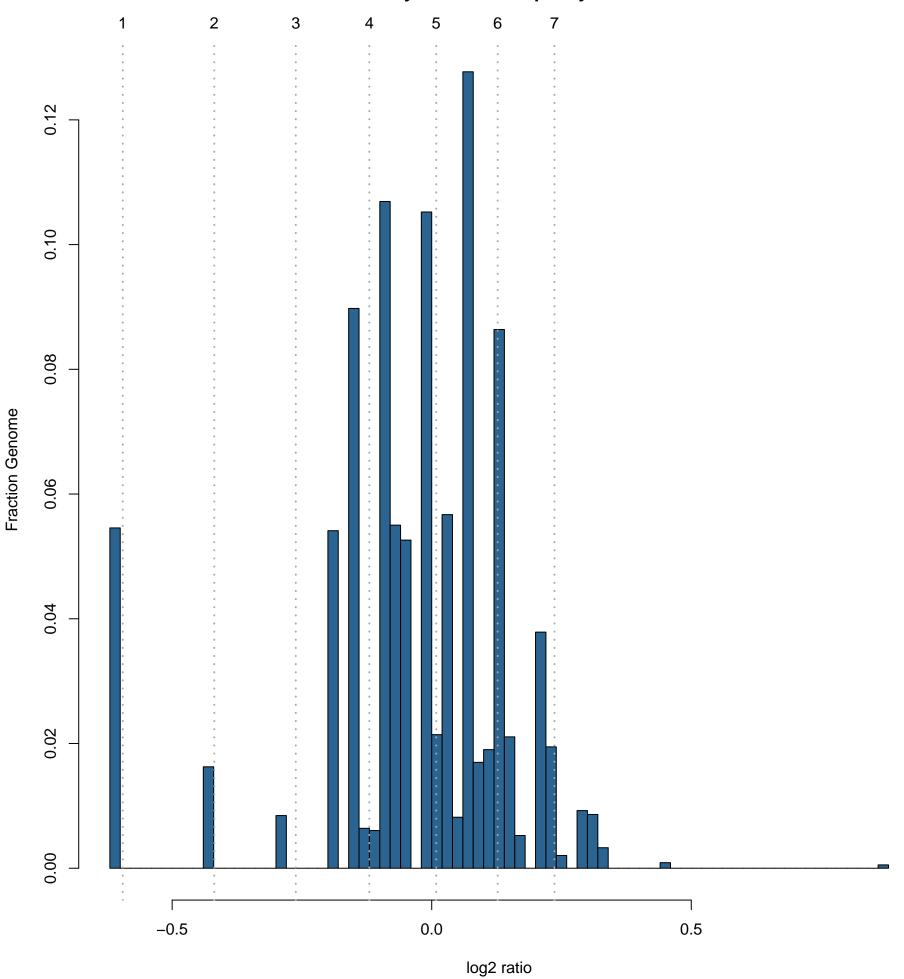
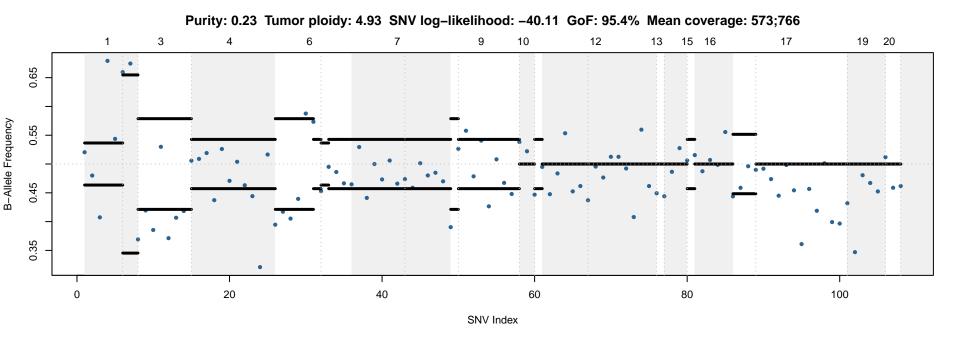
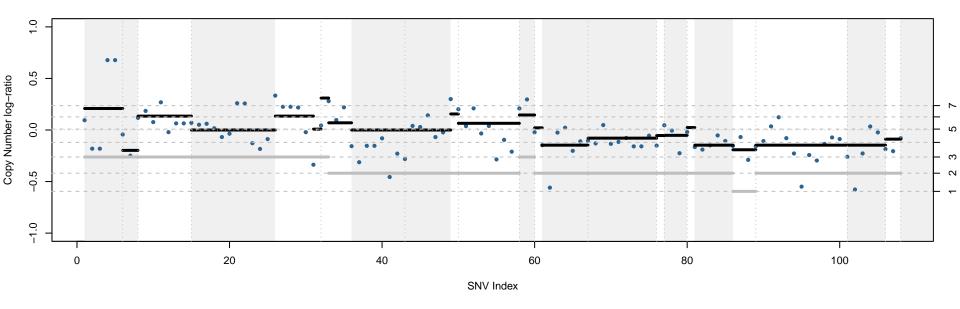
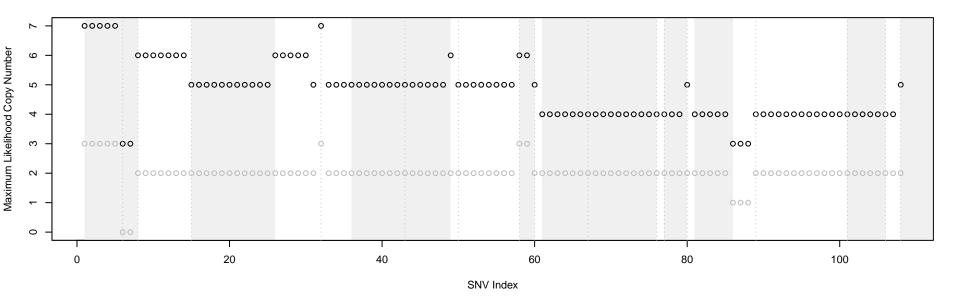
Purity: 0.23 Tumor ploidy: 4.93

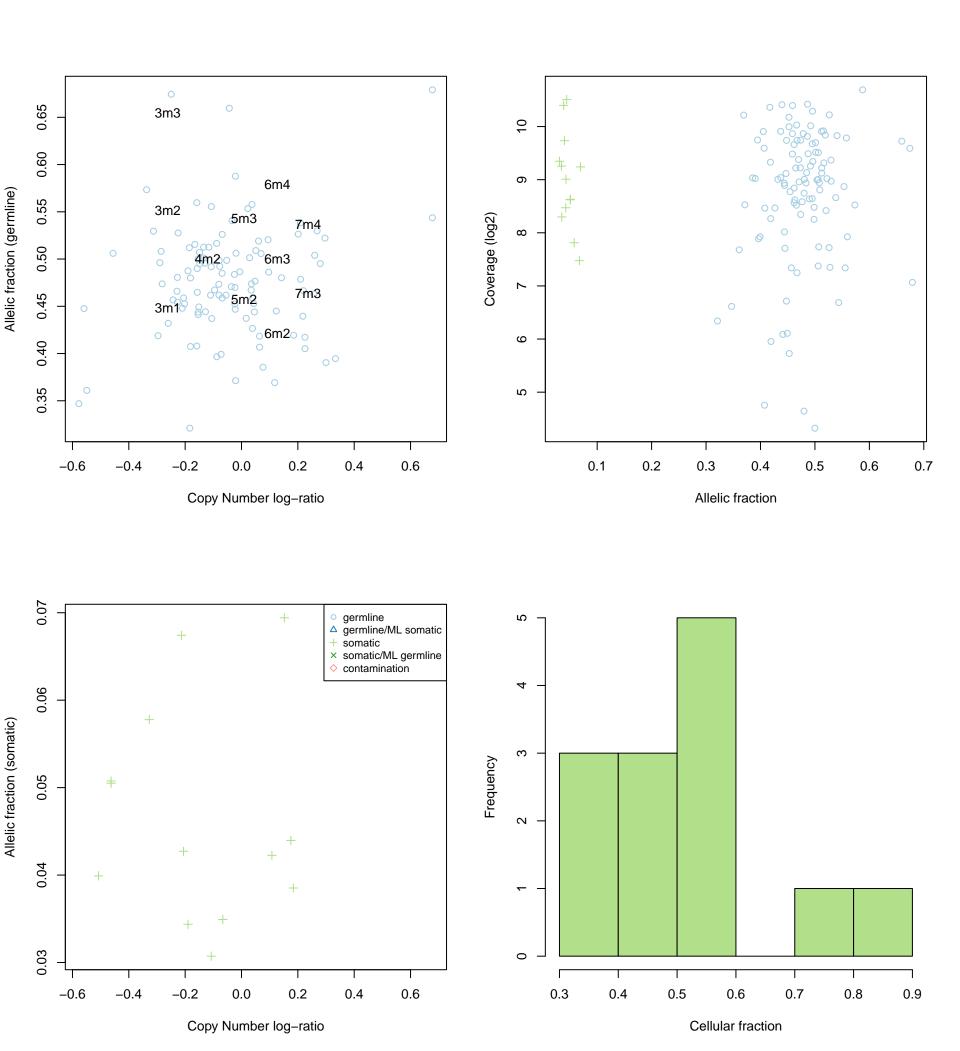




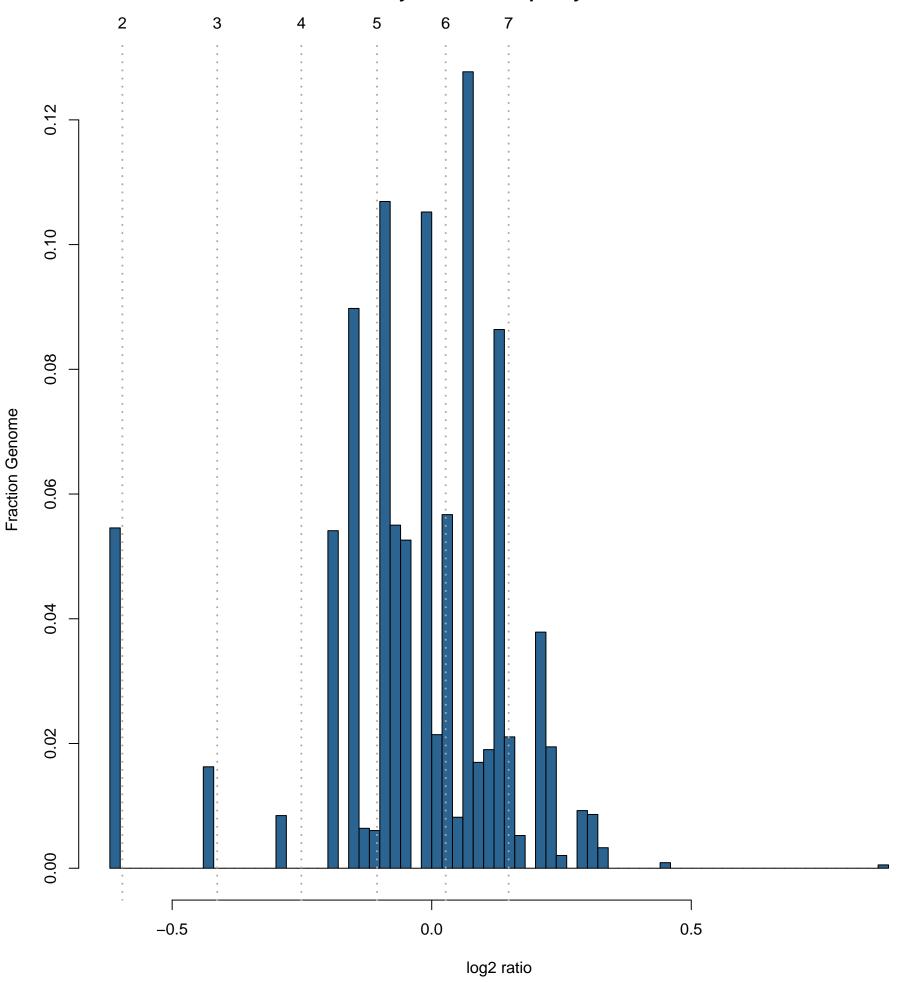
SCNA-fit log-likelihood: -1096.56

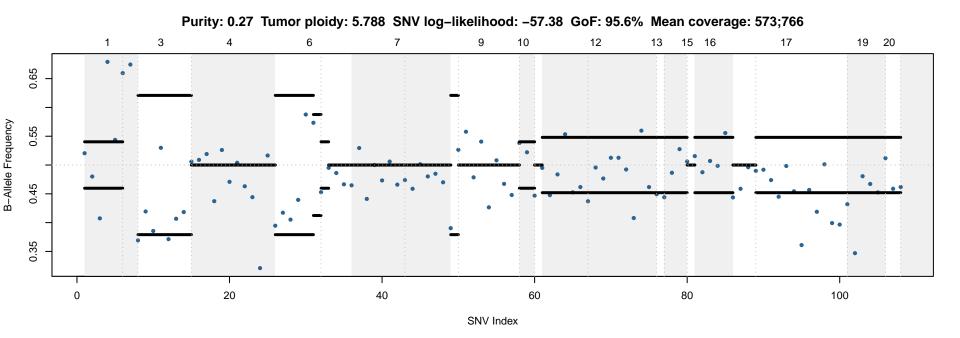




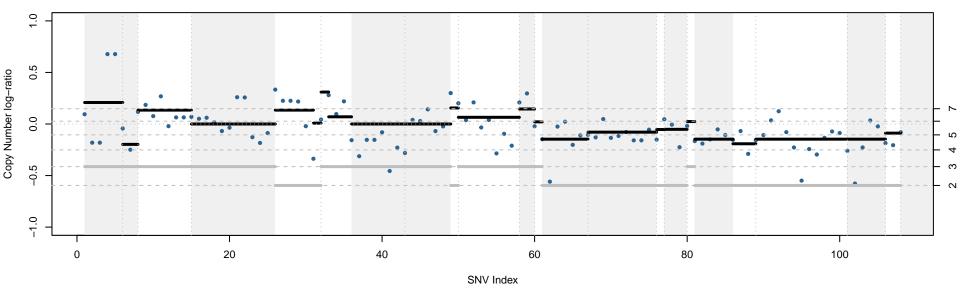


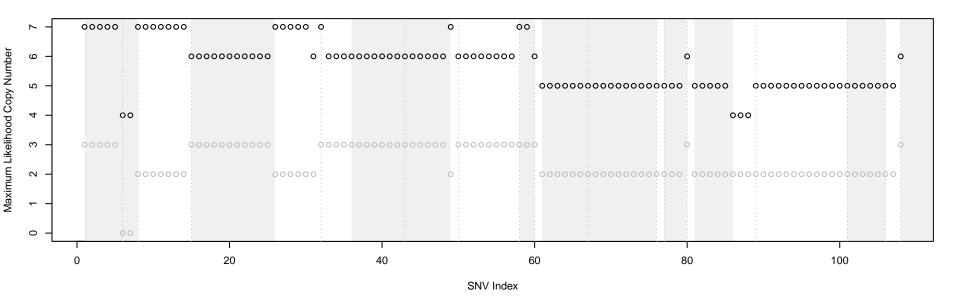
Purity: 0.27 Tumor ploidy: 5.788

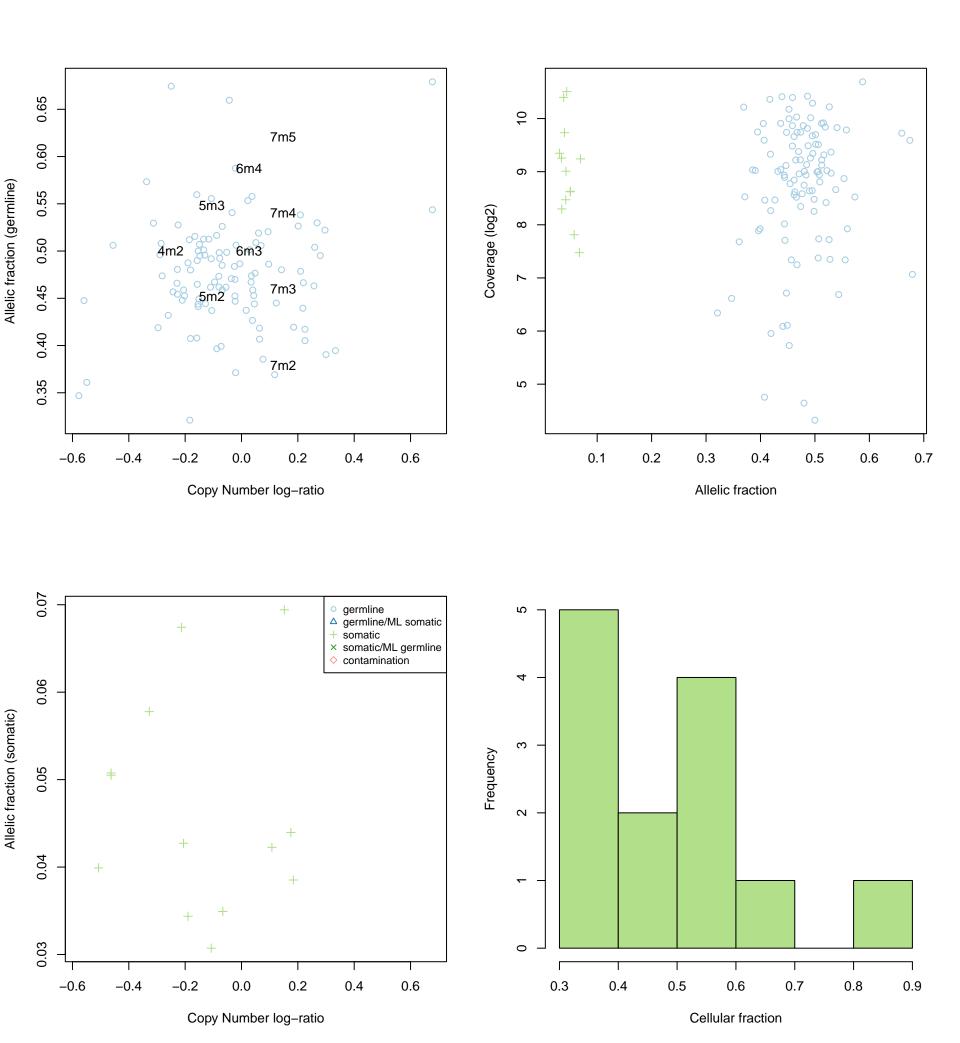




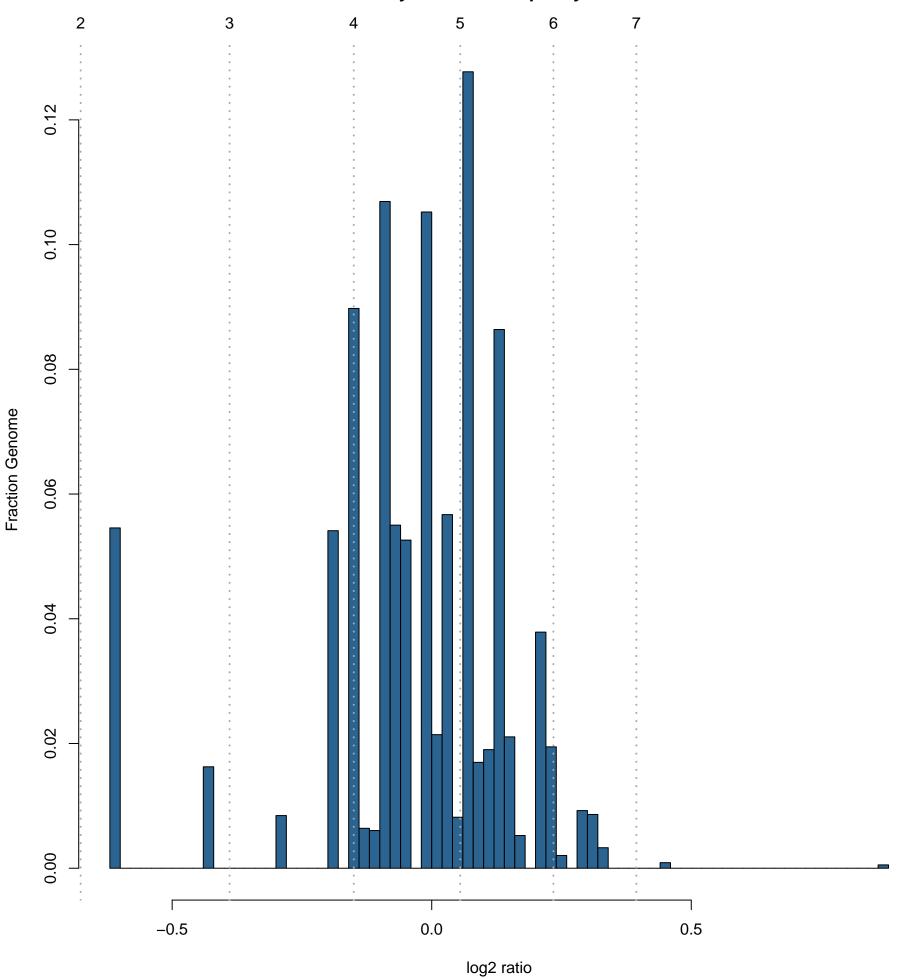
SCNA-fit log-likelihood: -1183.88

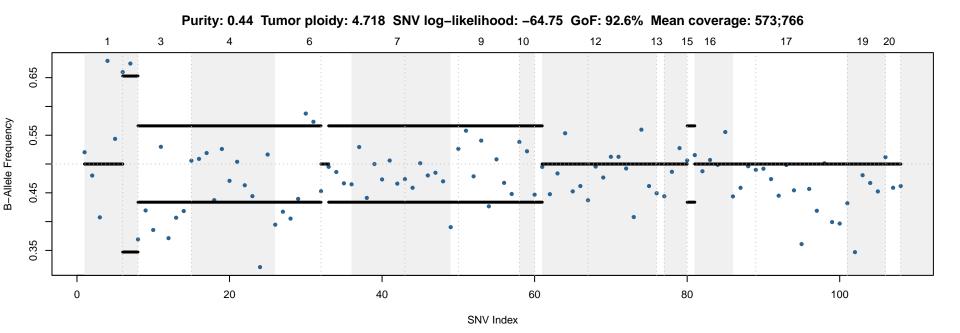




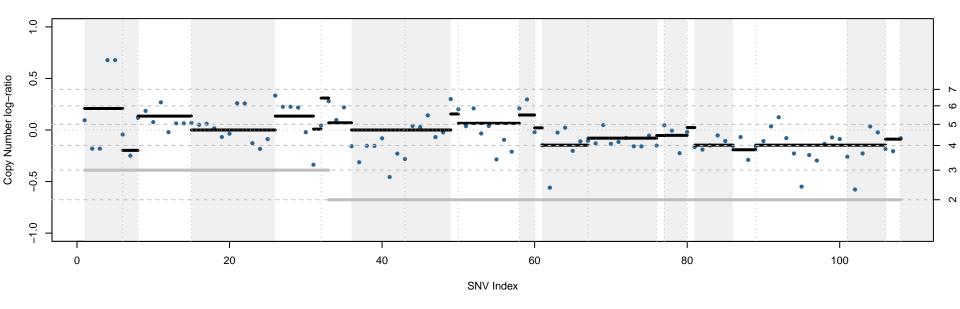


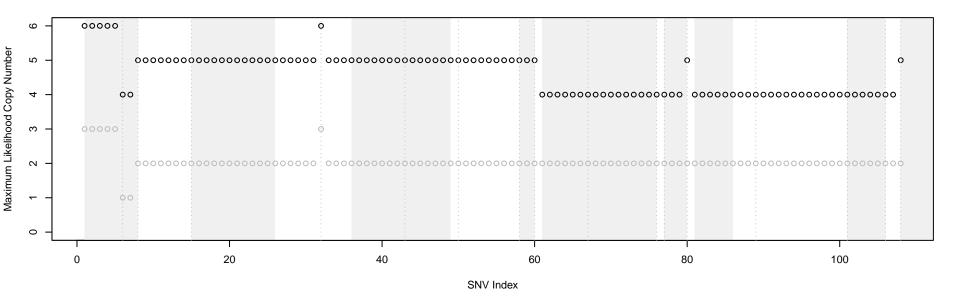
Purity: 0.44 Tumor ploidy: 4.718

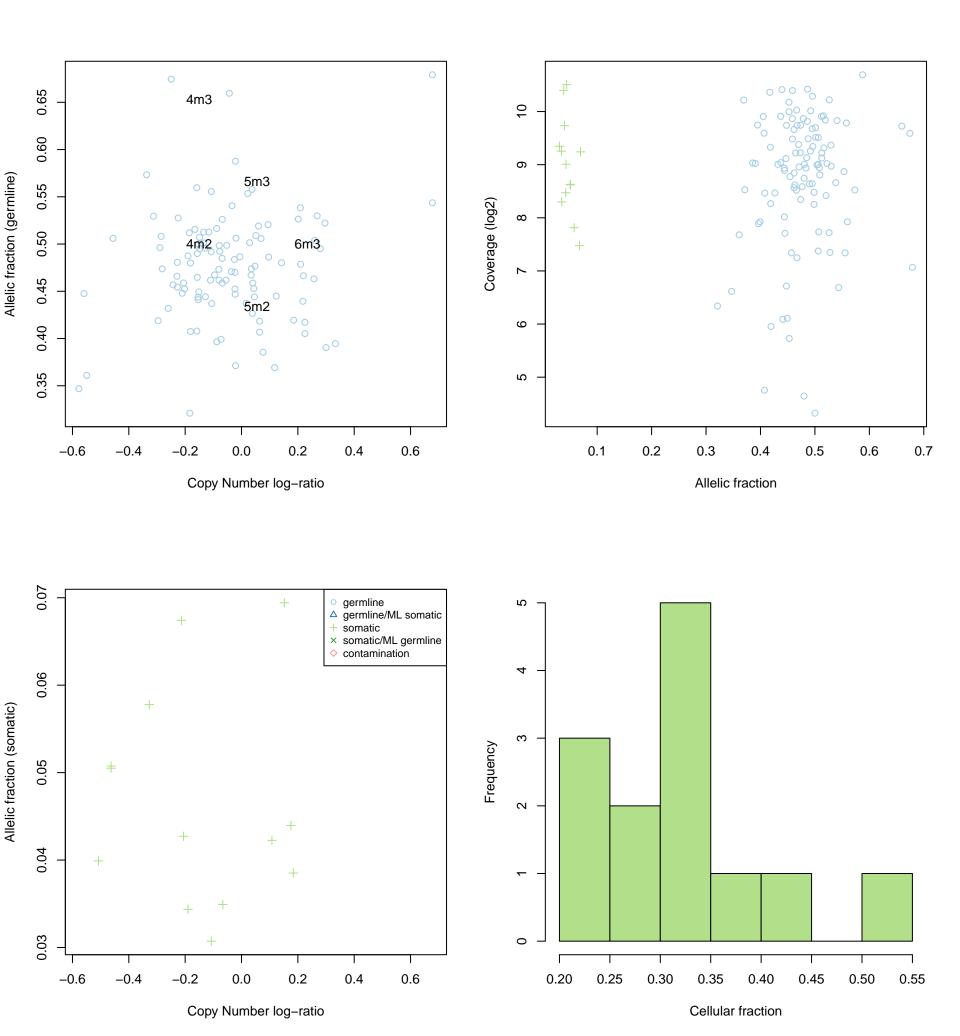




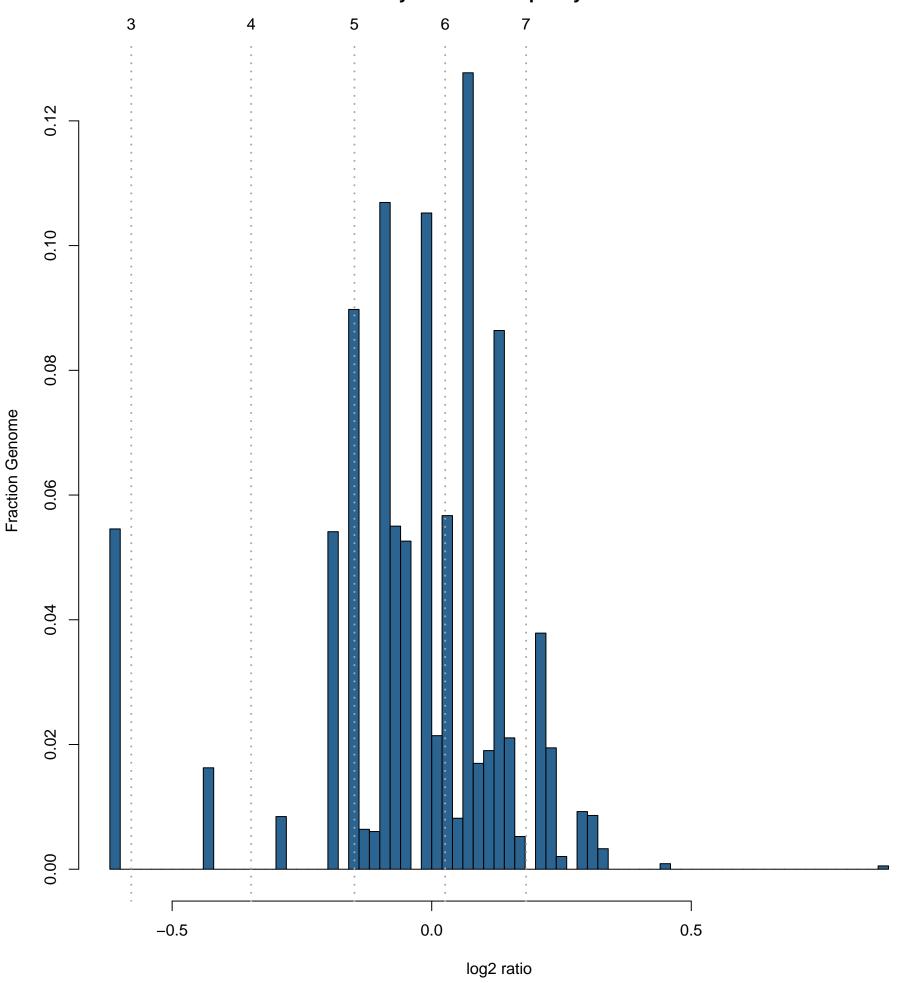
SCNA-fit log-likelihood: -1212.88

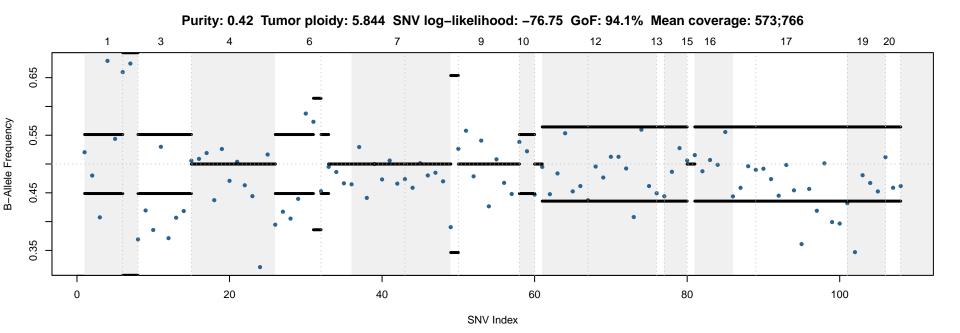




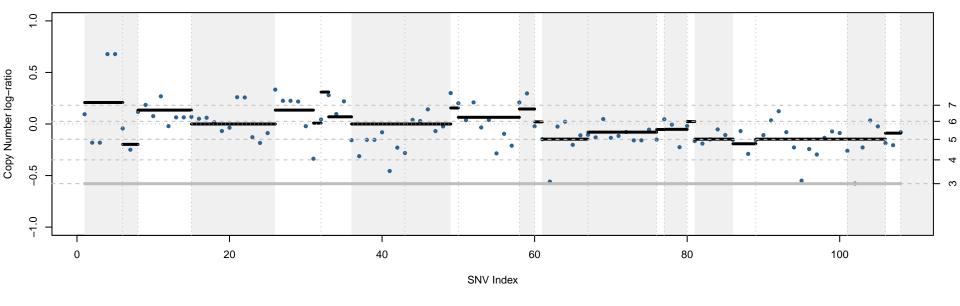


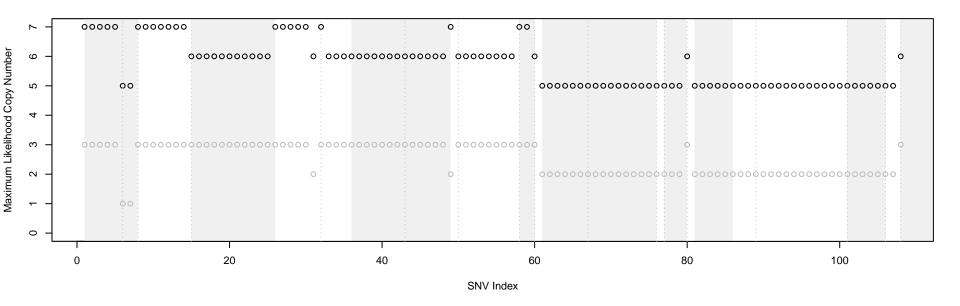
Purity: 0.42 Tumor ploidy: 5.844

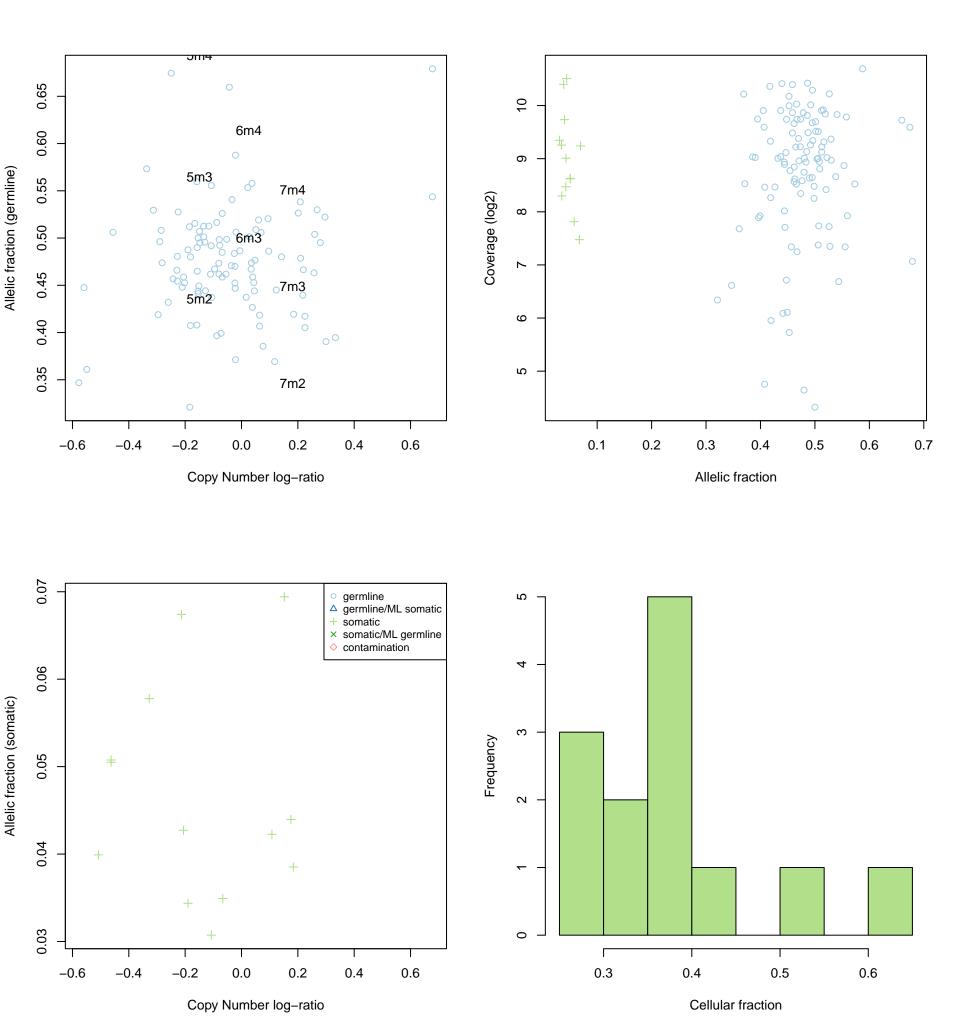




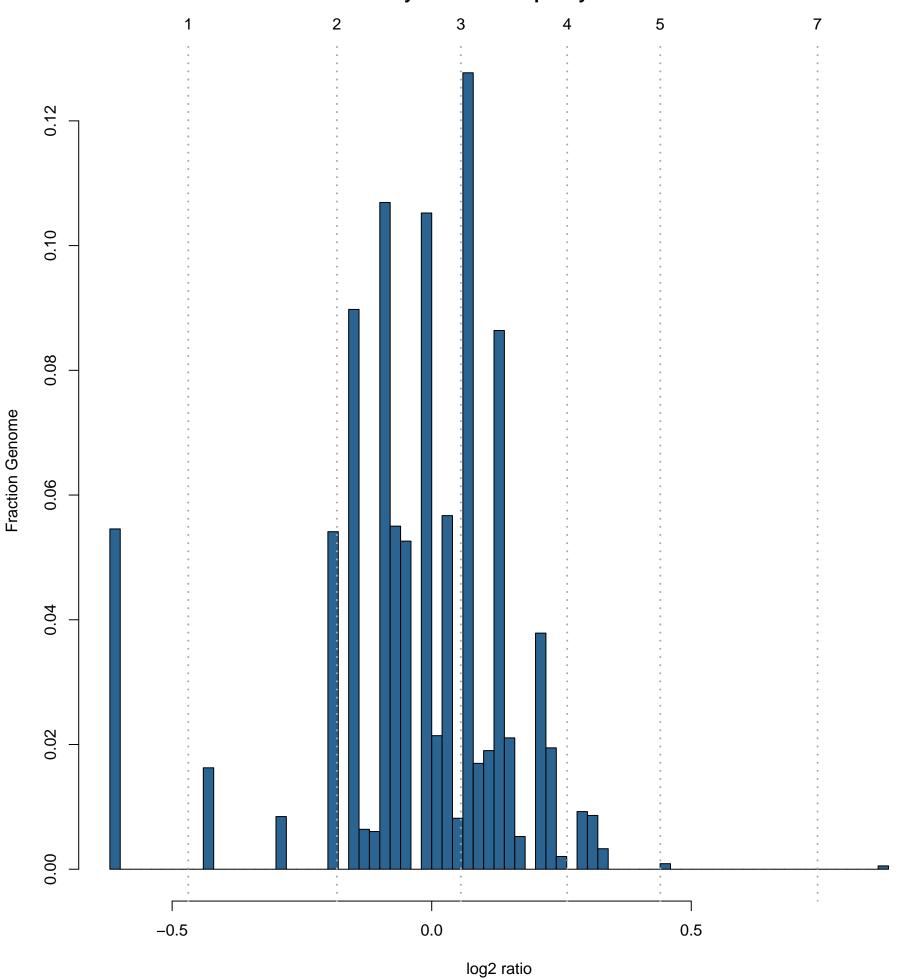
SCNA-fit log-likelihood: -1201.86

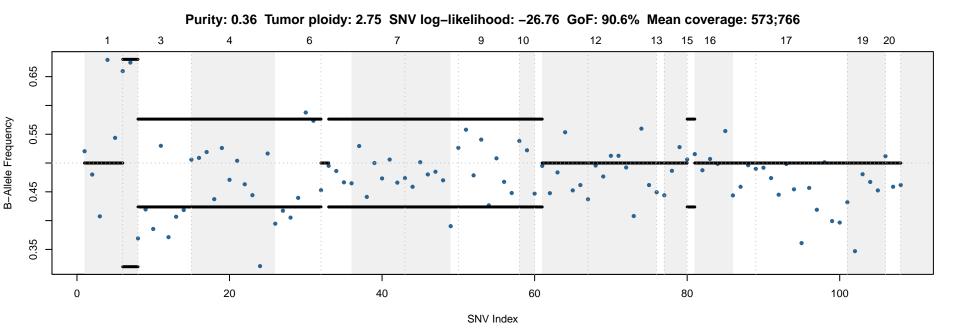




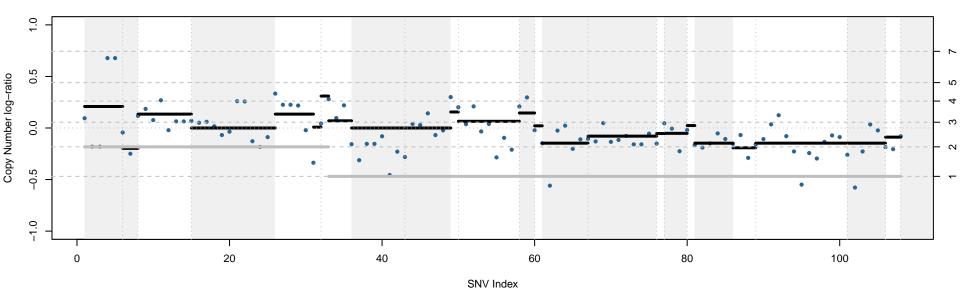


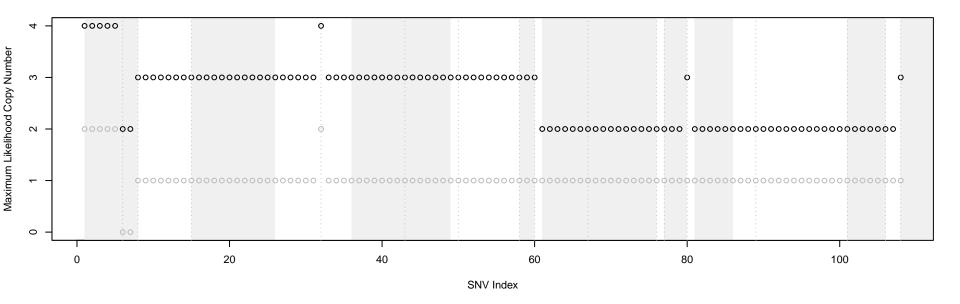
Purity: 0.36 Tumor ploidy: 2.75

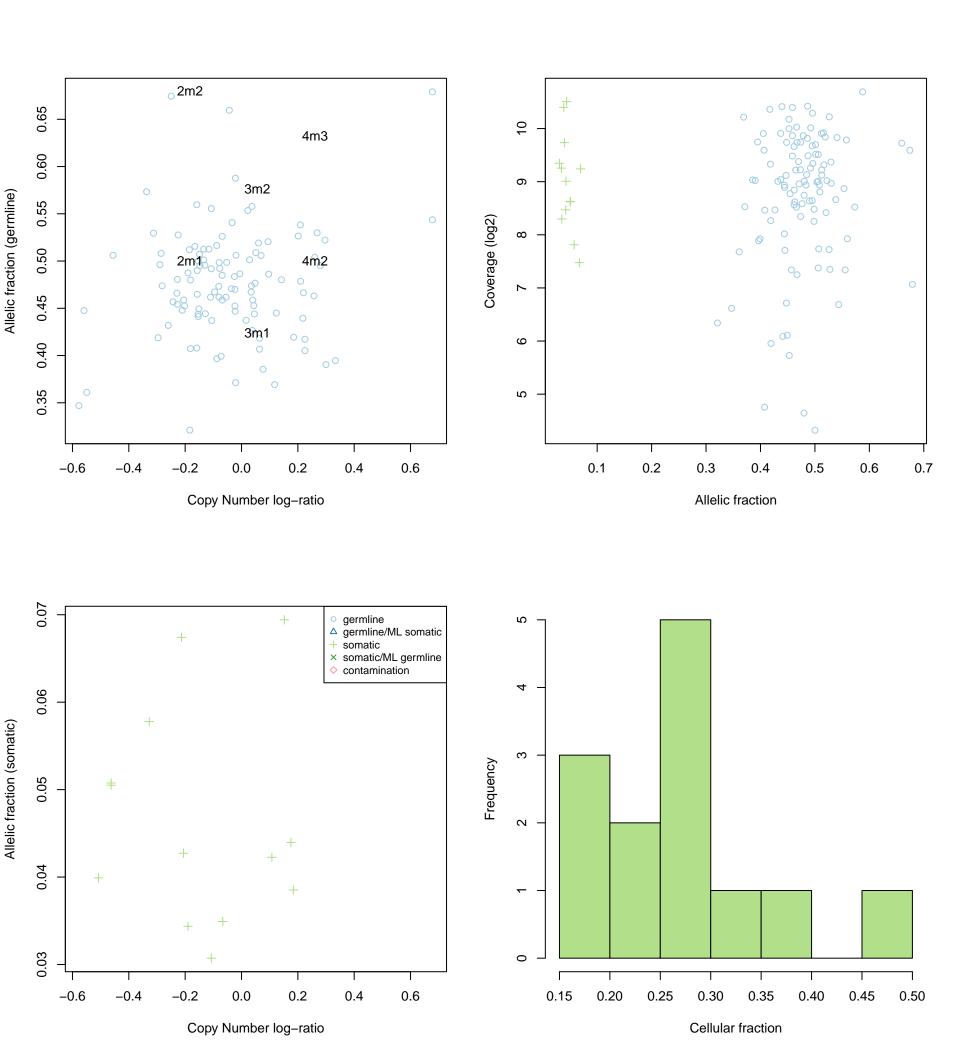




SCNA-fit log-likelihood: -1382.8

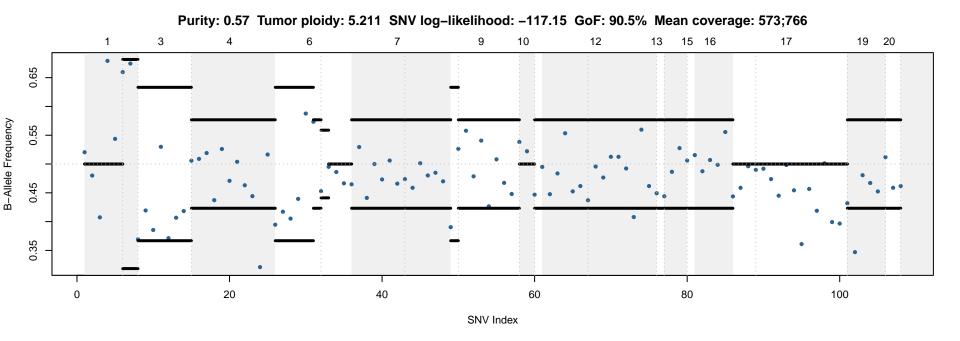




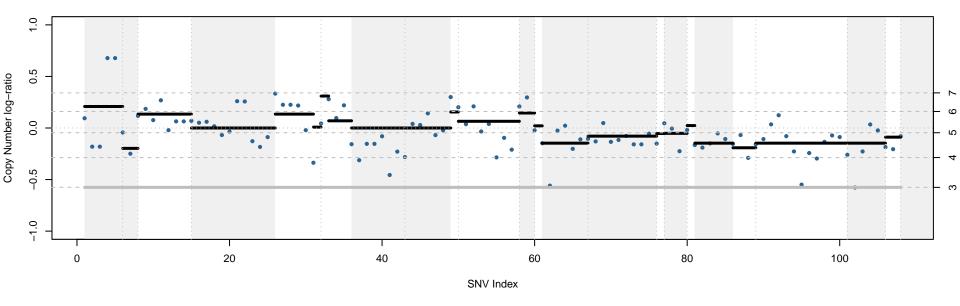


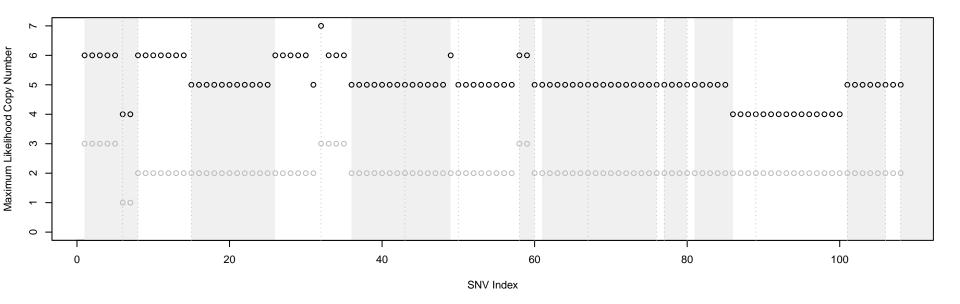
Purity: 0.57 Tumor ploidy: 5.211 3 6 0.12 0.10 0.08 Fraction Genome 90.0 0.04 0.02 0.00 -0.5 0.0 0.5

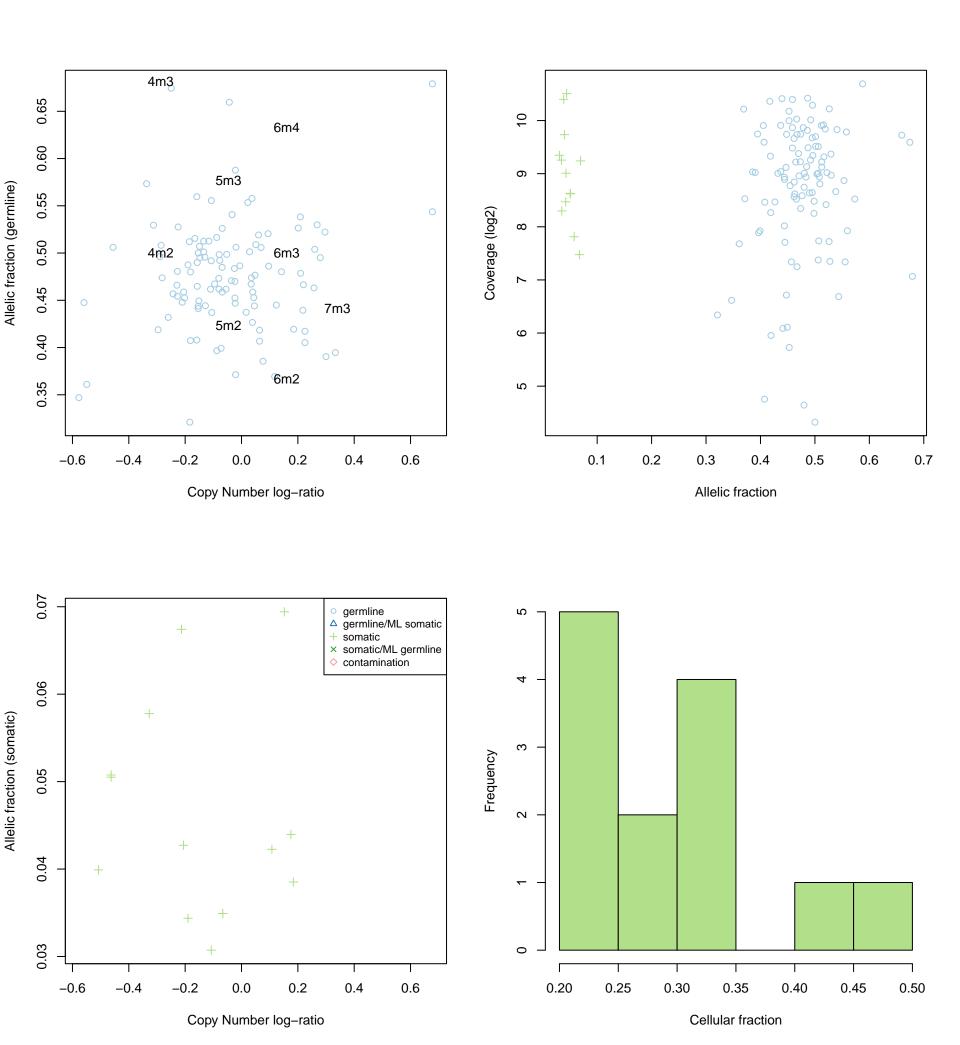
log2 ratio



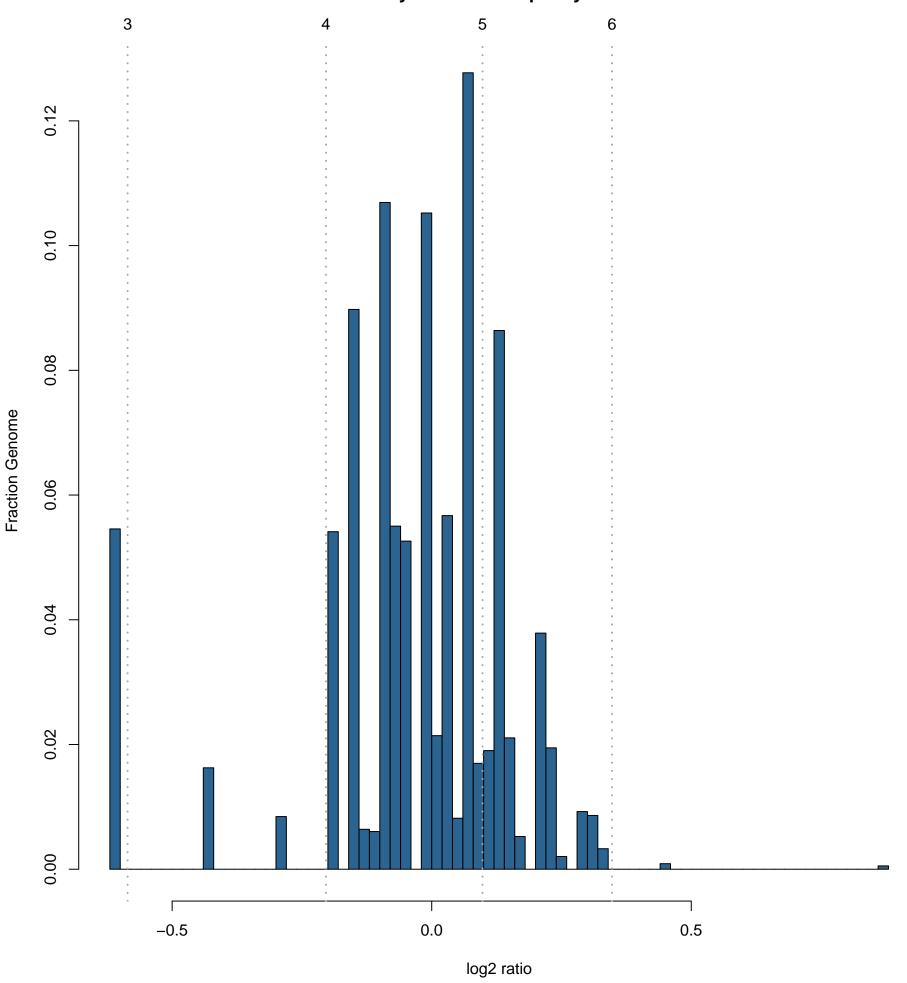
SCNA-fit log-likelihood: -1349.19

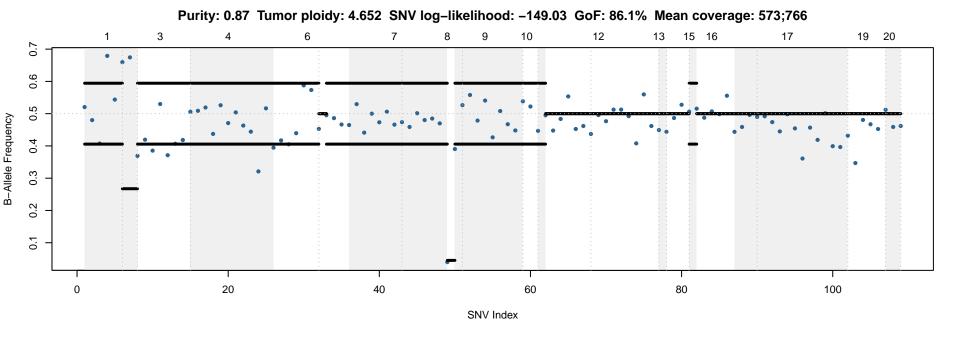




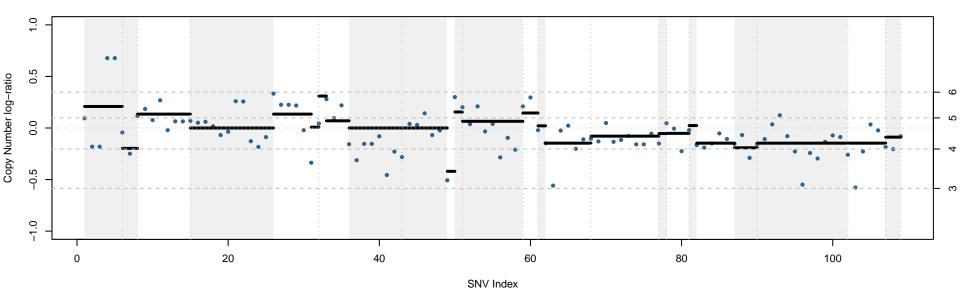


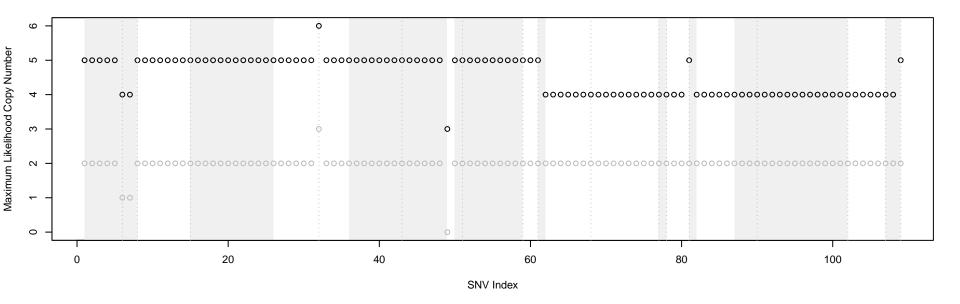
Purity: 0.87 Tumor ploidy: 4.652

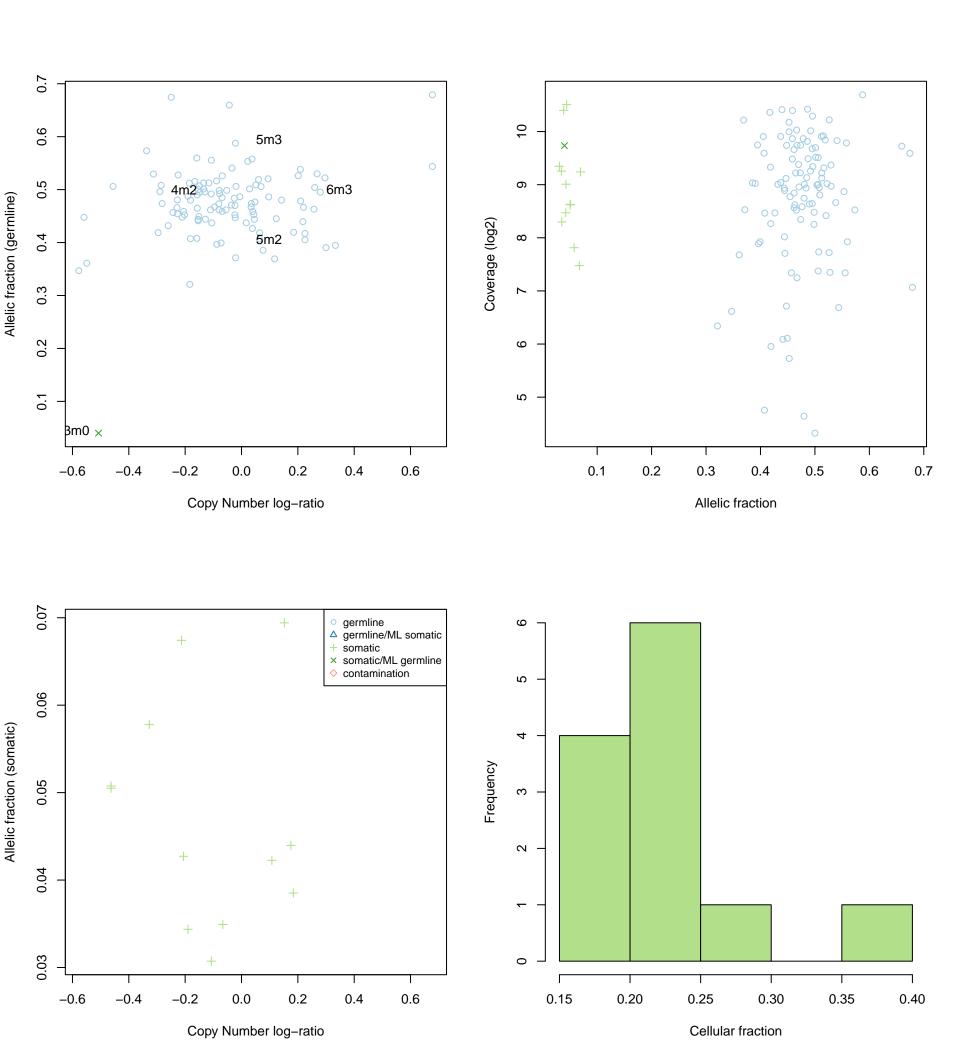




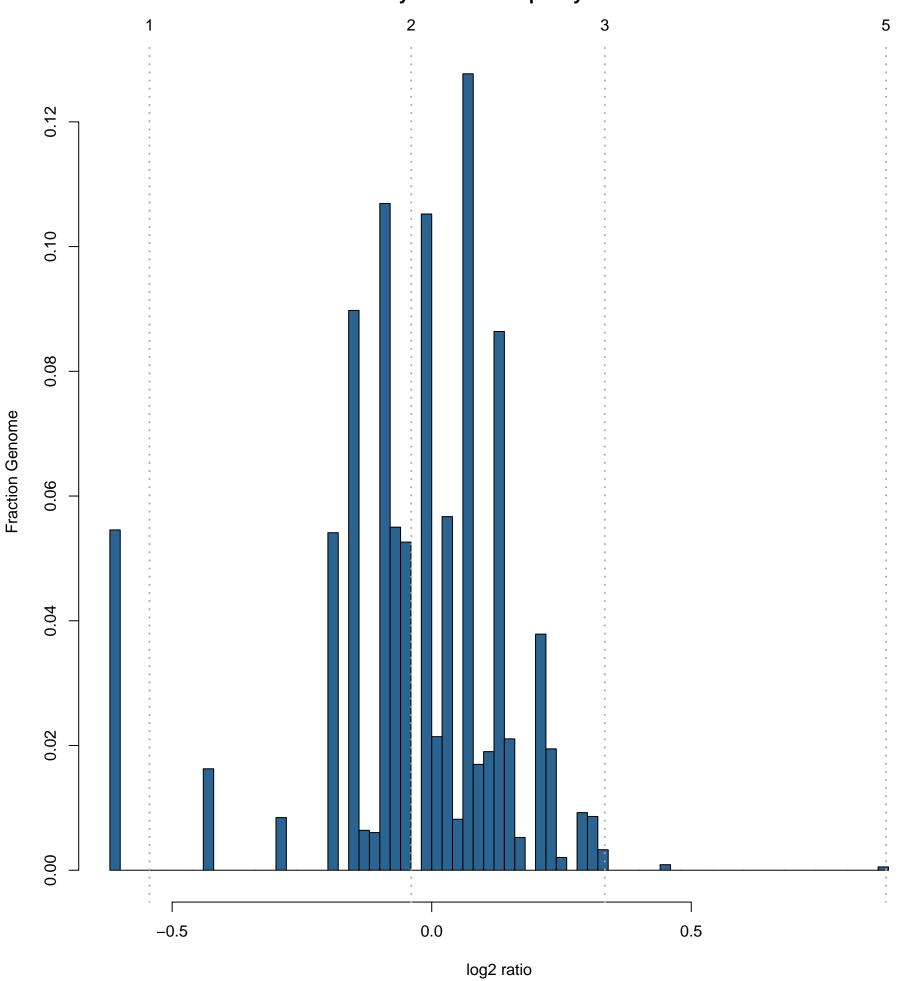
SCNA-fit log-likelihood: -1510.19

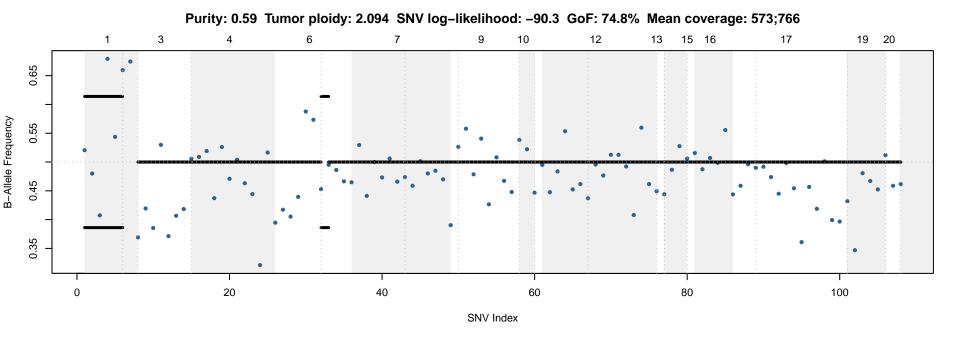




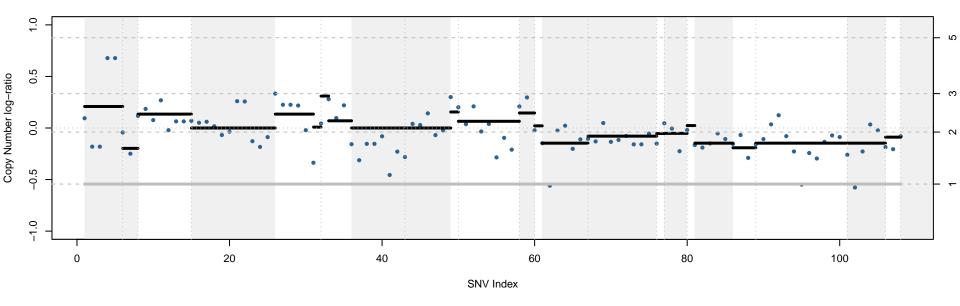


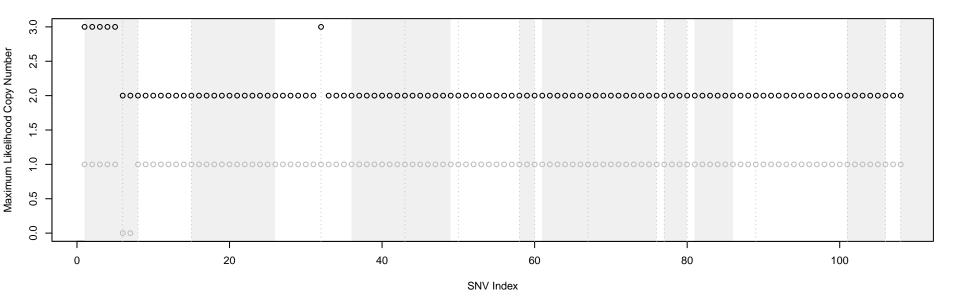
Purity: 0.59 Tumor ploidy: 2.094

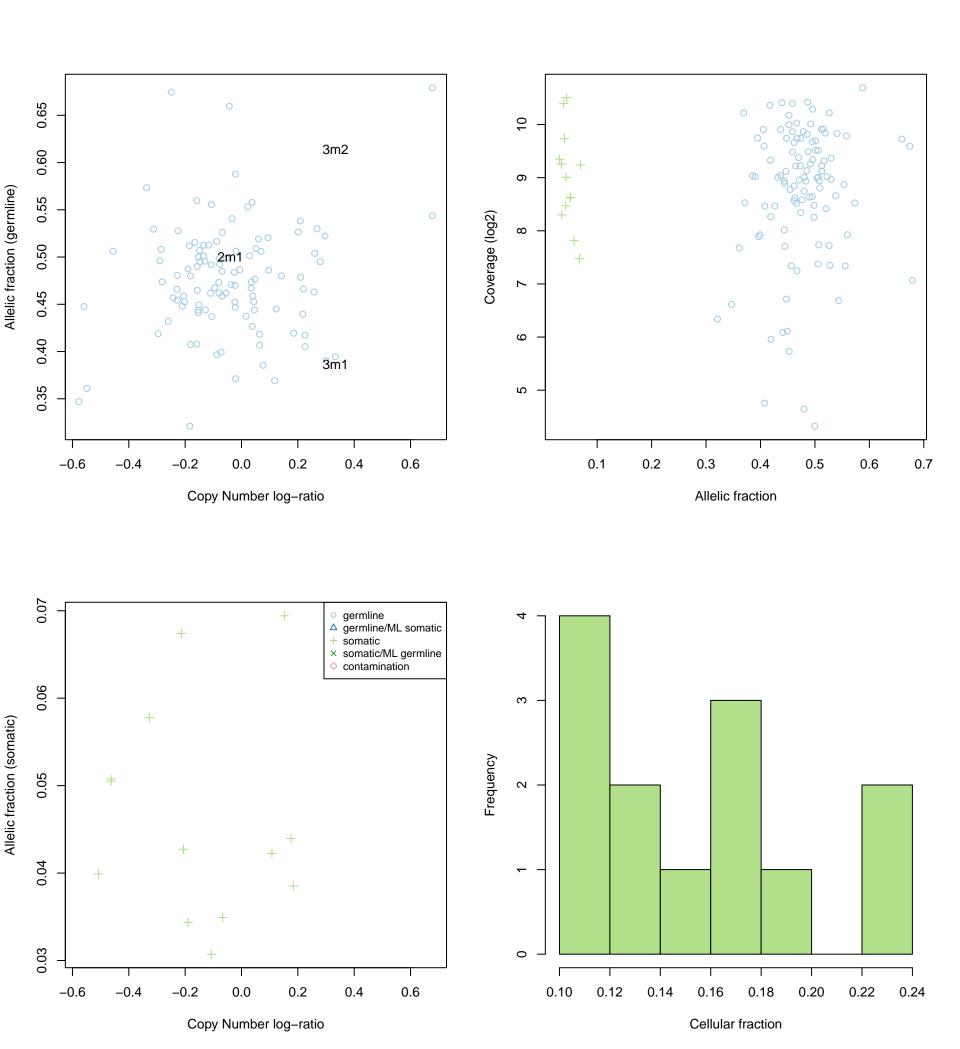




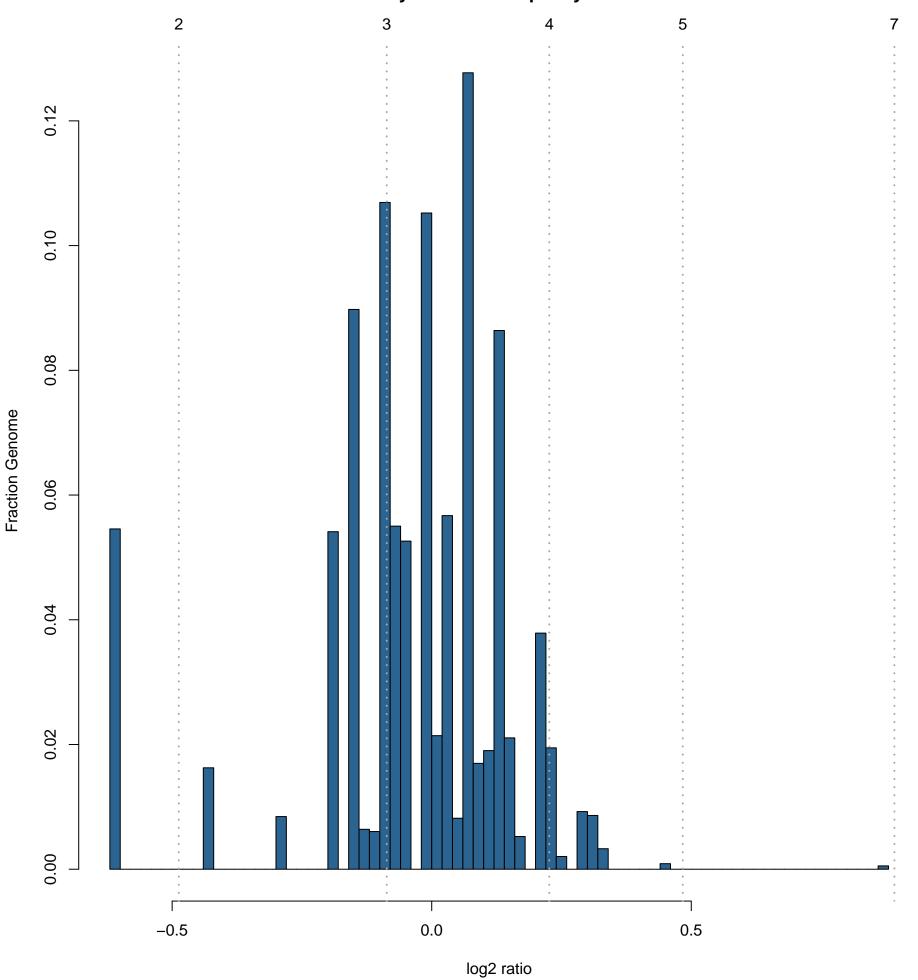
SCNA-fit log-likelihood: -1796.92

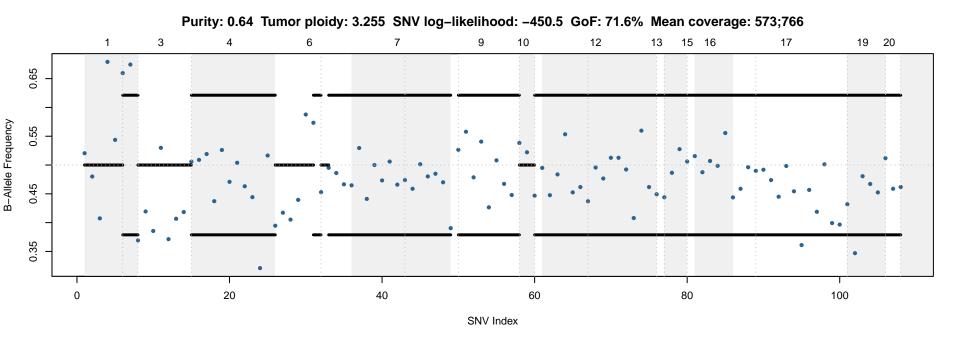






Purity: 0.64 Tumor ploidy: 3.255





SCNA-fit log-likelihood: -1656.16

