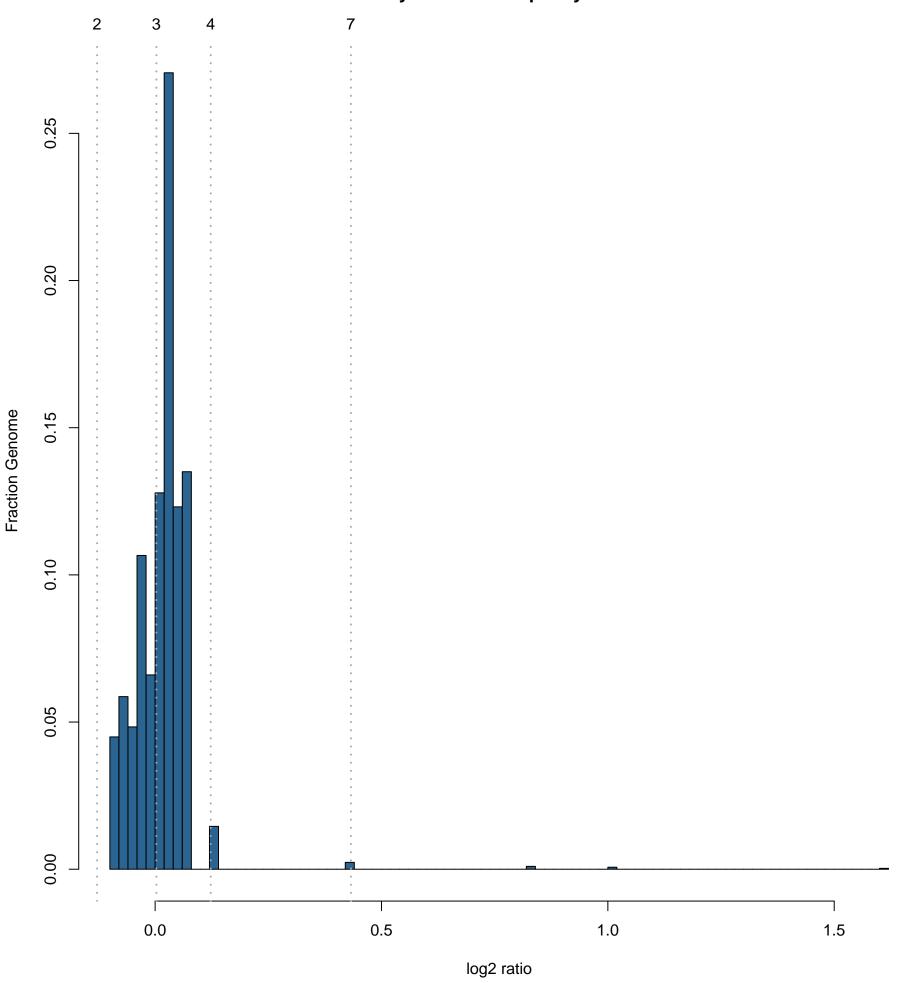
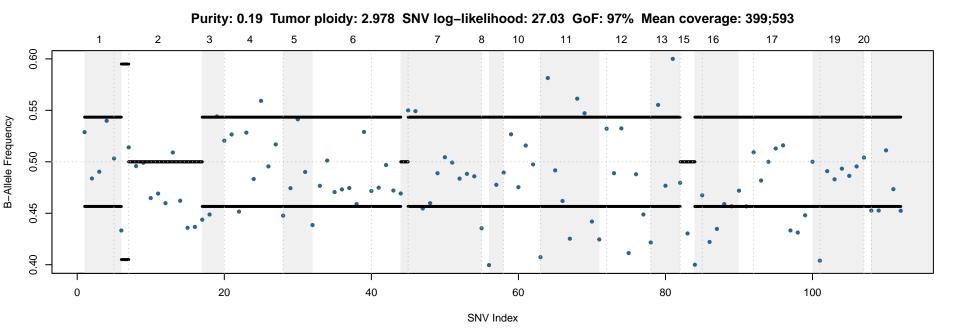
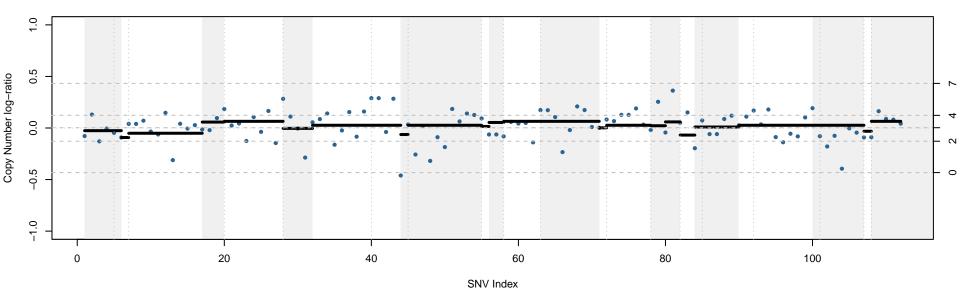
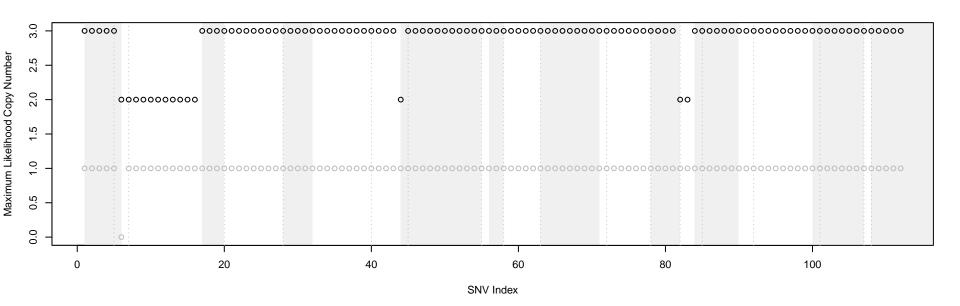
Purity: 0.19 Tumor ploidy: 2.978

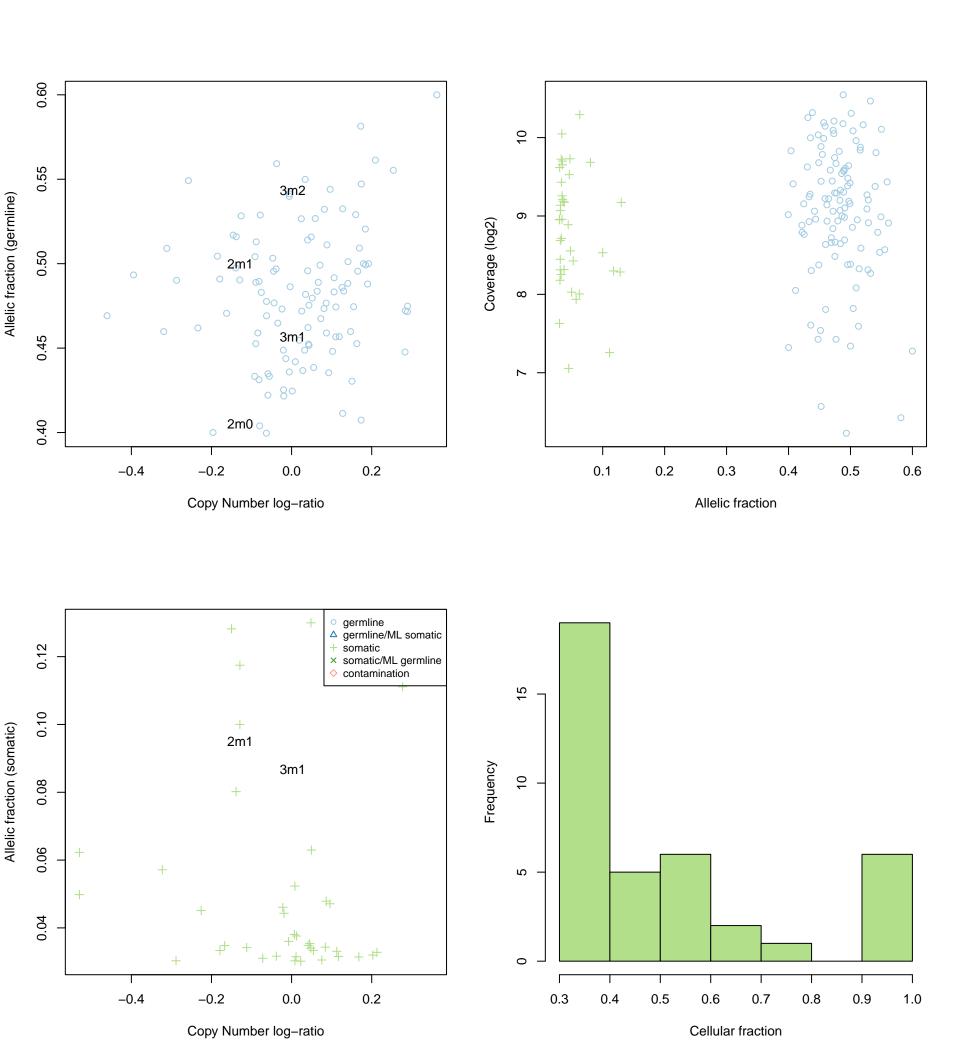




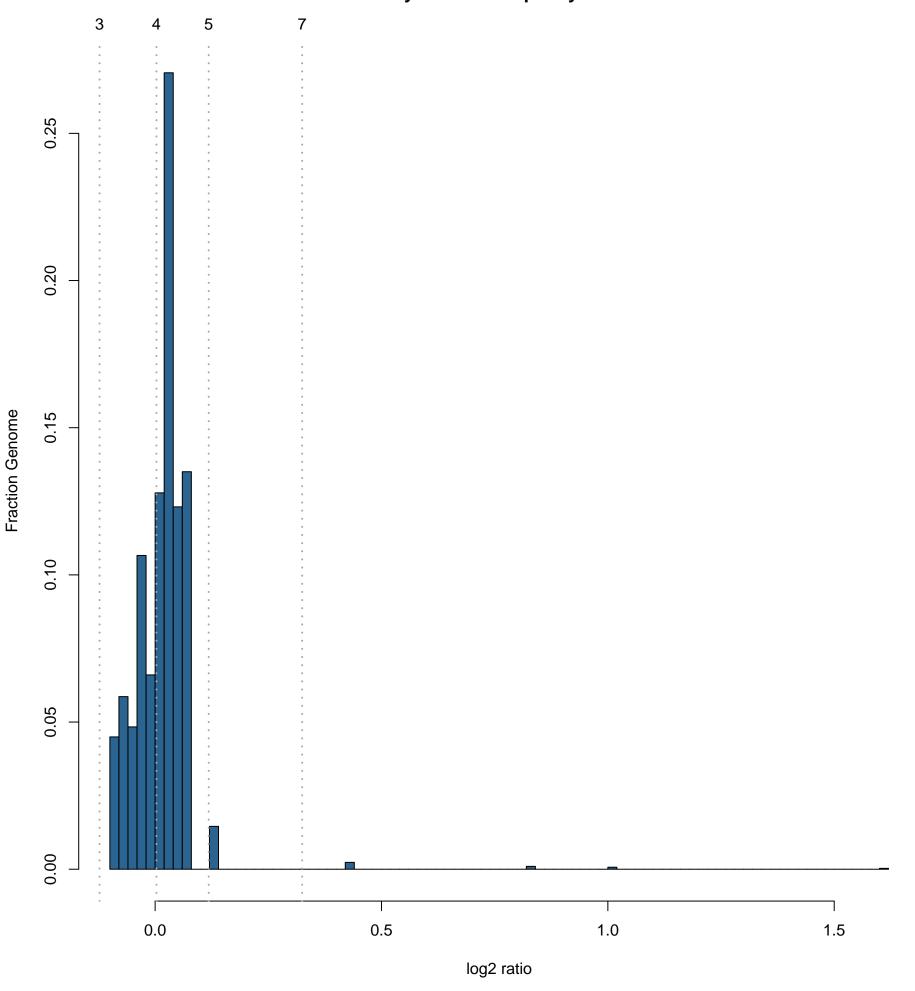
SCNA-fit log-likelihood: -5298.04

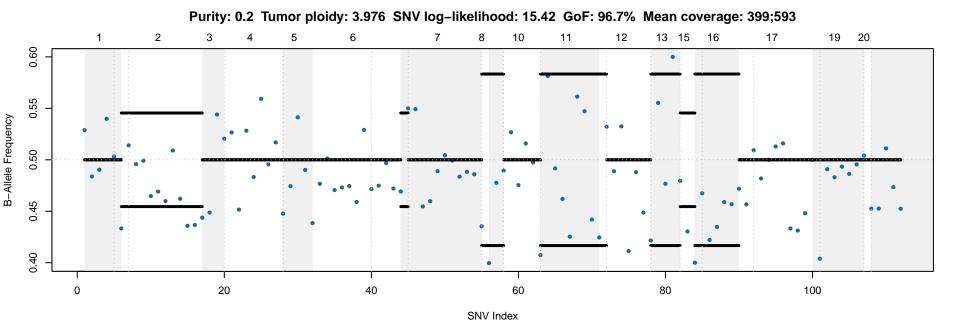




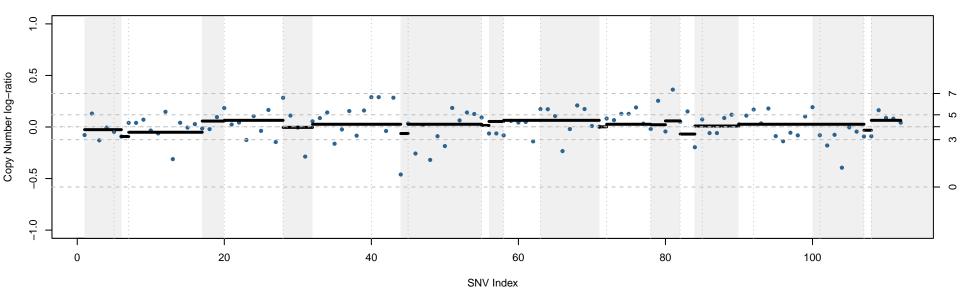


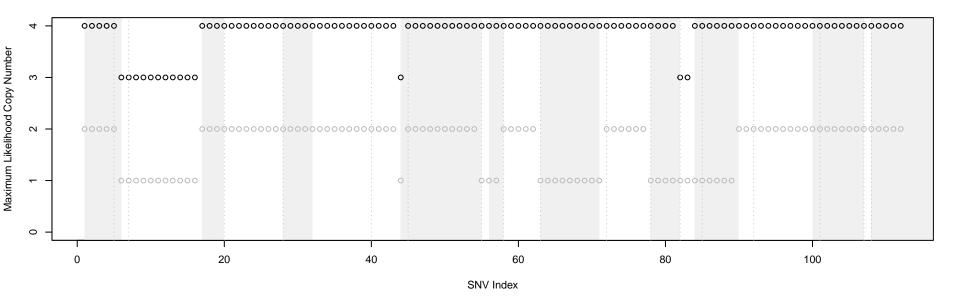
Purity: 0.2 Tumor ploidy: 3.976

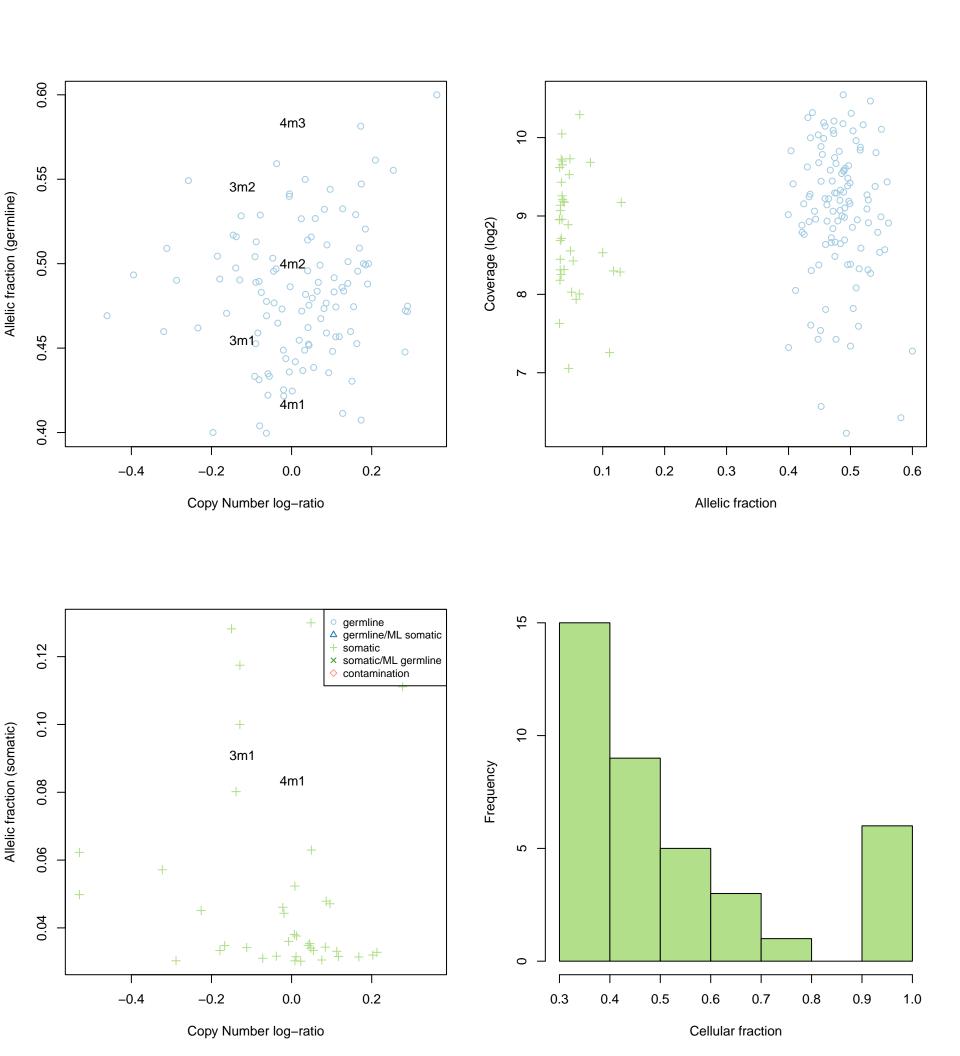




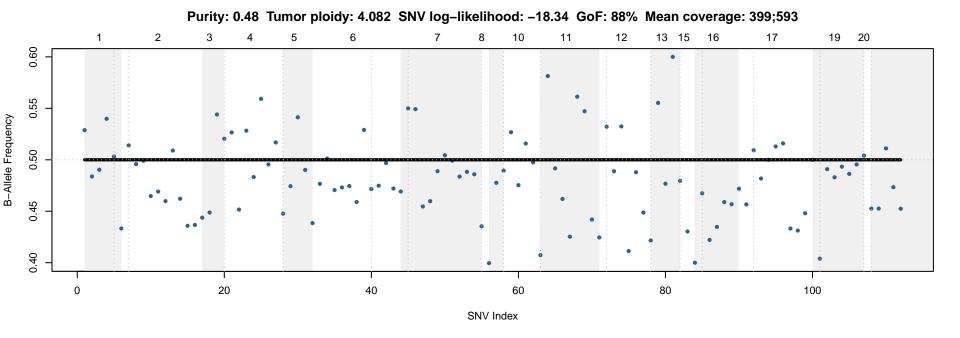
SCNA-fit log-likelihood: -5295.97



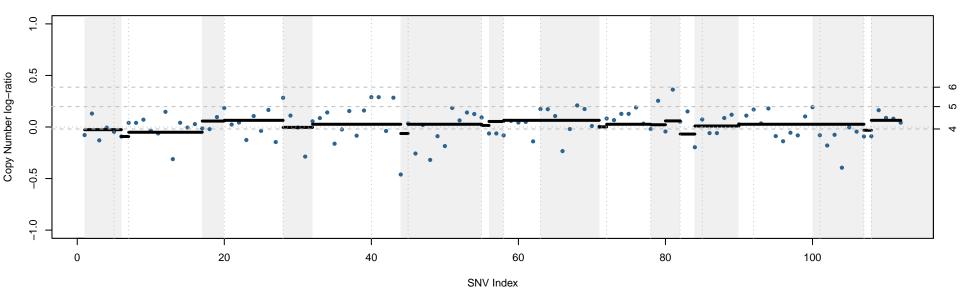


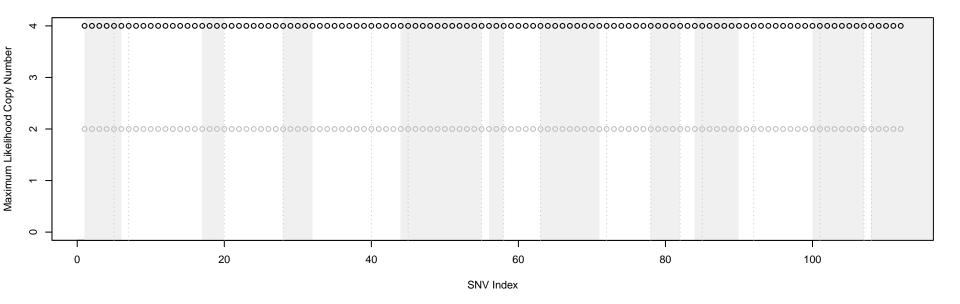


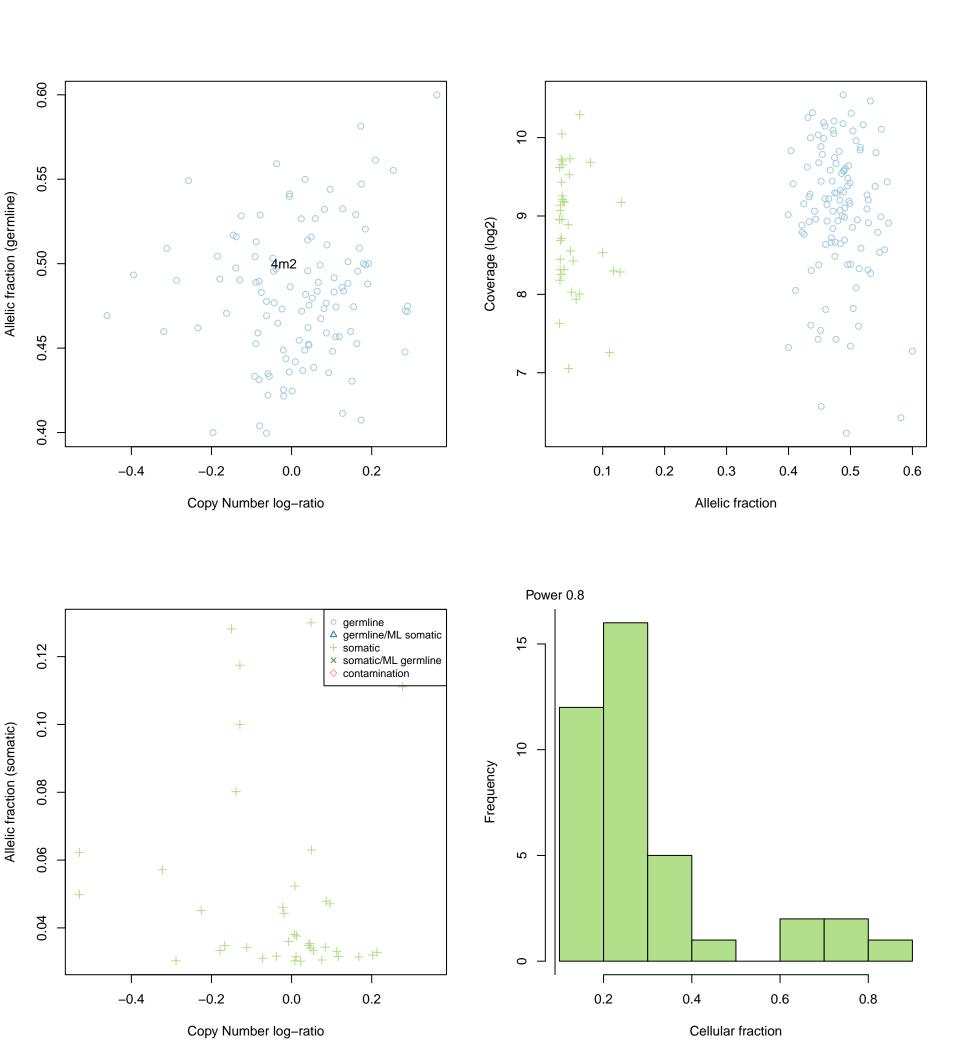
Purity: 0.48 Tumor ploidy: 4.082 0 6 5 9.0 0.3 Fraction Genome 0.2 0.1 0.0 -1.5 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



SCNA-fit log-likelihood: -5328.57







Purity: 0.23 Tumor ploidy: 4.861 6 0 5 0.4 0.3 Fraction Genome 0.2 0.1 0.0

-1.5

-1.0

-0.5

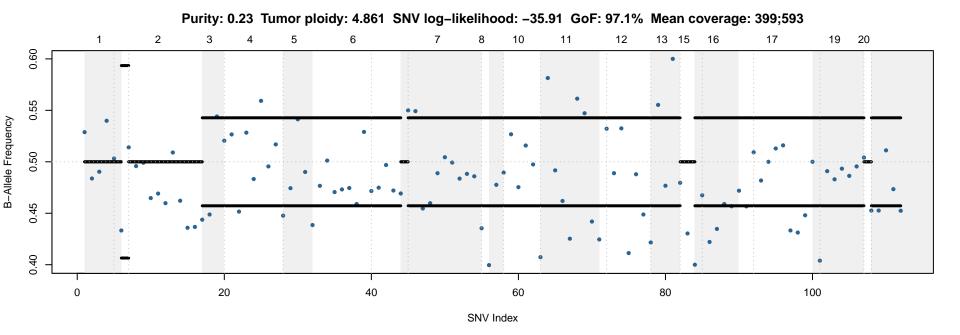
0.0

log2 ratio

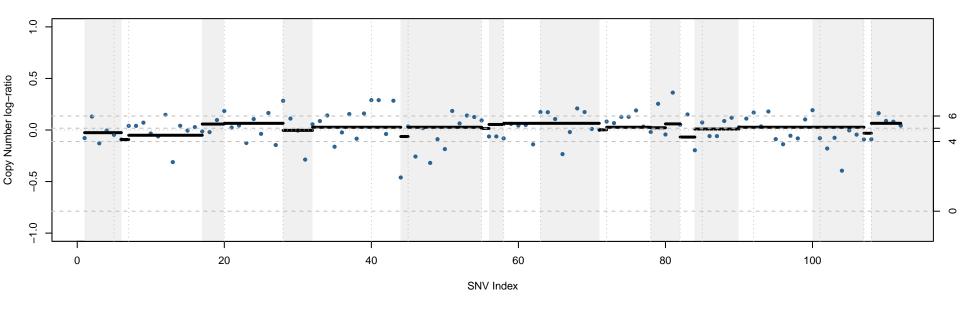
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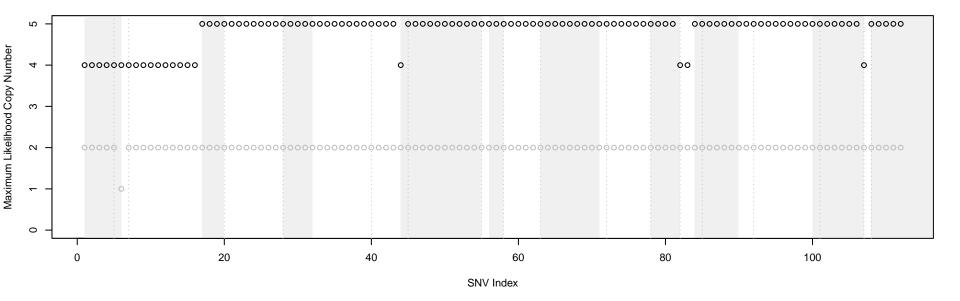
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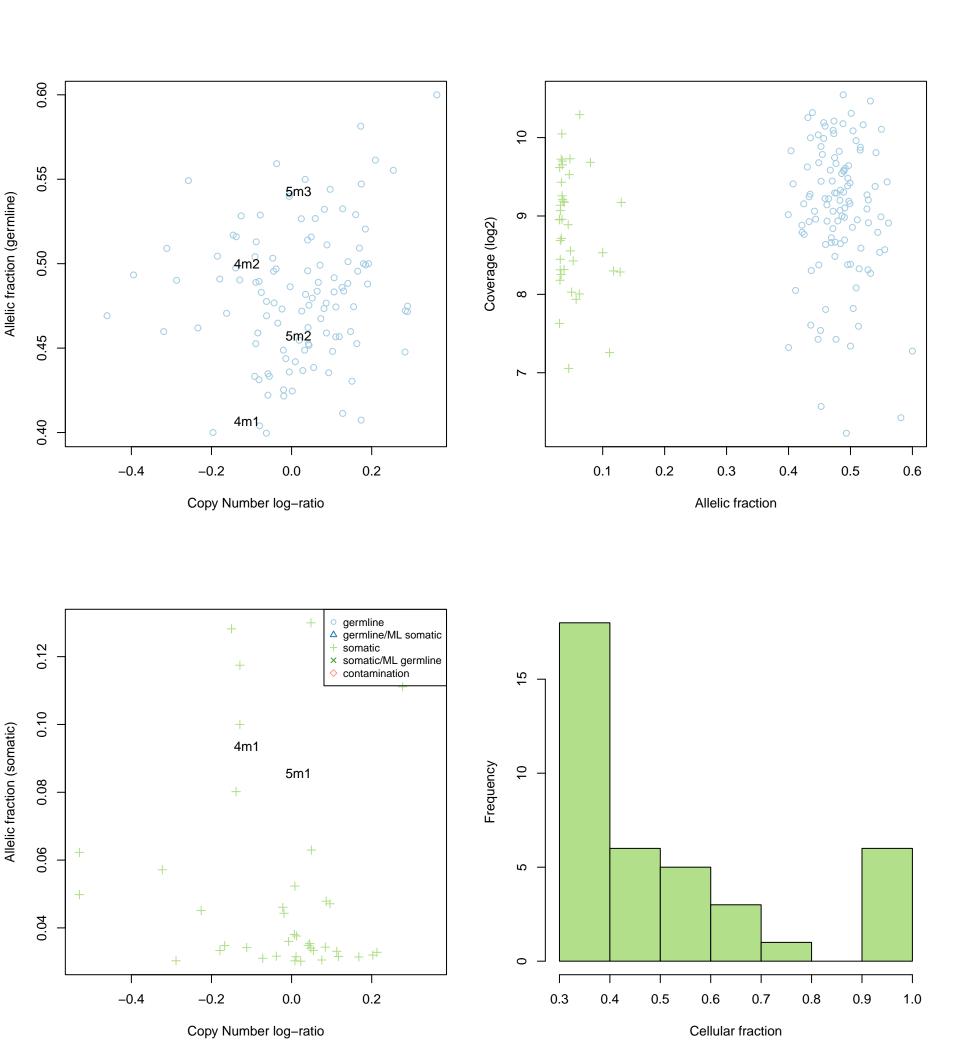
1.5



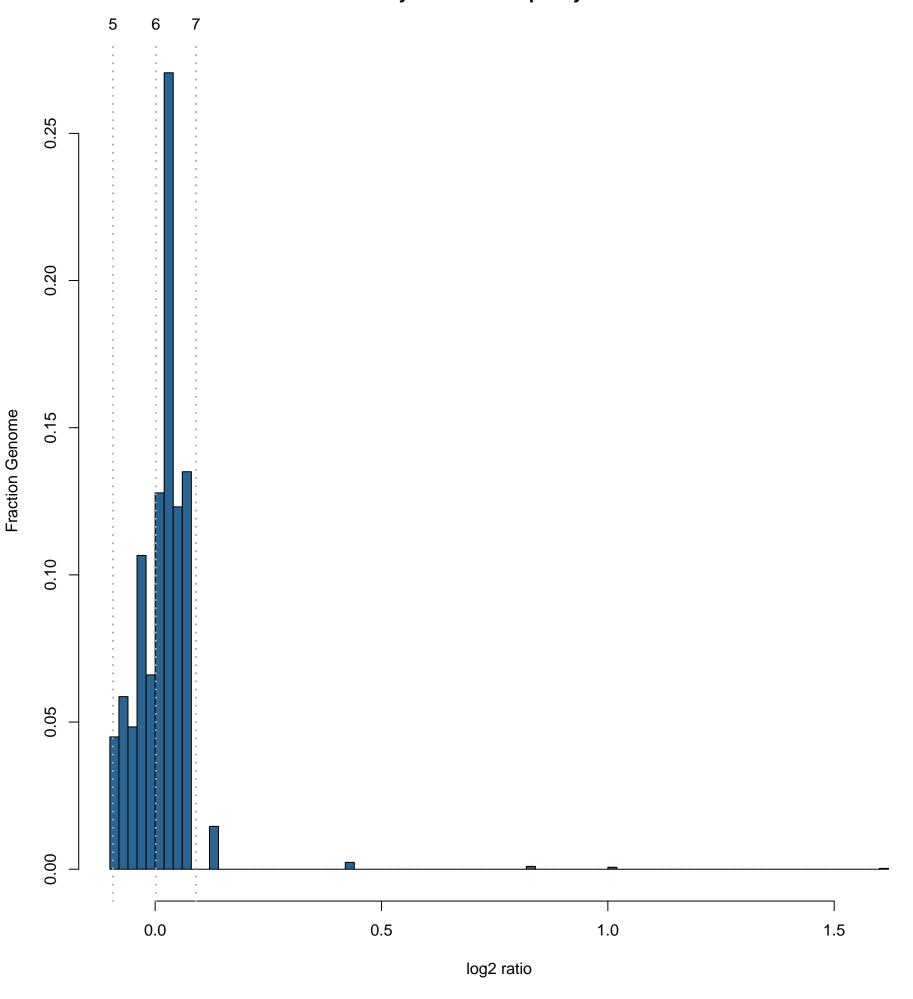
SCNA-fit log-likelihood: -5308.43

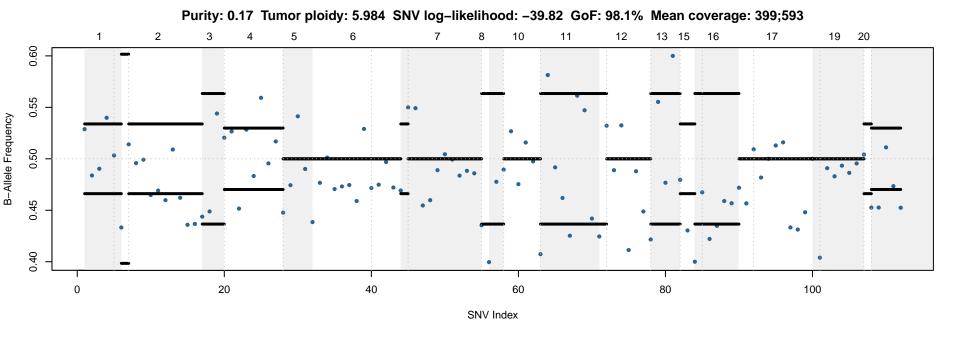




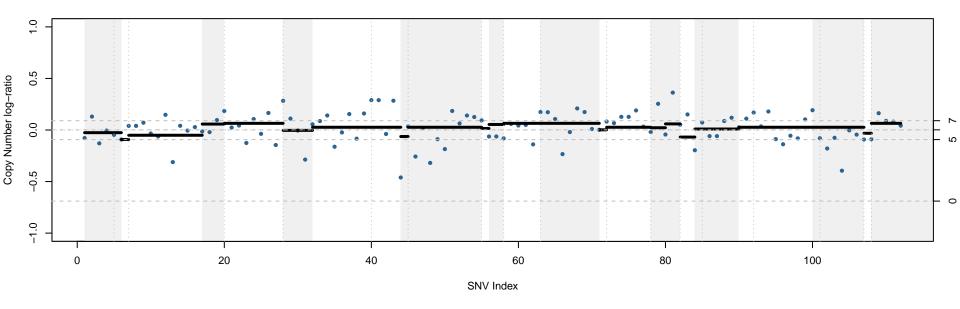


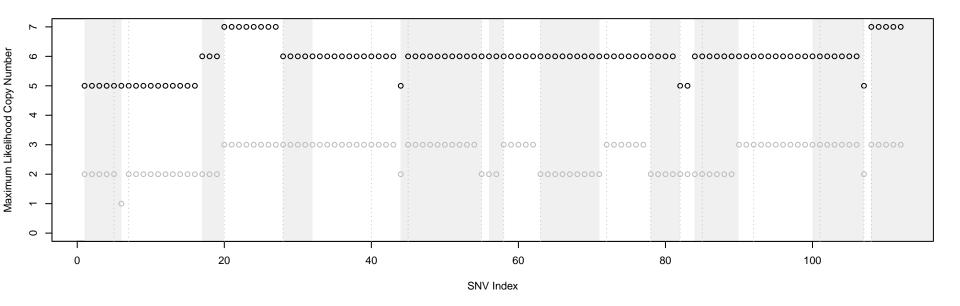
Purity: 0.17 Tumor ploidy: 5.984

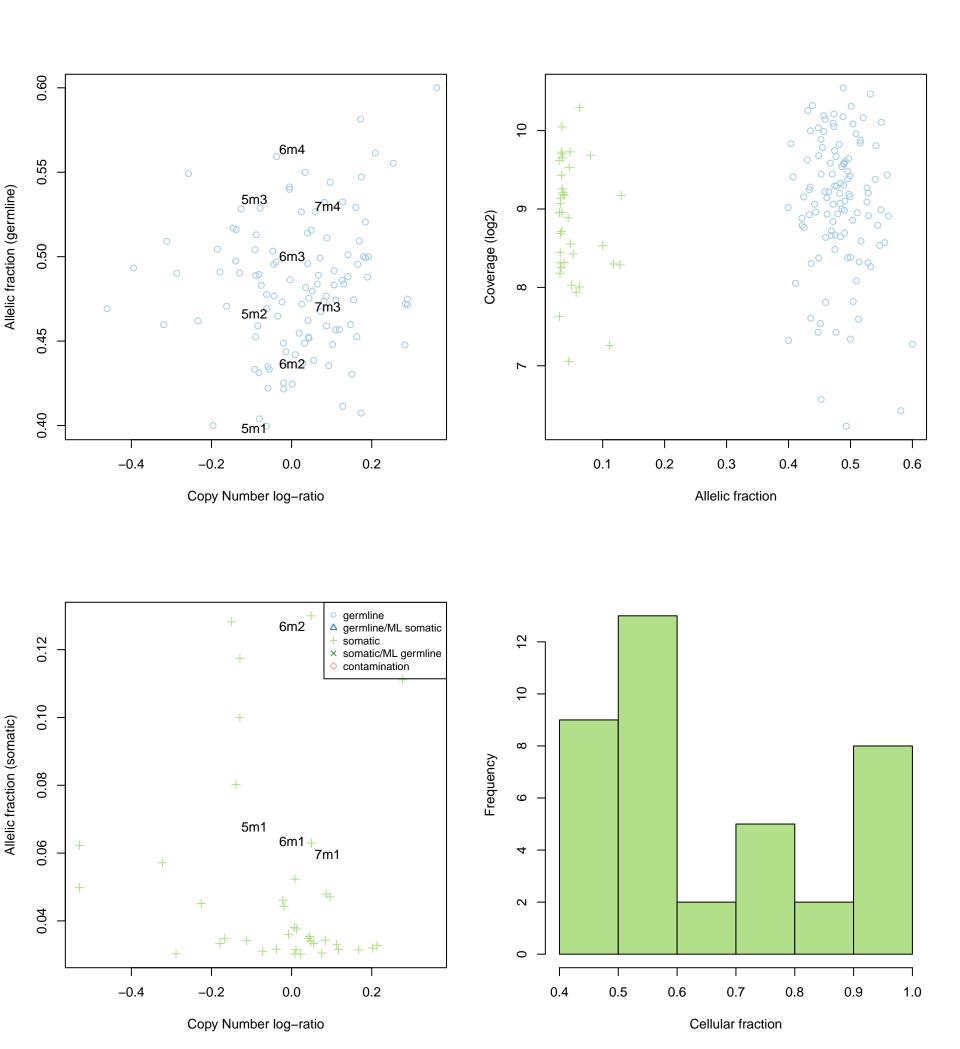




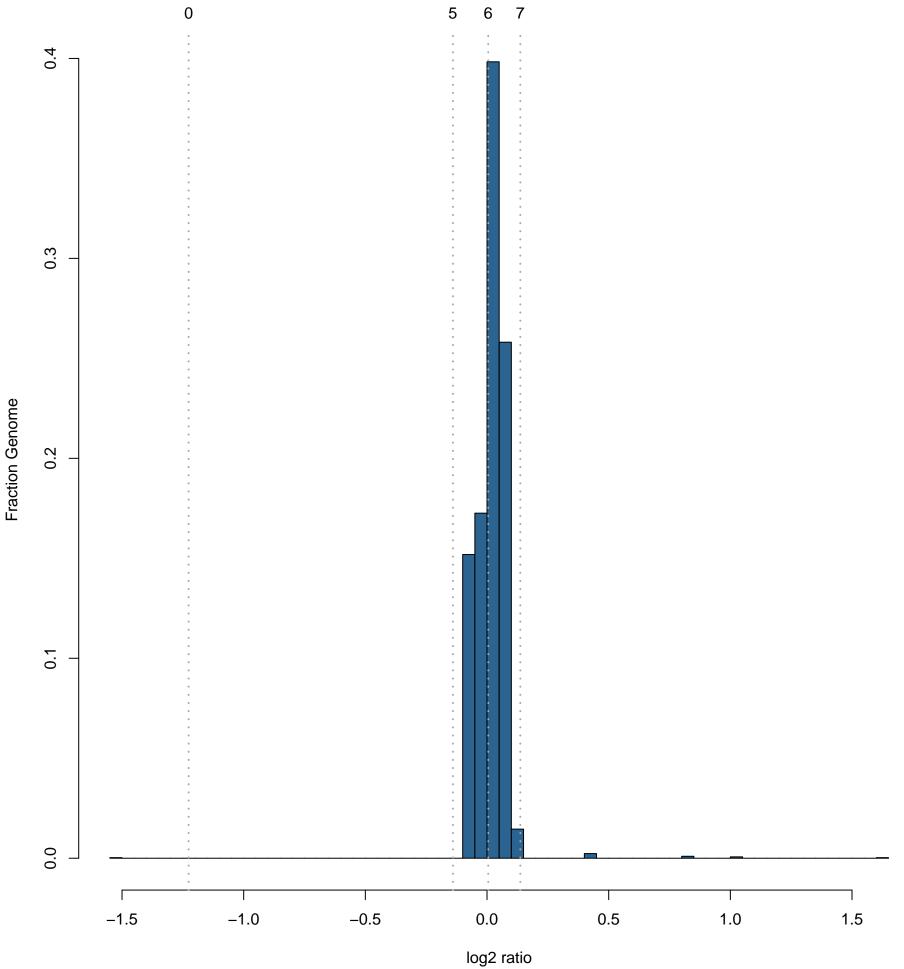
SCNA-fit log-likelihood: -5303.02

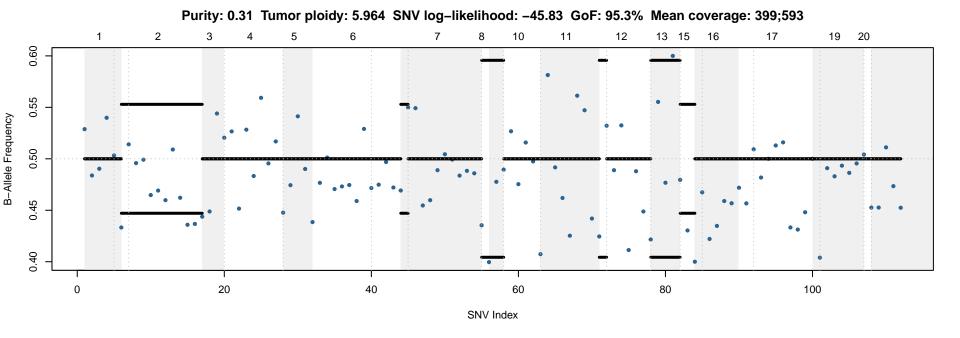




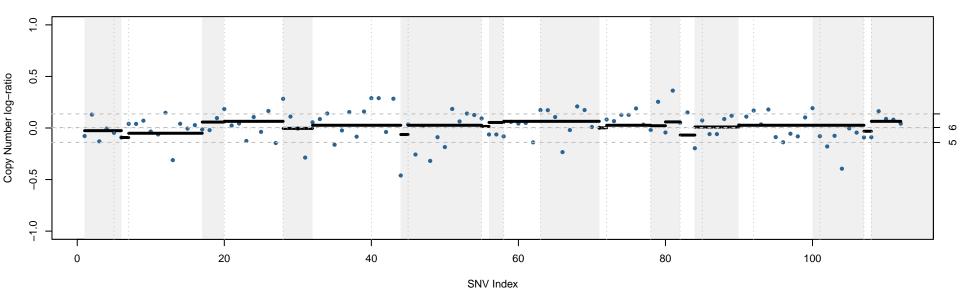


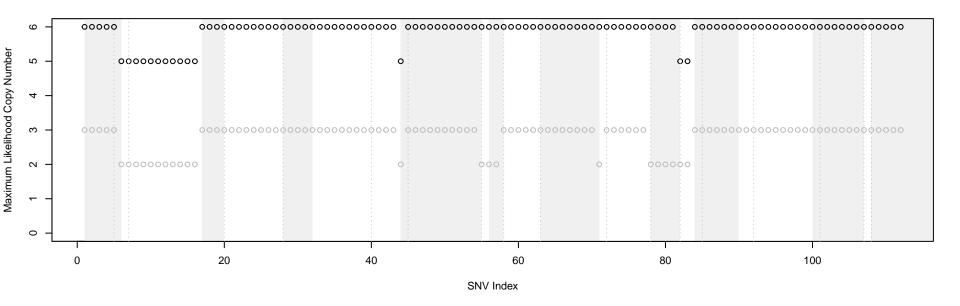
Purity: 0.31 Tumor ploidy: 5.964

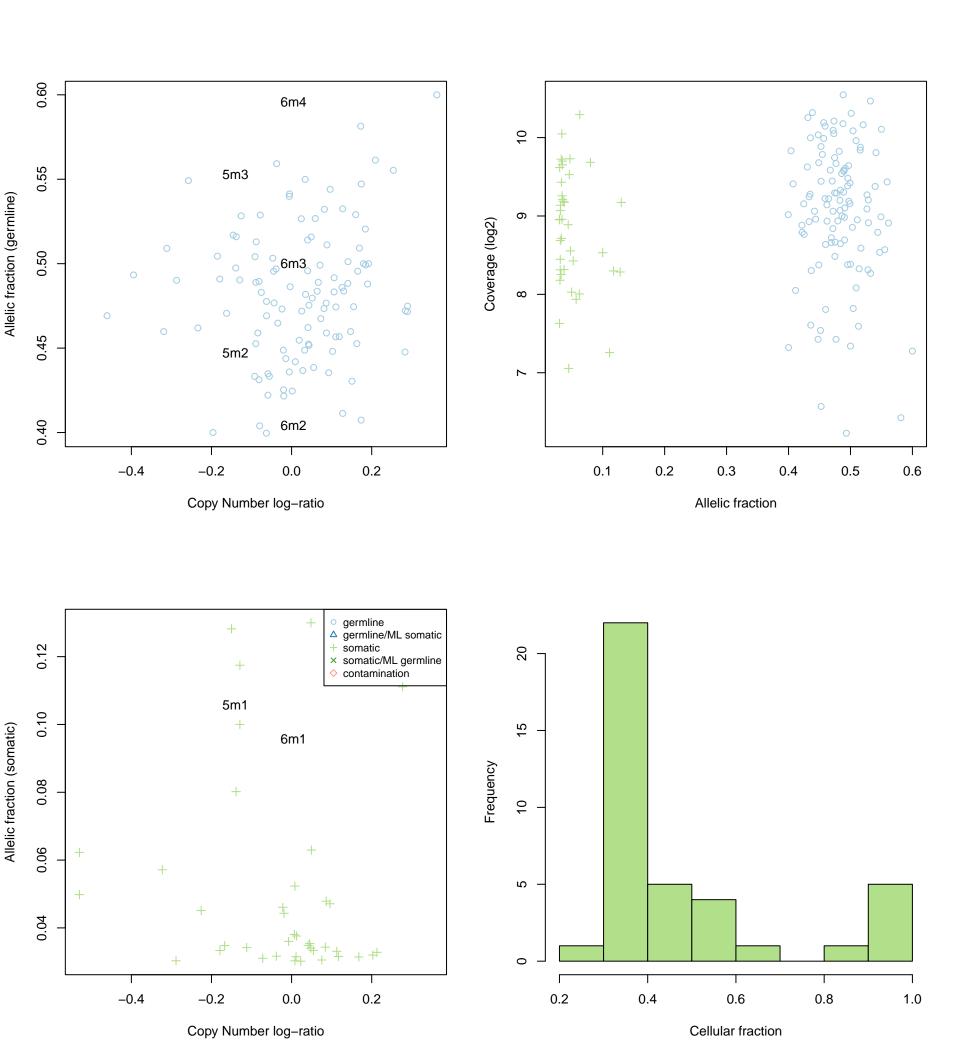




SCNA-fit log-likelihood: -5311.35







Purity: 0.55 Tumor ploidy: 5.982 5 1 6 9.0 0.3 Fraction Genome 0.2 0.1 0.0

-1.5

-1.0

-0.5

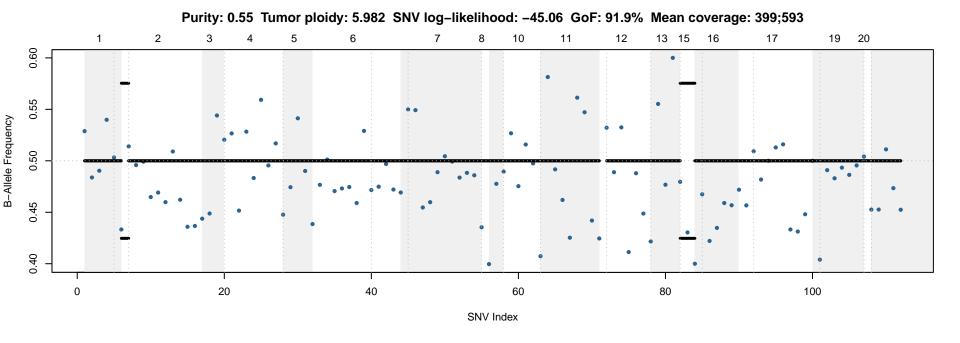
0.0

log2 ratio

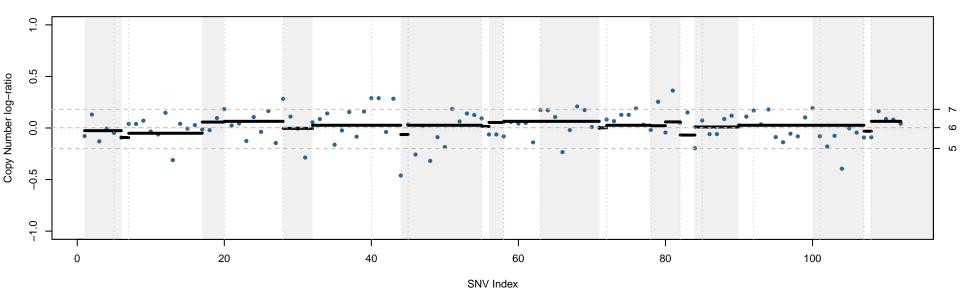
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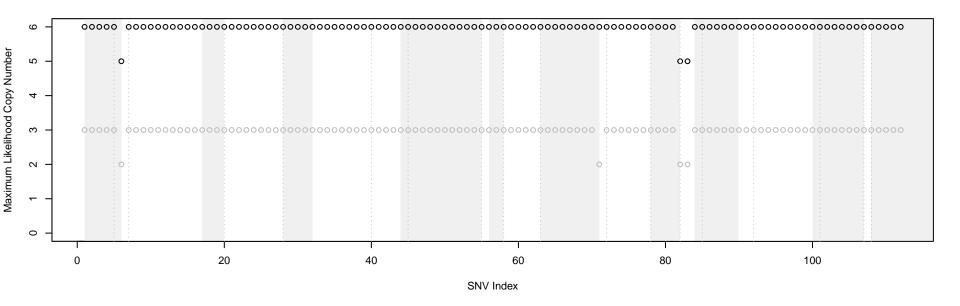
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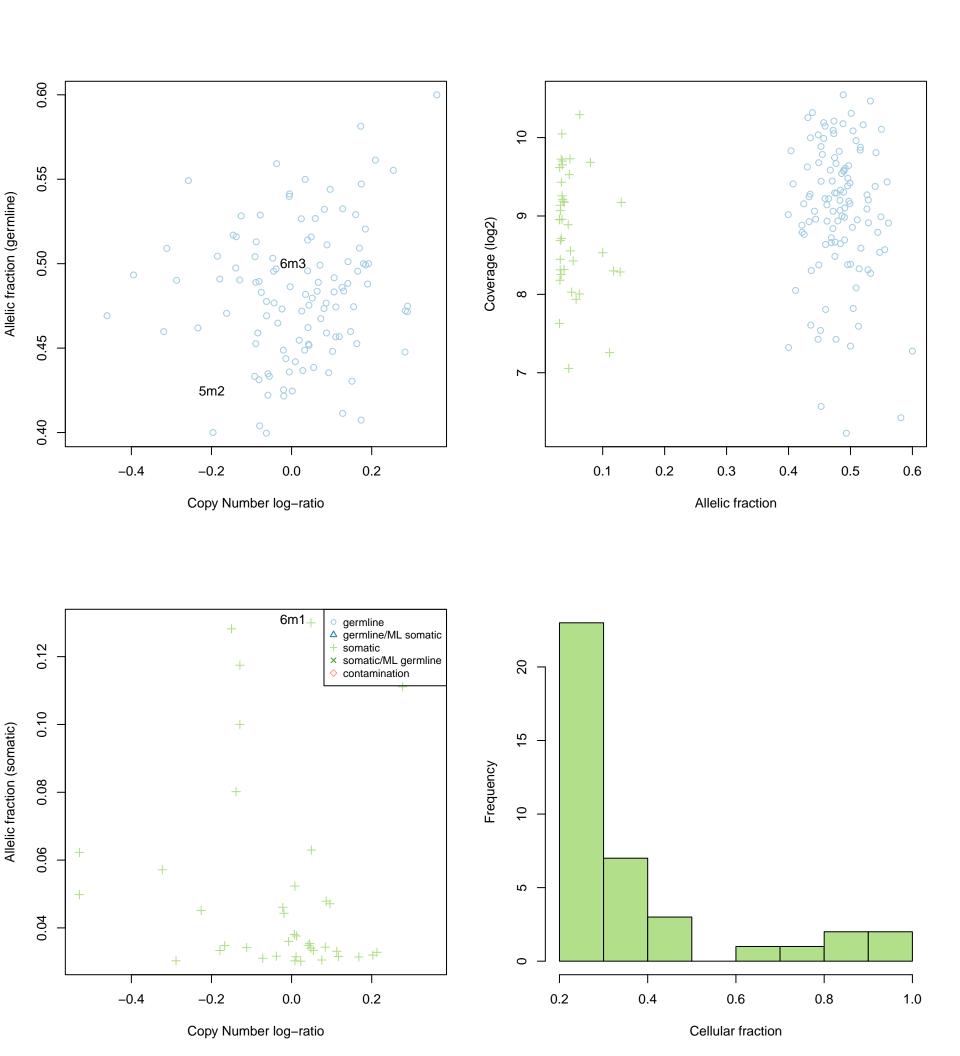
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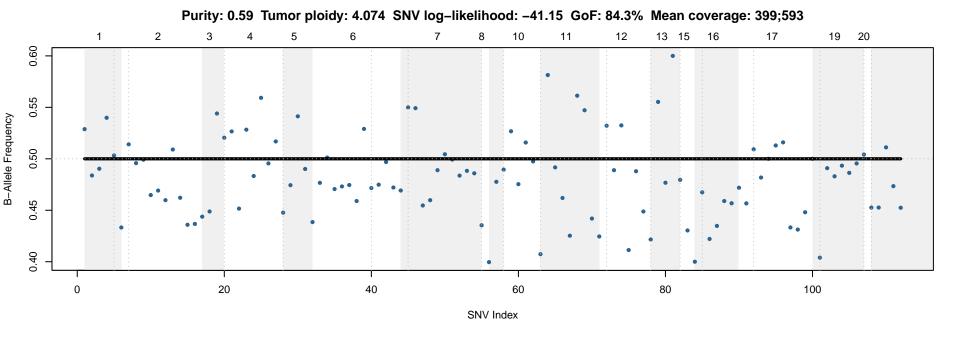




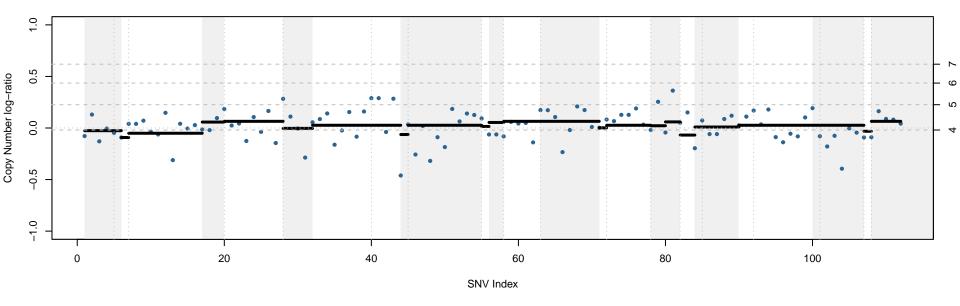


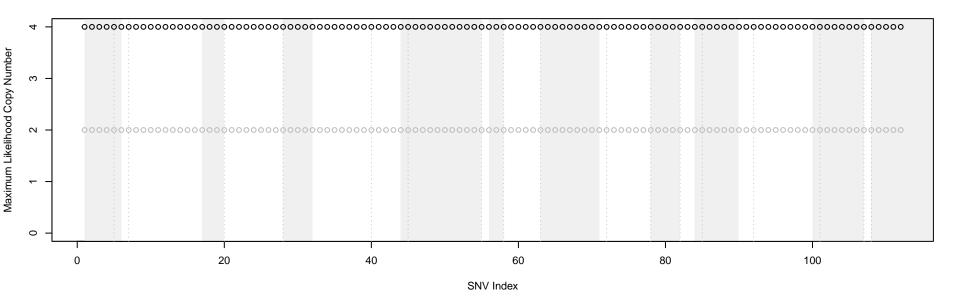


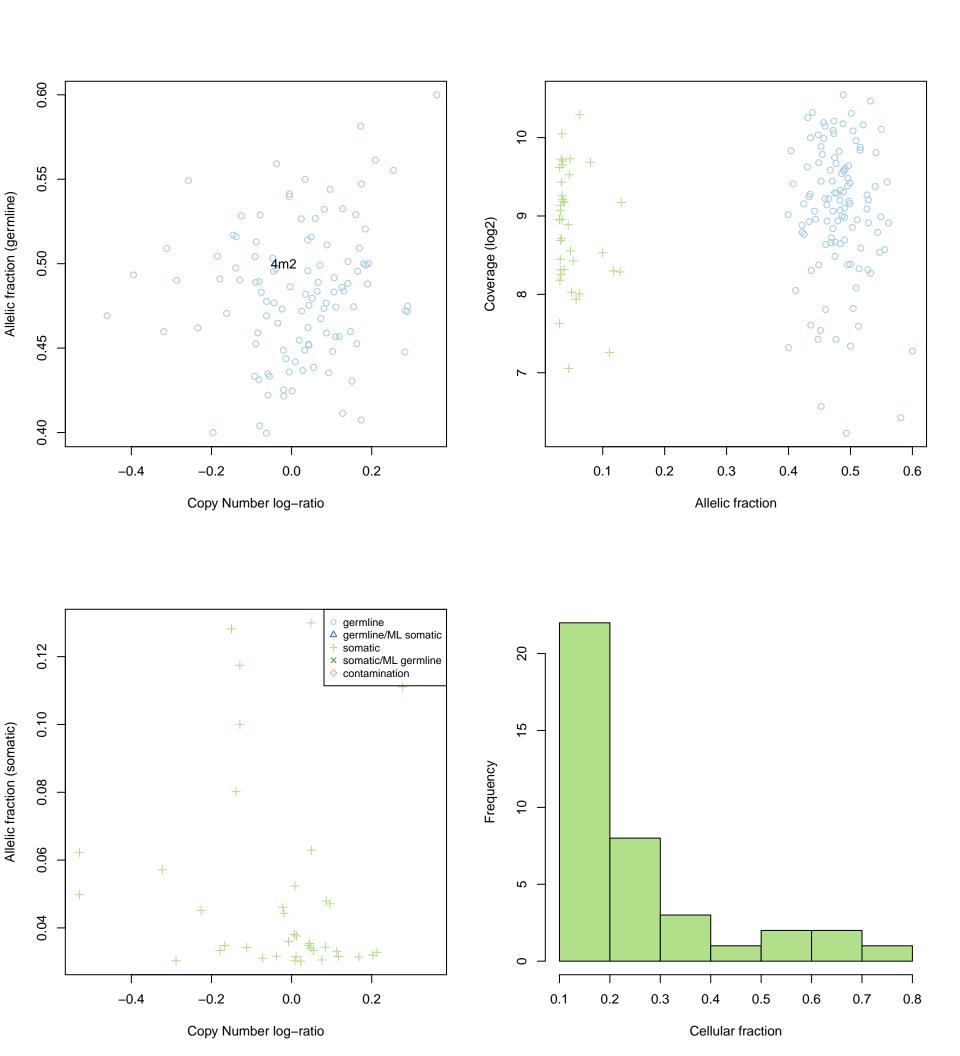
Purity: 0.59 Tumor ploidy: 4.074 5 6 1 9.0 0.3 Fraction Genome 0.2 0.1 0.0 -1.5 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



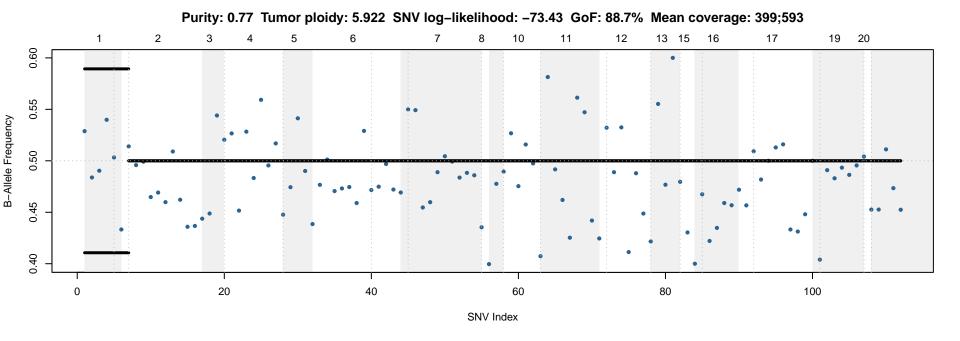
SCNA-fit log-likelihood: -5322.79



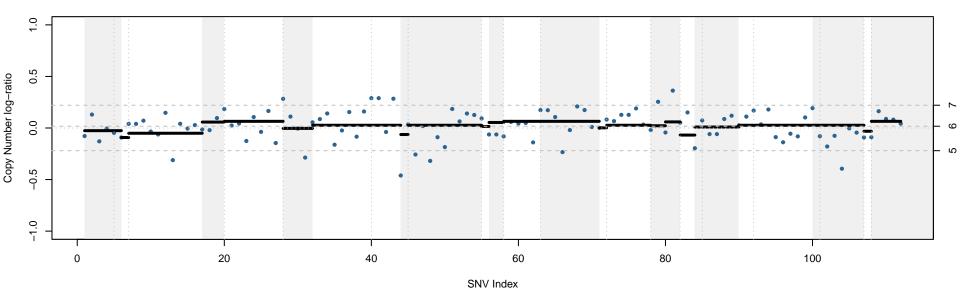


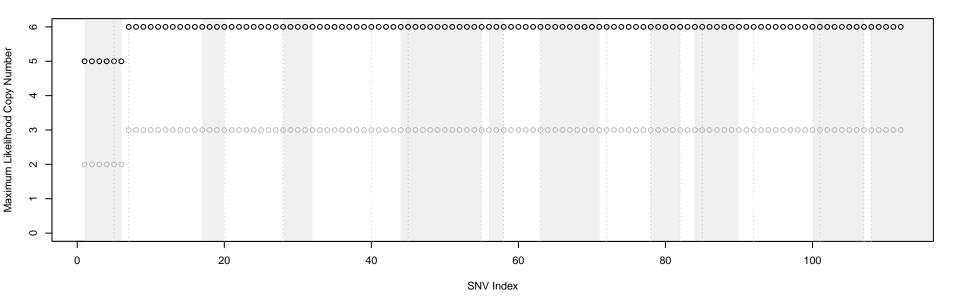


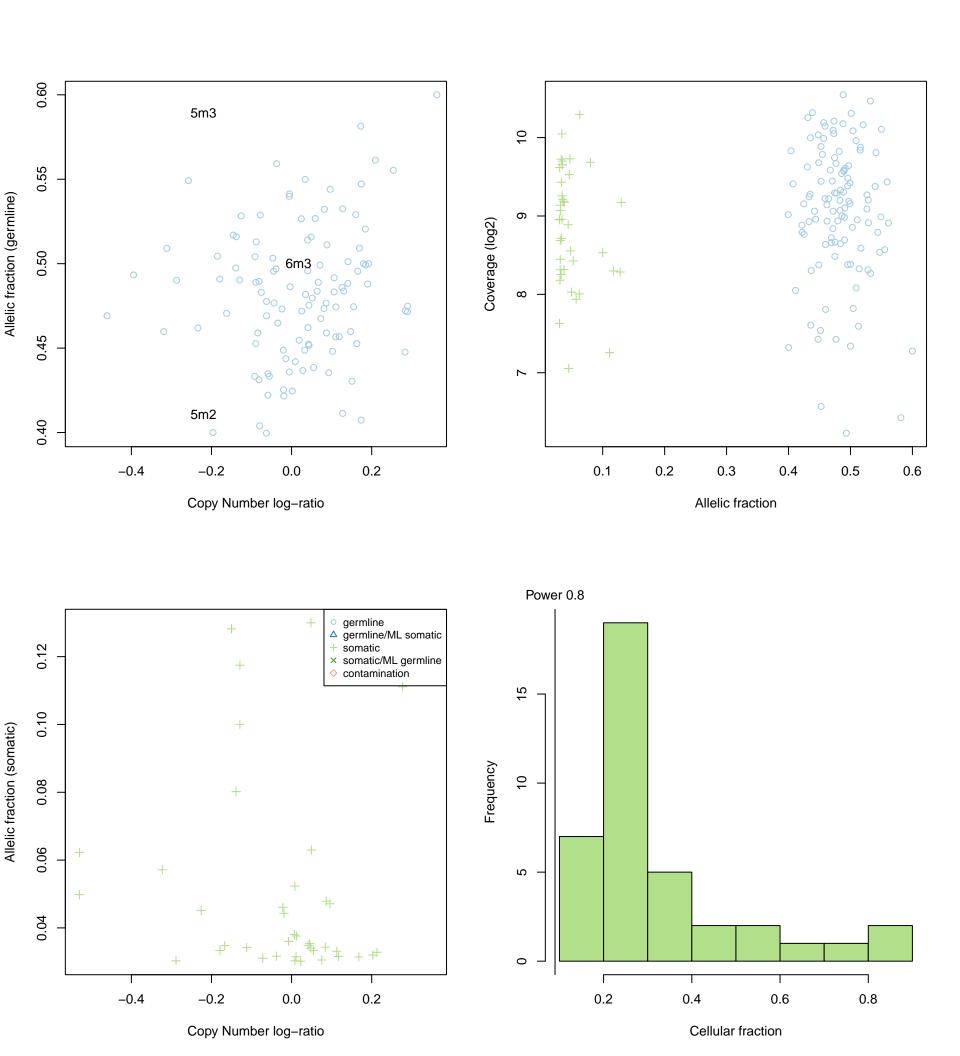
Purity: 0.77 Tumor ploidy: 5.922 2 6 5 7 9.0 0.3 Fraction Genome 0.2 0.1 0.0 -1.5 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



SCNA-fit log-likelihood: -5416.67

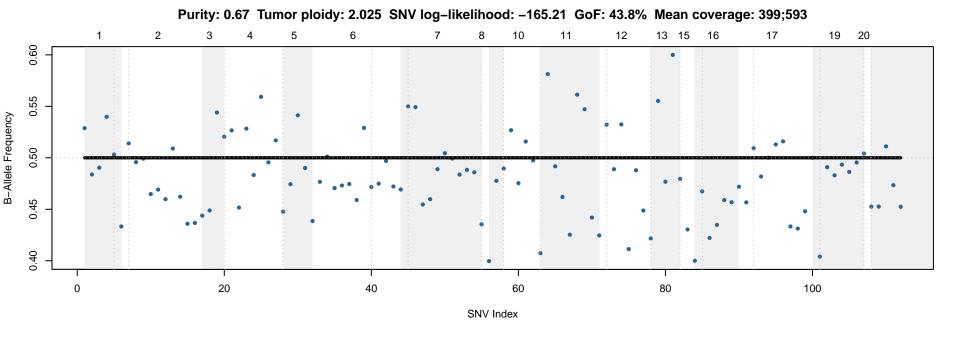




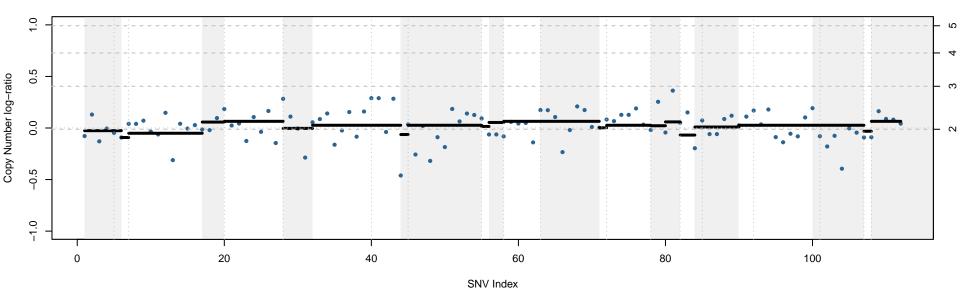


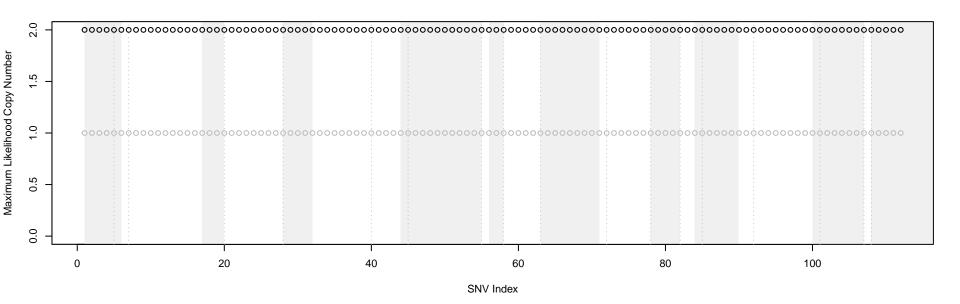
Purity: 0.67 Tumor ploidy: 2.025 2 0 5 7 0.3 Fraction Genome 0.2 0.1 0.0 -1.5 -1.0 -0.5 0.0 0.5 1.0 1.5

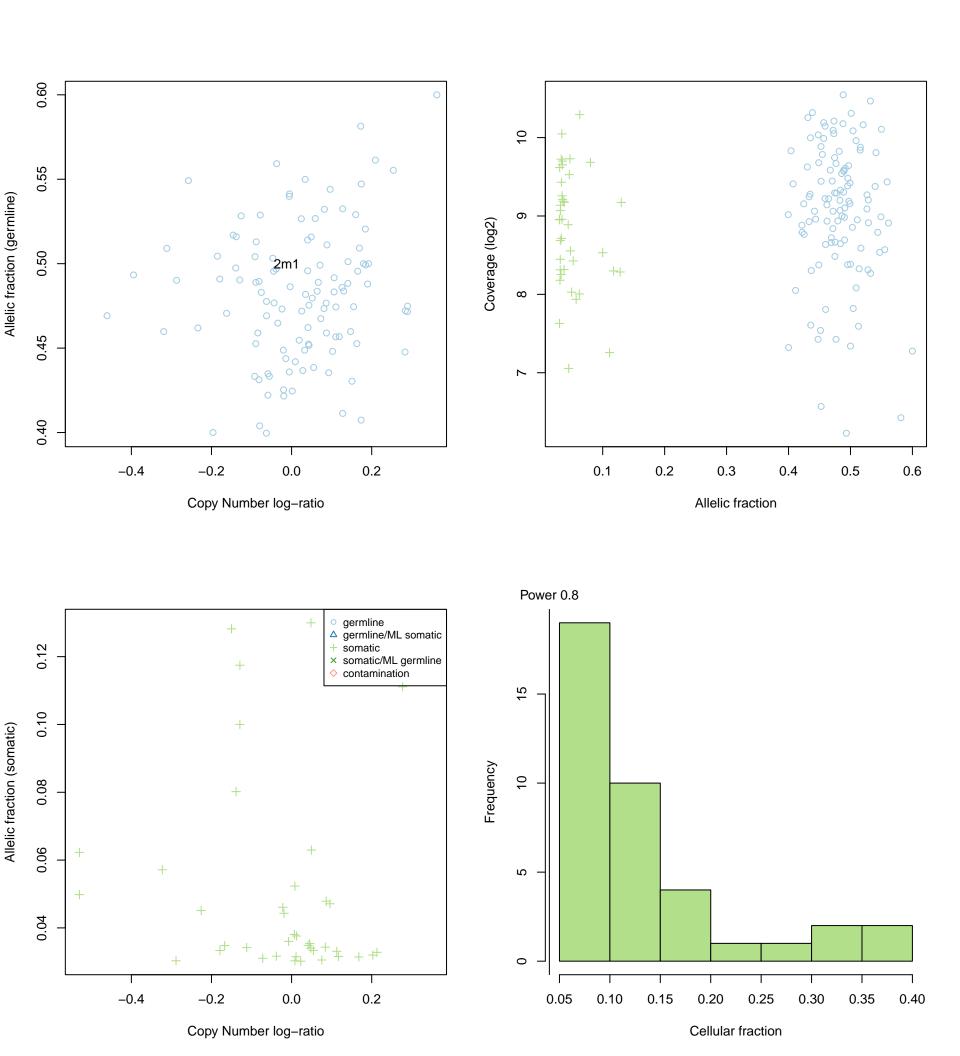
log2 ratio



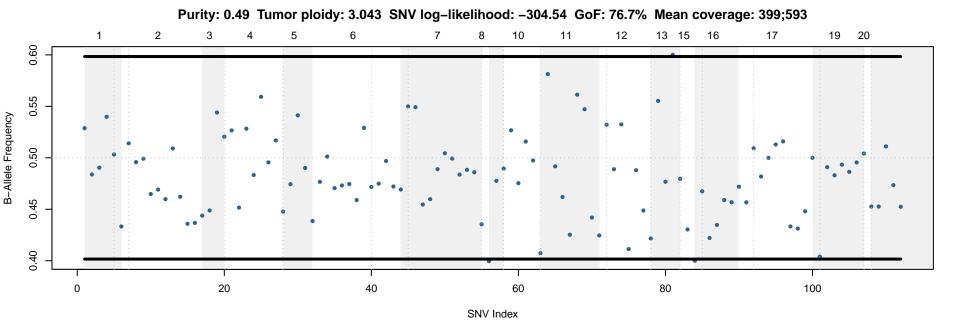
SCNA-fit log-likelihood: -5309.18



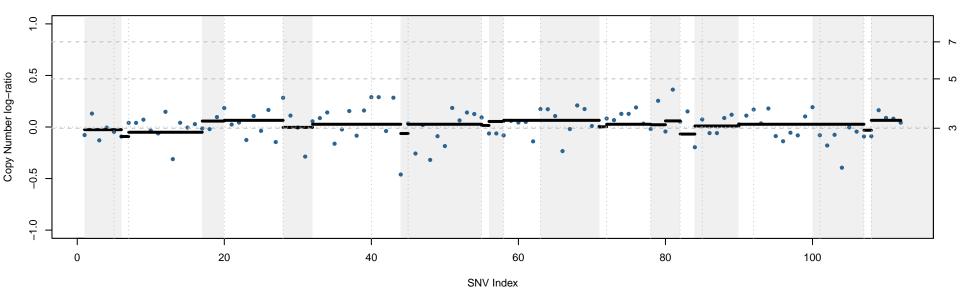


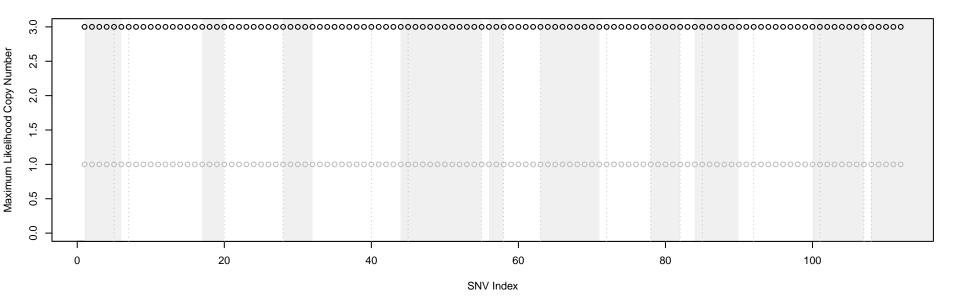


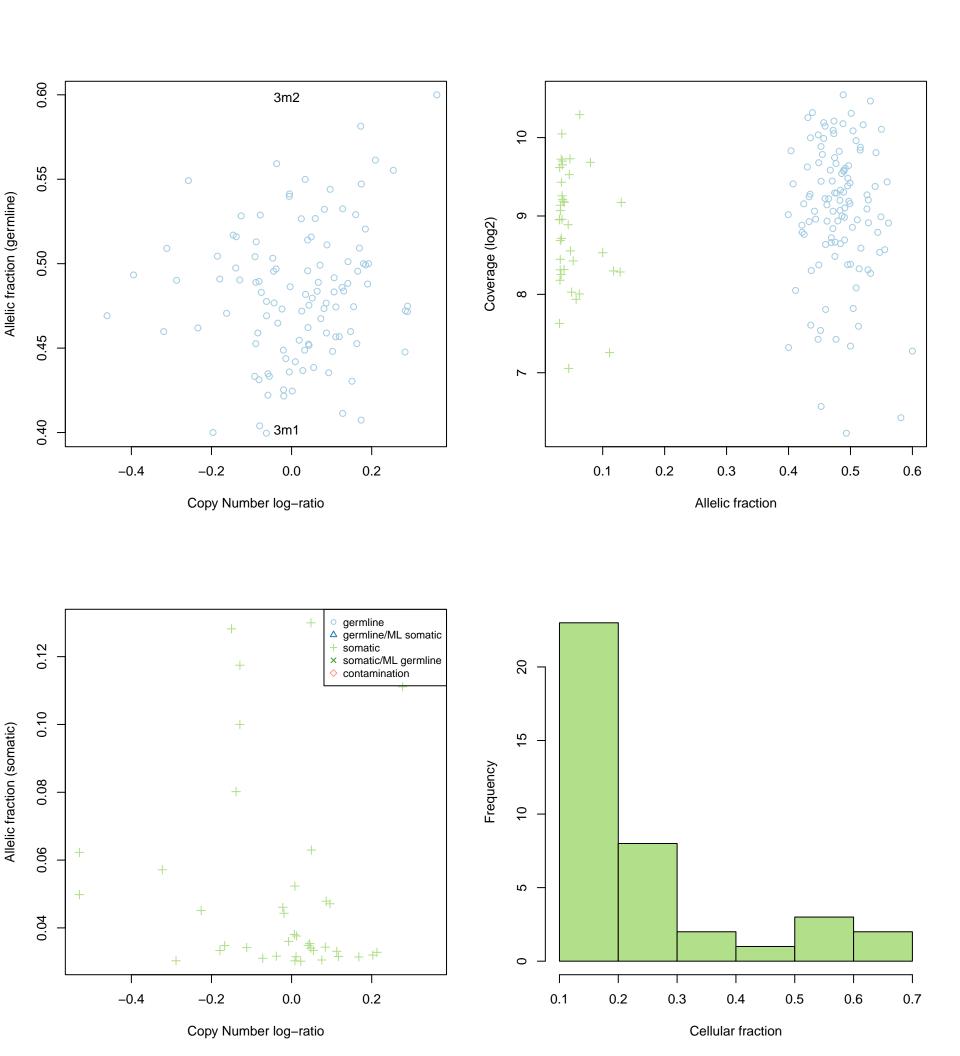
Purity: 0.49 Tumor ploidy: 3.043 0 3 7 9.0 0.3 Fraction Genome 0.2 0.1 0.0 -1.5 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



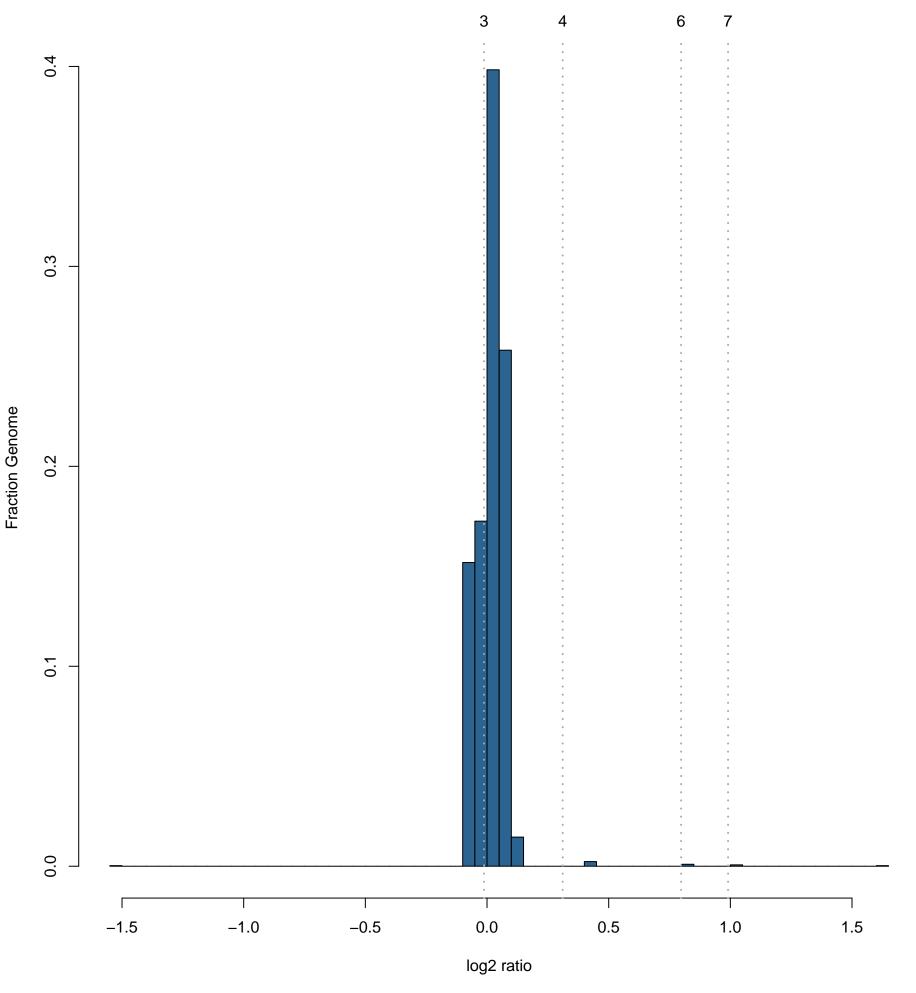
SCNA-fit log-likelihood: -5314.1

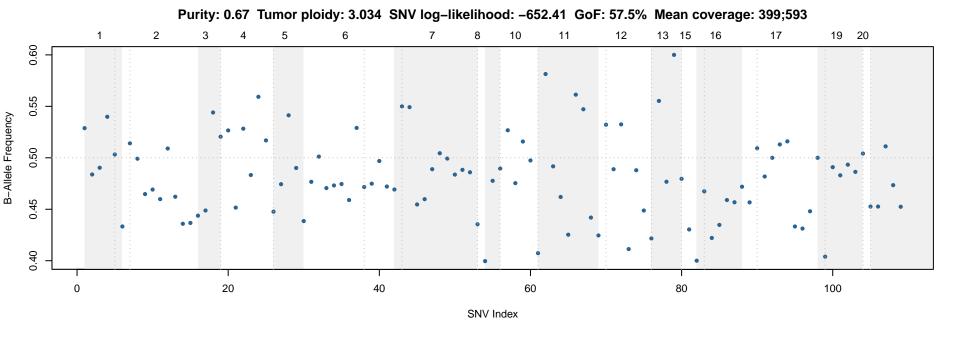




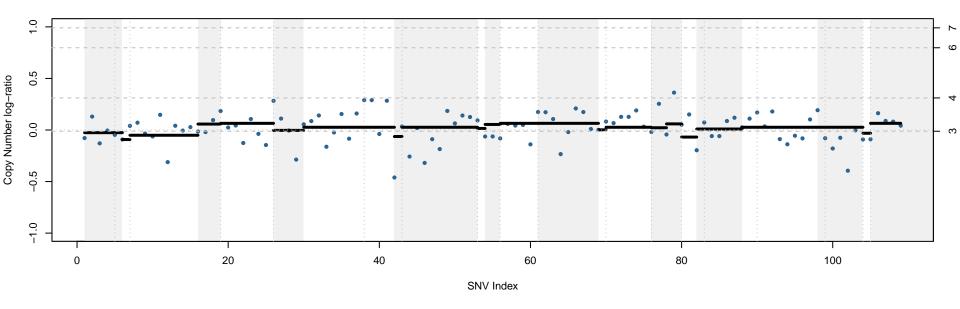


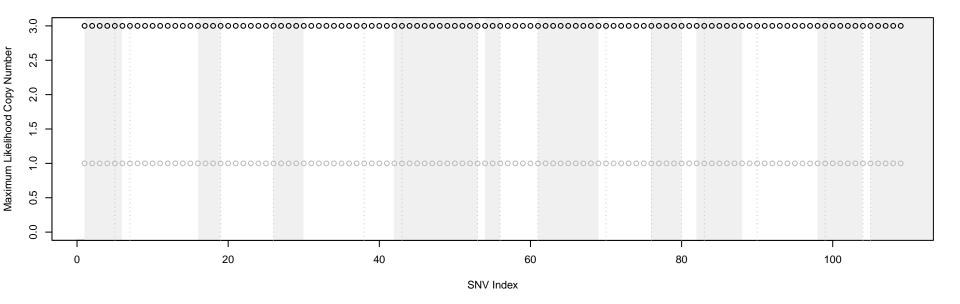
Purity: 0.67 Tumor ploidy: 3.034

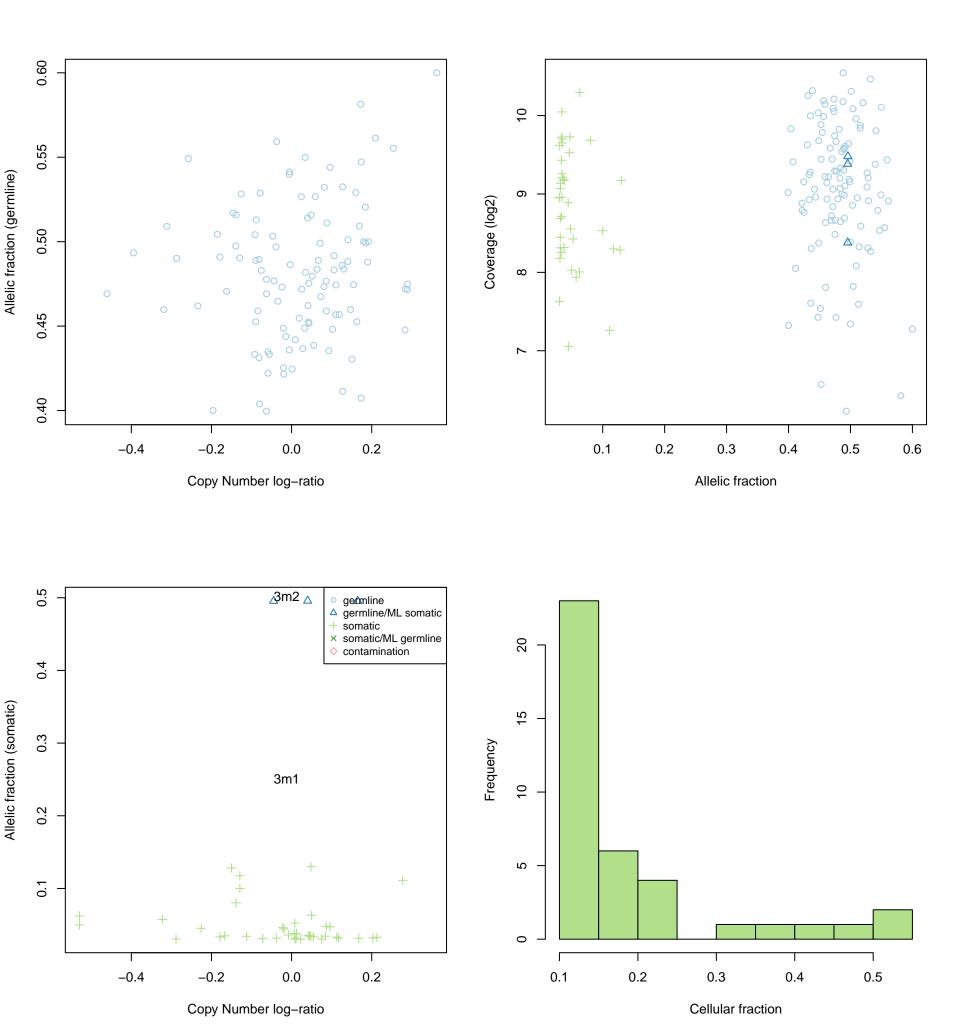




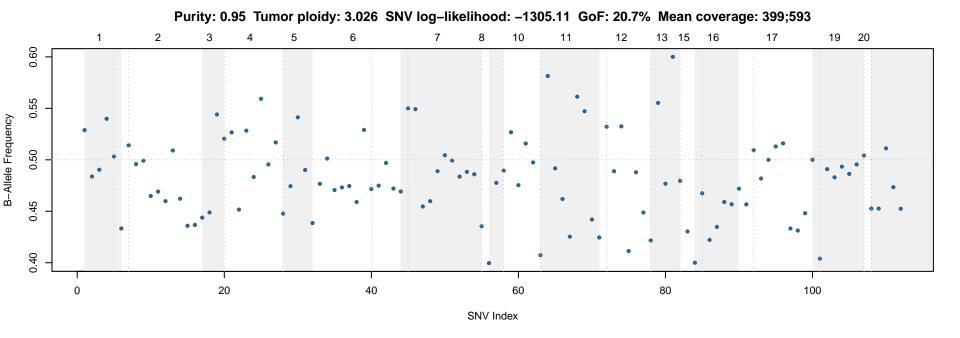
SCNA-fit log-likelihood: -5315.51







Purity: 0.95 Tumor ploidy: 3.026 3 5 6 1 9.0 0.3 Fraction Genome 0.2 0.1 0.0 -1.5 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



SCNA-fit log-likelihood: -5312.95

