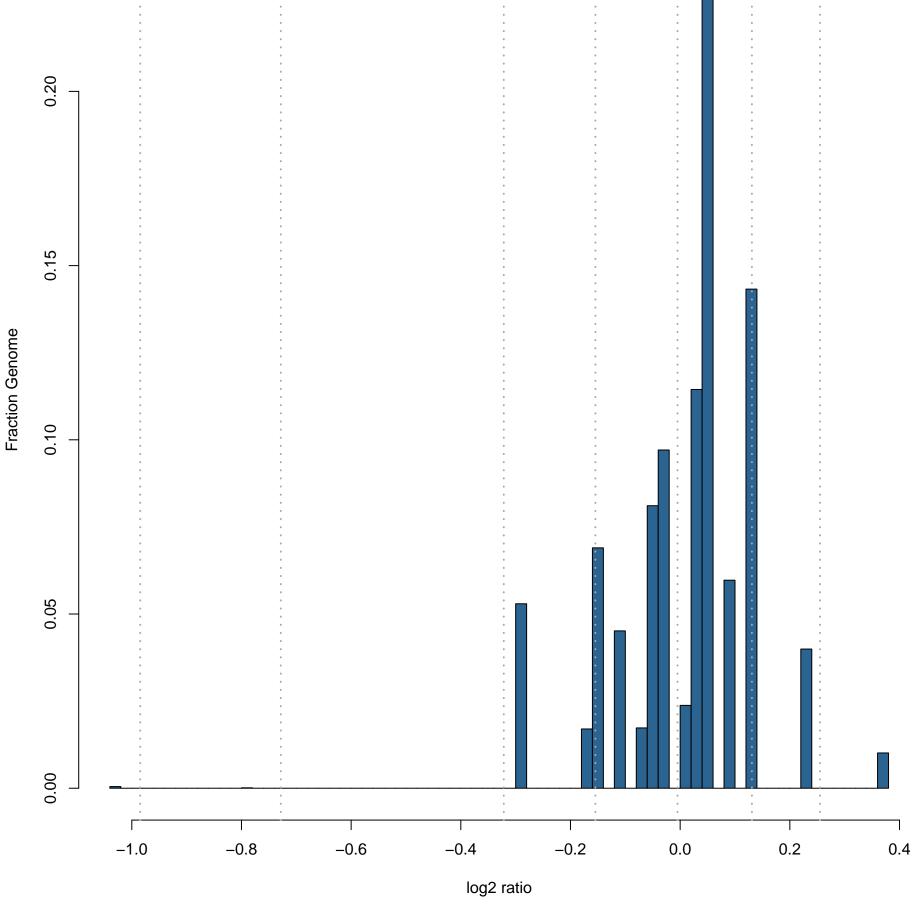
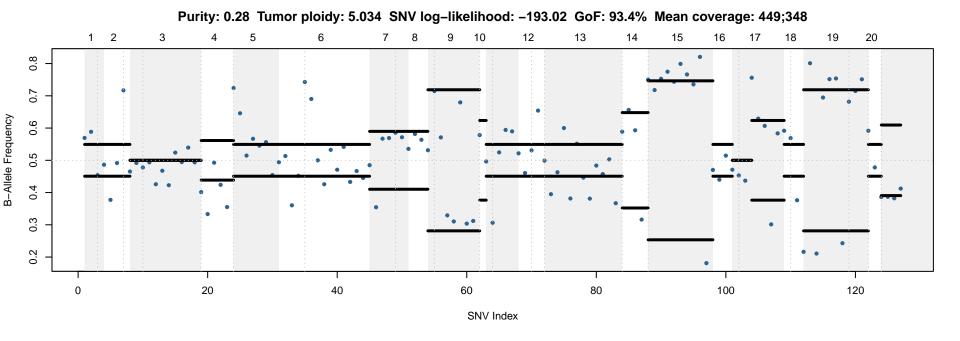
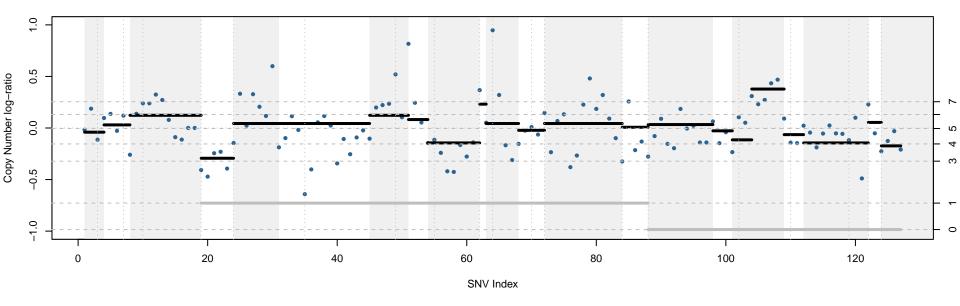
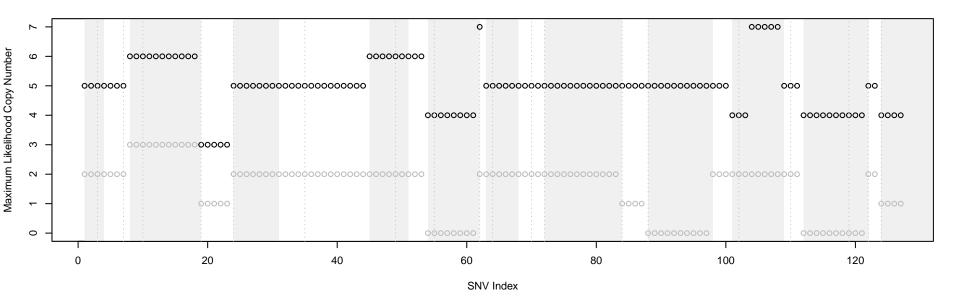
Purity: 0.28 Tumor ploidy: 5.034 

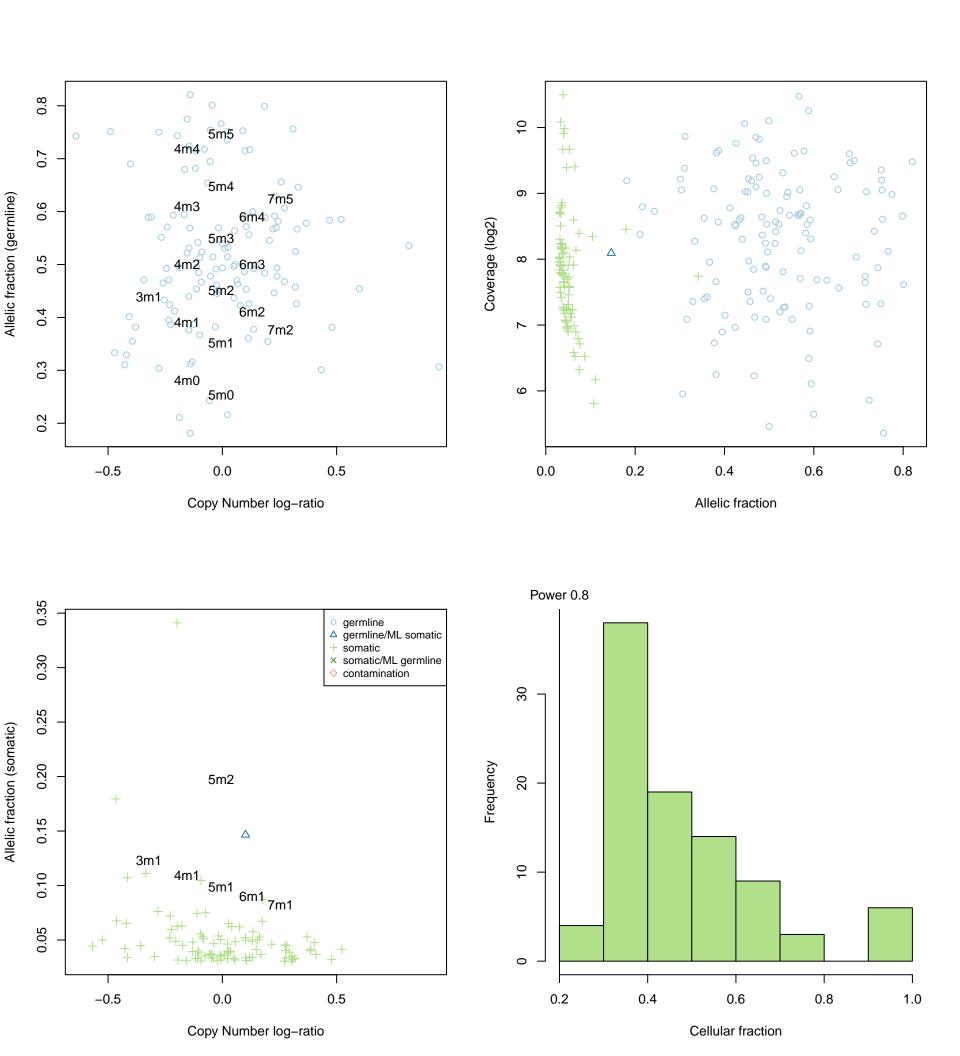




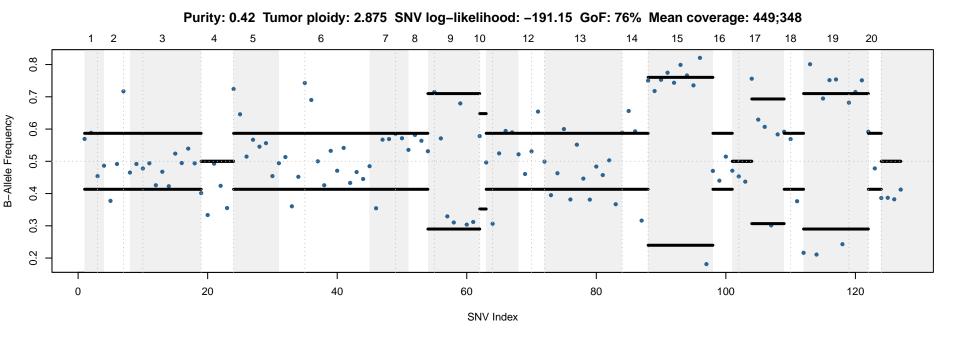
## SCNA-fit log-likelihood: -11100.21



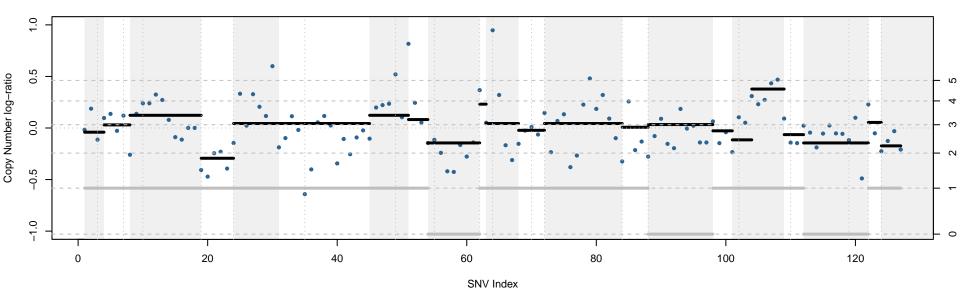


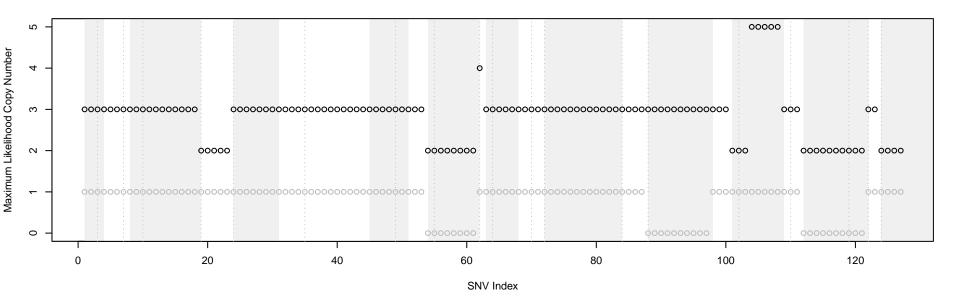


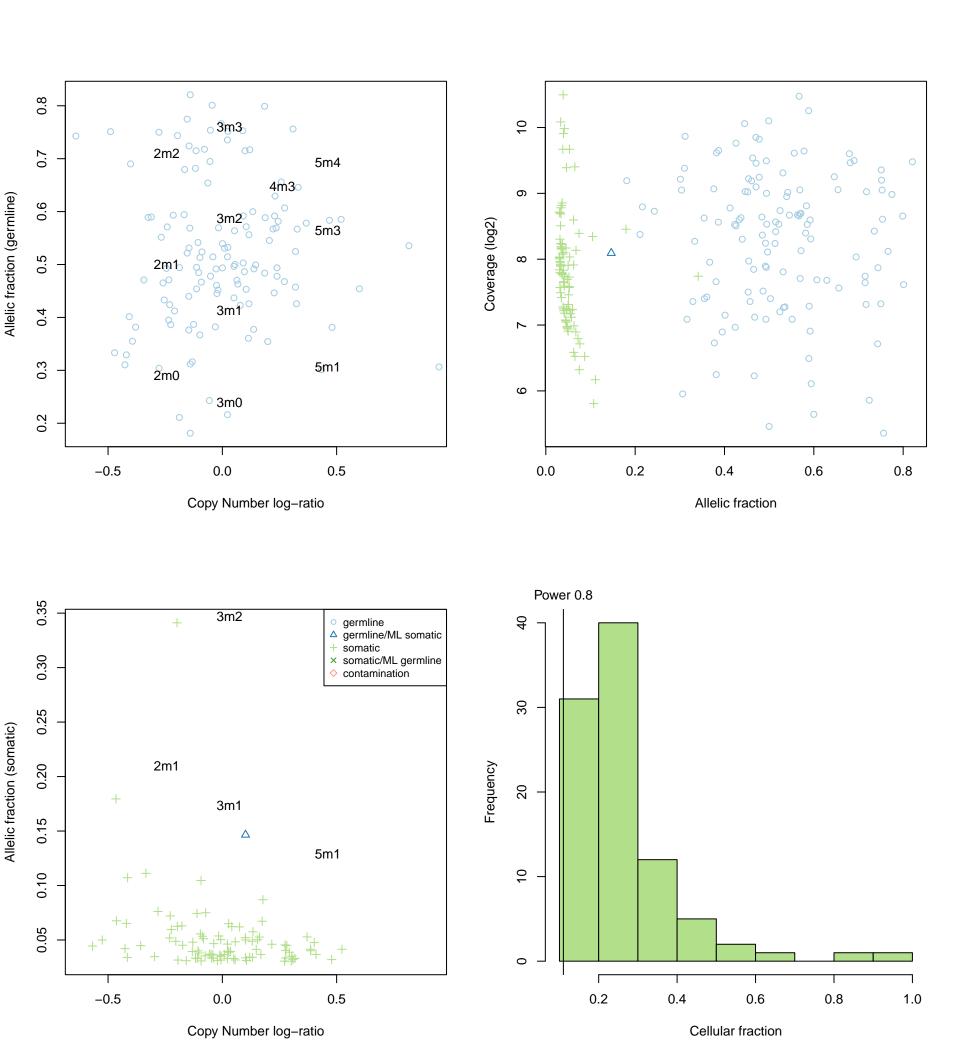
Purity: 0.42 Tumor ploidy: 2.875 3 0 Fraction Genome 0.10 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 0.4 log2 ratio



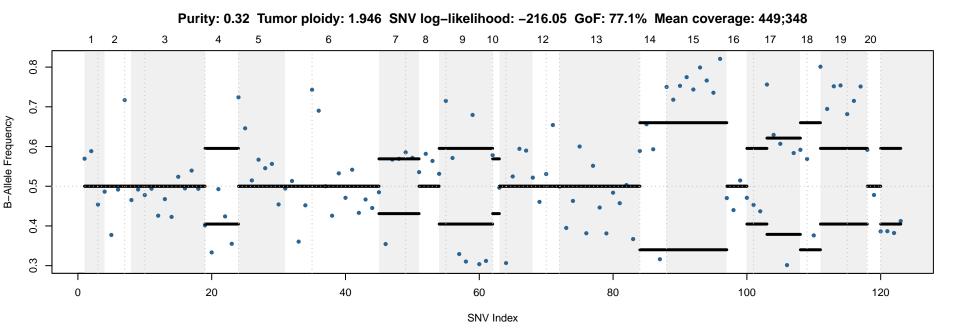
## SCNA-fit log-likelihood: -11198.08



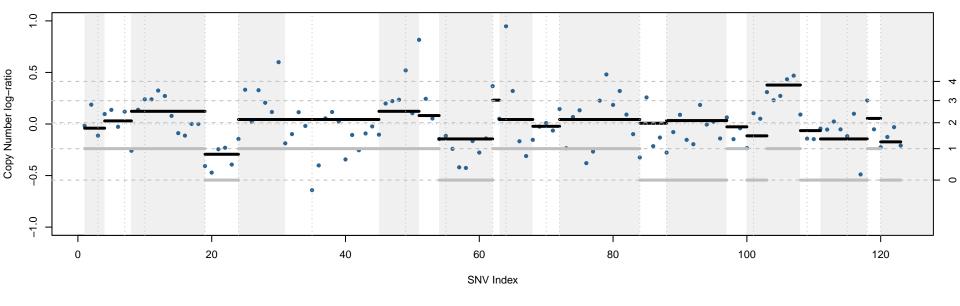


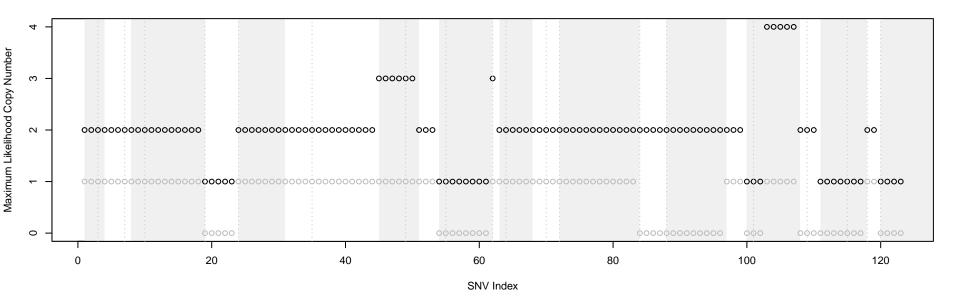


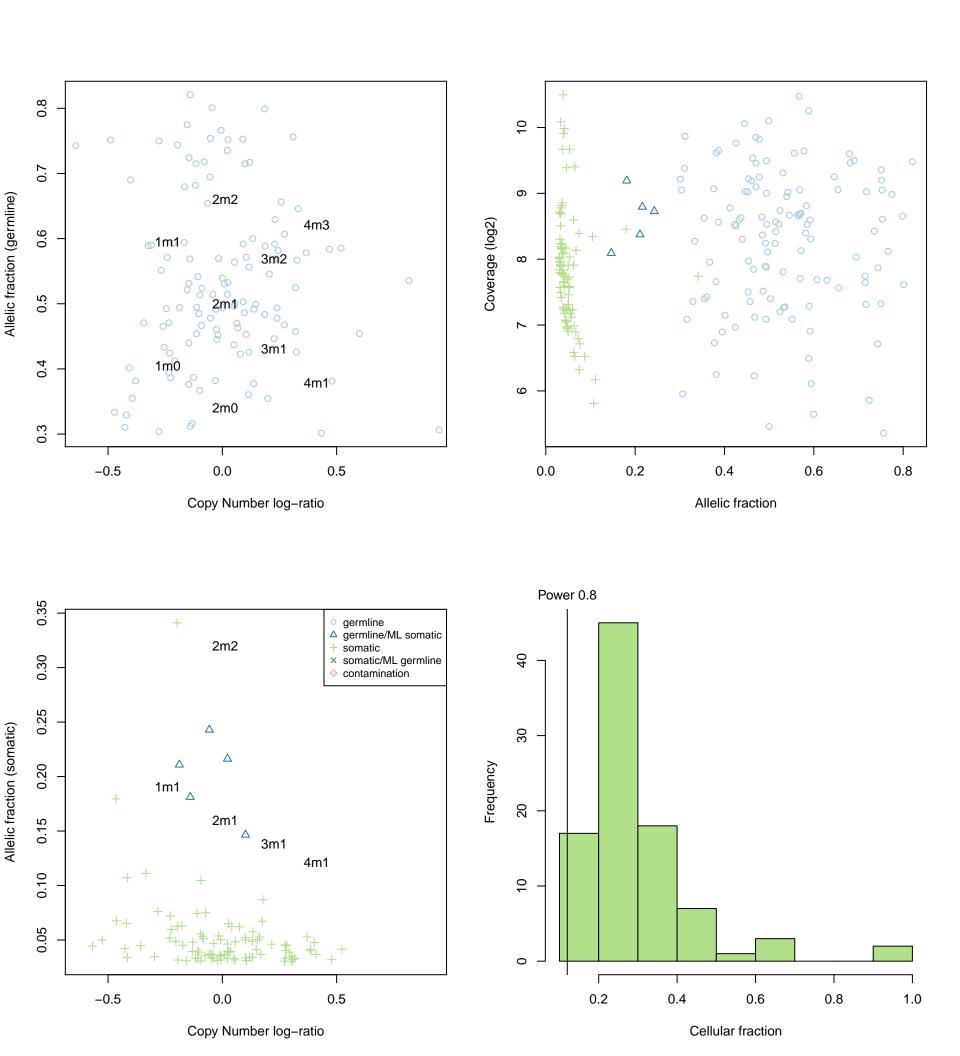
Purity: 0.32 Tumor ploidy: 1.946 2 3 Fraction Genome 0.02 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 0.4 log2 ratio



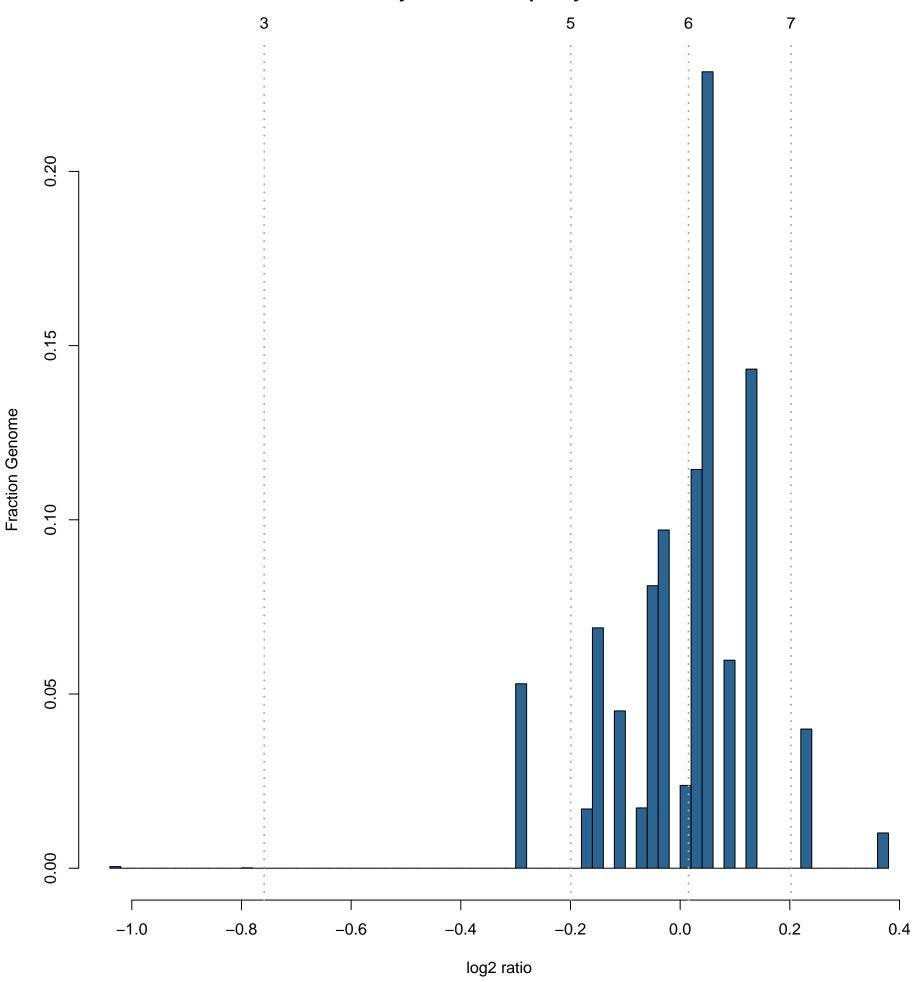
SCNA-fit log-likelihood: -11184.52

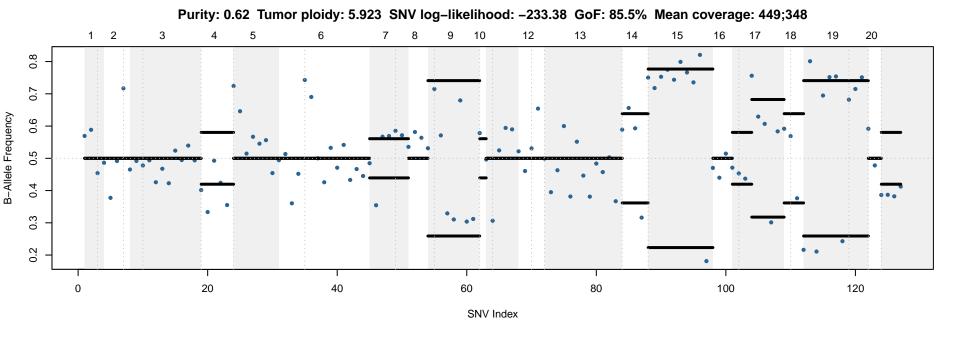




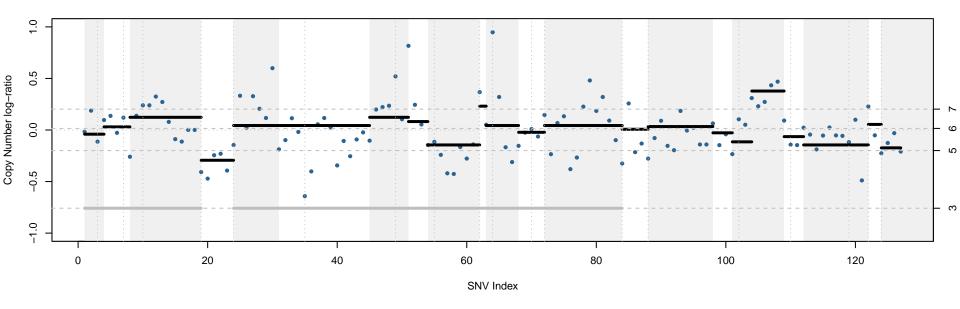


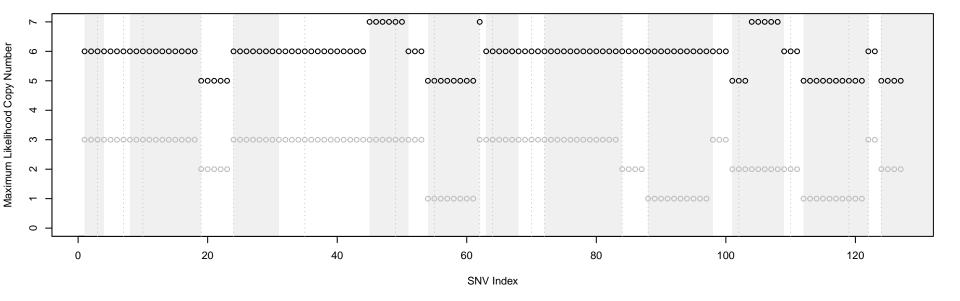
Purity: 0.62 Tumor ploidy: 5.923

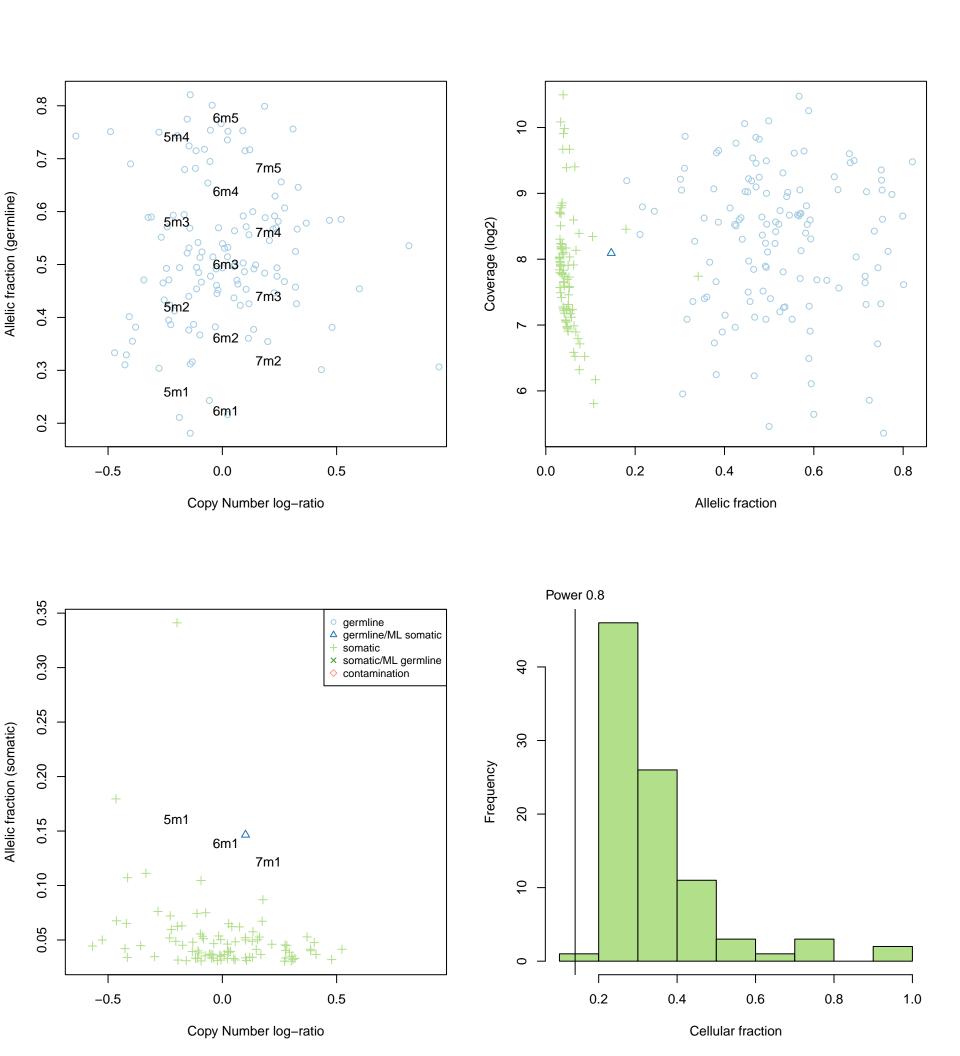




## SCNA-fit log-likelihood: -11167.33







Purity: 0.39 Tumor ploidy: 5.716 2 6 7 0.20 Fraction Genome 0.10 0.05 0.00

-0.4

log2 ratio

-0.2

0.0

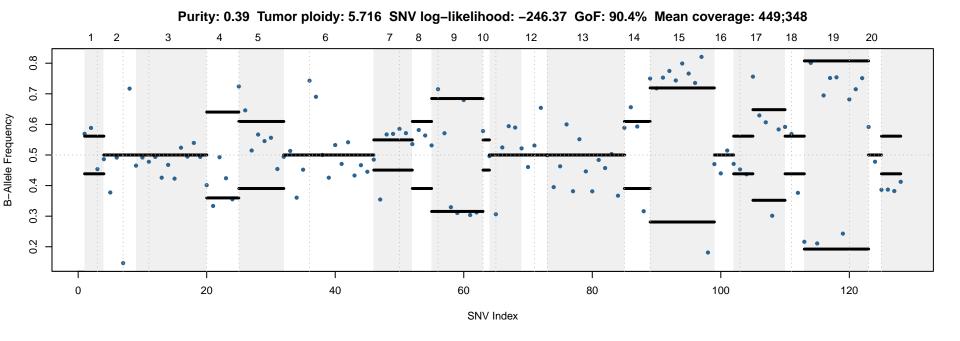
0.2

0.4

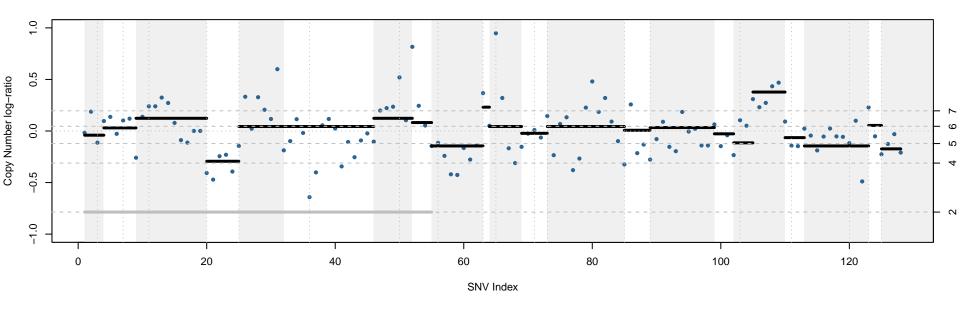
-1.0

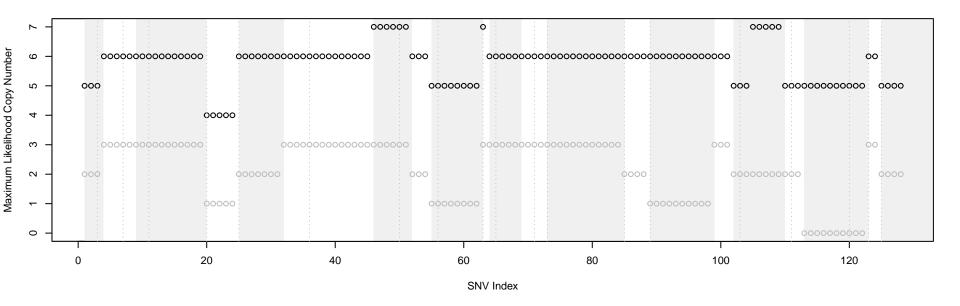
-0.8

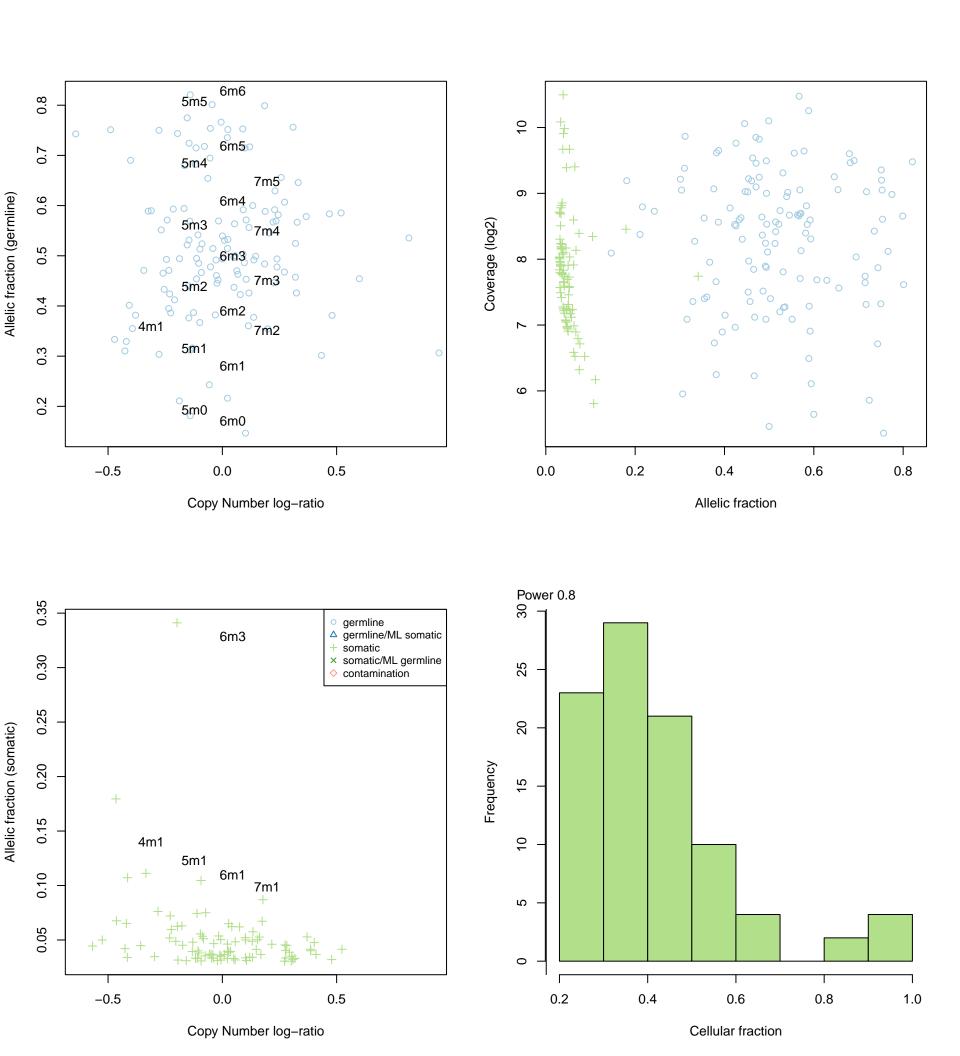
-0.6



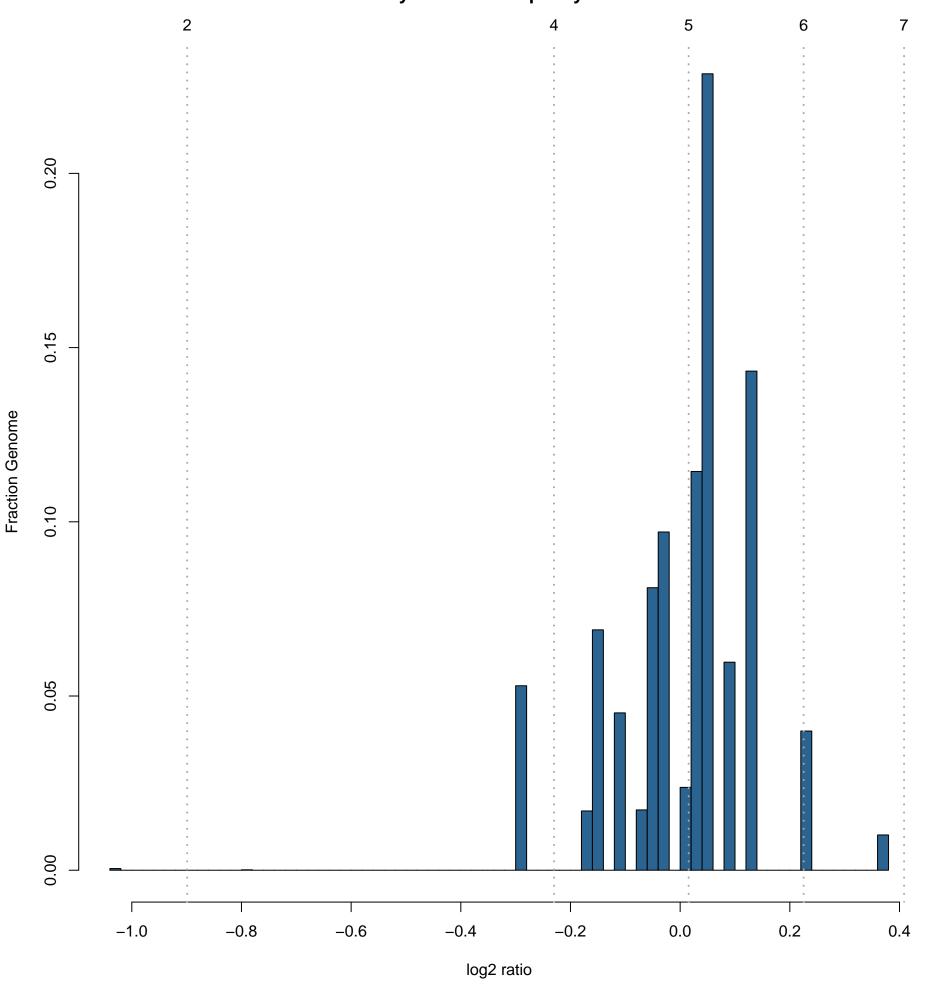
## SCNA-fit log-likelihood: -11132.49

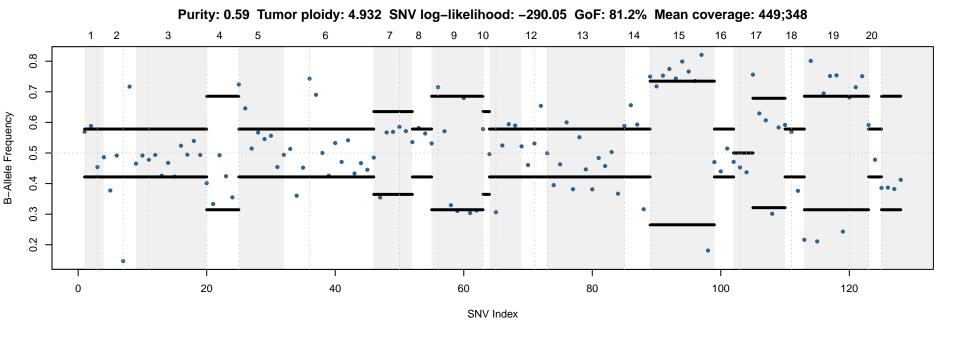




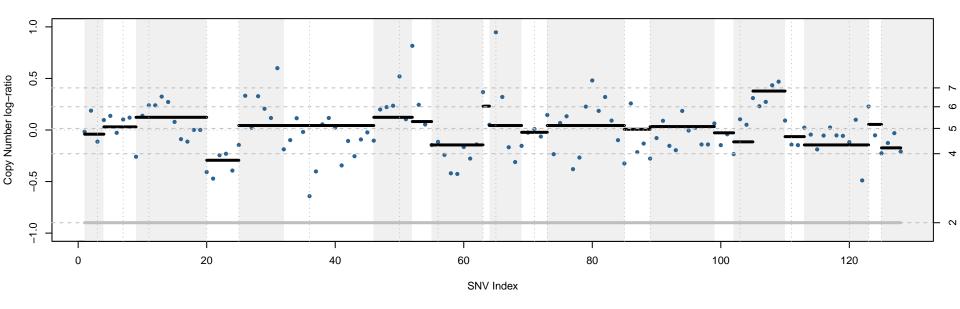


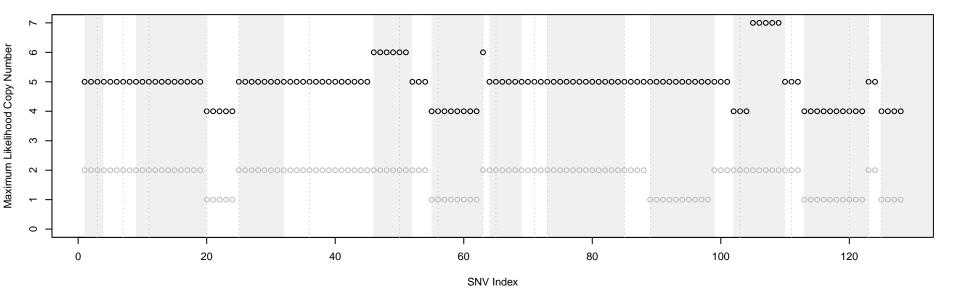
Purity: 0.59 Tumor ploidy: 4.932

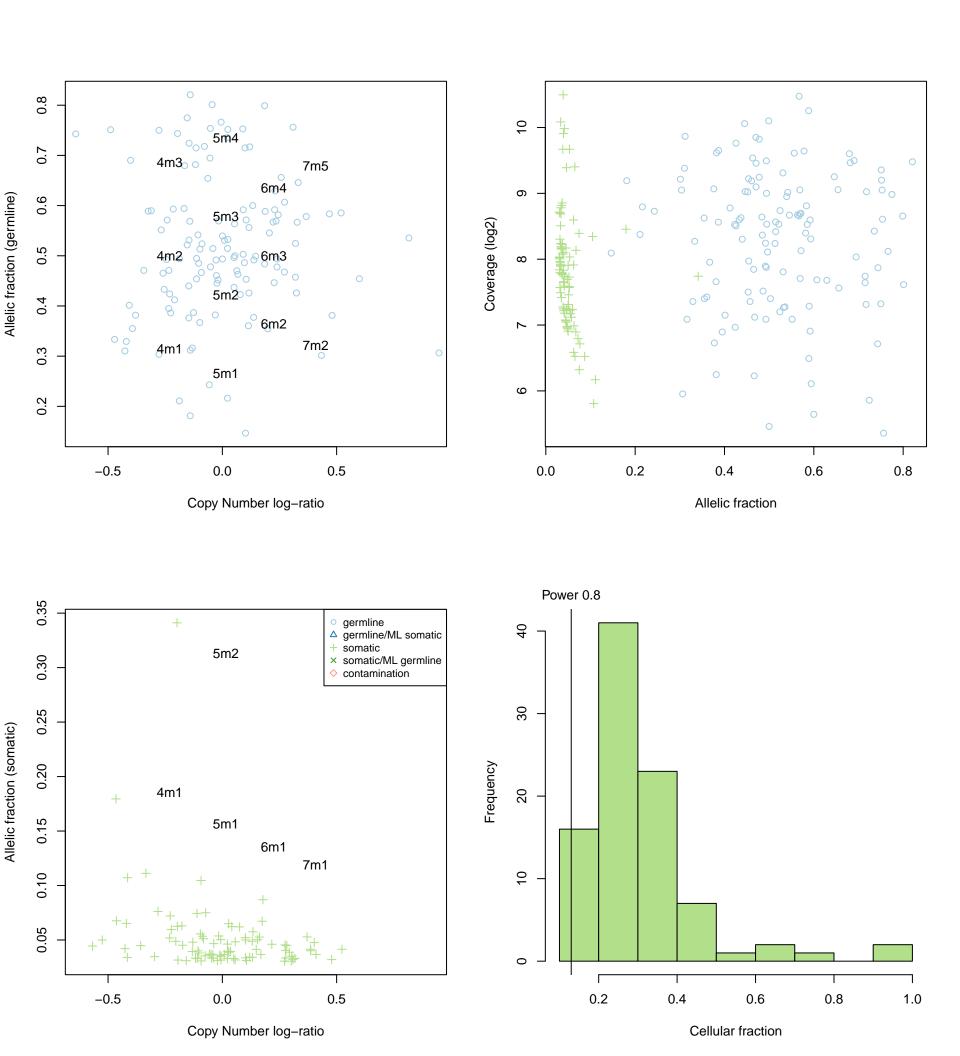




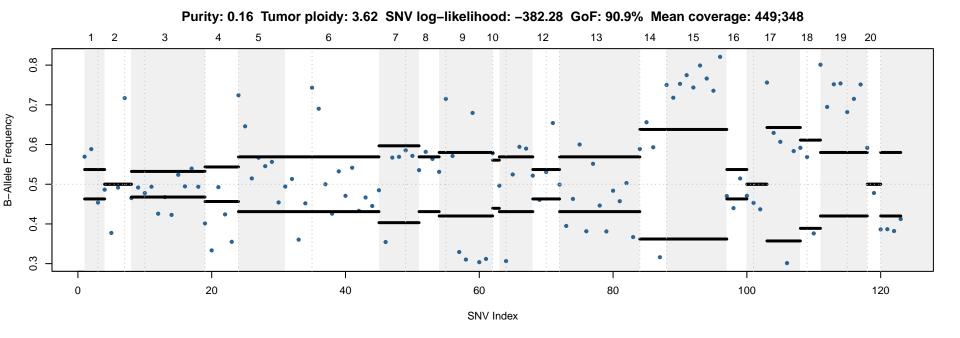
# SCNA-fit log-likelihood: -11175.38



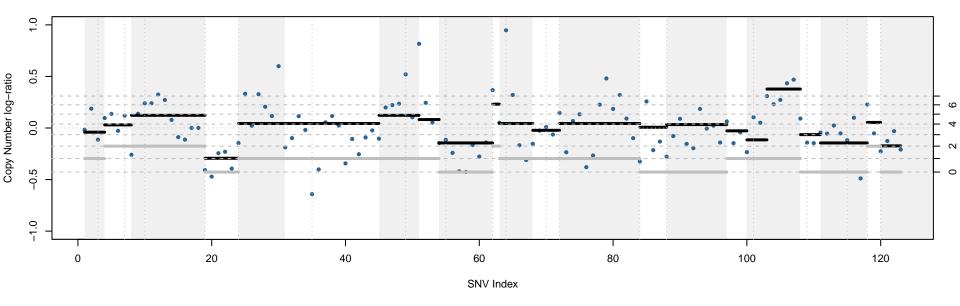


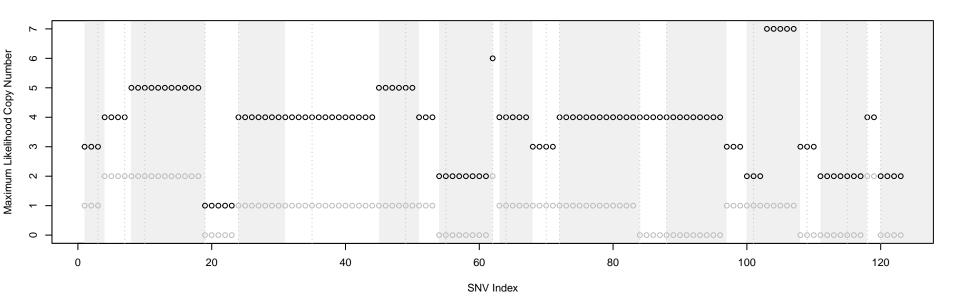


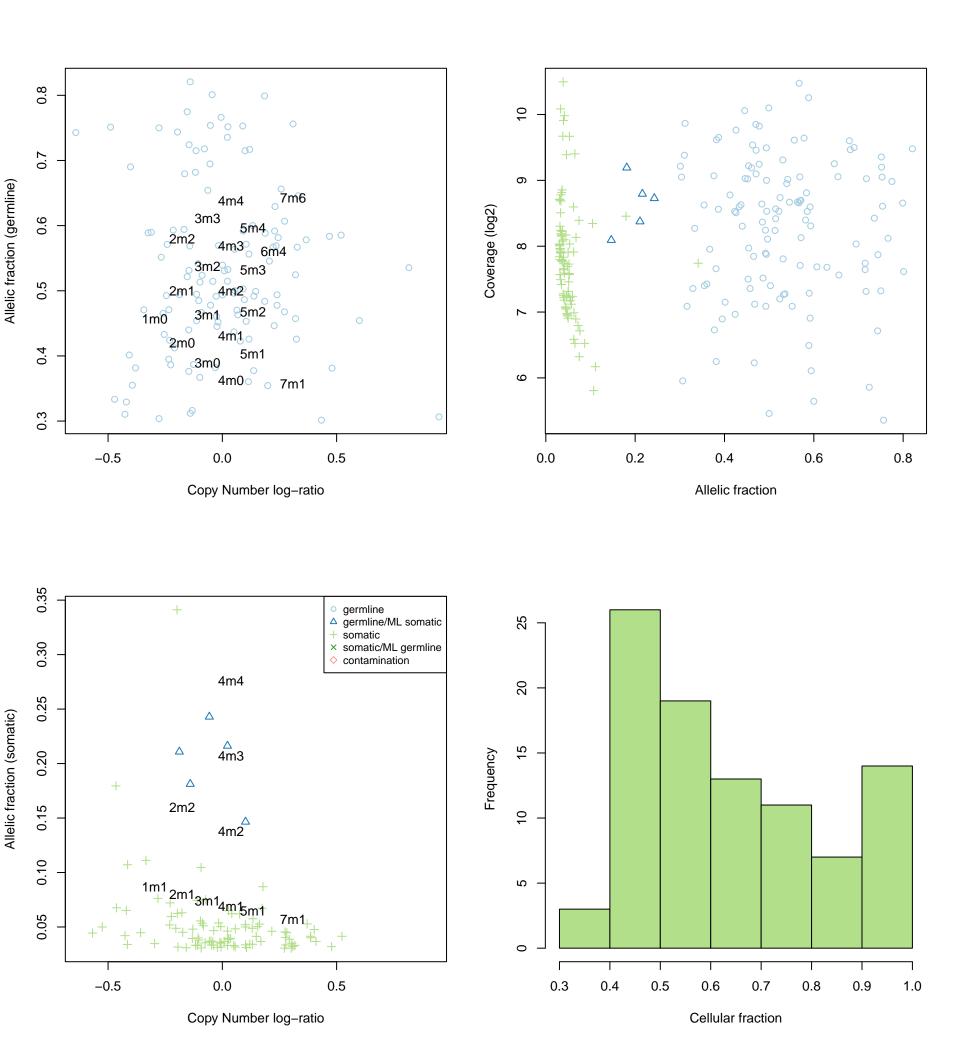
Purity: 0.16 Tumor ploidy: 3.62 2 3 7 5 6 Fraction Genome 0.10 0.05 0.00 -0.8 -0.6 -0.4 -0.2 0.0 0.2 0.4 log2 ratio



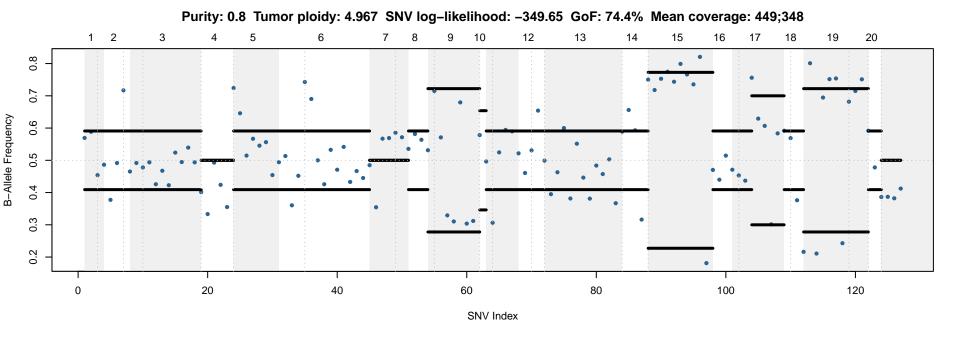
## SCNA-fit log-likelihood: -11078.48



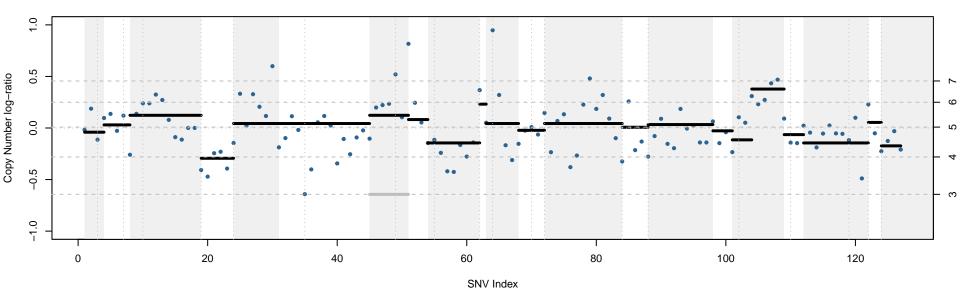


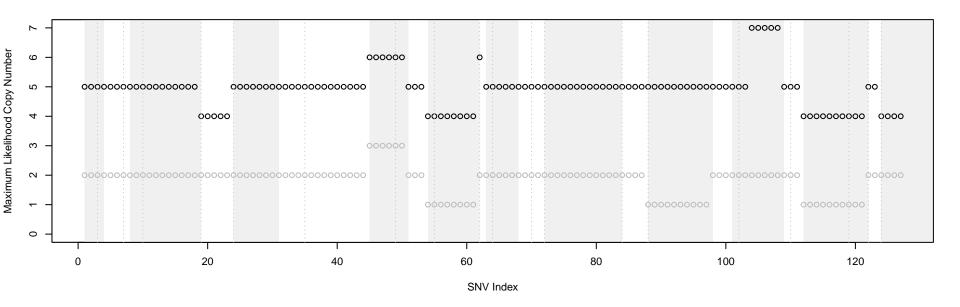


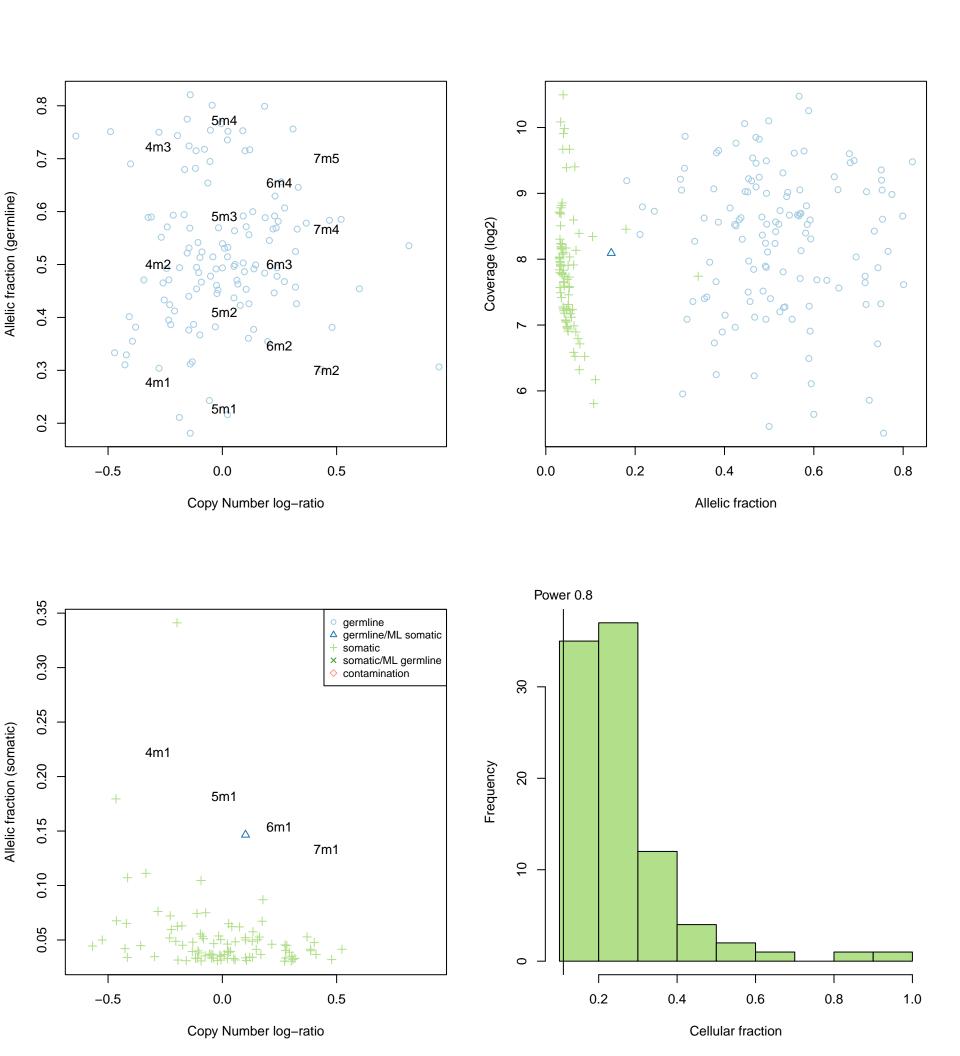
Purity: 0.8 Tumor ploidy: 4.967 6 3 5 Fraction Genome 0.10 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 0.4 log2 ratio



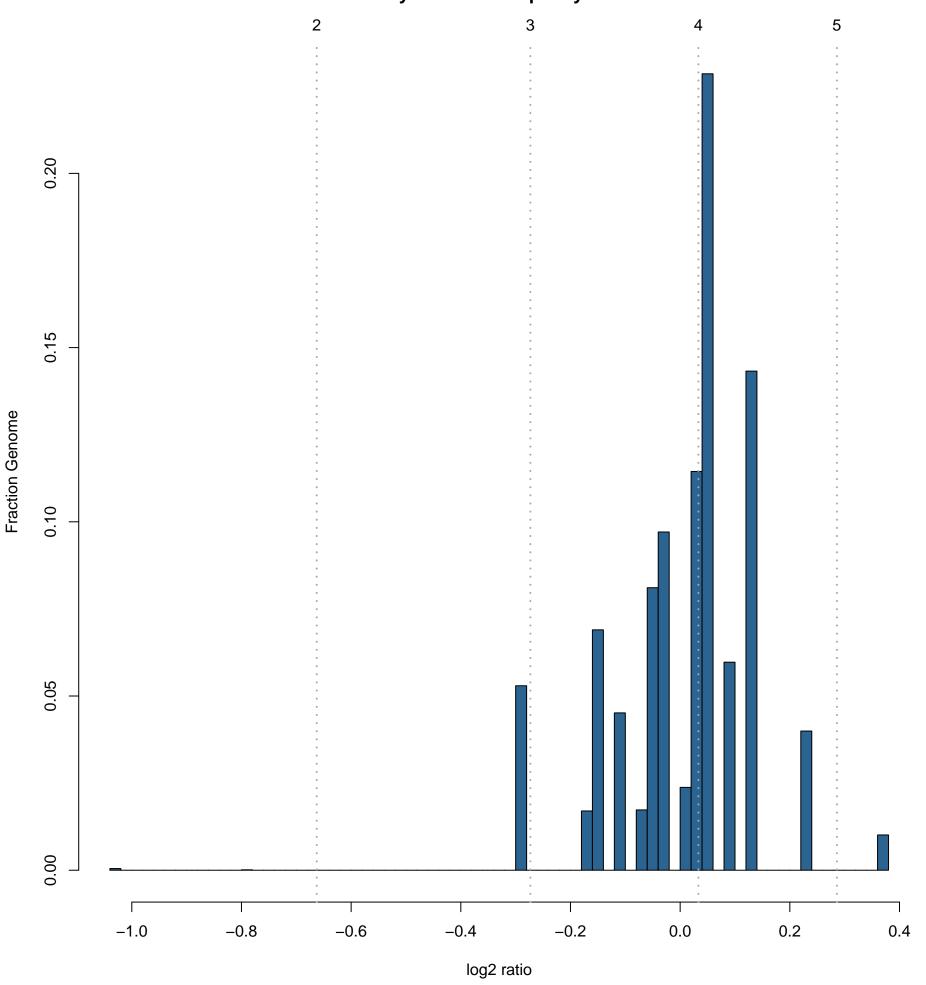
## SCNA-fit log-likelihood: -11220.35

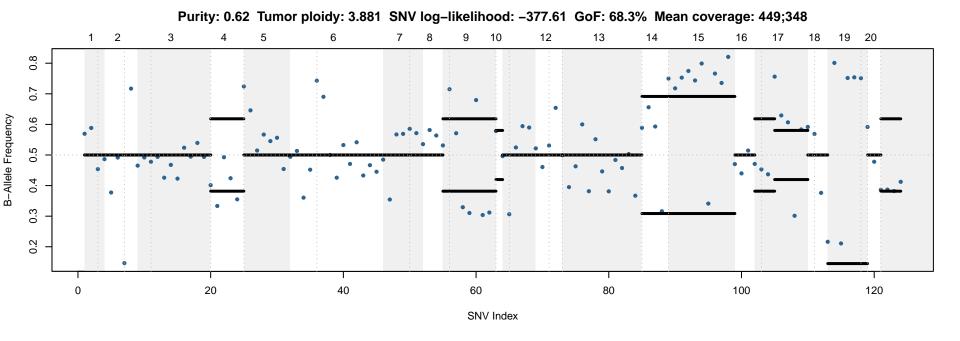




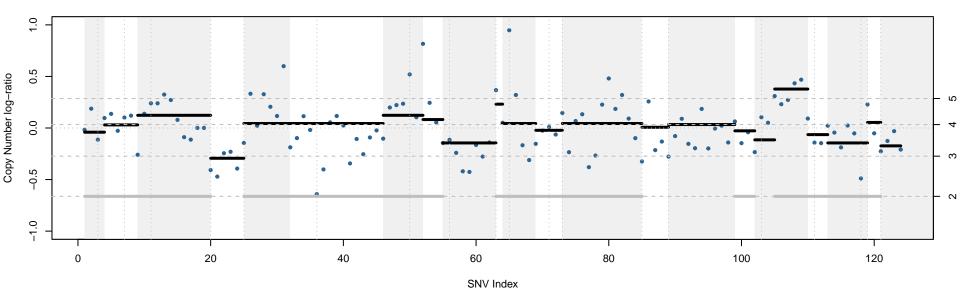


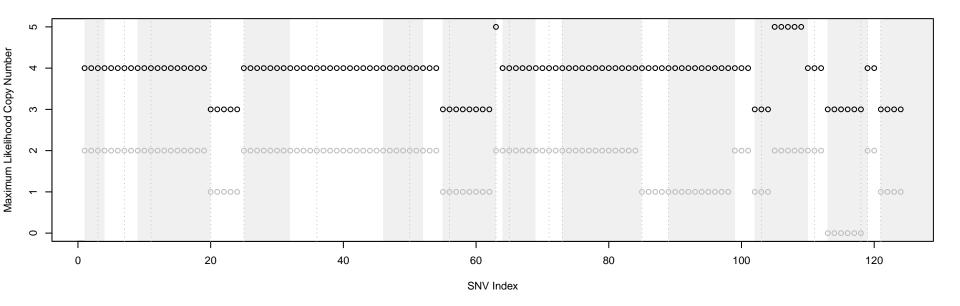
Purity: 0.62 Tumor ploidy: 3.881

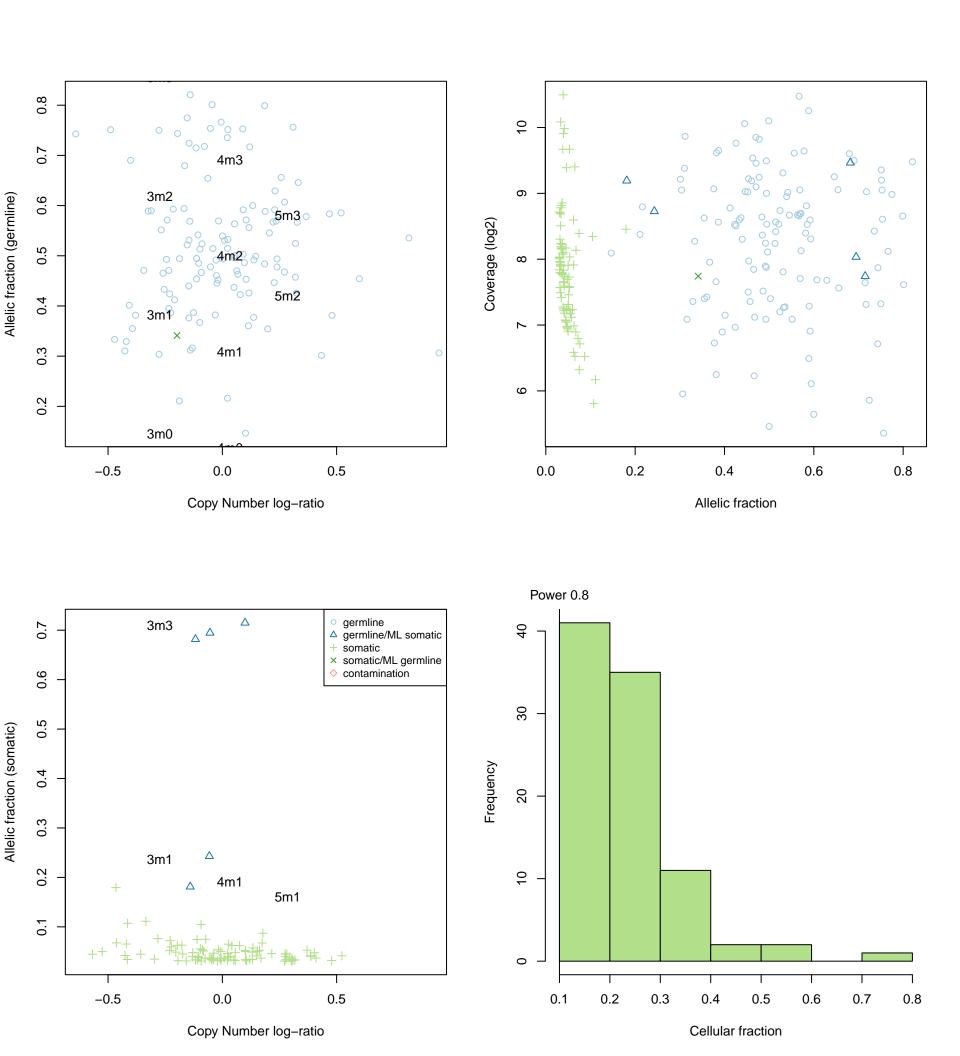




## SCNA-fit log-likelihood: -11224.92

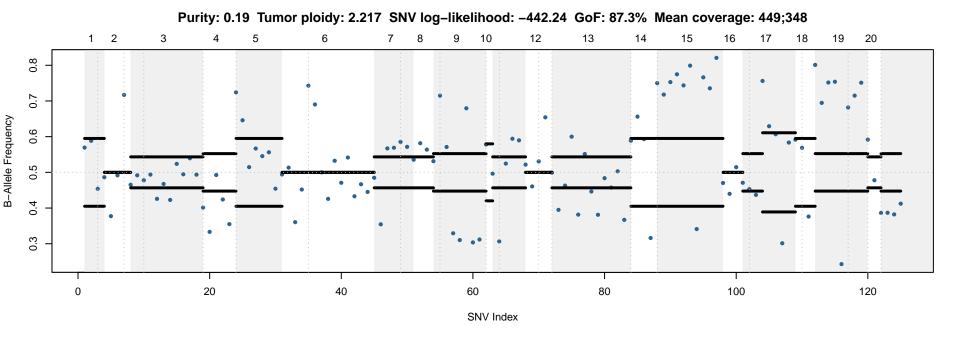




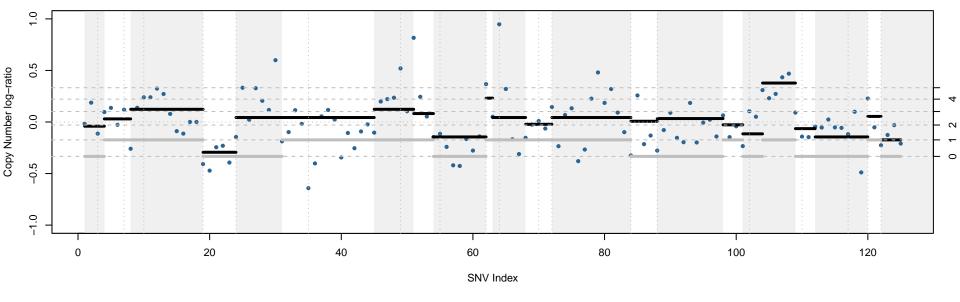


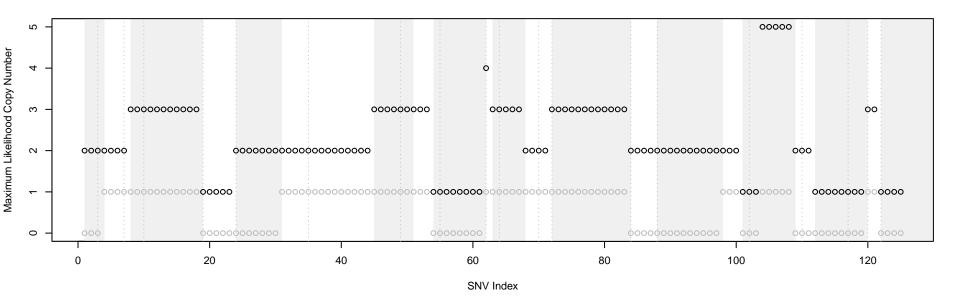
Purity: 0.19 Tumor ploidy: 2.217 3 5 Fraction Genome 0.05 0.00 -0.3 -0.2 -0.1 0.0 0.1 0.2 0.3 0.4

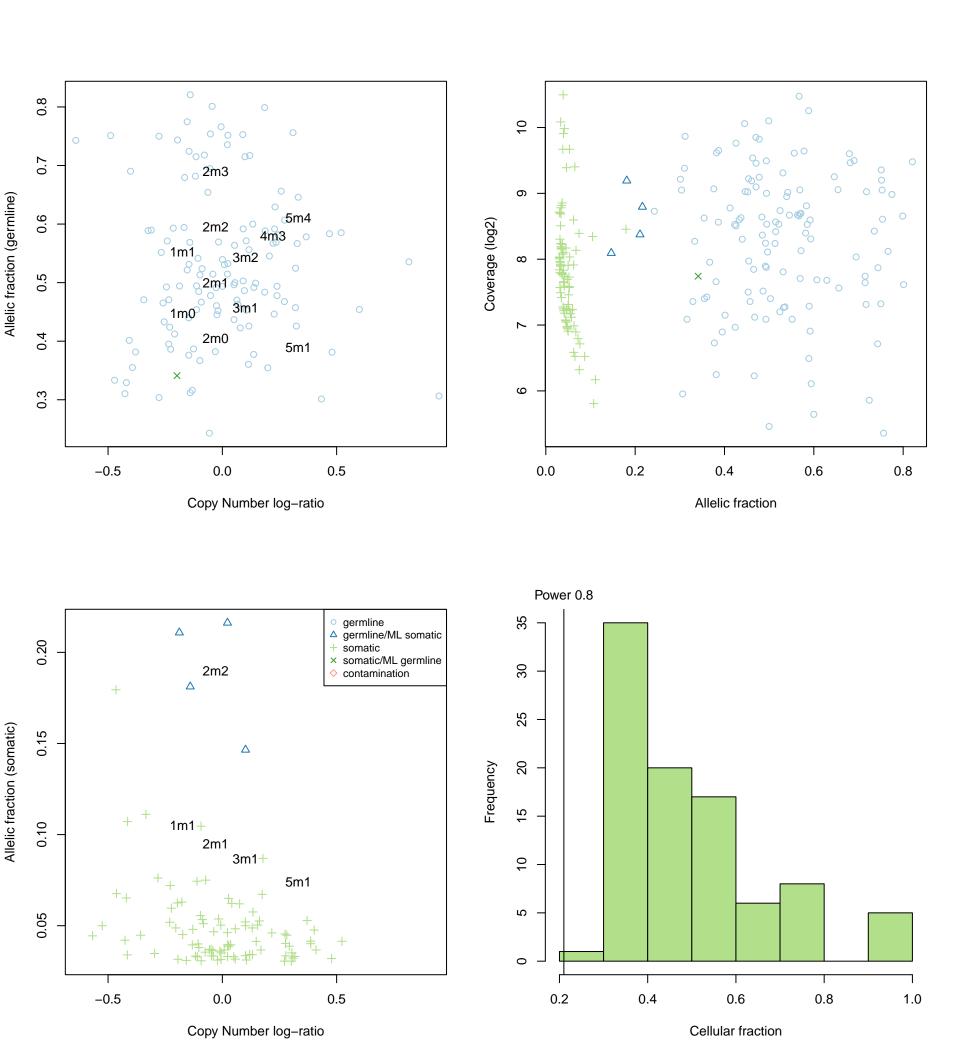
log2 ratio



## SCNA-fit log-likelihood: -11136.72

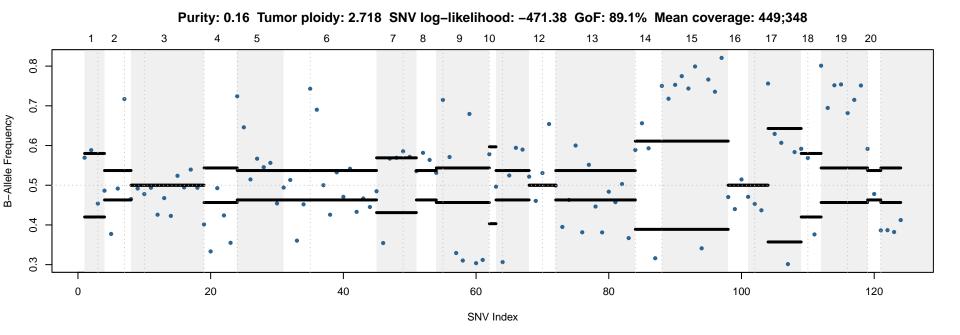




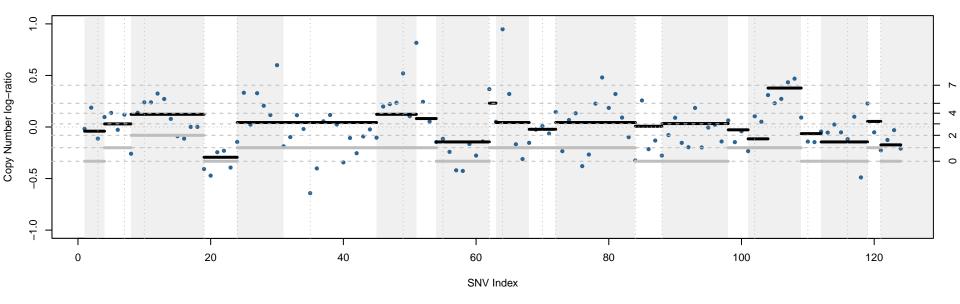


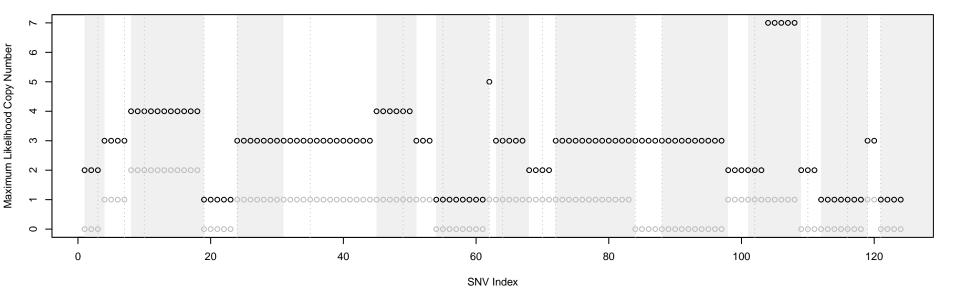
Purity: 0.16 Tumor ploidy: 2.718 2 3 5 0.15 Fraction Genome 0.10 0.05 0.00 -0.3 -0.2 -0.1 0.0 0.1 0.2 0.3 0.4

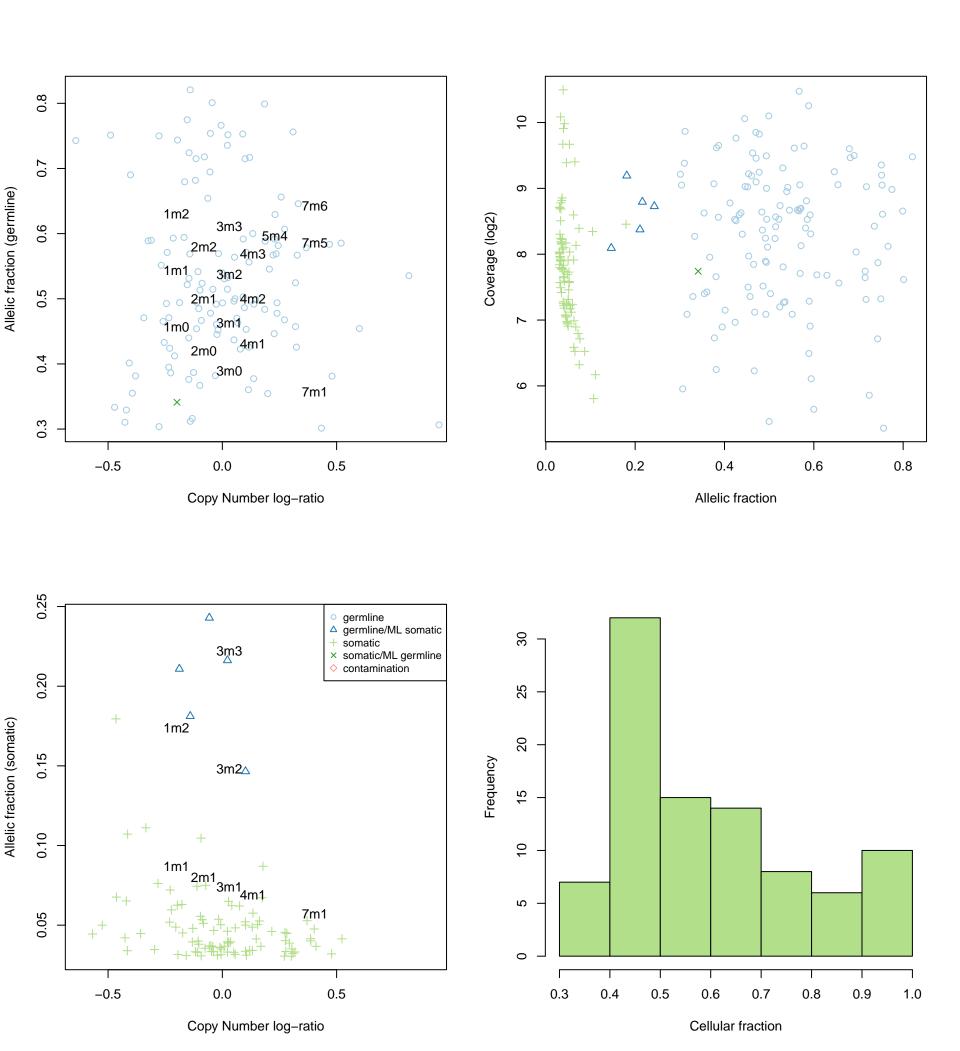
log2 ratio



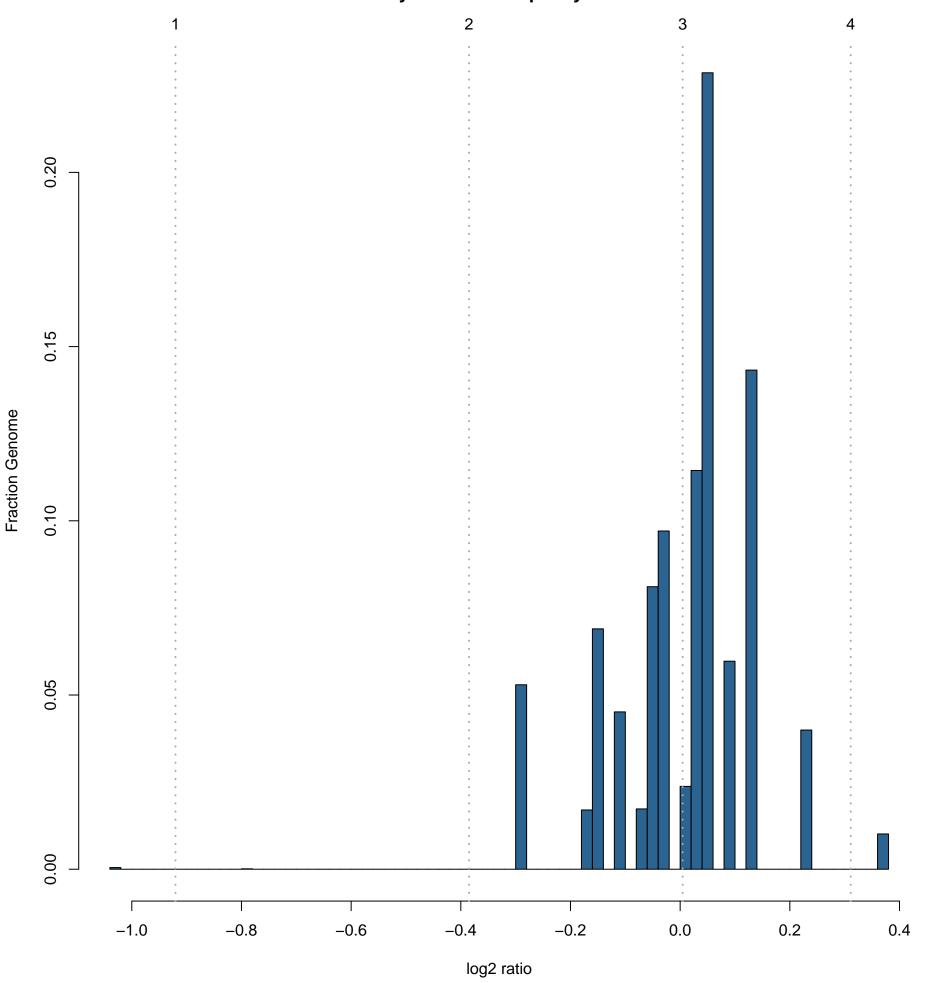
## SCNA-fit log-likelihood: -11108.88

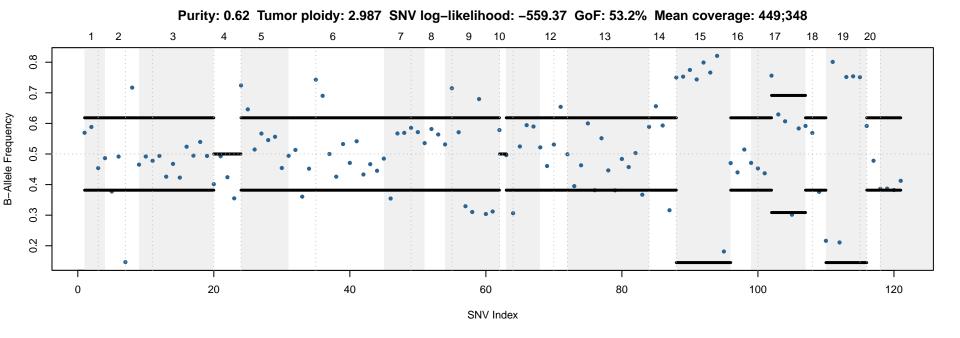




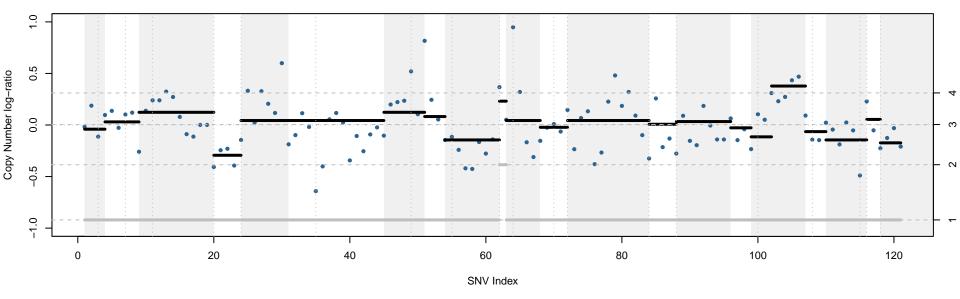


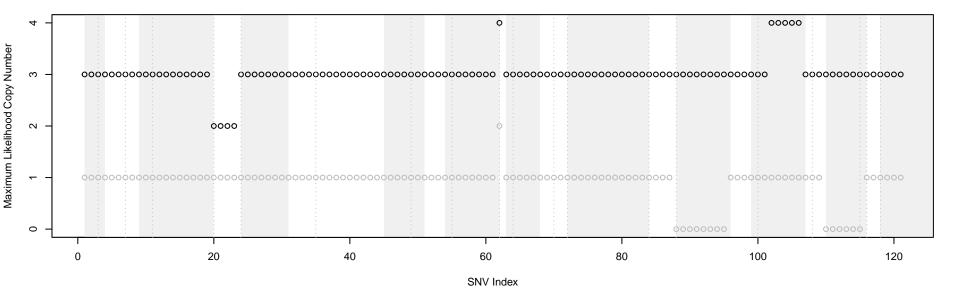
Purity: 0.62 Tumor ploidy: 2.987

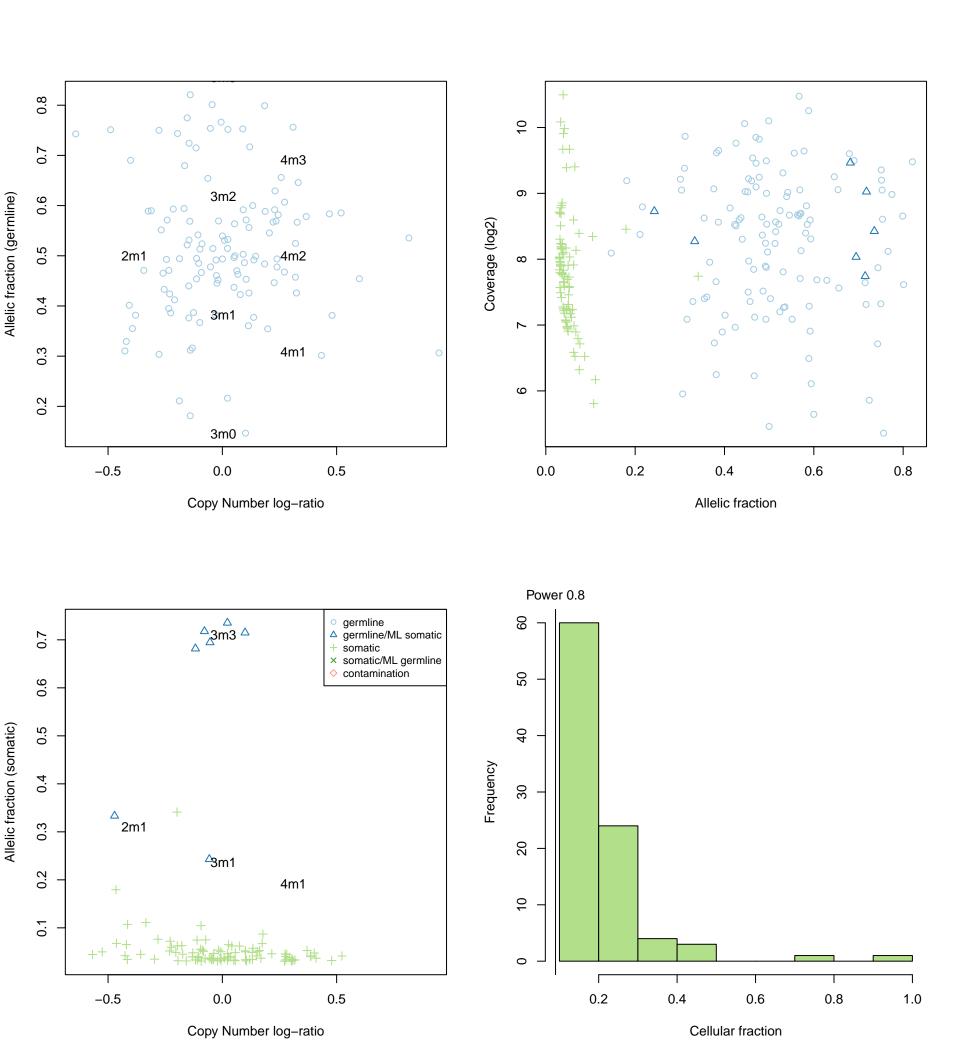




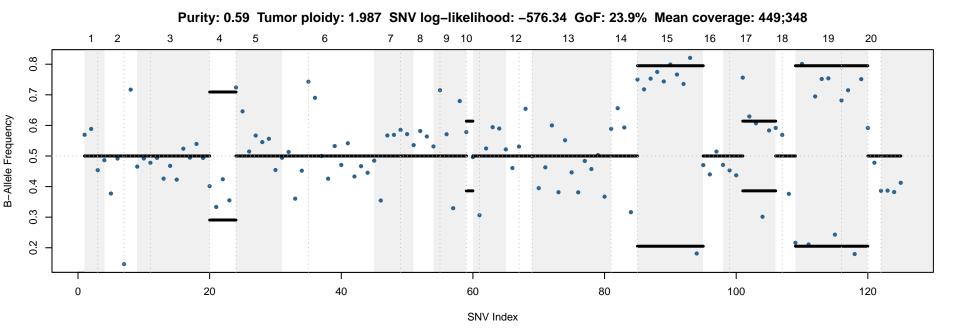
## SCNA-fit log-likelihood: -11295.43







Purity: 0.59 Tumor ploidy: 1.987 2 3 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 0.4 log2 ratio



SCNA-fit log-likelihood: -11380.87

