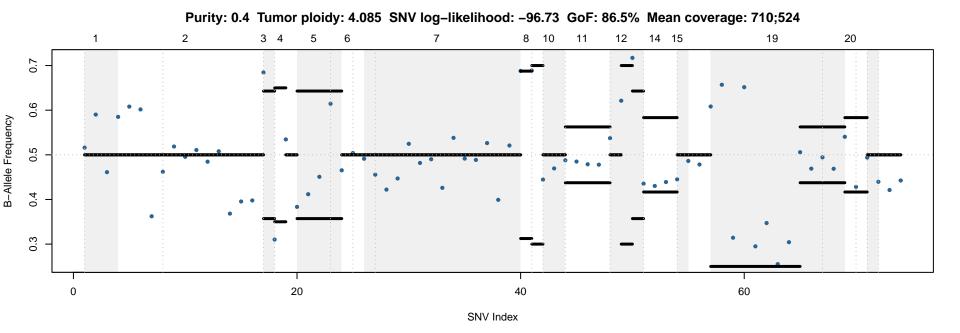
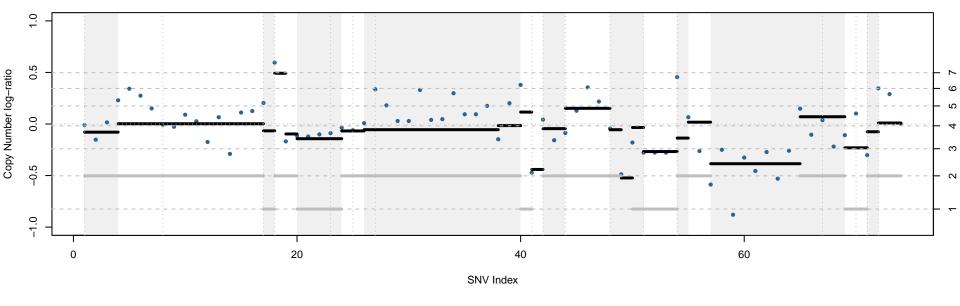
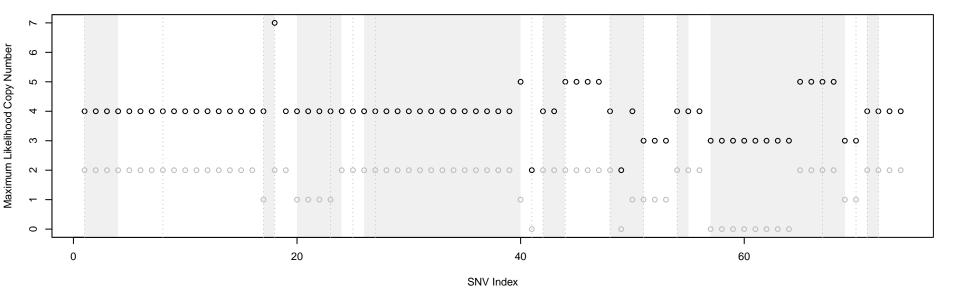
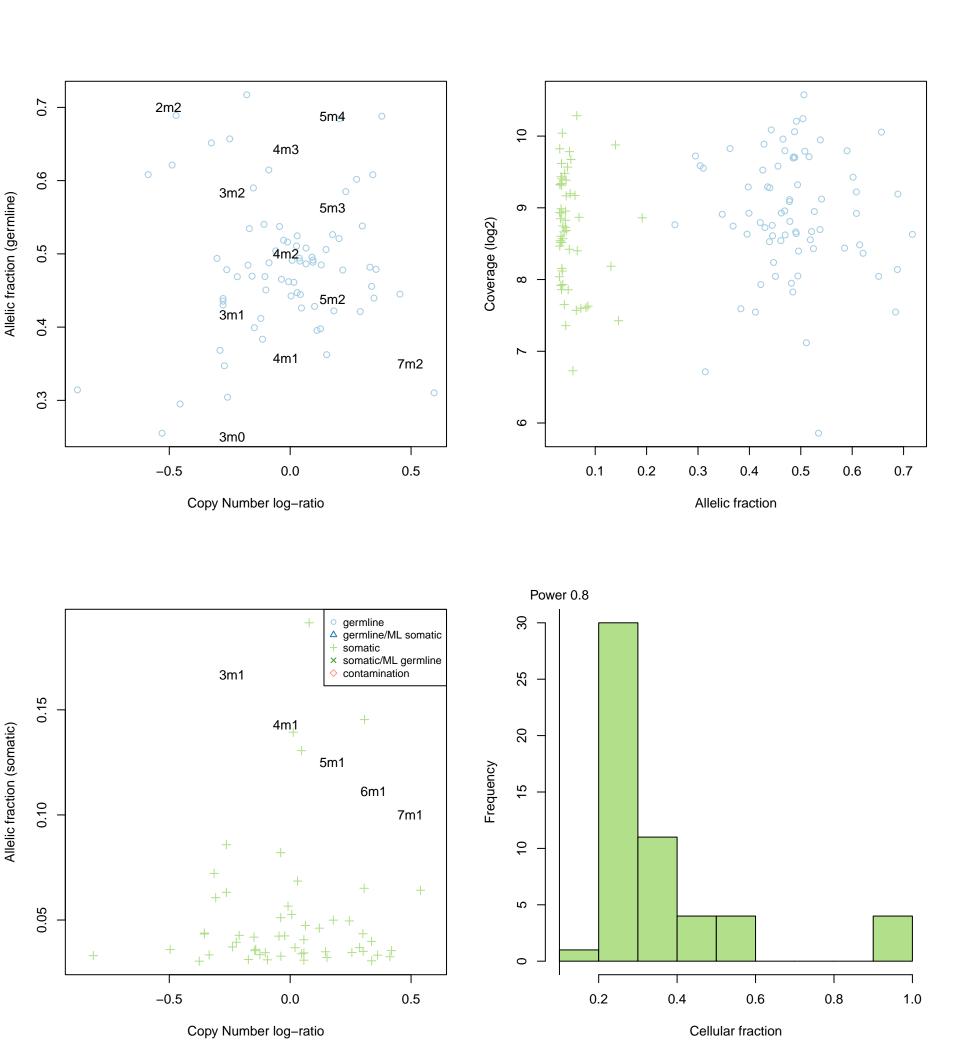
Purity: 0.4 Tumor ploidy: 4.085 3 6 0 2 5 7 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -1.5 -0.5 0.0 0.5 log2 ratio



SCNA-fit log-likelihood: -6664.66

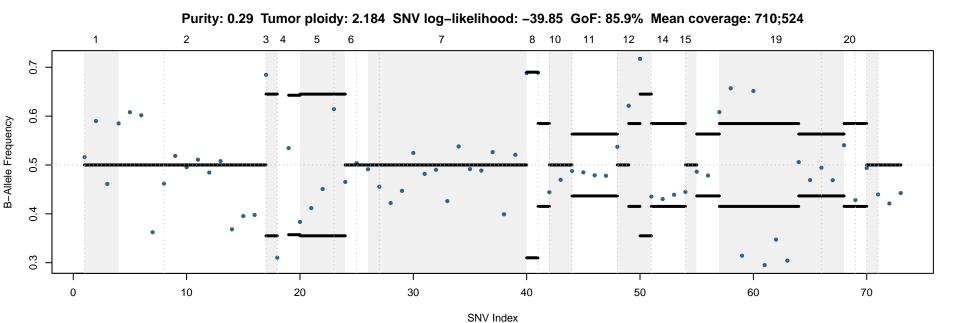




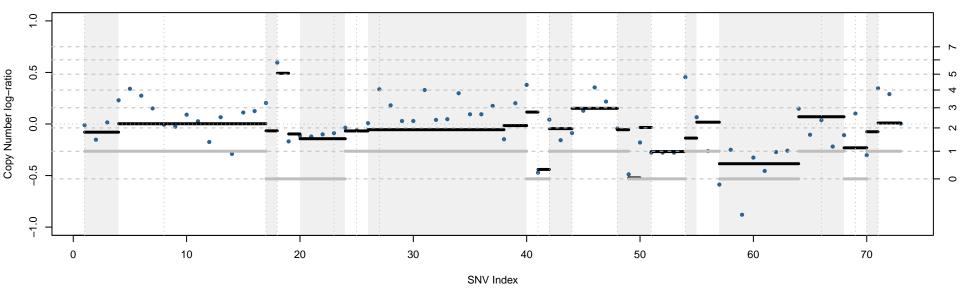


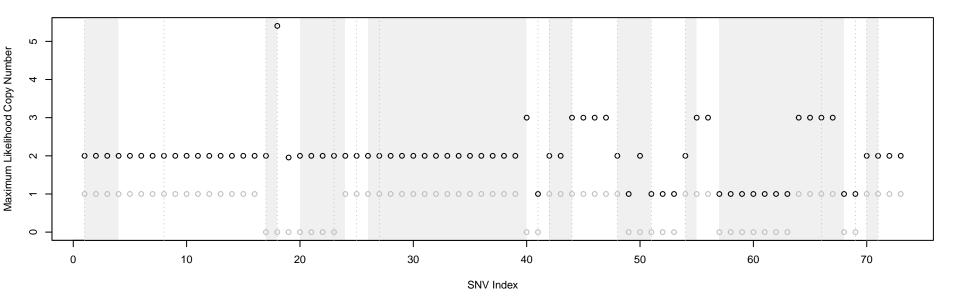
Purity: 0.29 Tumor ploidy: 2.184 0 3 5 6 7 Fraction Genome 0.05 0.00 -1.0 -0.5 0.0 0.5

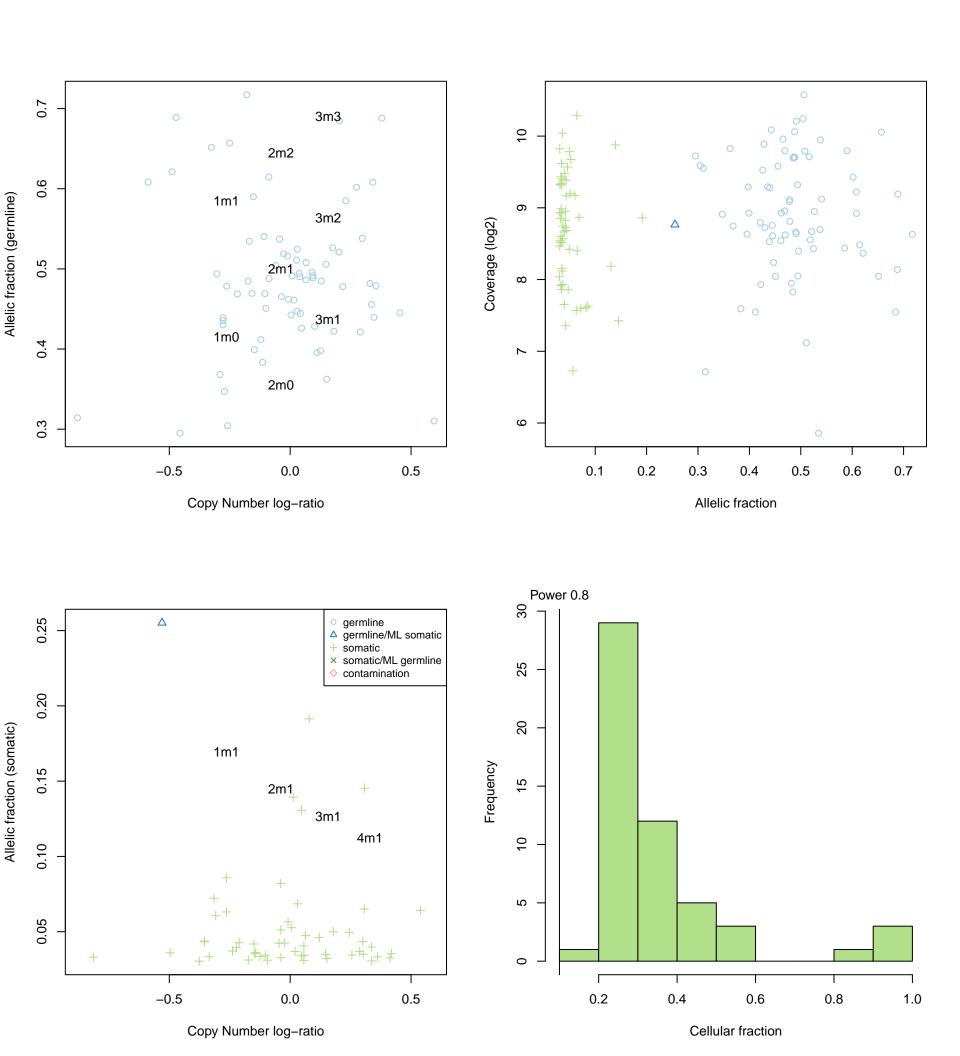
log2 ratio



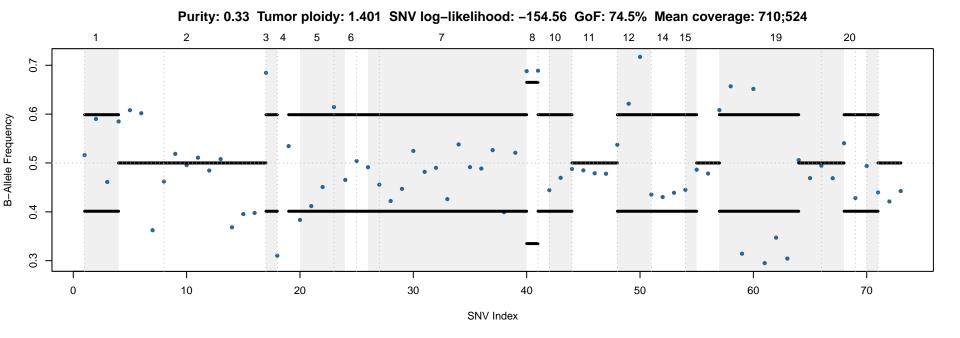
SCNA-fit log-likelihood: -7012.42



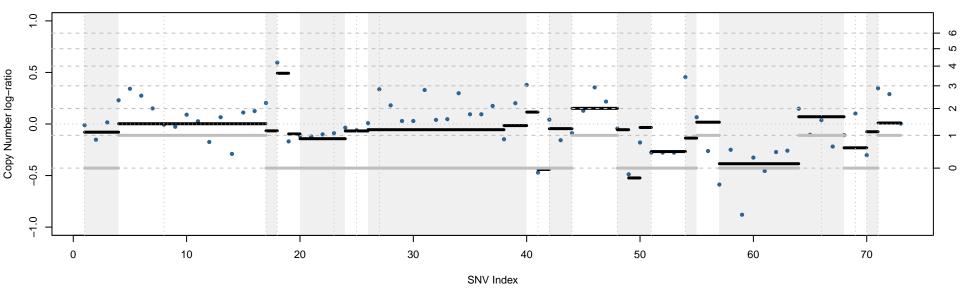


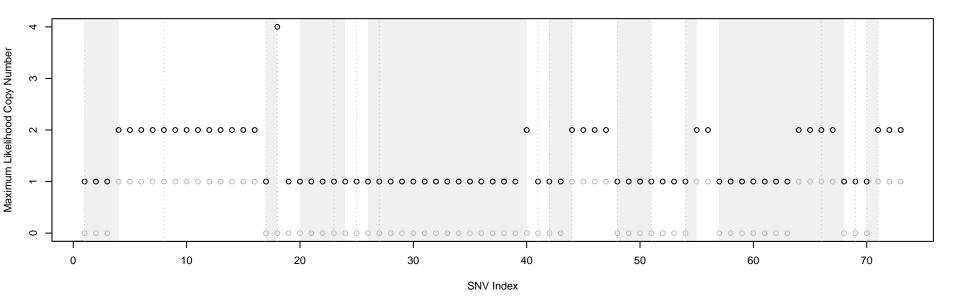


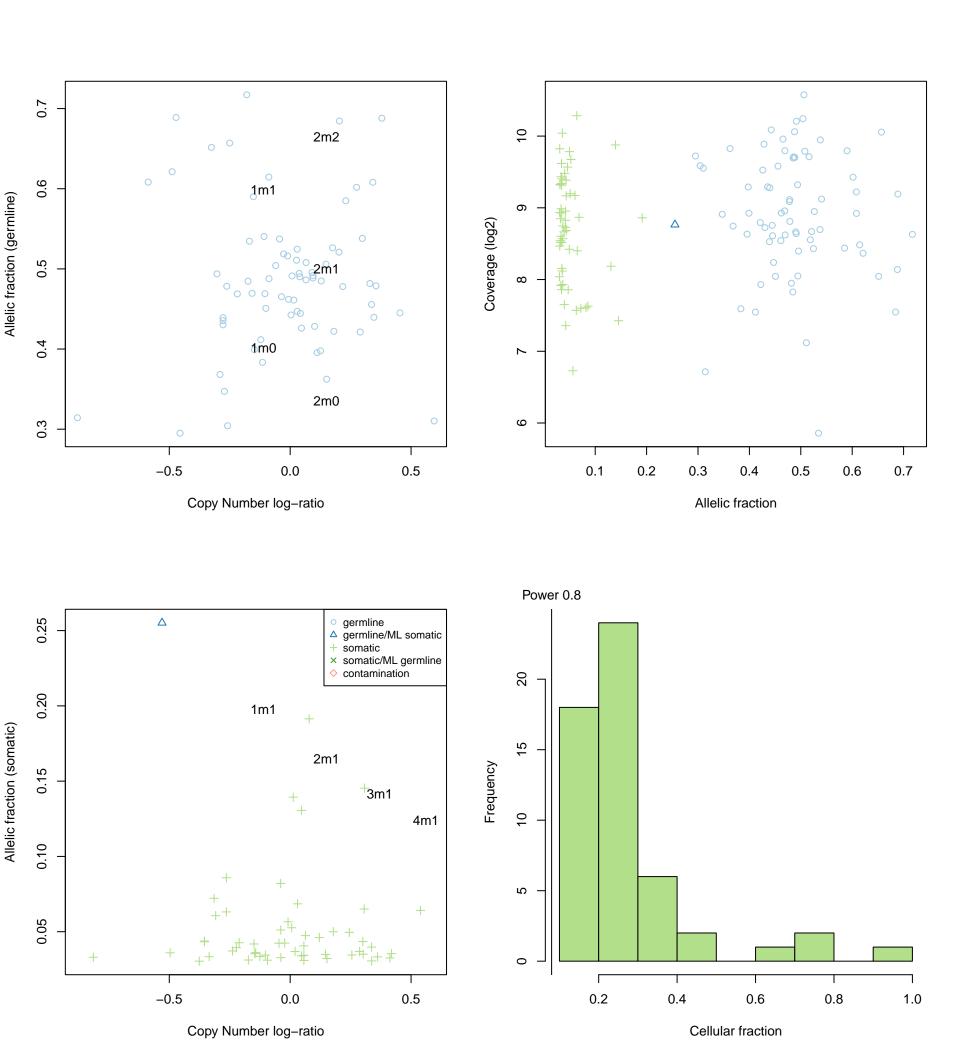
Purity: 0.33 Tumor ploidy: 1.401 0 3 5 6 Fraction Genome 0.00 -0.5 0.0 0.5 log2 ratio



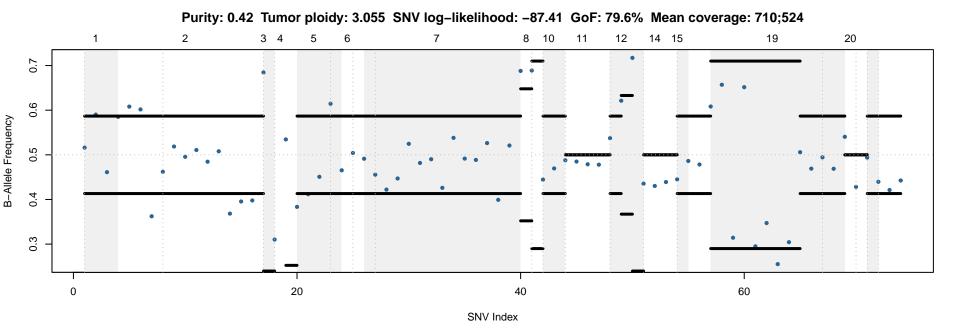
SCNA-fit log-likelihood: -6854.73



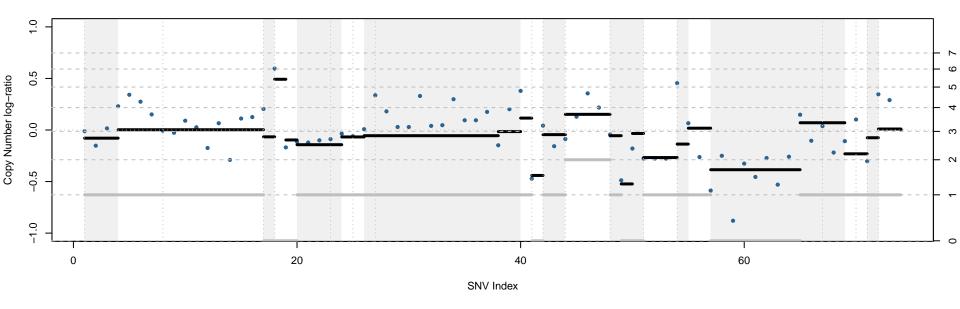


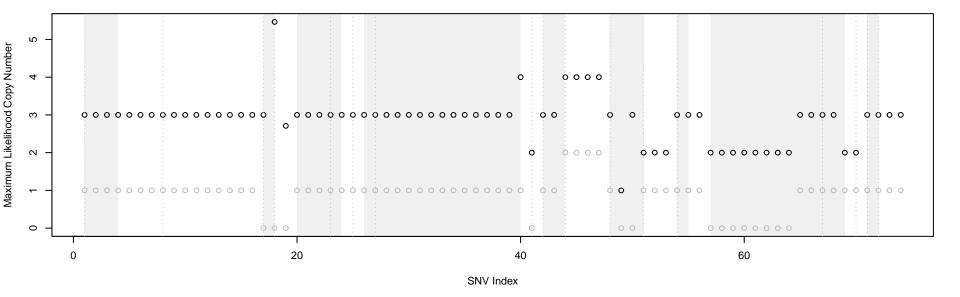


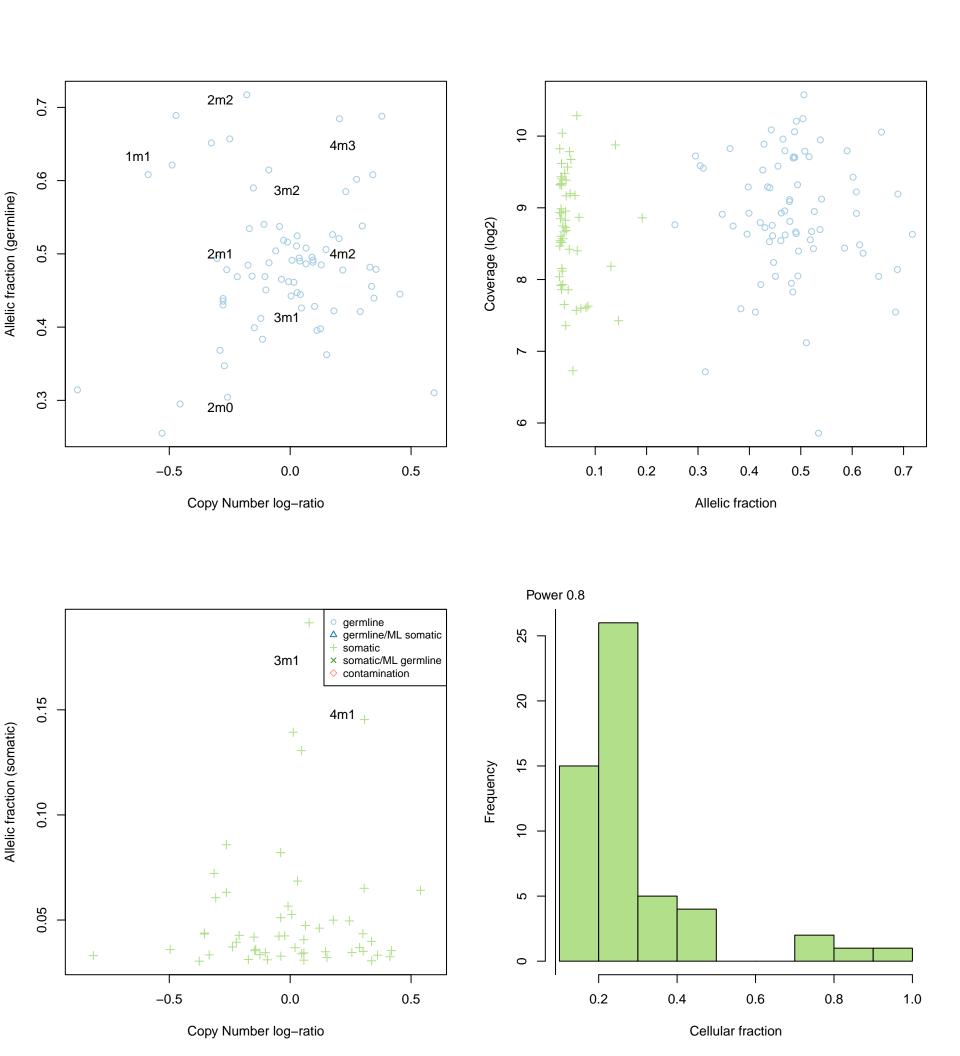
Purity: 0.42 Tumor ploidy: 3.055 2 0 5 6 0.20 Fraction Genome 0.05 0.00 -1.0 -1.5 -0.5 0.0 0.5 log2 ratio



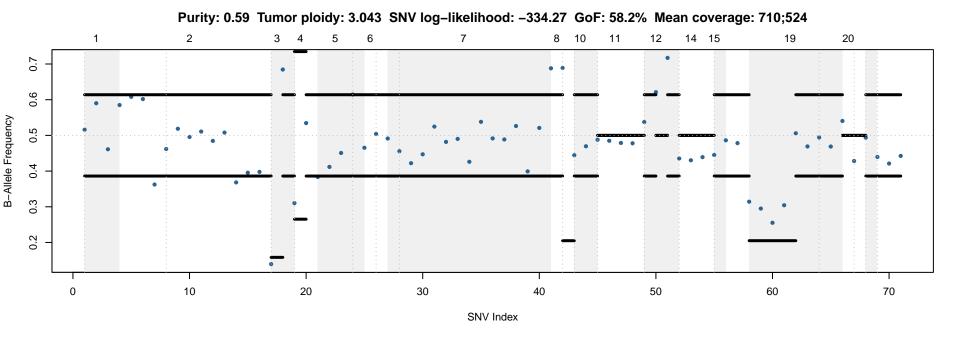
SCNA-fit log-likelihood: -7038.03



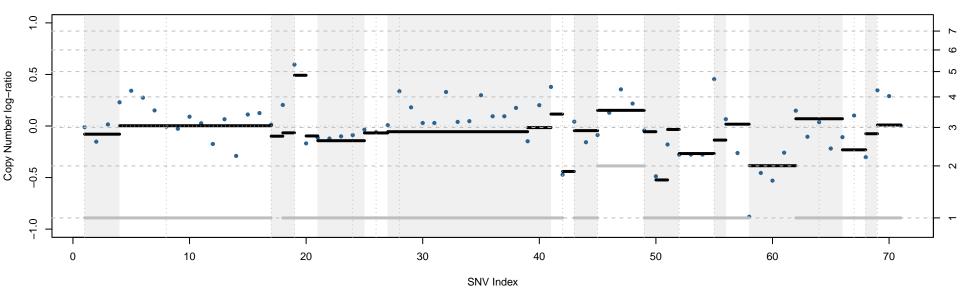


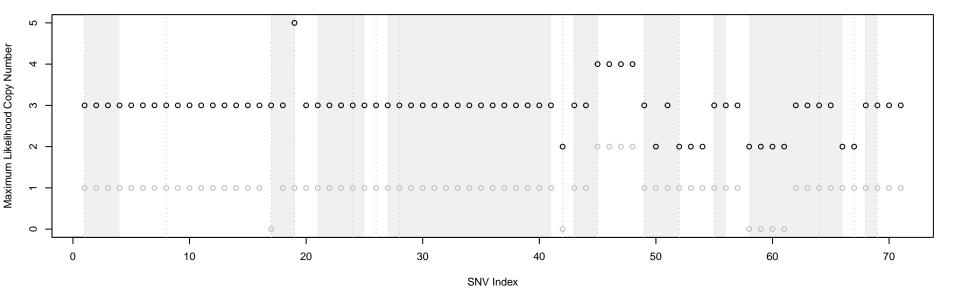


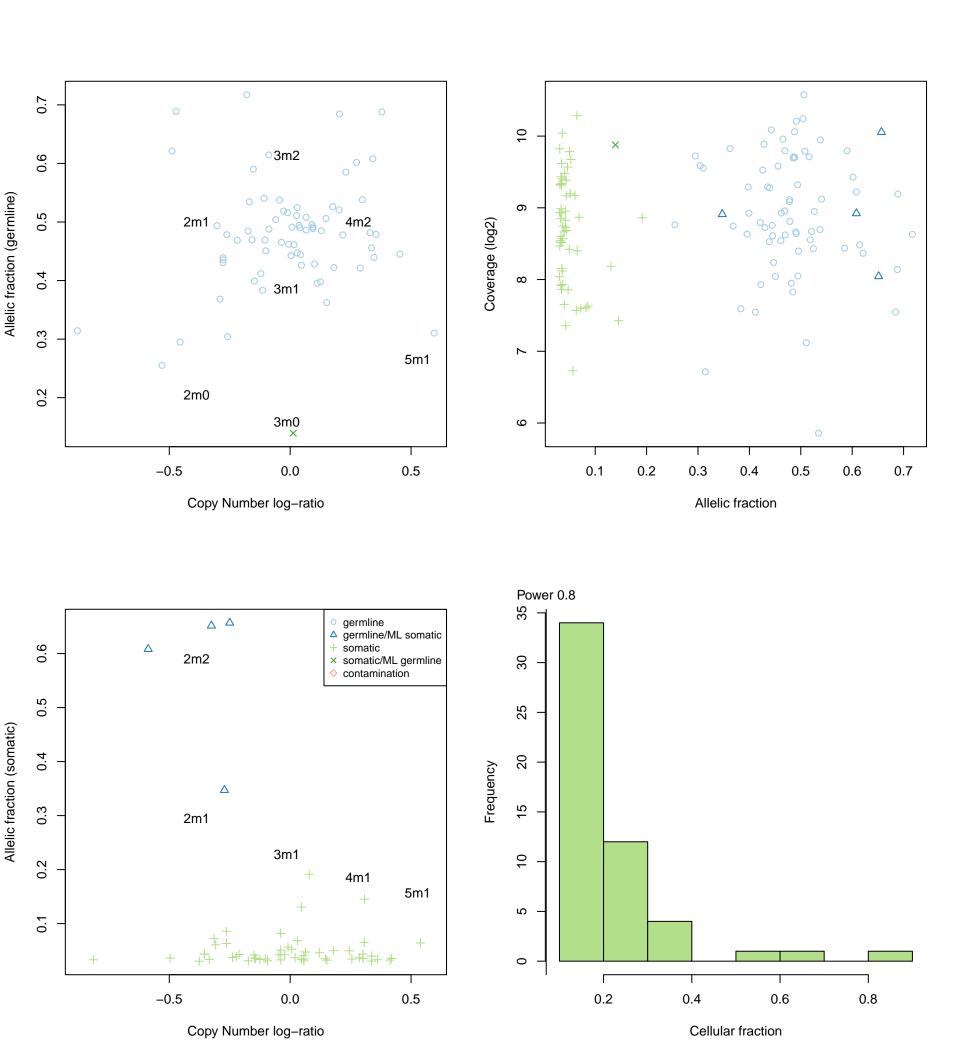
Purity: 0.59 Tumor ploidy: 3.043 0 5 6 0.20 Fraction Genome 0.05 0.00 -1.0 -0.5 -1.5 0.0 0.5 log2 ratio



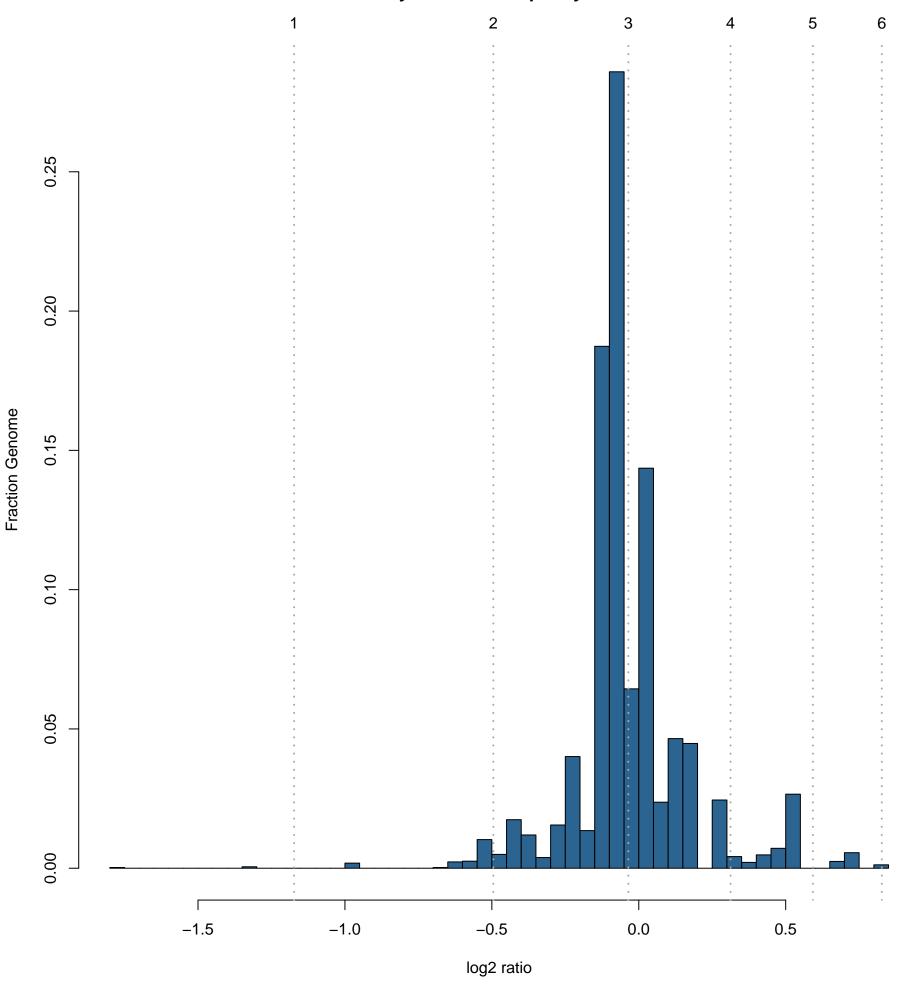
SCNA-fit log-likelihood: -6692

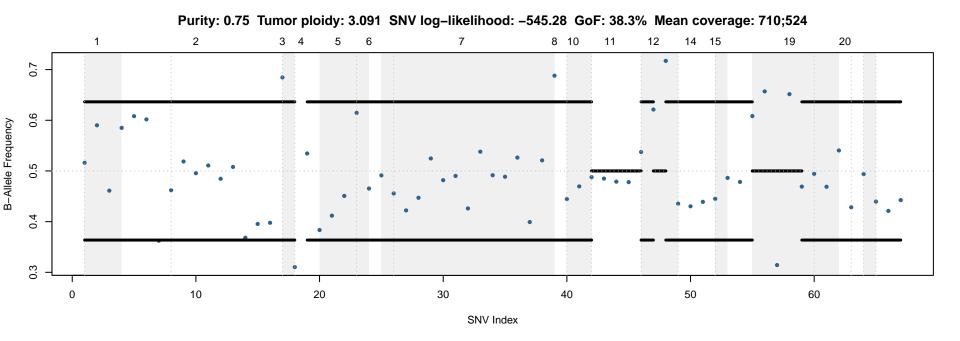




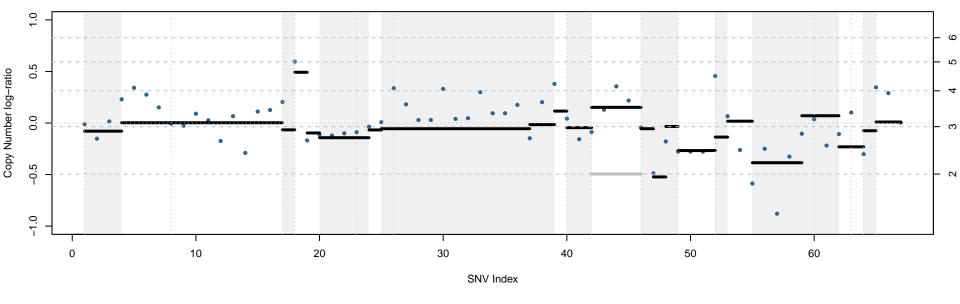


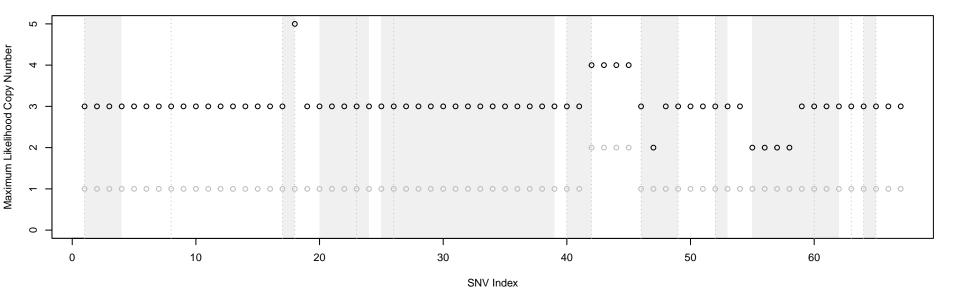
Purity: 0.75 Tumor ploidy: 3.091

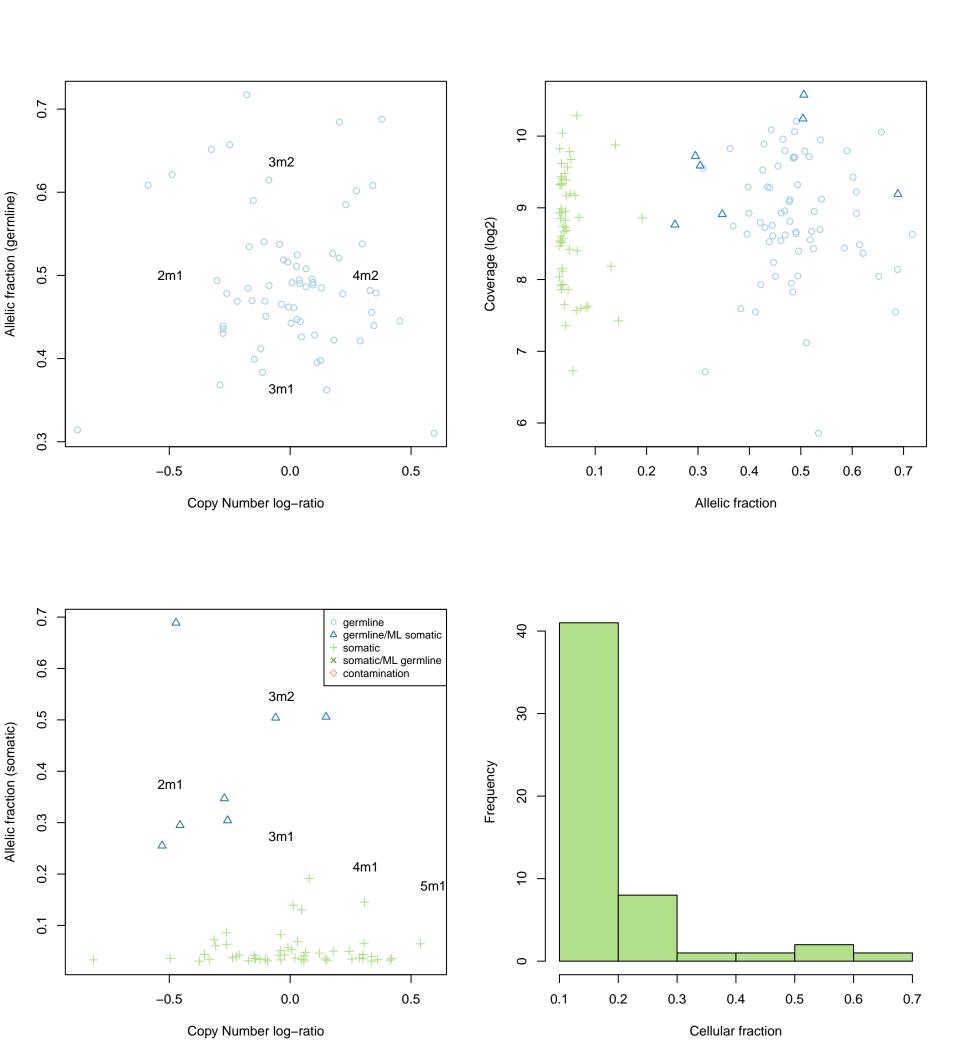




SCNA-fit log-likelihood: -6706.96

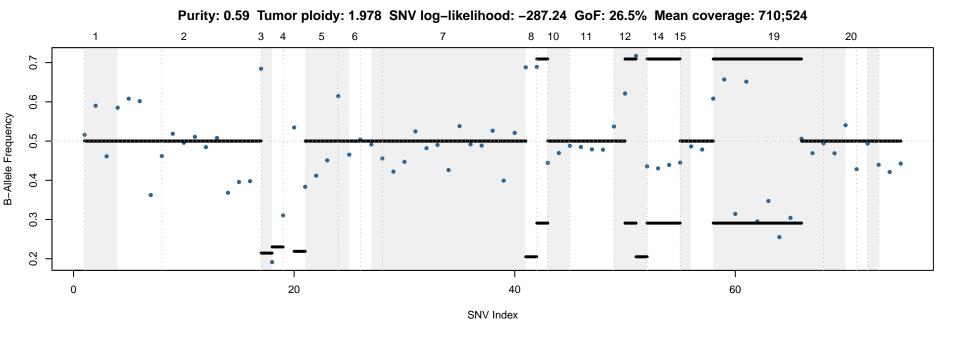






Purity: 0.59 Tumor ploidy: 1.978 3 5 0 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -1.0 -1.5 -0.5 0.0 0.5

log2 ratio



SCNA-fit log-likelihood: -7833.78

