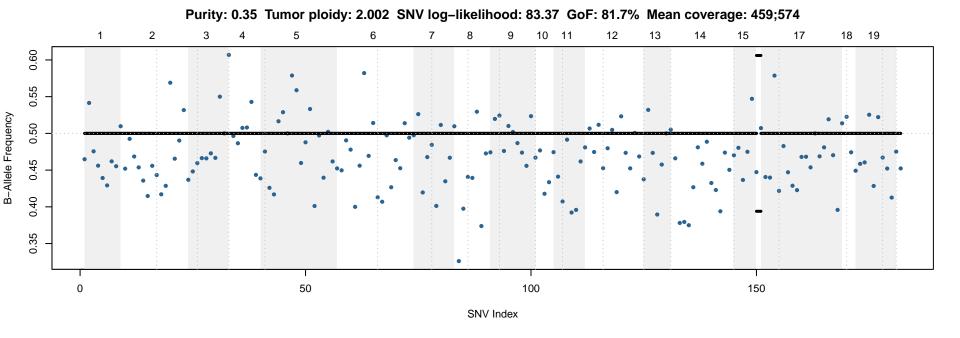
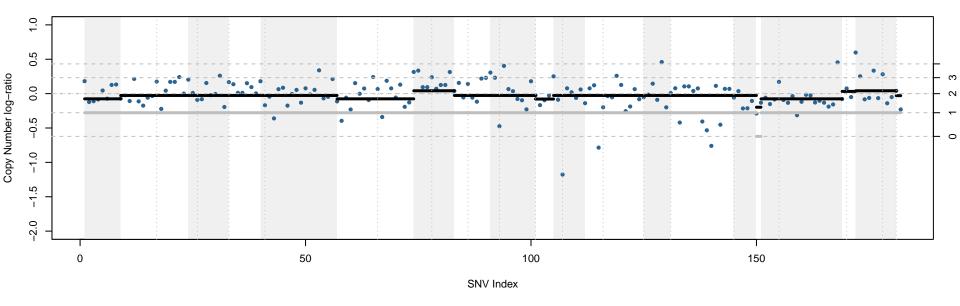
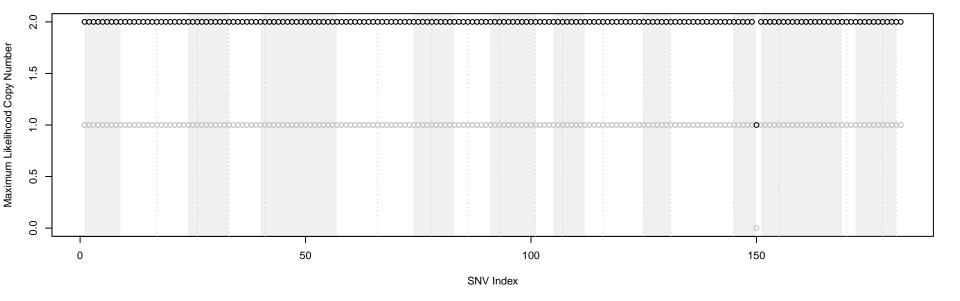
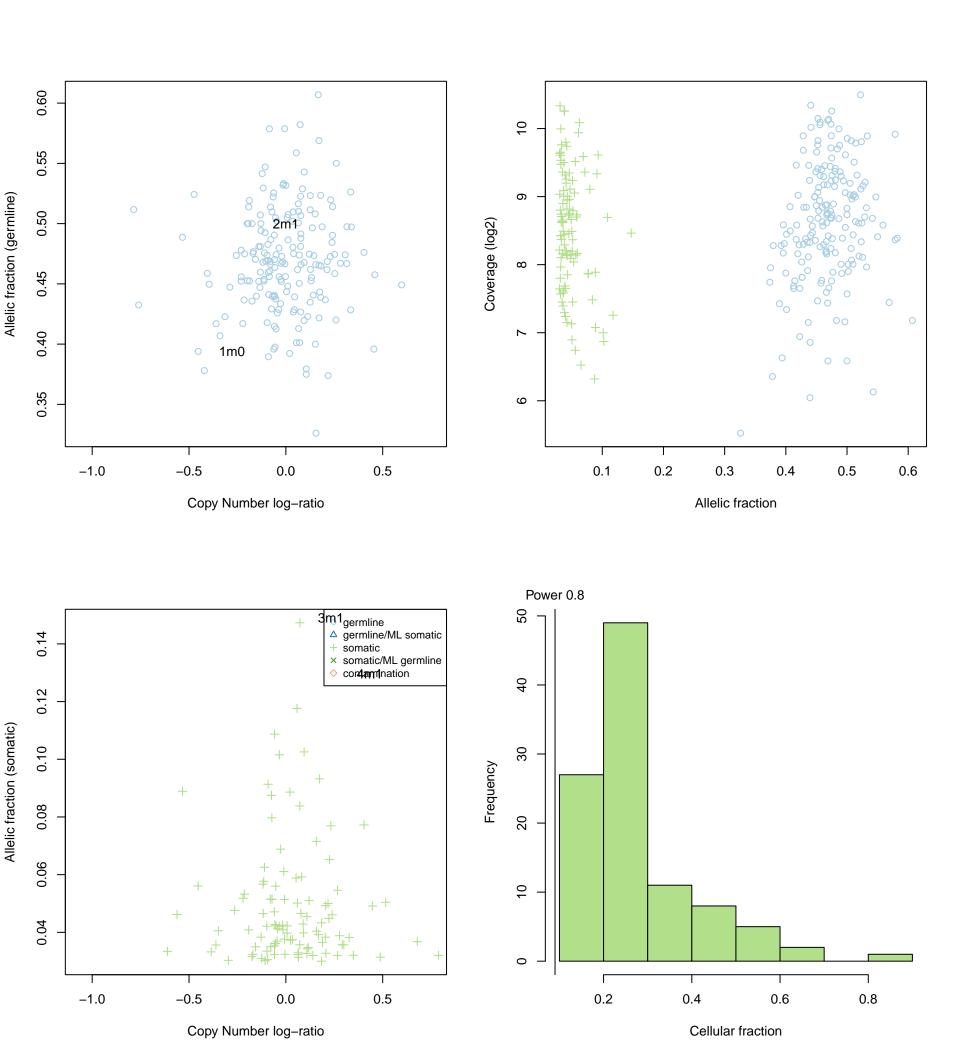
Purity: 0.35 Tumor ploidy: 2.002 0 2 3 0.5 Fraction Genome 0.3 0.2 0.1 0.0 -1.0 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



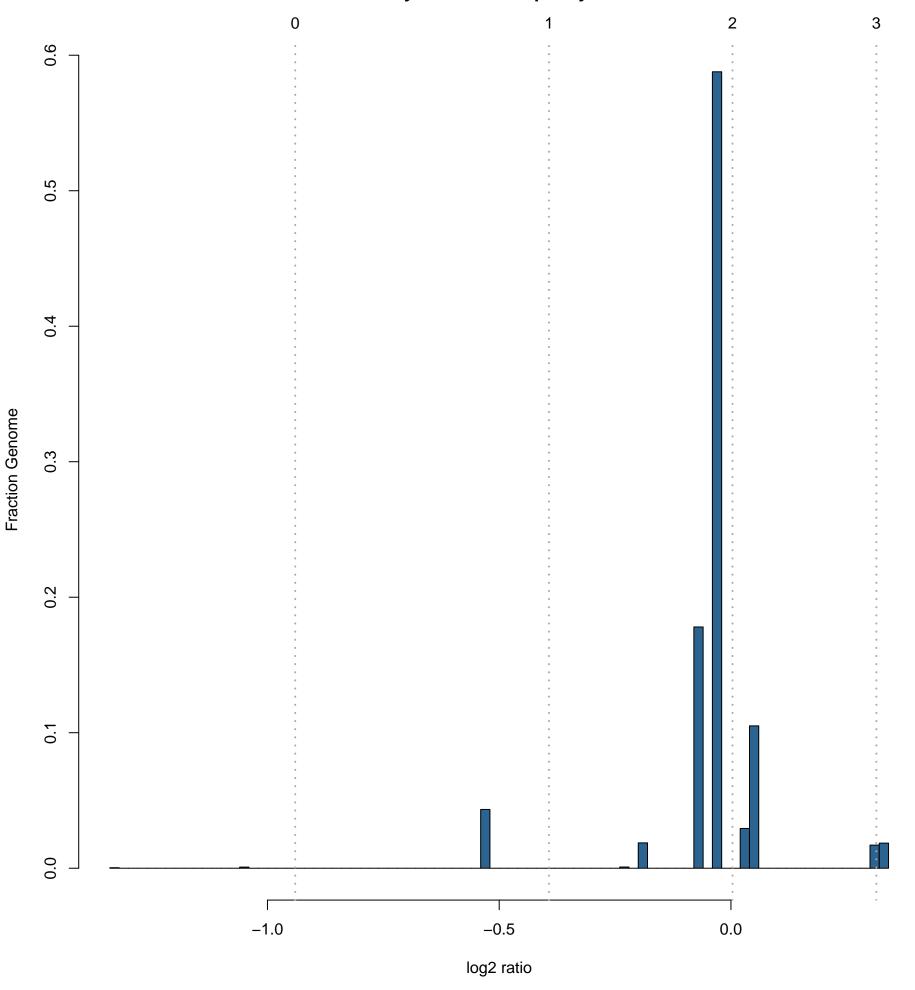
### SCNA-fit log-likelihood: -11774.32

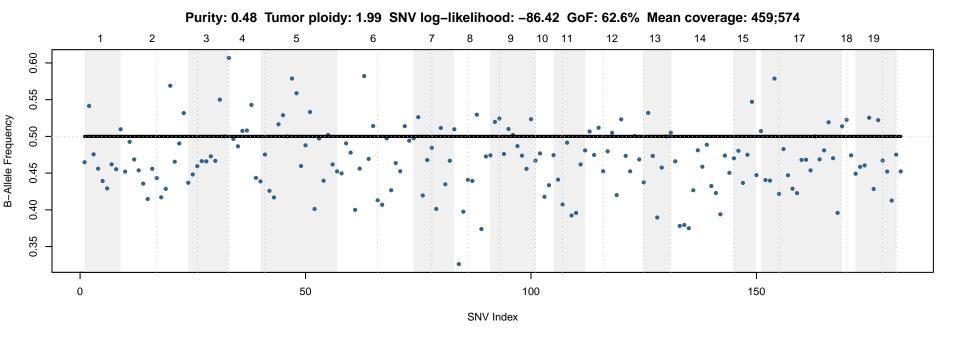




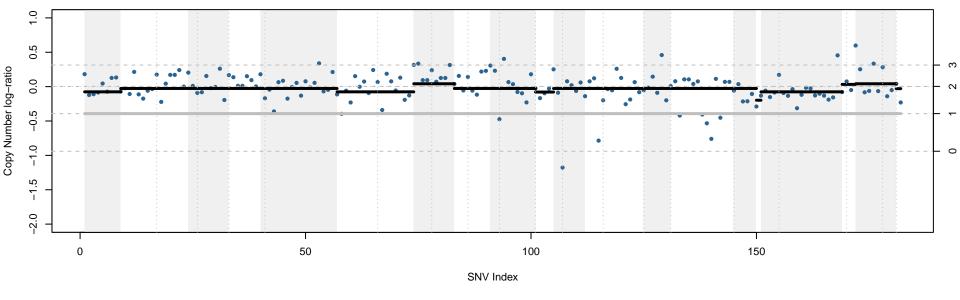


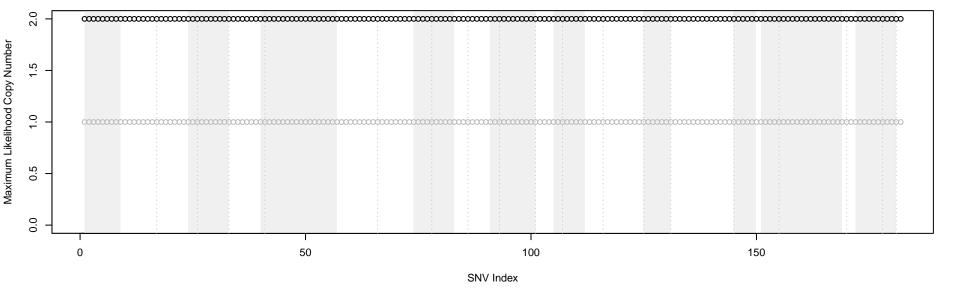
Purity: 0.48 Tumor ploidy: 1.99

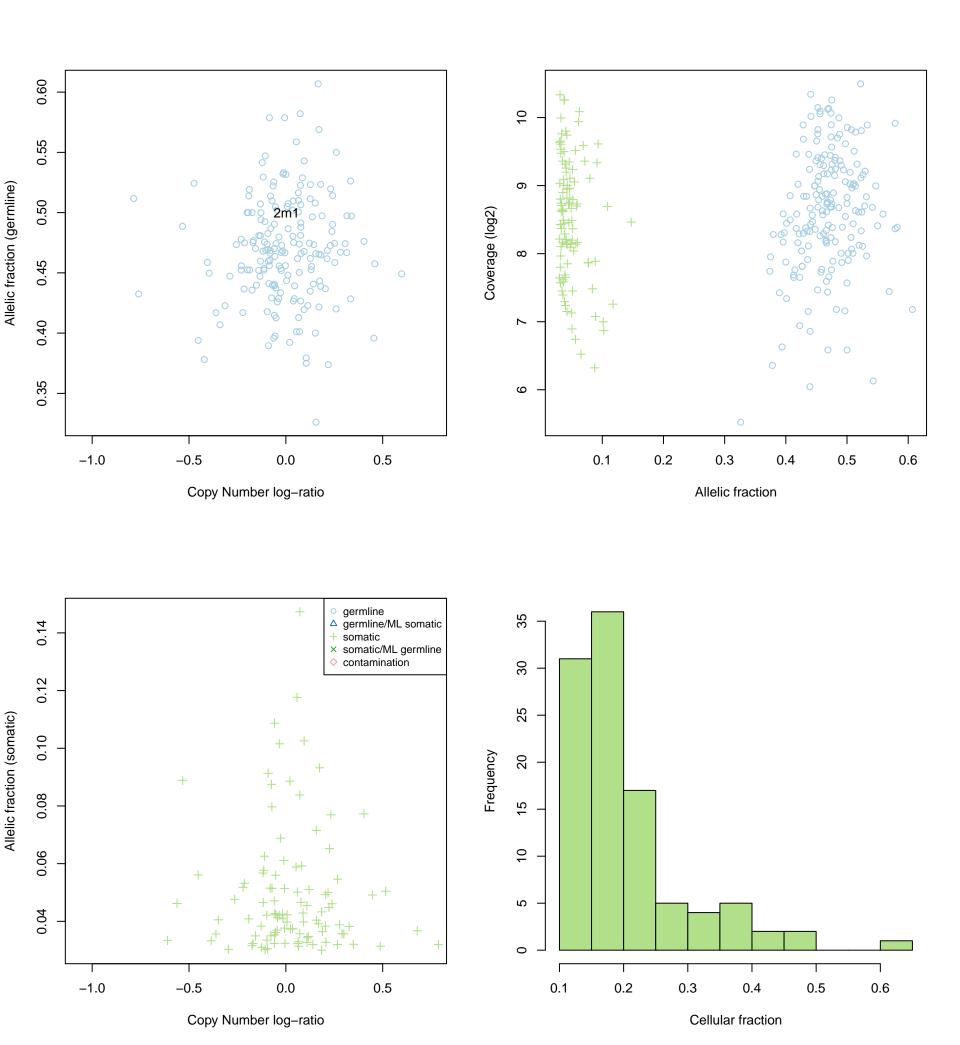




### SCNA-fit log-likelihood: -11726.33

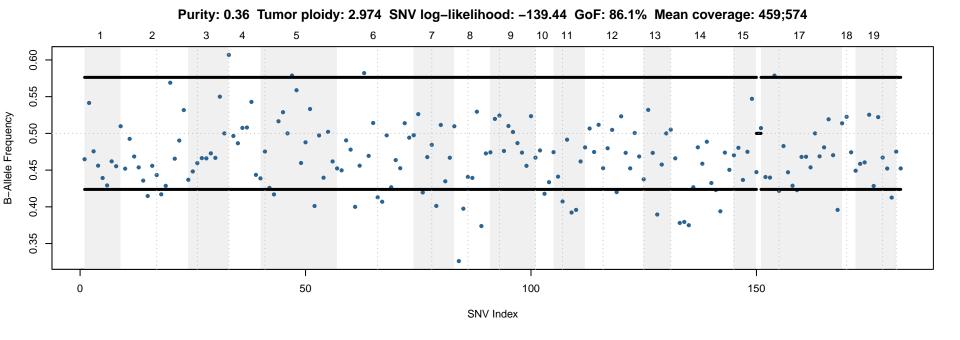




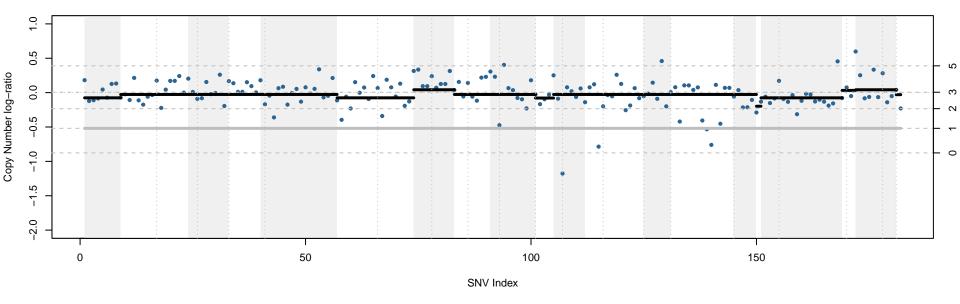


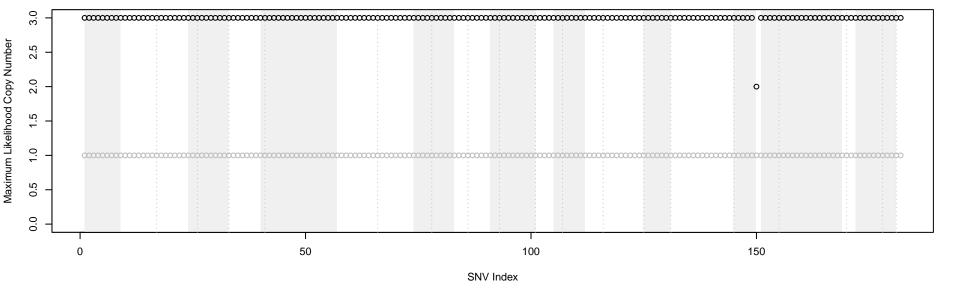
Purity: 0.36 Tumor ploidy: 2.974 3 5 0 0.5 Fraction Genome 0.3 0.2 0.1 0.0 -1.0 -0.5 0.0

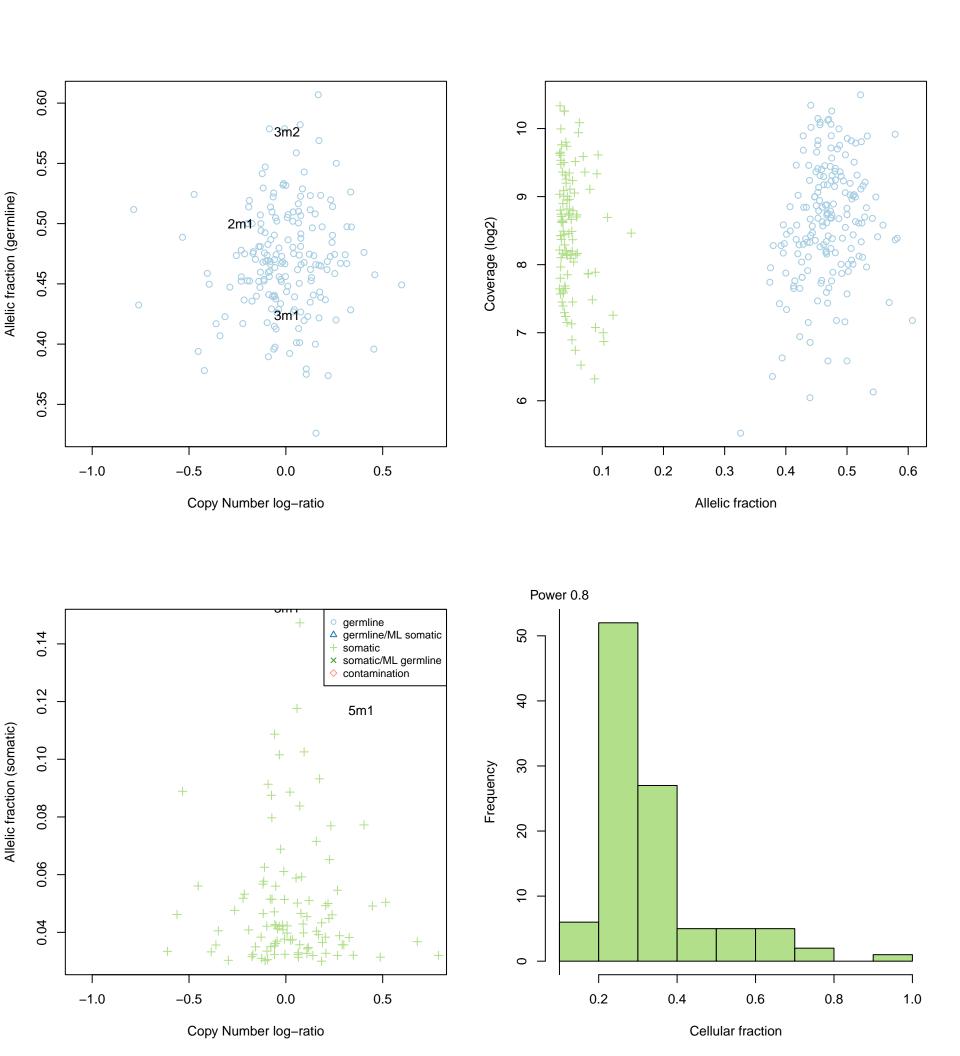
log2 ratio



# SCNA-fit log-likelihood: -11697.06

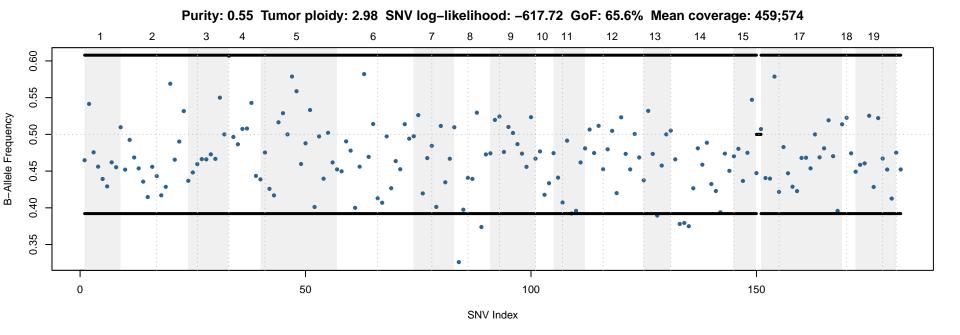




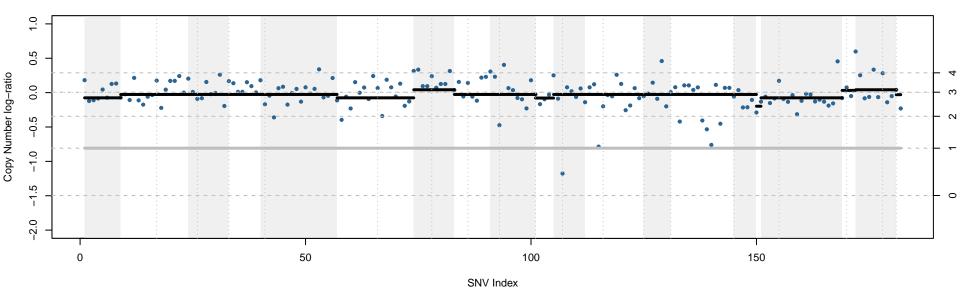


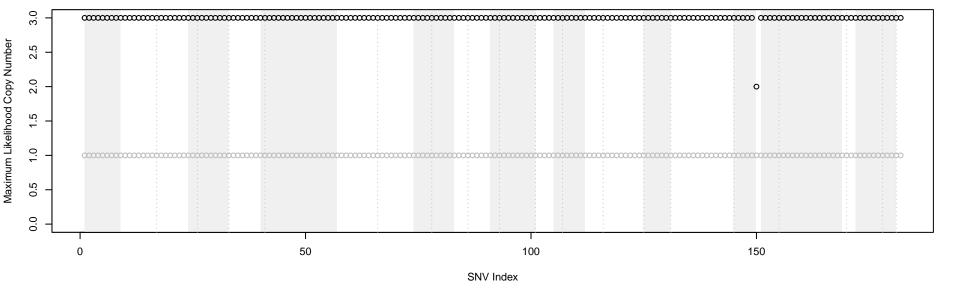
Purity: 0.55 Tumor ploidy: 2.98 2 3 0.5 Fraction Genome 0.3 0.2 0.1 0.0 -1.0 -0.5 0.0

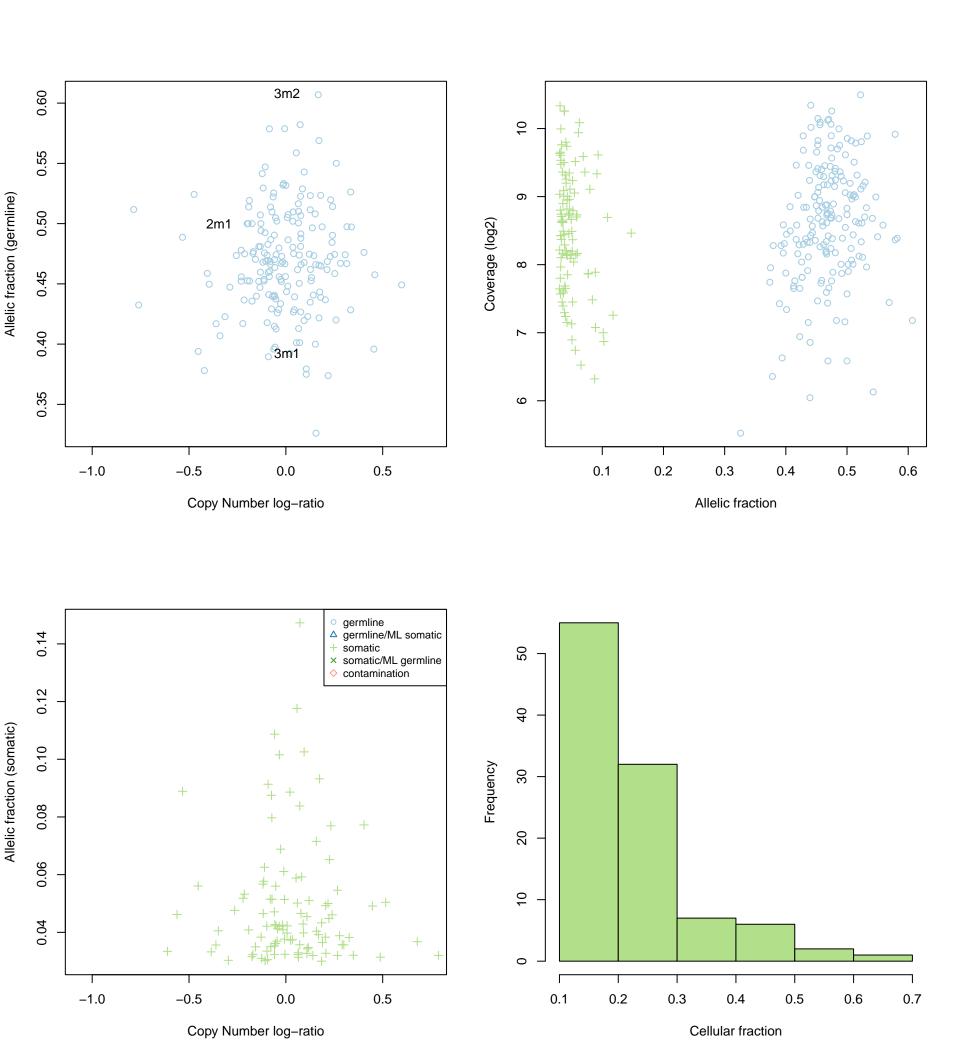
log2 ratio



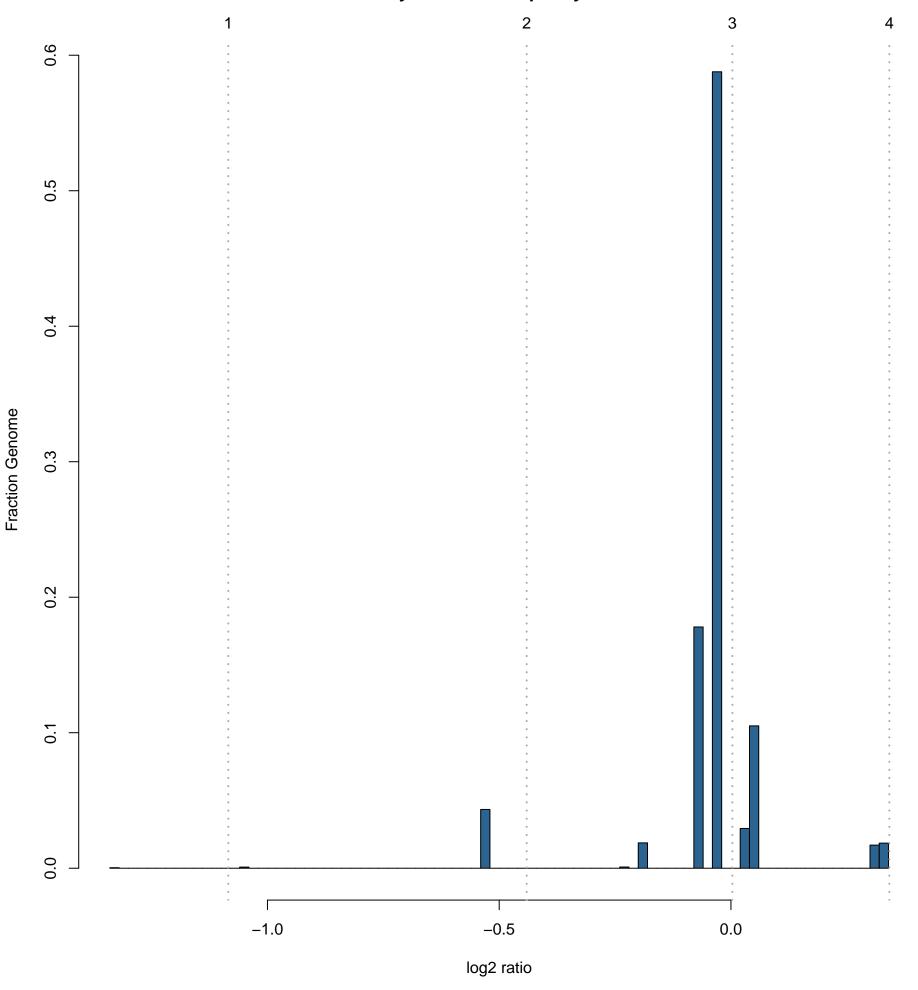
# SCNA-fit log-likelihood: -11741.07

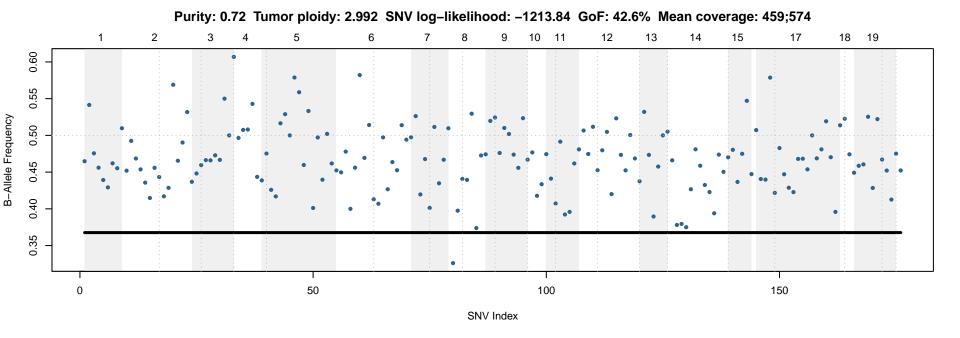






Purity: 0.72 Tumor ploidy: 2.992





# SCNA-fit log-likelihood: -11705.9

