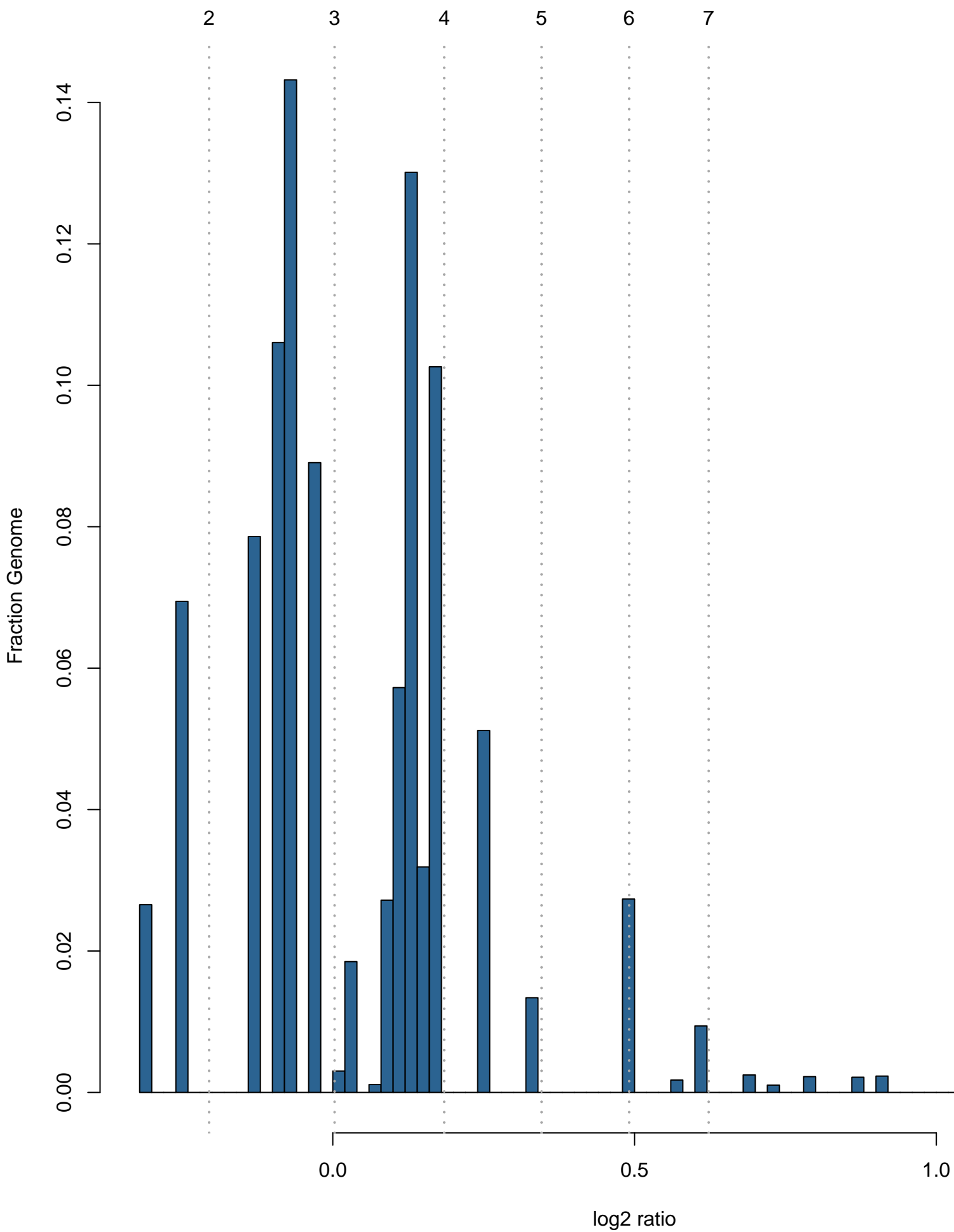
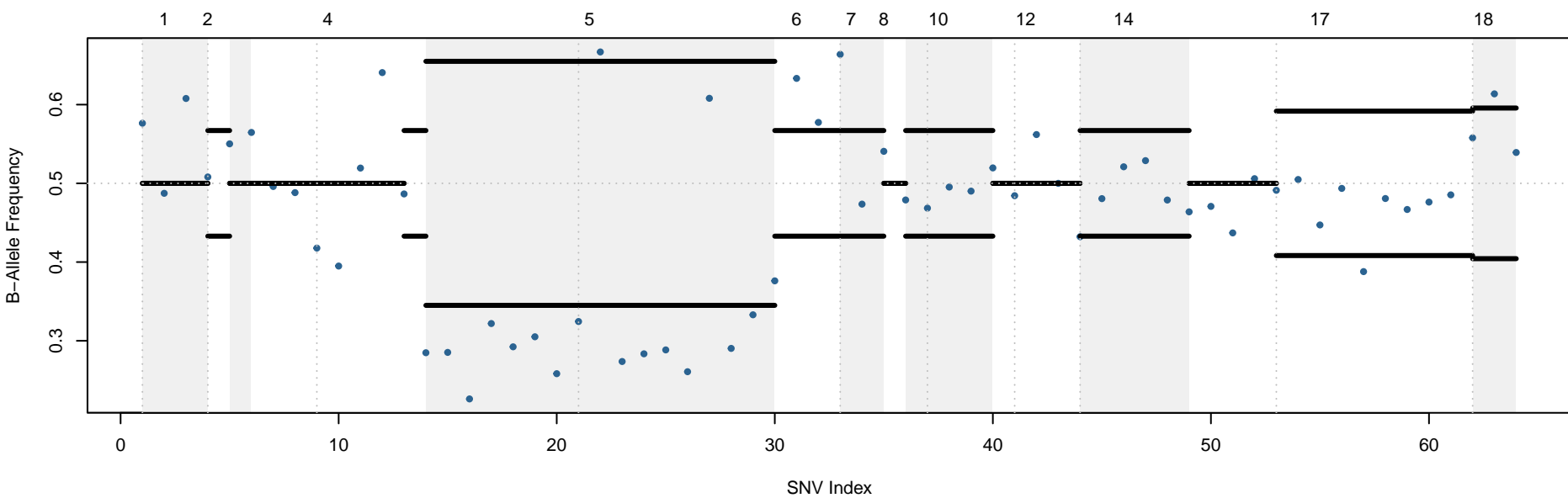


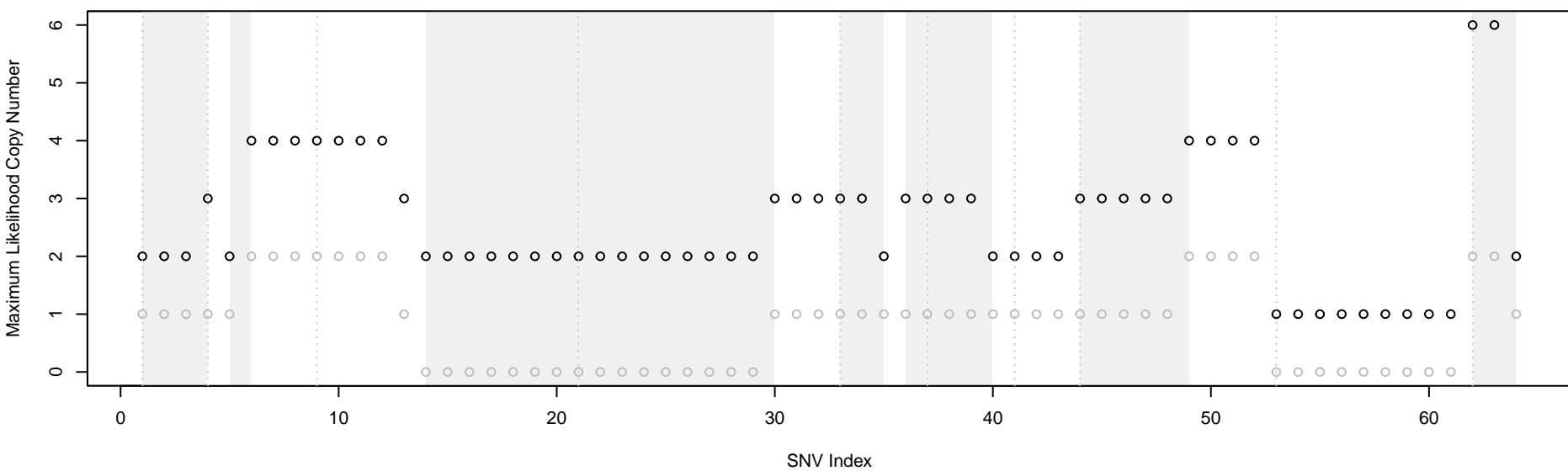
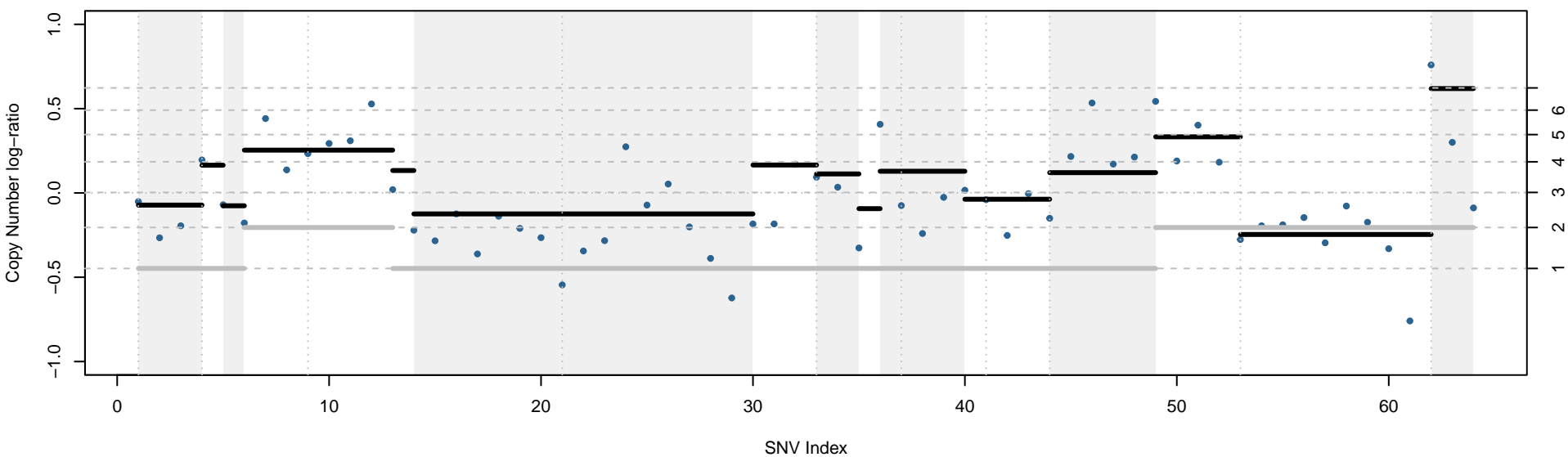
Purity: 0.31 Tumor ploidy: 2.985

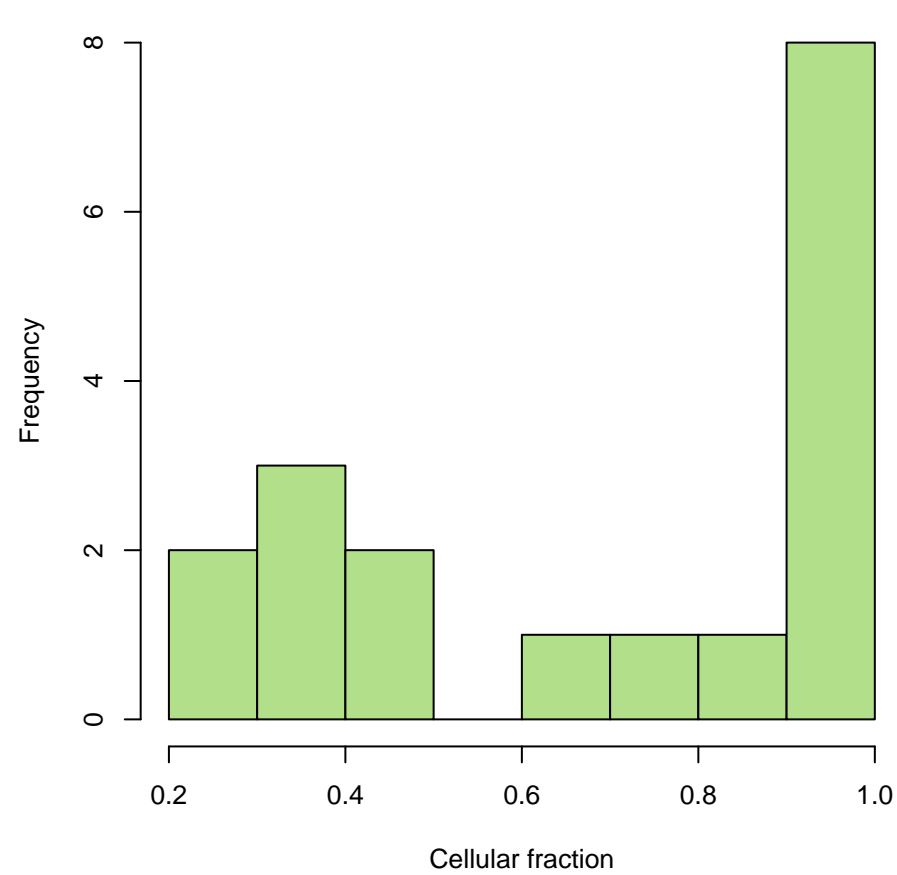
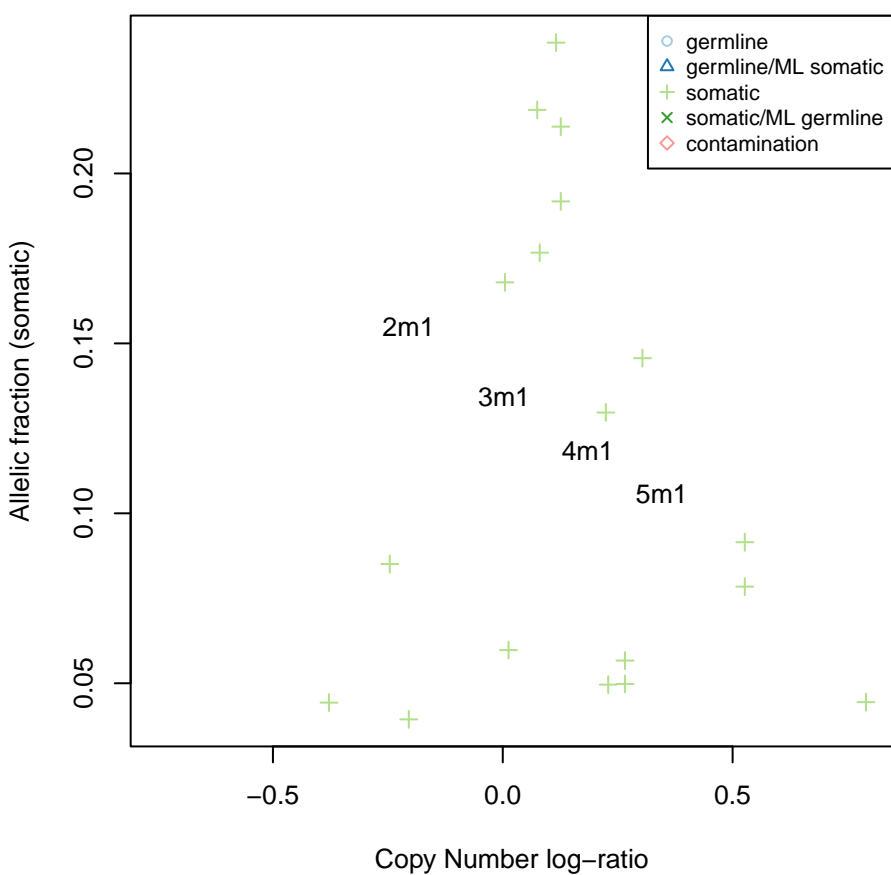
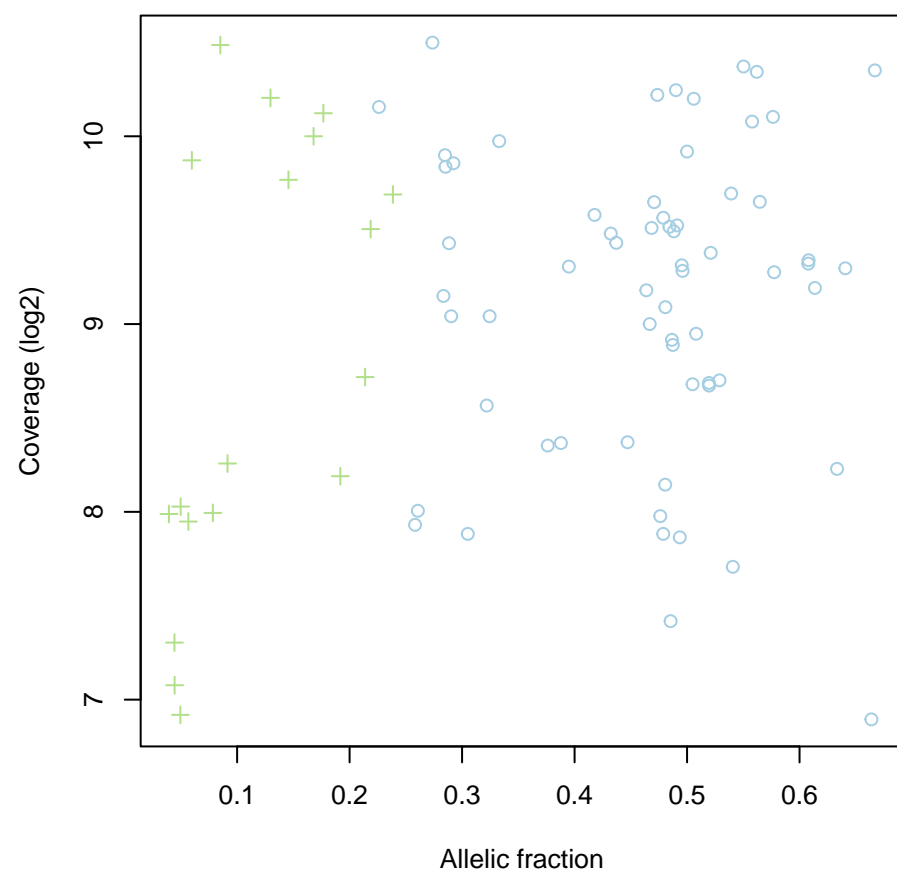
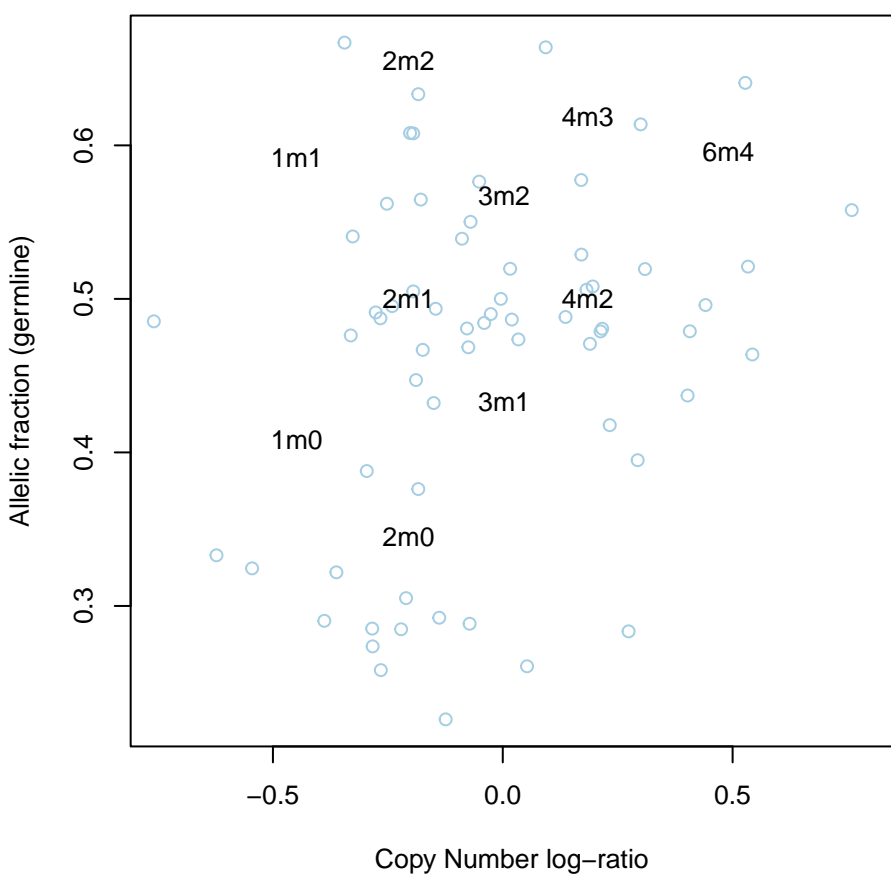


Purity: 0.31 Tumor ploidy: 2.985 SNV log-likelihood: -71.89 GoF: 91.7% Mean coverage: 586;641

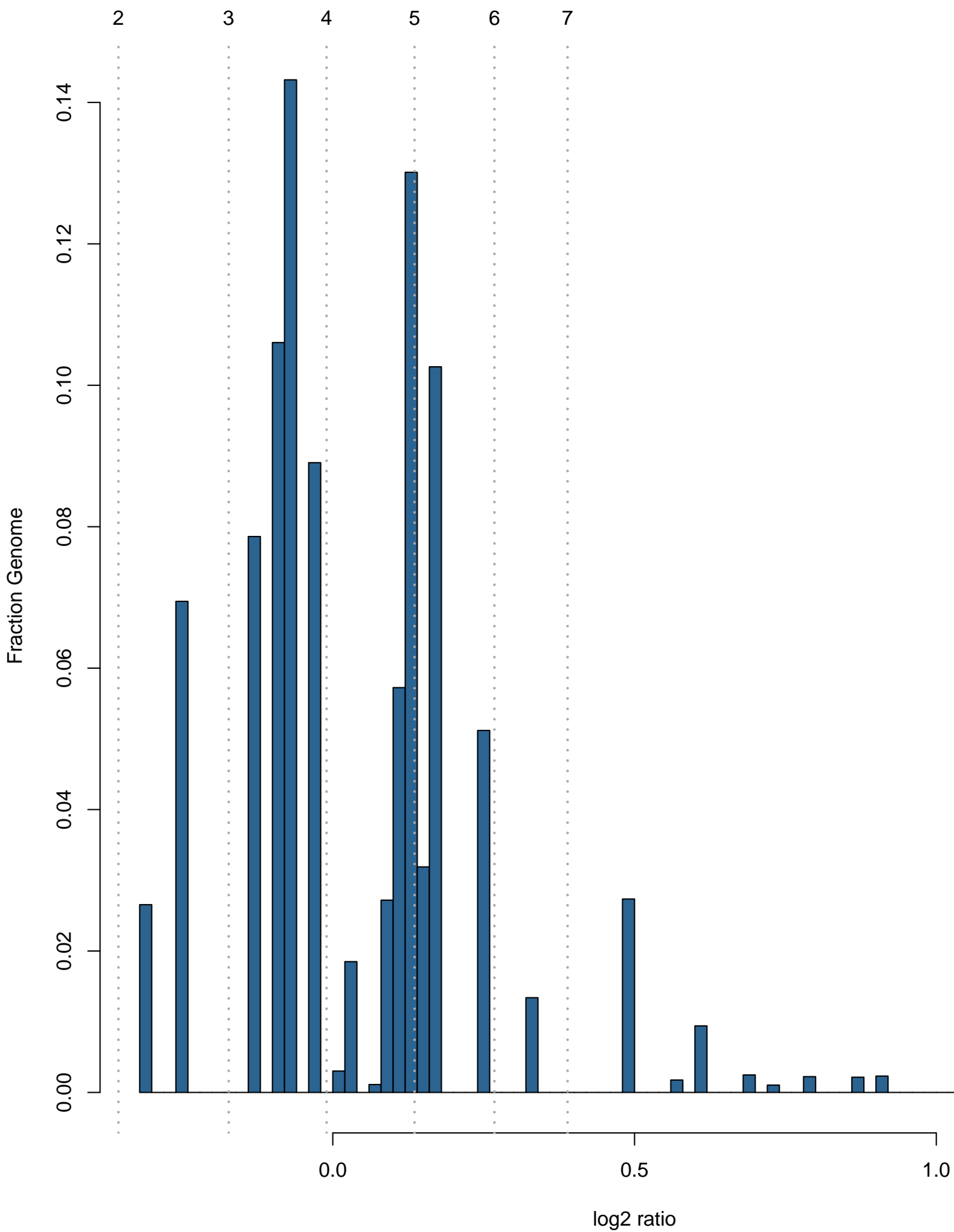


SCNA-fit log-likelihood: -6943.45

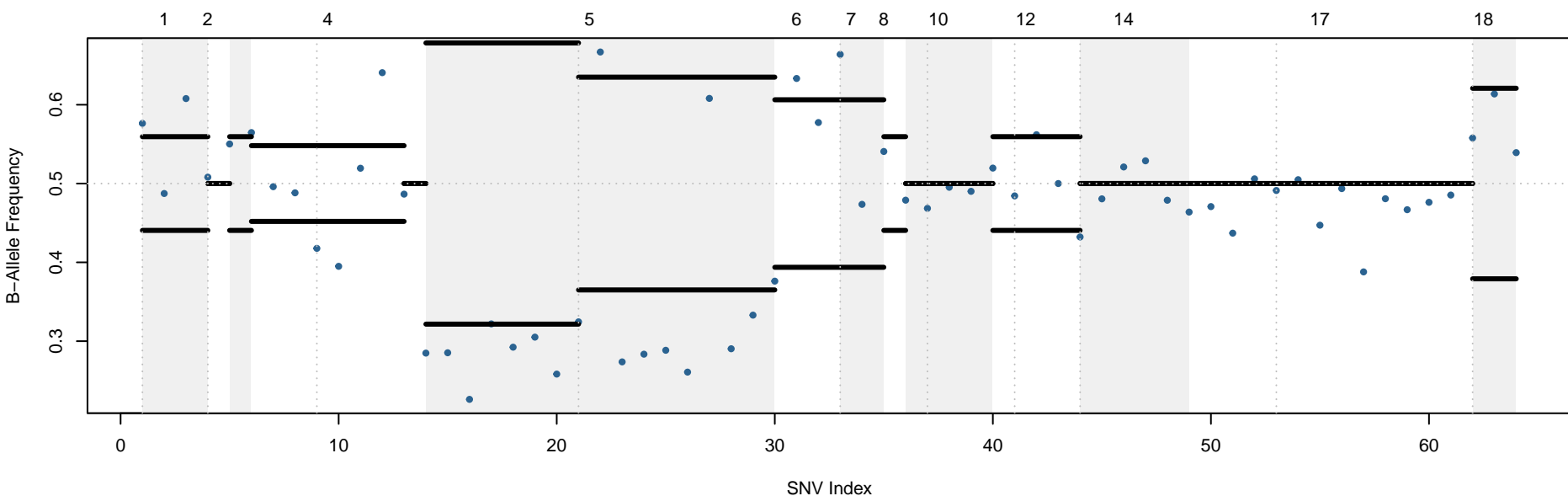




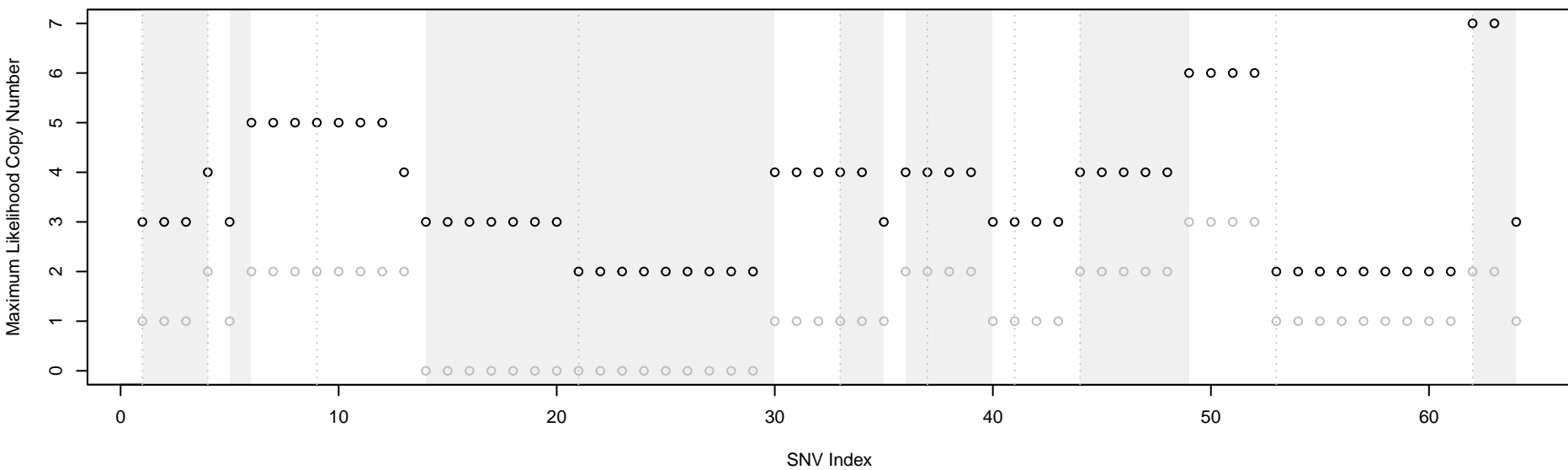
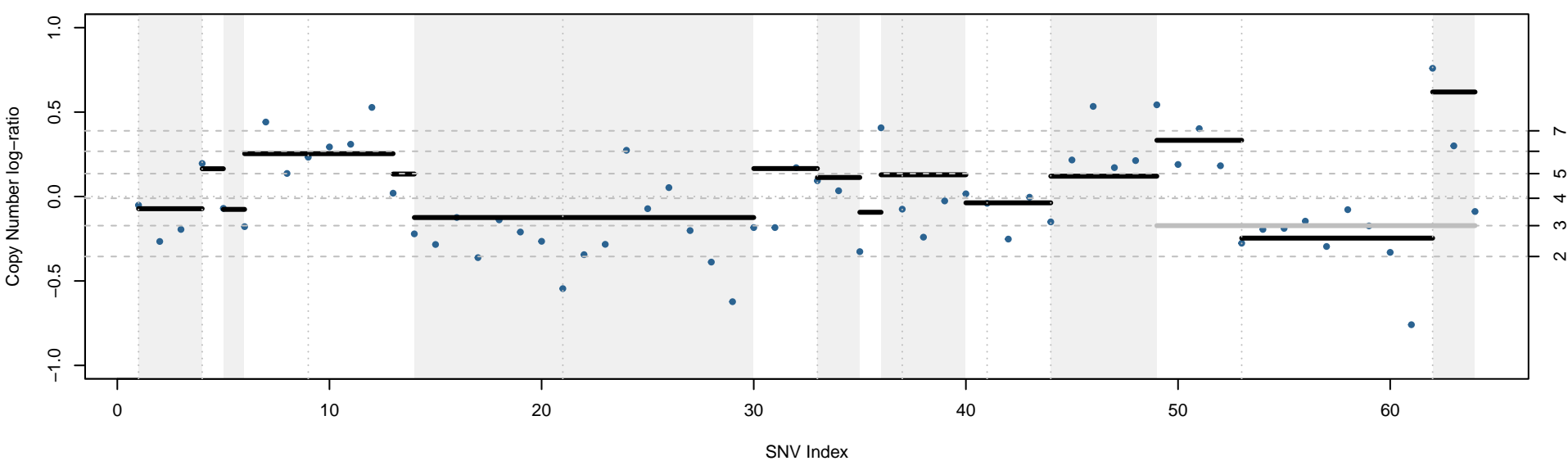
Purity: 0.27 Tumor ploidy: 4.067

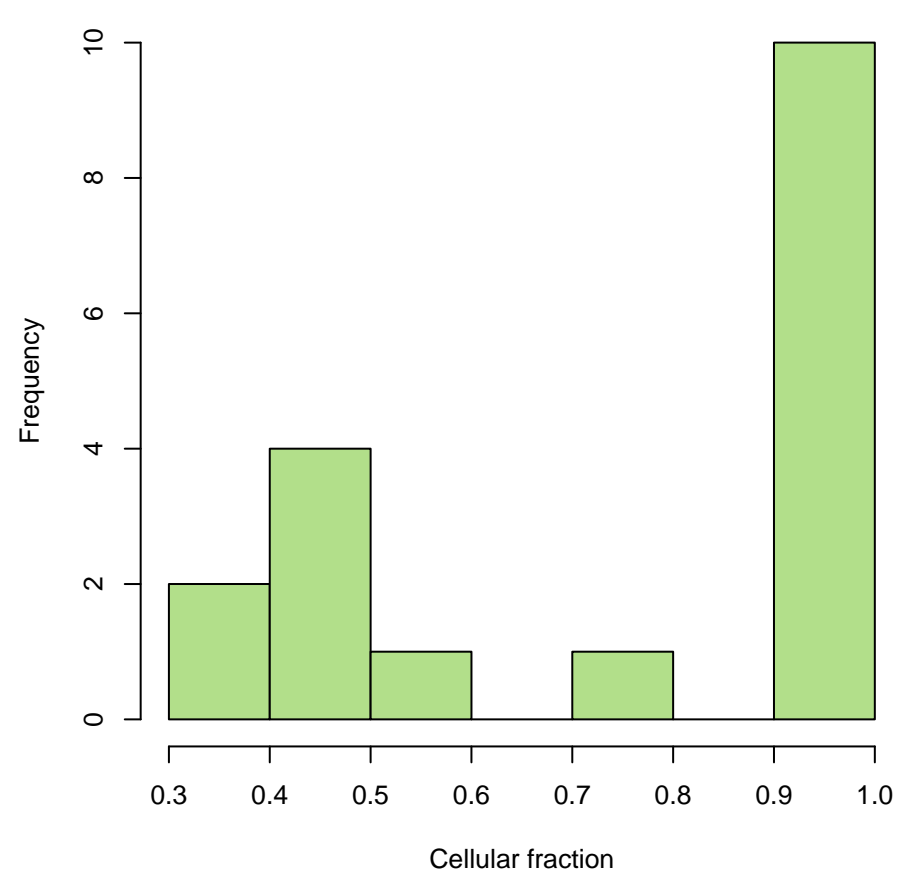
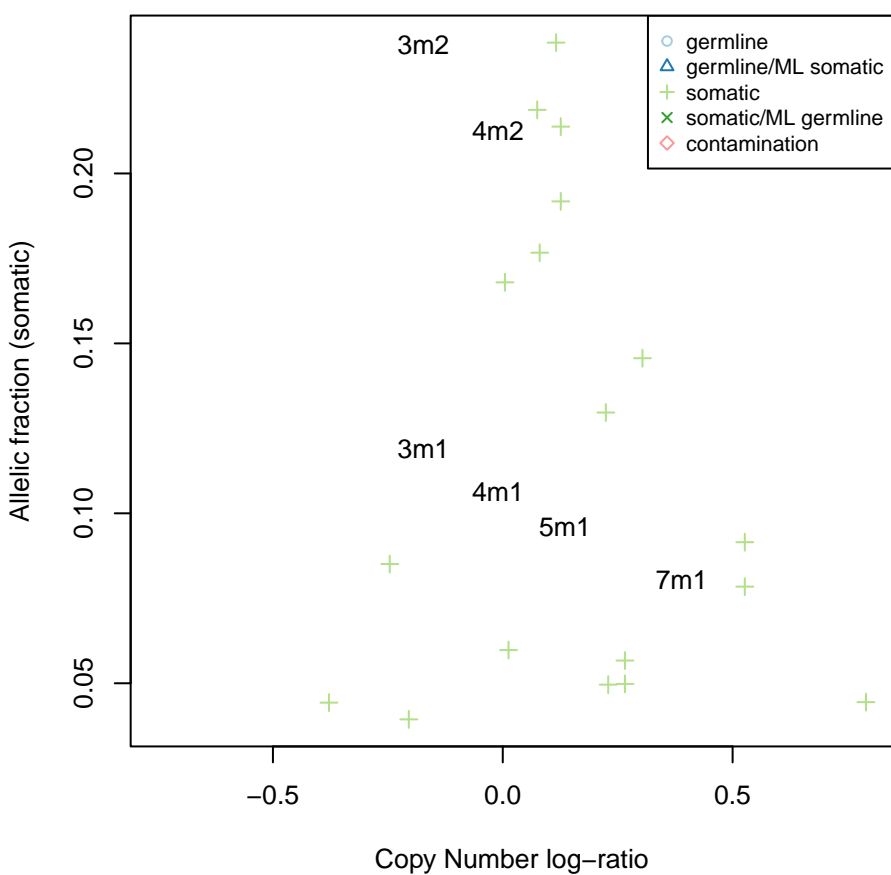
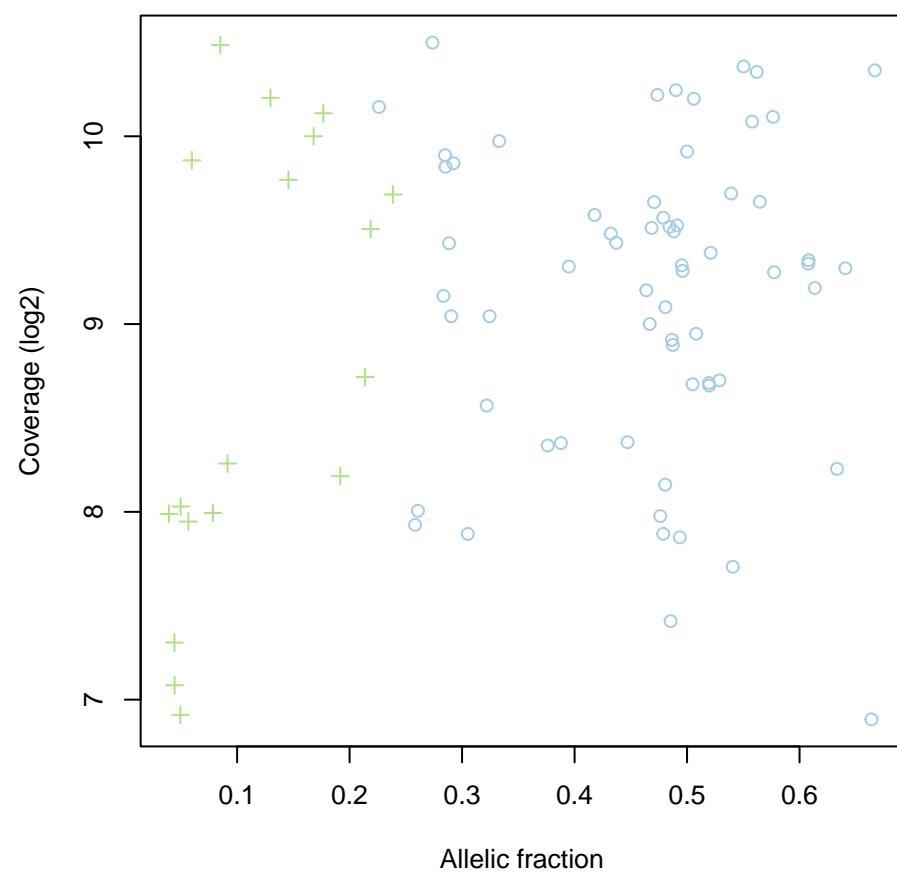
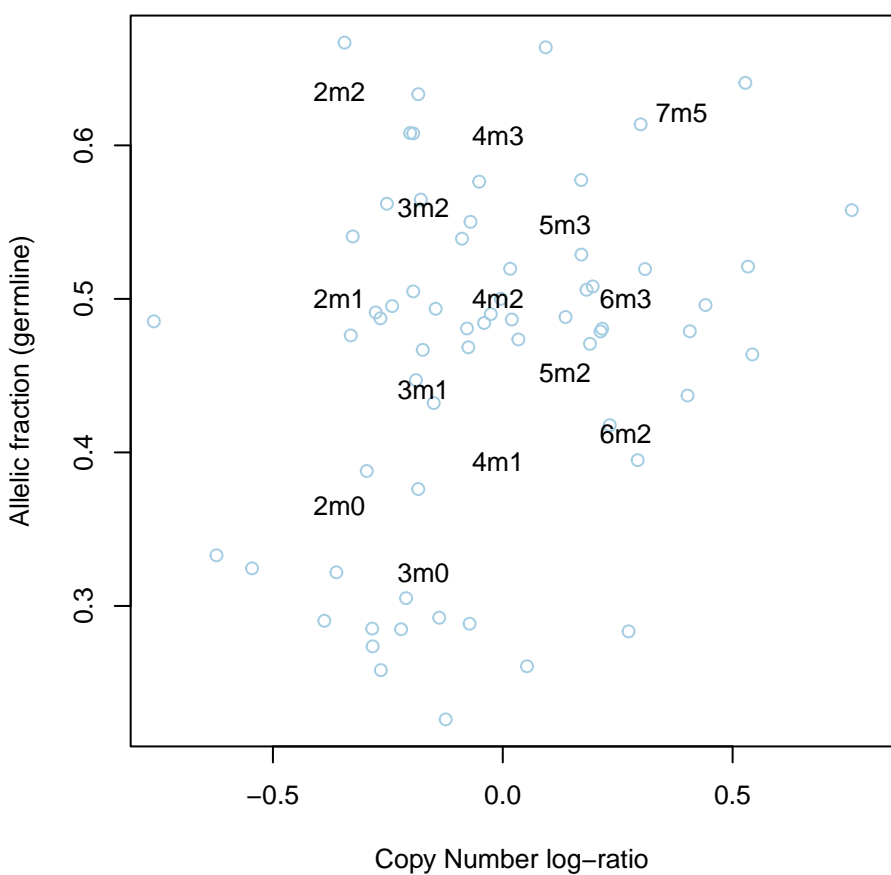


Purity: 0.27 Tumor ploidy: 4.067 SNV log-likelihood: -48.95 GoF: 94.7% Mean coverage: 586;641

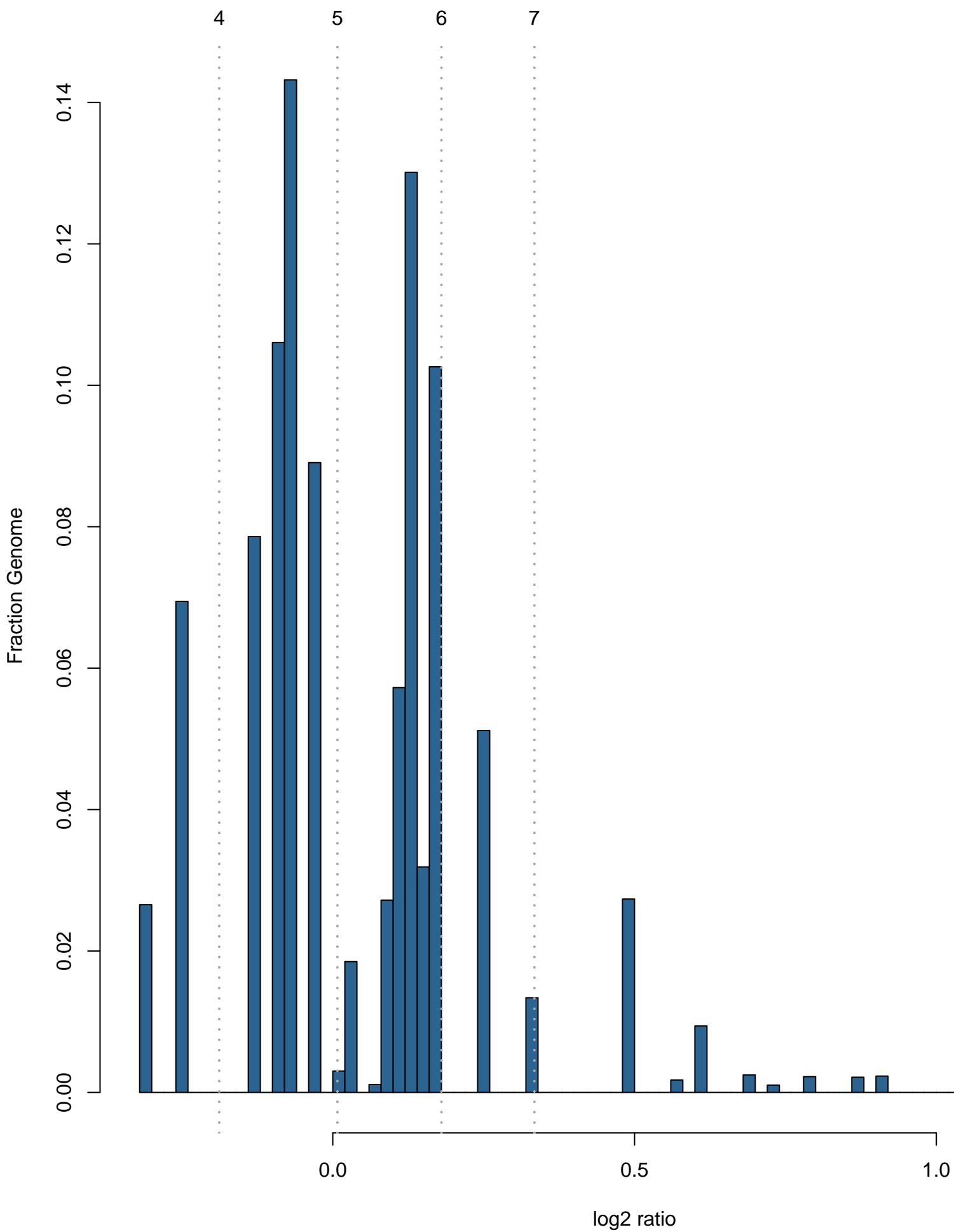


SCNA-fit log-likelihood: -7084.09

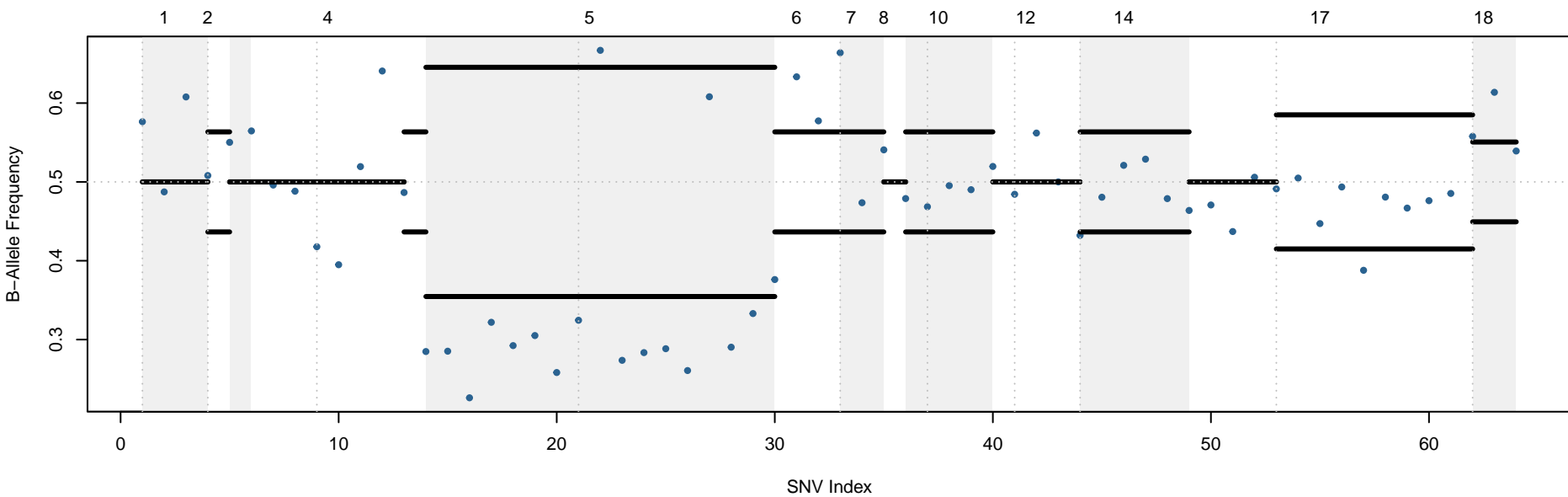




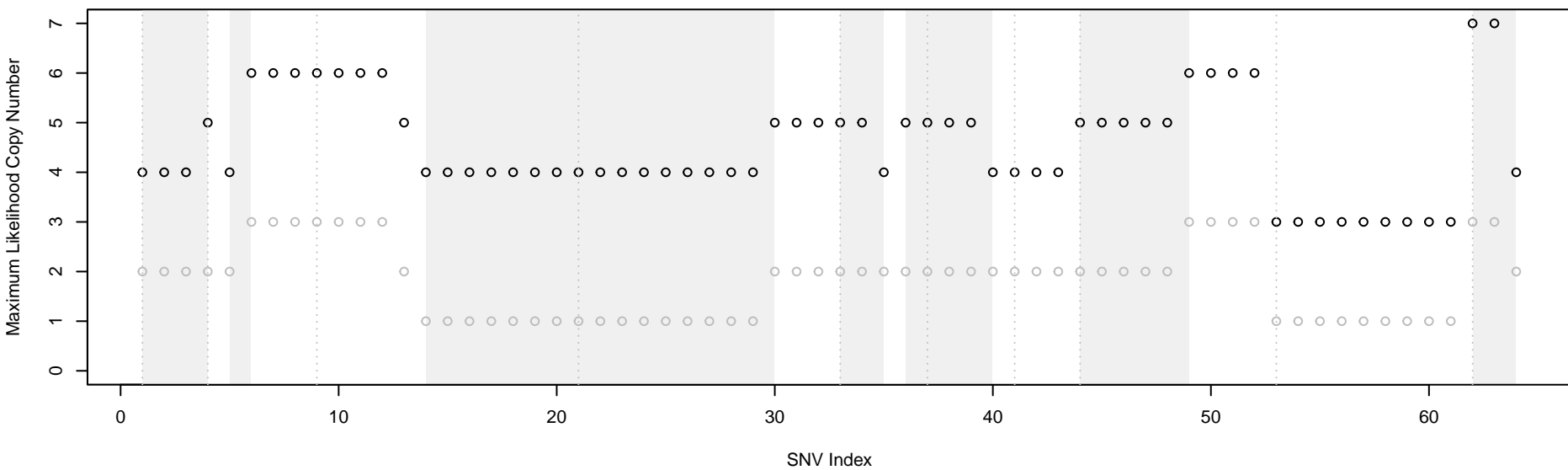
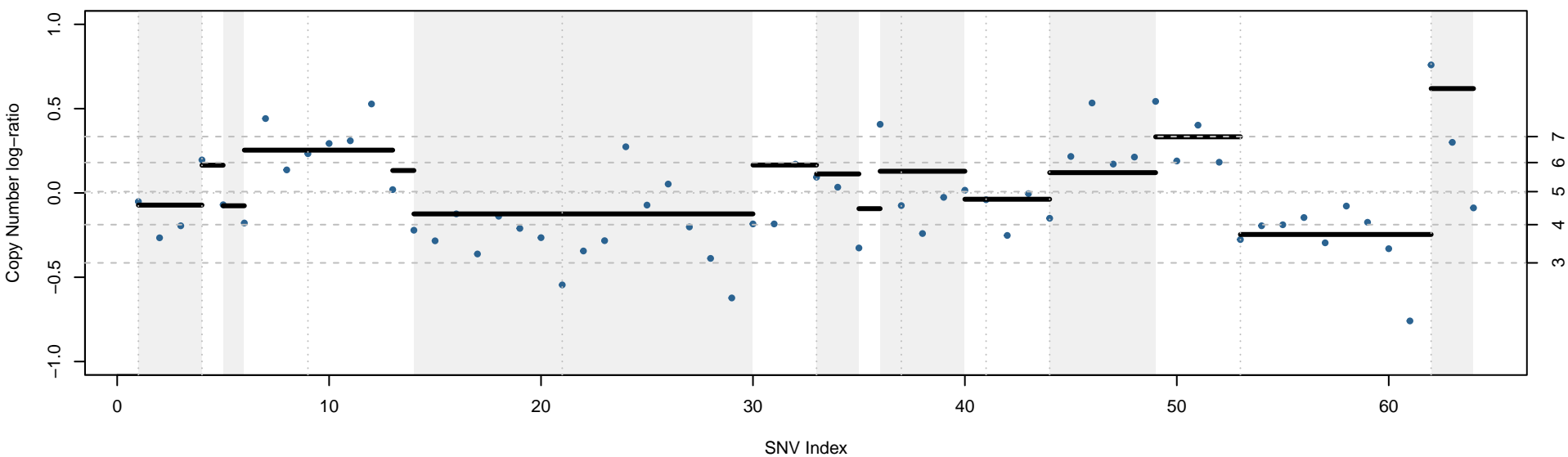
Purity: 0.41 Tumor ploidy: 4.958



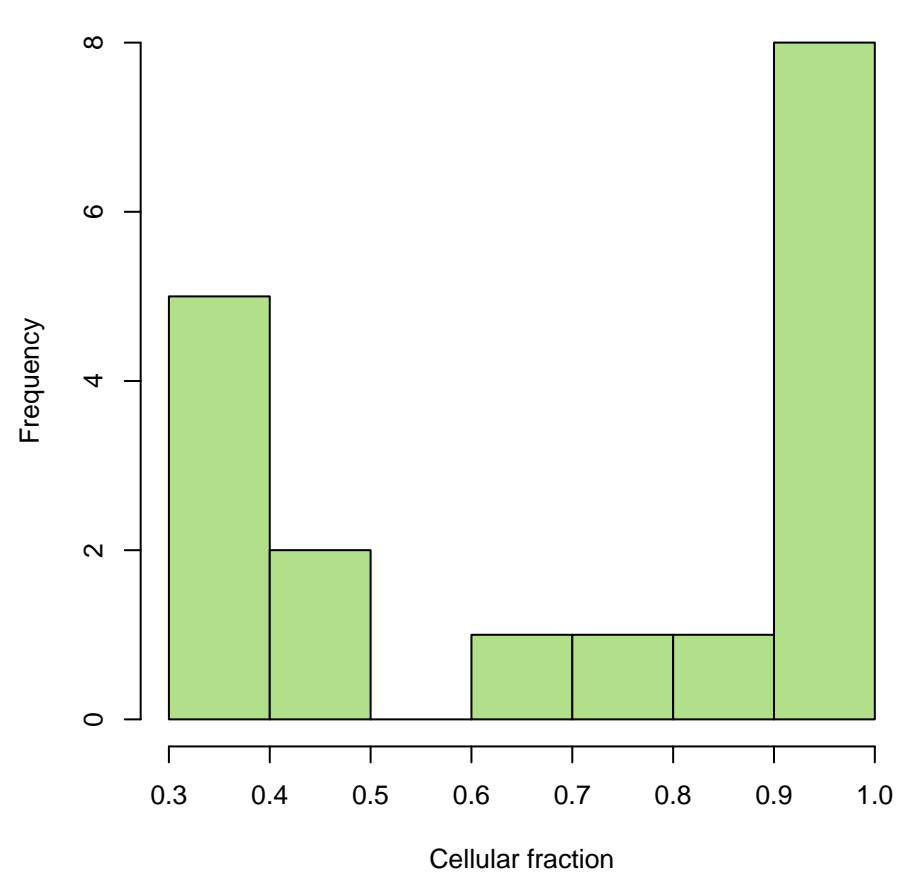
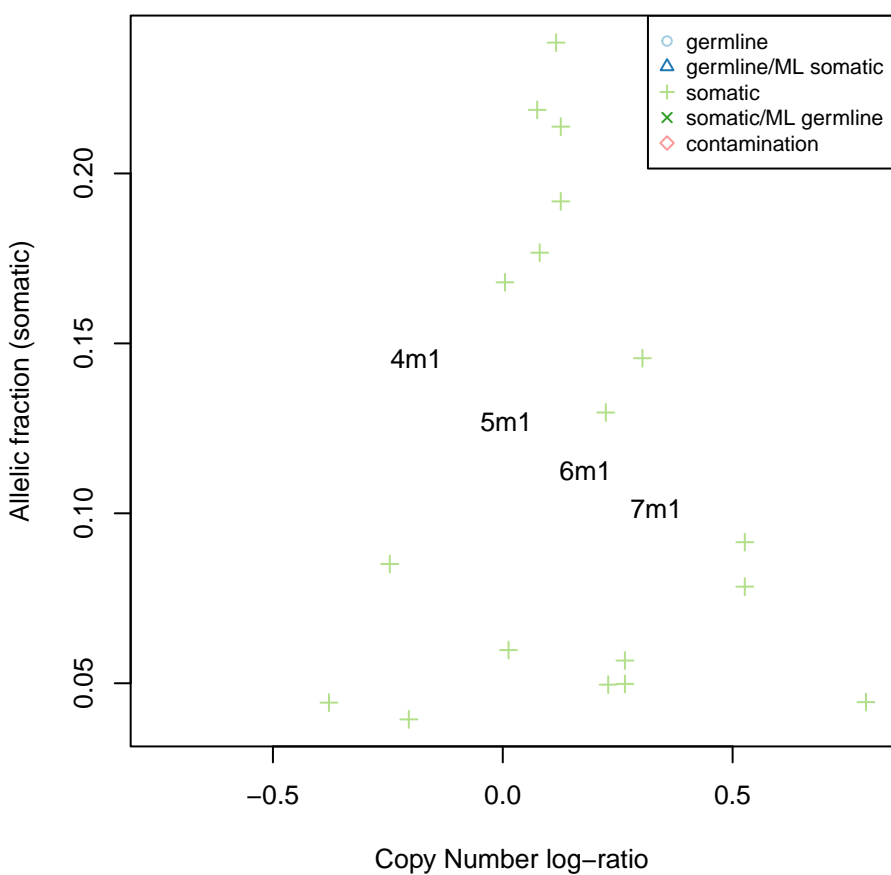
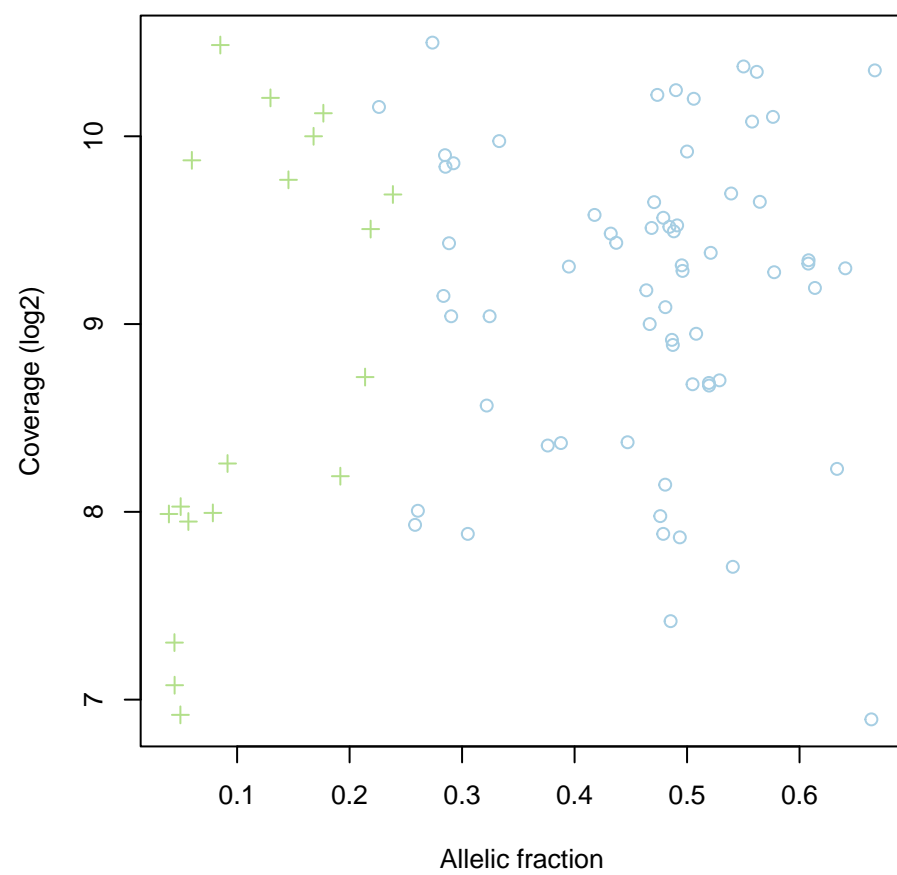
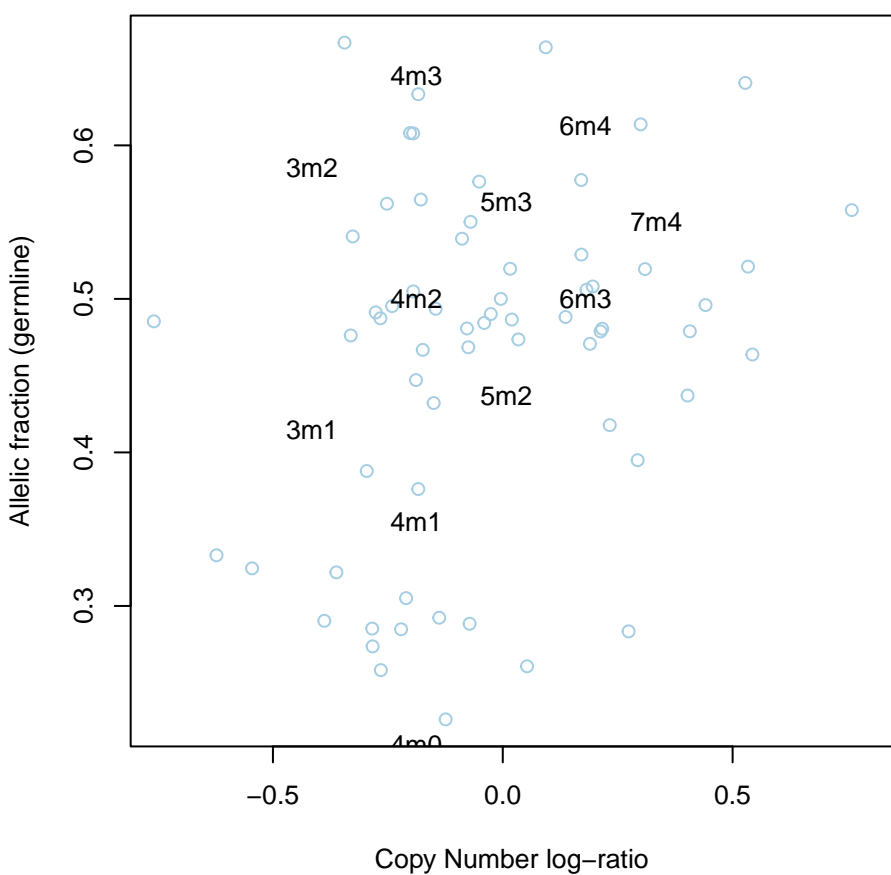
Purity: 0.41 Tumor ploidy: 4.958 SNV log-likelihood: -112.13 GoF: 92.1% Mean coverage: 586,641



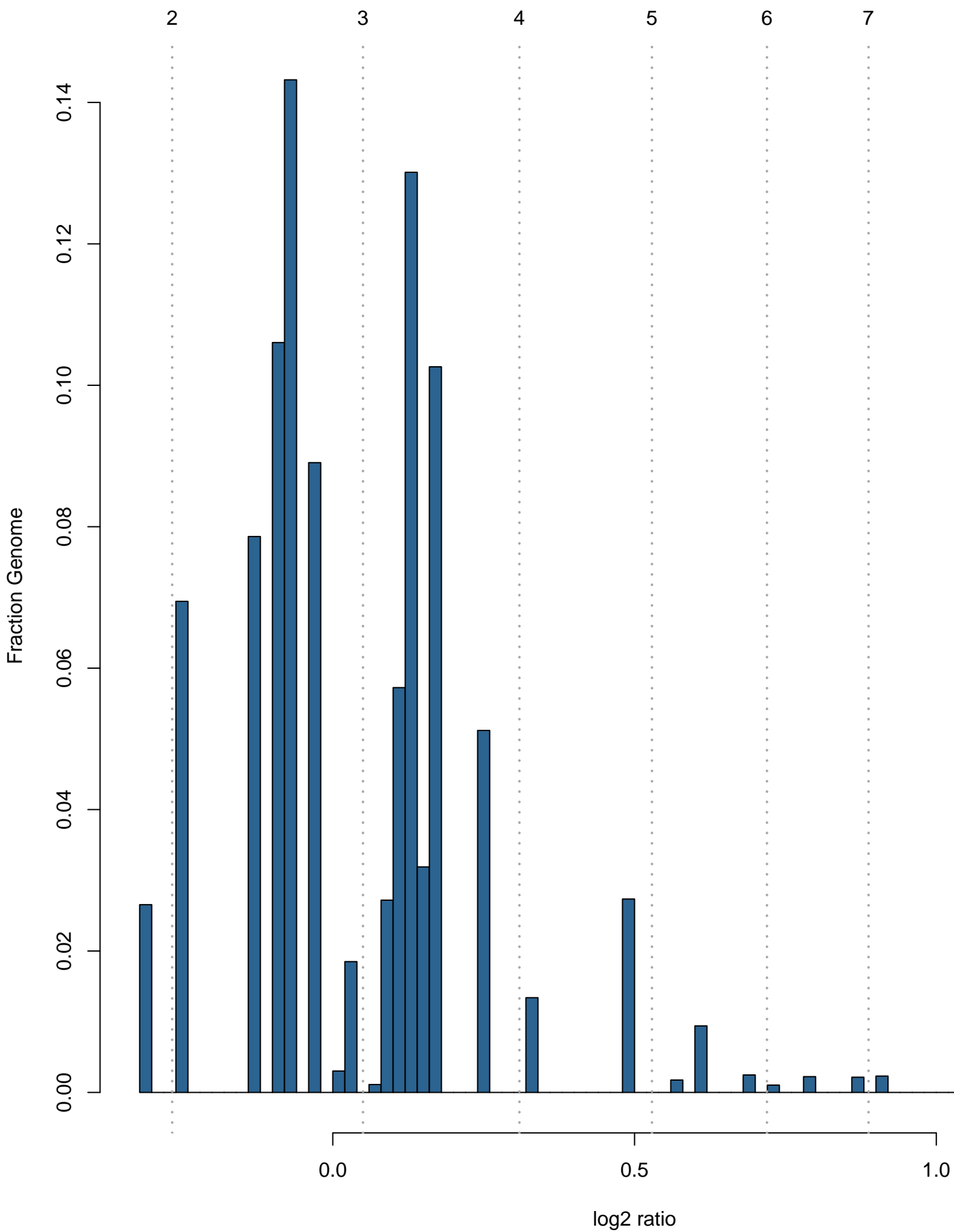
SCNA-fit log-likelihood: -6983.81



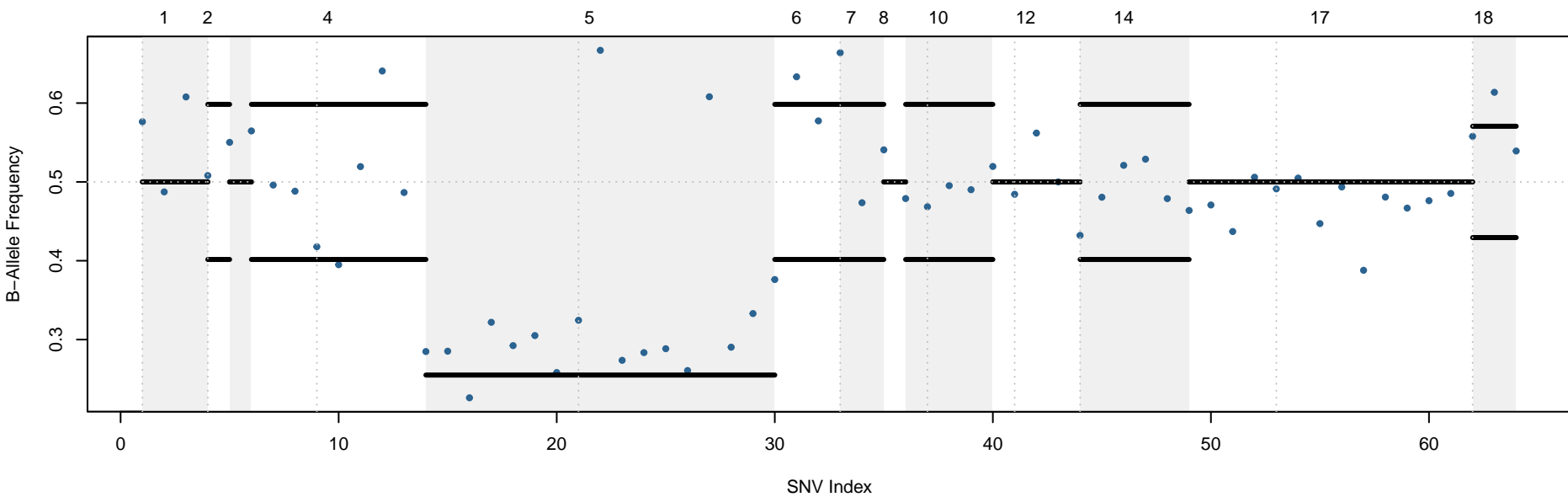




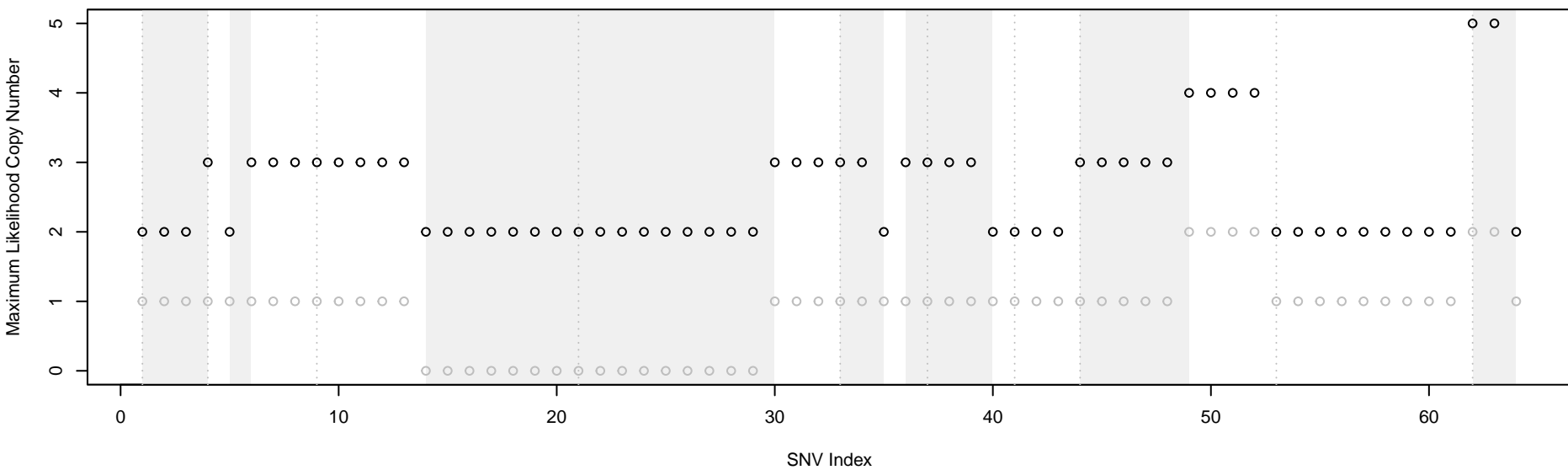
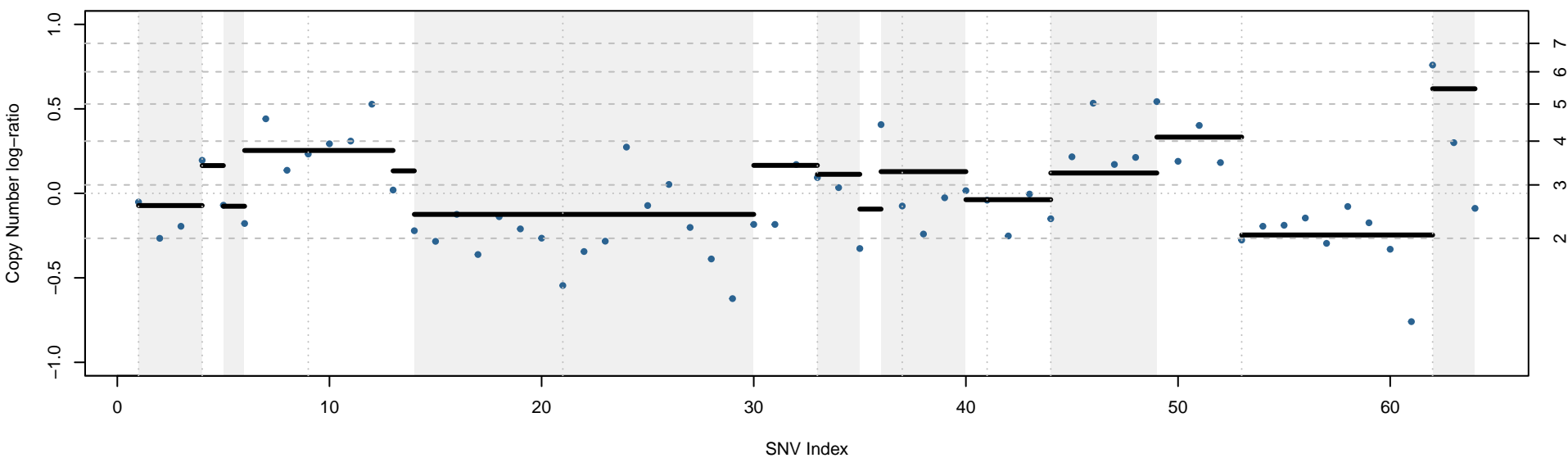
Purity: 0.49 Tumor ploidy: 2.827

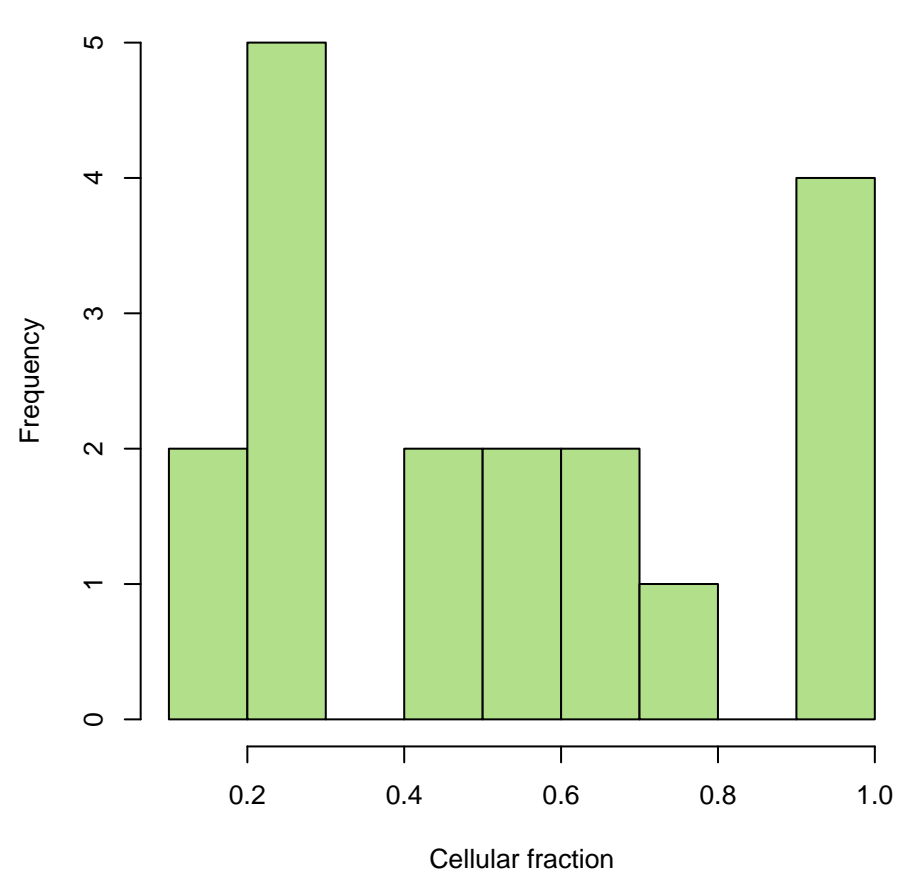
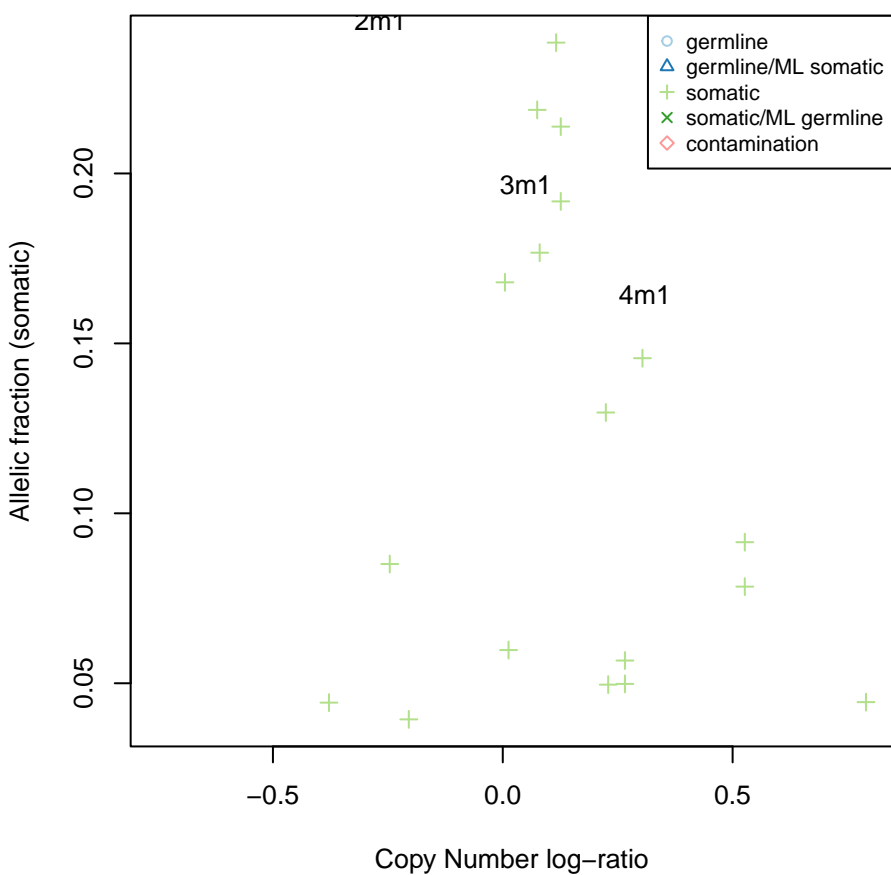
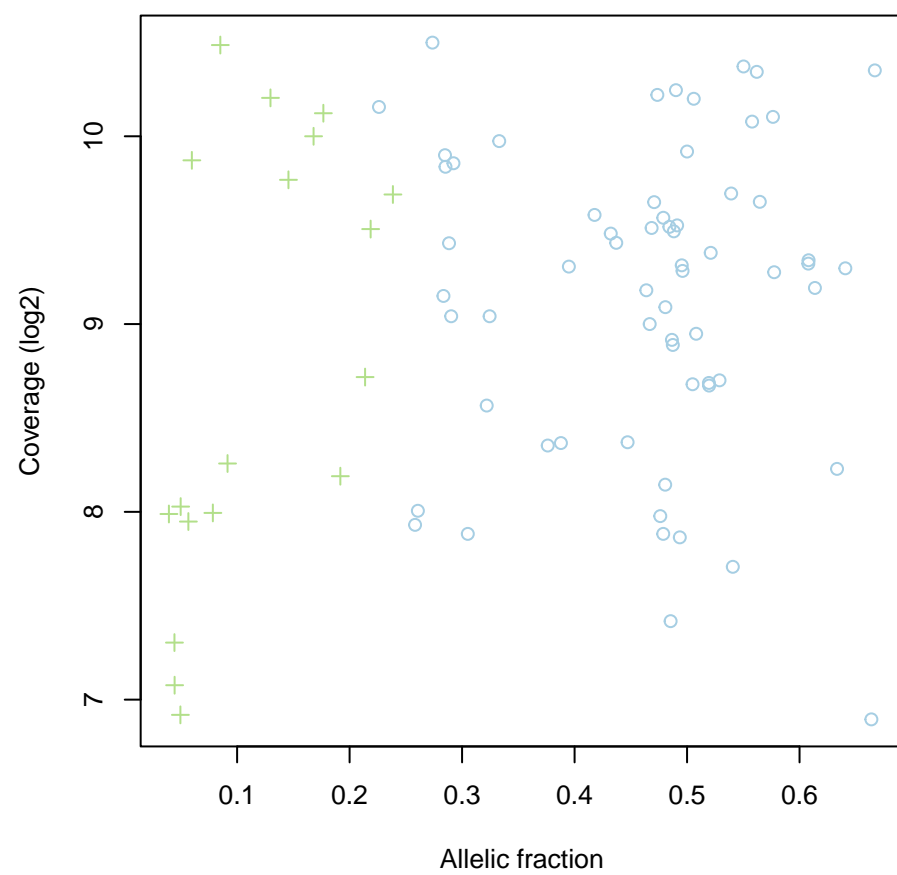
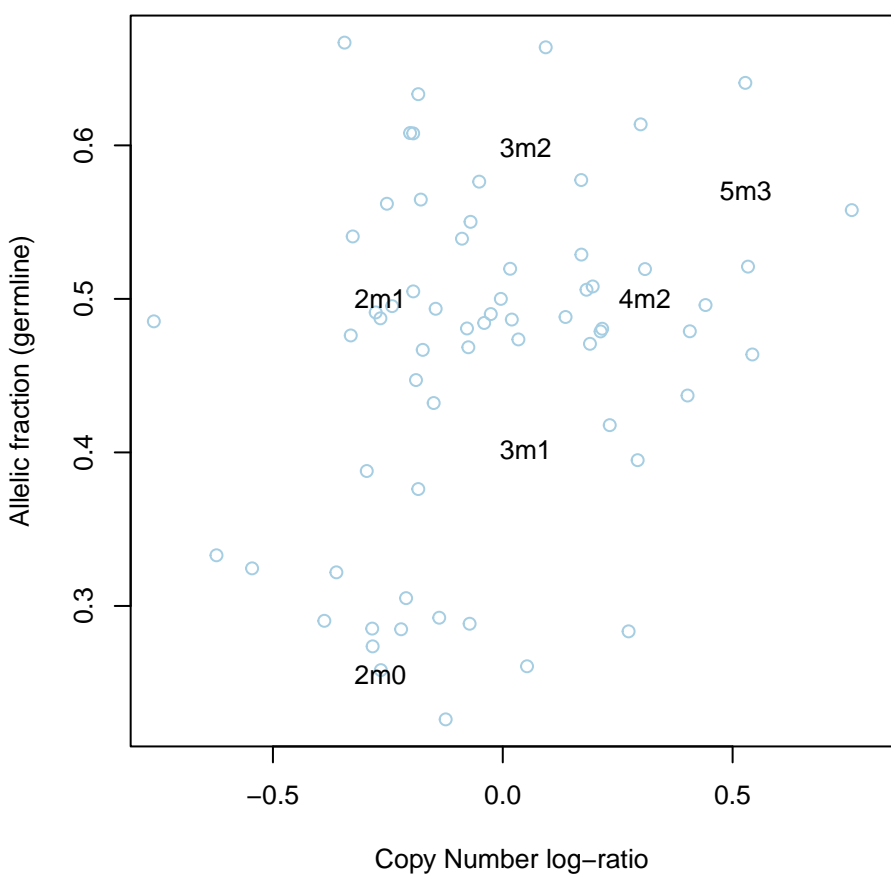


Purity: 0.49 Tumor ploidy: 2.827 SNV log-likelihood: -90.83 GoF: 87.1% Mean coverage: 586;641

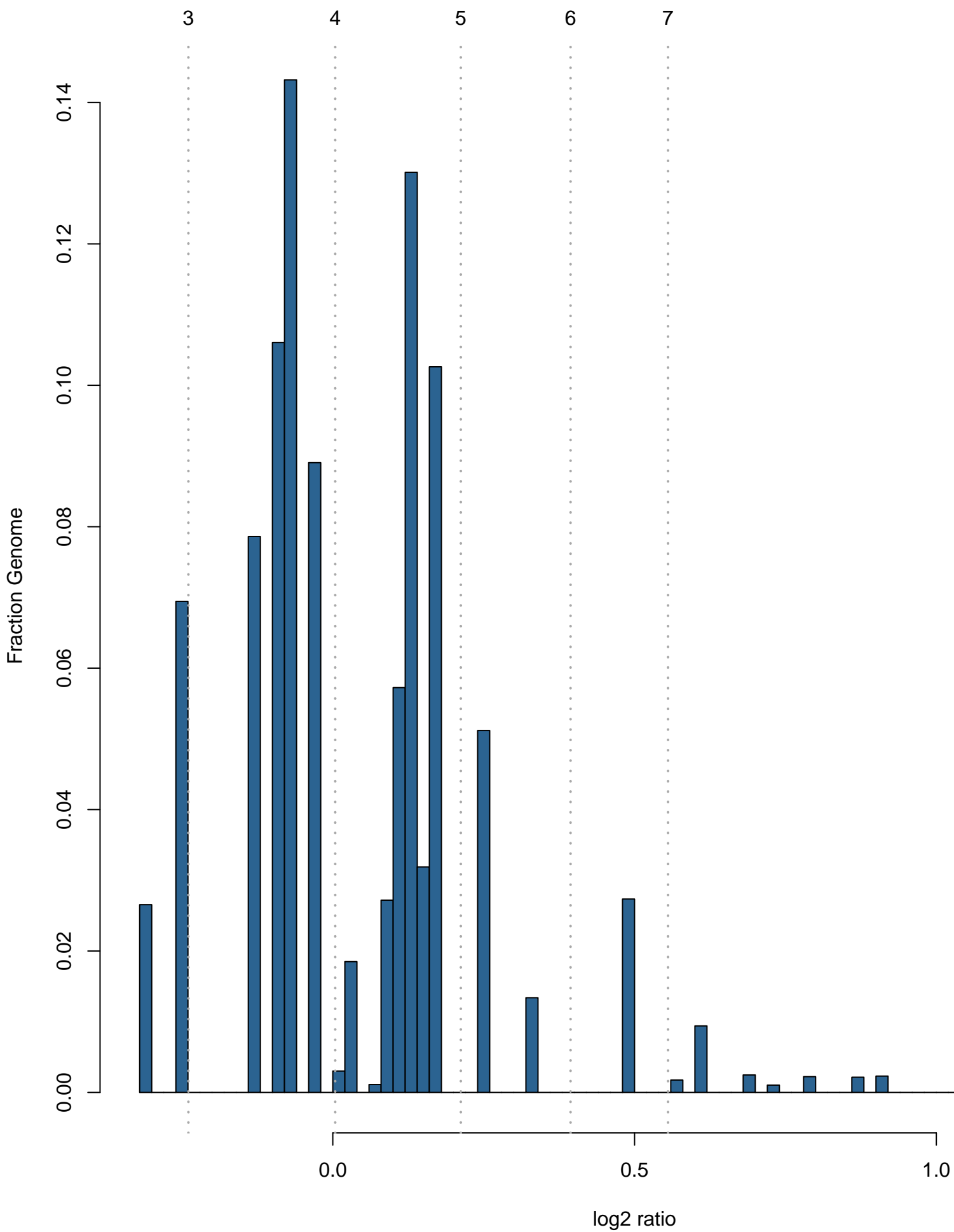


SCNA-fit log-likelihood: -7043.8

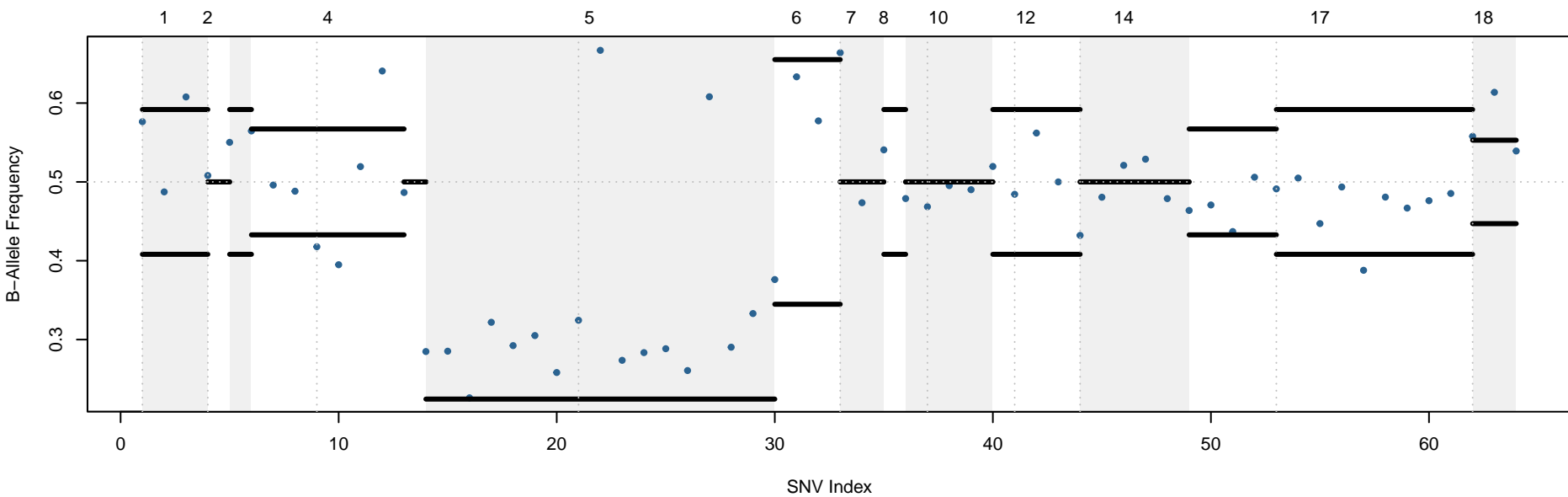




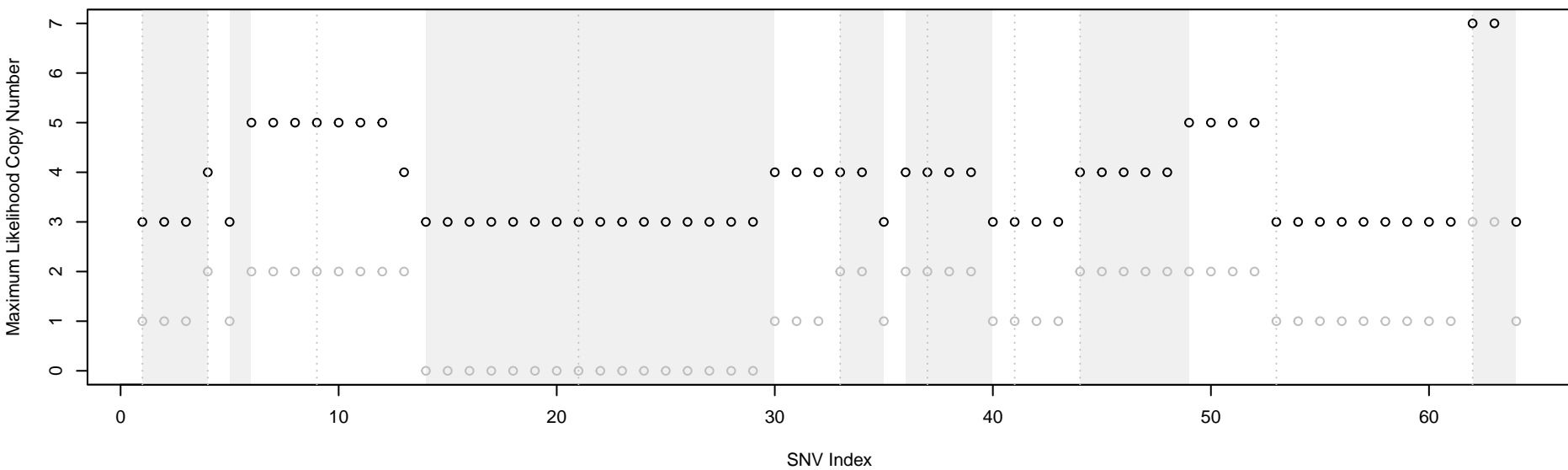
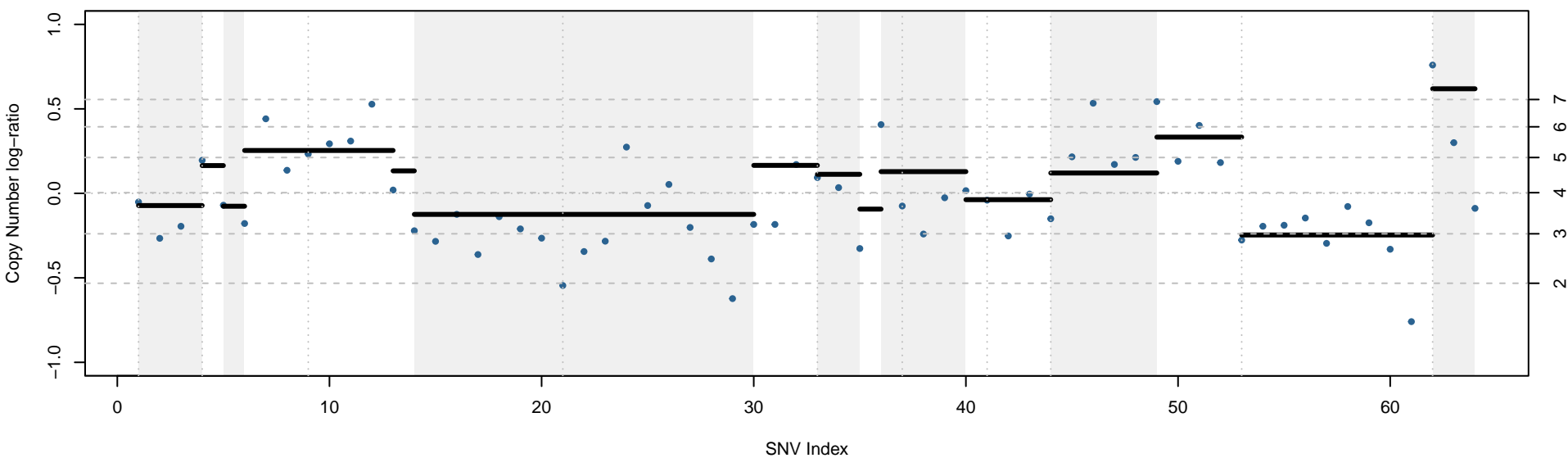
Purity: 0.45 Tumor ploidy: 3.982

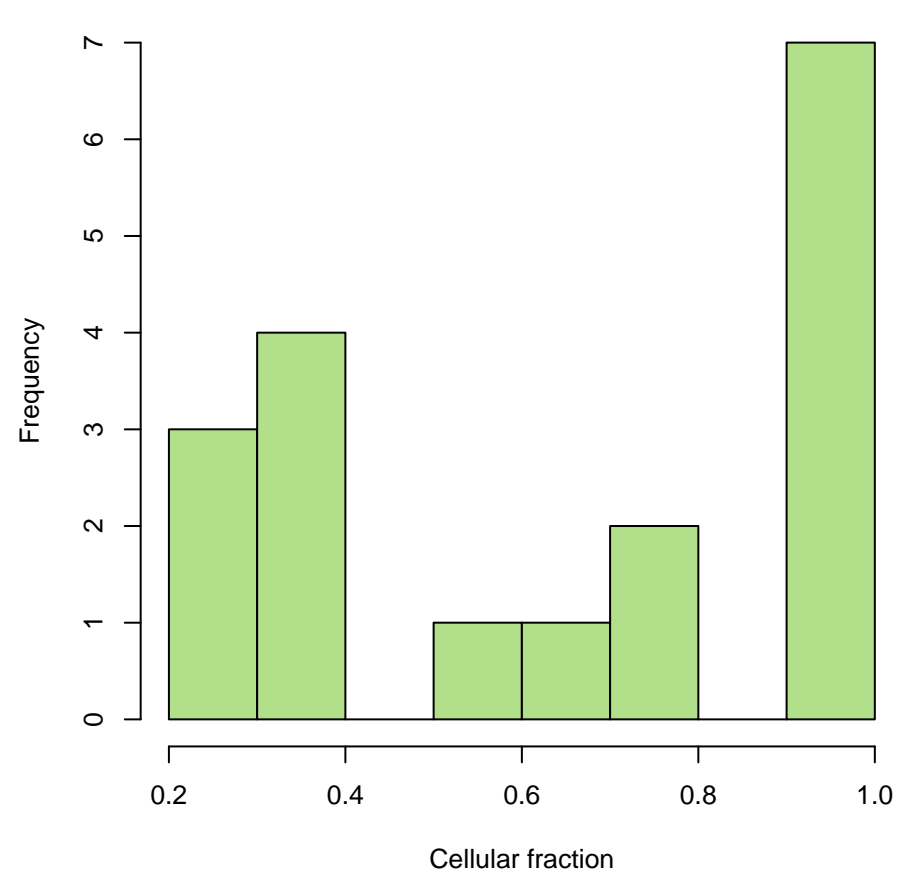
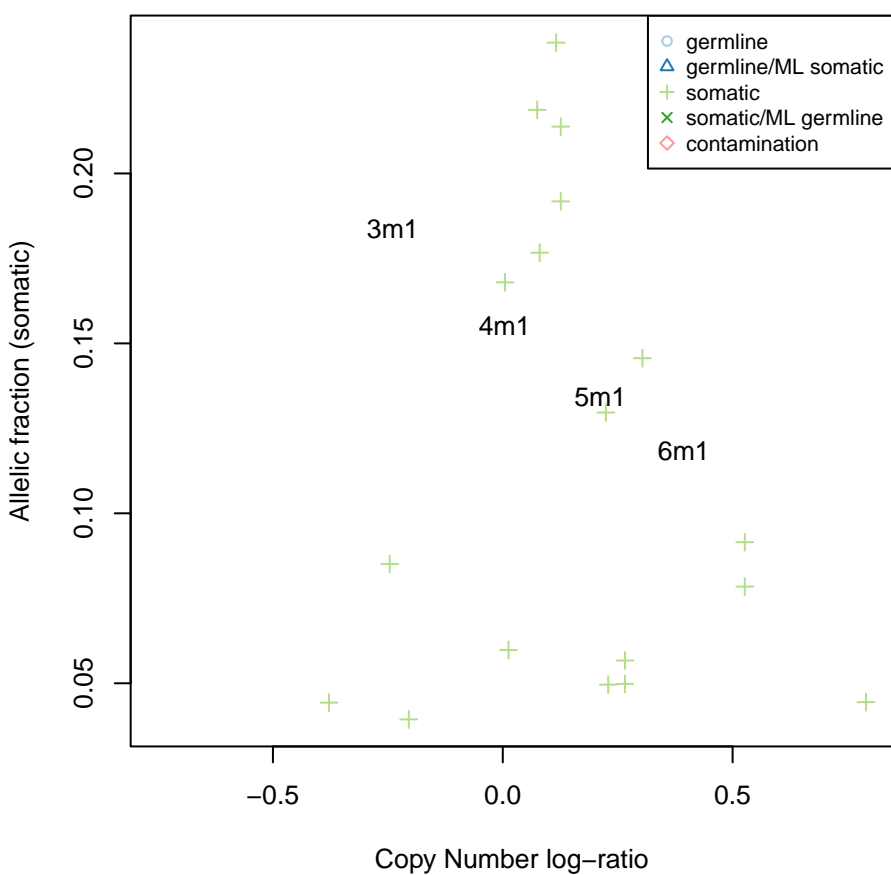
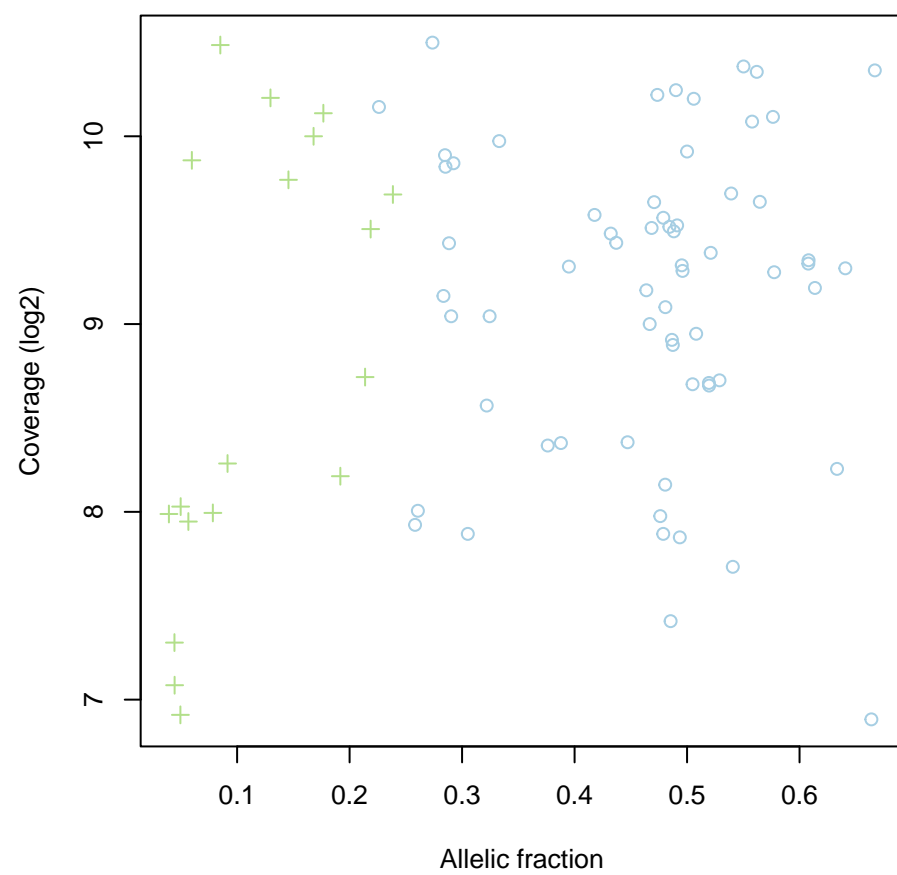
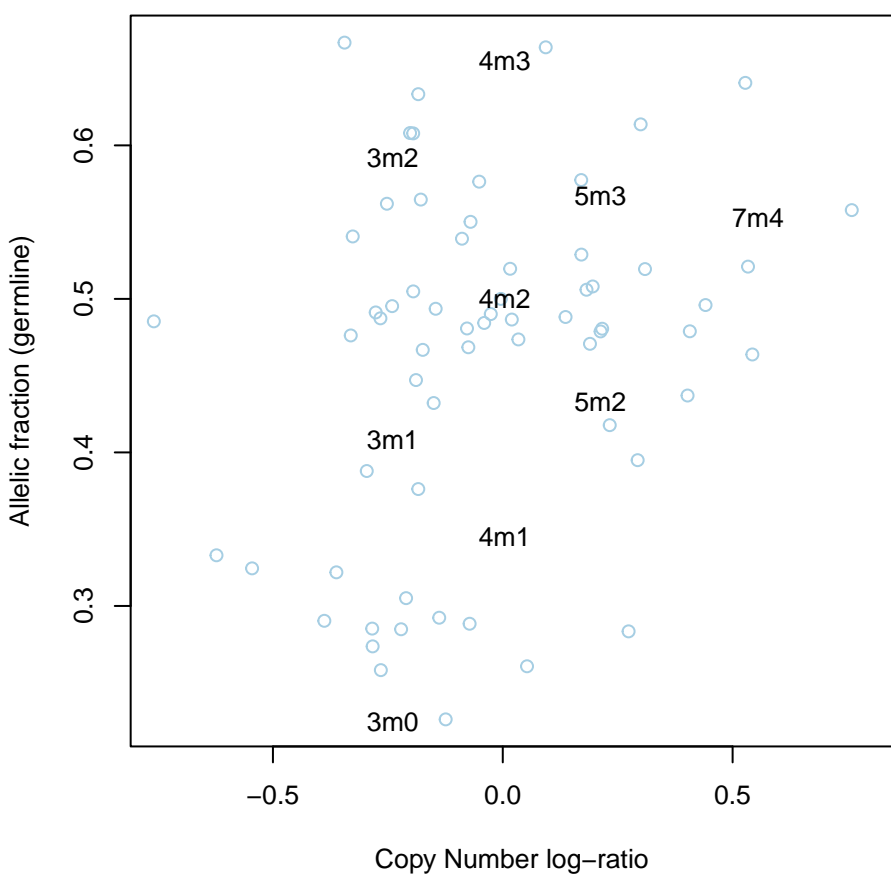


Purity: 0.45 Tumor ploidy: 3.982 SNV log-likelihood: -128.19 GoF: 89.7% Mean coverage: 586,641

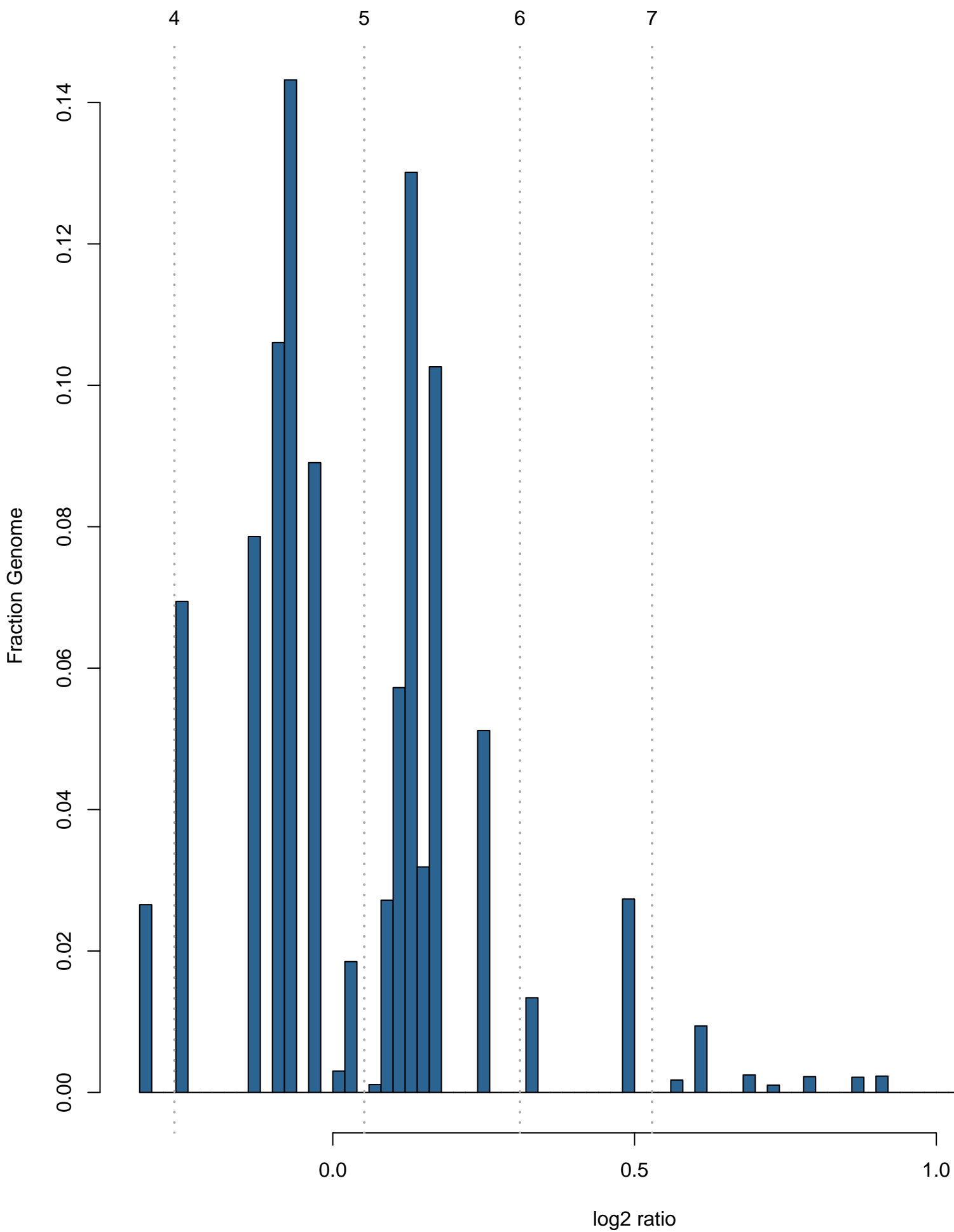


SCNA-fit log-likelihood: -7023.42



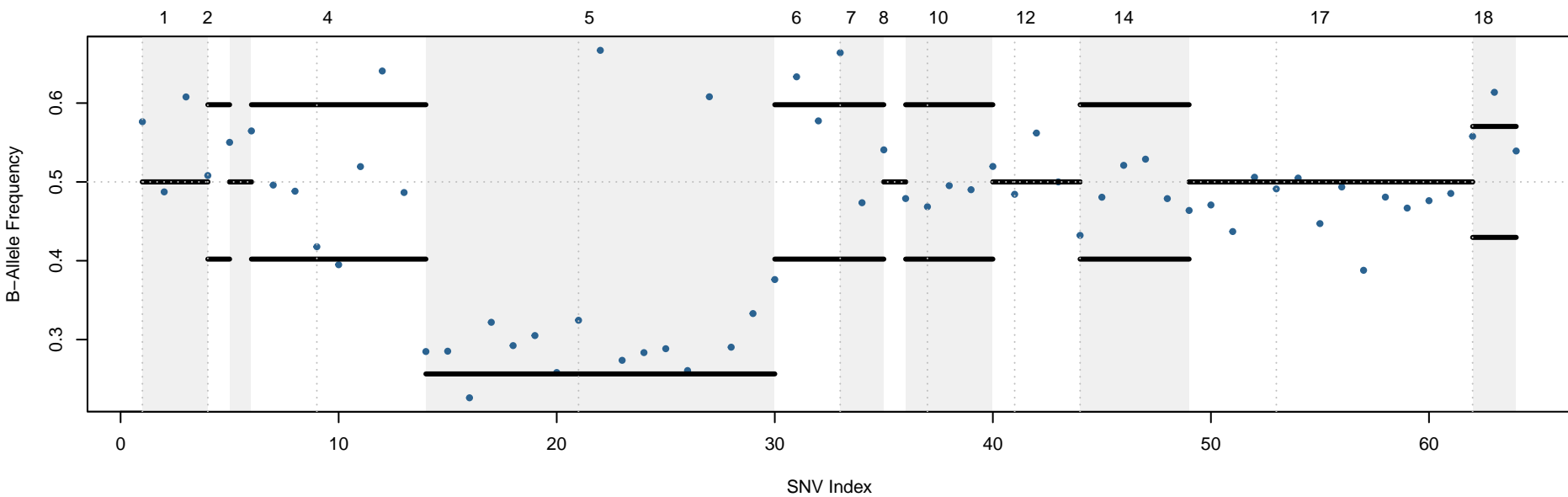


Purity: 0.95 Tumor ploidy: 4.819

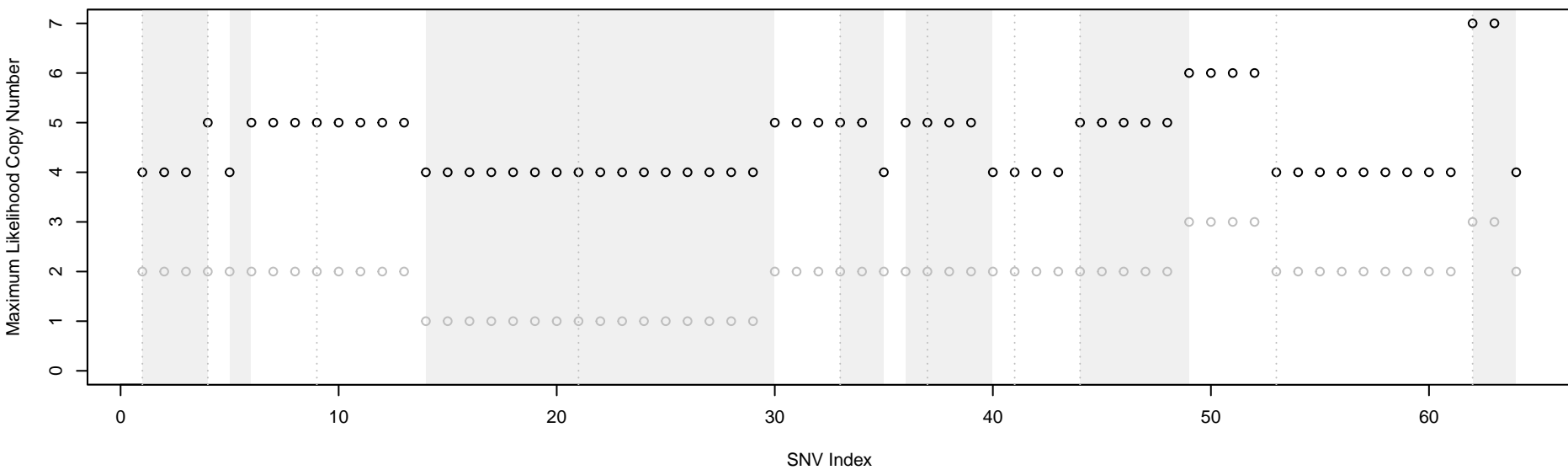
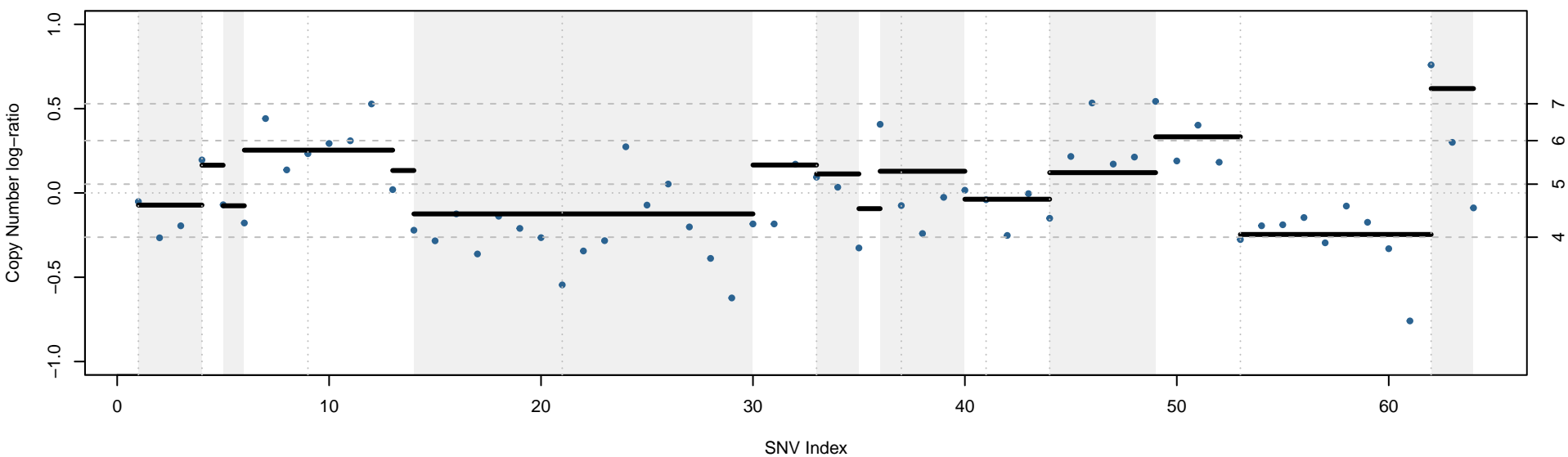


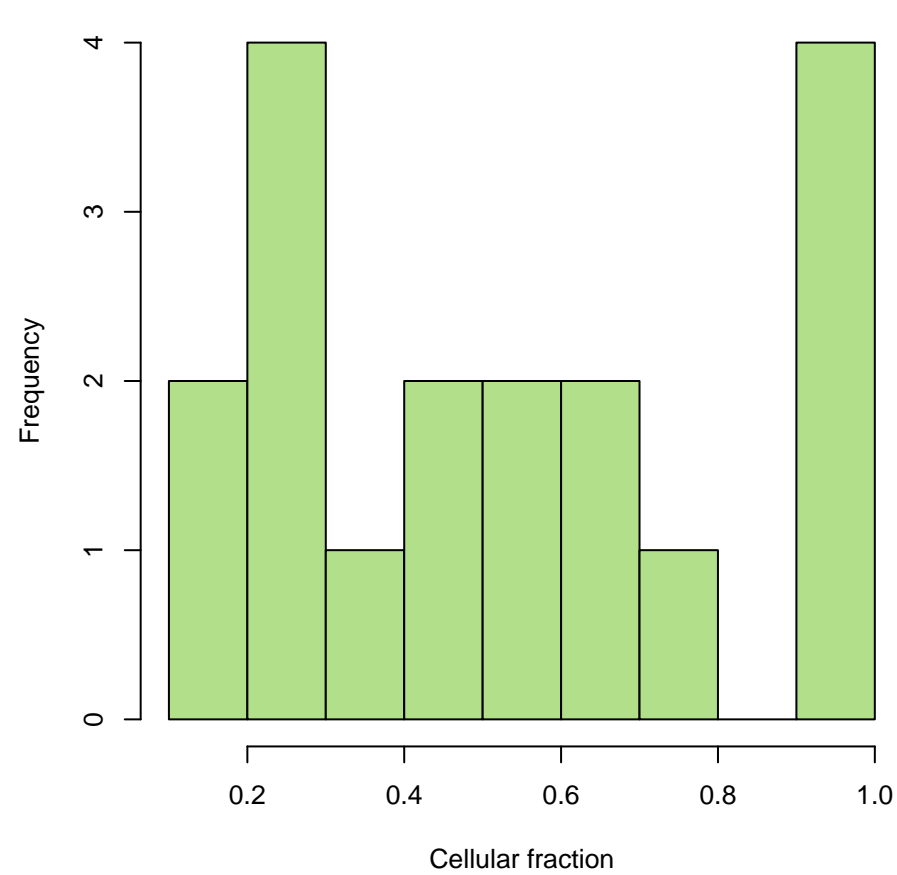
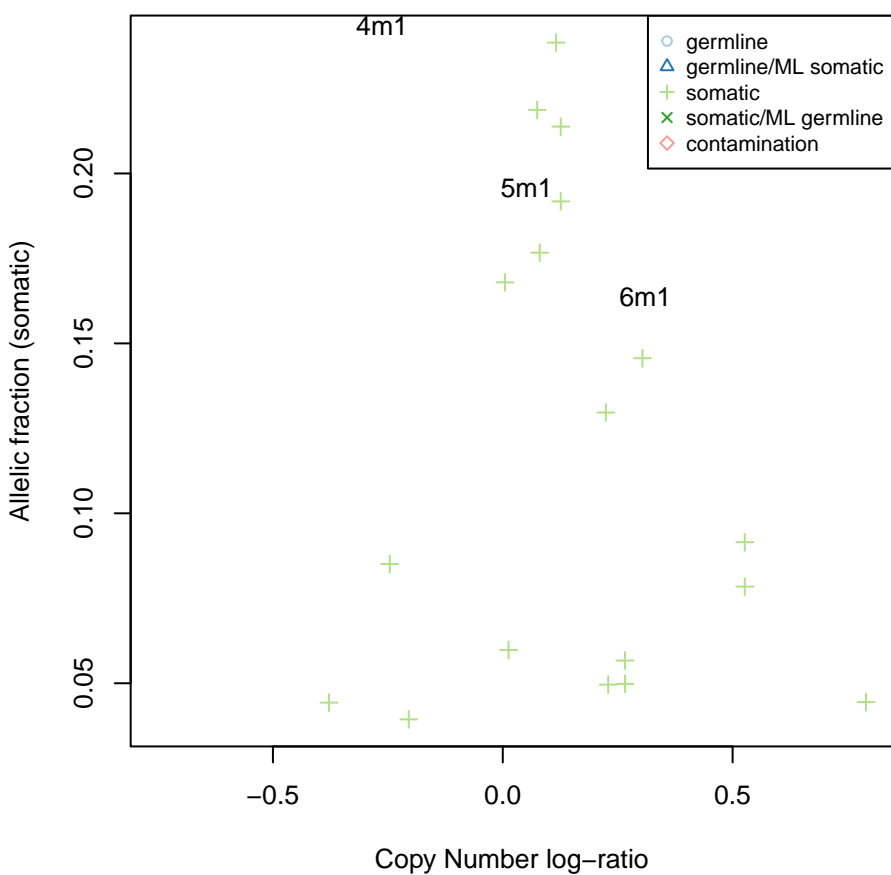
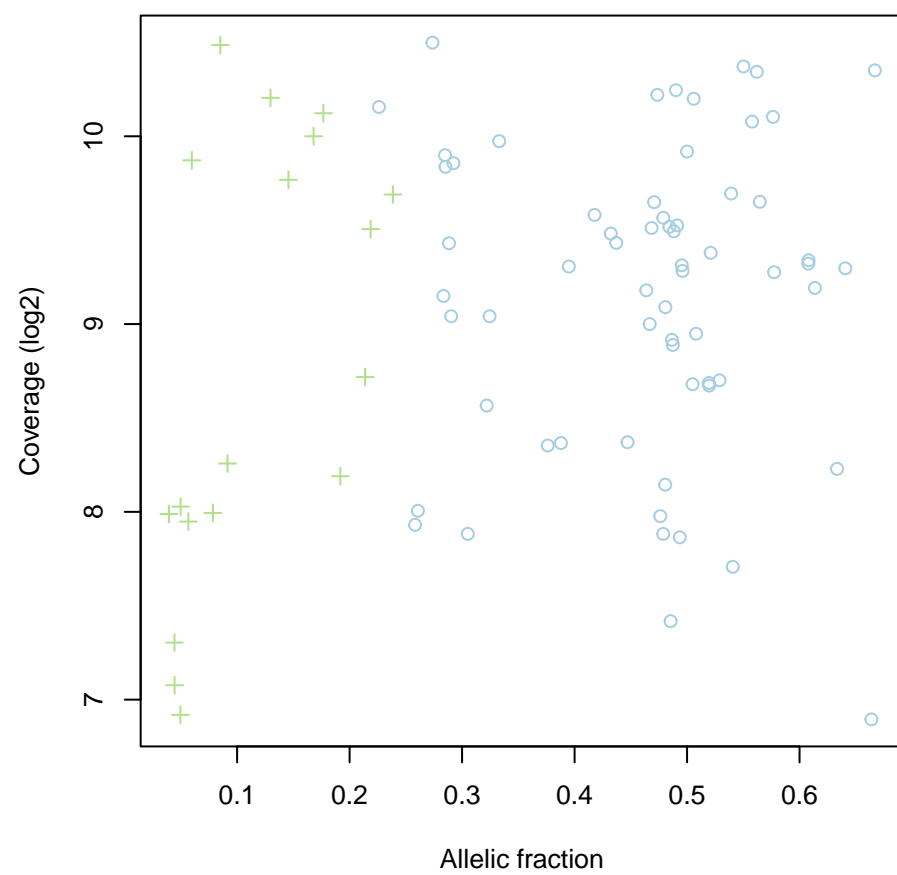
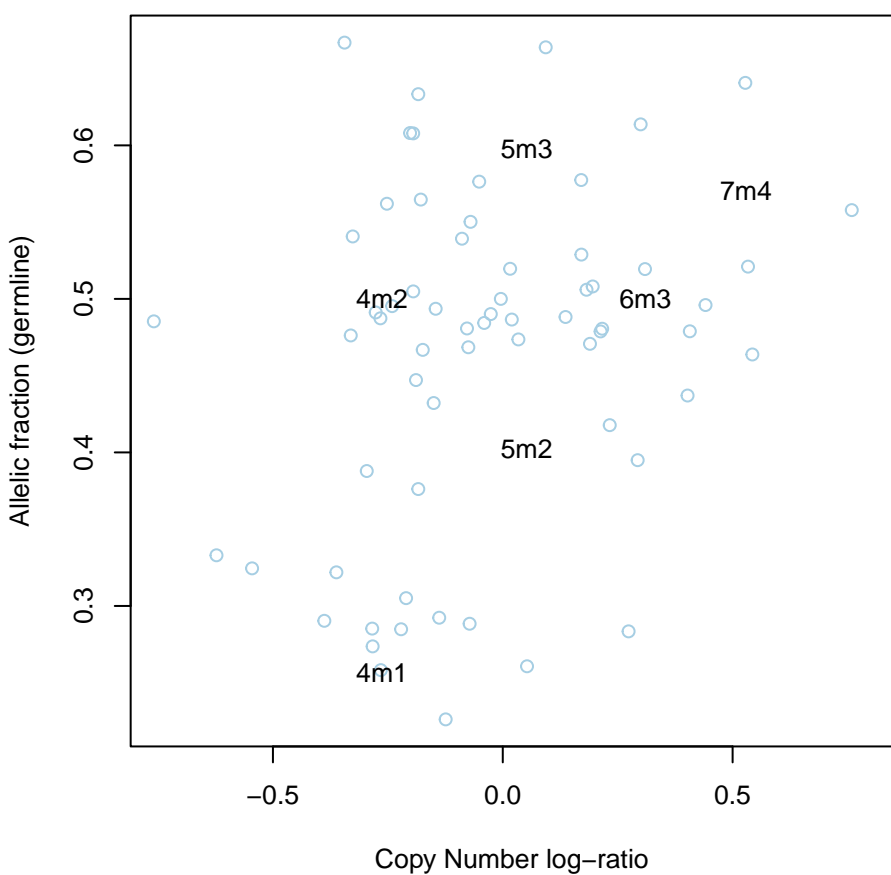


Purity: 0.95 Tumor ploidy: 4.819 SNV log-likelihood: -128.62 GoF: 87% Mean coverage: 586;641

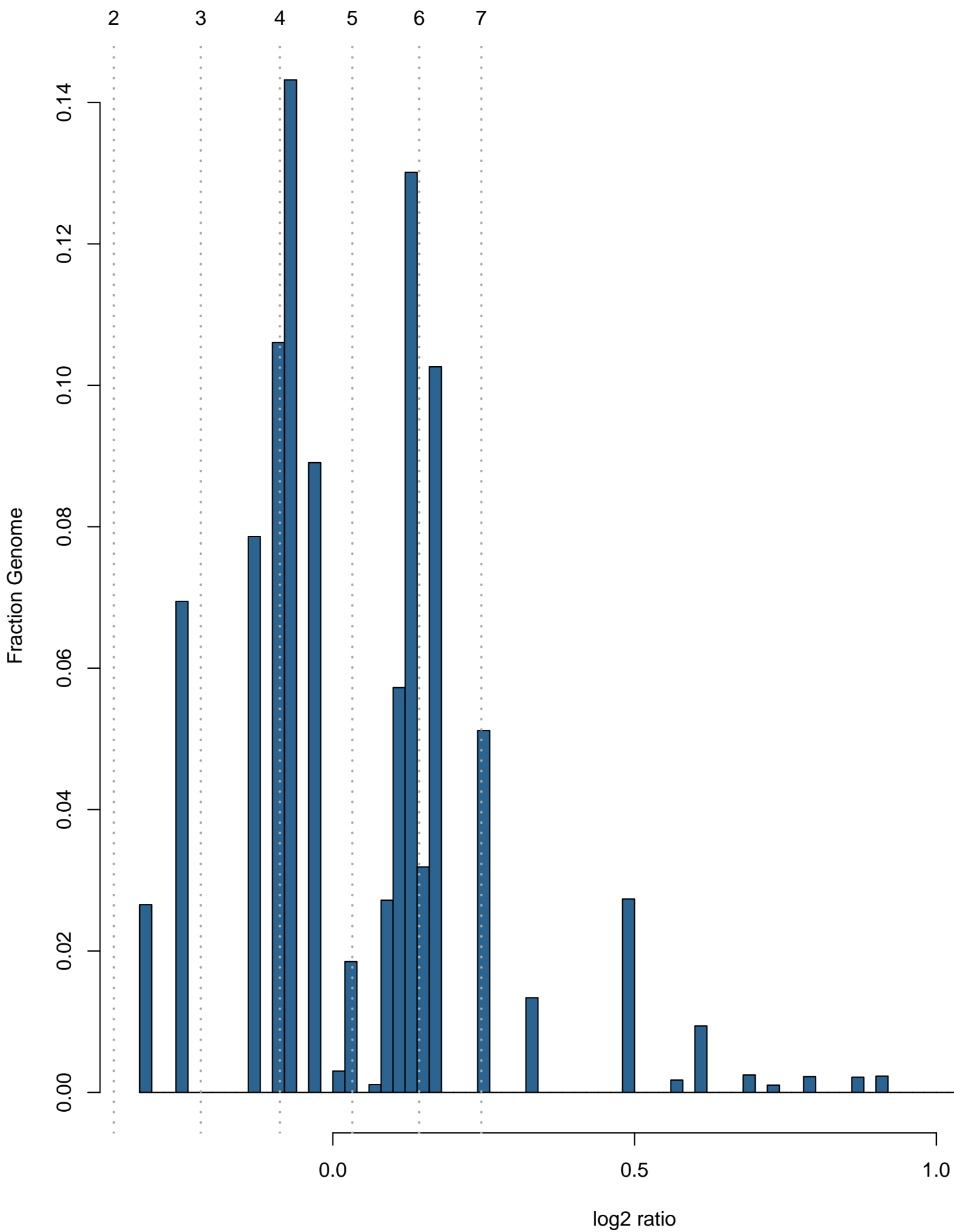


SCNA-fit log-likelihood: -7086.8

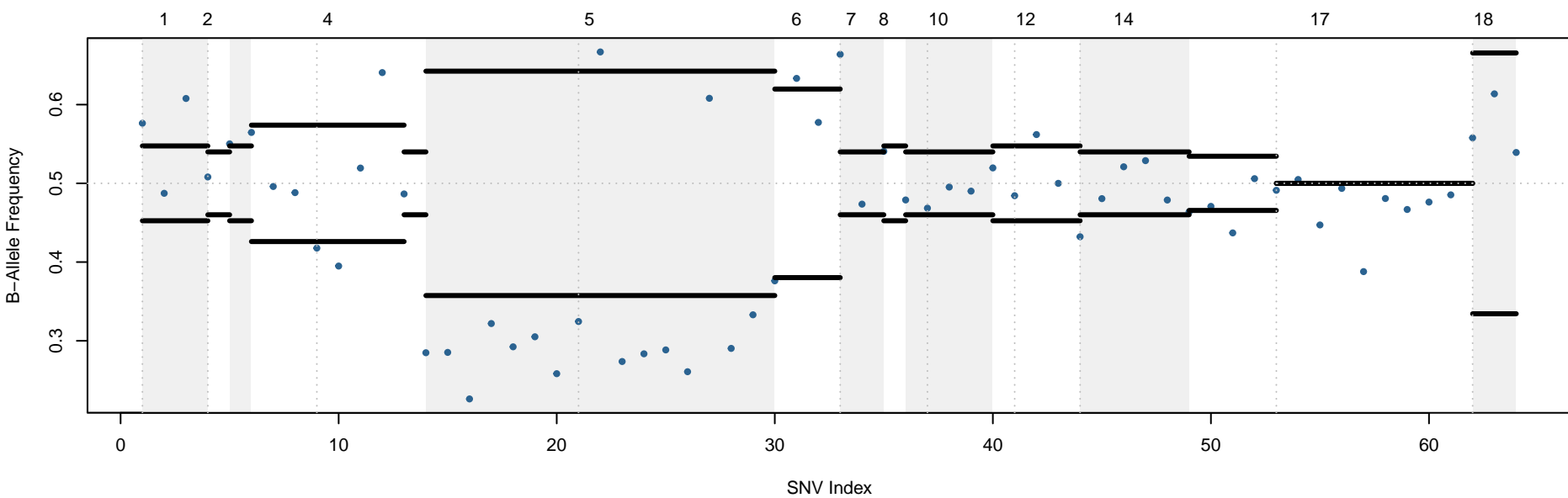




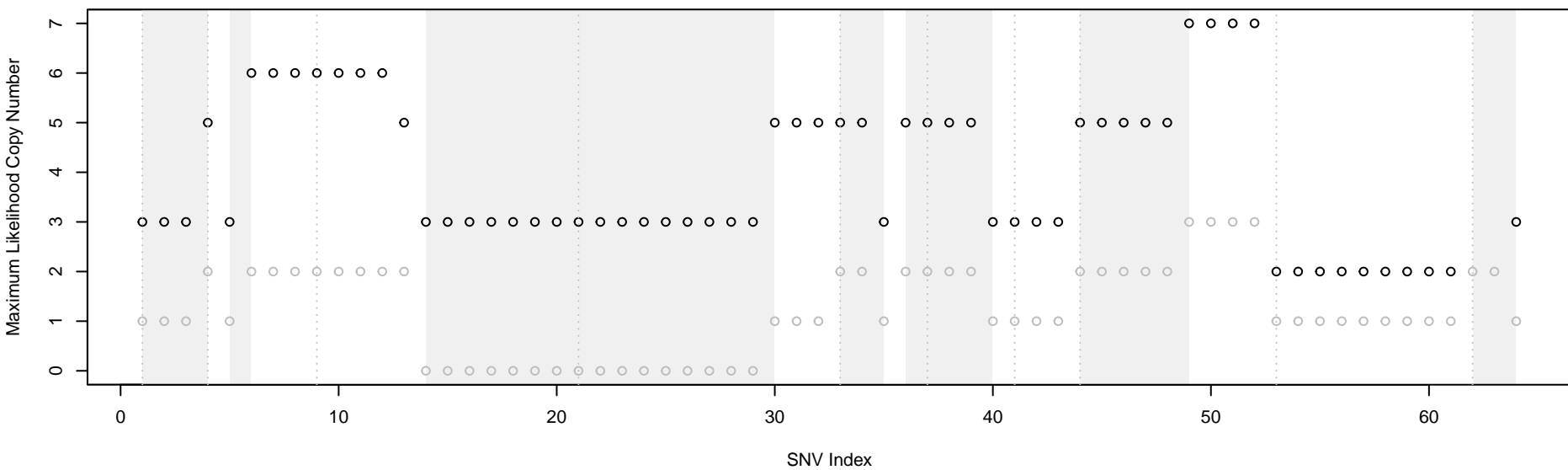
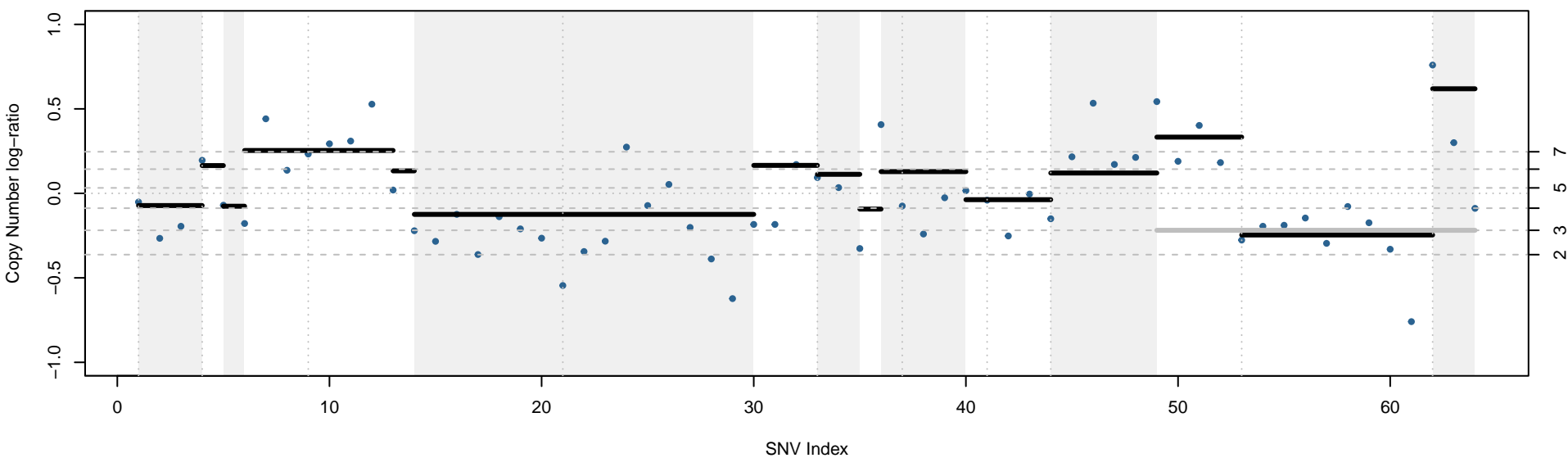
Purity: 0.21 Tumor ploidy: 4.722

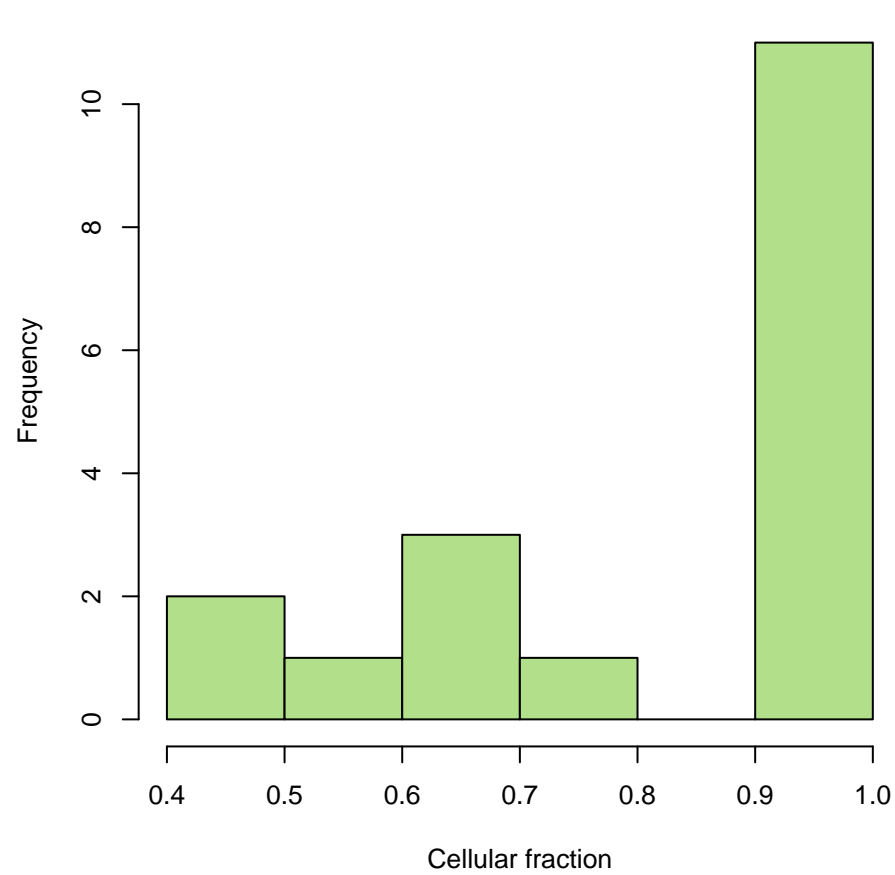
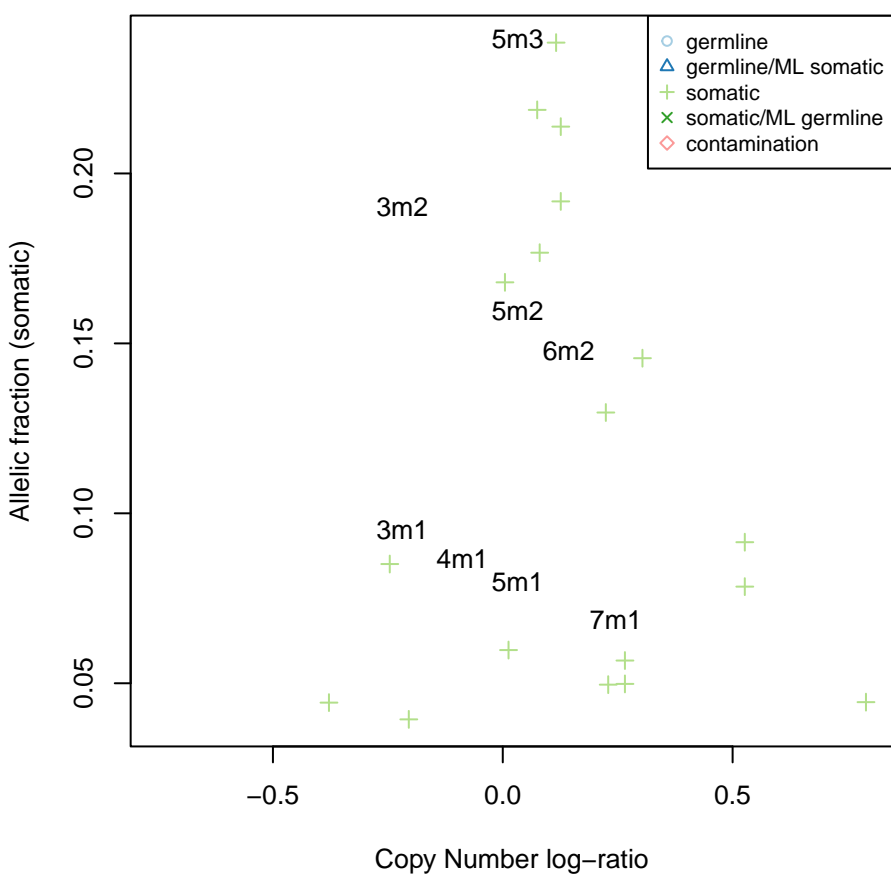
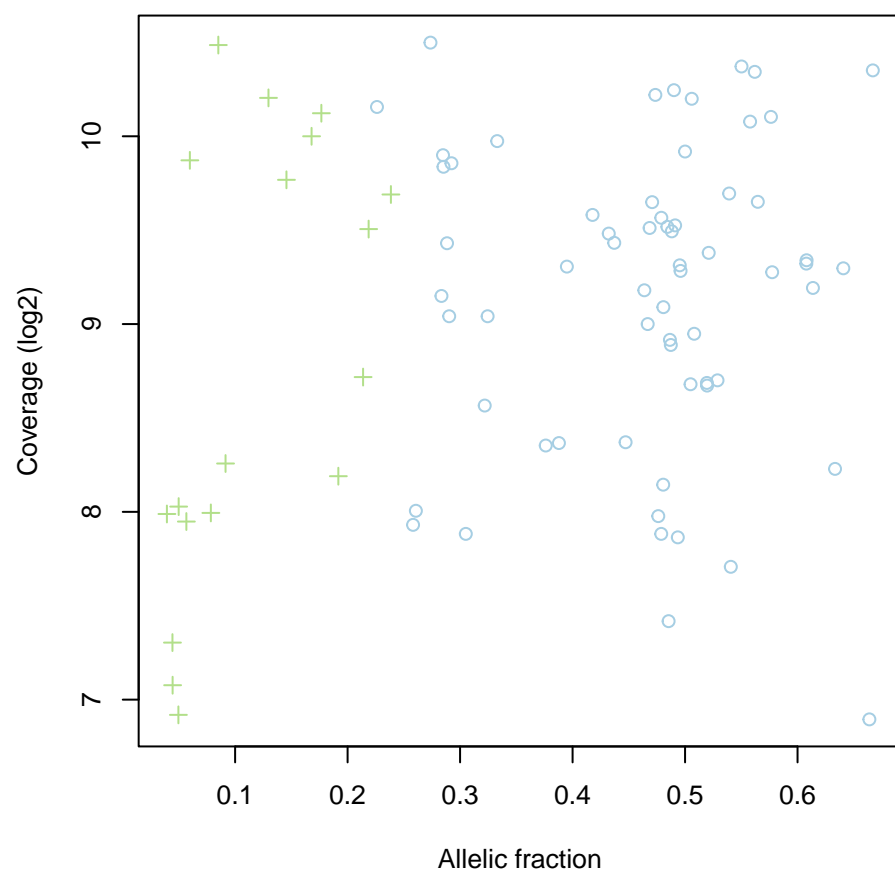
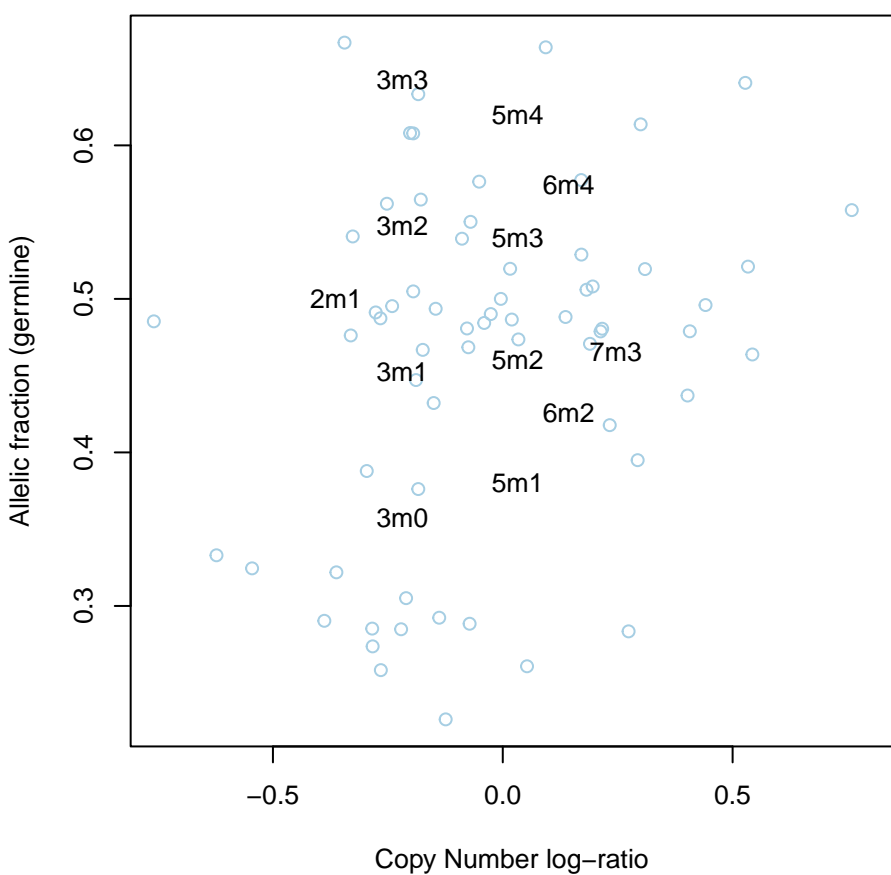


Purity: 0.21 Tumor ploidy: 4.722 SNV log-likelihood: -73.09 GoF: 94.2% Mean coverage: 586;641

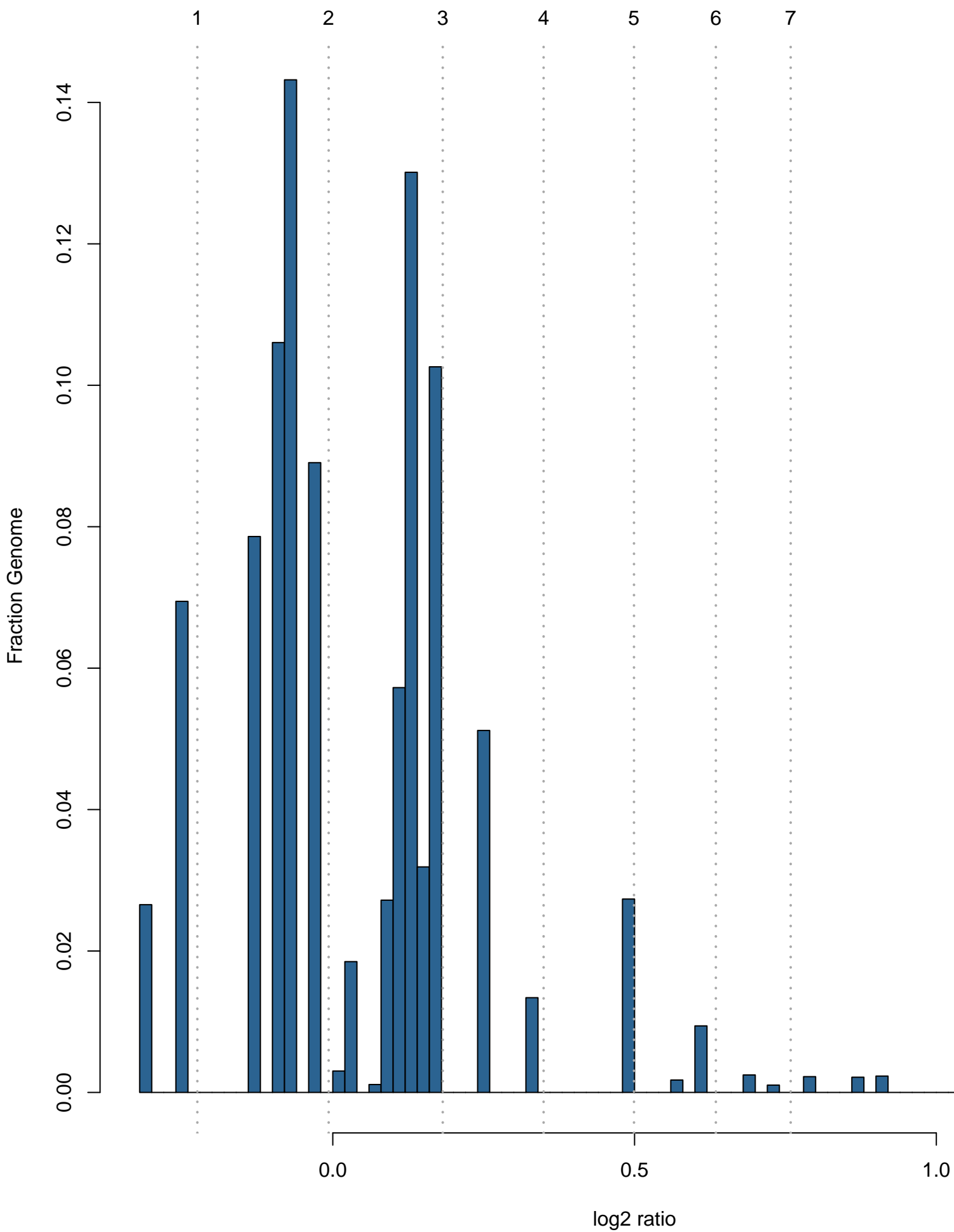


SCNA-fit log-likelihood: -7182.88

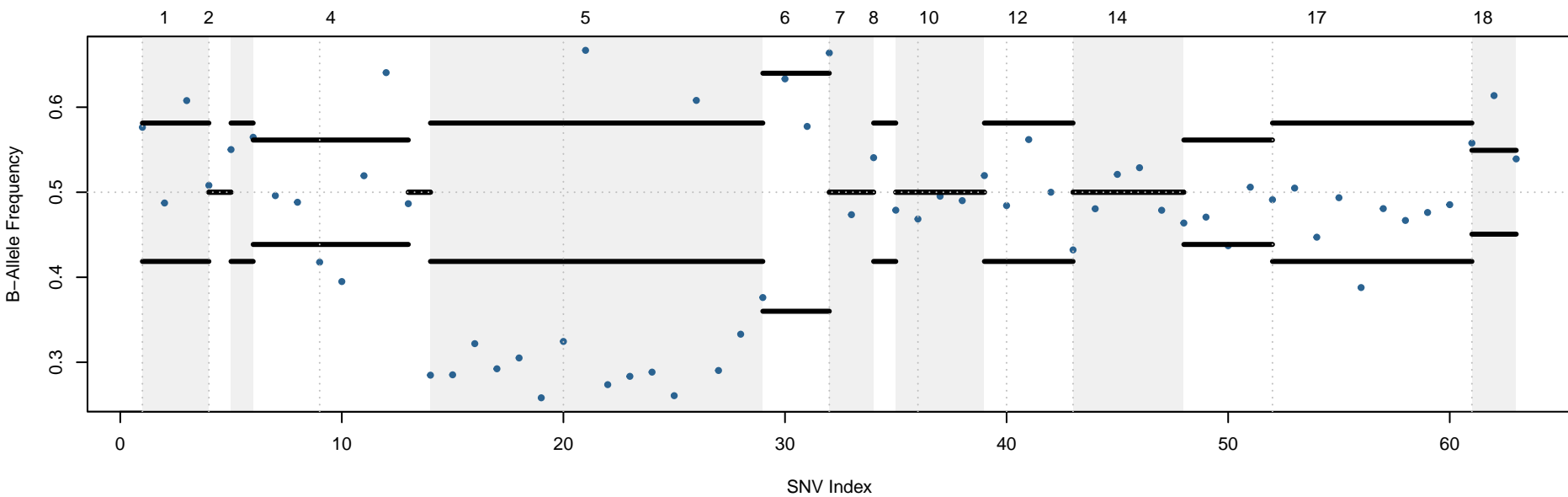




Purity: 0.28 Tumor ploidy: 2.034



Purity: 0.28 Tumor ploidy: 2.034 SNV log-likelihood: -183.24 GoF: 86.9% Mean coverage: 586,641



SCNA-fit log-likelihood: -7016.52

