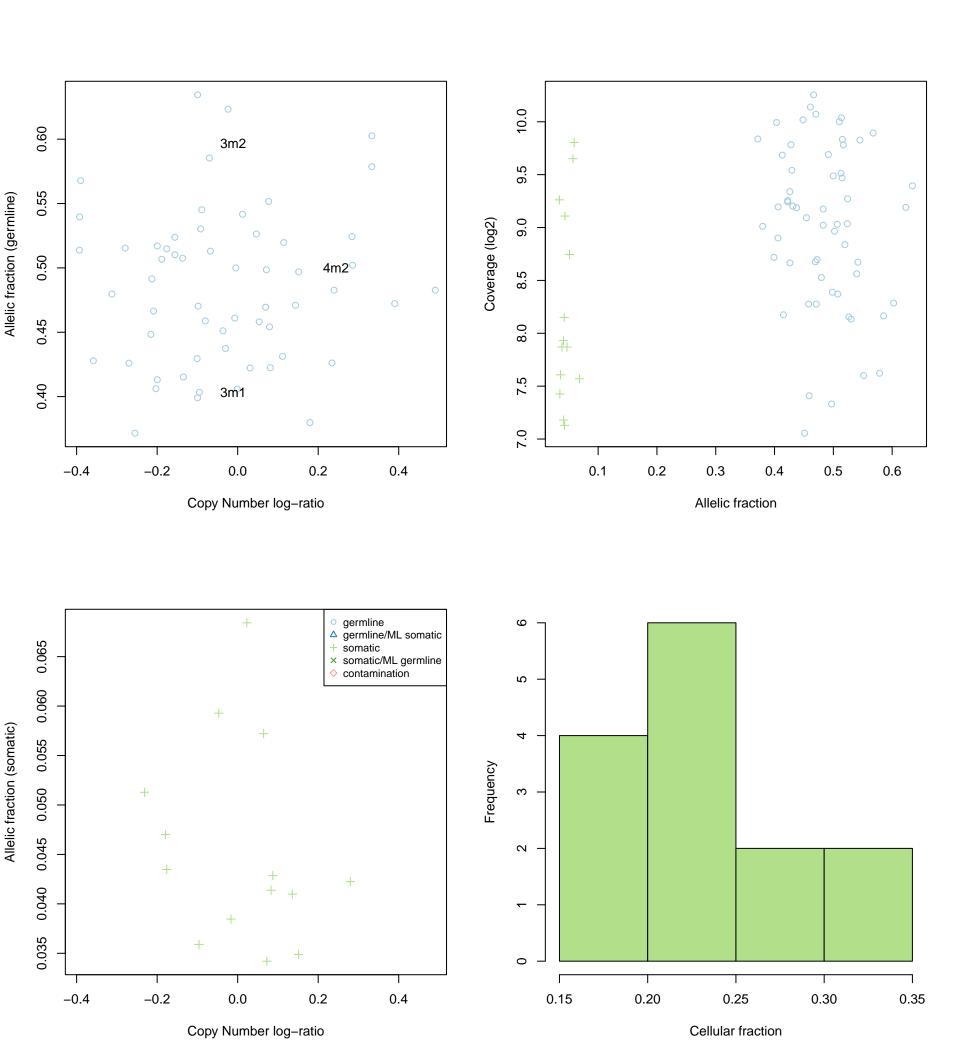
Purity: 0.48 Tumor ploidy: 3.04 3 2 5 6 Fraction Genome 0.0 -0.5 0.0 0.5 log2 ratio



SCNA-fit log-likelihood: -3398.8

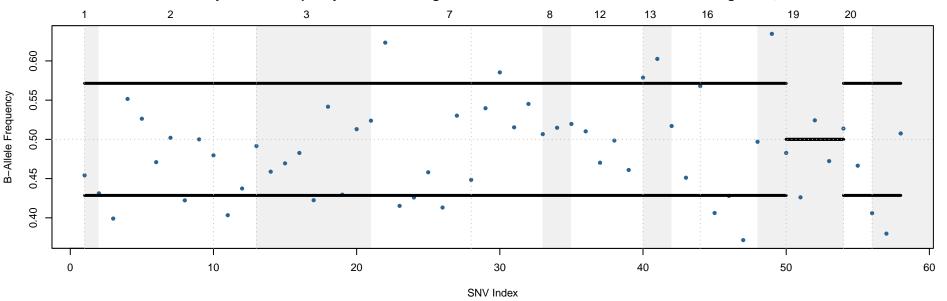




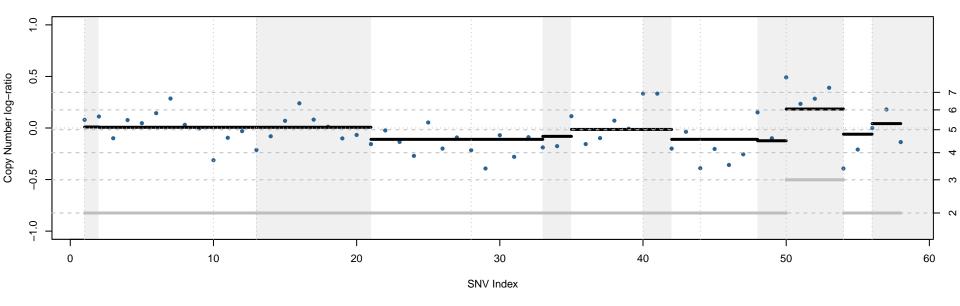


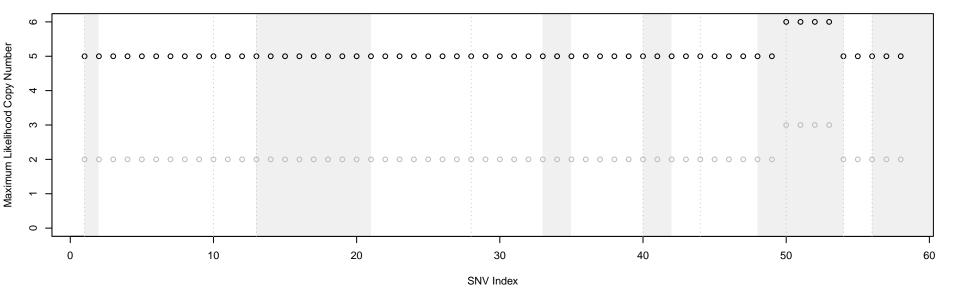
Purity: 0.5 Tumor ploidy: 5.082 2 3 Fraction Genome 0.2 0.1 0.0 -0.5 0.0 0.5 log2 ratio

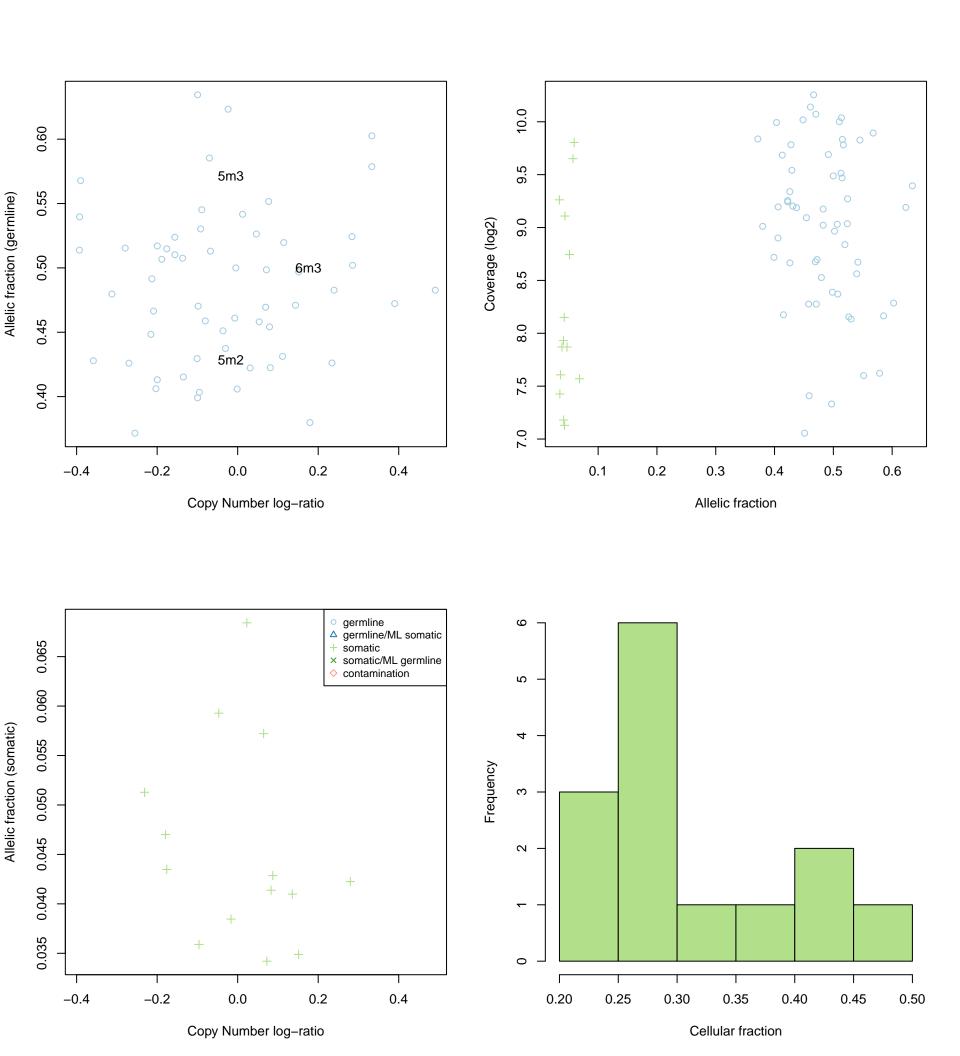
Purity: 0.5 Tumor ploidy: 5.082 SNV log-likelihood: -50.86 GoF: 92.1% Mean coverage: 545;642



SCNA-fit log-likelihood: -3465.9

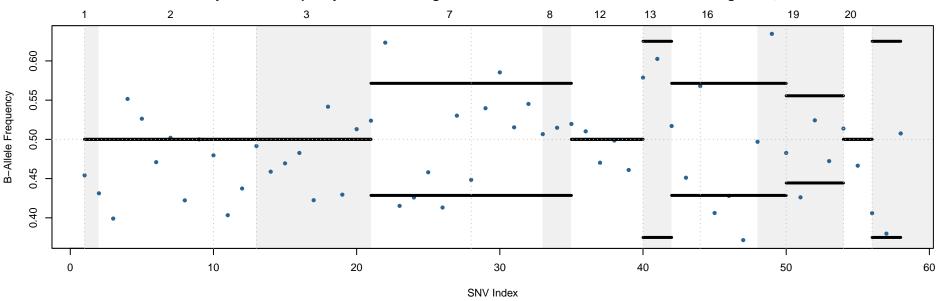




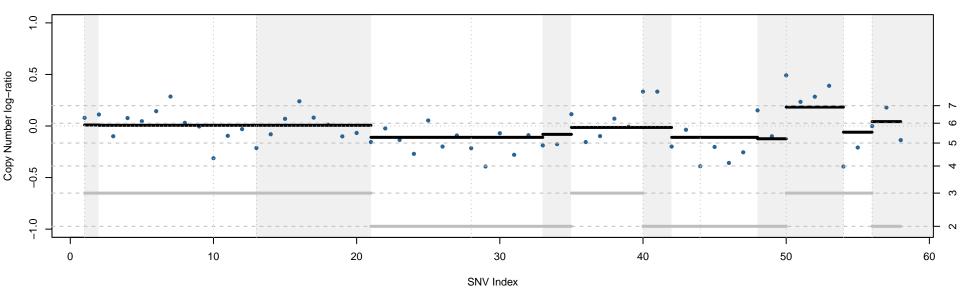


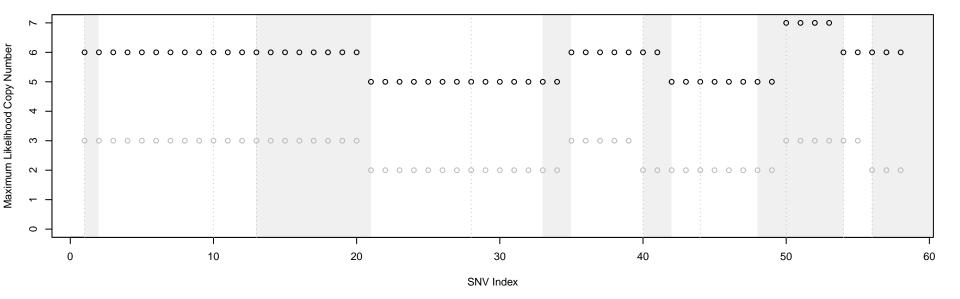
Purity: 0.5 Tumor ploidy: 5.851 3 5 6 Fraction Genome 0.1 0.0 -0.5 0.0 0.5 log2 ratio

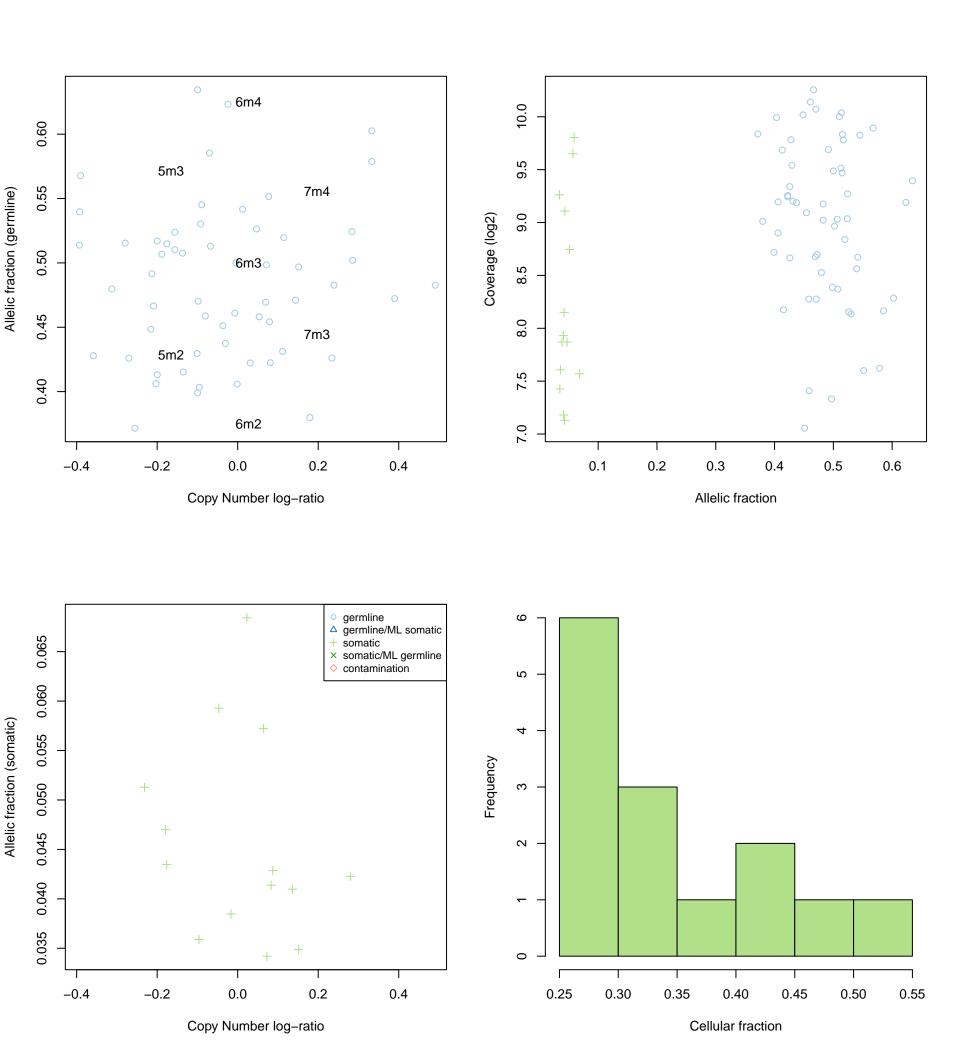
Purity: 0.5 Tumor ploidy: 5.851 SNV log-likelihood: -44.71 GoF: 92.9% Mean coverage: 545;642



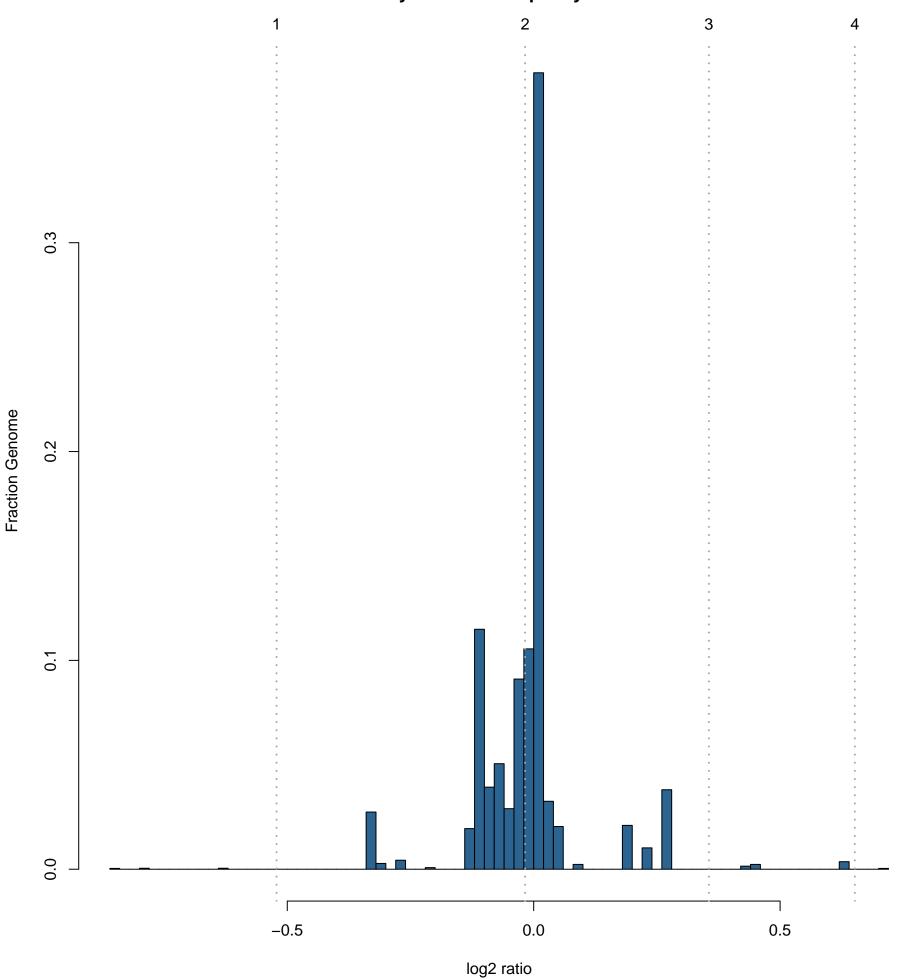
SCNA-fit log-likelihood: -3512.85



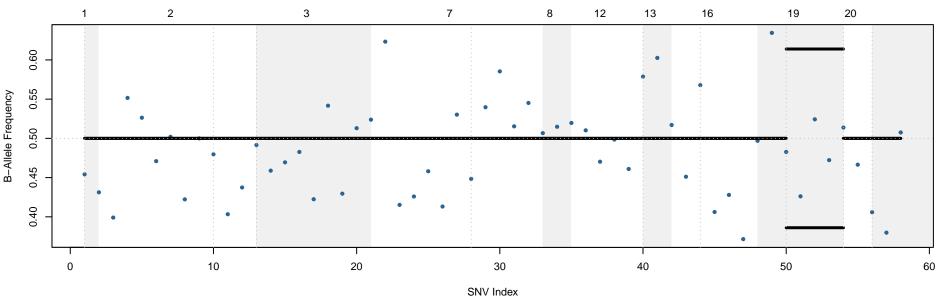




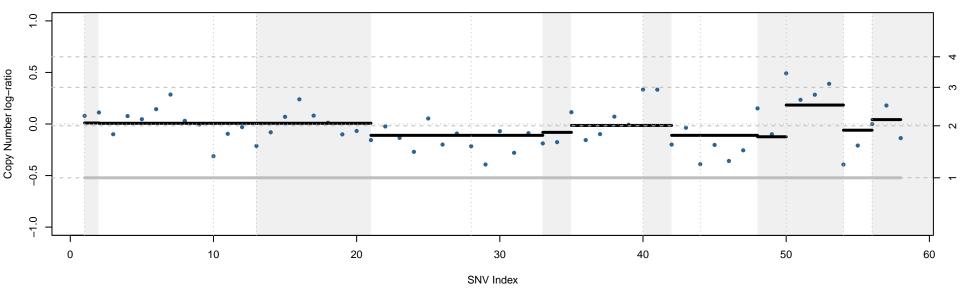
Purity: 0.59 Tumor ploidy: 2.041

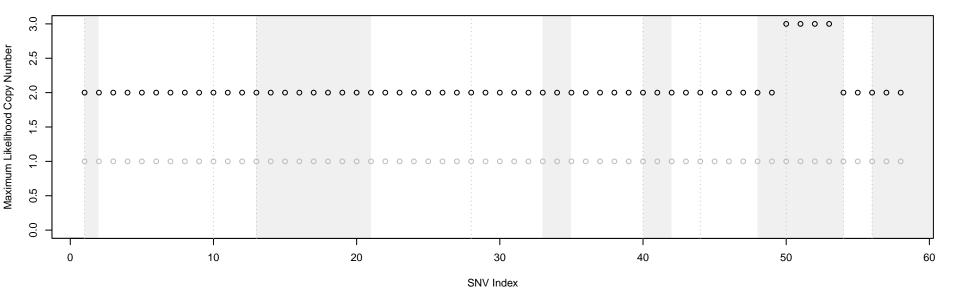


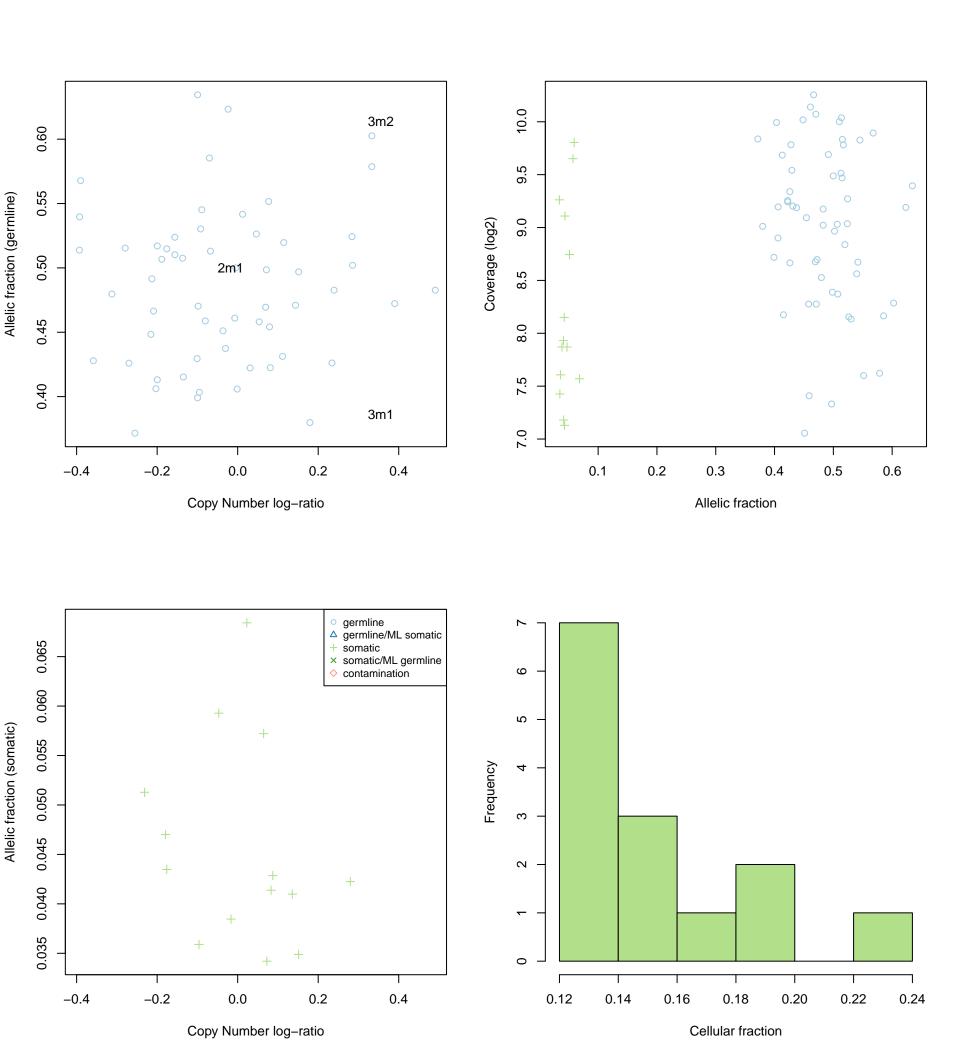
Purity: 0.59 Tumor ploidy: 2.041 SNV log-likelihood: -88.63 GoF: 61.7% Mean coverage: 545;642



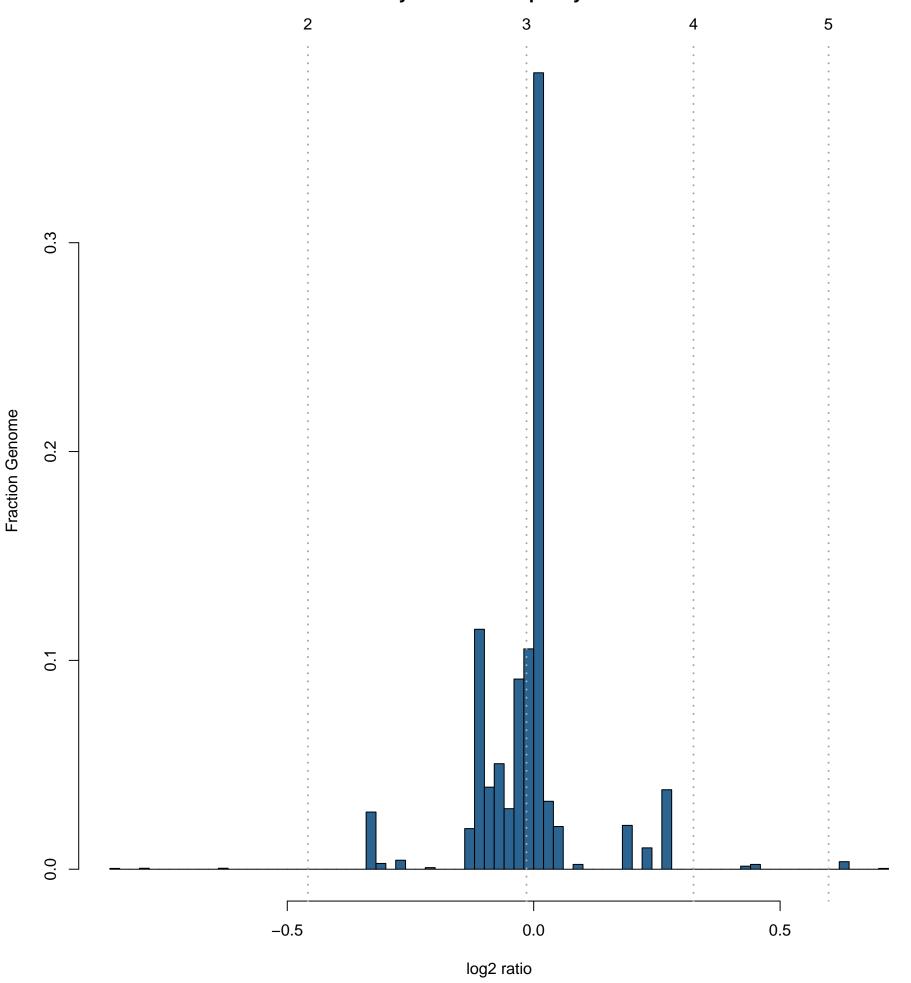
SCNA-fit log-likelihood: -3550.18



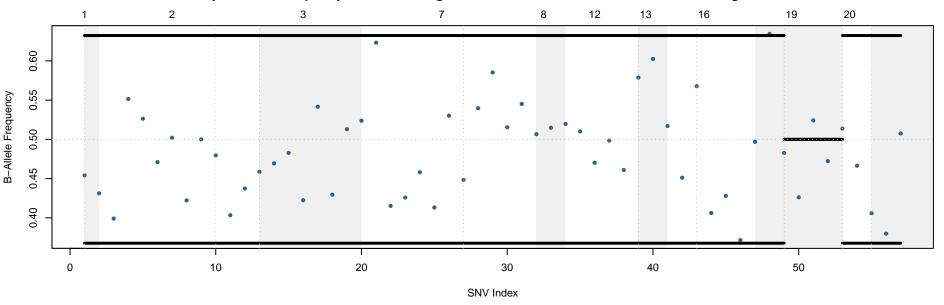




Purity: 0.72 Tumor ploidy: 3.038



Purity: 0.72 Tumor ploidy: 3.038 SNV log-likelihood: -251.5 GoF: 62.4% Mean coverage: 545;642



SCNA-fit log-likelihood: -3478.3

