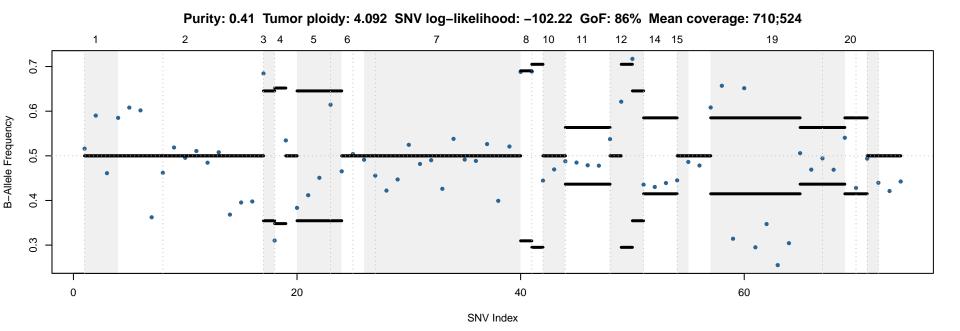
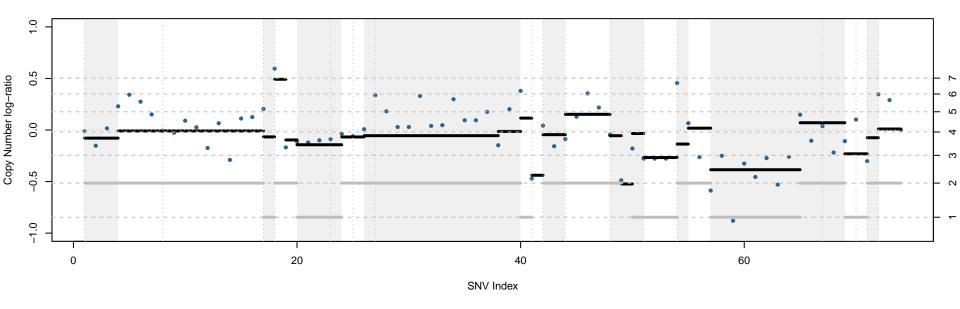
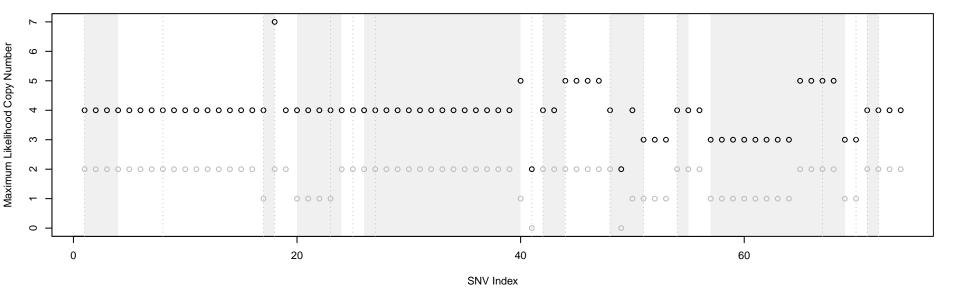
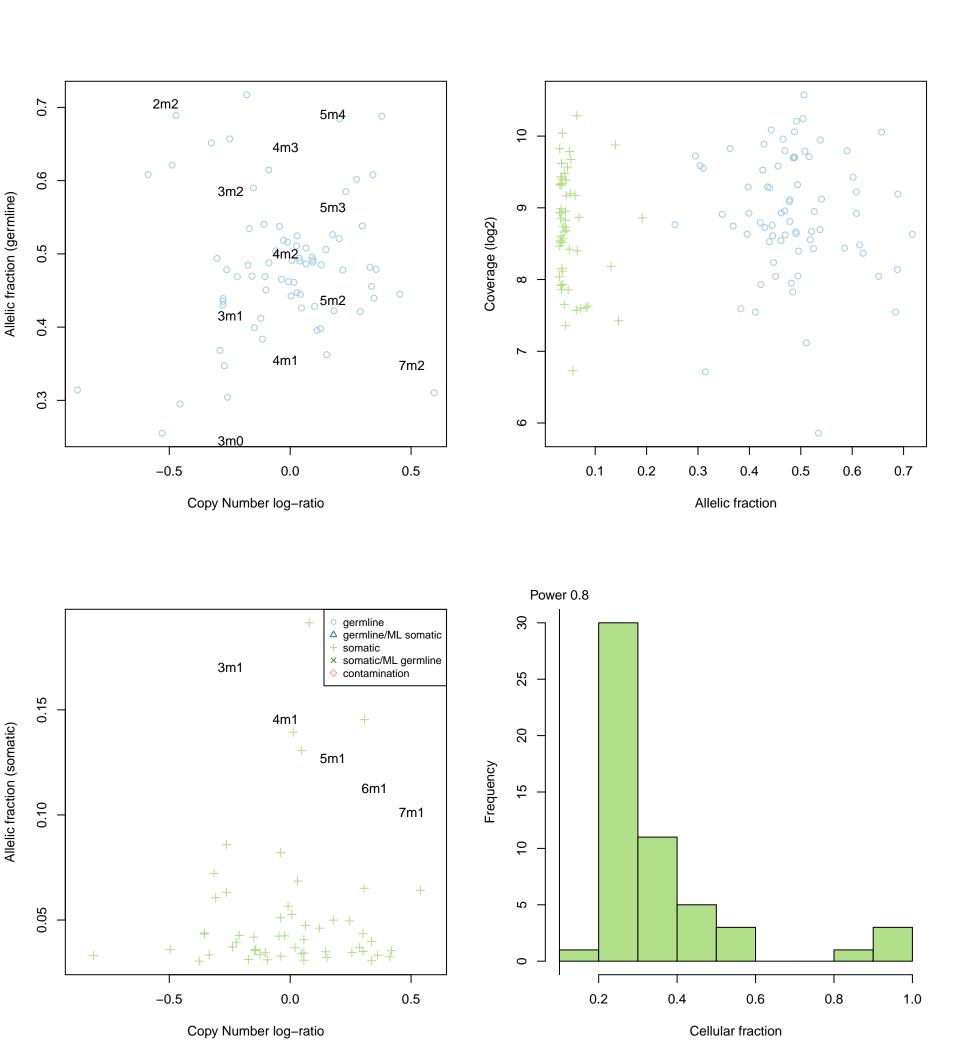
Purity: 0.41 Tumor ploidy: 4.092 3 5 6 0 2 7 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 -1.5 0.0 0.5 log2 ratio



SCNA-fit log-likelihood: -6679.11

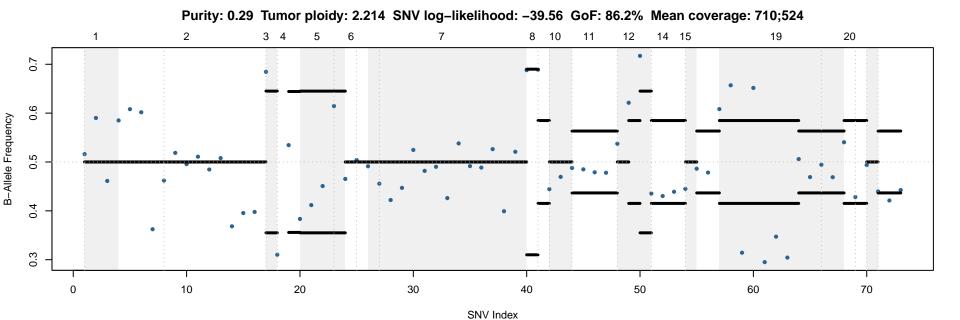




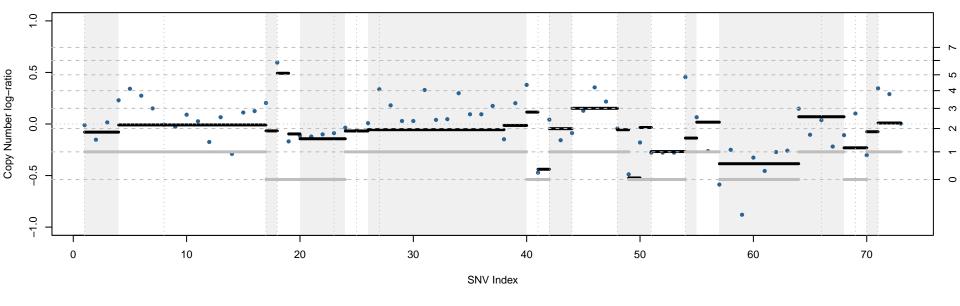


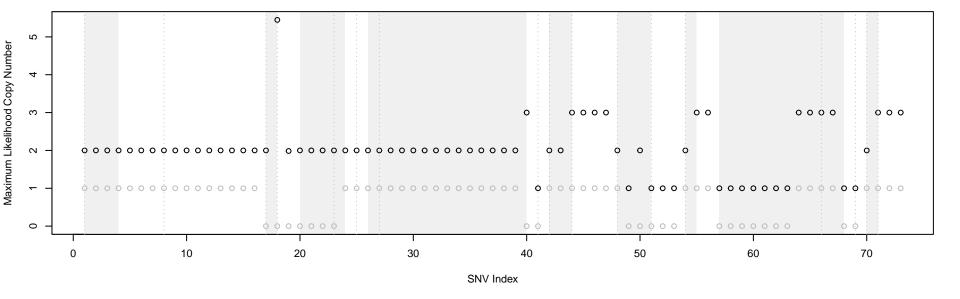
Purity: 0.29 Tumor ploidy: 2.214 2 3 5 0 6 7 Fraction Genome 0.05 0.00 -1.0 -0.5 0.0 0.5

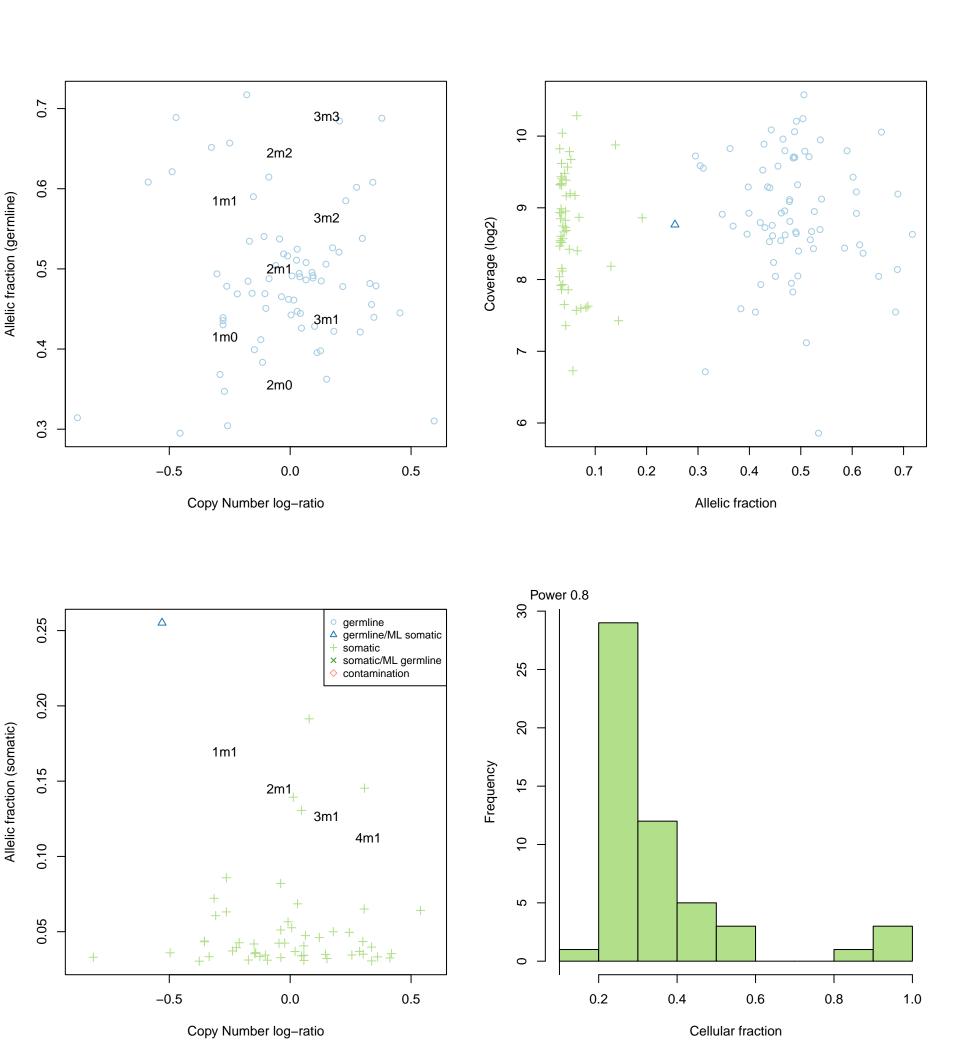
log2 ratio



SCNA-fit log-likelihood: -7026.84

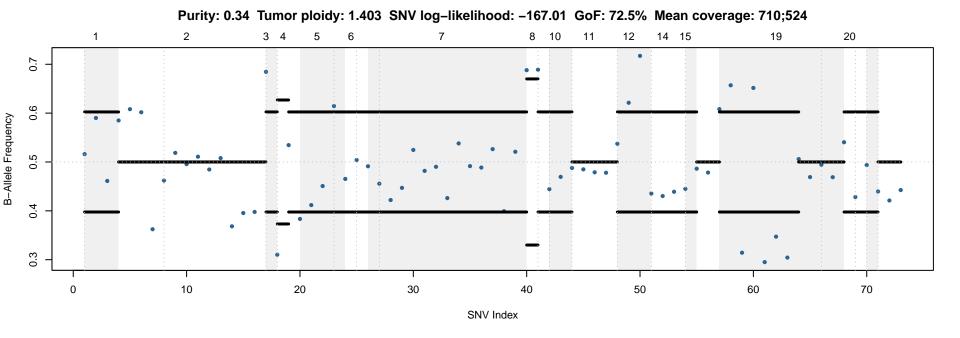




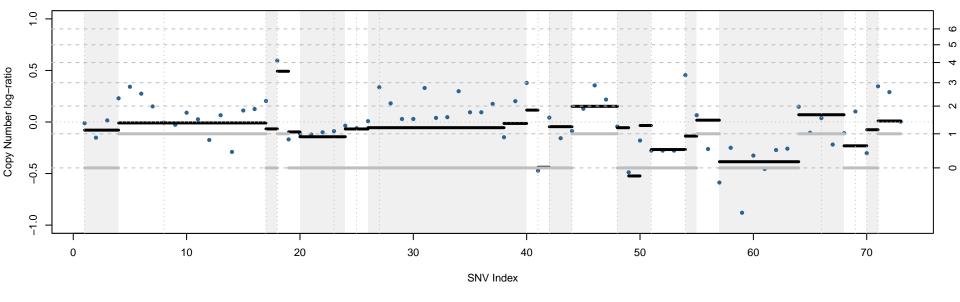


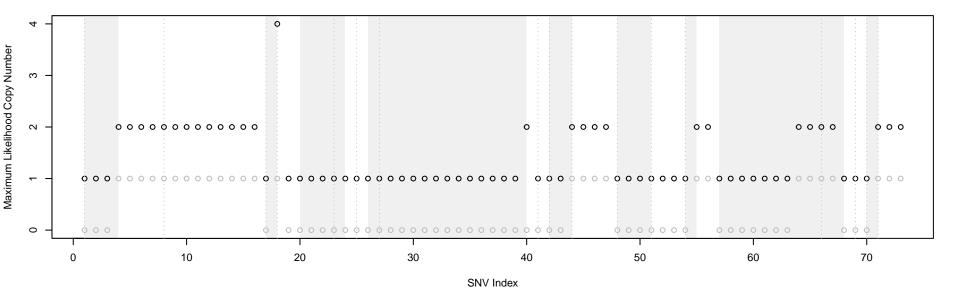
Purity: 0.34 Tumor ploidy: 1.403 0 5 Fraction Genome 0.05 0.00 -0.5 0.0 0.5

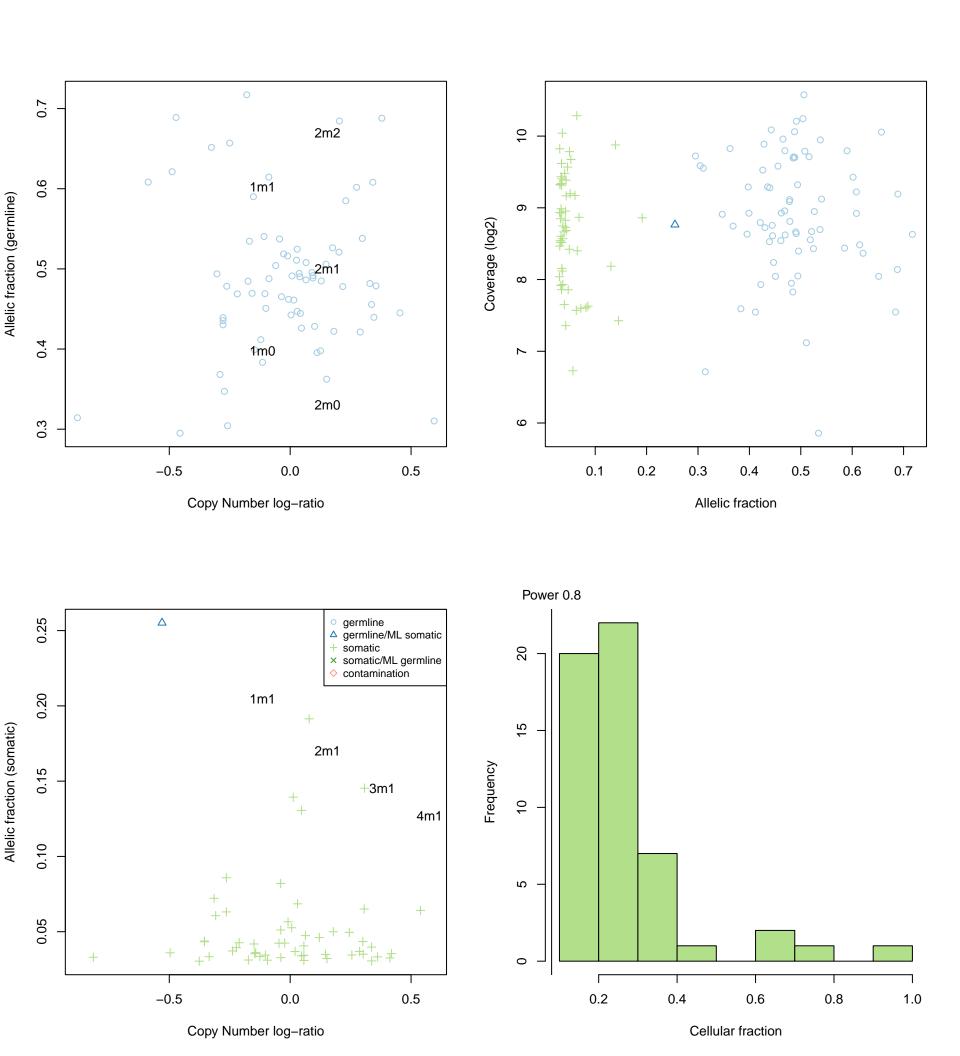
log2 ratio



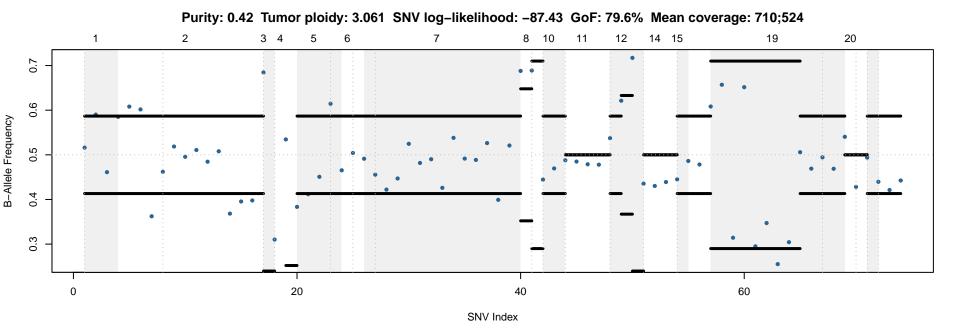
SCNA-fit log-likelihood: -6883.92



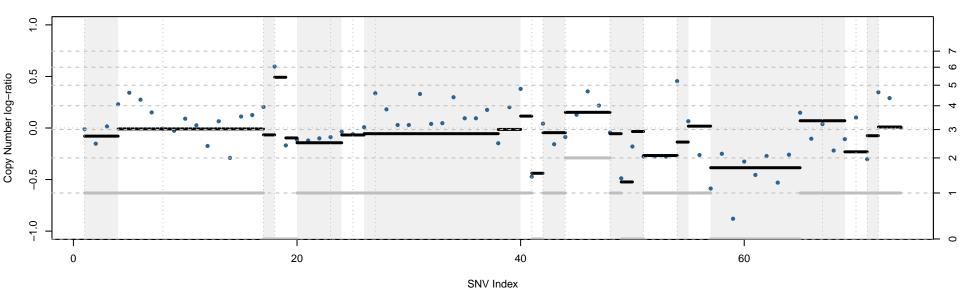


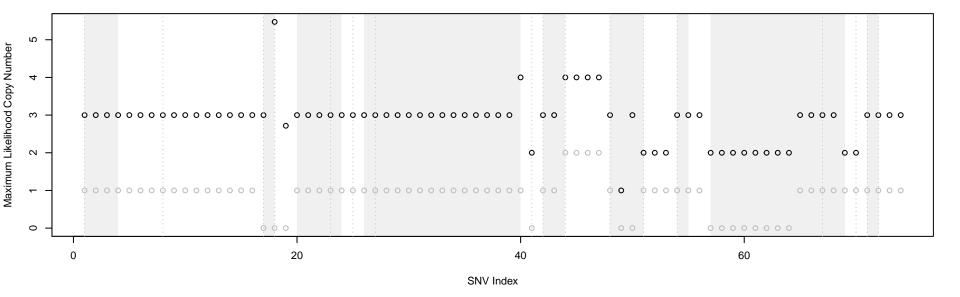


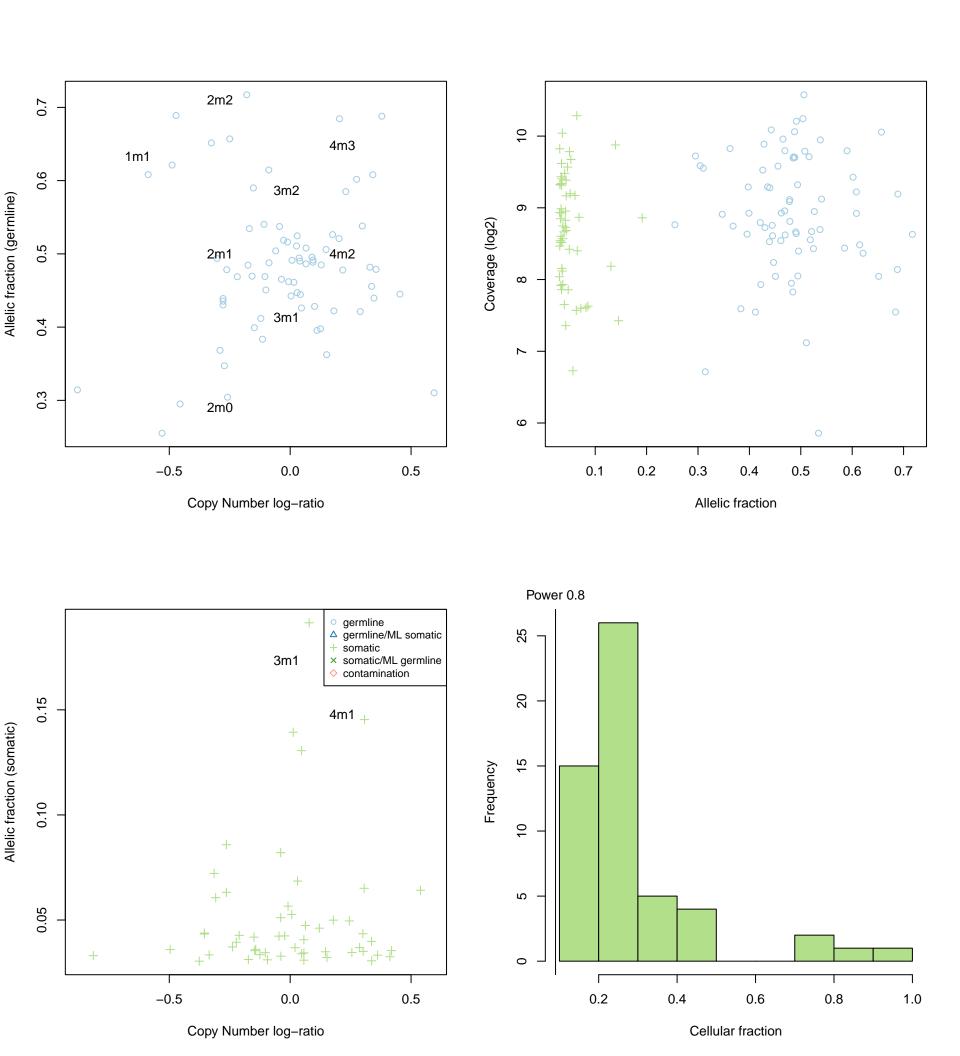
Purity: 0.42 Tumor ploidy: 3.061 2 0 5 6 Fraction Genome 0.05 0.00 -1.0 -1.5 -0.5 0.0 0.5 log2 ratio



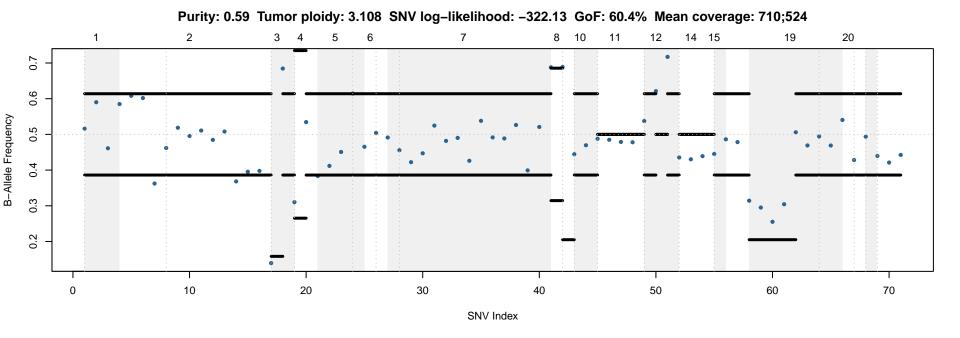
SCNA-fit log-likelihood: -7051.53



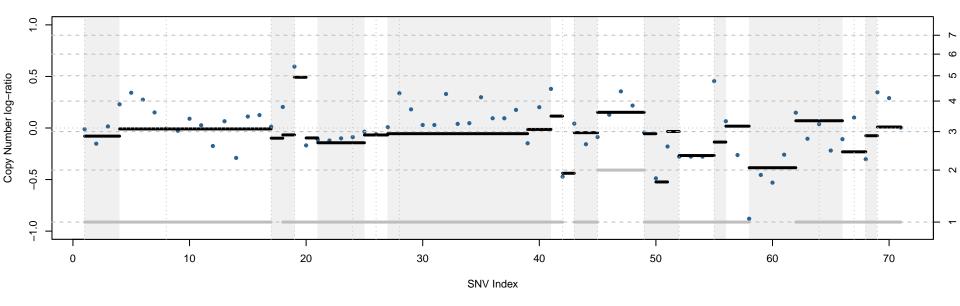


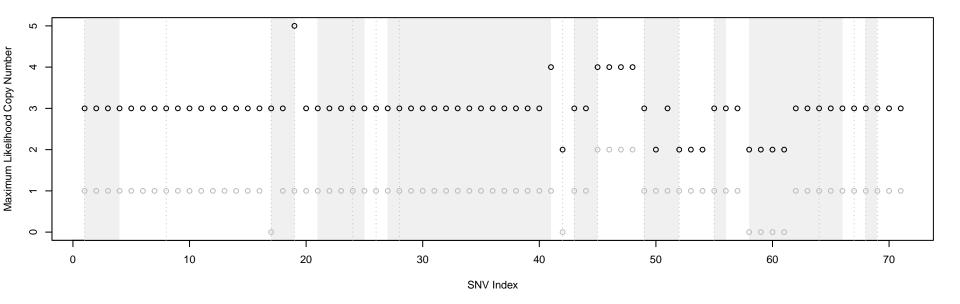


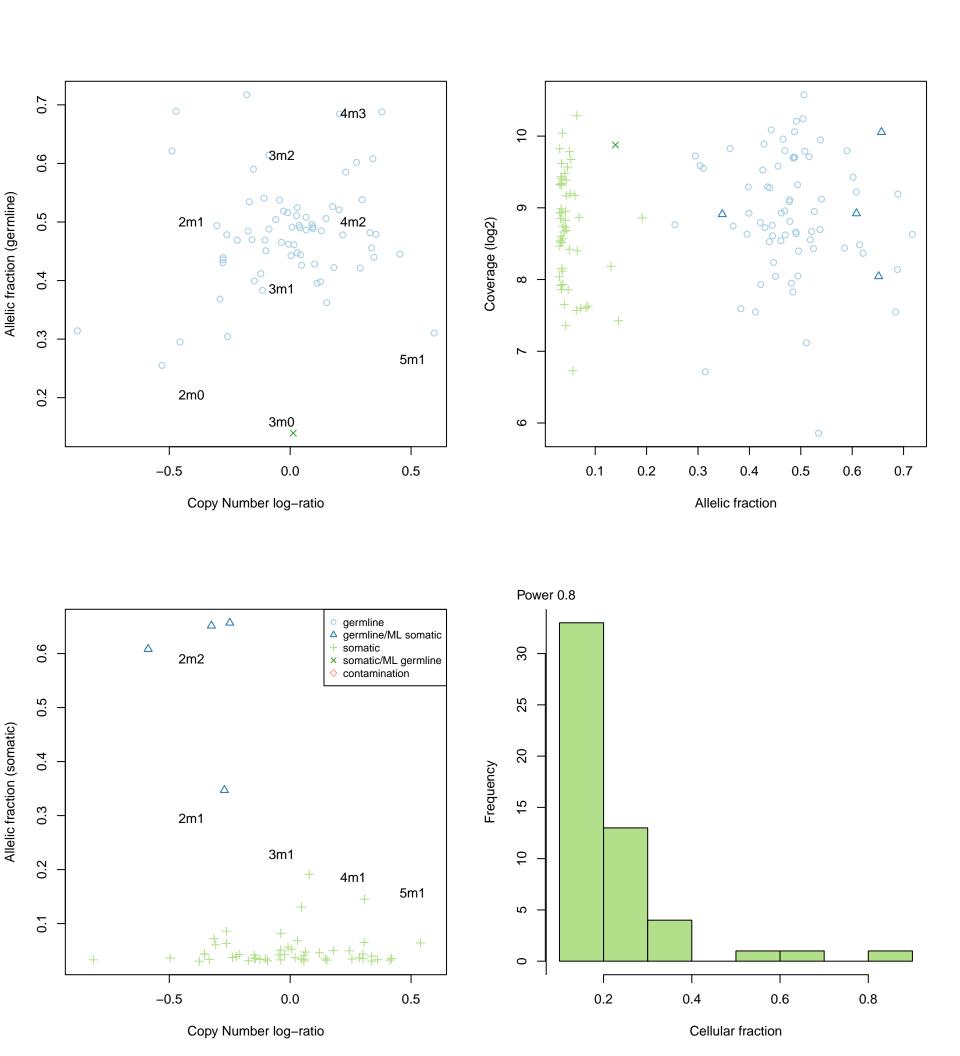
Purity: 0.59 Tumor ploidy: 3.108 0 5 6 Fraction Genome 0.05 0.00 -1.0 -0.5 -1.5 0.0 0.5 log2 ratio



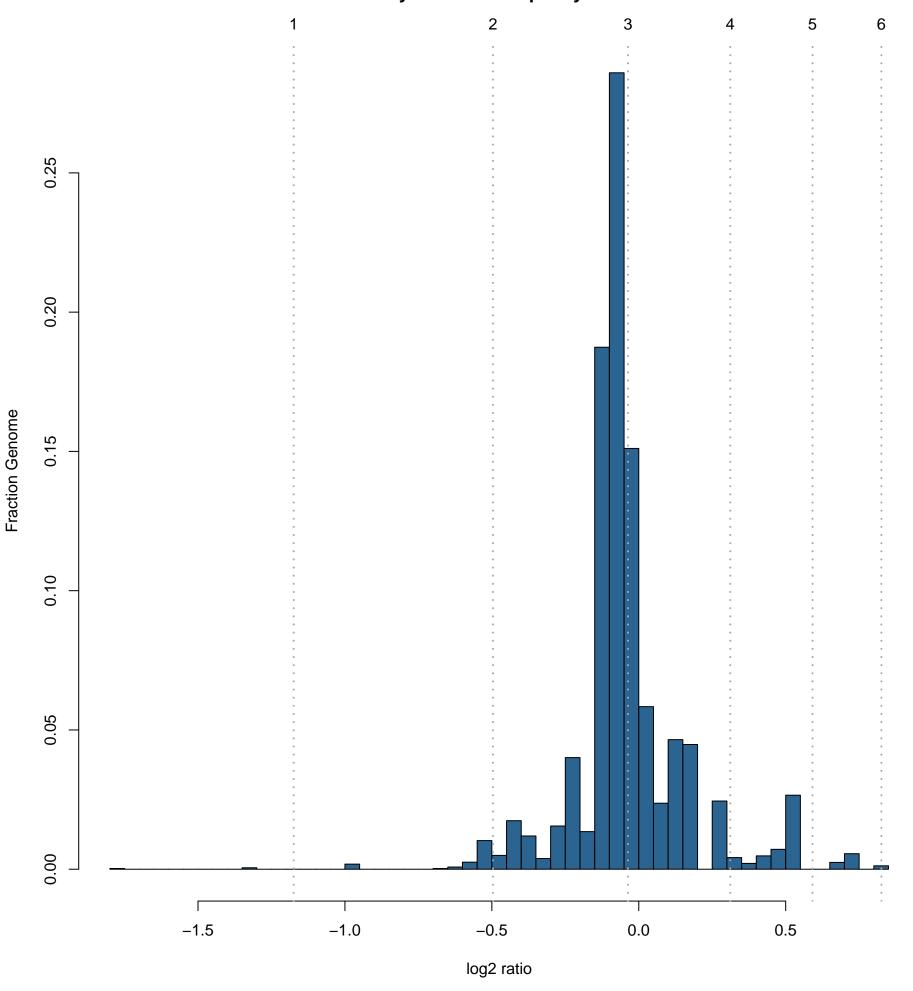
SCNA-fit log-likelihood: -6670.67

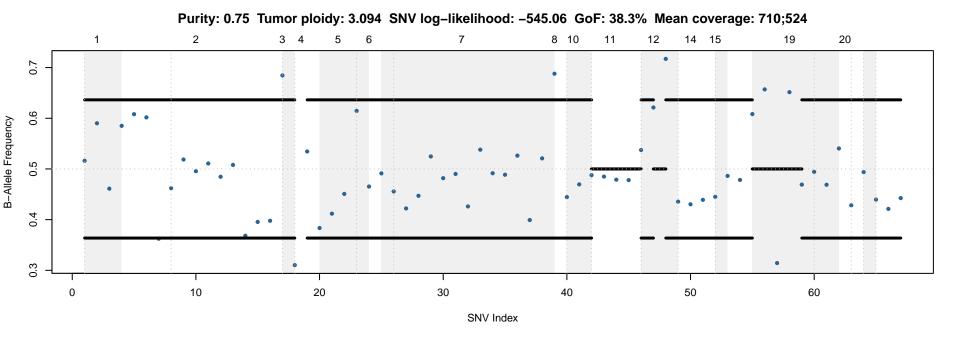




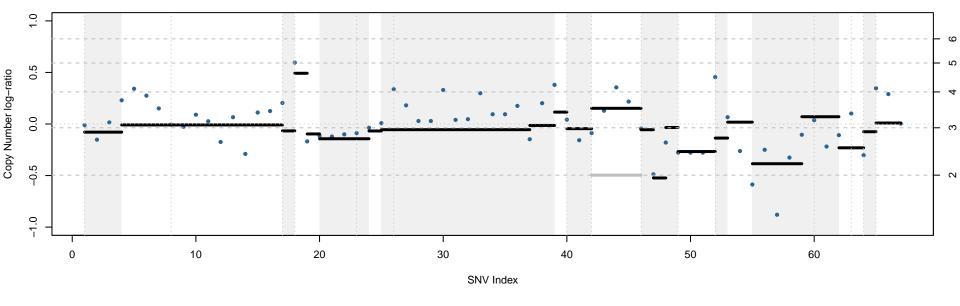


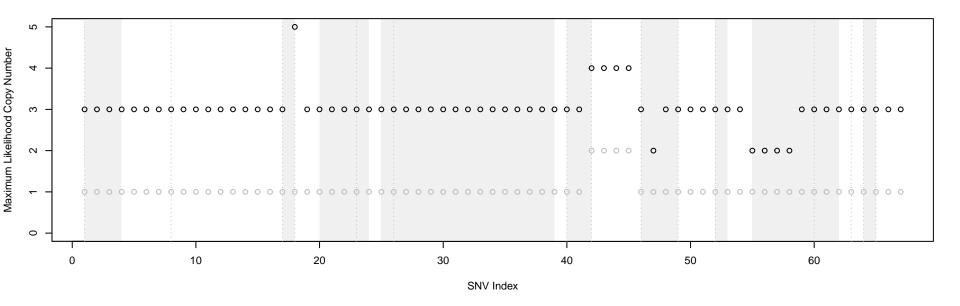
Purity: 0.75 Tumor ploidy: 3.094

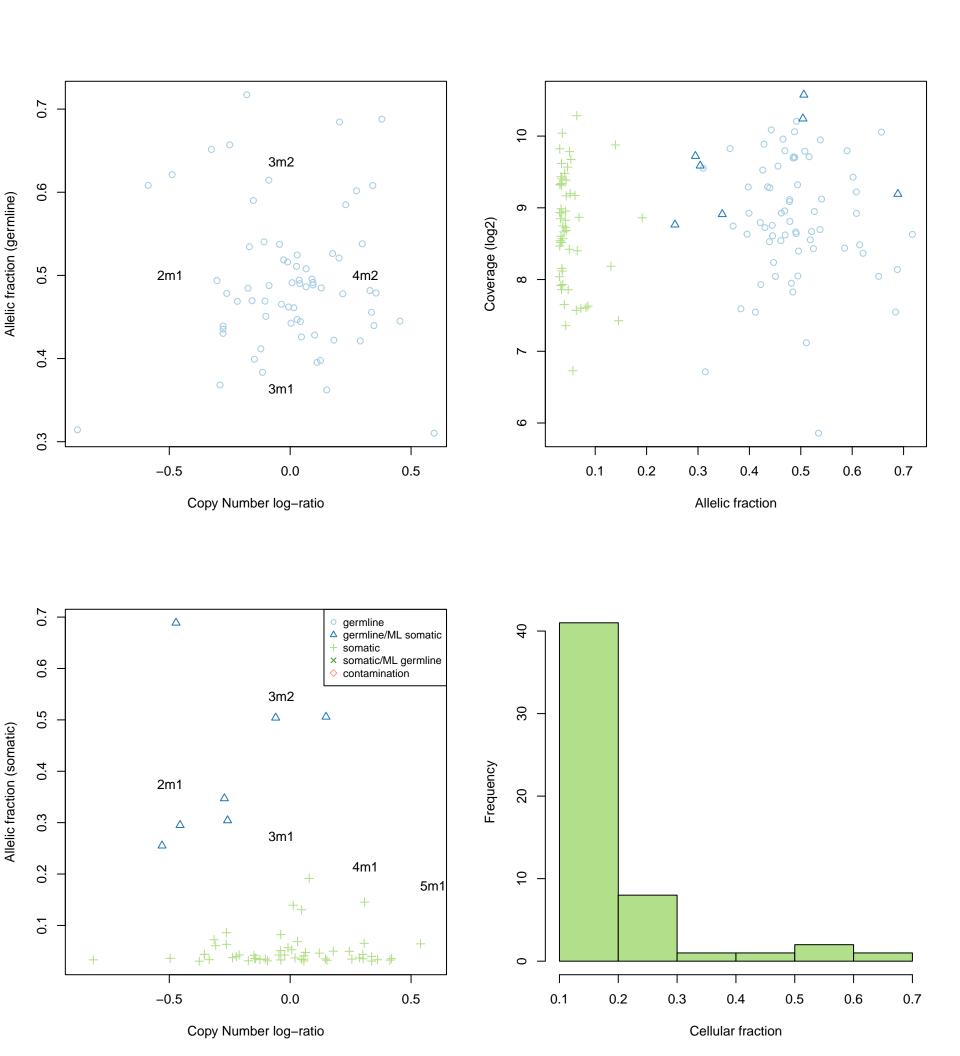




SCNA-fit log-likelihood: -6721.64

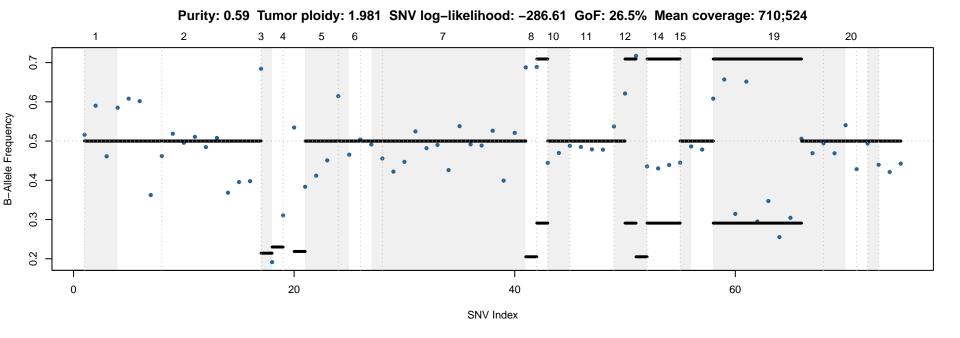






Purity: 0.59 Tumor ploidy: 1.981 0 3 5 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -1.5 -0.5 0.0 0.5

log2 ratio



SCNA-fit log-likelihood: -7851.32

