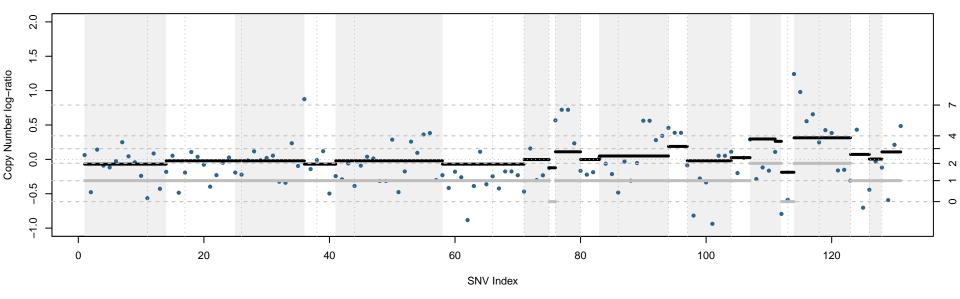
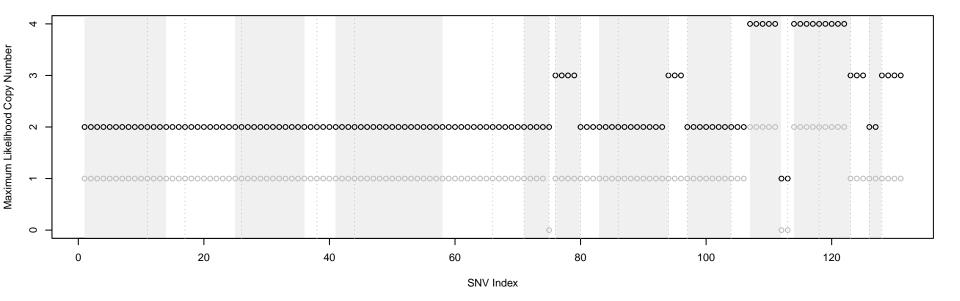
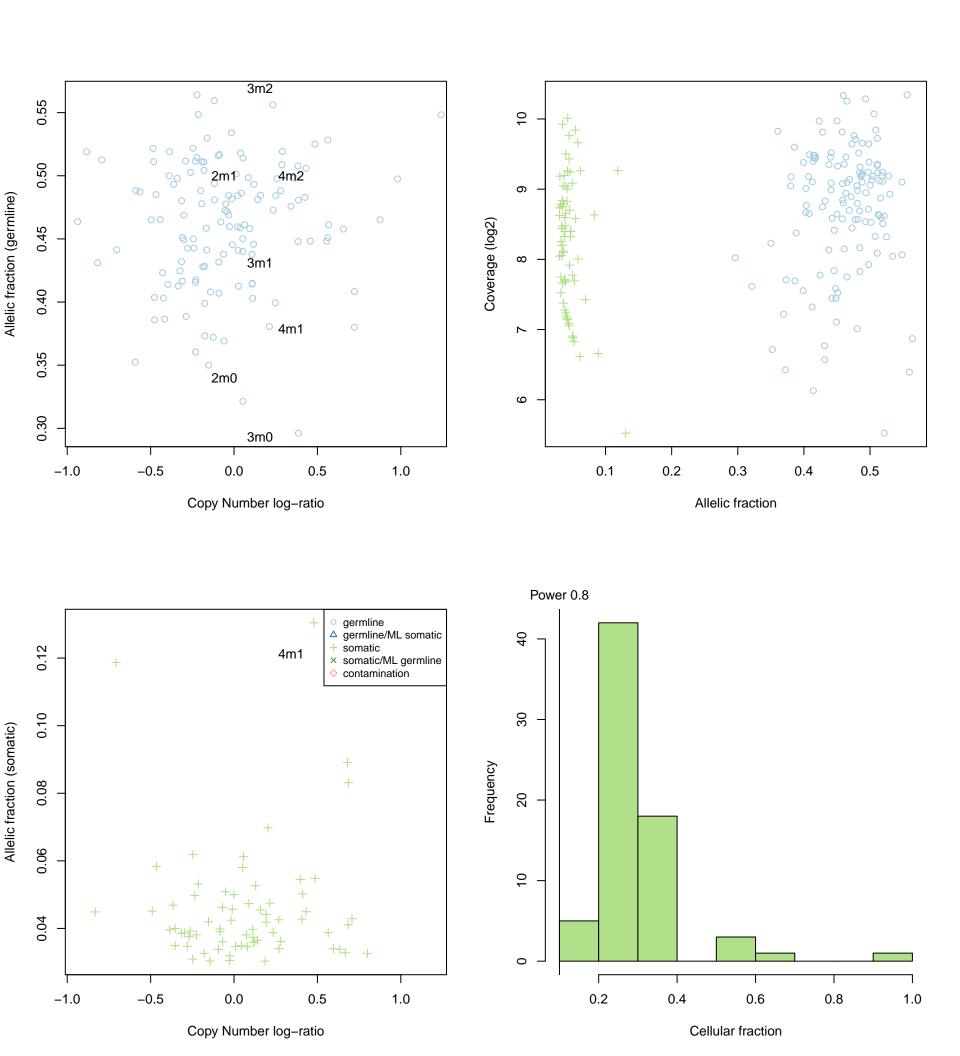


### SCNA-fit log-likelihood: -21584.2

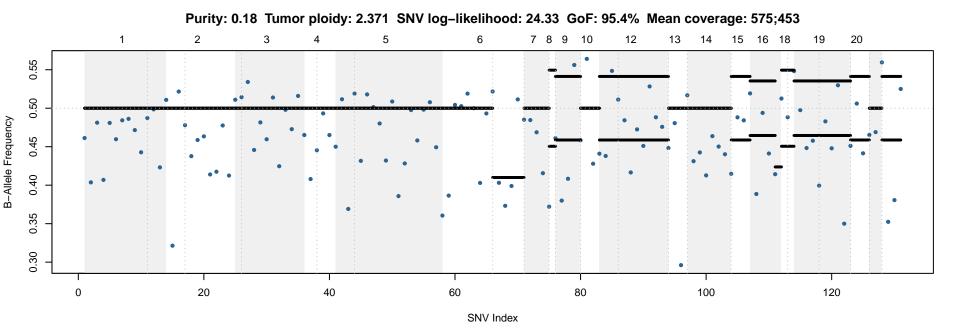




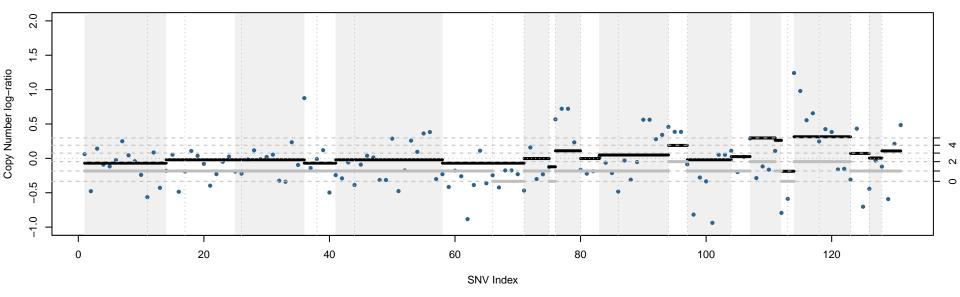


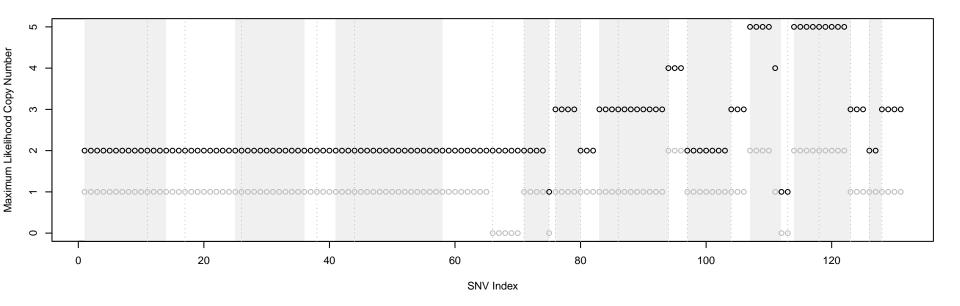
Purity: 0.18 Tumor ploidy: 2.371 2 3 0 5 0.25 0.20 Fraction Genome 0.05 0.00 -0.5 0.0 0.5 1.0

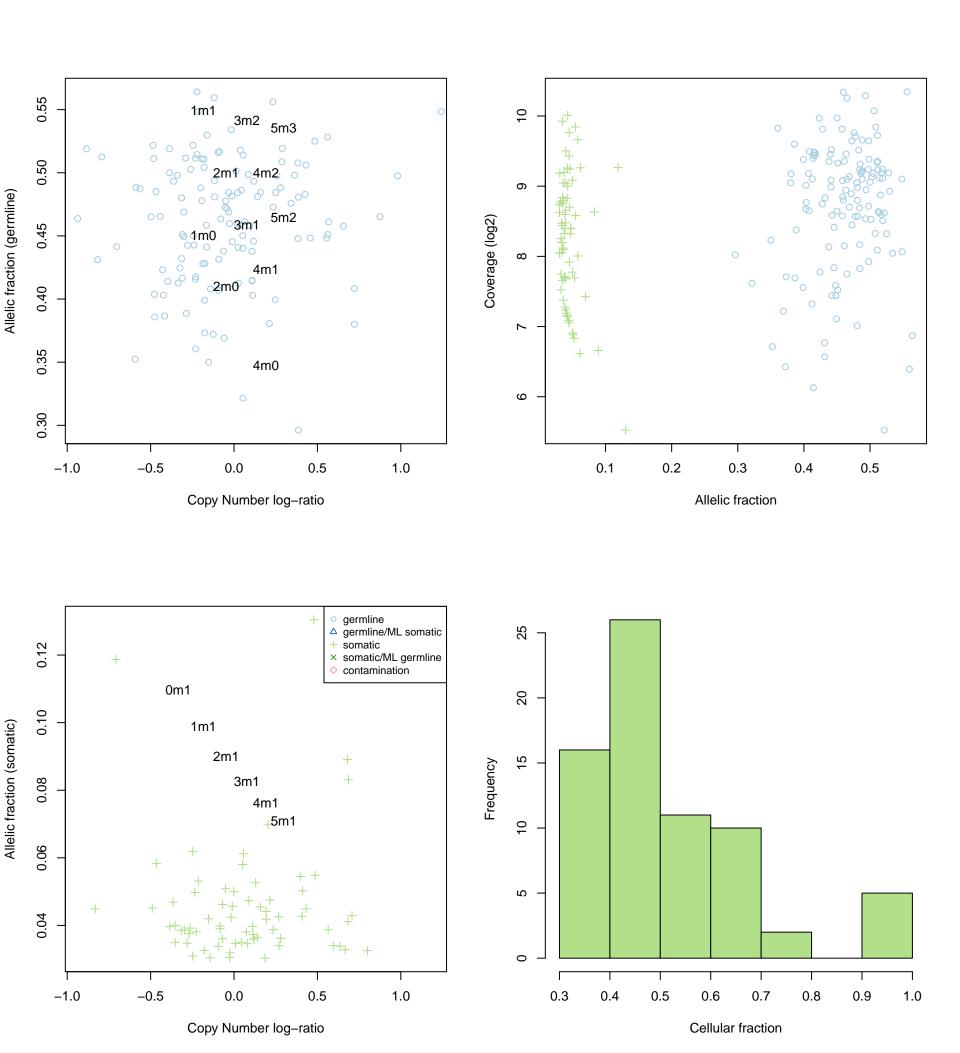
log2 ratio

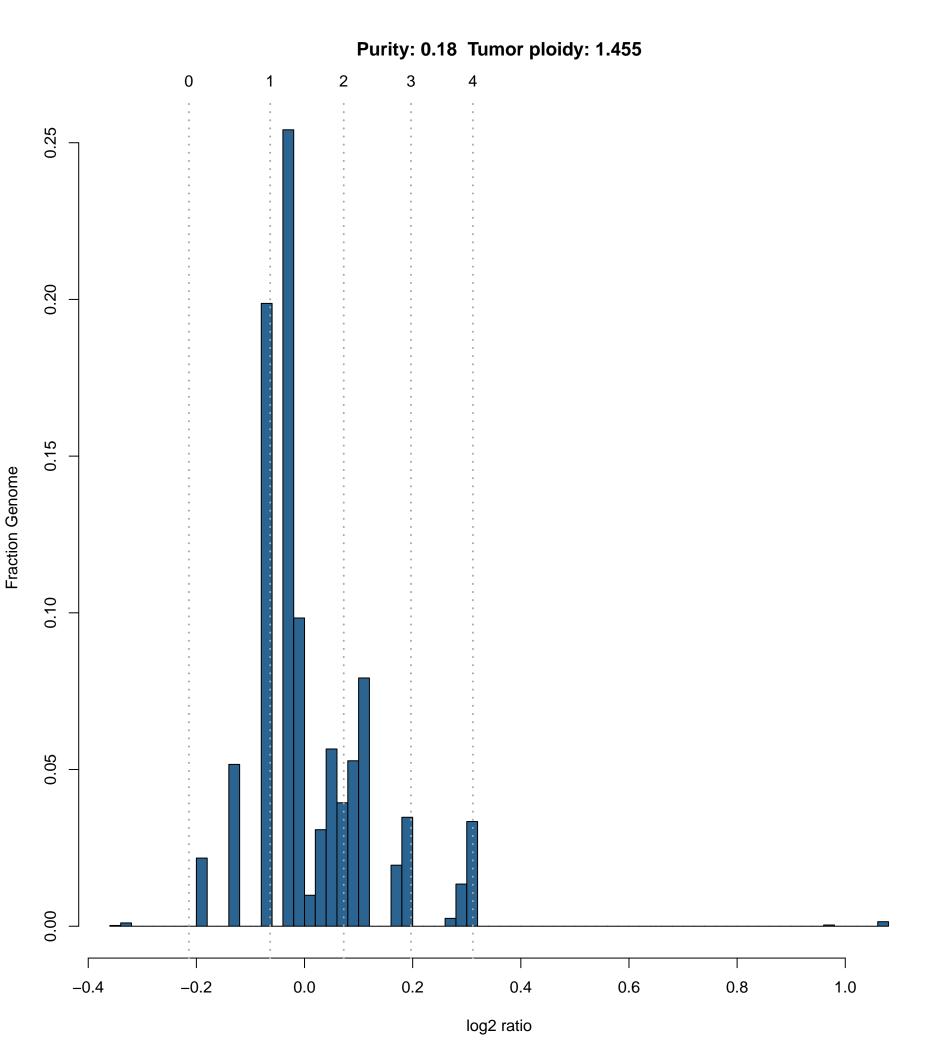


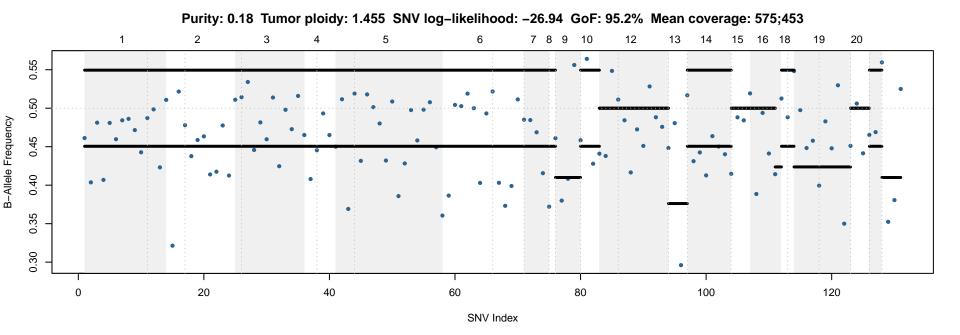
## SCNA-fit log-likelihood: -21562.59



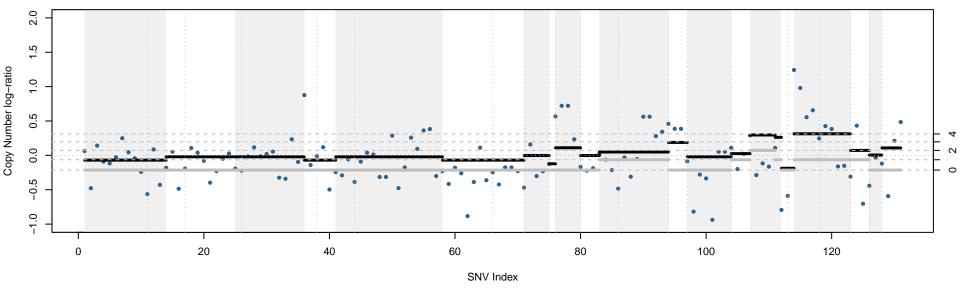


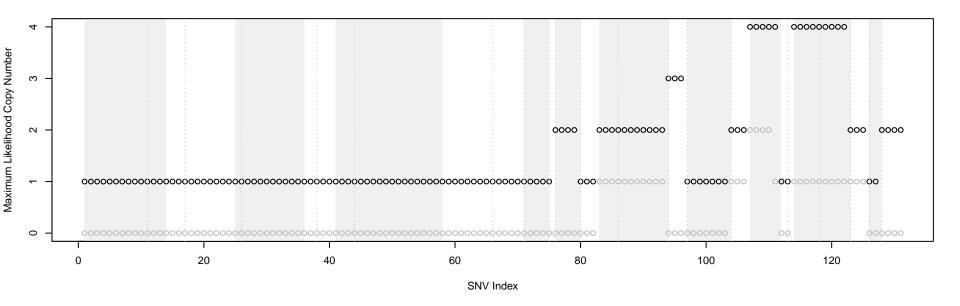


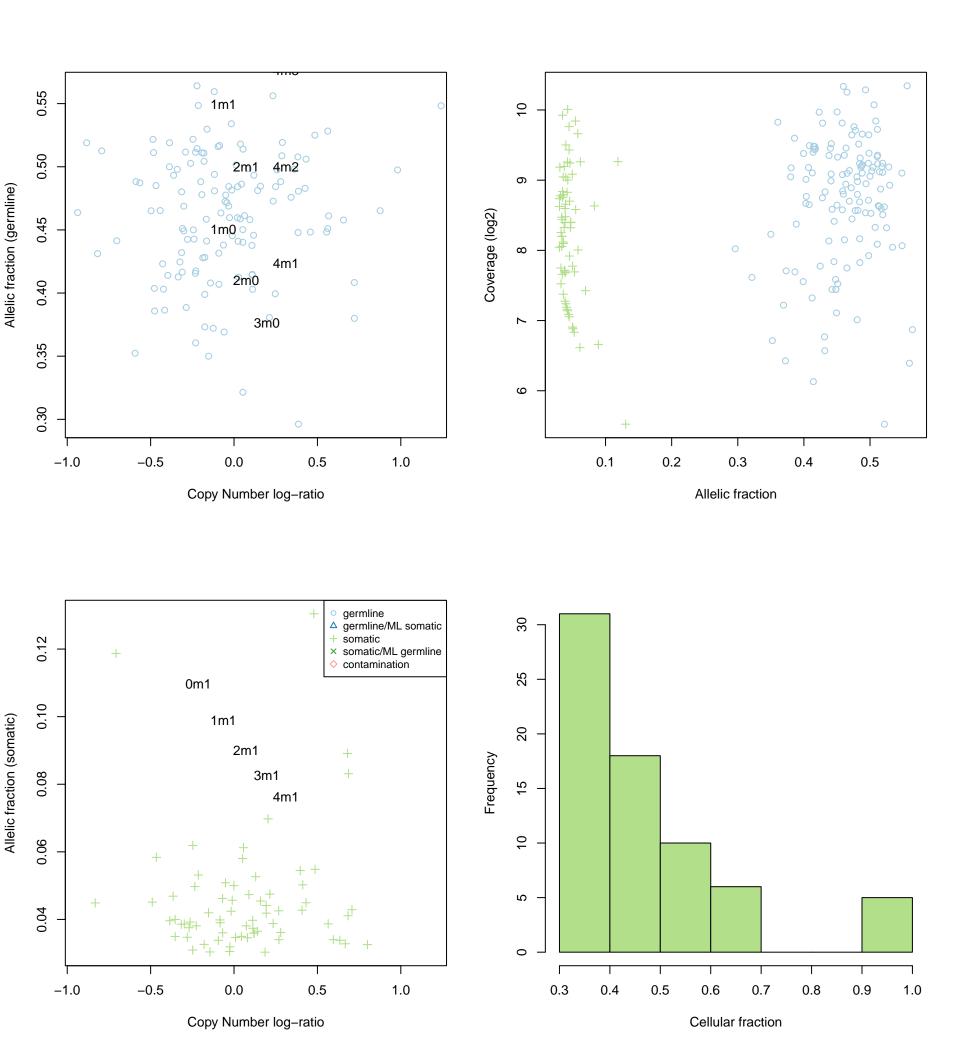


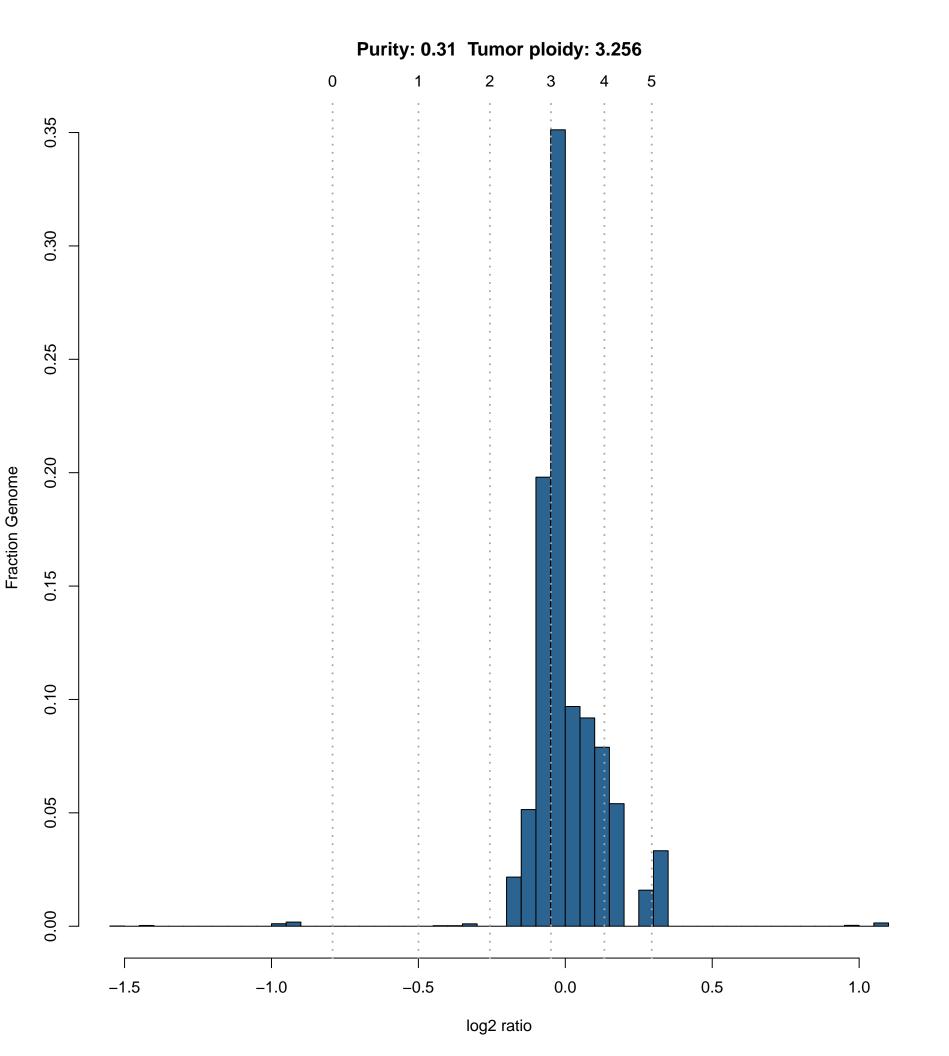


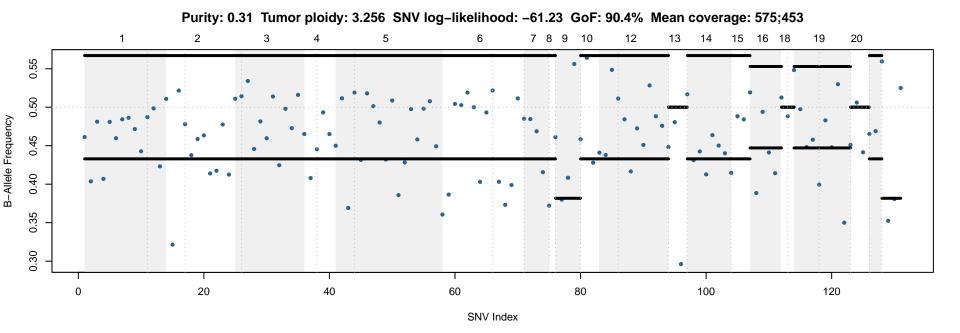
### SCNA-fit log-likelihood: -21593.53



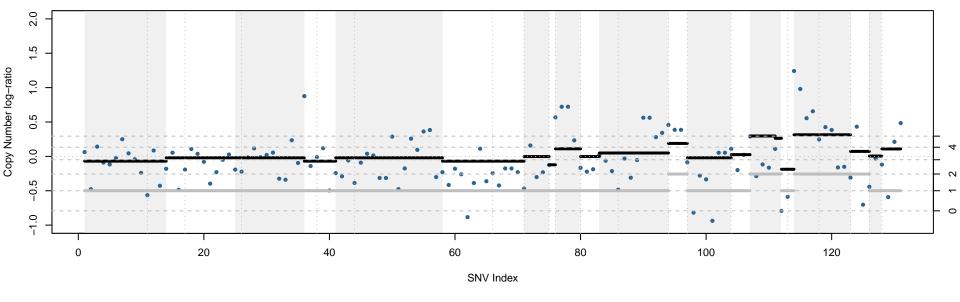


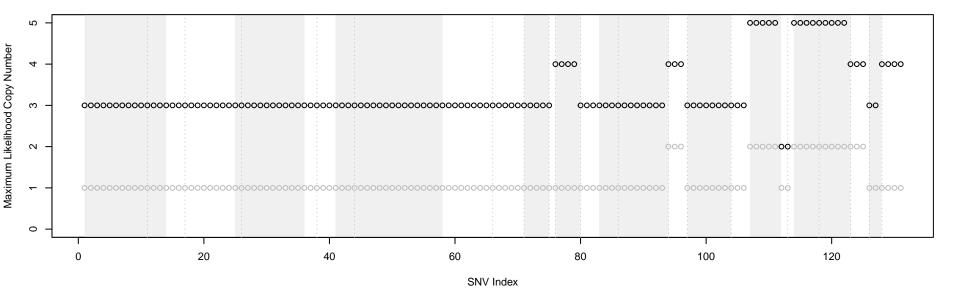


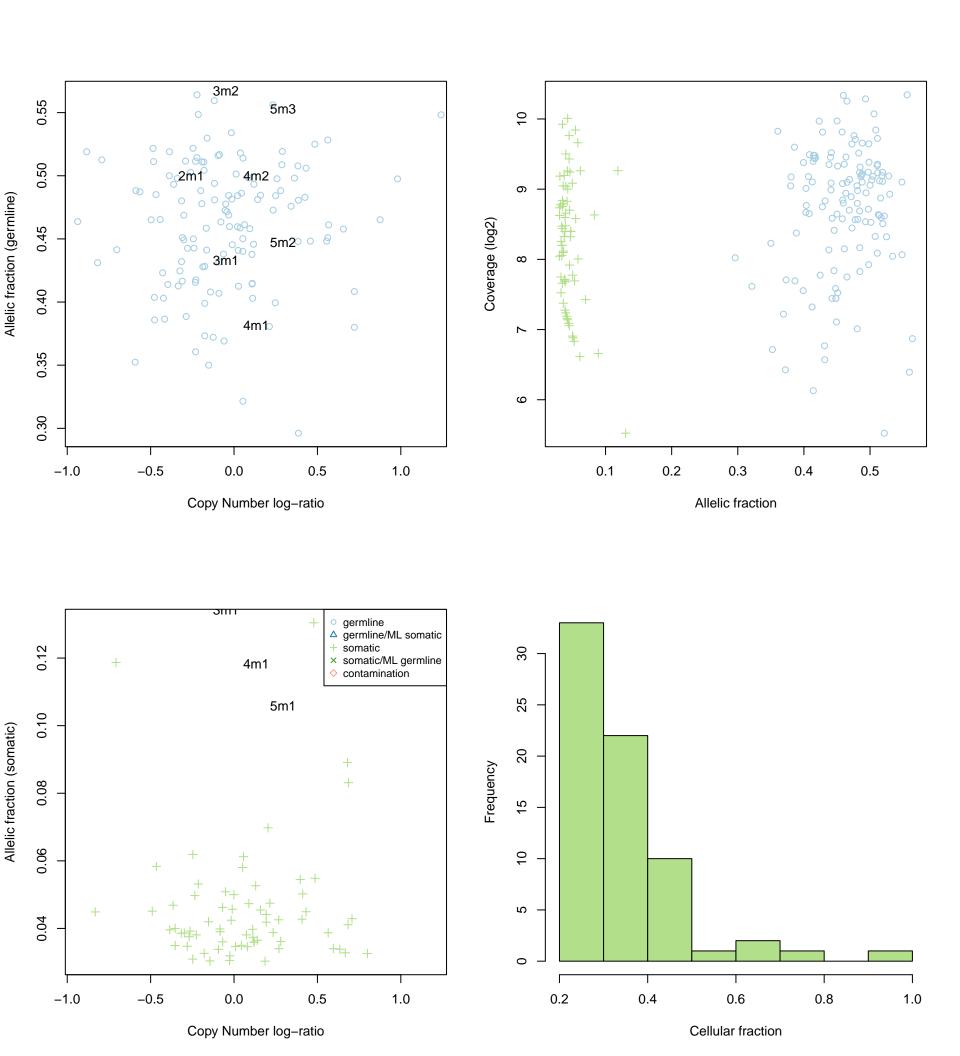




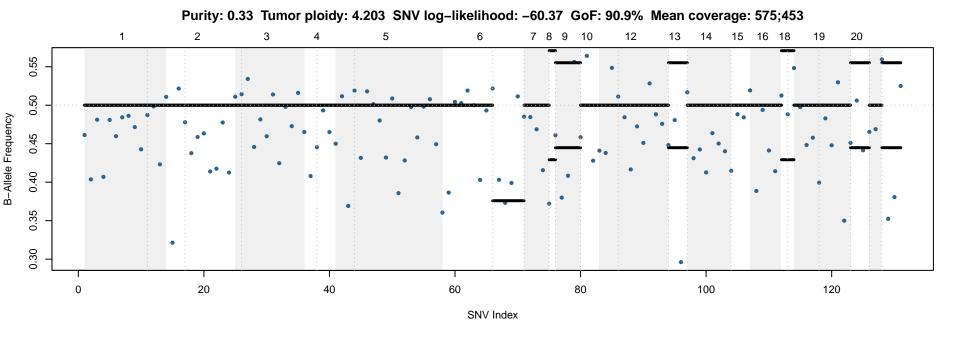
# SCNA-fit log-likelihood: -21564.45



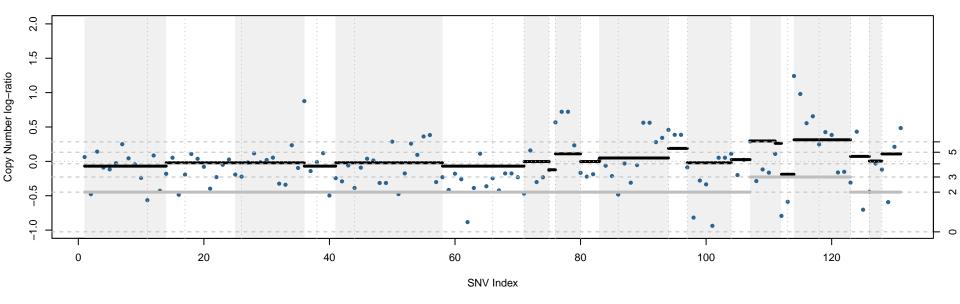


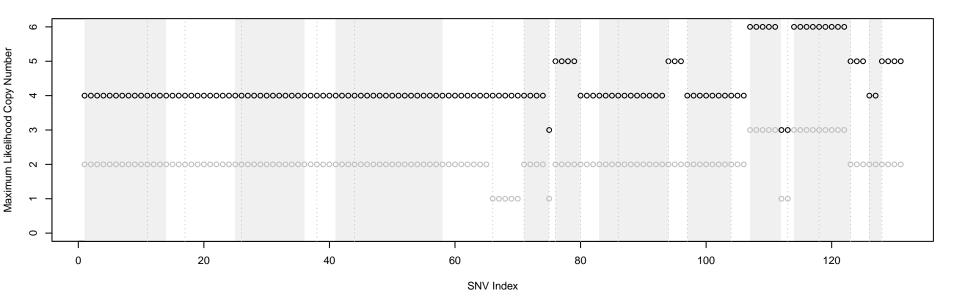


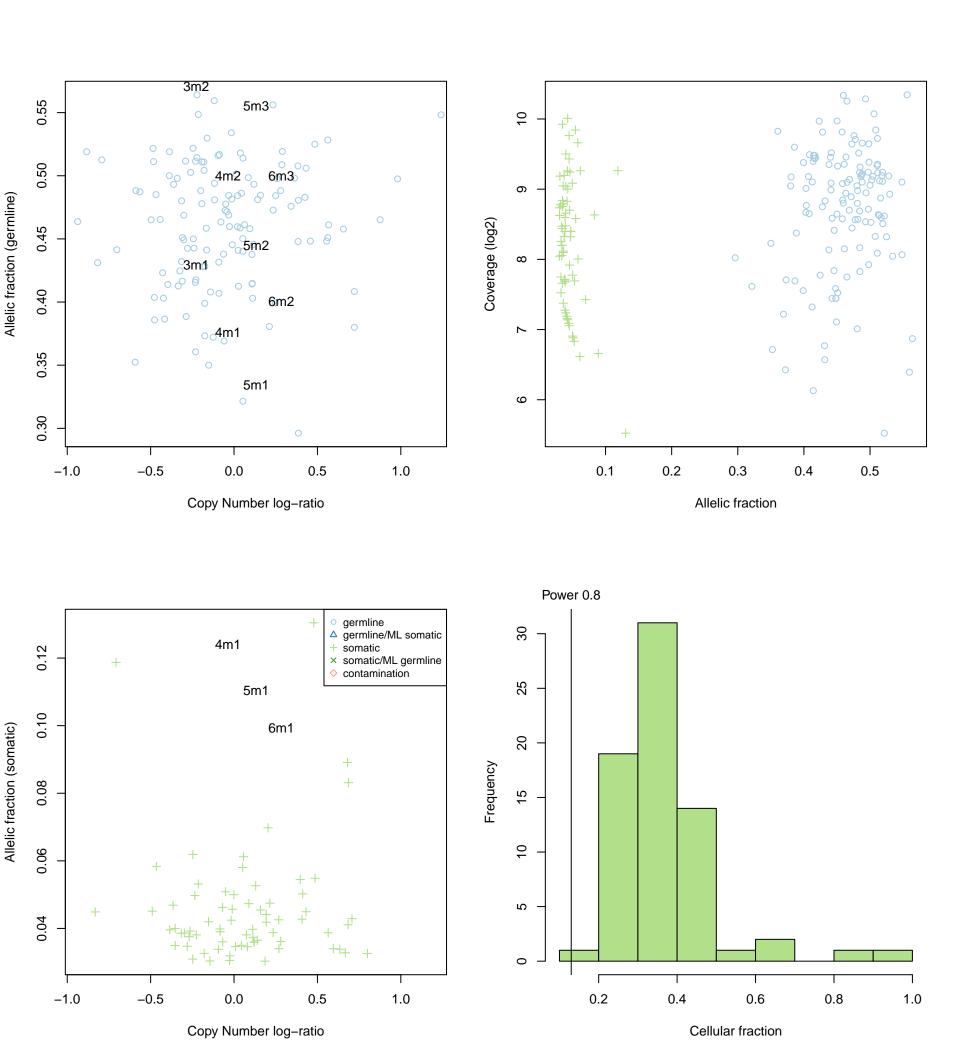
Purity: 0.33 Tumor ploidy: 4.203 3 5 6 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -2.0 -1.5 -1.0 -0.5 0.0 0.5 1.0 log2 ratio

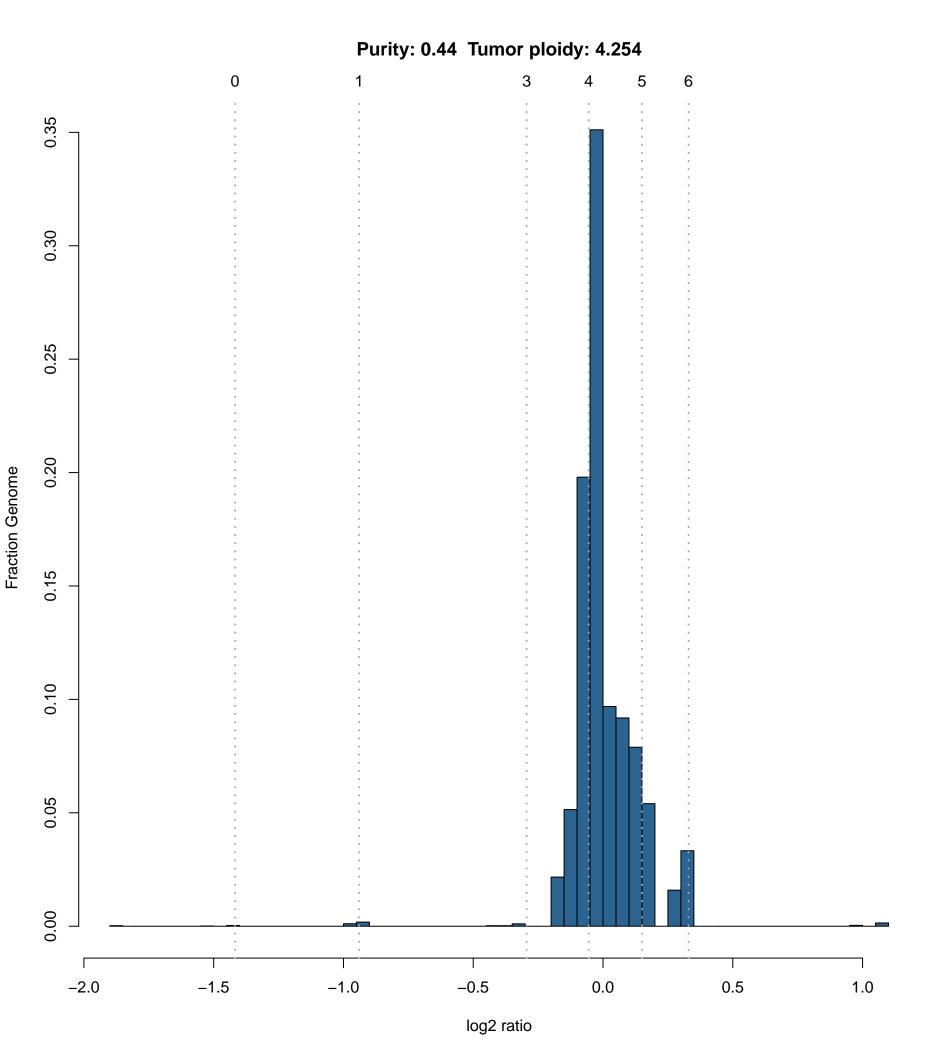


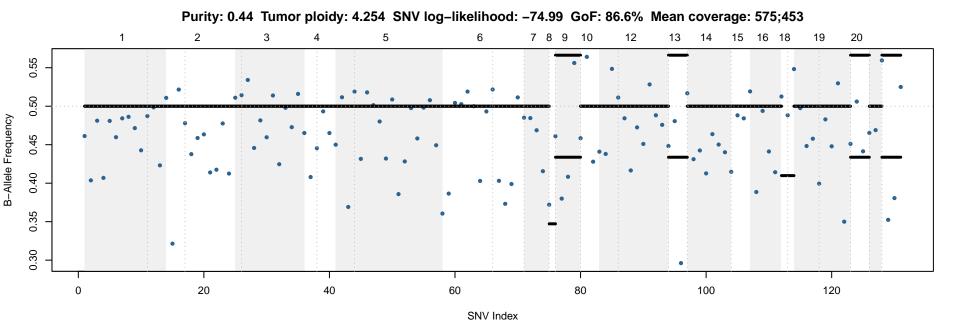
### SCNA-fit log-likelihood: -21557.49



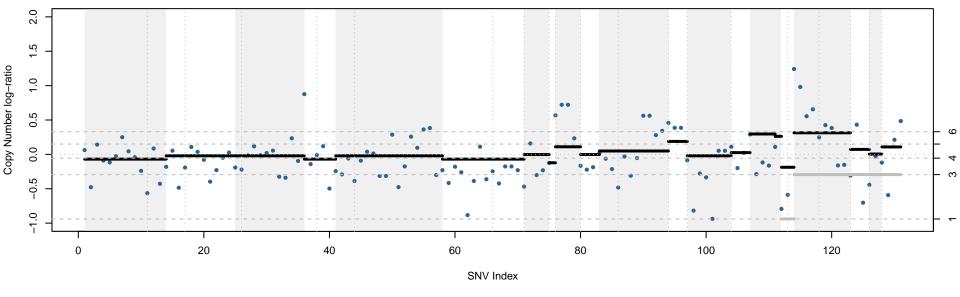


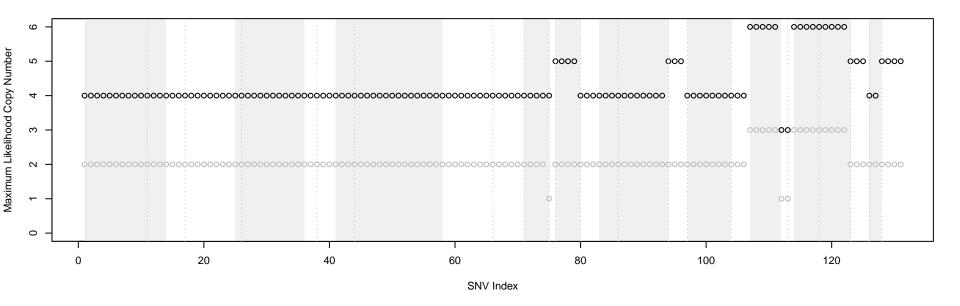


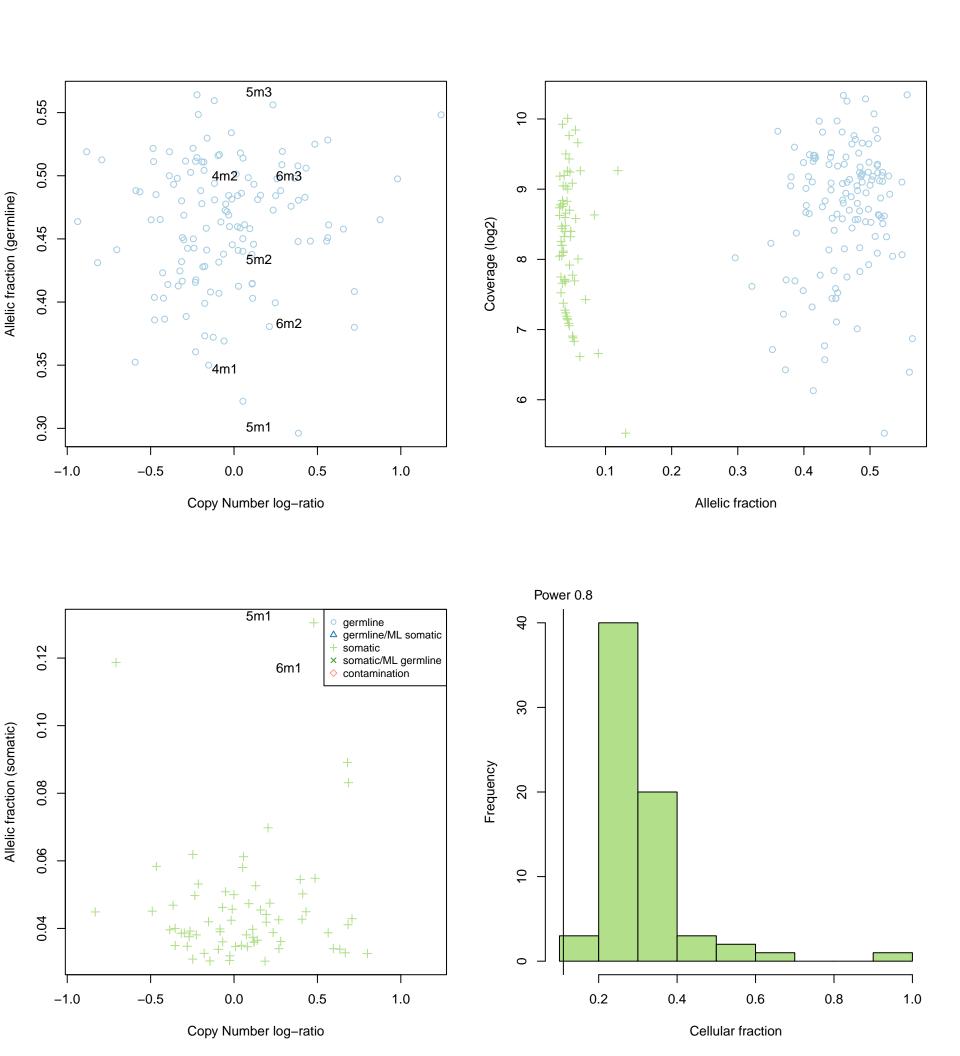


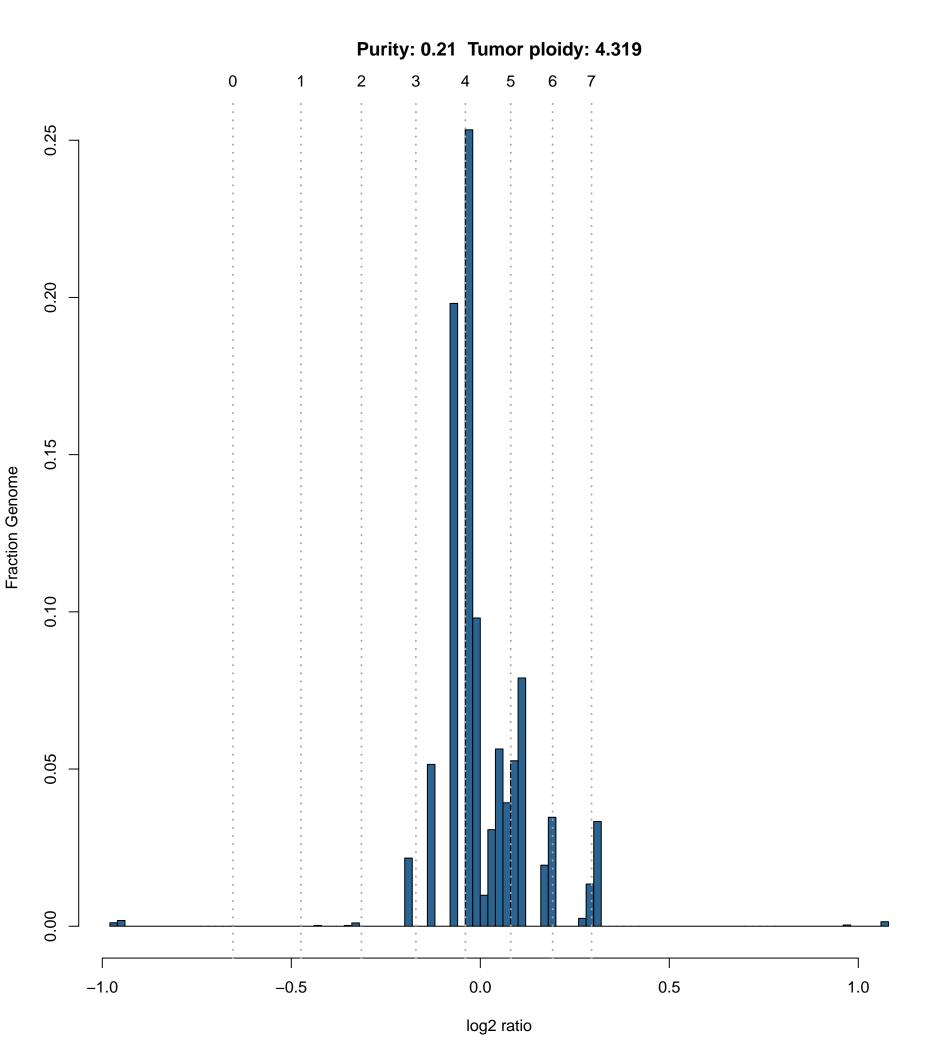


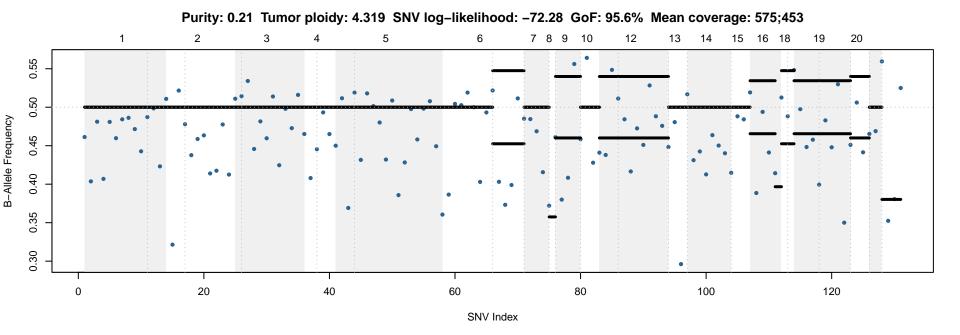
# SCNA-fit log-likelihood: -21573.21



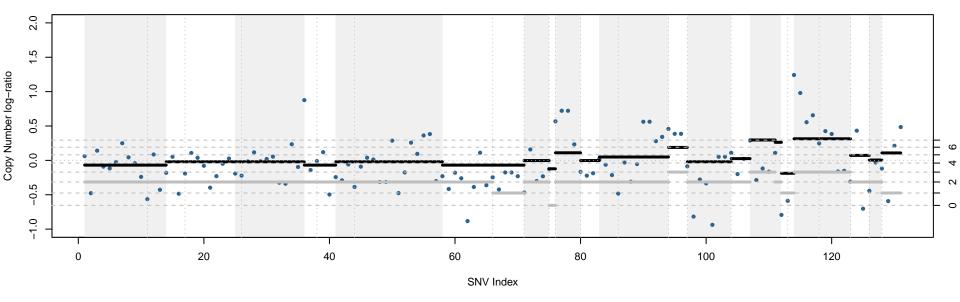


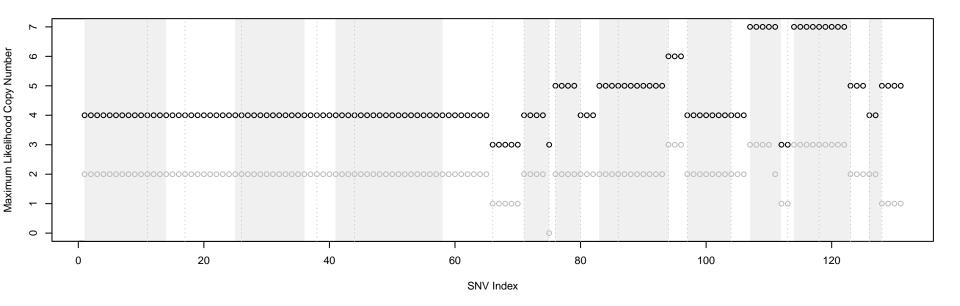


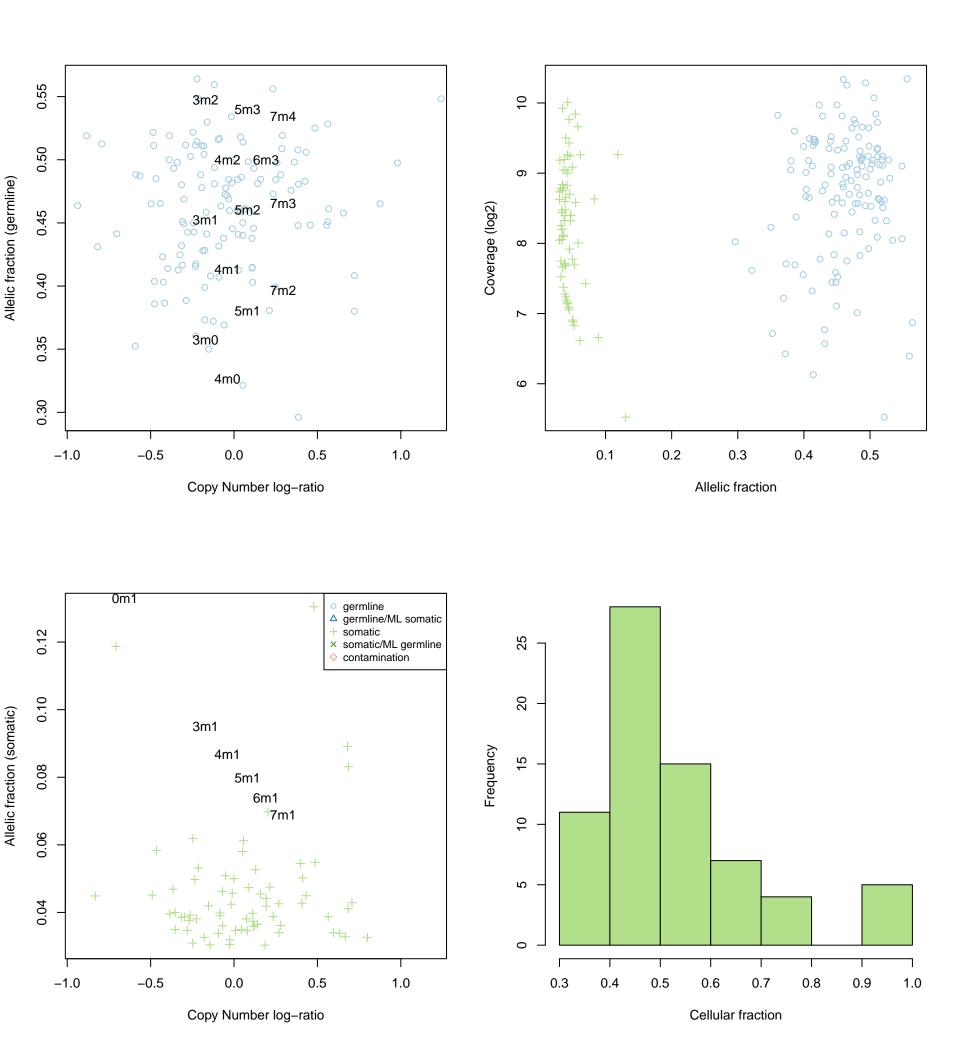




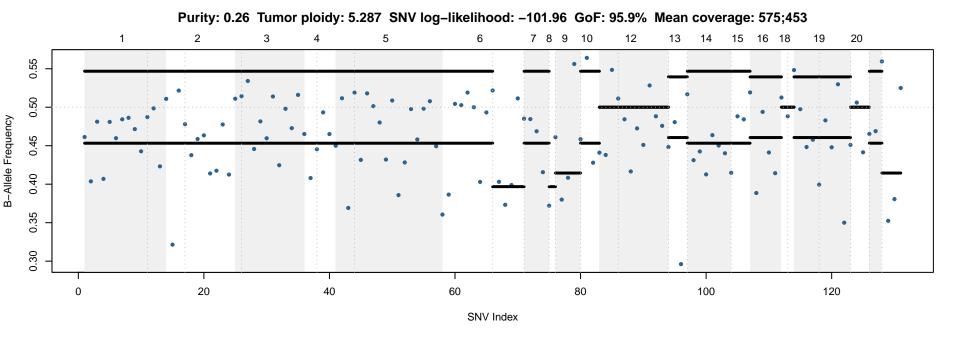
SCNA-fit log-likelihood: -21540.07



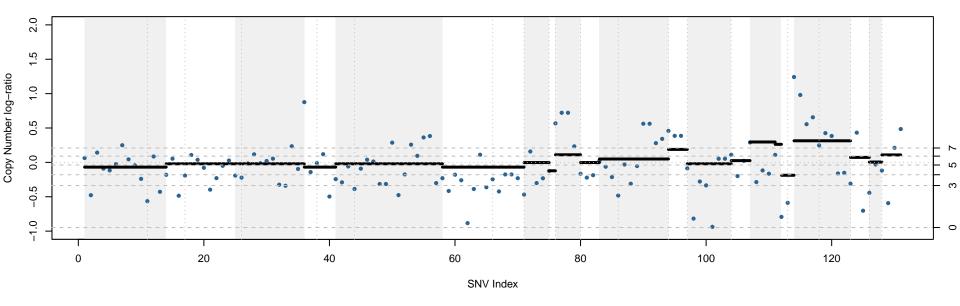


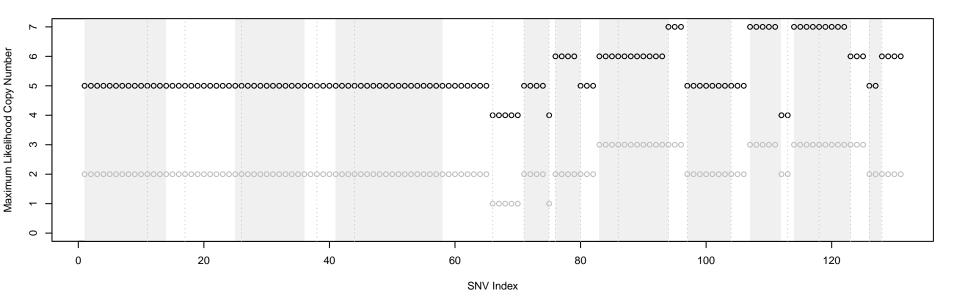


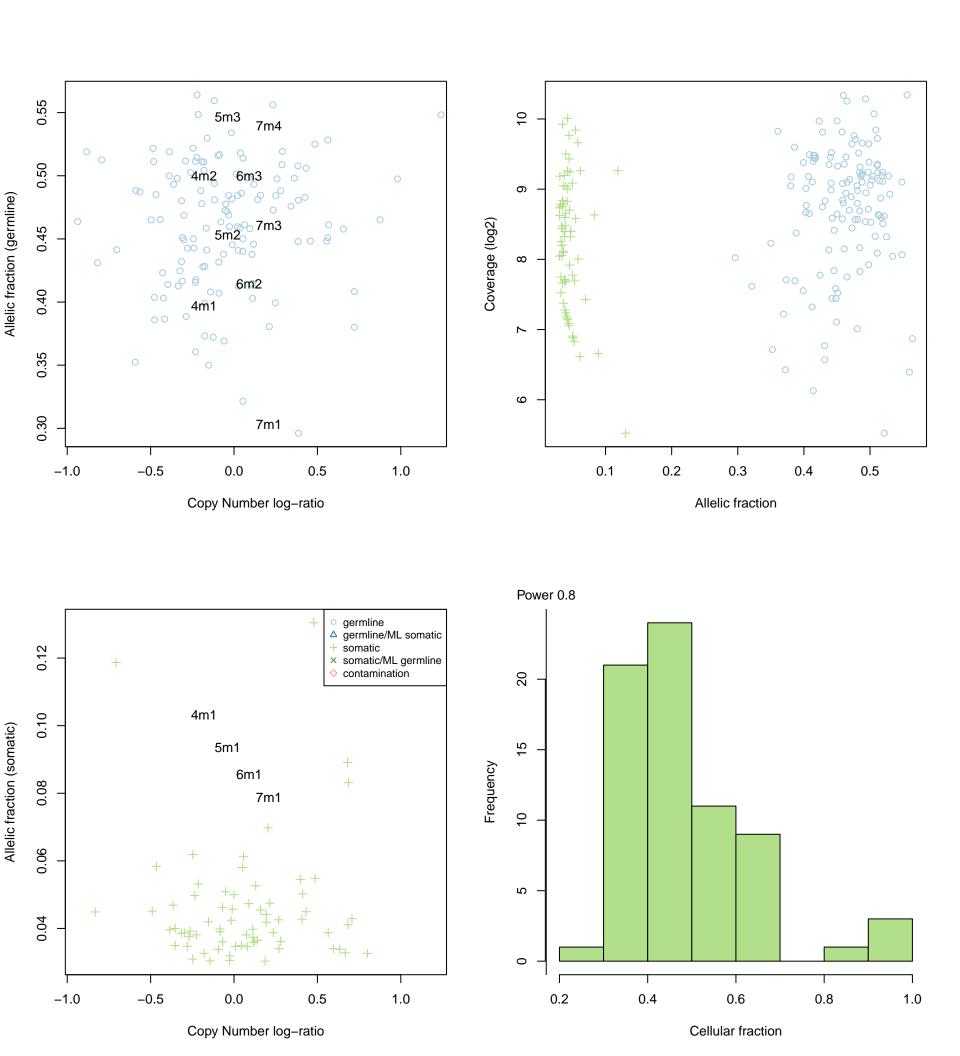
Purity: 0.26 Tumor ploidy: 5.287 7 5 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -2.0 -1.5 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



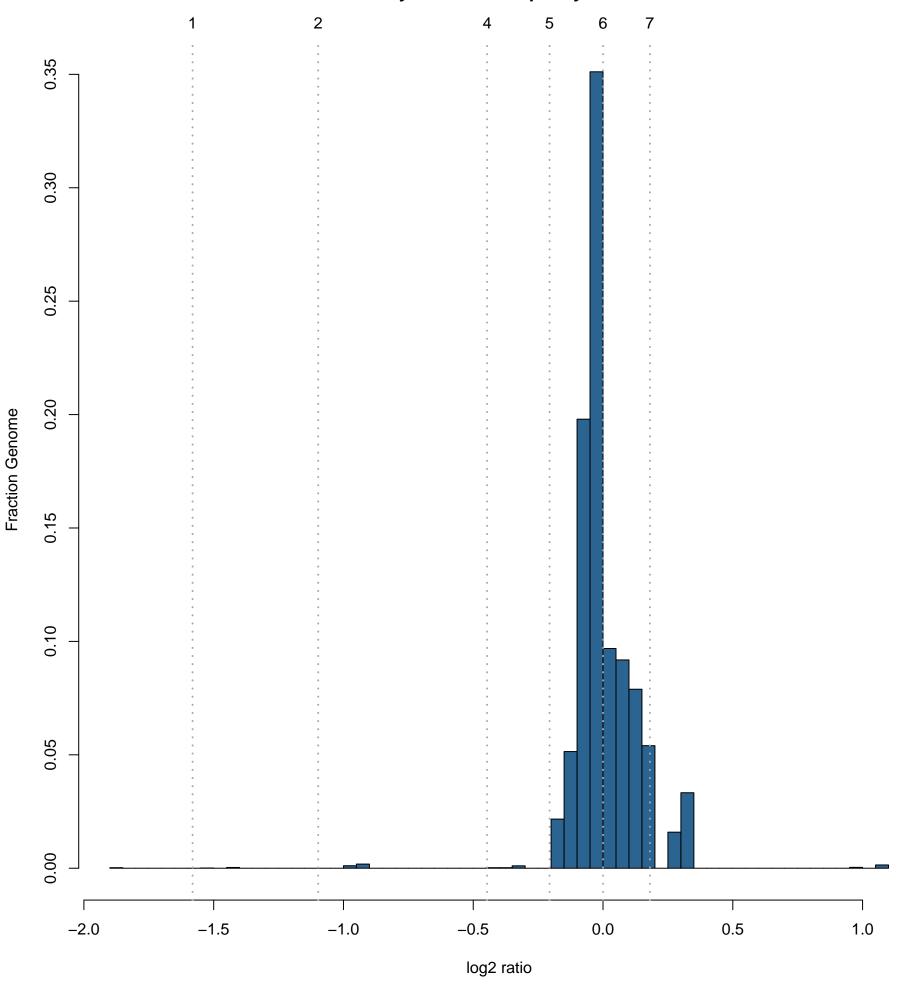


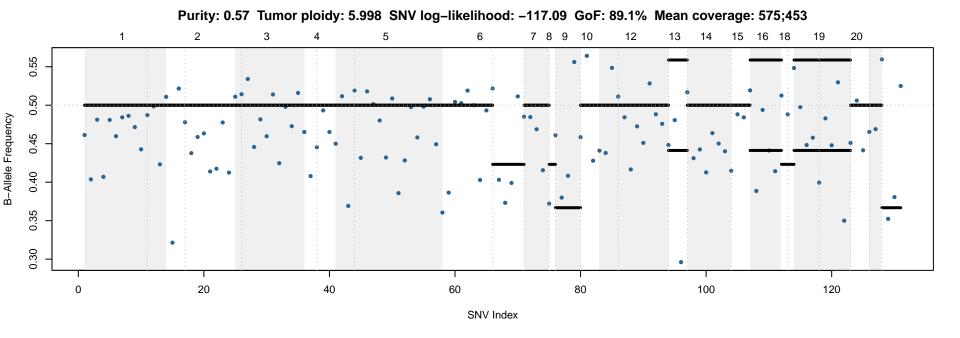




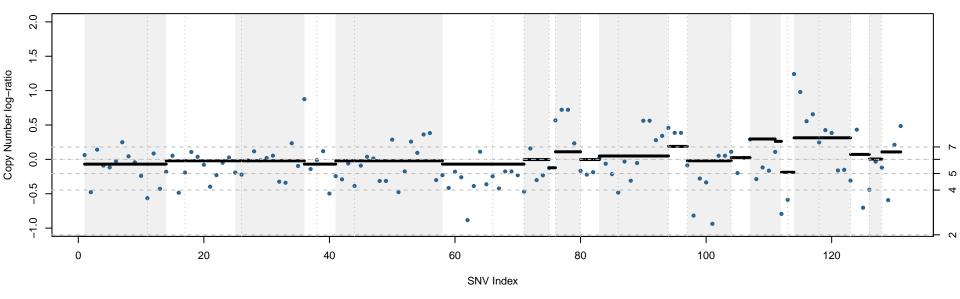


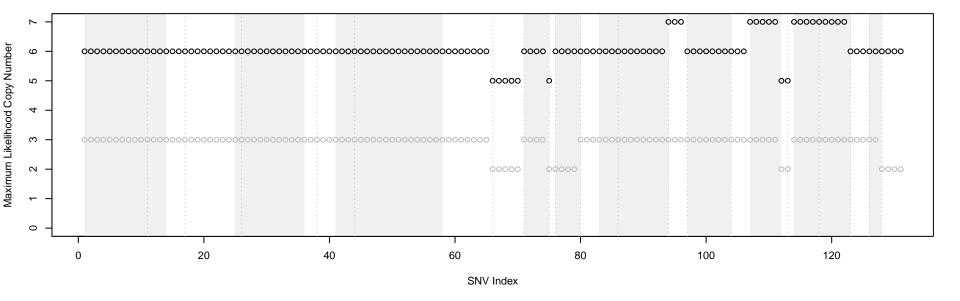
Purity: 0.57 Tumor ploidy: 5.998

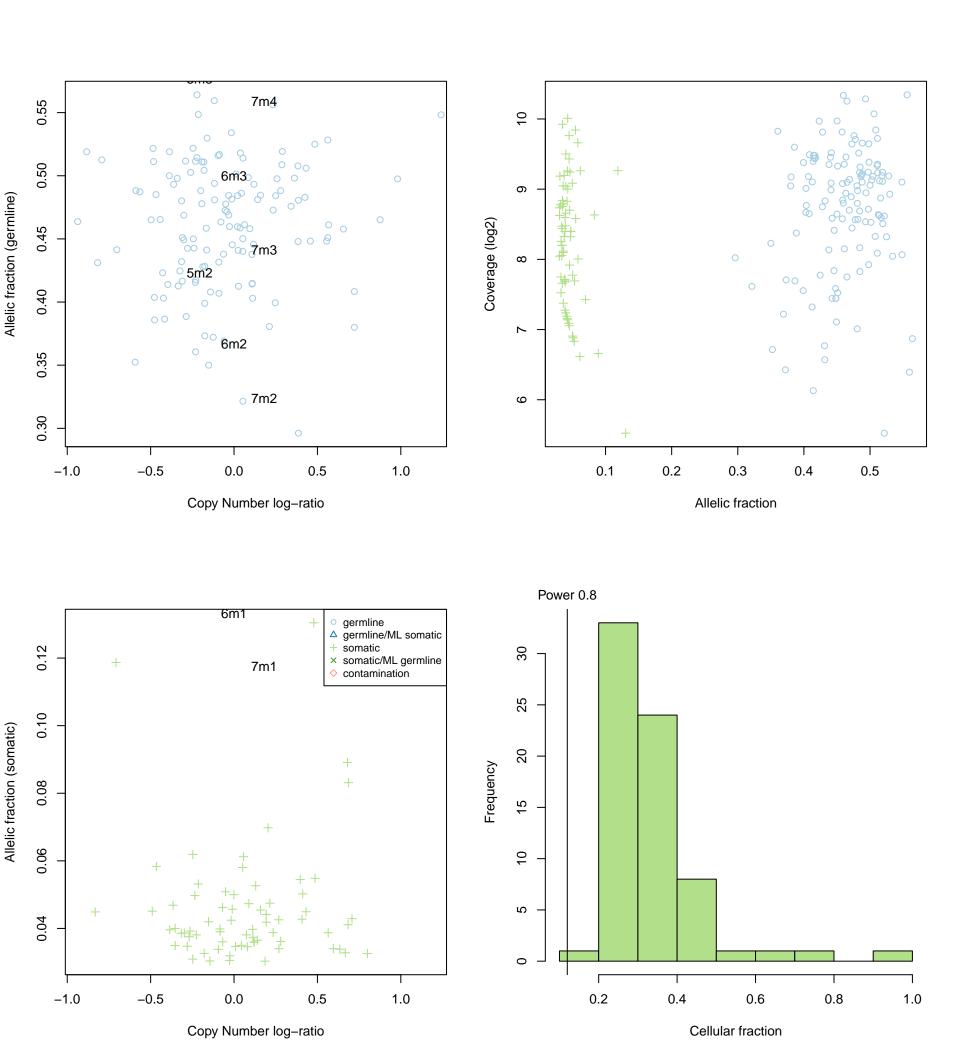




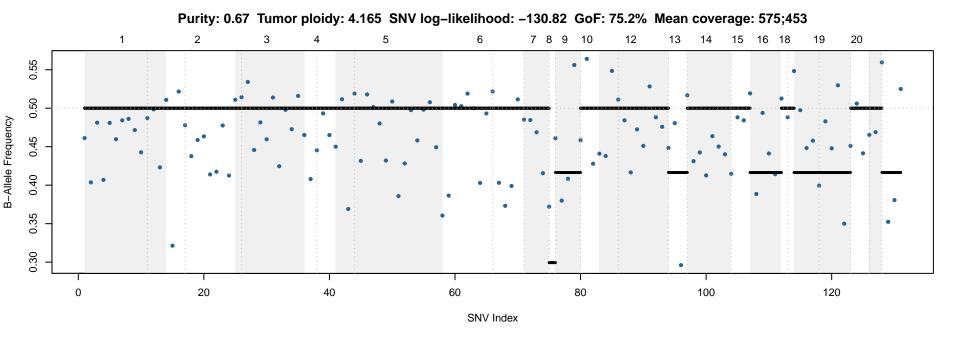
### SCNA-fit log-likelihood: -21600.37



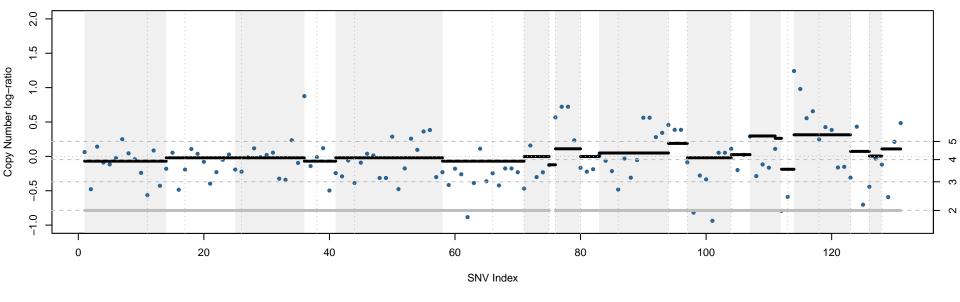


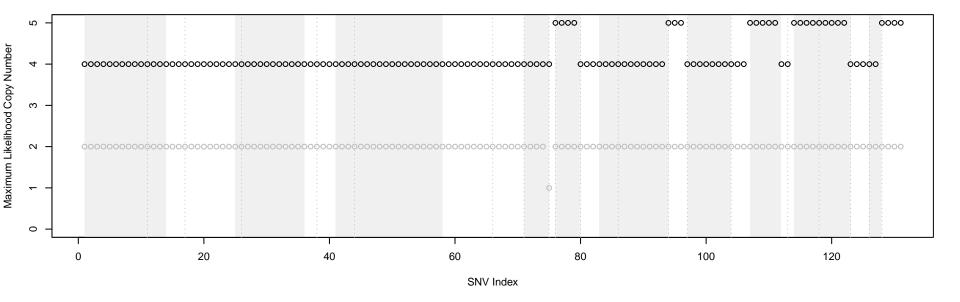


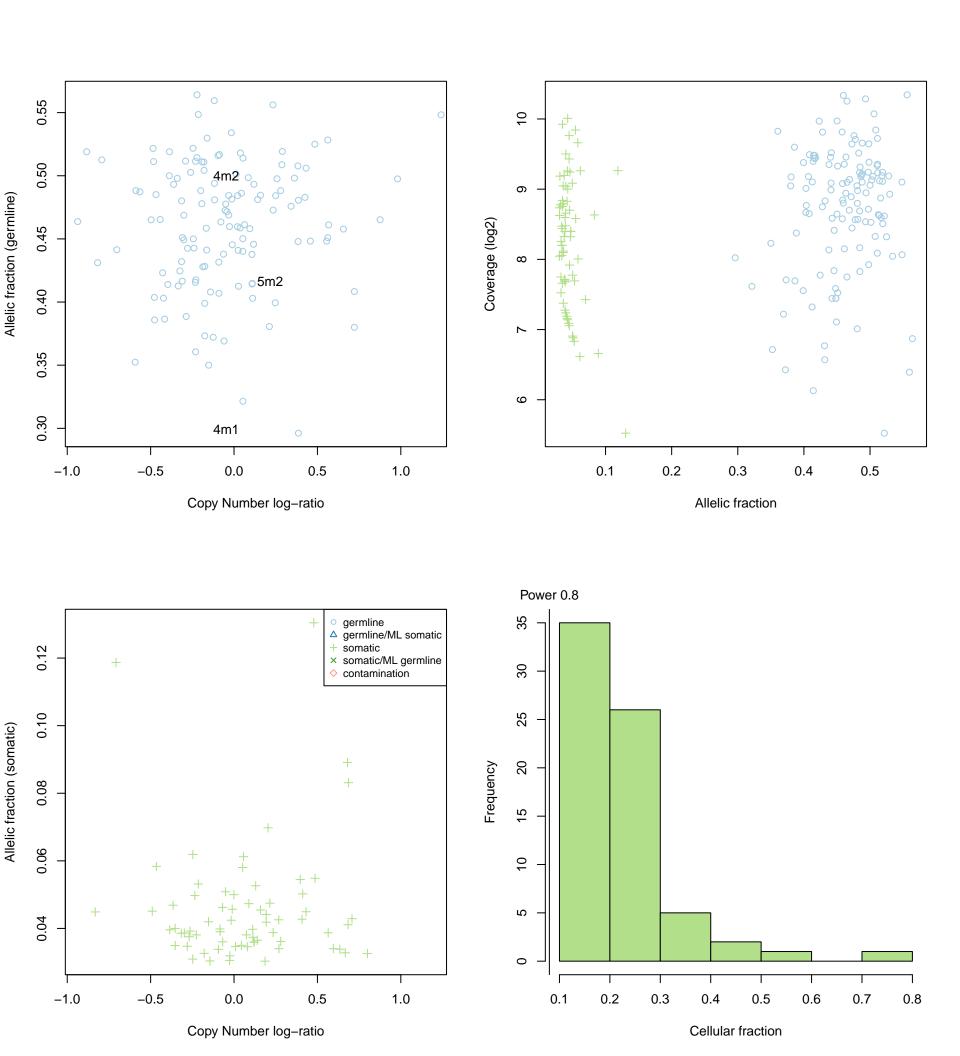
Purity: 0.67 Tumor ploidy: 4.165 3 5 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -2.0 -1.5 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



### SCNA-fit log-likelihood: -21622.55

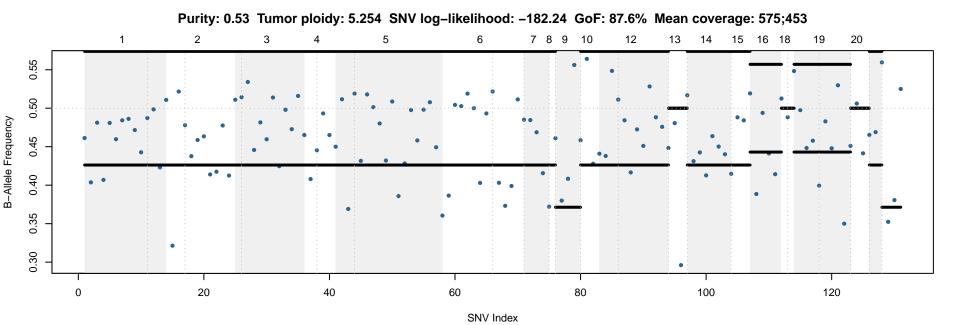




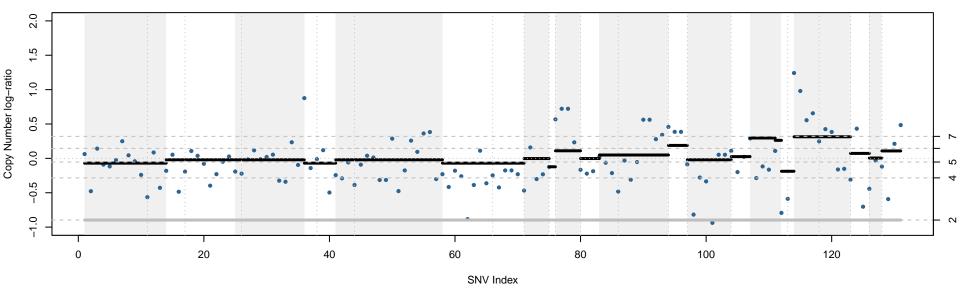


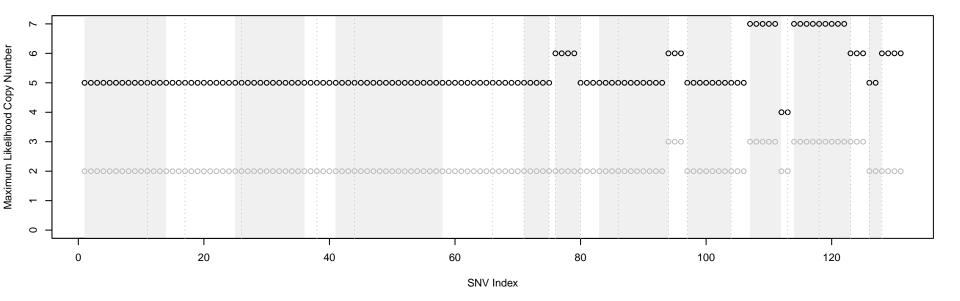
Purity: 0.53 Tumor ploidy: 5.254 7 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.05 0.00 -2.0 -1.5 -1.0 -0.5 0.0 0.5 1.0

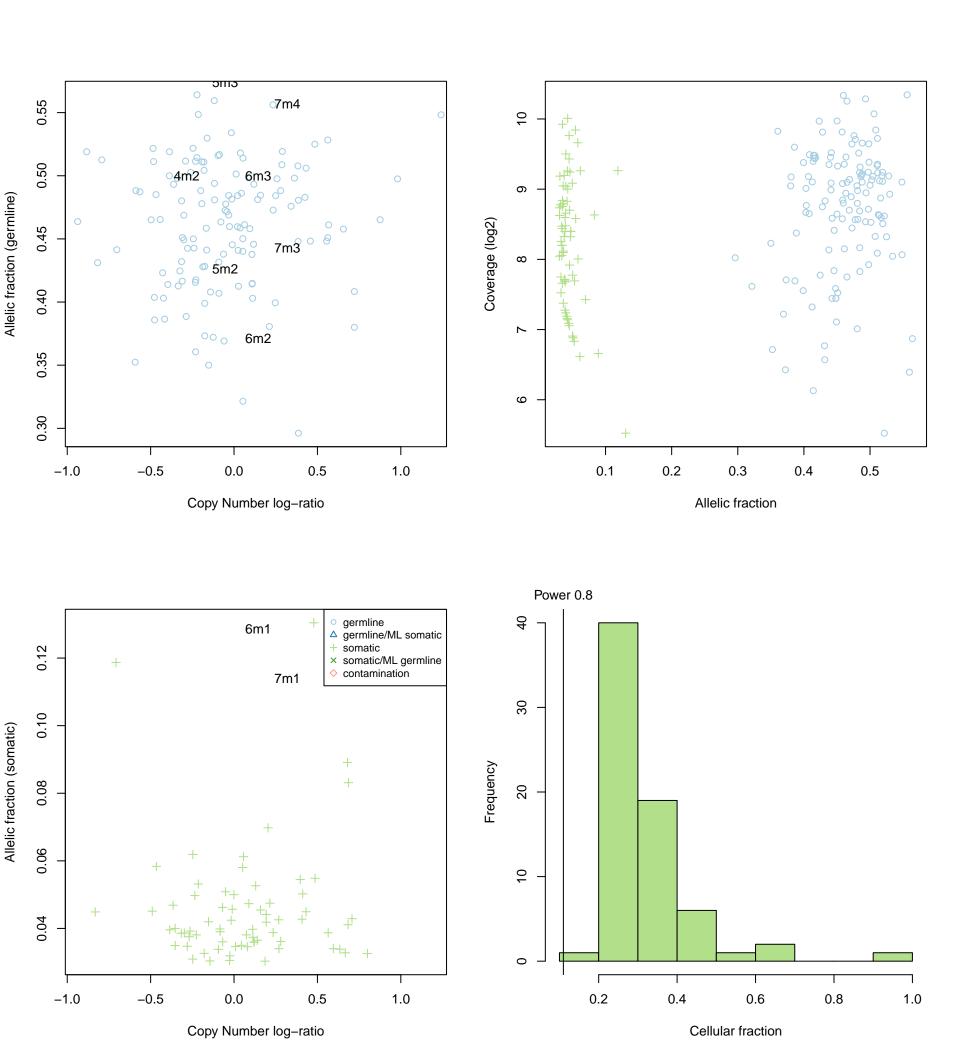
log2 ratio



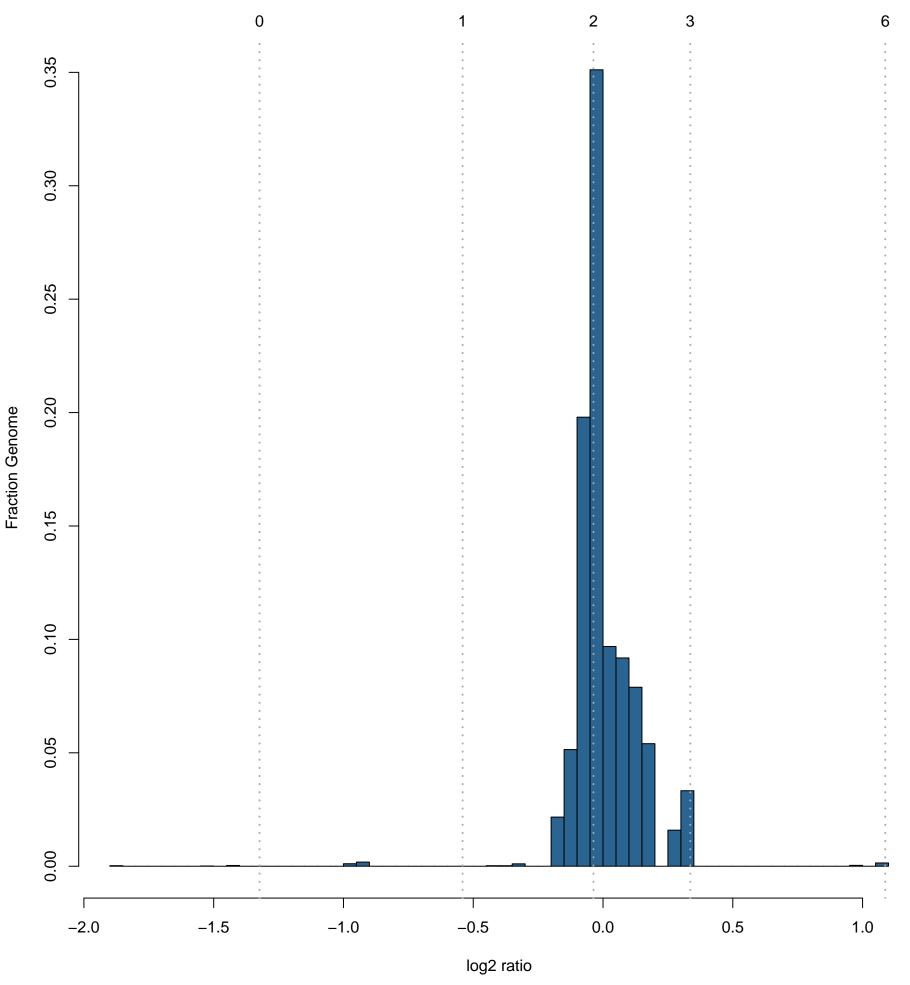
### SCNA-fit log-likelihood: -21569.49

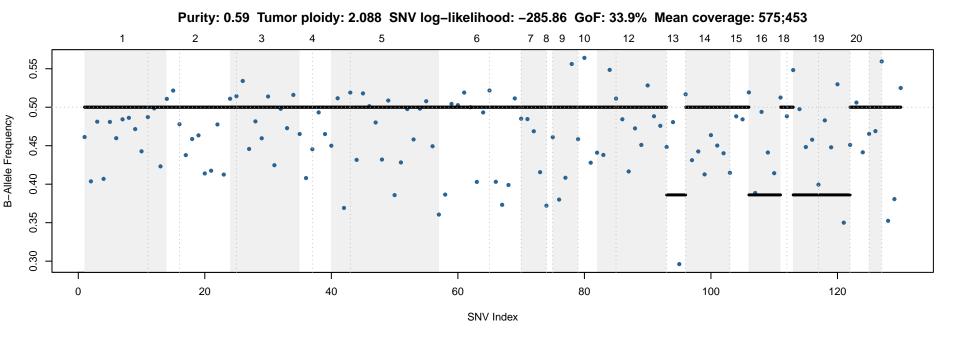




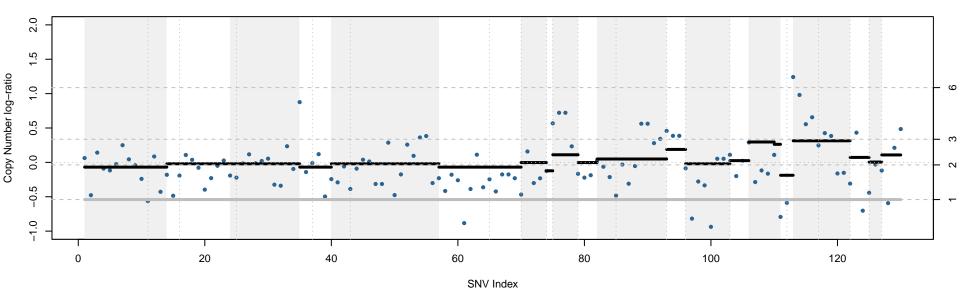


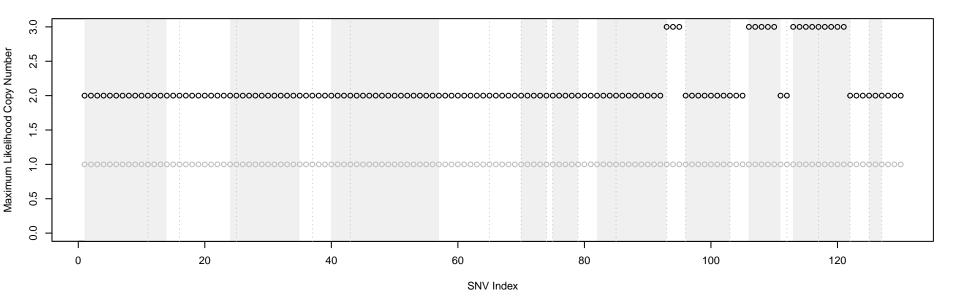
Purity: 0.59 Tumor ploidy: 2.088

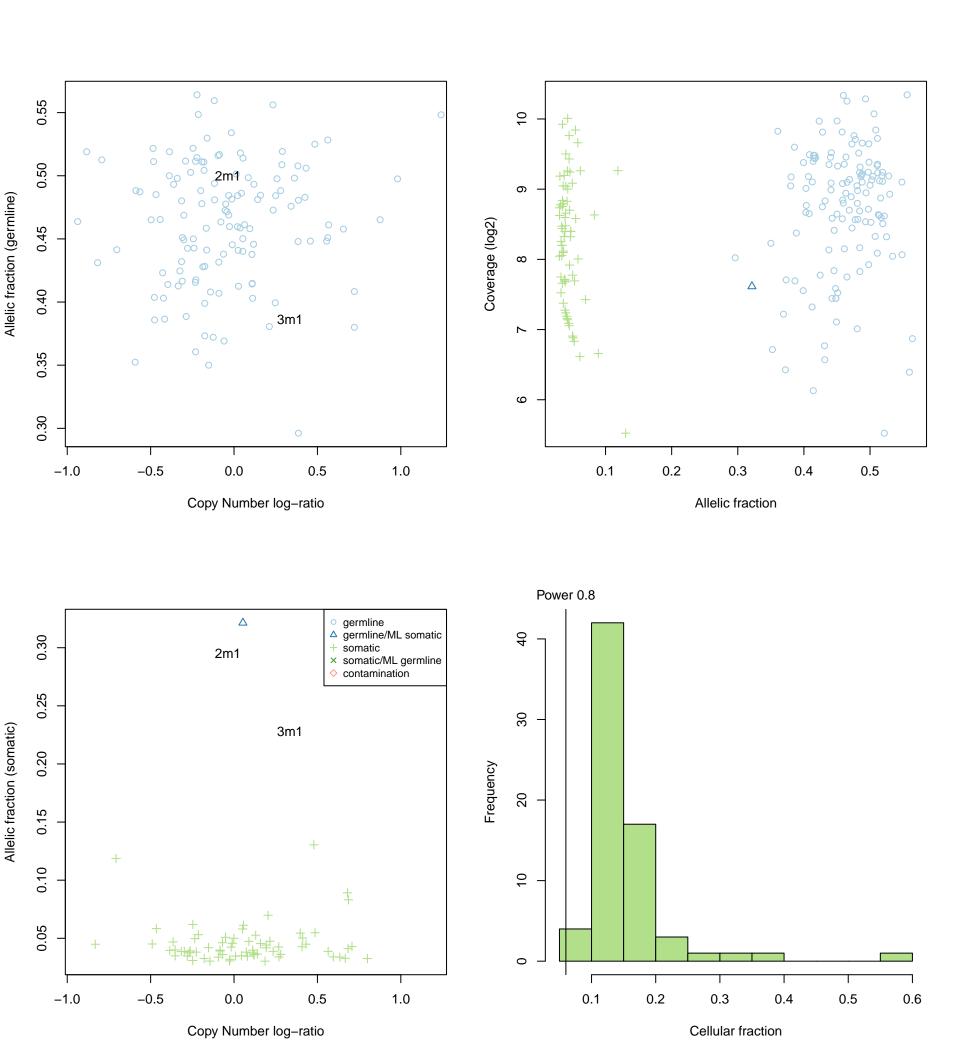




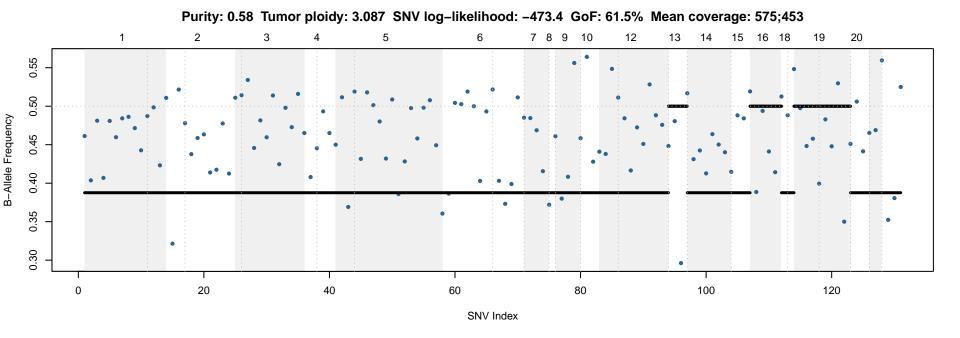
SCNA-fit log-likelihood: -21642.07



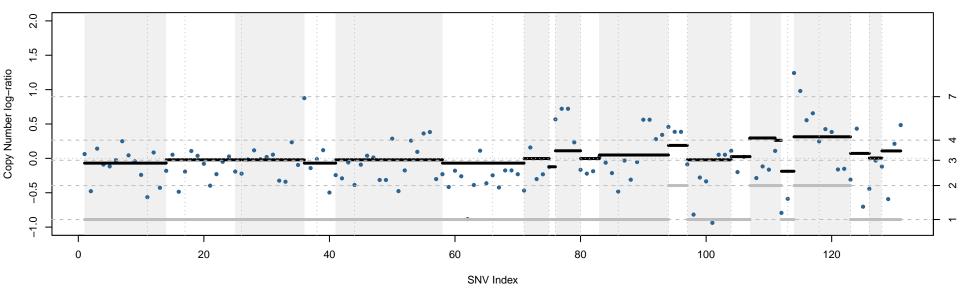


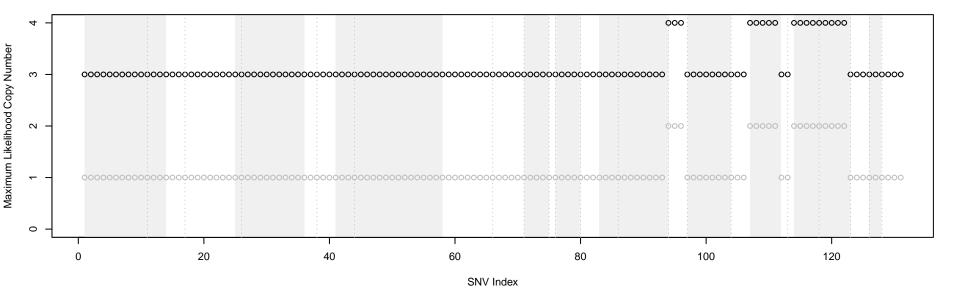


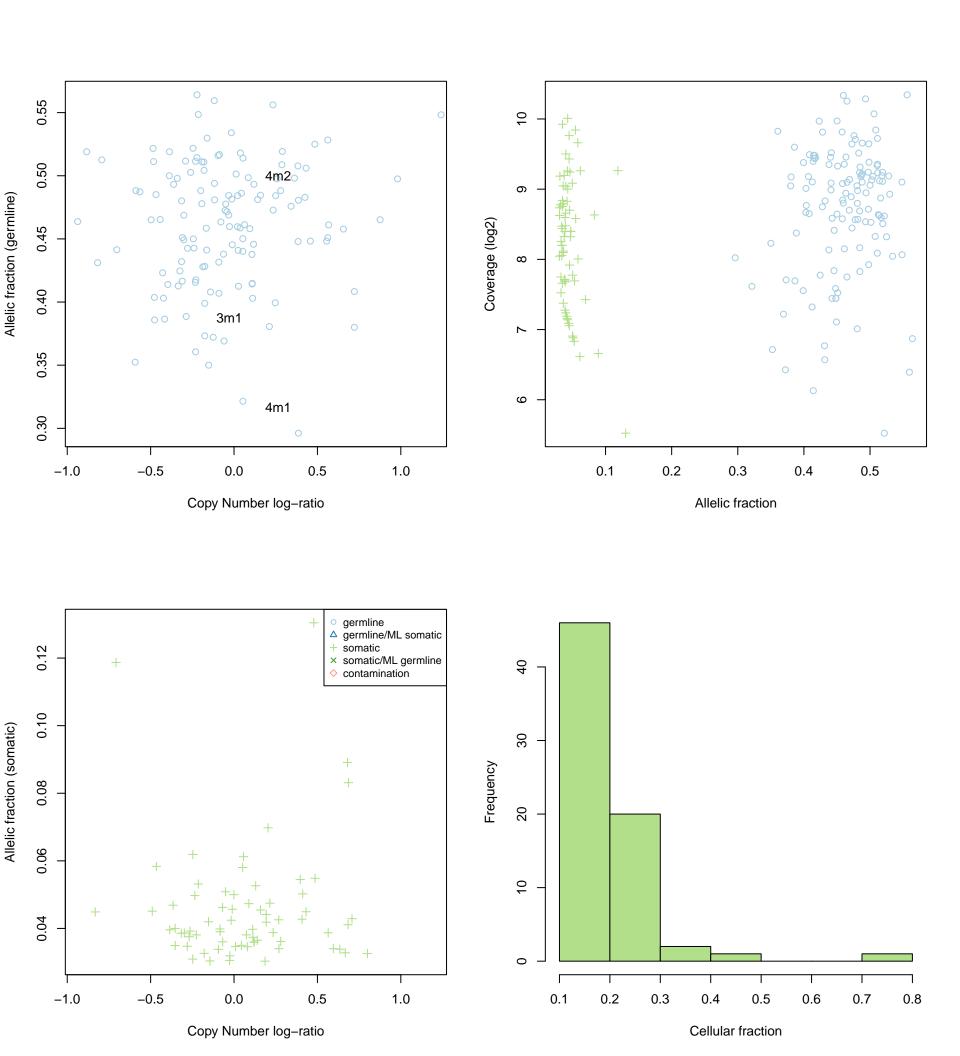
Purity: 0.58 Tumor ploidy: 3.087 0 2 3 7 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -2.0 -1.5 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



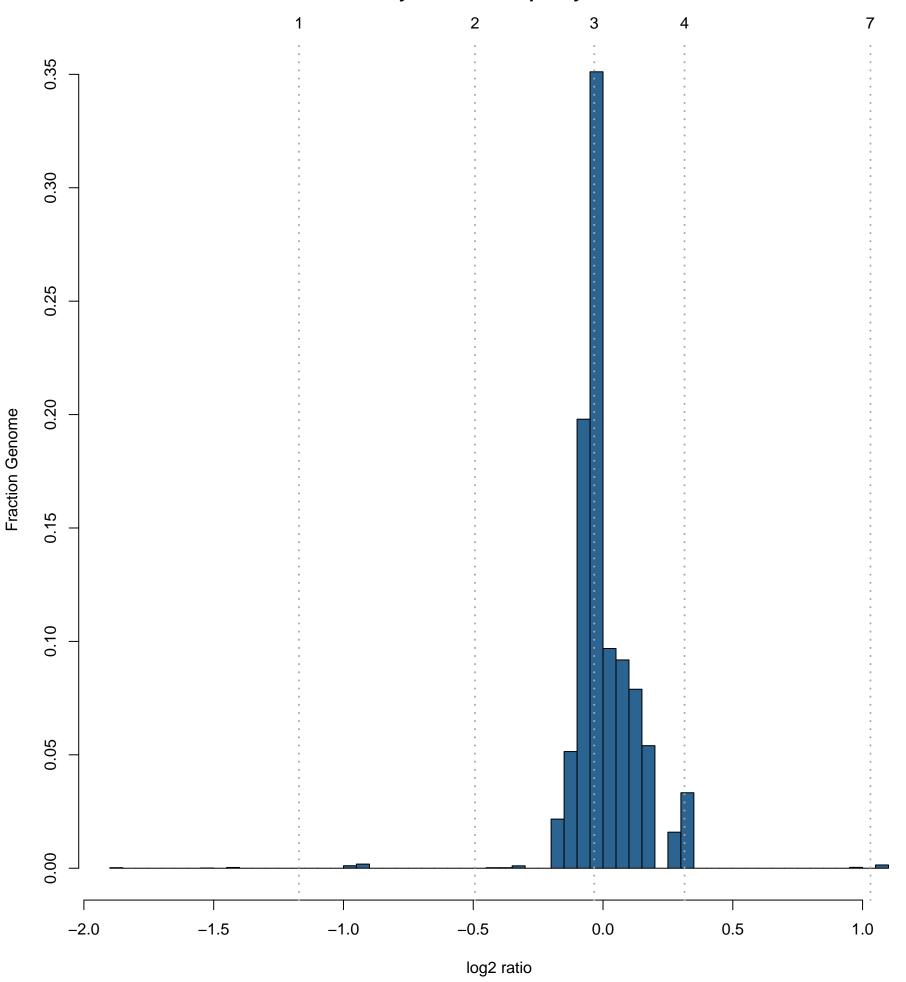
### SCNA-fit log-likelihood: -21610.14

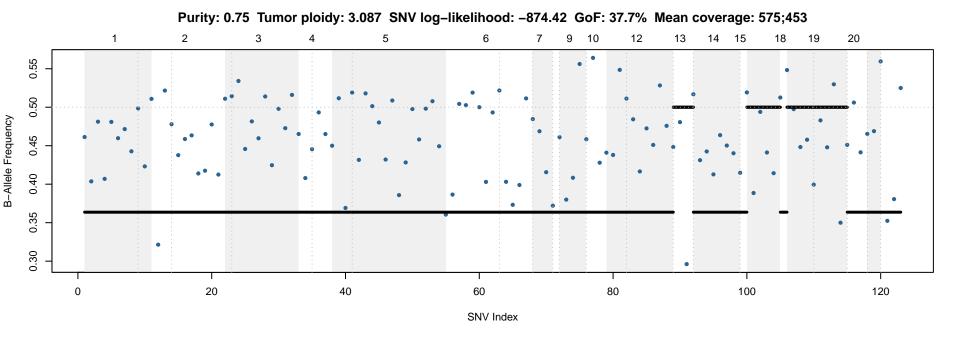






Purity: 0.75 Tumor ploidy: 3.087





### SCNA-fit log-likelihood: -21626.49

