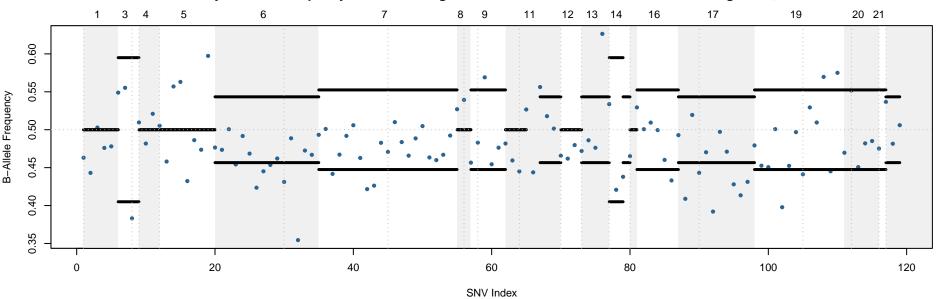
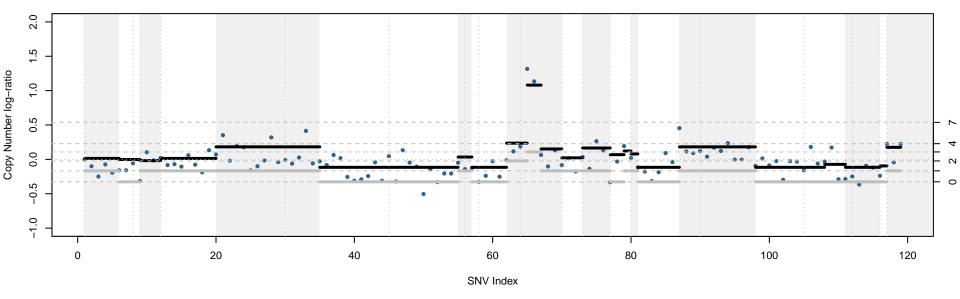
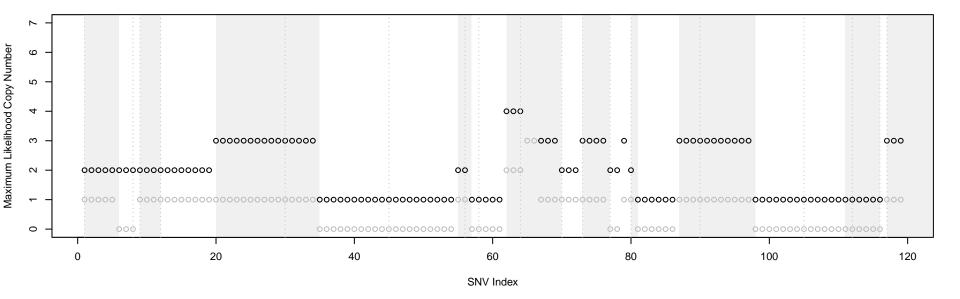
Purity: 0.19 Tumor ploidy: 2.166 0 2 Fraction Genome 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio

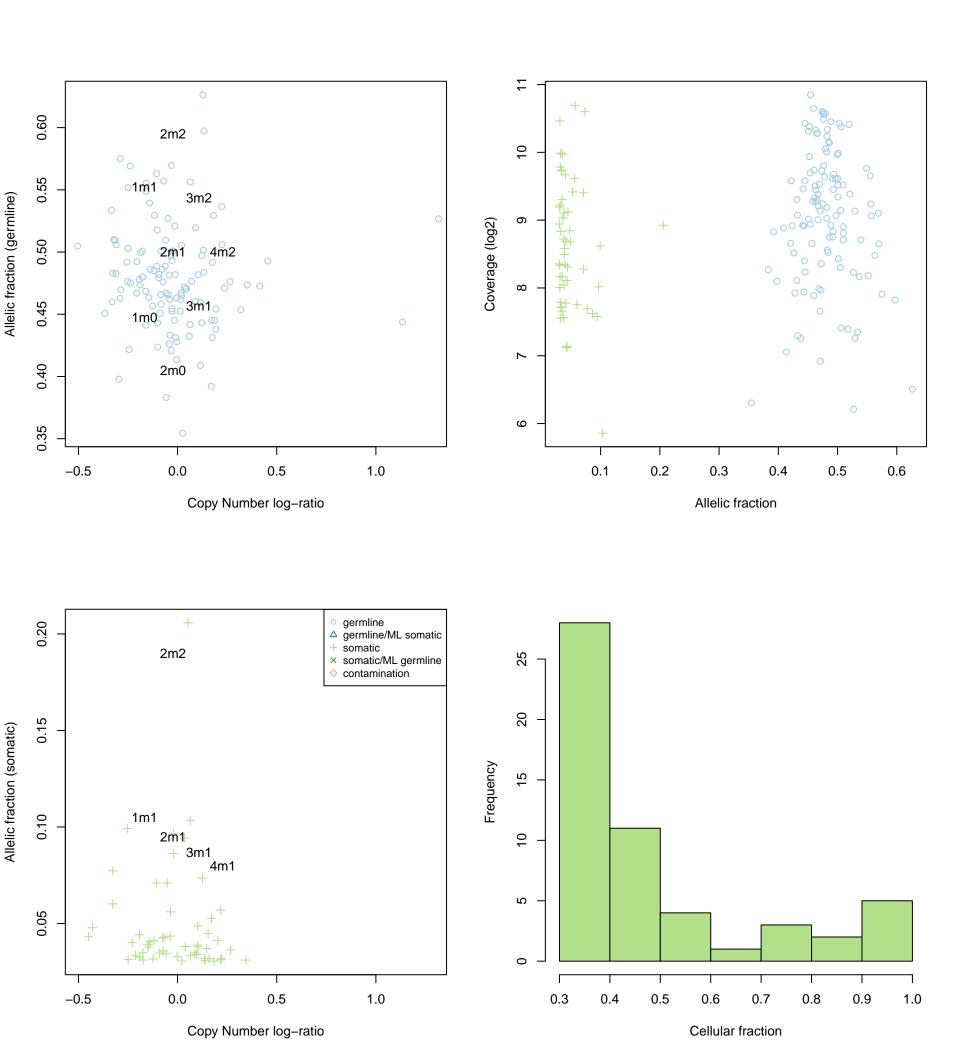




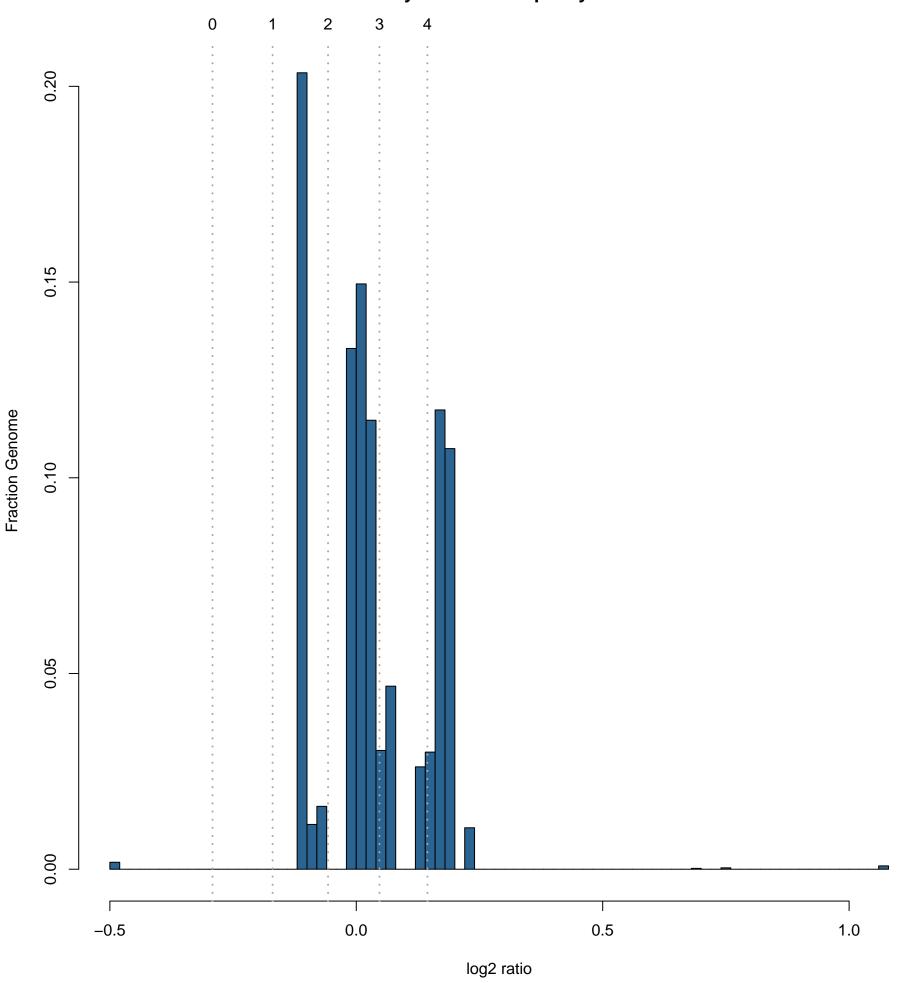
SCNA-fit log-likelihood: -5361.38



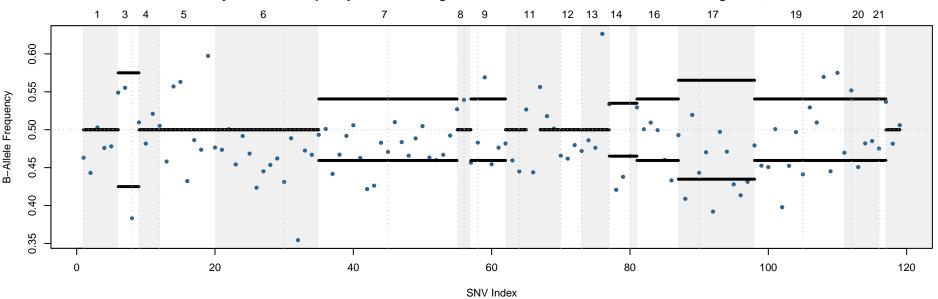




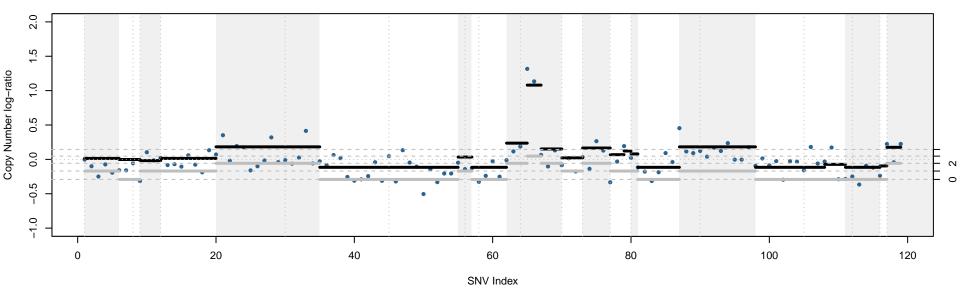
Purity: 0.15 Tumor ploidy: 2.54

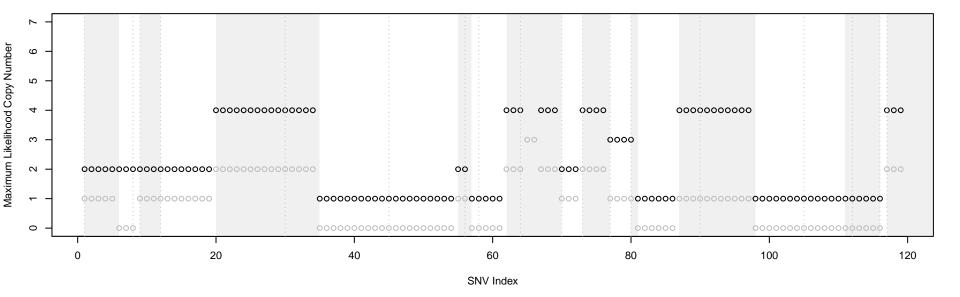


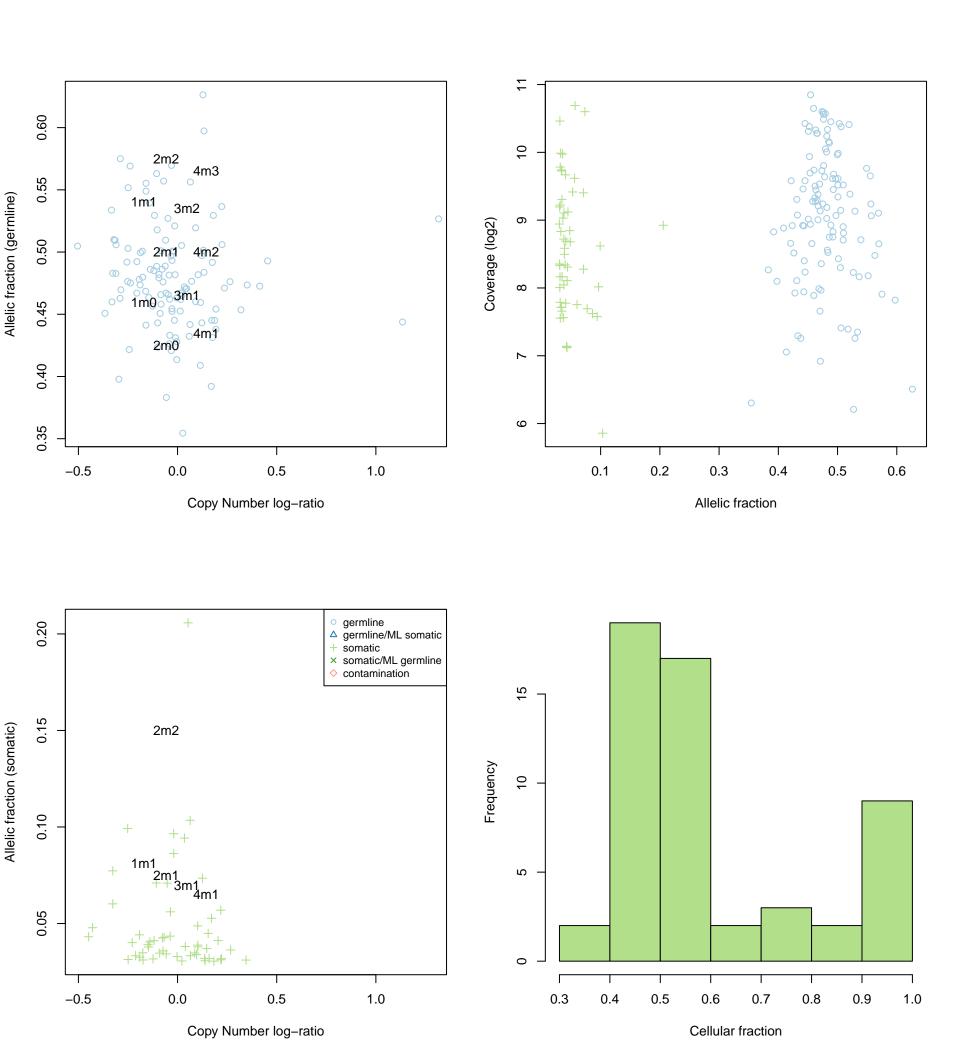
Purity: 0.15 Tumor ploidy: 2.54 SNV log-likelihood: 76.6 GoF: 96.1% Mean coverage: 597;603



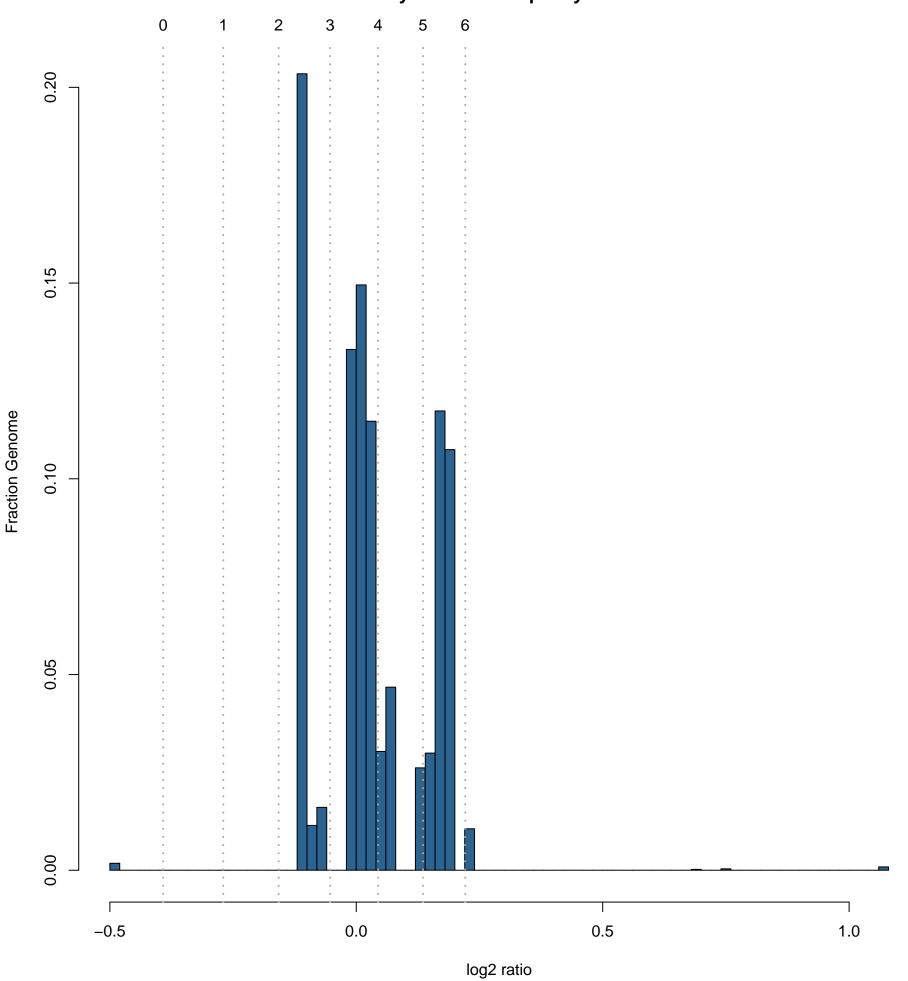
SCNA-fit log-likelihood: -5381.28







Purity: 0.15 Tumor ploidy: 3.537

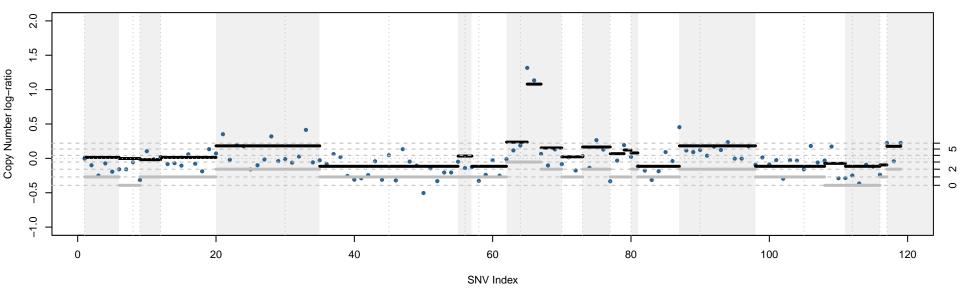


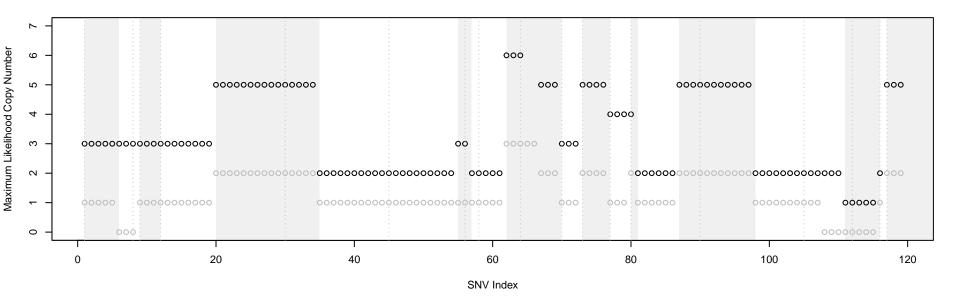
Purity: 0.15 Tumor ploidy: 3.537 SNV log-likelihood: 15.35 GoF: 96.7% Mean coverage: 597;603

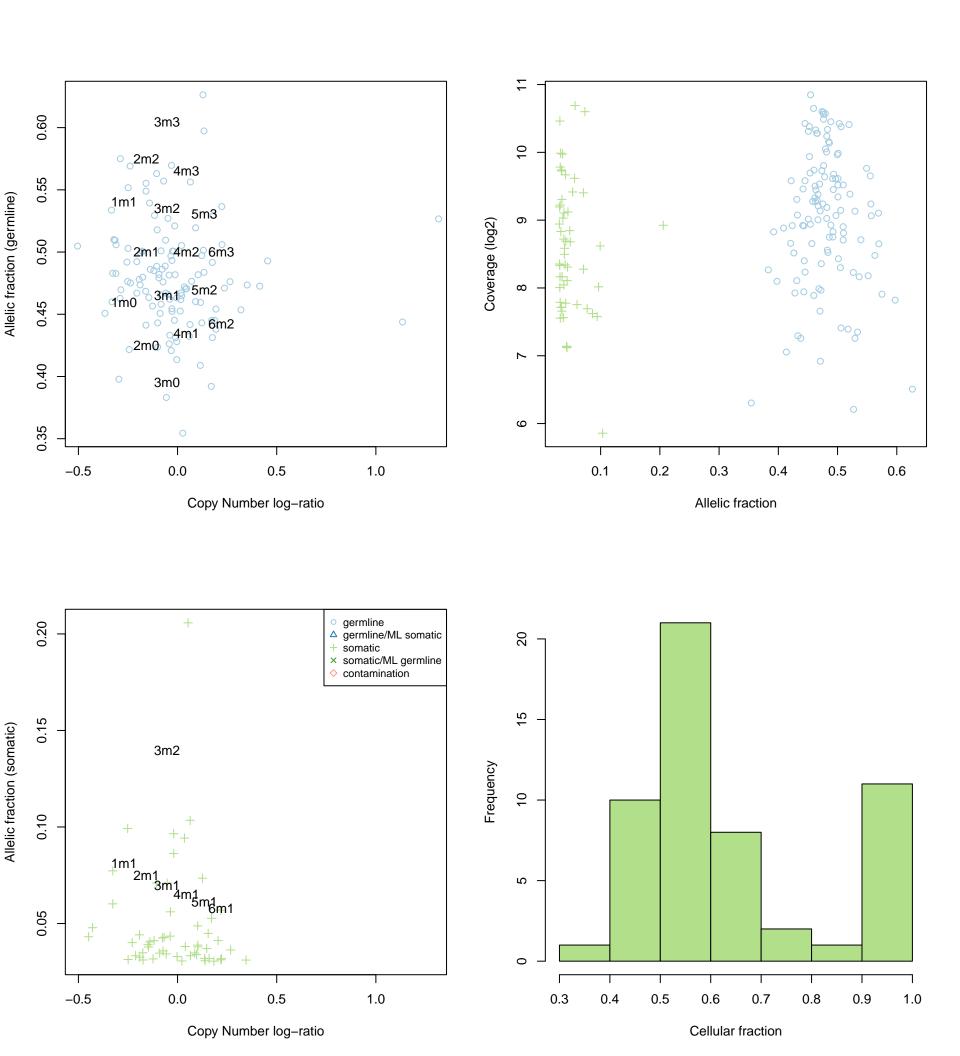
1 3 4 5 6 7 8 9 11 12 13 14 16 17 19 20 21

SCNA-fit log-likelihood: -5352.73

SNV Index







Purity: 0.32 Tumor ploidy: 2.418 0 2 3 6 Fraction Genome 0.05 0.00 0.0 -1.0 -0.5 0.5 1.0

log2 ratio

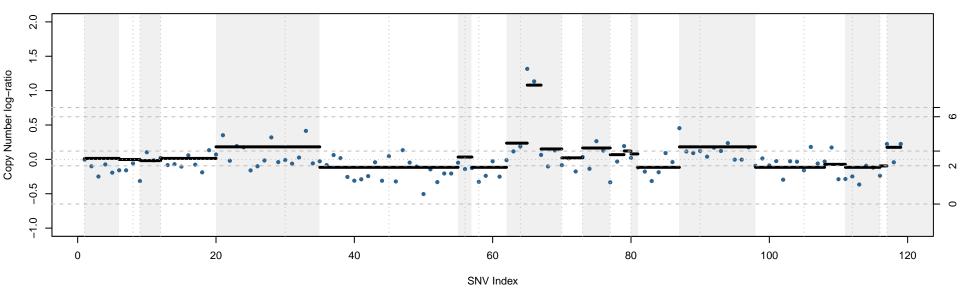
Purity: 0.32 Tumor ploidy: 2.418 SNV log-likelihood: 41.5 GoF: 87.9% Mean coverage: 597;603

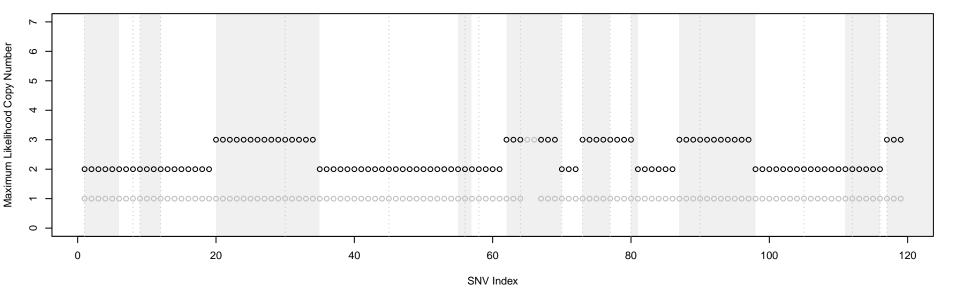
1 3 4 5 6 7 8 9 11 12 13 14 16 17 19 20 21

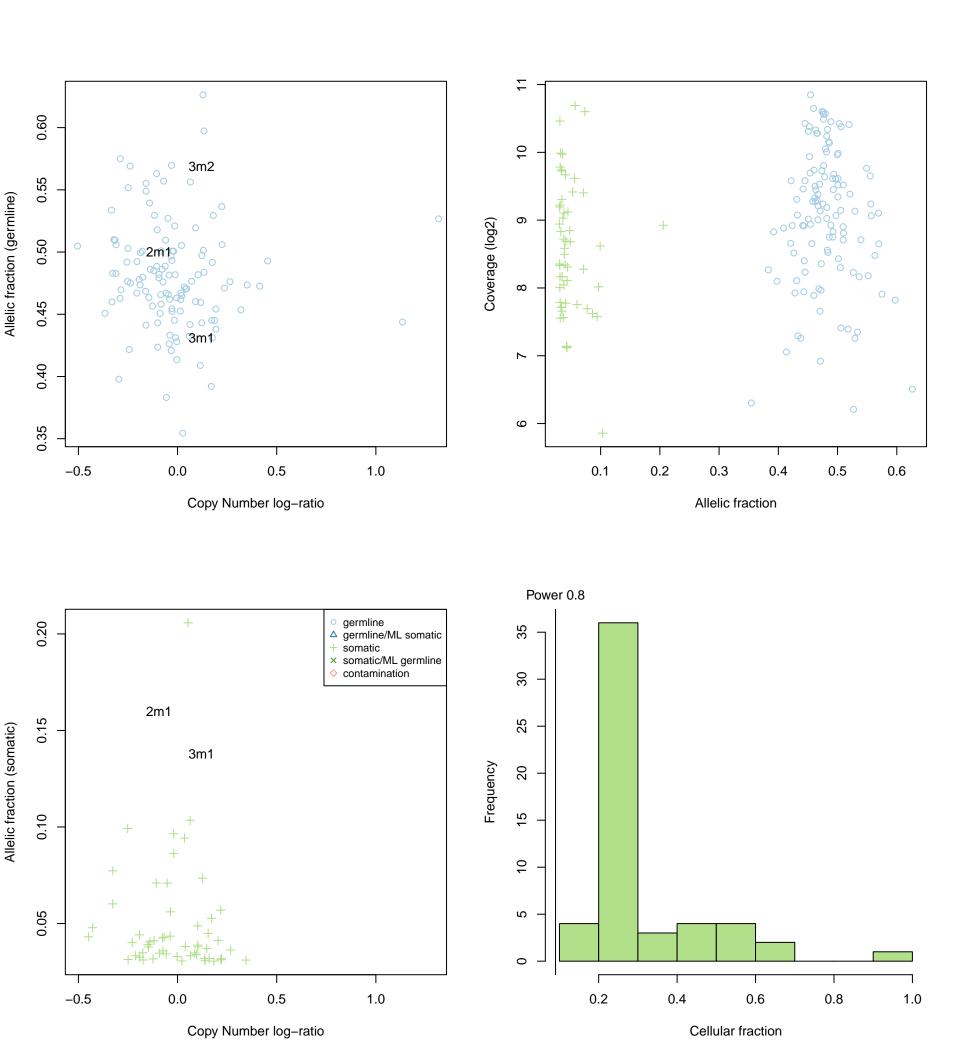
0.35

SCNA-fit log-likelihood: -5520.92

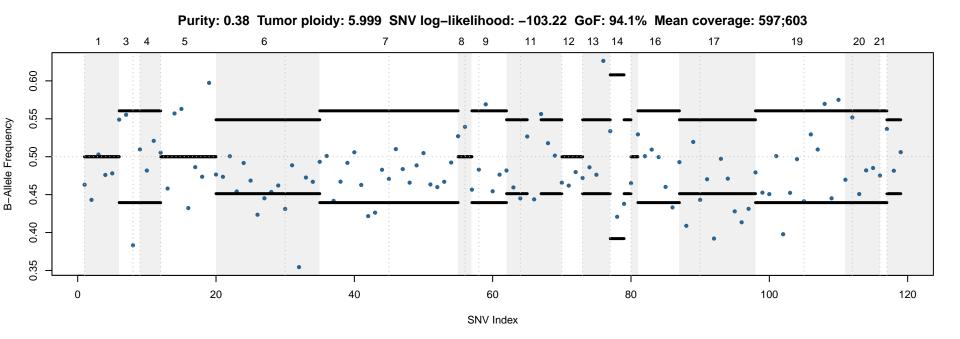
SNV Index



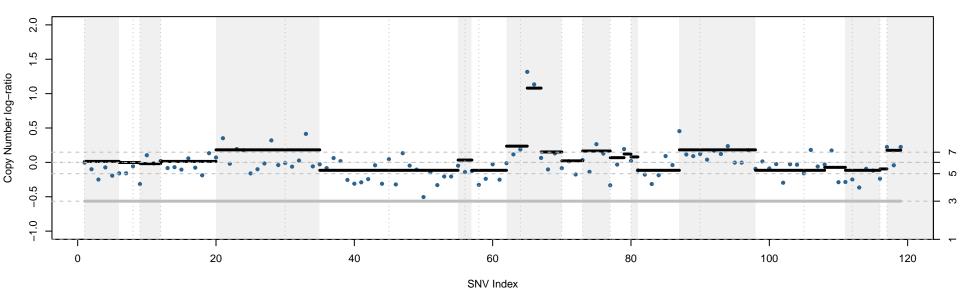


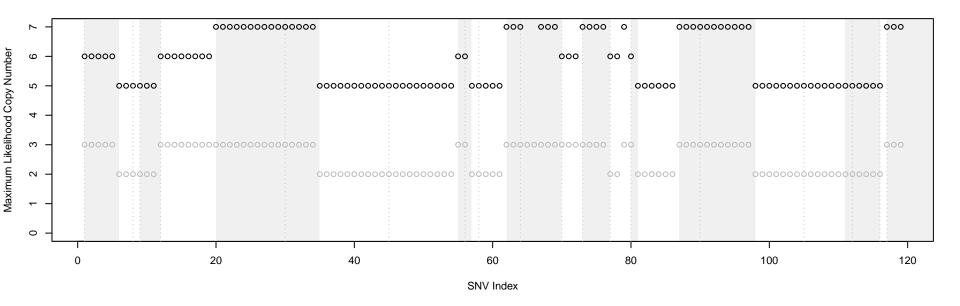


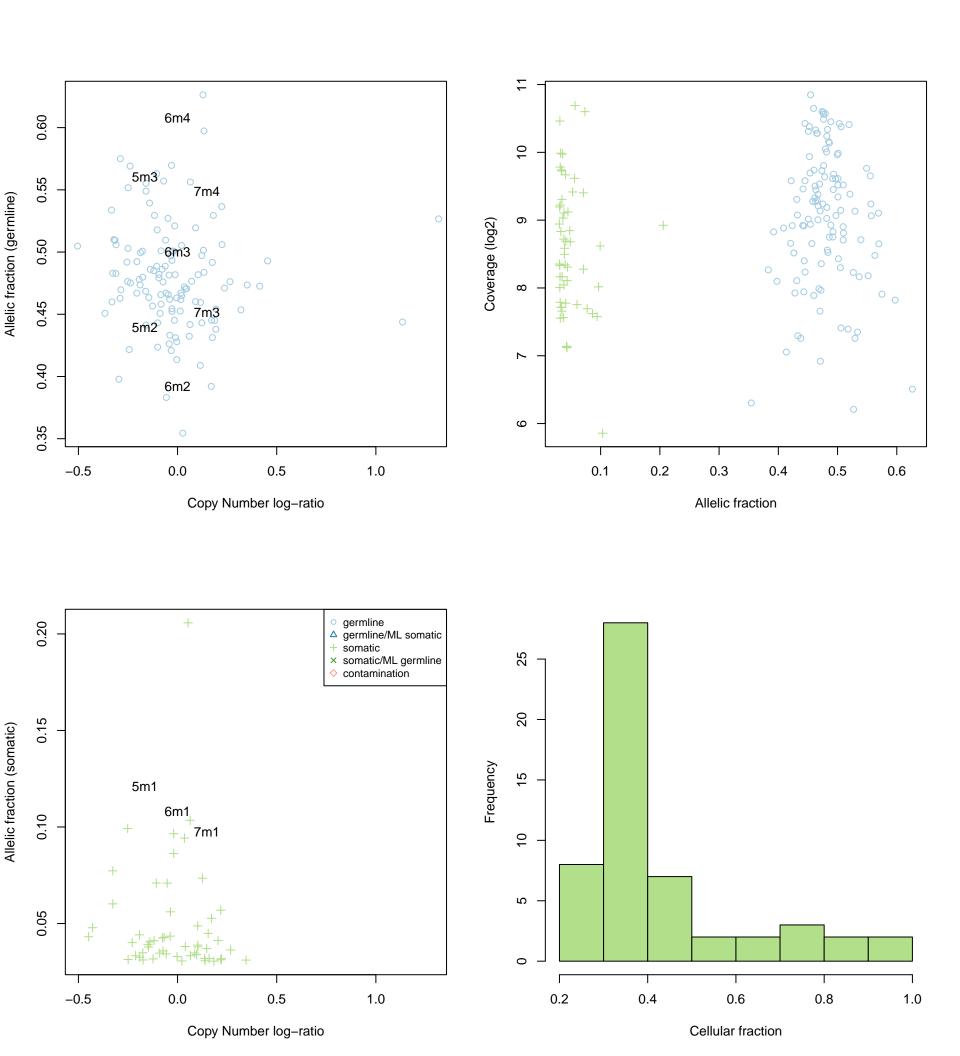
Purity: 0.38 Tumor ploidy: 5.999 5 3 6 7 Fraction Genome 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



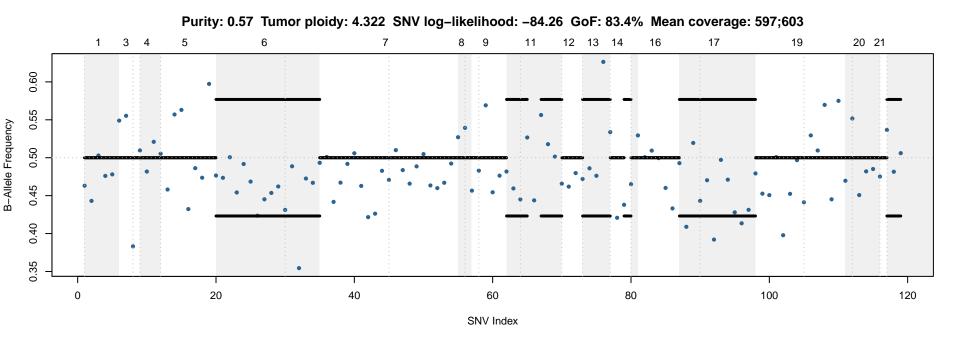
SCNA-fit log-likelihood: -5460.39



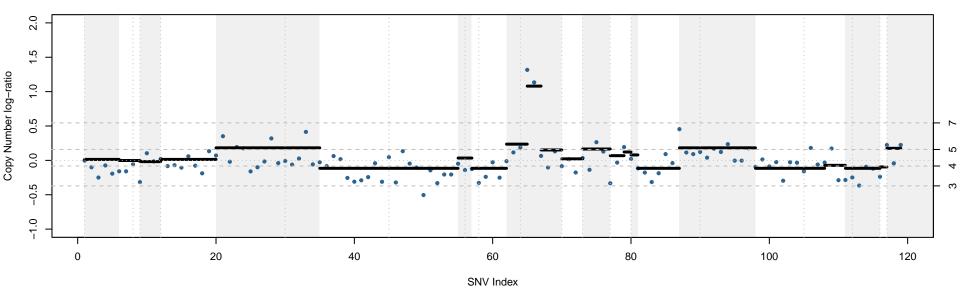


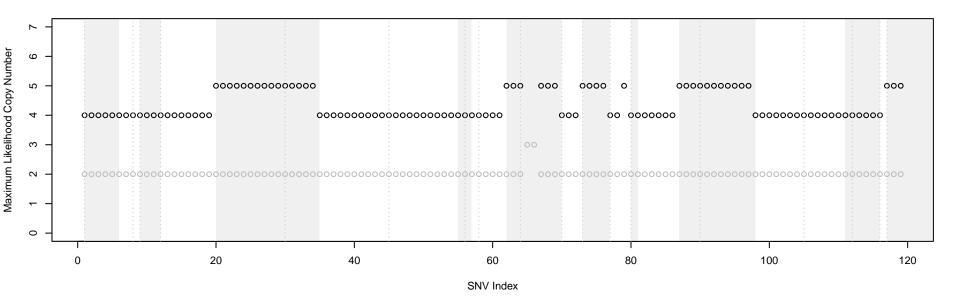


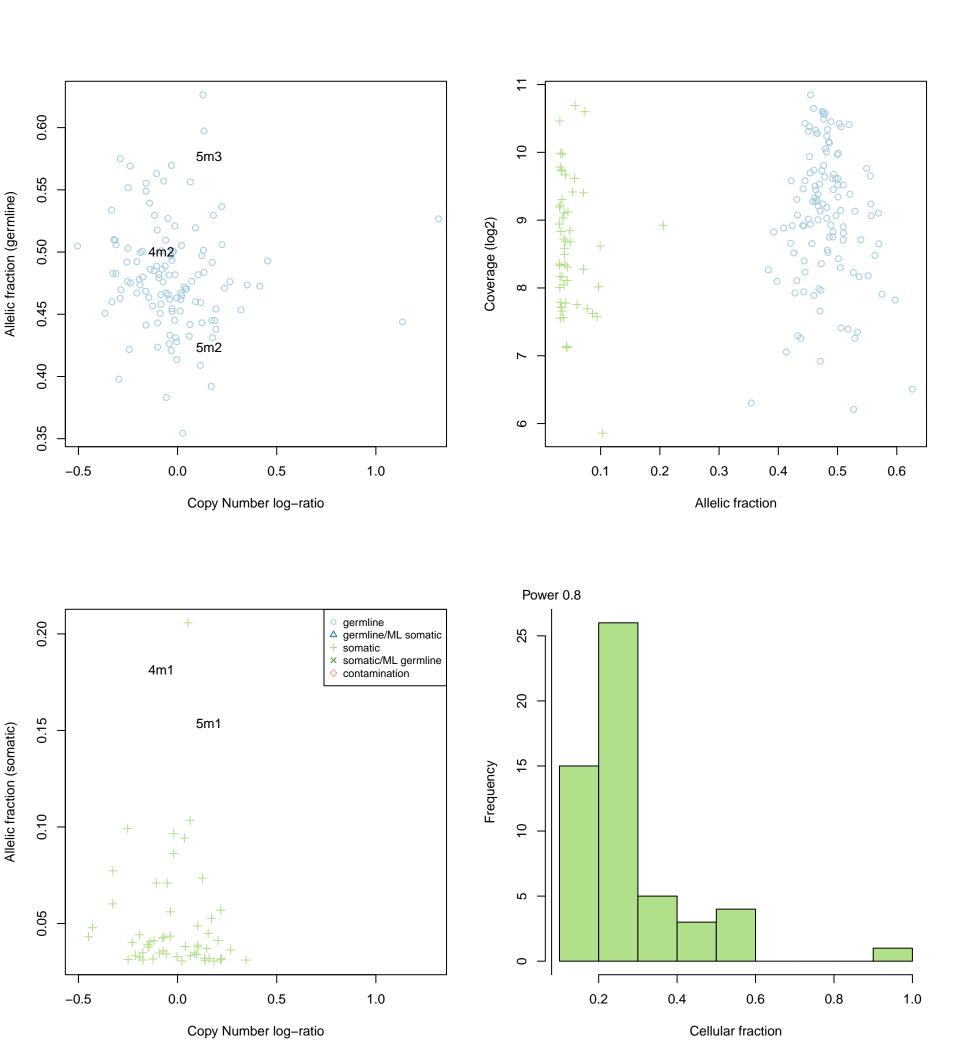
Purity: 0.57 Tumor ploidy: 4.322 5 3 7 Fraction Genome 0.05 0.00 0.0 -1.0 -0.5 0.5 1.0 log2 ratio



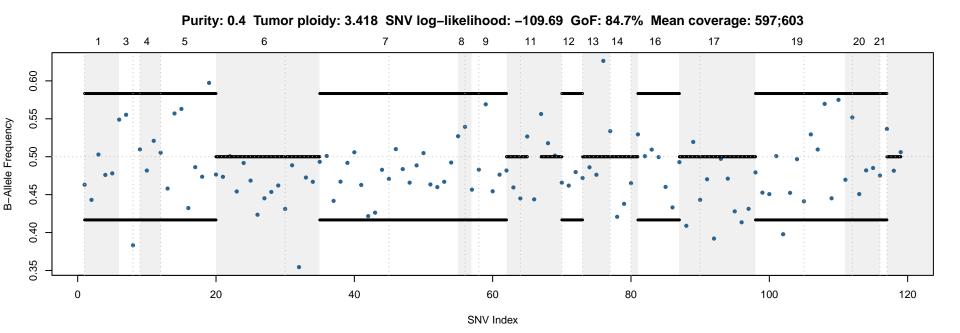
SCNA-fit log-likelihood: -5523.08



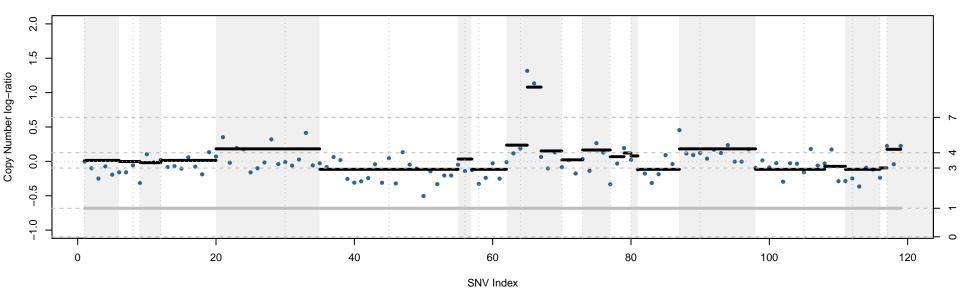


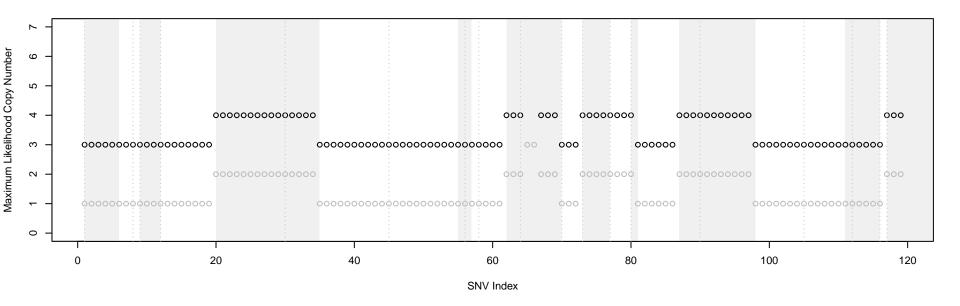


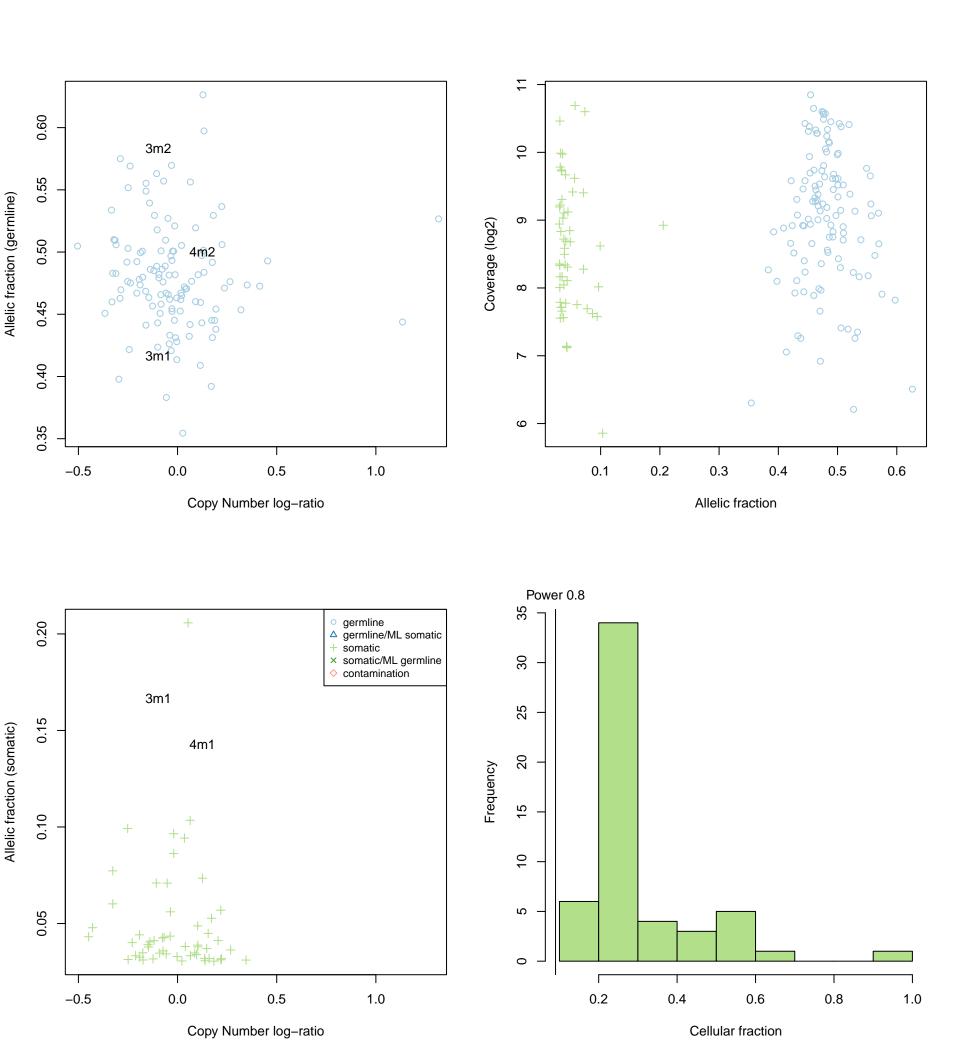
Purity: 0.4 Tumor ploidy: 3.418 0 3 7 Fraction Genome 0.05 0.00 0.0 -1.0 -0.5 0.5 1.0 log2 ratio



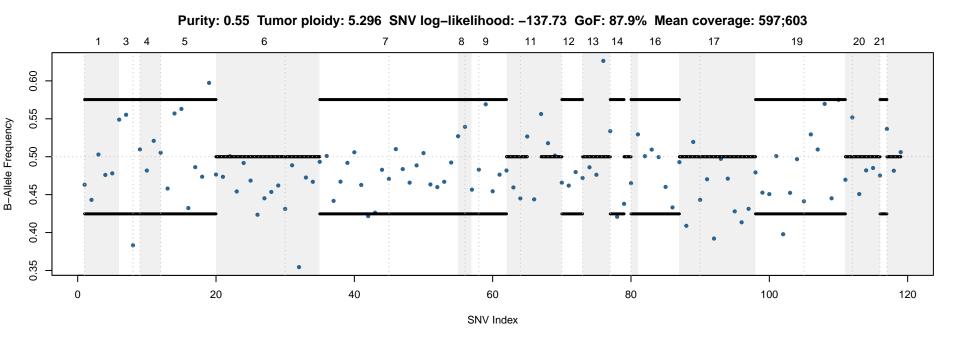
SCNA-fit log-likelihood: -5516.97



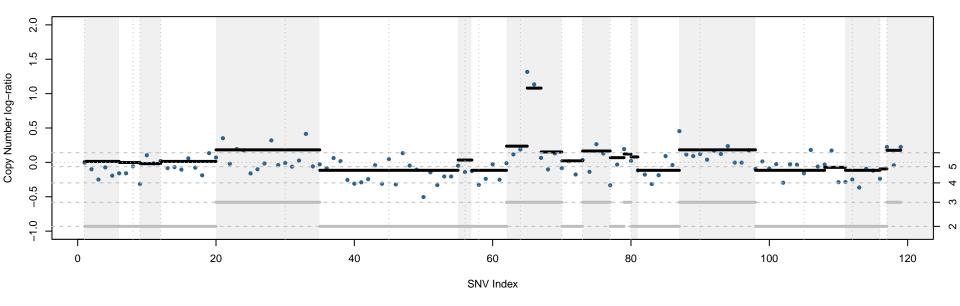


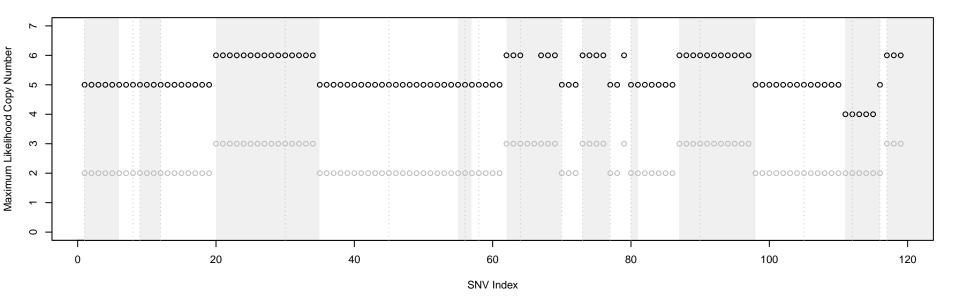


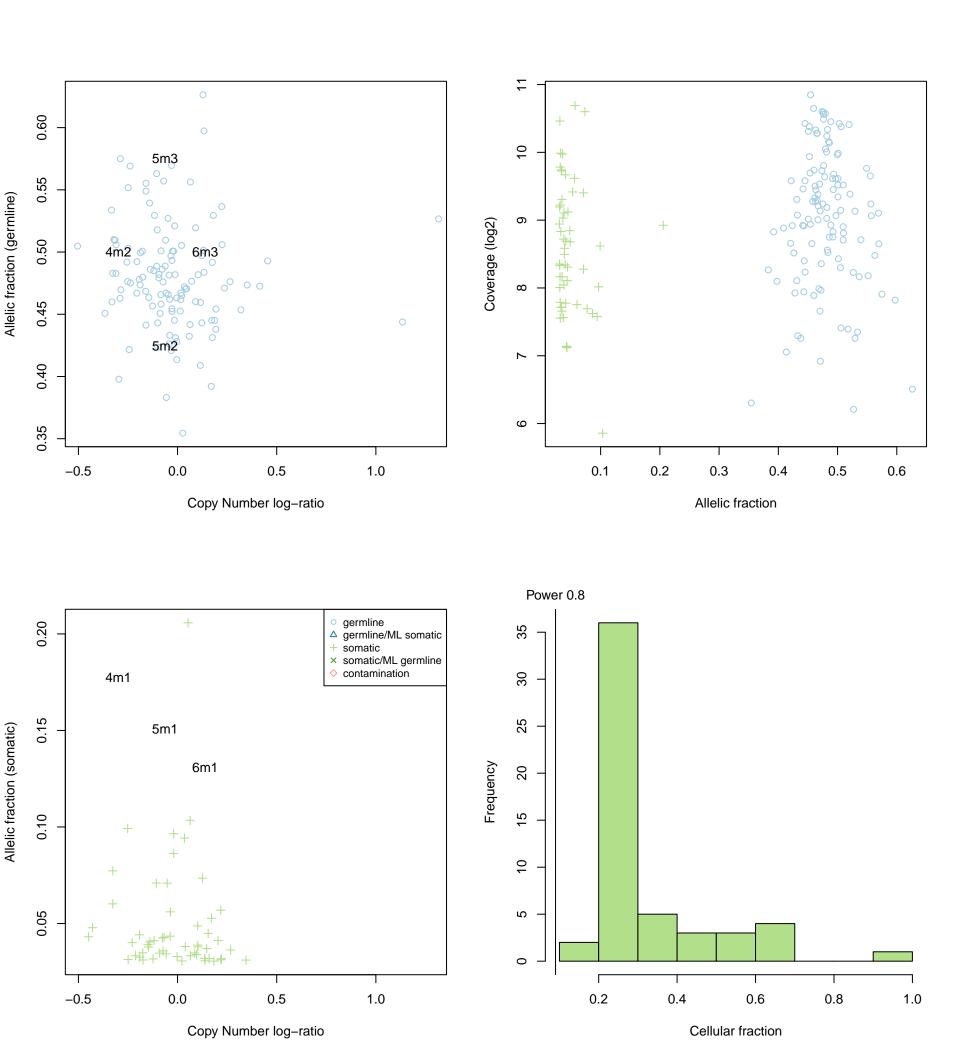
Purity: 0.55 Tumor ploidy: 5.296 2 3 5 6 Fraction Genome 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



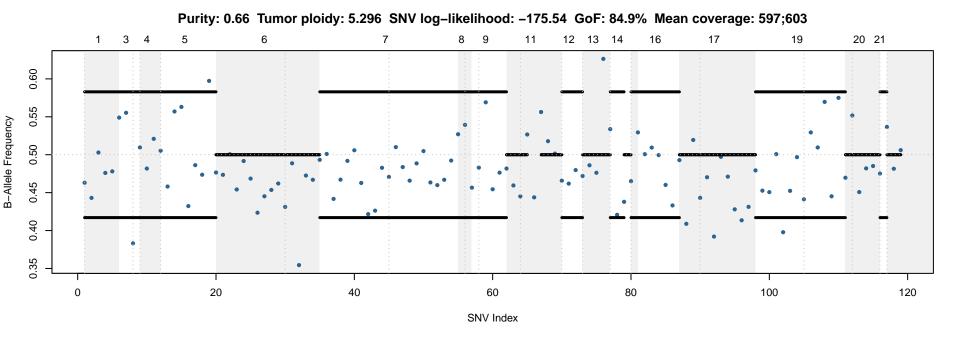
SCNA-fit log-likelihood: -5488.78



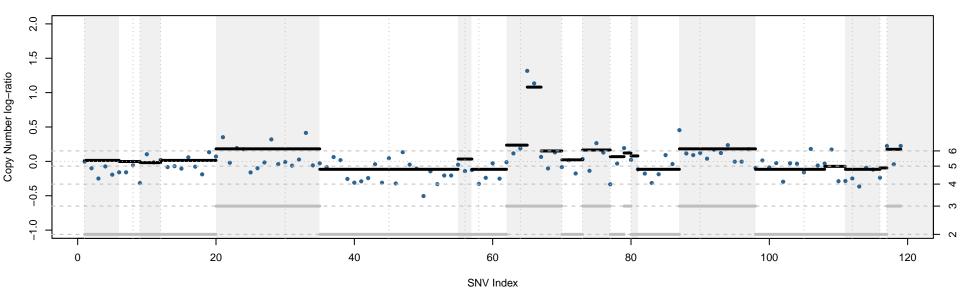


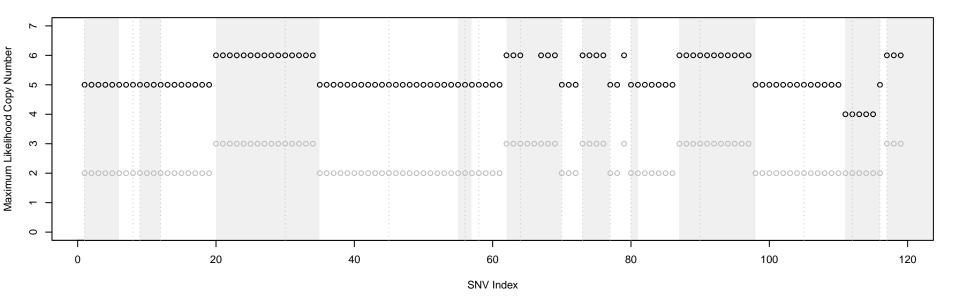


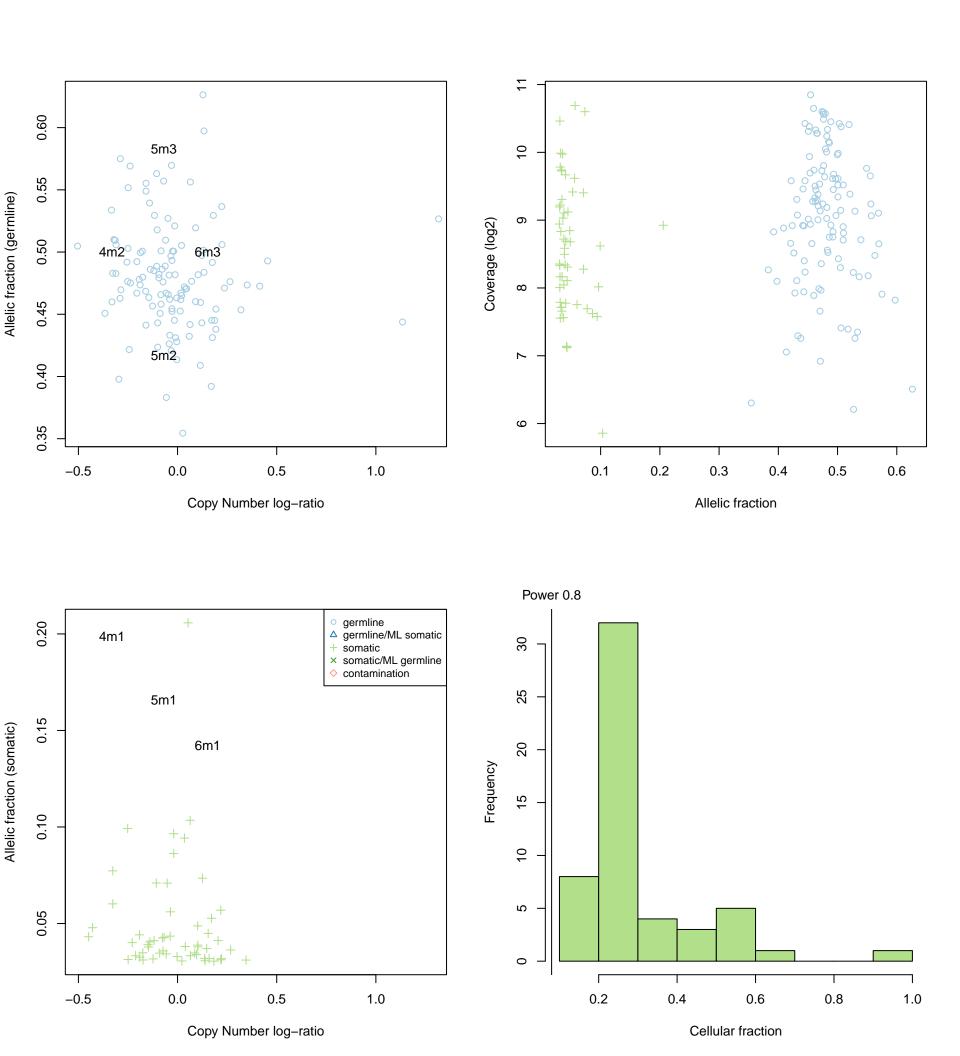
Purity: 0.66 Tumor ploidy: 5.296 2 3 6 Fraction Genome 0.05 0.00 0.0 -1.0 -0.5 0.5 1.0 log2 ratio



SCNA-fit log-likelihood: -5509.28

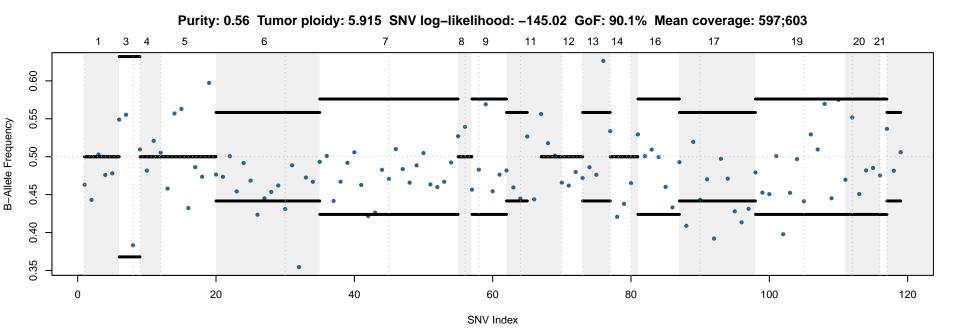




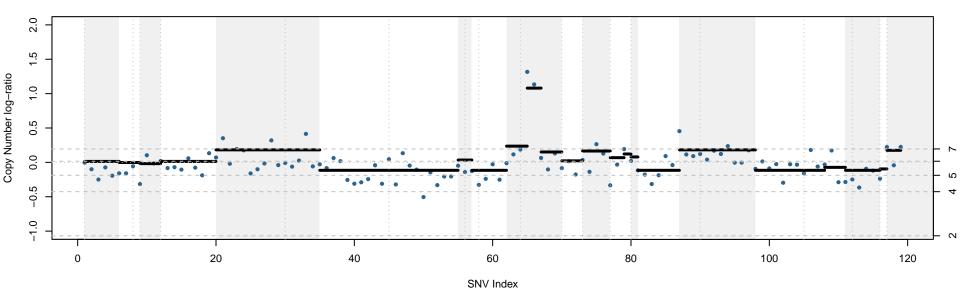


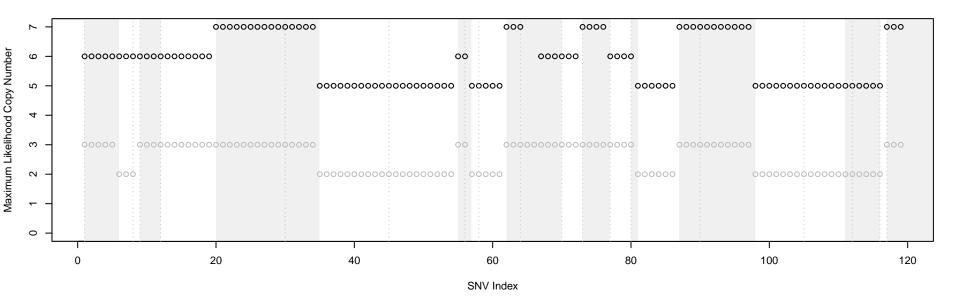
Purity: 0.56 Tumor ploidy: 5.915 2 5 7 6 0.20 Fraction Genome 0.05 0.00 0.0 -1.0 -0.5 0.5 1.0

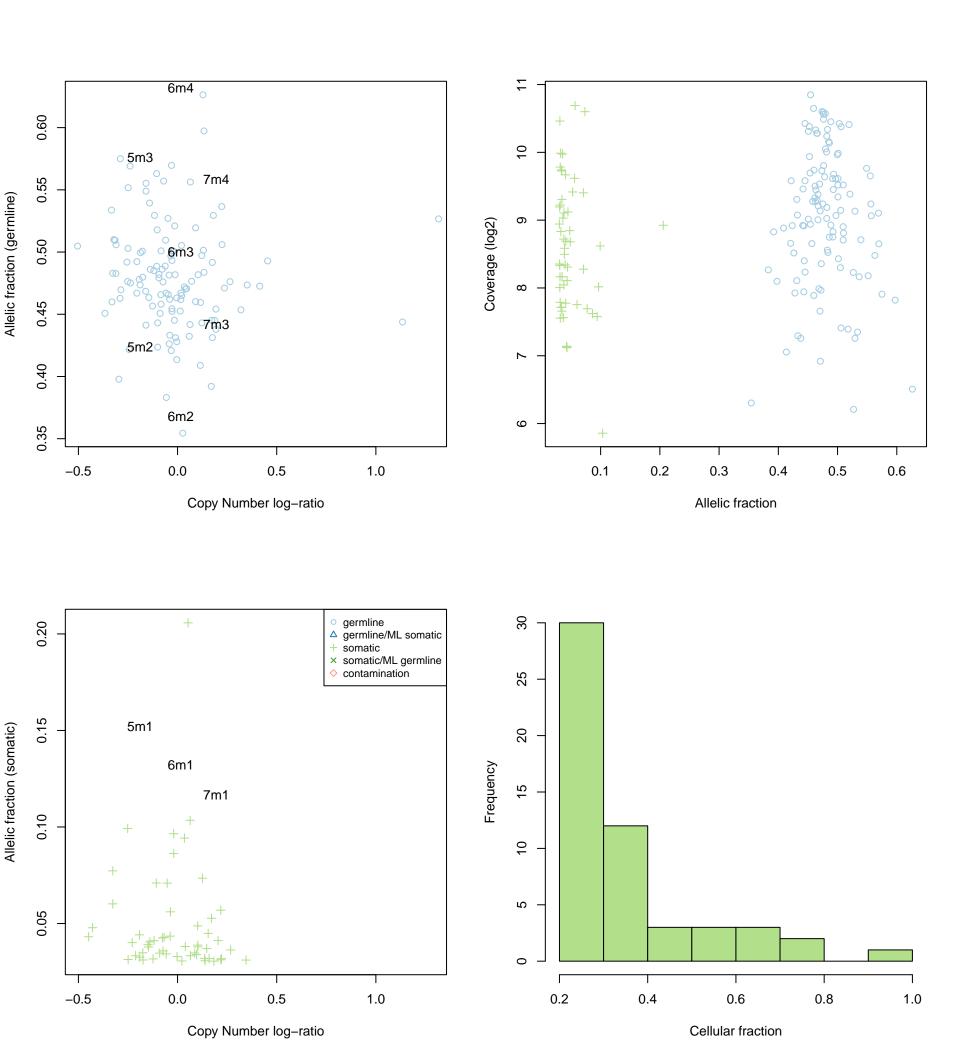
log2 ratio



SCNA-fit log-likelihood: -5835.98

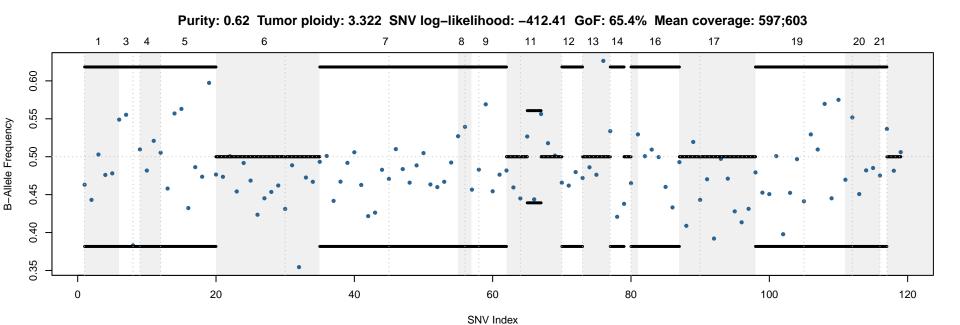




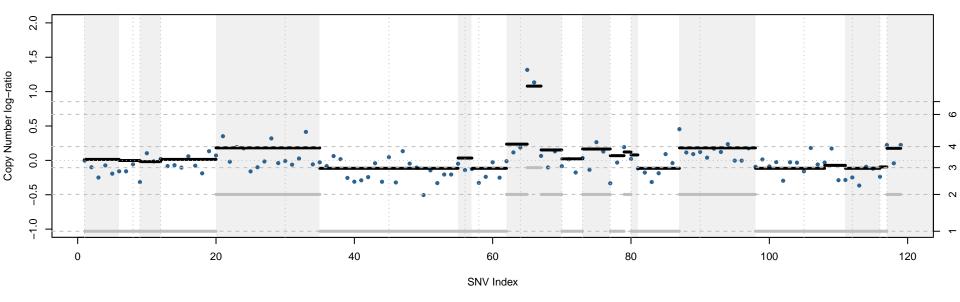


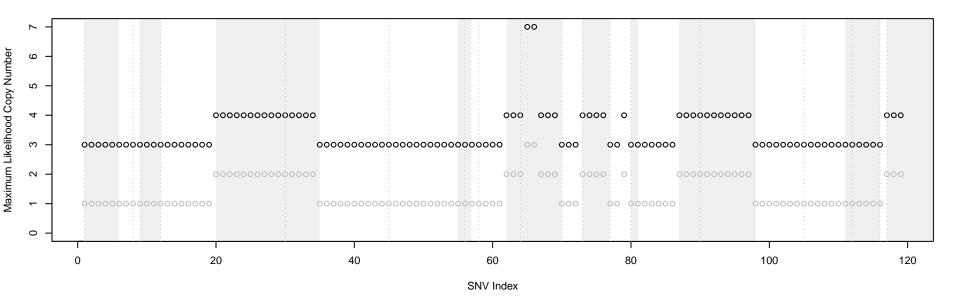
Purity: 0.62 Tumor ploidy: 3.322 2 6 7 Fraction Genome 0.05 0.00 0.0 -1.0 -0.5 0.5 1.0

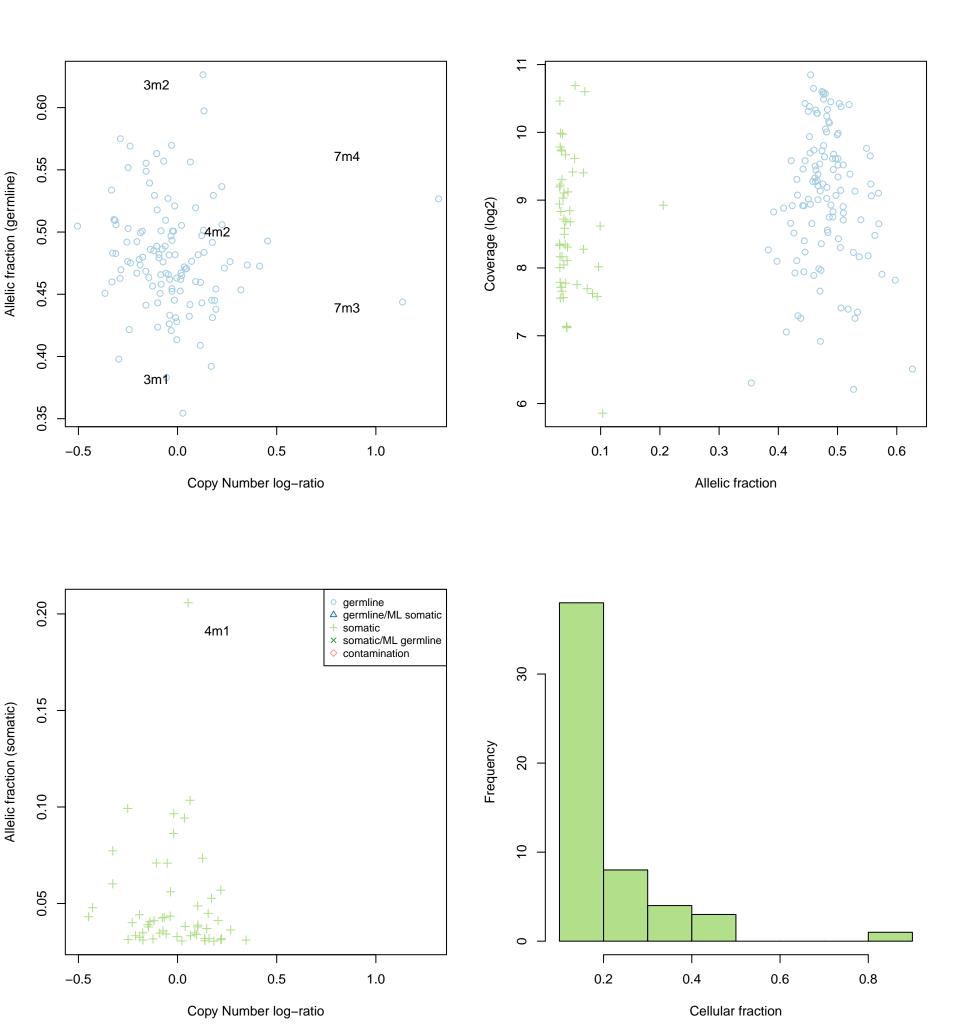
log2 ratio



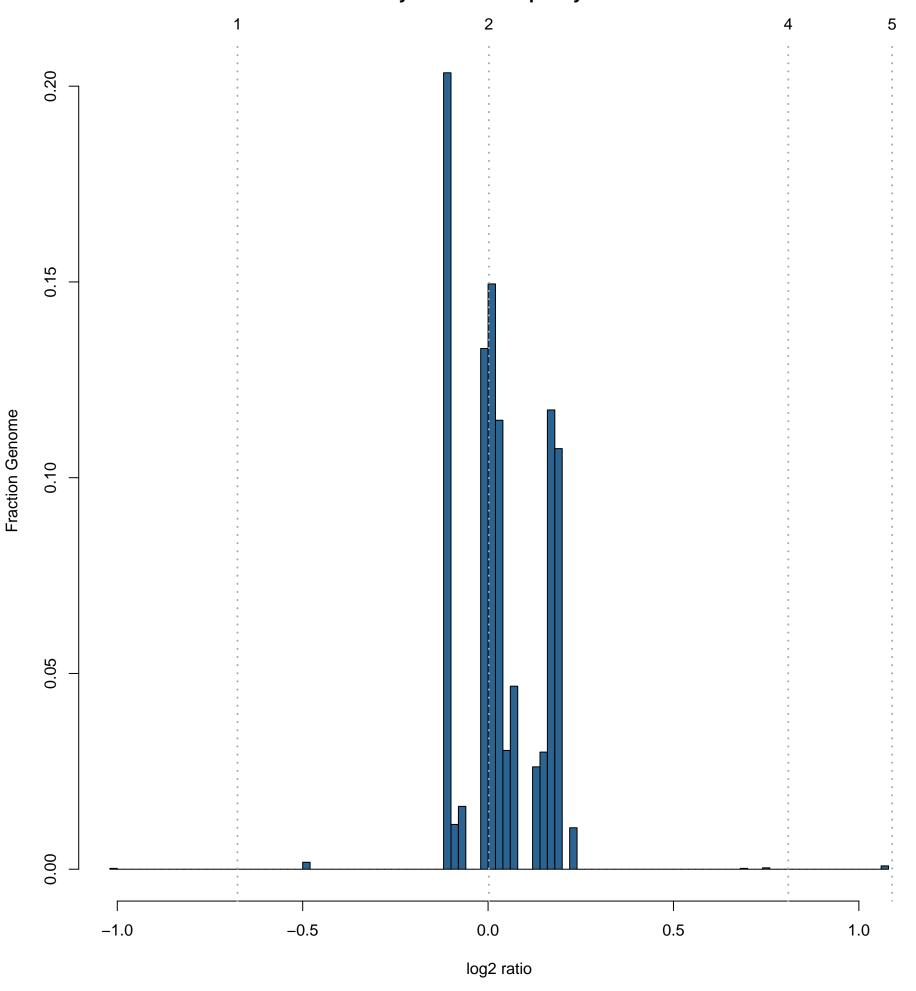
SCNA-fit log-likelihood: -5614.98

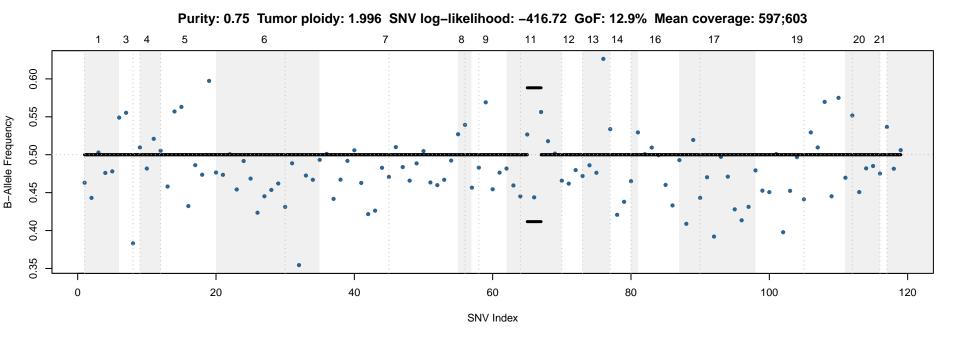






Purity: 0.75 Tumor ploidy: 1.996





SCNA-fit log-likelihood: -5897.89

