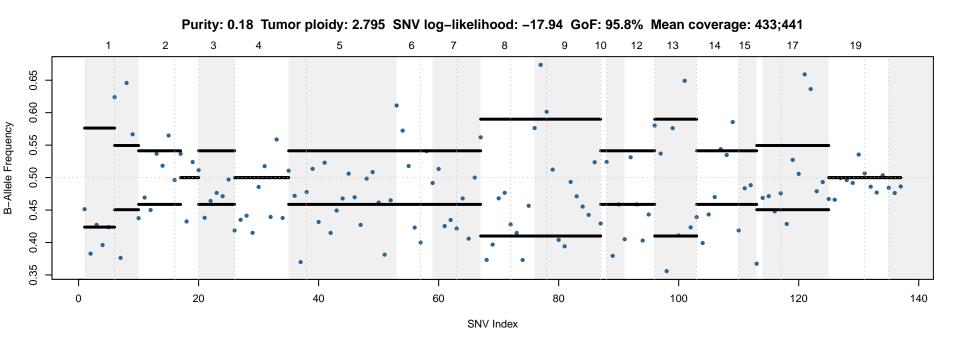
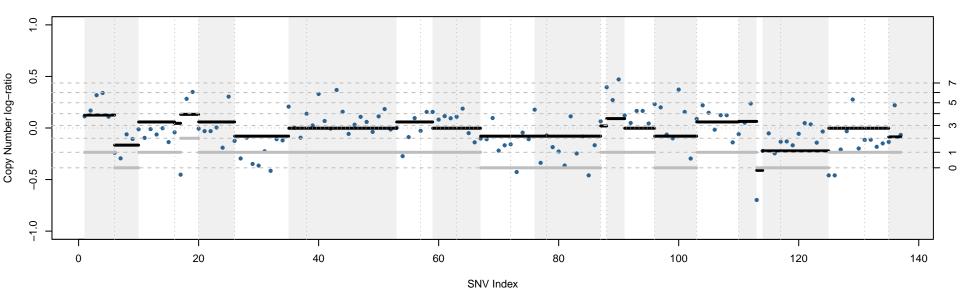
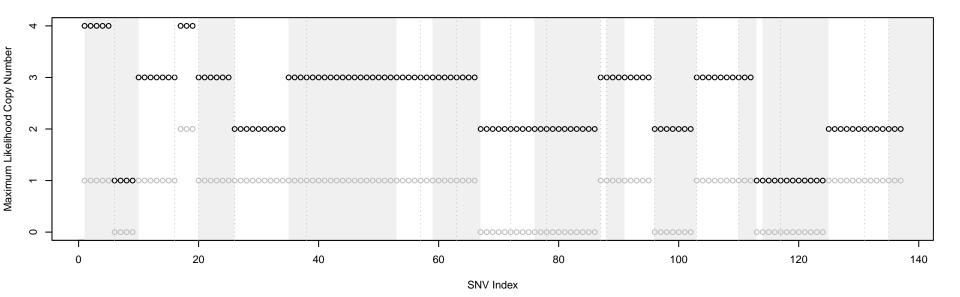
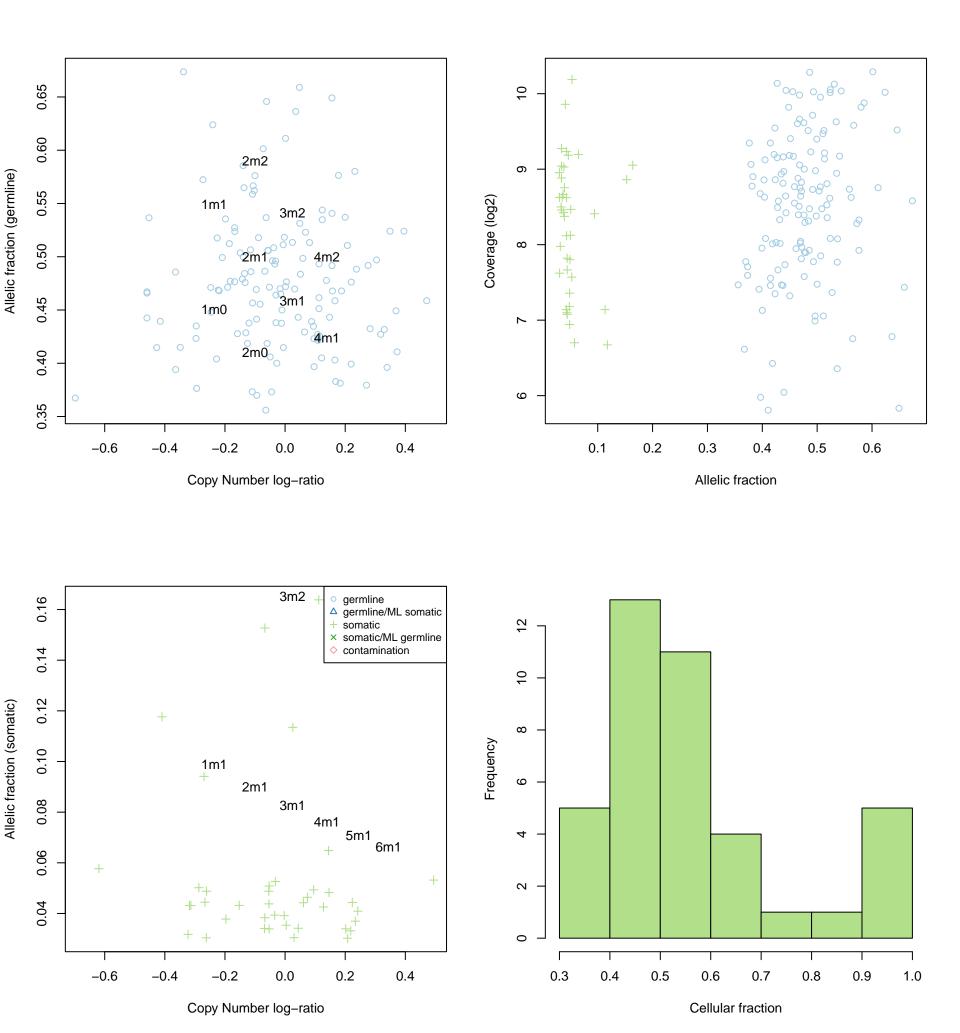
Purity: 0.18 Tumor ploidy: 2.795 0 2 3 5 6 1 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0

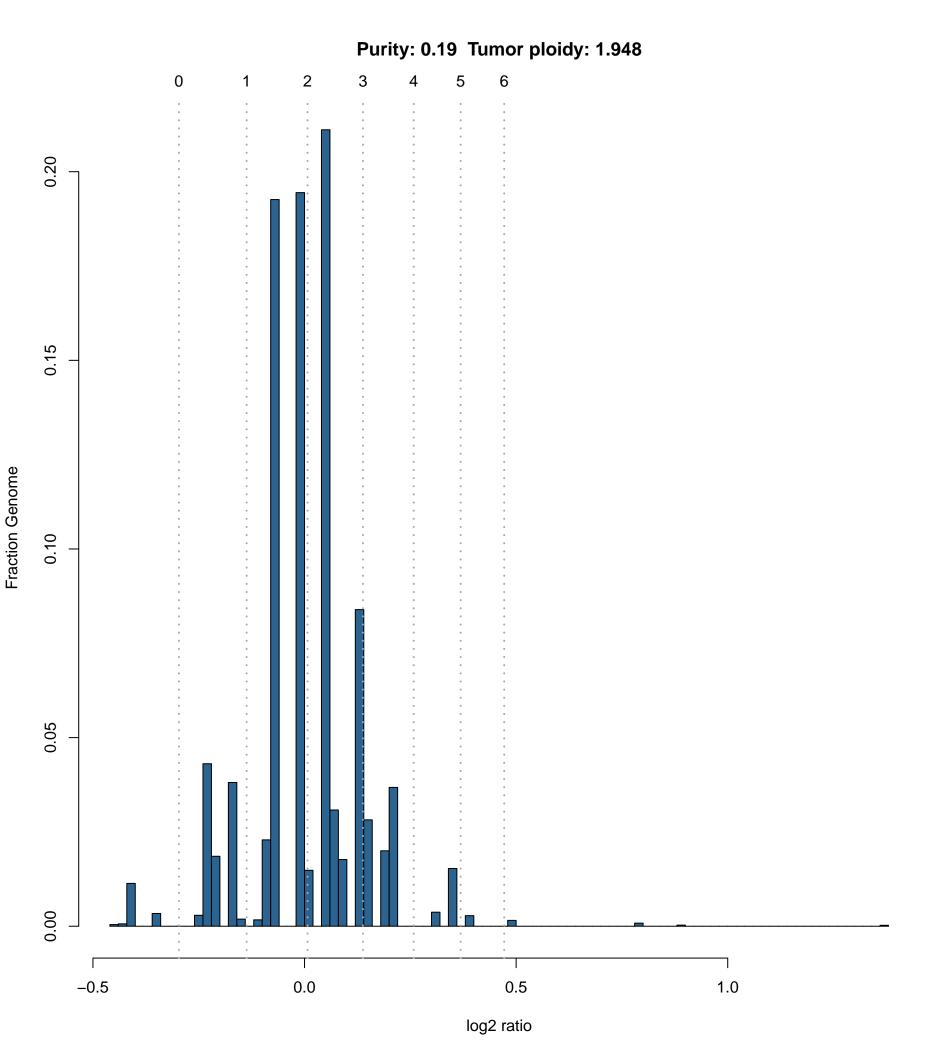


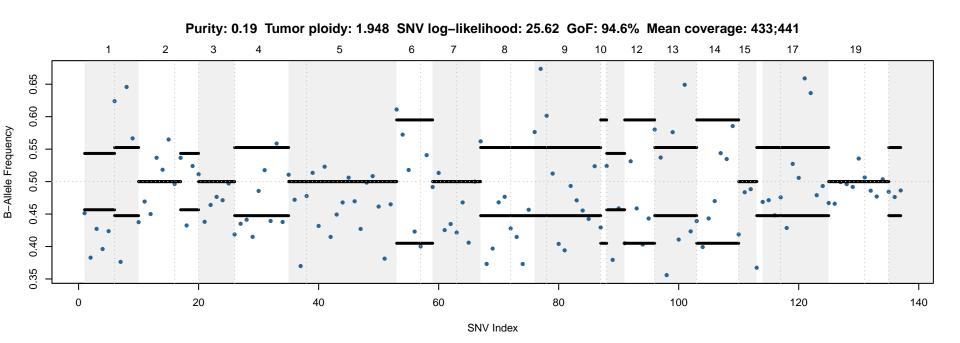
SCNA-fit log-likelihood: -8793.51



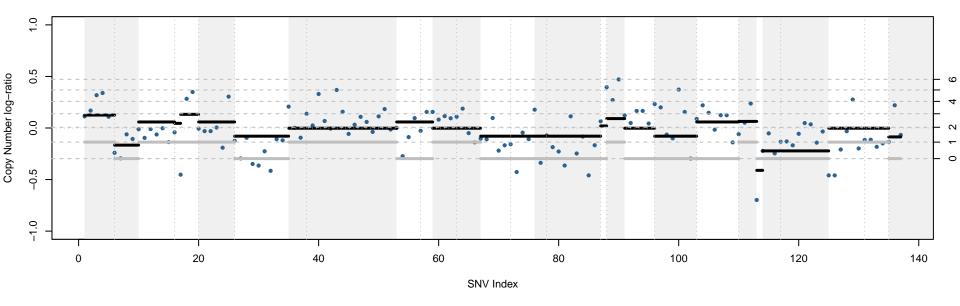


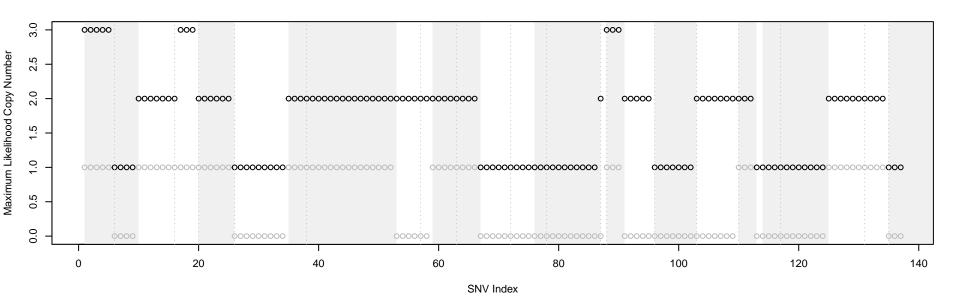


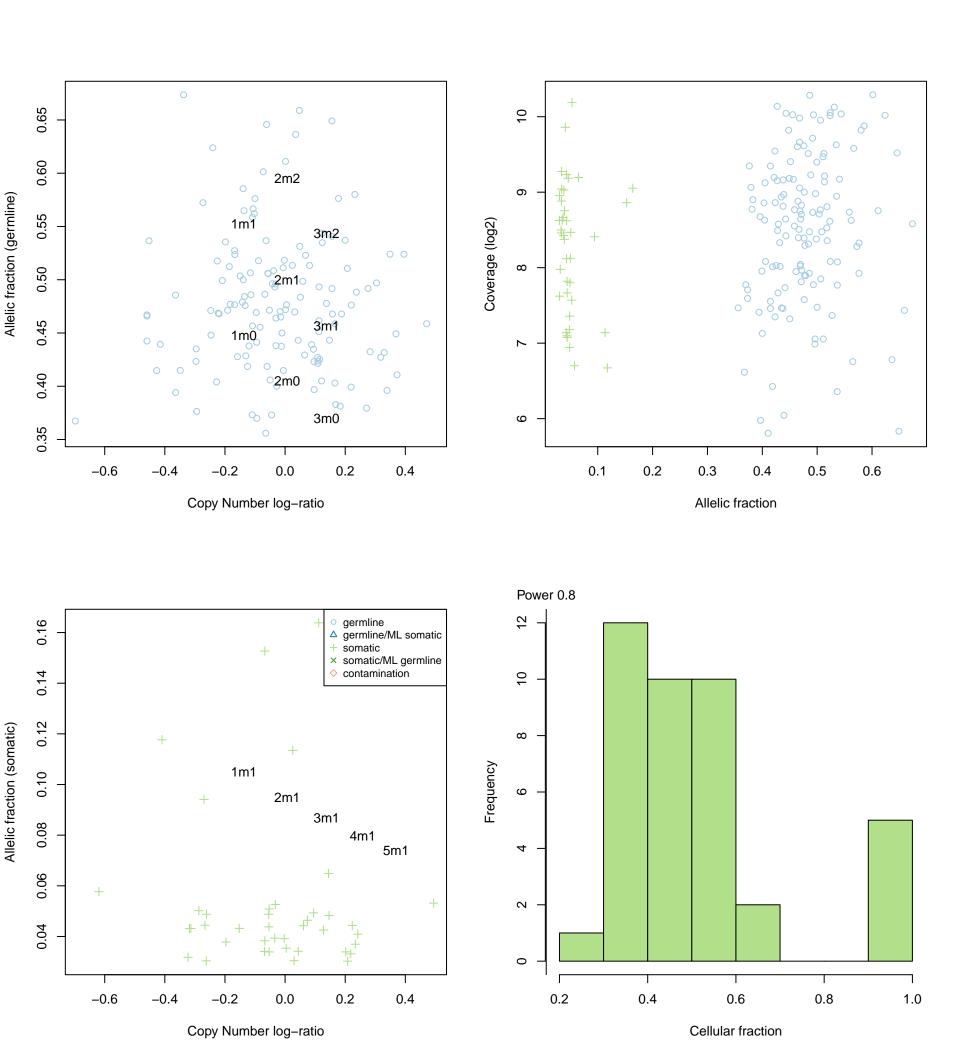




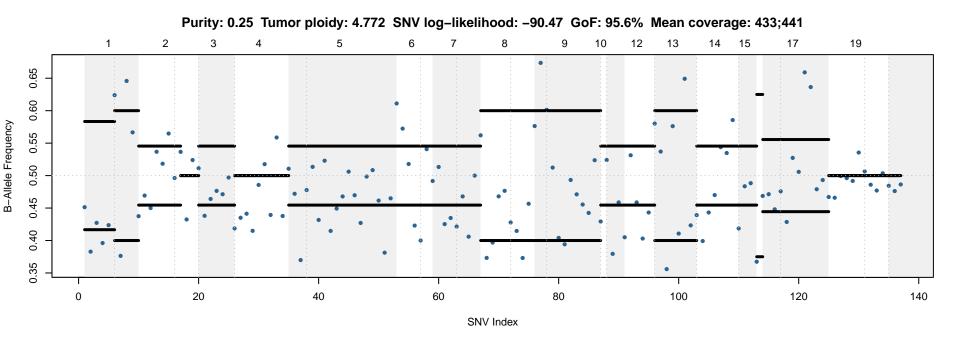
SCNA-fit log-likelihood: -8934.95



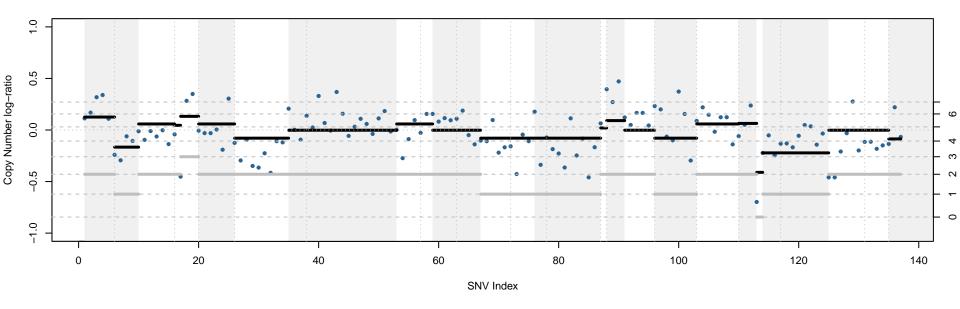


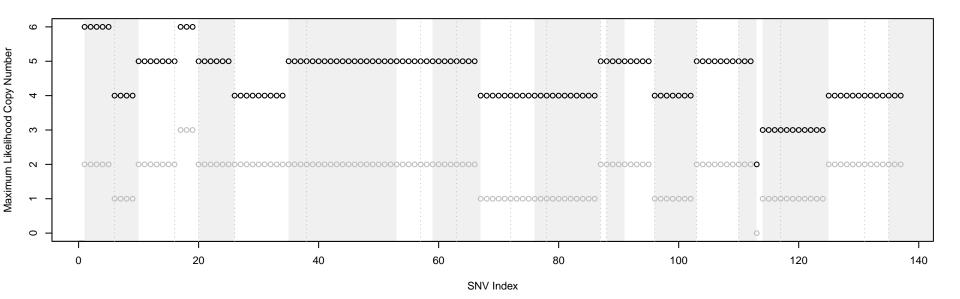


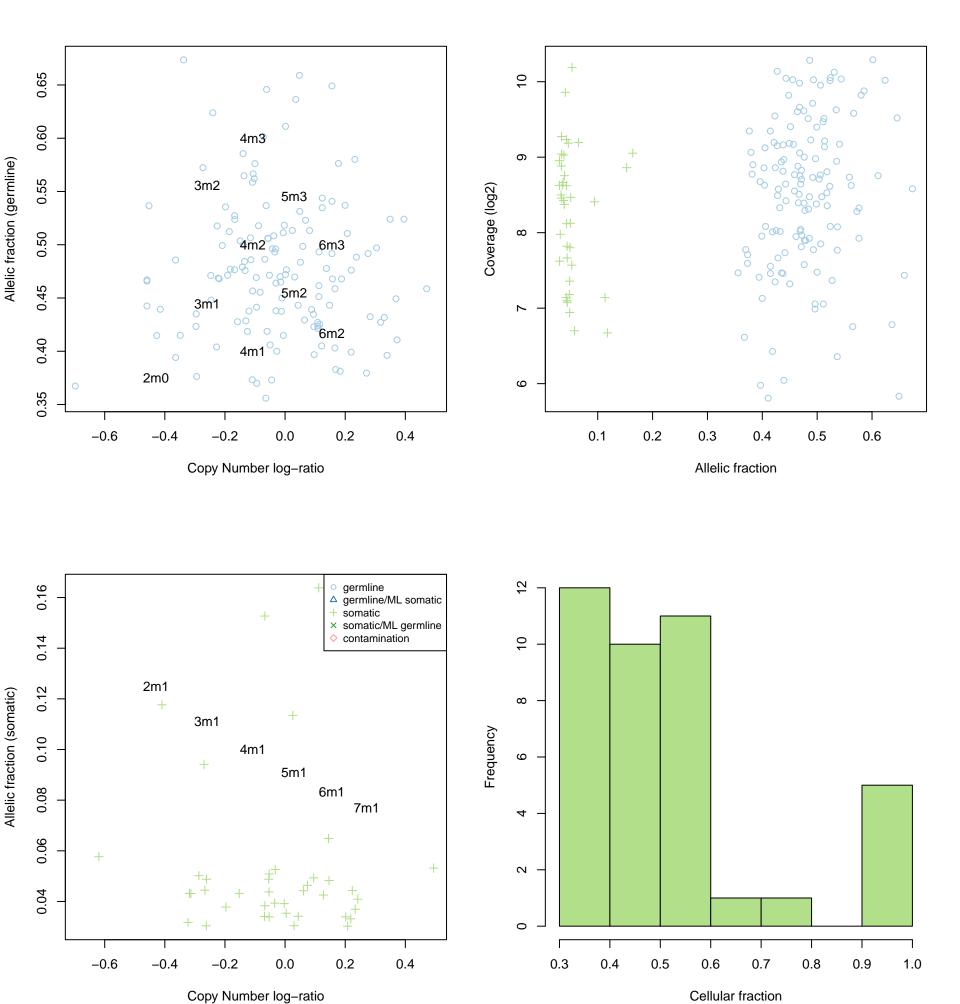
Purity: 0.25 Tumor ploidy: 4.772 6 2 3 7 0 5 0.25 0.20 Fraction Genome 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0



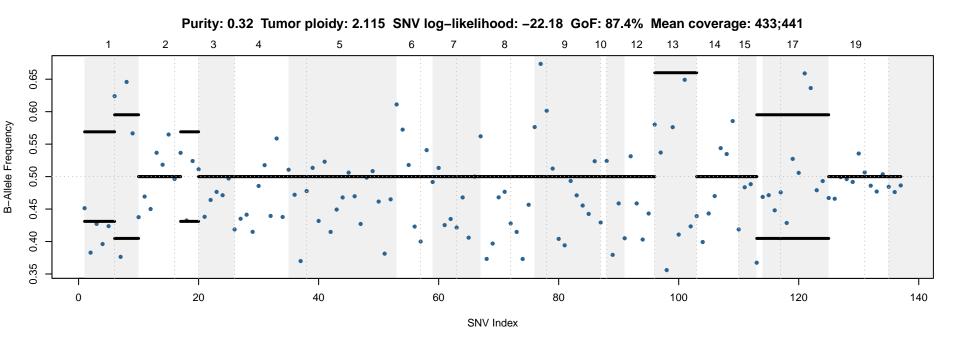
SCNA-fit log-likelihood: -8774.17



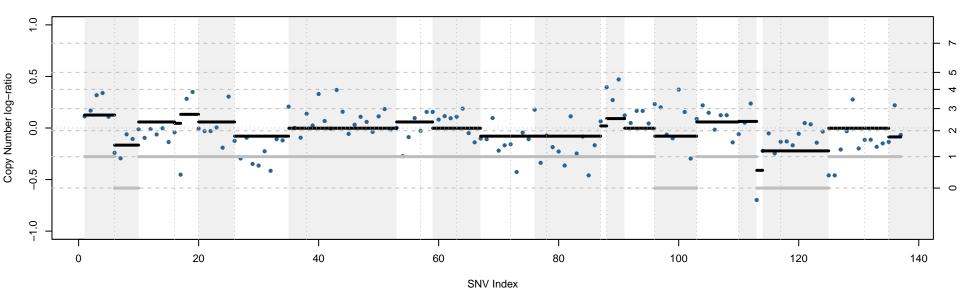


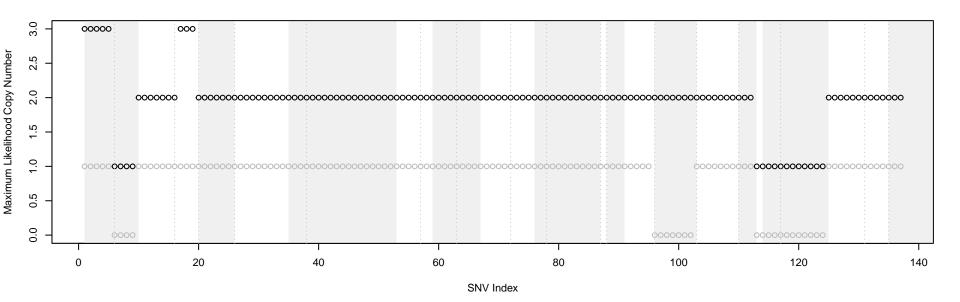


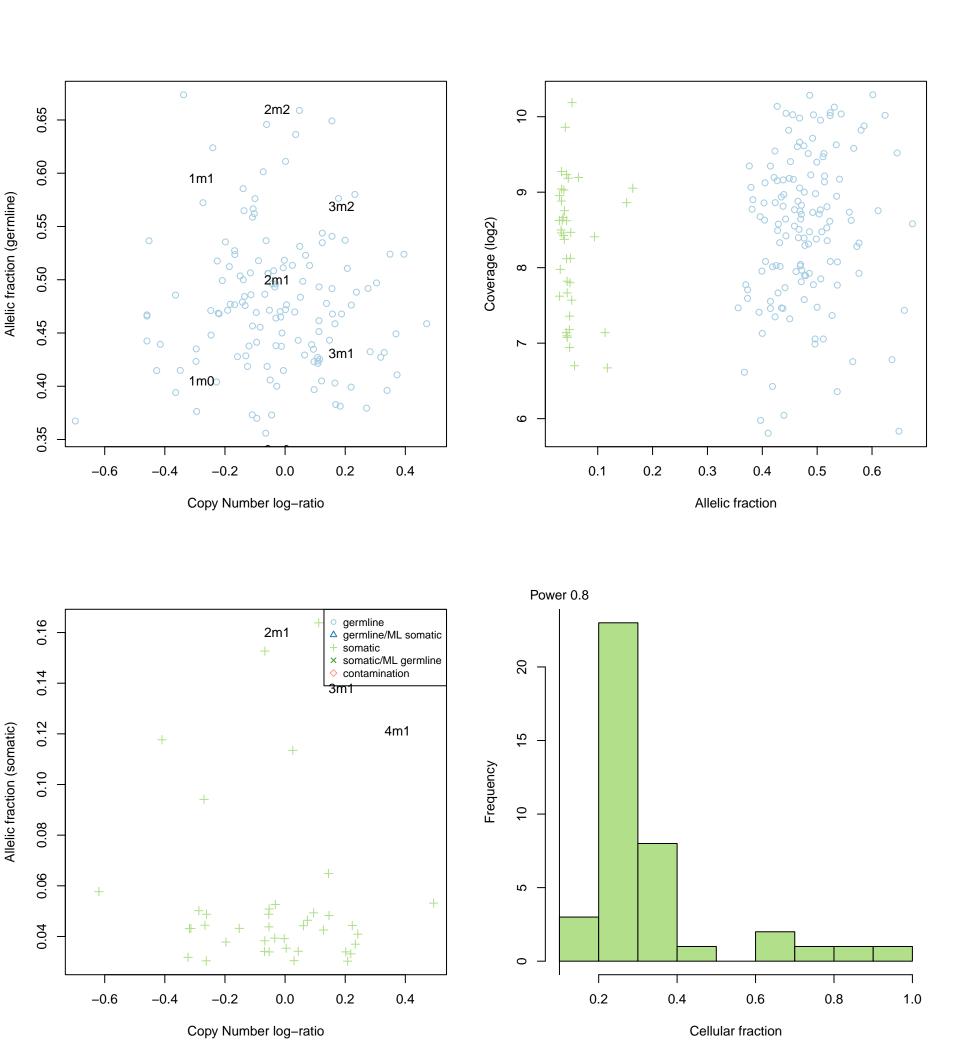
Purity: 0.32 Tumor ploidy: 2.115 3 0 2 5 7 0.20 Fraction Genome 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



SCNA-fit log-likelihood: -8973.69

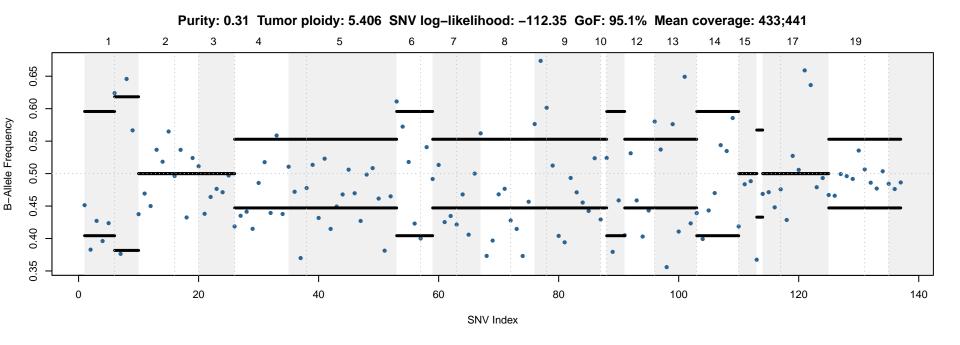




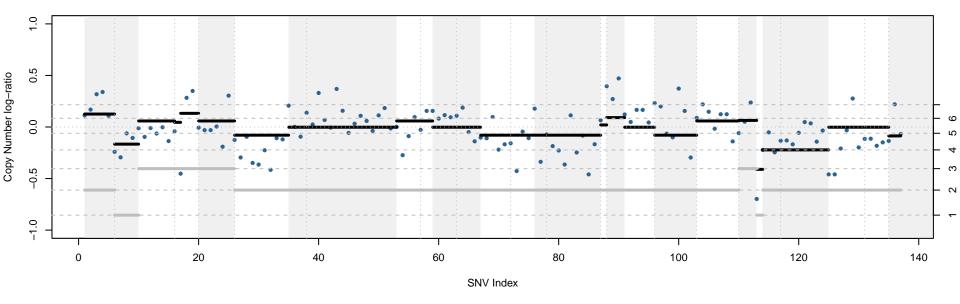


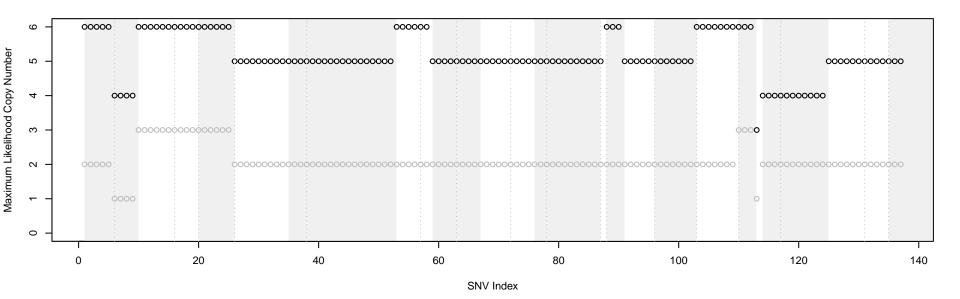
Purity: 0.31 Tumor ploidy: 5.406 3 7 2 5 6 0.25 0.20 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0

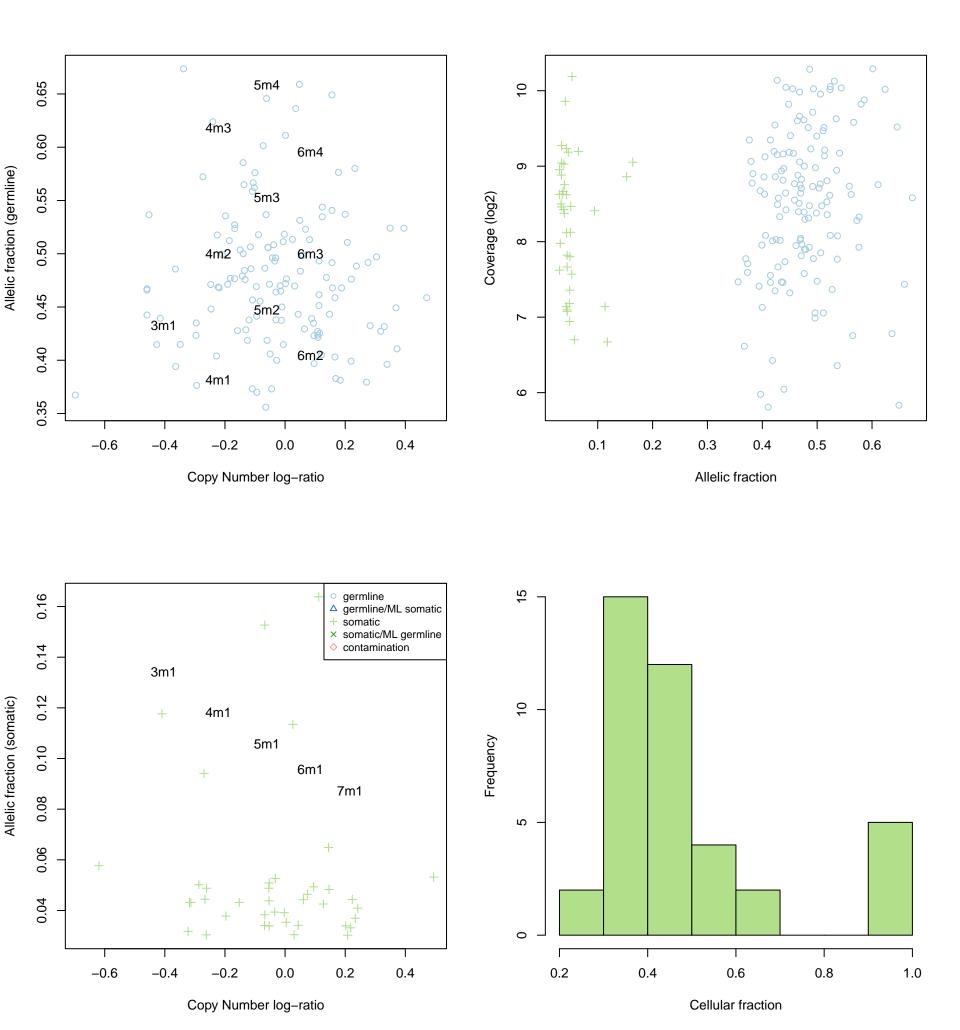
Fraction Genome



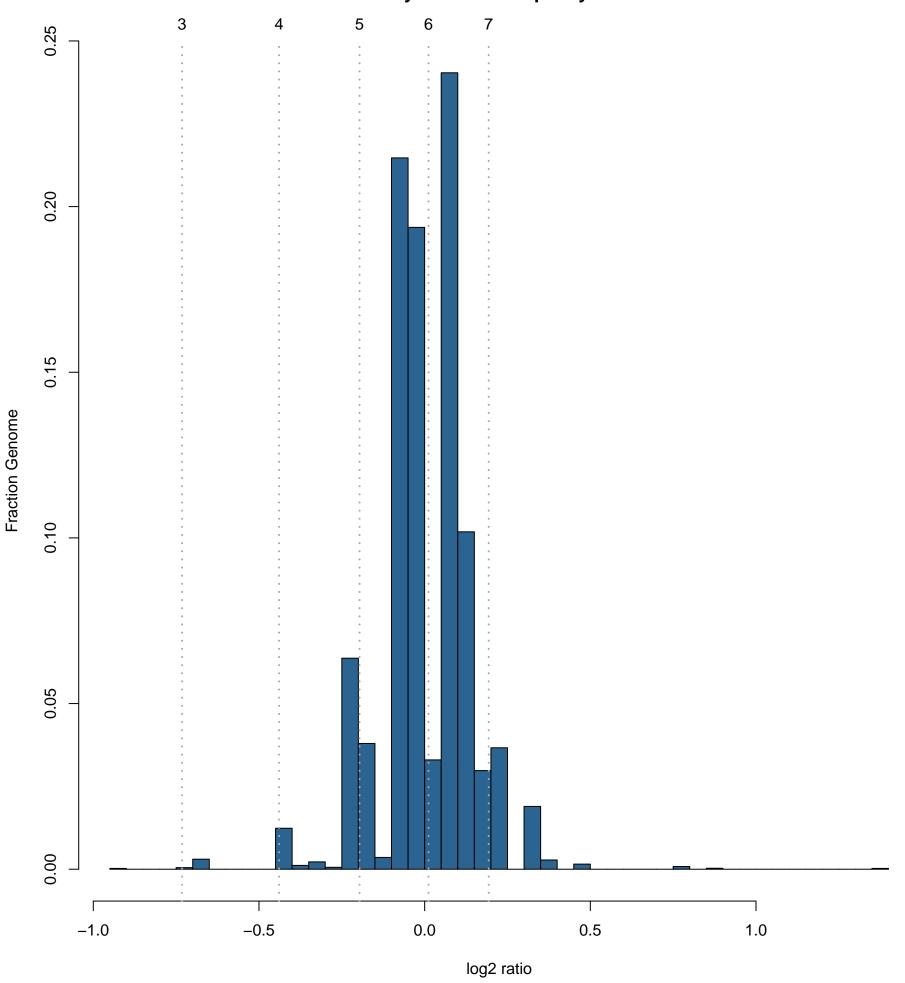
SCNA-fit log-likelihood: -8824.95

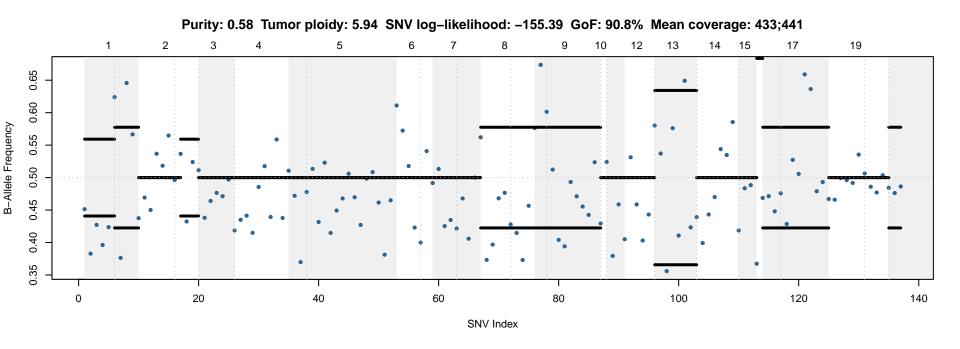




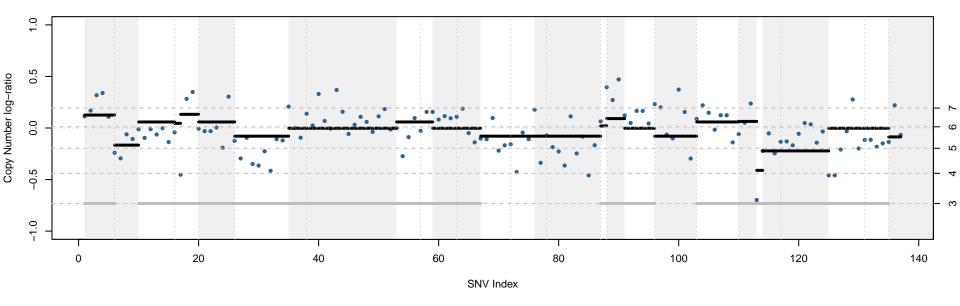


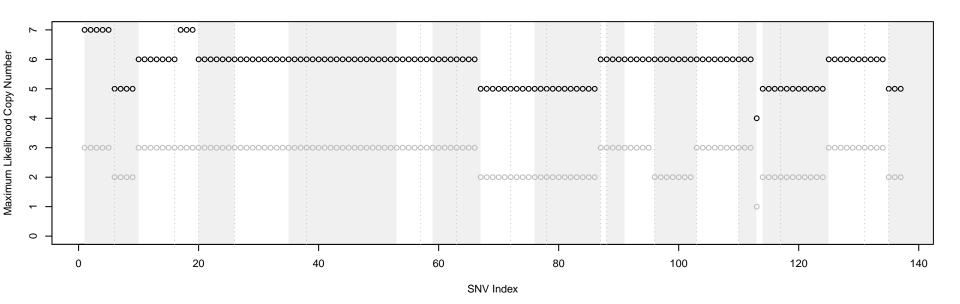
Purity: 0.58 Tumor ploidy: 5.94

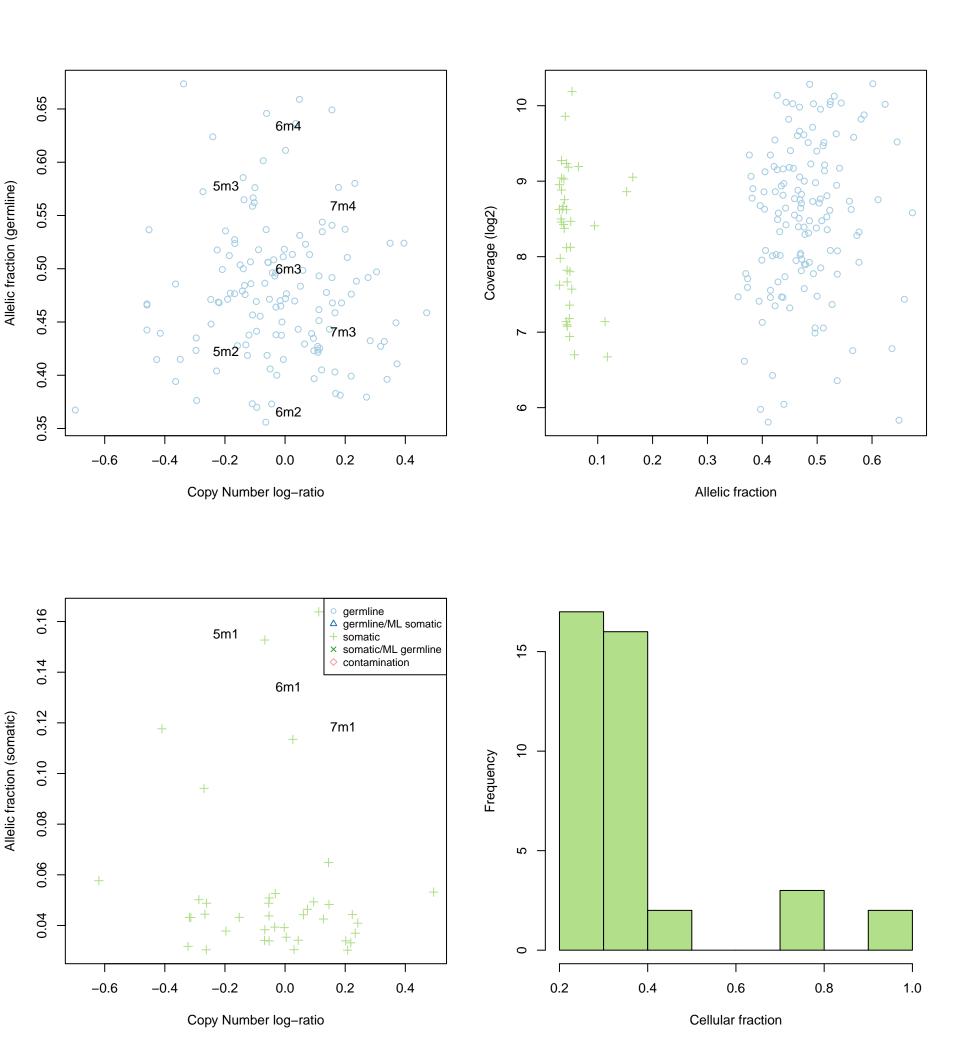




SCNA-fit log-likelihood: -8955.26

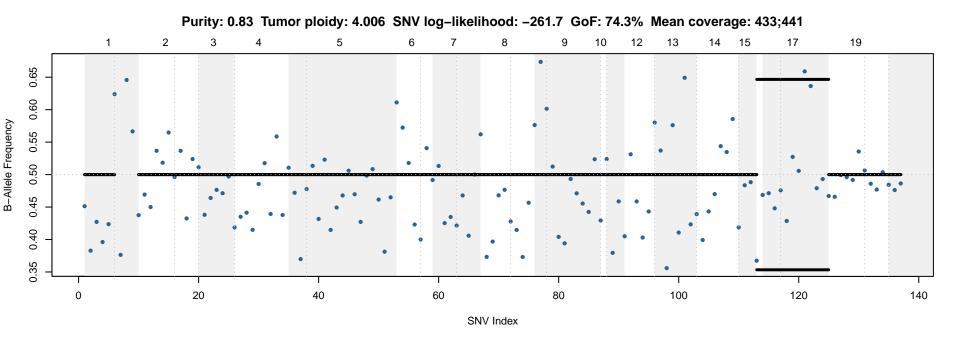




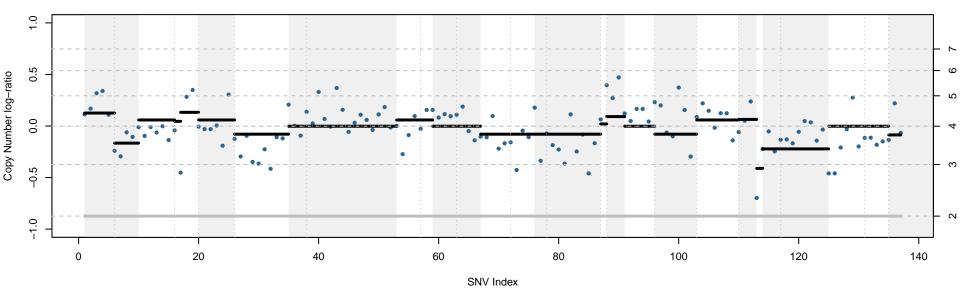


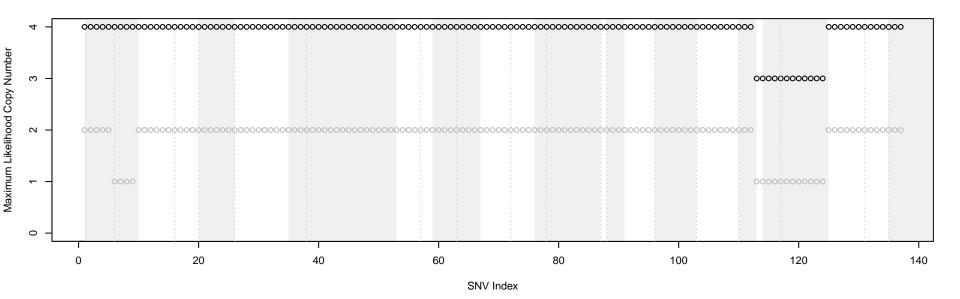
Purity: 0.83 Tumor ploidy: 4.006 5 2 3 6 7 0.25 0.20 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0

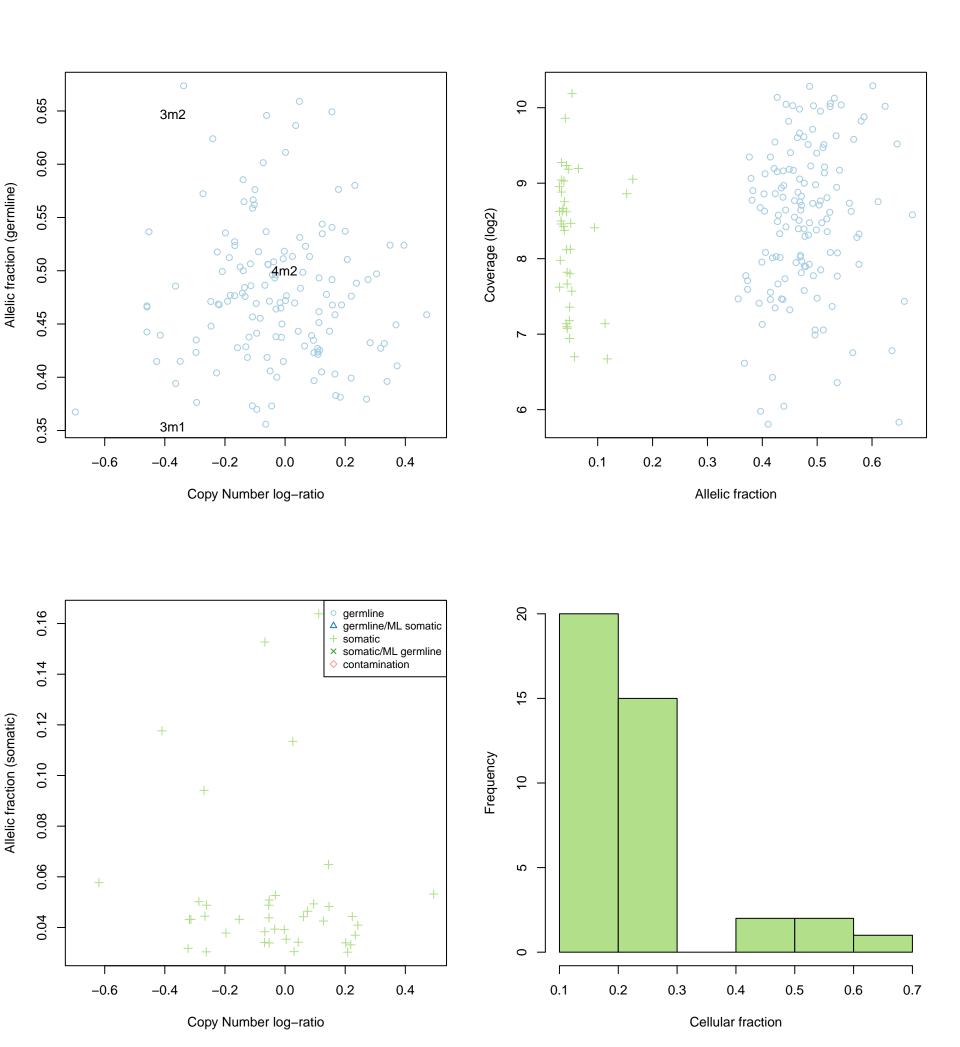
Fraction Genome



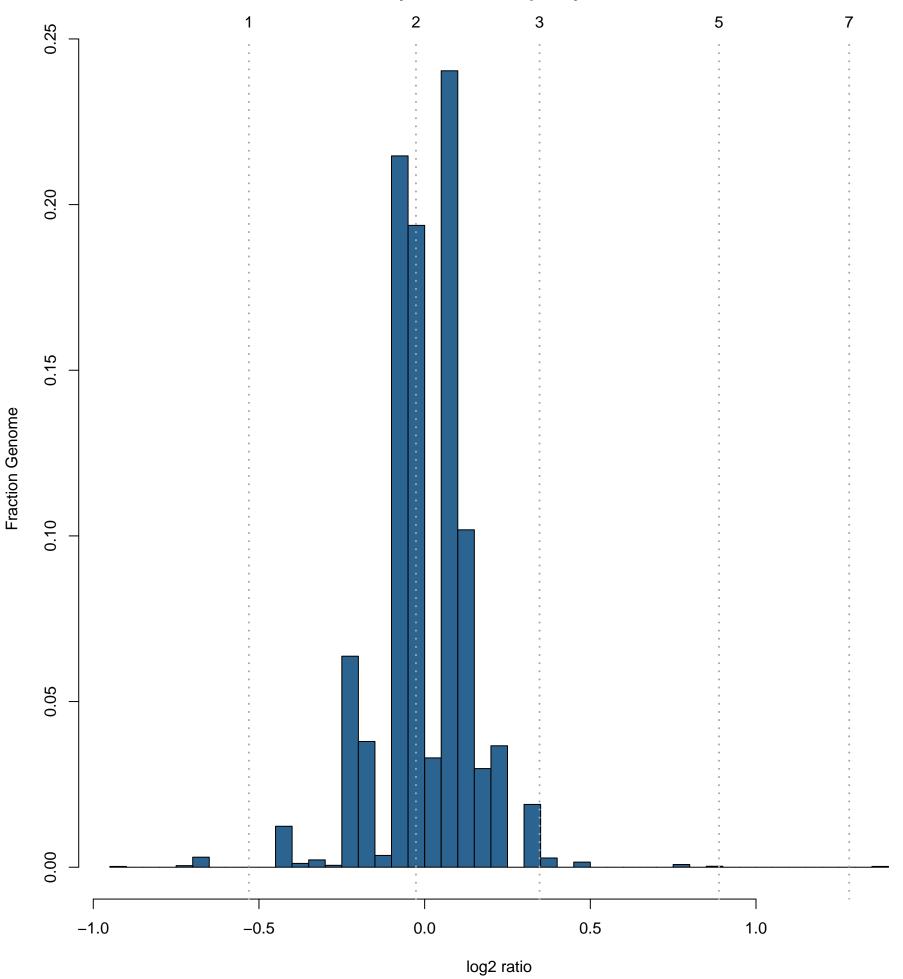
SCNA-fit log-likelihood: -9206.09

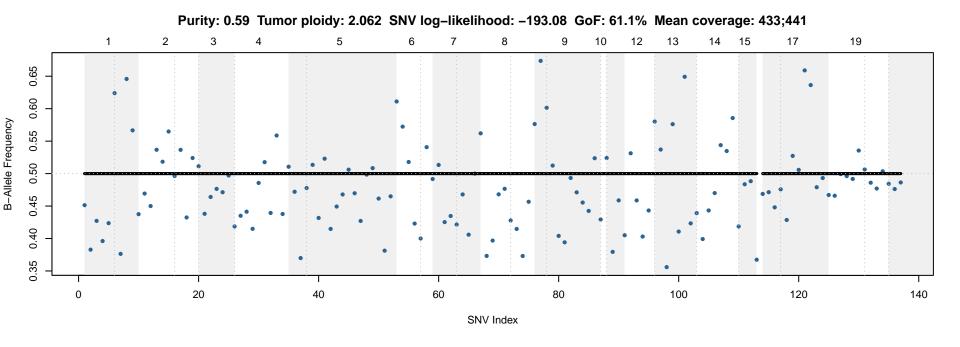




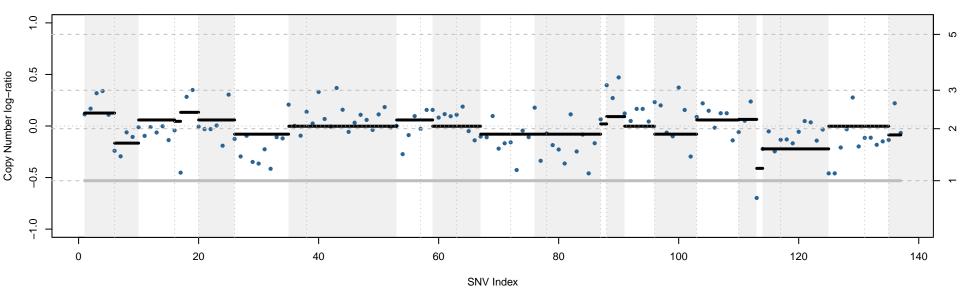


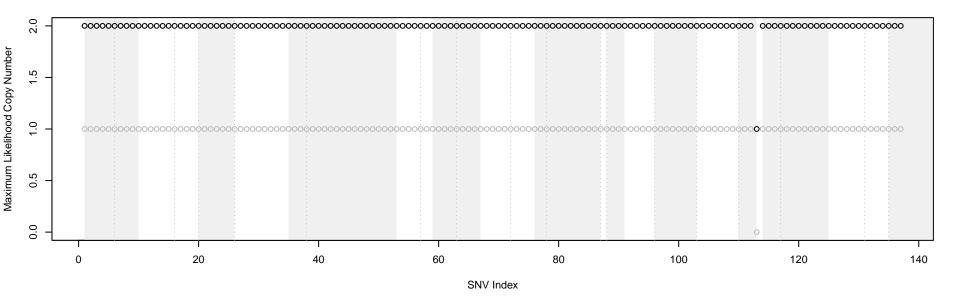
Purity: 0.59 Tumor ploidy: 2.062

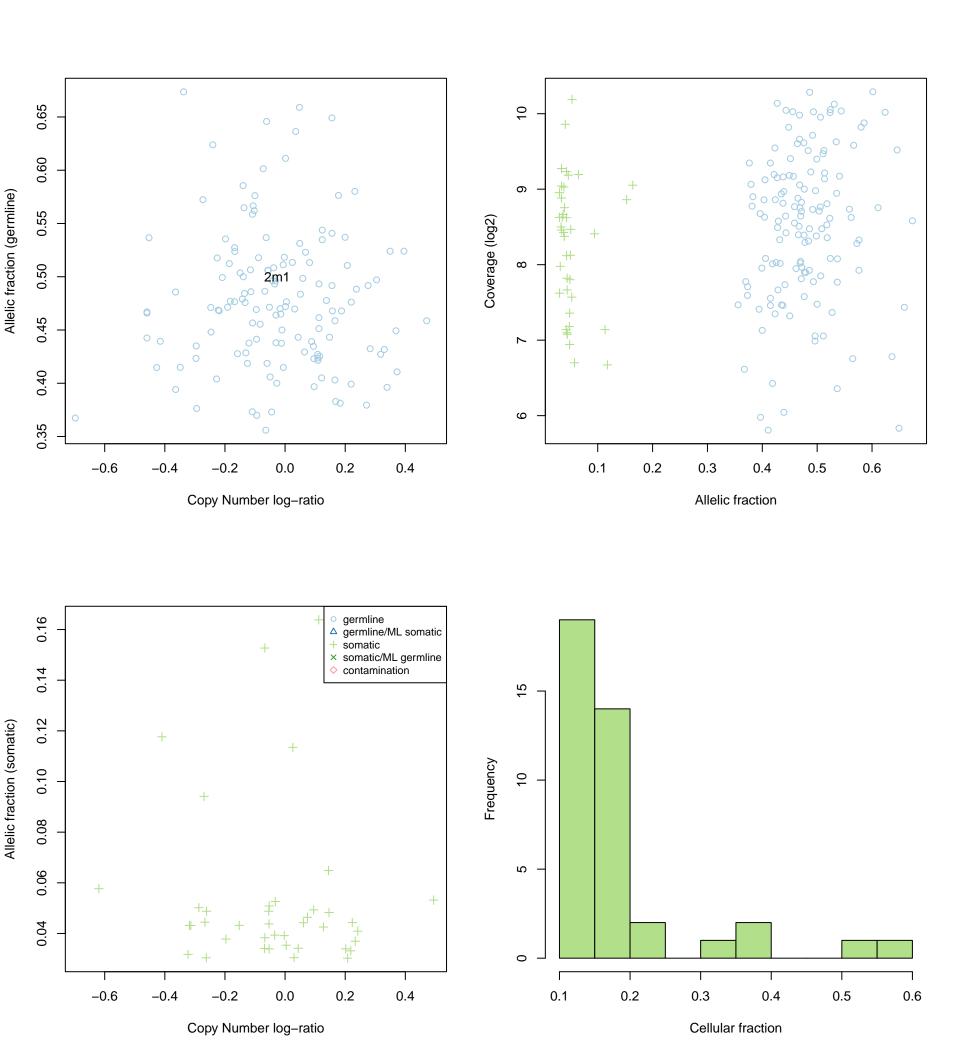


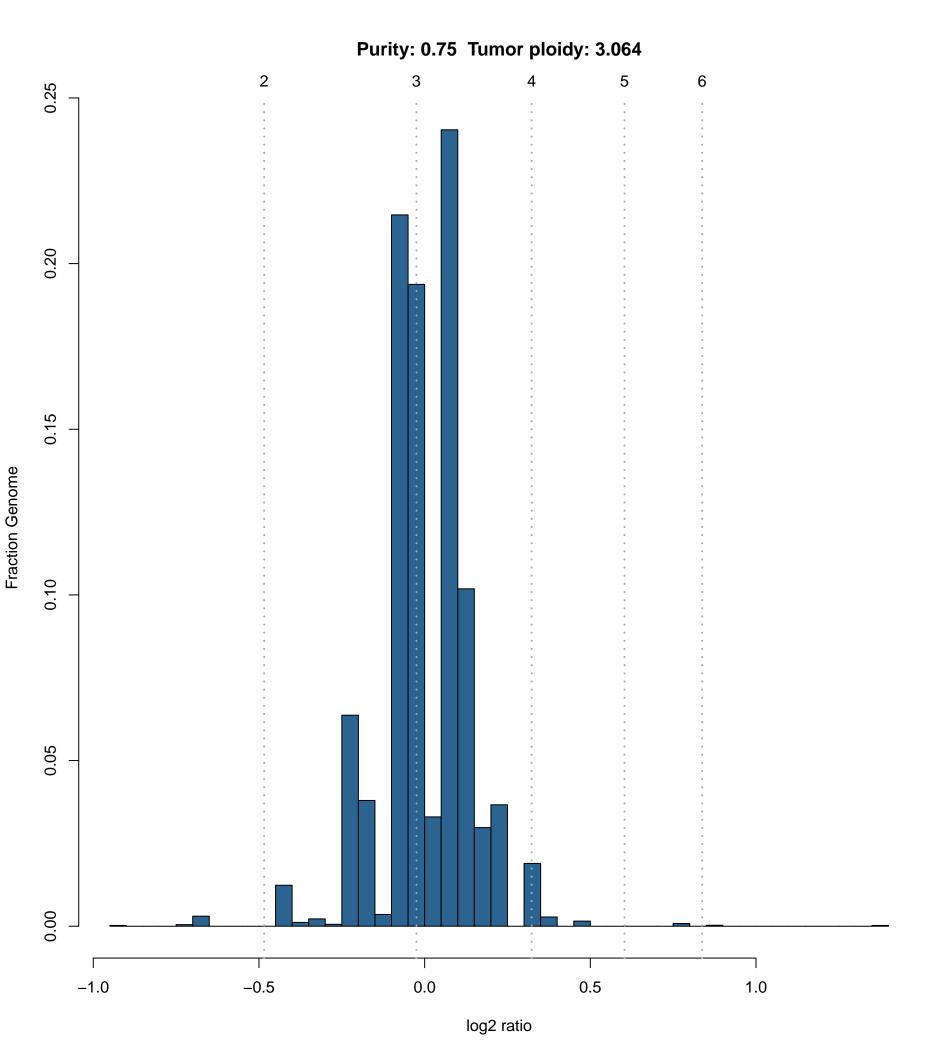


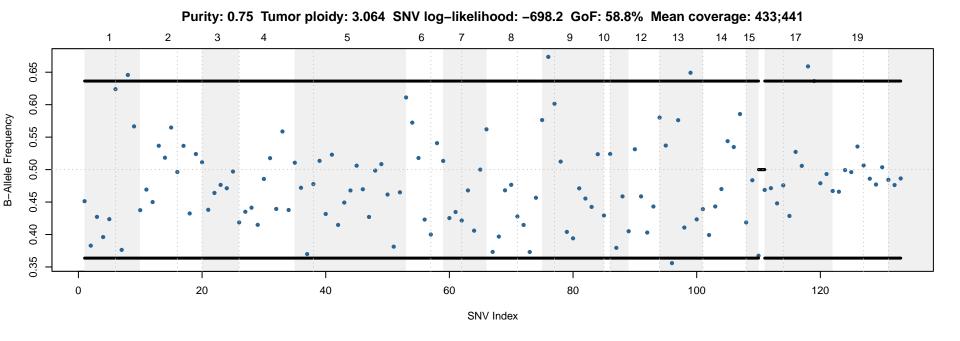
SCNA-fit log-likelihood: -9407.87











SCNA-fit log-likelihood: -9372.01

