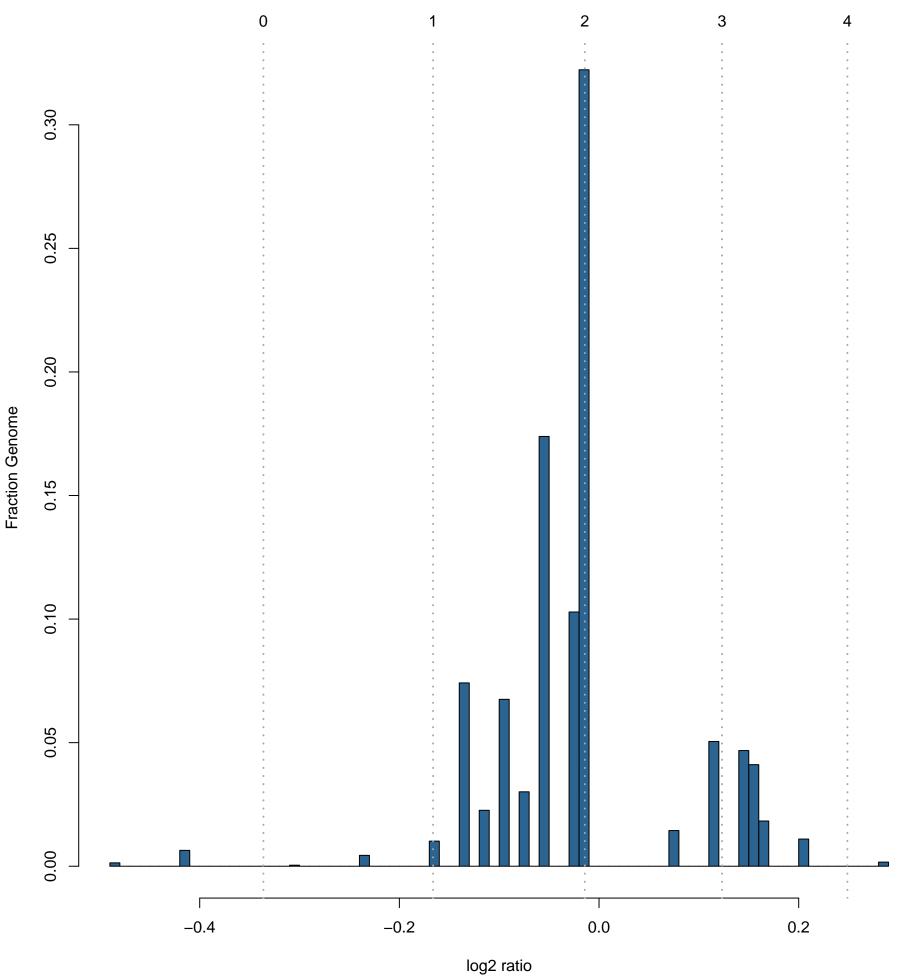
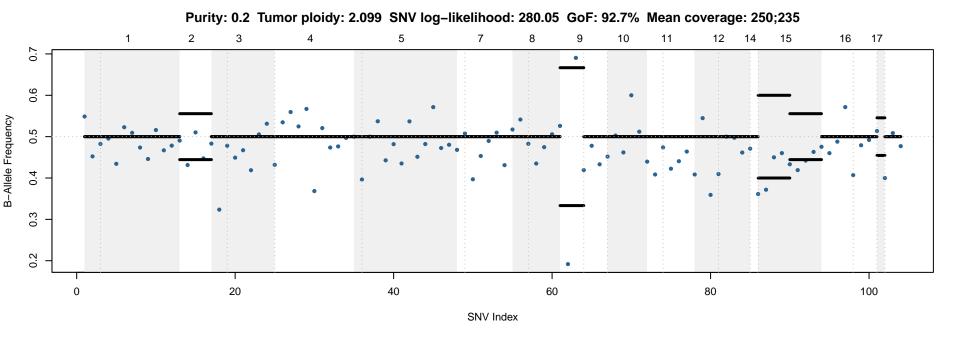
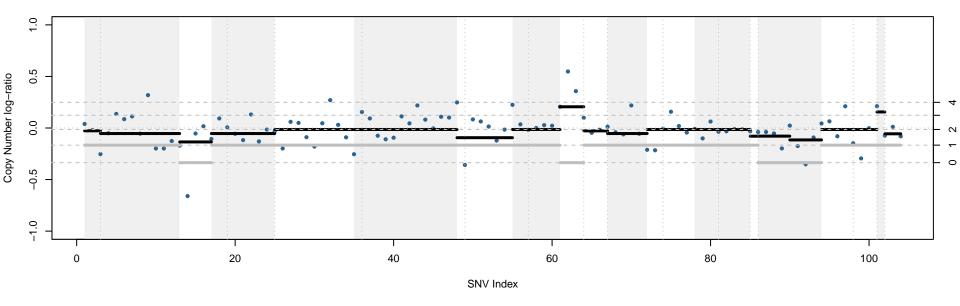
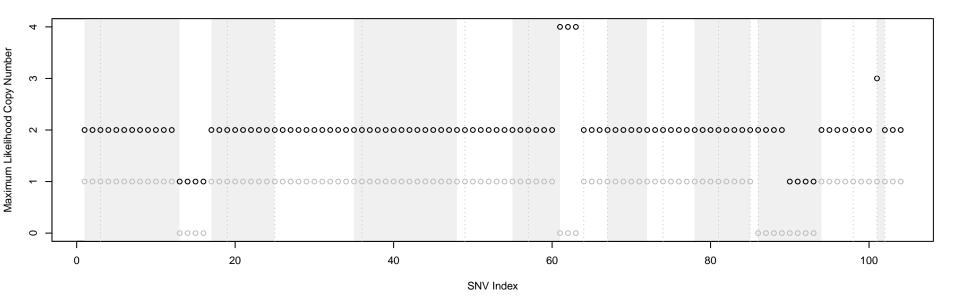
Purity: 0.2 Tumor ploidy: 2.099

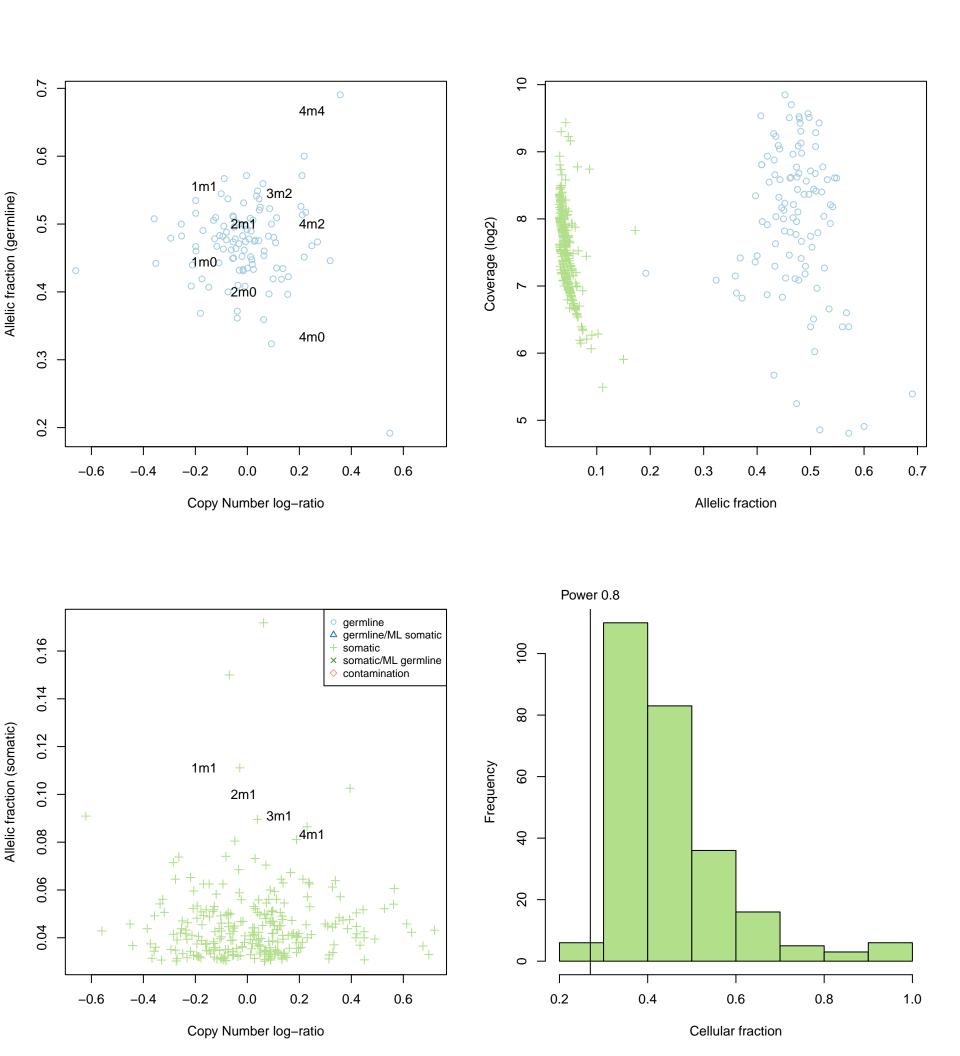




# SCNA-fit log-likelihood: -5443.29

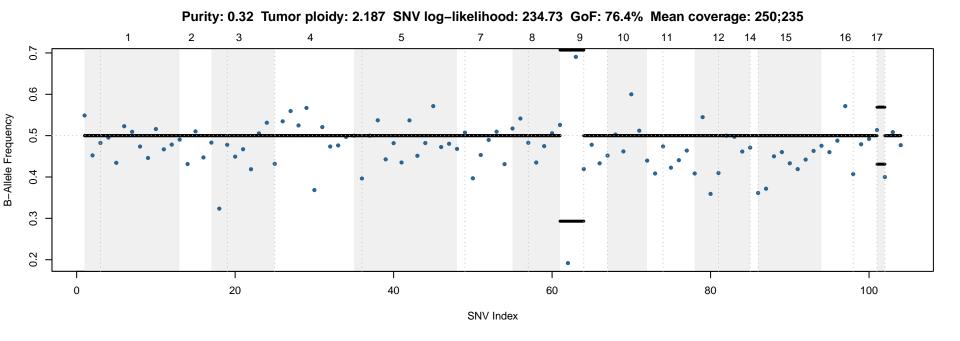




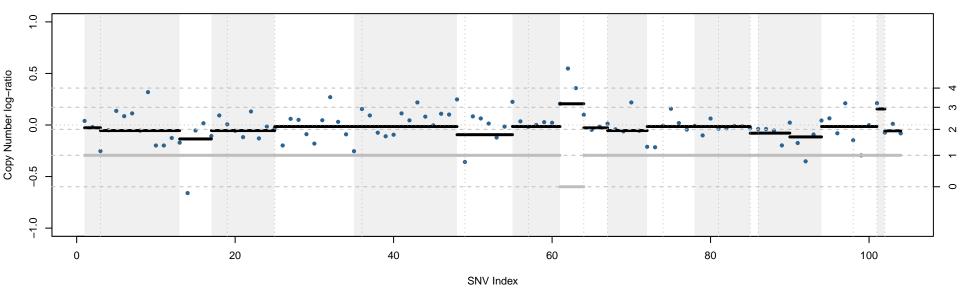


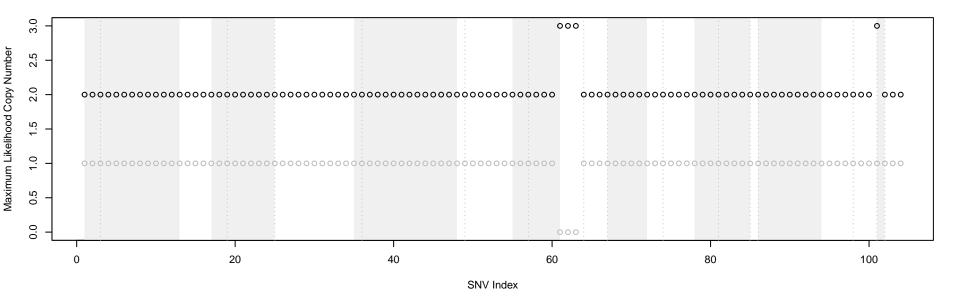
Purity: 0.32 Tumor ploidy: 2.187 2 0 3 0.30 0.25 0.20 Fraction Genome 0.15 0.05 0.00 -0.8 -0.6 -0.4 -0.2 0.0 0.2

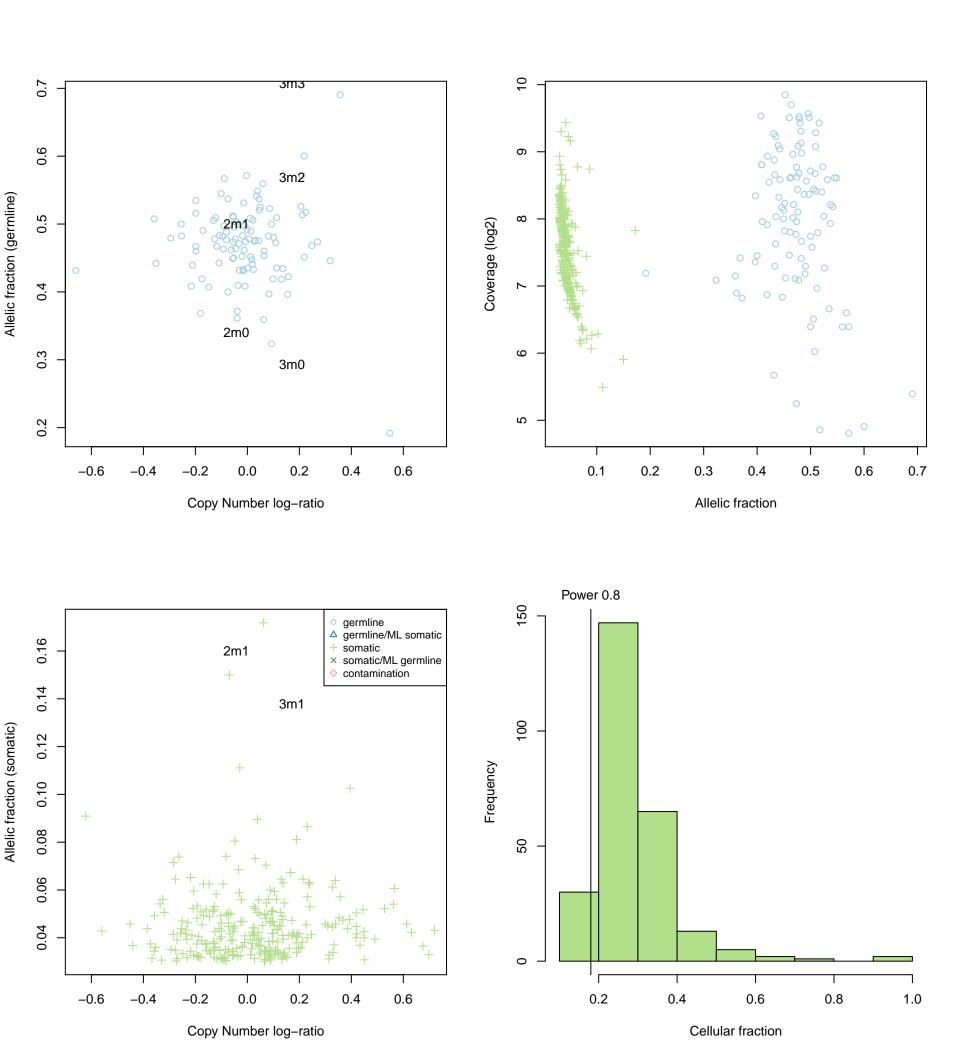
log2 ratio



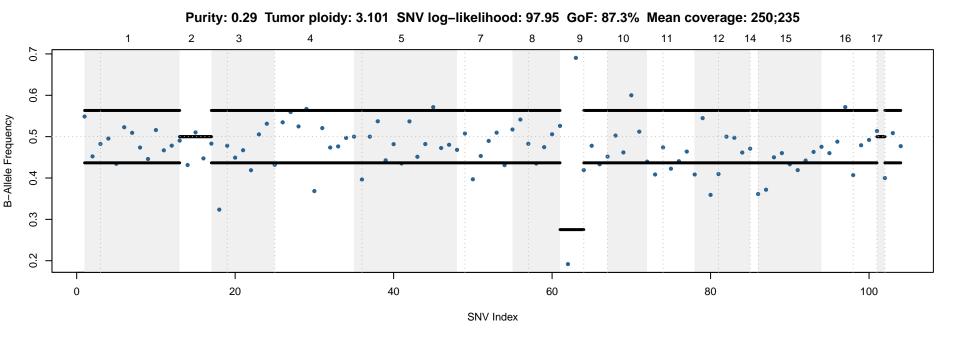
# SCNA-fit log-likelihood: -5457.56



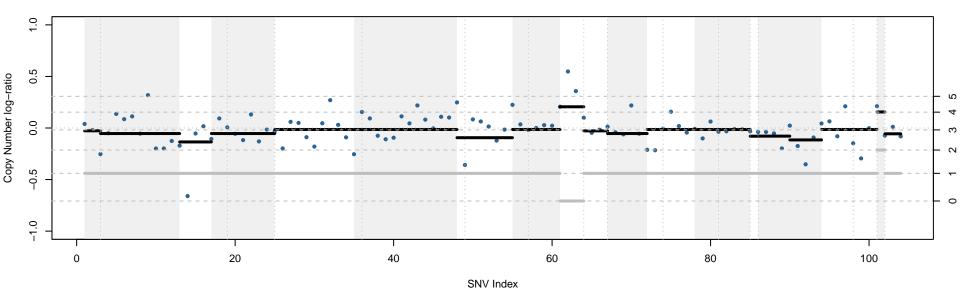


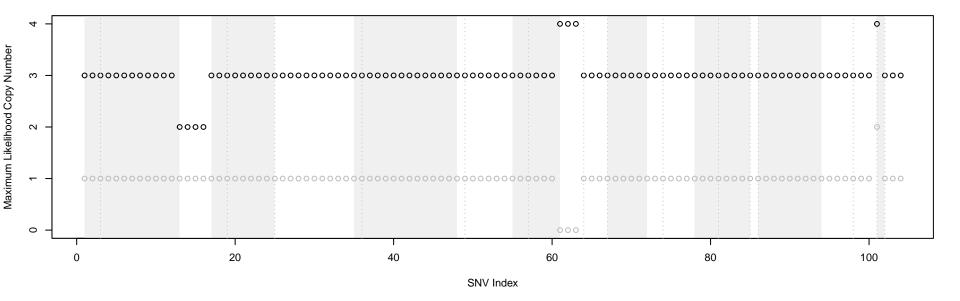


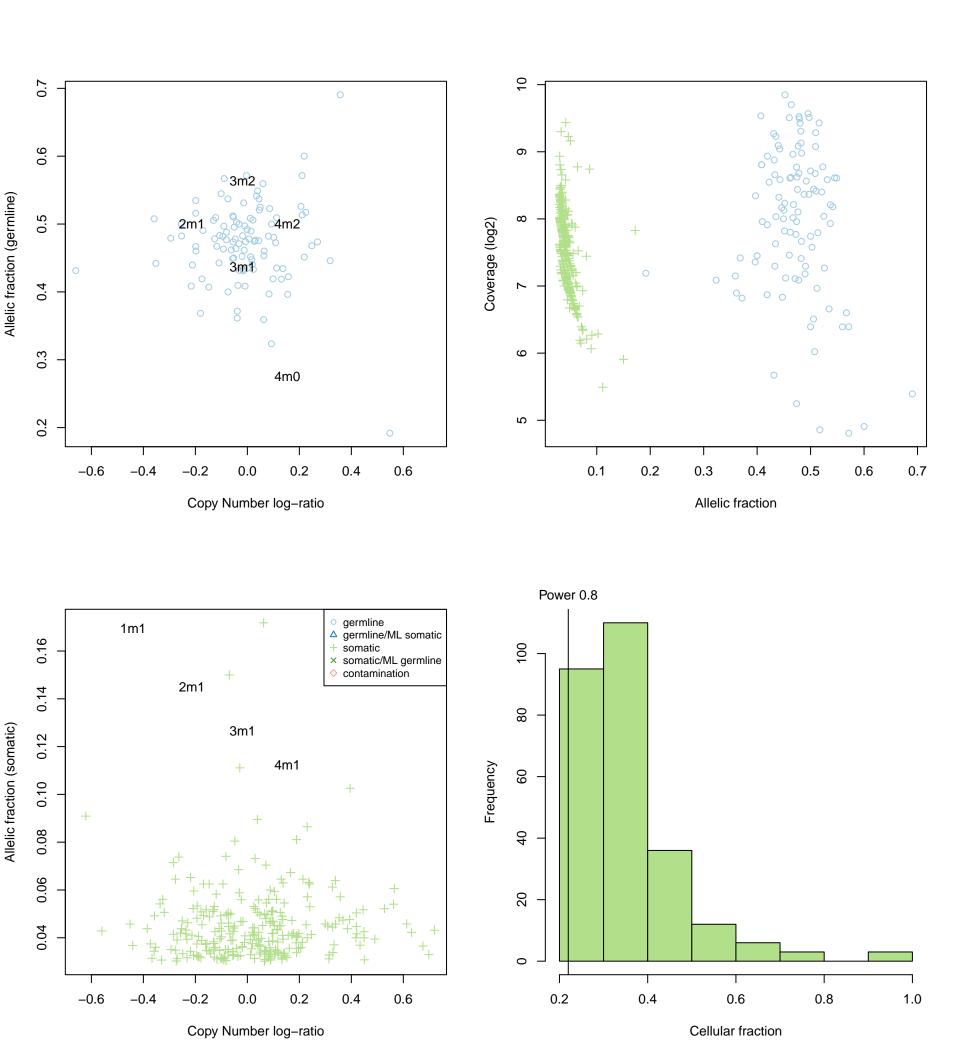
Purity: 0.29 Tumor ploidy: 3.101 3 5 0 2 0.30 0.25 Fraction Genome 0.15 0.05 0.00 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



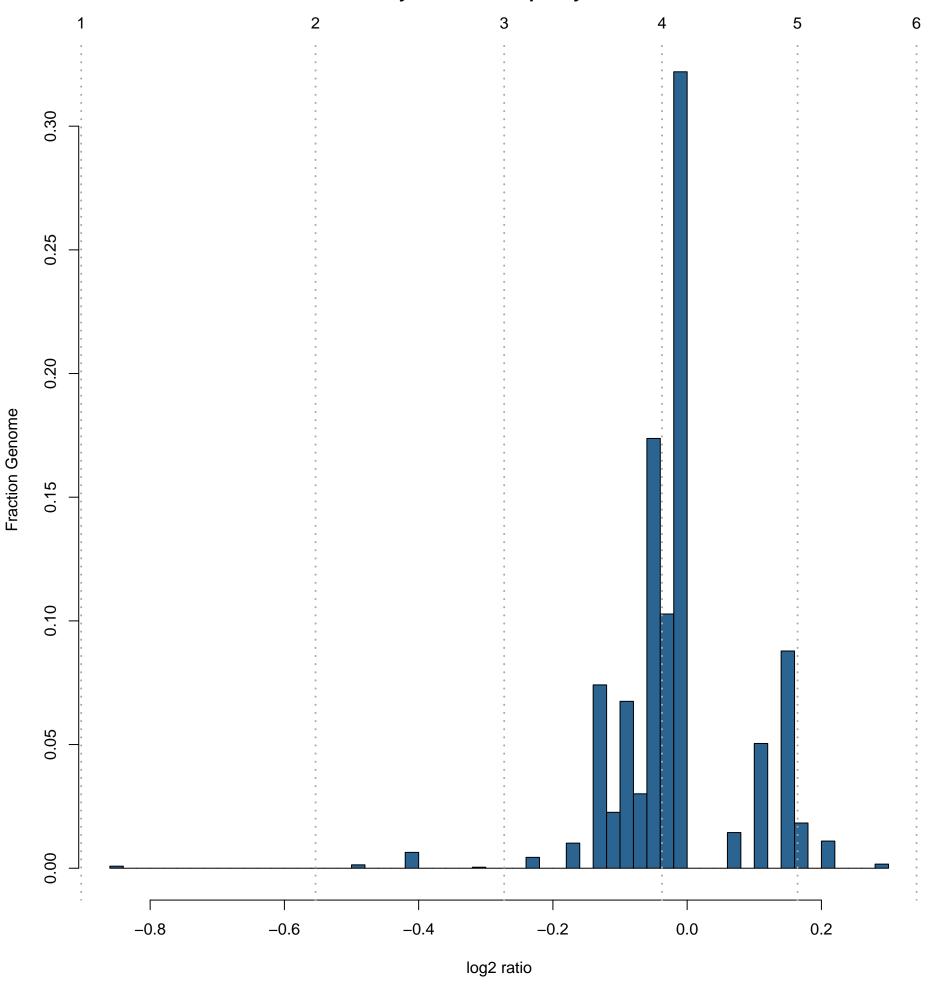
# SCNA-fit log-likelihood: -5435.16

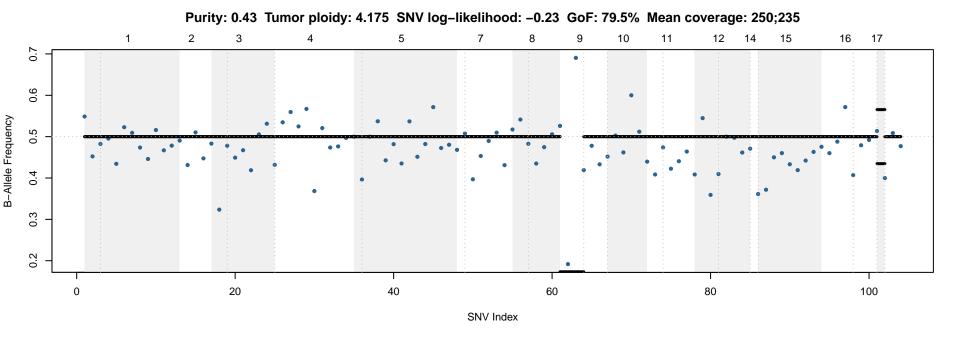




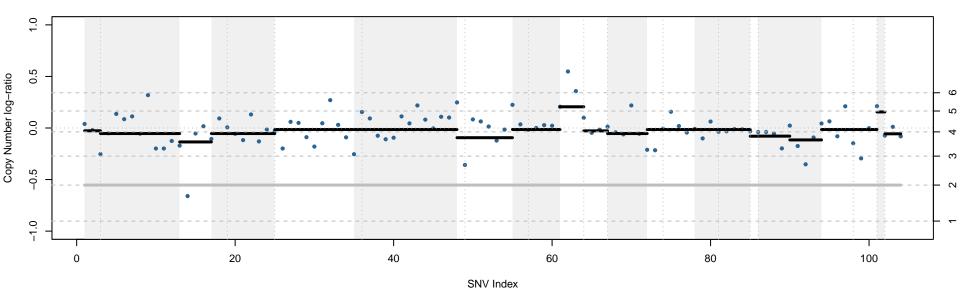


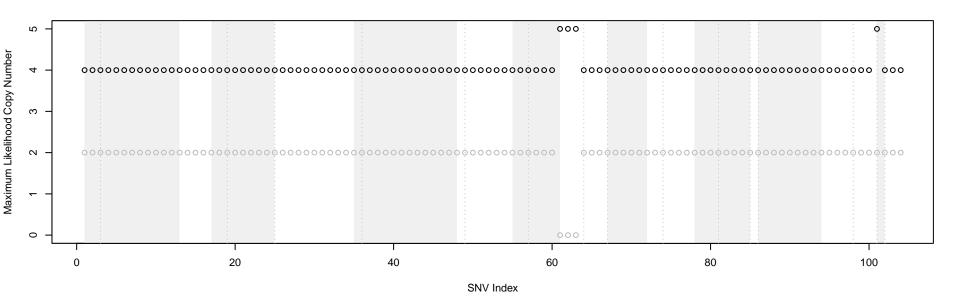
Purity: 0.43 Tumor ploidy: 4.175

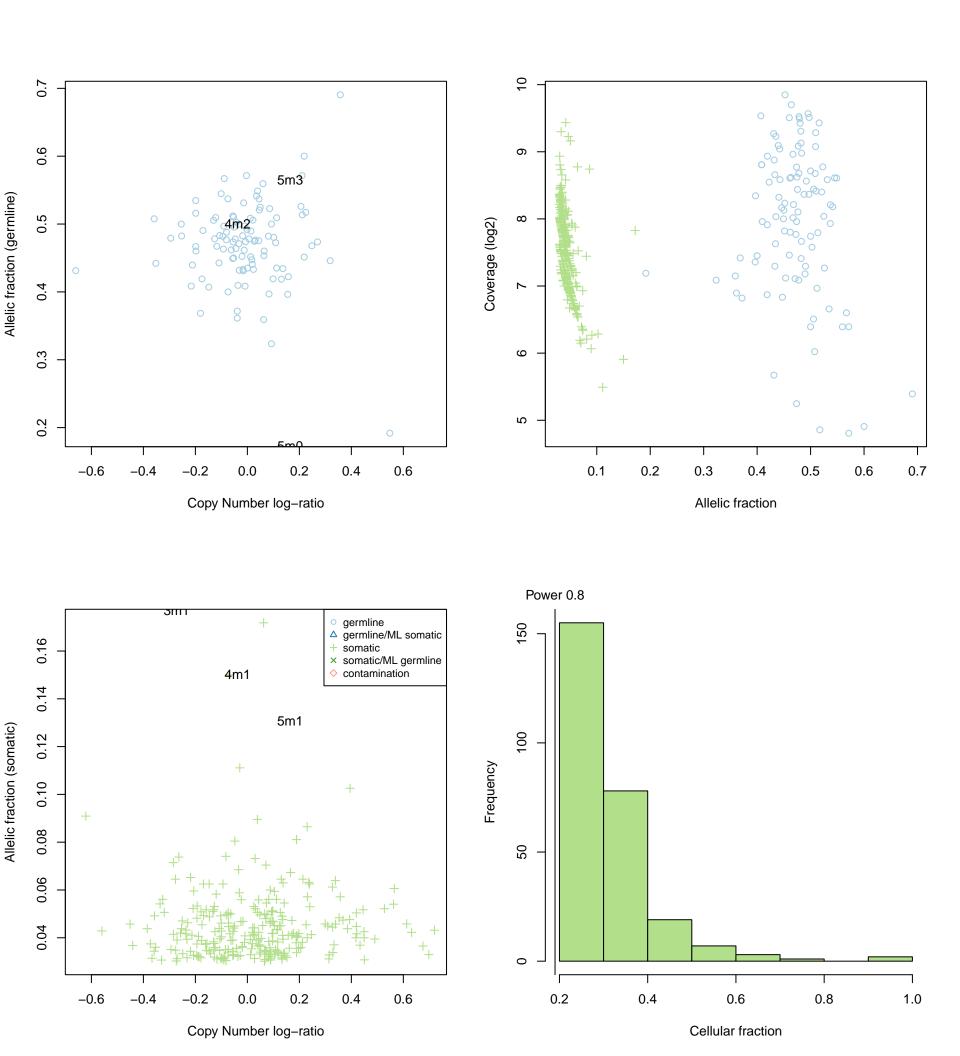


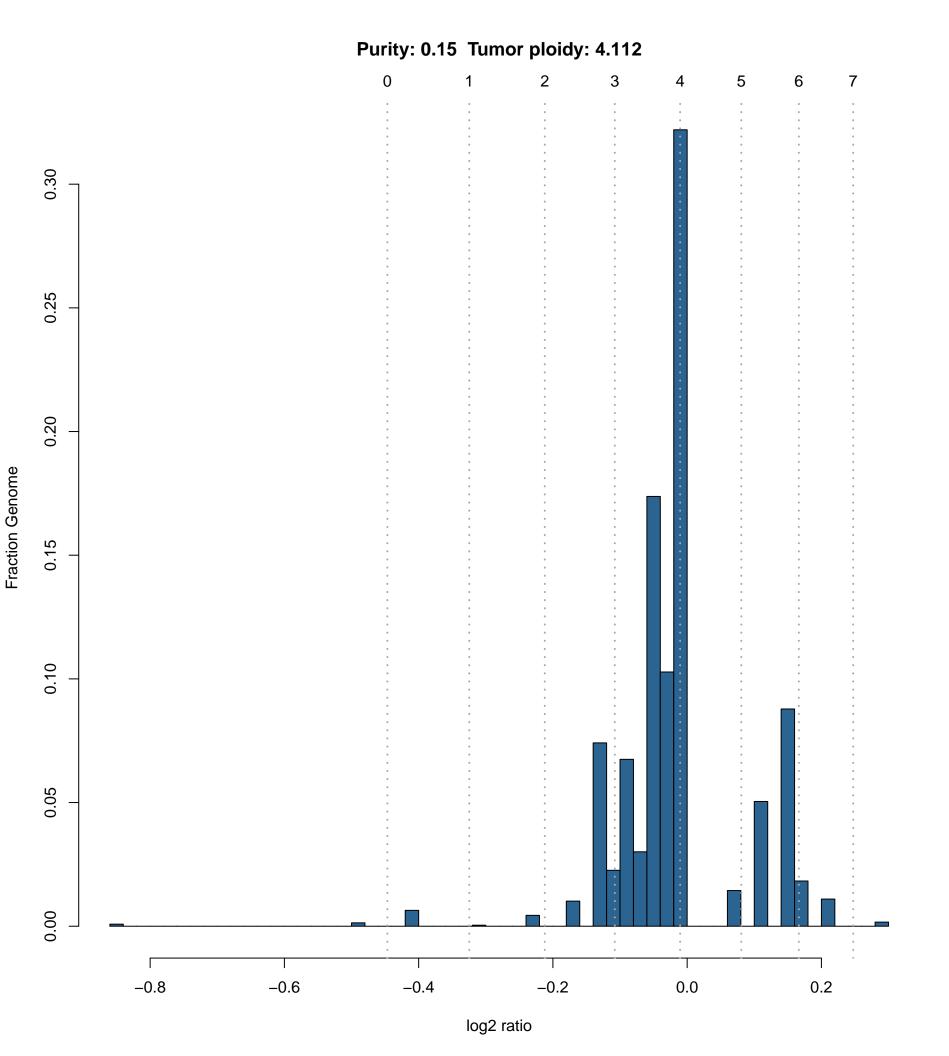


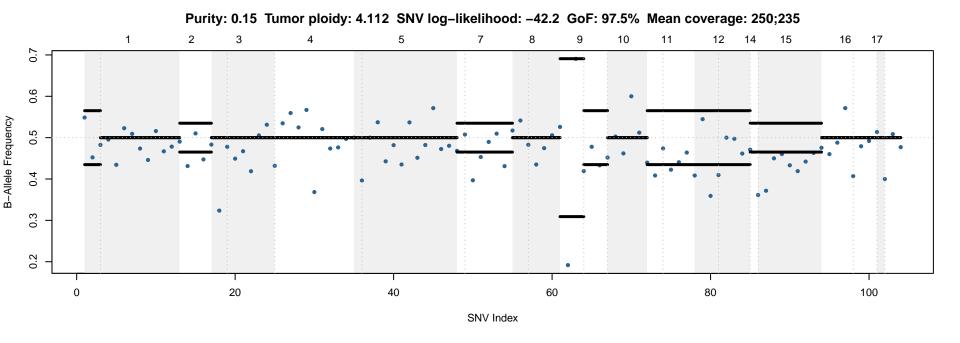
# SCNA-fit log-likelihood: -5448



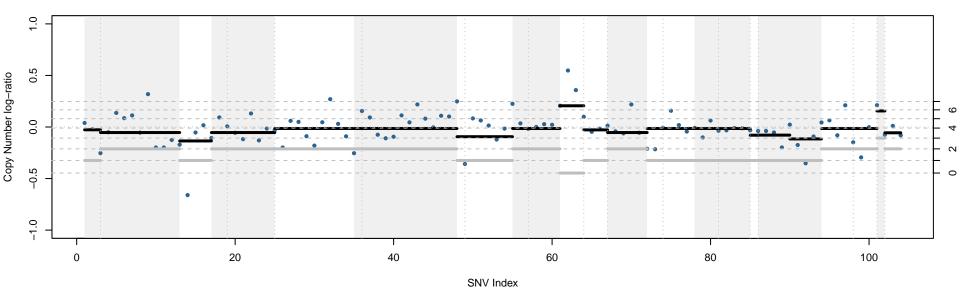


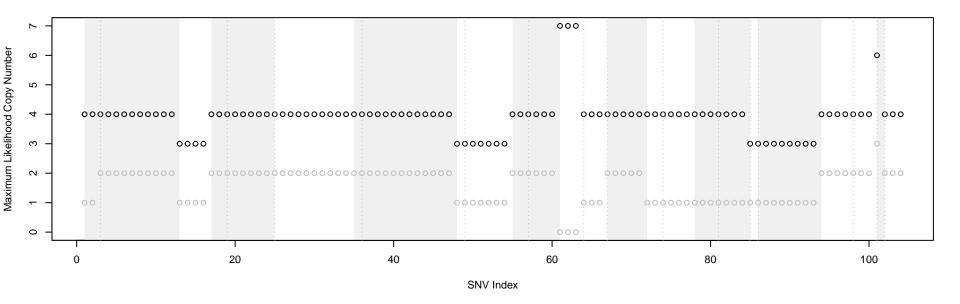


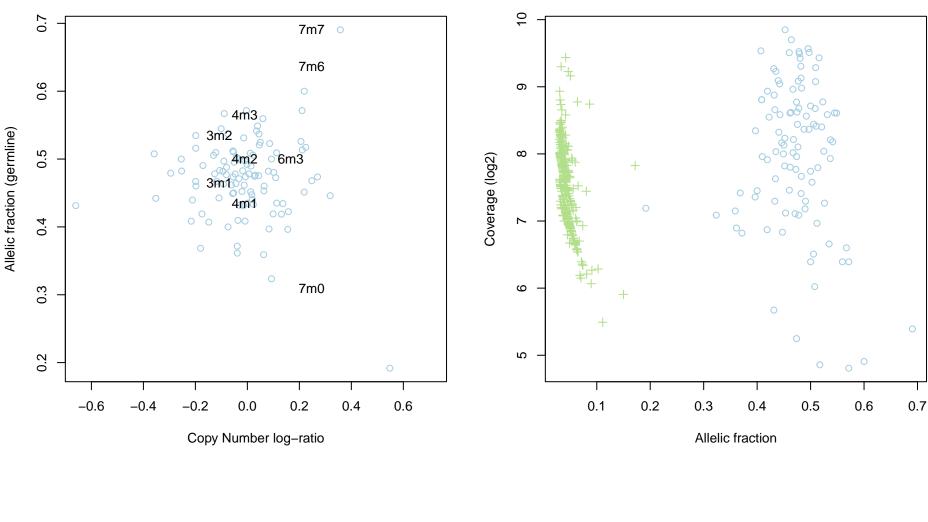


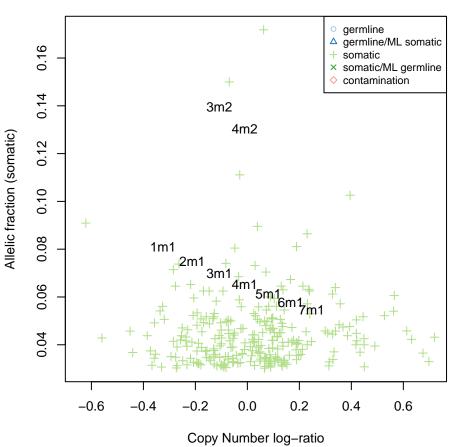


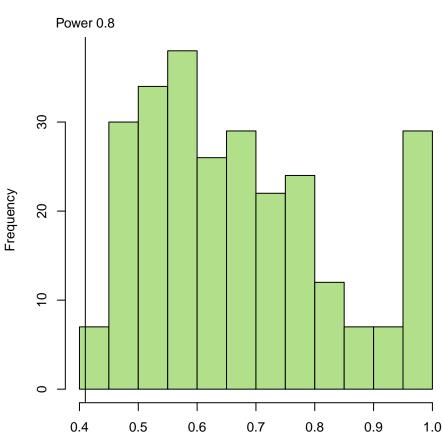
# SCNA-fit log-likelihood: -5366.71





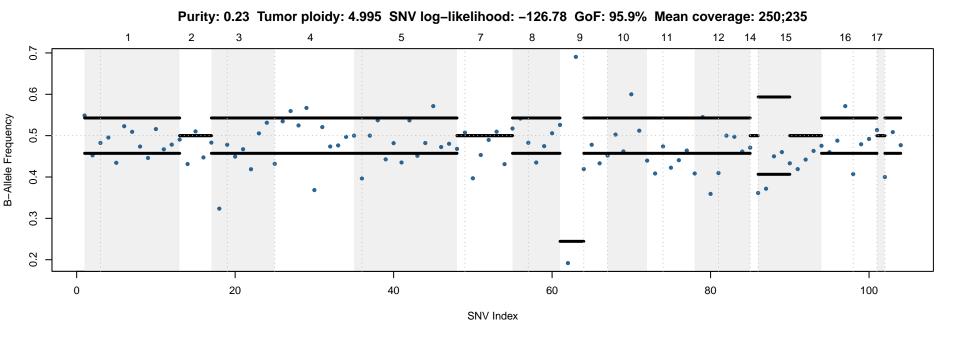




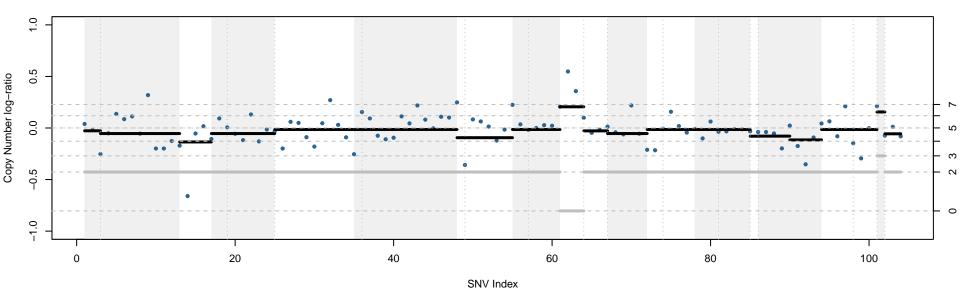


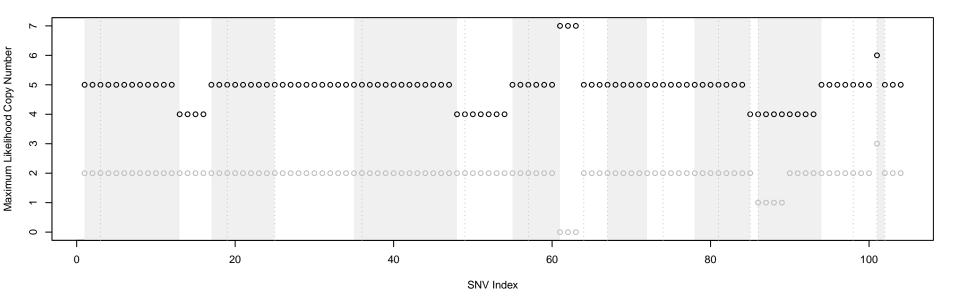
Cellular fraction

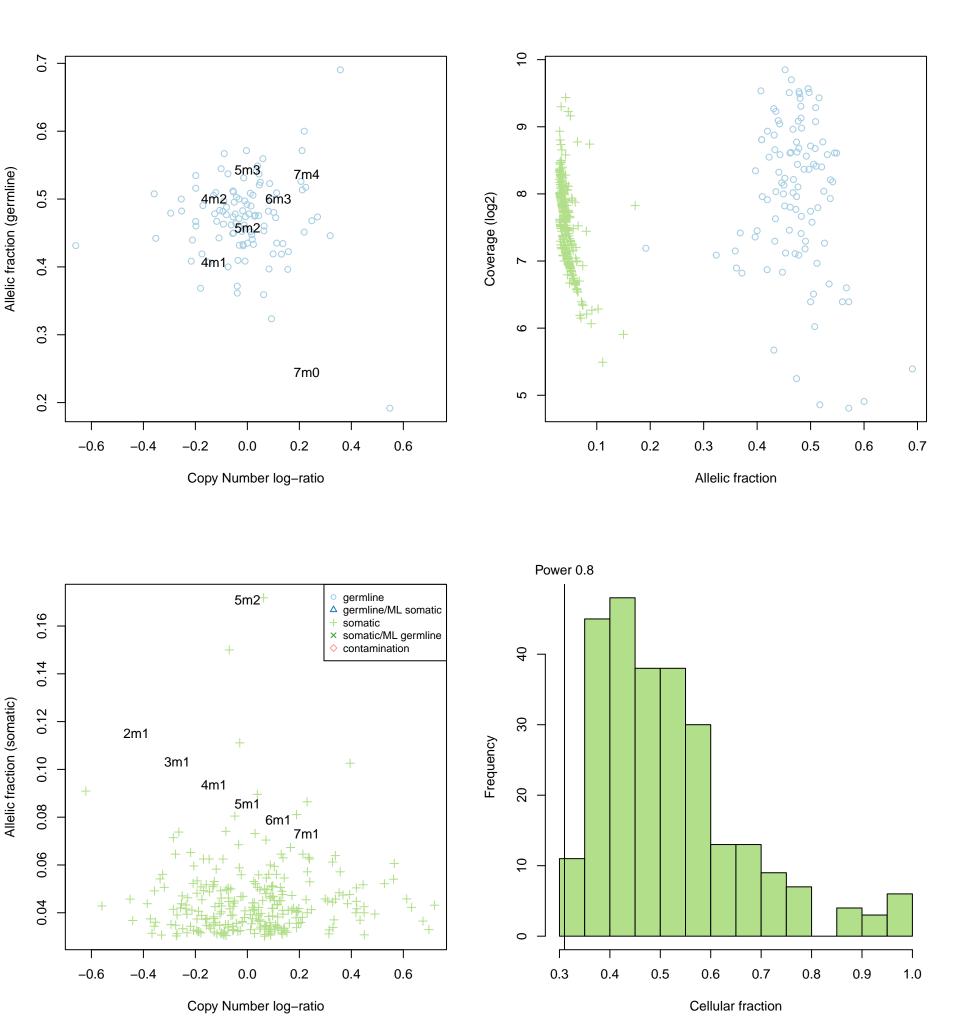
Purity: 0.23 Tumor ploidy: 4.995 3 0 2 5 7 6 0.30 0.25 0.20 Fraction Genome 0.15 0.05 0.00 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



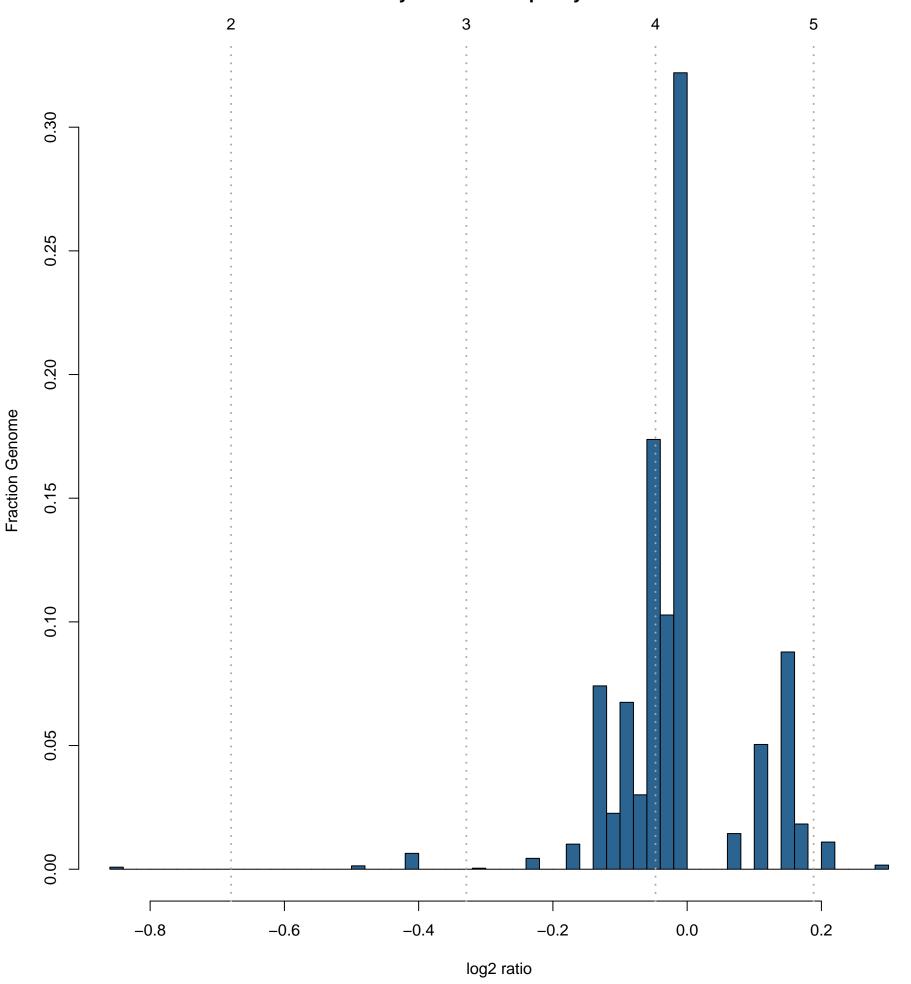
# SCNA-fit log-likelihood: -5384.32

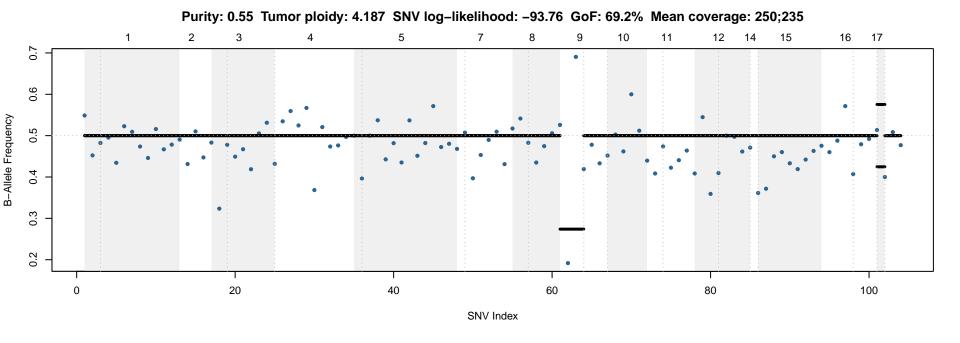




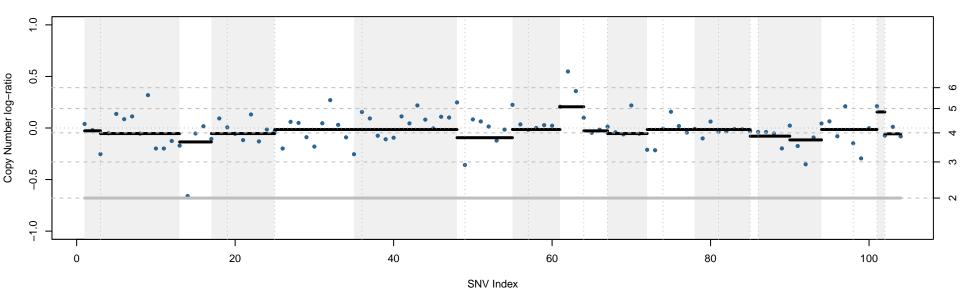


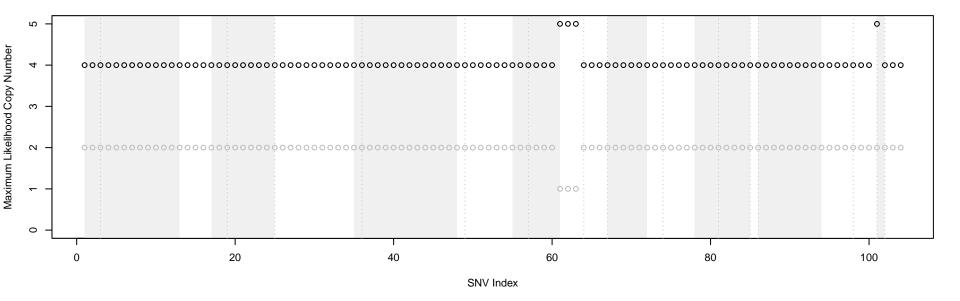
Purity: 0.55 Tumor ploidy: 4.187

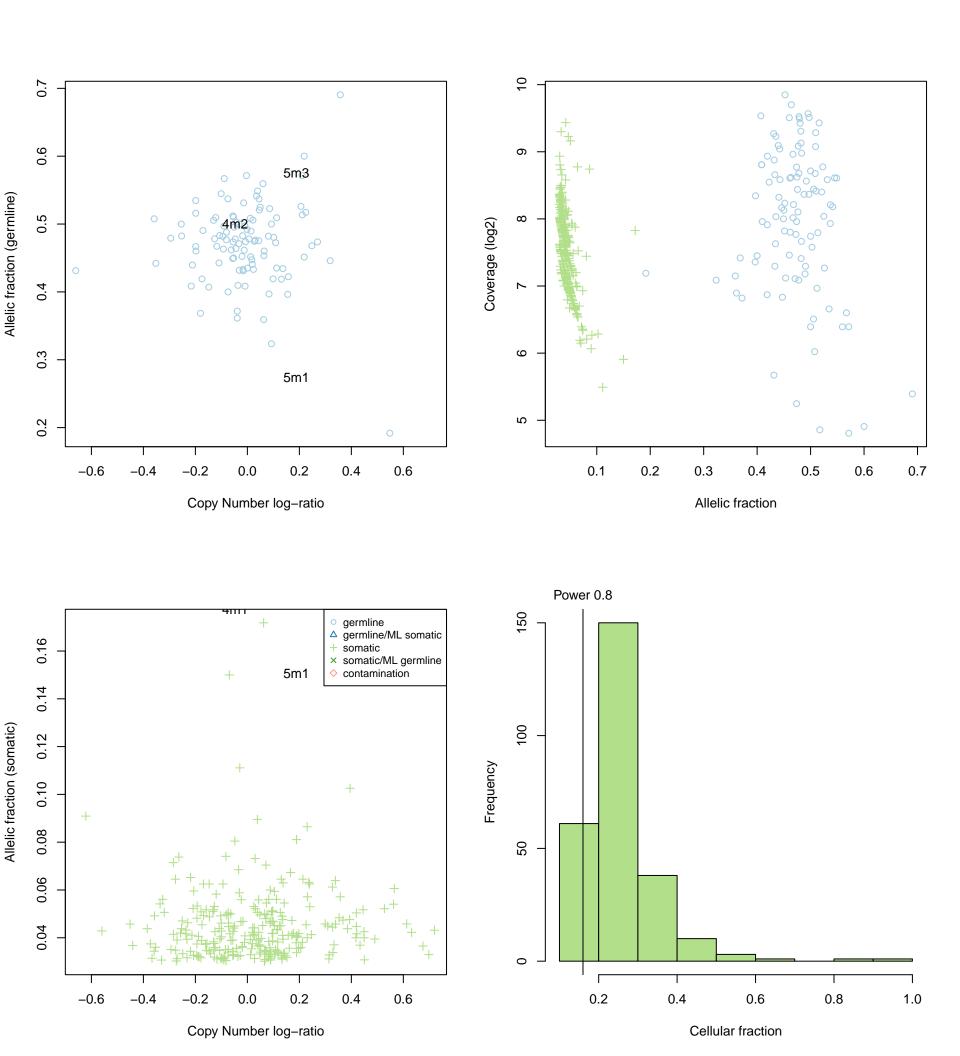




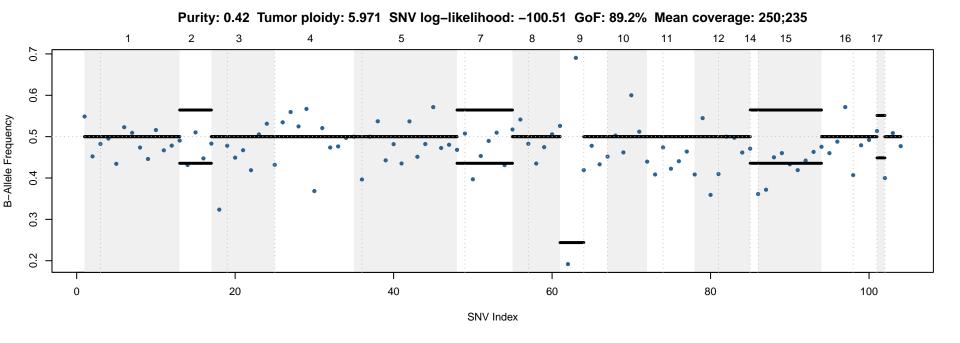
# SCNA-fit log-likelihood: -5472.42



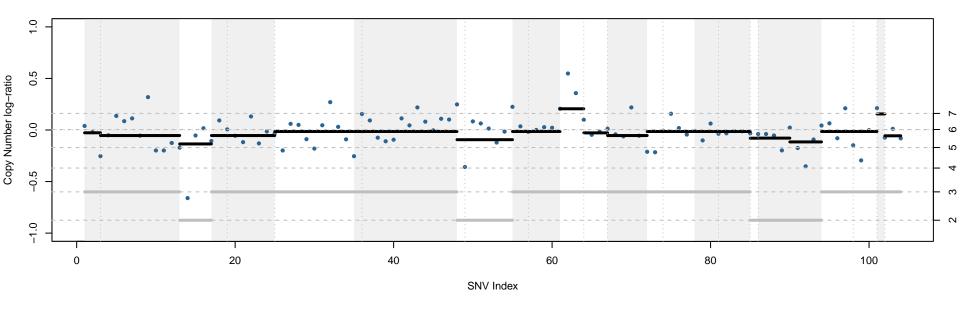


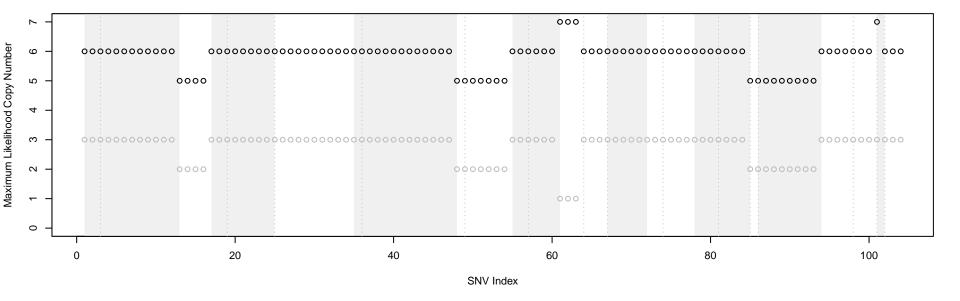


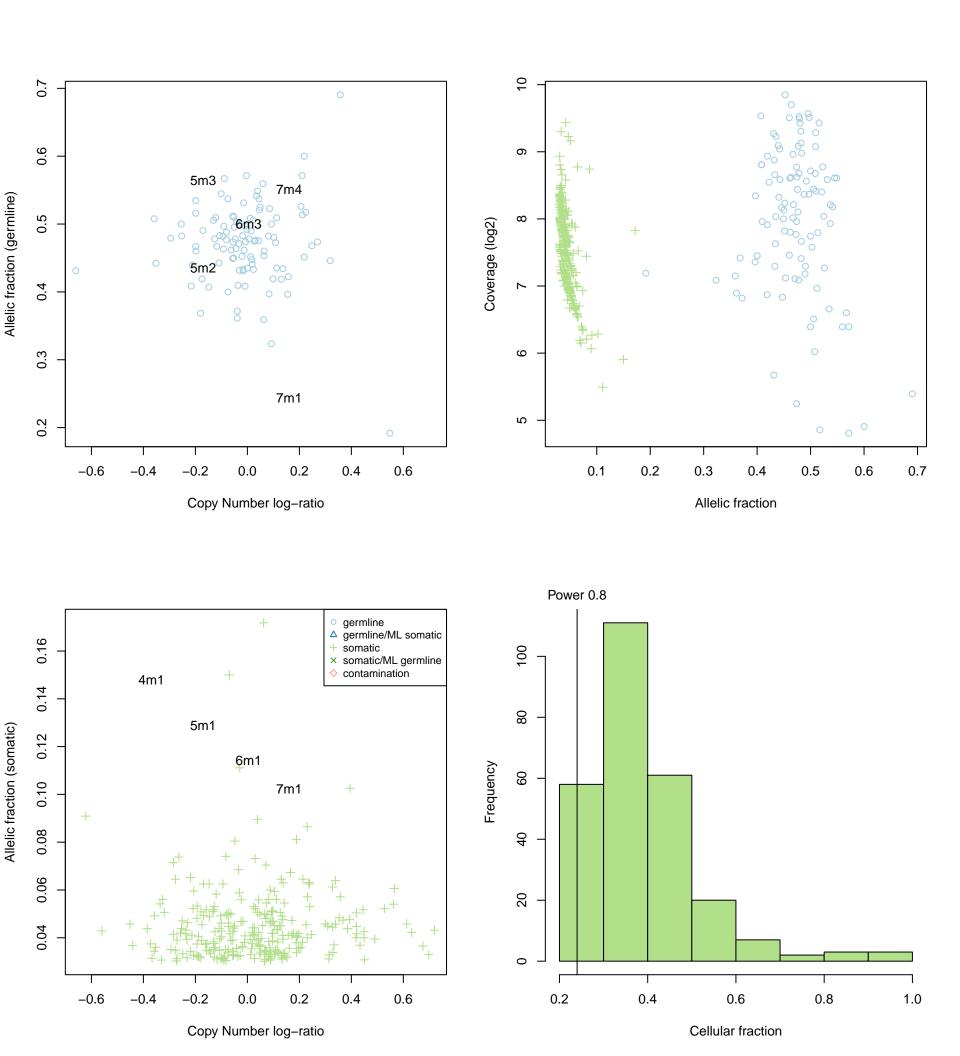
Purity: 0.42 Tumor ploidy: 5.971 2 5 3 6 0.30 0.25 0.20 Fraction Genome 0.15 0.05 0.00 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



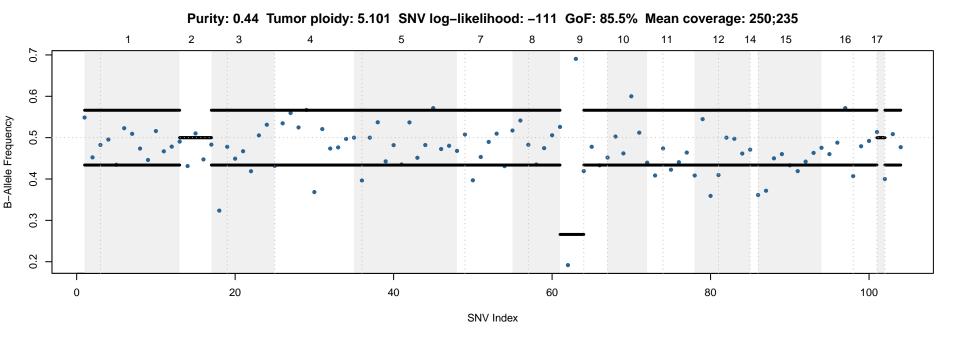
# SCNA-fit log-likelihood: -5474.31



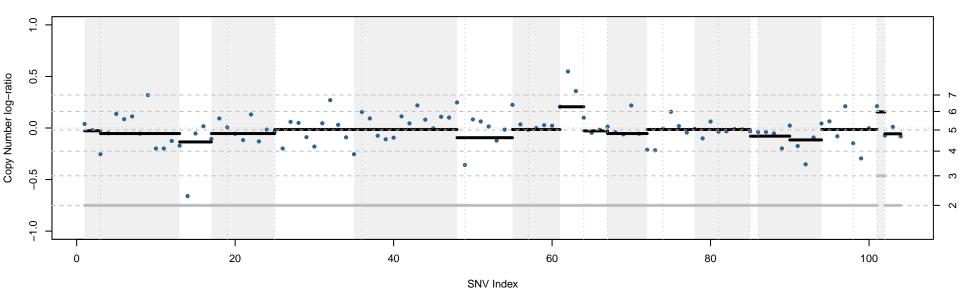


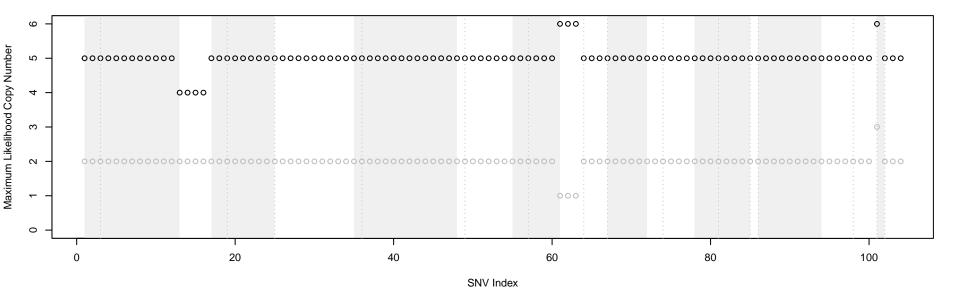


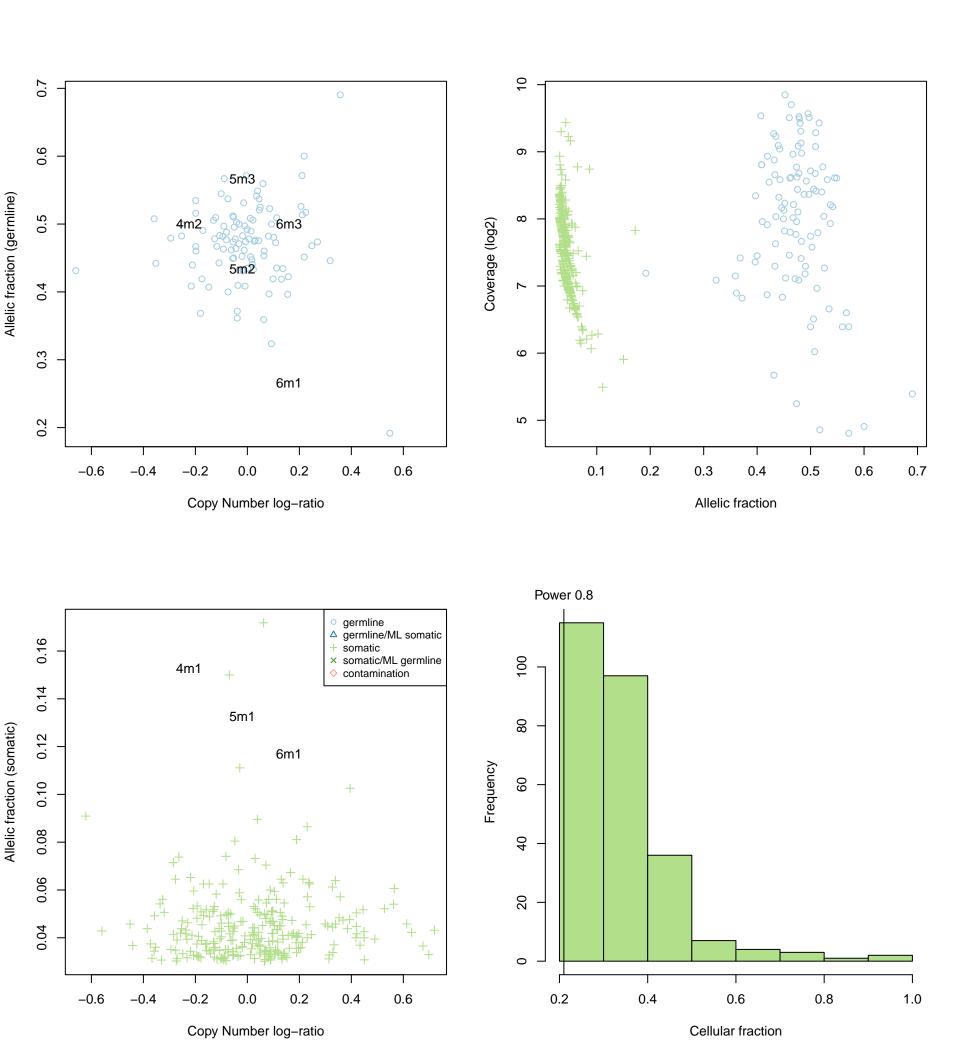
Purity: 0.44 Tumor ploidy: 5.101 2 5 6 7 3 0.30 0.25 Fraction Genome 0.15 0.05 0.00 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio

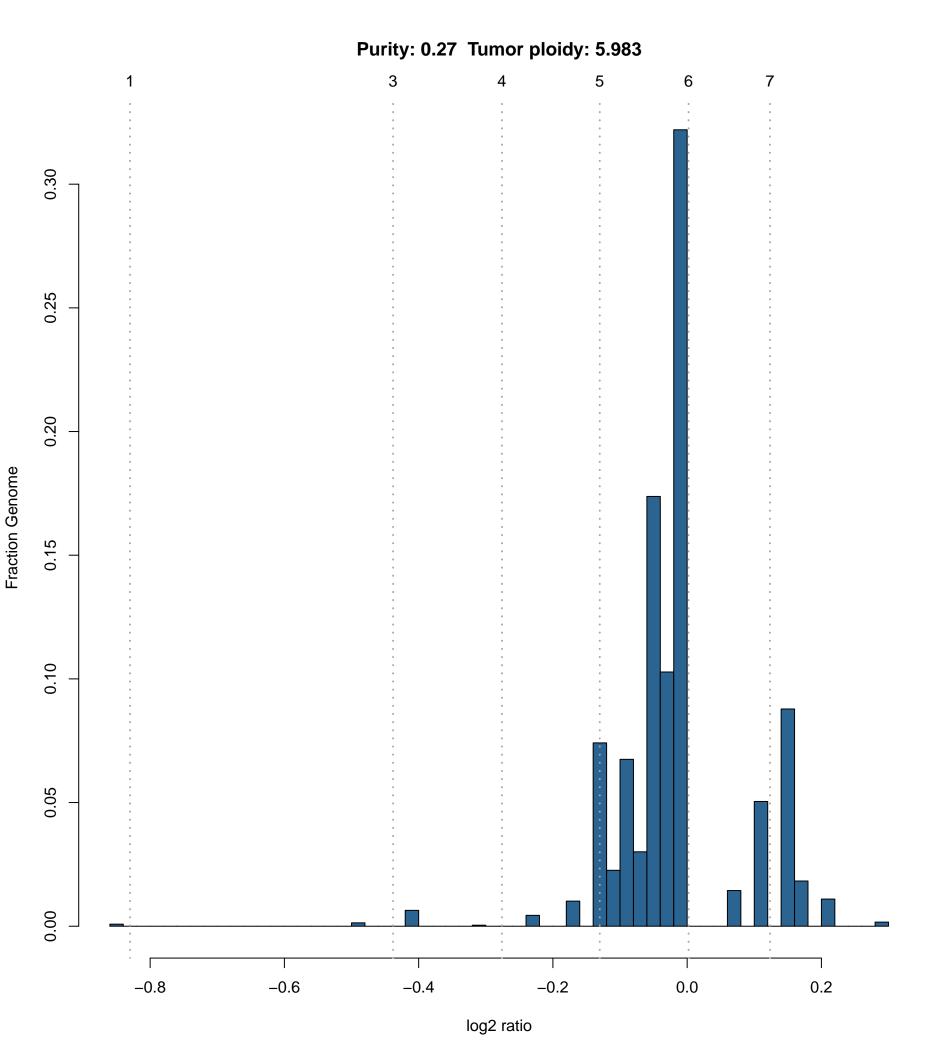


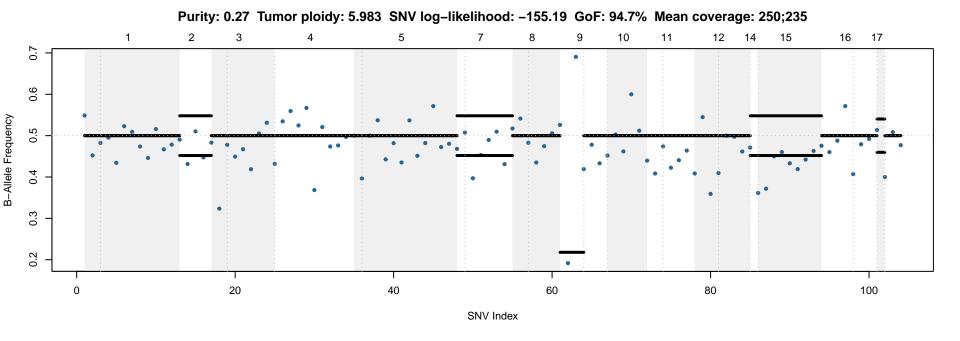
# SCNA-fit log-likelihood: -5447.16



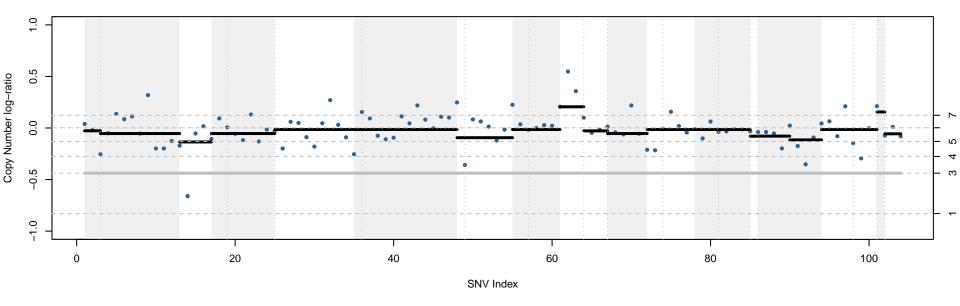


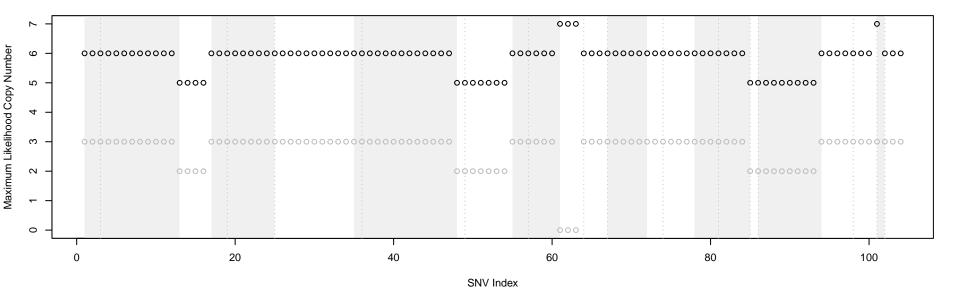


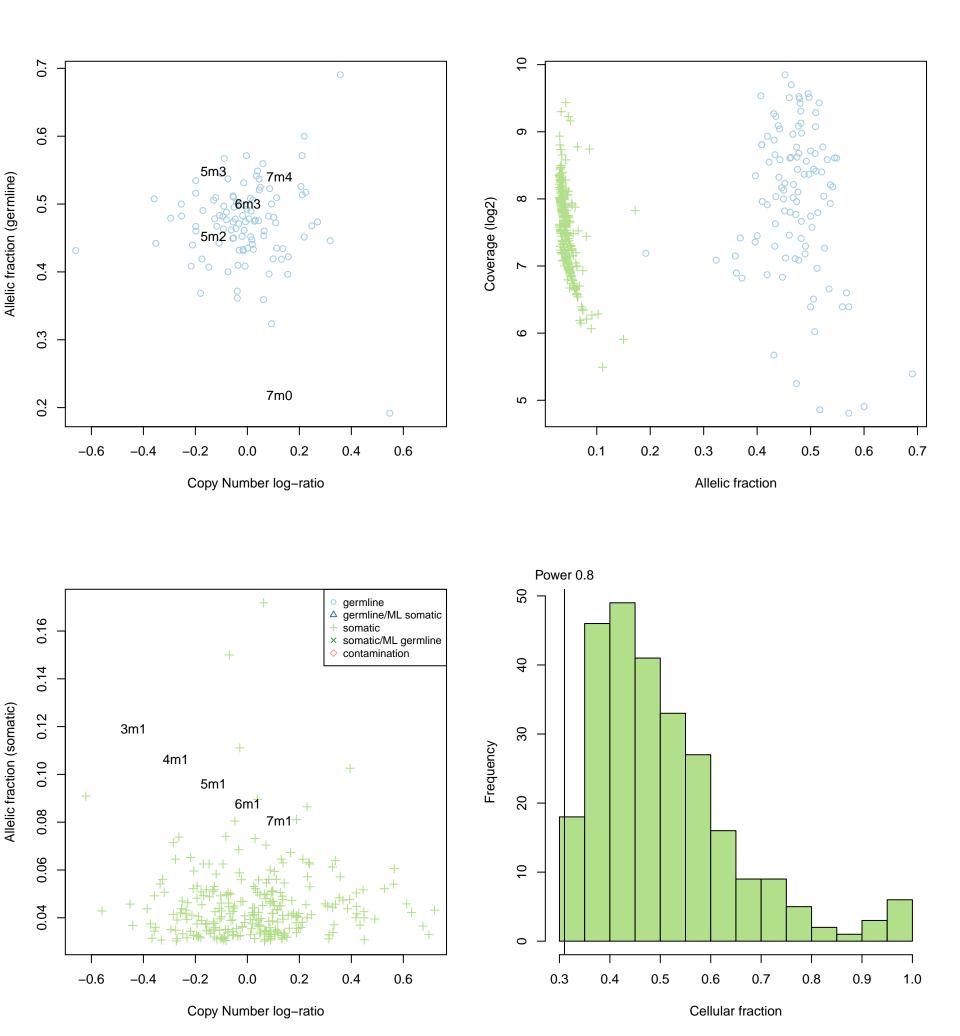




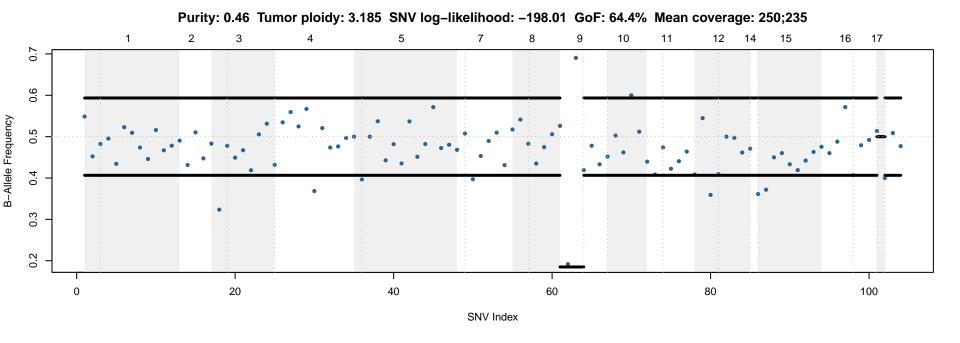
# SCNA-fit log-likelihood: -5407.21



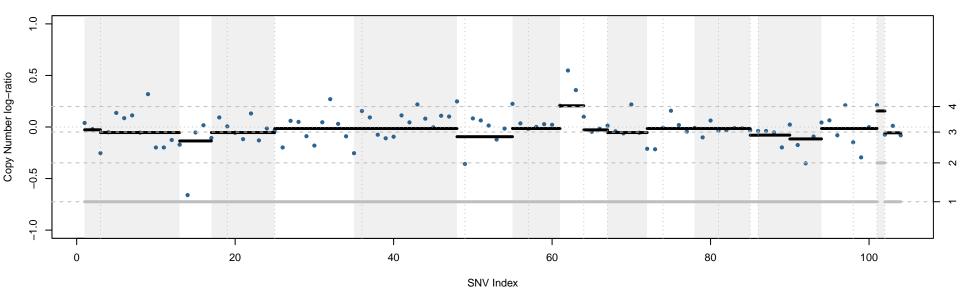


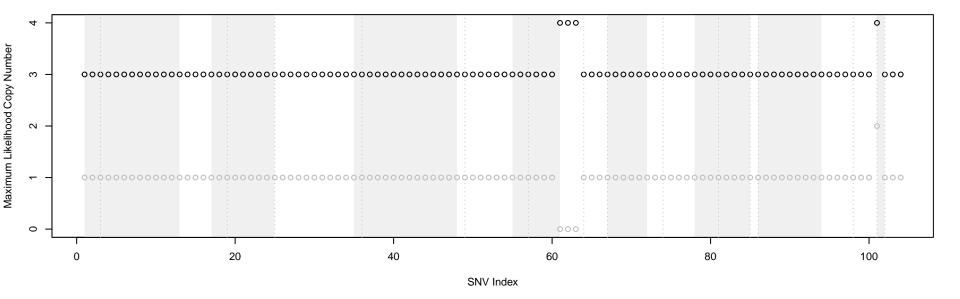


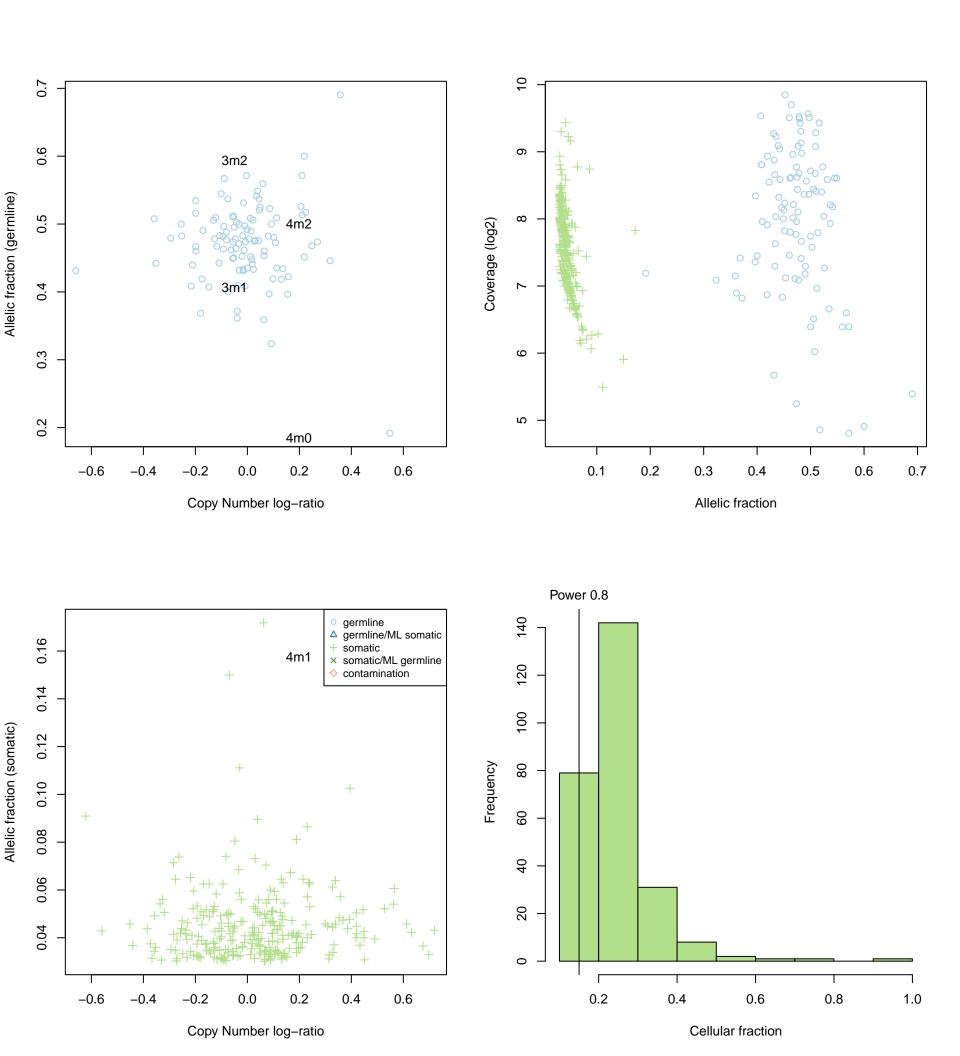
Purity: 0.46 Tumor ploidy: 3.185 2 3 0.30 0.25 0.20 Fraction Genome 0.15 0.05 0.00 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



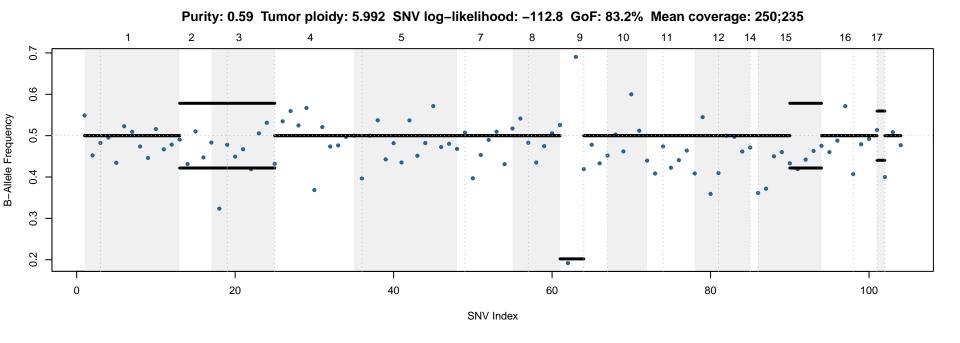
# SCNA-fit log-likelihood: -5486.6



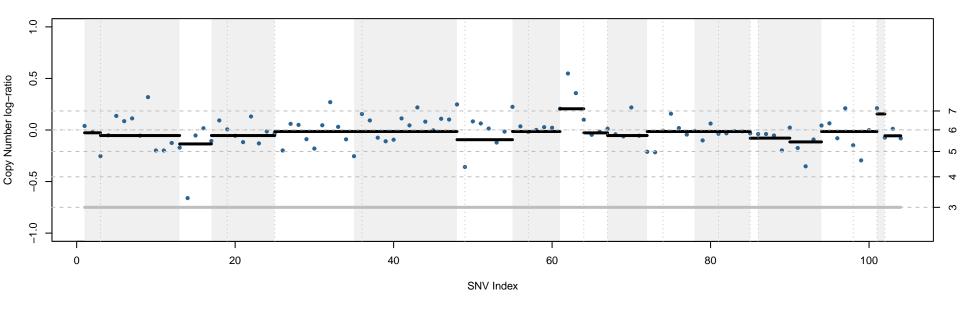


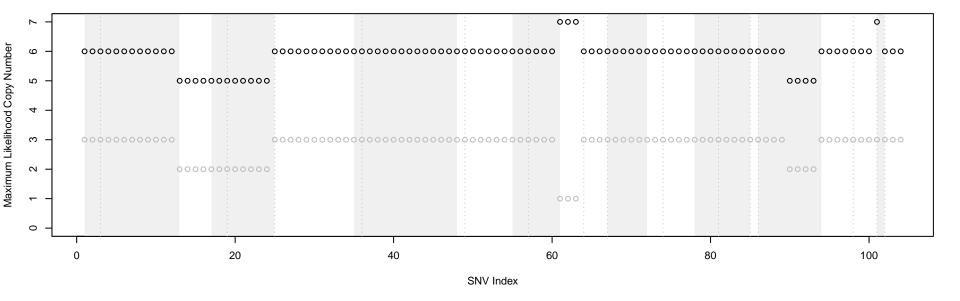


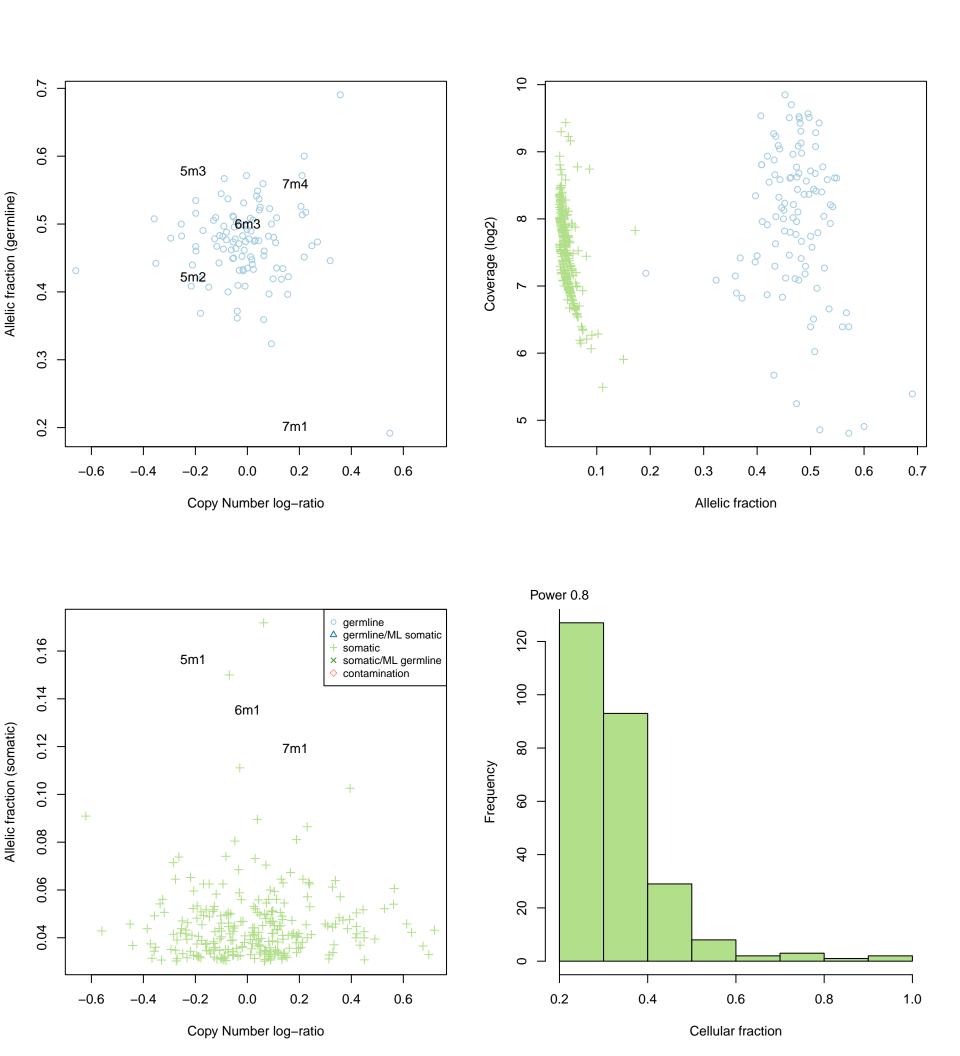
Purity: 0.59 Tumor ploidy: 5.992 5 6 7 3 0.30 0.25 Fraction Genome 0.15 0.05 0.00 -0.8 -0.6 -0.4 -0.2 0.0 0.2 log2 ratio



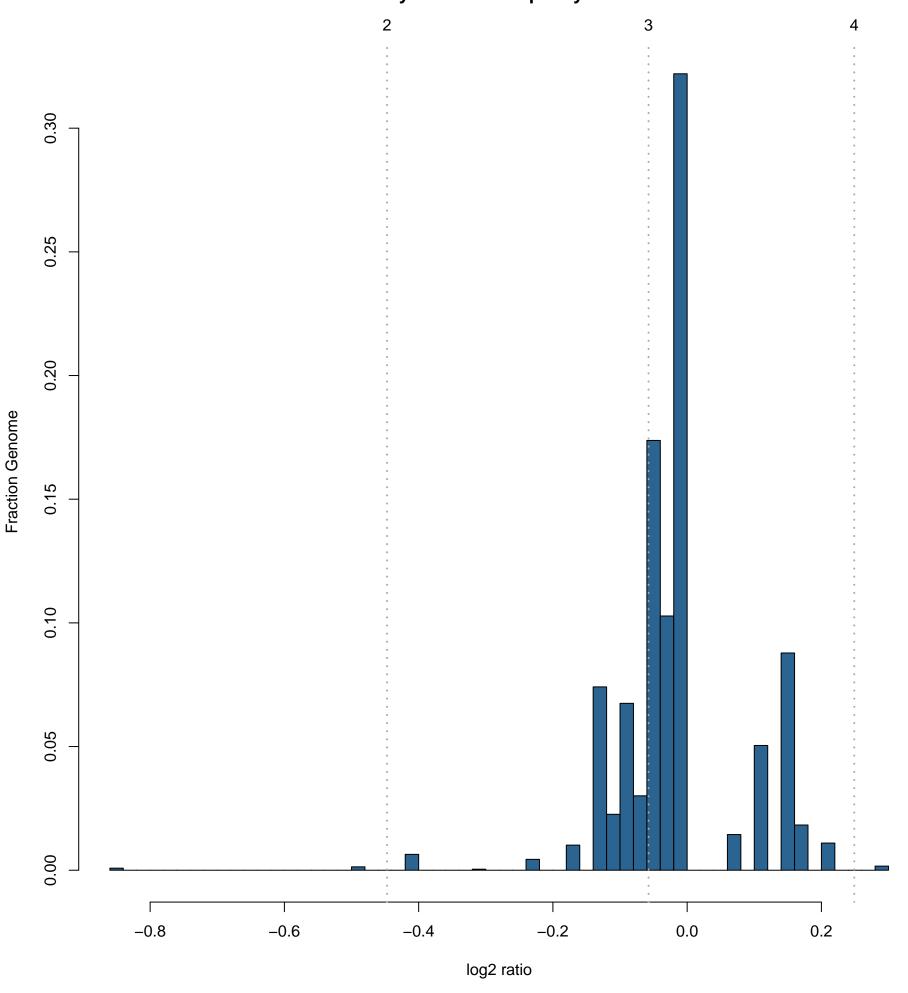
# SCNA-fit log-likelihood: -5626.14

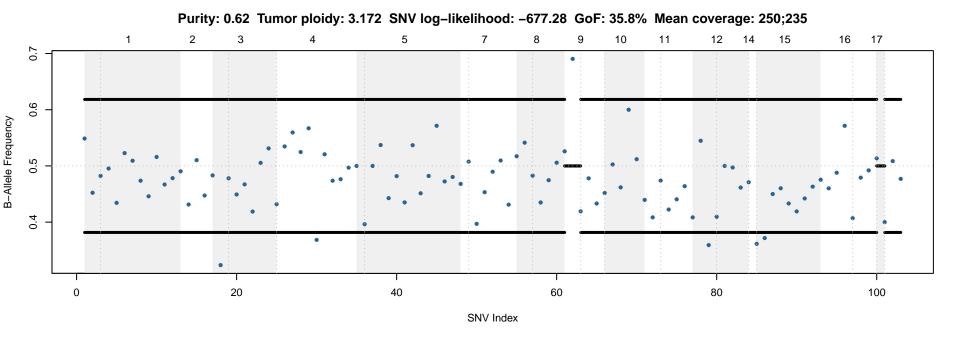




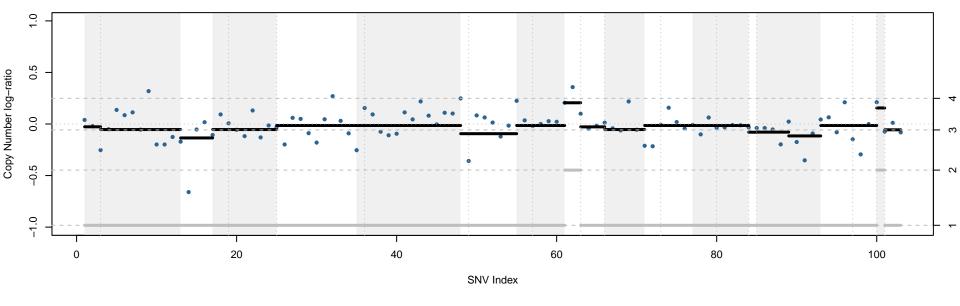


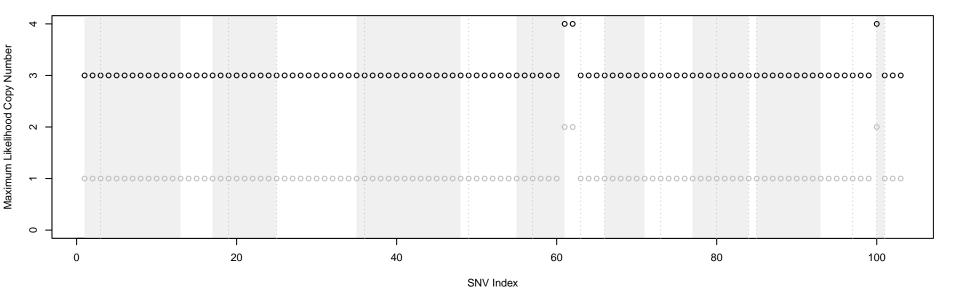
Purity: 0.62 Tumor ploidy: 3.172

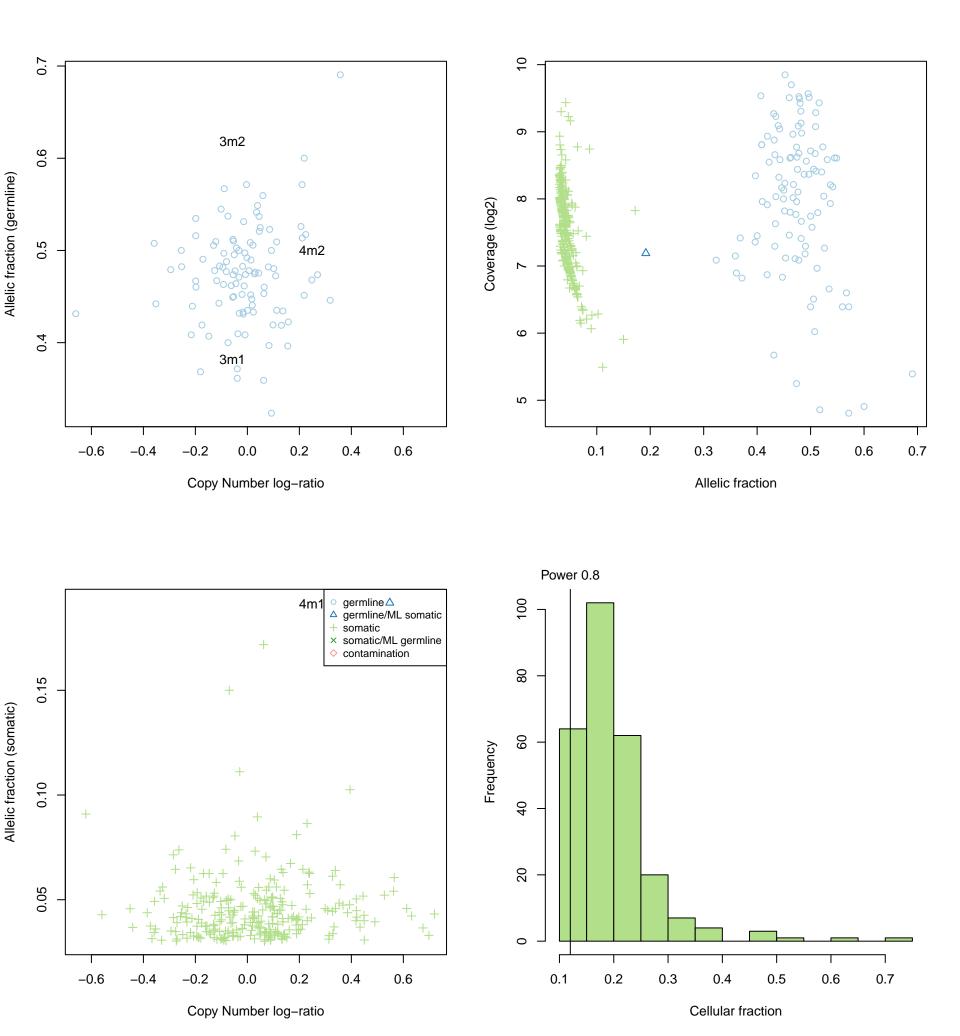




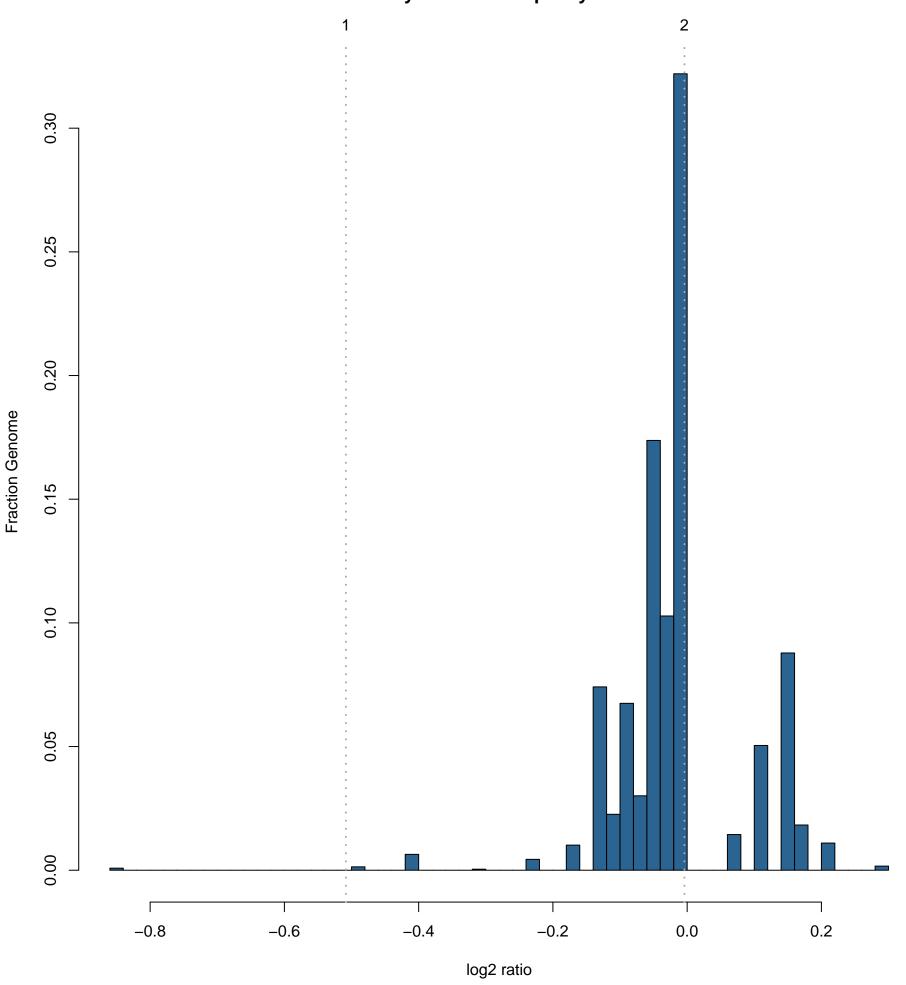
# SCNA-fit log-likelihood: -5597.78

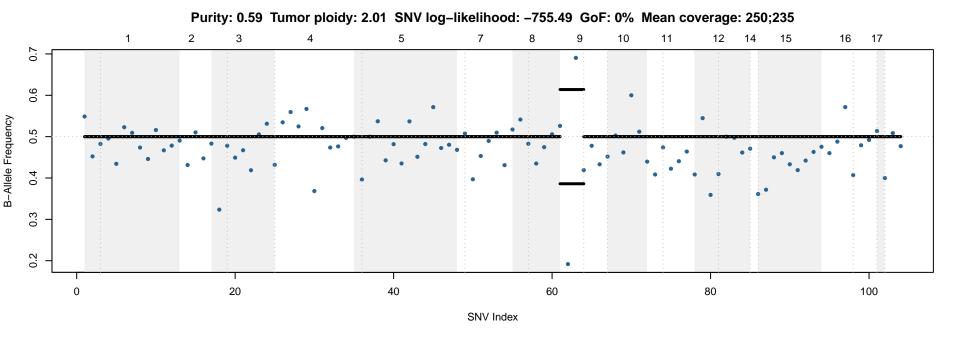




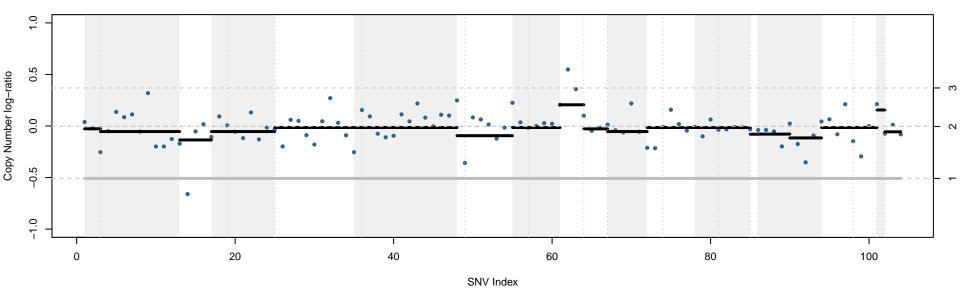


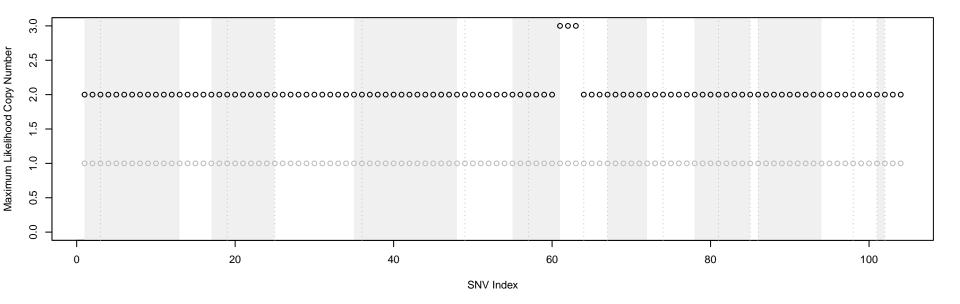
Purity: 0.59 Tumor ploidy: 2.01

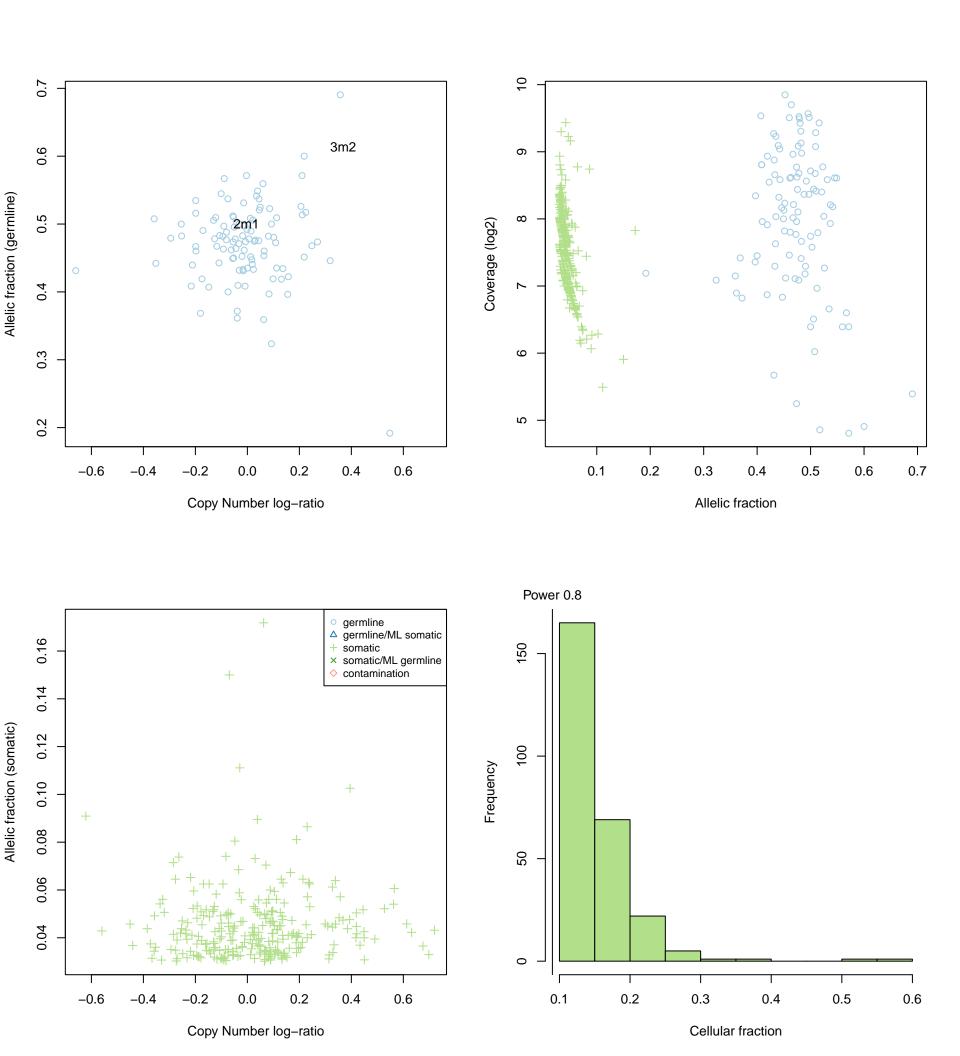




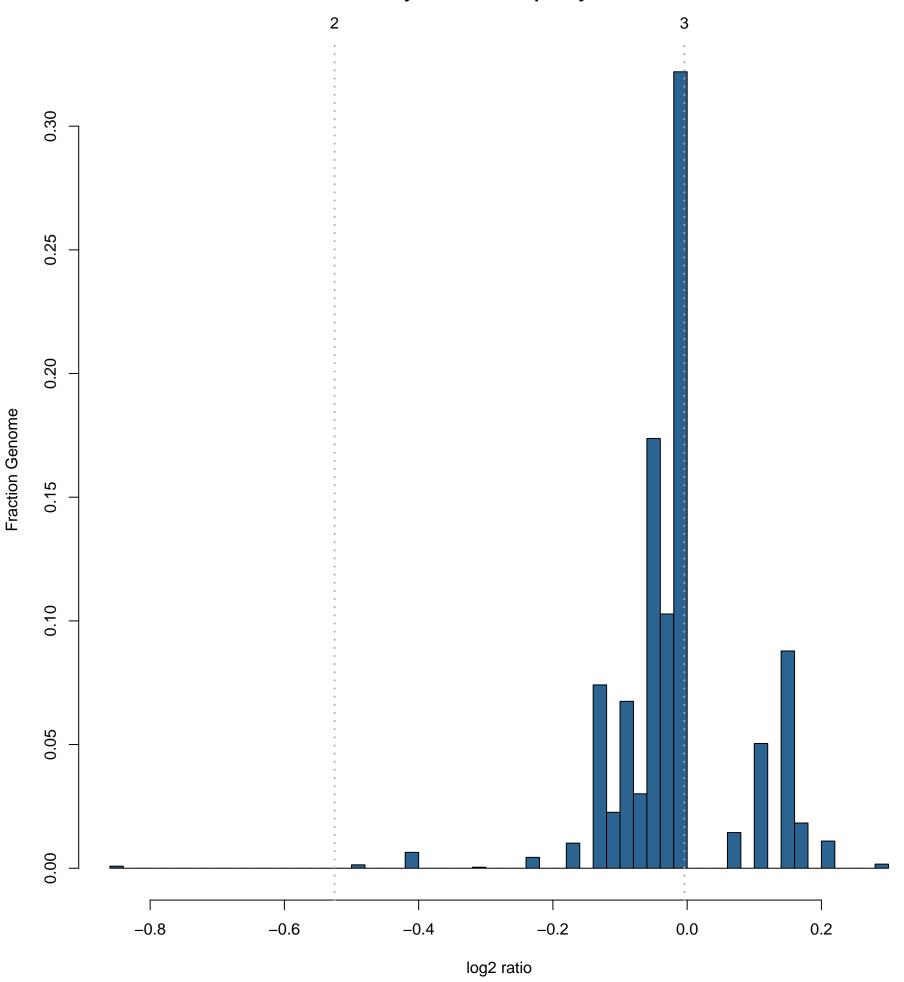
# SCNA-fit log-likelihood: -5822.8

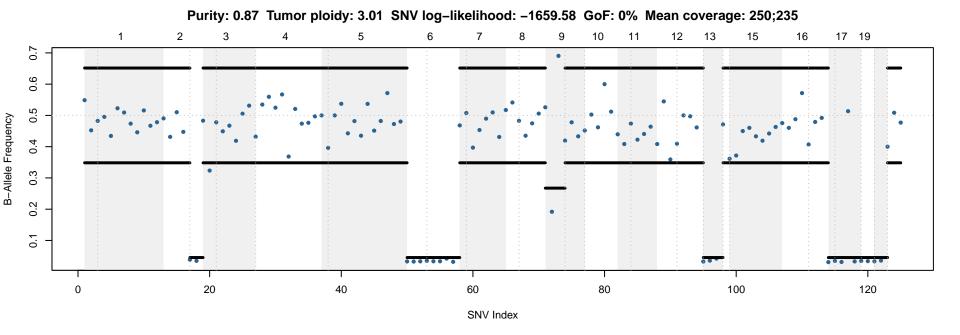






Purity: 0.87 Tumor ploidy: 3.01





# SCNA-fit log-likelihood: -5826.3

