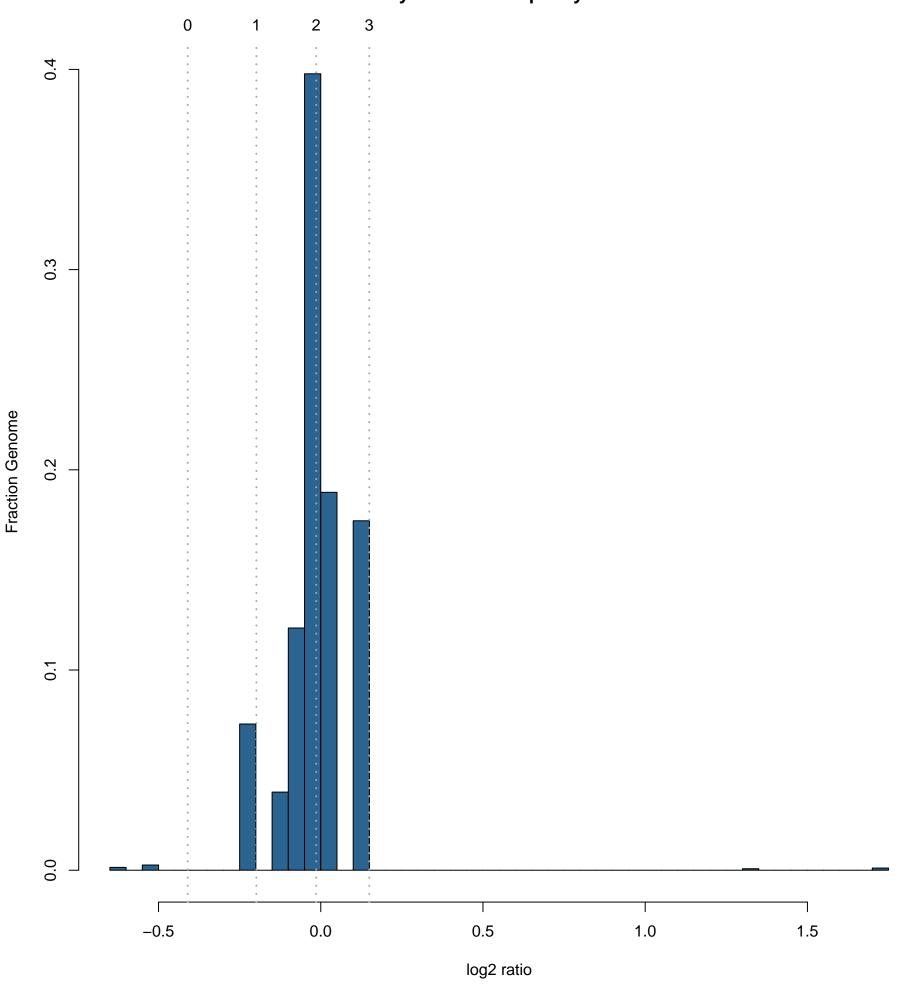
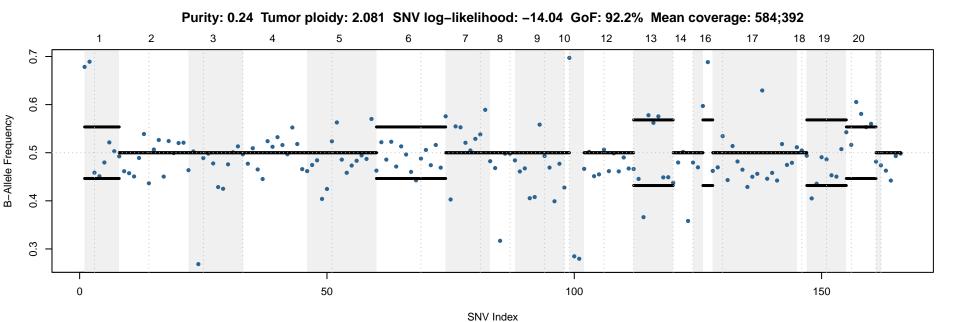
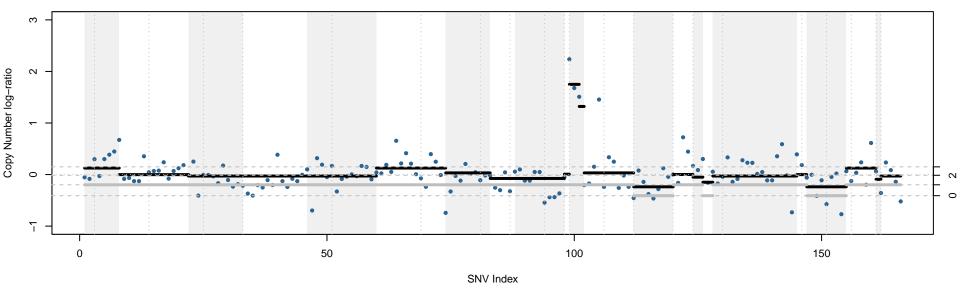
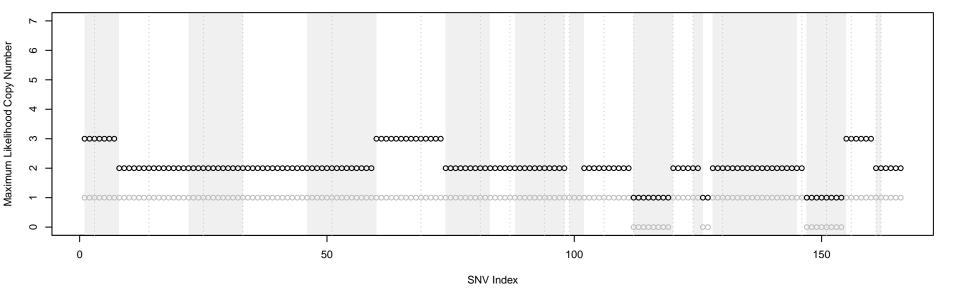
Purity: 0.24 Tumor ploidy: 2.081

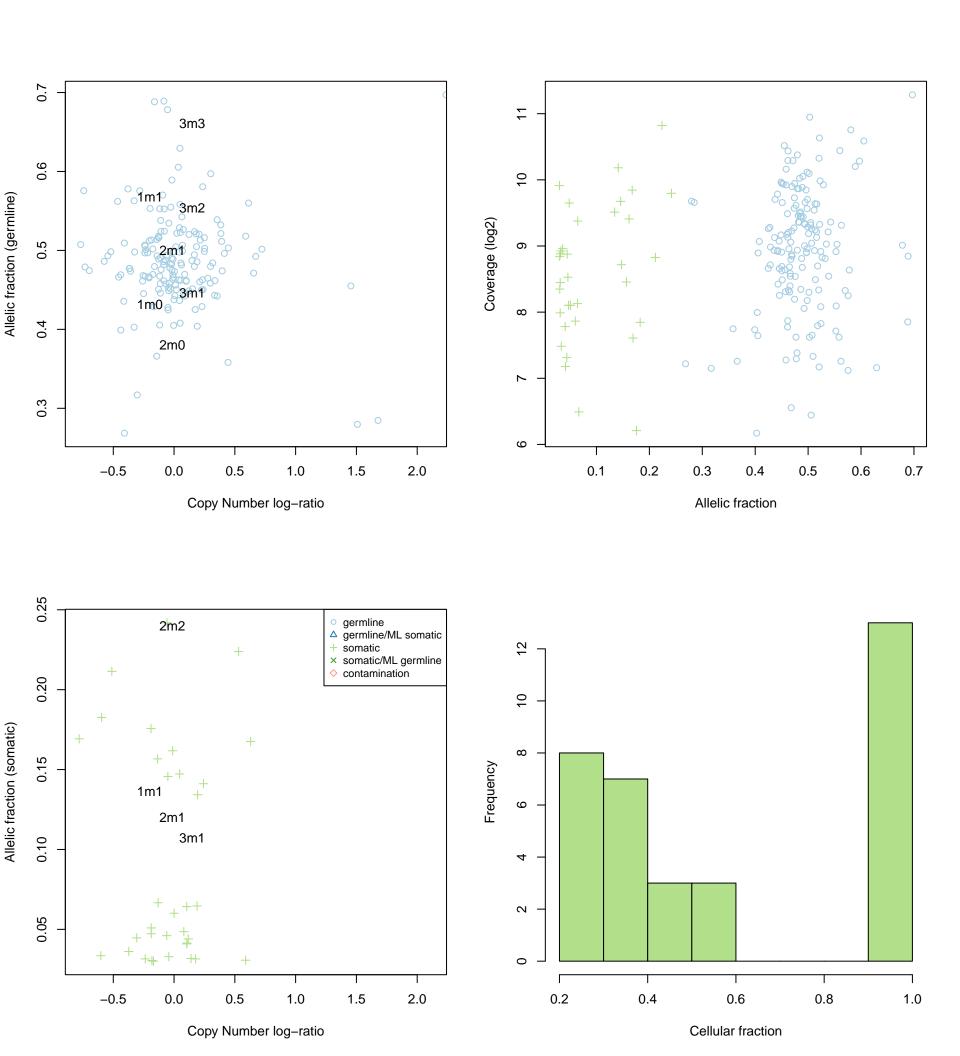




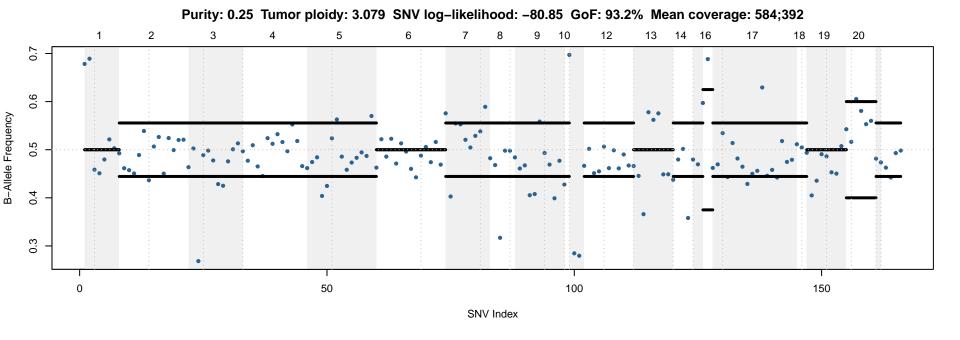
SCNA-fit log-likelihood: -8685.41



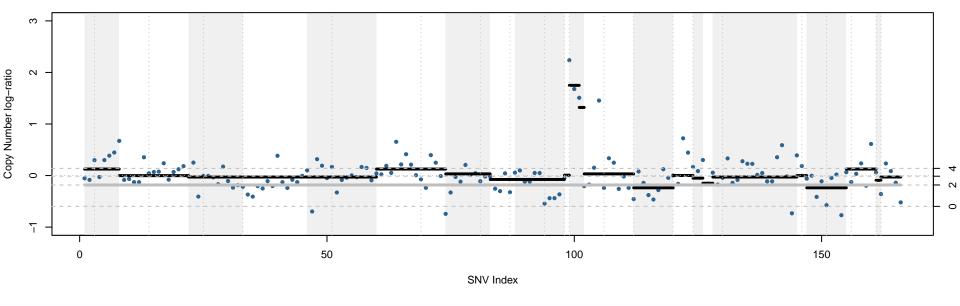


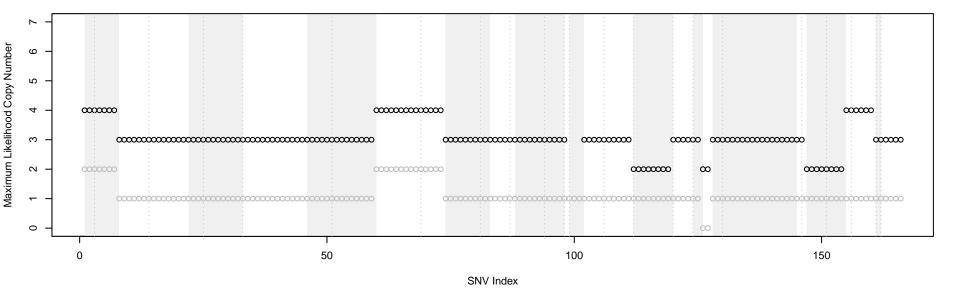


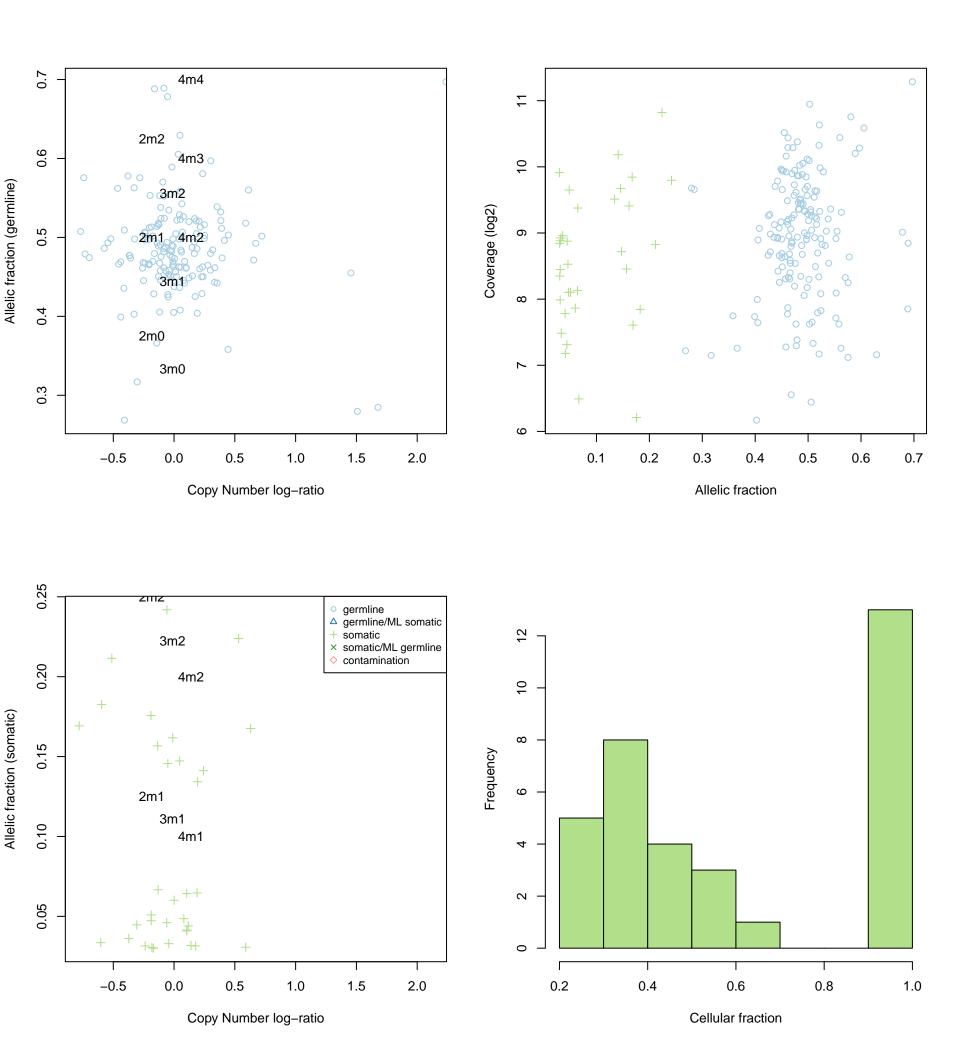
Purity: 0.25 Tumor ploidy: 3.079 0 2 3 0.3 Fraction Genome 0.2 0.1 0.0 -0.5 0.0 0.5 1.0 1.5 log2 ratio



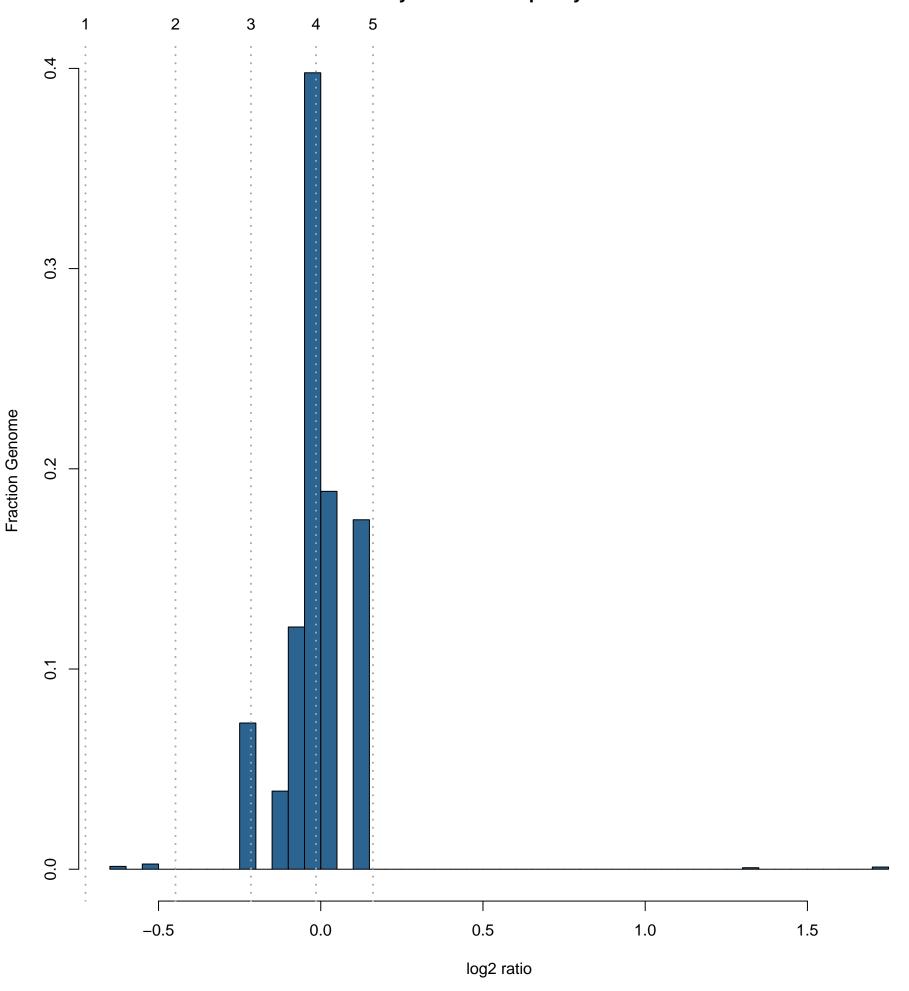
SCNA-fit log-likelihood: -8683.08

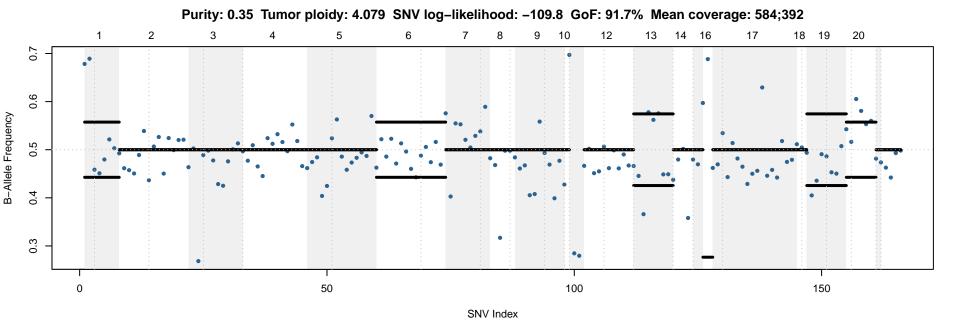




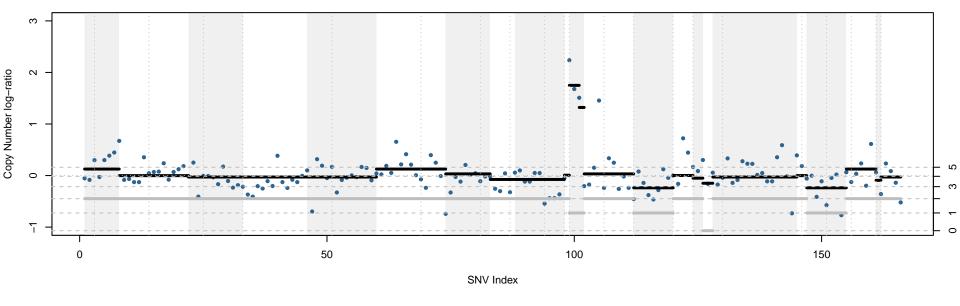


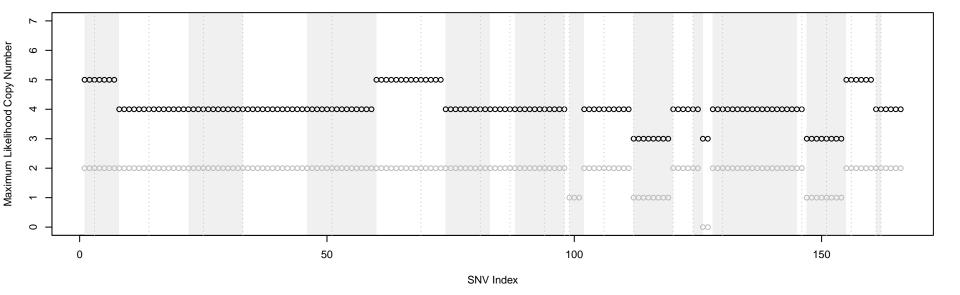
Purity: 0.35 Tumor ploidy: 4.079

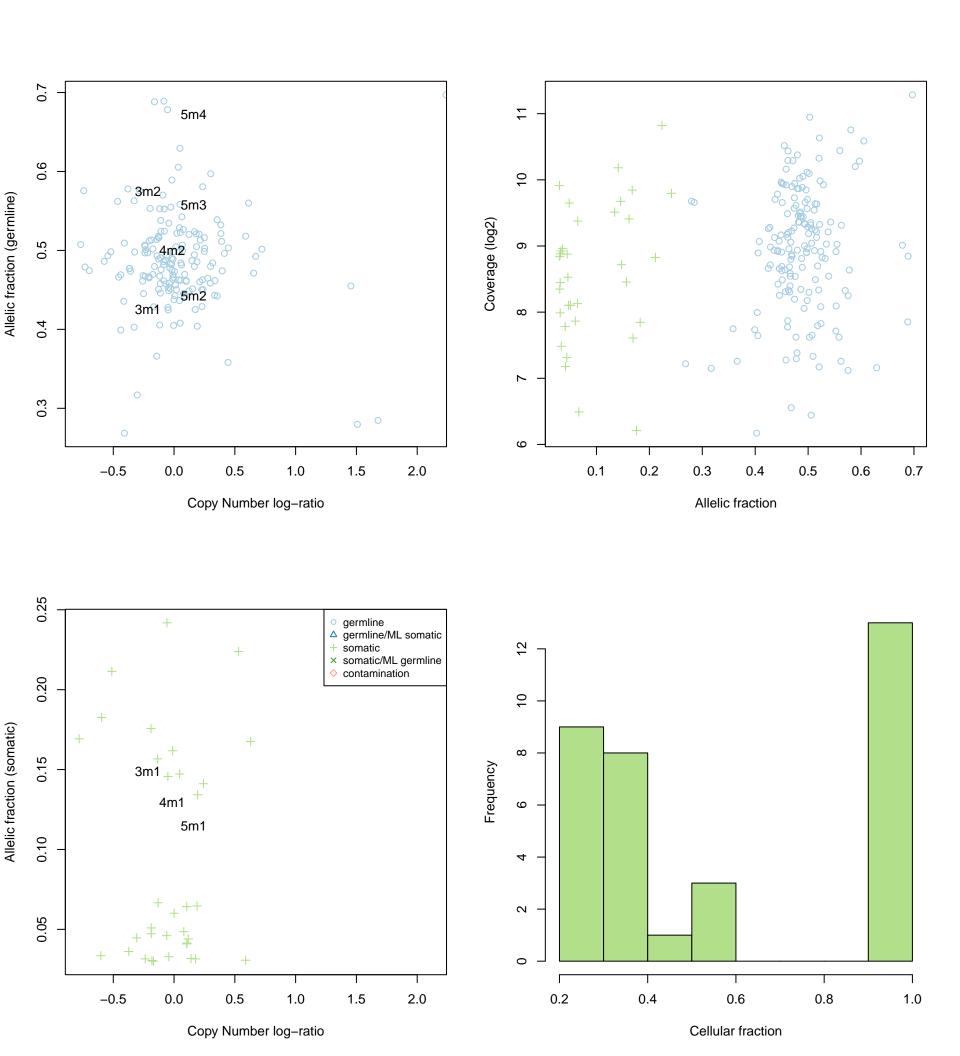




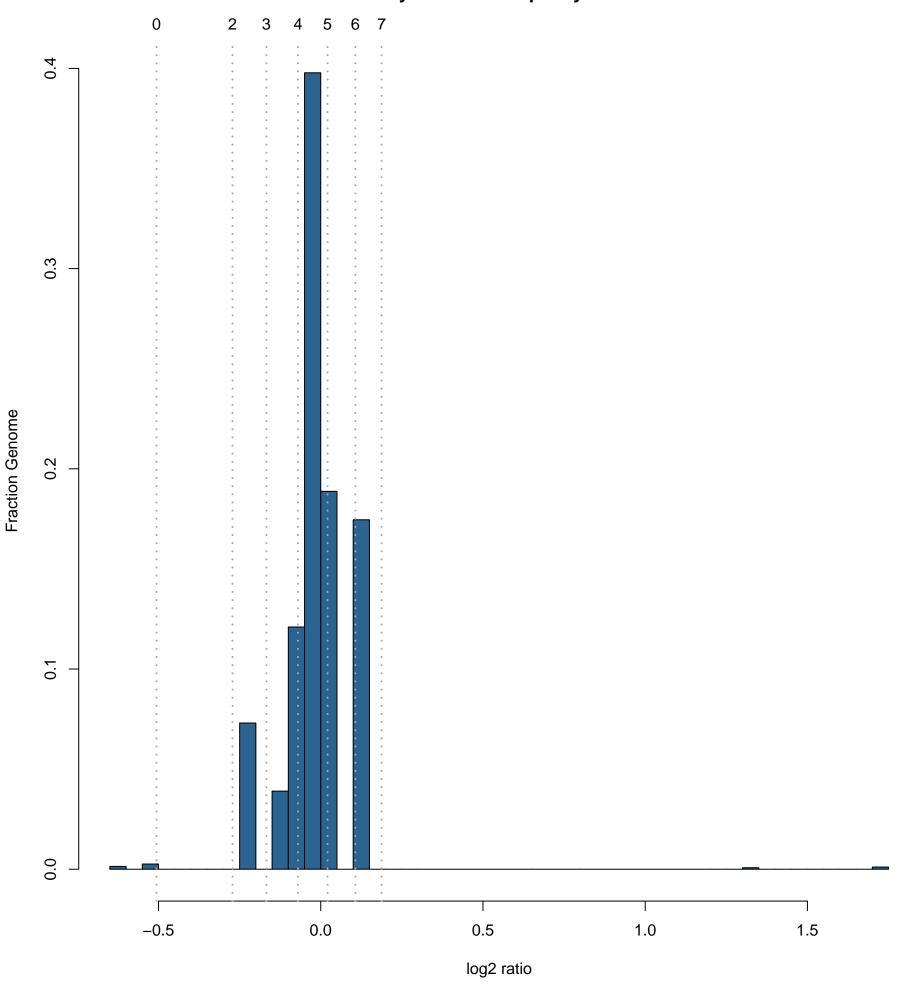
SCNA-fit log-likelihood: -8686.74

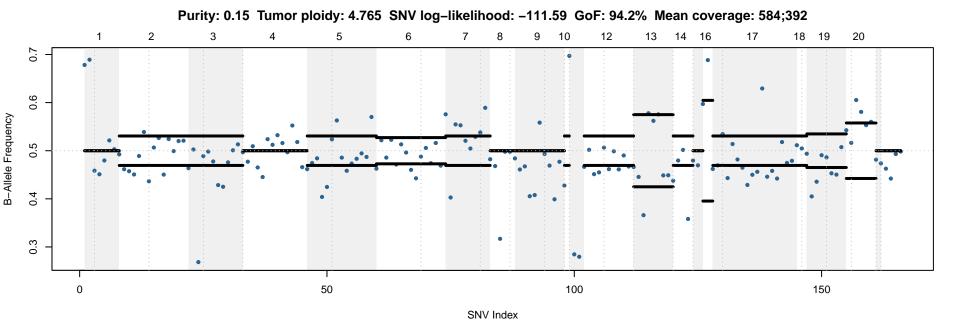




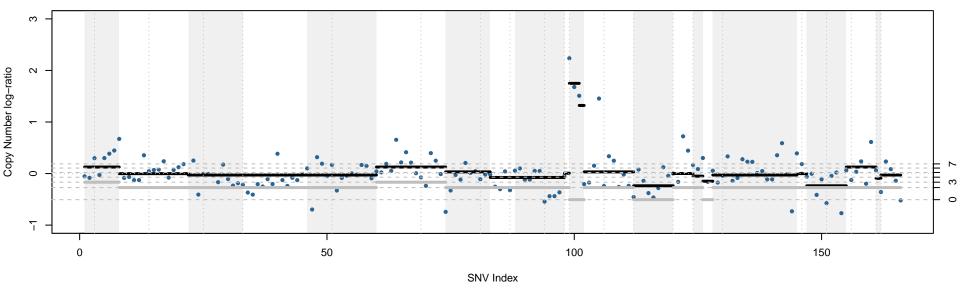


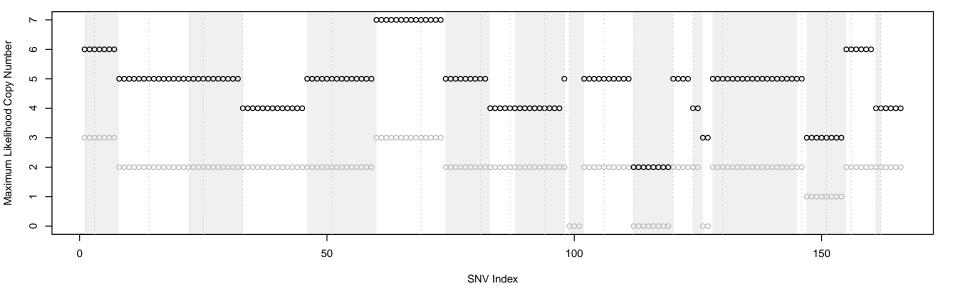
Purity: 0.15 Tumor ploidy: 4.765

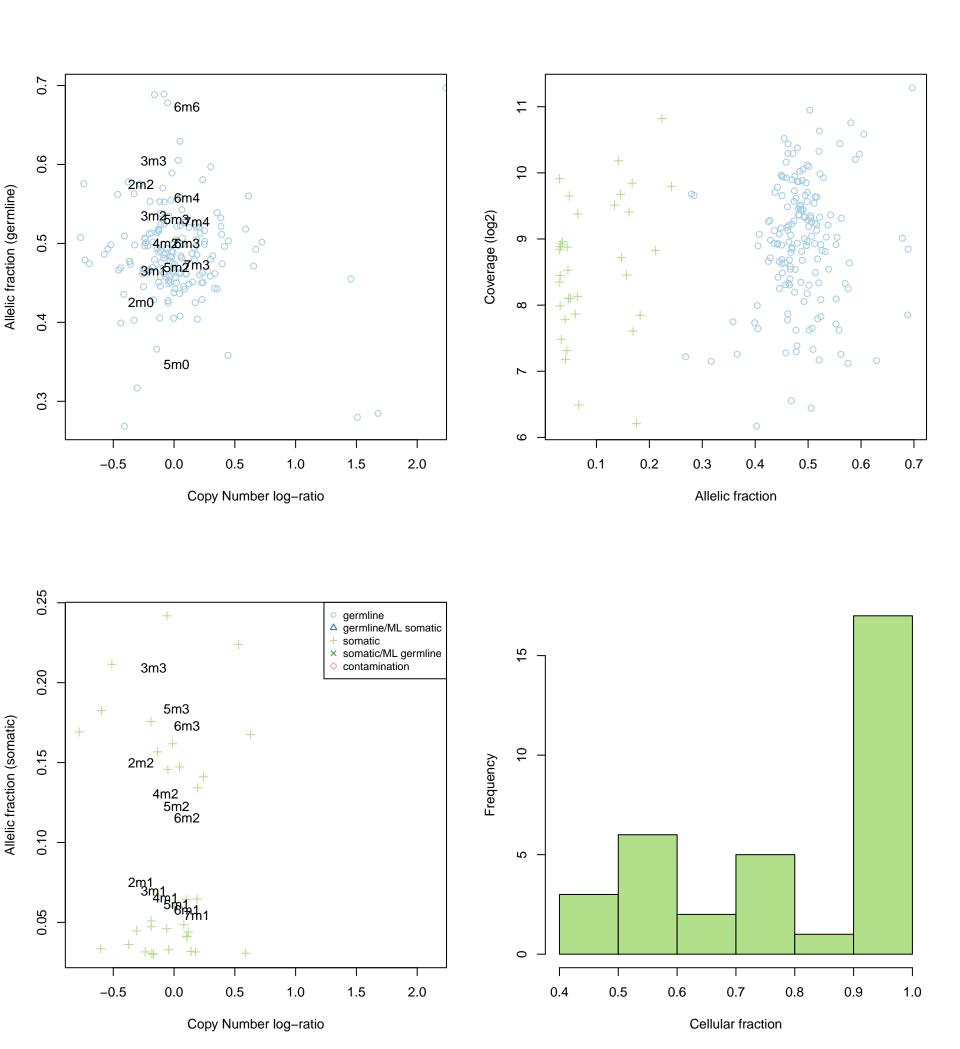




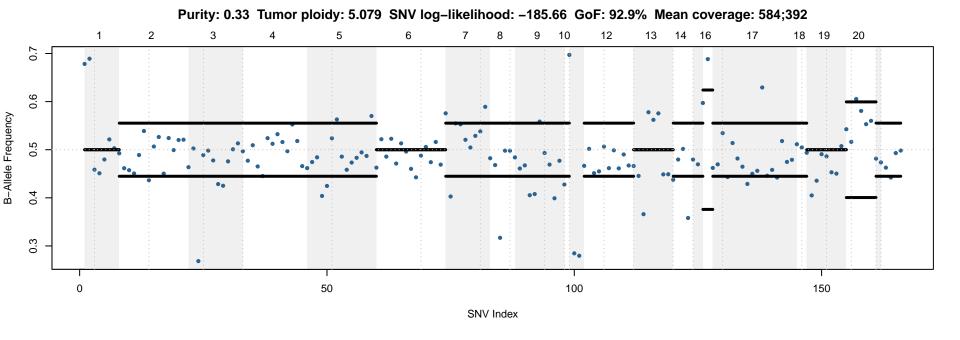
SCNA-fit log-likelihood: -8672.34



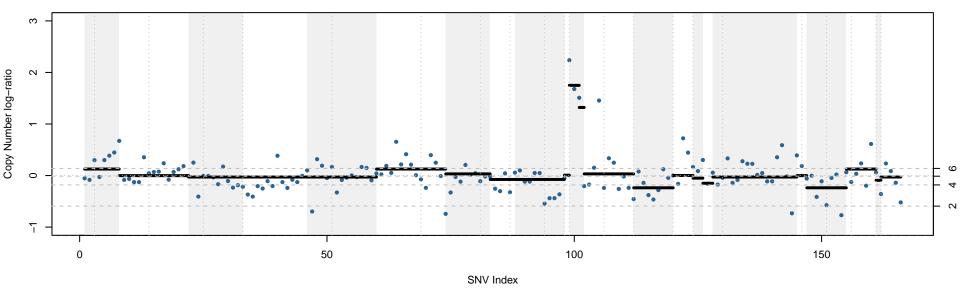


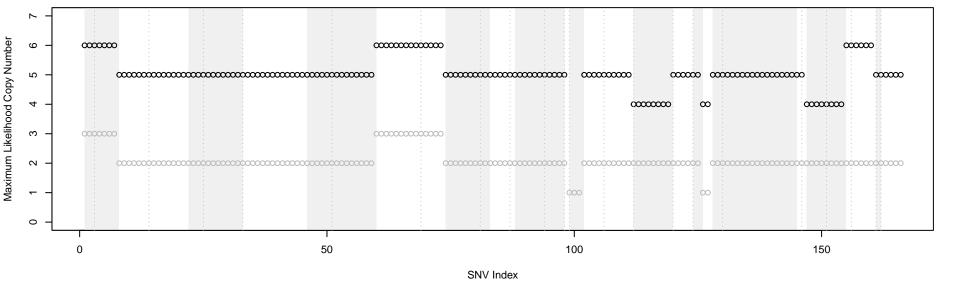


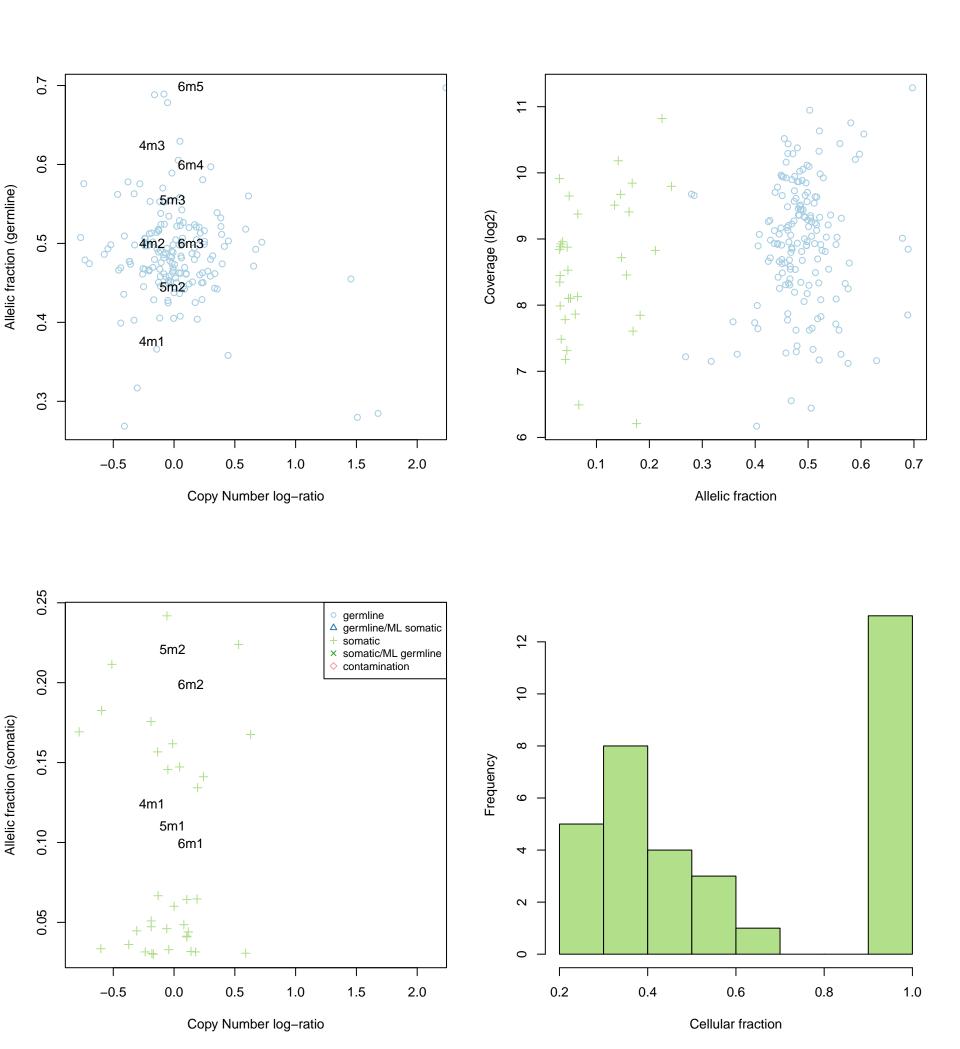
Purity: 0.33 Tumor ploidy: 5.079 0 0.3 Fraction Genome 0.2 0.1 0.0 -2 -1 0 log2 ratio



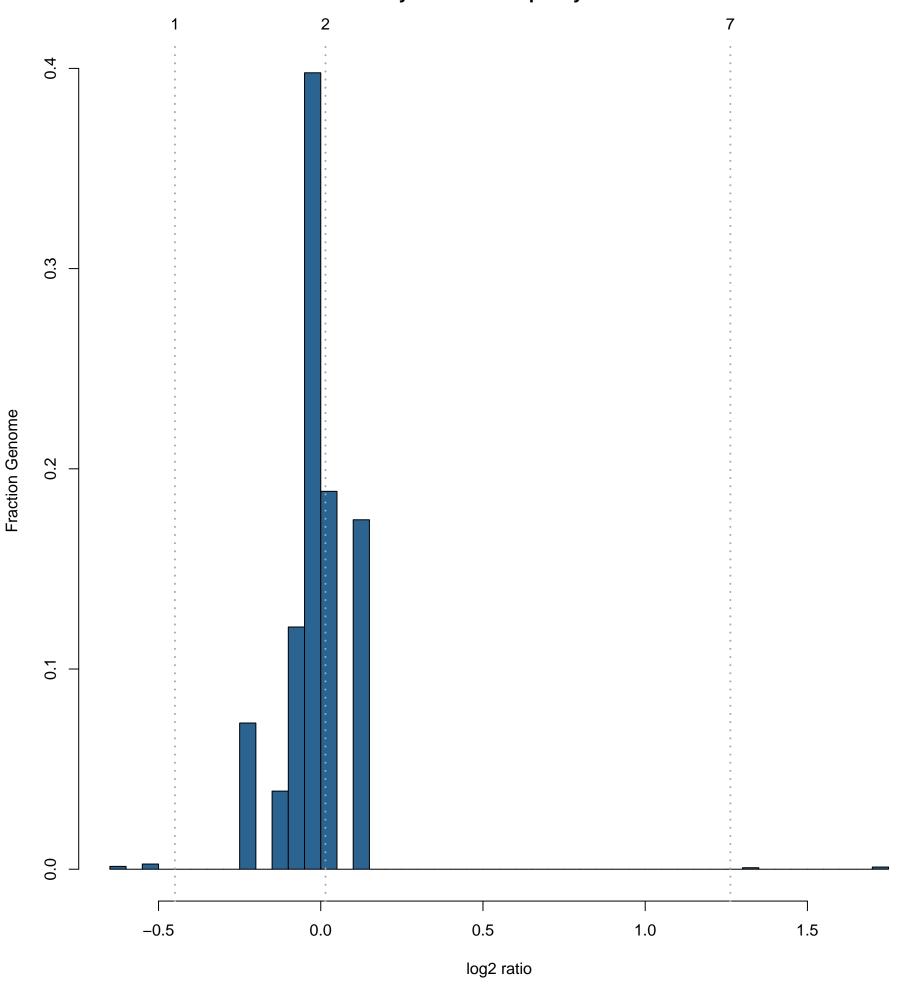
SCNA-fit log-likelihood: -8682.96

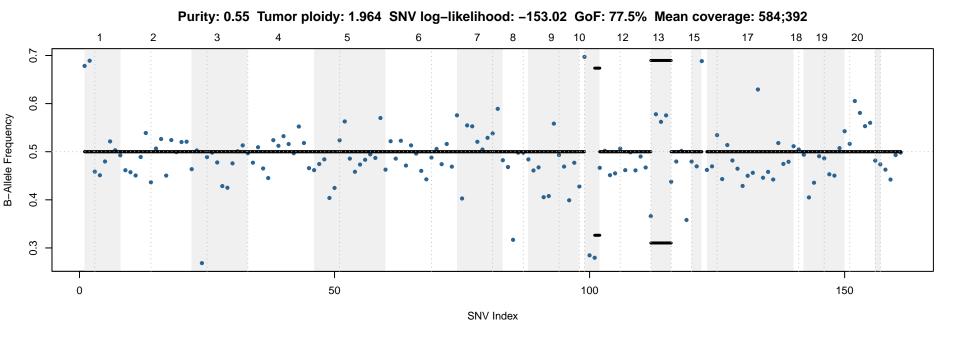




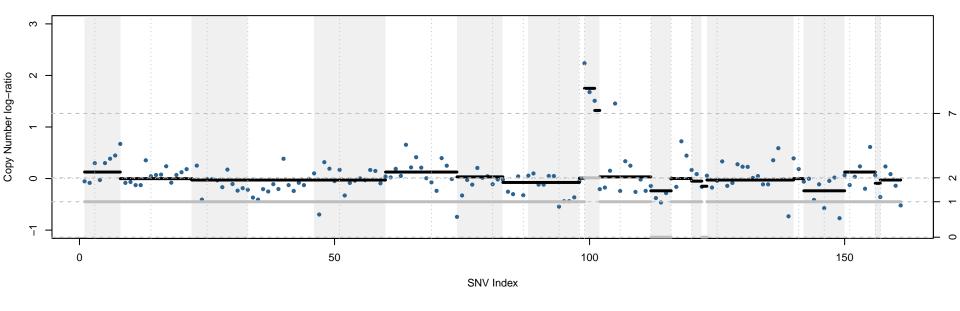


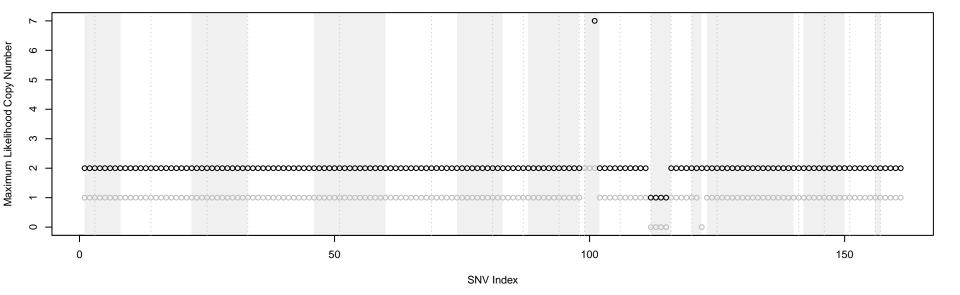
Purity: 0.55 Tumor ploidy: 1.964

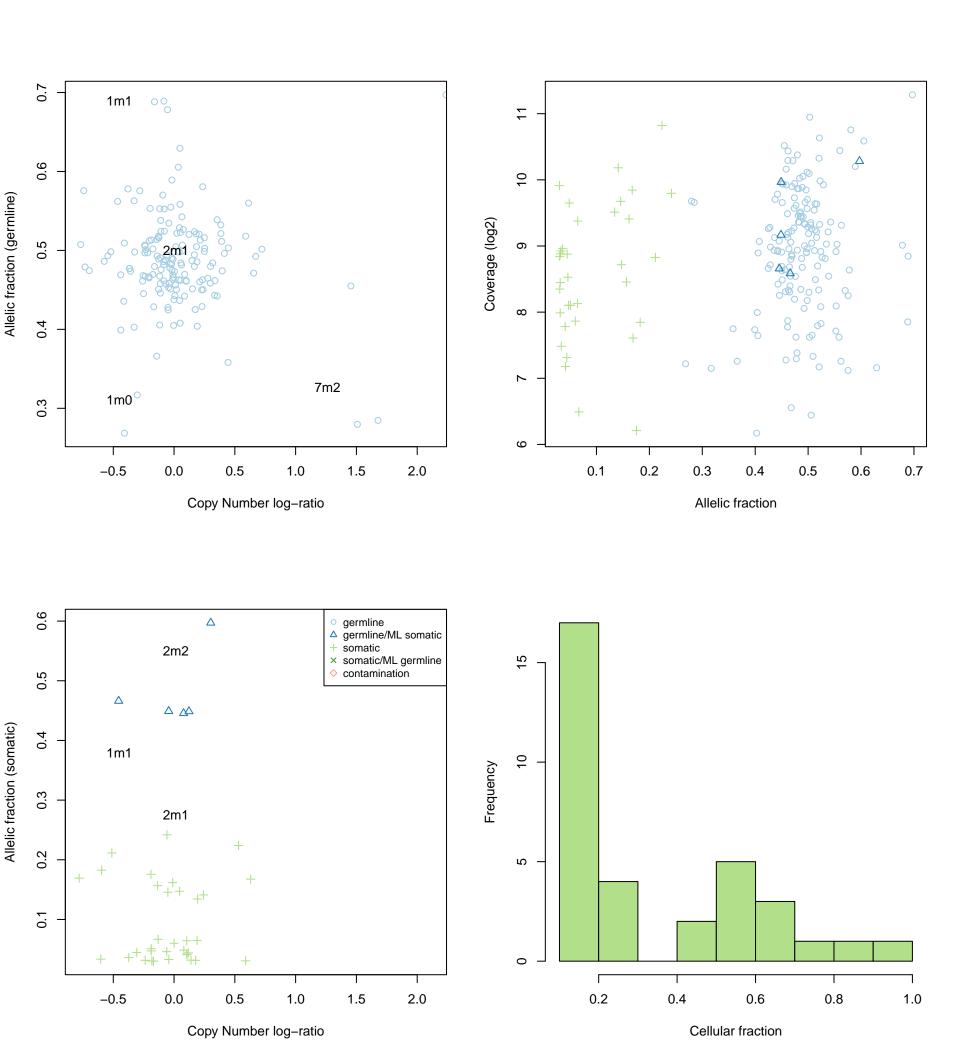


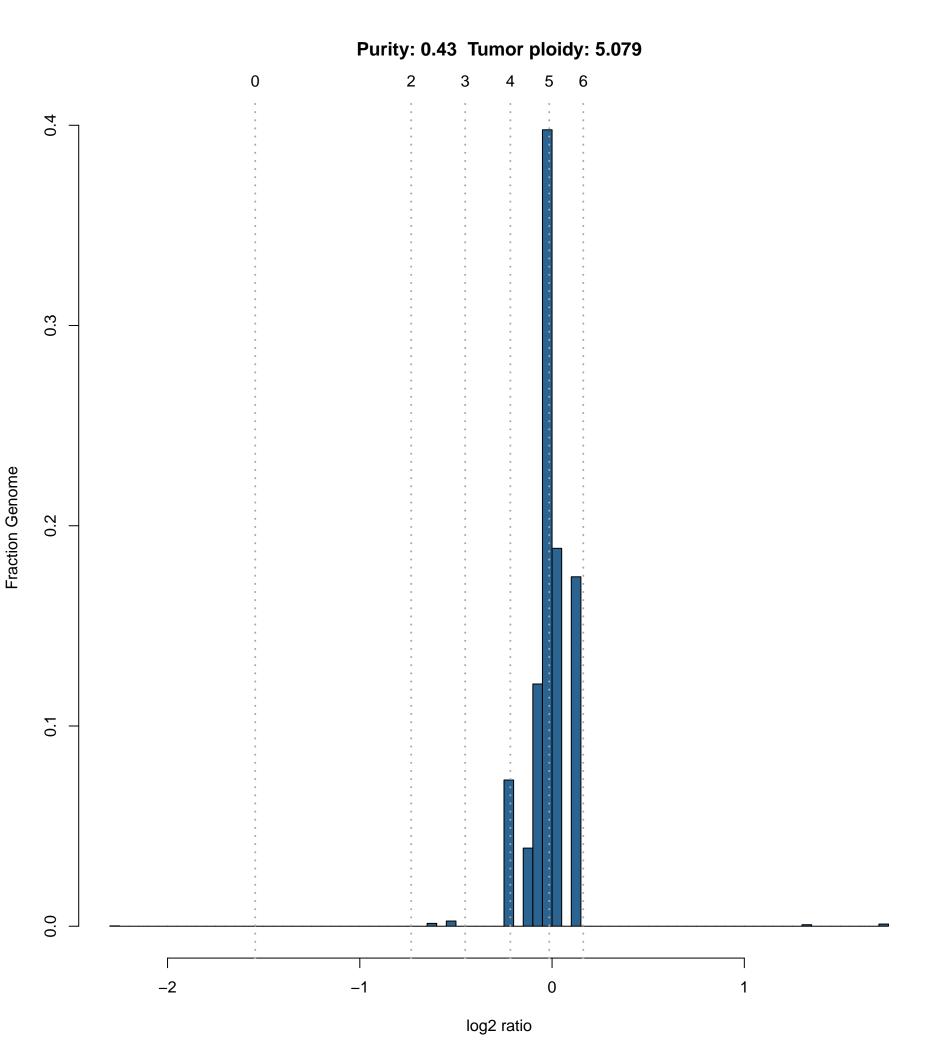


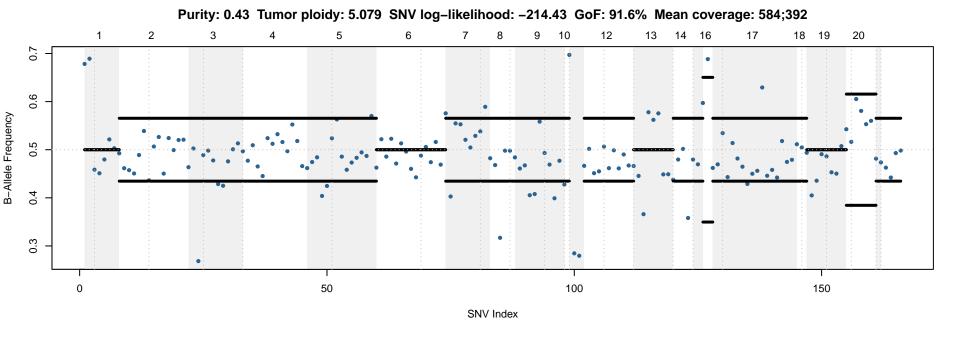
SCNA-fit log-likelihood: -8829.66



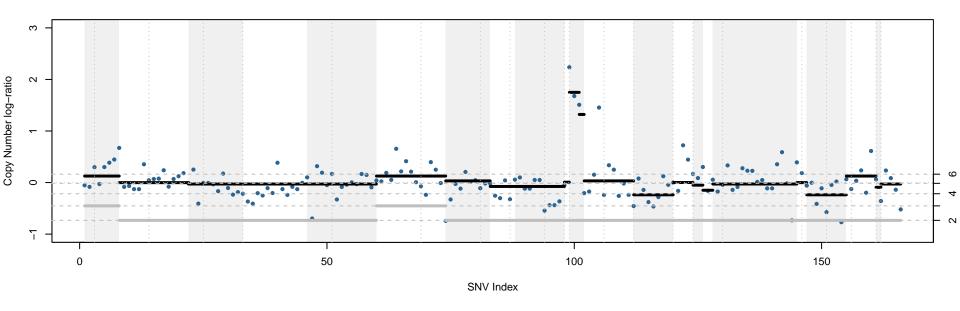


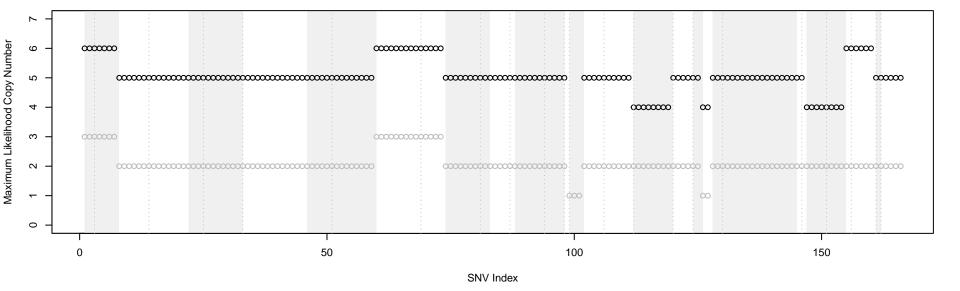


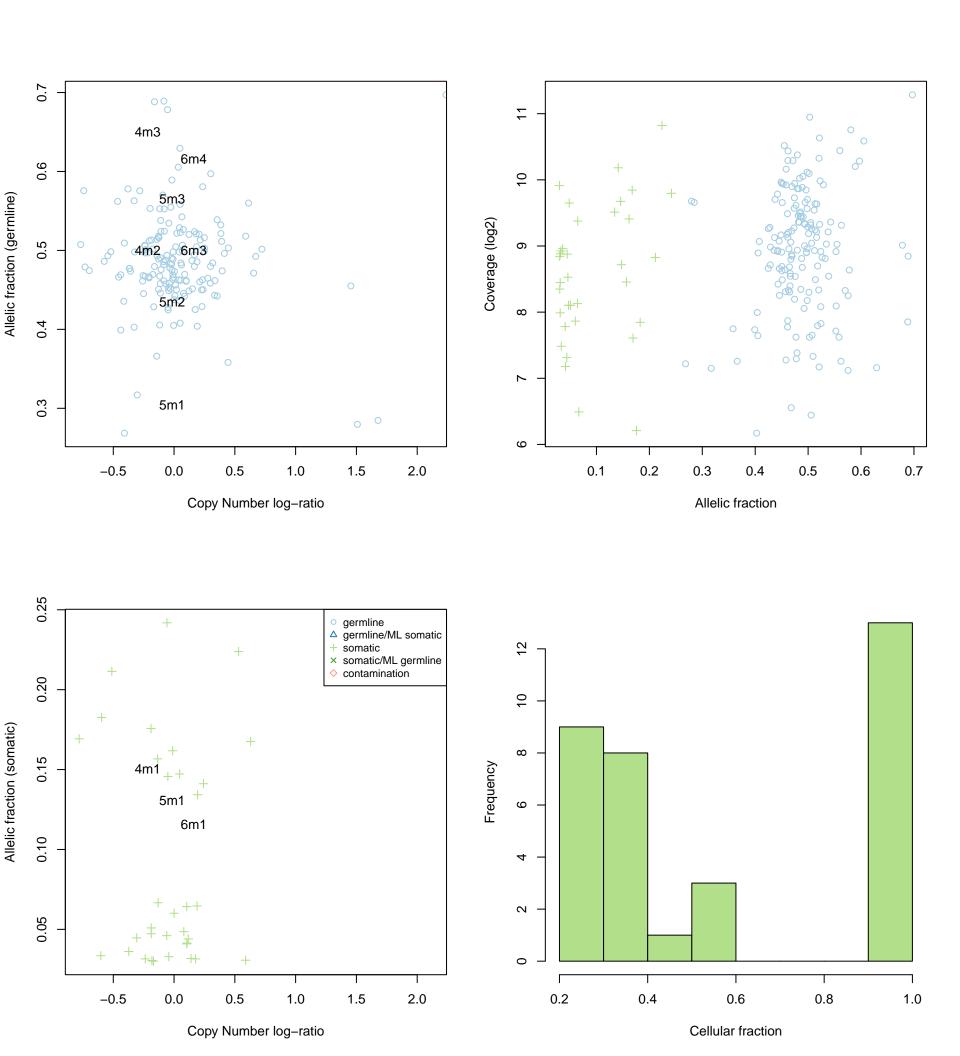


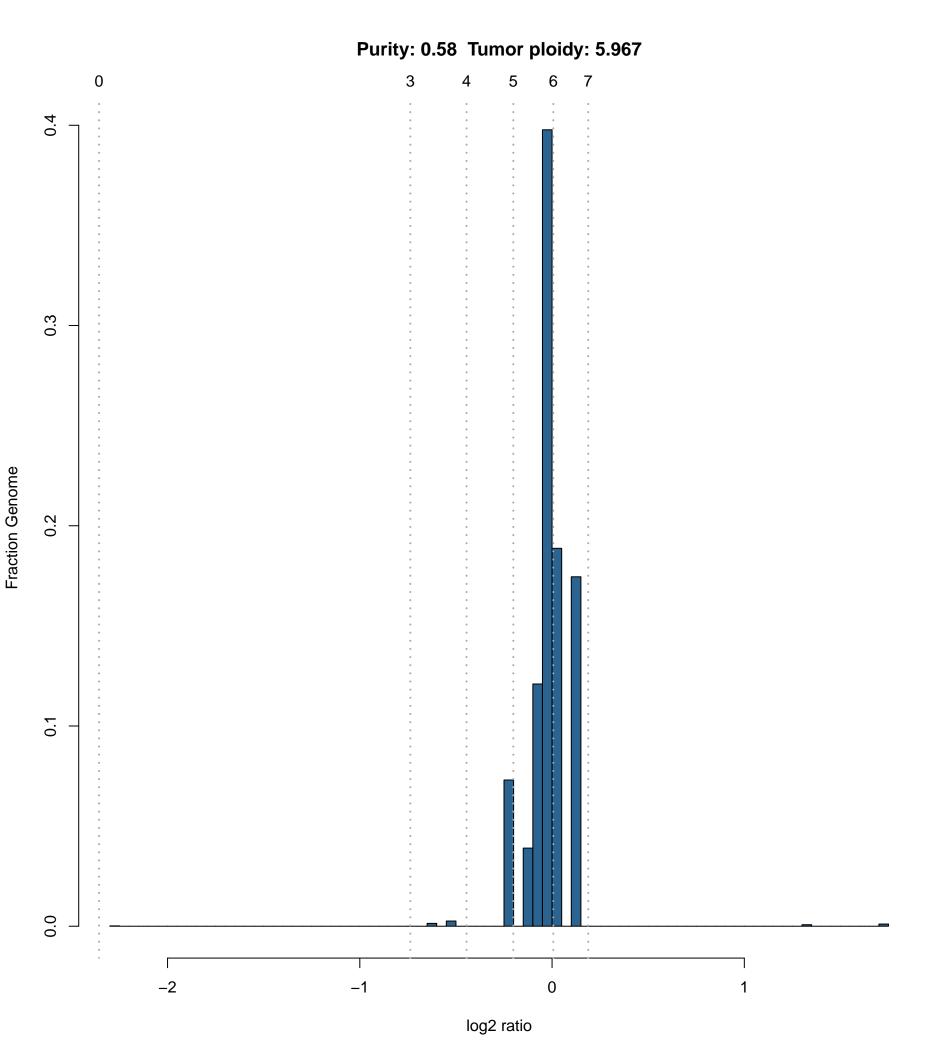


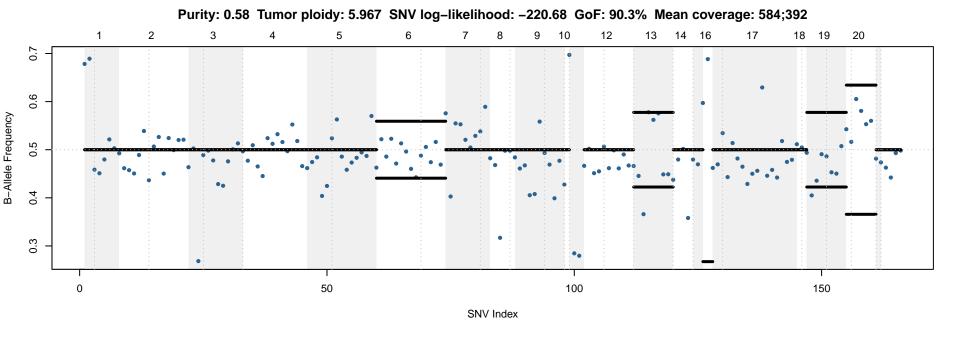
SCNA-fit log-likelihood: -8687.33



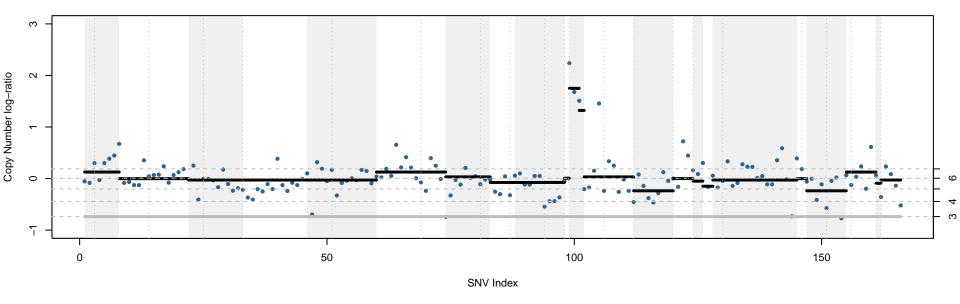


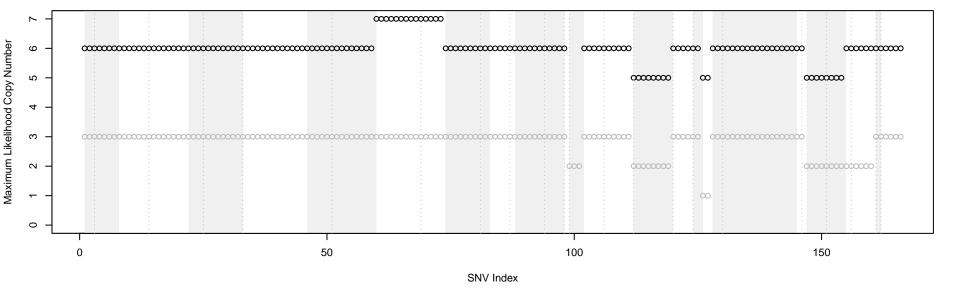


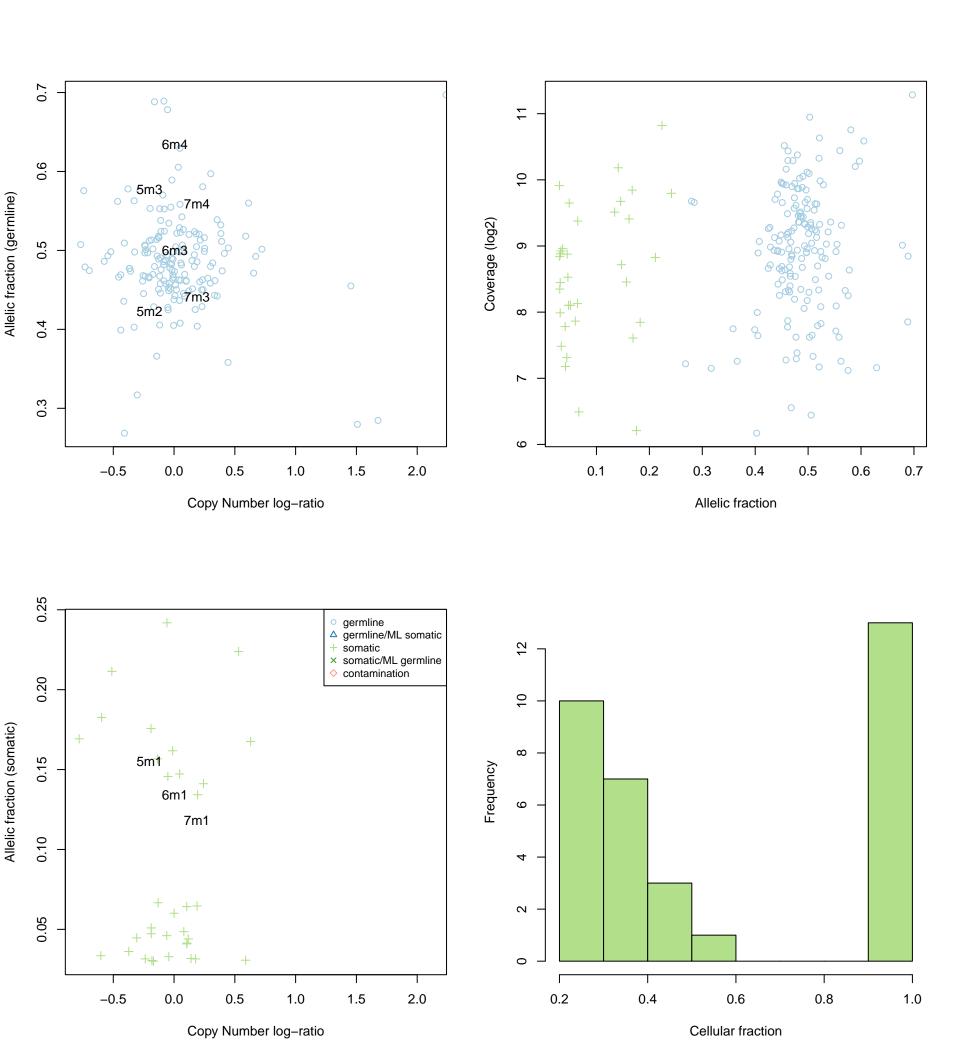


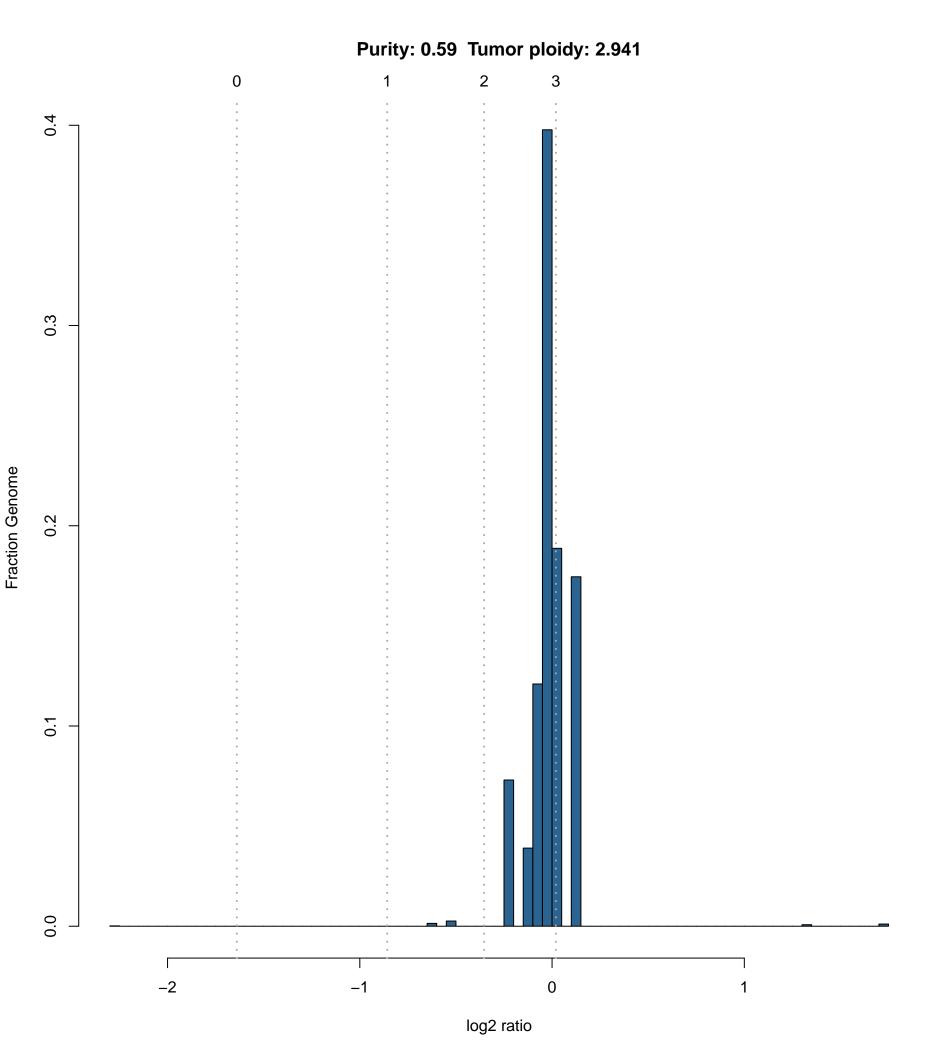


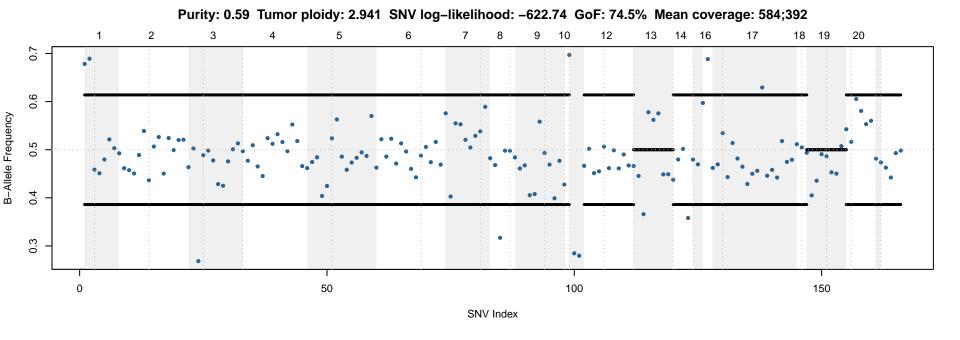
SCNA-fit log-likelihood: -8725.11



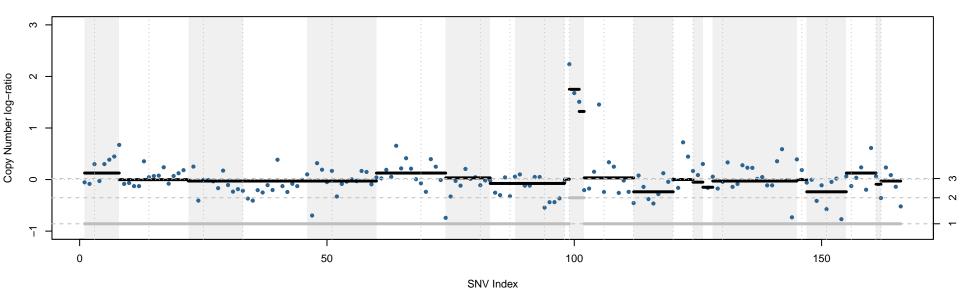


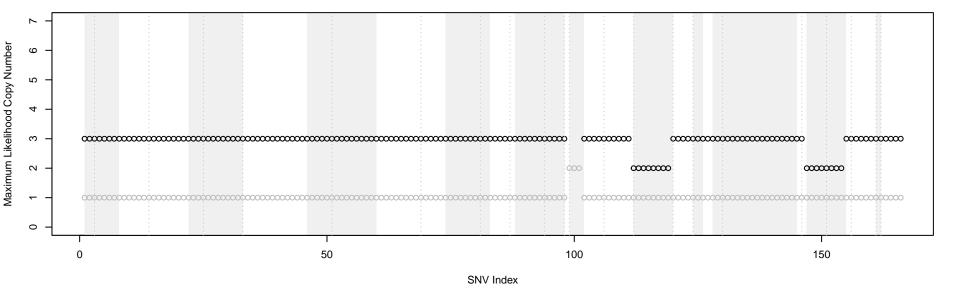


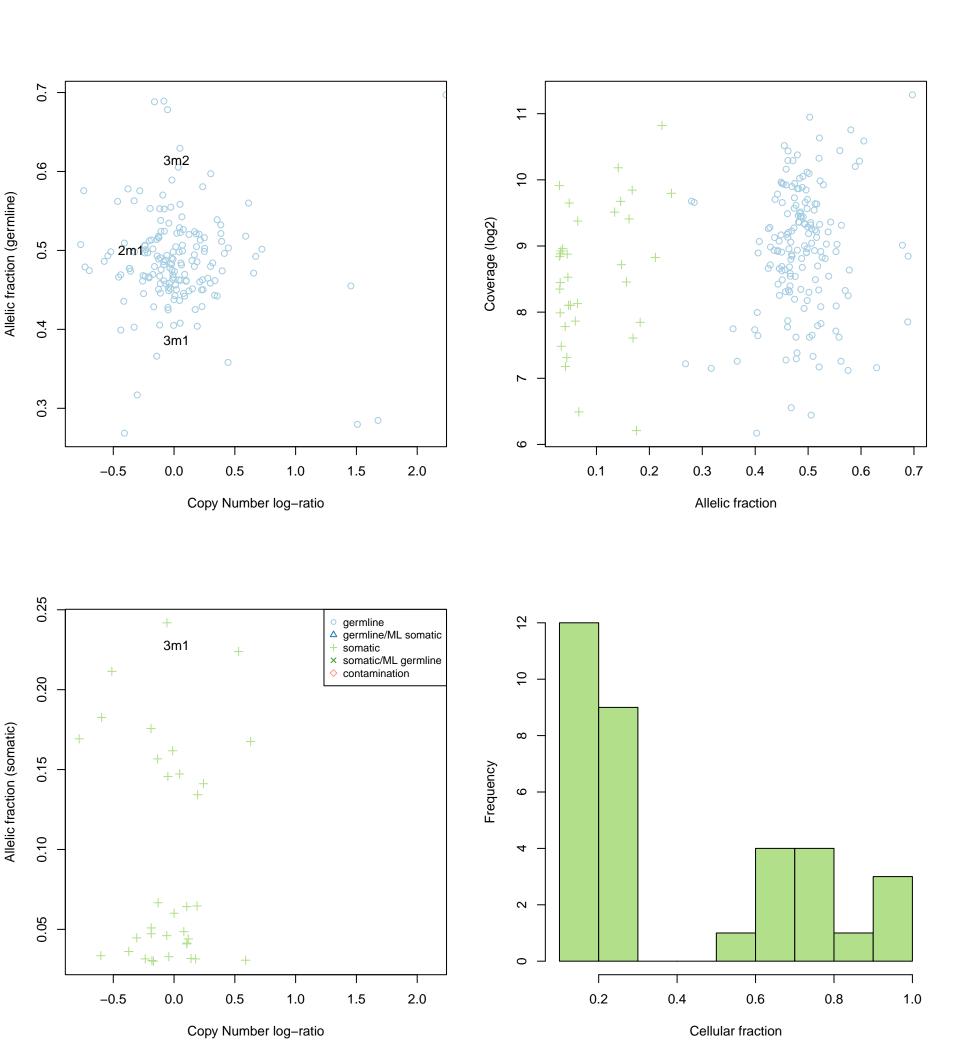




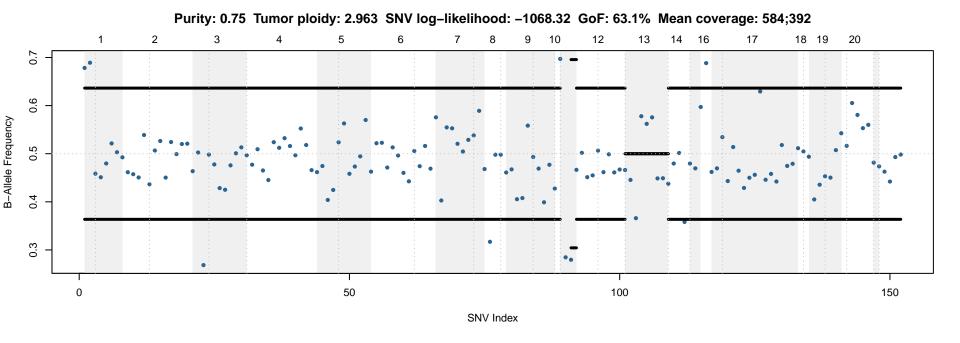
SCNA-fit log-likelihood: -8803.5







Purity: 0.75 Tumor ploidy: 2.963 3 0 7 Fraction Genome 0.2 0.1 0.0 -2 -1 0 log2 ratio



SCNA-fit log-likelihood: -8827.4

