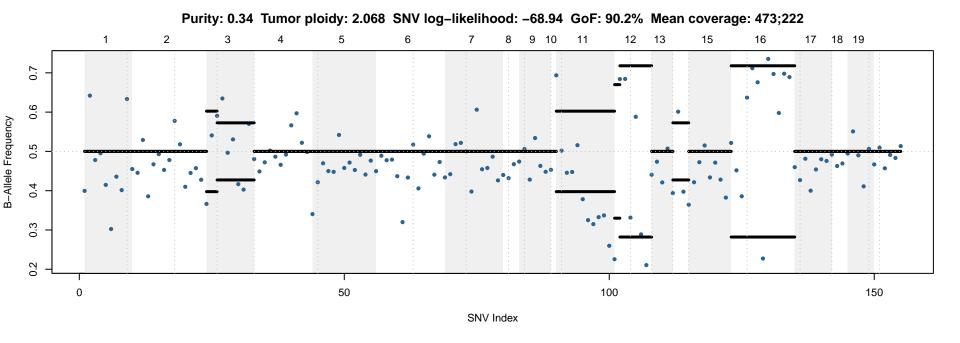
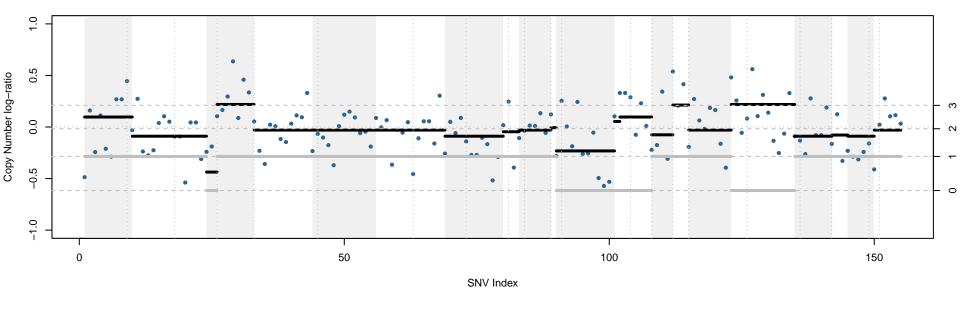
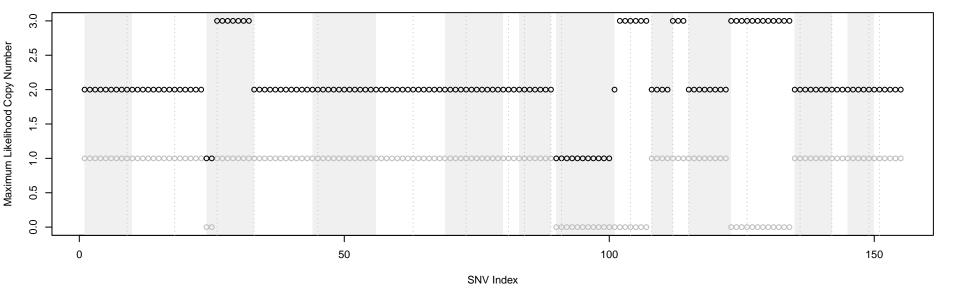
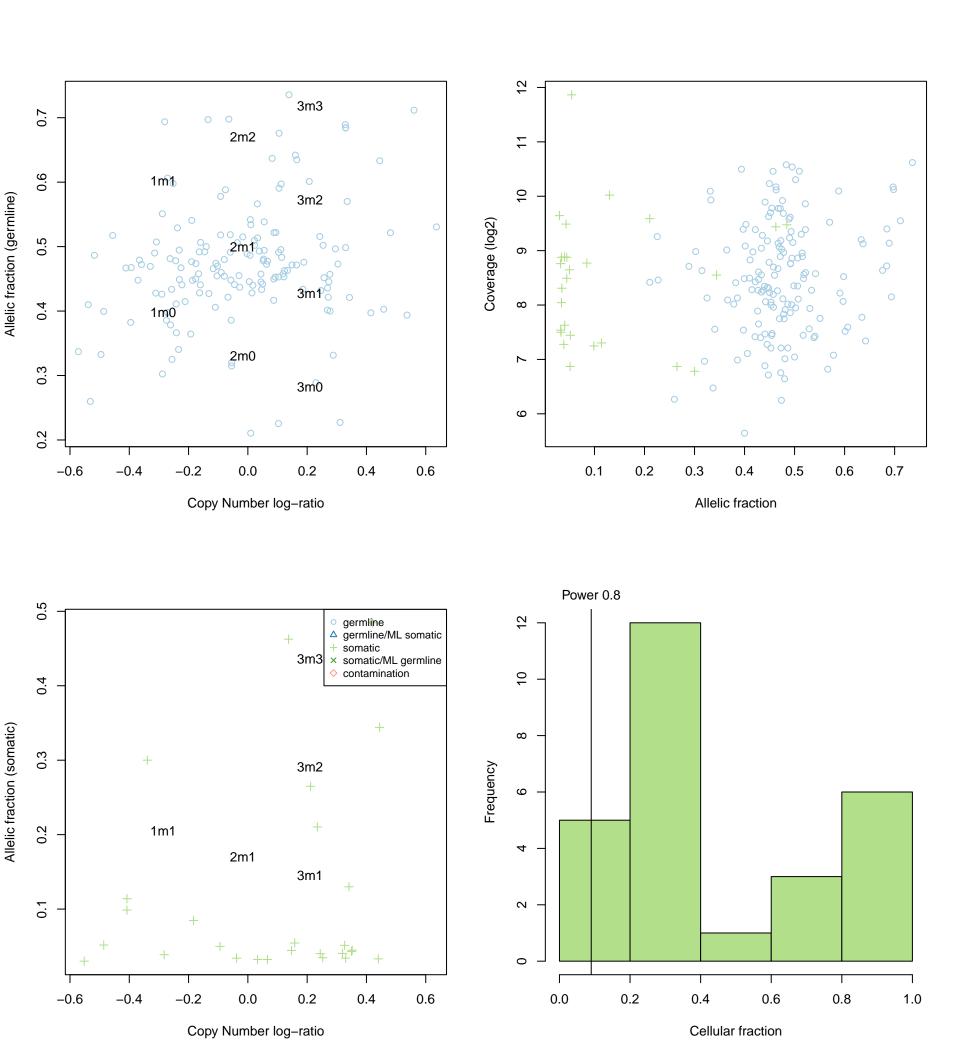
Purity: 0.34 Tumor ploidy: 2.068 3 0.20 Fraction Genome 0.10 0.05 0.00 -0.2 -0.4 0.0 0.2 log2 ratio



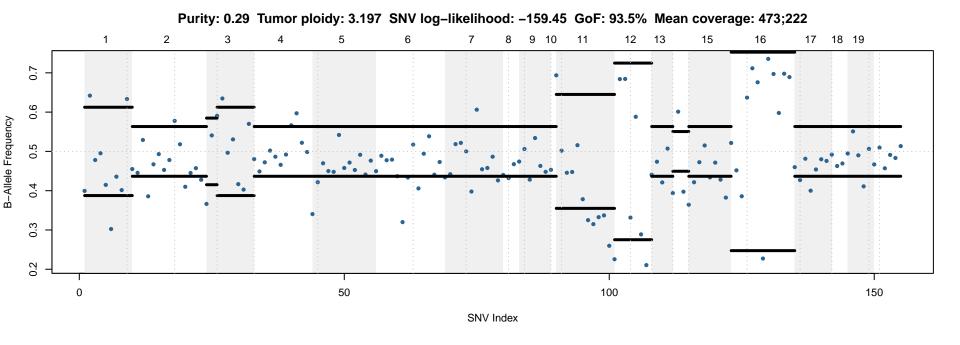
SCNA-fit log-likelihood: -15159.46



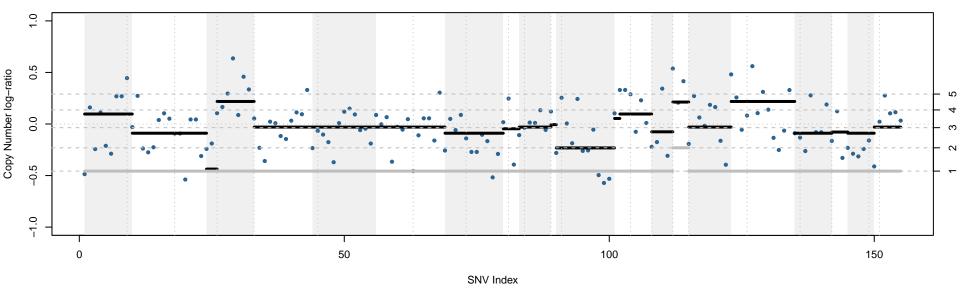


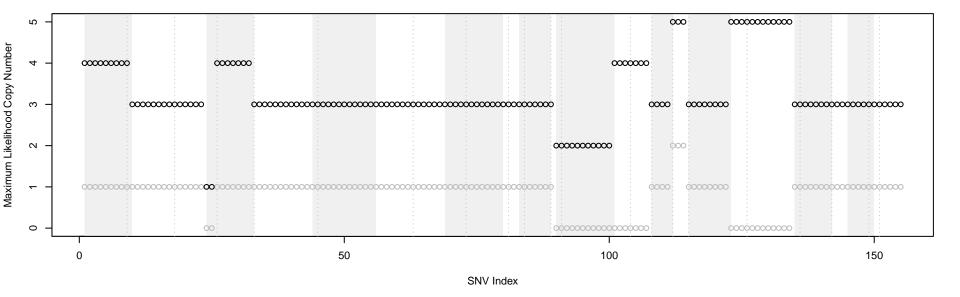


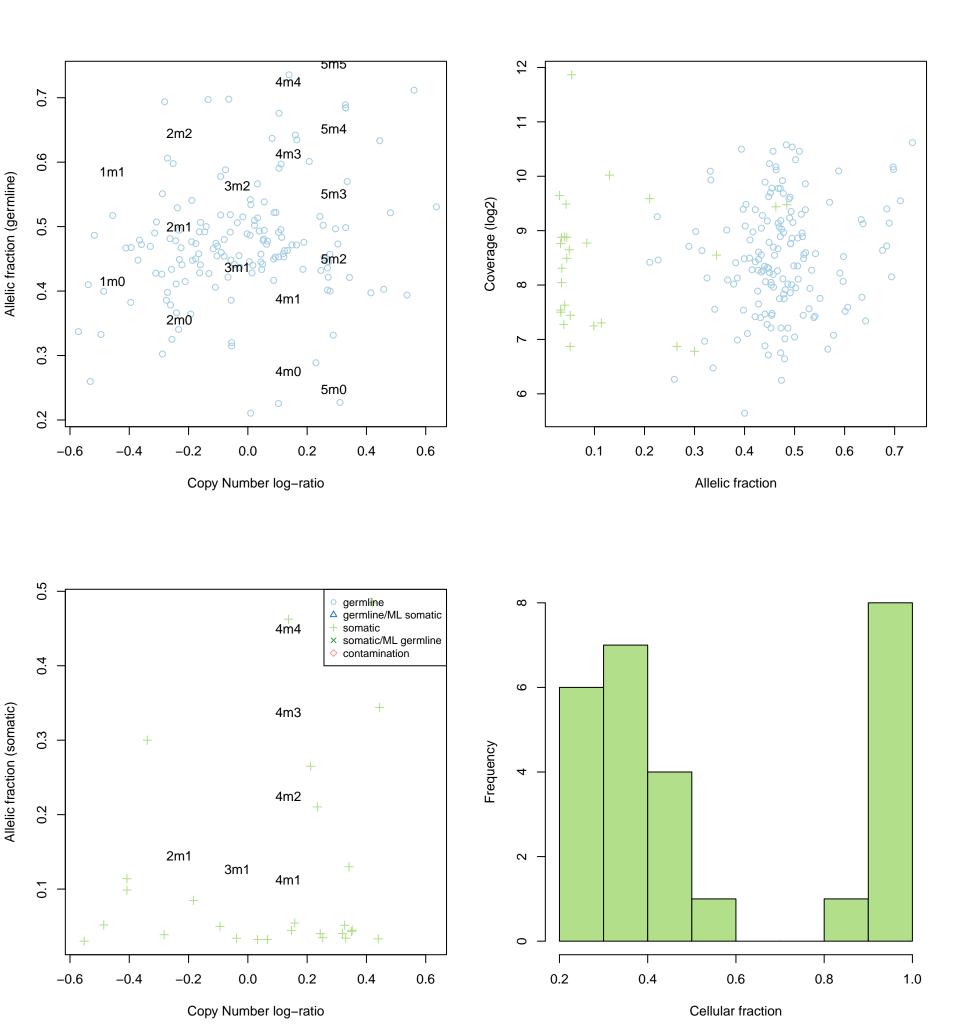
Purity: 0.29 Tumor ploidy: 3.197 3 5 0.20 Fraction Genome 0.10 0.05 0.00 -0.2 -0.4 0.0 0.2 log2 ratio



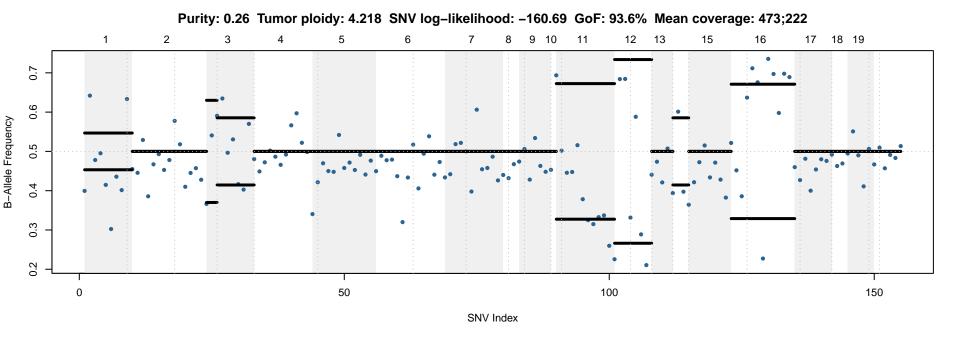
SCNA-fit log-likelihood: -15084.34



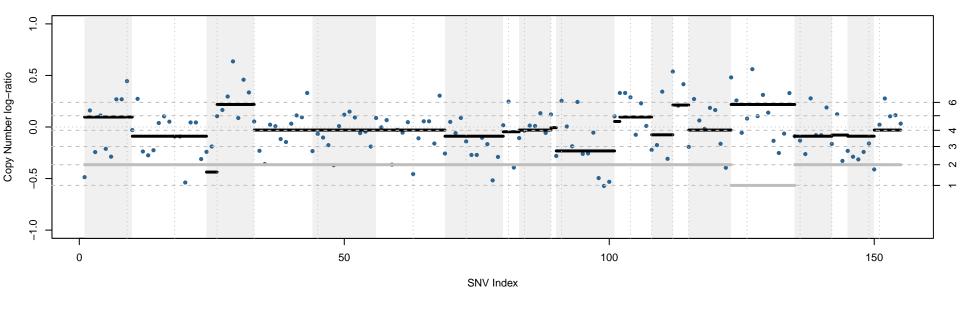


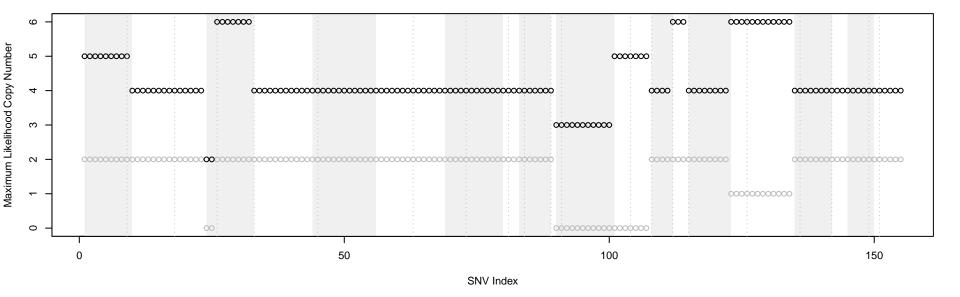


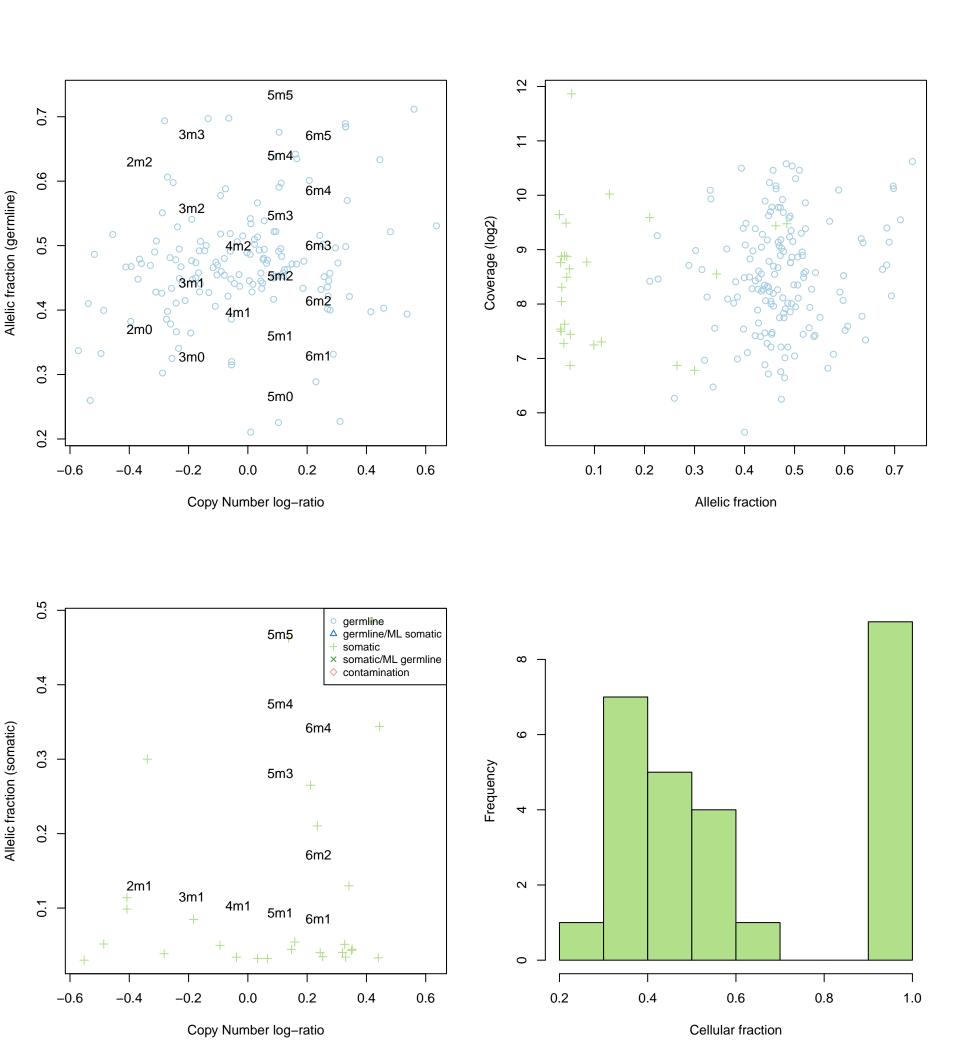
Purity: 0.26 Tumor ploidy: 4.218 2 3 5 6 0.25 0.20 Fraction Genome 0.10 0.05 0.00 -0.2 -0.4 0.0 0.2 log2 ratio



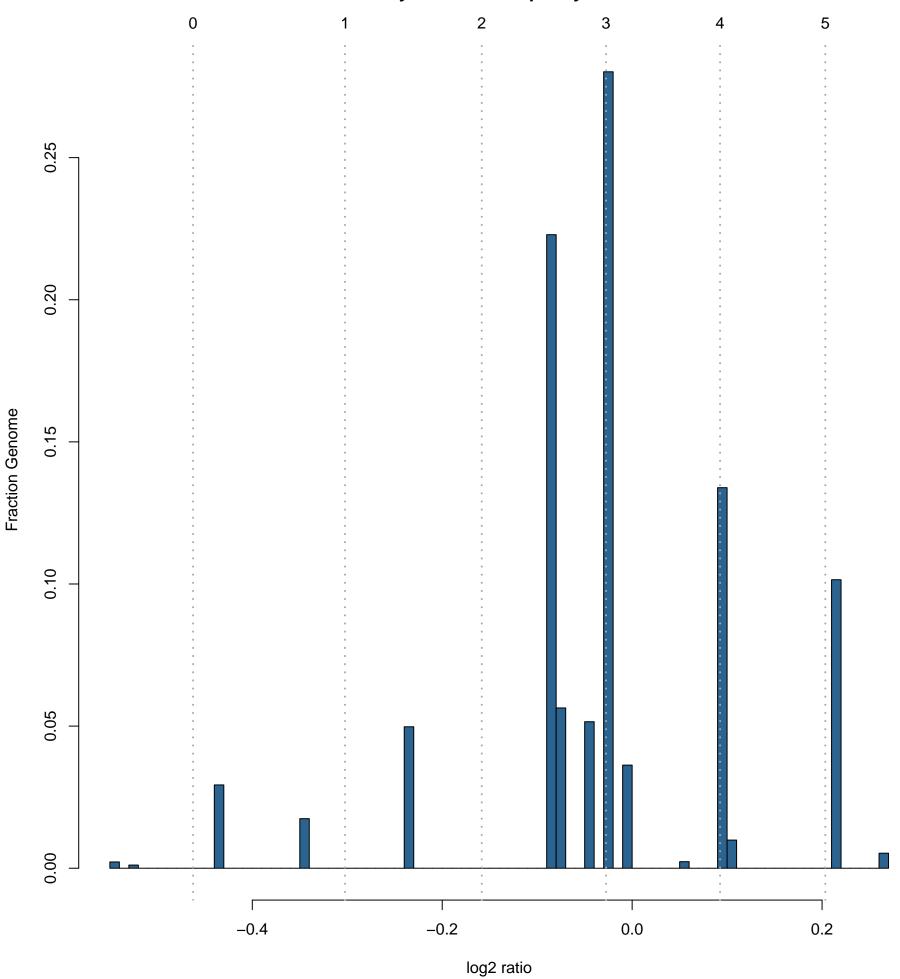
SCNA-fit log-likelihood: -15065.96

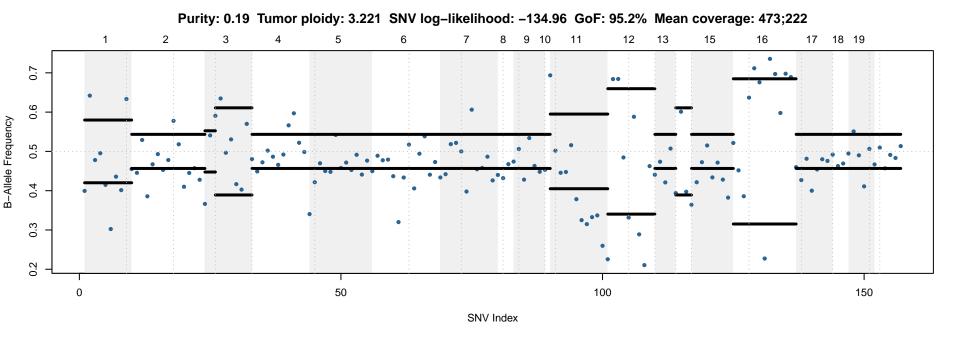




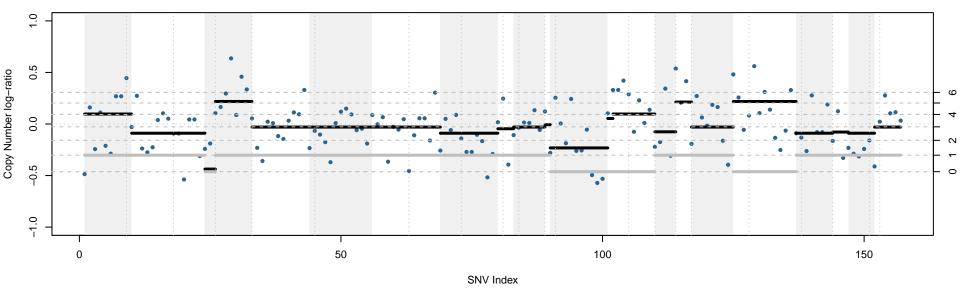


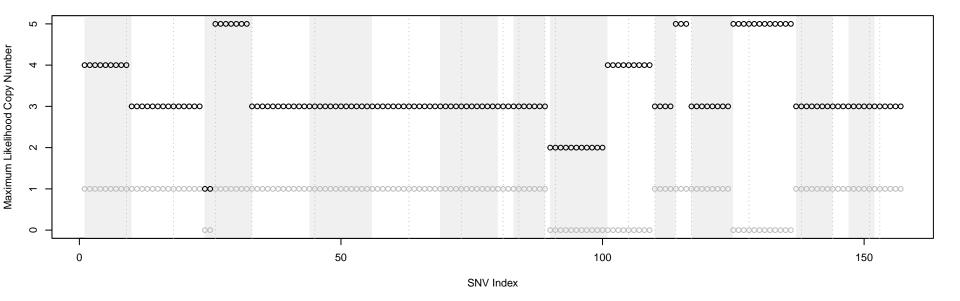
Purity: 0.19 Tumor ploidy: 3.221

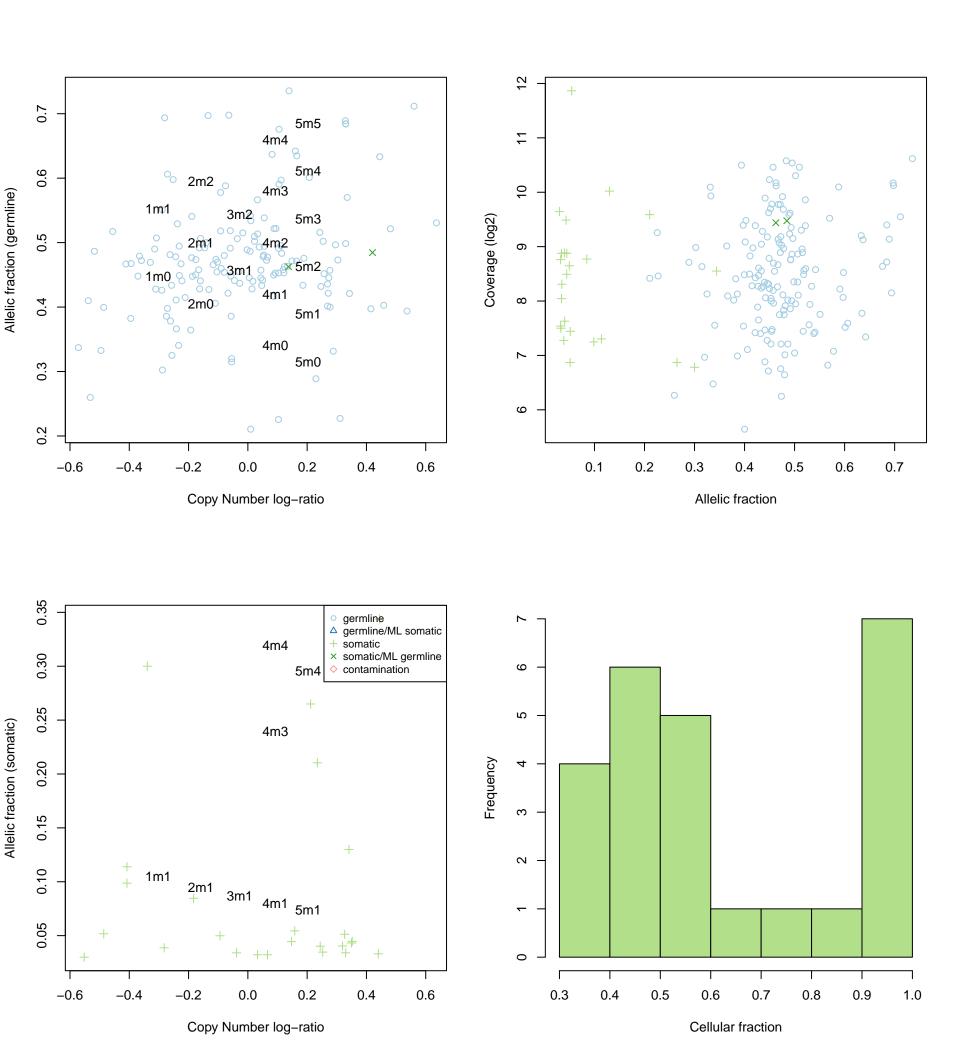




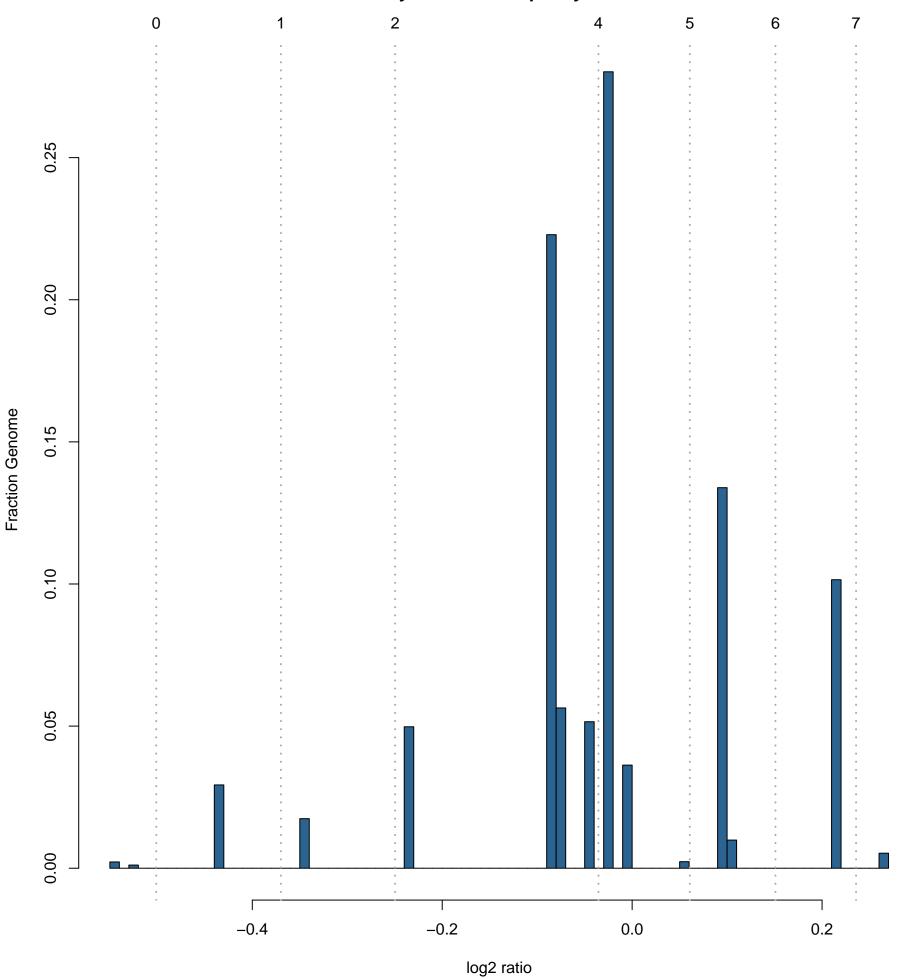
SCNA-fit log-likelihood: -15097.8

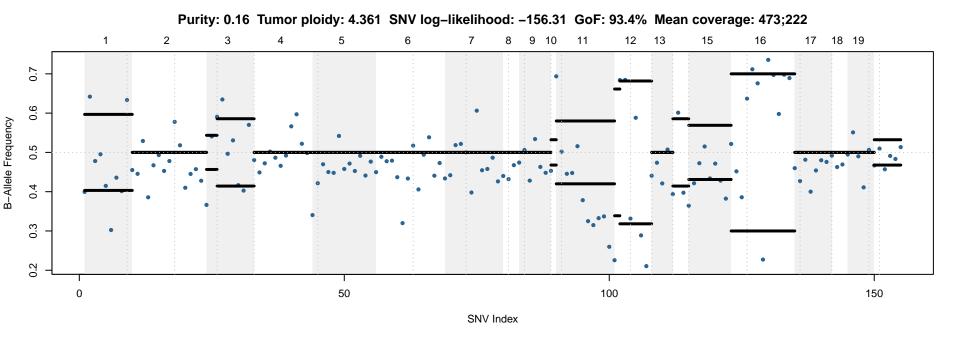




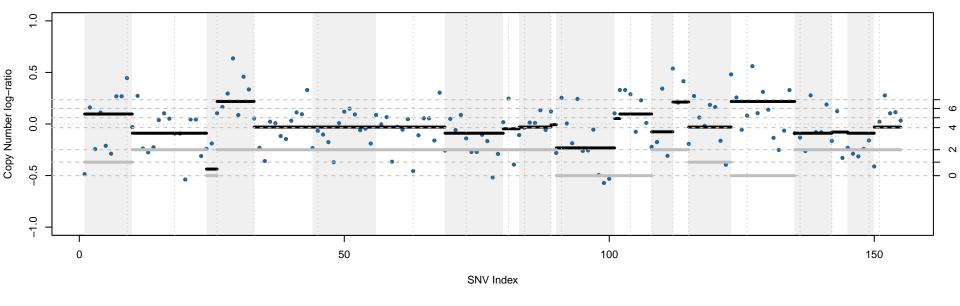


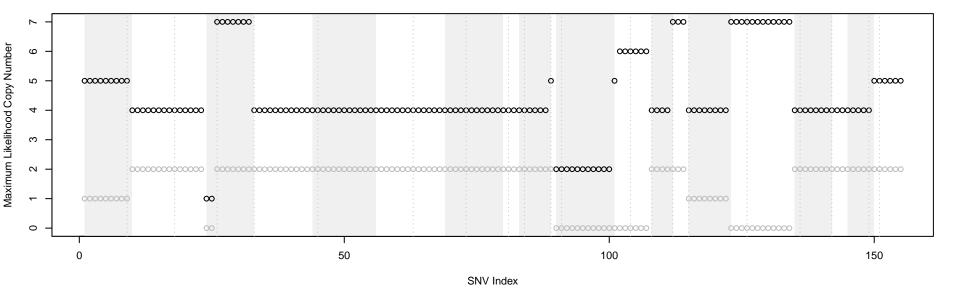
Purity: 0.16 Tumor ploidy: 4.361

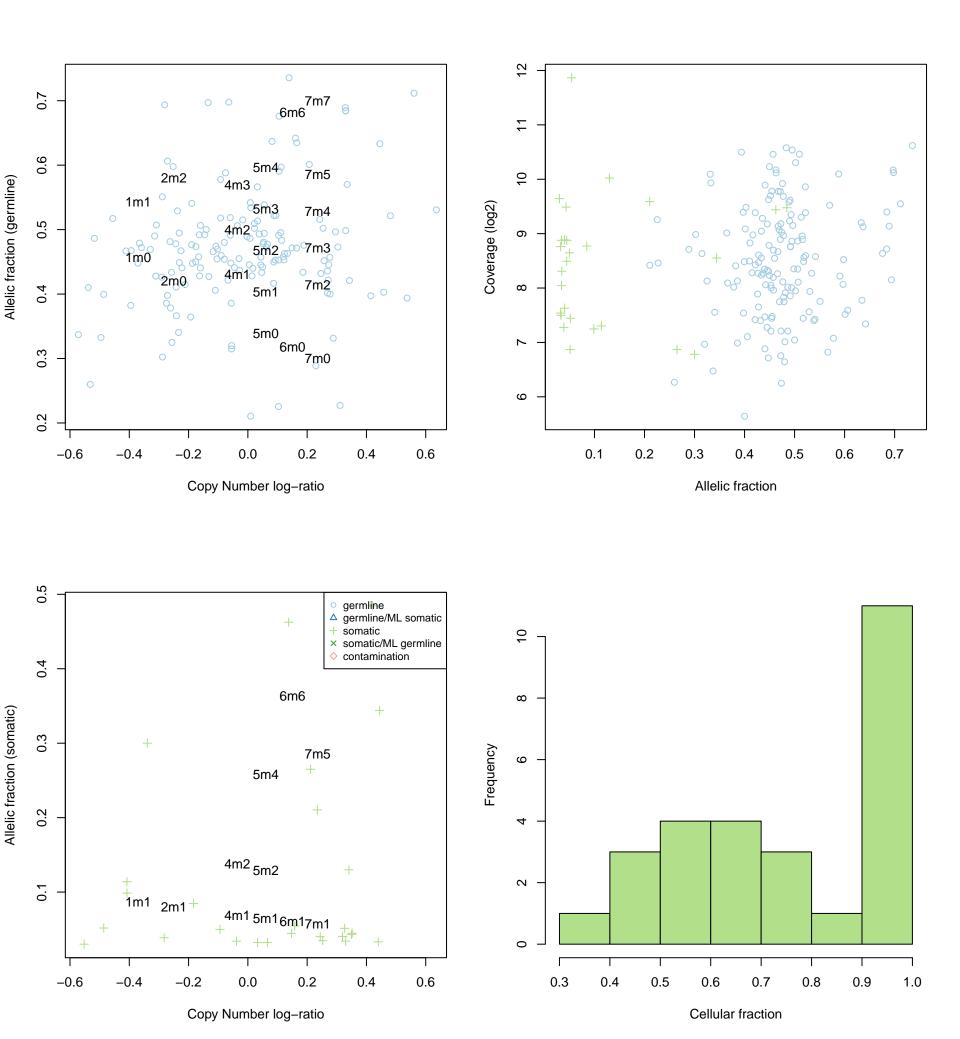




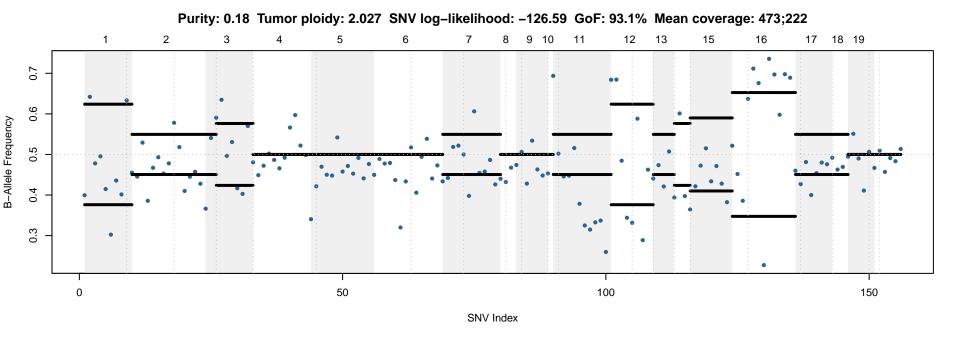
SCNA-fit log-likelihood: -15055.62



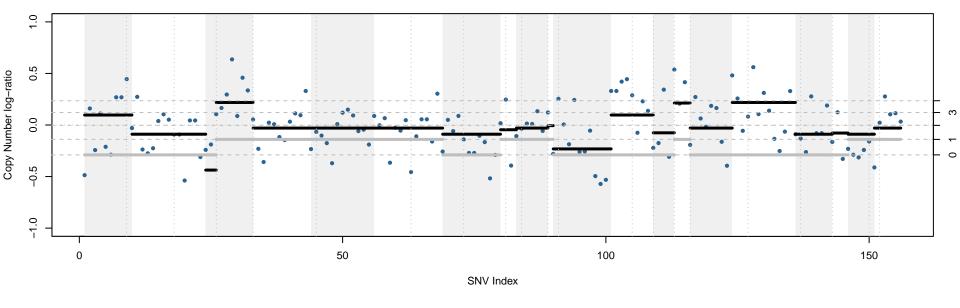


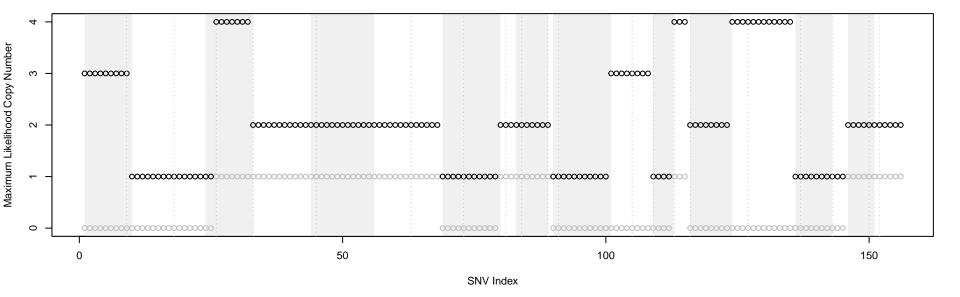


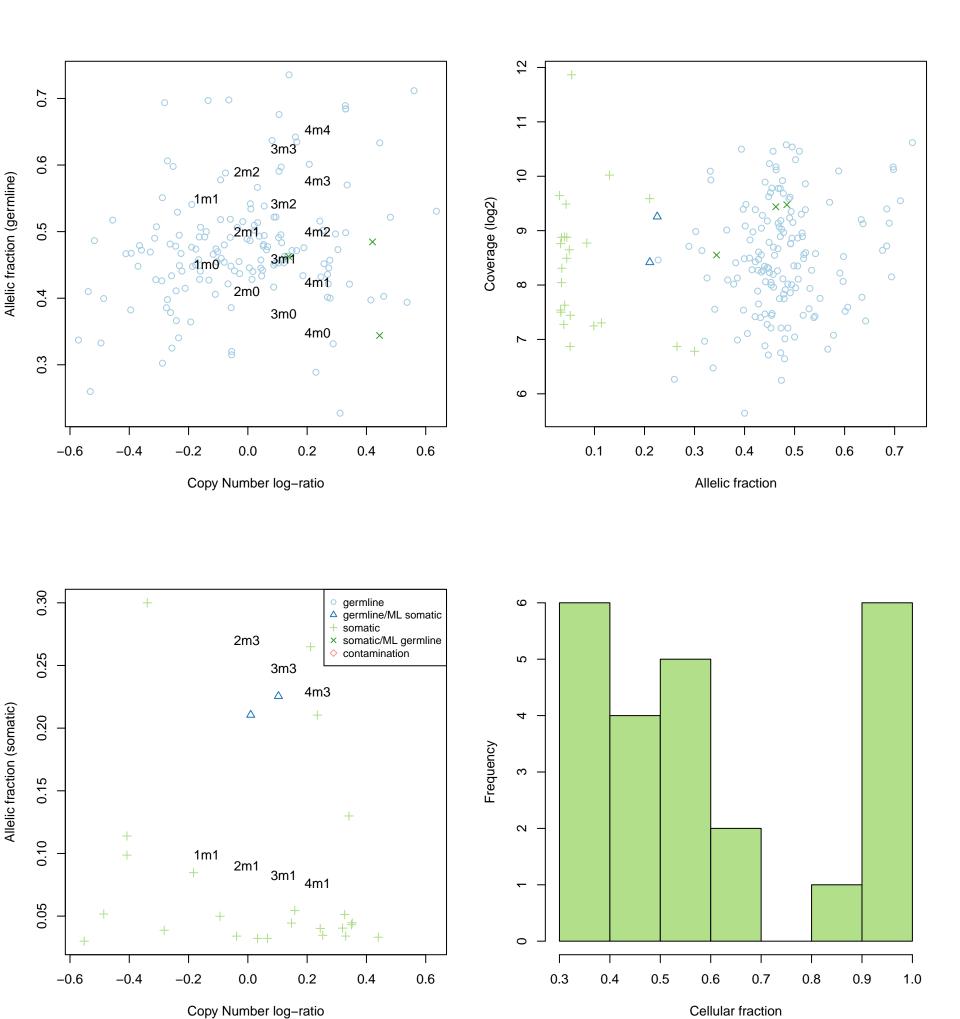
Purity: 0.18 Tumor ploidy: 2.027 3 0.20 Fraction Genome 0.10 0.05 0.00 -0.2 -0.4 0.0 0.2 log2 ratio



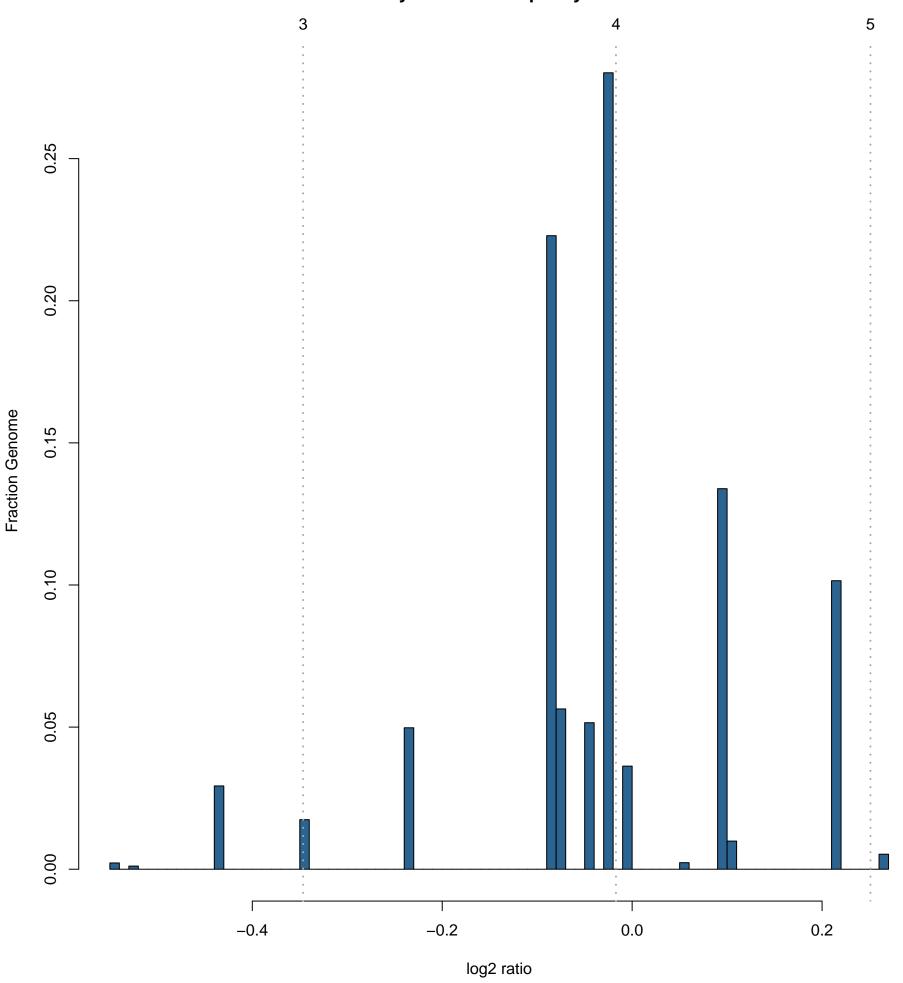
SCNA-fit log-likelihood: -15237.28

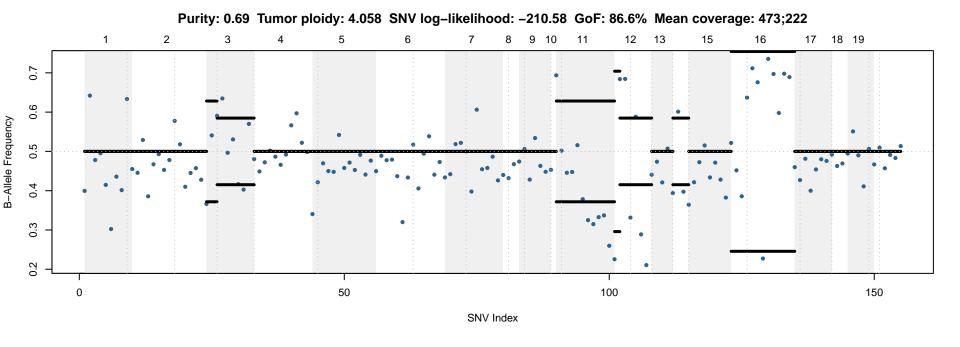




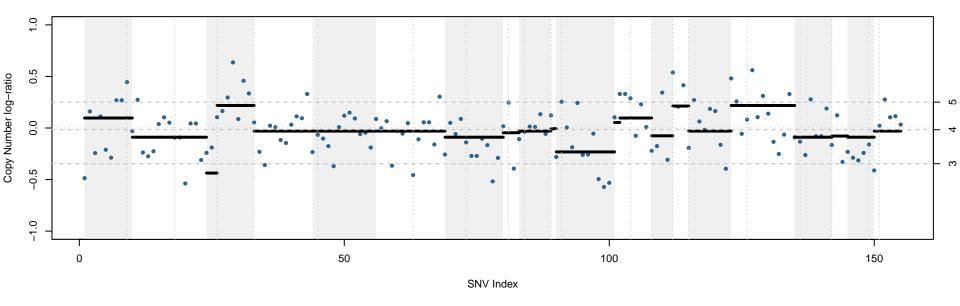


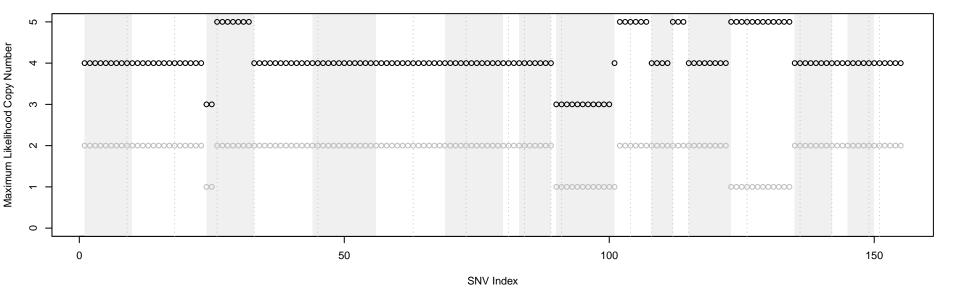
Purity: 0.69 Tumor ploidy: 4.058

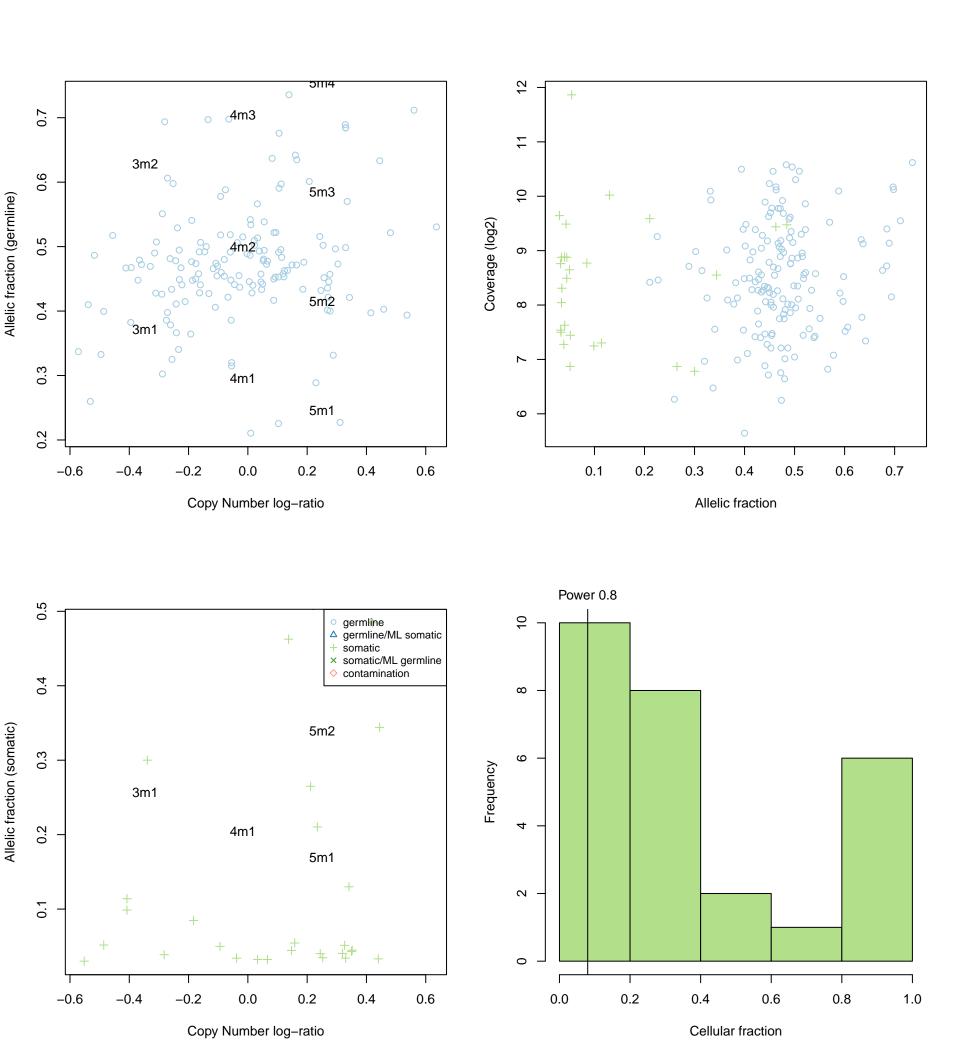




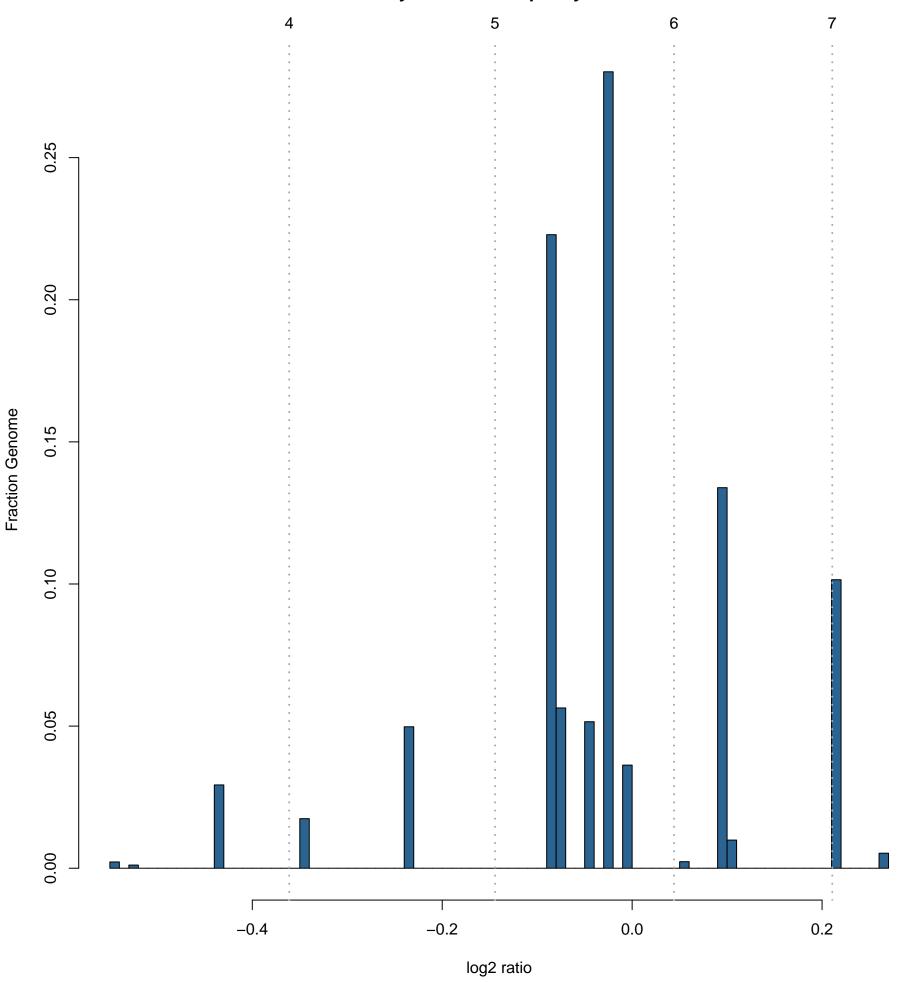
SCNA-fit log-likelihood: -15179.86

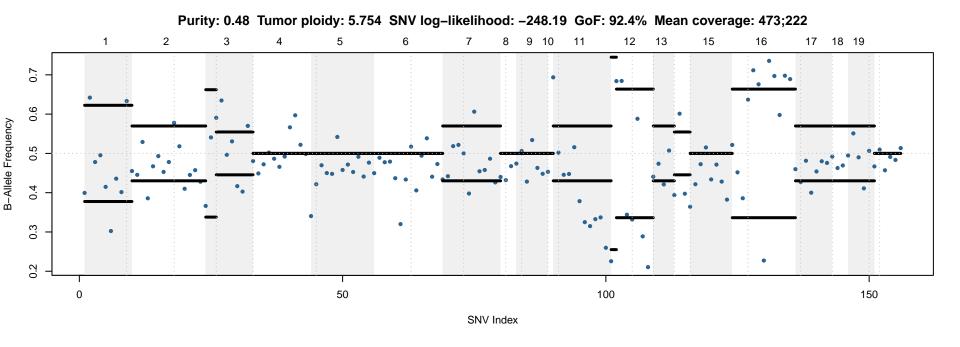




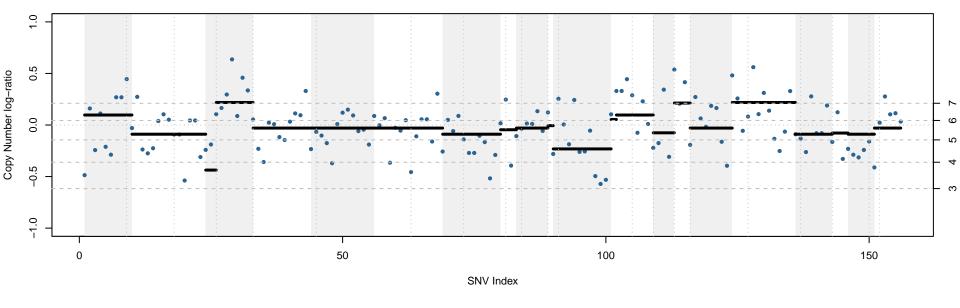


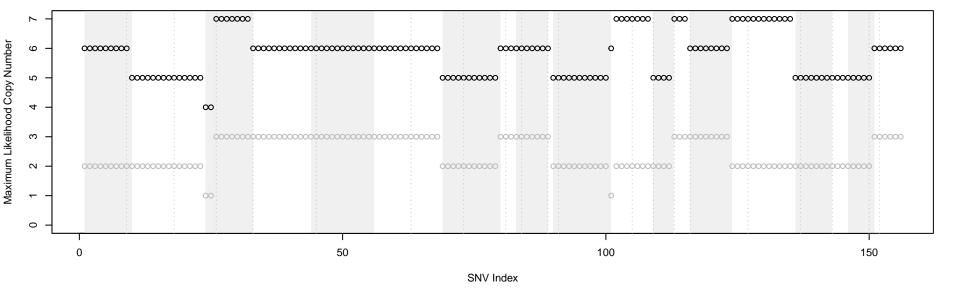
Purity: 0.48 Tumor ploidy: 5.754

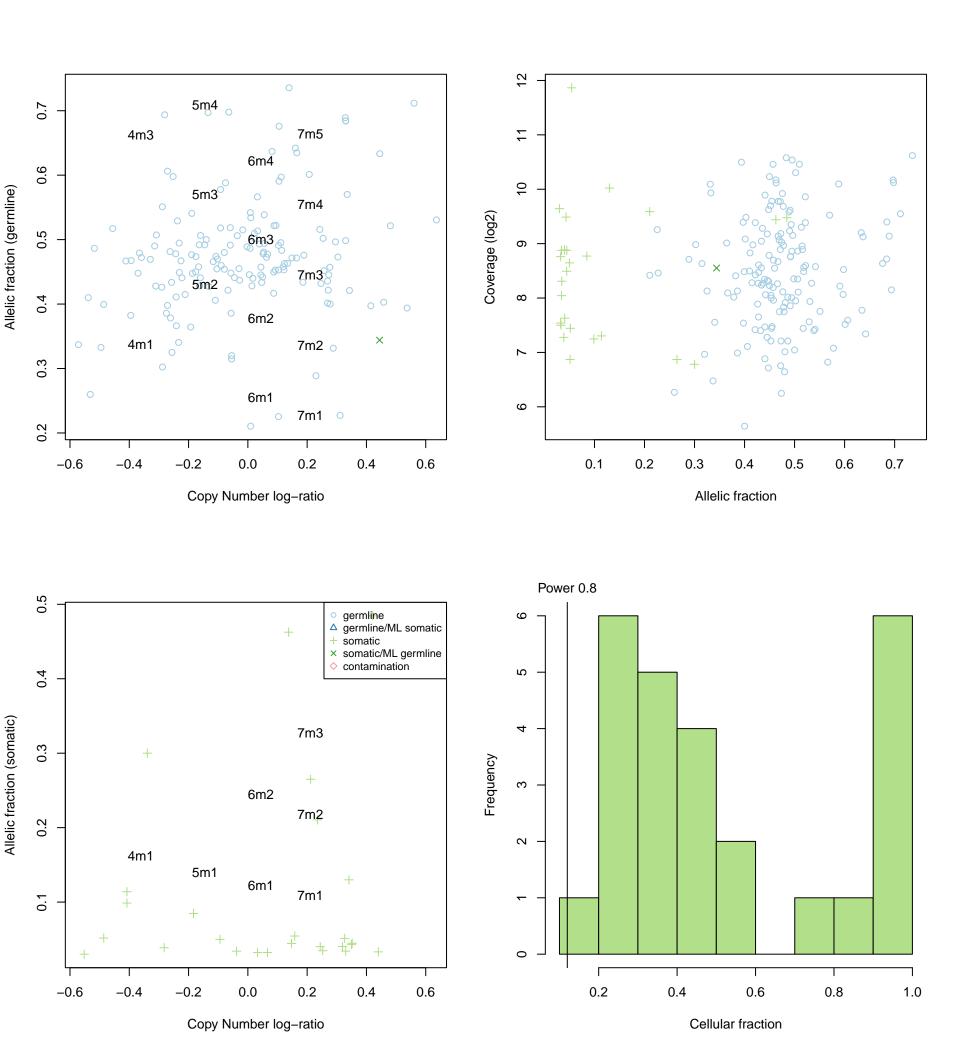




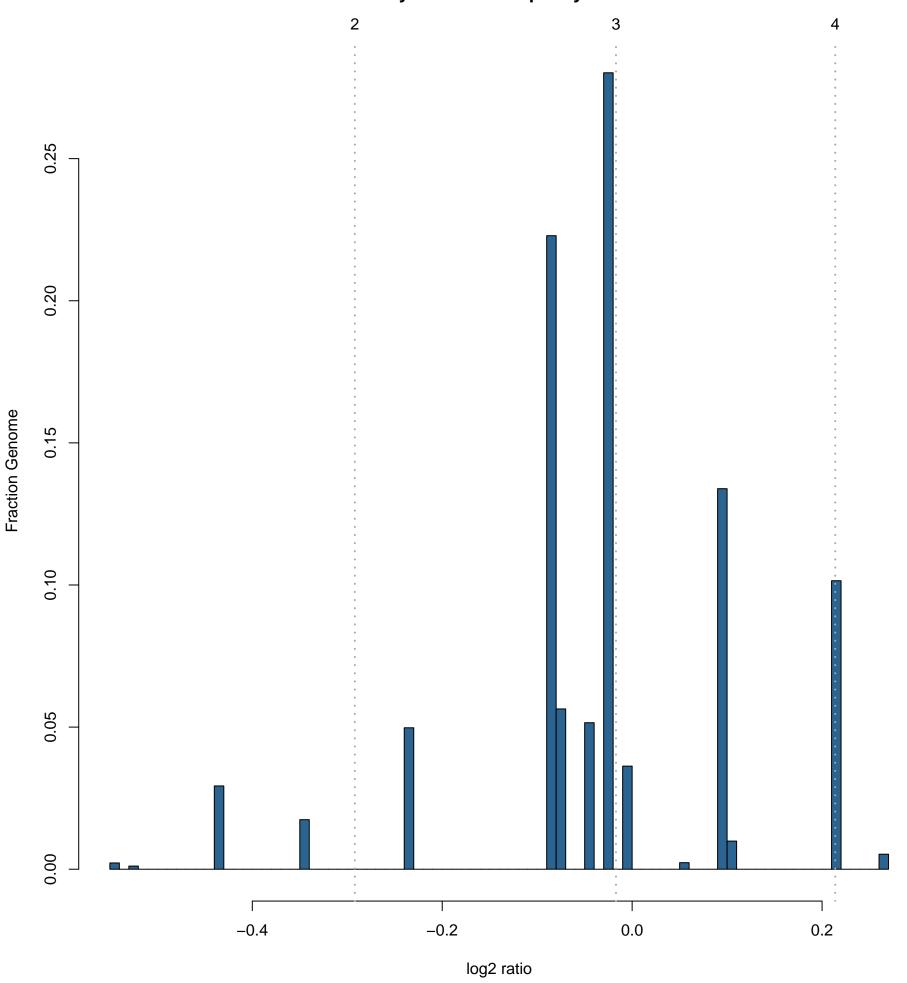
SCNA-fit log-likelihood: -15176.58

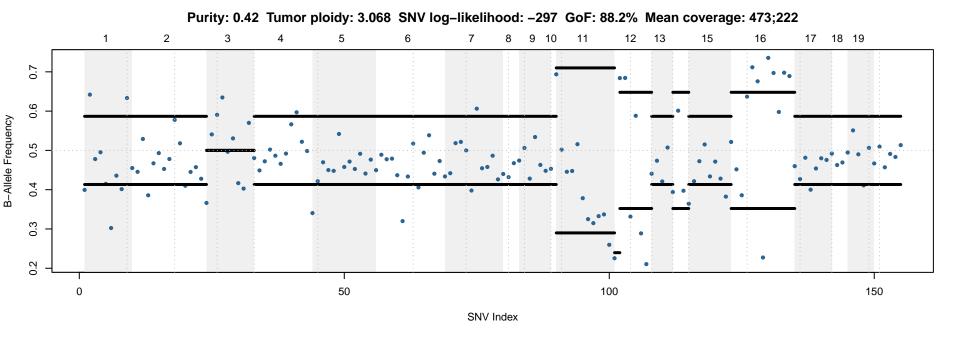




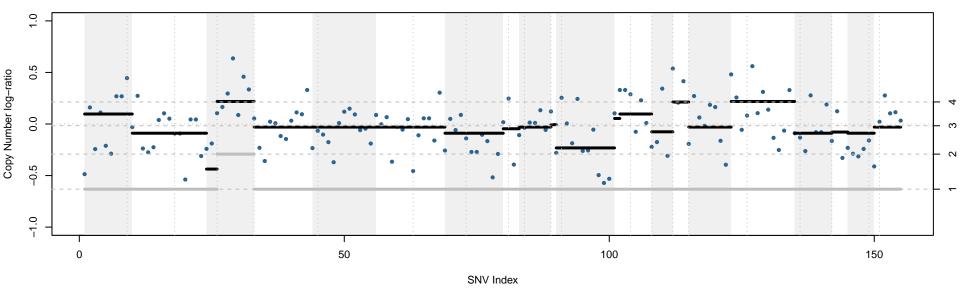


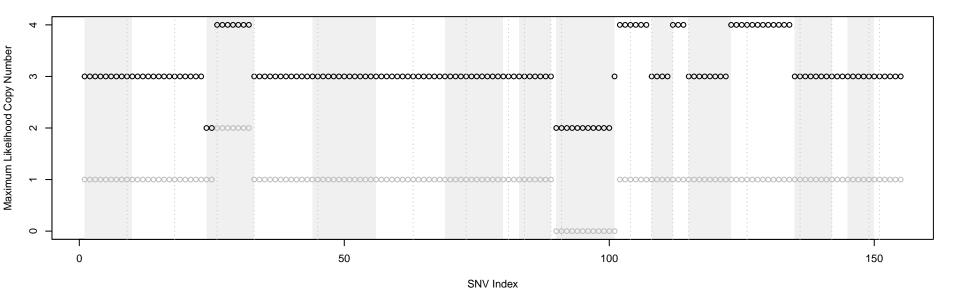
Purity: 0.42 Tumor ploidy: 3.068

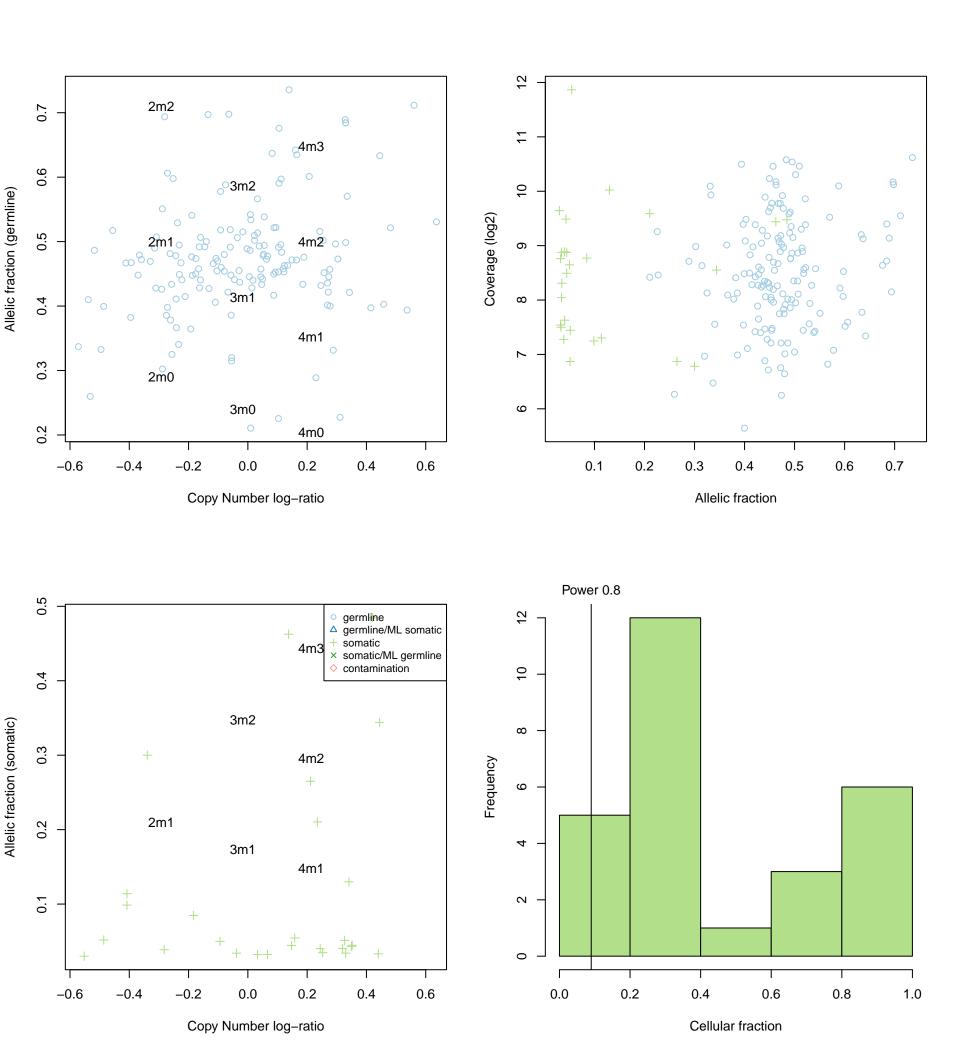




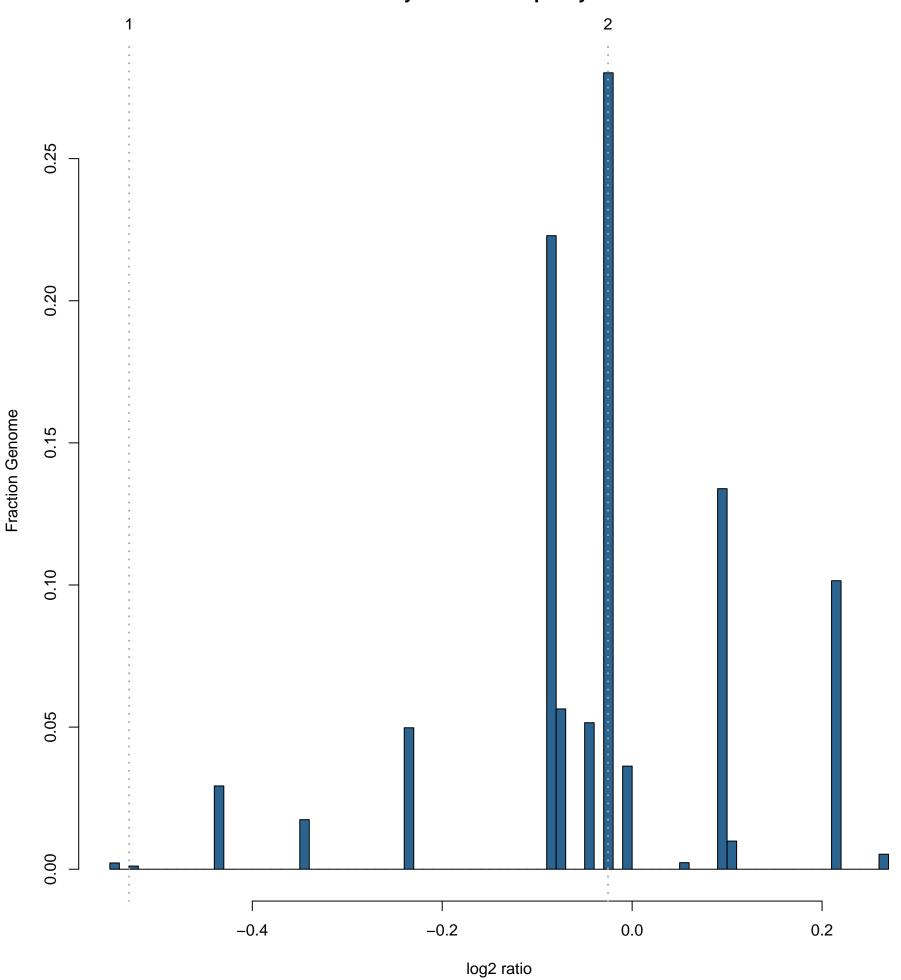
SCNA-fit log-likelihood: -15157.44

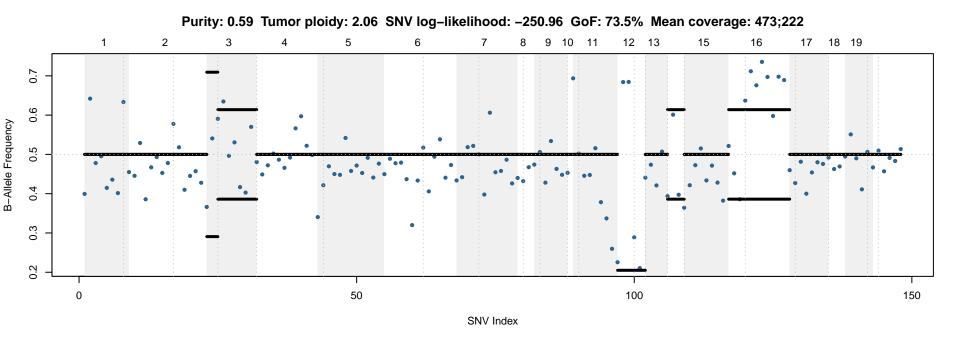




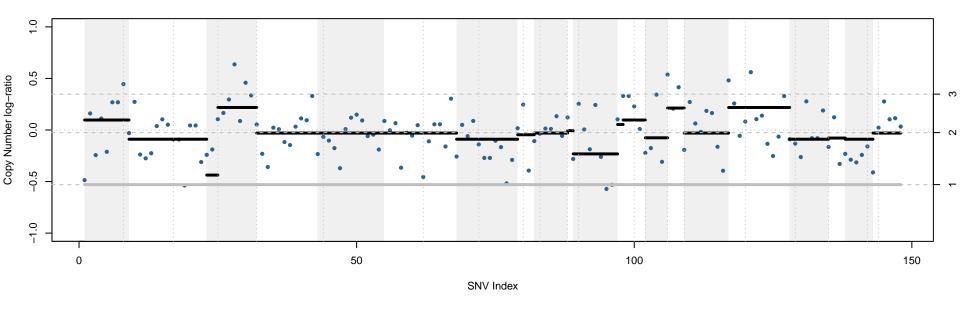


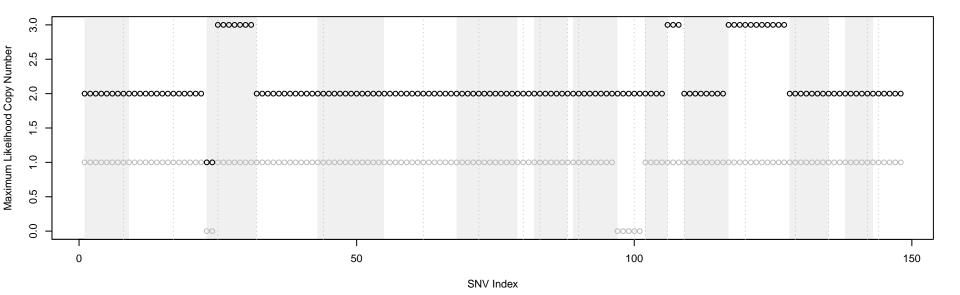
Purity: 0.59 Tumor ploidy: 2.06

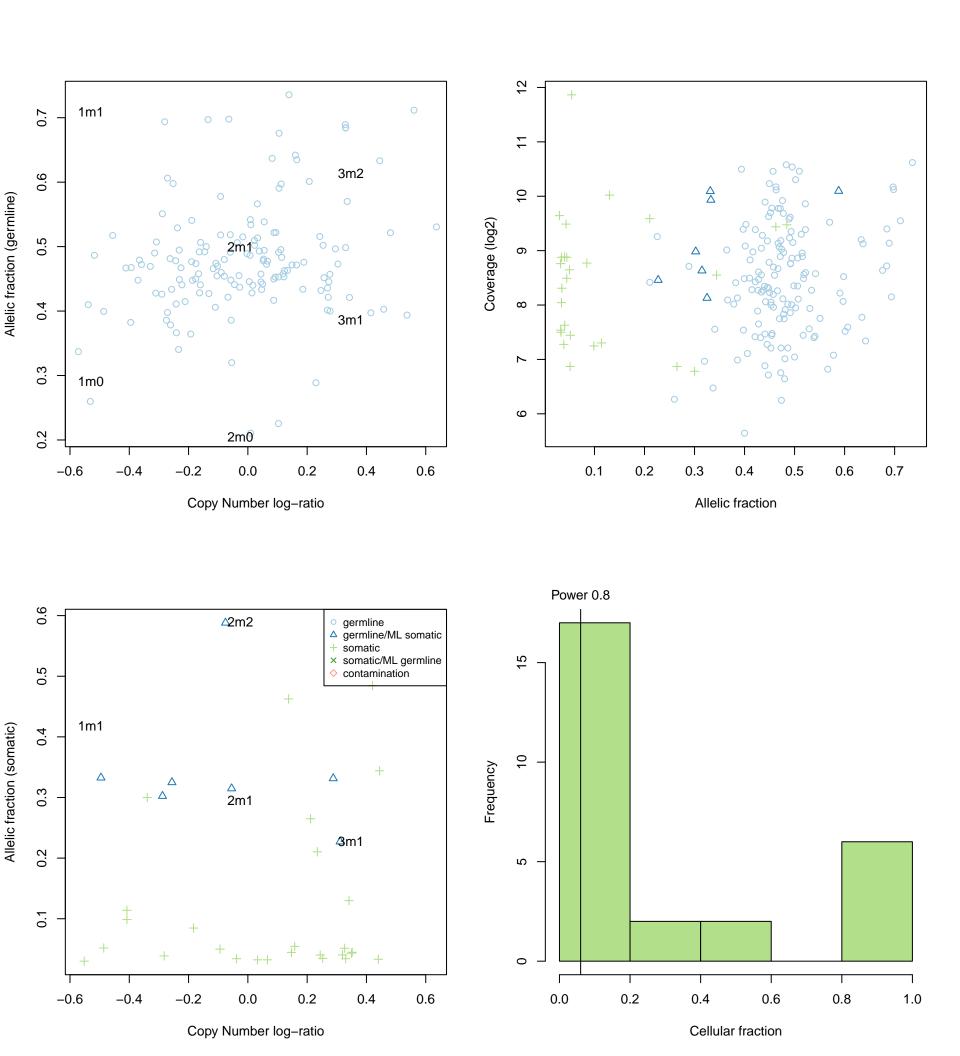




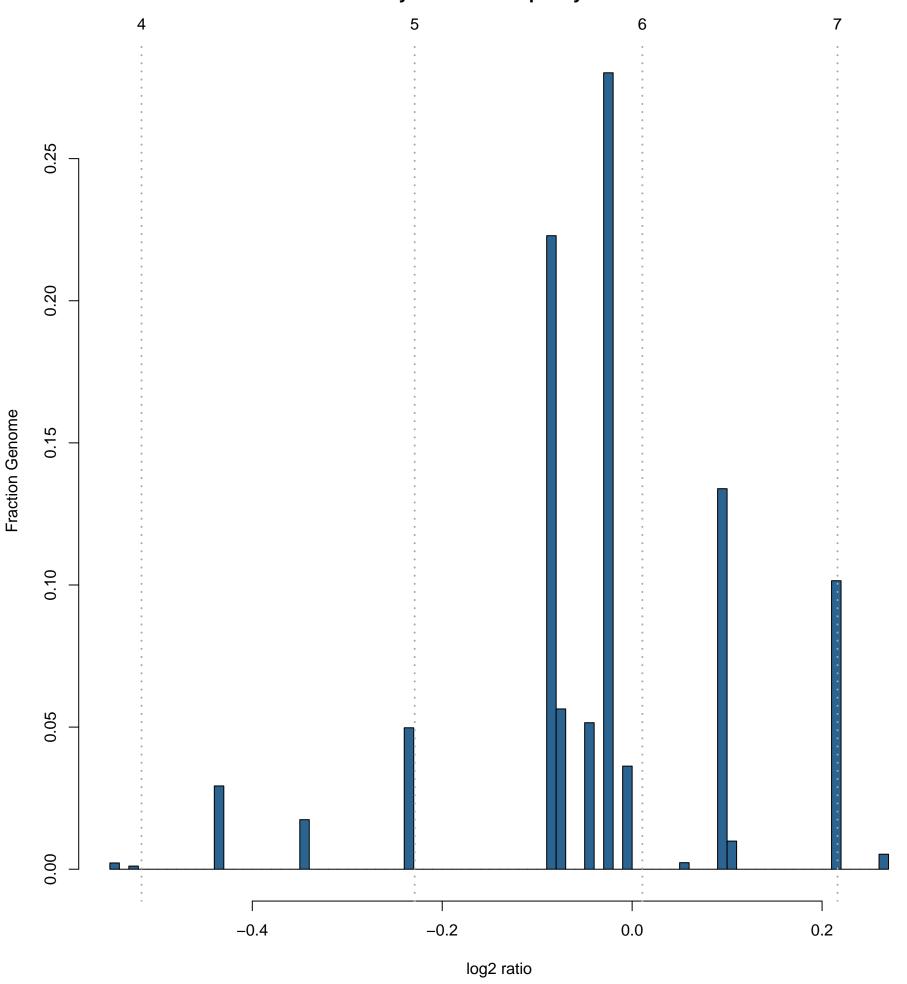
SCNA-fit log-likelihood: -15347.95

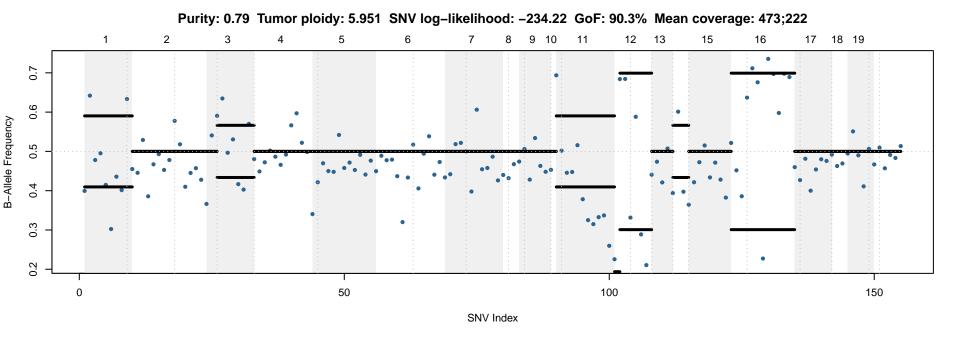




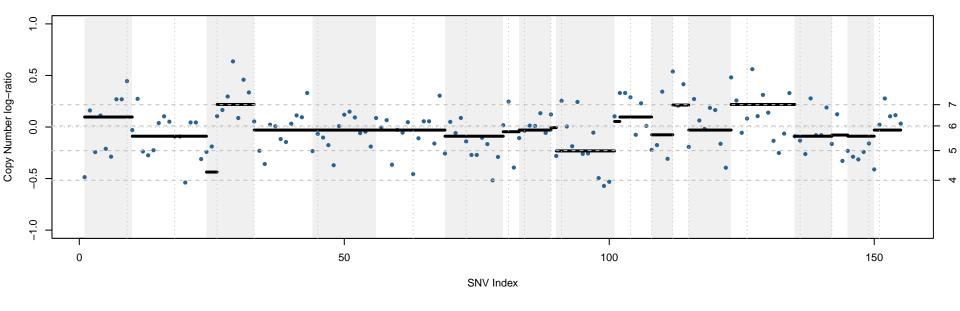


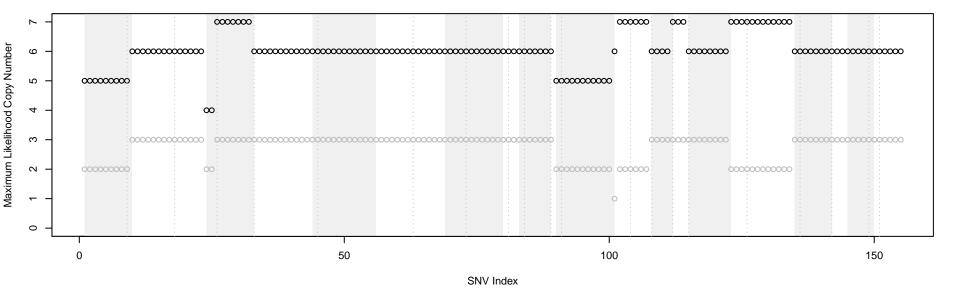
Purity: 0.79 Tumor ploidy: 5.951

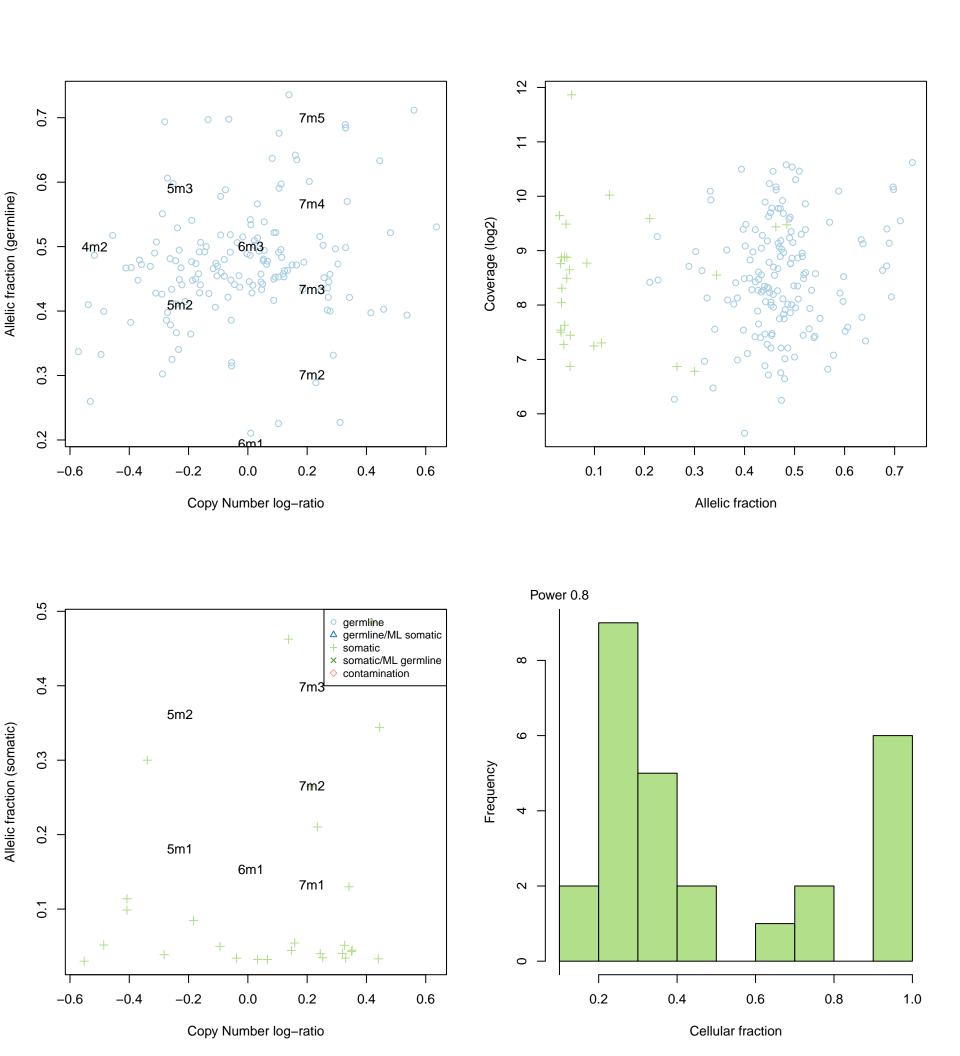




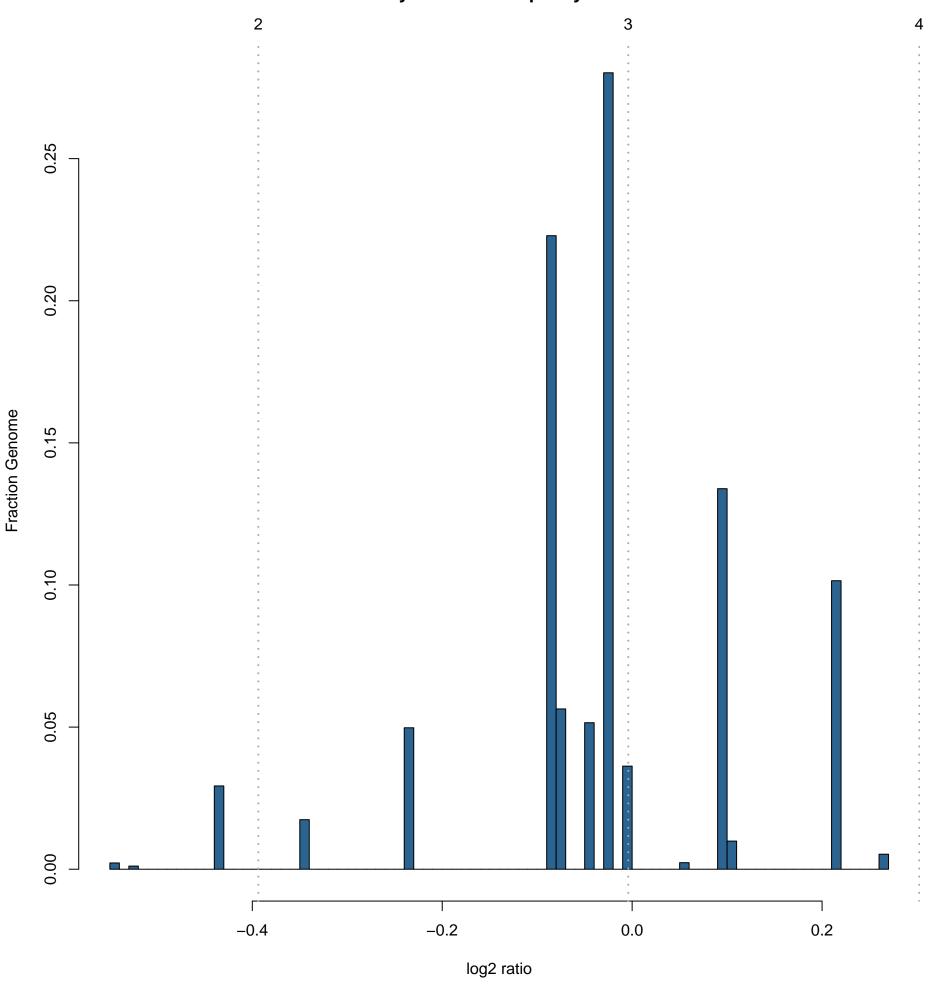
SCNA-fit log-likelihood: -15492.86

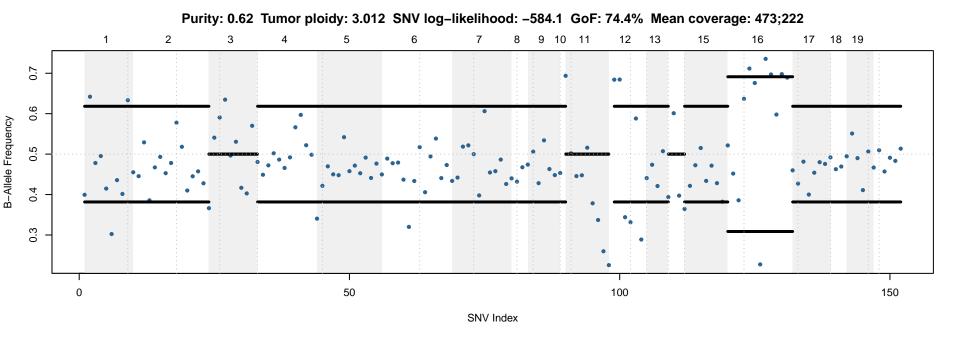






Purity: 0.62 Tumor ploidy: 3.012





SCNA-fit log-likelihood: -15257.55

