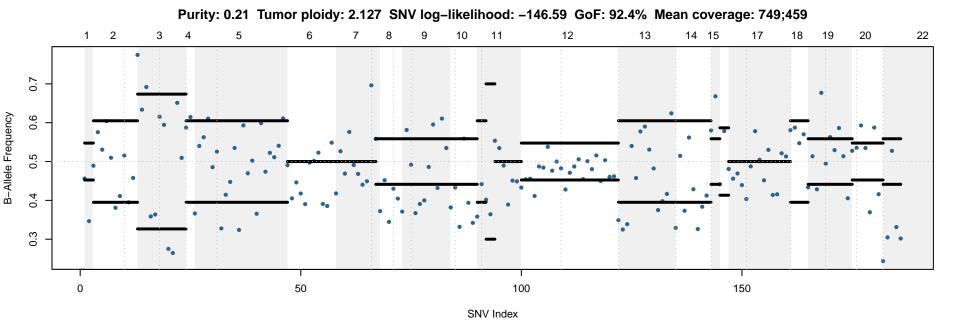
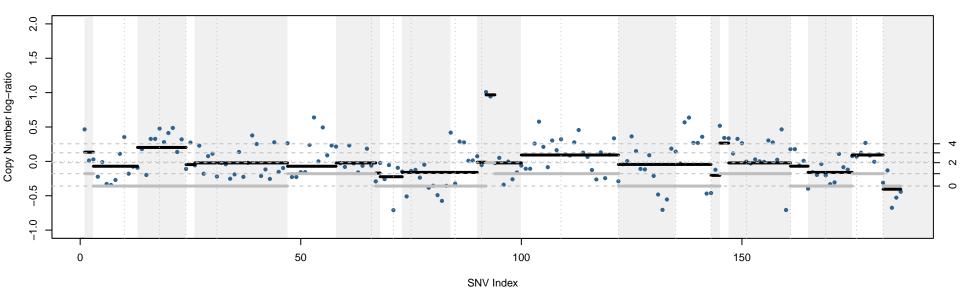
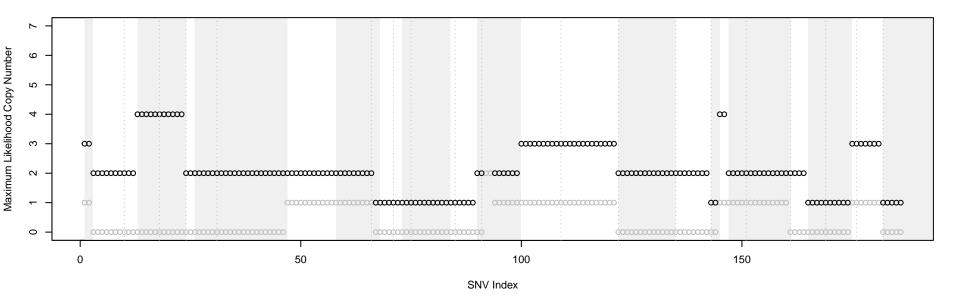
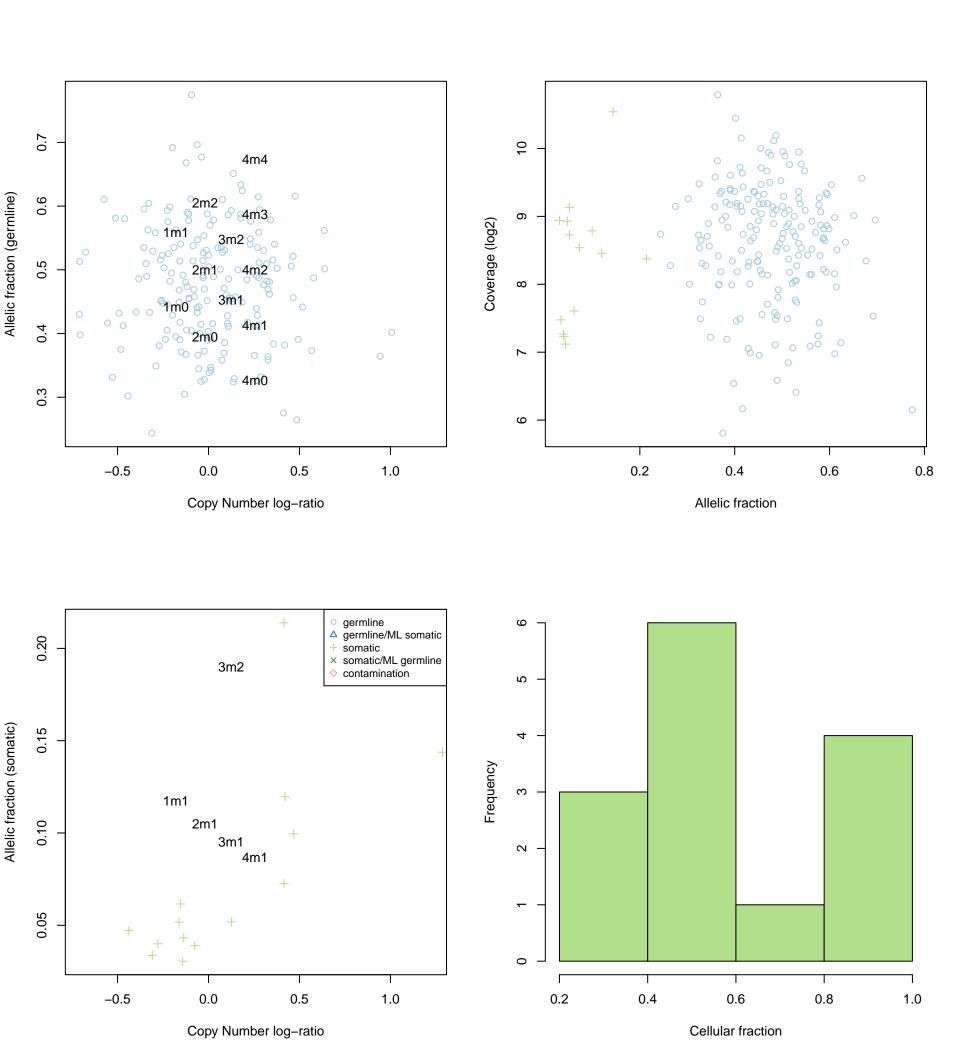
Purity: 0.21 Tumor ploidy: 2.127 2 0 3 0.20 Fraction Genome 0.10 0.05 0.00 0.2 -0.4 -0.2 0.0 0.4 0.6 0.8 1.0 log2 ratio



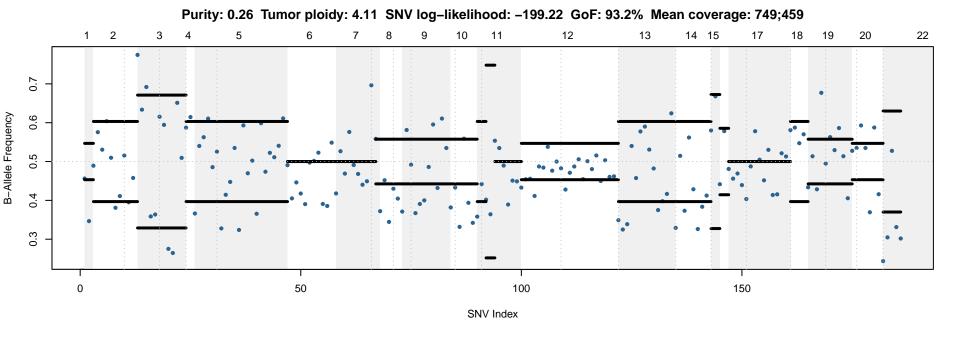
SCNA-fit log-likelihood: -10142.17



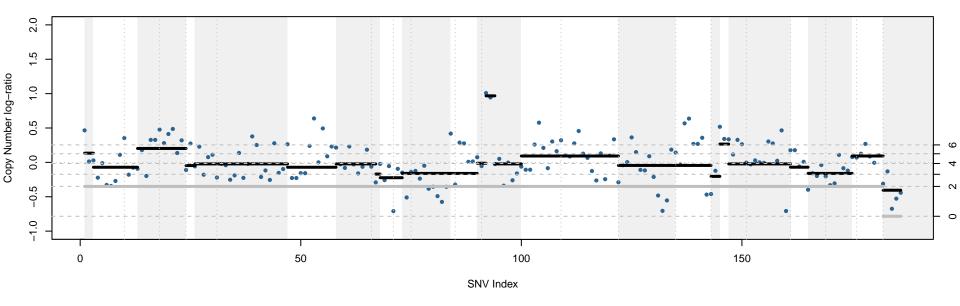


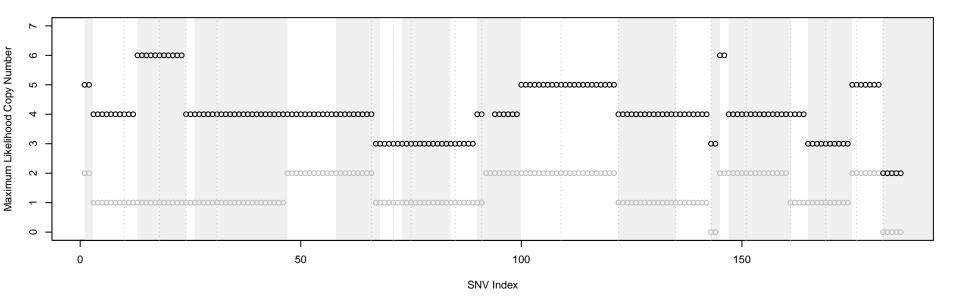


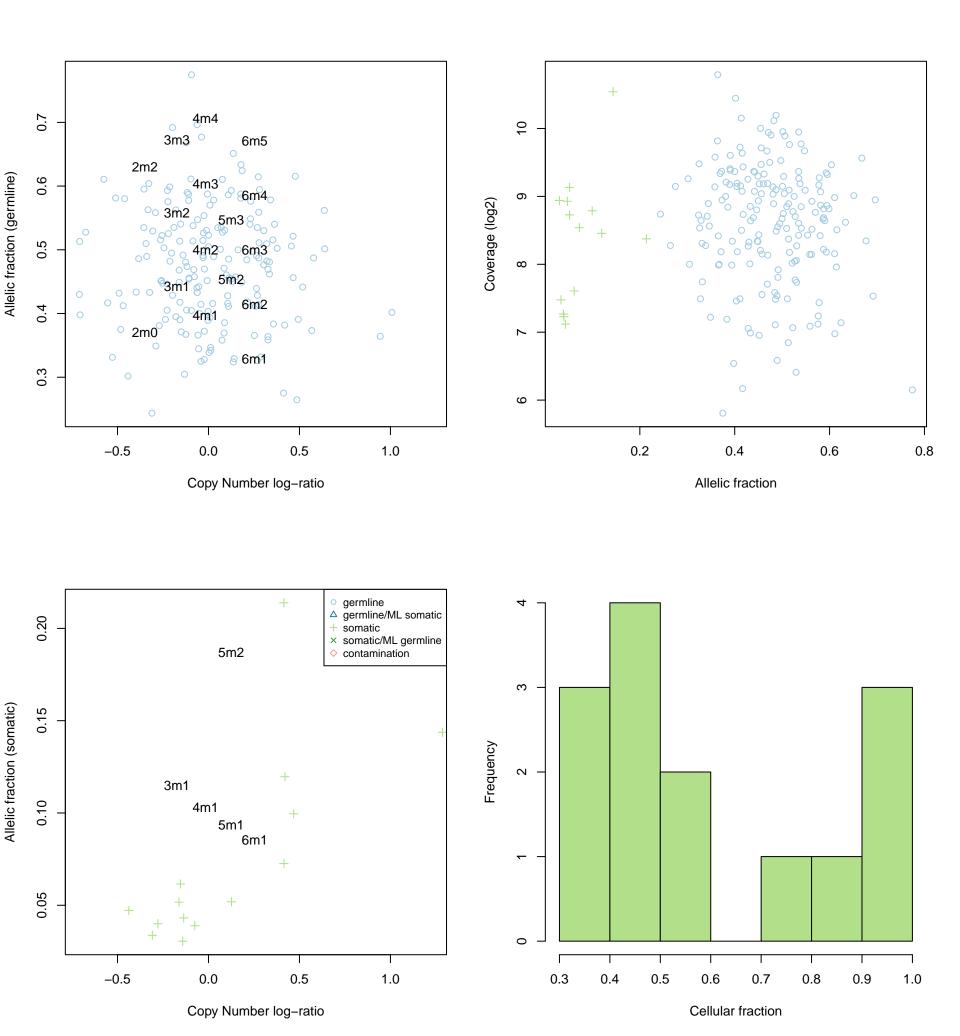
Purity: 0.26 Tumor ploidy: 4.11 3 6 2 0 5 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio



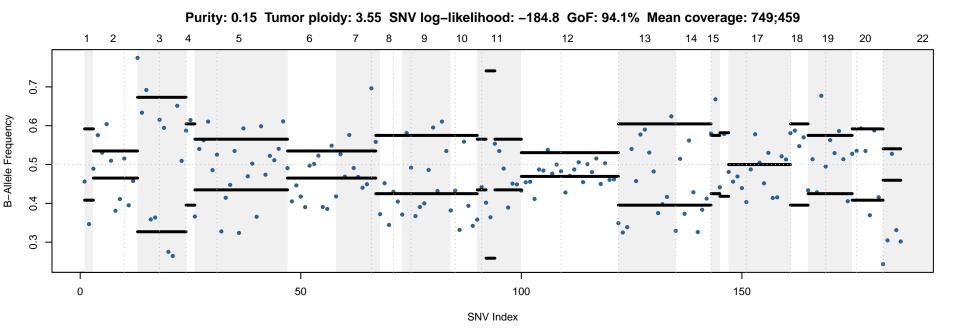
SCNA-fit log-likelihood: -10117.03



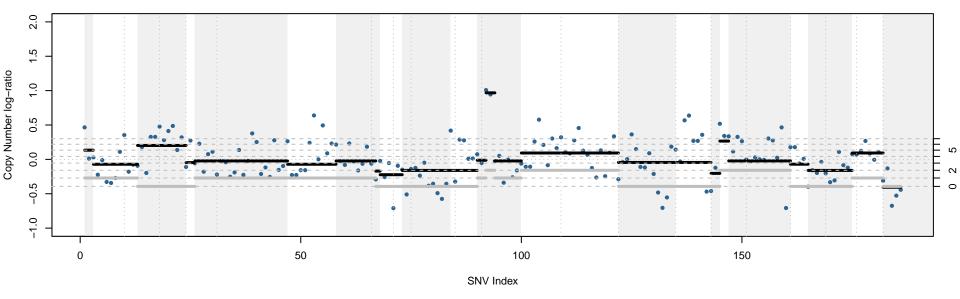


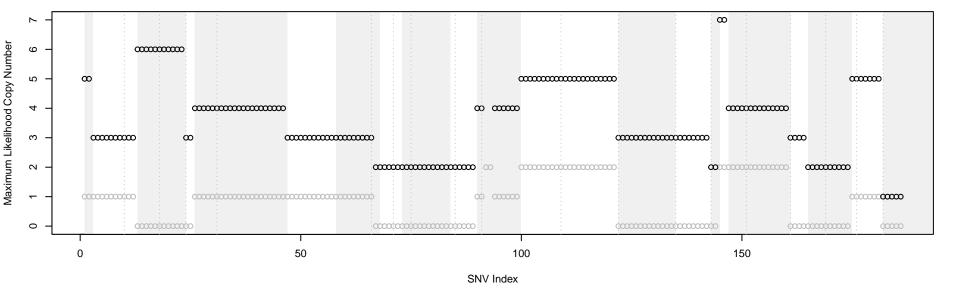


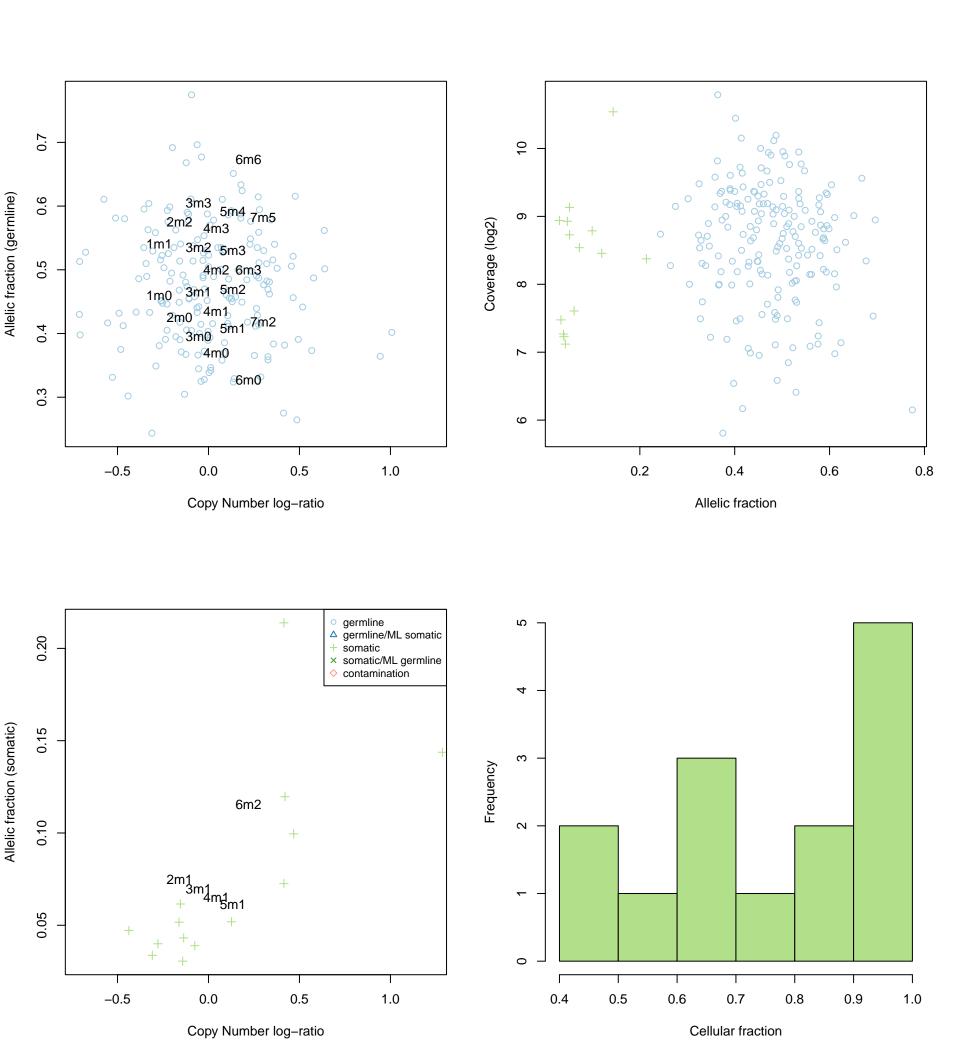
Purity: 0.15 Tumor ploidy: 3.55 2 3 0 5 6 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio



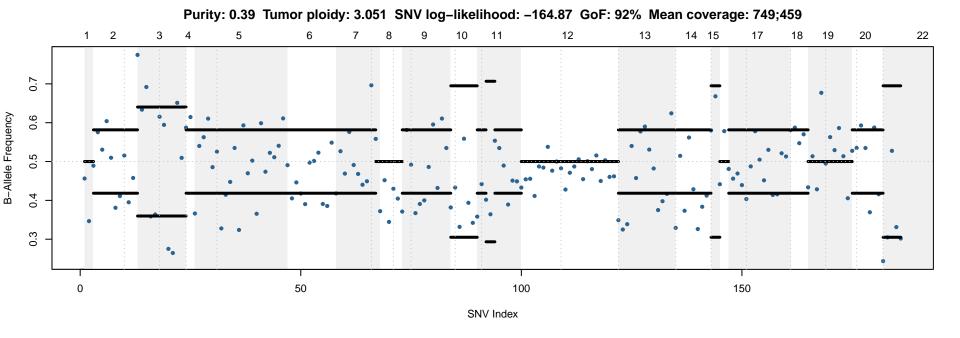
SCNA-fit log-likelihood: -10109.91



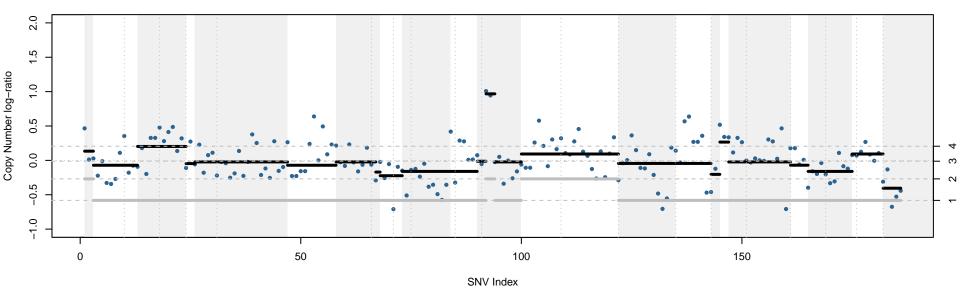


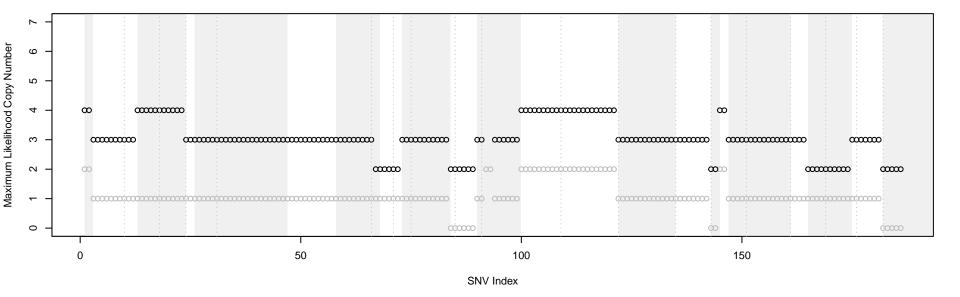


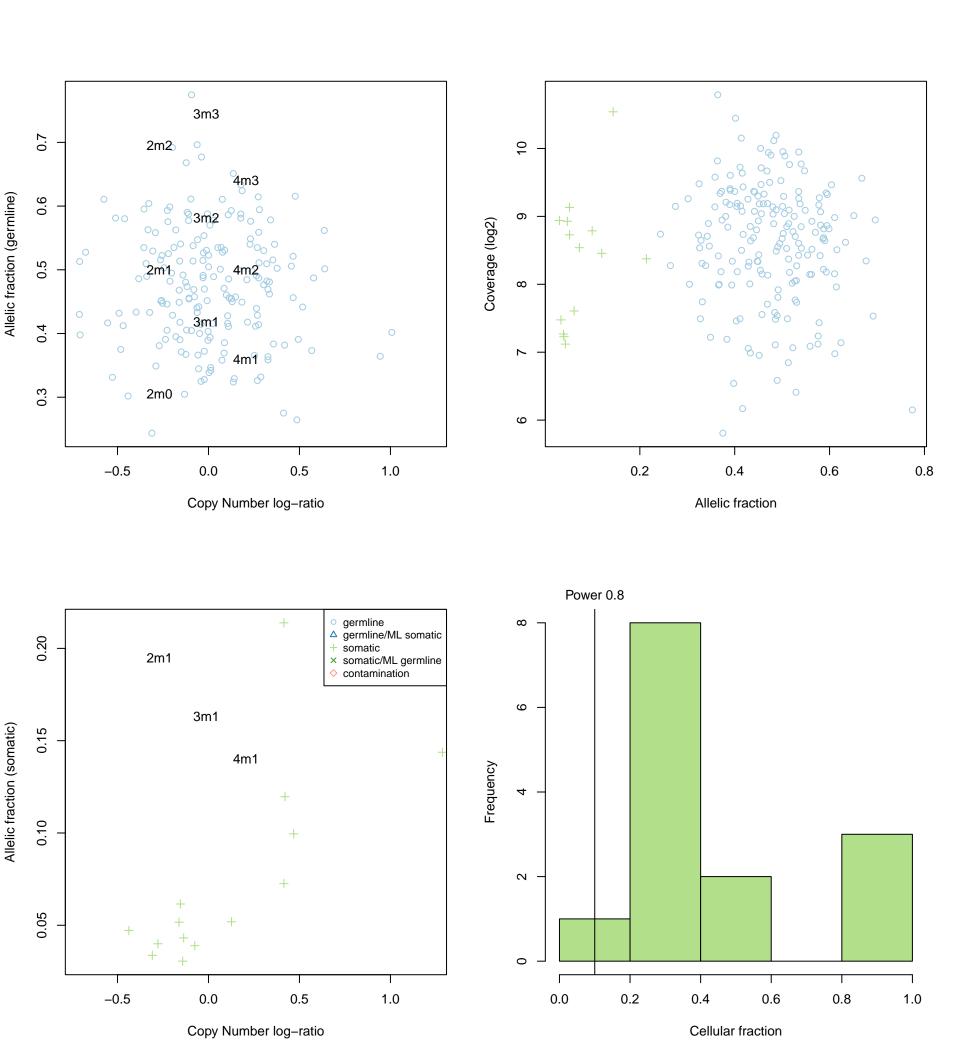
Purity: 0.39 Tumor ploidy: 3.051 2 3 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio

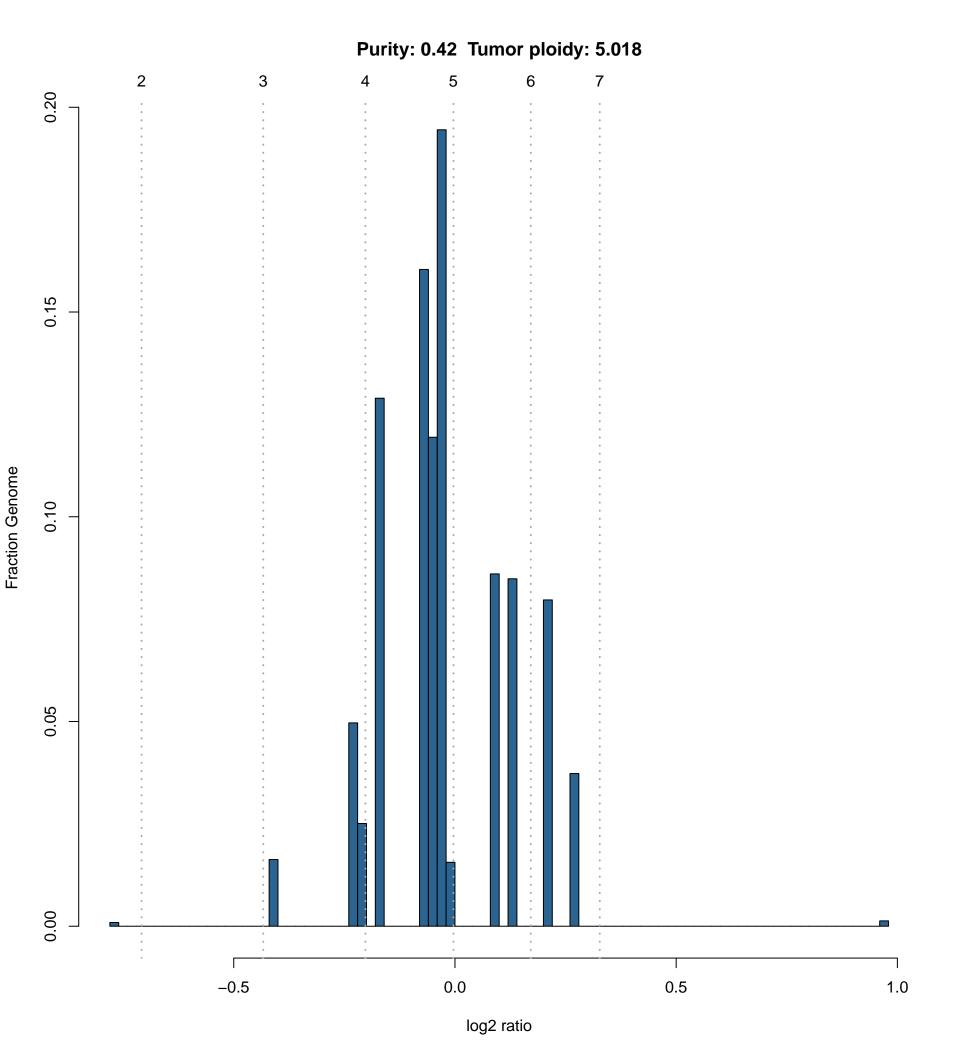


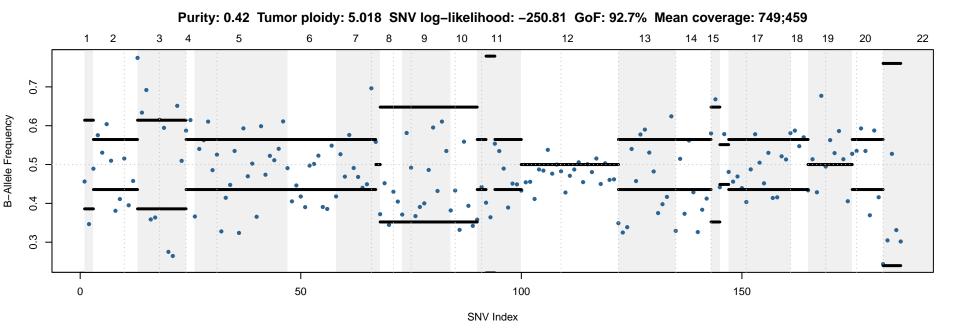
SCNA-fit log-likelihood: -10254.2



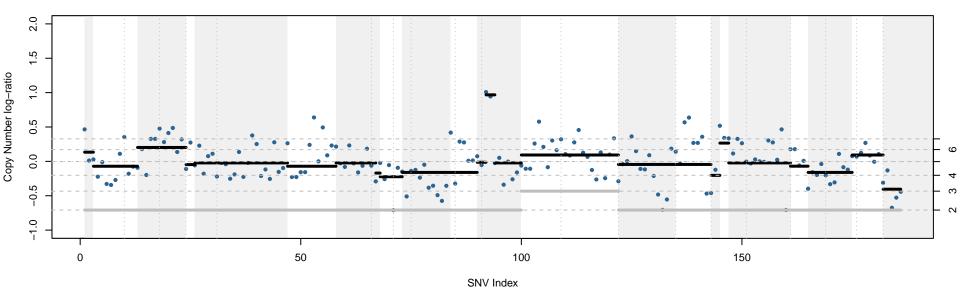


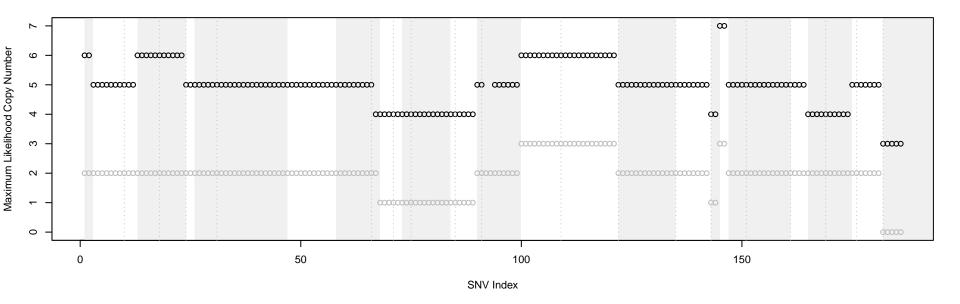


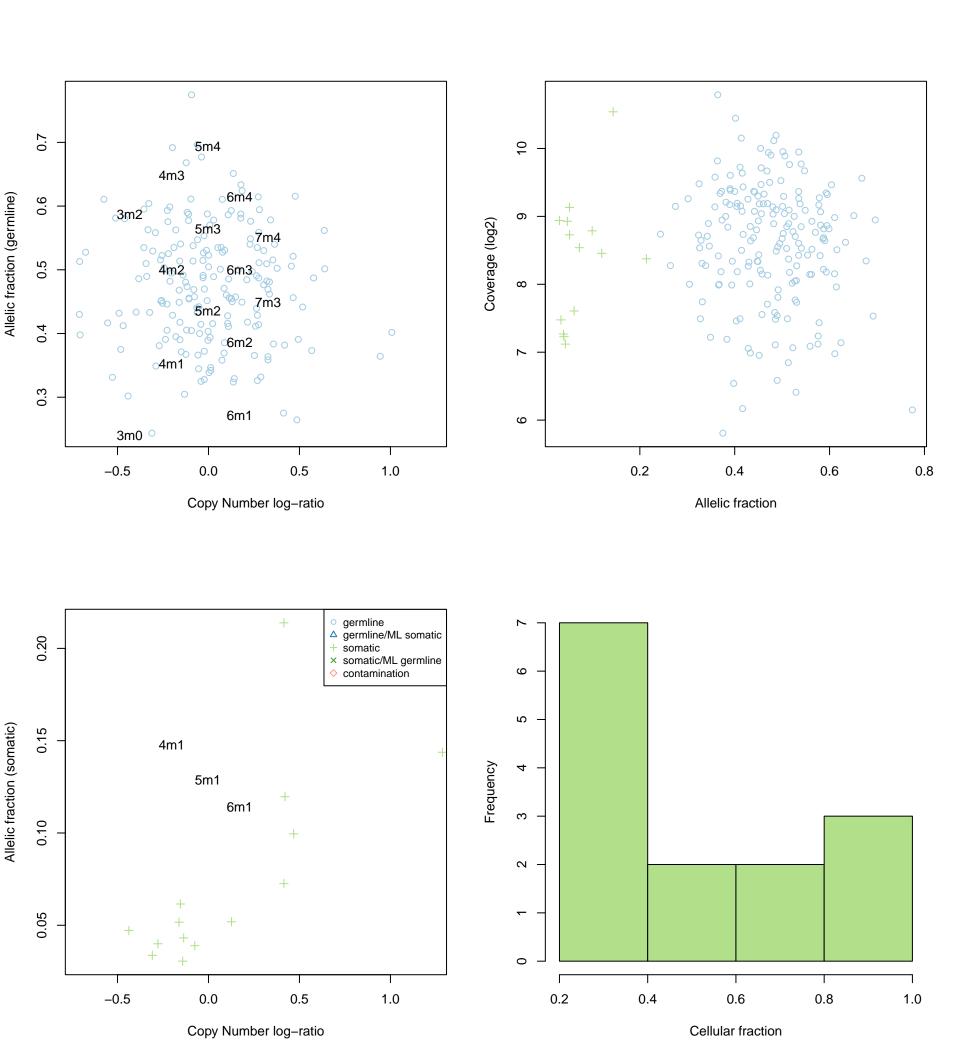




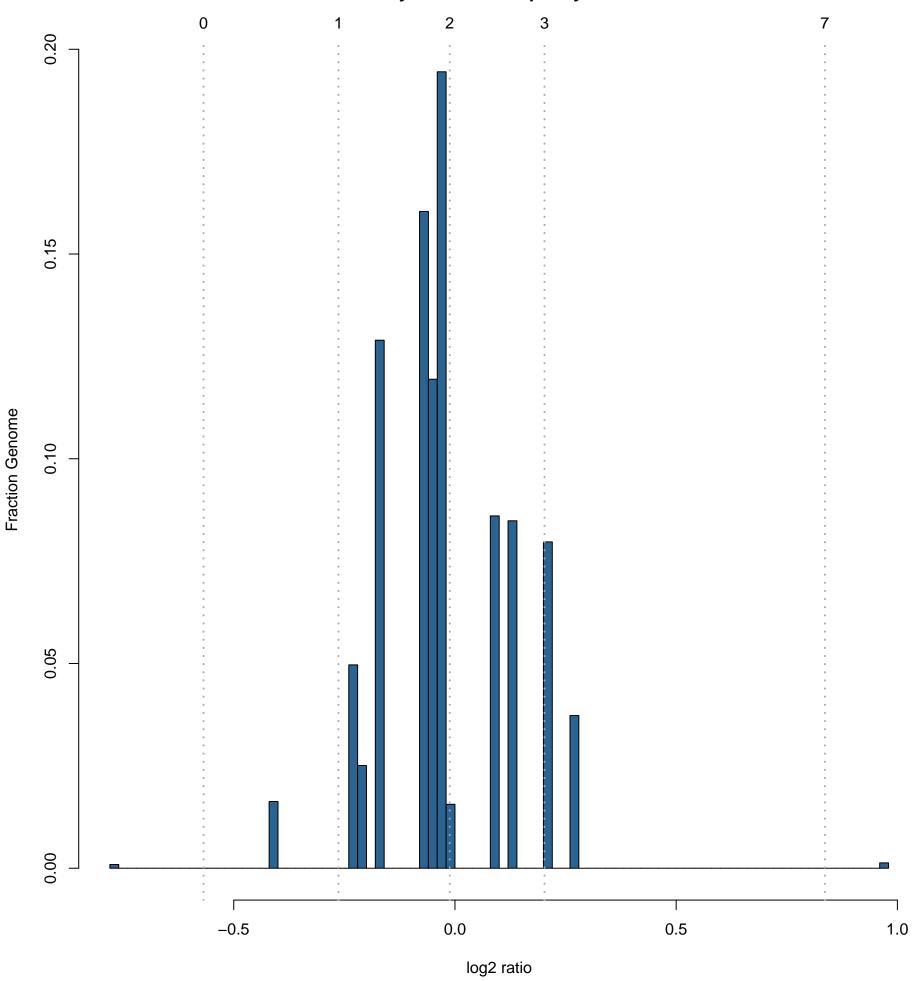
SCNA-fit log-likelihood: -10154.19

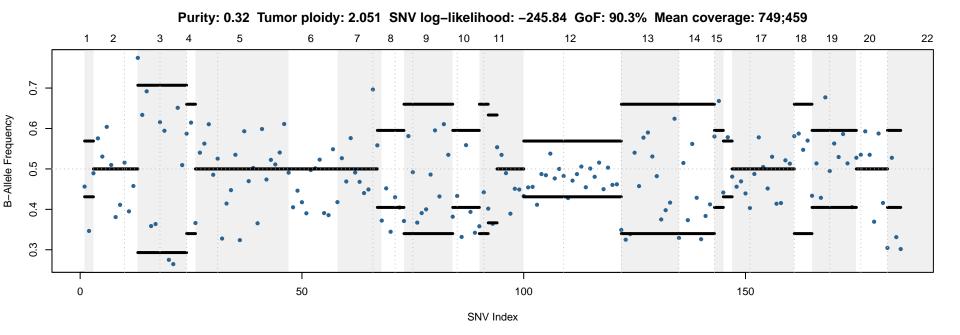




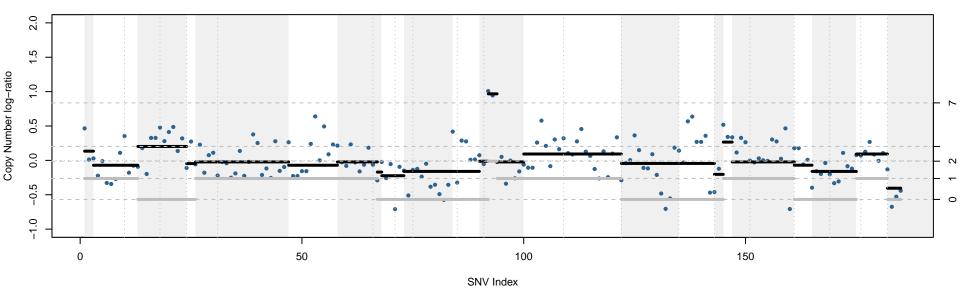


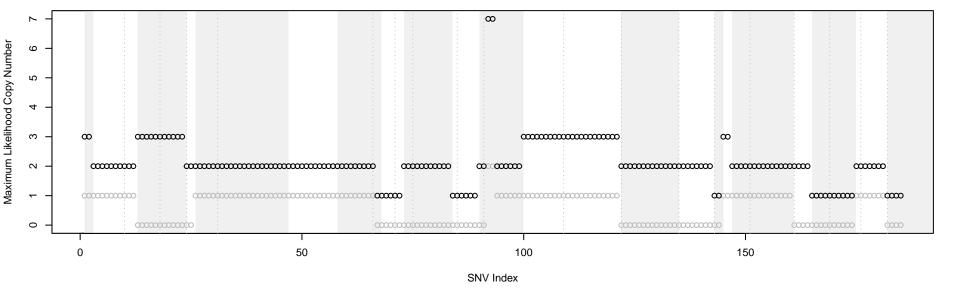
Purity: 0.32 Tumor ploidy: 2.051

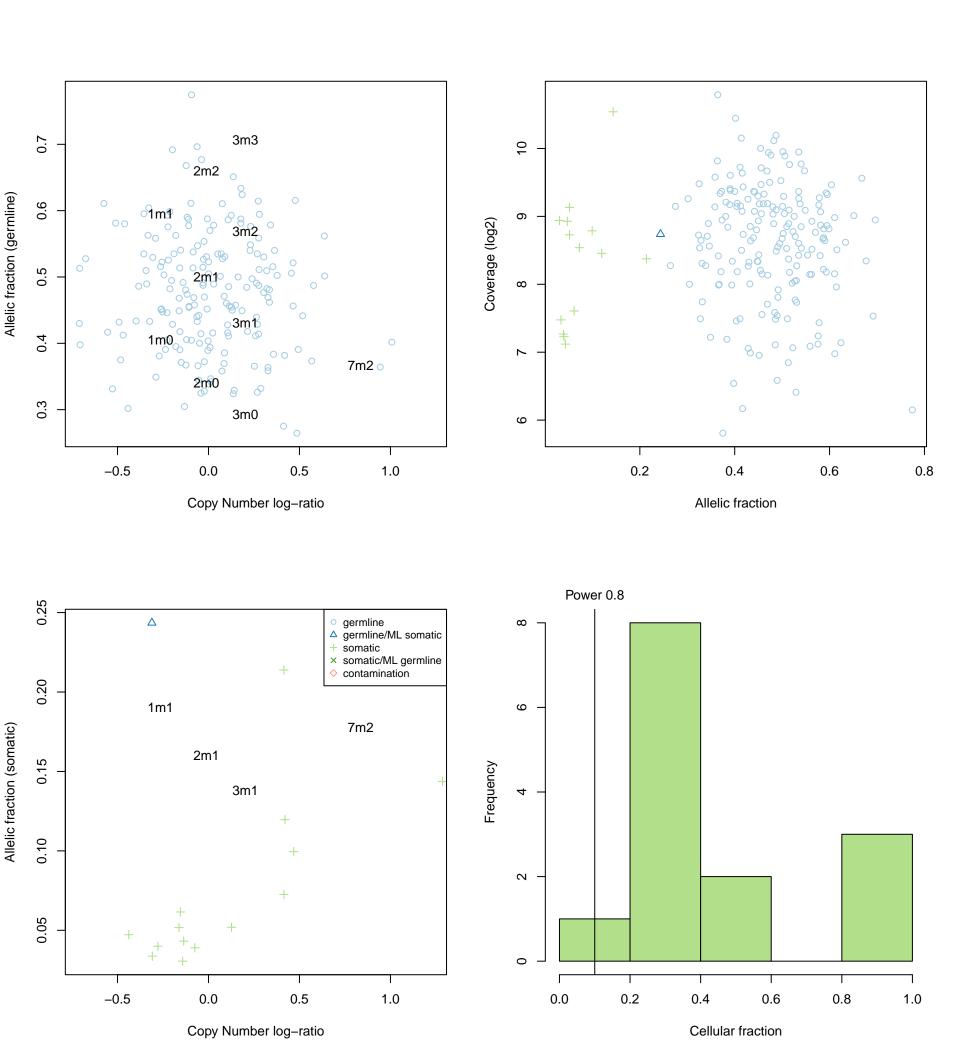


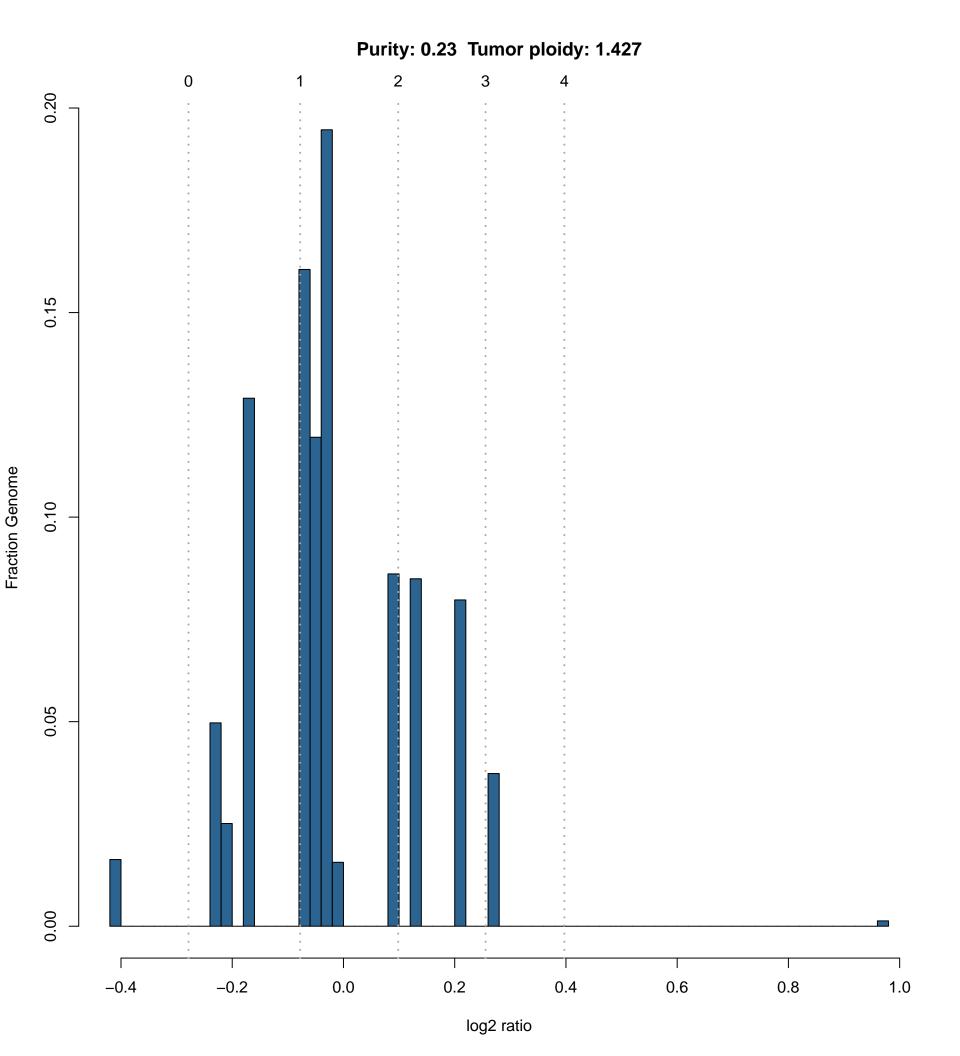


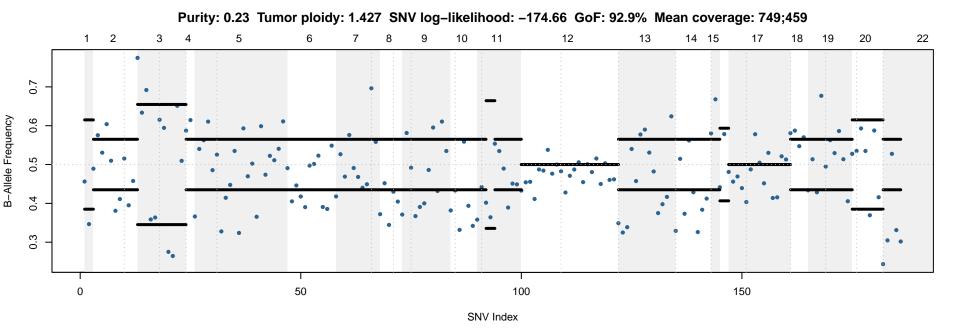
SCNA-fit log-likelihood: -10219.66



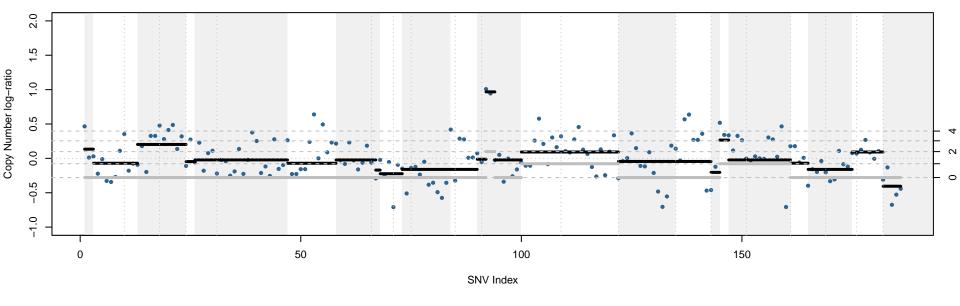


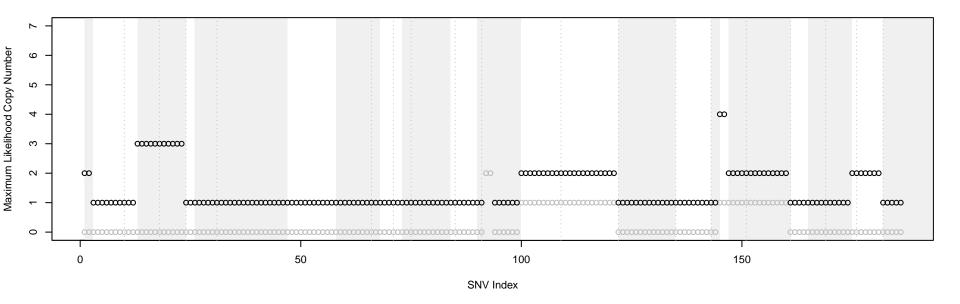


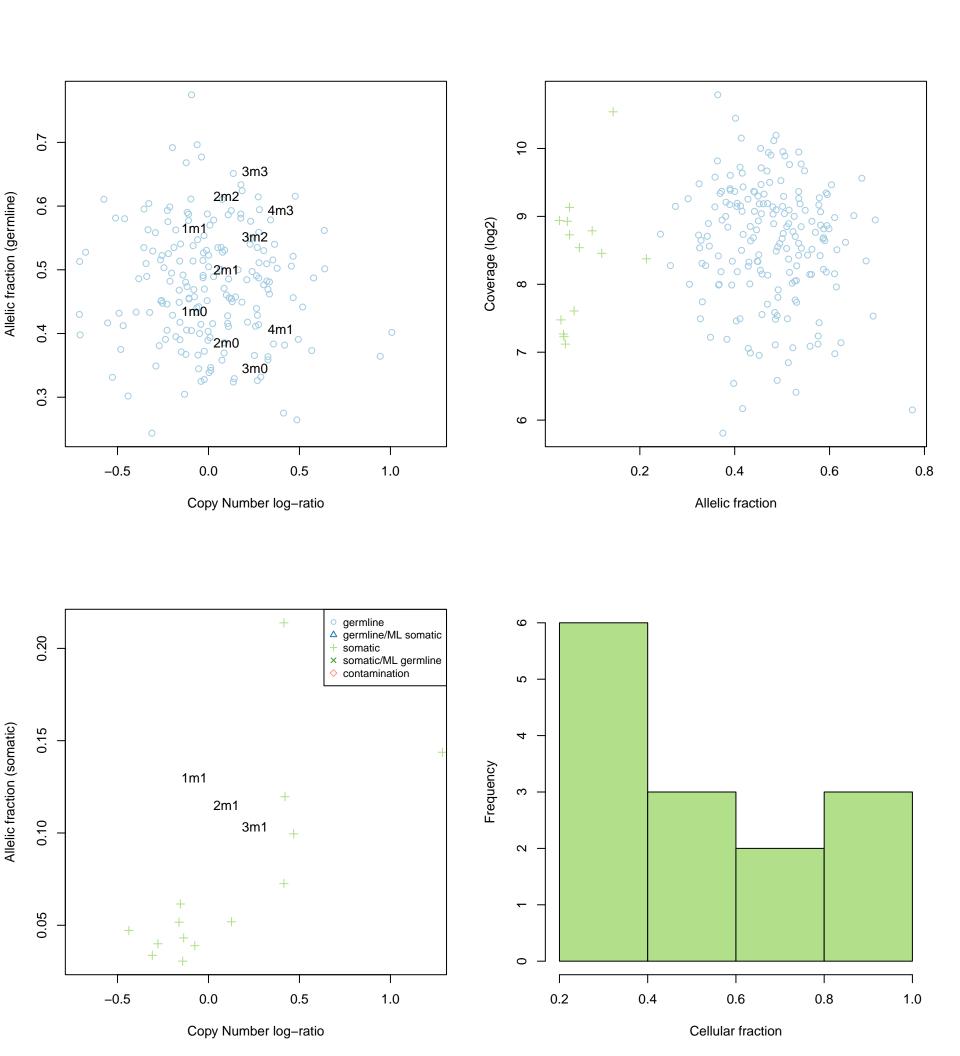




SCNA-fit log-likelihood: -10356.77

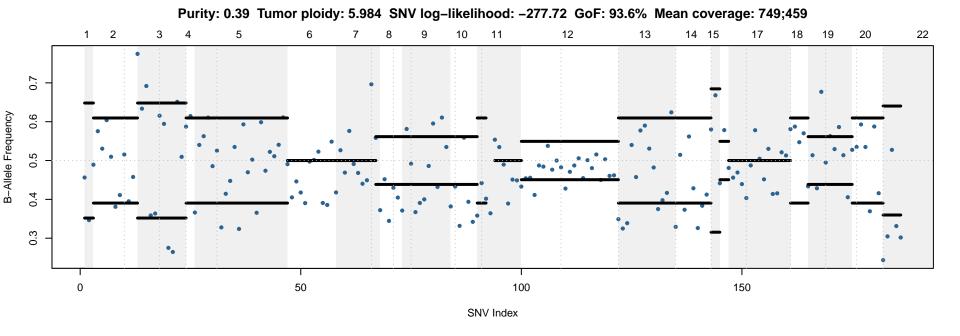




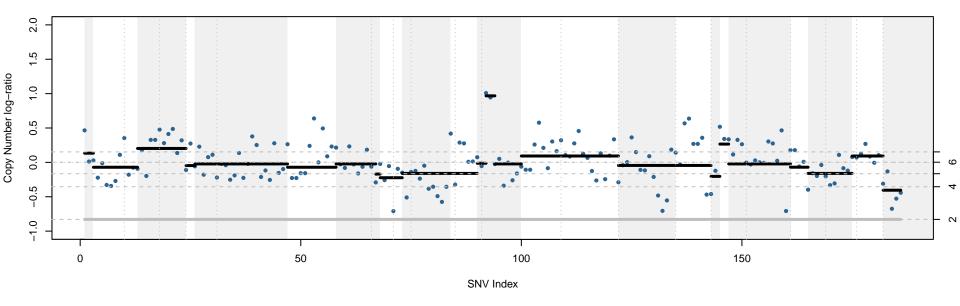


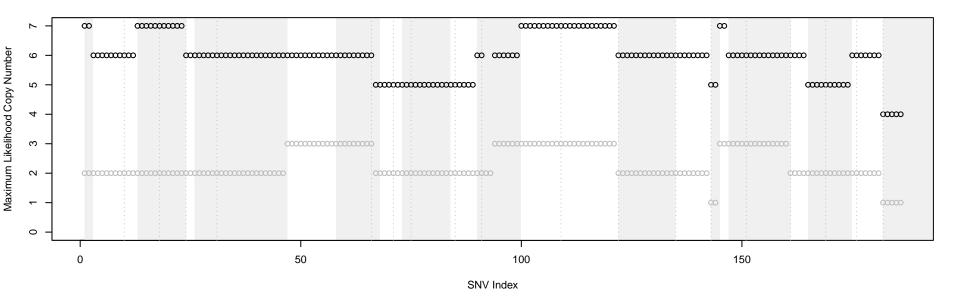
Purity: 0.39 Tumor ploidy: 5.984 6 2 5 7 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0

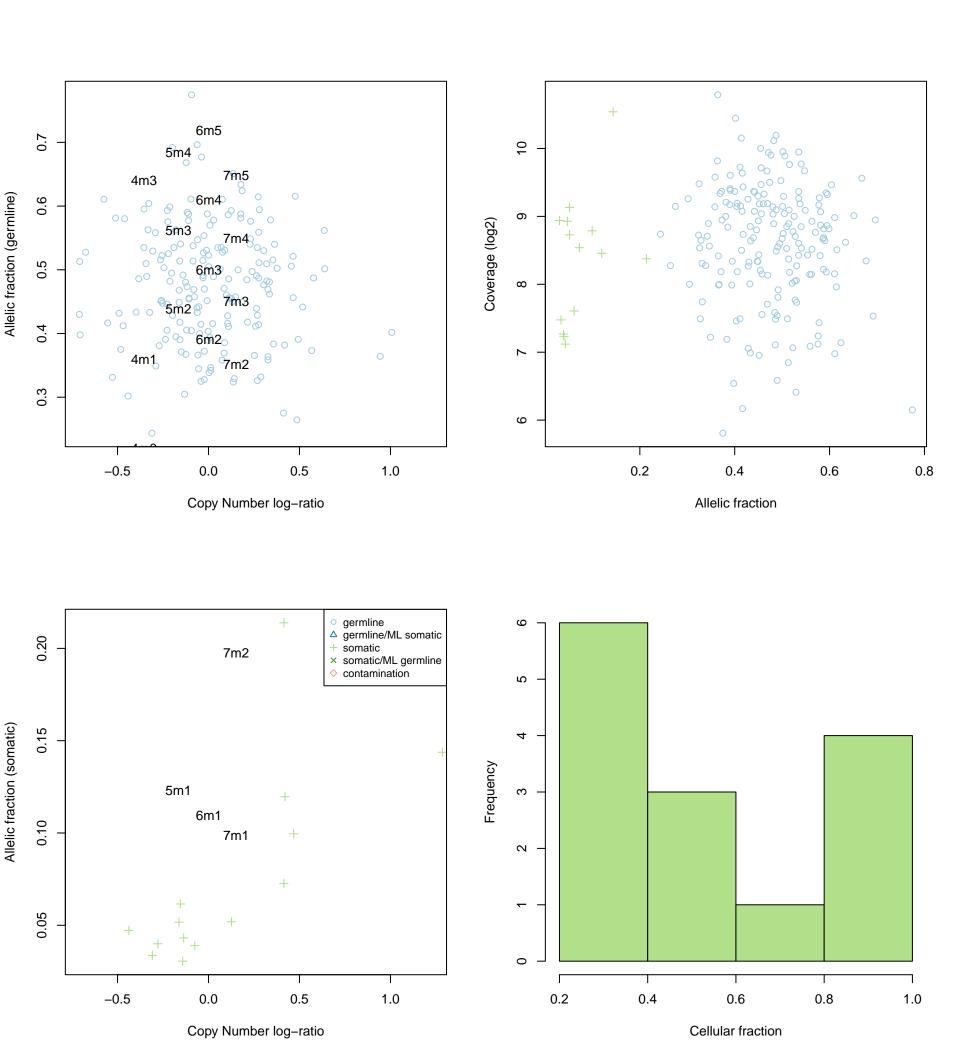
log2 ratio



SCNA-fit log-likelihood: -10173.18

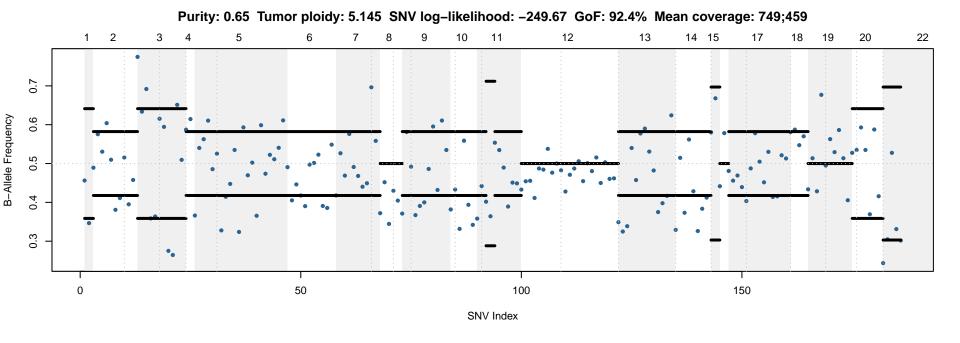




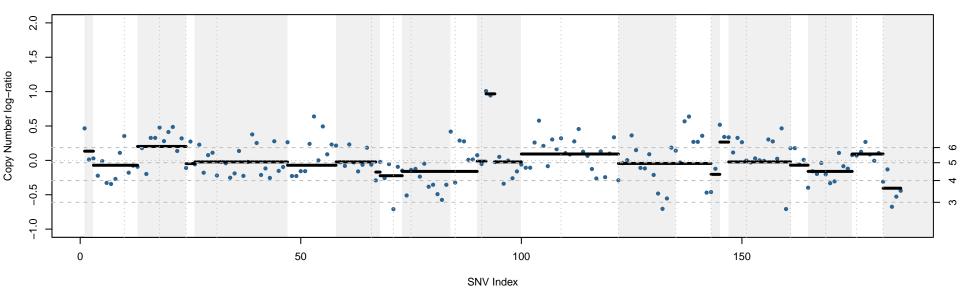


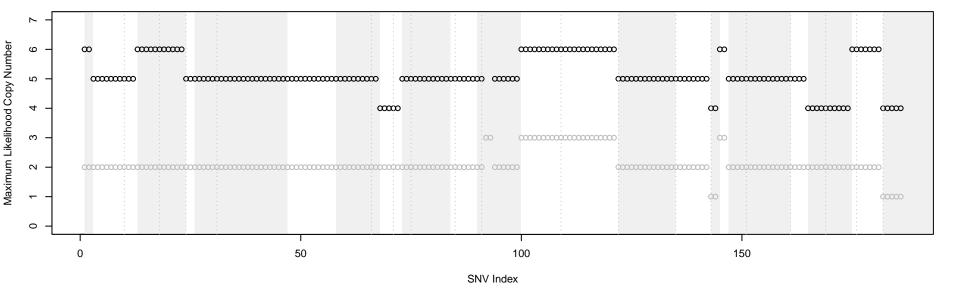
Purity: 0.65 Tumor ploidy: 5.145 3 5 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0

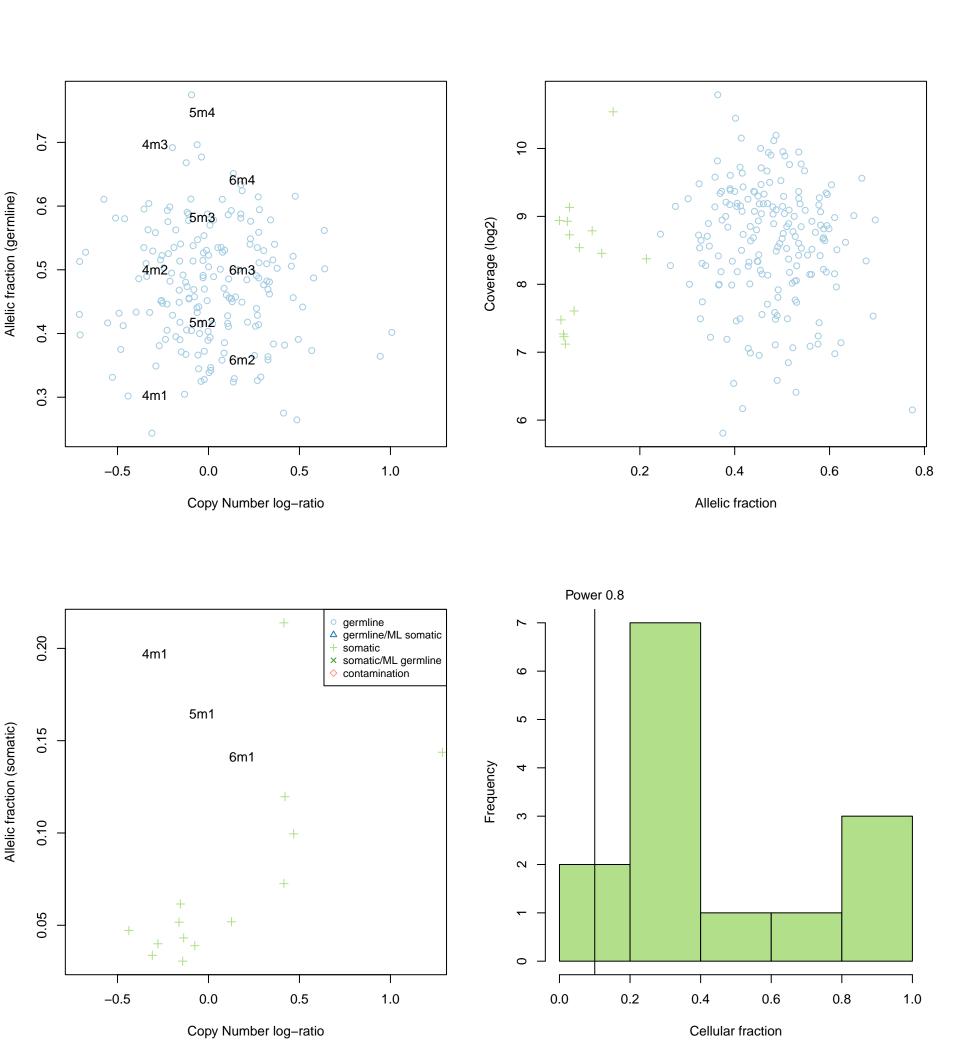
log2 ratio



SCNA-fit log-likelihood: -10242.4

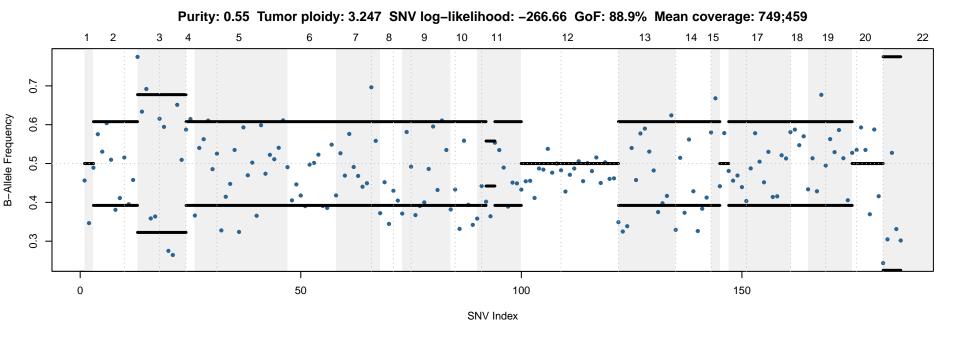




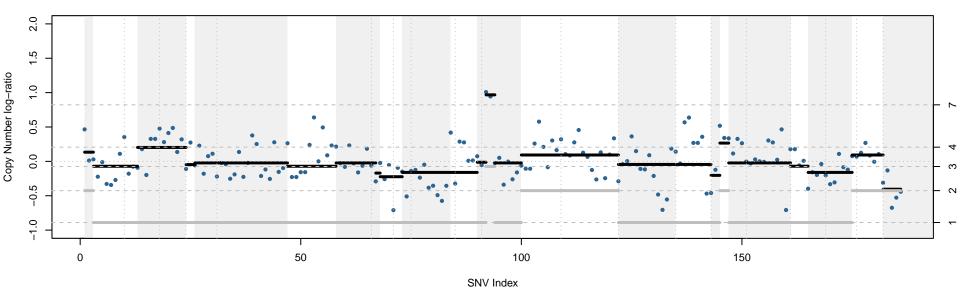


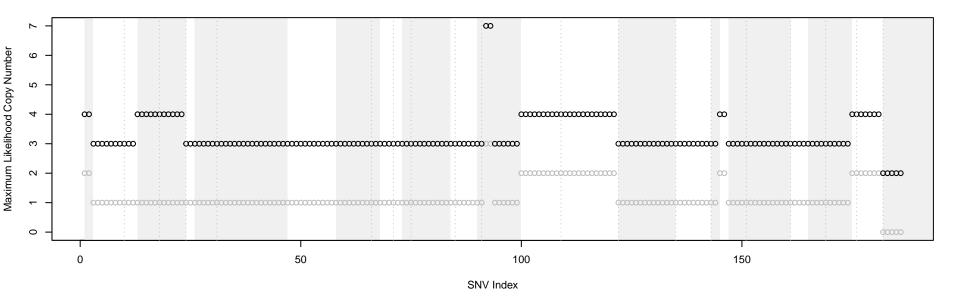
Purity: 0.55 Tumor ploidy: 3.247 2 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0

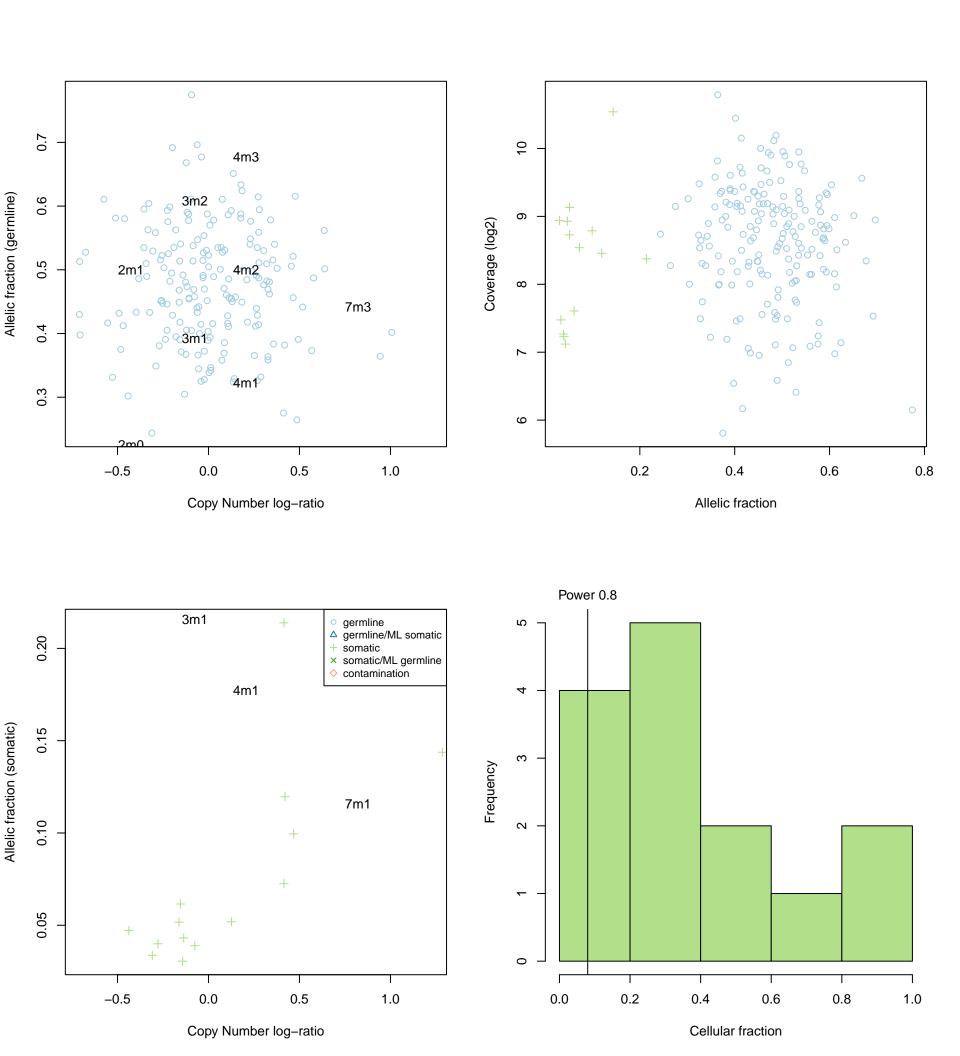
log2 ratio



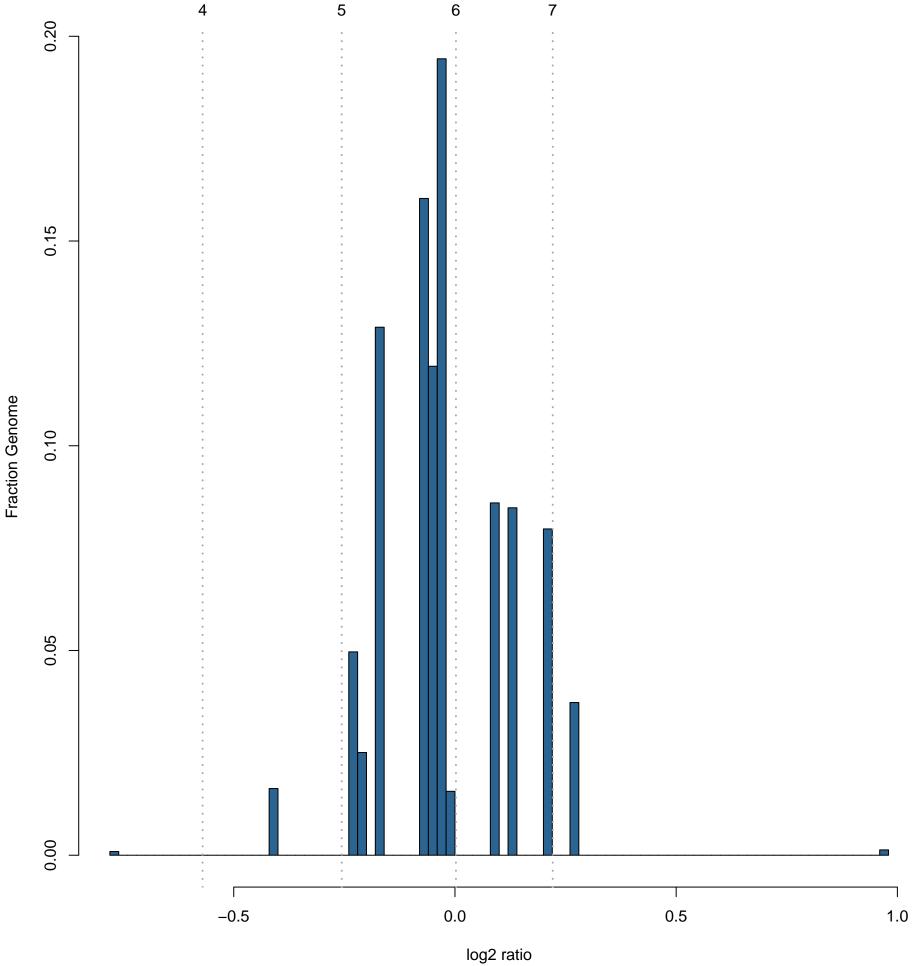
SCNA-fit log-likelihood: -10256.33

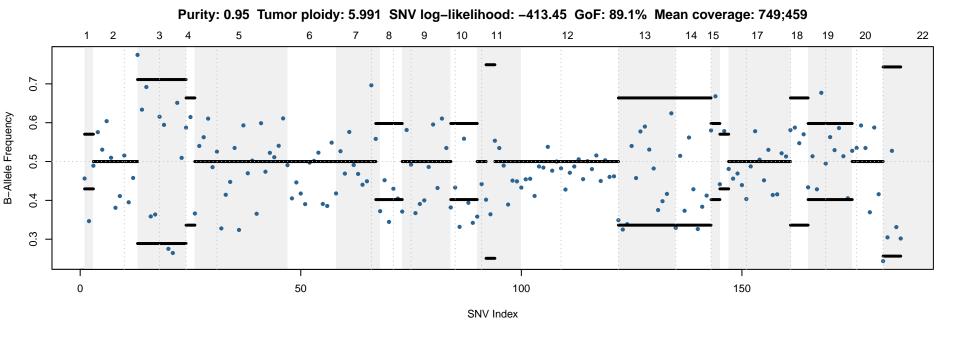




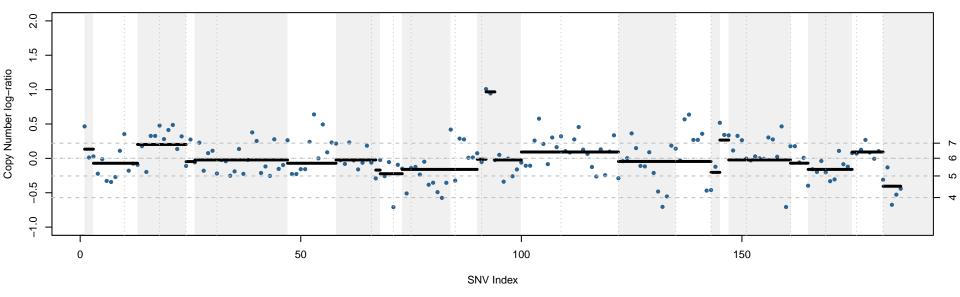


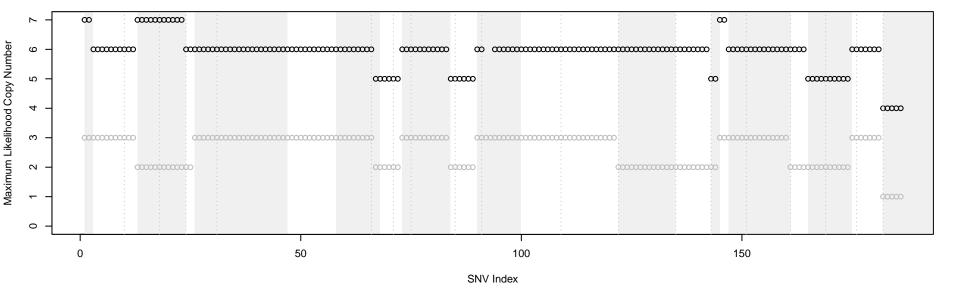
Purity: **0.95** Tumor ploidy: **5.991**6 7

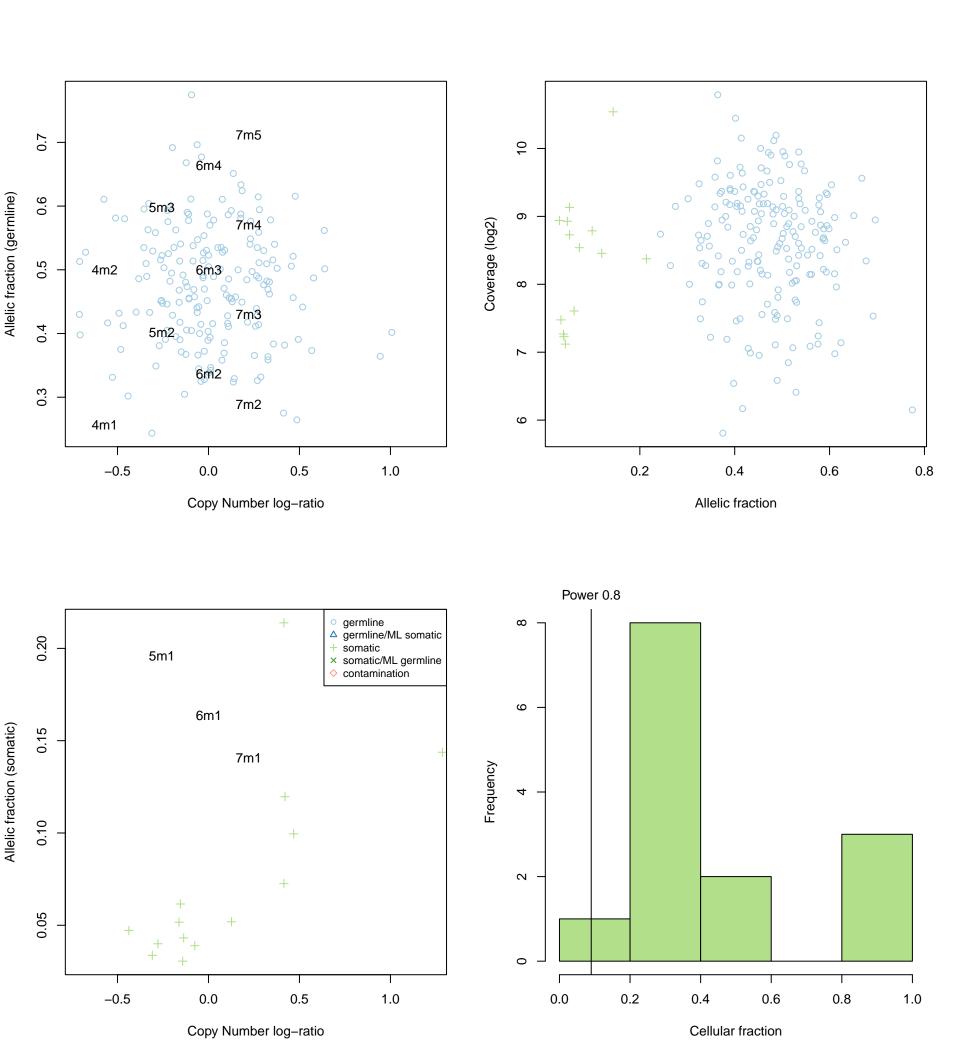




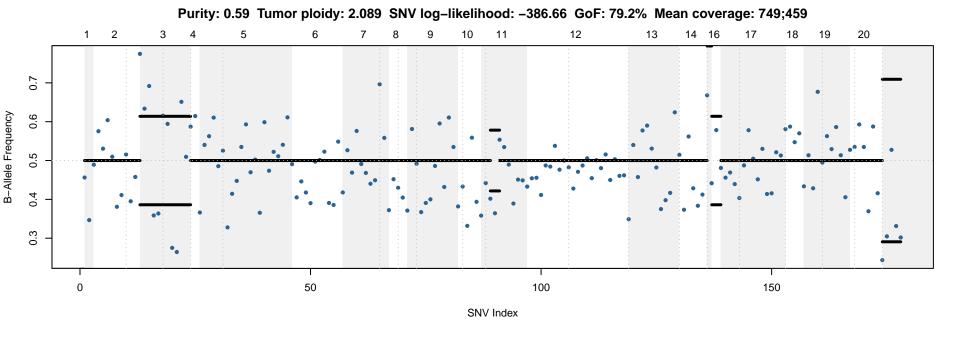
SCNA-fit log-likelihood: -10294.51







Purity: 0.59 Tumor ploidy: 2.089 5 0.20 Fraction Genome 0.10 0.05 0.00 -0.5 0.0 0.5 1.0 log2 ratio



SCNA-fit log-likelihood: -10532.74

