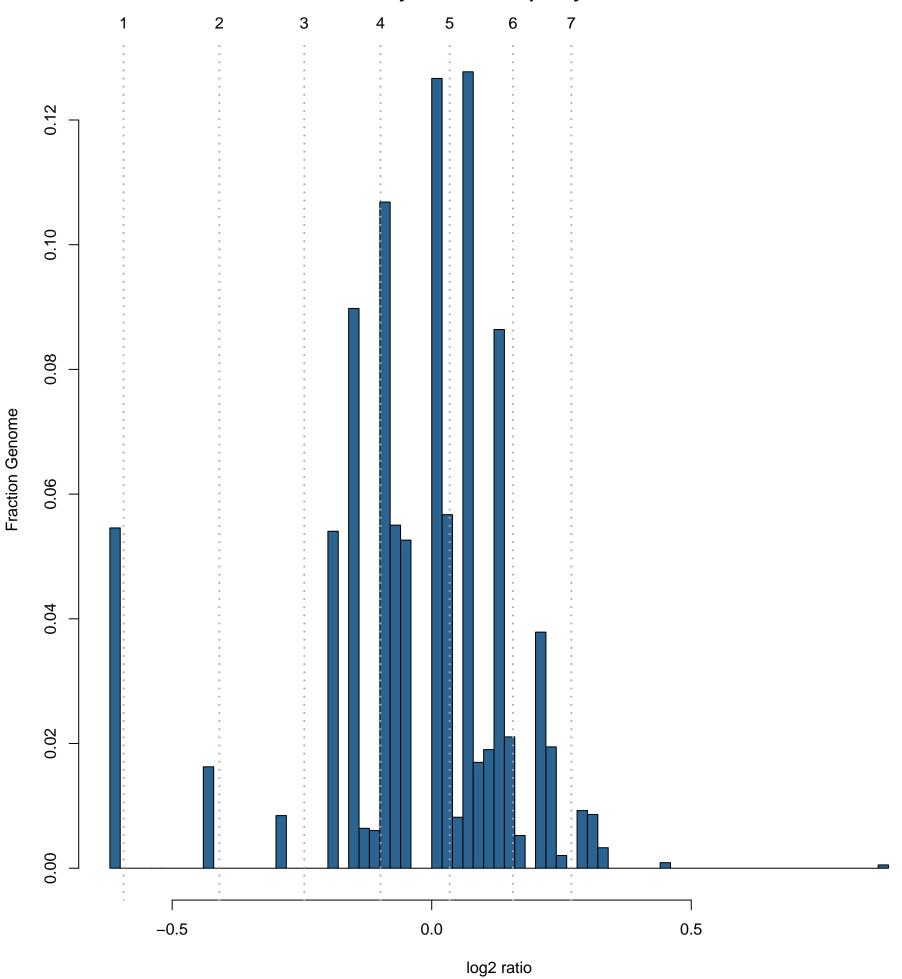
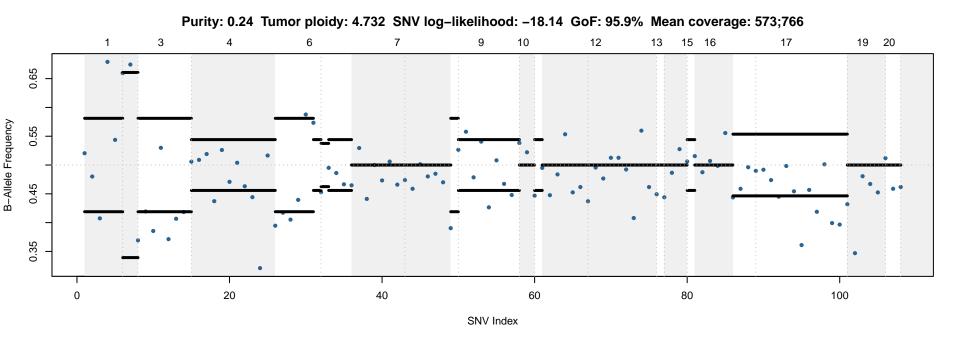
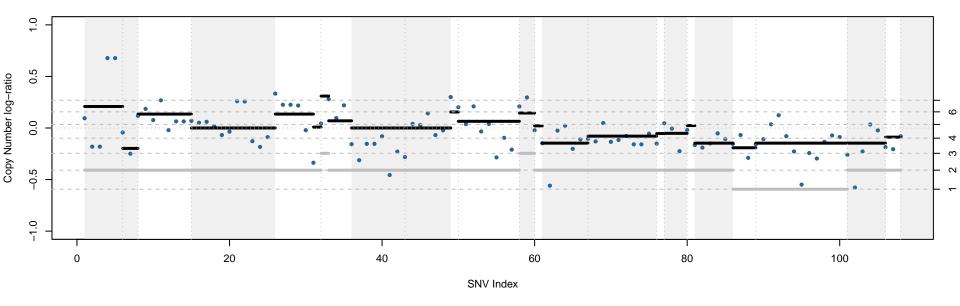
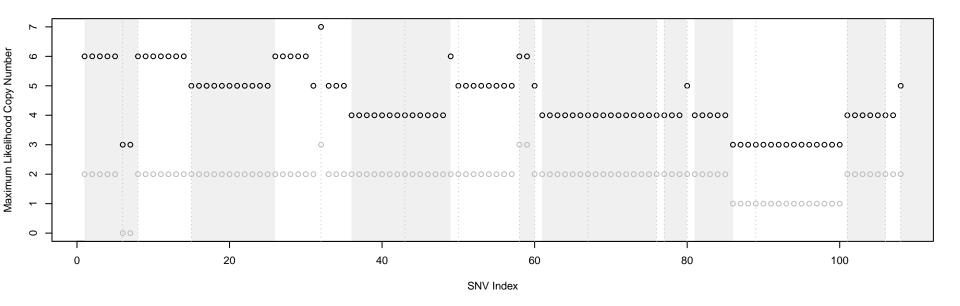
Purity: 0.24 Tumor ploidy: 4.732

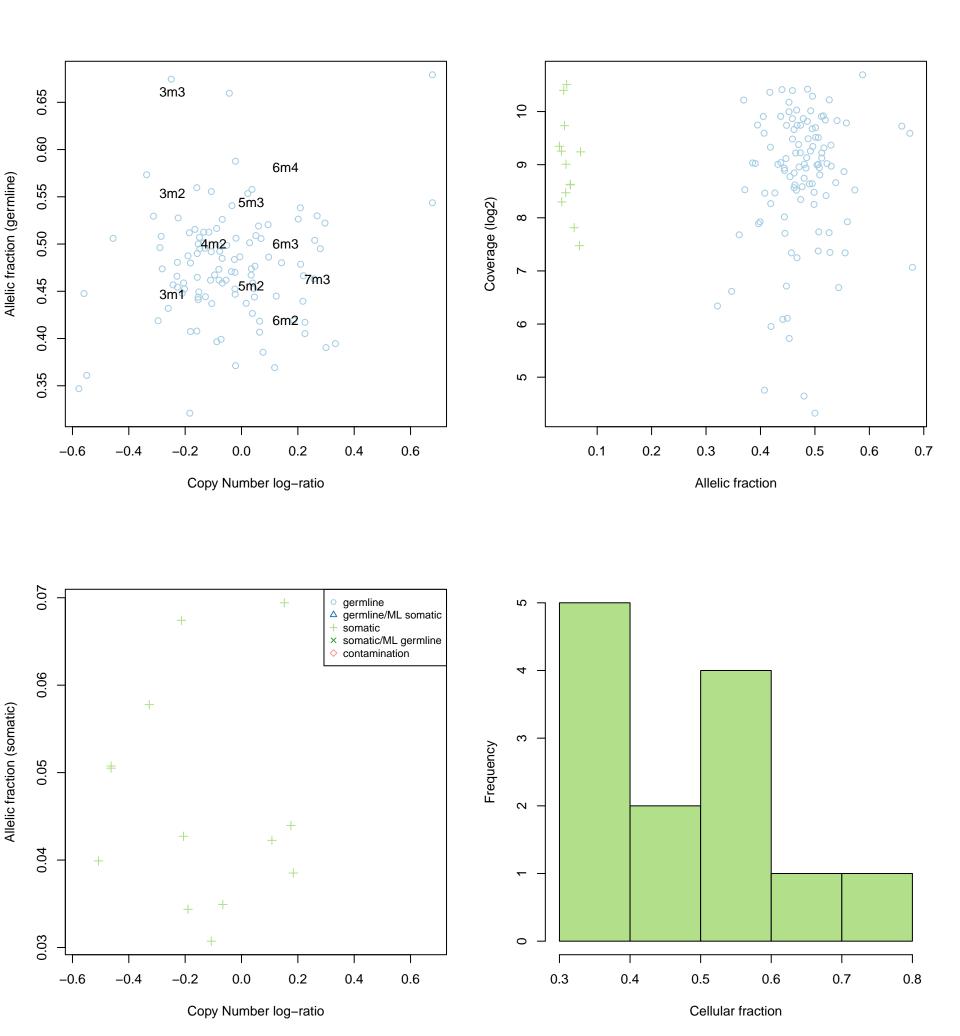




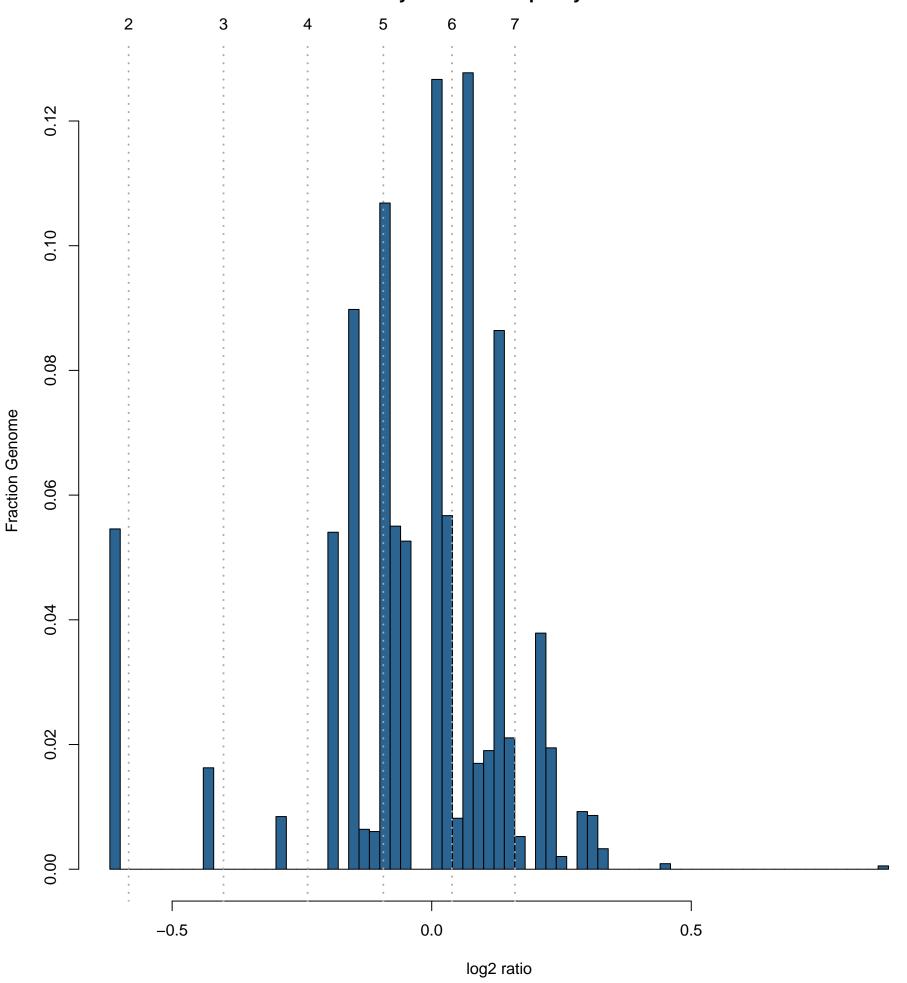
SCNA-fit log-likelihood: -1110.11

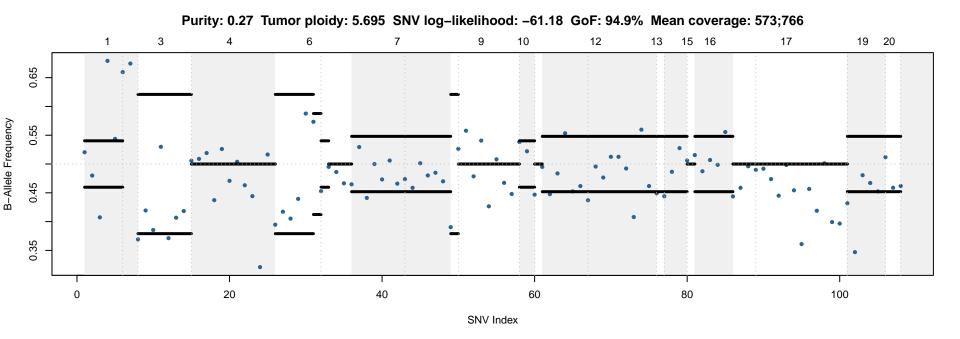




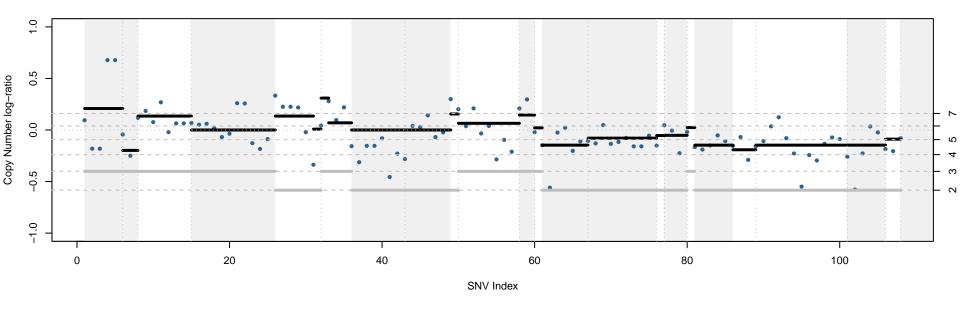


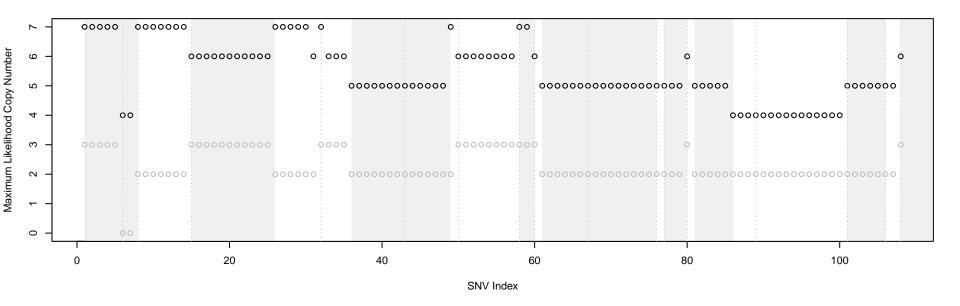
Purity: 0.27 Tumor ploidy: 5.695

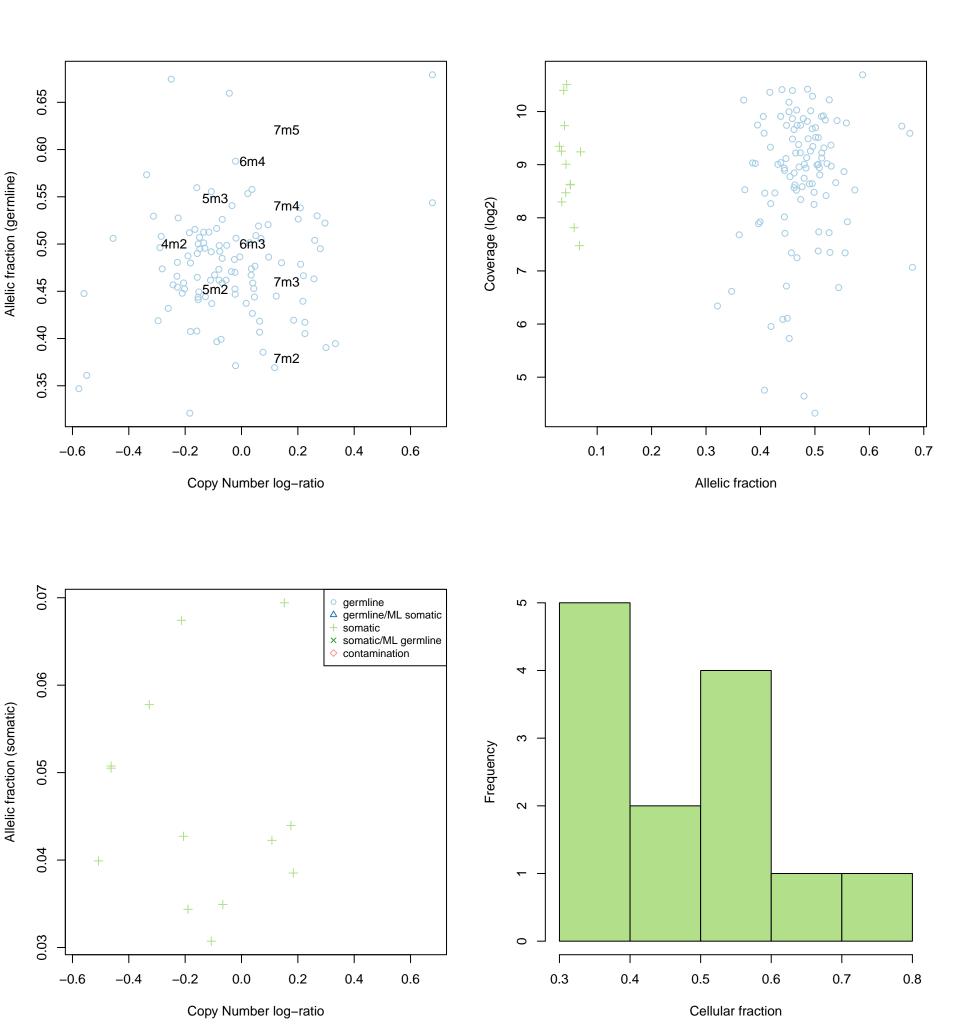




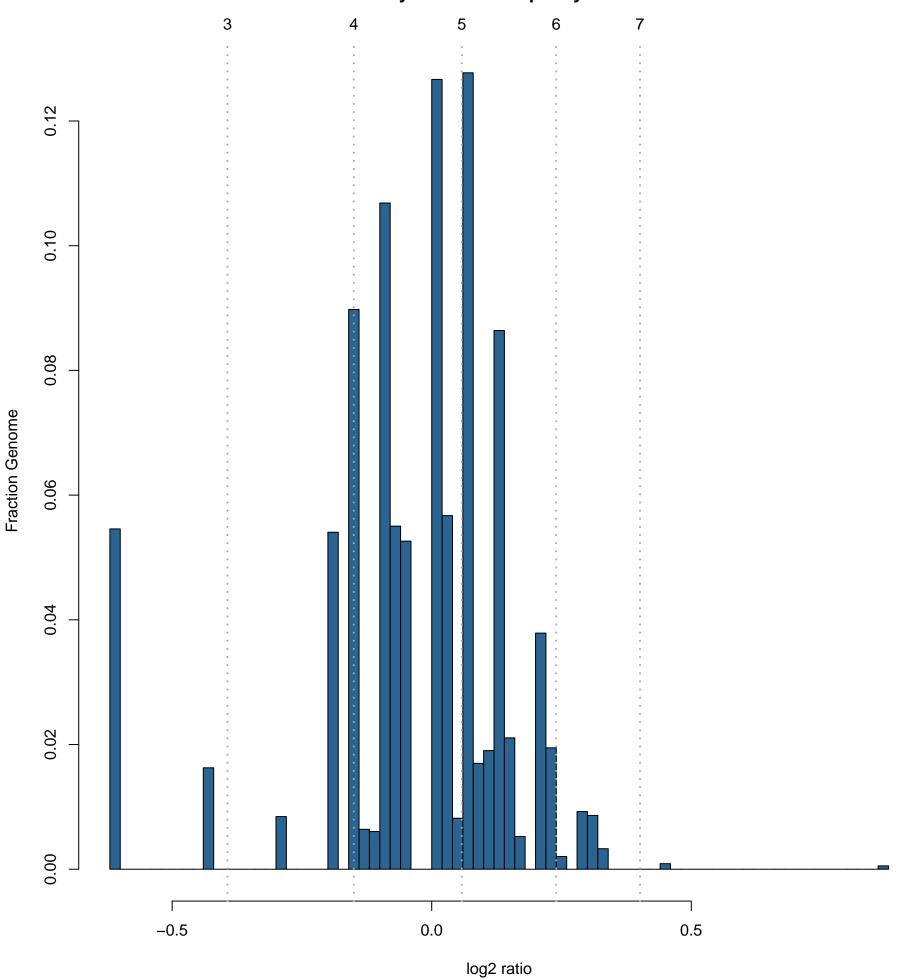
SCNA-fit log-likelihood: -1139.31

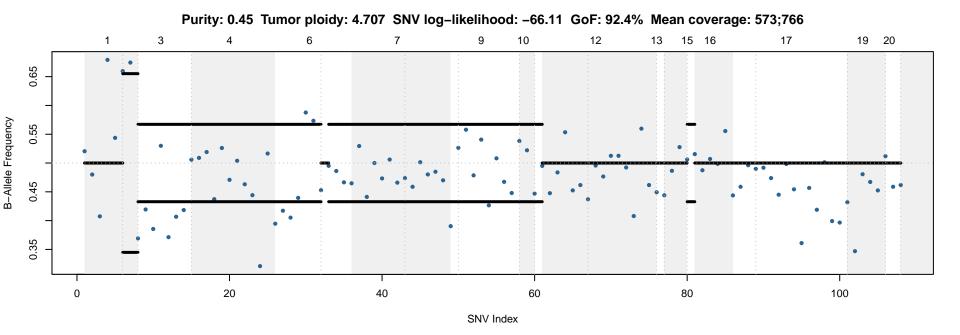




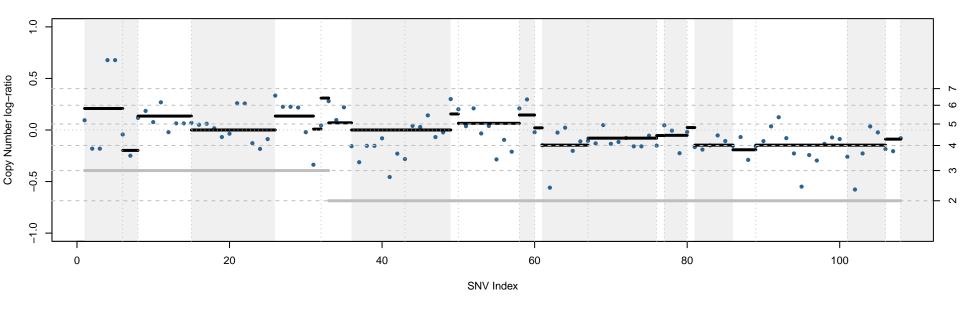


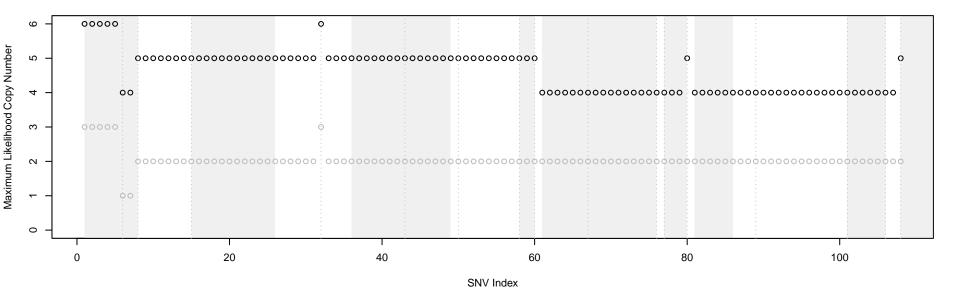
Purity: 0.45 Tumor ploidy: 4.707

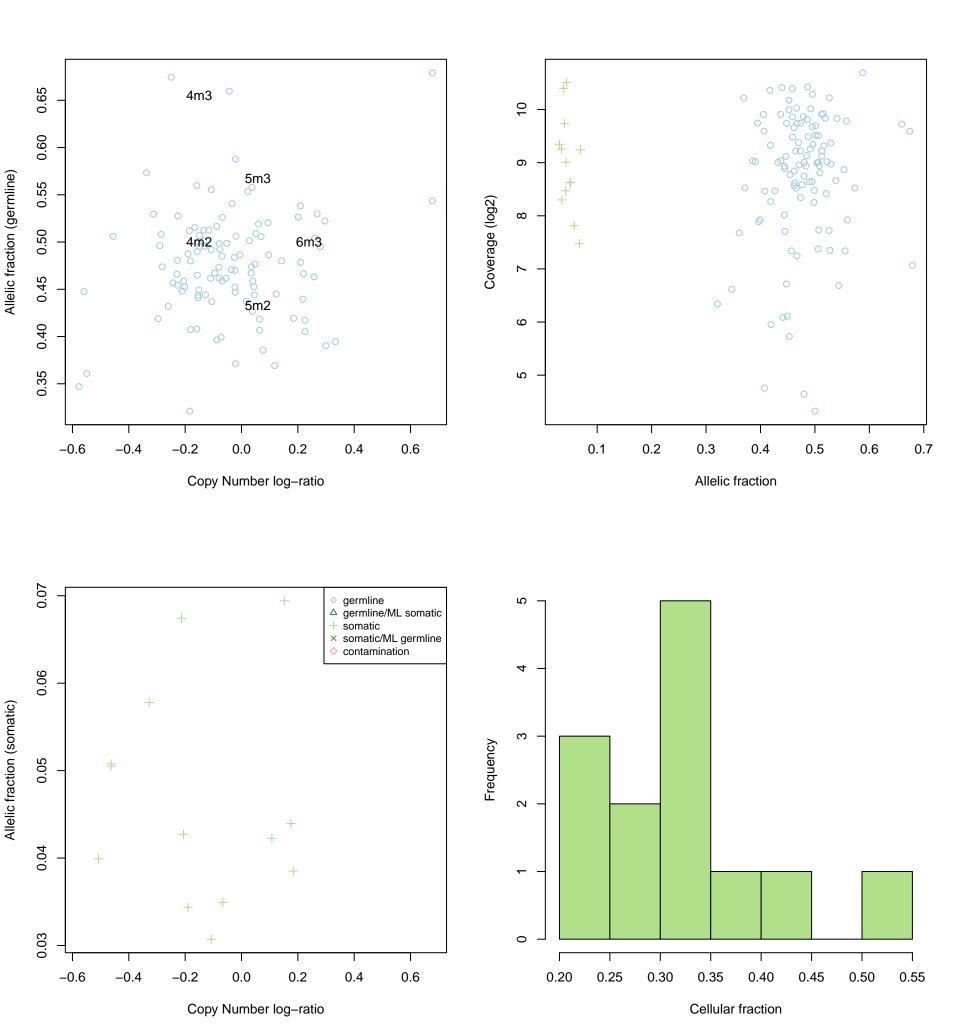




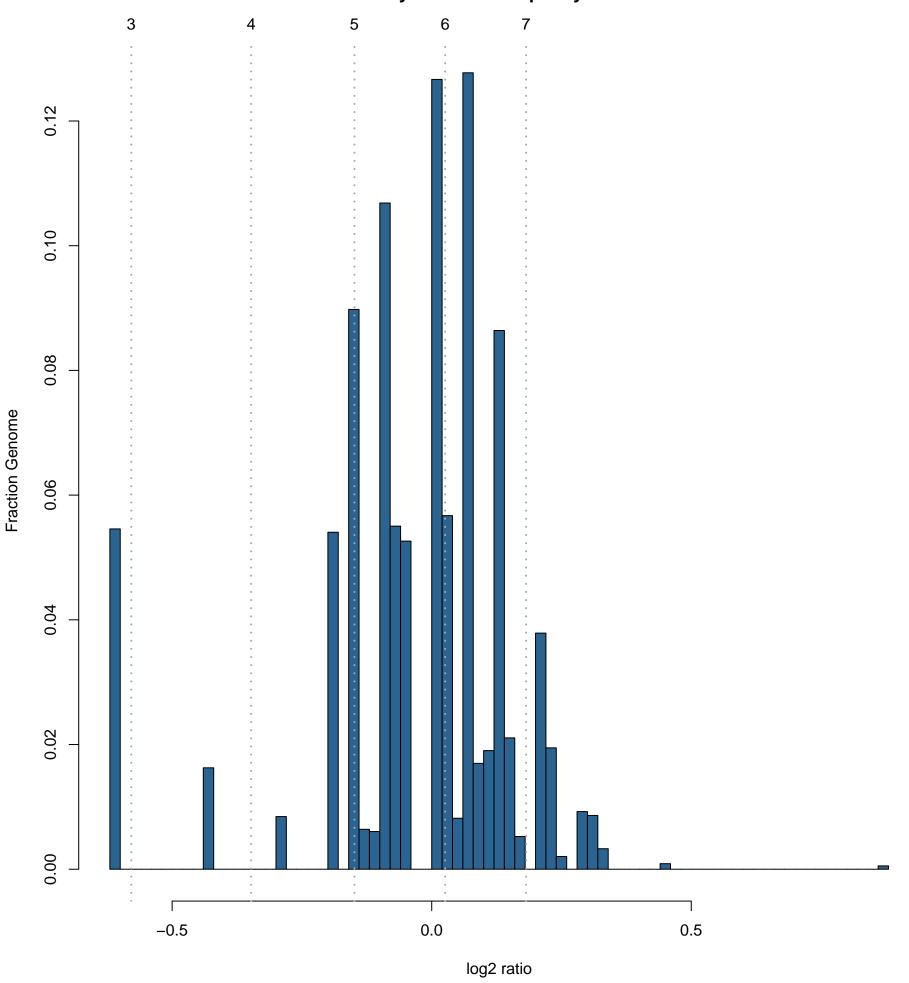
SCNA-fit log-likelihood: -1221.79

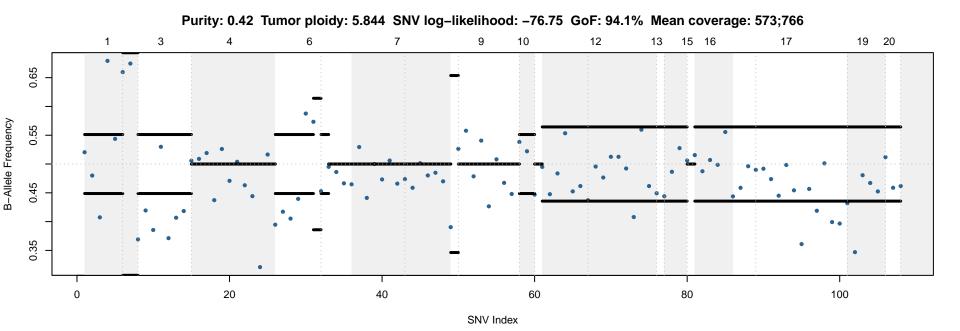




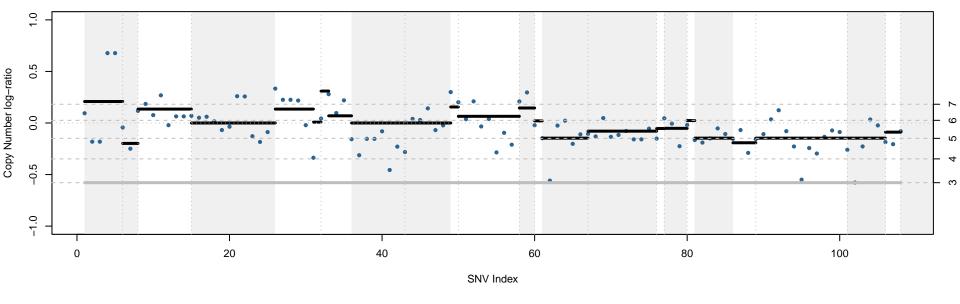


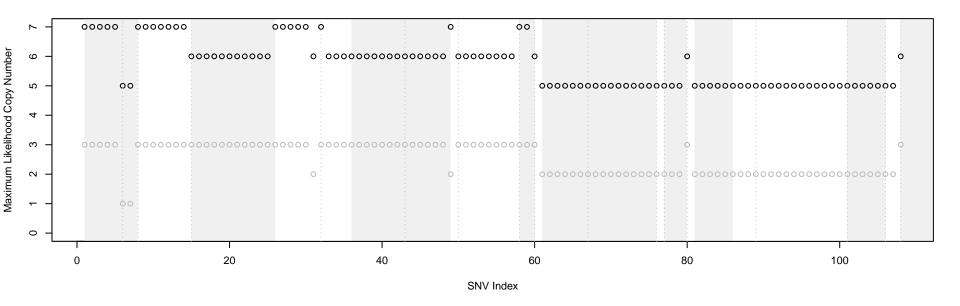
Purity: 0.42 Tumor ploidy: 5.844

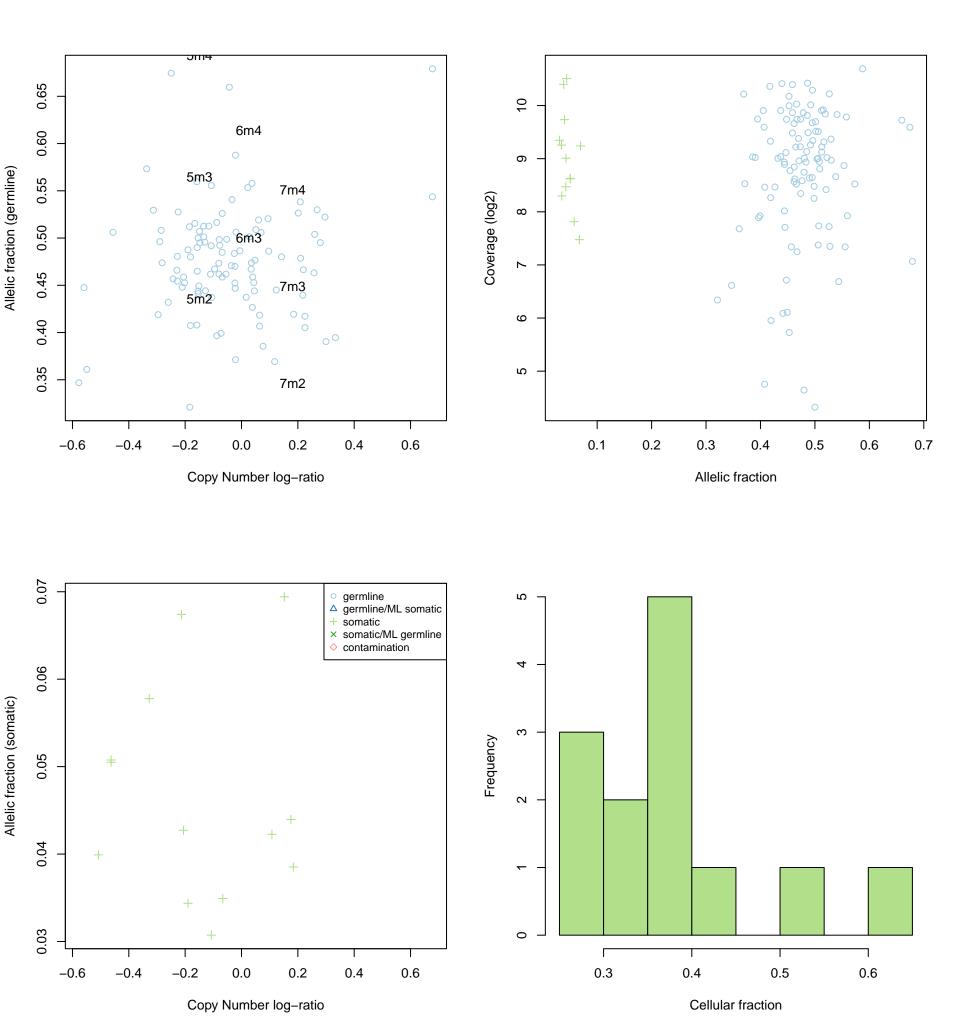




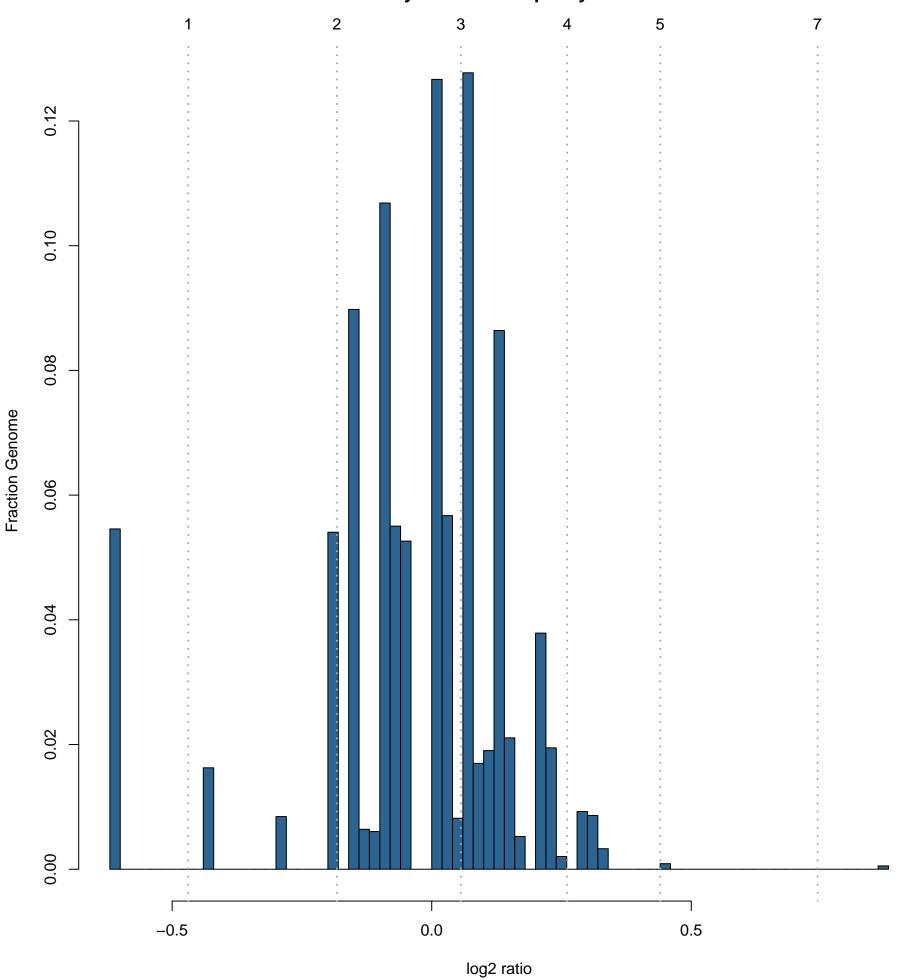
SCNA-fit log-likelihood: -1202.17

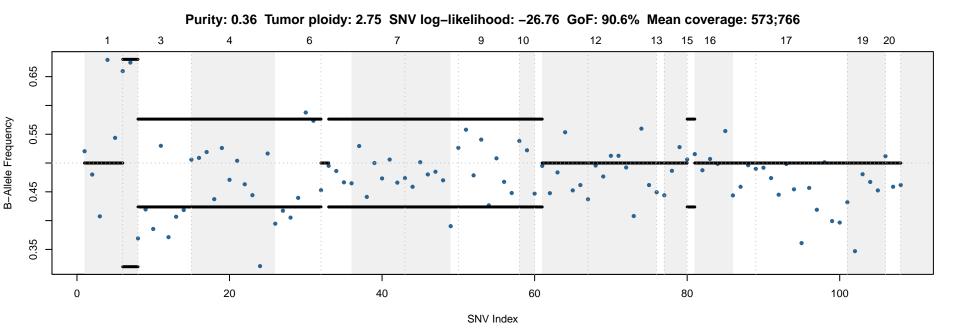




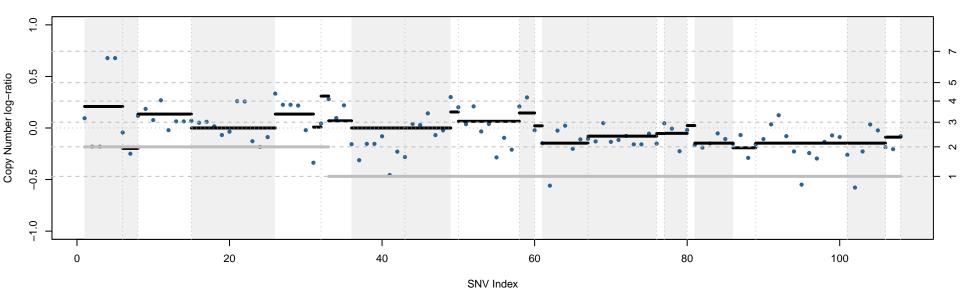


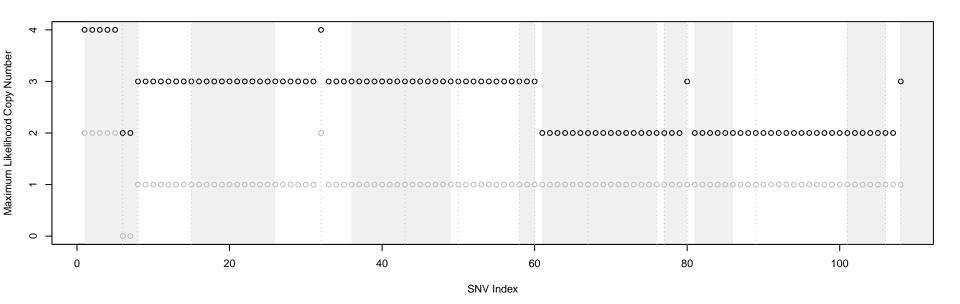
Purity: 0.36 Tumor ploidy: 2.75

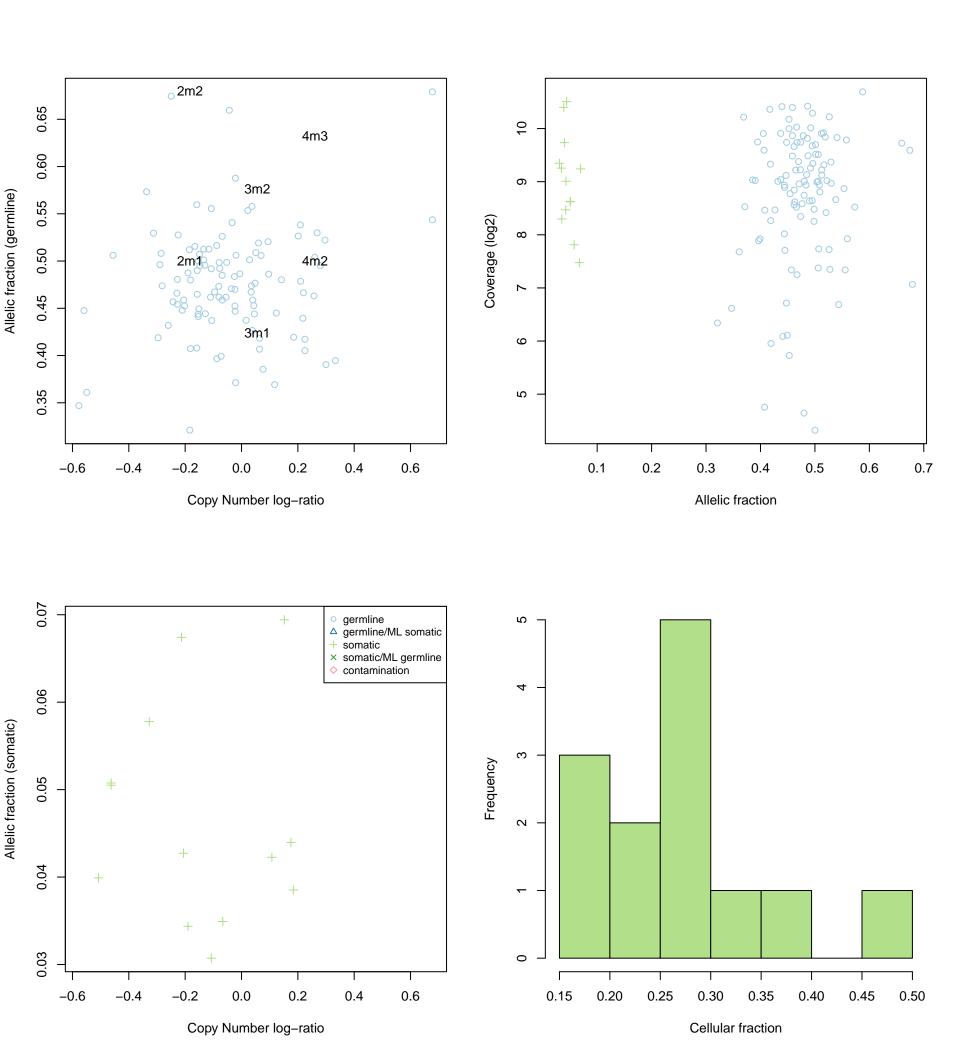




SCNA-fit log-likelihood: -1382.98

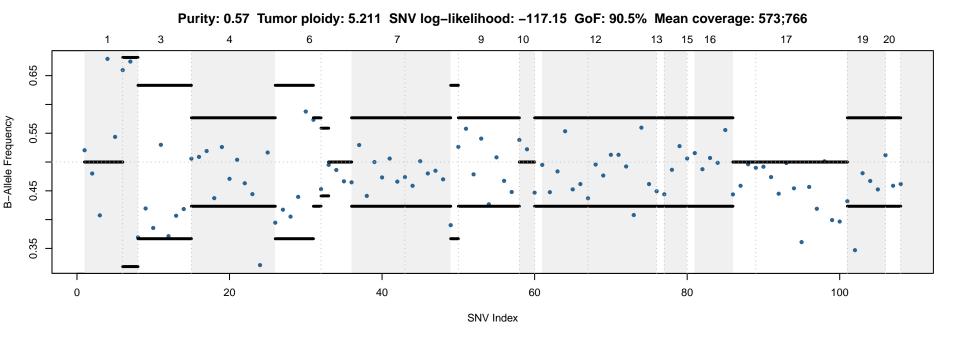




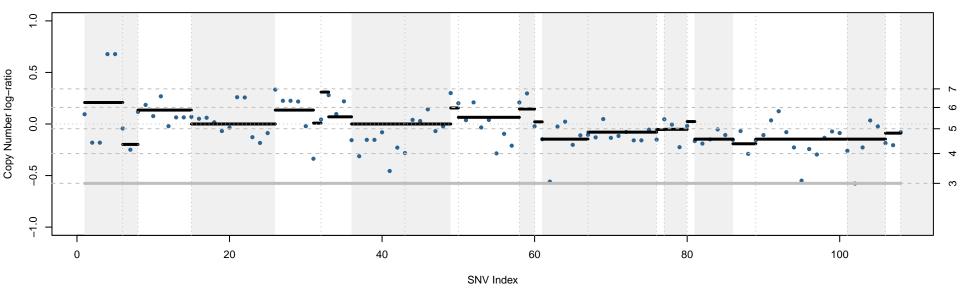


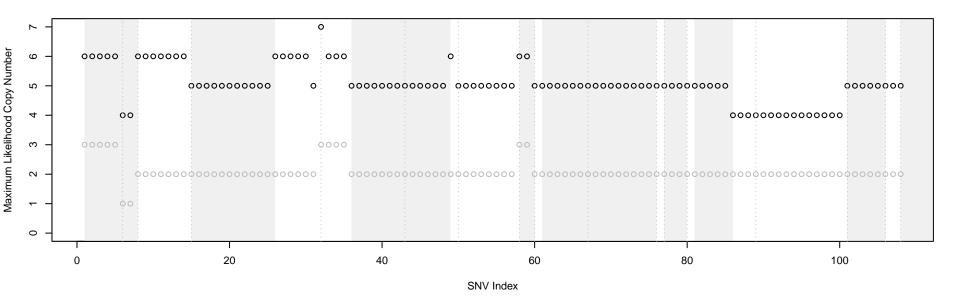
Purity: 0.57 Tumor ploidy: 5.211 3 0.12 0.10 0.08 Fraction Genome 90.0 0.04 0.02 0.00 -0.5 0.0 0.5

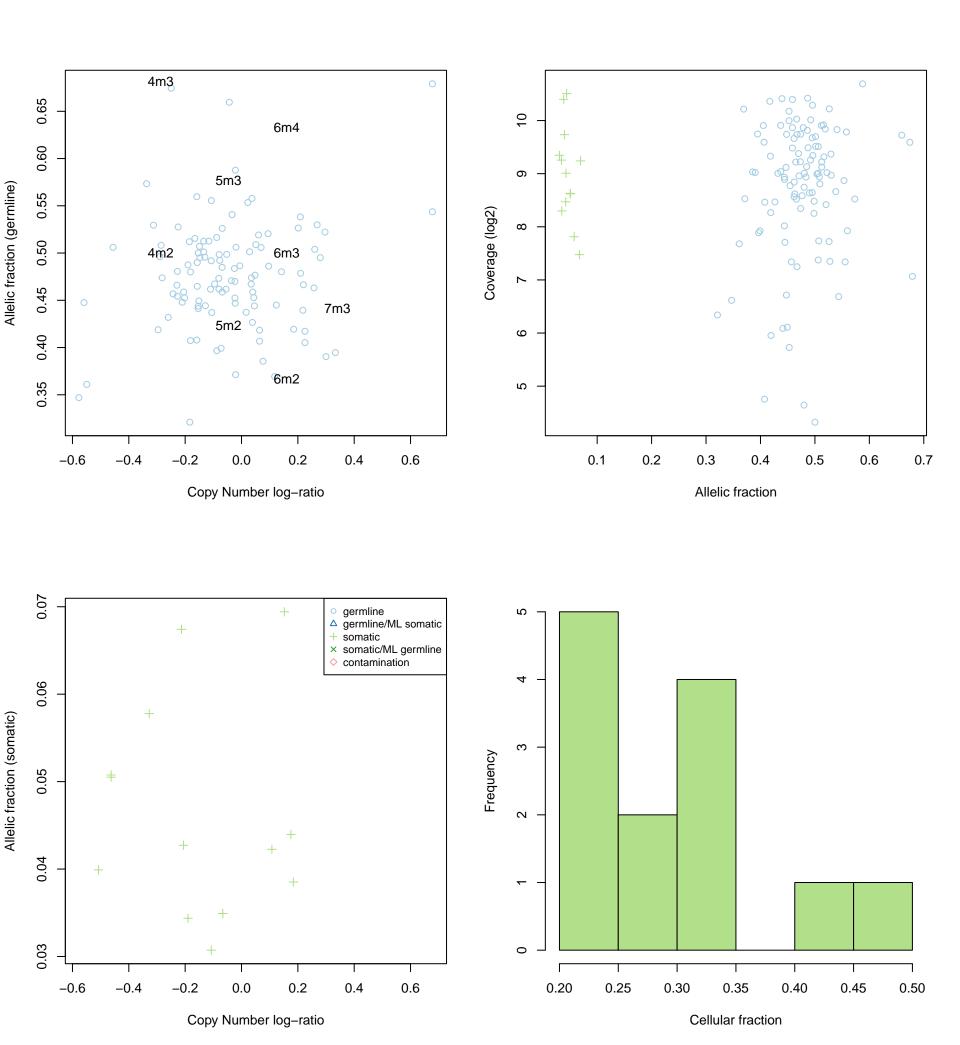
log2 ratio



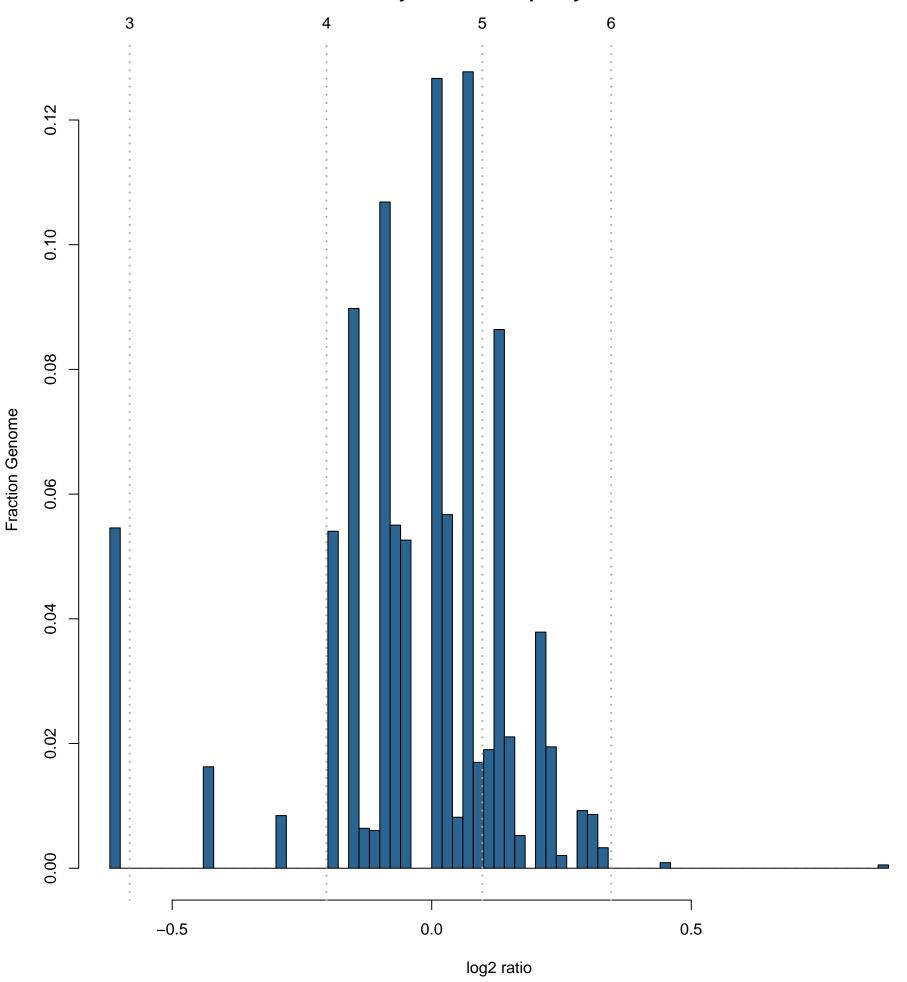
SCNA-fit log-likelihood: -1349.43

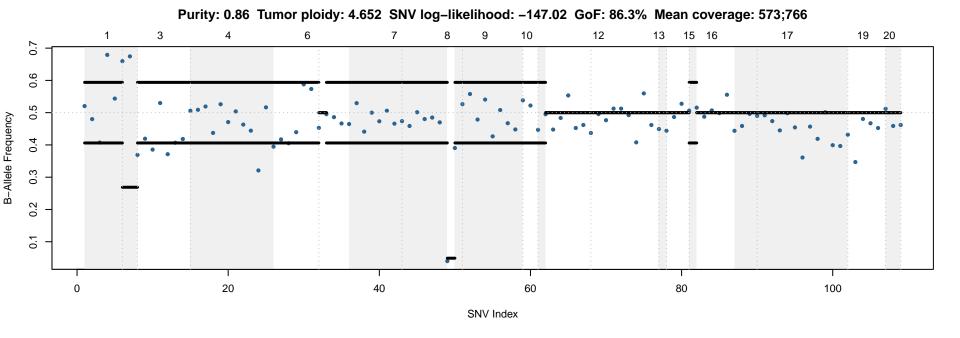




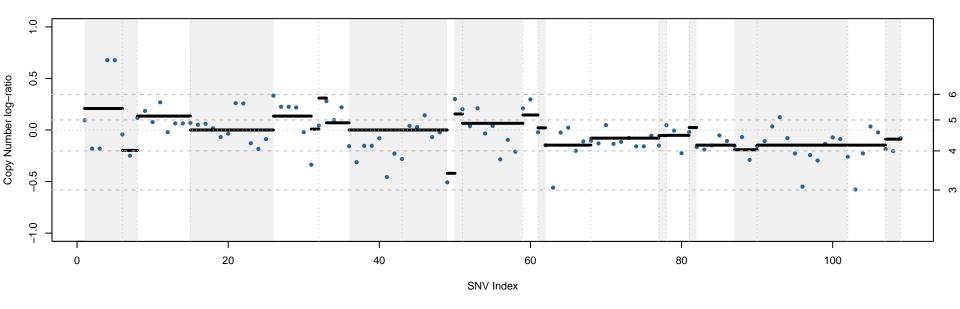


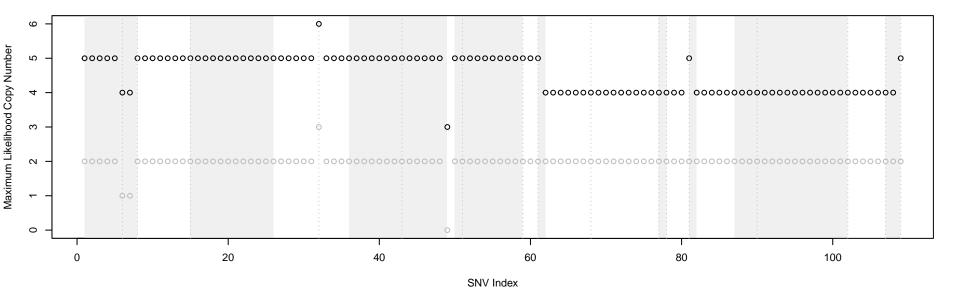
Purity: 0.86 Tumor ploidy: 4.652

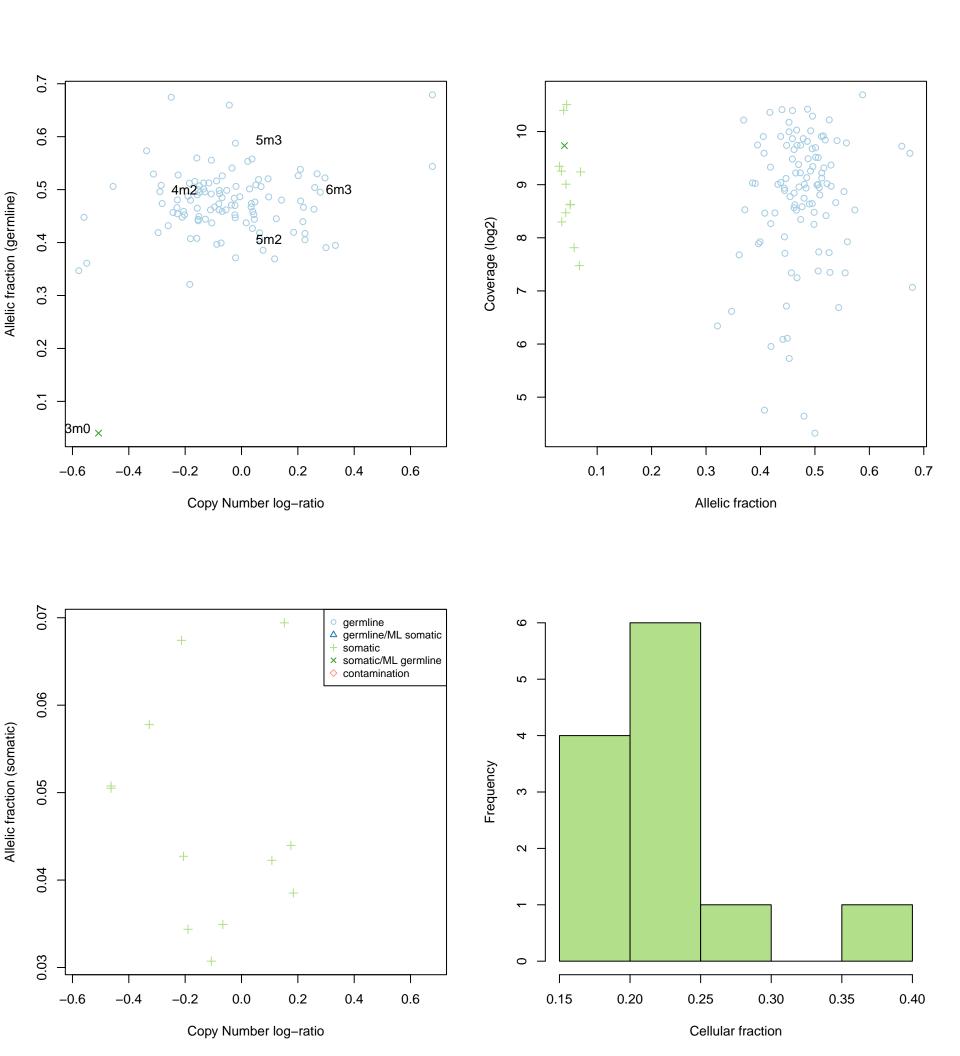




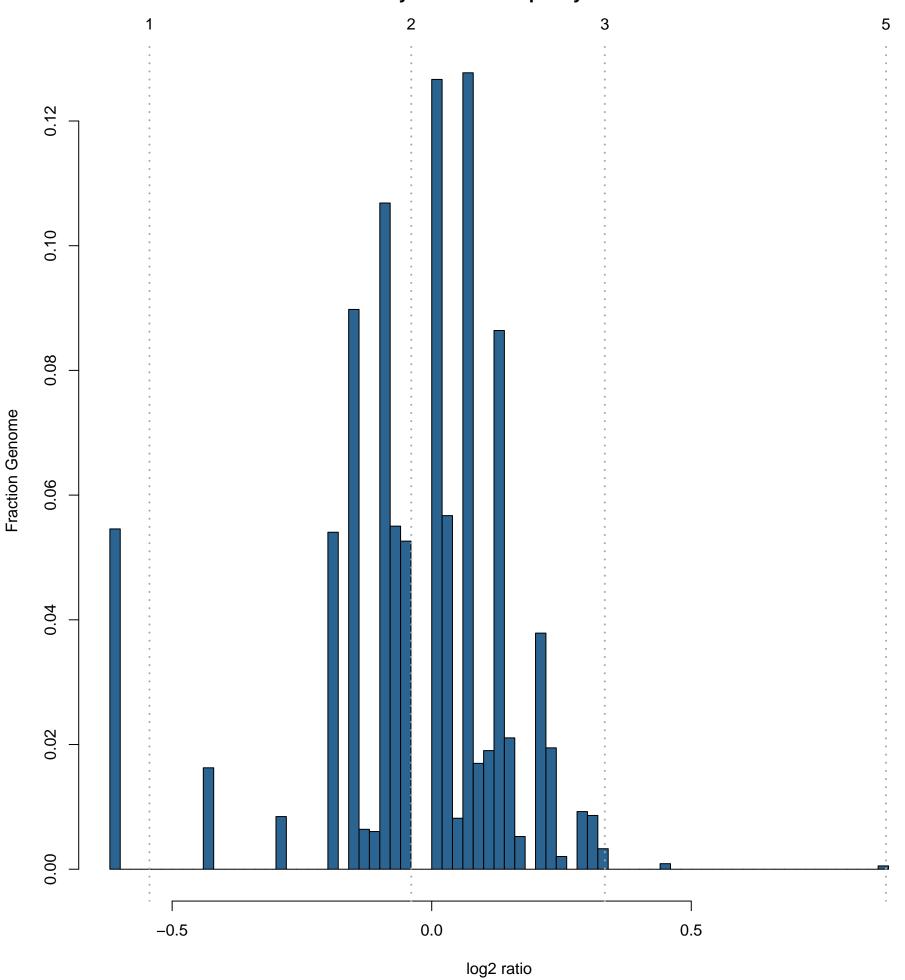
SCNA-fit log-likelihood: -1504.23

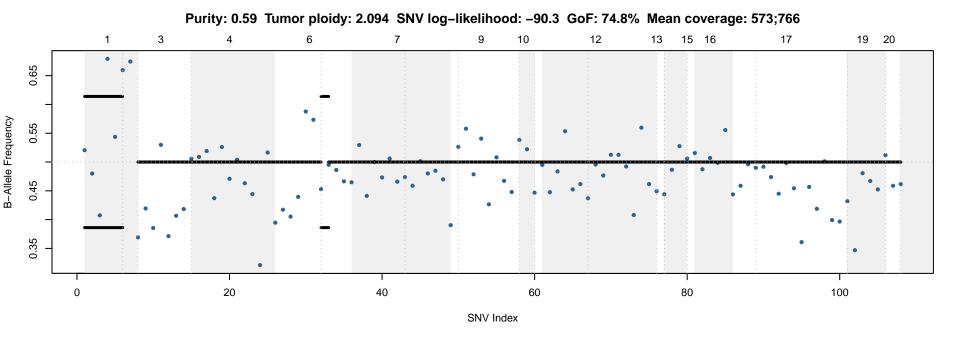




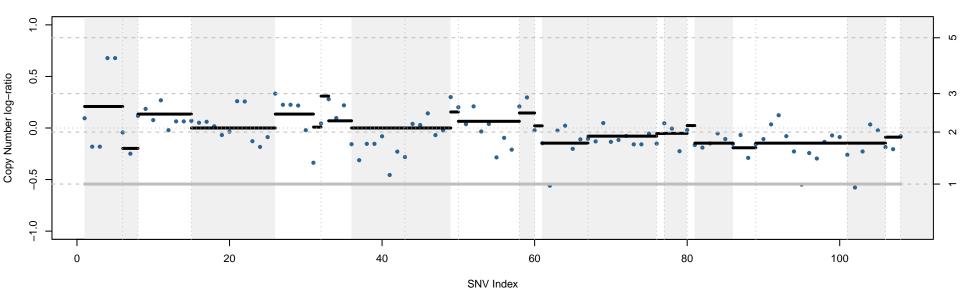


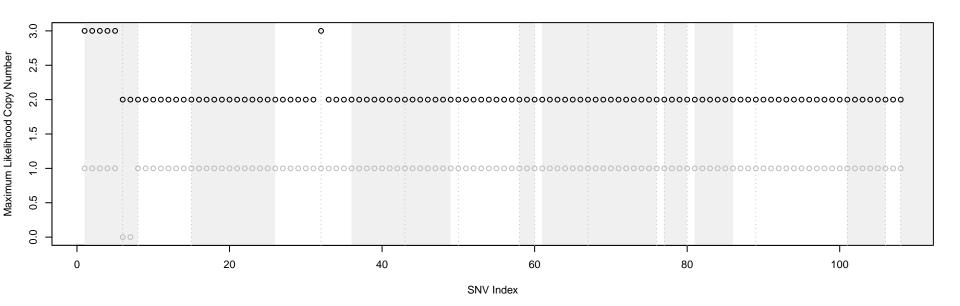
Purity: 0.59 Tumor ploidy: 2.094

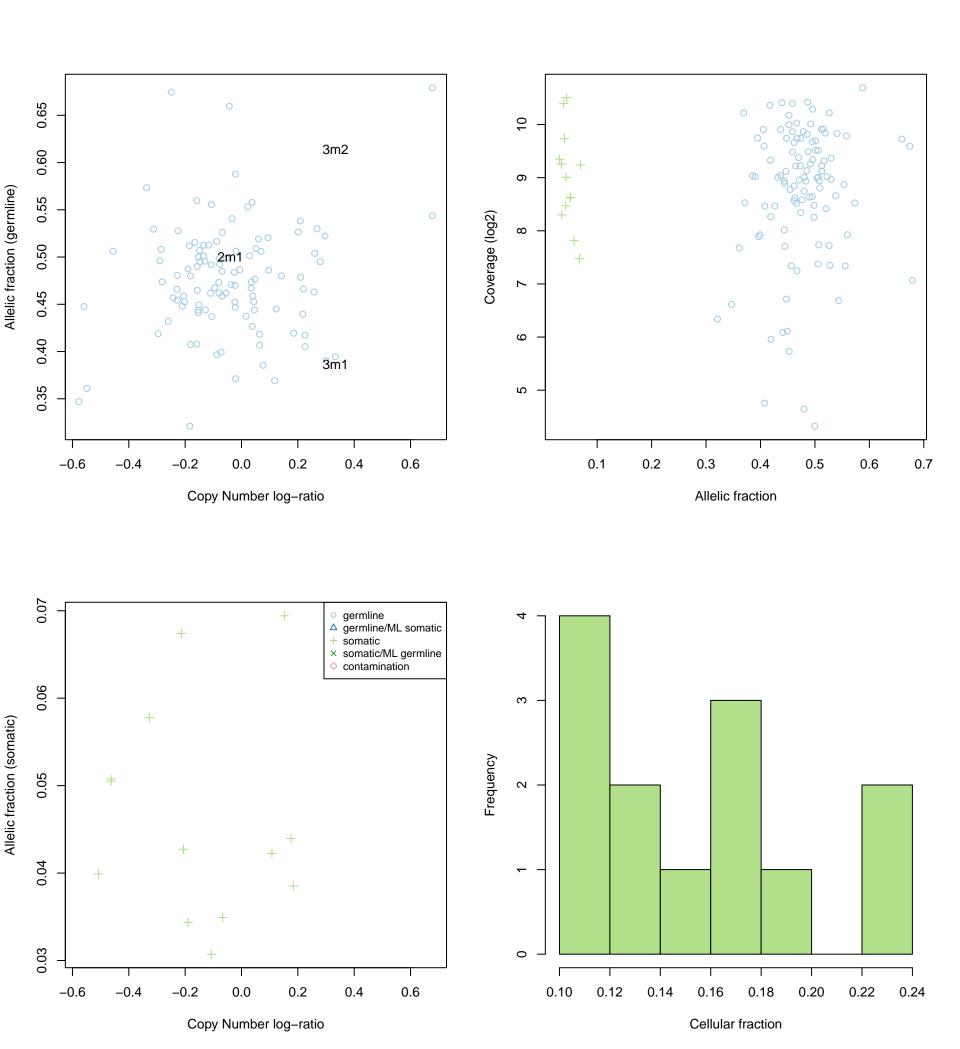




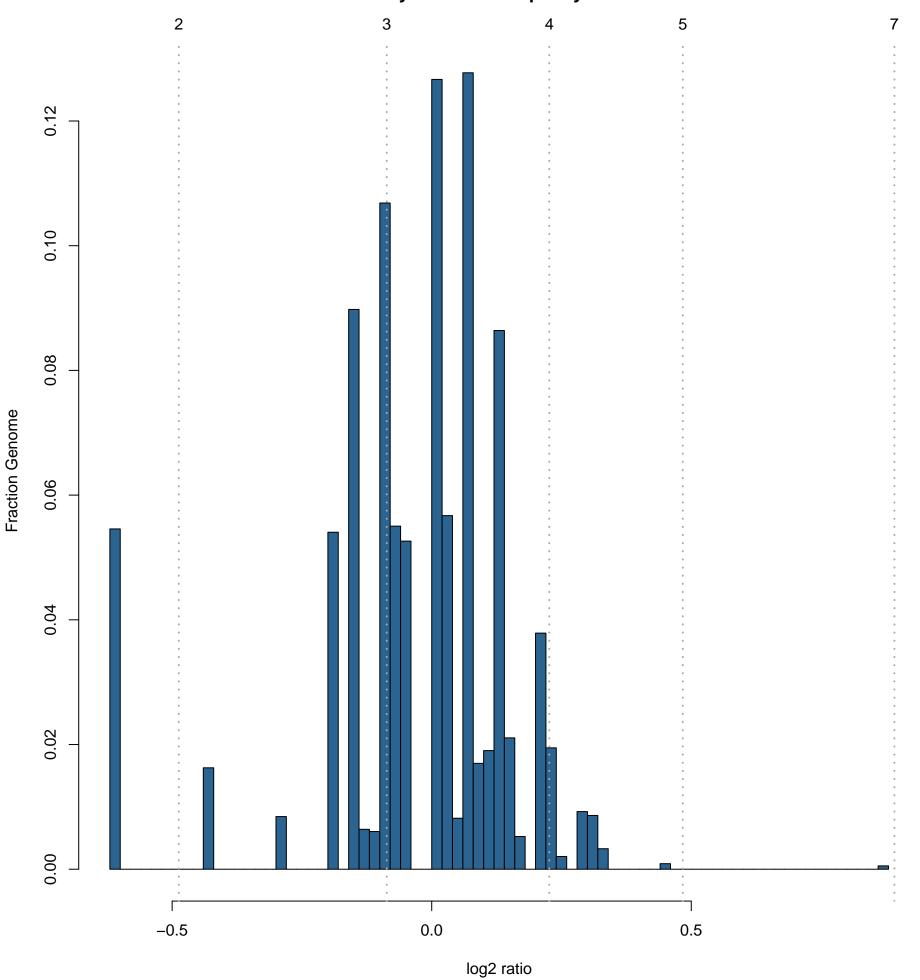
SCNA-fit log-likelihood: -1797.5

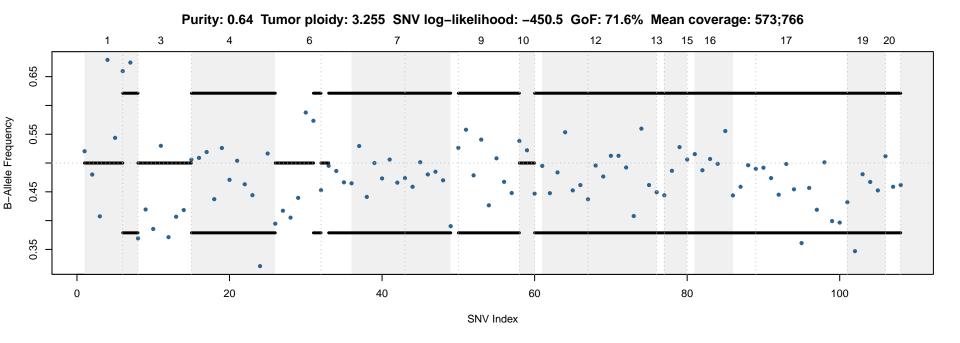






Purity: 0.64 Tumor ploidy: 3.255





SCNA-fit log-likelihood: -1656.69

