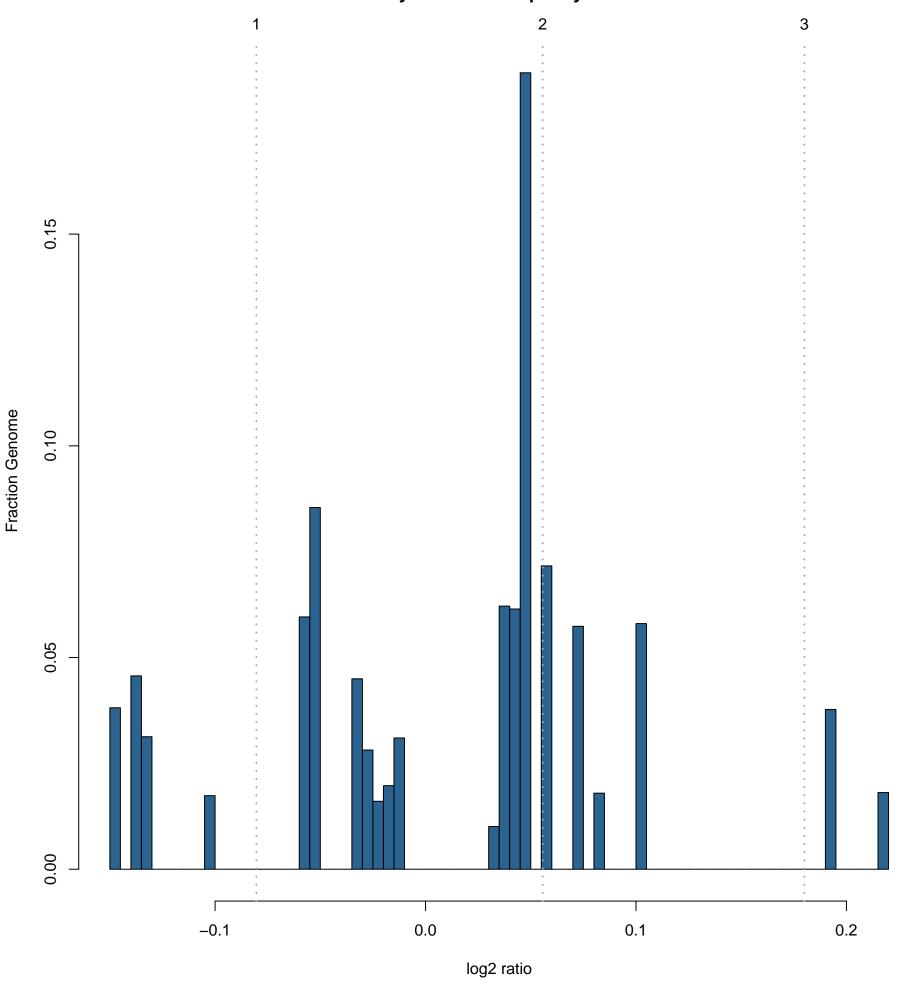
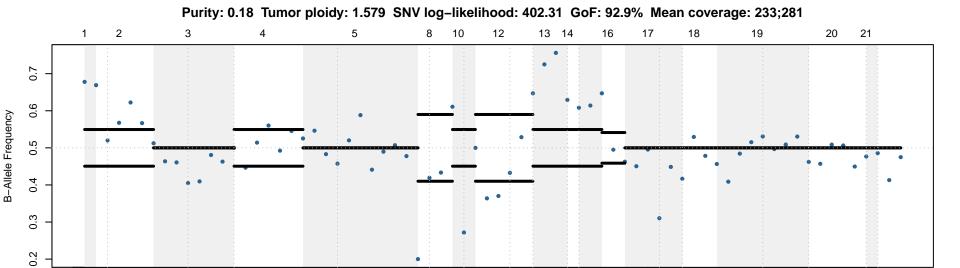
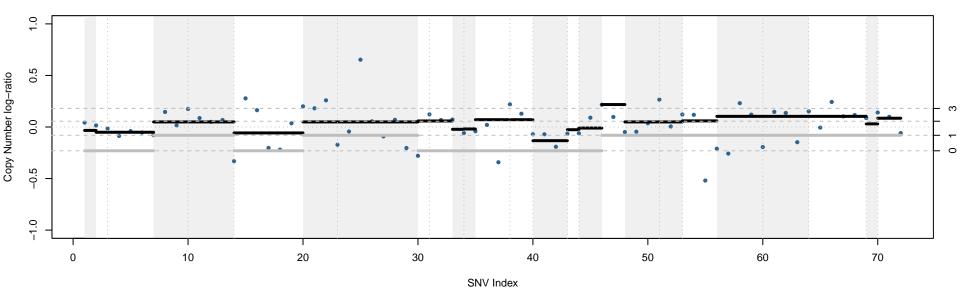
Purity: 0.18 Tumor ploidy: 1.579

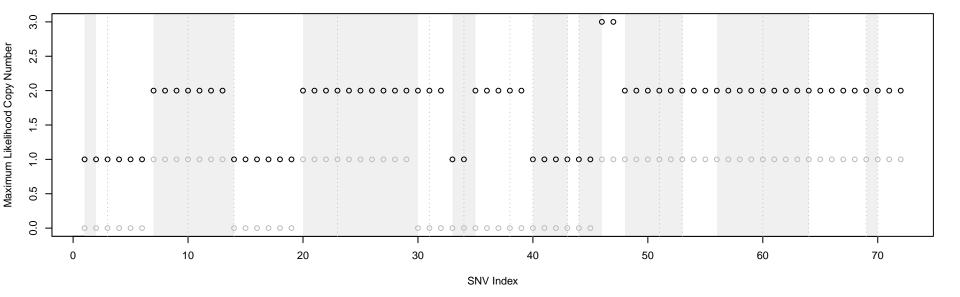


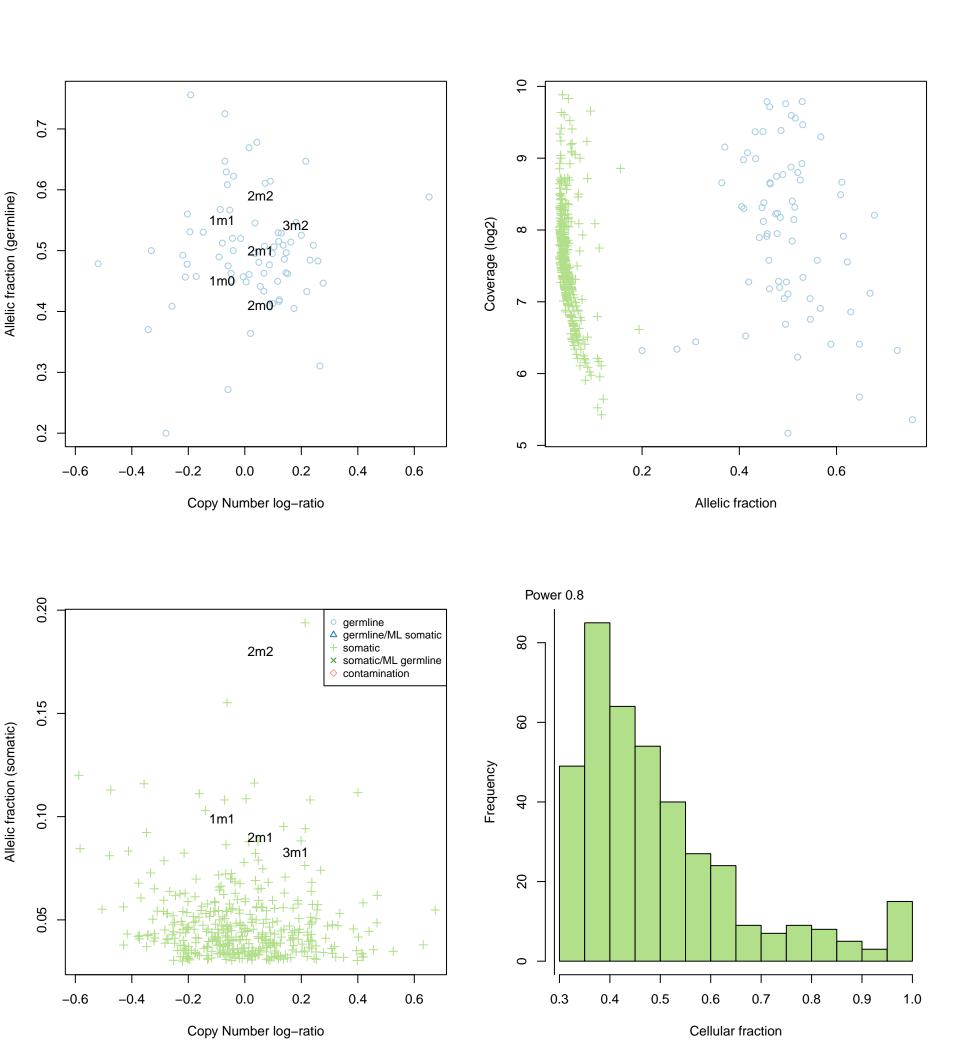


## SCNA-fit log-likelihood: -5119.38

SNV Index

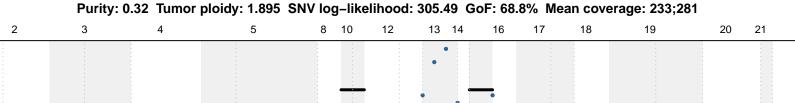


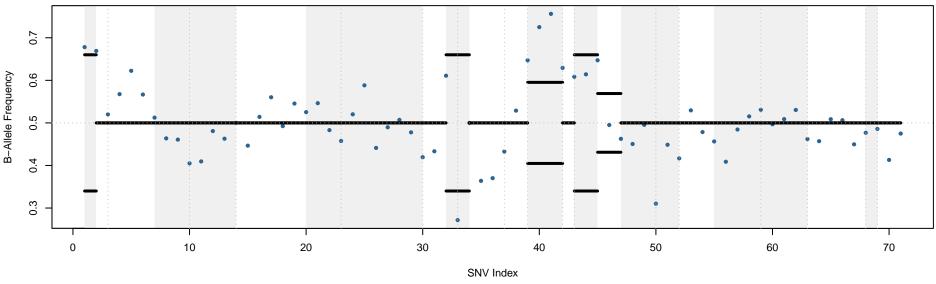




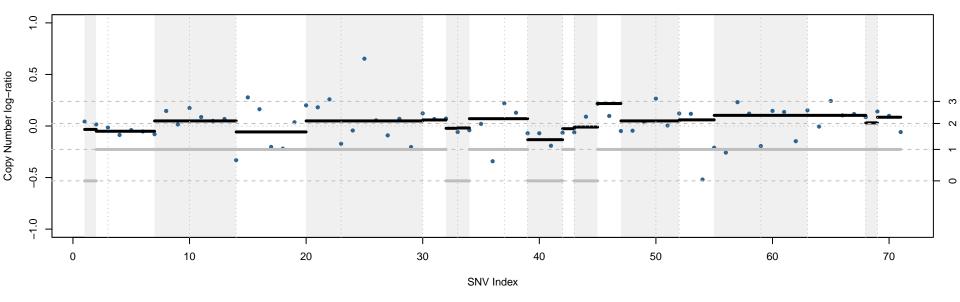
Purity: 0.32 Tumor ploidy: 1.895 2 0 3 0.25 0.20 Fraction Genome 0.00 -0.6 -0.4 -0.2 0.0 0.2

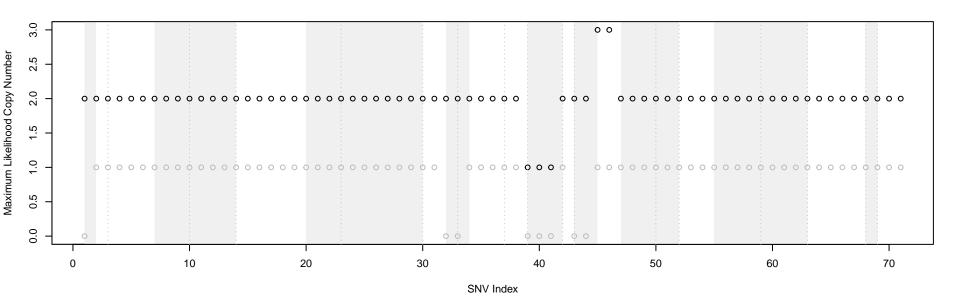
log2 ratio

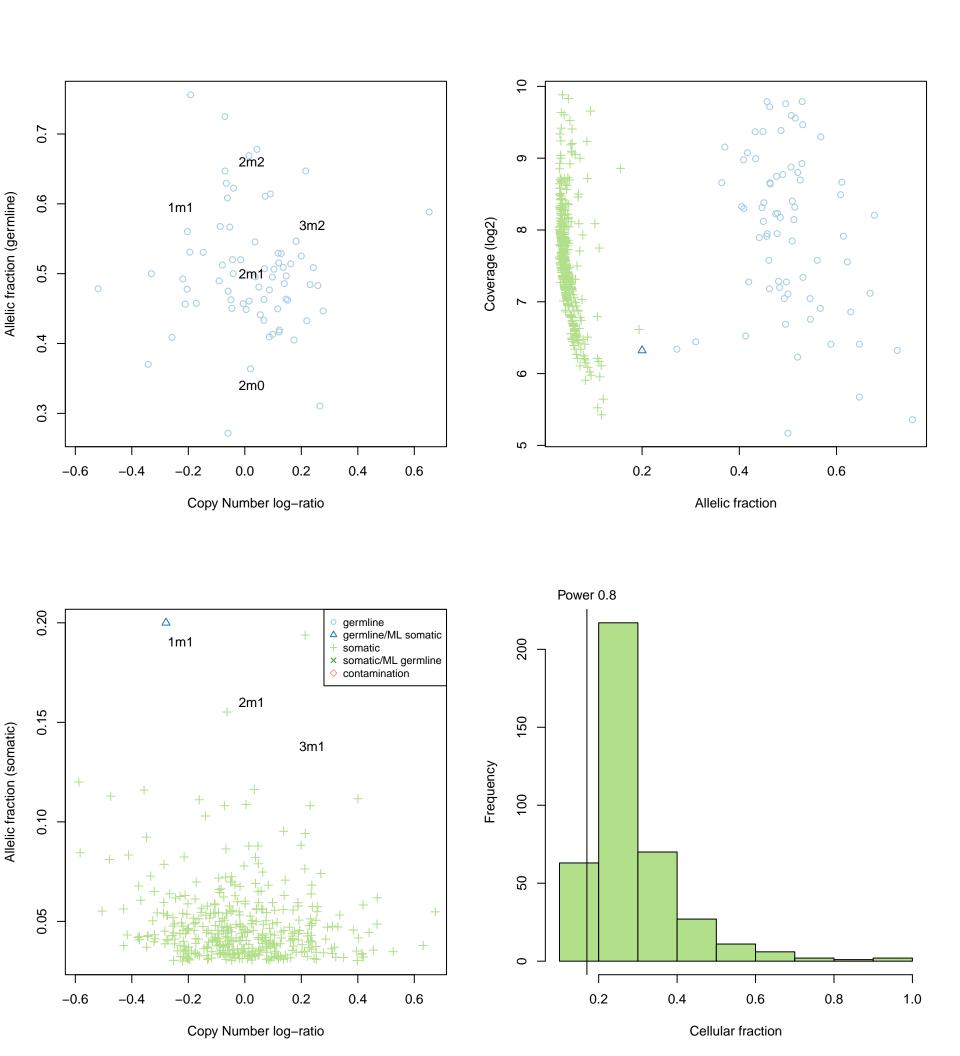




## SCNA-fit log-likelihood: -5311.82







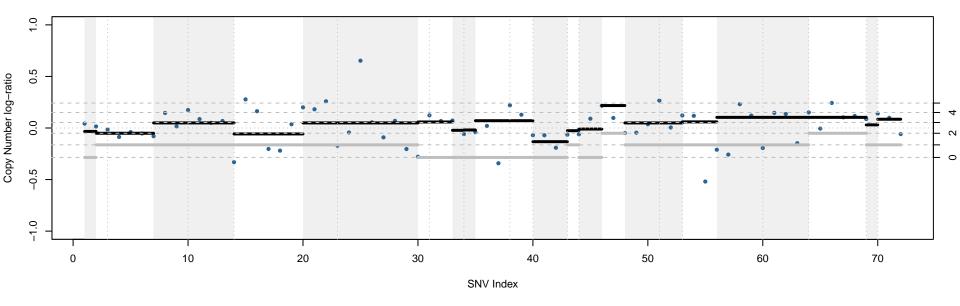
Purity: 0.15 Tumor ploidy: 2.481 3 5 0.25 0.20 Fraction Genome 0.00 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio

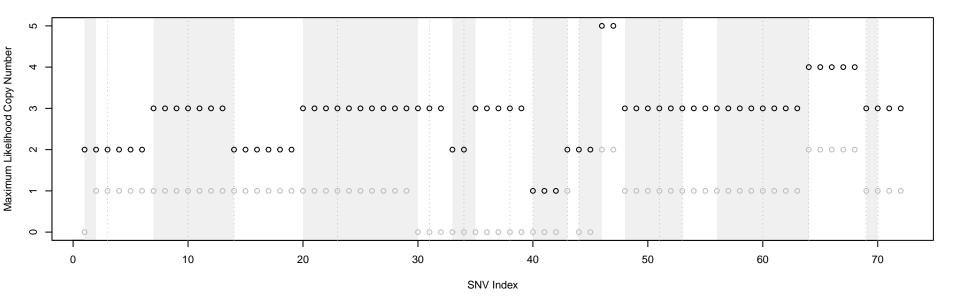
Purity: 0.15 Tumor ploidy: 2.481 SNV log-likelihood: 131.58 GoF: 96.2% Mean coverage: 233;281

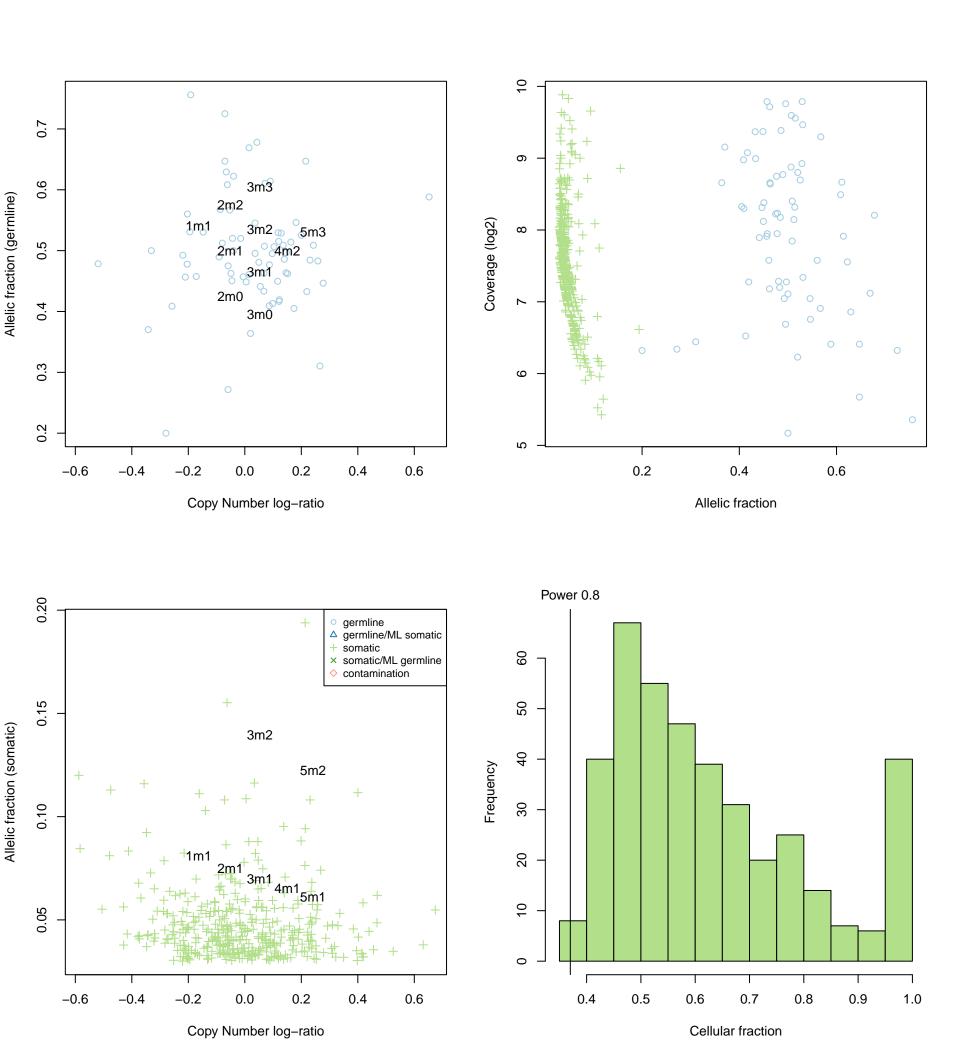
1 2 3 4 5 8 10 12 13 14 16 17 18 19 20 21

SCNA-fit log-likelihood: -5040.58

SNV Index

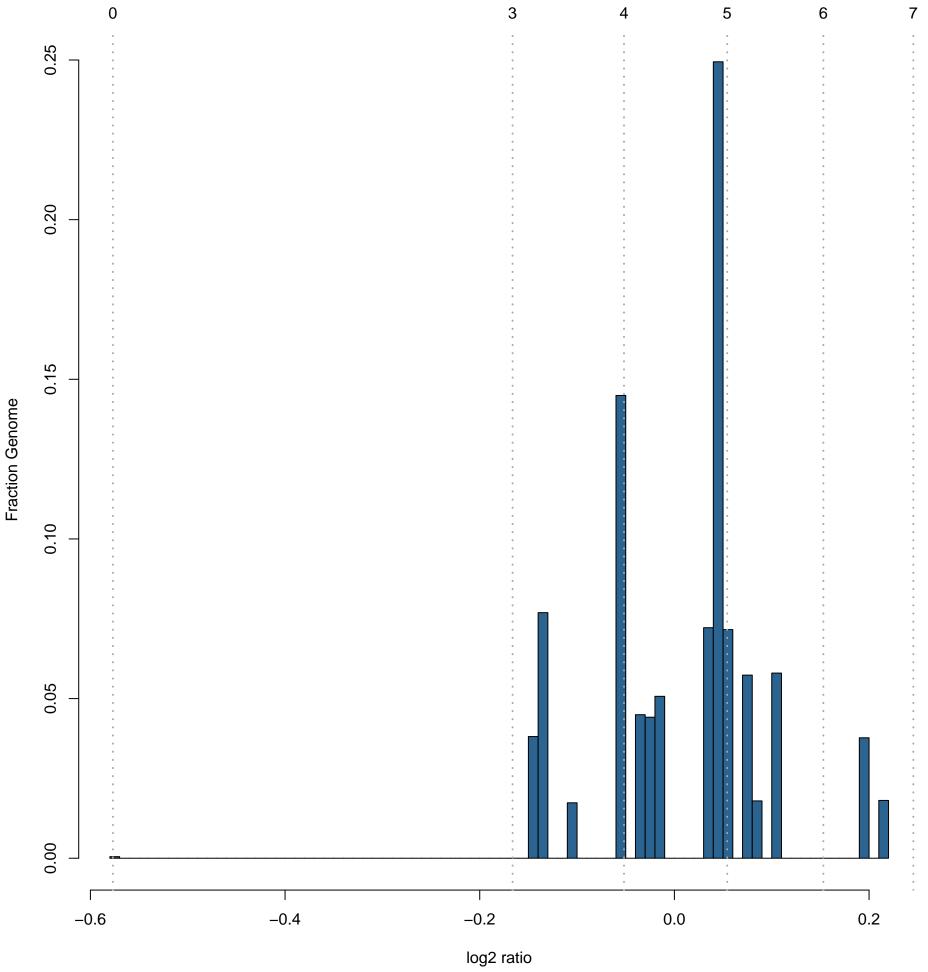


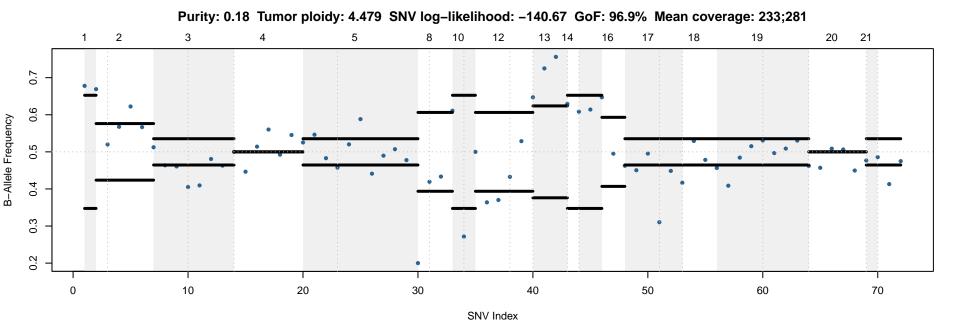




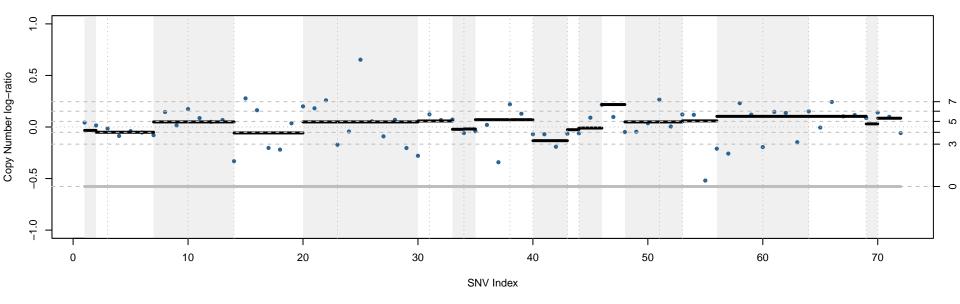
Purity: 0.18 Tumor ploidy: 4.479

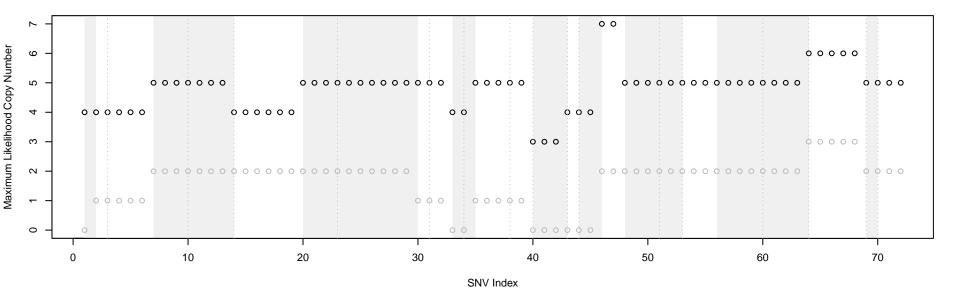
3 4
: : :

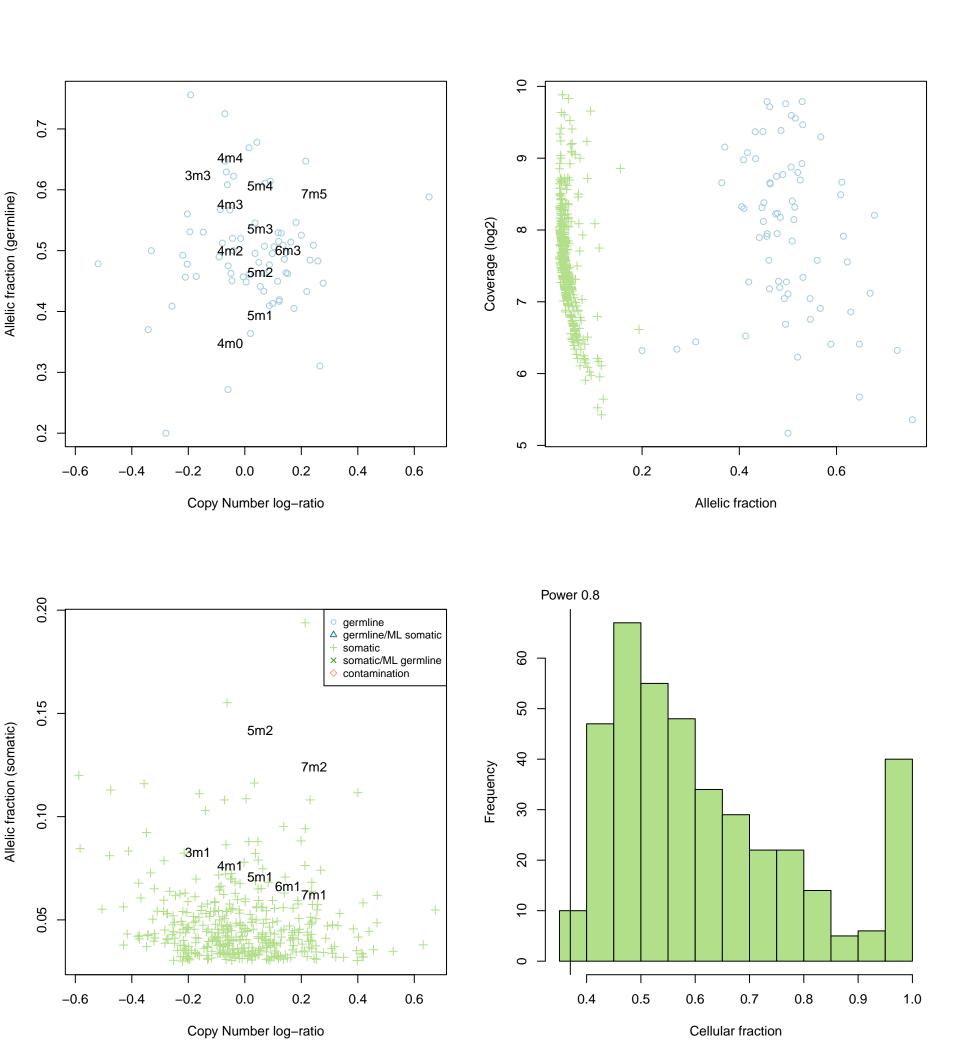




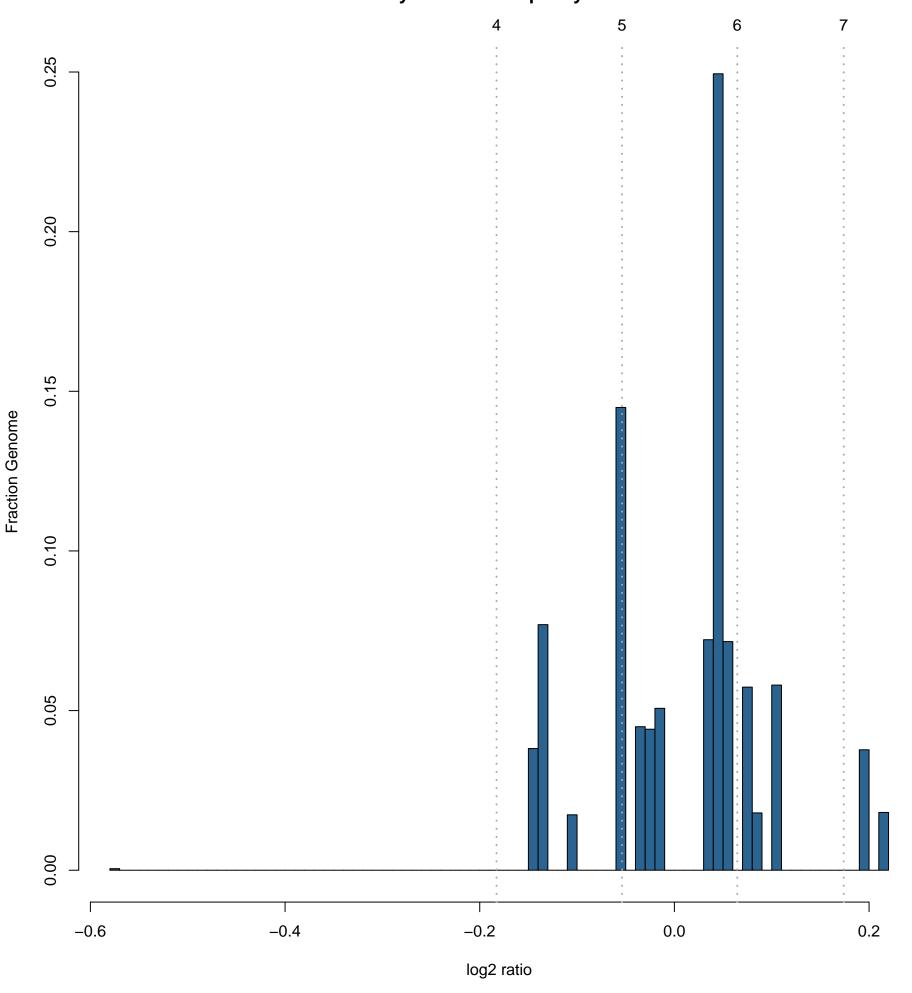
## SCNA-fit log-likelihood: -5038.4

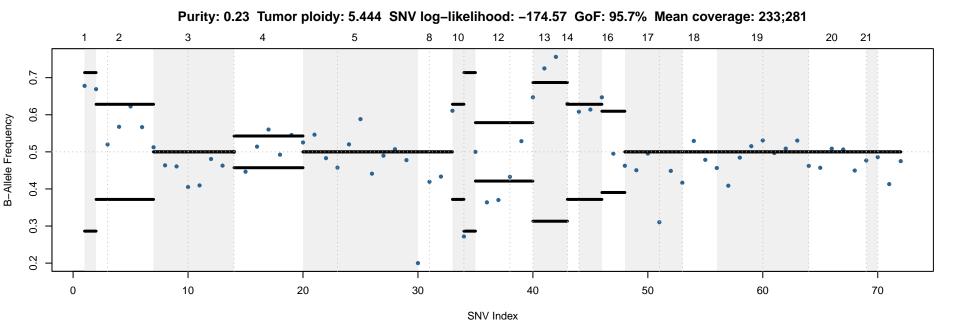




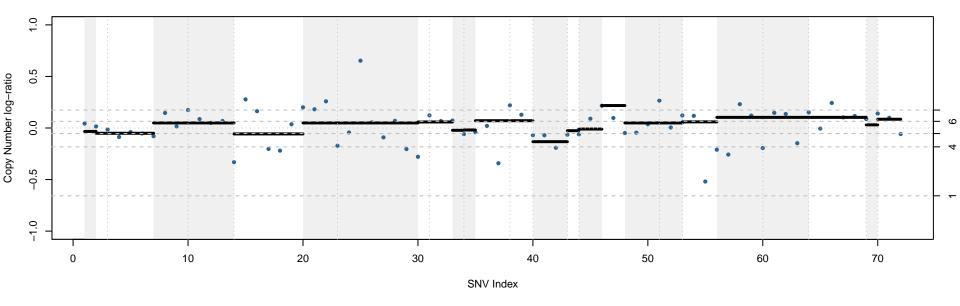


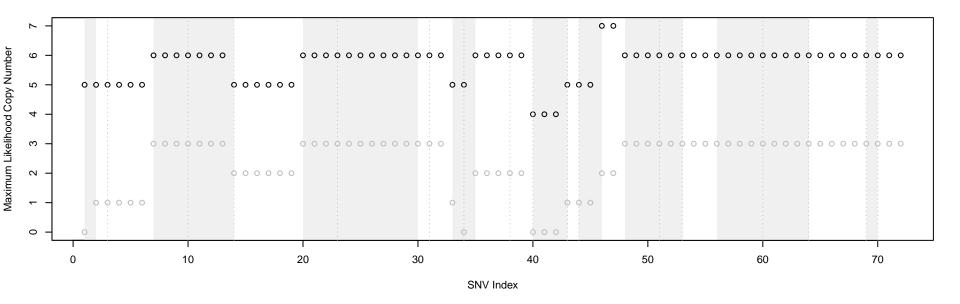
Purity: 0.23 Tumor ploidy: 5.444

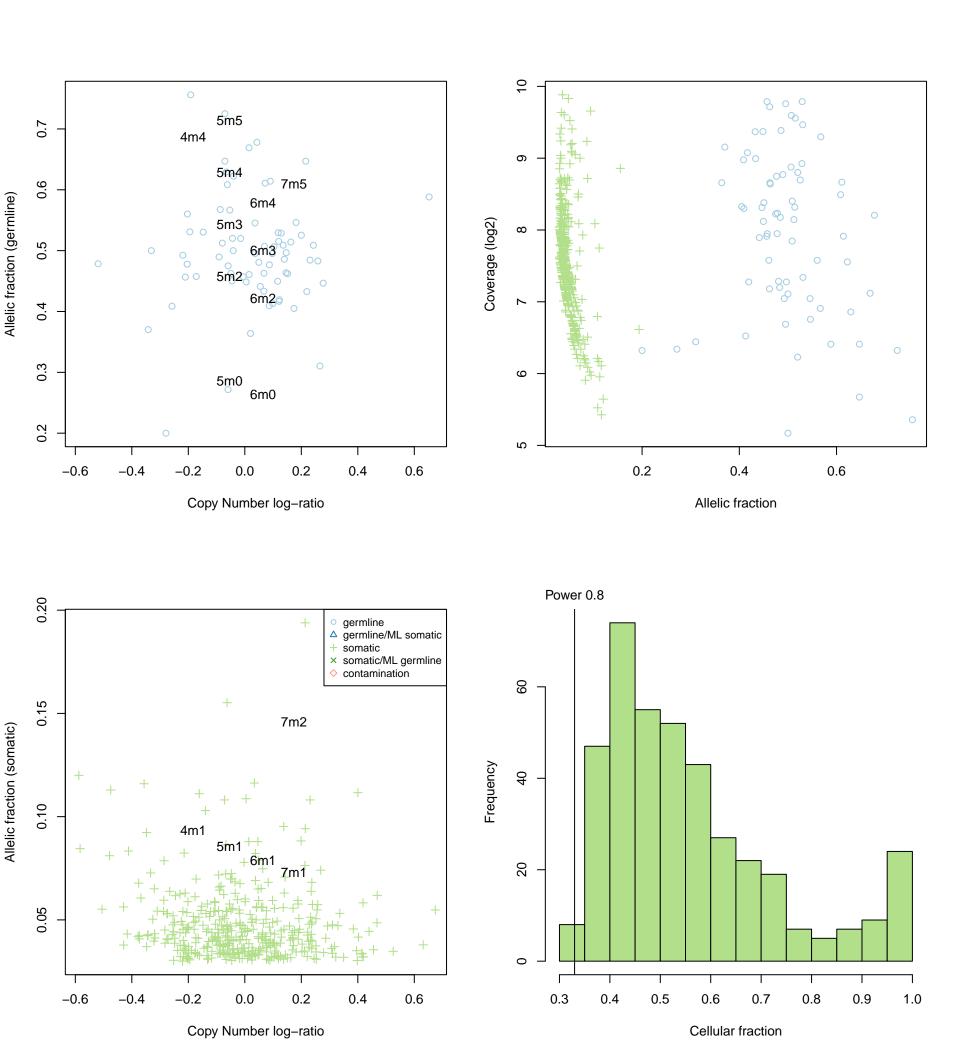




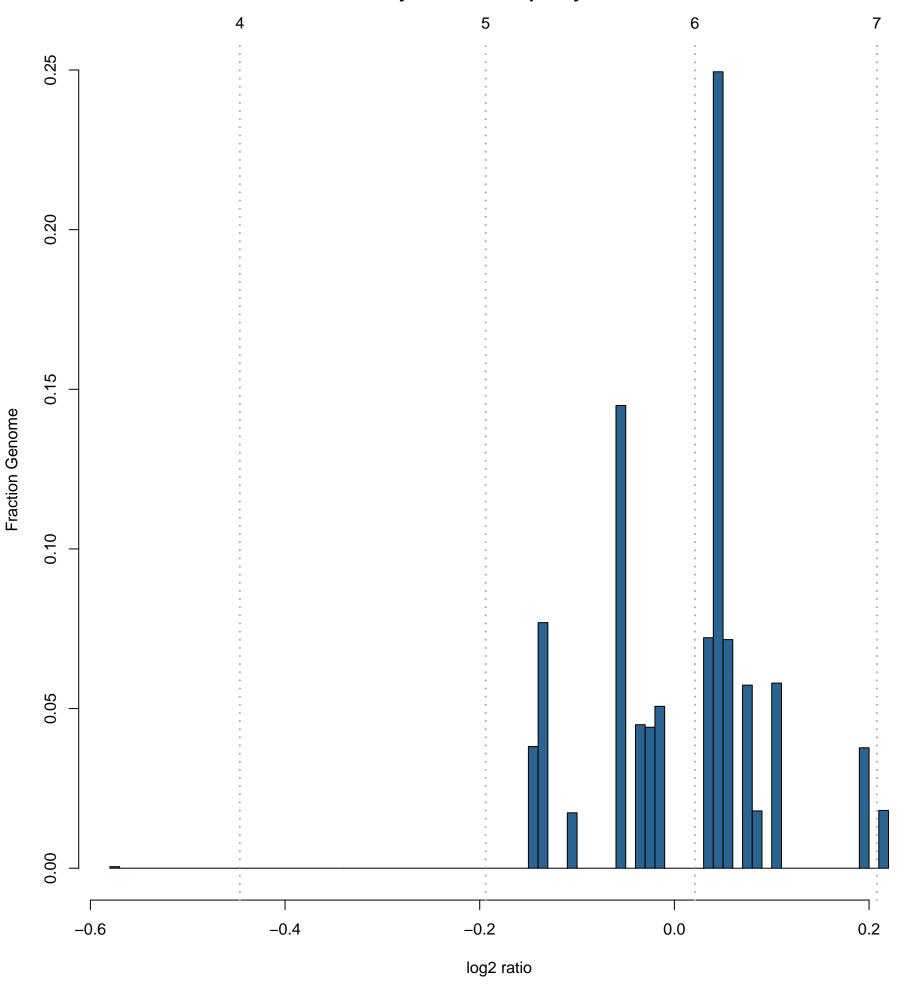
## SCNA-fit log-likelihood: -5057.28

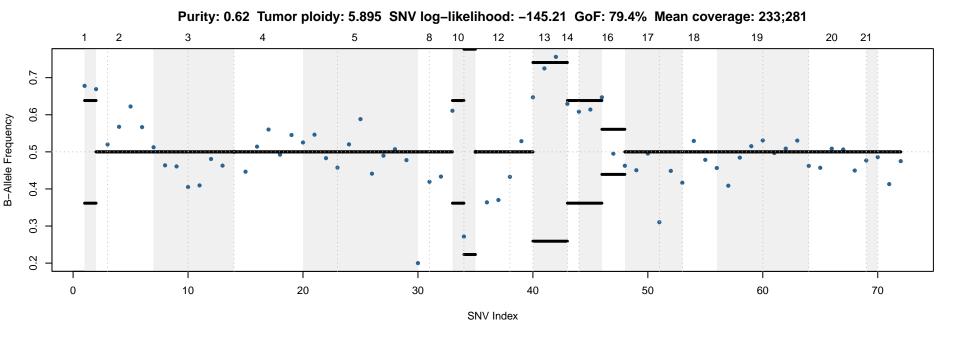




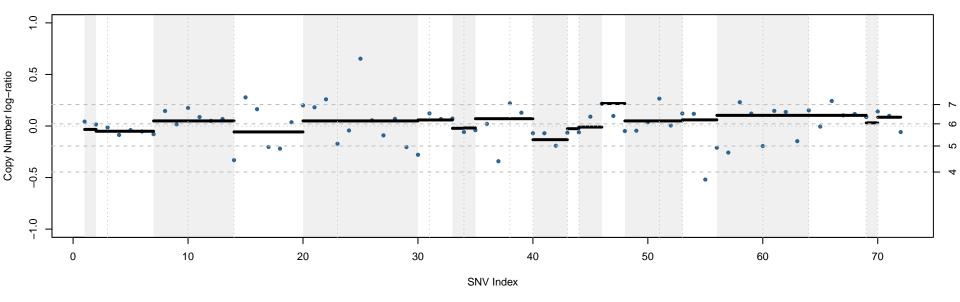


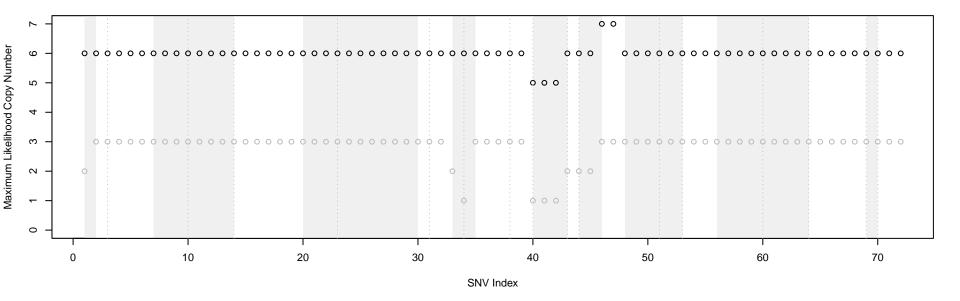
Purity: 0.62 Tumor ploidy: 5.895

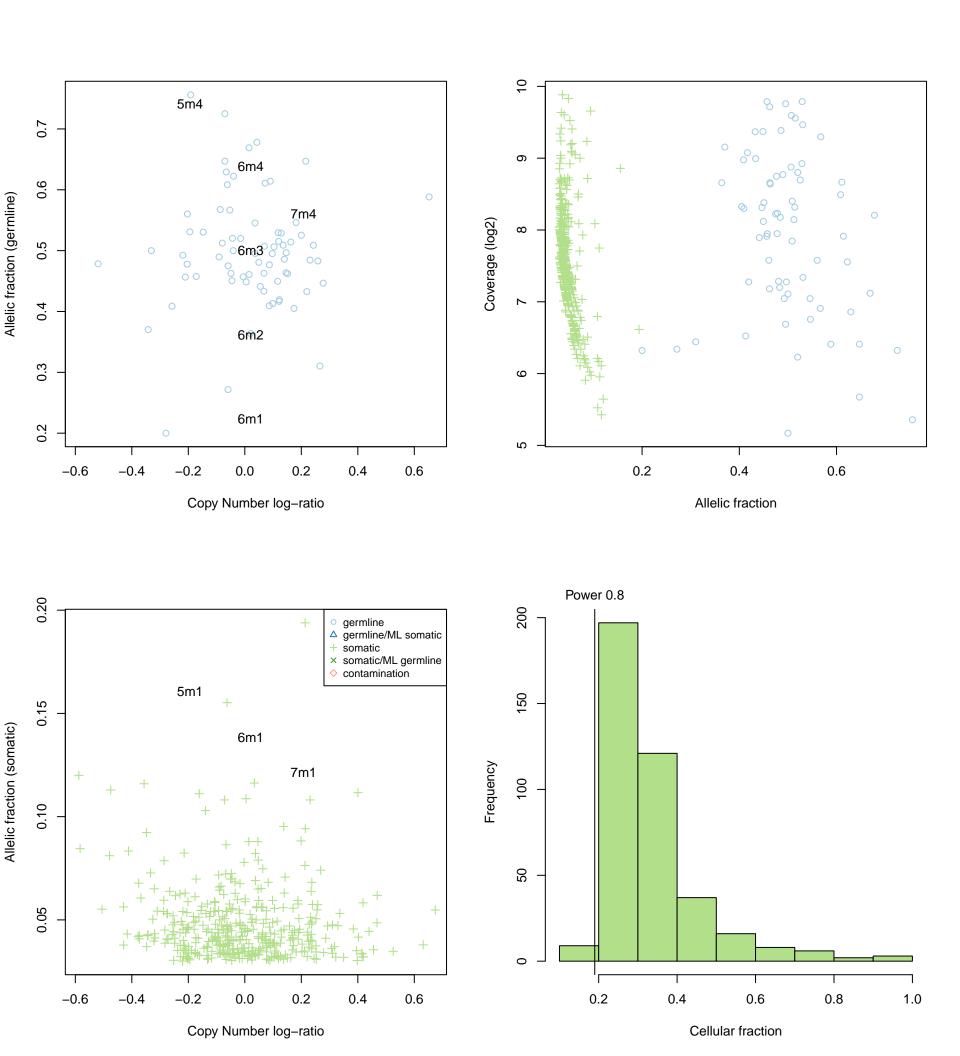




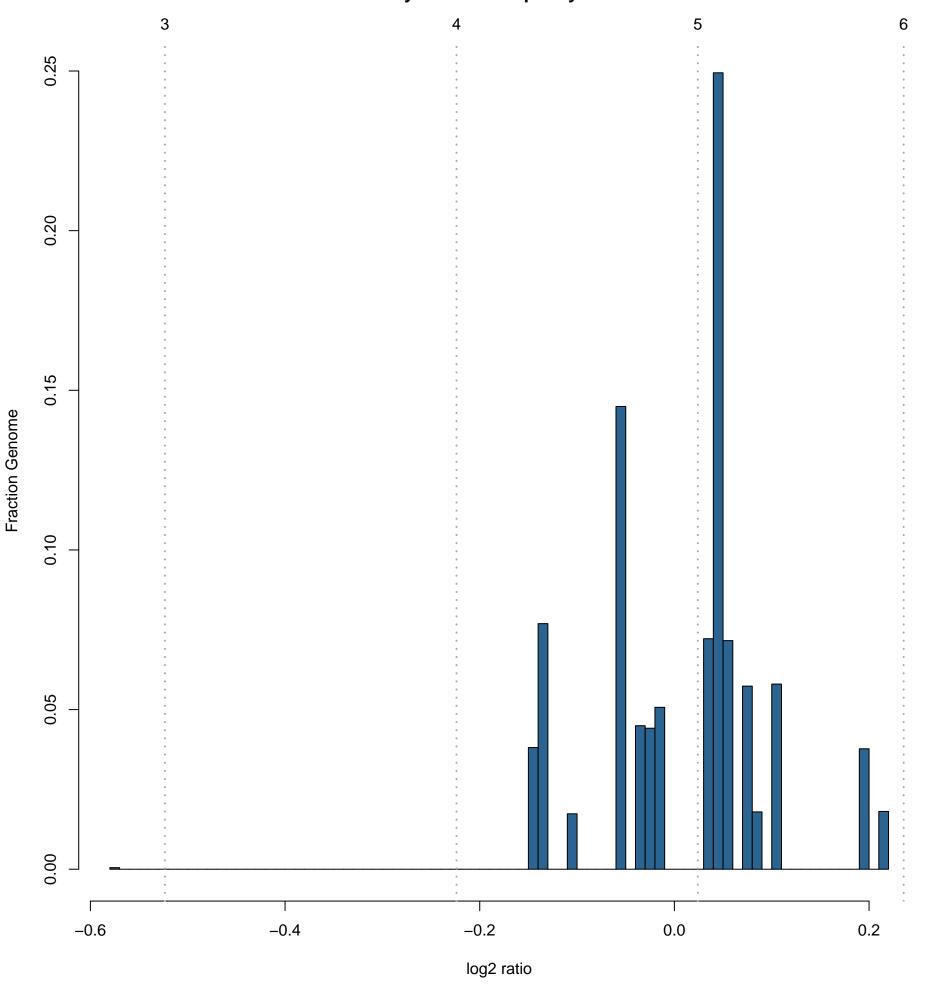
## SCNA-fit log-likelihood: -5238.16

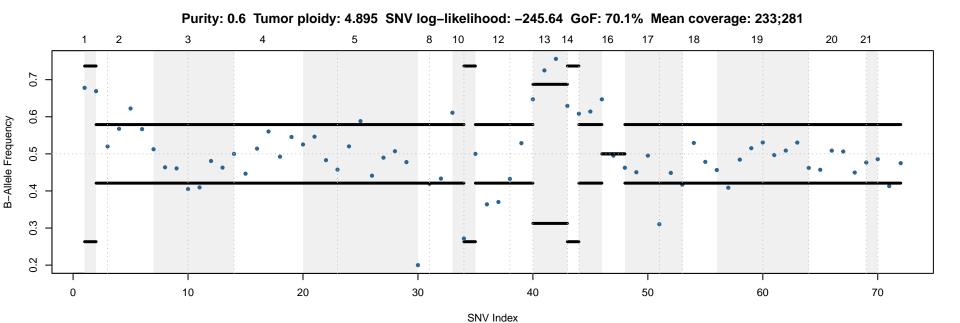




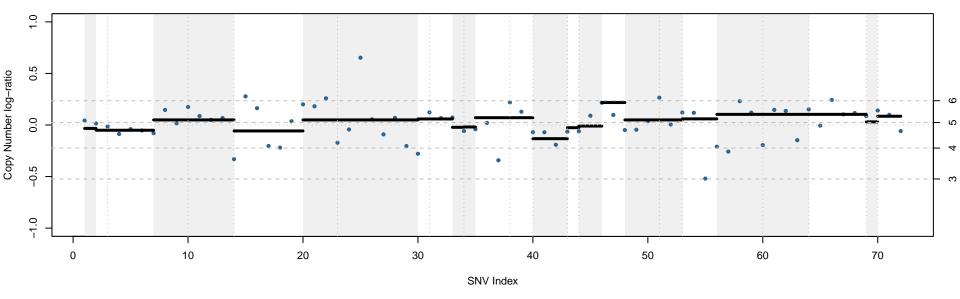


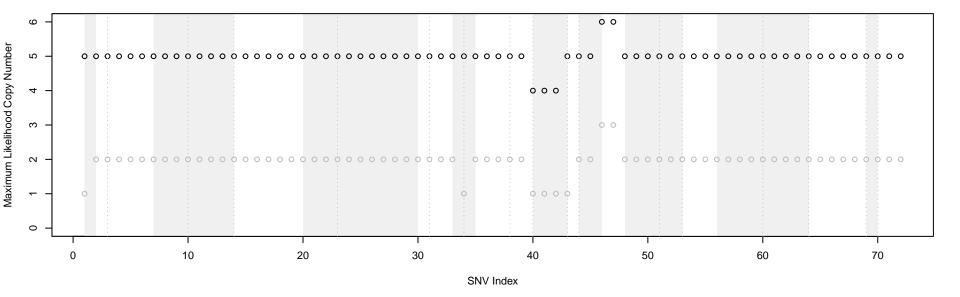
Purity: 0.6 Tumor ploidy: 4.895

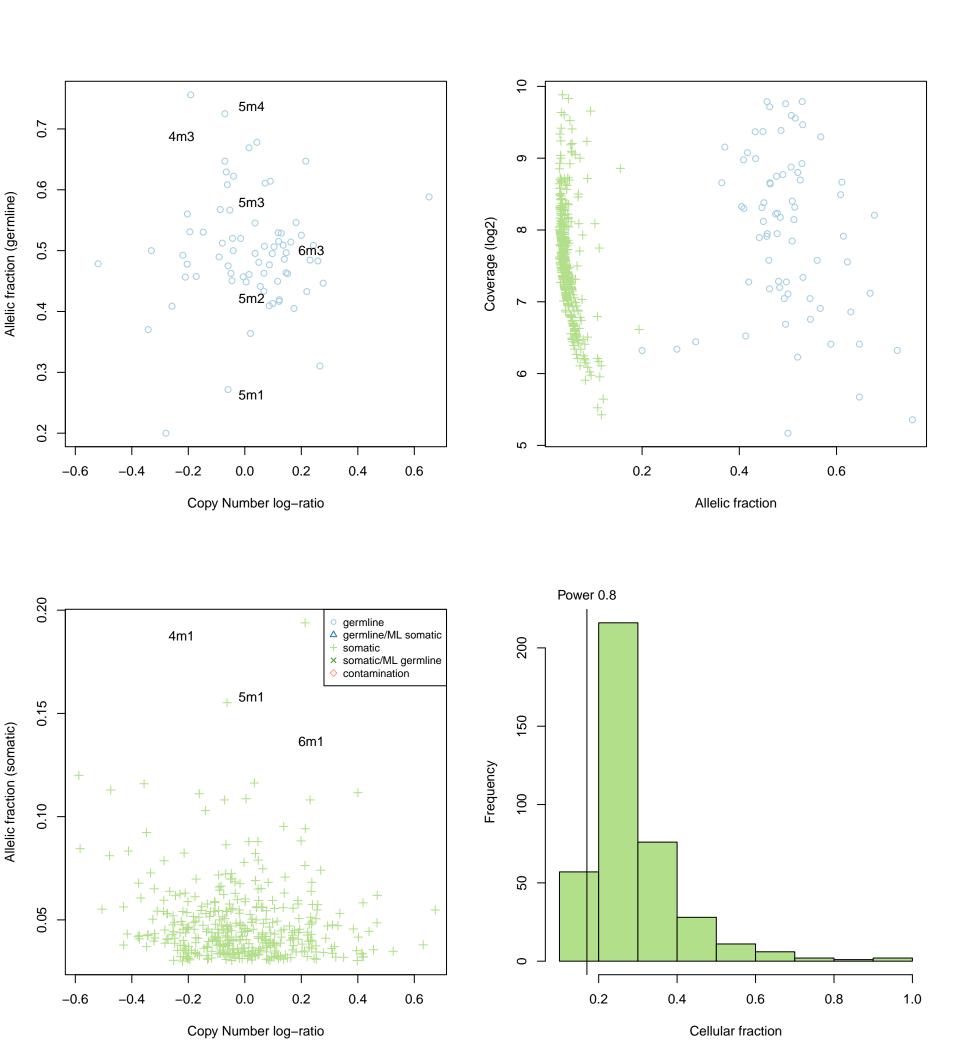




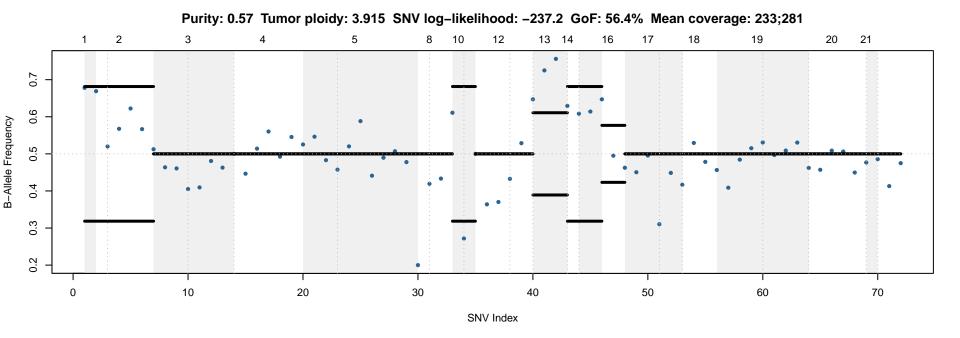
## SCNA-fit log-likelihood: -5302.86



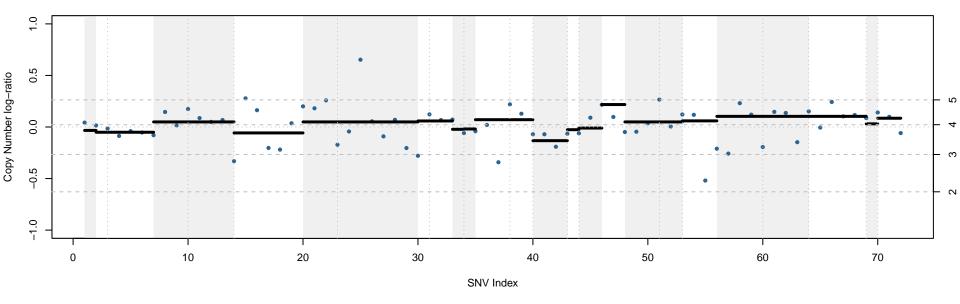


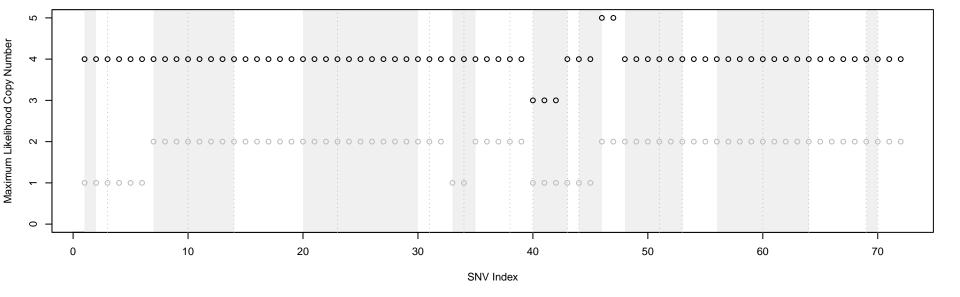


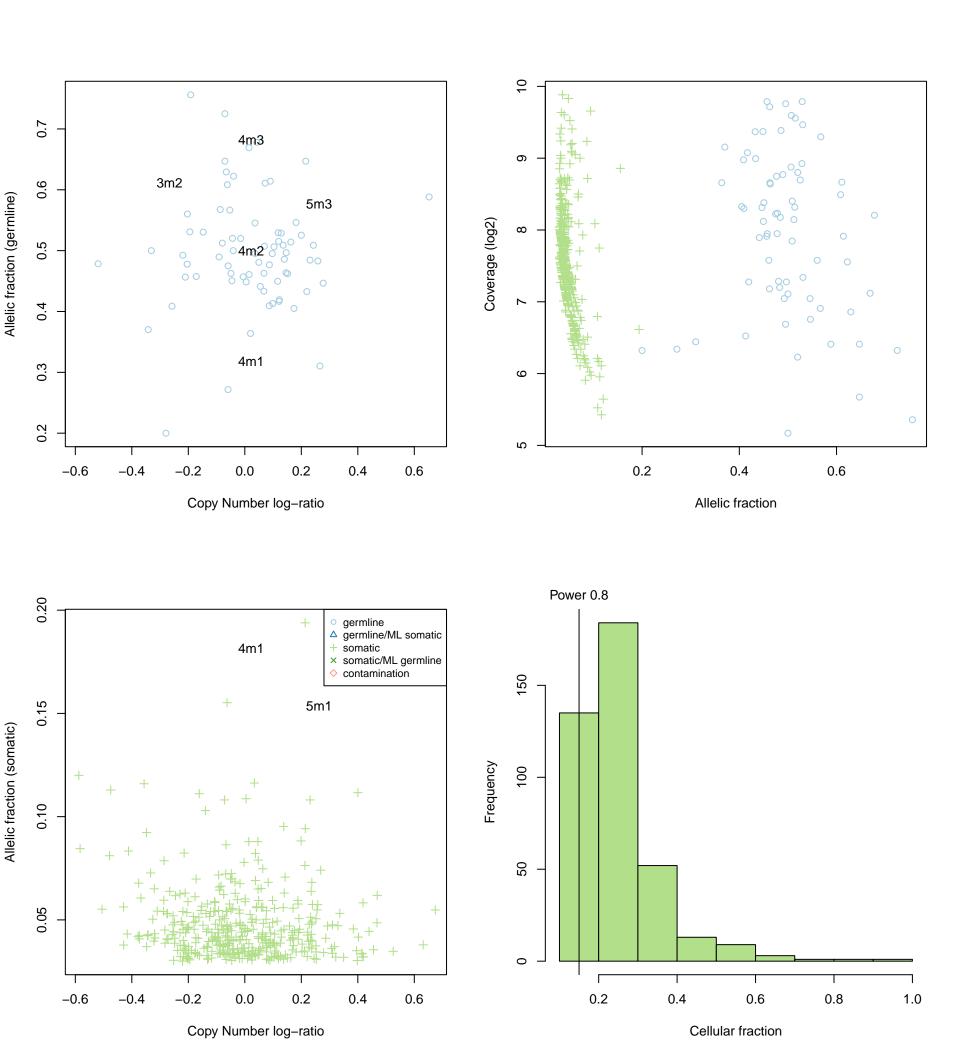
Purity: 0.57 Tumor ploidy: 3.915 3 4 0.20 Fraction Genome 0.05 0.00 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



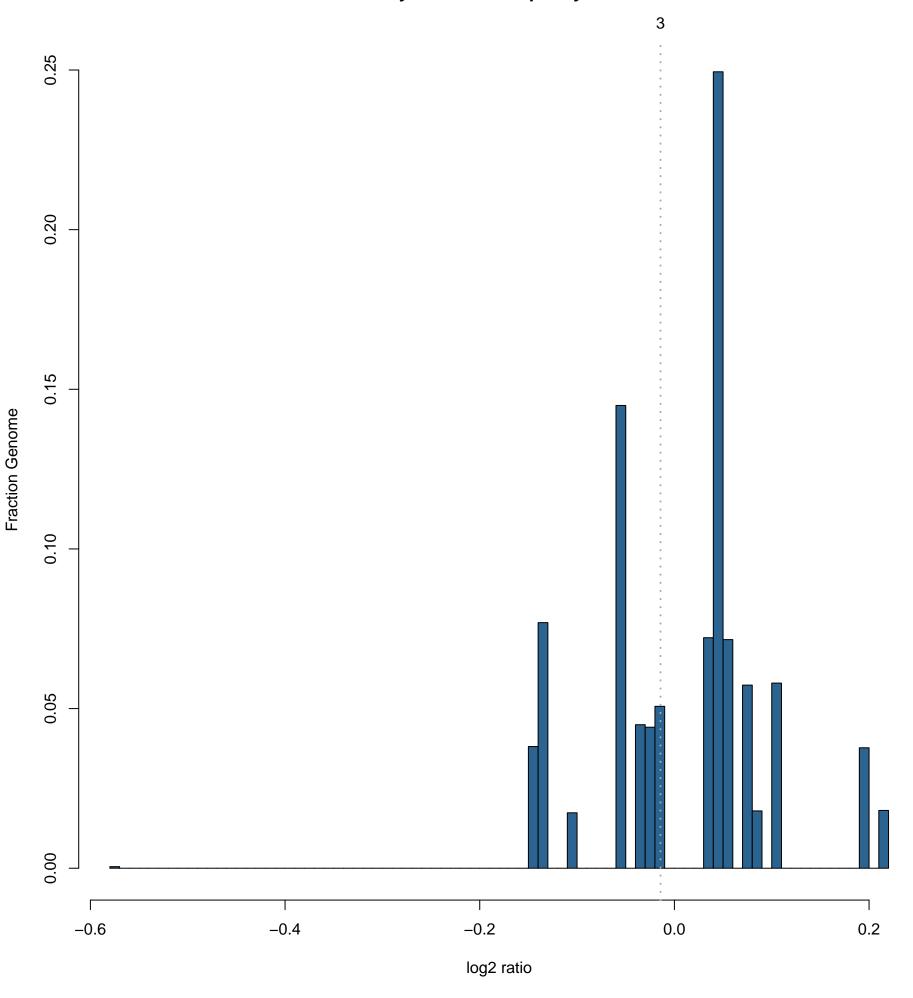
# SCNA-fit log-likelihood: -5421.05

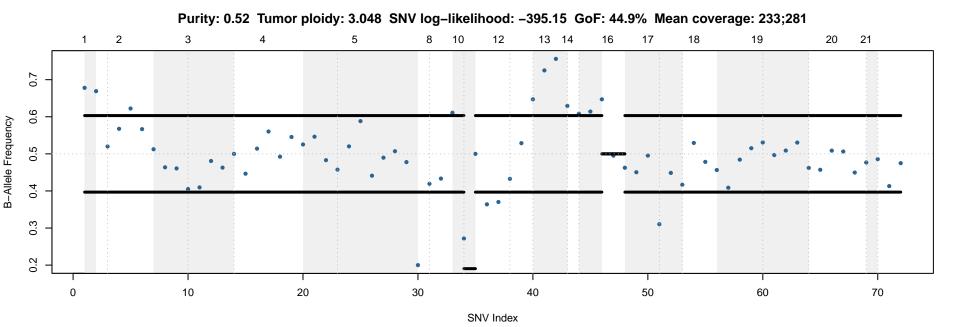




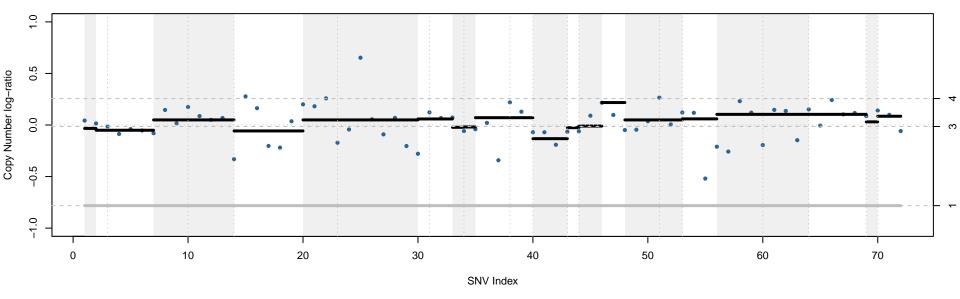


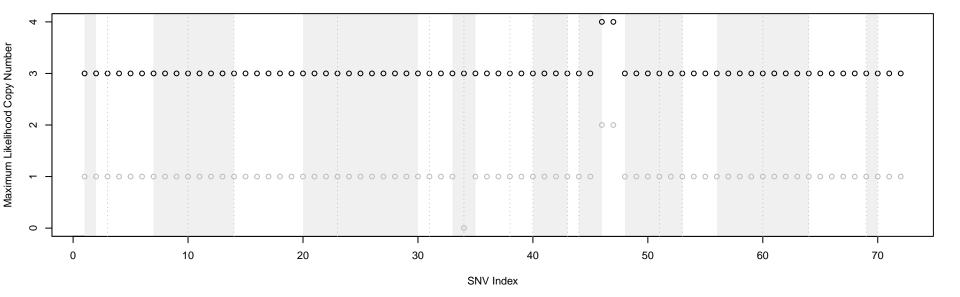
Purity: 0.52 Tumor ploidy: 3.048

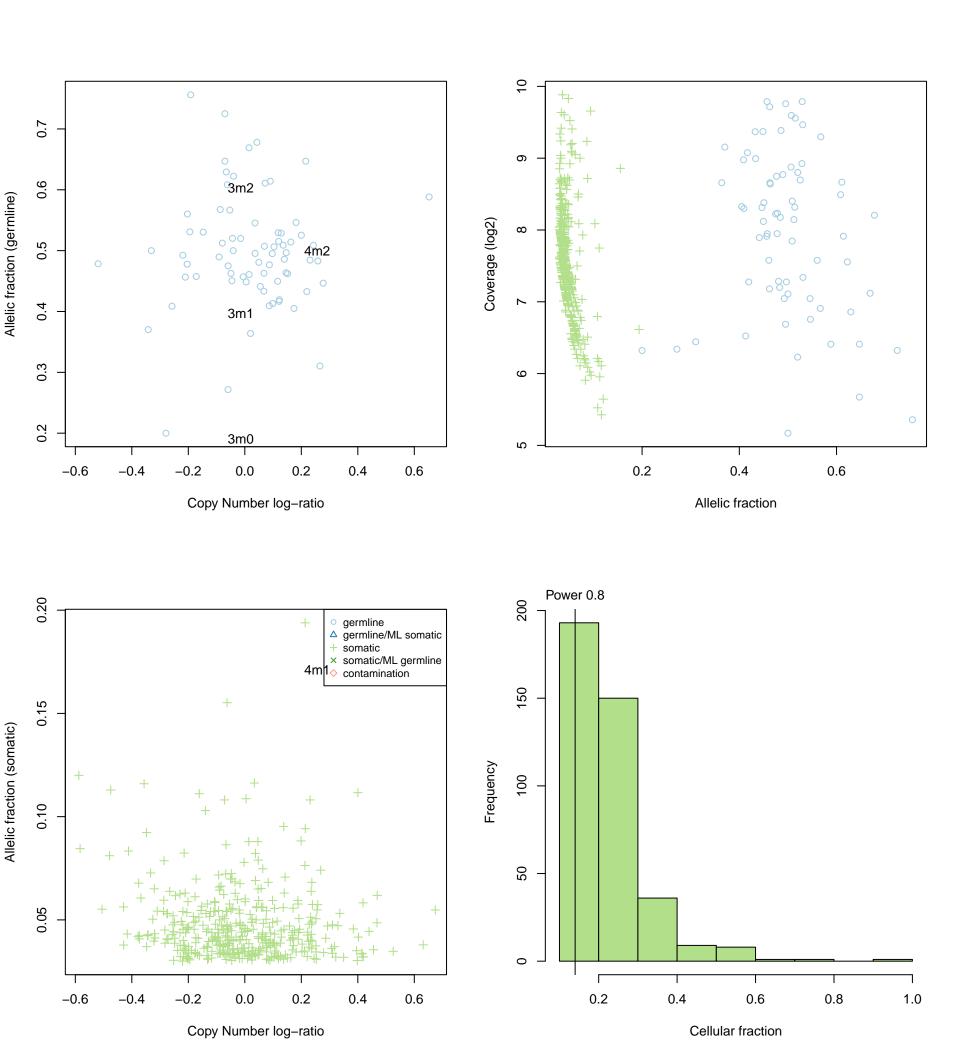




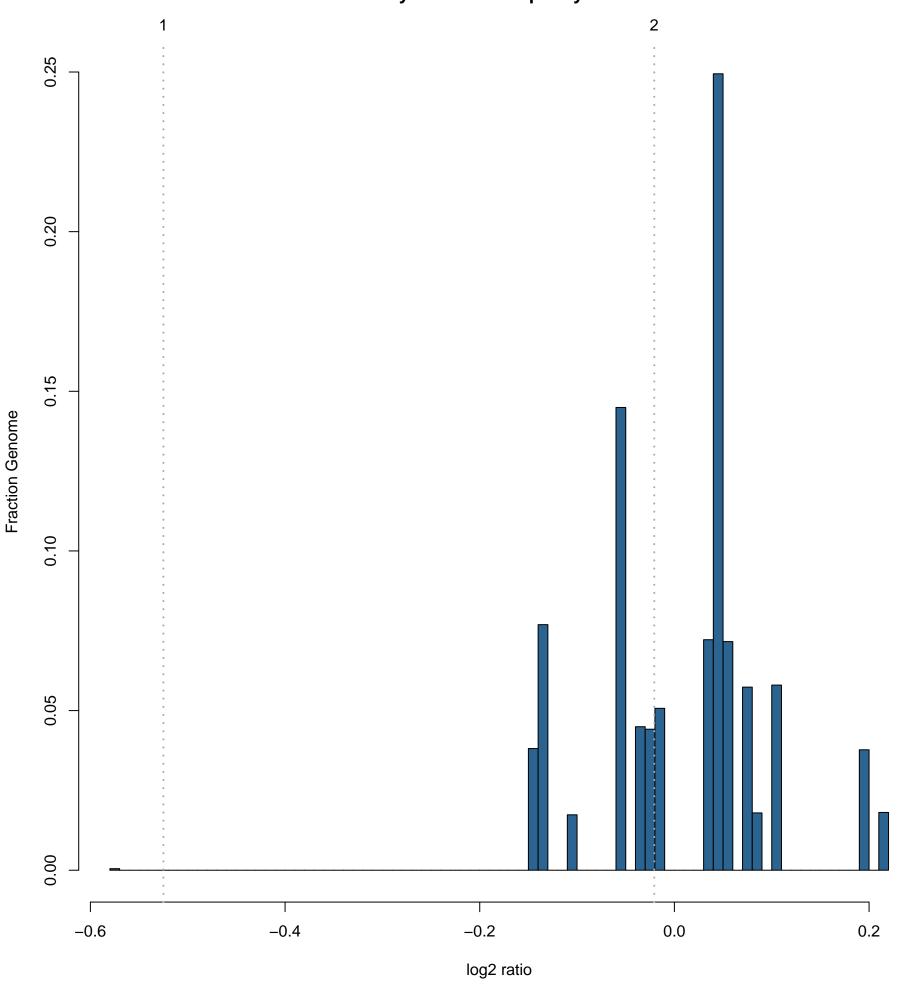
## SCNA-fit log-likelihood: -5518.46

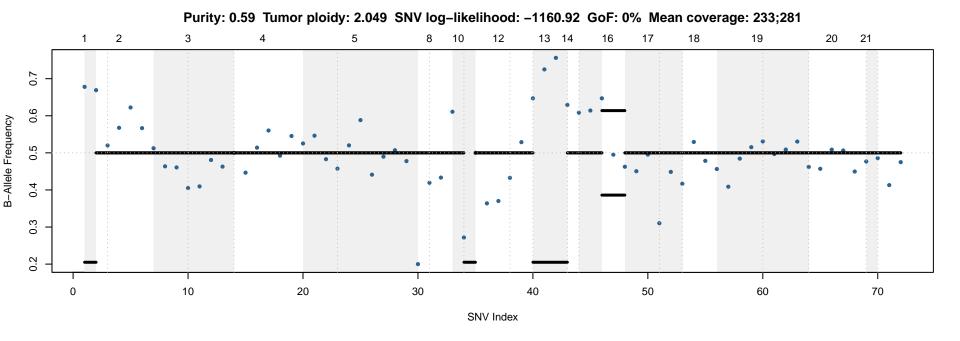




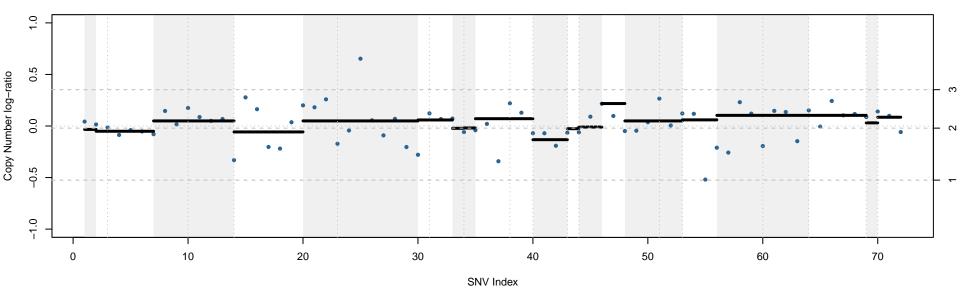


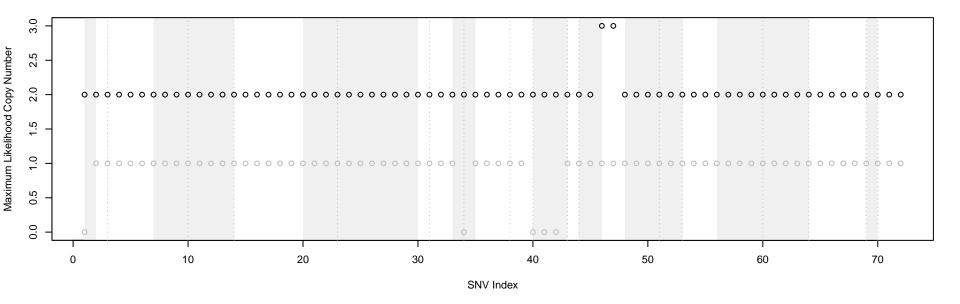
Purity: 0.59 Tumor ploidy: 2.049

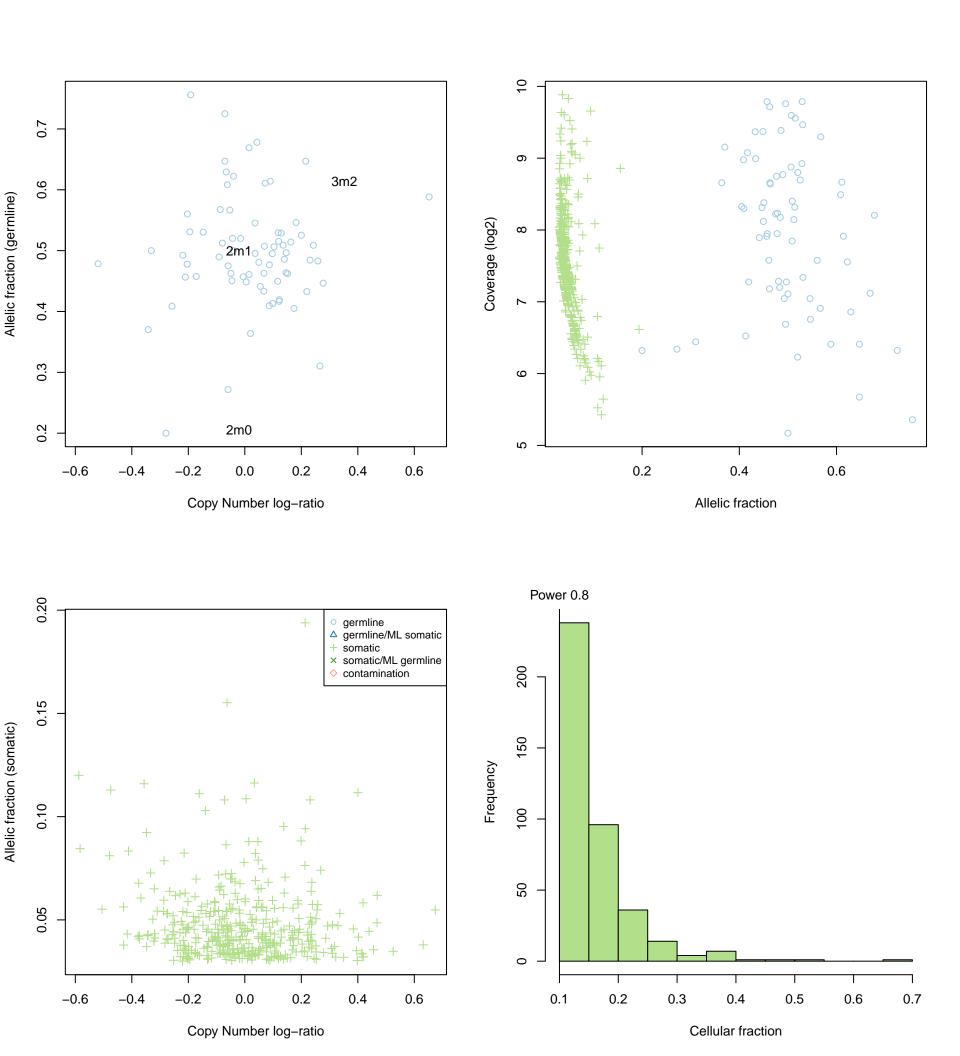




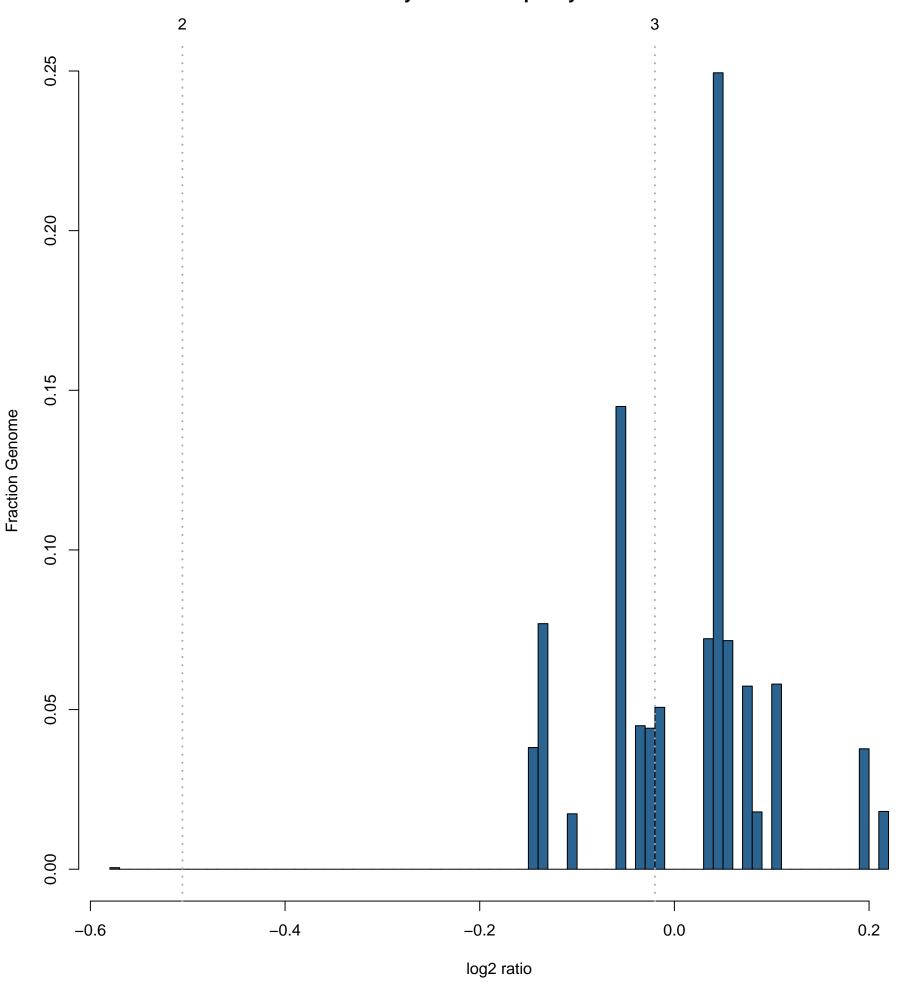
## SCNA-fit log-likelihood: -5649.55

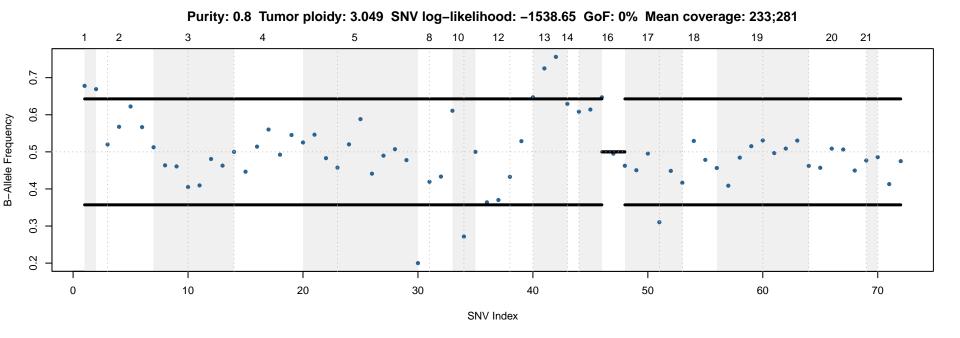






Purity: 0.8 Tumor ploidy: 3.049





## SCNA-fit log-likelihood: -5631.41

