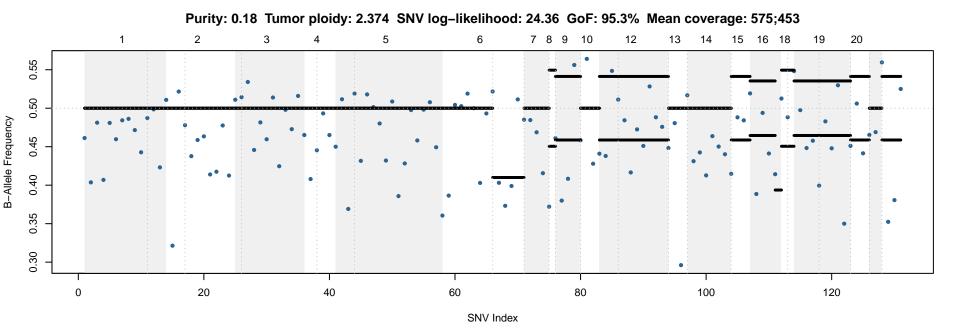
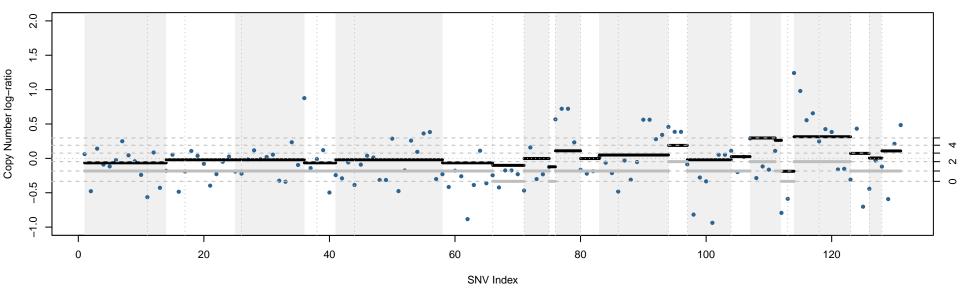
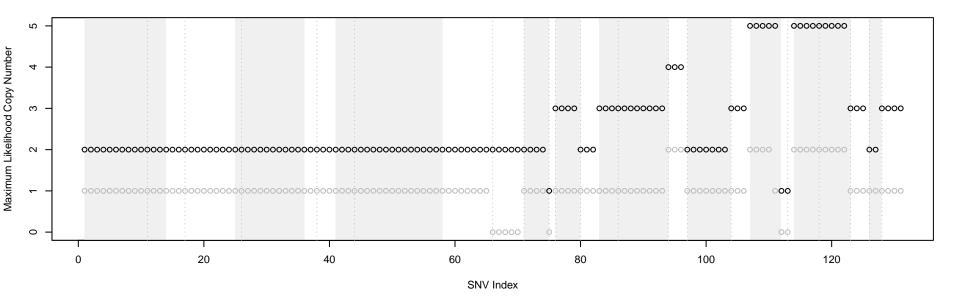
Purity: 0.18 Tumor ploidy: 2.374 0 2 3 5 0.25 0.20 Fraction Genome 0.05 0.00 -0.5 0.0 0.5 1.0

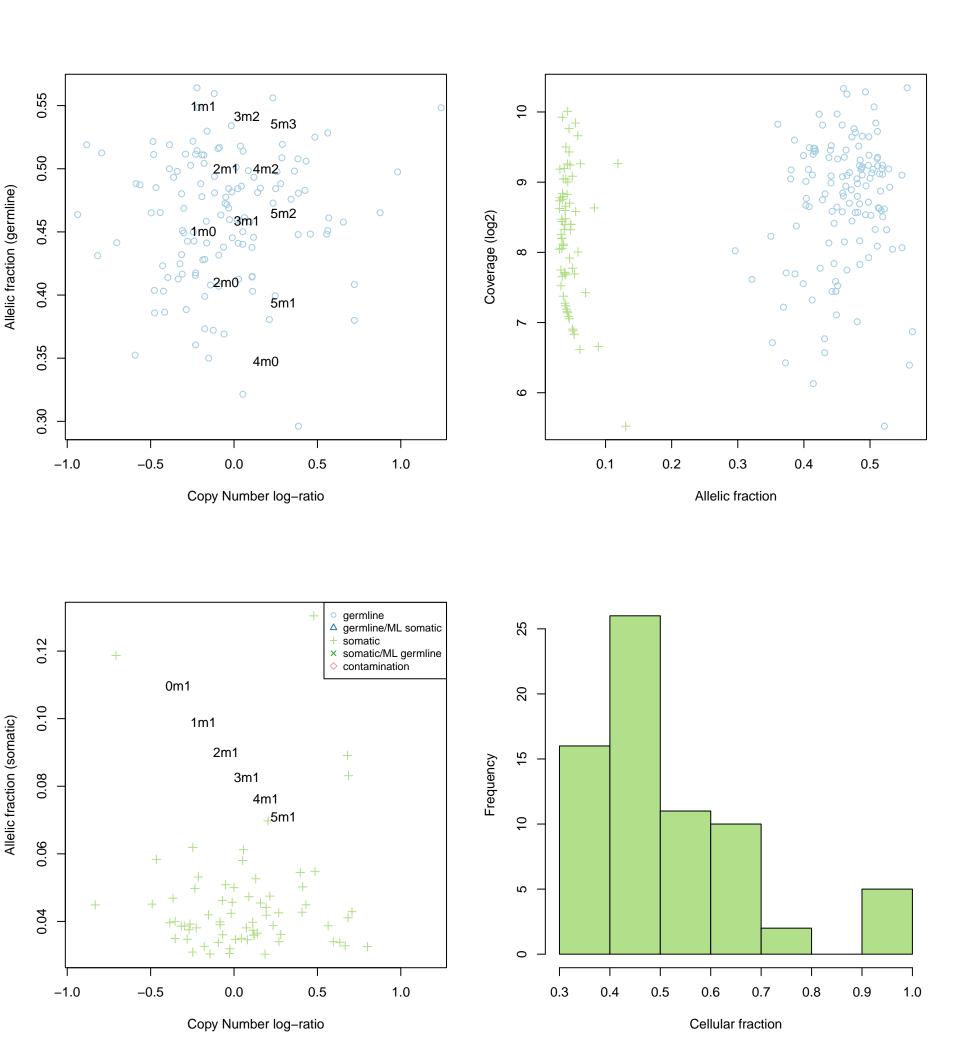
log2 ratio

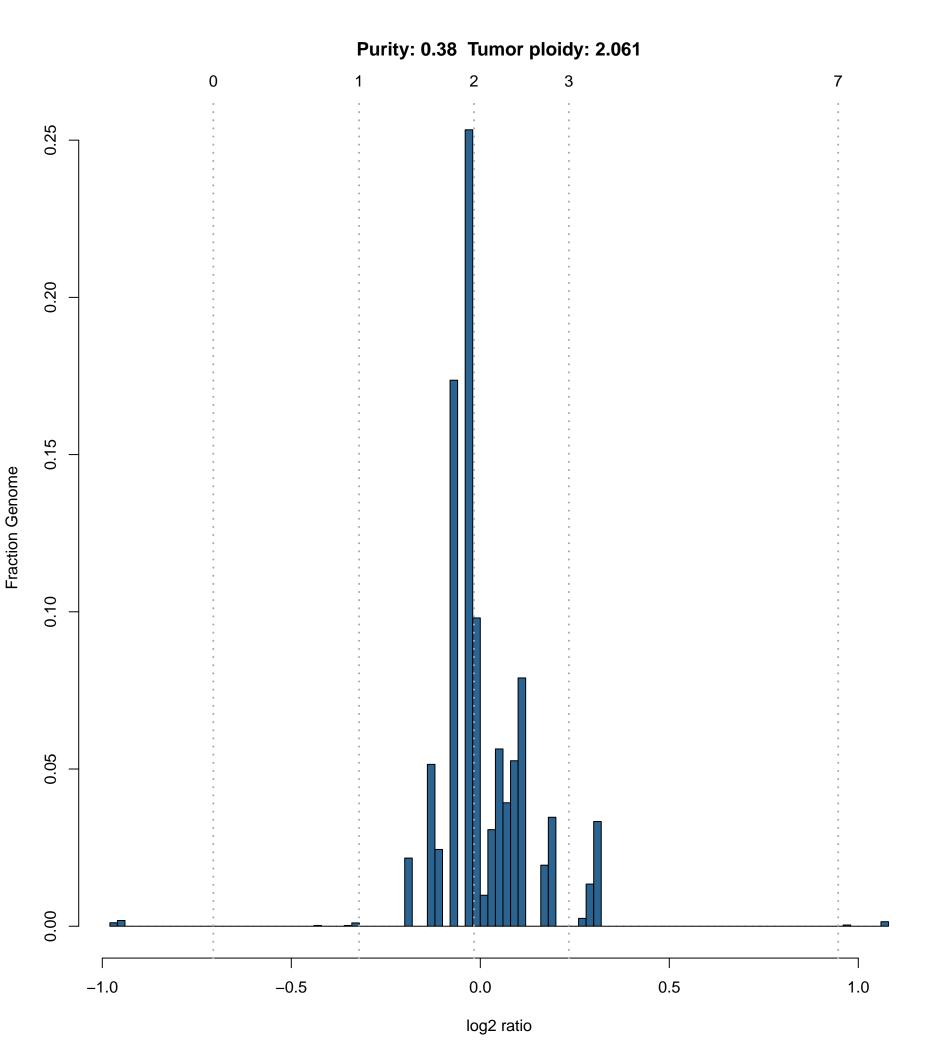


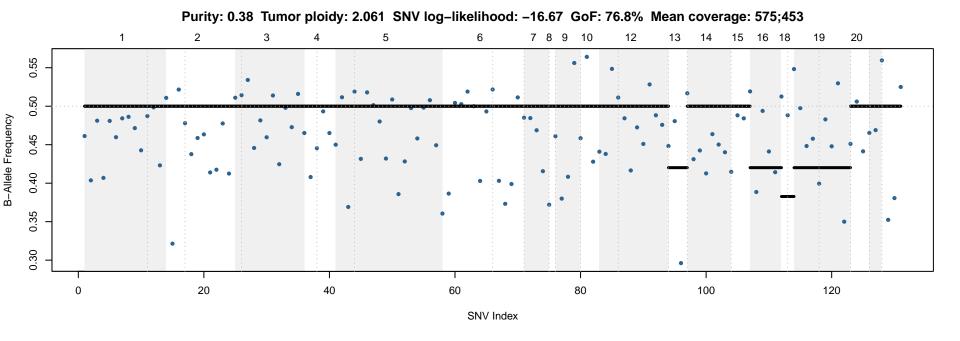
# SCNA-fit log-likelihood: -21560.62



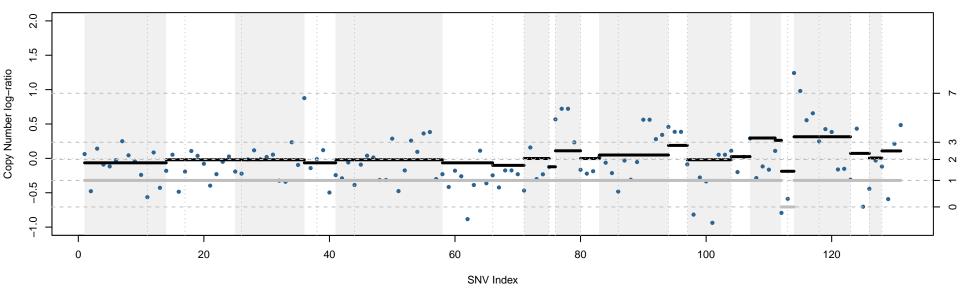


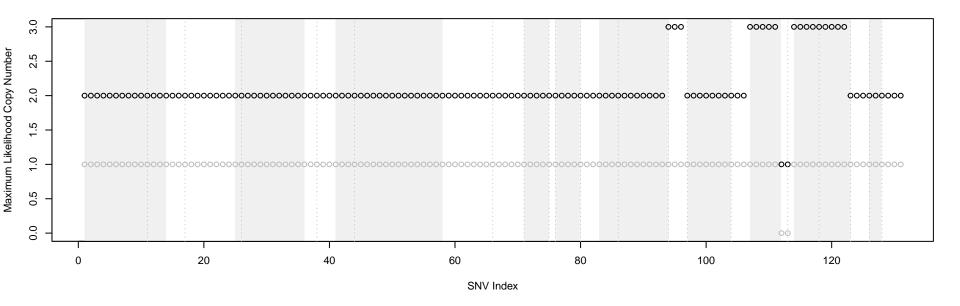


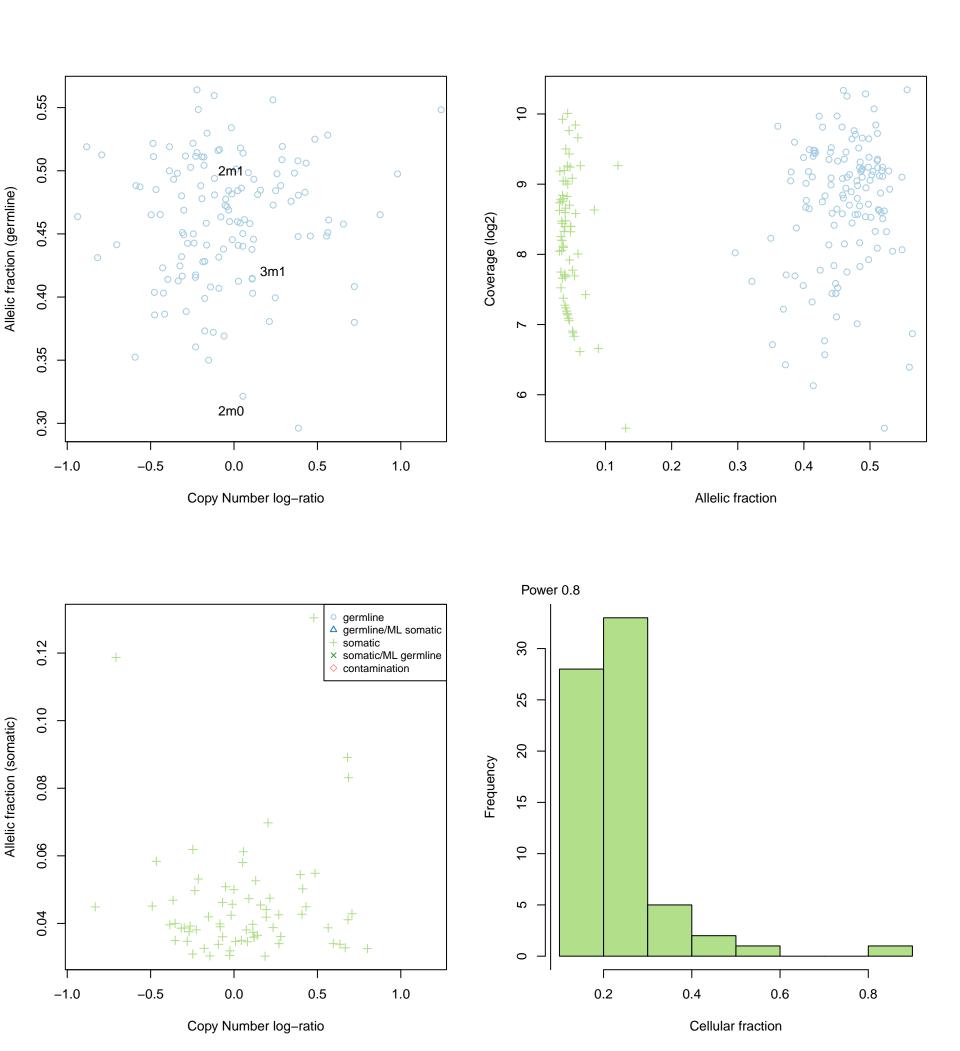


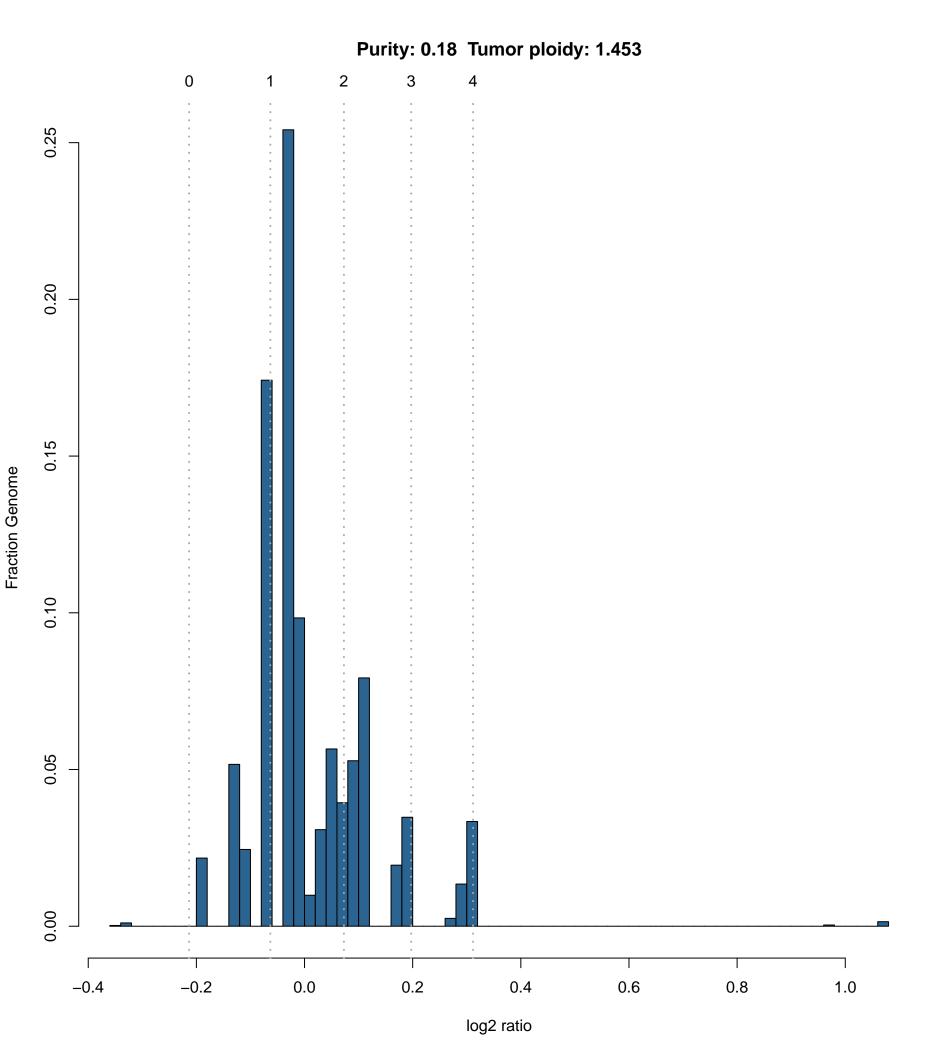


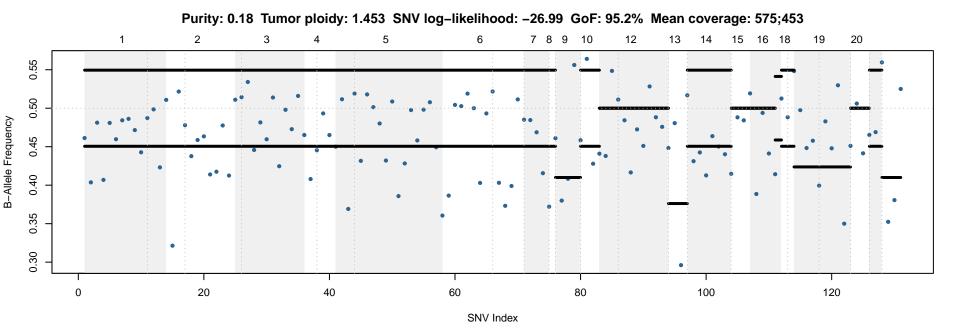
### SCNA-fit log-likelihood: -21601.99



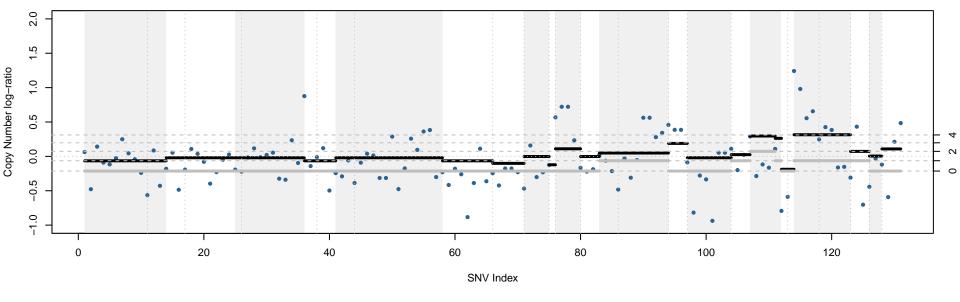


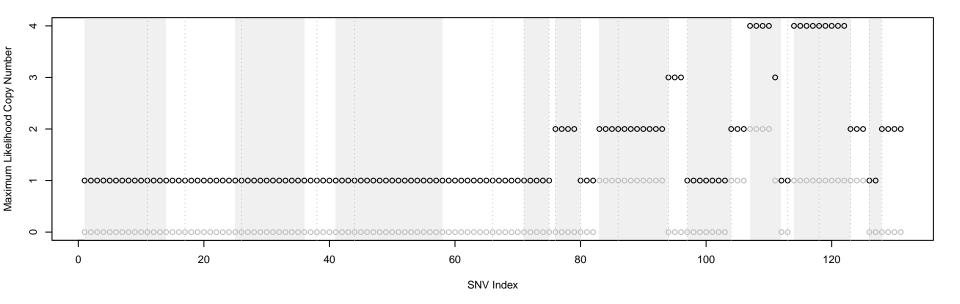


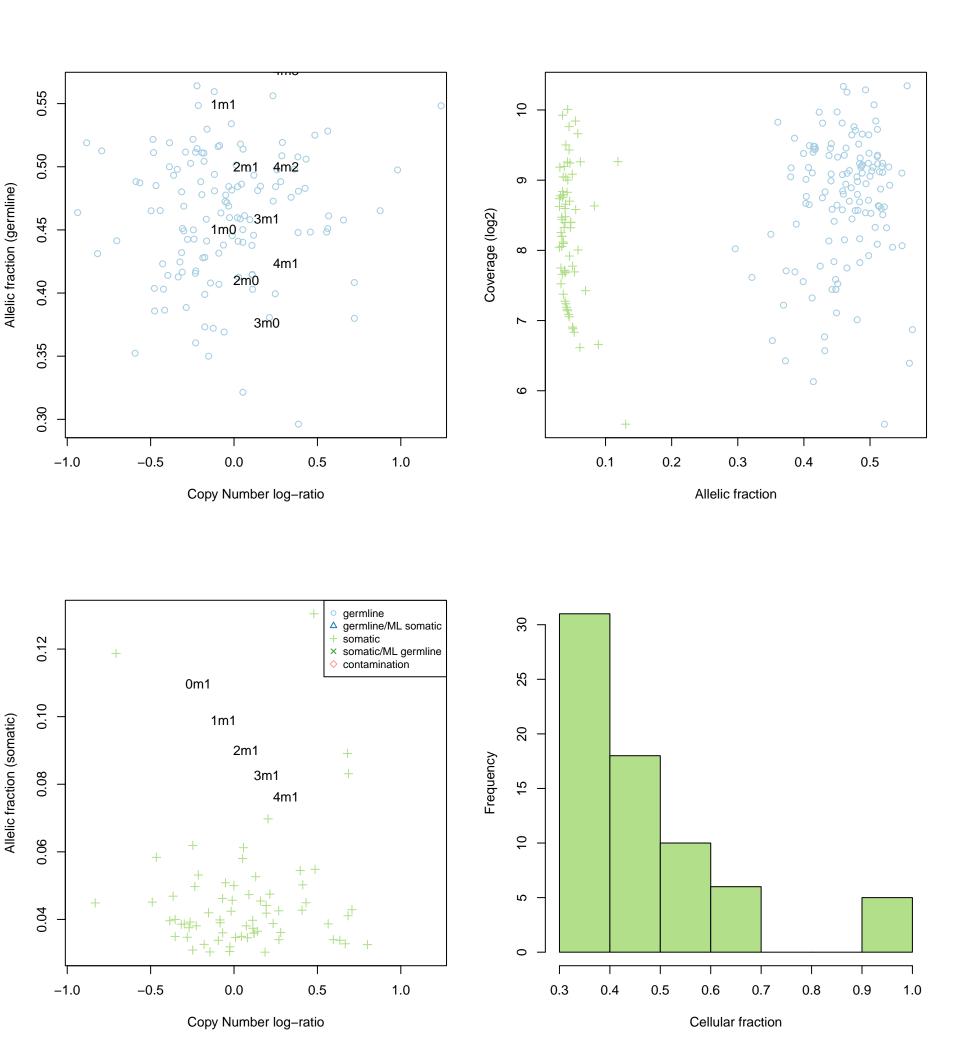


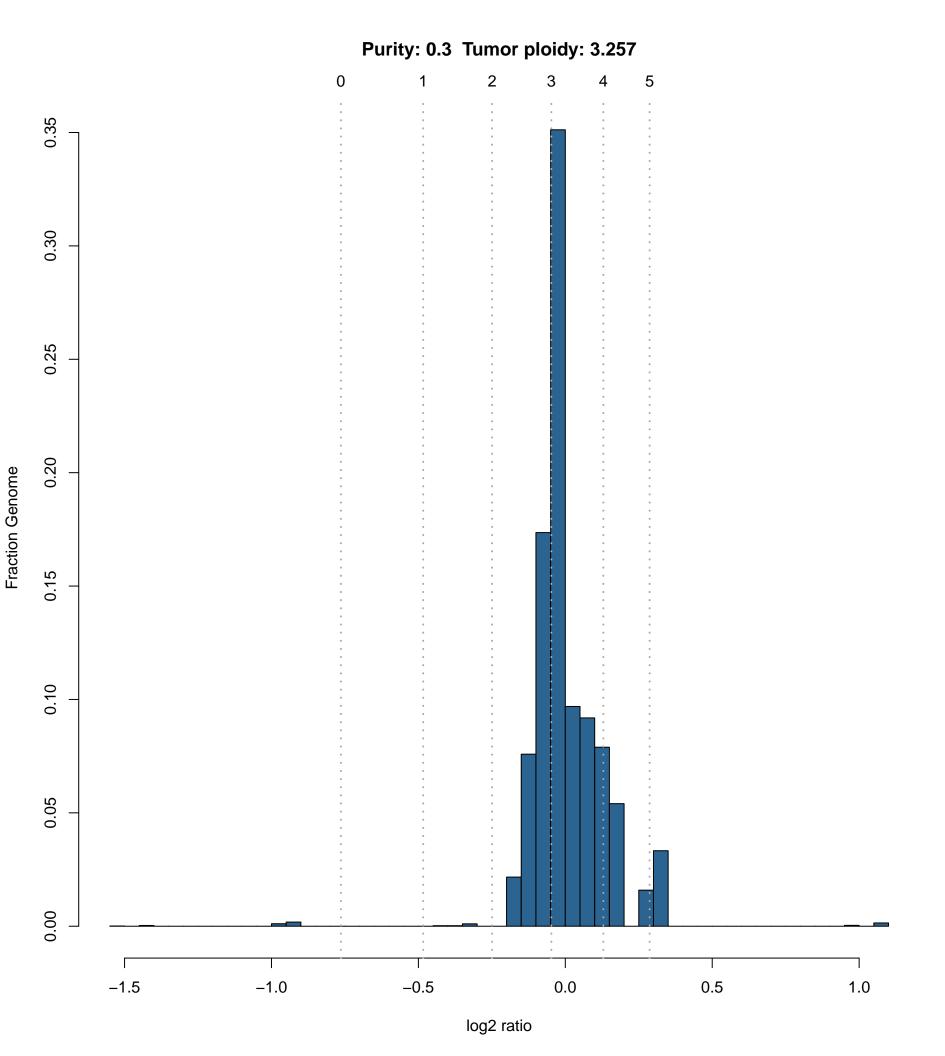


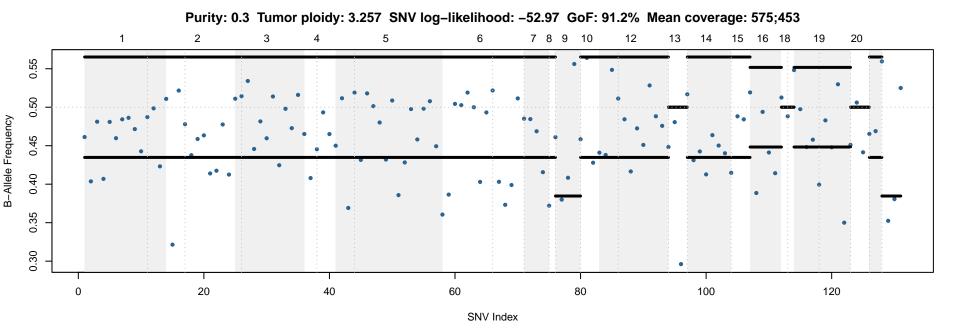
SCNA-fit log-likelihood: -21591.52



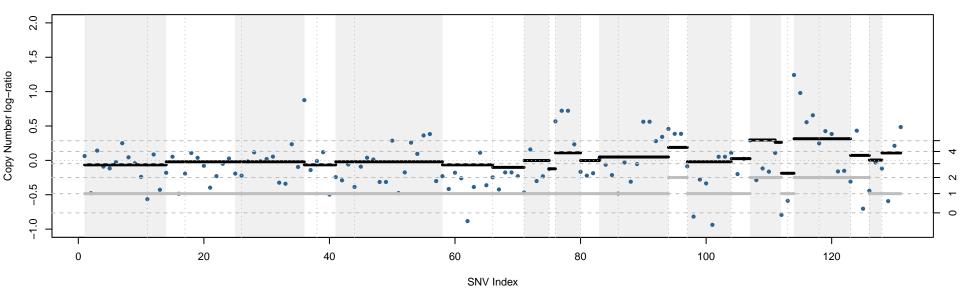


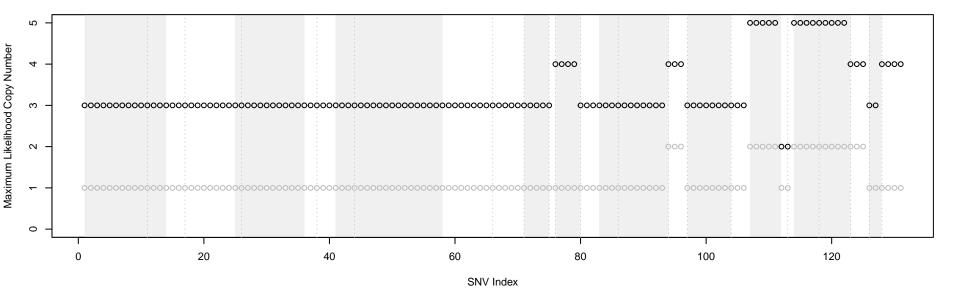


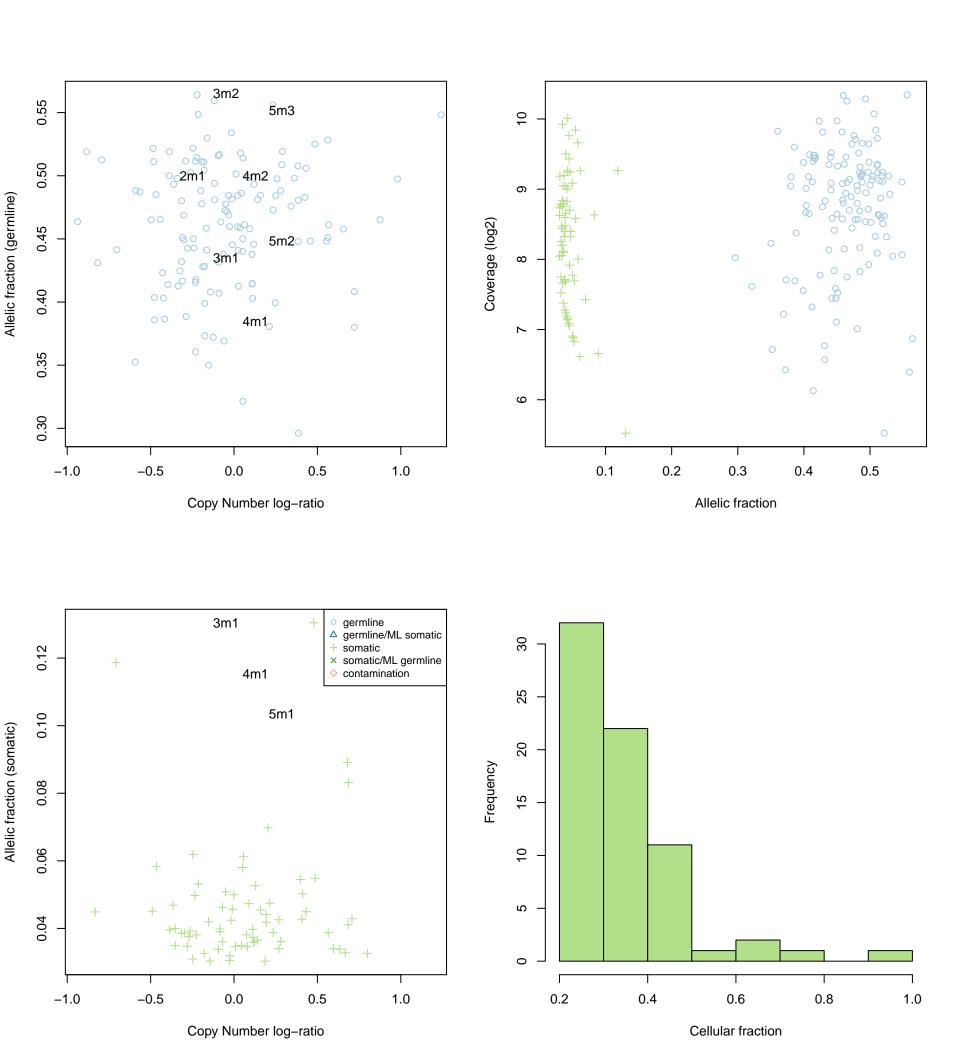




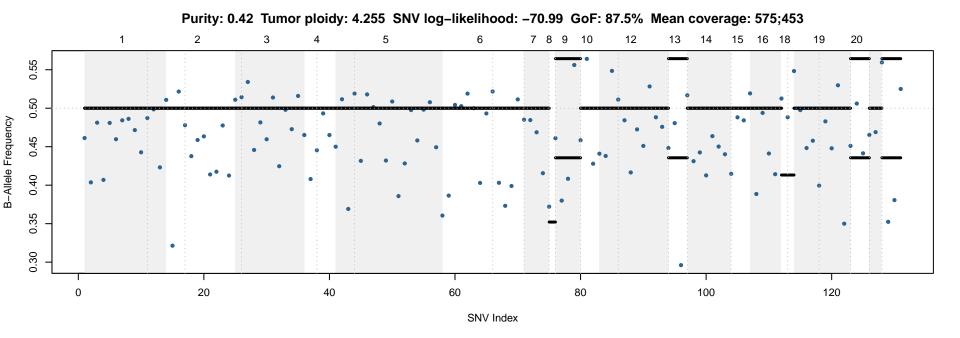
## SCNA-fit log-likelihood: -21561.93



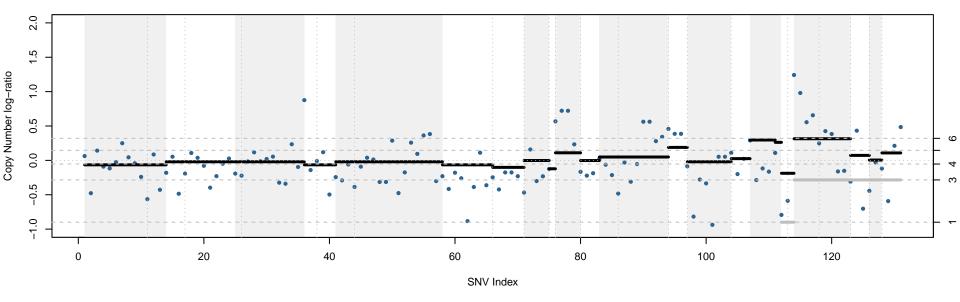


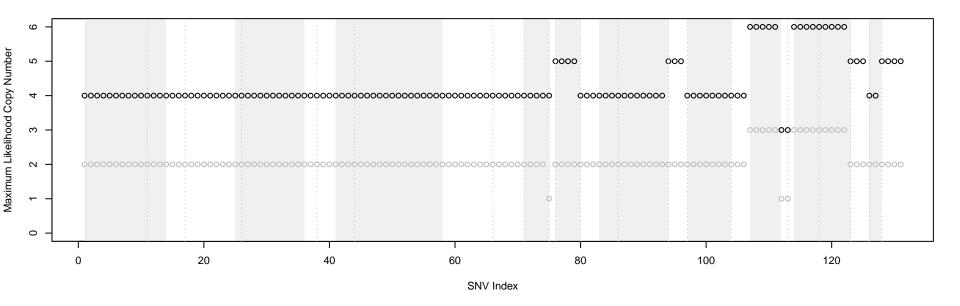


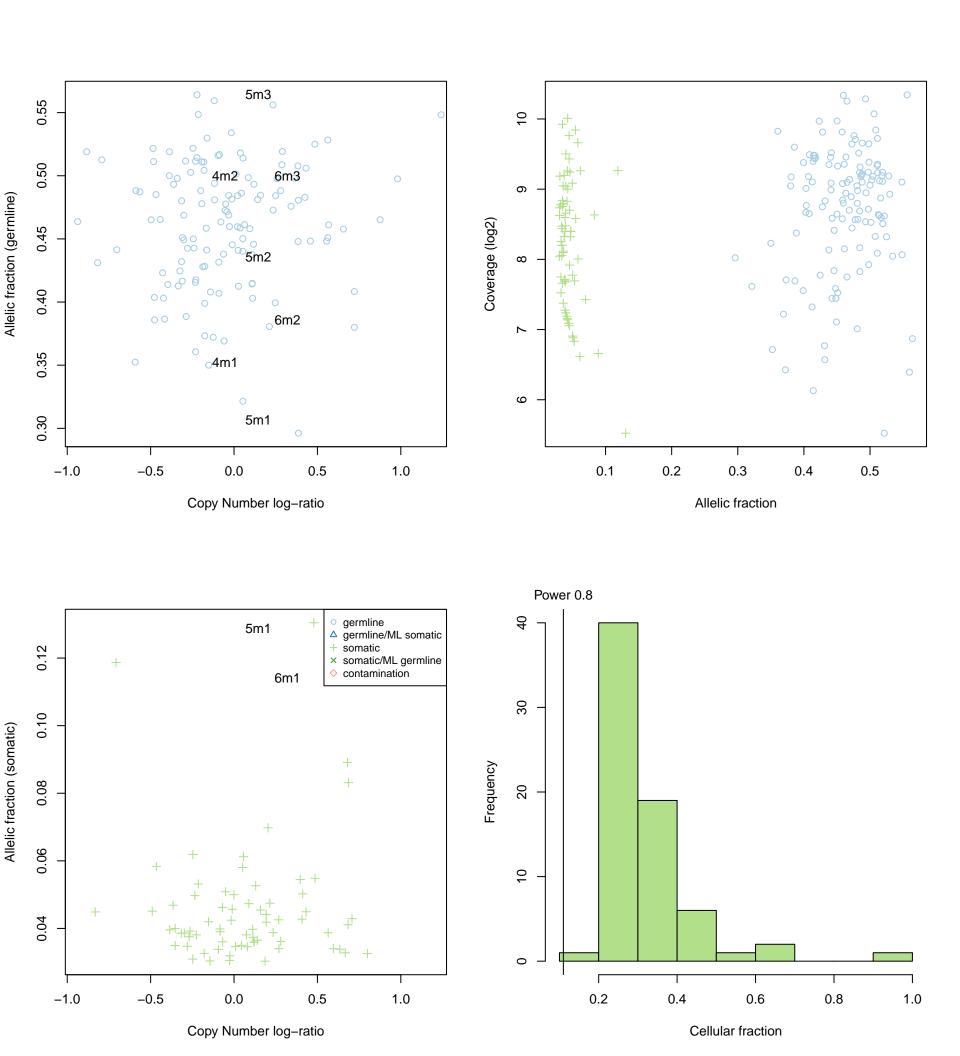
Purity: 0.42 Tumor ploidy: 4.255 0 3 6 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -2.0 -1.5 -1.0 -0.5 0.0 0.5 1.0 log2 ratio

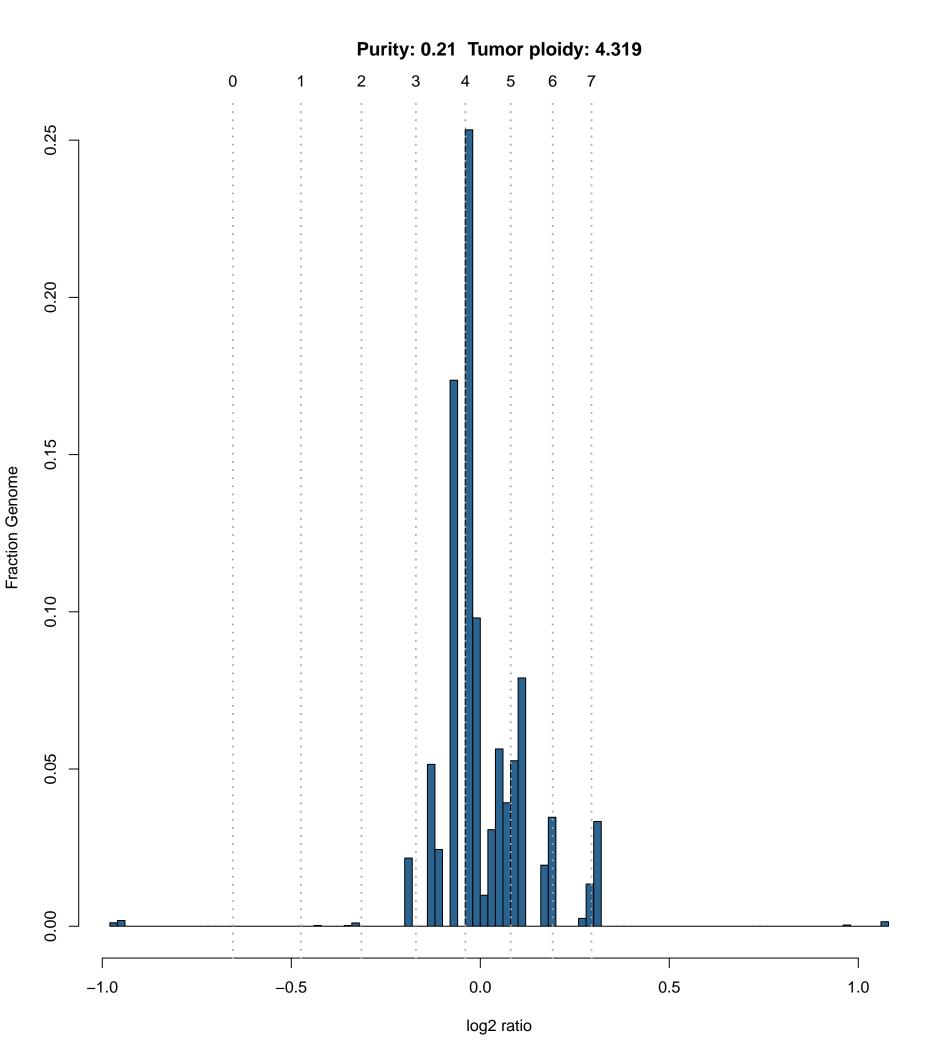


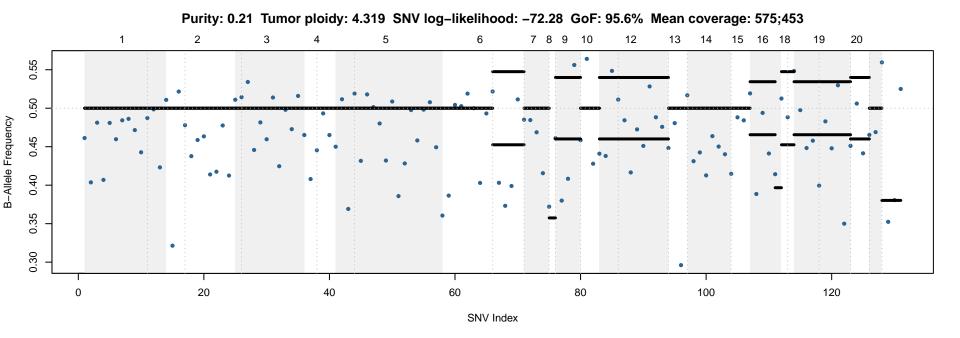
## SCNA-fit log-likelihood: -21567.54



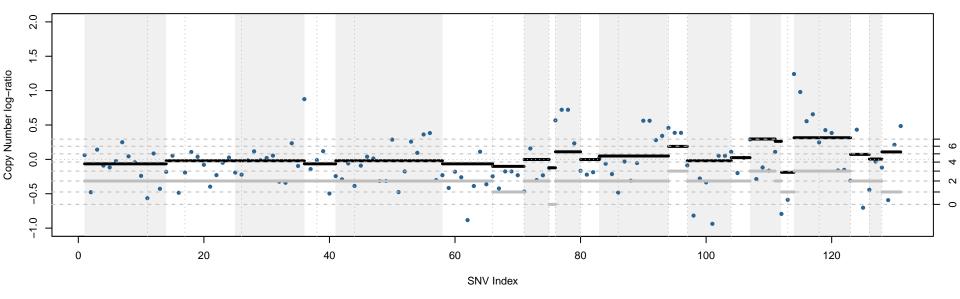


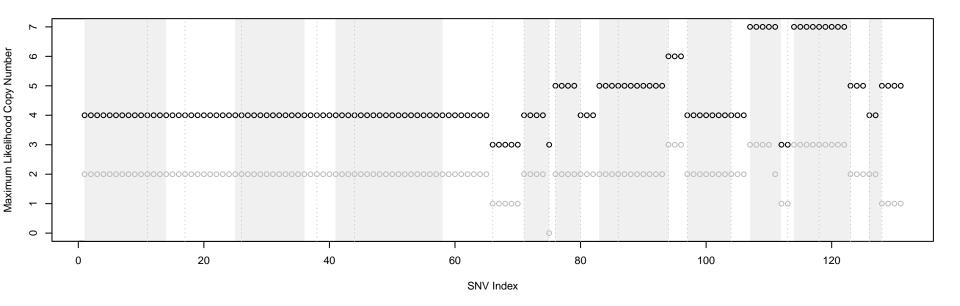


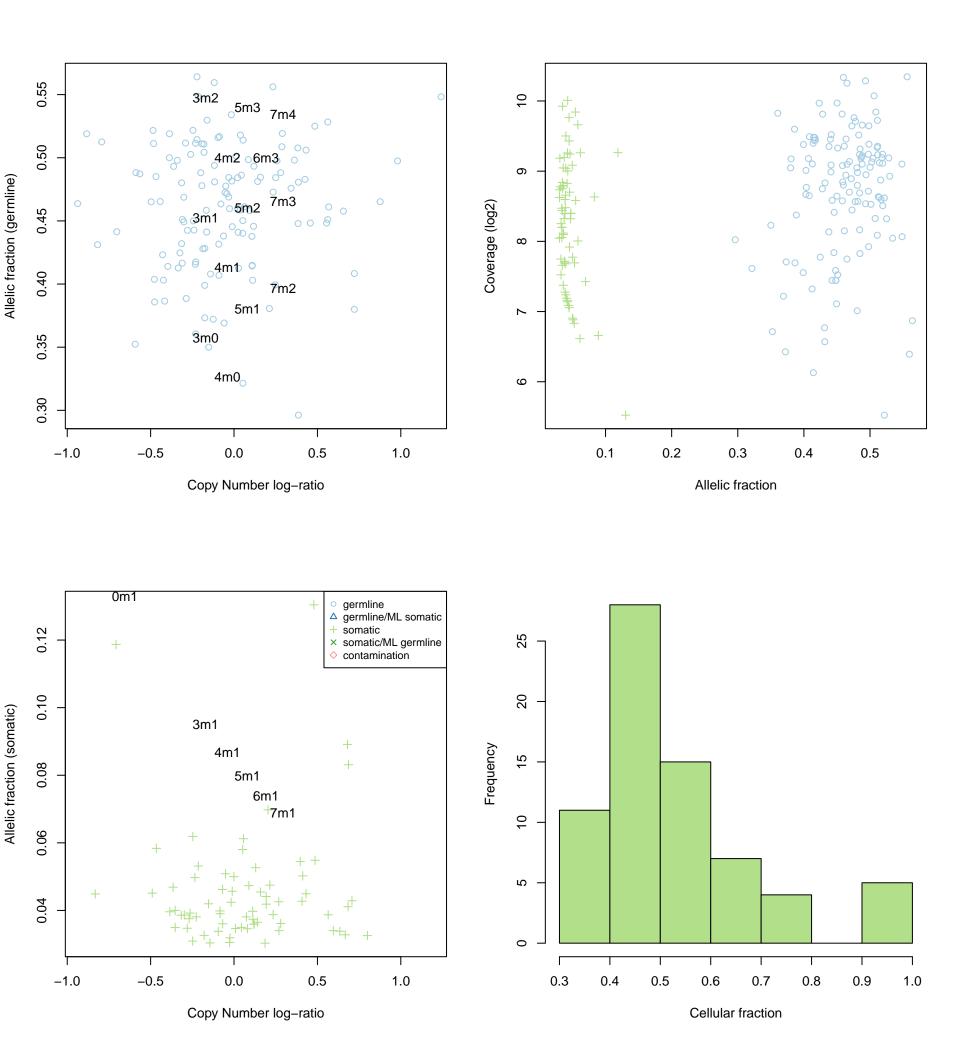




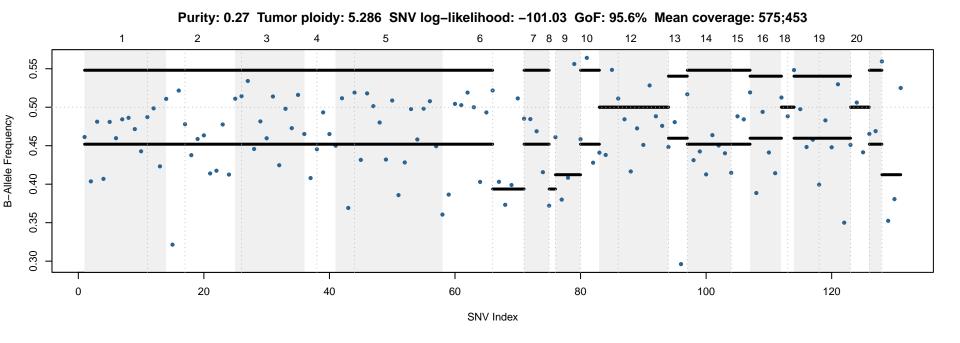
#### SCNA-fit log-likelihood: -21538.13



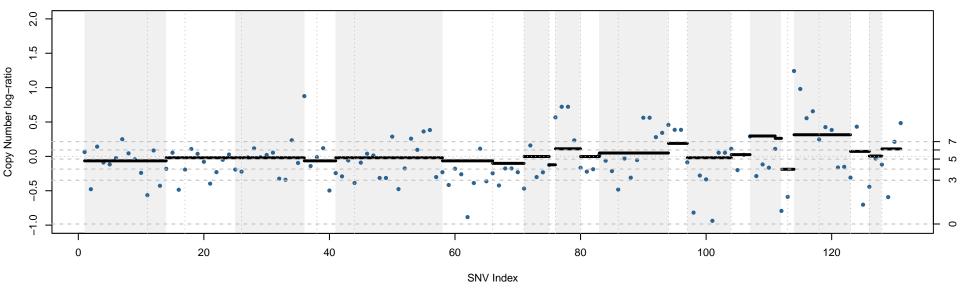


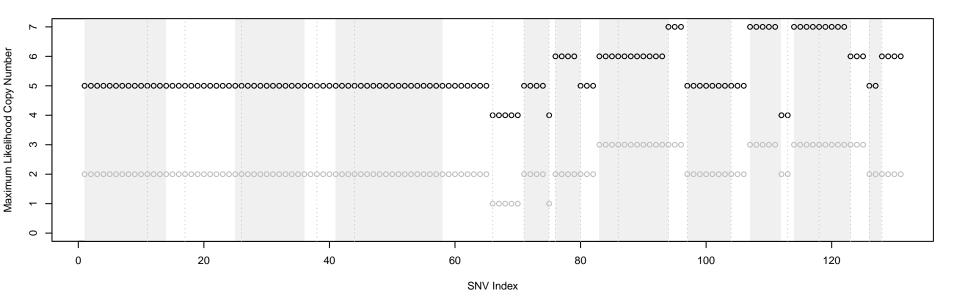


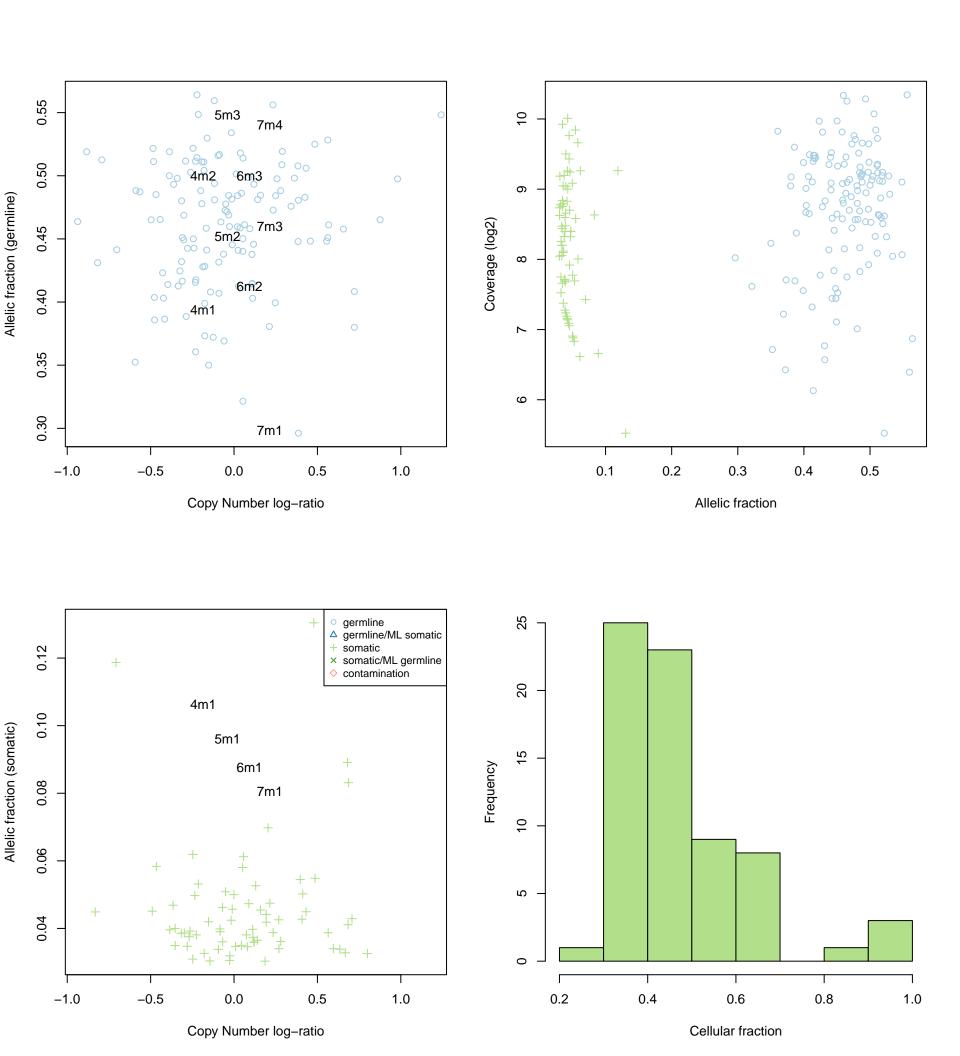
Purity: 0.27 Tumor ploidy: 5.286 5 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -2.0 -1.5 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



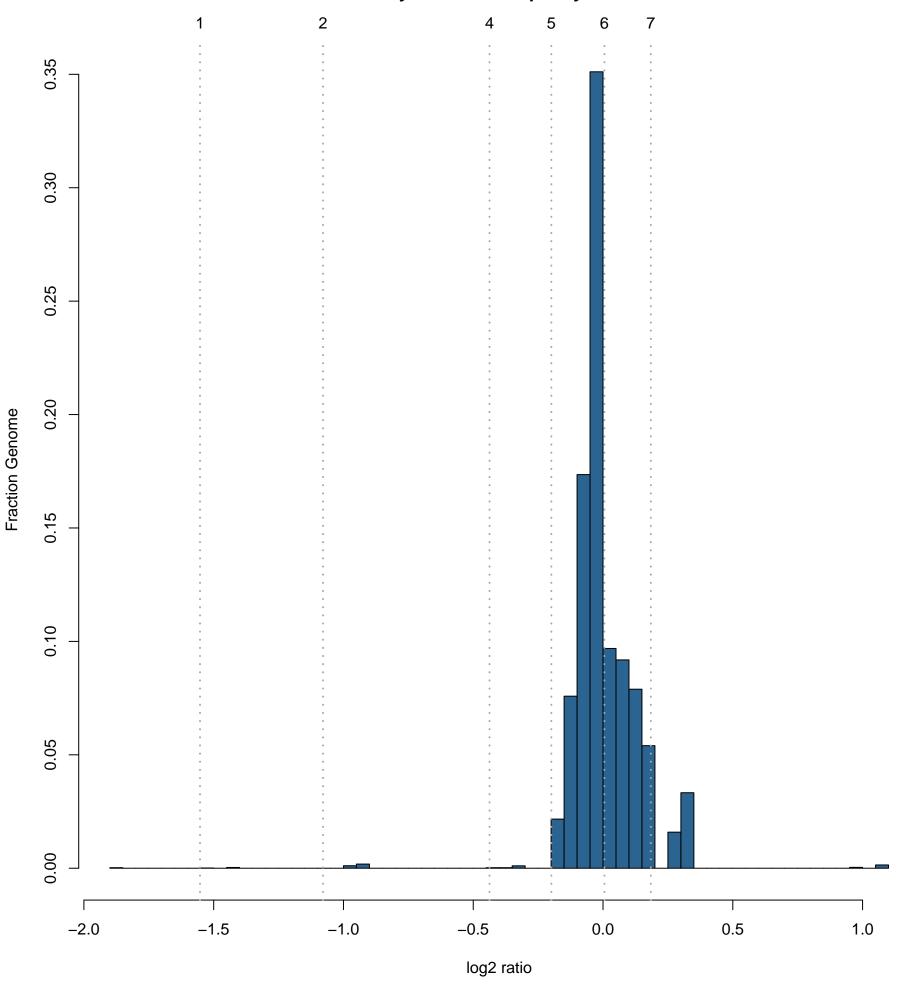


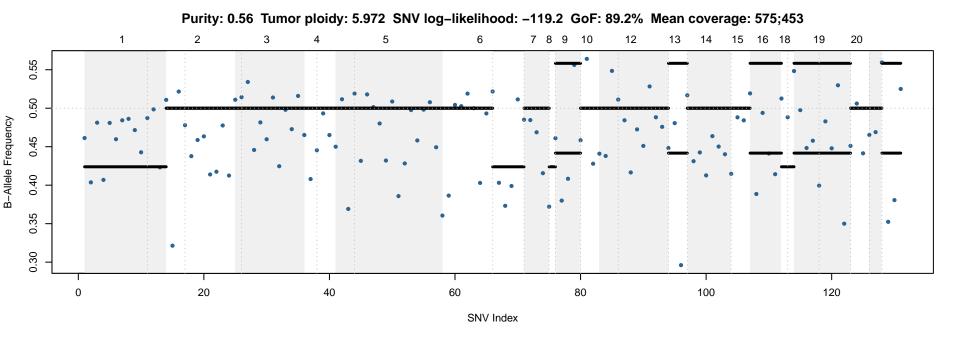




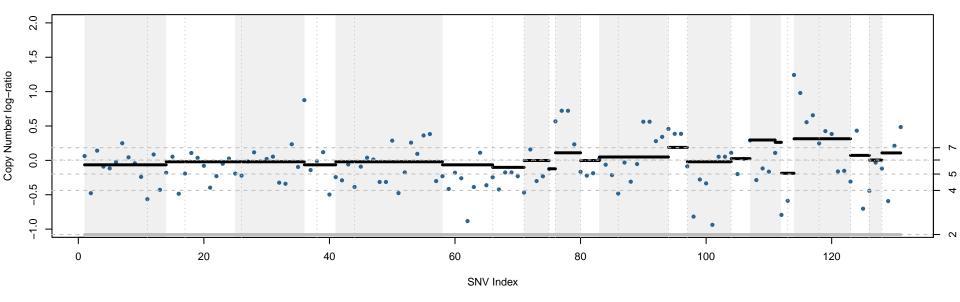


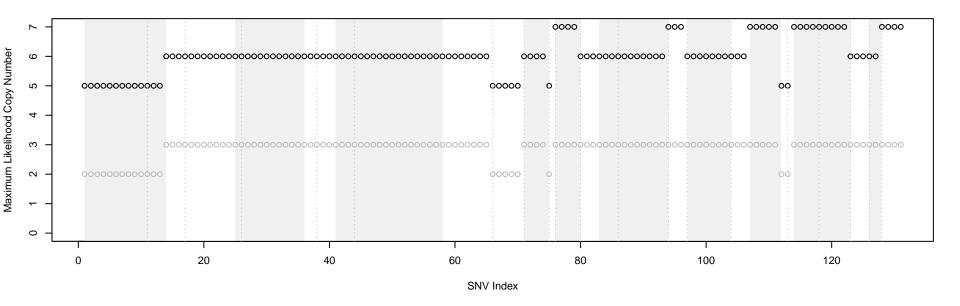
Purity: 0.56 Tumor ploidy: 5.972

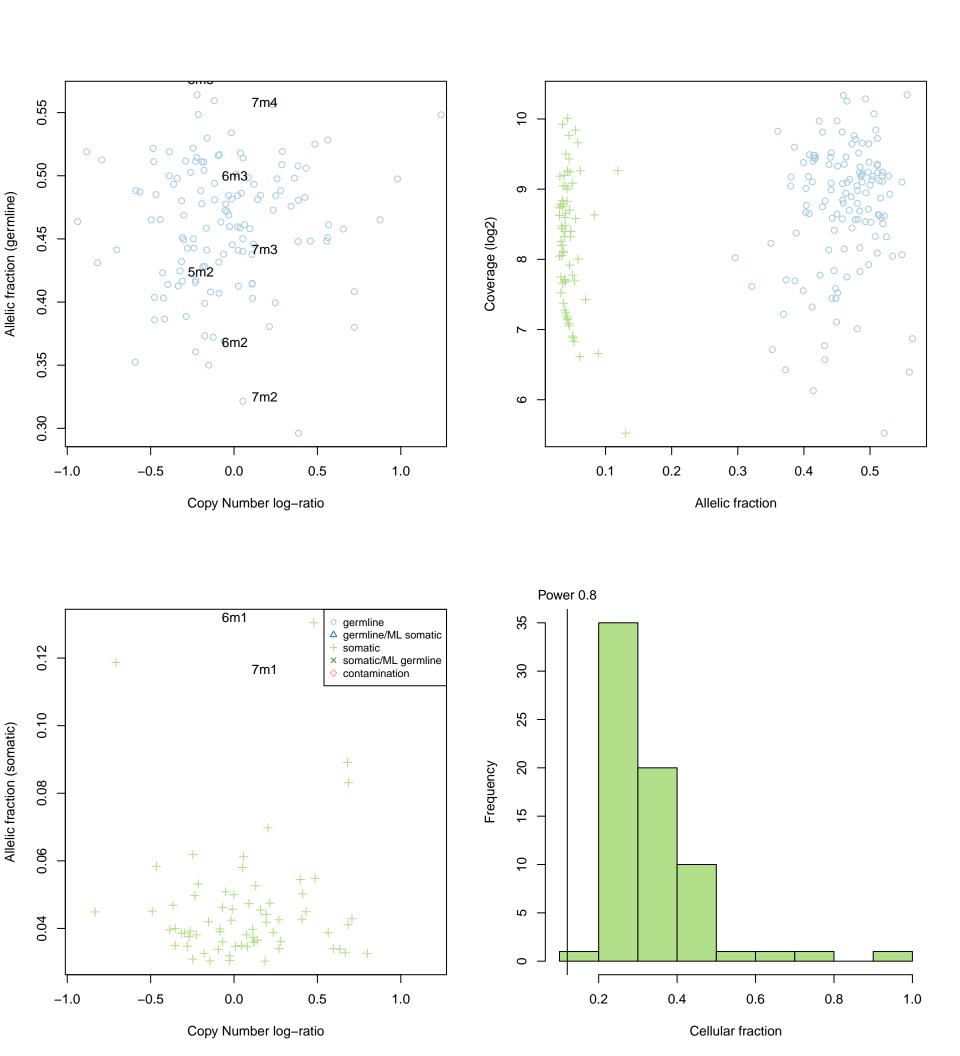




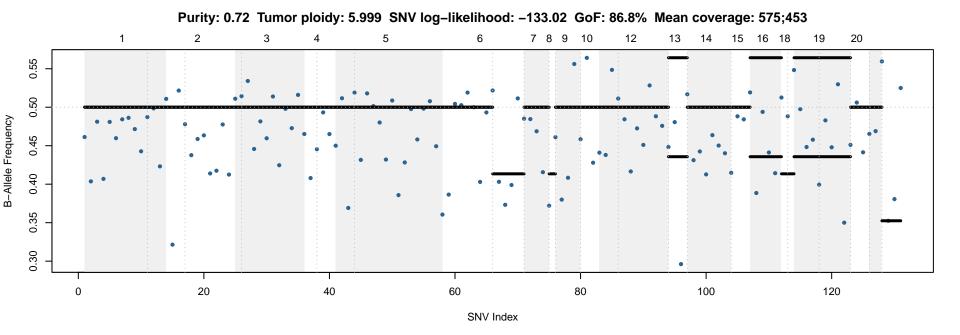
## SCNA-fit log-likelihood: -21611.54



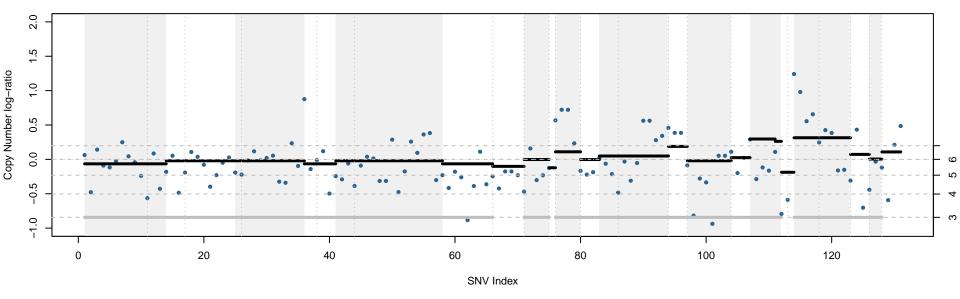


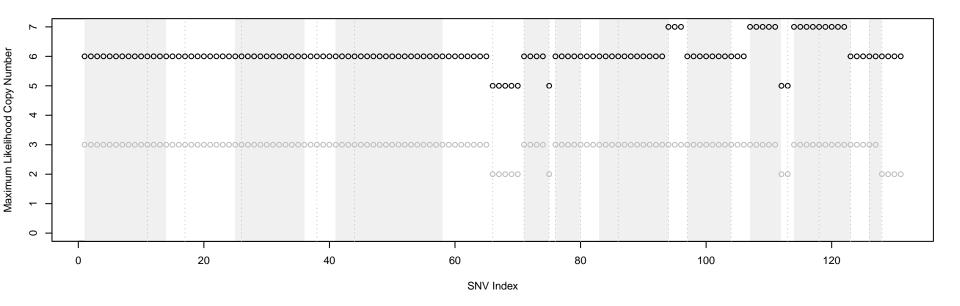


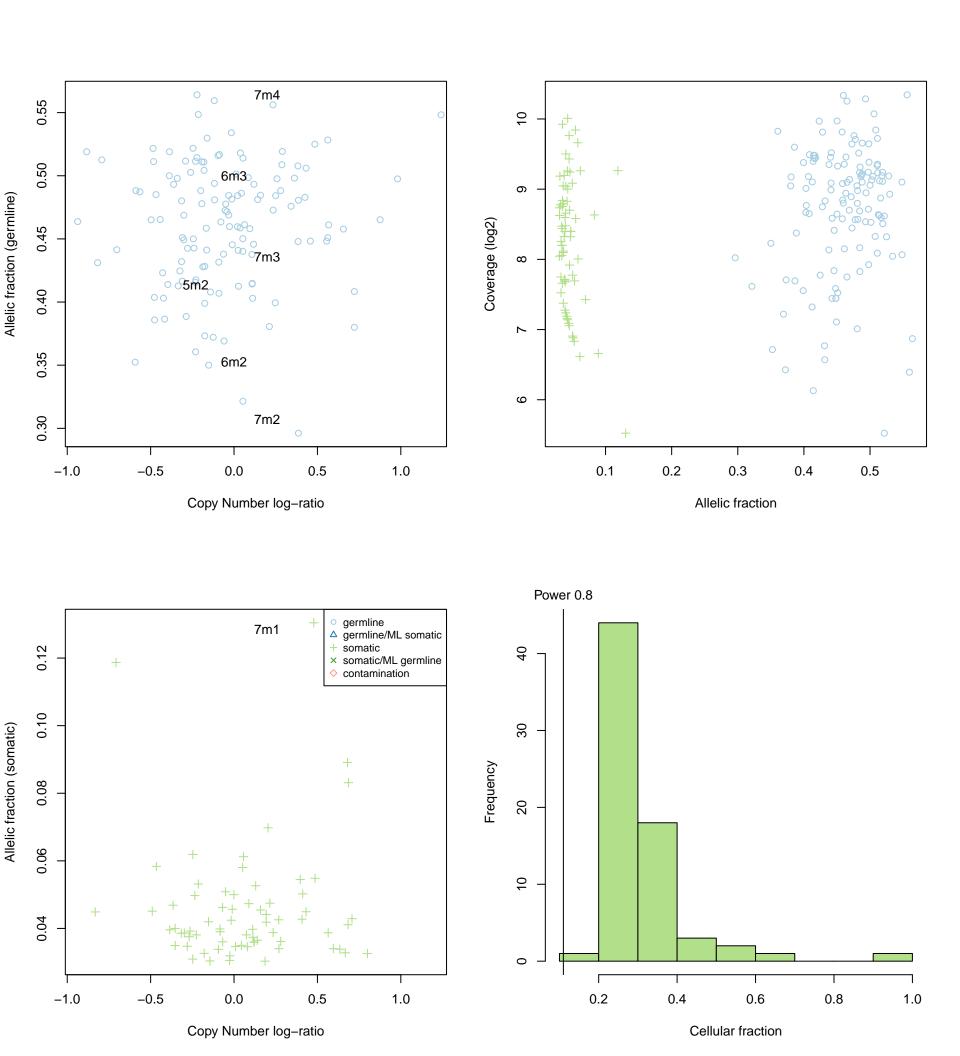
Purity: 0.72 Tumor ploidy: 5.999 2 5 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -2.0 -1.5 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



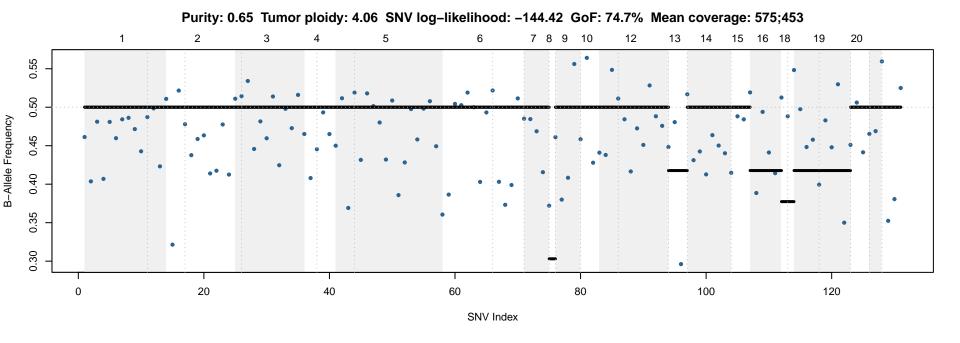
### SCNA-fit log-likelihood: -21604.06



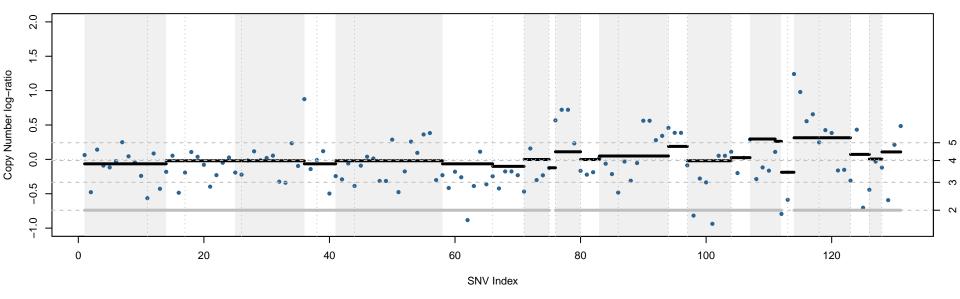


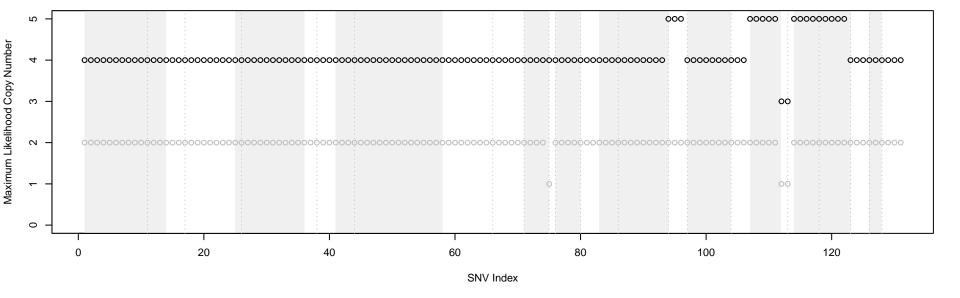


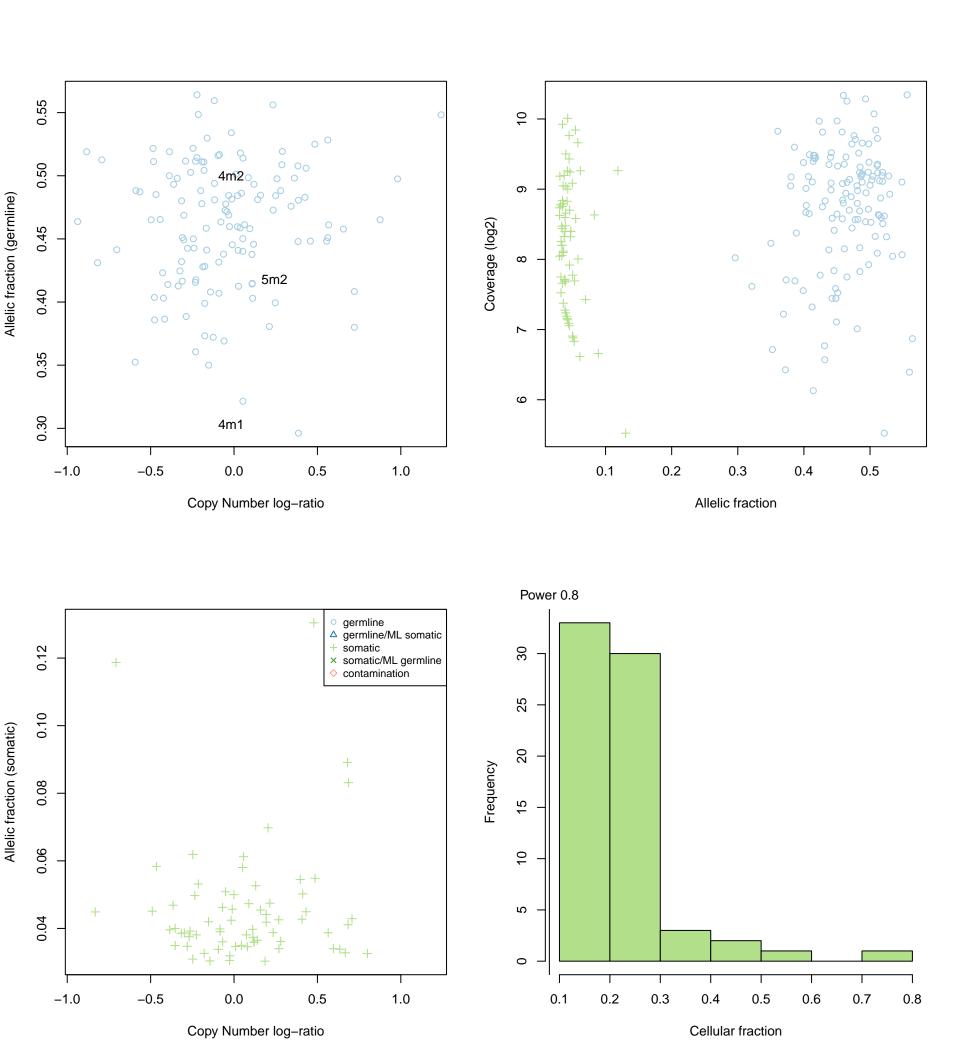
Purity: 0.65 Tumor ploidy: 4.06 3 5 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -2.0 -1.5 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



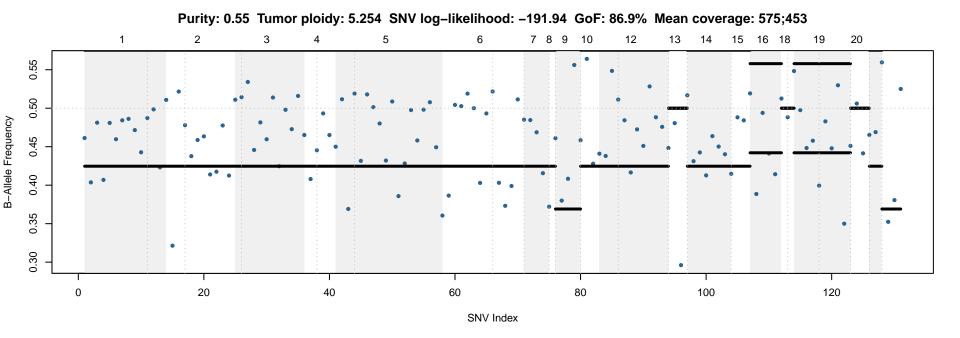
### SCNA-fit log-likelihood: -21618.76



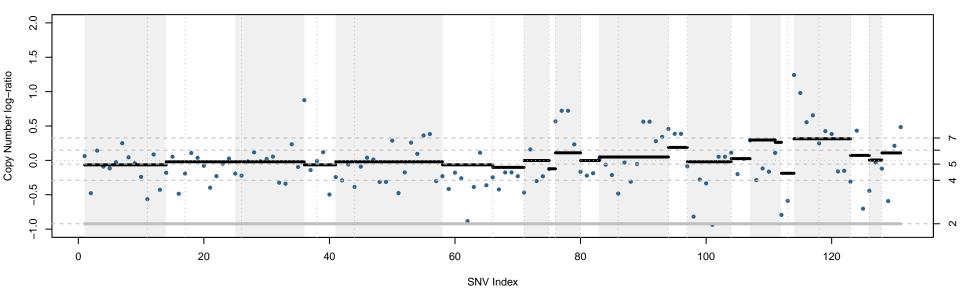


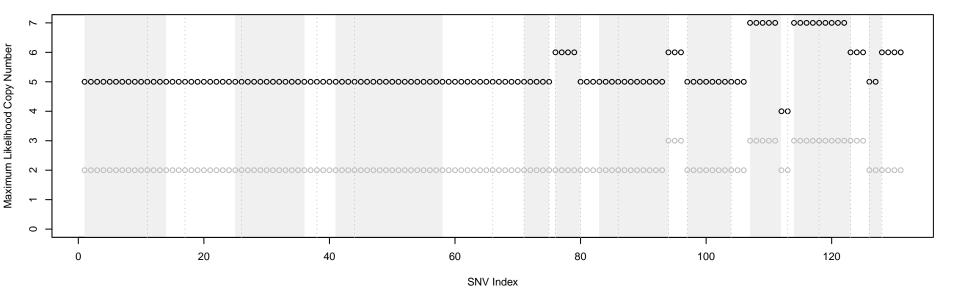


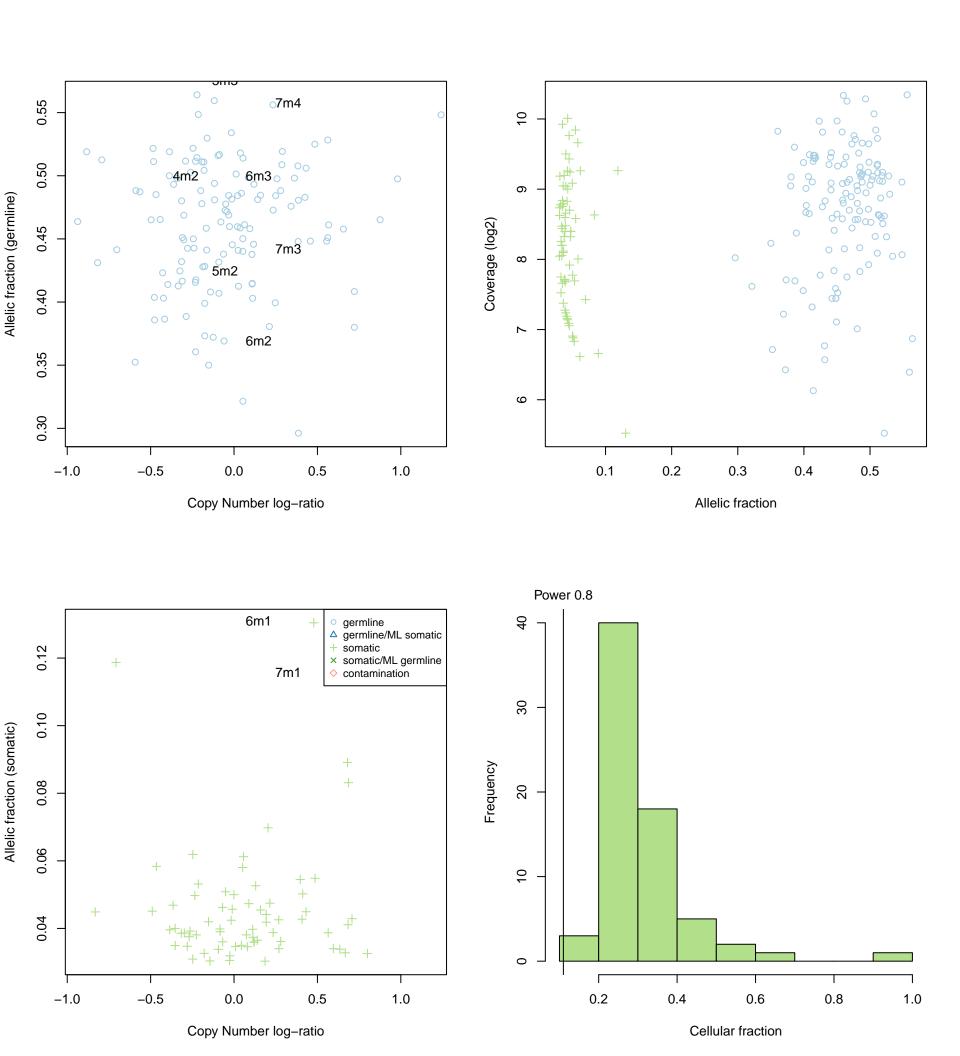
Purity: 0.55 Tumor ploidy: 5.254 2 7 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.05 0.00 -2.0 -1.5 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



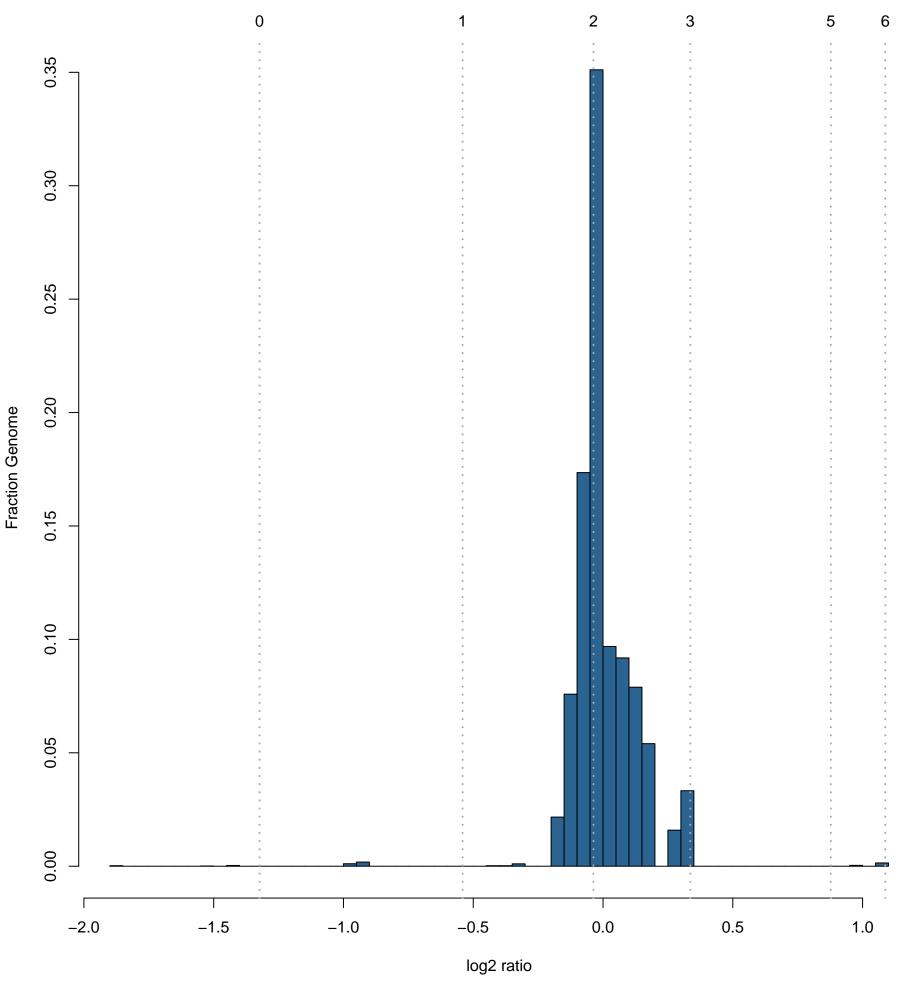
### SCNA-fit log-likelihood: -21569.64

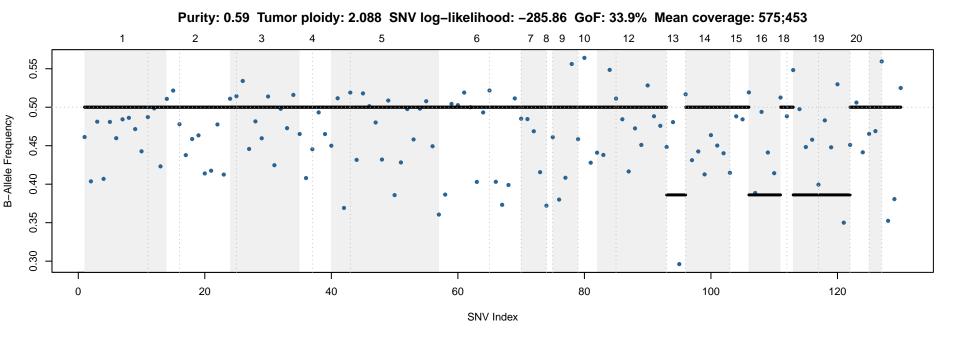




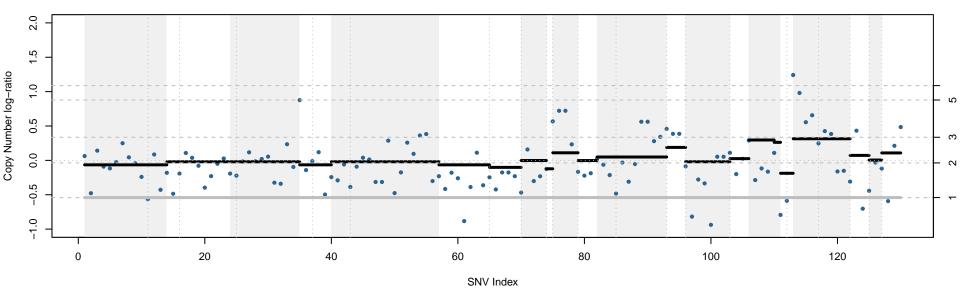


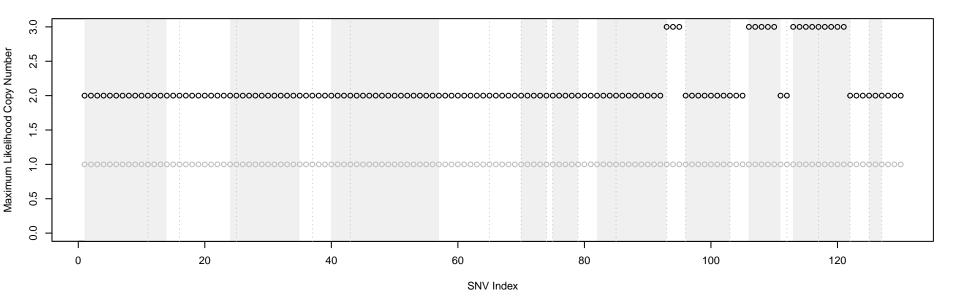
Purity: 0.59 Tumor ploidy: 2.088

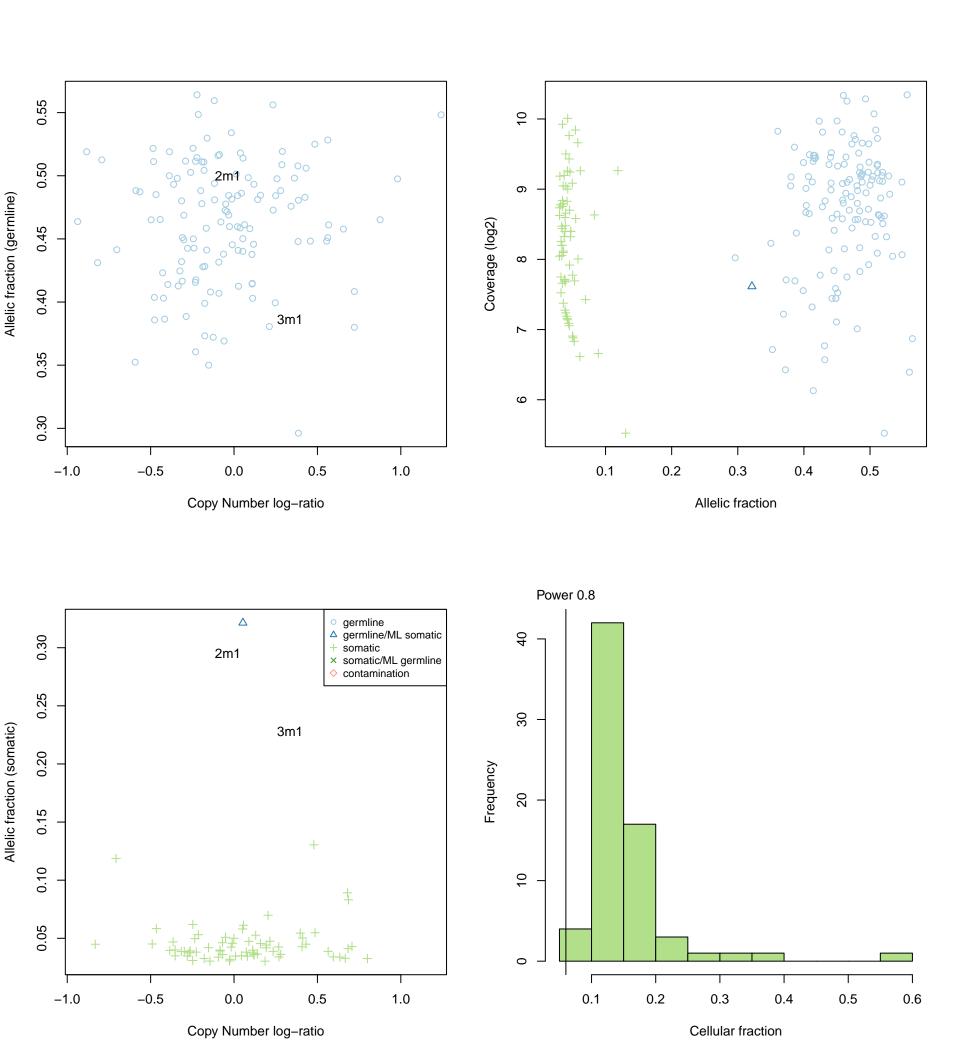




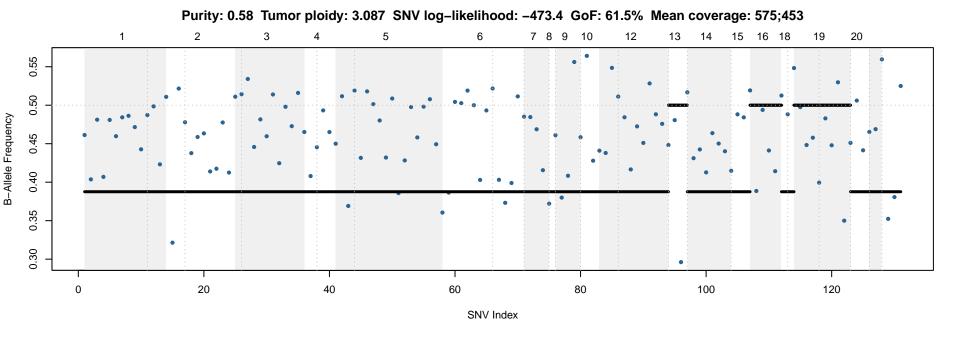
### SCNA-fit log-likelihood: -21640.13



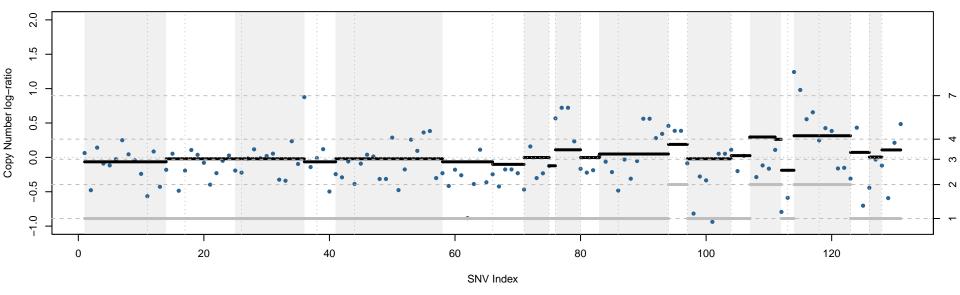


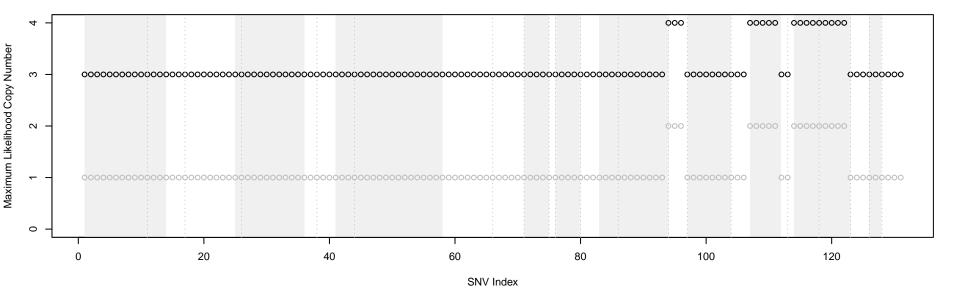


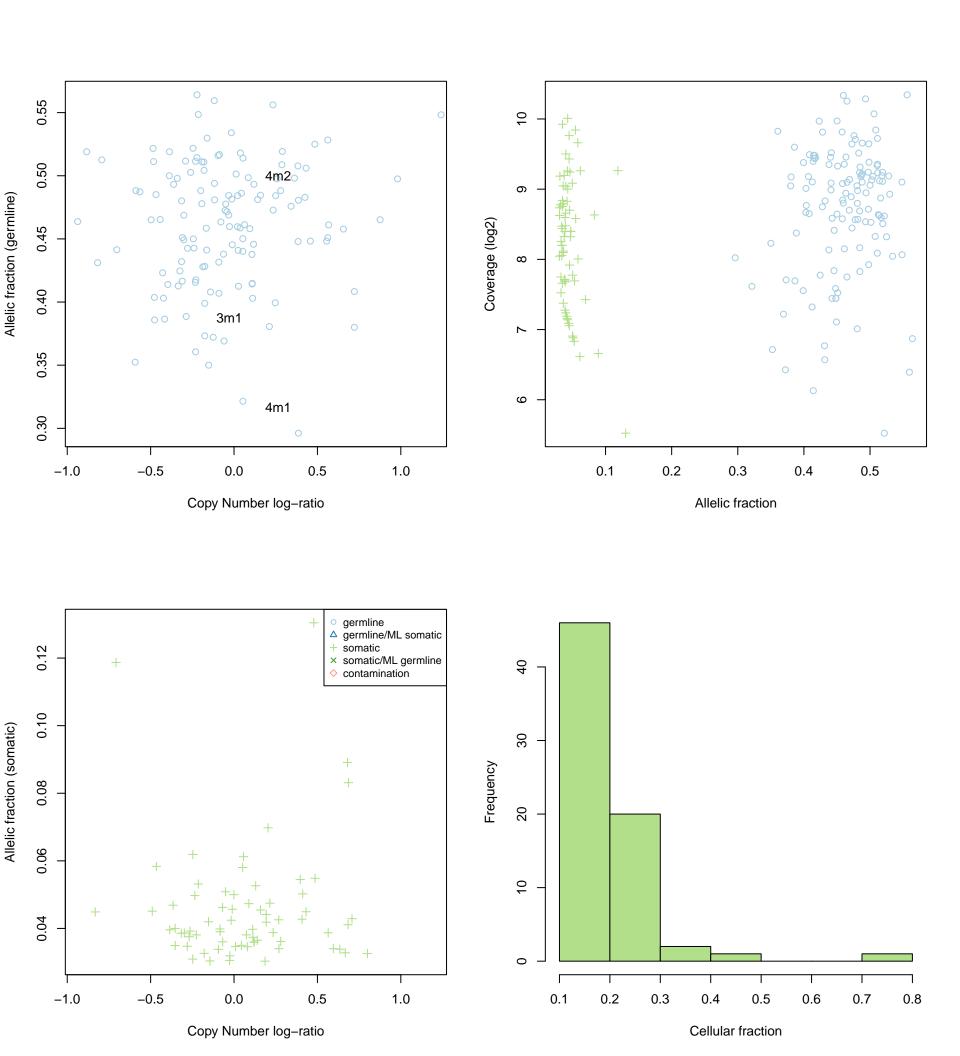
Purity: 0.58 Tumor ploidy: 3.087 0 2 3 7 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -2.0 -1.5 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



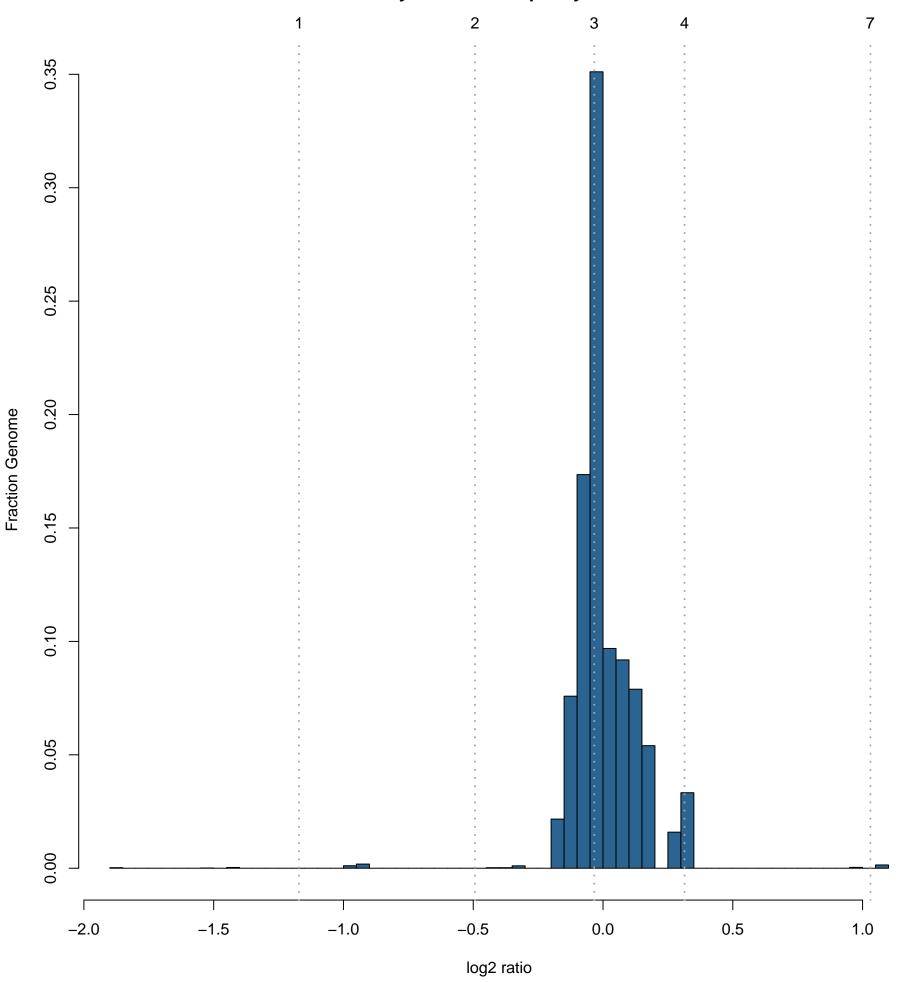
### SCNA-fit log-likelihood: -21608.21

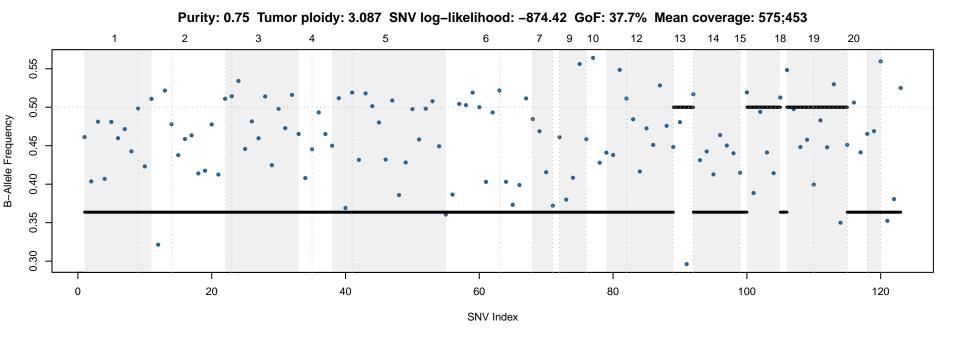






Purity: 0.75 Tumor ploidy: 3.087





### SCNA-fit log-likelihood: -21624.54

