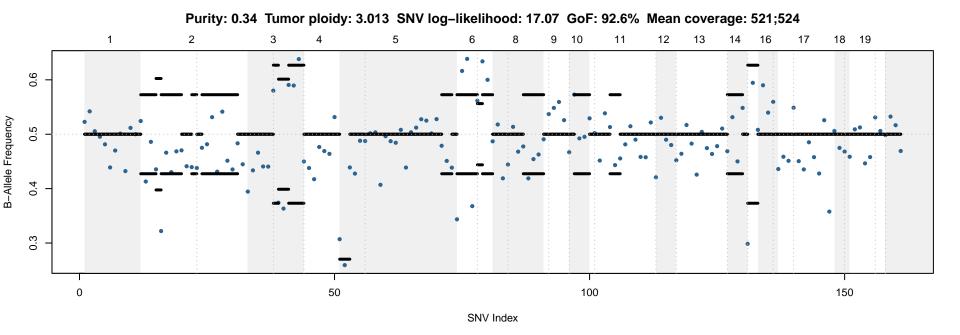
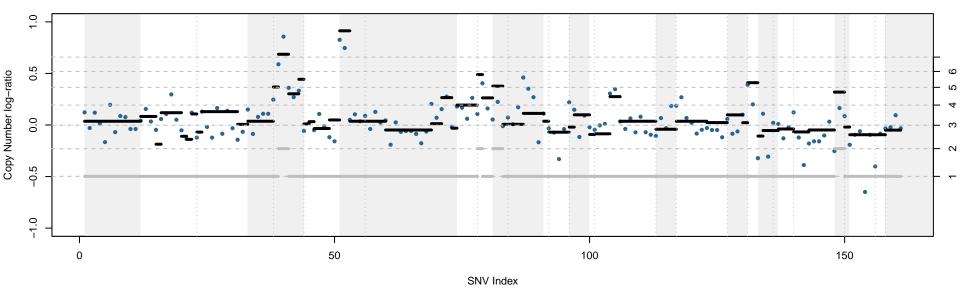
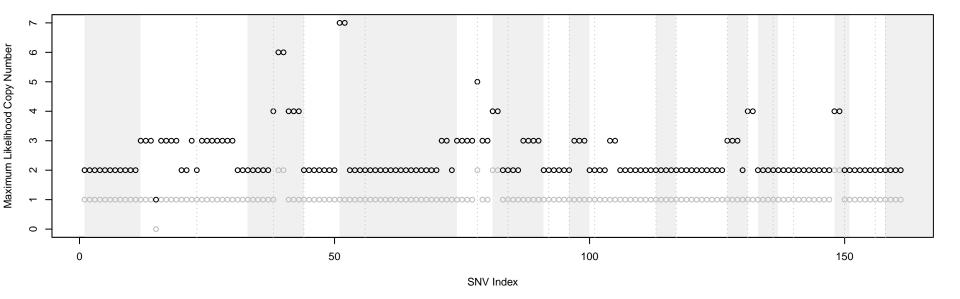
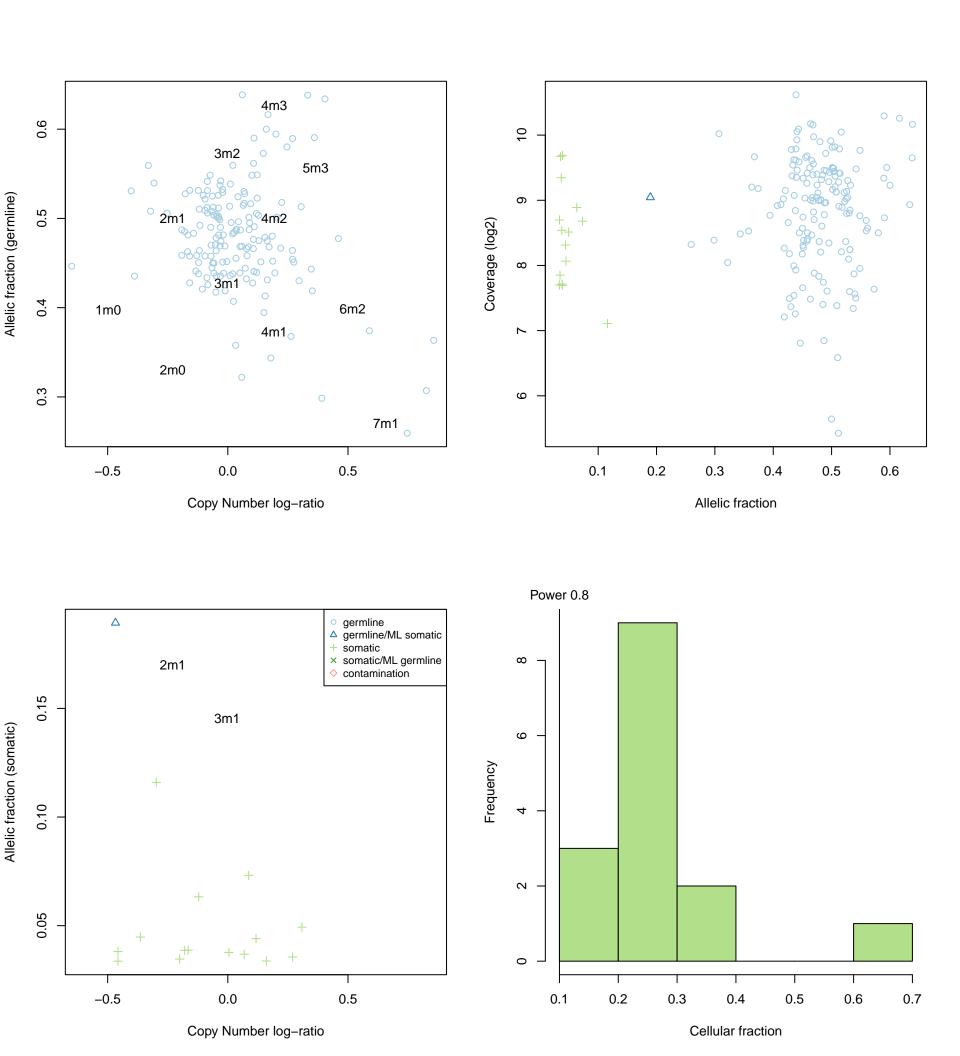
Purity: 0.34 Tumor ploidy: 3.013 2 3 5 6 7 Fraction Genome 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio



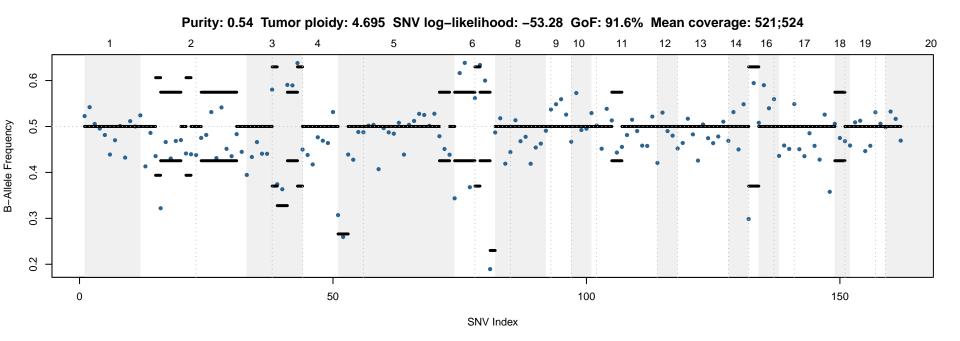
SCNA-fit log-likelihood: -152.66



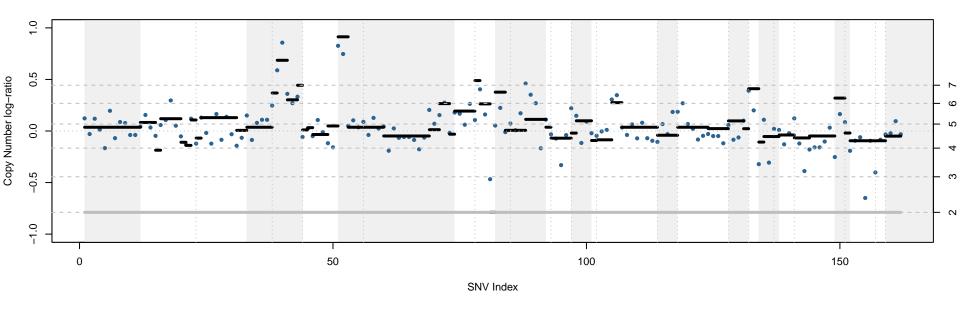


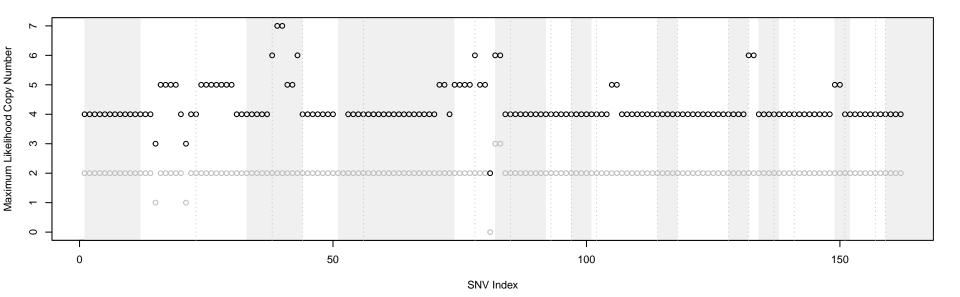


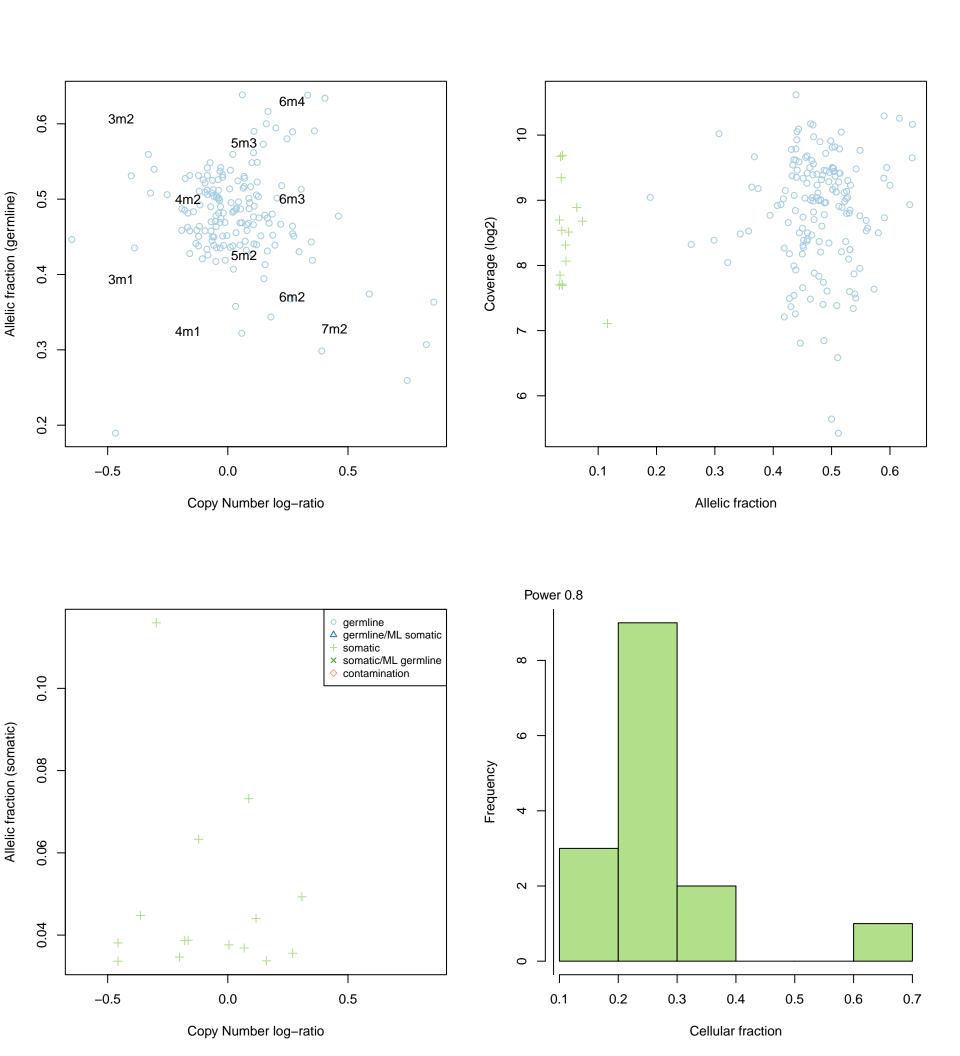
Purity: 0.54 Tumor ploidy: 4.695 2 3 5 0.20 Fraction Genome 0.05 0.00 0.0 -0.5 0.5 1.0 log2 ratio

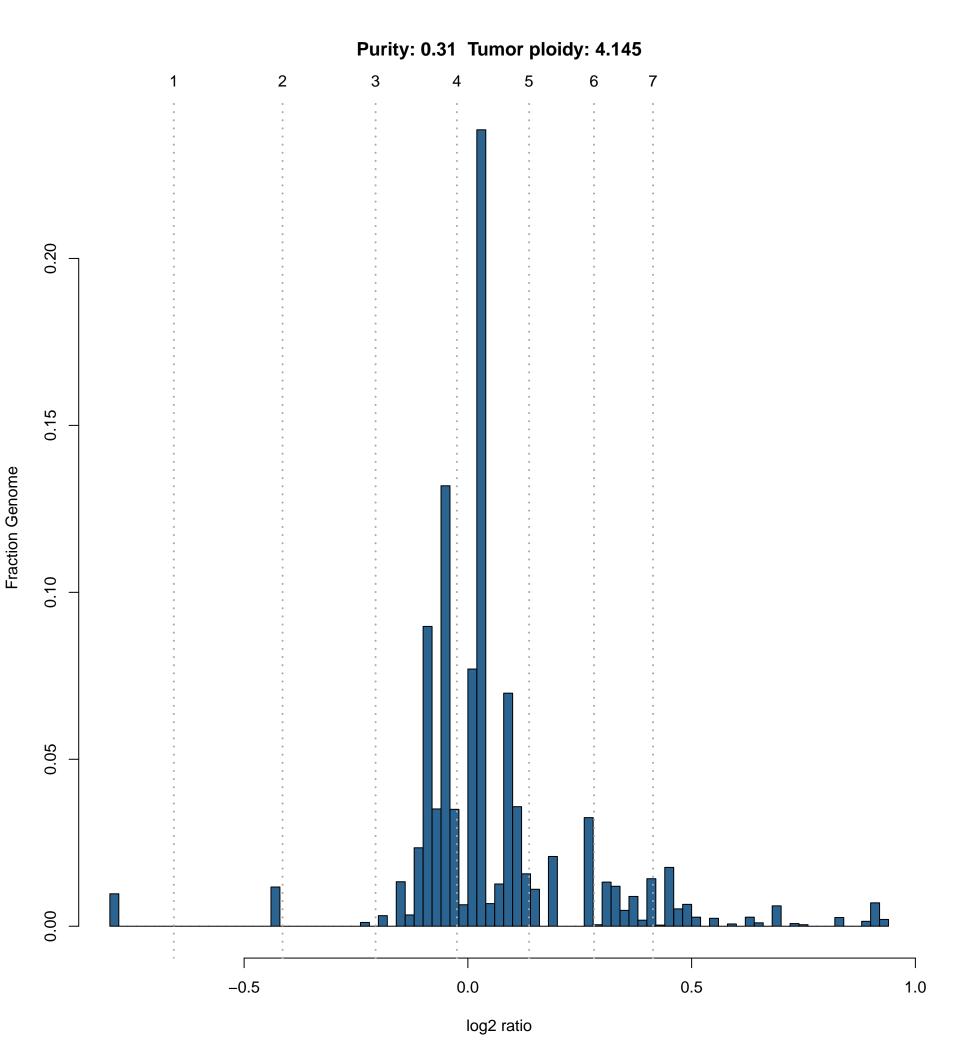


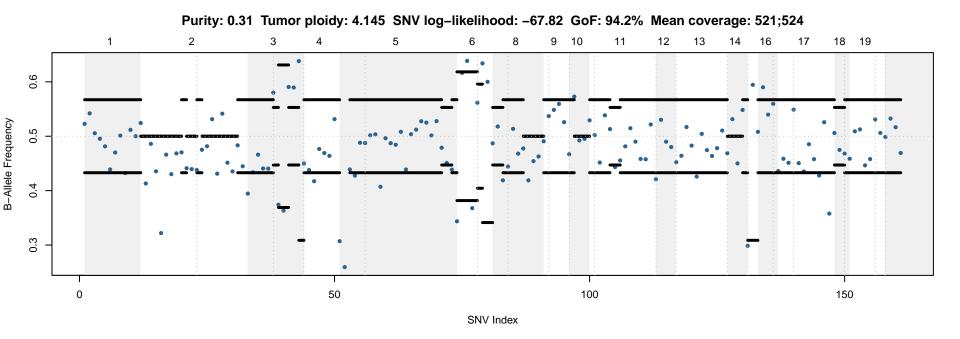
SCNA-fit log-likelihood: -119.35



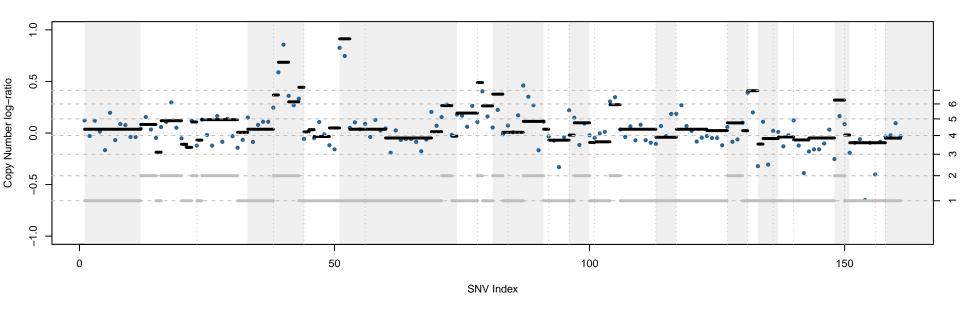


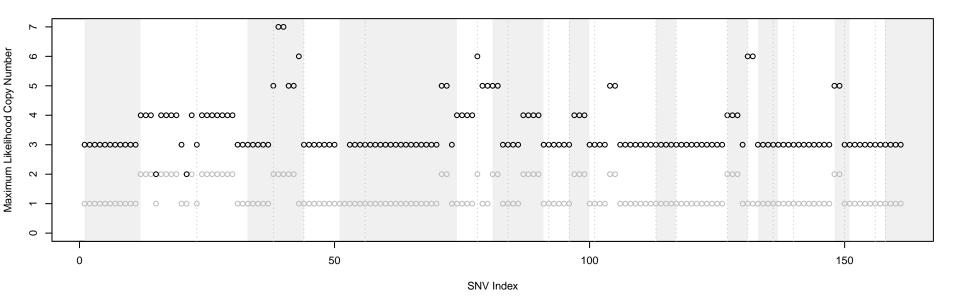


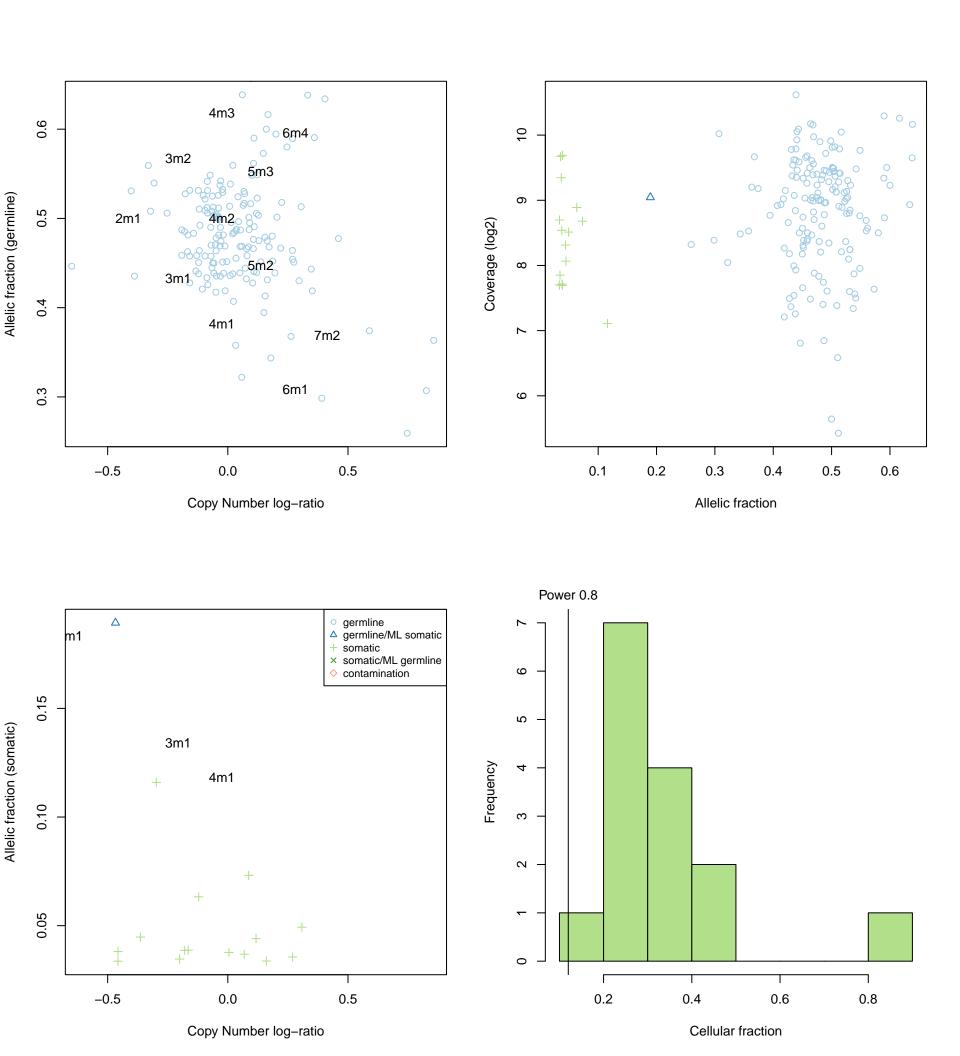




SCNA-fit log-likelihood: -99.39

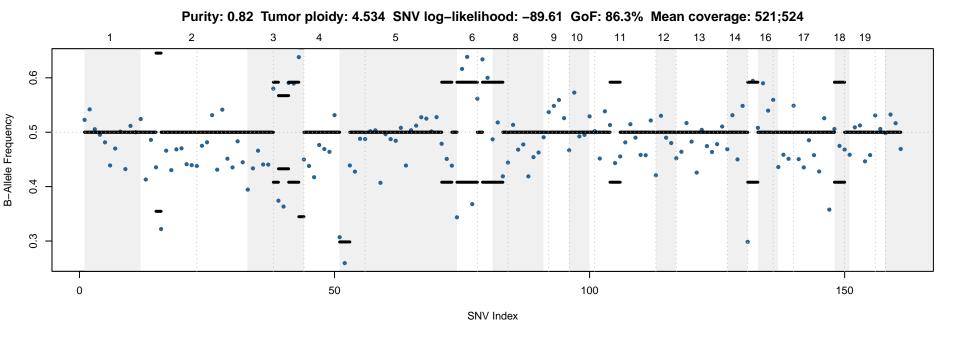




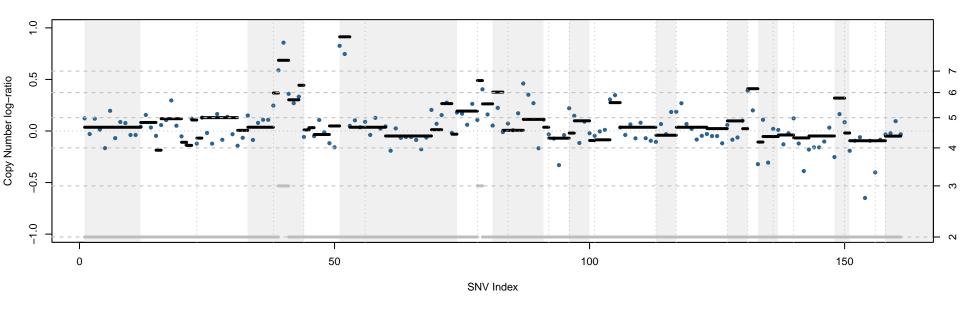


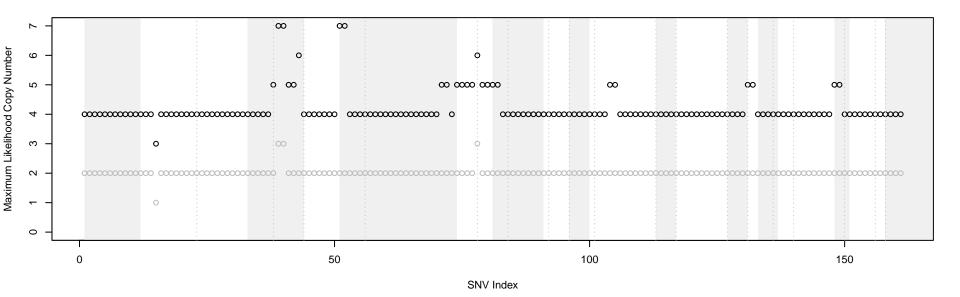
Purity: 0.82 Tumor ploidy: 4.534 3 6 7 Fraction Genome 0.05 0.00 0.0 -0.5 0.5 1.0

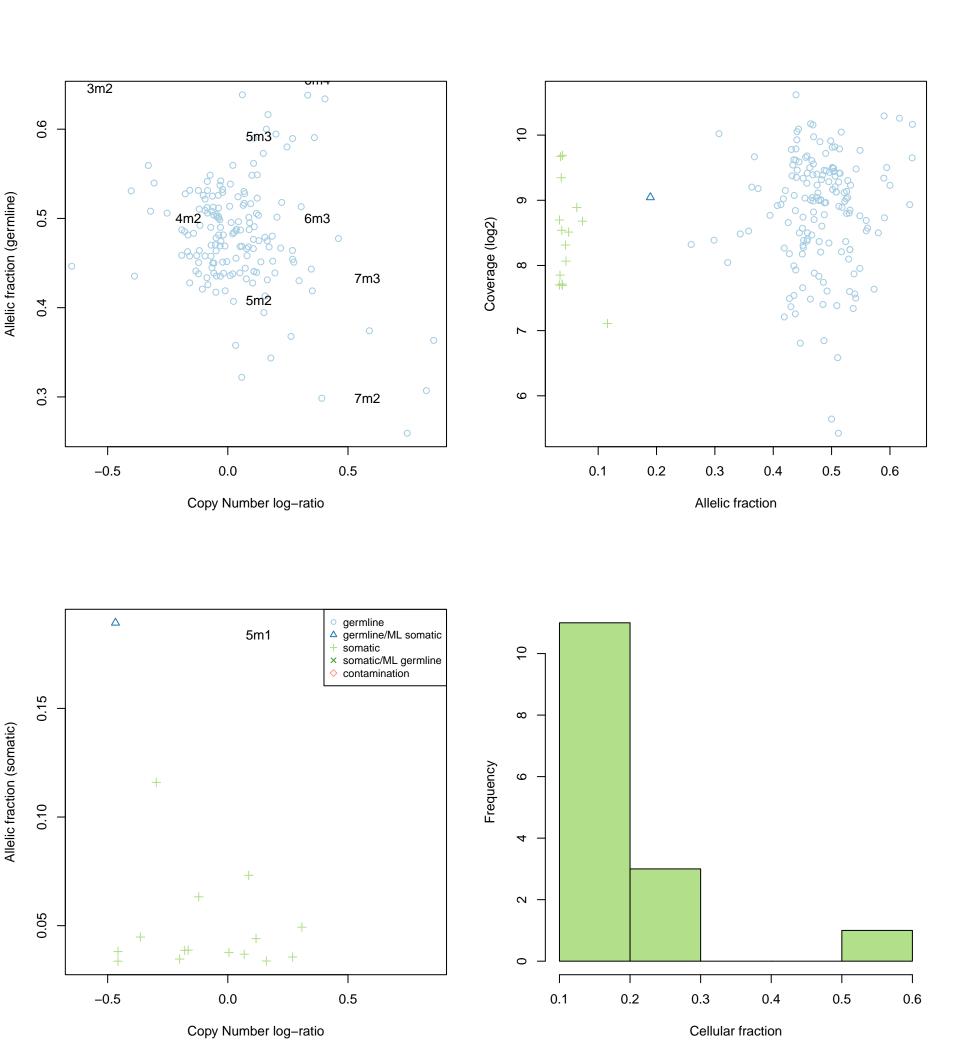
log2 ratio

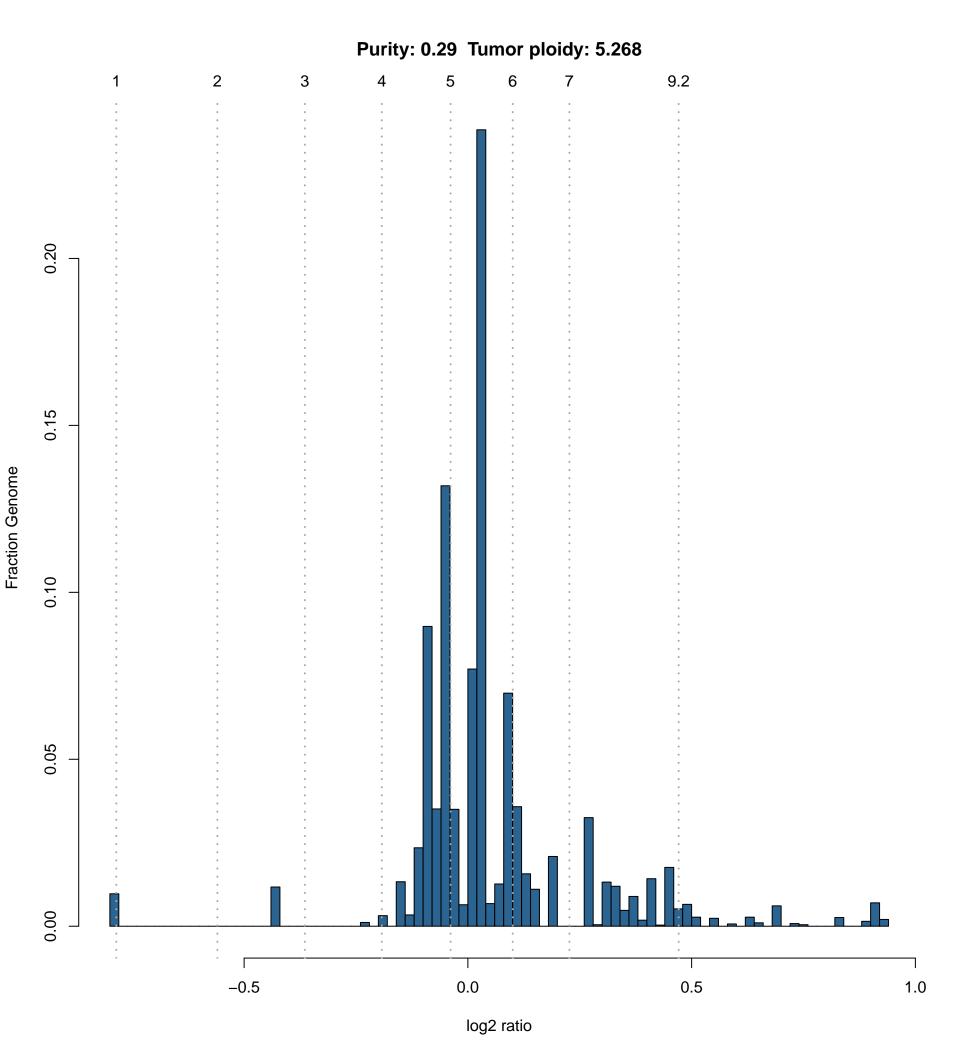


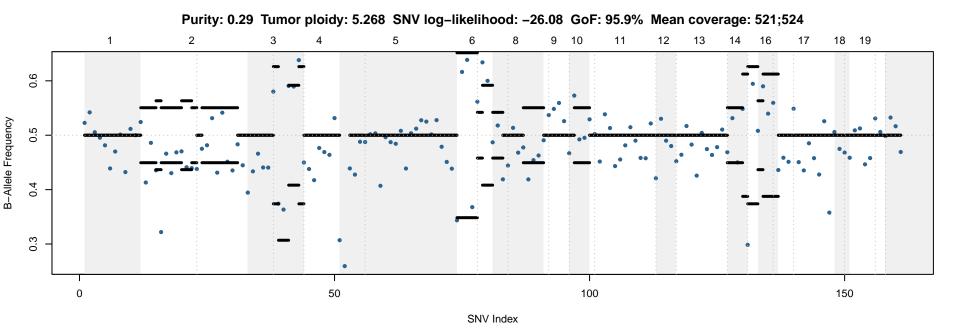
SCNA-fit log-likelihood: -80.36



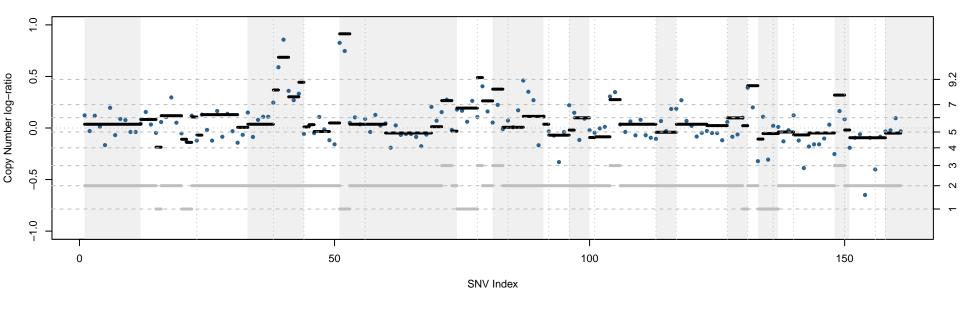


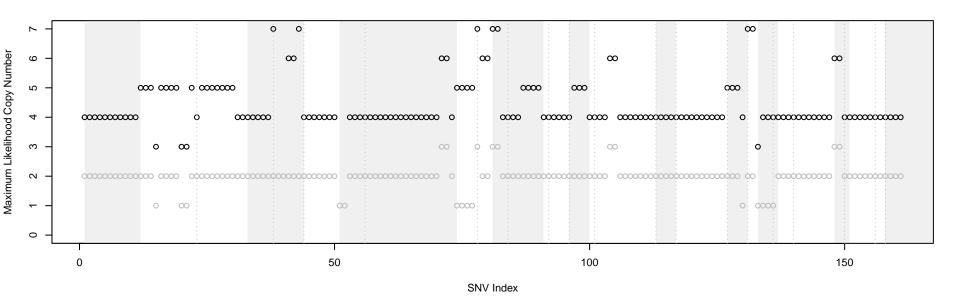


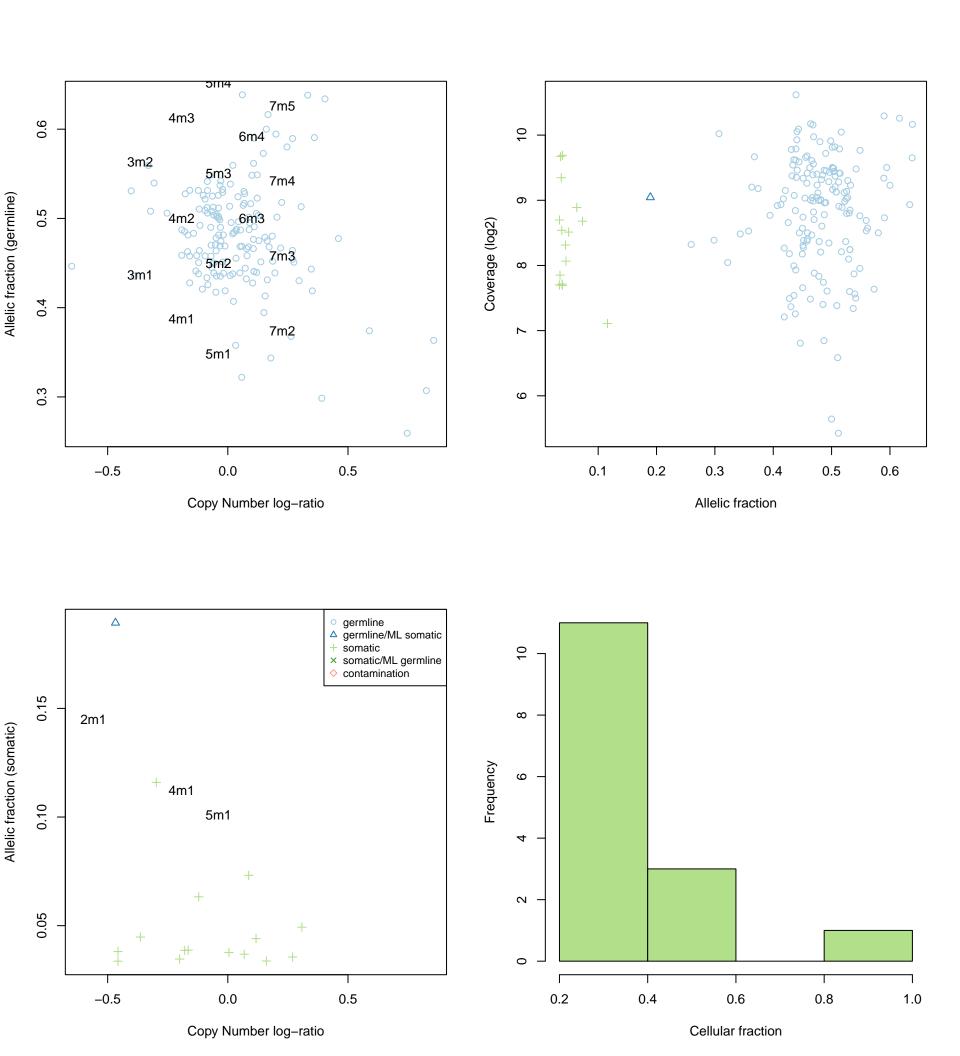




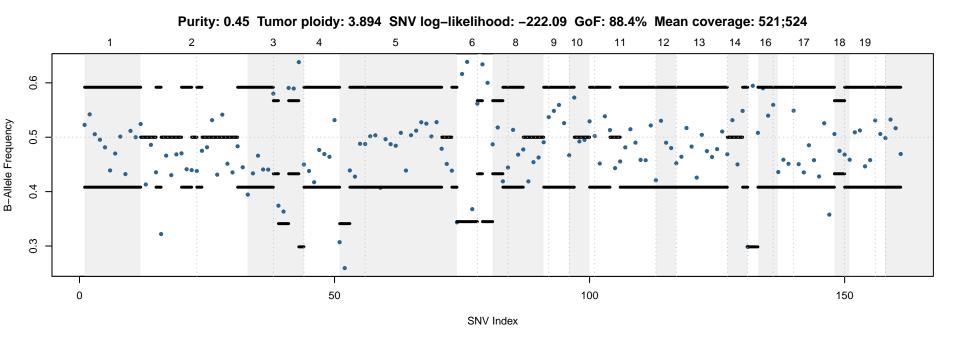
SCNA-fit log-likelihood: -249.74



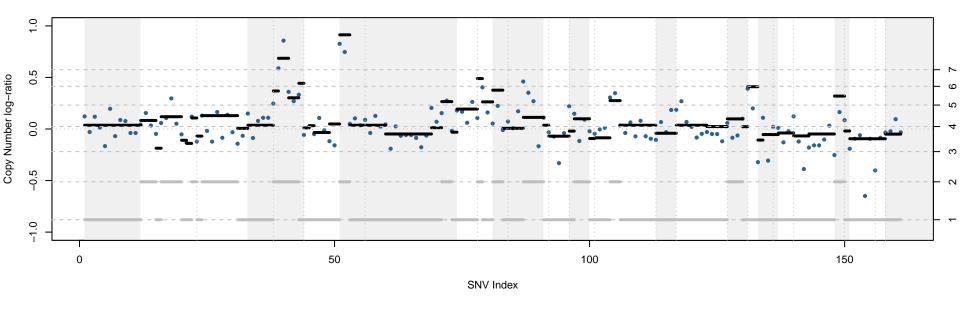


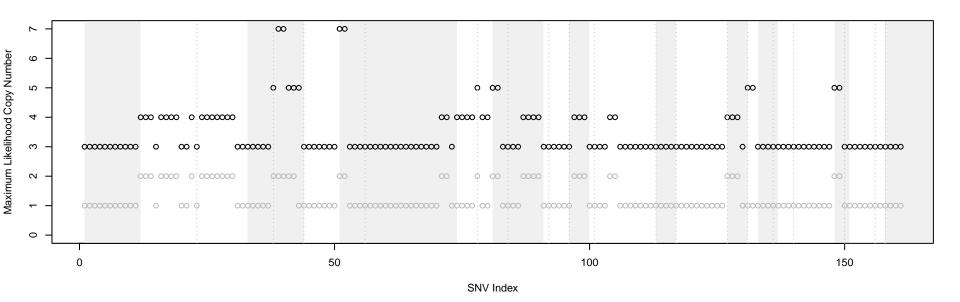


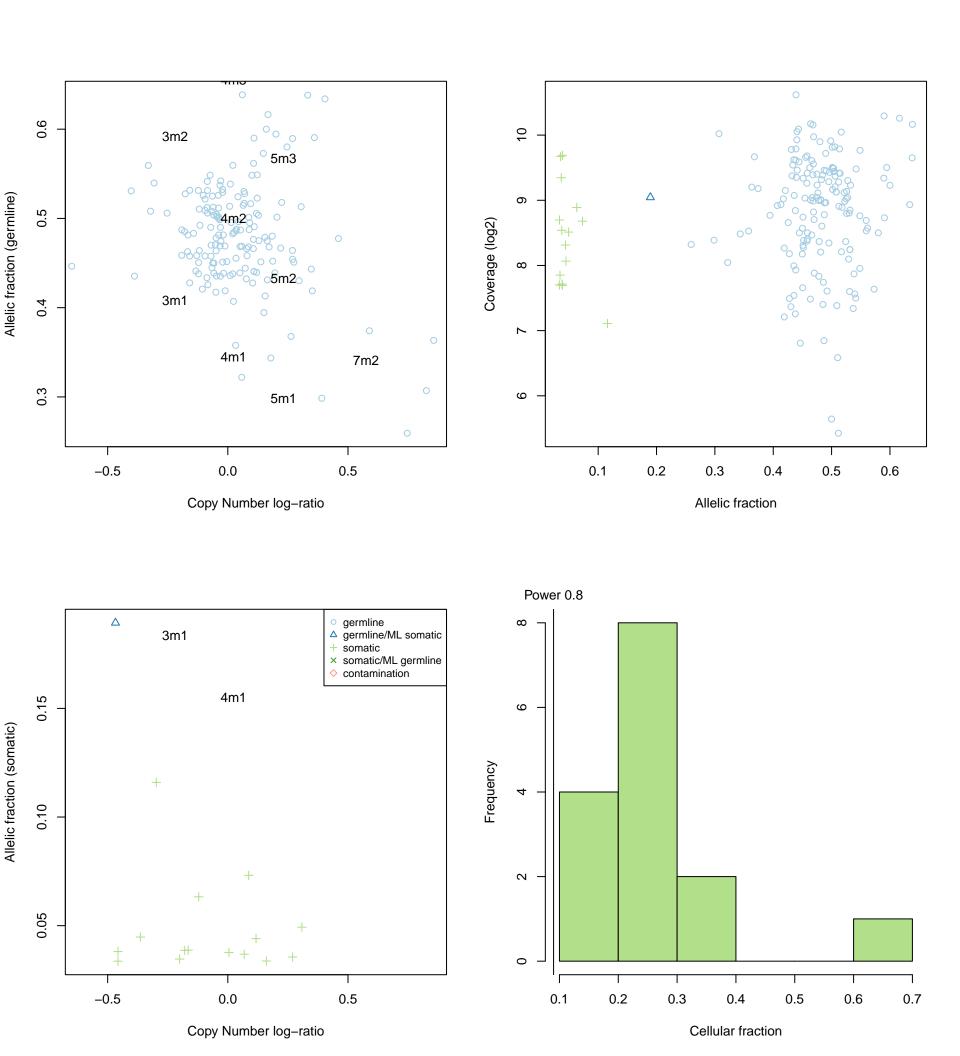
Purity: 0.45 Tumor ploidy: 3.894 2 3 5 7 Fraction Genome 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio



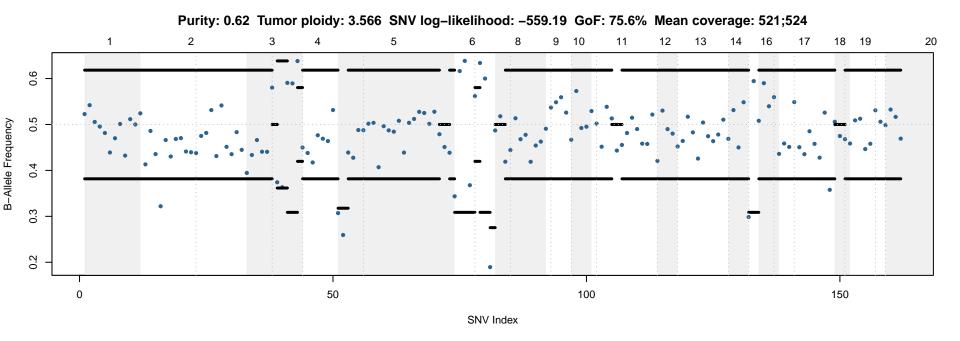
SCNA-fit log-likelihood: -49.09



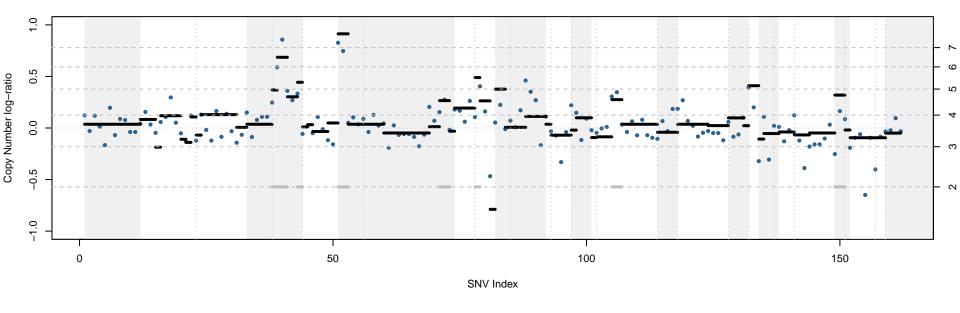


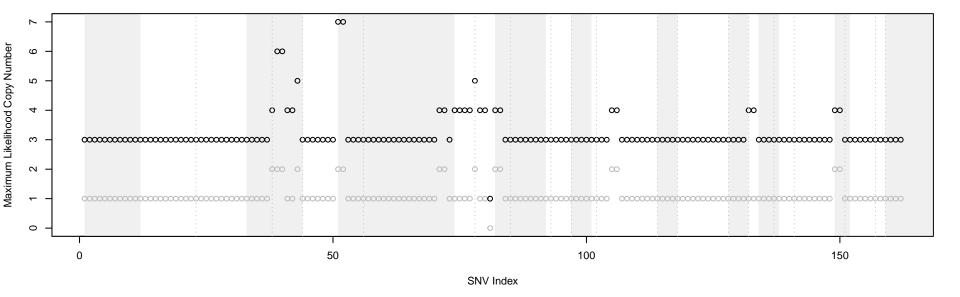


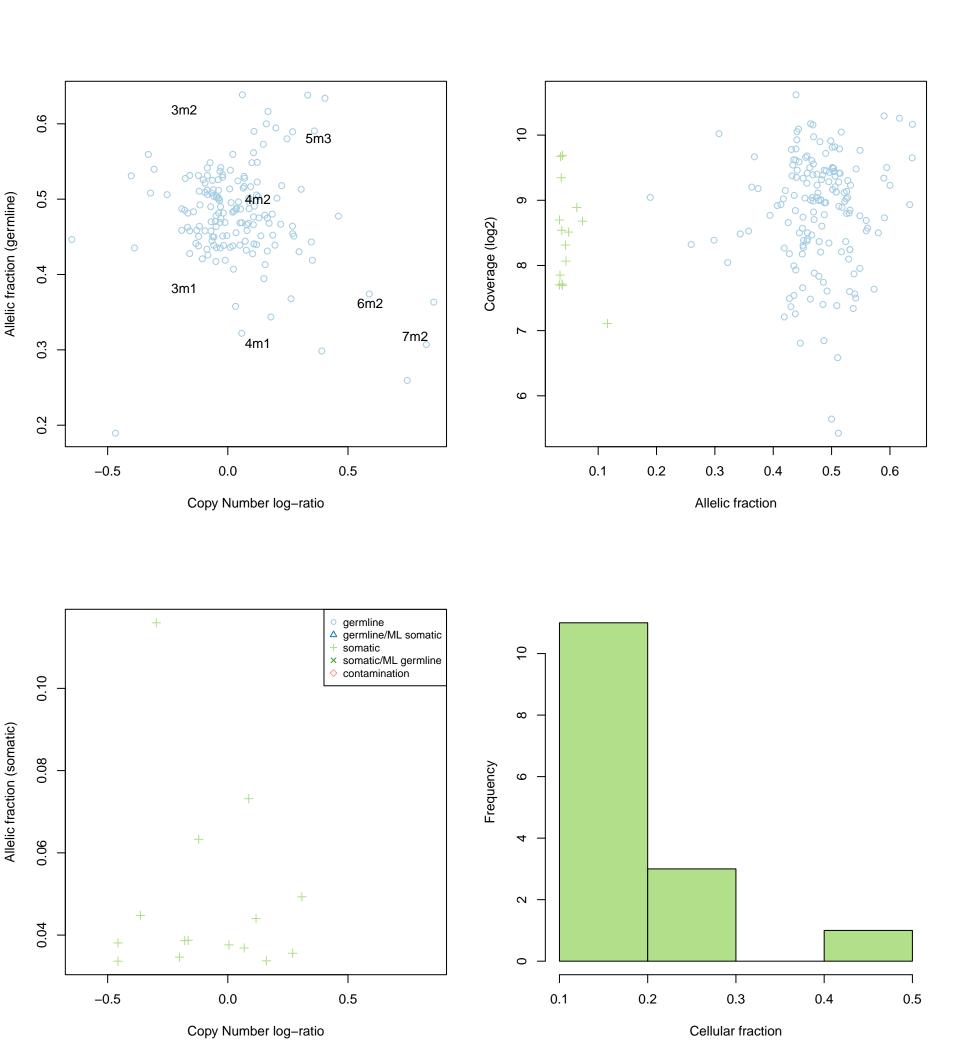
Purity: 0.62 Tumor ploidy: 3.566 2 6 7 Fraction Genome 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio



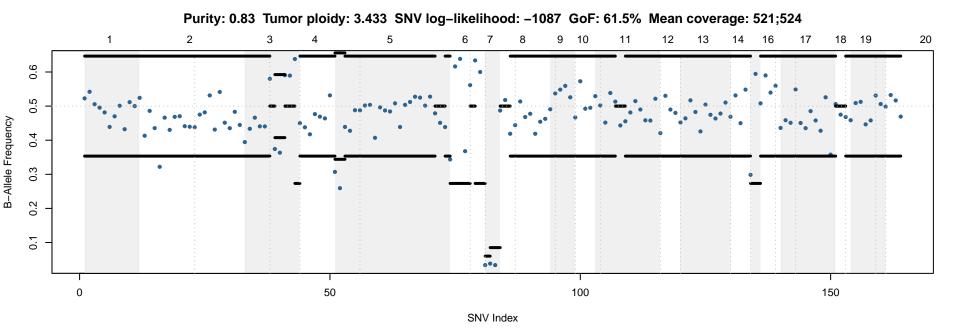
SCNA-fit log-likelihood: -80.77







Purity: 0.83 Tumor ploidy: 3.433 3 2 5 6 Fraction Genome 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio



SCNA-fit log-likelihood: -161.03

