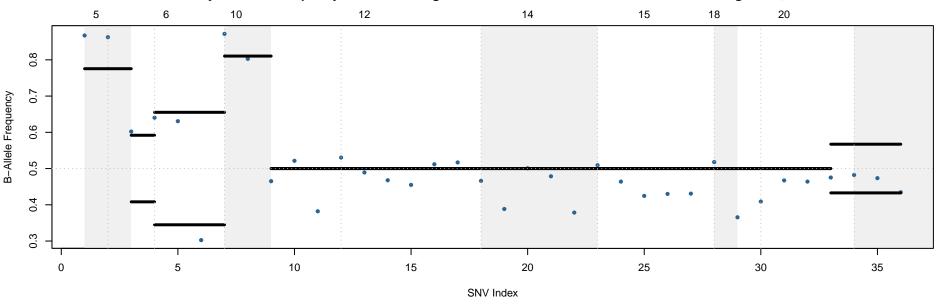
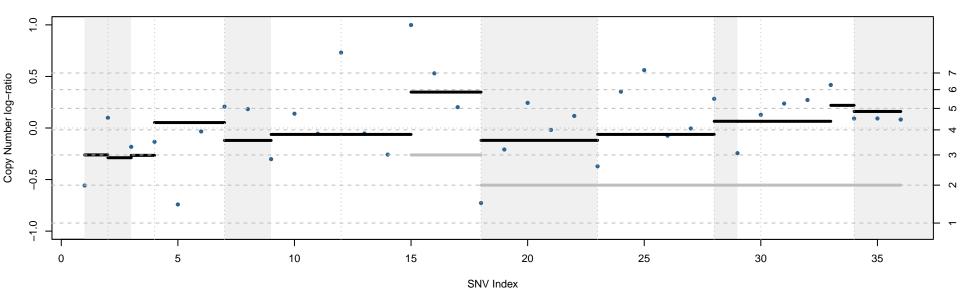
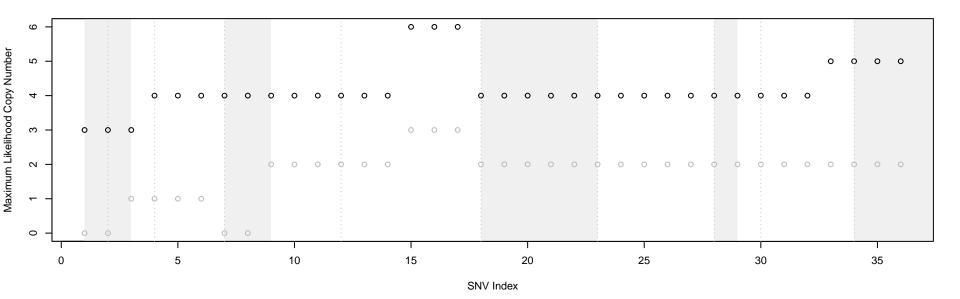


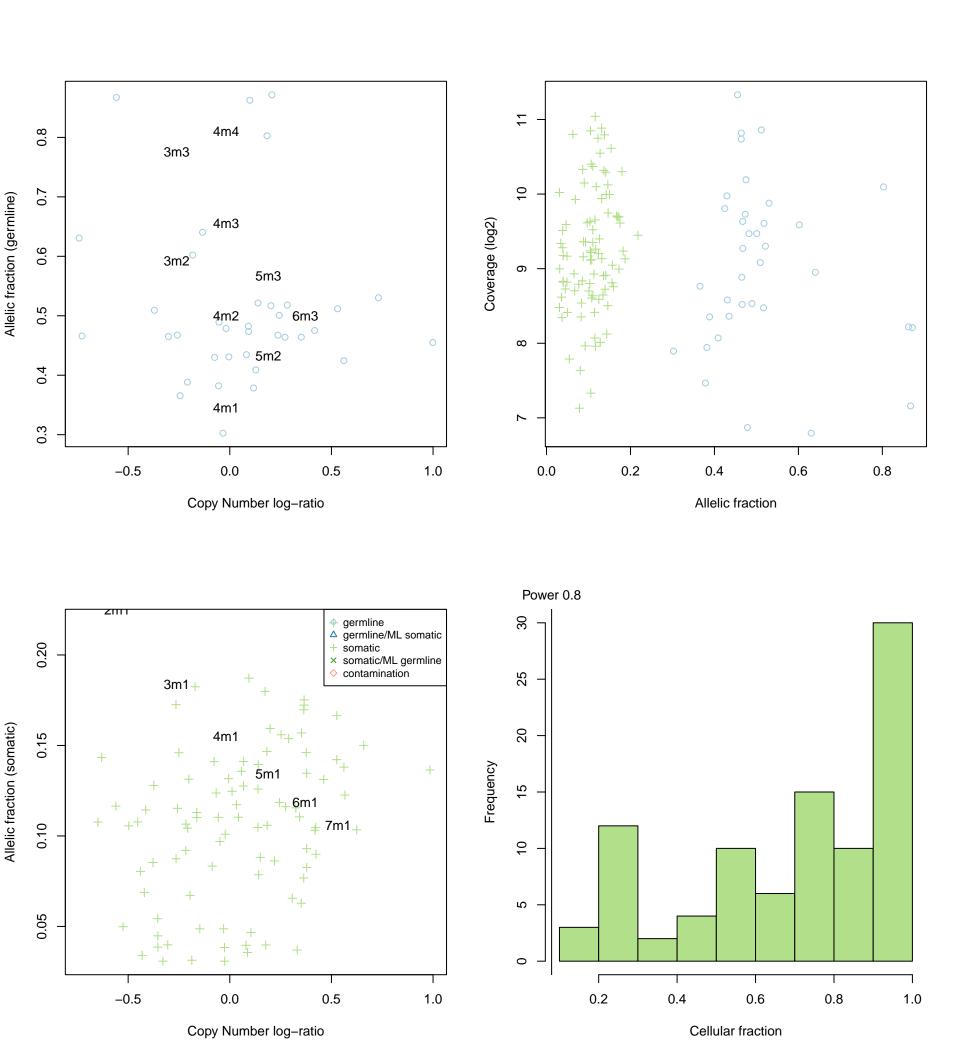
Purity: 0.45 Tumor ploidy: 4.081 SNV log-likelihood: -122.67 GoF: 89.6% Mean coverage: 350;709



SCNA-fit log-likelihood: -4008.23

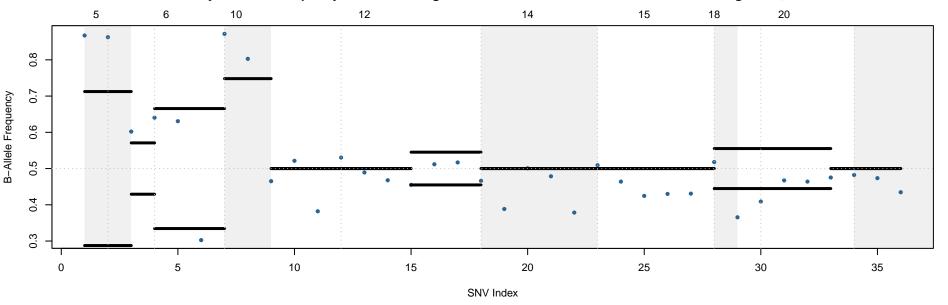




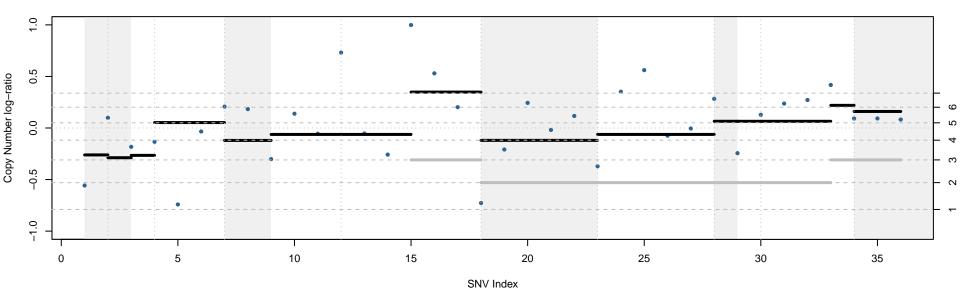


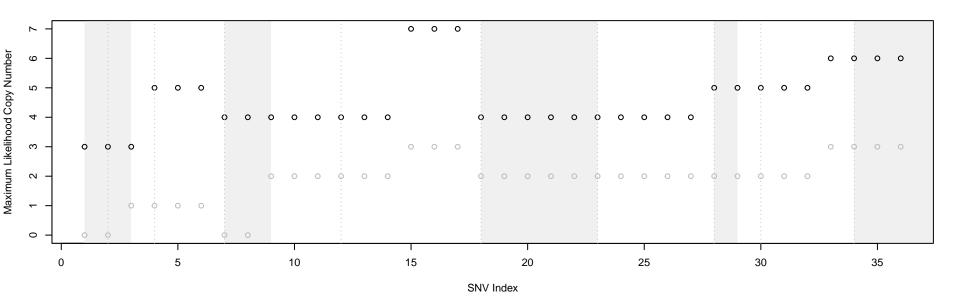
Purity: 0.33 Tumor ploidy: 4.689 2 3 5 6 7 1 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0

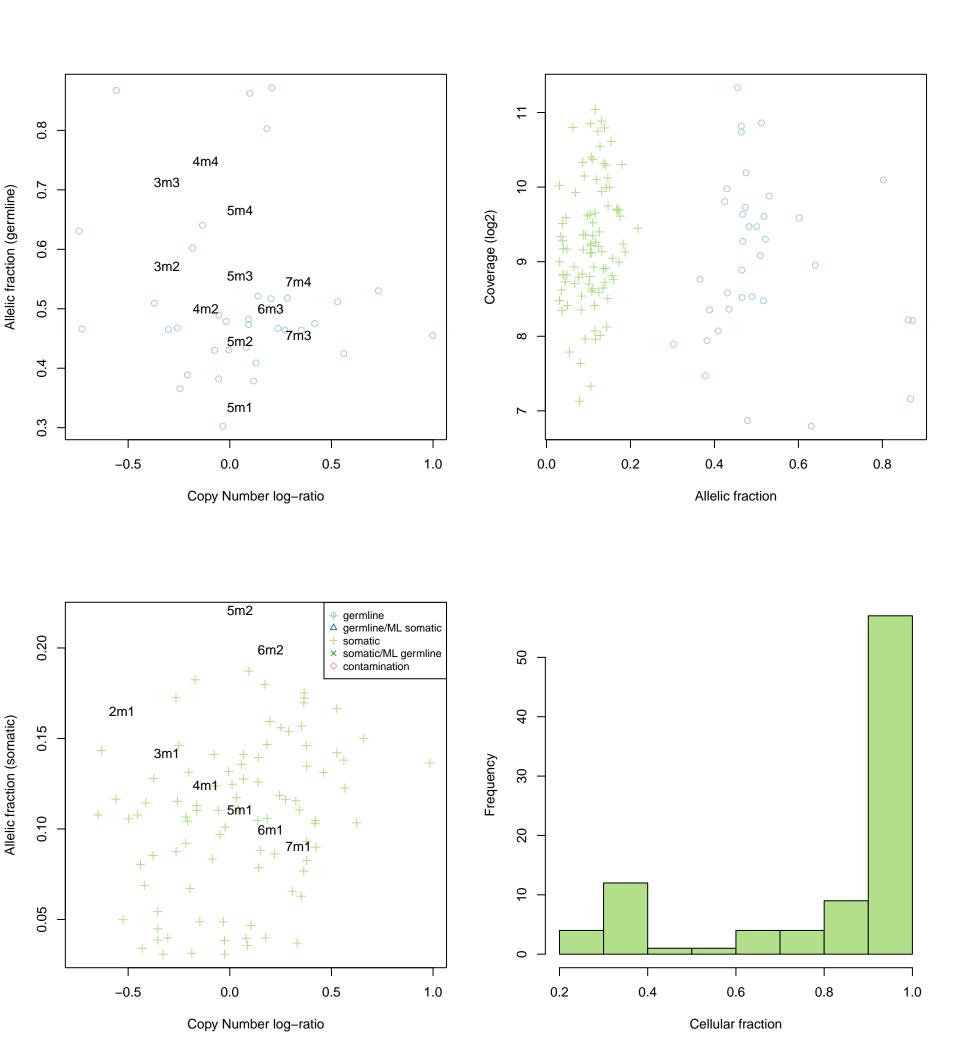
Purity: 0.33 Tumor ploidy: 4.689 SNV log-likelihood: -142.28 GoF: 93.2% Mean coverage: 350;709

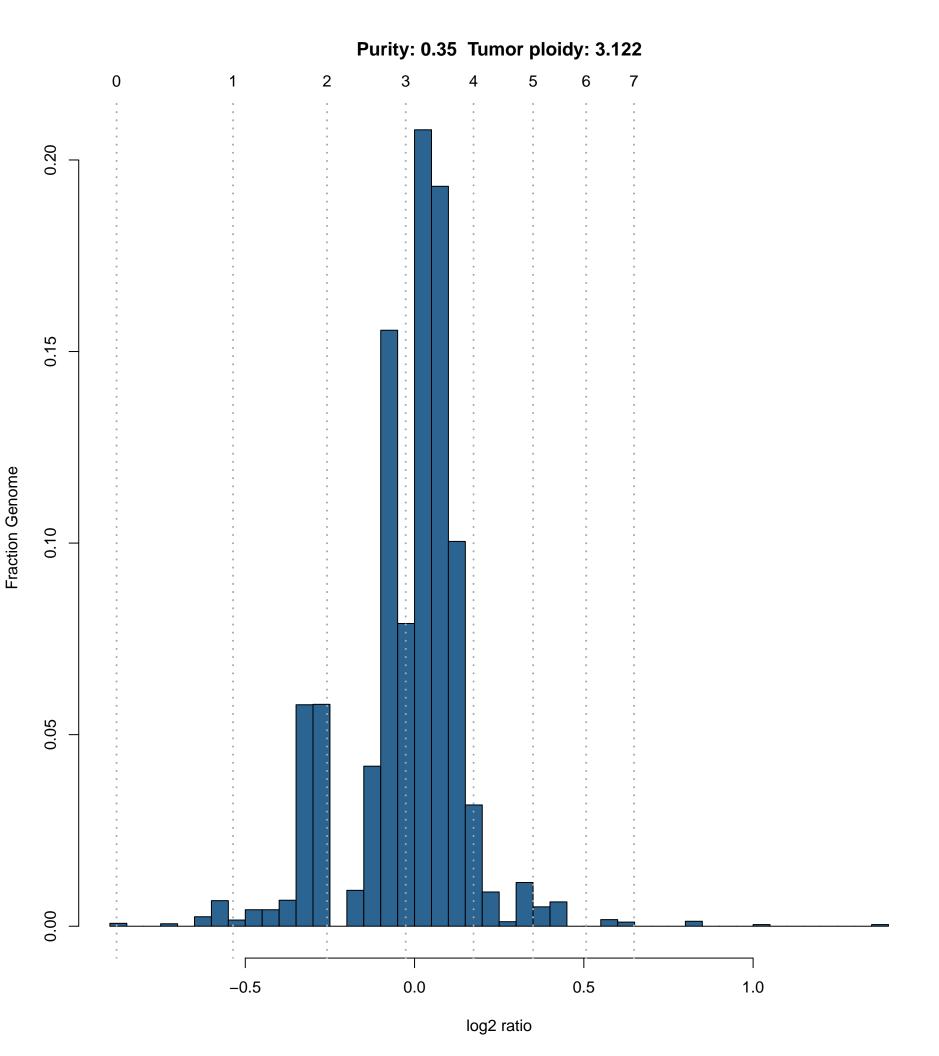


SCNA-fit log-likelihood: -3983.02

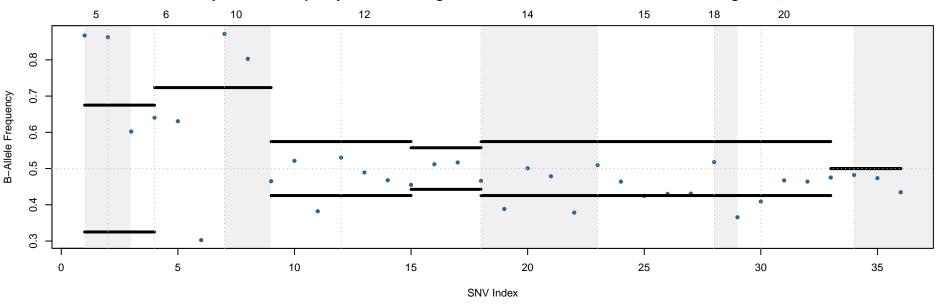




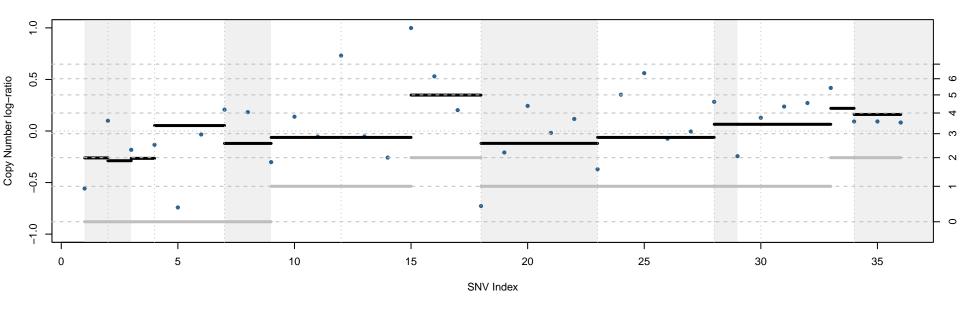


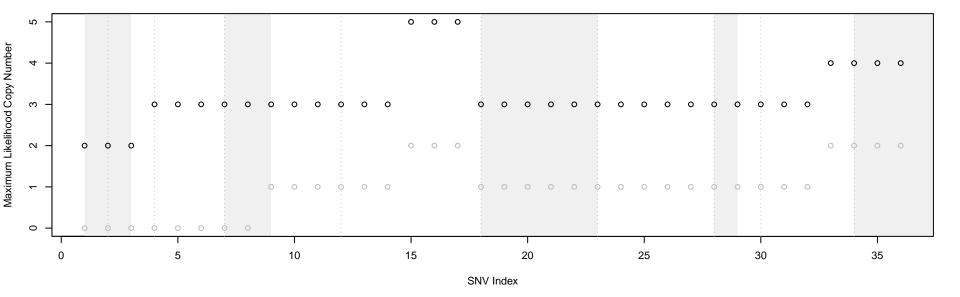


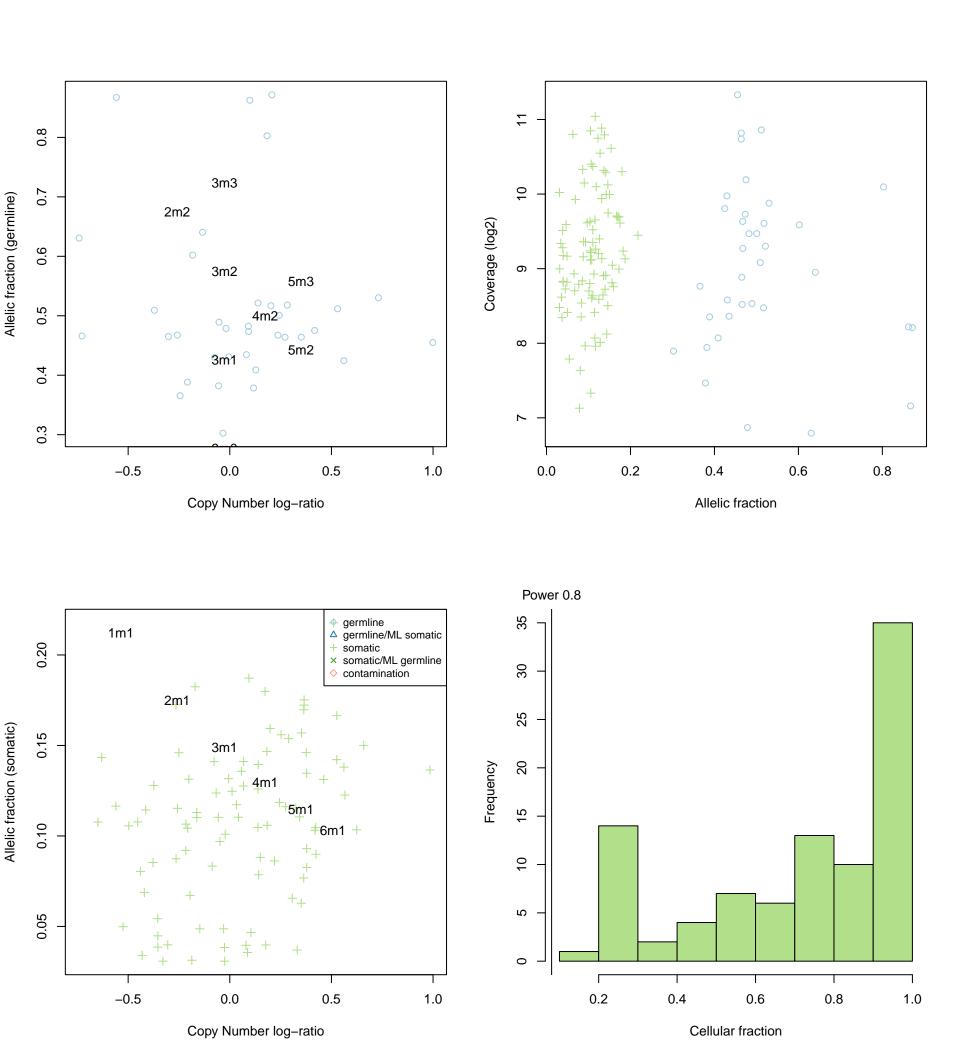
Purity: 0.35 Tumor ploidy: 3.122 SNV log-likelihood: -144.9 GoF: 89.6% Mean coverage: 350;709



SCNA-fit log-likelihood: -3993.34

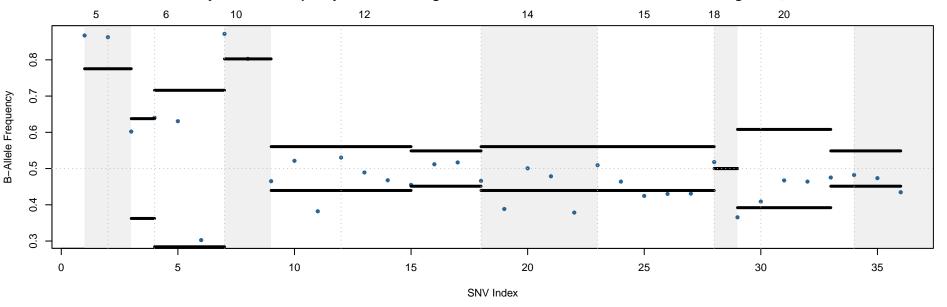




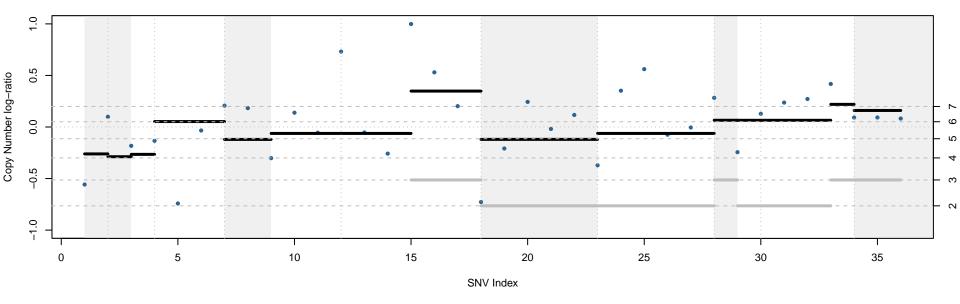


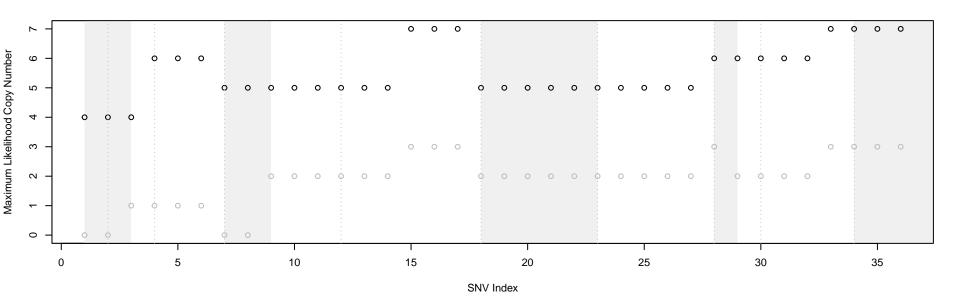
Purity: 0.38 Tumor ploidy: 5.677 2 6 5 3 4 7 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio

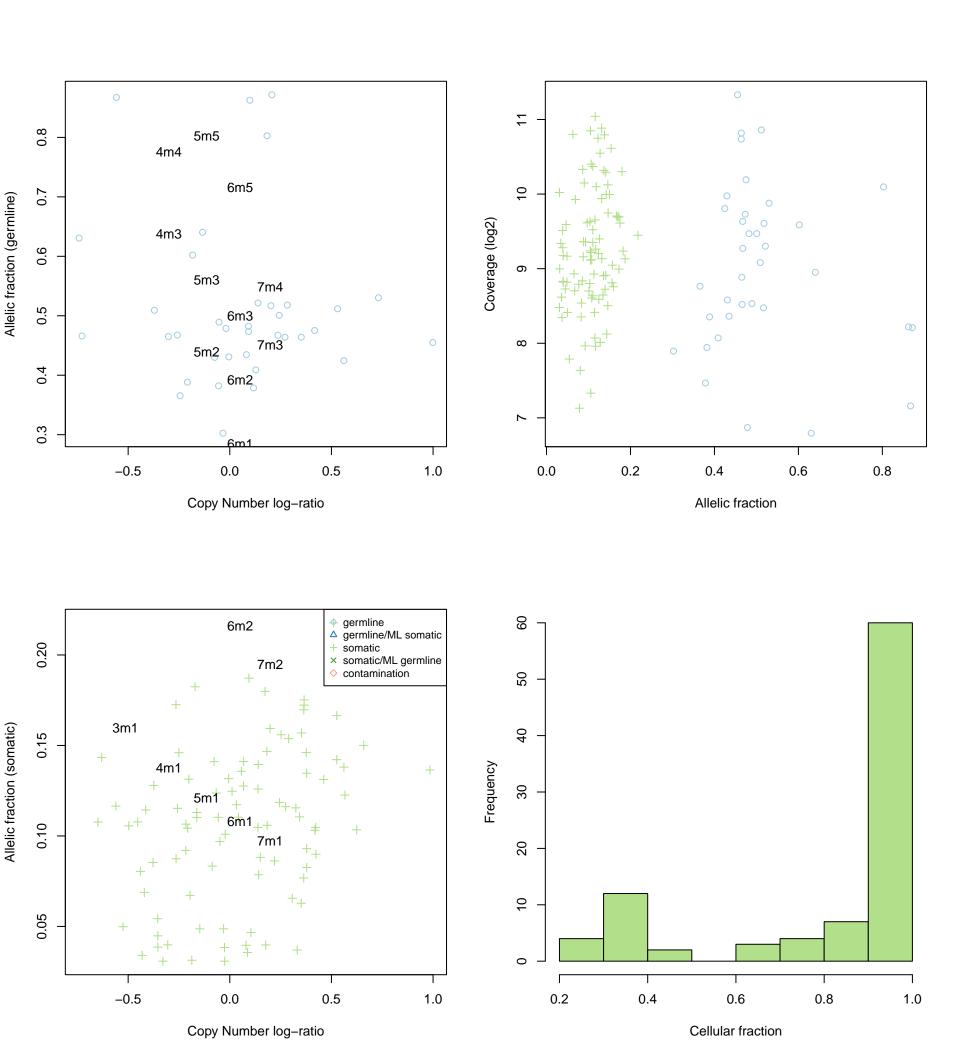
Purity: 0.38 Tumor ploidy: 5.677 SNV log-likelihood: -130.92 GoF: 94.7% Mean coverage: 350;709



SCNA-fit log-likelihood: -4060.05

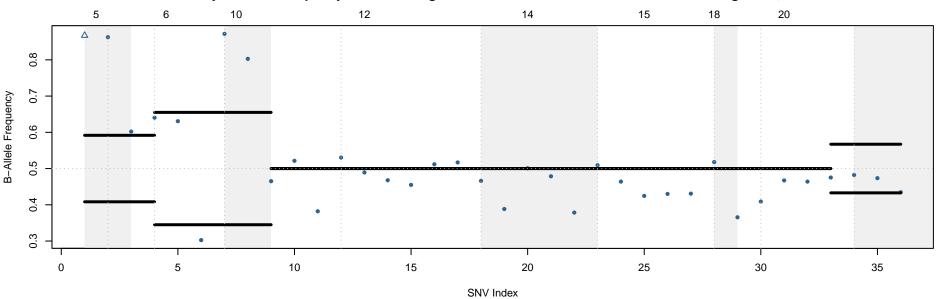




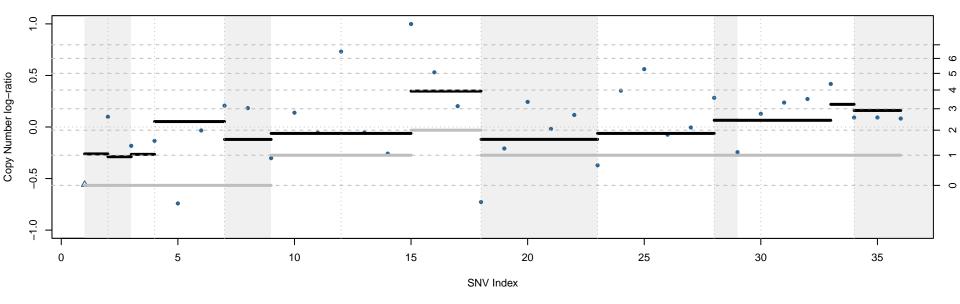


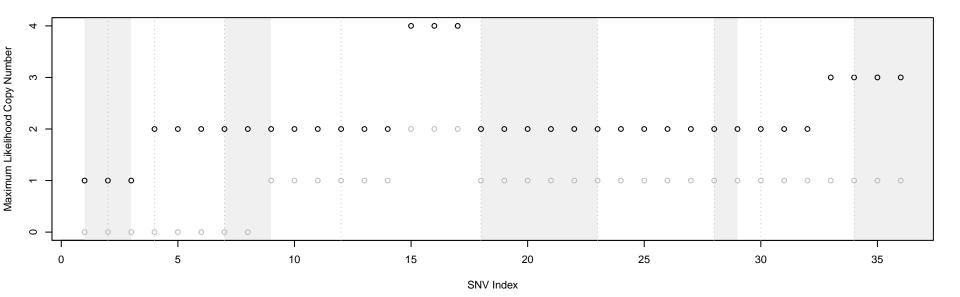
Purity: 0.31 Tumor ploidy: 2.14 2 0 3 7 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio

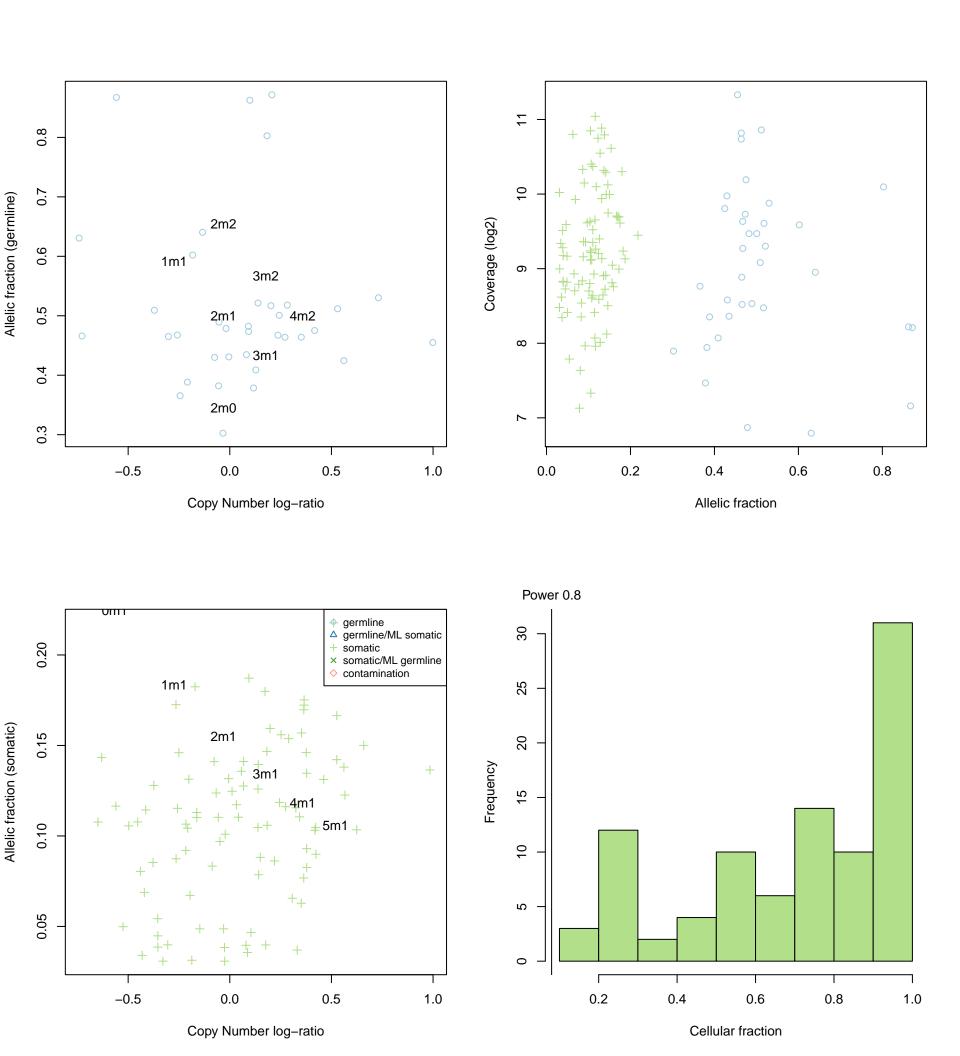
Purity: 0.31 Tumor ploidy: 2.14 SNV log-likelihood: -162.89 GoF: 87.3% Mean coverage: 350;709



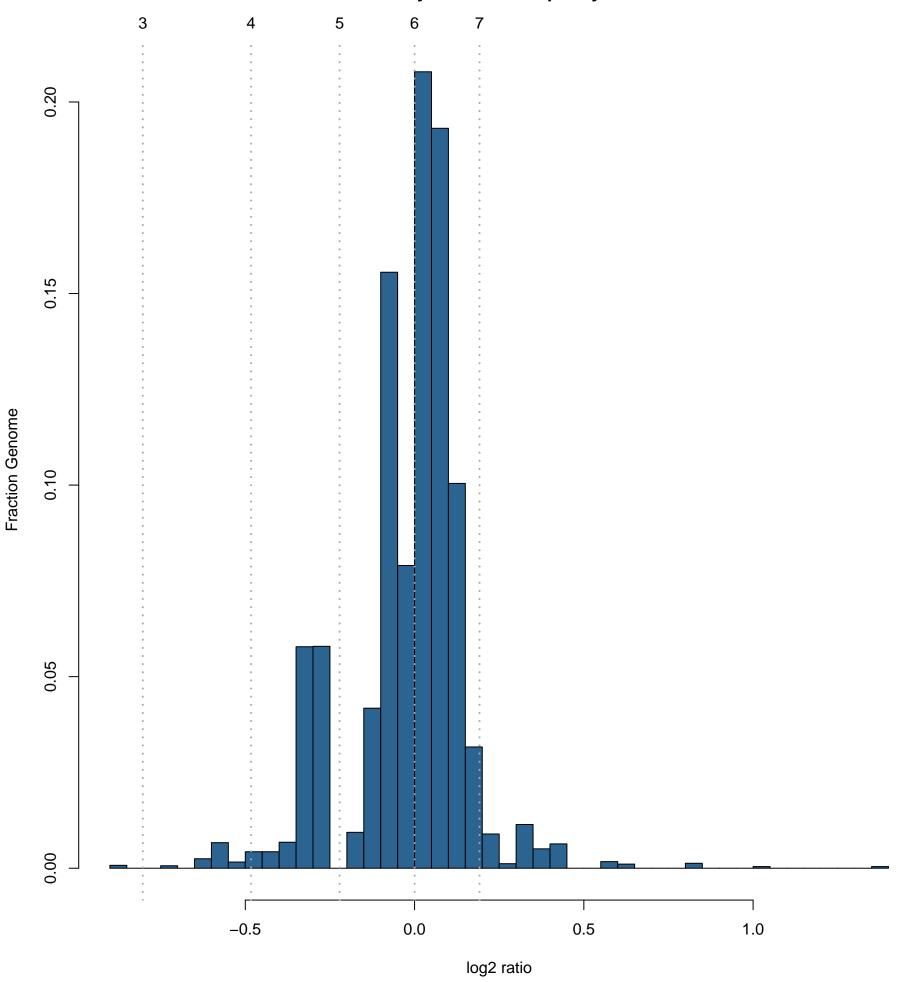
SCNA-fit log-likelihood: -4014.34



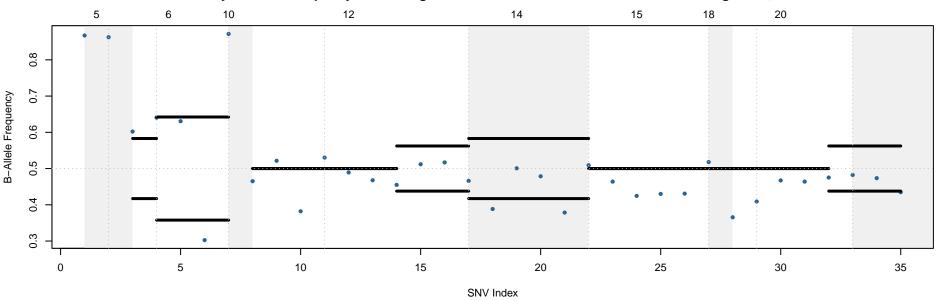




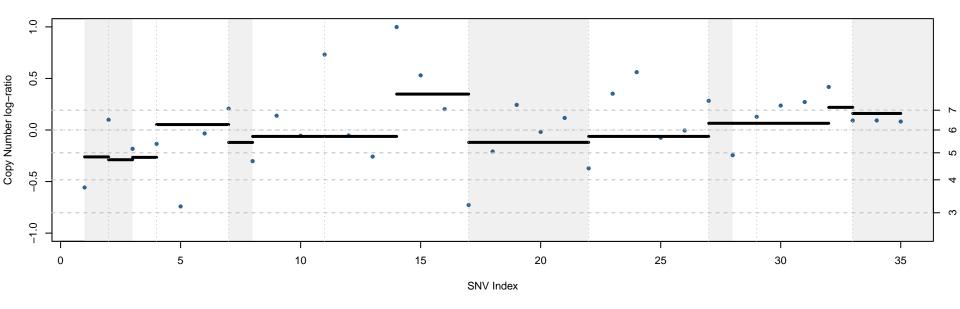
Purity: 0.66 Tumor ploidy: 6

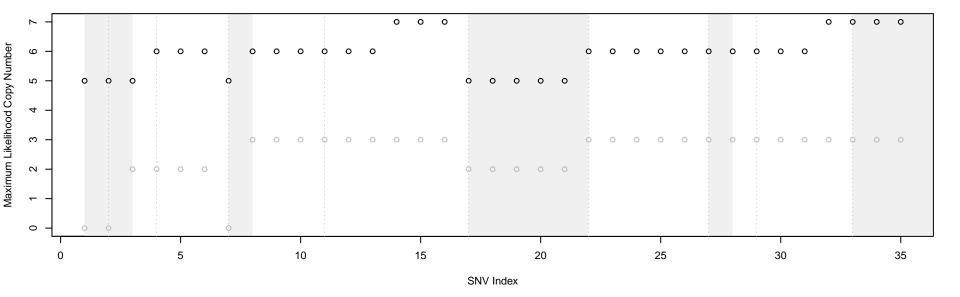


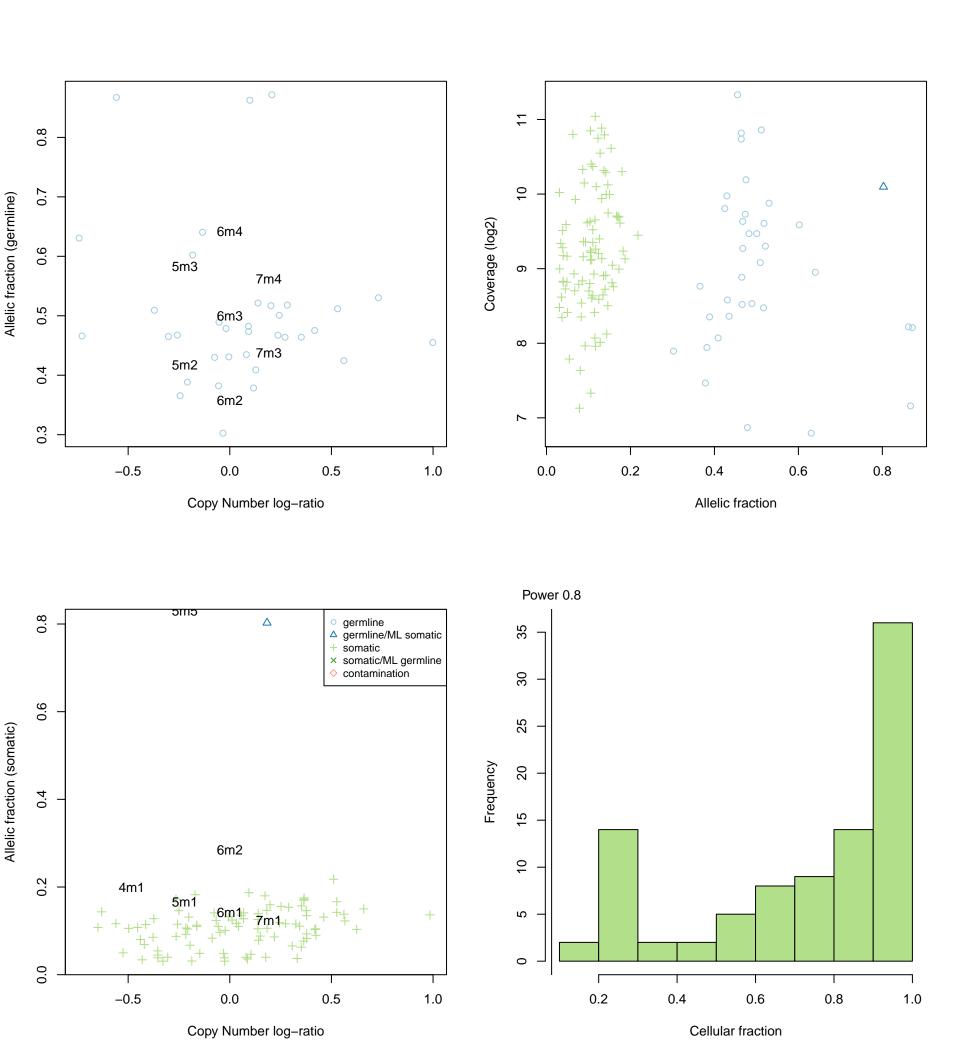
Purity: 0.66 Tumor ploidy: 6 SNV log-likelihood: -144.45 GoF: 92.4% Mean coverage: 350;709

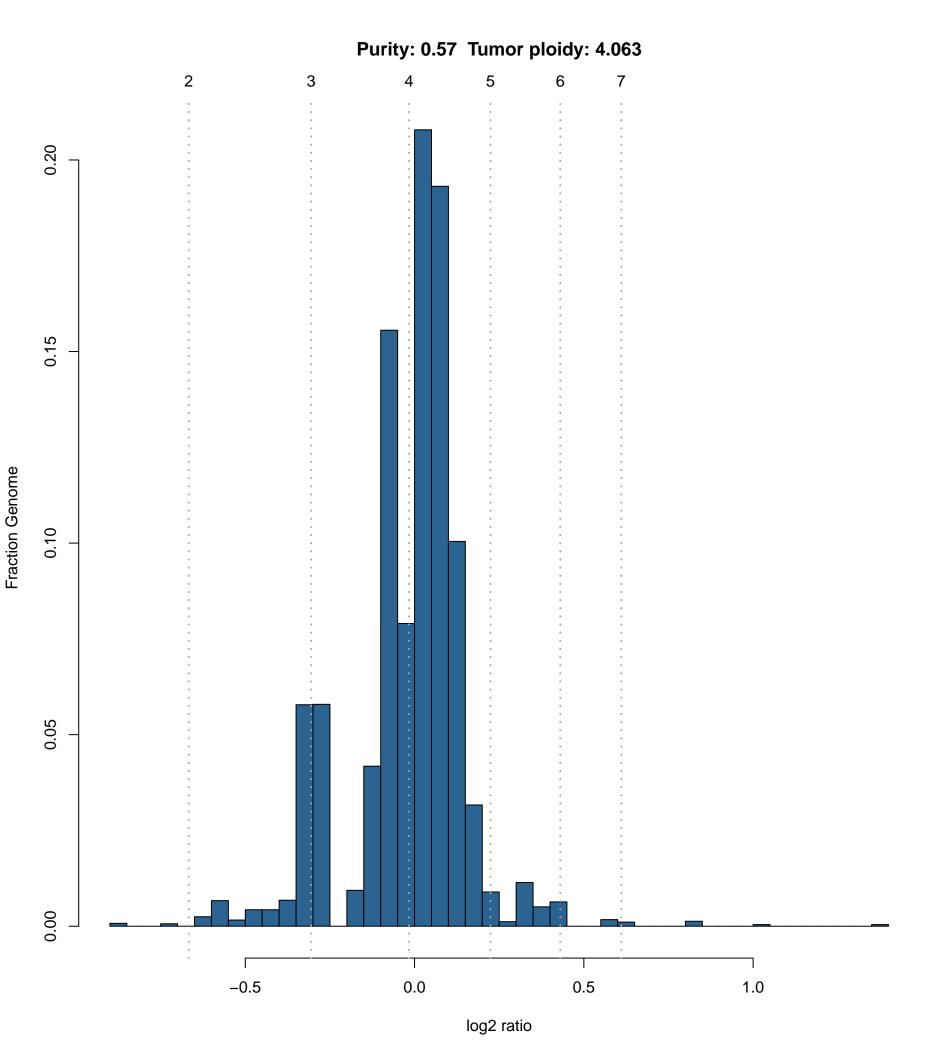


SCNA-fit log-likelihood: -4076.05

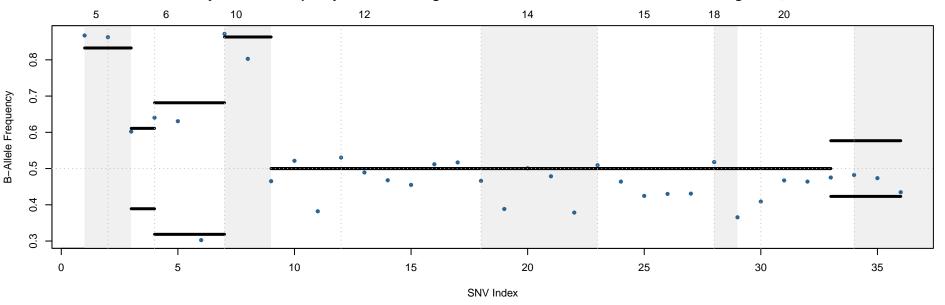




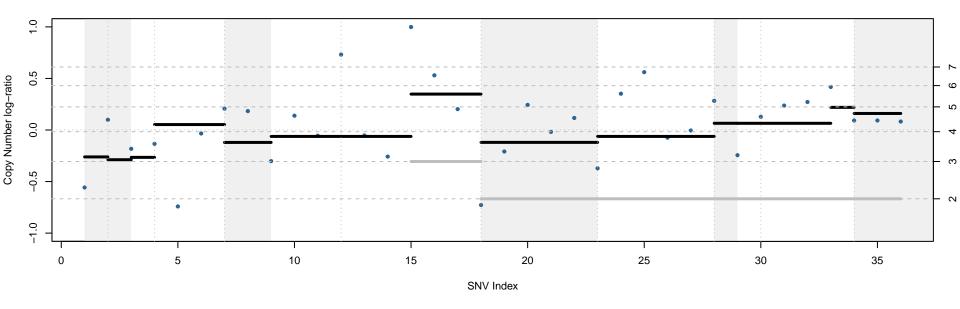


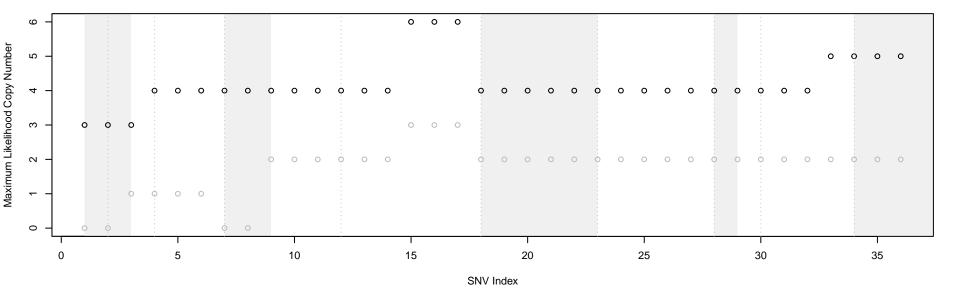


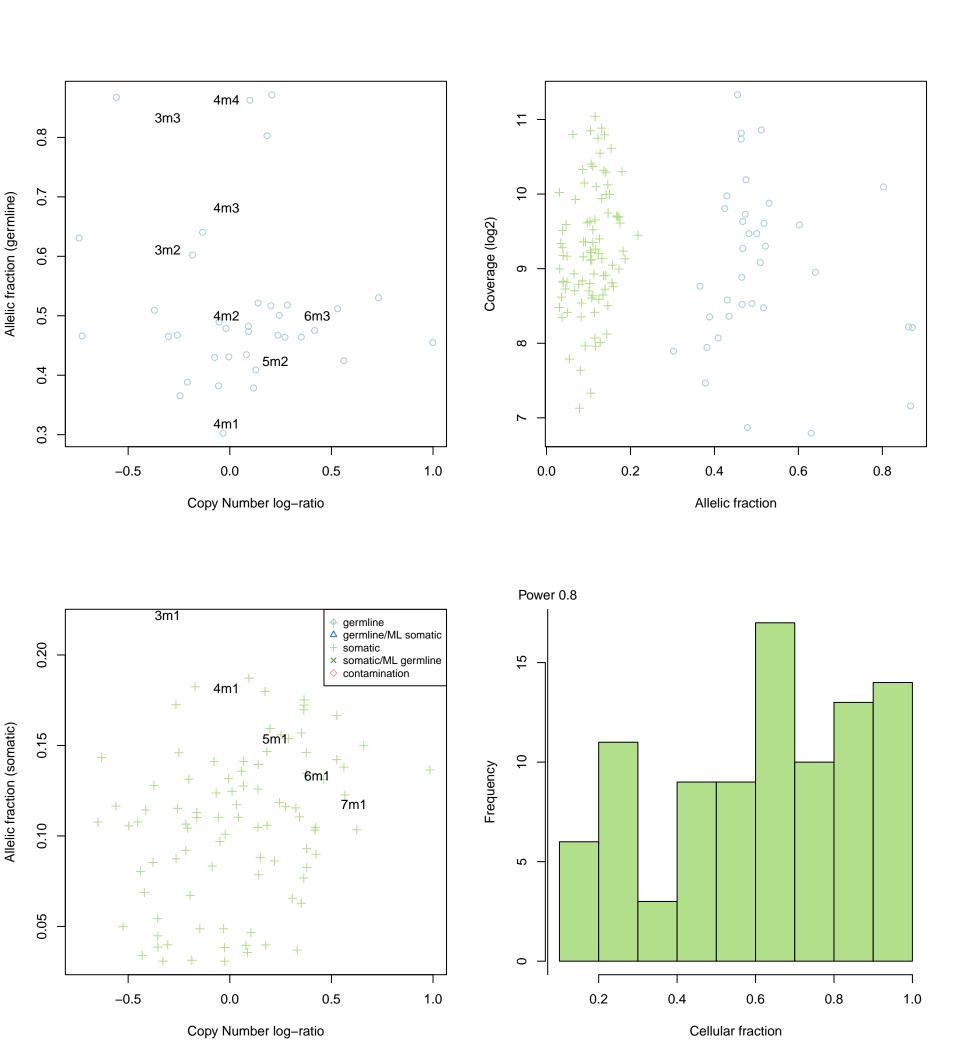
Purity: 0.57 Tumor ploidy: 4.063 SNV log-likelihood: -174.49 GoF: 84.2% Mean coverage: 350;709



SCNA-fit log-likelihood: -4017.13

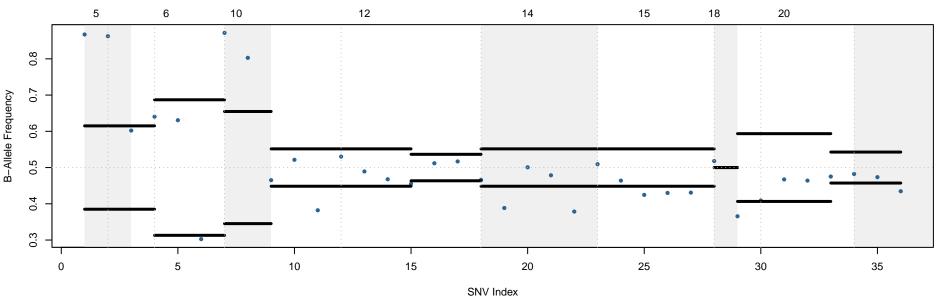




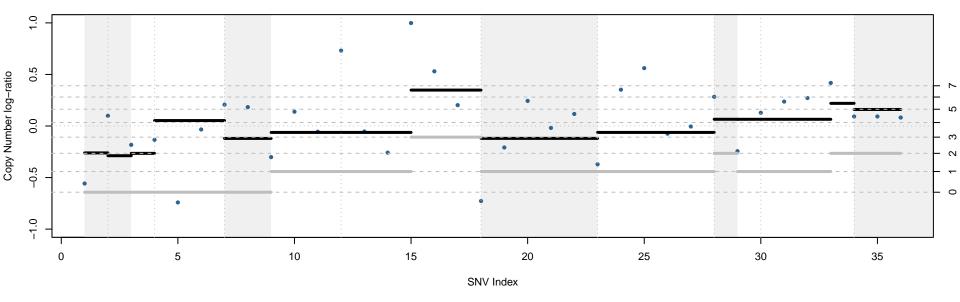


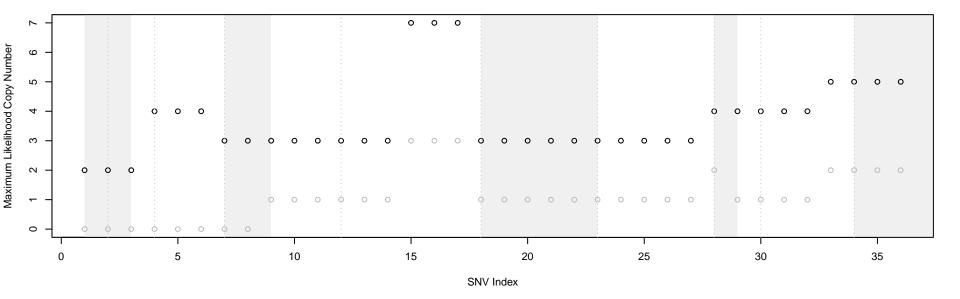
Purity: 0.23 Tumor ploidy: 3.755 3 0 2 5 6 7 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0

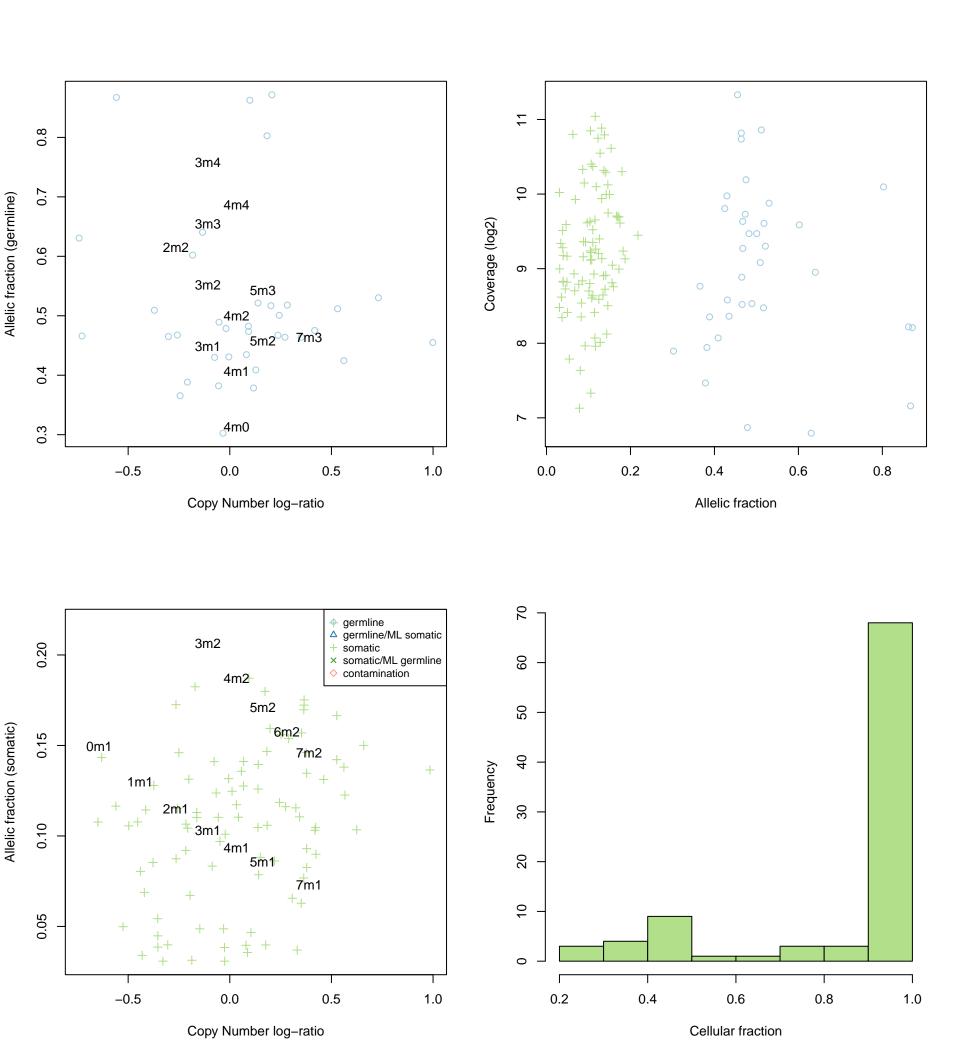
Purity: 0.23 Tumor ploidy: 3.755 SNV log-likelihood: -179.61 GoF: 93.1% Mean coverage: 350;709

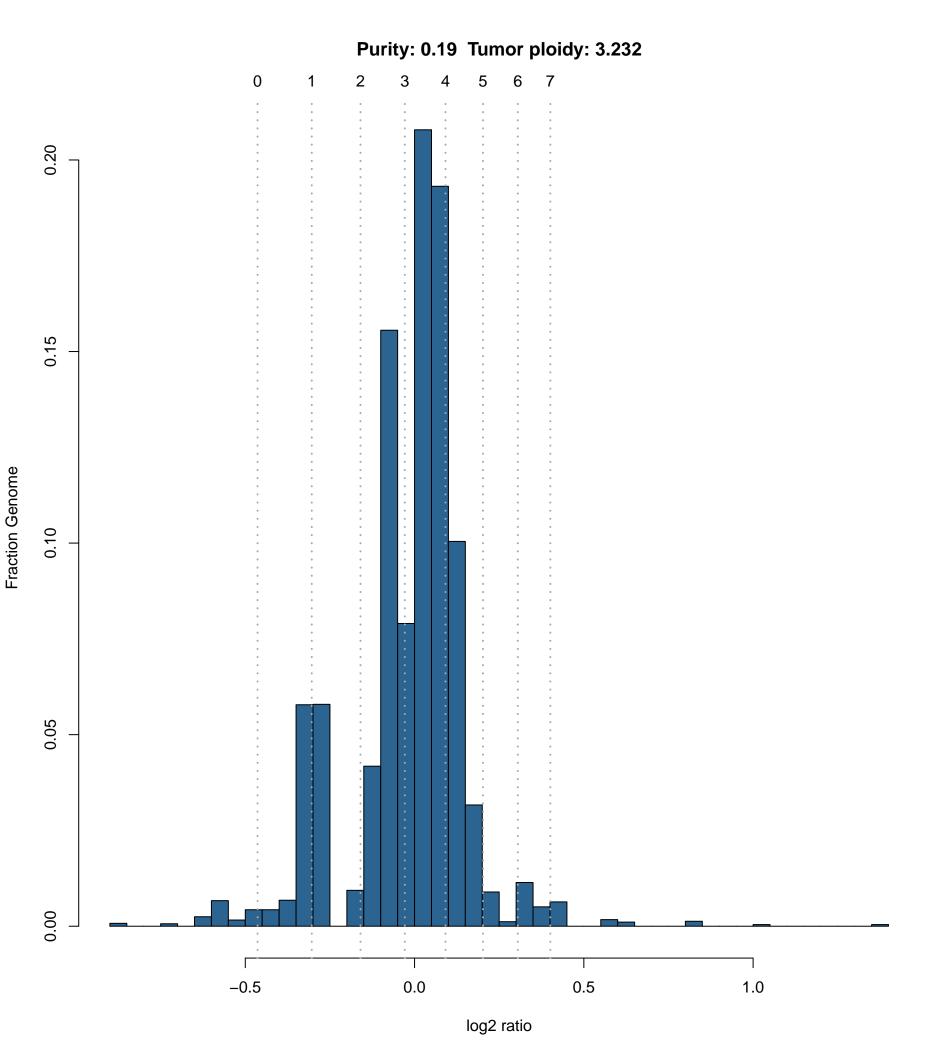


SCNA-fit log-likelihood: -3971.47

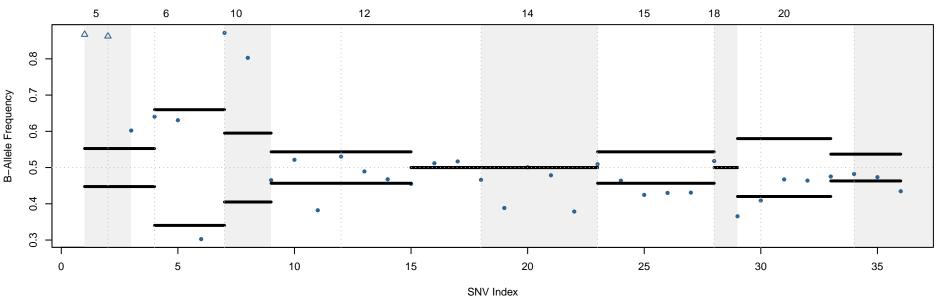




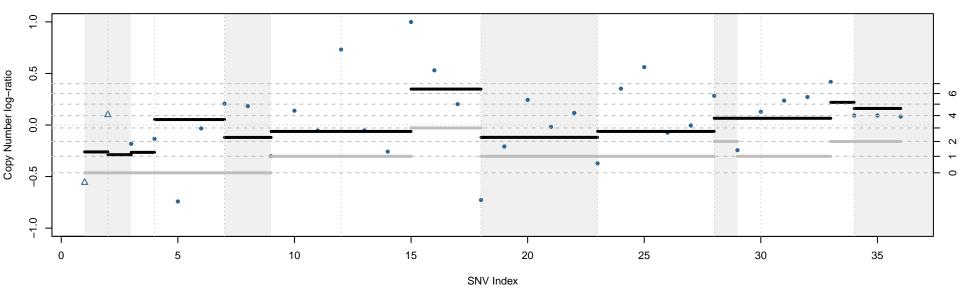


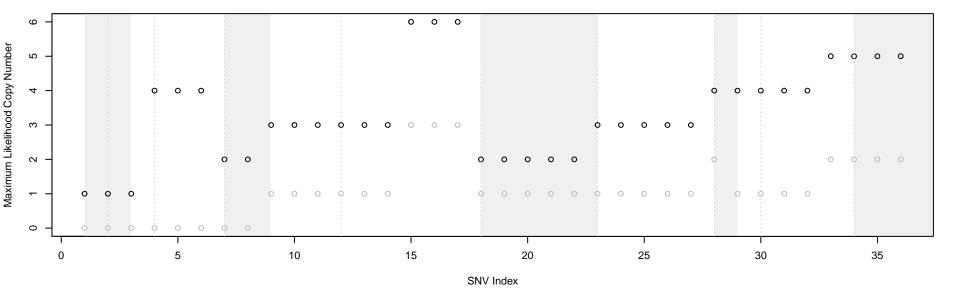


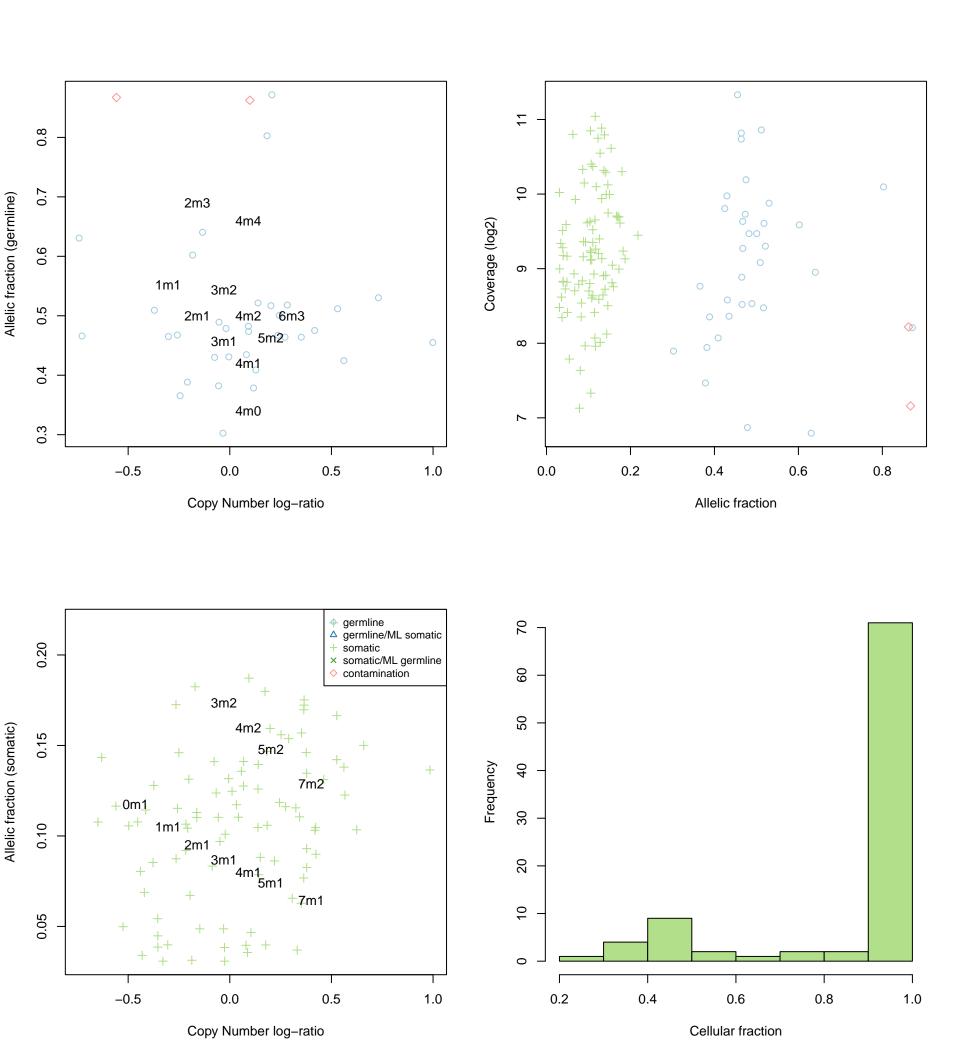
Purity: 0.19 Tumor ploidy: 3.232 SNV log-likelihood: -182.38 GoF: 96.2% Mean coverage: 350;709



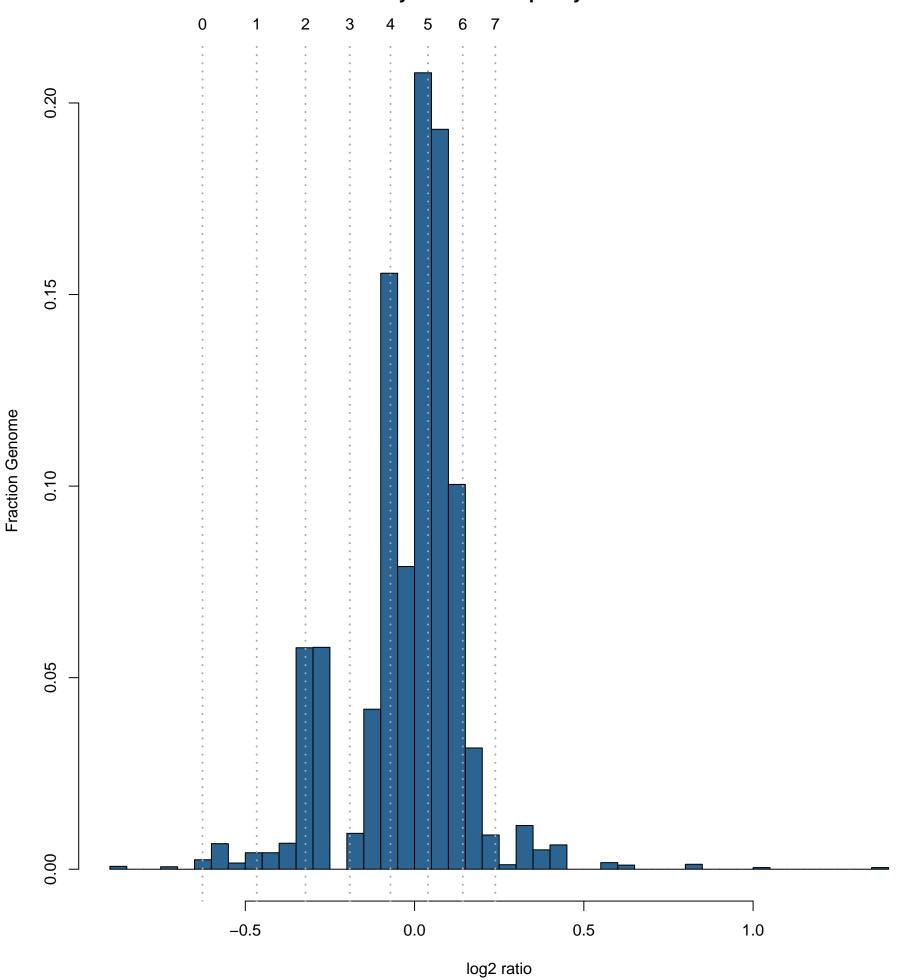
SCNA-fit log-likelihood: -3998.73



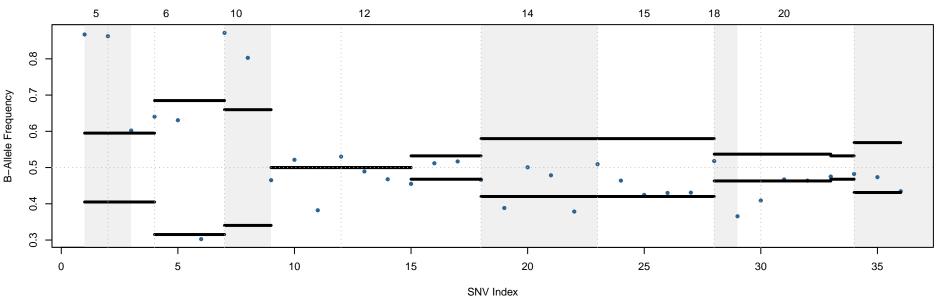




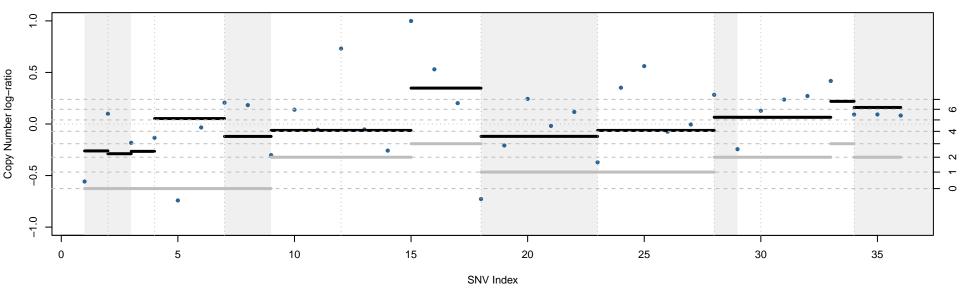
Purity: 0.19 Tumor ploidy: 4.634

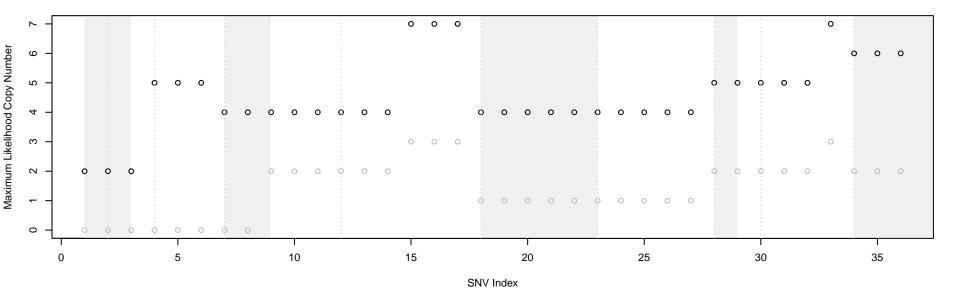


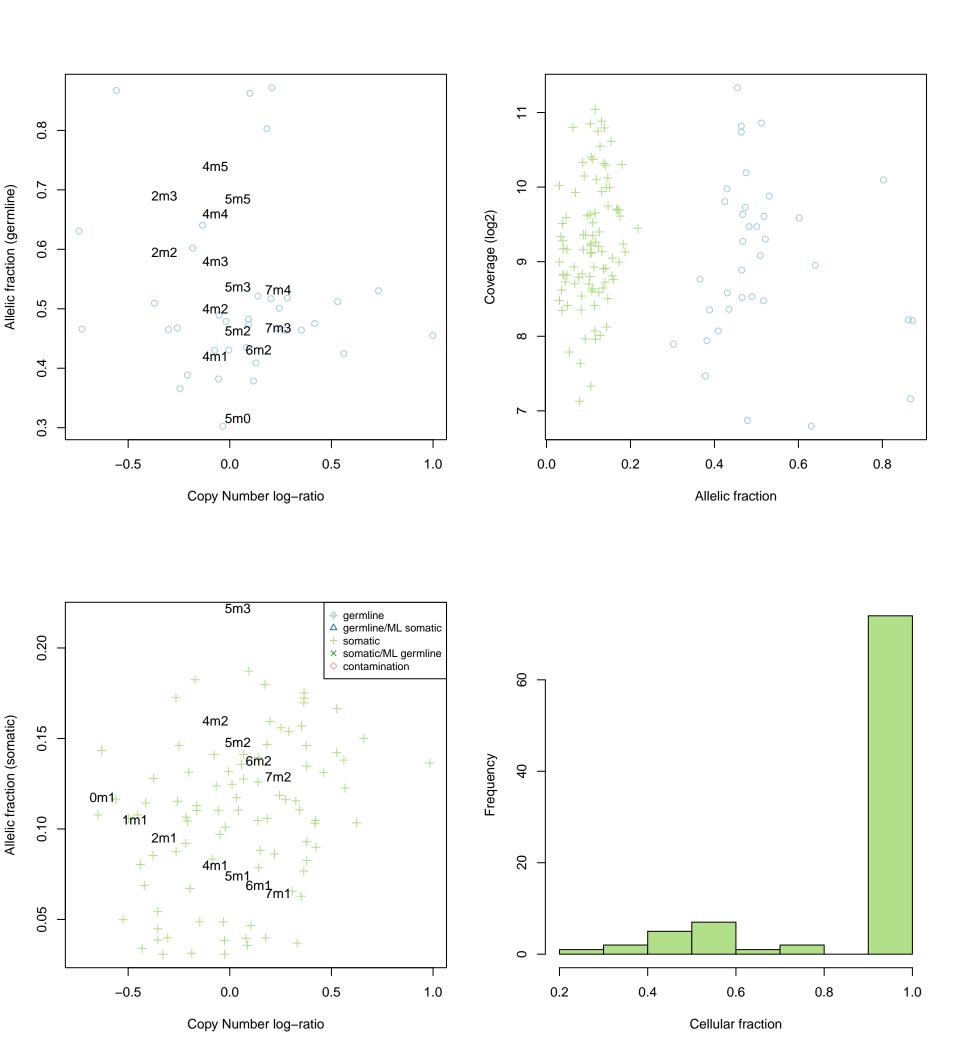
Purity: 0.19 Tumor ploidy: 4.634 SNV log-likelihood: -212.31 GoF: 94.4% Mean coverage: 350;709

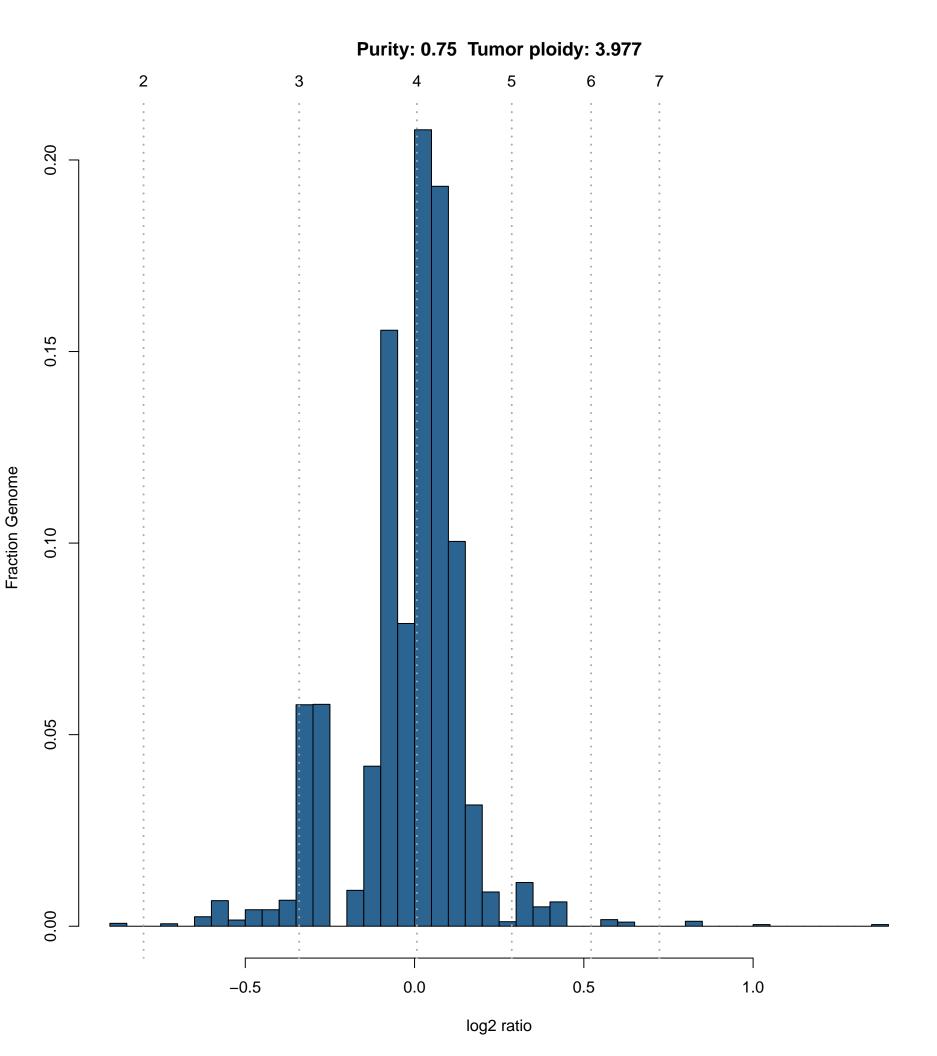


SCNA-fit log-likelihood: -4026.29

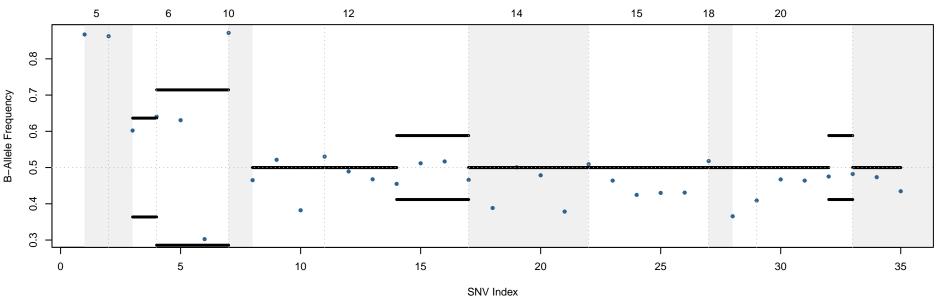




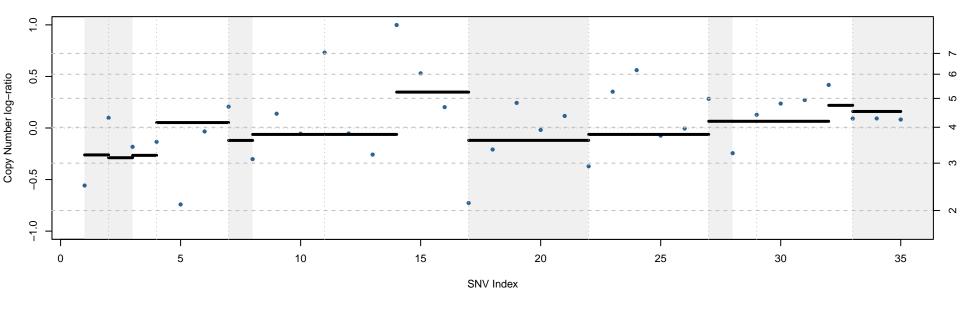


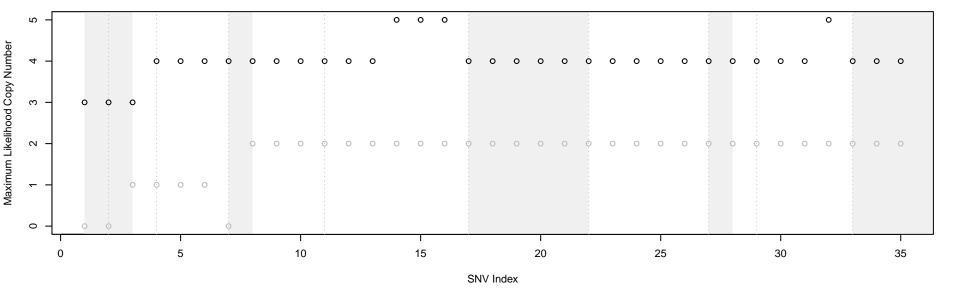


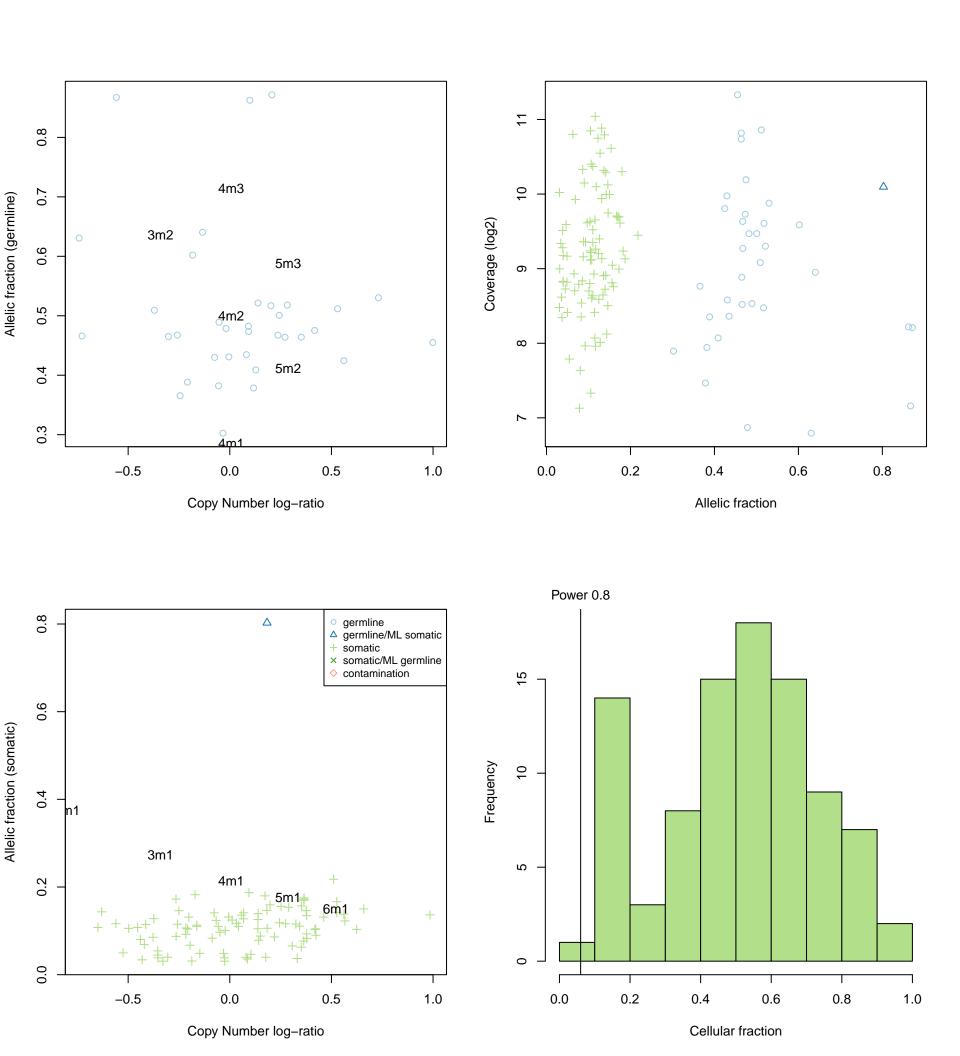
Purity: 0.75 Tumor ploidy: 3.977 SNV log-likelihood: -272.75 GoF: 70.2% Mean coverage: 350;709

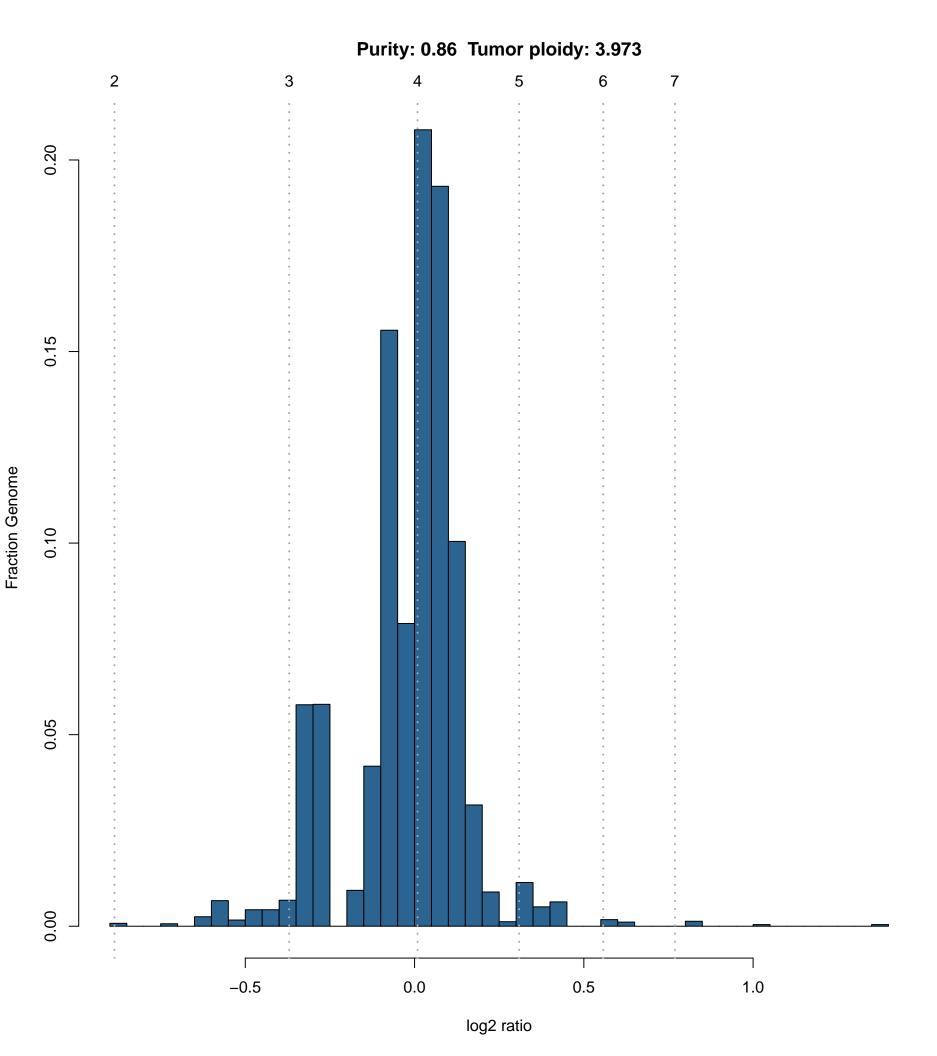


SCNA-fit log-likelihood: -4063.13

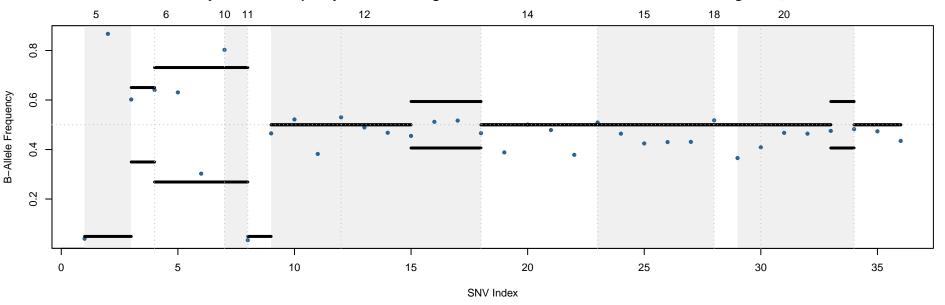




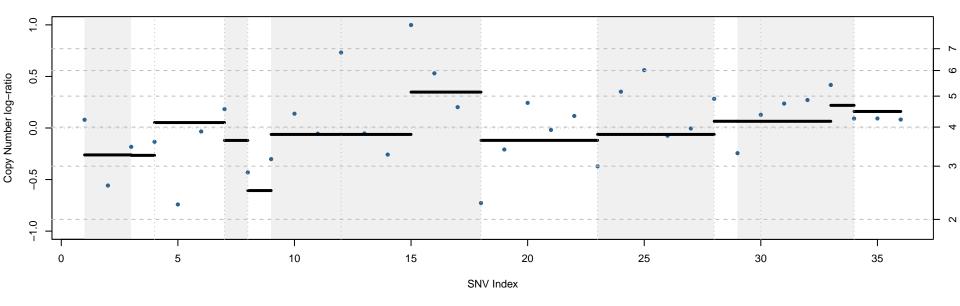


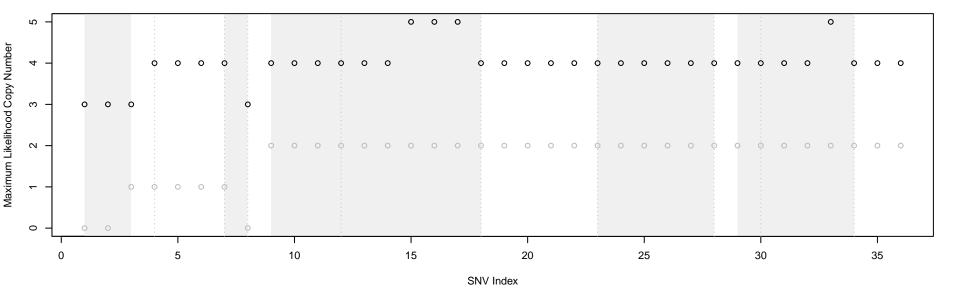


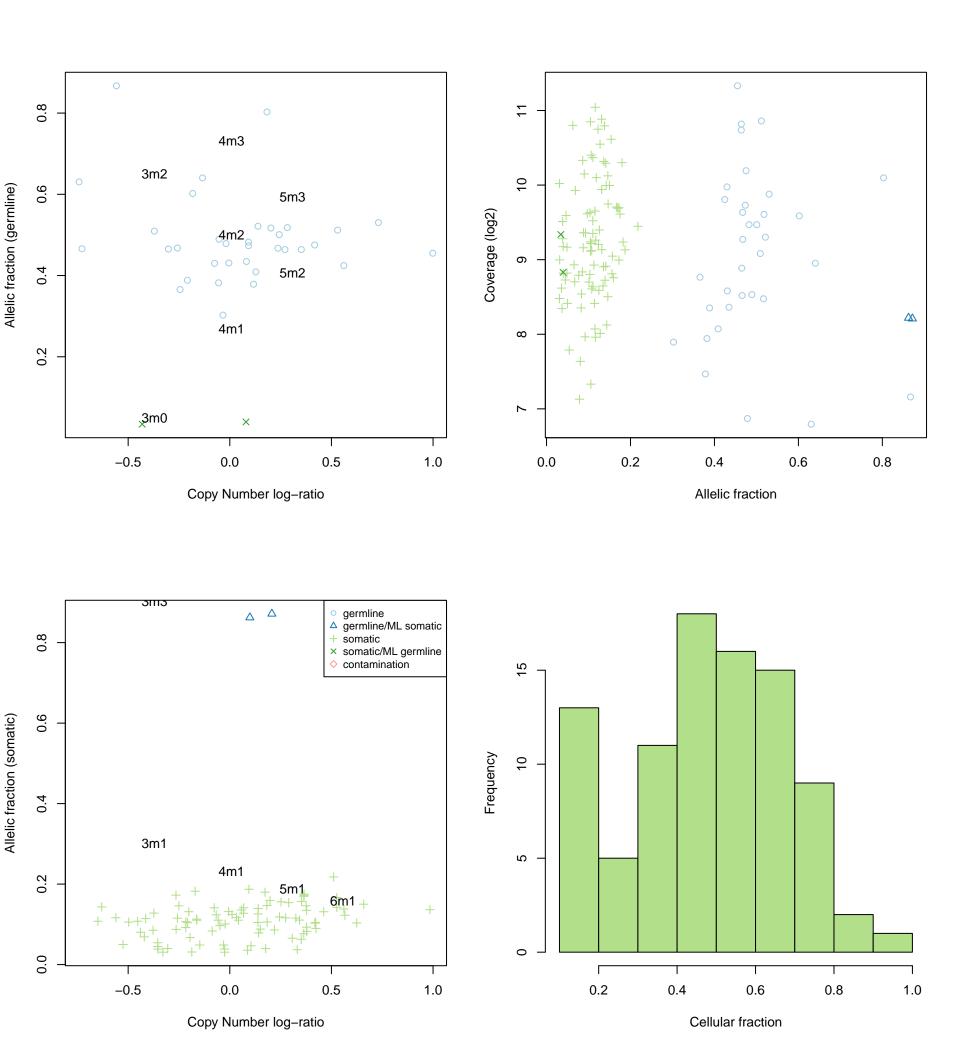
Purity: 0.86 Tumor ploidy: 3.973 SNV log-likelihood: -319.73 GoF: 67.3% Mean coverage: 350;709



SCNA-fit log-likelihood: -4078.43

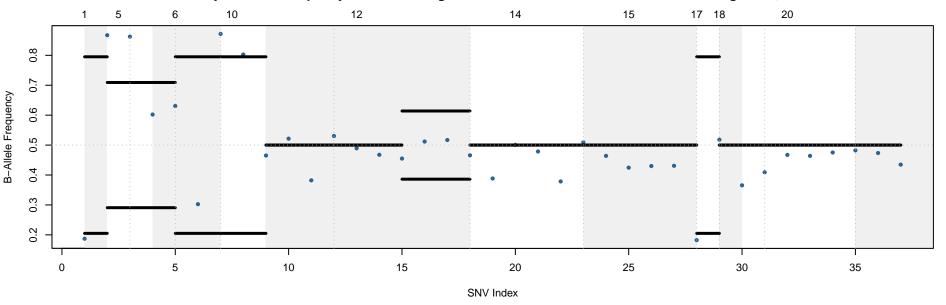




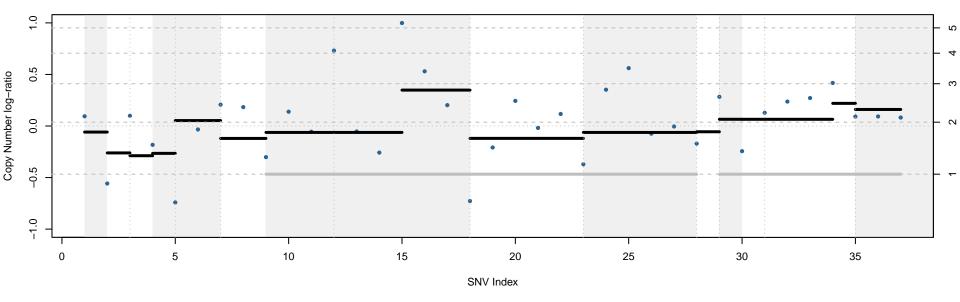


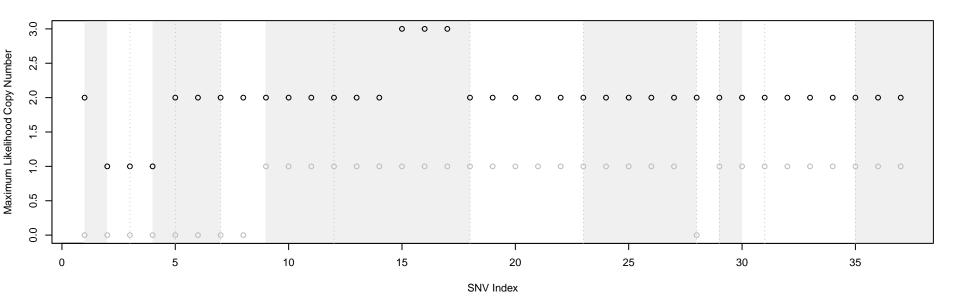
Purity: 0.59 Tumor ploidy: 1.914 3 2 5 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0

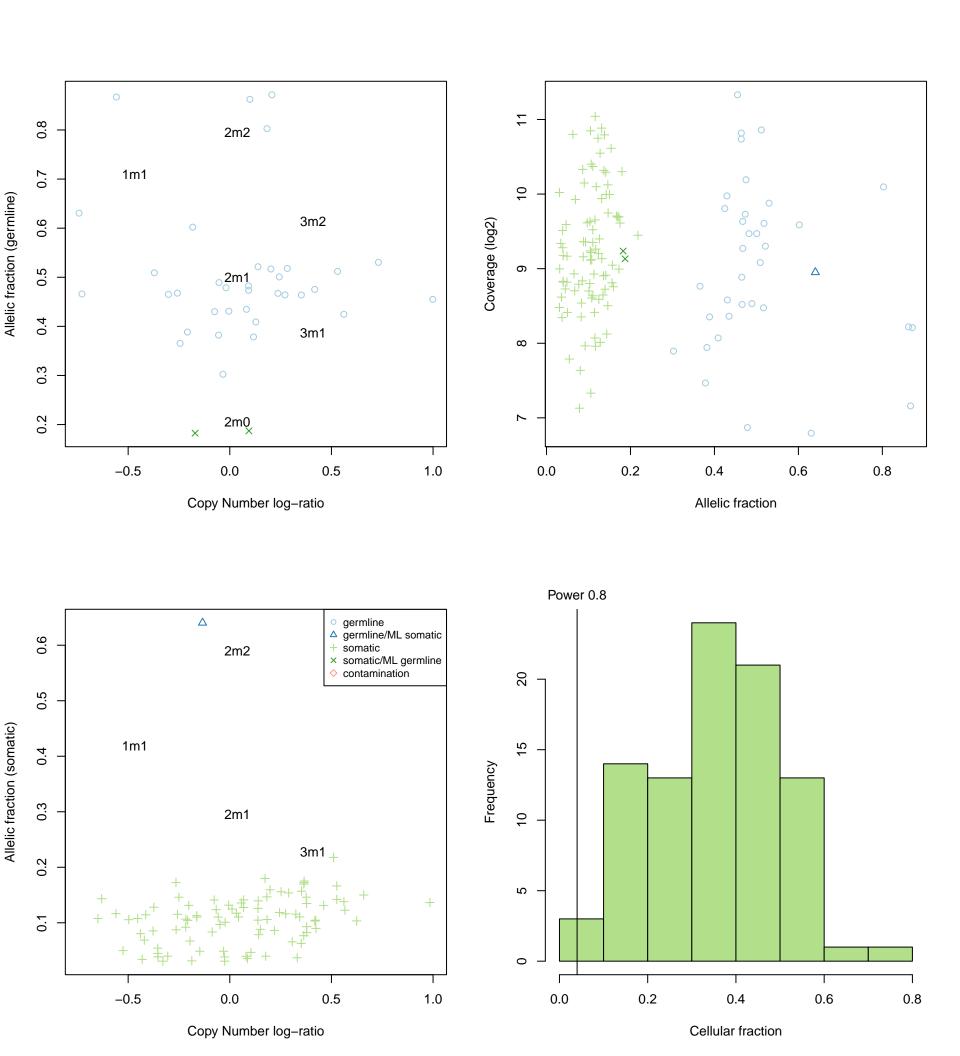
Purity: 0.59 Tumor ploidy: 1.914 SNV log-likelihood: -281.09 GoF: 22% Mean coverage: 350;709



SCNA-fit log-likelihood: -4184.42

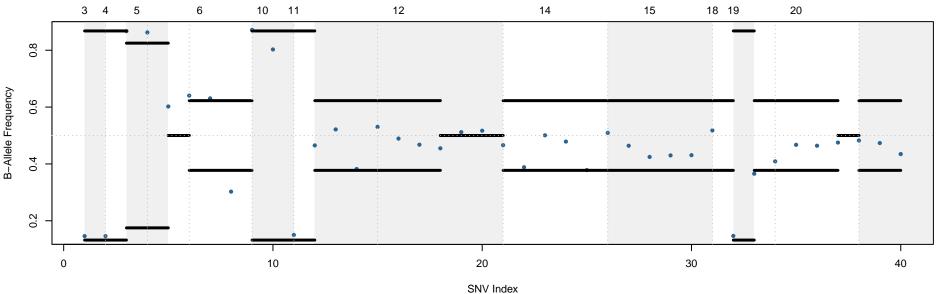






Purity: 0.65 Tumor ploidy: 2.935 2 6 1 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0





SCNA-fit log-likelihood: -4091.03

