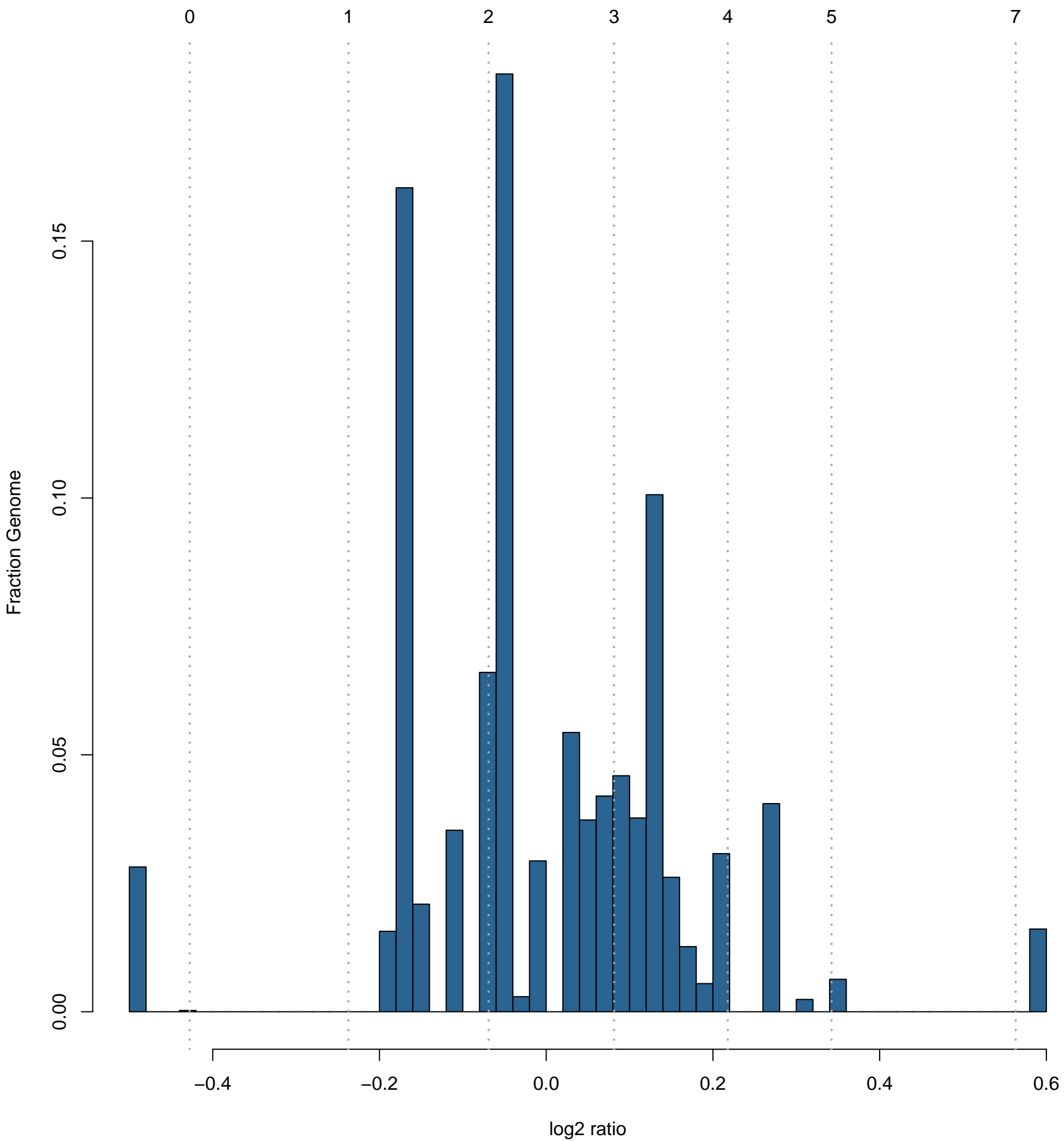
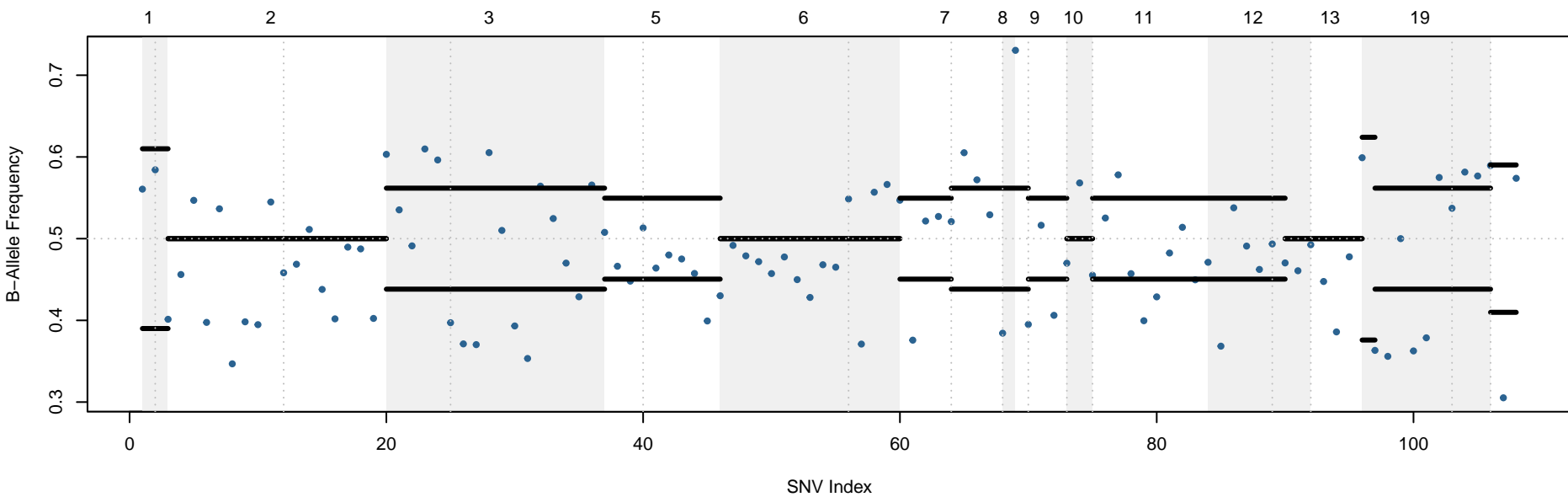


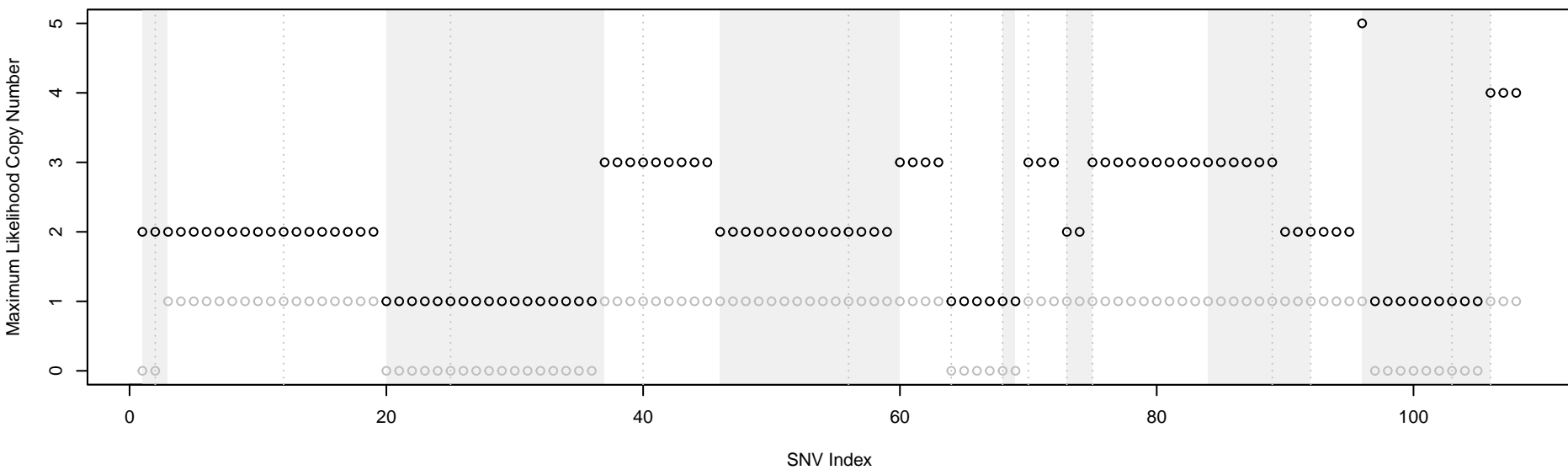
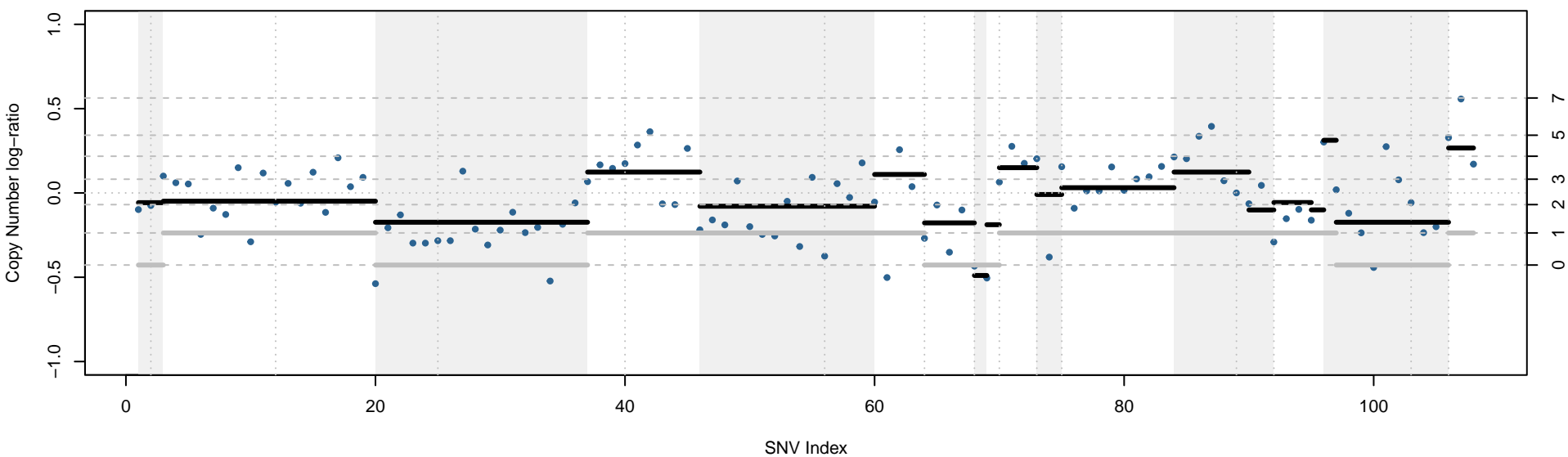
Purity: 0.22 Tumor ploidy: 2.446

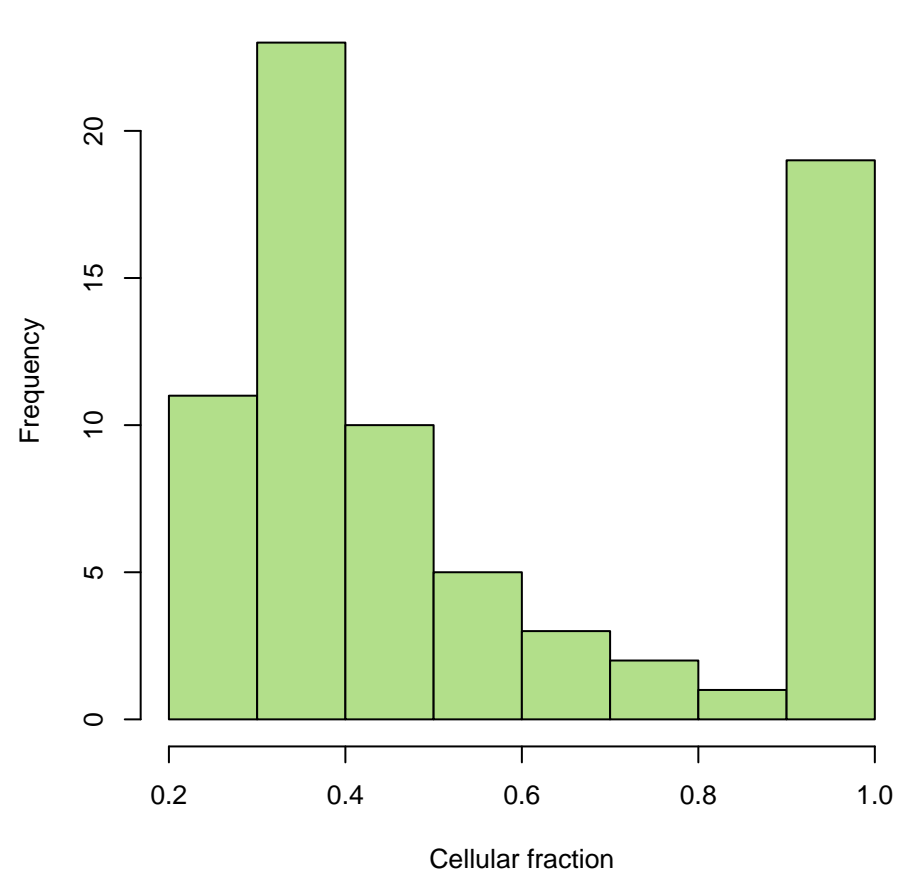
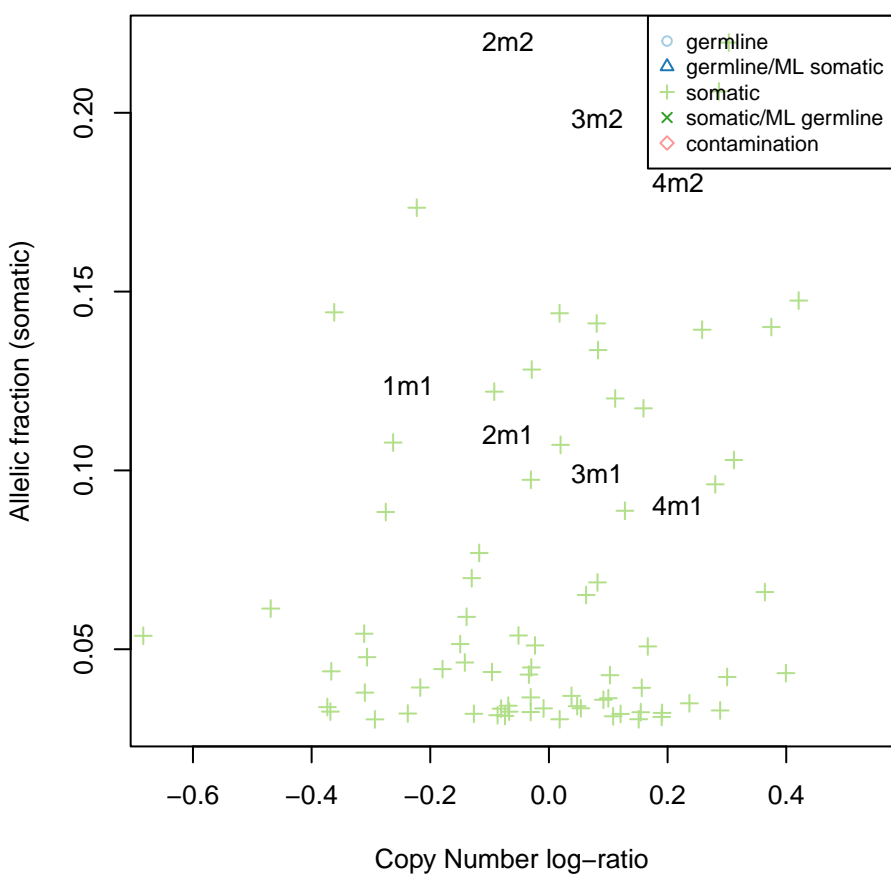
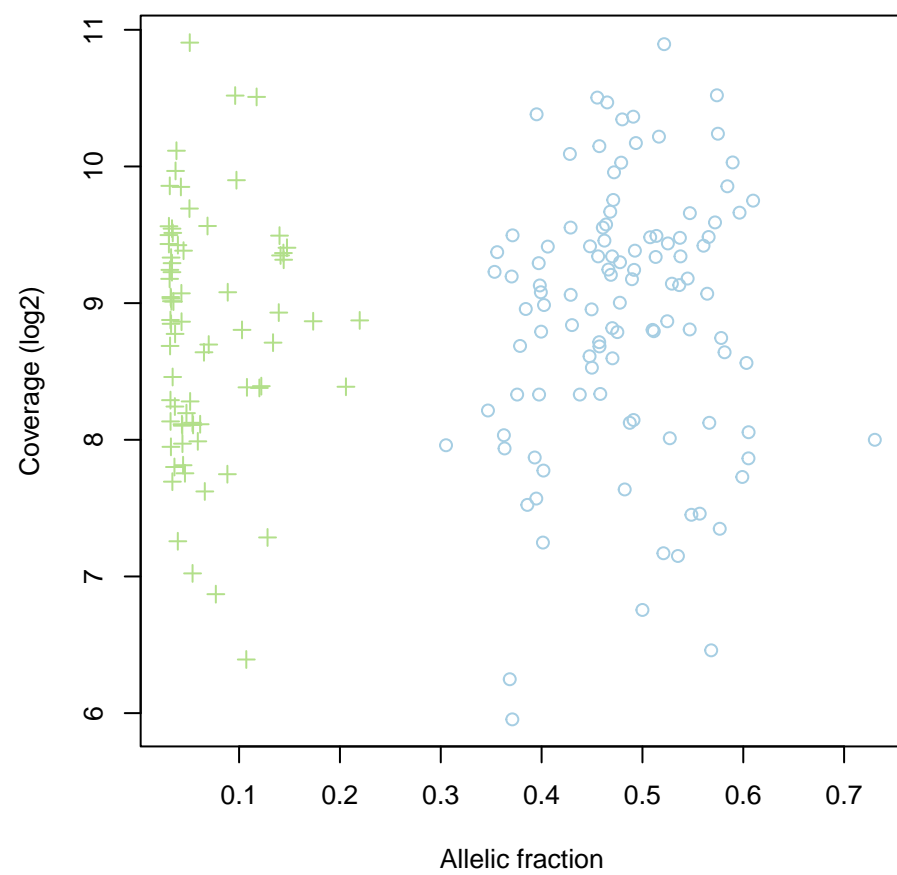
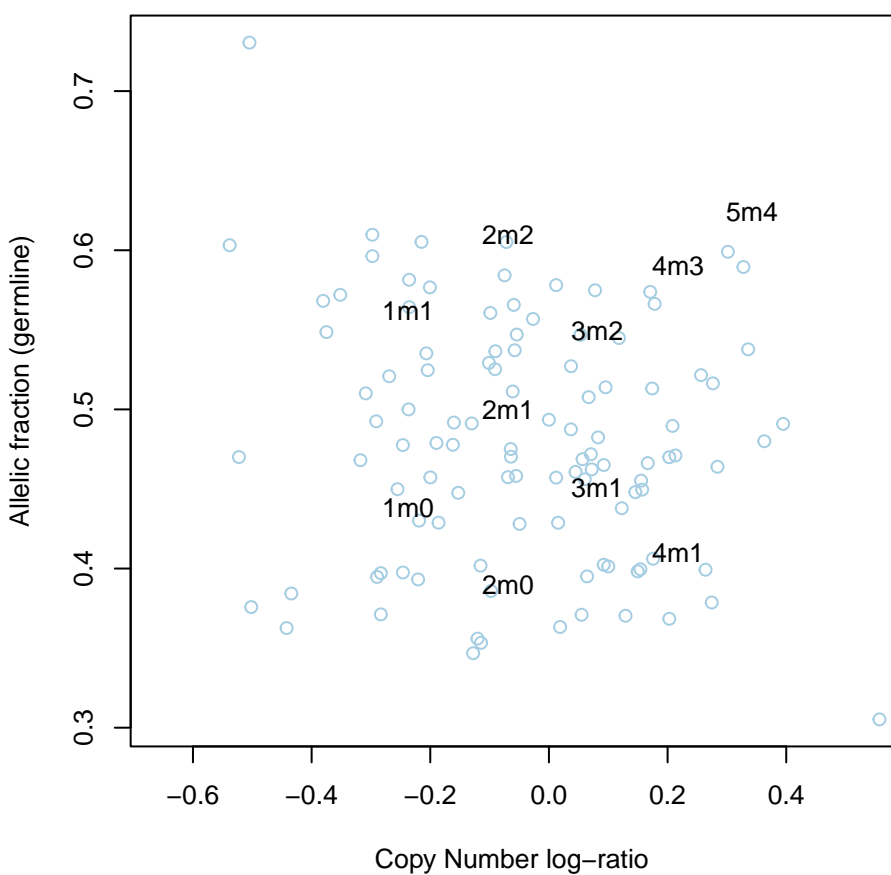


Purity: 0.22 Tumor ploidy: 2.446 SNV log-likelihood: 2.98 GoF: 92.7% Mean coverage: 466;556

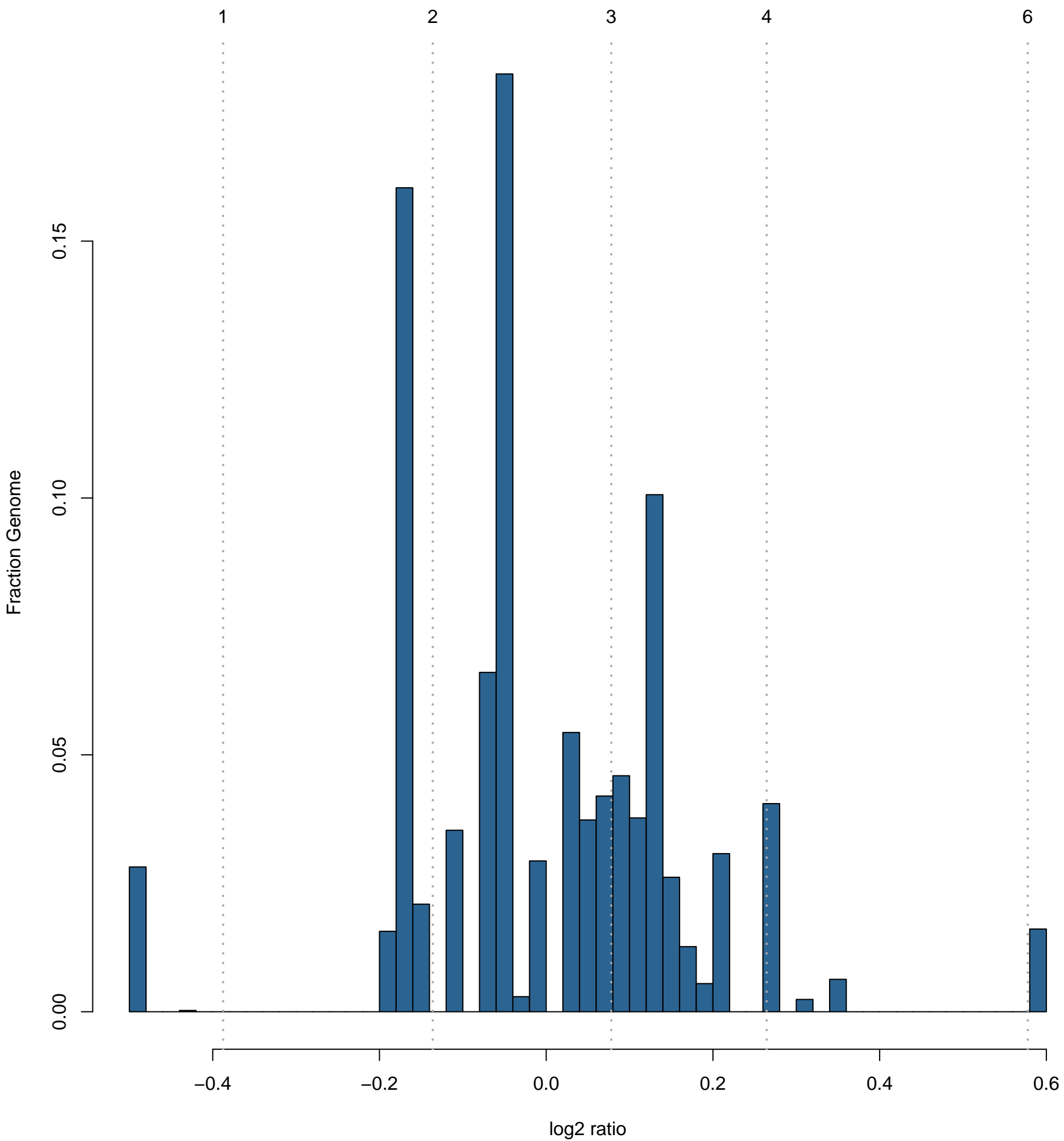


SCNA-fit log-likelihood: -5271.55

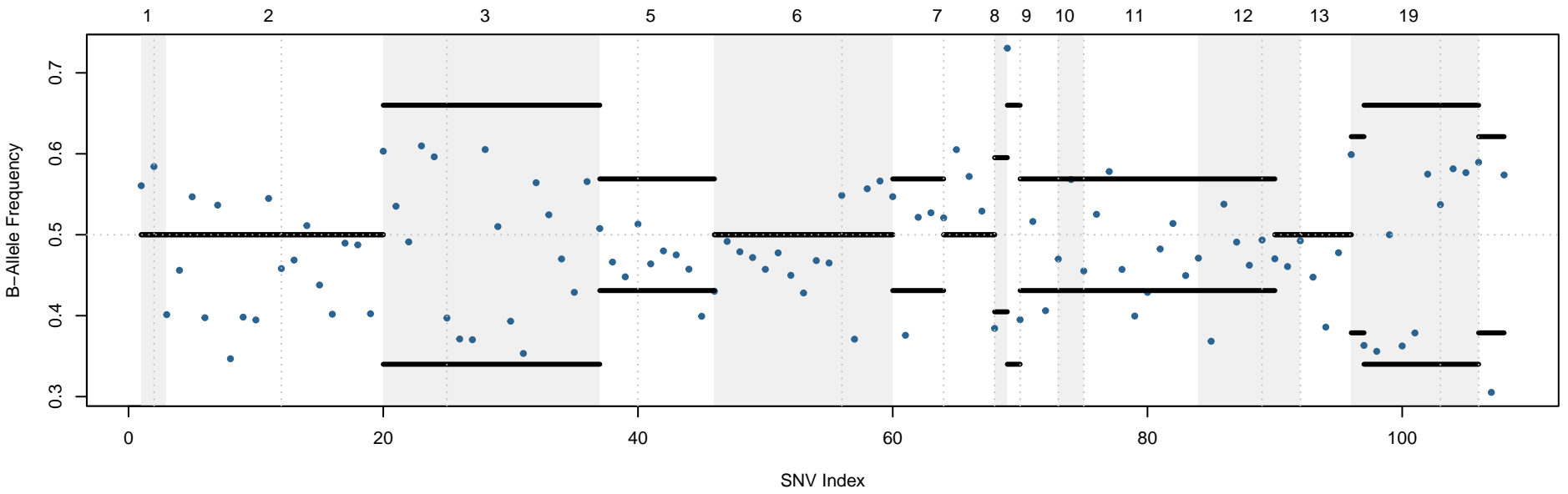




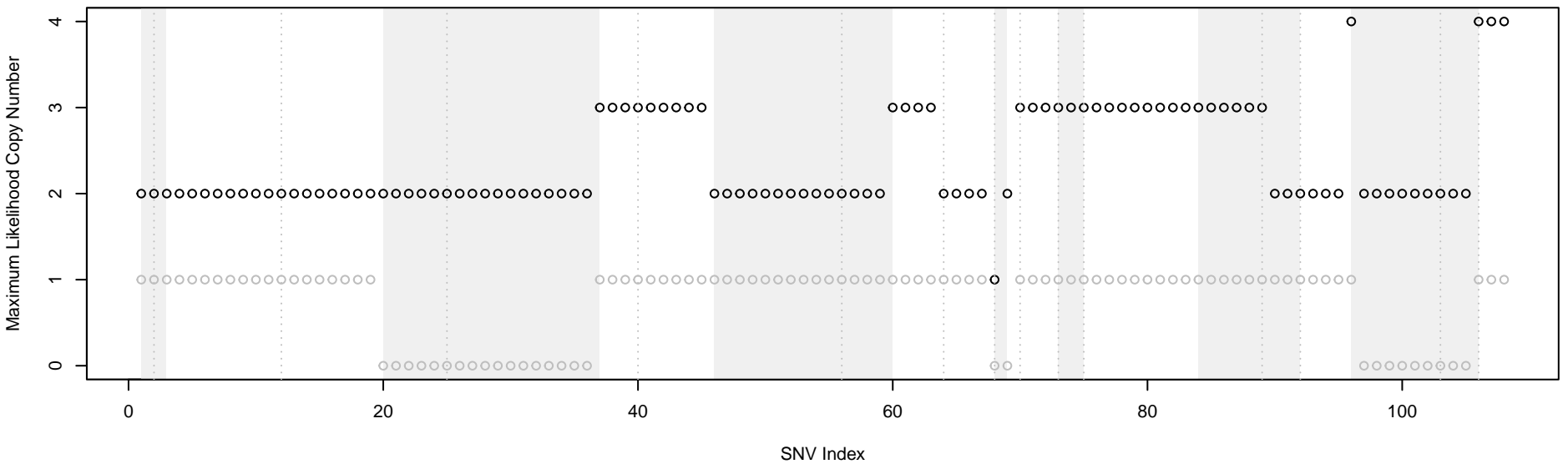
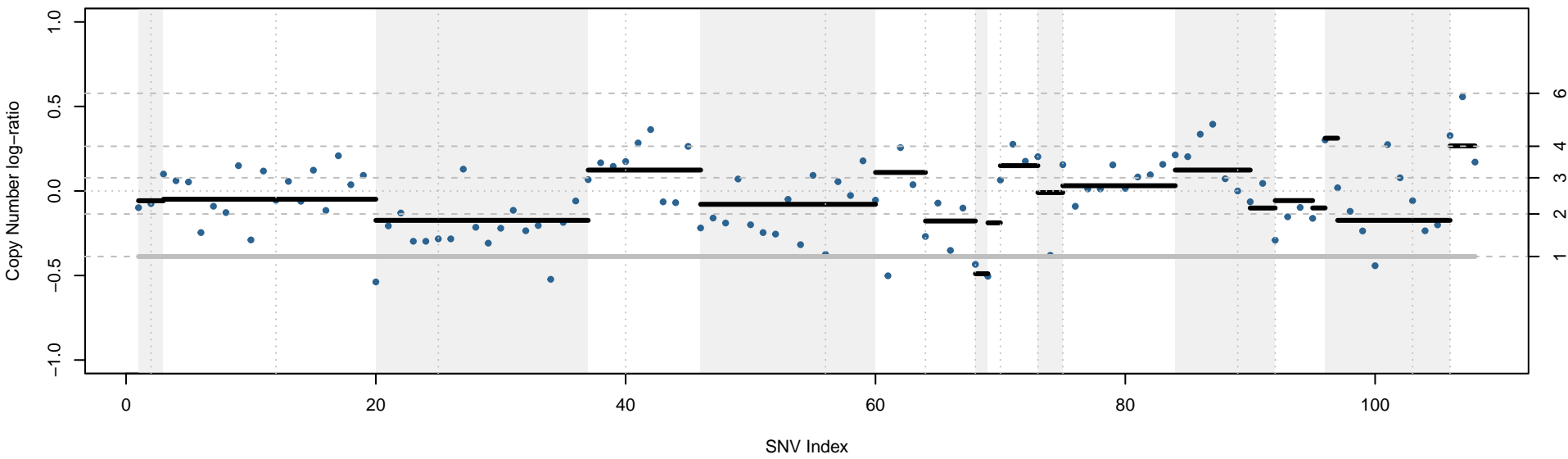
Purity: 0.32 Tumor ploidy: 2.618

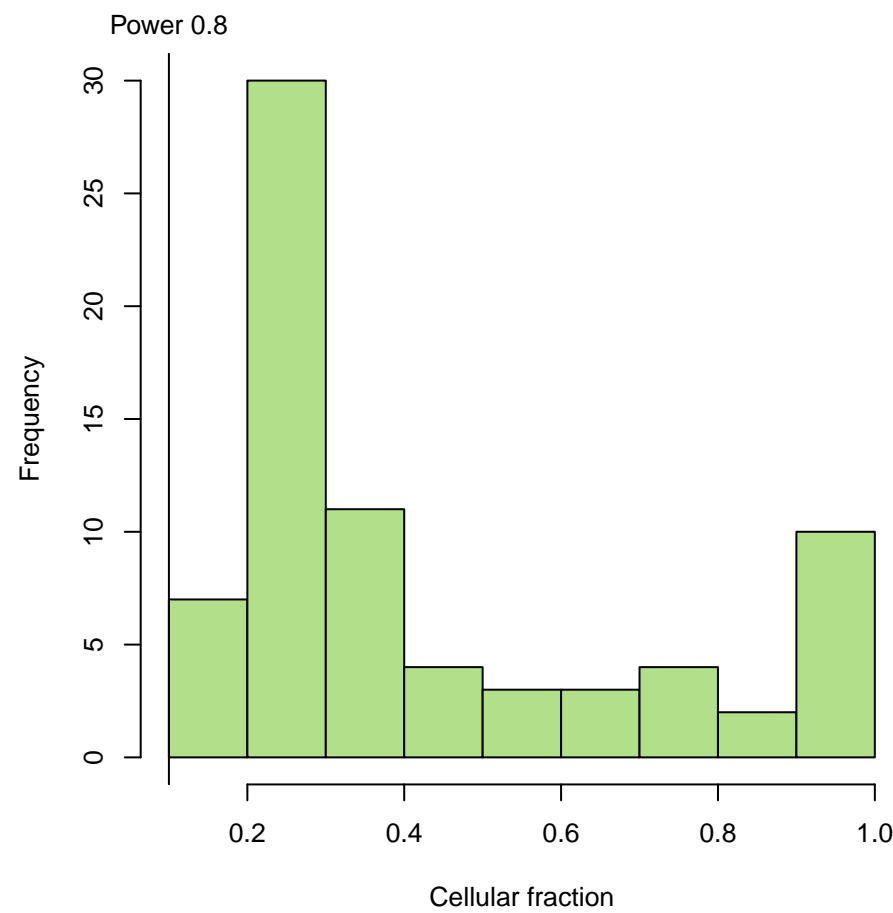
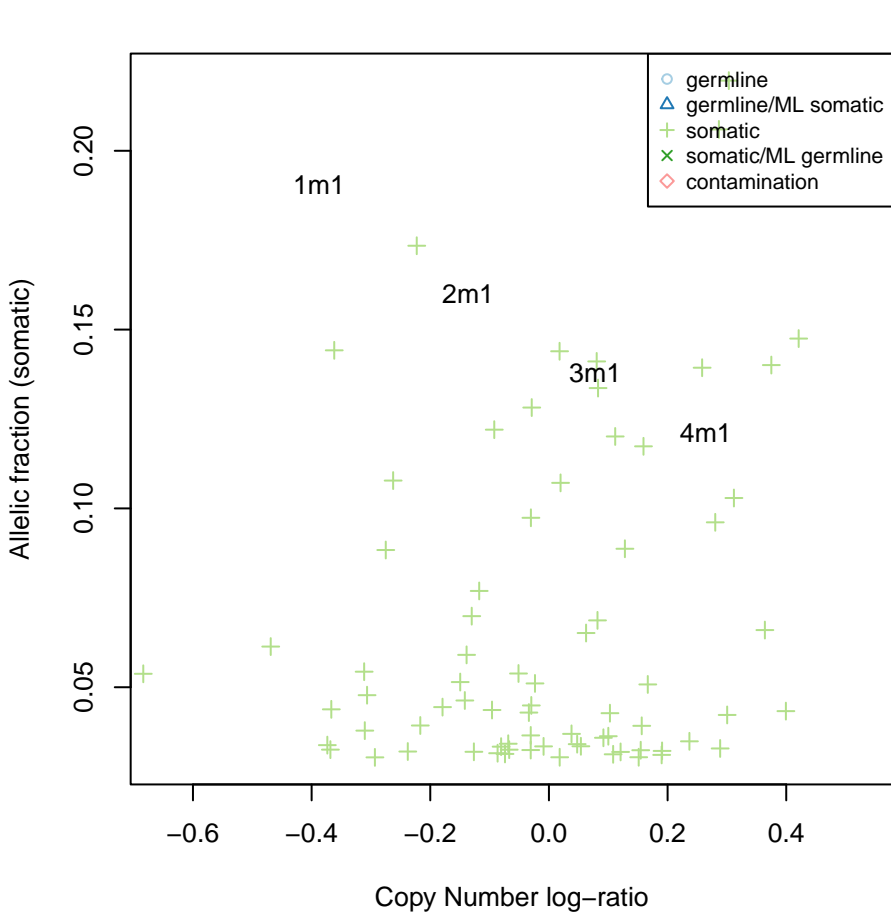
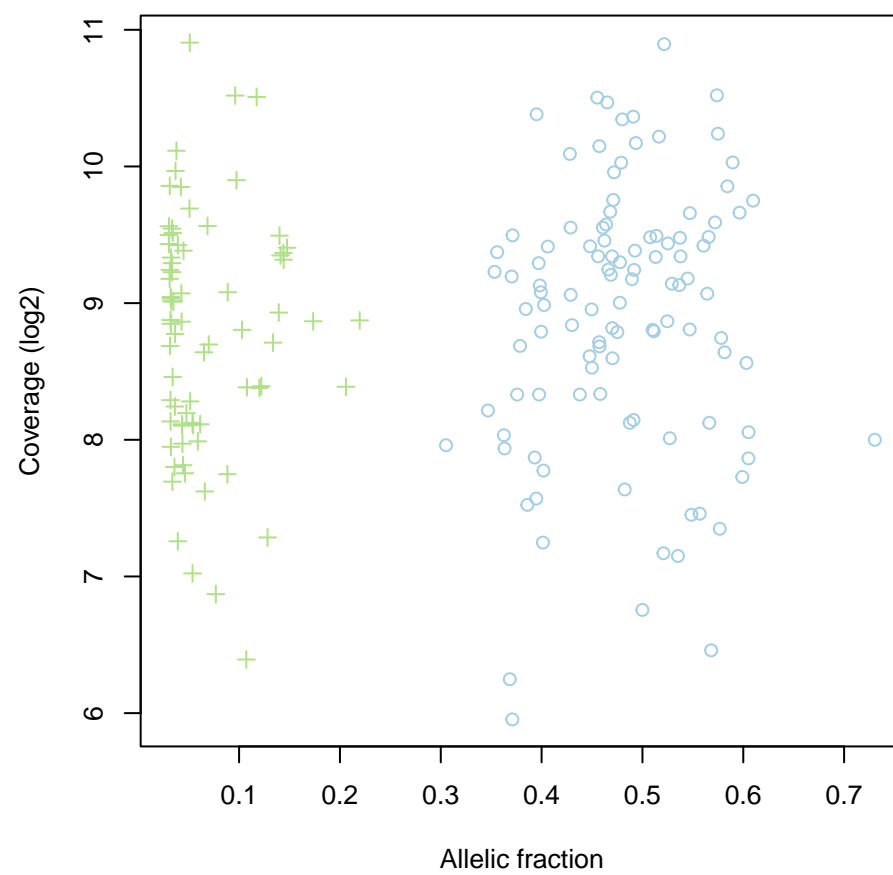
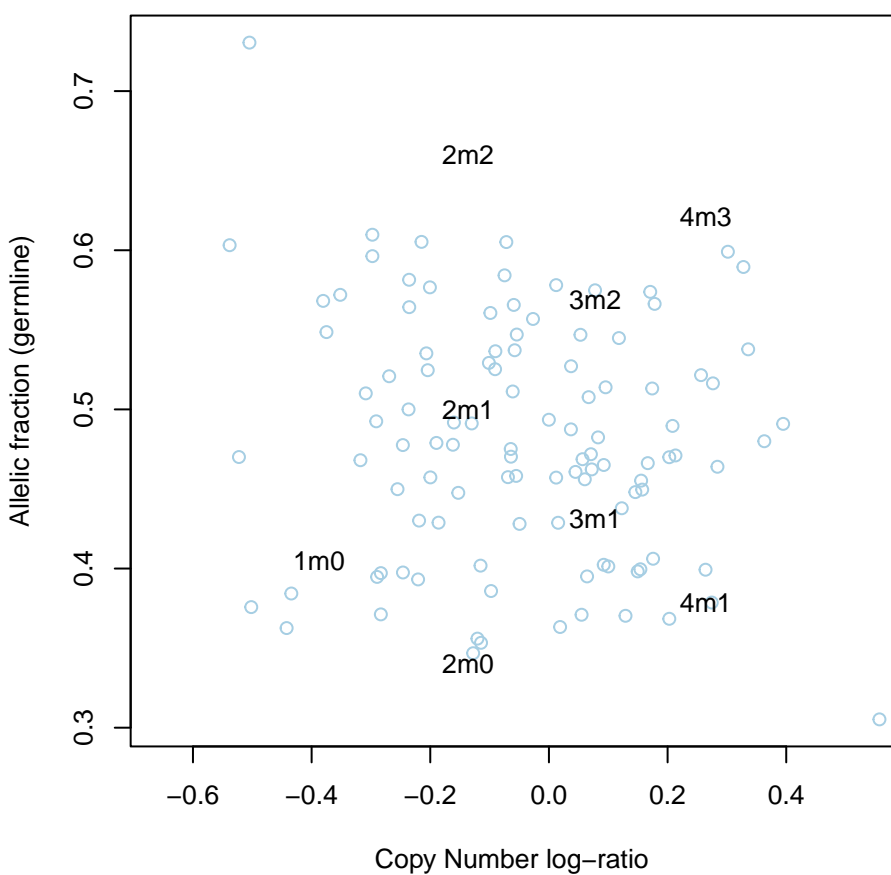


Purity: 0.32 Tumor ploidy: 2.618 SNV log-likelihood: -91.69 GoF: 86.2% Mean coverage: 466;556

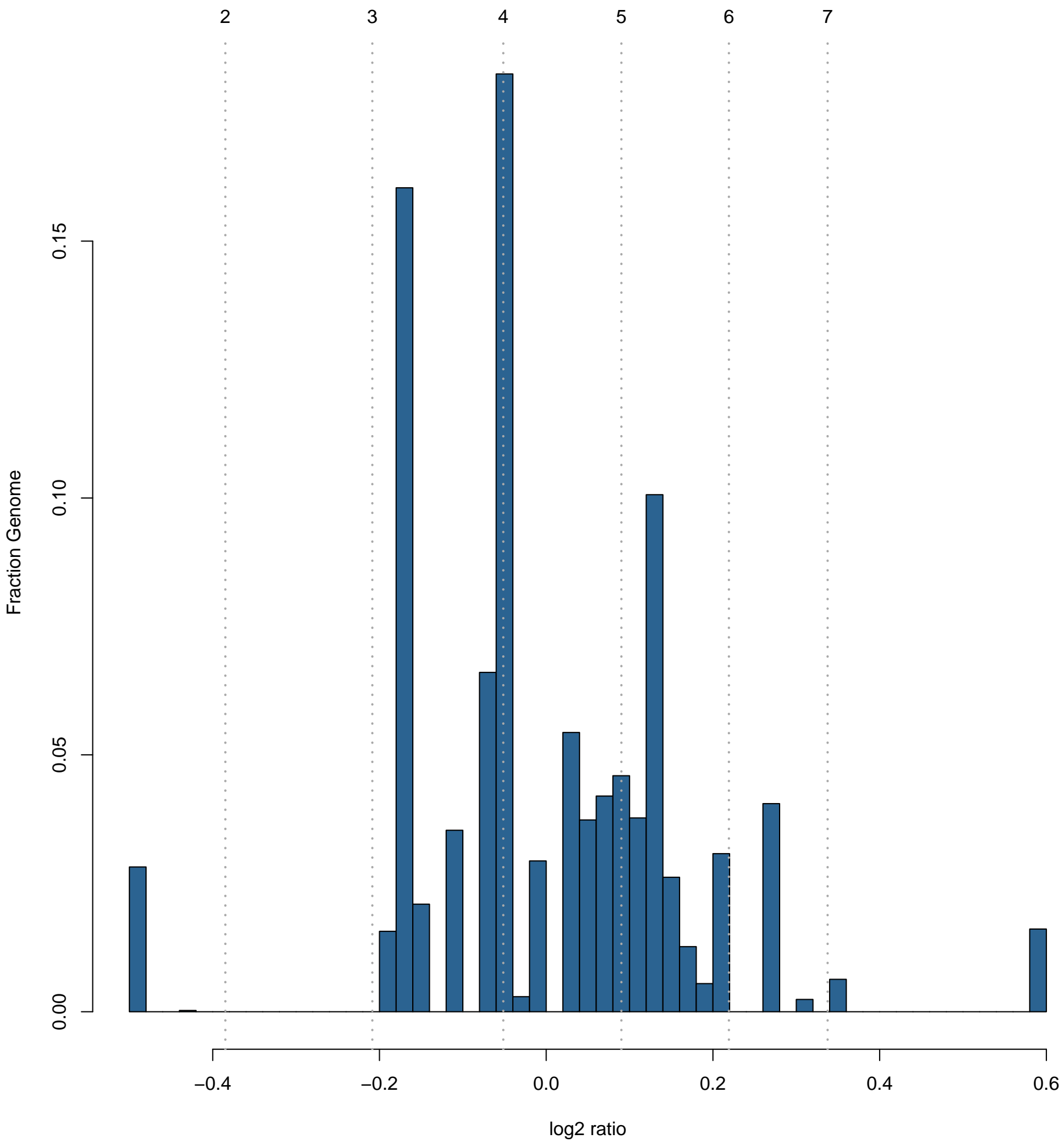


SCNA-fit log-likelihood: -5241.35

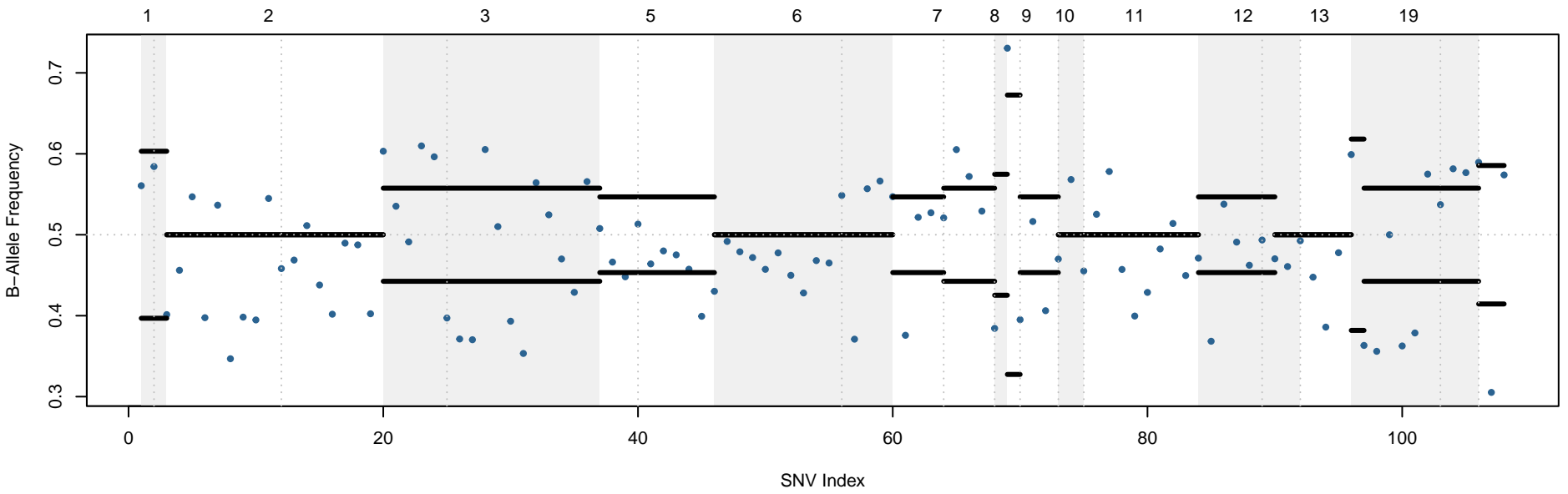




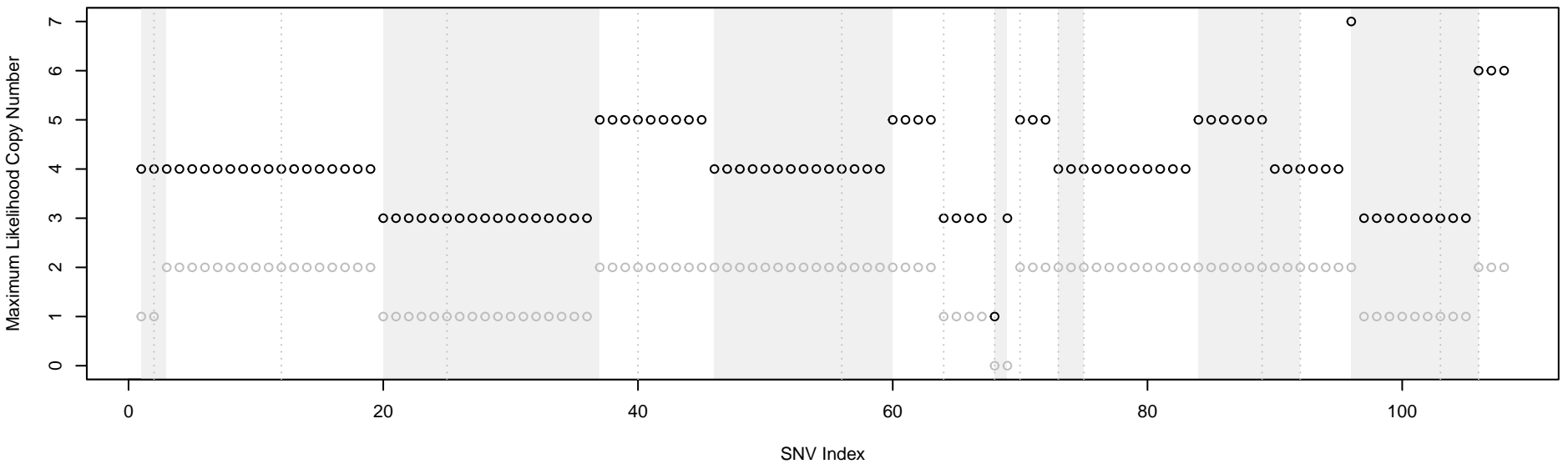
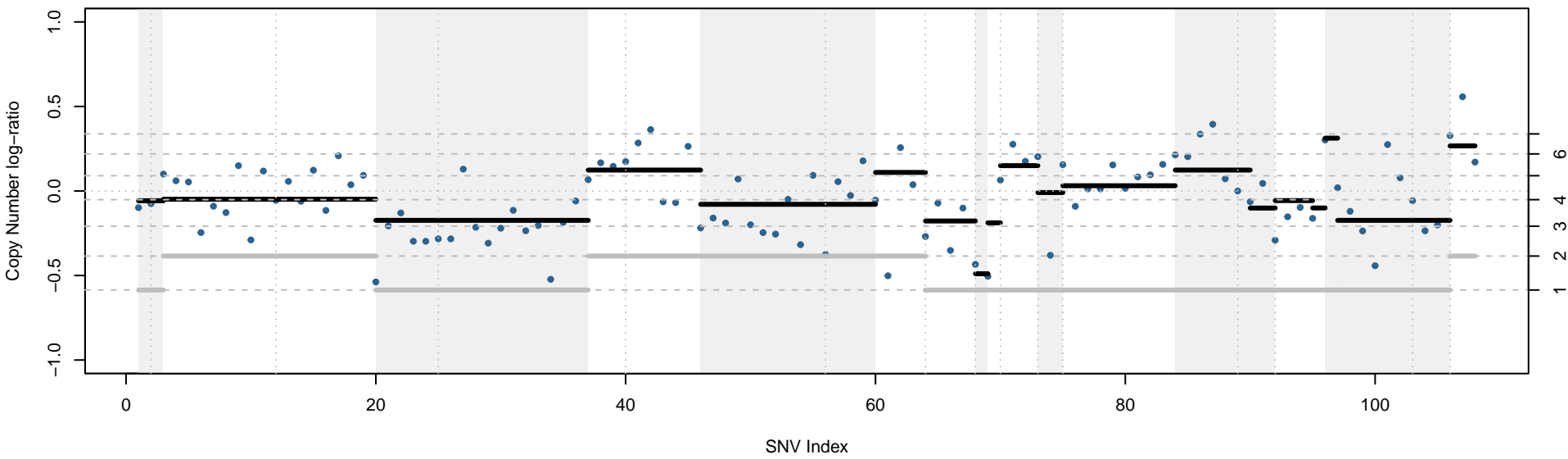
Purity: 0.26 Tumor ploidy: 4.352



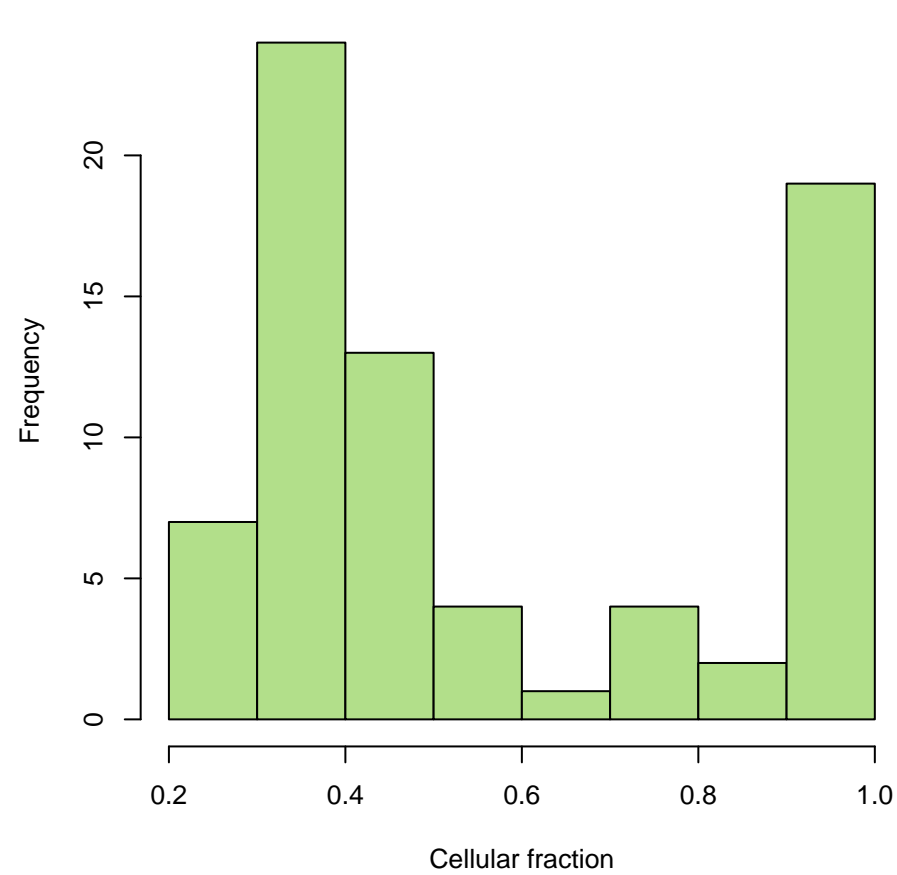
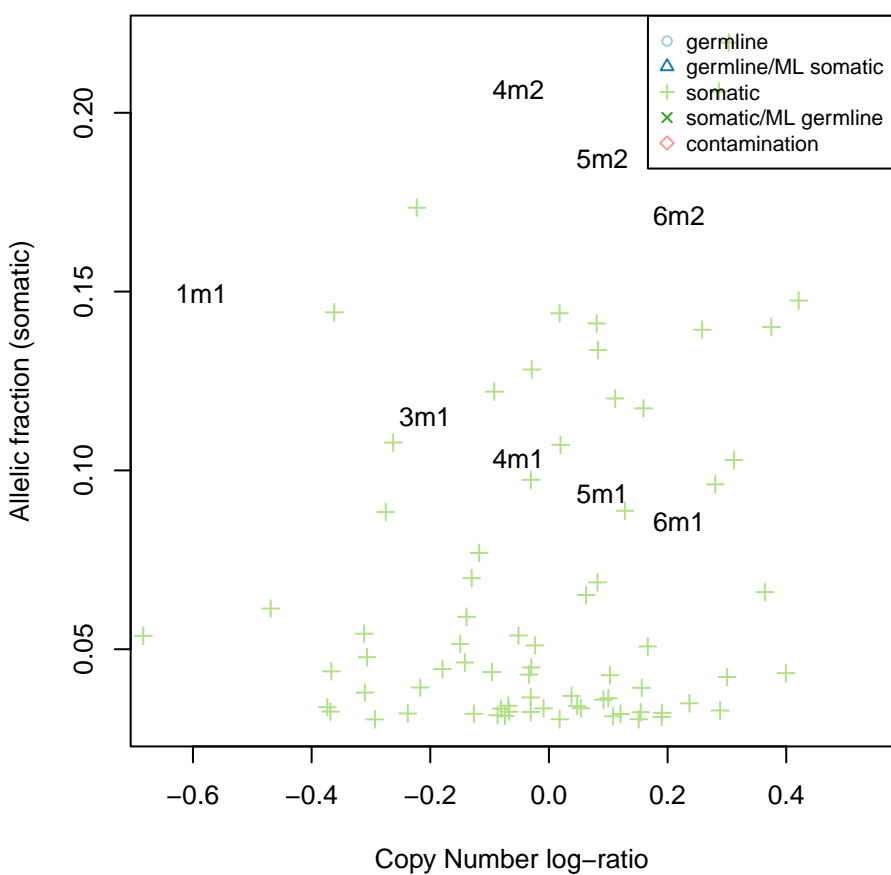
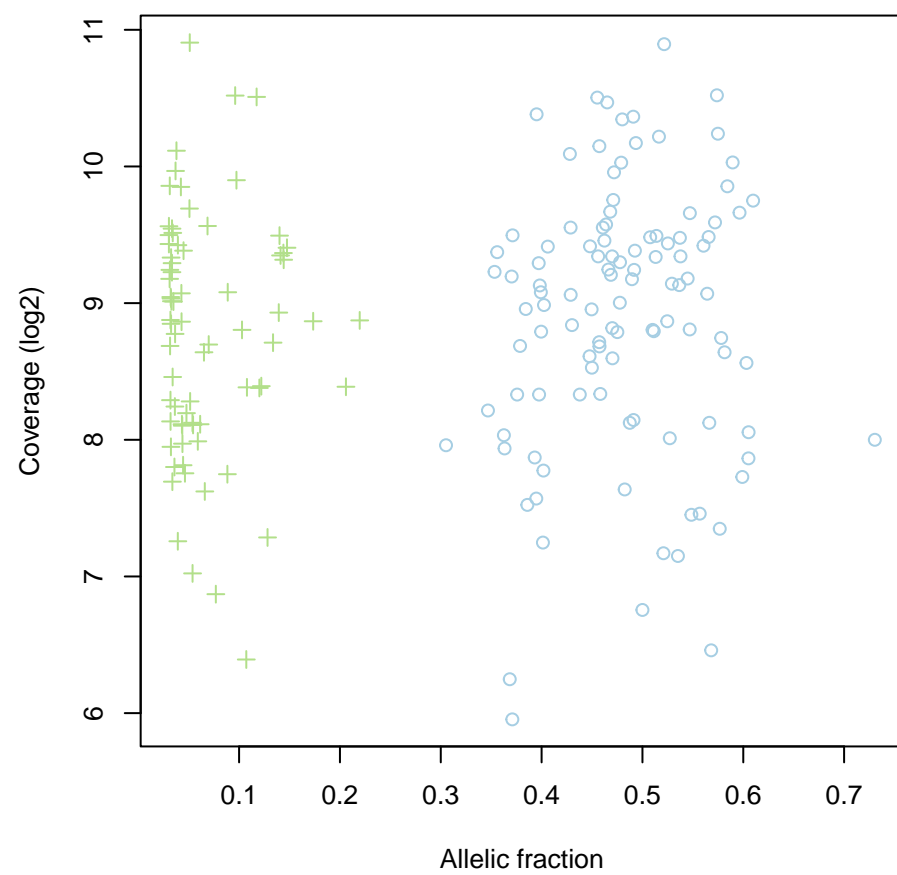
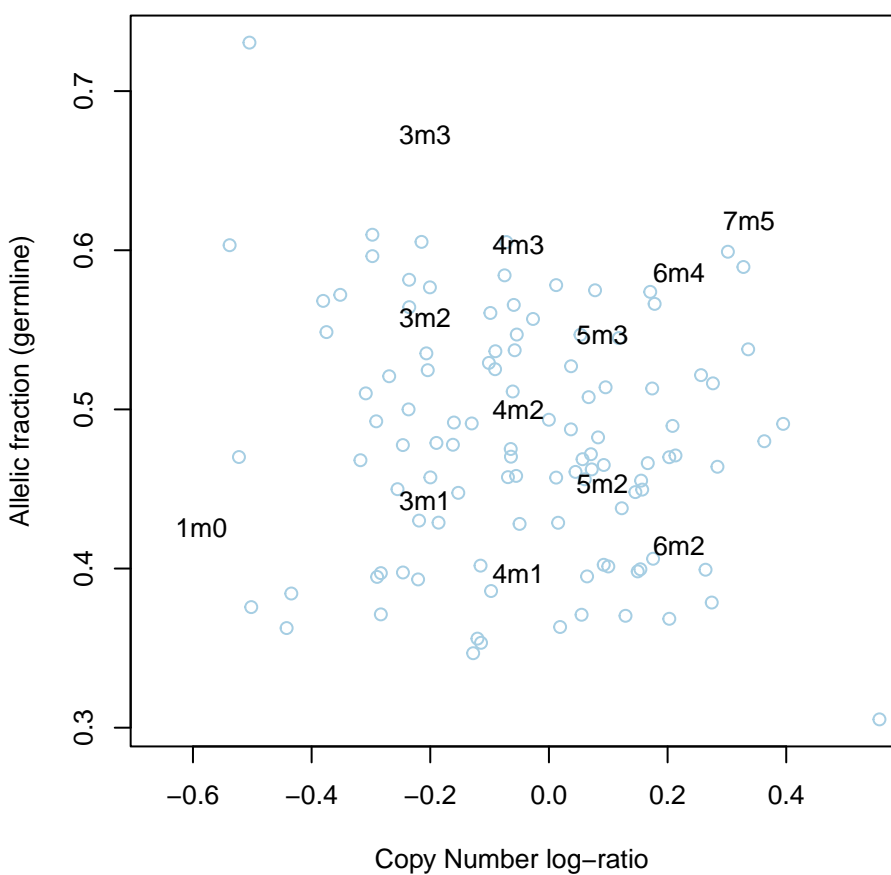
Purity: 0.26 Tumor ploidy: 4.352 SNV log-likelihood: -91.59 GoF: 93.1% Mean coverage: 466;556



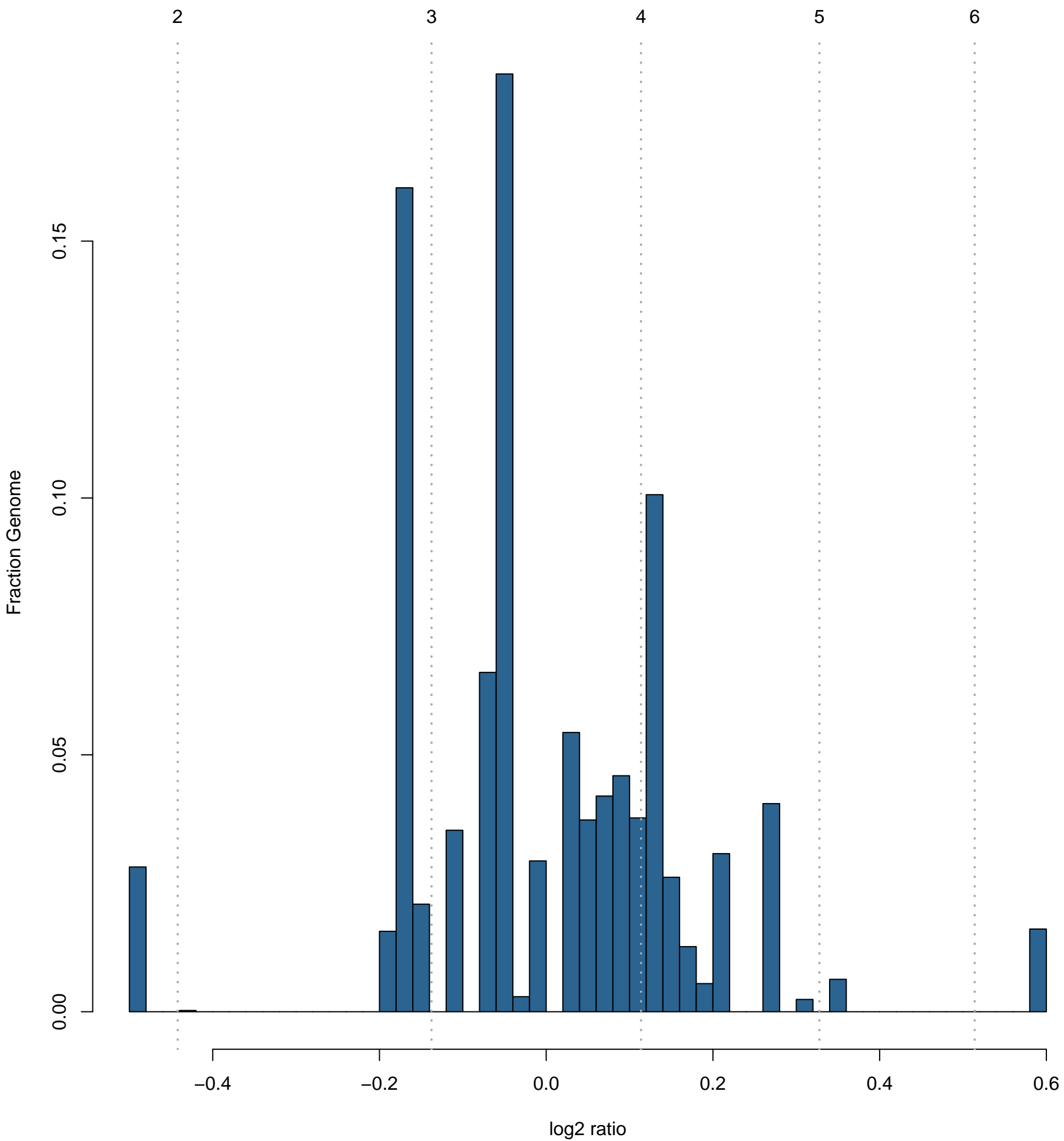
SCNA-fit log-likelihood: -5397.2



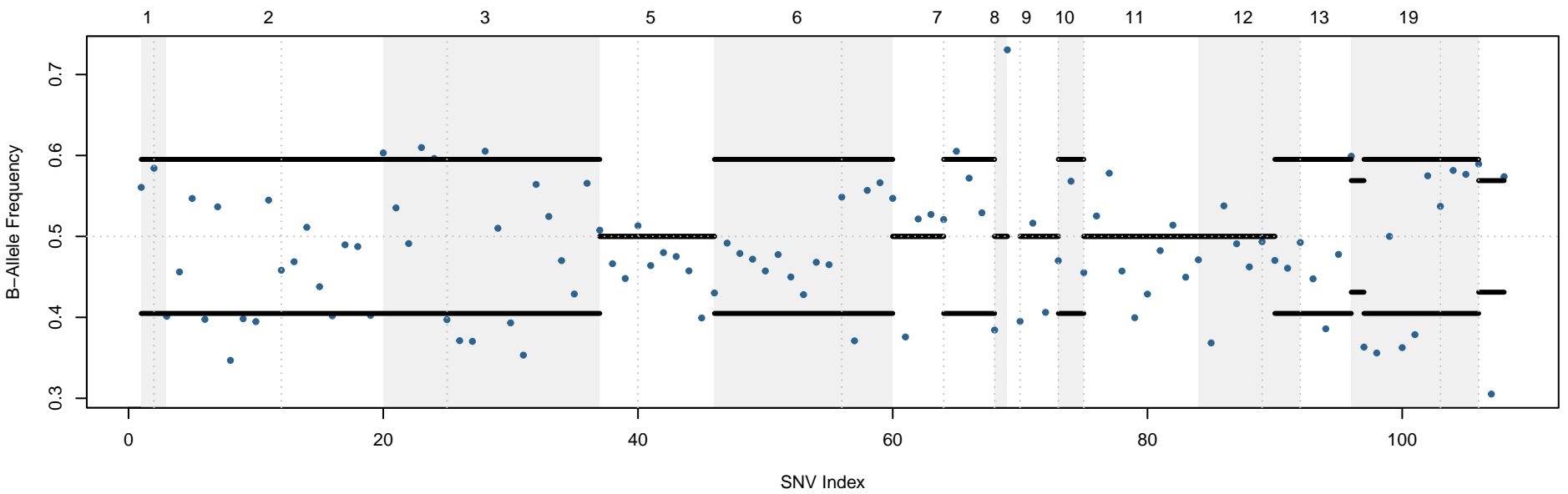




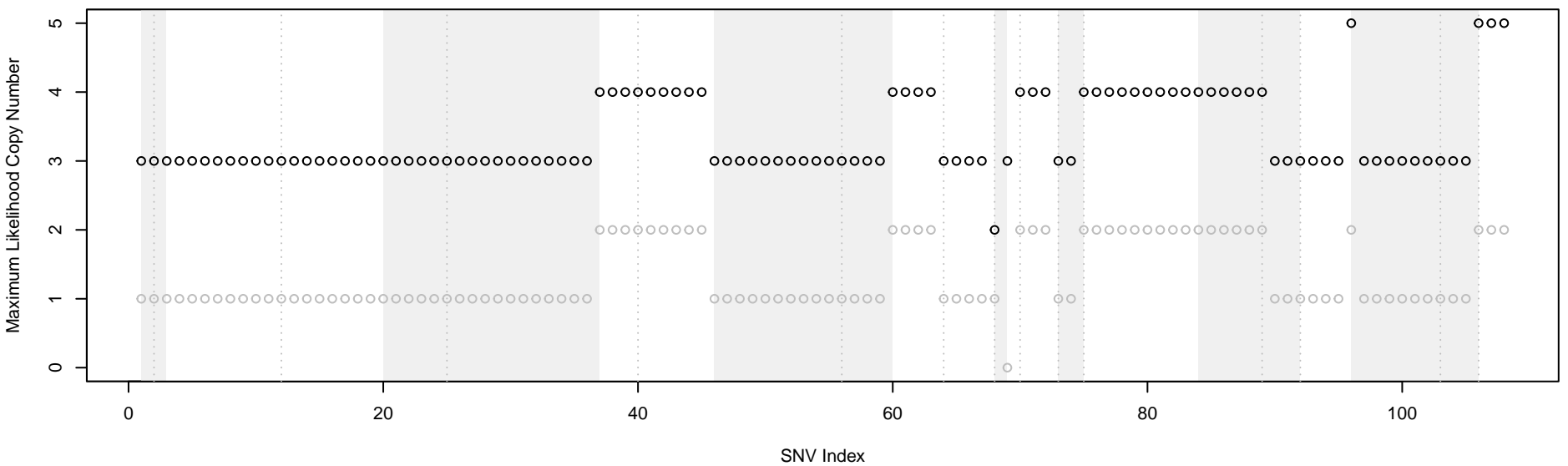
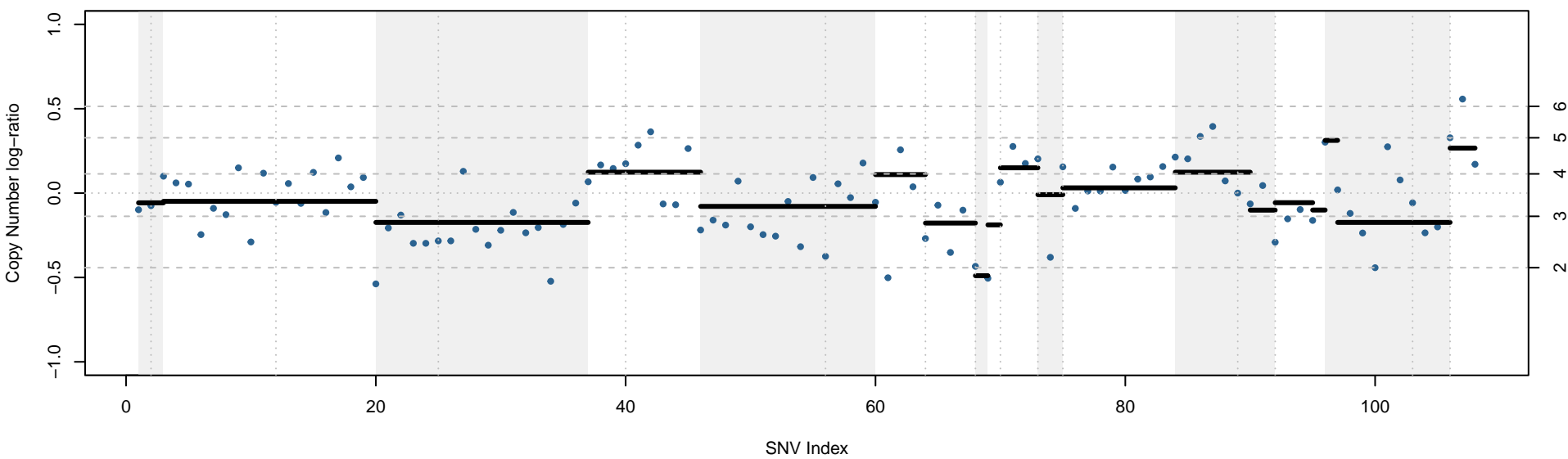
Purity: 0.47 Tumor ploidy: 3.526

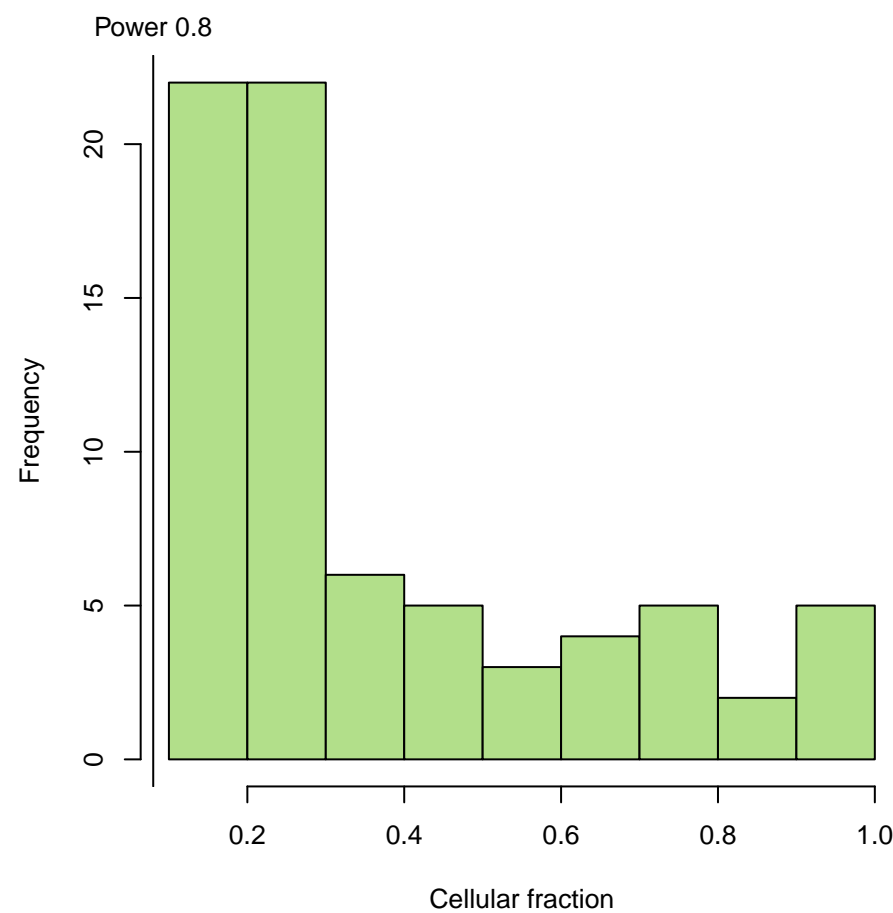
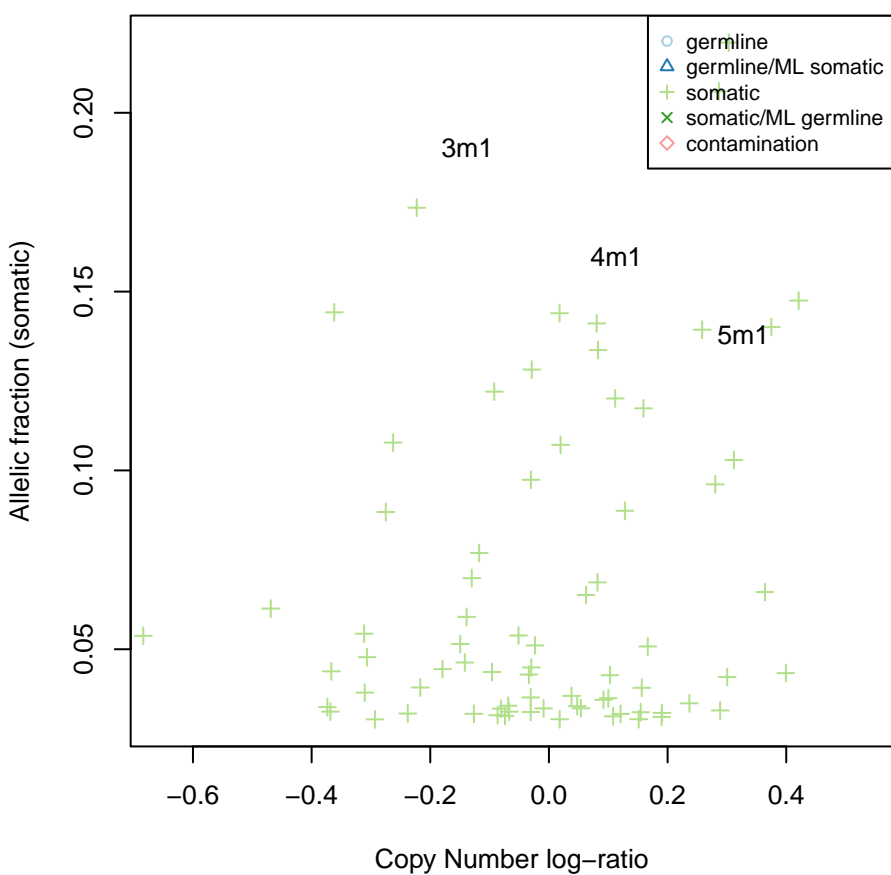
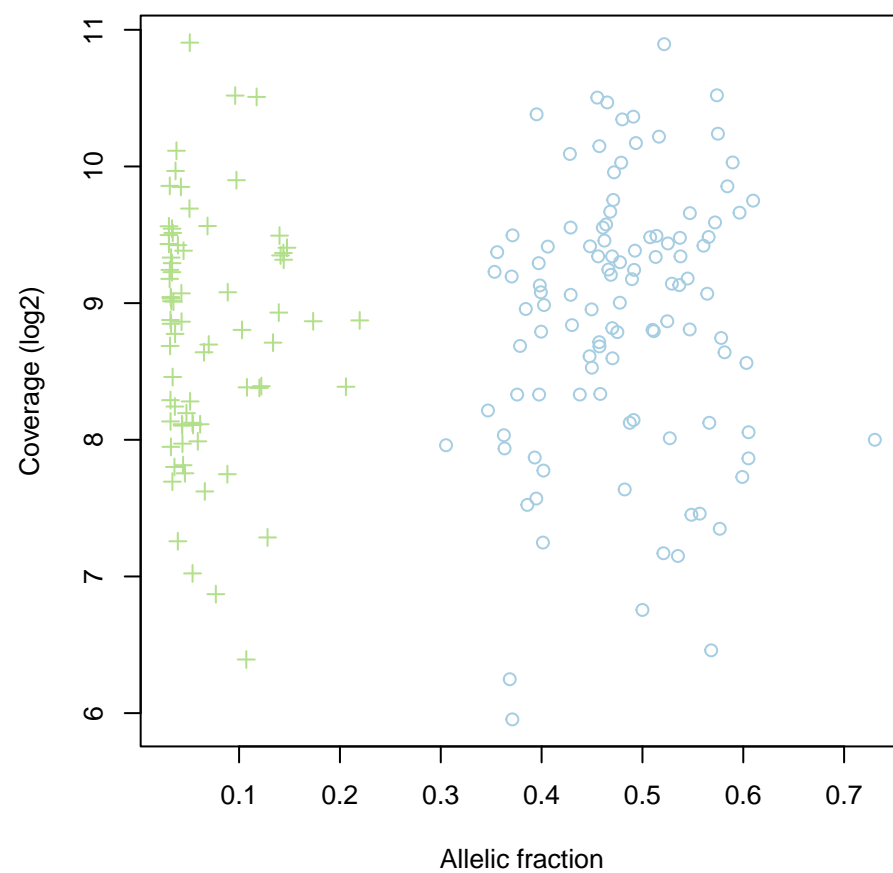
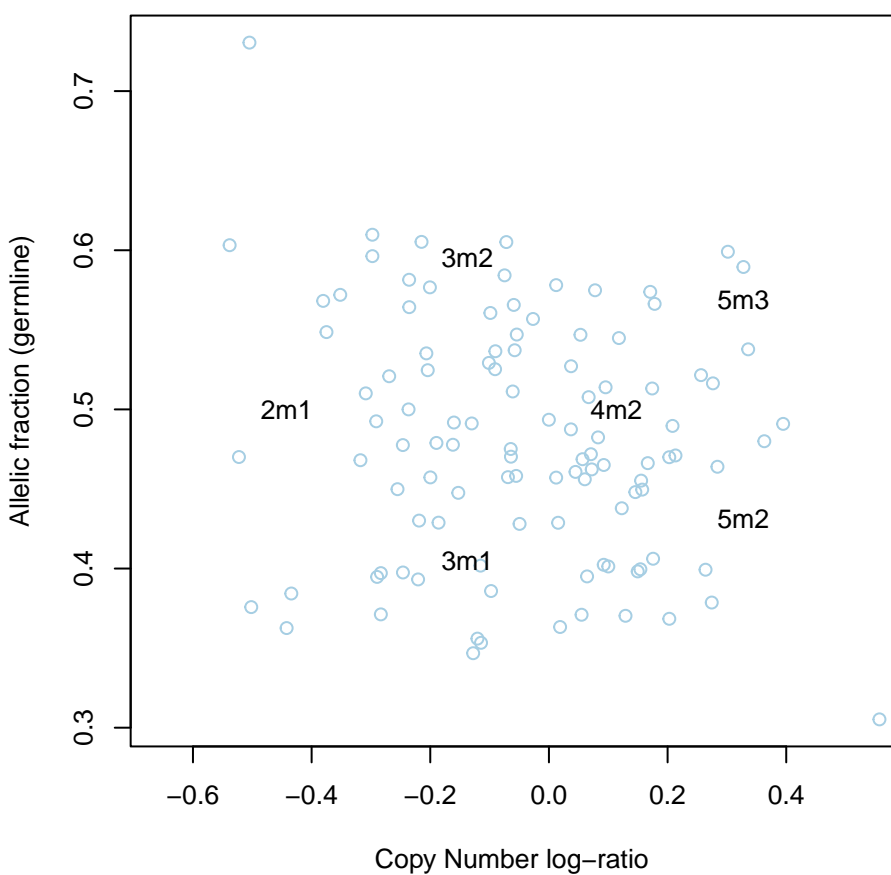


Purity: 0.47 Tumor ploidy: 3.526 SNV log-likelihood: -171.79 GoF: 81% Mean coverage: 466;556

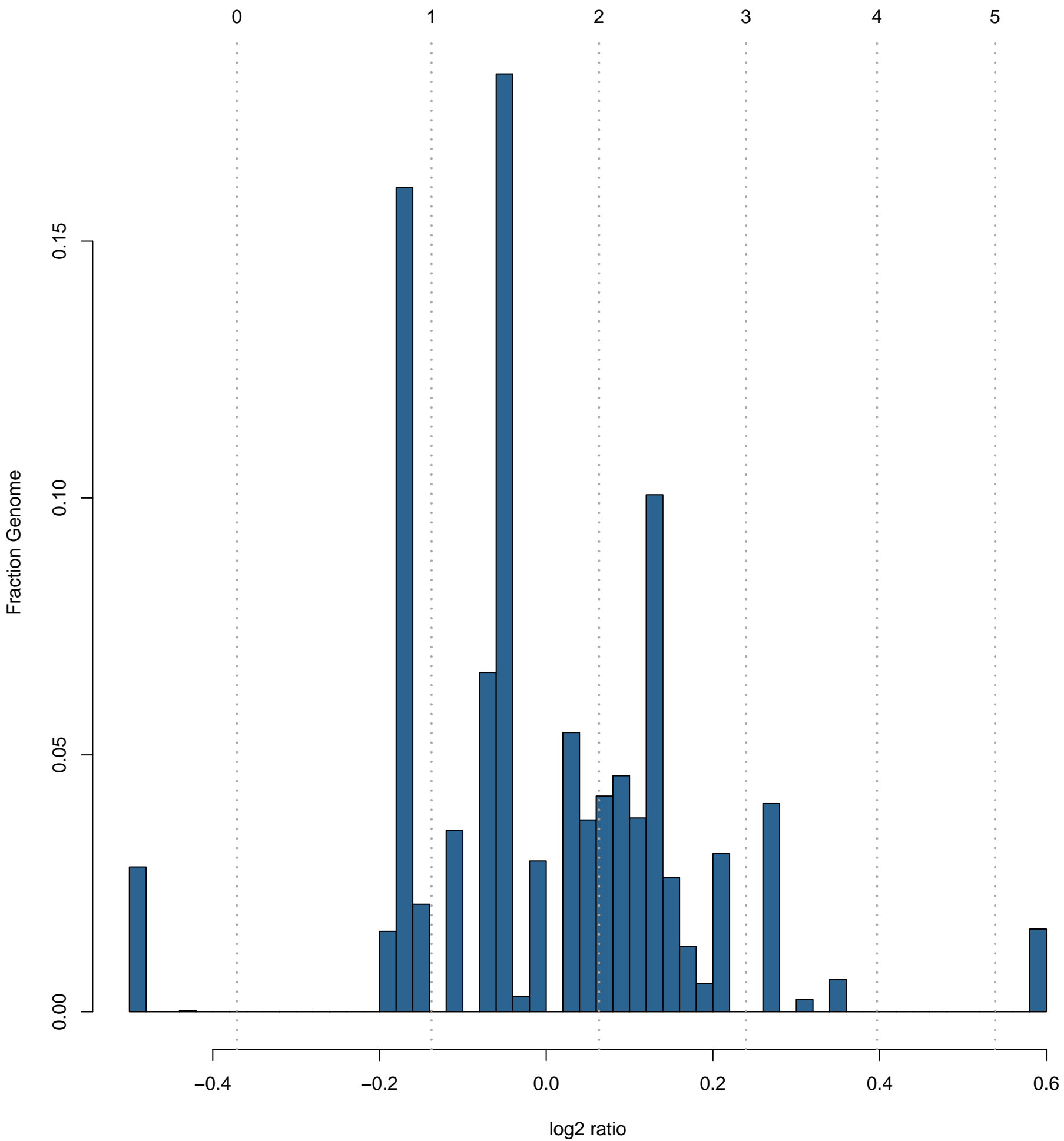


SCNA-fit log-likelihood: -5314.9

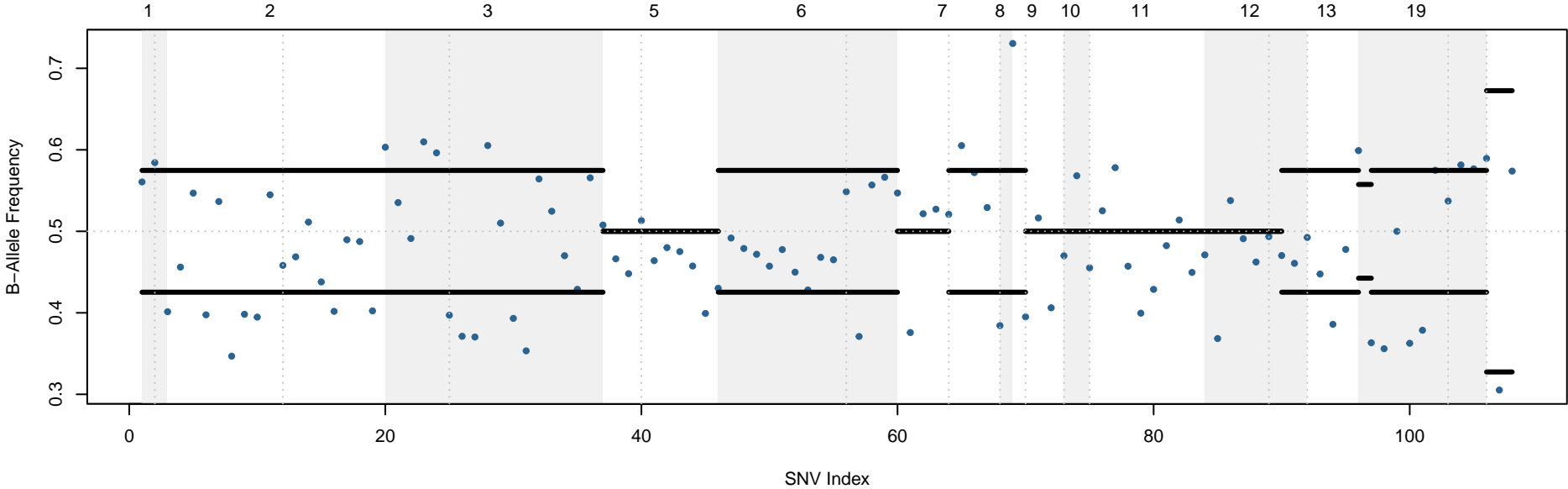




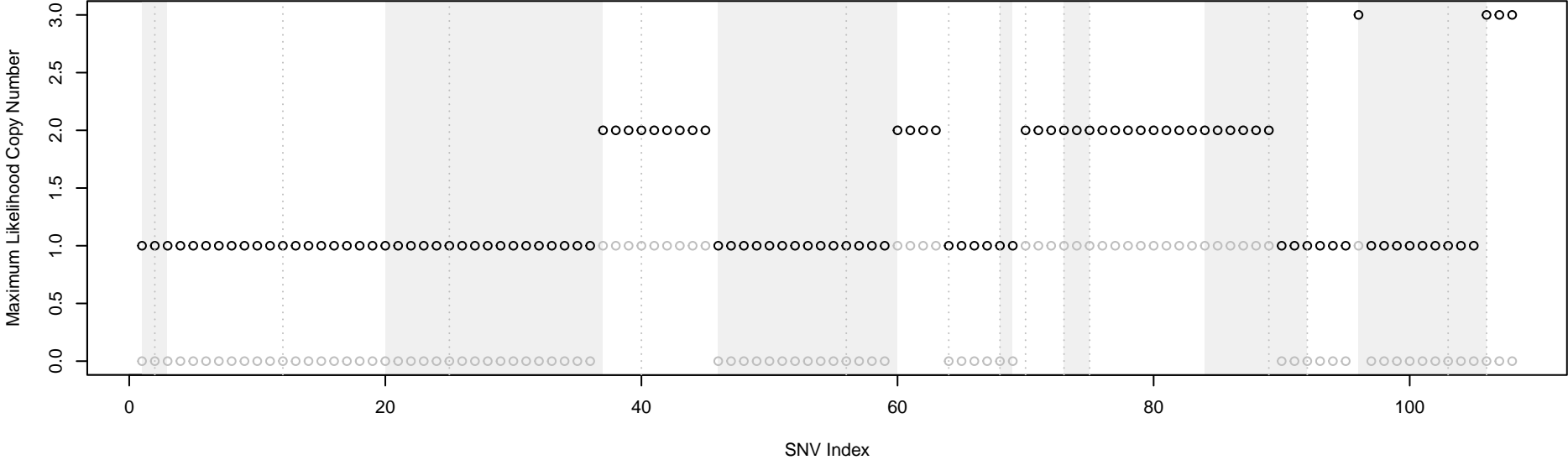
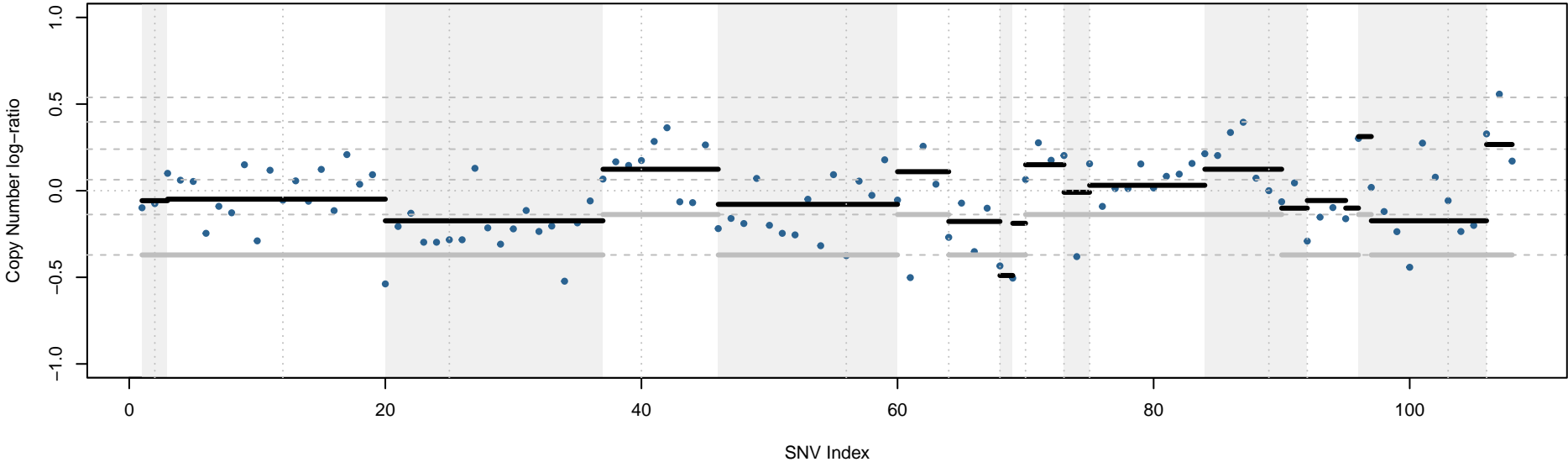
Purity: 0.26 Tumor ploidy: 1.669

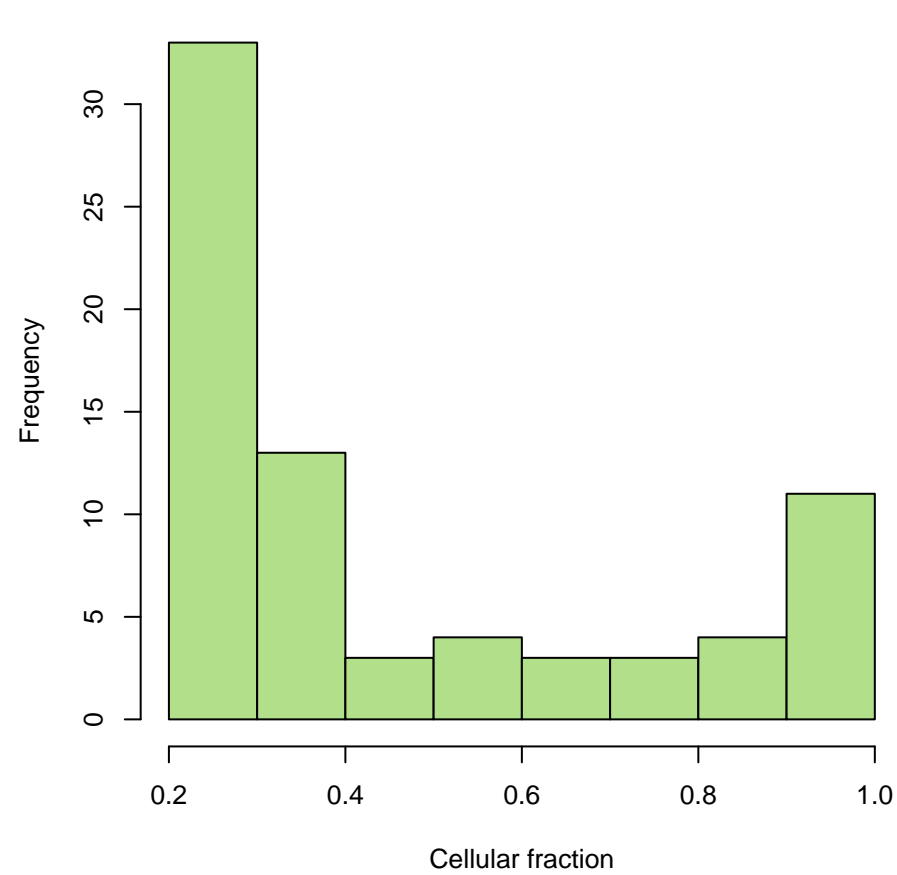
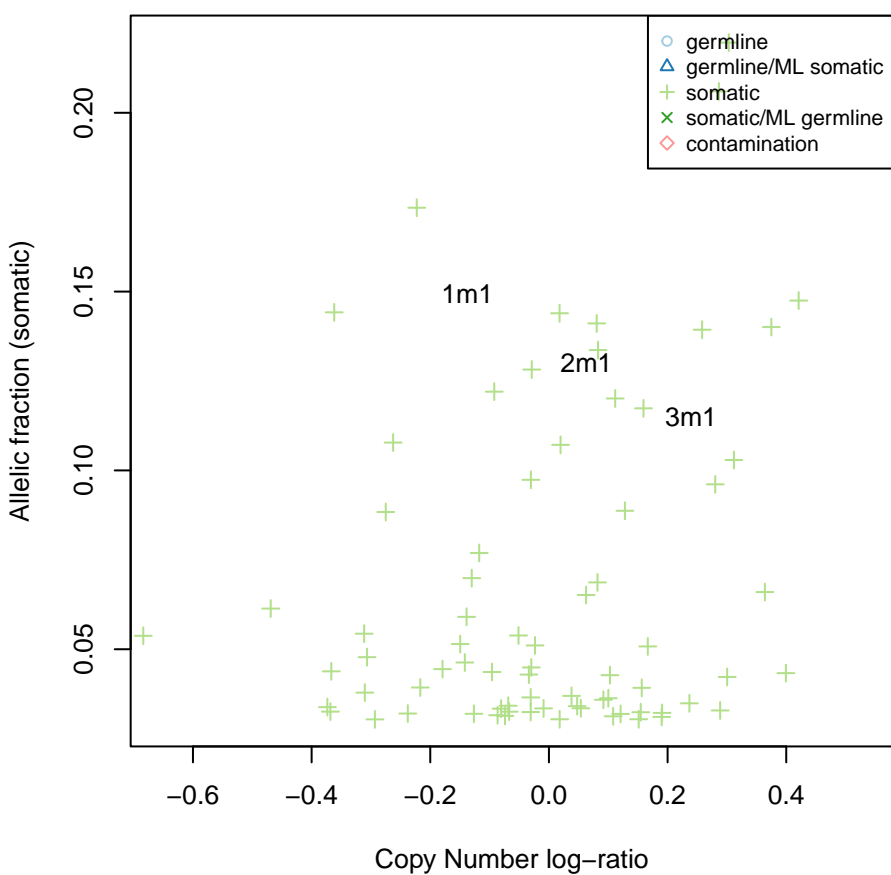
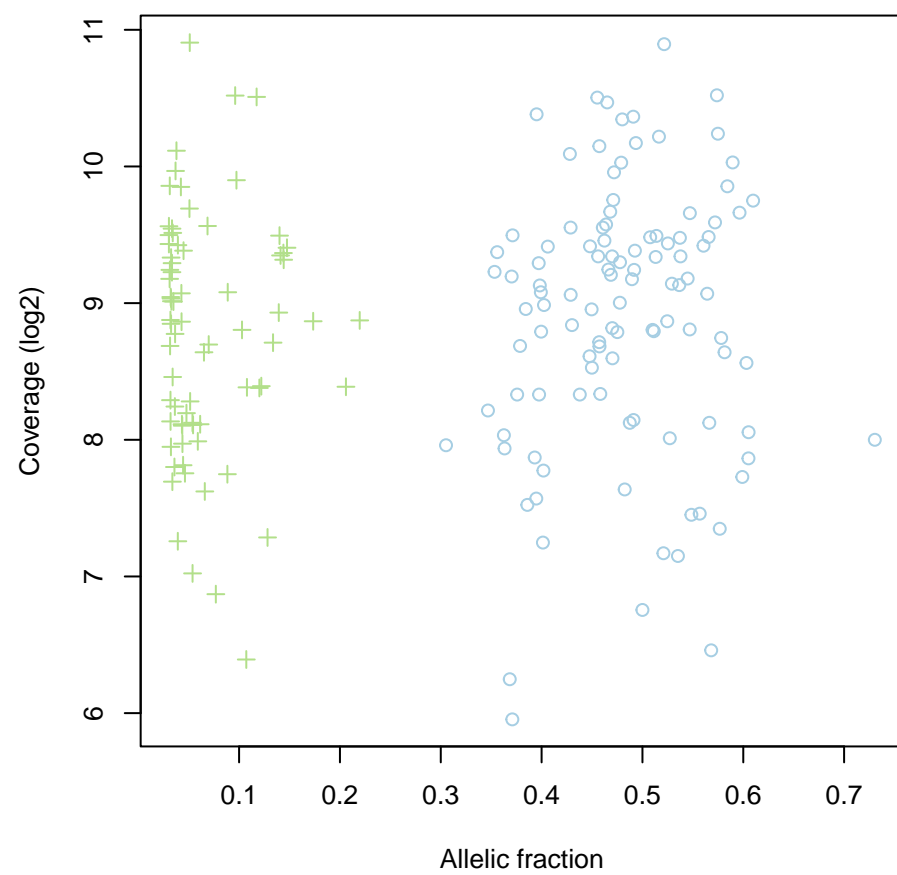
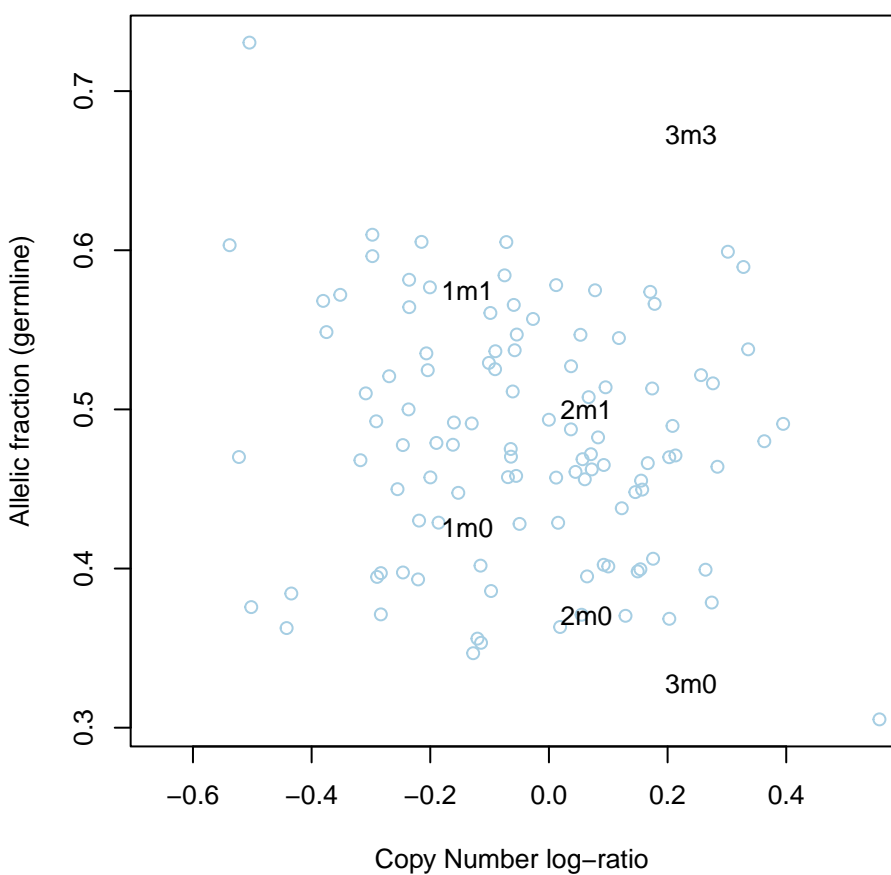


Purity: 0.26 Tumor ploidy: 1.669 SNV log-likelihood: -67.47 GoF: 89% Mean coverage: 466;556

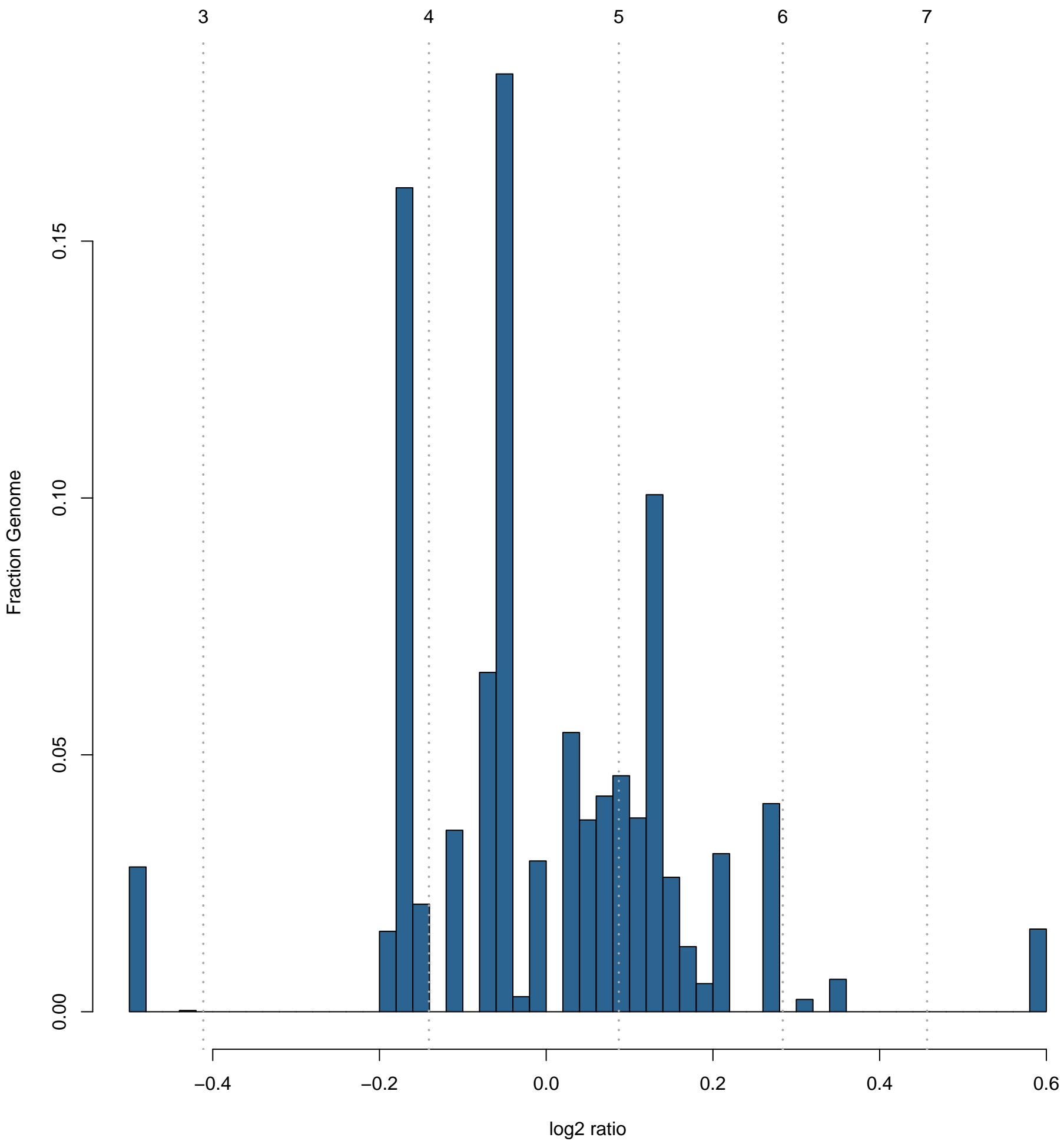


SCNA-fit log-likelihood: -5577.48



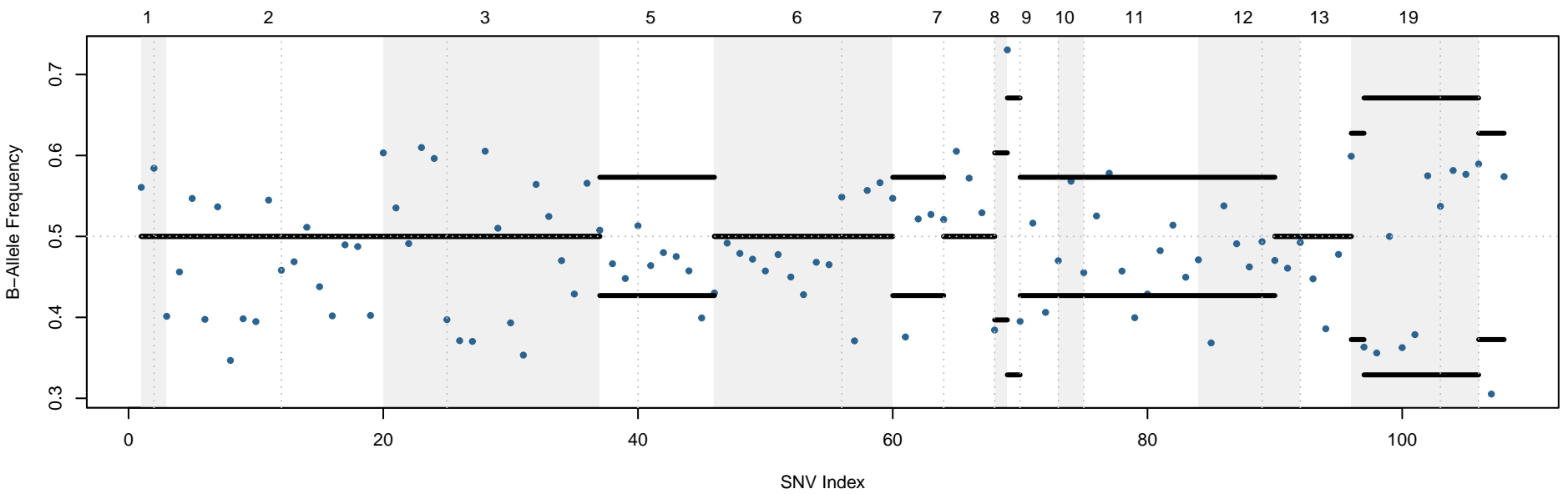


Purity: 0.52 Tumor ploidy: 4.599

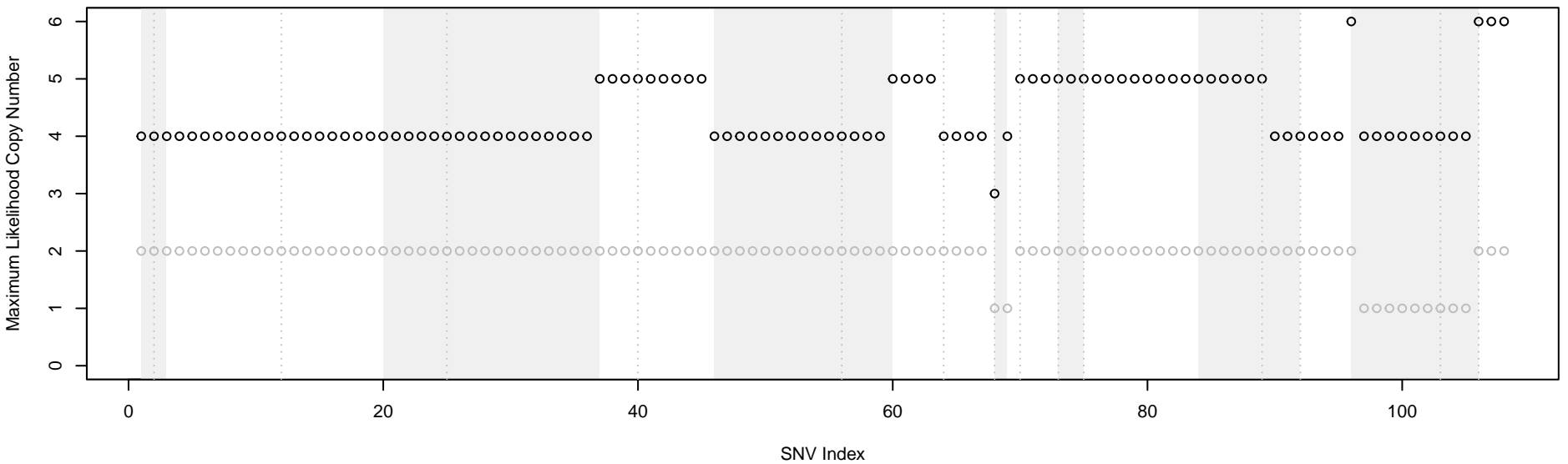
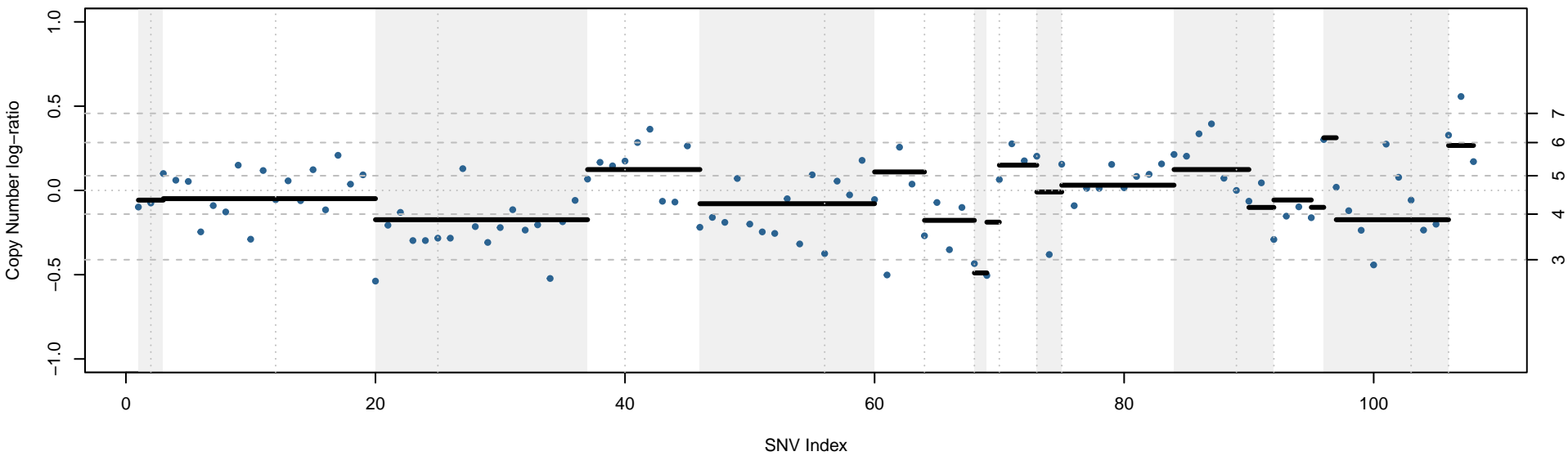


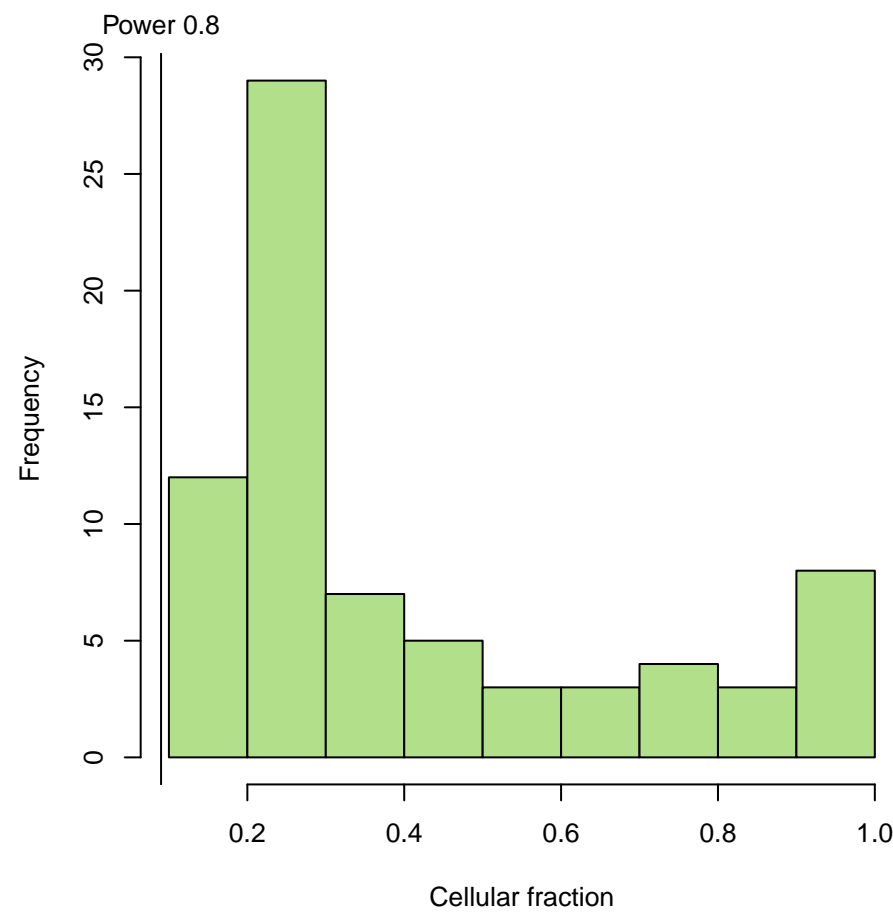
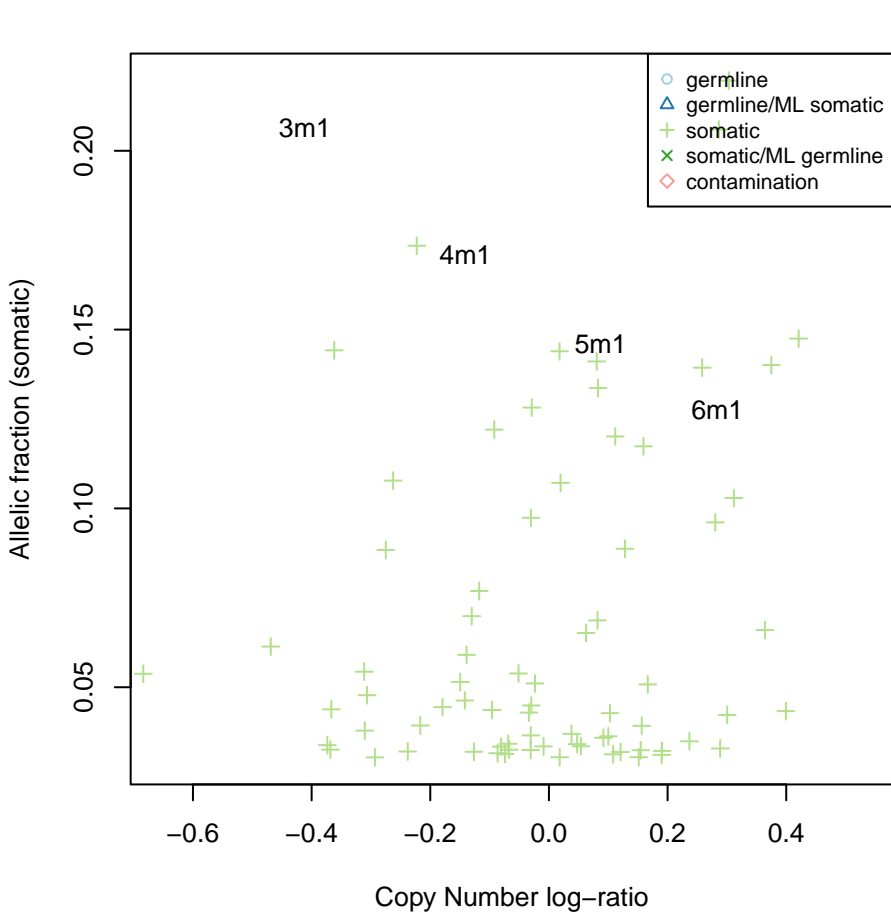
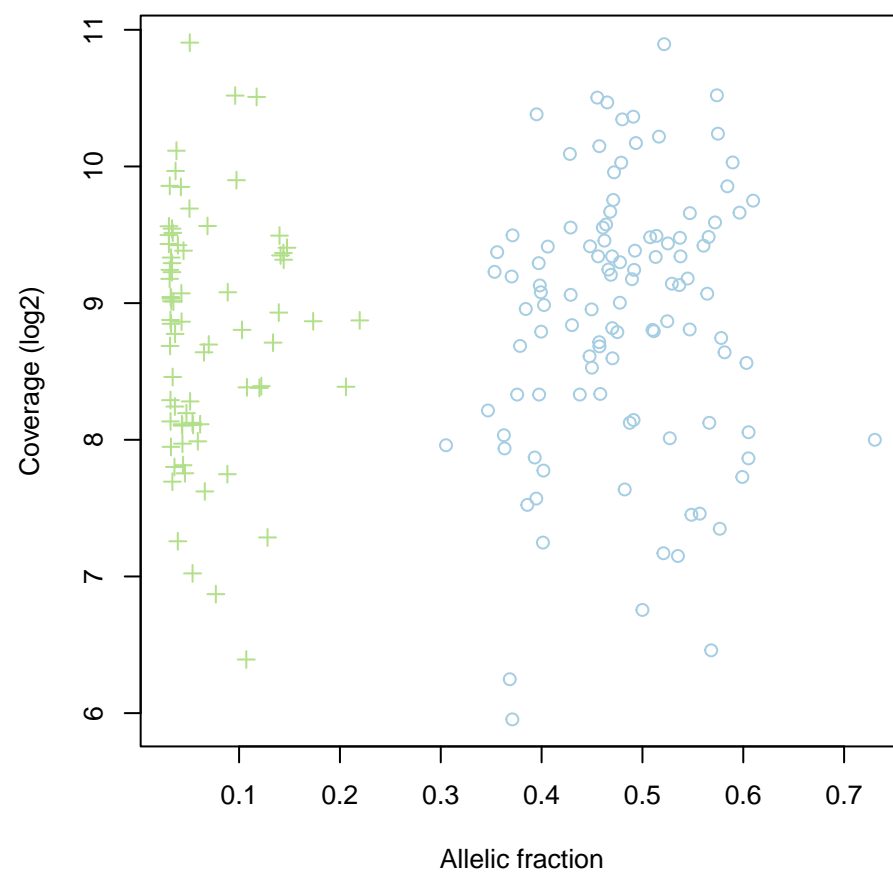
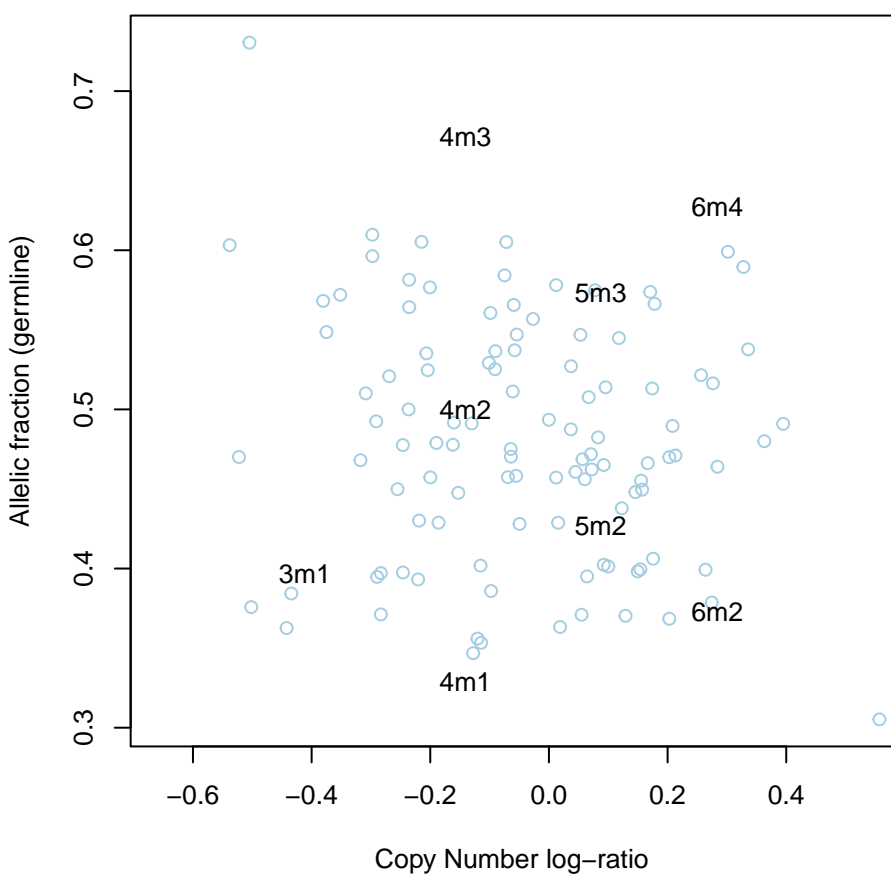


Purity: 0.52 Tumor ploidy: 4.599 SNV log-likelihood: -230.13 GoF: 83.4% Mean coverage: 466;556

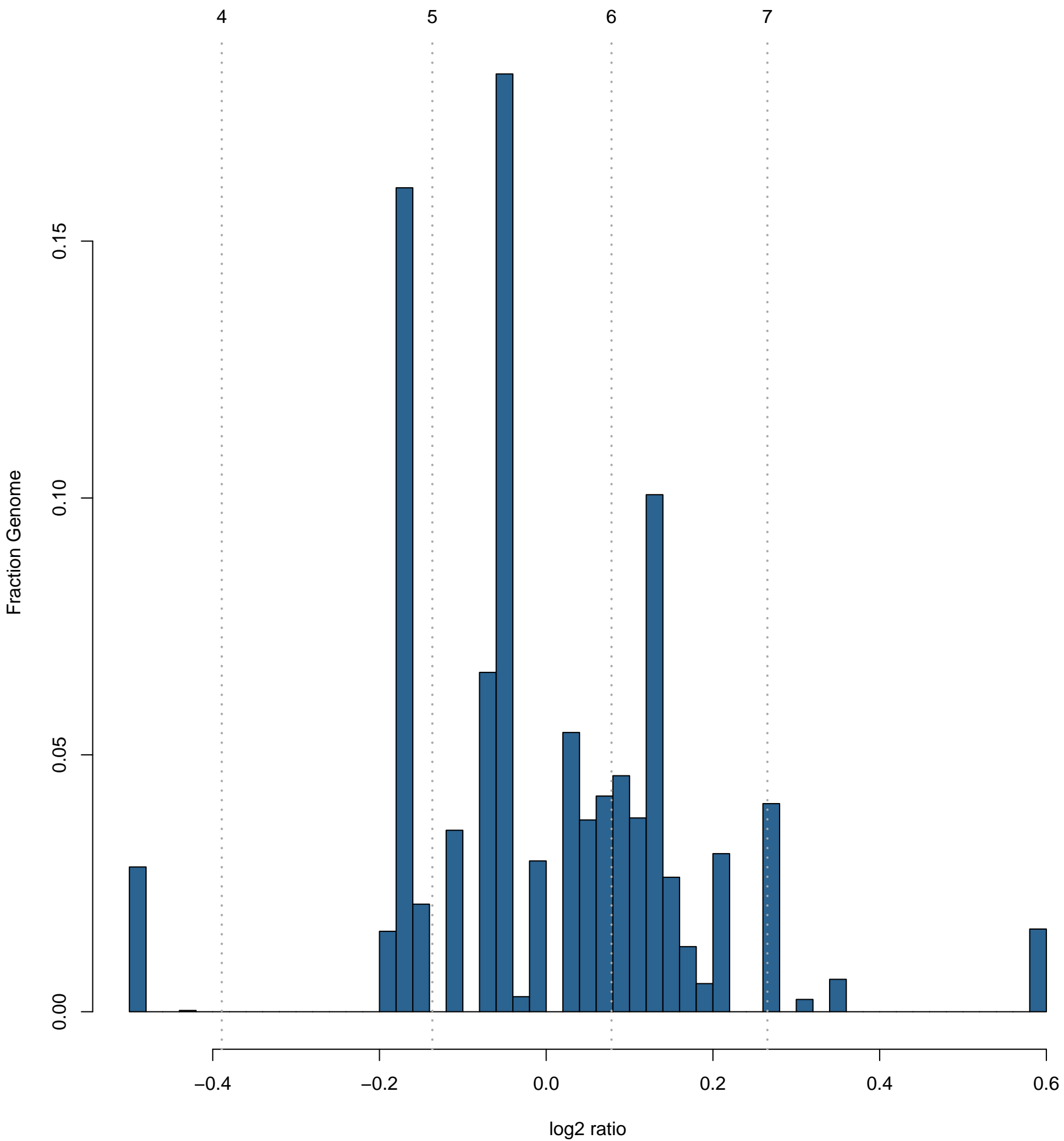


SCNA-fit log-likelihood: -5282.64

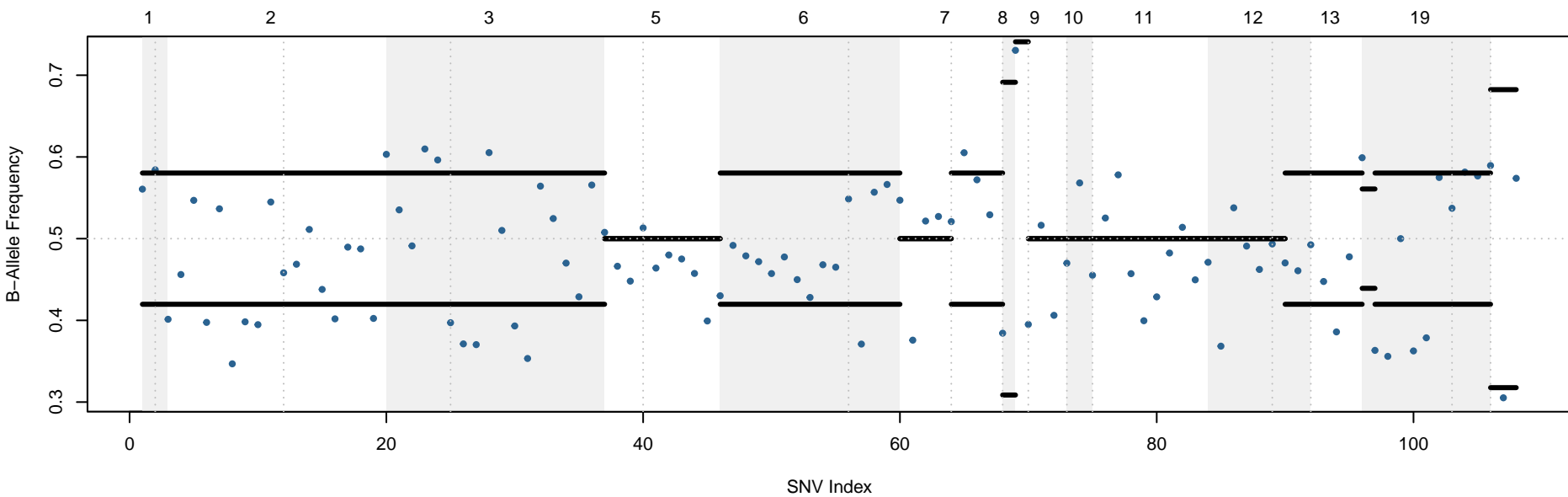




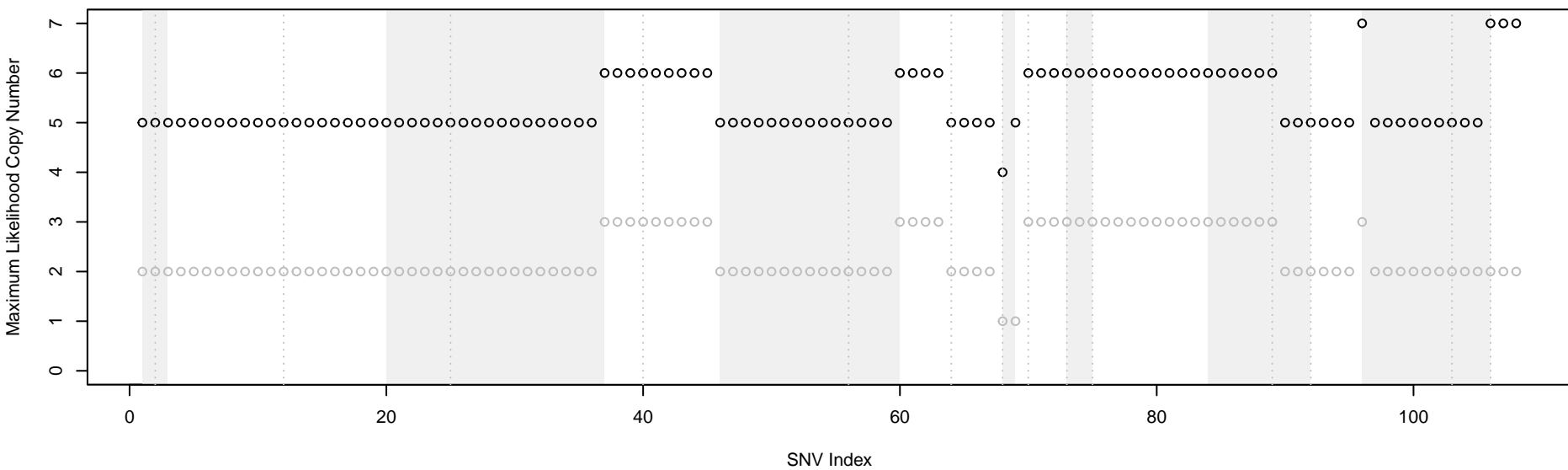
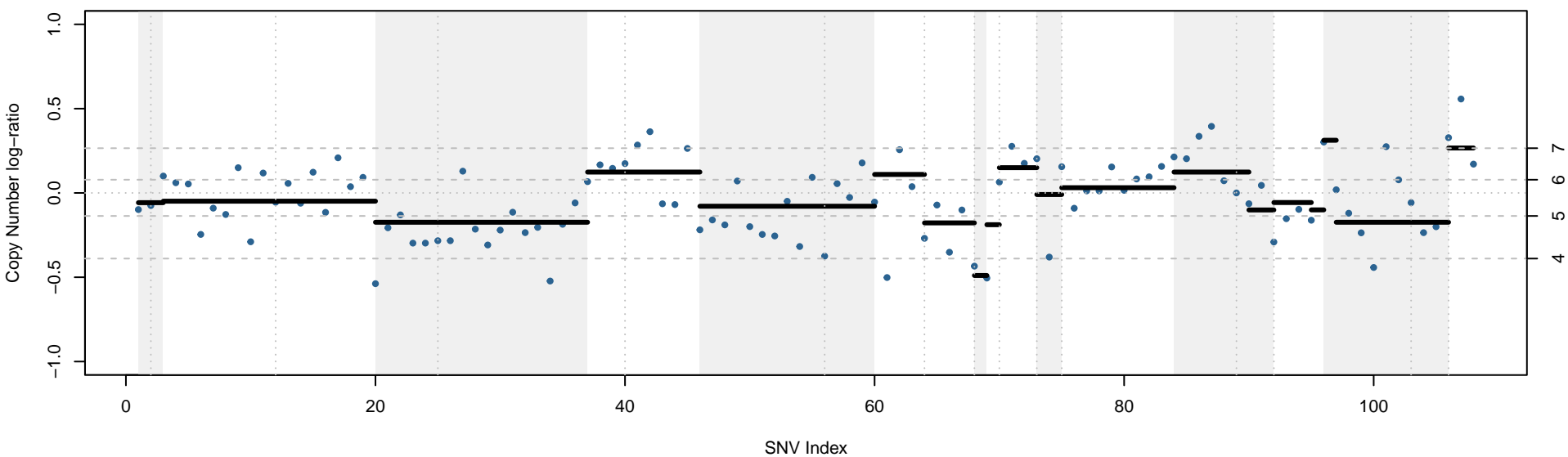
Purity: 0.62 Tumor ploidy: 5.618

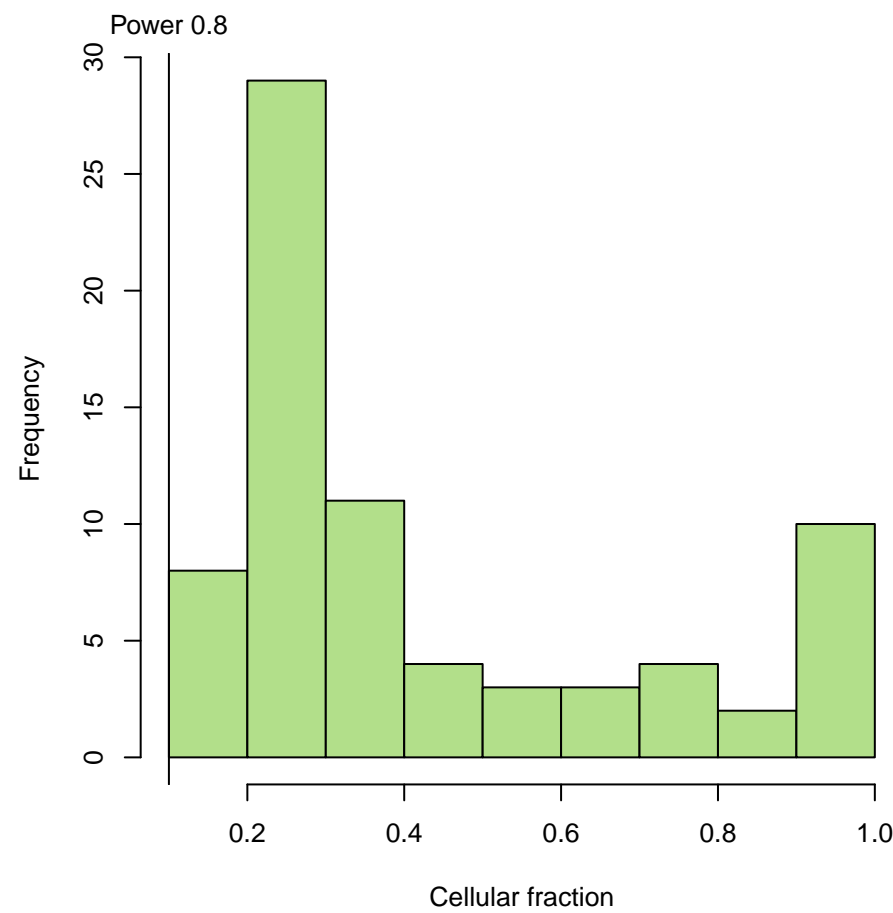
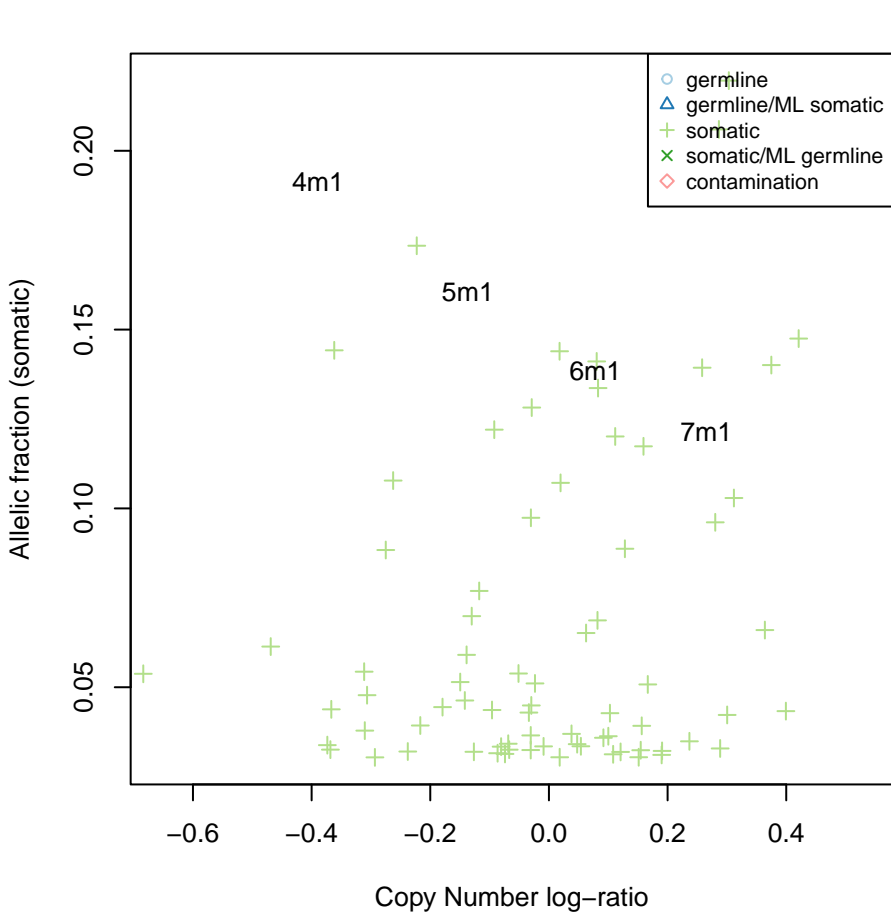
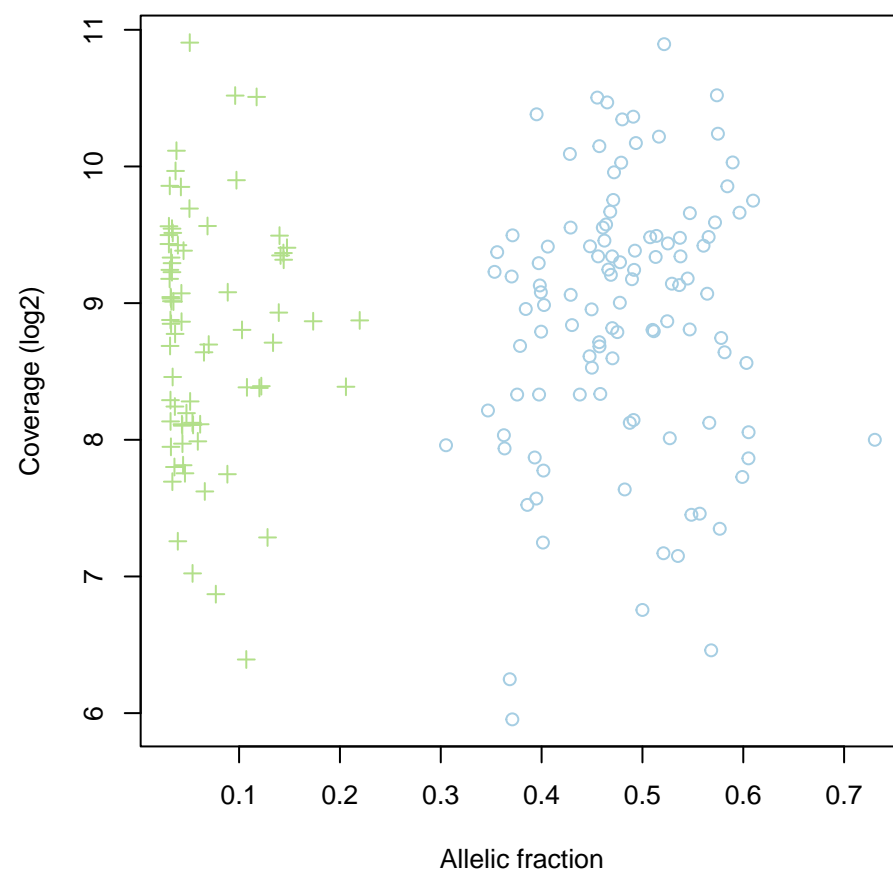
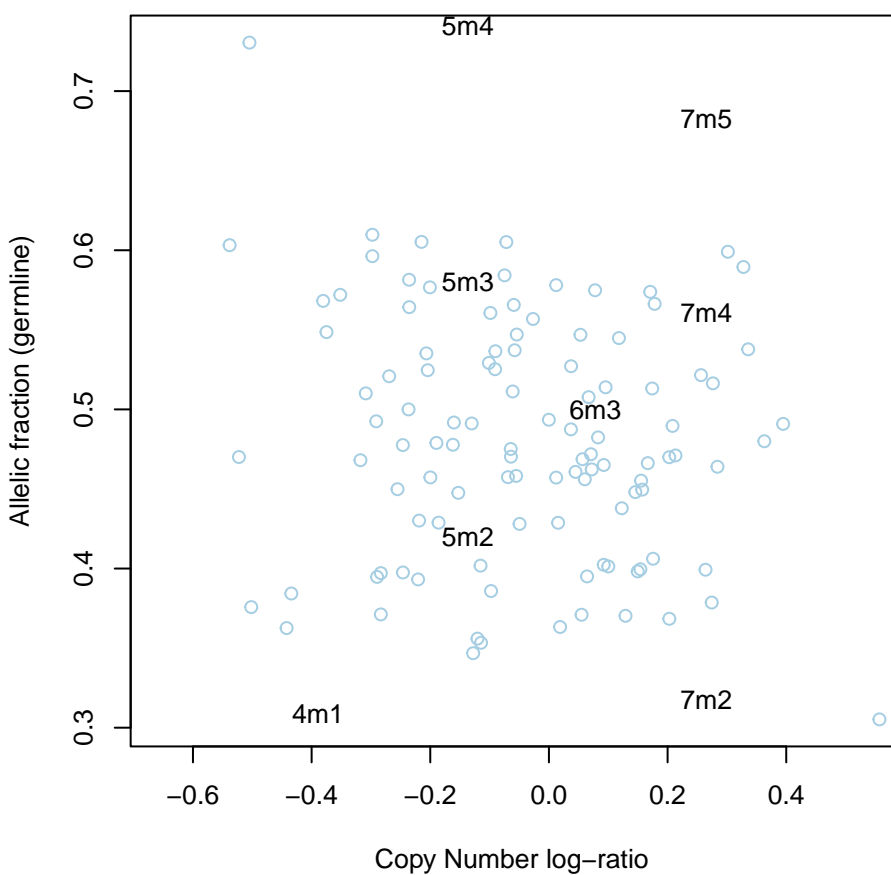


Purity: 0.62 Tumor ploidy: 5.618 SNV log-likelihood: -170.28 GoF: 87.1% Mean coverage: 466;556

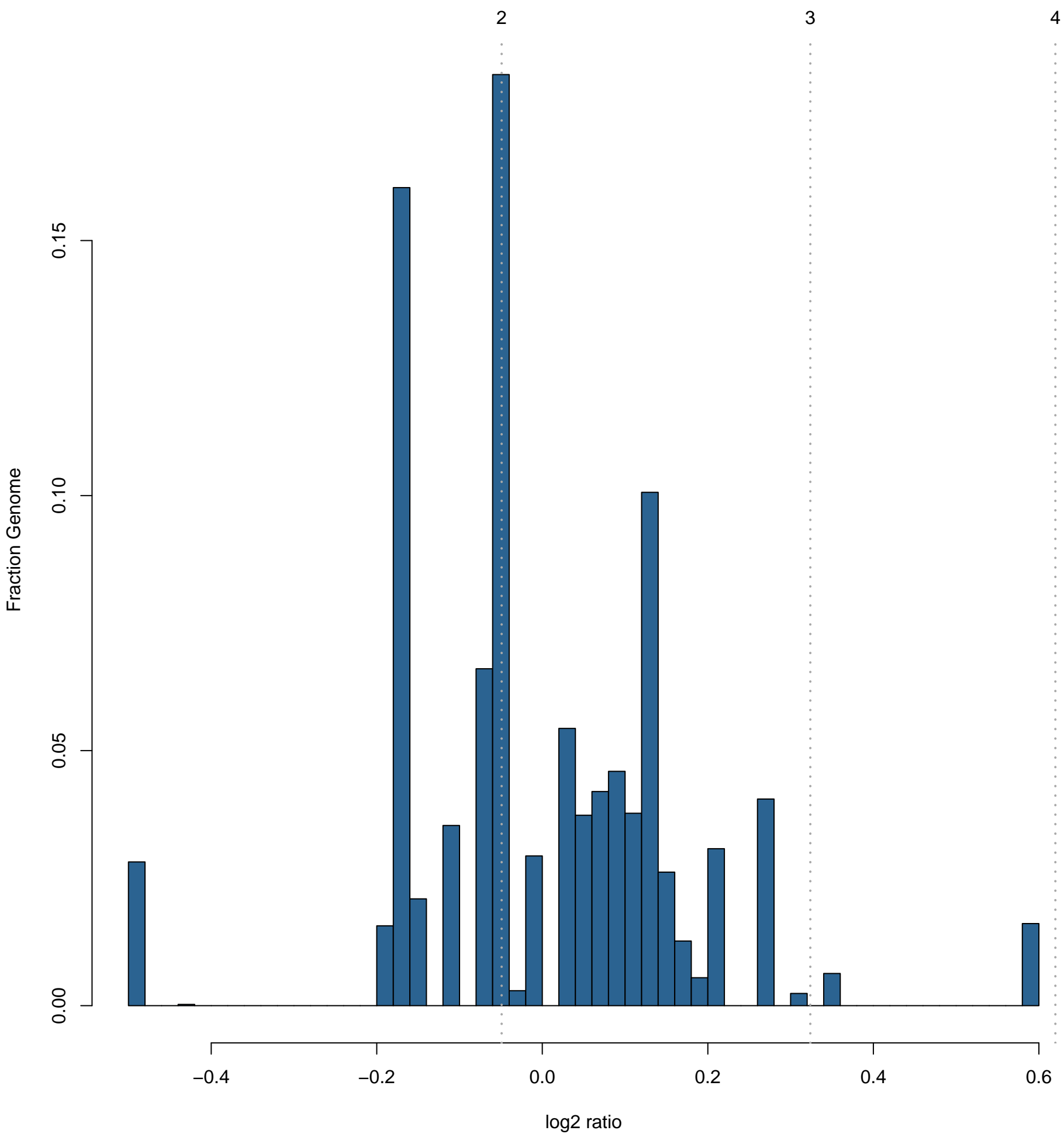


SCNA-fit log-likelihood: -5594.2

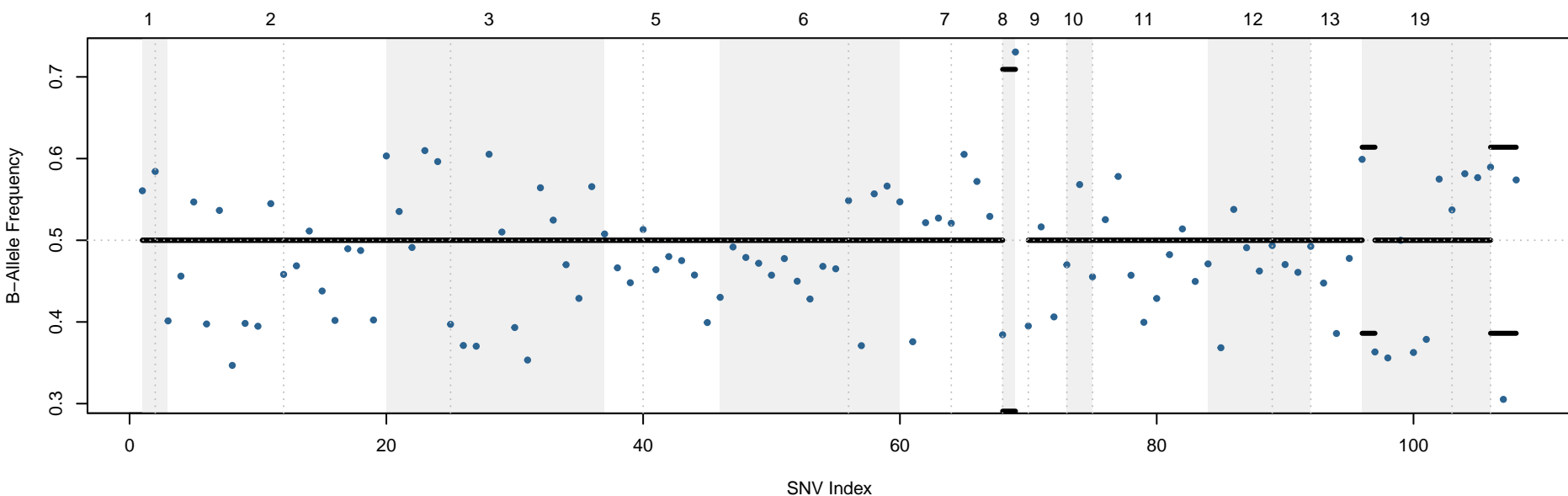




Purity: 0.59 Tumor ploidy: 2.117



Purity: 0.59 Tumor ploidy: 2.117 SNV log-likelihood: -382.43 GoF: 37.3% Mean coverage: 466;556



SCNA-fit log-likelihood: -6048.96

