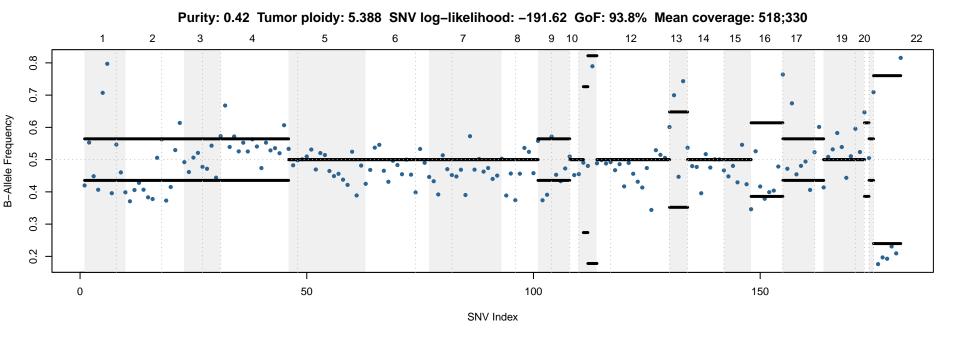
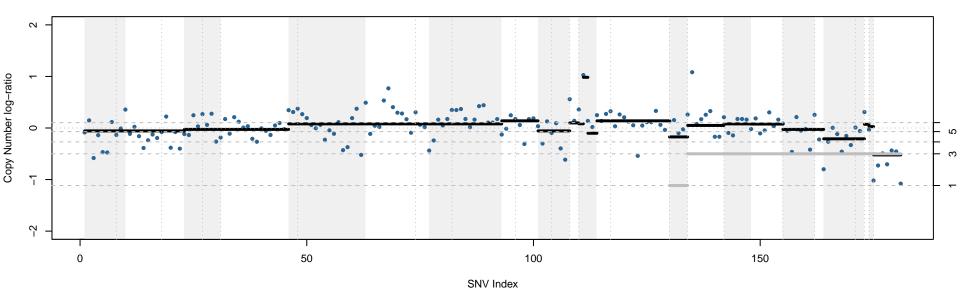
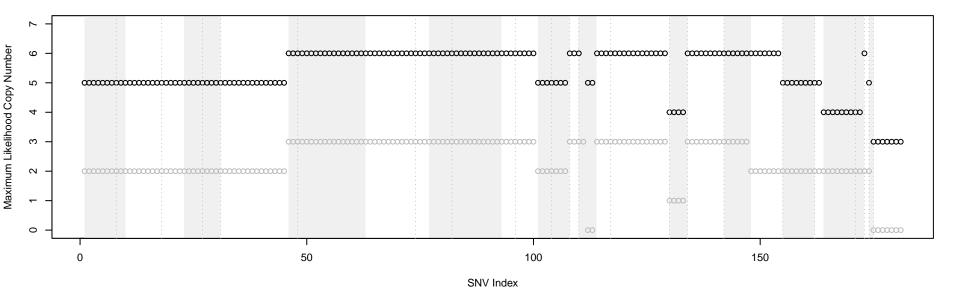
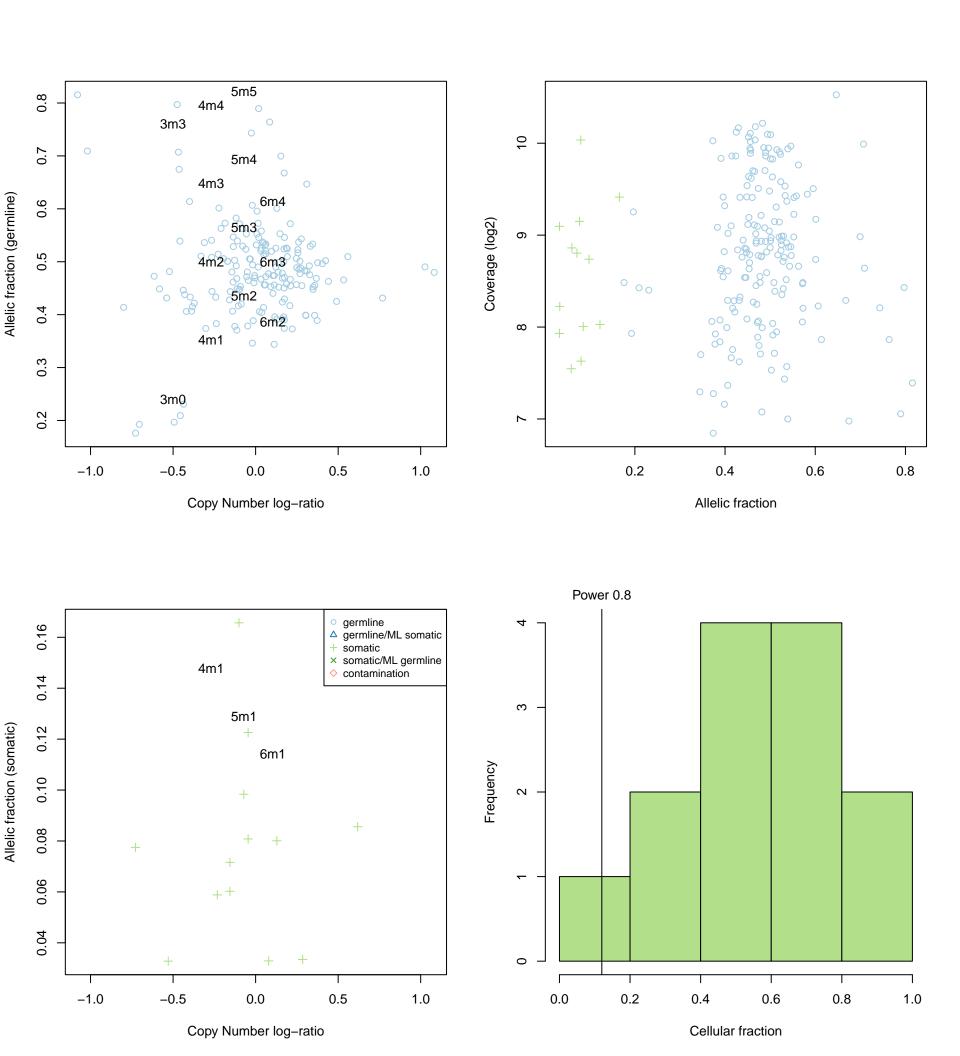
Purity: 0.42 Tumor ploidy: 5.388 6 5 3 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



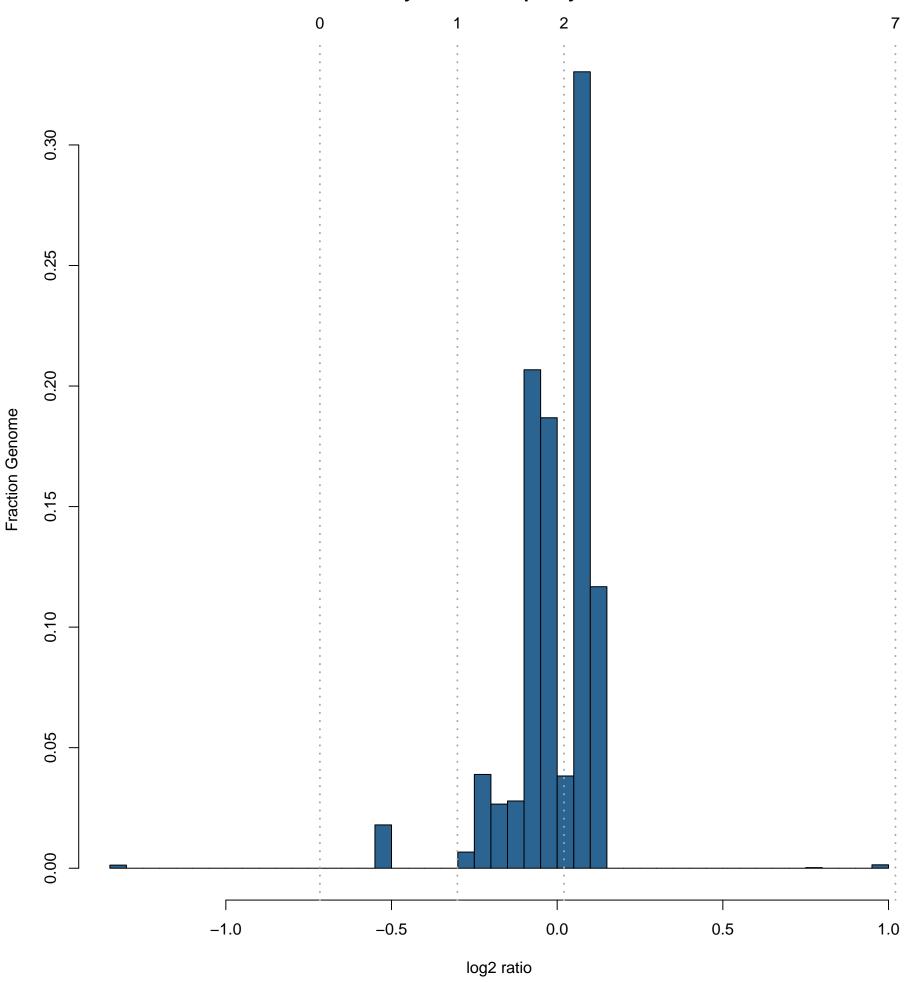
SCNA-fit log-likelihood: -12942.29

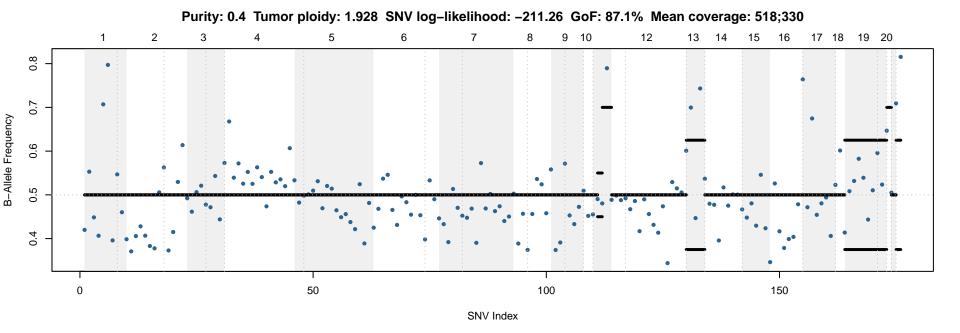




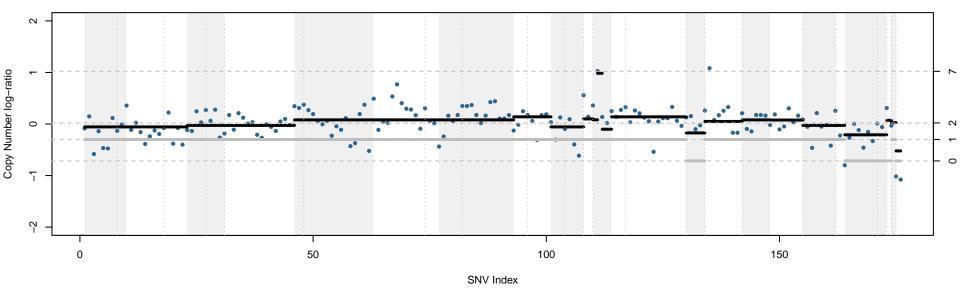


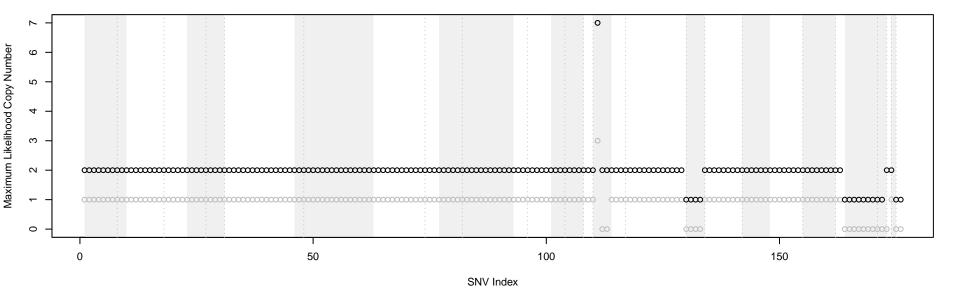
Purity: 0.4 Tumor ploidy: 1.928

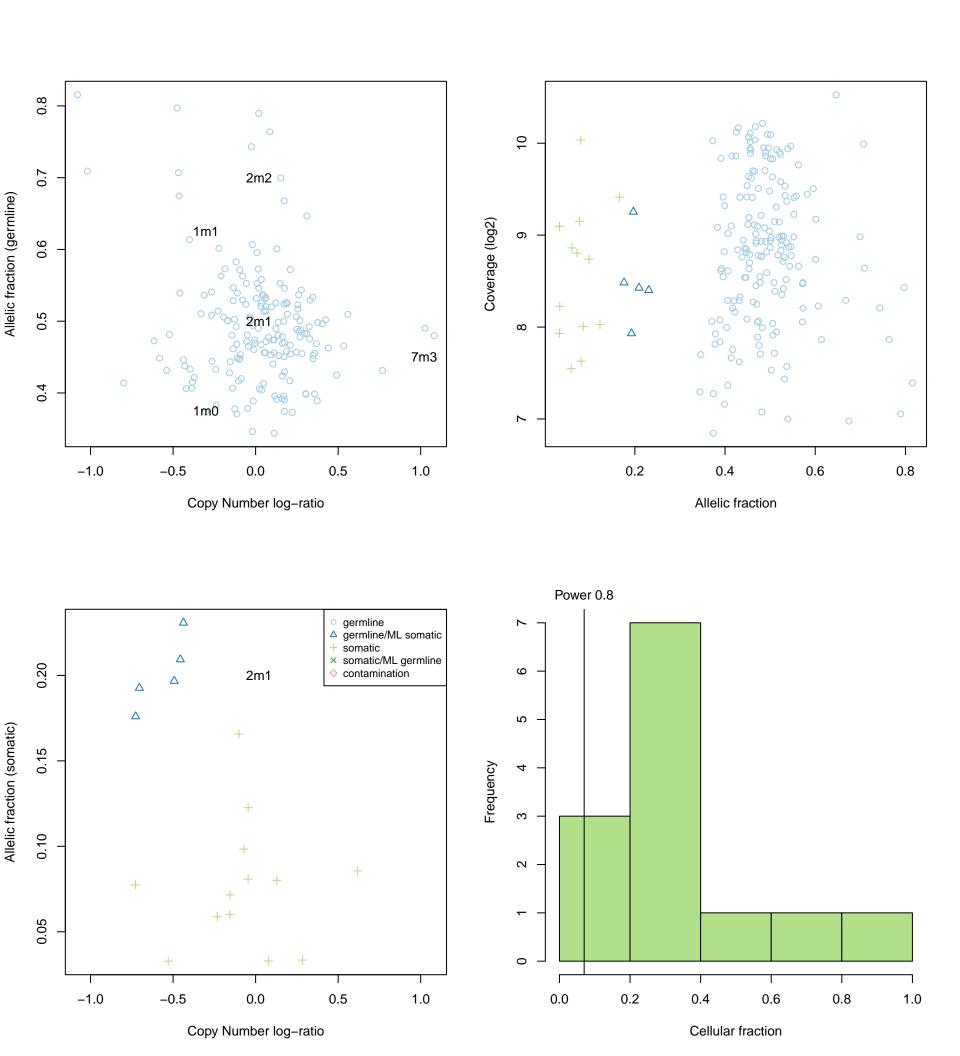




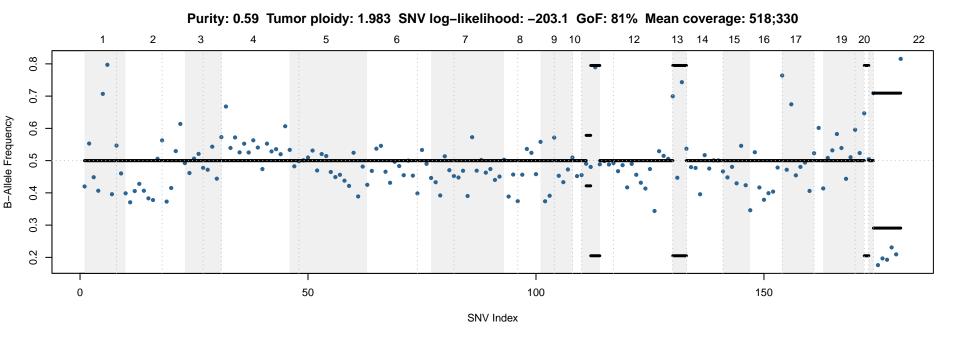
SCNA-fit log-likelihood: -13062.35



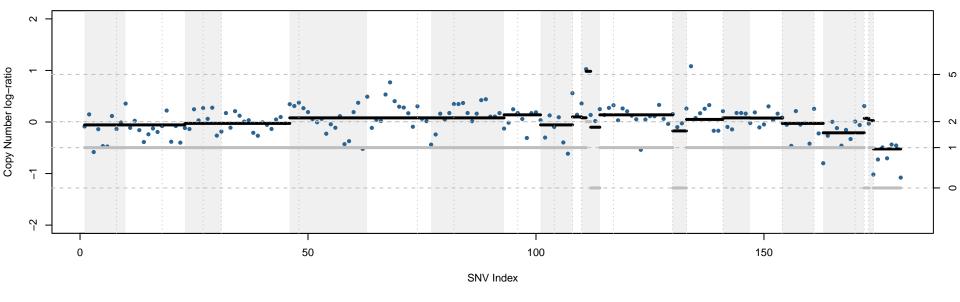


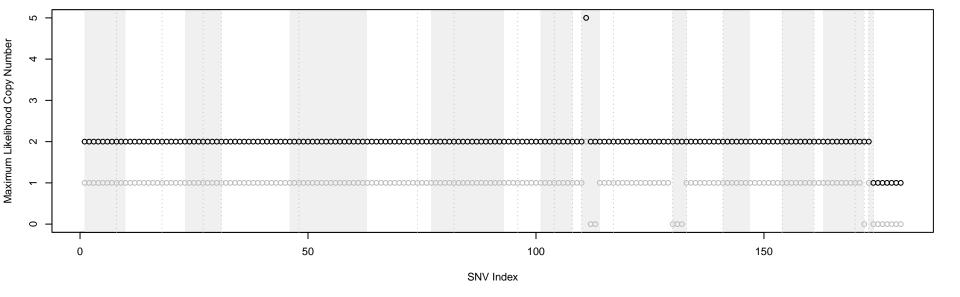


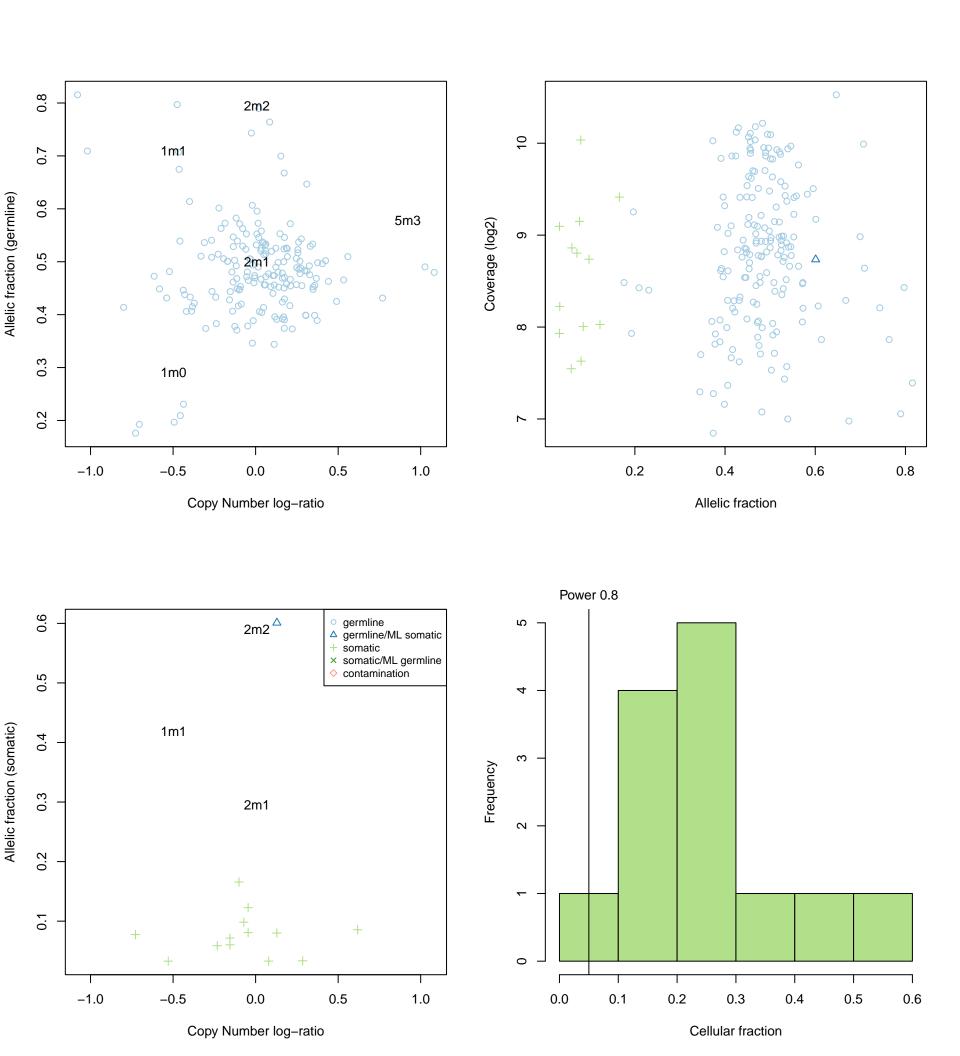
Purity: 0.59 Tumor ploidy: 1.983 0 2 5 0.25 0.20 Fraction Genome 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio

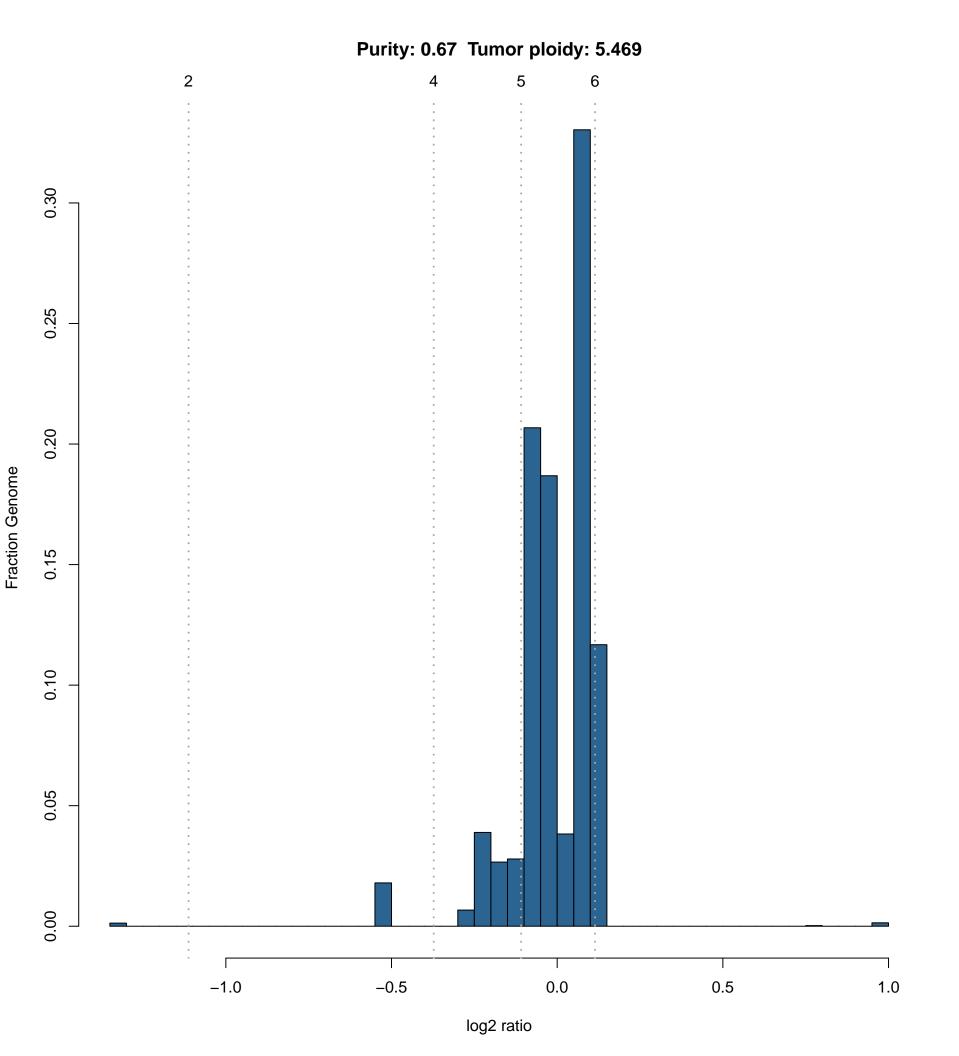


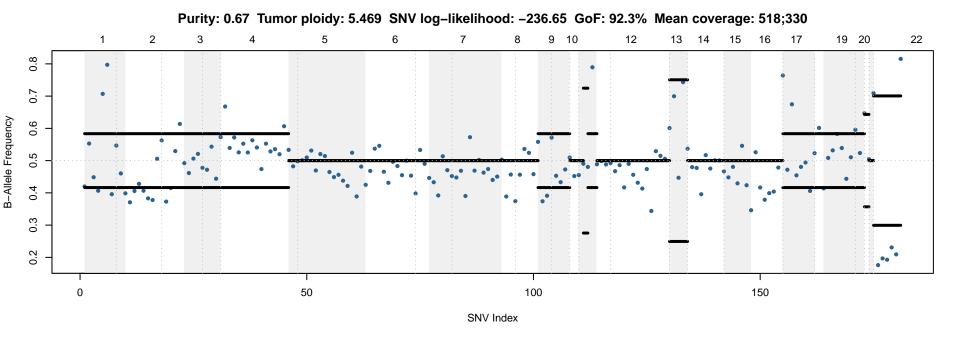
SCNA-fit log-likelihood: -13096.51



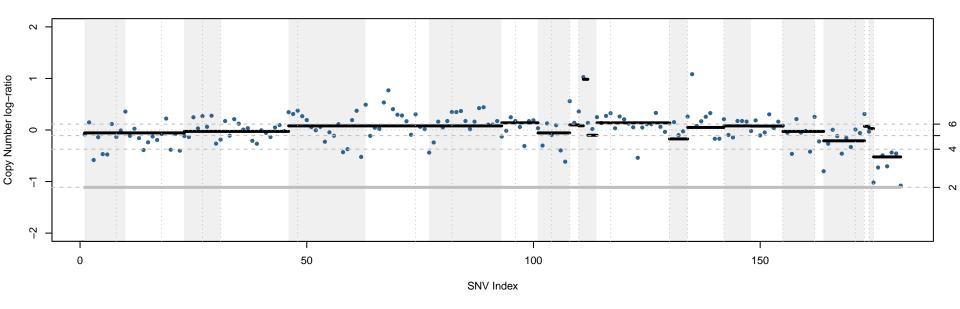


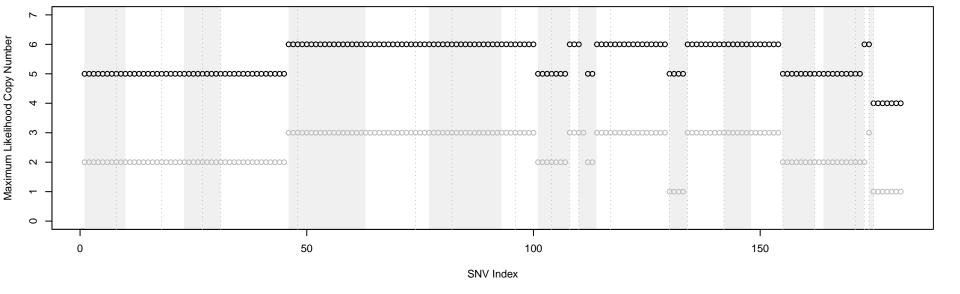


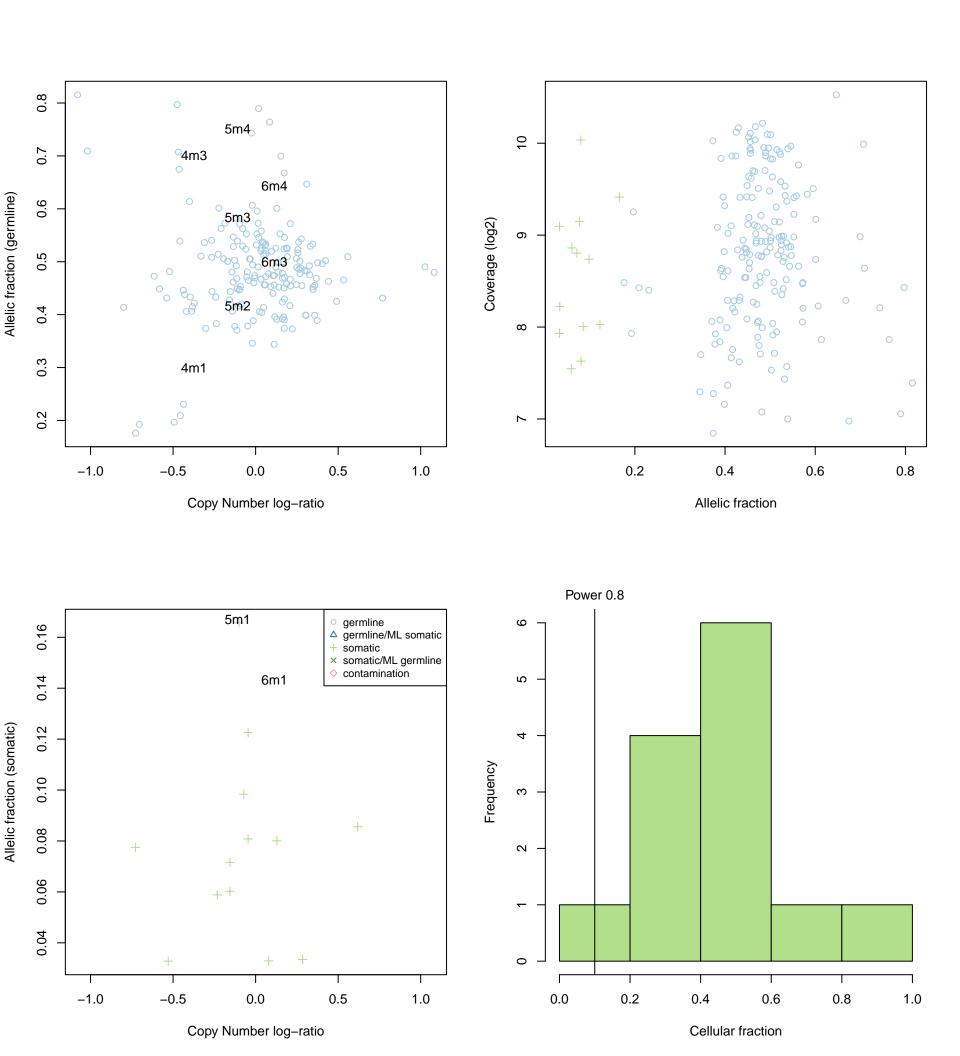


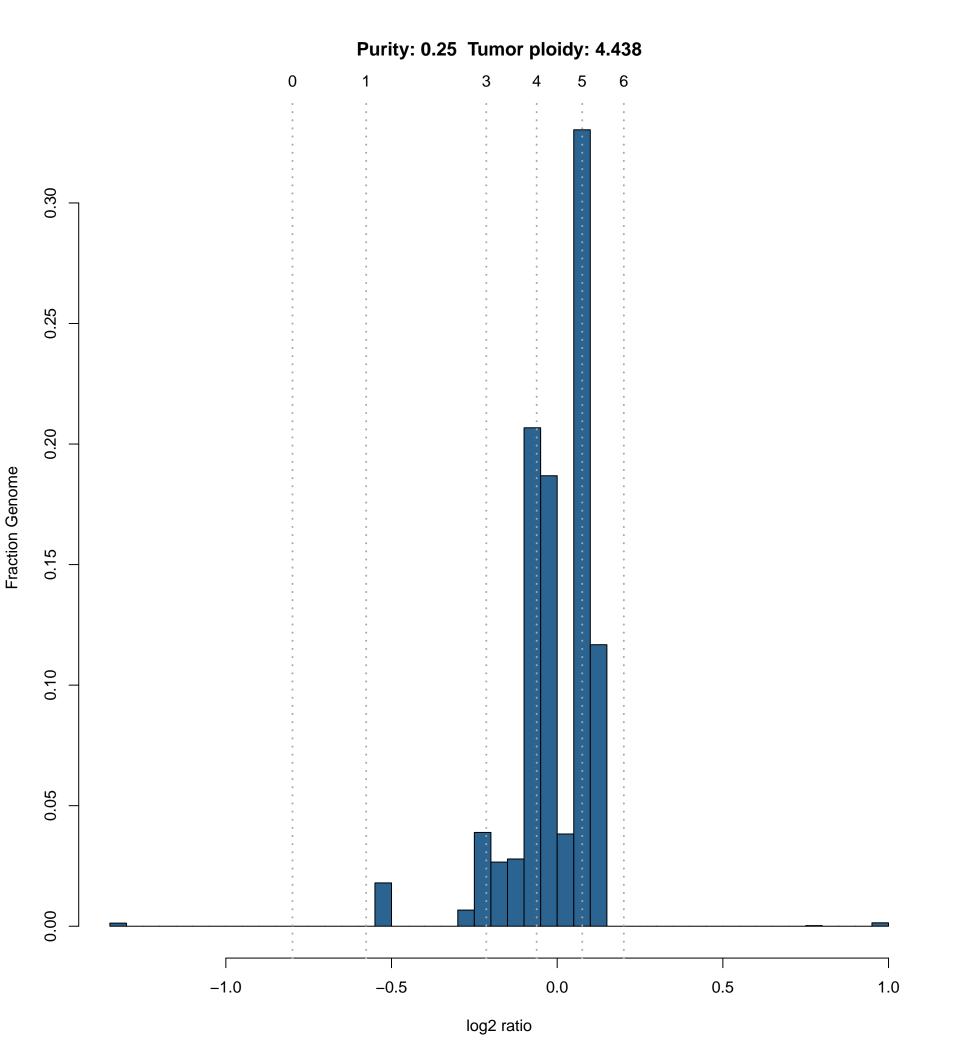


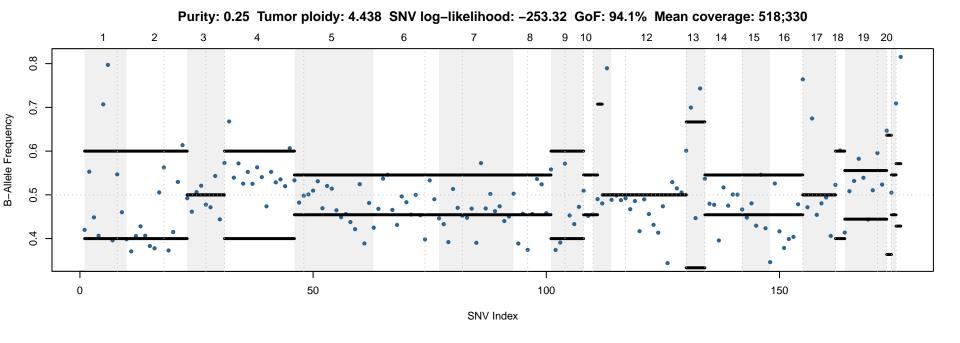
SCNA-fit log-likelihood: -12997.53



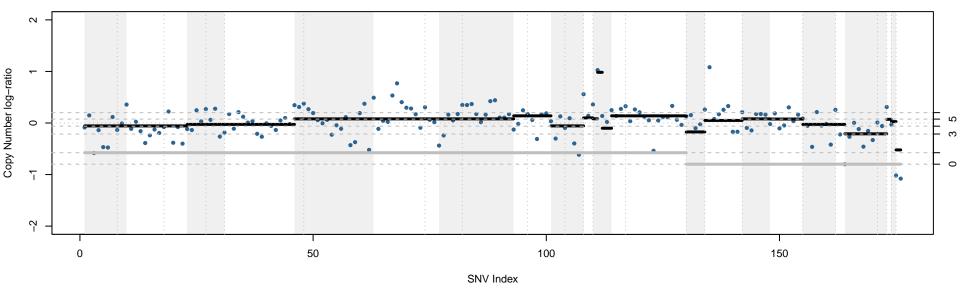


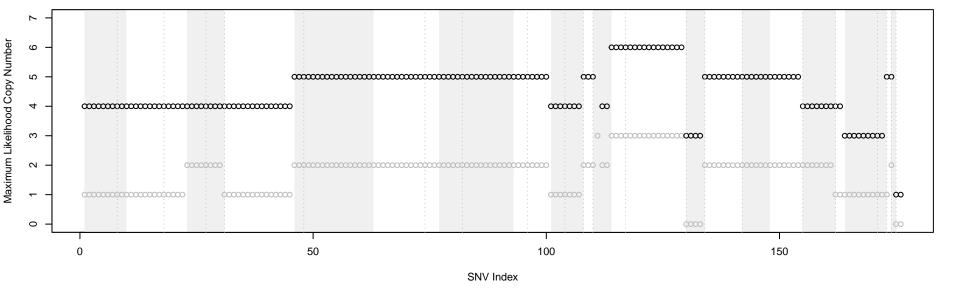


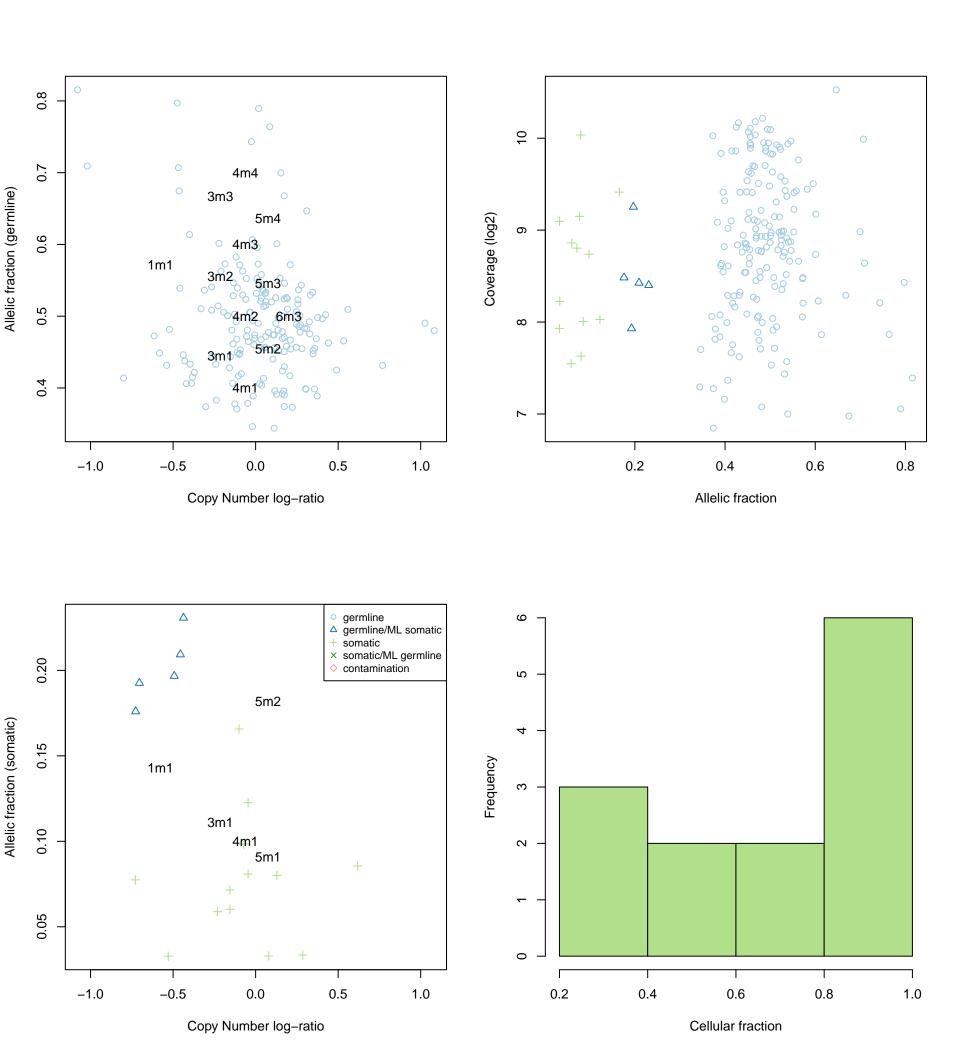




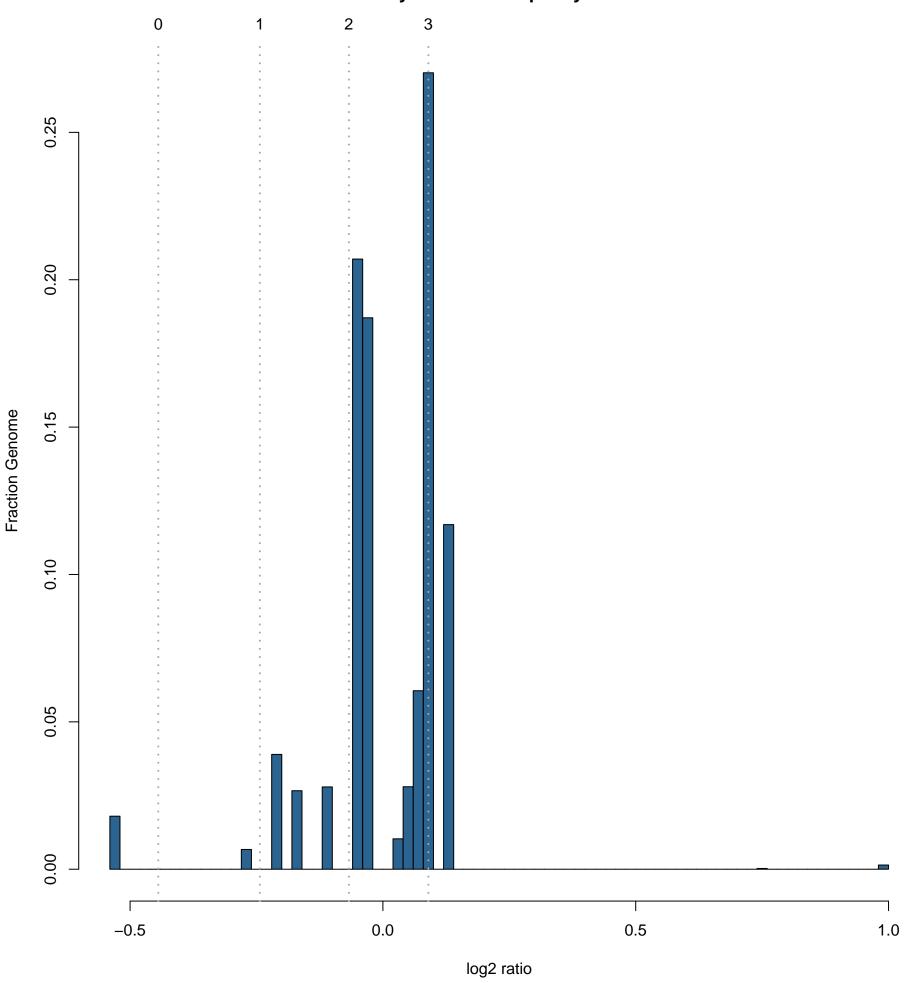
SCNA-fit log-likelihood: -12933.78

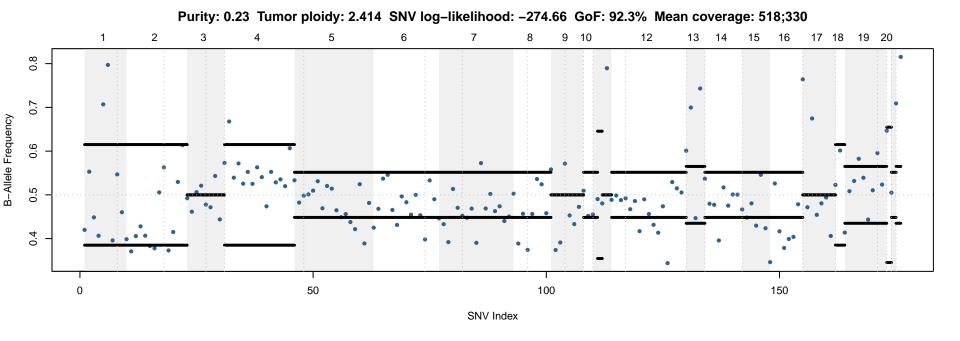




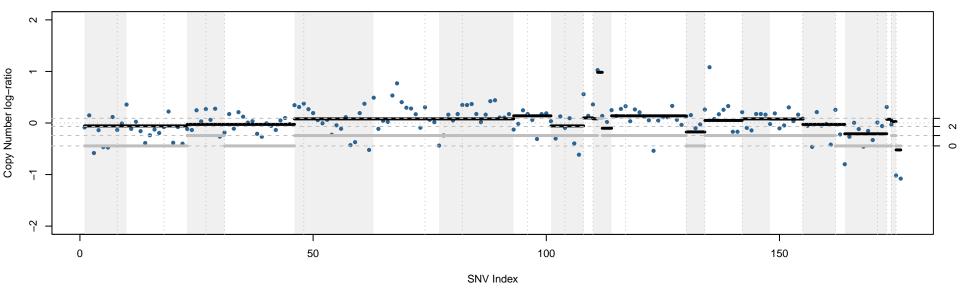


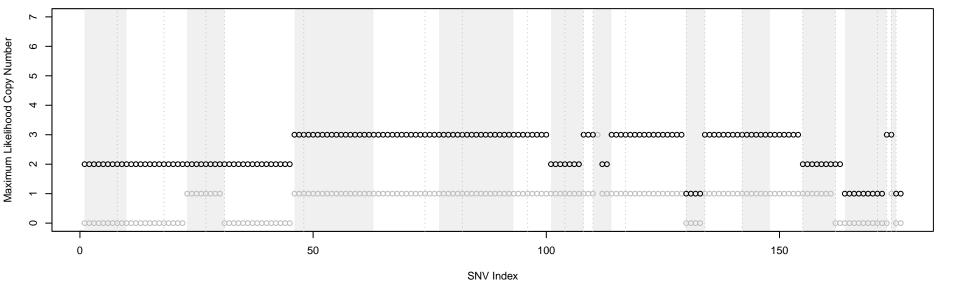
Purity: 0.23 Tumor ploidy: 2.414

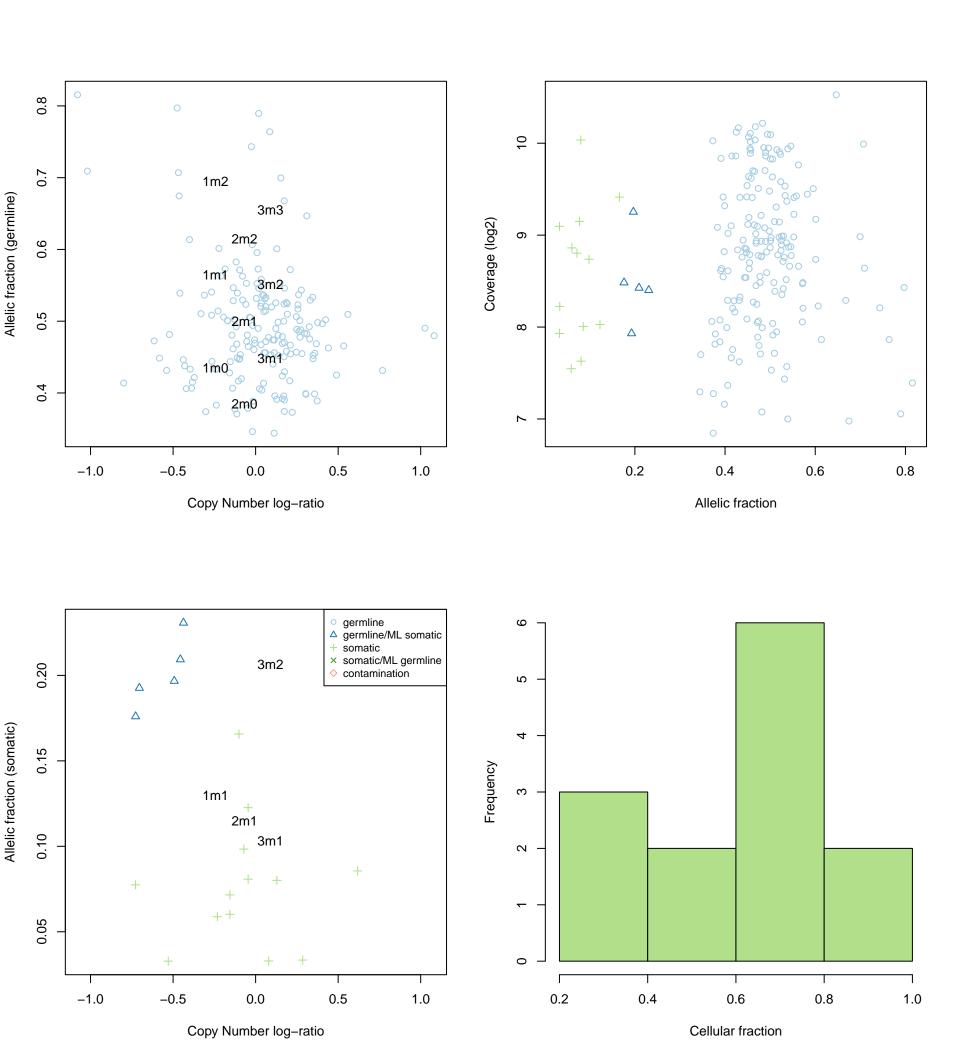


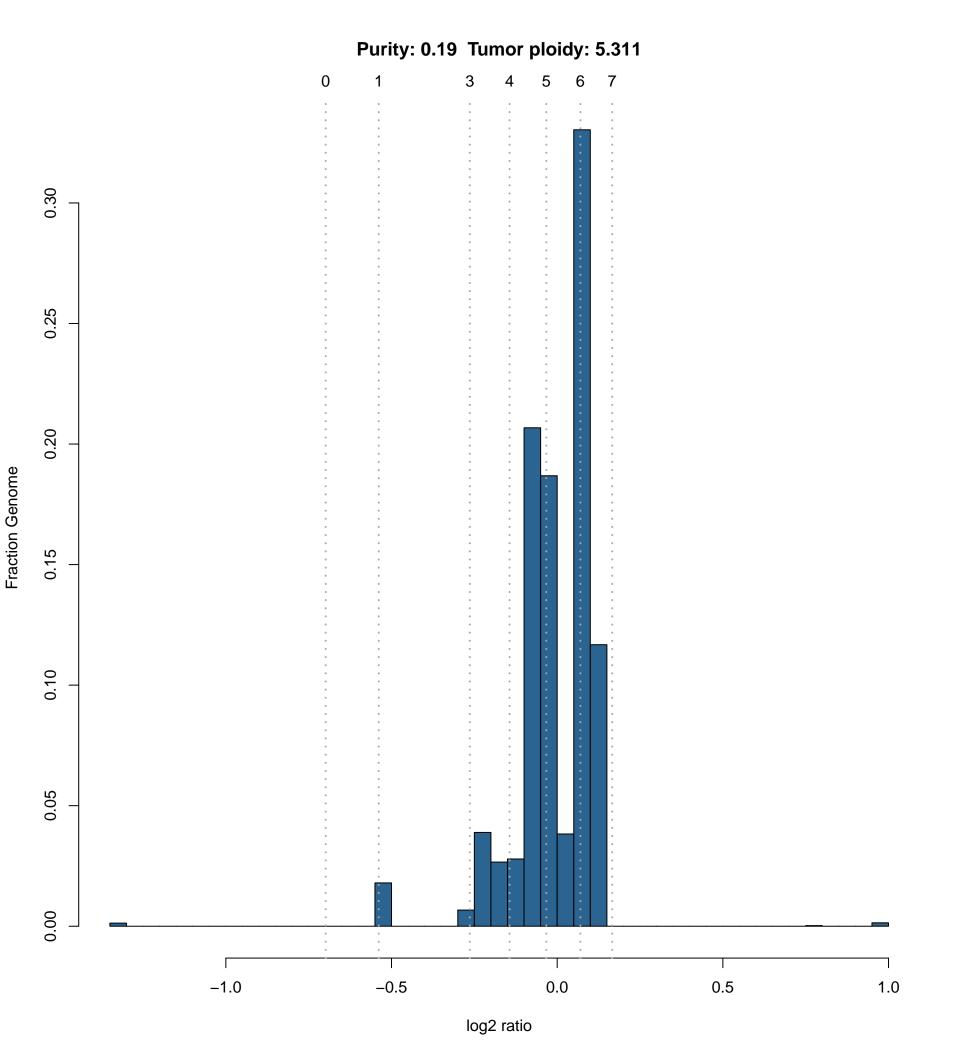


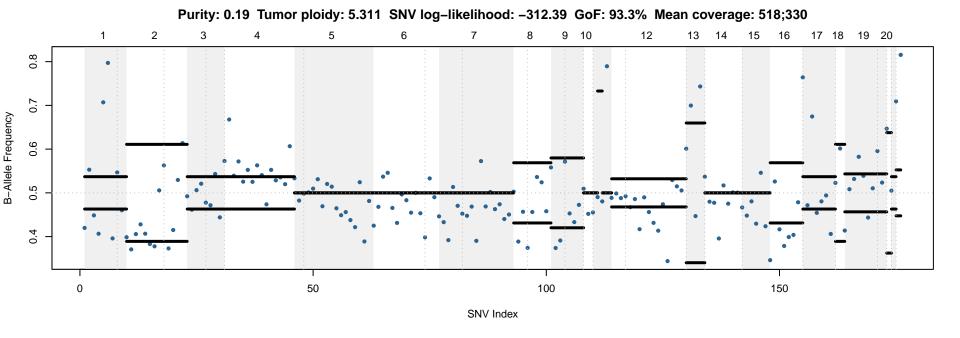
SCNA-fit log-likelihood: -12987.98



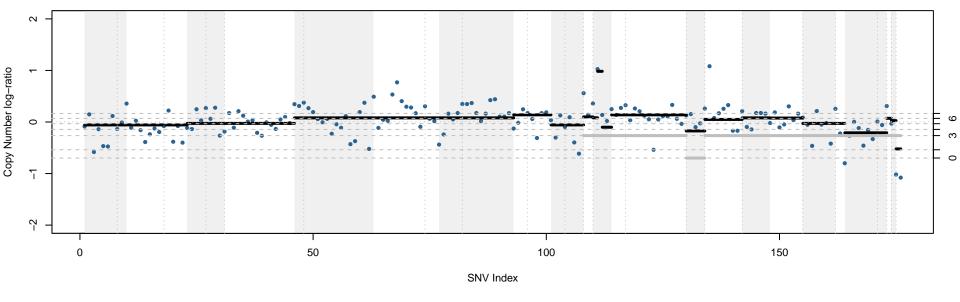


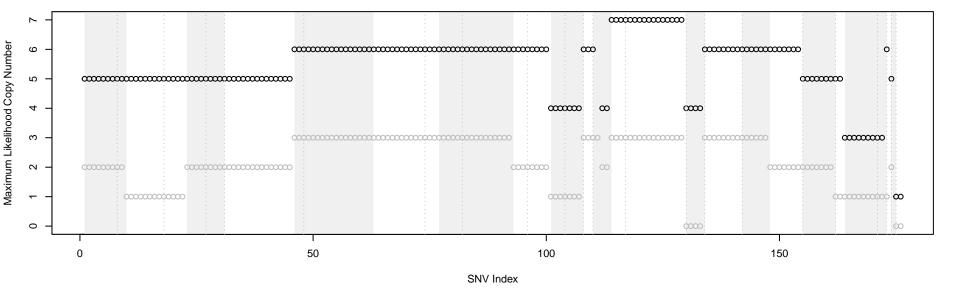


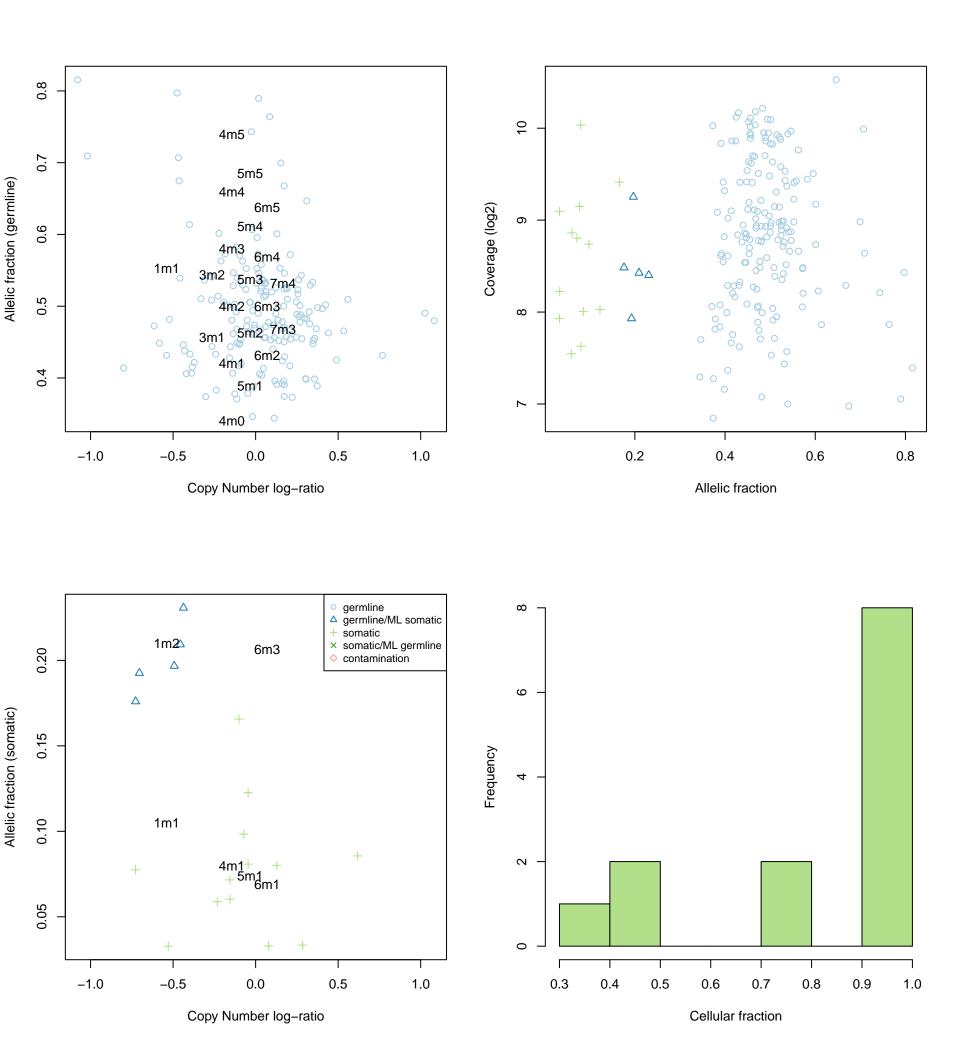




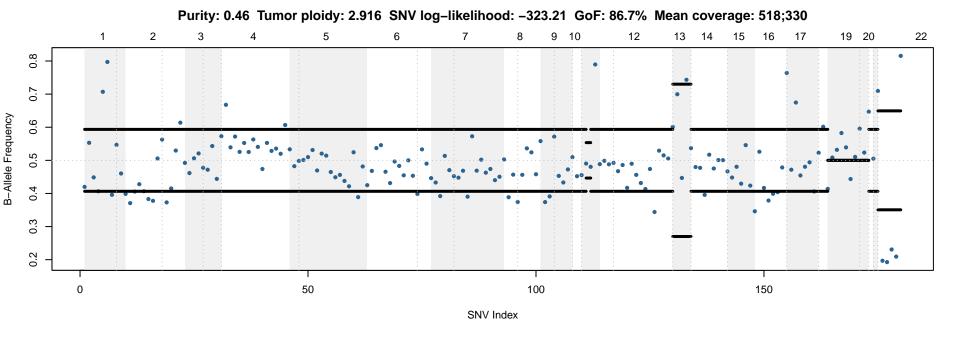
SCNA-fit log-likelihood: -12932.46



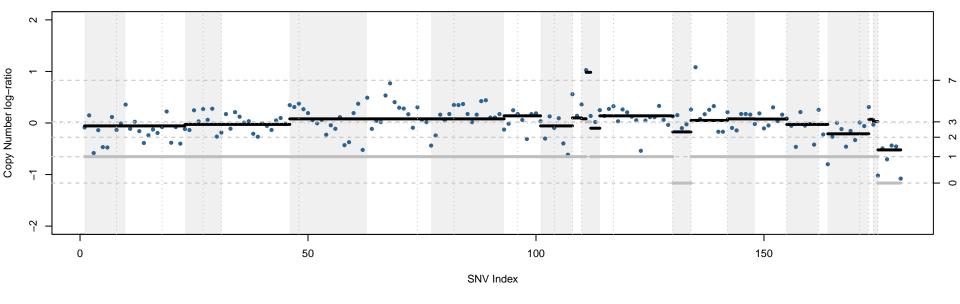


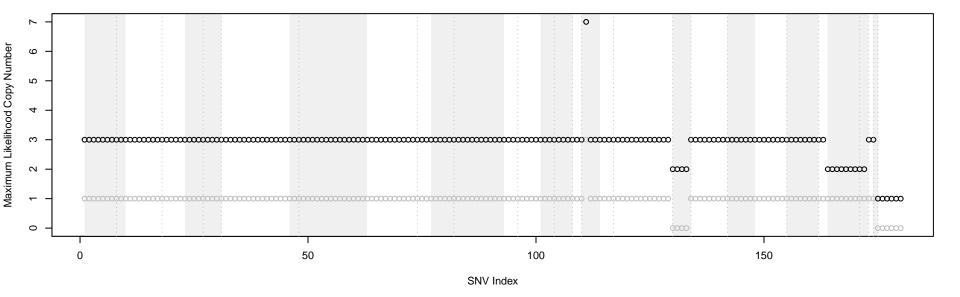


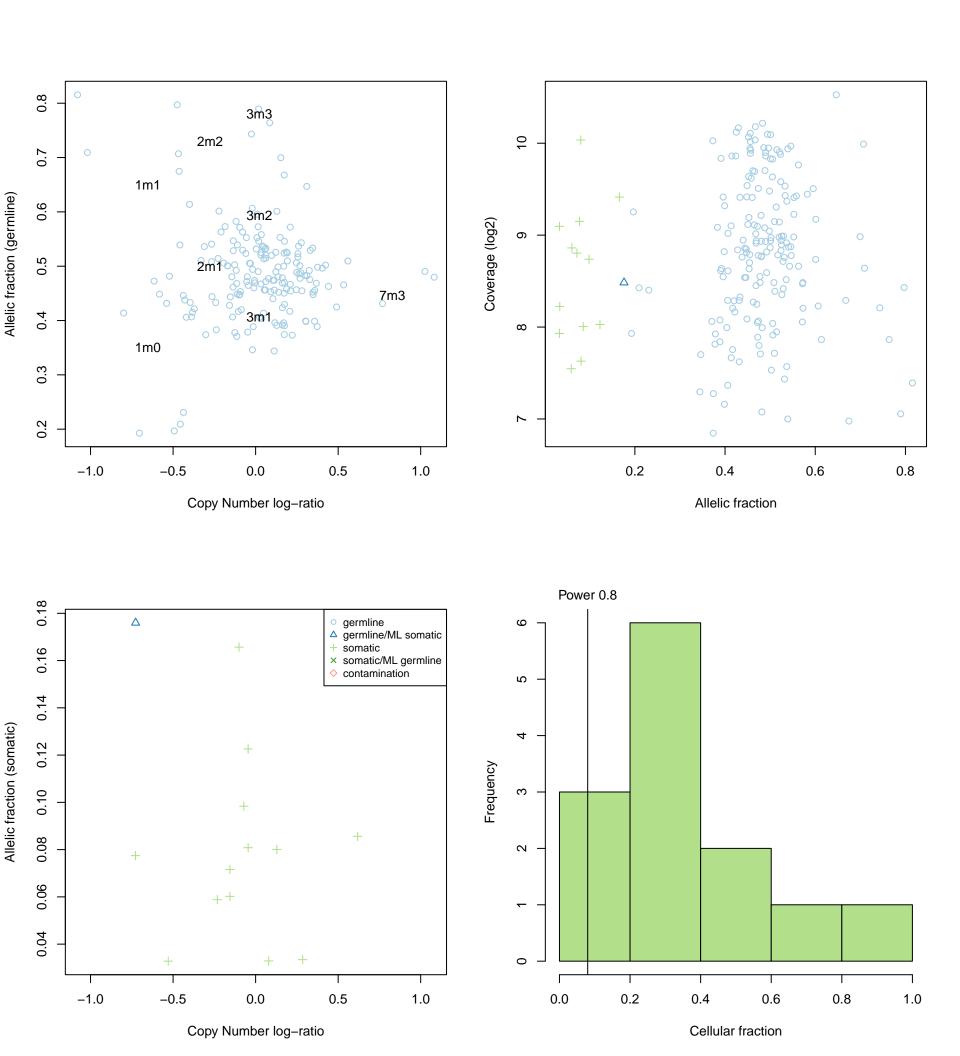
Purity: 0.46 Tumor ploidy: 2.916 0 2 7 3 0.25 0.20 Fraction Genome 0.15 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio

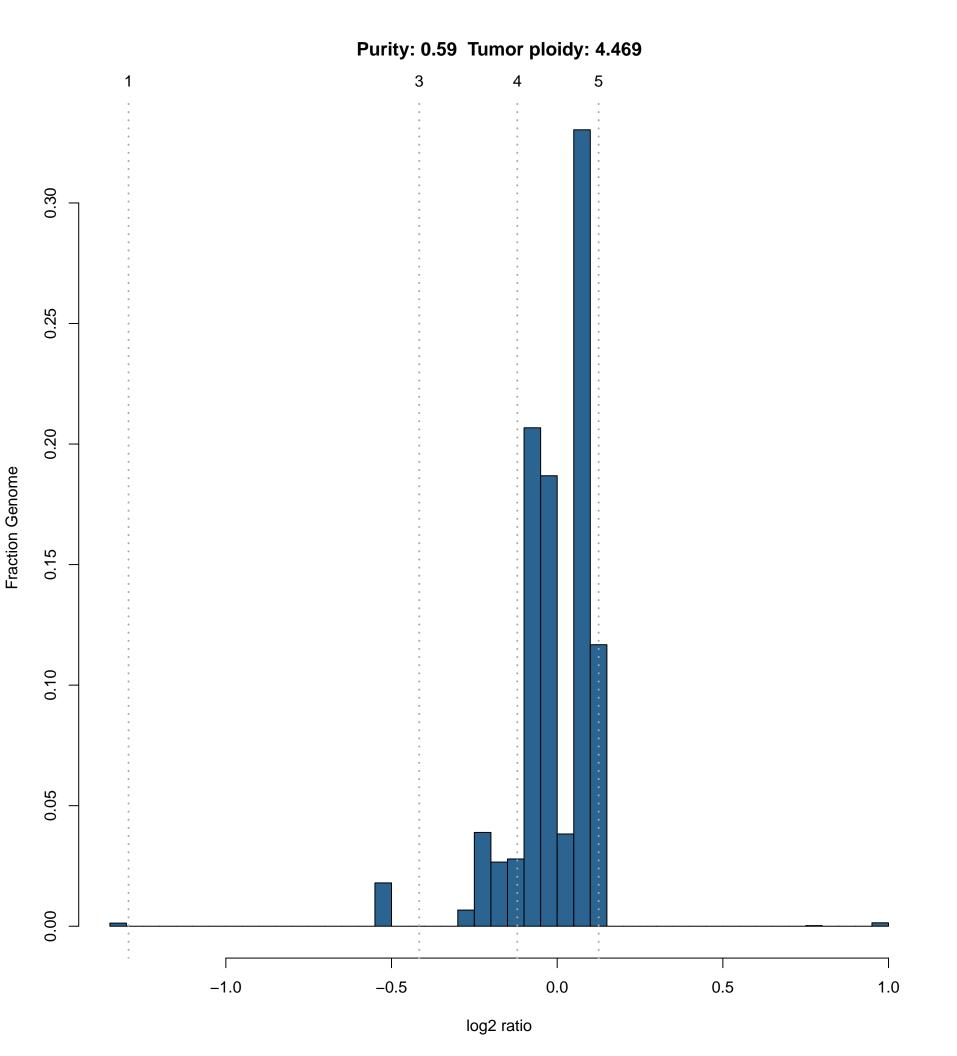


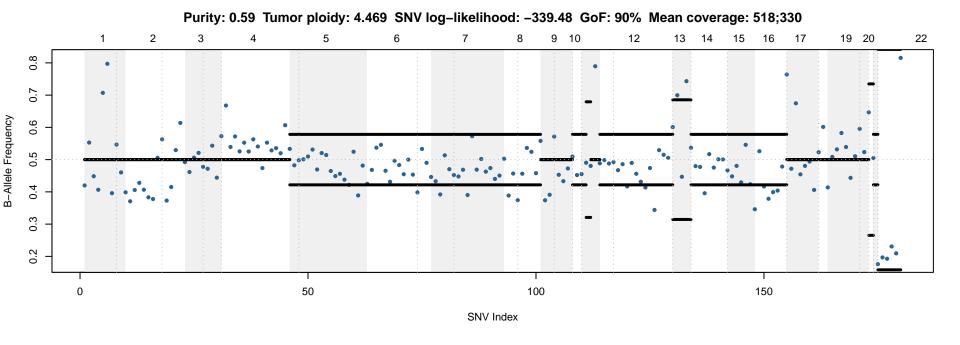
SCNA-fit log-likelihood: -13027.51



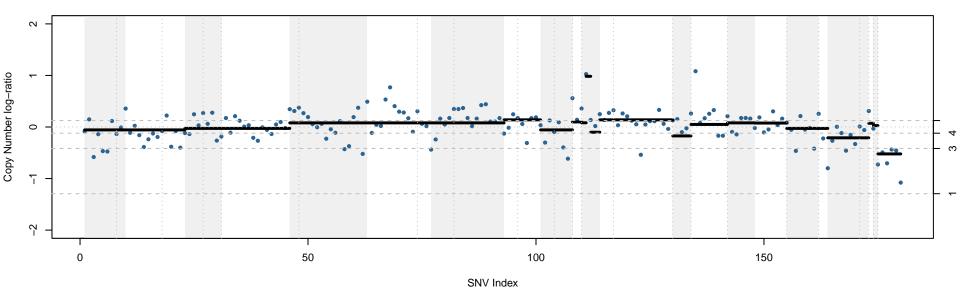


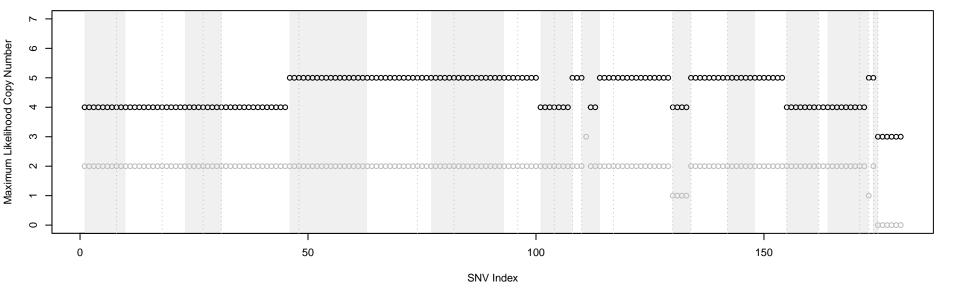


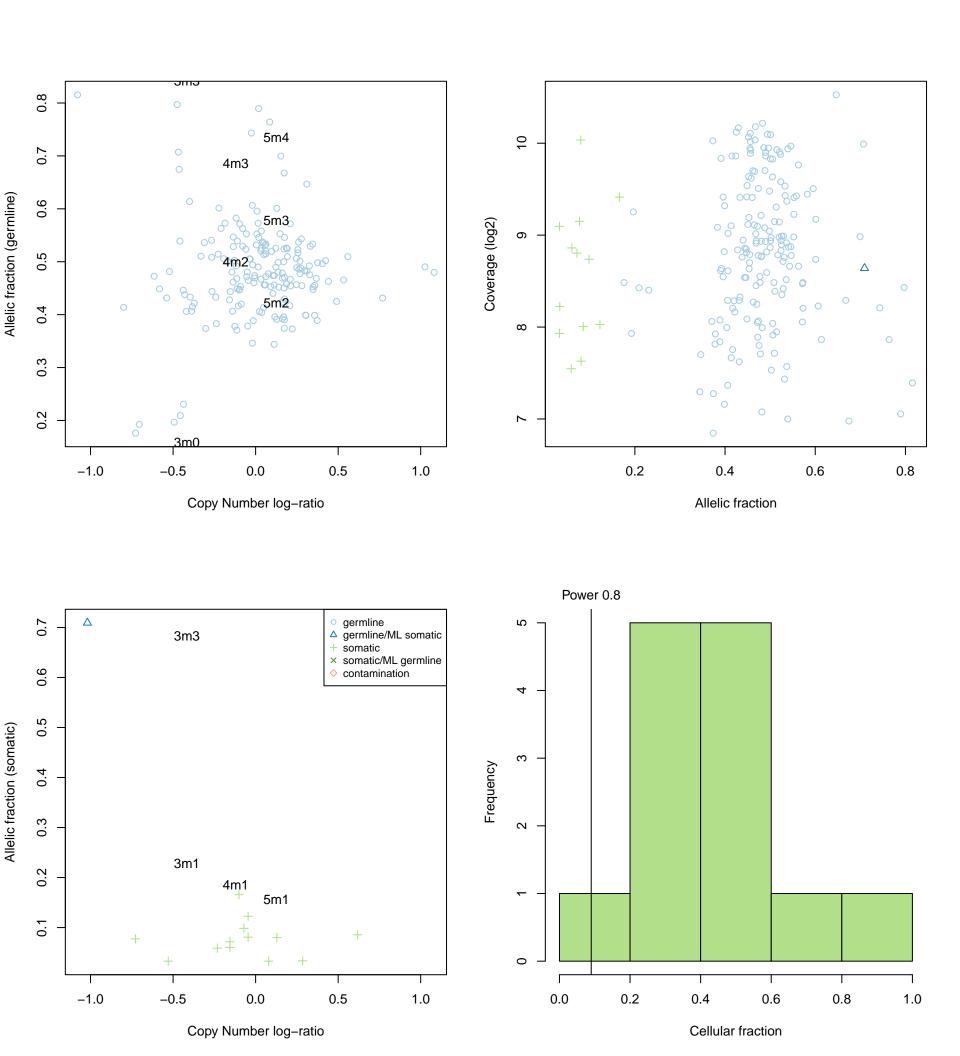




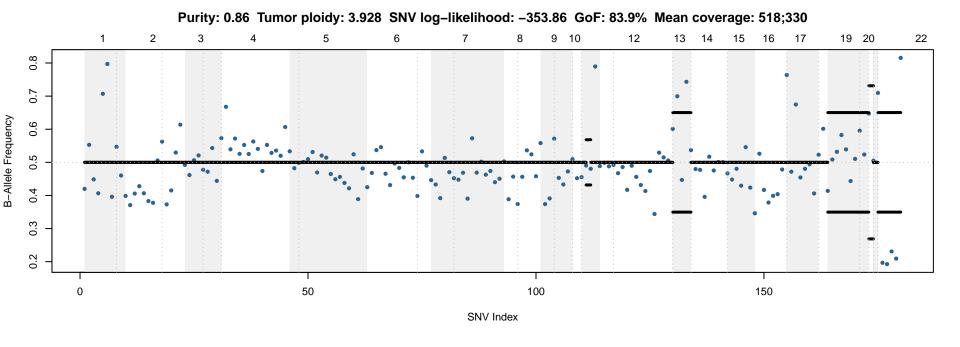
SCNA-fit log-likelihood: -13013.44



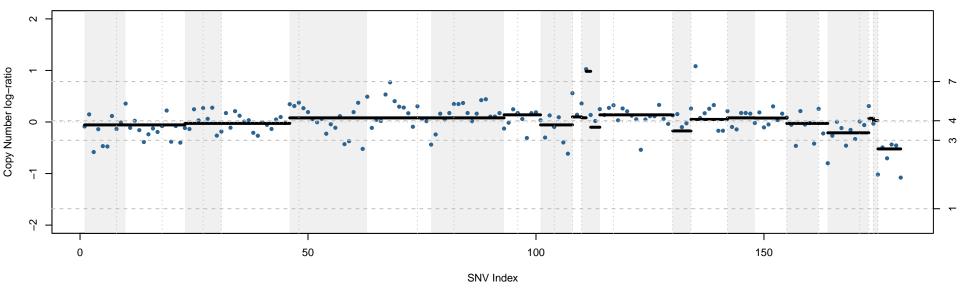


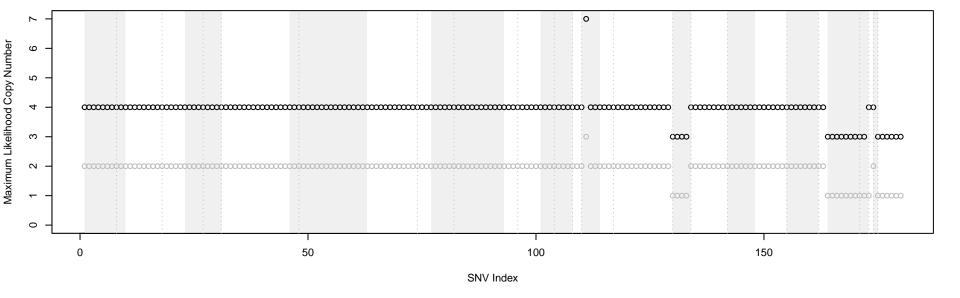


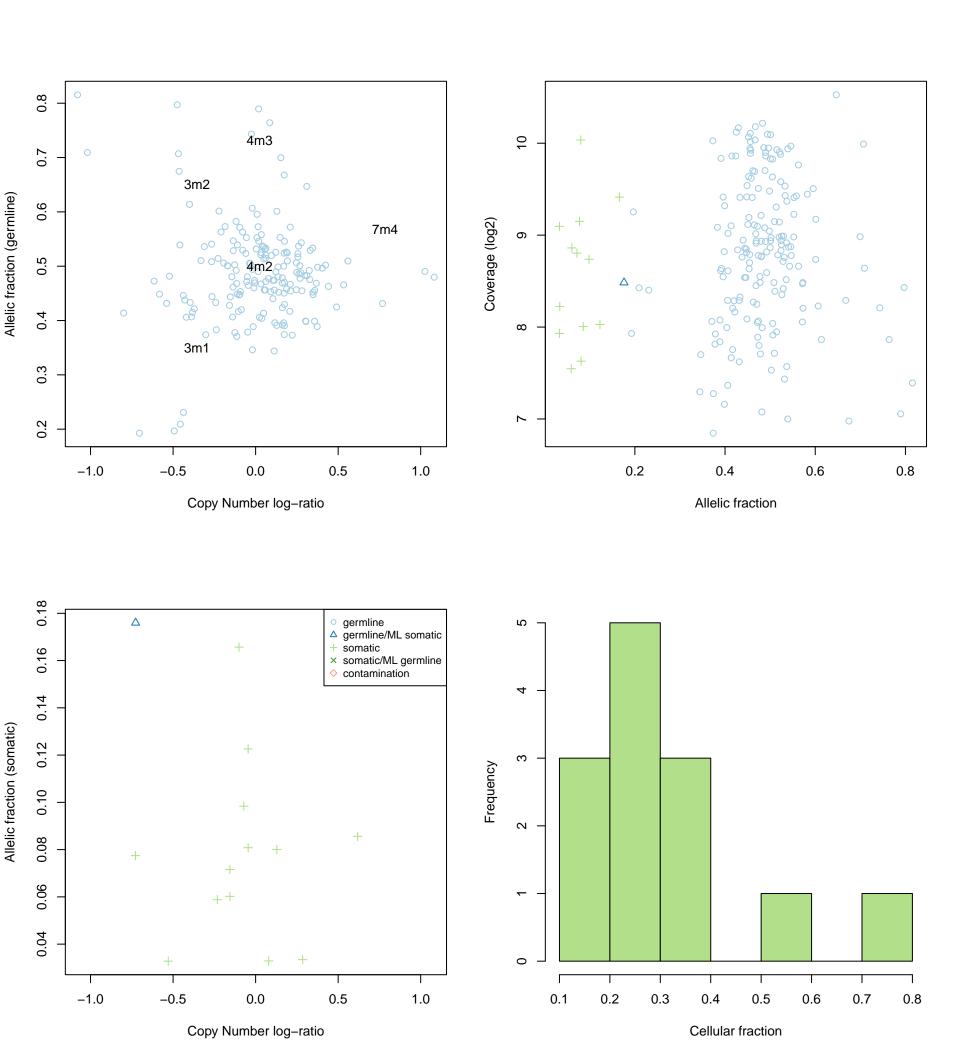
Purity: 0.86 Tumor ploidy: 3.928 3 7 0.25 0.20 Fraction Genome 0.15 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



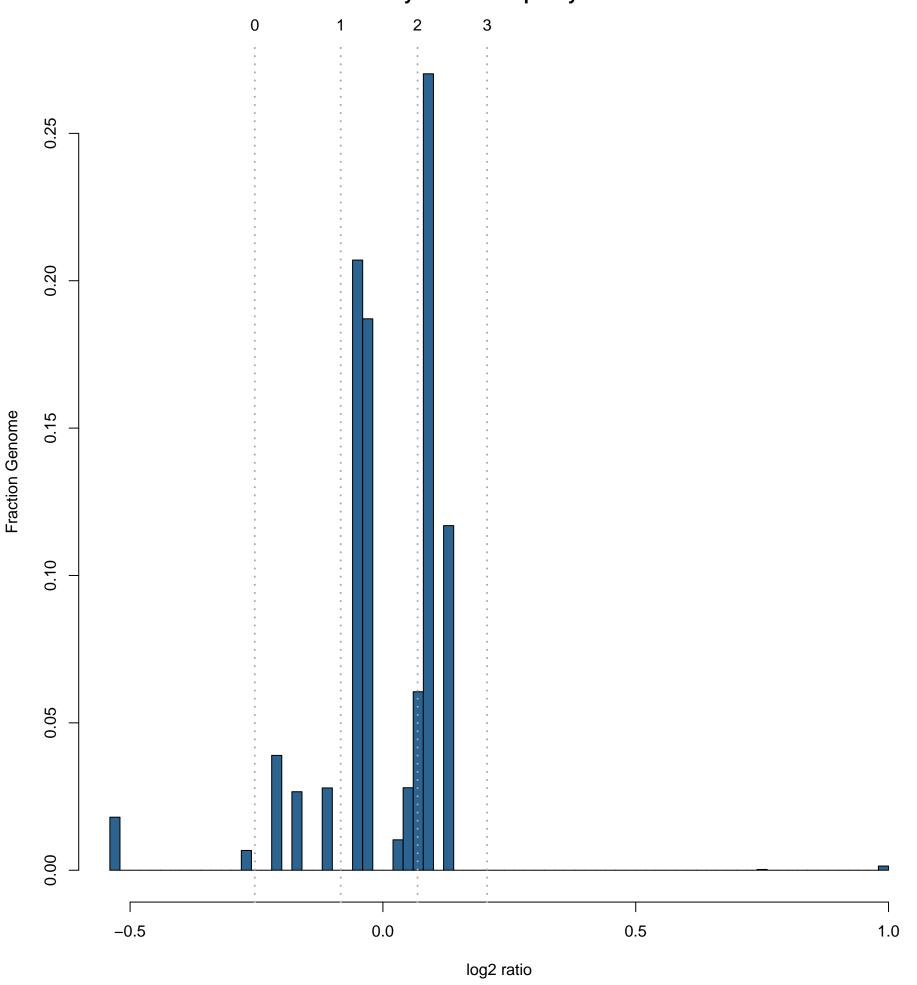
SCNA-fit log-likelihood: -13068.28

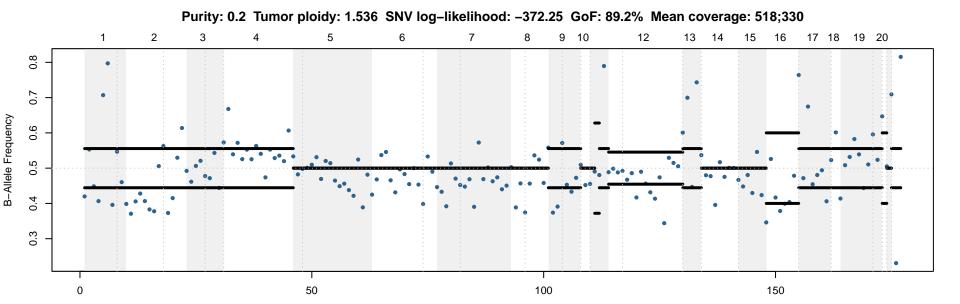






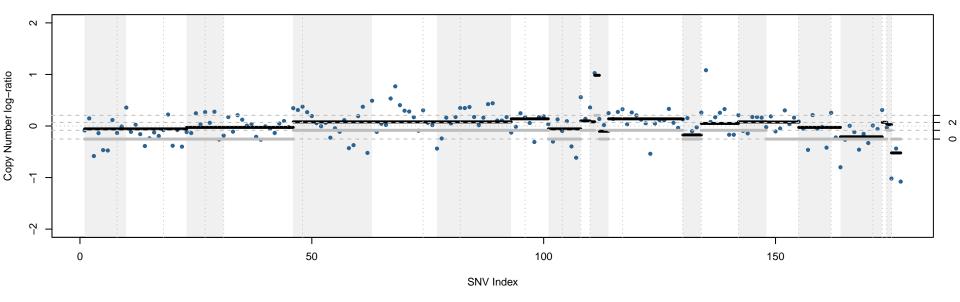
Purity: 0.2 Tumor ploidy: 1.536

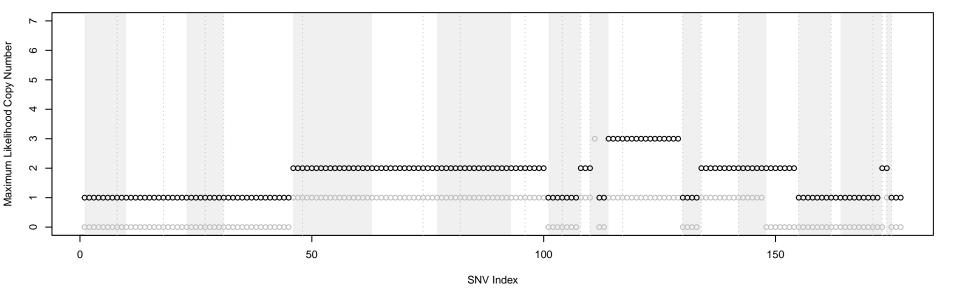


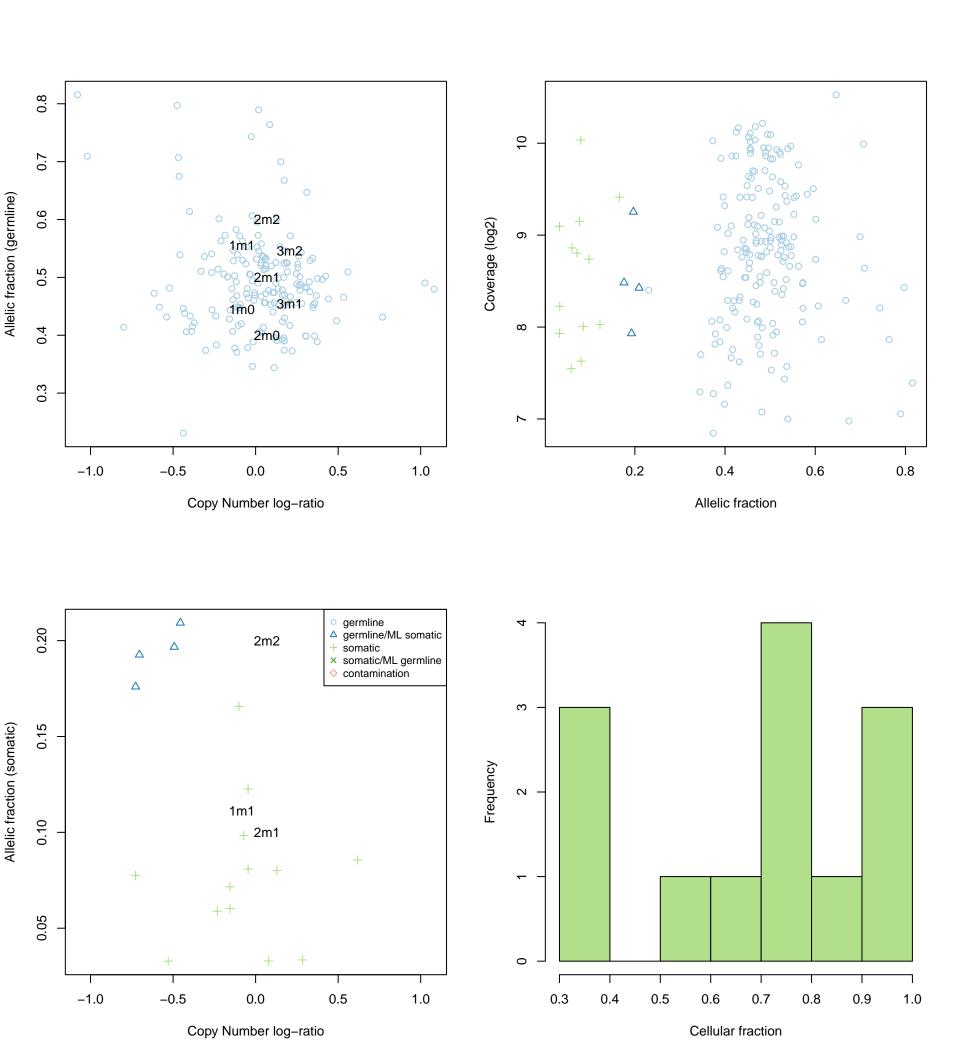


SCNA-fit log-likelihood: -13072.24

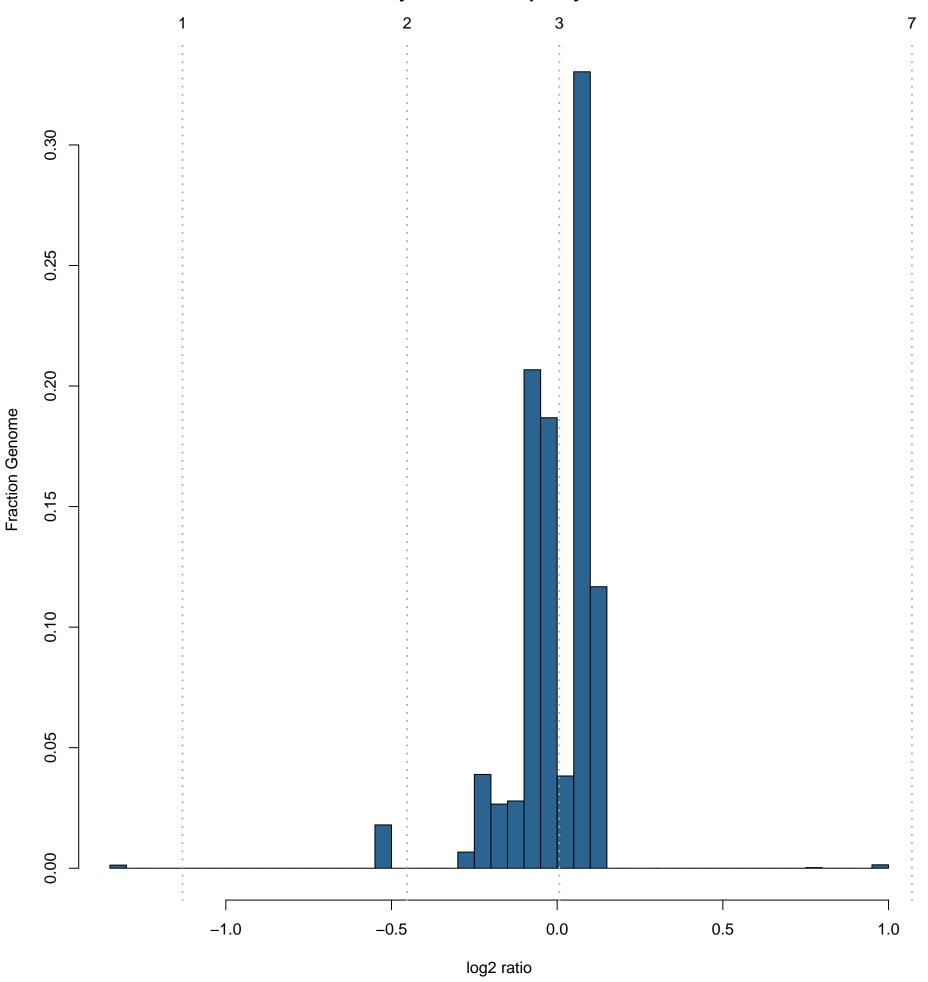
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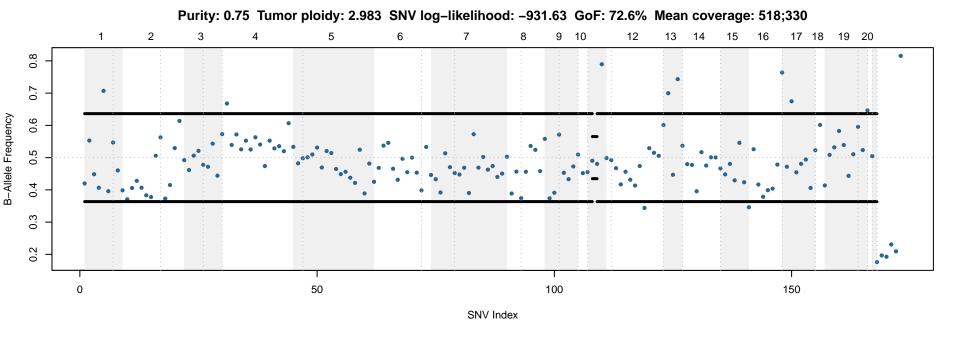






Purity: 0.75 Tumor ploidy: 2.983





SCNA-fit log-likelihood: -13097.38

