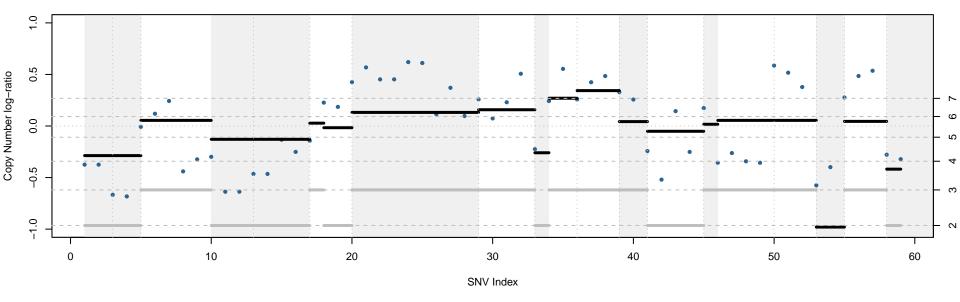
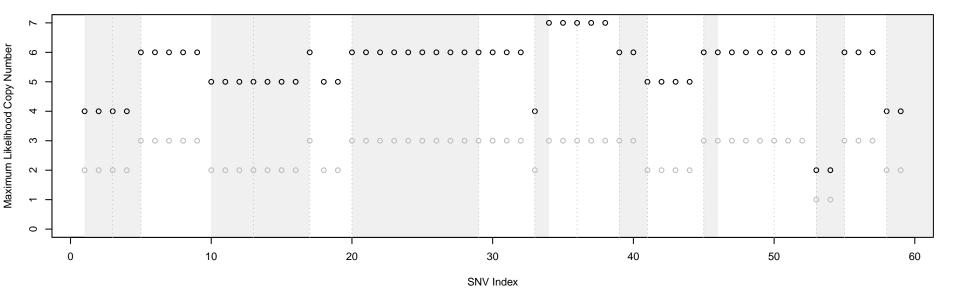
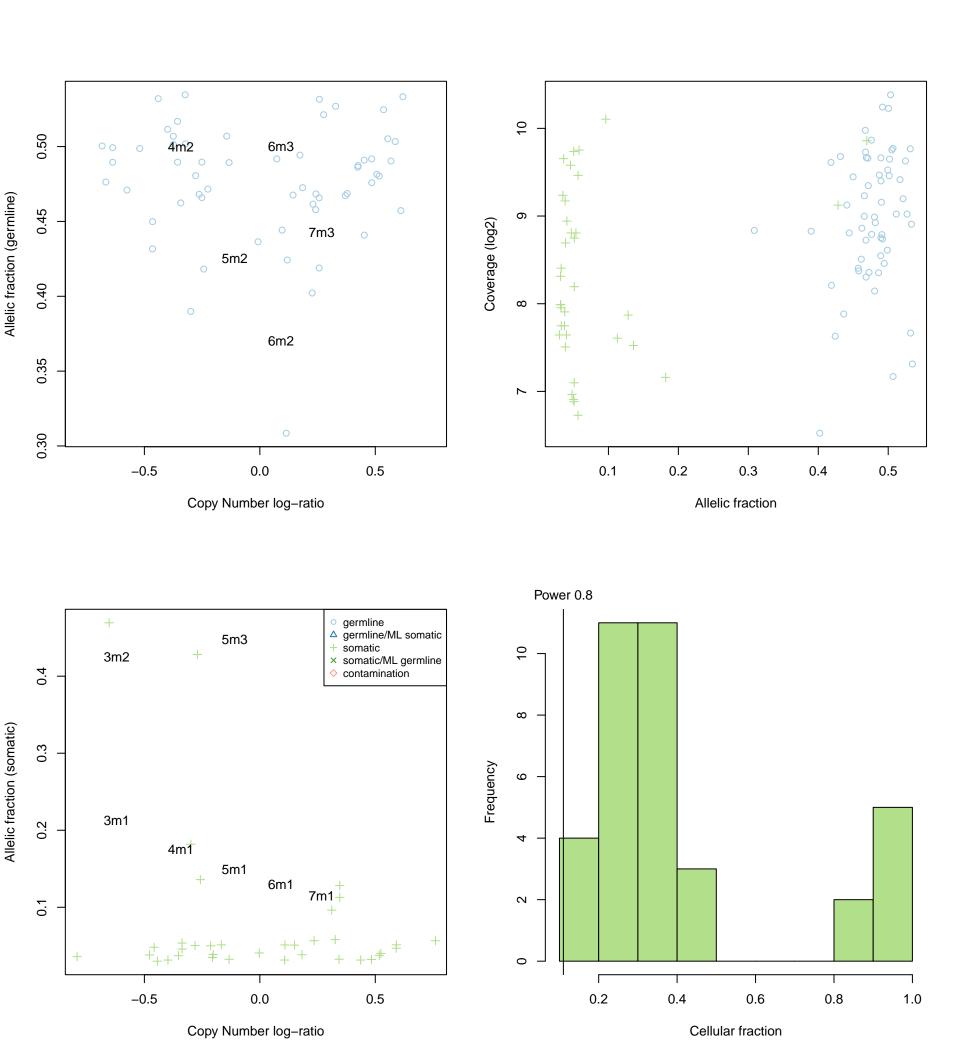


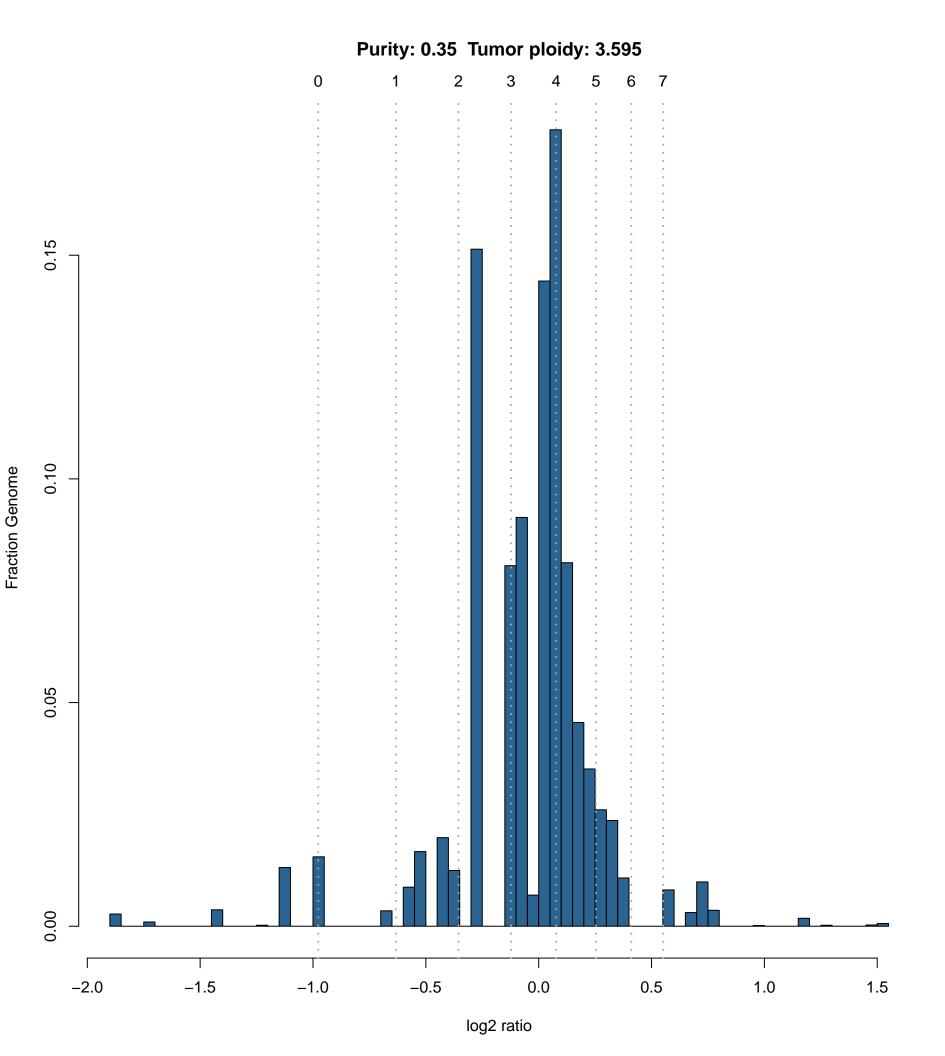
SCNA-fit log-likelihood: -18807.03

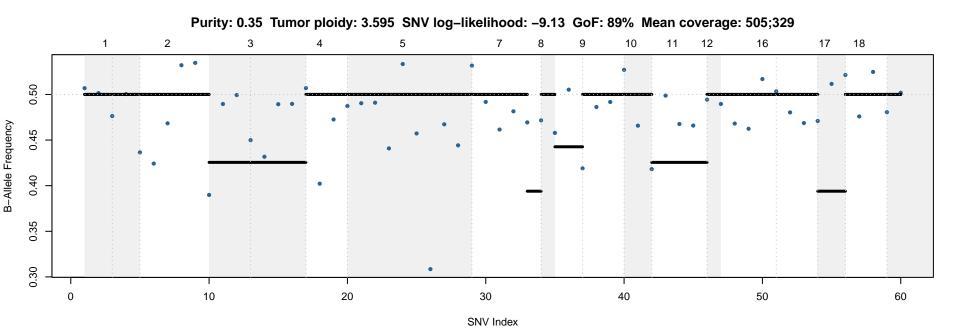
SNV Index



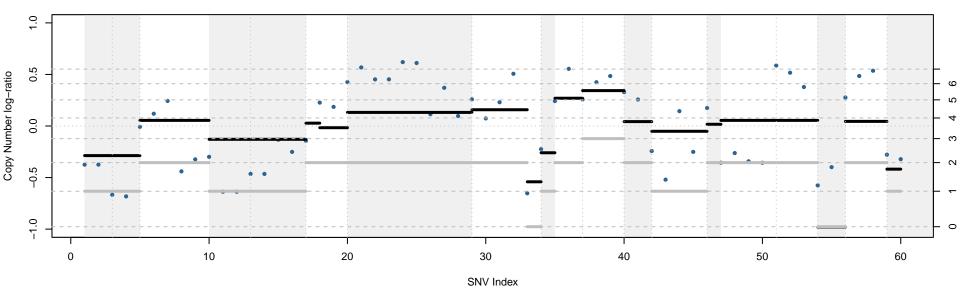


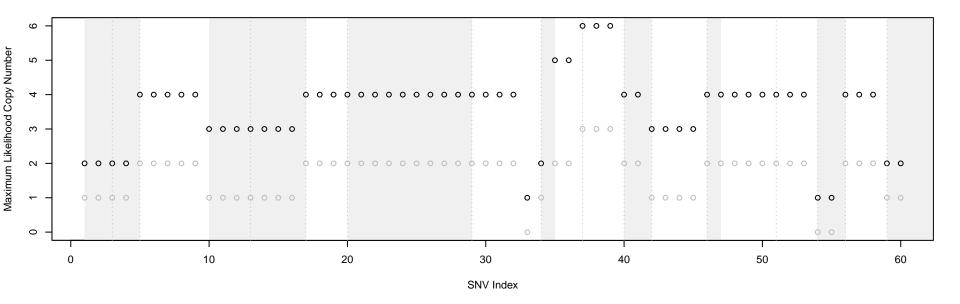


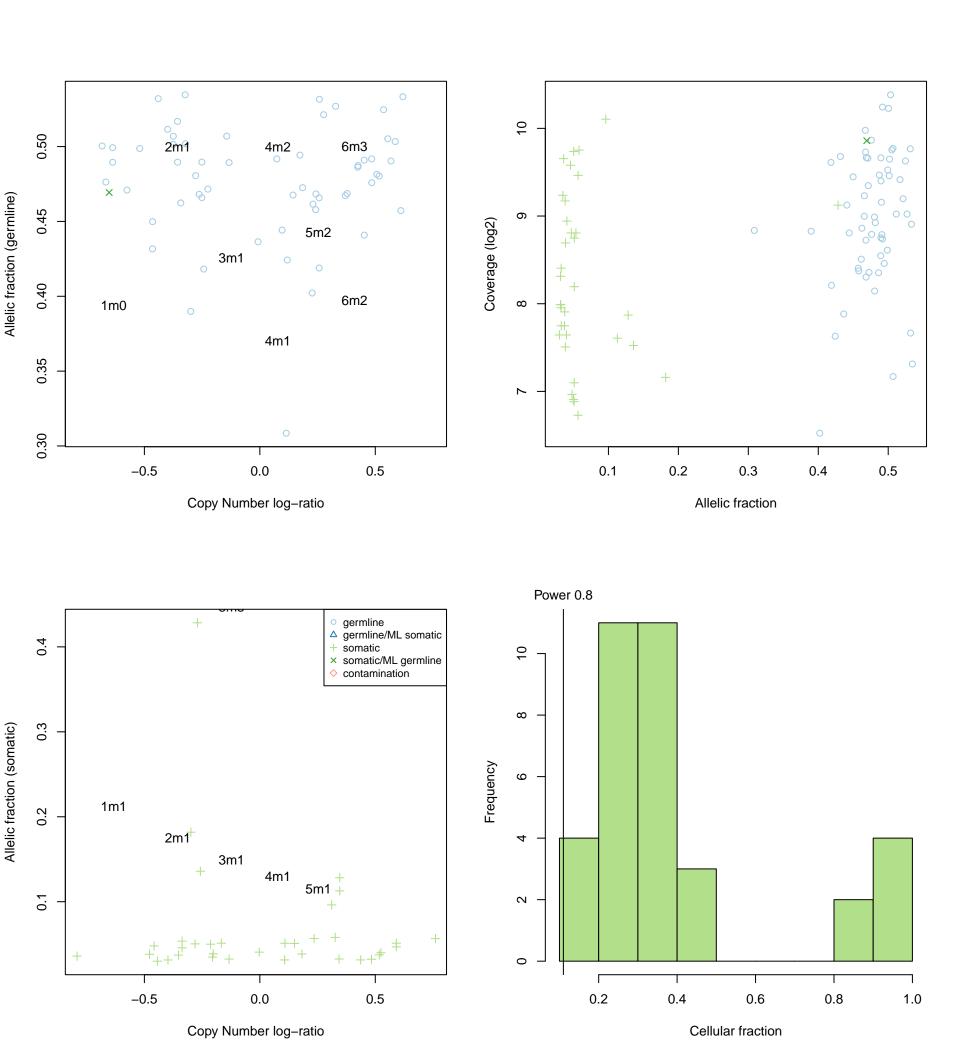


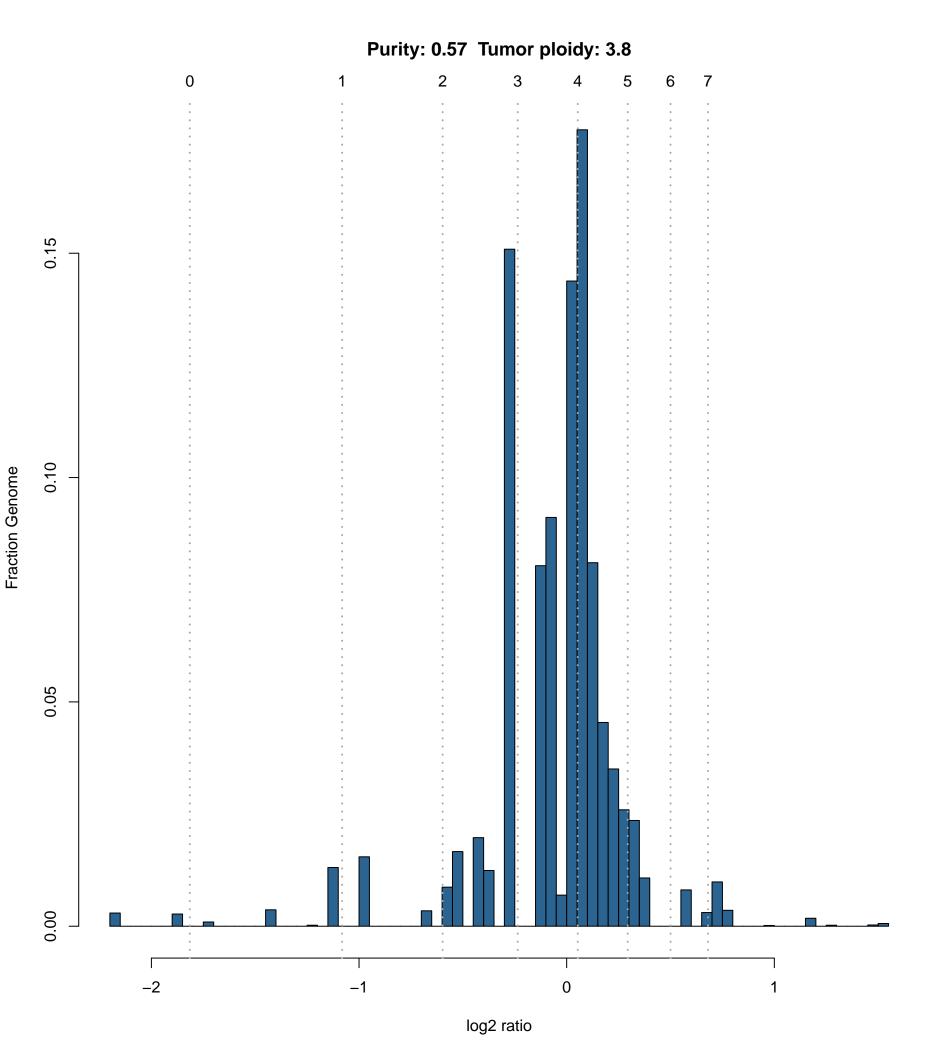


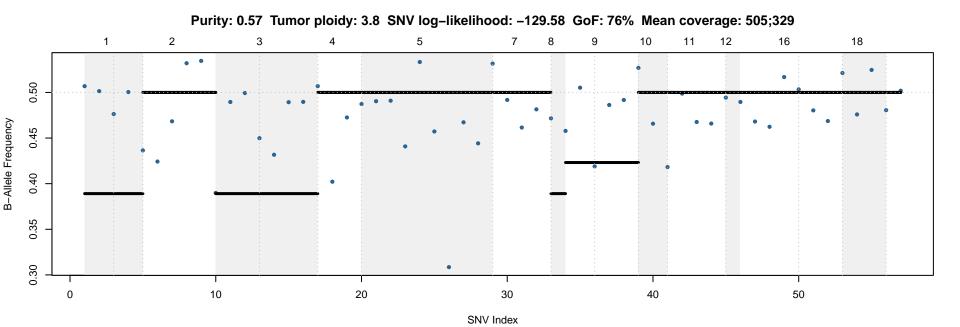
SCNA-fit log-likelihood: -18960.86



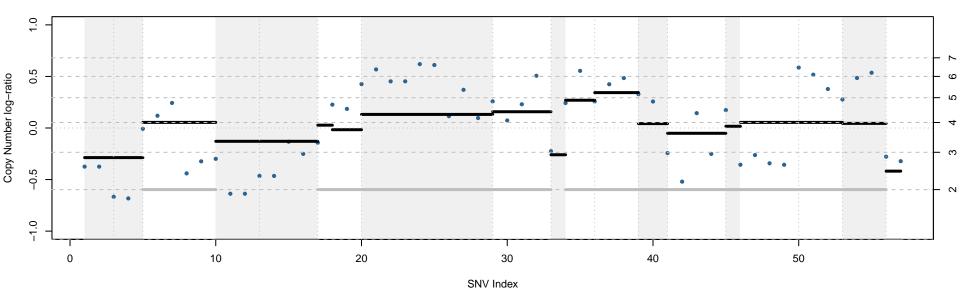


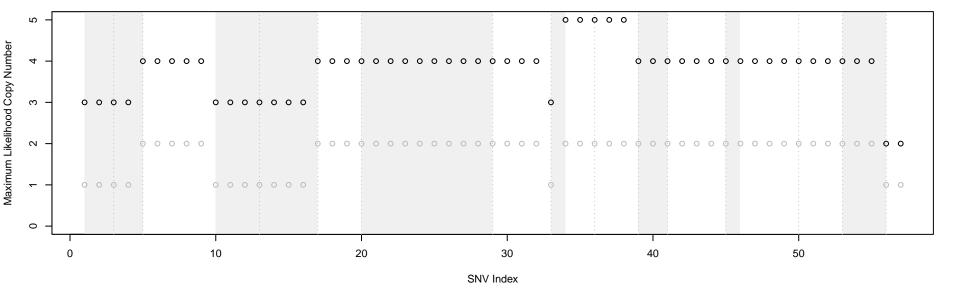


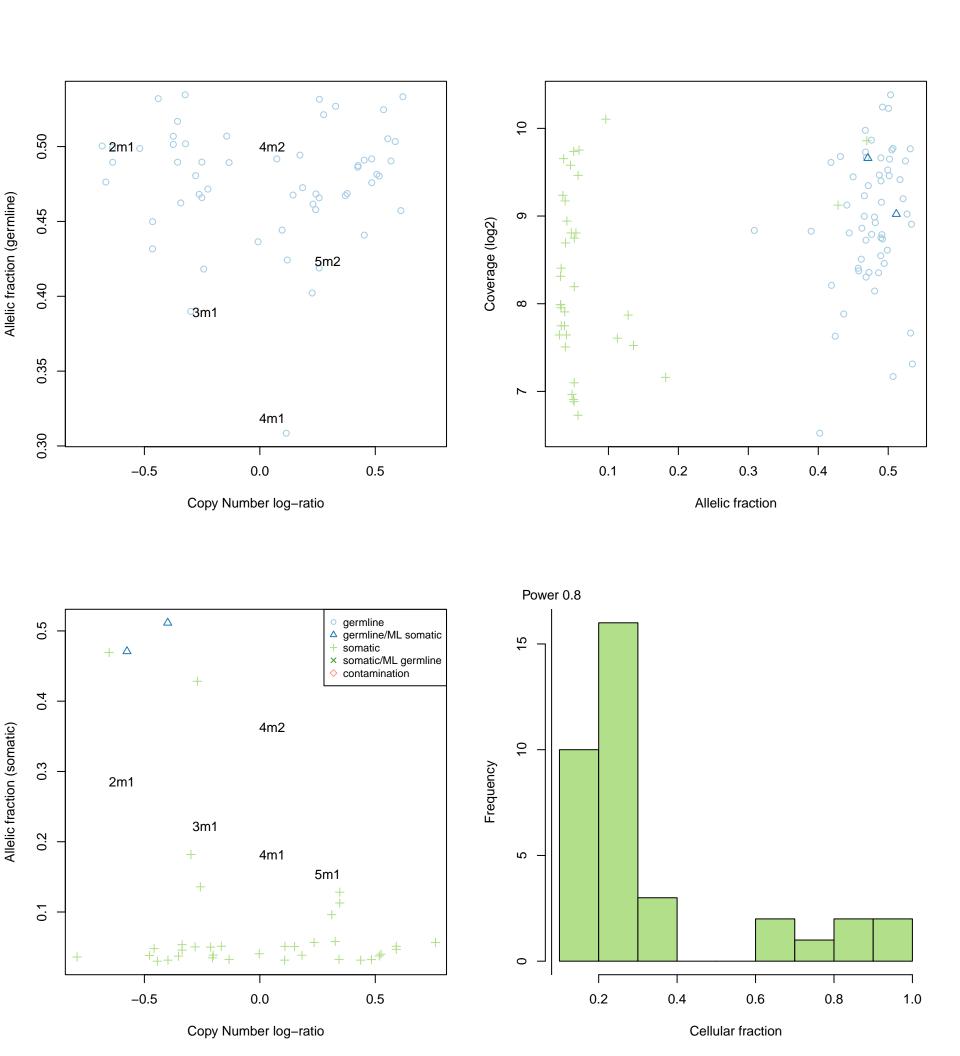




SCNA-fit log-likelihood: -18741.58







Purity: 0.73 Tumor ploidy: 5.912 6 2 3 5 7 0.10 Fraction Genome 0.05 0.00 -2 -1 0 1 log2 ratio

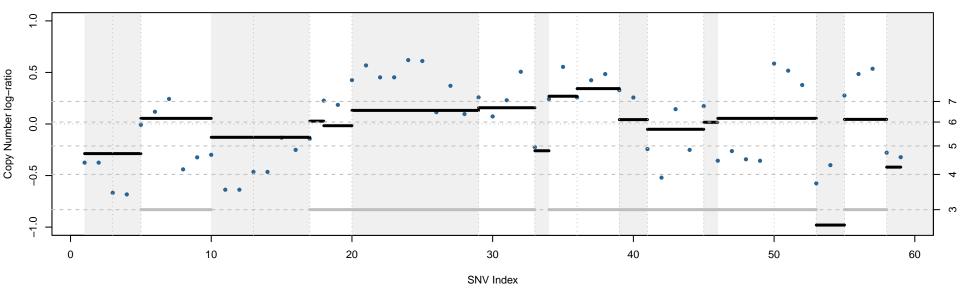
Purity: 0.73 Tumor ploidy: 5.912 SNV log-likelihood: -100.2 GoF: 86.2% Mean coverage: 505;329

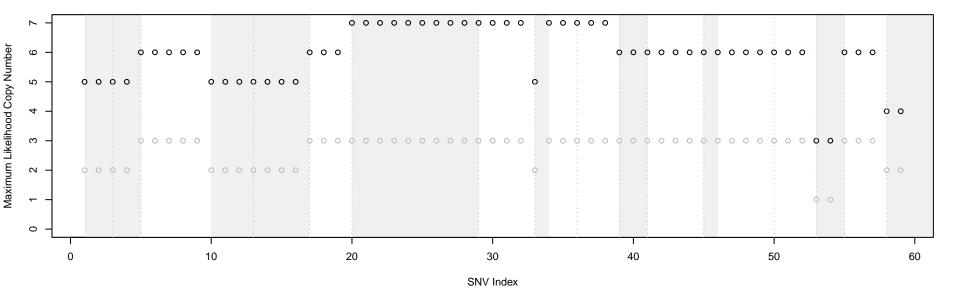
1 2 3 4 5 7 8 9 10 11 12 16 17 18

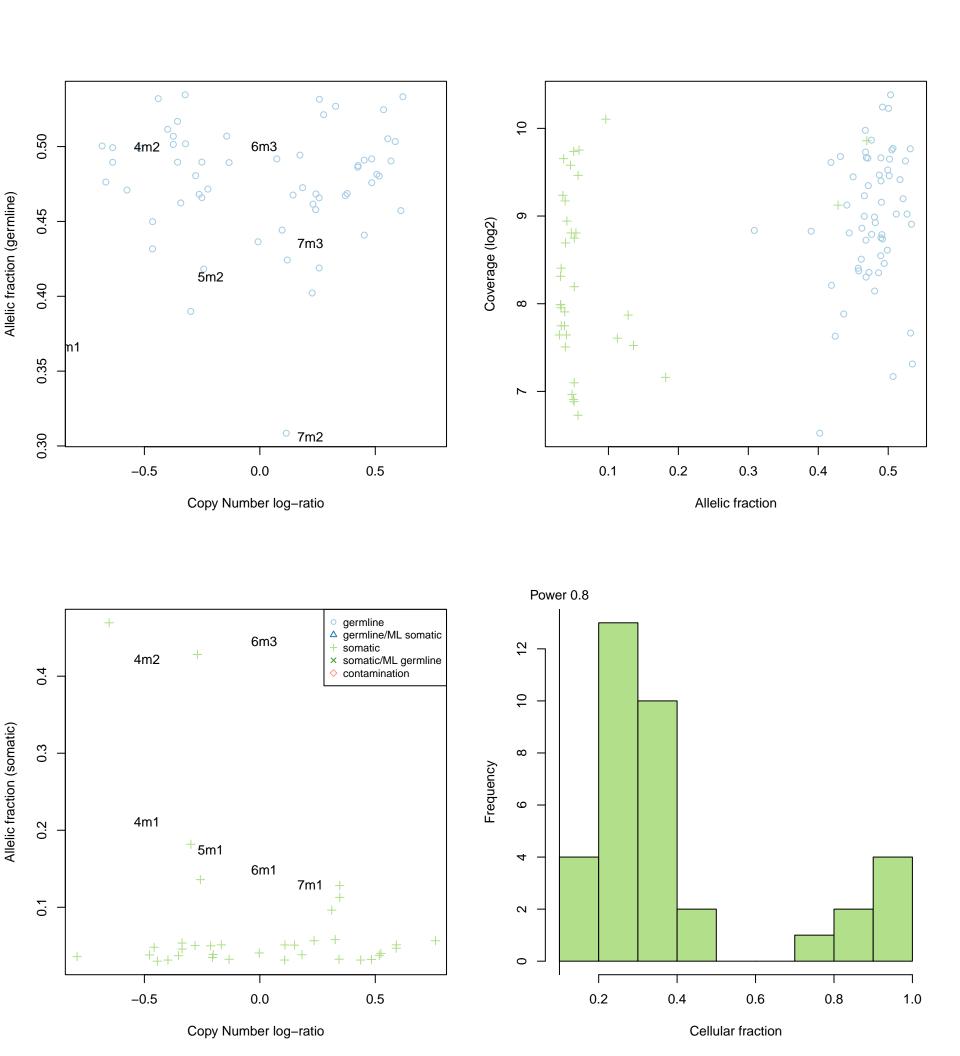
Ogroup of the control of t

SCNA-fit log-likelihood: -18848.45

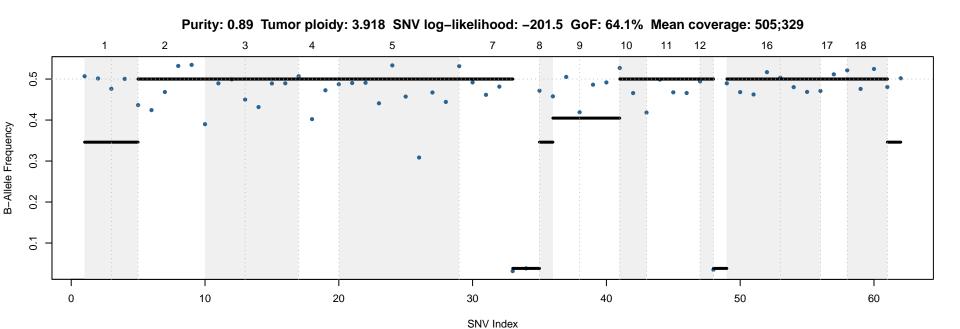
SNV Index



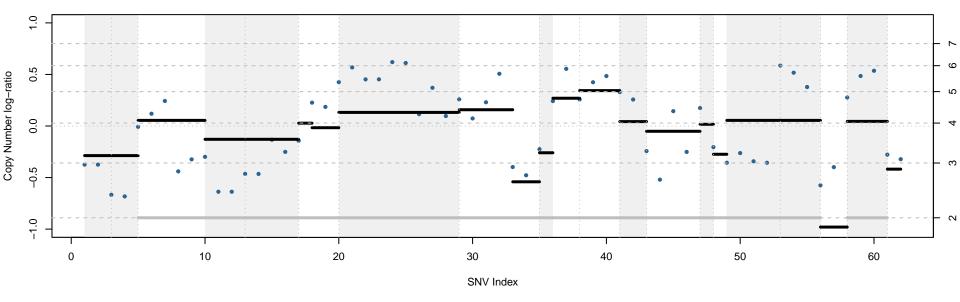


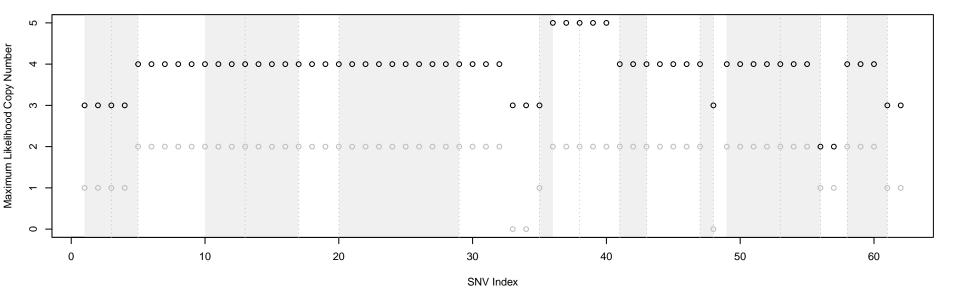


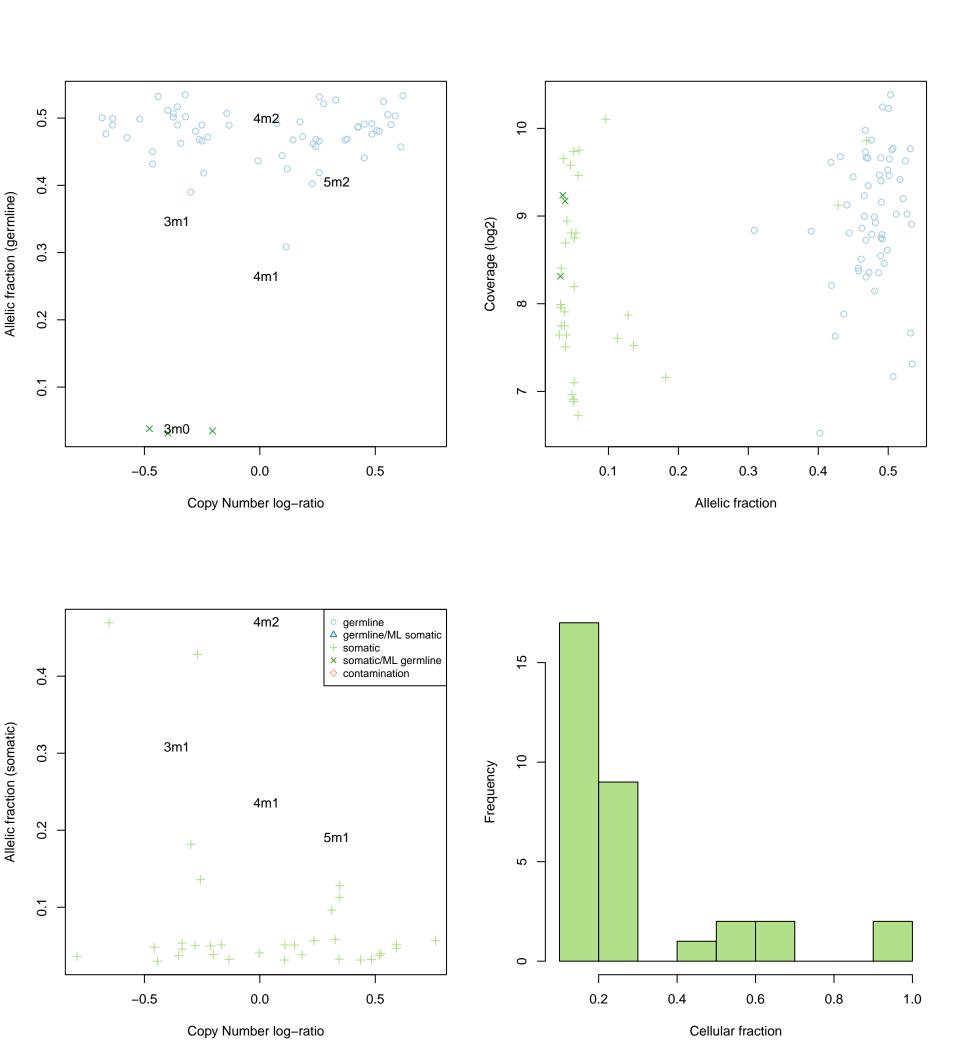
Purity: 0.89 Tumor ploidy: 3.918 3 6 7 0.10 Fraction Genome 0.02 0.00 -2 -1 0 log2 ratio

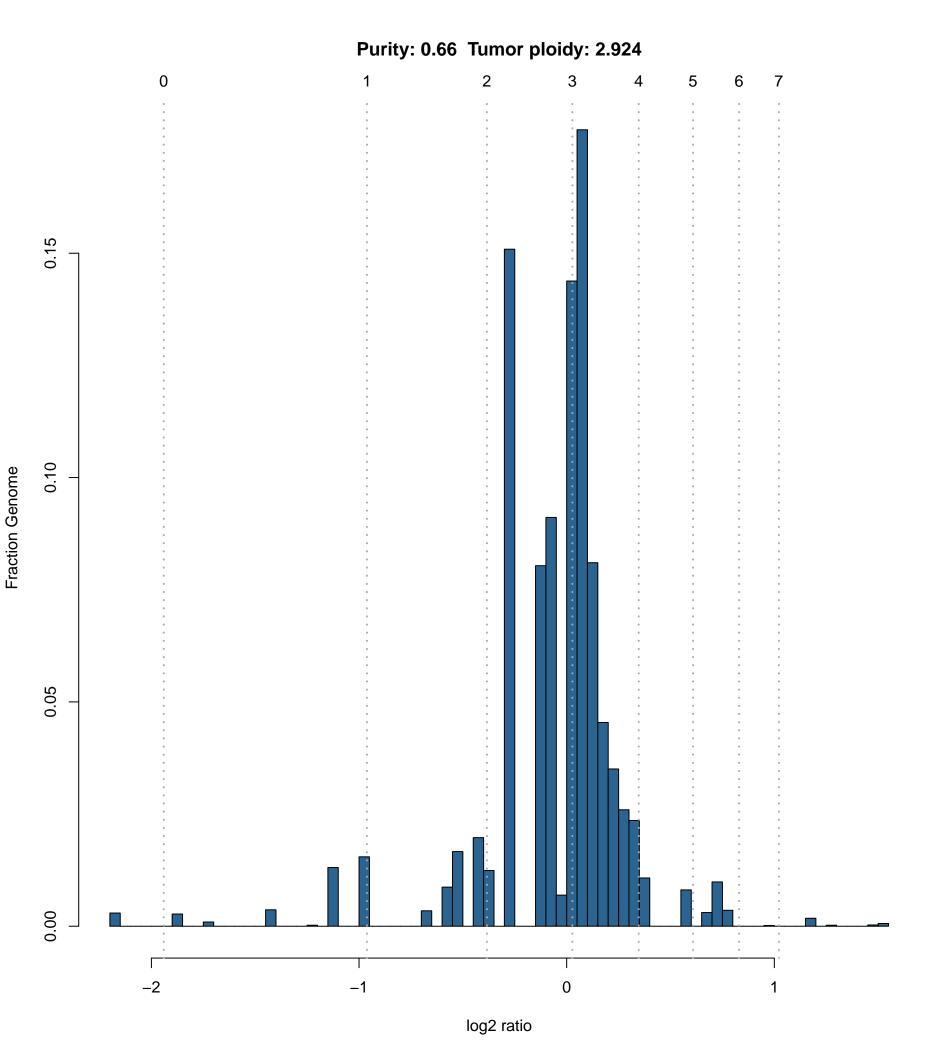


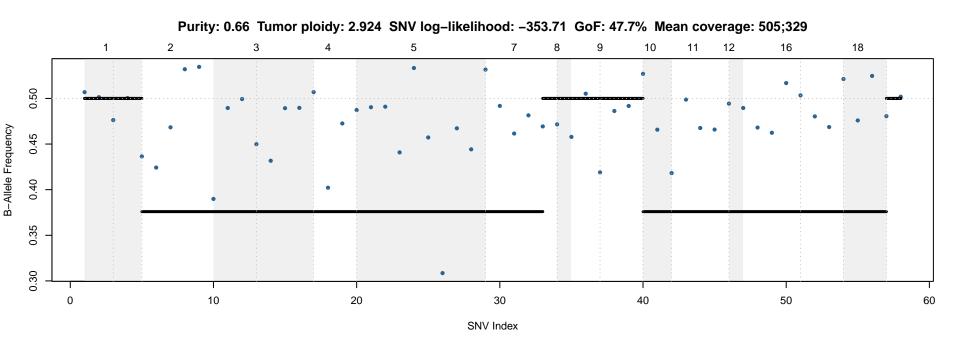
SCNA-fit log-likelihood: -18811.55



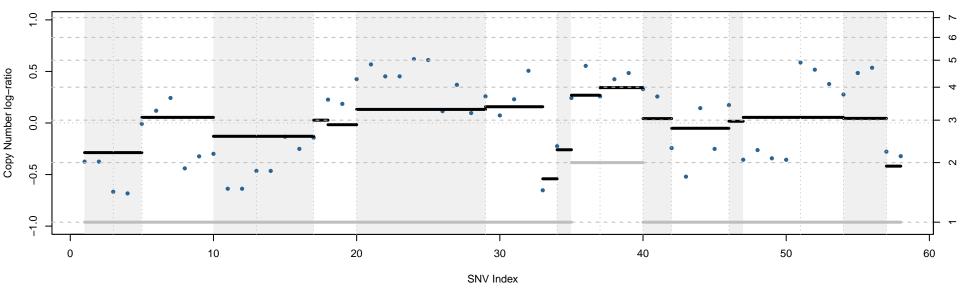


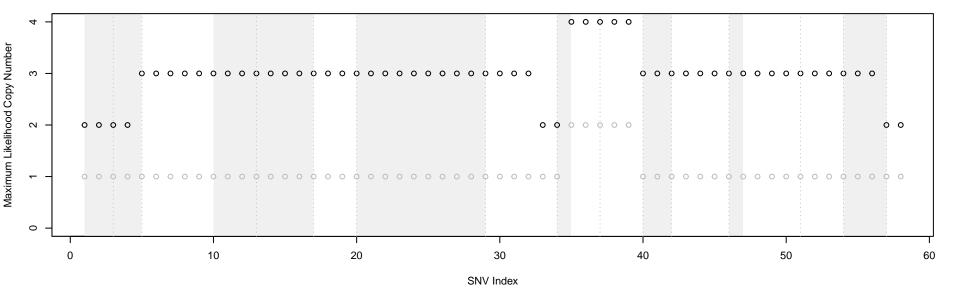


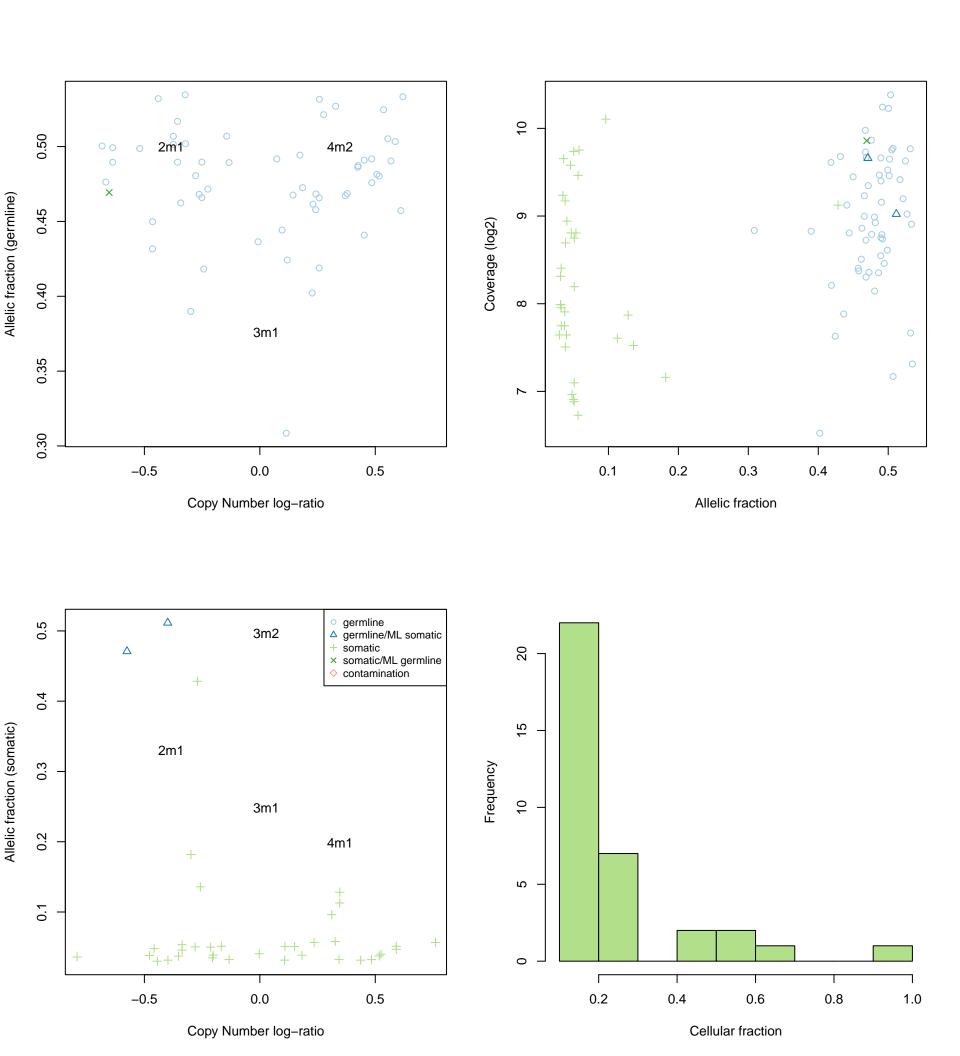




SCNA-fit log-likelihood: -18788.07

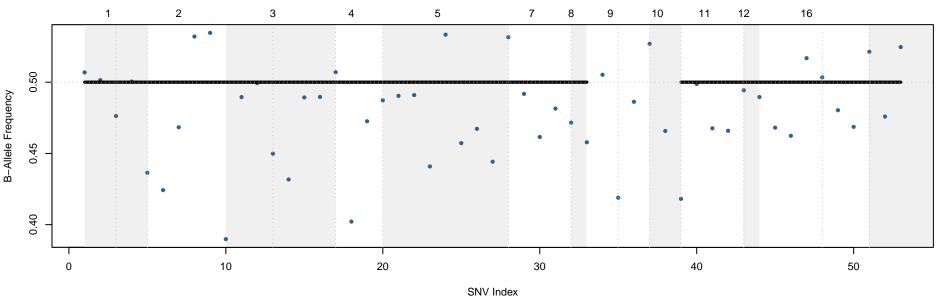




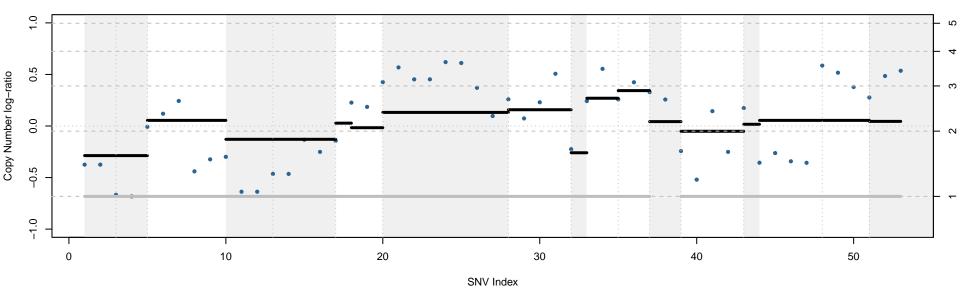


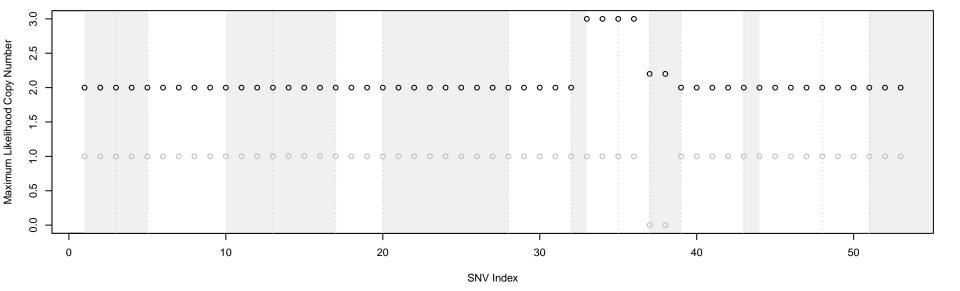
Purity: 0.71 Tumor ploidy: 2.099 0 2 7 3 5 6 0.10 Fraction Genome 0.05 0.00 -2 -1 0 log2 ratio

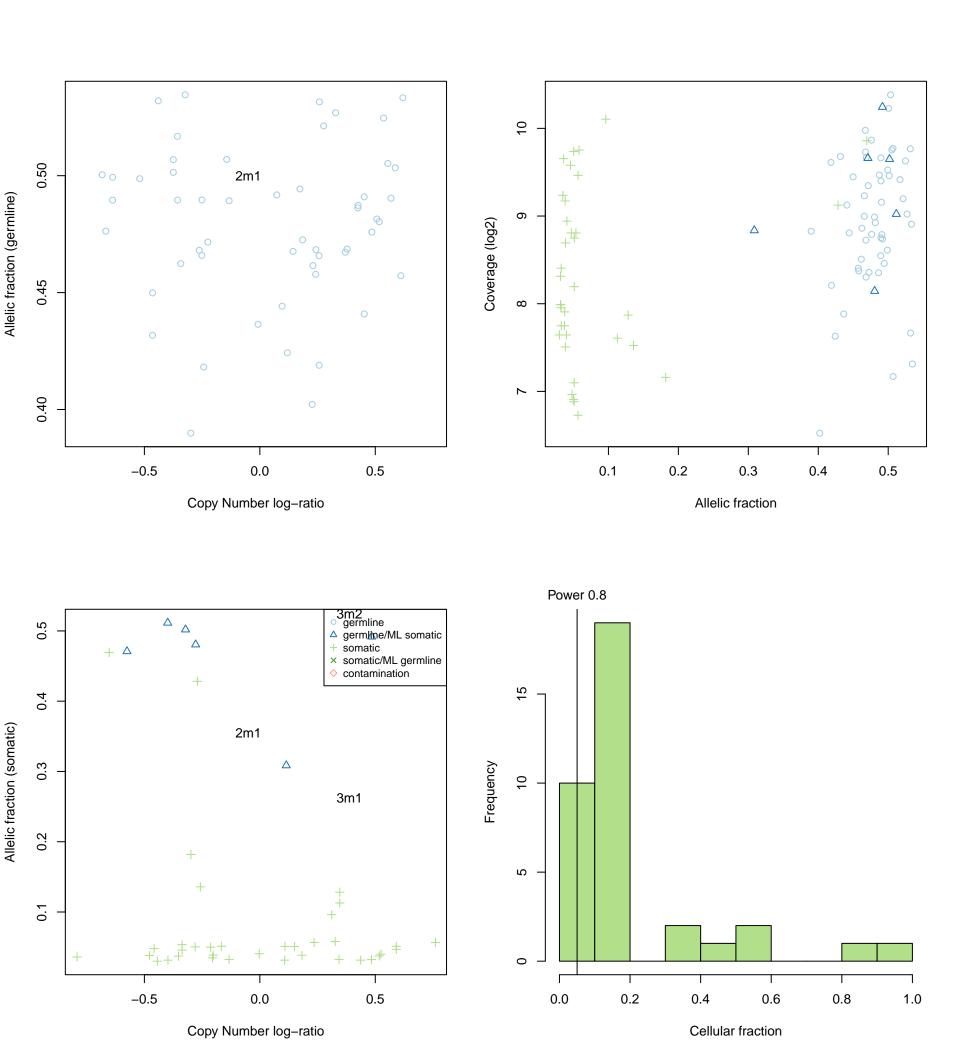




SCNA-fit log-likelihood: -19216.36

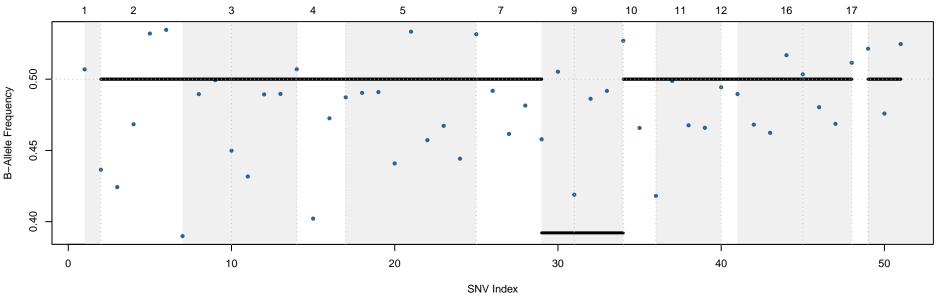






Purity: 0.55 Tumor ploidy: 1.935 2 3 6 0.10 Fraction Genome 0.05 0.00 -2 -1 0 1 log2 ratio





SCNA-fit log-likelihood: -19397.45

