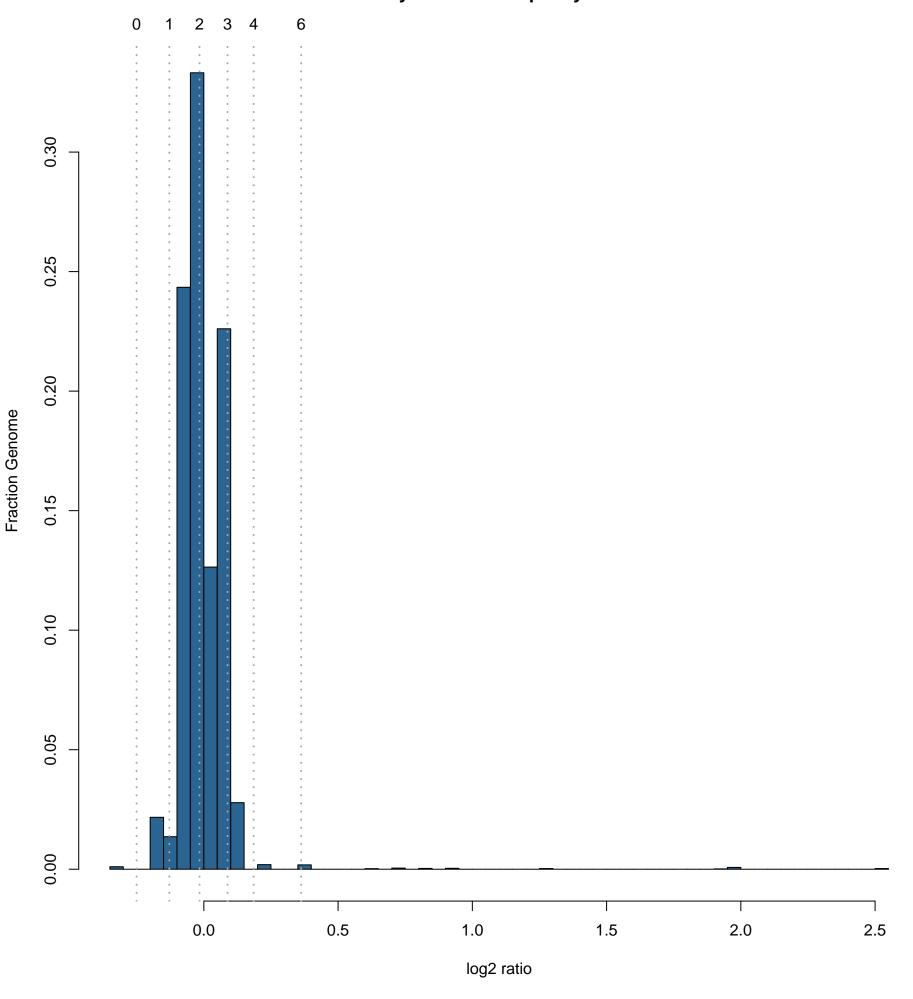
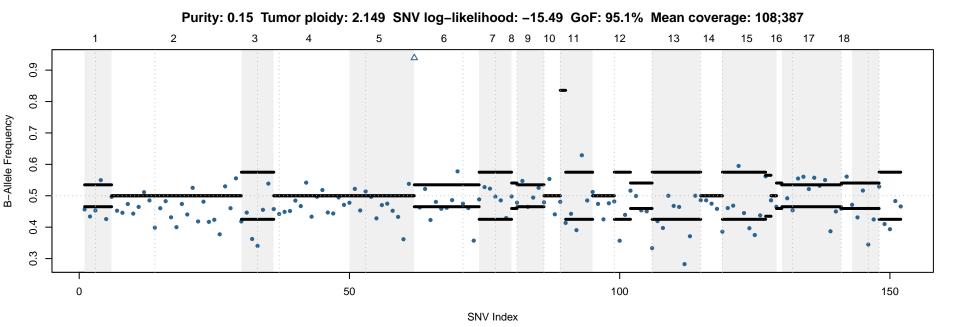
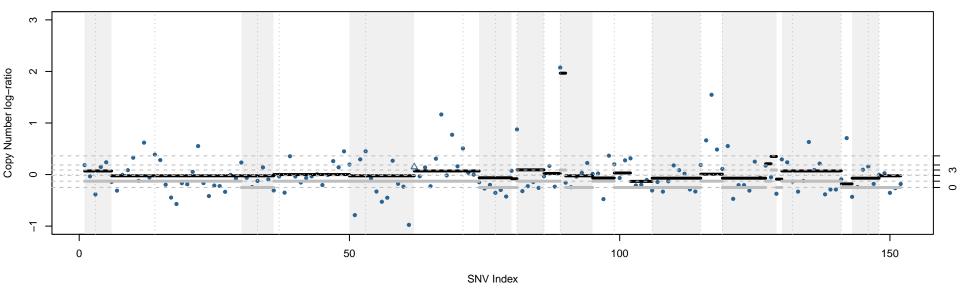
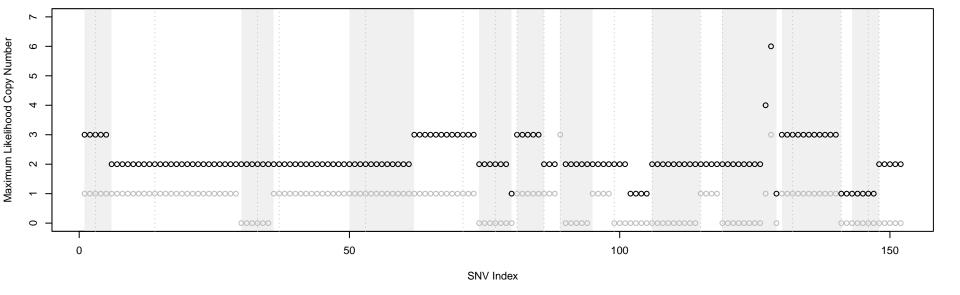
Purity: 0.15 Tumor ploidy: 2.149

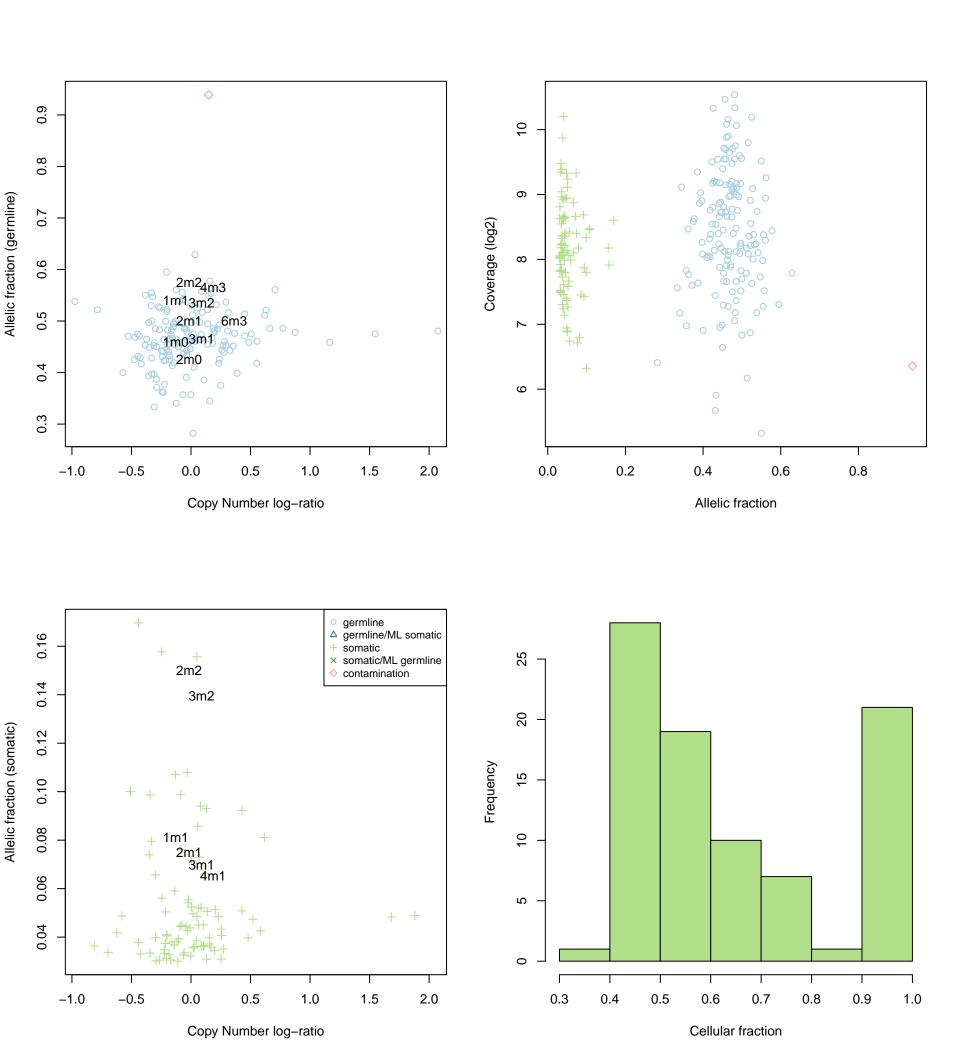




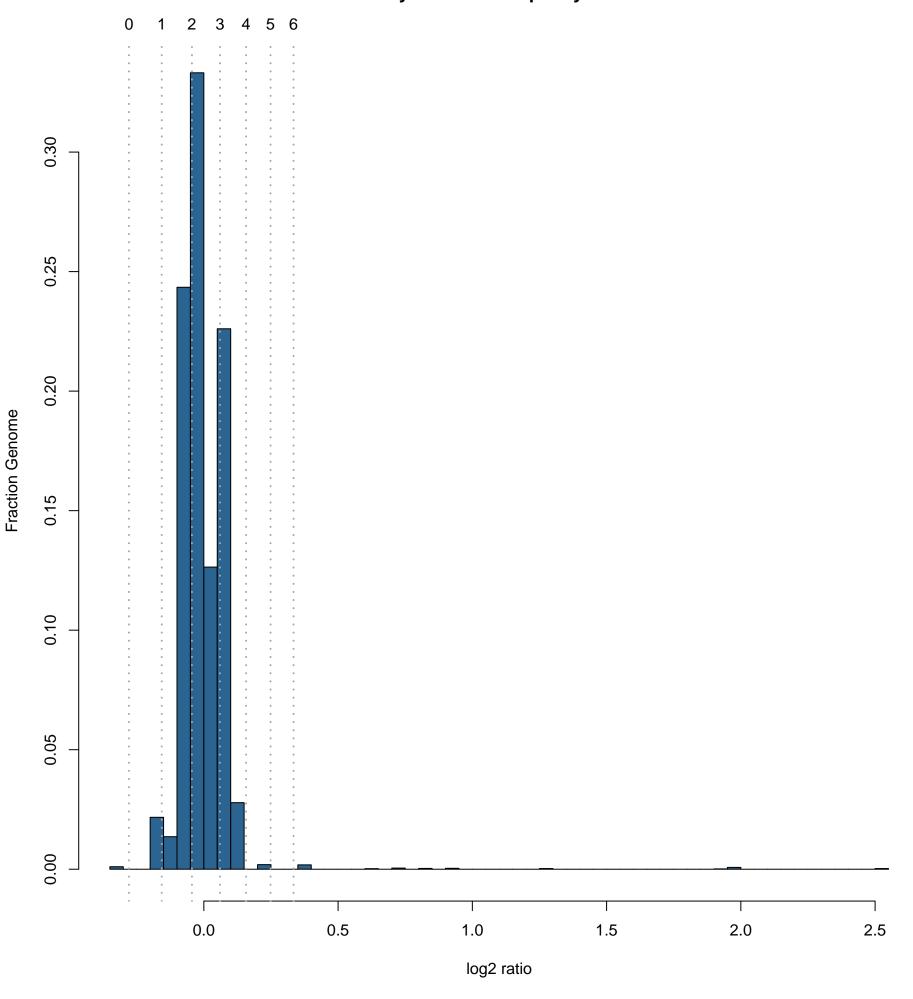
SCNA-fit log-likelihood: -15714.15

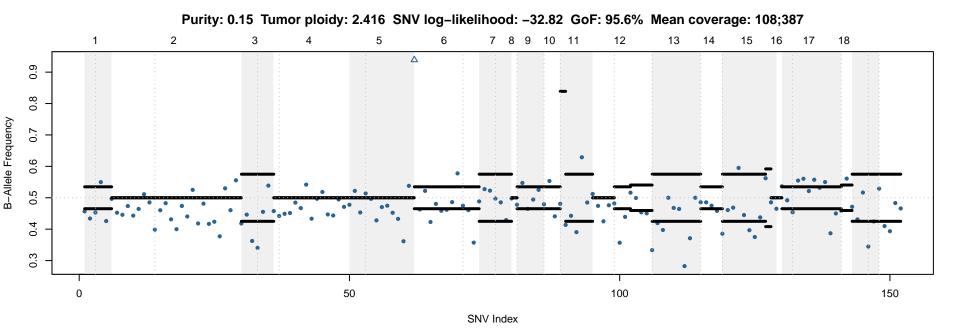




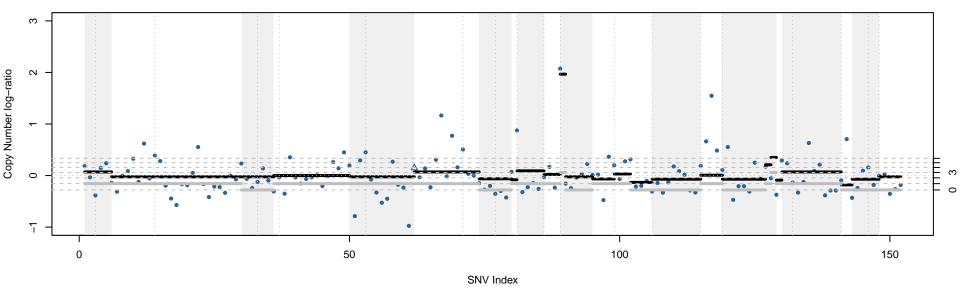


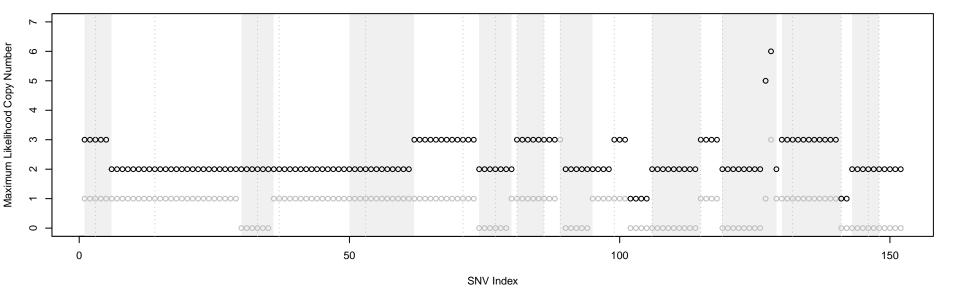
Purity: 0.15 Tumor ploidy: 2.416

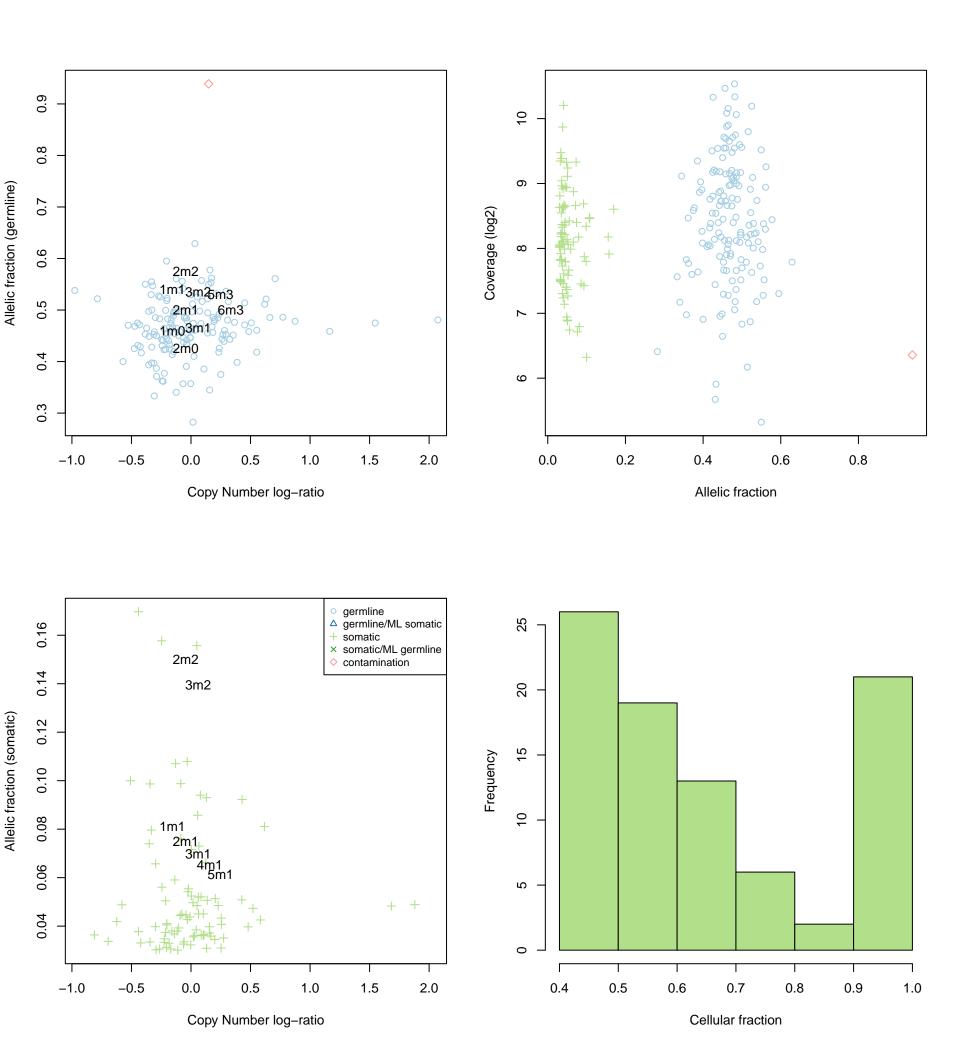




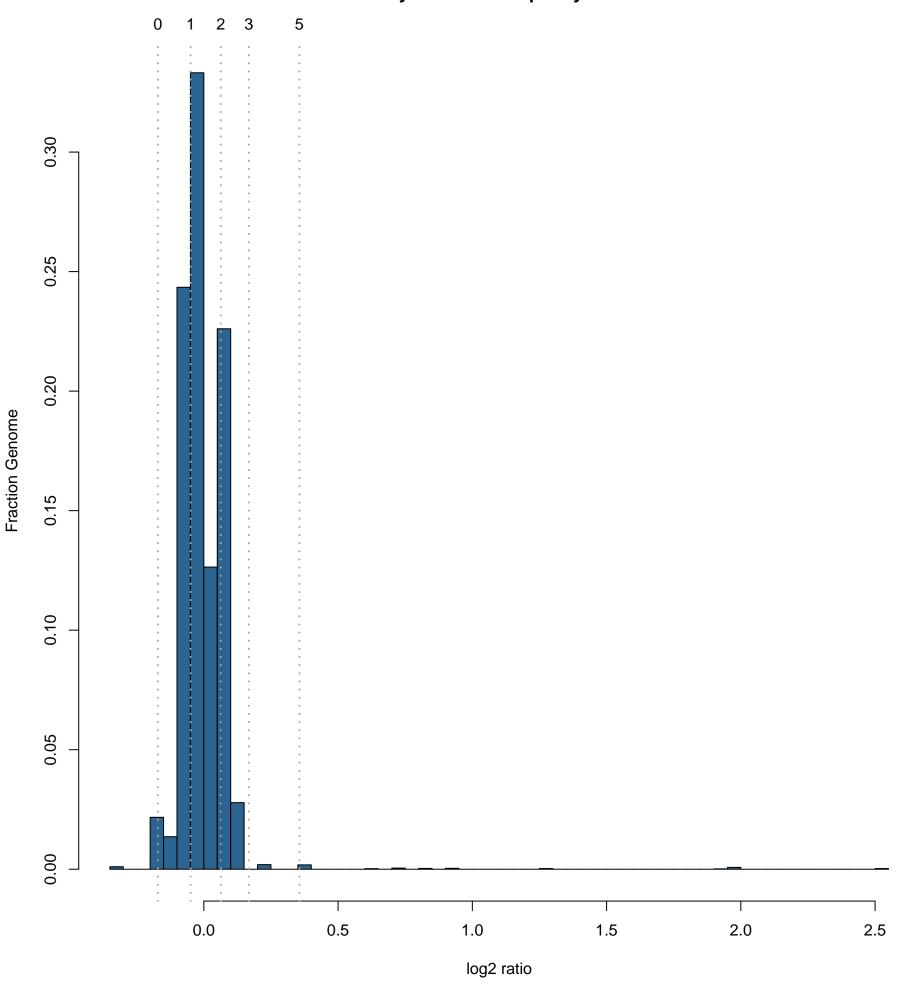
SCNA-fit log-likelihood: -15712.8

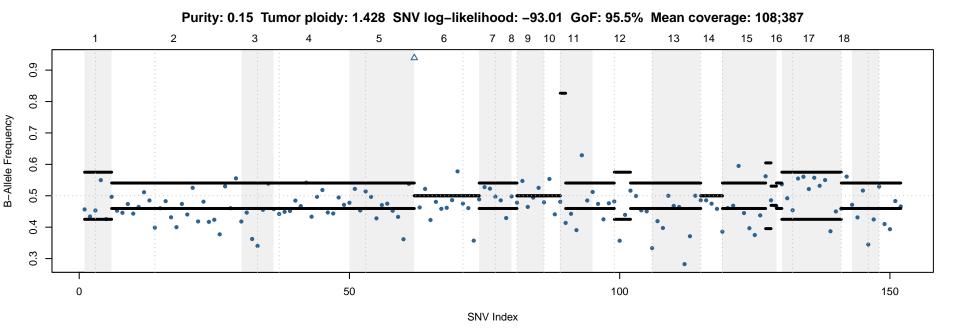




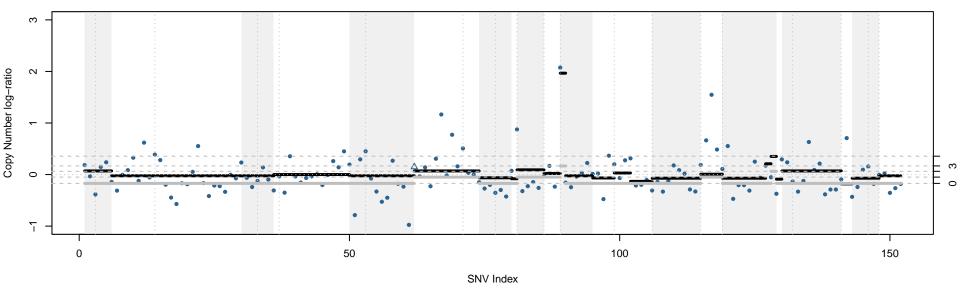


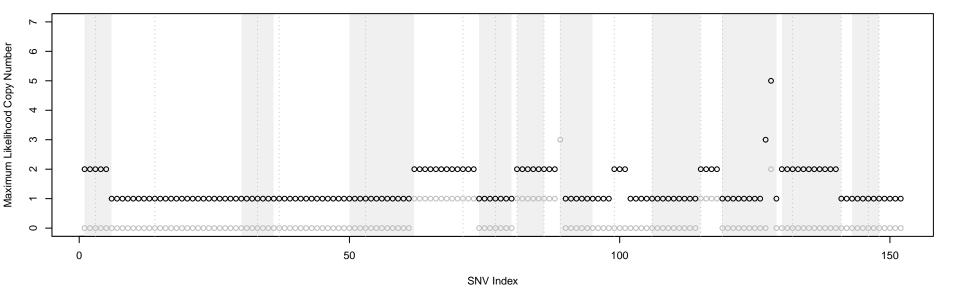
Purity: 0.15 Tumor ploidy: 1.428

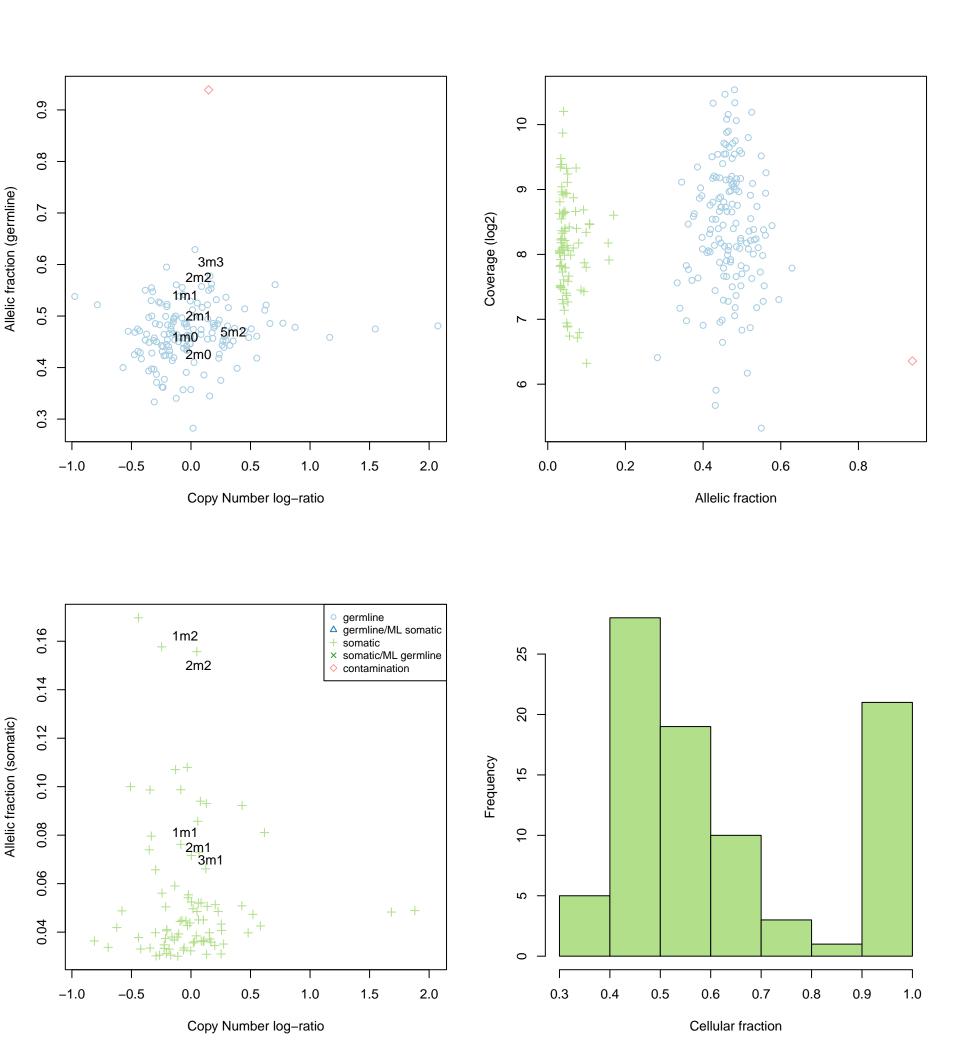




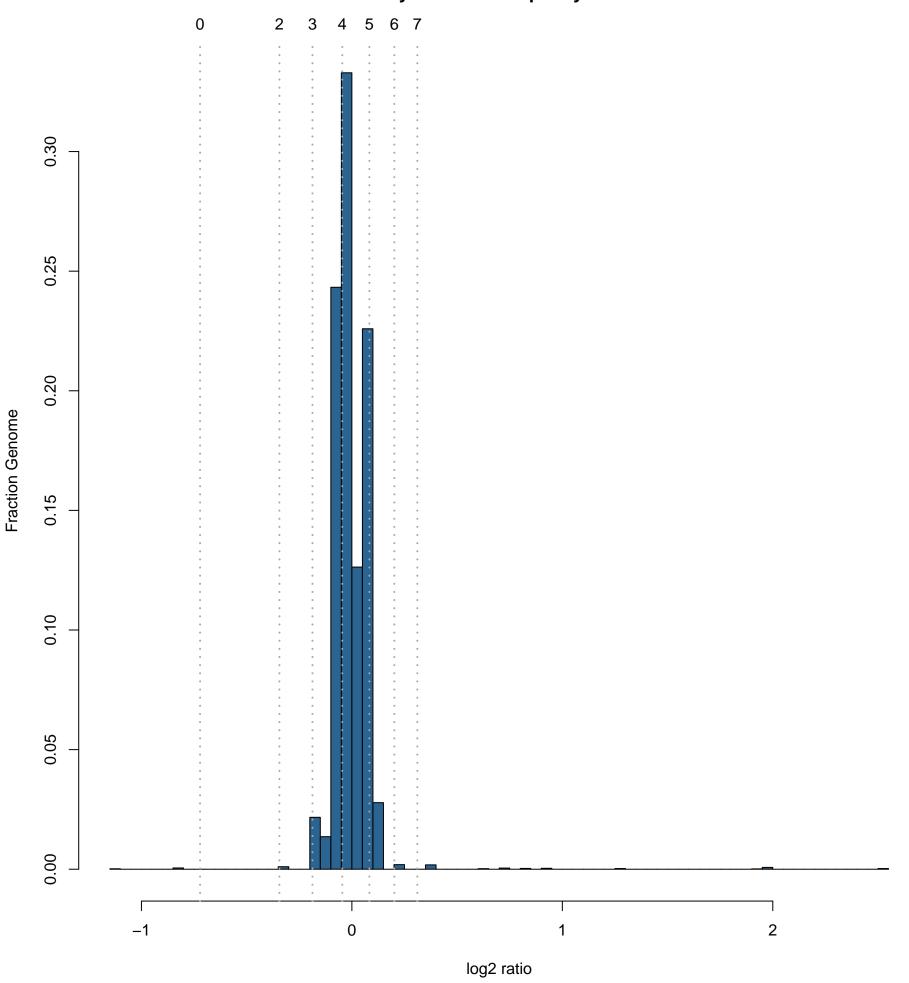
SCNA-fit log-likelihood: -15734.95

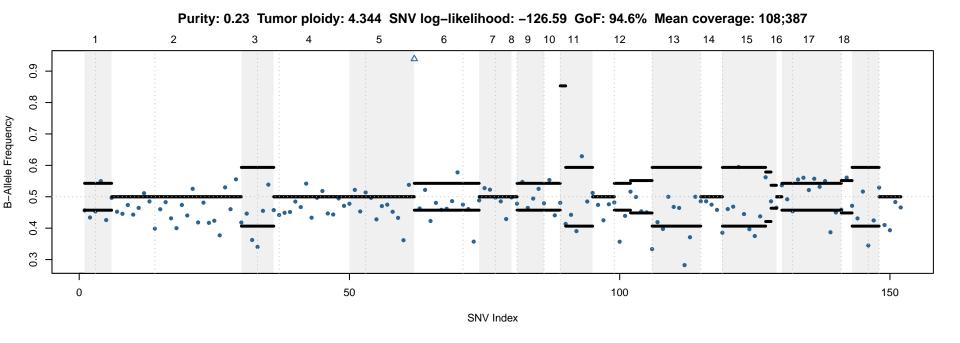




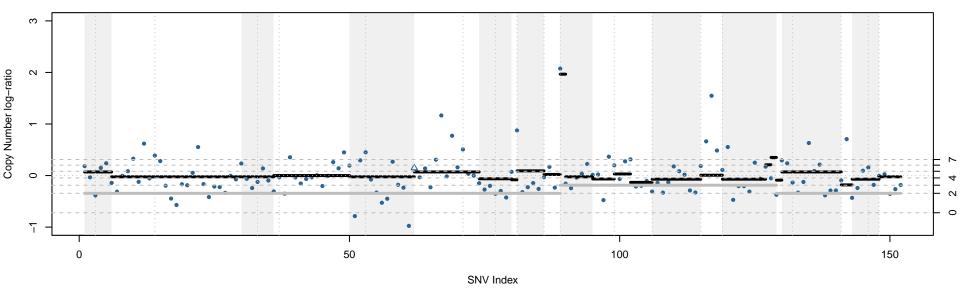


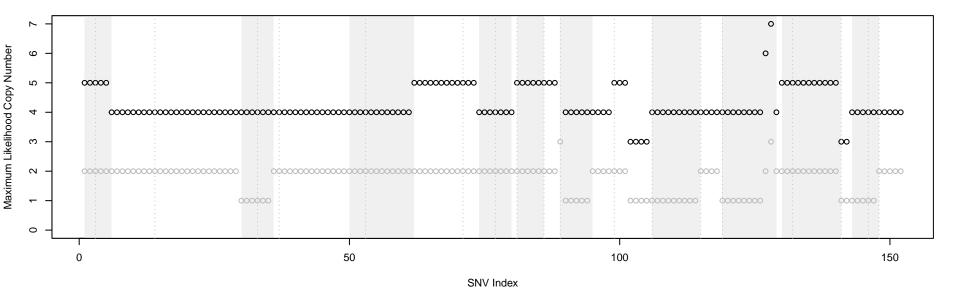
Purity: 0.23 Tumor ploidy: 4.344

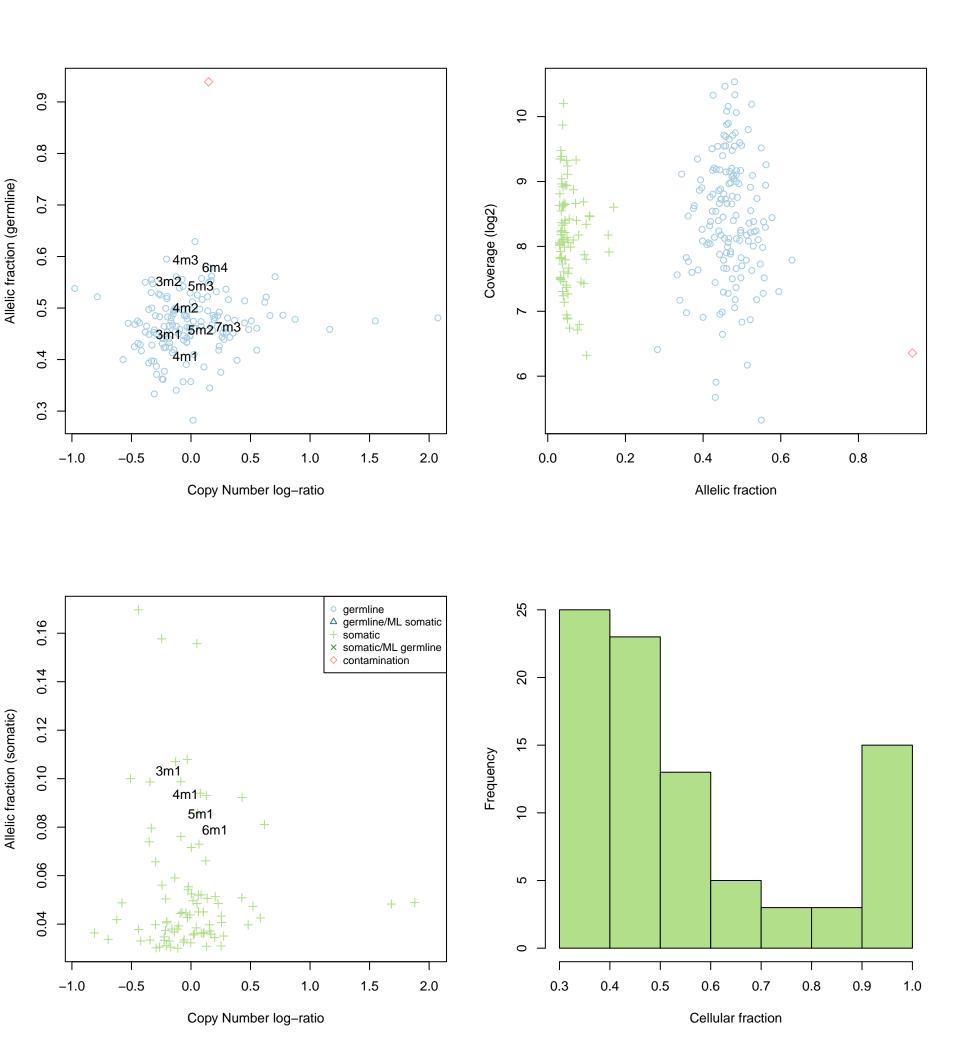




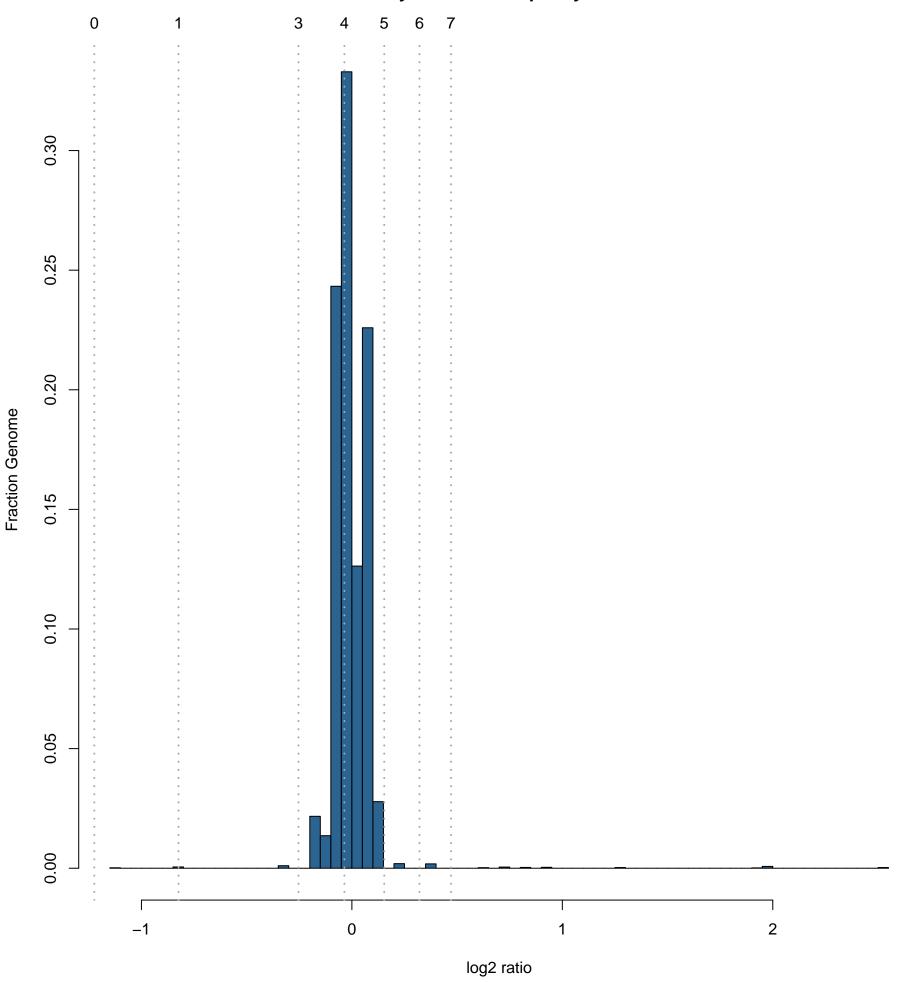
SCNA-fit log-likelihood: -15709.06

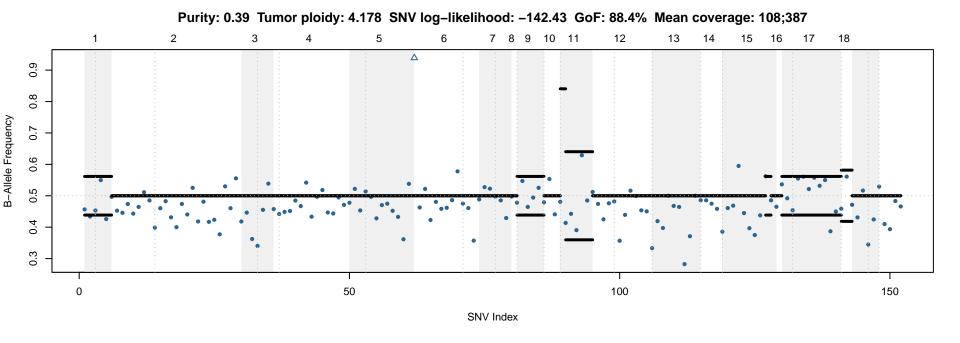




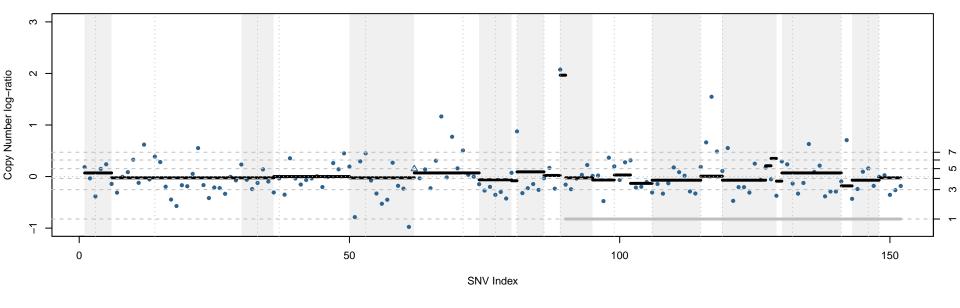


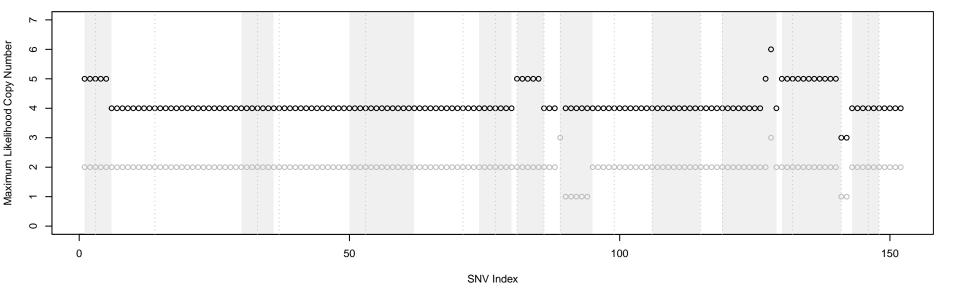
Purity: 0.39 Tumor ploidy: 4.178

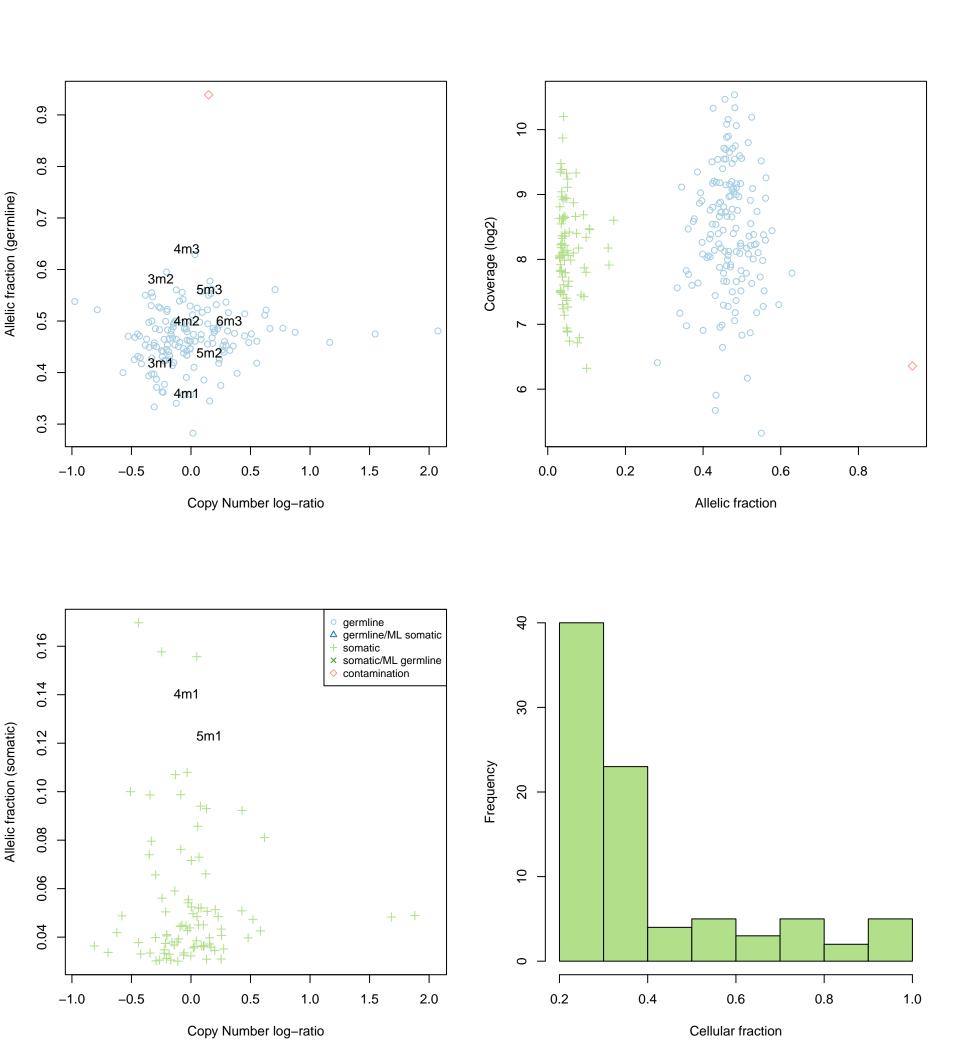




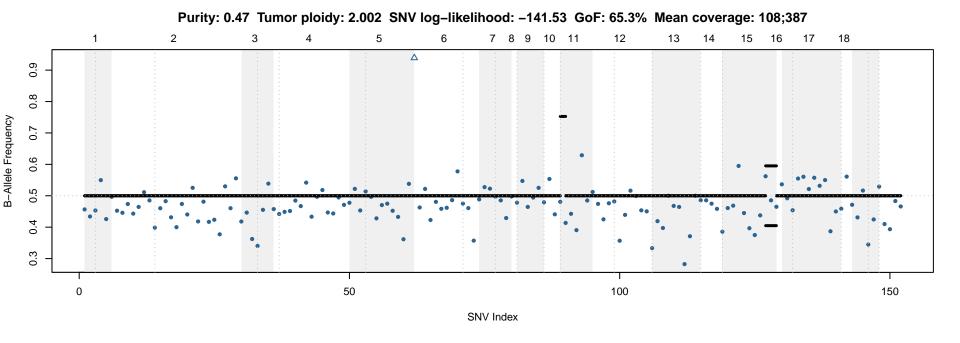
SCNA-fit log-likelihood: -15763.29



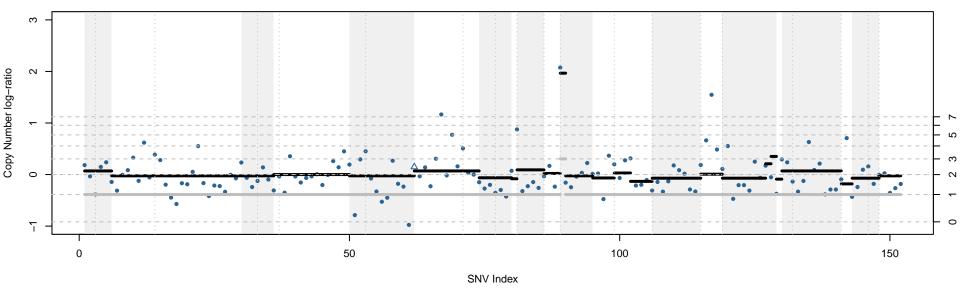


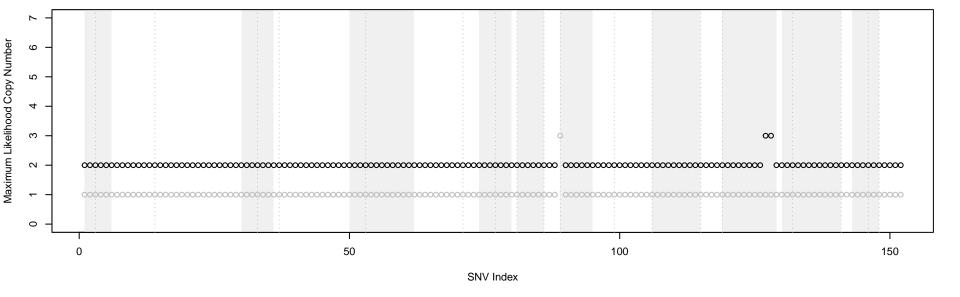


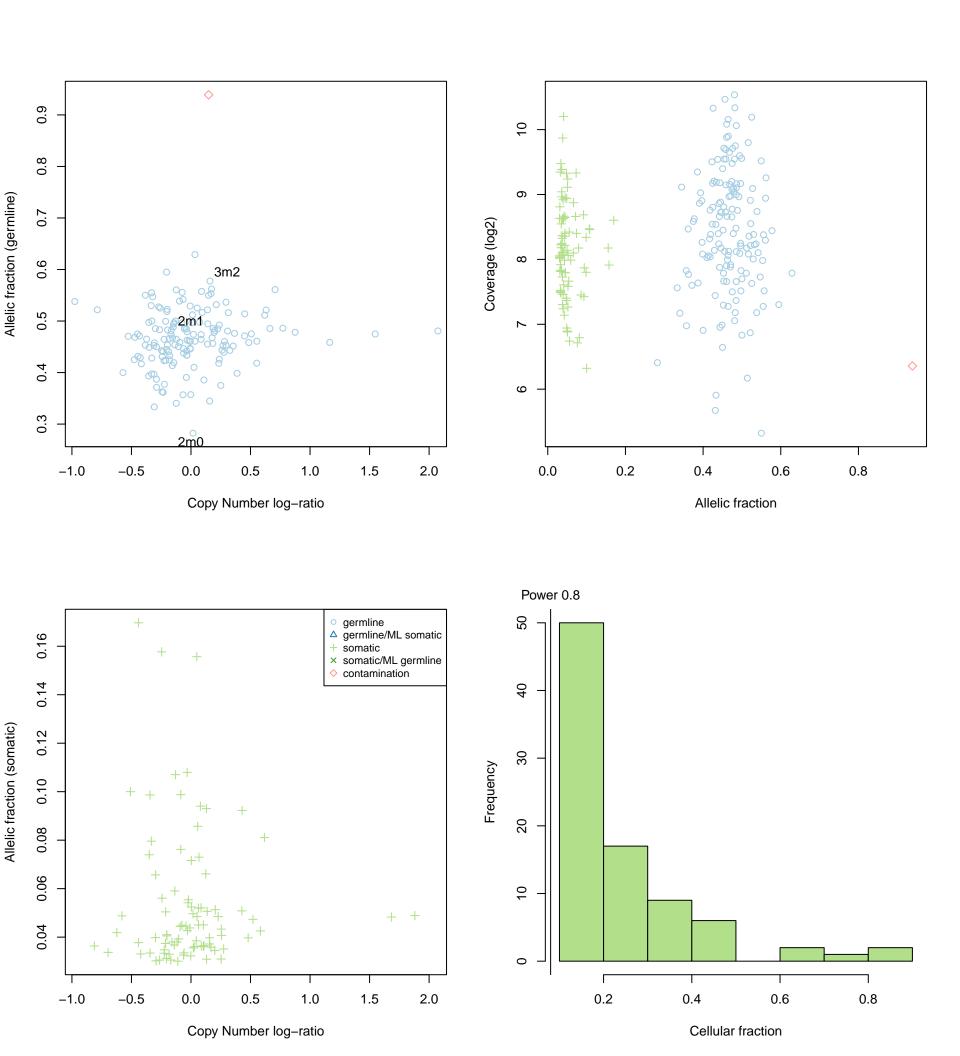
Purity: 0.47 Tumor ploidy: 2.002 3 2 0 5 6 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 0 2 1 log2 ratio



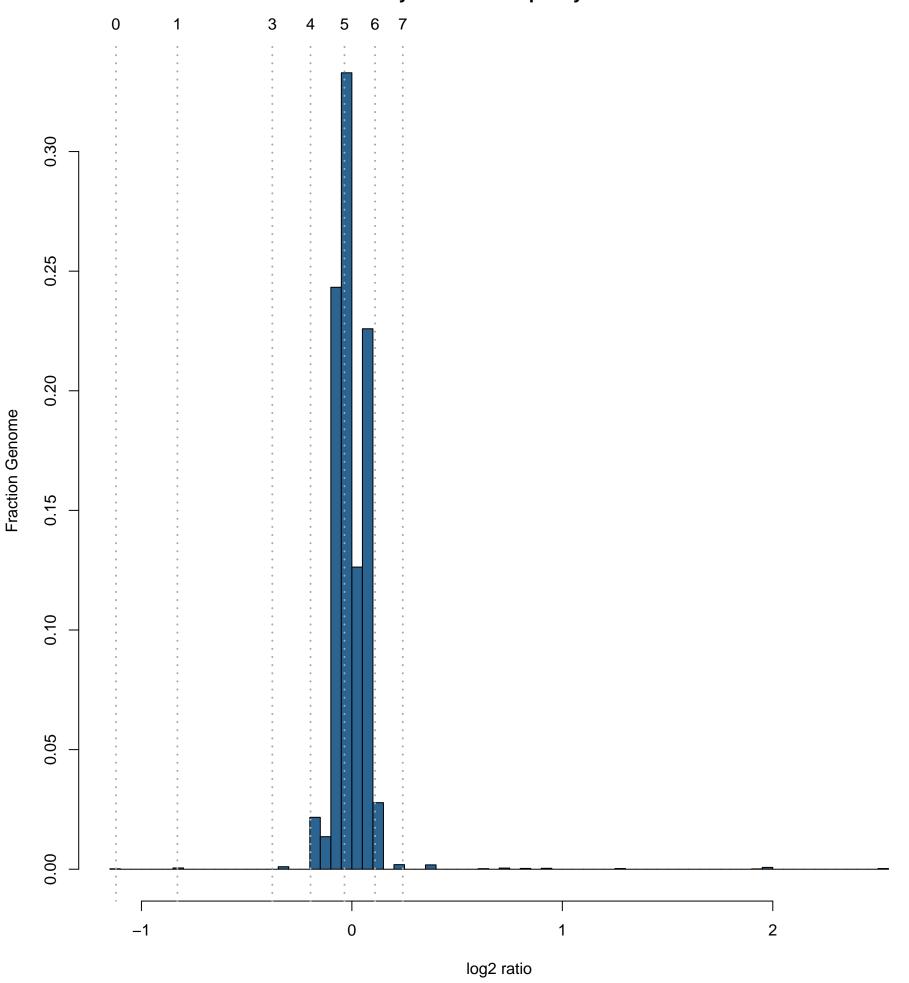
SCNA-fit log-likelihood: -15808.57

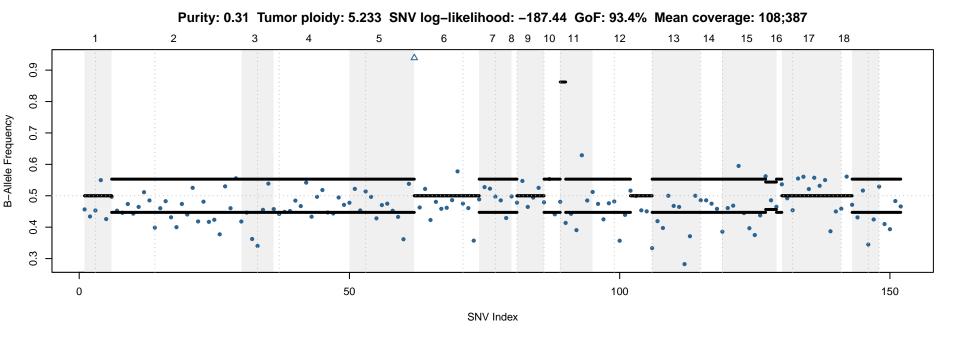




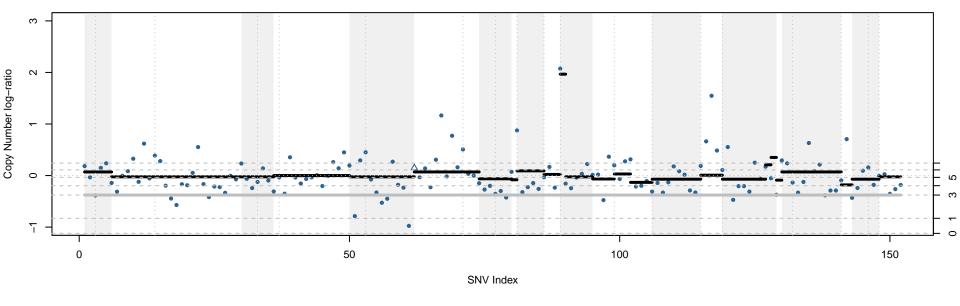


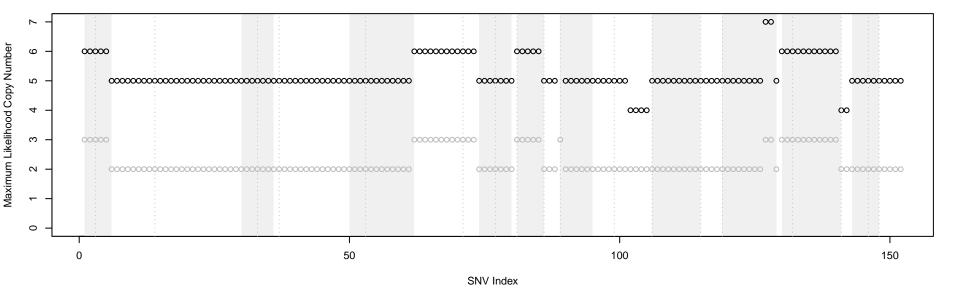
Purity: 0.31 Tumor ploidy: 5.233

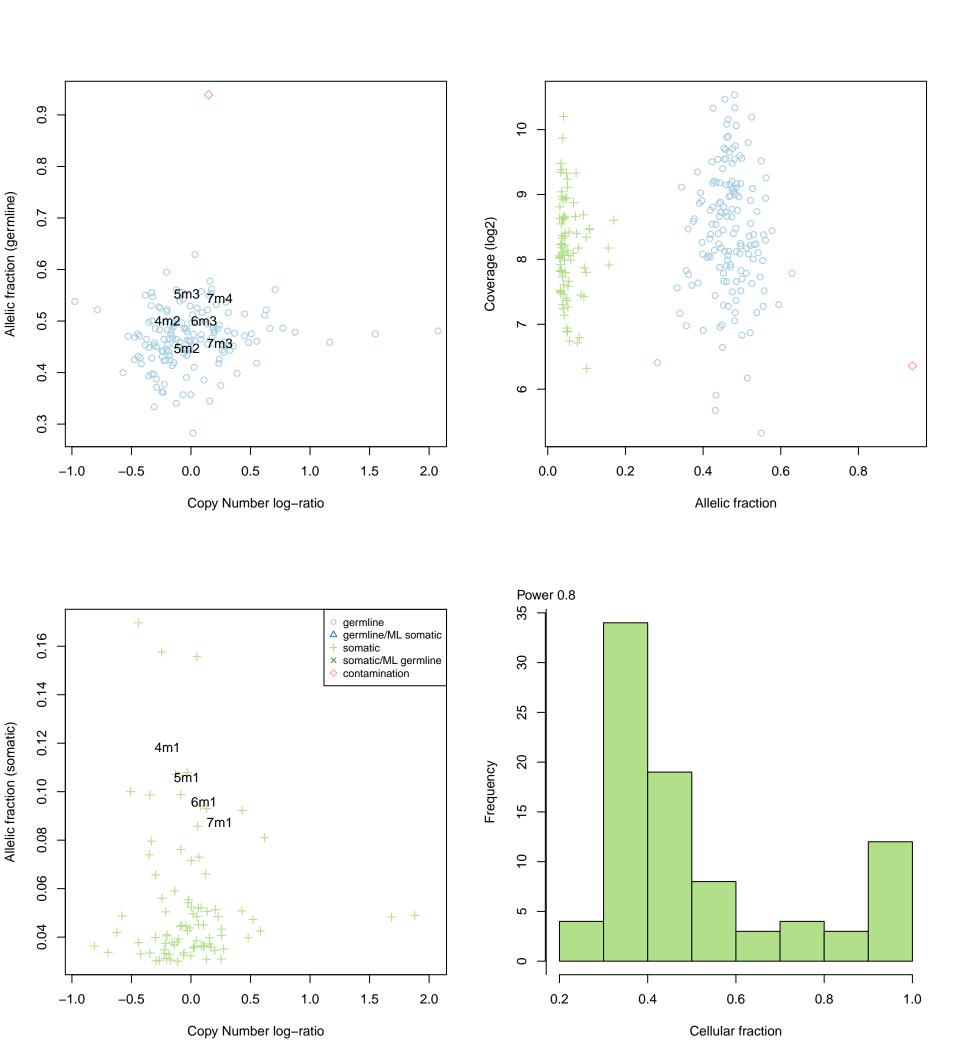




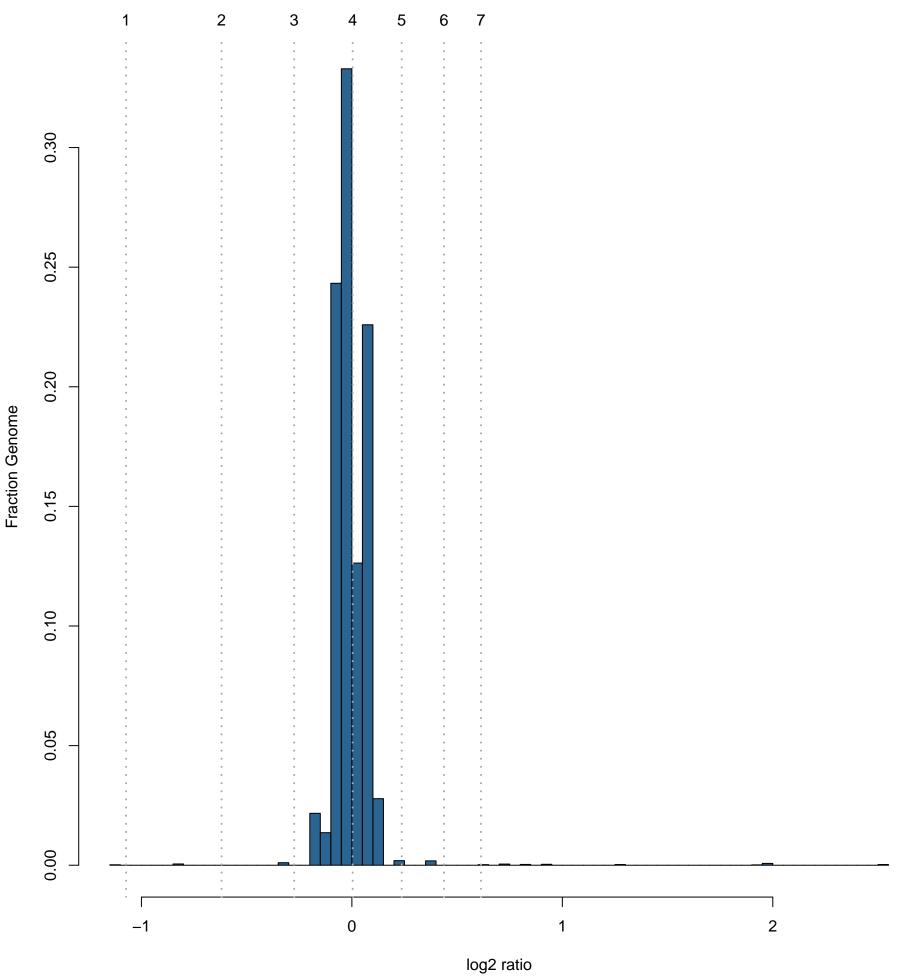
SCNA-fit log-likelihood: -15718.74

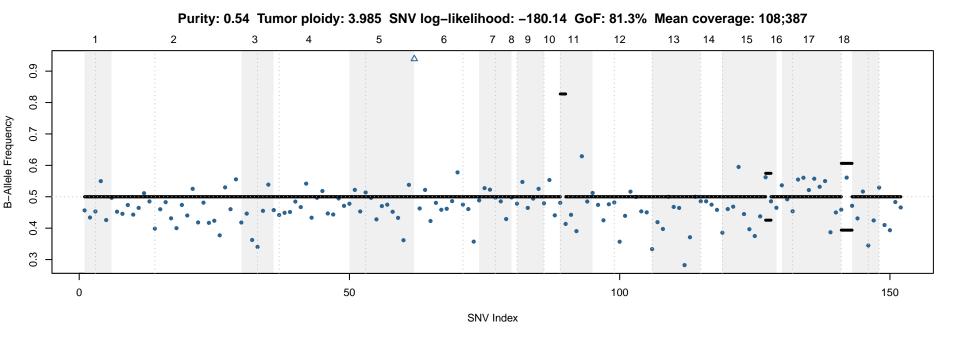




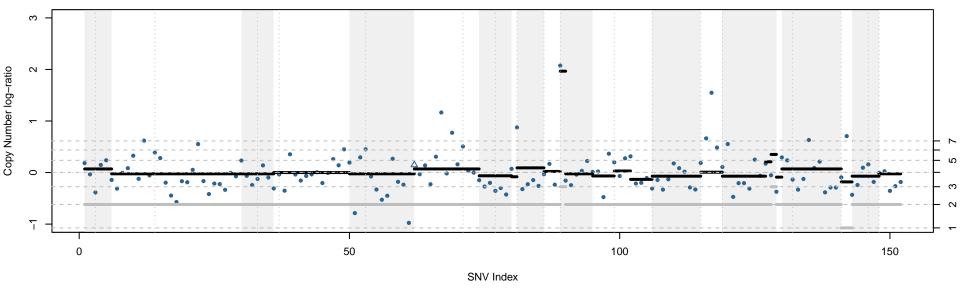


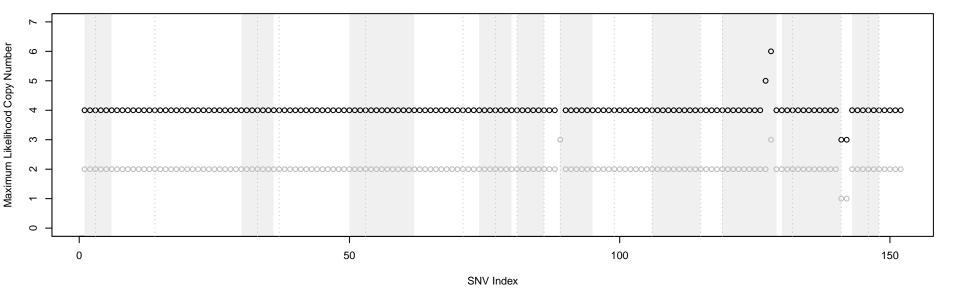
Purity: 0.54 Tumor ploidy: 3.985

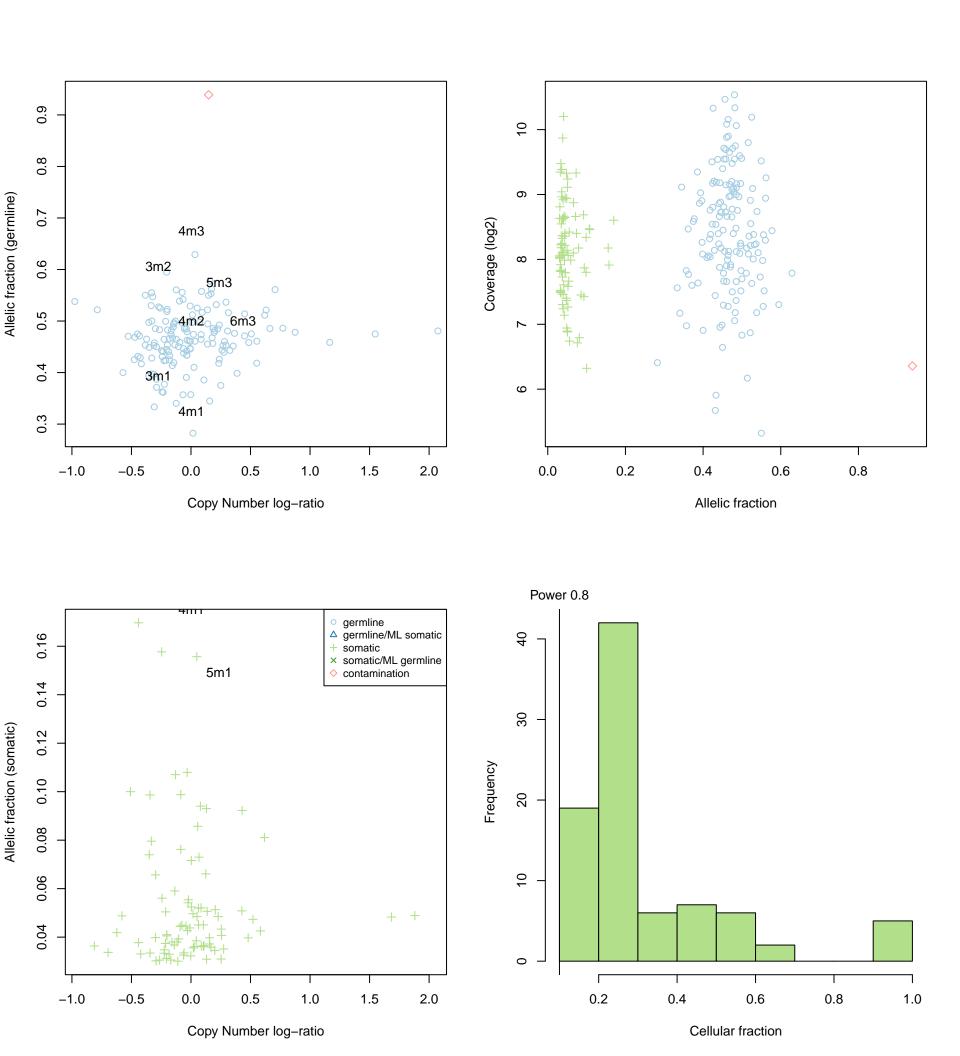




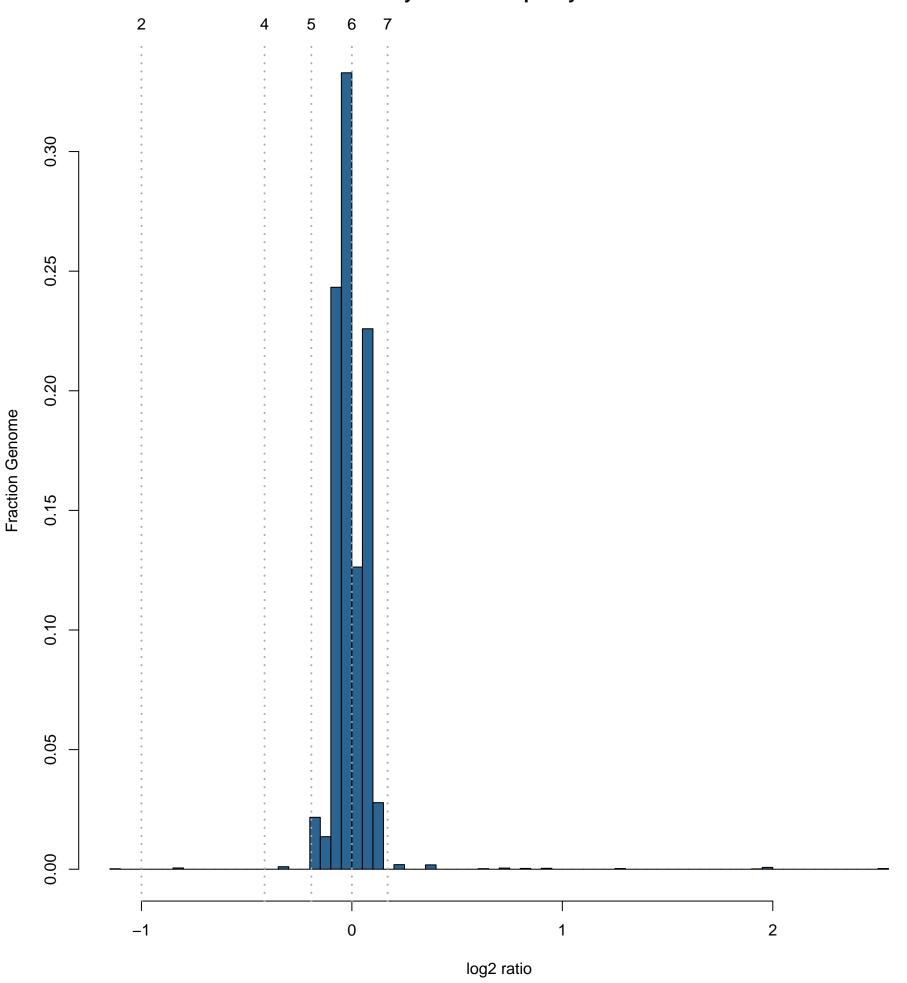
SCNA-fit log-likelihood: -15800.47

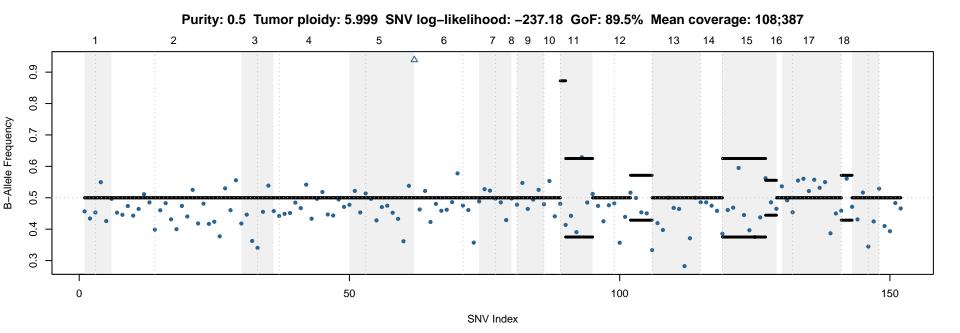




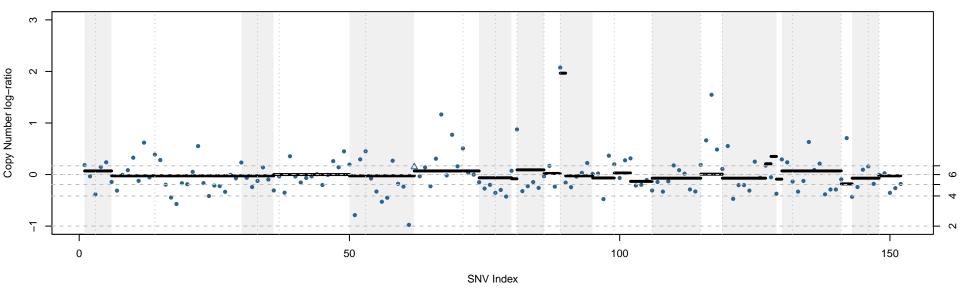


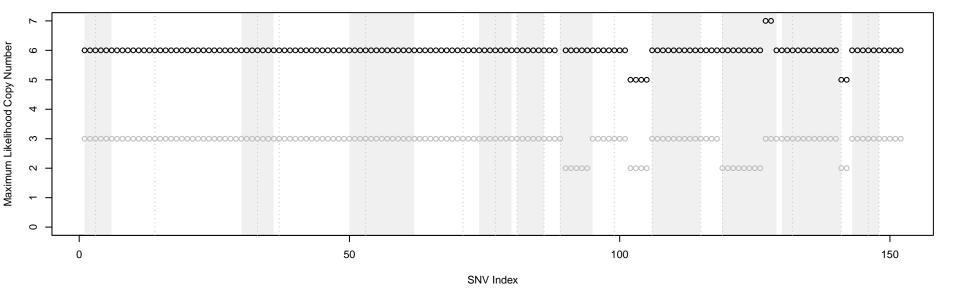
Purity: 0.5 Tumor ploidy: 5.999

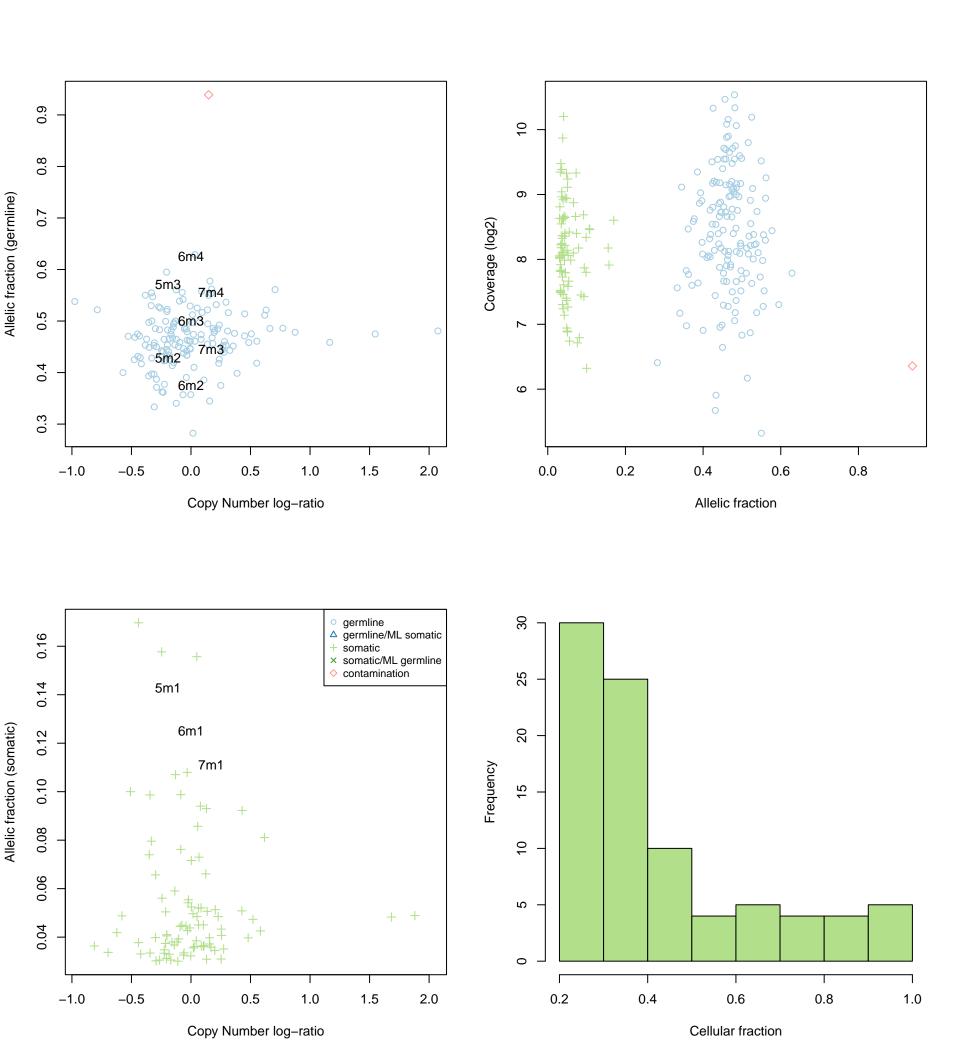




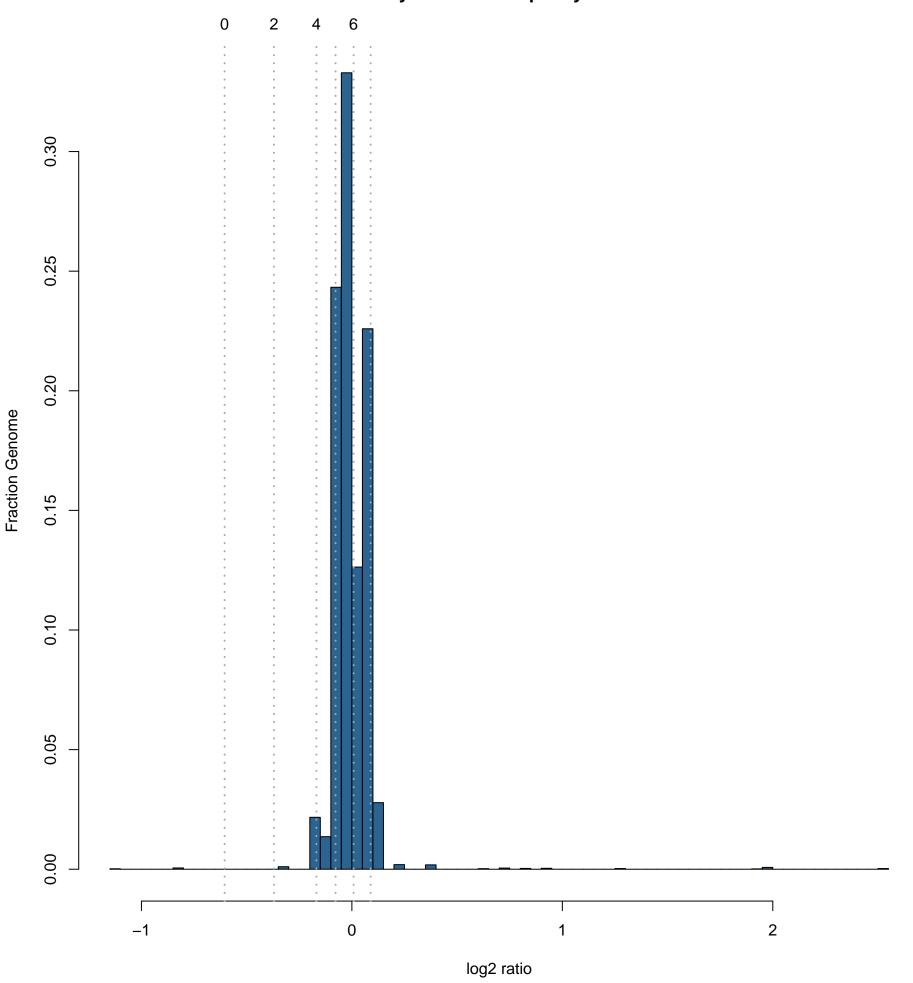
SCNA-fit log-likelihood: -15790.71

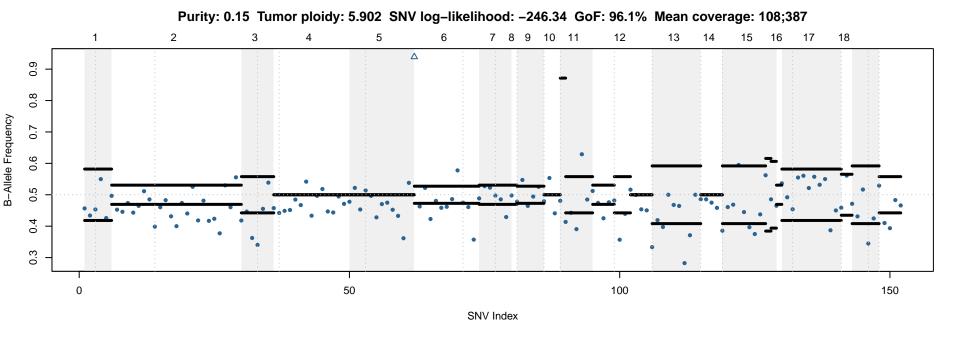




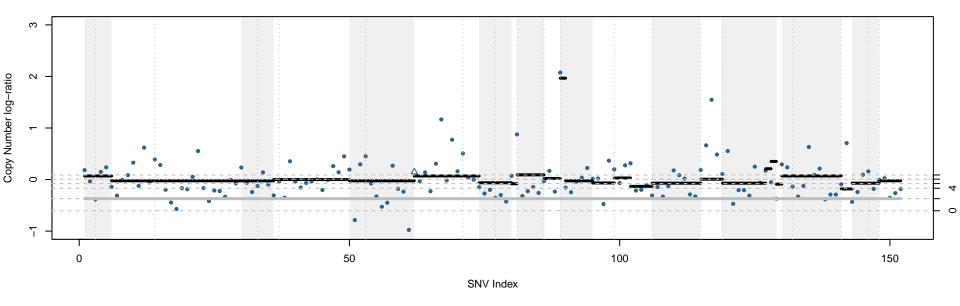


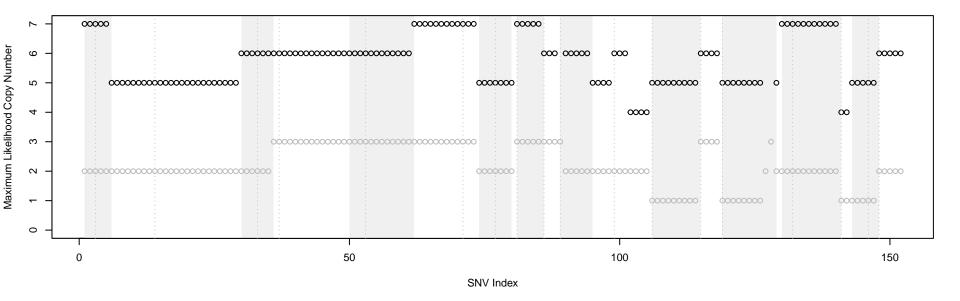
Purity: 0.15 Tumor ploidy: 5.902

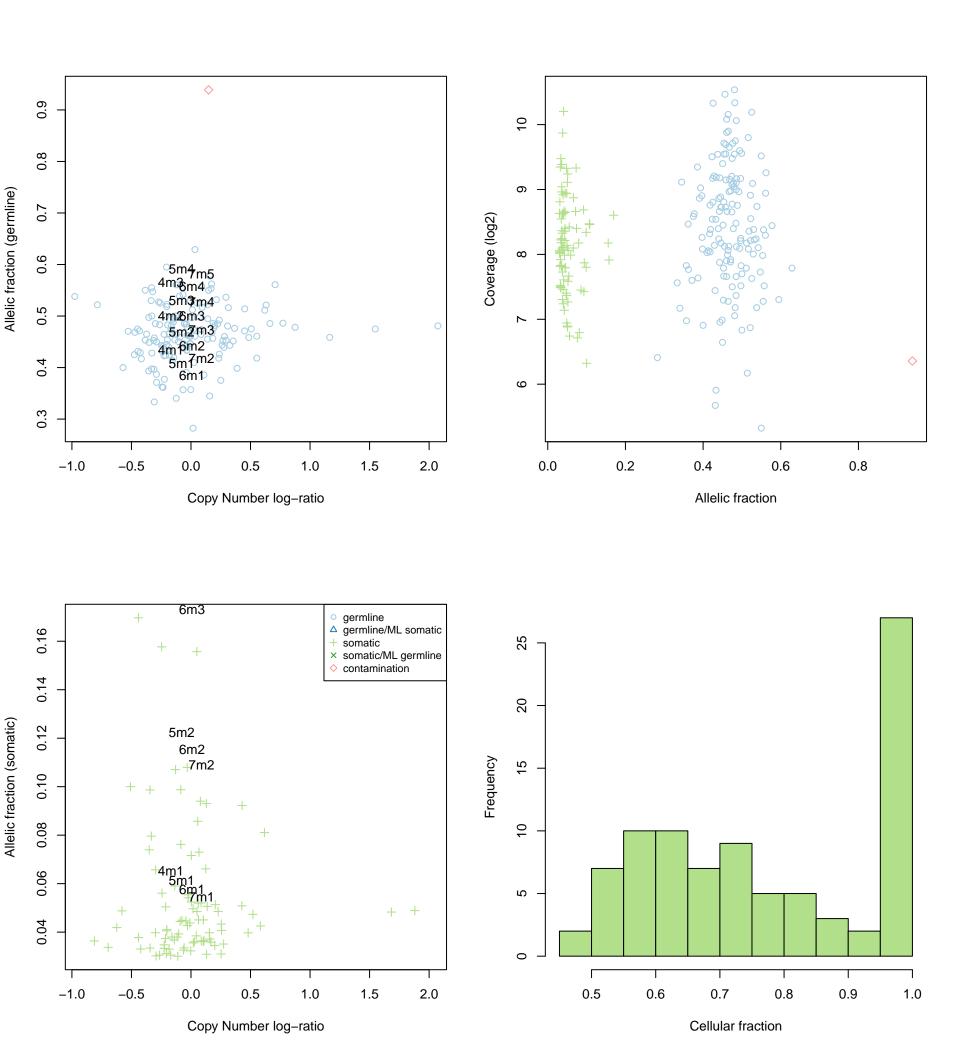




SCNA-fit log-likelihood: -15756.11

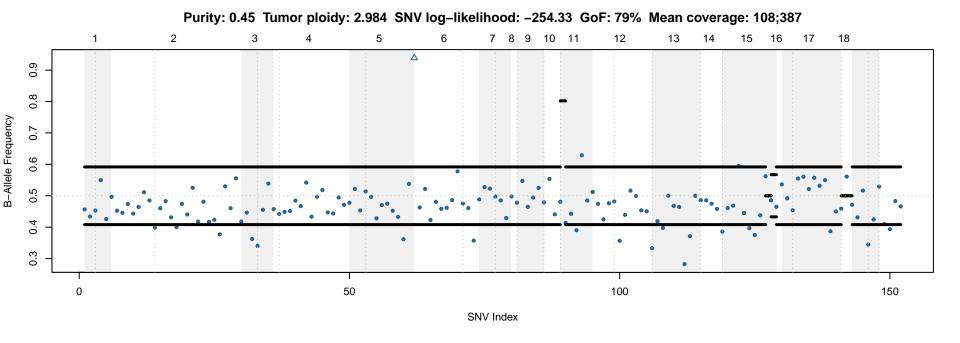




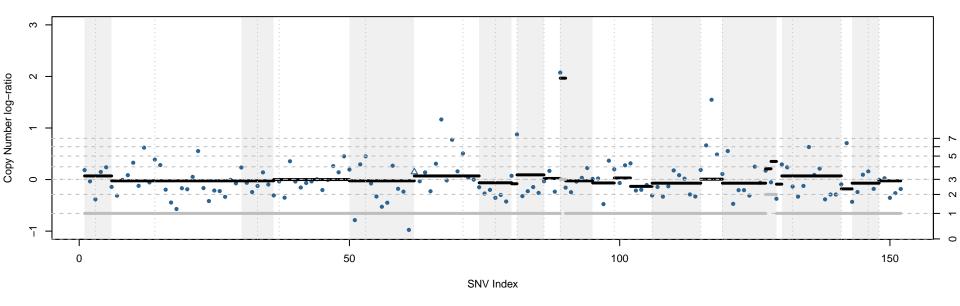


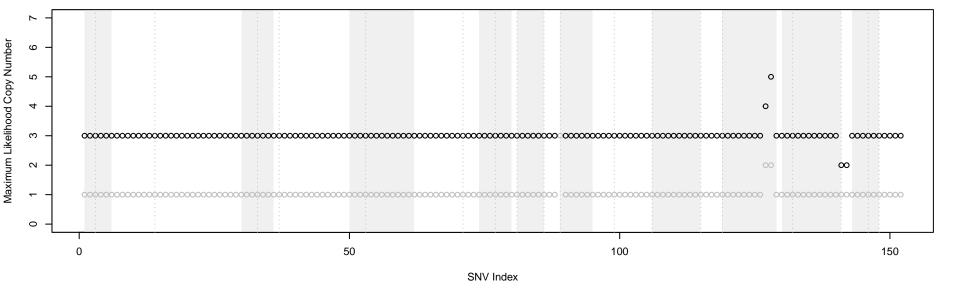
Purity: 0.45 Tumor ploidy: 2.984 2 0 3 6 7 0.30 0.25 0.20 Fraction Genome 0.15 0.10 0.05 0.00 -1 0 2 1

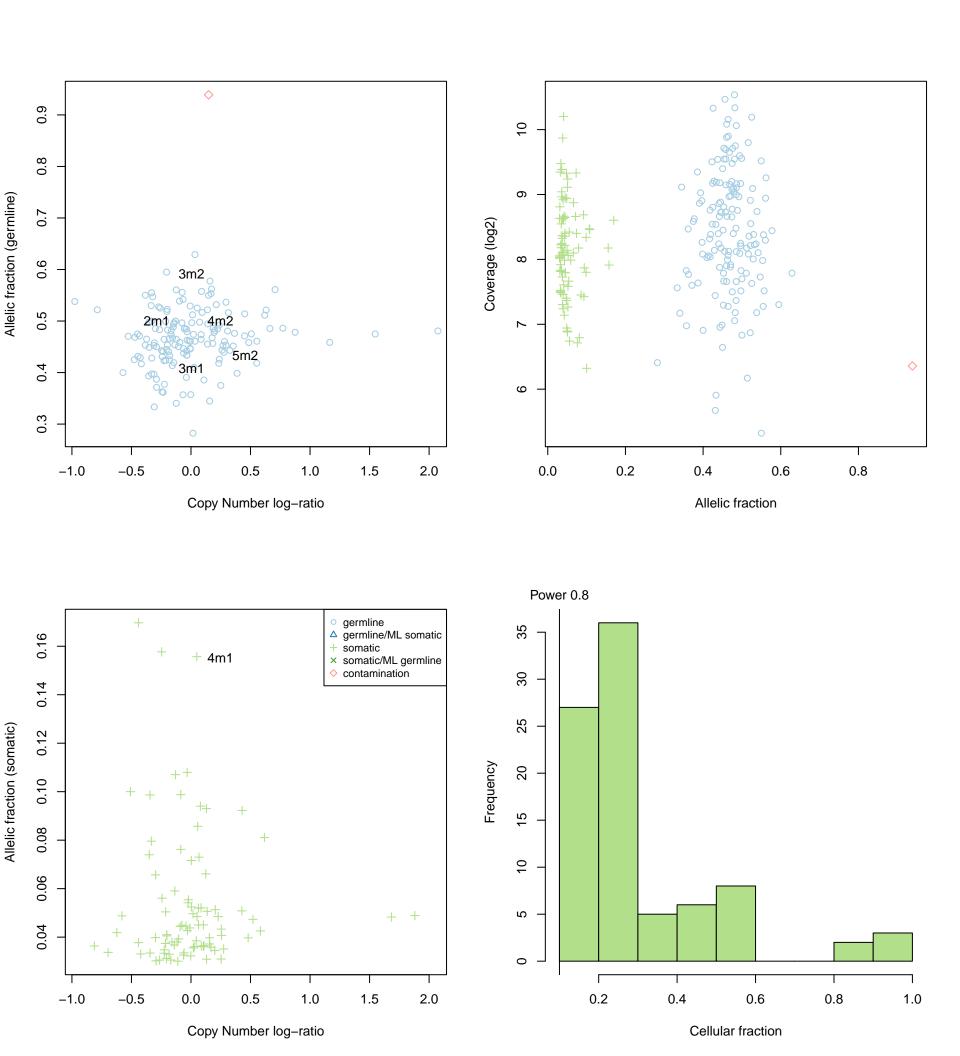
log2 ratio



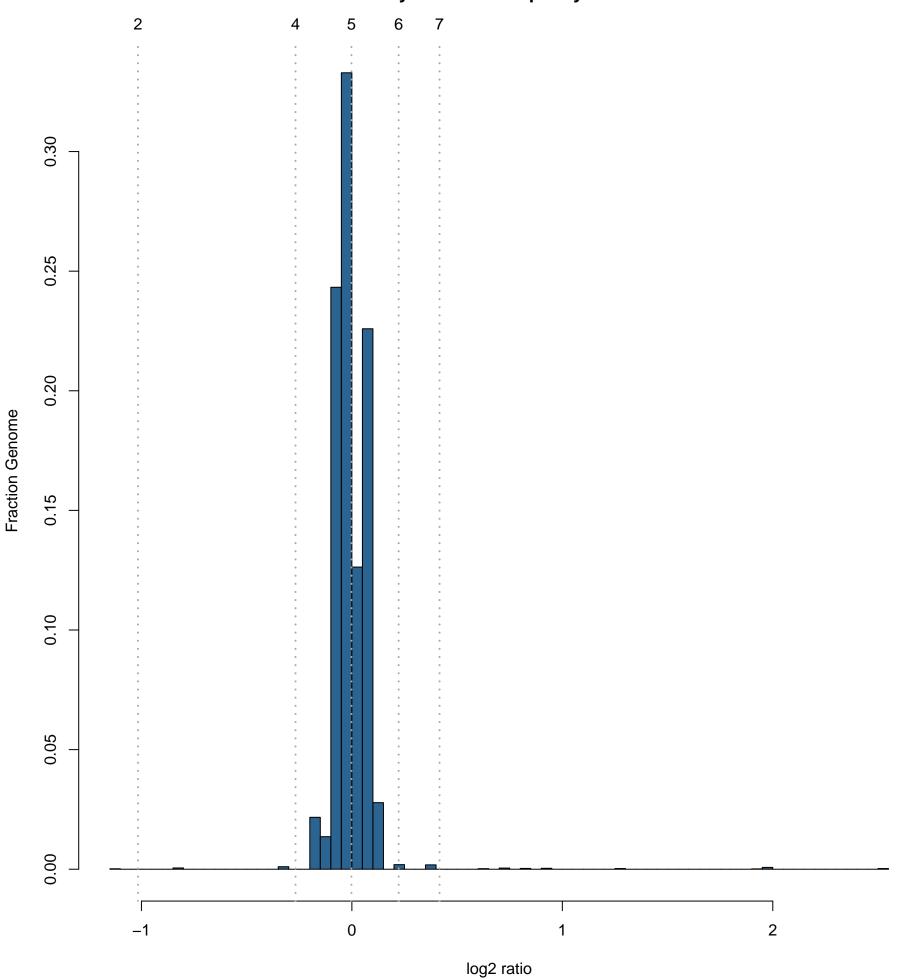
SCNA-fit log-likelihood: -15796

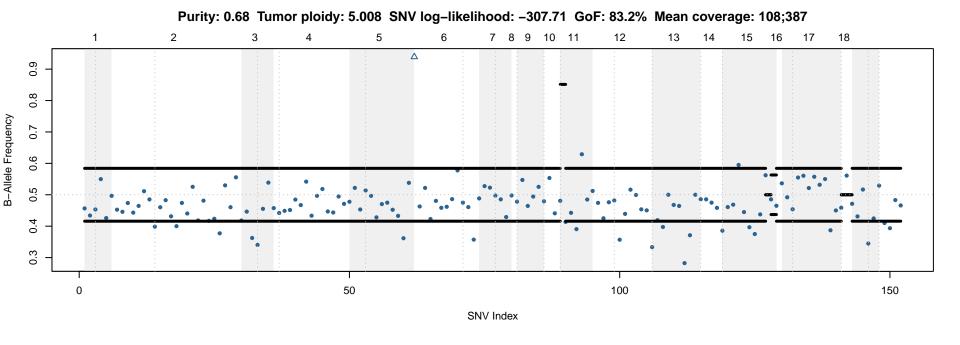




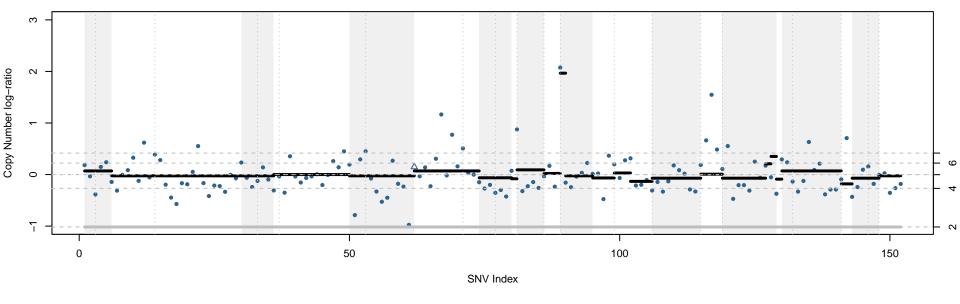


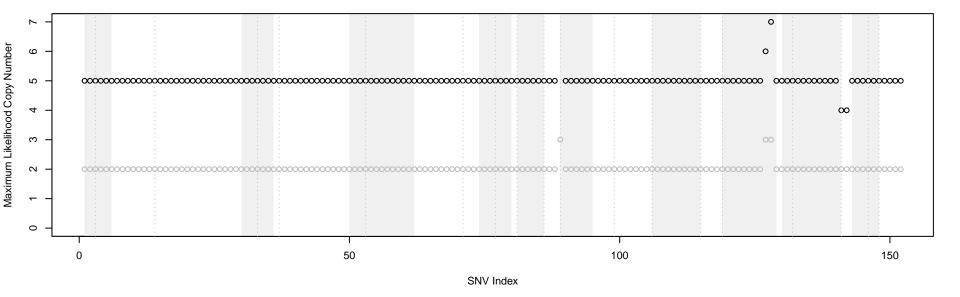
Purity: 0.68 Tumor ploidy: 5.008

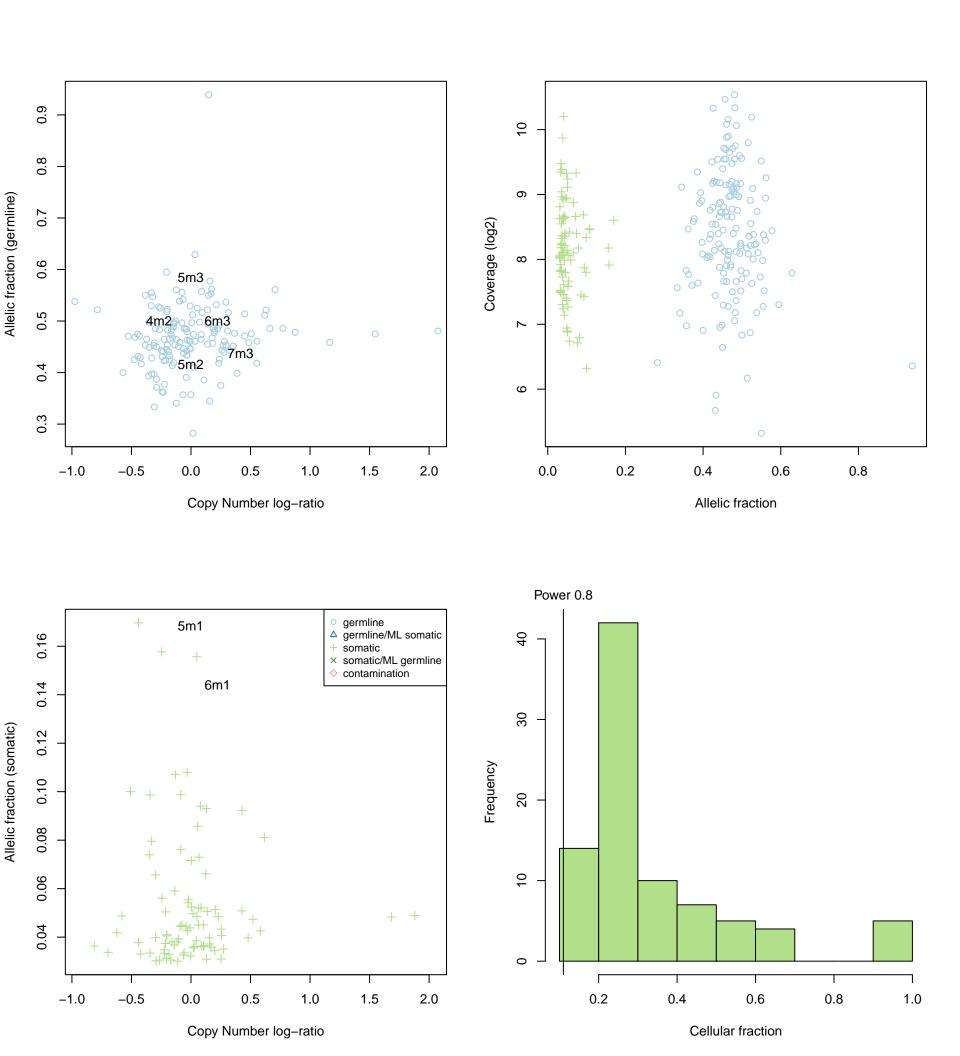




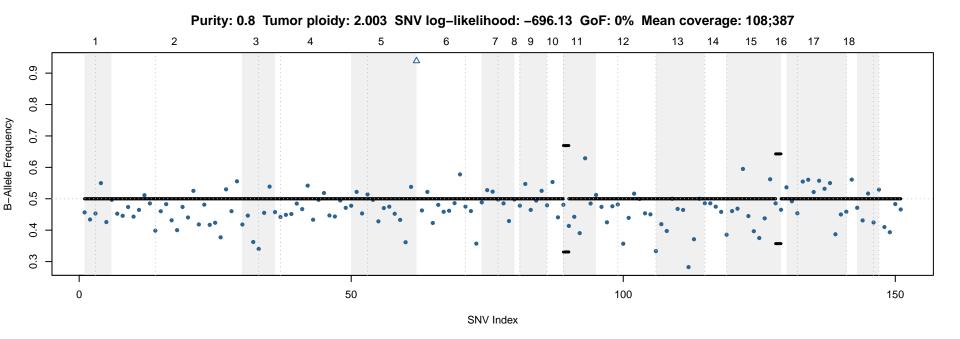
SCNA-fit log-likelihood: -15805.93



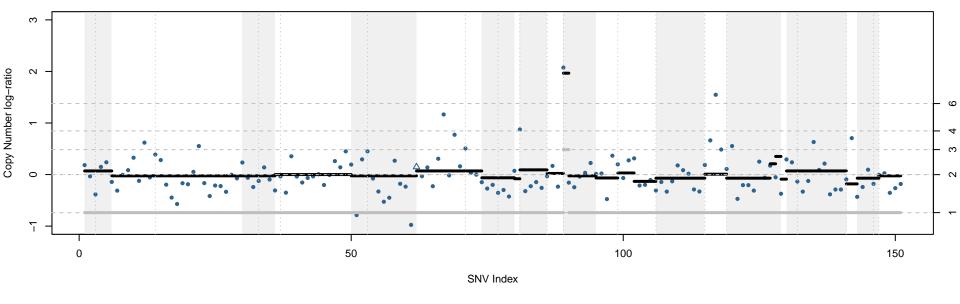


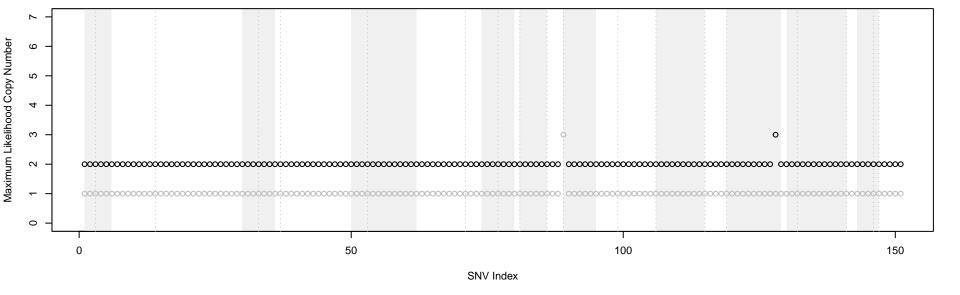


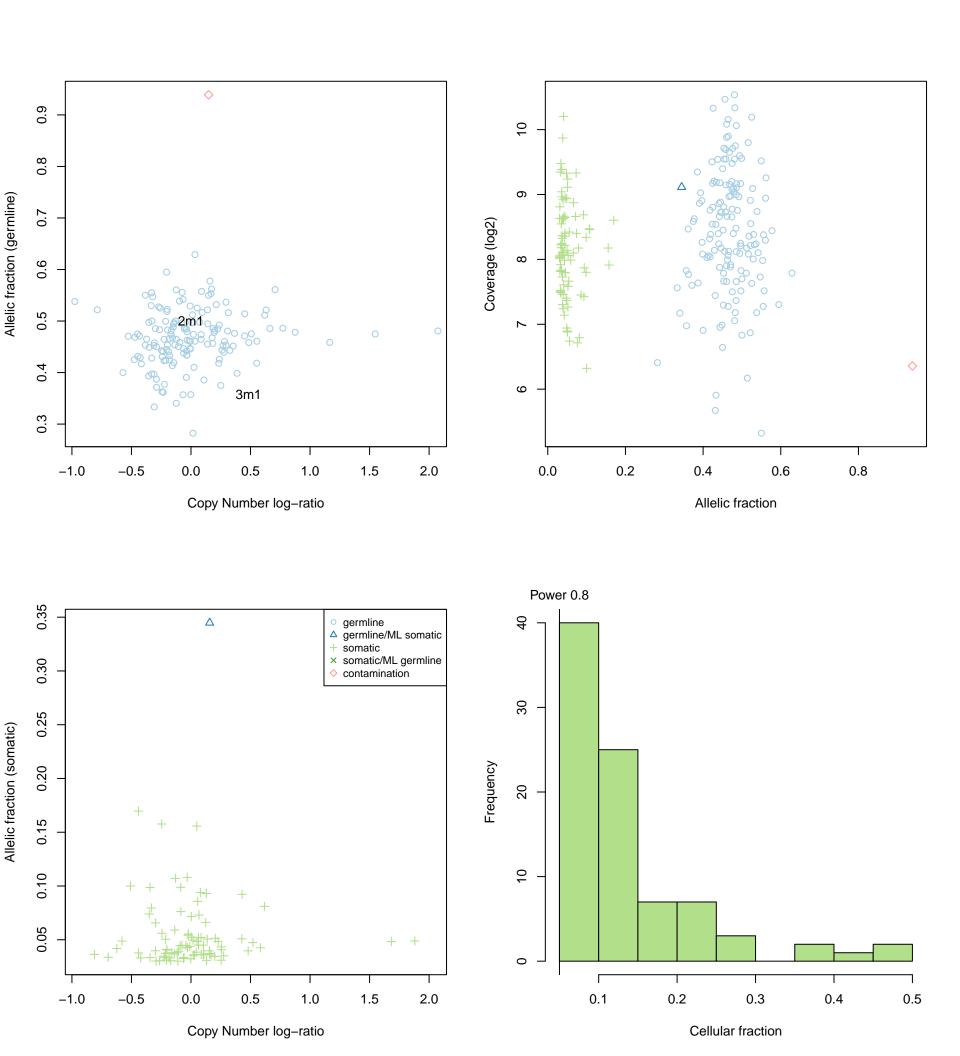
Purity: 0.8 Tumor ploidy: 2.003 3 2 0.30 0.25 0.20 Fraction Genome 0.10 0.05 0.00 -1 0 1 2 log2 ratio

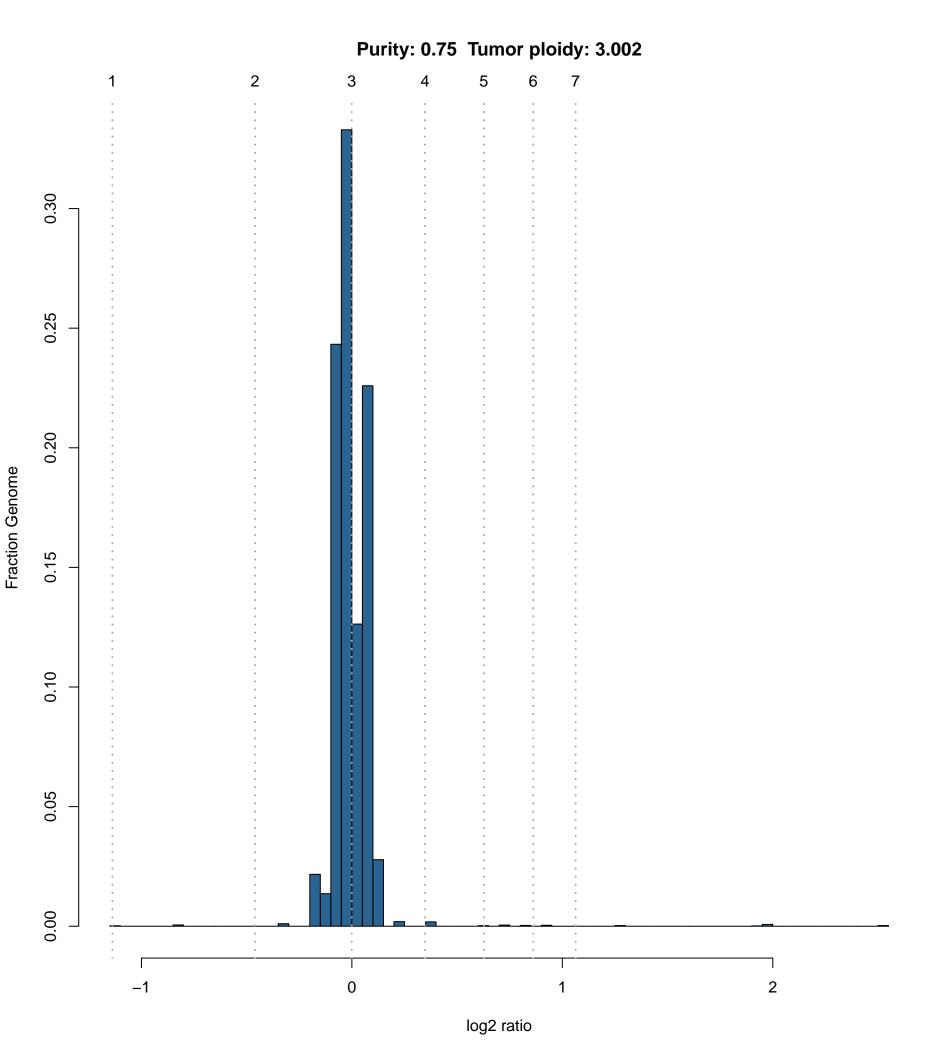


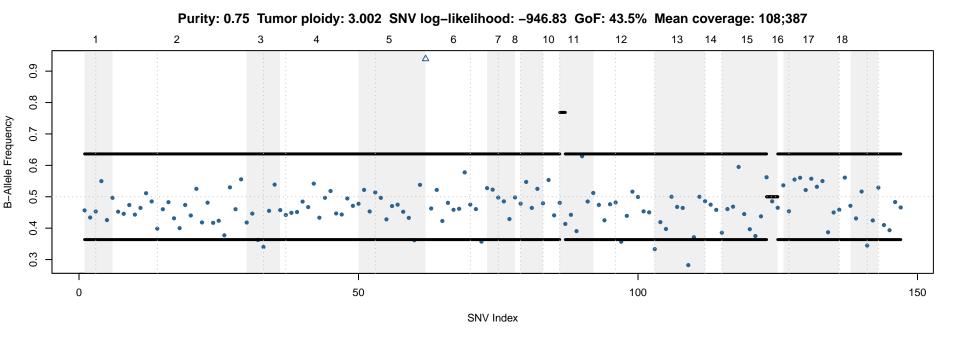
SCNA-fit log-likelihood: -15818.04



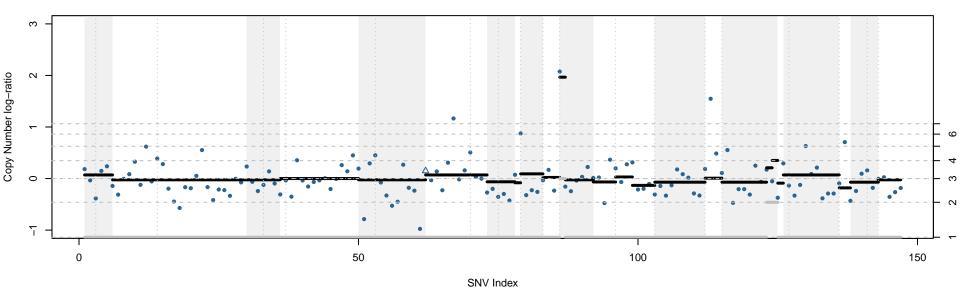


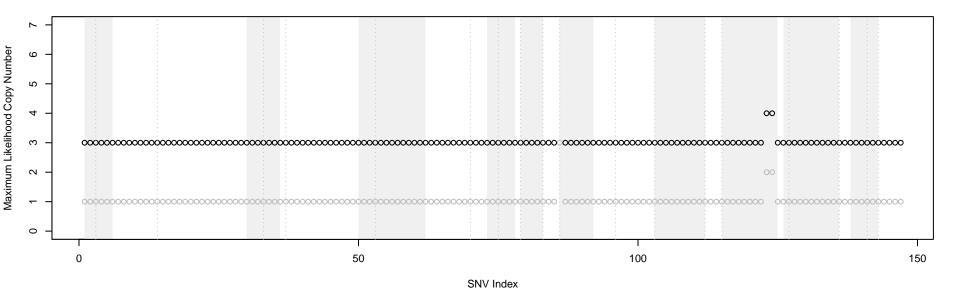


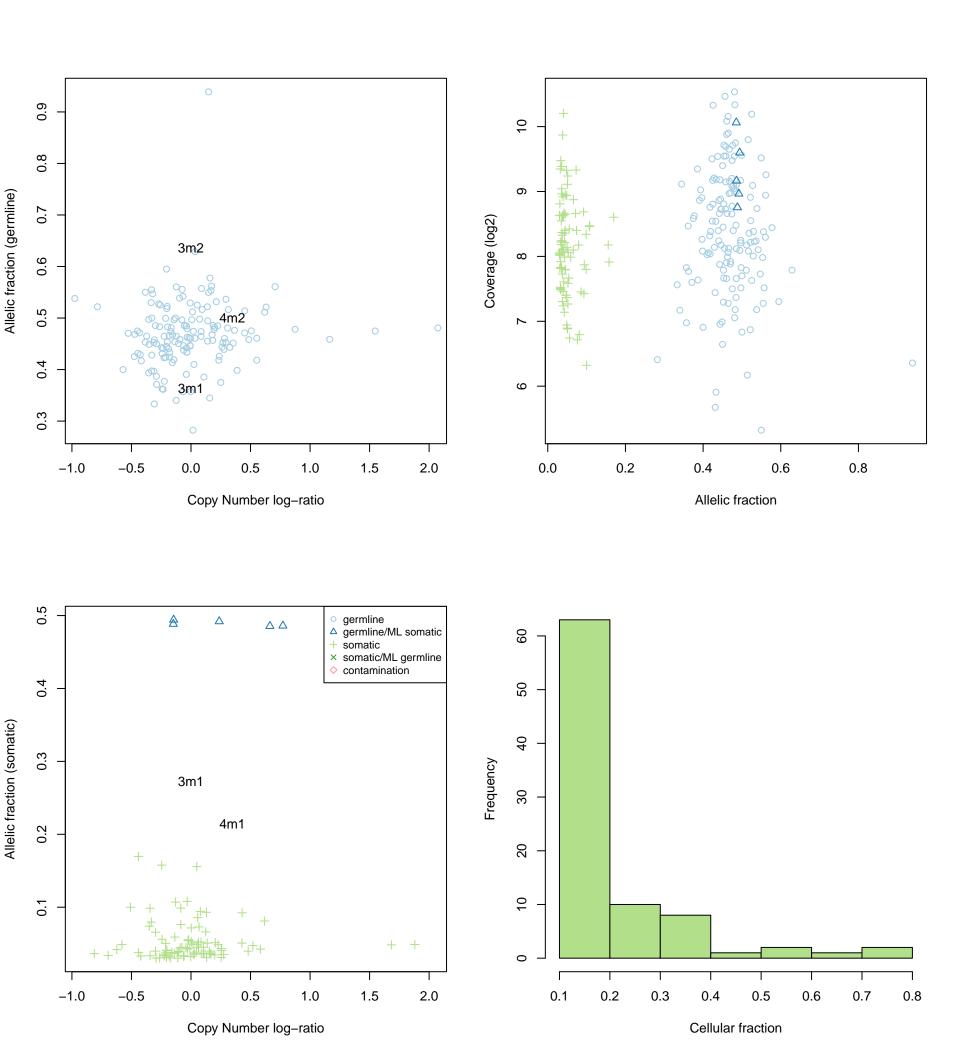


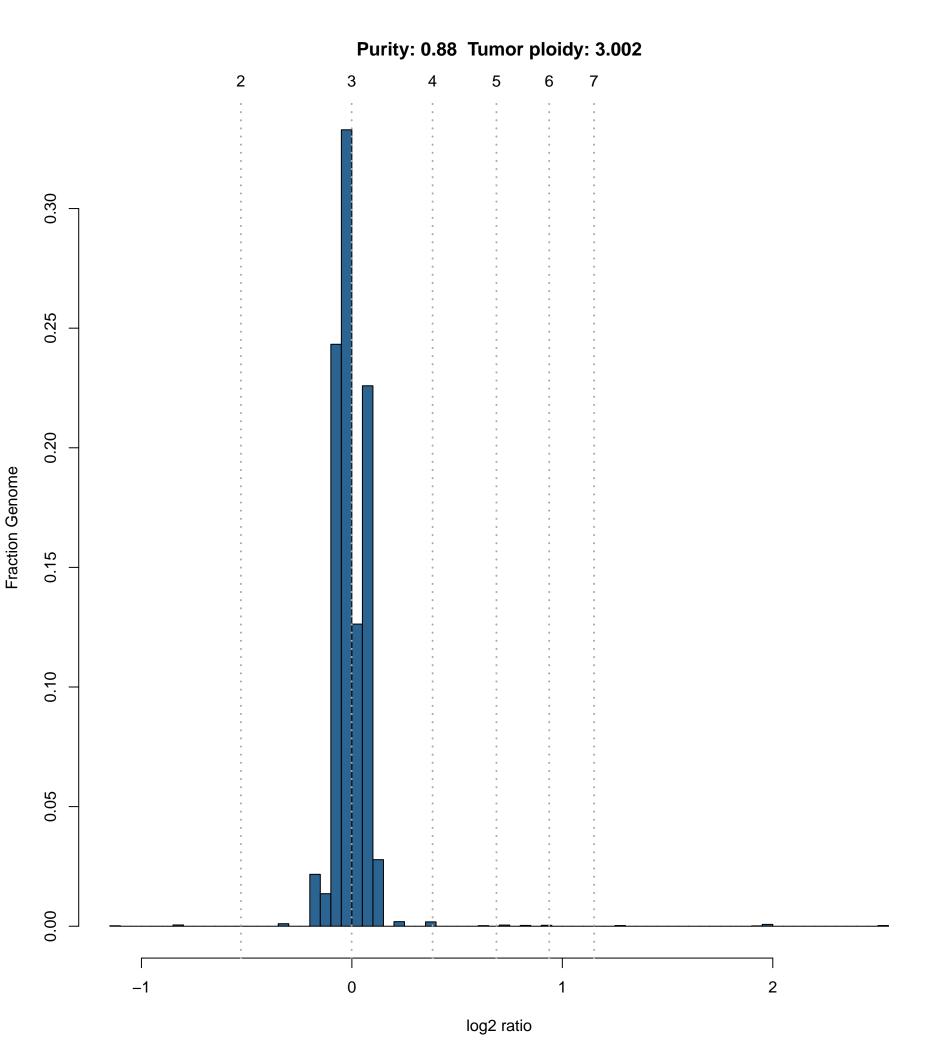


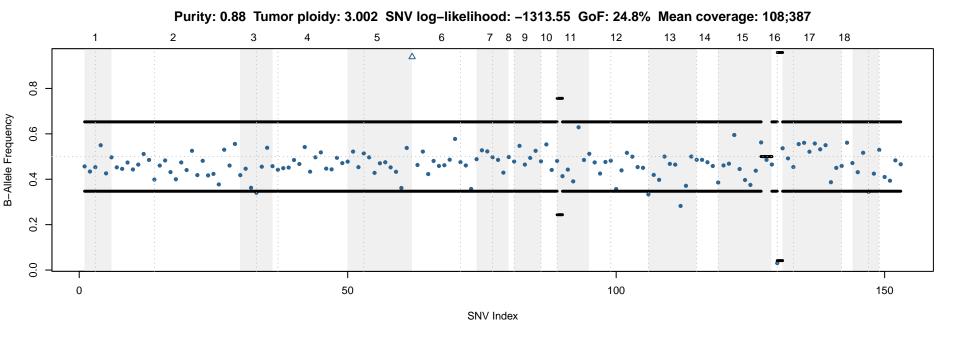
SCNA-fit log-likelihood: -15811.35











SCNA-fit log-likelihood: -15813.62

