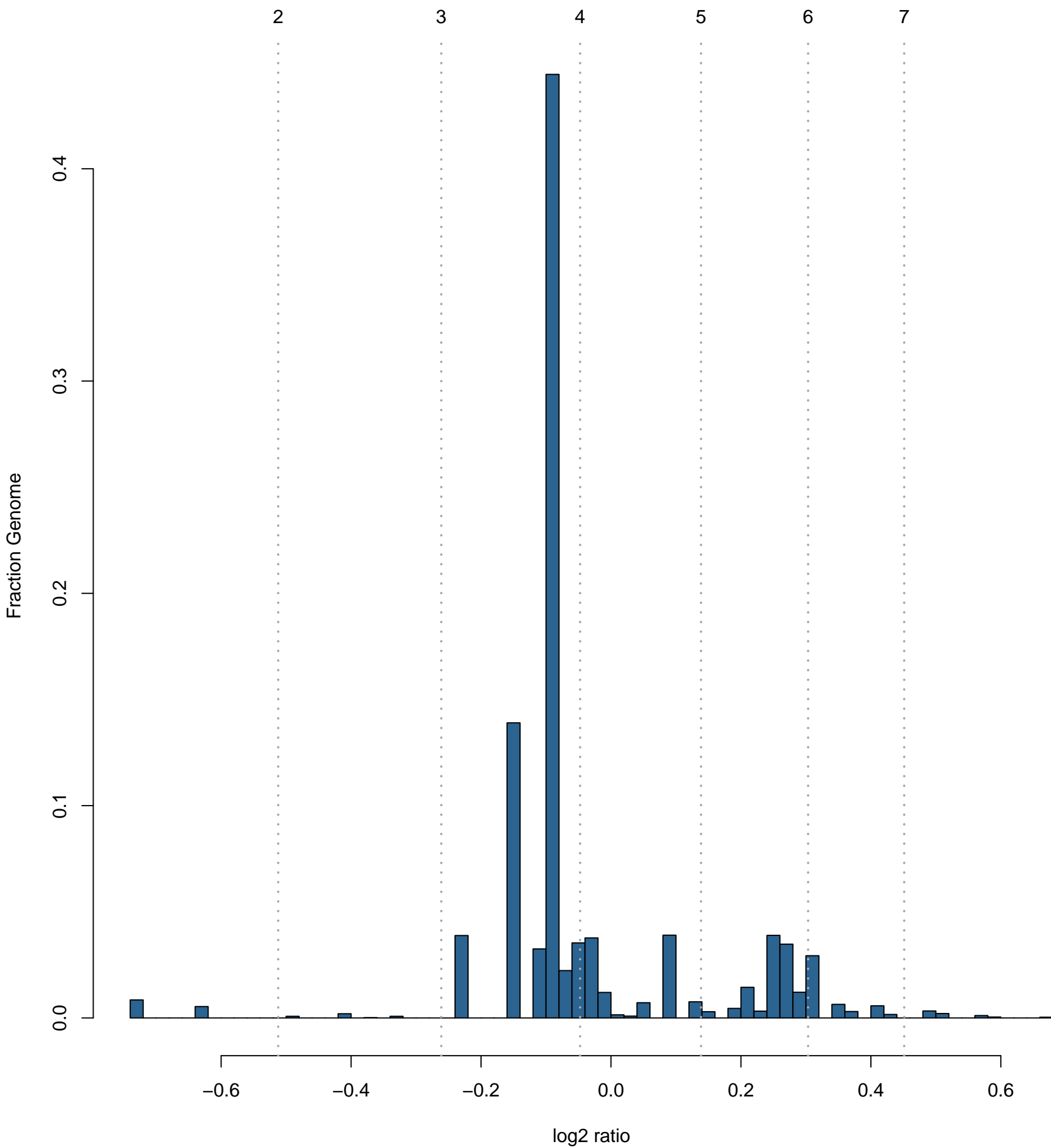
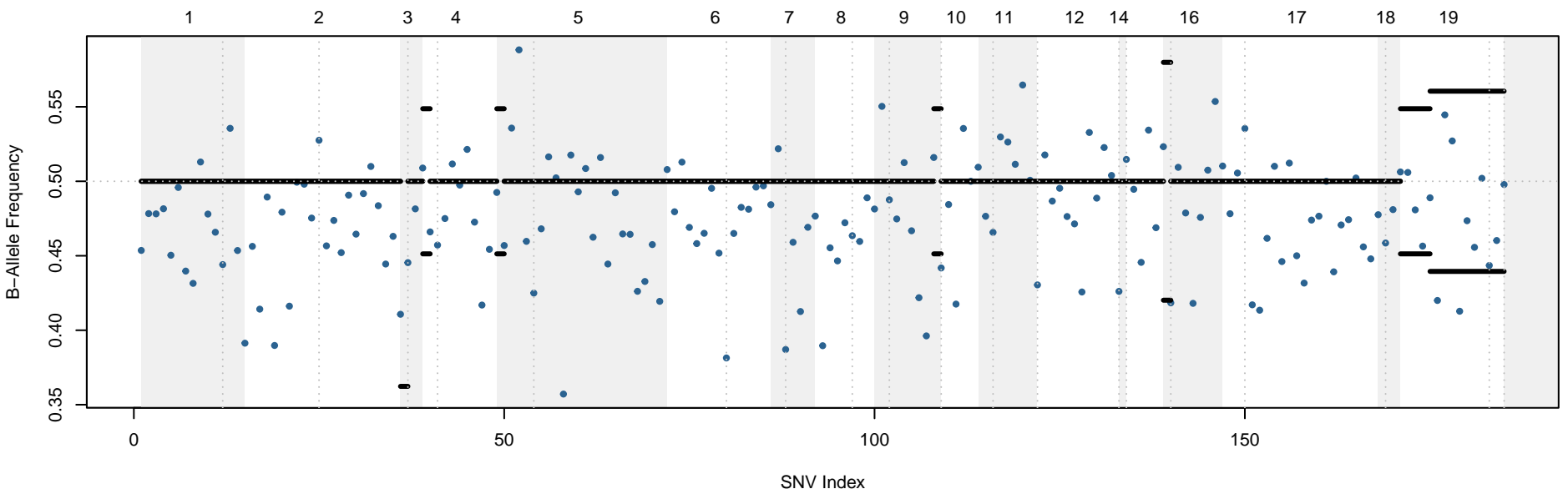


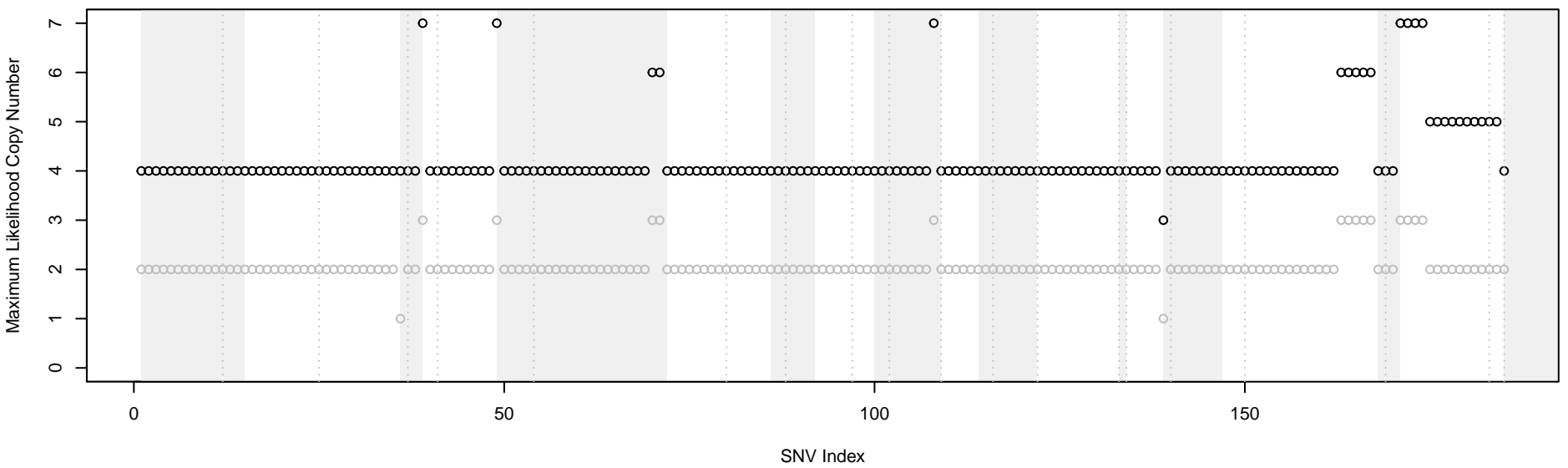
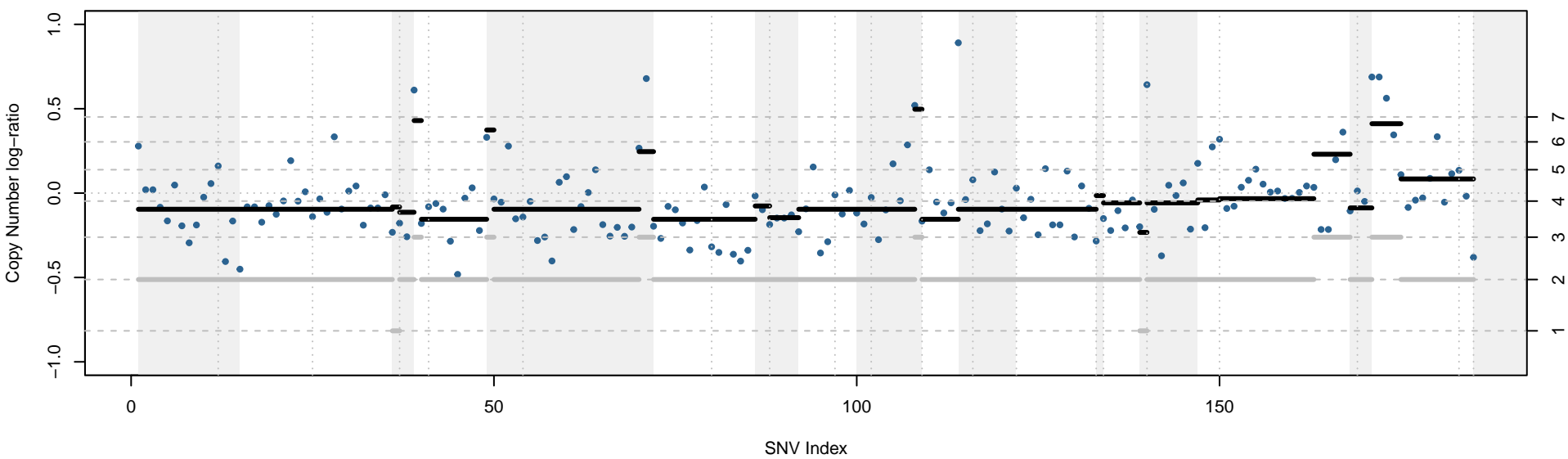
Purity: 0.38 Tumor ploidy: 4.243

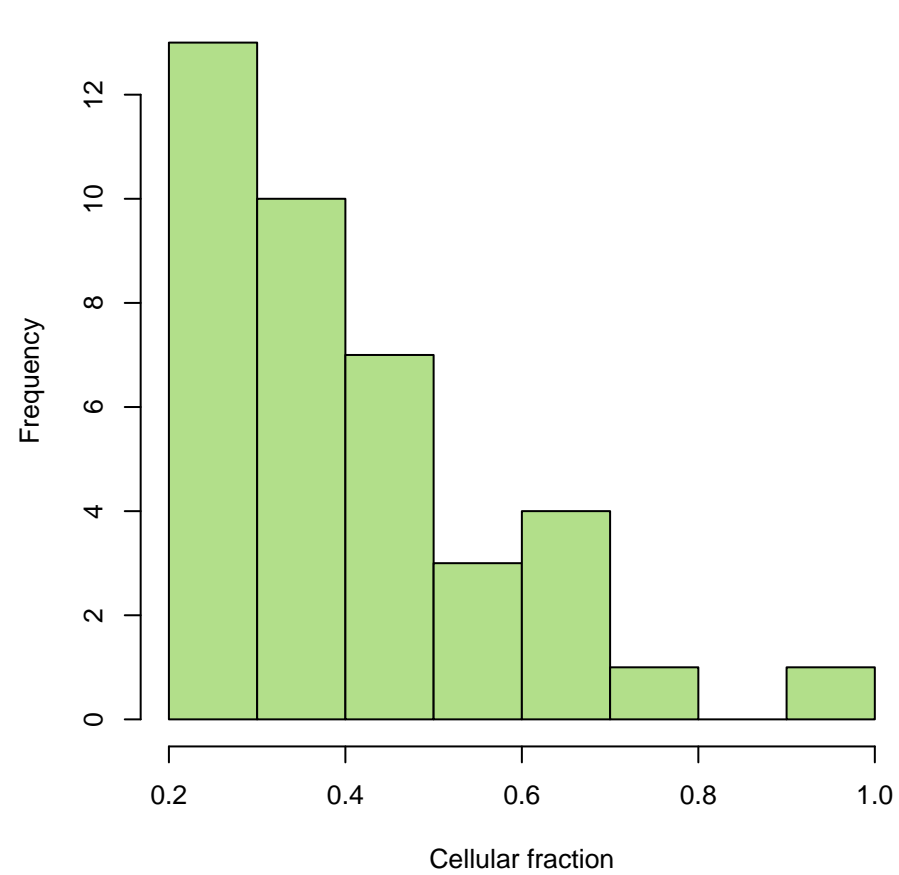
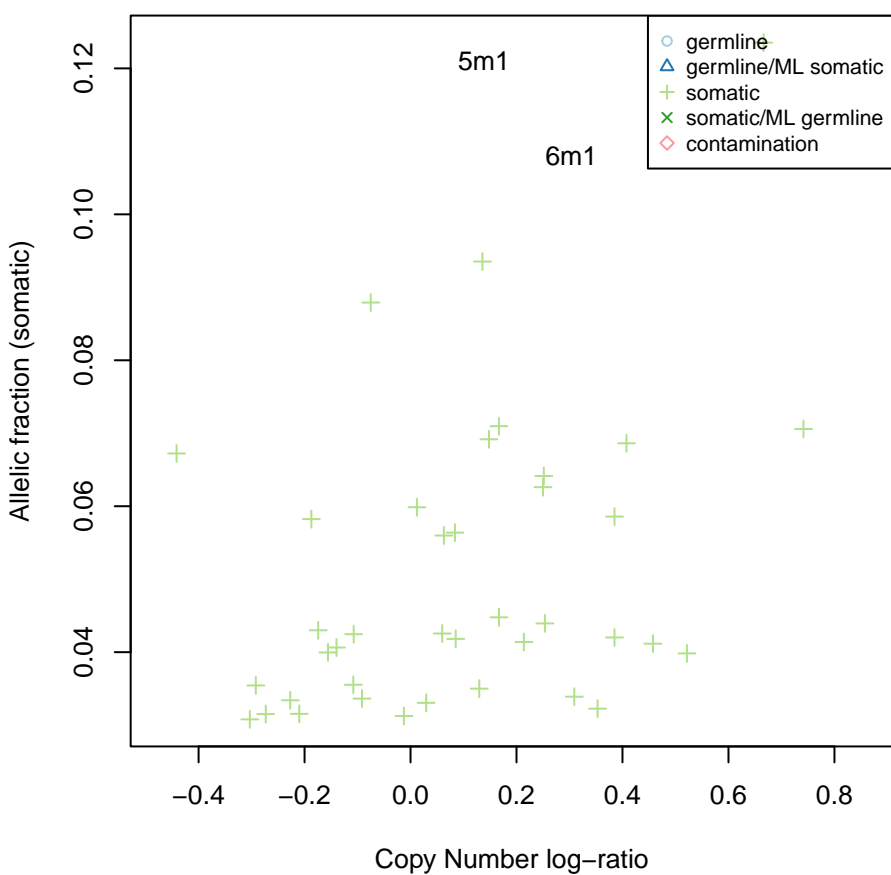
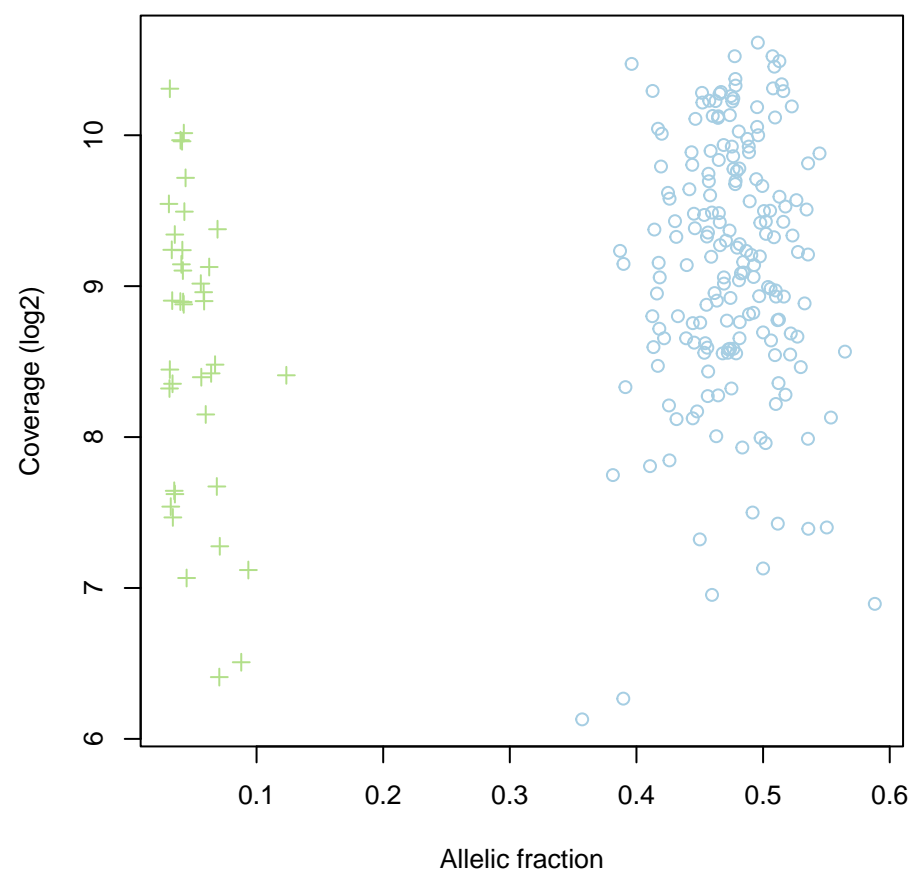
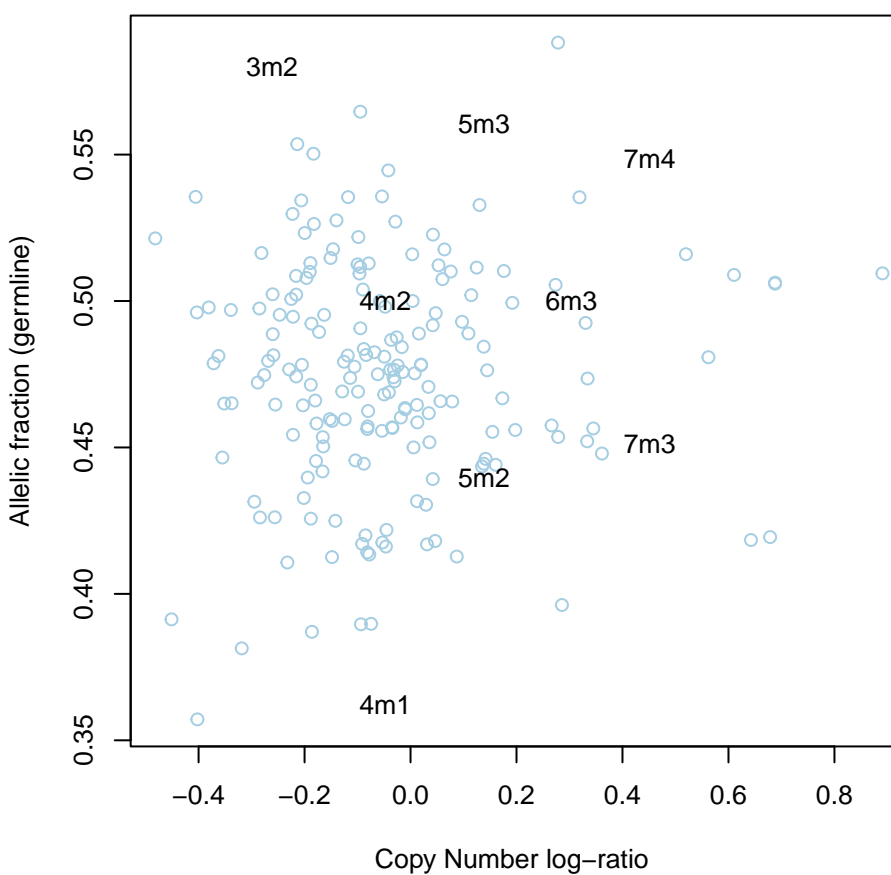


Purity: 0.38 Tumor ploidy: 4.243 SNV log-likelihood: 2.82 GoF: 93.7% Mean coverage: 889;627

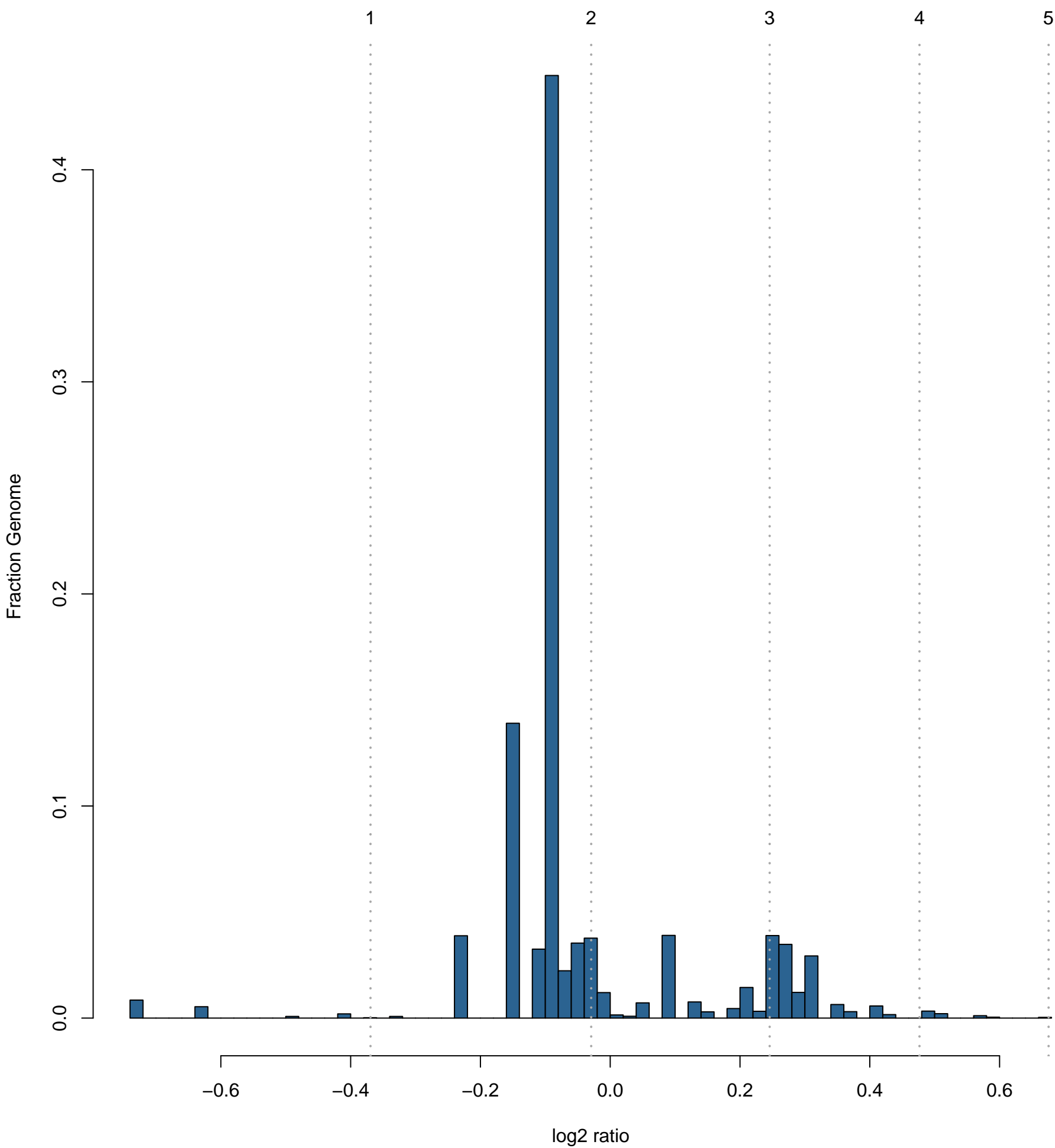


SCNA-fit log-likelihood: -3107.21

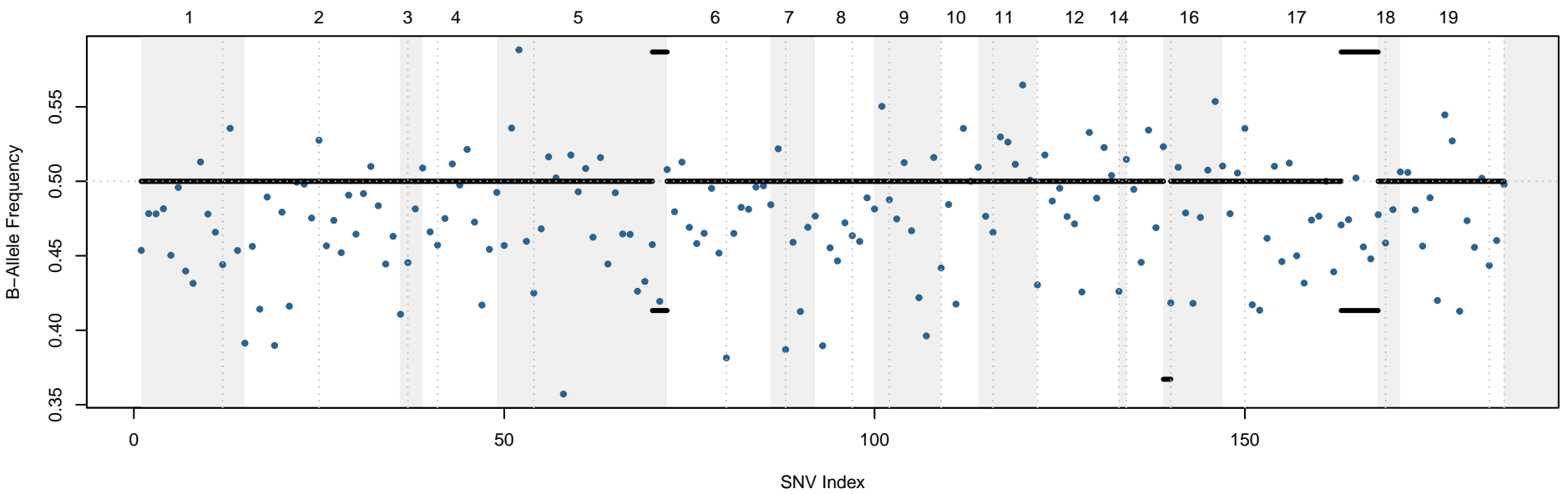




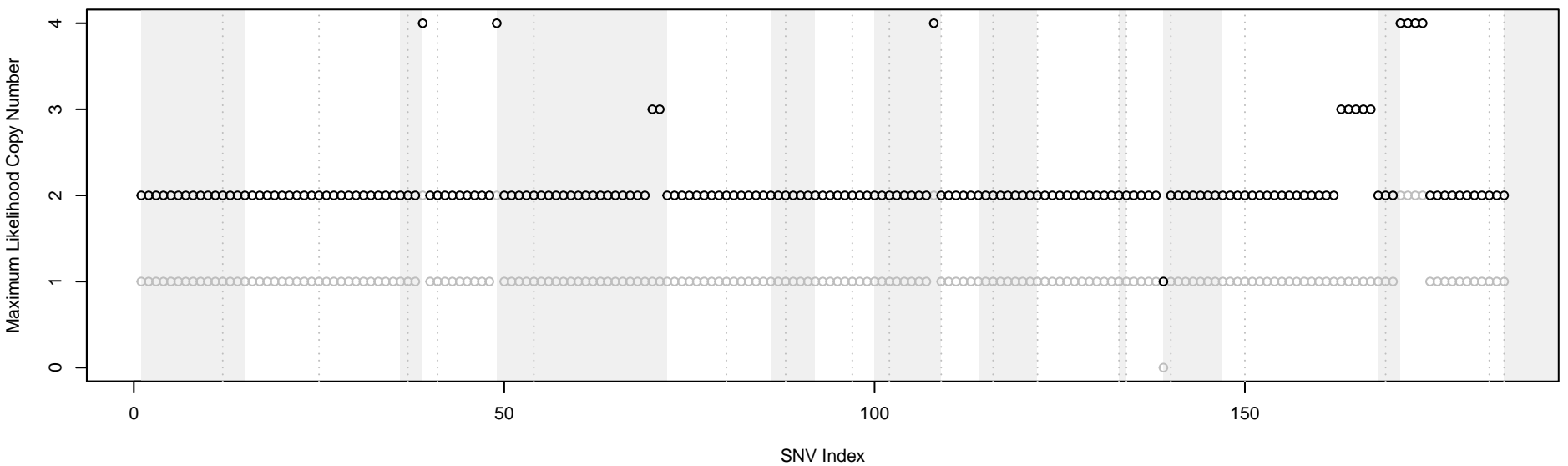
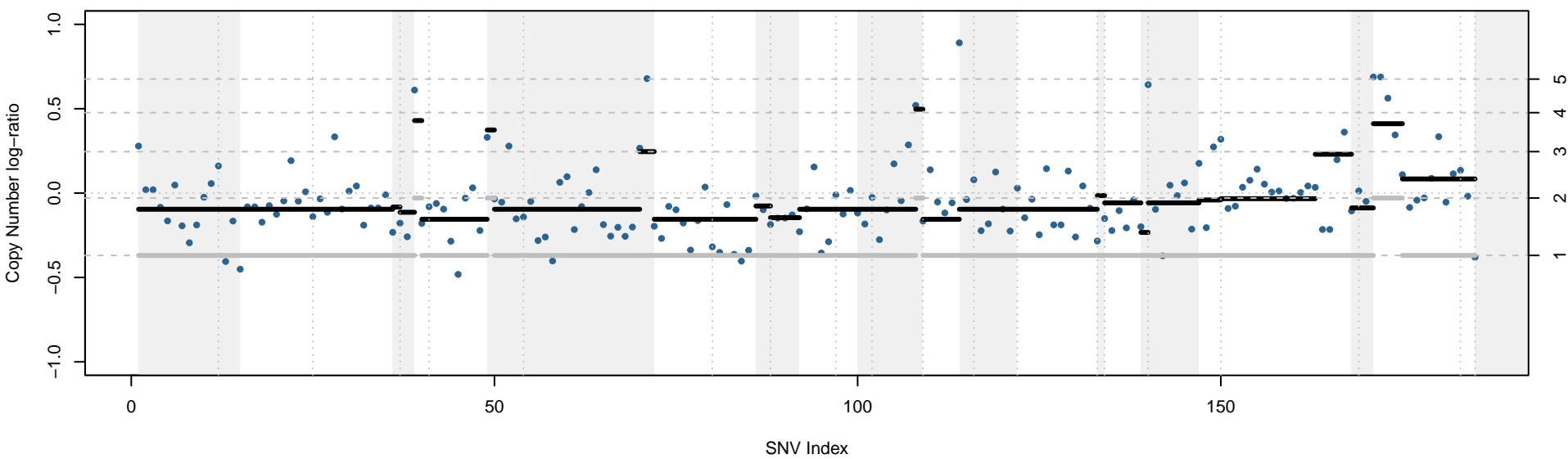
Purity: 0.42 Tumor ploidy: 2.098

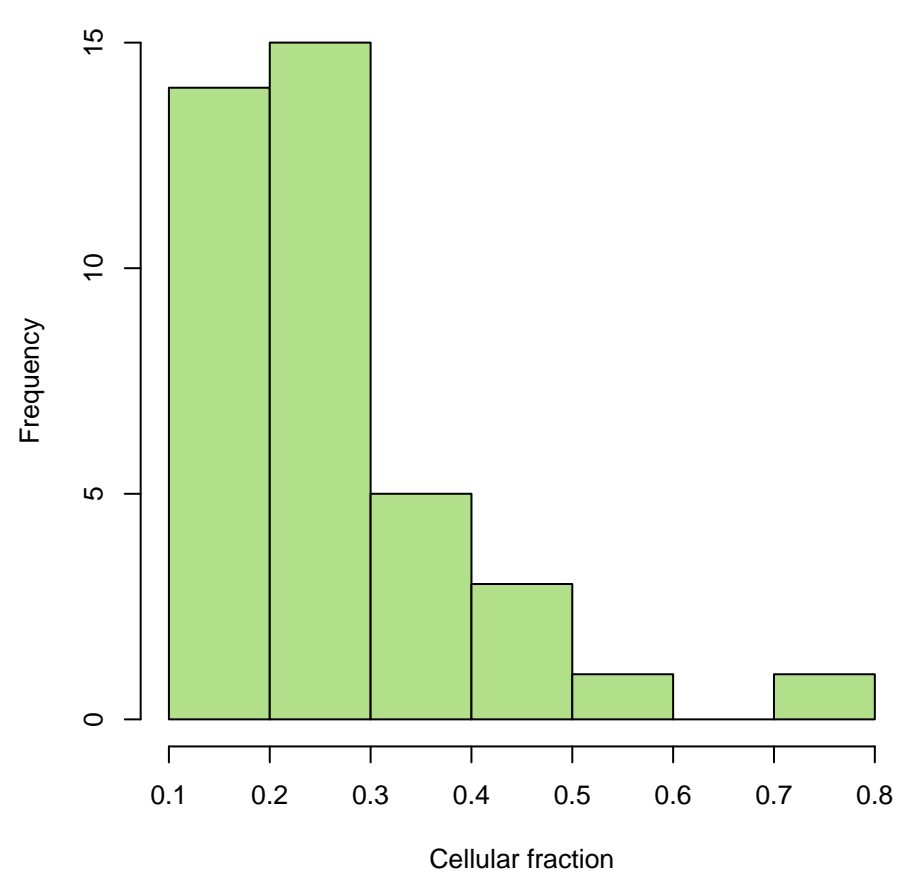
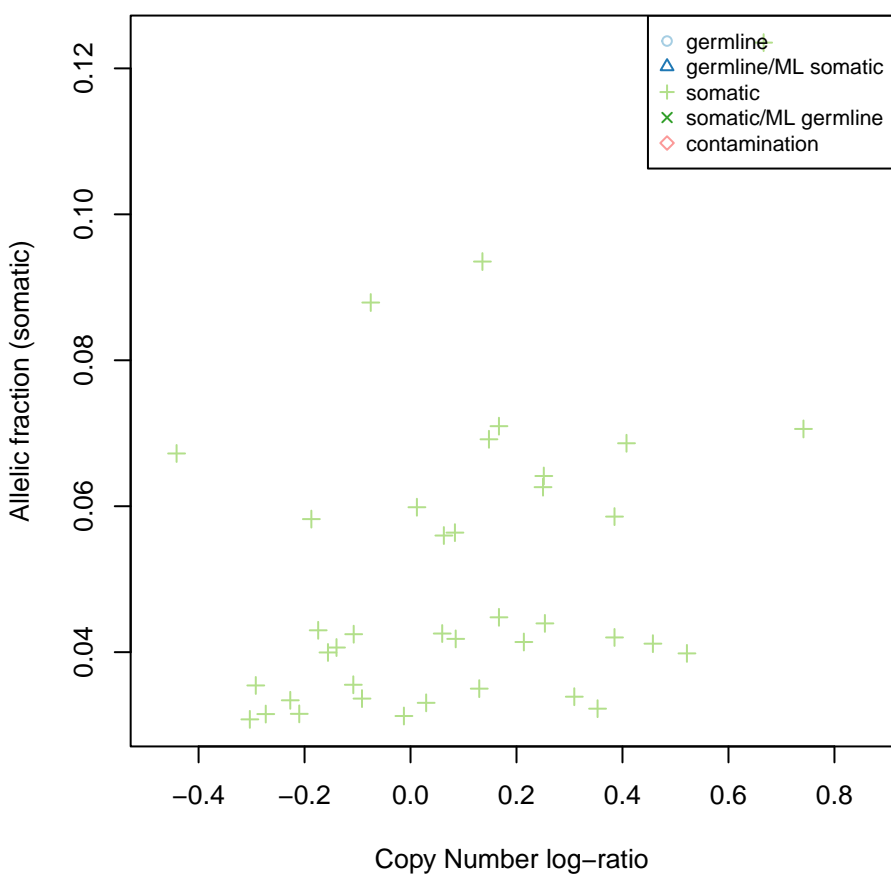
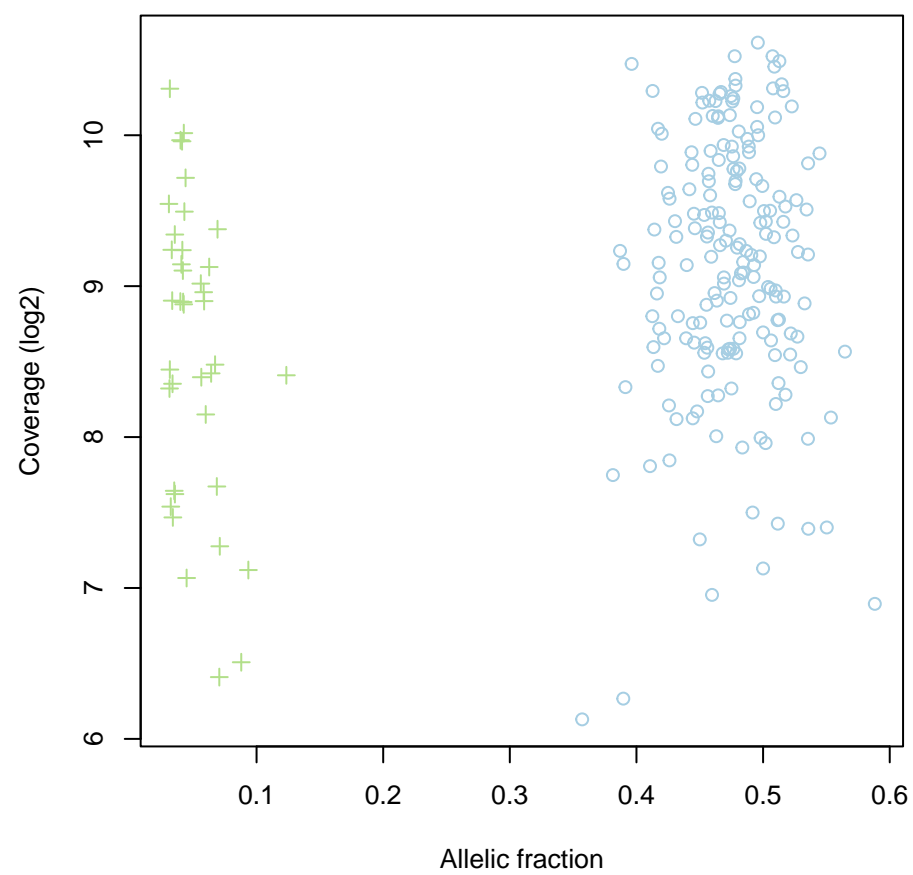
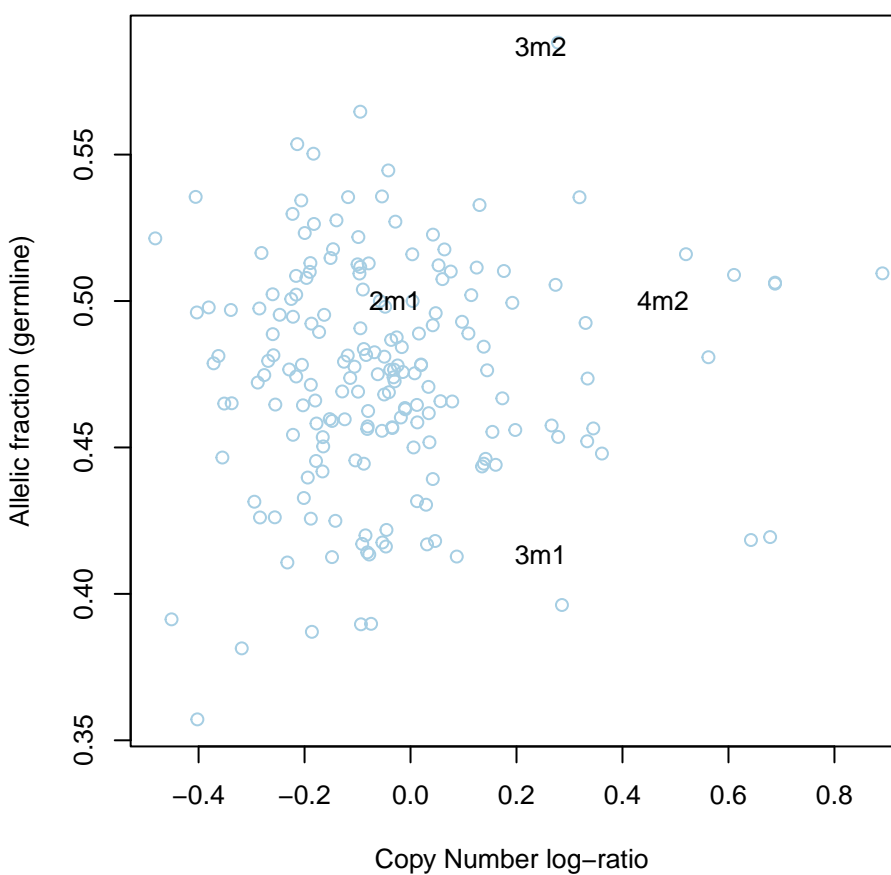


Purity: 0.42 Tumor ploidy: 2.098 SNV log-likelihood: 77.1 GoF: 86.3% Mean coverage: 889;627

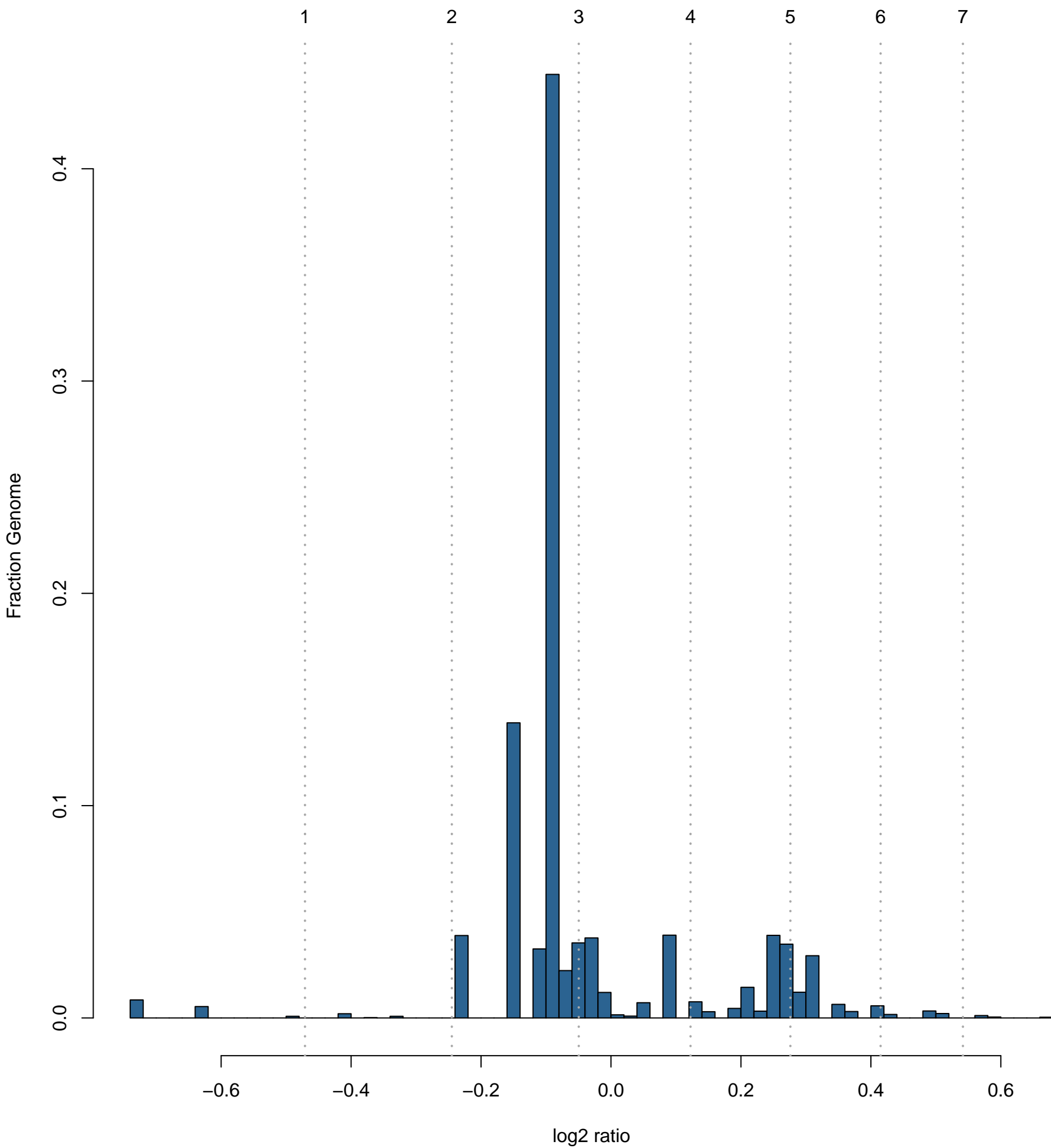


SCNA-fit log-likelihood: -3373.73

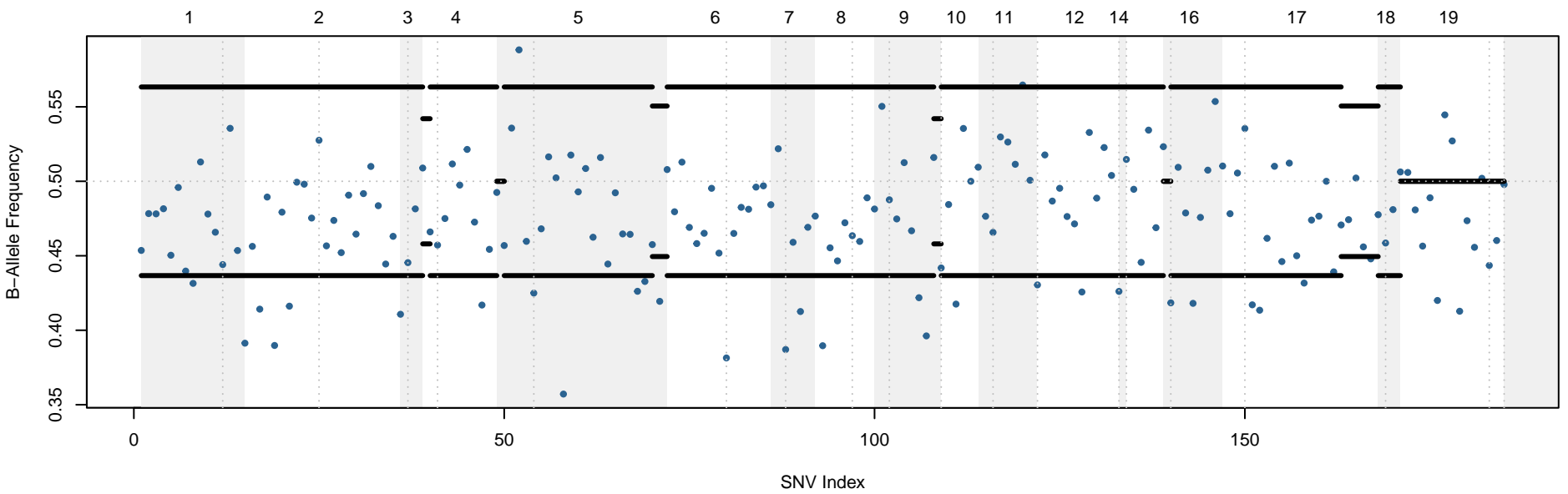




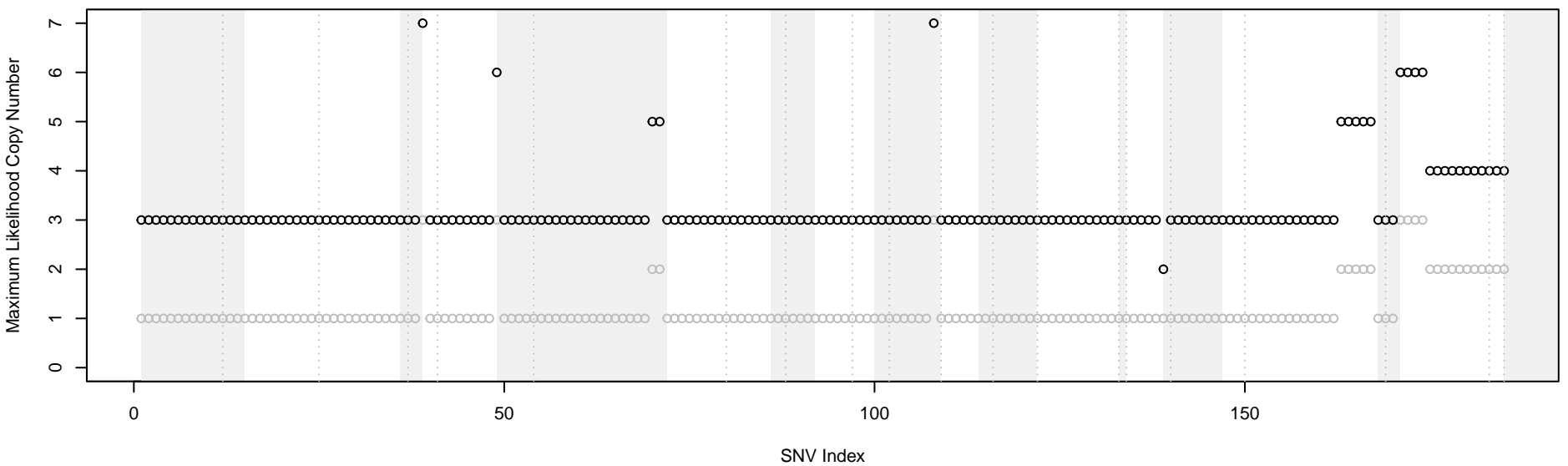
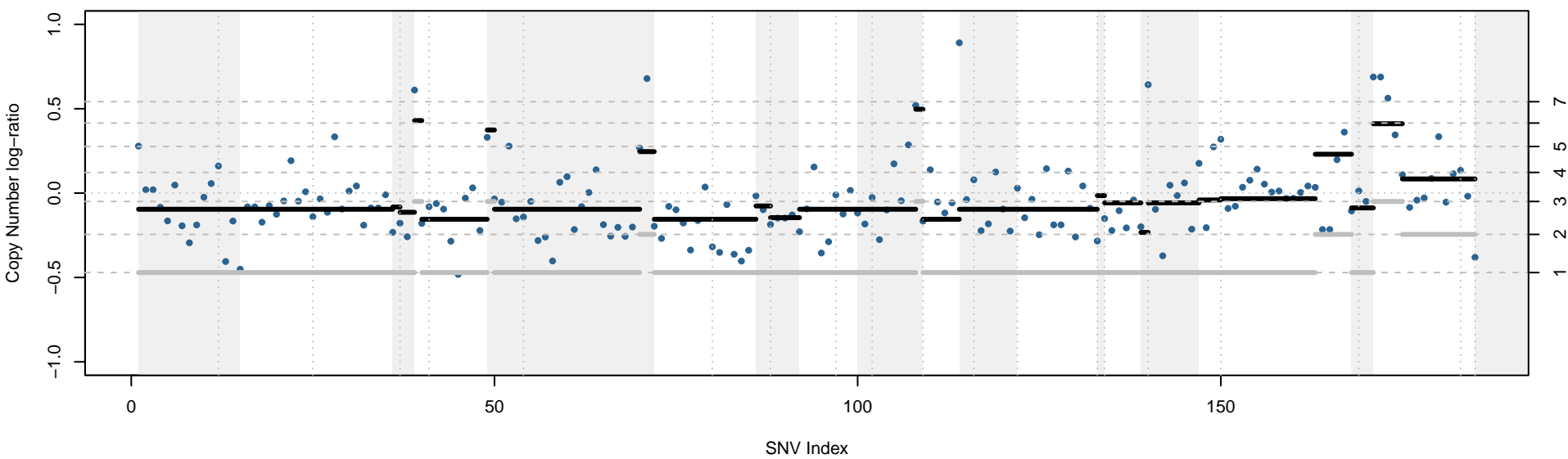
Purity: 0.29 Tumor ploidy: 3.276



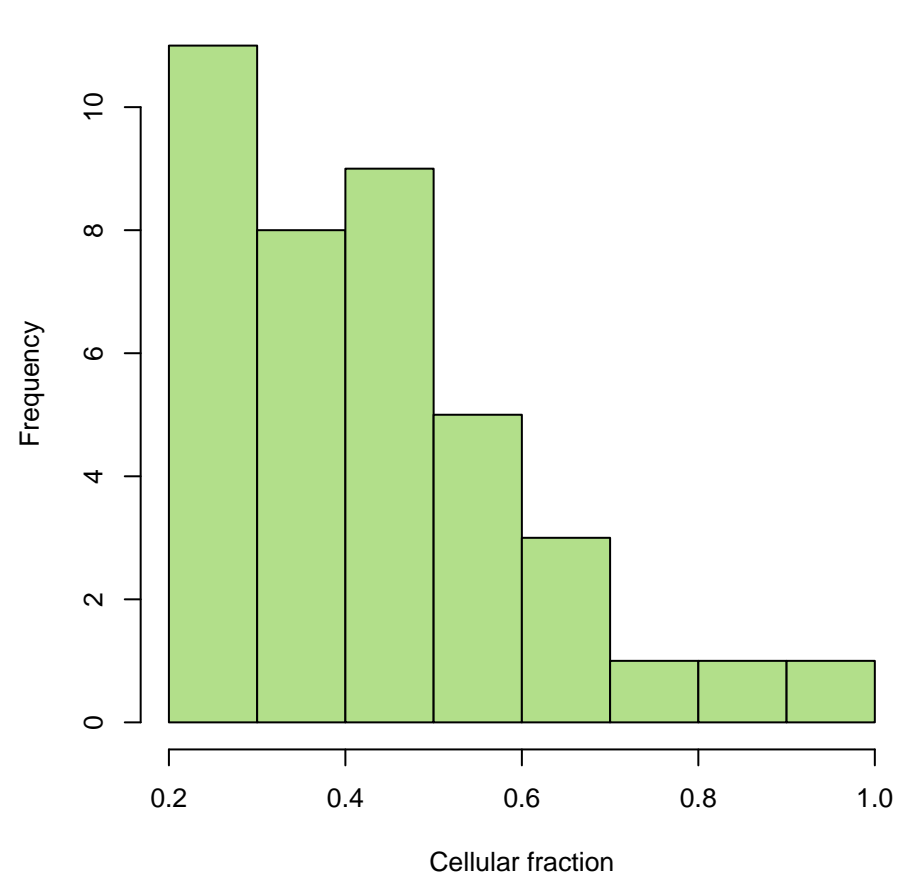
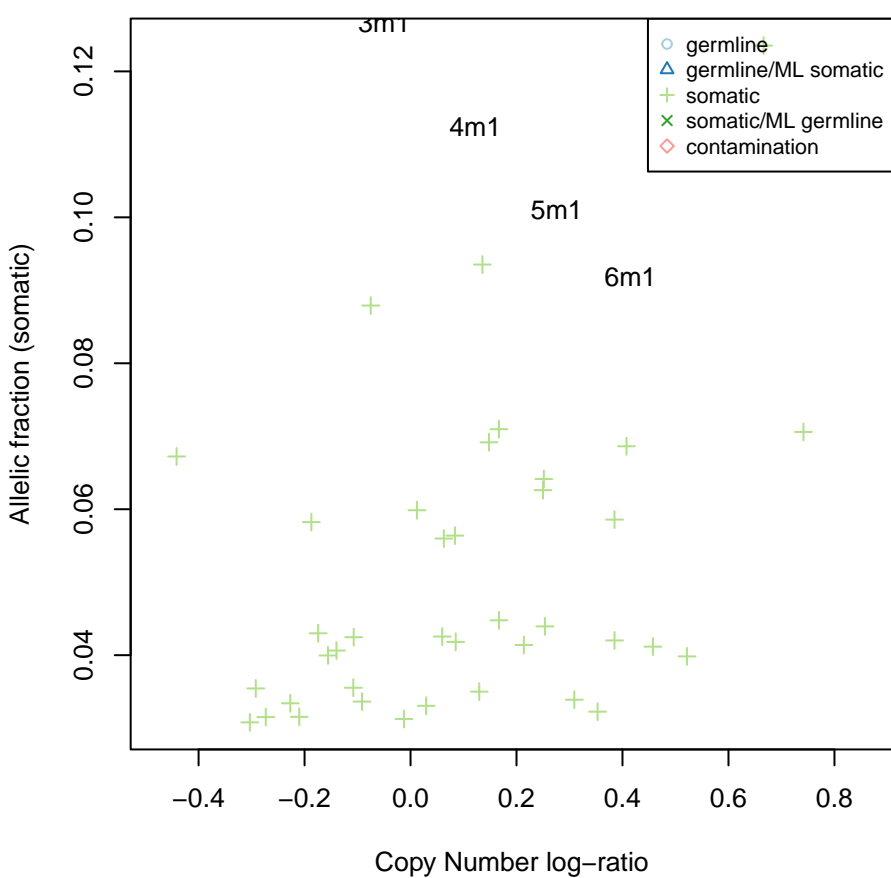
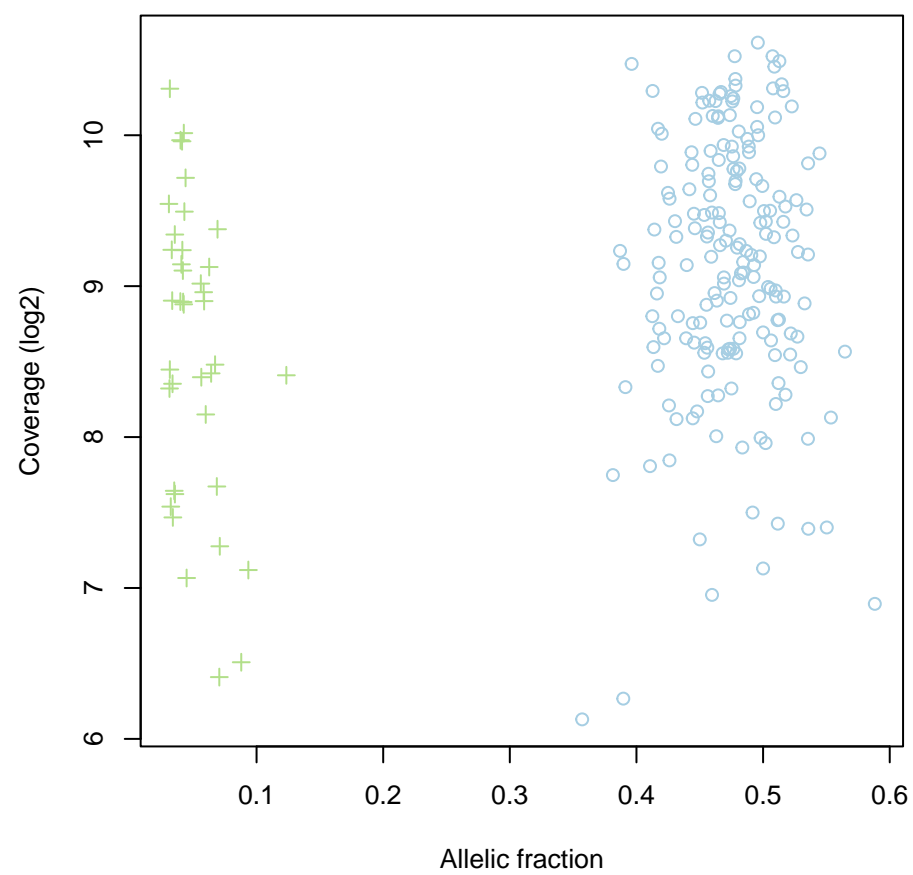
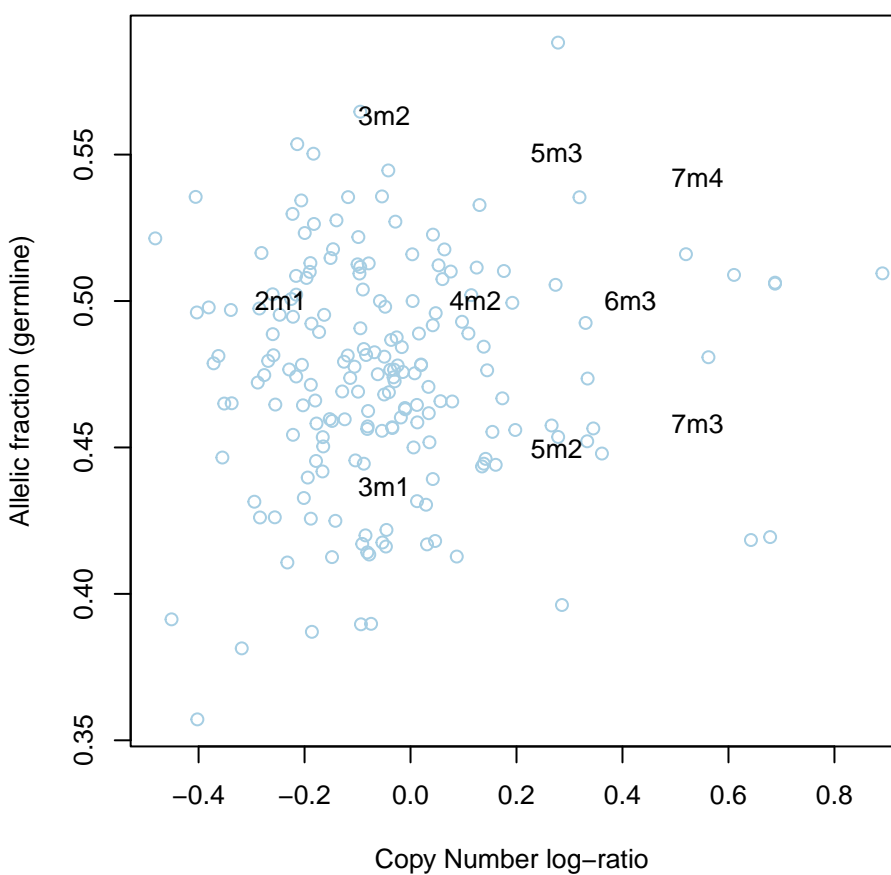
Purity: 0.29 Tumor ploidy: 3.276 SNV log-likelihood: -61.88 GoF: 94.5% Mean coverage: 889;627



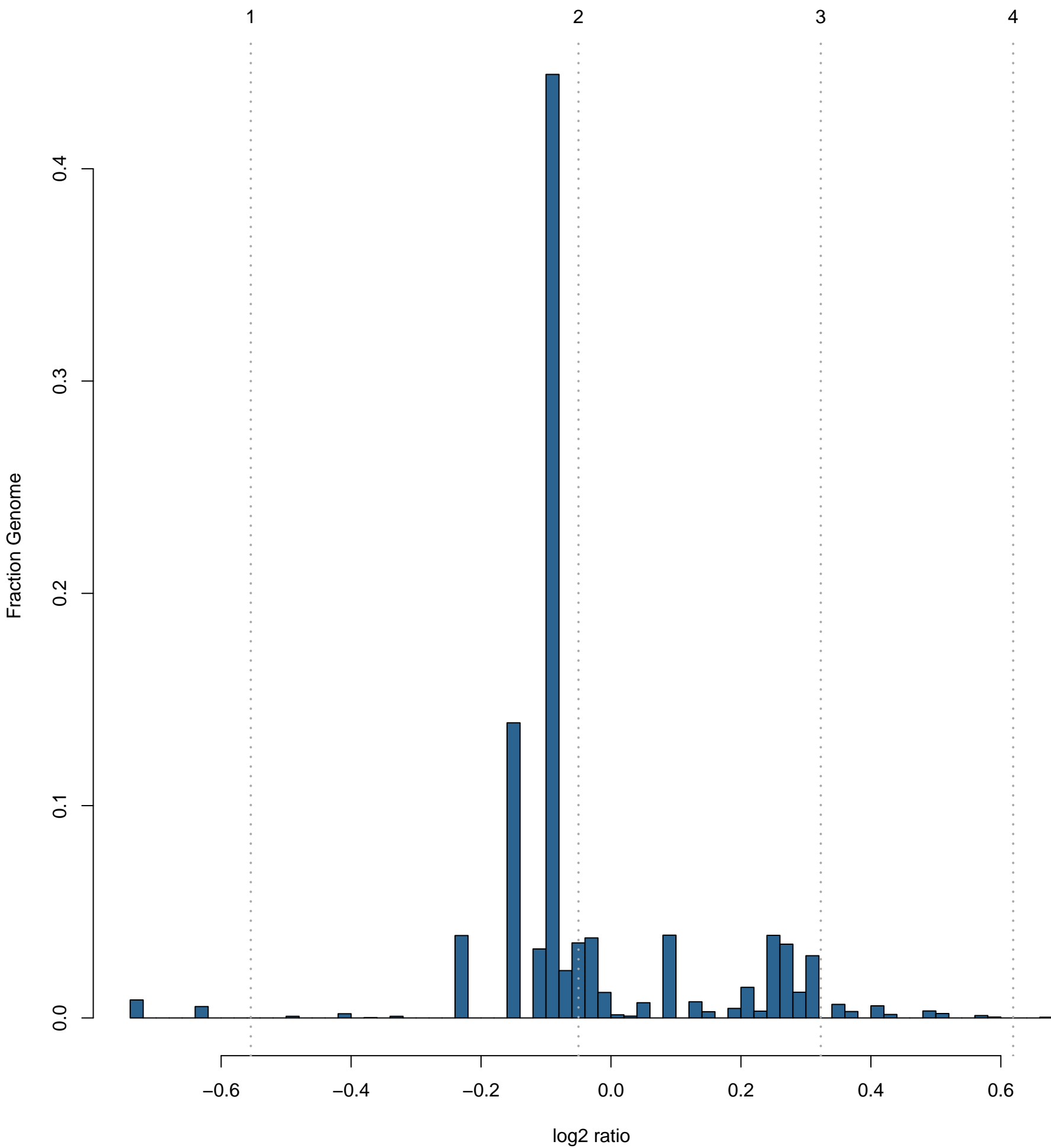
SCNA-fit log-likelihood: -3078.31



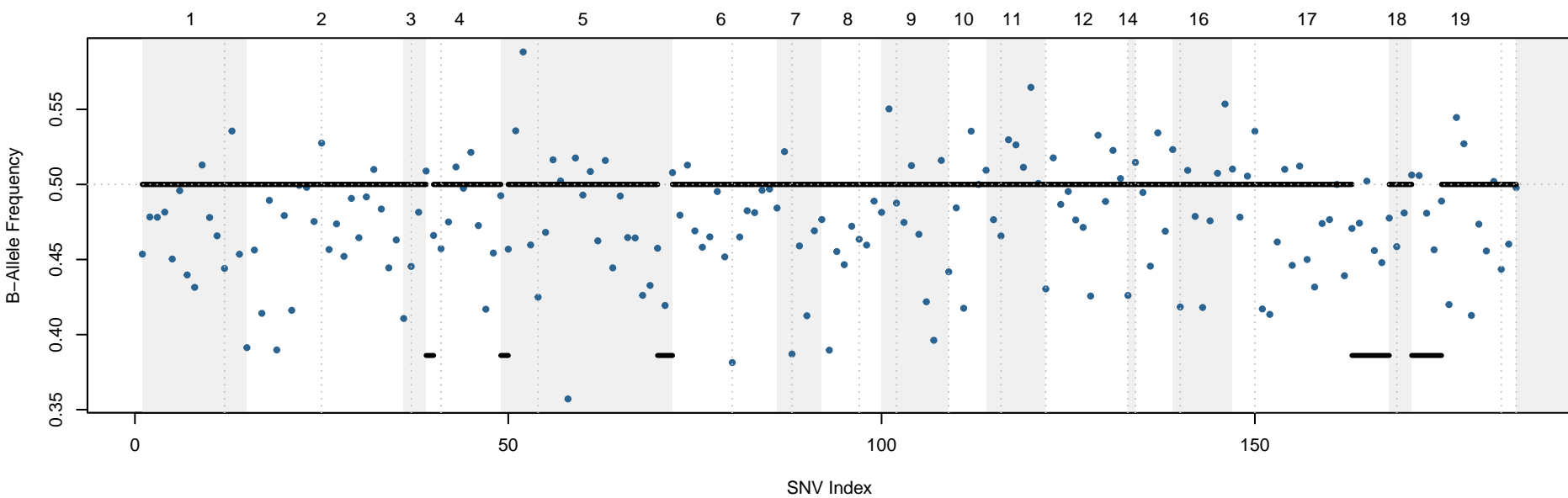




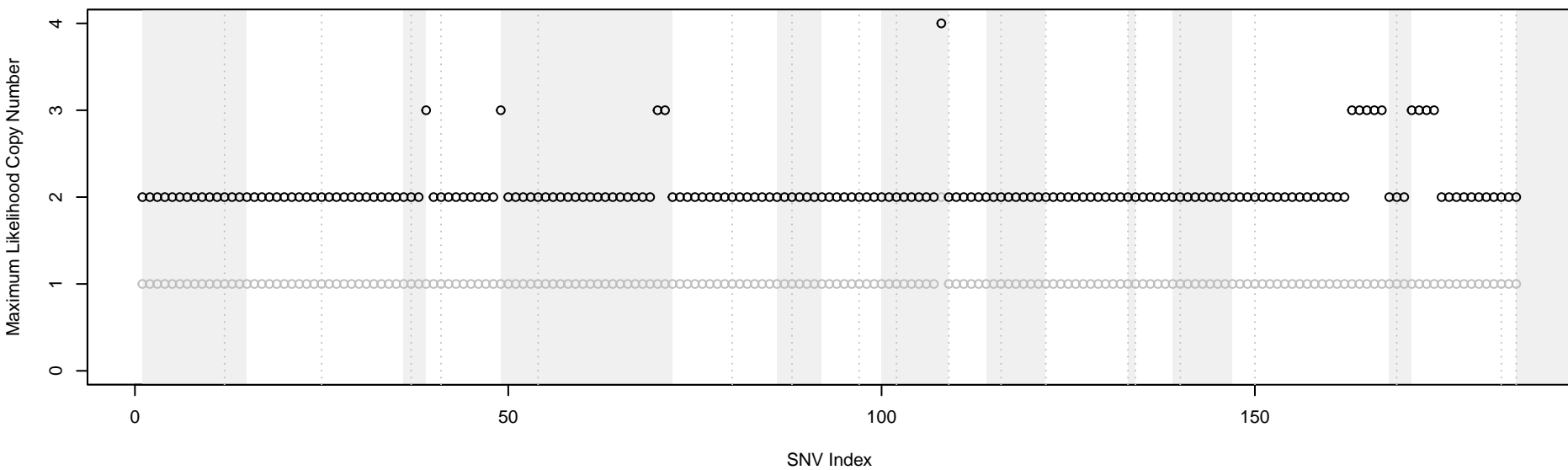
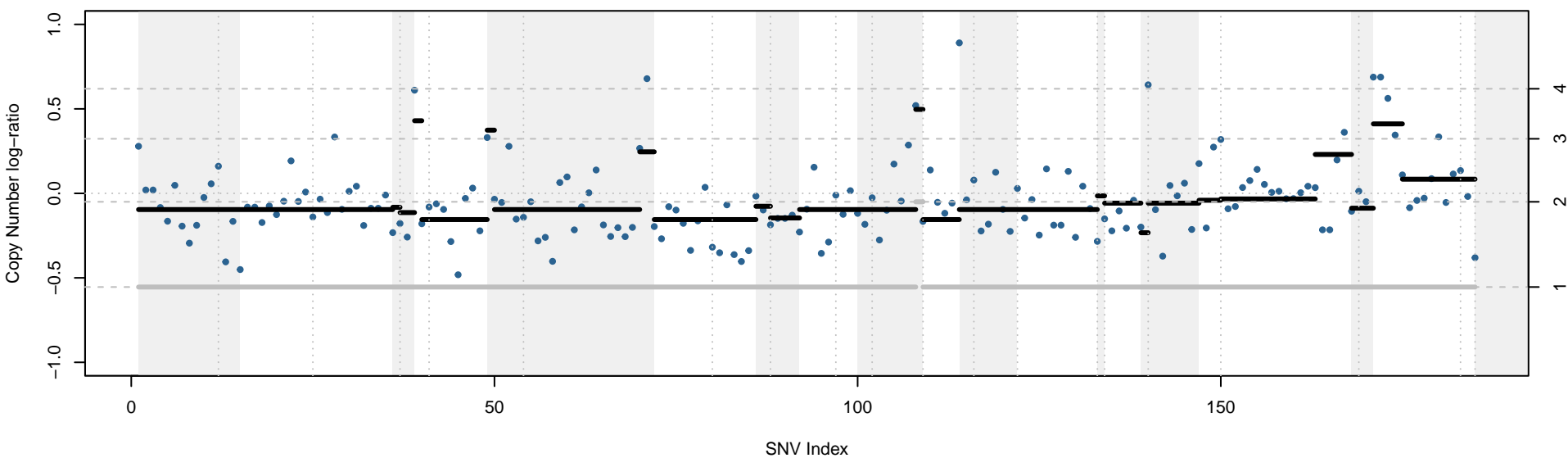
Purity: 0.59 Tumor ploidy: 2.12

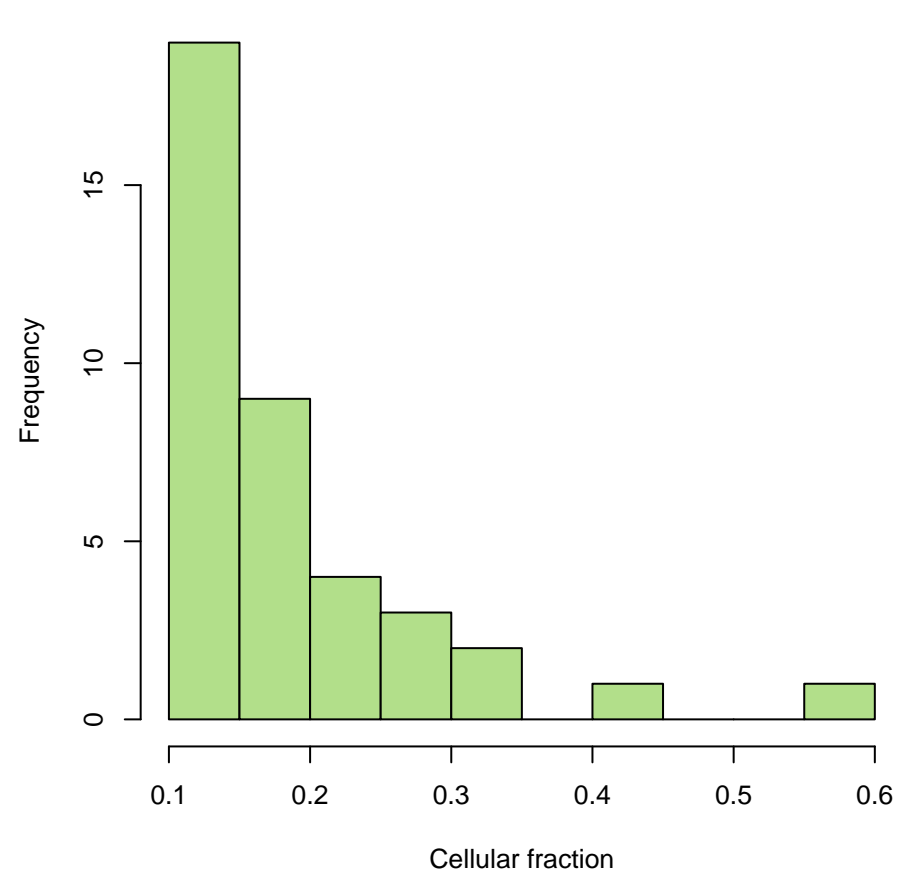
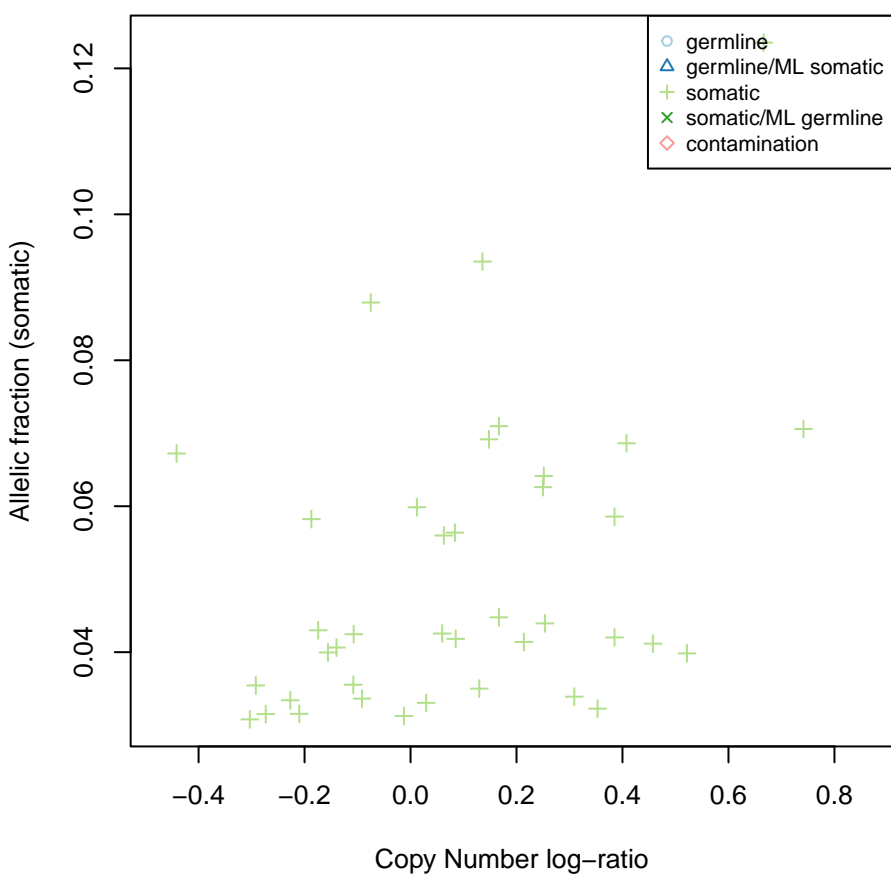
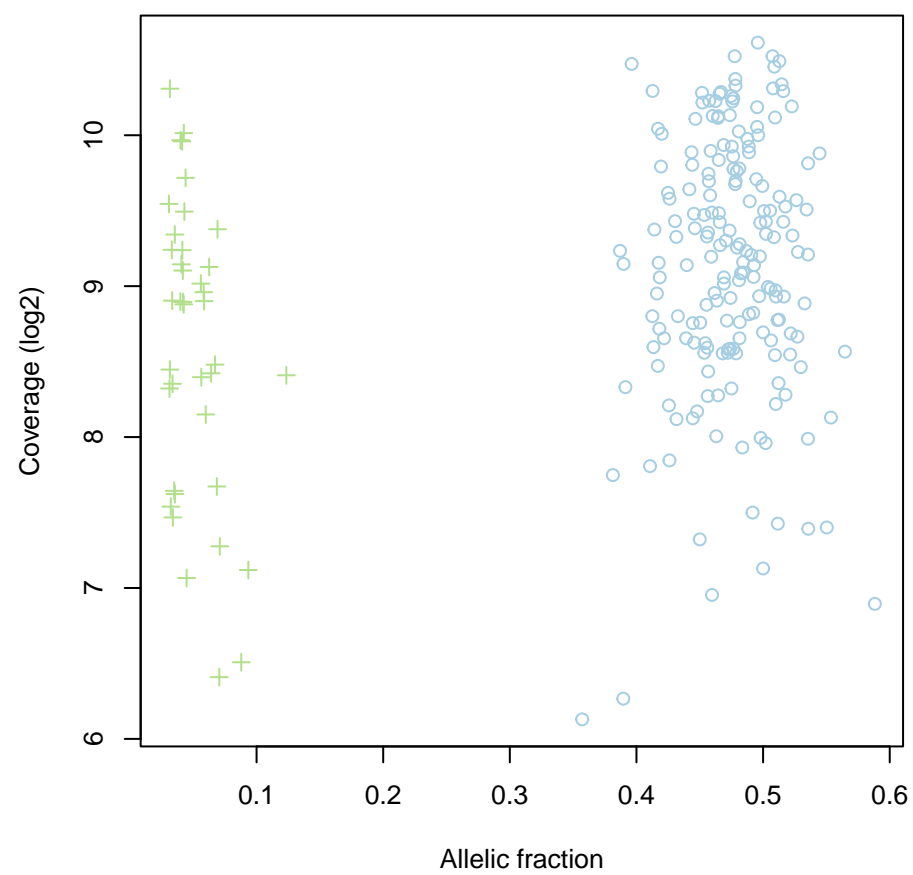
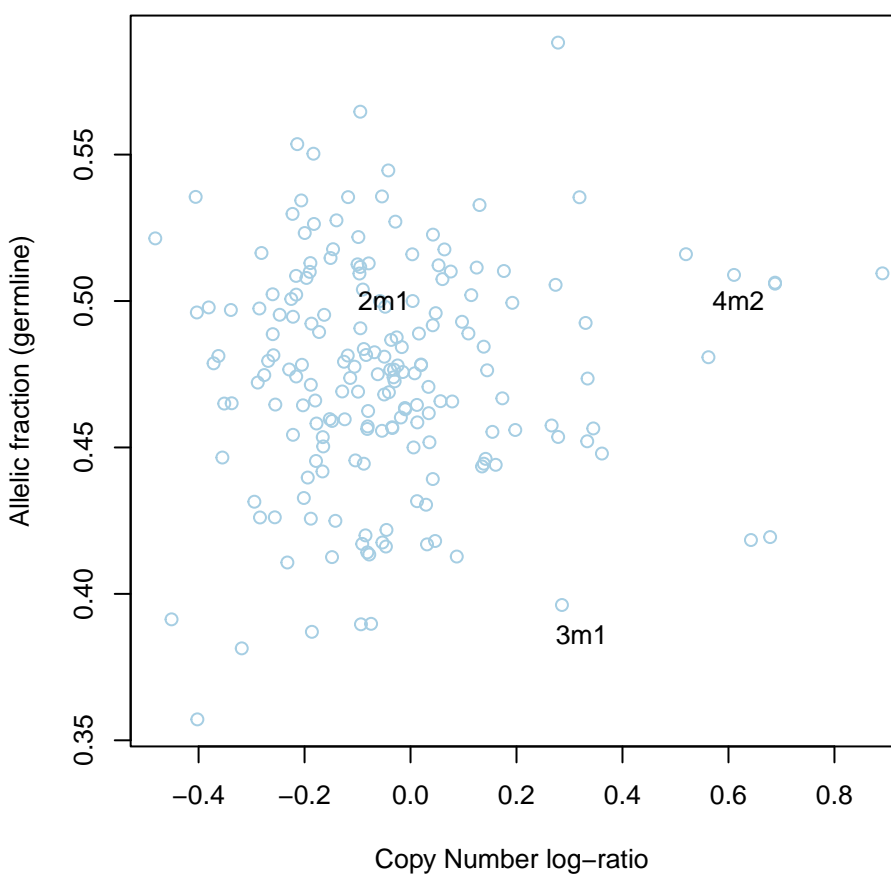


Purity: 0.59 Tumor ploidy: 2.12 SNV log-likelihood: -58.97 GoF: 73.2% Mean coverage: 889,627

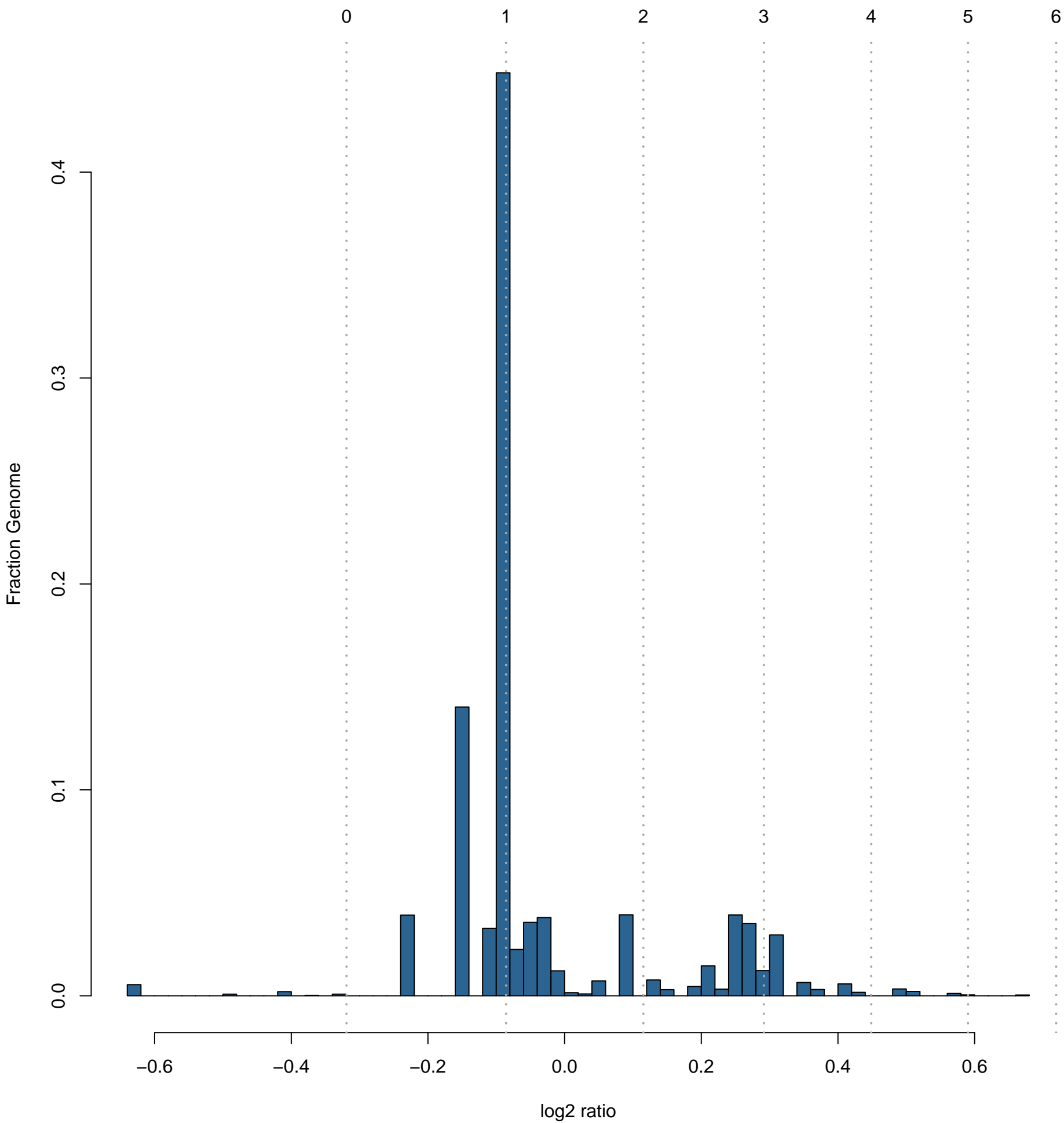


SCNA-fit log-likelihood: -3266.98

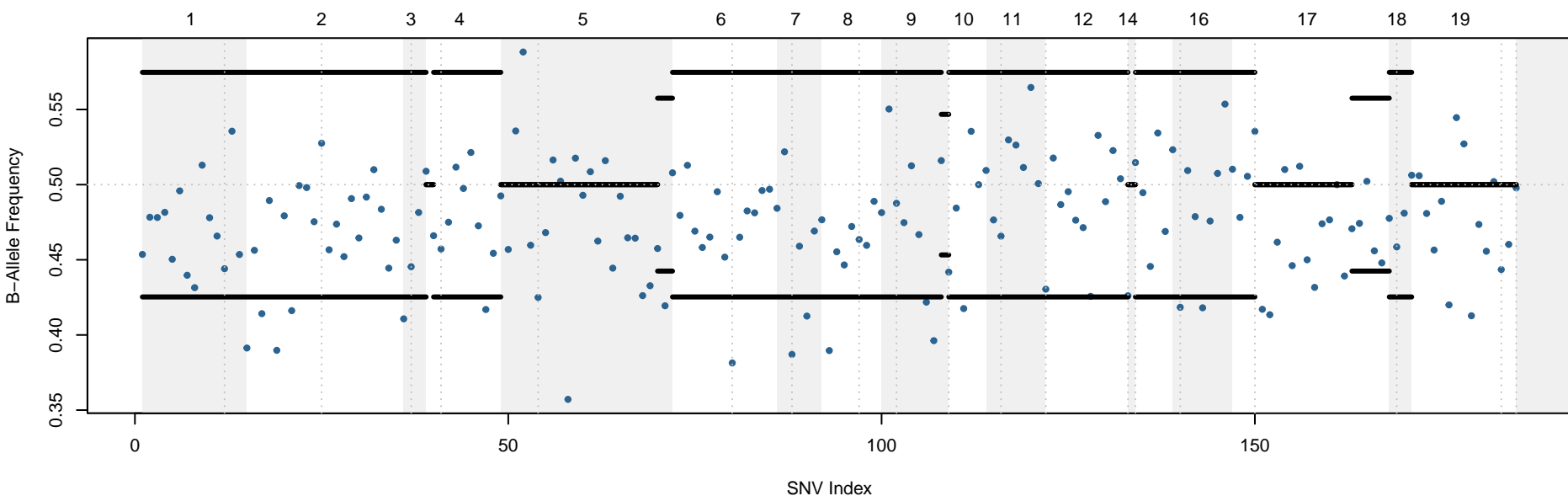




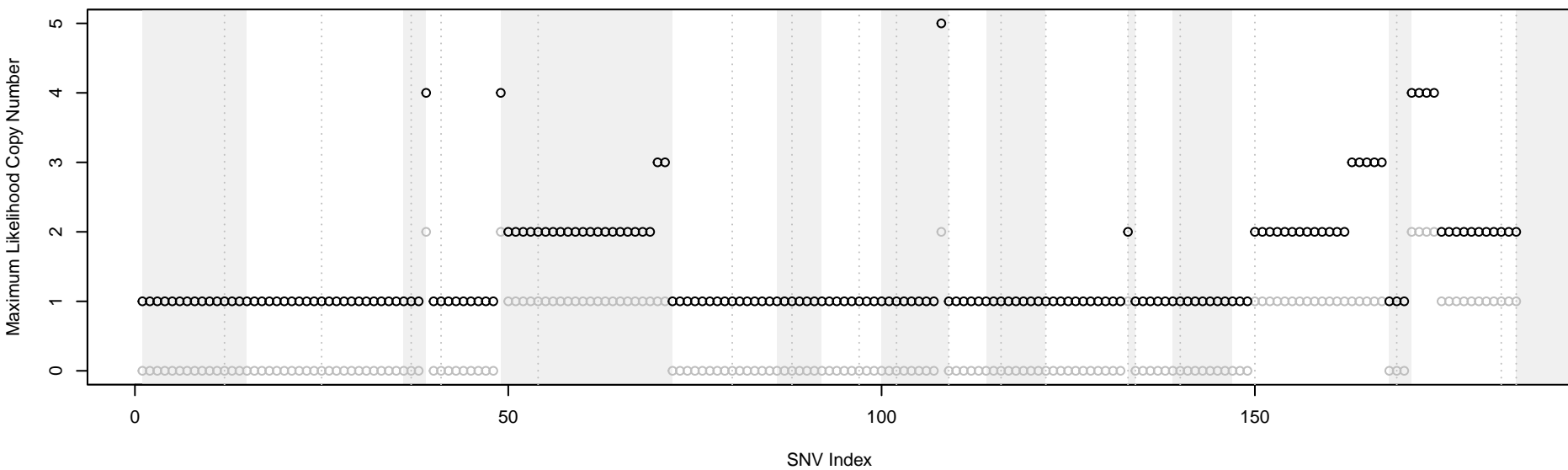
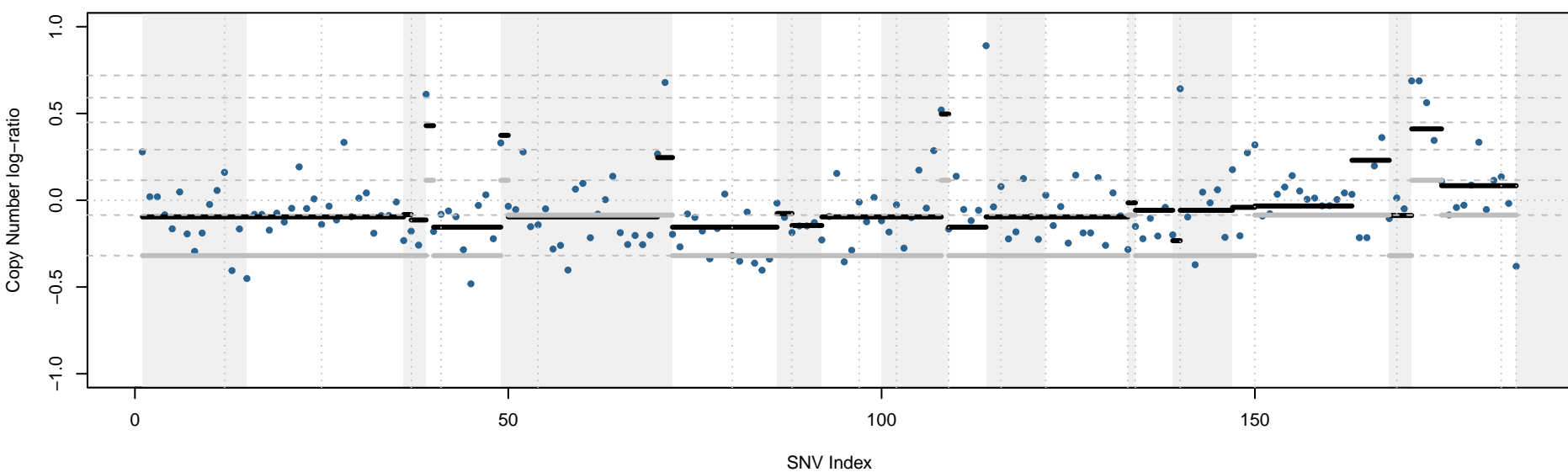
Purity: 0.26 Tumor ploidy: 1.409

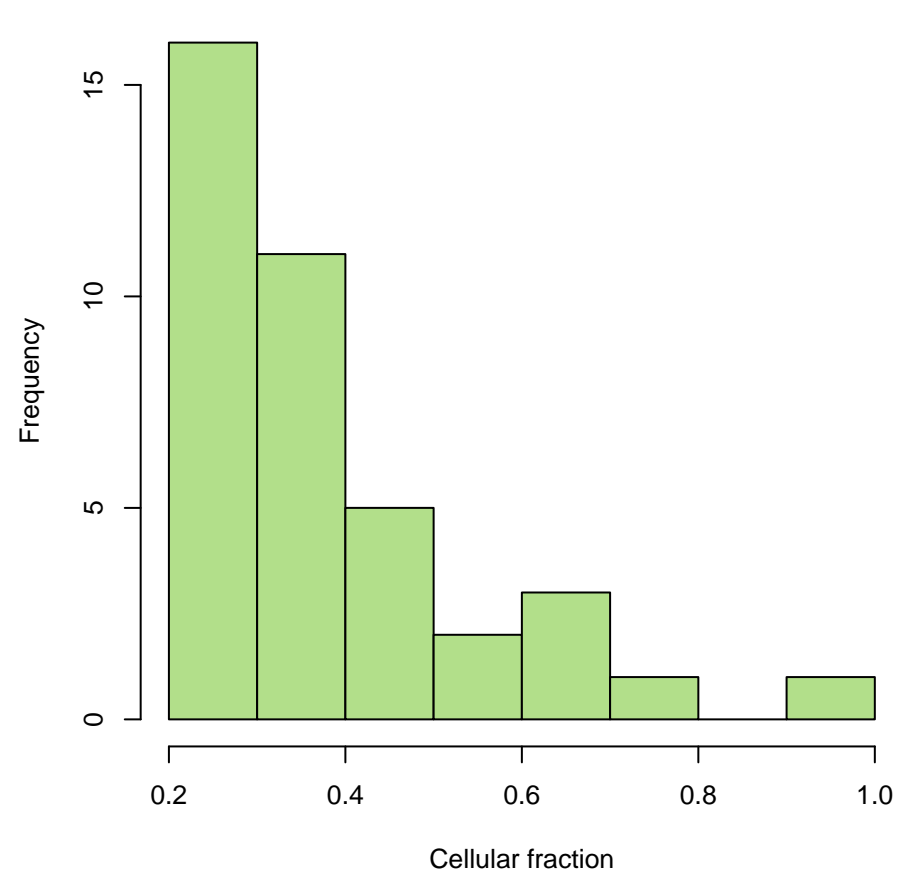
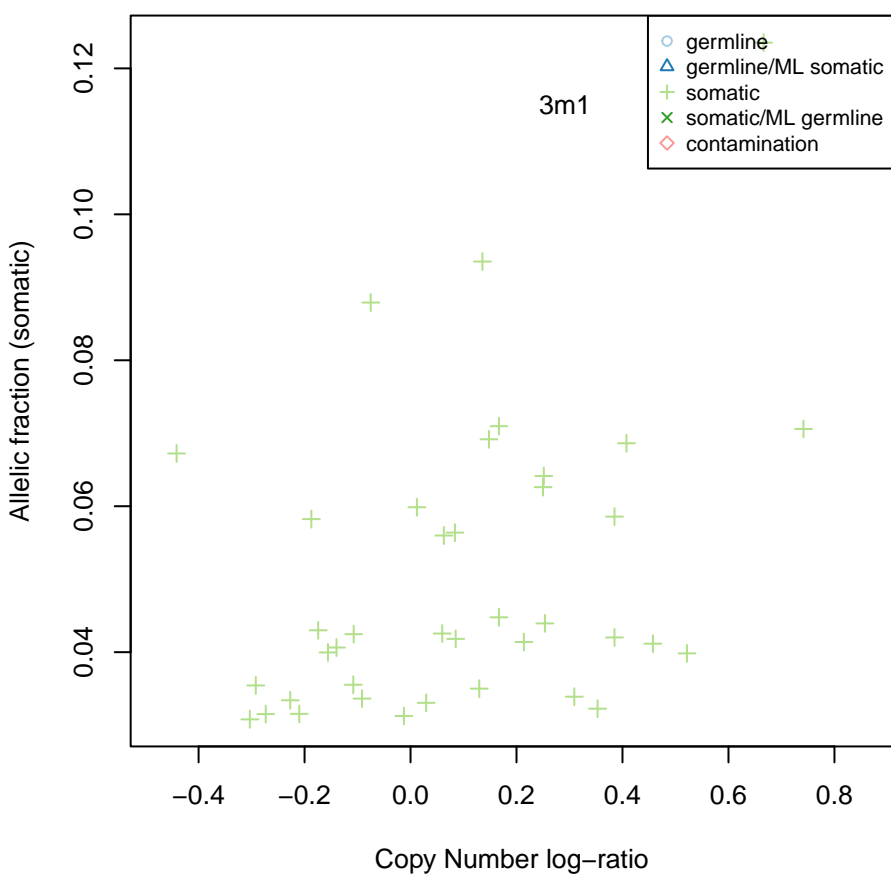
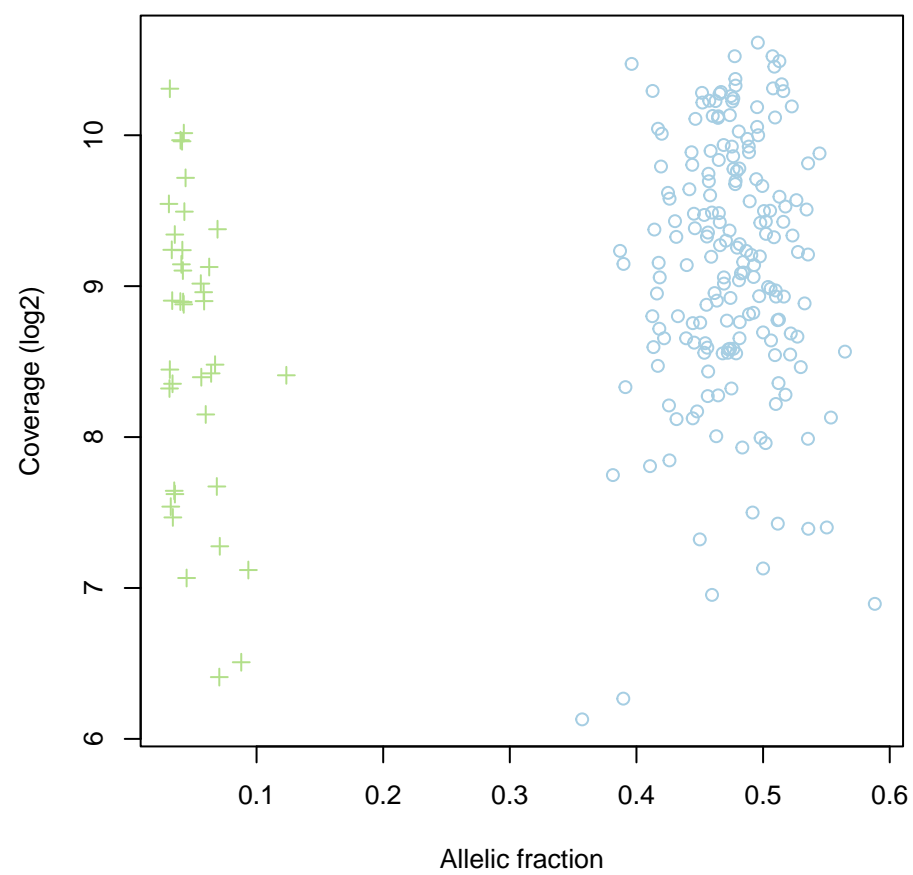
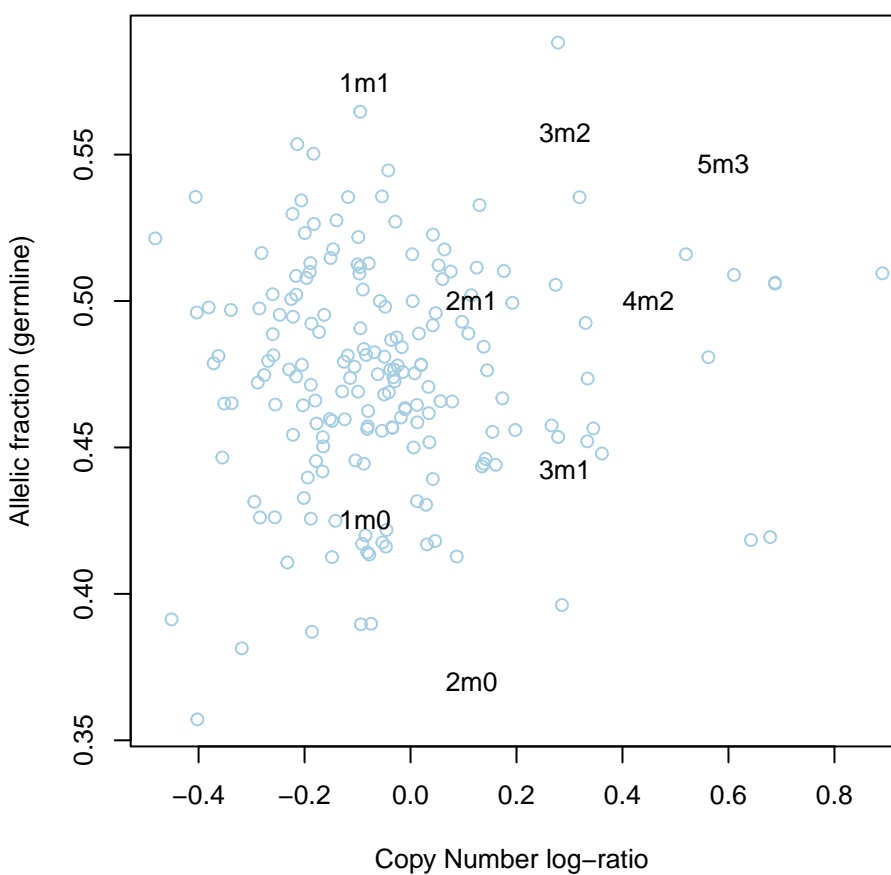


Purity: 0.26 Tumor ploidy: 1.409 SNV log-likelihood: -114.72 GoF: 91.7% Mean coverage: 889,627

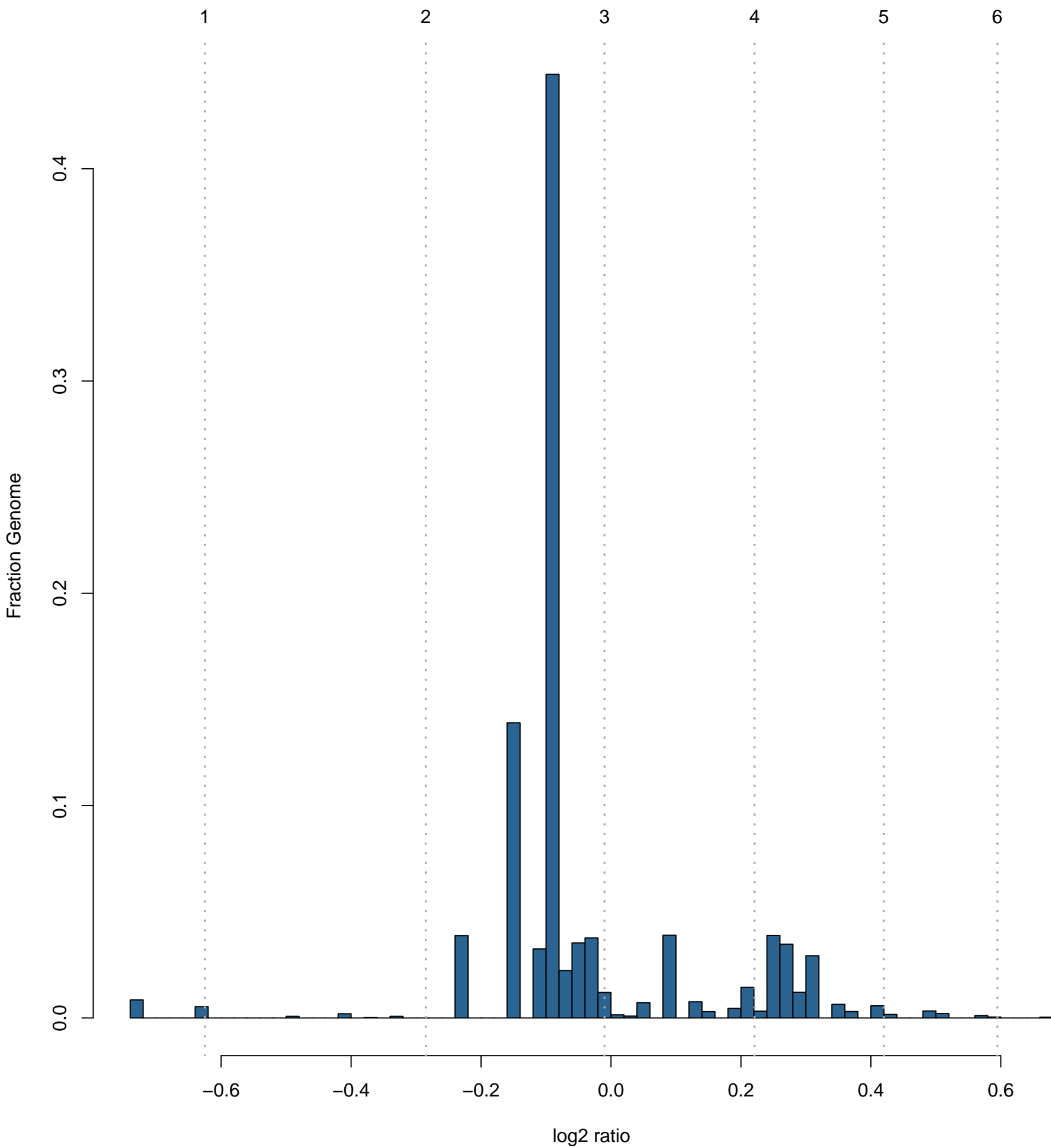


SCNA-fit log-likelihood: -3449.15



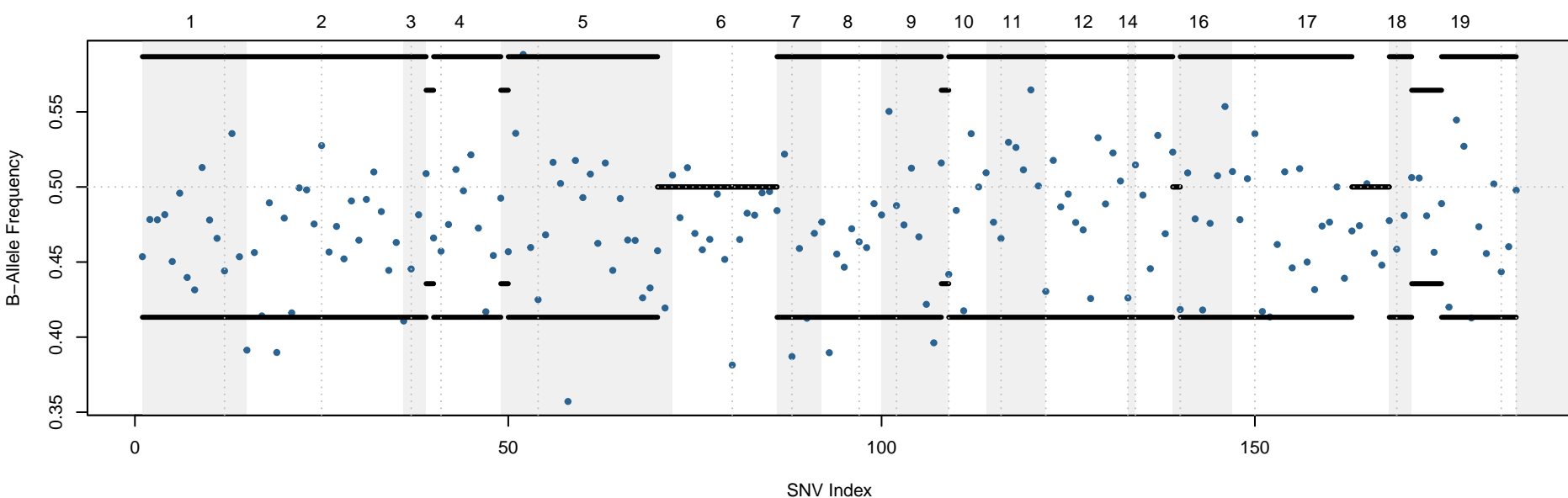


Purity: 0.42 Tumor ploidy: 3.04

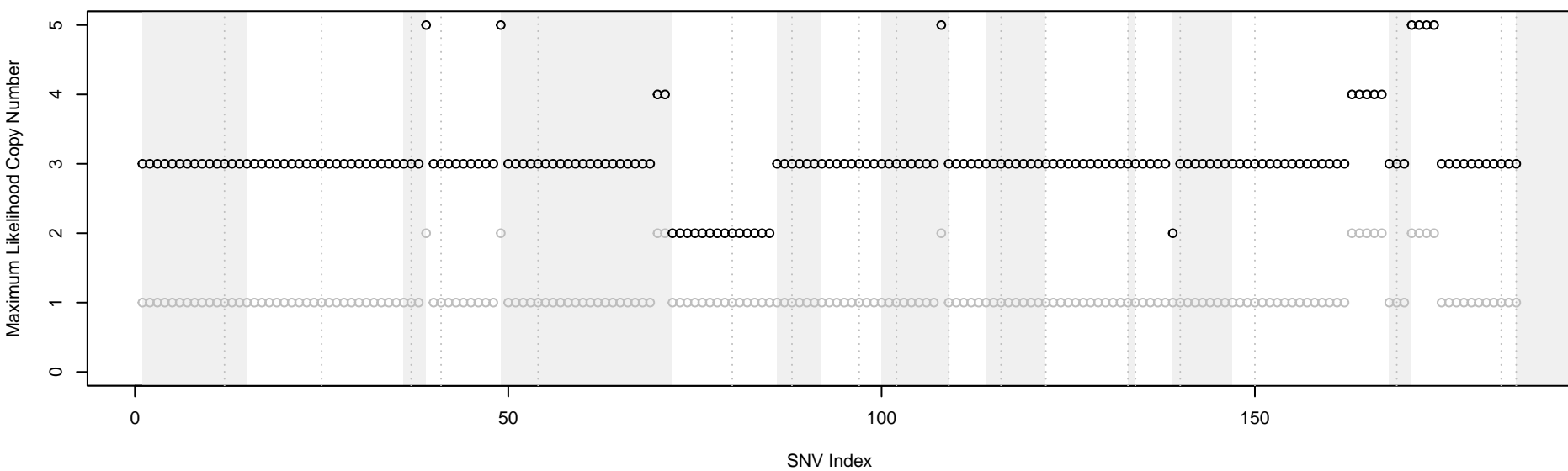
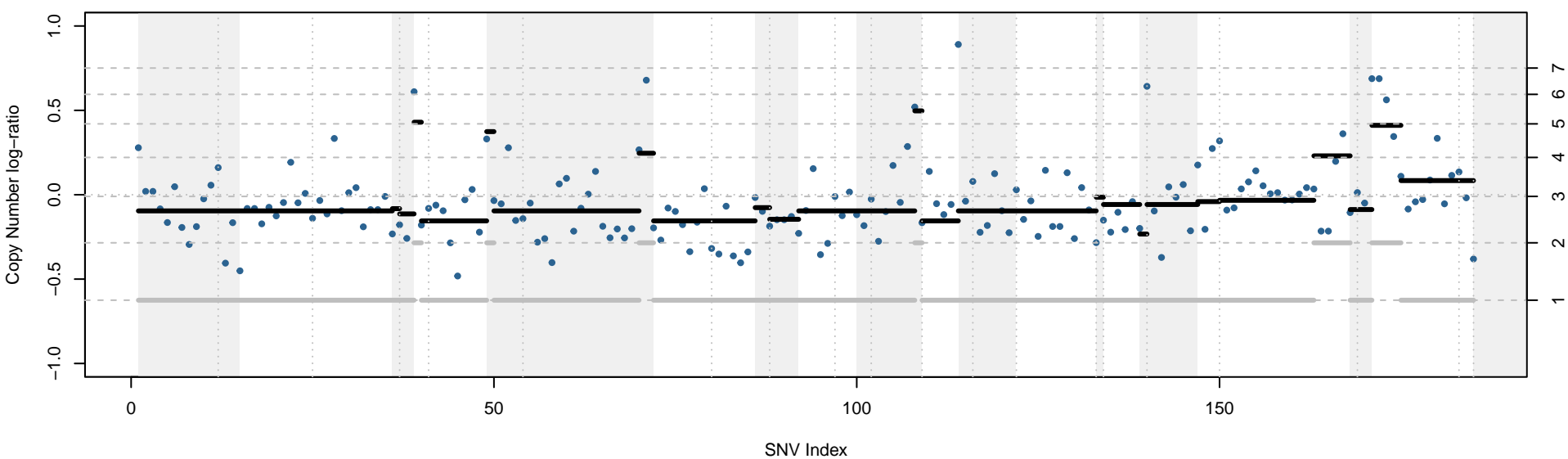


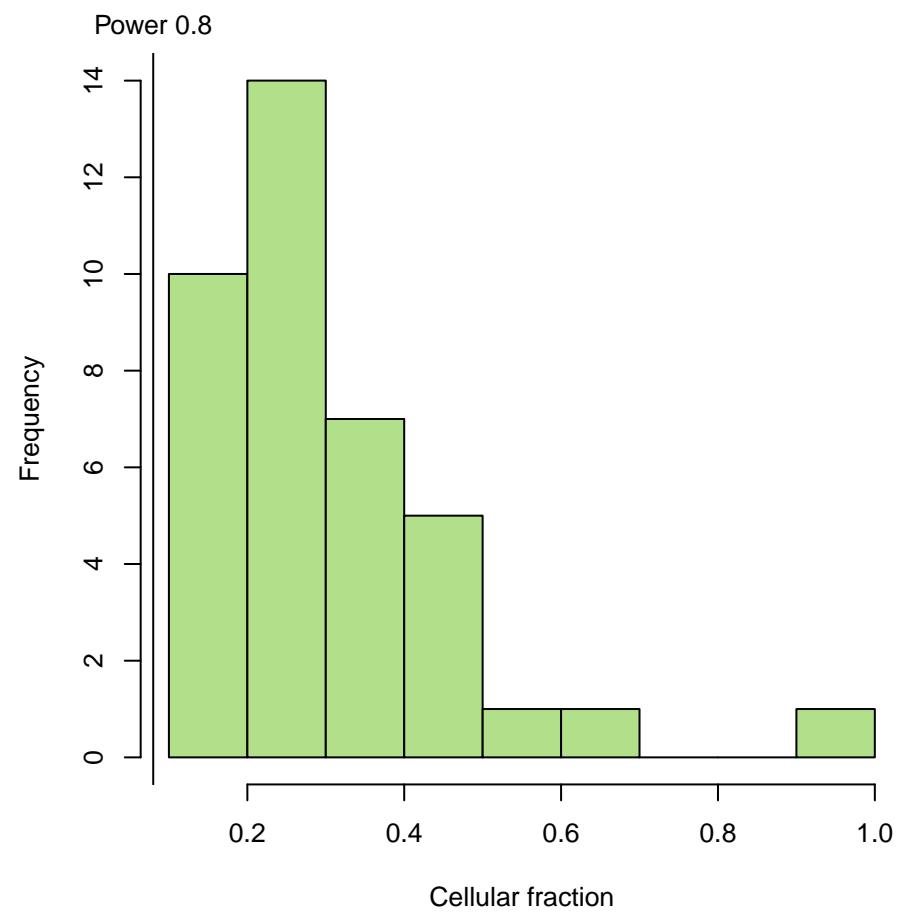
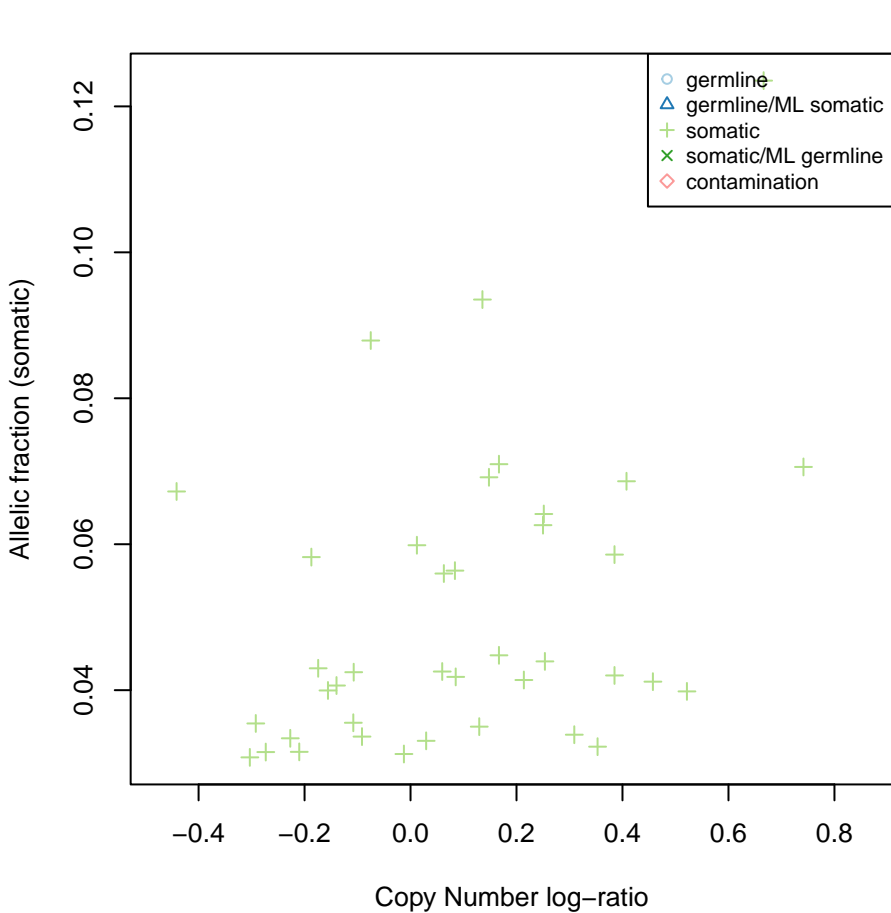
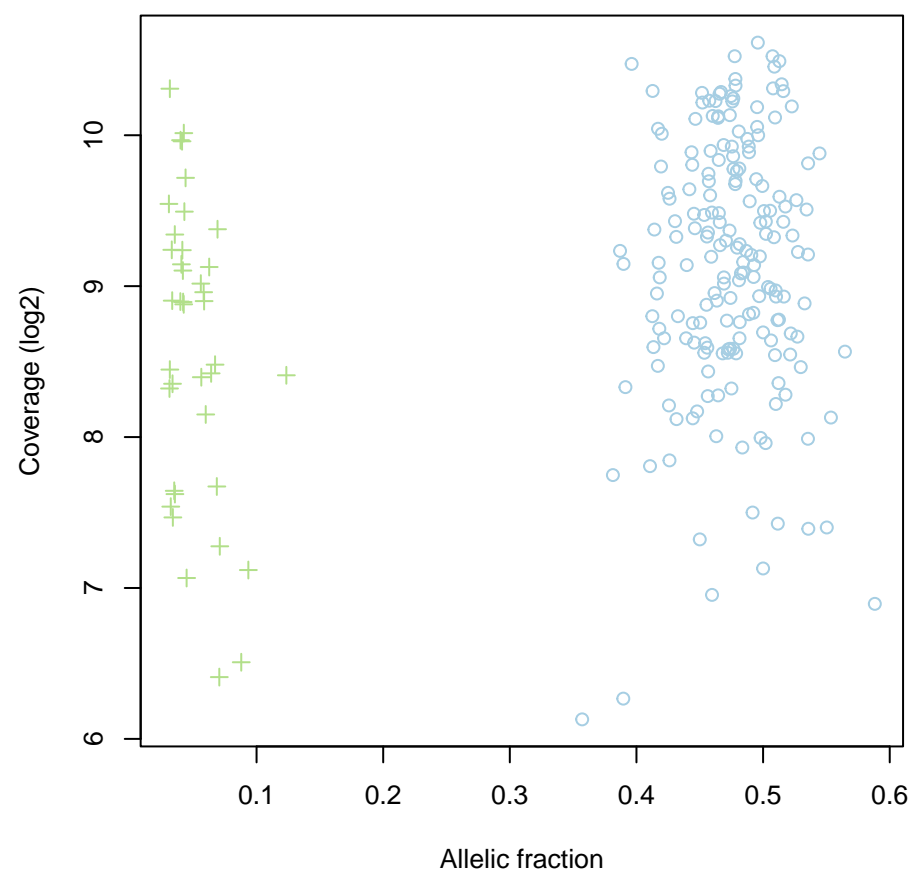
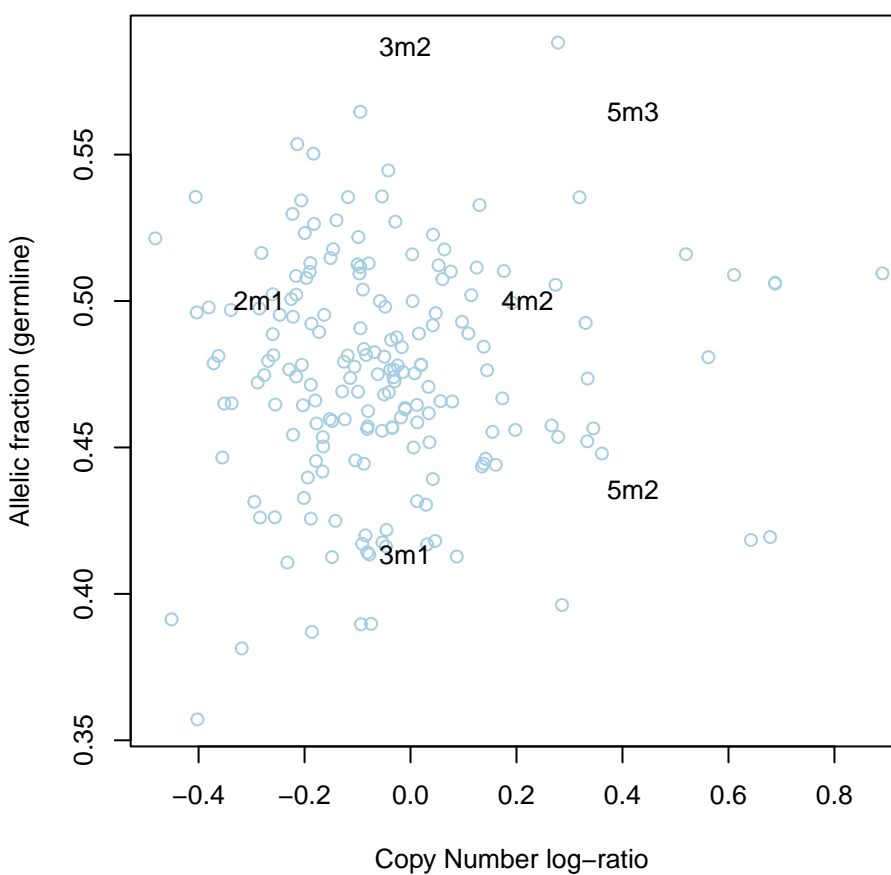


Purity: 0.42 Tumor ploidy: 3.04 SNV log-likelihood: -234 GoF: 87.3% Mean coverage: 889;627

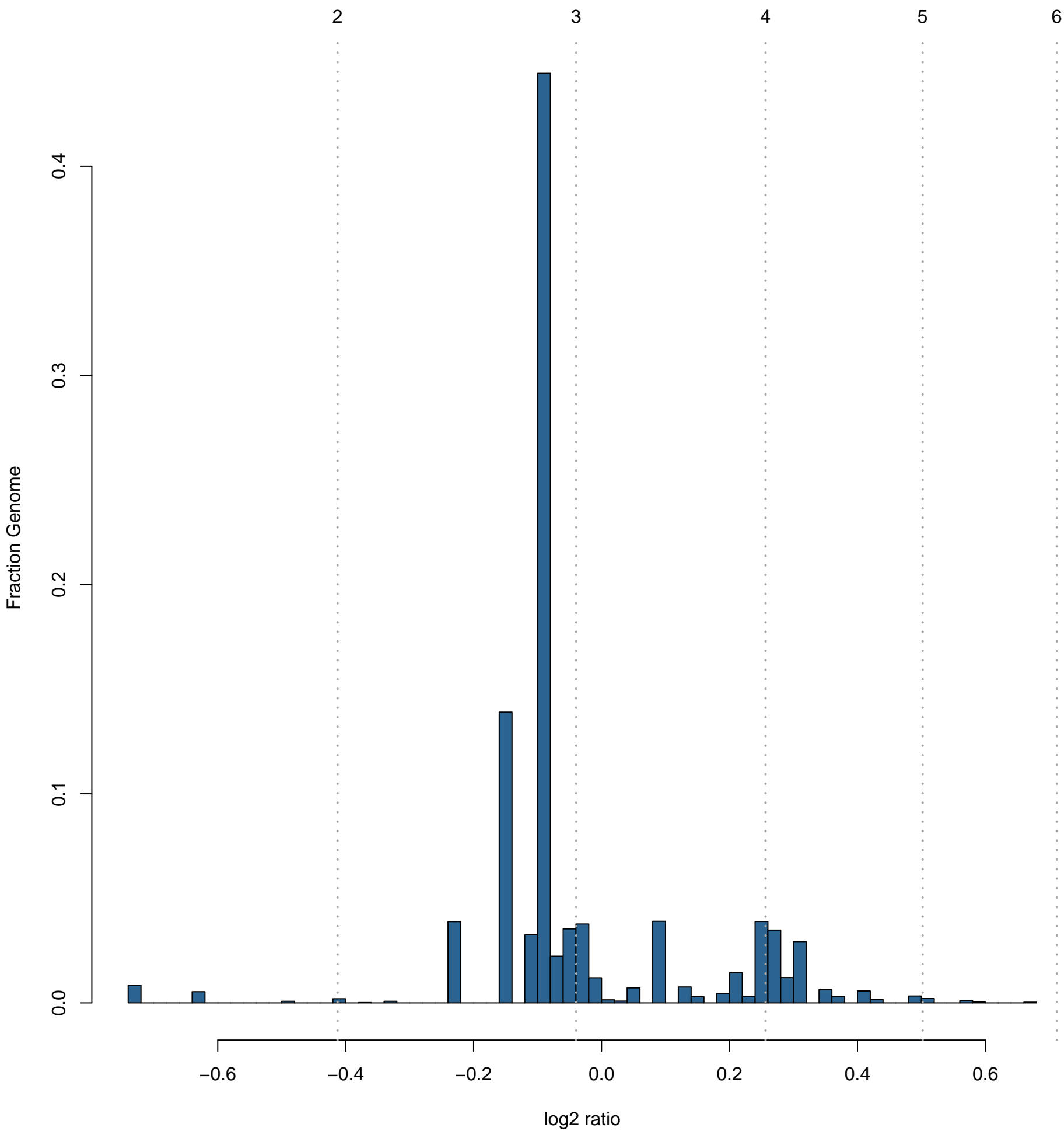


SCNA-fit log-likelihood: -3339.68

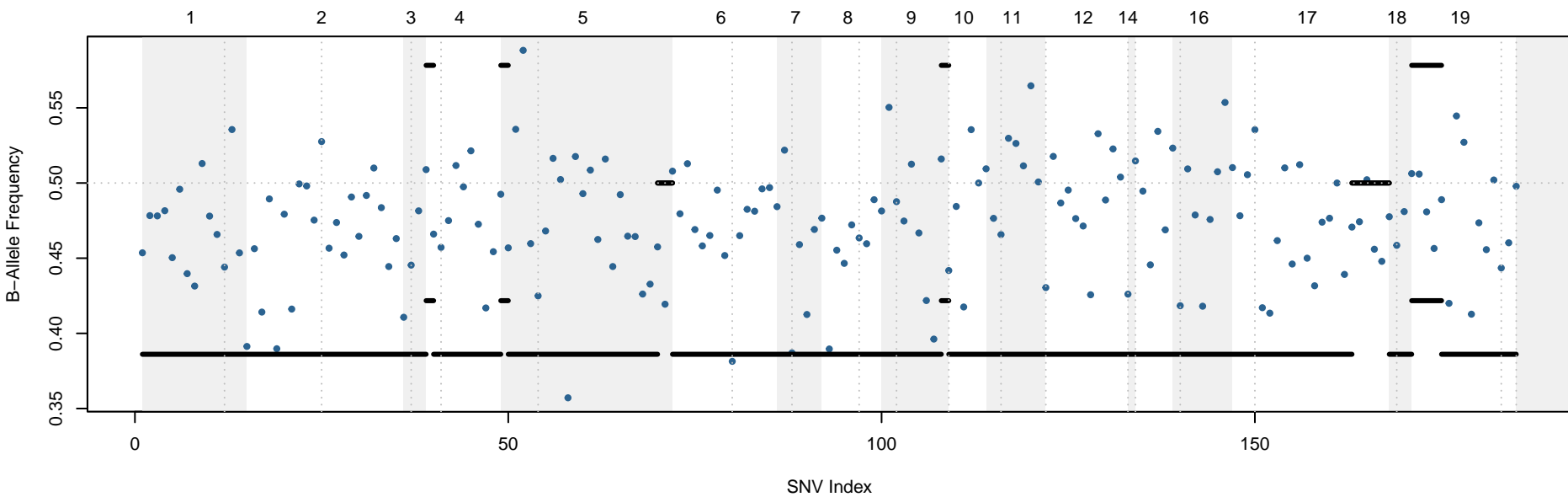




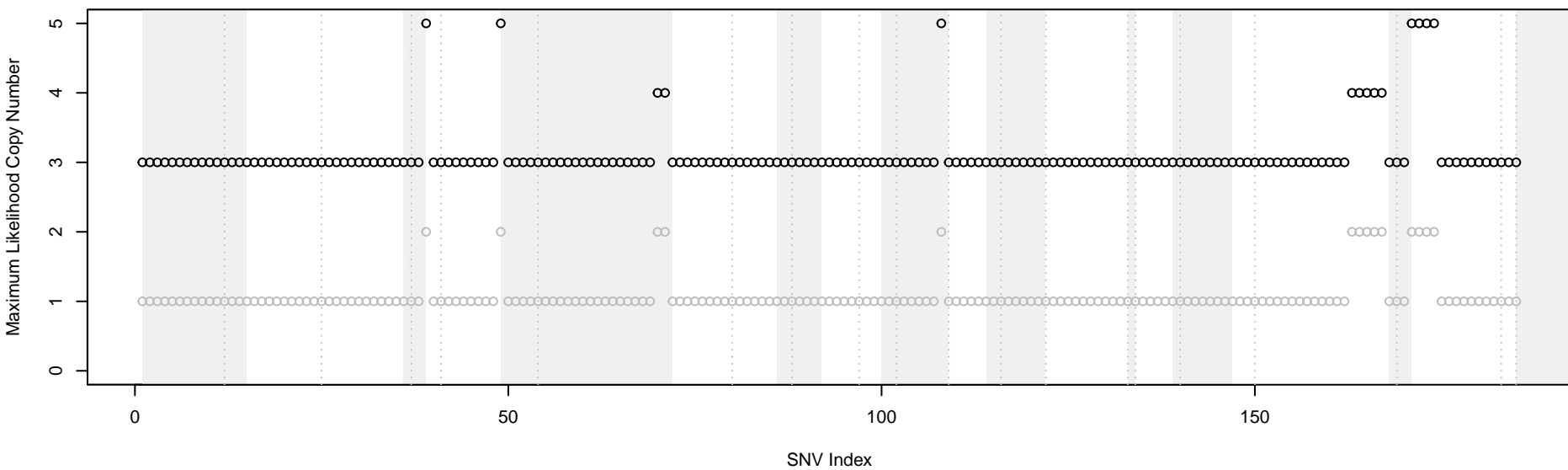
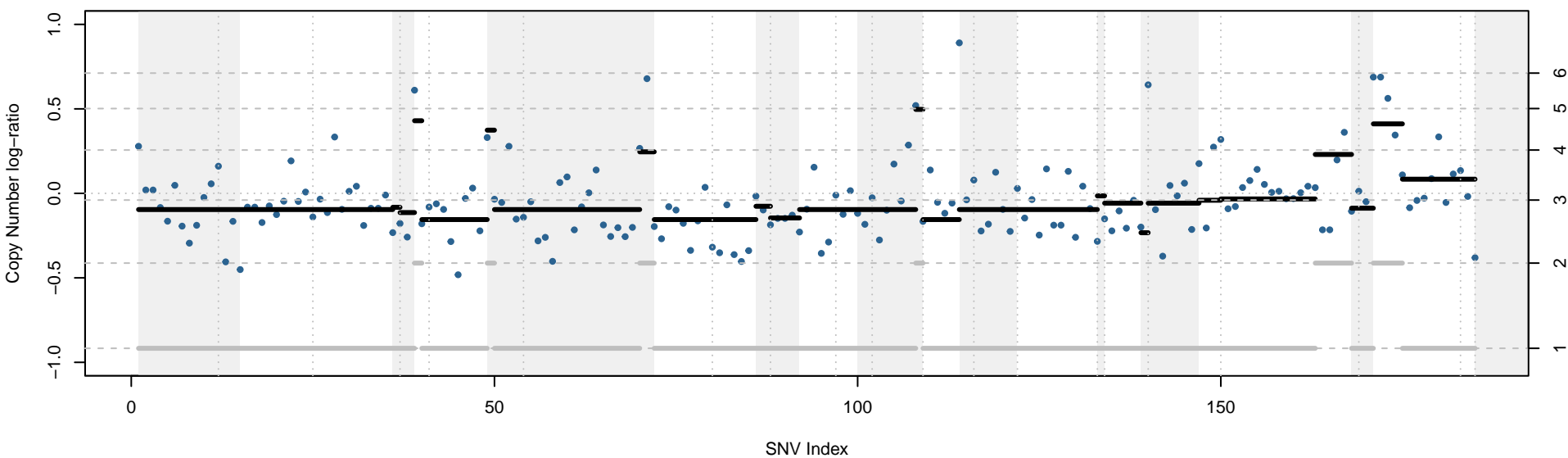
Purity: 0.59 Tumor ploidy: 3.122

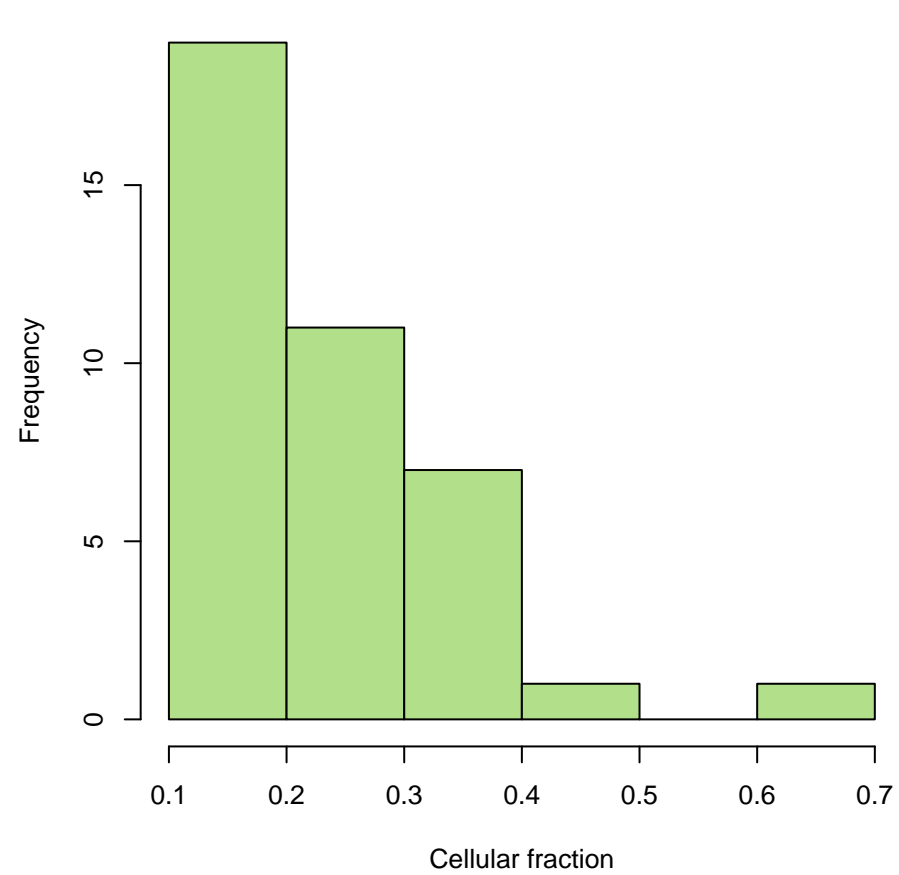
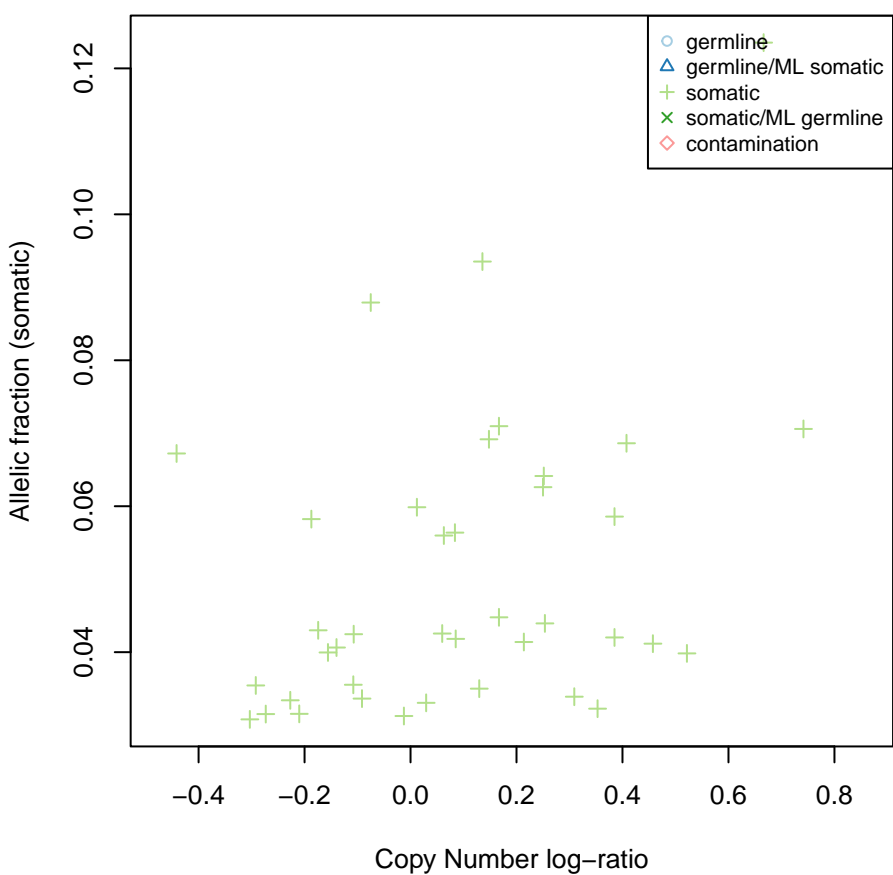
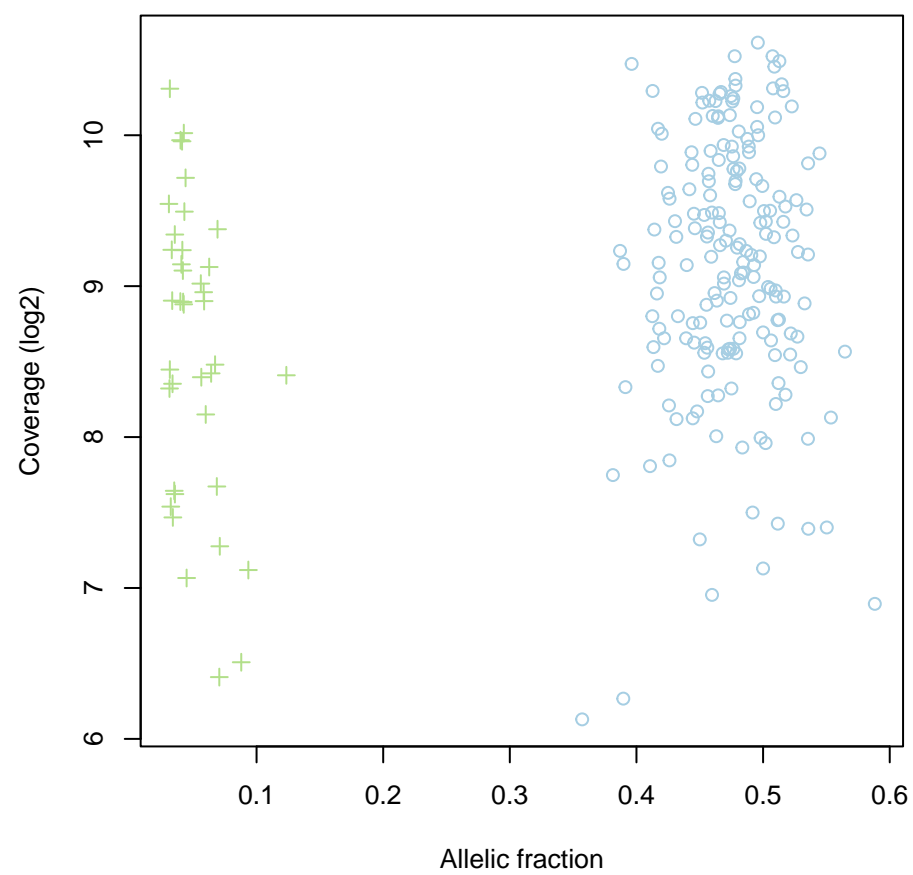
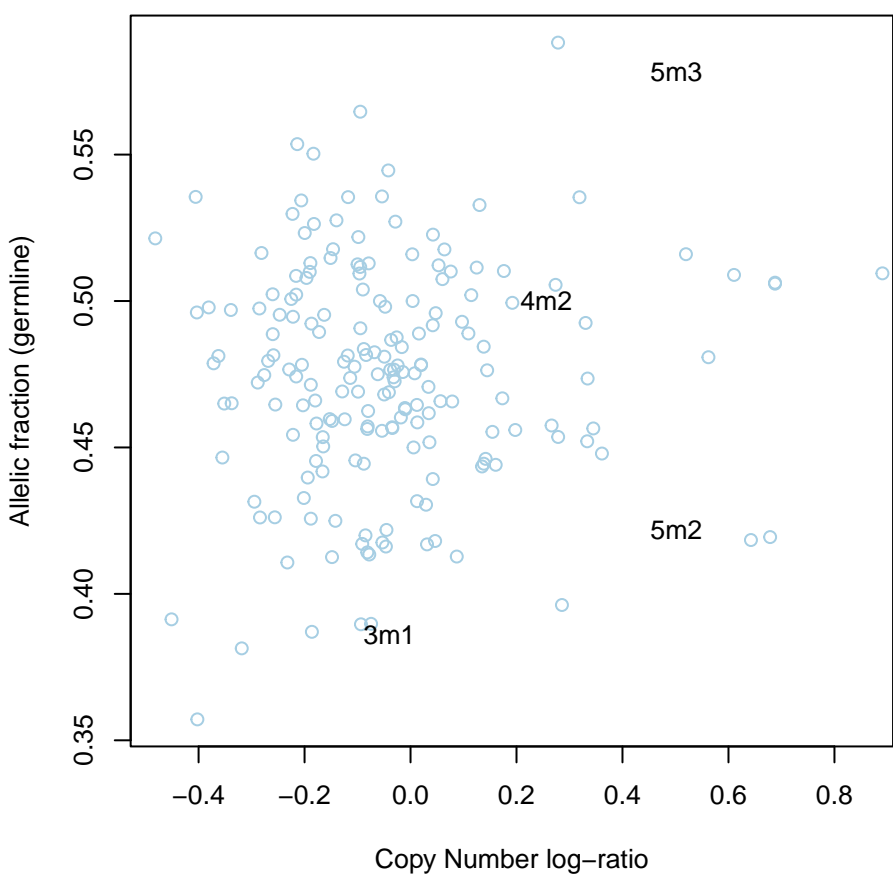


Purity: 0.59 Tumor ploidy: 3.122 SNV log-likelihood: -712.92 GoF: 73.7% Mean coverage: 889,627

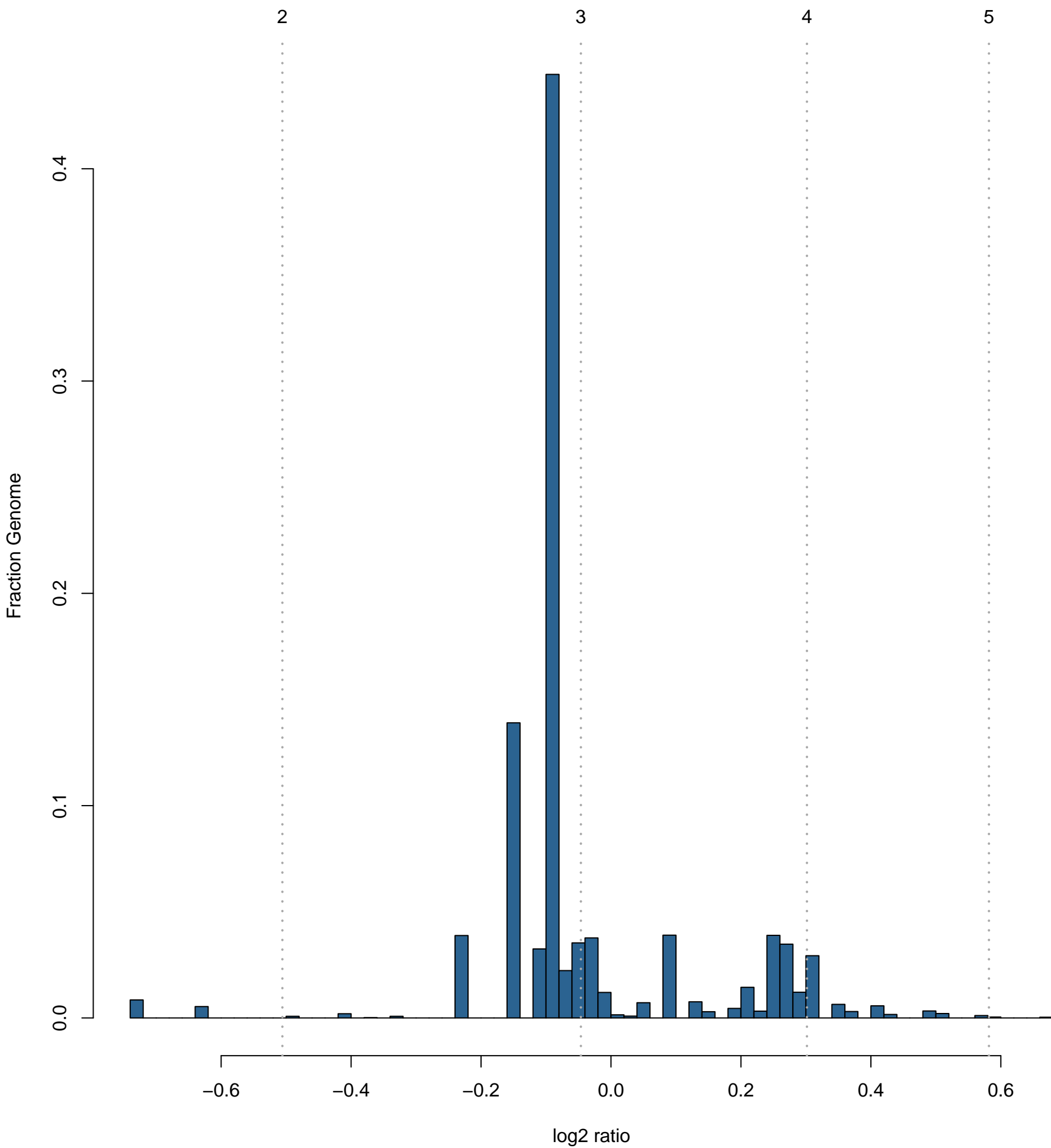


SCNA-fit log-likelihood: -3296.06

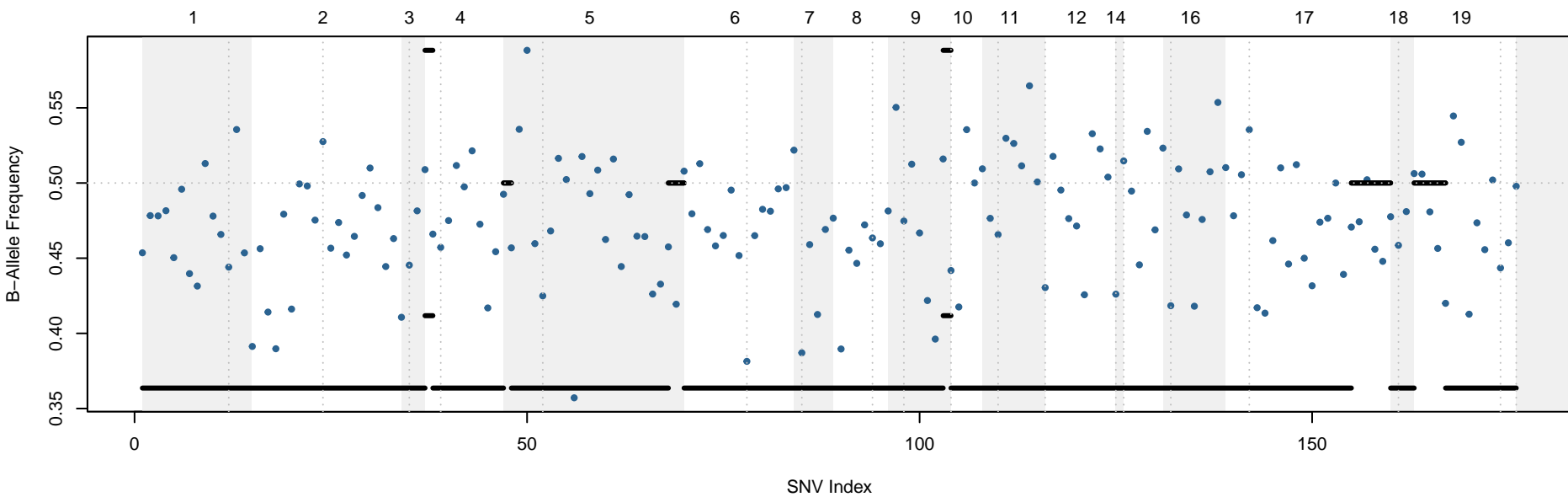




Purity: 0.75 Tumor ploidy: 3.12



Purity: 0.75 Tumor ploidy: 3.12 SNV log-likelihood: -1190.37 GoF: 61% Mean coverage: 889;627



SCNA-fit log-likelihood: -3260.84

