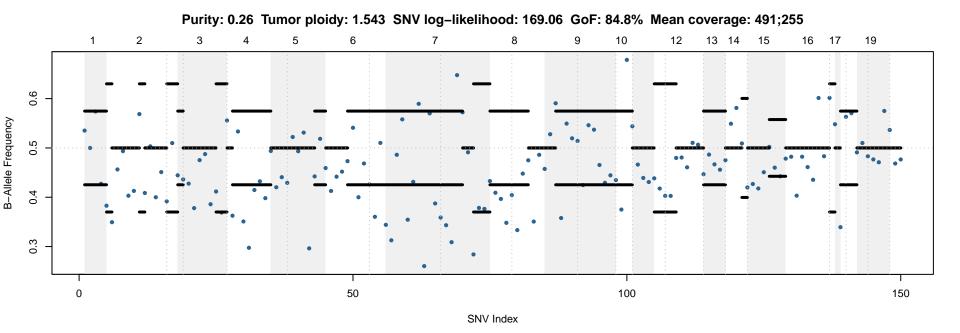
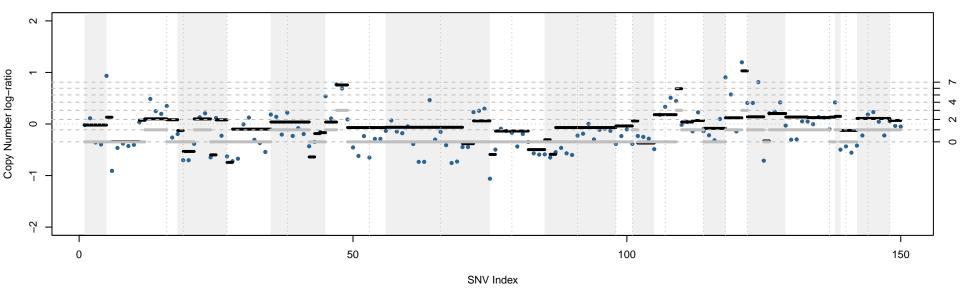
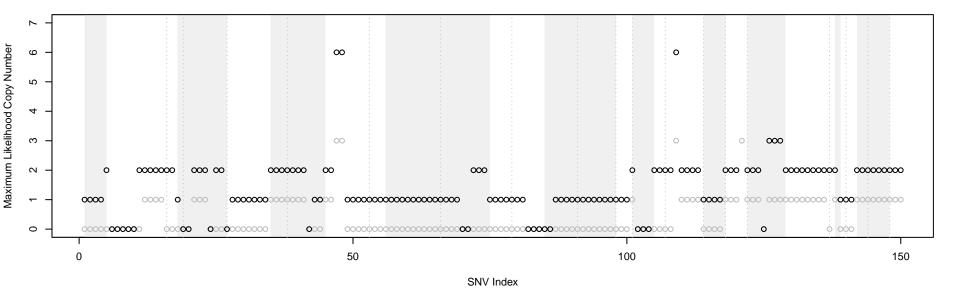
Purity: 0.26 Tumor ploidy: 1.543 3 0 7 0.08 Fraction Genome 90.0 0.04 0.02 0.00 0.0 -0.5 0.5 1.0

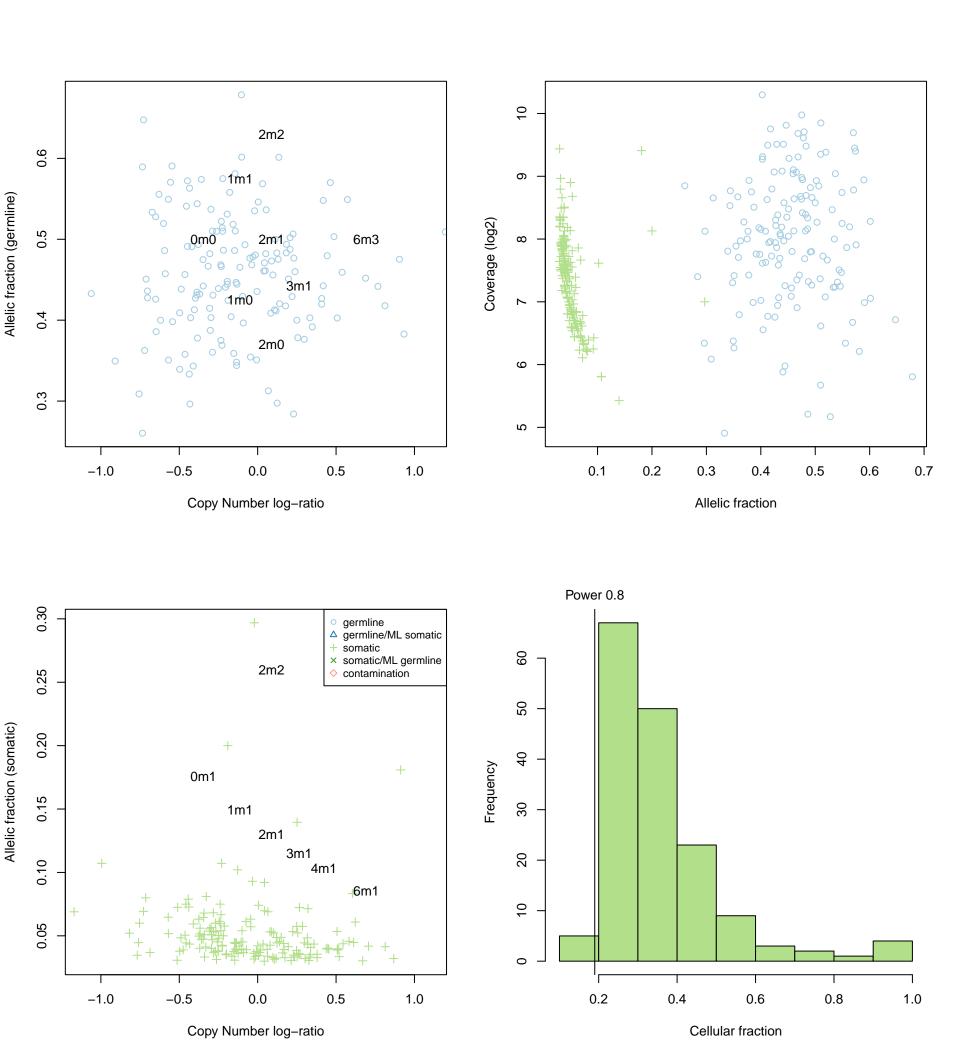
log2 ratio

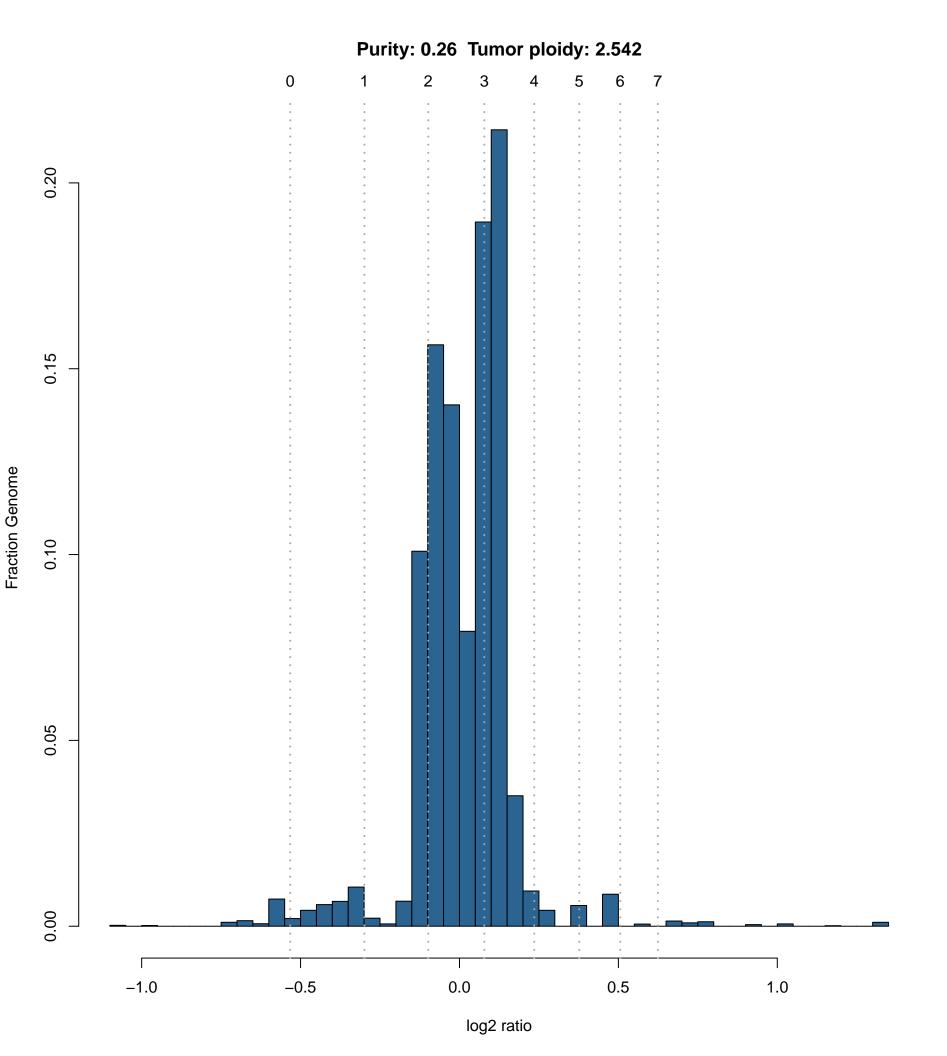


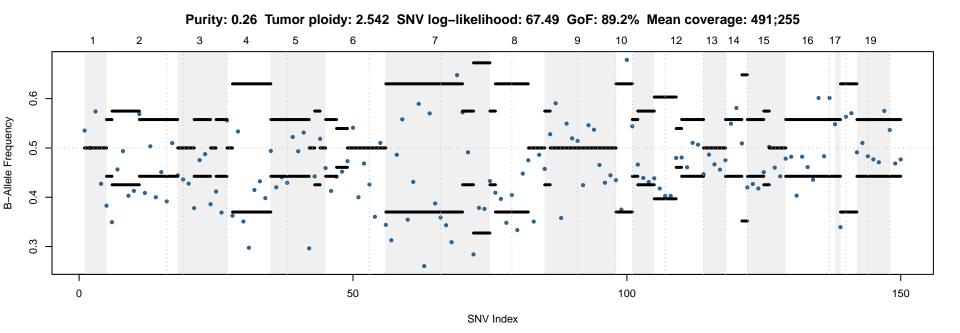
SCNA-fit log-likelihood: -10617.31



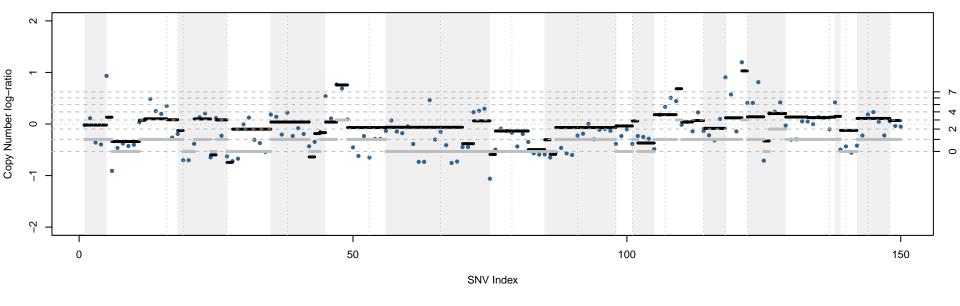


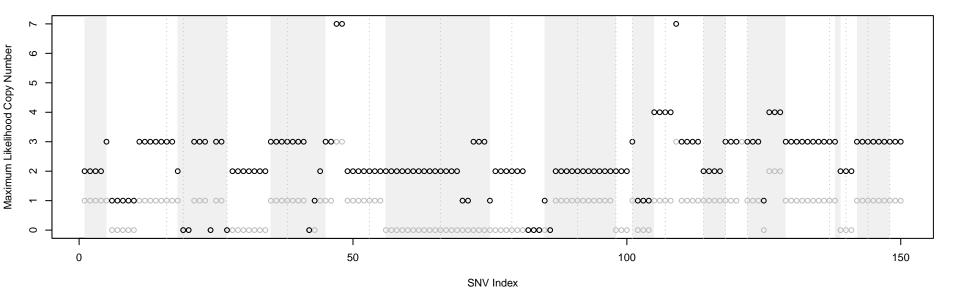


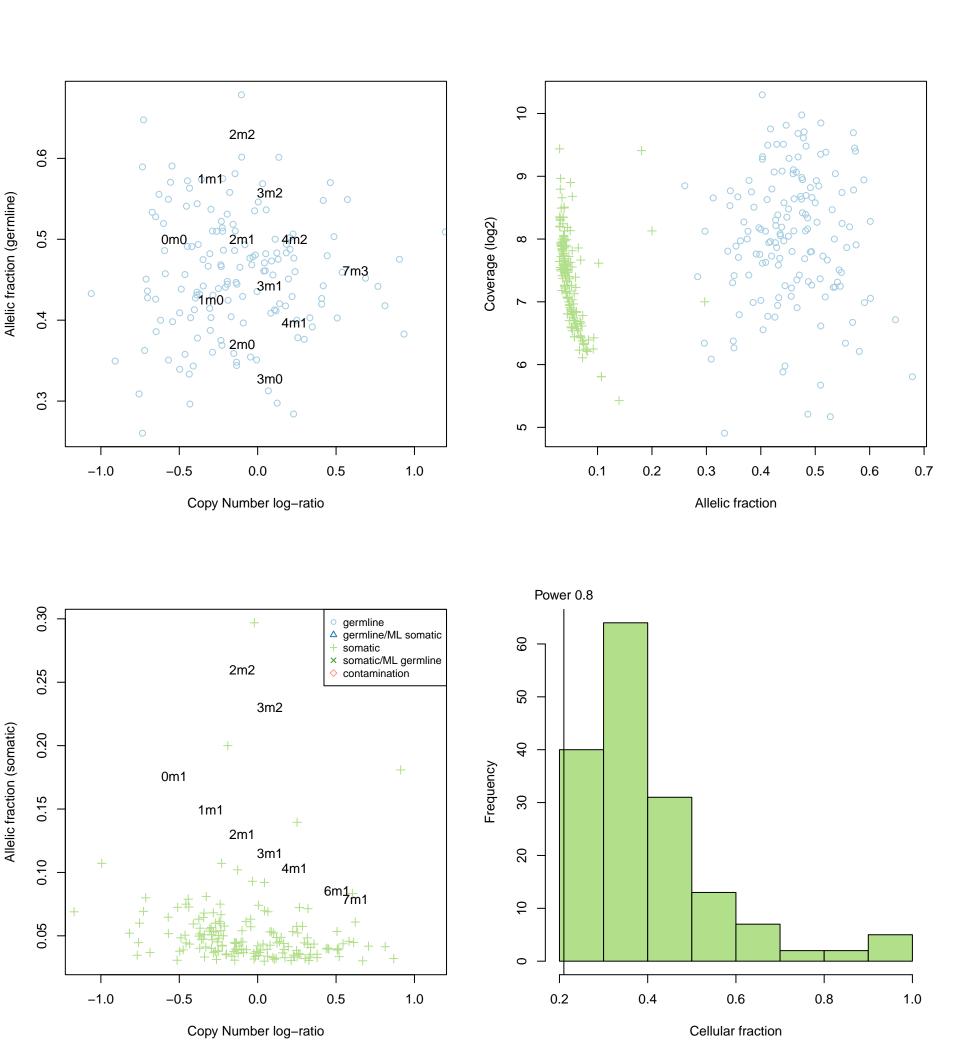


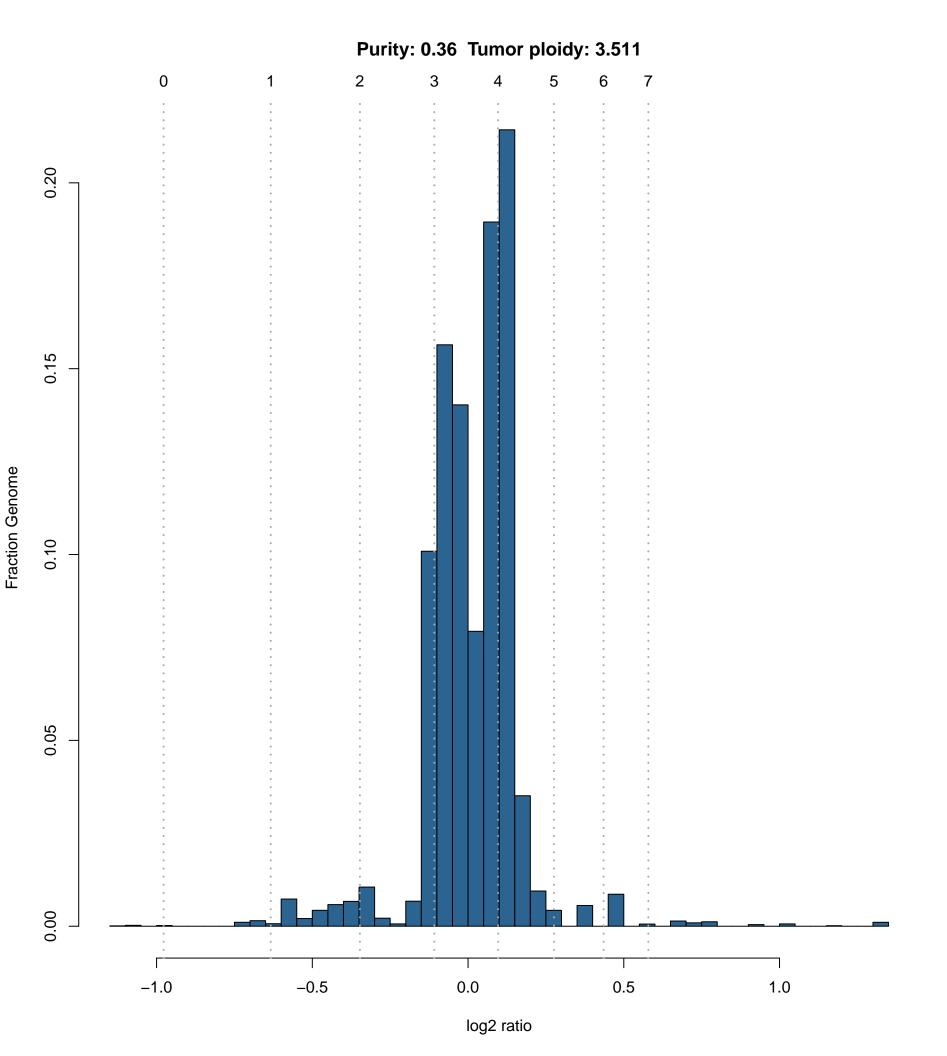


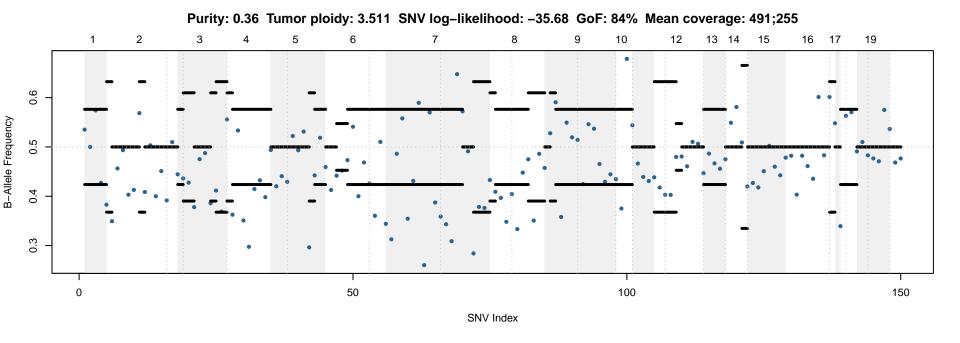
SCNA-fit log-likelihood: -10507.42



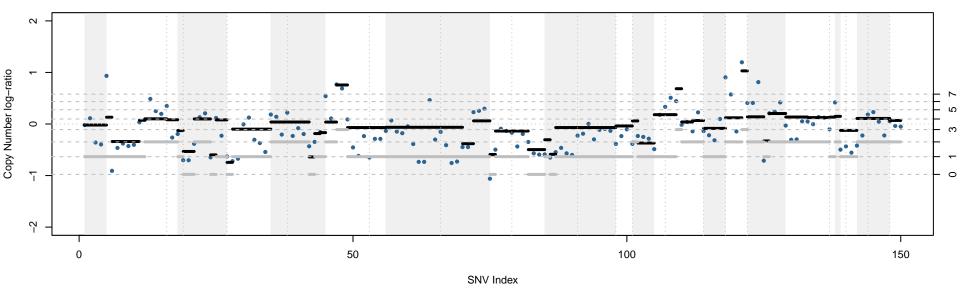


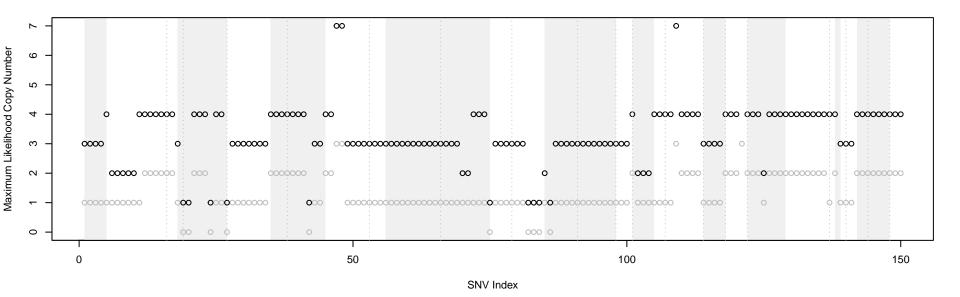


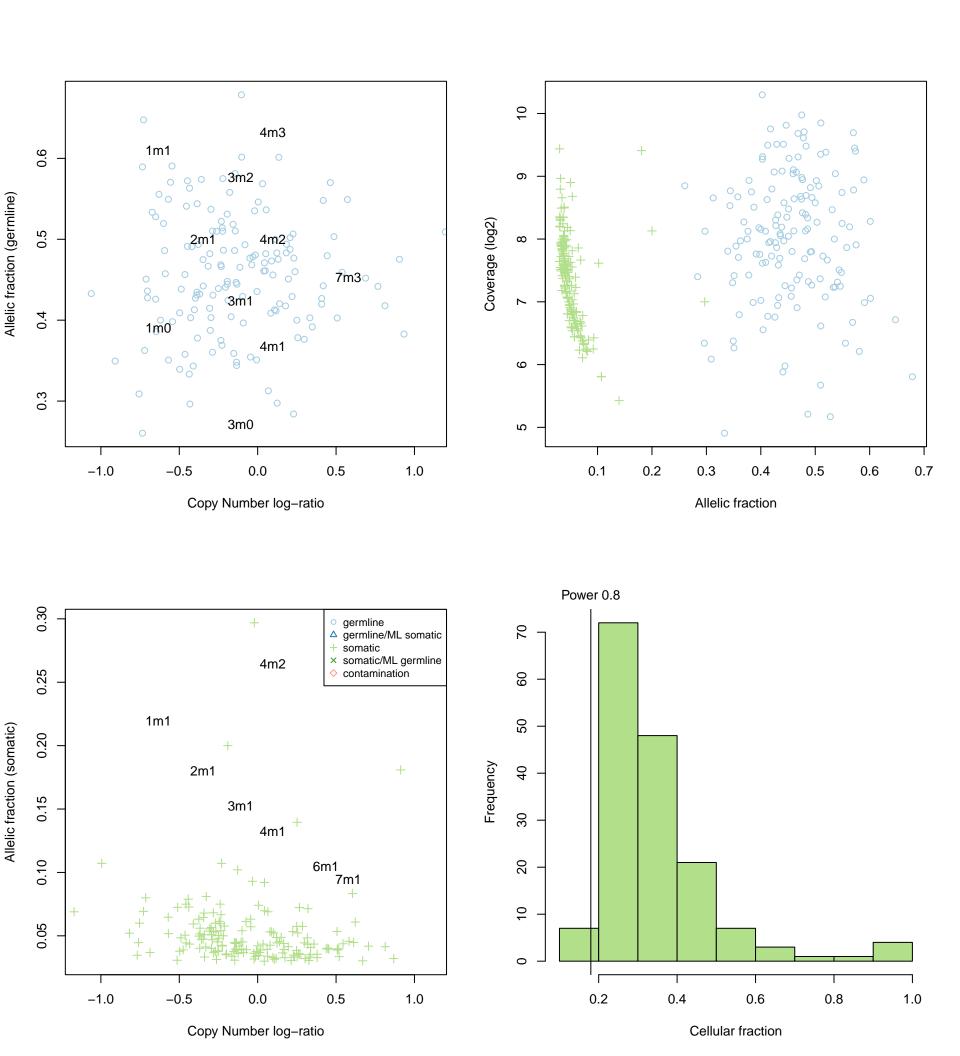




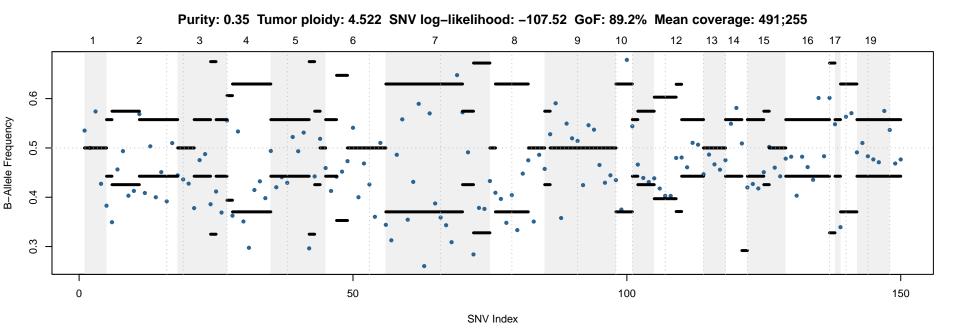
SCNA-fit log-likelihood: -10512.48



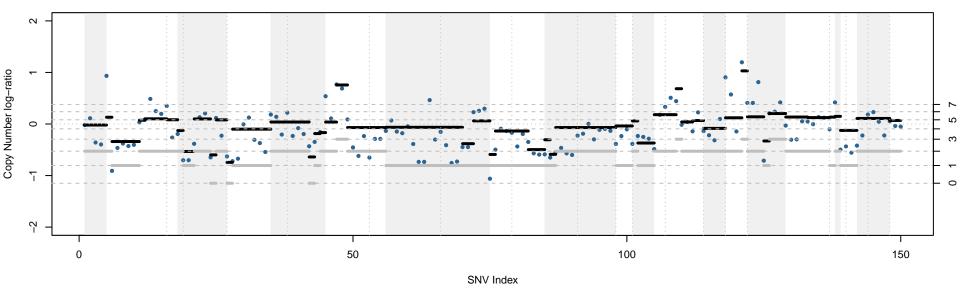


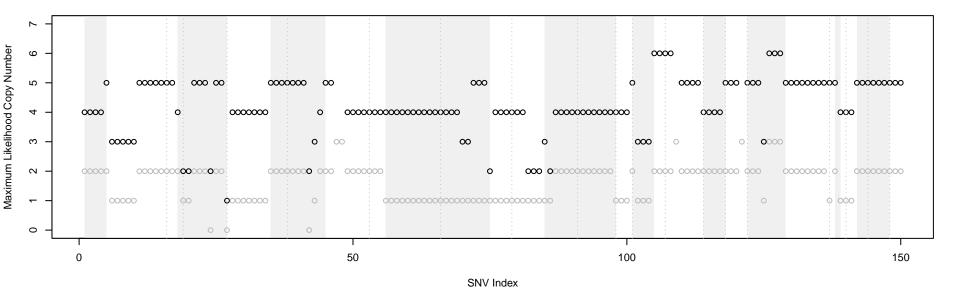


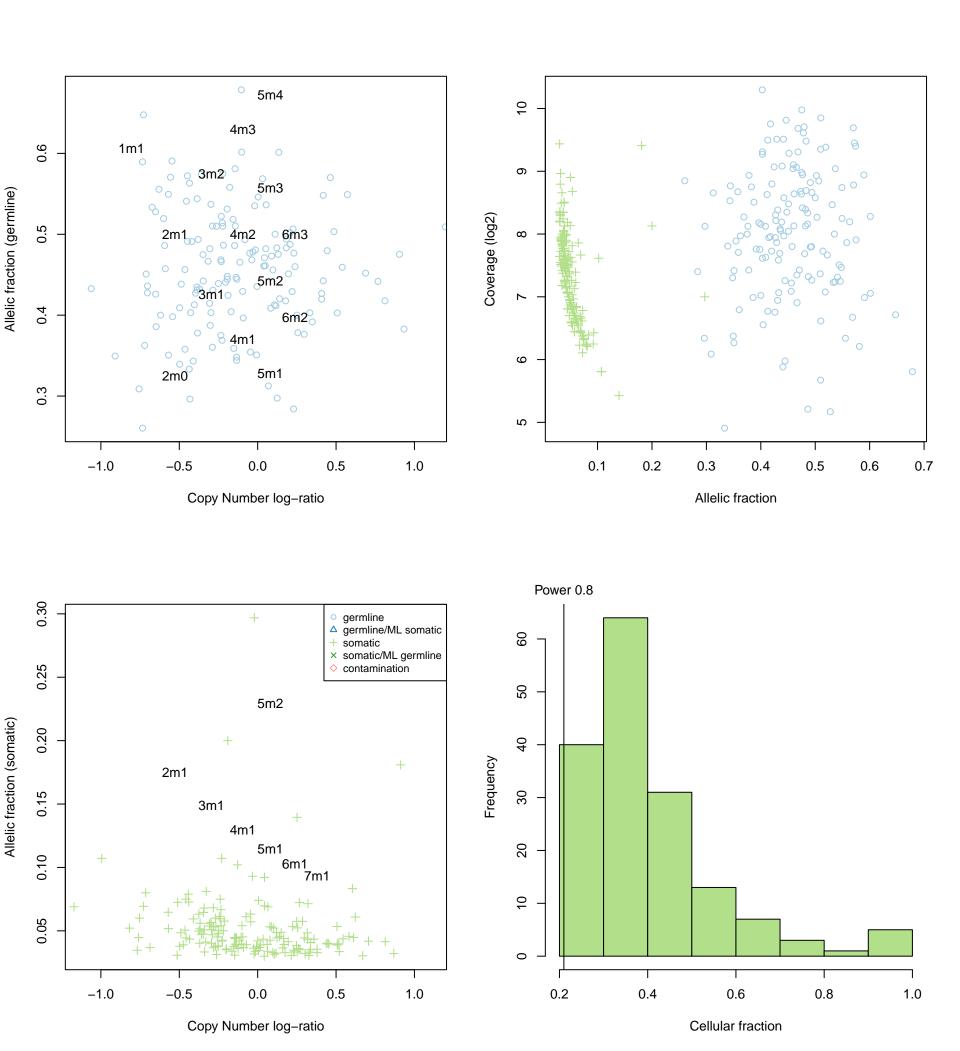
Purity: 0.35 Tumor ploidy: 4.522 2 3 0 5 6 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



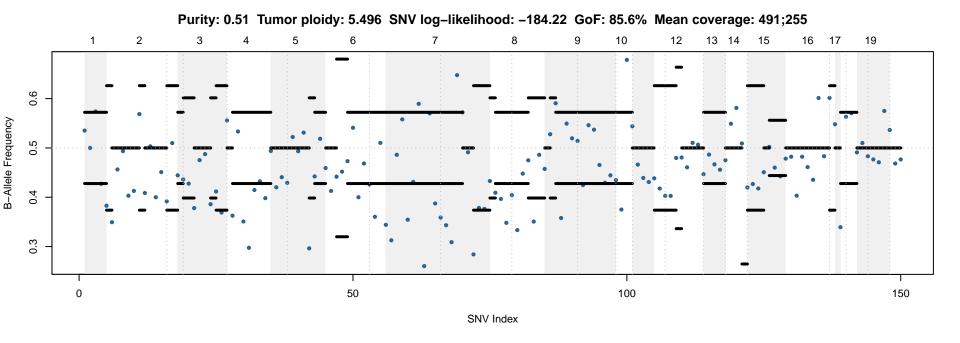
SCNA-fit log-likelihood: -10576.55



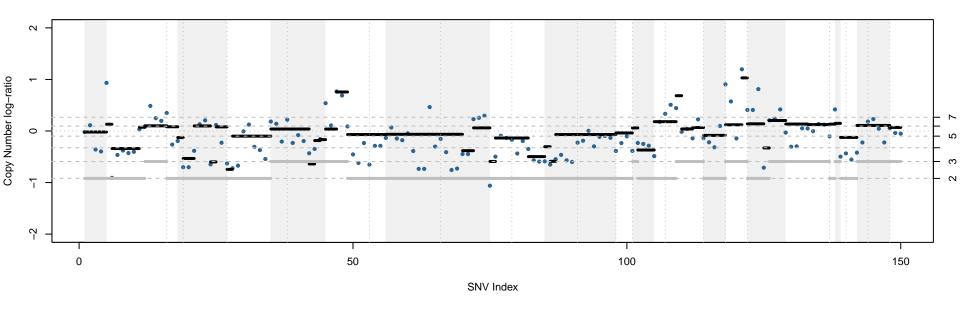


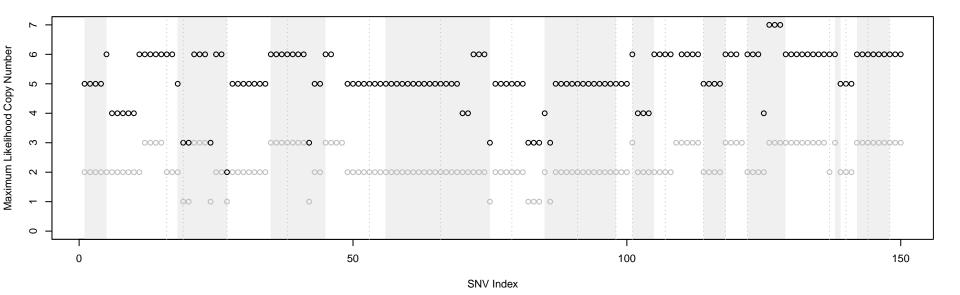


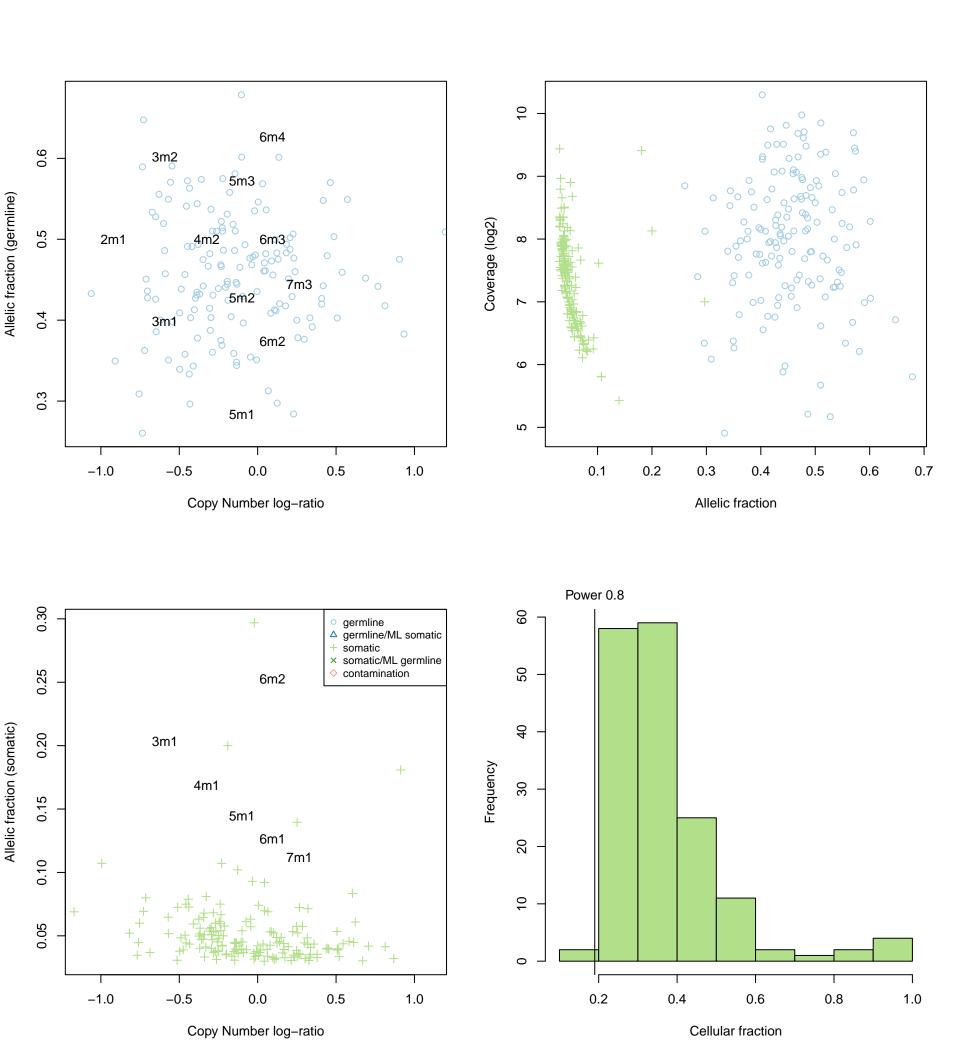
Purity: 0.51 Tumor ploidy: 5.496 6 2 3 5 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio

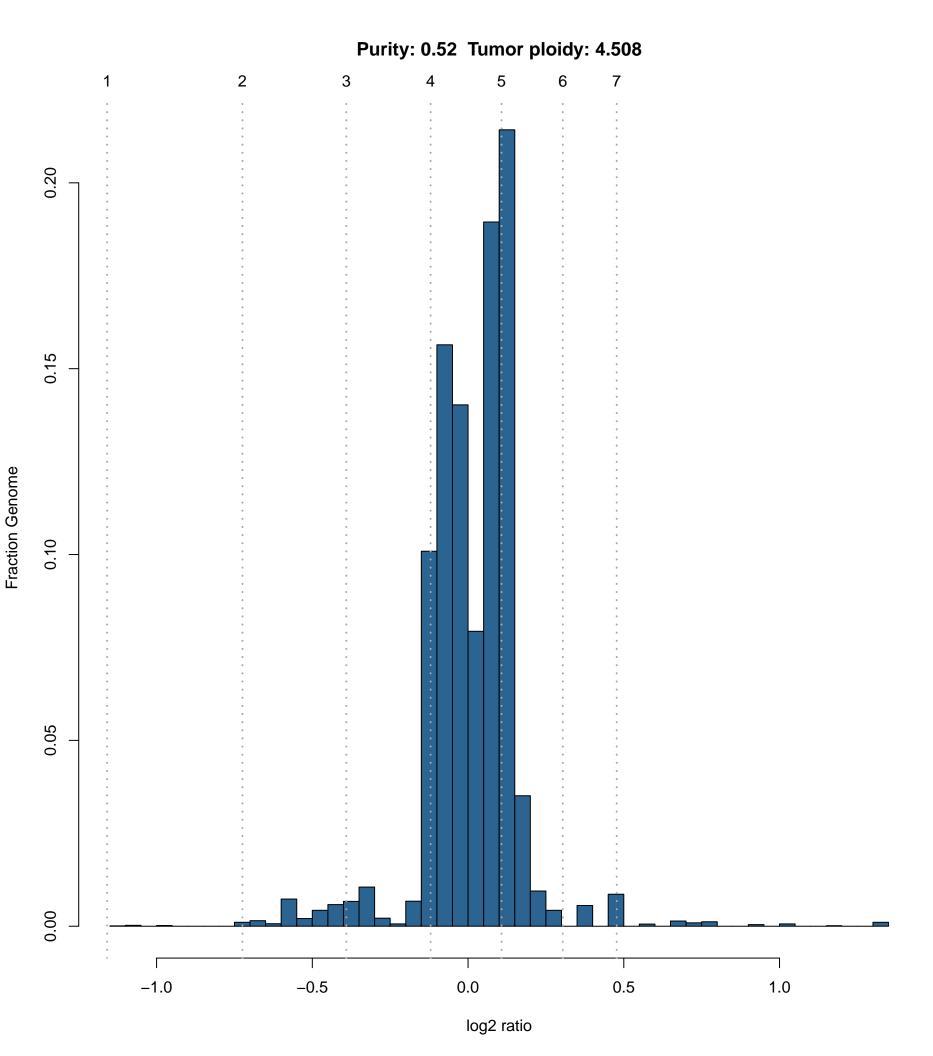


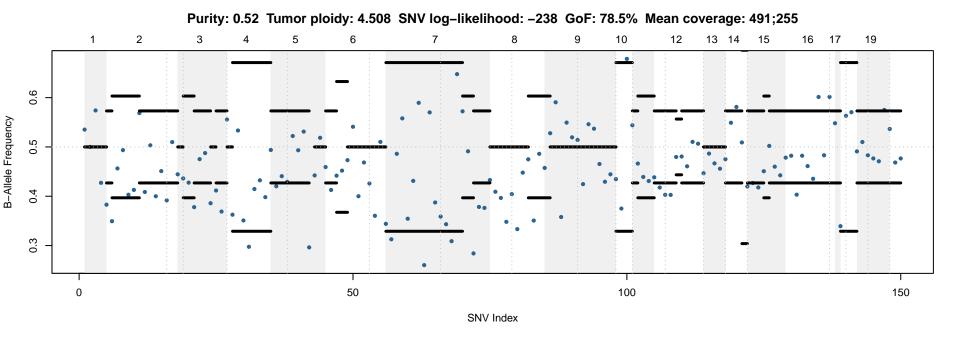
SCNA-fit log-likelihood: -10628.3



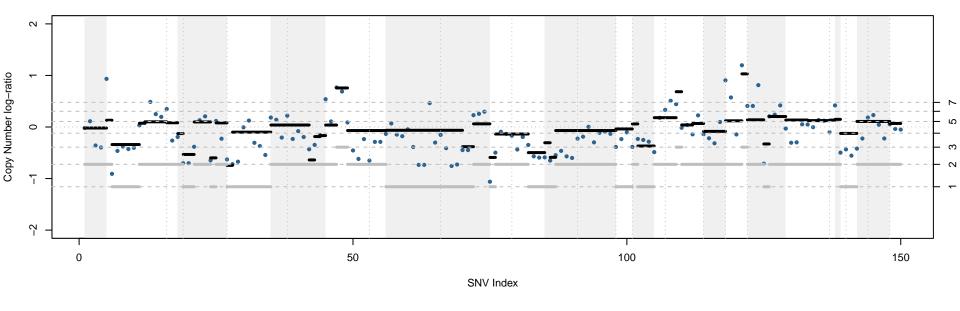


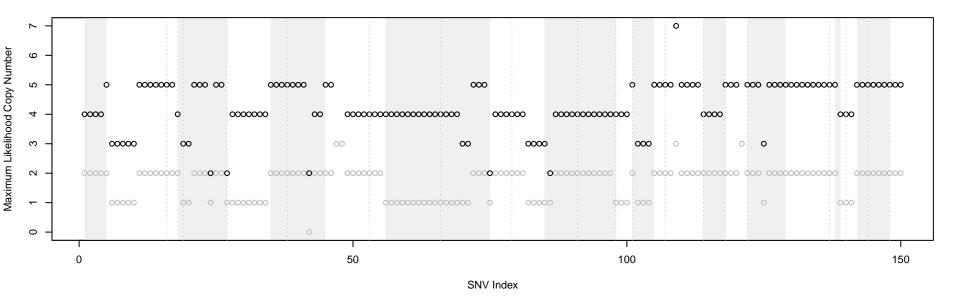


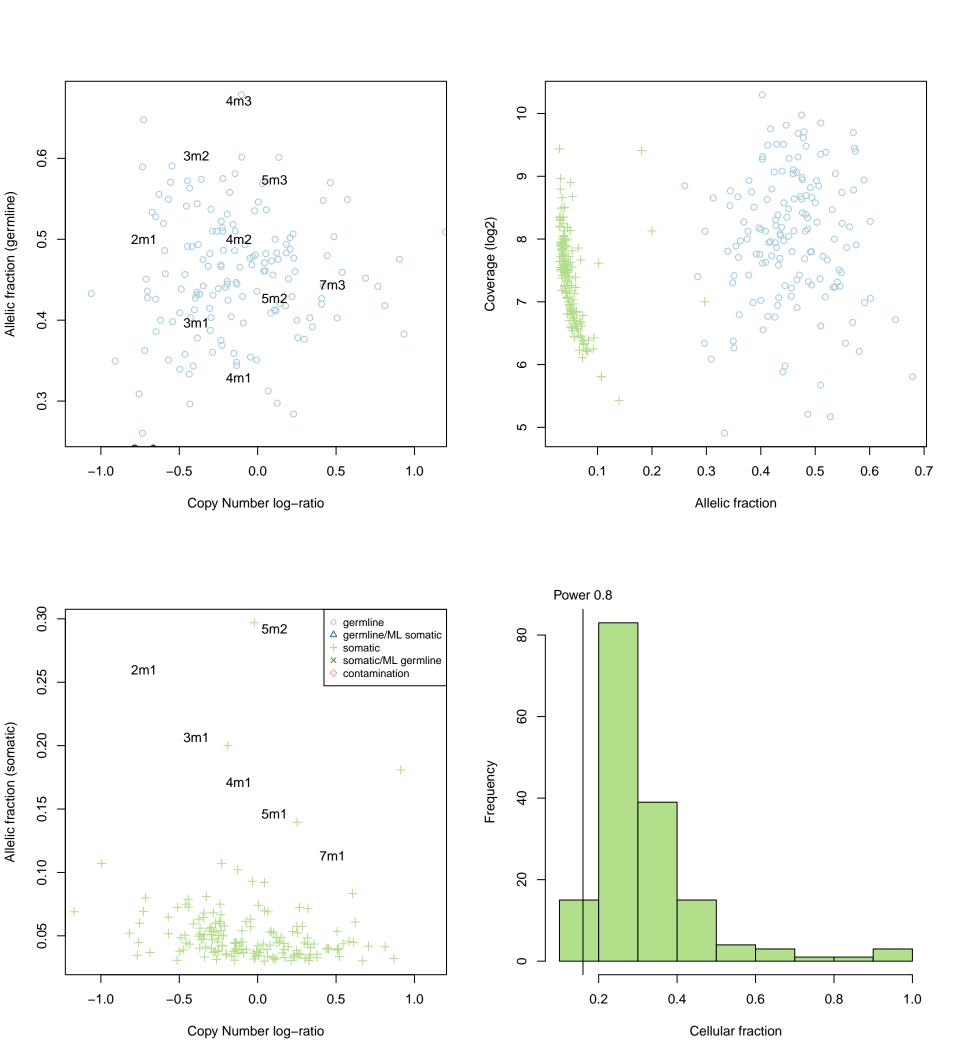




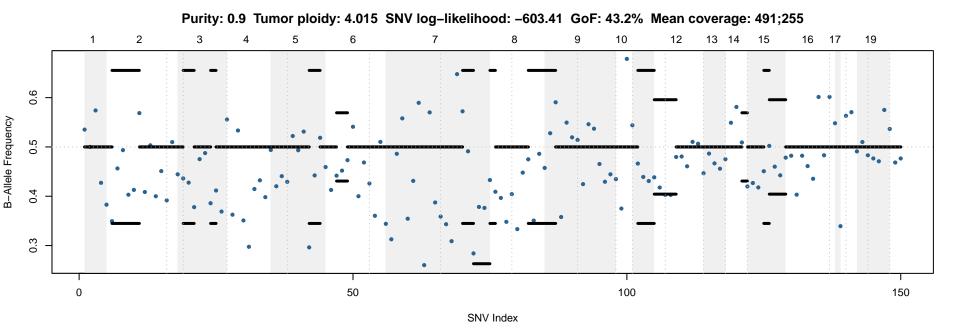
SCNA-fit log-likelihood: -10599.6



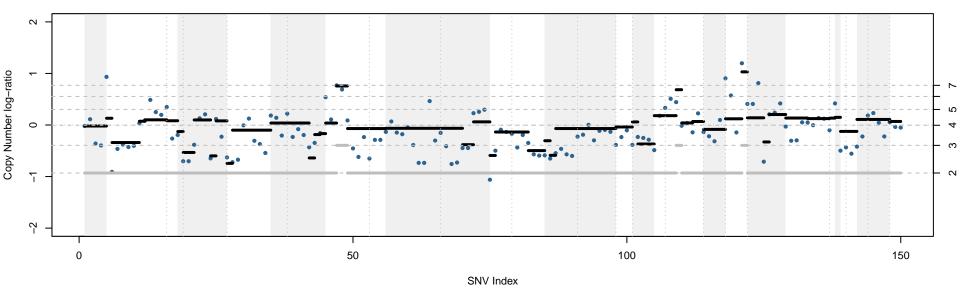


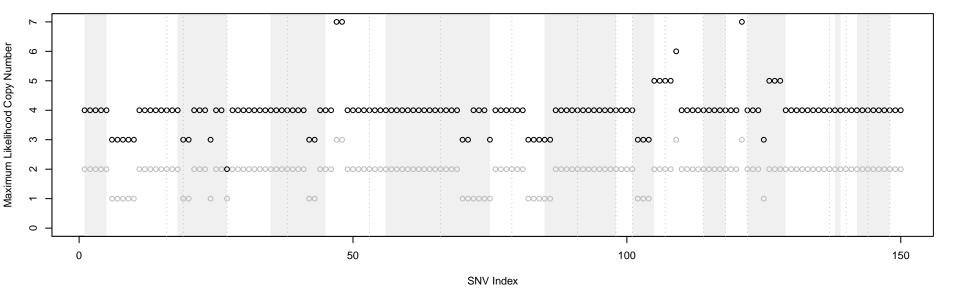


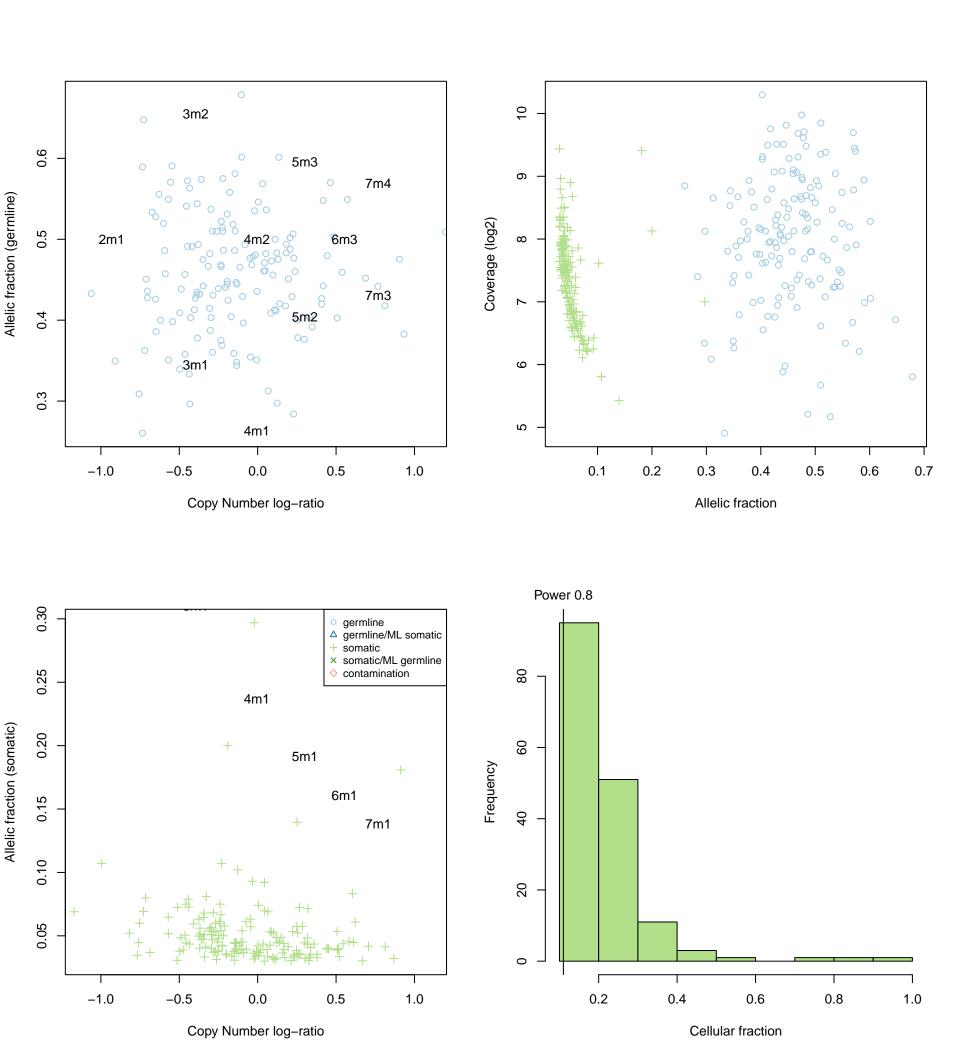
Purity: 0.9 Tumor ploidy: 4.015 2 3 7 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



SCNA-fit log-likelihood: -10879.31







Purity: 0.59 Tumor ploidy: 1.99 2 6 7 5 Fraction Genome 0.05 0.00

0.0

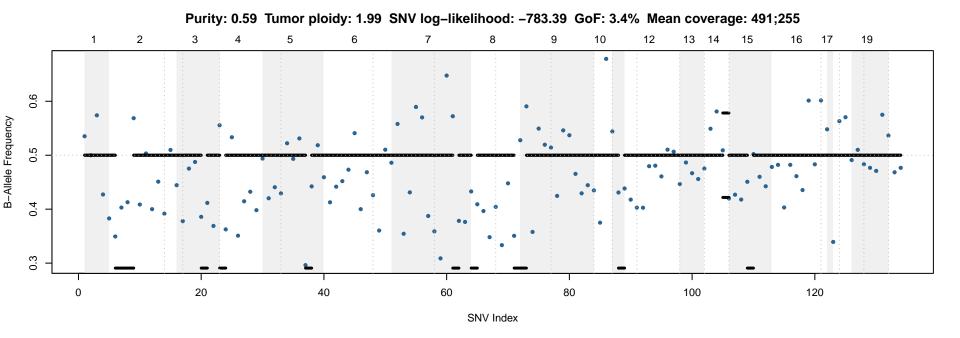
log2 ratio

0.5

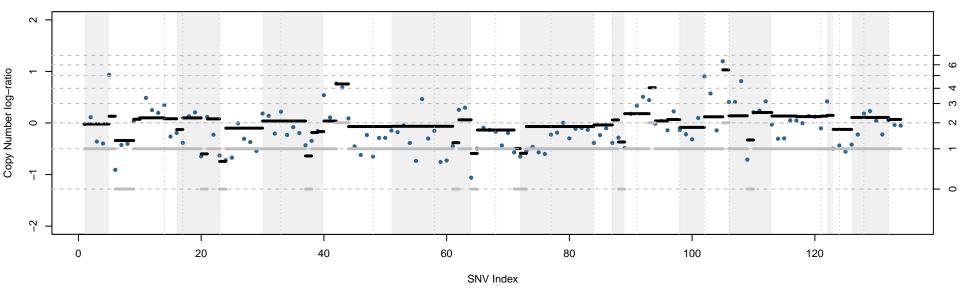
1.0

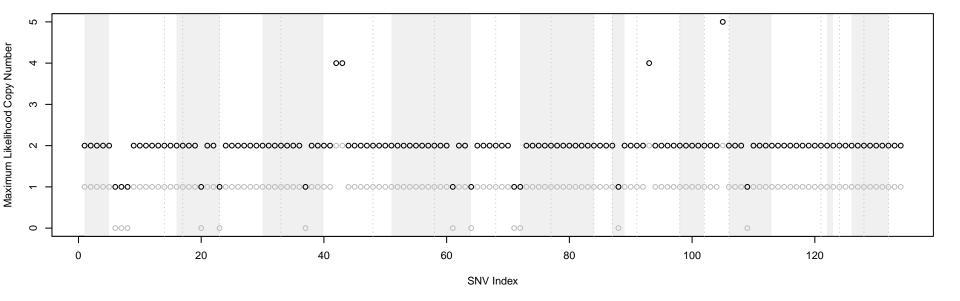
-1.0

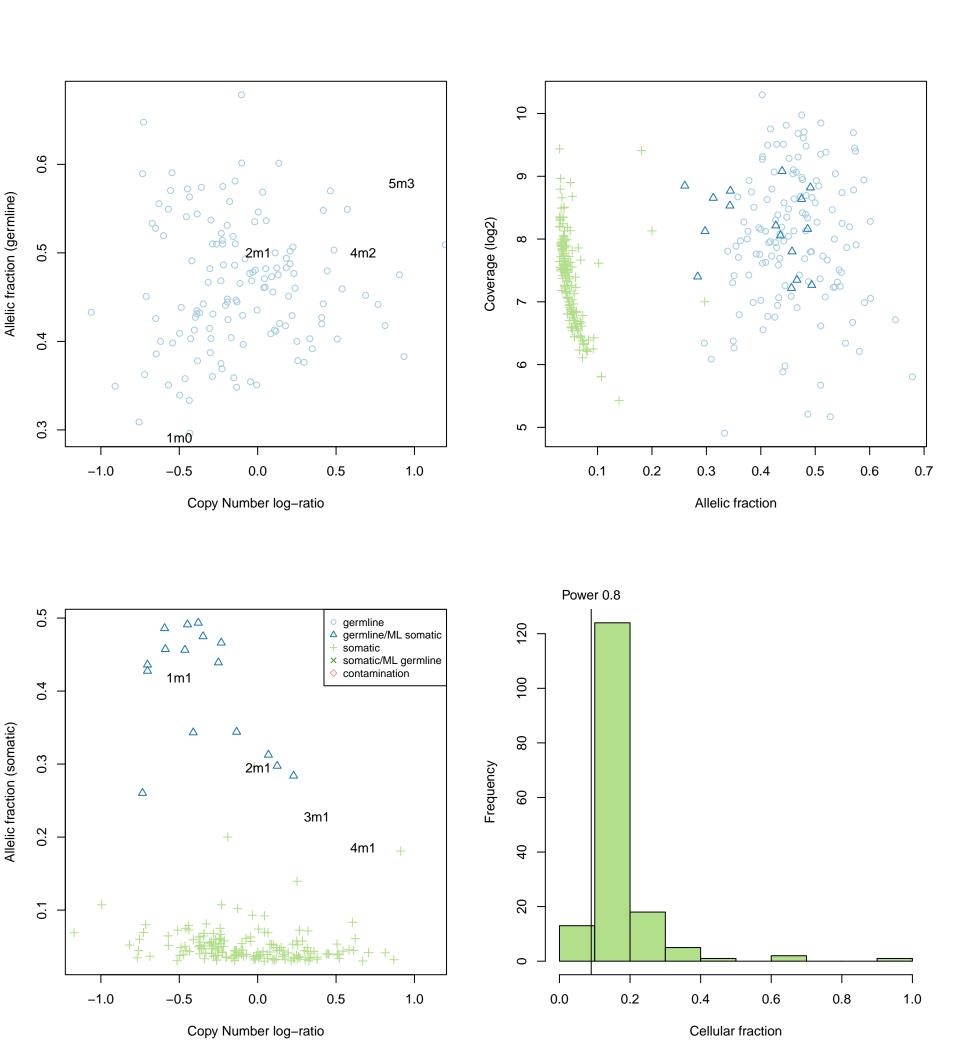
-0.5



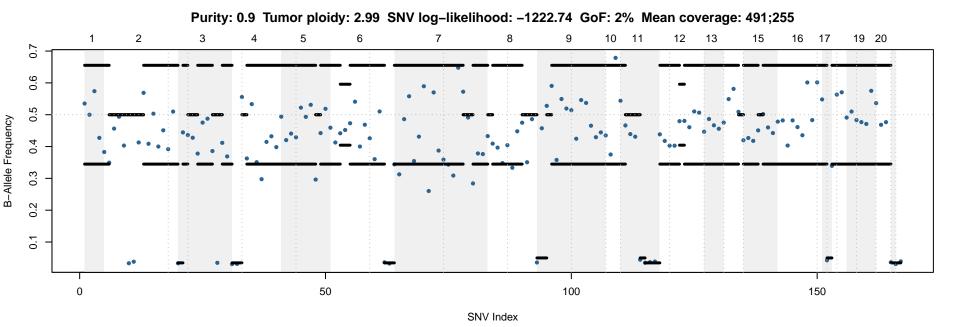
SCNA-fit log-likelihood: -10869.78







Purity: 0.9 Tumor ploidy: 2.99 2 3 5 6 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 log2 ratio



SCNA-fit log-likelihood: -10881.62

