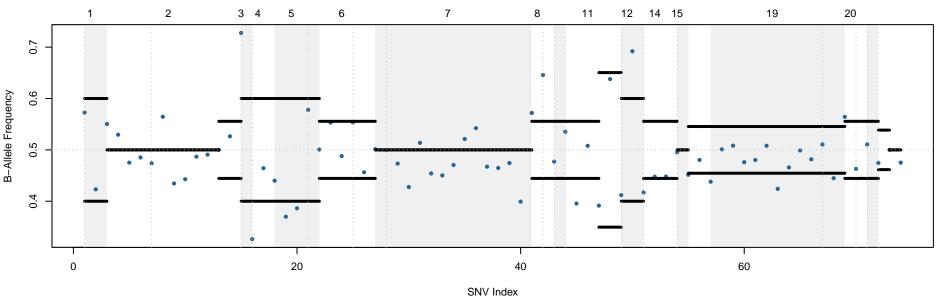
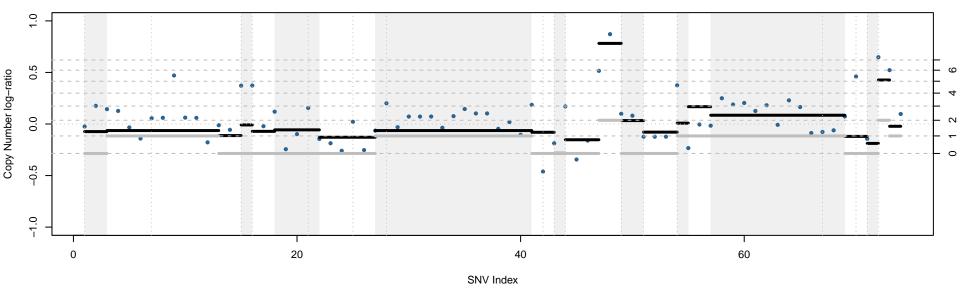
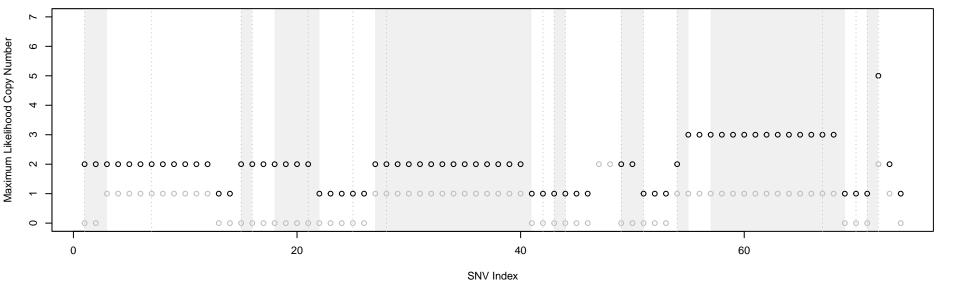
Purity: 0.2 Tumor ploidy: 1.752 3 0 2 6 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -0.4 -0.2 0.0 0.2 0.4 0.6 0.8 log2 ratio

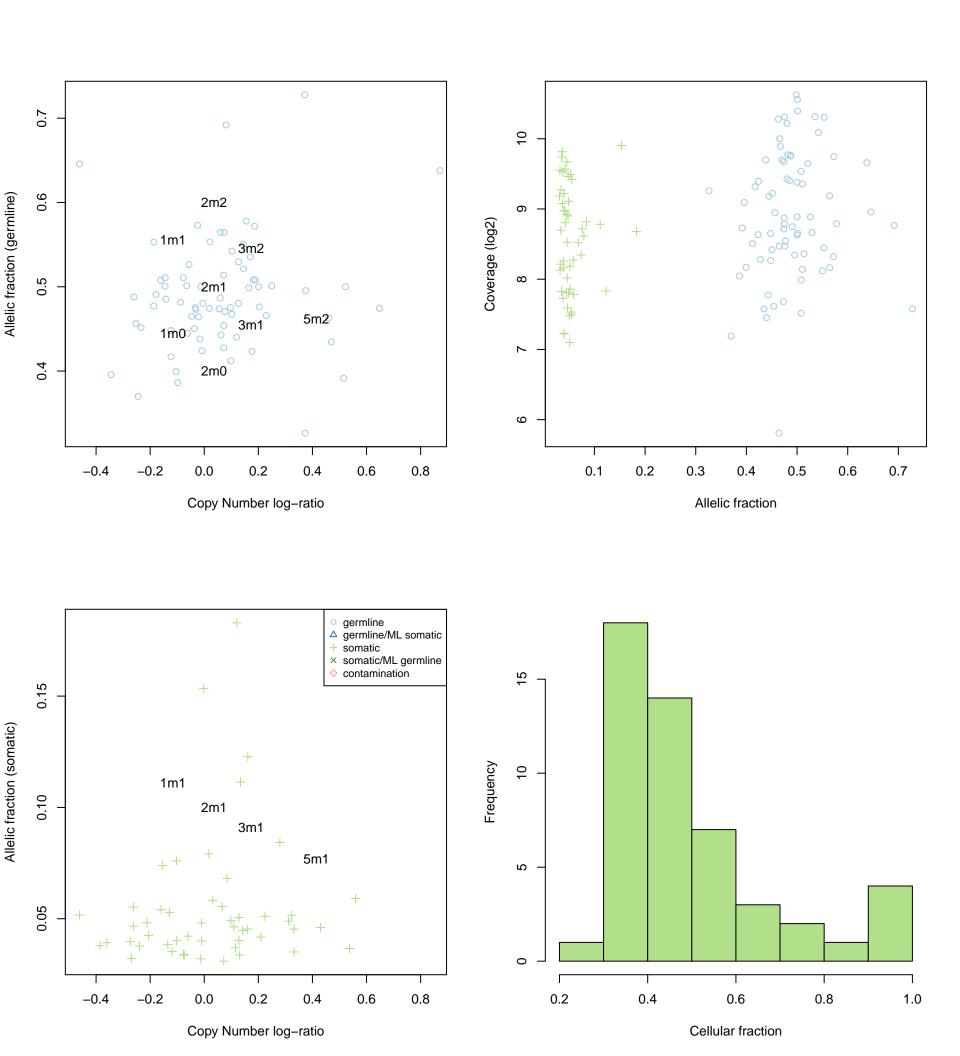
Purity: 0.2 Tumor ploidy: 1.752 SNV log-likelihood: 40.73 GoF: 94.1% Mean coverage: 520;712

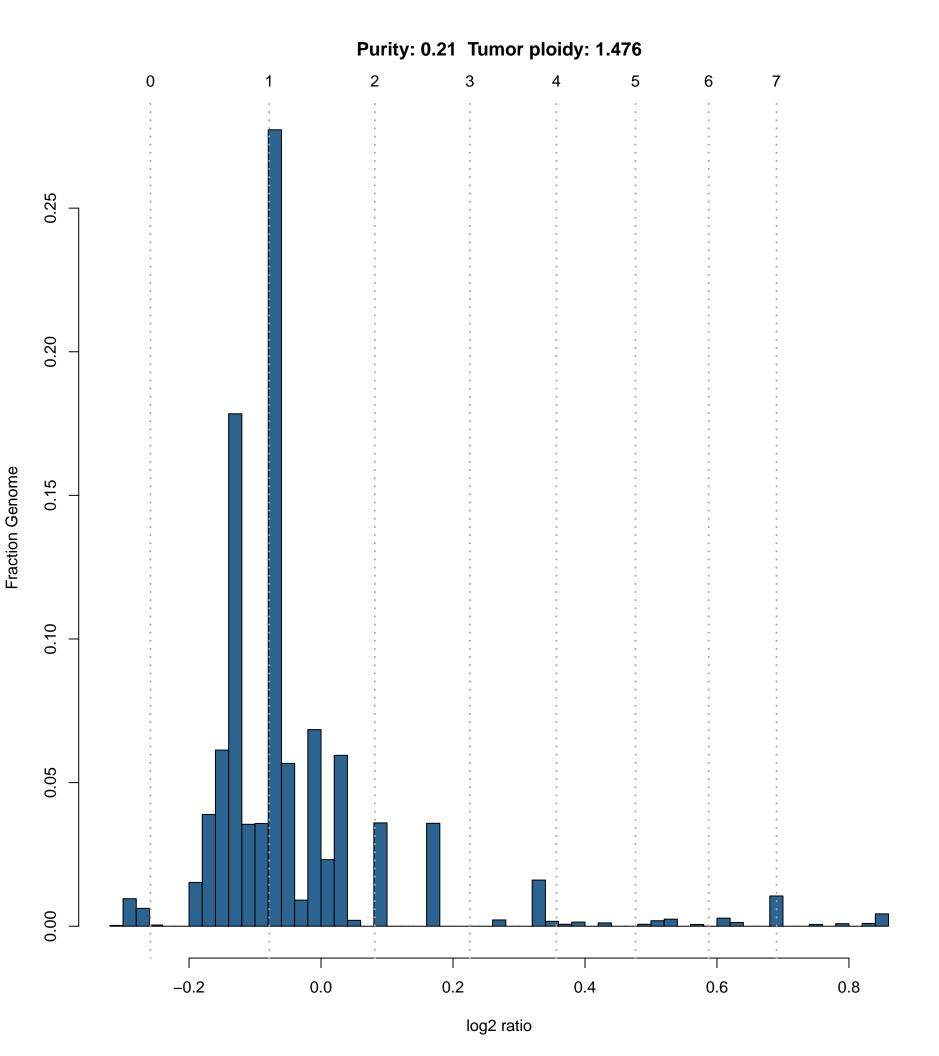


SCNA-fit log-likelihood: -9686.16

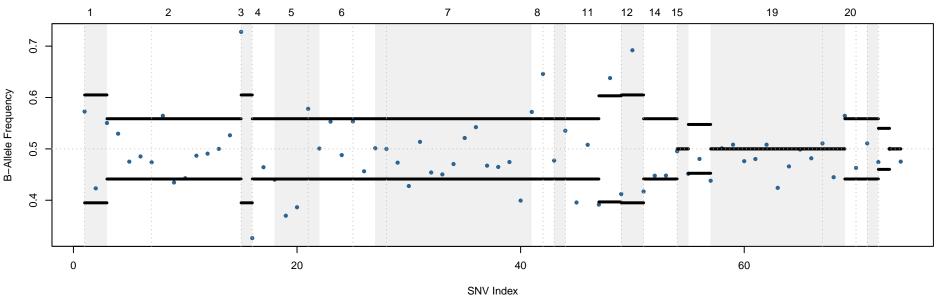




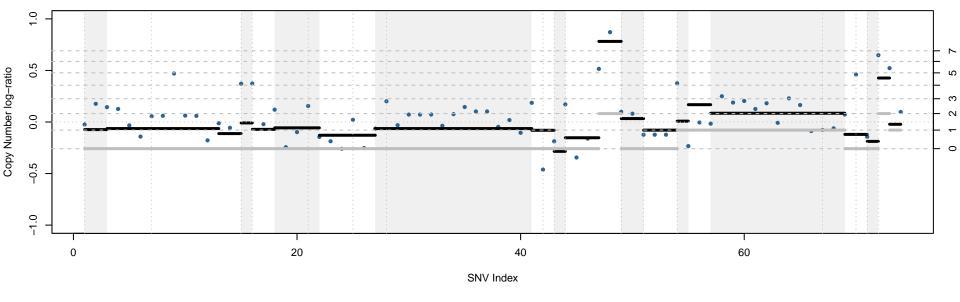


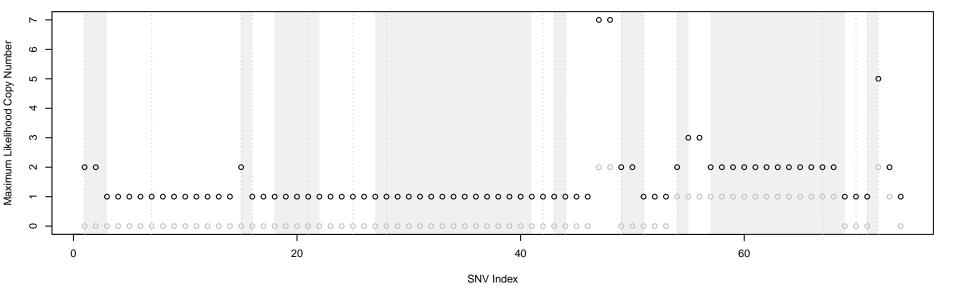


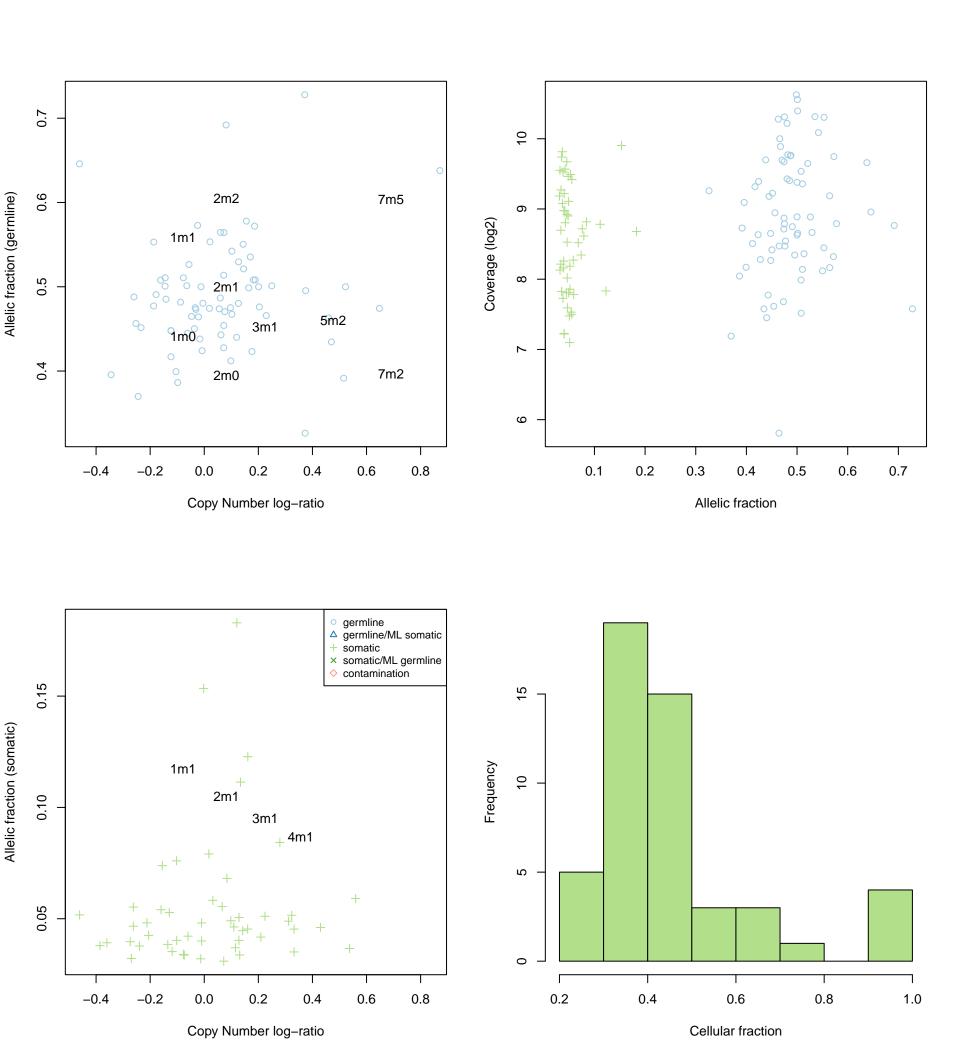


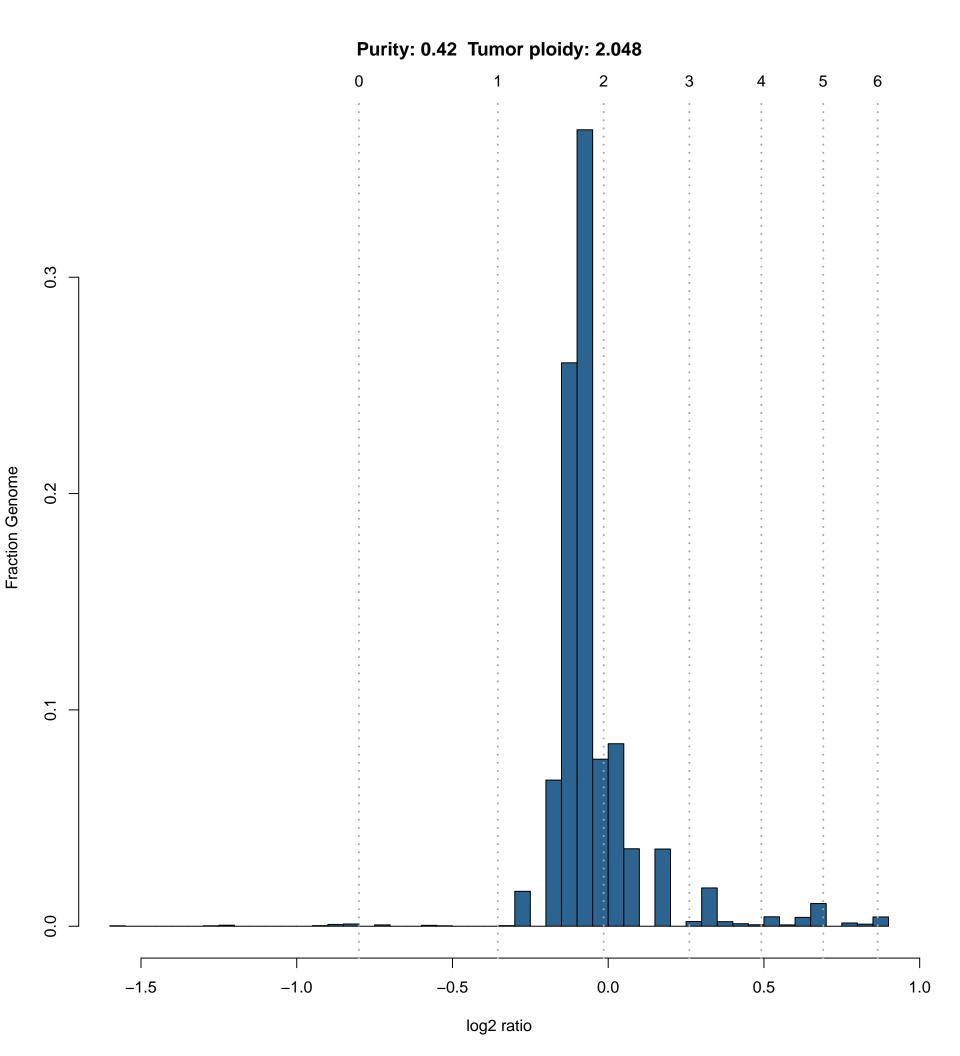


SCNA-fit log-likelihood: -9688.87

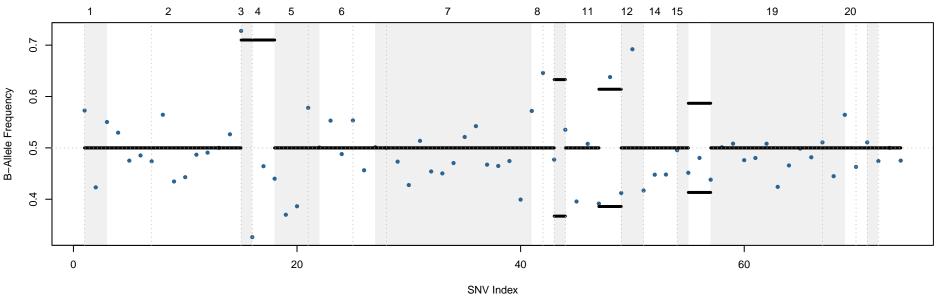




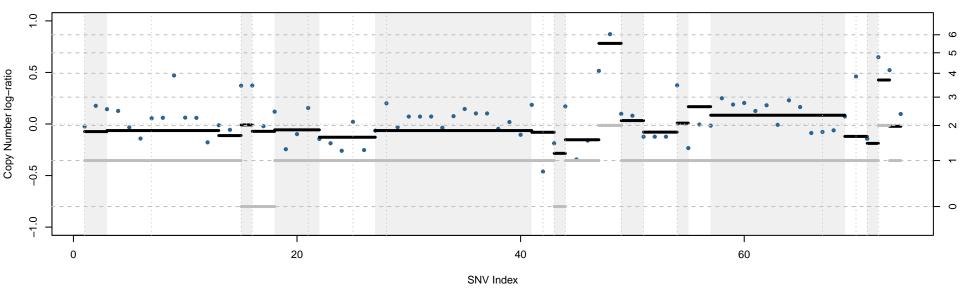


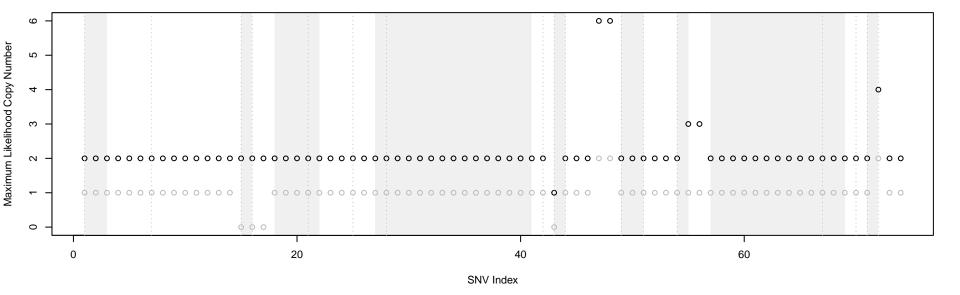


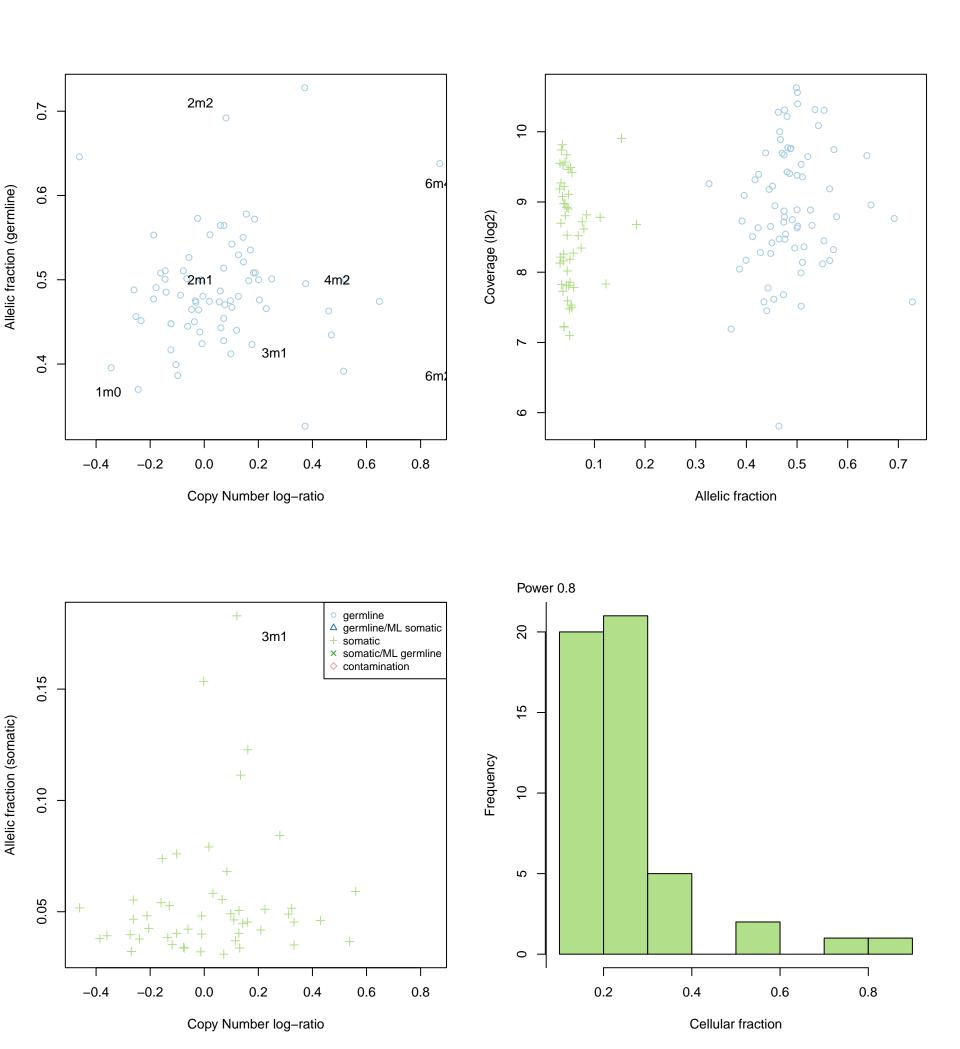




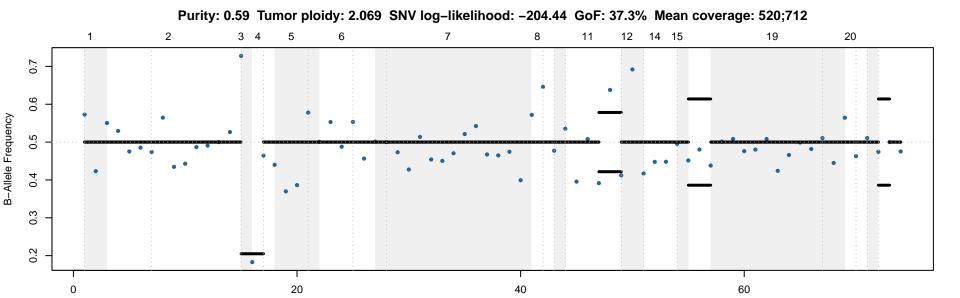
SCNA-fit log-likelihood: -9713.27





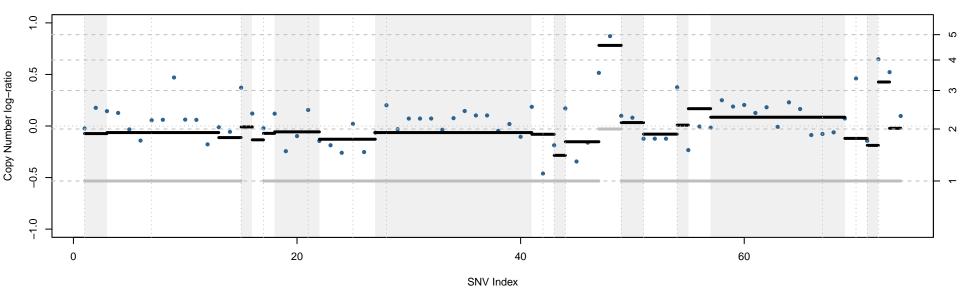


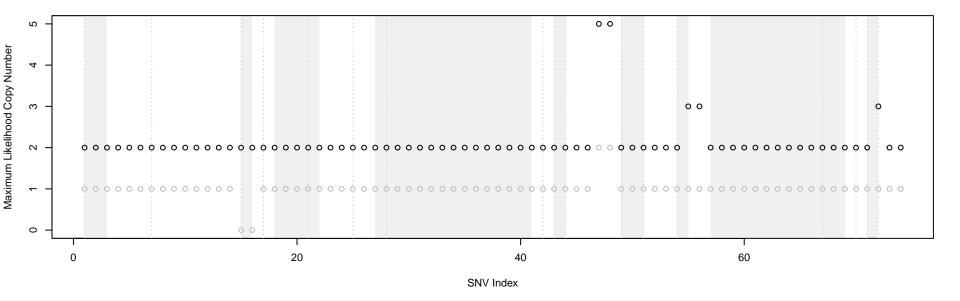
Purity: 0.59 Tumor ploidy: 2.069 3 5 0 4 Fraction Genome 0.2 0.0 -1.5 -1.0 -0.5 0.0 0.5 1.0 log2 ratio

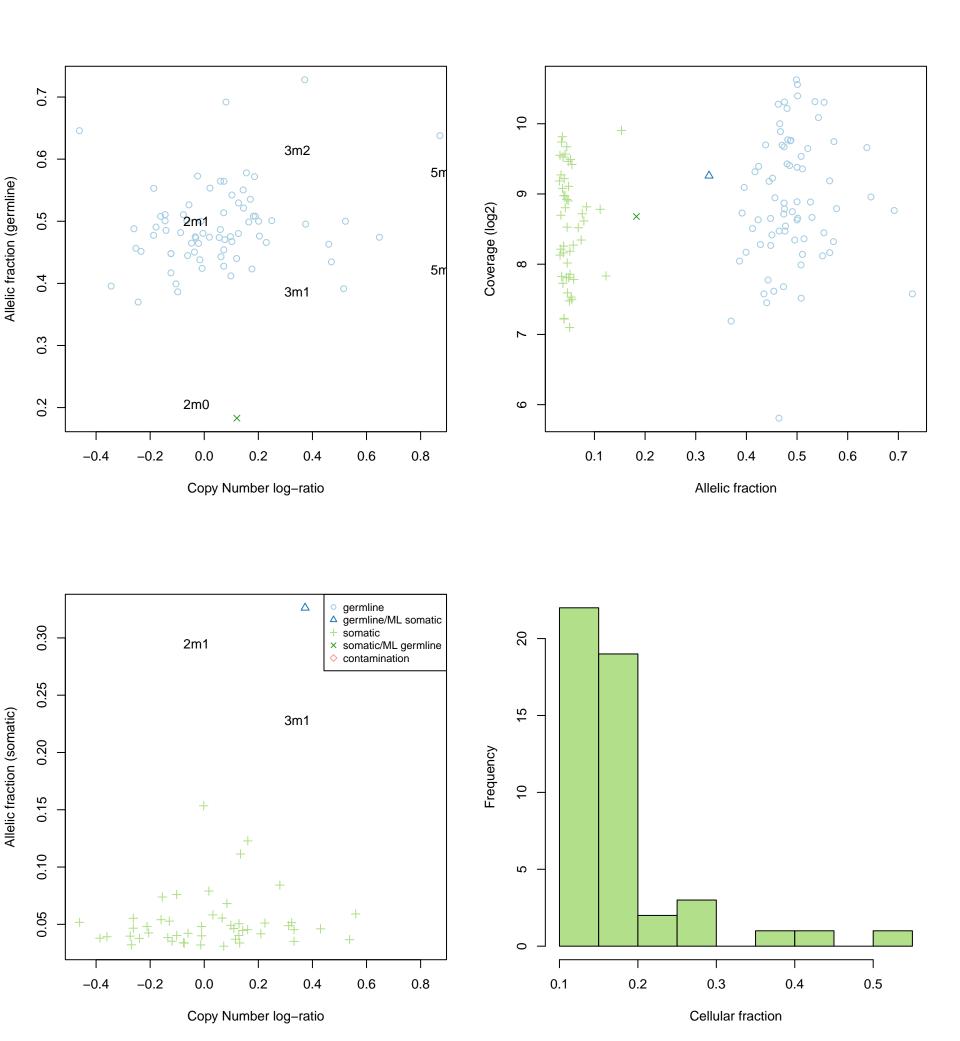


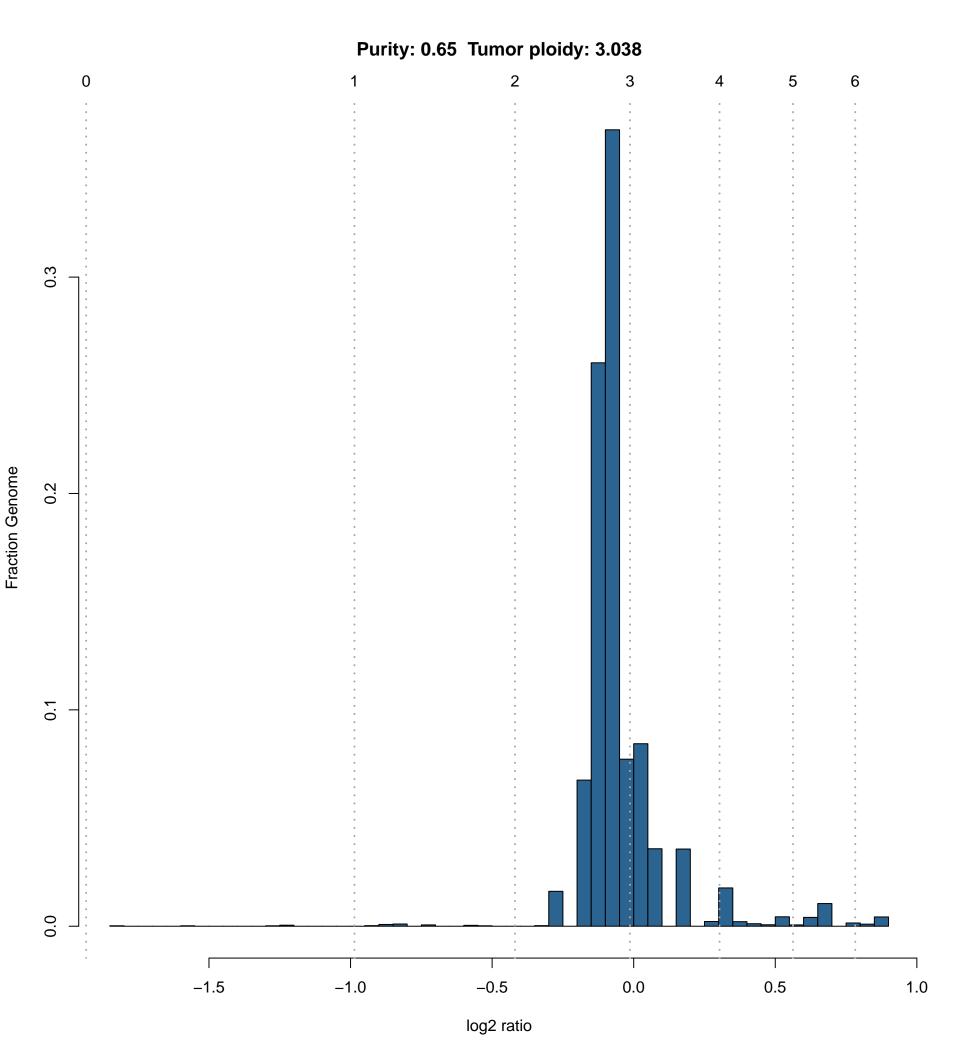
SCNA-fit log-likelihood: -9706.22

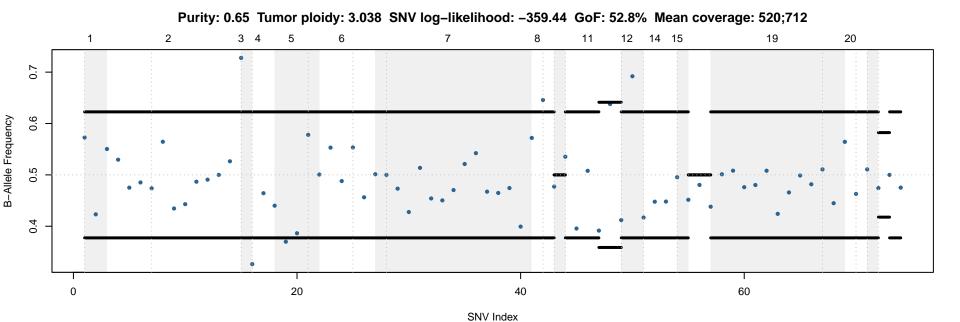
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SCNA-fit log-likelihood: -9709.7

