

Purity: 0.4 Tumor ploidy: 3.74 SNV log-likelihood: -57.73 GoF: 87% Mean coverage: 505;489

SCNA-fit log-likelihood: -11769.52

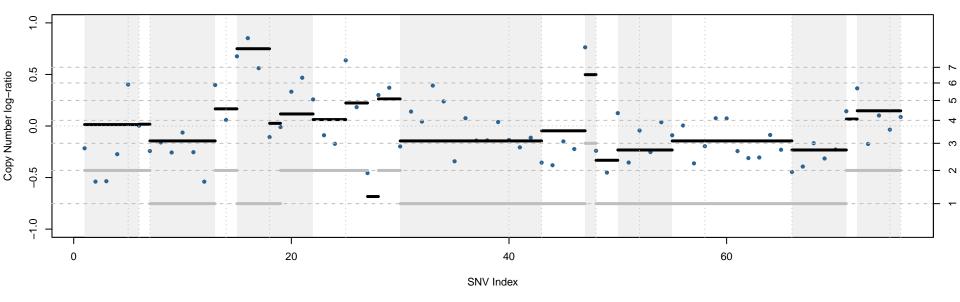
SNV Index

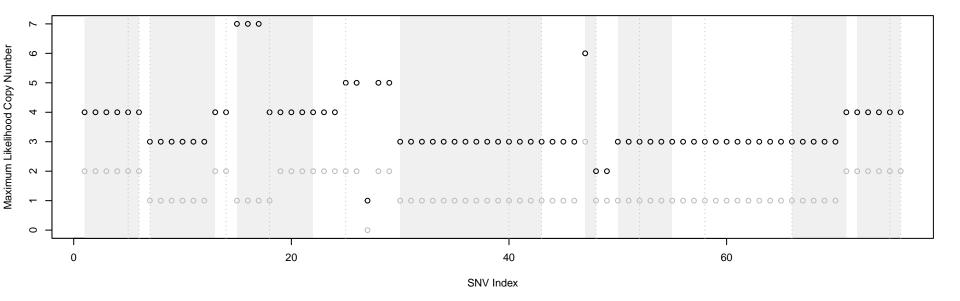
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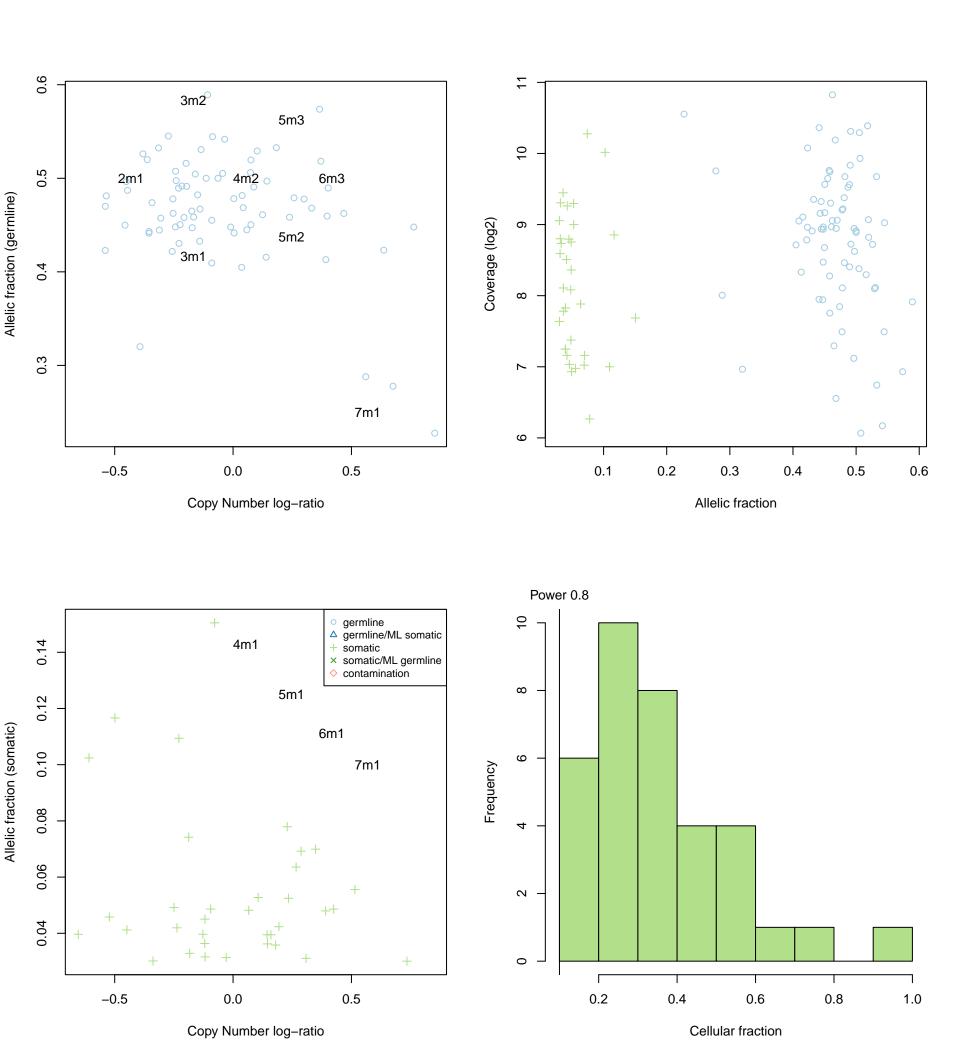
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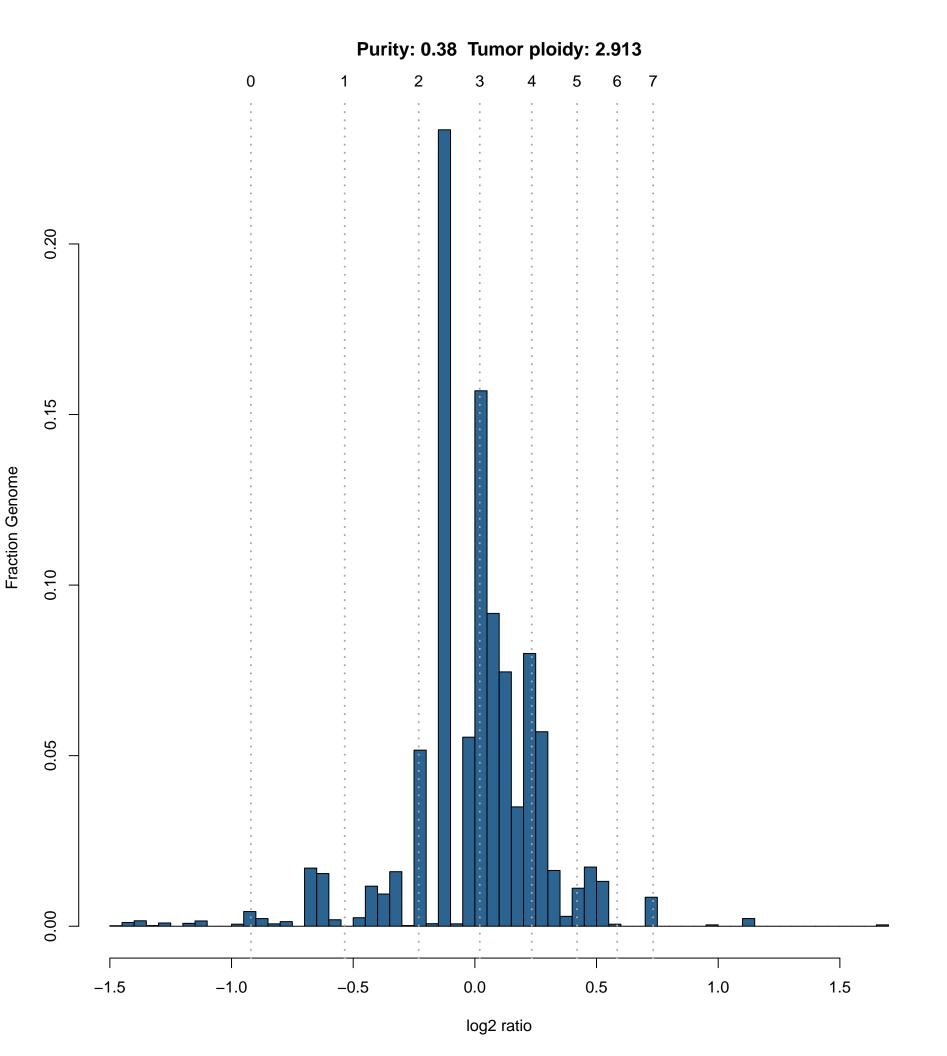
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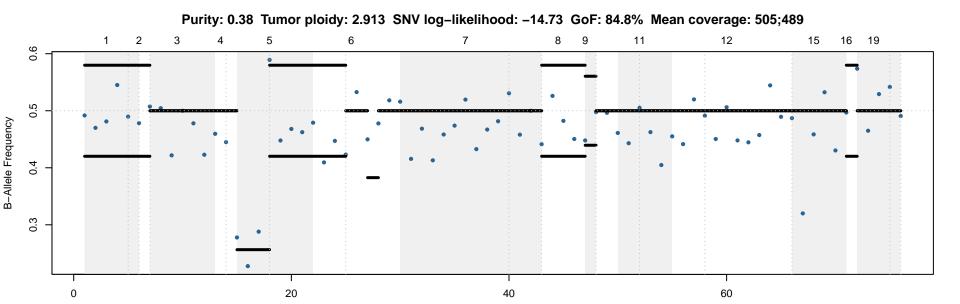
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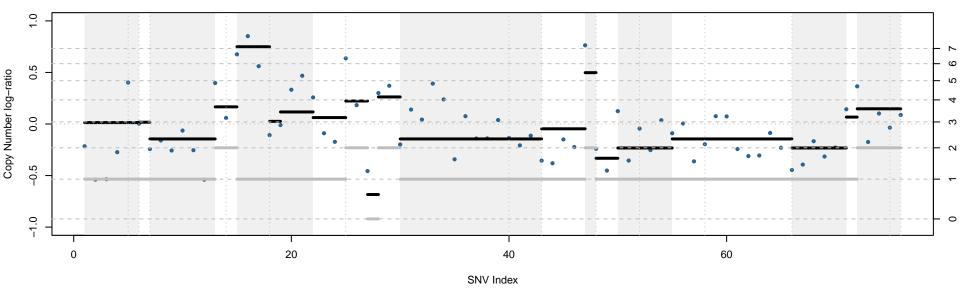


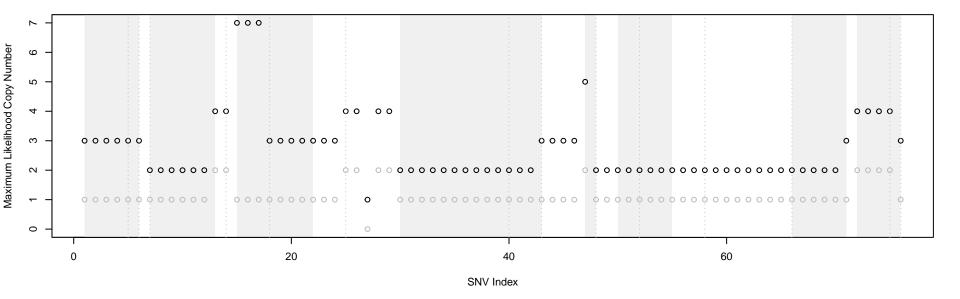


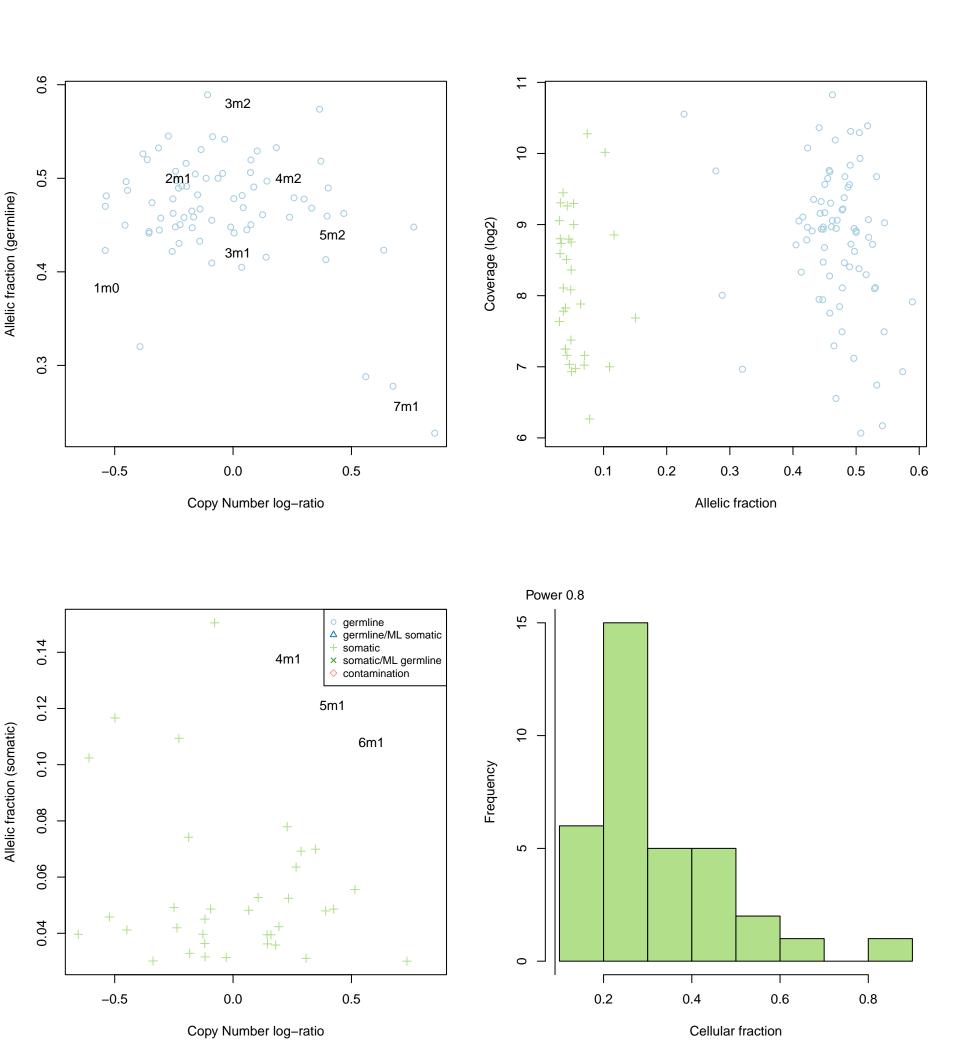


SCNA-fit log-likelihood: -11942.63

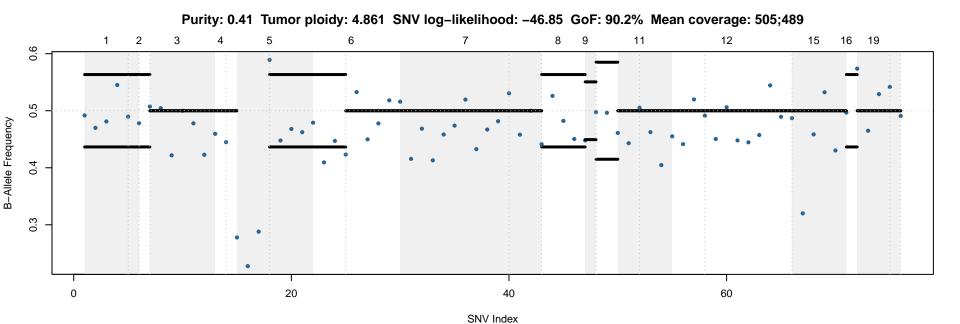
SNV Index



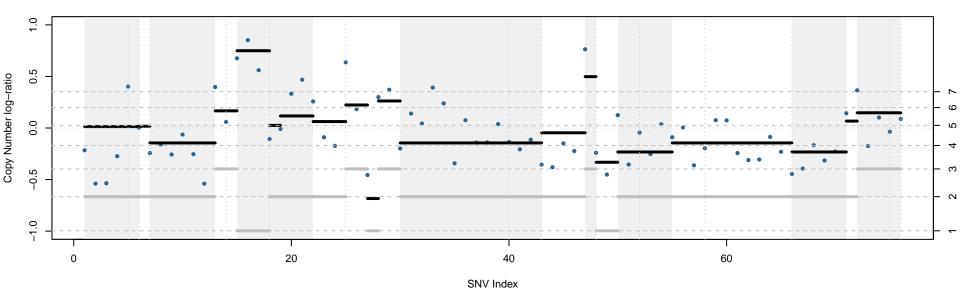


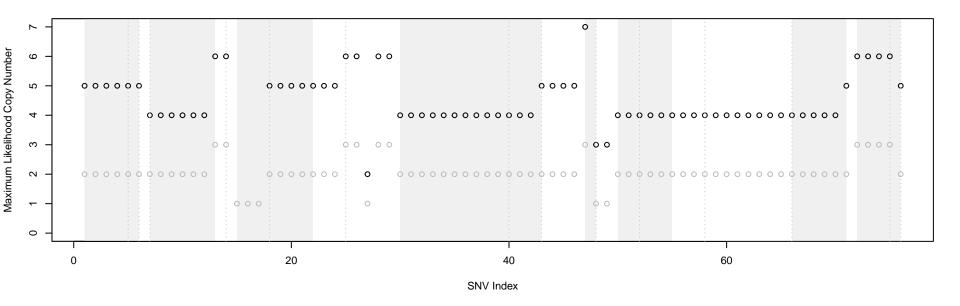


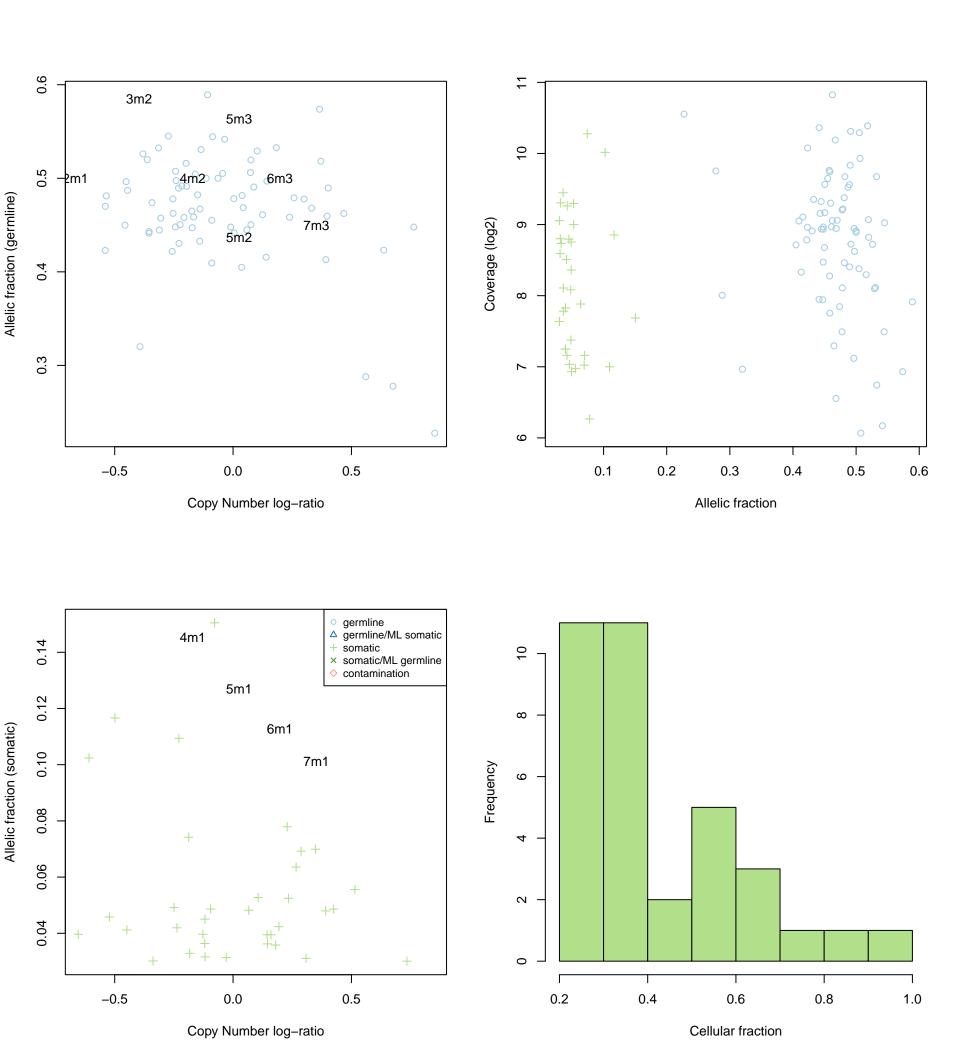
Purity: 0.41 Tumor ploidy: 4.861 3 0 2 5 7 6 0.20 Fraction Genome 0.10 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



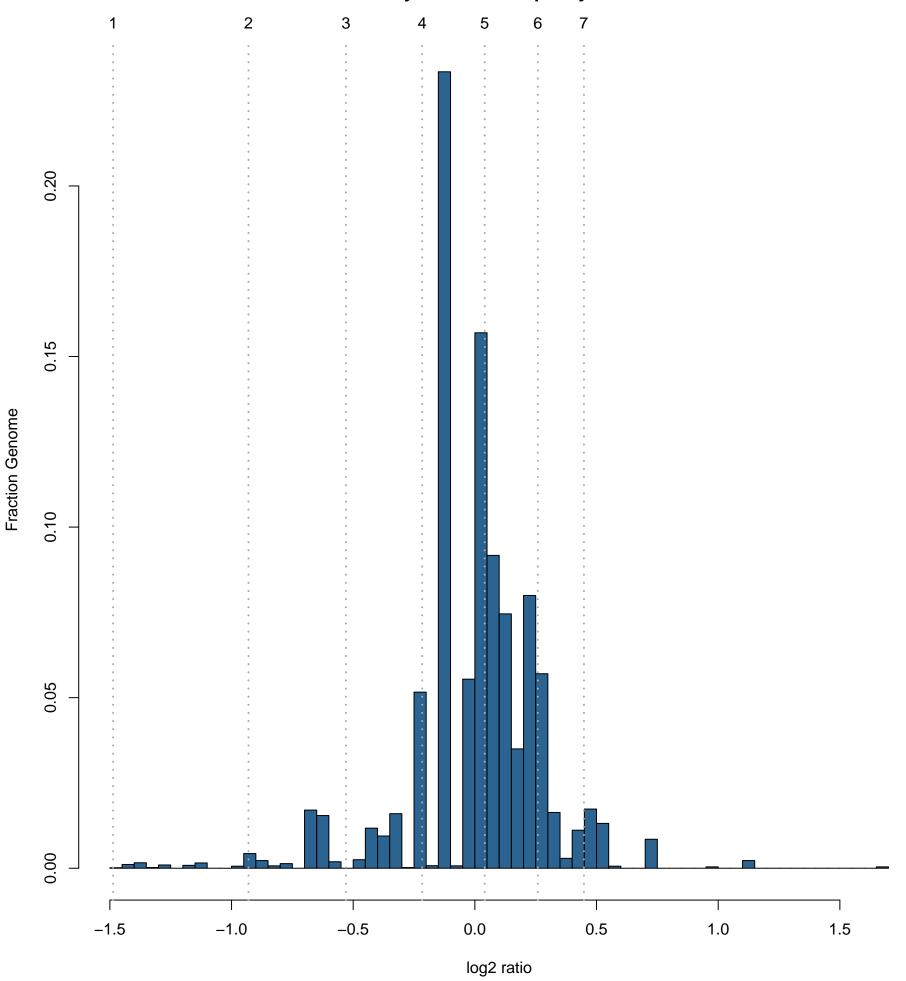
SCNA-fit log-likelihood: -11882.7

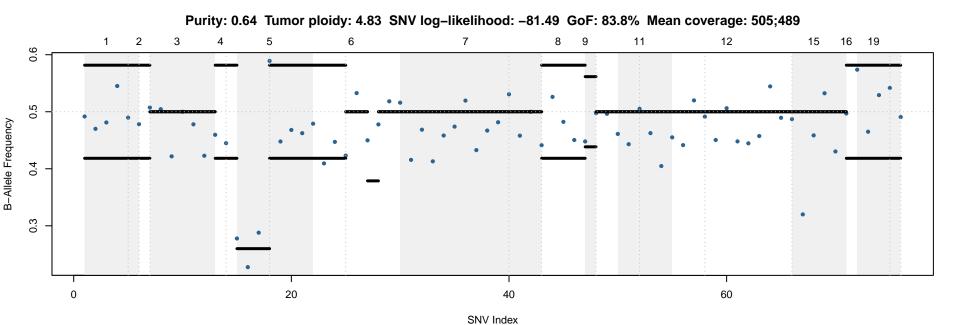




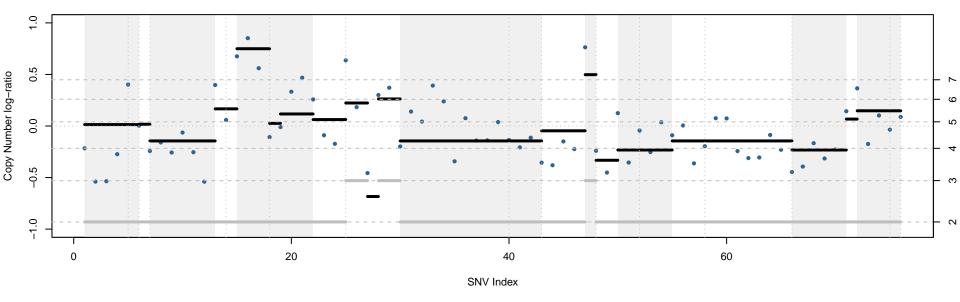


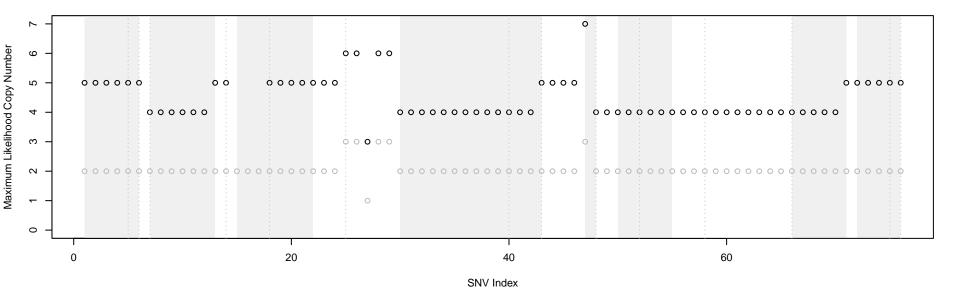
Purity: 0.64 Tumor ploidy: 4.83

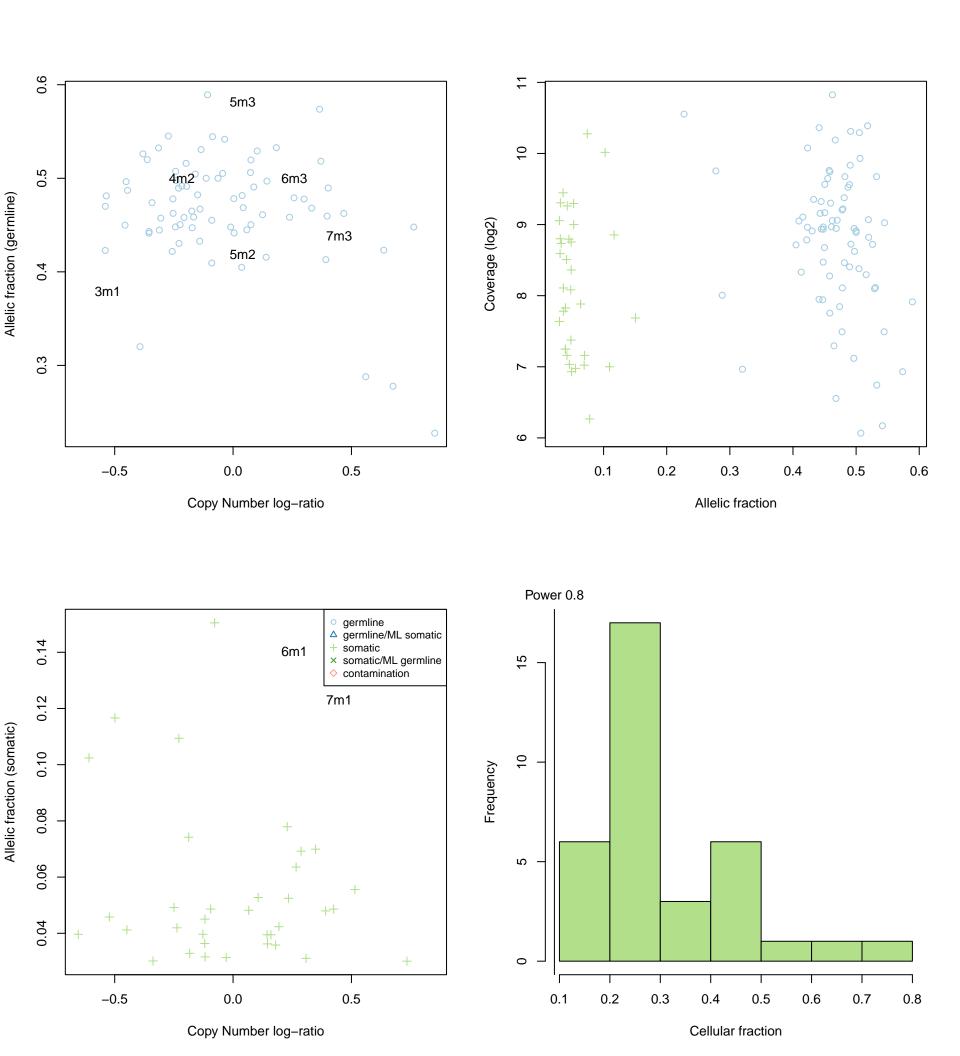




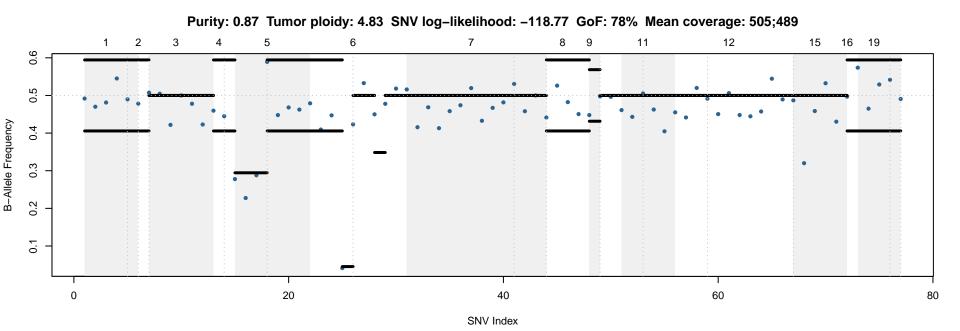
SCNA-fit log-likelihood: -11958.23



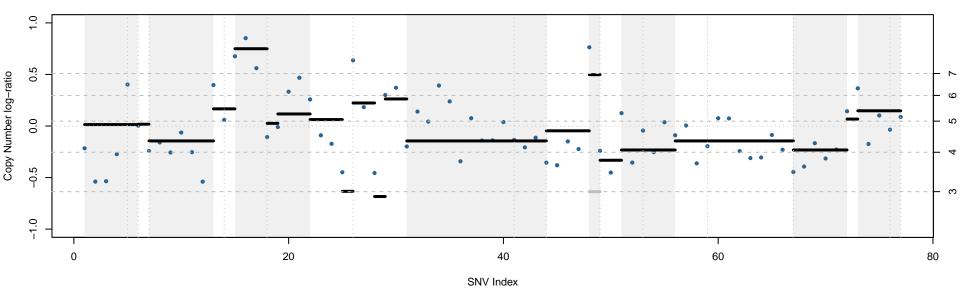


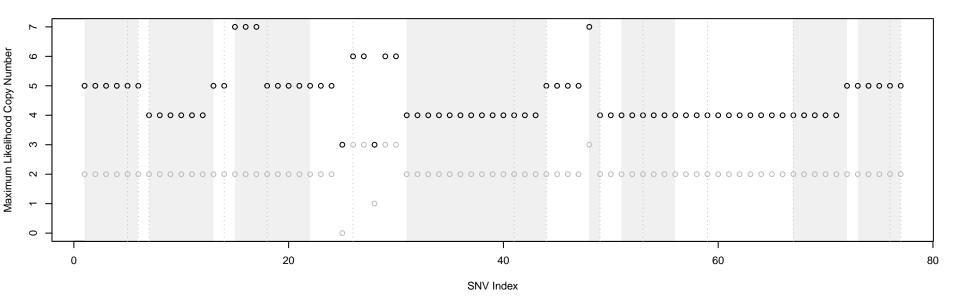


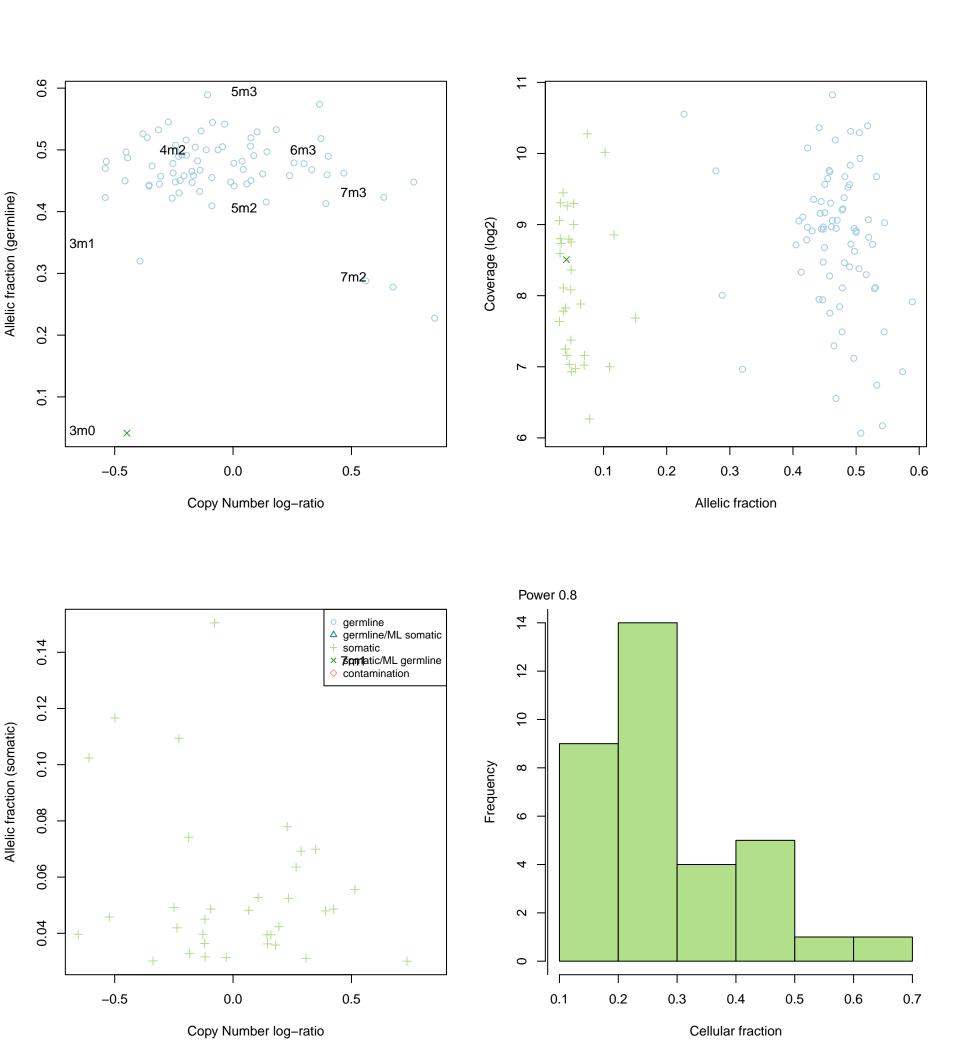
Purity: 0.87 Tumor ploidy: 4.83 7 6 2 3 5 0.20 Fraction Genome 0.10 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio

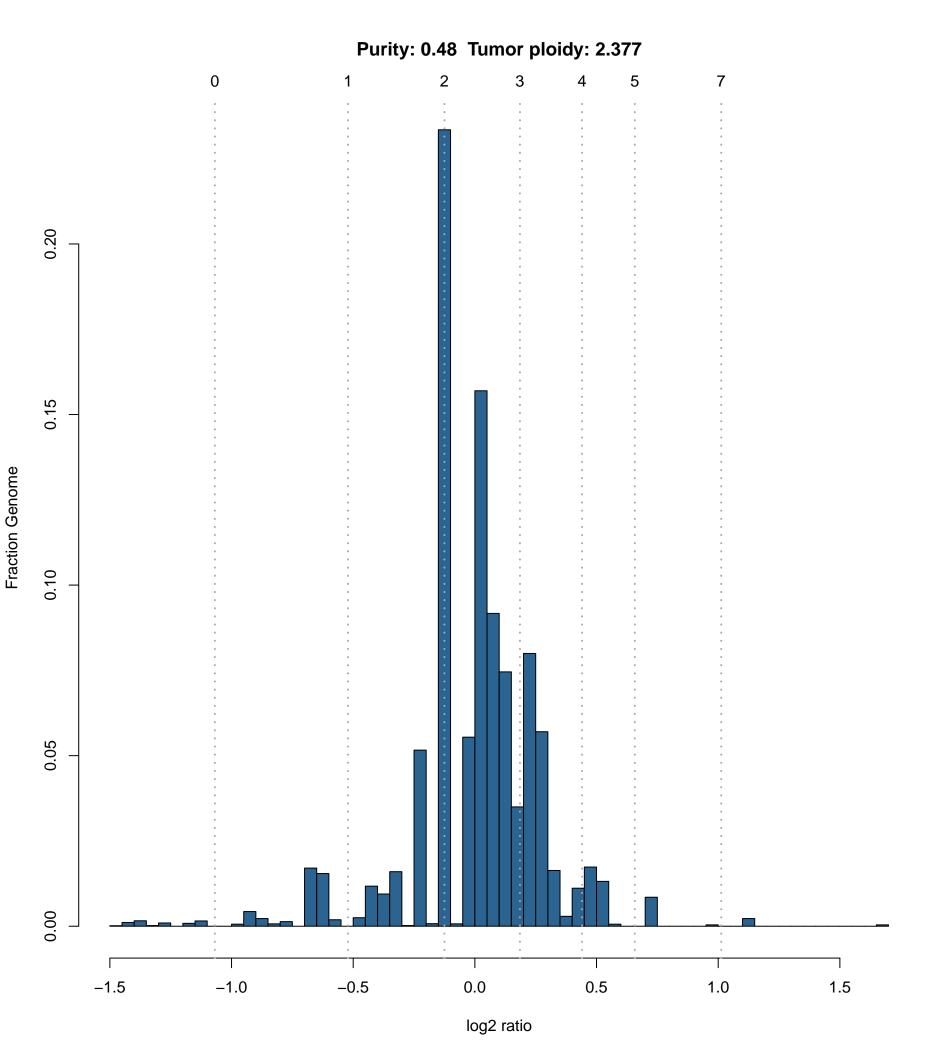


SCNA-fit log-likelihood: -11943.25

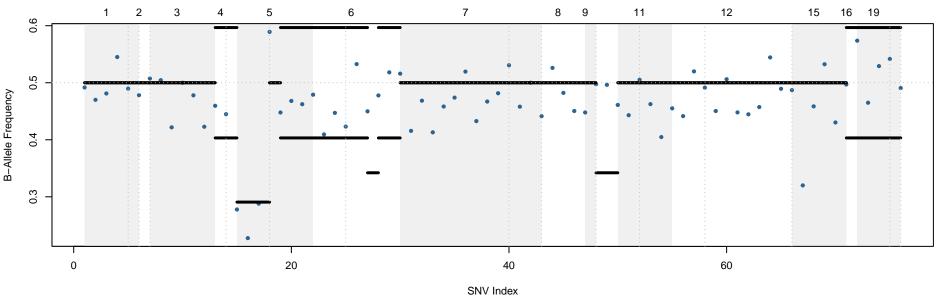




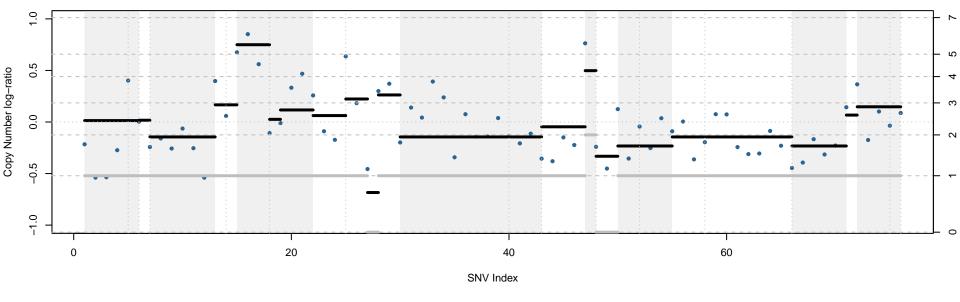


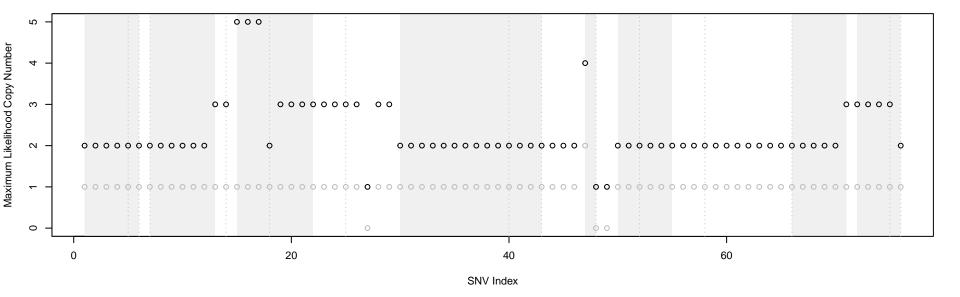


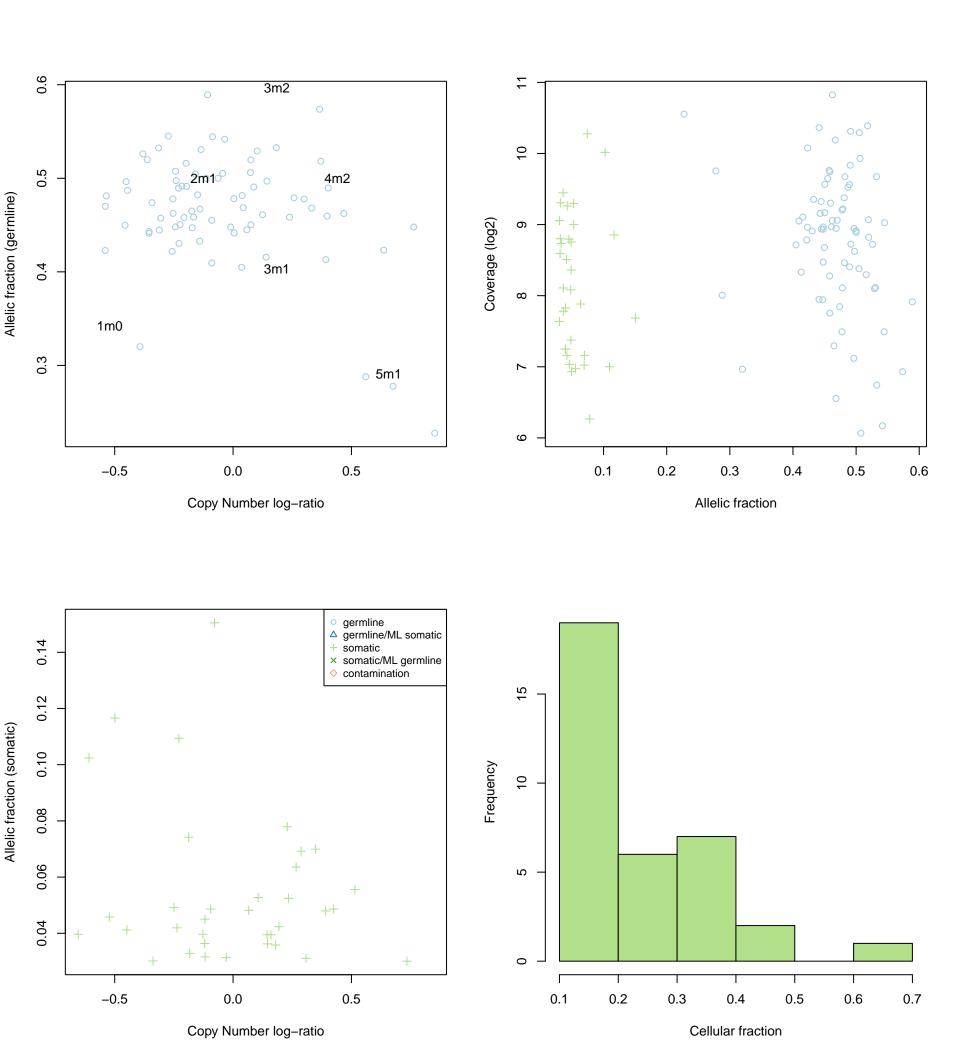




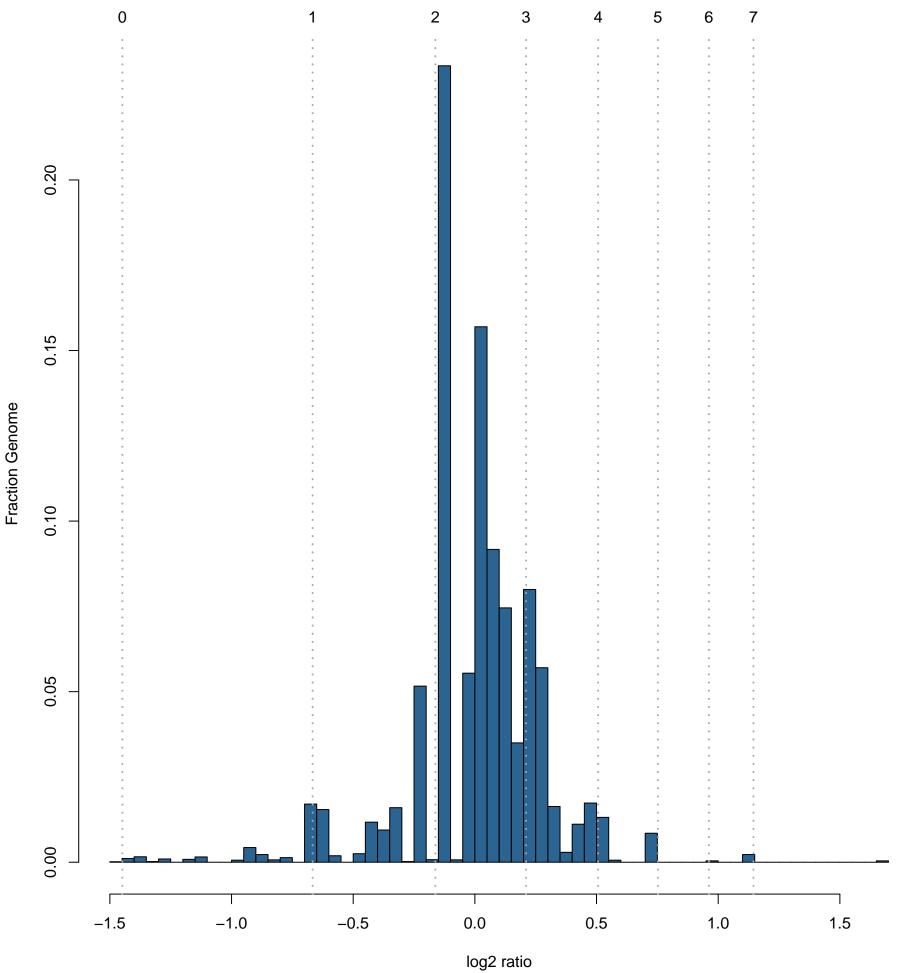
SCNA-fit log-likelihood: -12088.31



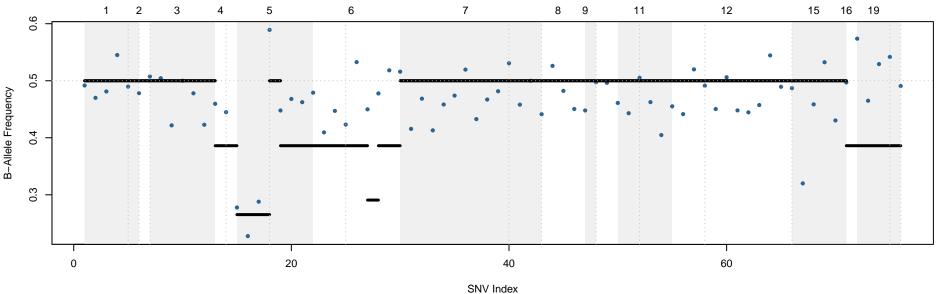




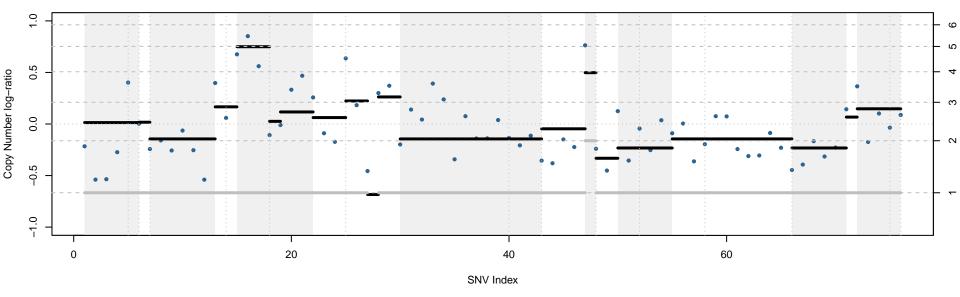
Purity: 0.59 Tumor ploidy: 2.404

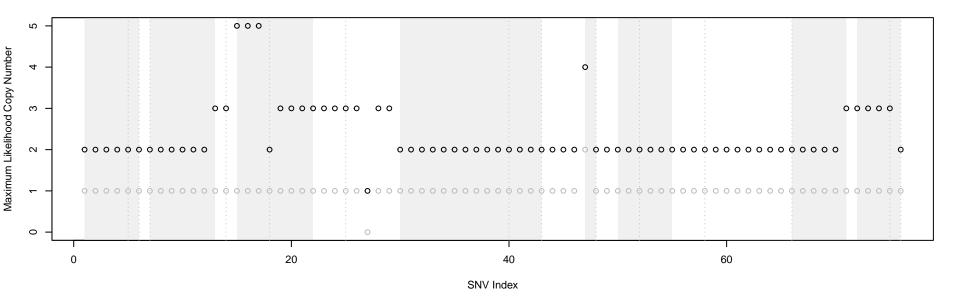


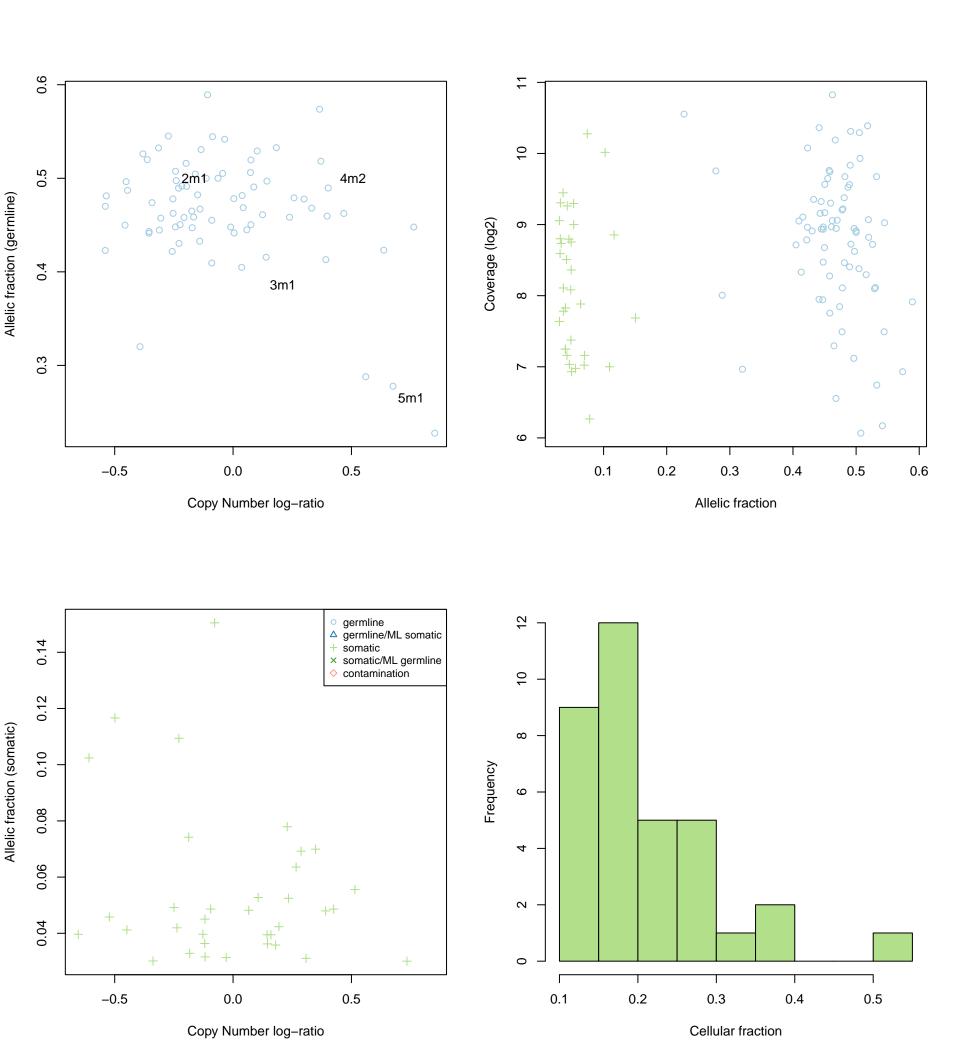
Purity: 0.59 Tumor ploidy: 2.404 SNV log-likelihood: -100 GoF: 56.4% Mean coverage: 505;489

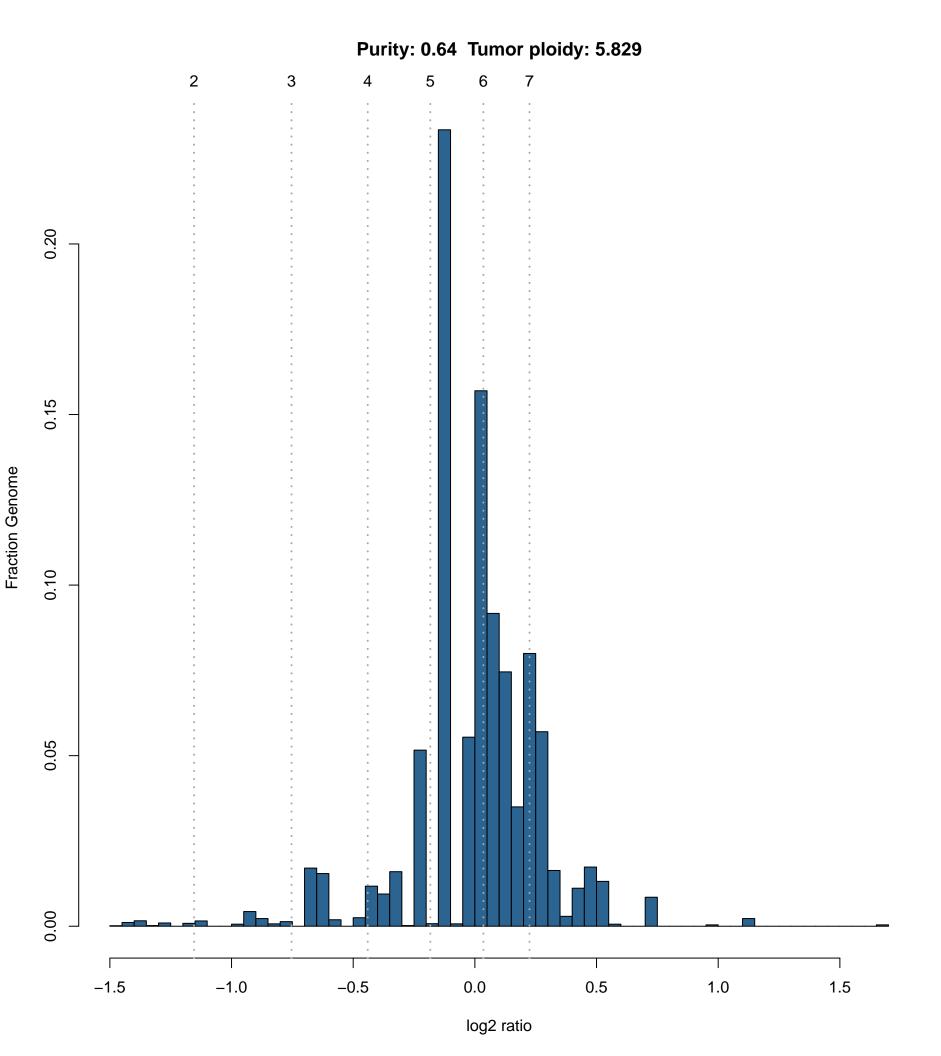


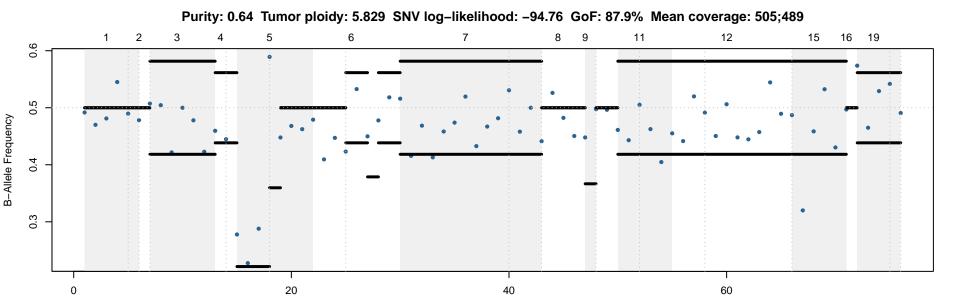
SCNA-fit log-likelihood: -12139.43











SCNA-fit log-likelihood: -12307.97

SNV Index

