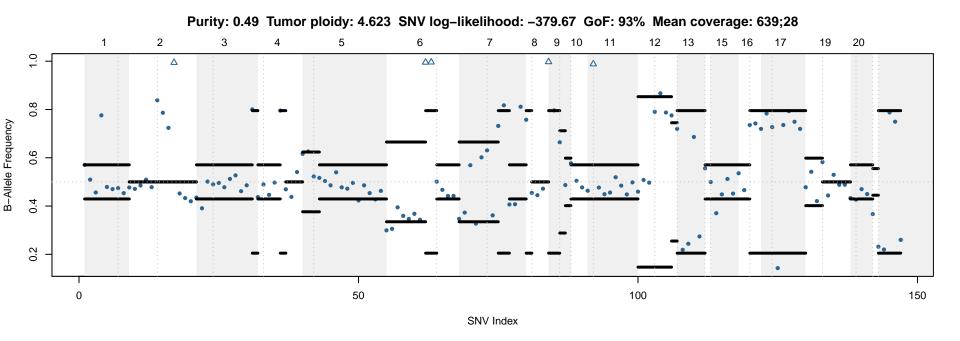
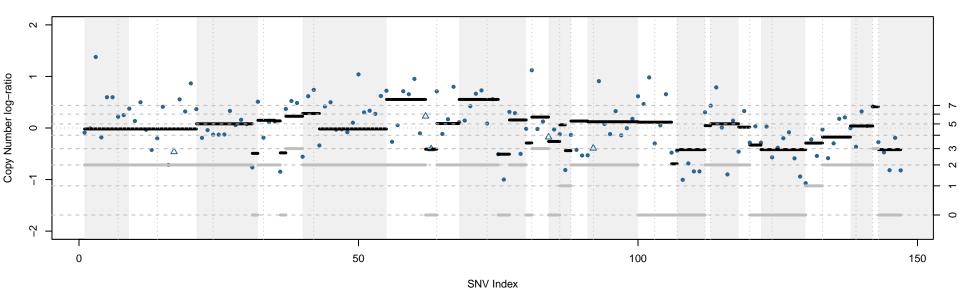
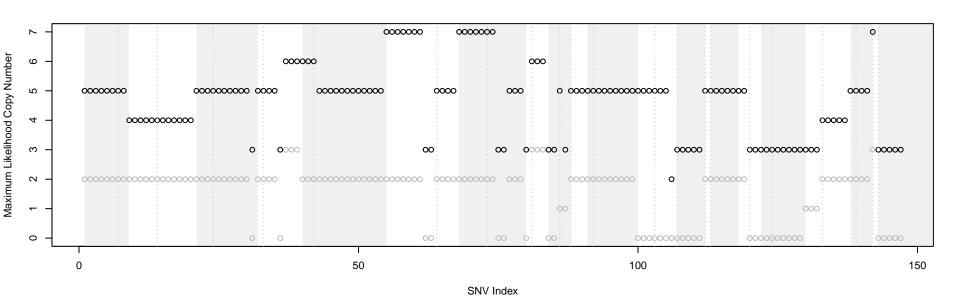
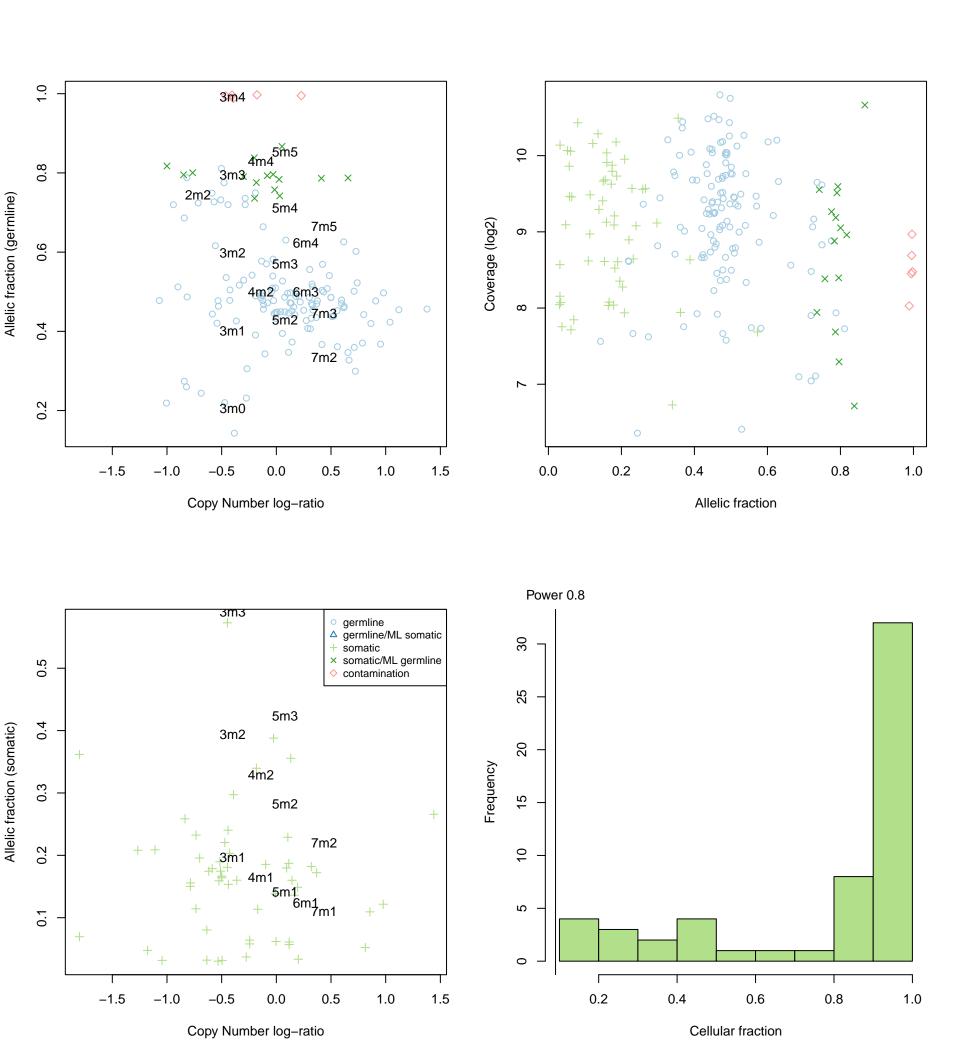
Purity: 0.49 Tumor ploidy: 4.623 3 2 6 0.20 Fraction Genome 0.10 0.05 0.00 -1 0 2 1 log2 ratio



SCNA-fit log-likelihood: -18038.95







Purity: 0.65 Tumor ploidy: 5.344 6 2 3 5

0.20

Fraction Genome

0.10

0.05

0.00

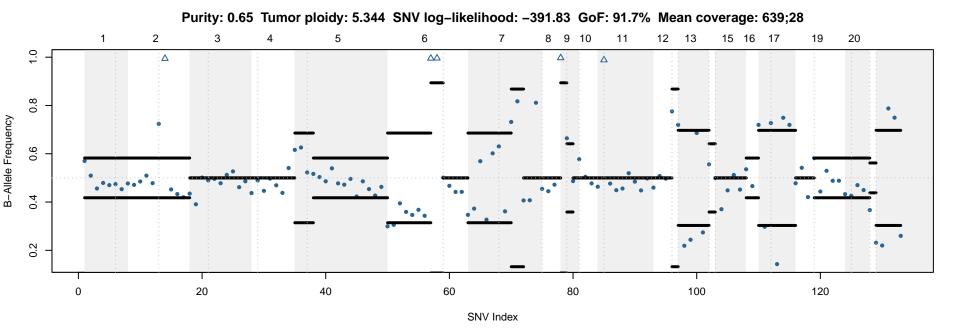
-1

0

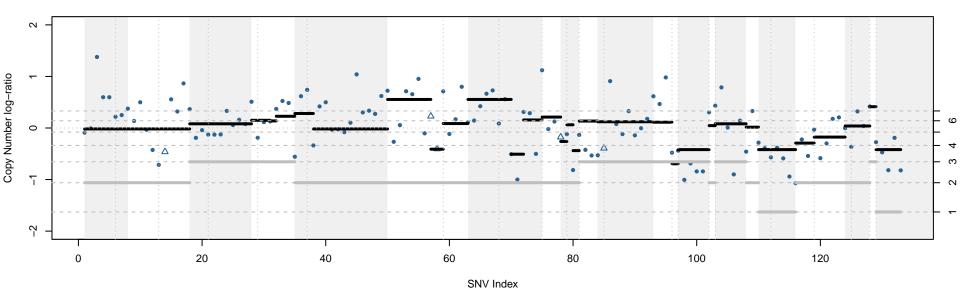
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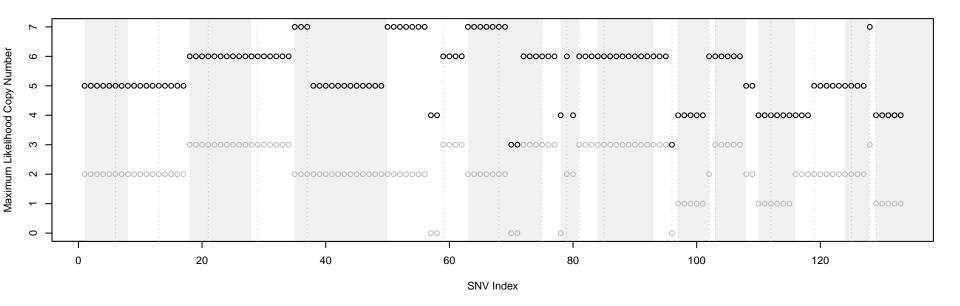
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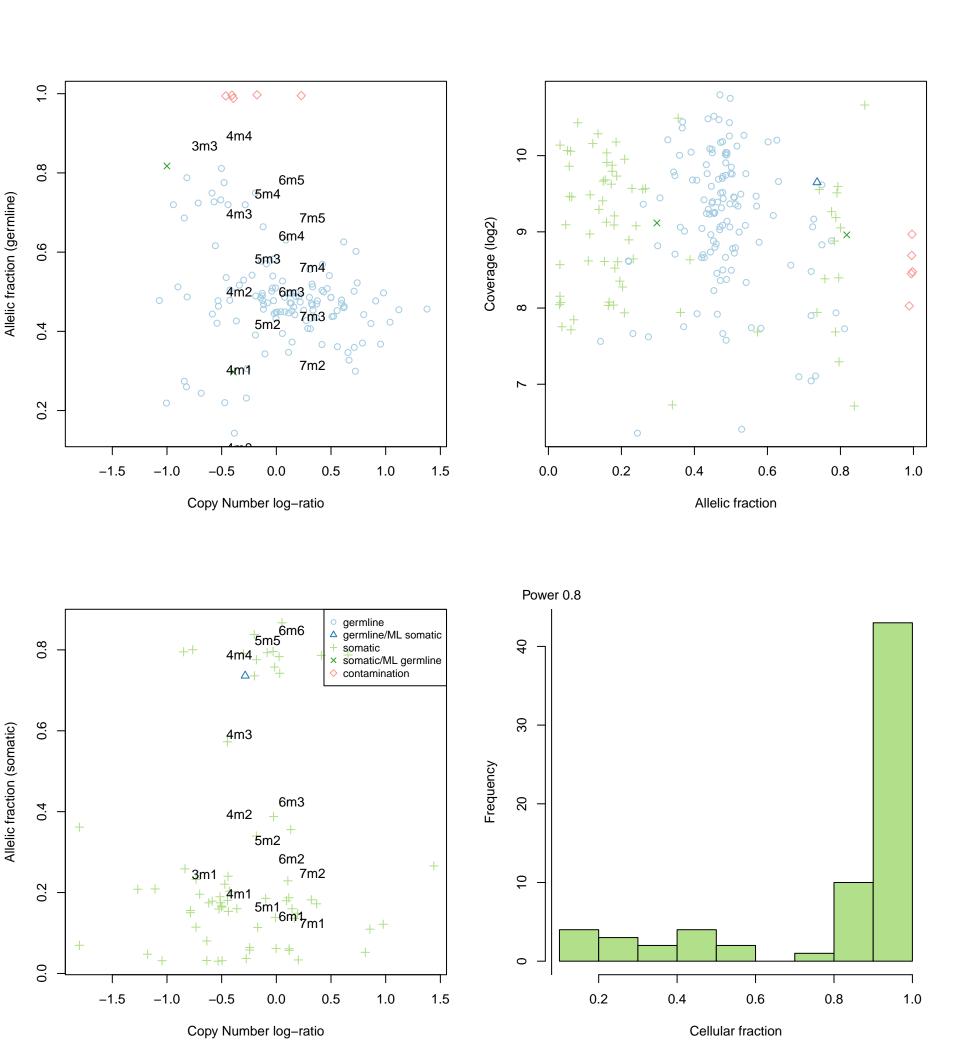
log2 ratio



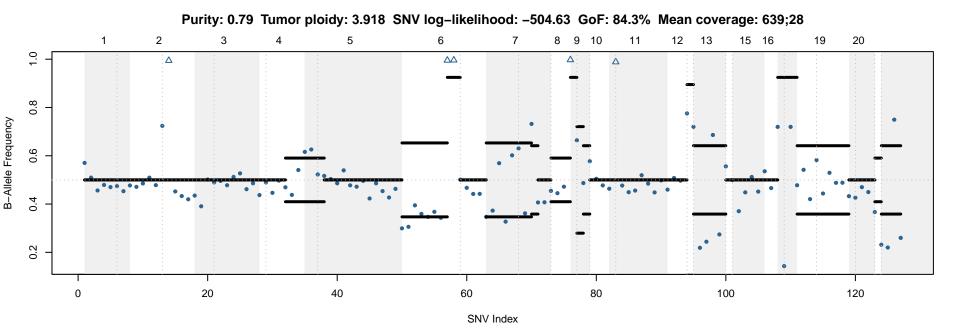
SCNA-fit log-likelihood: -18109.92



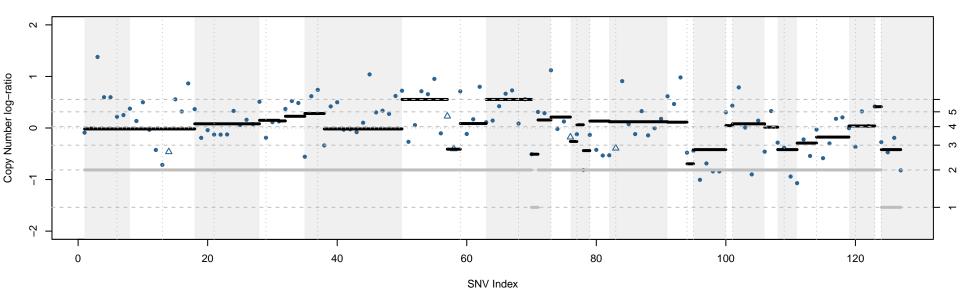


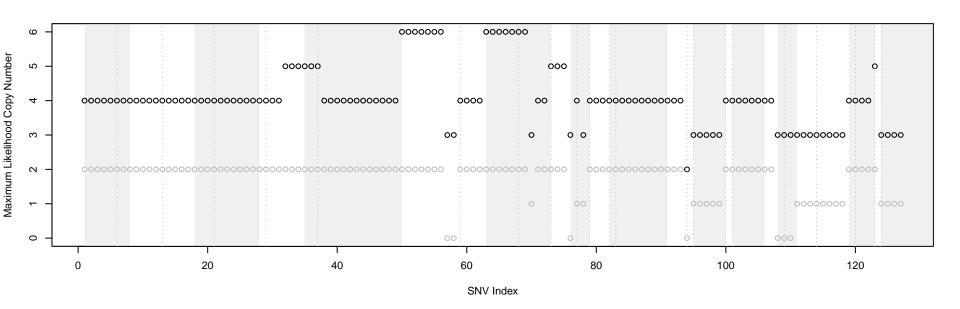


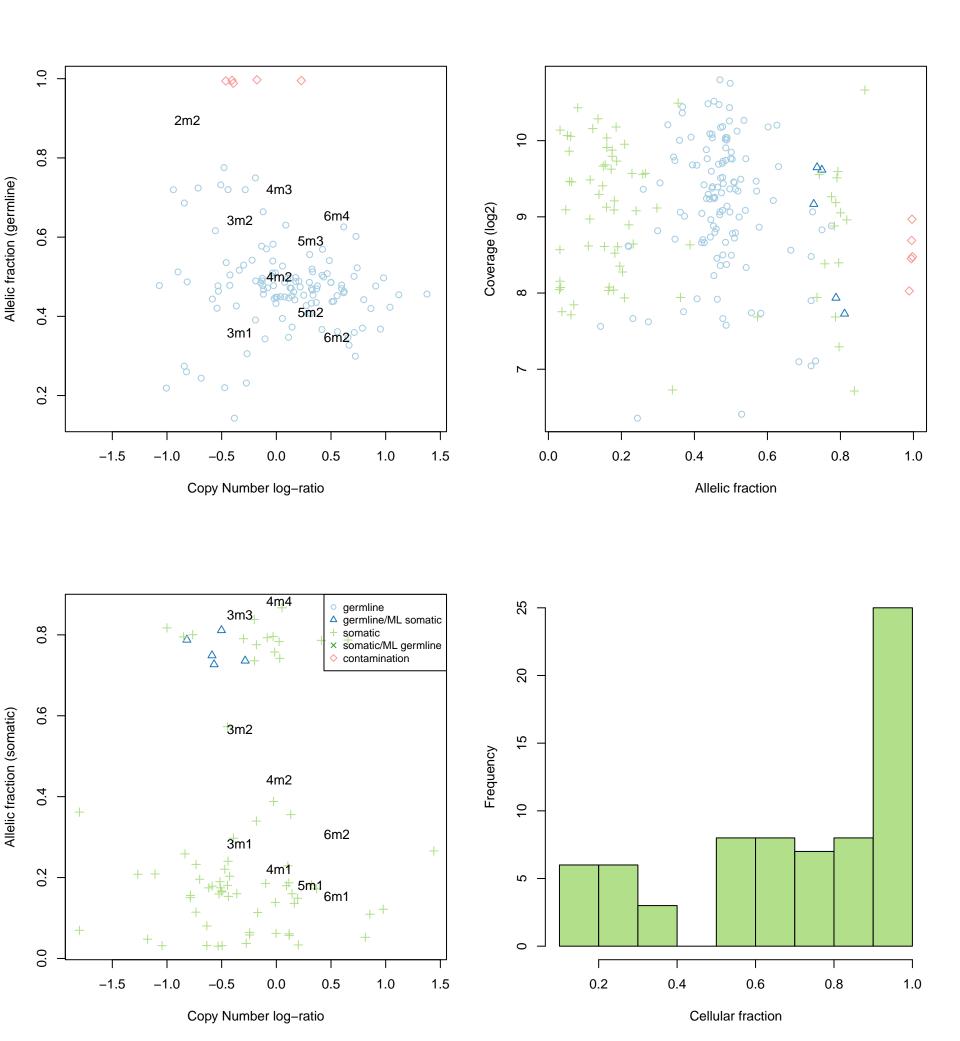
Purity: 0.79 Tumor ploidy: 3.918 3 6 2 5 0.20 0.15 Fraction Genome 0.10 0.05 0.00 0 -1 2 1 log2 ratio



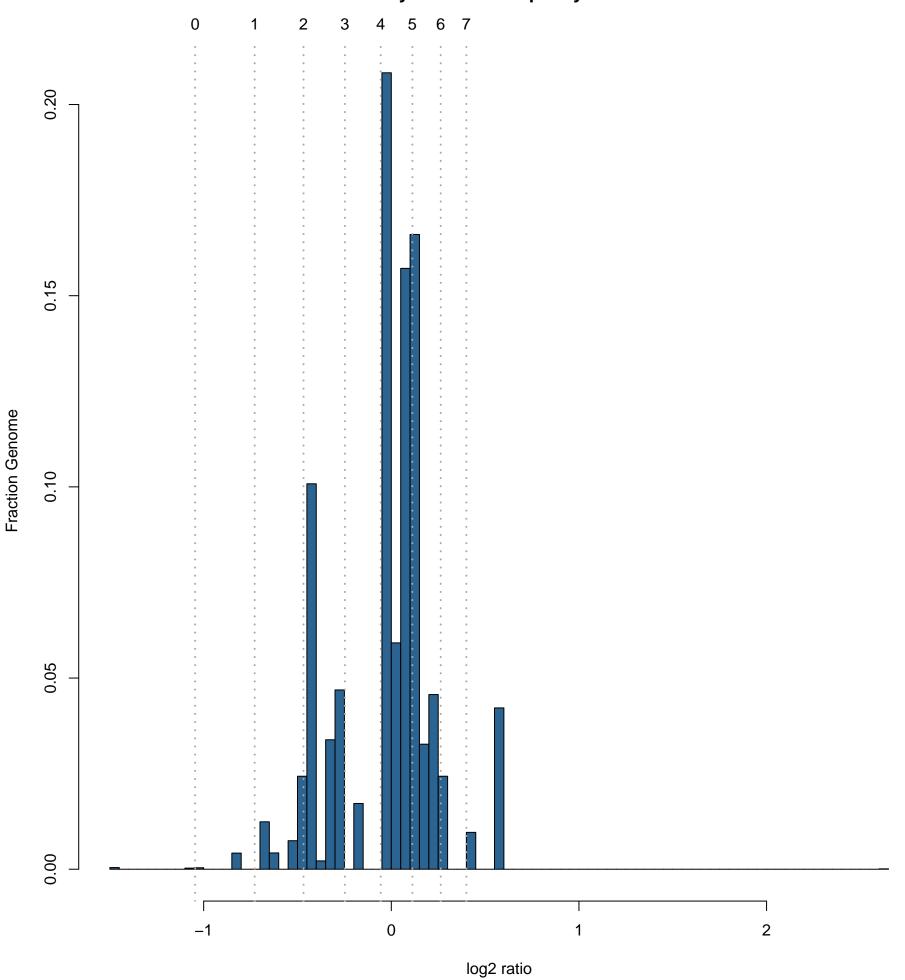
SCNA-fit log-likelihood: -18109.69

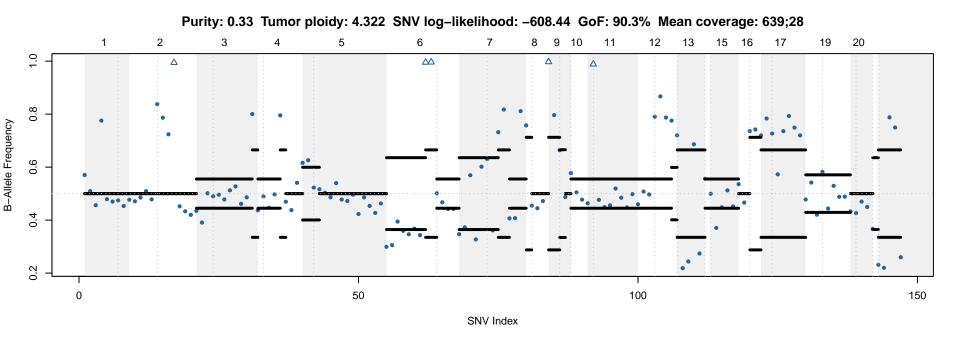




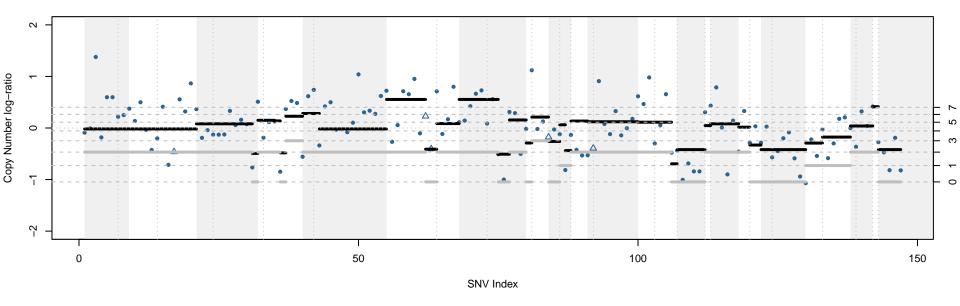


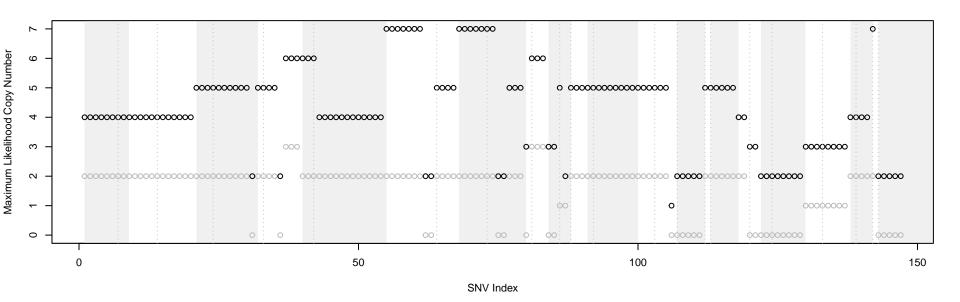
Purity: 0.33 Tumor ploidy: 4.322

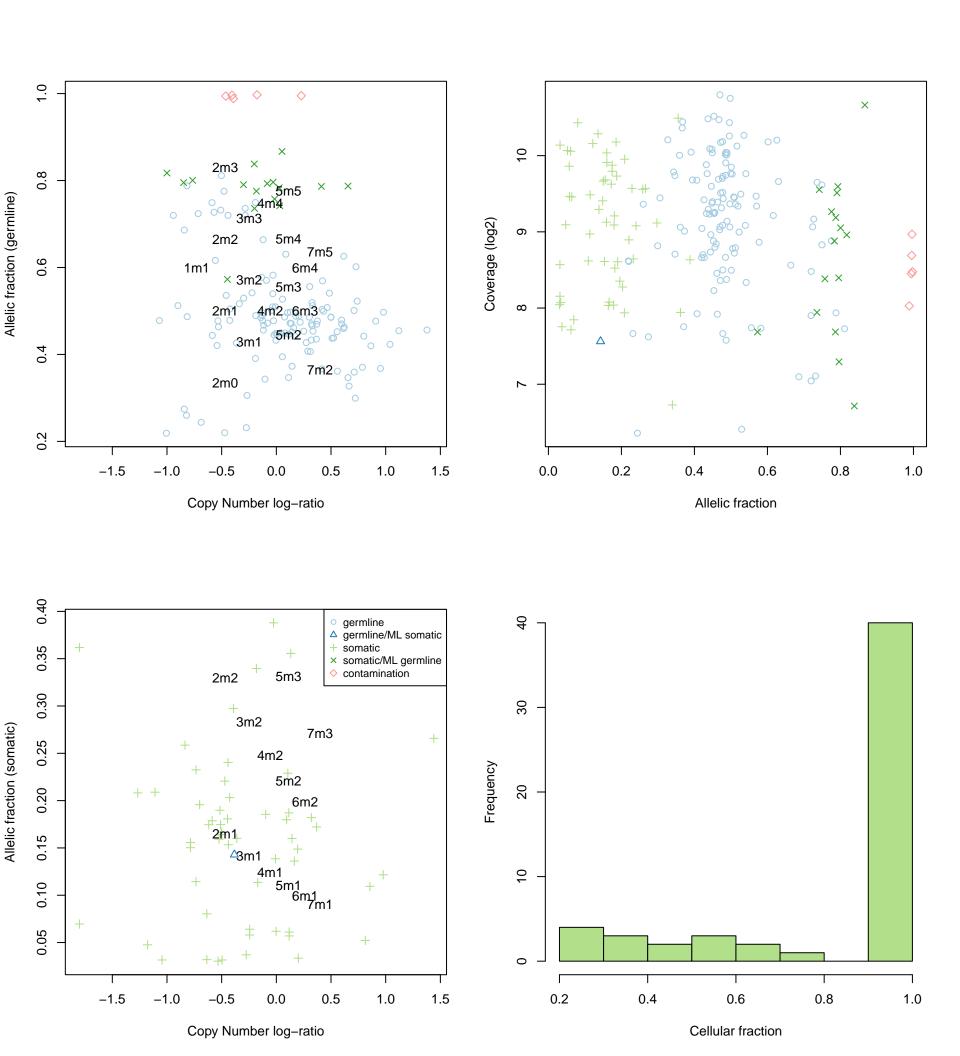




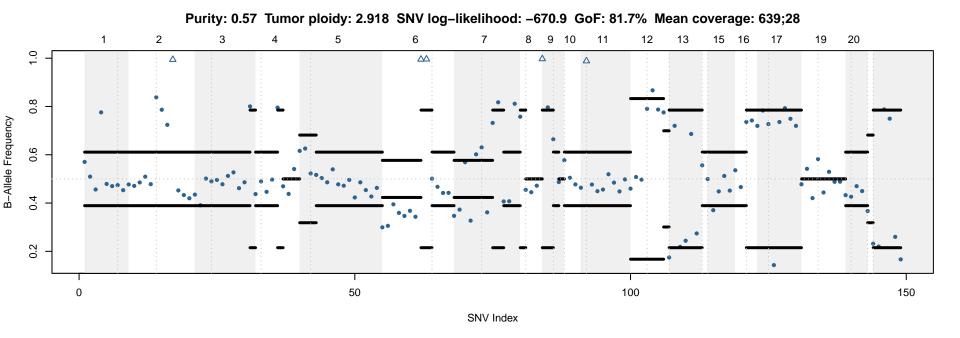
SCNA-fit log-likelihood: -18003.14



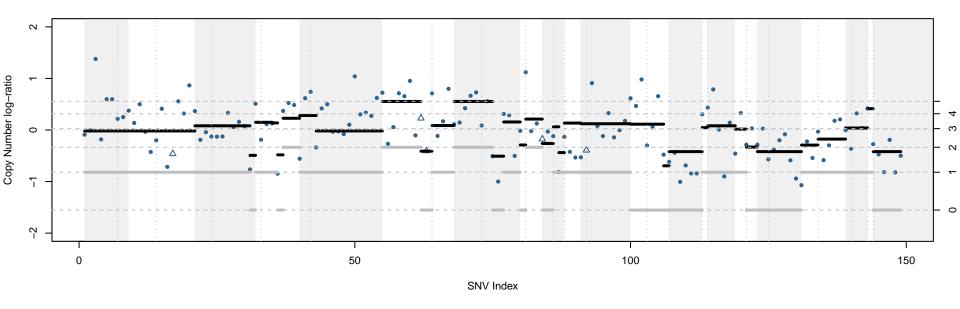


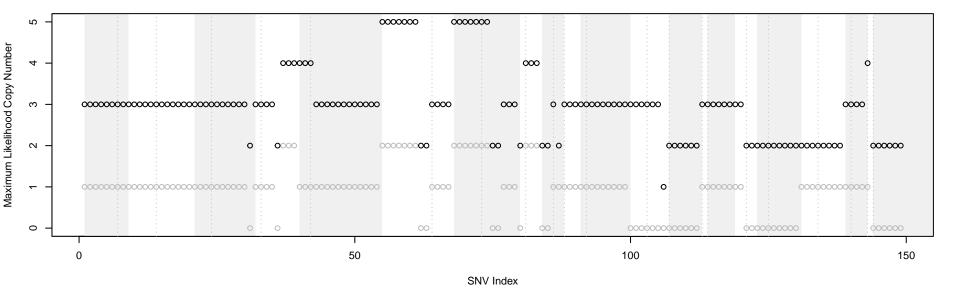


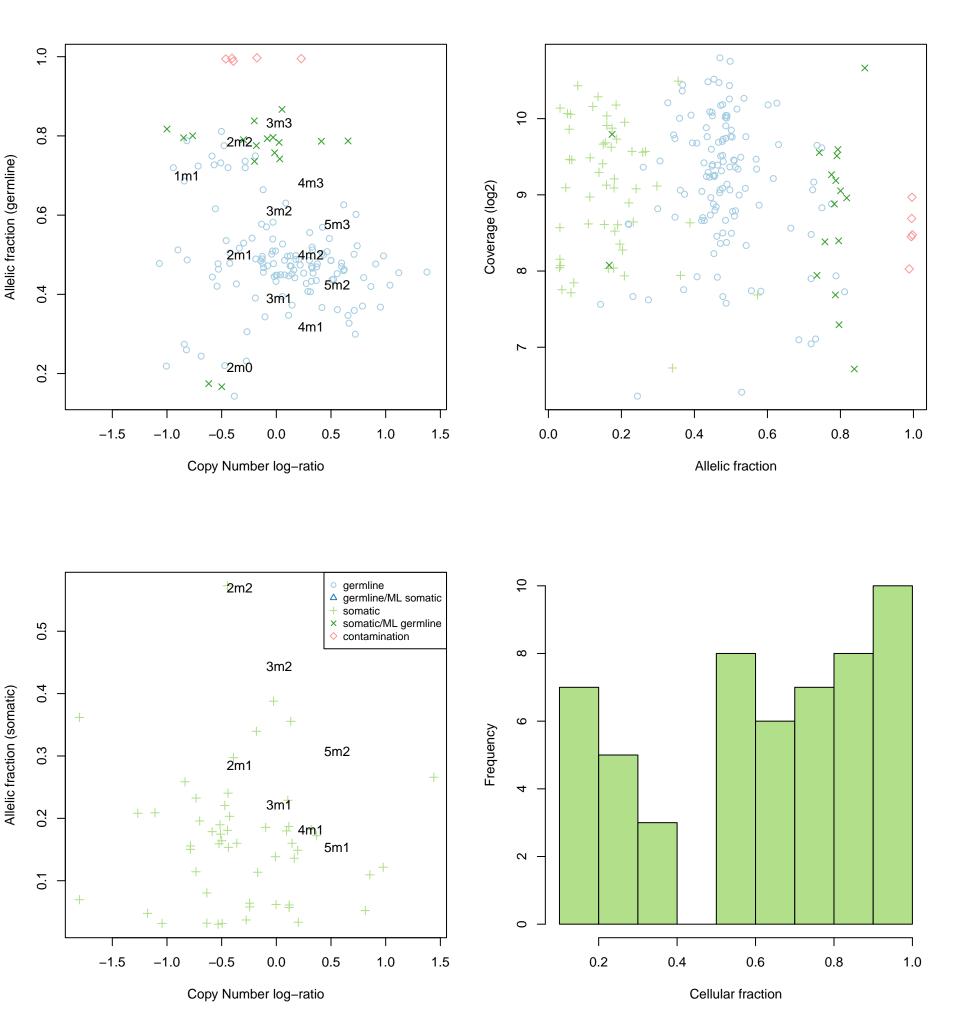
Purity: 0.57 Tumor ploidy: 2.918 2 5 0 0.20 0.15 Fraction Genome 0.10 0.05 0.00 0 -1 2 1 log2 ratio



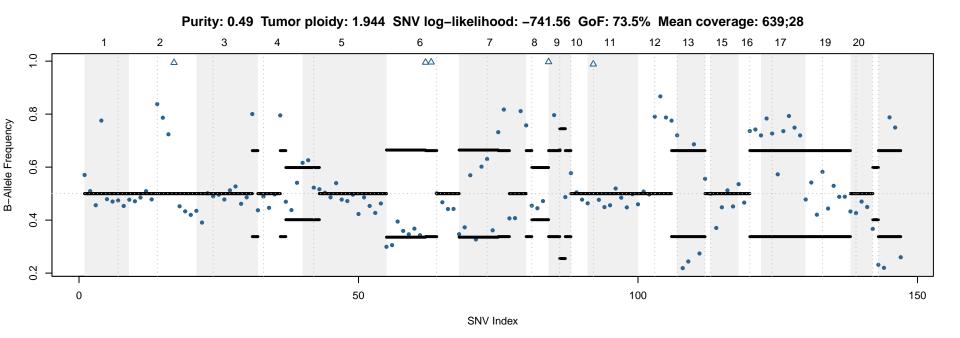
SCNA-fit log-likelihood: -18109.75



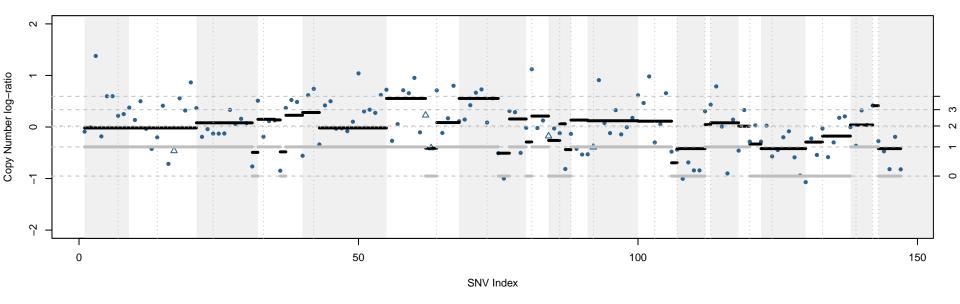


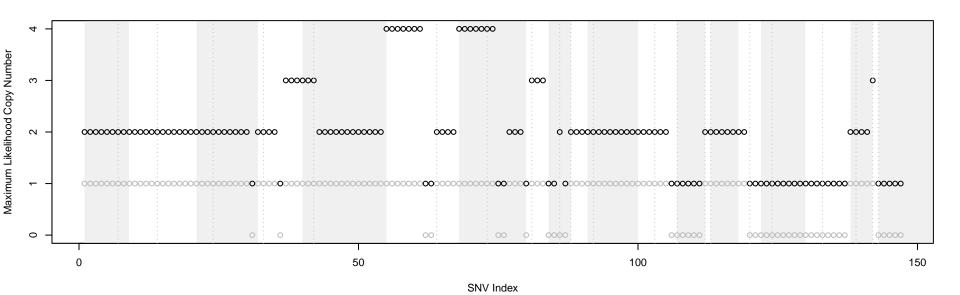


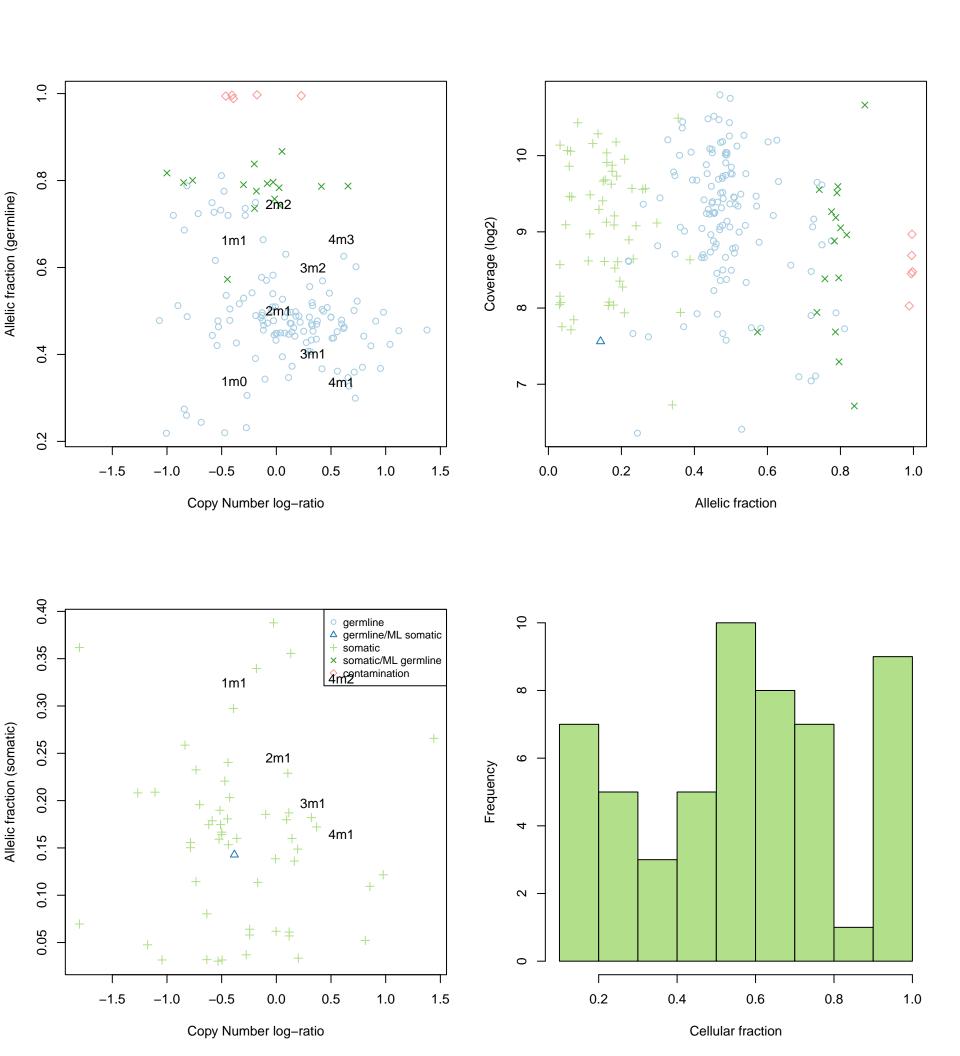
Purity: 0.49 Tumor ploidy: 1.944 0 2 3 4 0.20 Fraction Genome 0.10 0.05 0.00 0 -1 2 1 log2 ratio



SCNA-fit log-likelihood: -18186.63

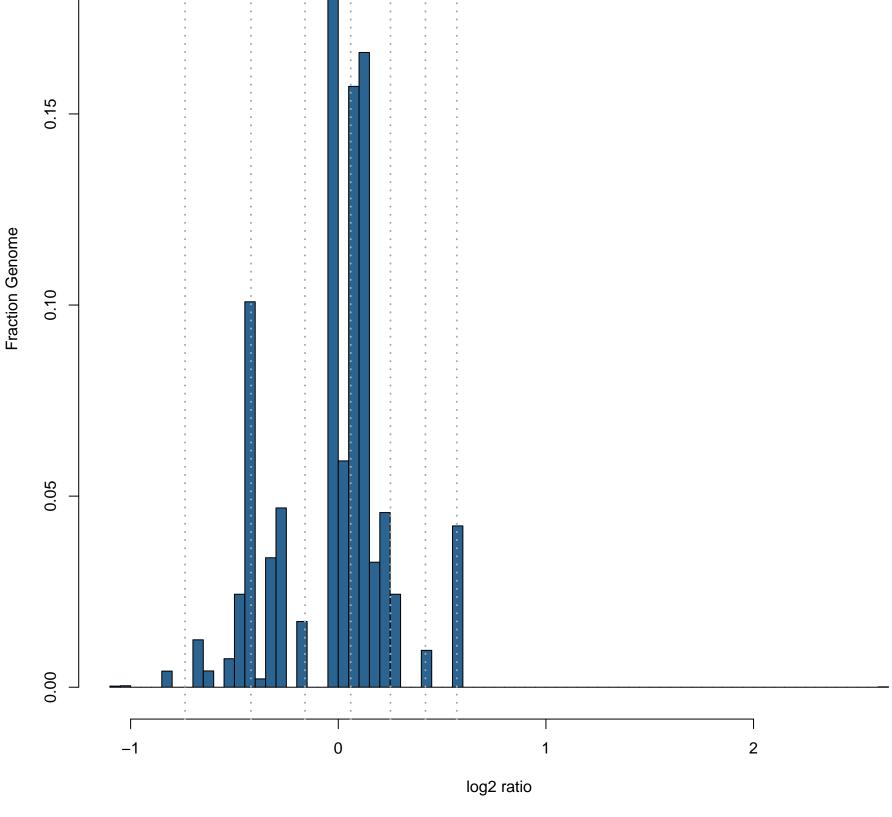


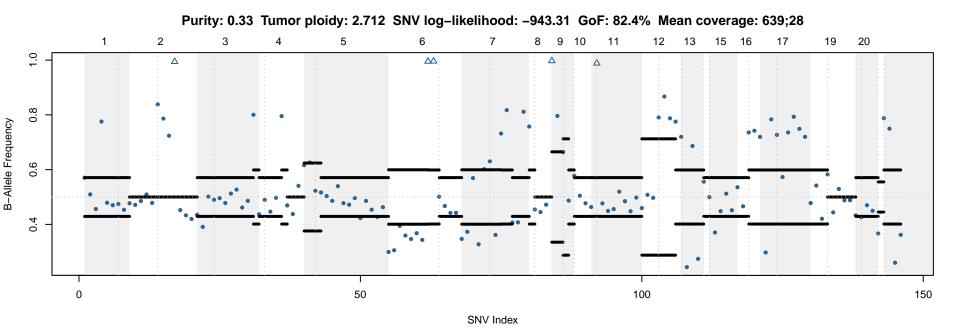




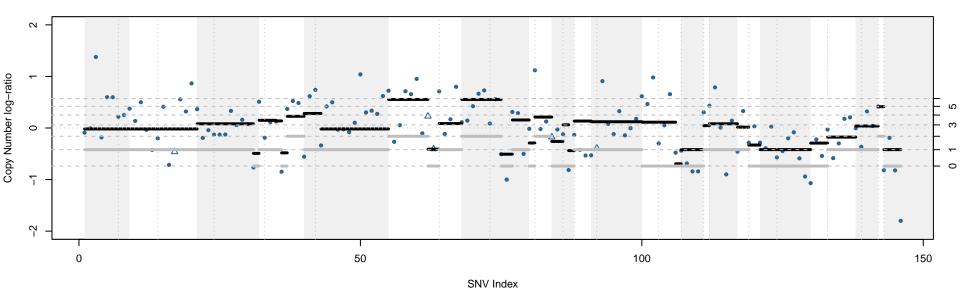
Purity: 0.33 Tumor ploidy: 2.712

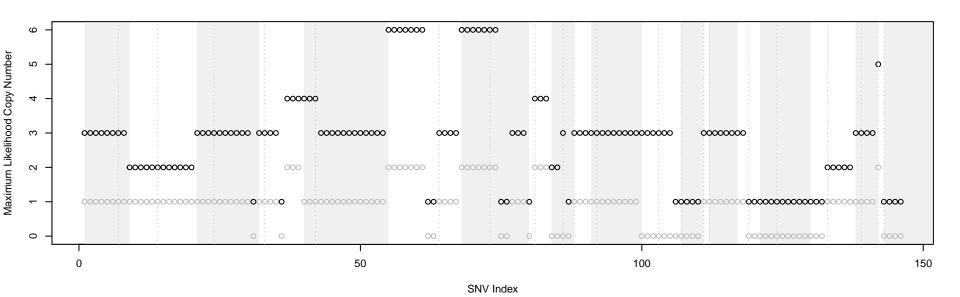
0.20

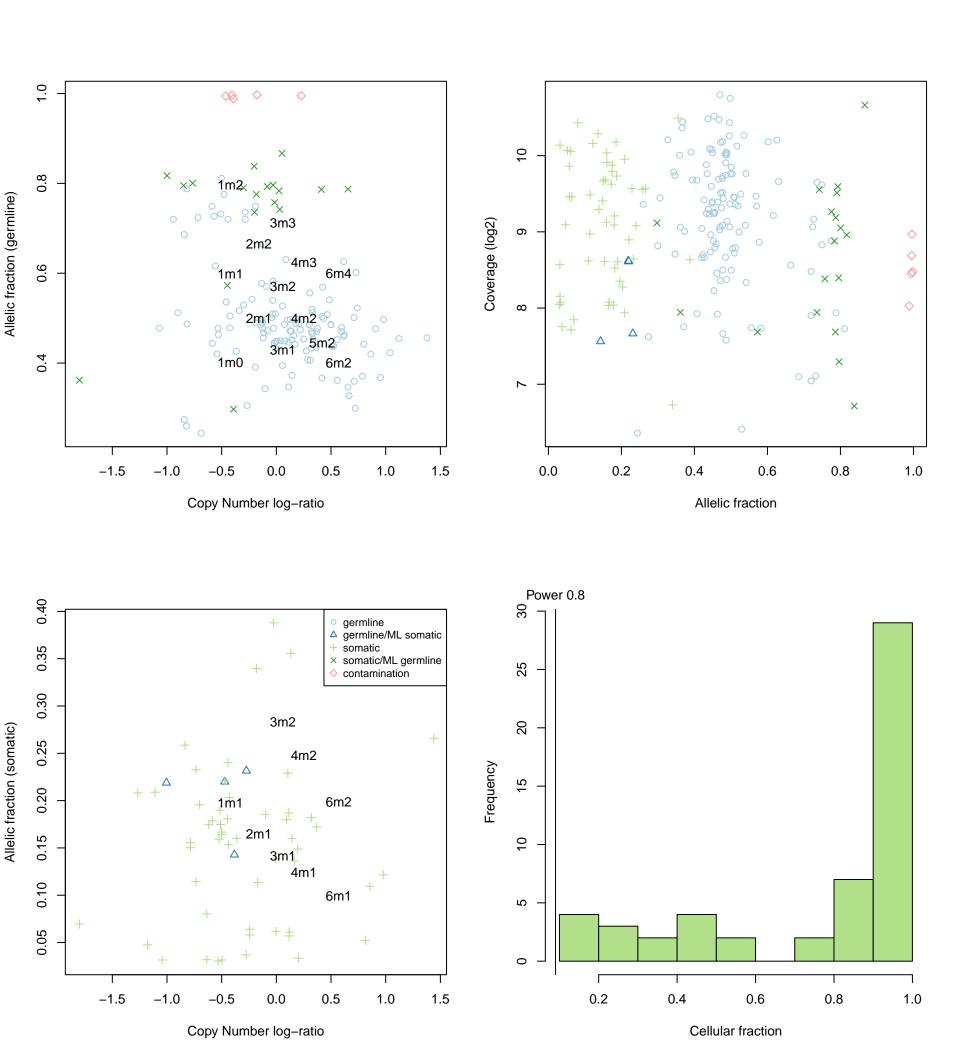




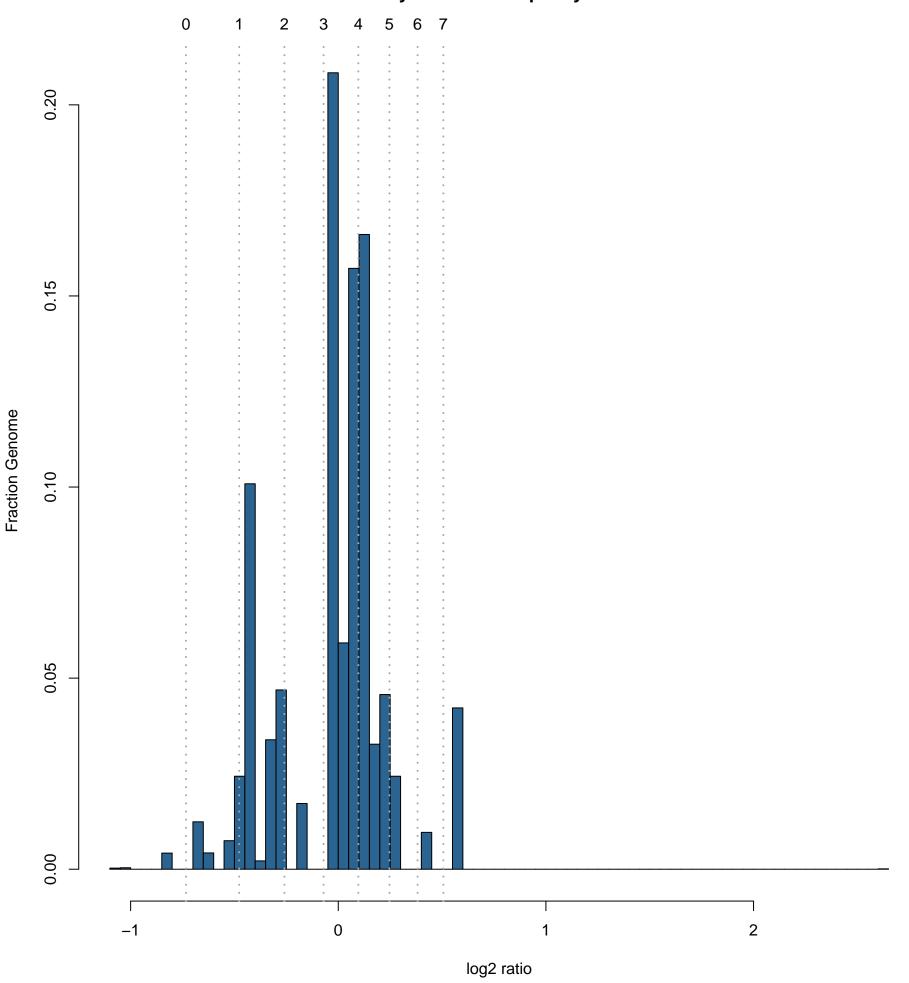
SCNA-fit log-likelihood: -18093.26

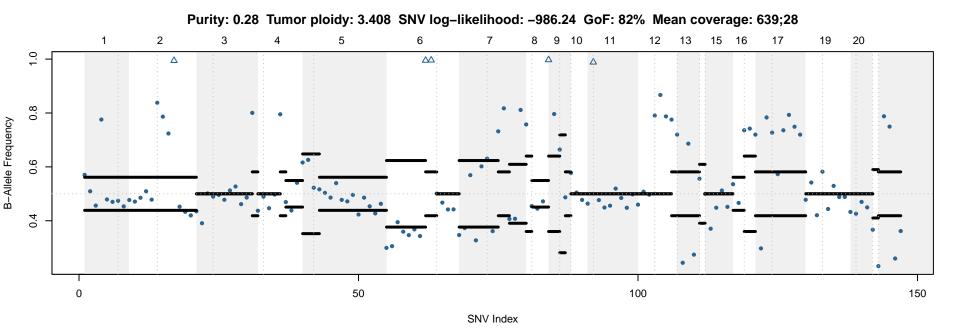




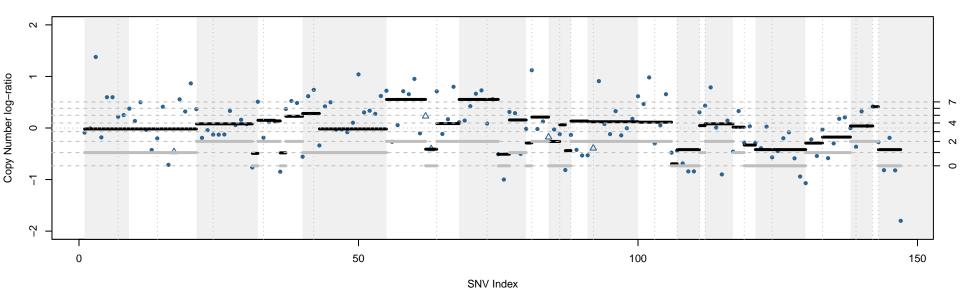


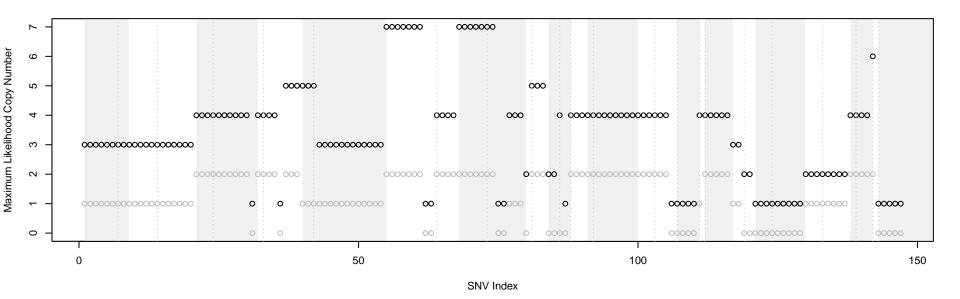
Purity: 0.28 Tumor ploidy: 3.408

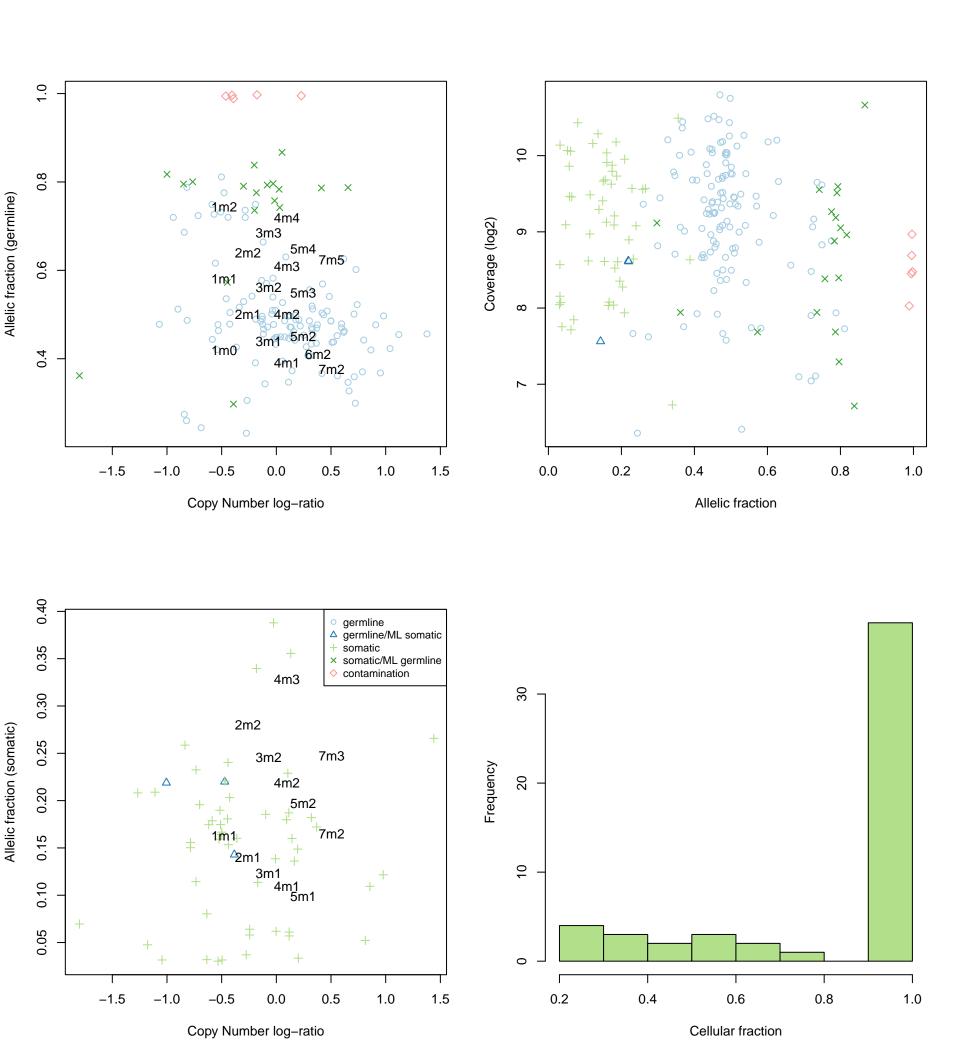




SCNA-fit log-likelihood: -18019.99

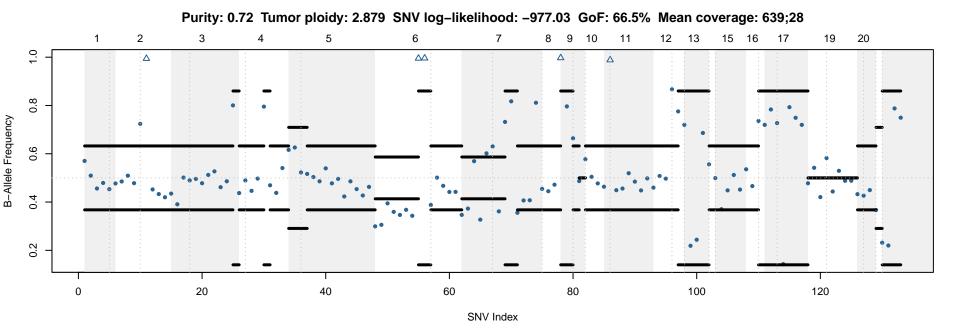






Purity: 0.72 Tumor ploidy: 2.879 2 3 5 0.20 Fraction Genome 0.10 0.05 0.00 0 -1 2 1

log2 ratio



SCNA-fit log-likelihood: -18165.41

