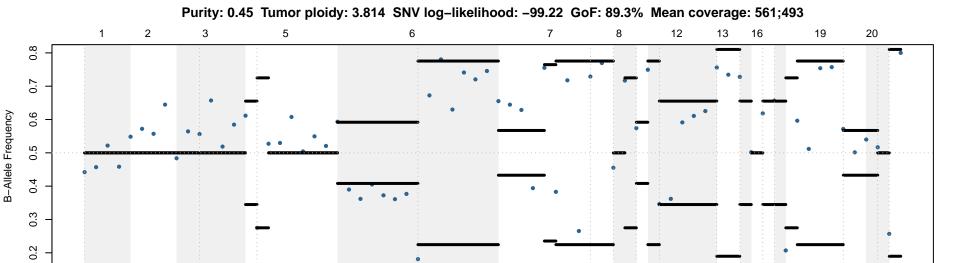
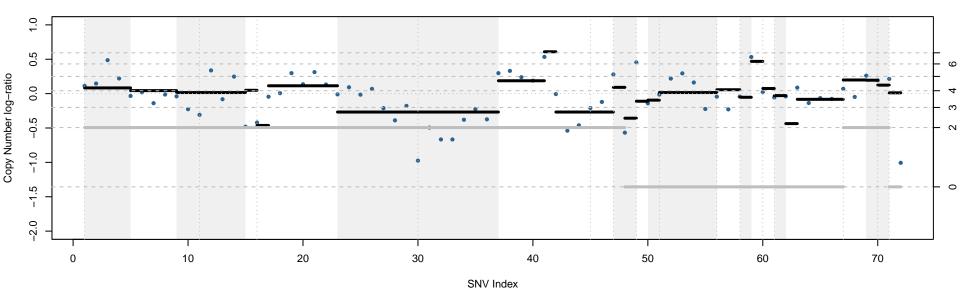
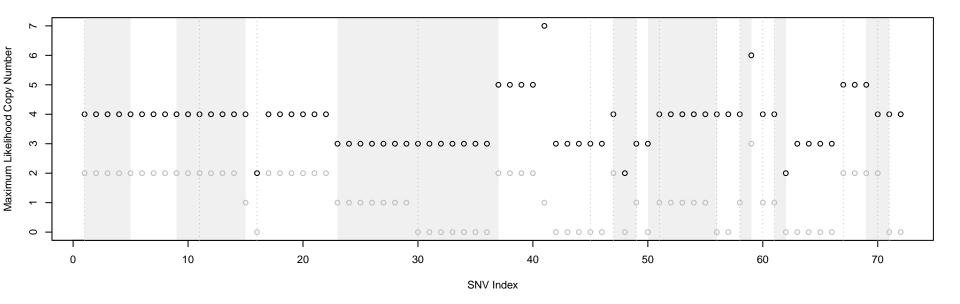
Purity: 0.45 Tumor ploidy: 3.814 0 3 2 5 6 7 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio

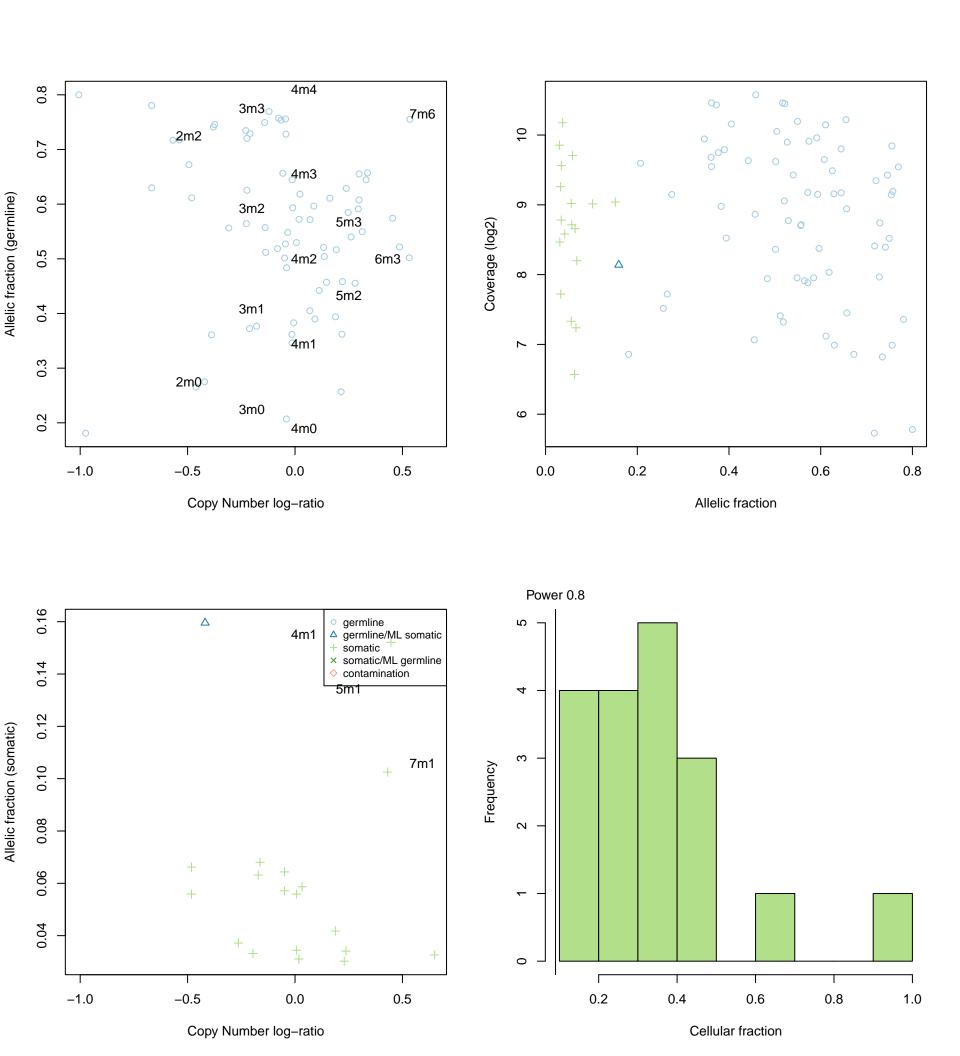


SCNA-fit log-likelihood: -10268.56

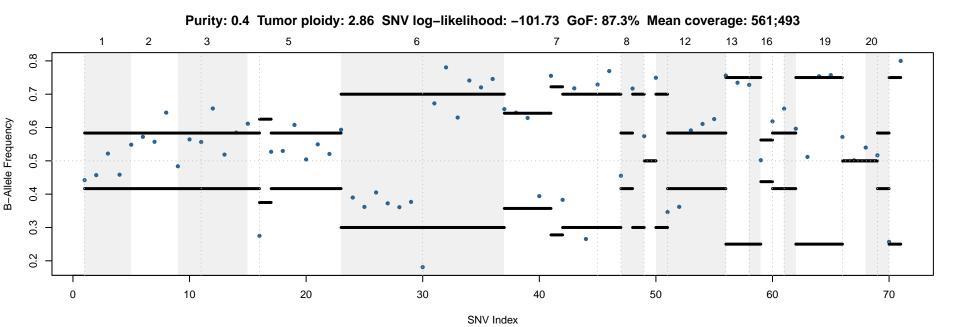
SNV Index



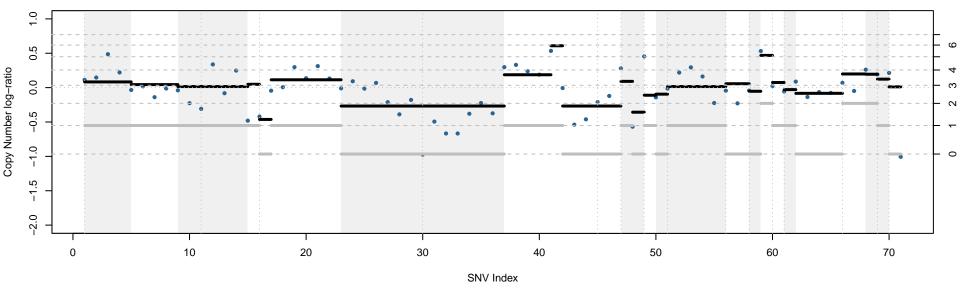


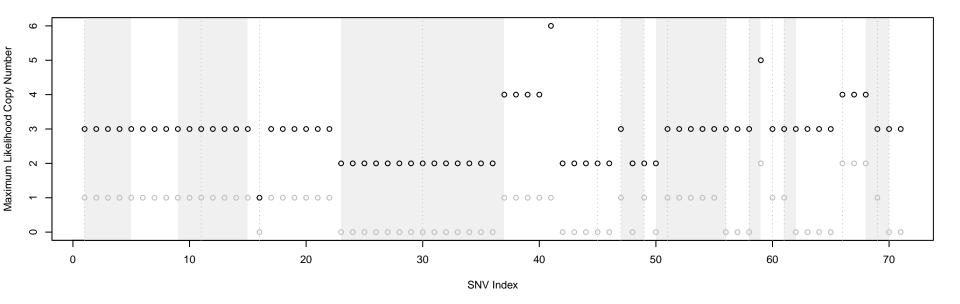


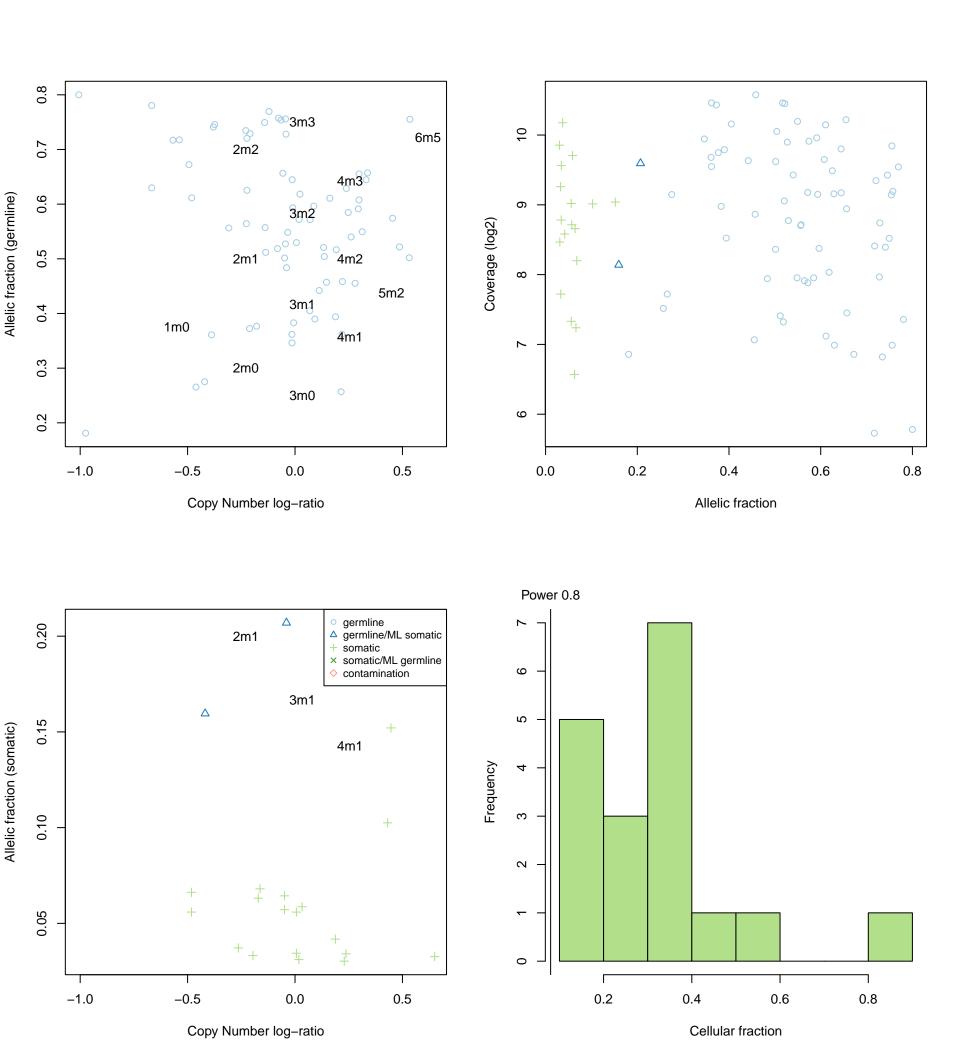
Purity: 0.4 Tumor ploidy: 2.86 2 0 5 3 6 0.25 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio

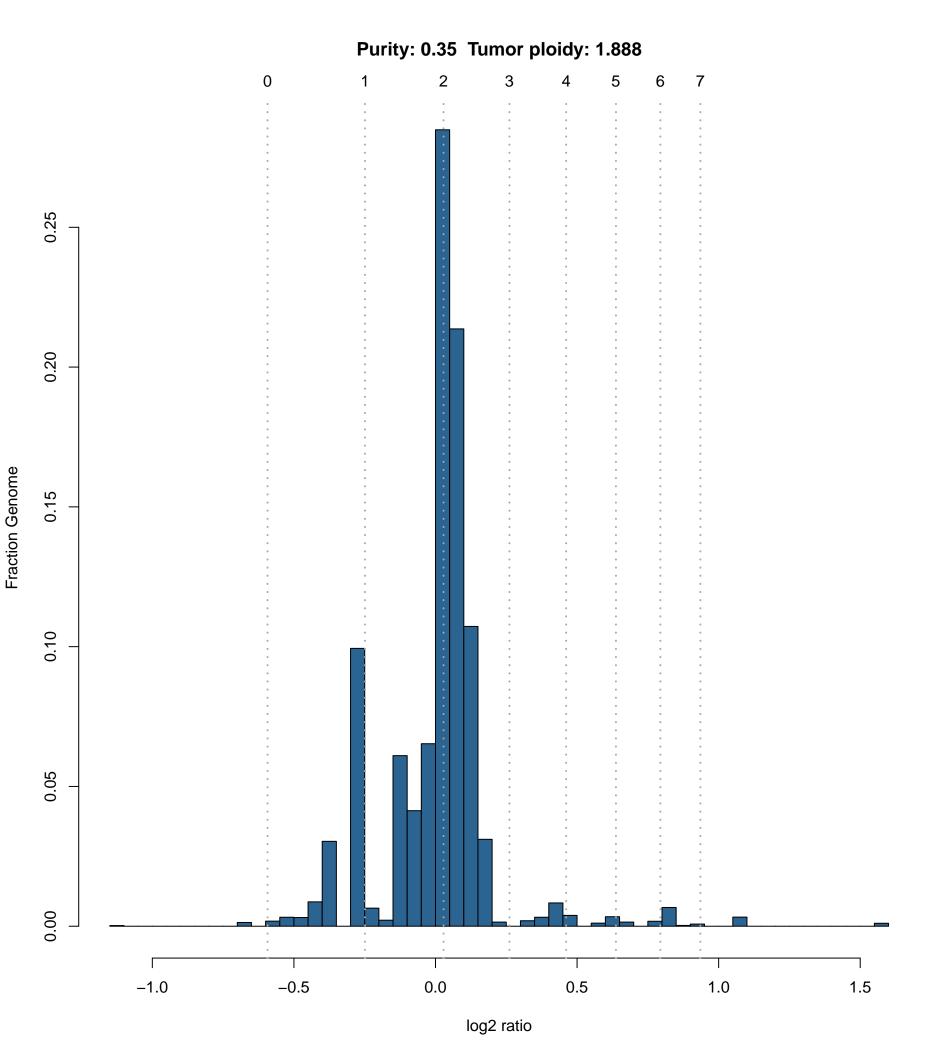


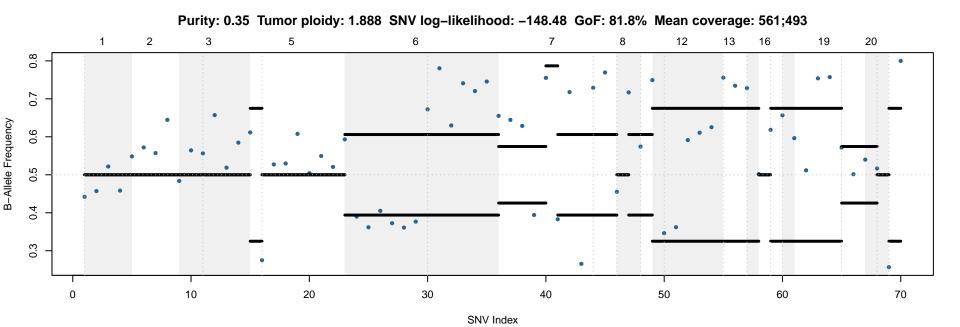
SCNA-fit log-likelihood: -10249.56



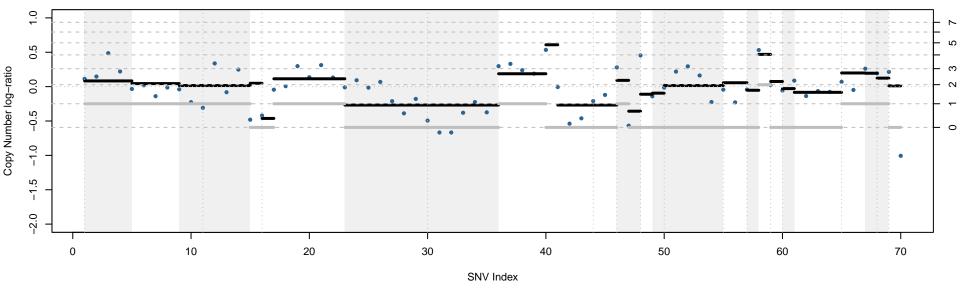


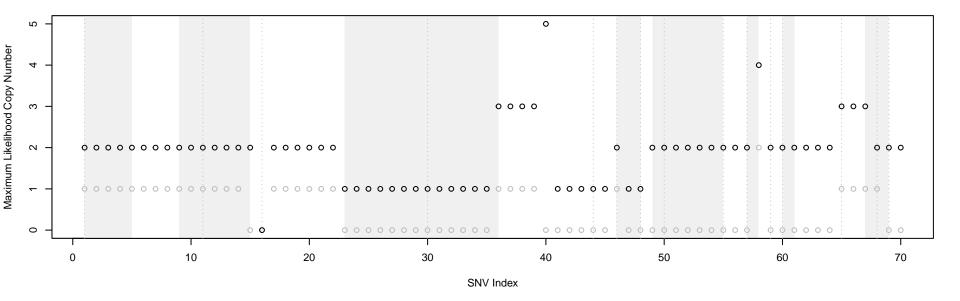


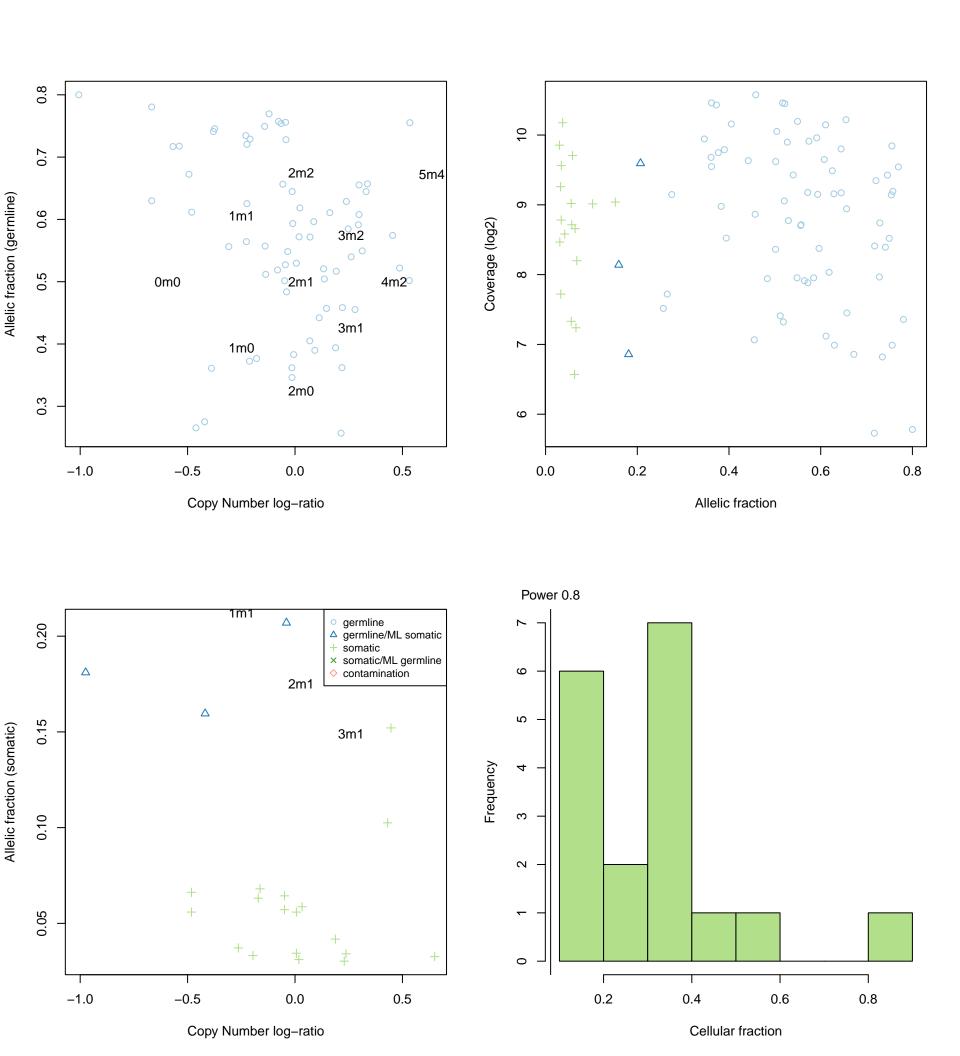




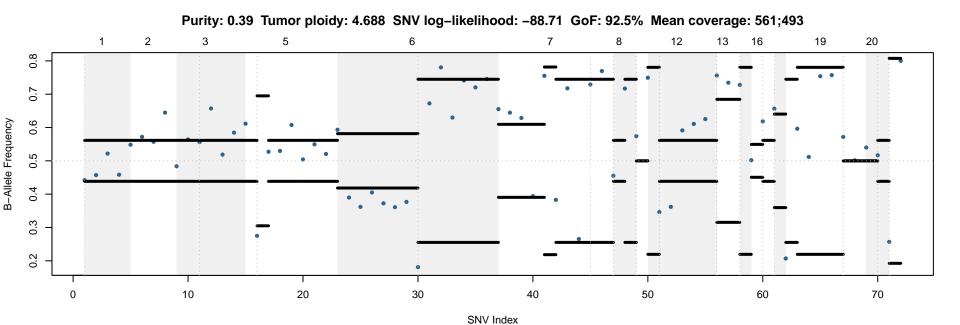
SCNA-fit log-likelihood: -10208.93



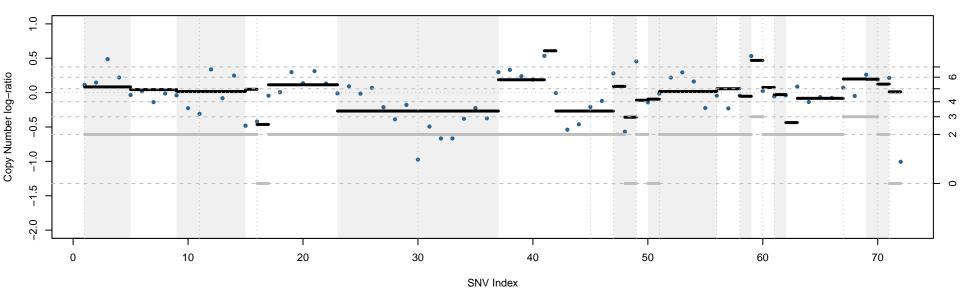


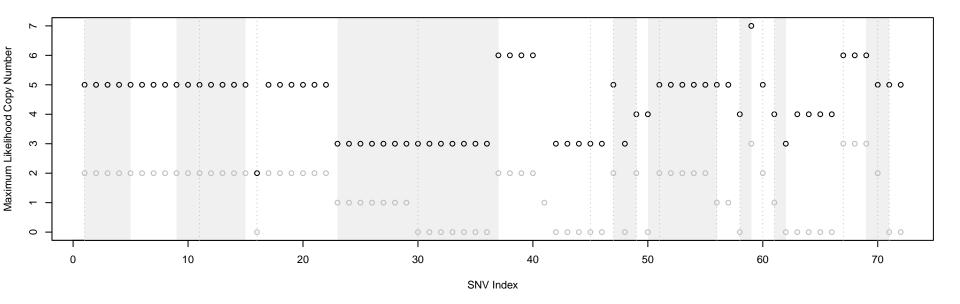


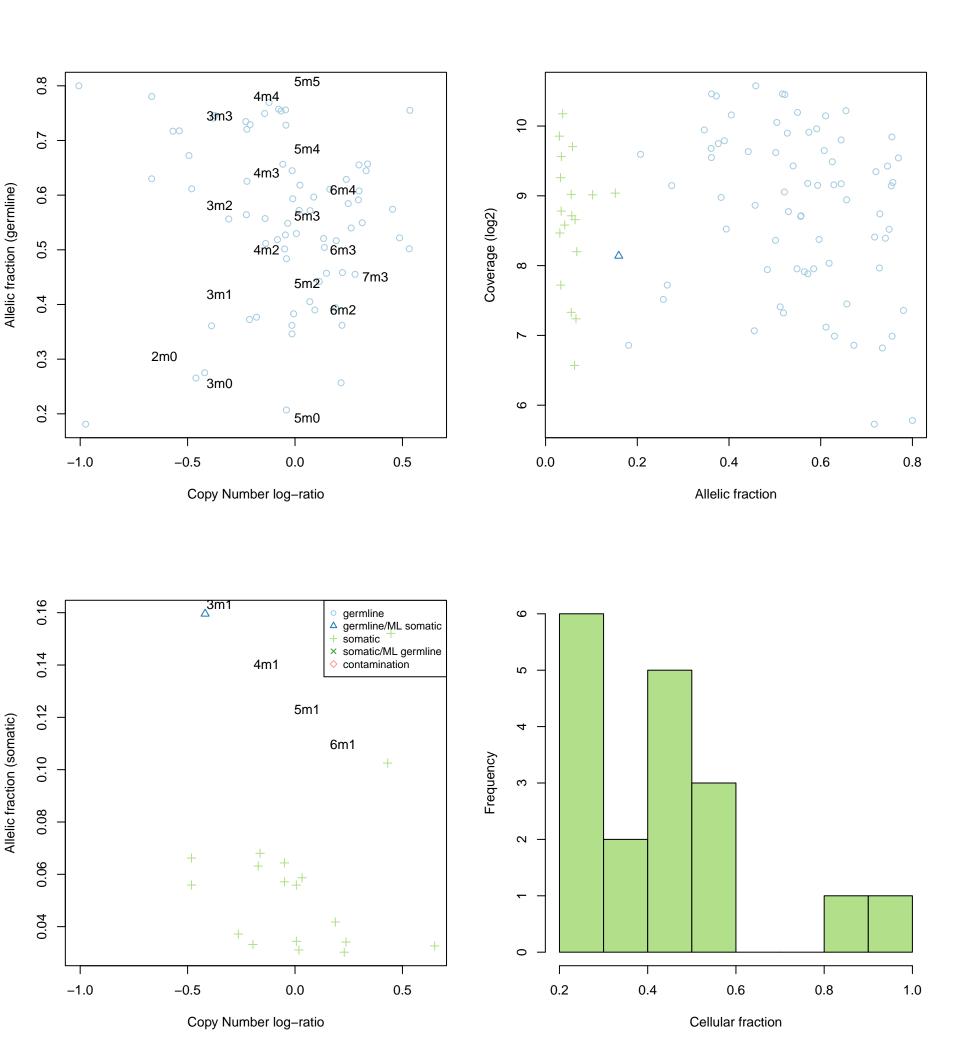
Purity: 0.39 Tumor ploidy: 4.688 0 5 2 3 6 0.25 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



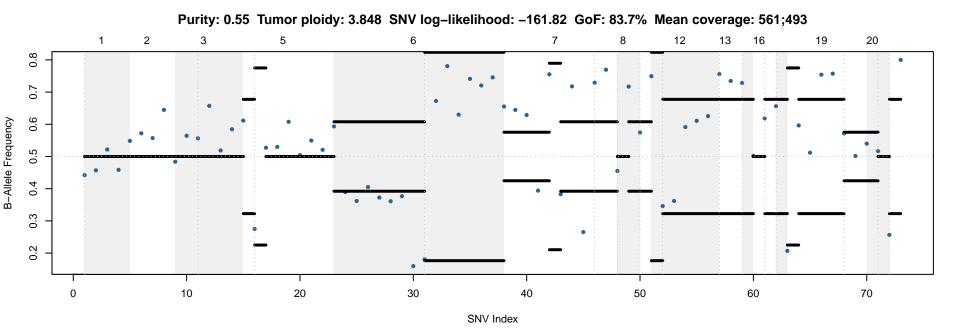
SCNA-fit log-likelihood: -10437.16



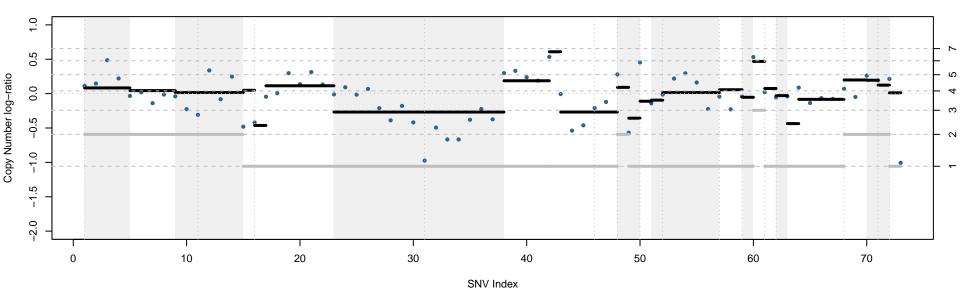


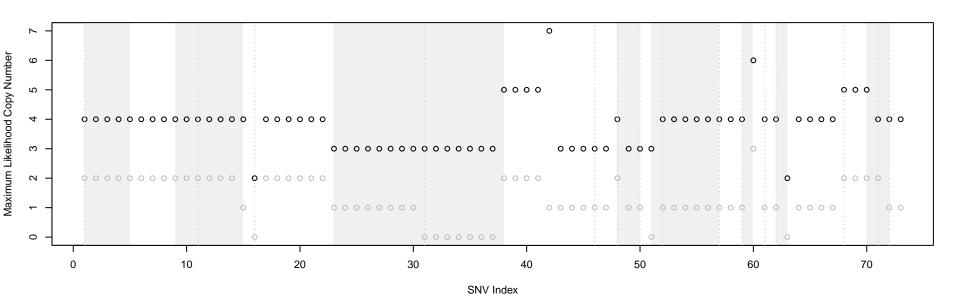


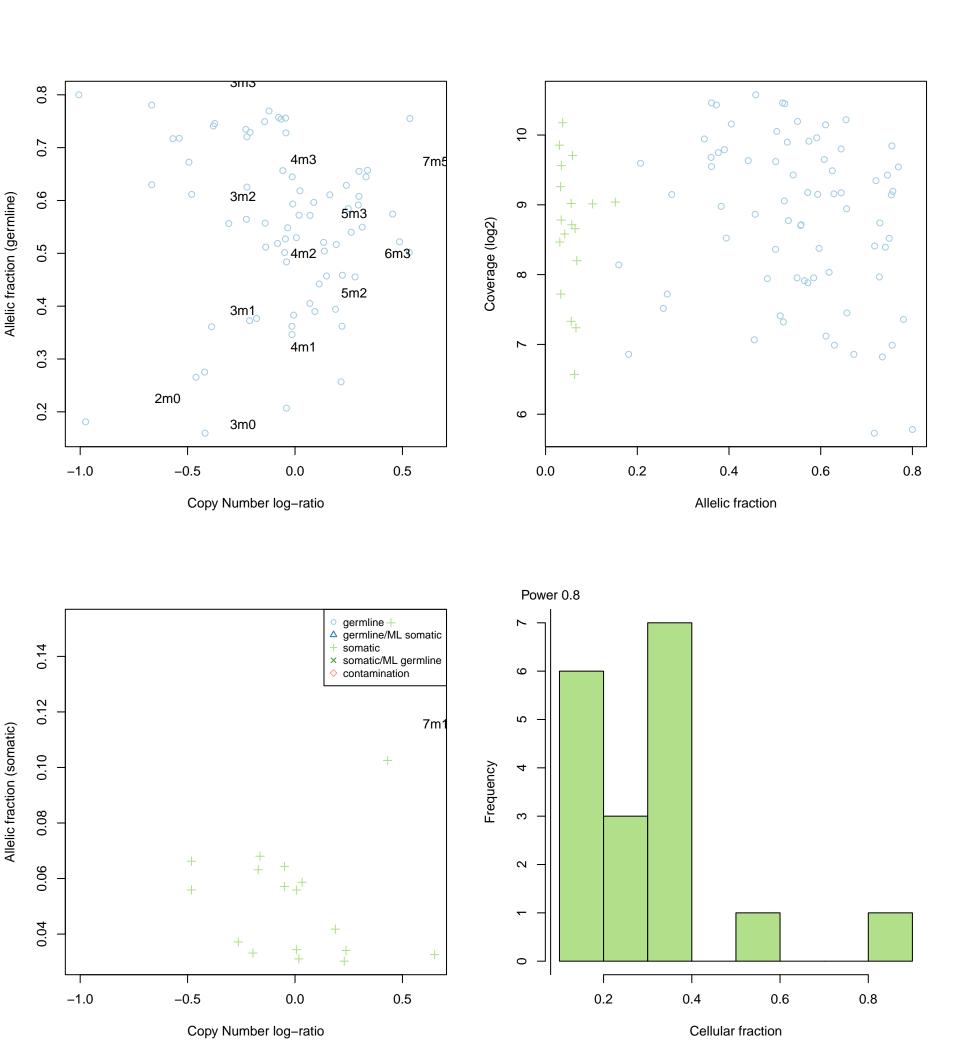
Purity: 0.55 Tumor ploidy: 3.848 3 2 5 6 4 0.25 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



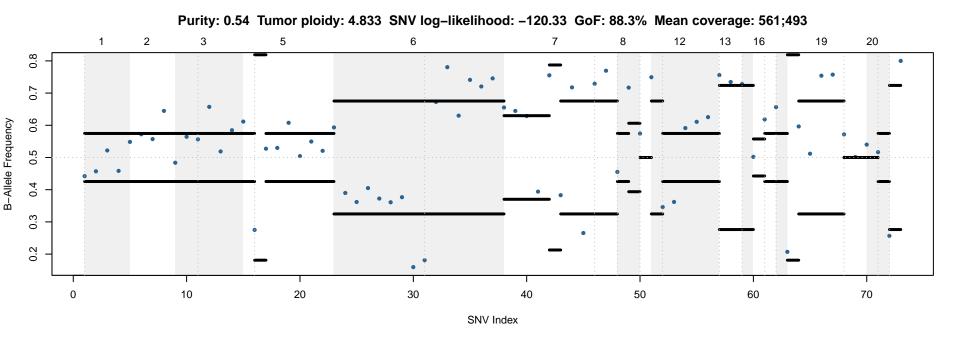
SCNA-fit log-likelihood: -10295.3



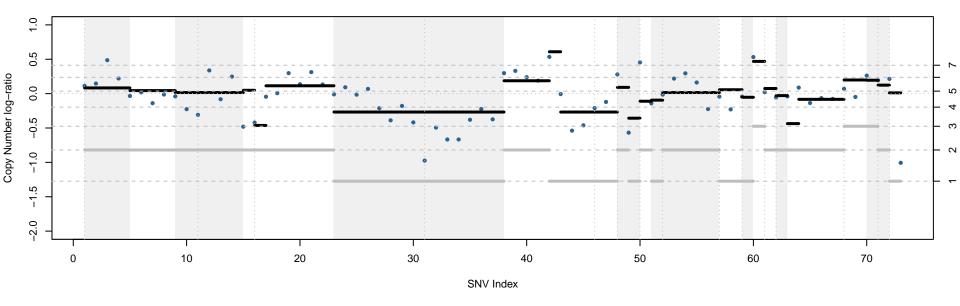


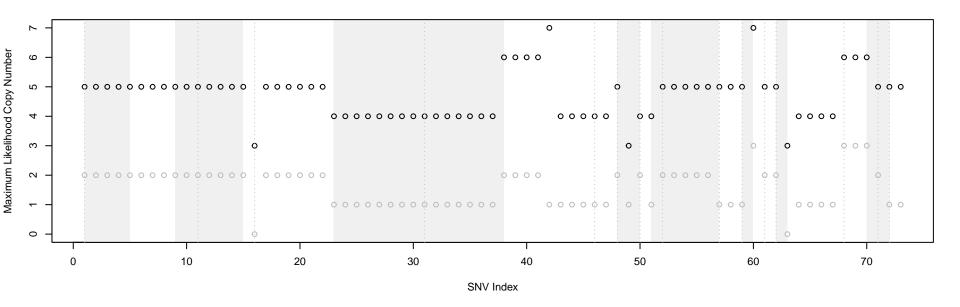


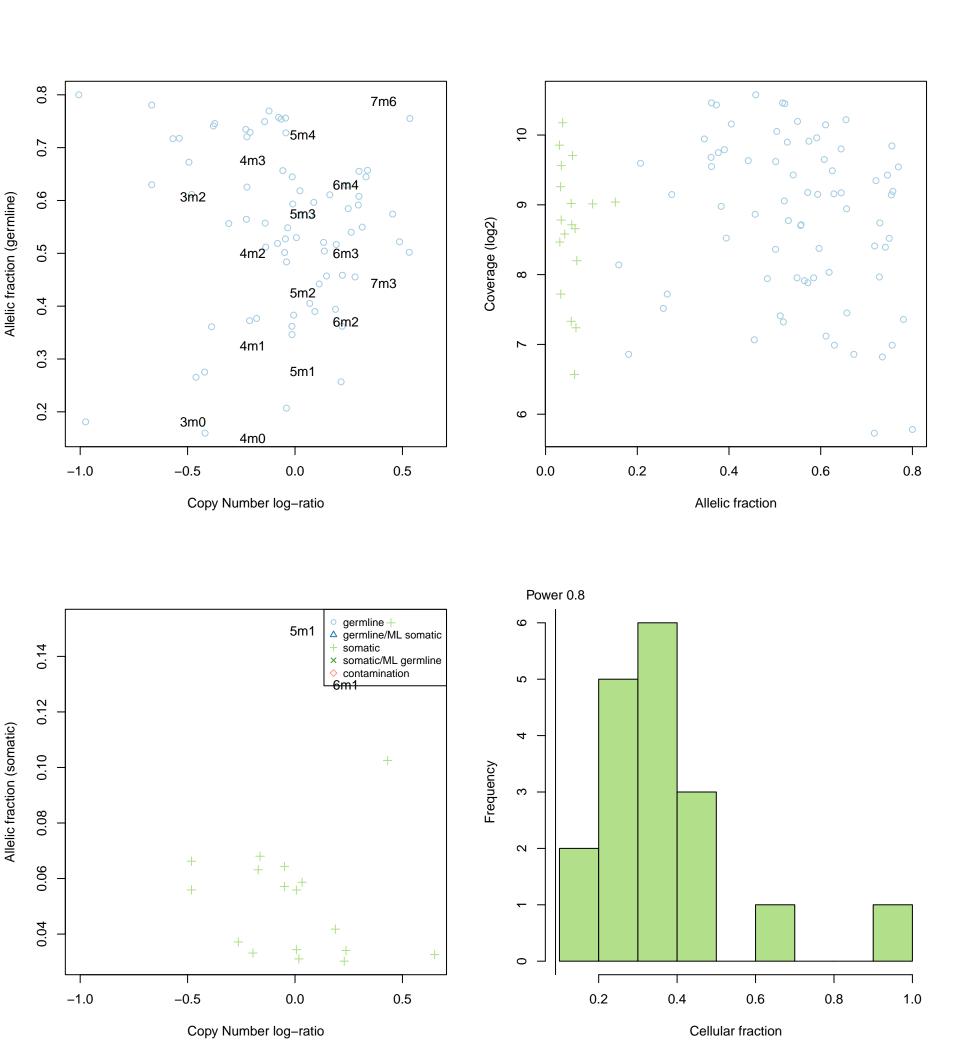
Purity: 0.54 Tumor ploidy: 4.833 6 3 5 2 0.25 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



SCNA-fit log-likelihood: -10429.26

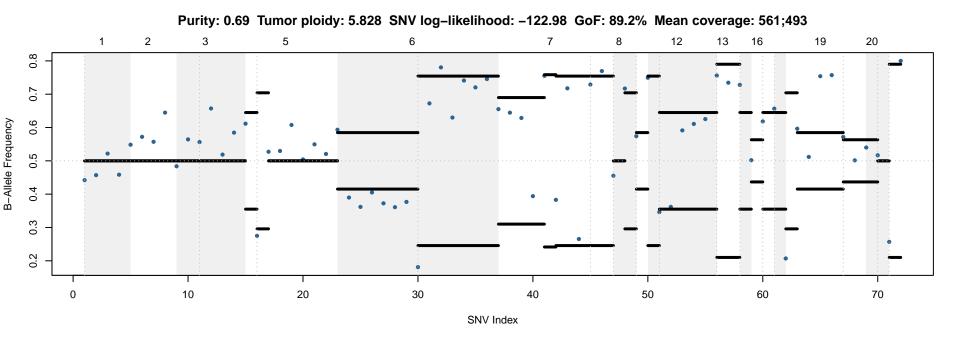




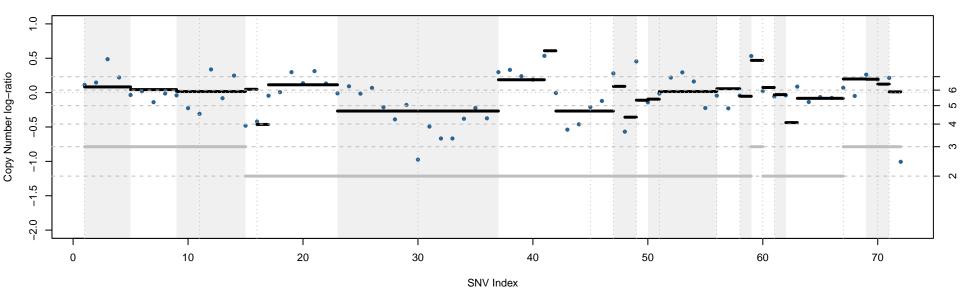


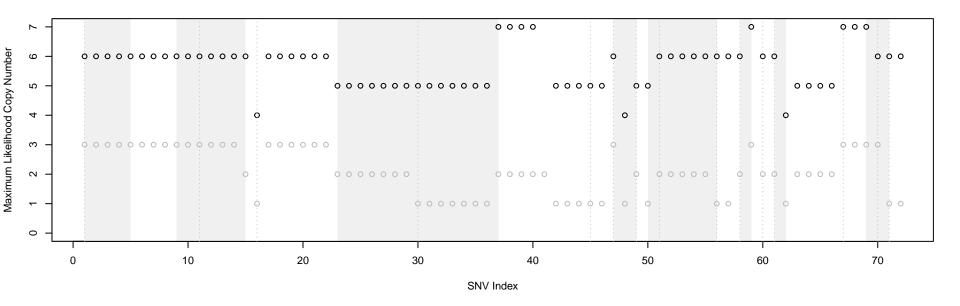
Purity: 0.69 Tumor ploidy: 5.828 2 5 6 7 3 0.25 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5

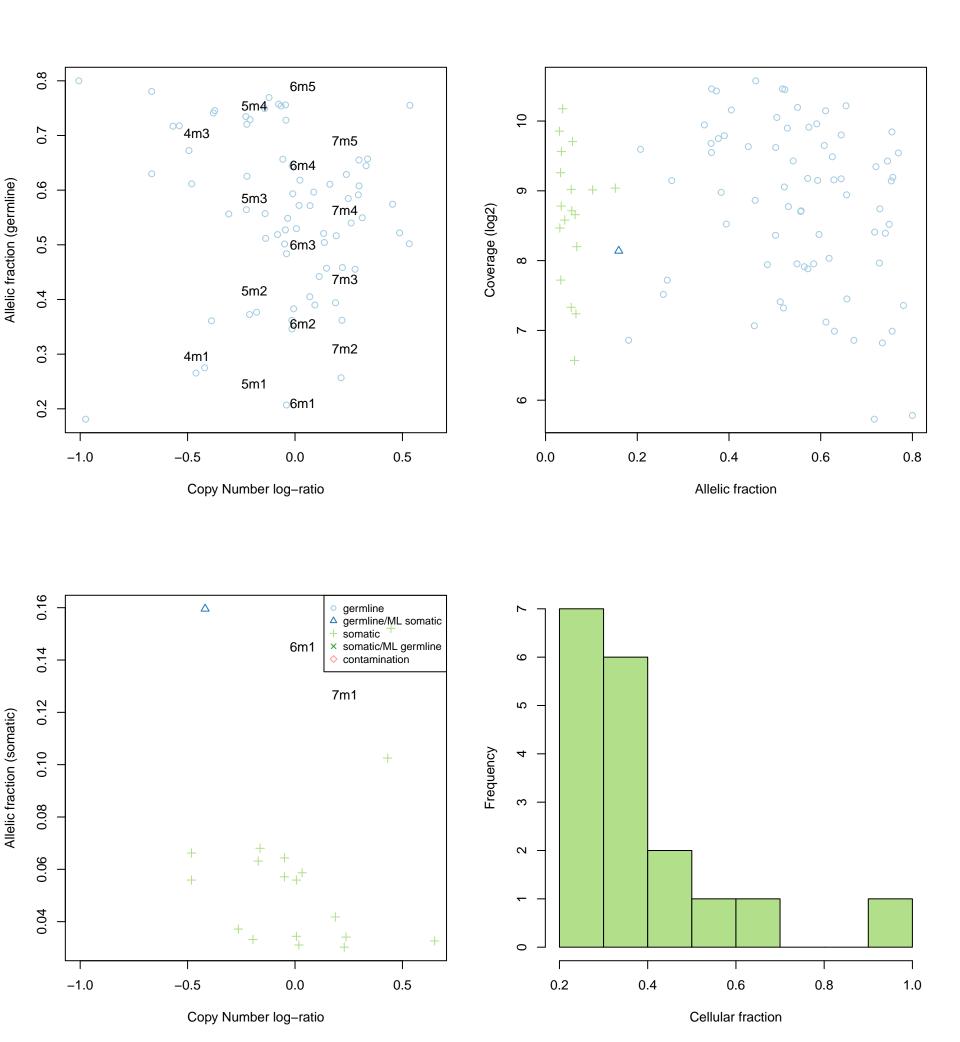
log2 ratio



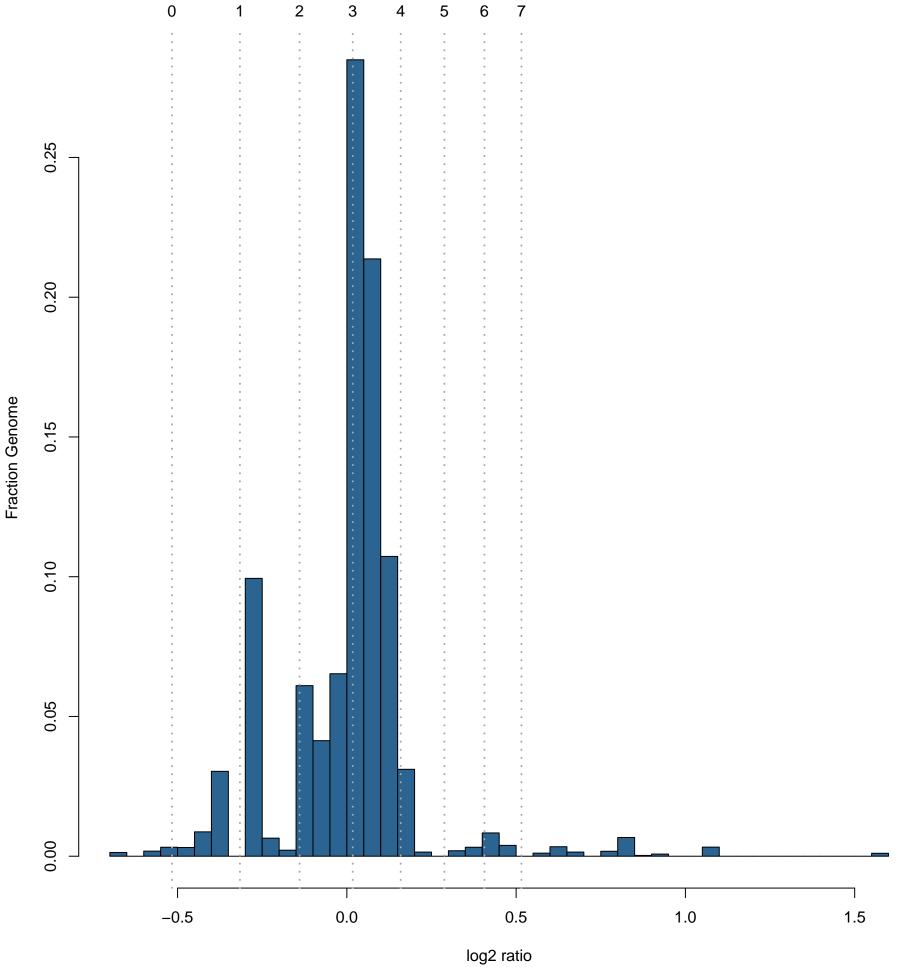
SCNA-fit log-likelihood: -10558.69

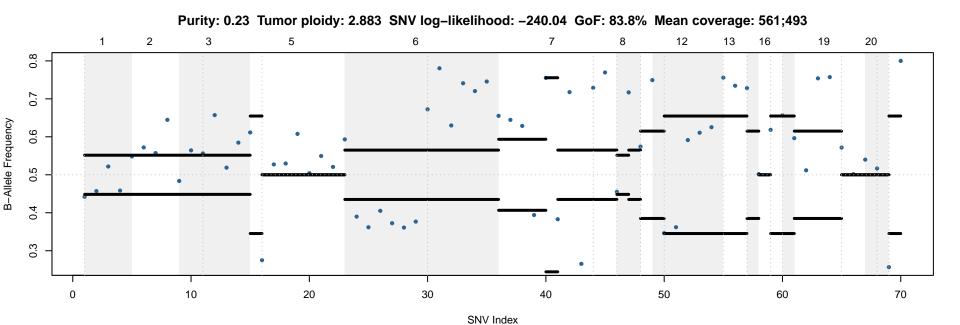




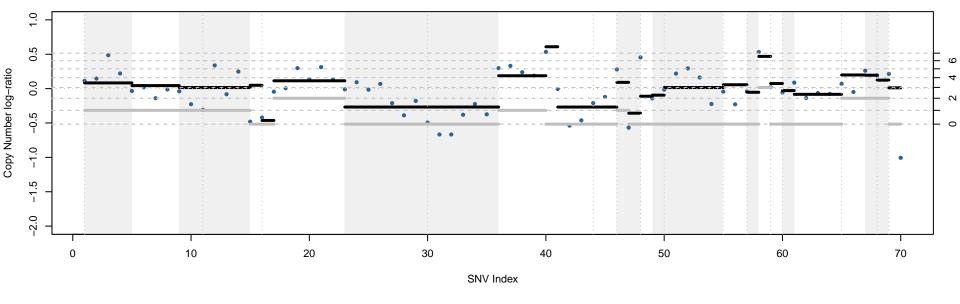


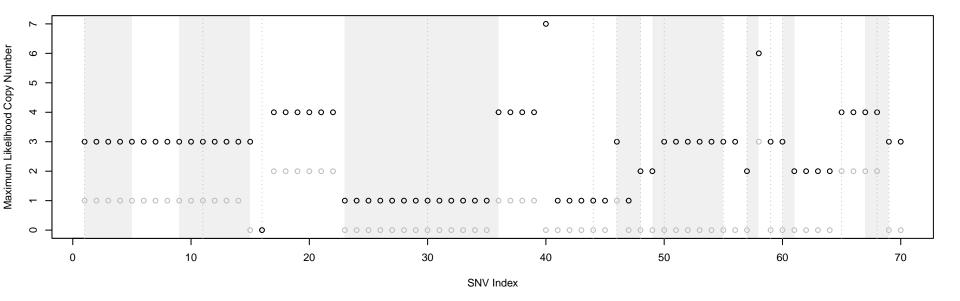
Purity: 0.23 Tumor ploidy: 2.883

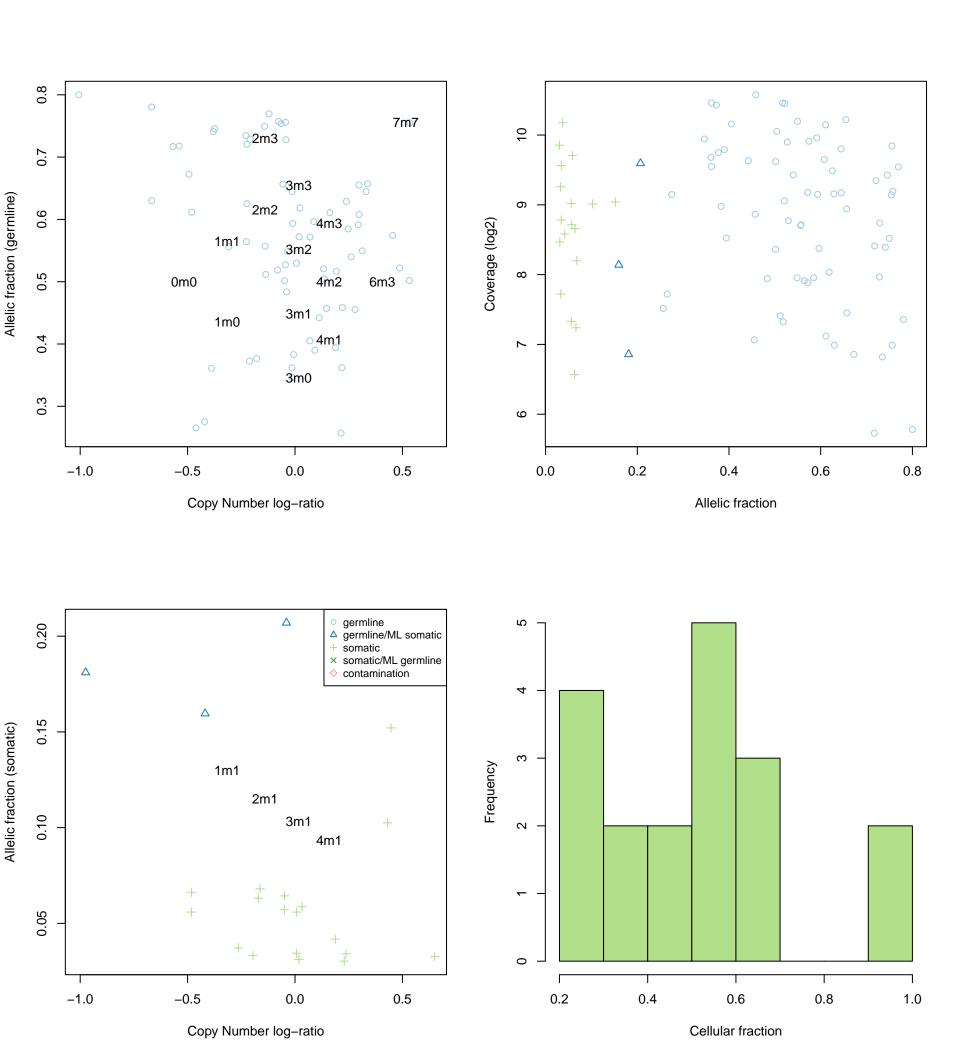




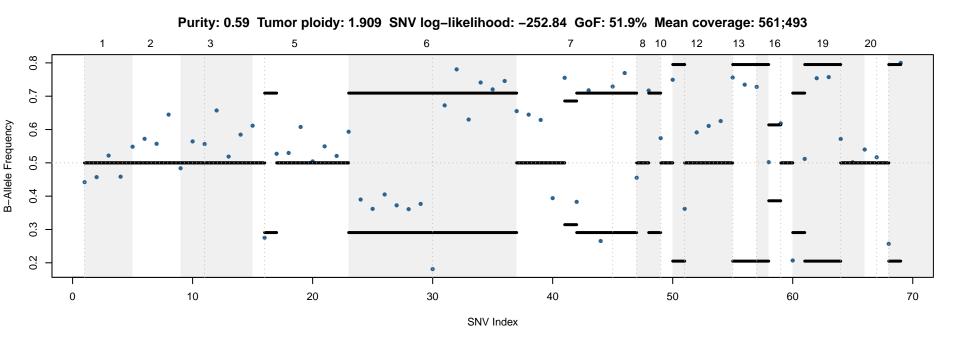
SCNA-fit log-likelihood: -10284.9



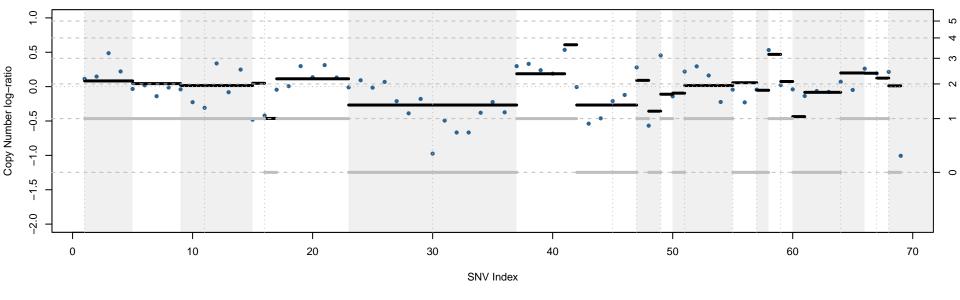


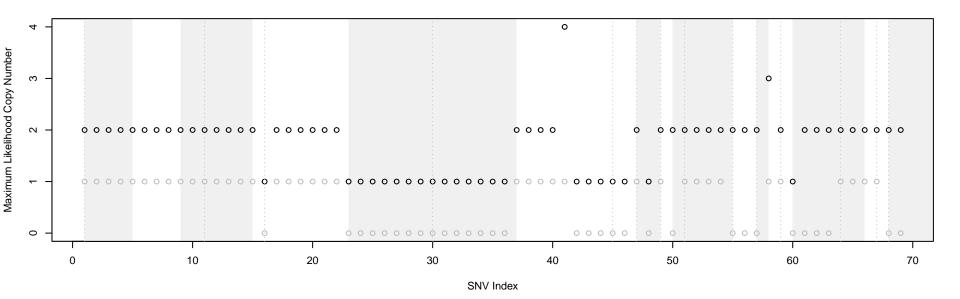


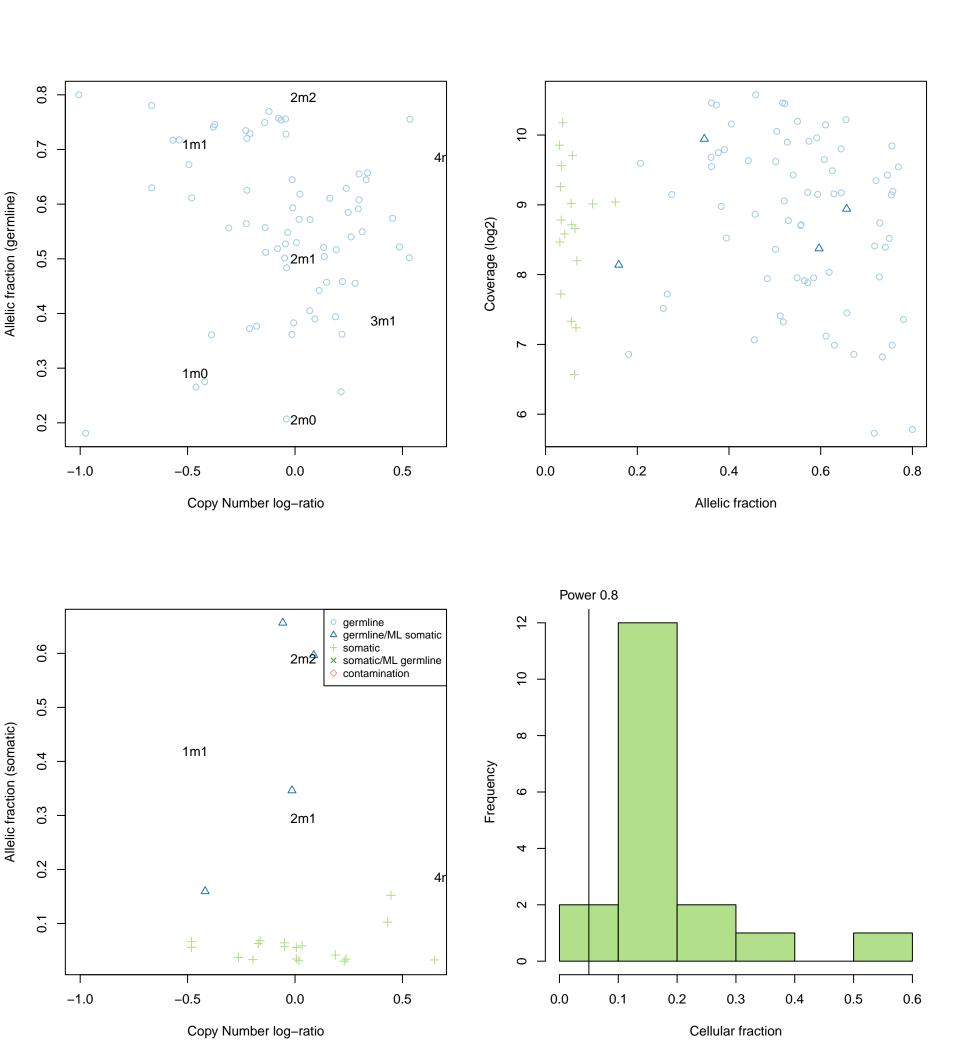
Purity: 0.59 Tumor ploidy: 1.909 2 3 0 6 5 0.20 Fraction Genome 0.10 0.05 0.00 -1.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



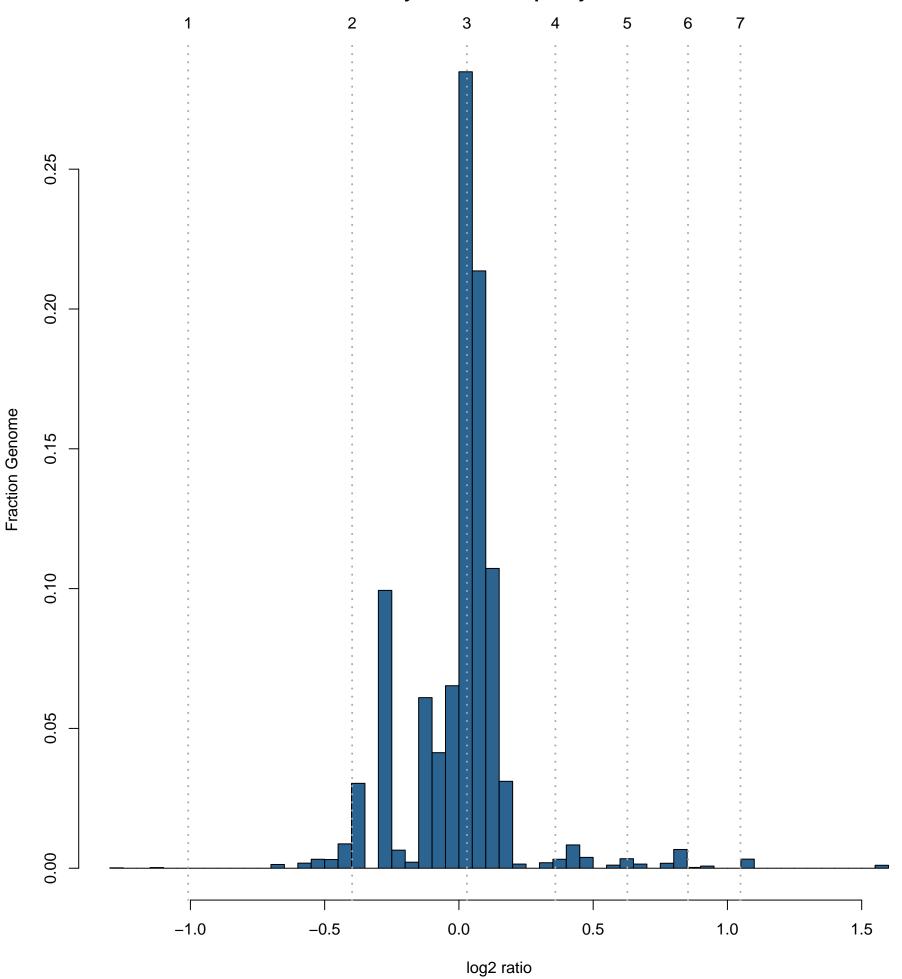
SCNA-fit log-likelihood: -10527.04







Purity: 0.69 Tumor ploidy: 2.92



SCNA-fit log-likelihood: -10362.38

