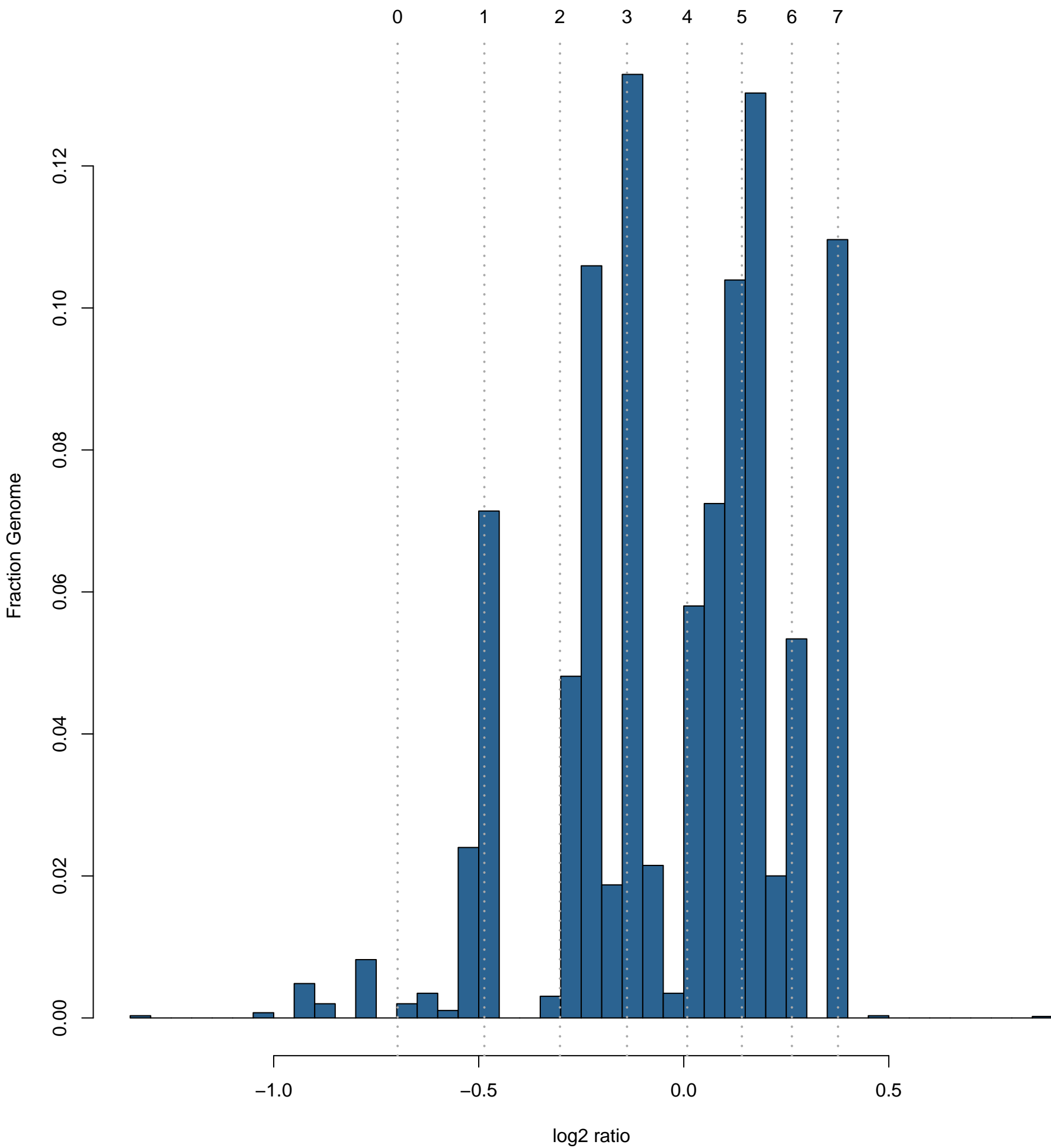
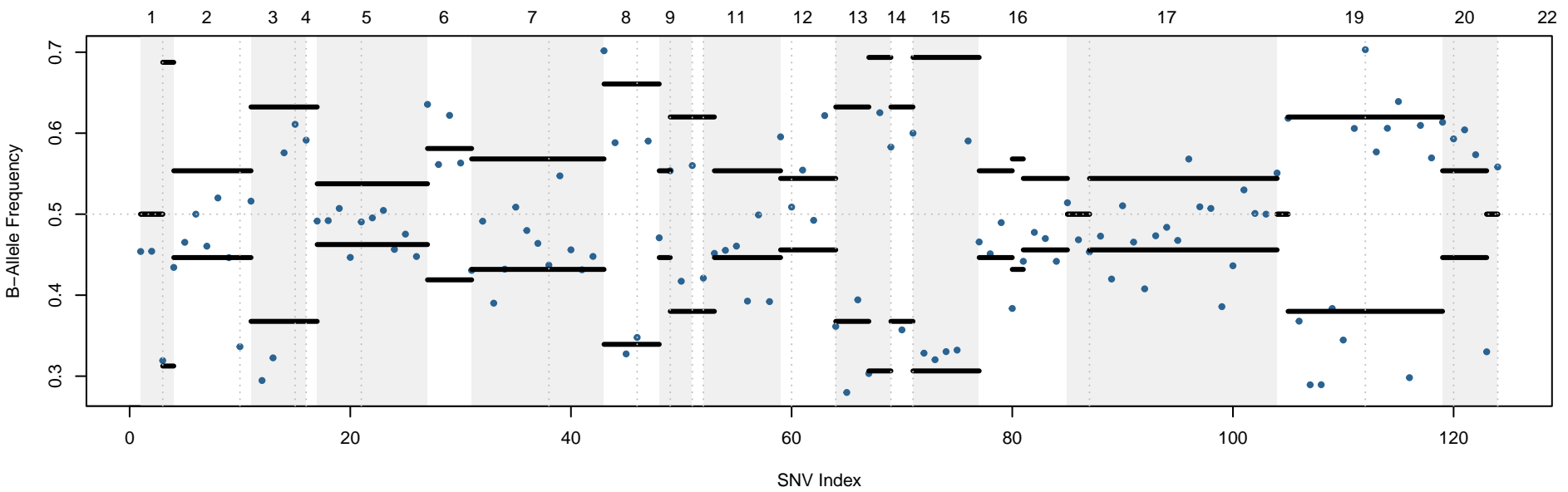


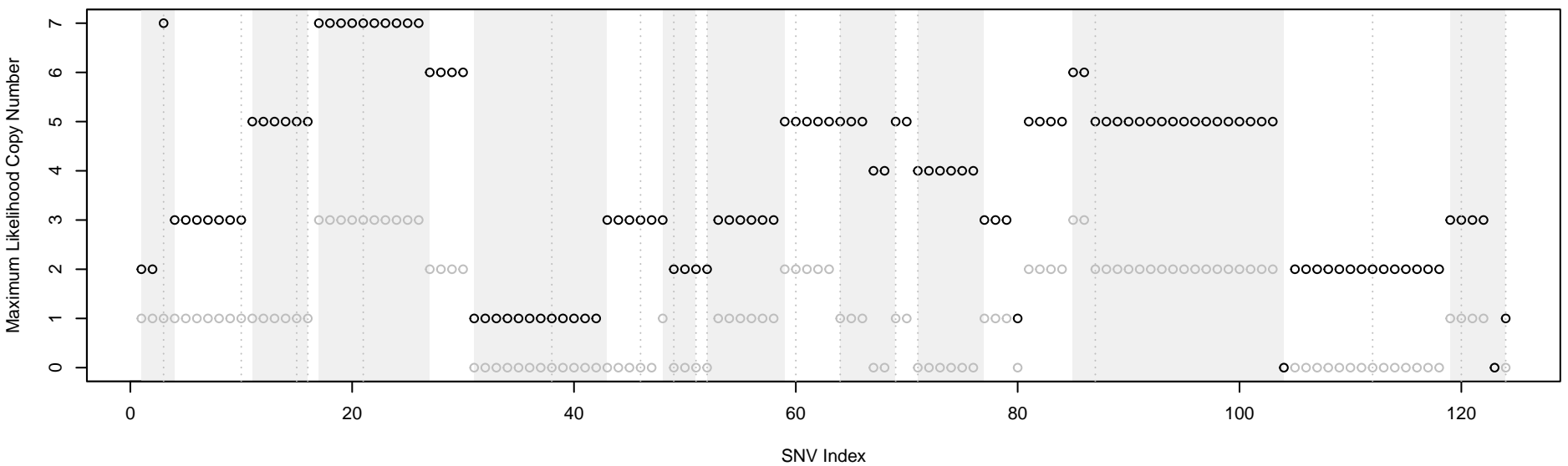
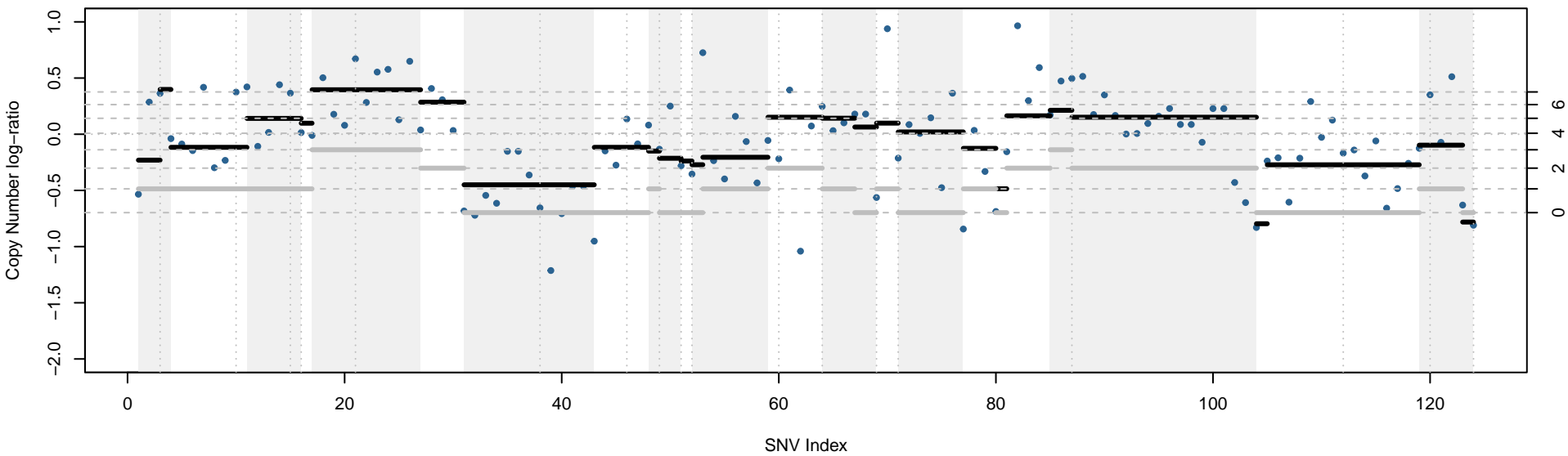
Purity: 0.24 Tumor ploidy: 3.94

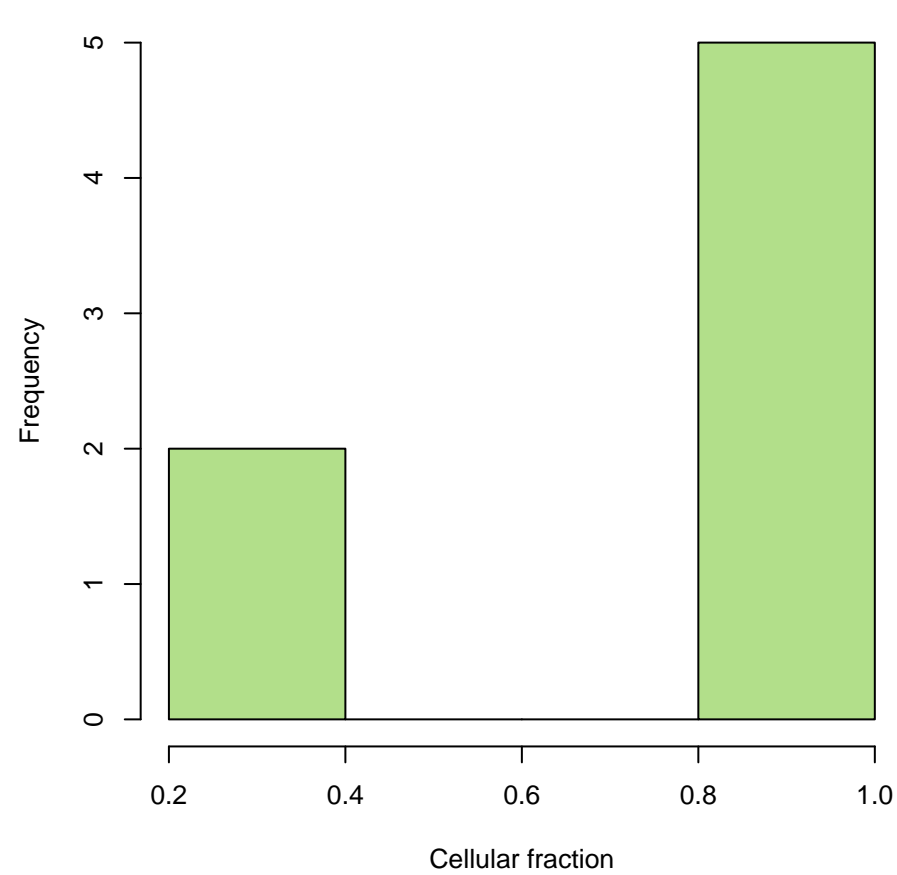
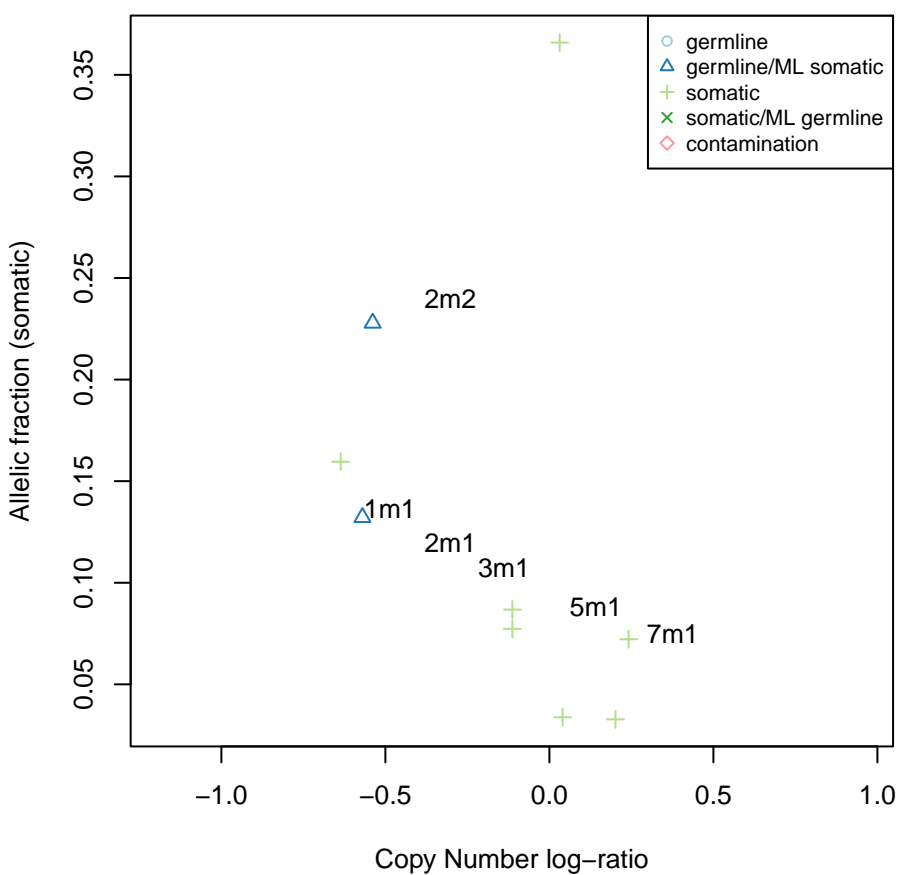
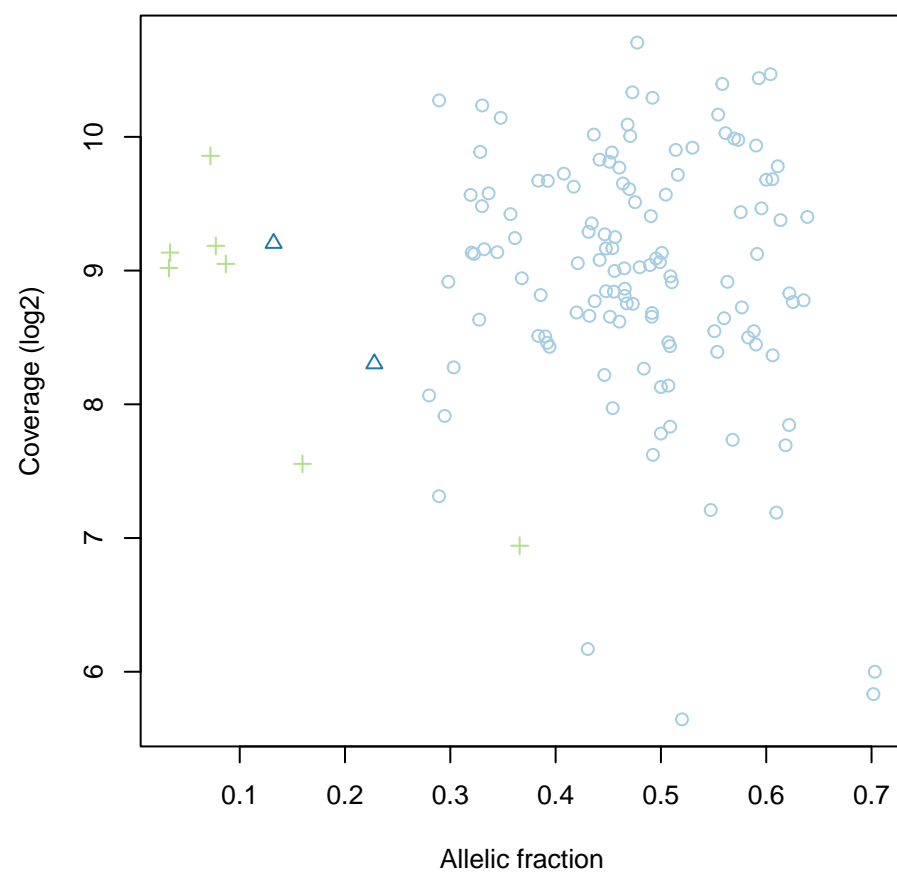
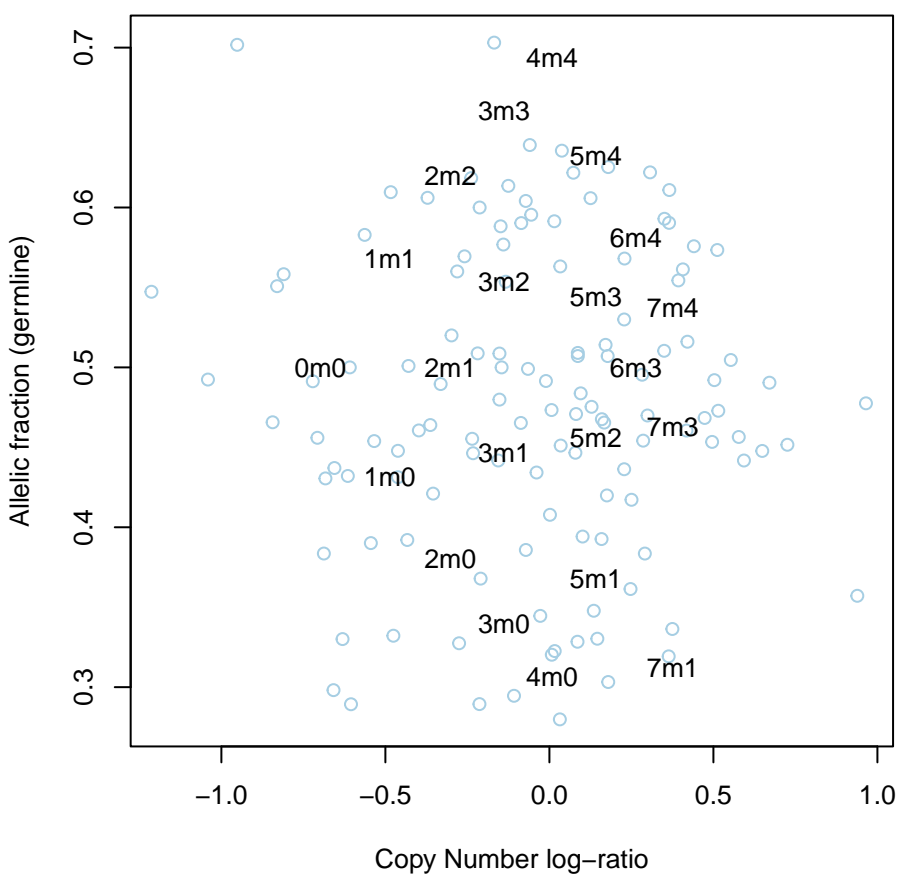


Purity: 0.24 Tumor ploidy: 3.94 SNV log-likelihood: -103.11 GoF: 94.9% Mean coverage: 459;590

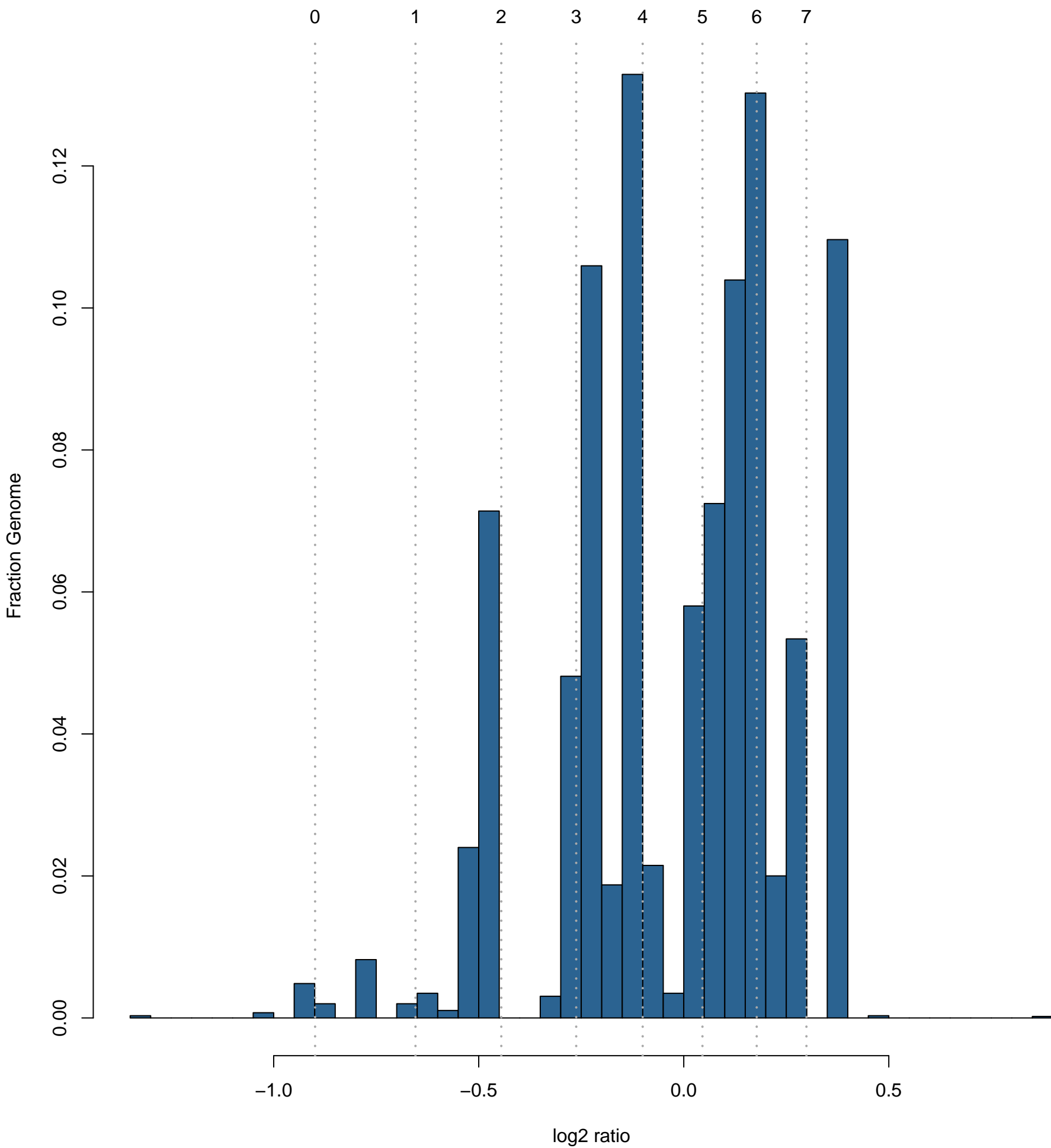


SCNA-fit log-likelihood: -3702.56

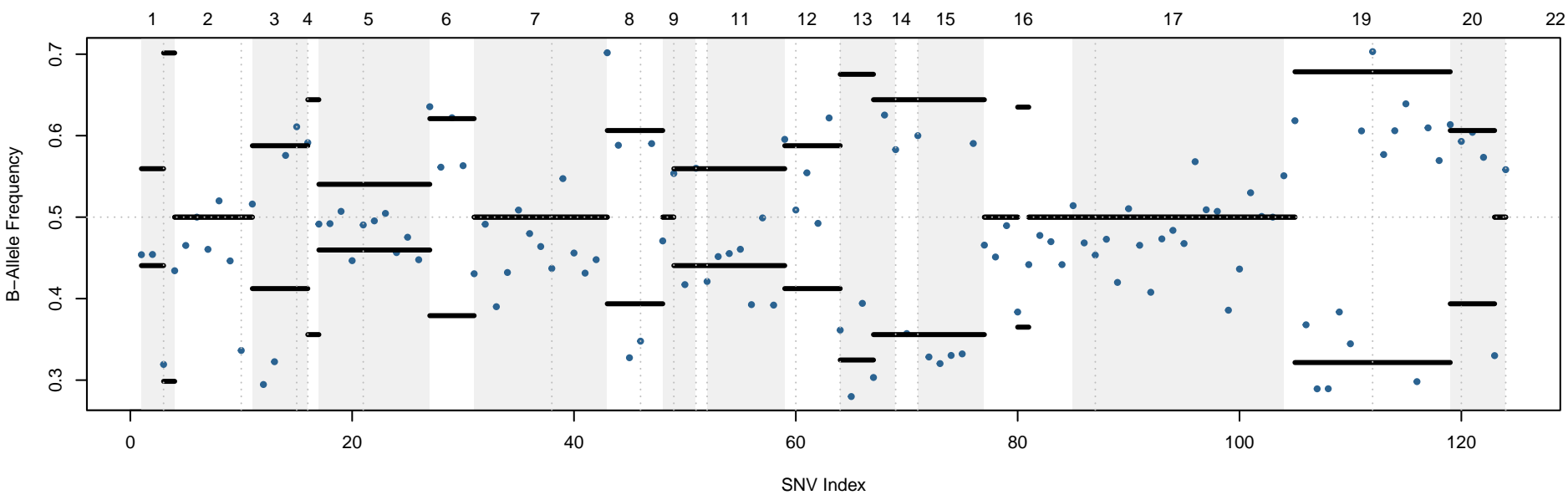




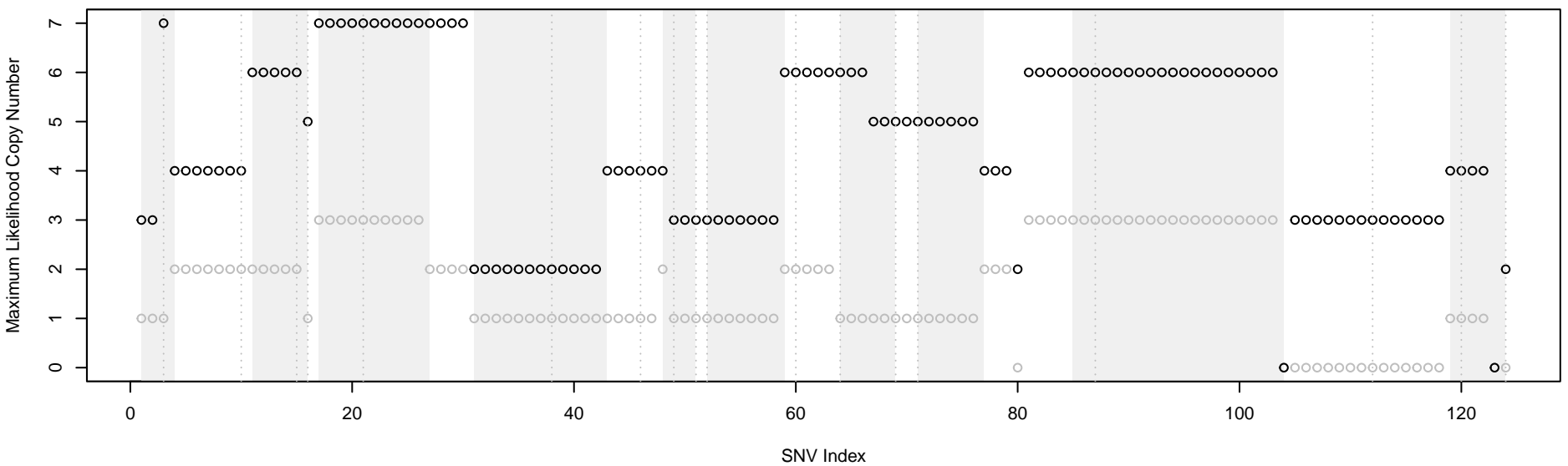
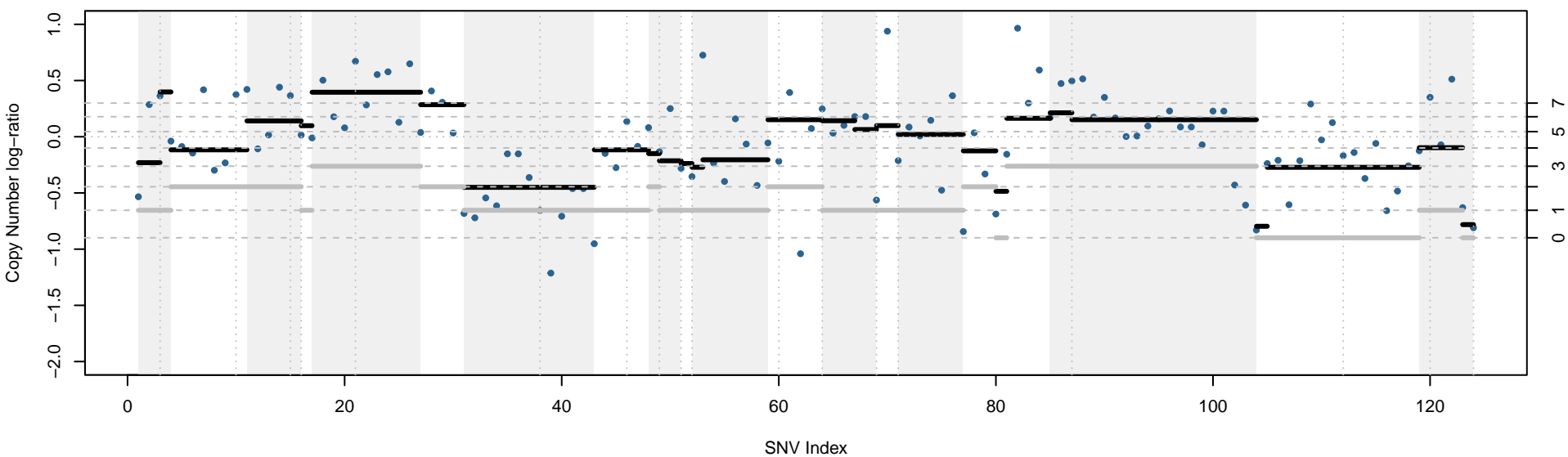
Purity: 0.27 Tumor ploidy: 4.676

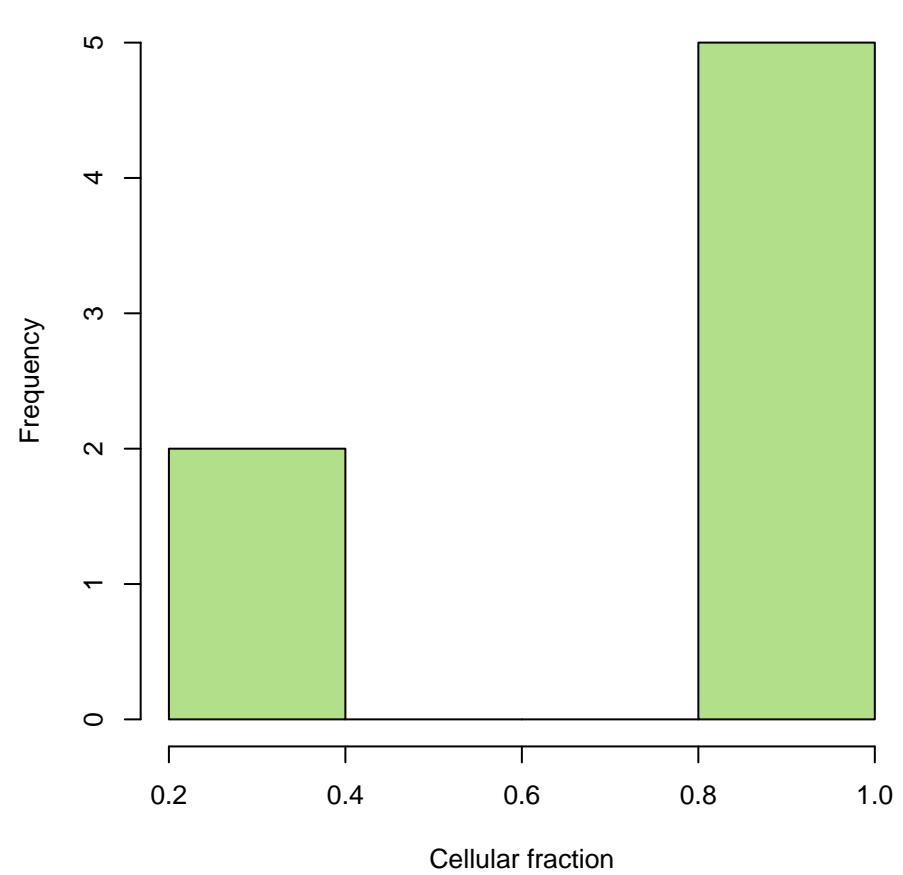
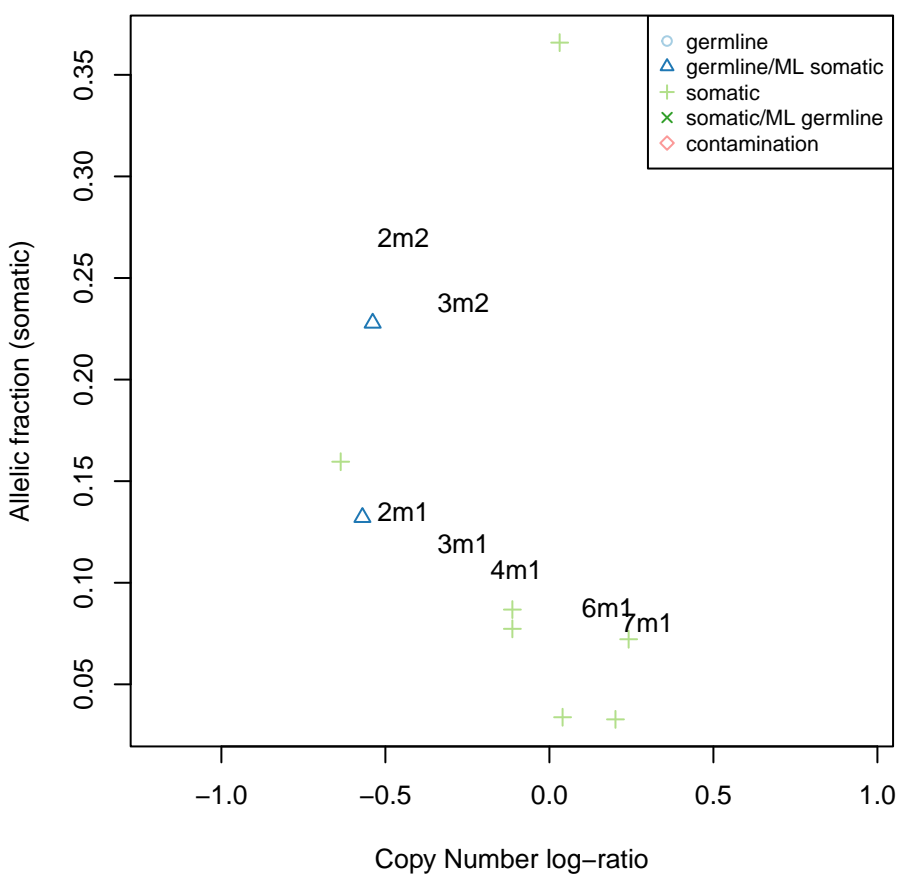
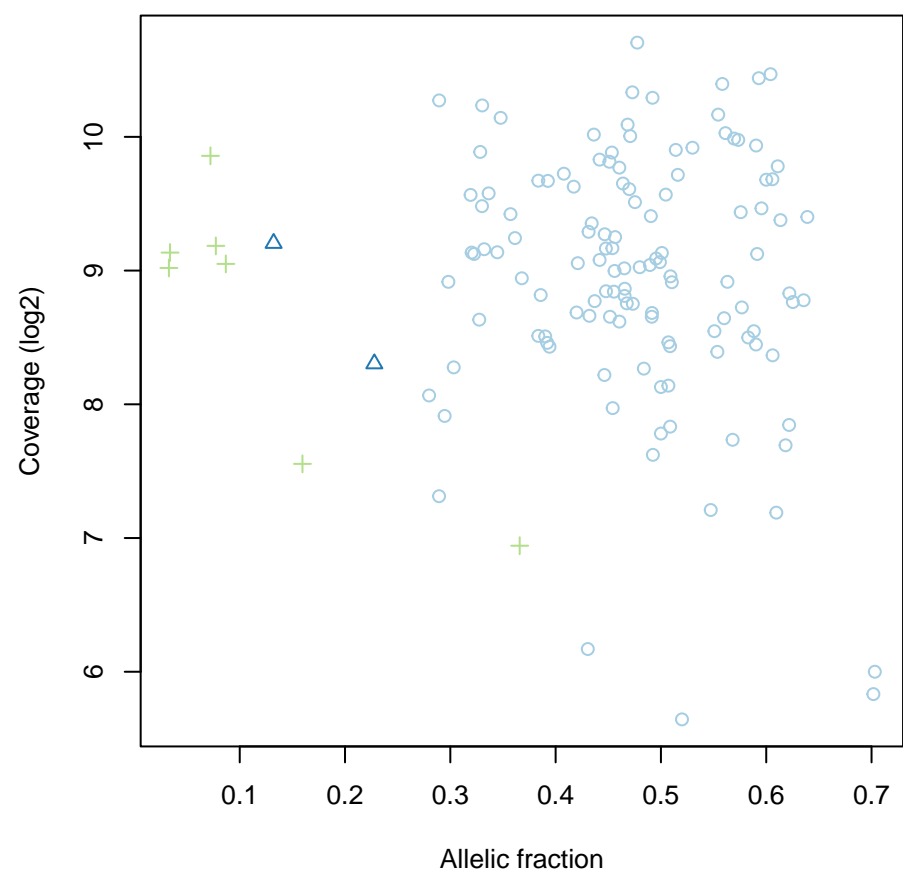
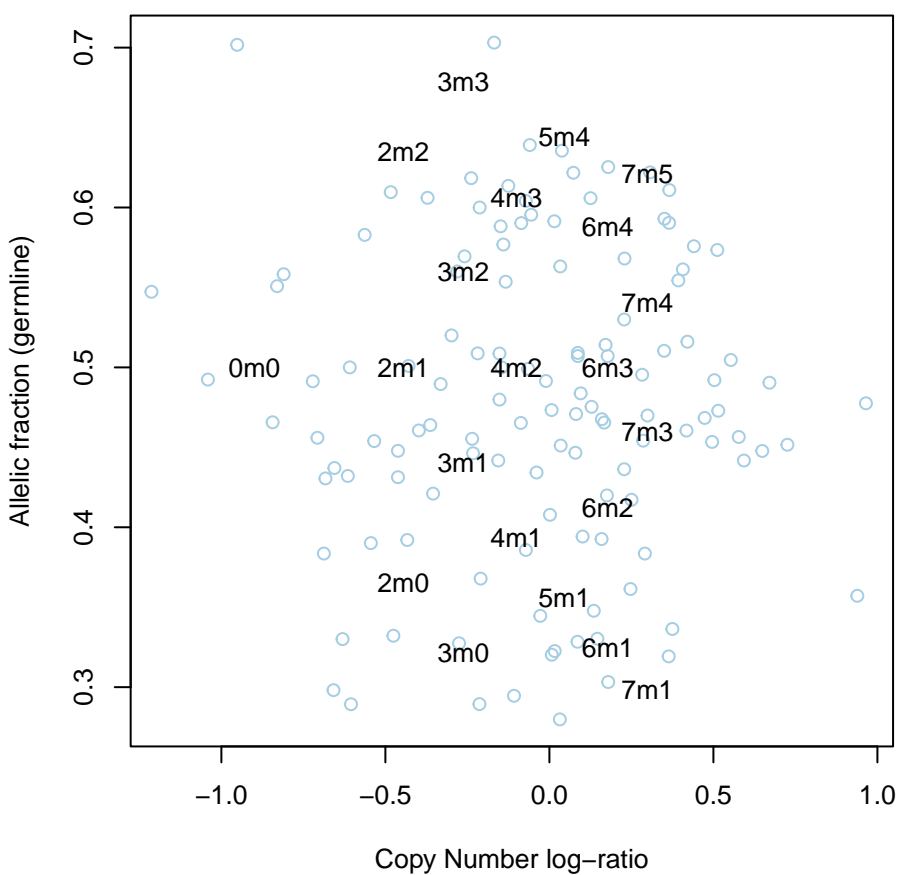


Purity: 0.27 Tumor ploidy: 4.676 SNV log-likelihood: -121.71 GoF: 94% Mean coverage: 459;590

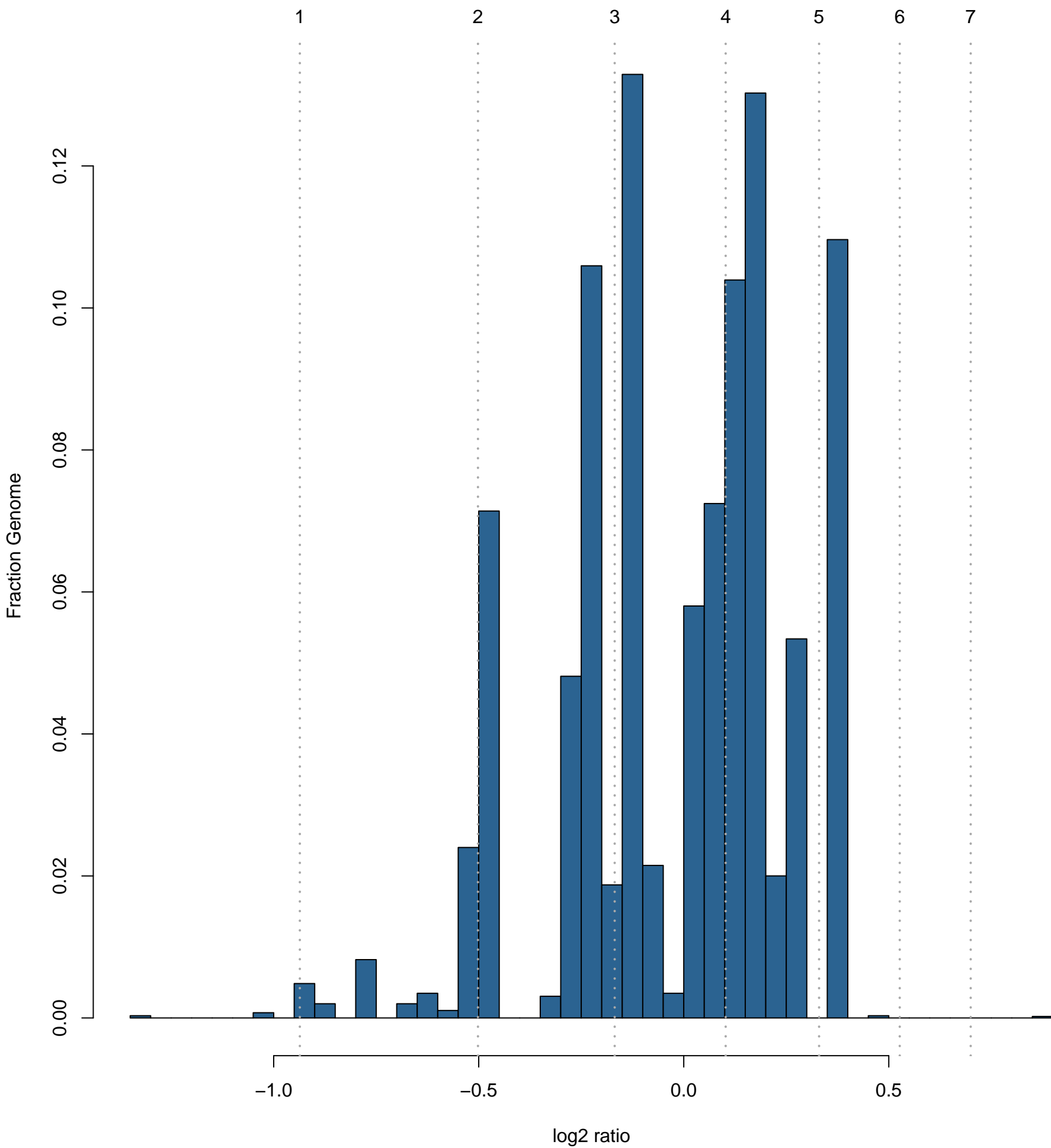


SCNA-fit log-likelihood: -3721.67

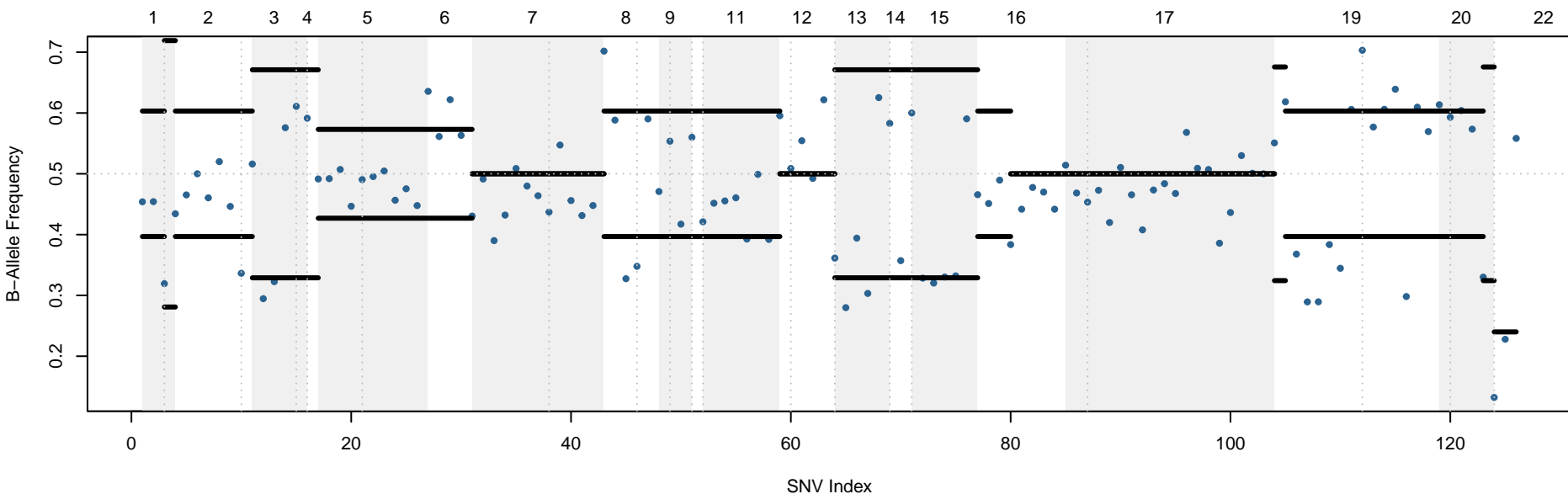




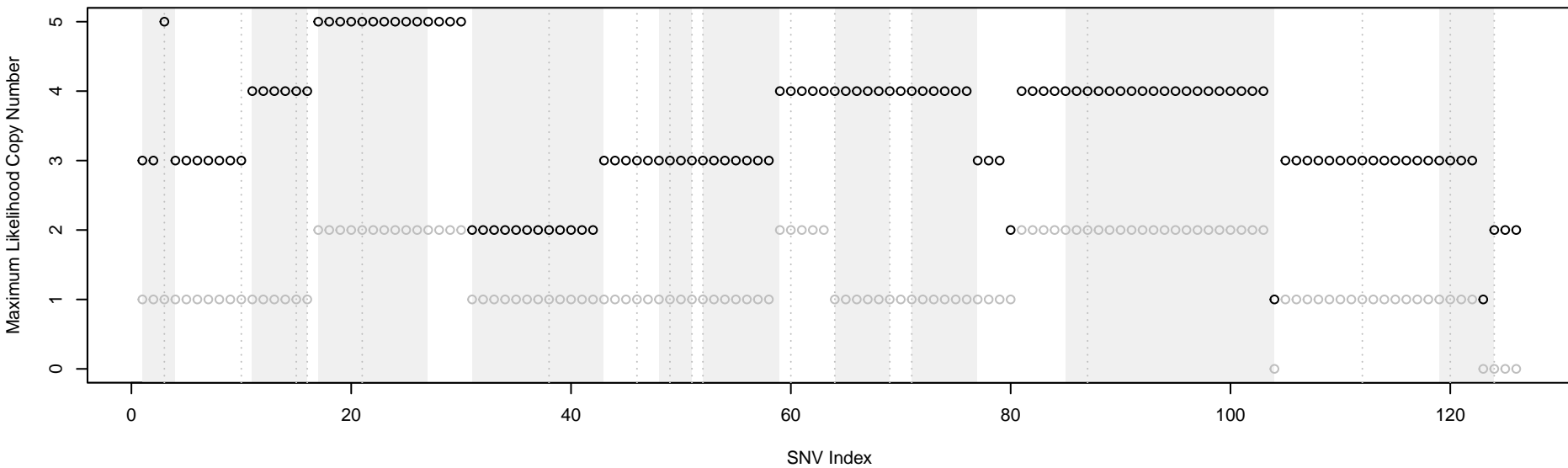
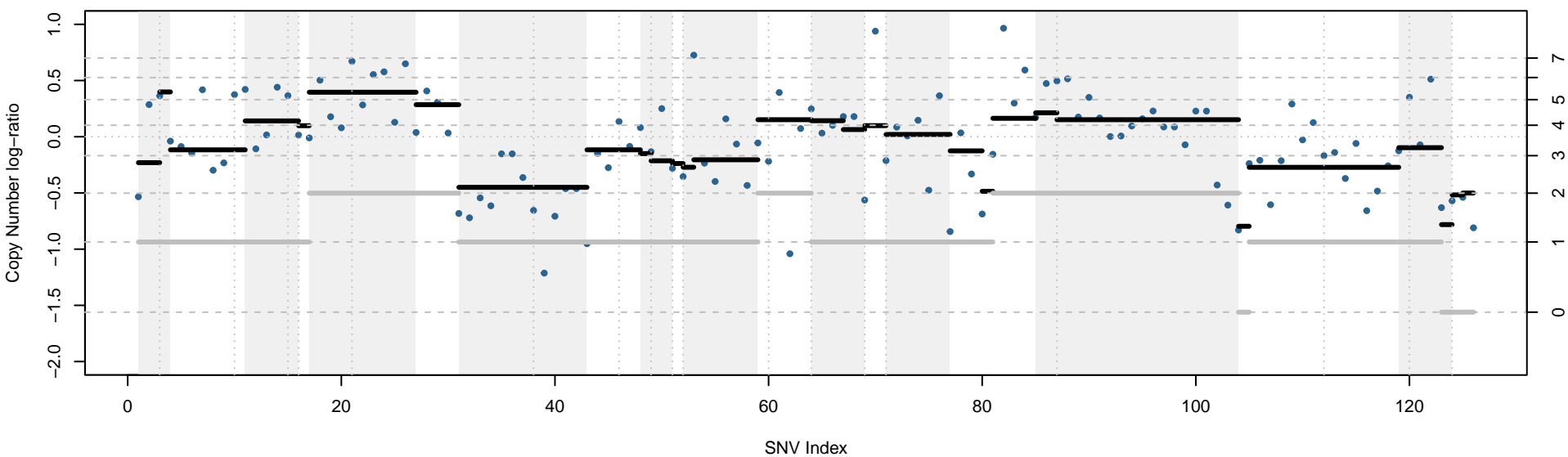
Purity: 0.52 Tumor ploidy: 3.6



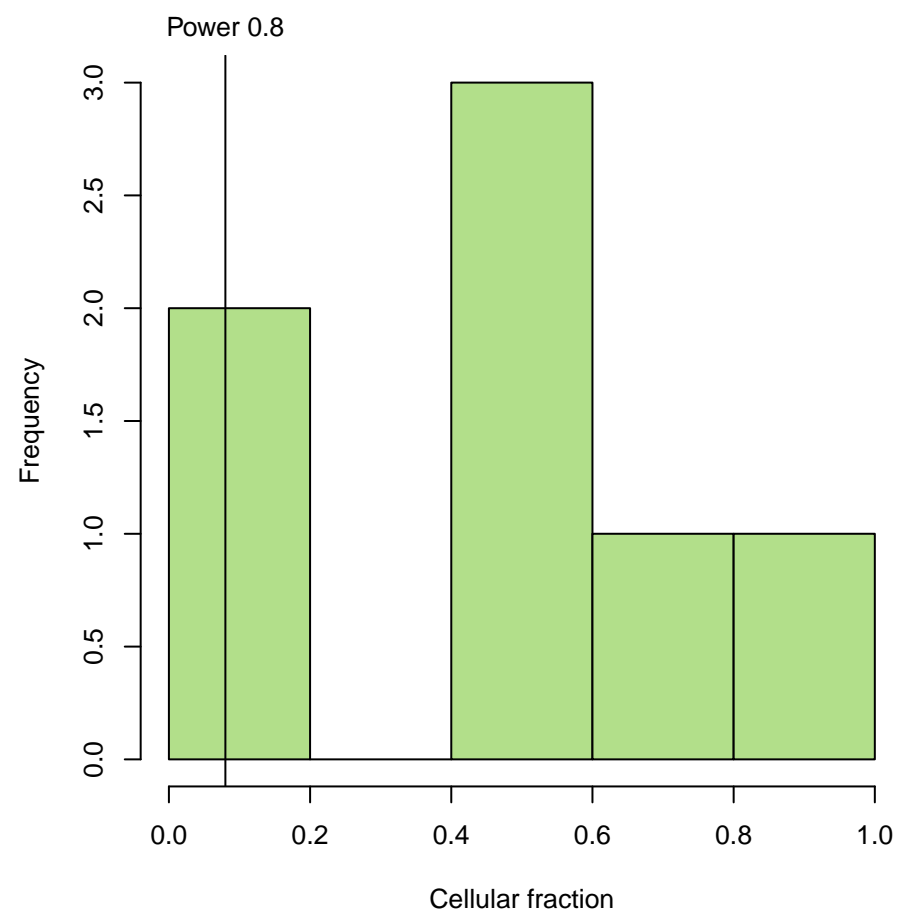
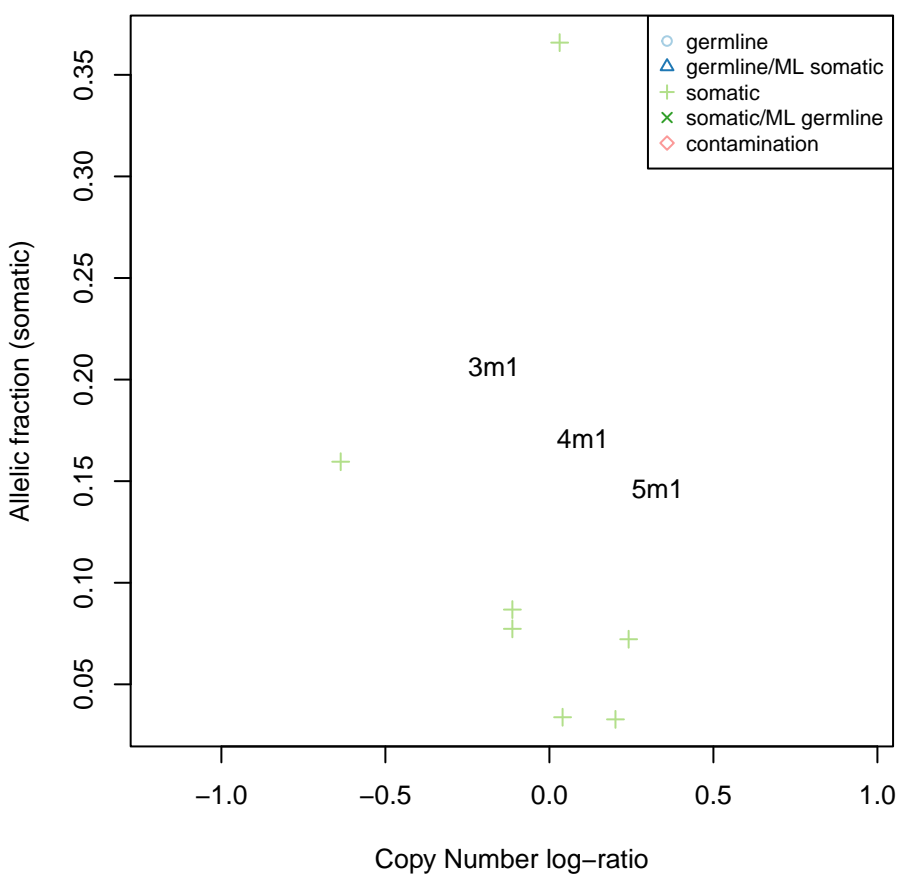
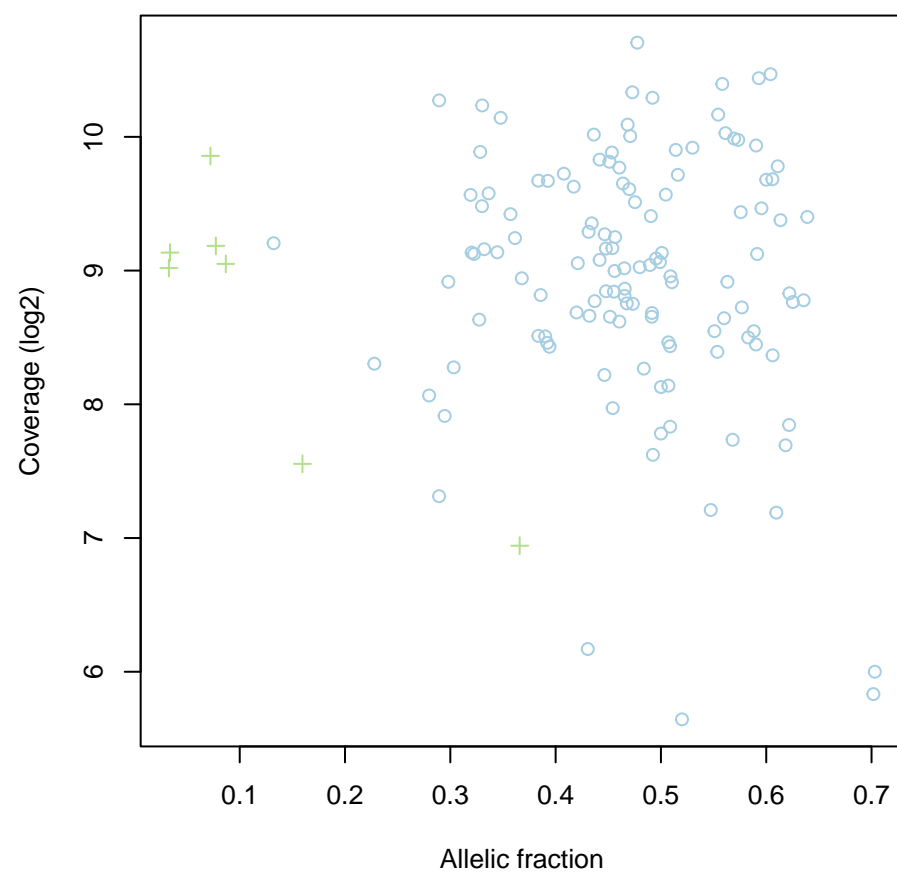
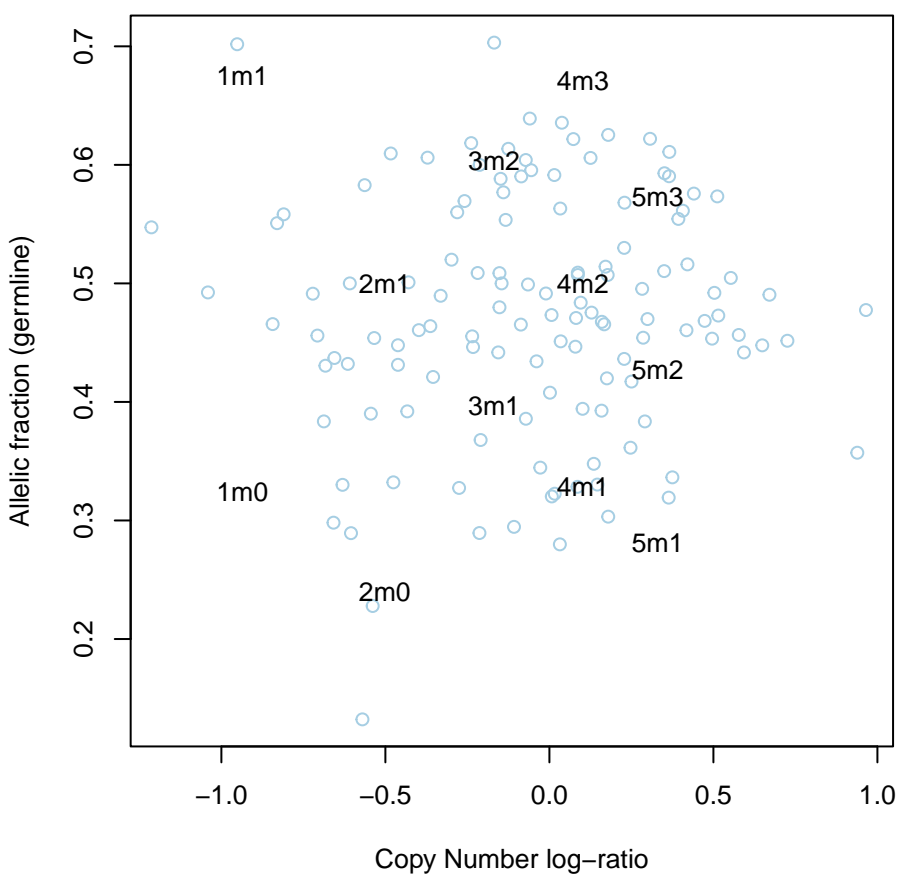
Purity: 0.52 Tumor ploidy: 3.6 SNV log-likelihood: -170.98 GoF: 91% Mean coverage: 459;590



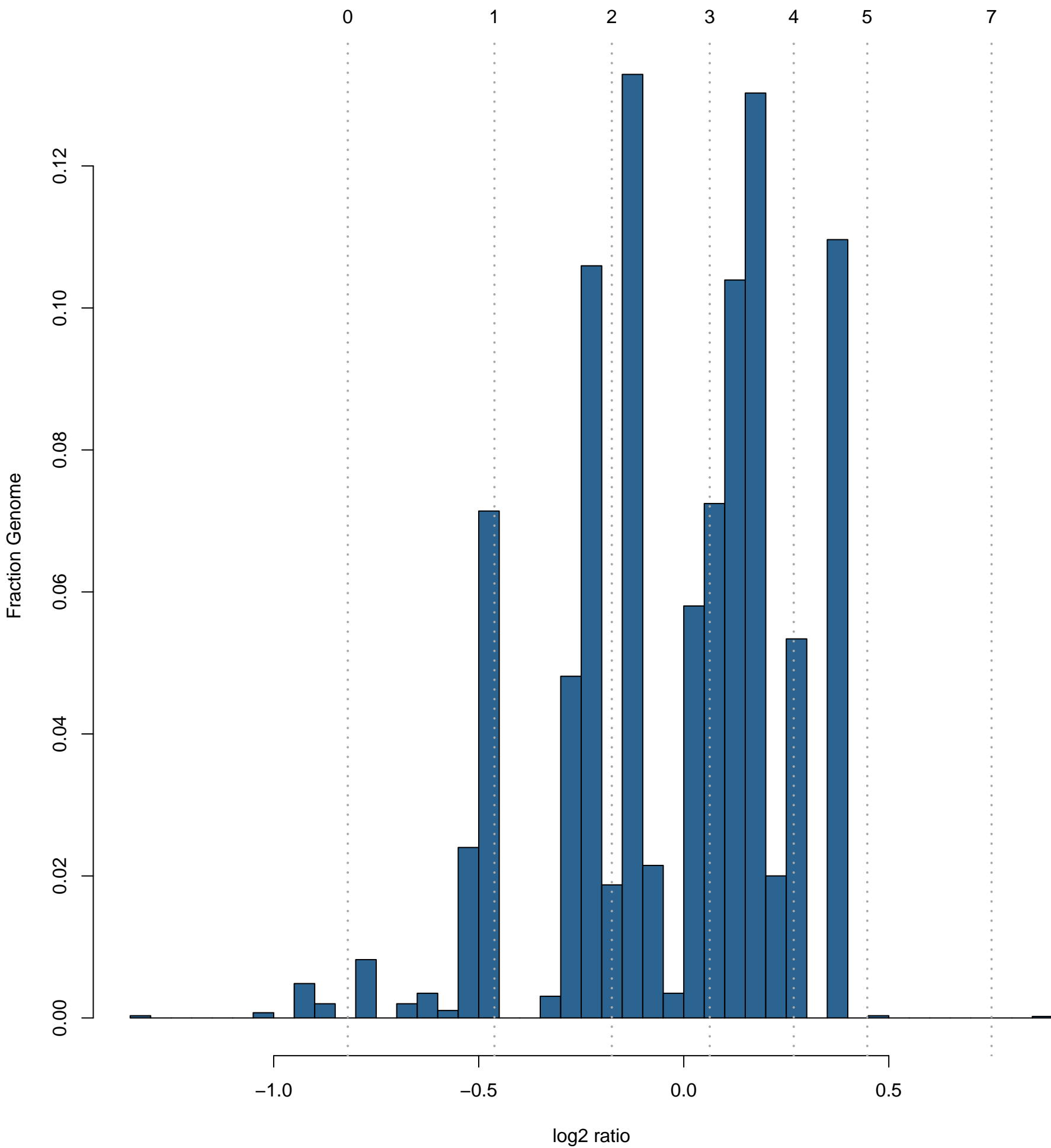
SCNA-fit log-likelihood: -3774.23



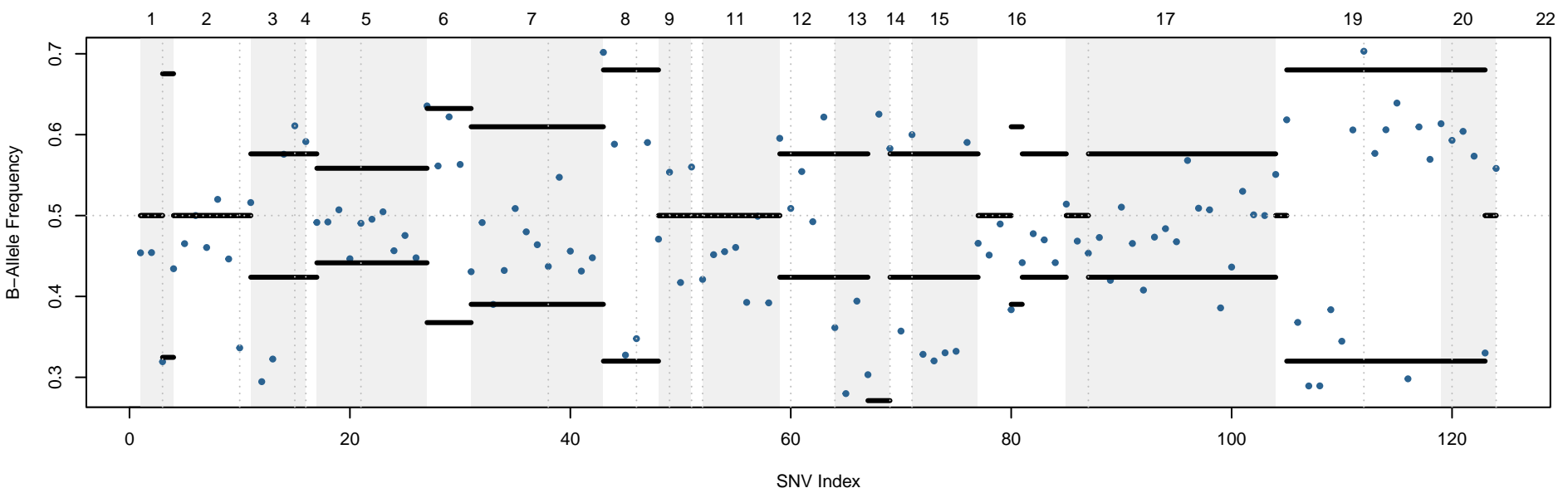




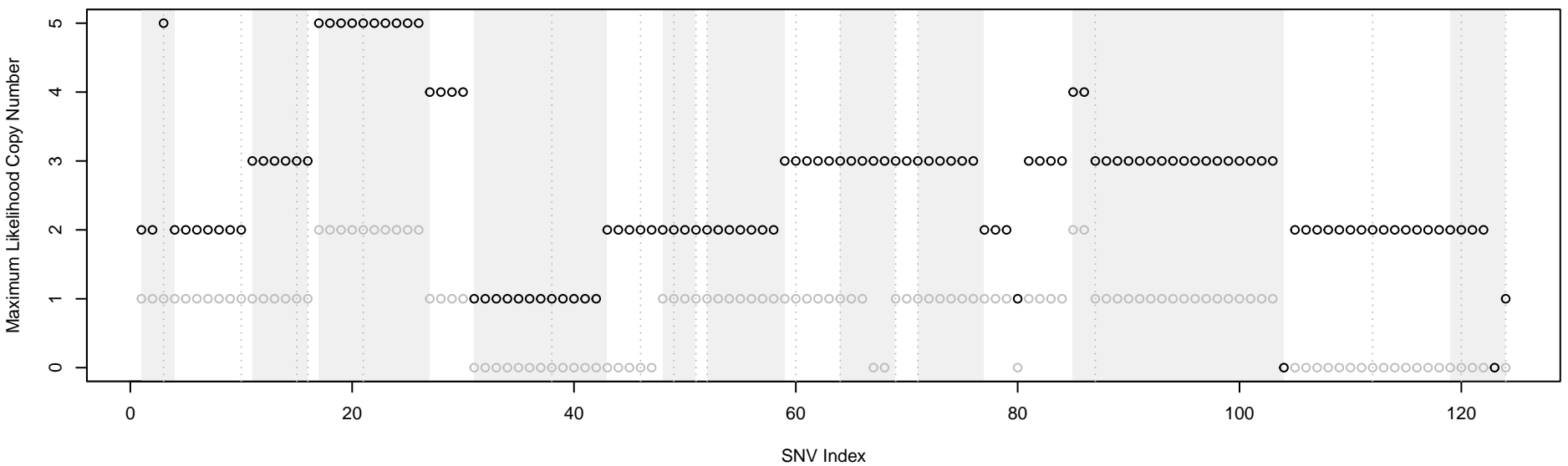
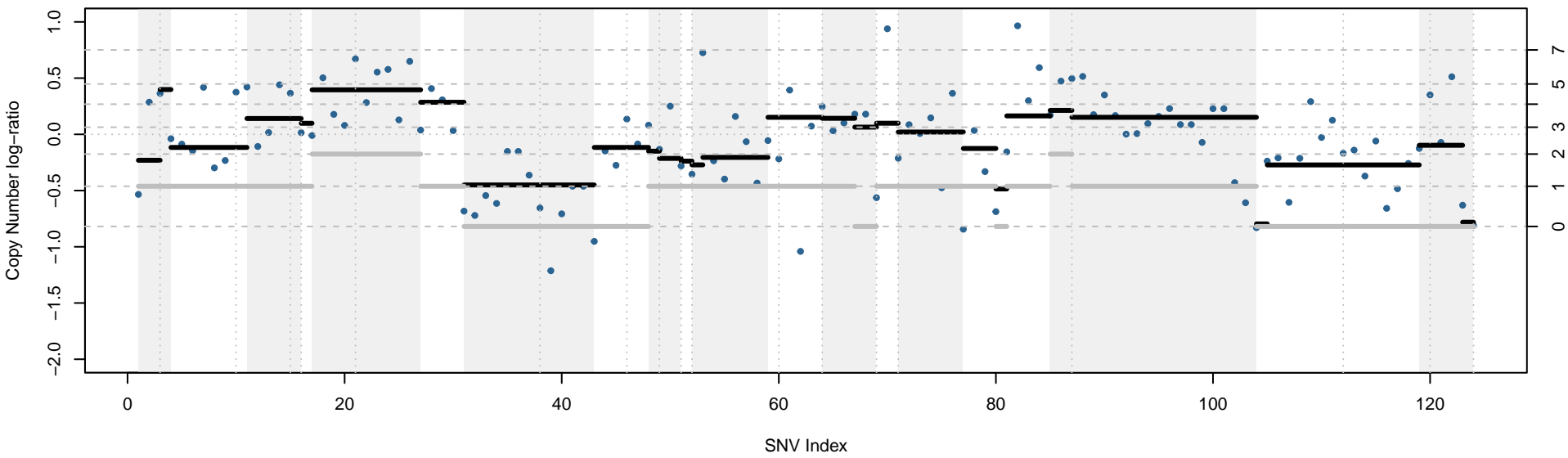
Purity: 0.36 Tumor ploidy: 2.718

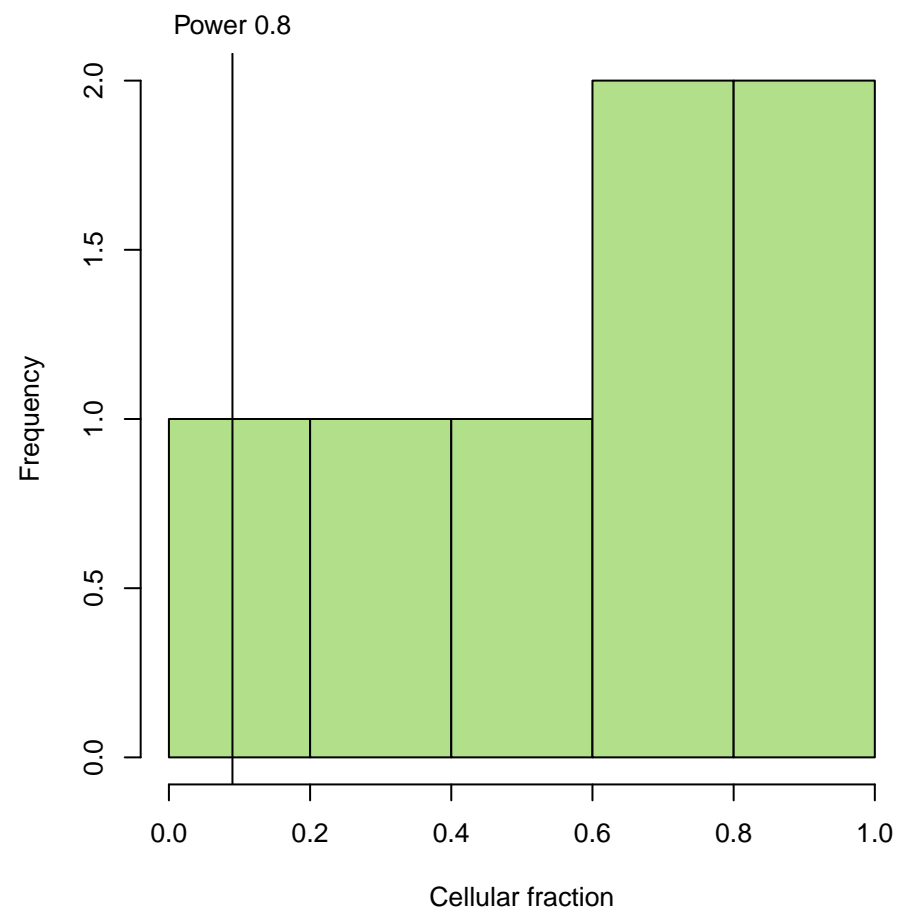
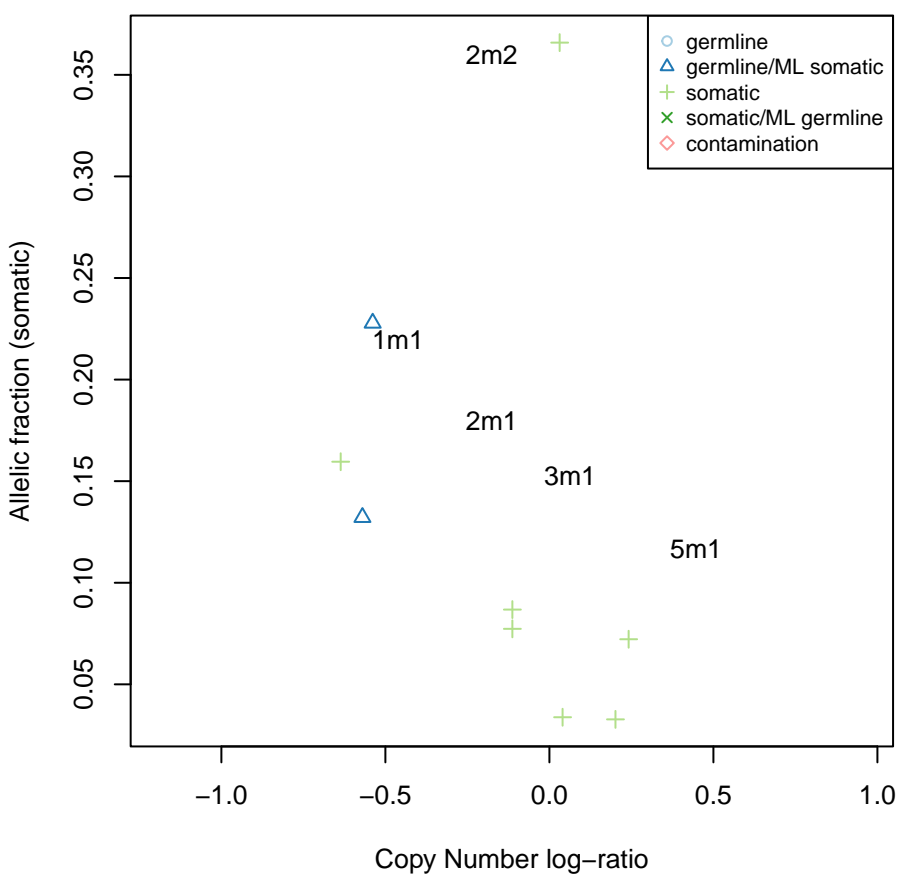
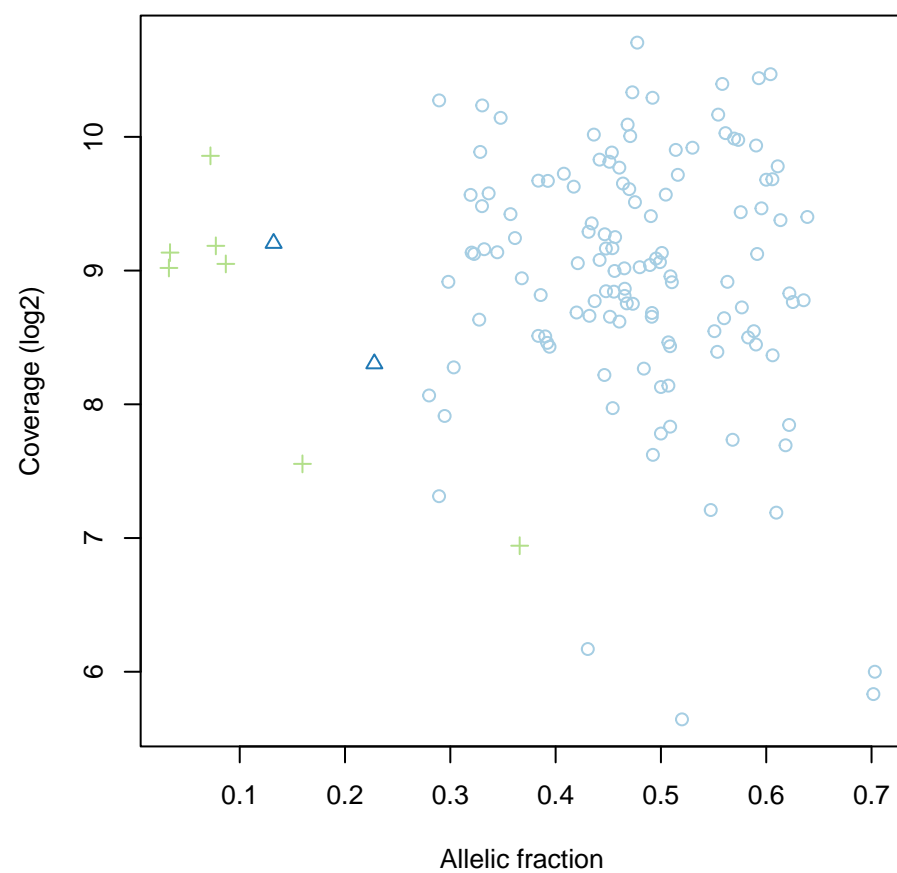
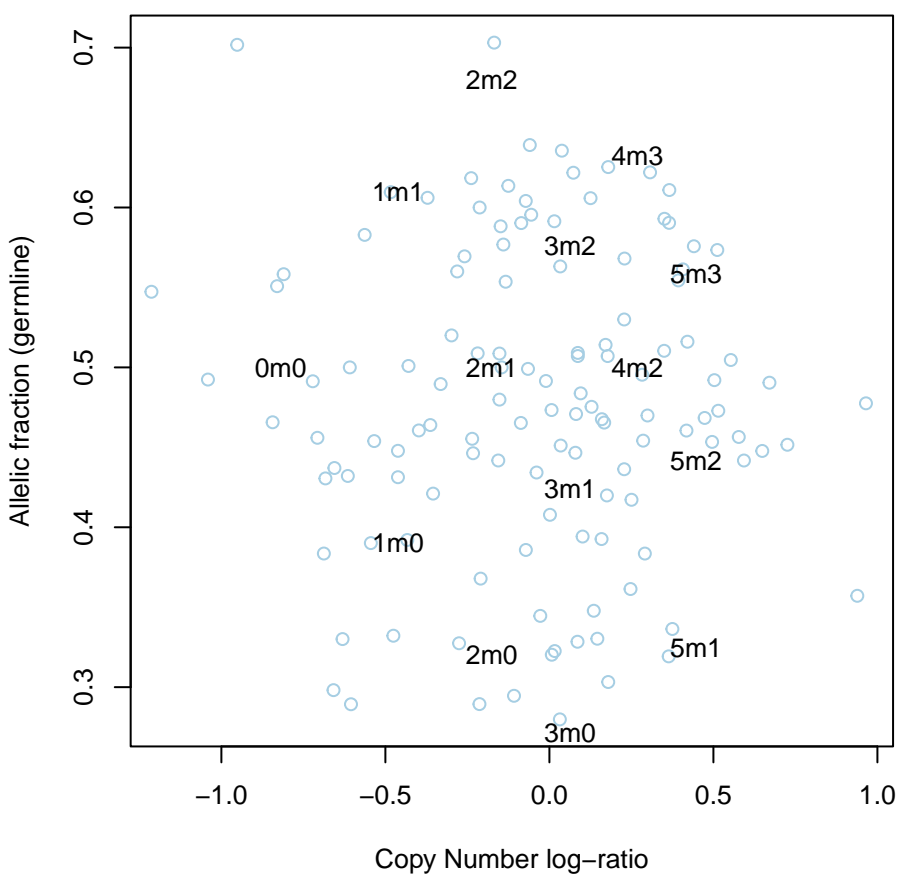


Purity: 0.36 Tumor ploidy: 2.718 SNV log-likelihood: -180.93 GoF: 91.5% Mean coverage: 459,590

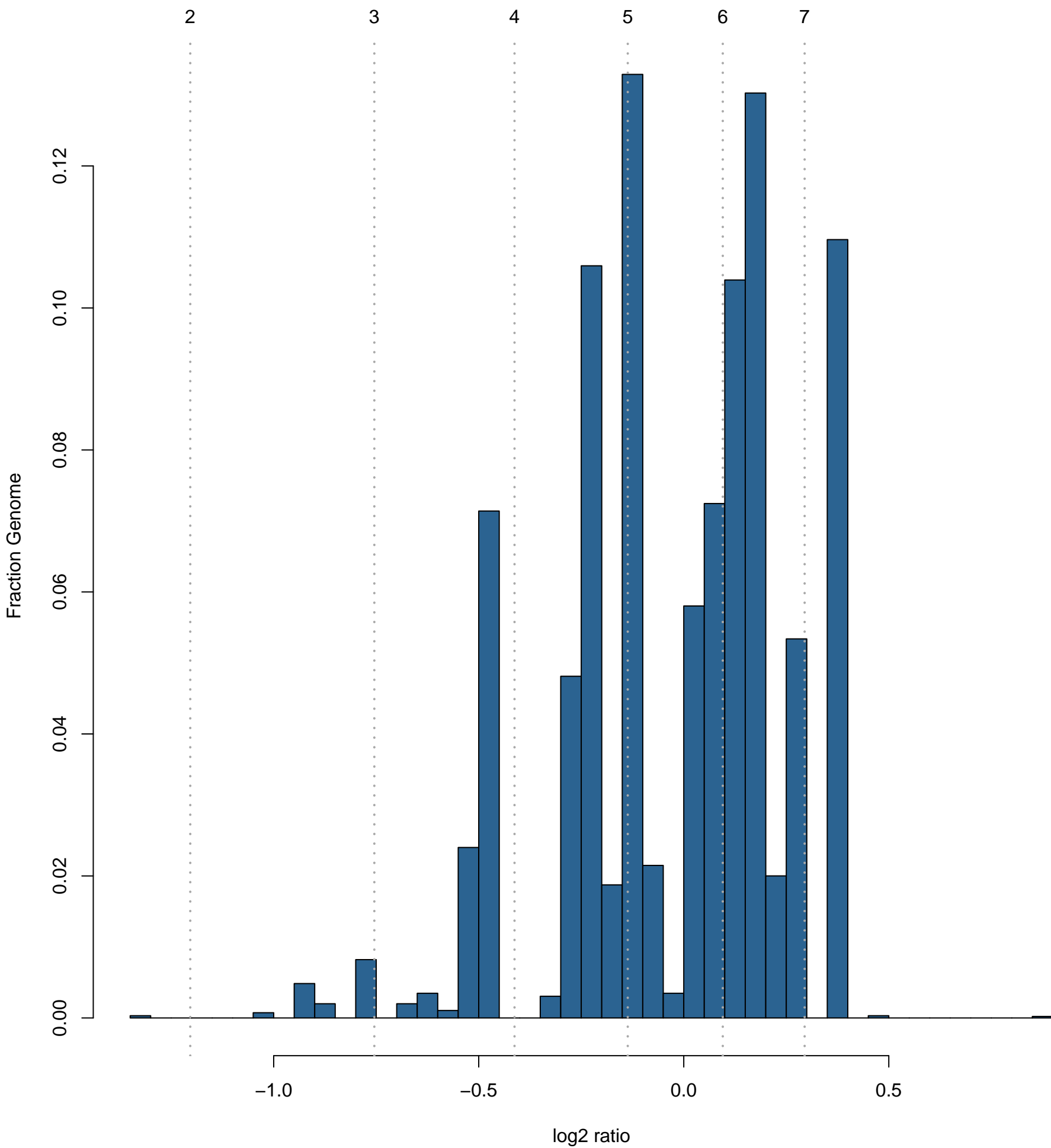


SCNA-fit log-likelihood: -3786.83

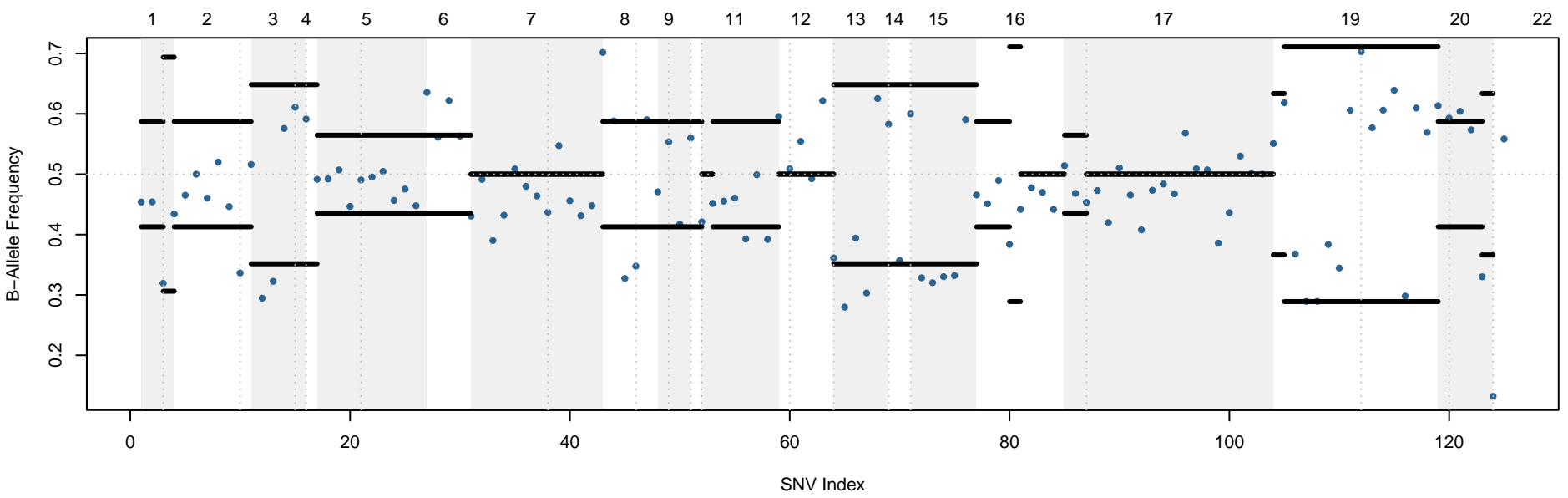




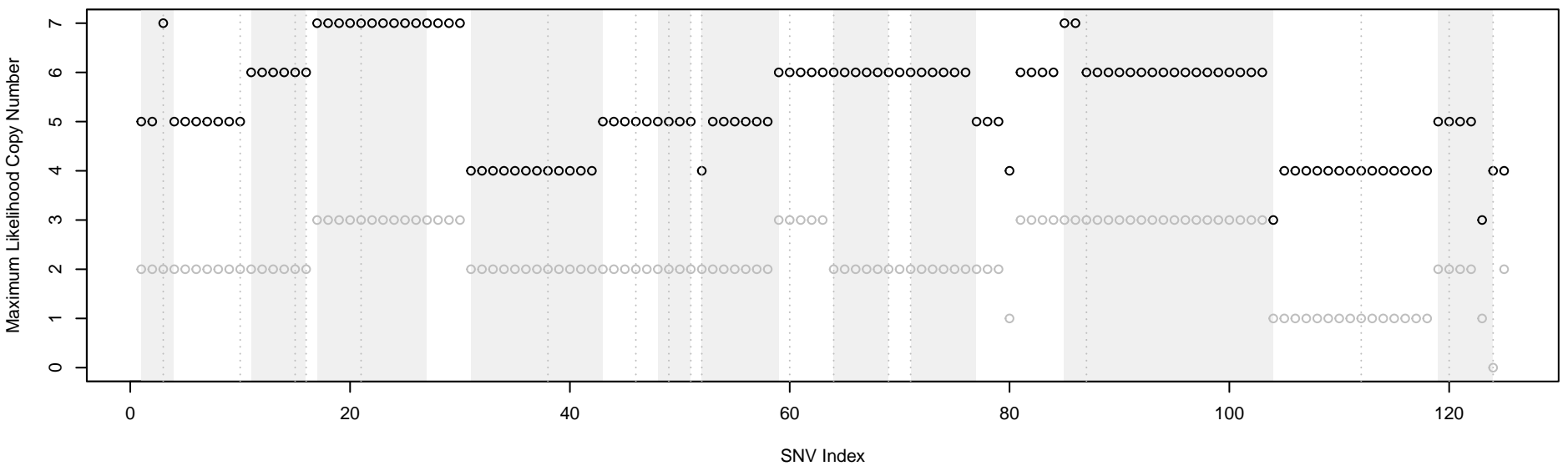
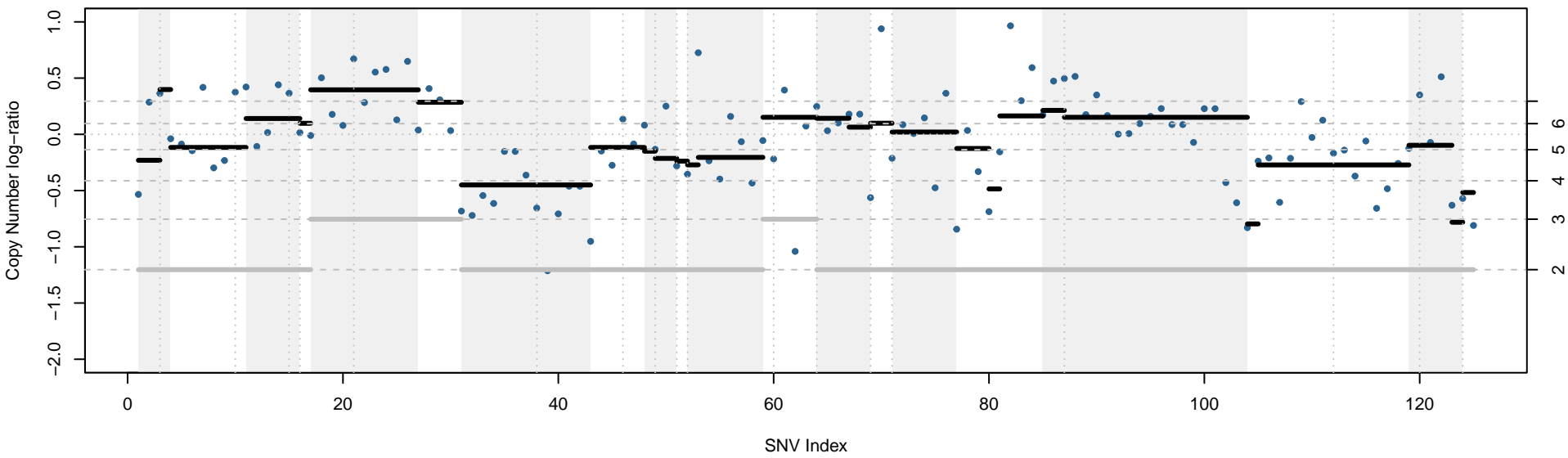
Purity: 0.73 Tumor ploidy: 5.57

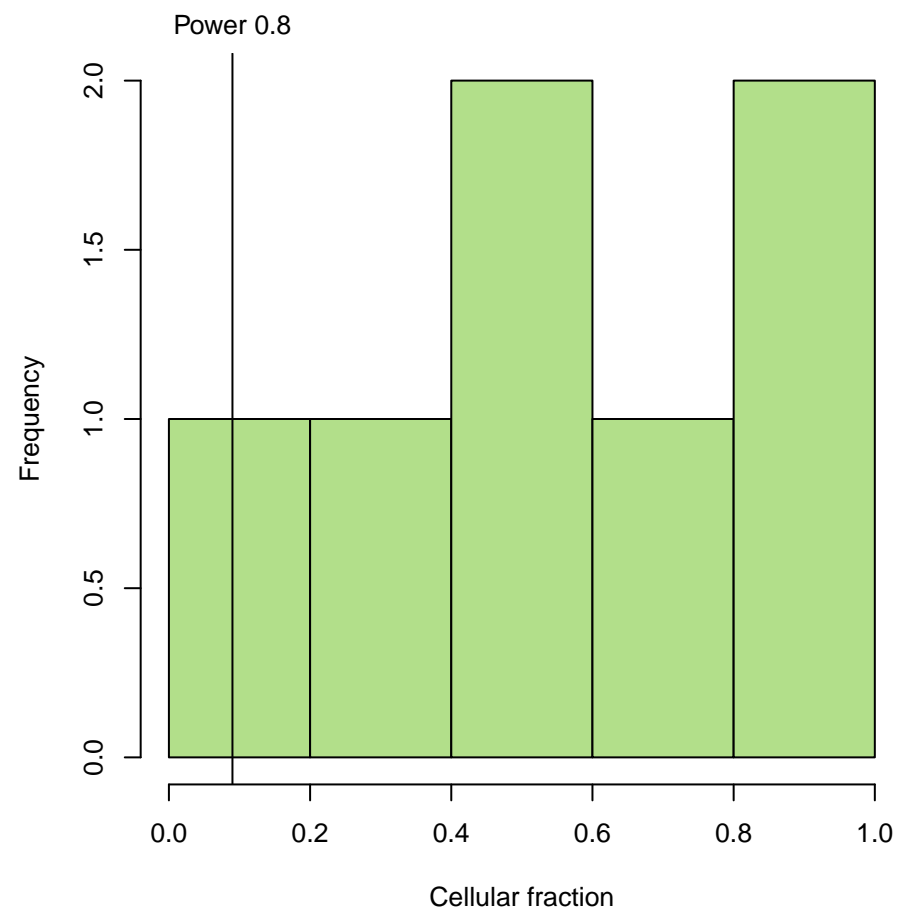
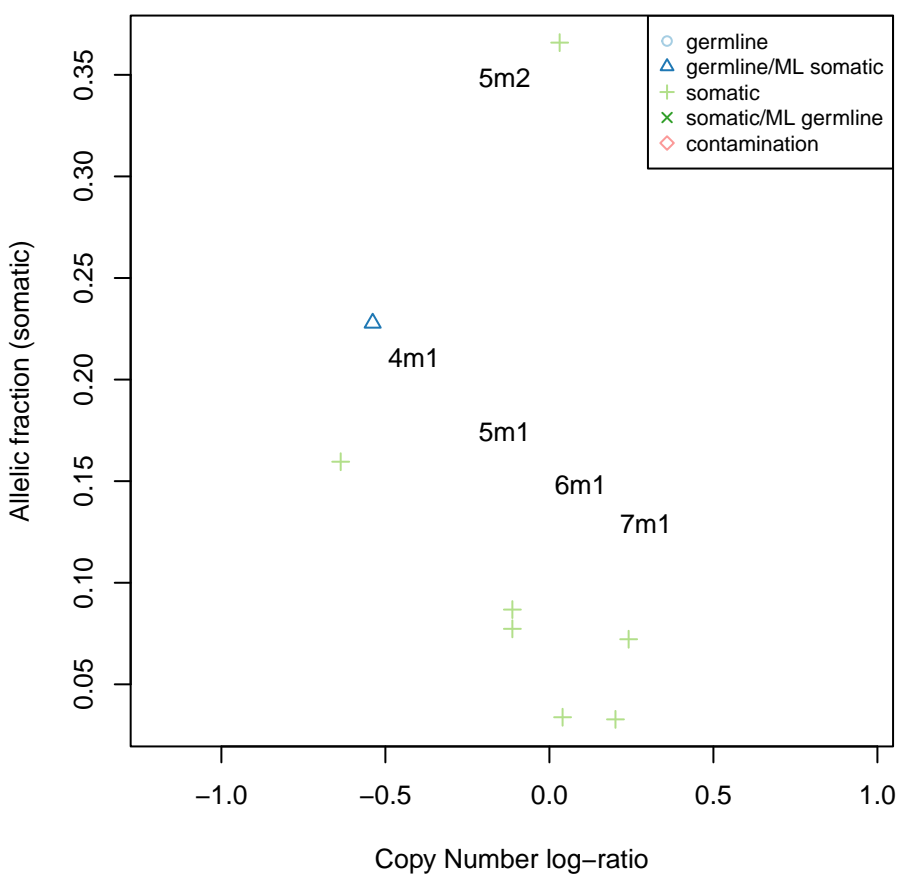
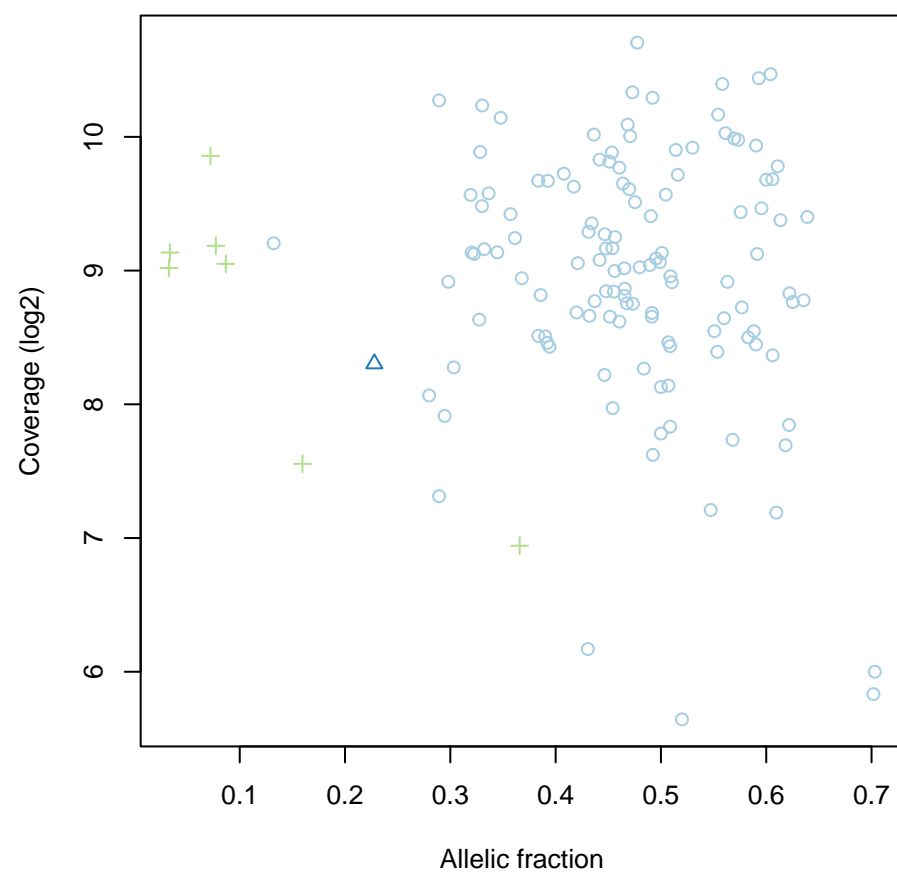
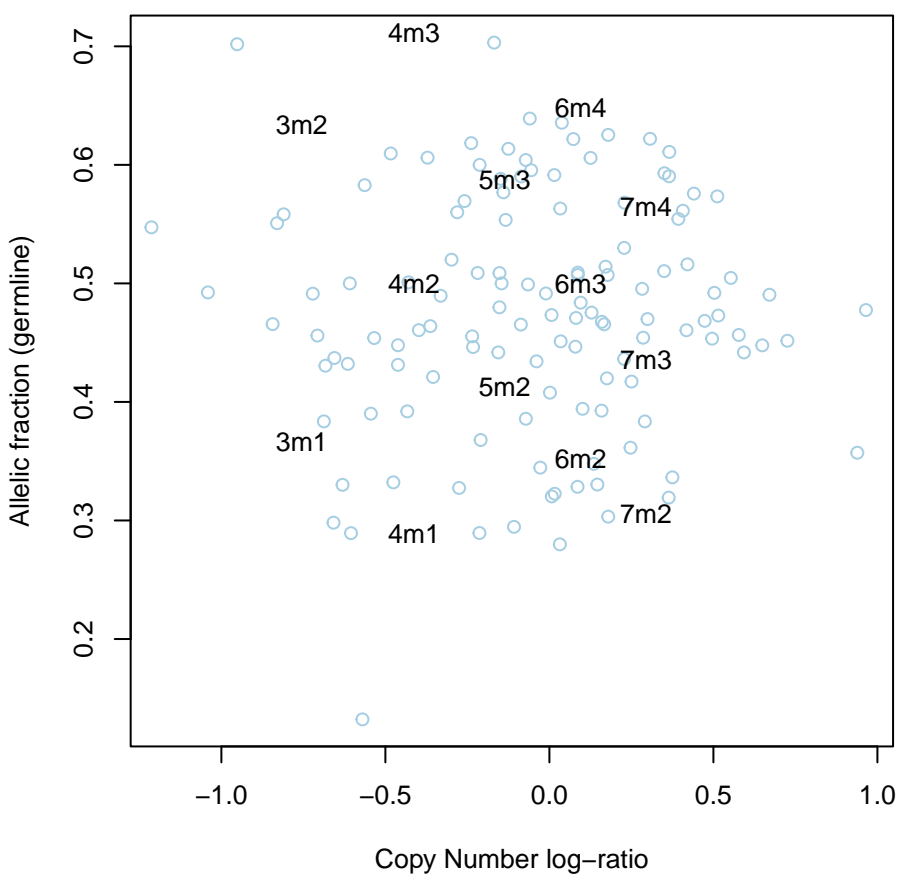


Purity: 0.73 Tumor ploidy: 5.57 SNV log-likelihood: -218.79 GoF: 91.9% Mean coverage: 459;590

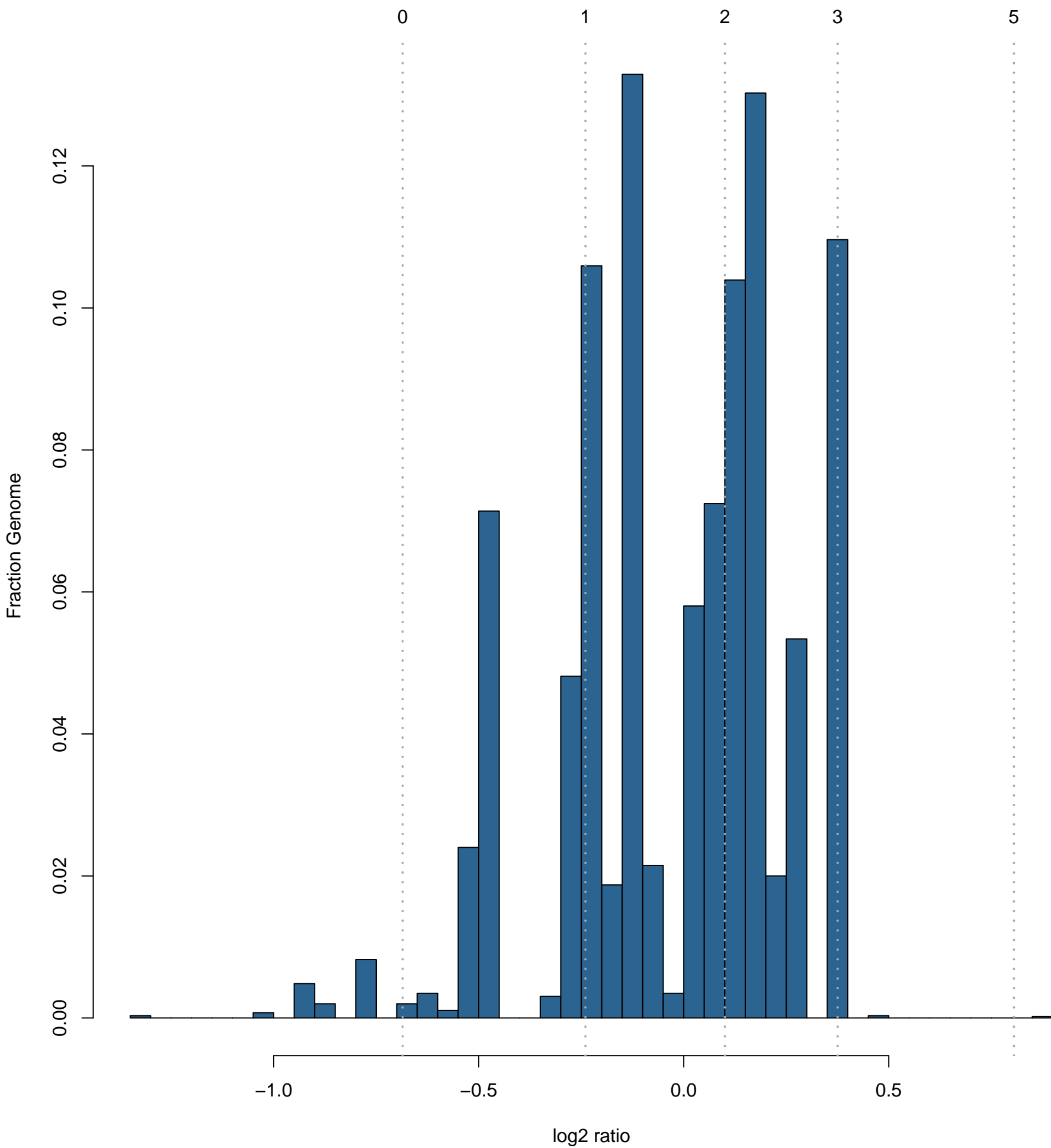


SCNA-fit log-likelihood: -3816.48



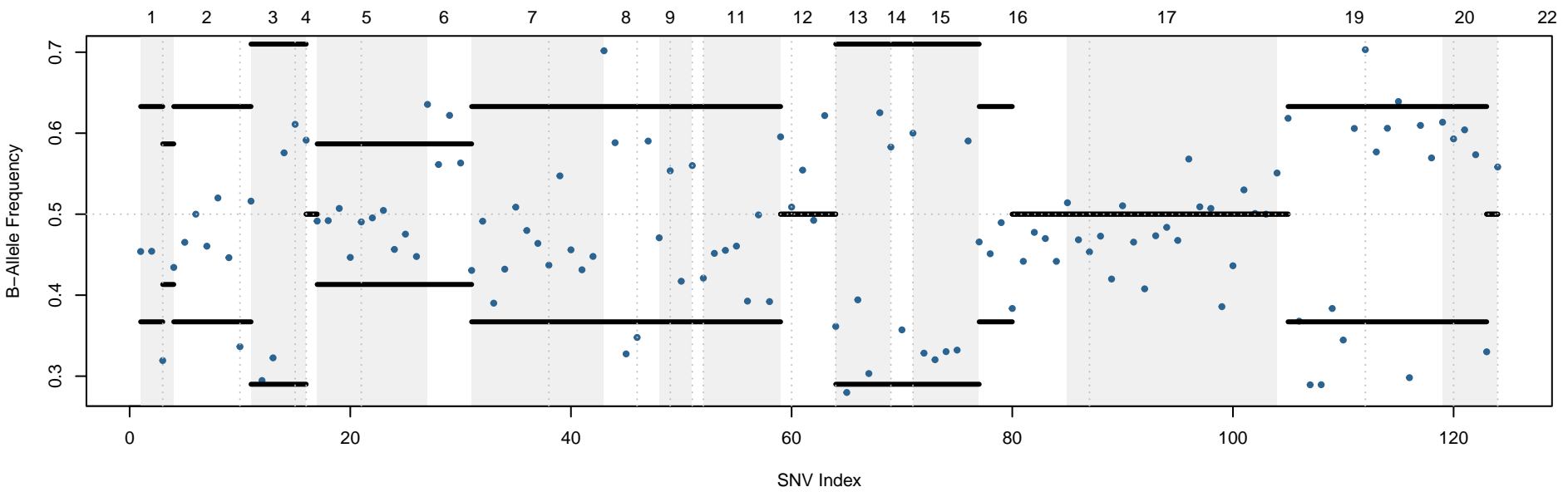


Purity: 0.42 Tumor ploidy: 1.68

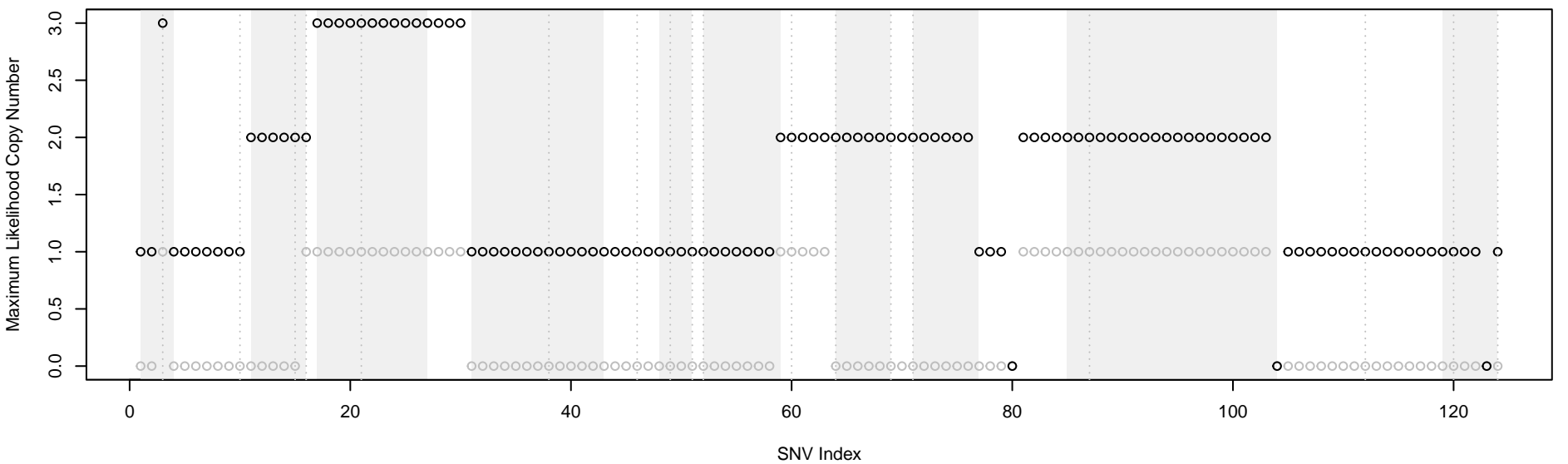
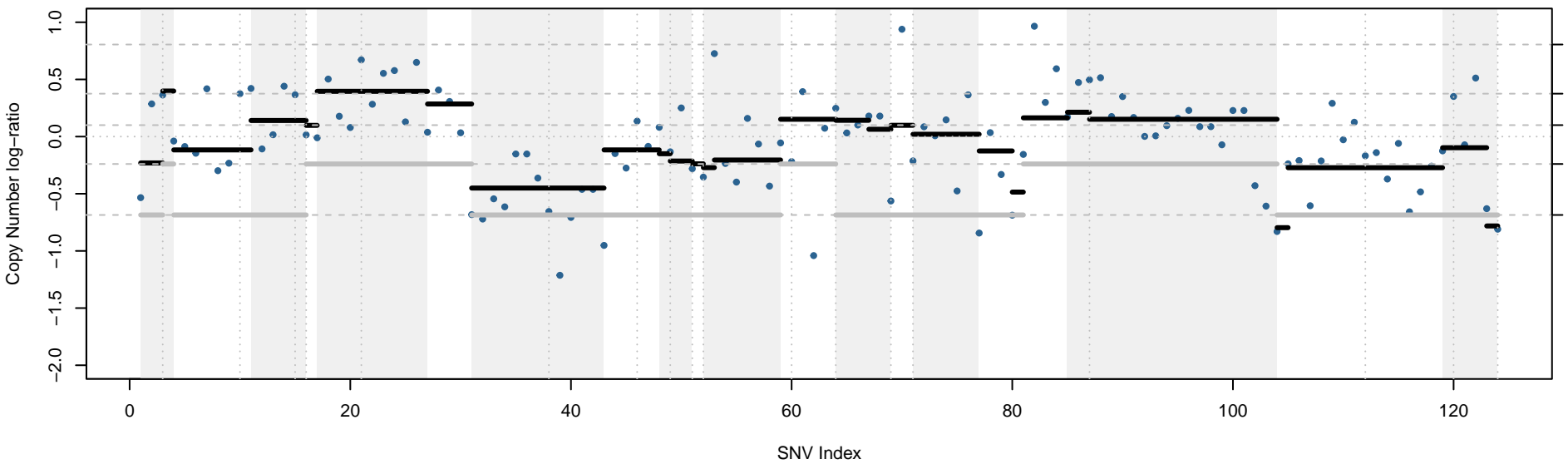


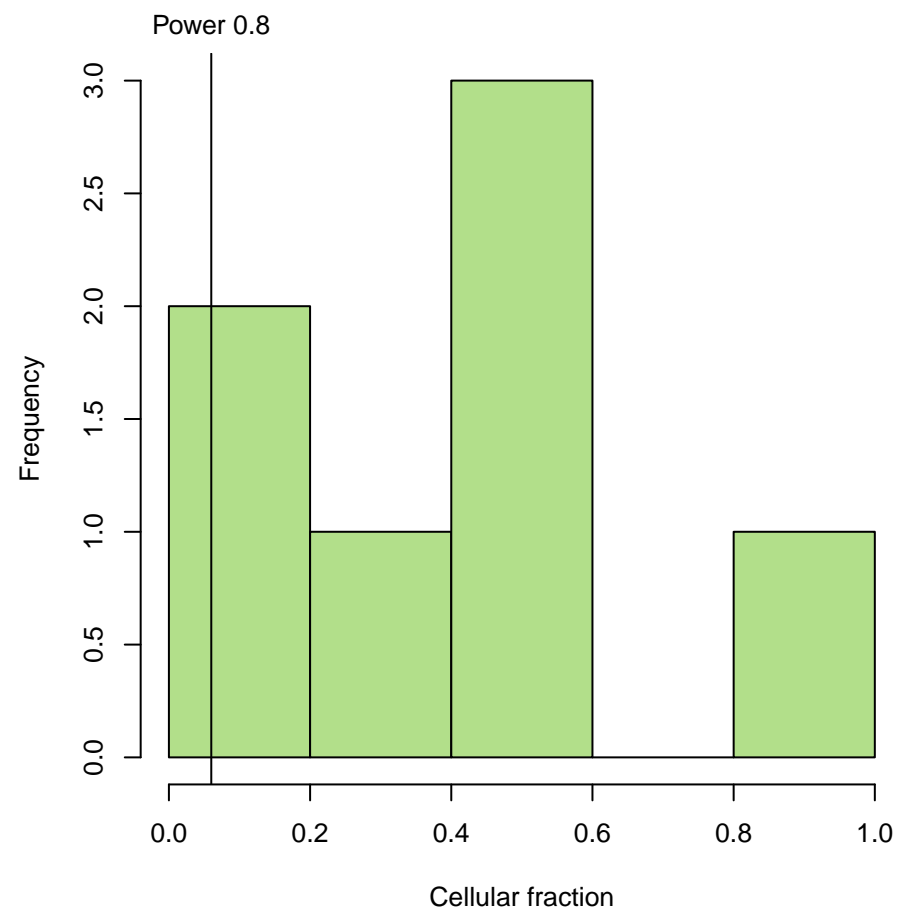
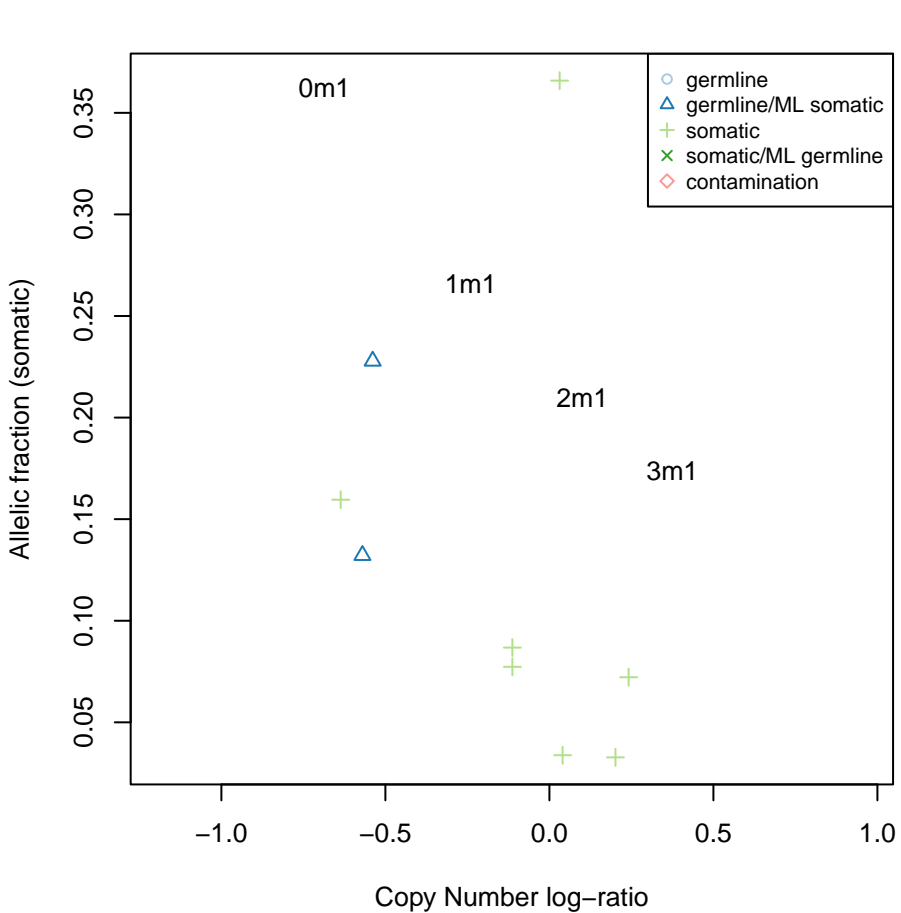
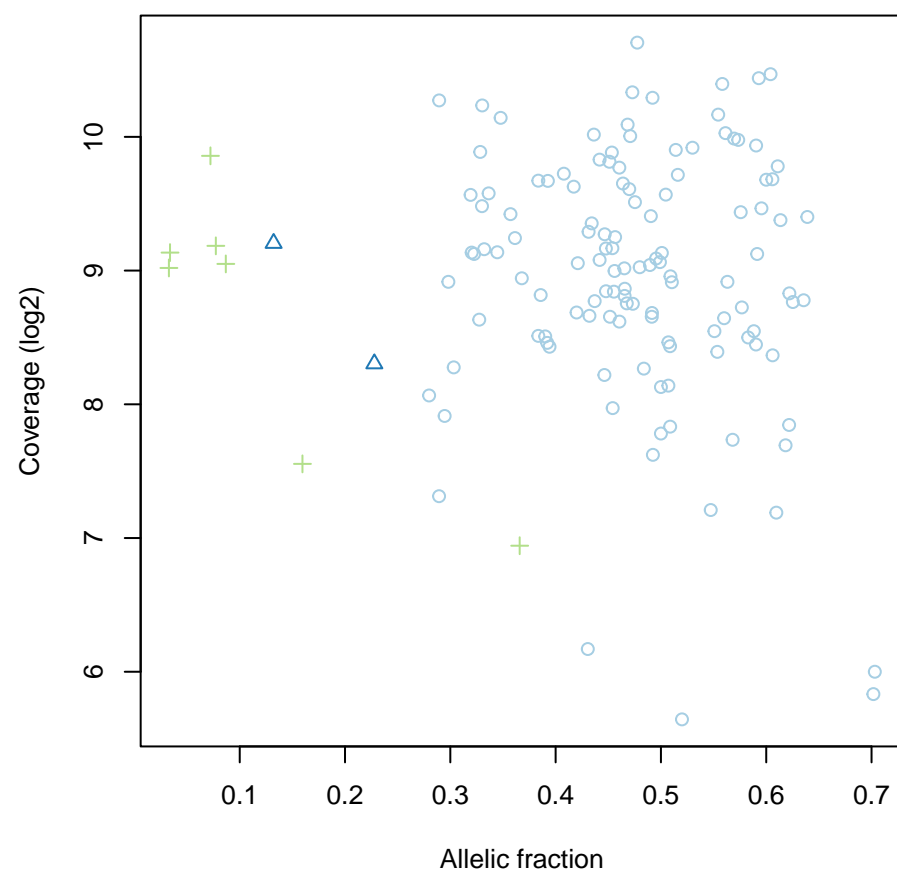
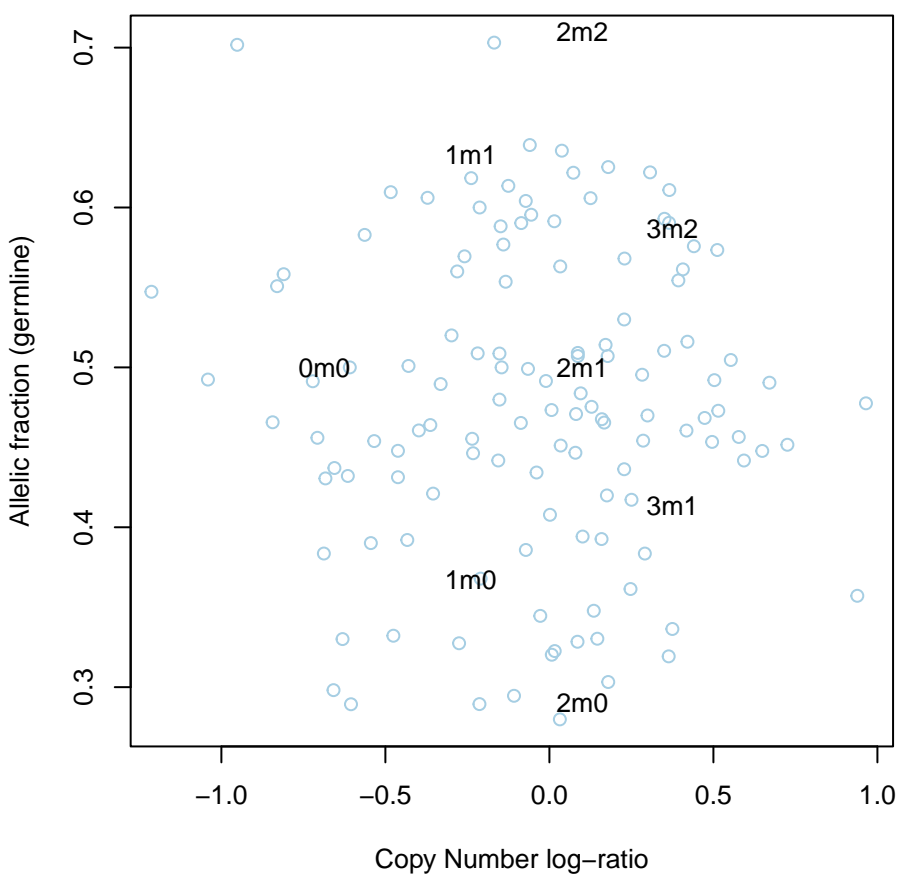


Purity: 0.42 Tumor ploidy: 1.68 SNV log-likelihood: -245.63 GoF: 83.9% Mean coverage: 459;590

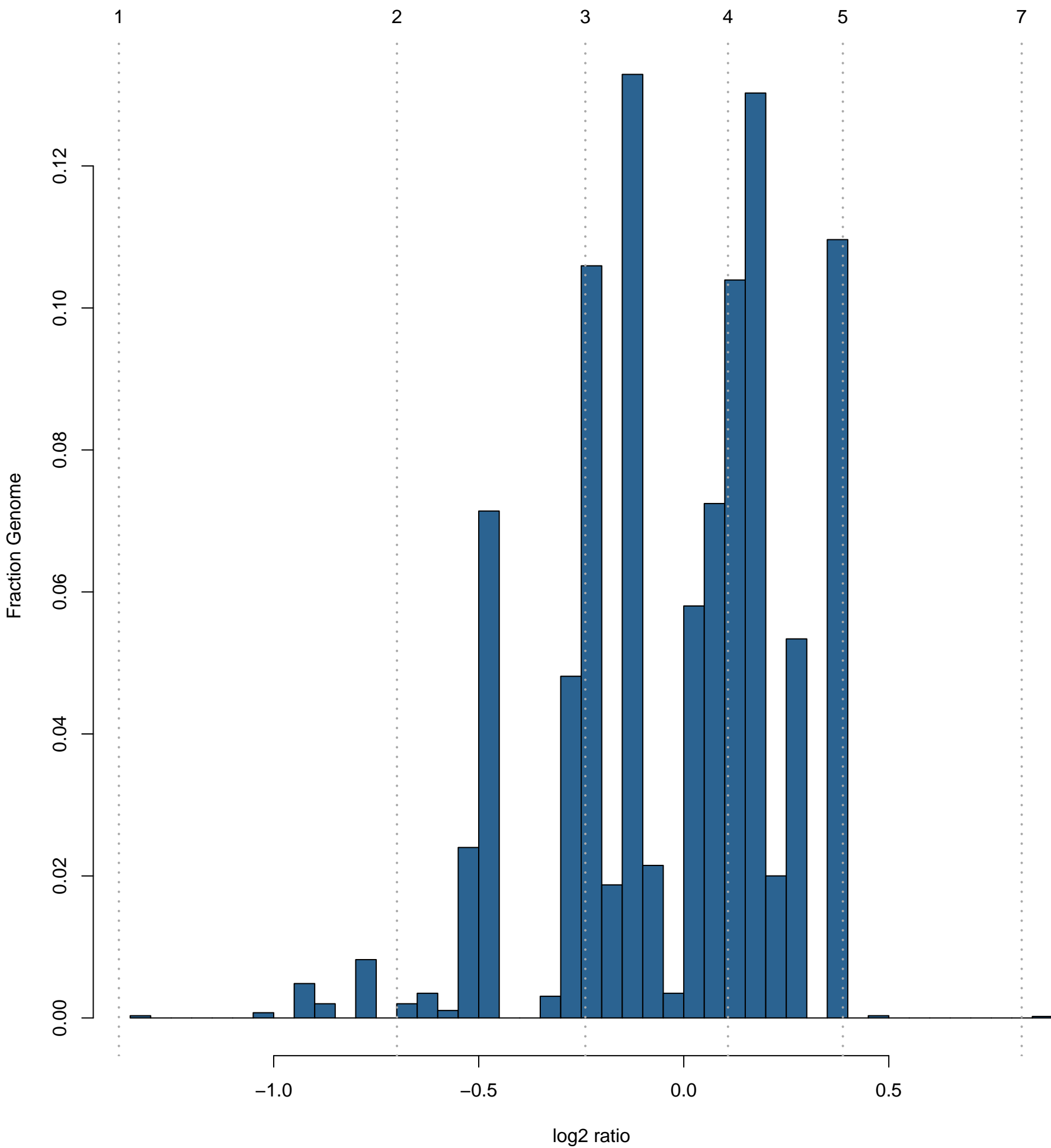


SCNA-fit log-likelihood: -3990.7

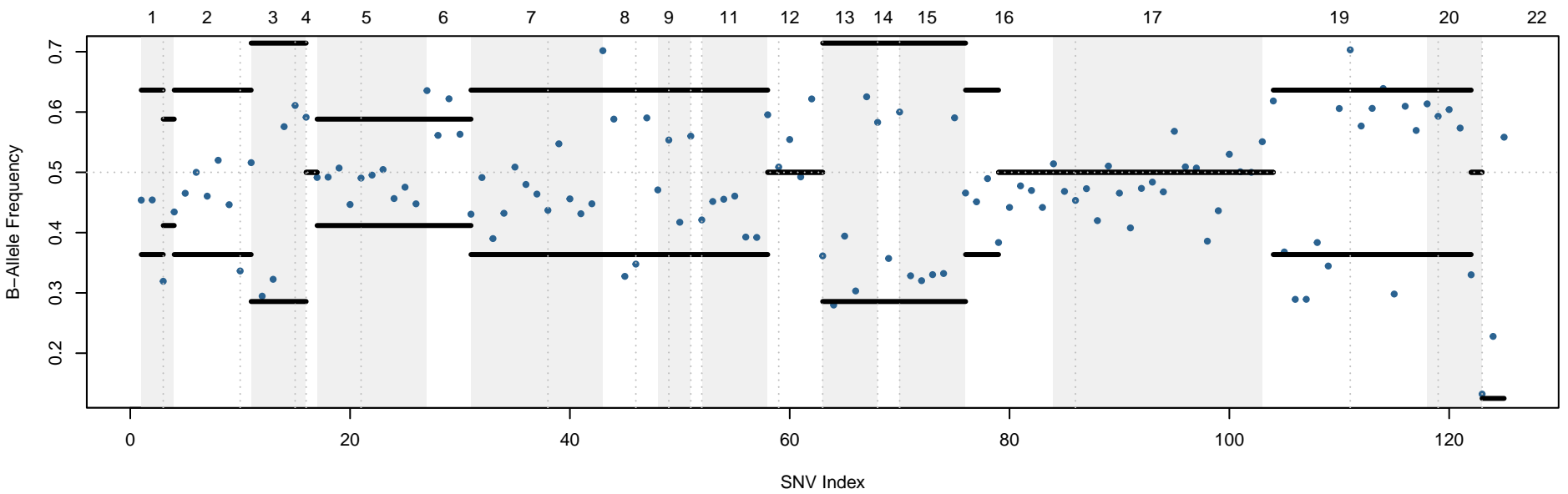




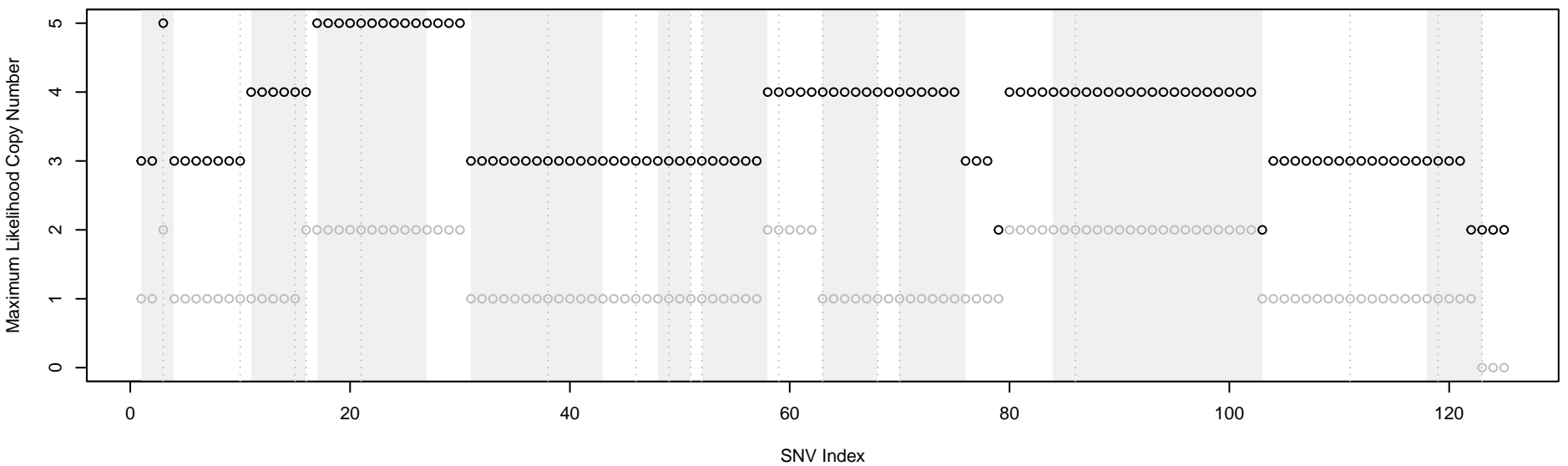
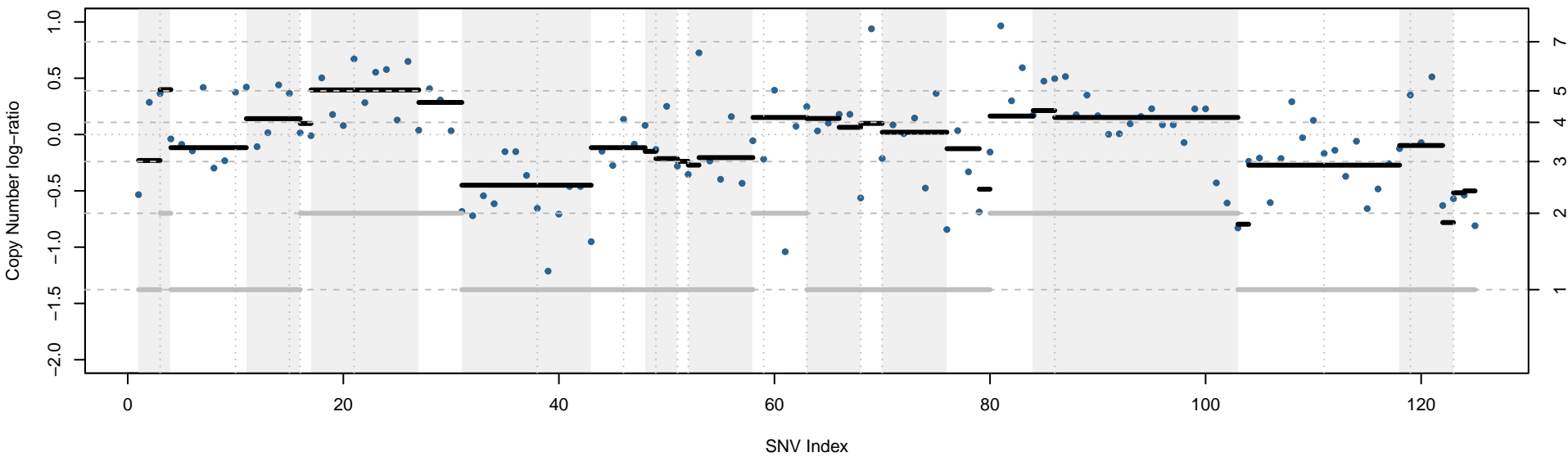
Purity: 0.75 Tumor ploidy: 3.664

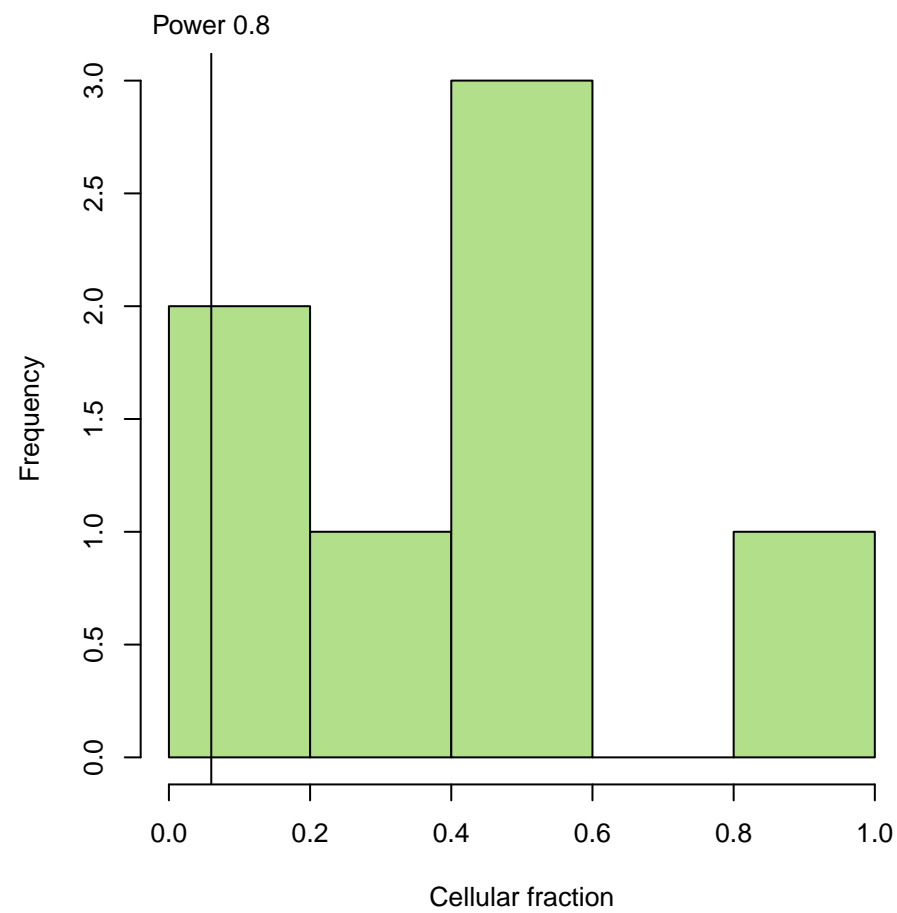
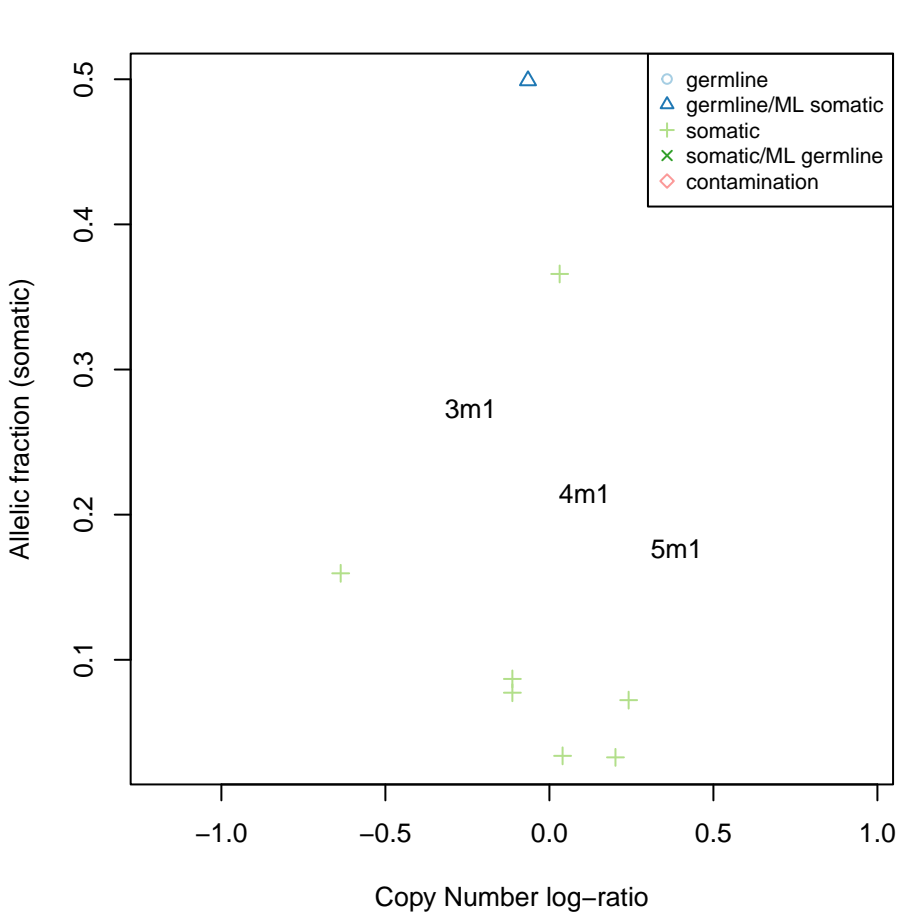
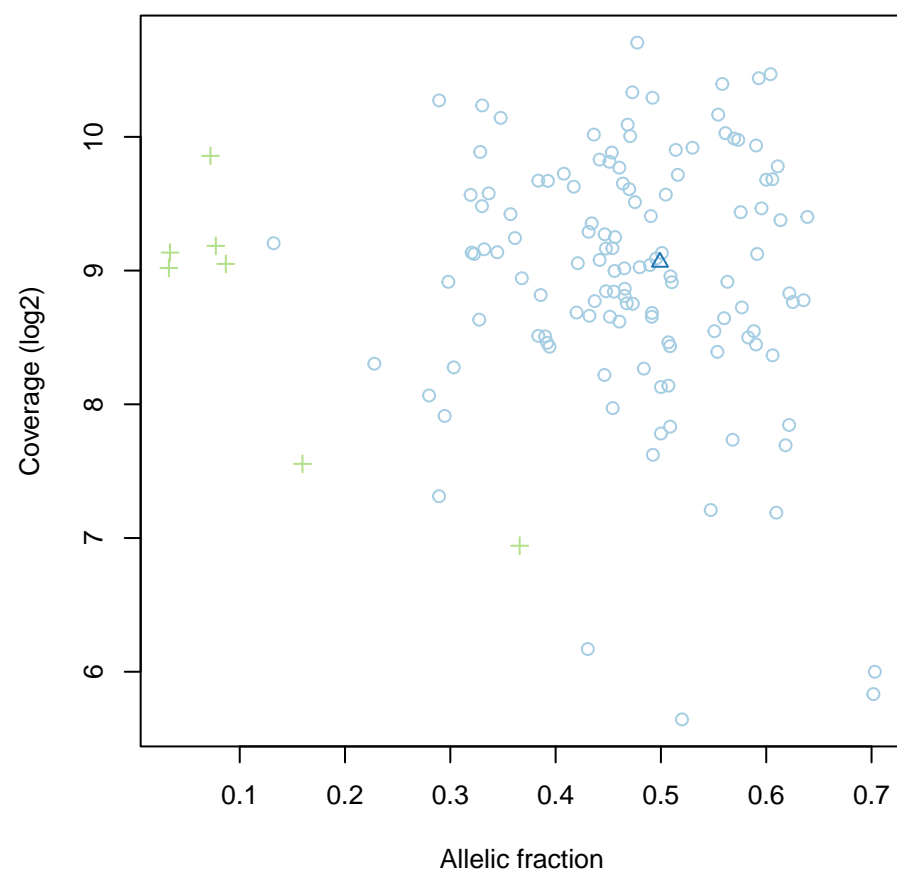
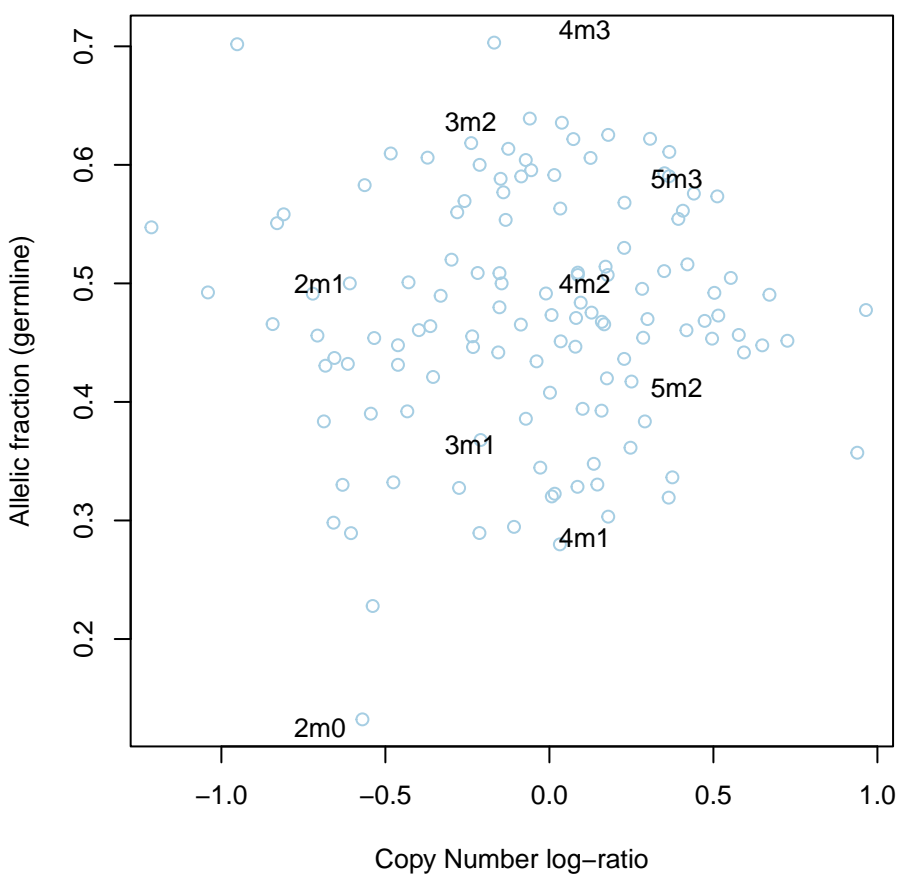


Purity: 0.75 Tumor ploidy: 3.664 SNV log-likelihood: -342.87 GoF: 84.3% Mean coverage: 459,590

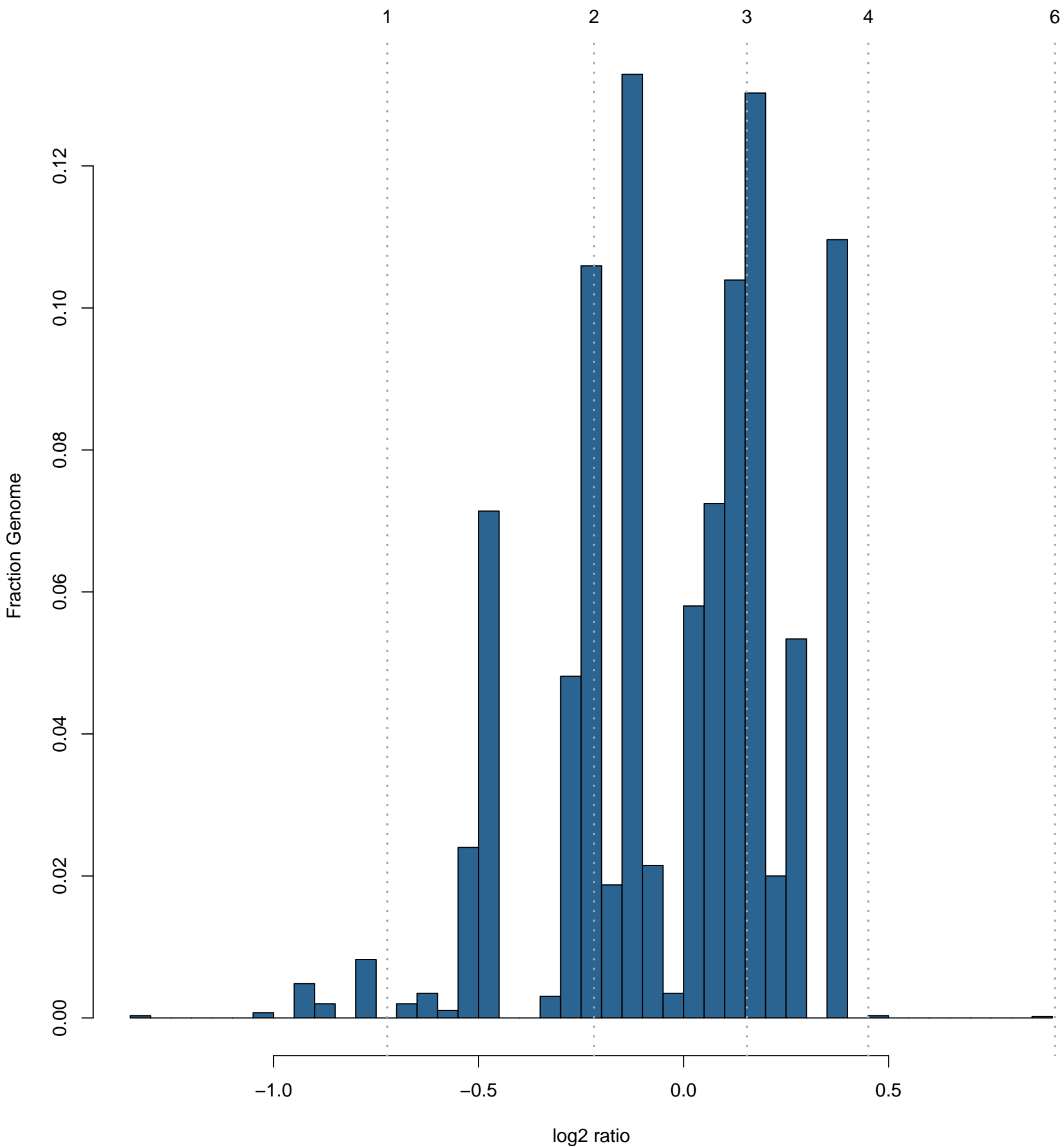


SCNA-fit log-likelihood: -3963.46

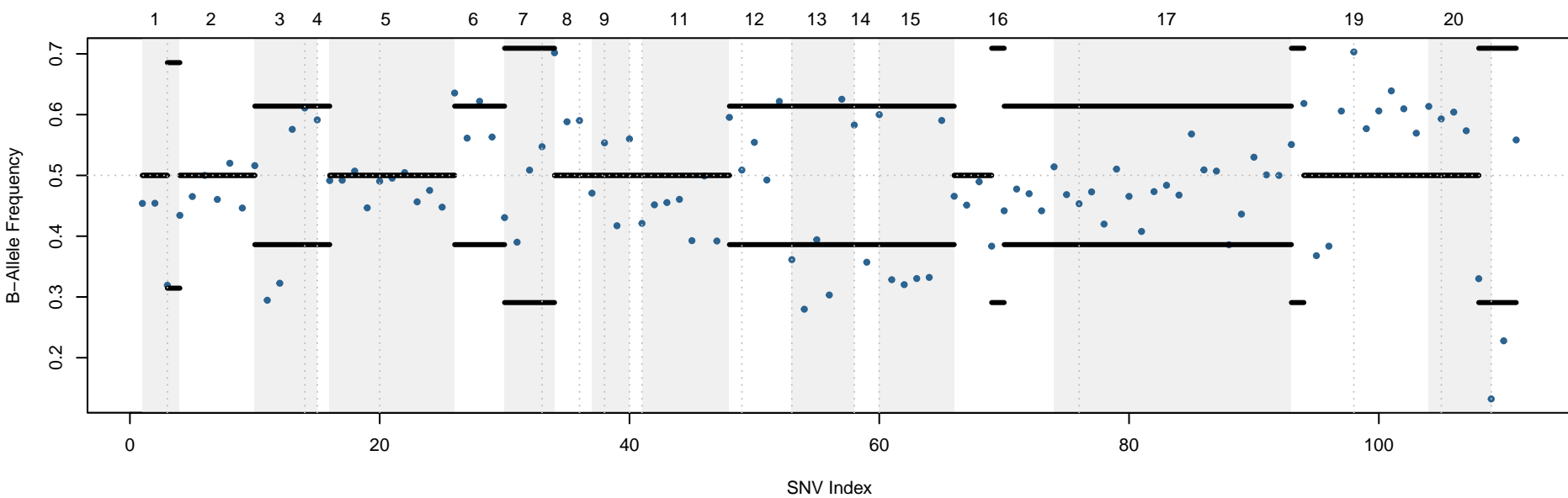




Purity: 0.59 Tumor ploidy: 2.554



Purity: 0.59 Tumor ploidy: 2.554 SNV log-likelihood: -416.31 GoF: 82.1% Mean coverage: 459,590



SCNA-fit log-likelihood: -4028.18

