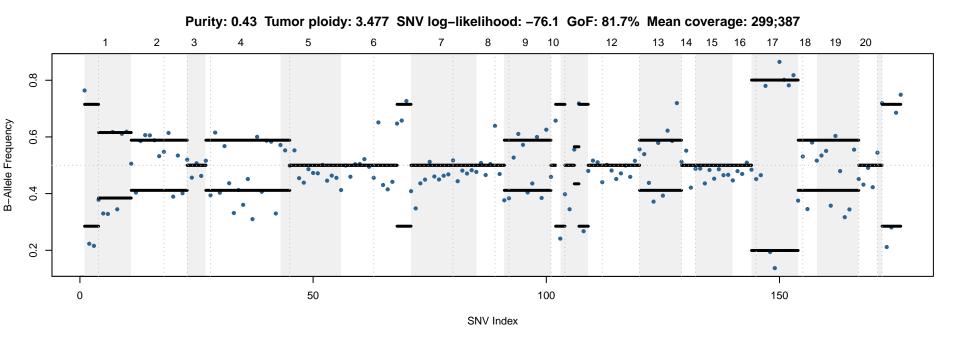
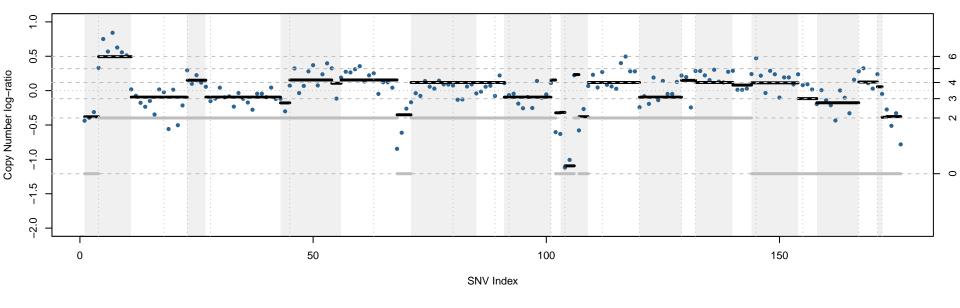
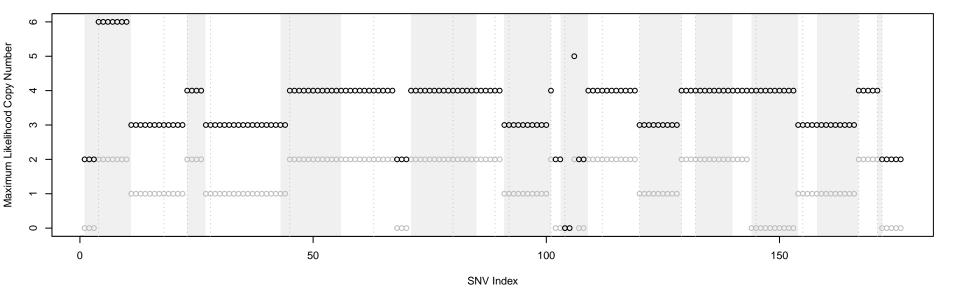
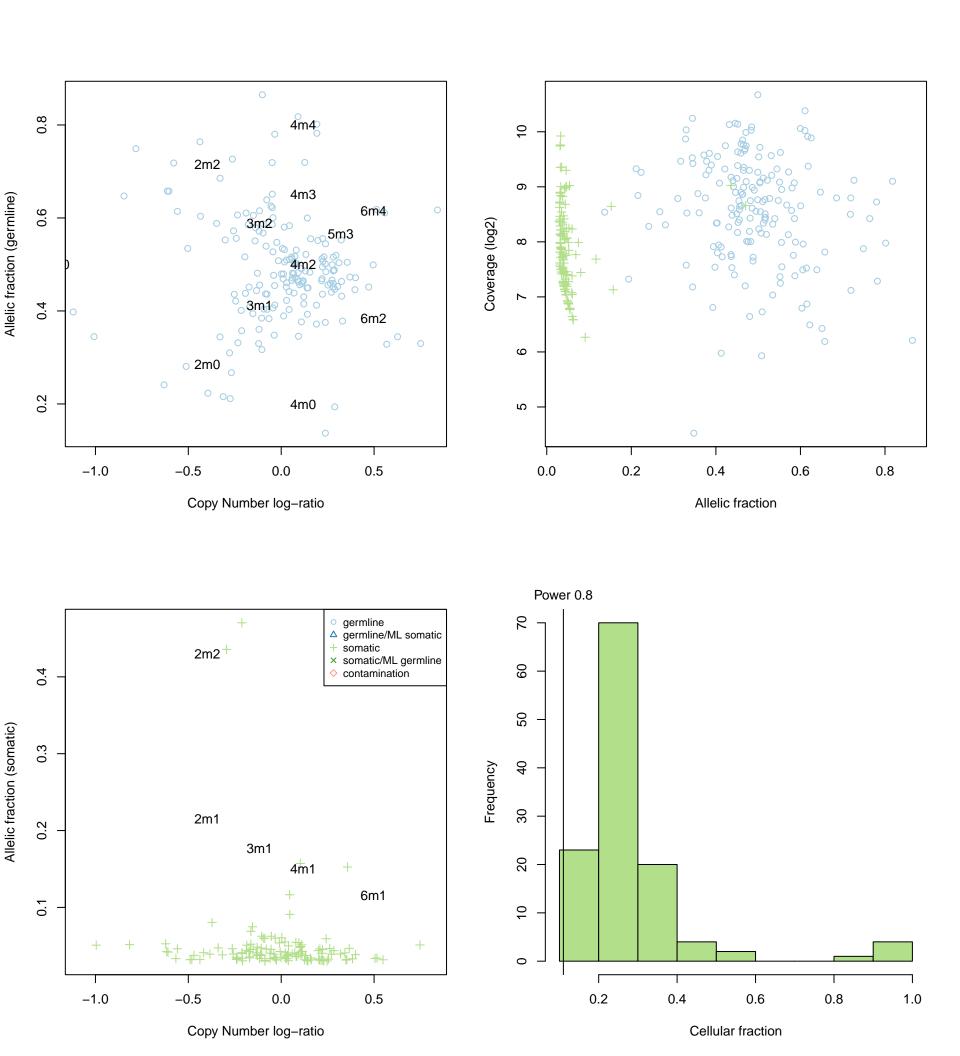
Purity: 0.43 Tumor ploidy: 3.477 0 3 6 2 5 0.30 0.25 0.20 Fraction Genome 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



SCNA-fit log-likelihood: -5533.26

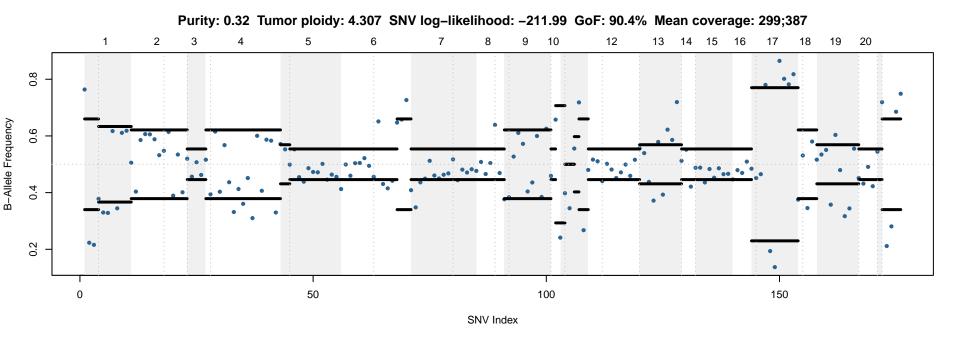




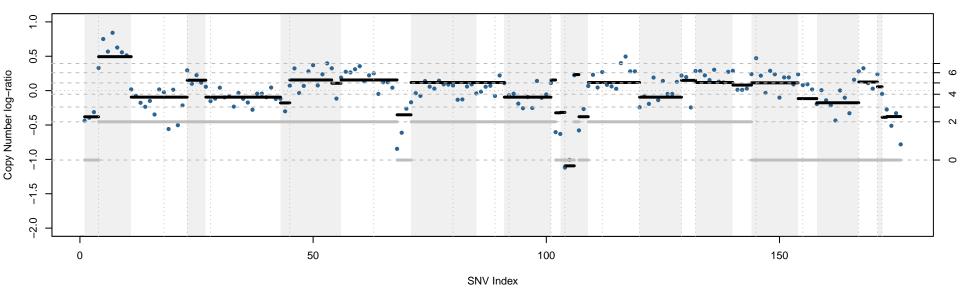


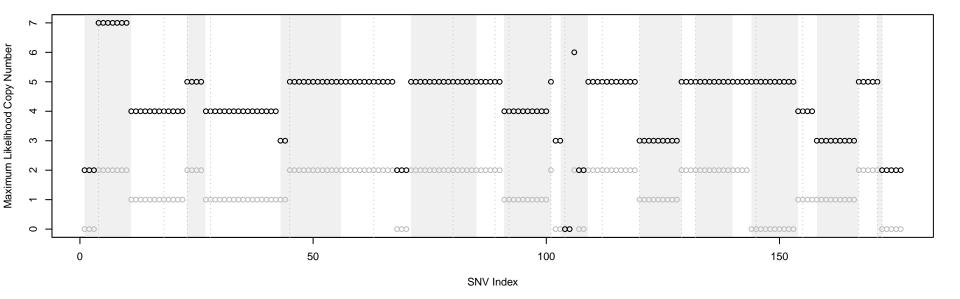
Purity: 0.32 Tumor ploidy: 4.307 0 6 2 3 5 7 0.30 0.25 0.20 Fraction Genome 0.15 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5

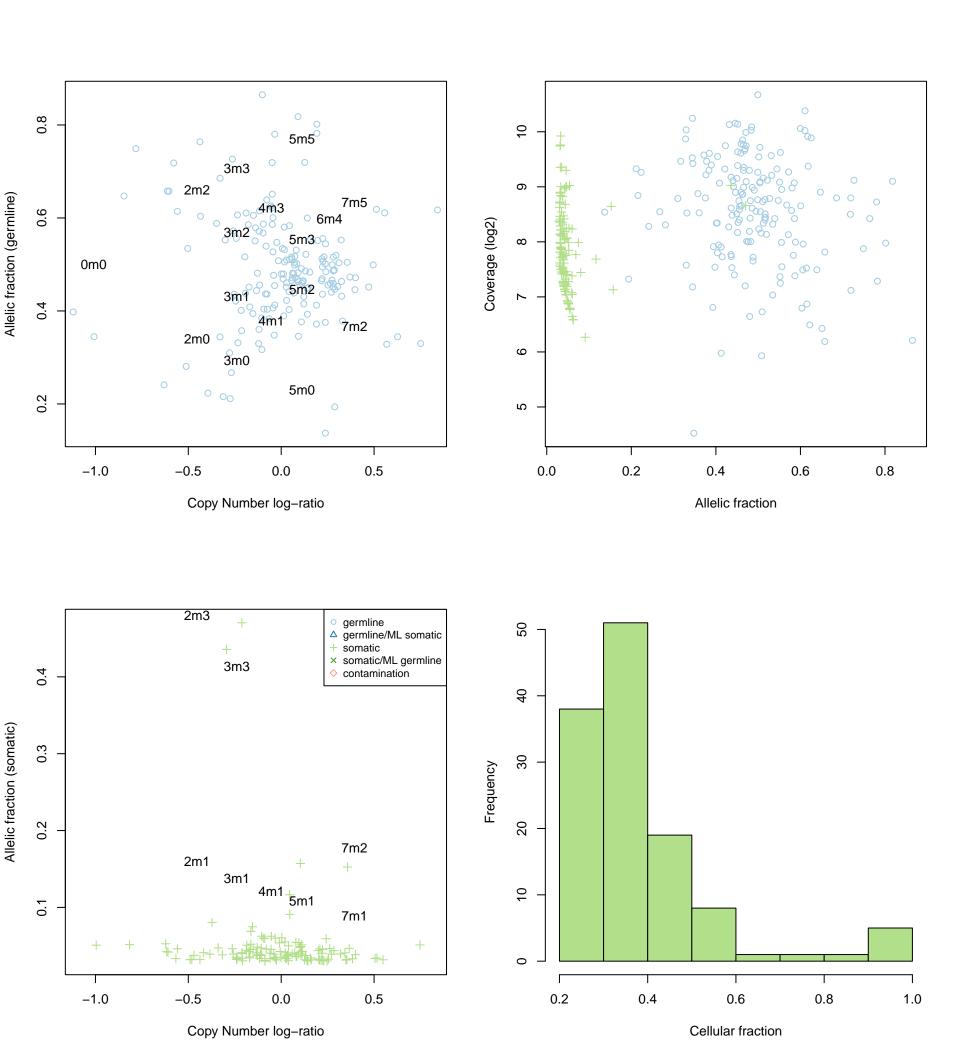
log2 ratio



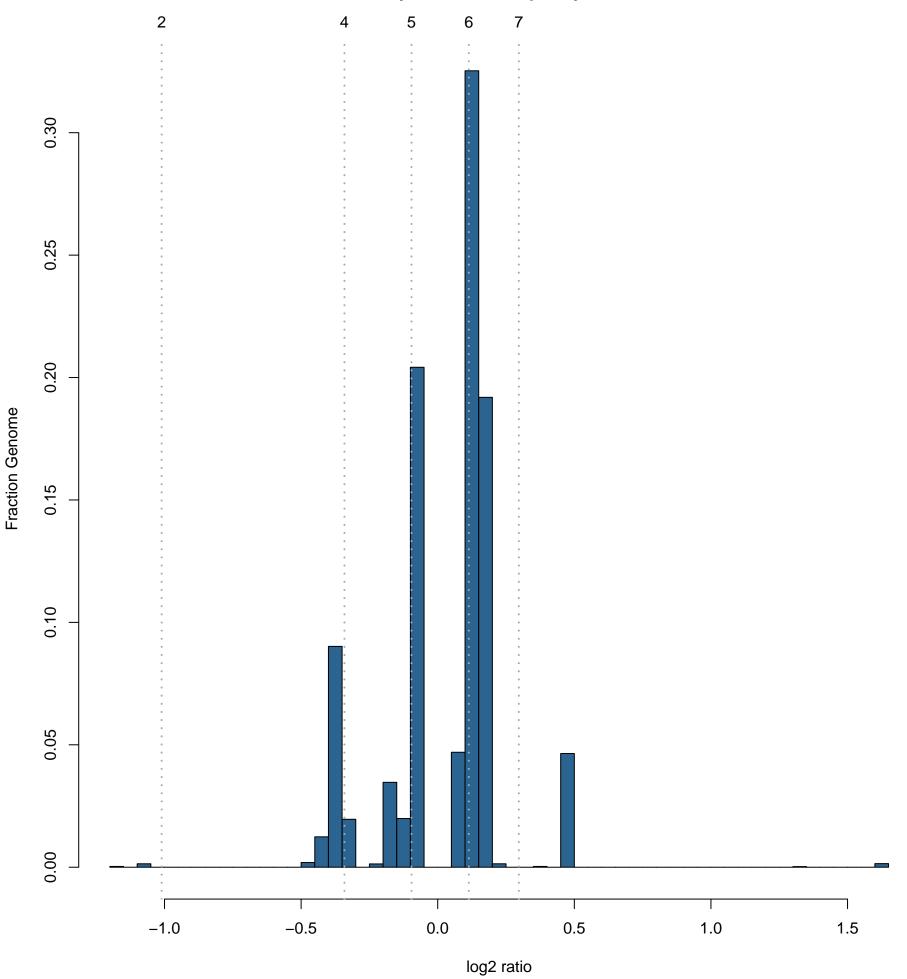
SCNA-fit log-likelihood: -5618.9

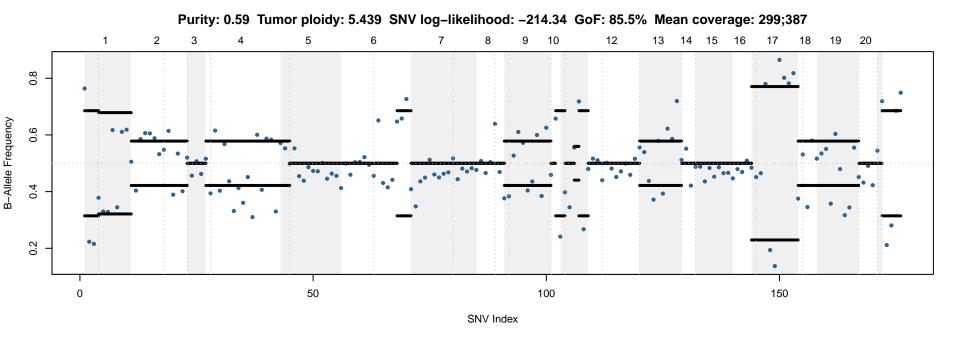




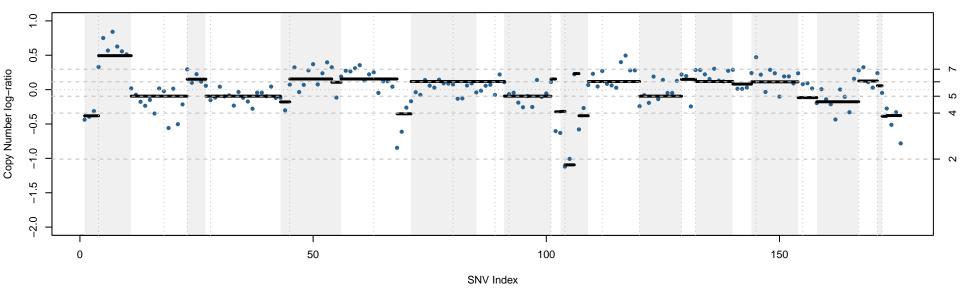


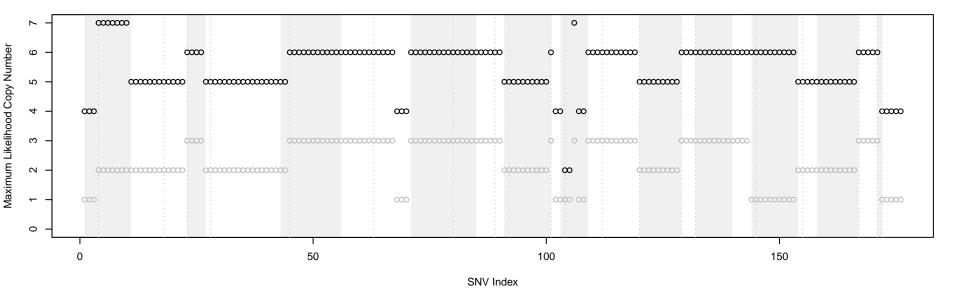
Purity: 0.59 Tumor ploidy: 5.439

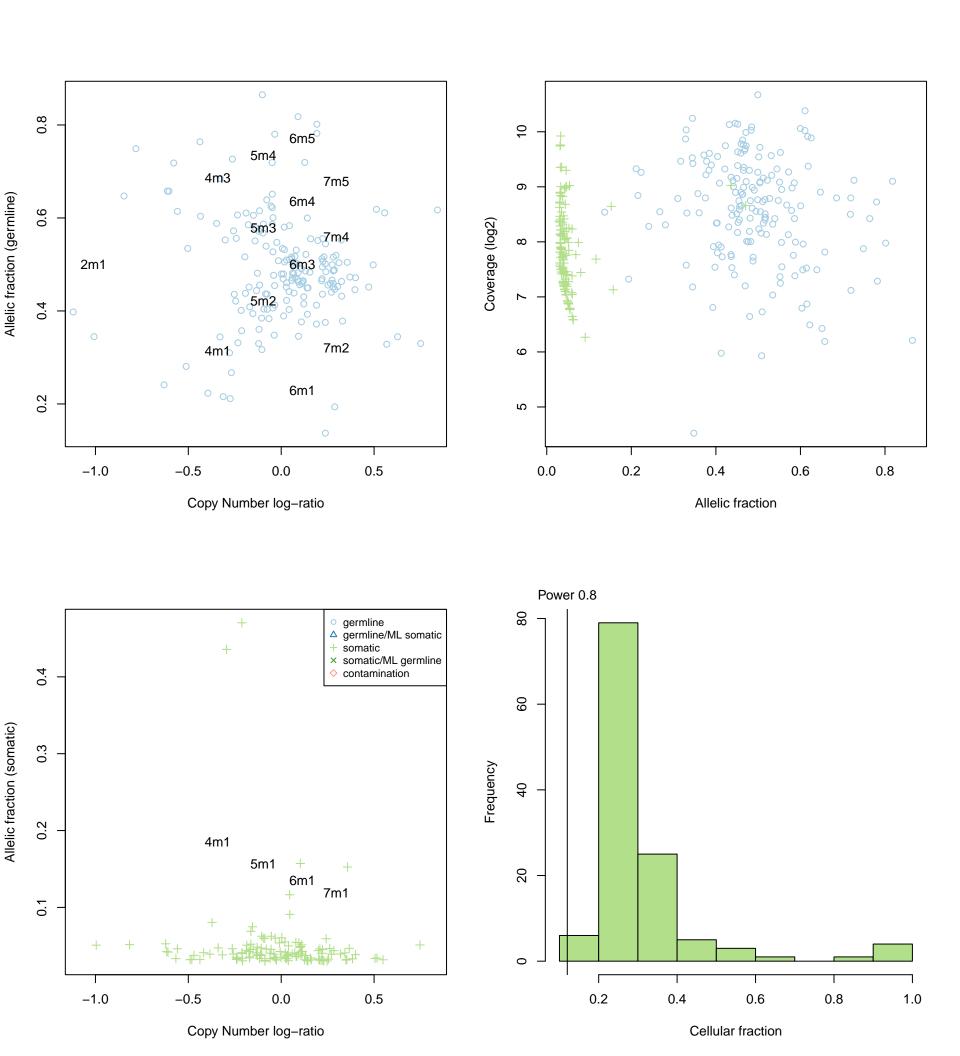




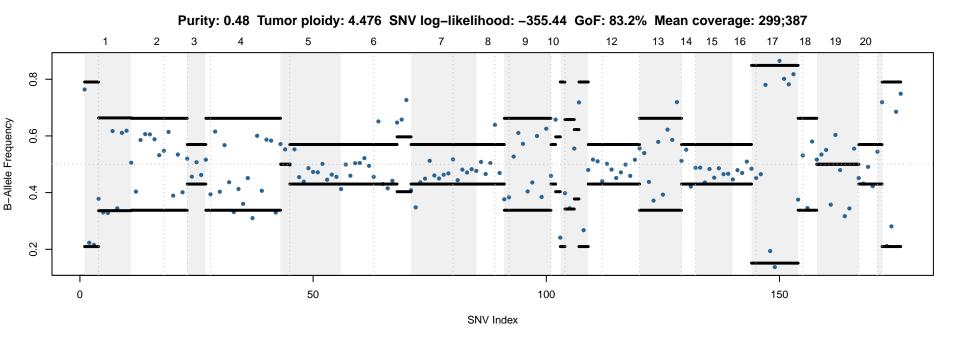
SCNA-fit log-likelihood: -5660.49



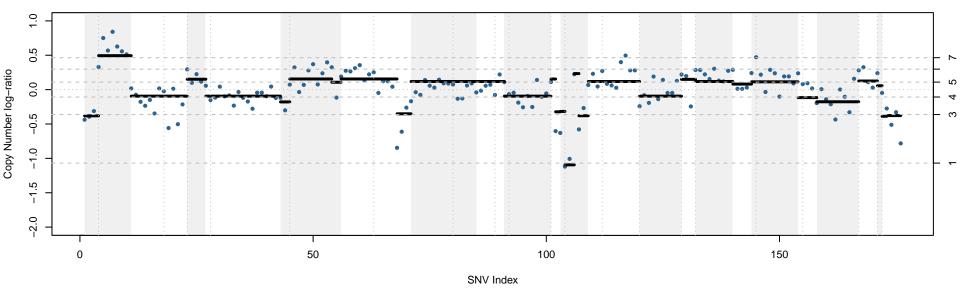


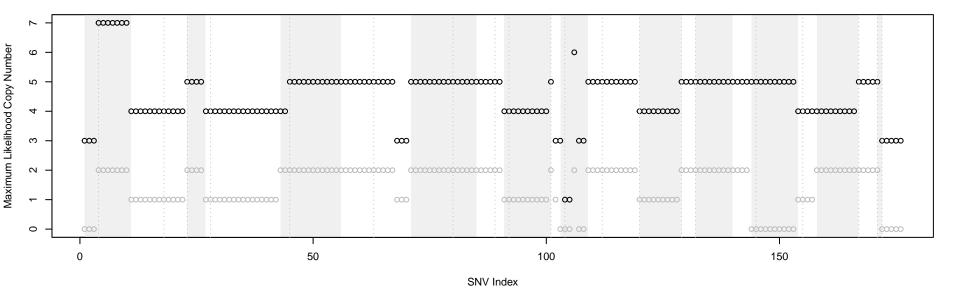


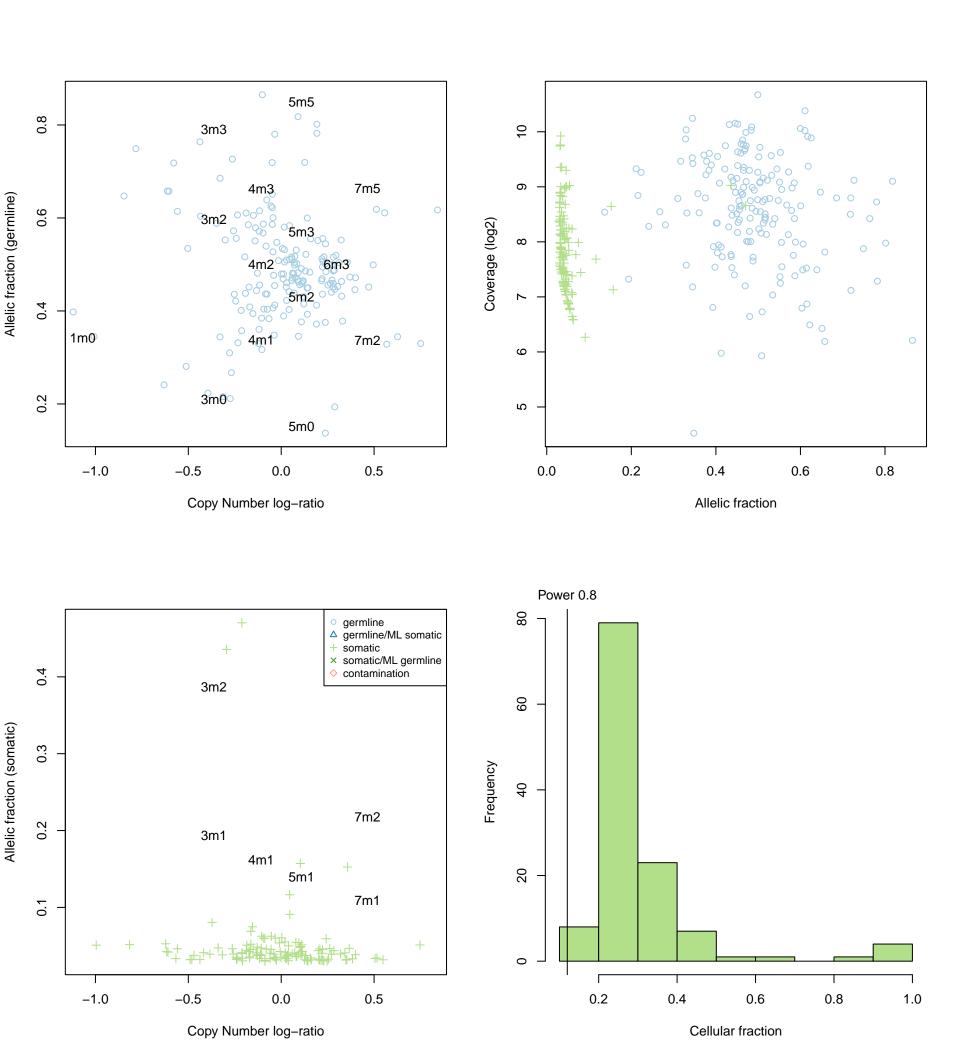
Purity: 0.48 Tumor ploidy: 4.476 6 3 5 1 0.30 0.25 0.20 Fraction Genome 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



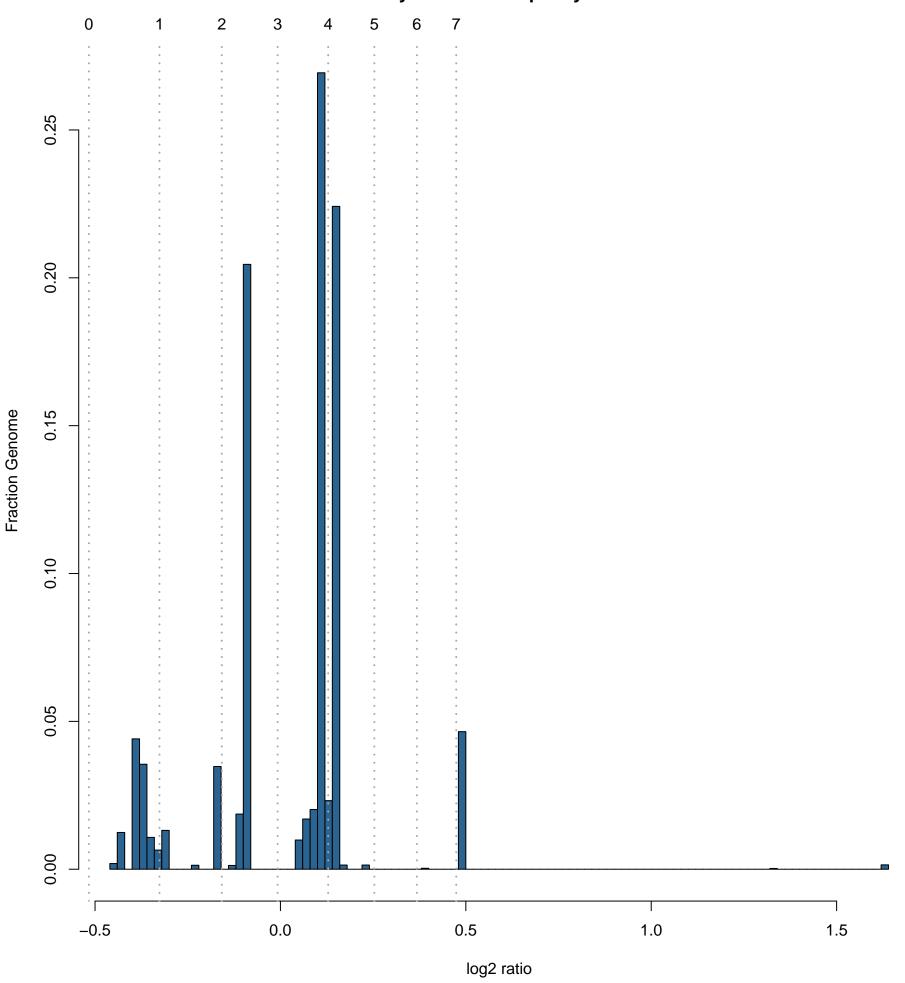
SCNA-fit log-likelihood: -5540.12

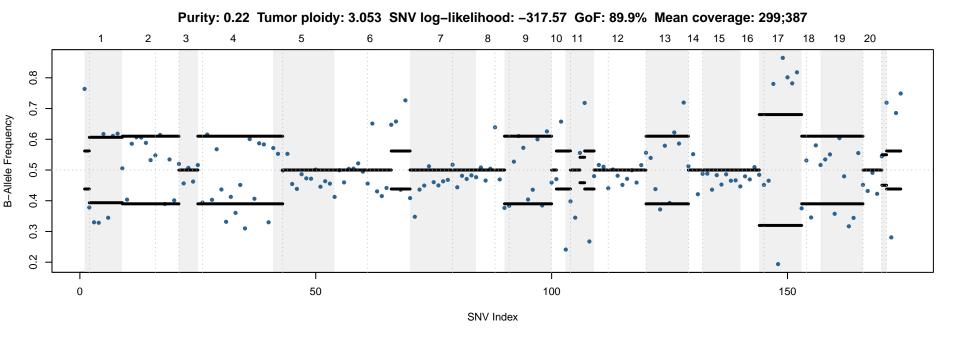




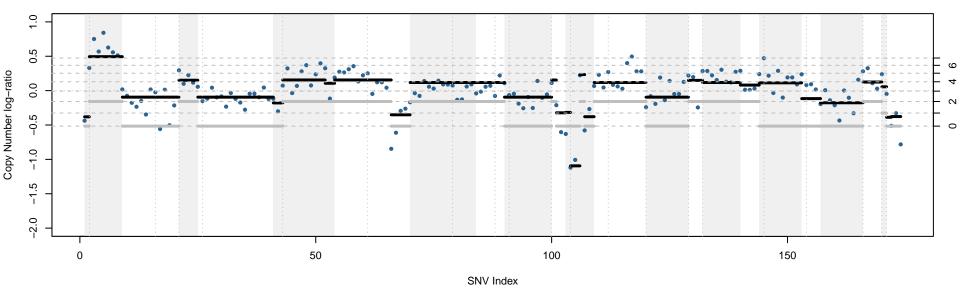


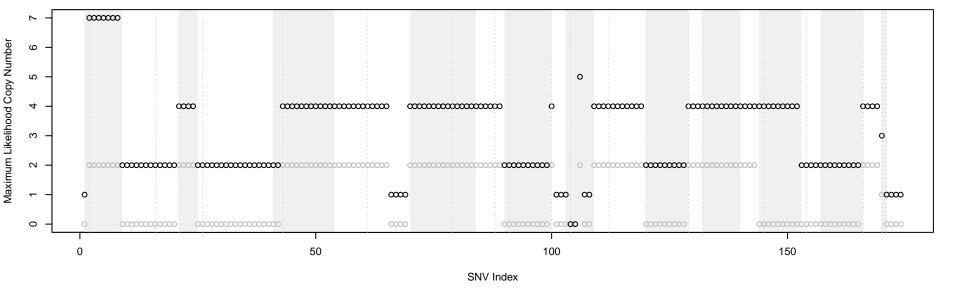
Purity: 0.22 Tumor ploidy: 3.053

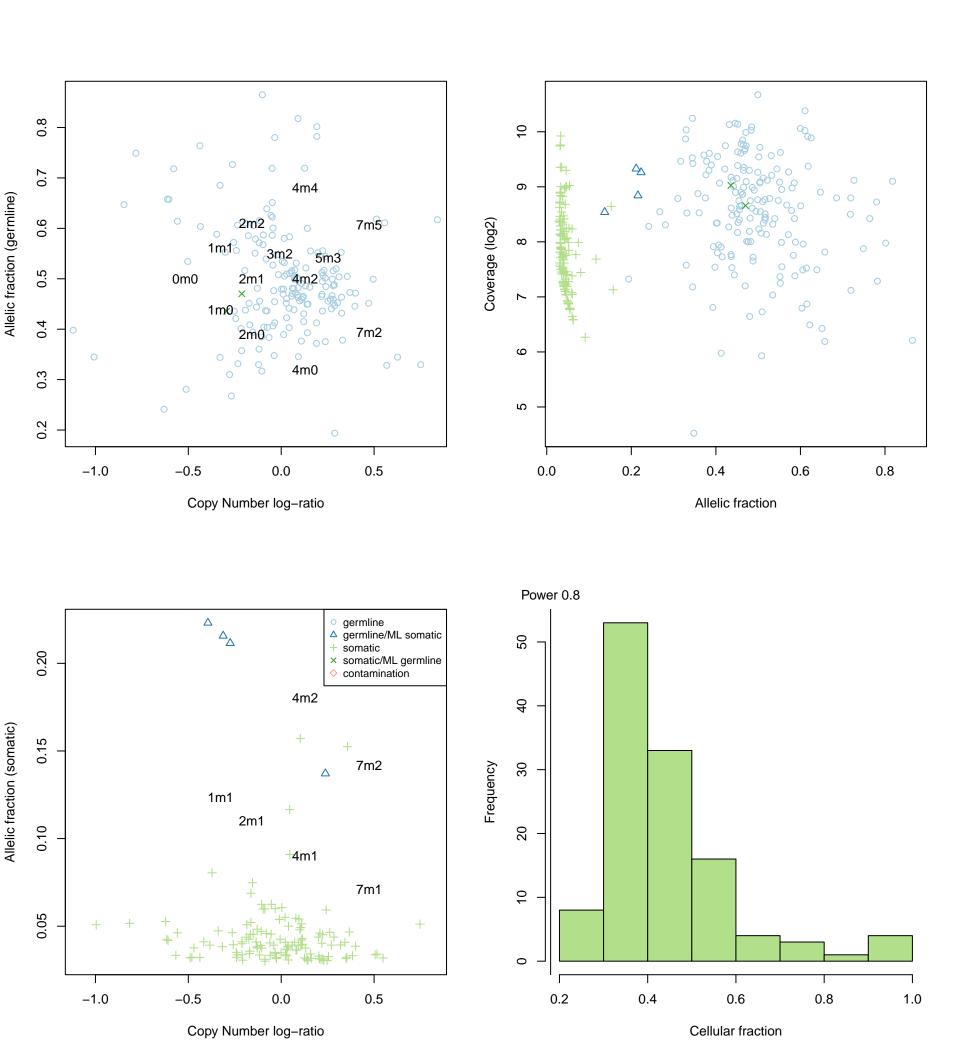


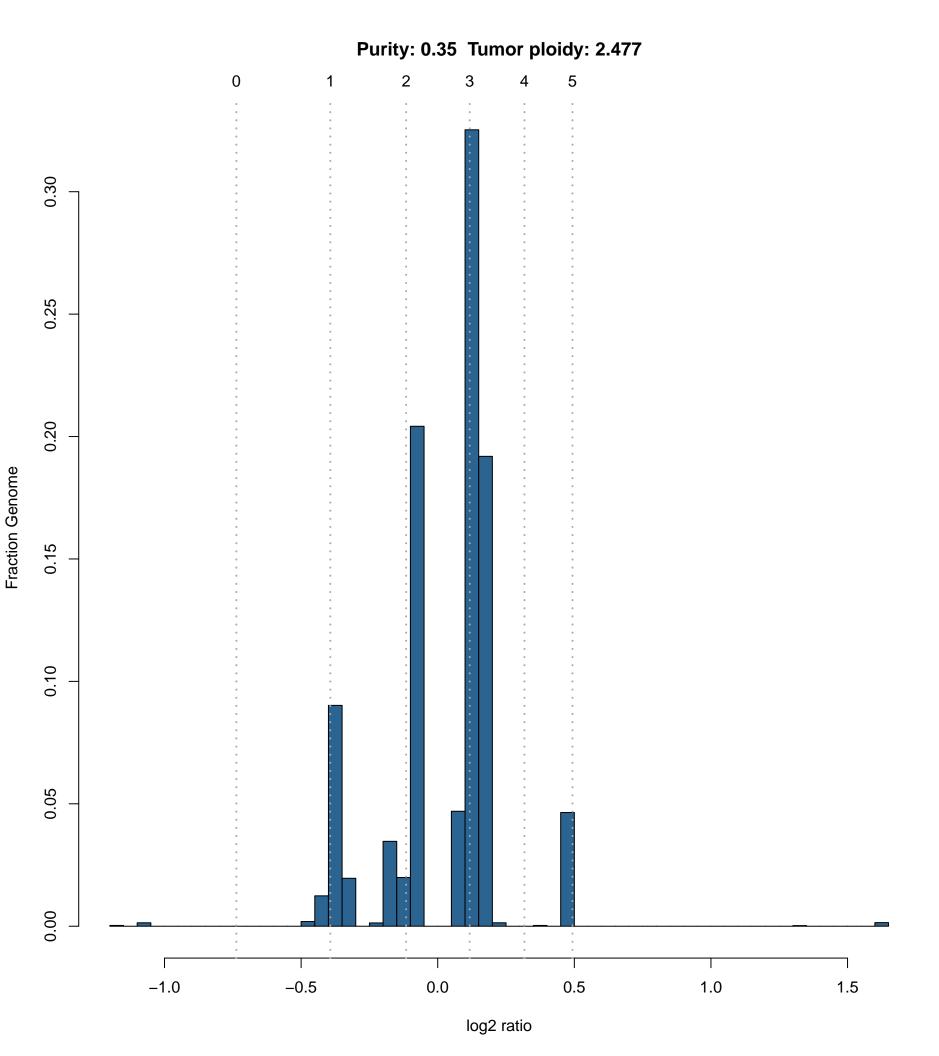


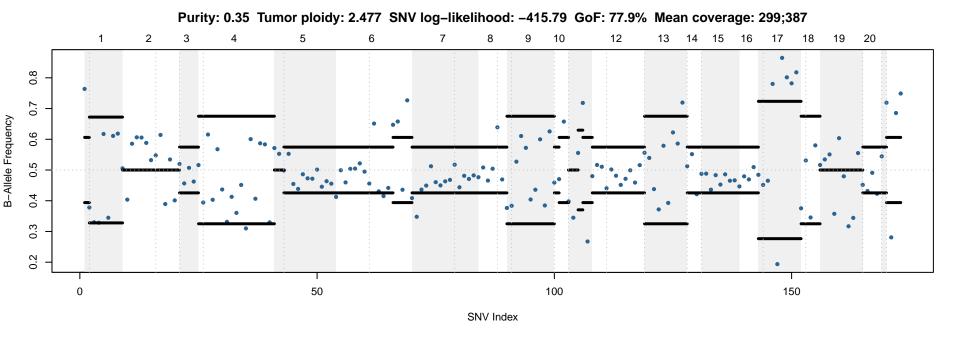
SCNA-fit log-likelihood: -5619.19



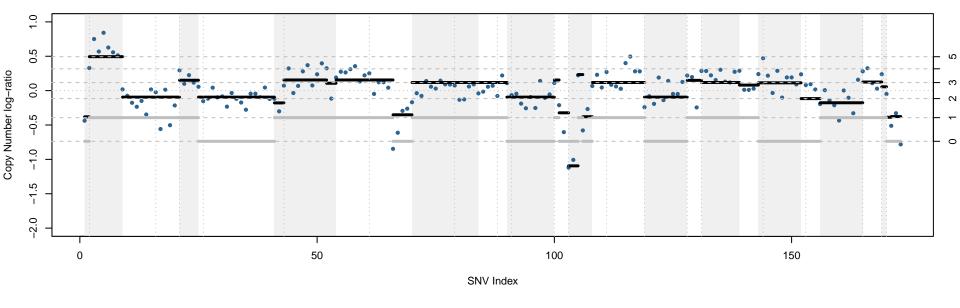


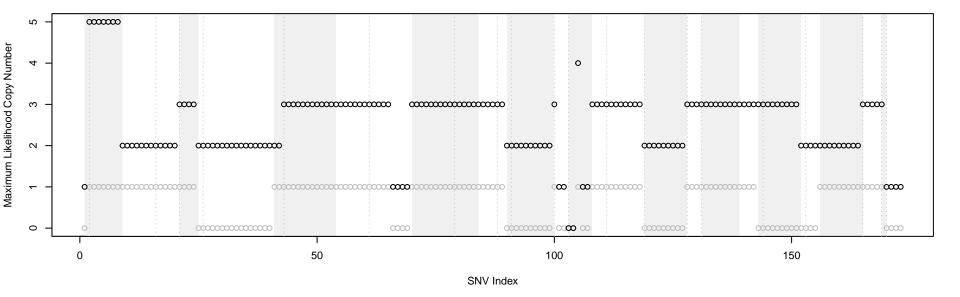


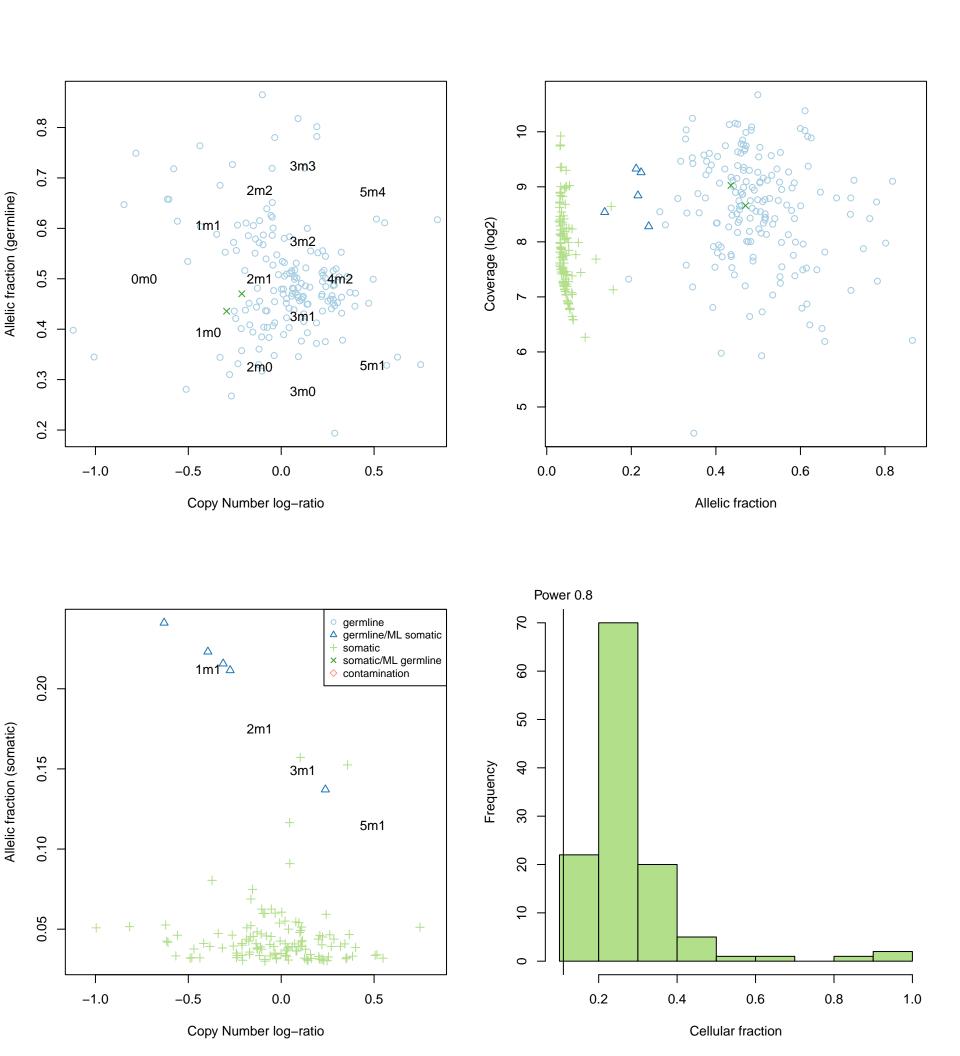




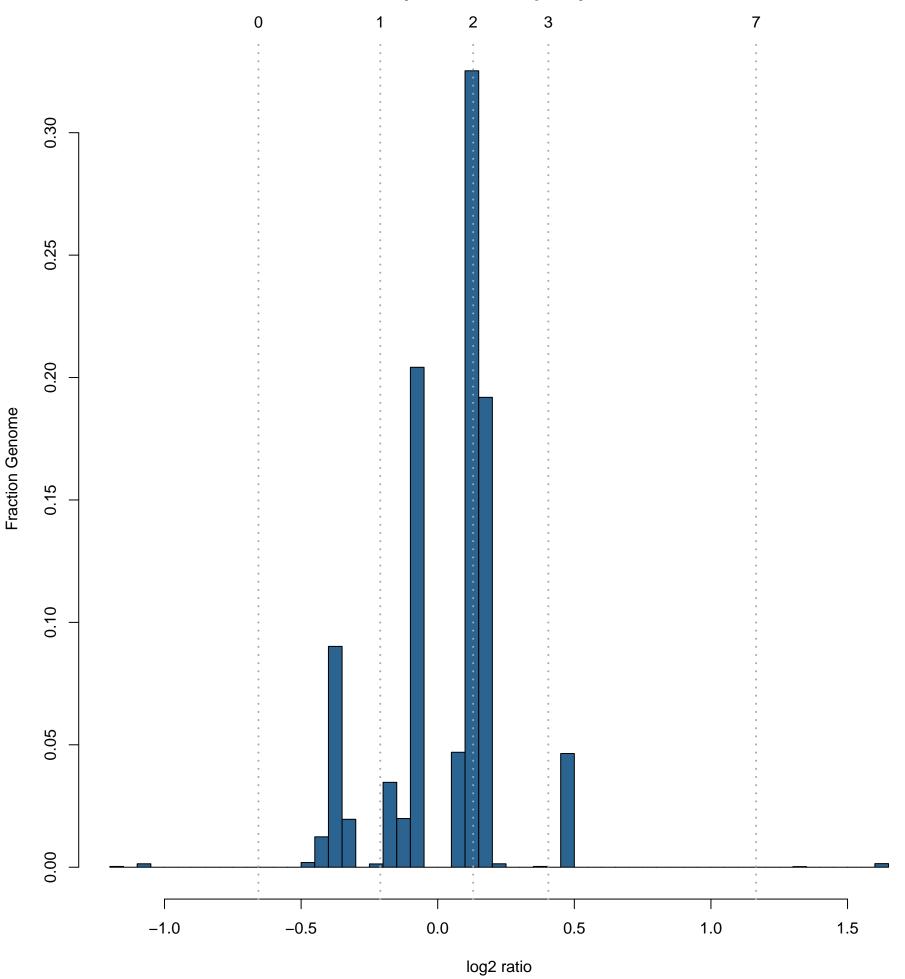
SCNA-fit log-likelihood: -5547.34

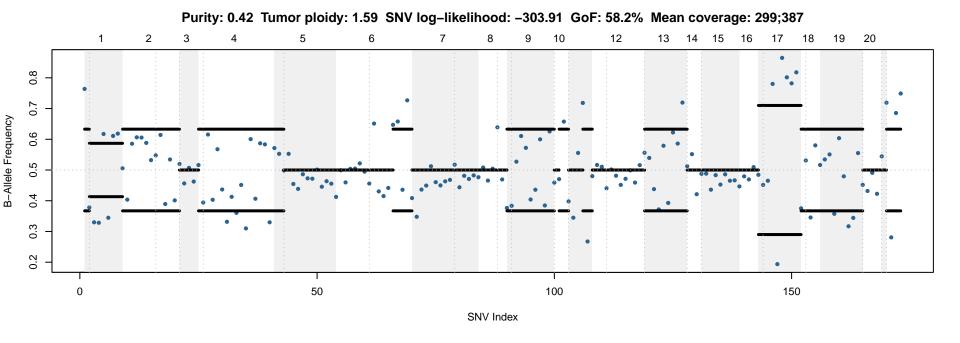




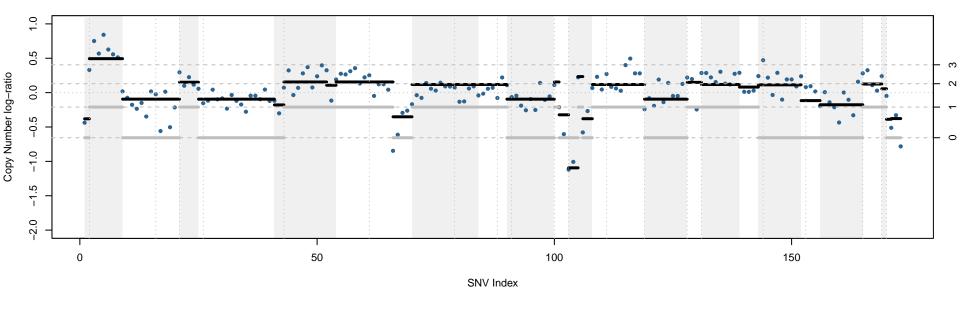


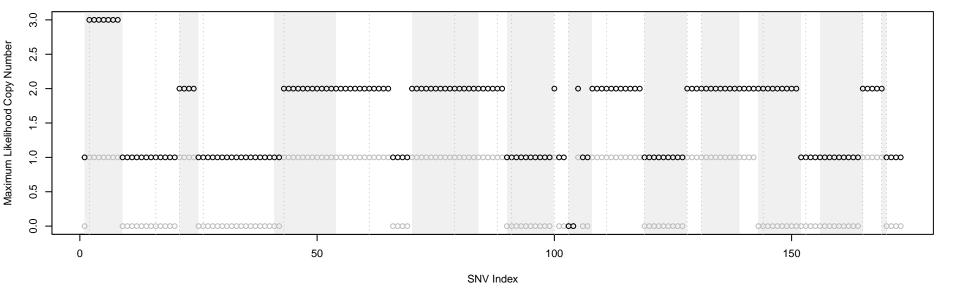
Purity: 0.42 Tumor ploidy: 1.59

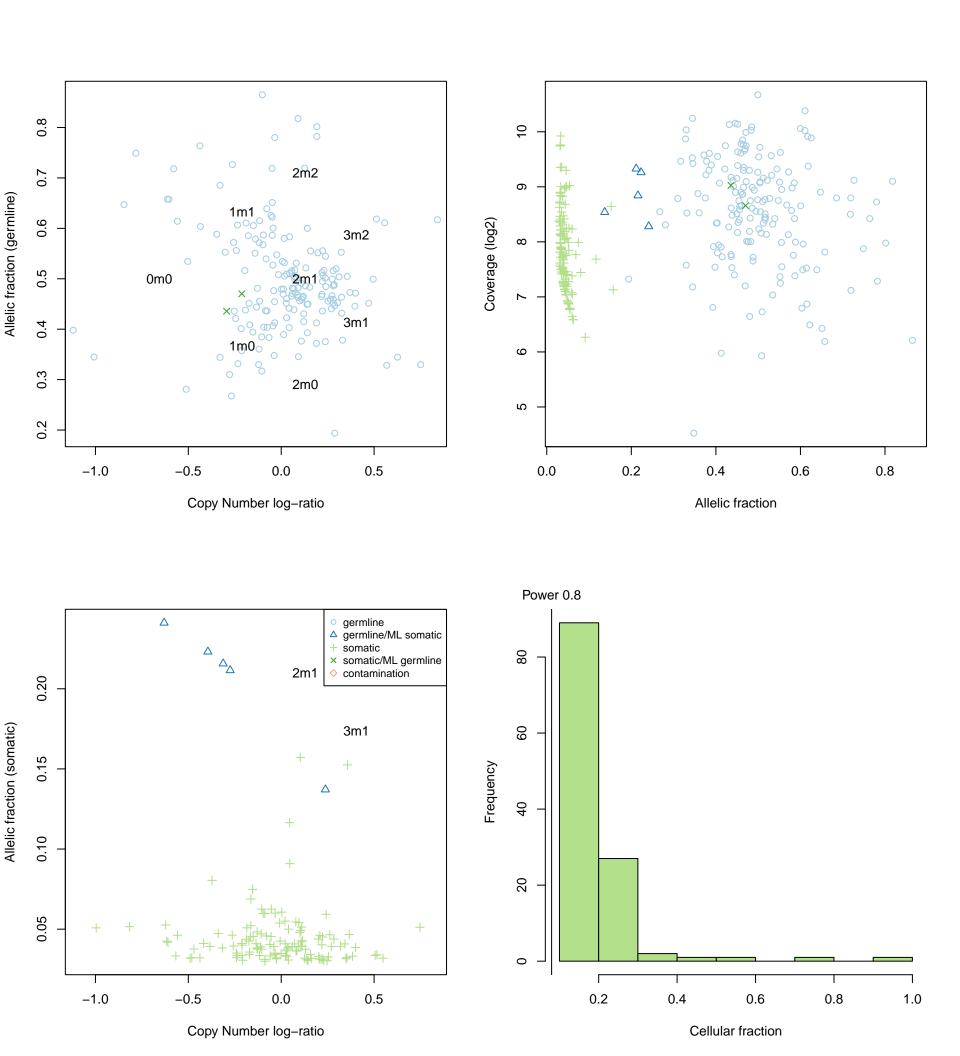




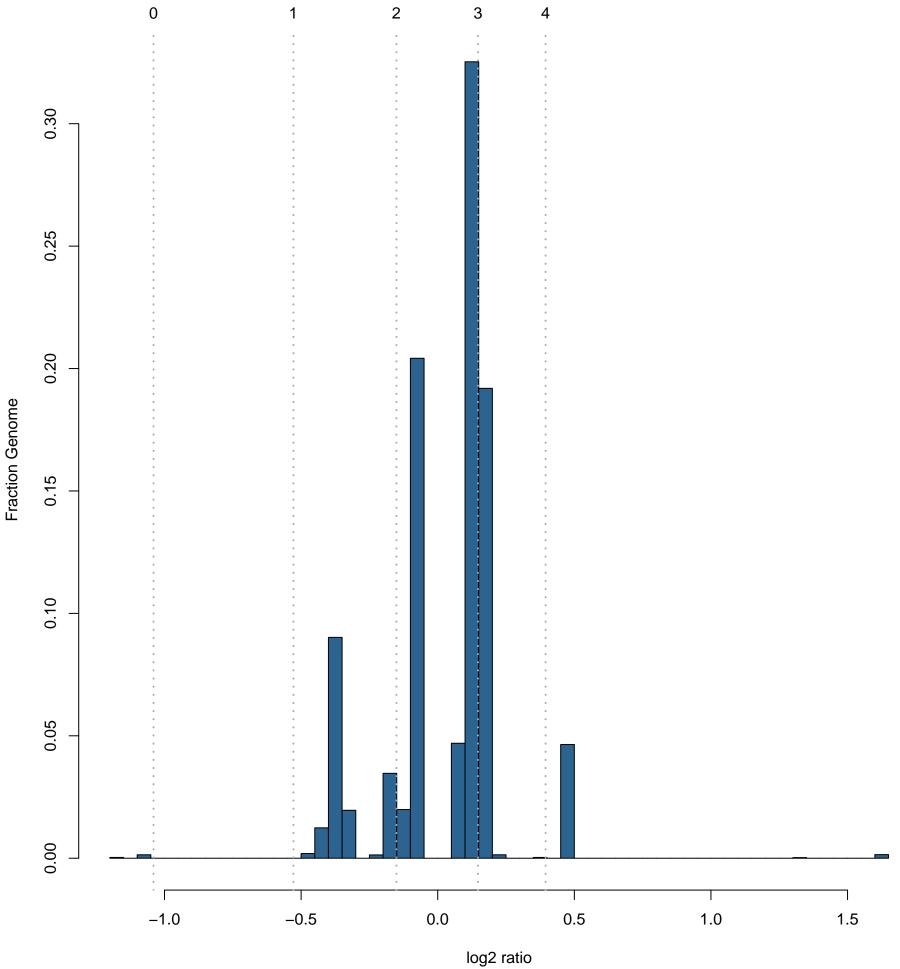
SCNA-fit log-likelihood: -5957.1

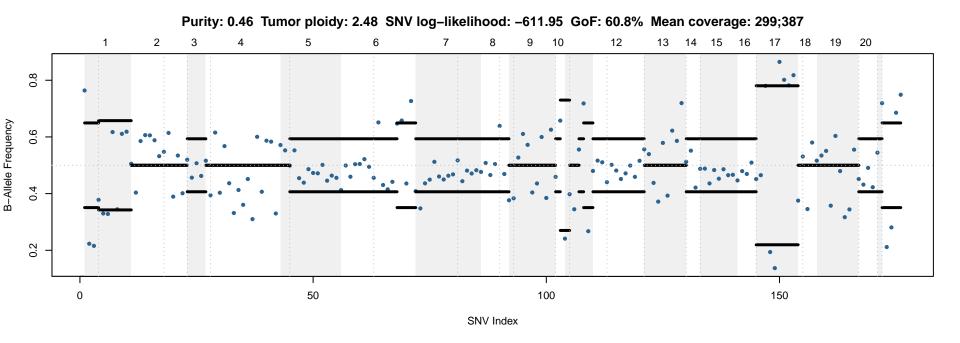




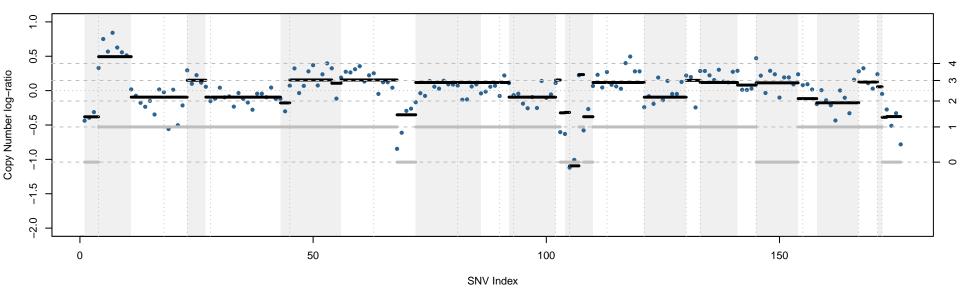


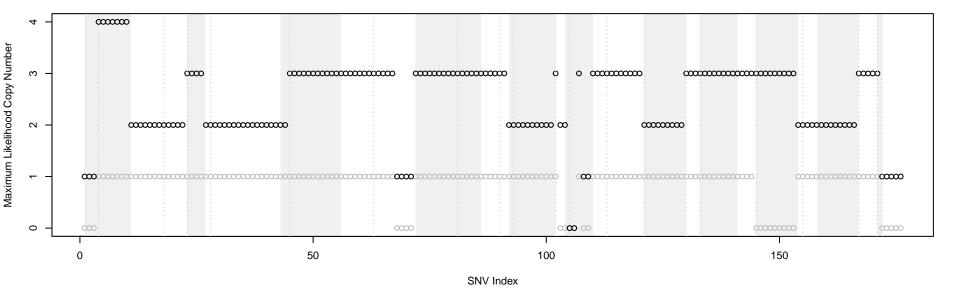
Purity: 0.46 Tumor ploidy: 2.48

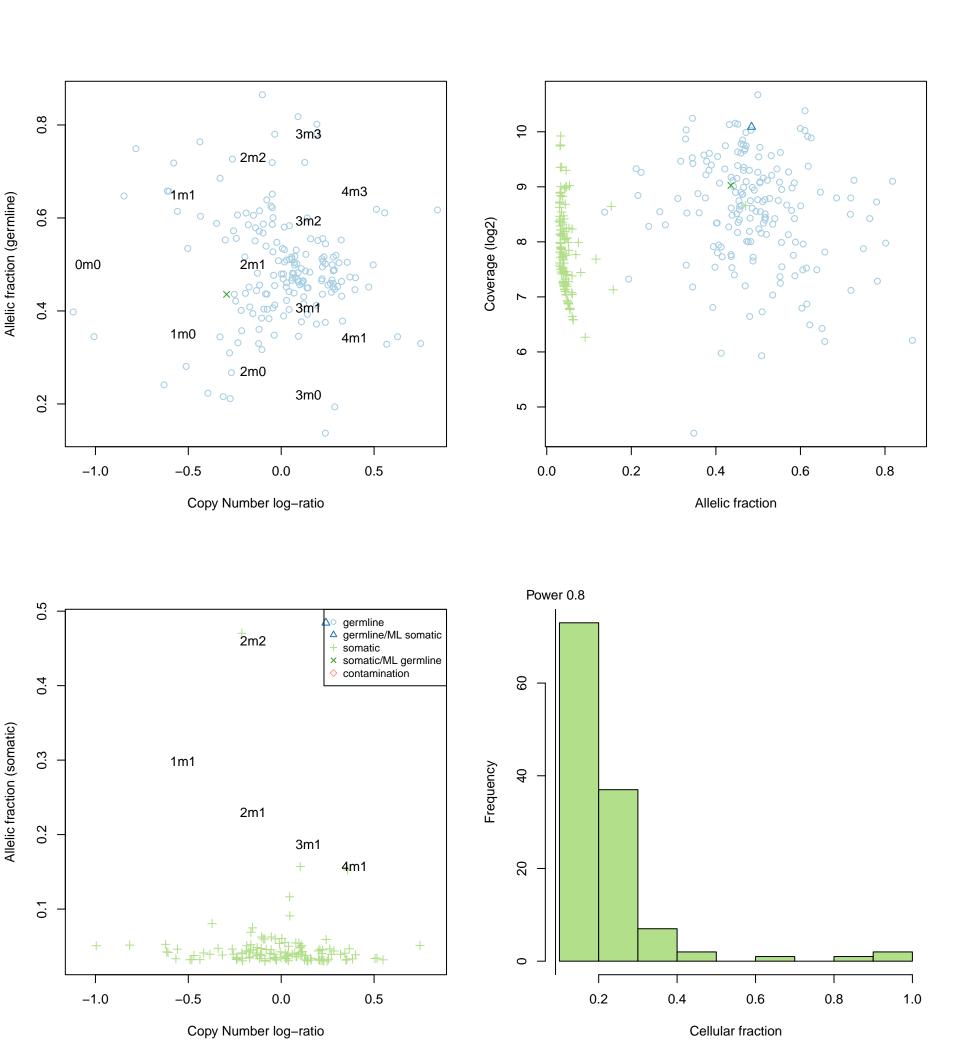




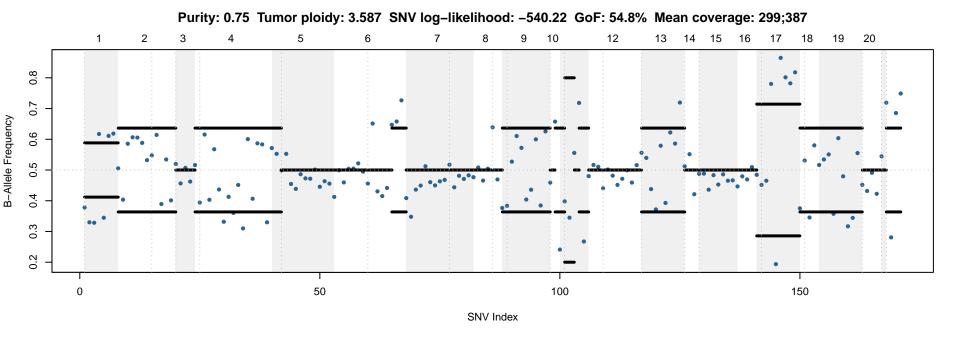
SCNA-fit log-likelihood: -5759.03



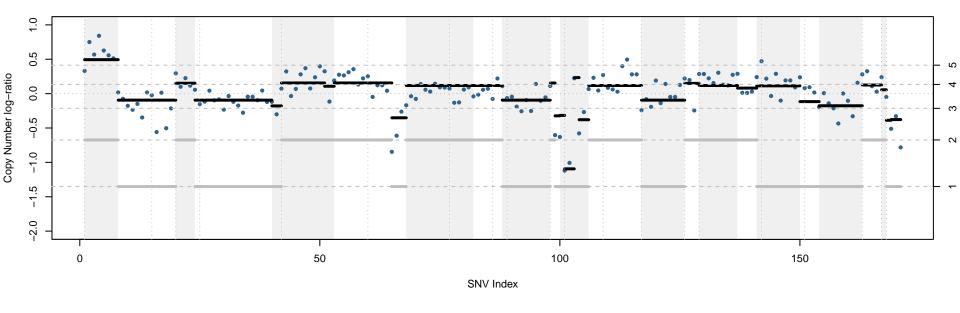


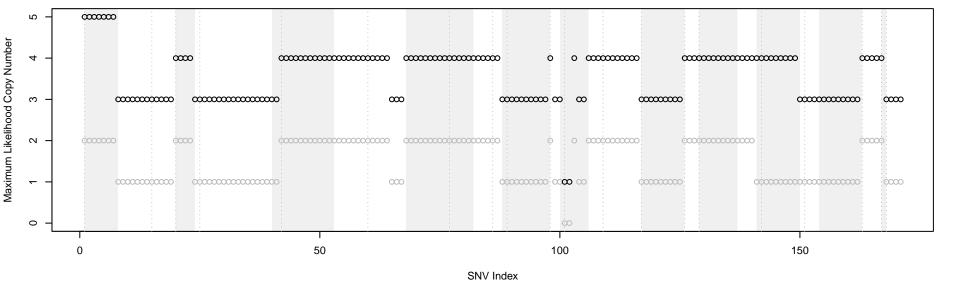


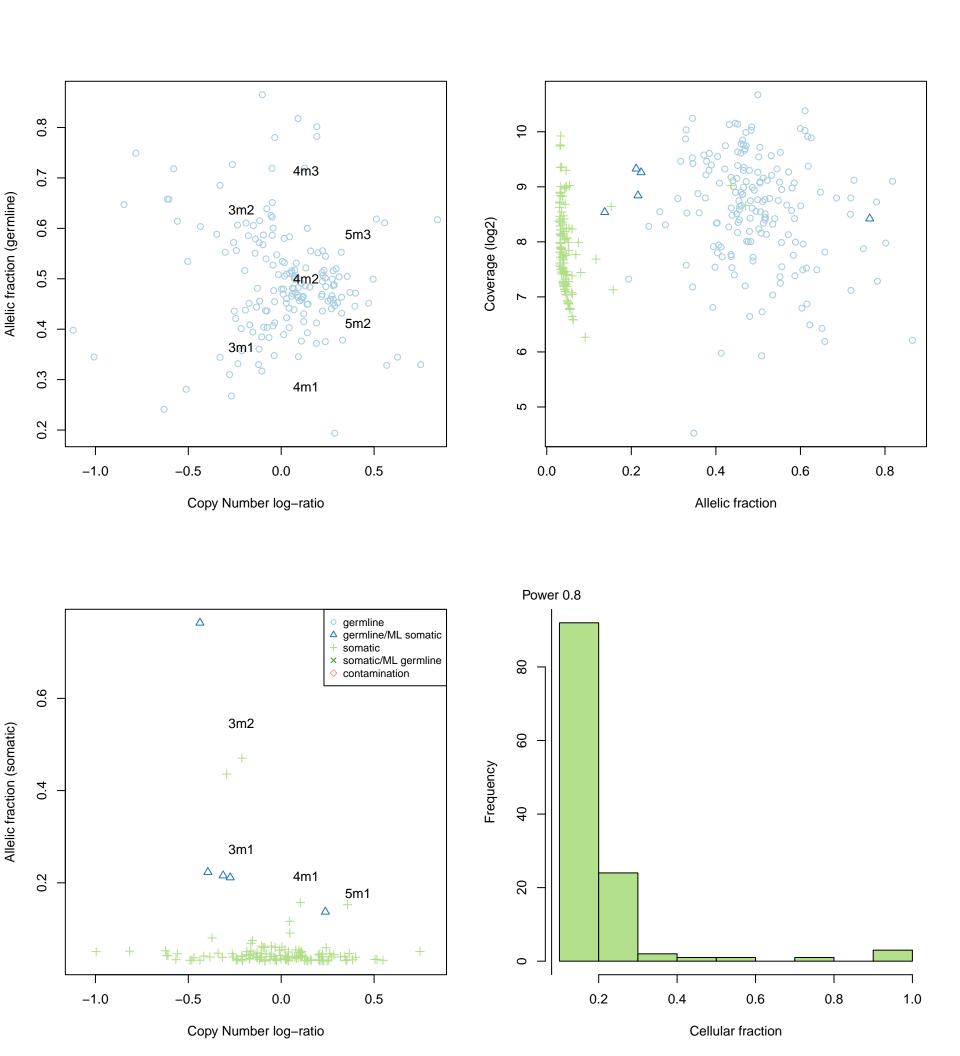
Purity: 0.75 Tumor ploidy: 3.587 2 5 3 0.30 0.25 0.20 Fraction Genome 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



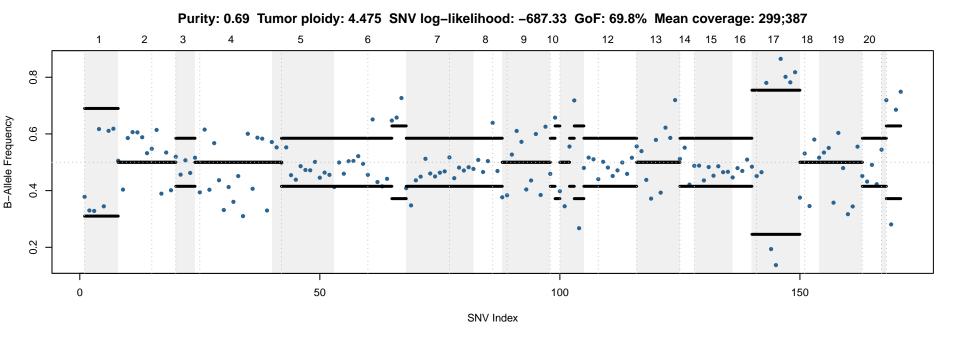
SCNA-fit log-likelihood: -5945.46



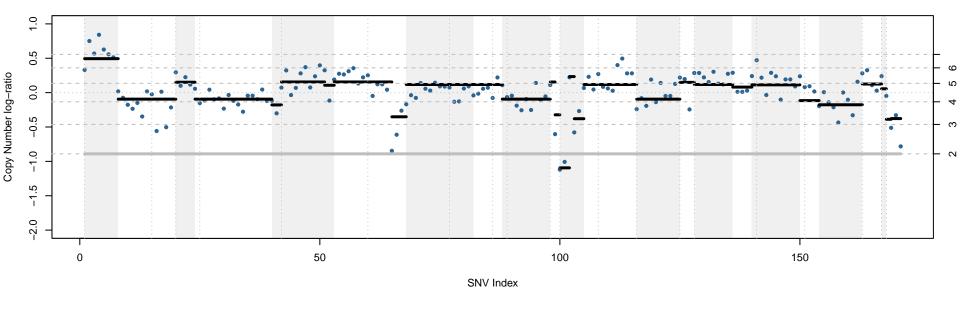


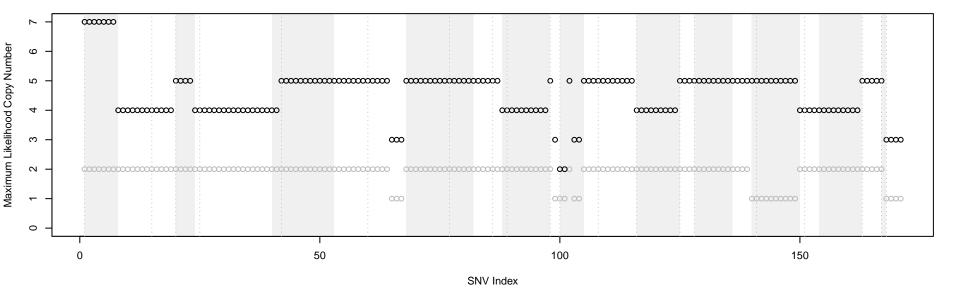


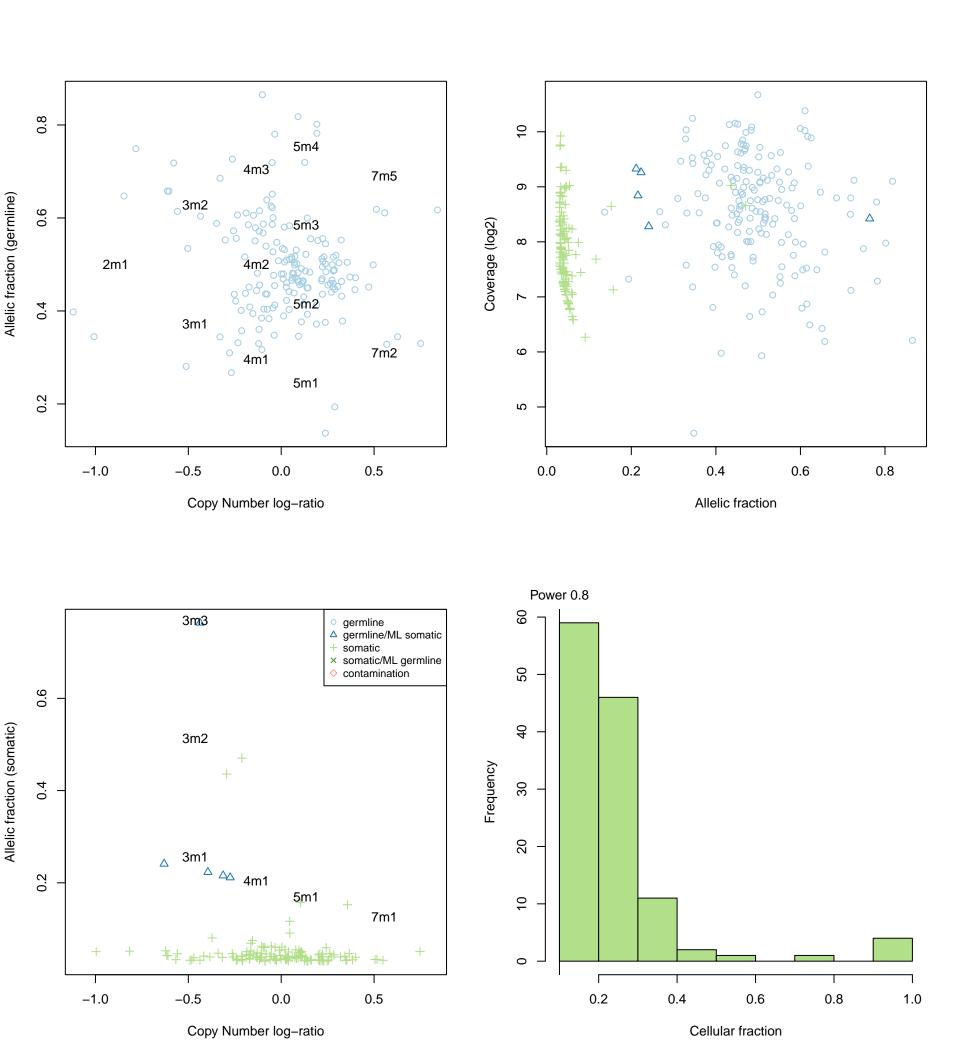
Purity: 0.69 Tumor ploidy: 4.475 2 5 6 3 0.30 0.25 0.20 Fraction Genome 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



SCNA-fit log-likelihood: -5615







Purity: 0.47 Tumor ploidy: 1.796 2 0 7 0.25 0.20 Fraction Genome 0.05 0.00

0.0

log2 ratio

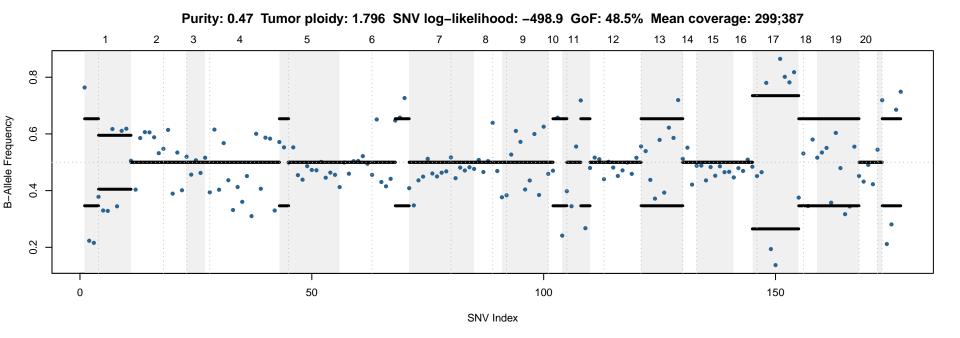
0.5

1.0

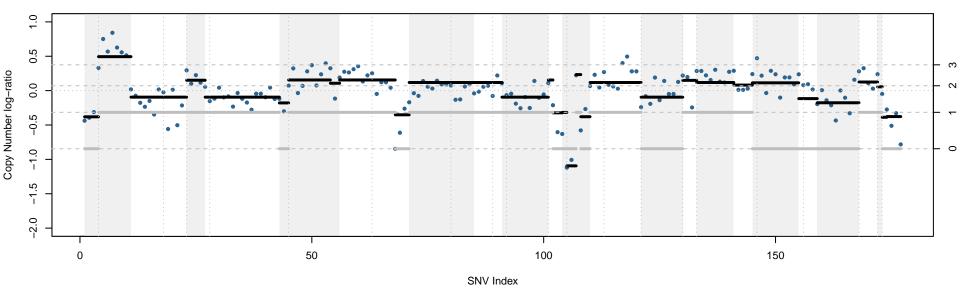
1.5

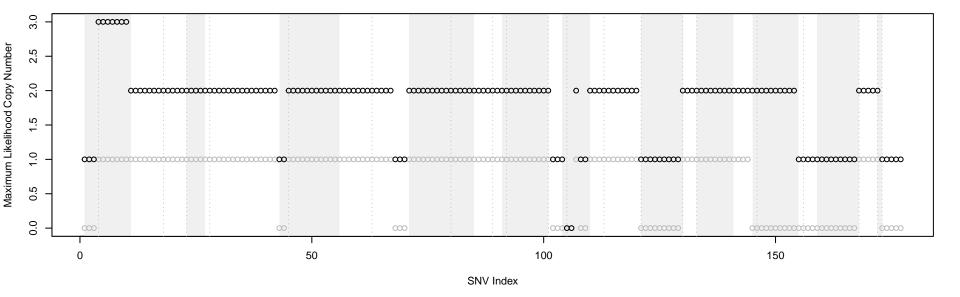
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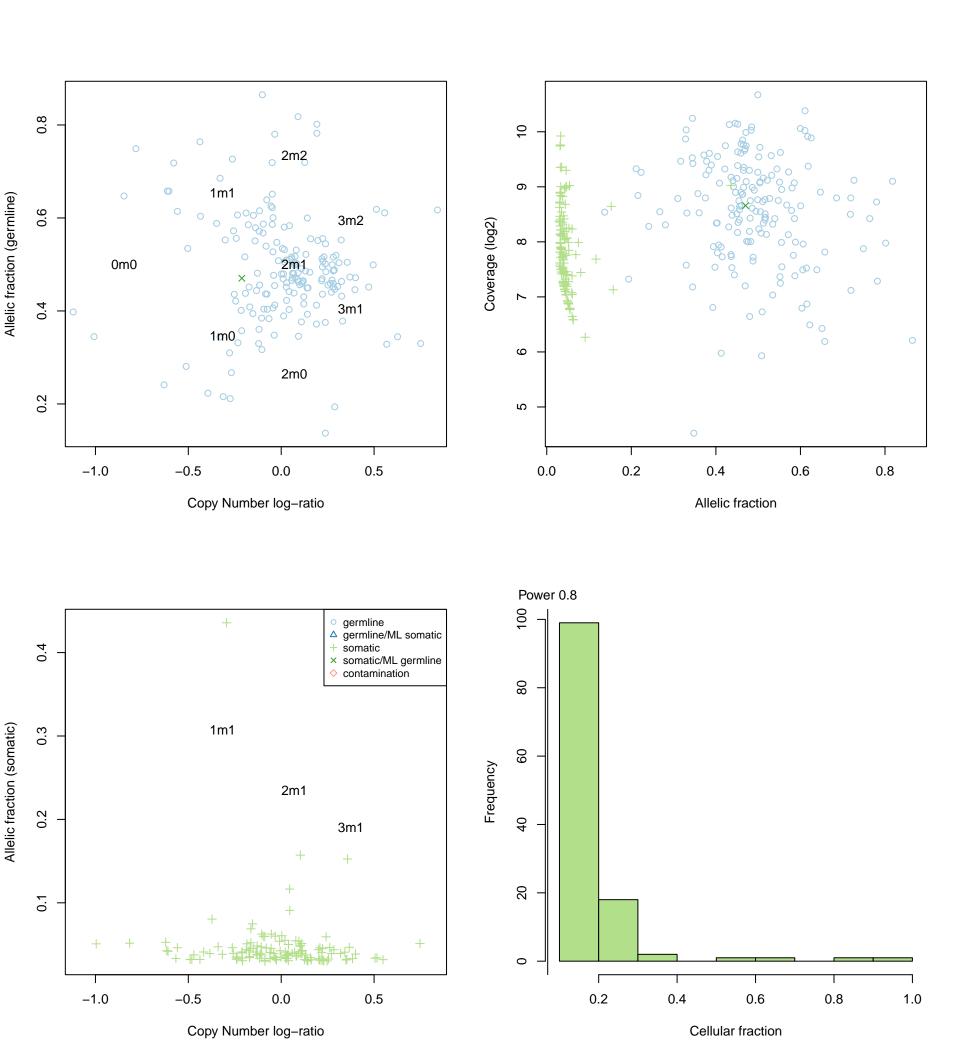
-0.5



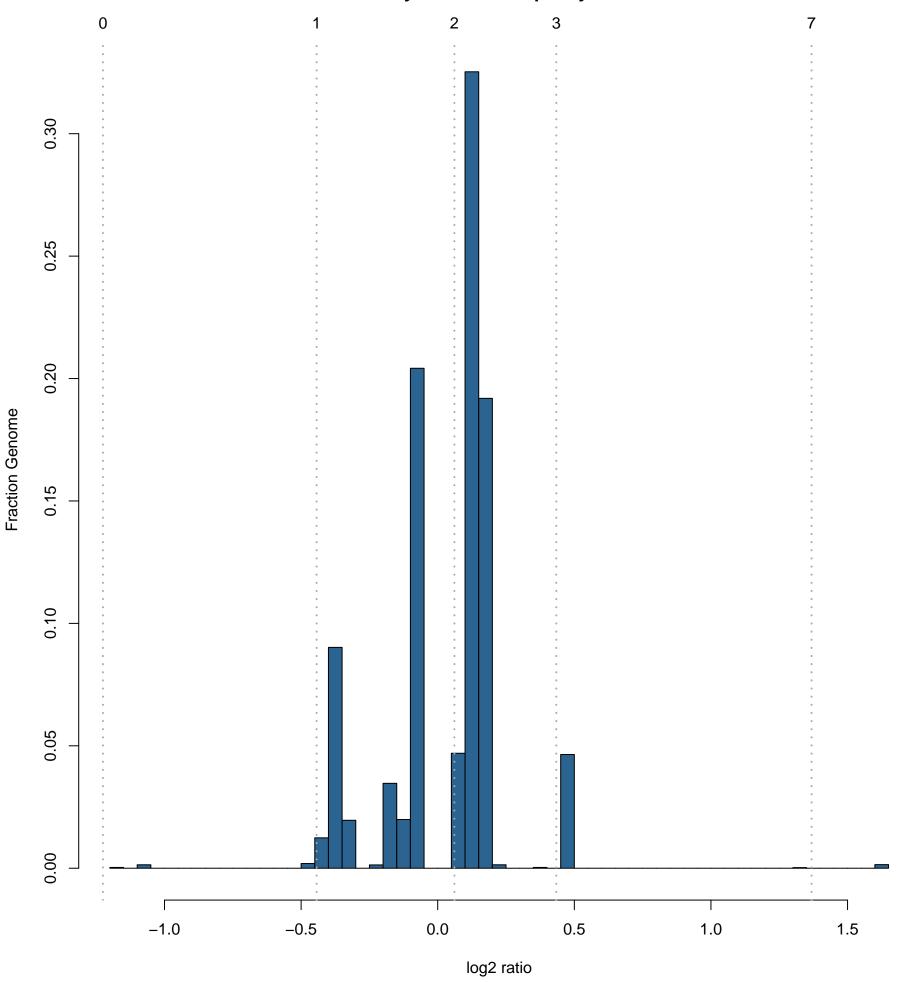
SCNA-fit log-likelihood: -6122.07

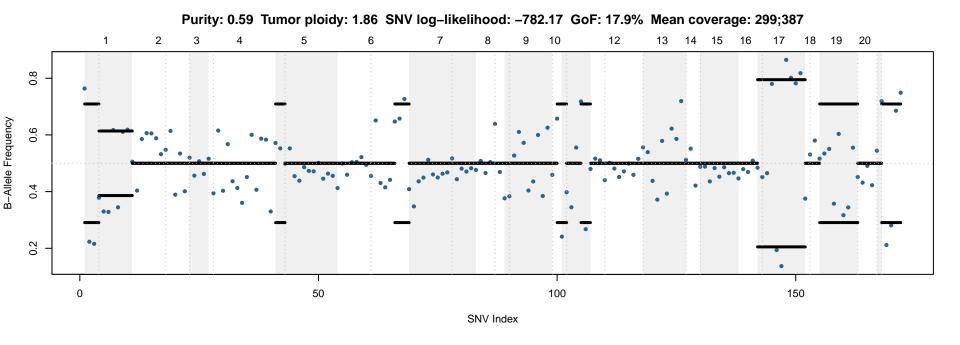




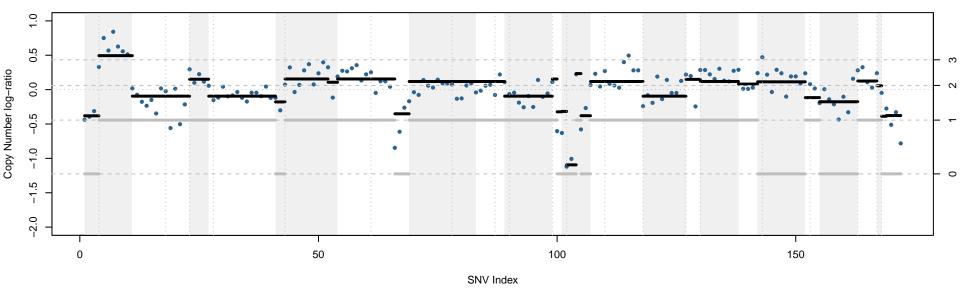


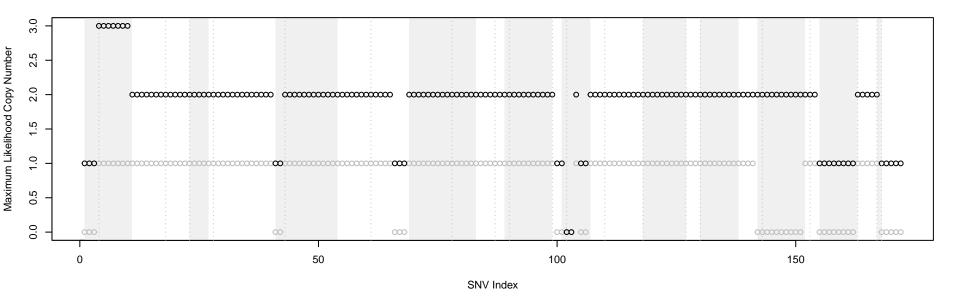
Purity: 0.59 Tumor ploidy: 1.86

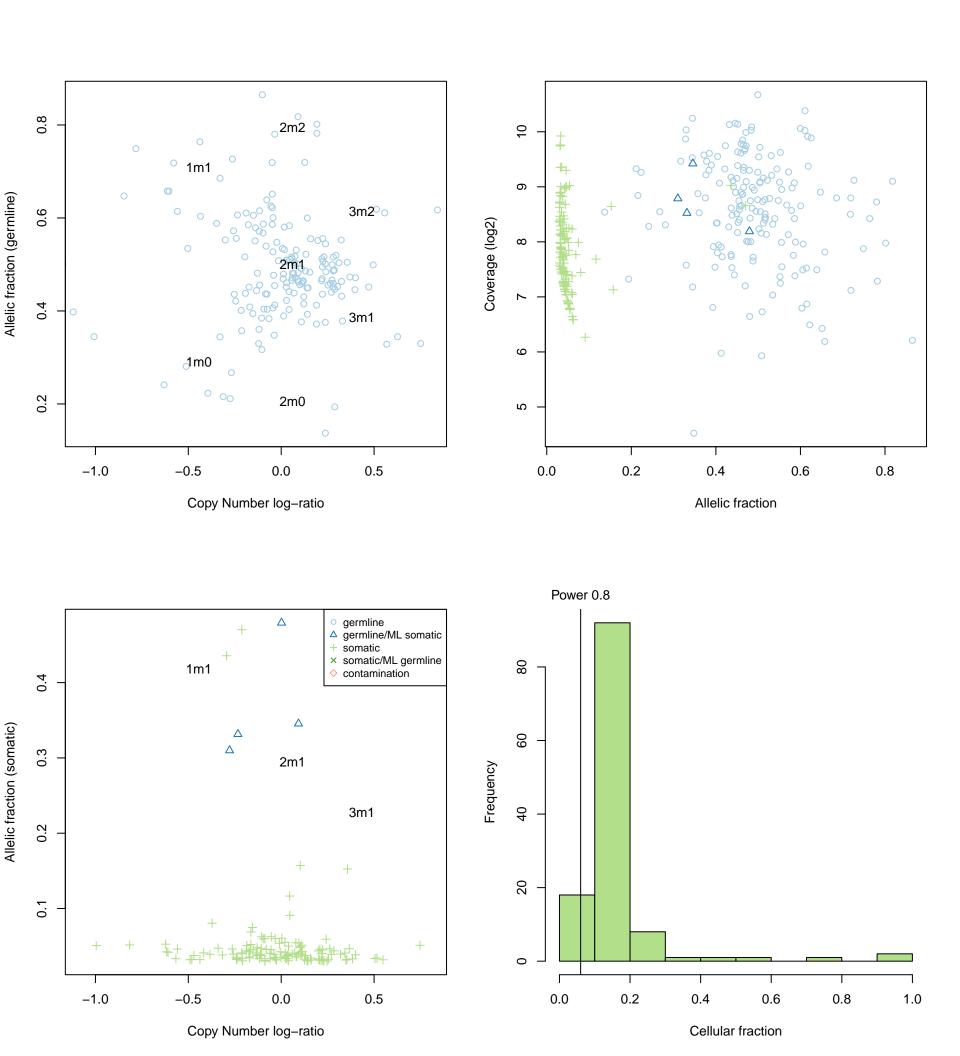




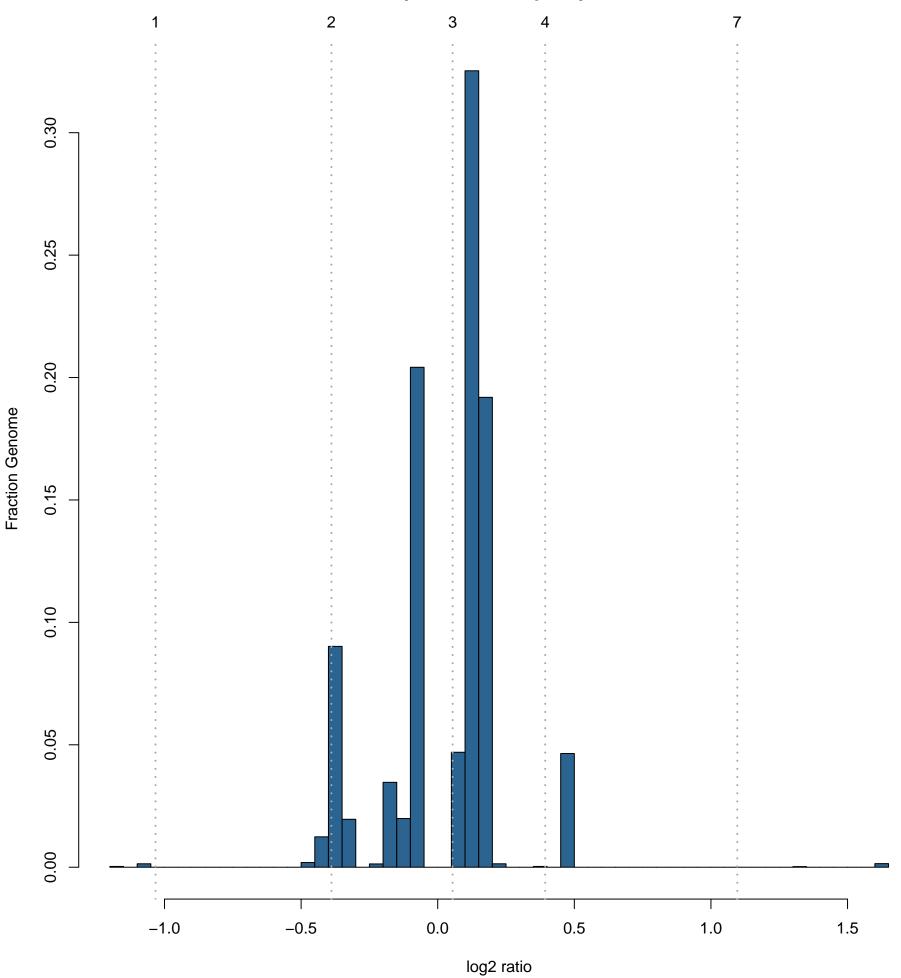
SCNA-fit log-likelihood: -6204.29

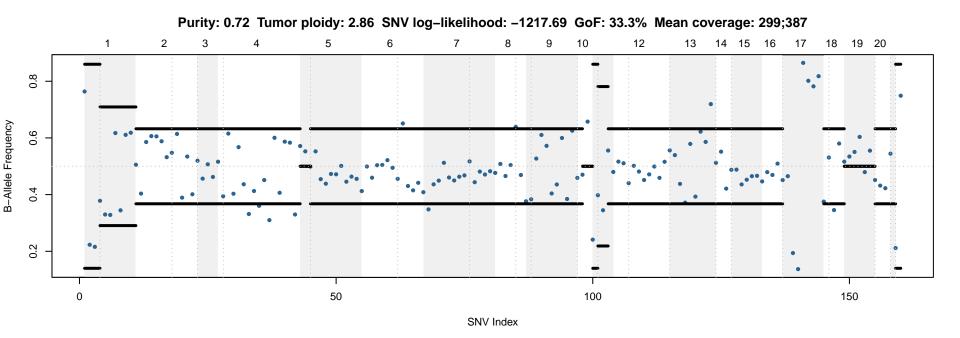






Purity: 0.72 Tumor ploidy: 2.86





SCNA-fit log-likelihood: -6142.86

