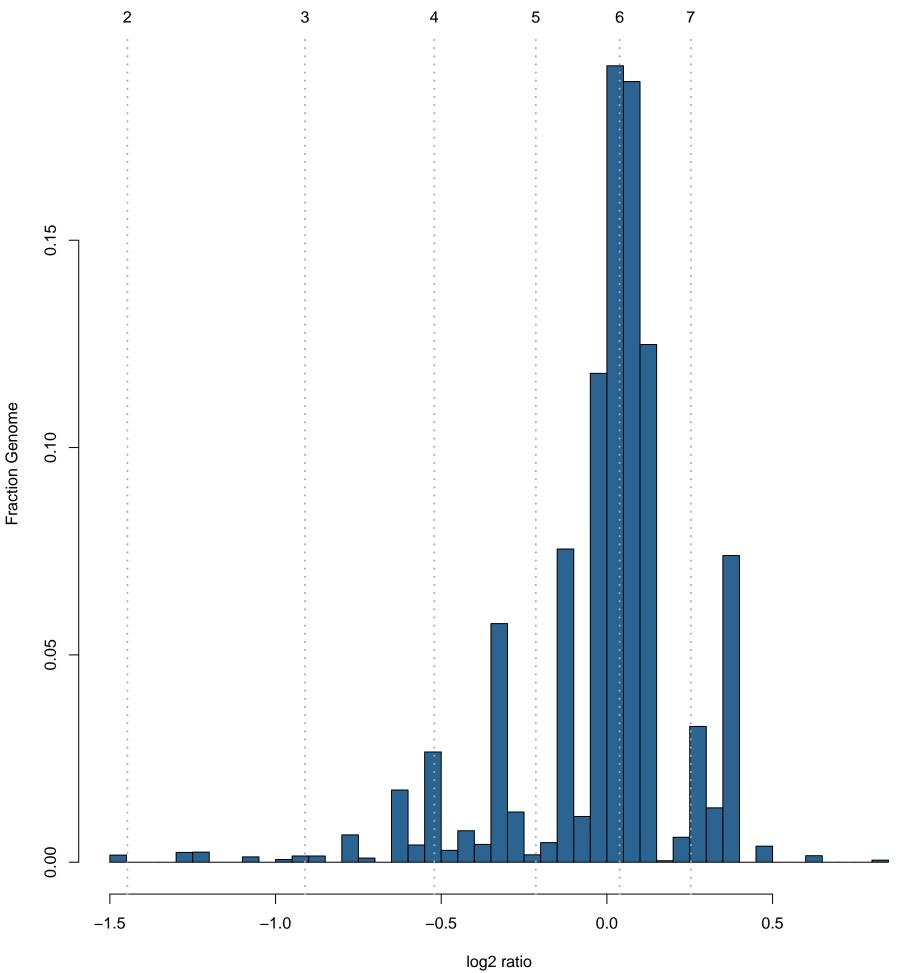
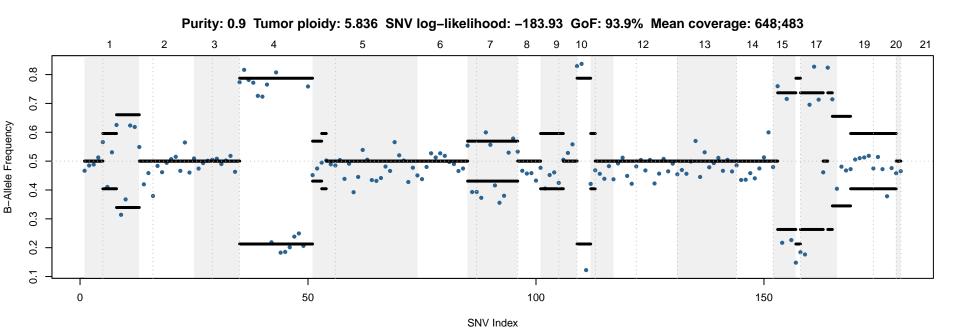
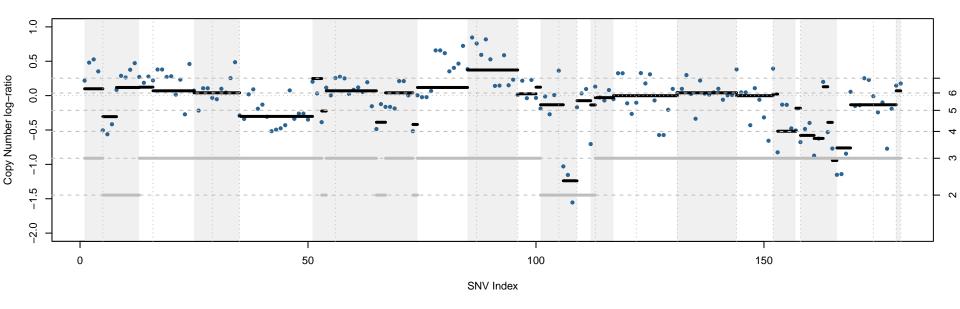
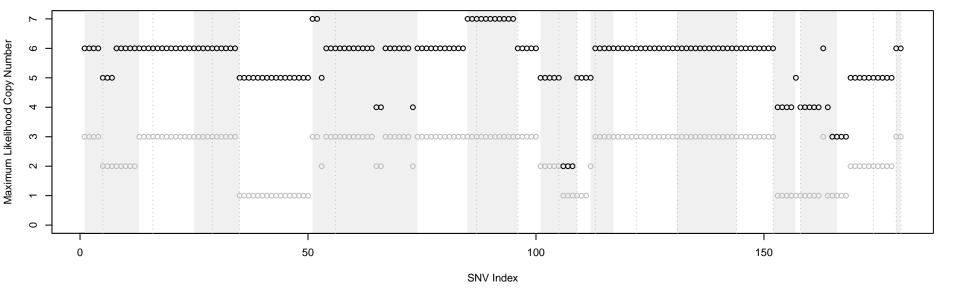
Purity: 0.9 Tumor ploidy: 5.836

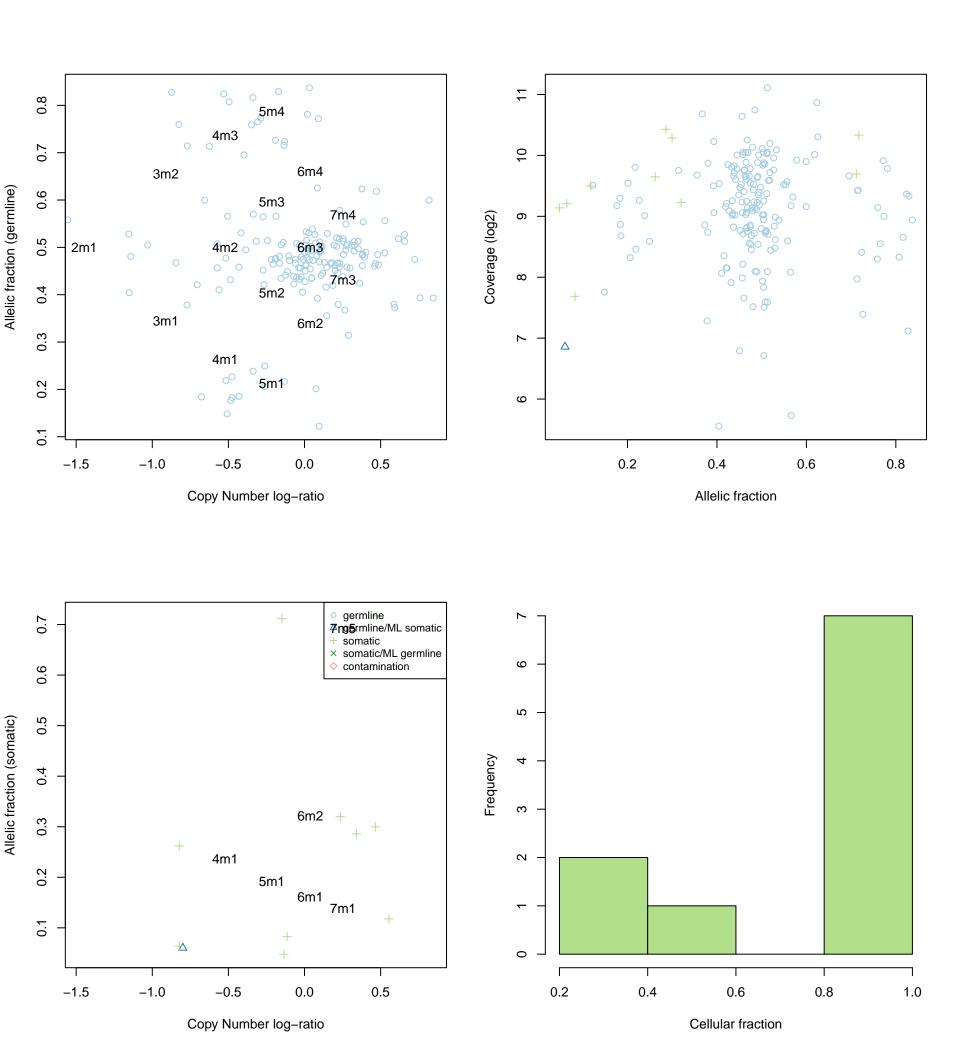




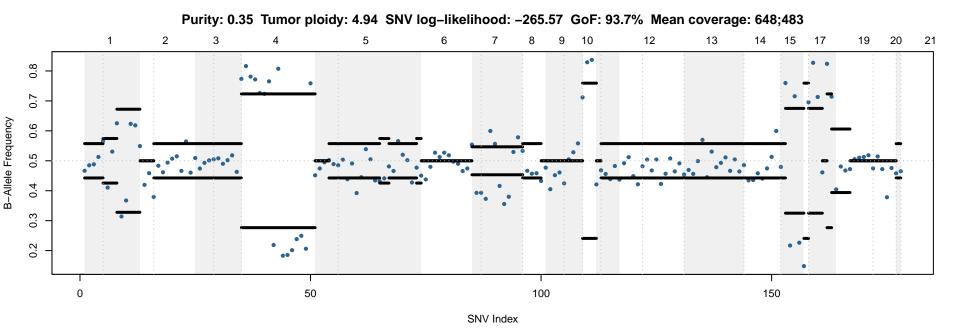
#### SCNA-fit log-likelihood: -4815.01



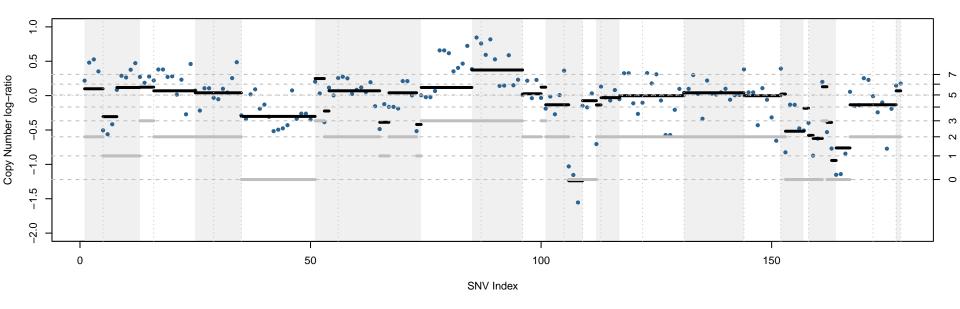


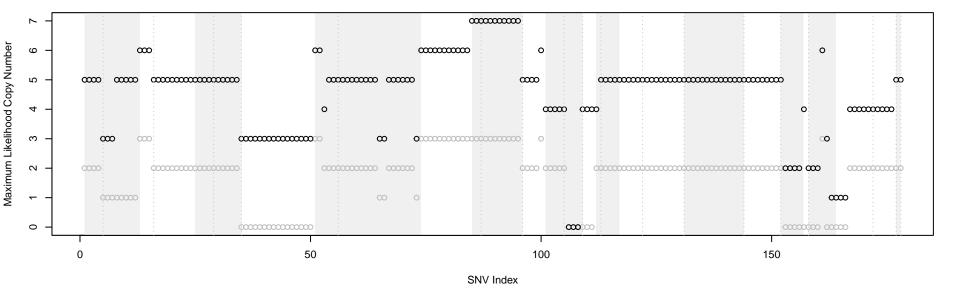


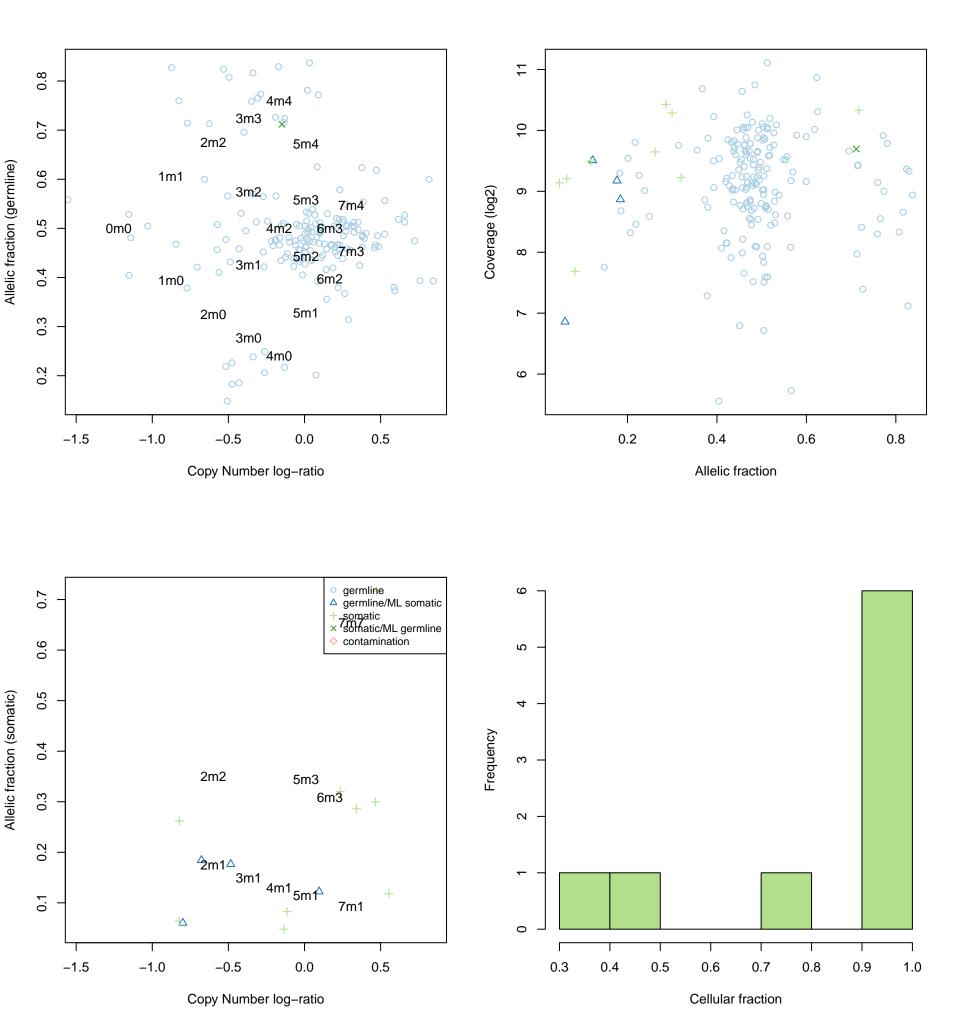
Purity: 0.35 Tumor ploidy: 4.94 3 0 2 5 6 7 1 Fraction Genome 0.10 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio



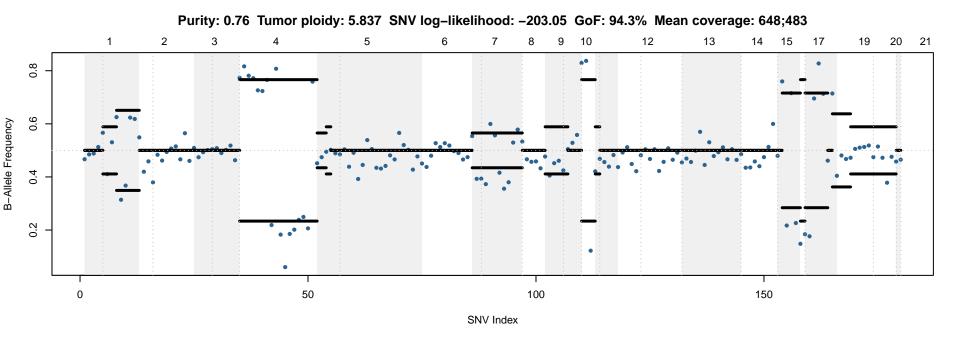
### SCNA-fit log-likelihood: -4690.93



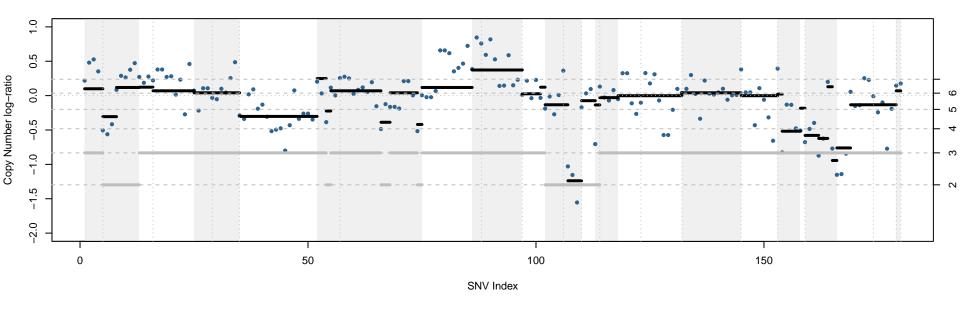


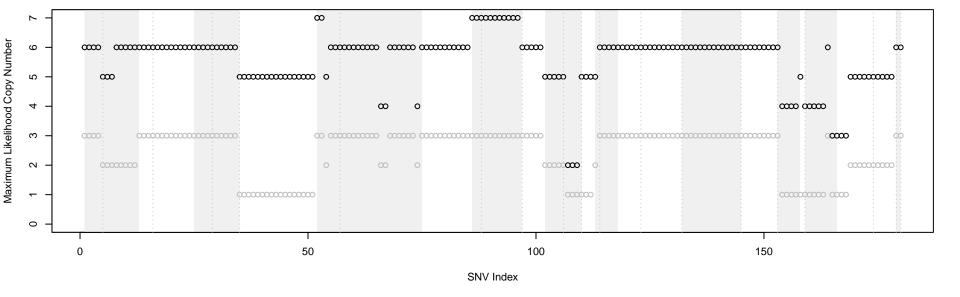


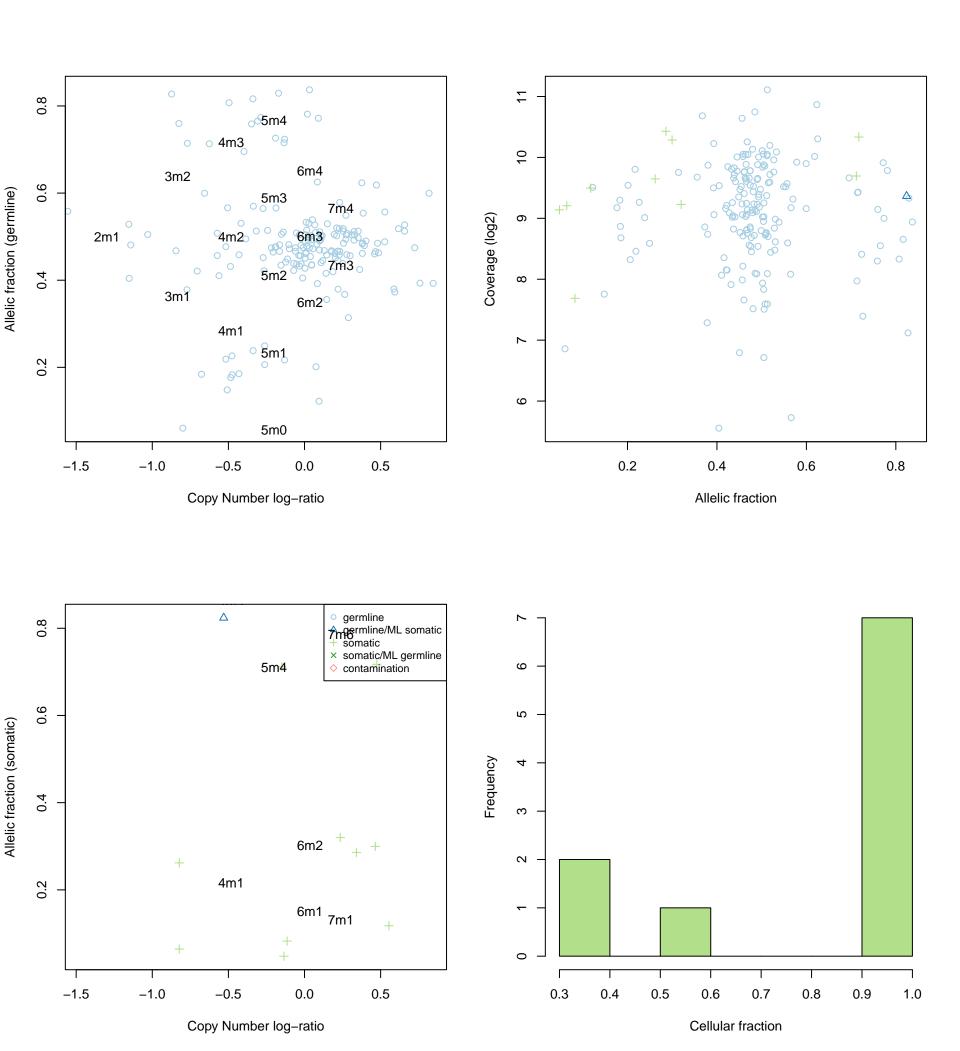
Purity: 0.76 Tumor ploidy: 5.837 2 3 6 7 Fraction Genome 0.10 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio



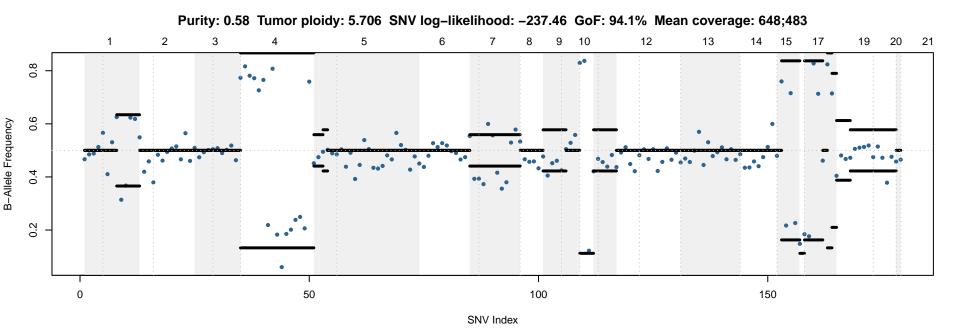
#### SCNA-fit log-likelihood: -4840.21



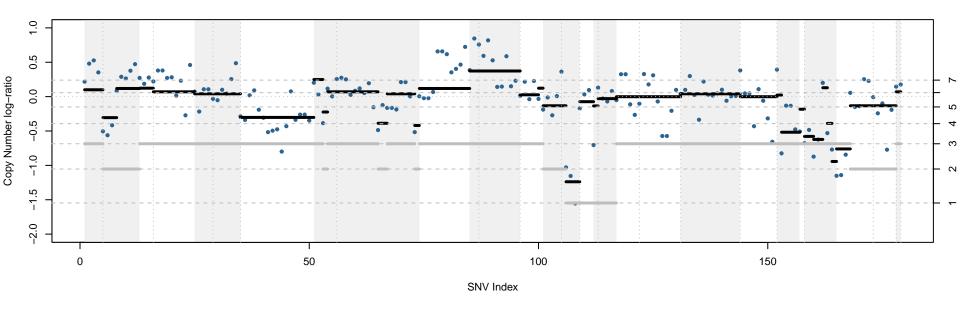


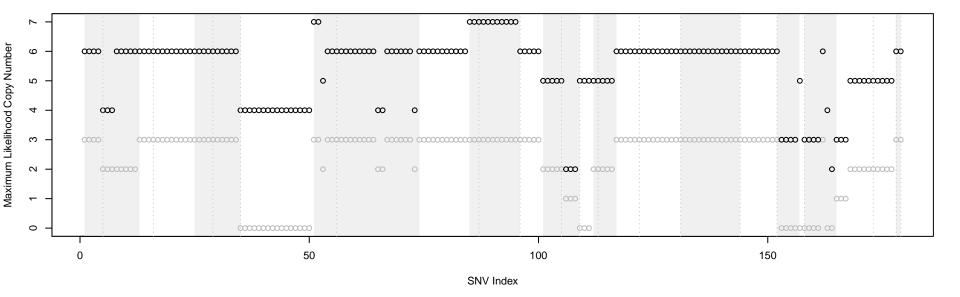


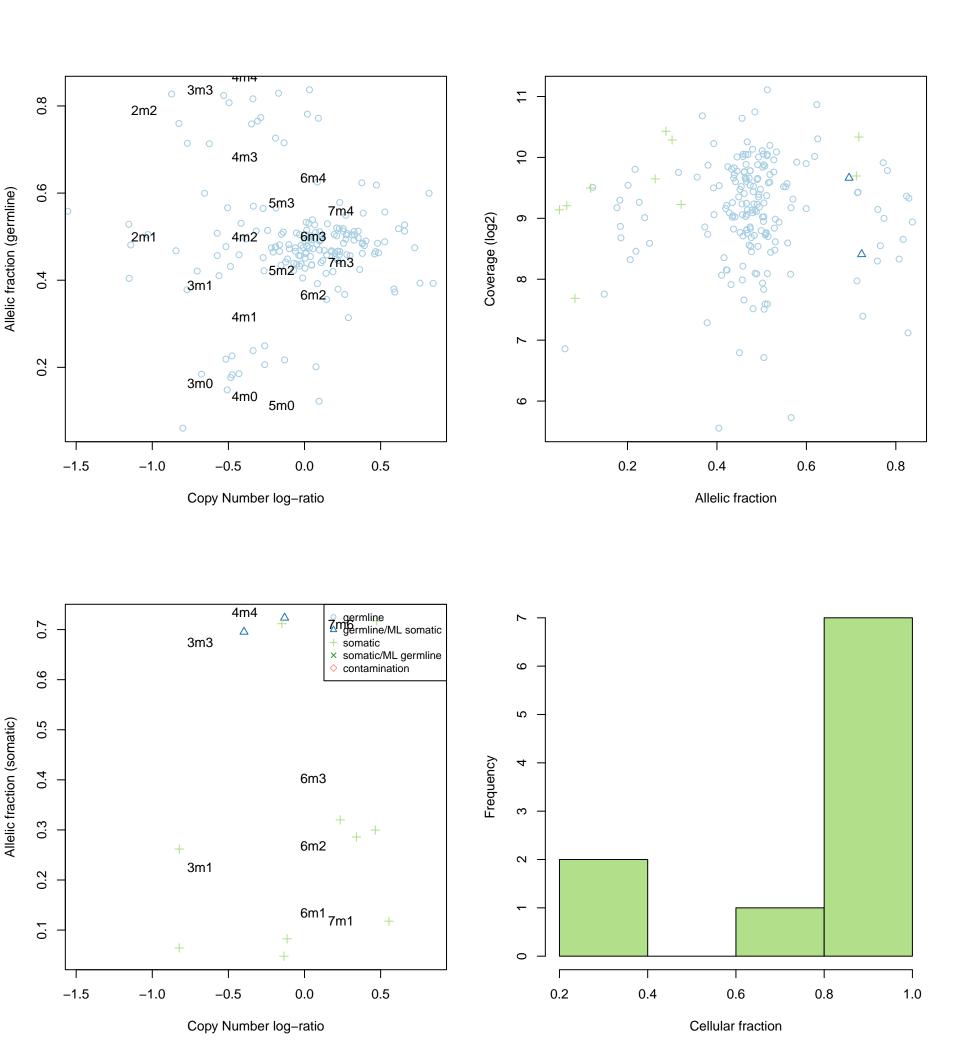
Purity: 0.58 Tumor ploidy: 5.706 5 2 3 7 0.15 Fraction Genome 0.10 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio



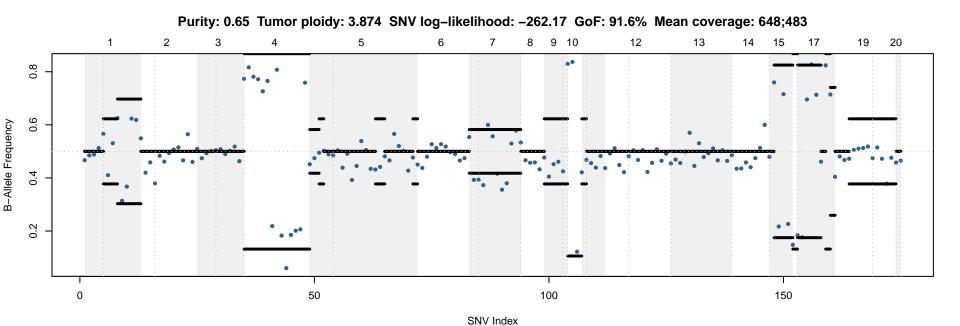
# SCNA-fit log-likelihood: -4811.19



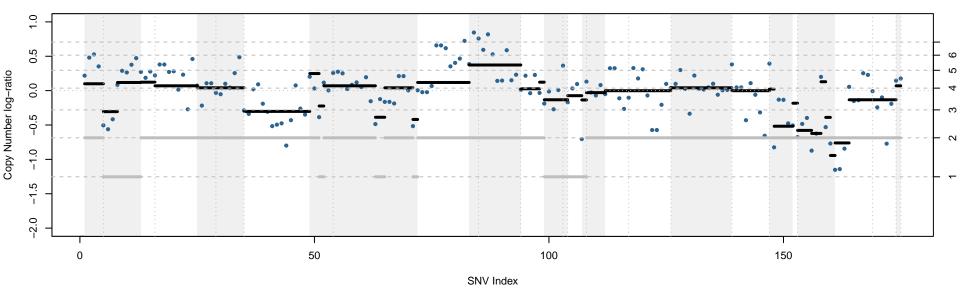


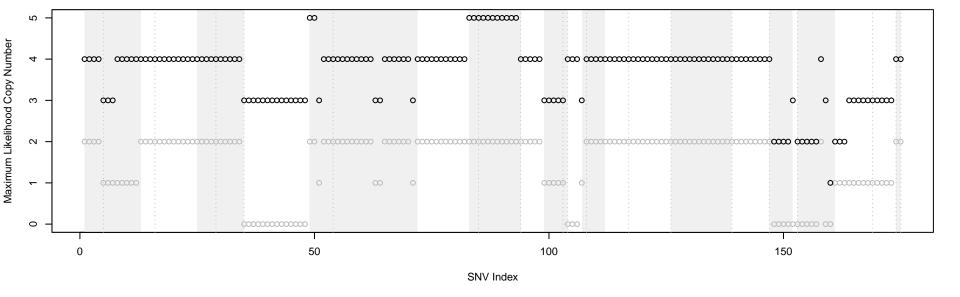


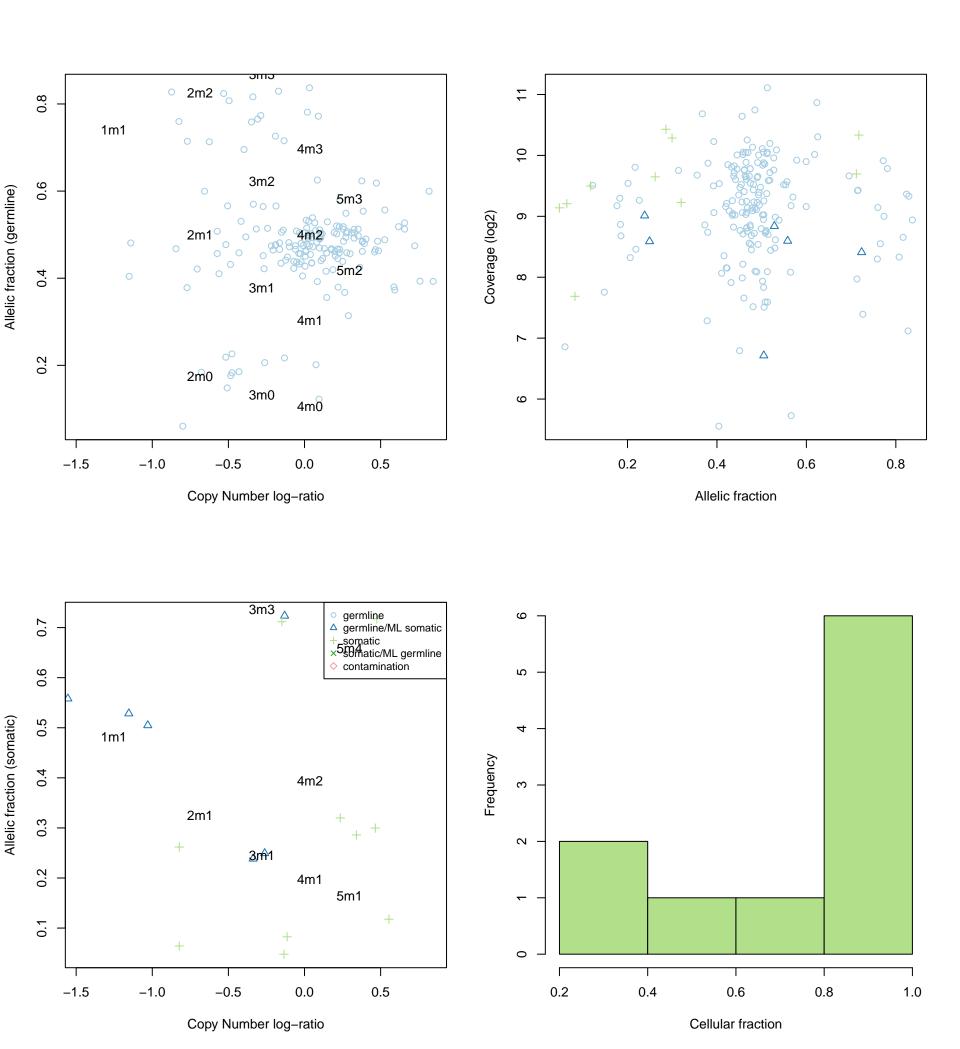
Purity: 0.65 Tumor ploidy: 3.874 3 5 6 7 2 Fraction Genome 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio



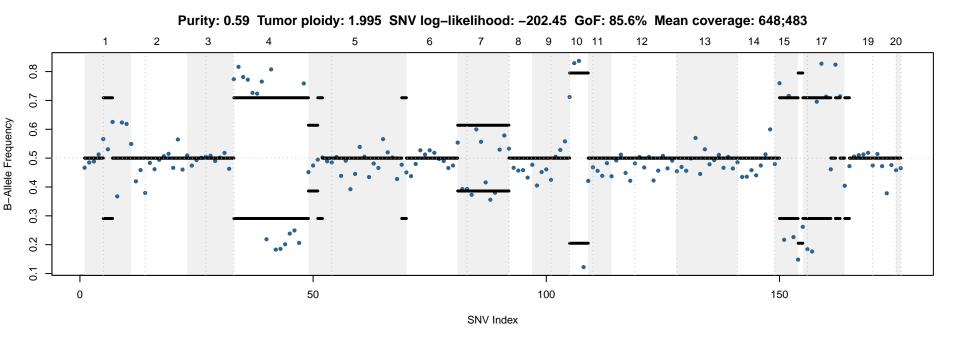
### SCNA-fit log-likelihood: -4789.54



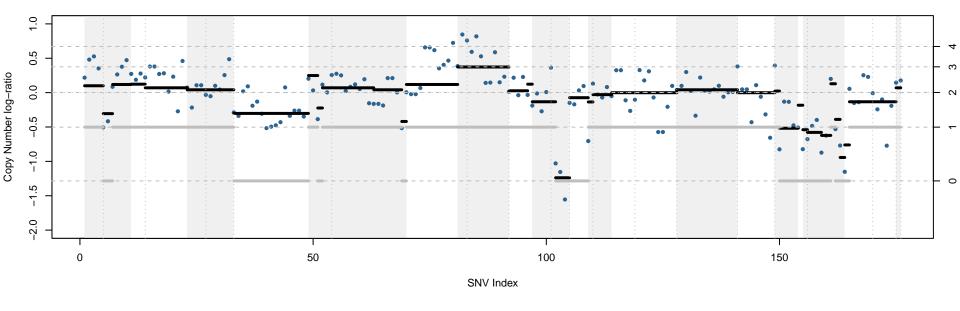


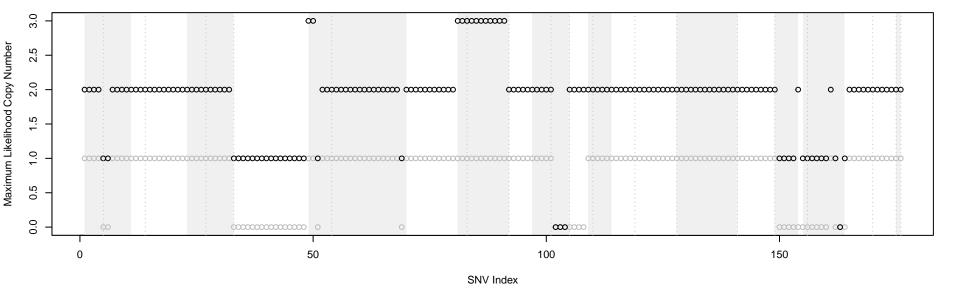


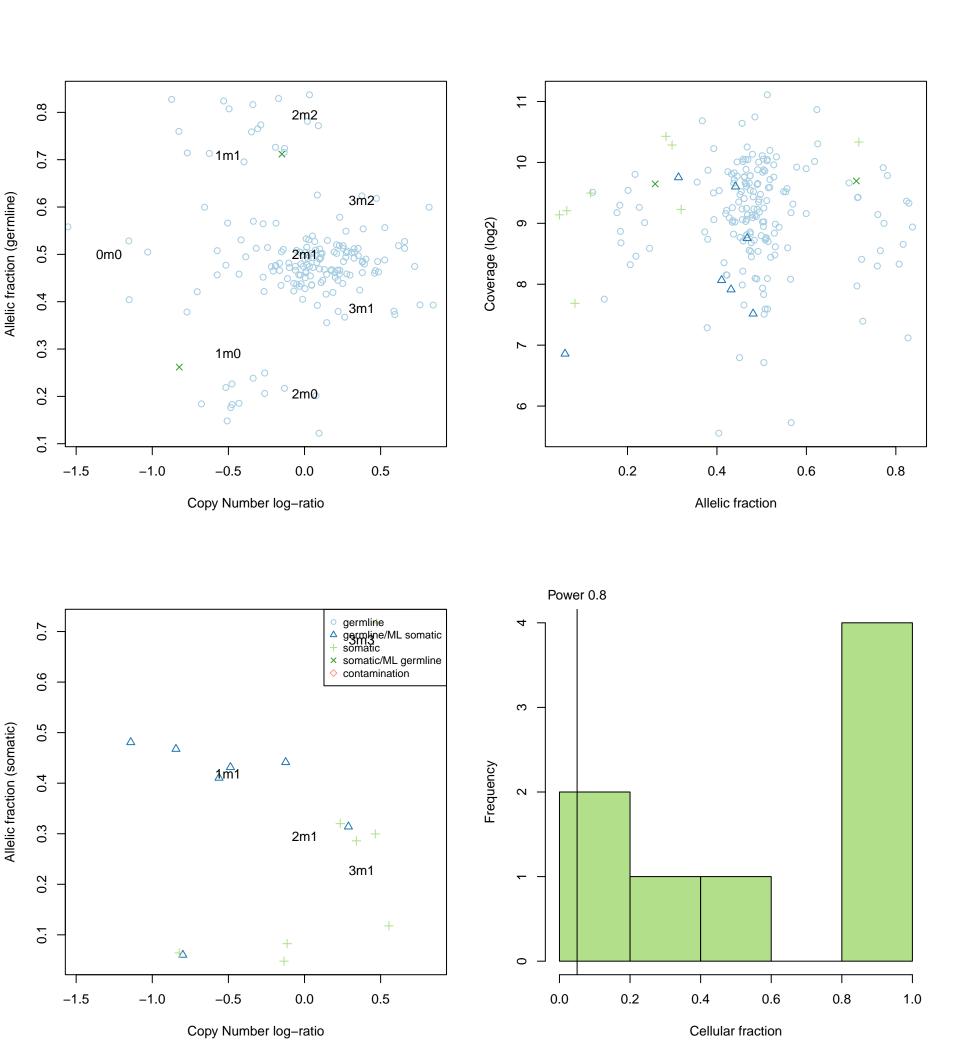
Purity: 0.59 Tumor ploidy: 1.995 2 0 3 Fraction Genome 0.10 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio



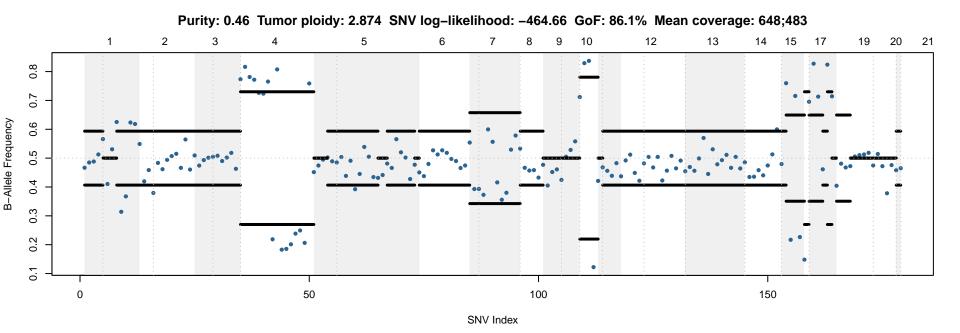
## SCNA-fit log-likelihood: -5057.04



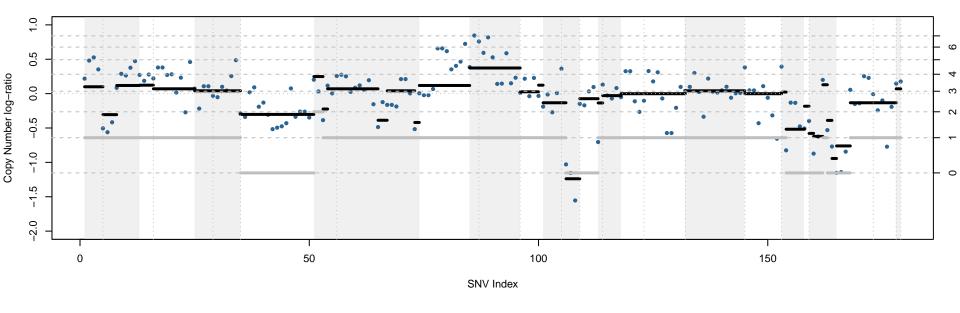


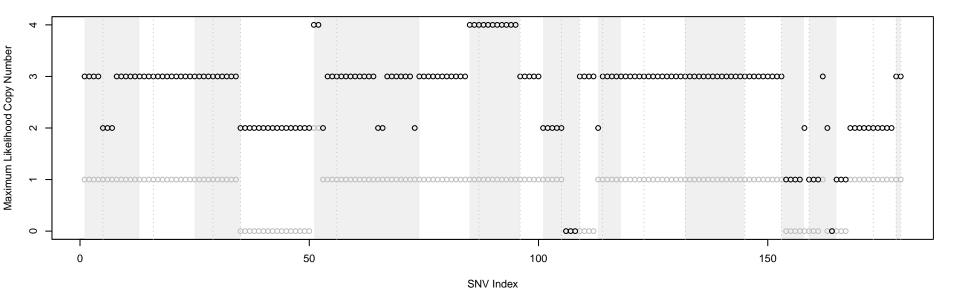


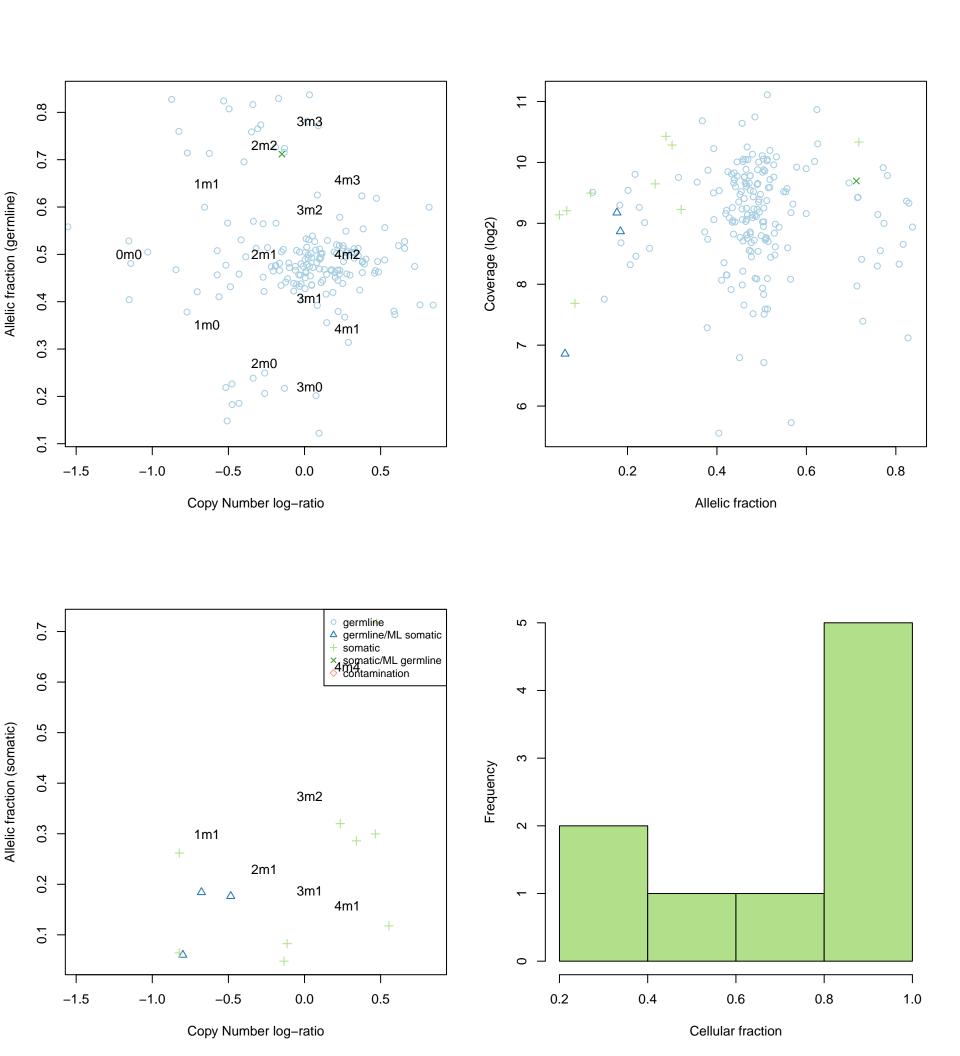
Purity: 0.46 Tumor ploidy: 2.874 0 2 5 4 6 Fraction Genome 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio

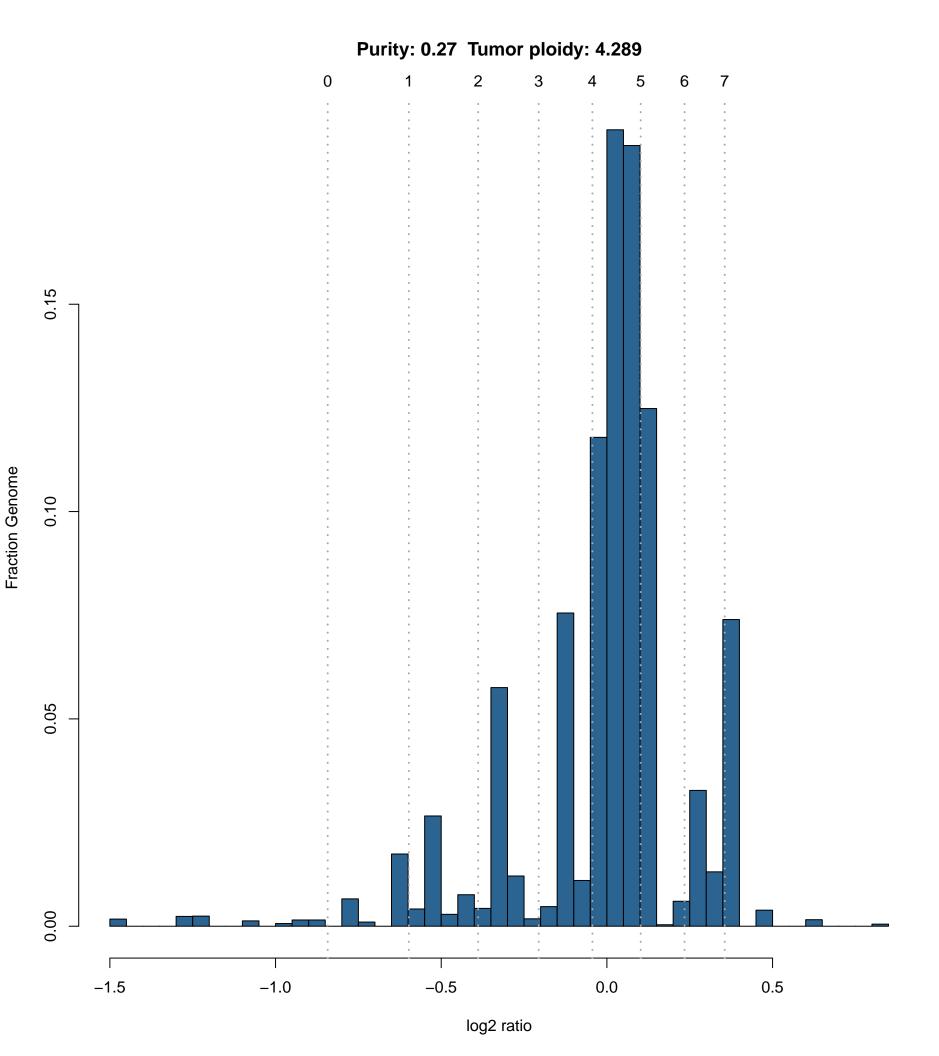


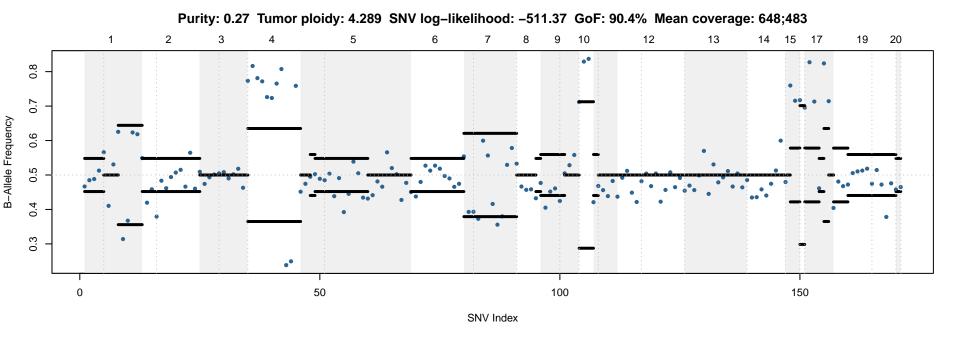
SCNA-fit log-likelihood: -4773.53



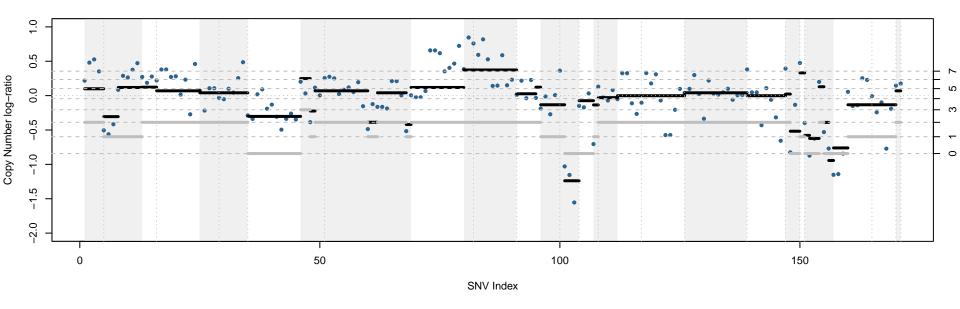


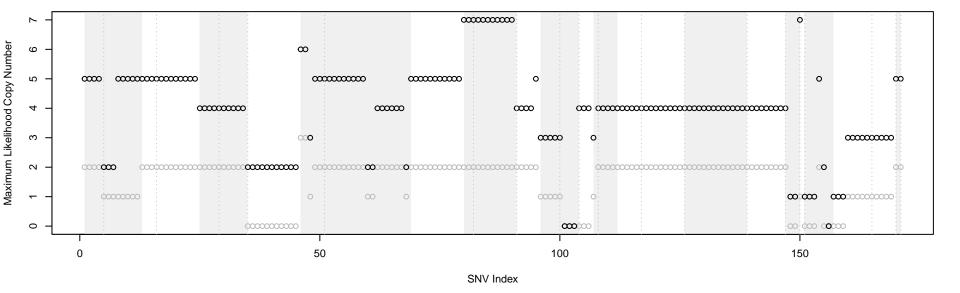


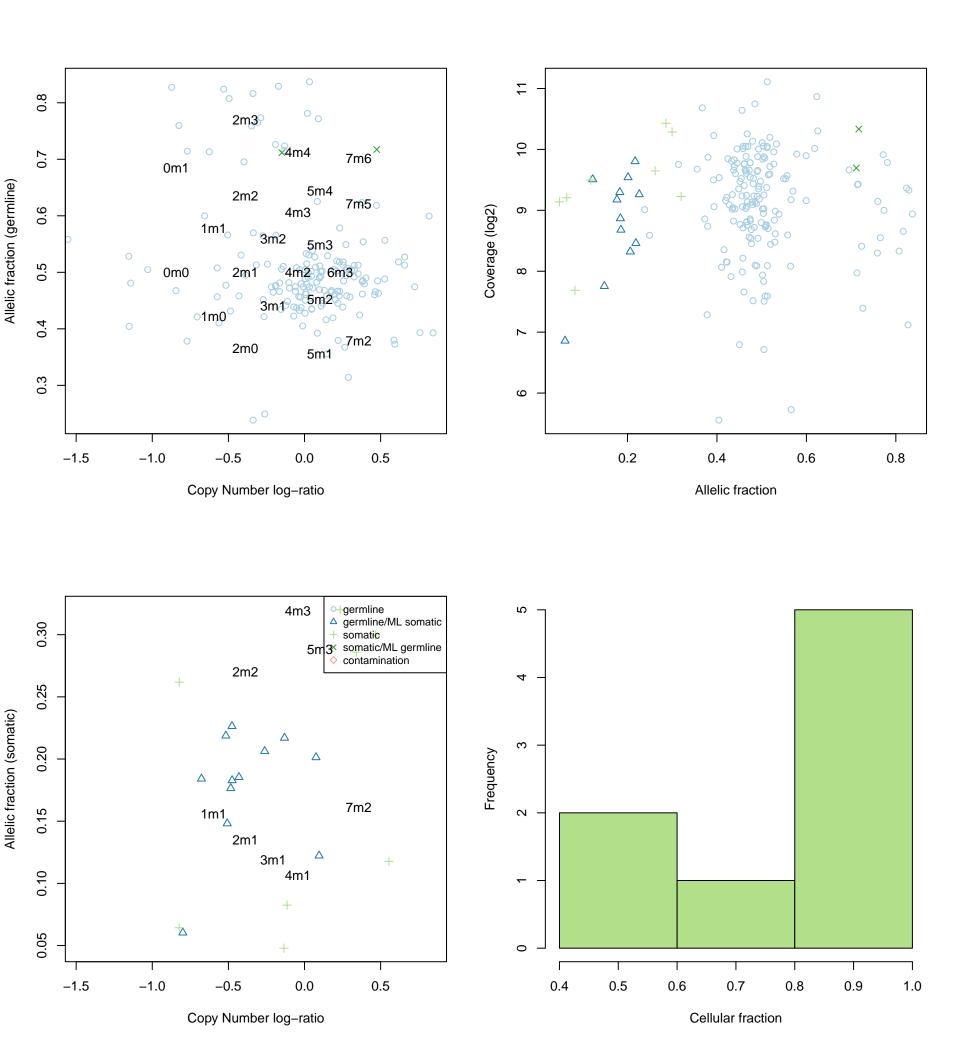




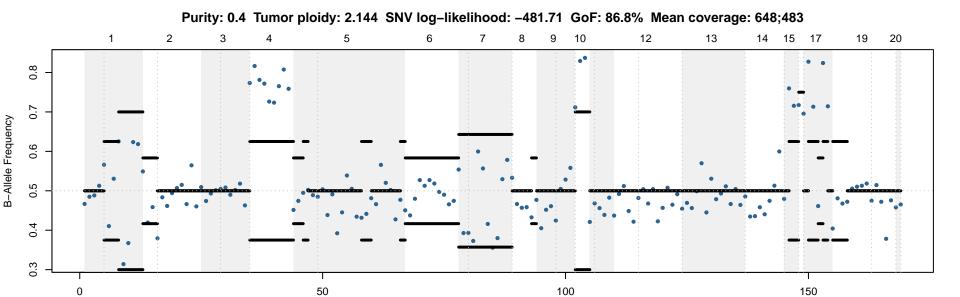
#### SCNA-fit log-likelihood: -4780.87





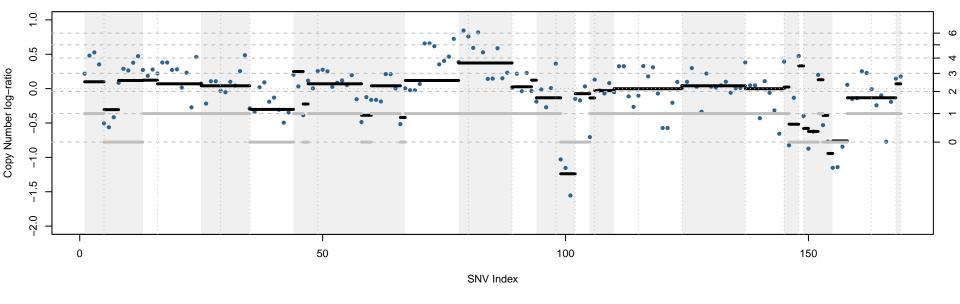


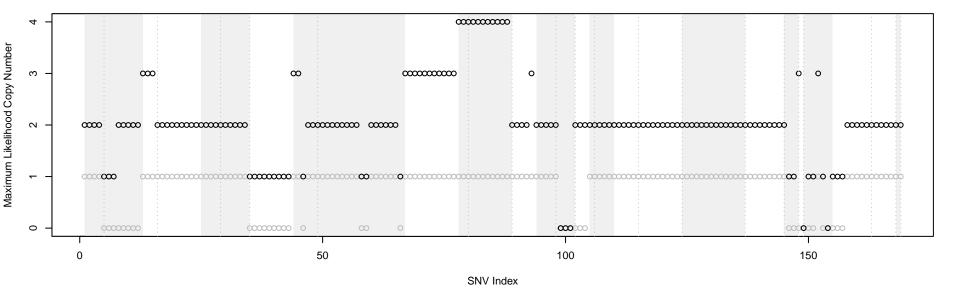
Purity: 0.4 Tumor ploidy: 2.144 0 2 3 6 5 Fraction Genome 0.10 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 log2 ratio

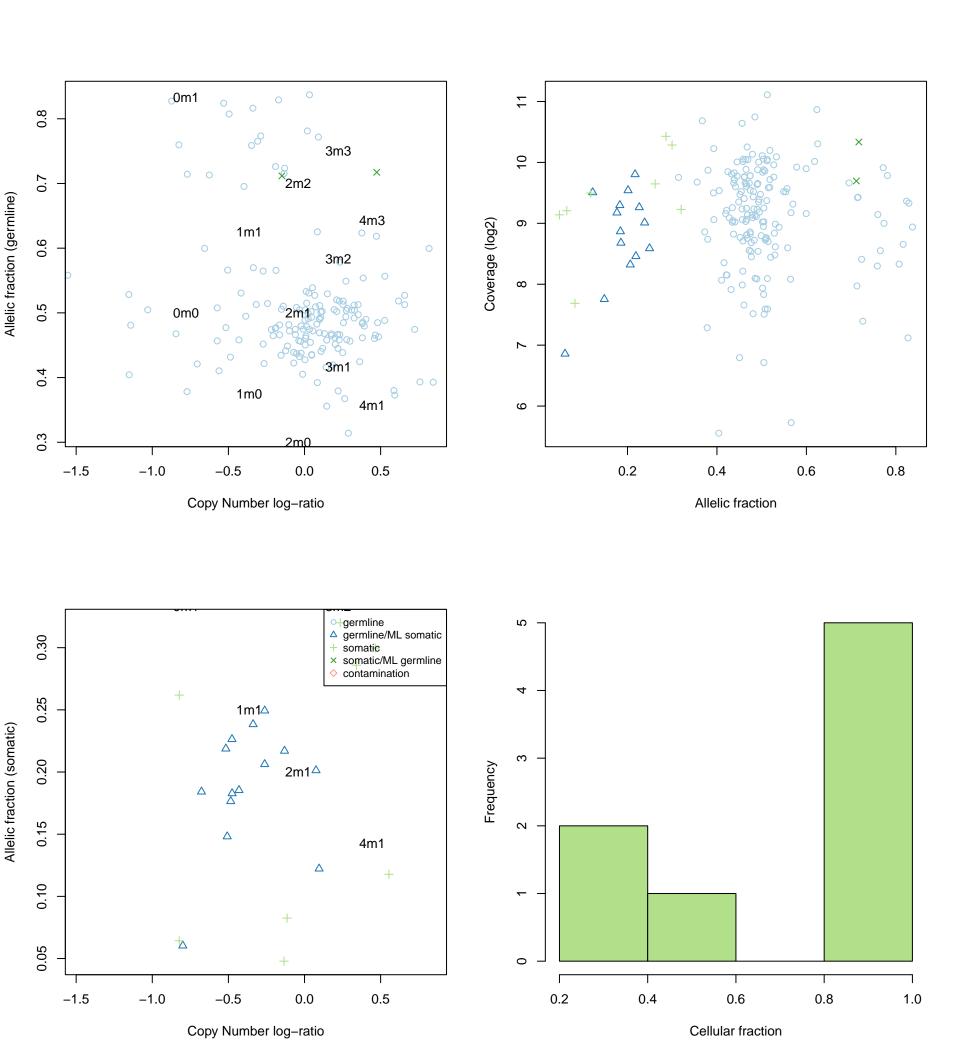


### SCNA-fit log-likelihood: -5195.58

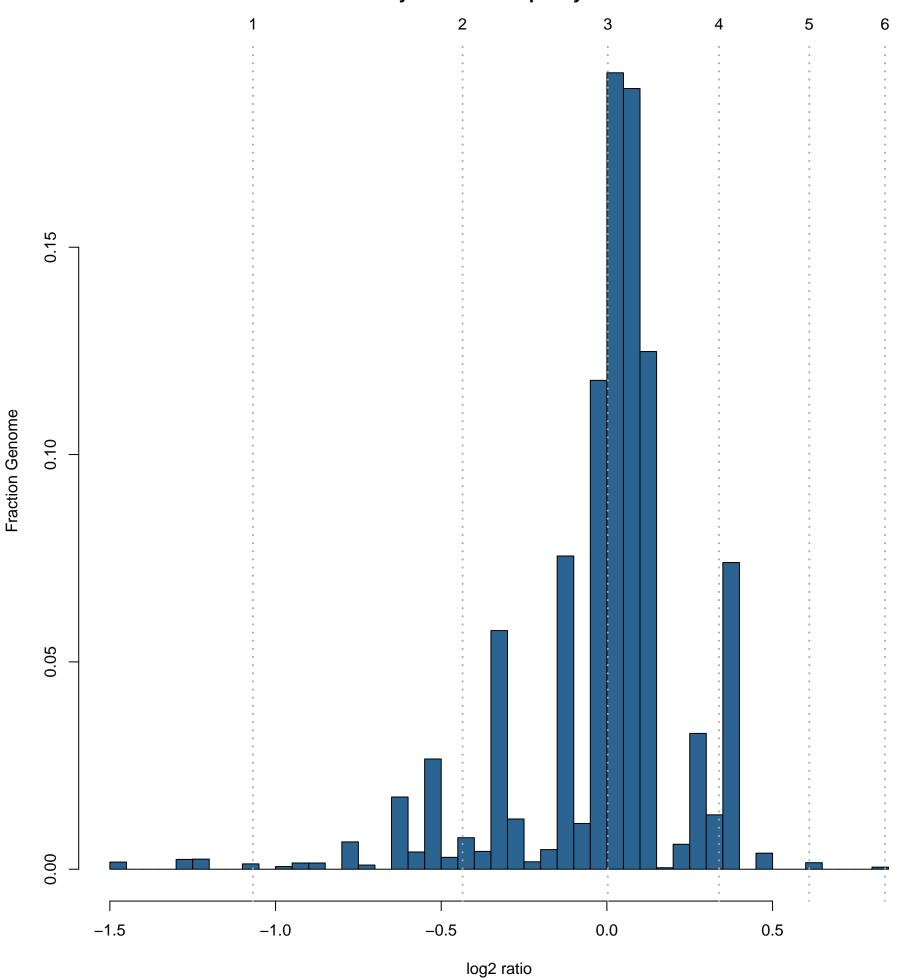
SNV Index

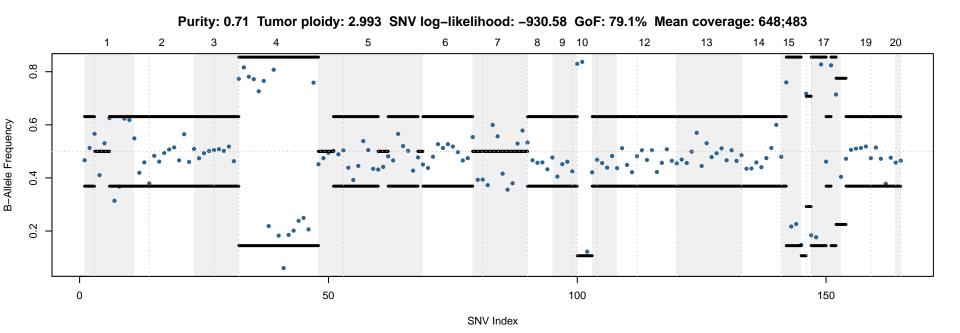






Purity: 0.71 Tumor ploidy: 2.993





### SCNA-fit log-likelihood: -4994.99

