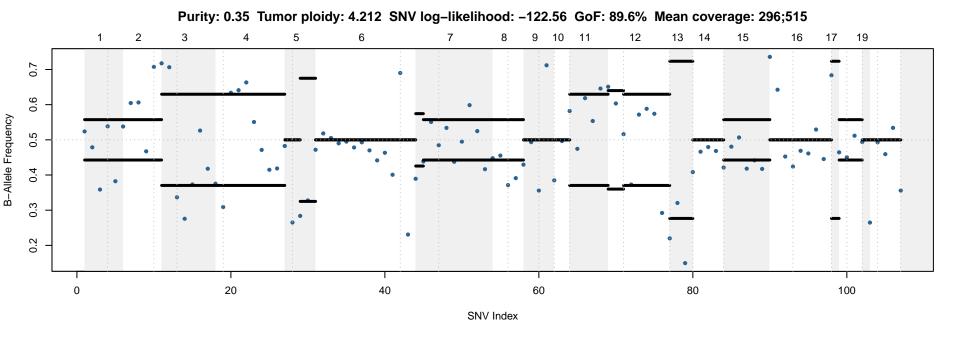
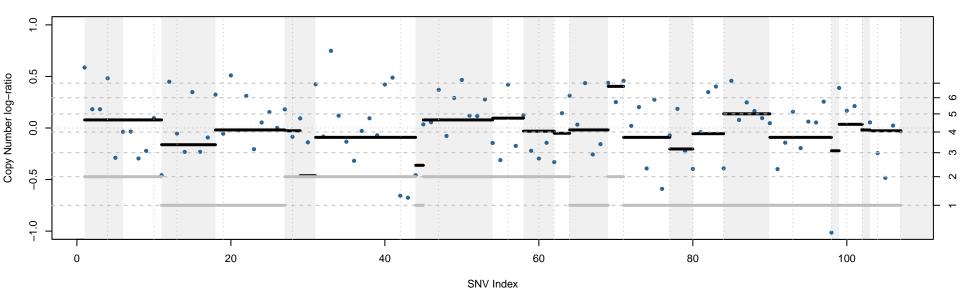
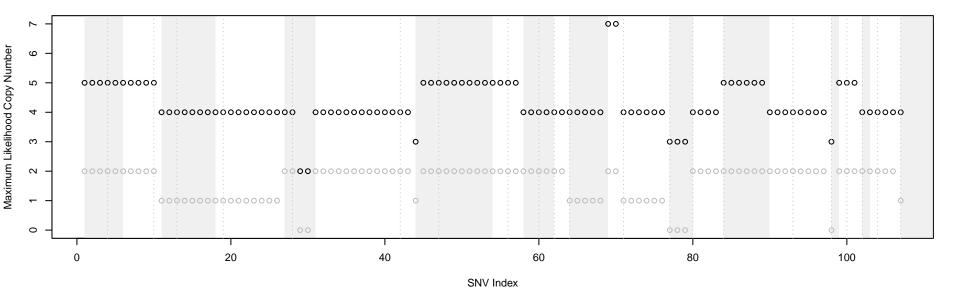
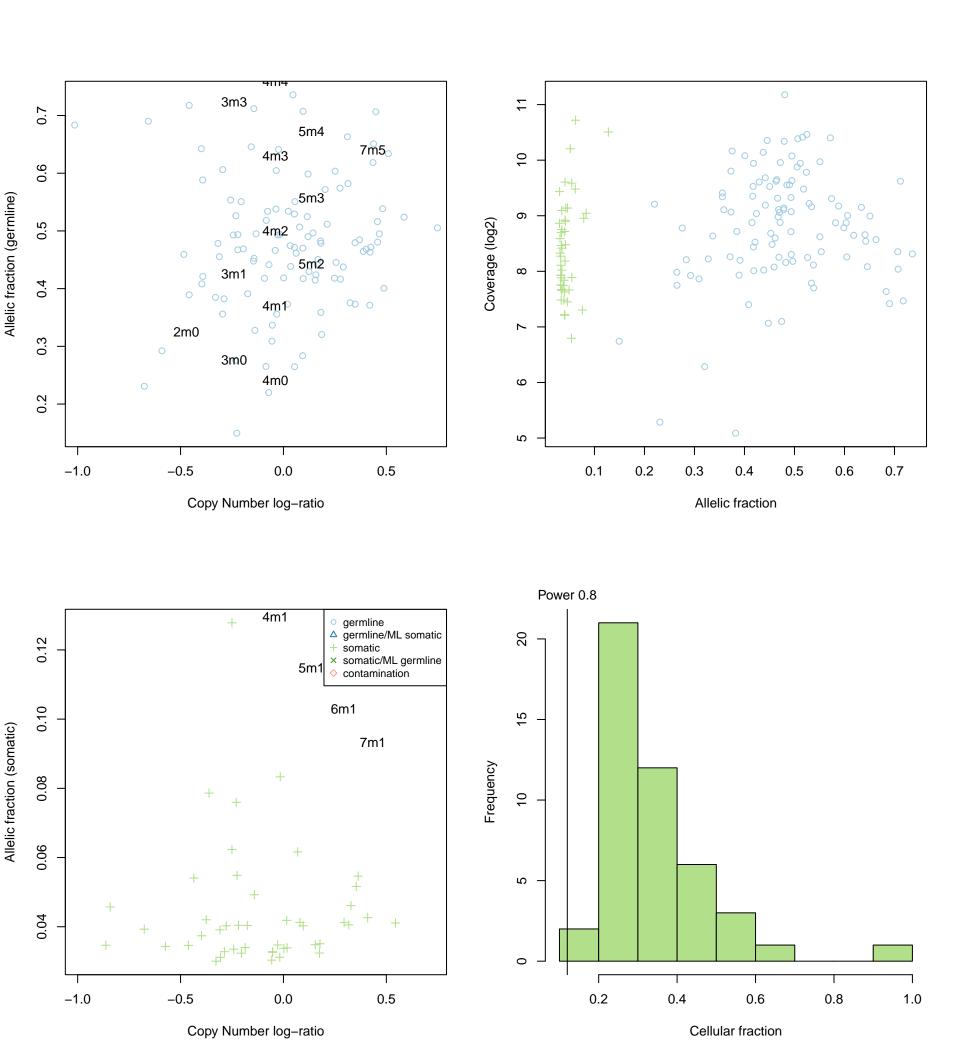
Purity: 0.35 Tumor ploidy: 4.212 2 3 6 5 0.25 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio

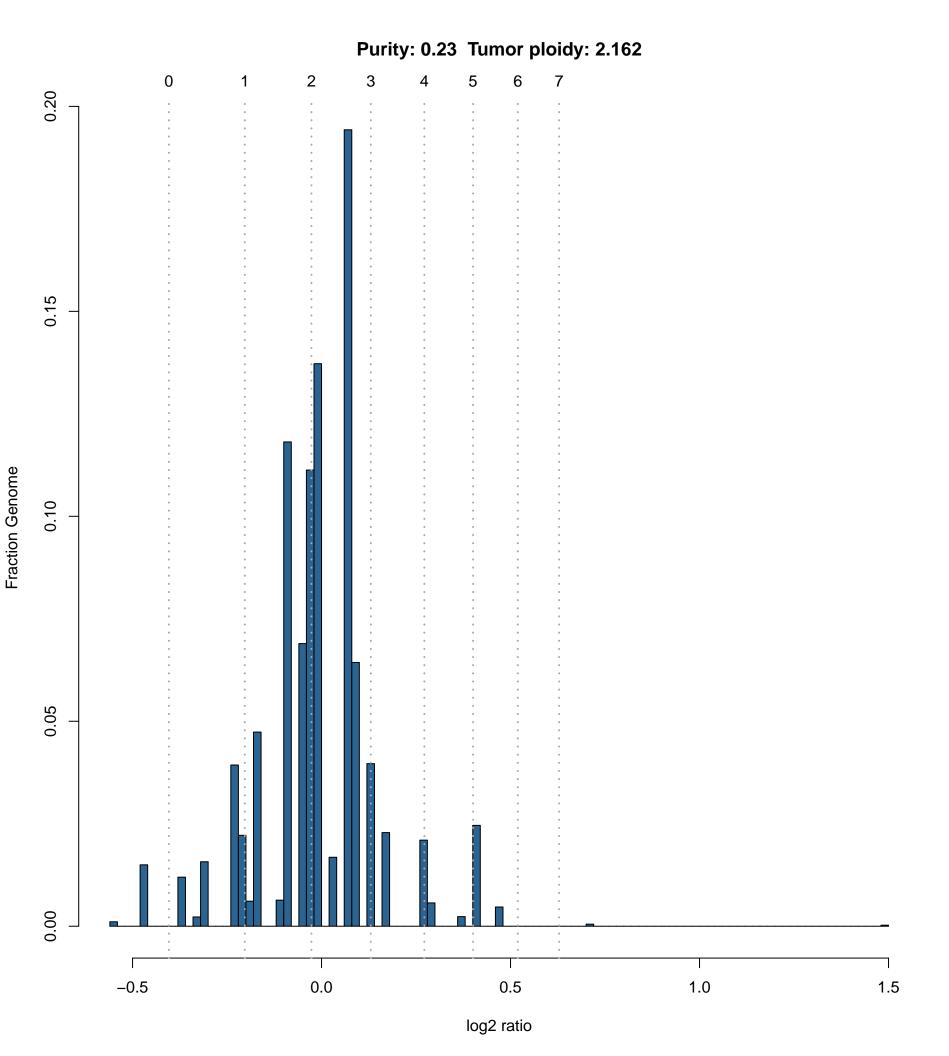


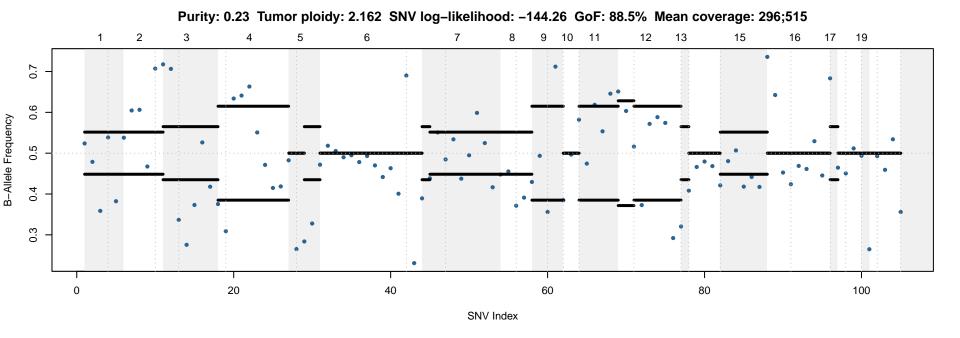
SCNA-fit log-likelihood: -5493.82



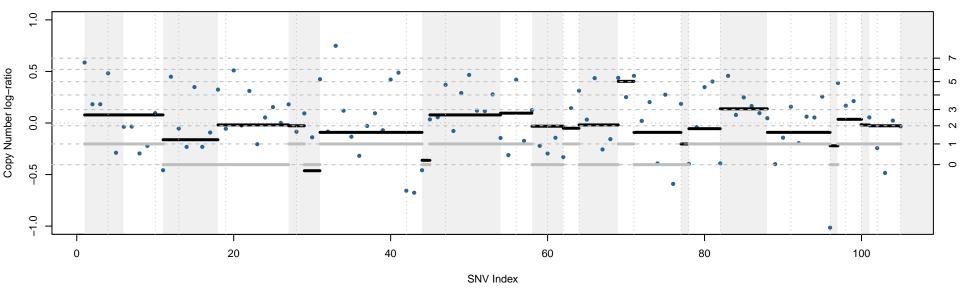


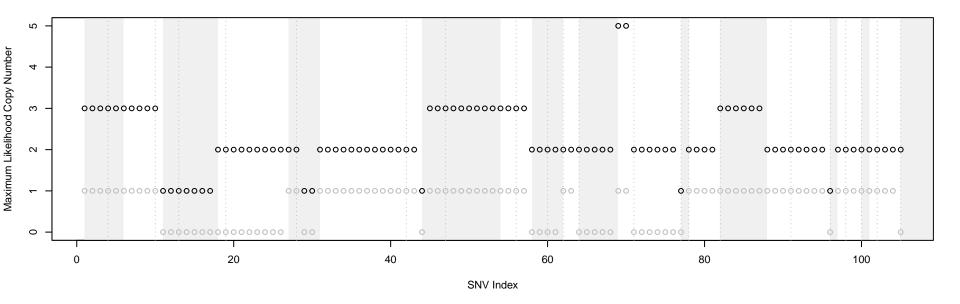


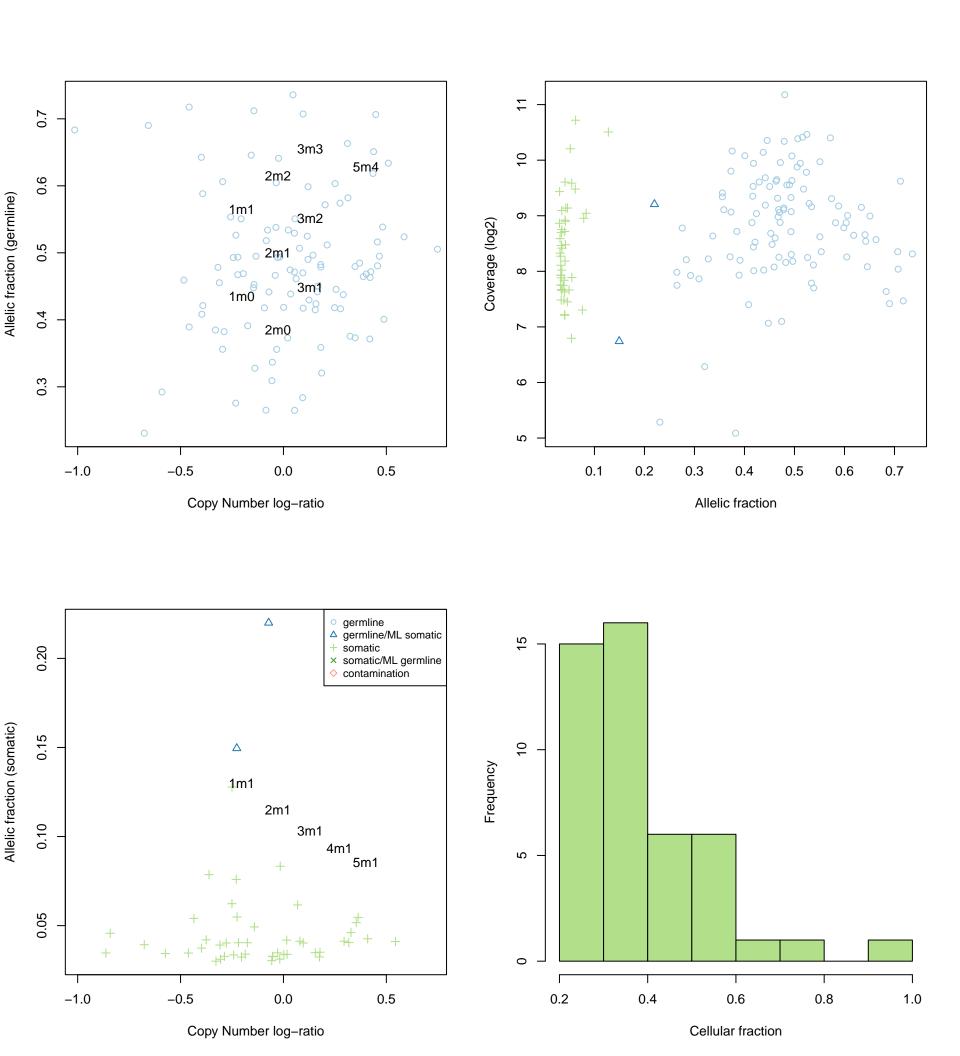


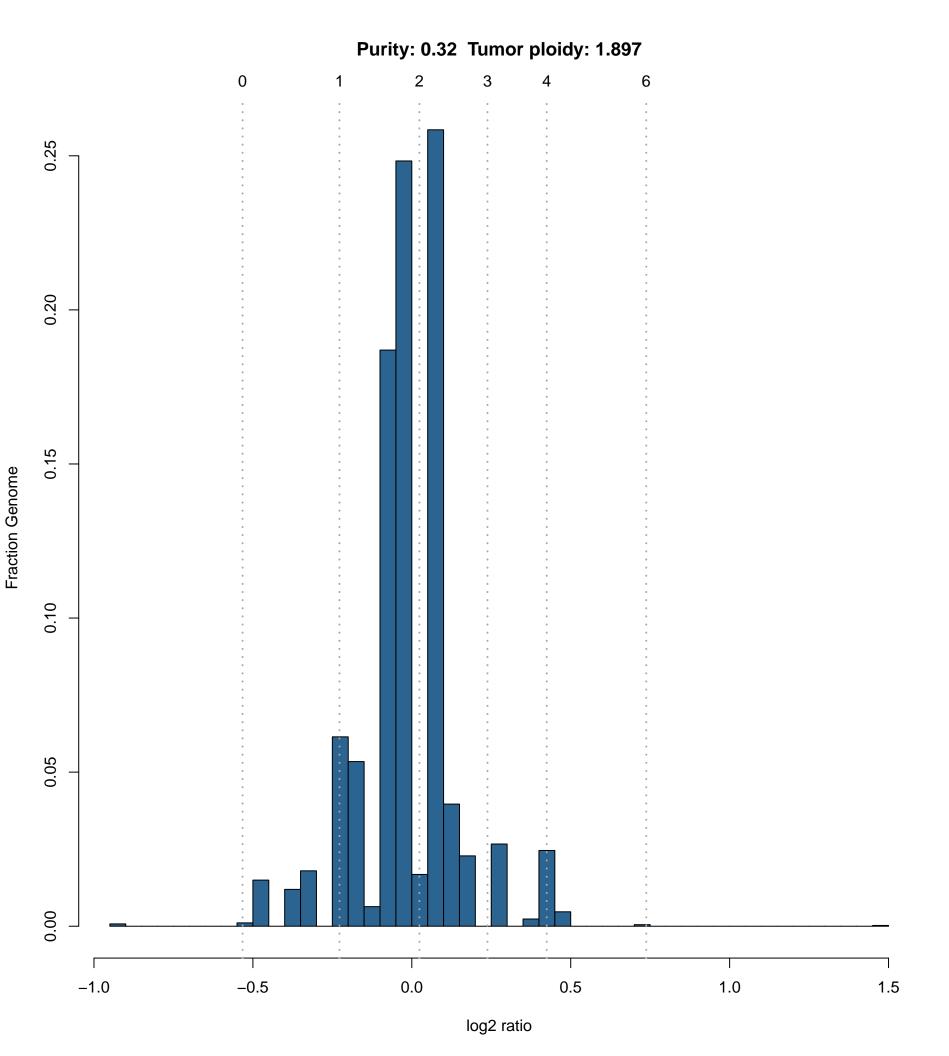


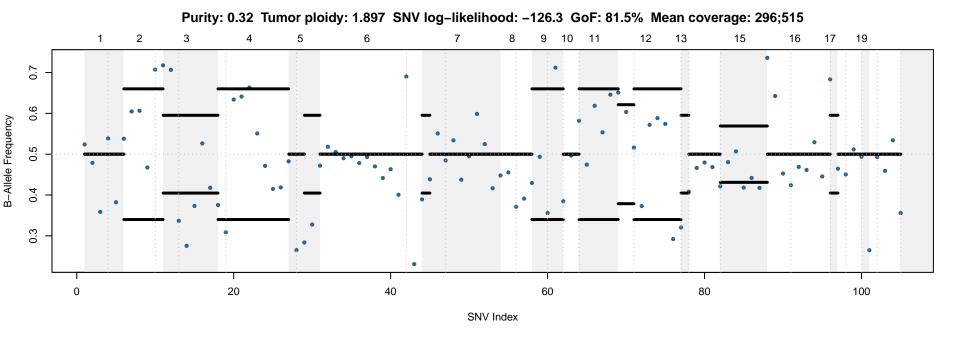
SCNA-fit log-likelihood: -5531.91



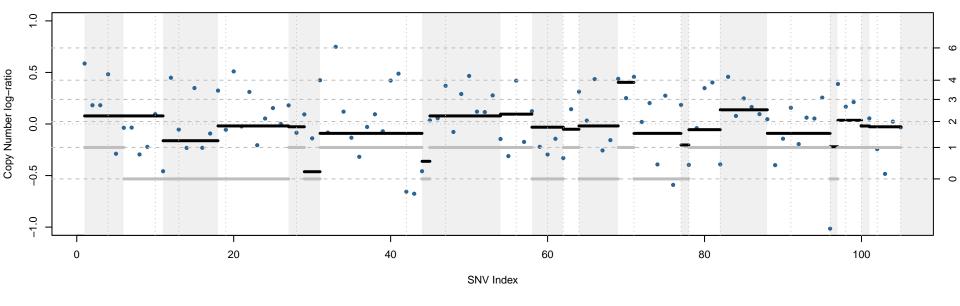


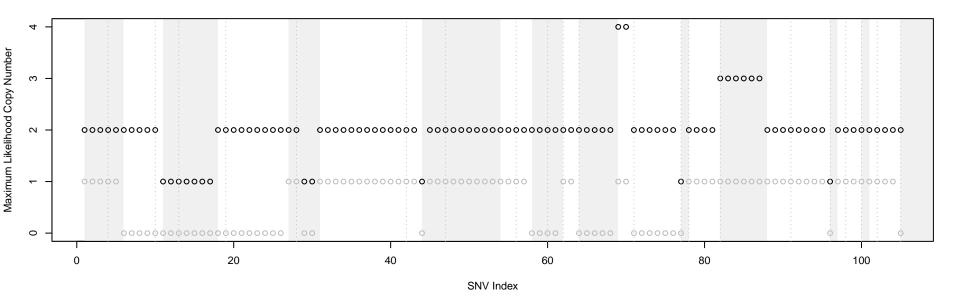


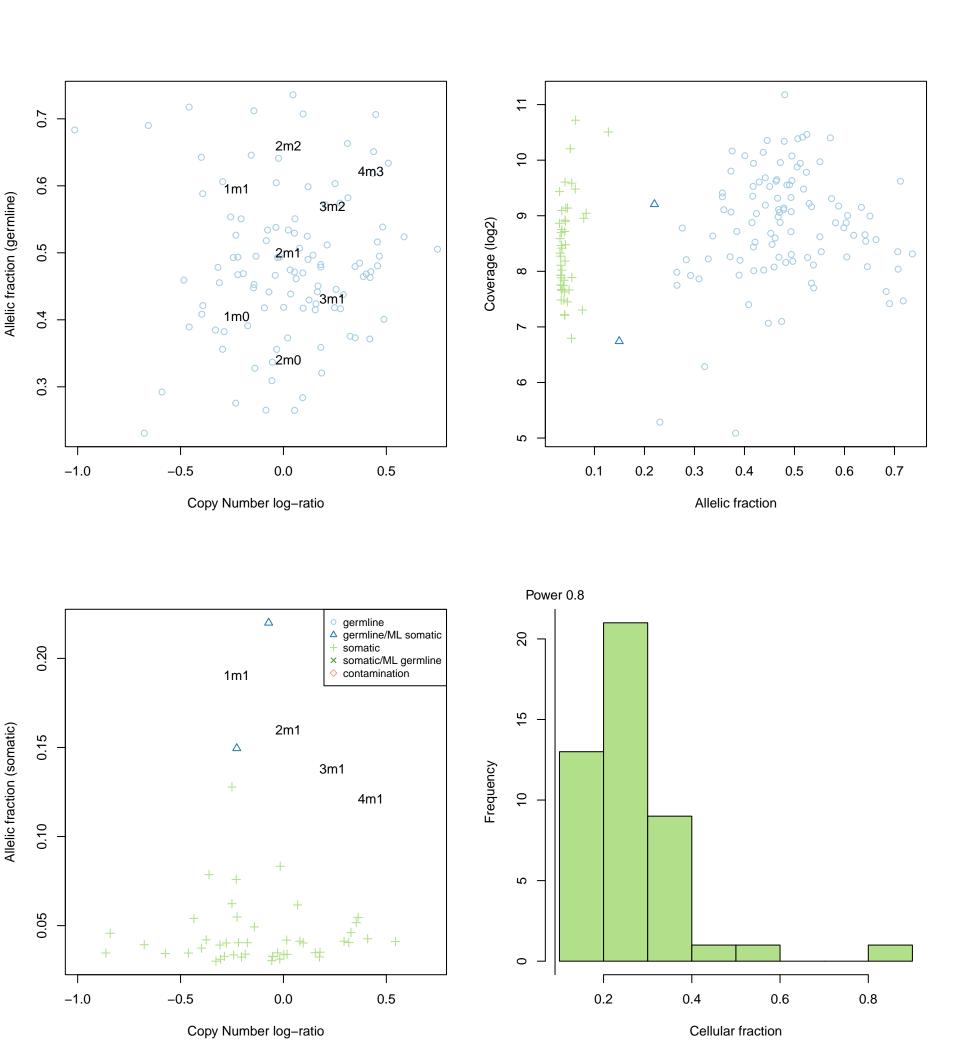




SCNA-fit log-likelihood: -5629.28

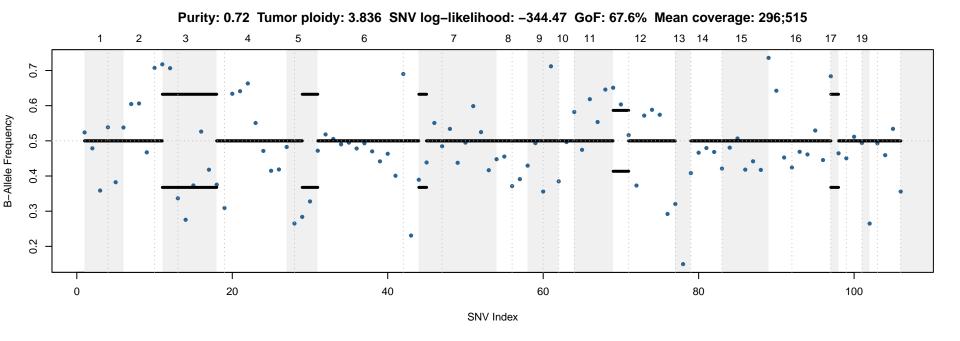




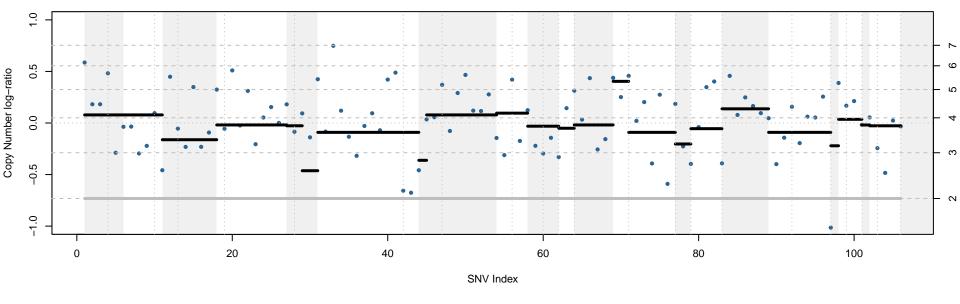


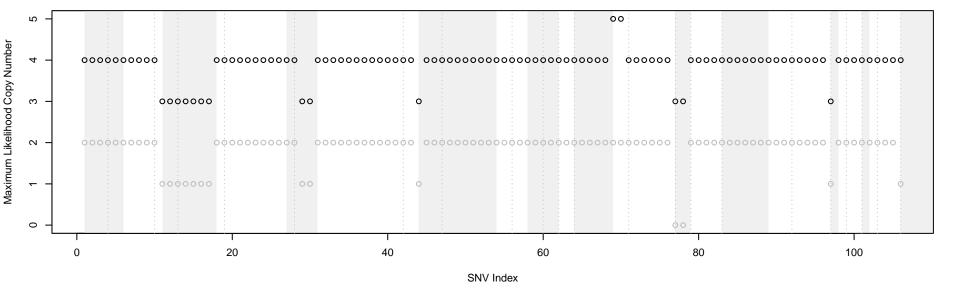
Purity: 0.72 Tumor ploidy: 3.836 2 3 5 0.25 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5

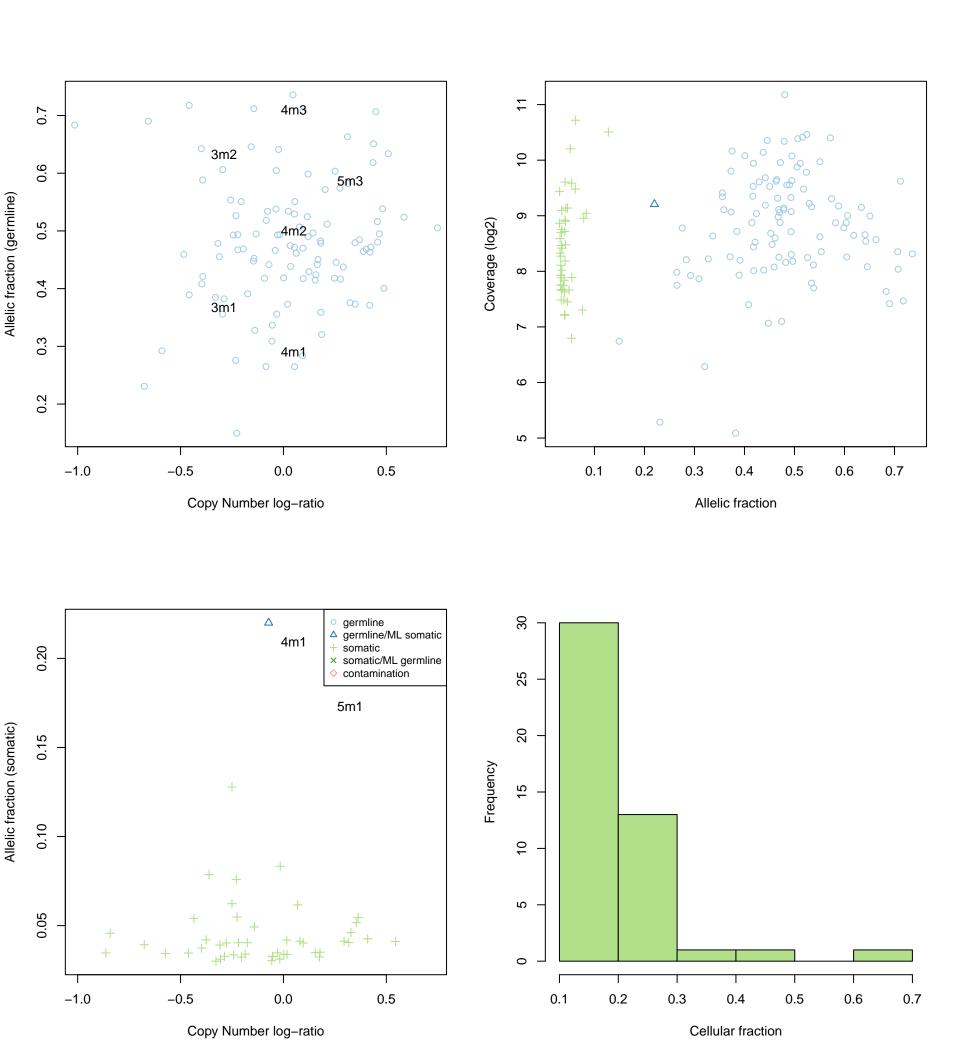
log2 ratio



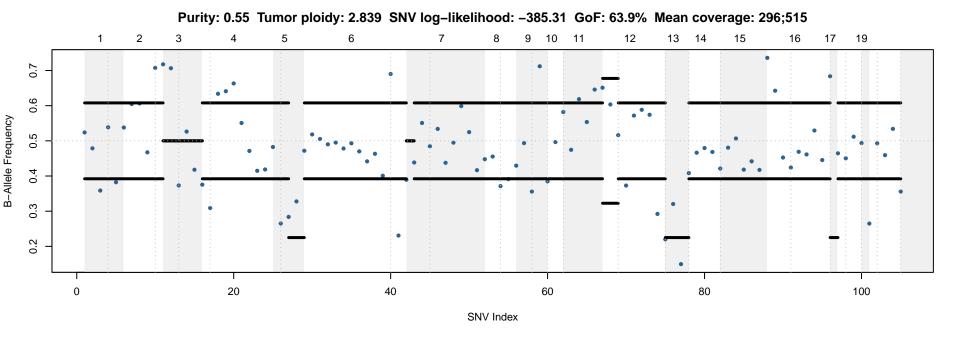
SCNA-fit log-likelihood: -5696.17



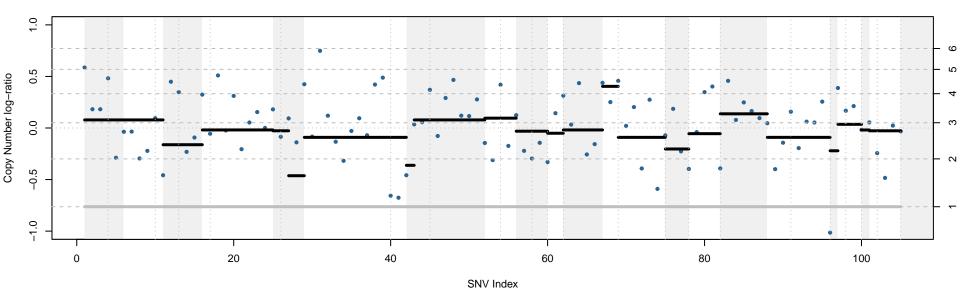


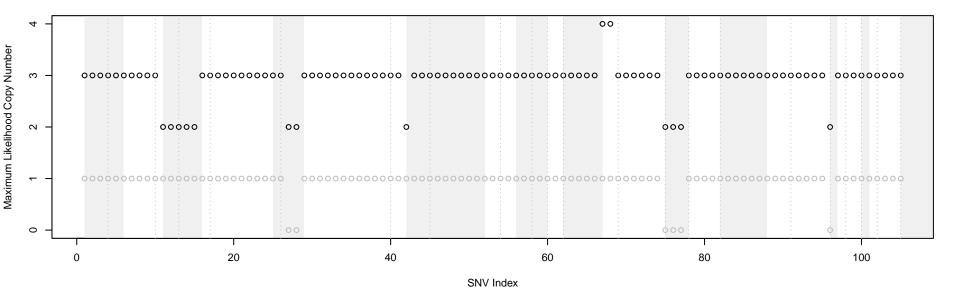


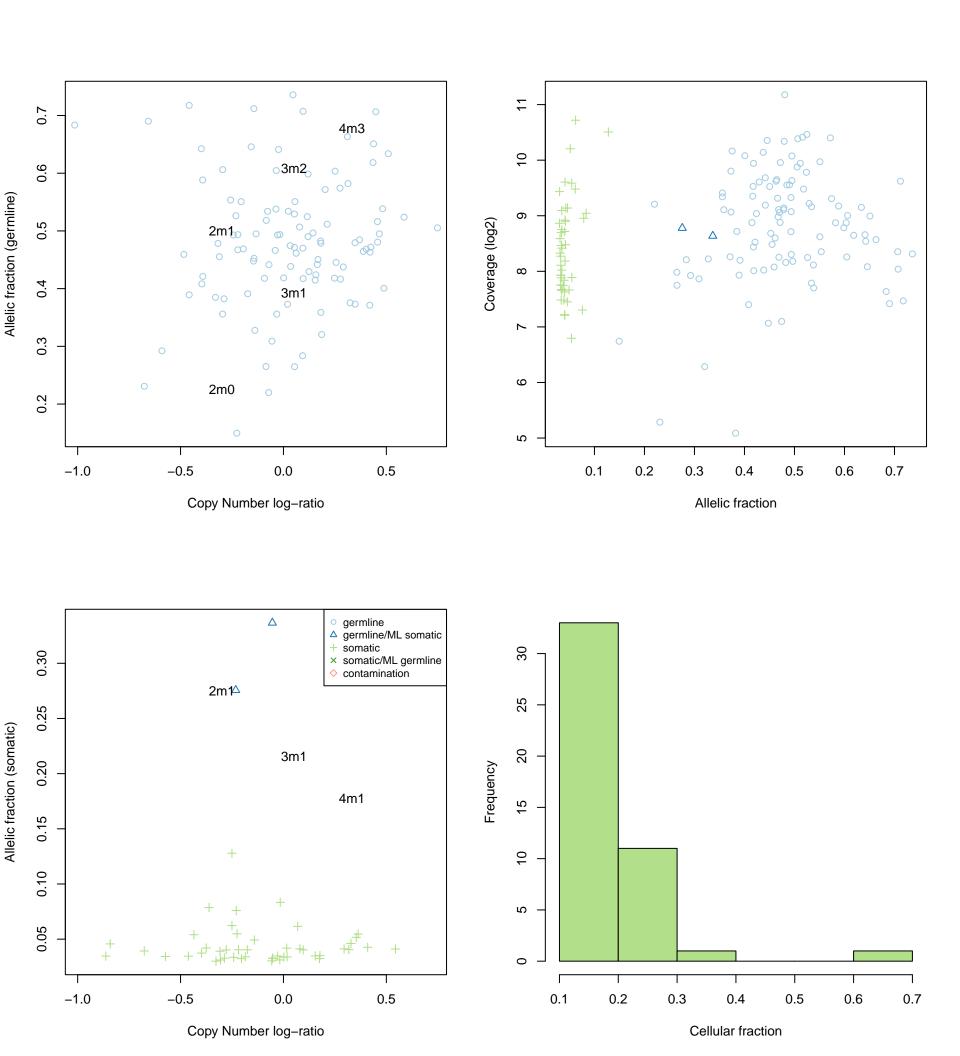
Purity: 0.55 Tumor ploidy: 2.839 2 3 5 4 6 0.25 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



SCNA-fit log-likelihood: -5708.86

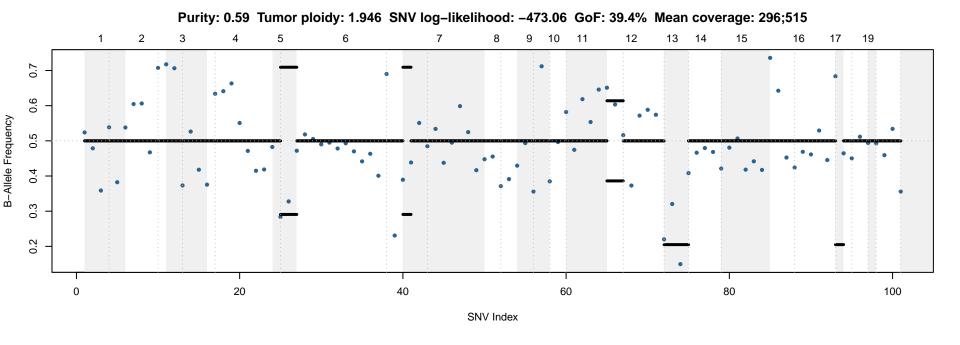




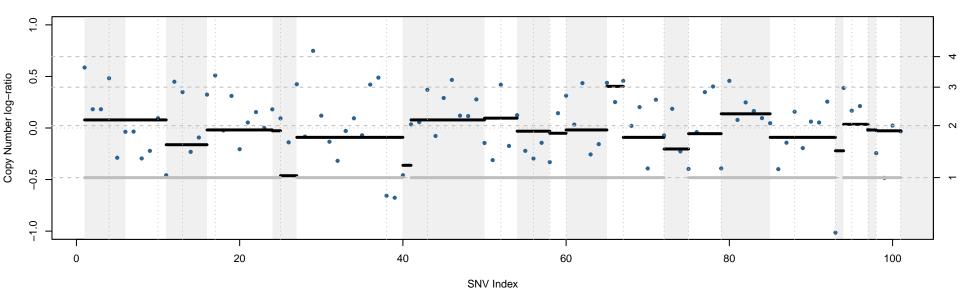


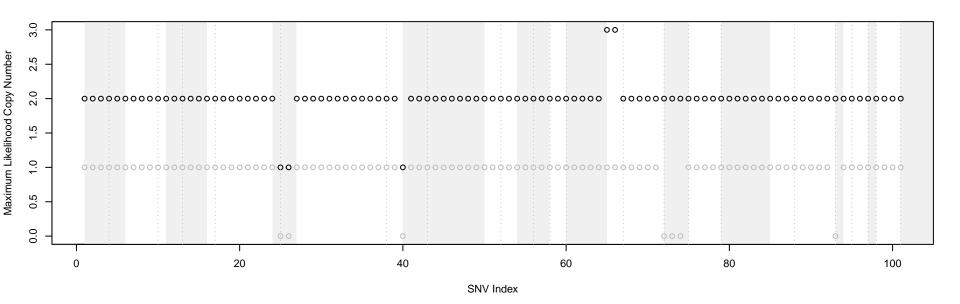
Purity: 0.59 Tumor ploidy: 1.946 2 7 0.25 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5

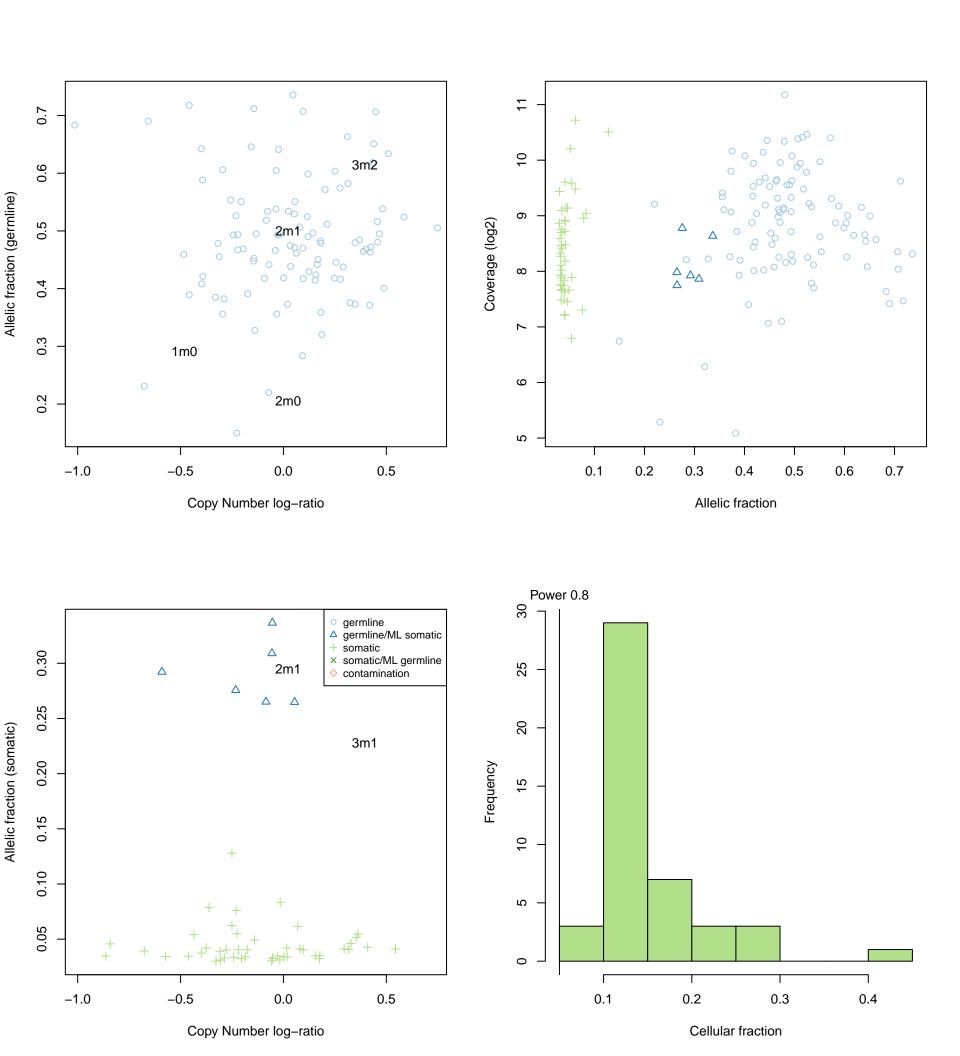
log2 ratio

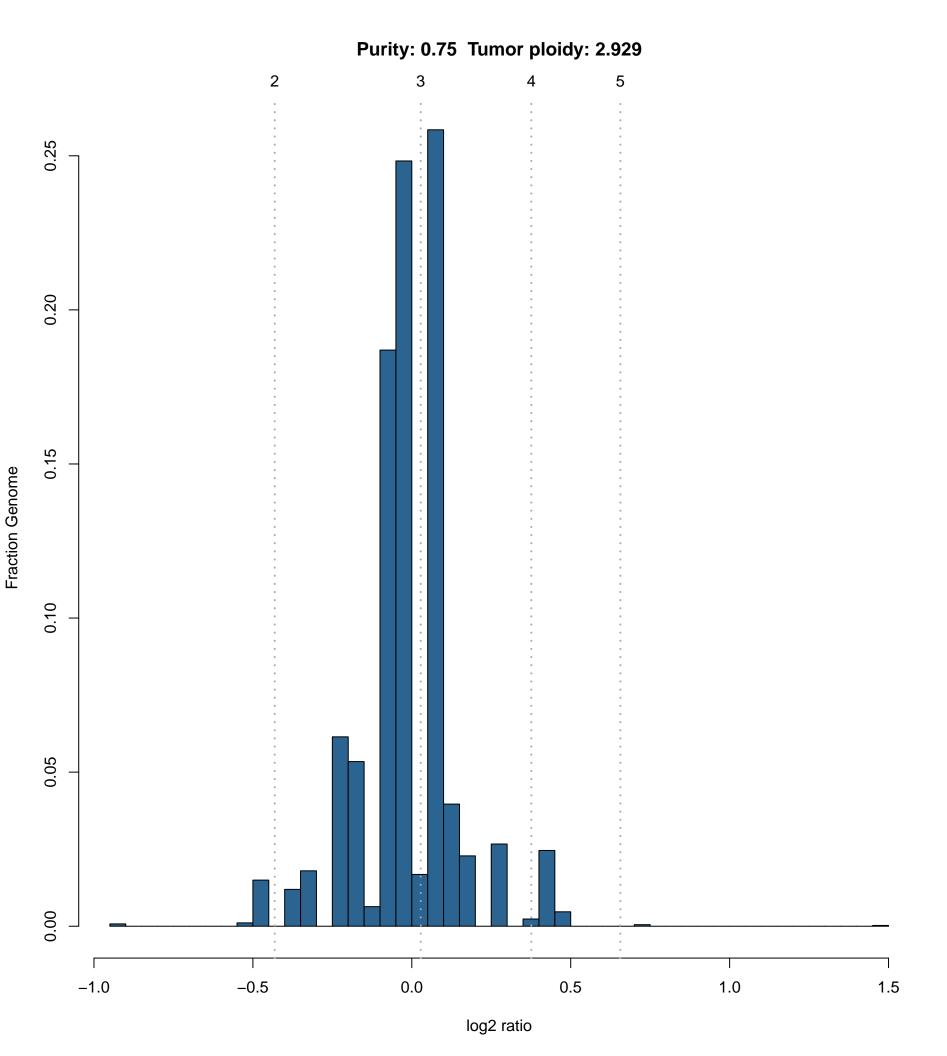


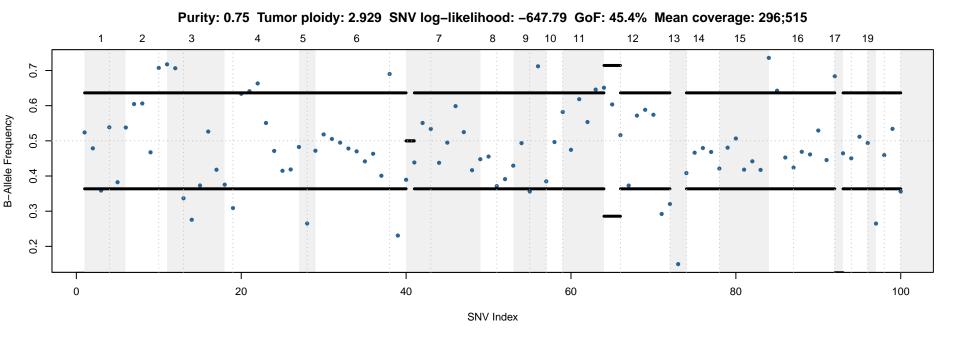
SCNA-fit log-likelihood: -5824.46











SCNA-fit log-likelihood: -5808.78

