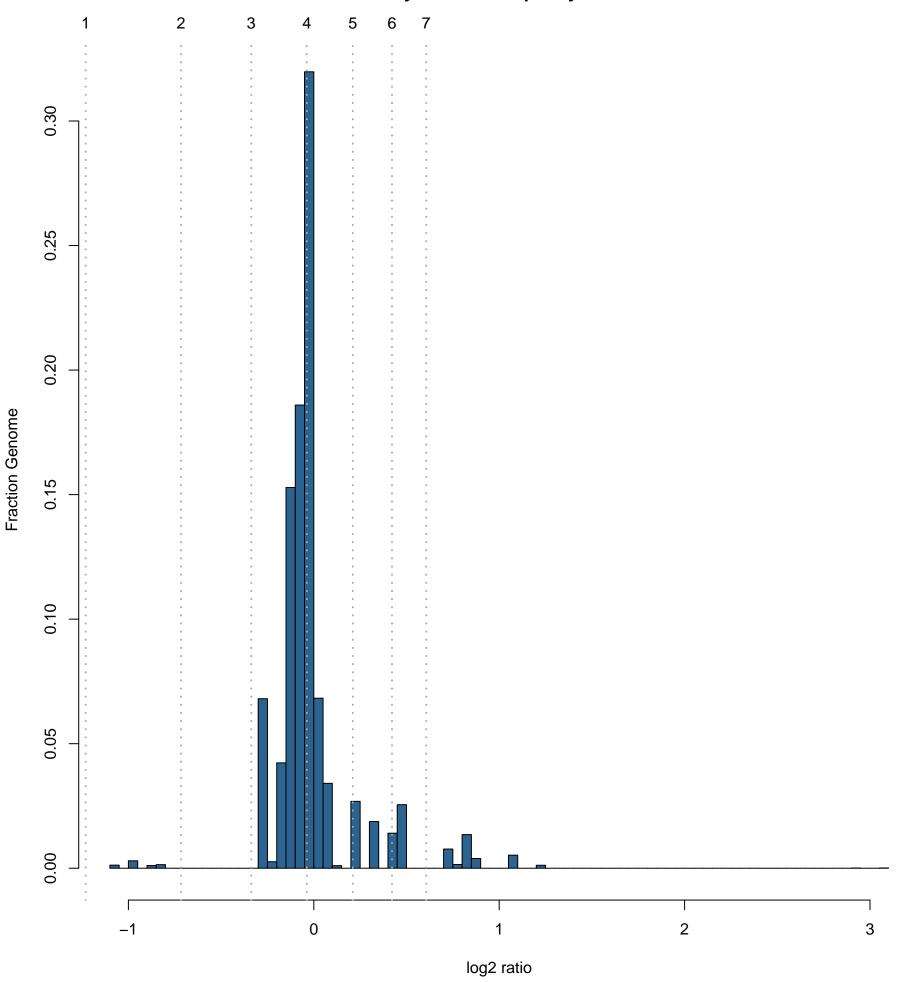
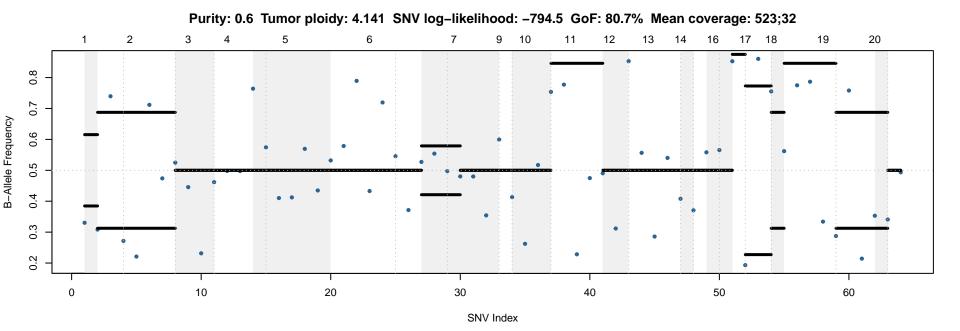
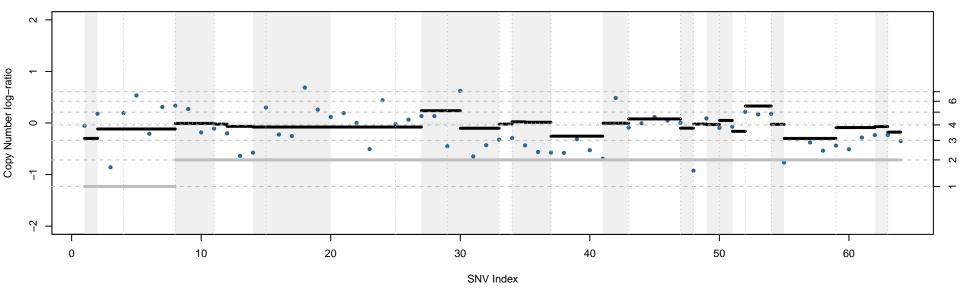
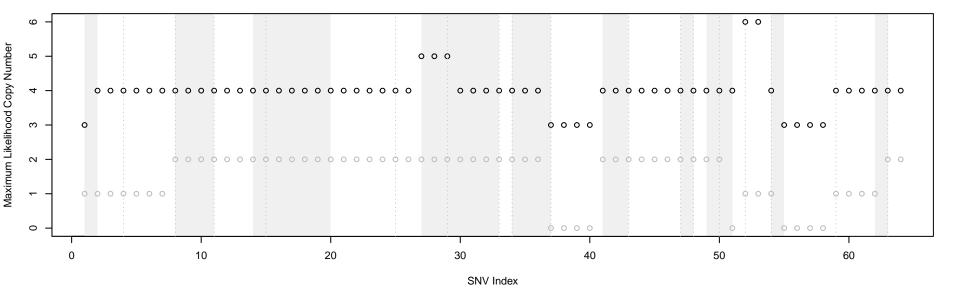
Purity: 0.6 Tumor ploidy: 4.141

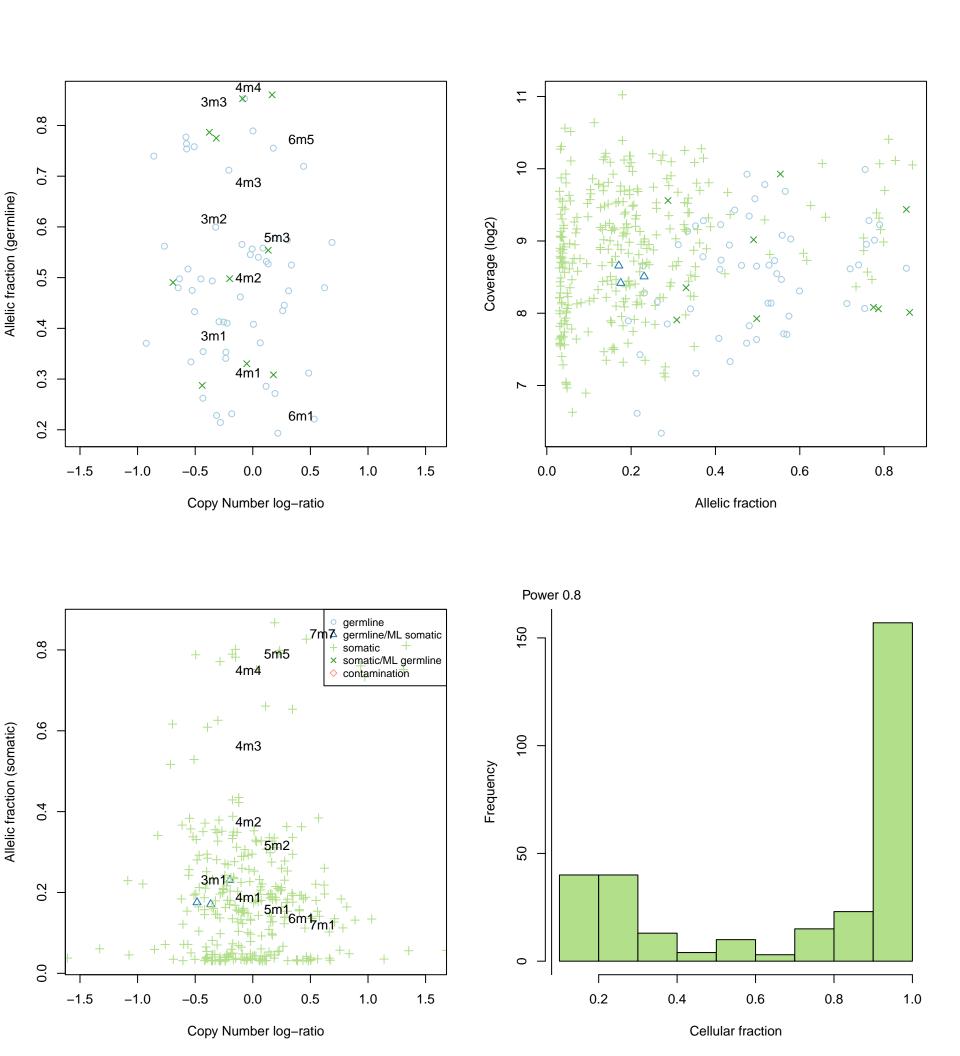




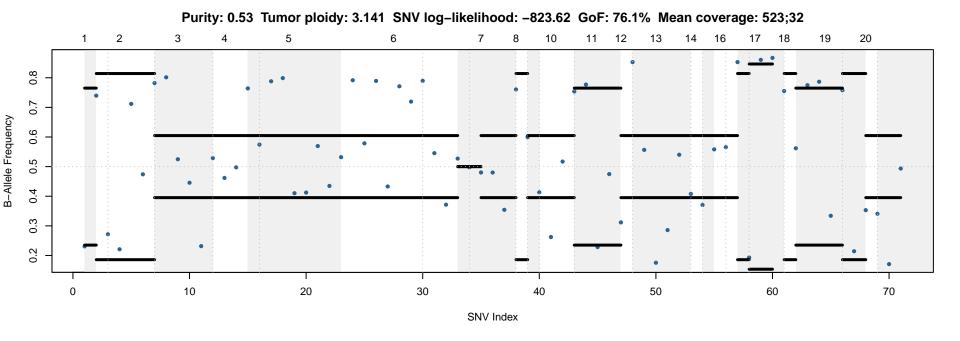
SCNA-fit log-likelihood: -16960.31



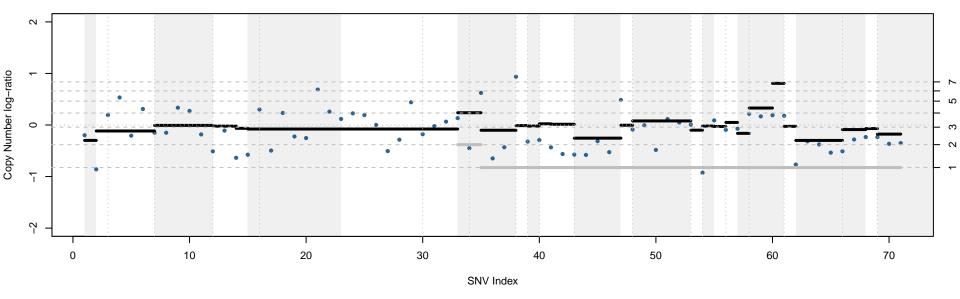


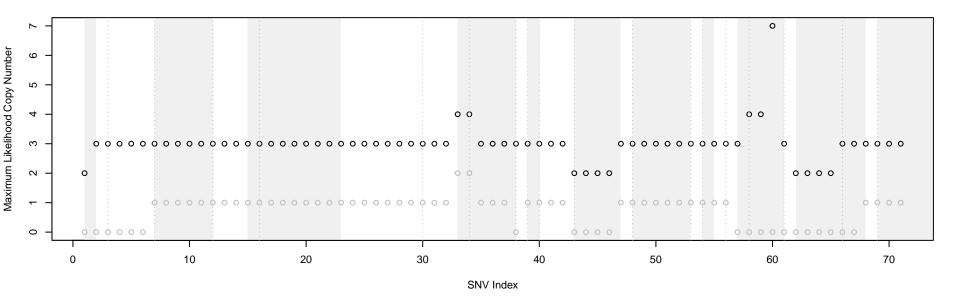


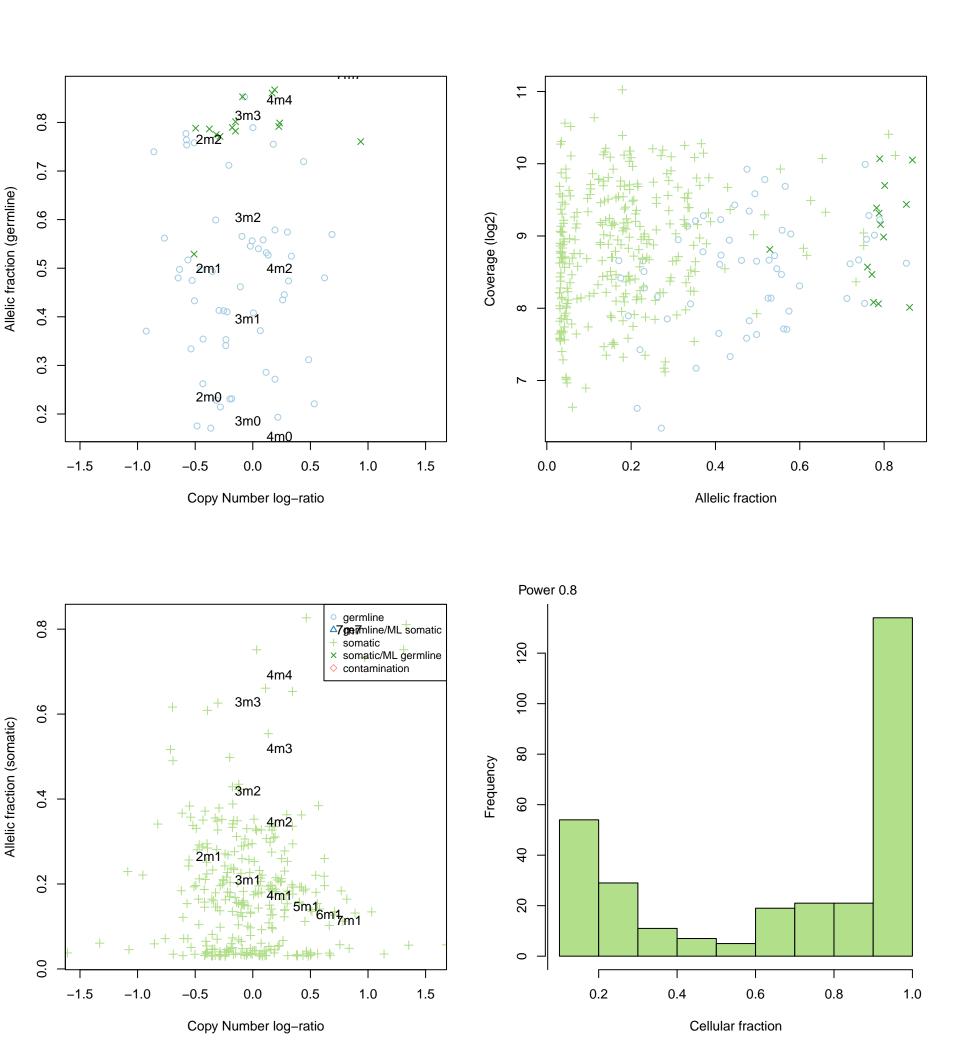
Purity: 0.53 Tumor ploidy: 3.141 3 2 6 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 0 -1 2 3 1 log2 ratio



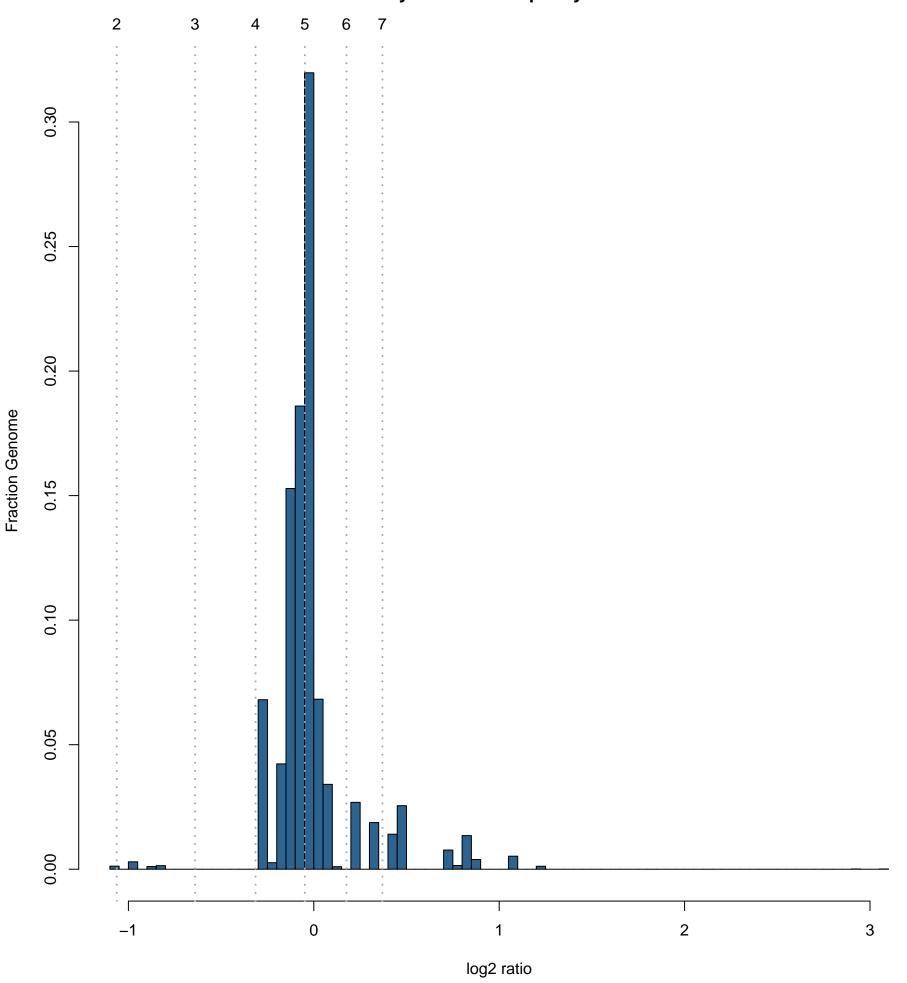
SCNA-fit log-likelihood: -16923.52

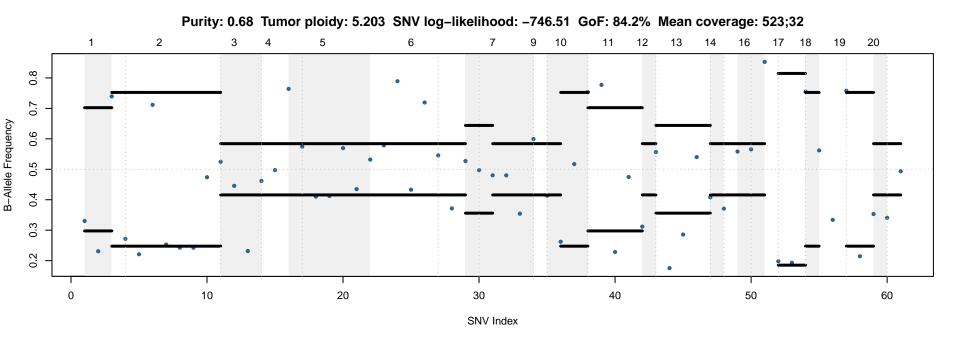




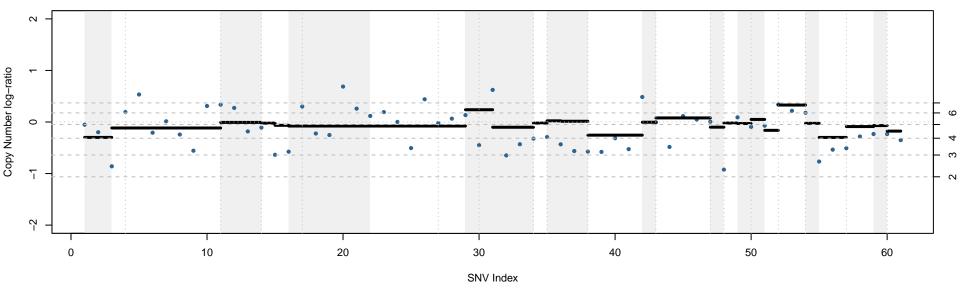


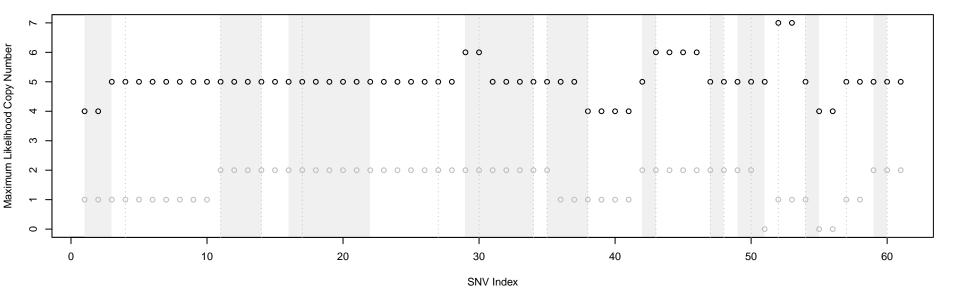
Purity: 0.68 Tumor ploidy: 5.203

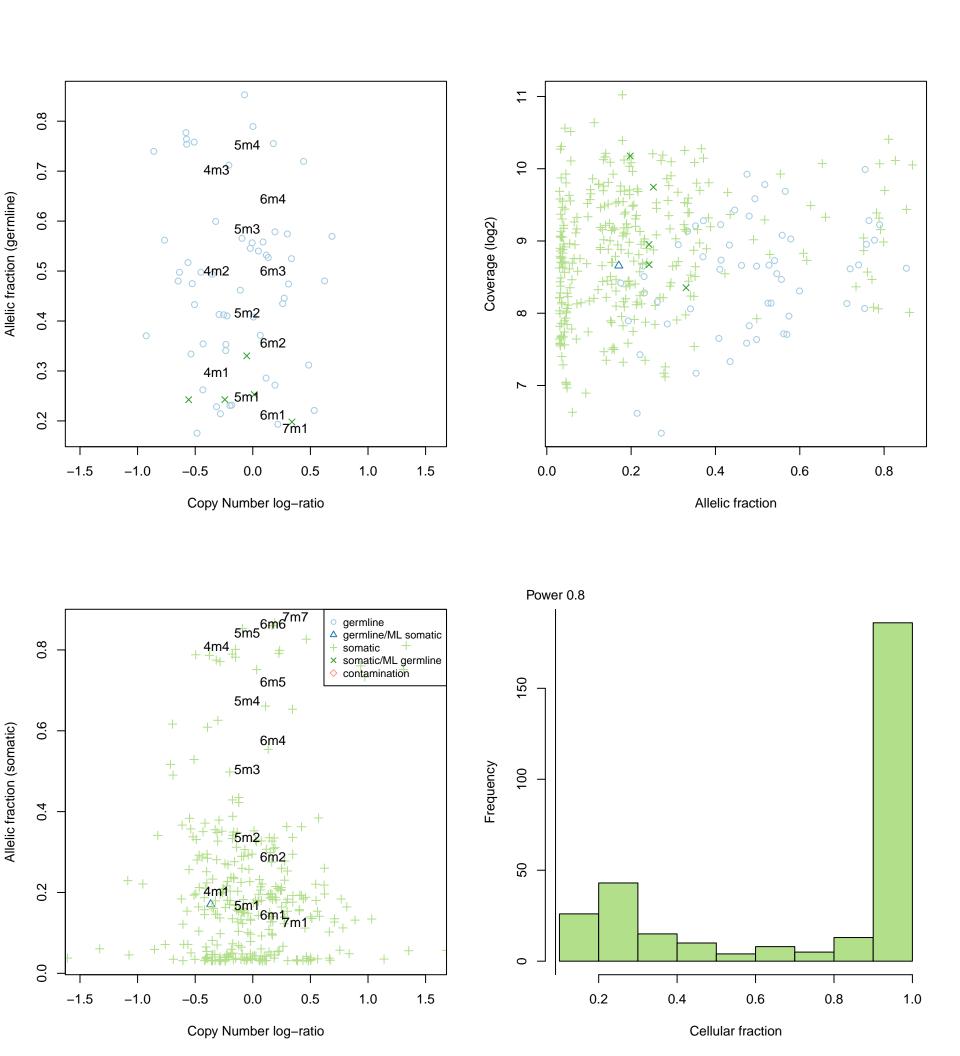




SCNA-fit log-likelihood: -17125.16



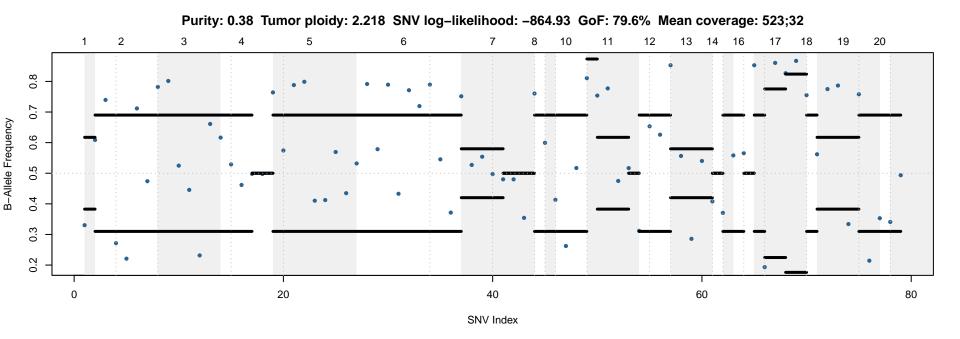




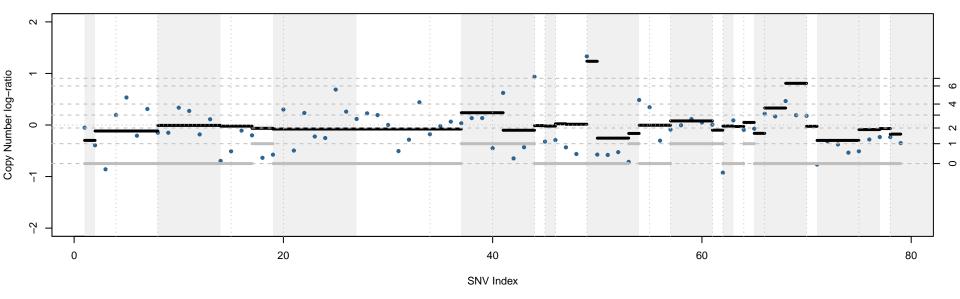
Purity: 0.38 Tumor ploidy: 2.218 0 2 1 3 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -1 0 2 3

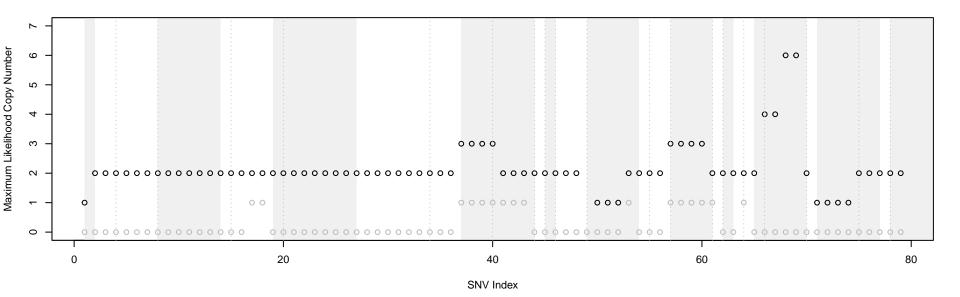
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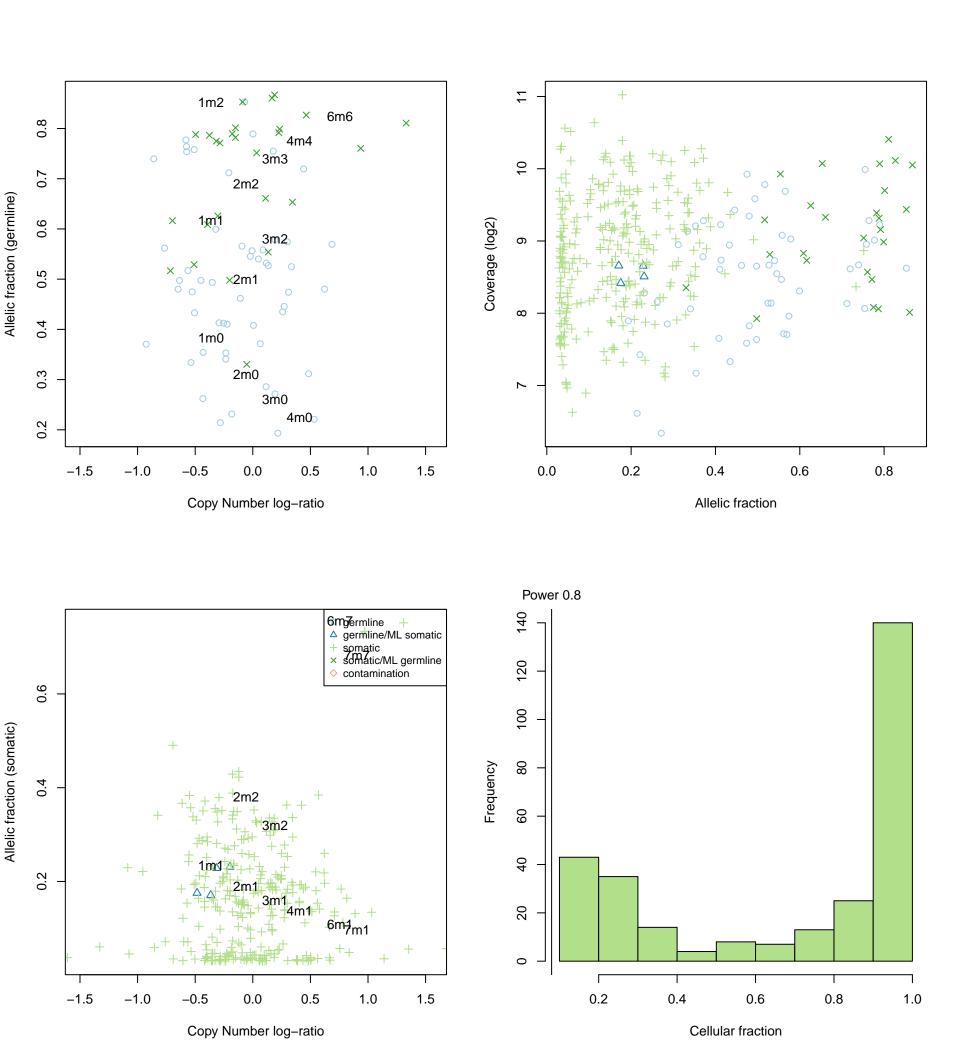
log2 ratio



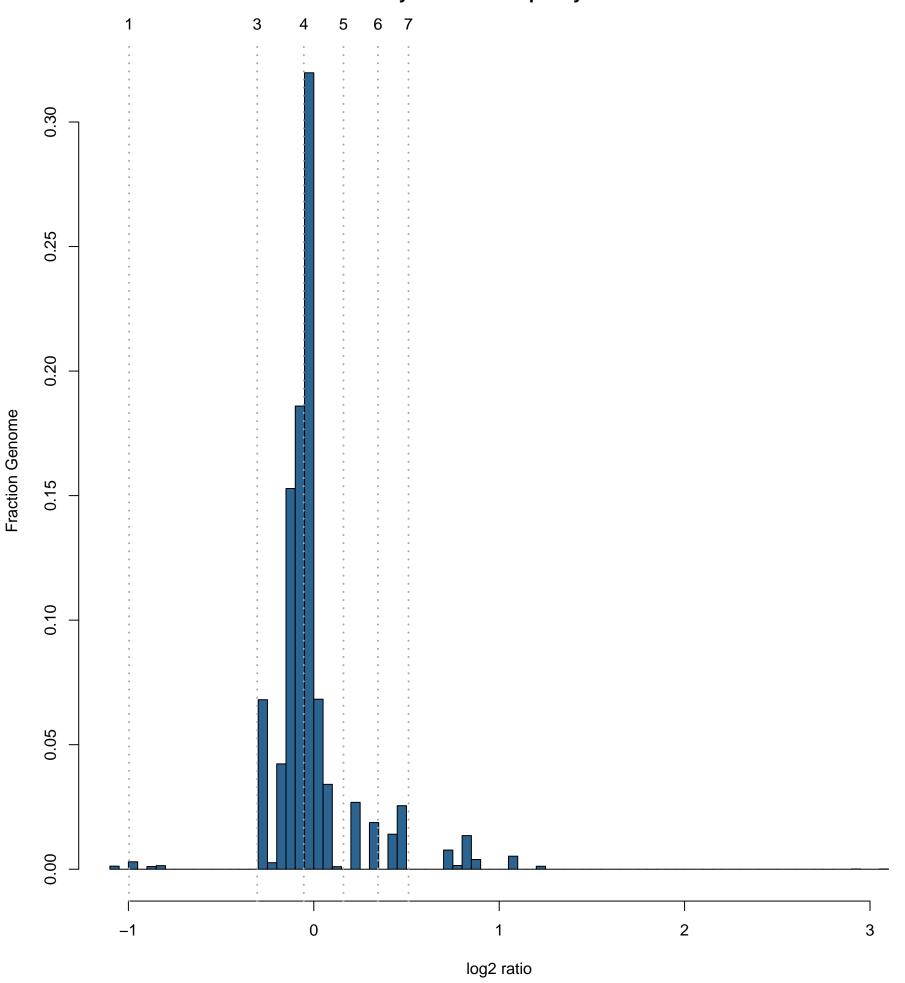
SCNA-fit log-likelihood: -16904.84

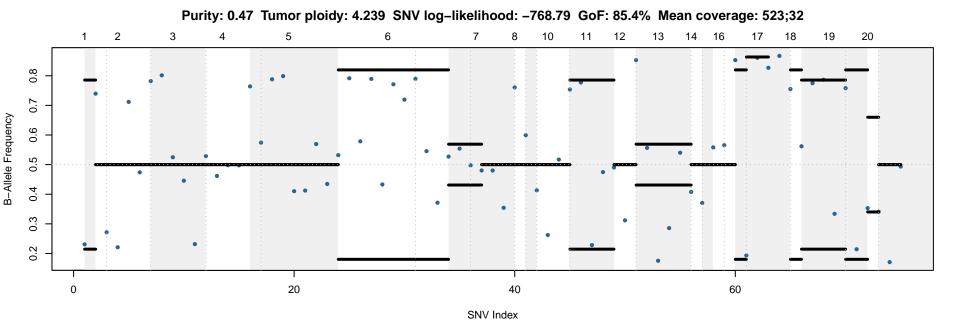




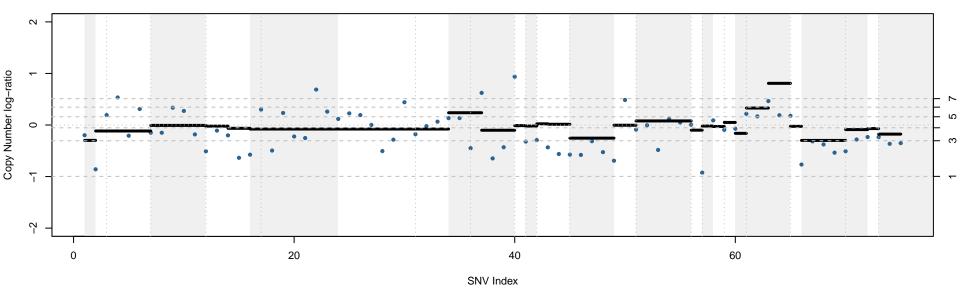


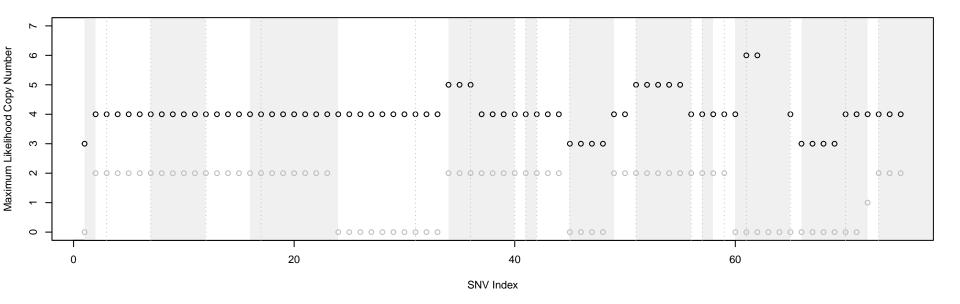
Purity: 0.47 Tumor ploidy: 4.239

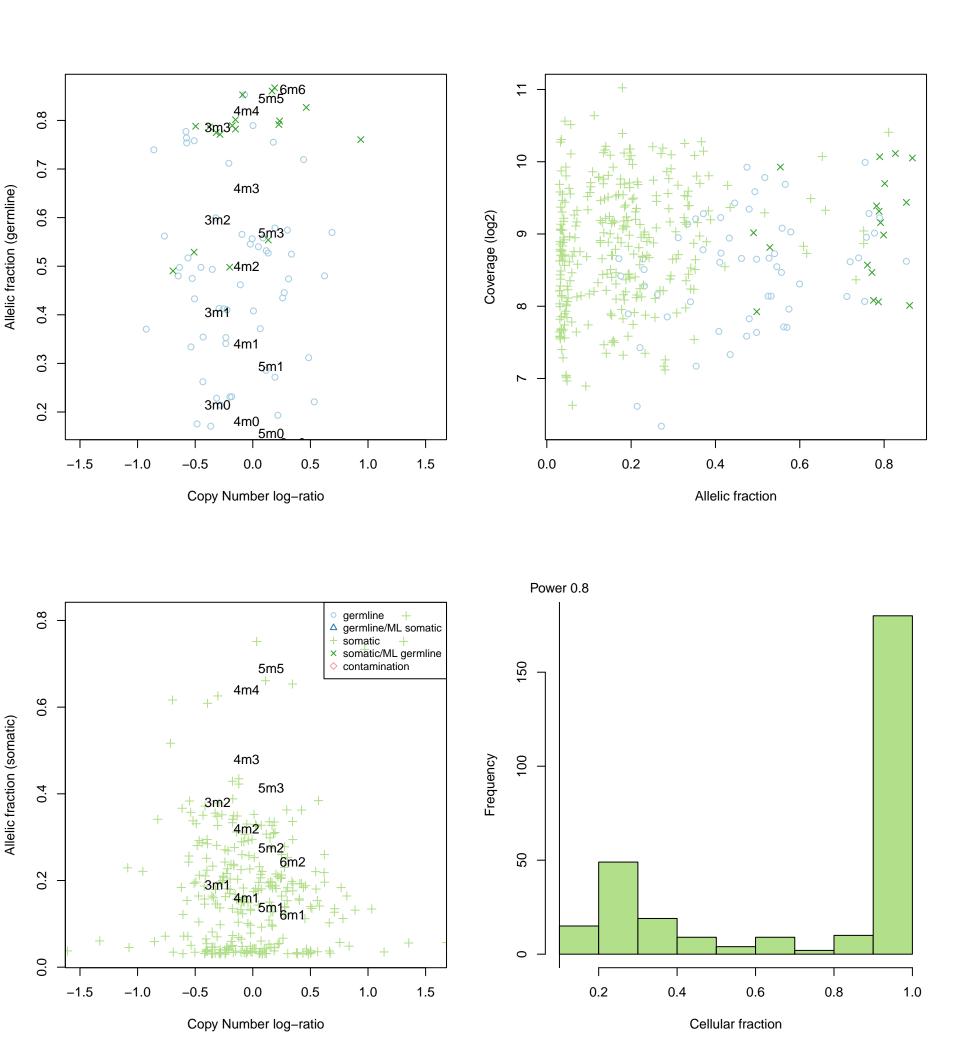




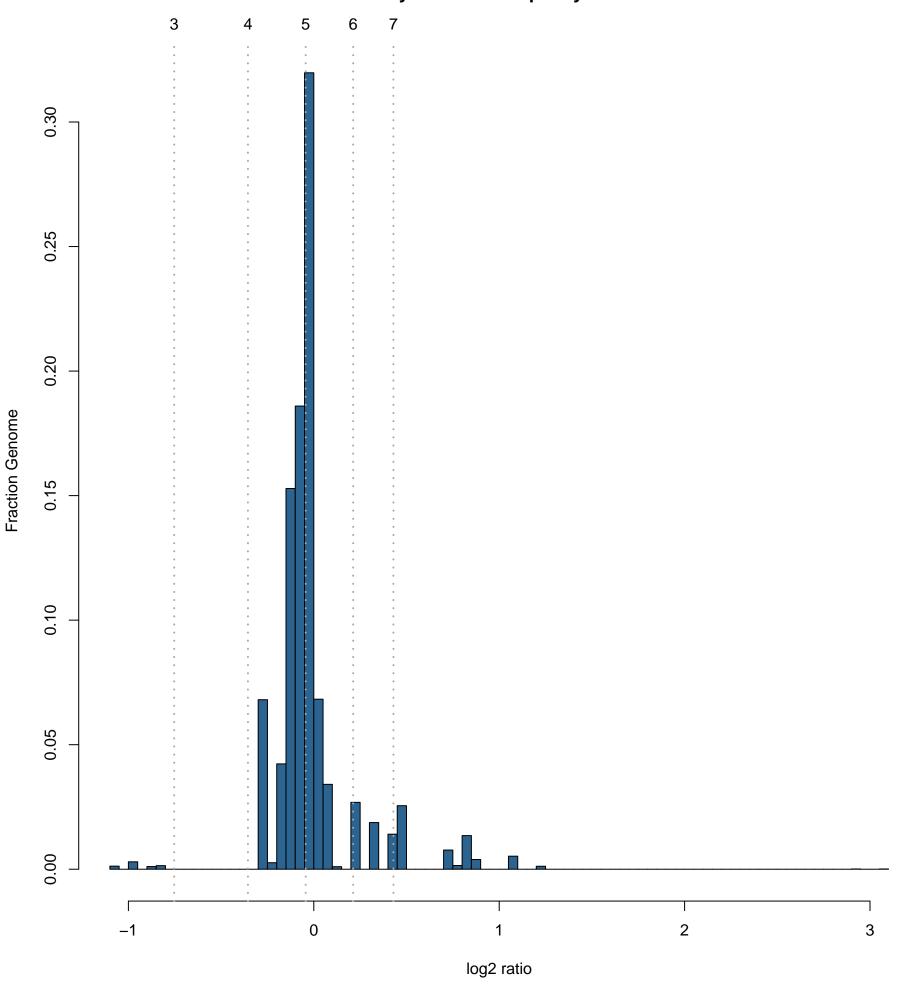
SCNA-fit log-likelihood: -17119.52

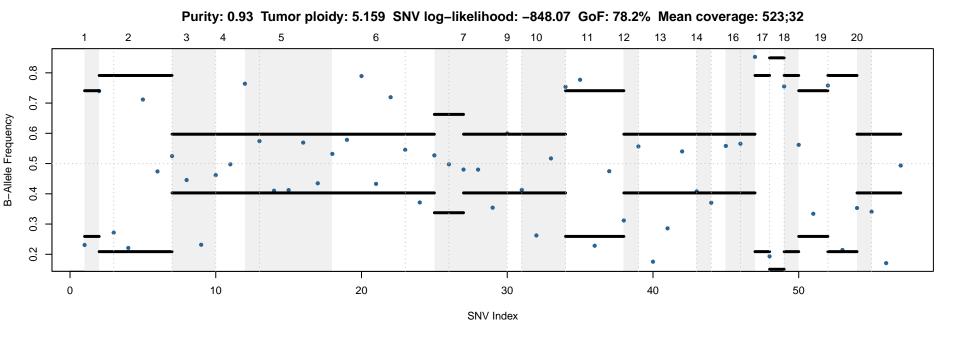




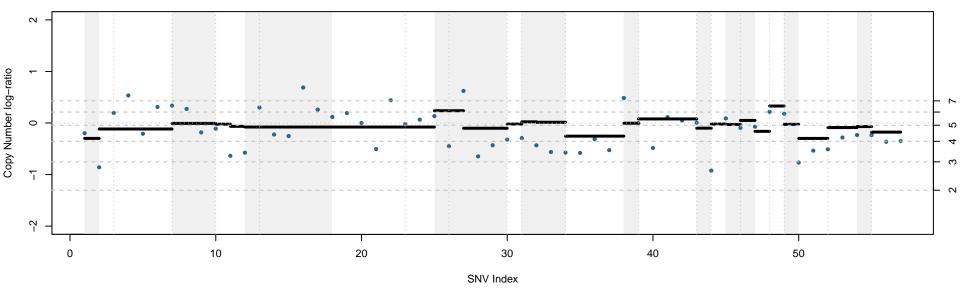


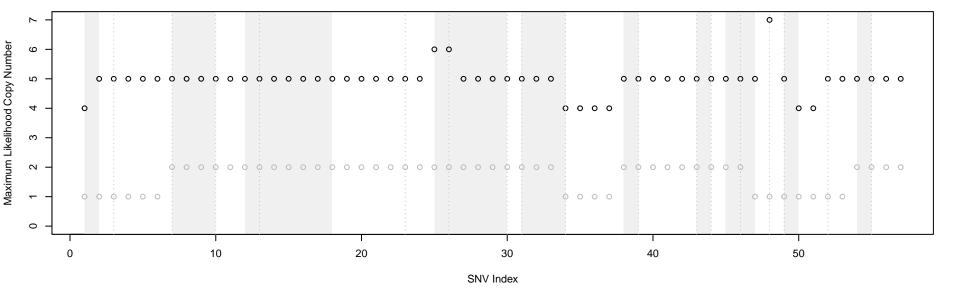
Purity: 0.93 Tumor ploidy: 5.159

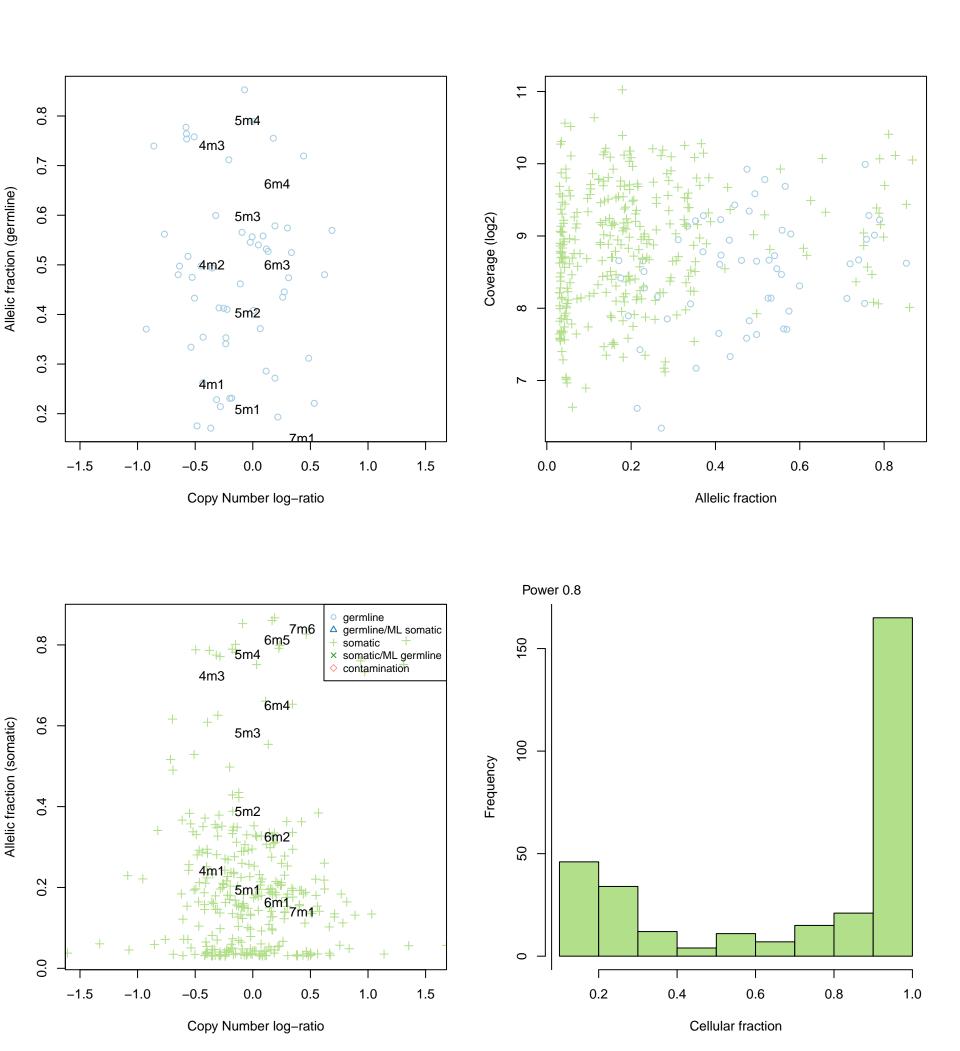


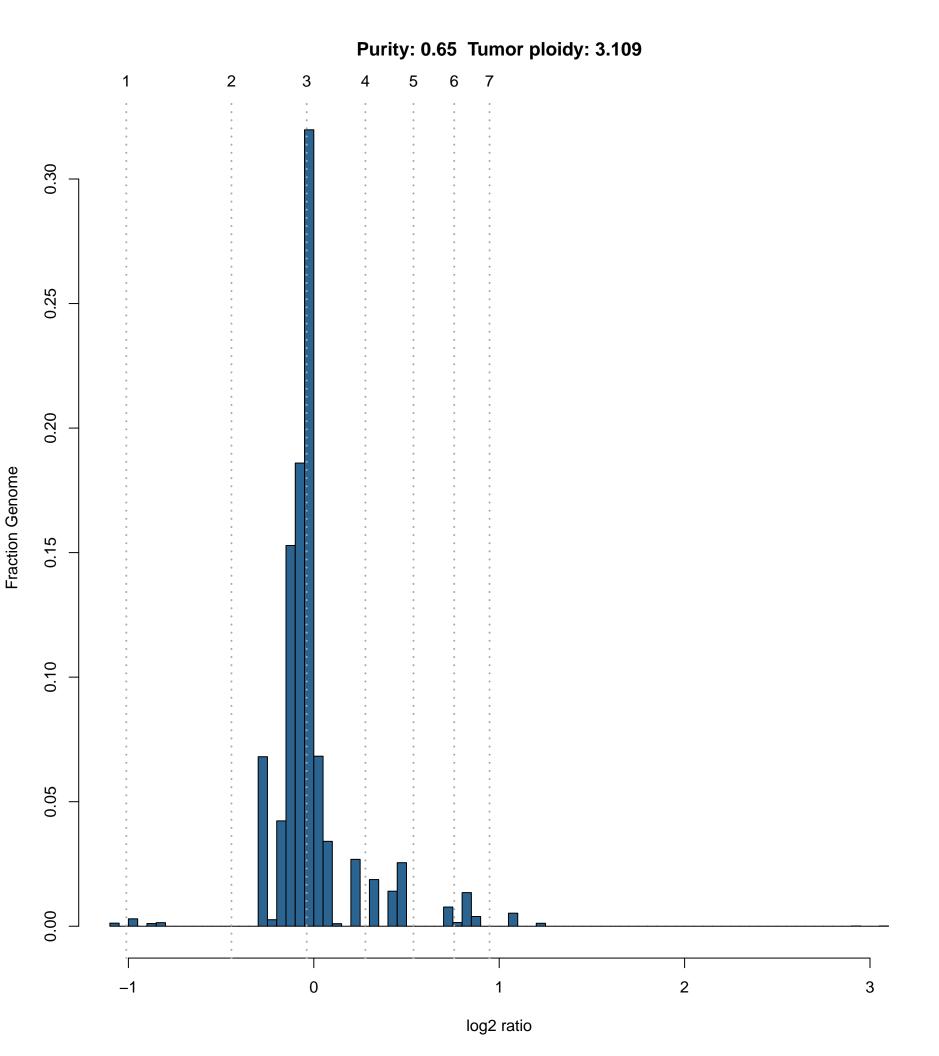


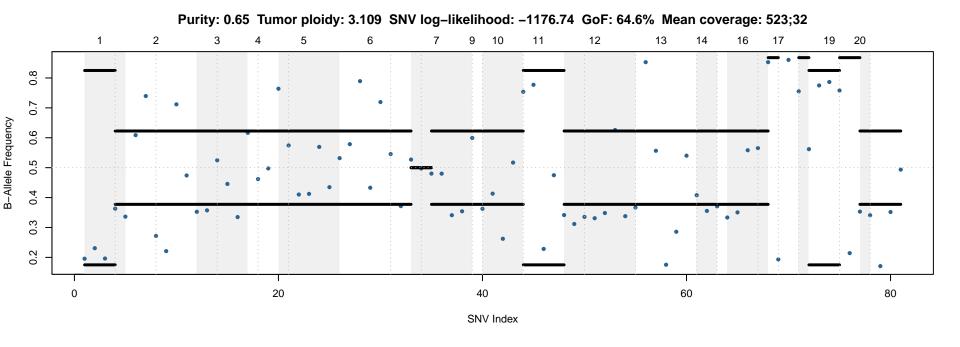
SCNA-fit log-likelihood: -17135.65



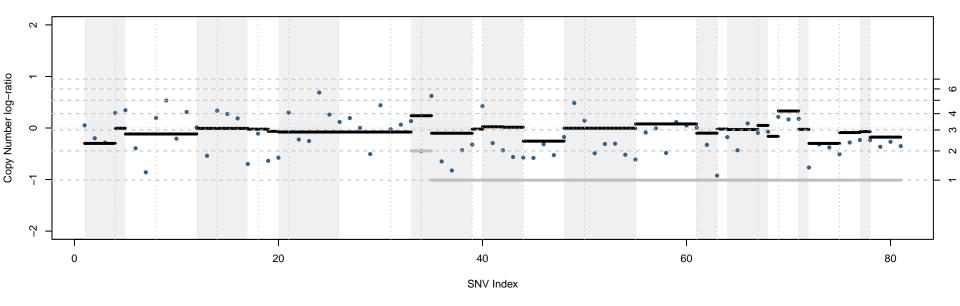


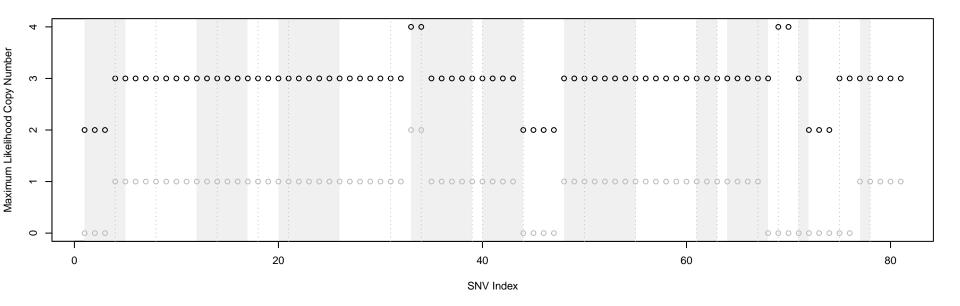


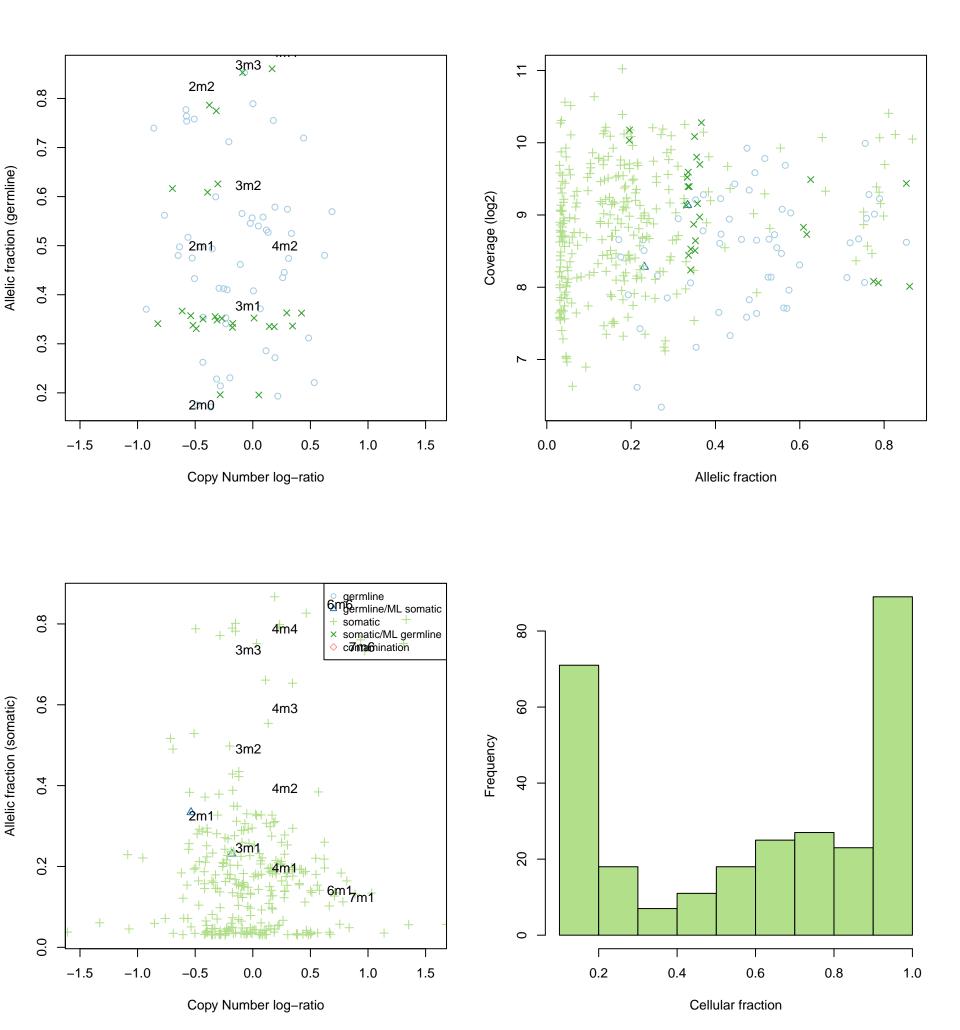




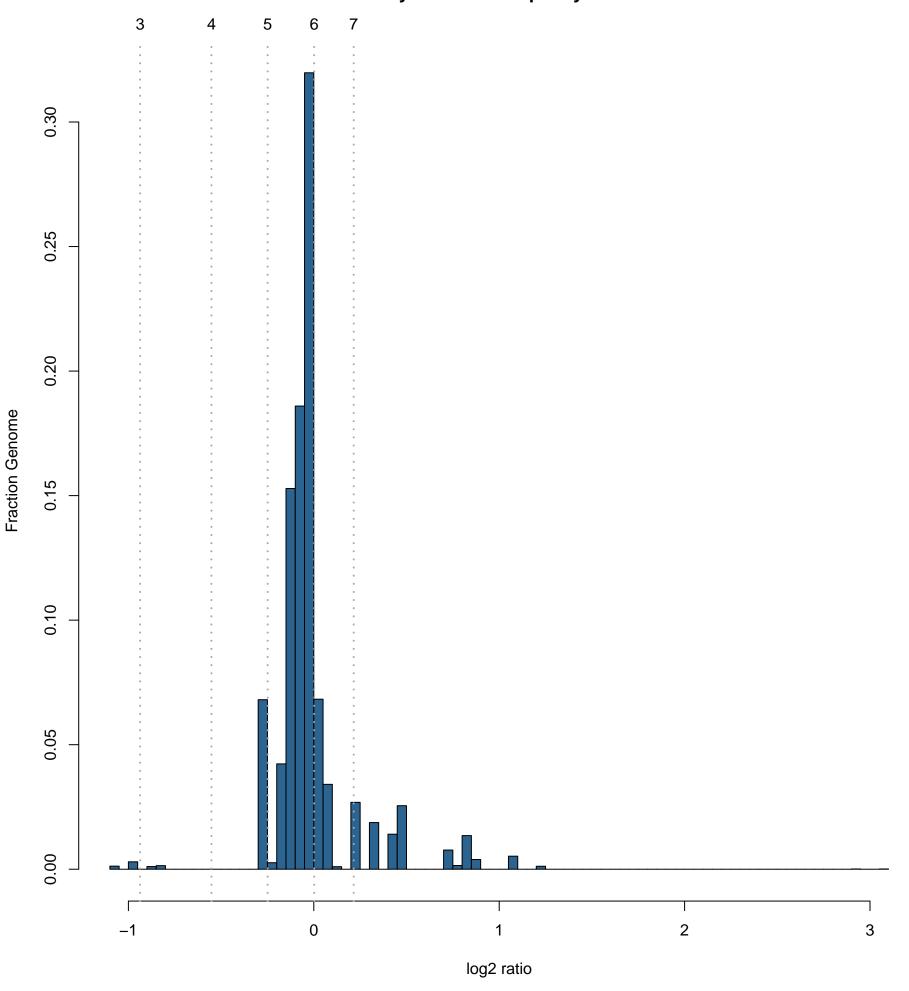
SCNA-fit log-likelihood: -16901.02

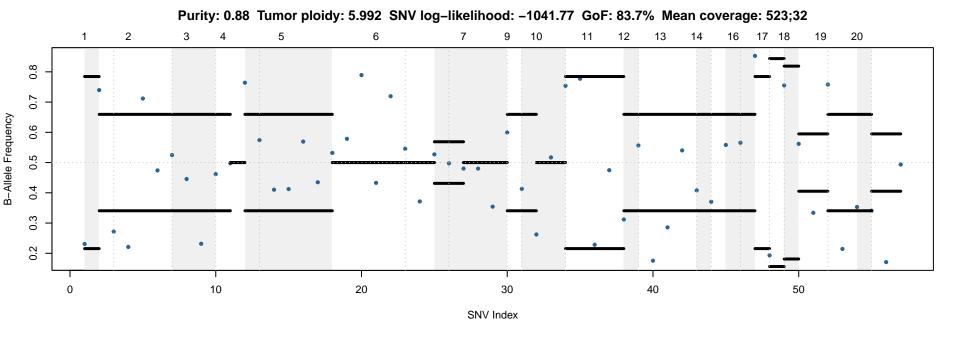




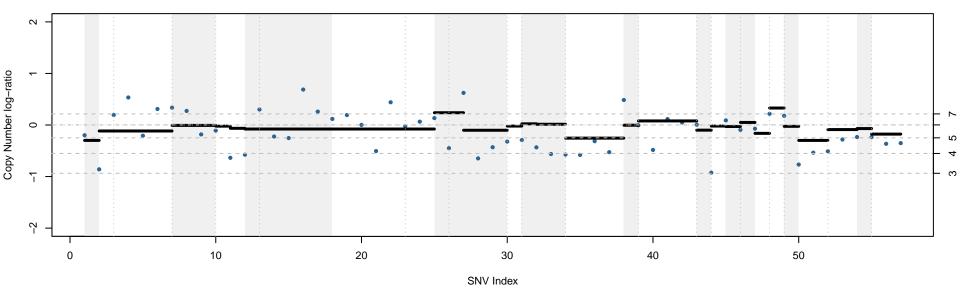


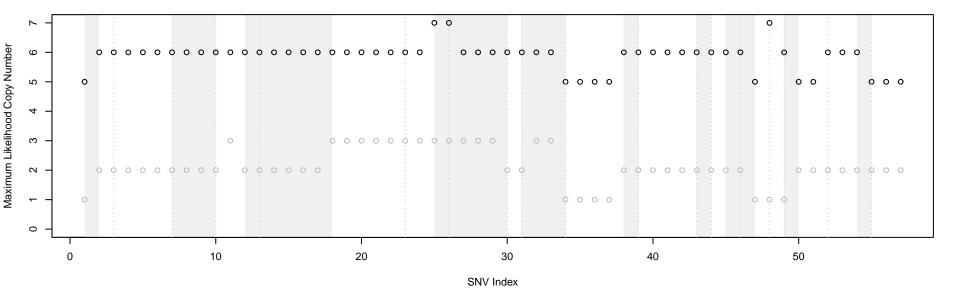
Purity: 0.88 Tumor ploidy: 5.992

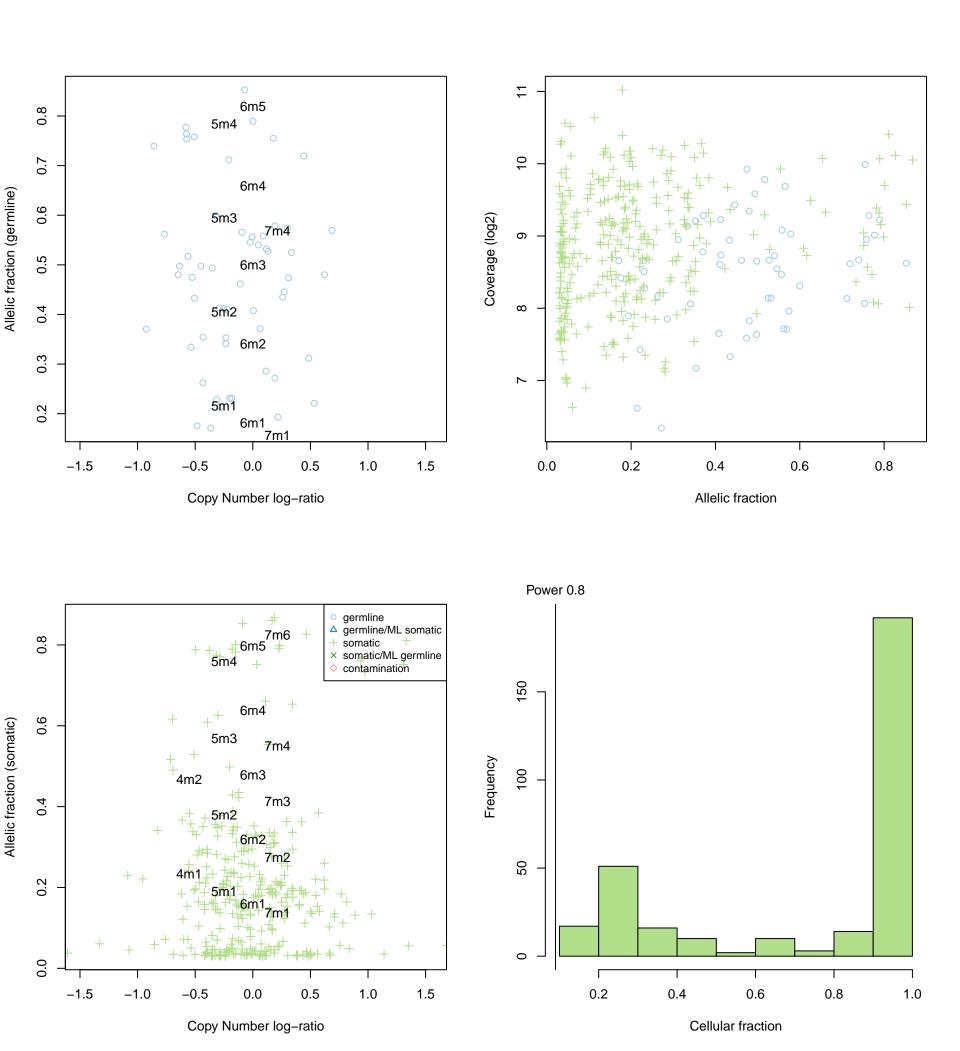




SCNA-fit log-likelihood: -17538.56

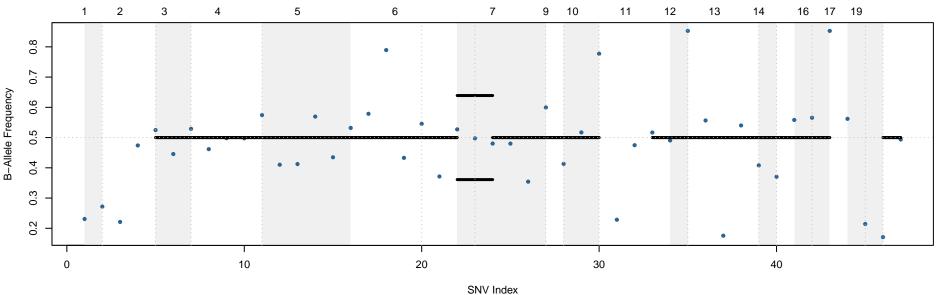






Purity: 0.77 Tumor ploidy: 2.123 2 3 5 6 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -1 0 1 2 3 log2 ratio





SCNA-fit log-likelihood: -16969.37

