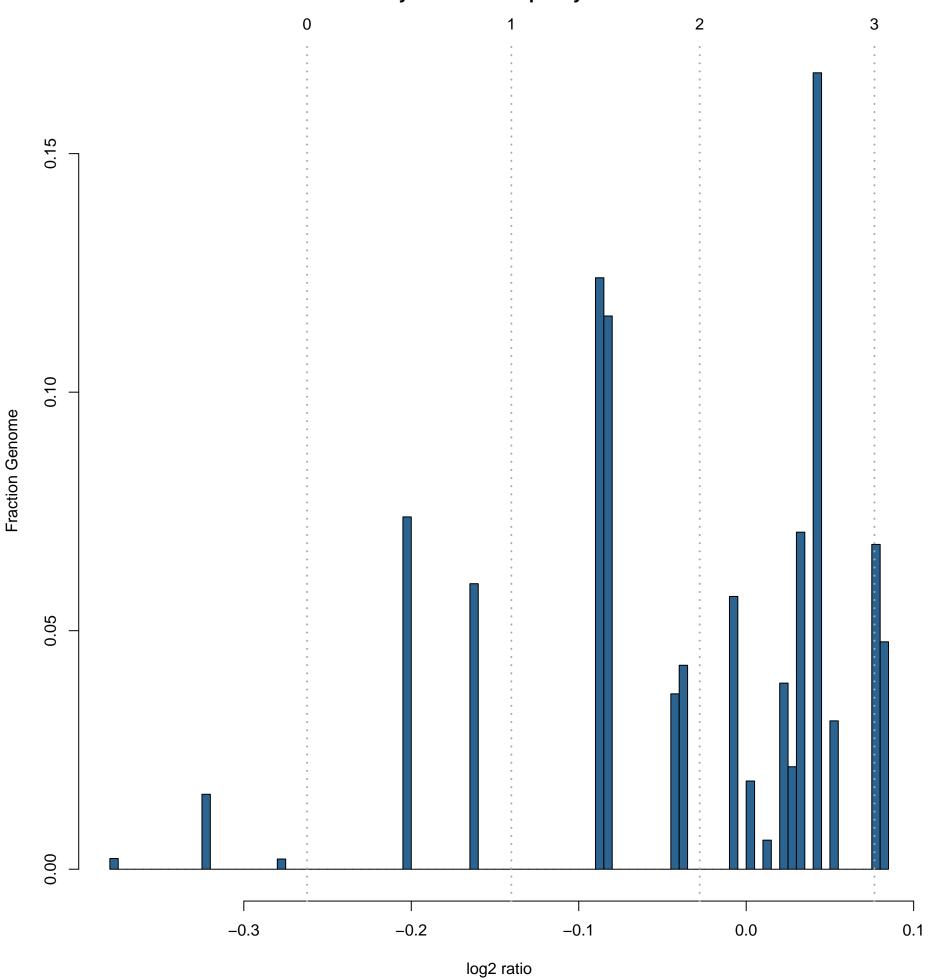
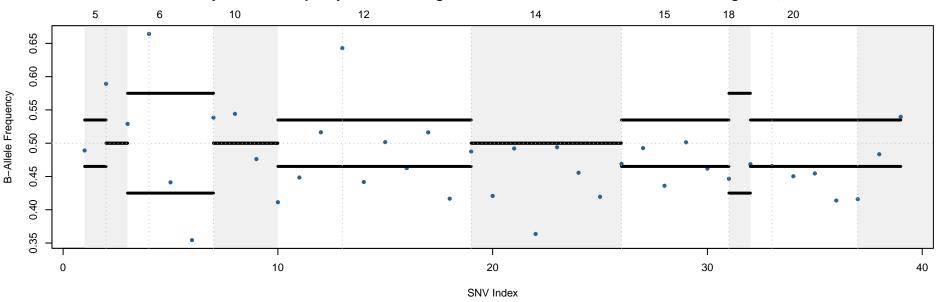
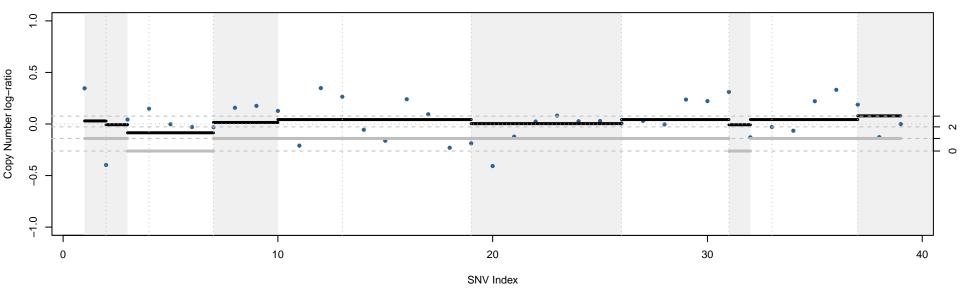
Purity: 0.15 Tumor ploidy: 2.259

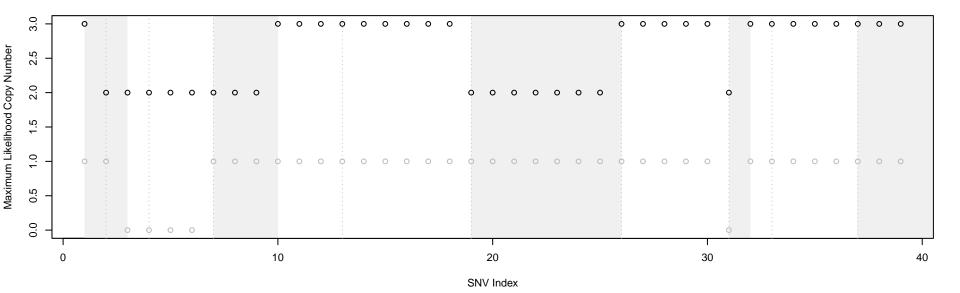


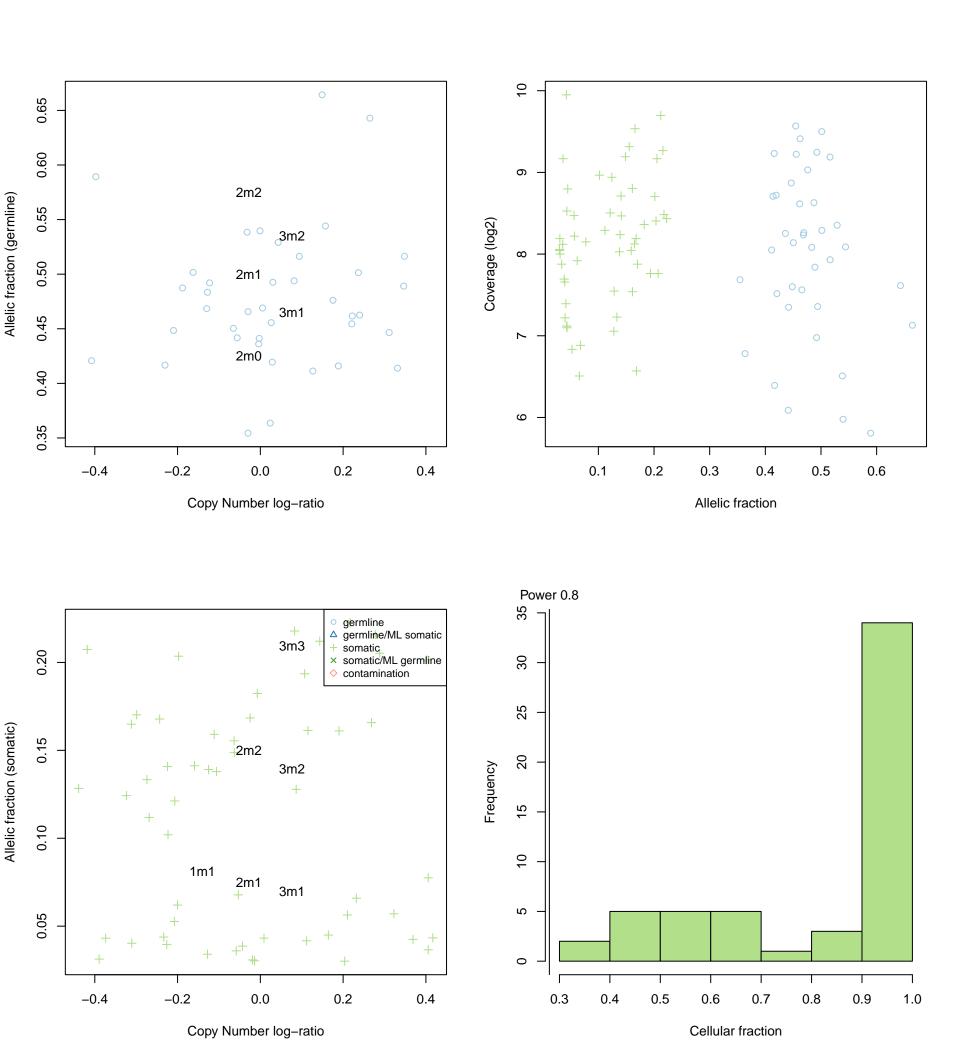
Purity: 0.15 Tumor ploidy: 2.259 SNV log-likelihood: -16.35 GoF: 95.8% Mean coverage: 315;324



SCNA-fit log-likelihood: -475.85

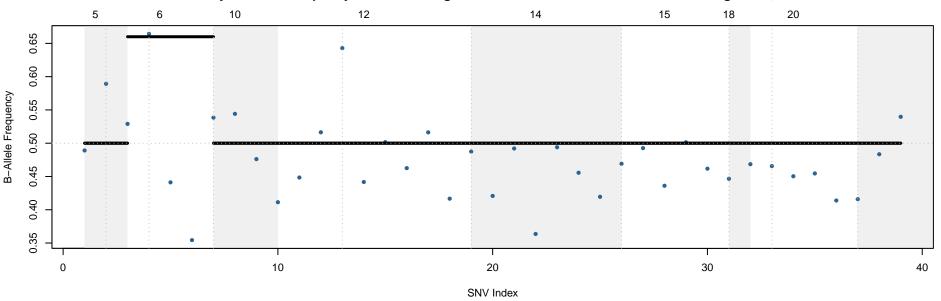




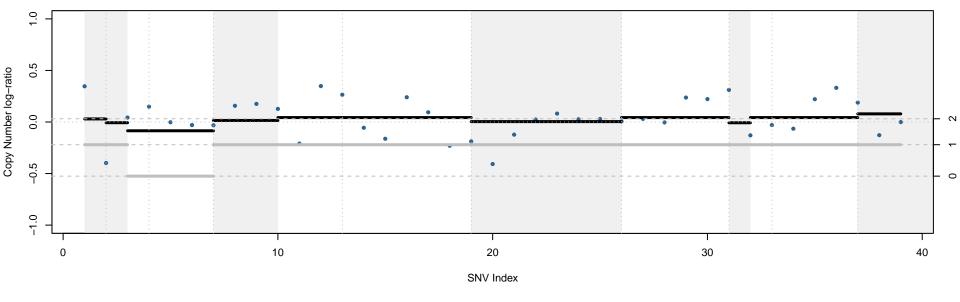


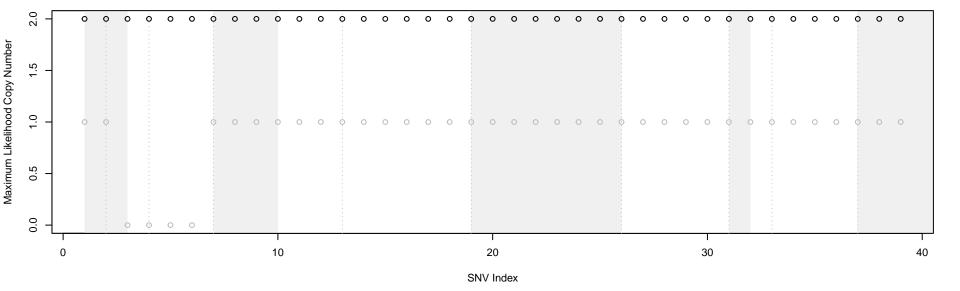
Purity: 0.32 Tumor ploidy: 1.866 2 Fraction Genome 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 log2 ratio

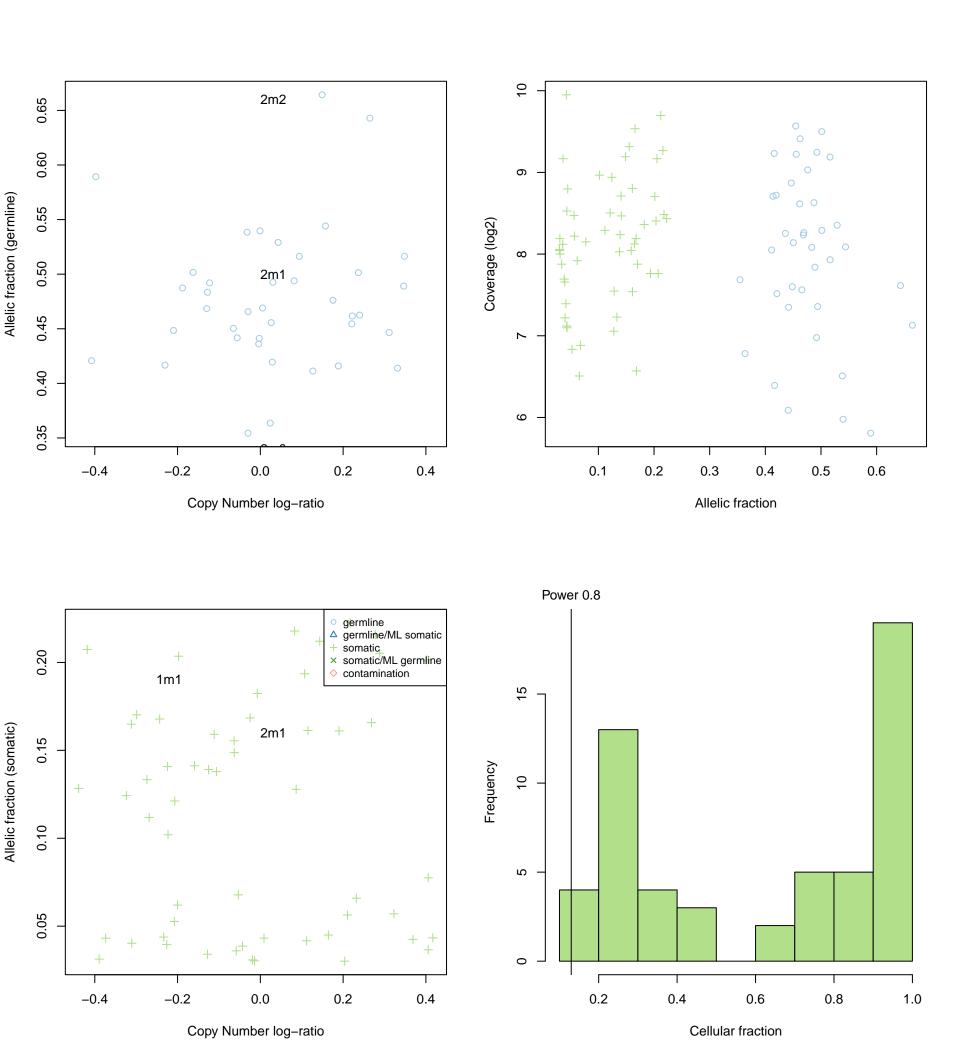
Purity: 0.32 Tumor ploidy: 1.866 SNV log-likelihood: 6.76 GoF: 87.3% Mean coverage: 315;324



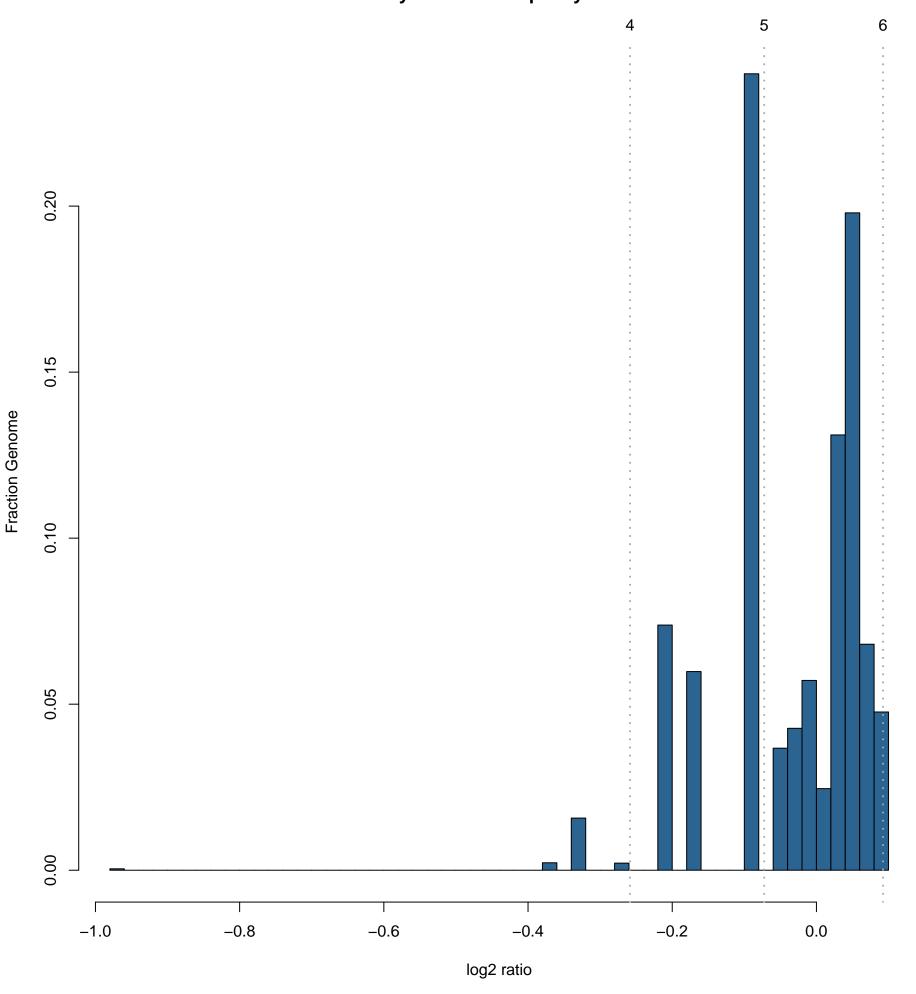
SCNA-fit log-likelihood: -624.33



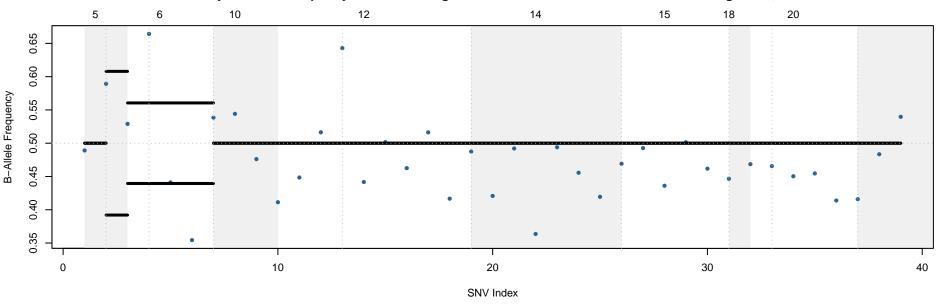




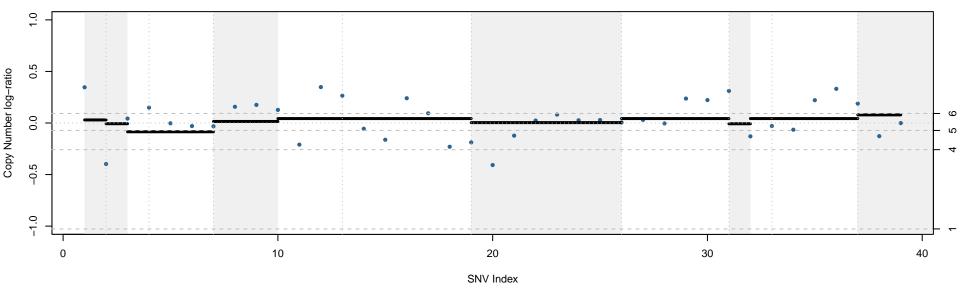
Purity: 0.38 Tumor ploidy: 5.426

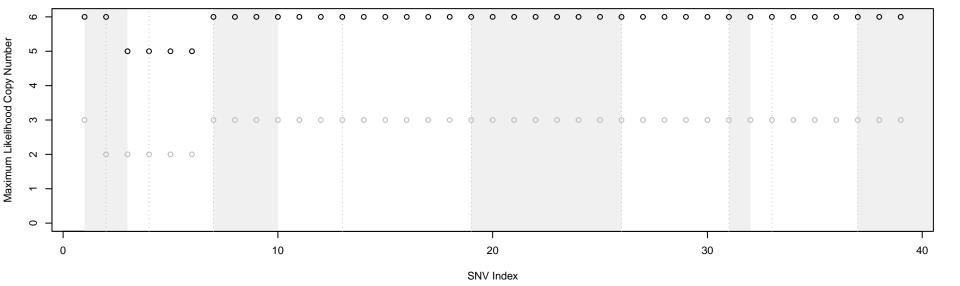


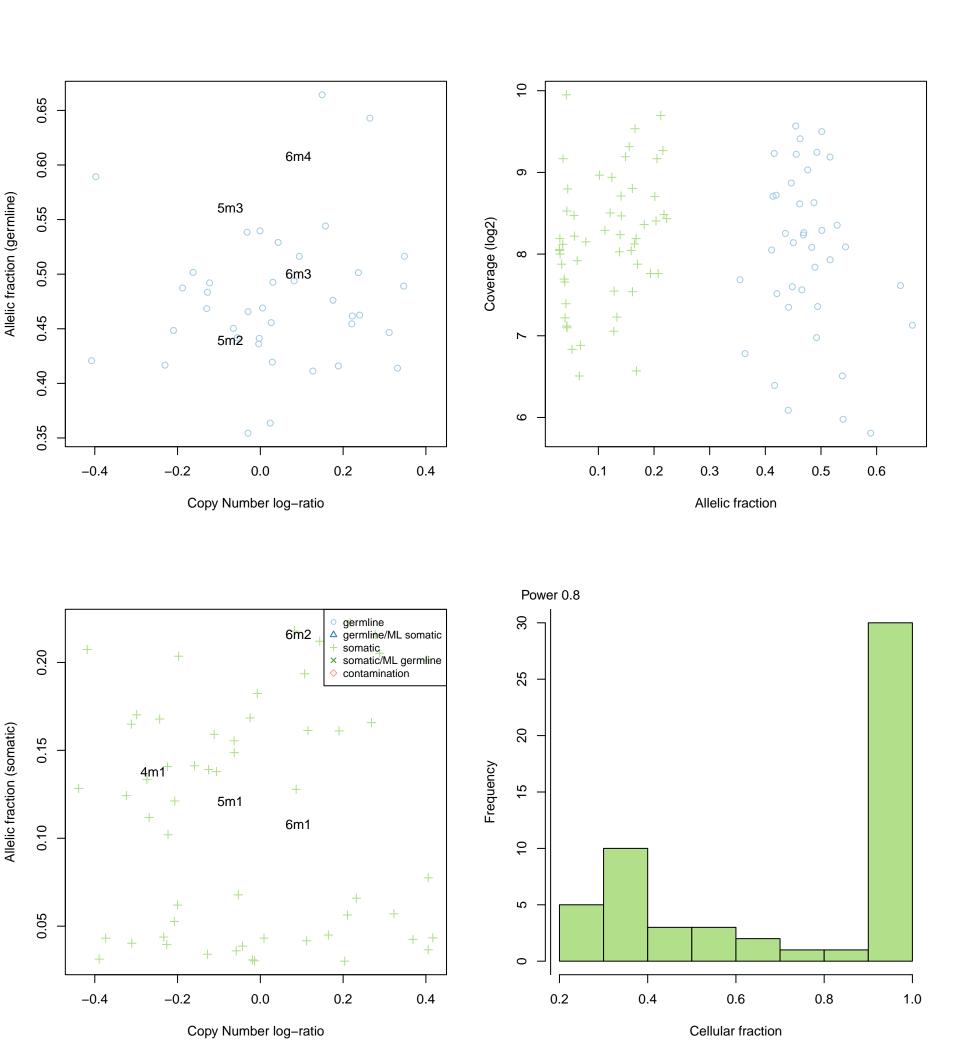
Purity: 0.38 Tumor ploidy: 5.426 SNV log-likelihood: -75.37 GoF: 93% Mean coverage: 315;324



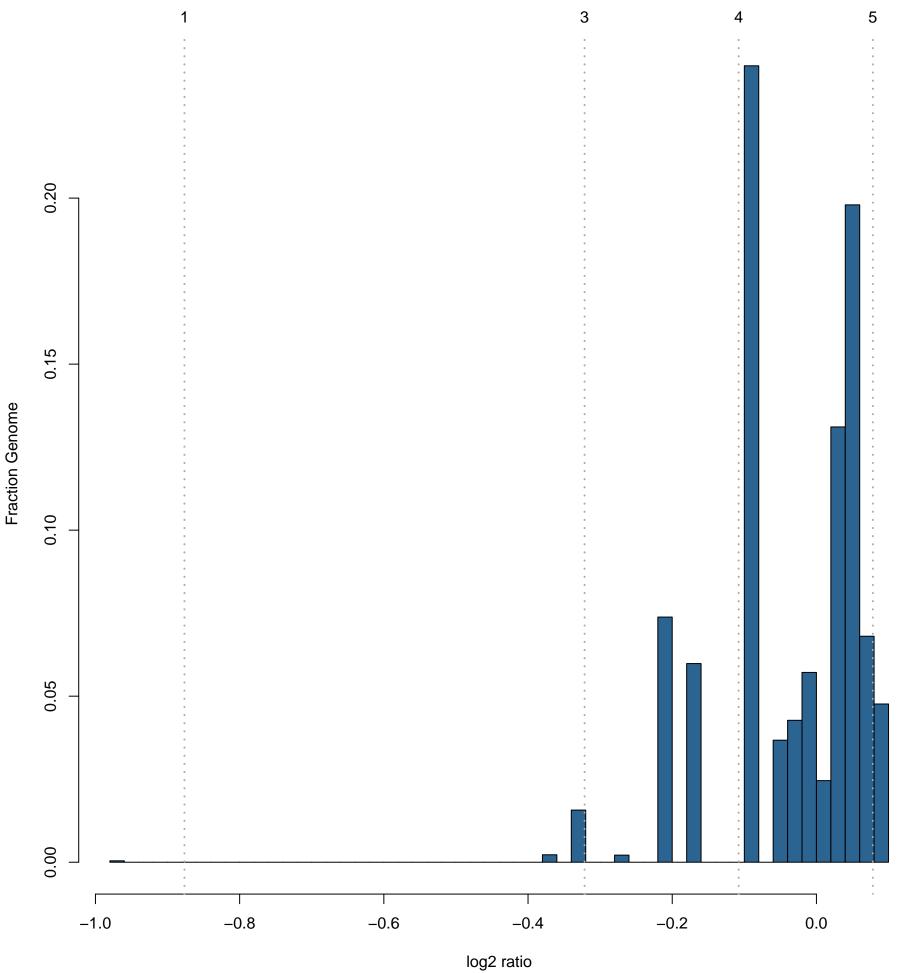
SCNA-fit log-likelihood: -449.44



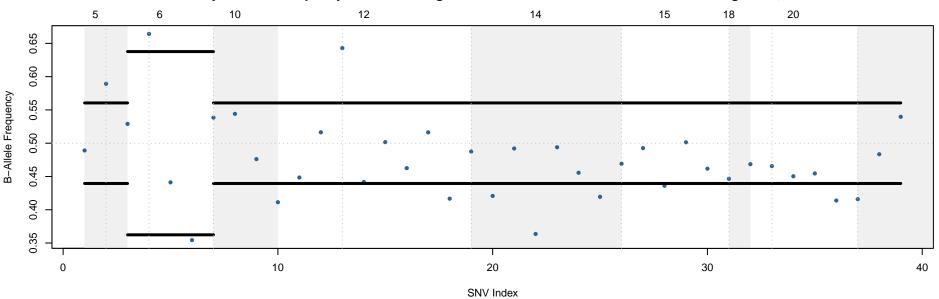




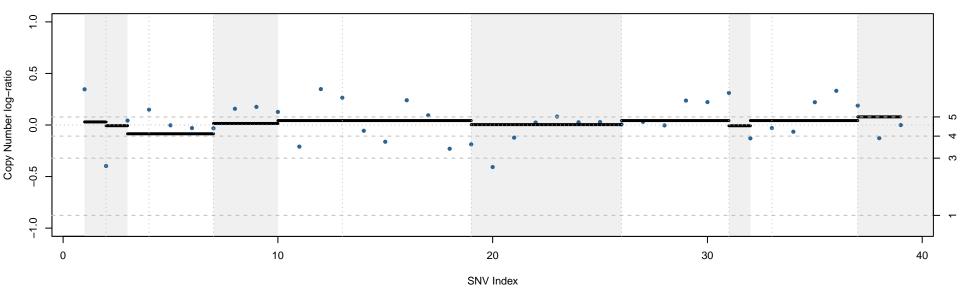
Purity: 0.38 Tumor ploidy: 4.564

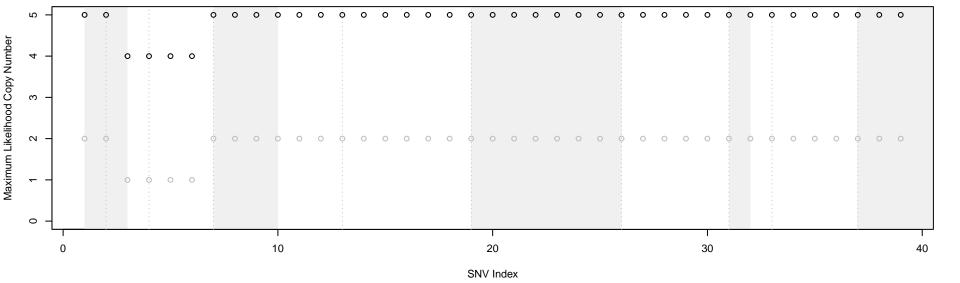


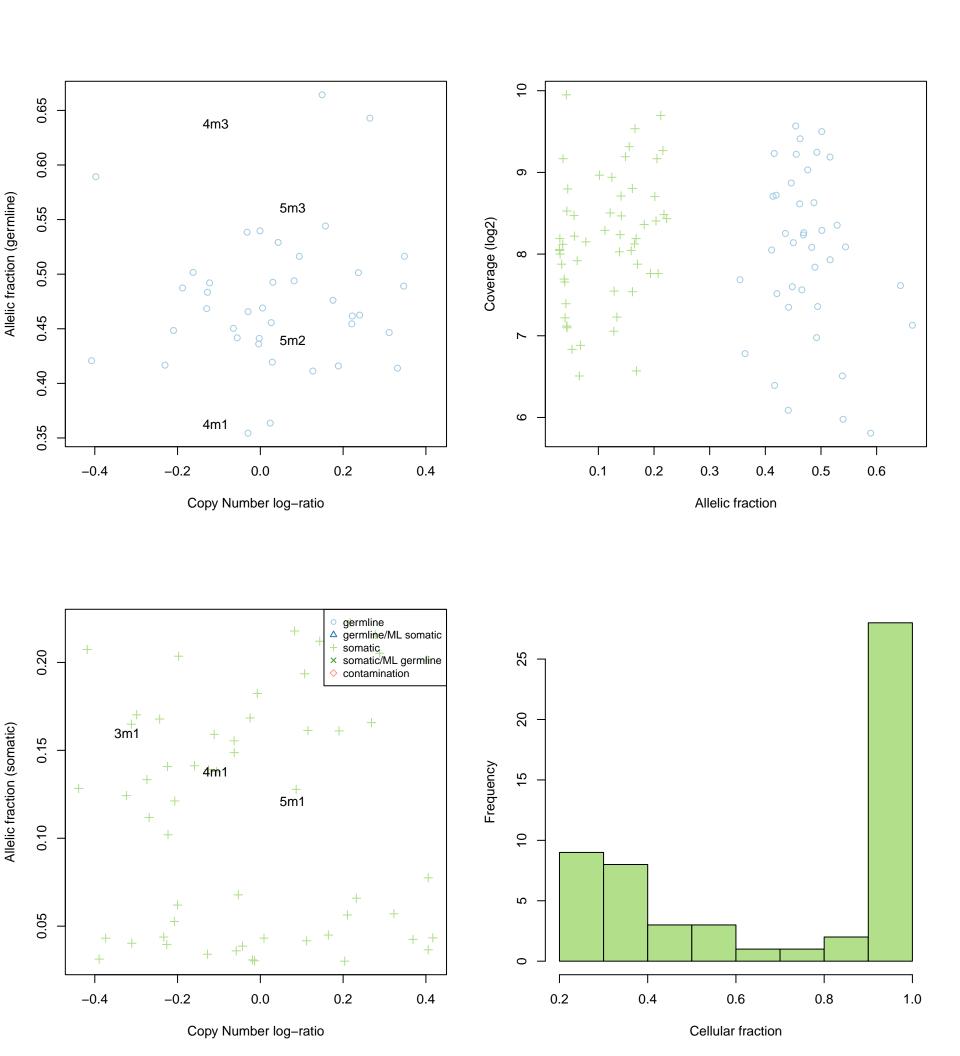
Purity: 0.38 Tumor ploidy: 4.564 SNV log-likelihood: -72.21 GoF: 92.9% Mean coverage: 315;324



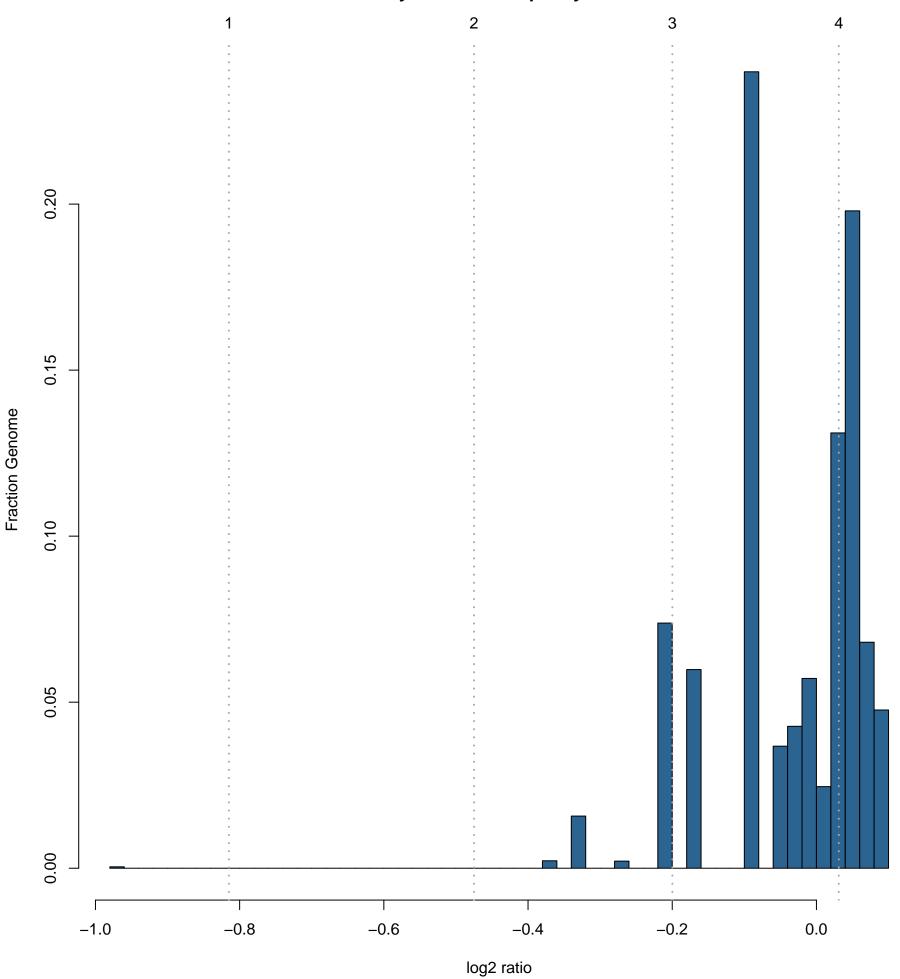
SCNA-fit log-likelihood: -473.5



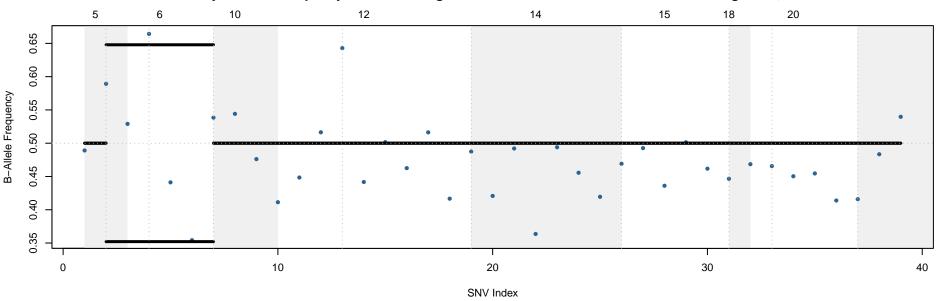




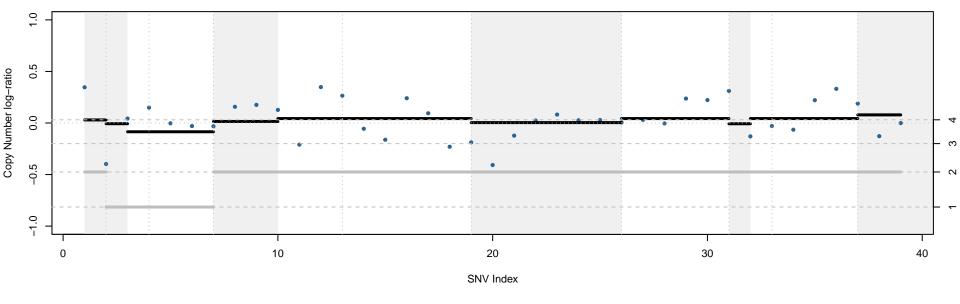
Purity: 0.42 Tumor ploidy: 3.856

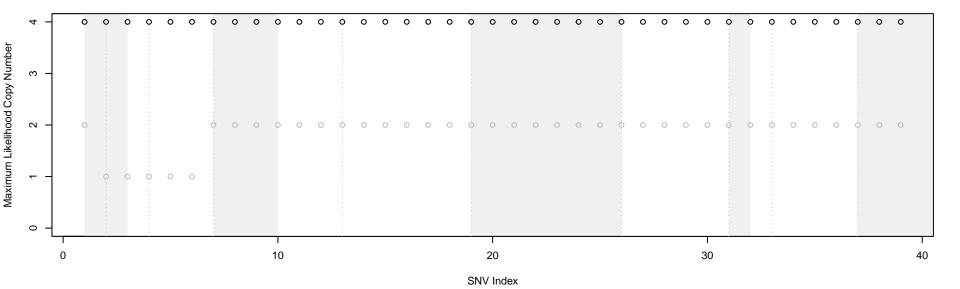


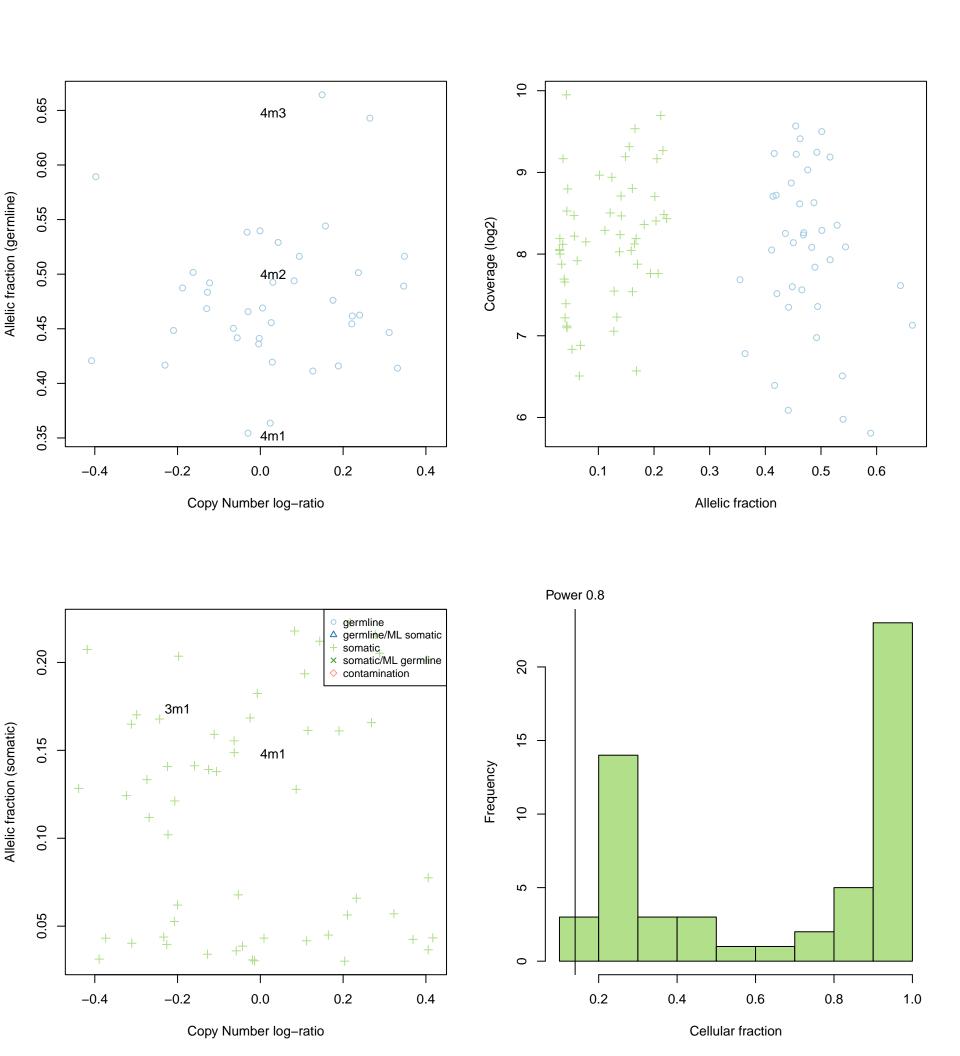
Purity: 0.42 Tumor ploidy: 3.856 SNV log-likelihood: -62.98 GoF: 88.8% Mean coverage: 315;324



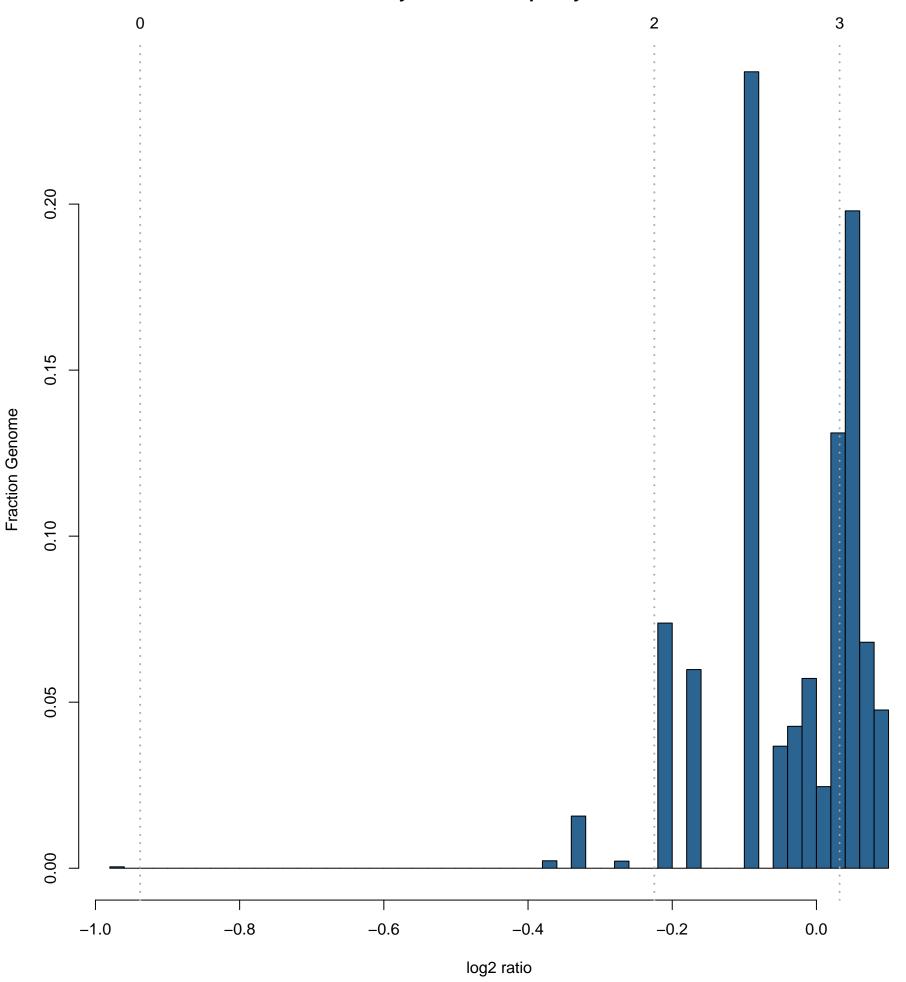
SCNA-fit log-likelihood: -602.37



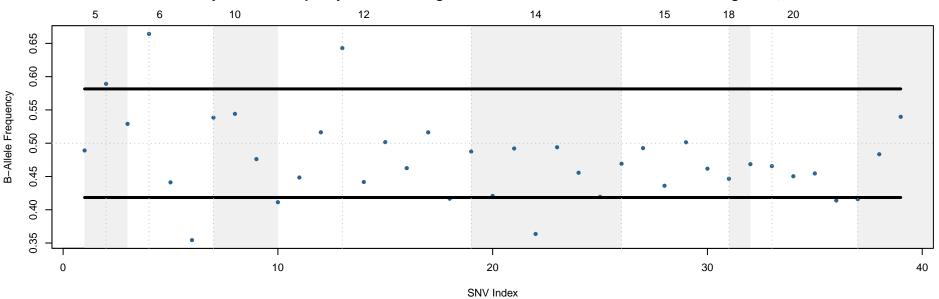




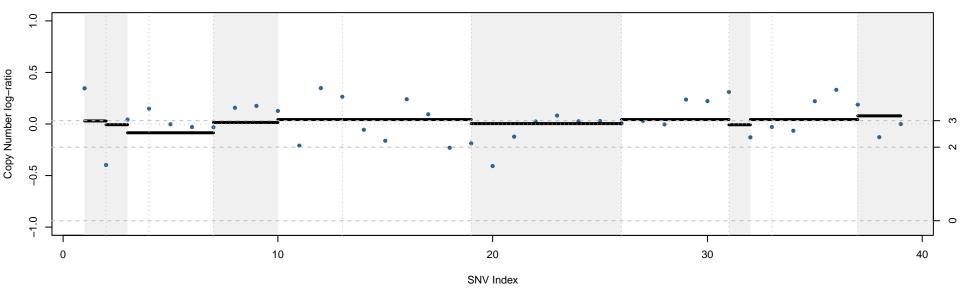
Purity: 0.39 Tumor ploidy: 2.865

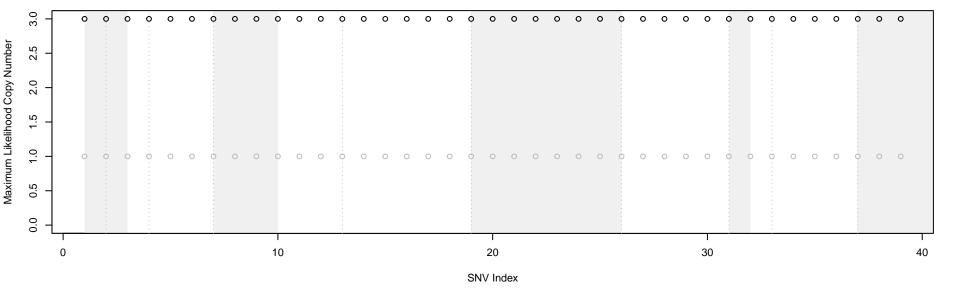


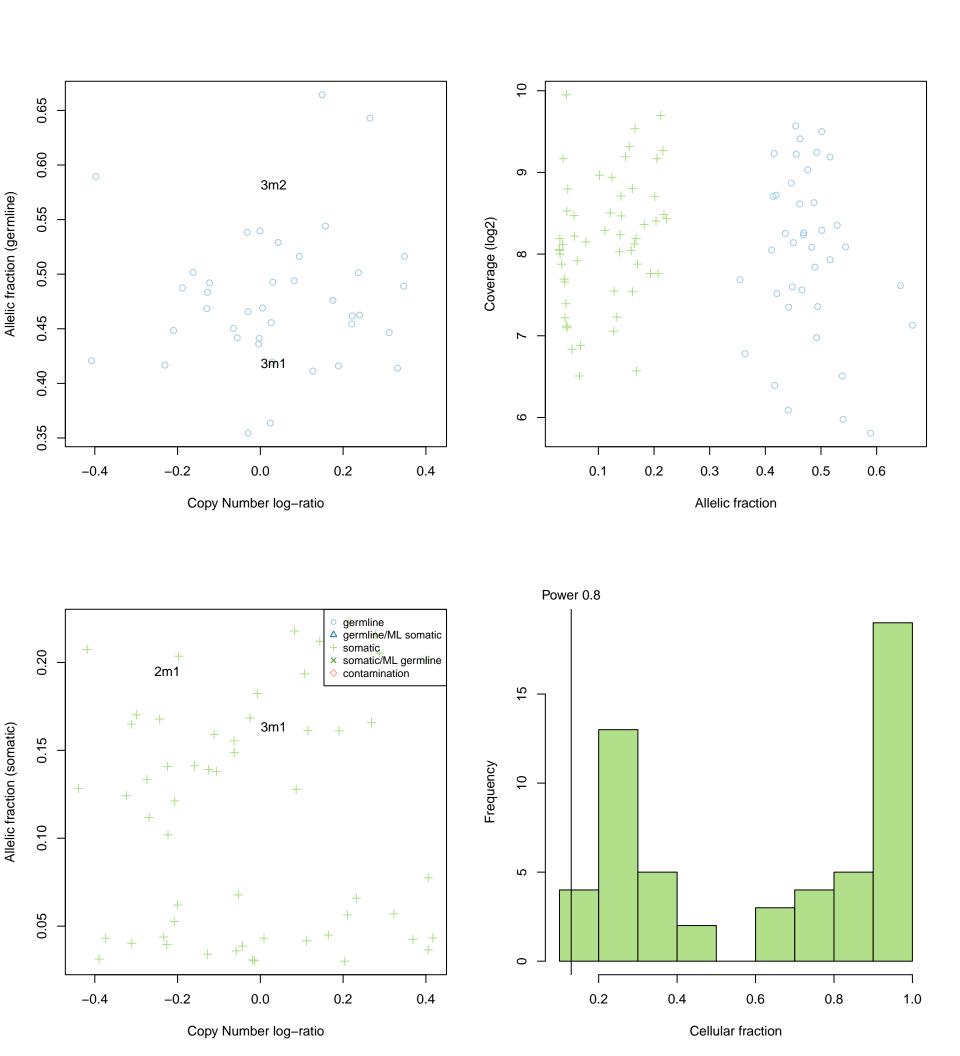
Purity: 0.39 Tumor ploidy: 2.865 SNV log-likelihood: -66.02 GoF: 86.6% Mean coverage: 315;324



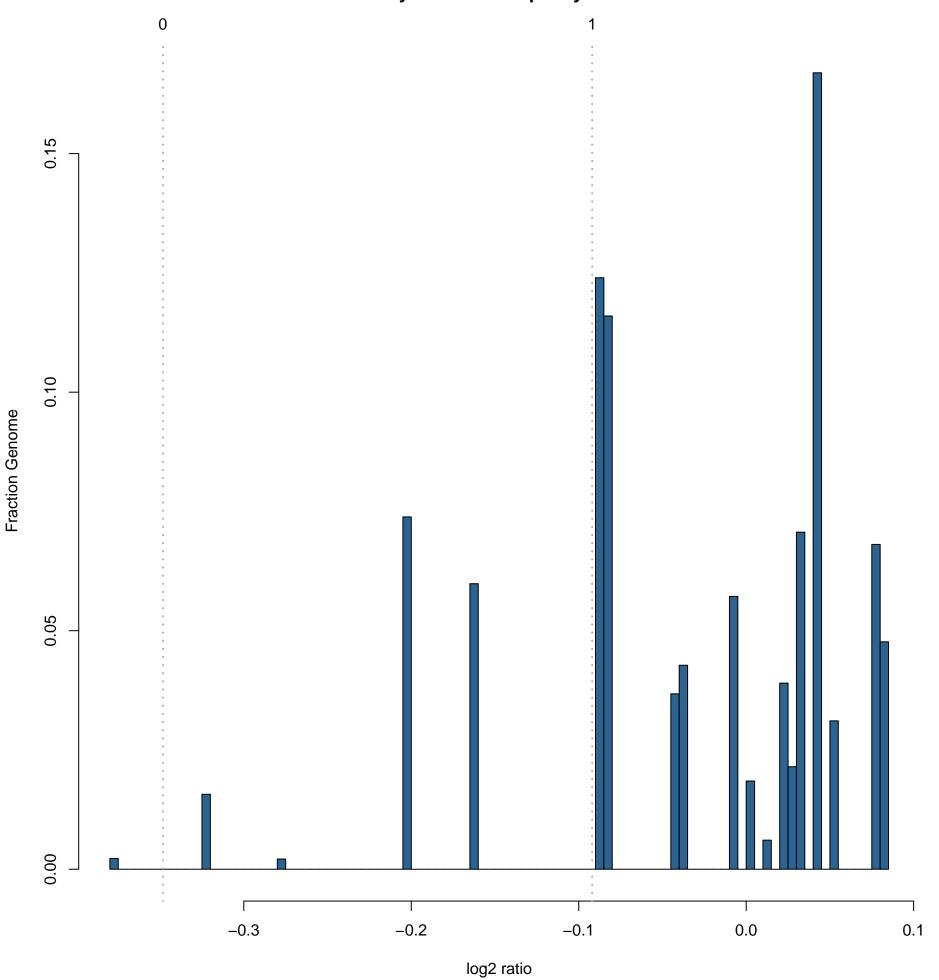
SCNA-fit log-likelihood: -620.18



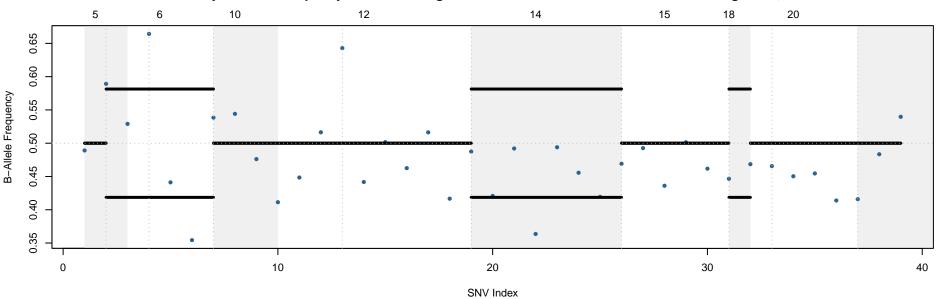




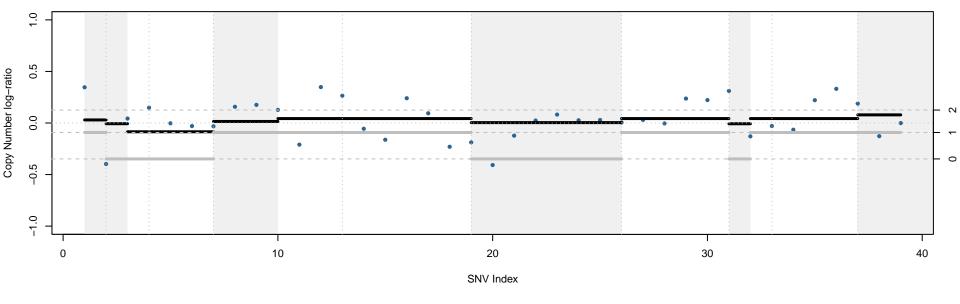
Purity: 0.28 Tumor ploidy: 1.405

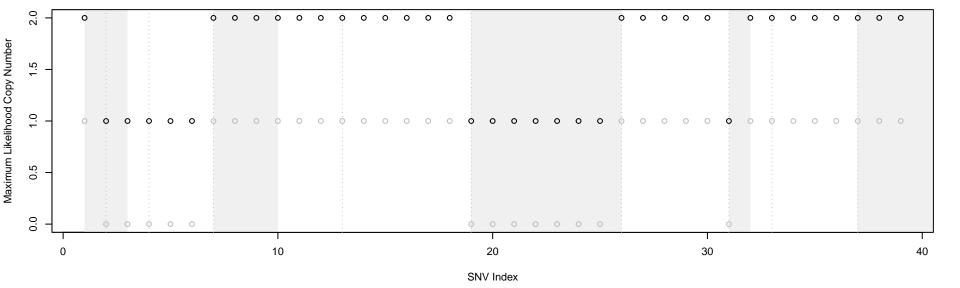


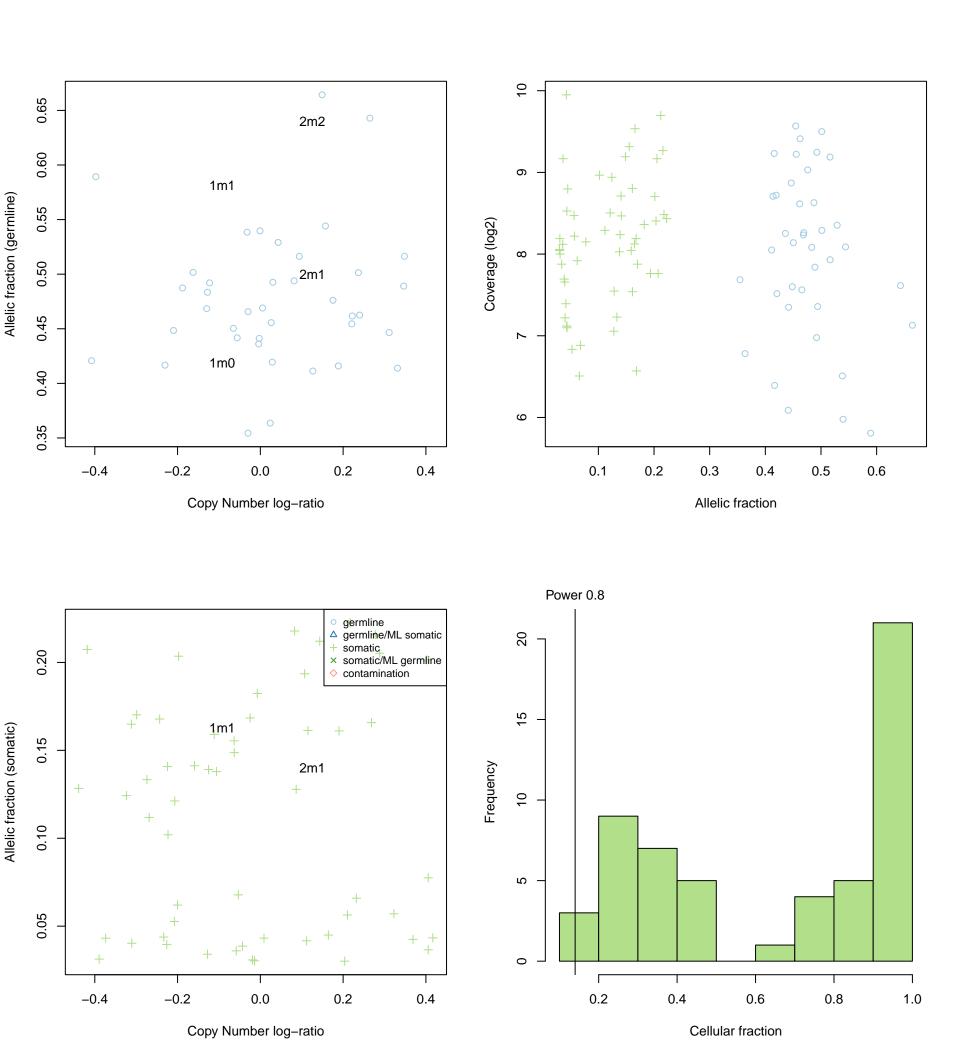
Purity: 0.28 Tumor ploidy: 1.405 SNV log-likelihood: -31.88 GoF: 89.5% Mean coverage: 315;324



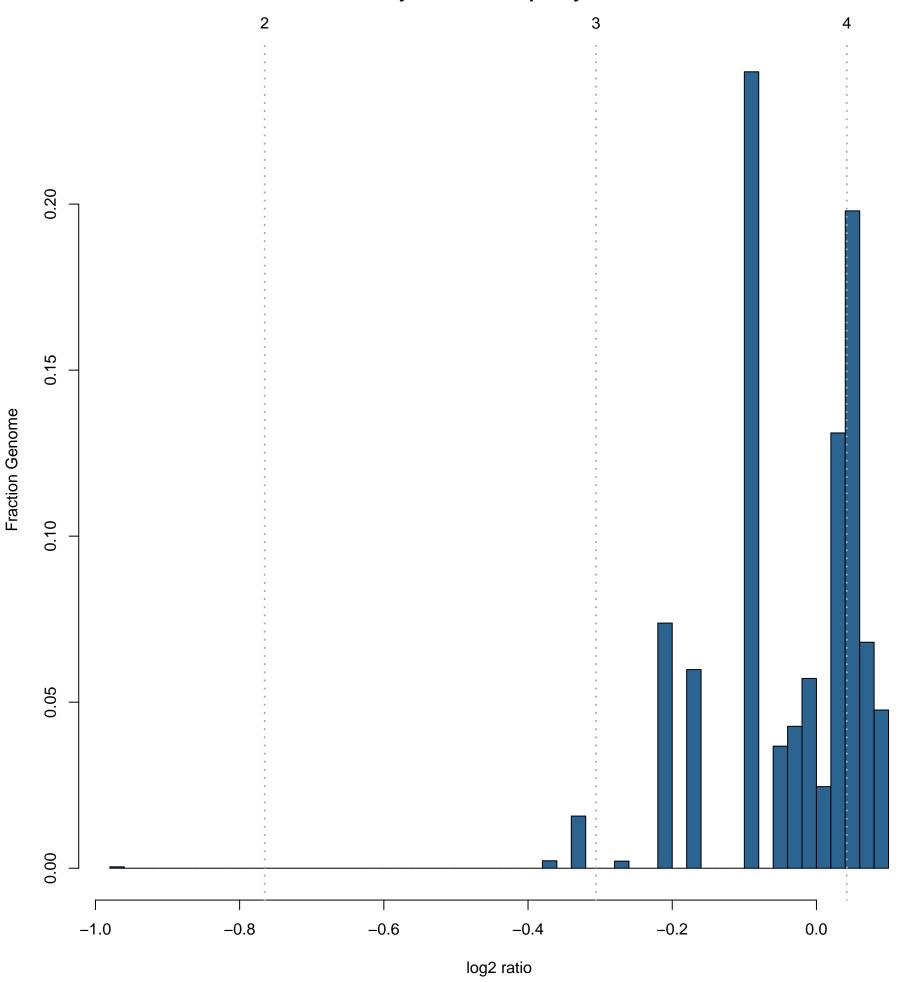
SCNA-fit log-likelihood: -718.29



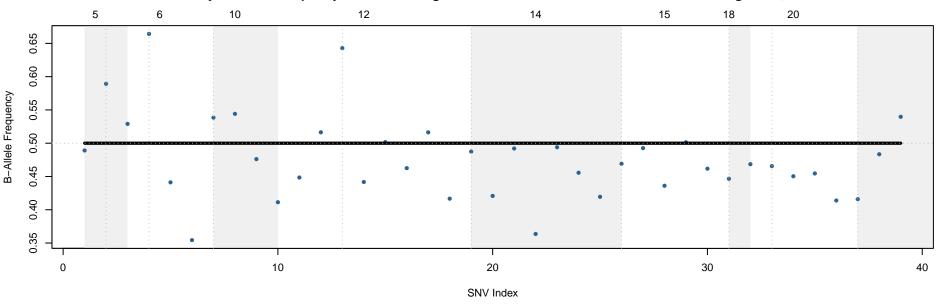




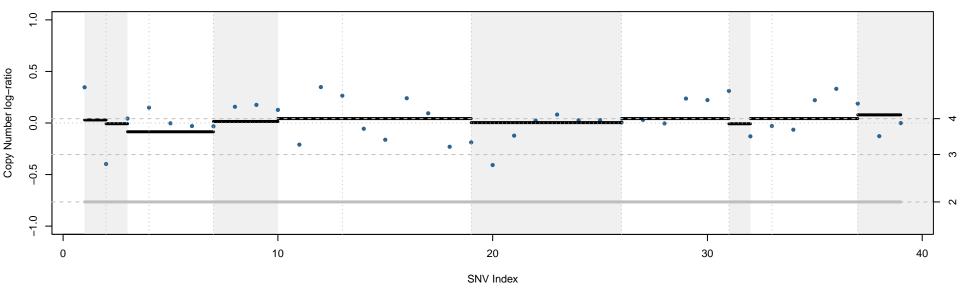
Purity: 0.75 Tumor ploidy: 3.866

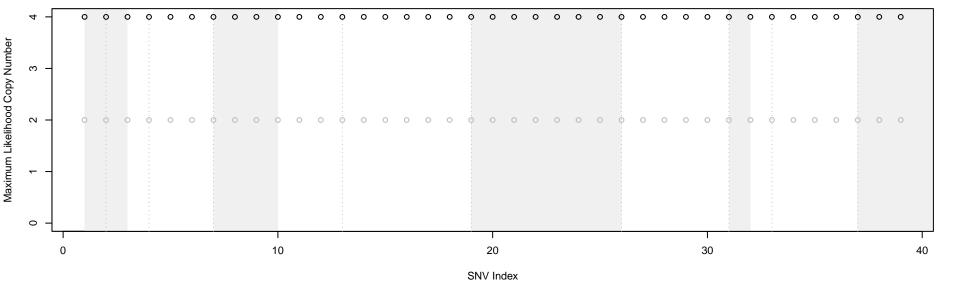


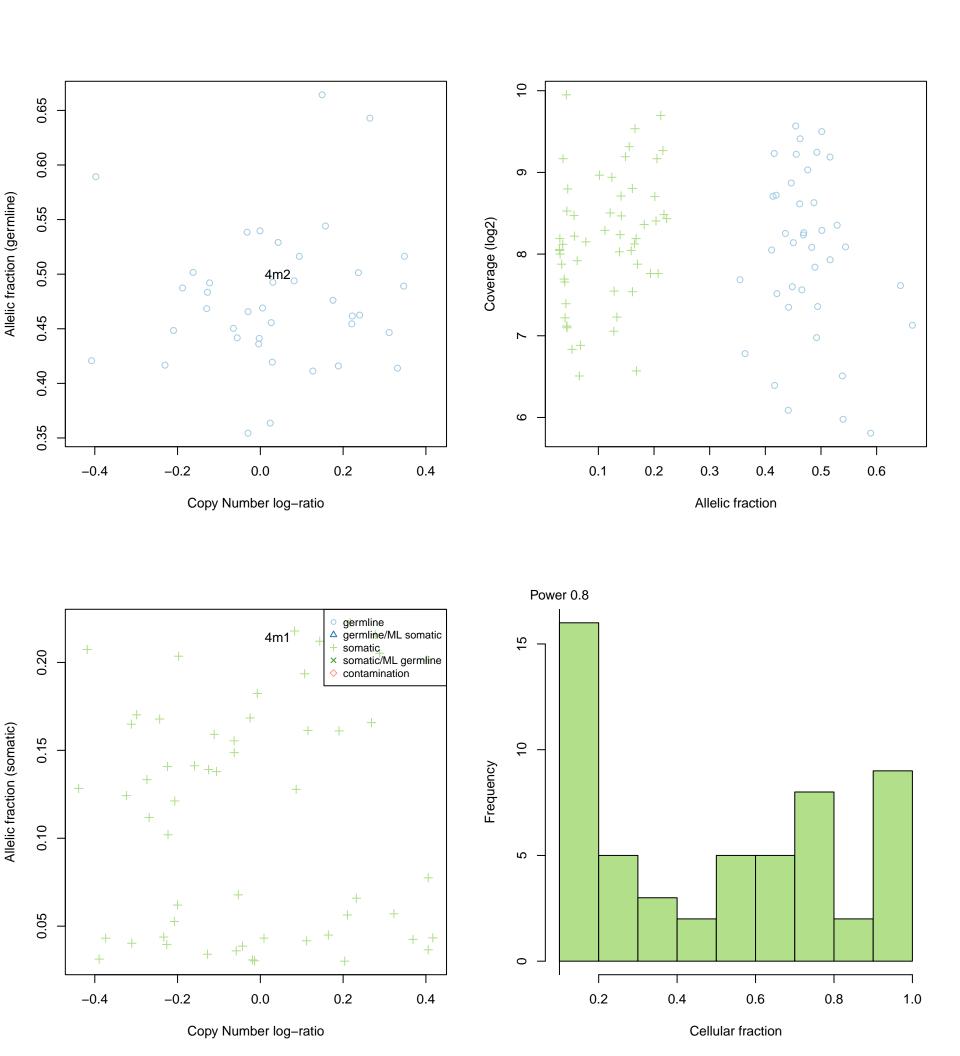
Purity: 0.75 Tumor ploidy: 3.866 SNV log-likelihood: -122.28 GoF: 73.2% Mean coverage: 315;324



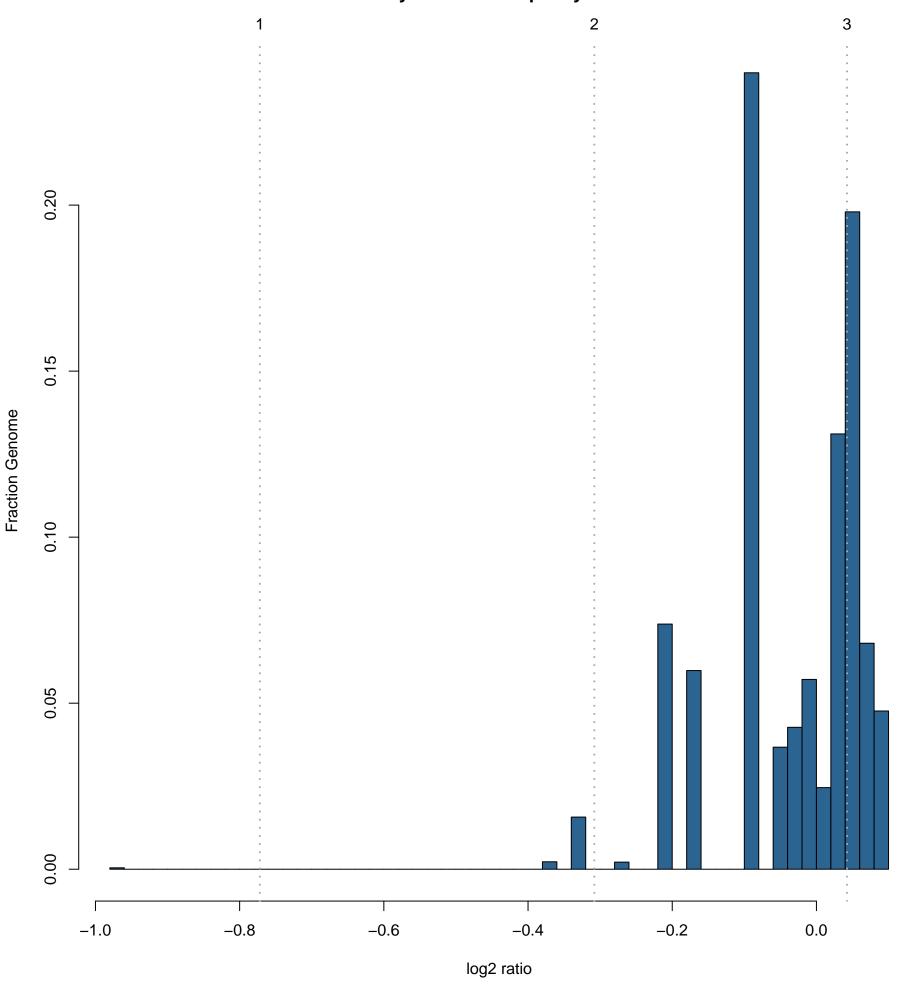
SCNA-fit log-likelihood: -772.59



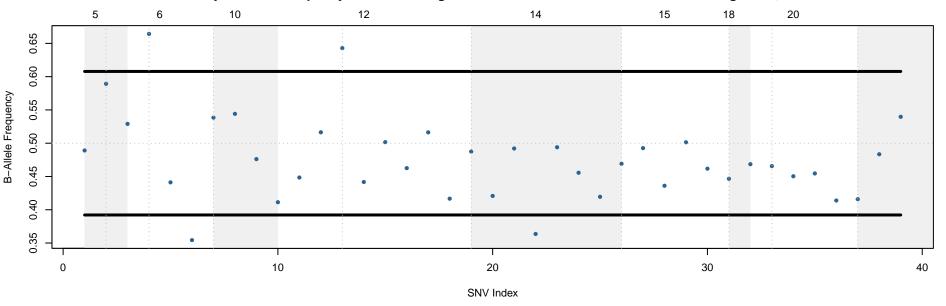




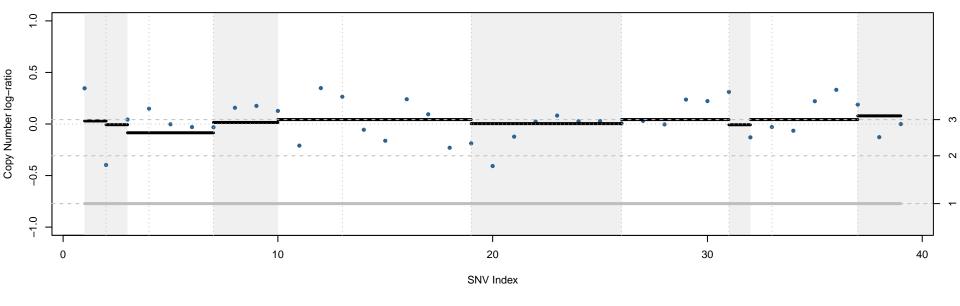
Purity: 0.55 Tumor ploidy: 2.866

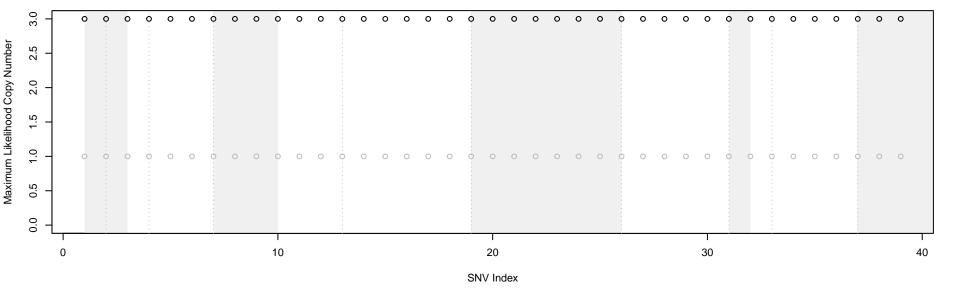


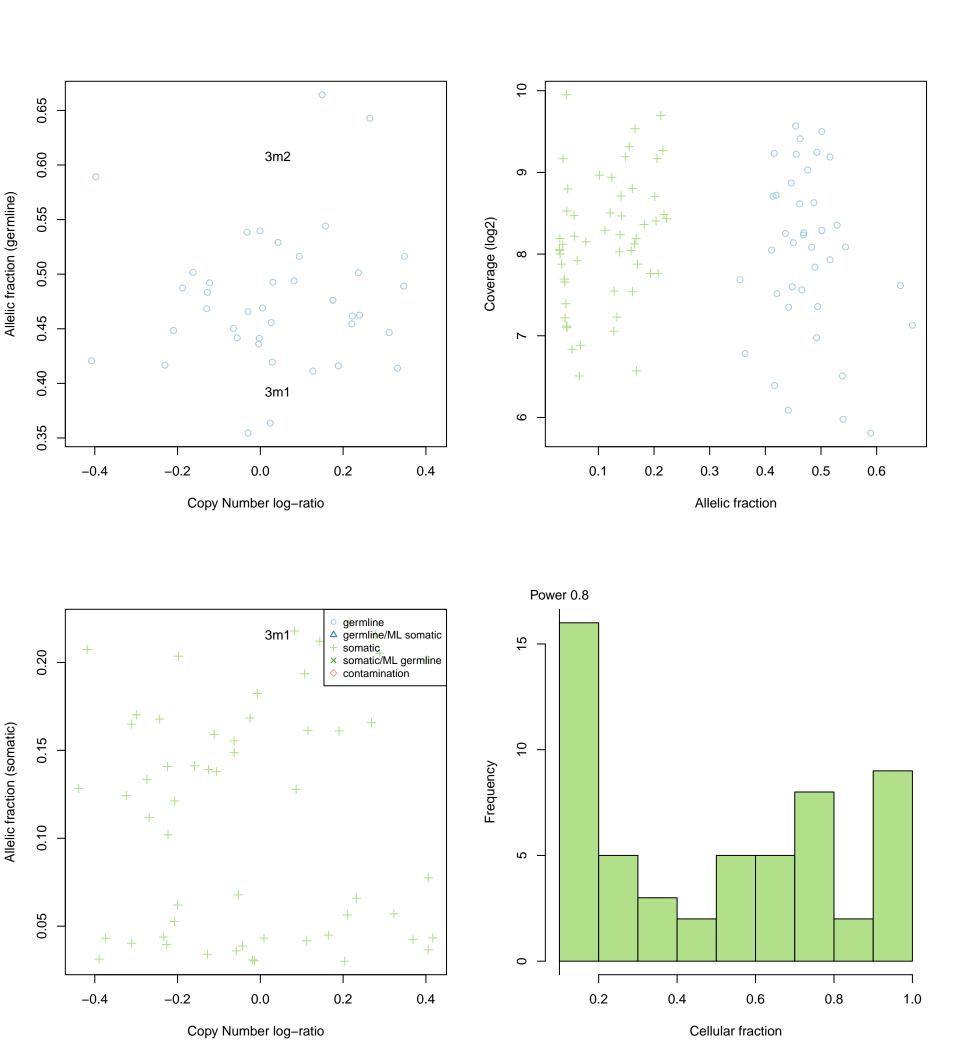
Purity: 0.55 Tumor ploidy: 2.866 SNV log-likelihood: -168.92 GoF: 71% Mean coverage: 315;324



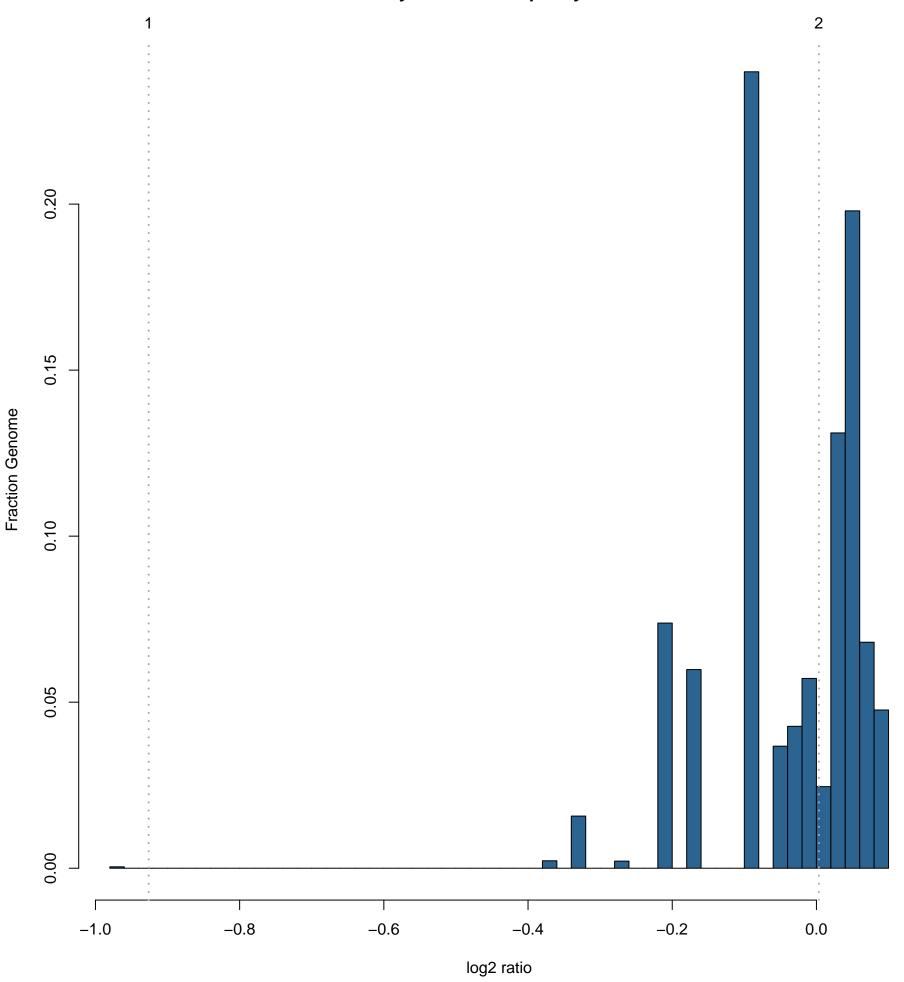
SCNA-fit log-likelihood: -783.45

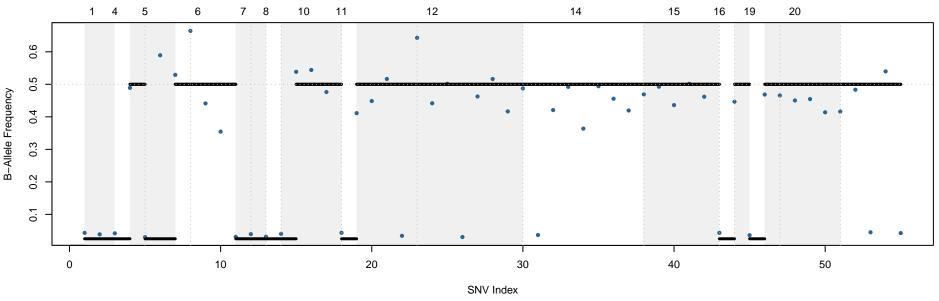




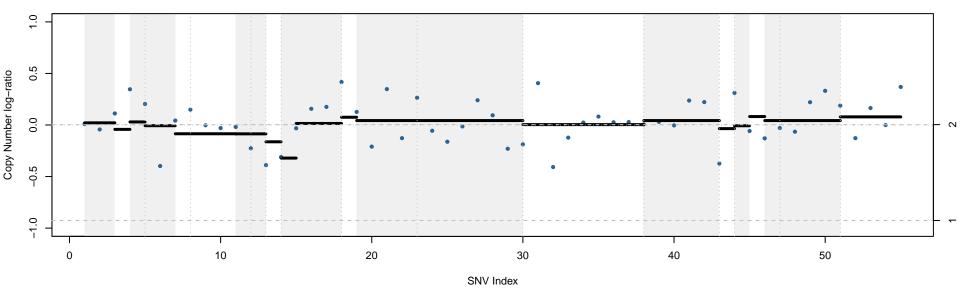


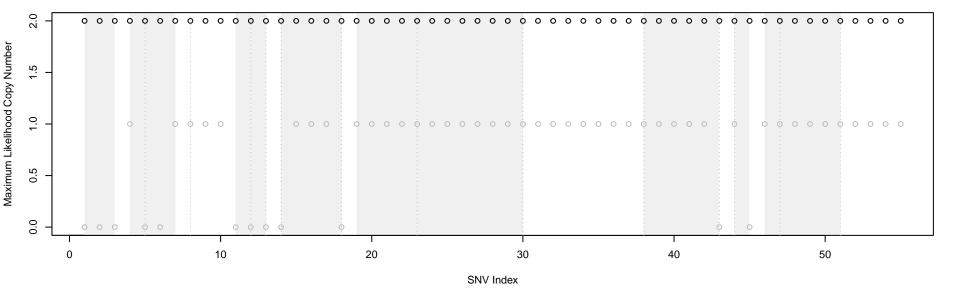
Purity: 0.95 Tumor ploidy: 1.995

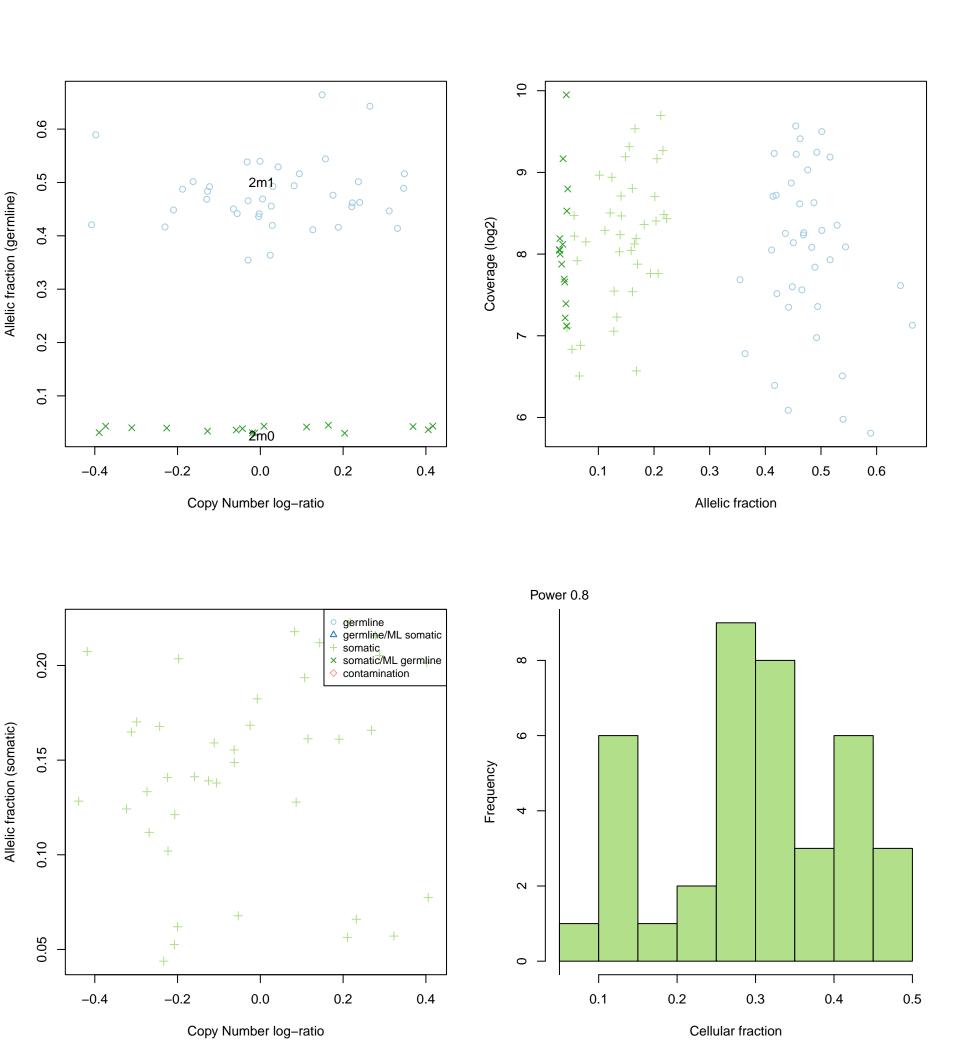




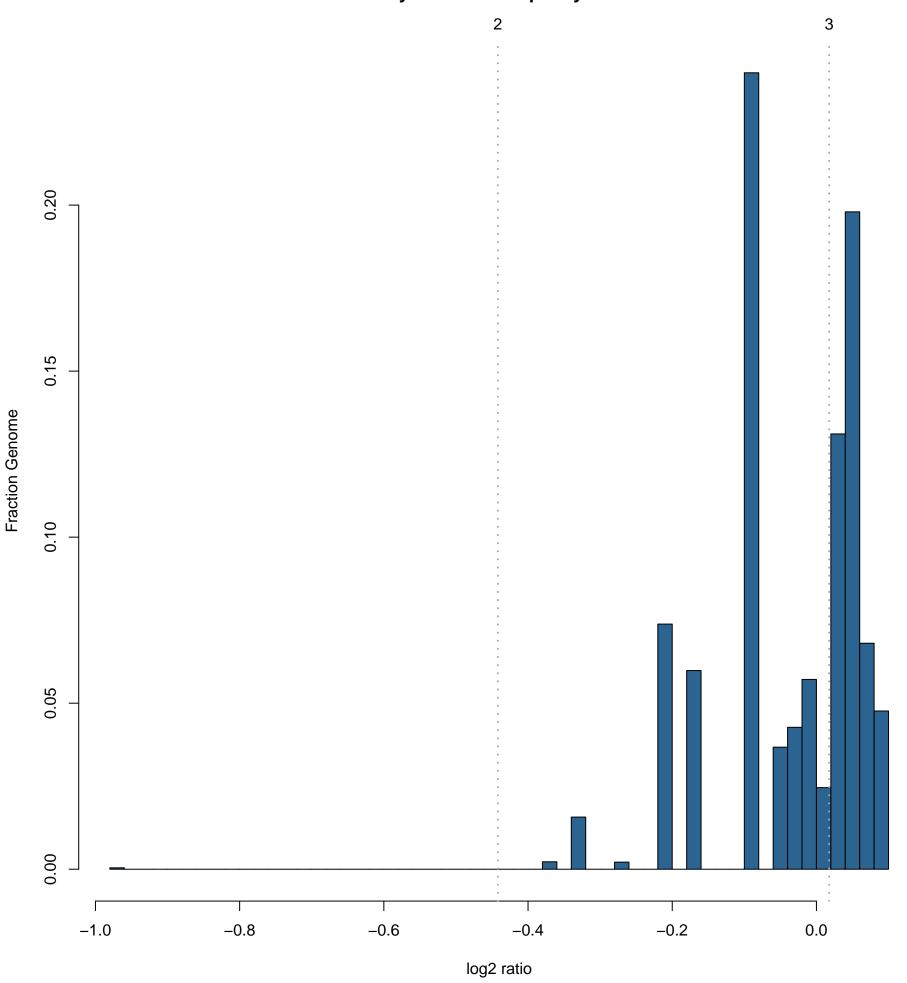
SCNA-fit log-likelihood: -934.13



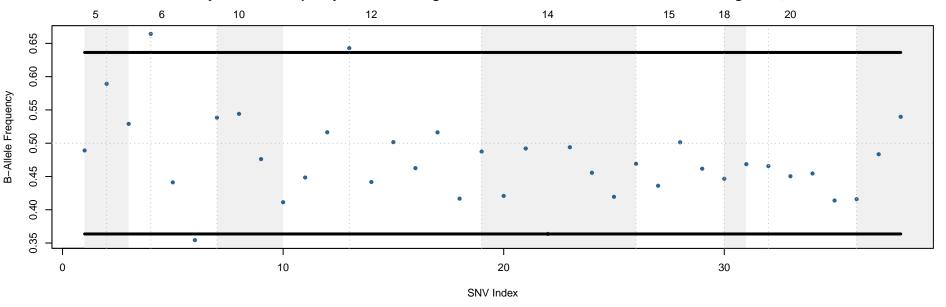




Purity: 0.75 Tumor ploidy: 2.955



Purity: 0.75 Tumor ploidy: 2.955 SNV log-likelihood: -357.18 GoF: 46.3% Mean coverage: 315;324



SCNA-fit log-likelihood: -887.06

