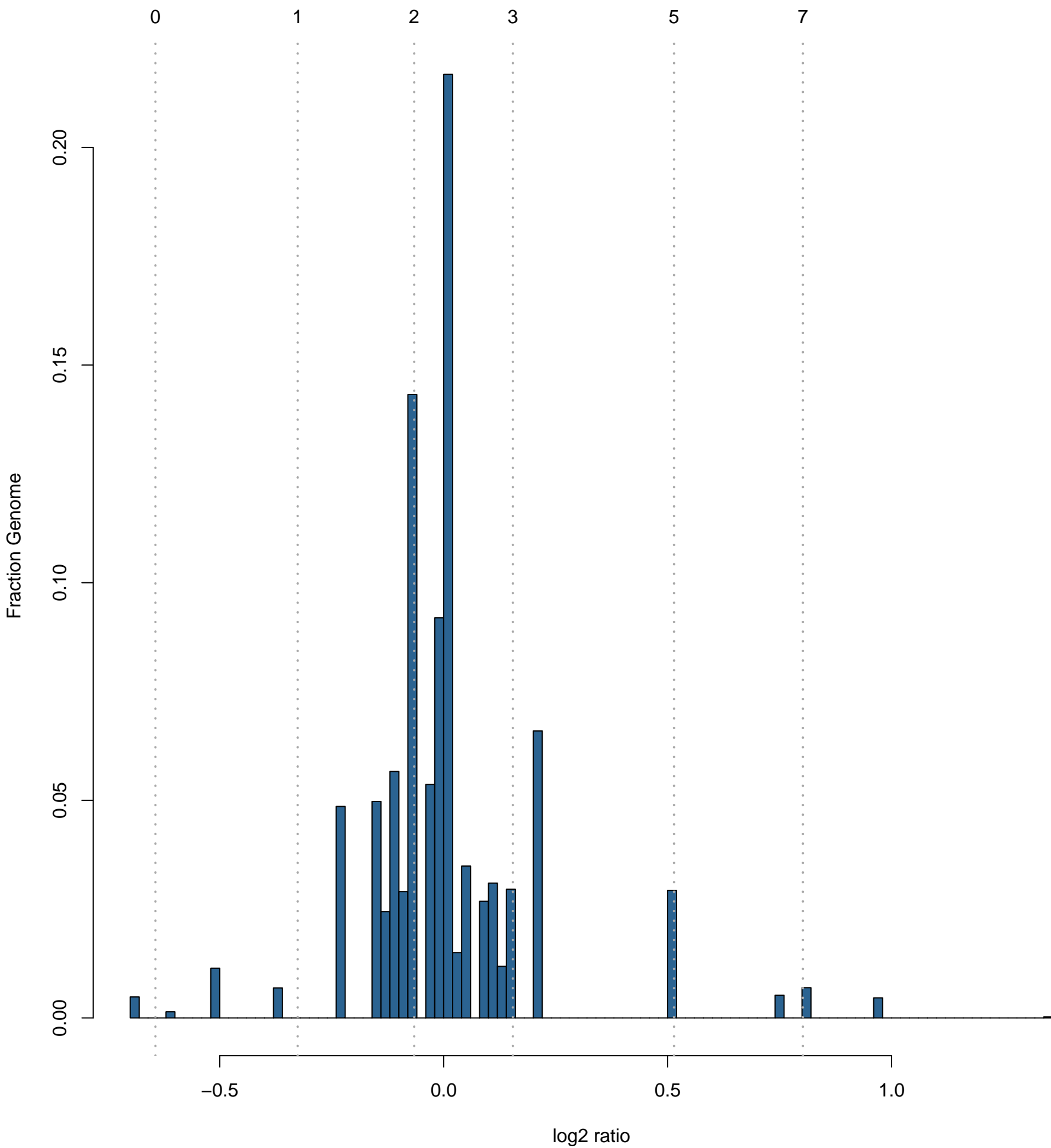
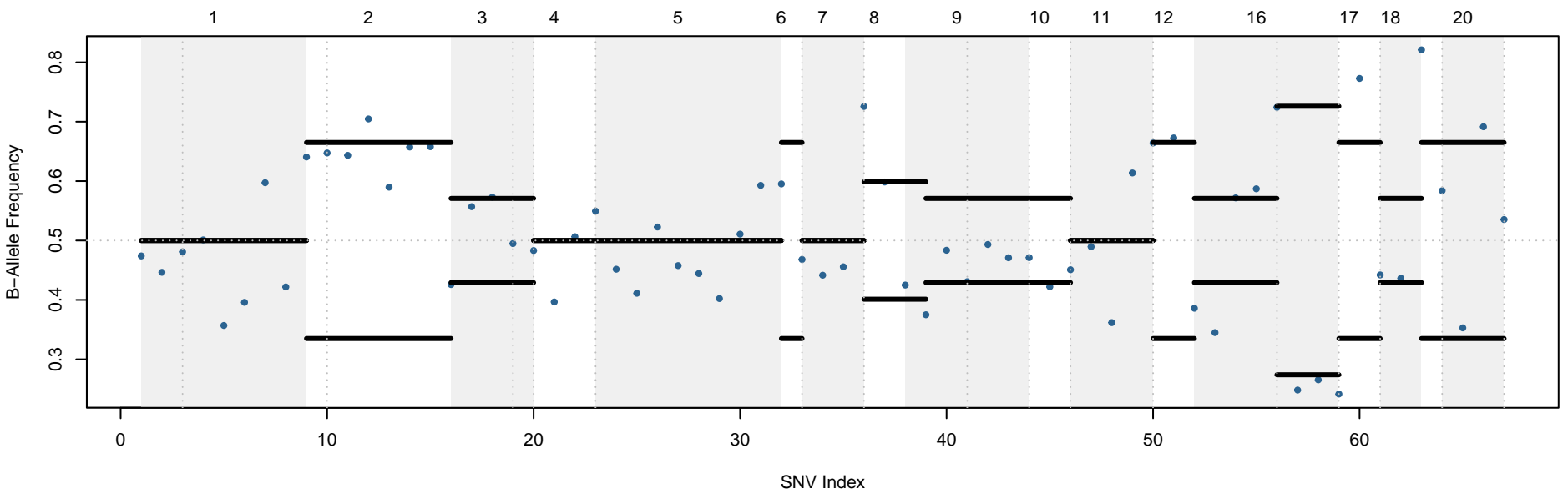


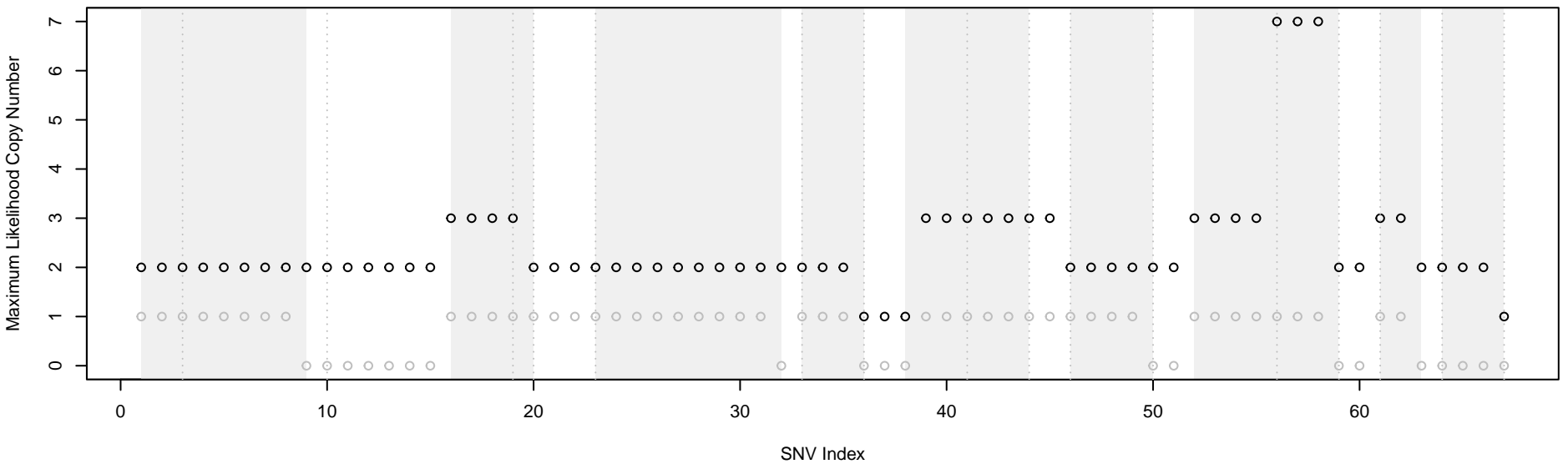
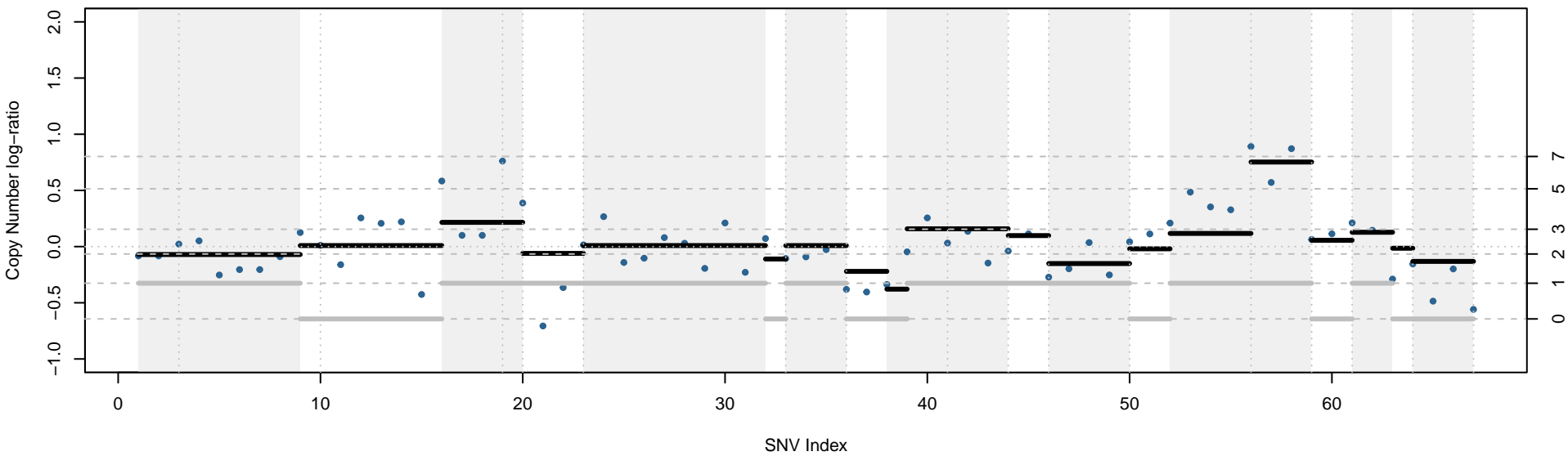
Purity: 0.33 Tumor ploidy: 2.283

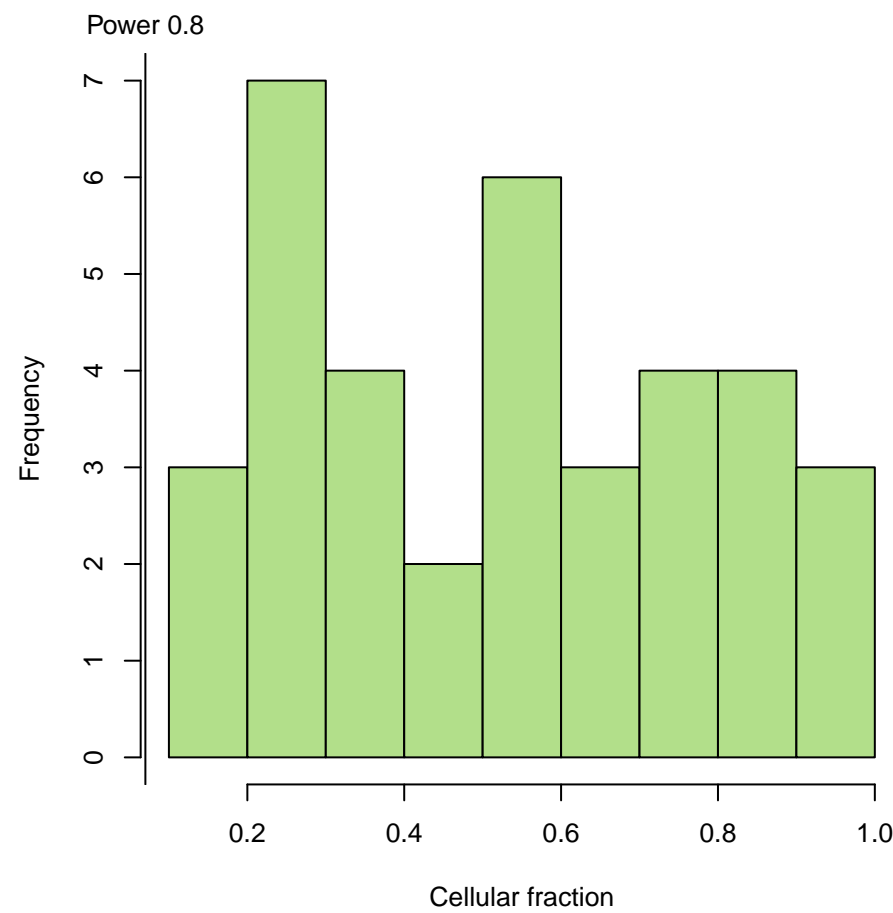
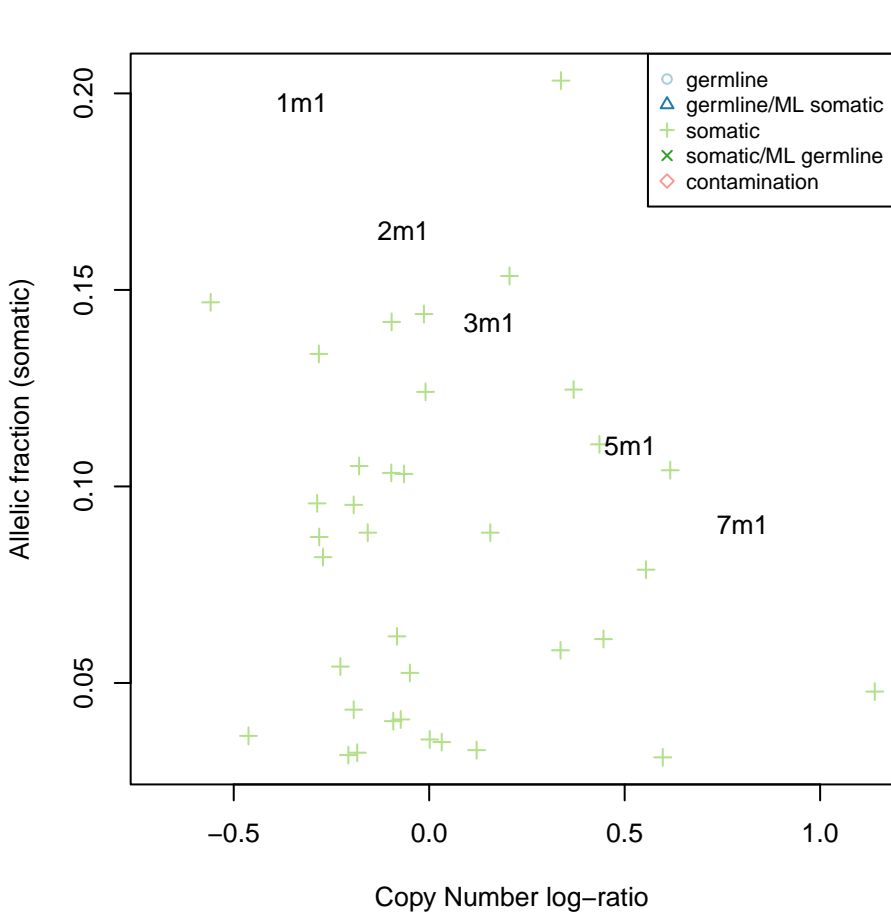
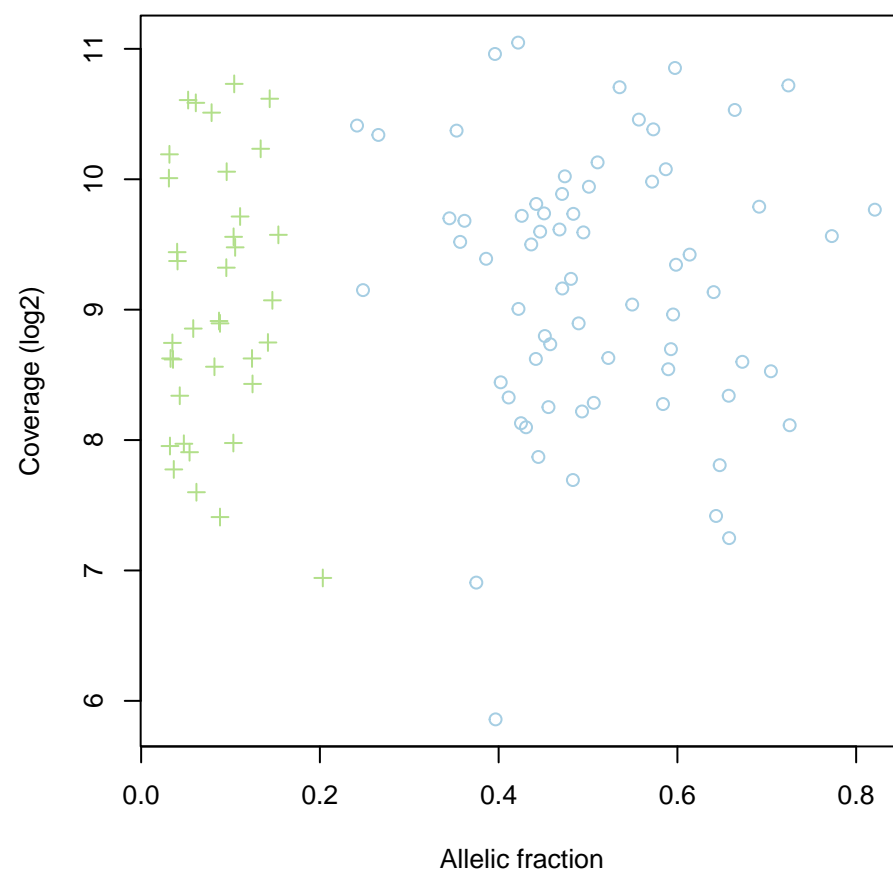
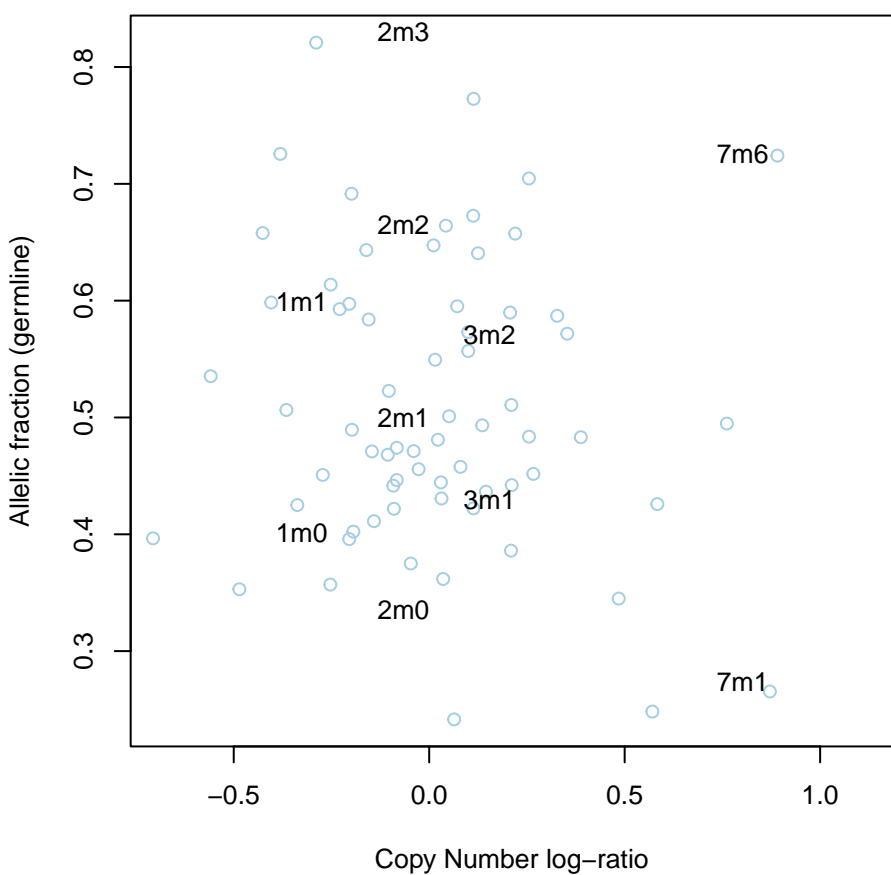


Purity: 0.33 Tumor ploidy: 2.283 SNV log-likelihood: -92.82 GoF: 88.7% Mean coverage: 385;708

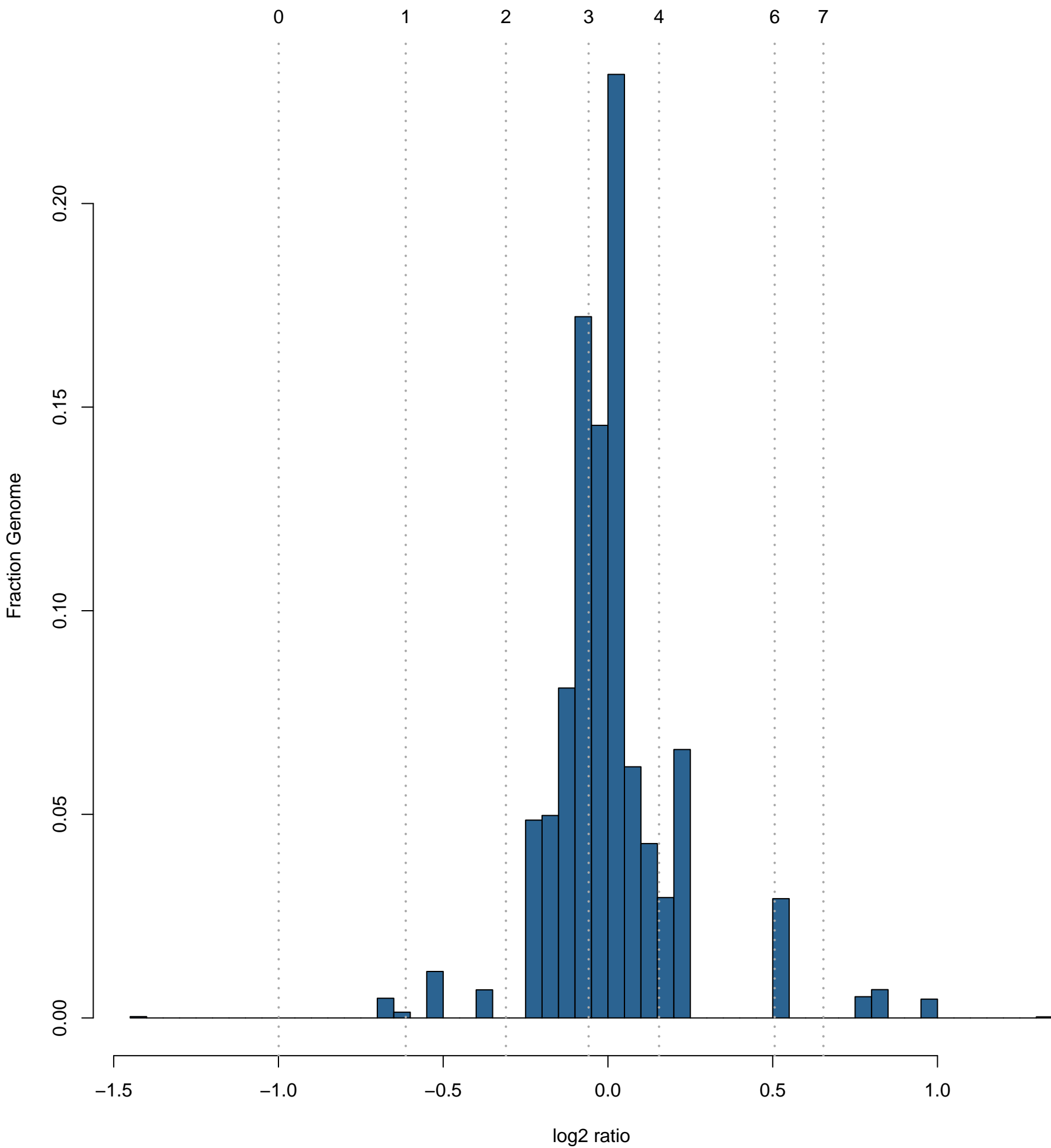


SCNA-fit log-likelihood: -16516.01

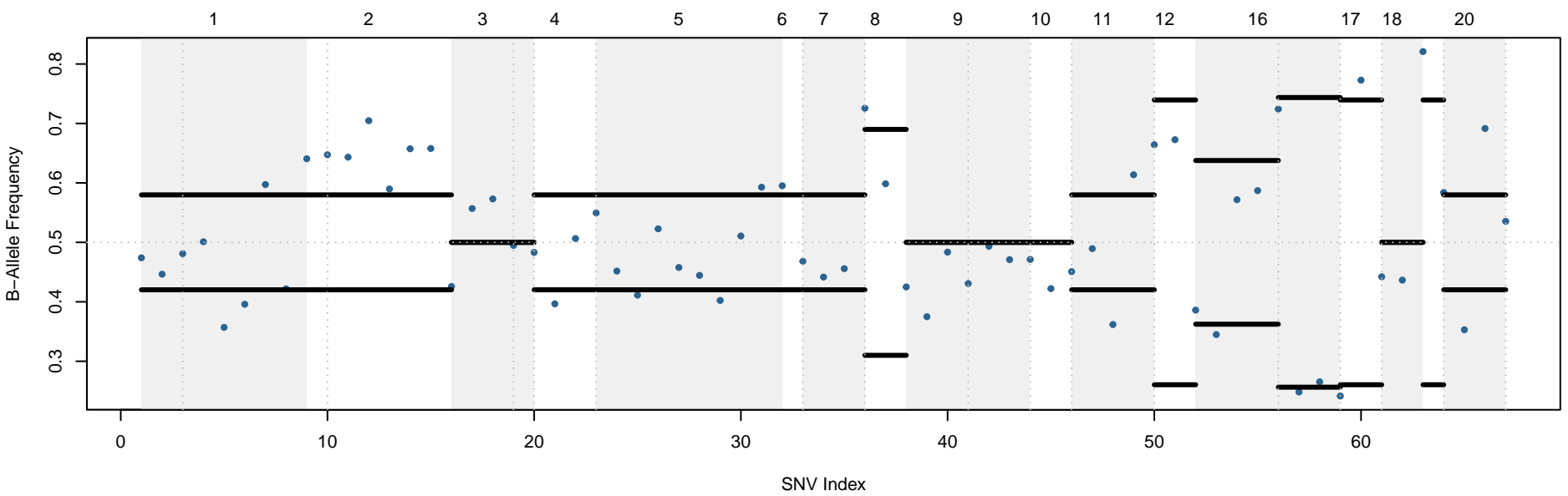




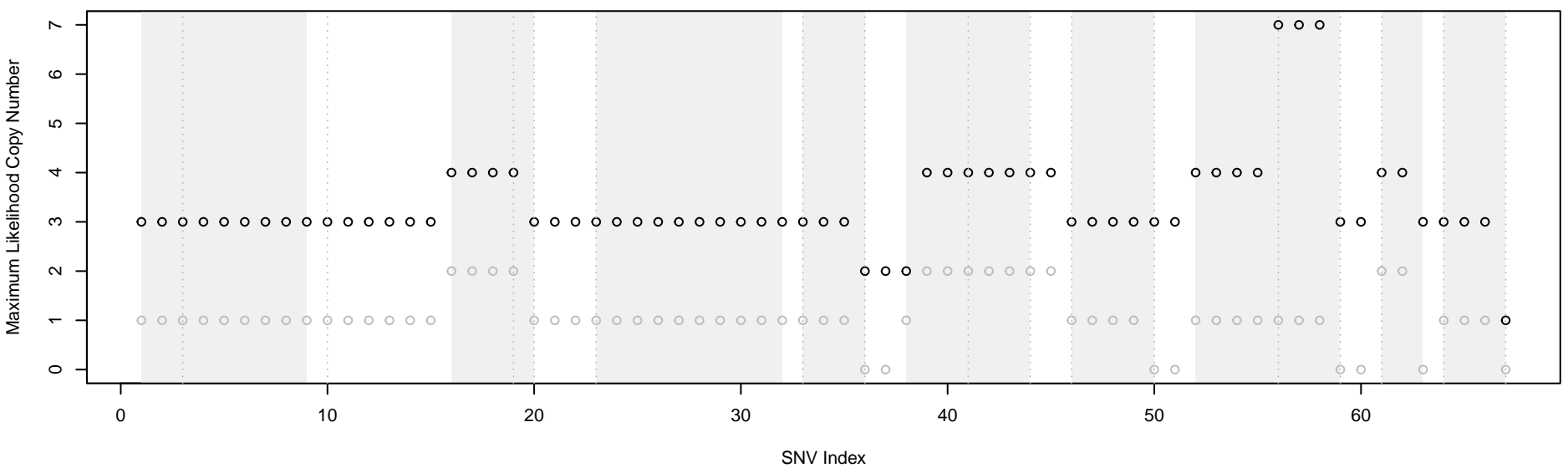
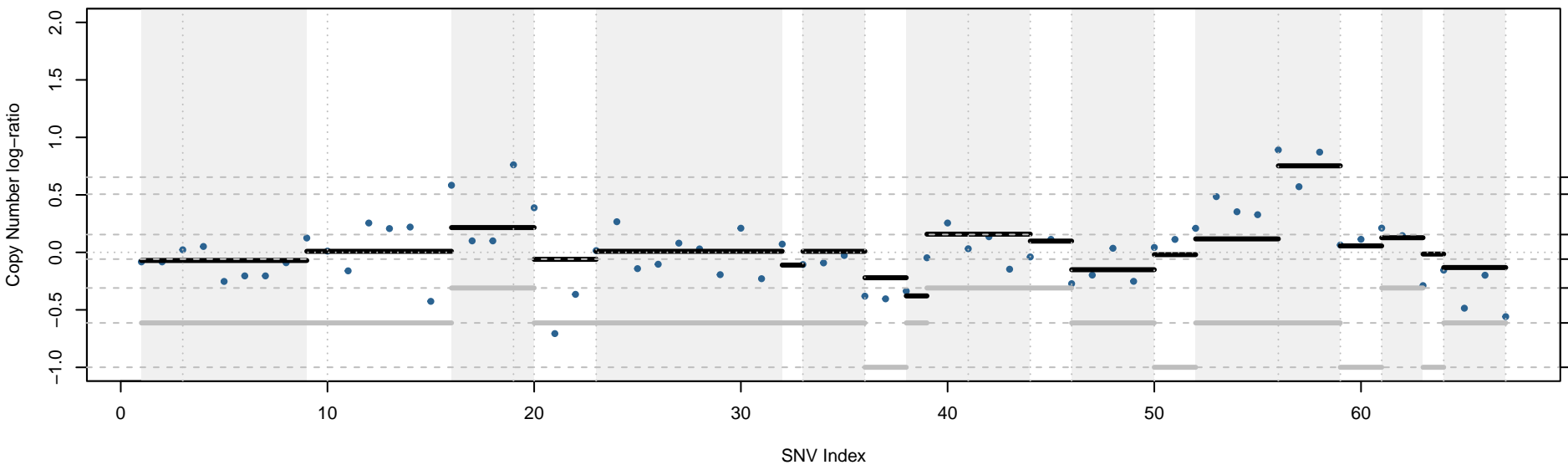
Purity: 0.38 Tumor ploidy: 3.26

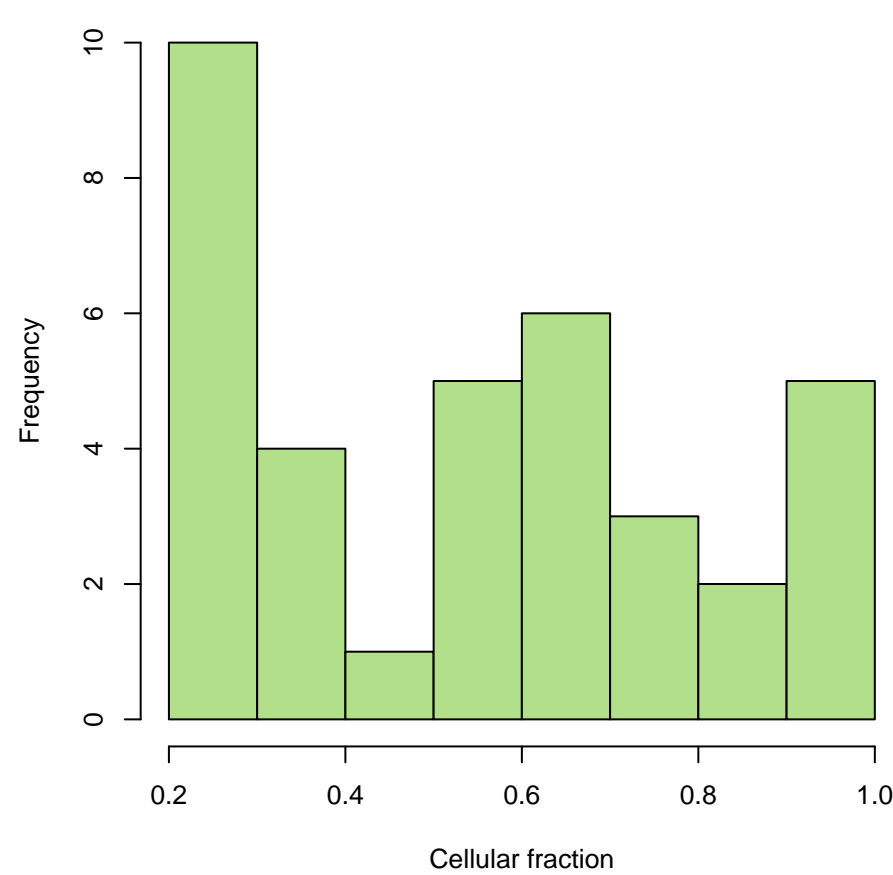
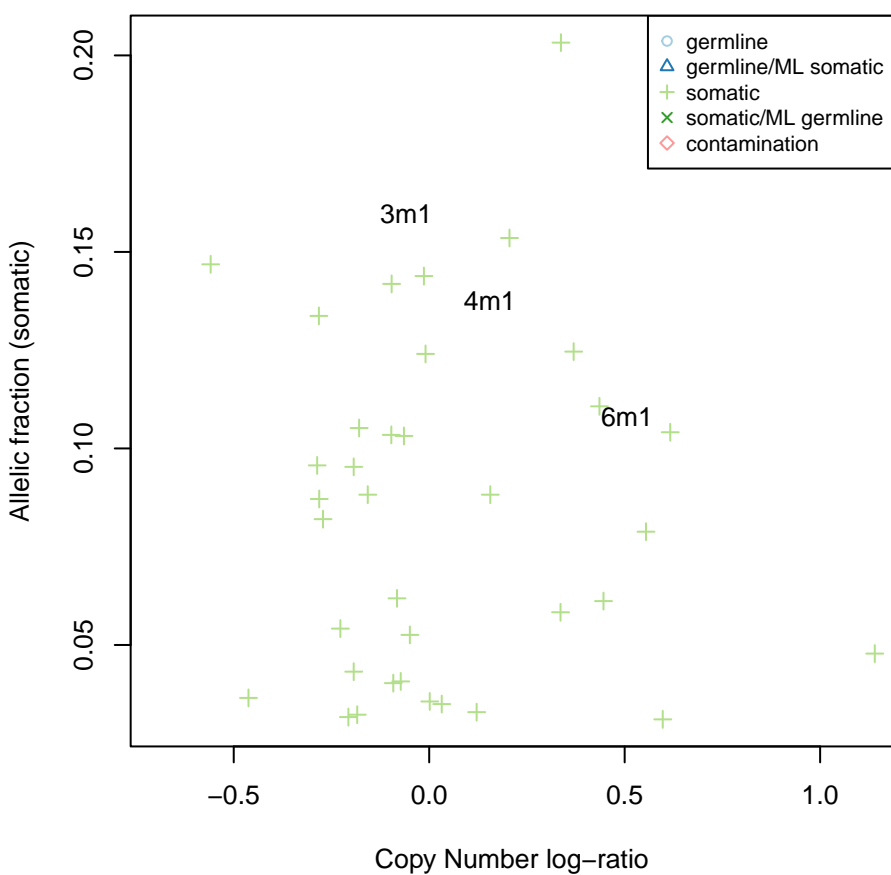
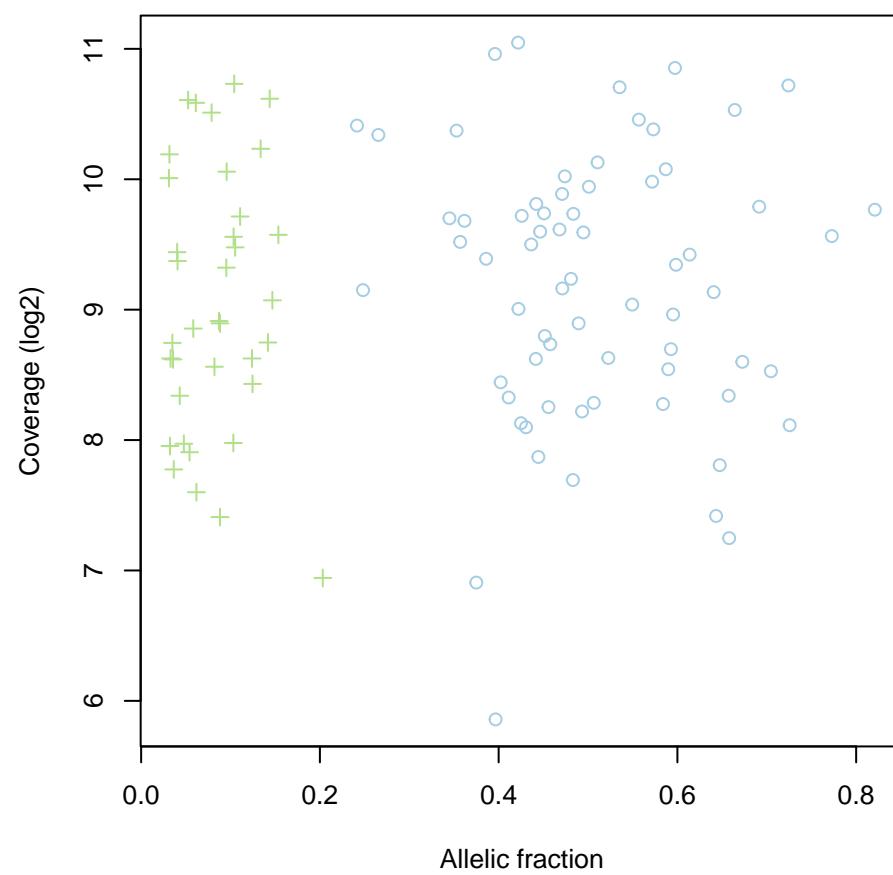
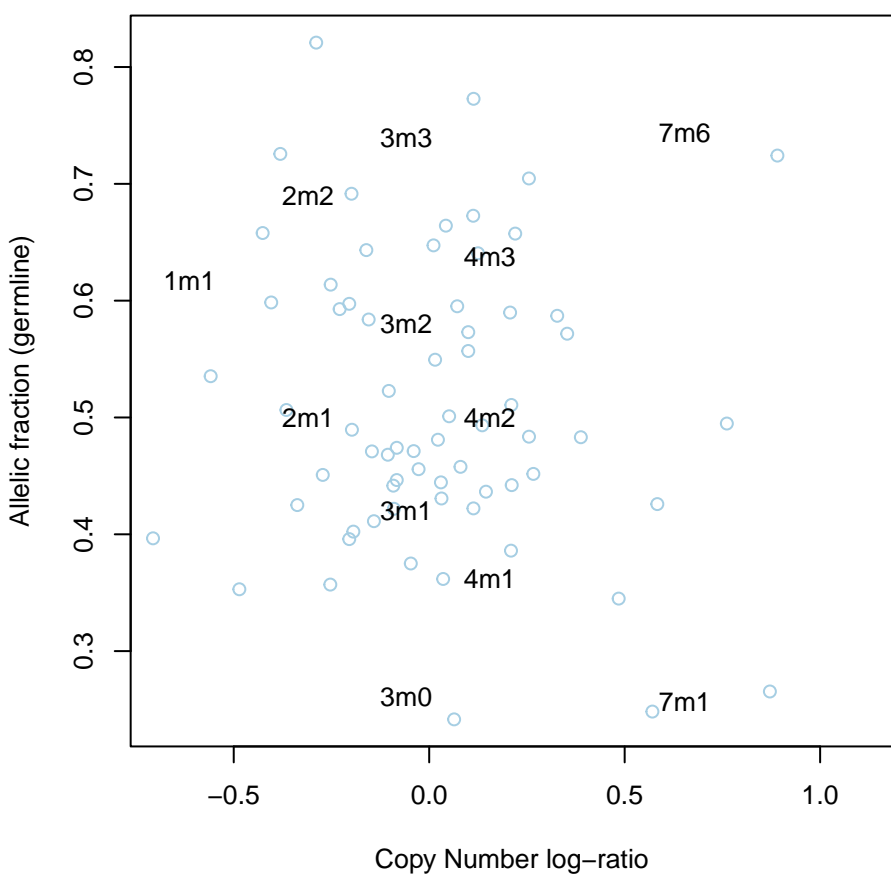


Purity: 0.38 Tumor ploidy: 3.26 SNV log-likelihood: -108.91 GoF: 89.7% Mean coverage: 385;708

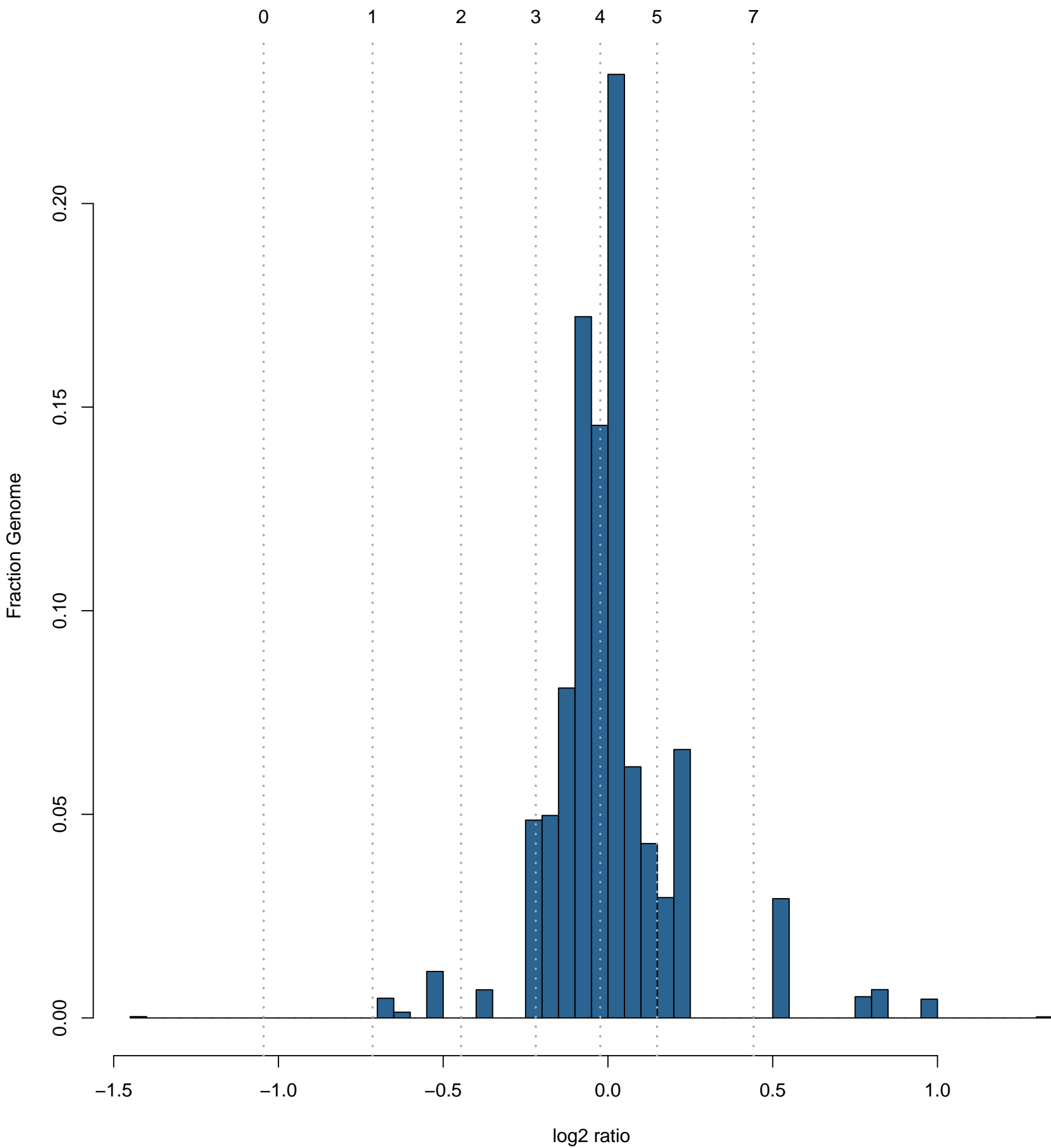


SCNA-fit log-likelihood: -16512.82

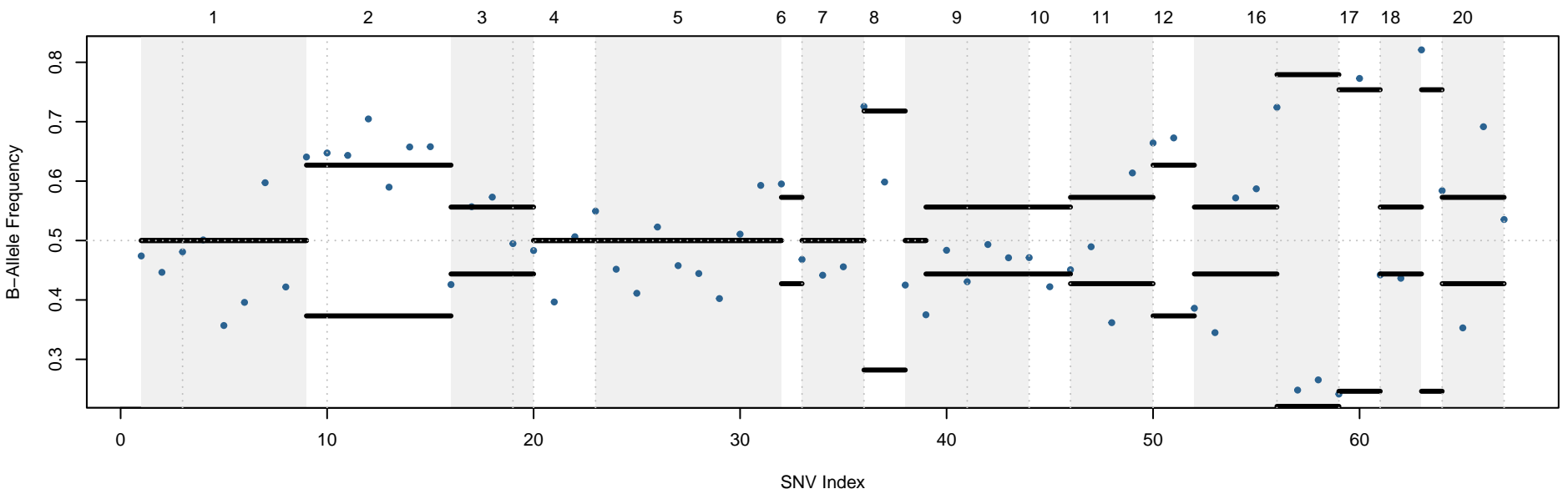




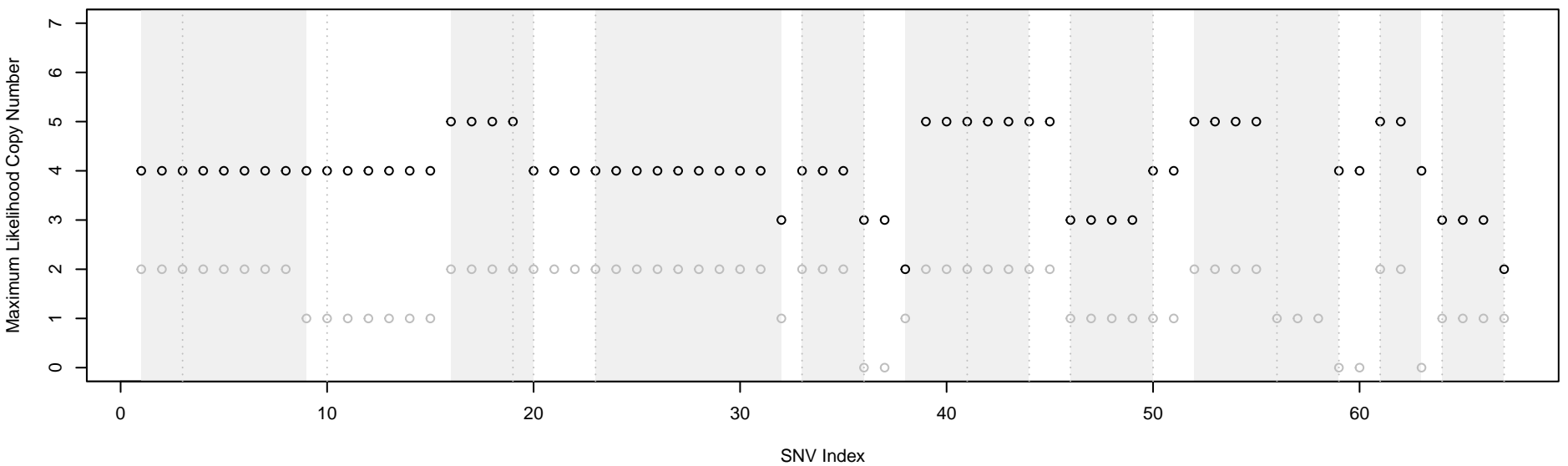
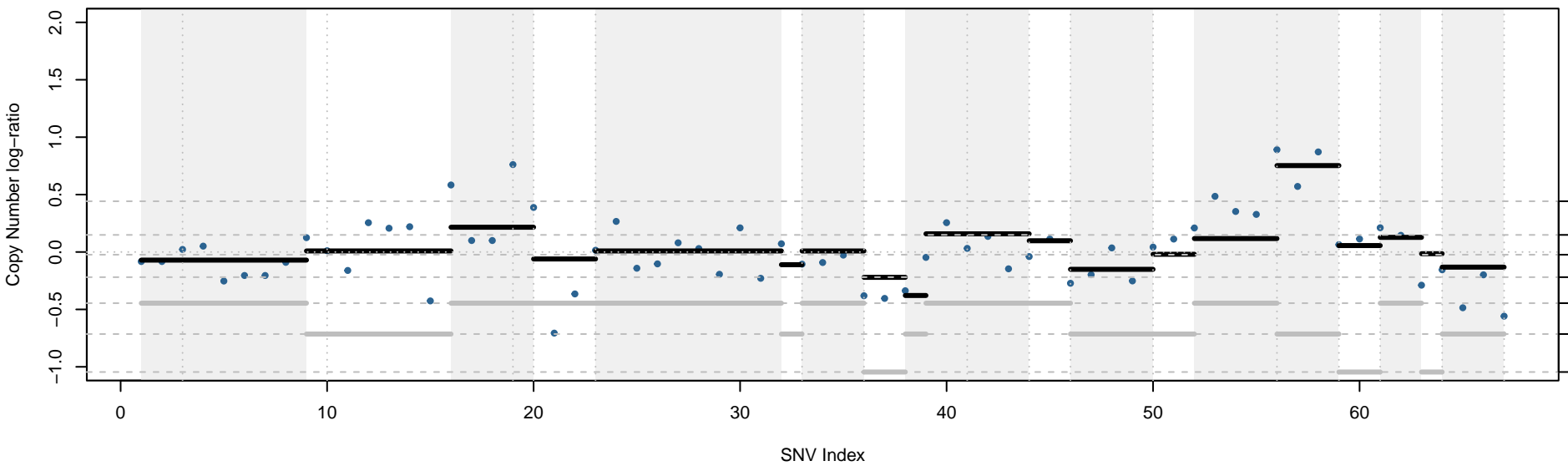
Purity: 0.34 Tumor ploidy: 4.129



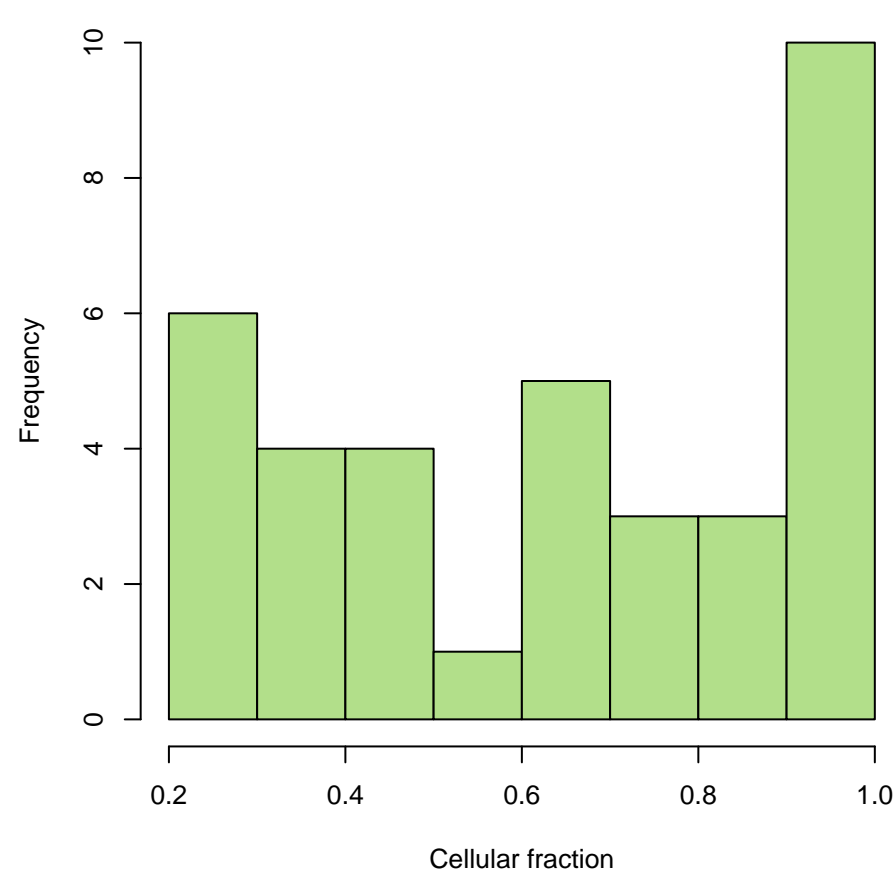
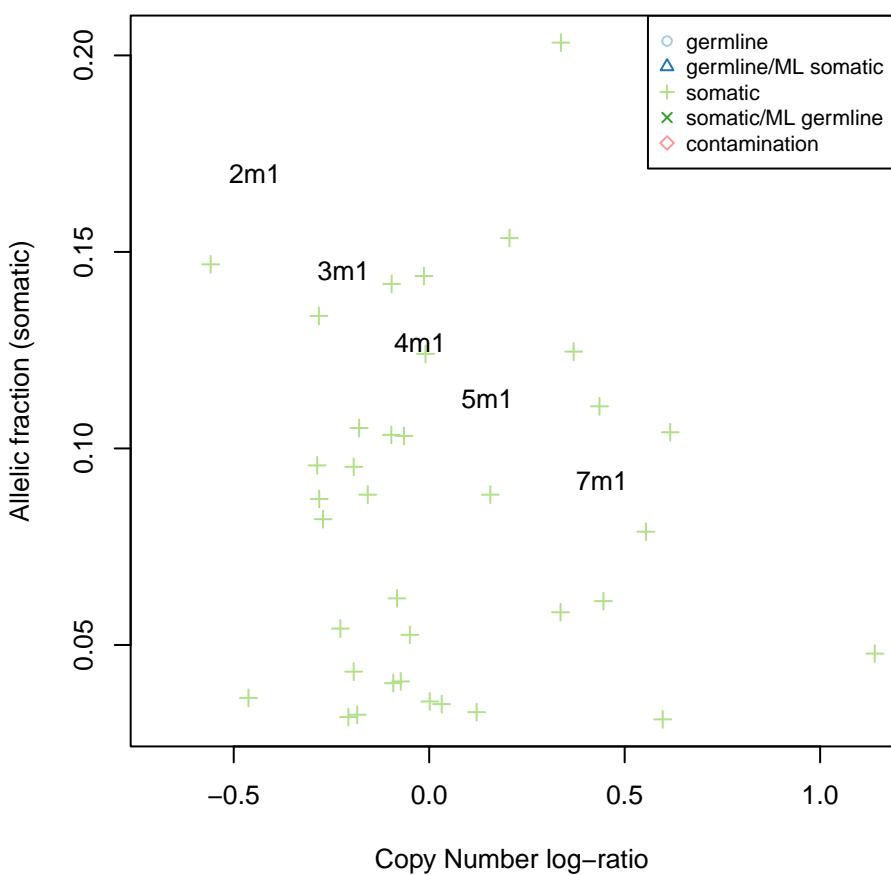
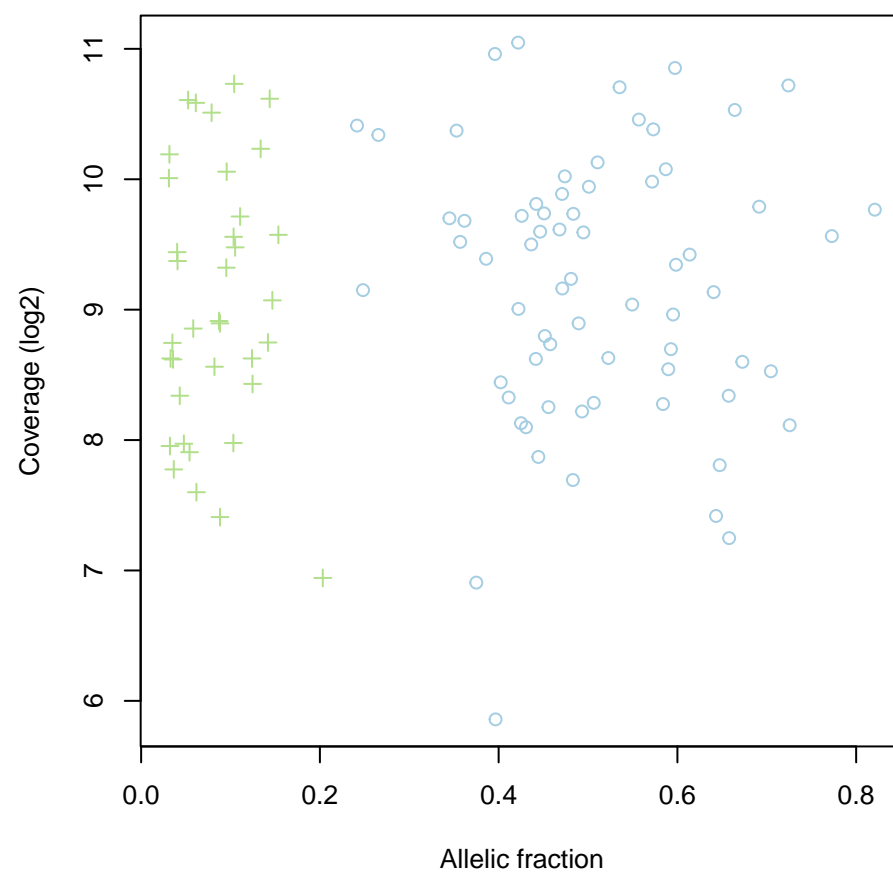
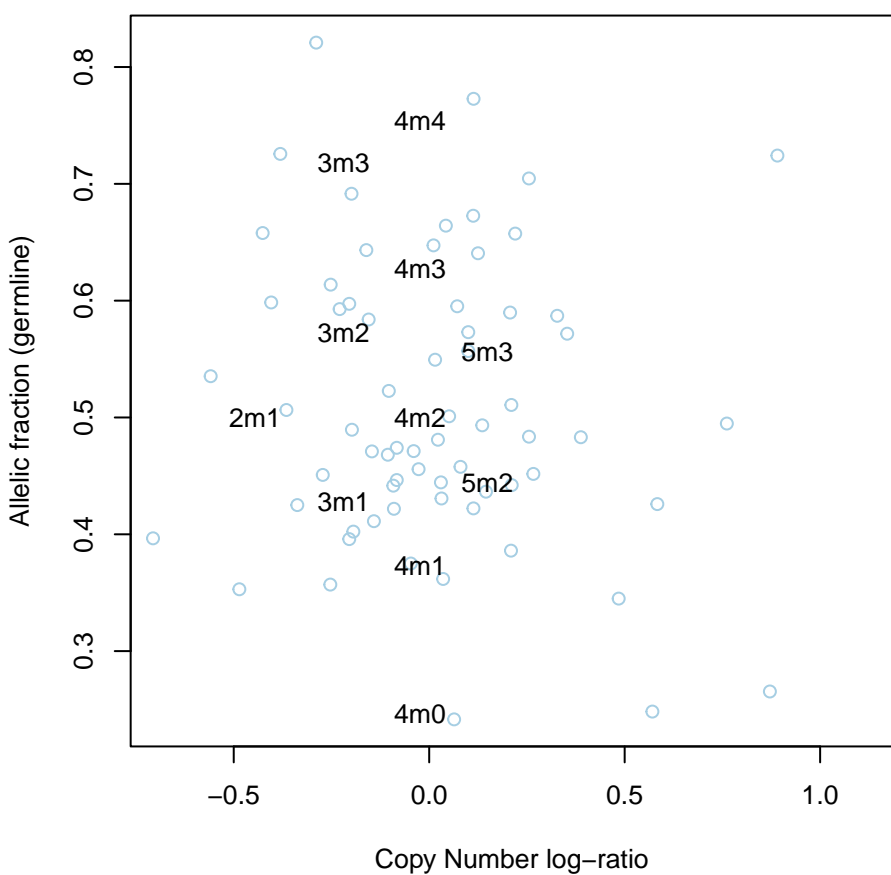
Purity: 0.34 Tumor ploidy: 4.129 SNV log-likelihood: -88.87 GoF: 92.8% Mean coverage: 385;708



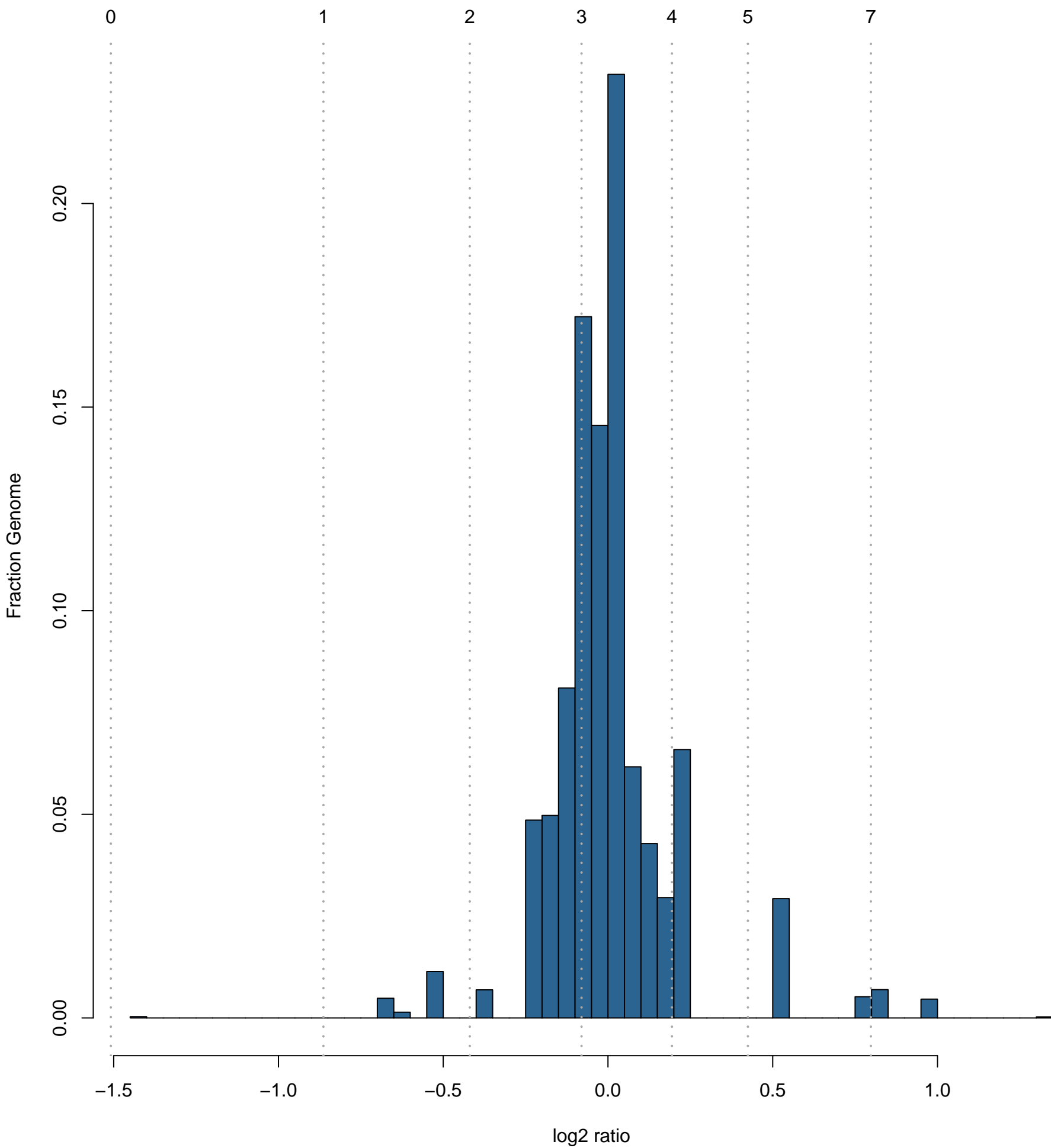
SCNA-fit log-likelihood: -16612.67



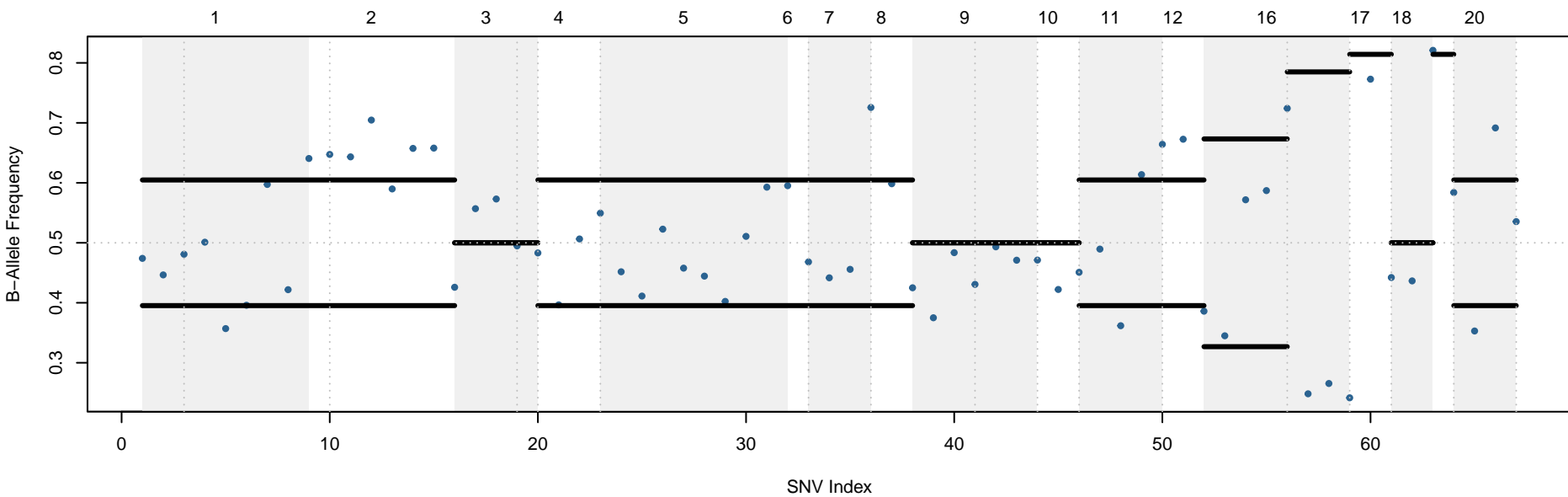




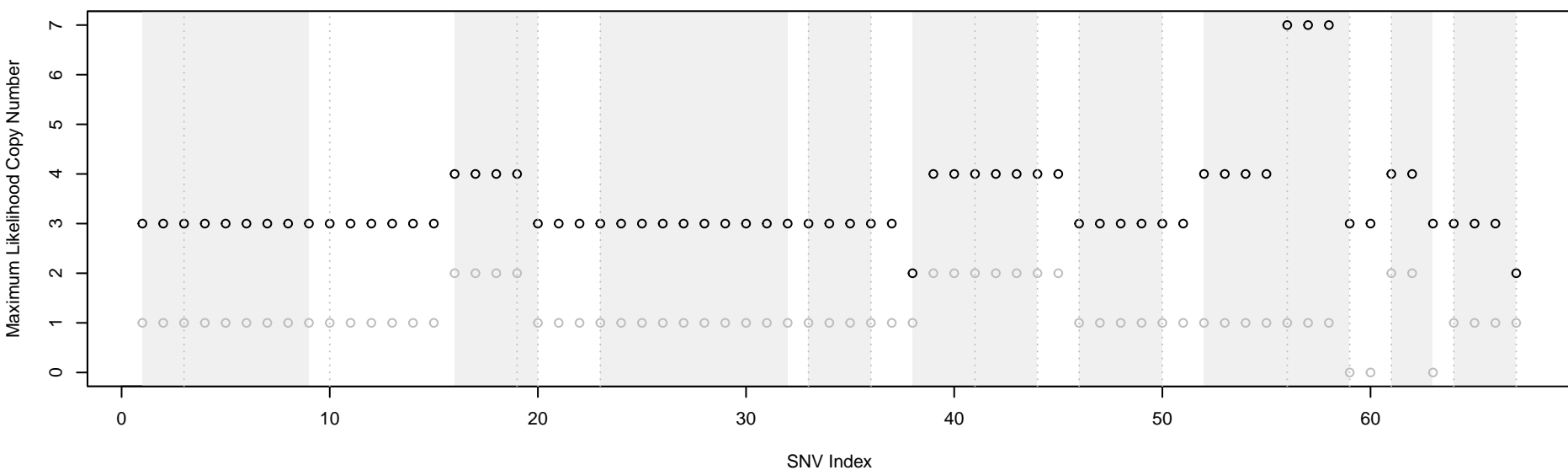
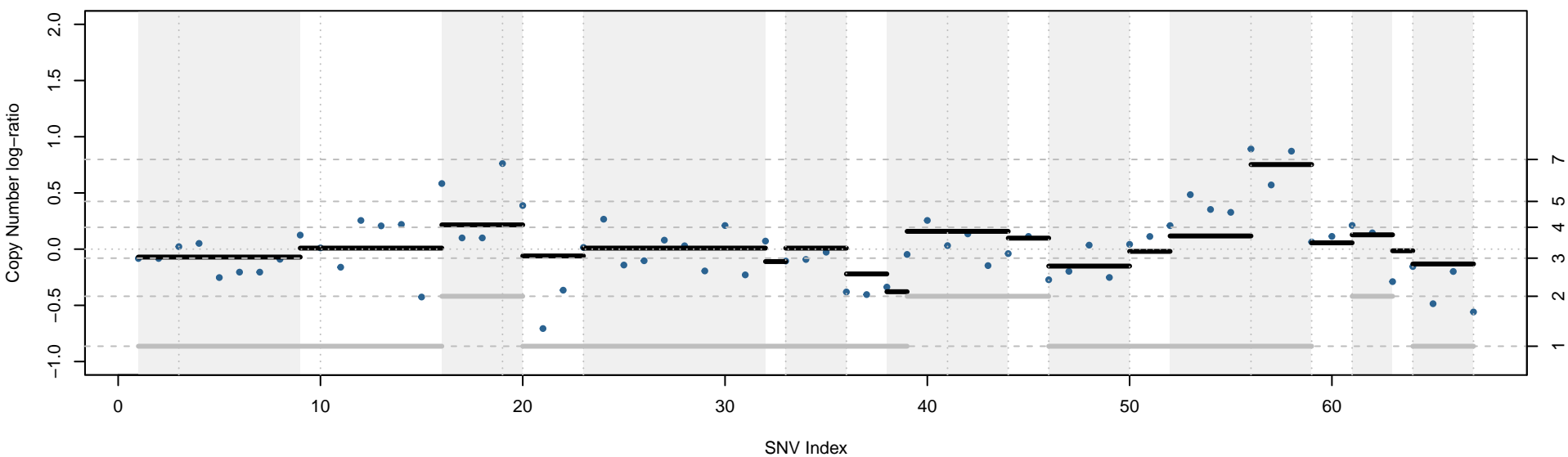
Purity: 0.53 Tumor ploidy: 3.273

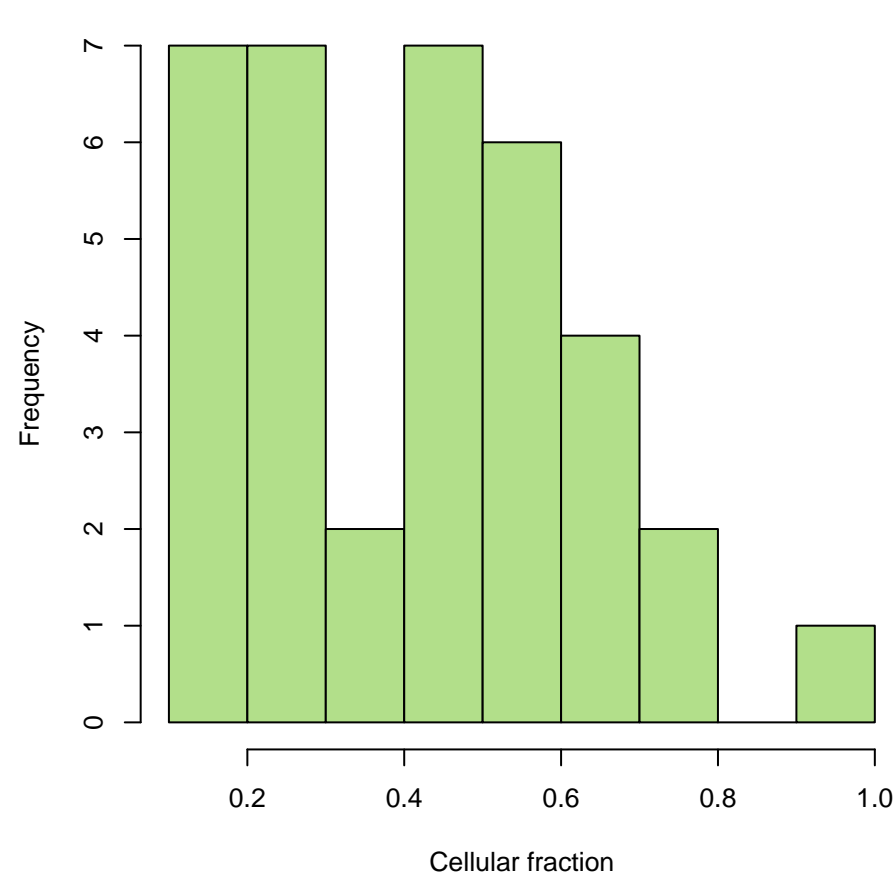
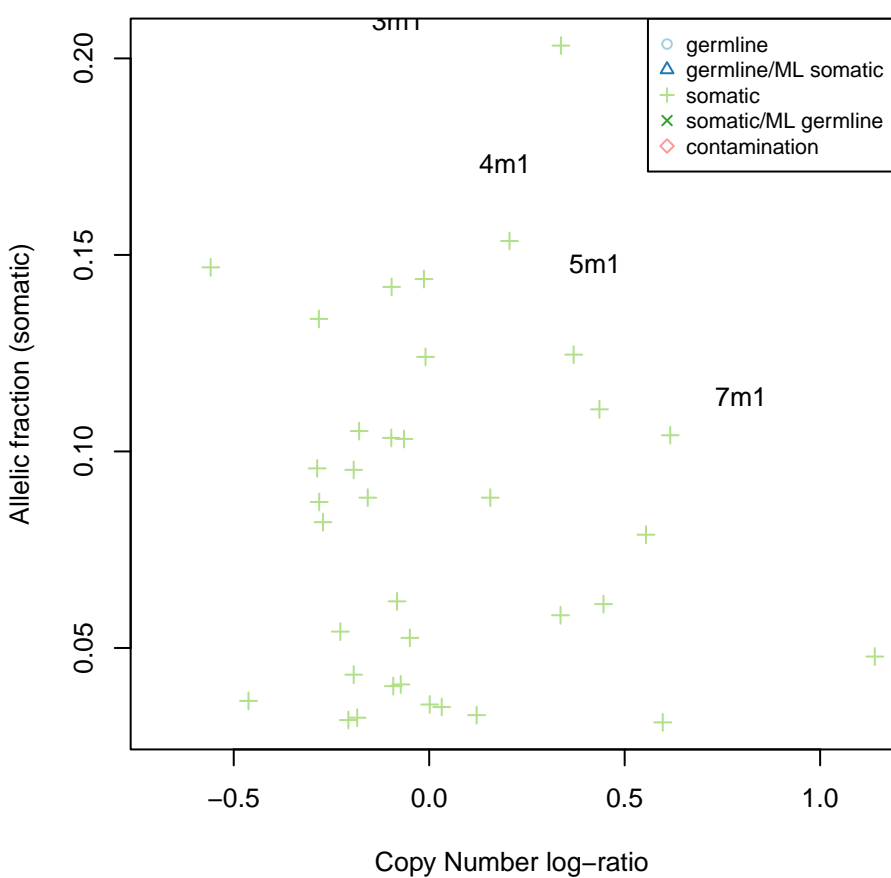
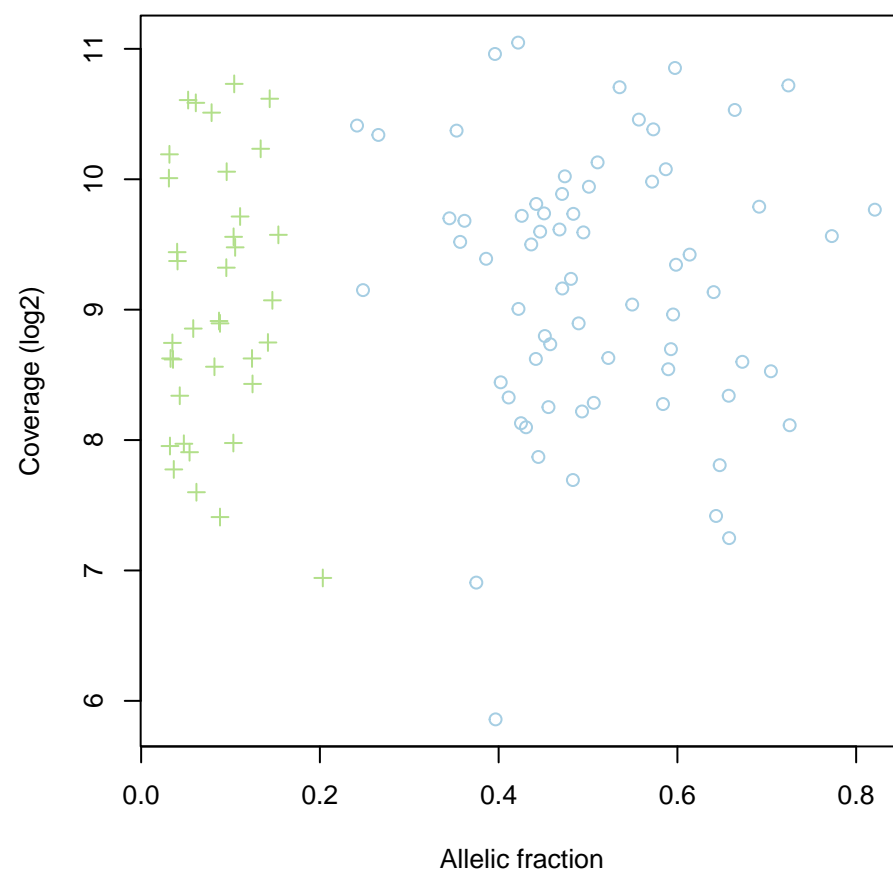
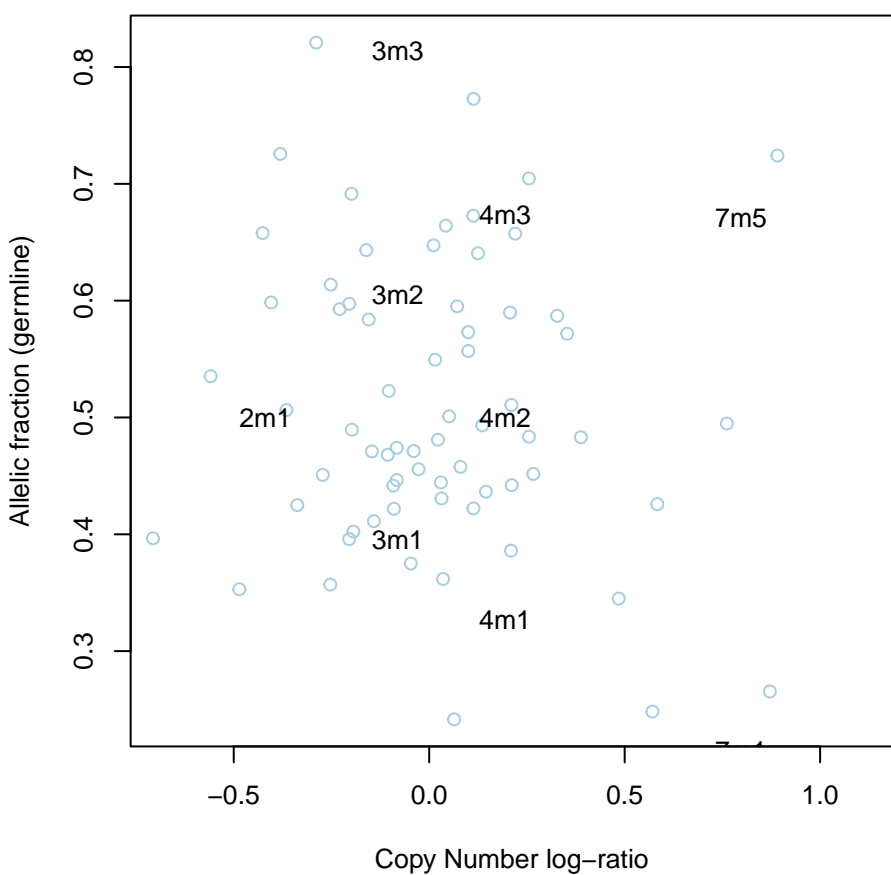


Purity: 0.53 Tumor ploidy: 3.273 SNV log-likelihood: -154.55 GoF: 80.5% Mean coverage: 385,708

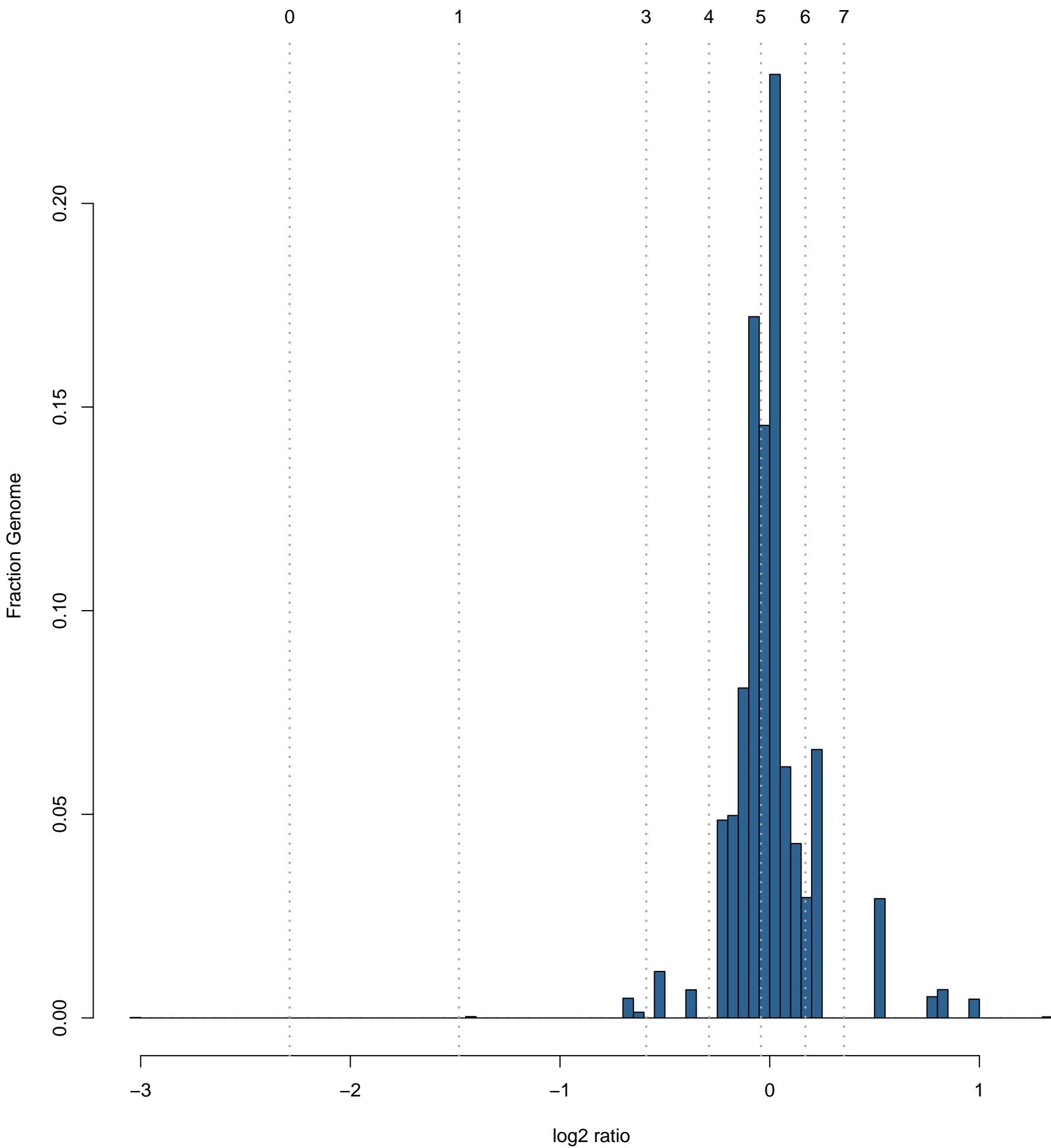


SCNA-fit log-likelihood: -16535.64

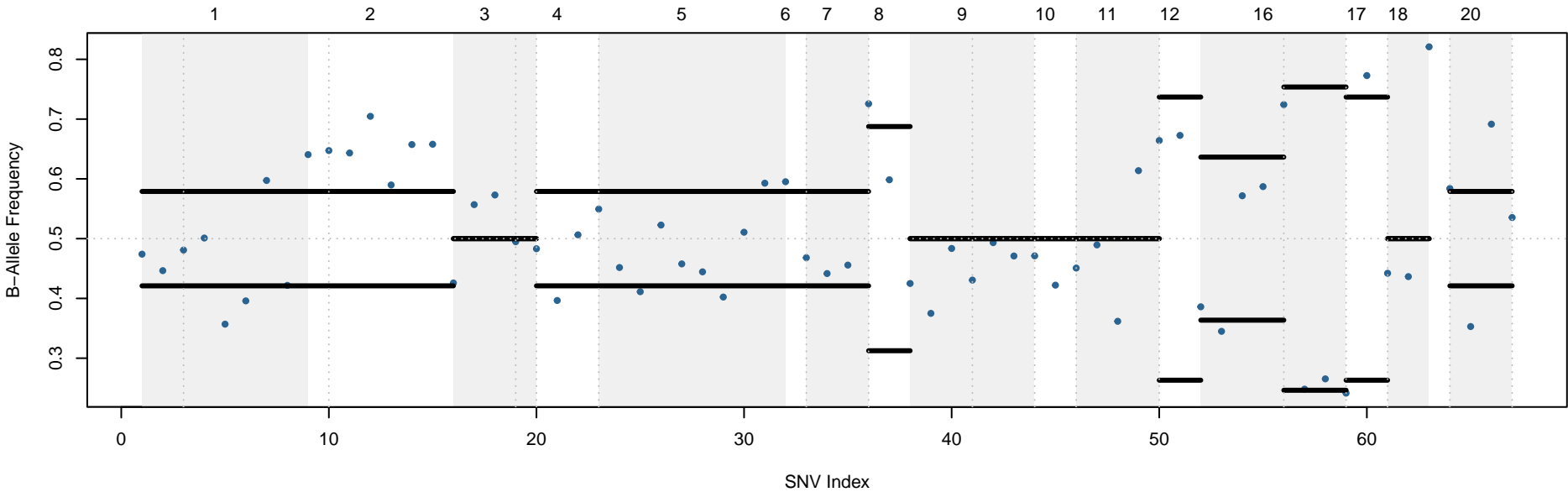




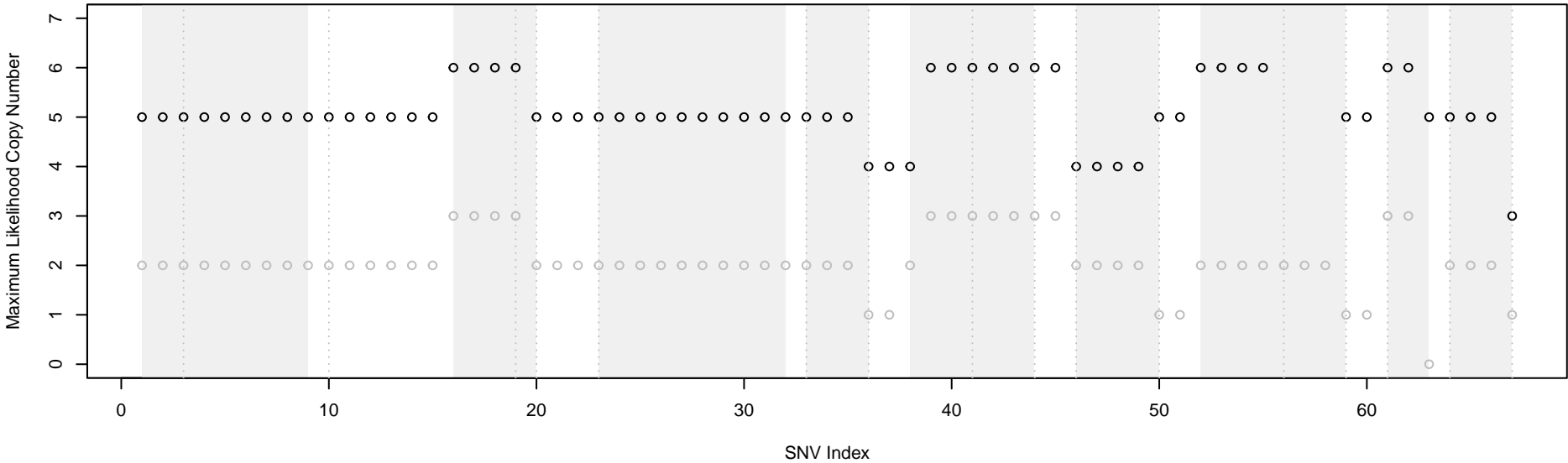
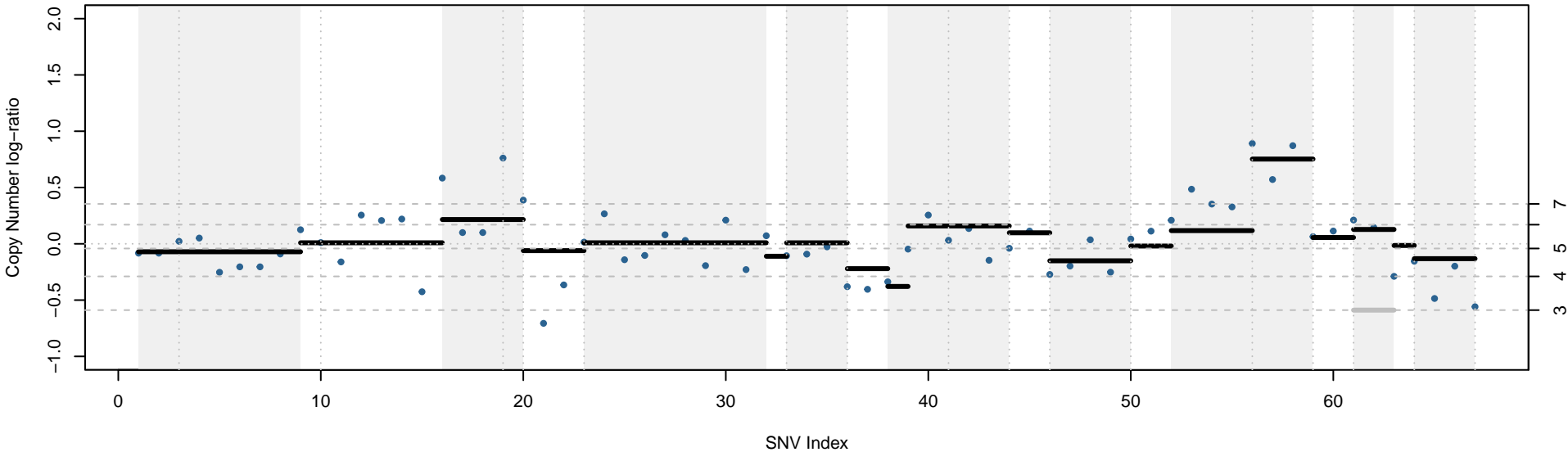
Purity: 0.6 Tumor ploidy: 5.185

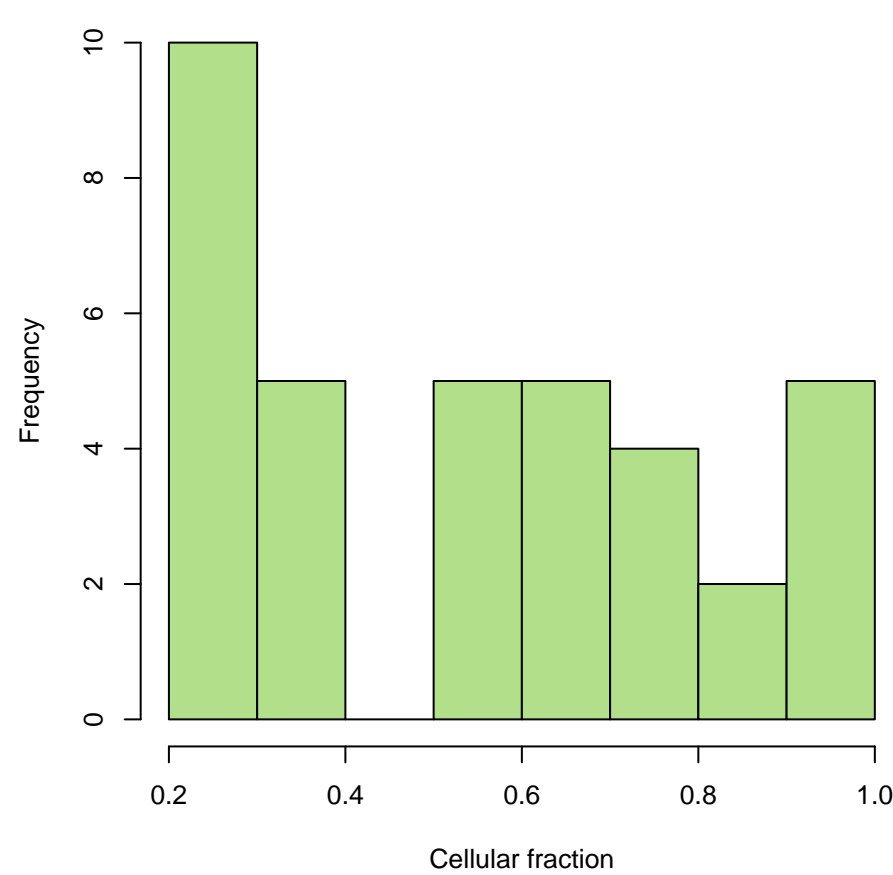
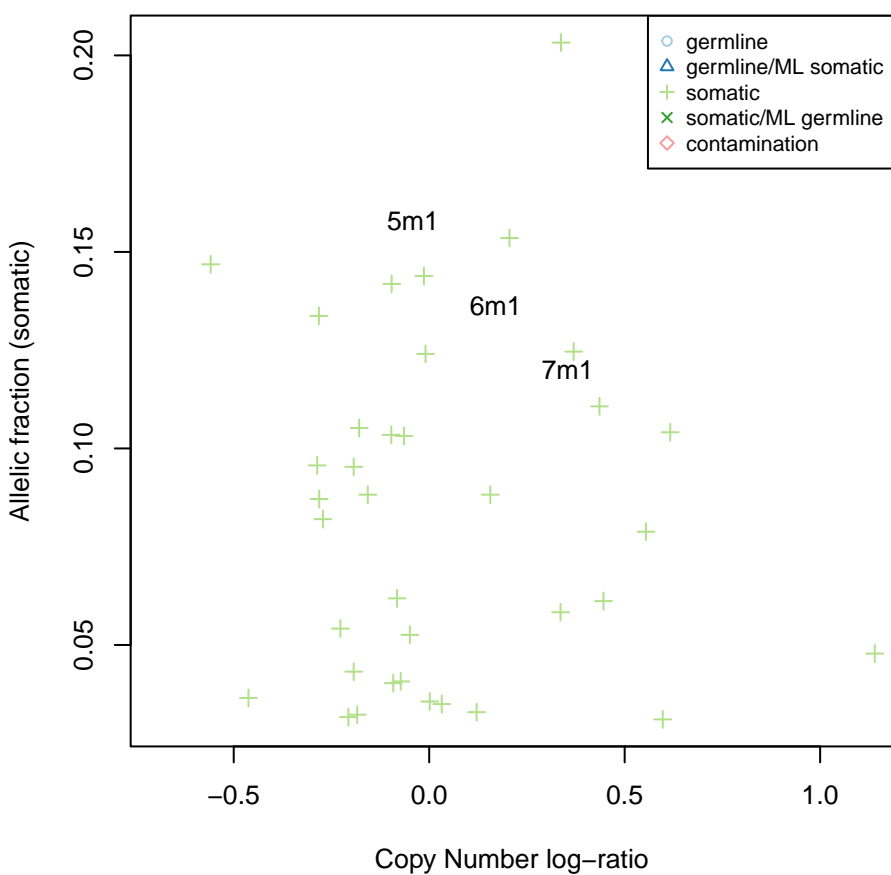
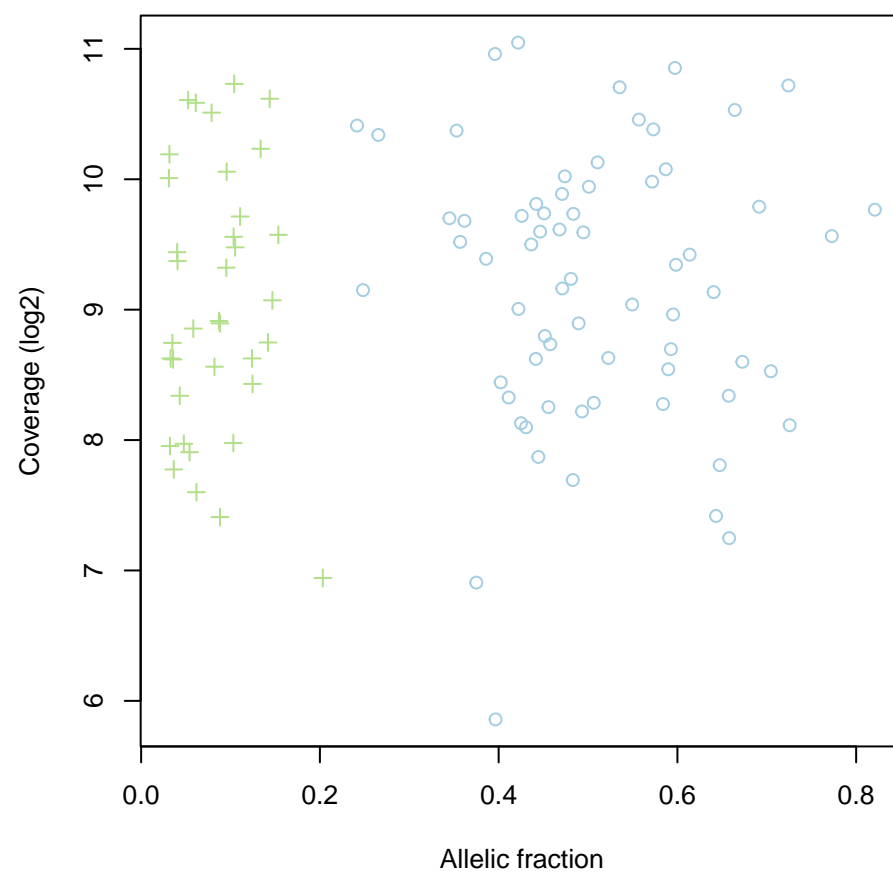
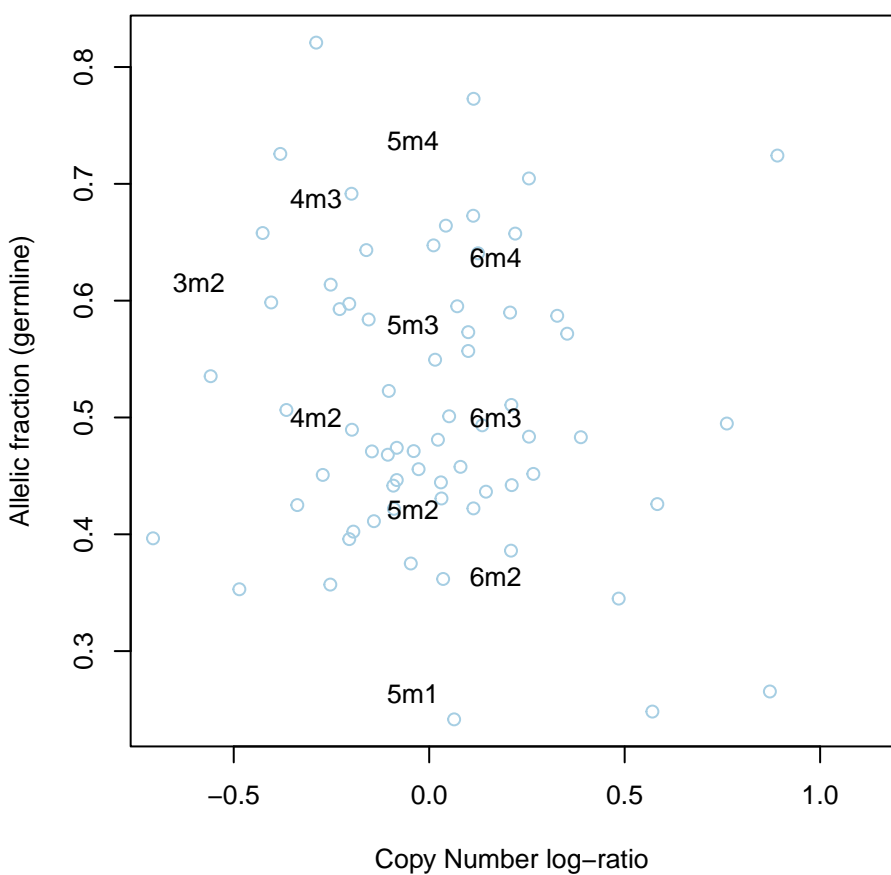


Purity: 0.6 Tumor ploidy: 5.185 SNV log-likelihood: -159.77 GoF: 88% Mean coverage: 385;708

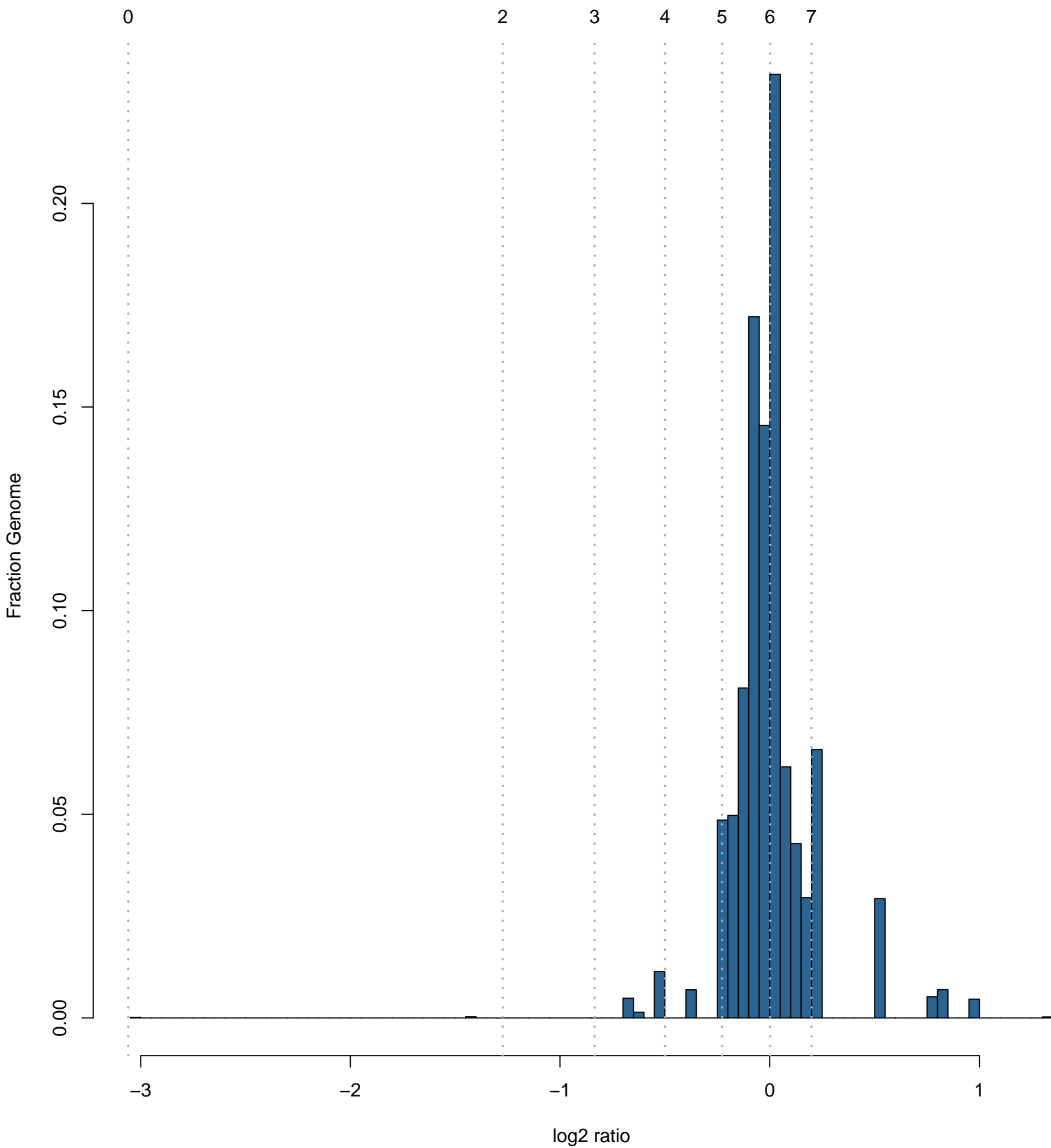


SCNA-fit log-likelihood: -16649.23



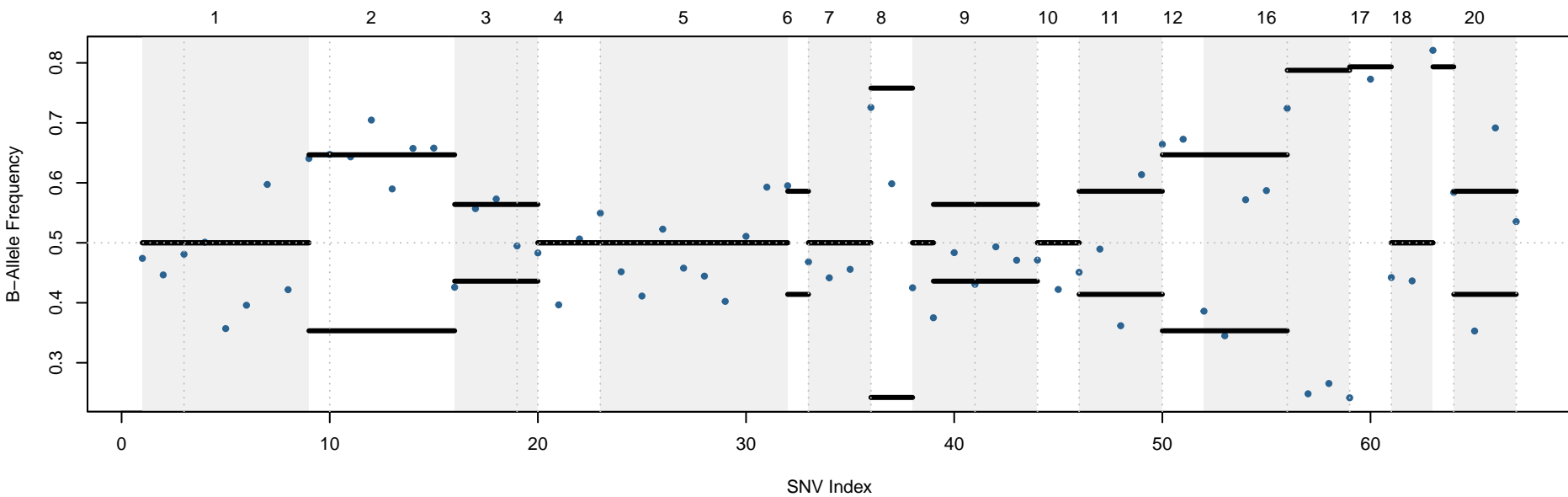


Purity: 0.71 Tumor ploidy: 5.992

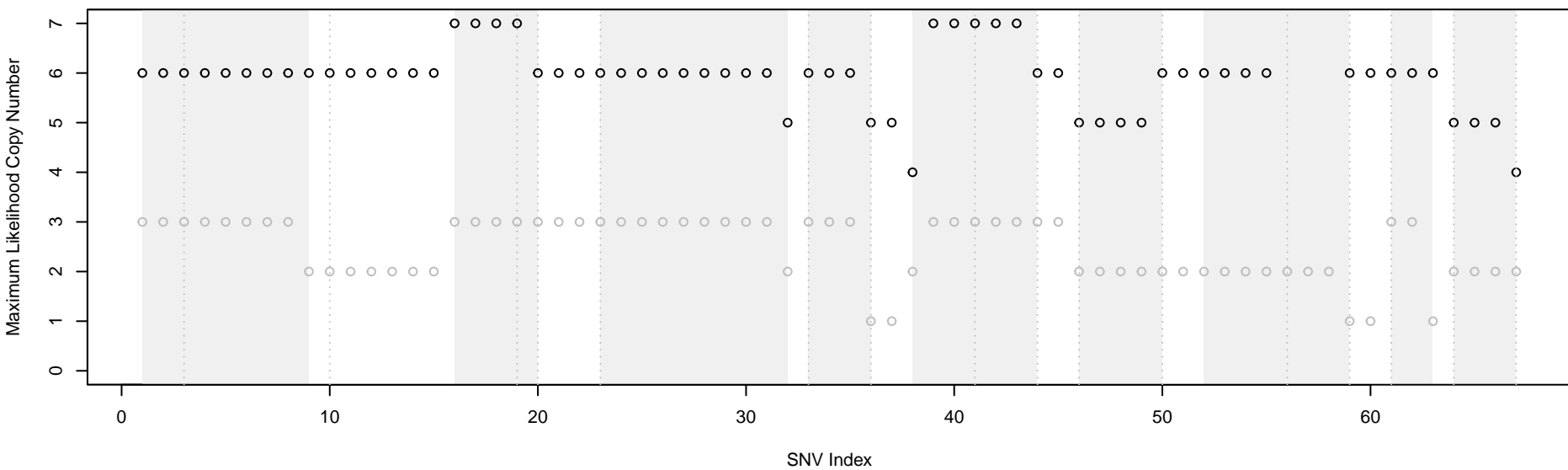
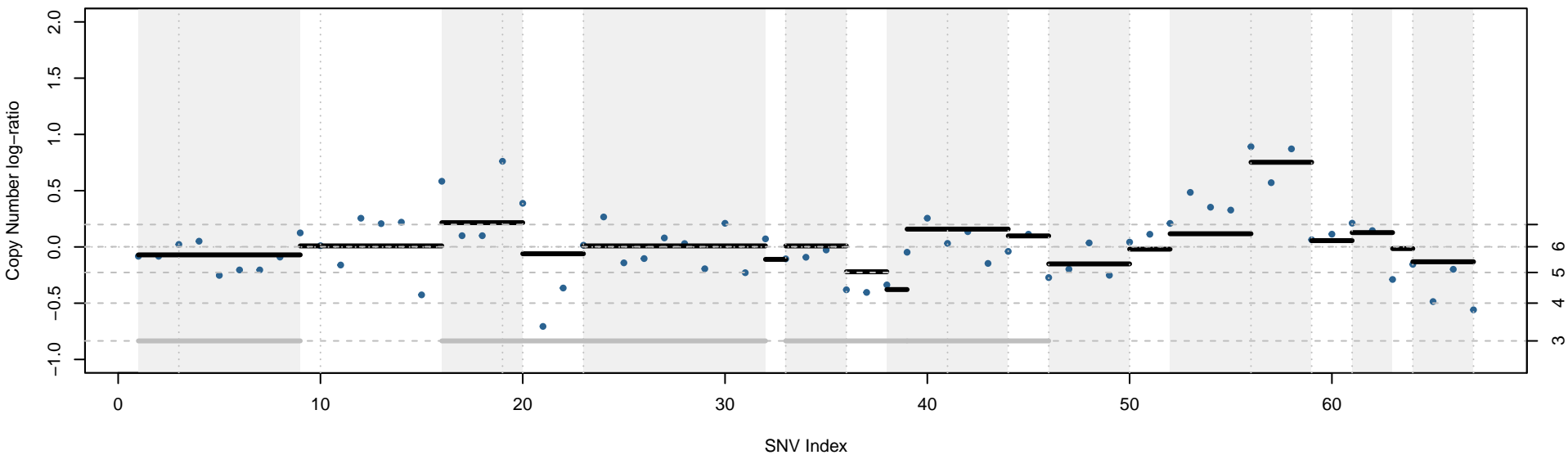


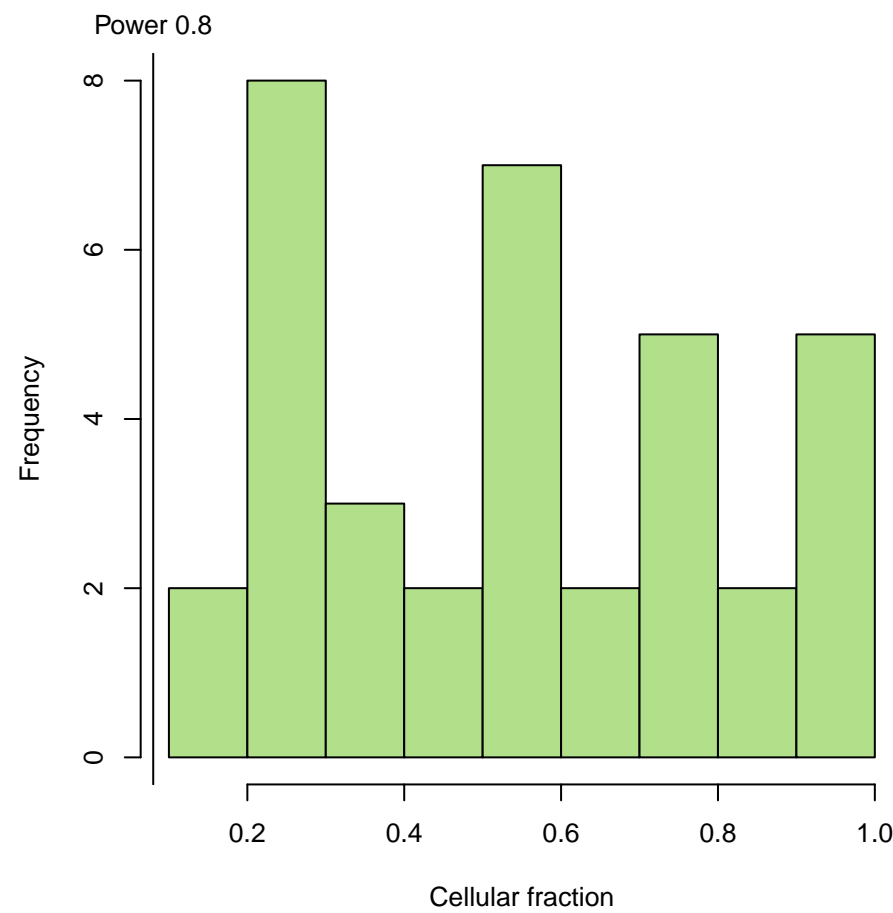
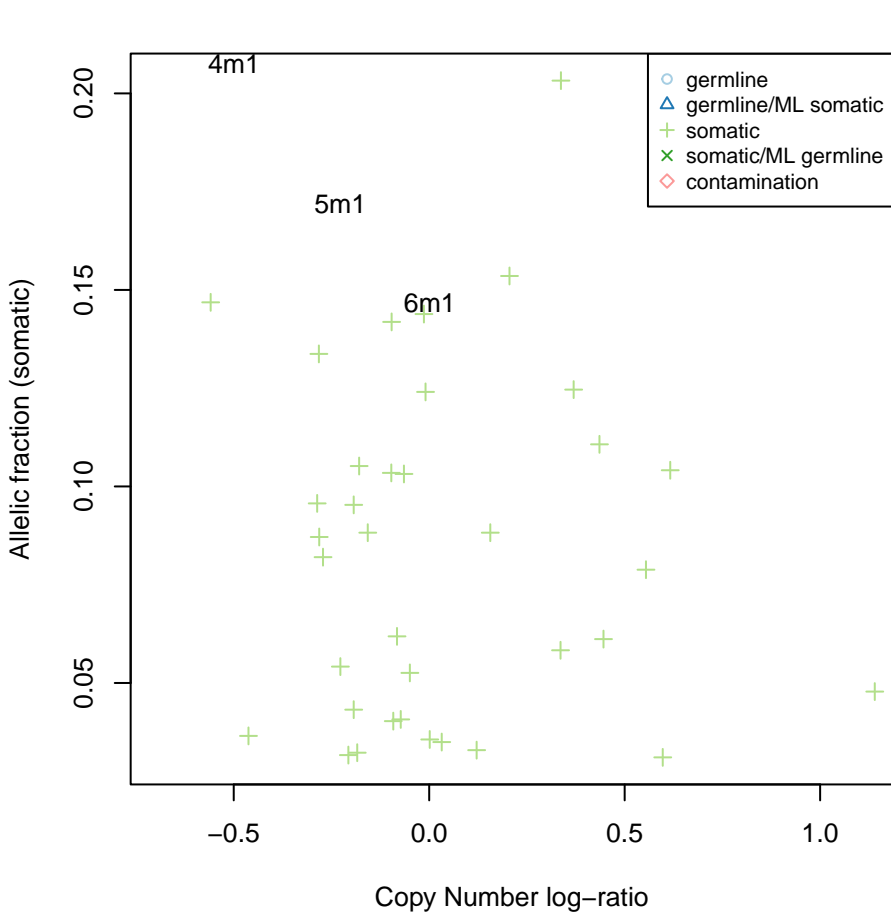
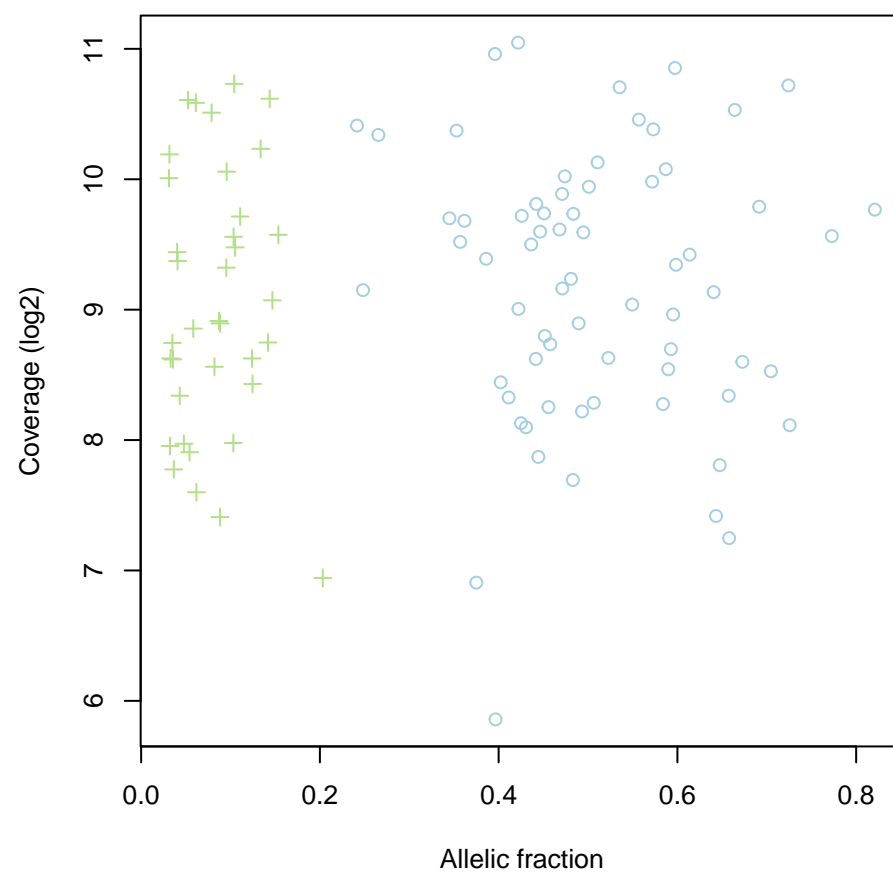
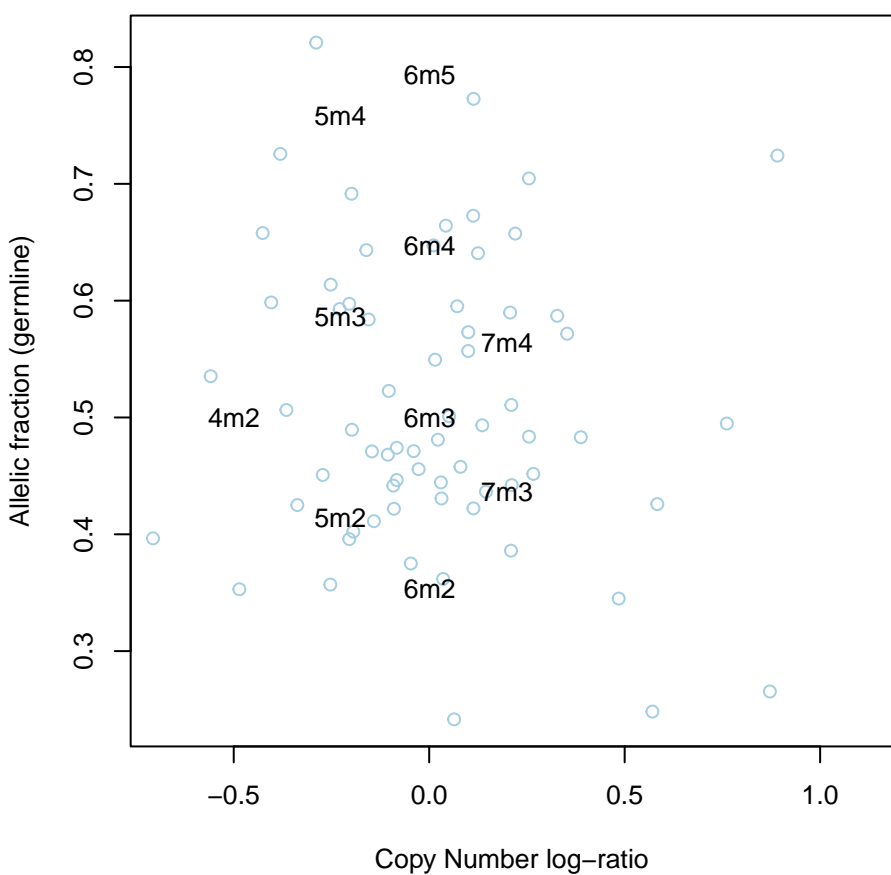


Purity: 0.71 Tumor ploidy: 5.992 SNV log-likelihood: -140.37 GoF: 88.9% Mean coverage: 385,708

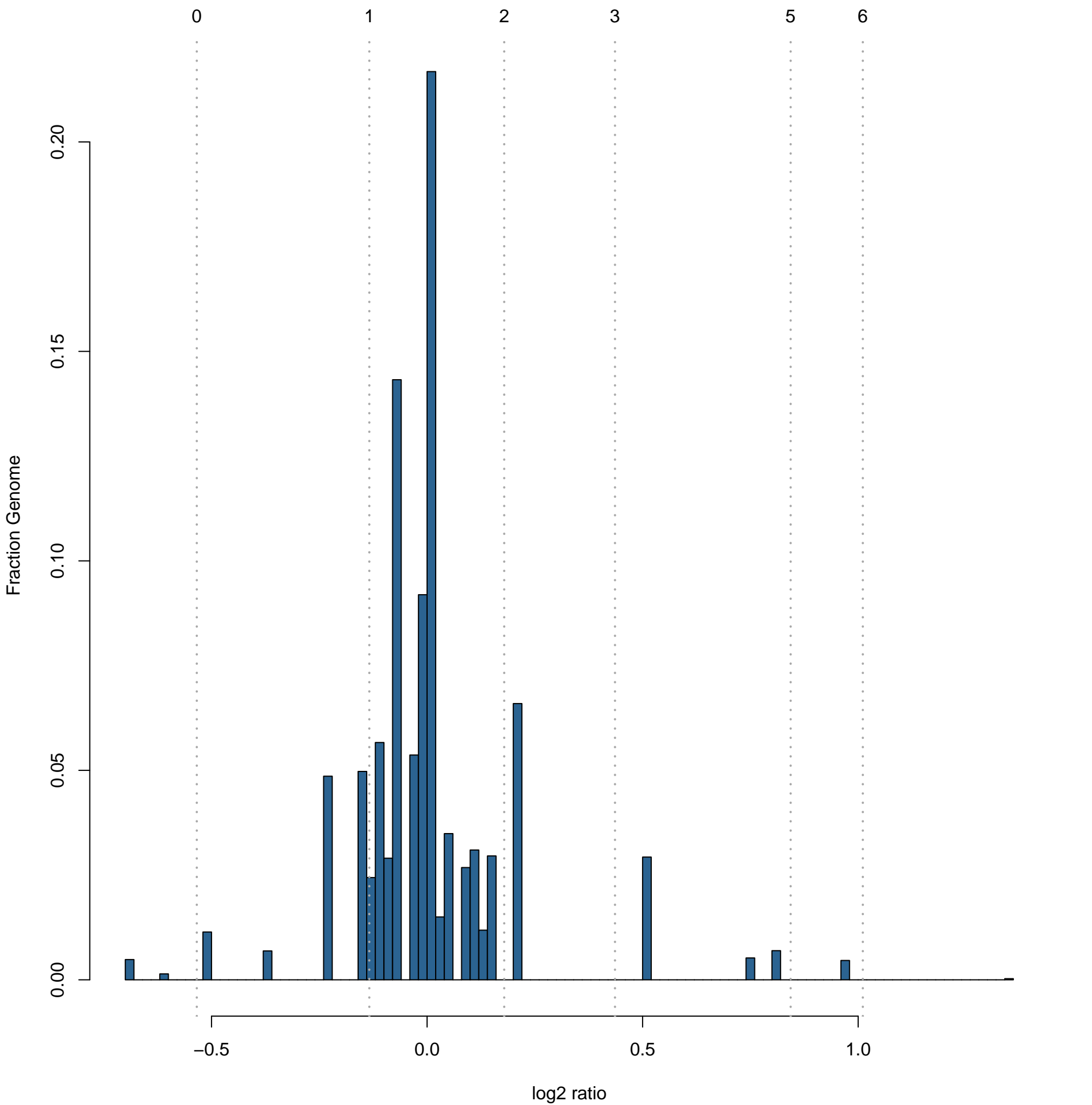


SCNA-fit log-likelihood: -16845.03

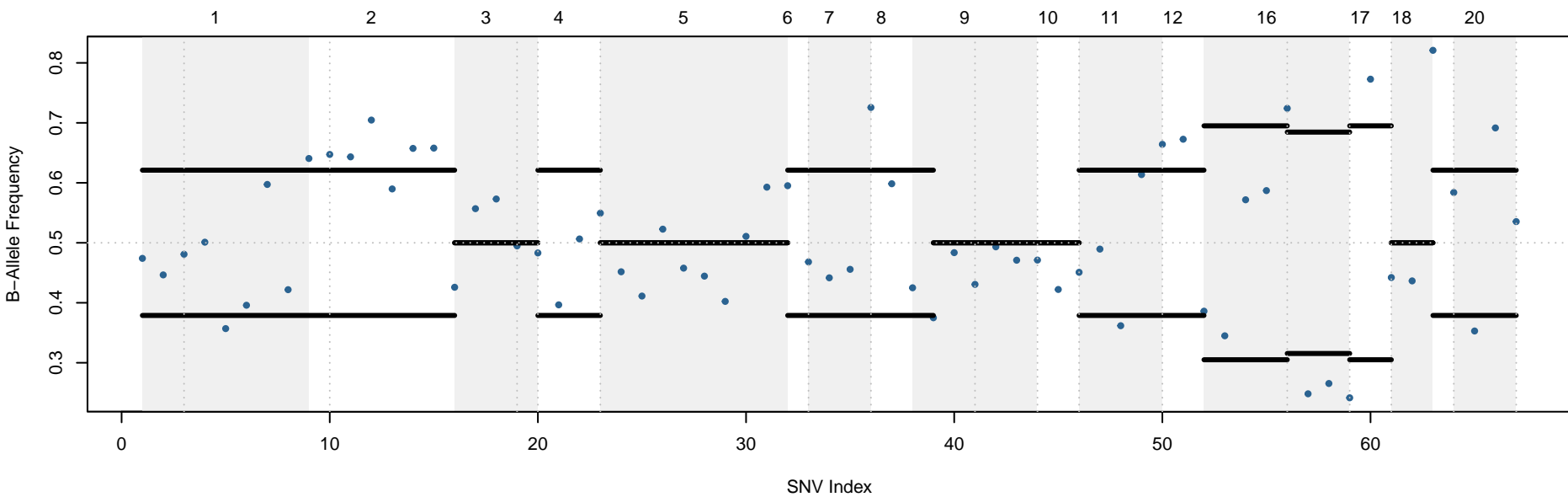




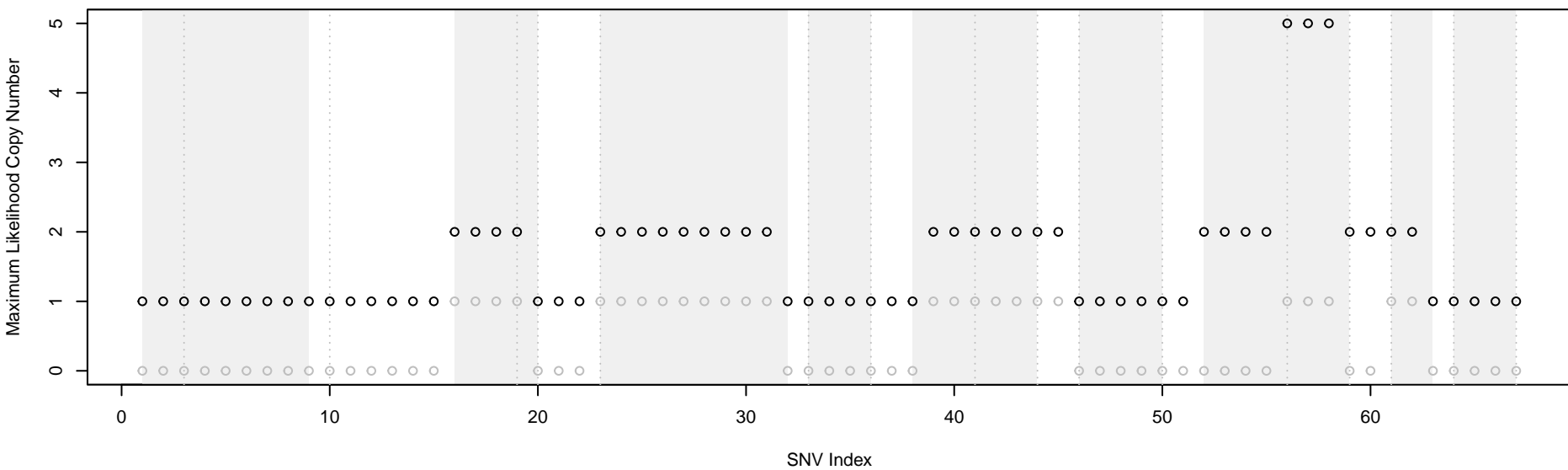
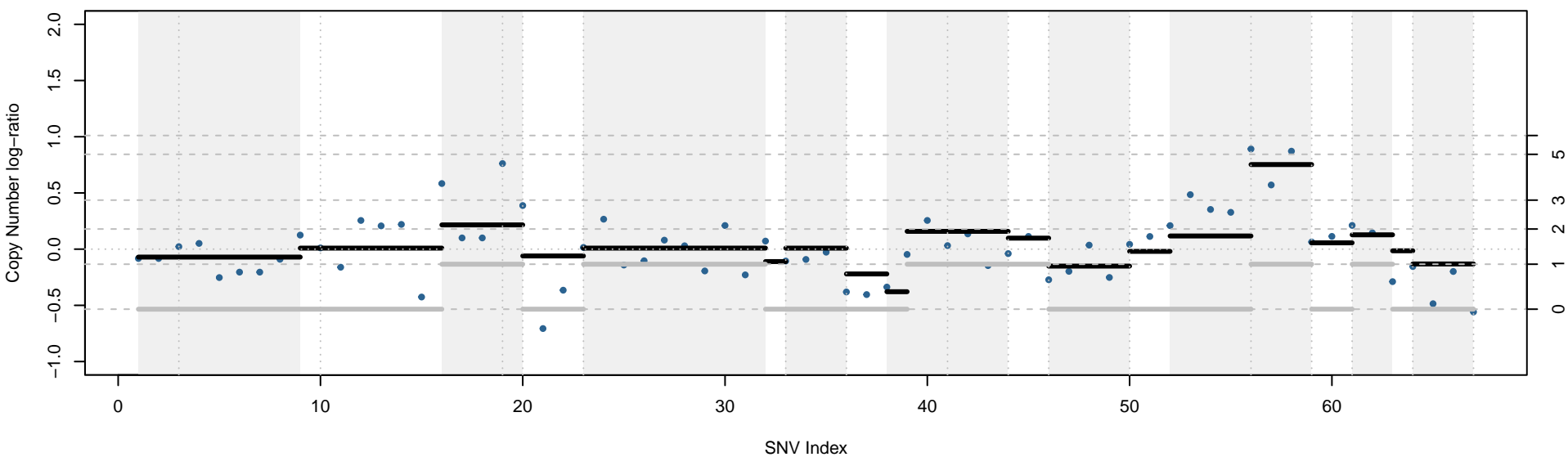
Purity: 0.39 Tumor ploidy: 1.402

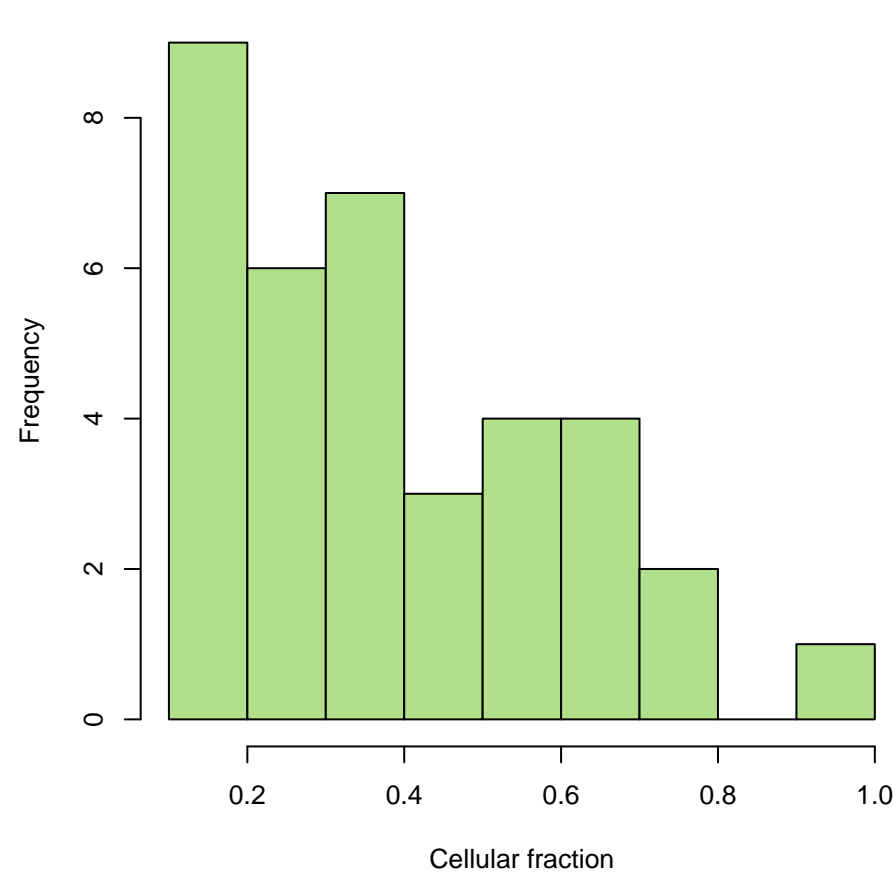
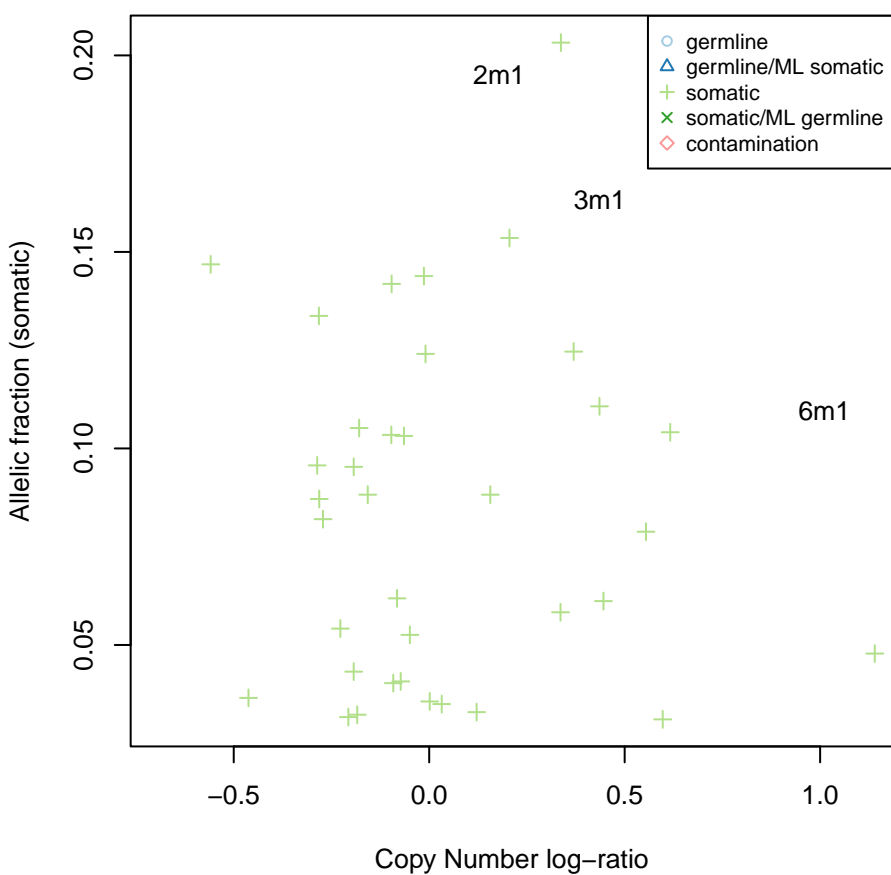
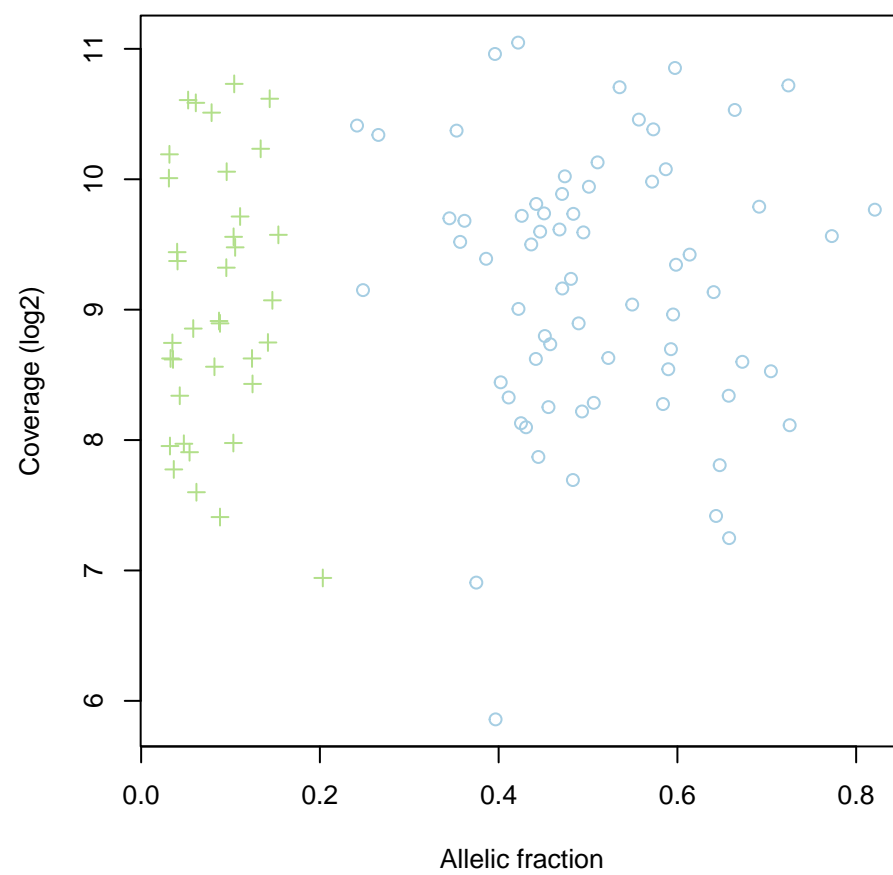
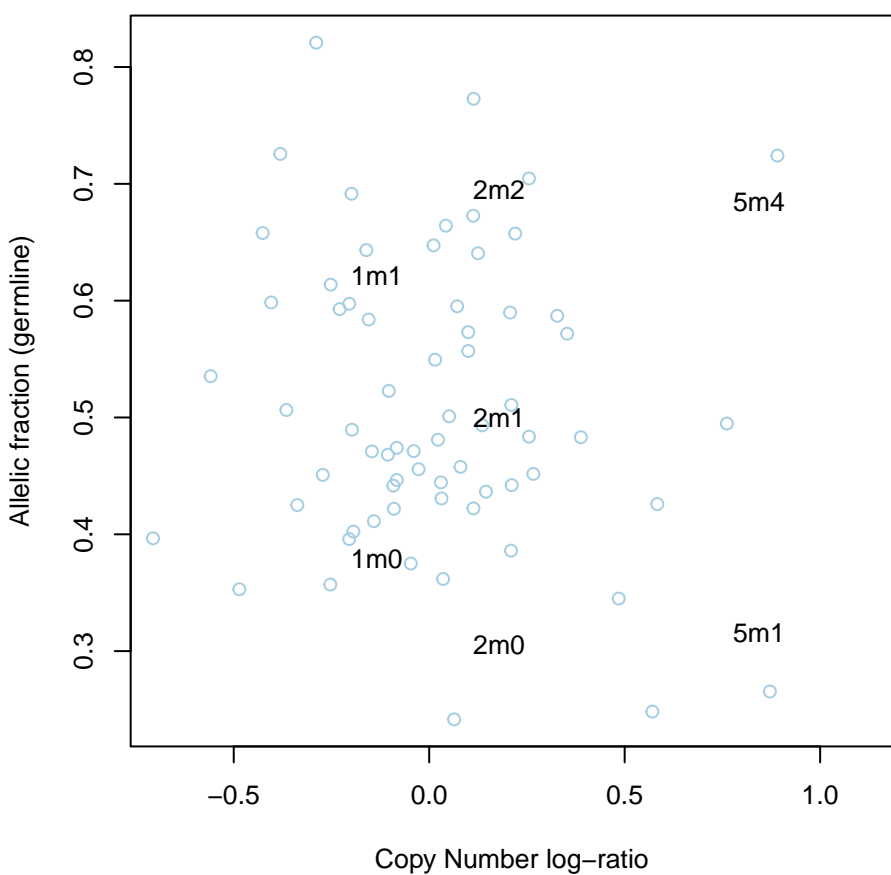


Purity: 0.39 Tumor ploidy: 1.402 SNV log-likelihood: -219.16 GoF: 72.7% Mean coverage: 385,708

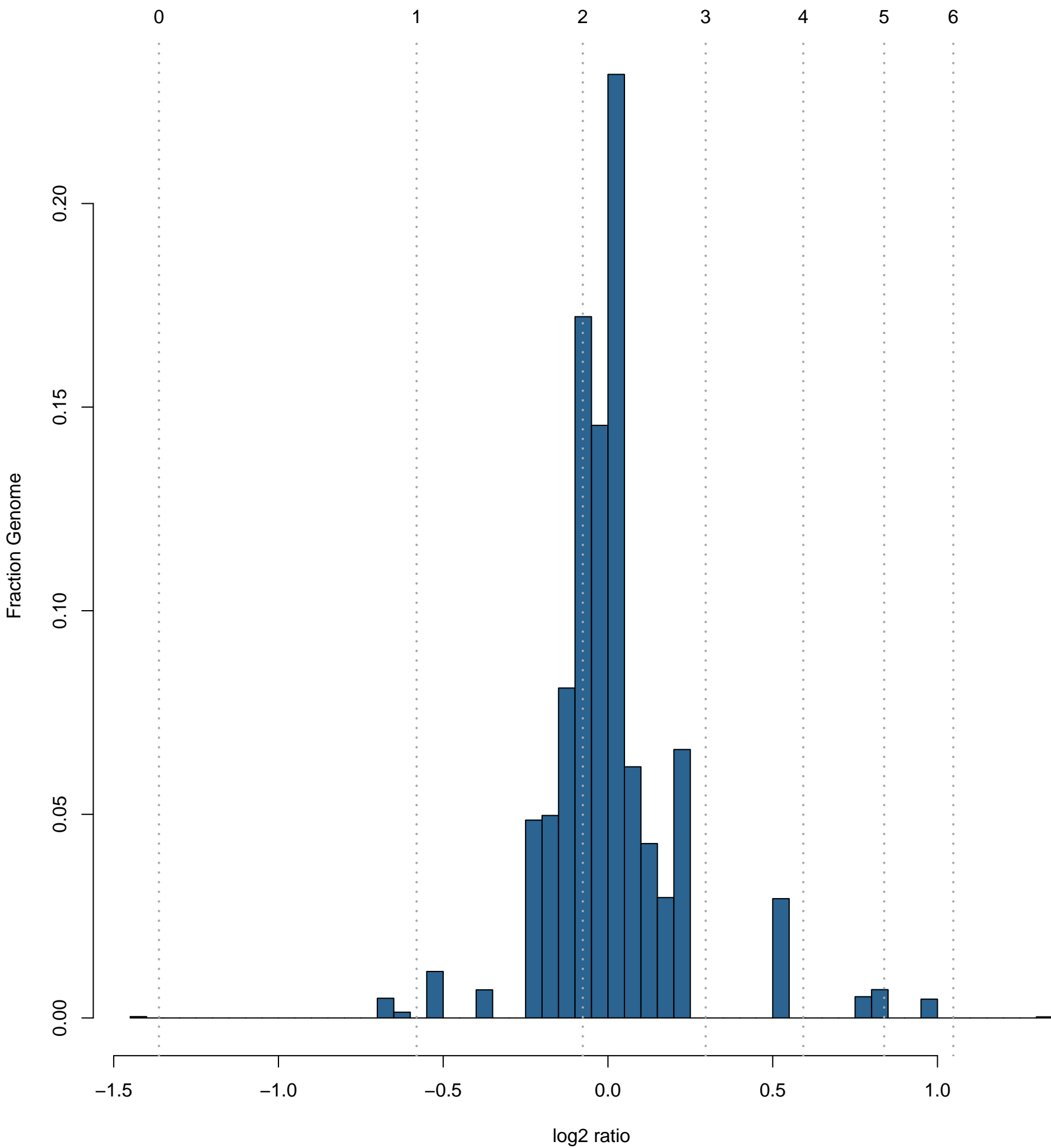


SCNA-fit log-likelihood: -16752.02

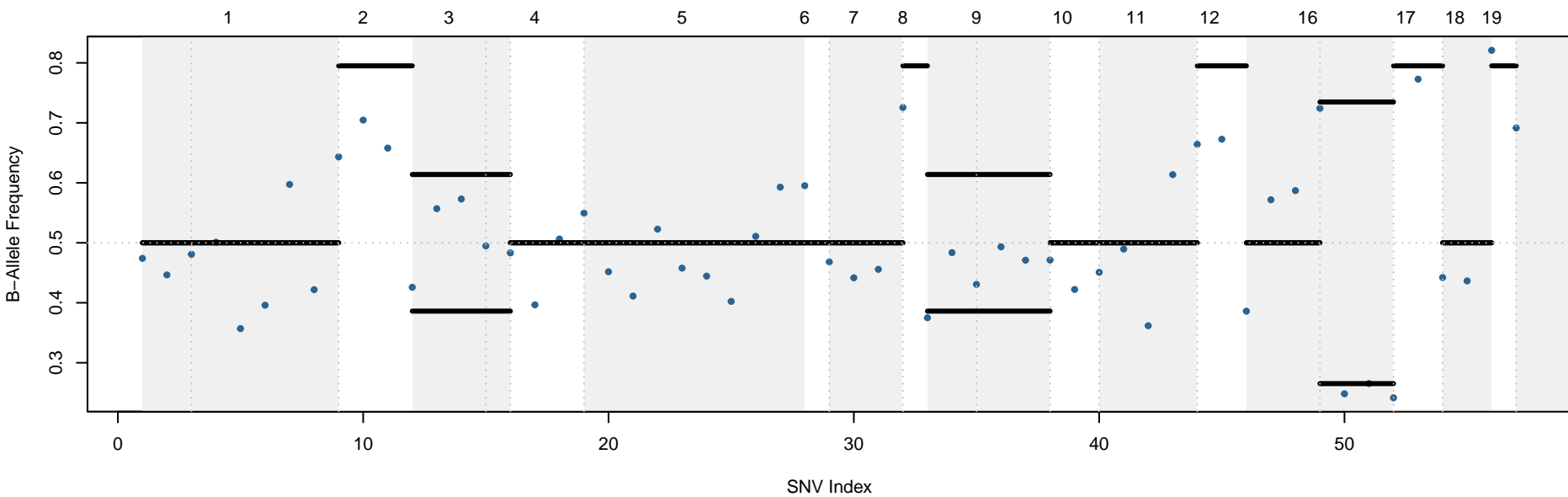




Purity: 0.59 Tumor ploidy: 2.184



Purity: 0.59 Tumor ploidy: 2.184 SNV log-likelihood: -285.87 GoF: 54.5% Mean coverage: 385,708



SCNA-fit log-likelihood: -16606.23

