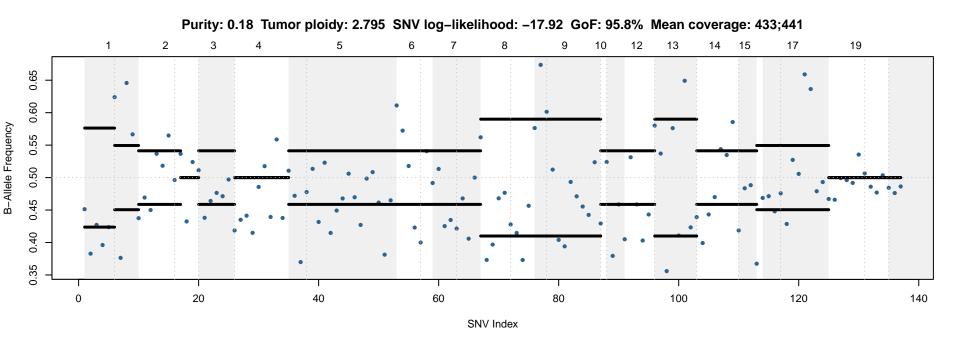
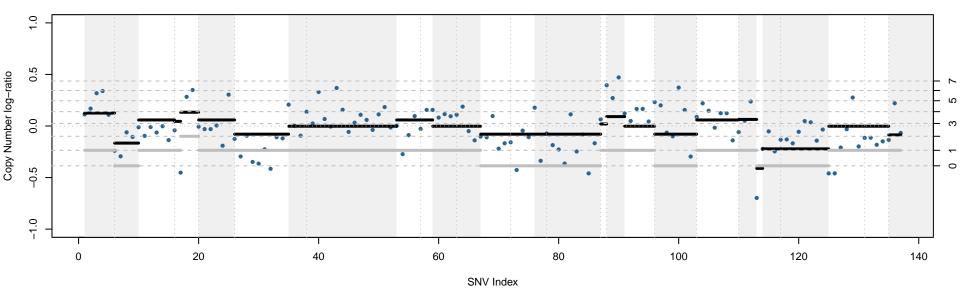
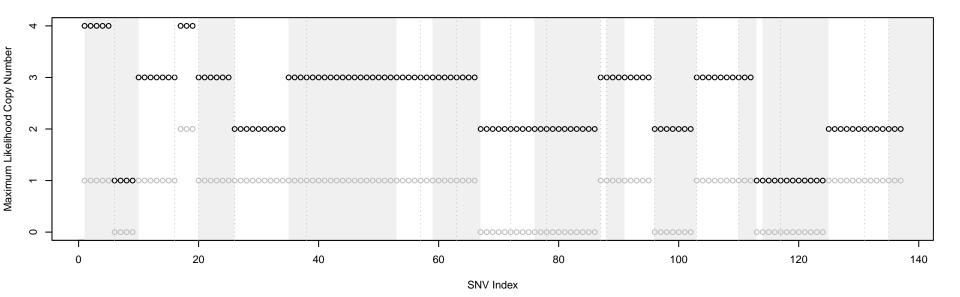
Purity: 0.18 Tumor ploidy: 2.795 0 2 3 5 6 1 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0

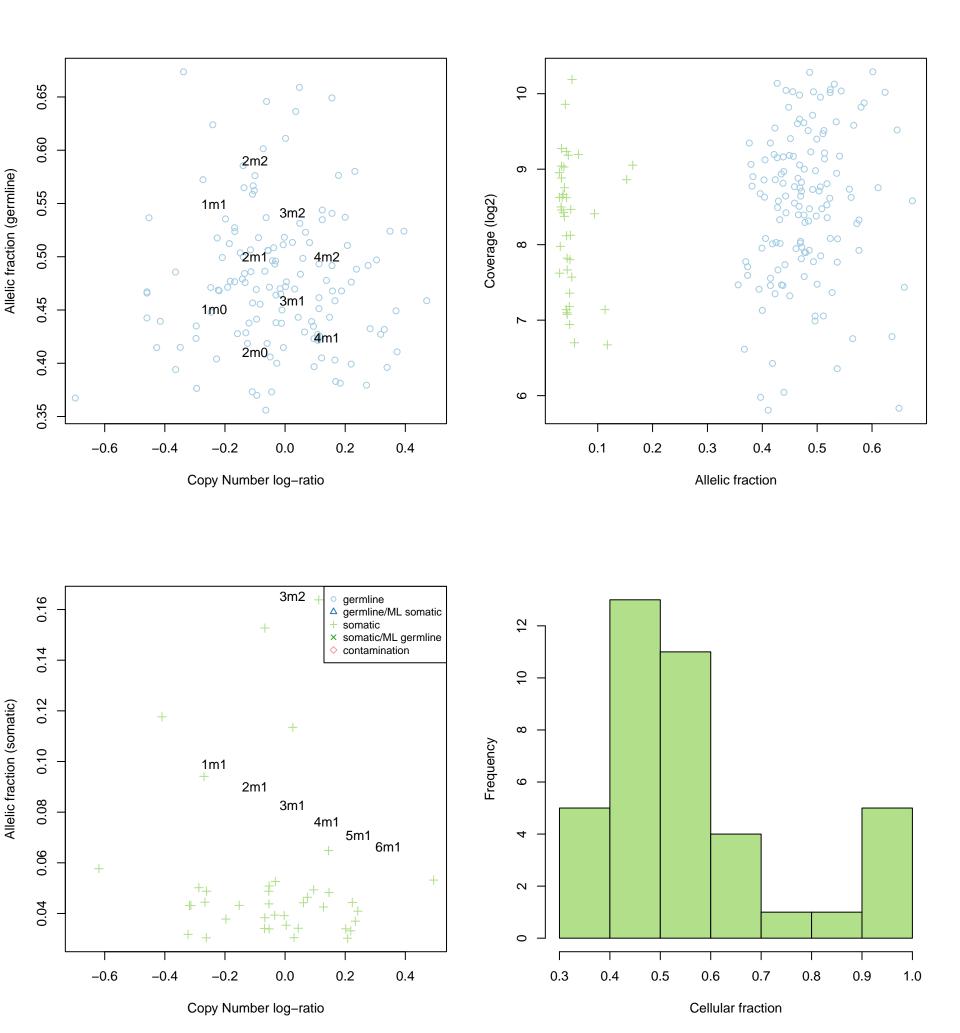
log2 ratio

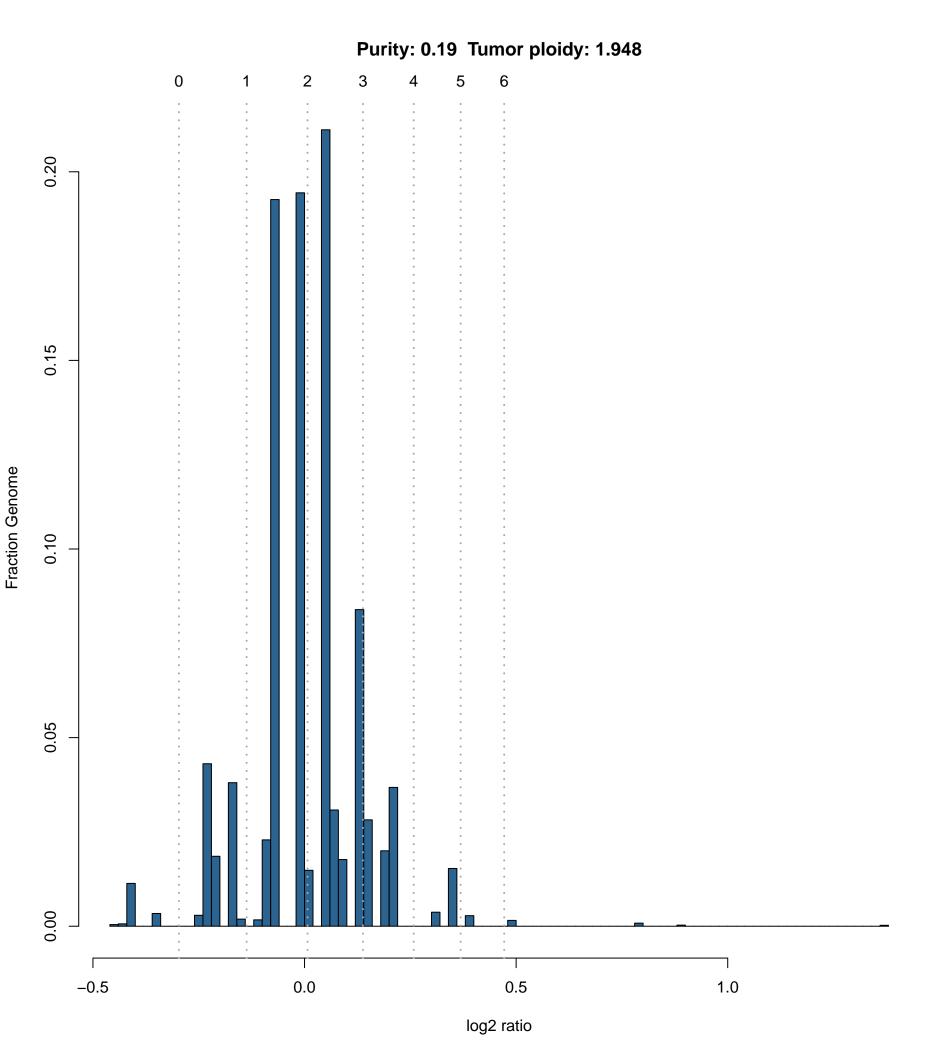


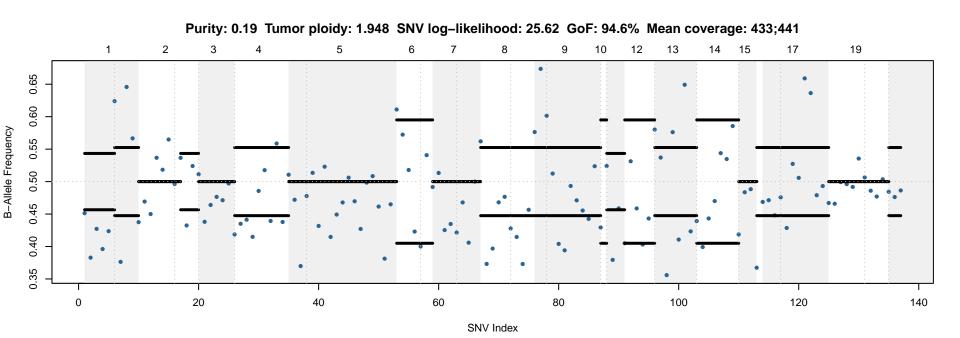
SCNA-fit log-likelihood: -8793.14



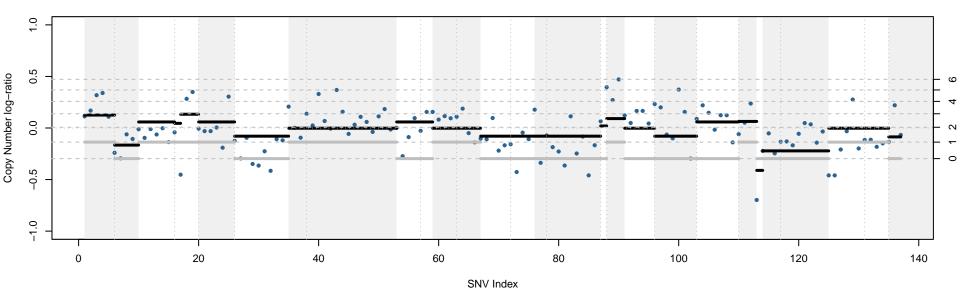


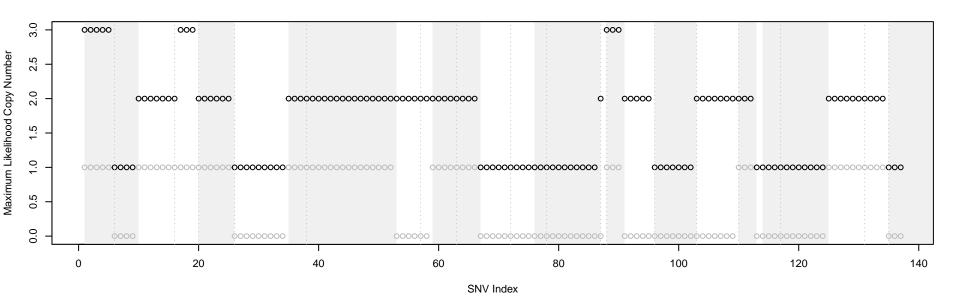


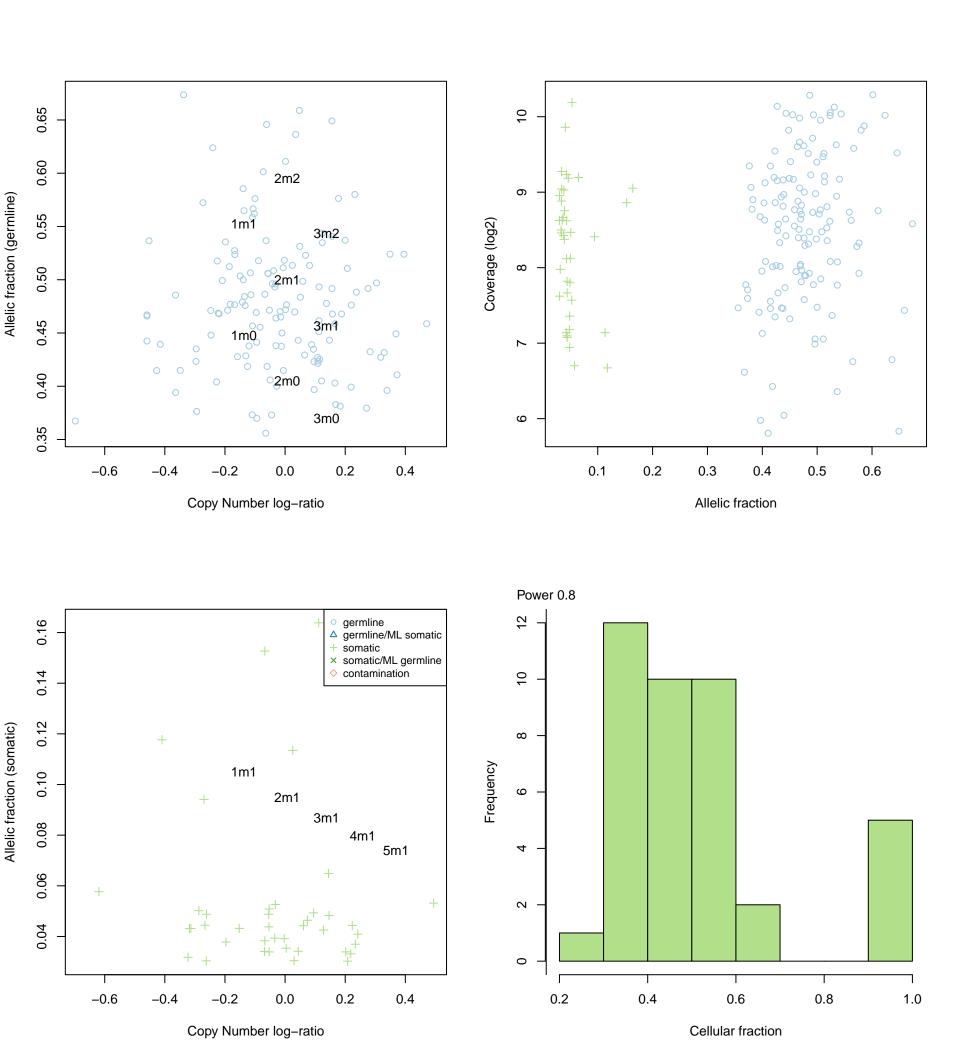




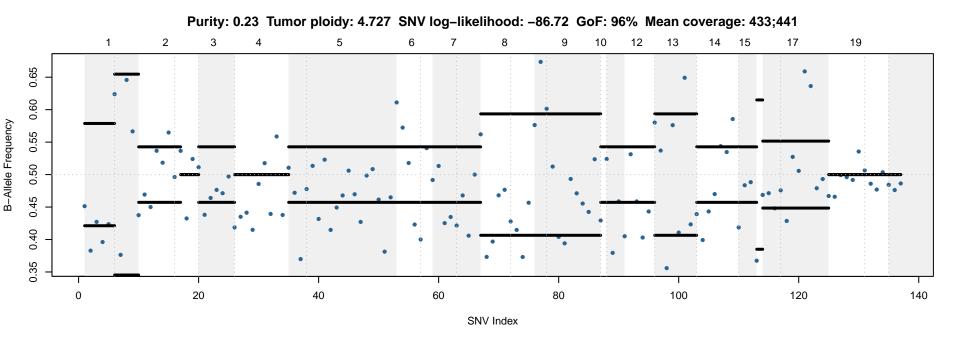
SCNA-fit log-likelihood: -8934.82



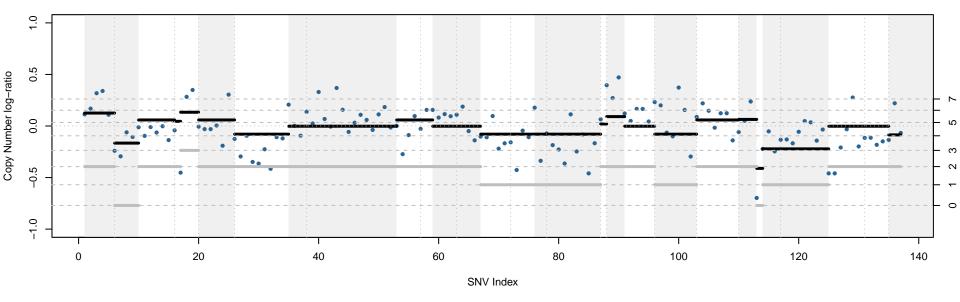


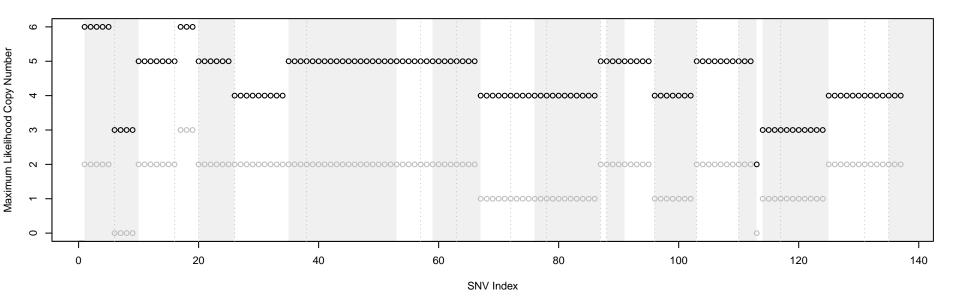


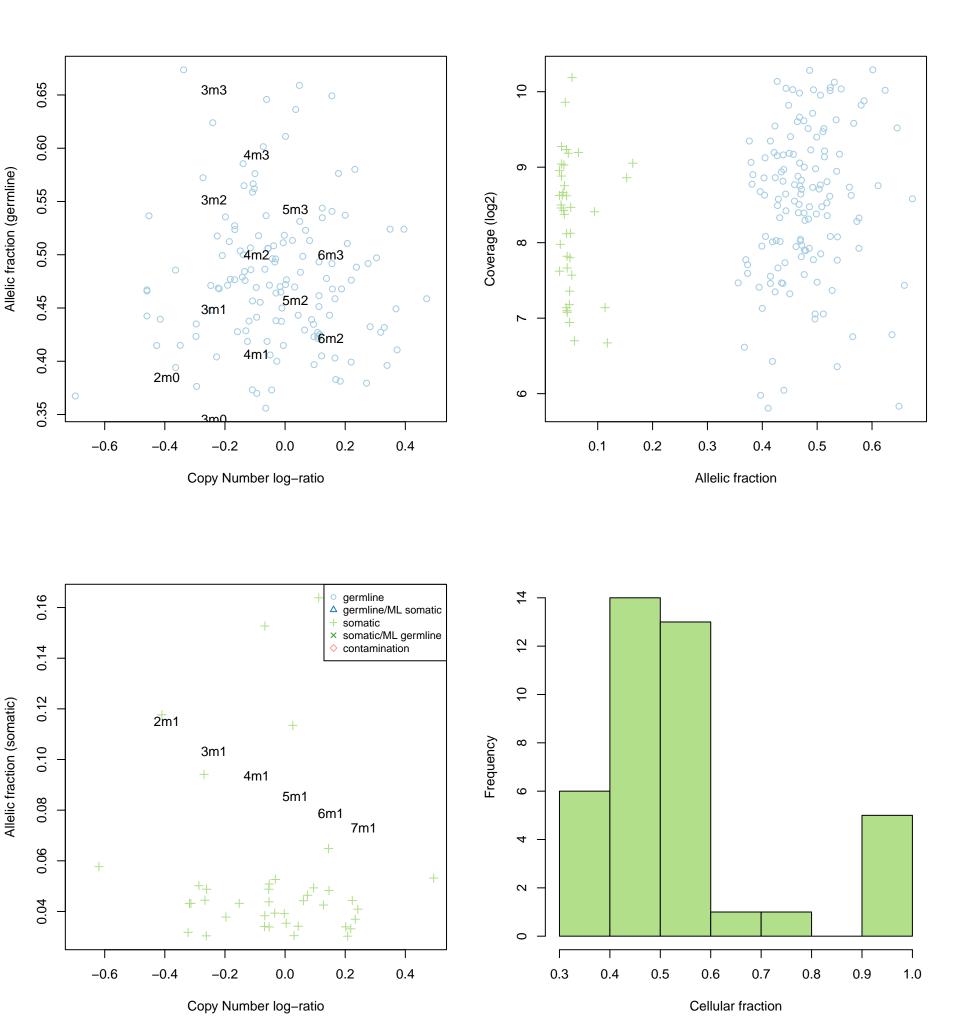
Purity: 0.23 Tumor ploidy: 4.727 0 2 3 6 5 0.25 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



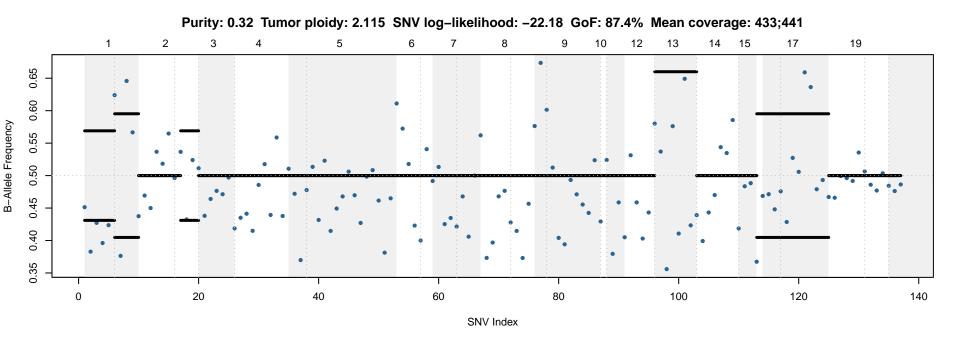
SCNA-fit log-likelihood: -8766.28



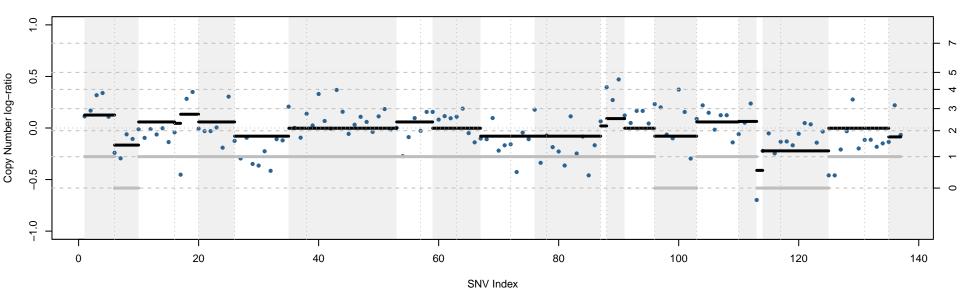


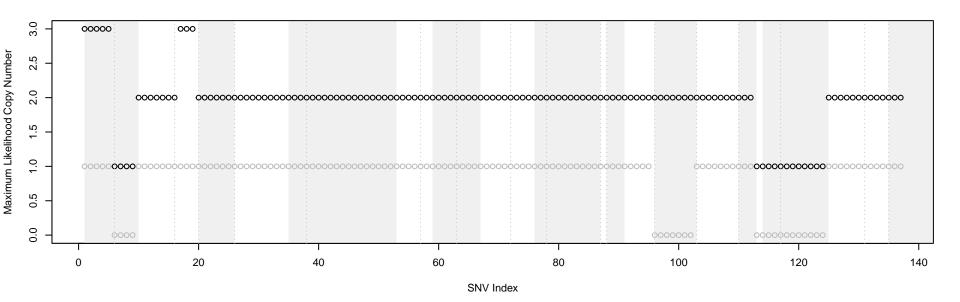


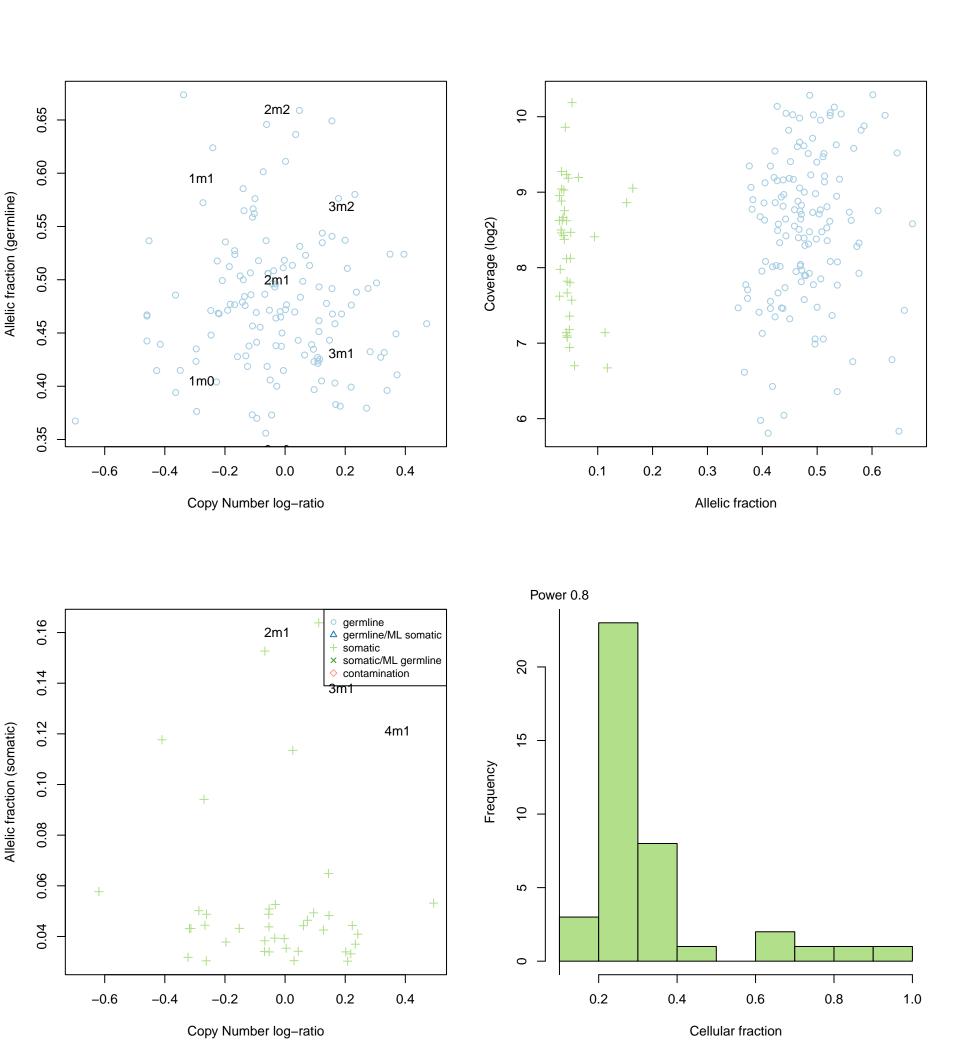
Purity: 0.32 Tumor ploidy: 2.115 3 0 2 5 7 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



SCNA-fit log-likelihood: -8973.64



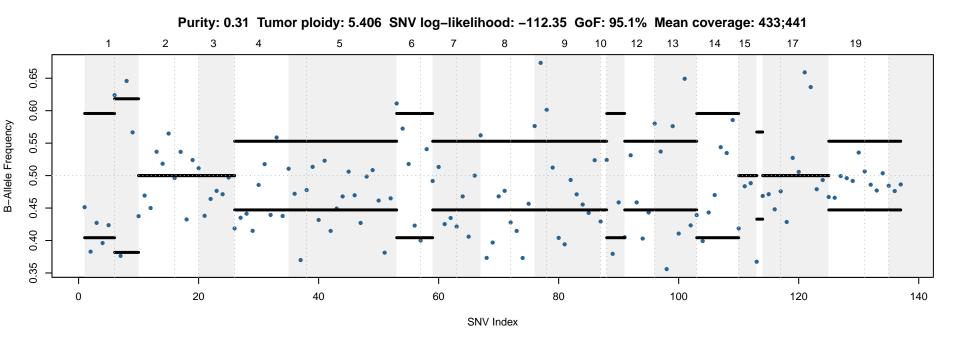




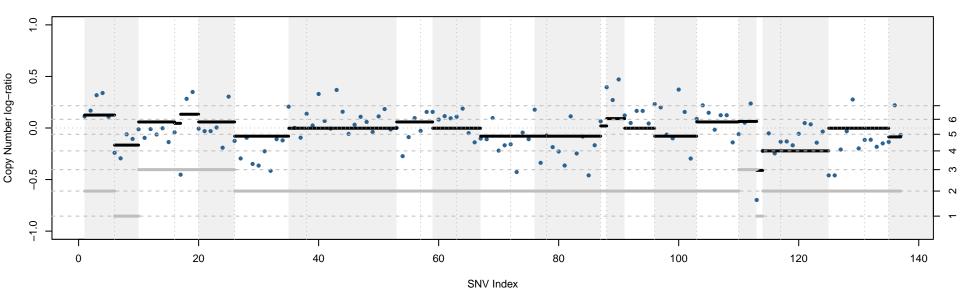
Purity: 0.31 Tumor ploidy: 5.406 3 7 2 5 6 0.25 0.20 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0

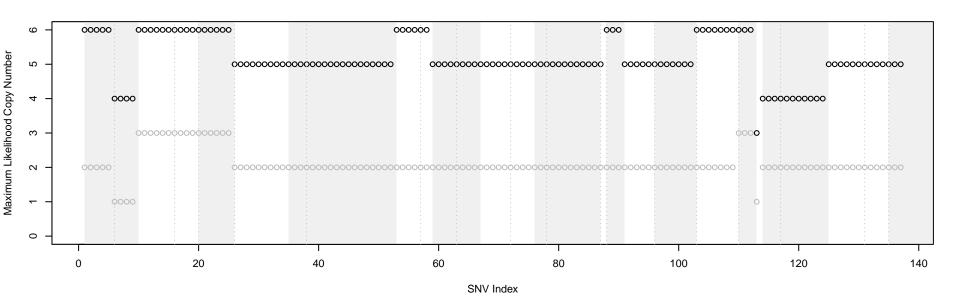
log2 ratio

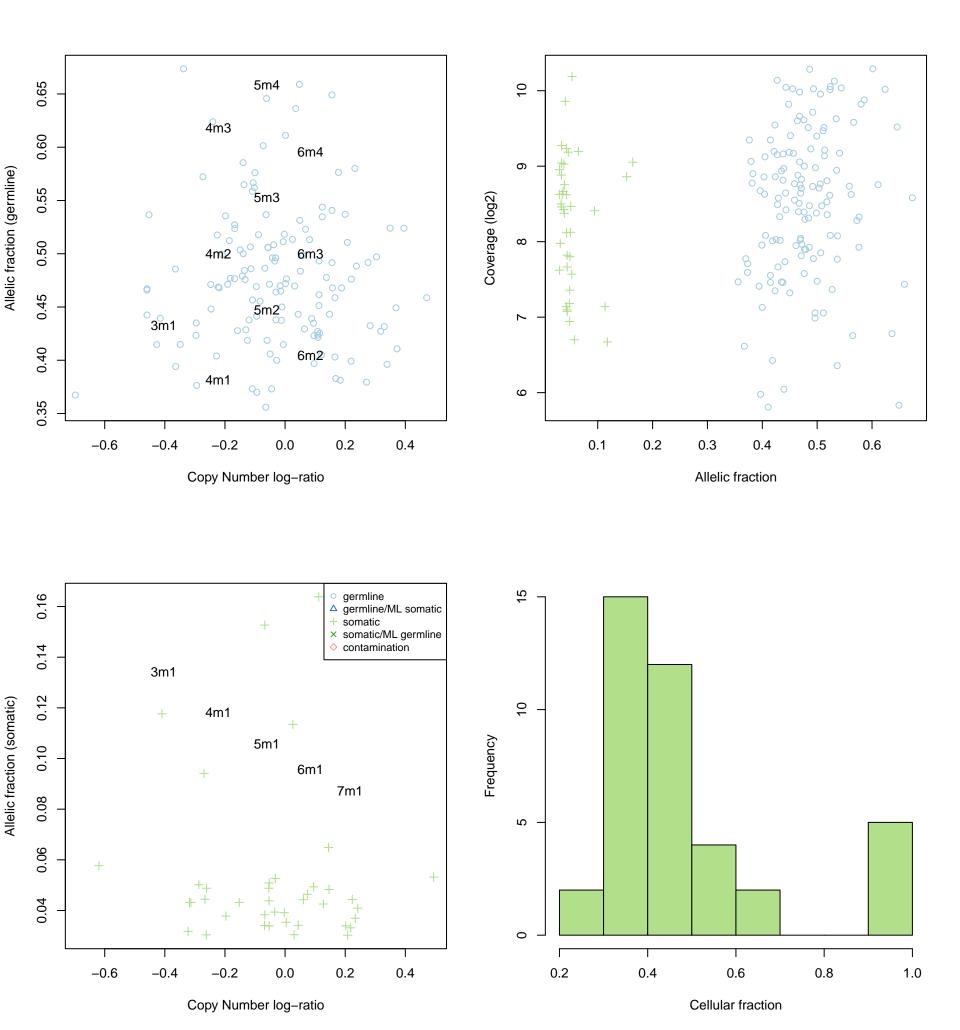
Fraction Genome



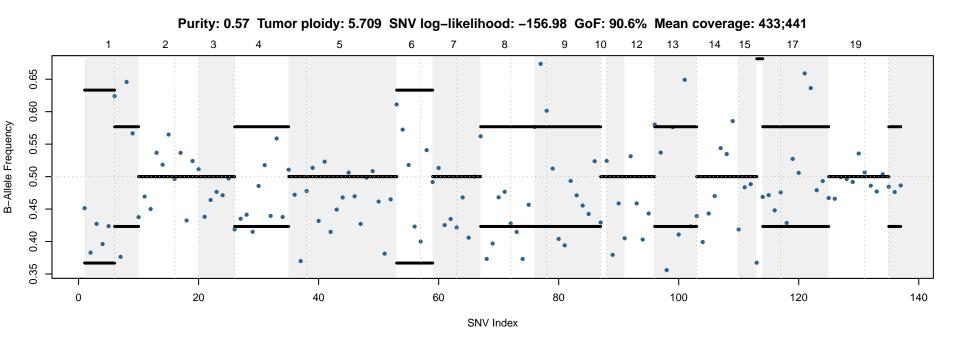
SCNA-fit log-likelihood: -8824.95



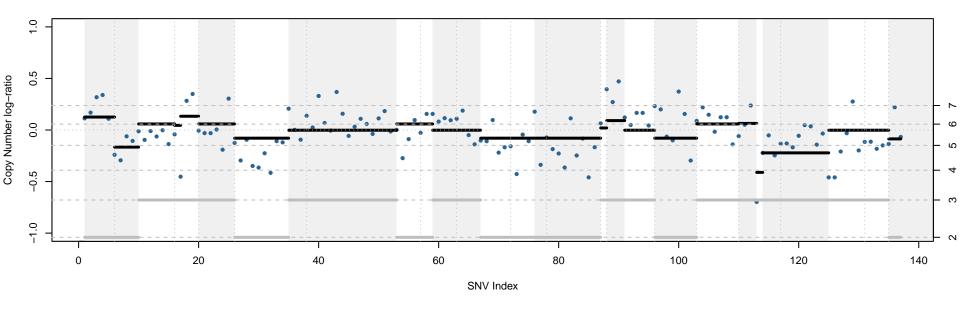


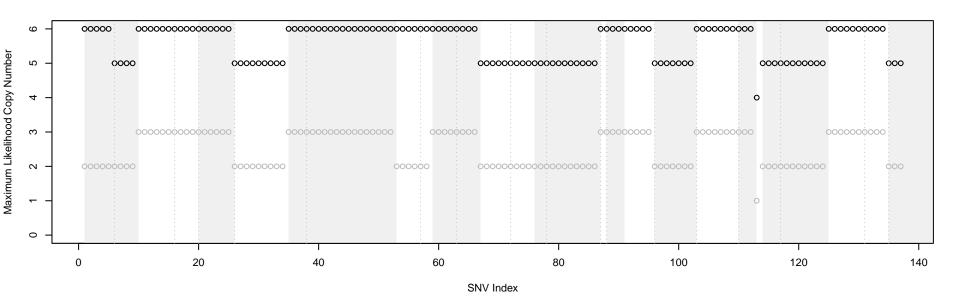


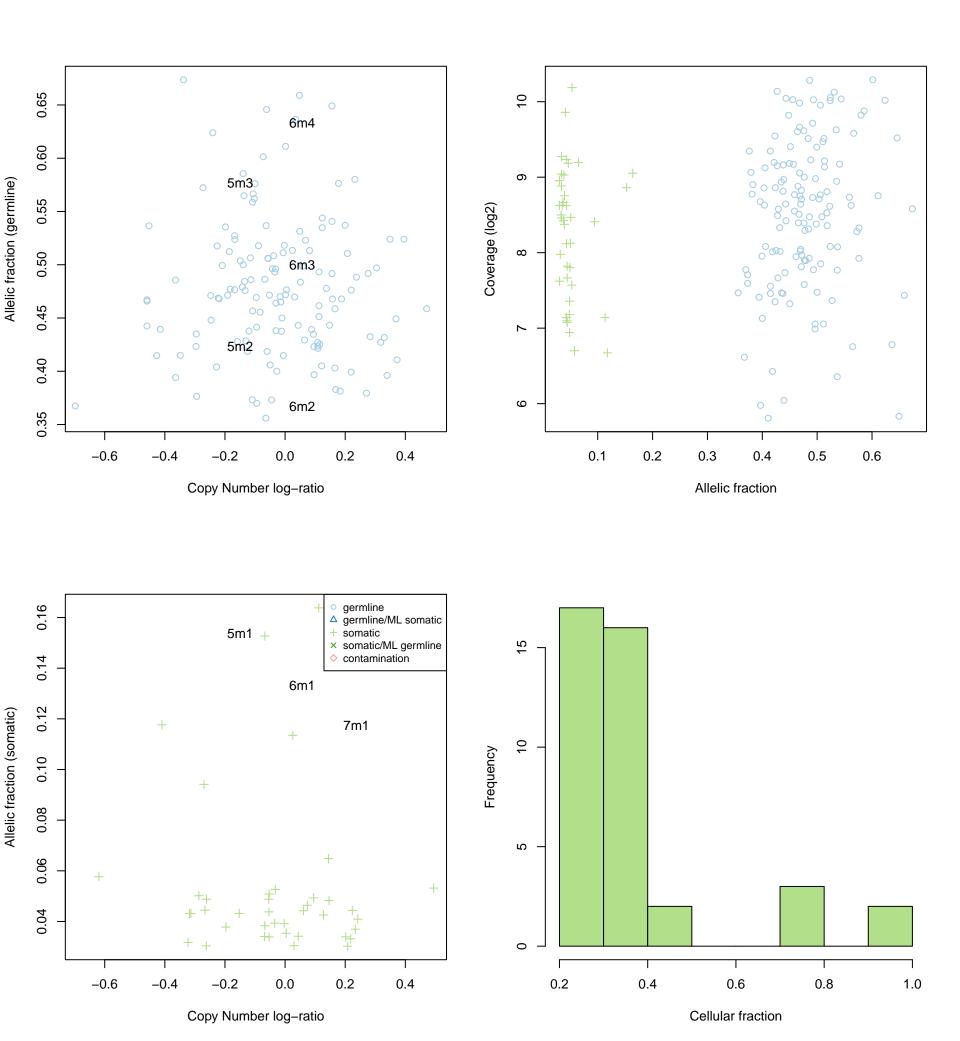
Purity: 0.57 Tumor ploidy: 5.709 6 3 5 7 4 0.25 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



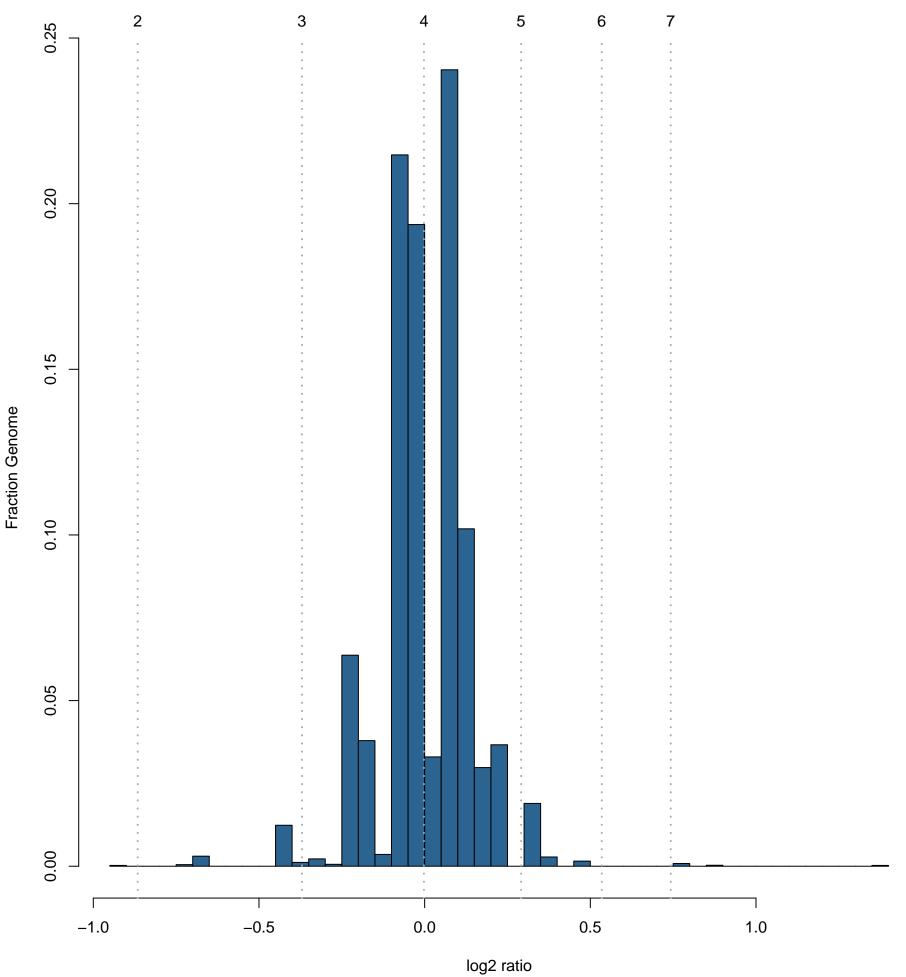
SCNA-fit log-likelihood: -8920.27

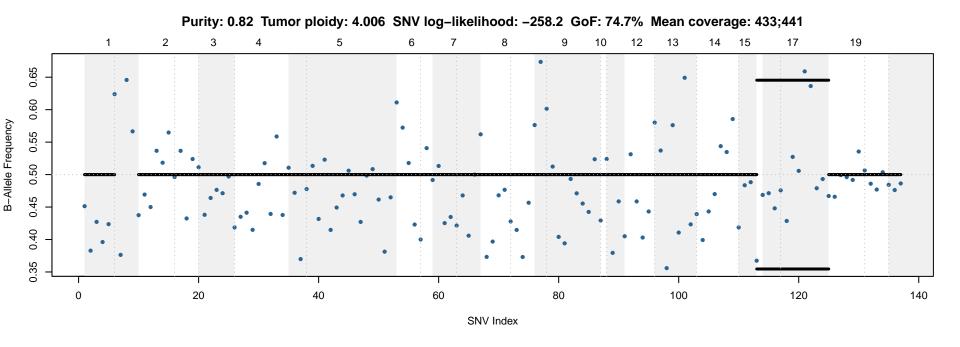




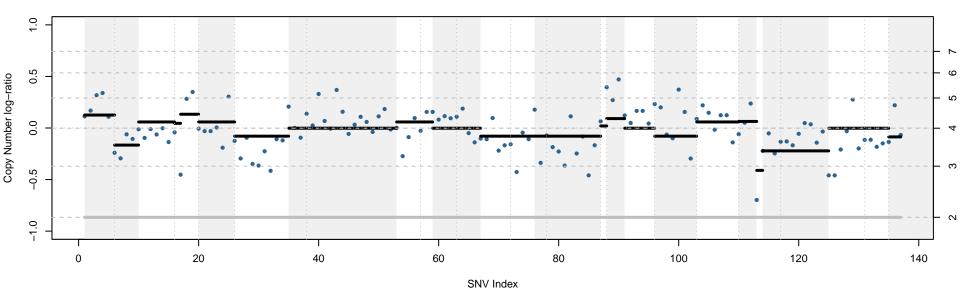


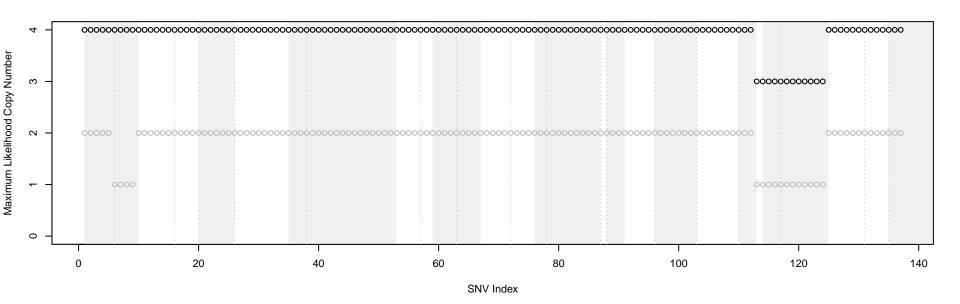
Purity: 0.82 Tumor ploidy: 4.006

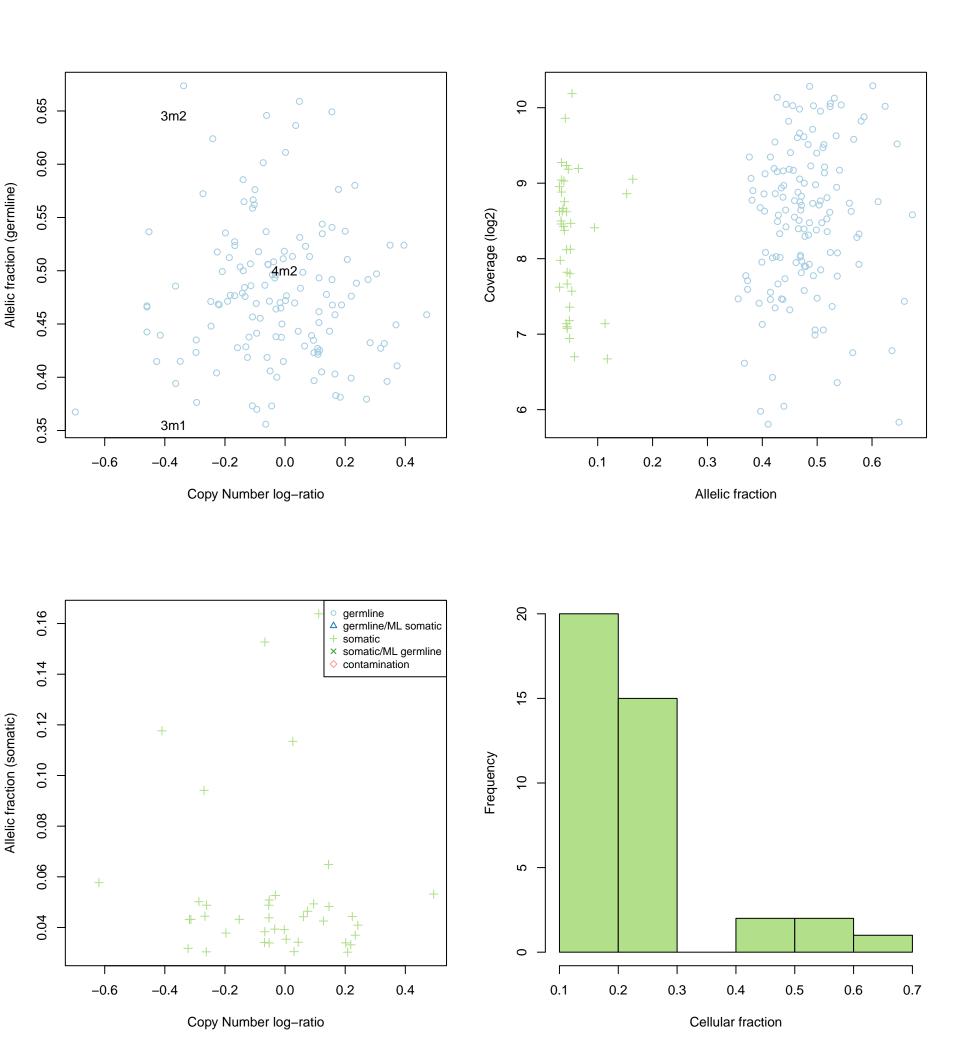




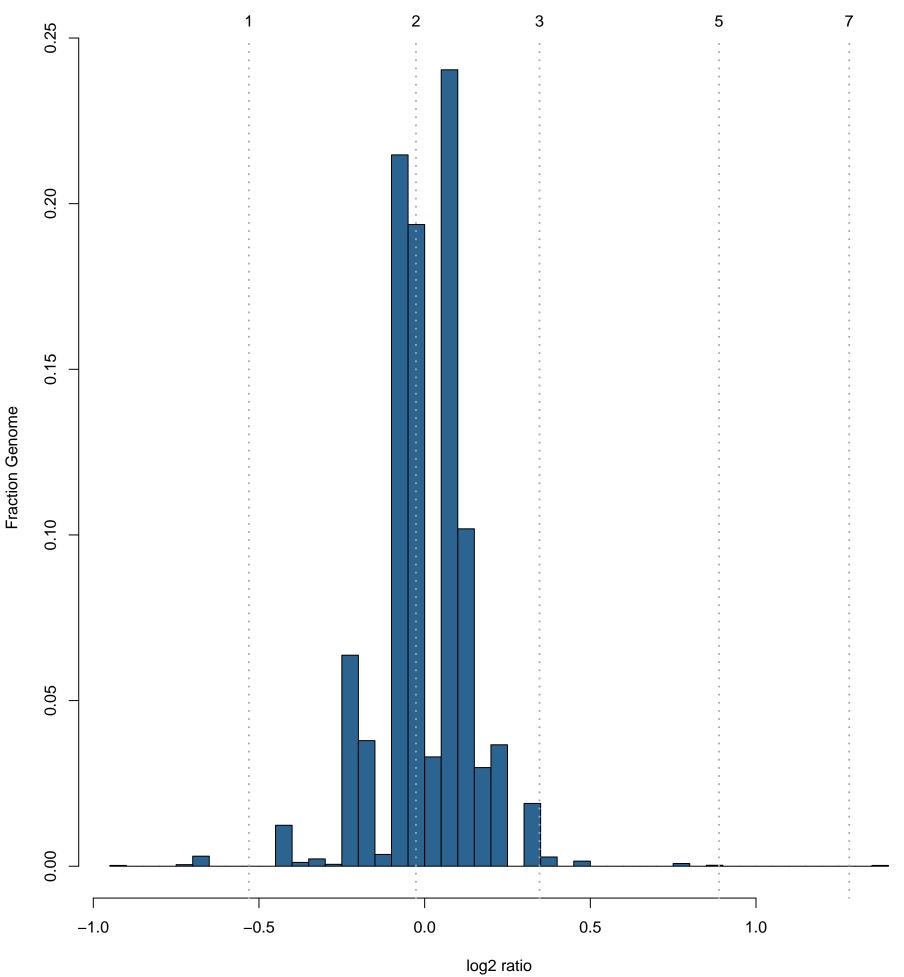
SCNA-fit log-likelihood: -9200.45

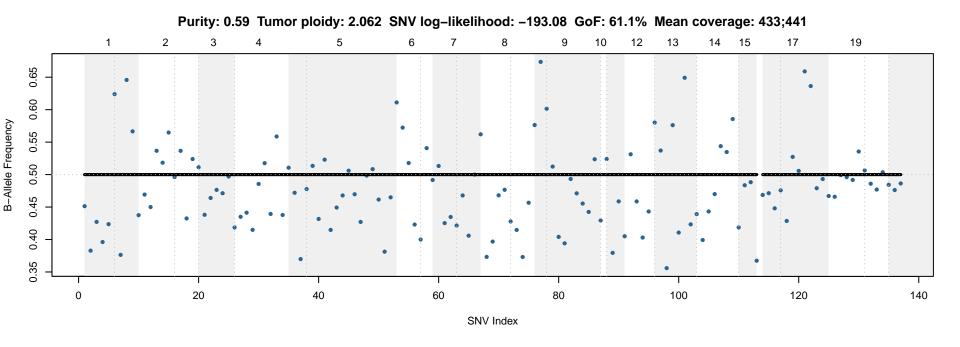




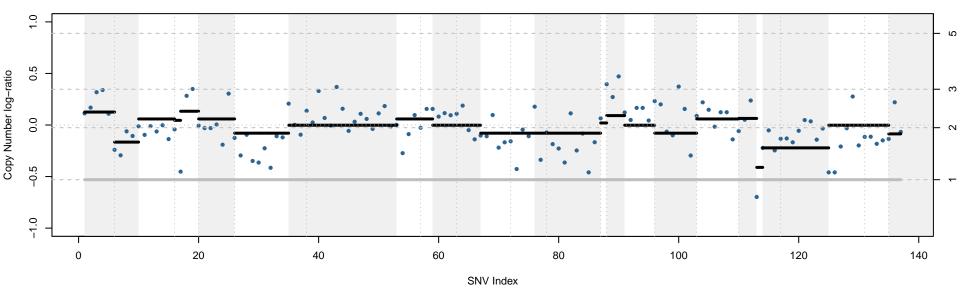


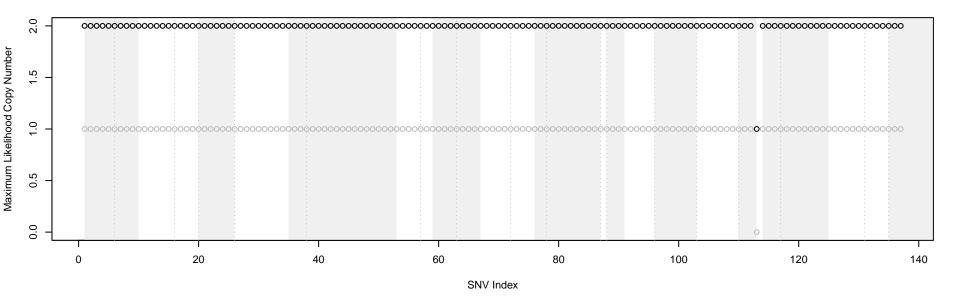
Purity: 0.59 Tumor ploidy: 2.062

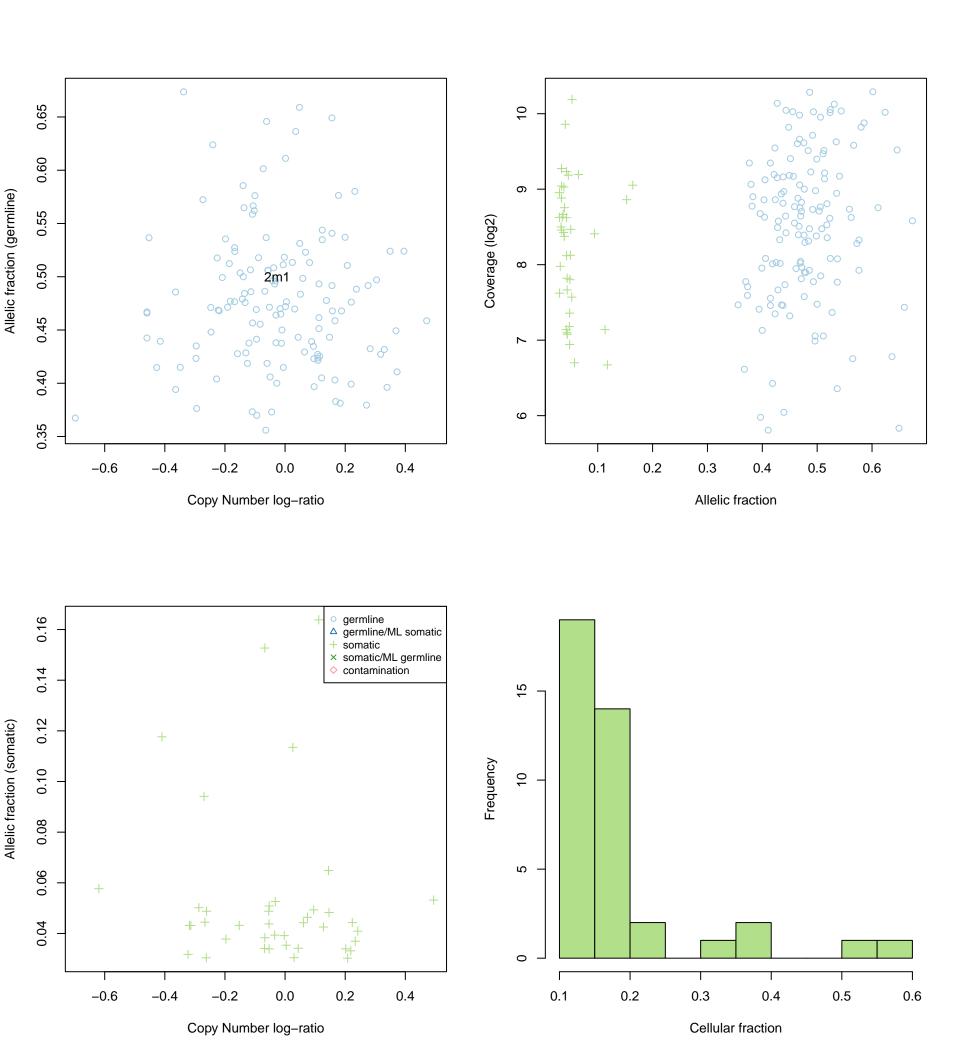


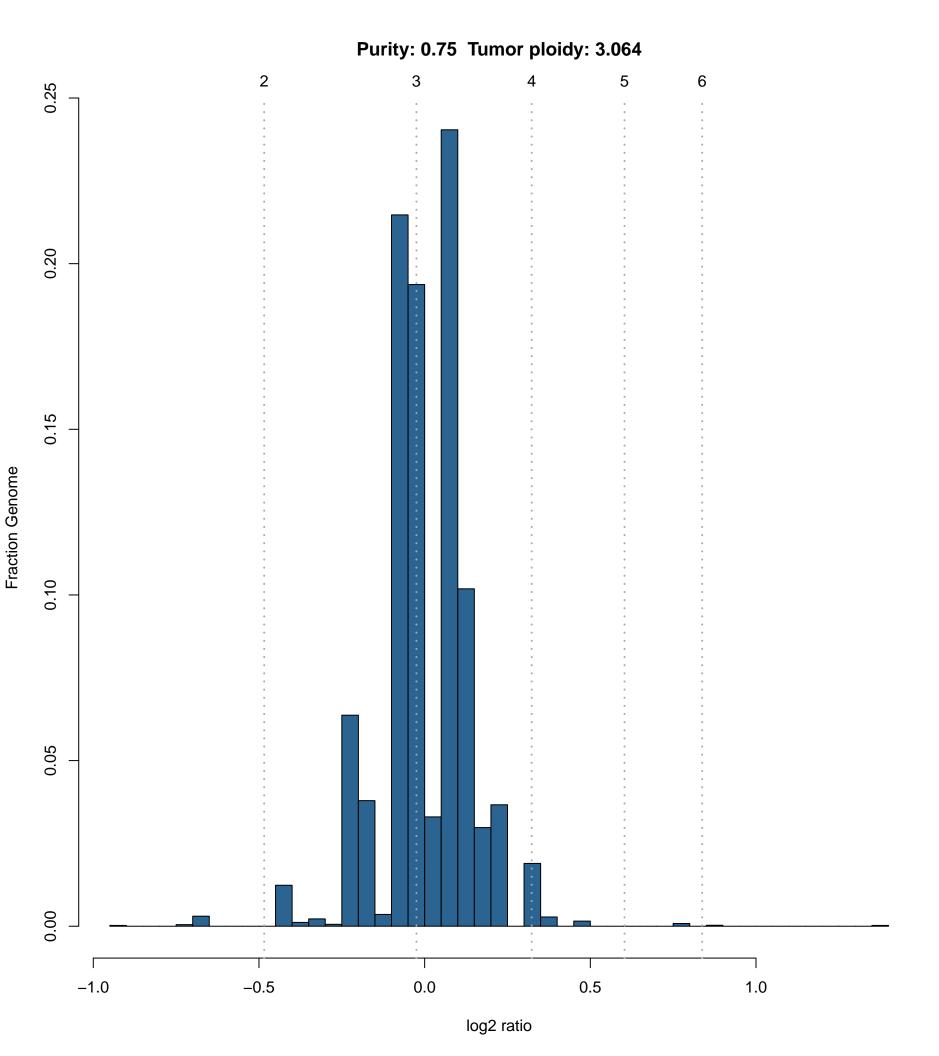


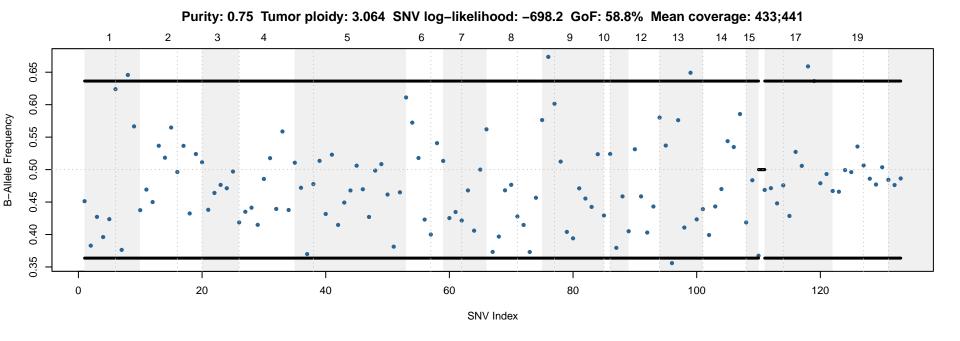
SCNA-fit log-likelihood: -9407.67











SCNA-fit log-likelihood: -9371.8

