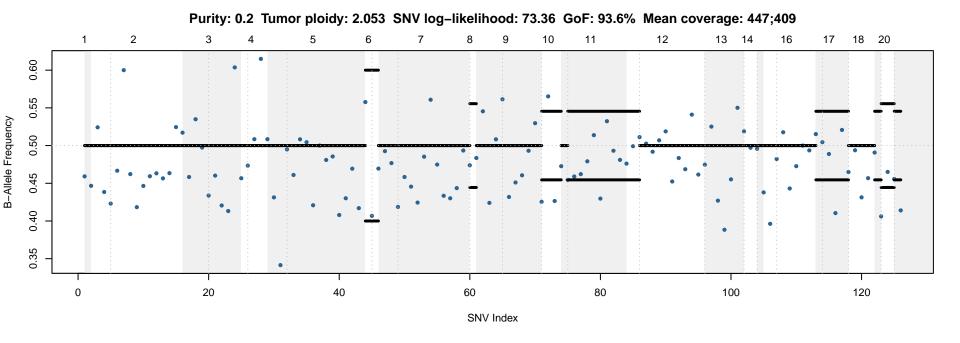
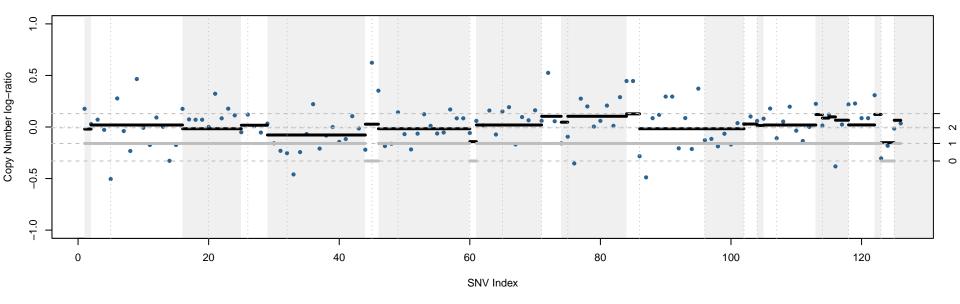
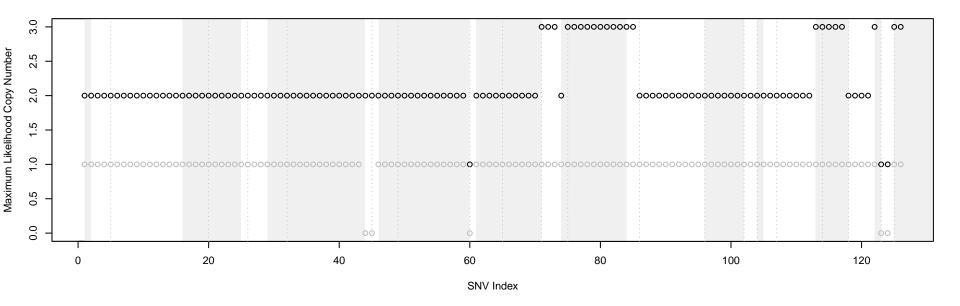
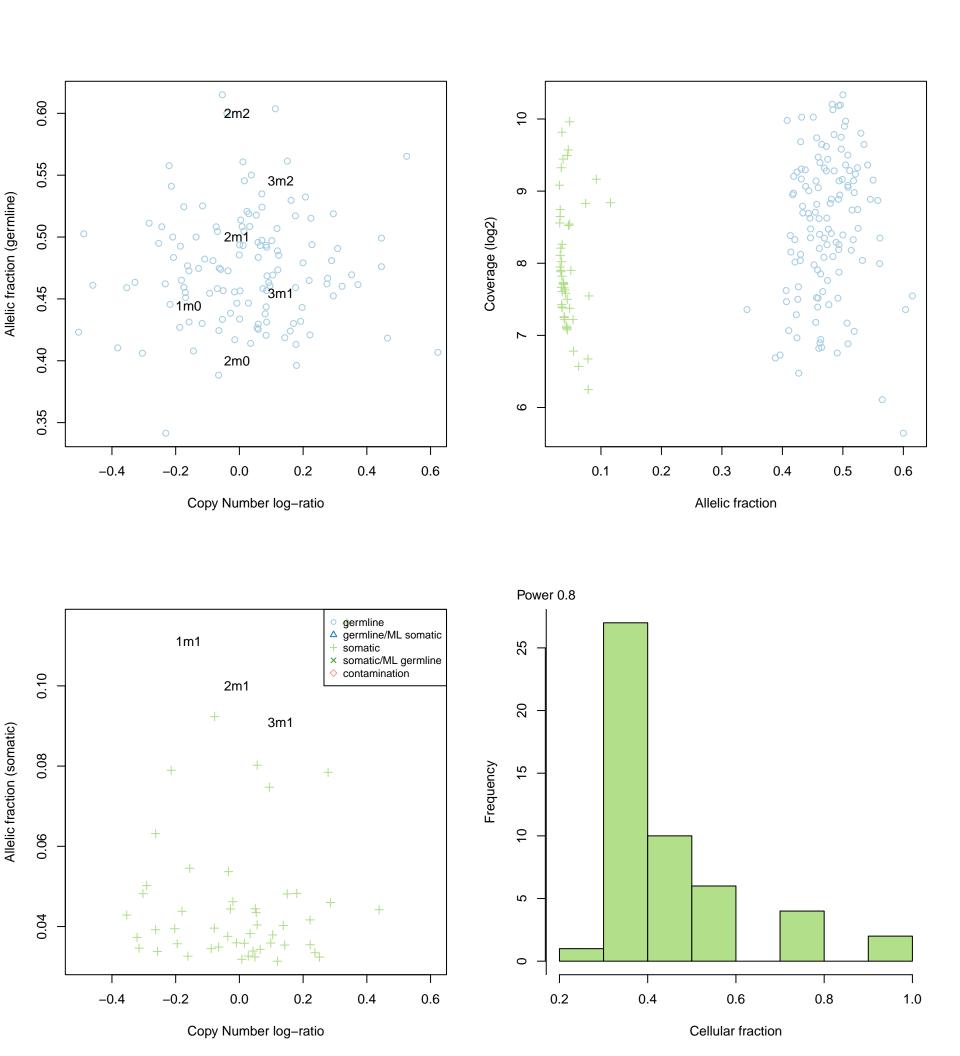
Purity: 0.2 Tumor ploidy: 2.053 2 3 0.20 Fraction Genome 0.05 0.00 -0.2 -0.6 -0.4 0.0 0.2 log2 ratio



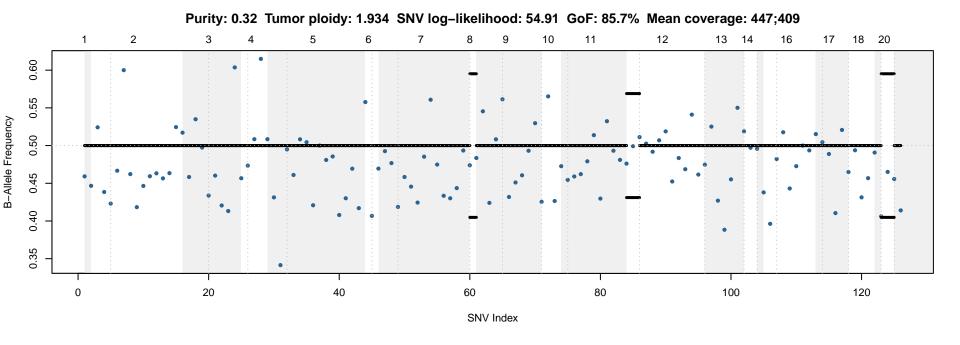
# SCNA-fit log-likelihood: -7201.15



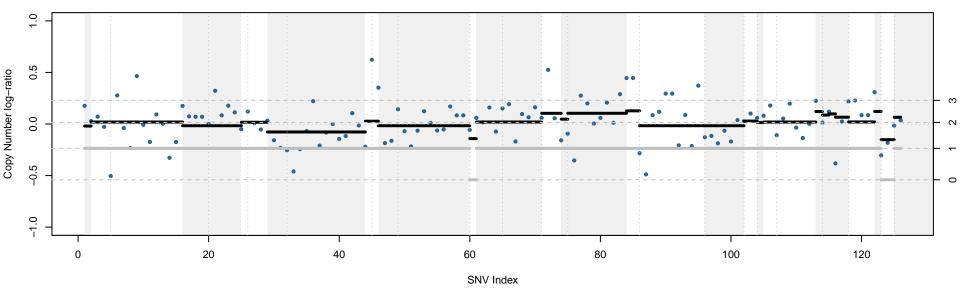


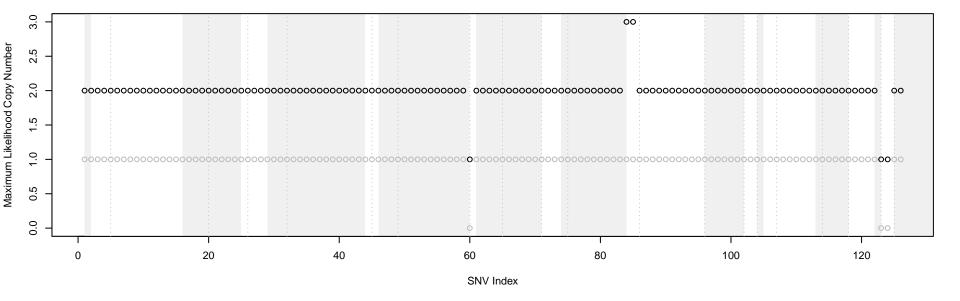


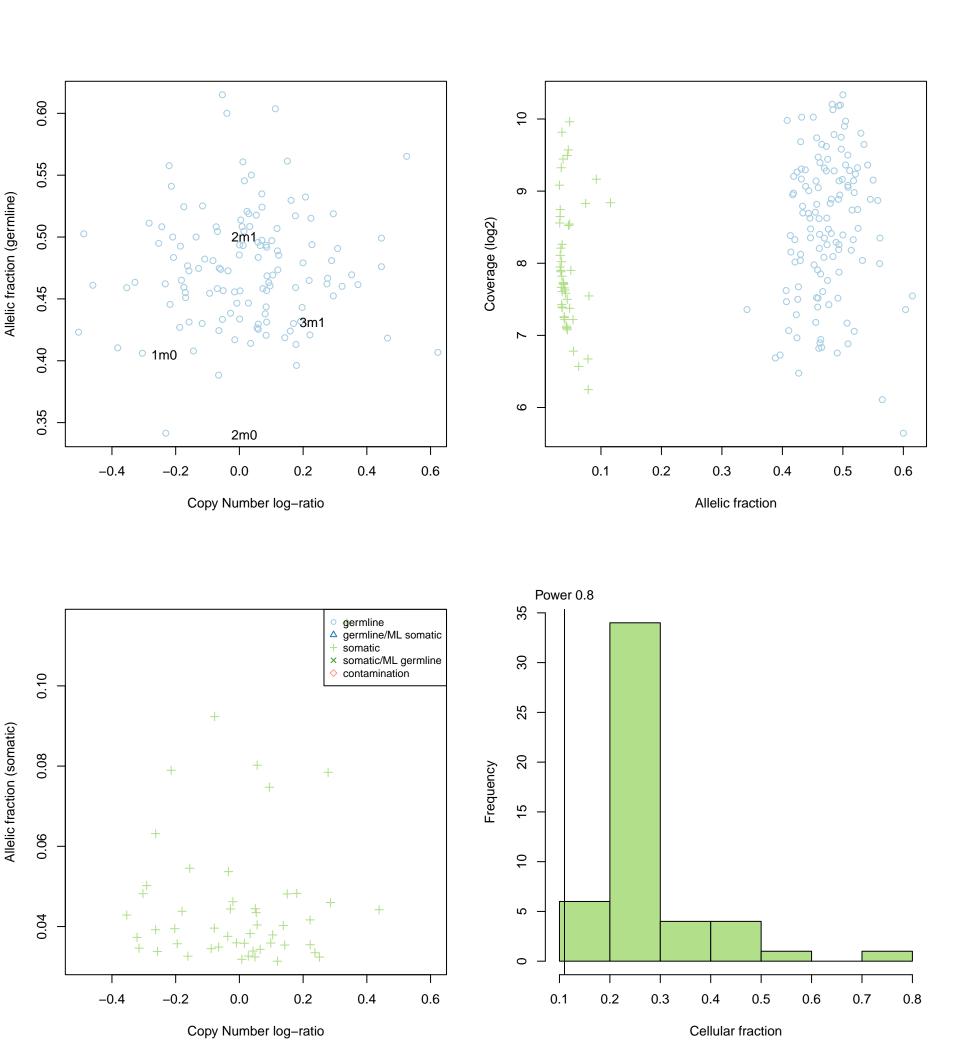
Purity: 0.32 Tumor ploidy: 1.934 2 3 0.20 Fraction Genome 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



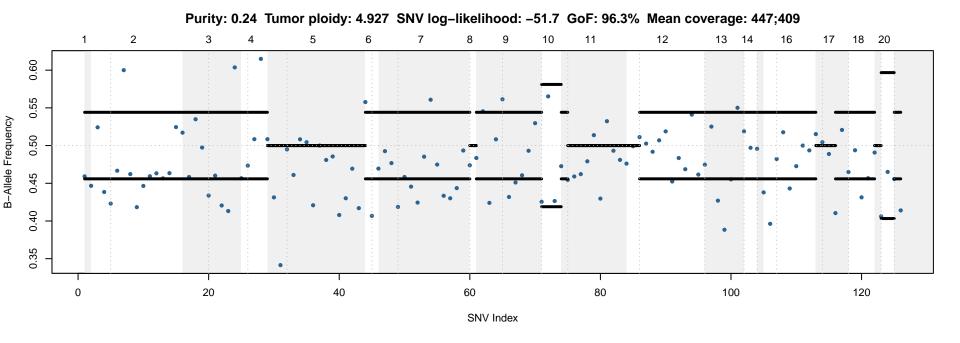
## SCNA-fit log-likelihood: -7280.38



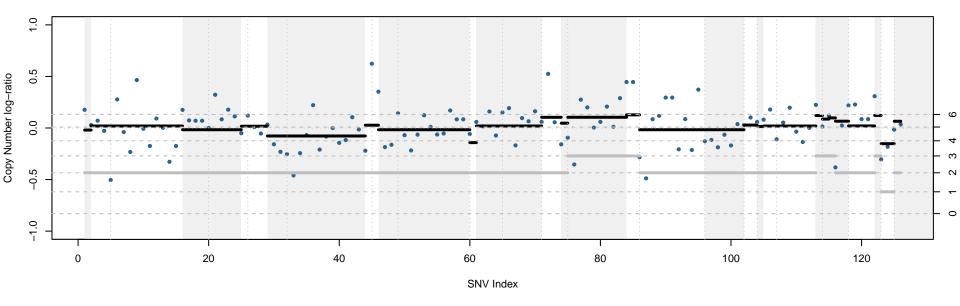


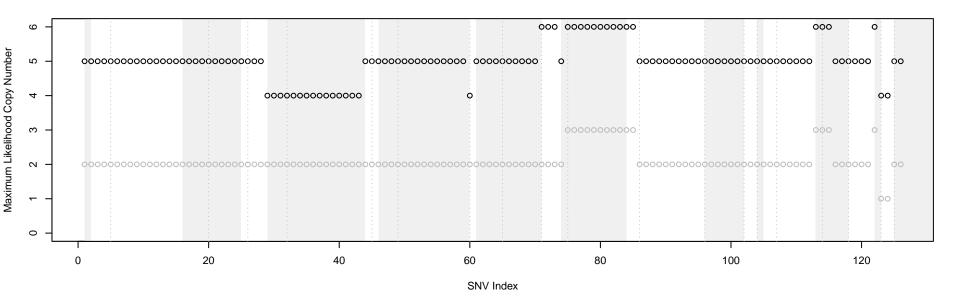


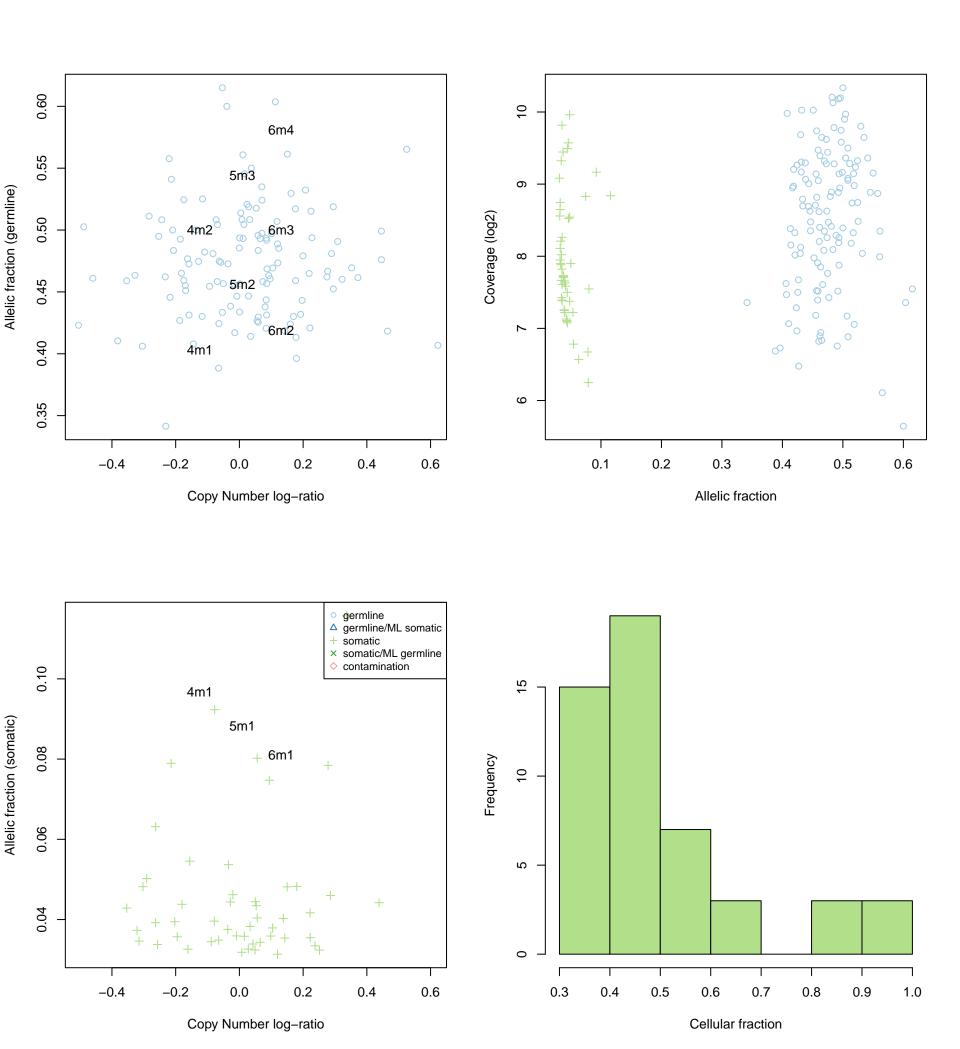
Purity: 0.24 Tumor ploidy: 4.927 2 3 5 6 0 0.20 0.15 Fraction Genome 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



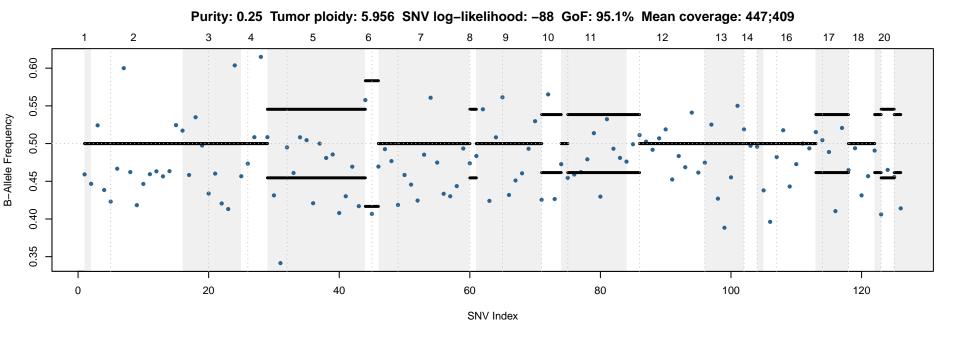
## SCNA-fit log-likelihood: -7160.15



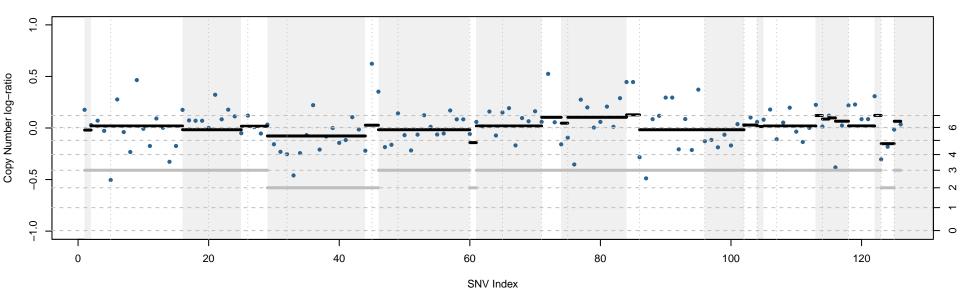


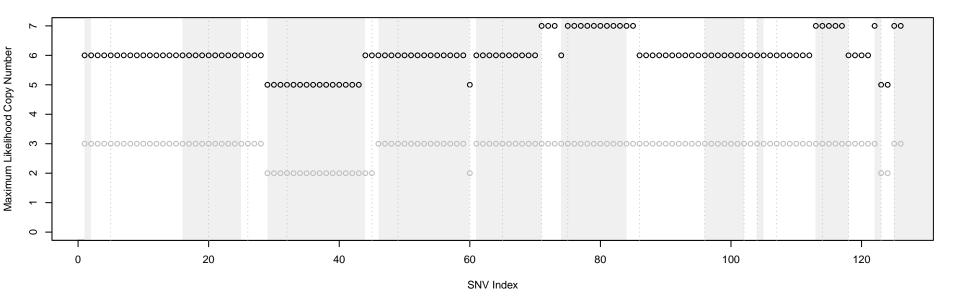


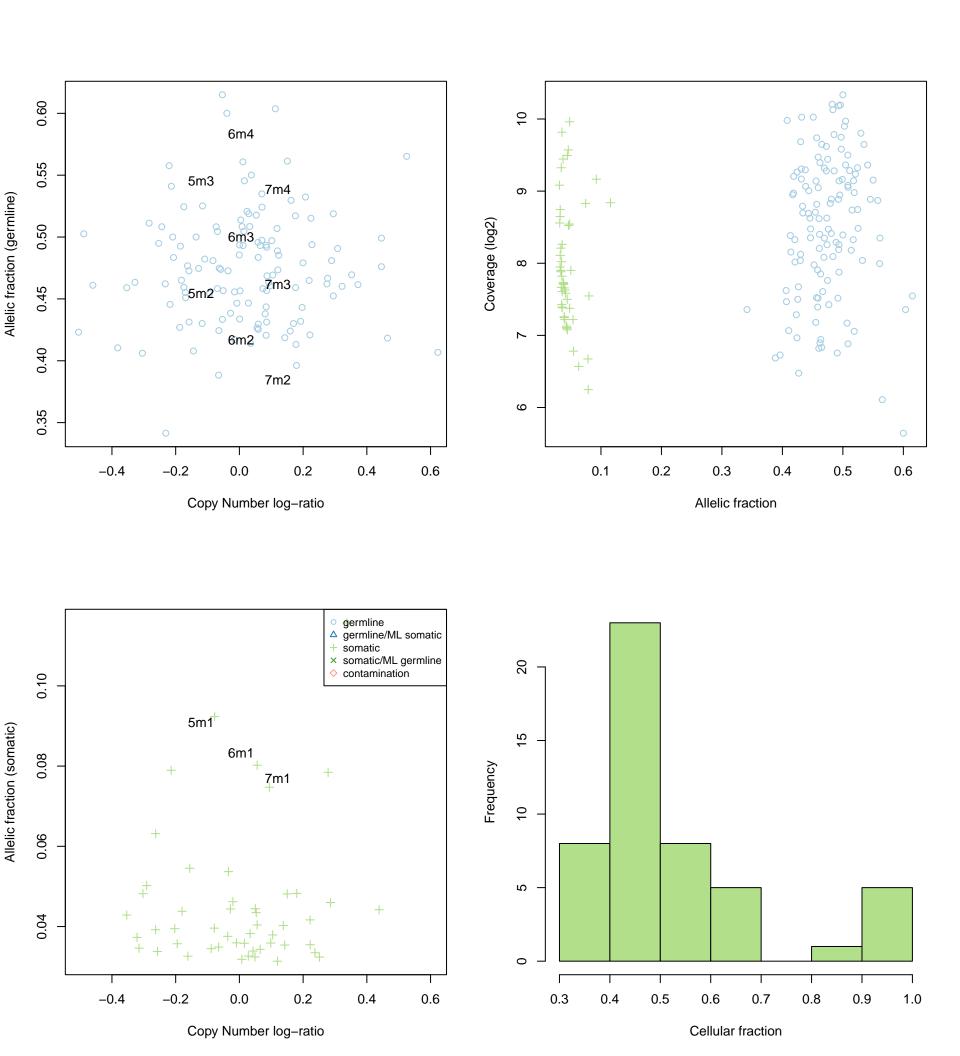
Purity: 0.25 Tumor ploidy: 5.956 6 0 3 5 7 0.25 0.20 0.15 Fraction Genome 0.10 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio

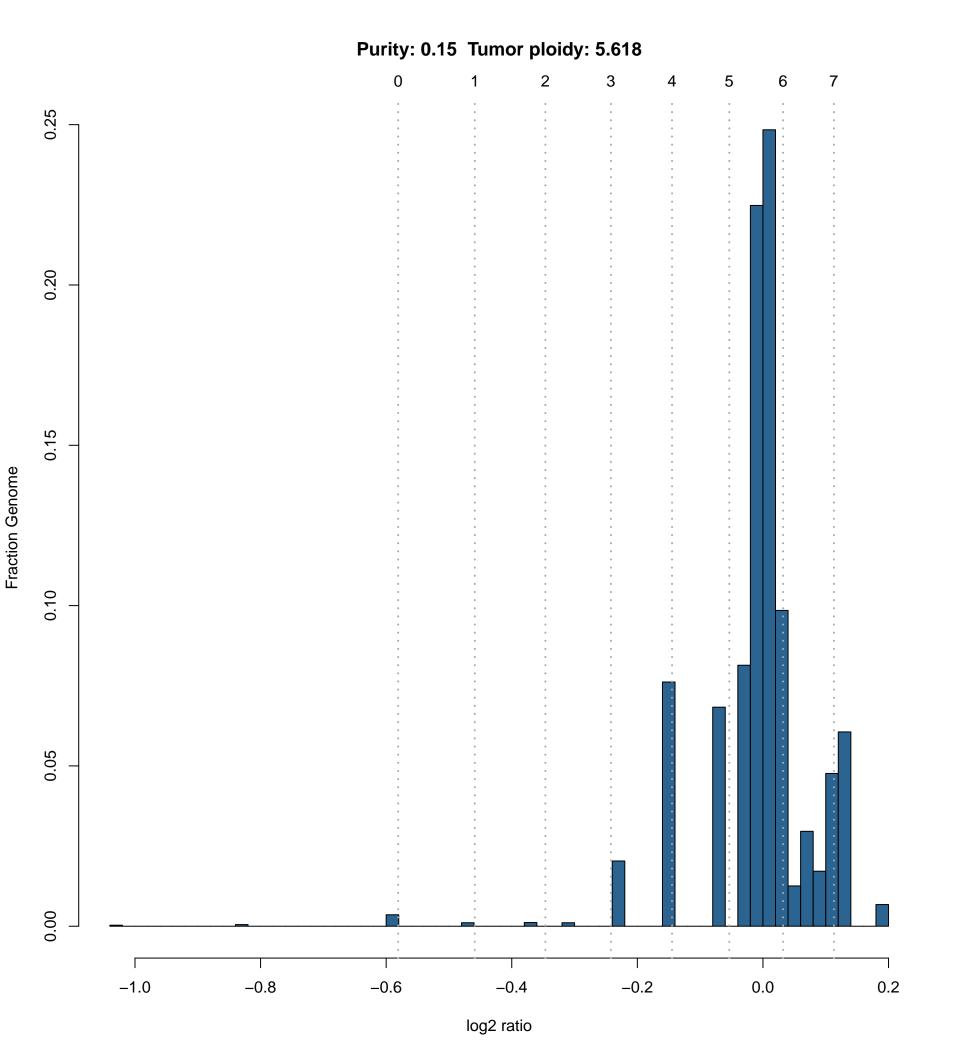


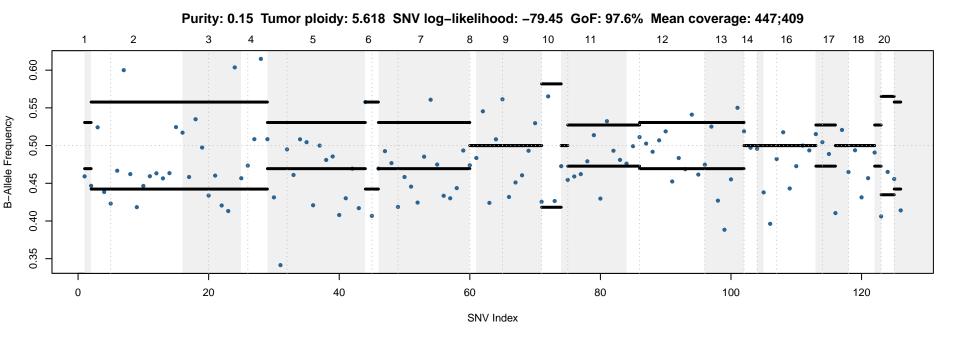
## SCNA-fit log-likelihood: -7152.41



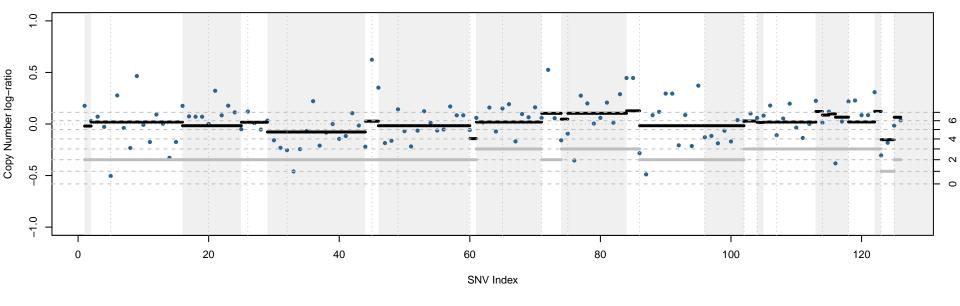


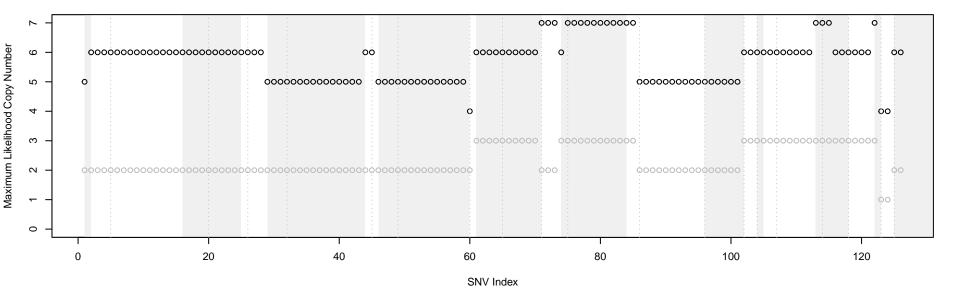


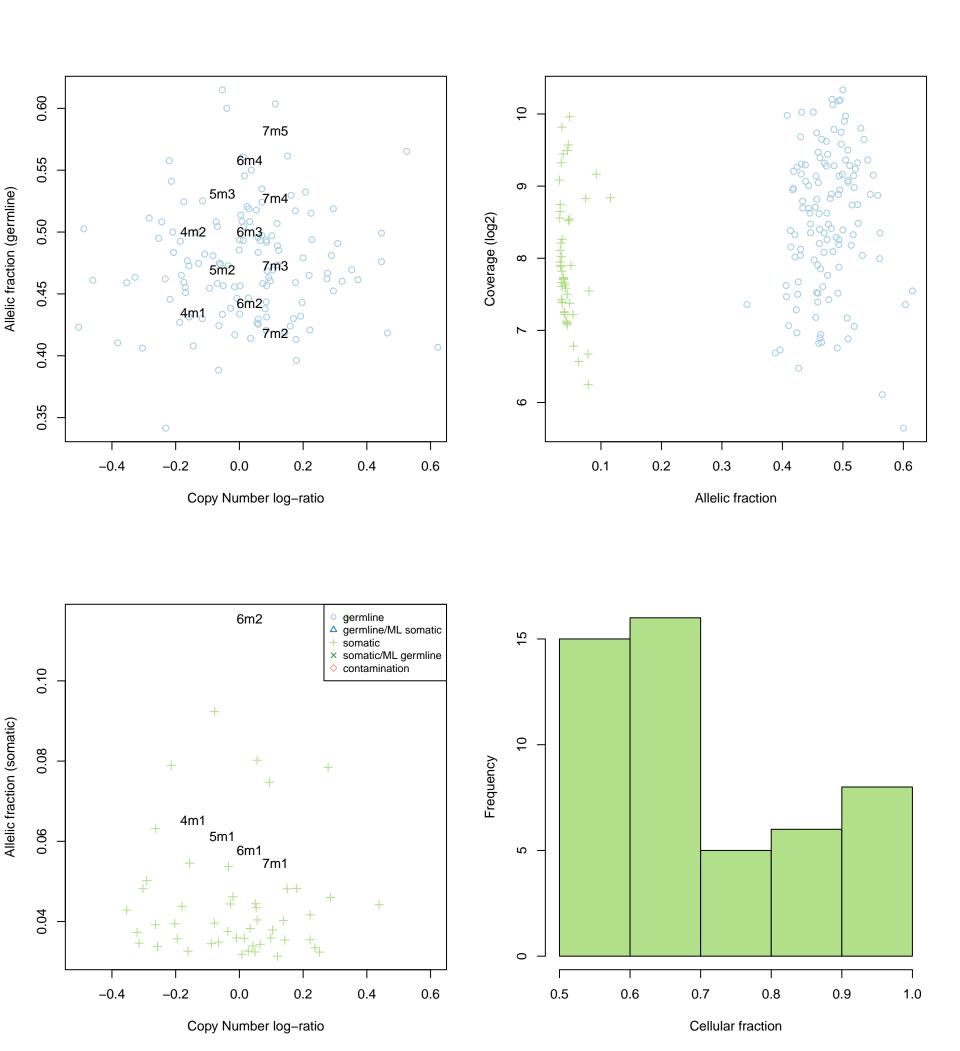




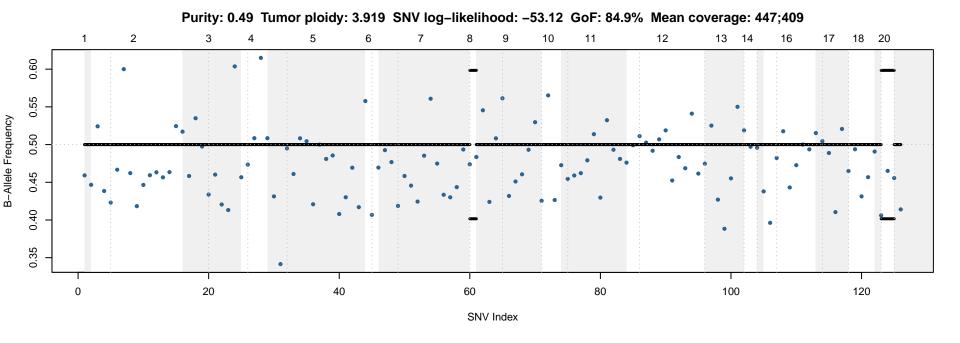
## SCNA-fit log-likelihood: -7155.5



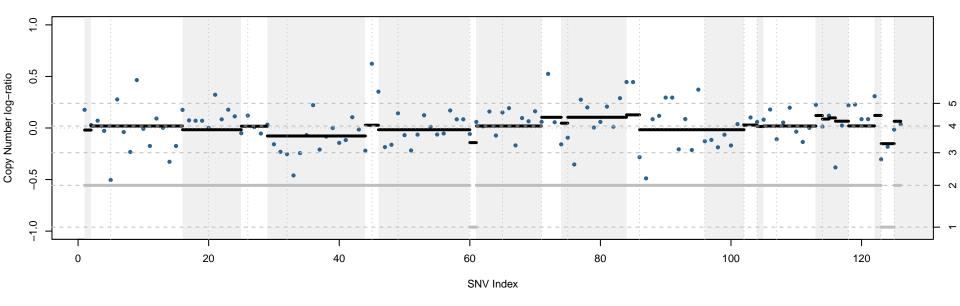


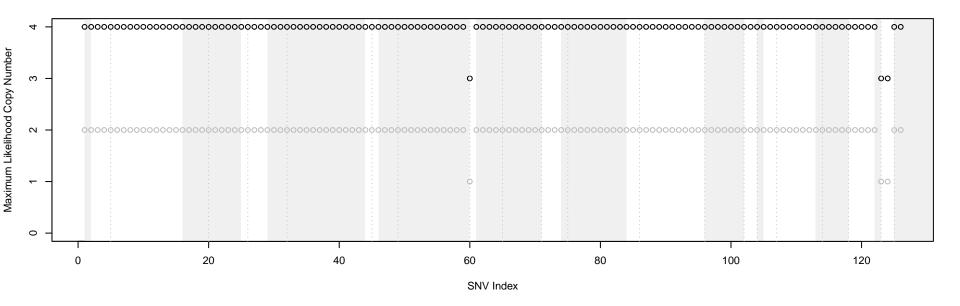


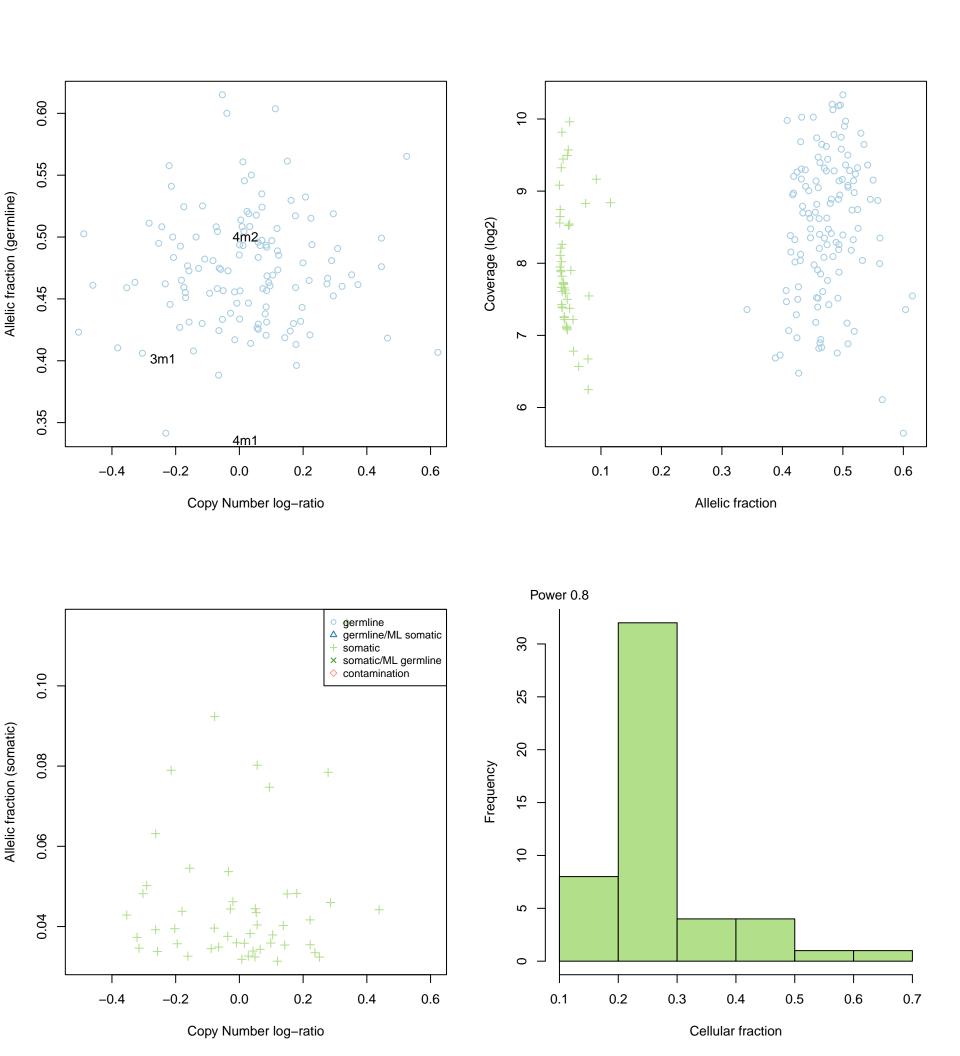
Purity: 0.49 Tumor ploidy: 3.919 5 0.25 0.20 0.15 Fraction Genome 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



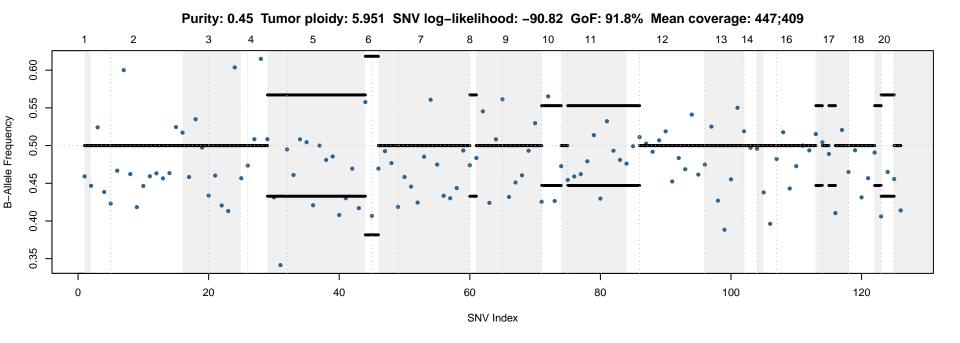
## SCNA-fit log-likelihood: -7280.14



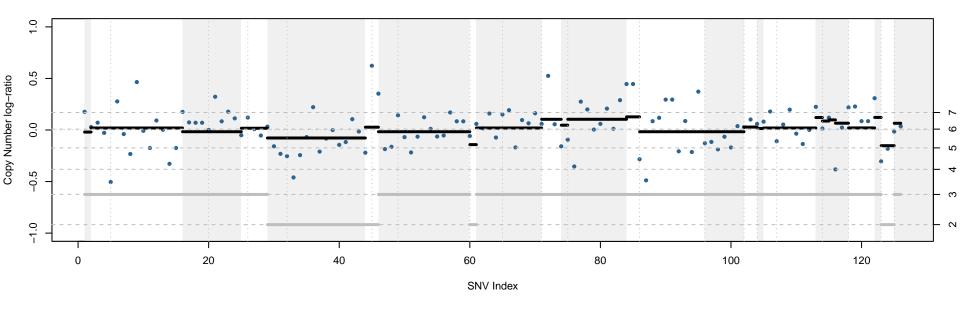


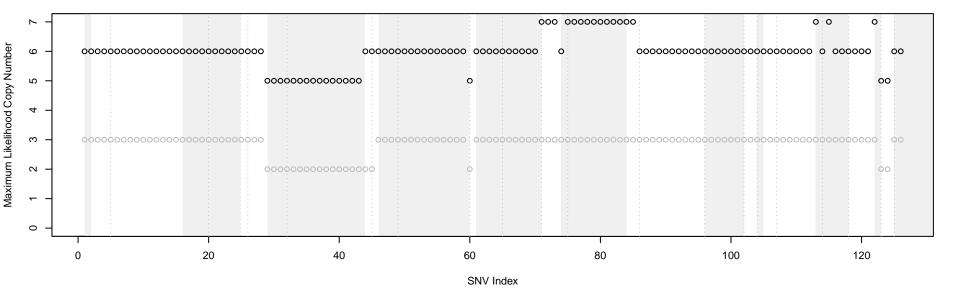


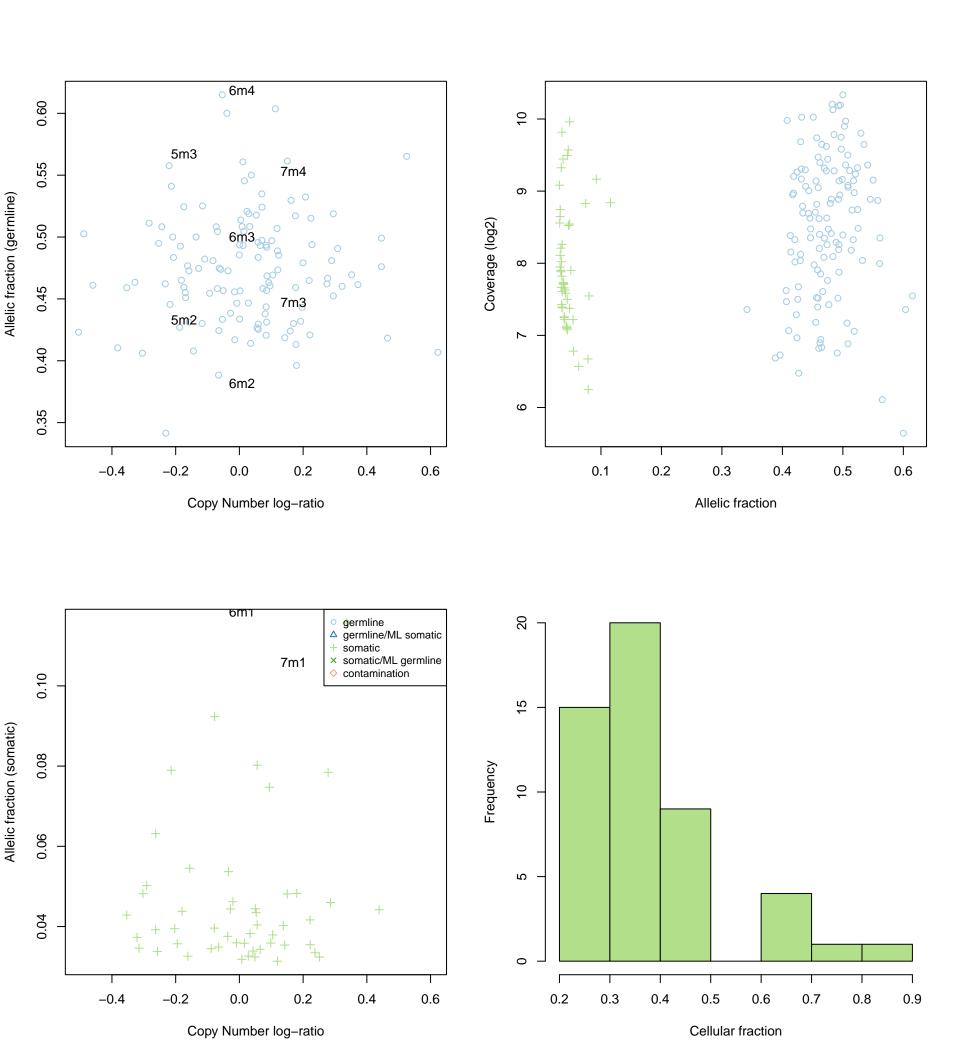
Purity: 0.45 Tumor ploidy: 5.951 7 2 6 5 0.20 Fraction Genome 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



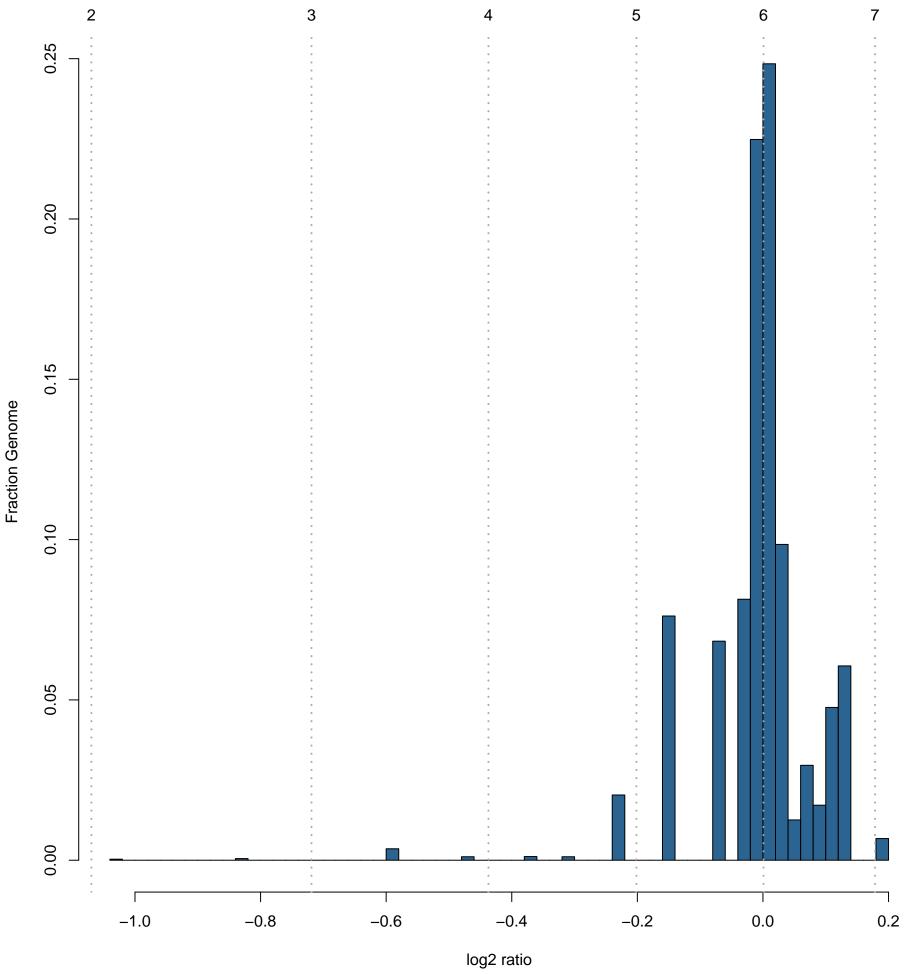
## SCNA-fit log-likelihood: -7205.21

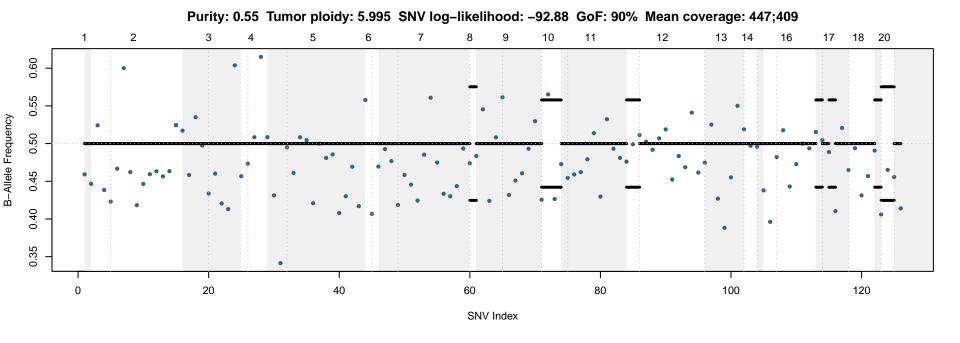




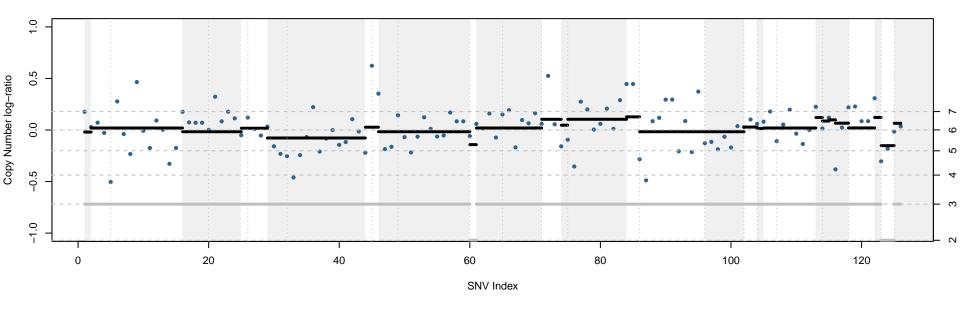


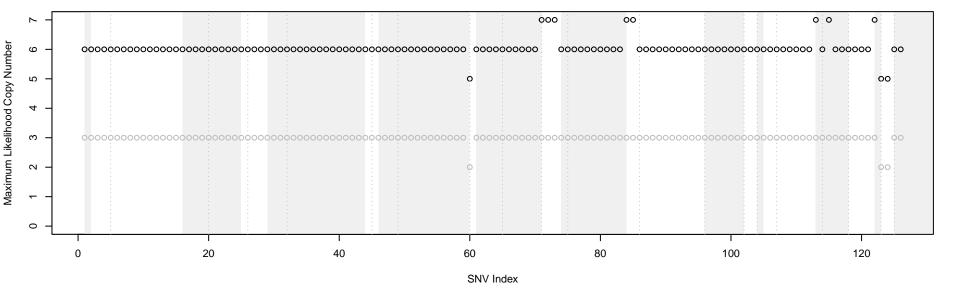
Purity: 0.55 Tumor ploidy: 5.995

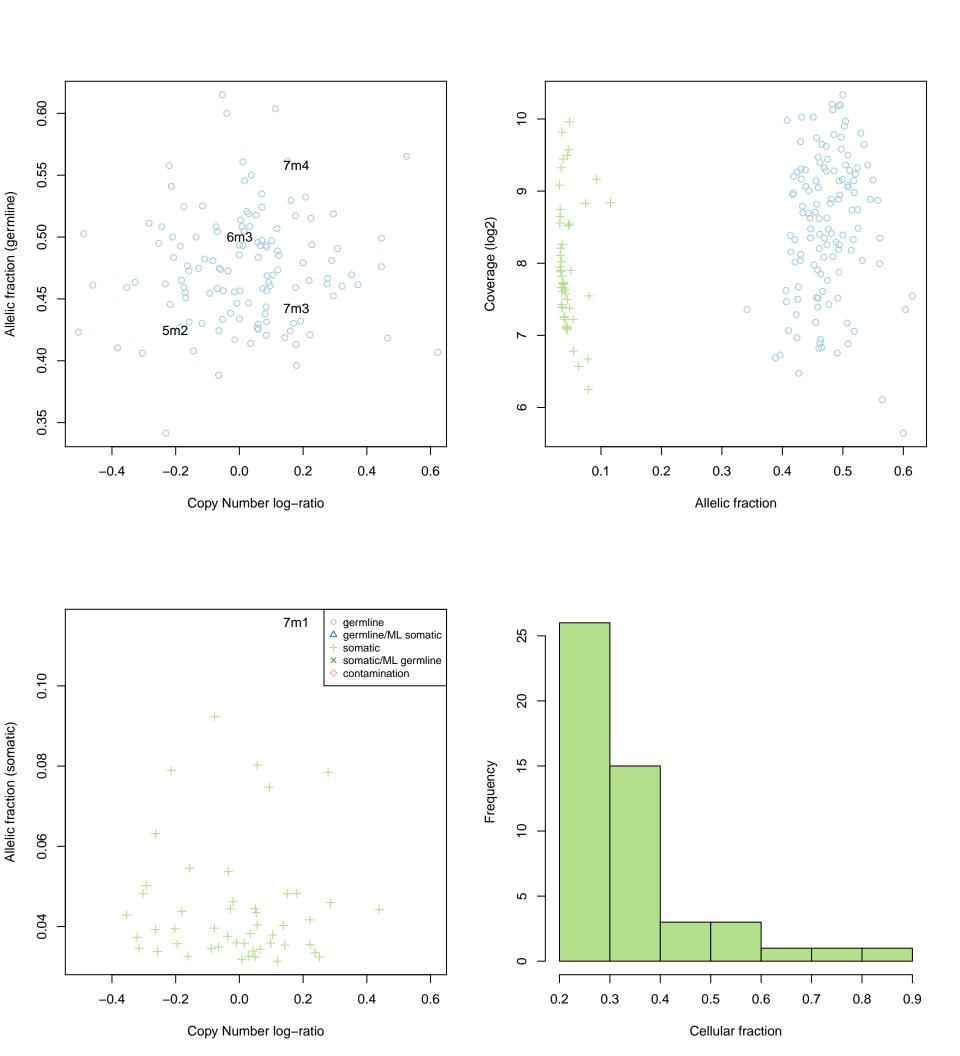




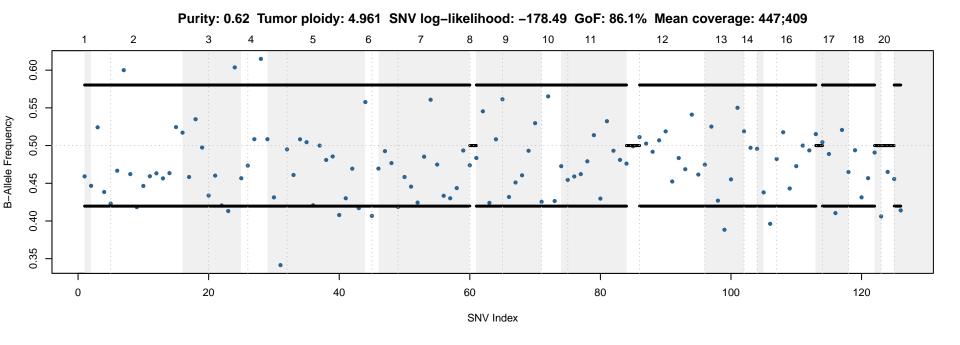
# SCNA-fit log-likelihood: -7222.73



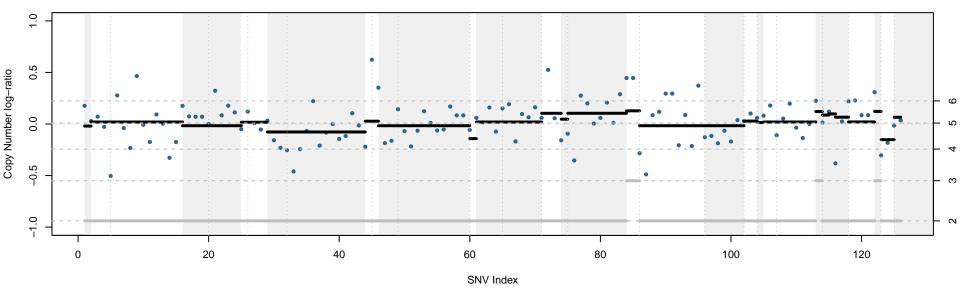


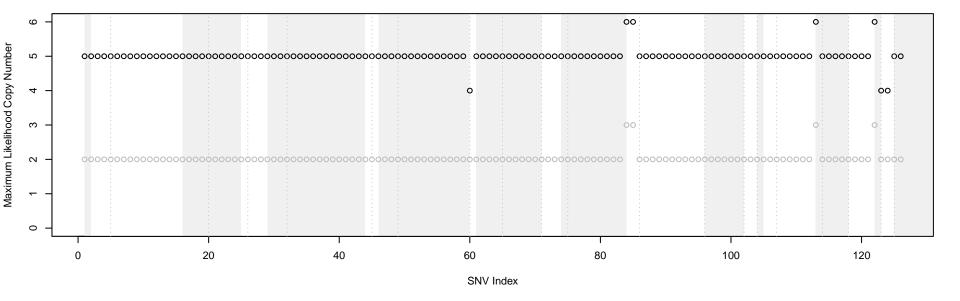


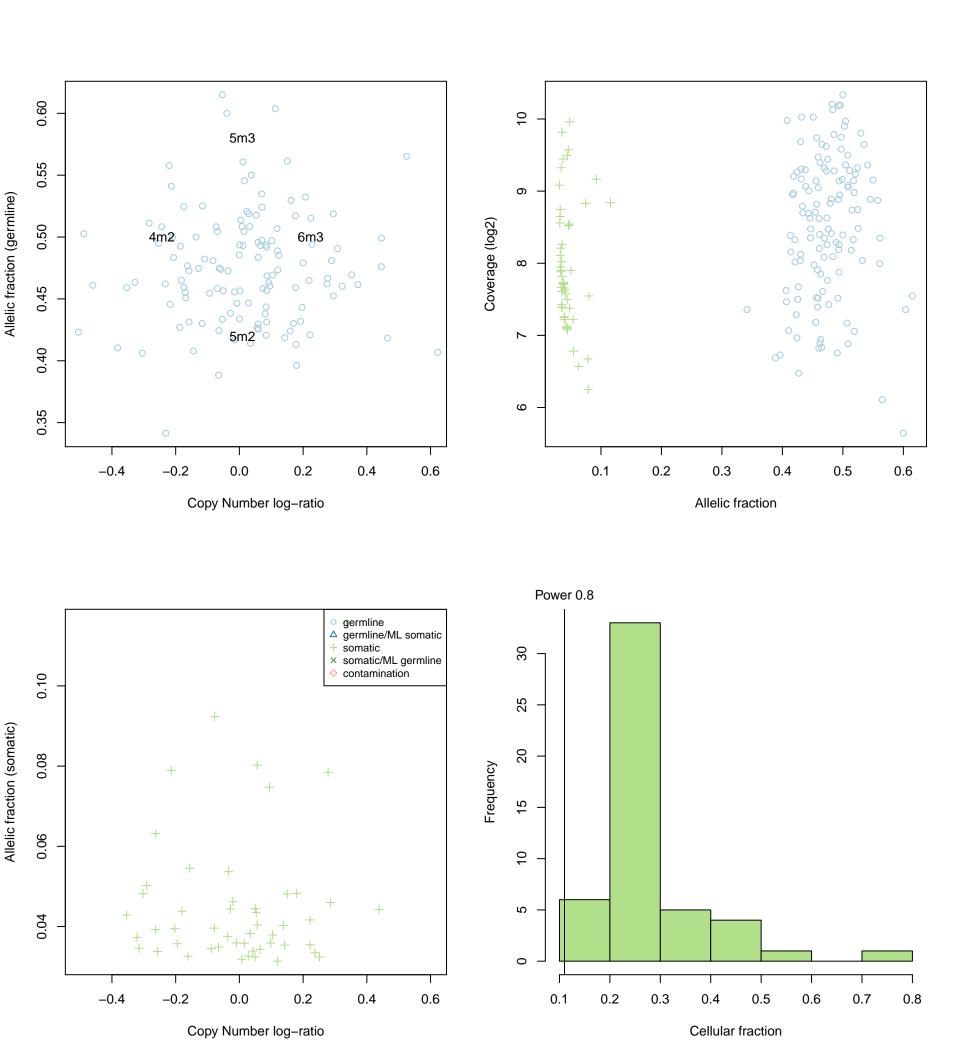
Purity: 0.62 Tumor ploidy: 4.961 2 5 6 3 0.20 Fraction Genome 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



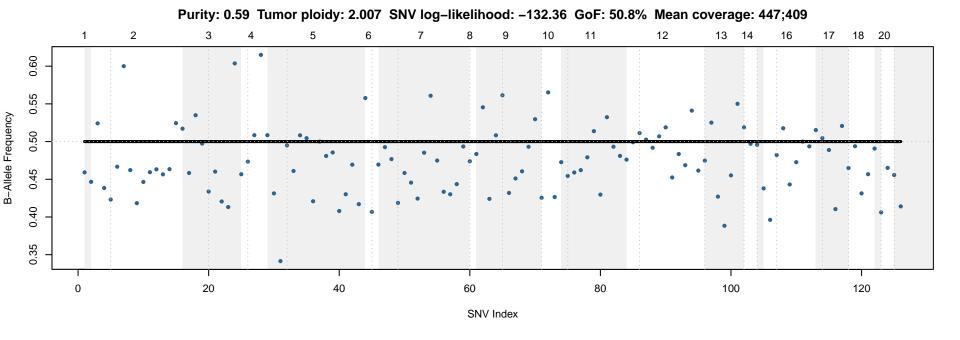
## SCNA-fit log-likelihood: -7275.38



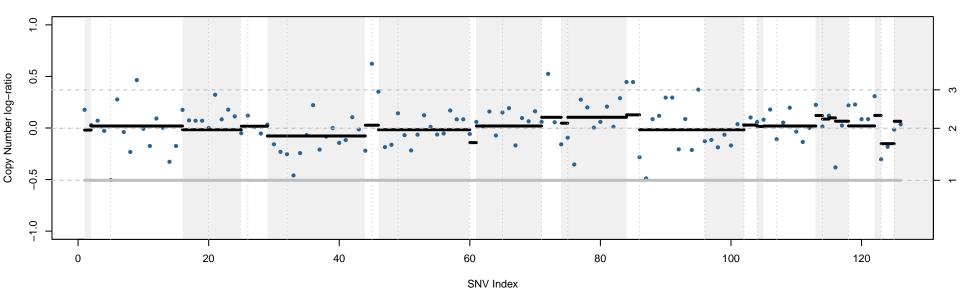


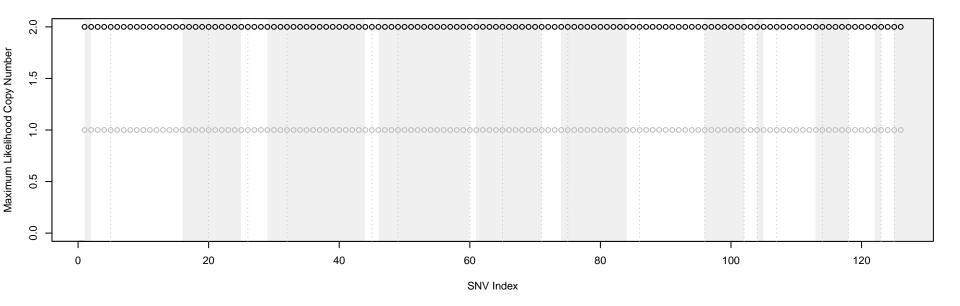


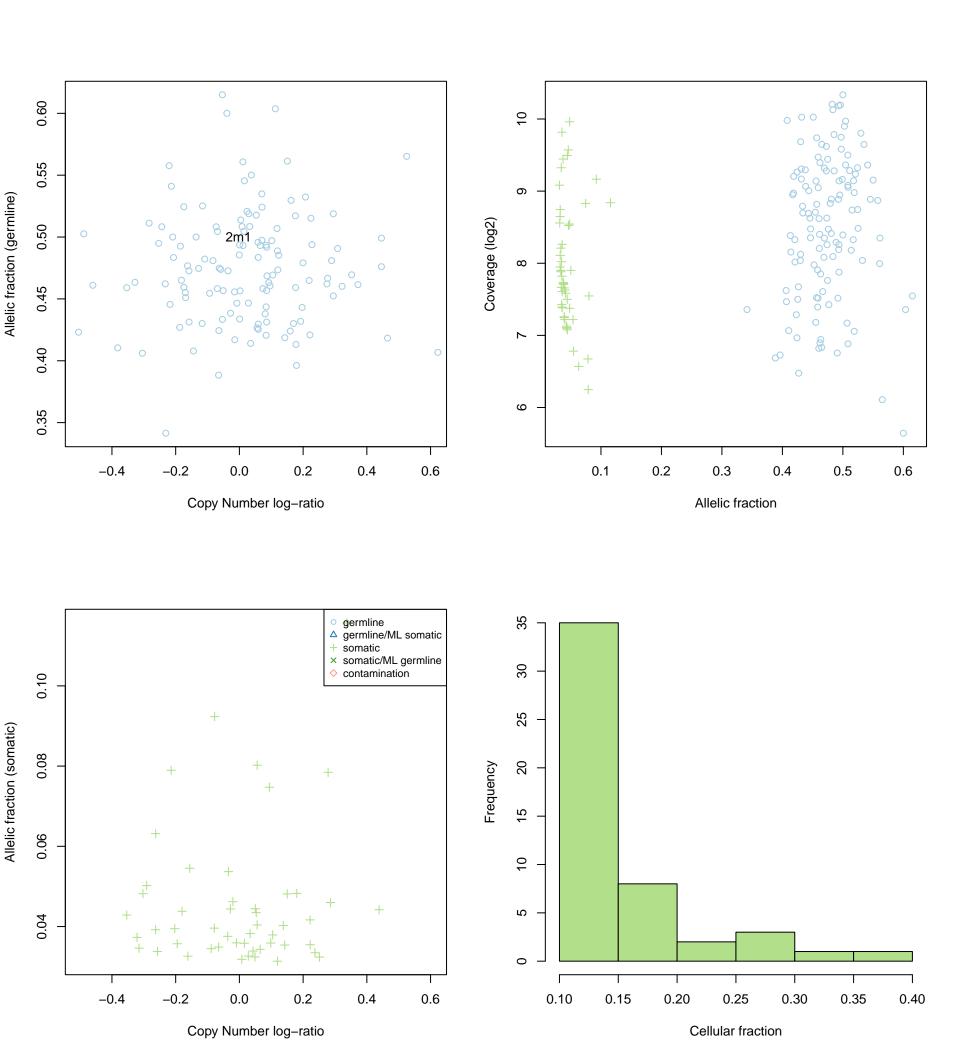
Purity: 0.59 Tumor ploidy: 2.007 2 0.25 0.20 0.15 Fraction Genome 0.10 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



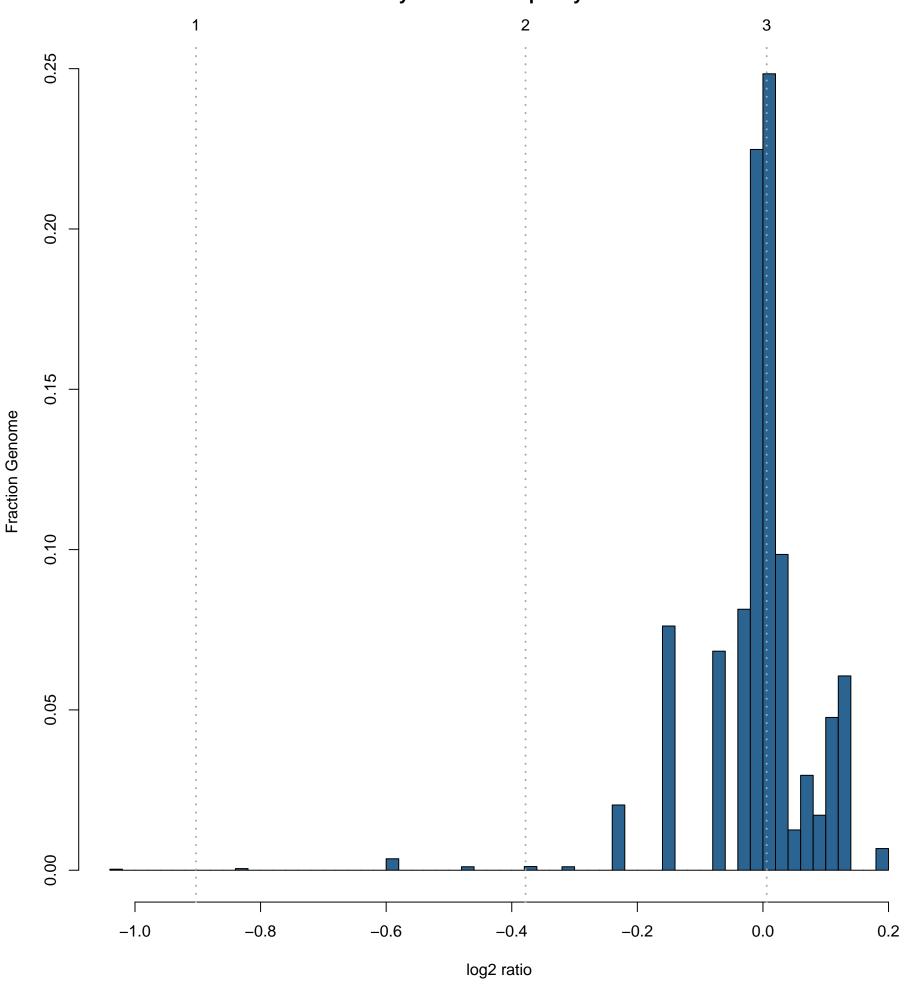
## SCNA-fit log-likelihood: -7412.74

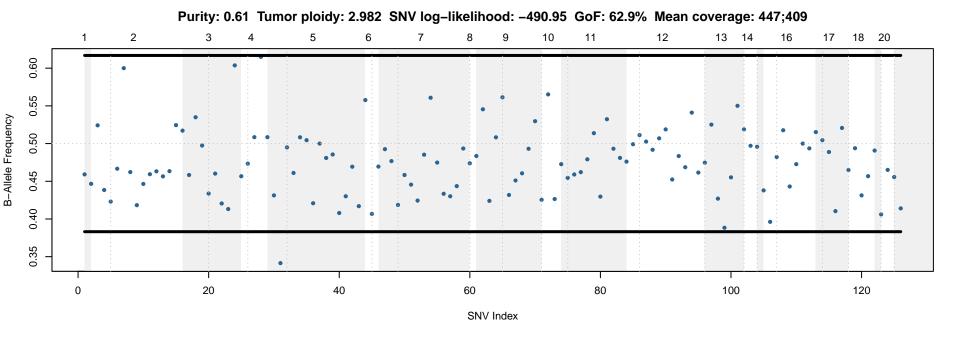






Purity: 0.61 Tumor ploidy: 2.982





## SCNA-fit log-likelihood: -7377.51

