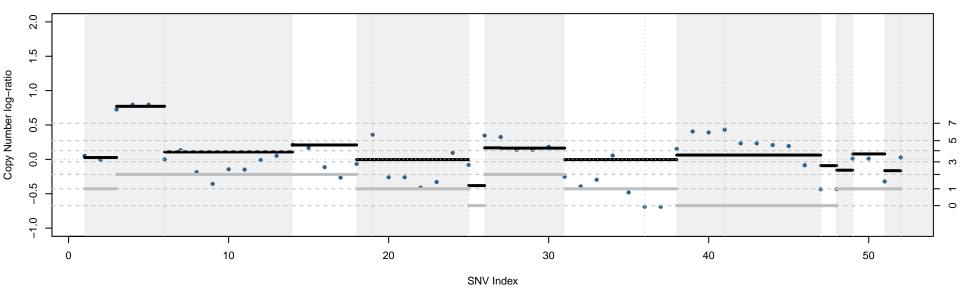
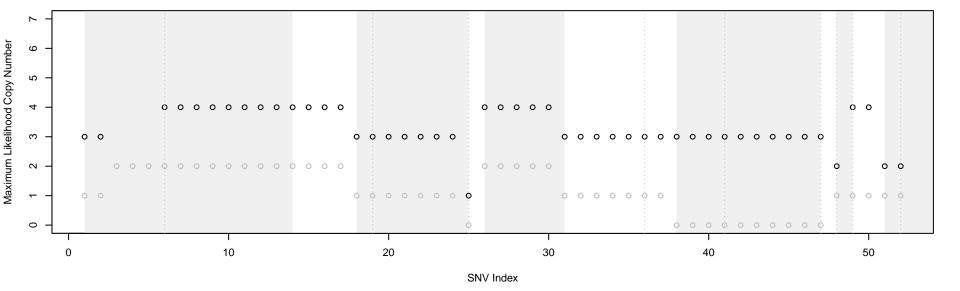
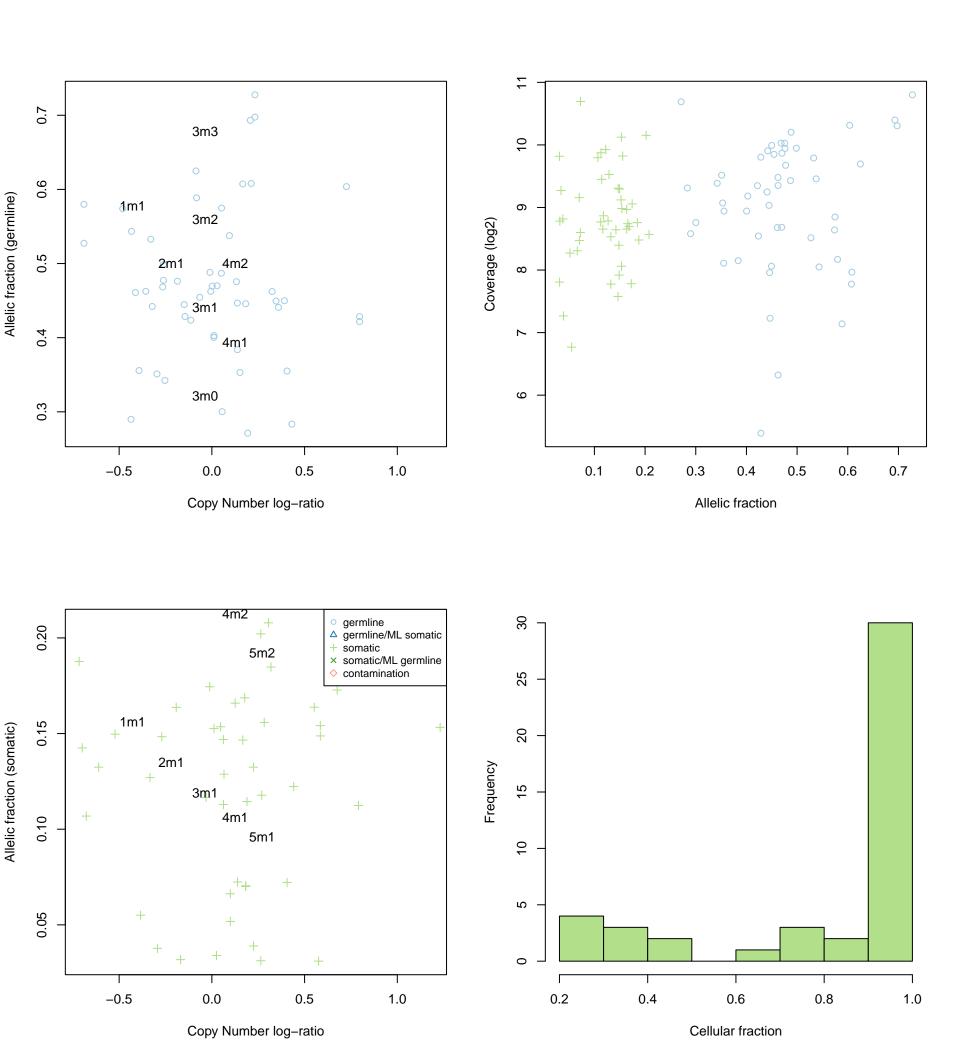
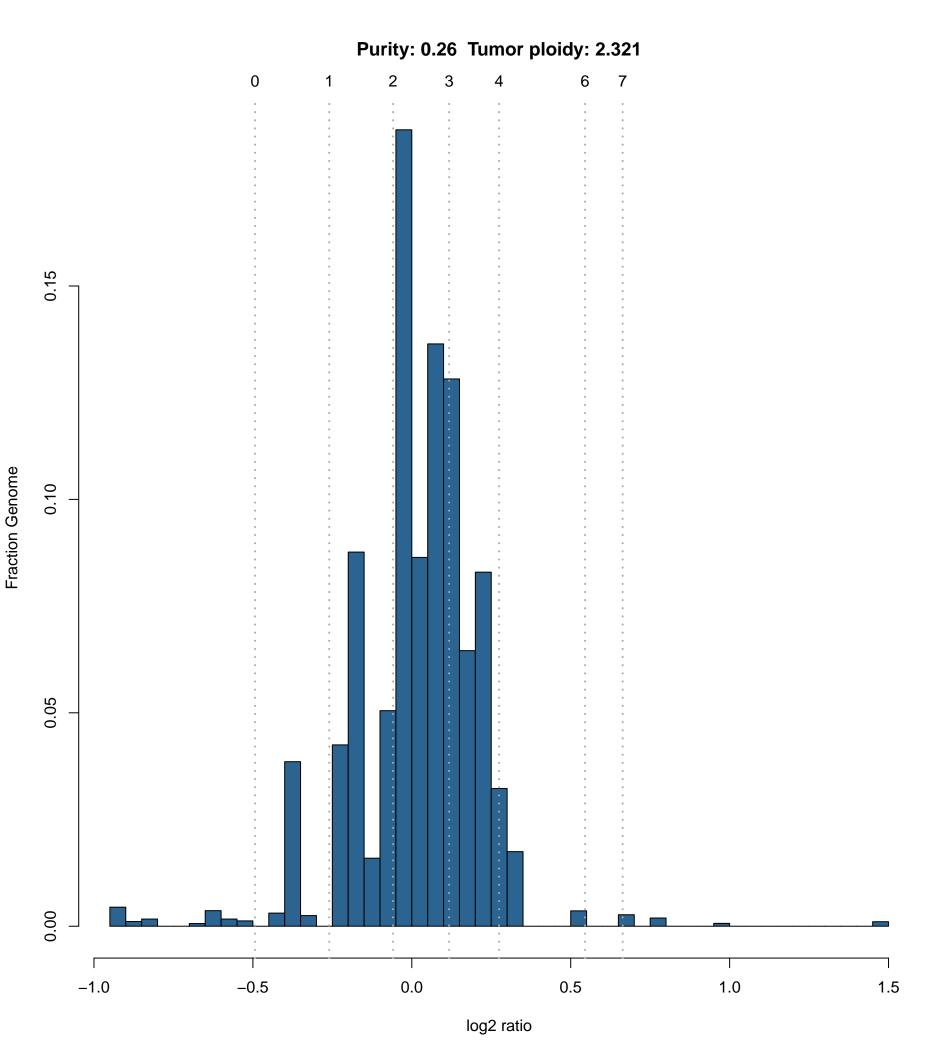


SCNA-fit log-likelihood: -14636.56









Purity: 0.26 Tumor ploidy: 2.321 SNV log-likelihood: -40.35 GoF: 94.4% Mean coverage: 586;597

1 2 3 4 5 6 7 9 14

2 0 4 5 6 7 9 14

B-Allele Frequency

0.3

0

10

SCNA-fit log-likelihood: -14706.3

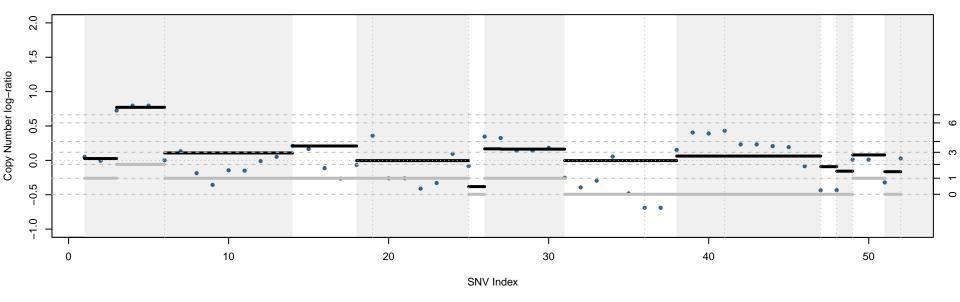
SNV Index

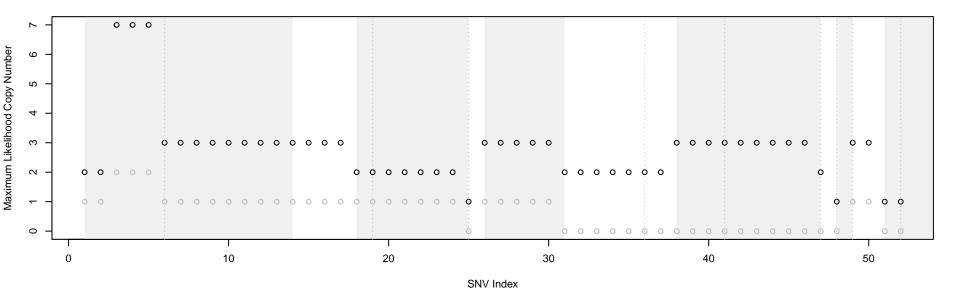
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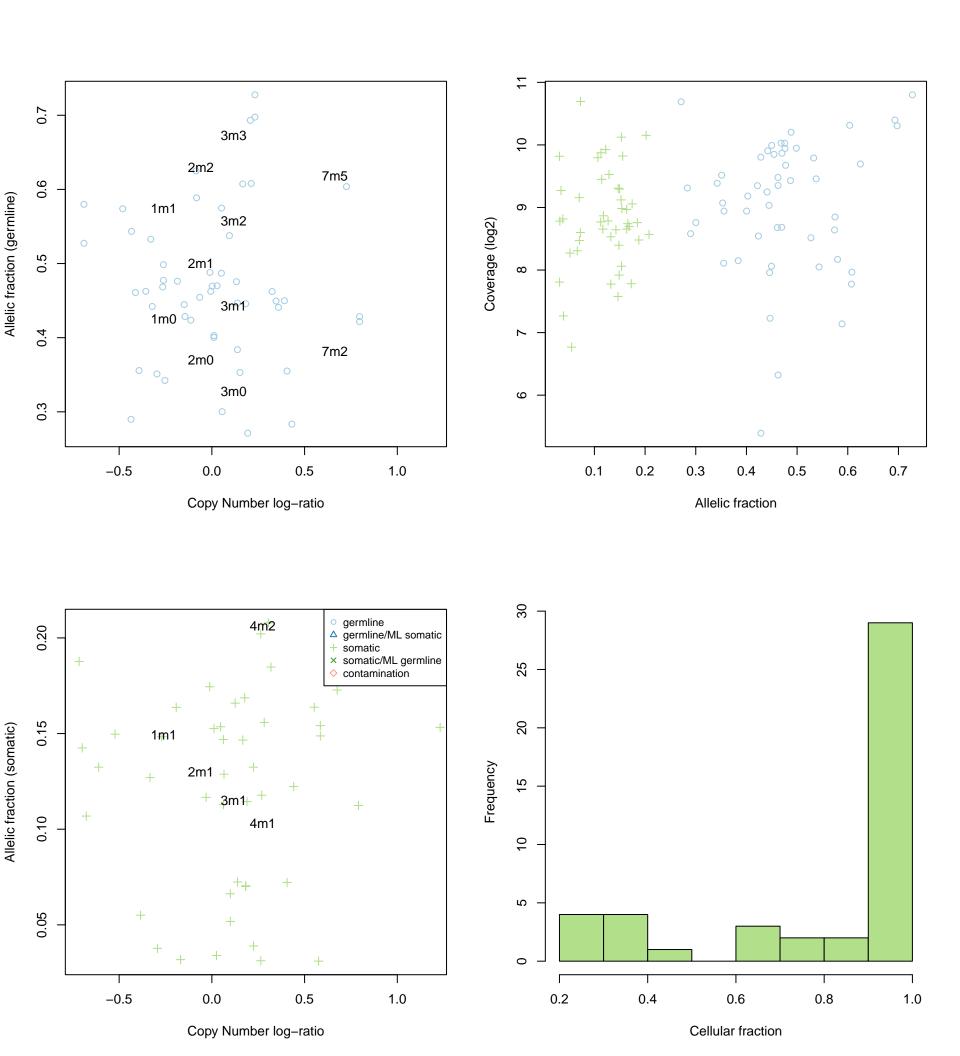
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50

20







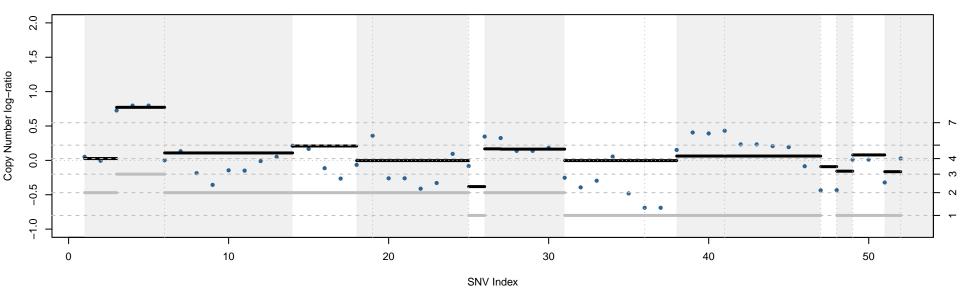
Purity: 0.41 Tumor ploidy: 3.878 0 3 7 Fraction Genome 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio

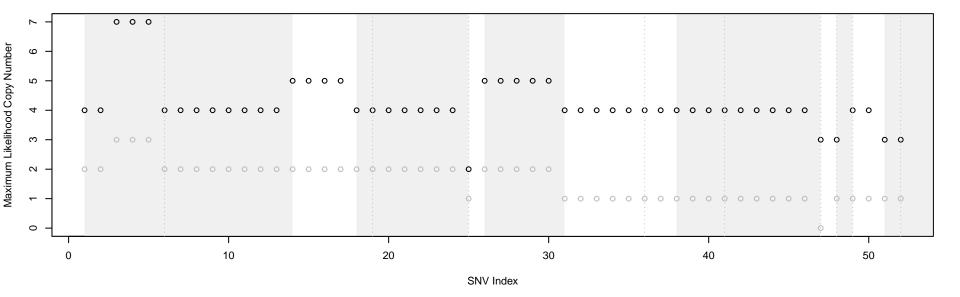
Purity: 0.41 Tumor ploidy: 3.878 SNV log-likelihood: -95.96 GoF: 91.5% Mean coverage: 586;597

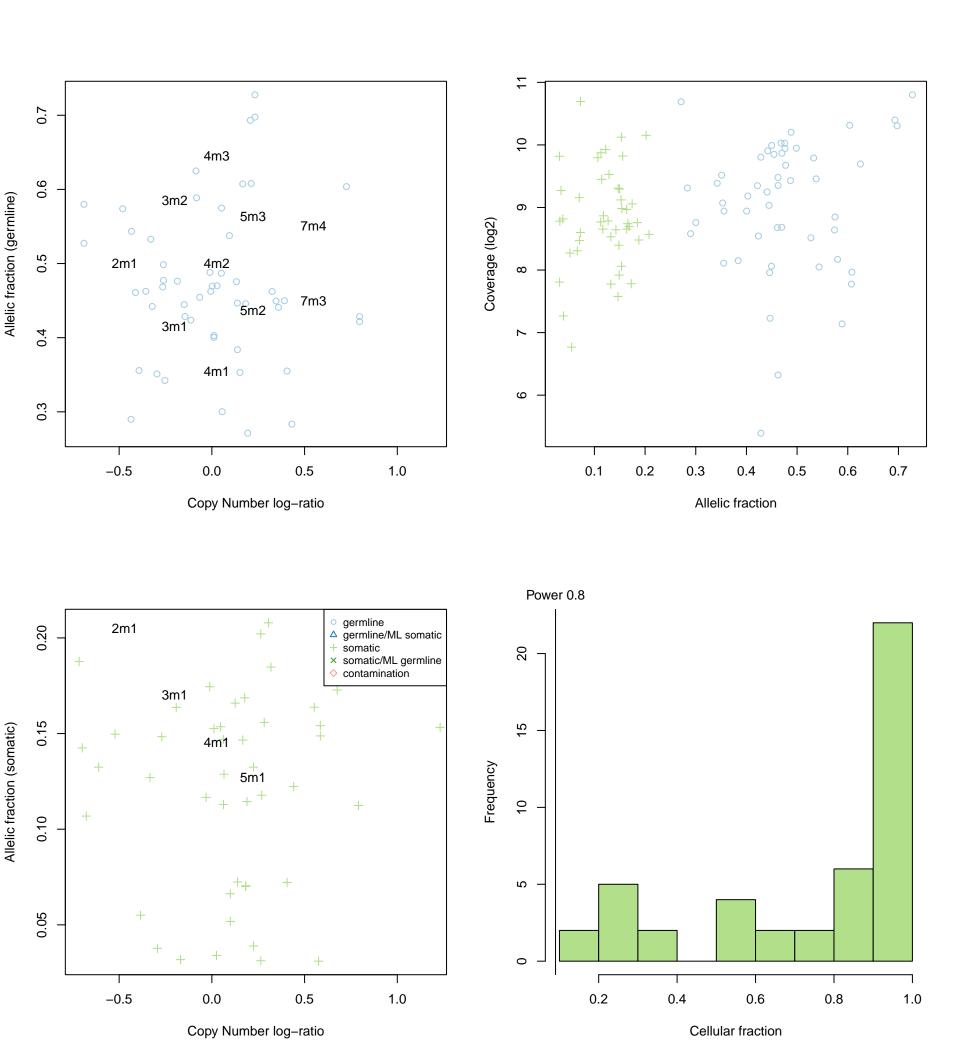
1 2 3 4 5 6 7 9 14

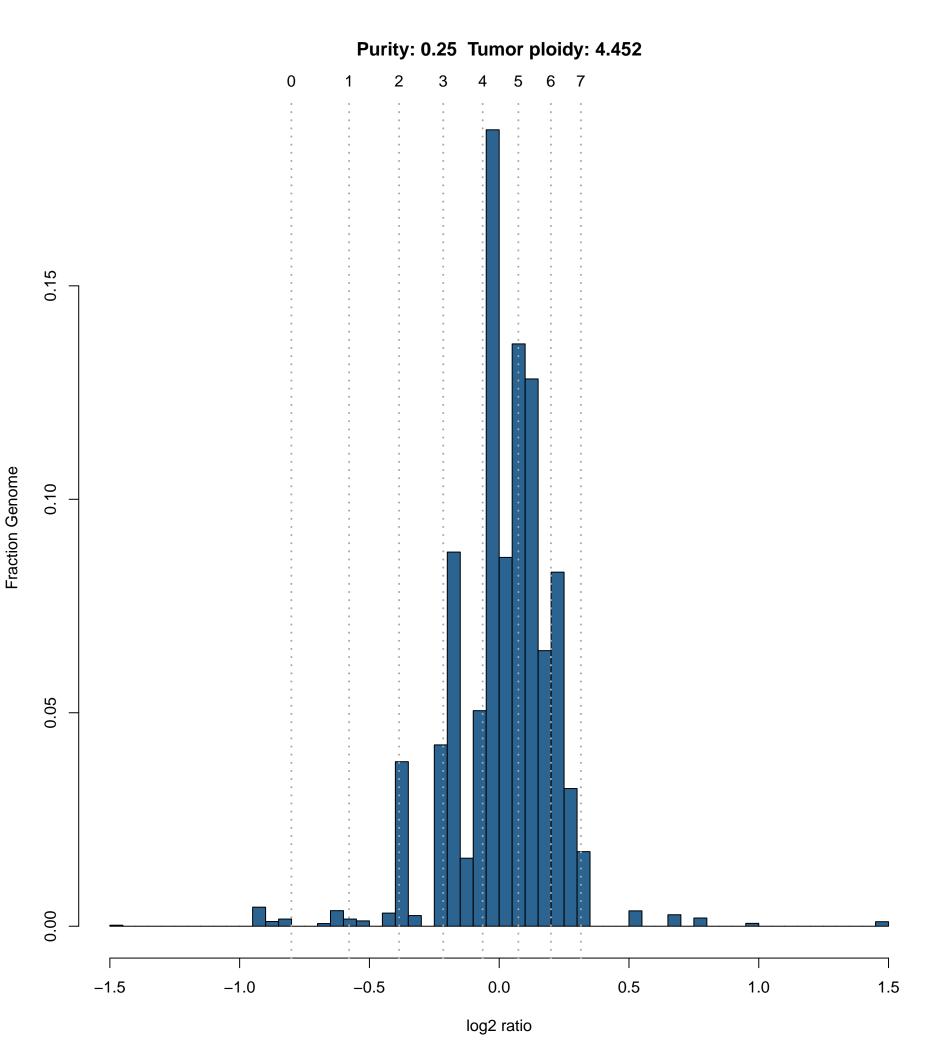
SCNA-fit log-likelihood: -14617.3

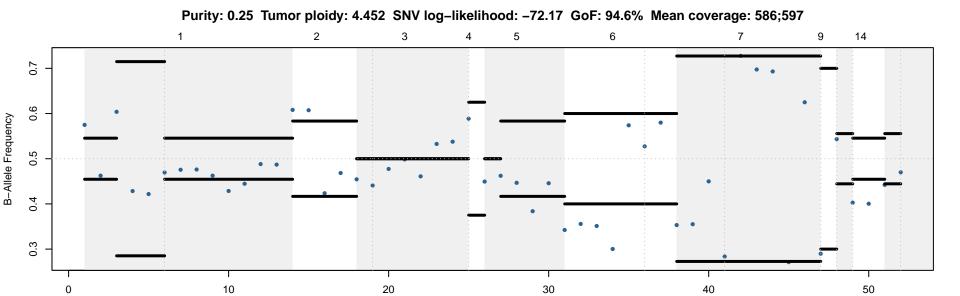
SNV Index





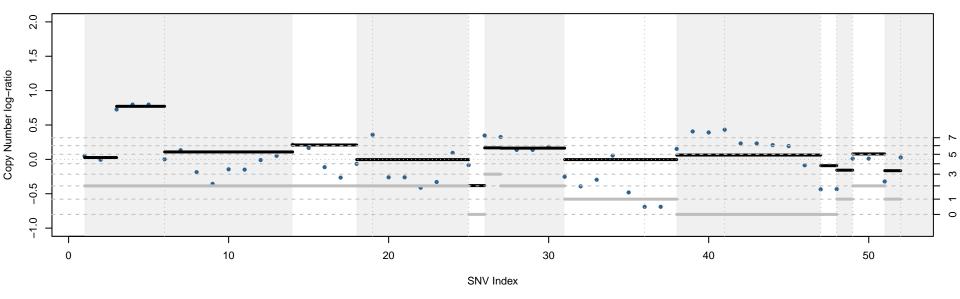


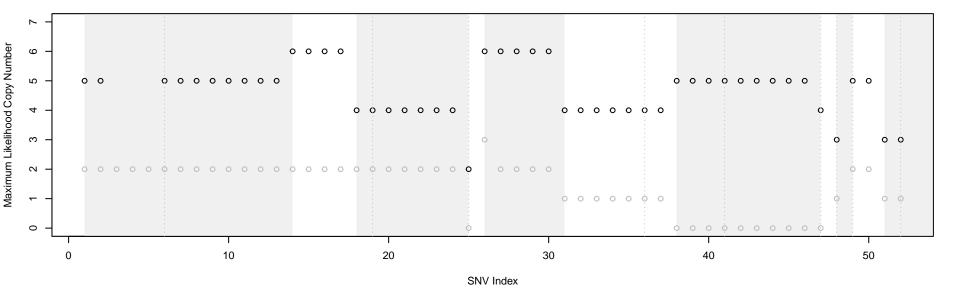


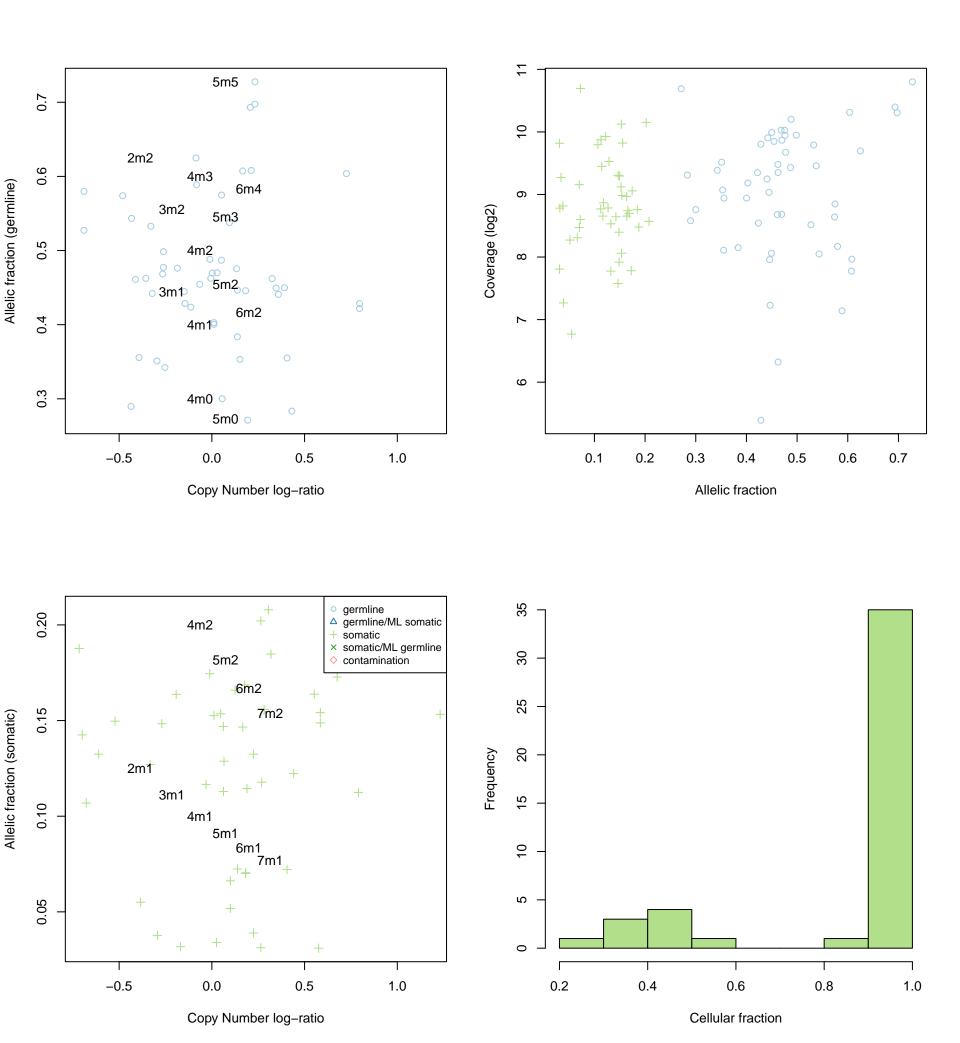


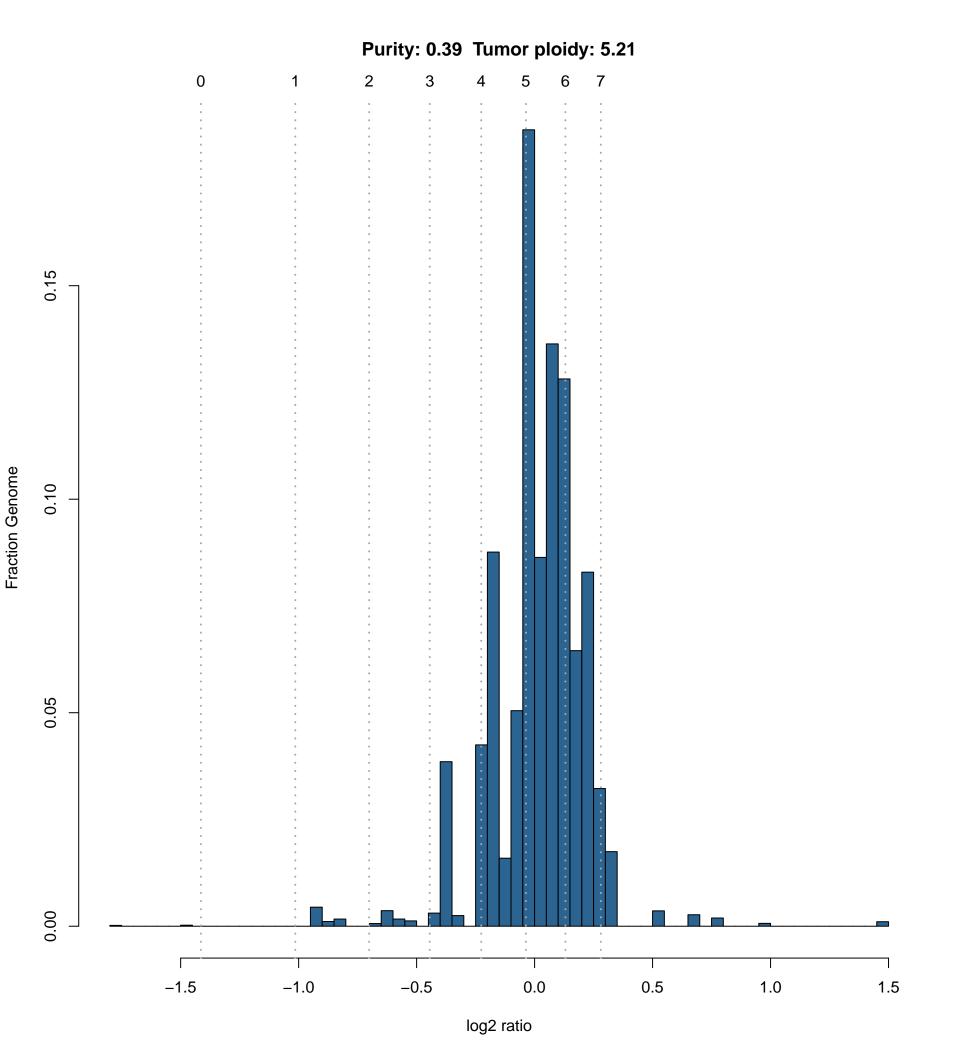
SCNA-fit log-likelihood: -14718.93

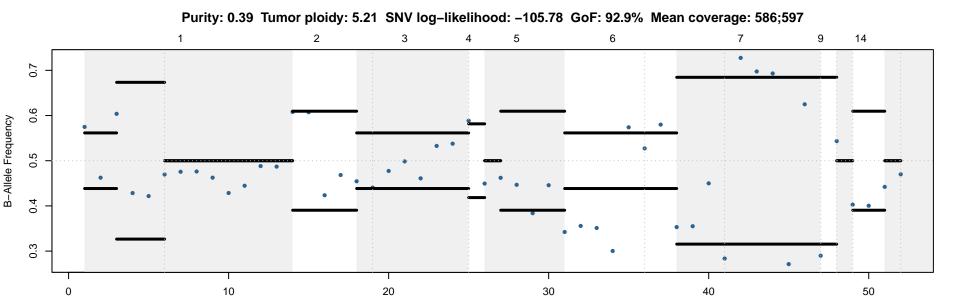
SNV Index





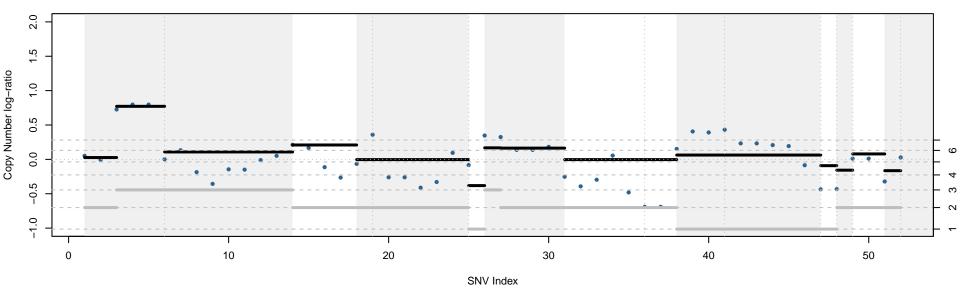


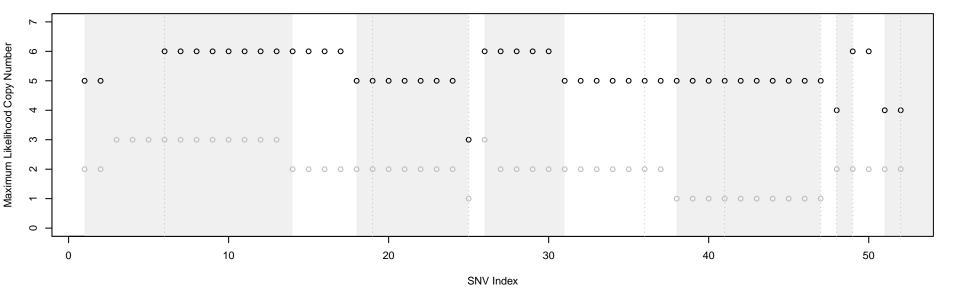


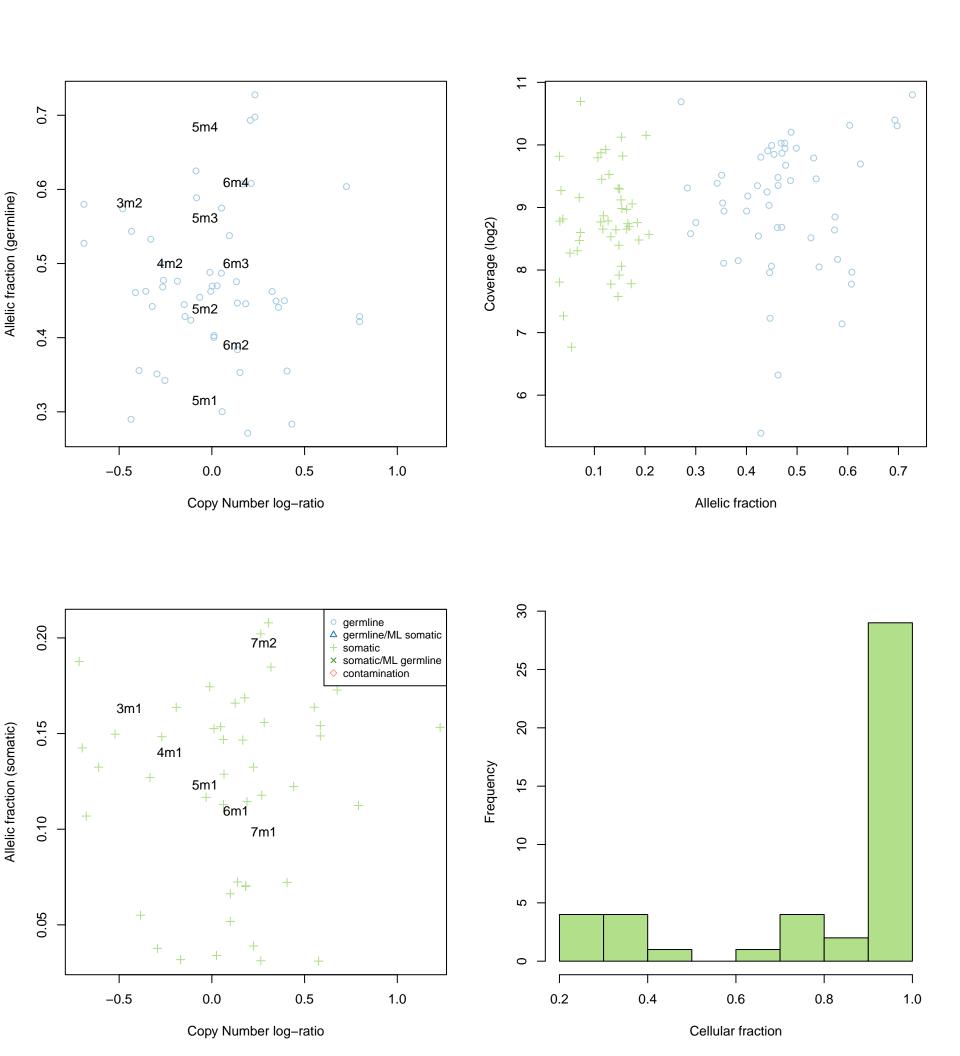


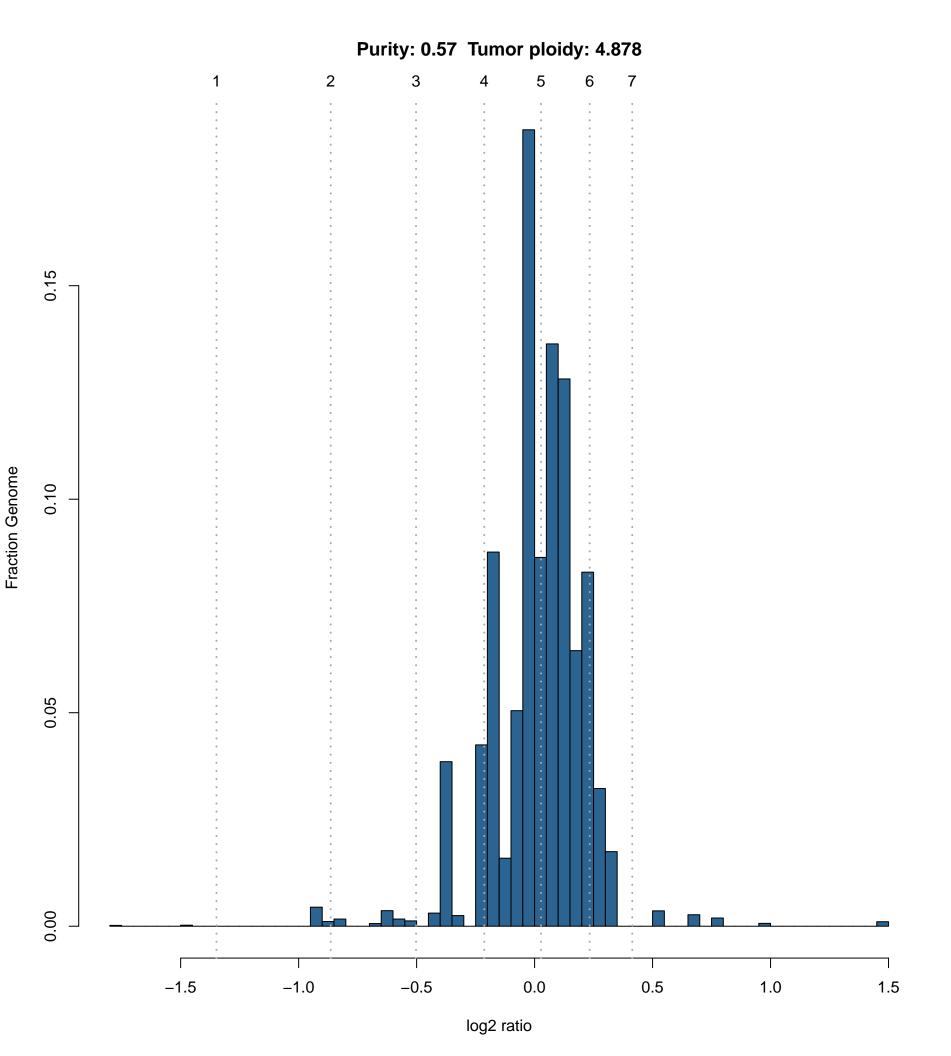
SCNA-fit log-likelihood: -14741.66

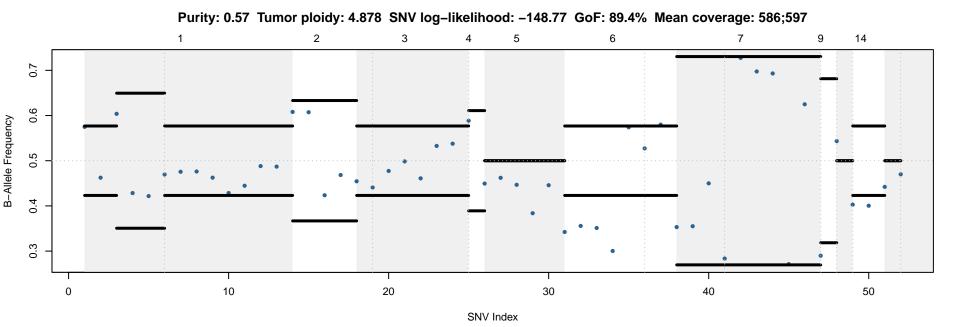
SNV Index



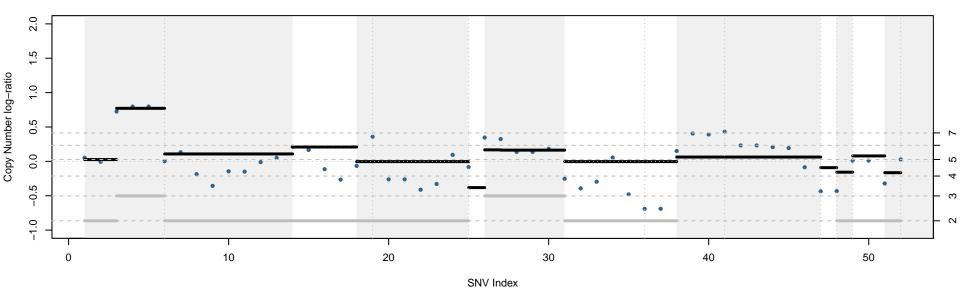


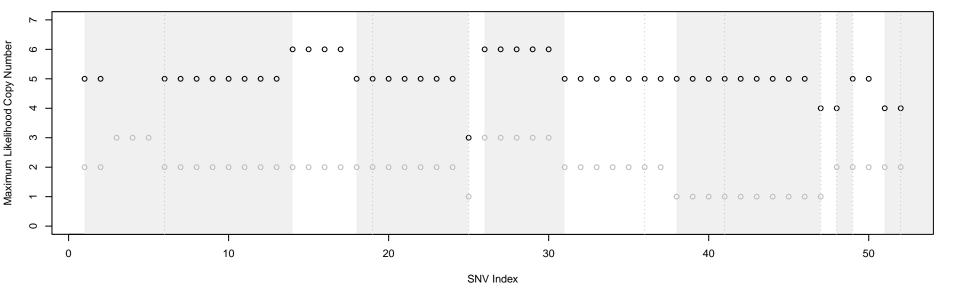


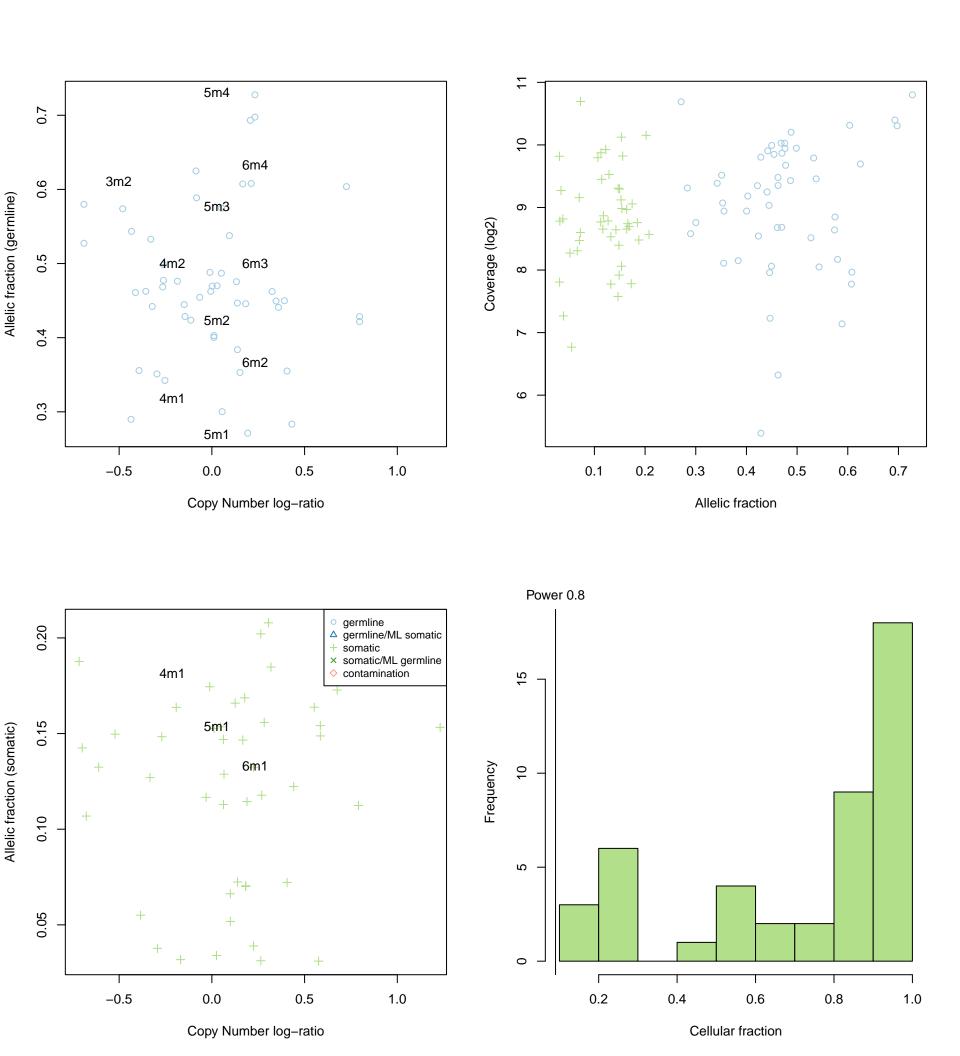




SCNA-fit log-likelihood: -14681.45

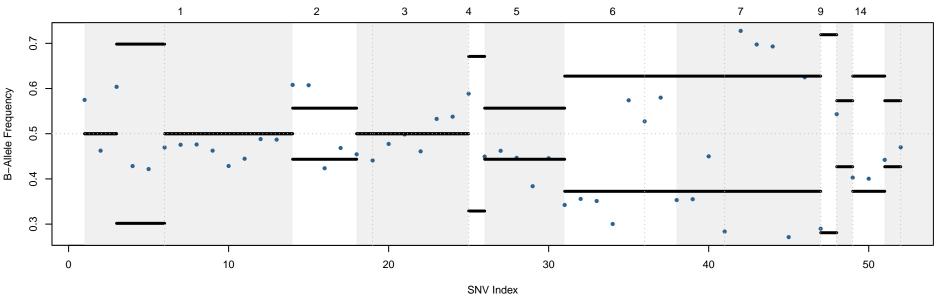




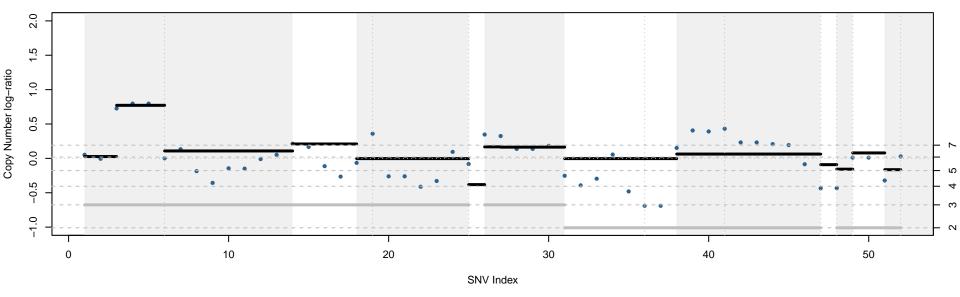


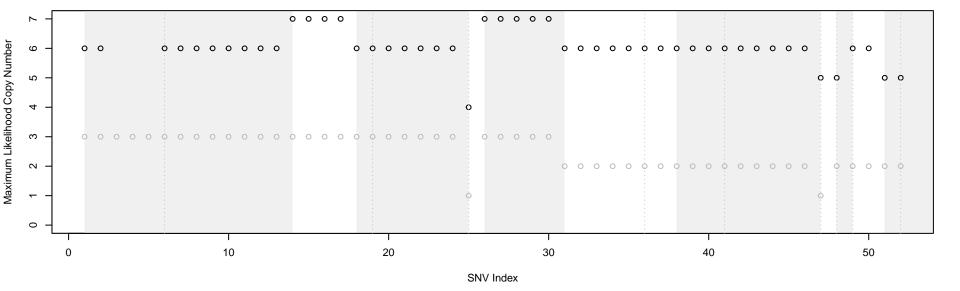
Purity: 0.52 Tumor ploidy: 5.897 2 3 5 7 6 Fraction Genome 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio

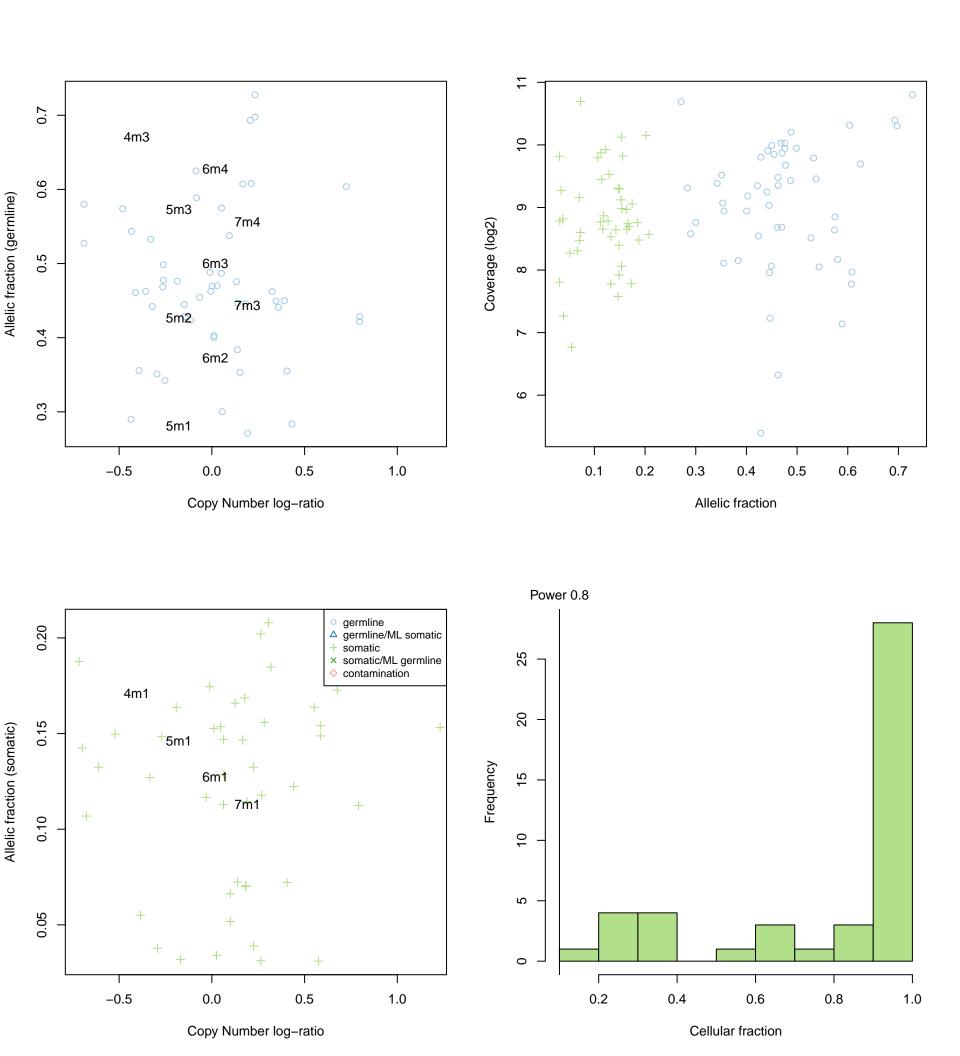


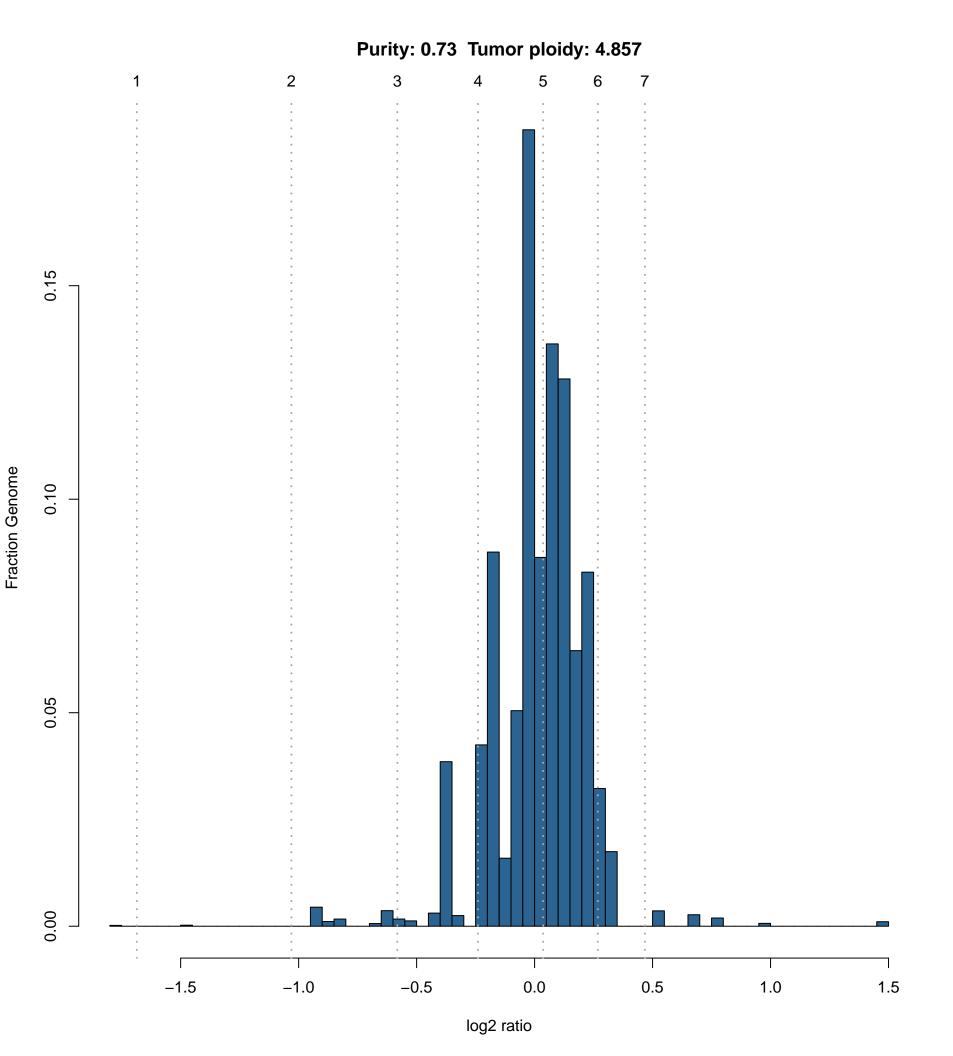


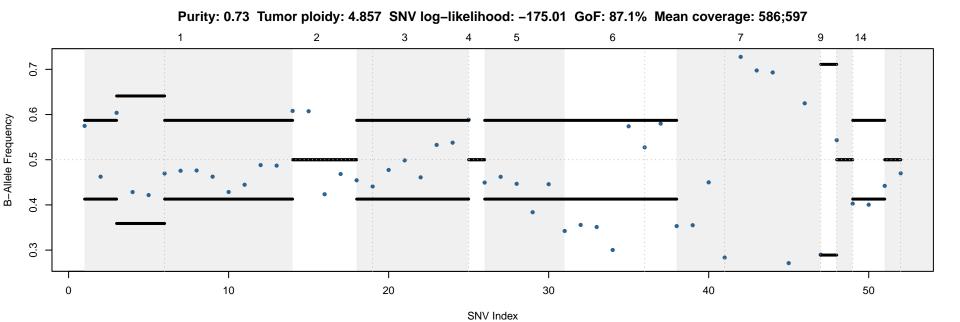
SCNA-fit log-likelihood: -14750.54



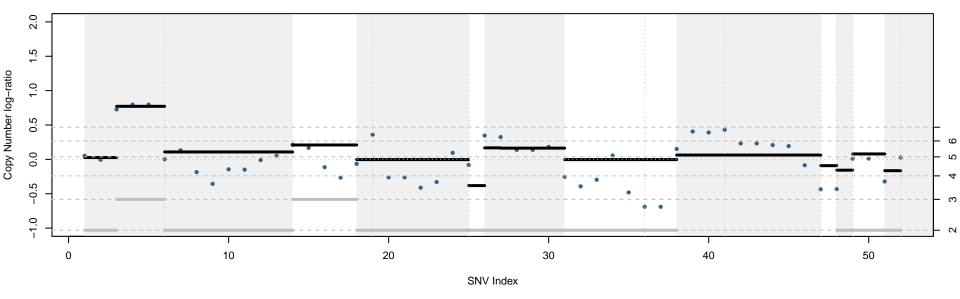


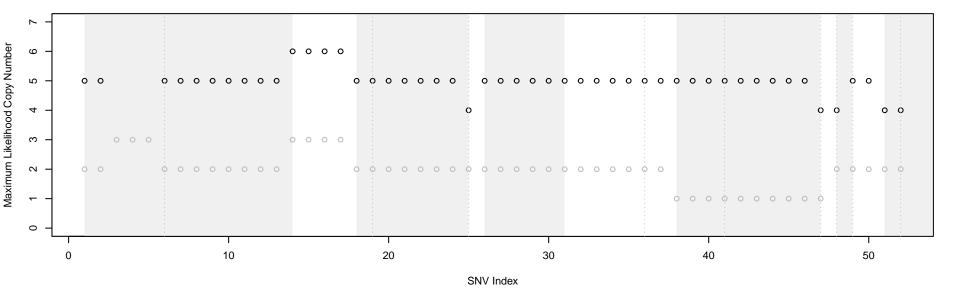


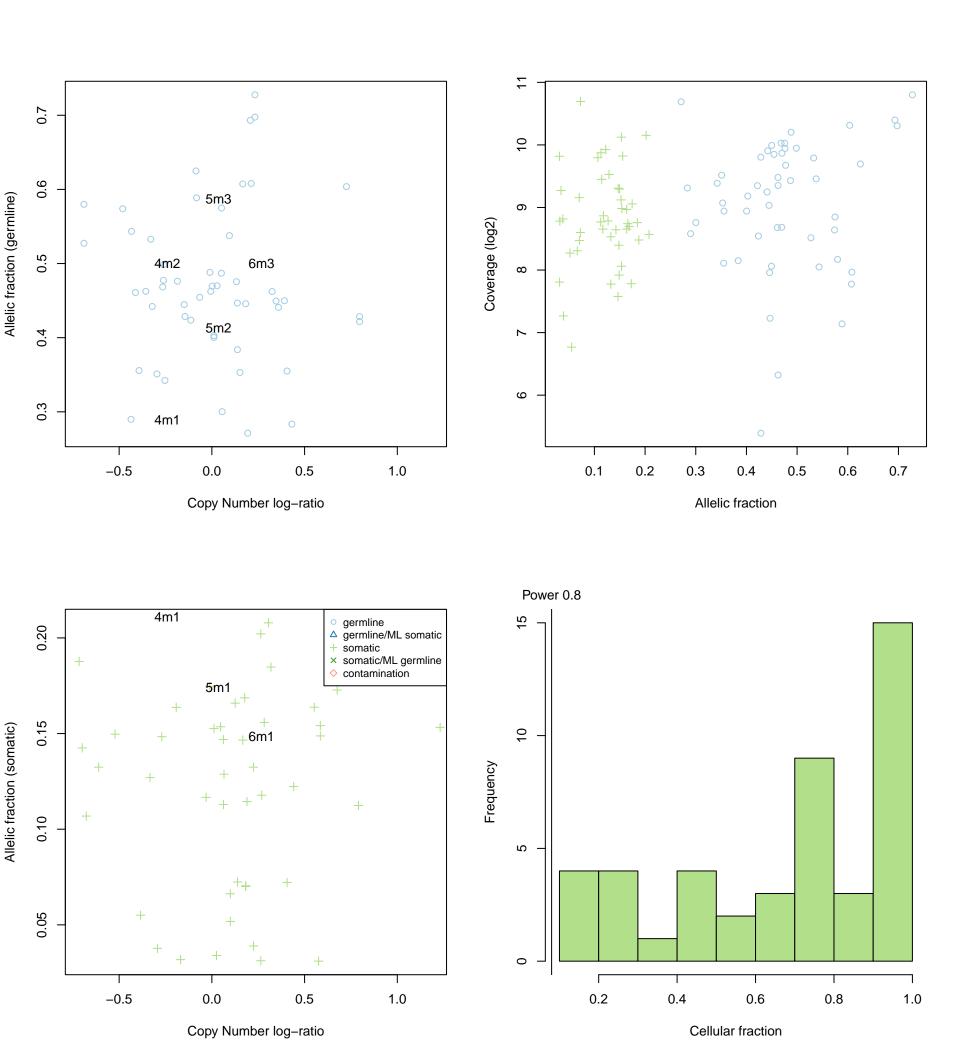




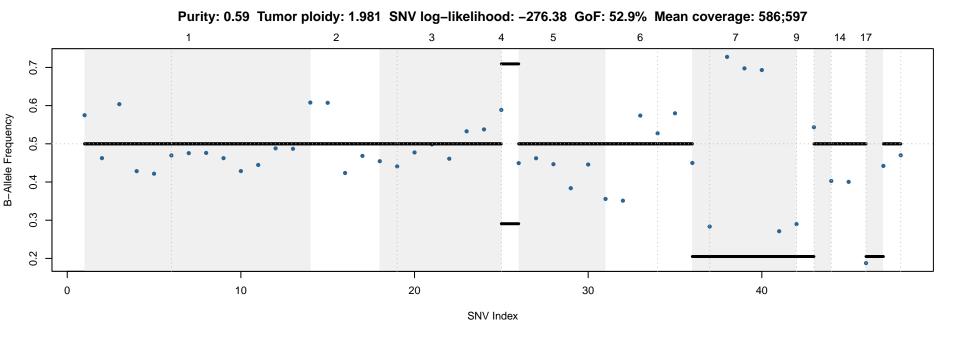
SCNA-fit log-likelihood: -14747.34







Purity: 0.59 Tumor ploidy: 1.981 0 5 Fraction Genome 0.05 0.00 -1.5 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



SCNA-fit log-likelihood: -15052.32

