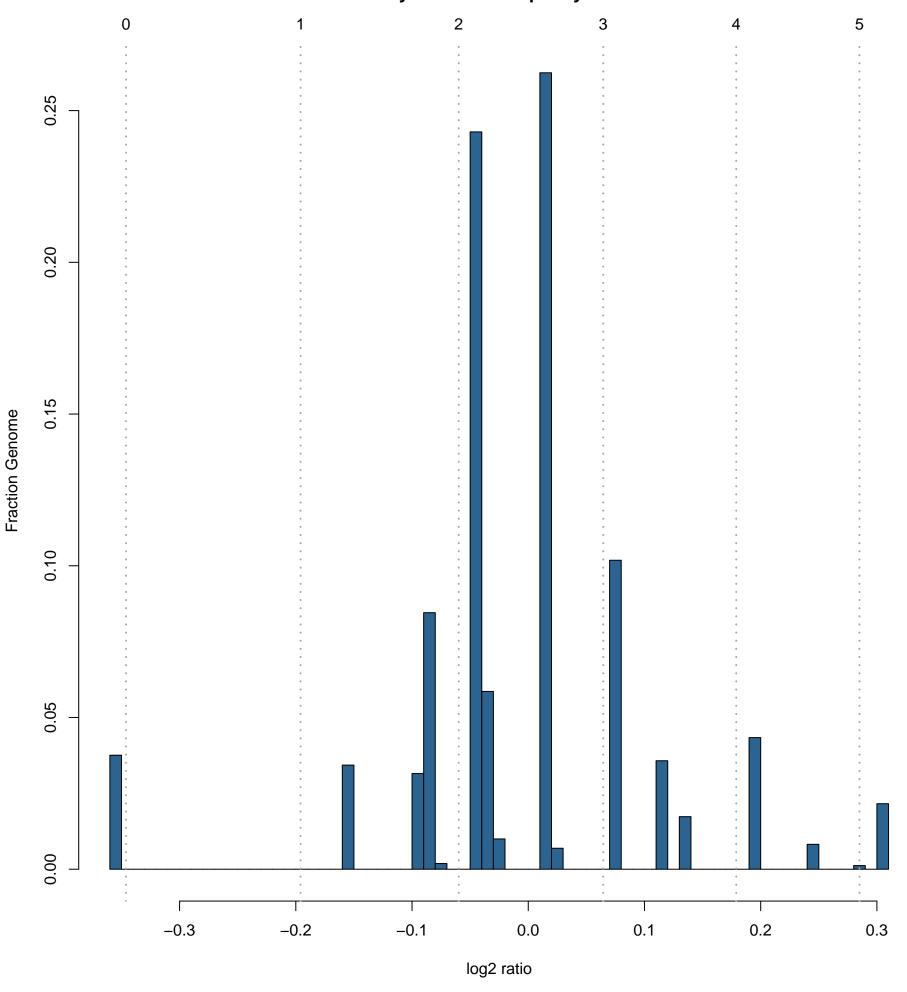
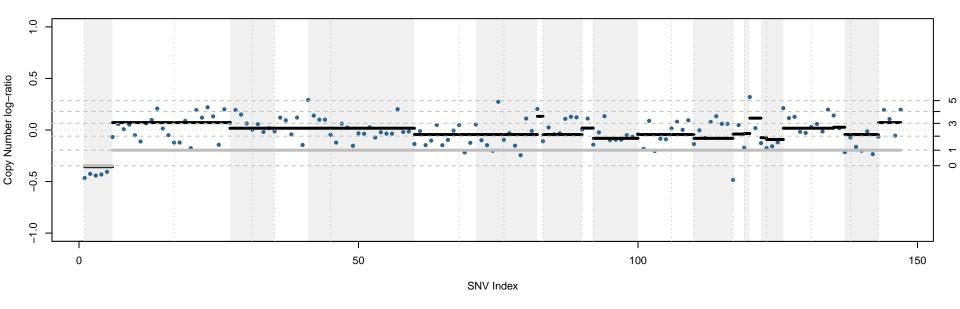
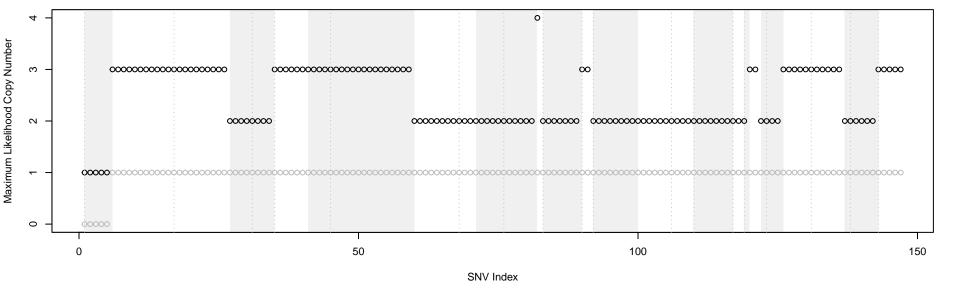
Purity: 0.18 Tumor ploidy: 2.471

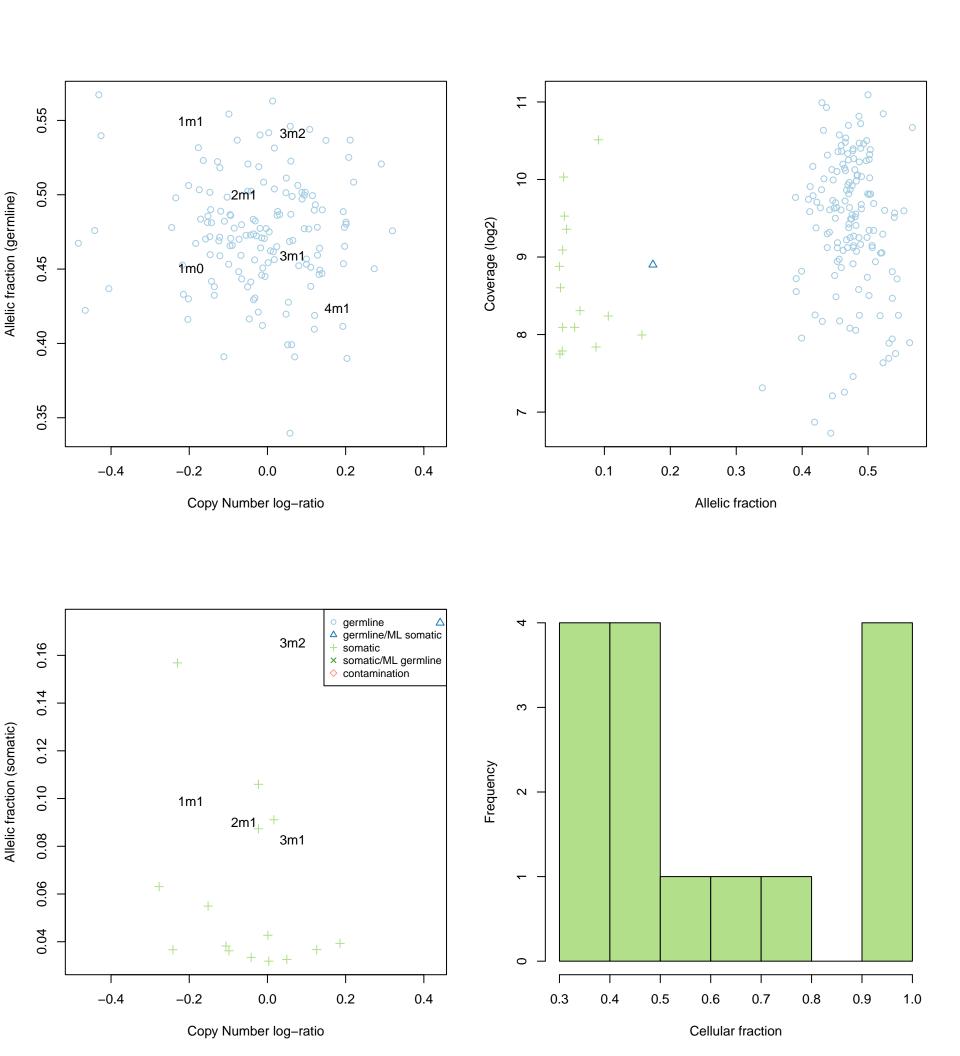


SCNA-fit log-likelihood: -9296.13

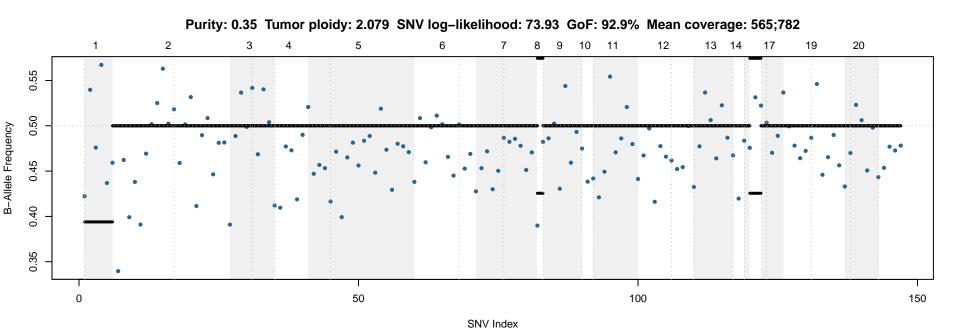
SNV Index



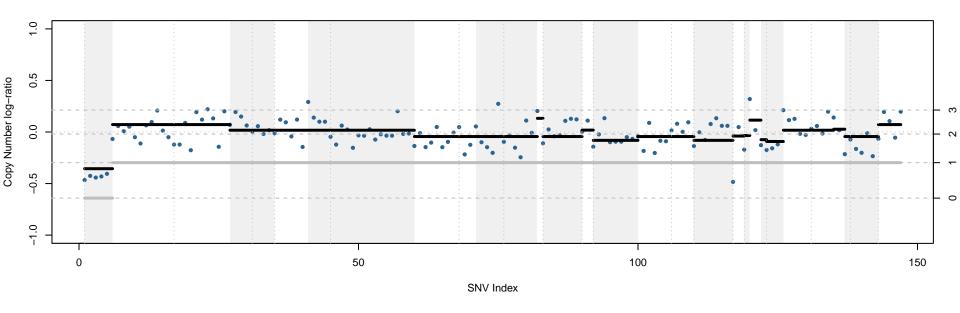


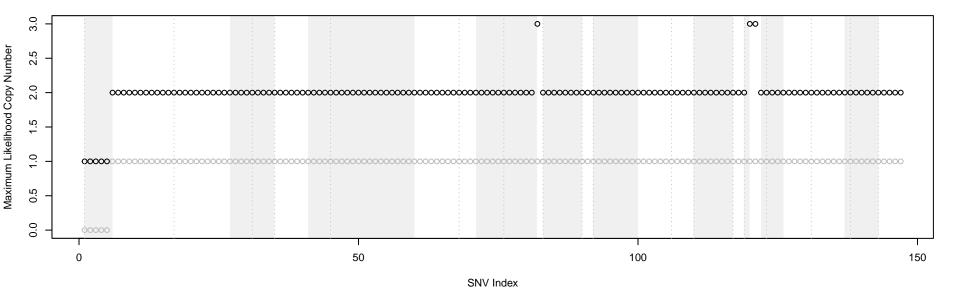


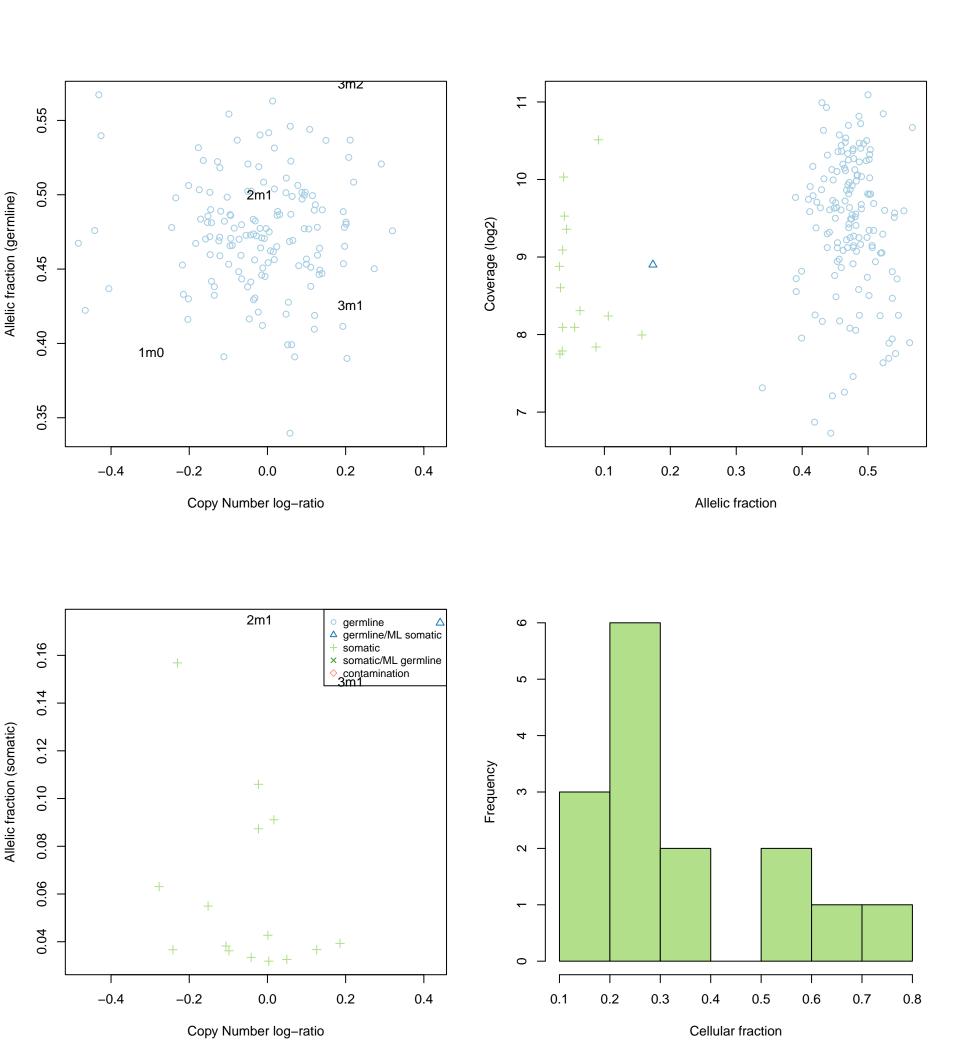
Purity: 0.35 Tumor ploidy: 2.079 2 0 3 0.20 Fraction Genome 0.05 0.00 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



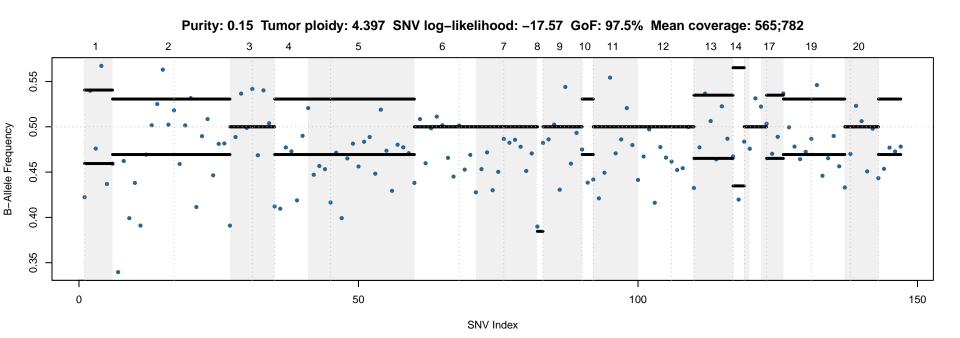
SCNA-fit log-likelihood: -9392.84



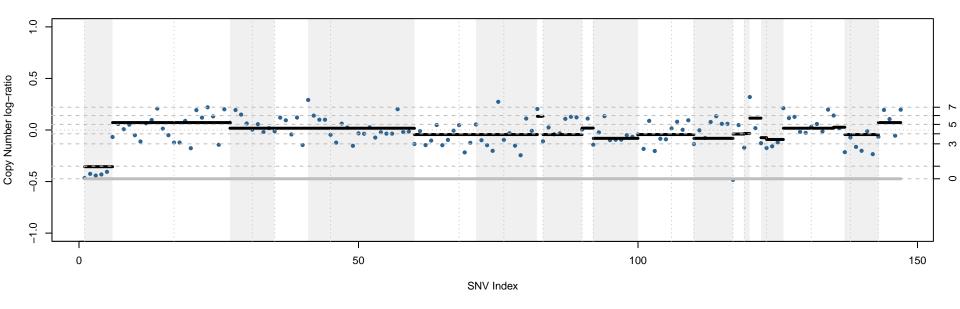


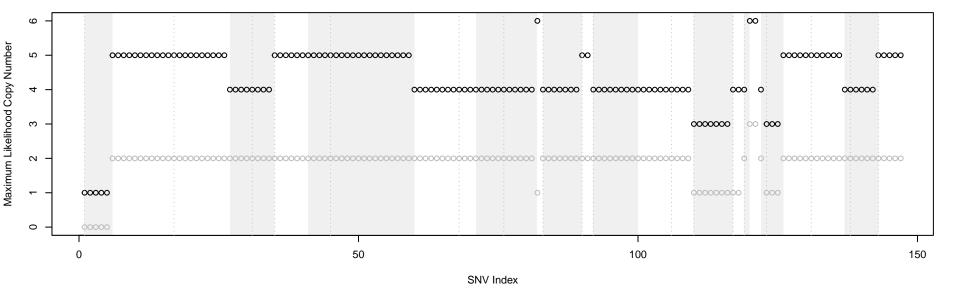


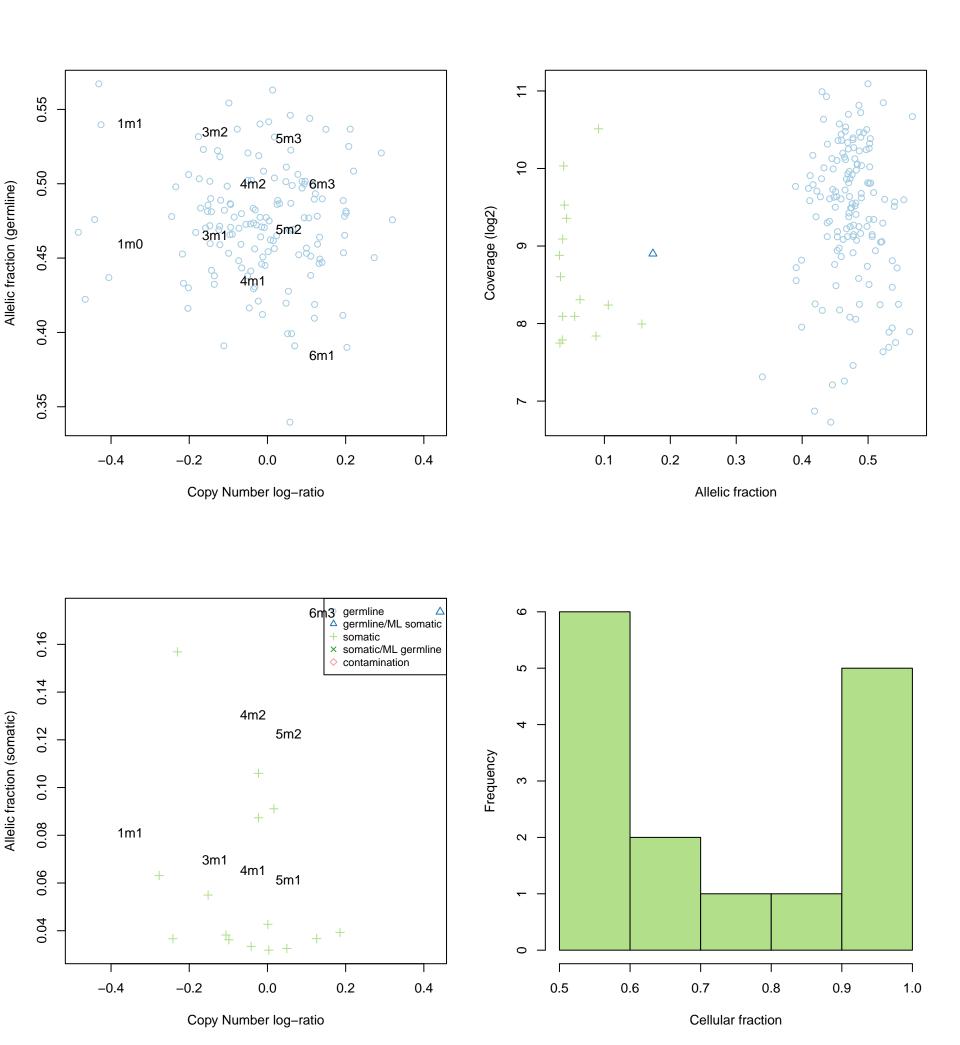
Purity: 0.15 Tumor ploidy: 4.397 0 5 6 7 Fraction Genome 0.05 0.00 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



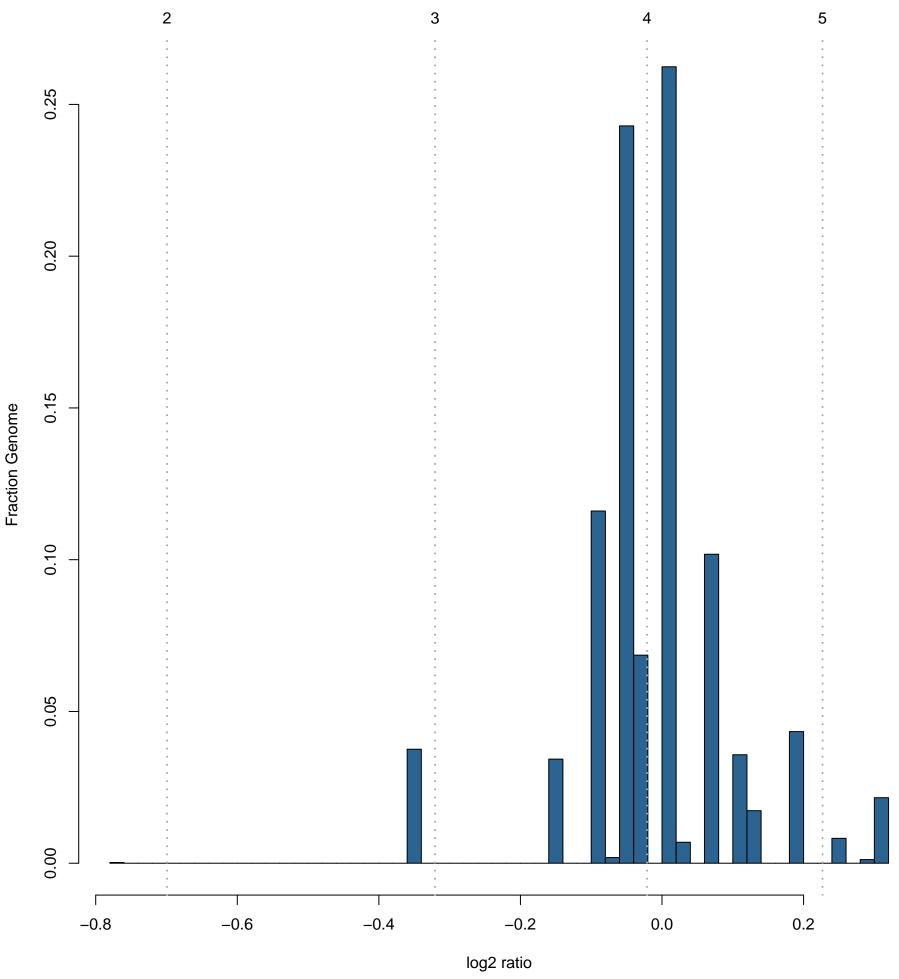
SCNA-fit log-likelihood: -9195.38

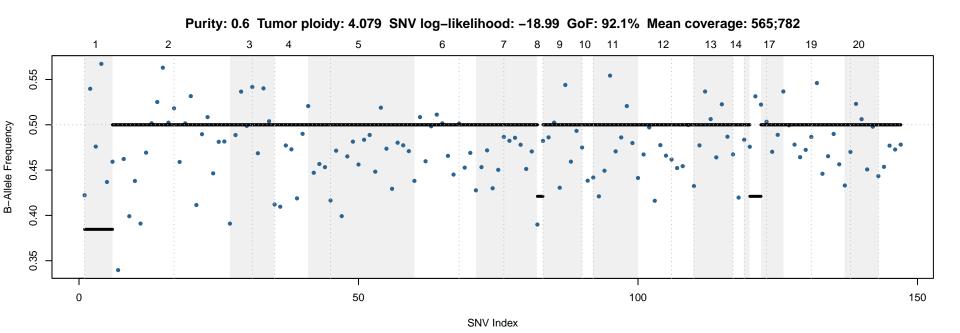




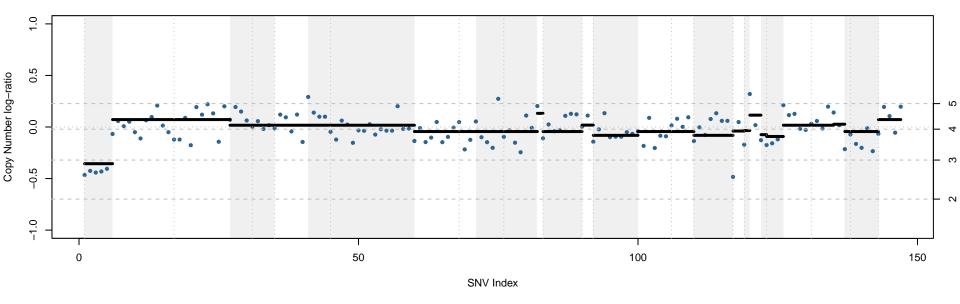


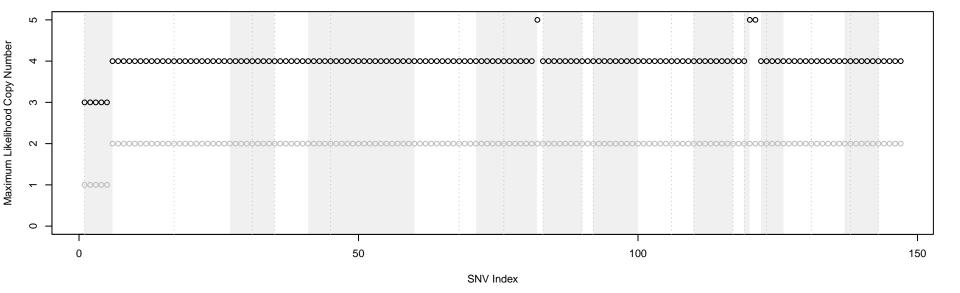
Purity: 0.6 Tumor ploidy: 4.079

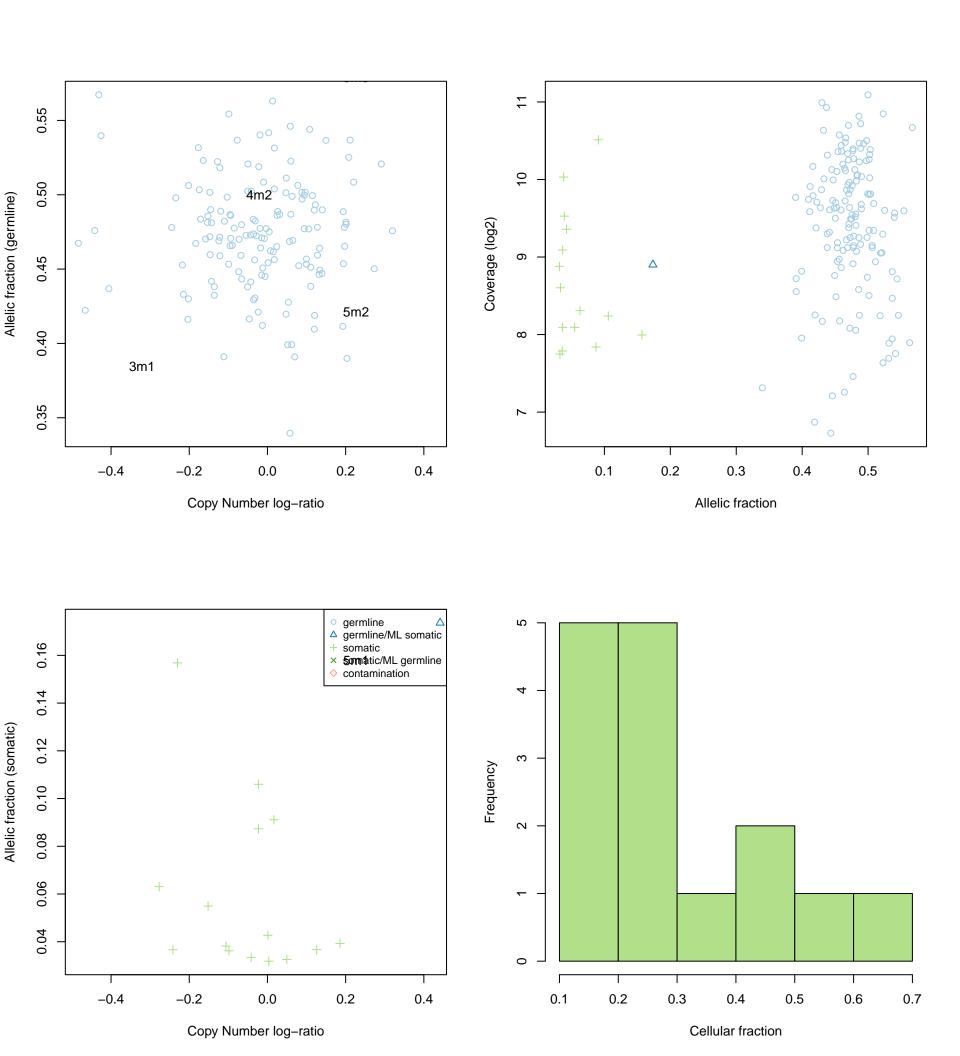




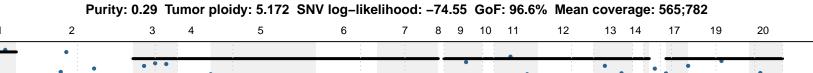
SCNA-fit log-likelihood: -9395.17

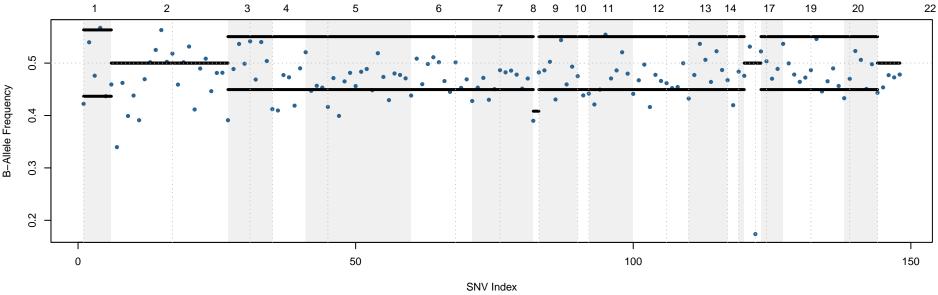




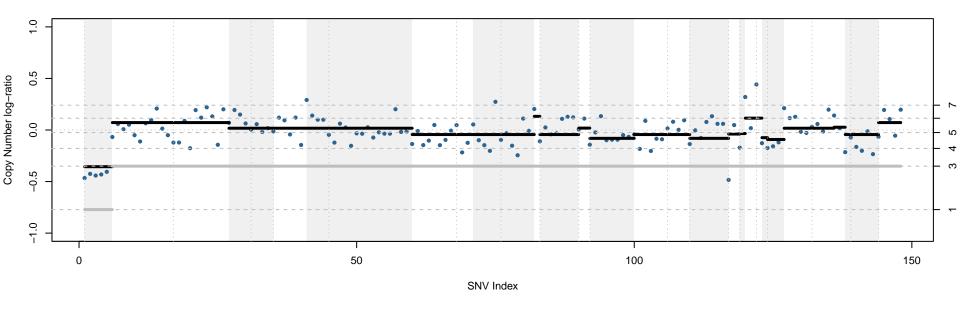


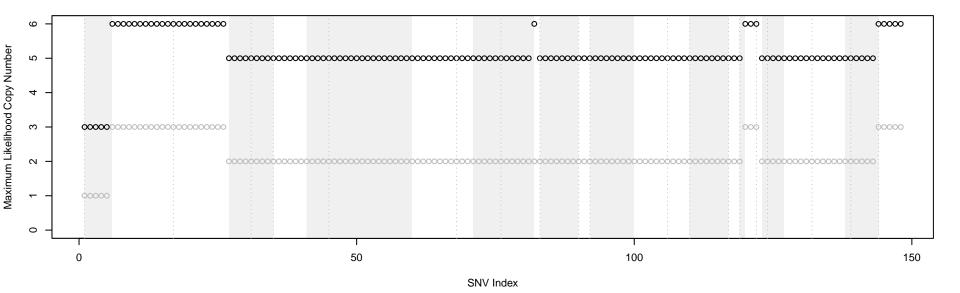
Purity: 0.29 Tumor ploidy: 5.172 6 1 5 0.25 0.20 Fraction Genome 0.05 0.00 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio

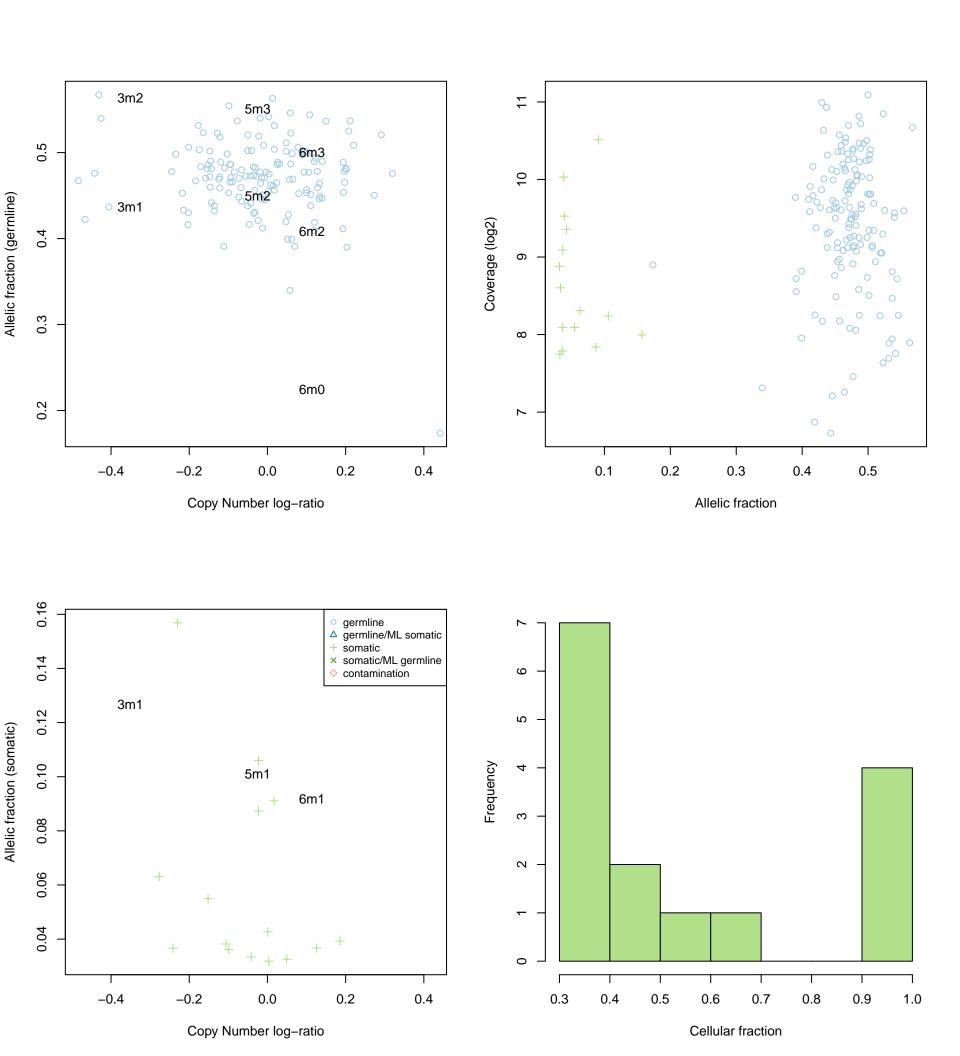




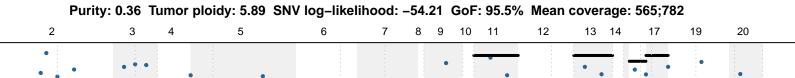
SCNA-fit log-likelihood: -9250.14

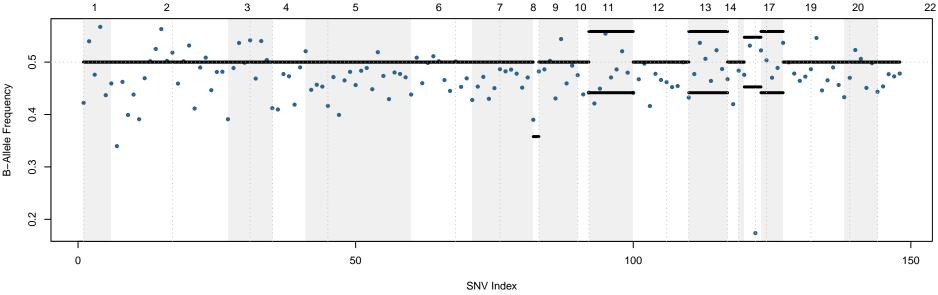




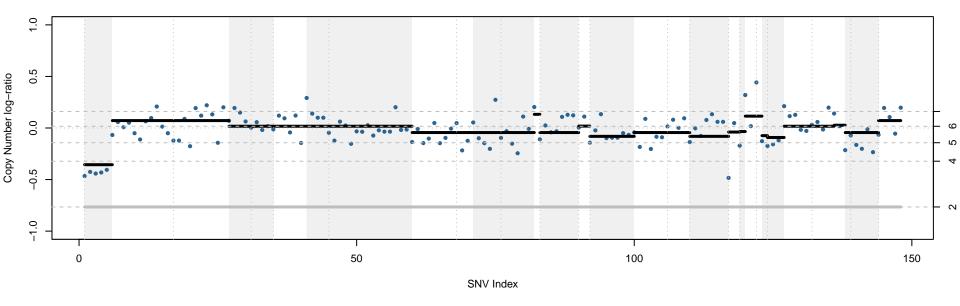


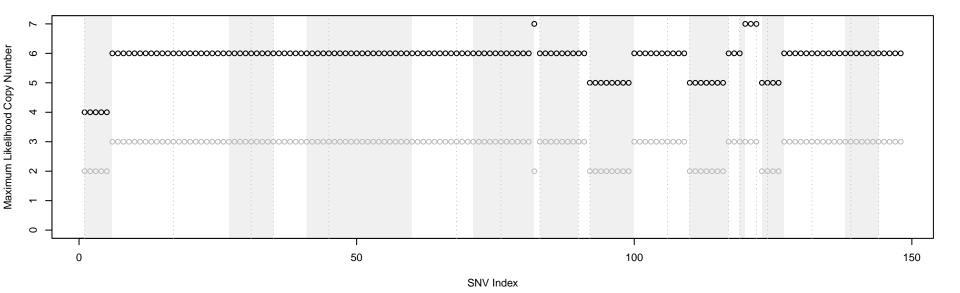
Purity: 0.36 Tumor ploidy: 5.89 2 5 6 7 0.20 Fraction Genome 0.05 0.00 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio

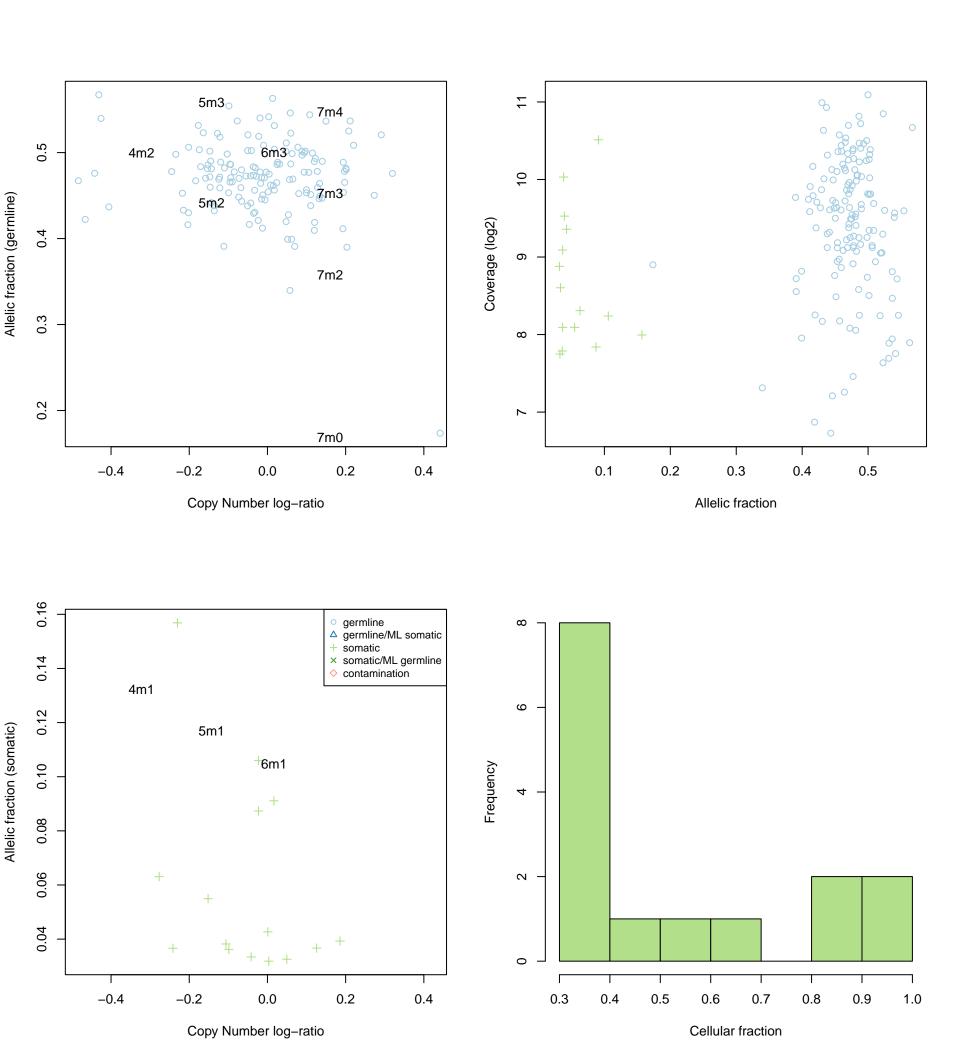




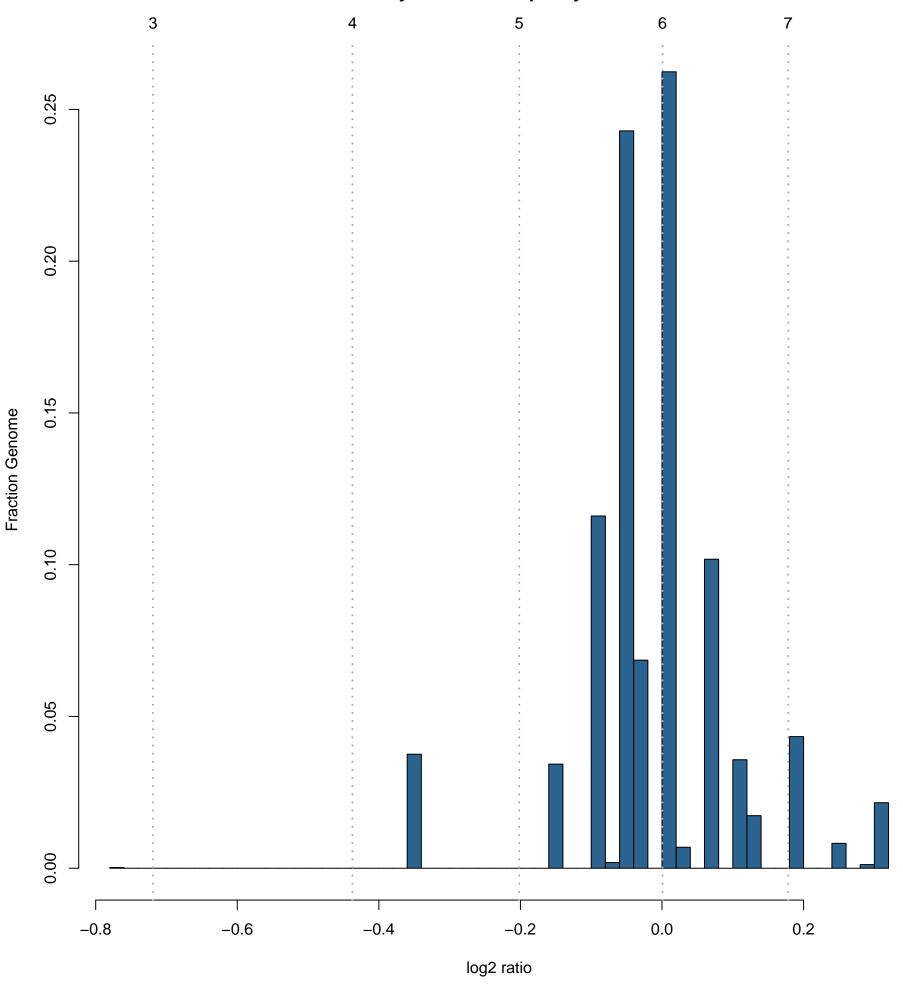
SCNA-fit log-likelihood: -9334.21

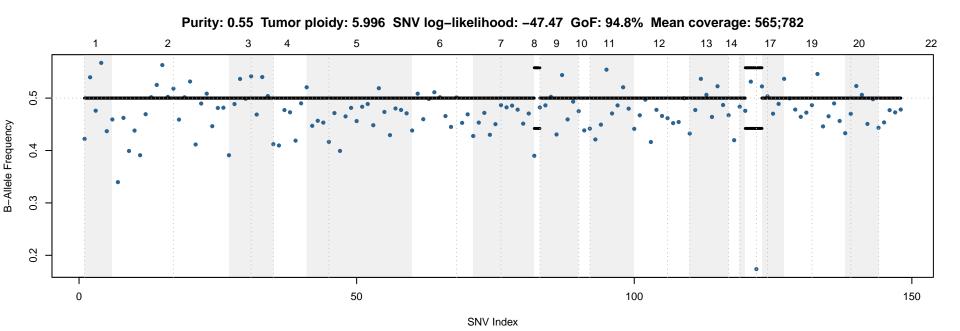




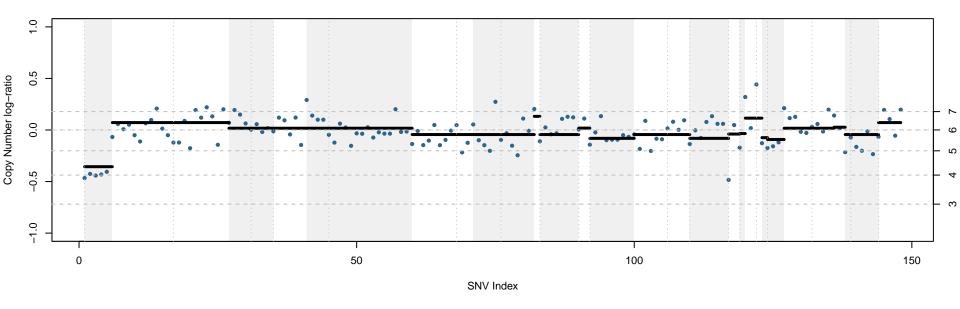


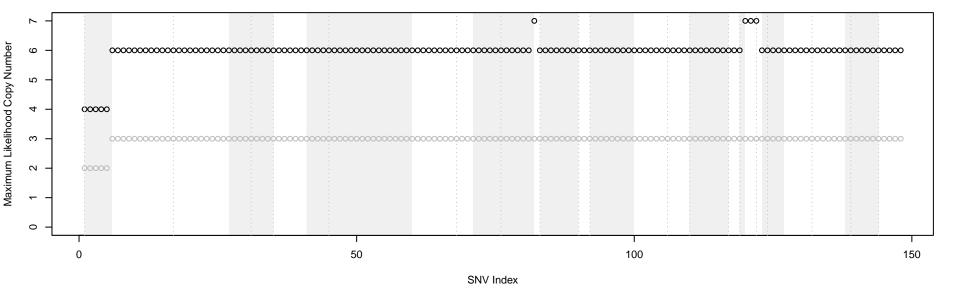
Purity: 0.55 Tumor ploidy: 5.996

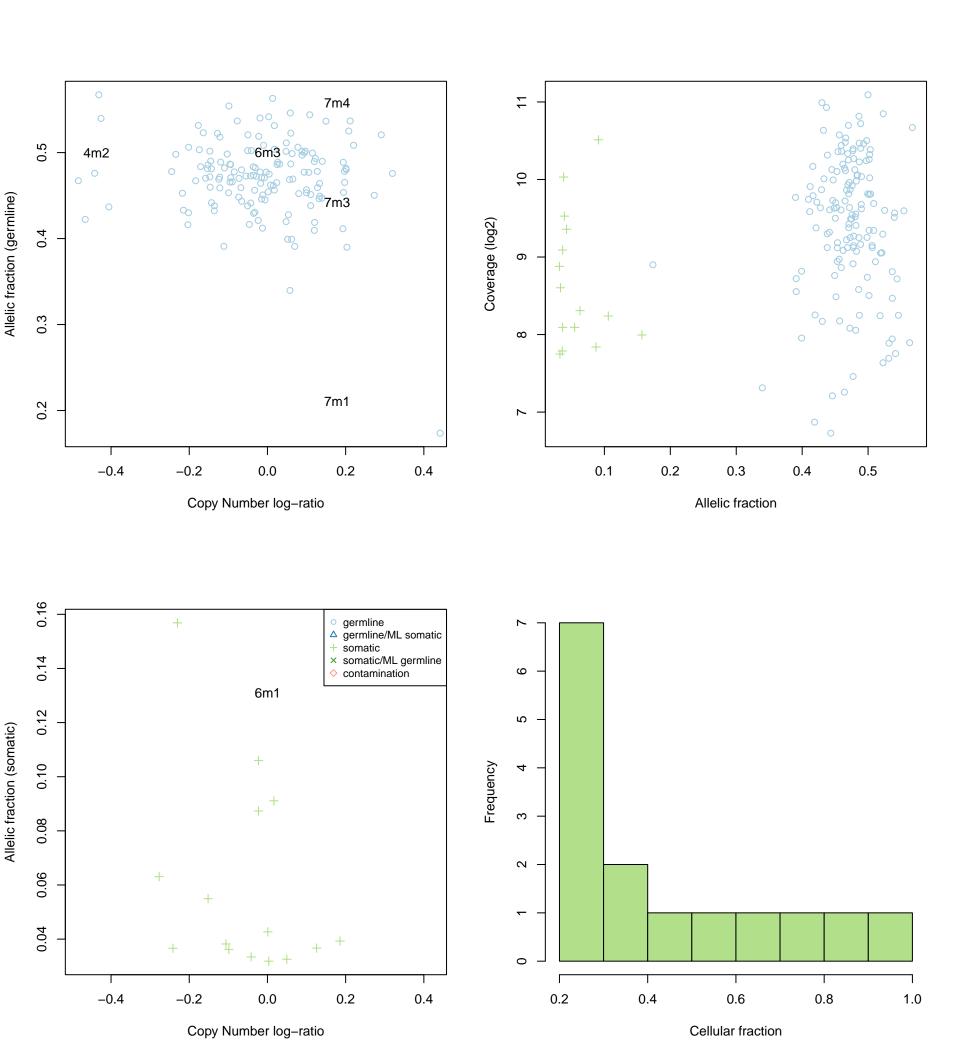




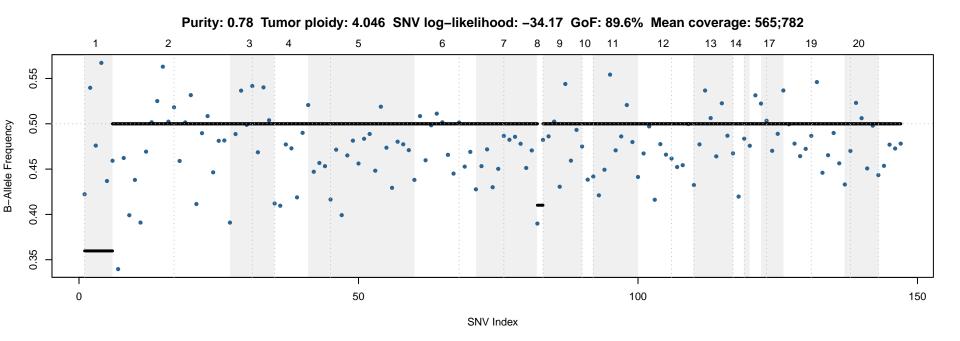
SCNA-fit log-likelihood: -9363.82



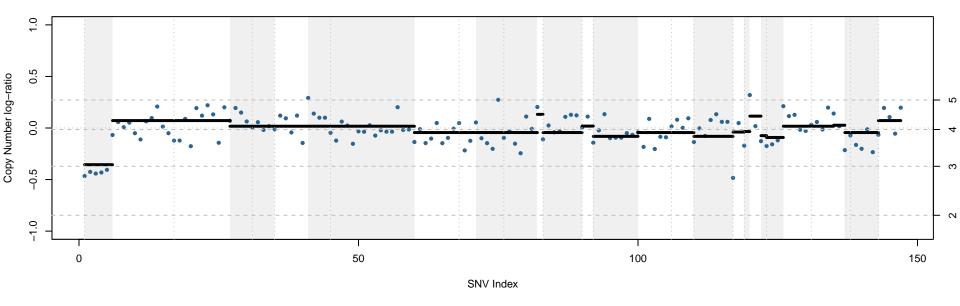


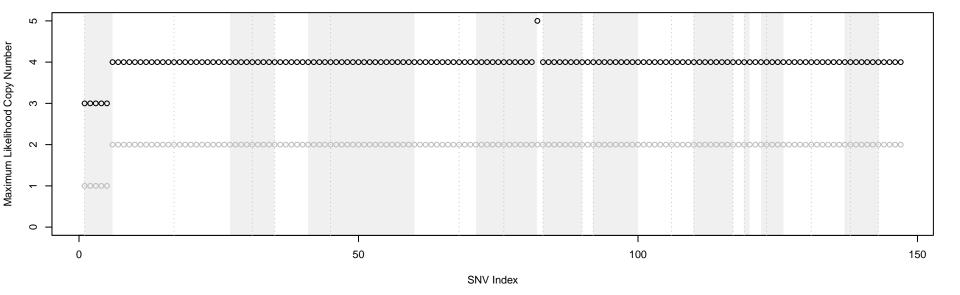


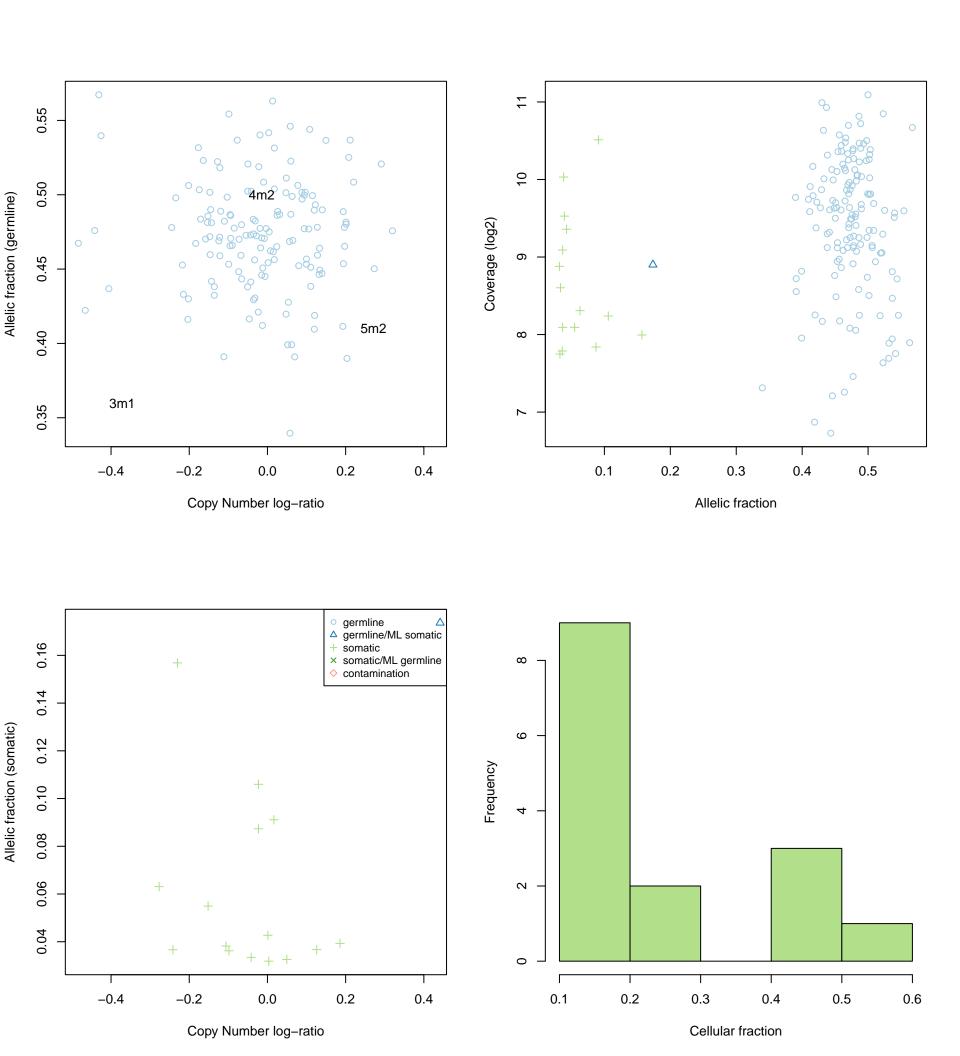
Purity: 0.78 Tumor ploidy: 4.046 3 5 0.20 Fraction Genome 0.05 0.00 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



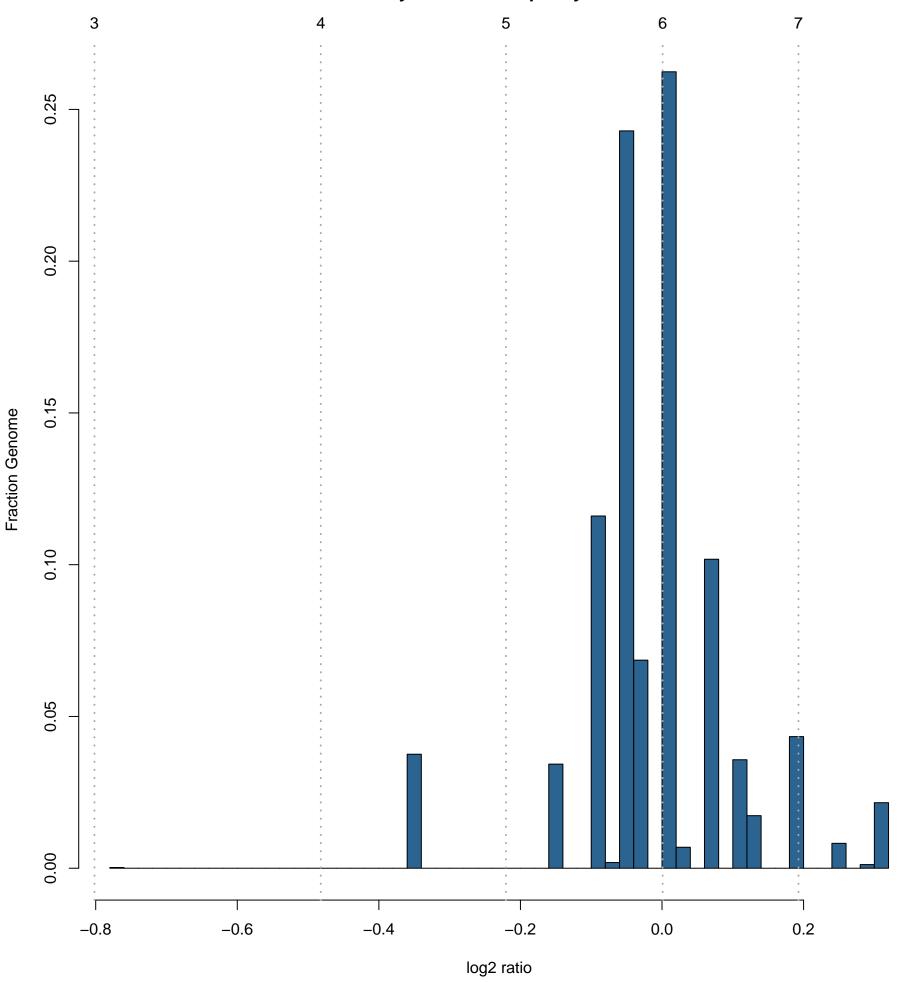
SCNA-fit log-likelihood: -9428.95

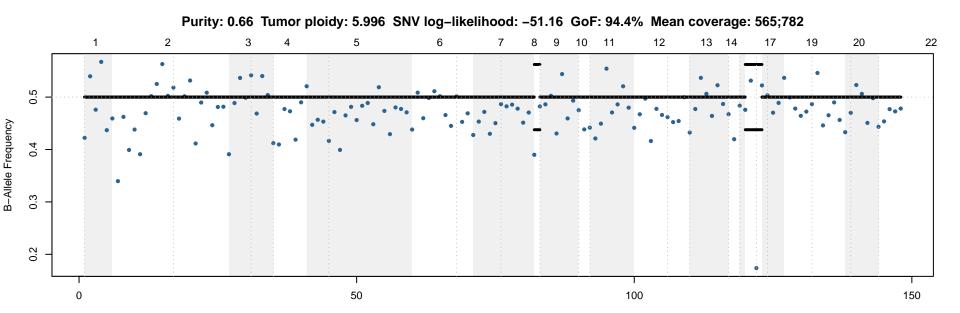






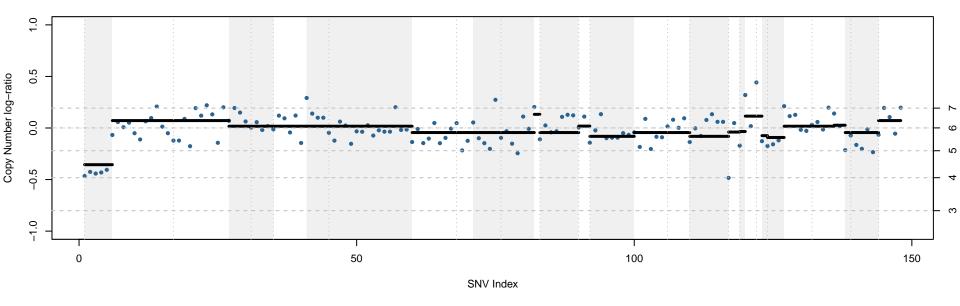
Purity: 0.66 Tumor ploidy: 5.996

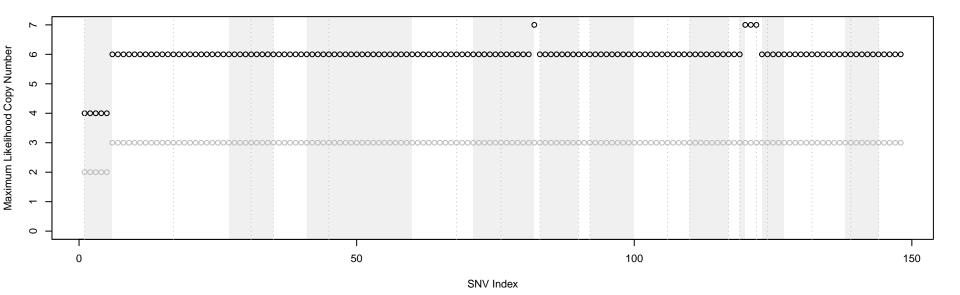


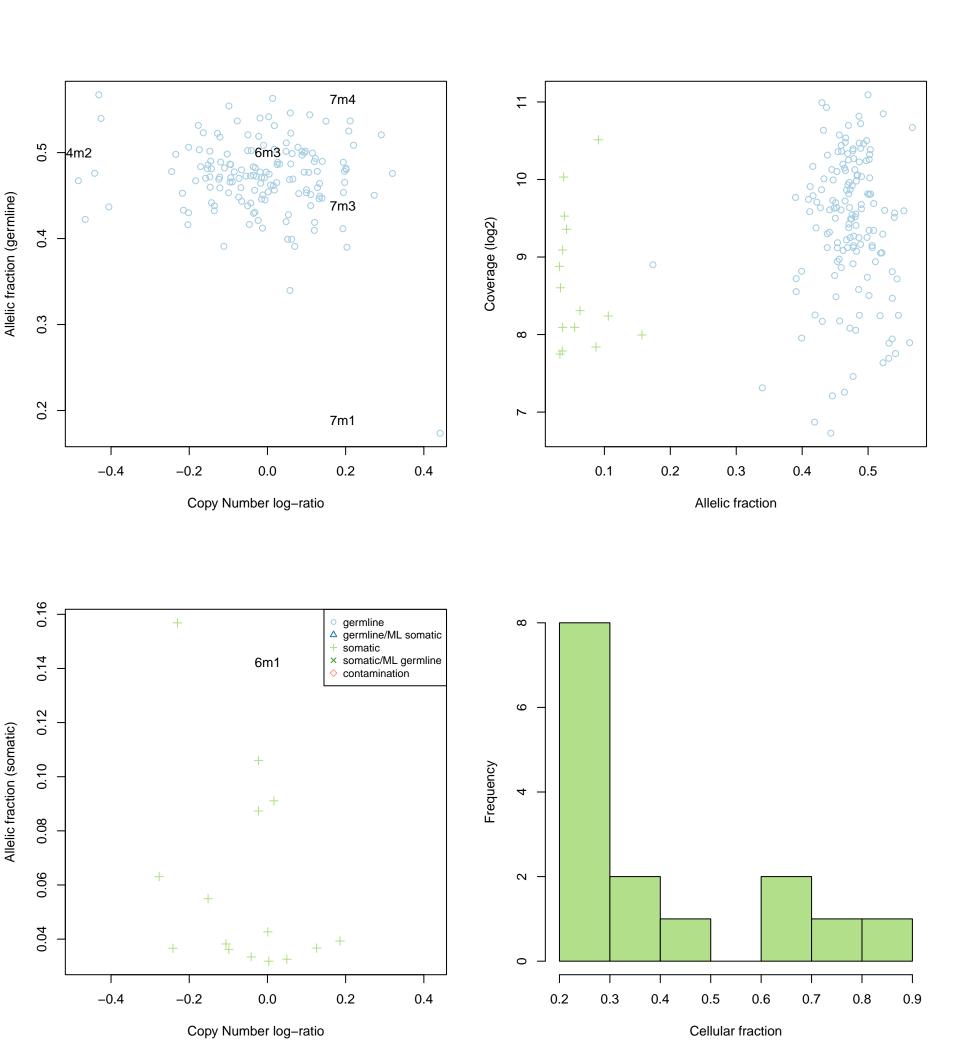


SCNA-fit log-likelihood: -9394.77

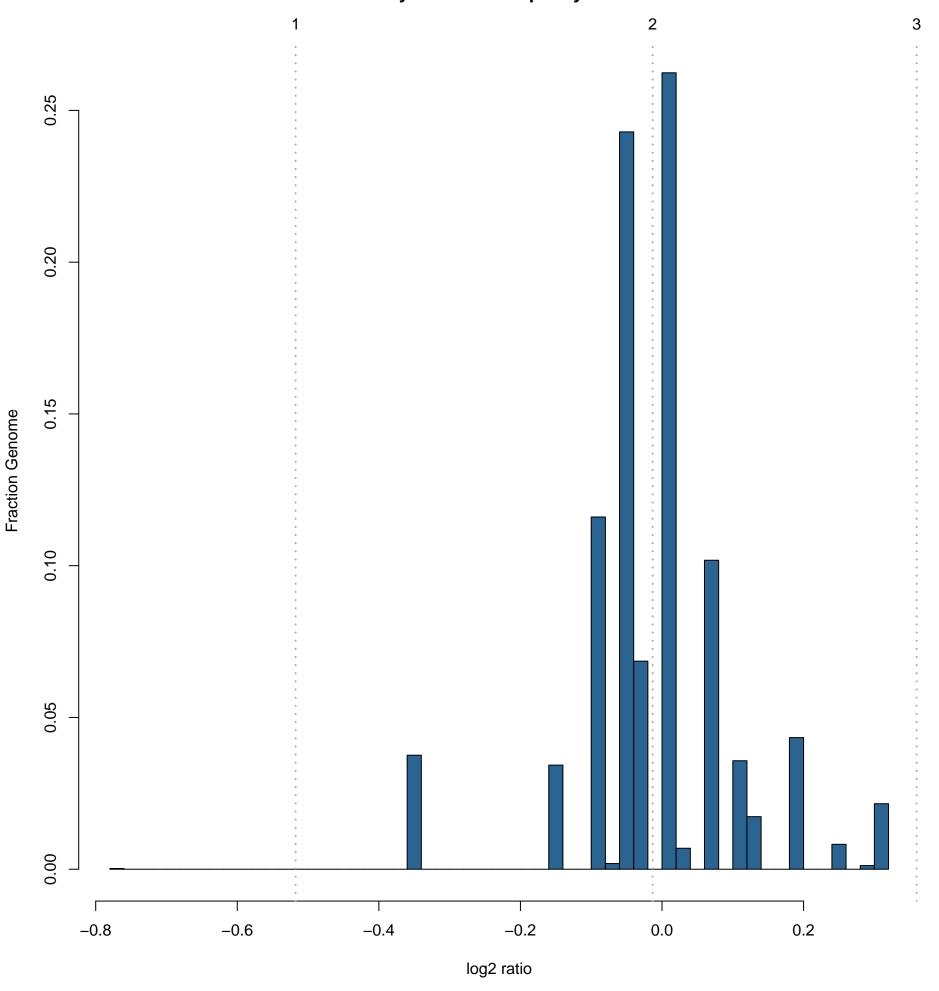
SNV Index

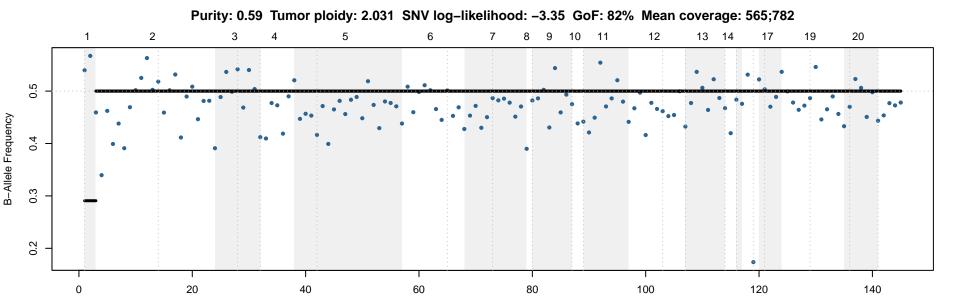






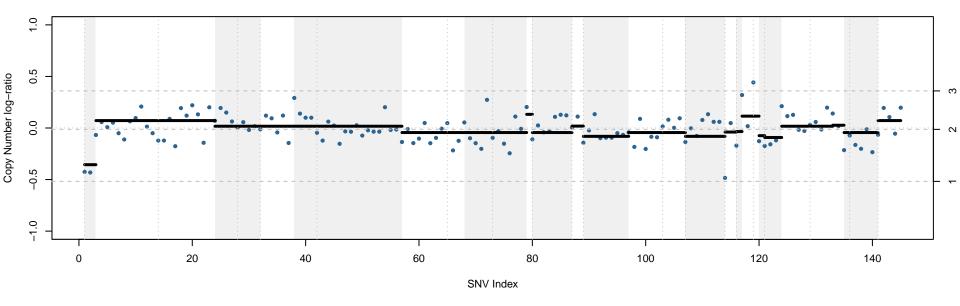
Purity: 0.59 Tumor ploidy: 2.031

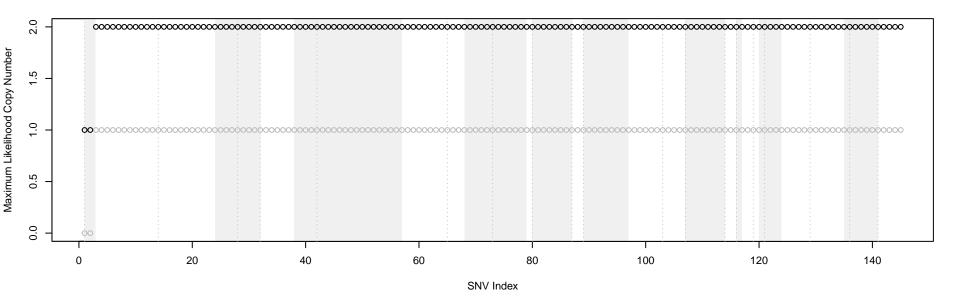


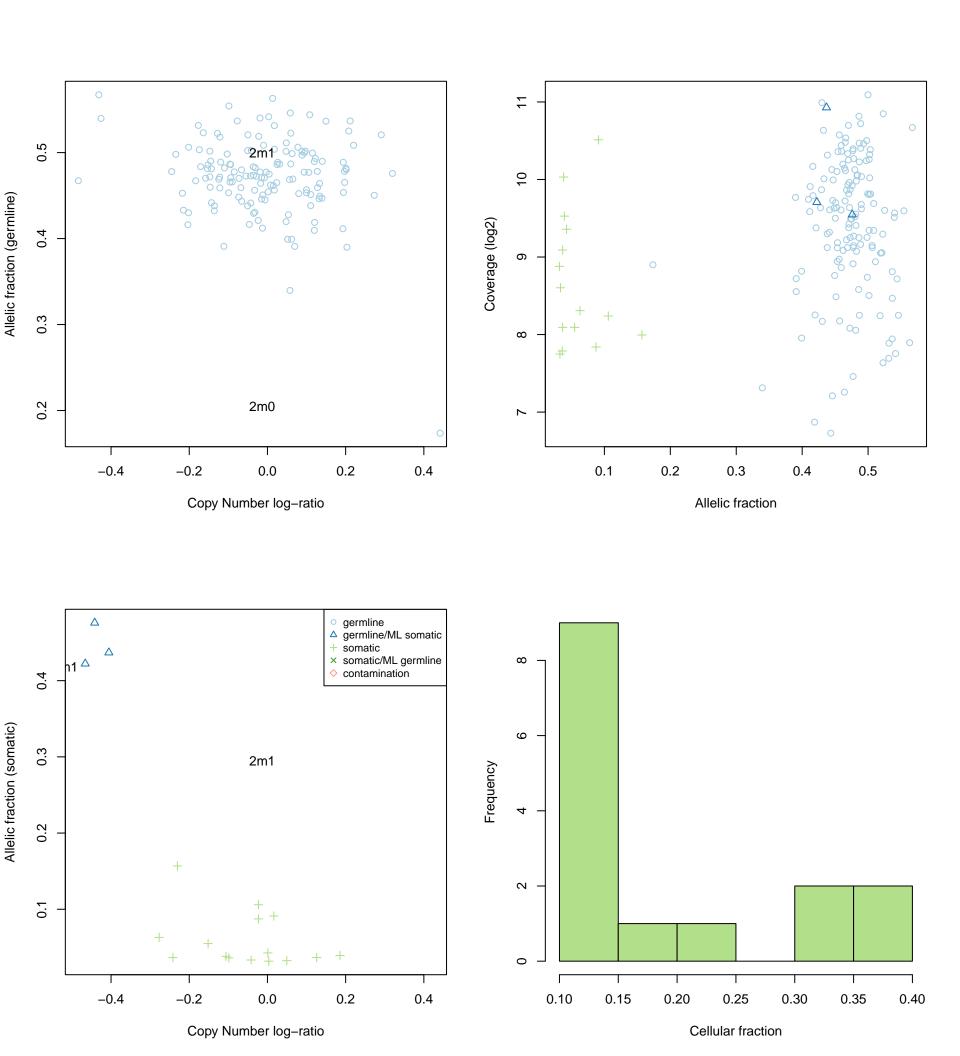


SCNA-fit log-likelihood: -9574.8

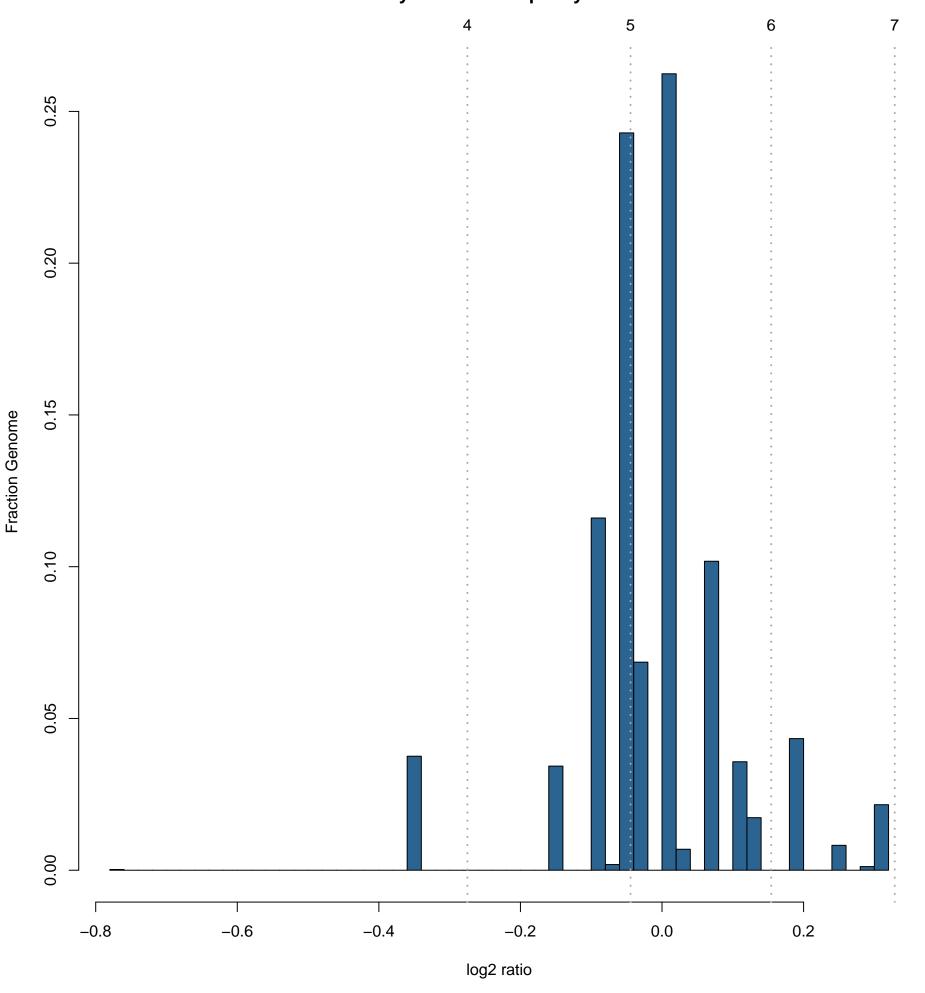
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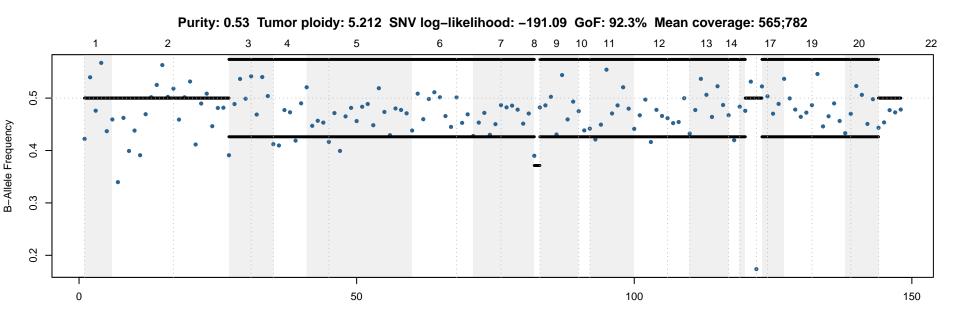






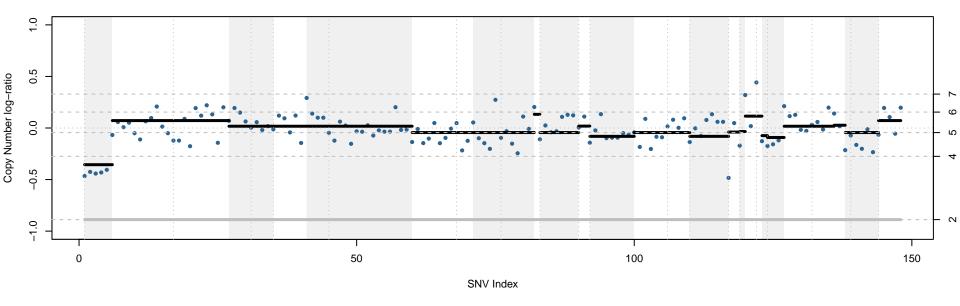
Purity: 0.53 Tumor ploidy: 5.212

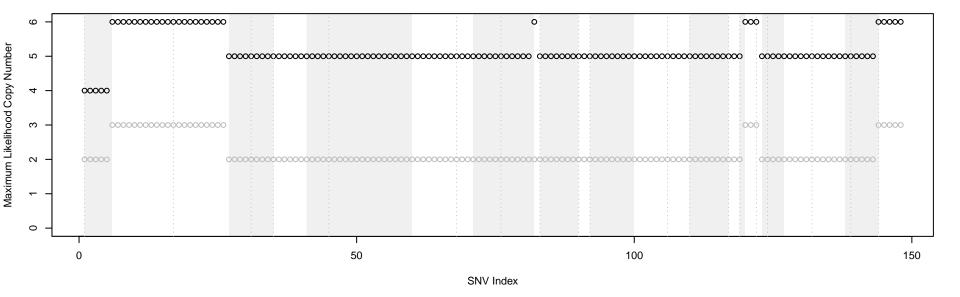


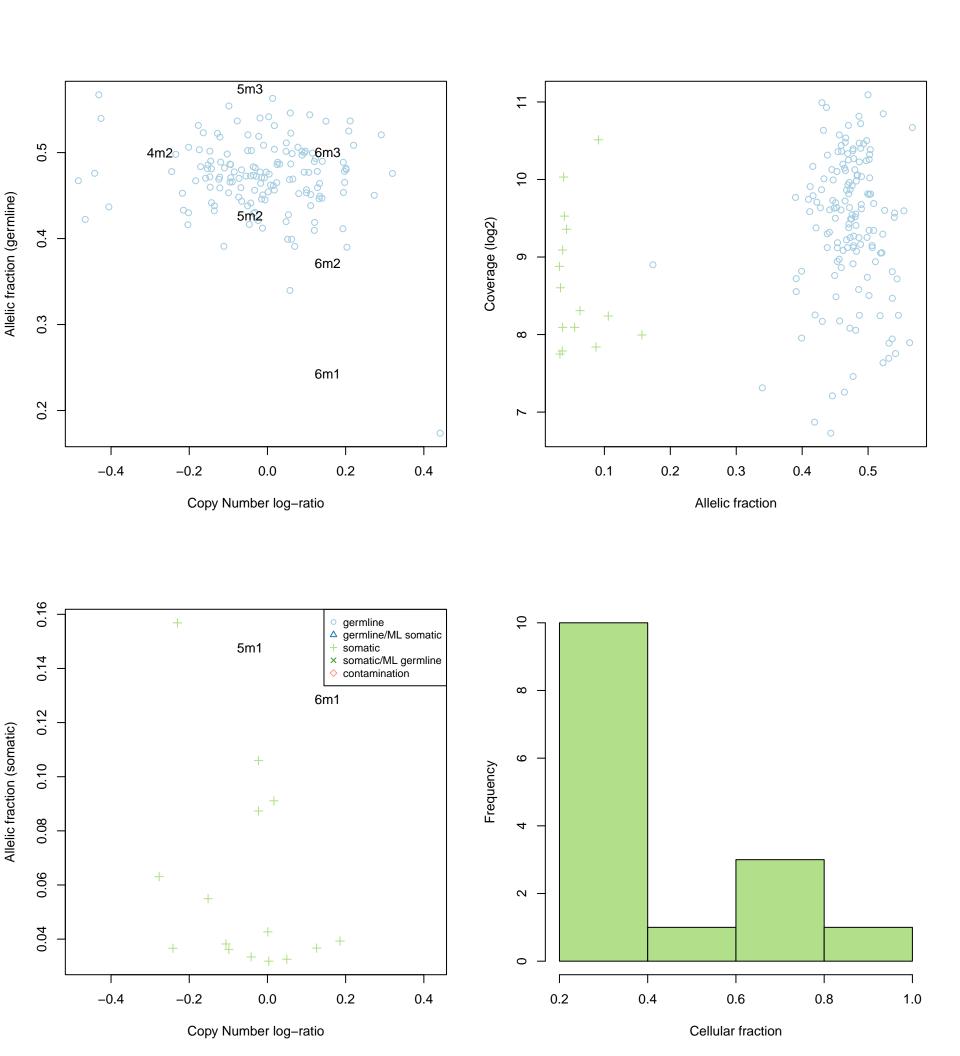


SCNA-fit log-likelihood: -9356.94

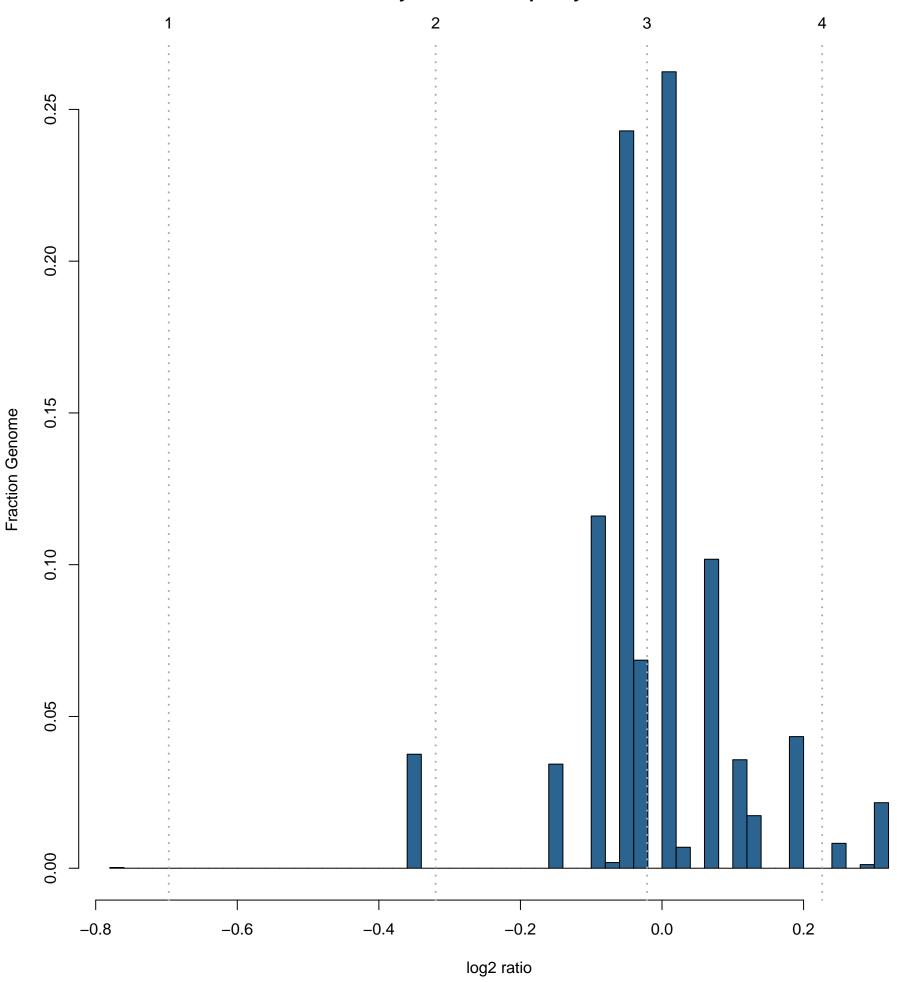
SNV Index

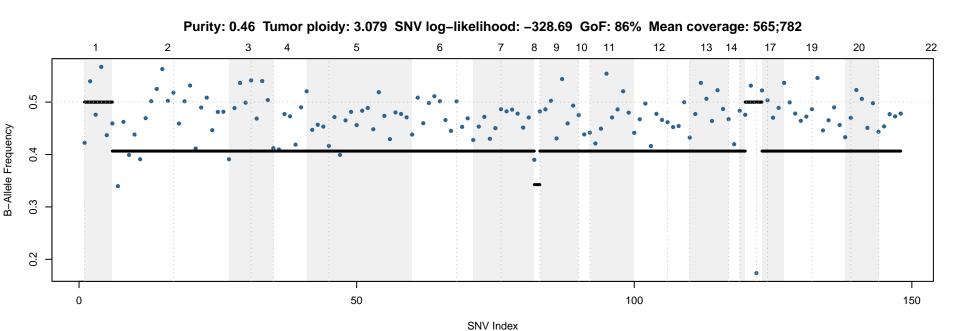




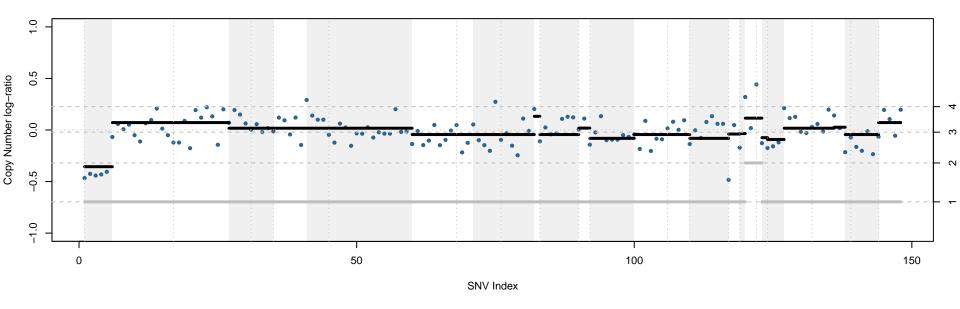


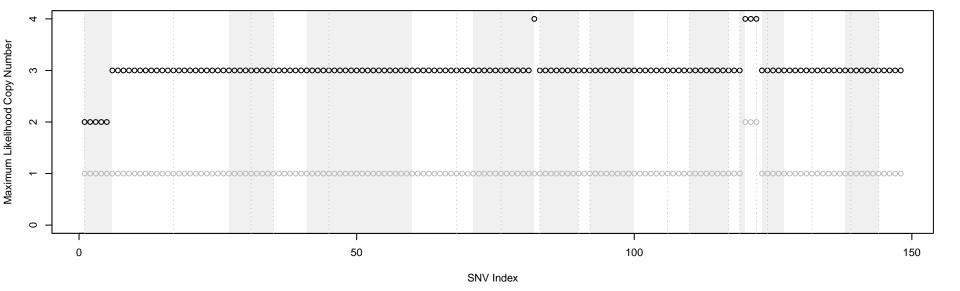
Purity: 0.46 Tumor ploidy: 3.079

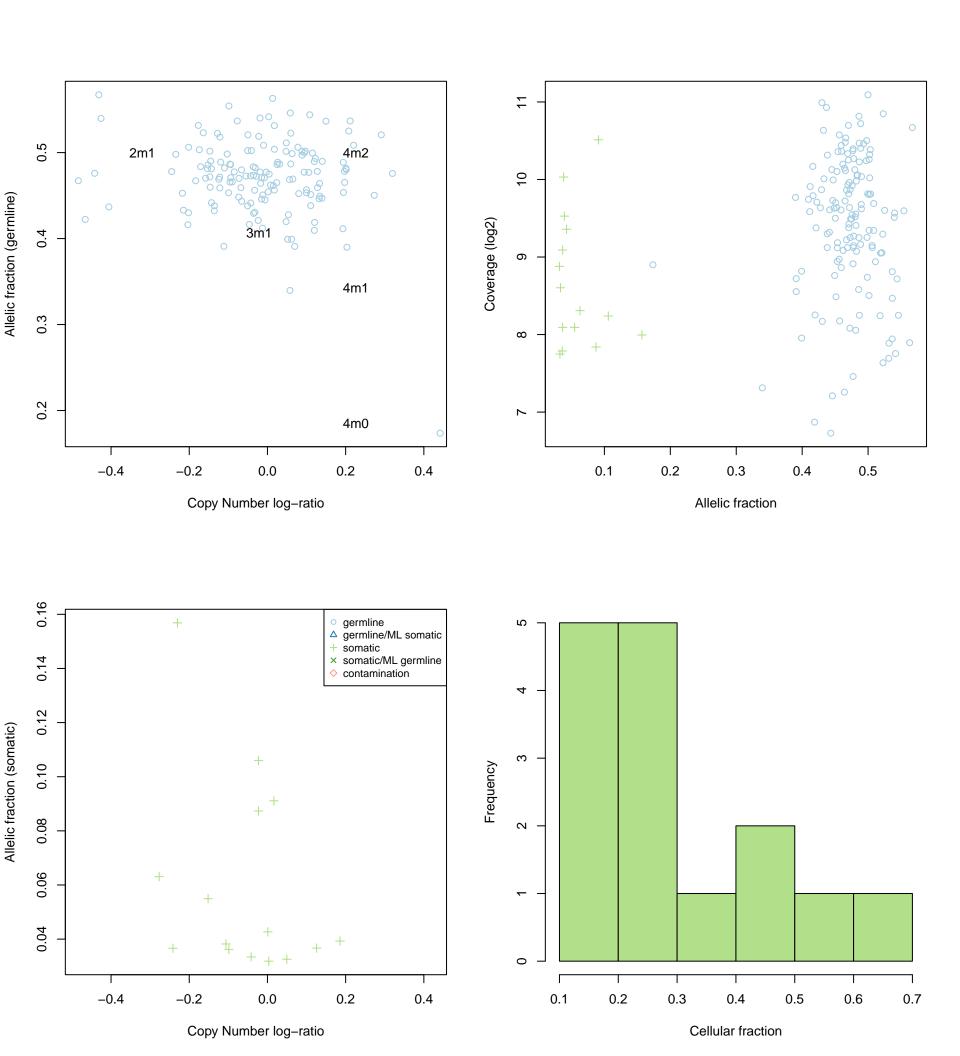




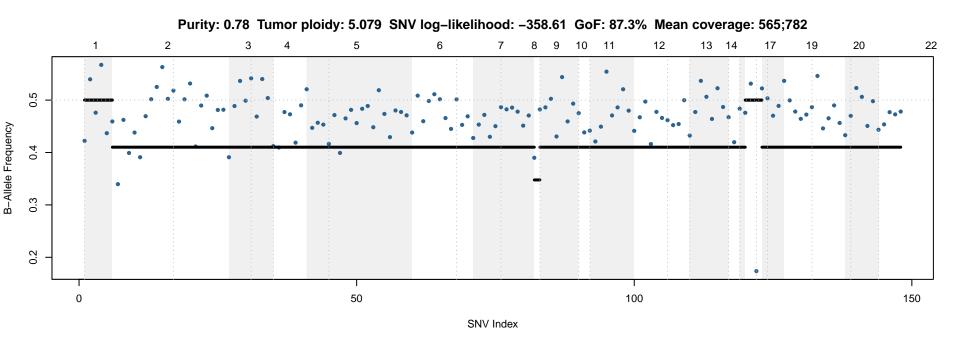
SCNA-fit log-likelihood: -9395.06



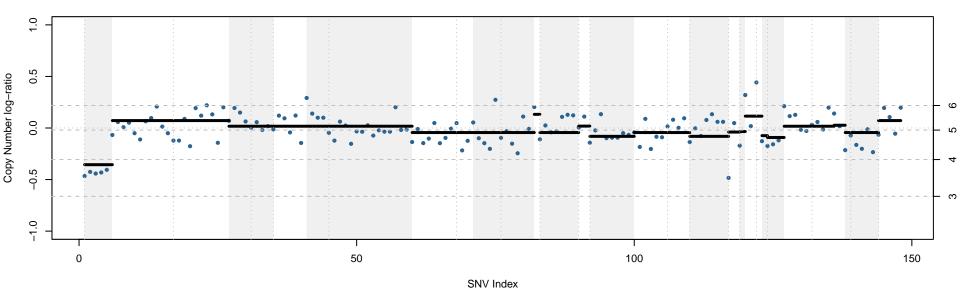


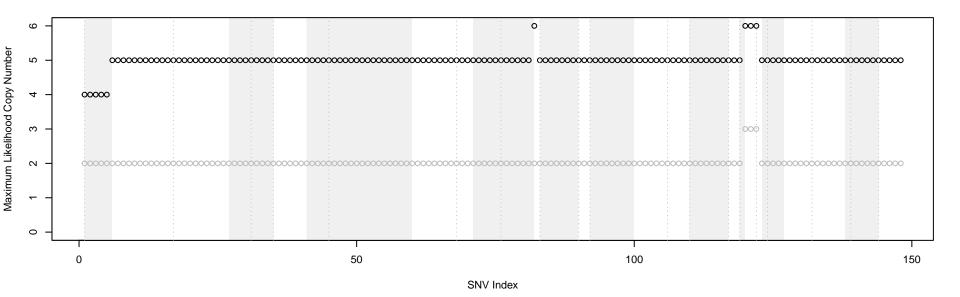


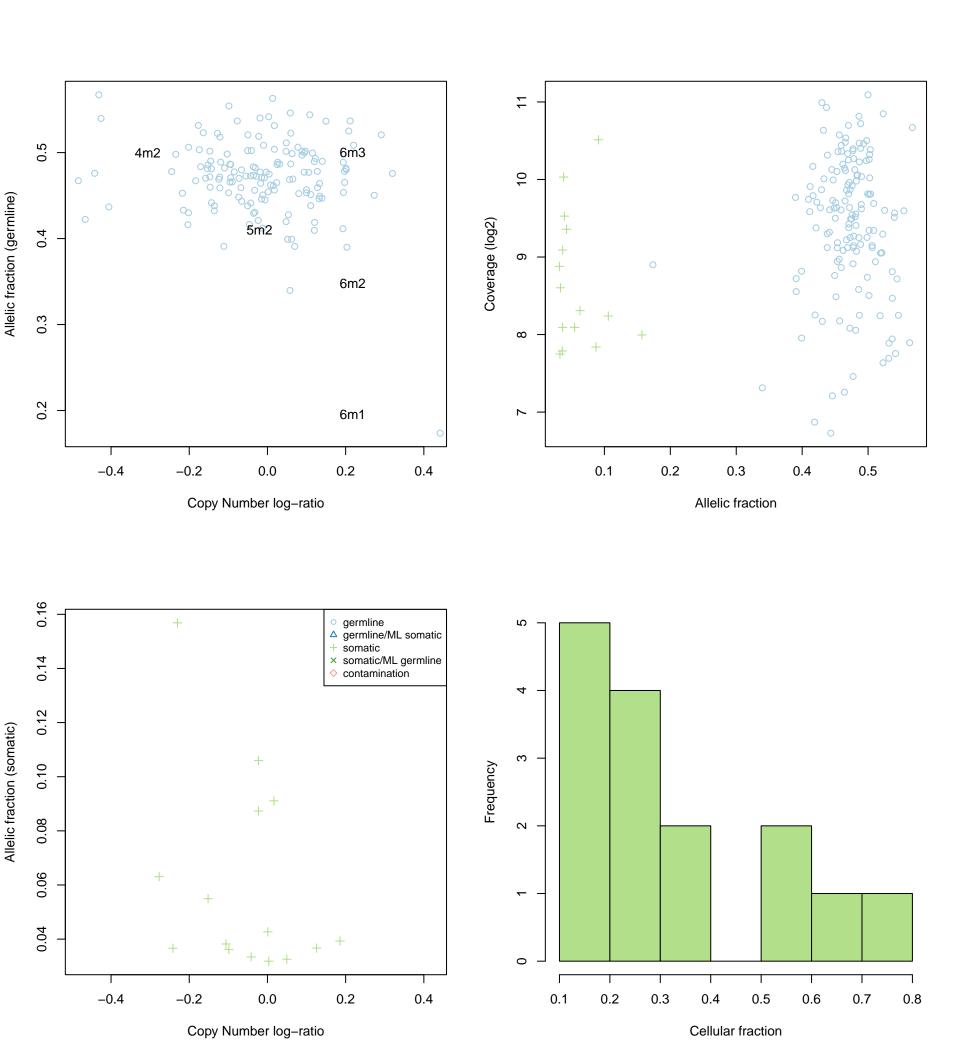
Purity: 0.78 Tumor ploidy: 5.079 6 3 5 0.20 Fraction Genome 0.05 0.00 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



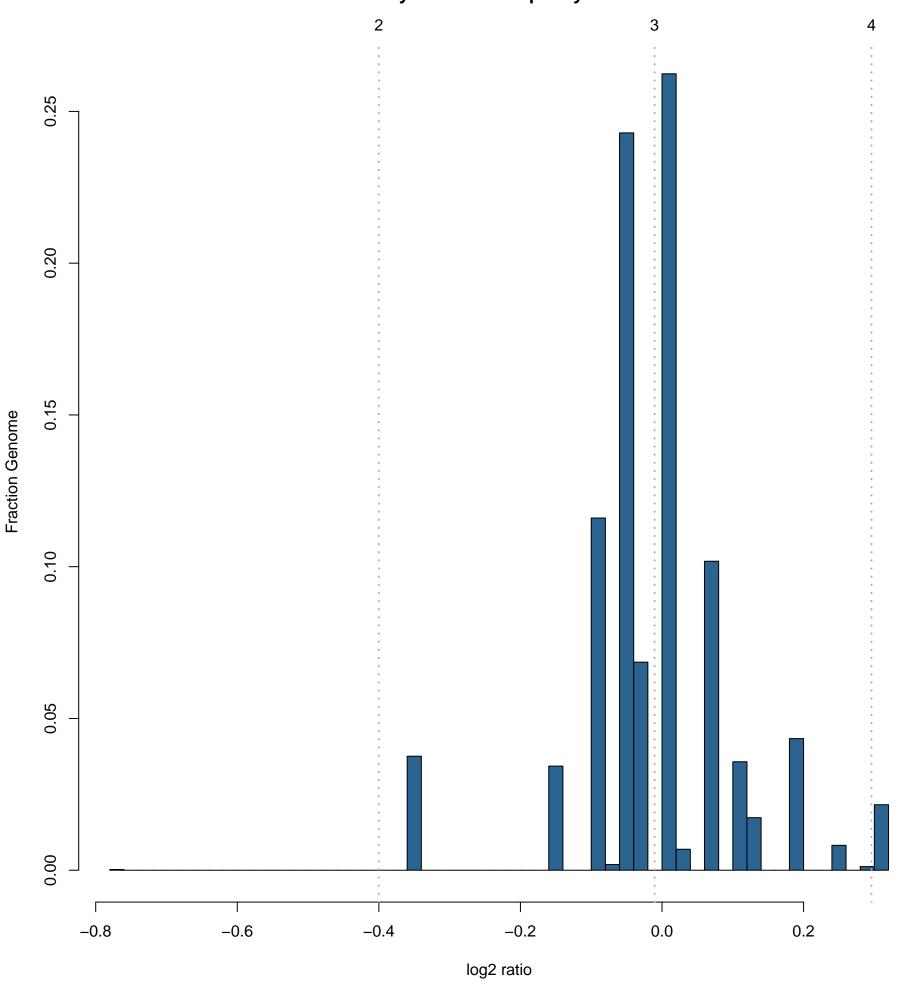
SCNA-fit log-likelihood: -9393.04

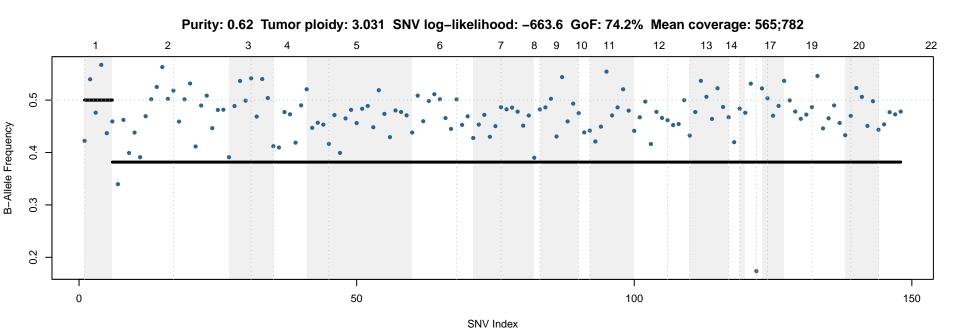




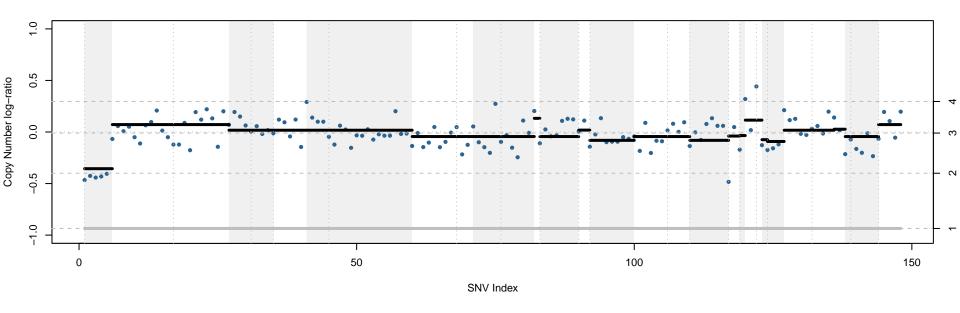


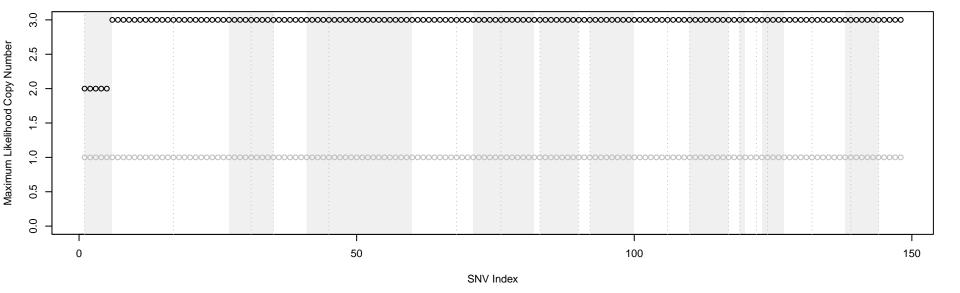
Purity: 0.62 Tumor ploidy: 3.031

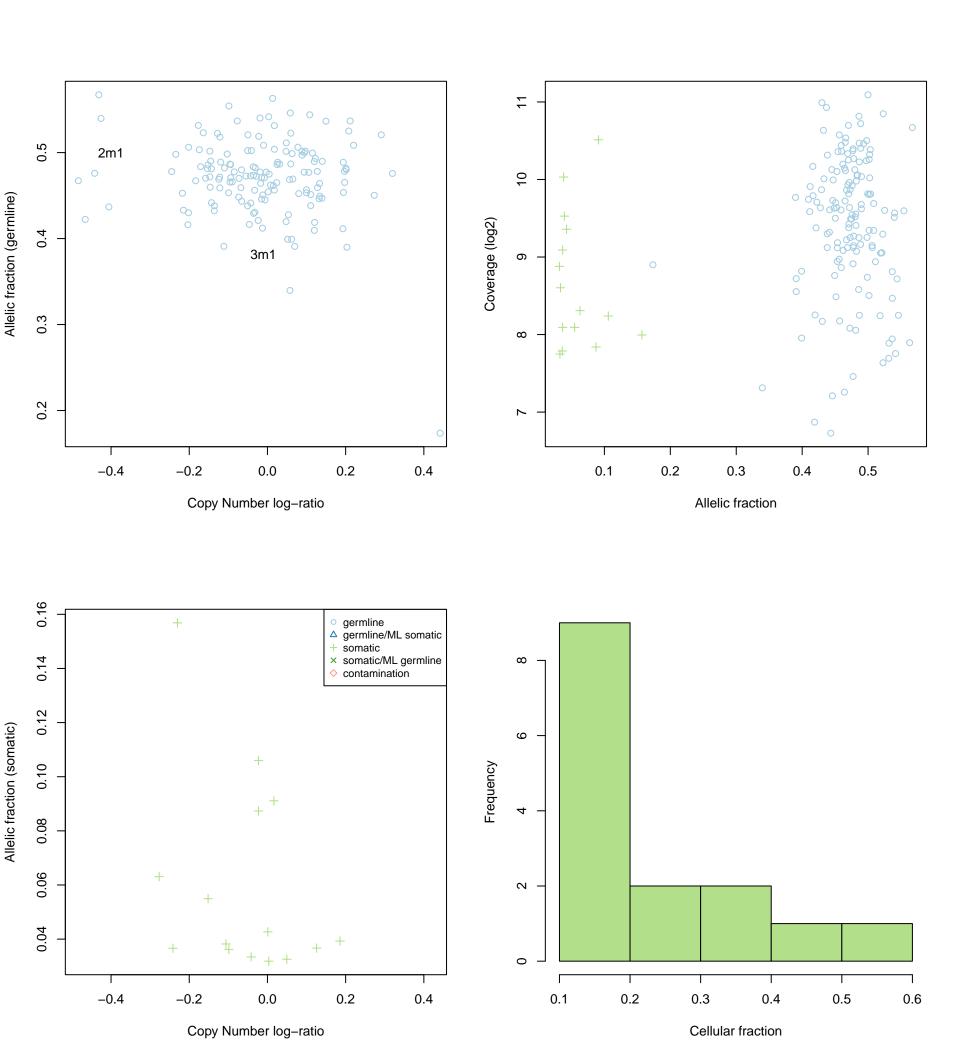




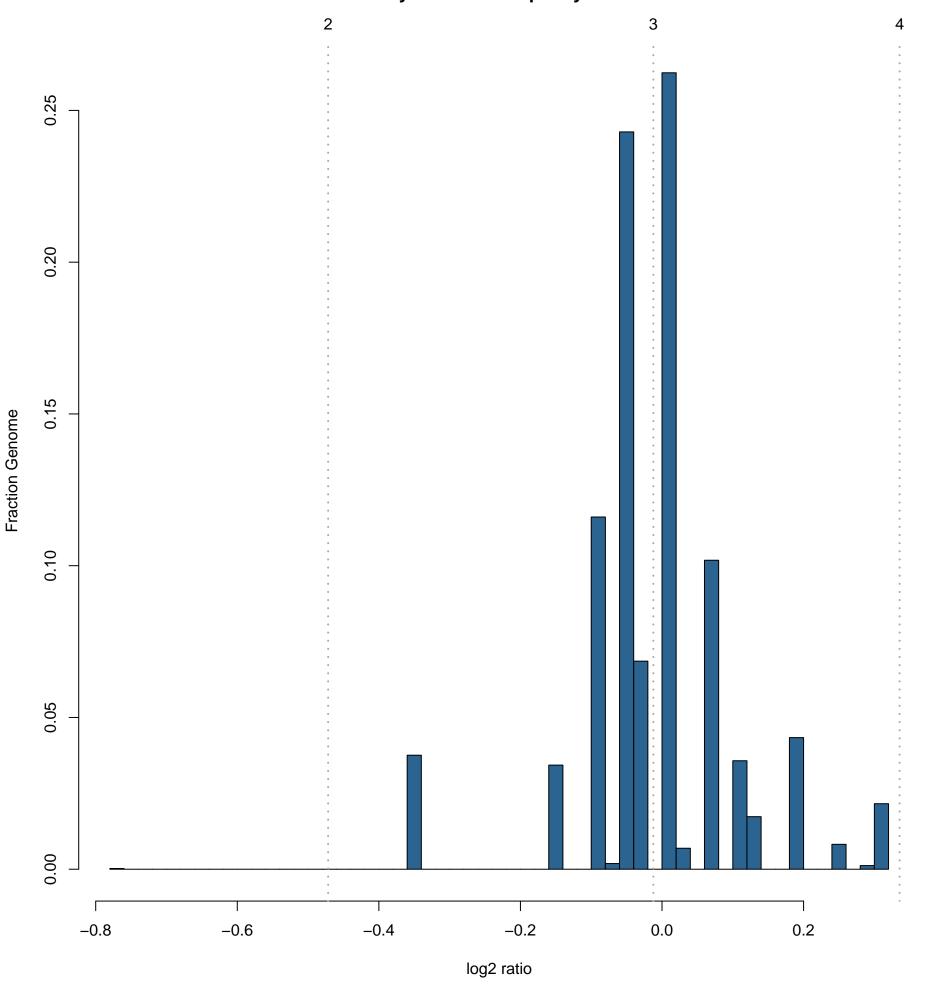
SCNA-fit log-likelihood: -9448.9

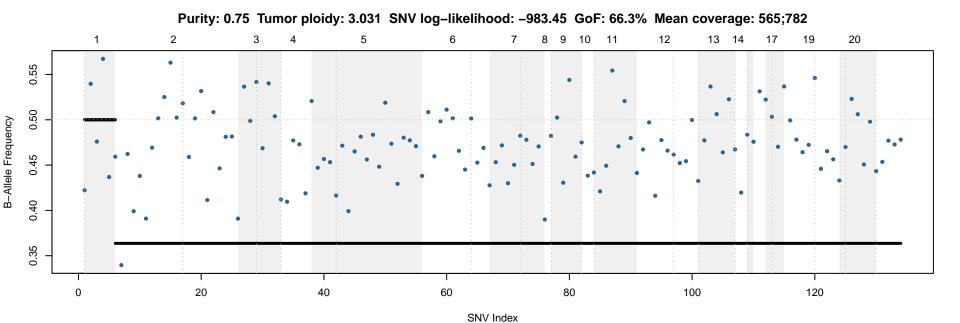






Purity: 0.75 Tumor ploidy: 3.031





SCNA-fit log-likelihood: -9514.26

