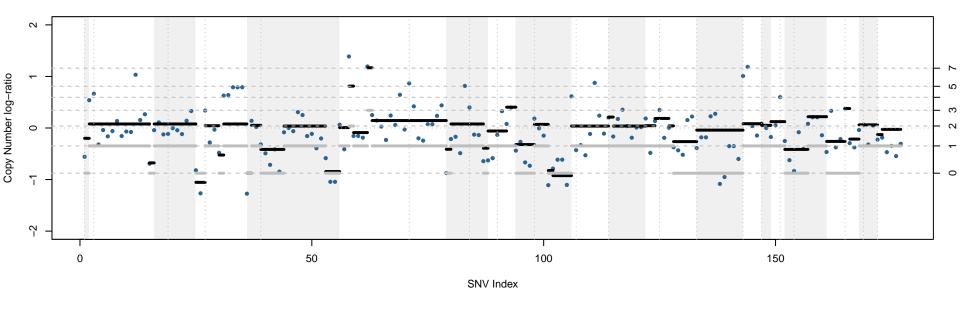
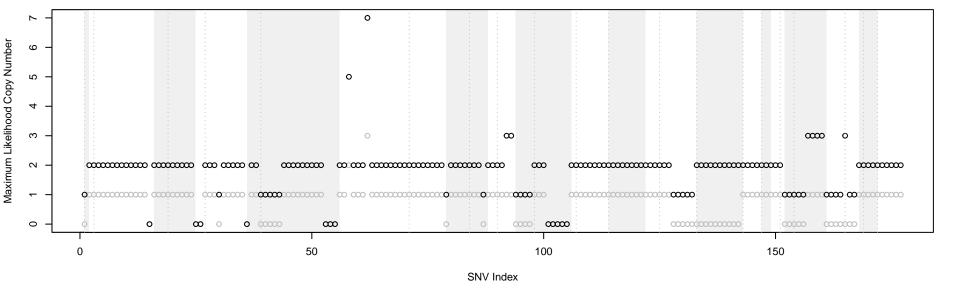
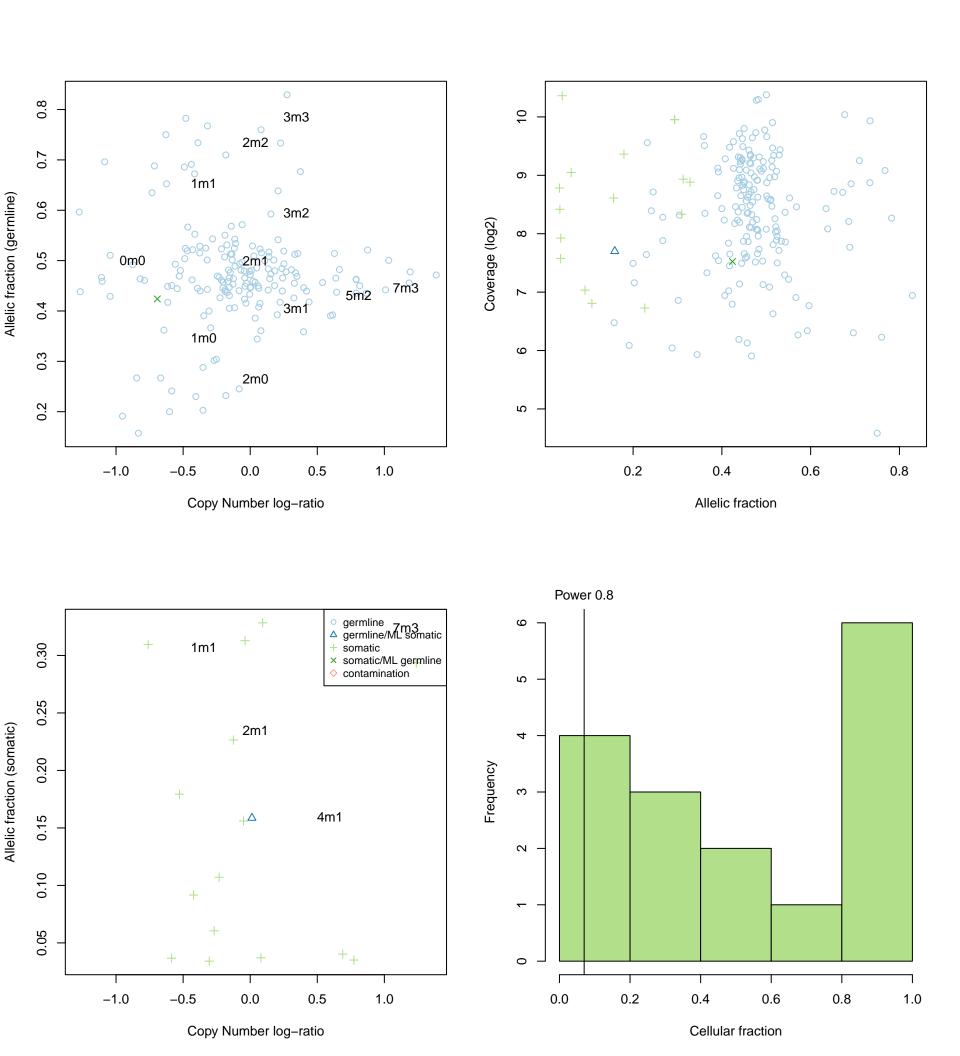


SCNA-fit log-likelihood: -13100







Purity: 0.45 Tumor ploidy: 3.856 2 3 5 6 1 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00

-1.0

-0.5

0.0

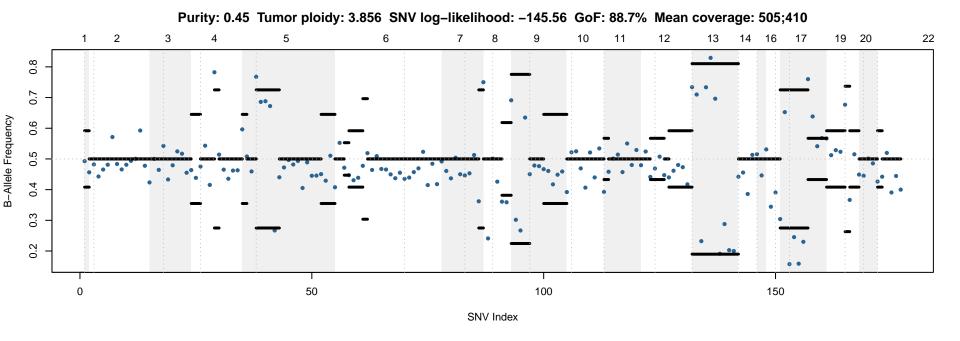
0.5

log2 ratio

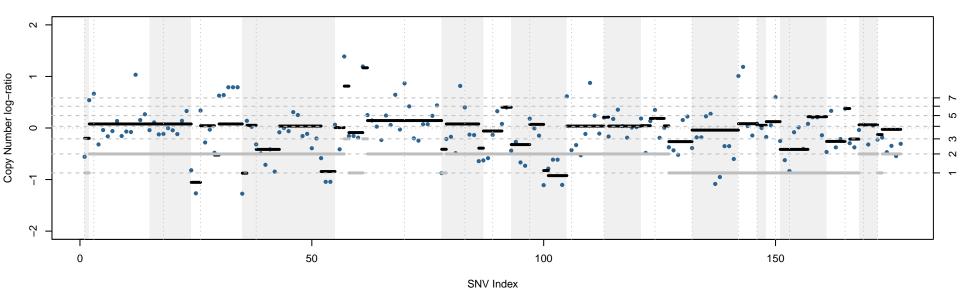
1.0

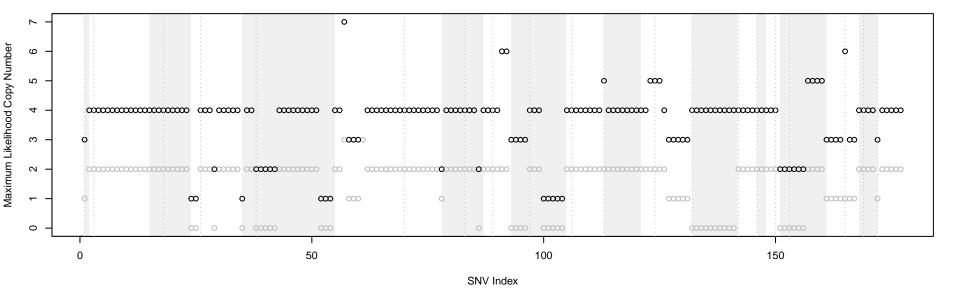
1.5

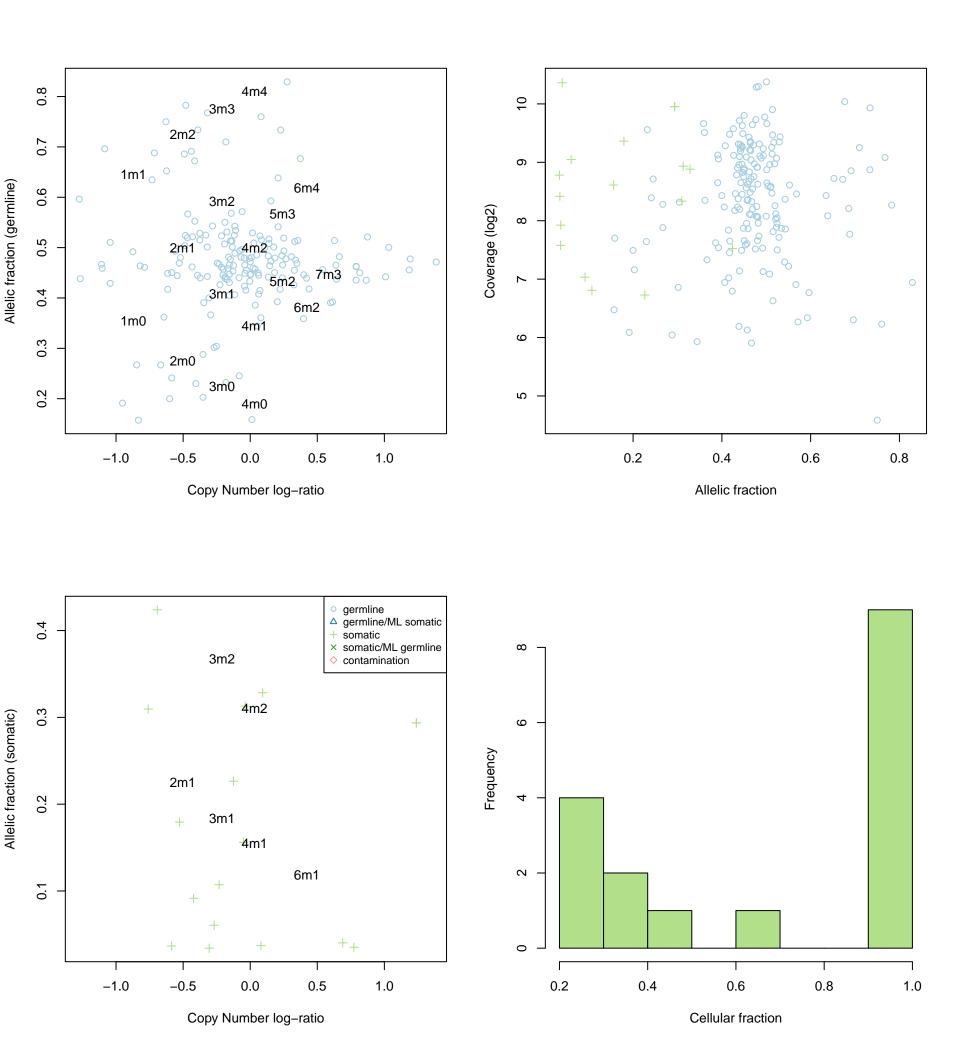
2.0



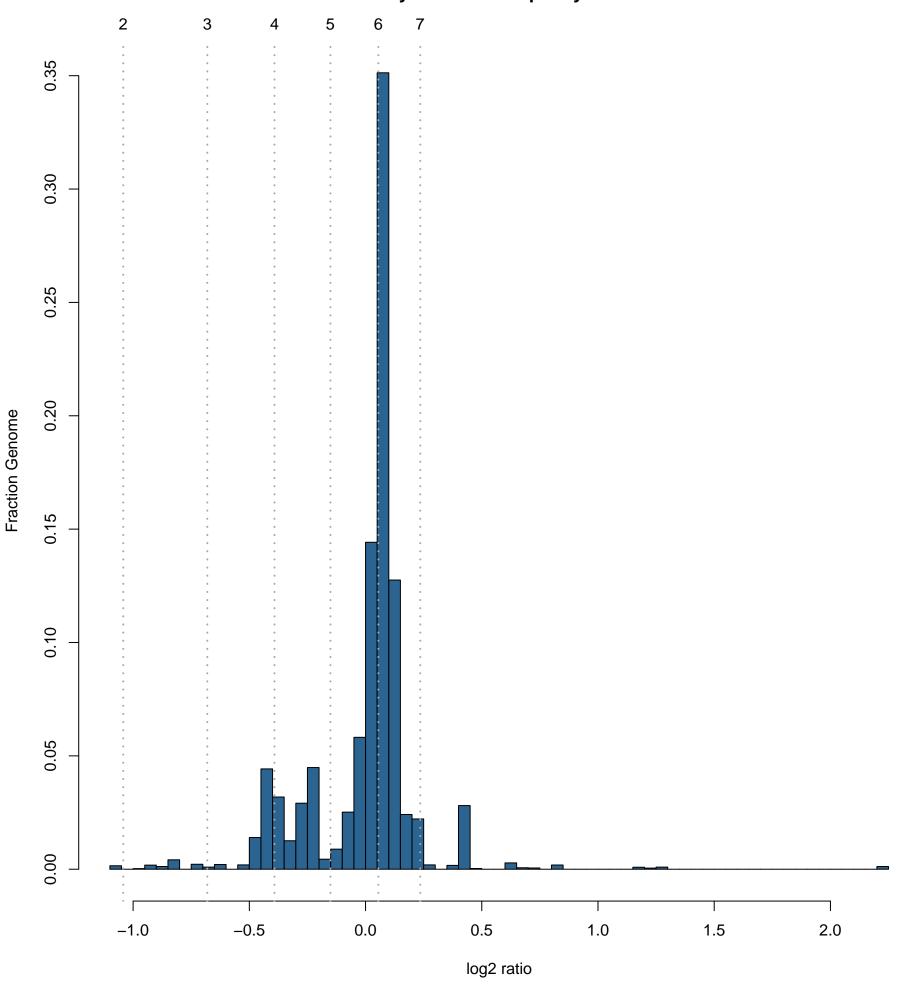
SCNA-fit log-likelihood: -13070.54

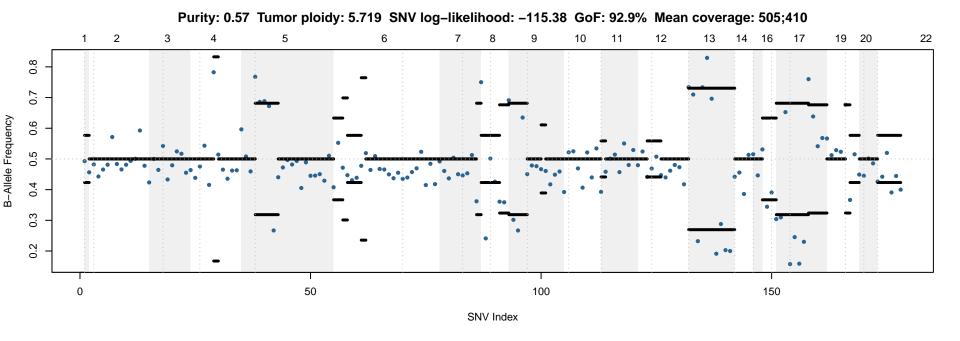




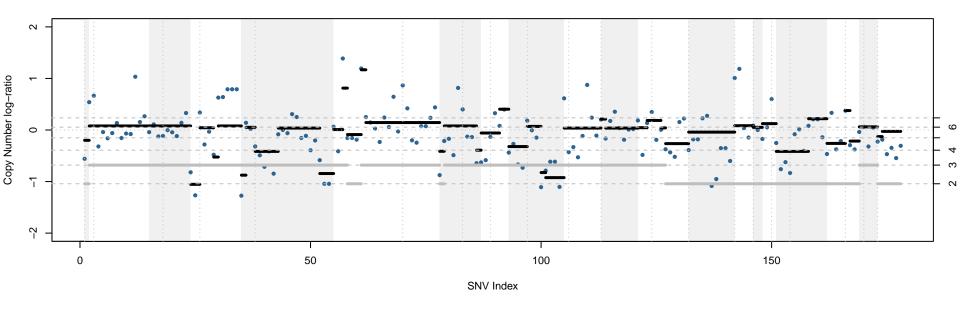


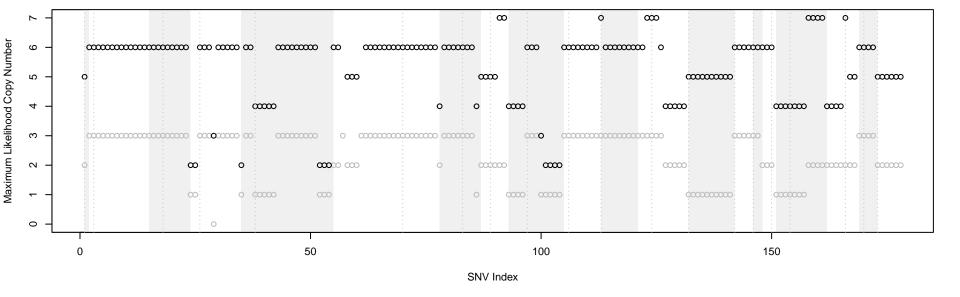
Purity: 0.57 Tumor ploidy: 5.719

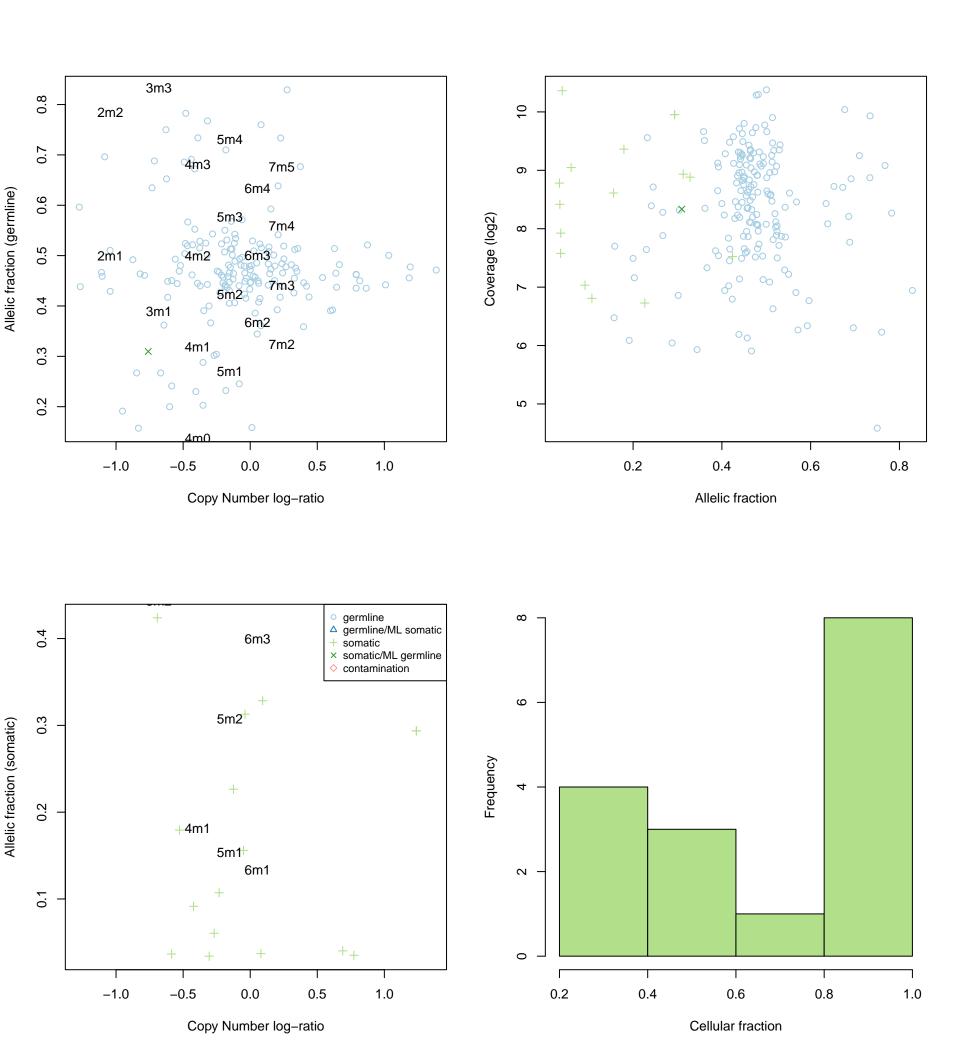




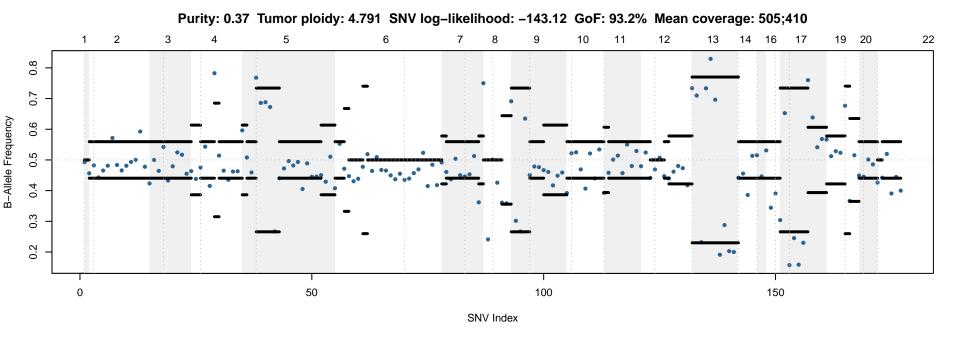
SCNA-fit log-likelihood: -13172.78



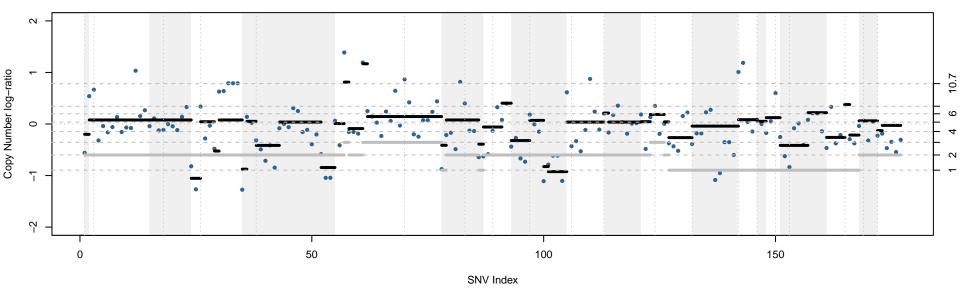


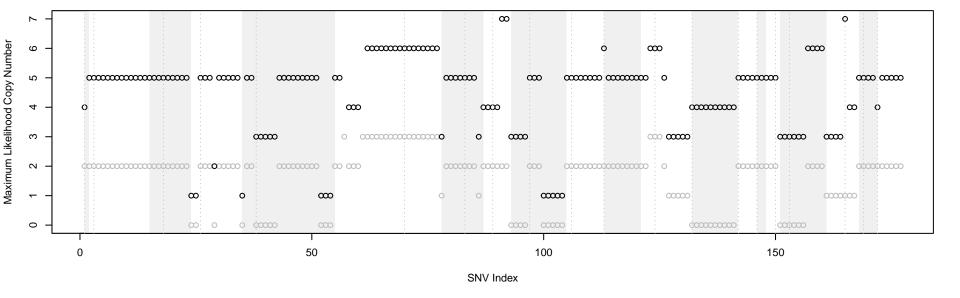


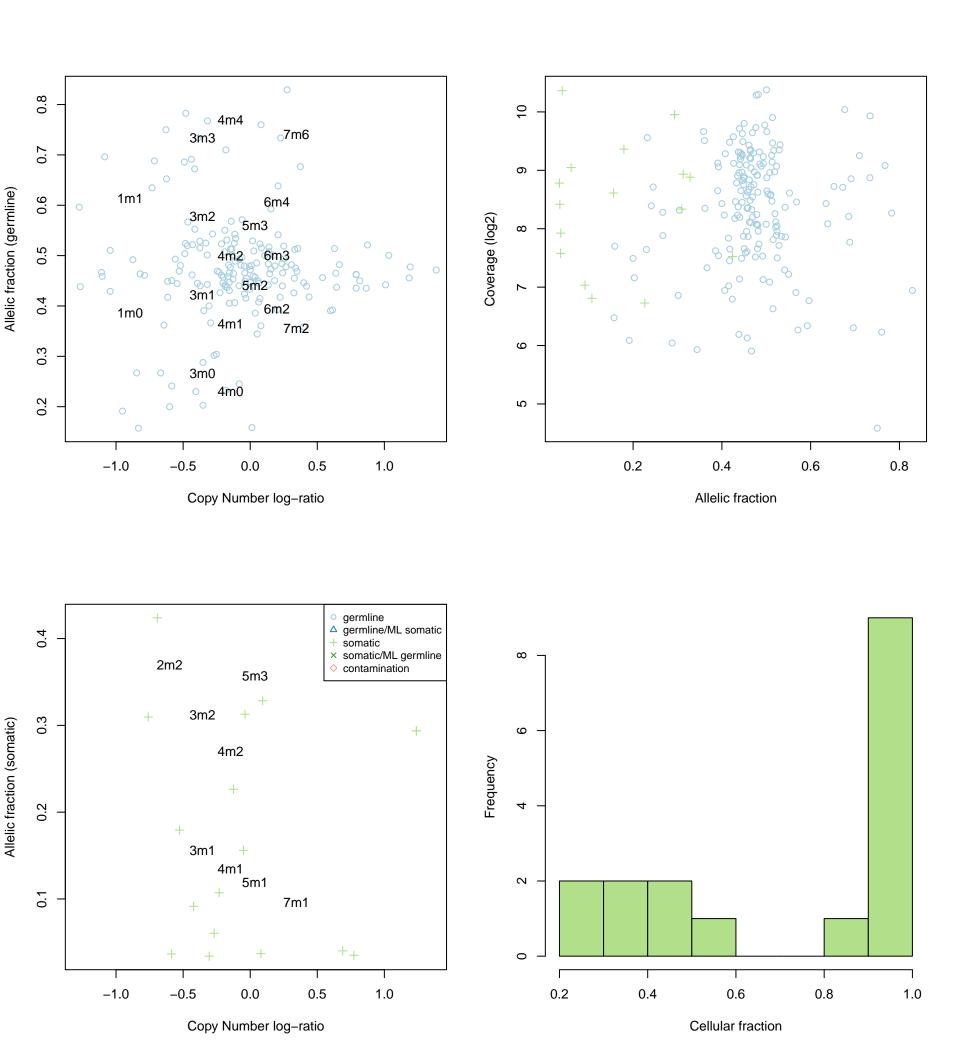
Purity: 0.37 Tumor ploidy: 4.791 10.7 2 3 5 7 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 2.0 log2 ratio



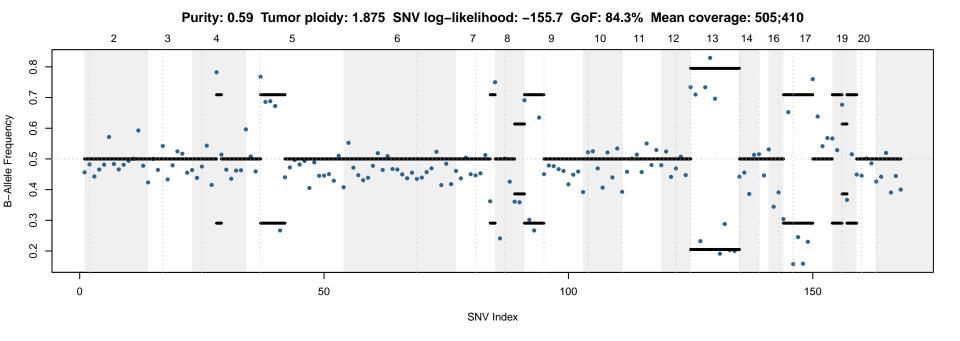
SCNA-fit log-likelihood: -13141.4



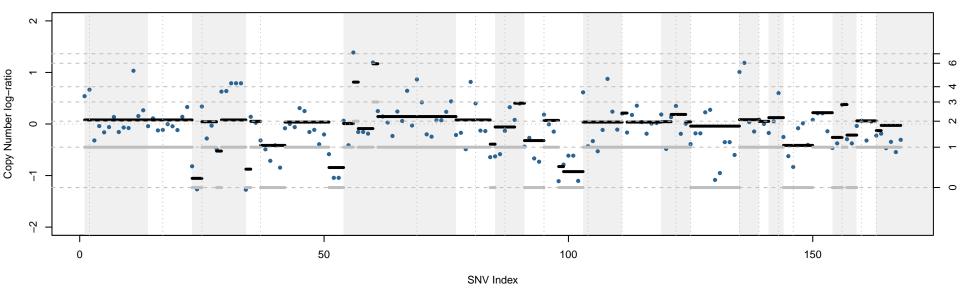


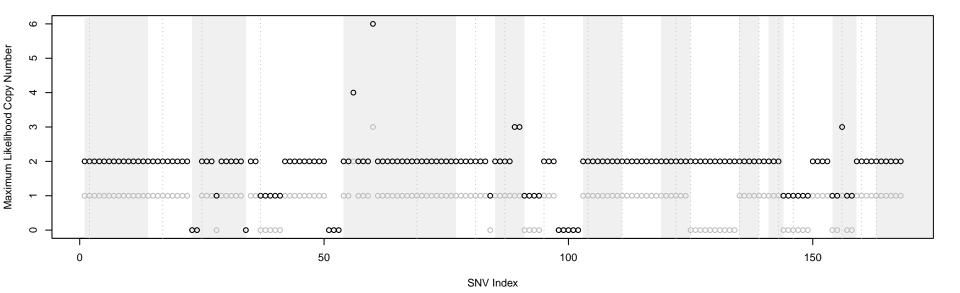


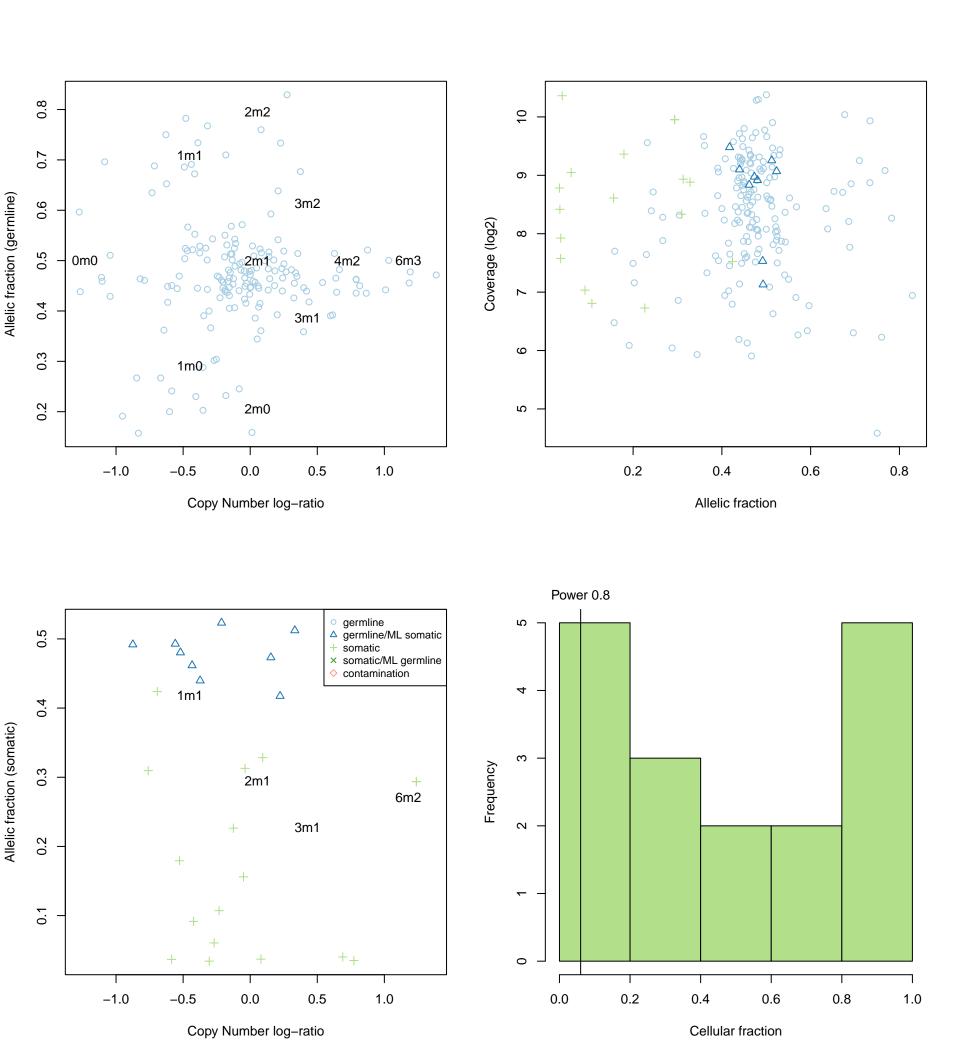
Purity: 0.59 Tumor ploidy: 1.875 2 0 3 7 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 2.0 log2 ratio



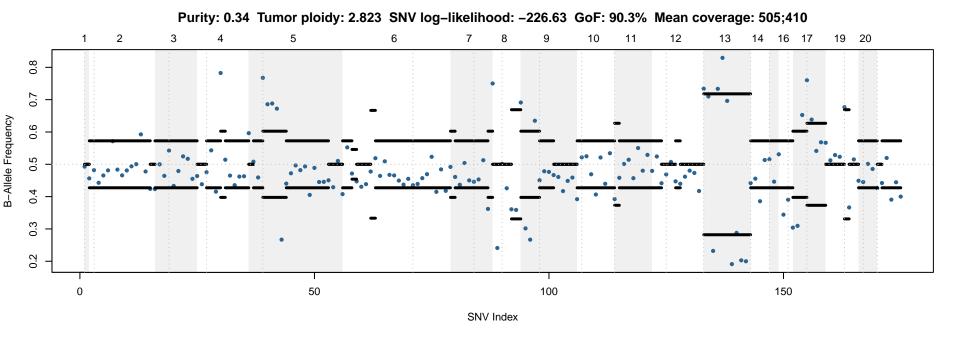
SCNA-fit log-likelihood: -13201.68



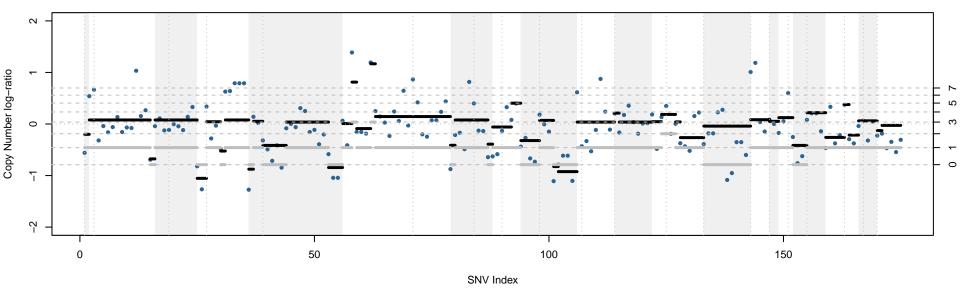


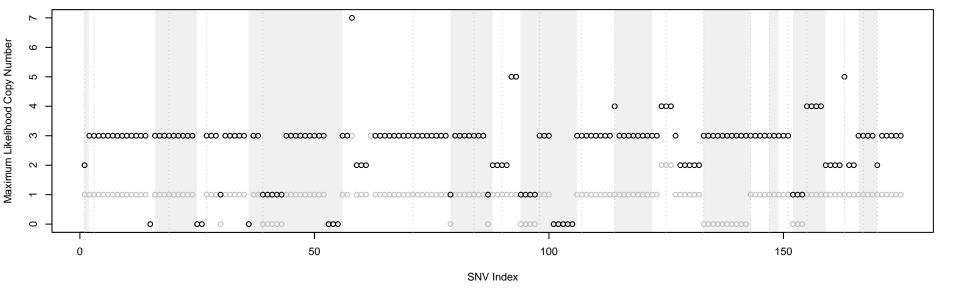


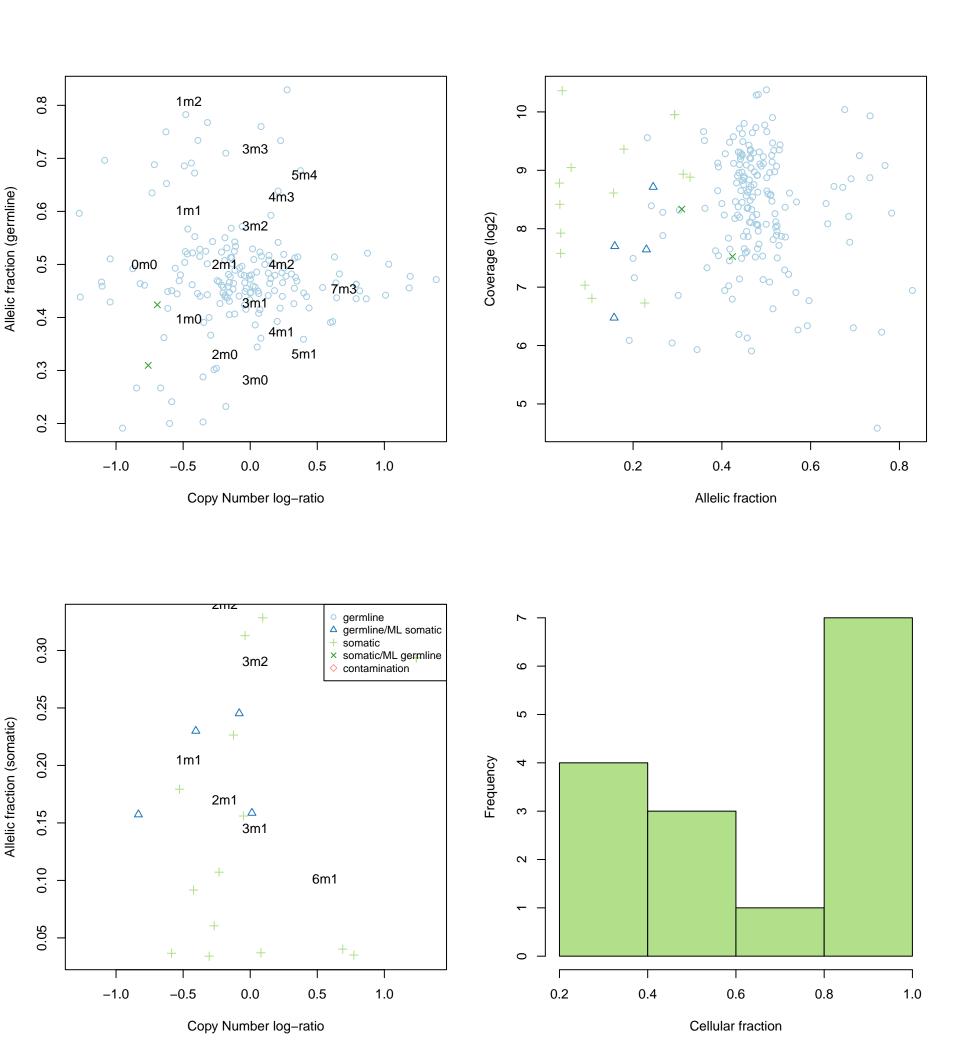
Purity: 0.34 Tumor ploidy: 2.823 3 0 2 6 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 2.0 log2 ratio



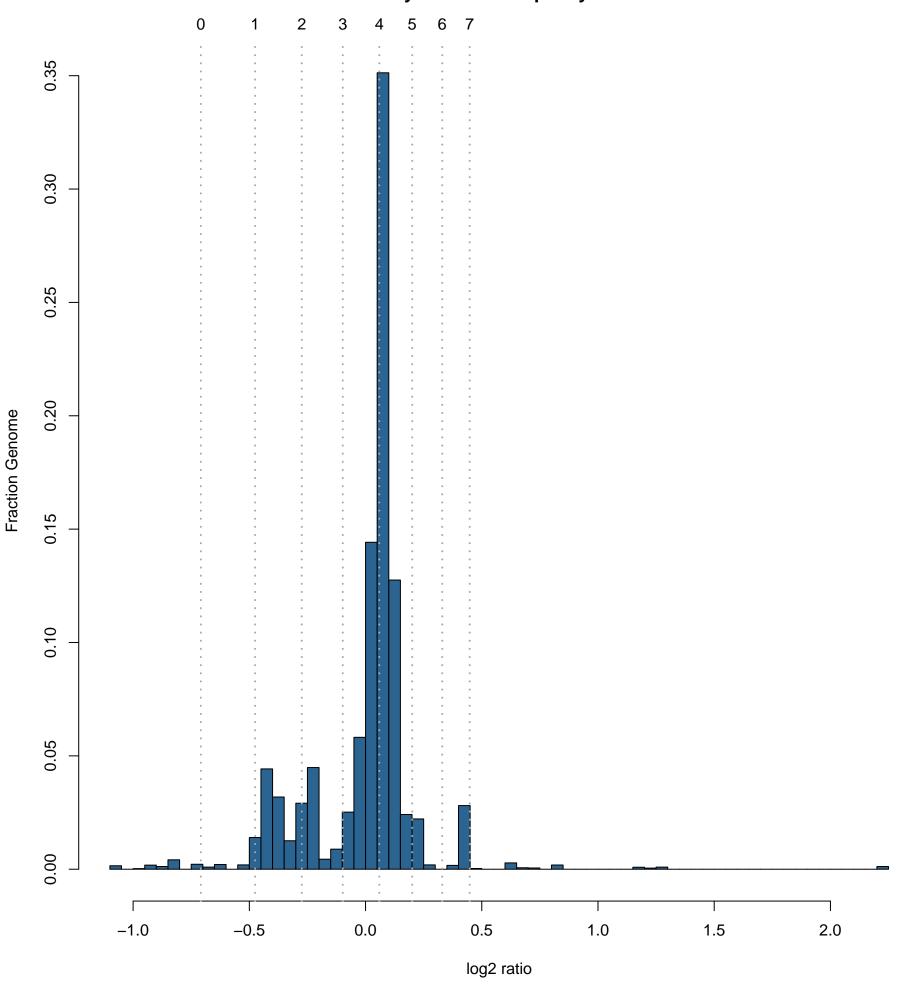
SCNA-fit log-likelihood: -13057.2

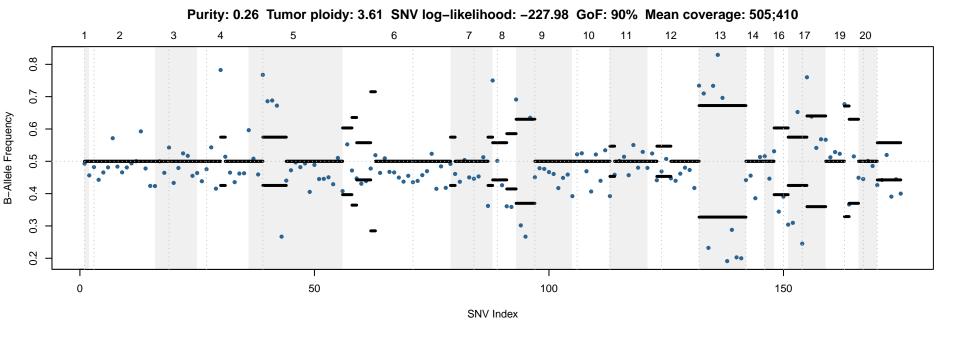




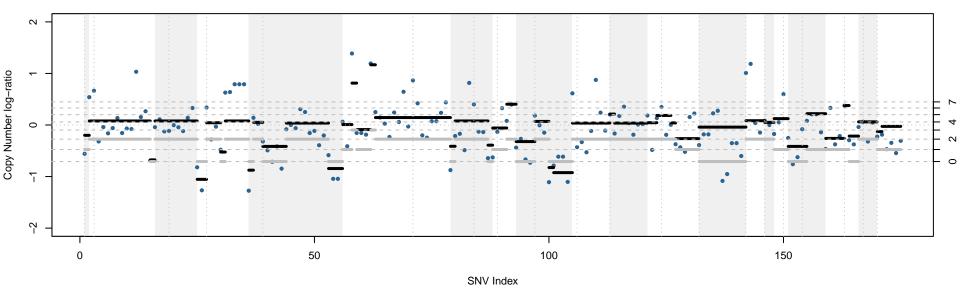


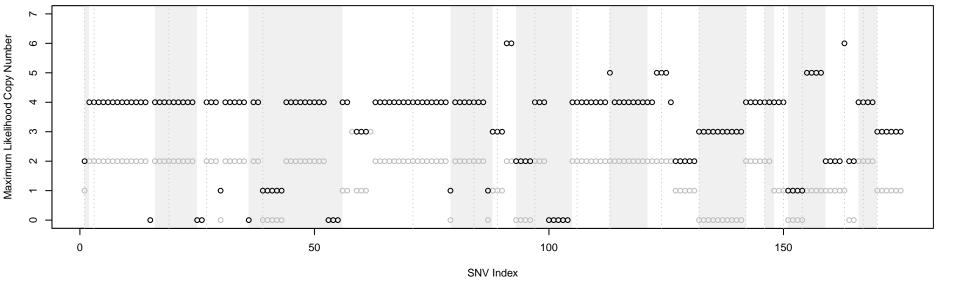
Purity: 0.26 Tumor ploidy: 3.61

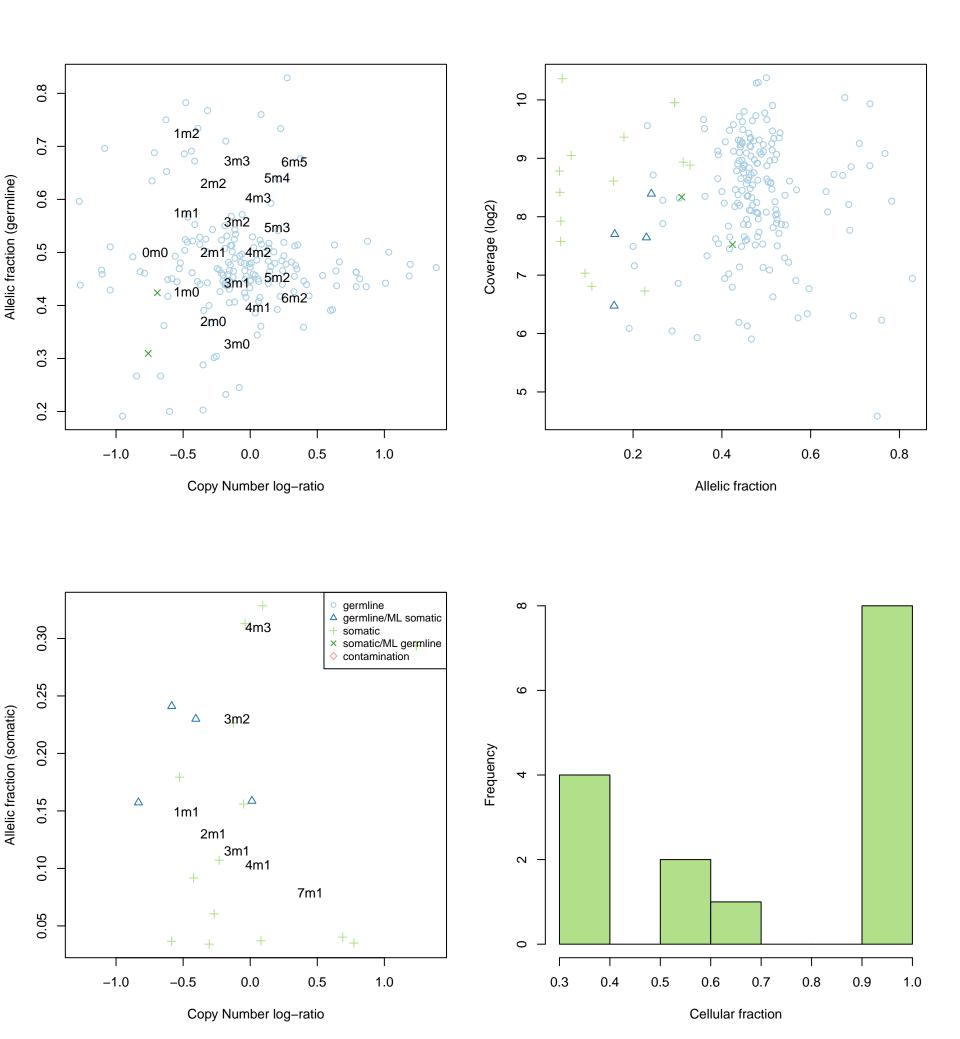


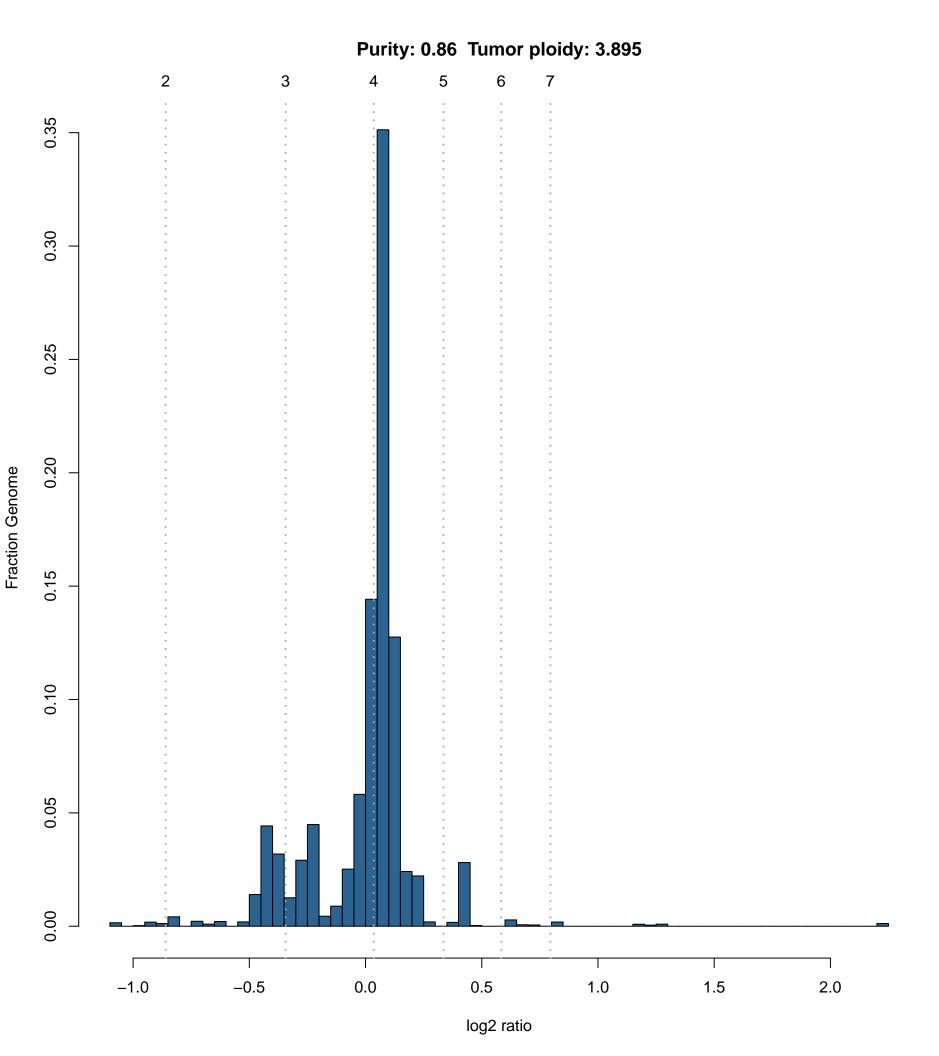


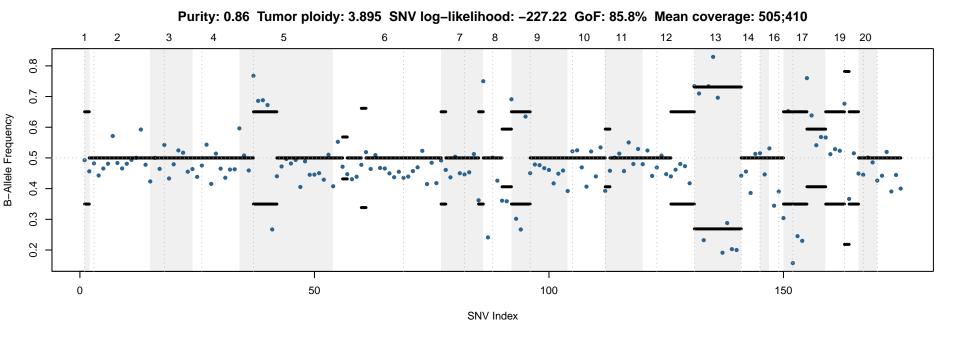
SCNA-fit log-likelihood: -13071.08



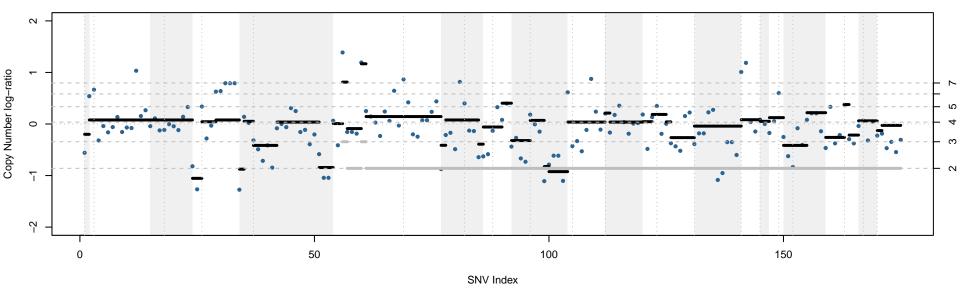


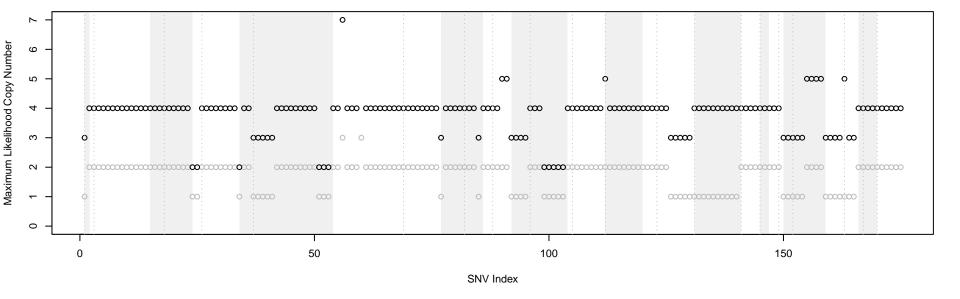


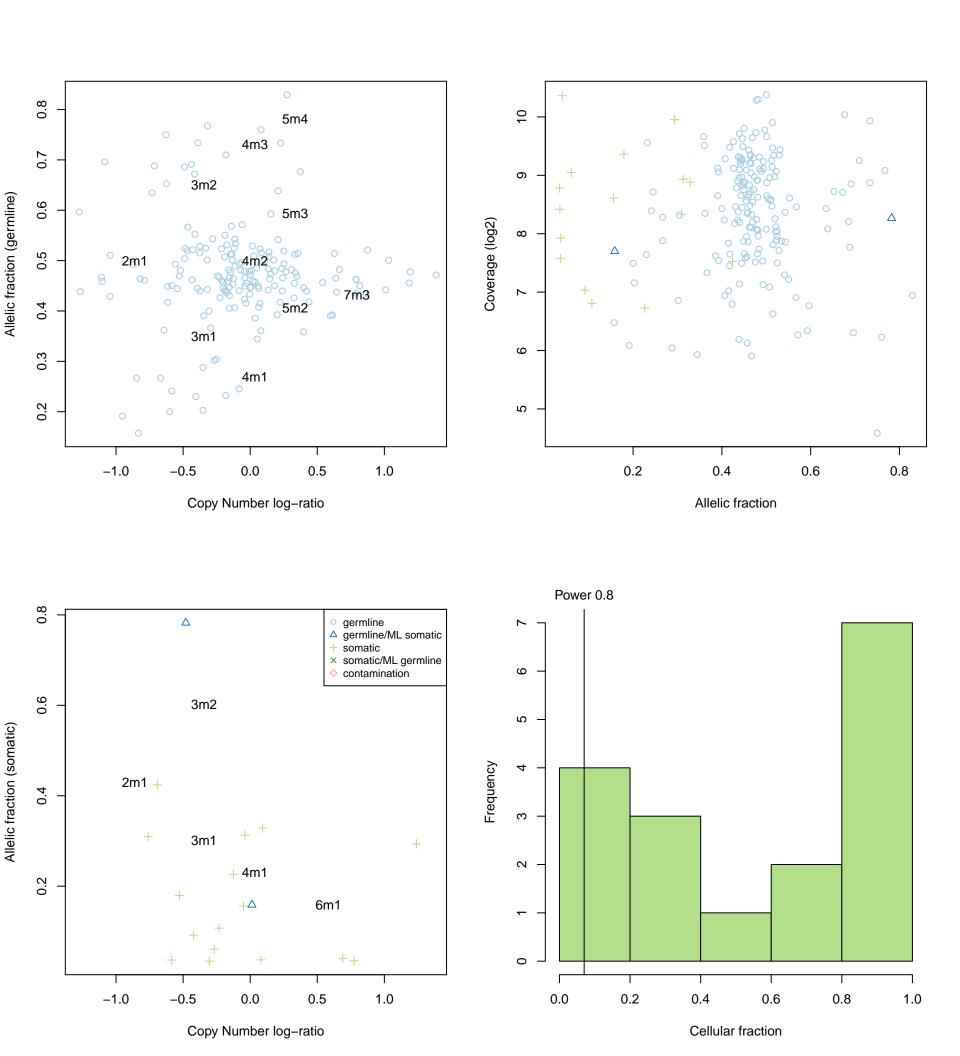




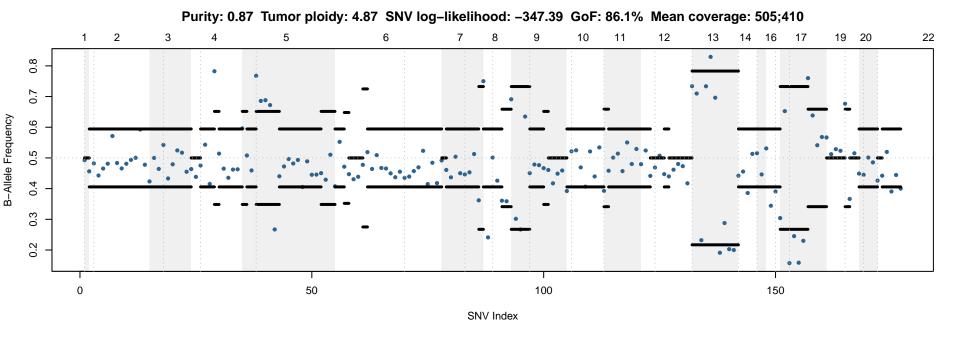
SCNA-fit log-likelihood: -13140.62



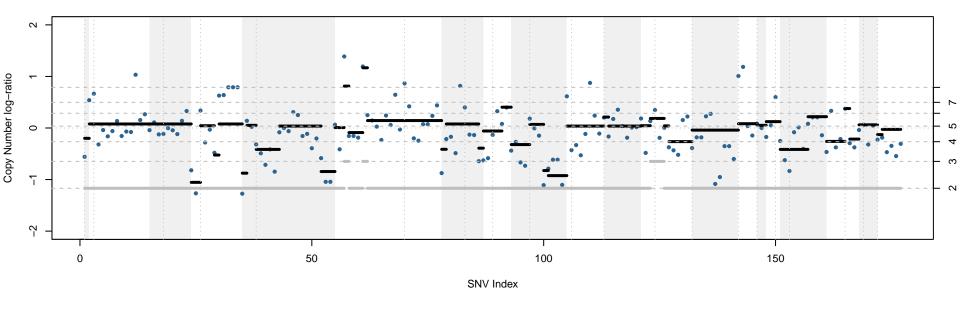


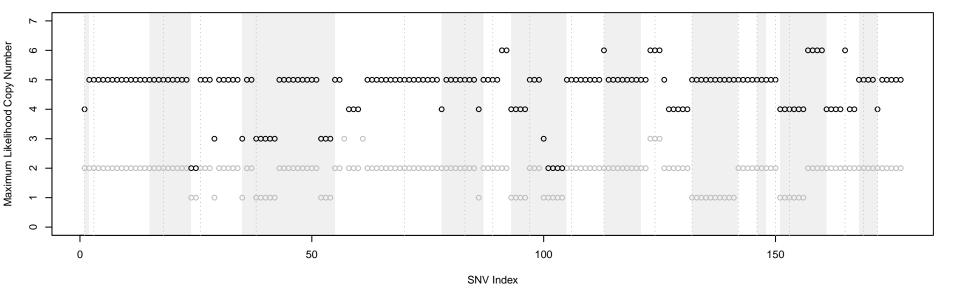


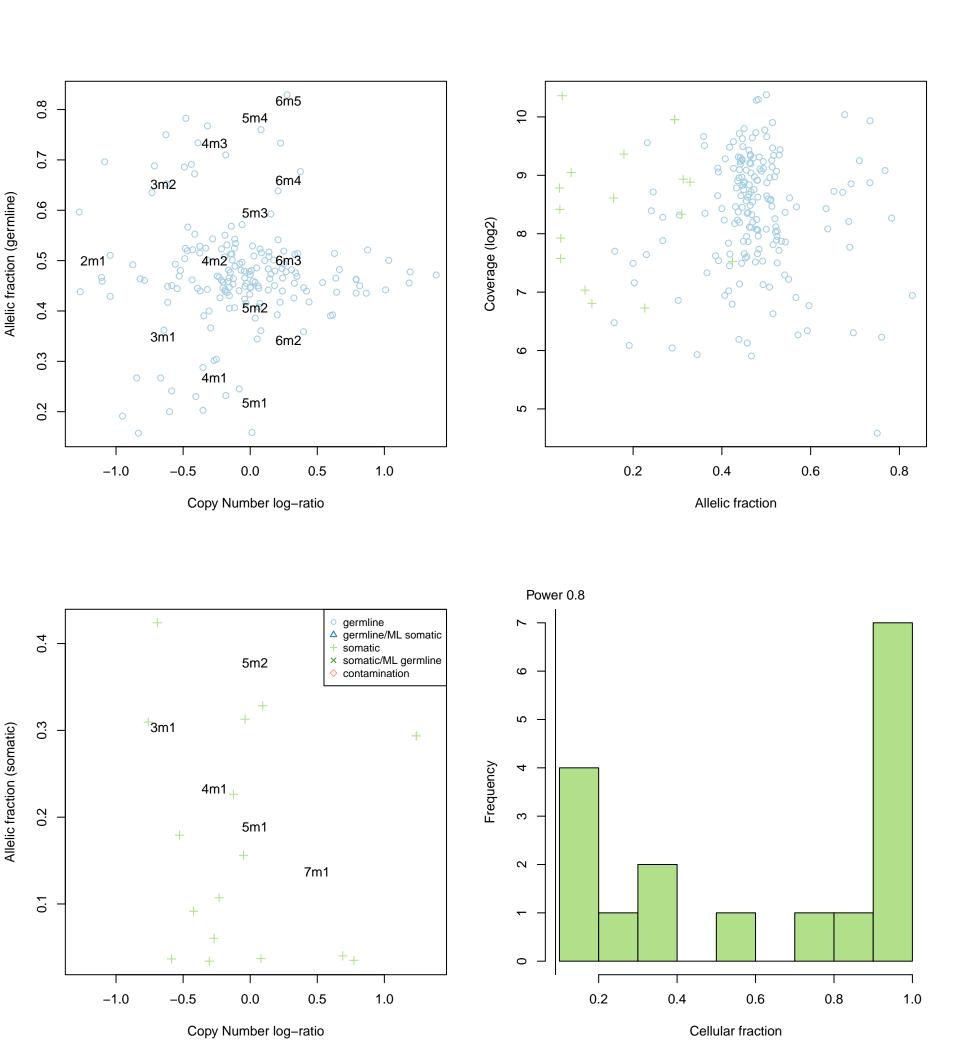
Purity: 0.87 Tumor ploidy: 4.87 8.6 2 3 4 5 6 7 0.35 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 2.0 log2 ratio

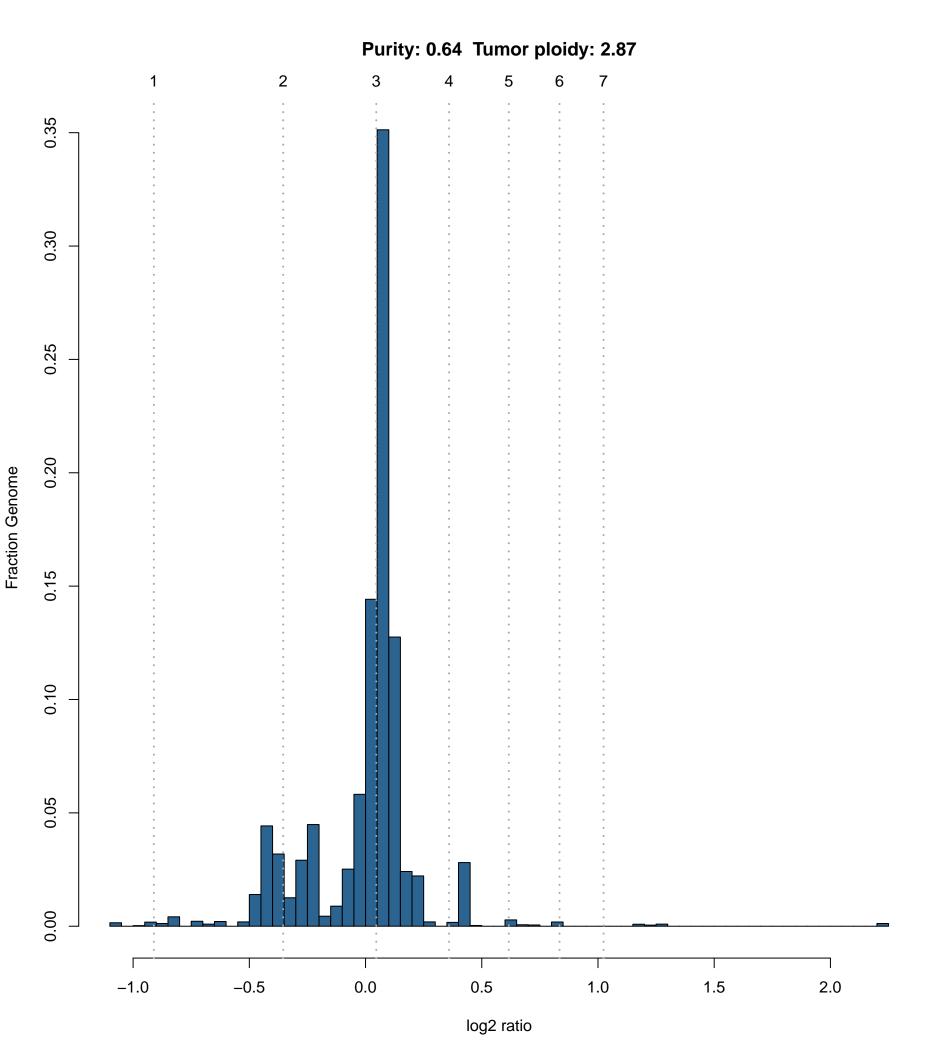


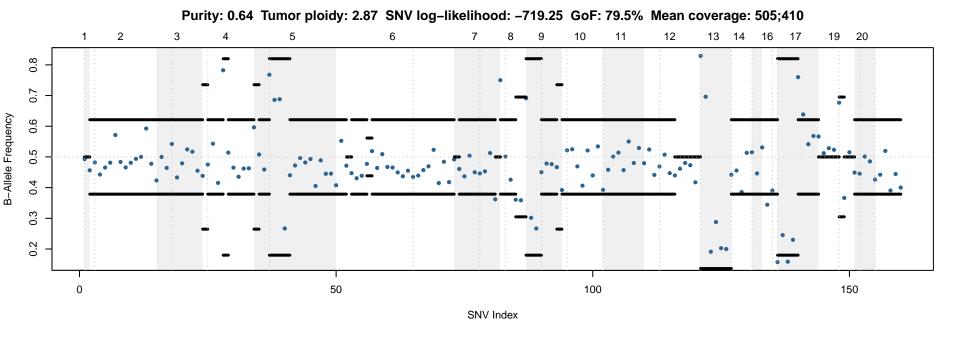
SCNA-fit log-likelihood: -13190.78











SCNA-fit log-likelihood: -13104.51

