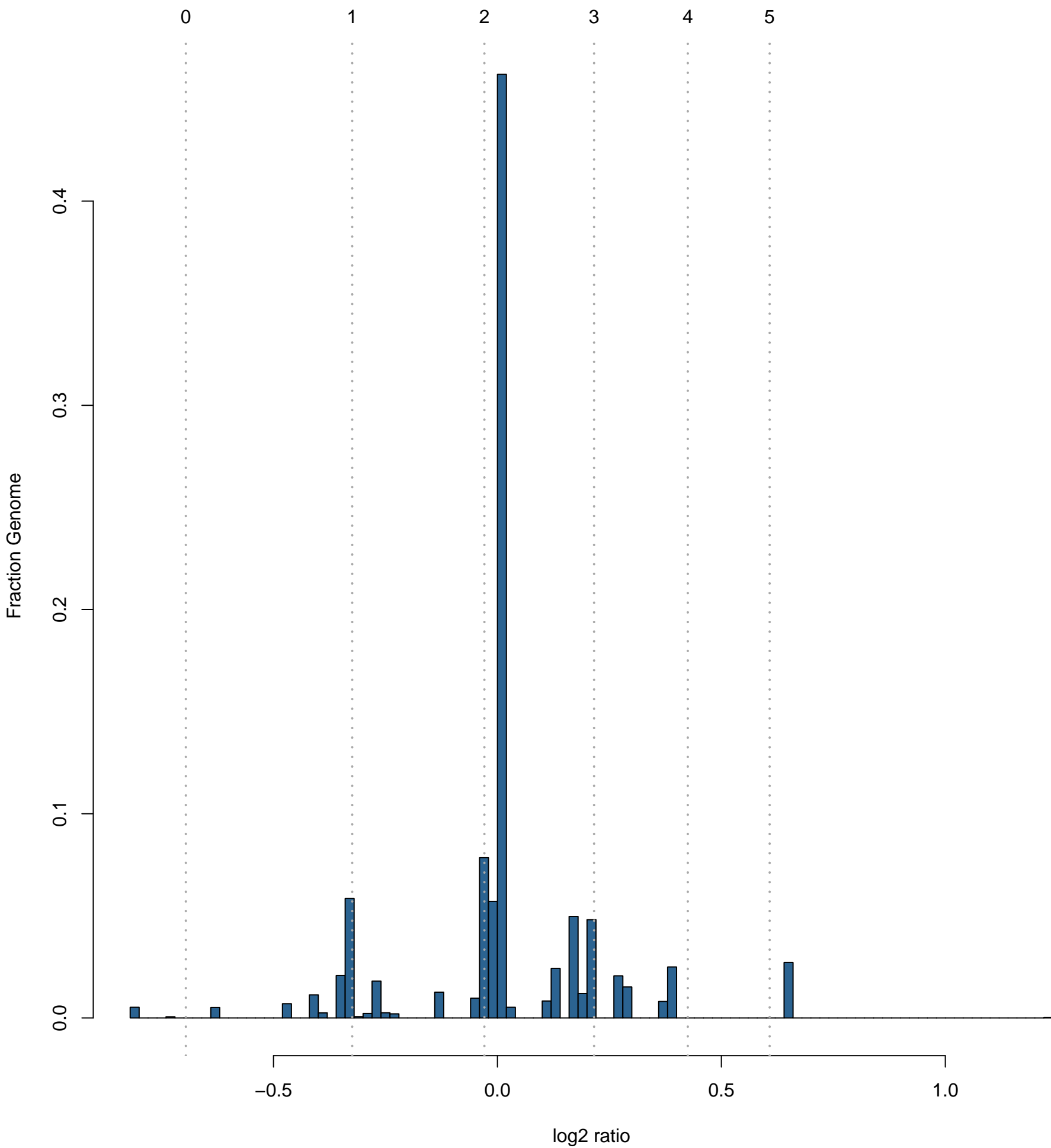
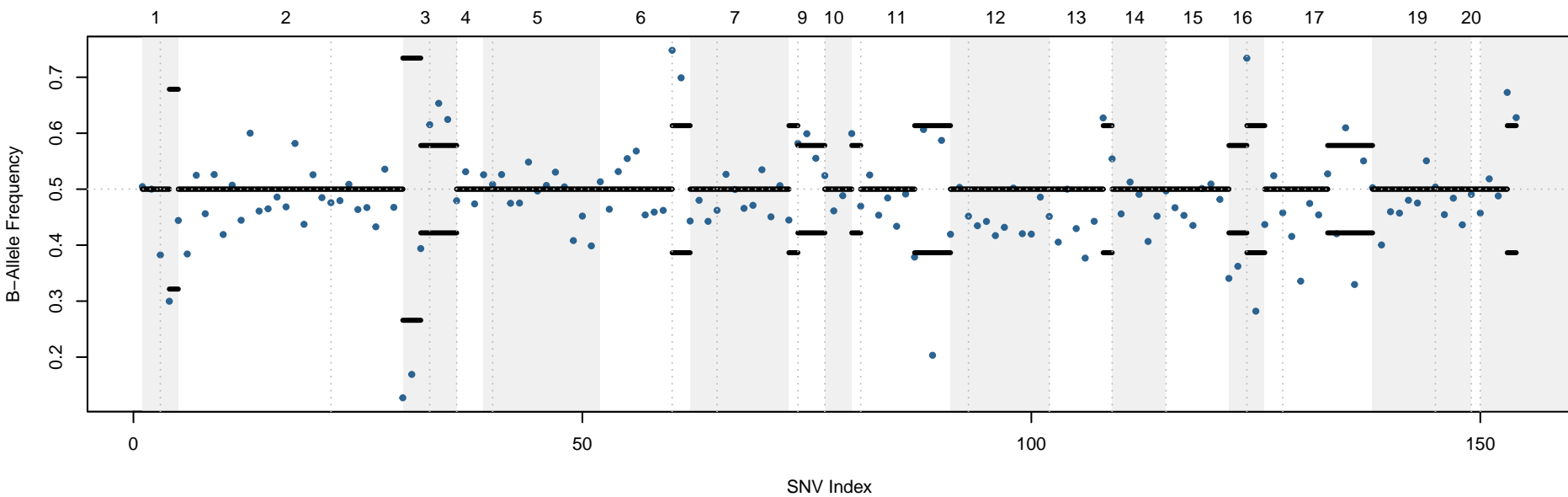


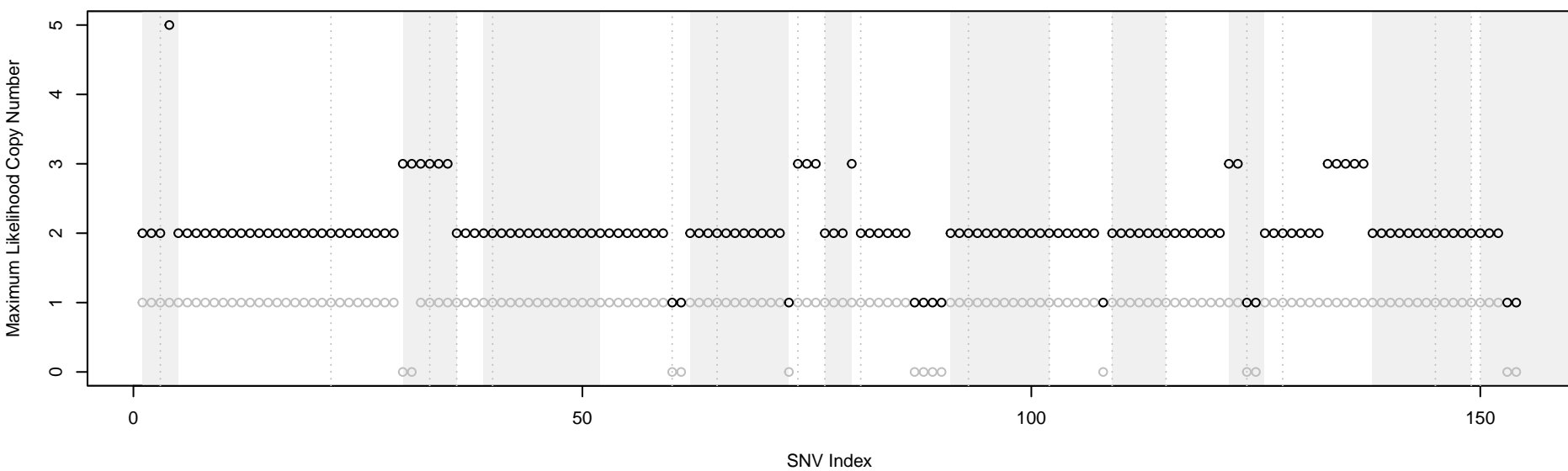
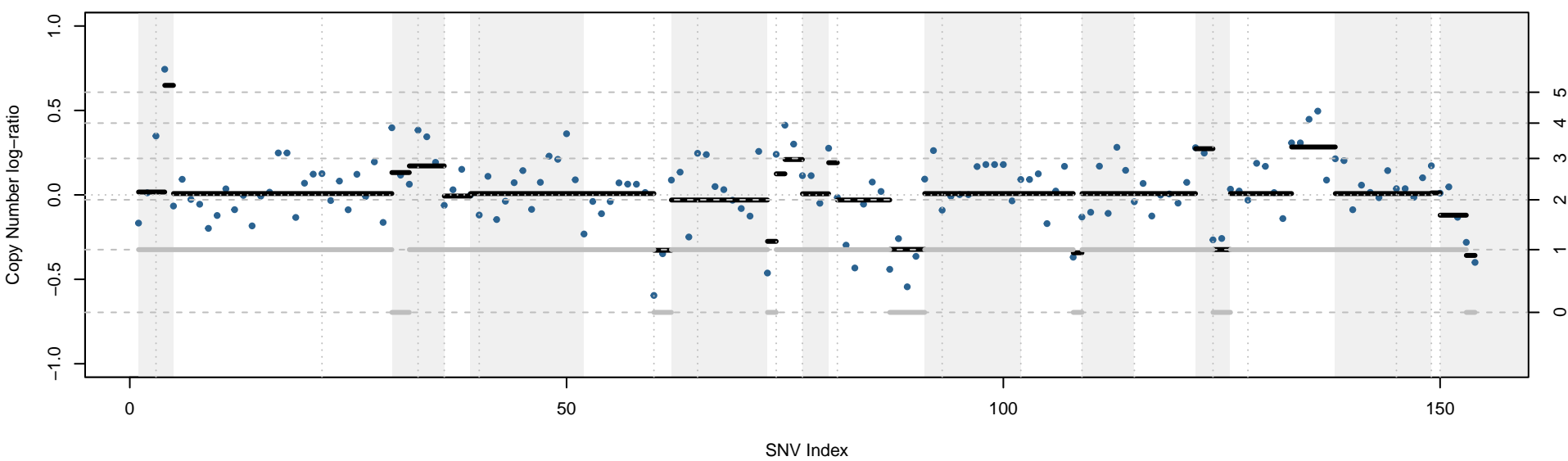
Purity: 0.37 Tumor ploidy: 2.11

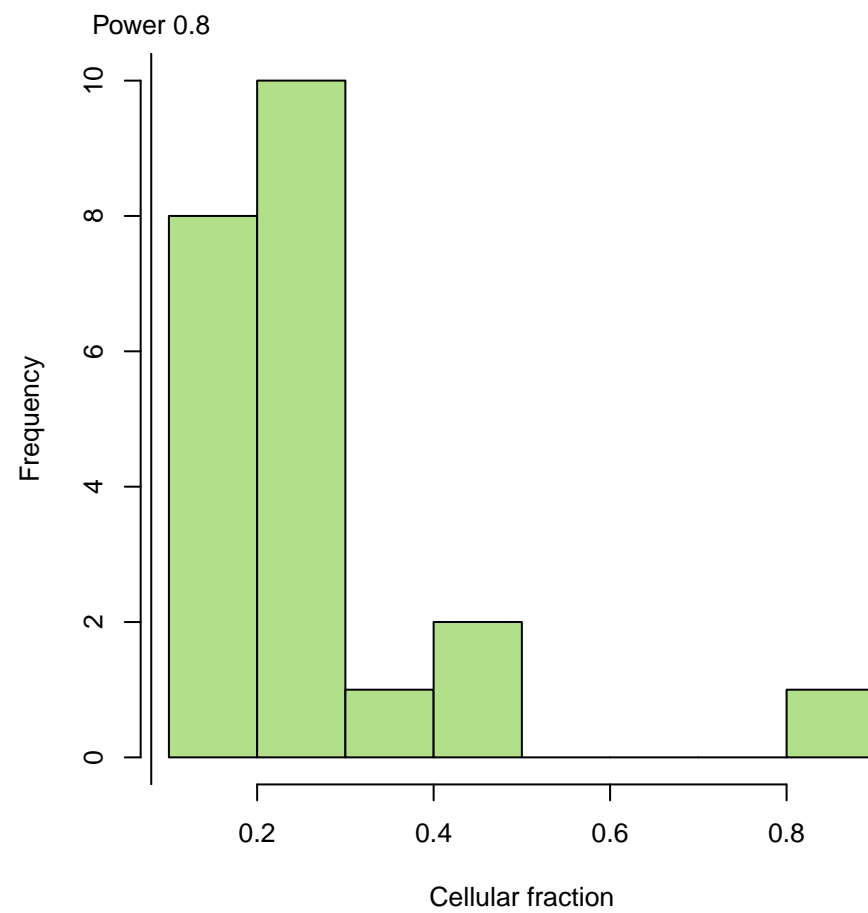
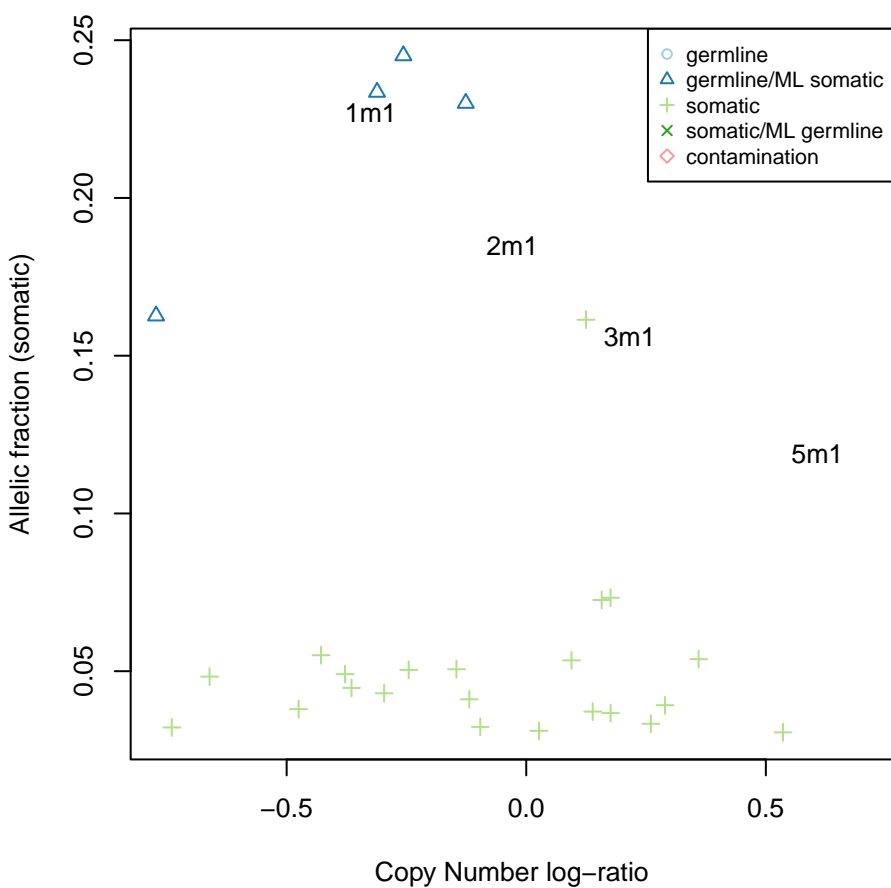
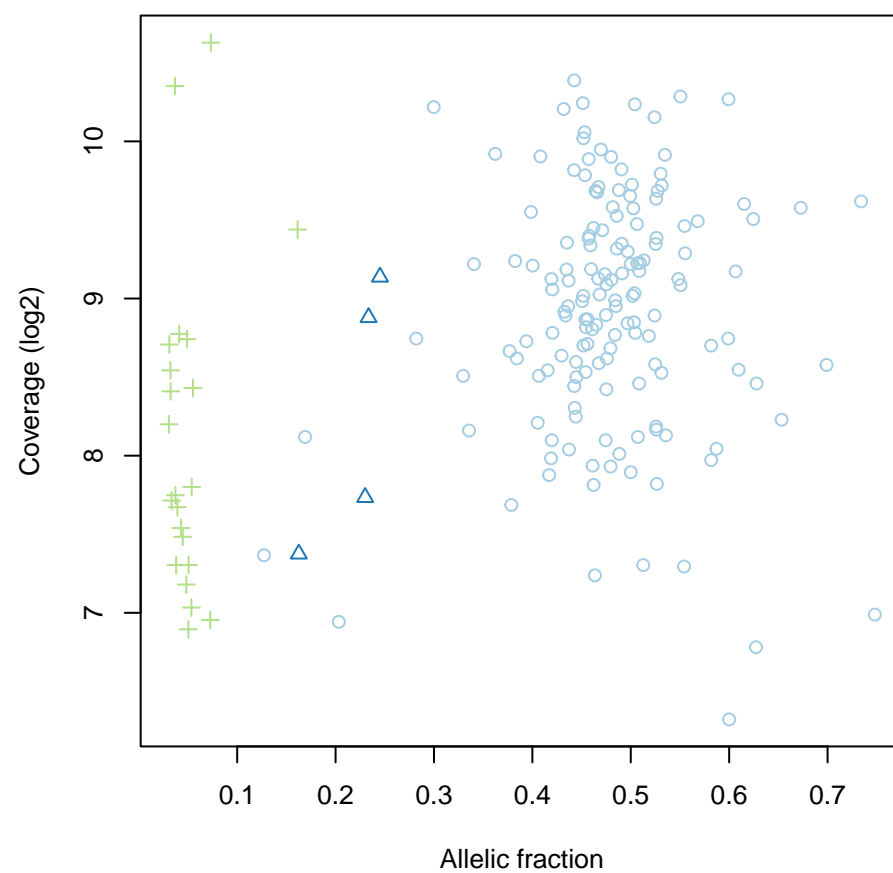
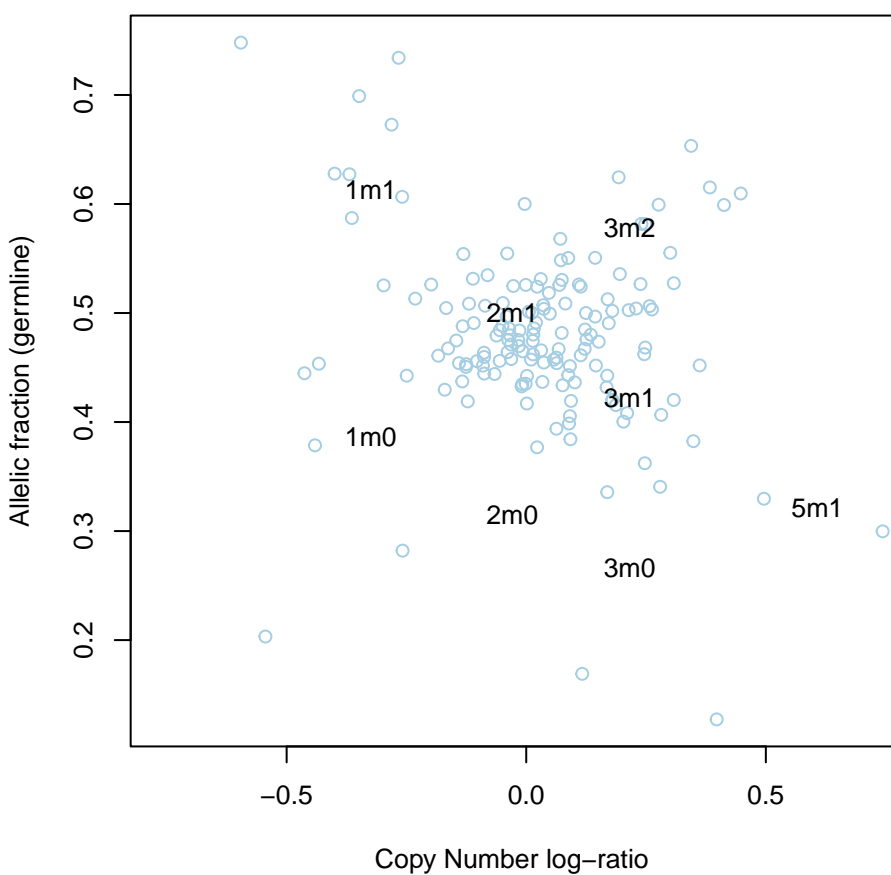


Purity: 0.37 Tumor ploidy: 2.11 SNV log-likelihood: -63.57 GoF: 87% Mean coverage: 527;500

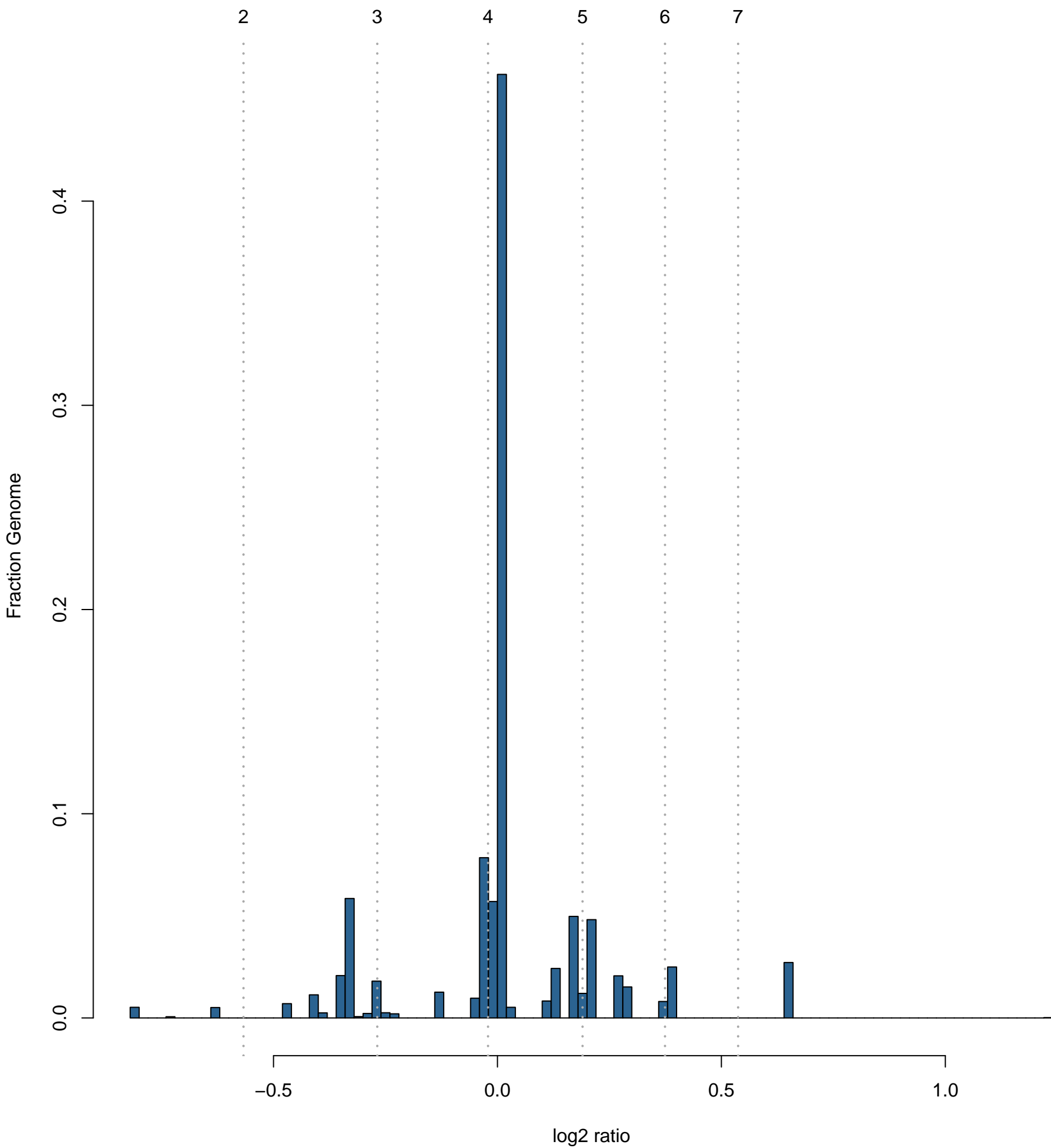


SCNA-fit log-likelihood: -4571.8

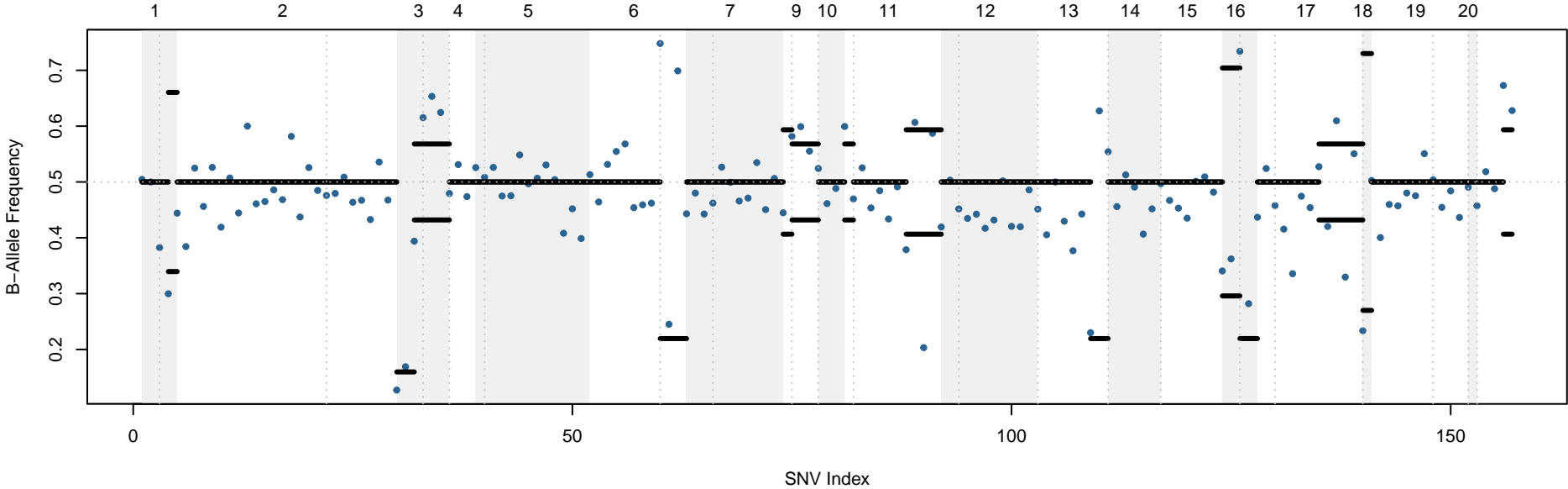




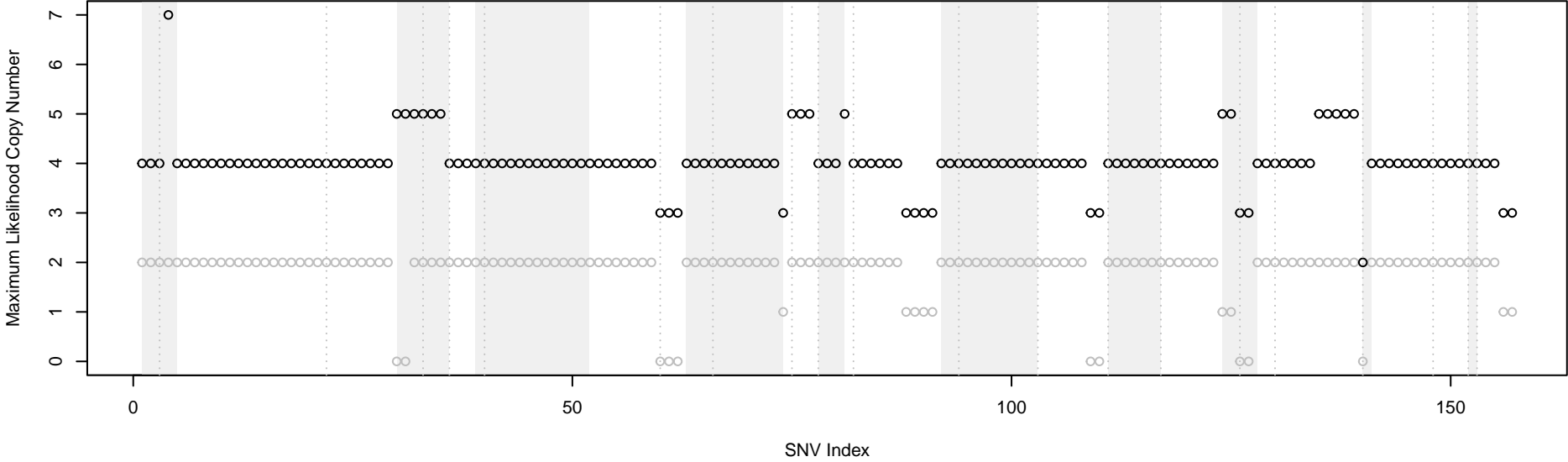
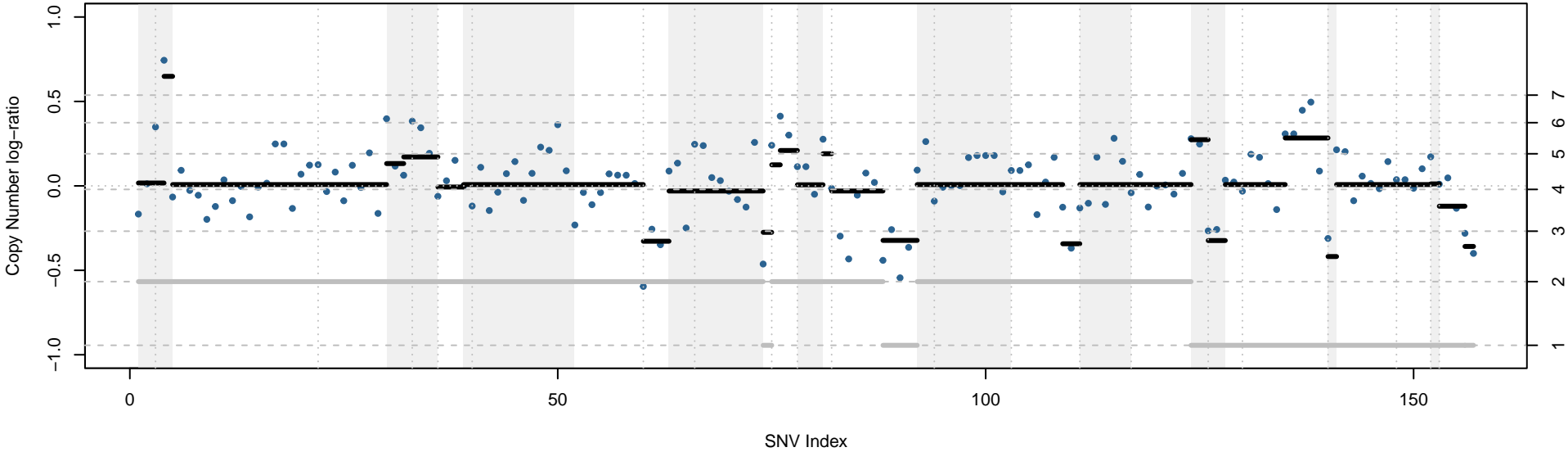
Purity: 0.46 Tumor ploidy: 4.093

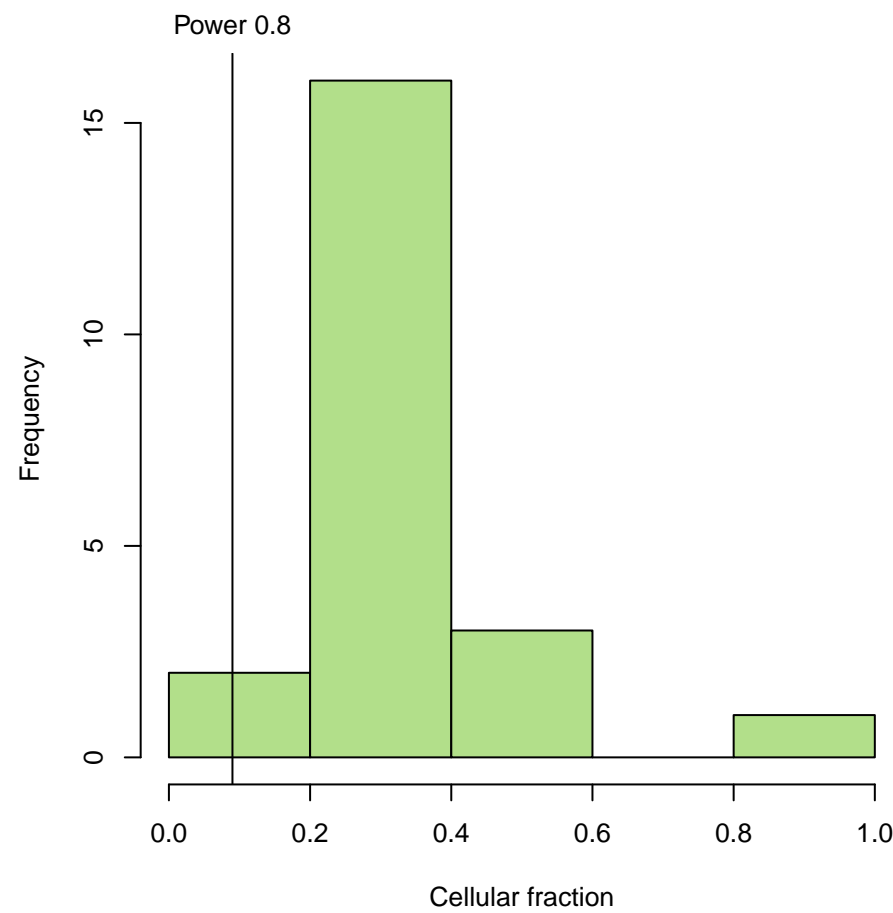
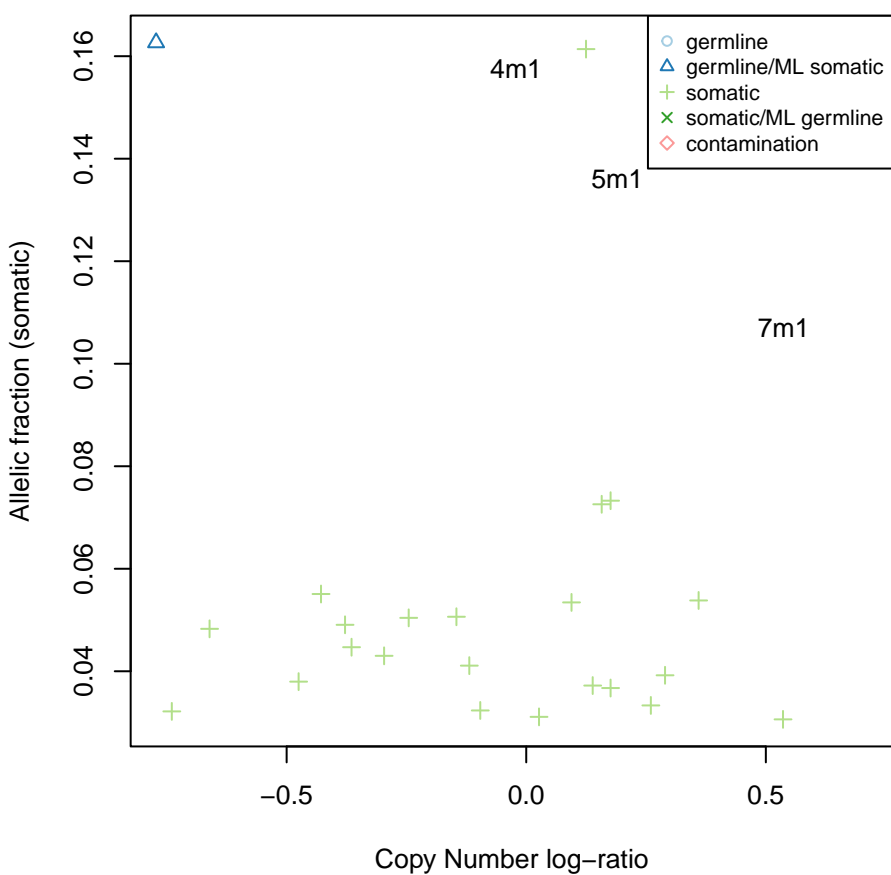
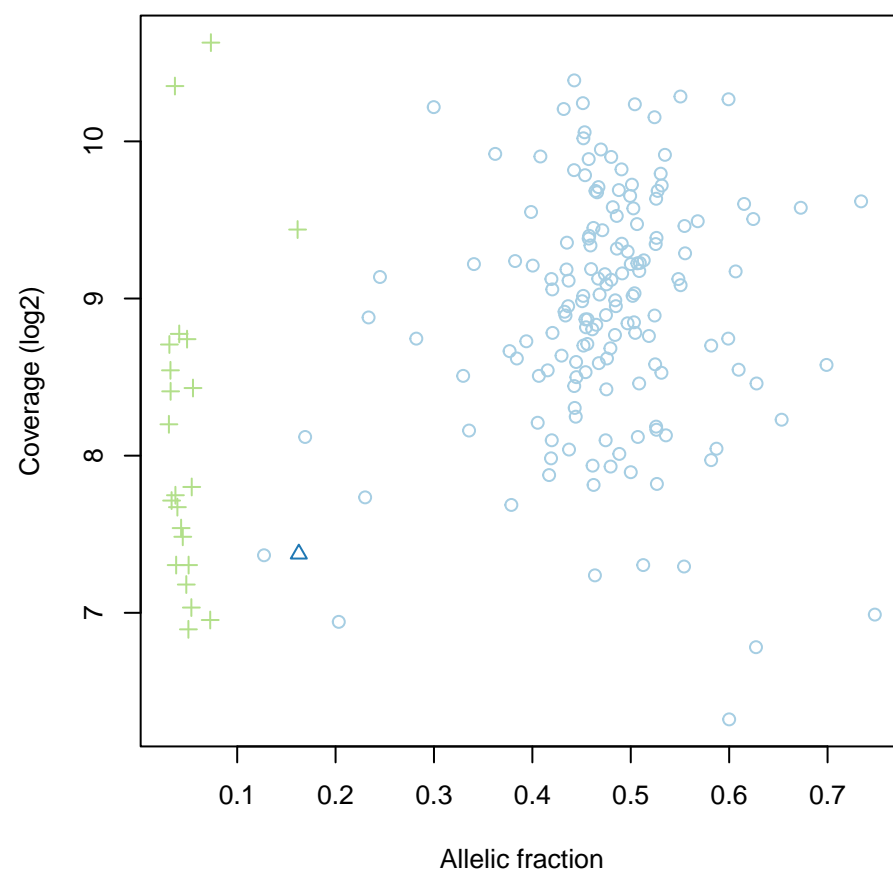


Purity: 0.46 Tumor ploidy: 4.093 SNV log-likelihood: -99.23 GoF: 90% Mean coverage: 527;500

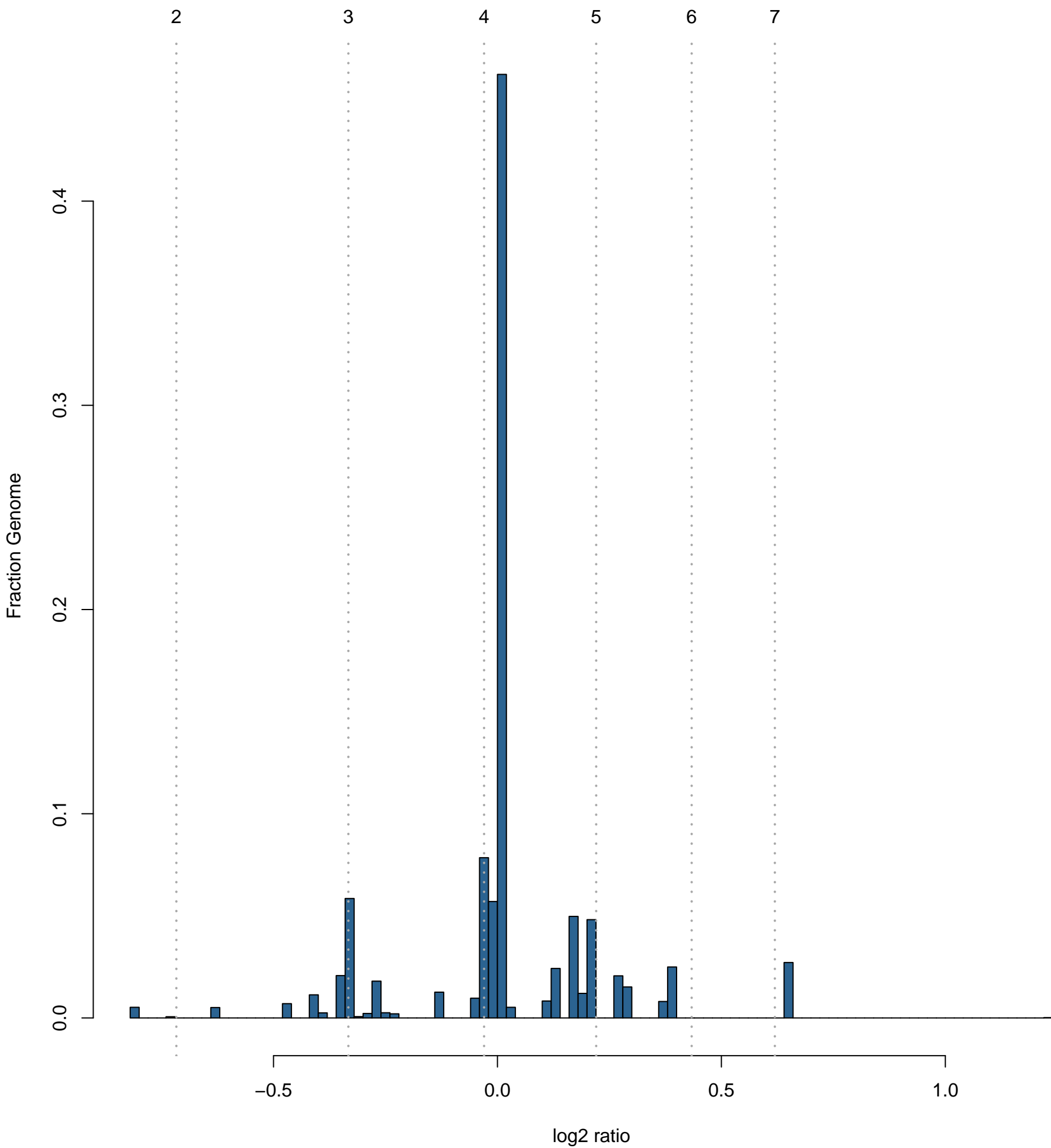


SCNA-fit log-likelihood: -4597.23

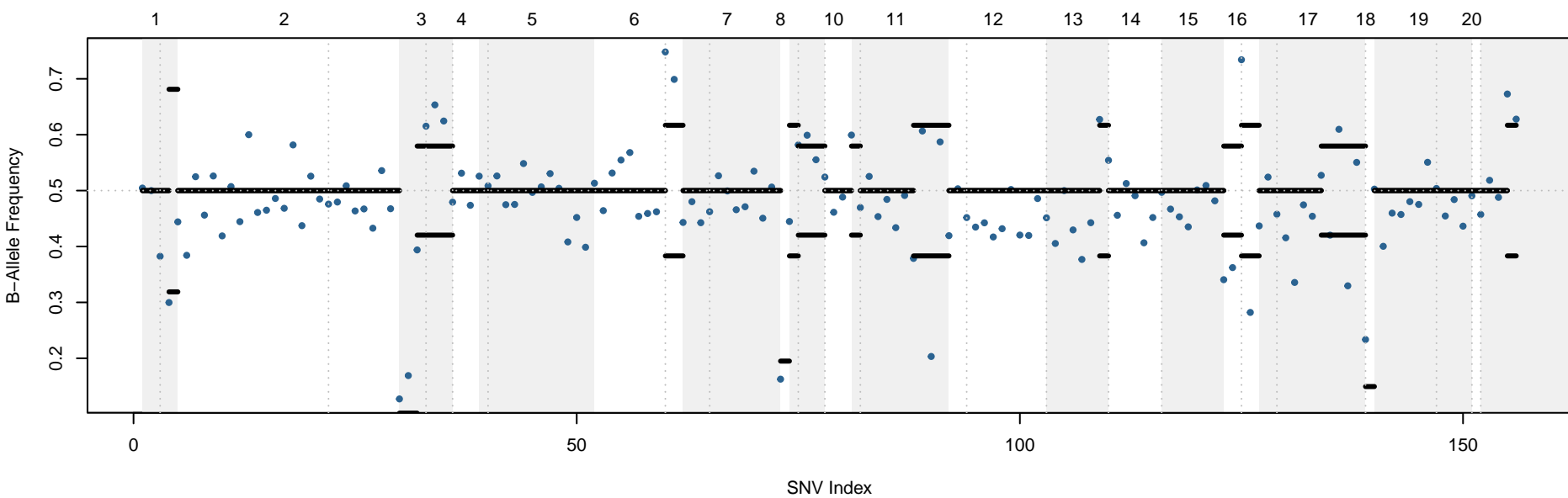




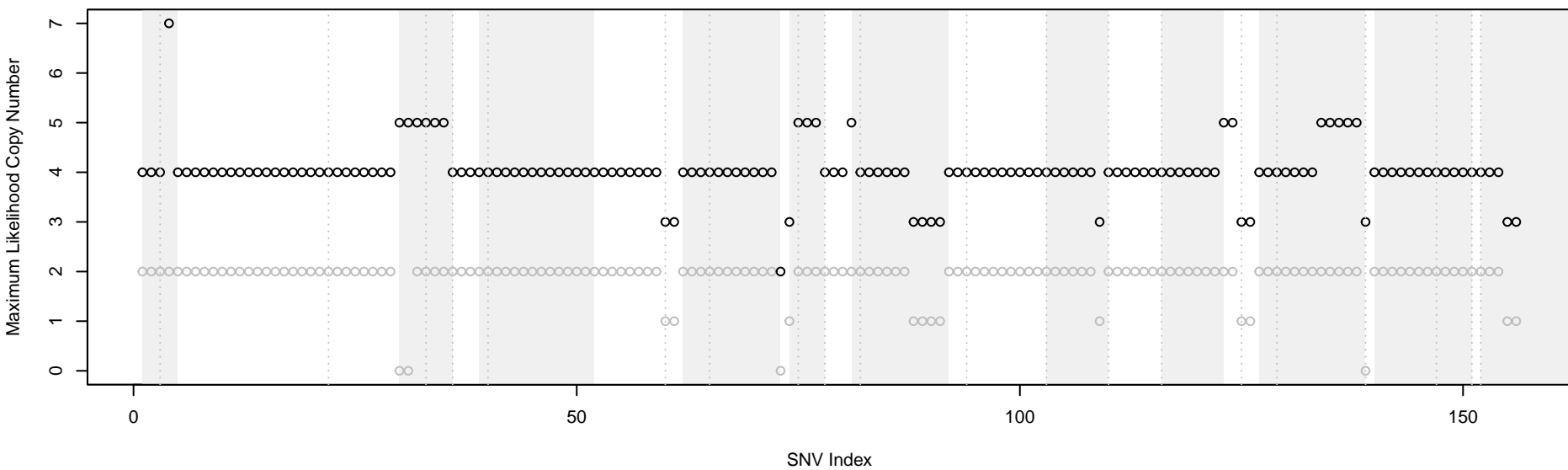
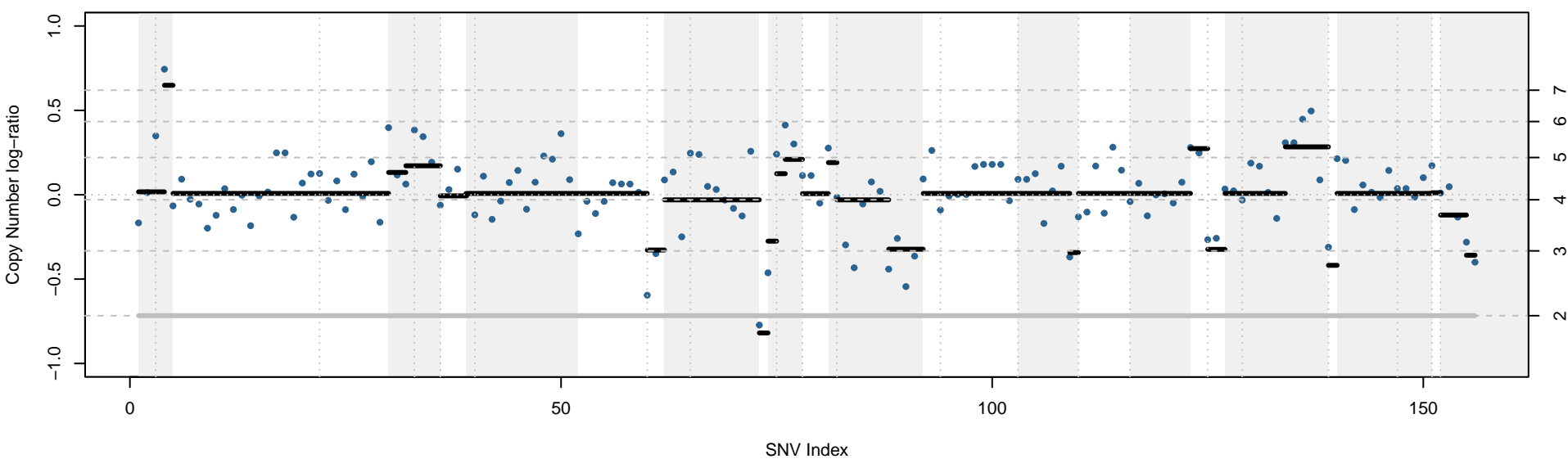
Purity: 0.61 Tumor ploidy: 4.11



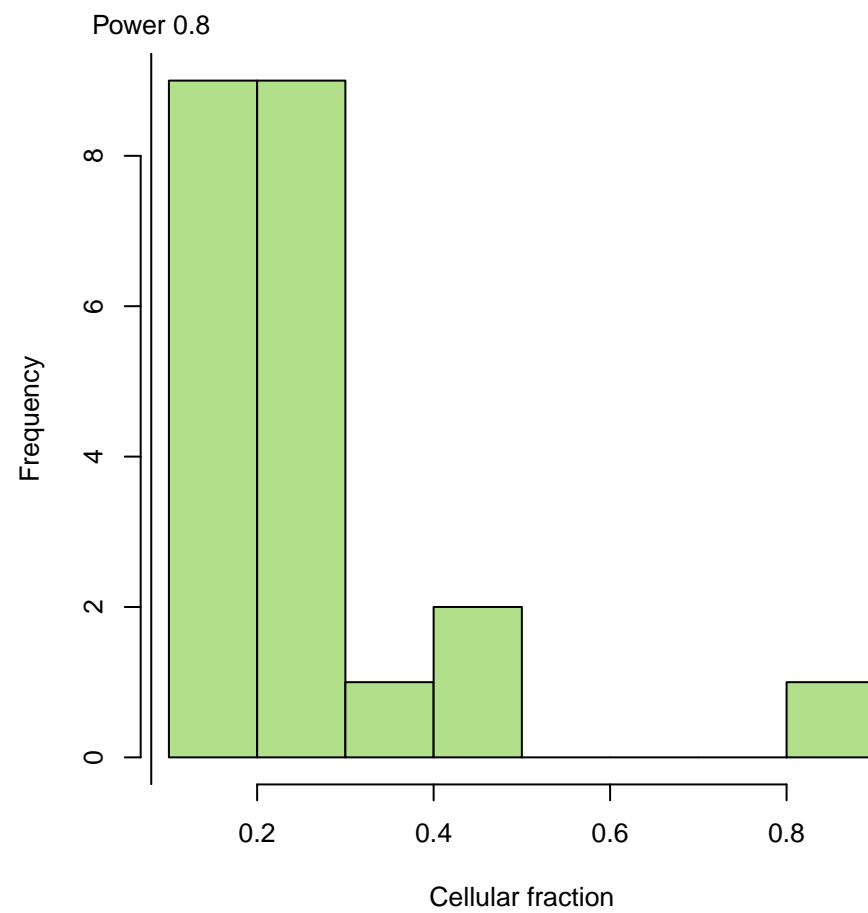
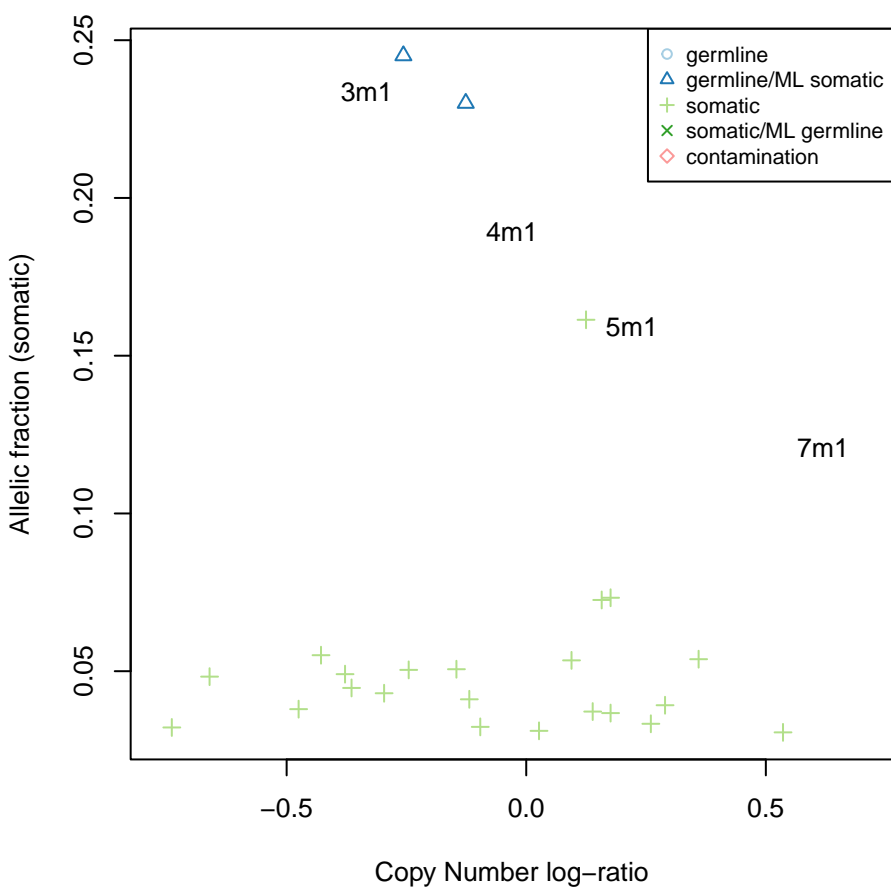
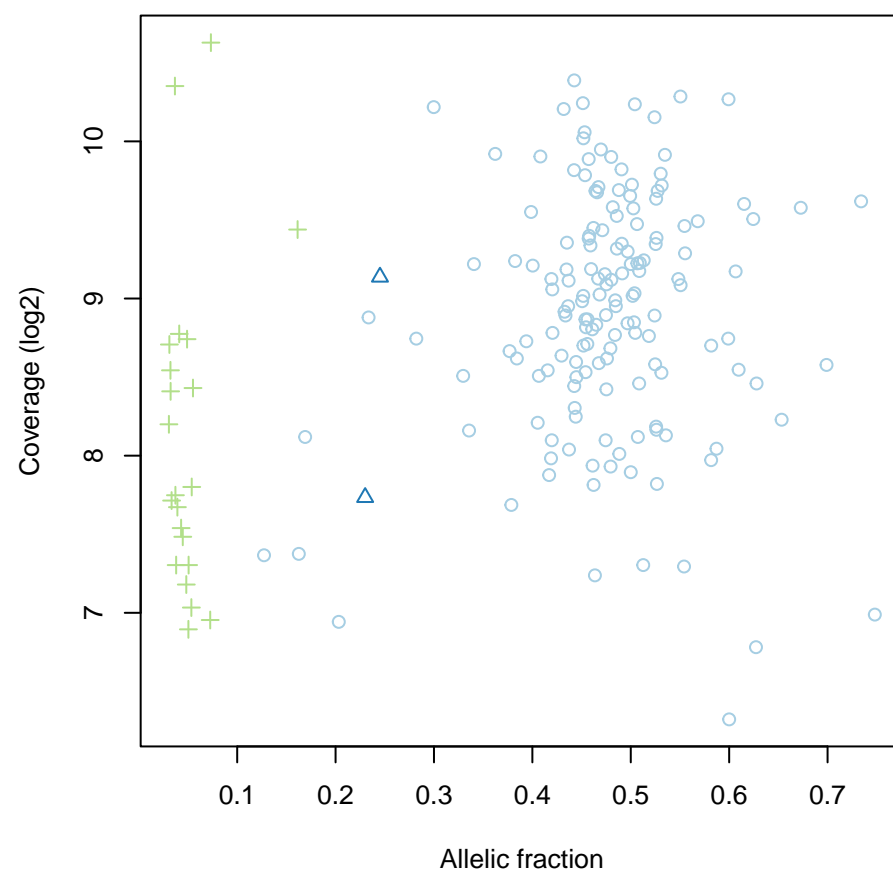
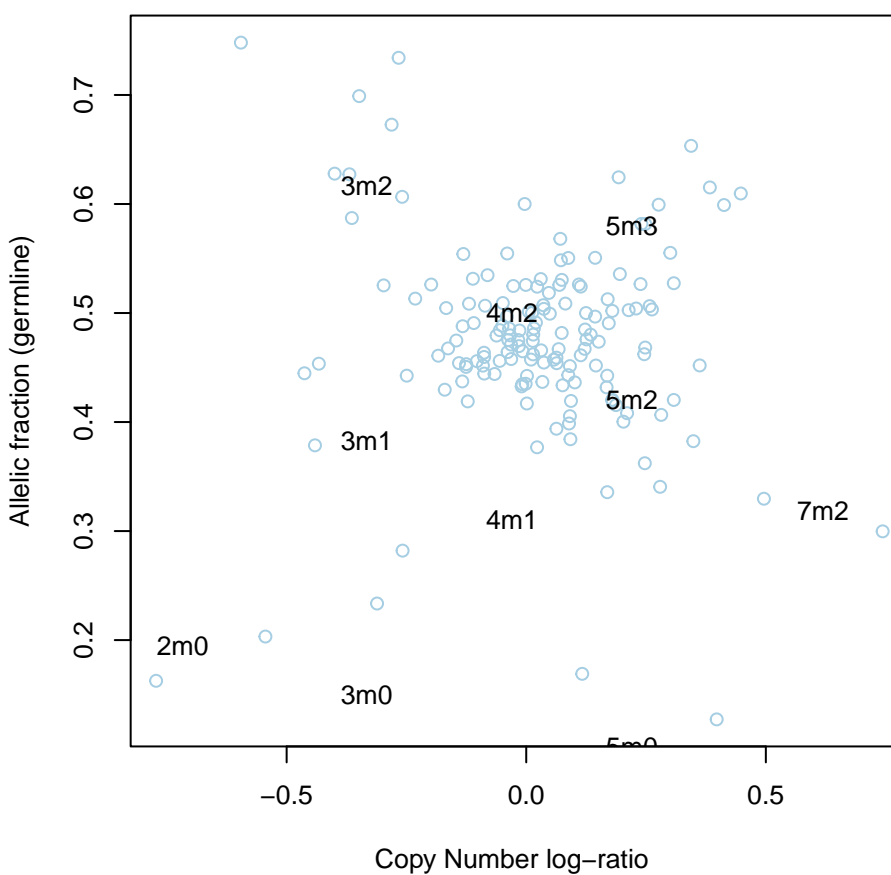
Purity: 0.61 Tumor ploidy: 4.11 SNV log-likelihood: -140.75 GoF: 87.3% Mean coverage: 527;500



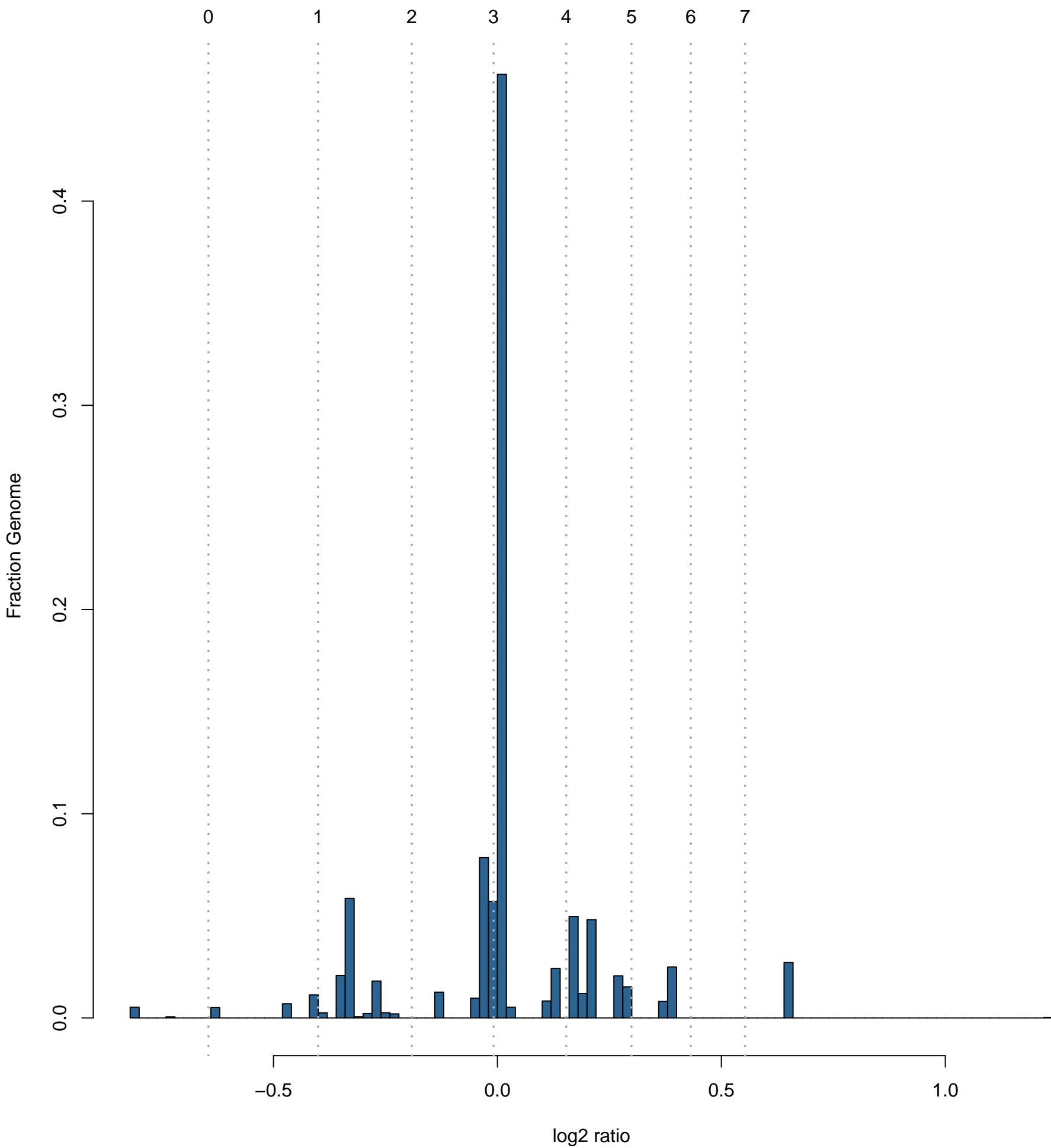
SCNA-fit log-likelihood: -4573.3



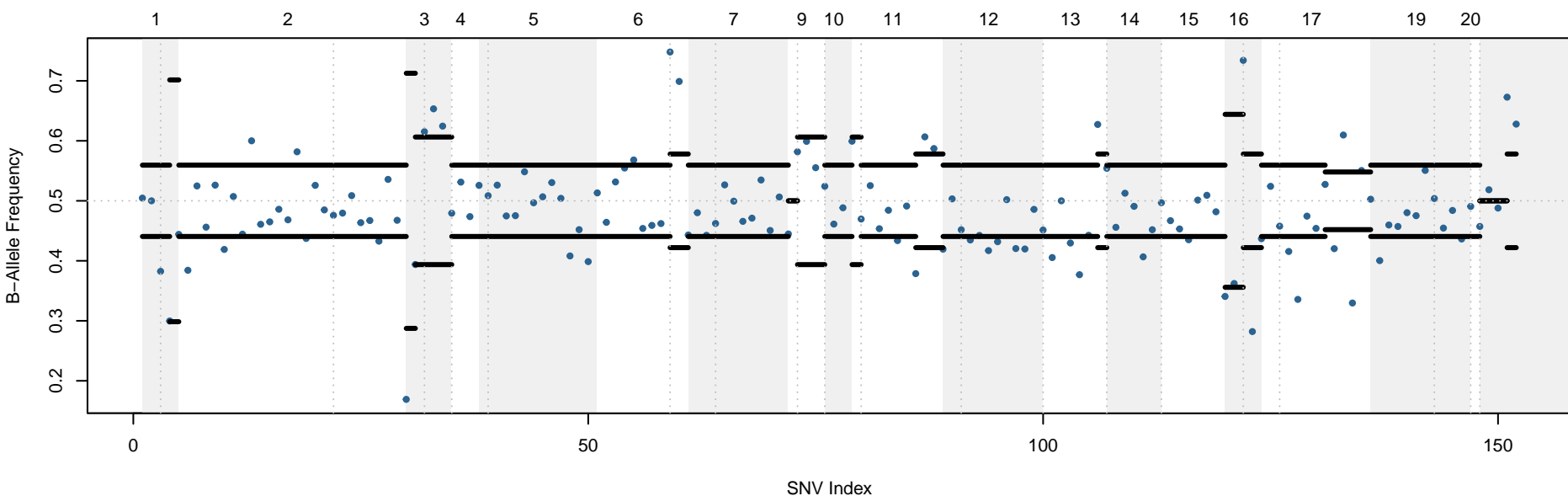




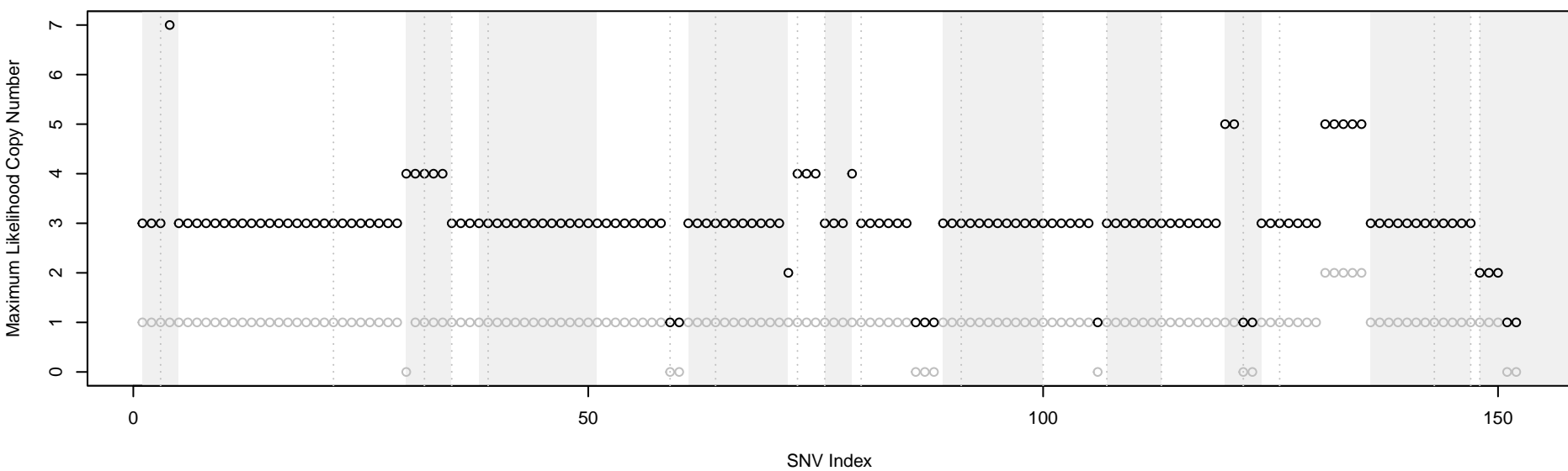
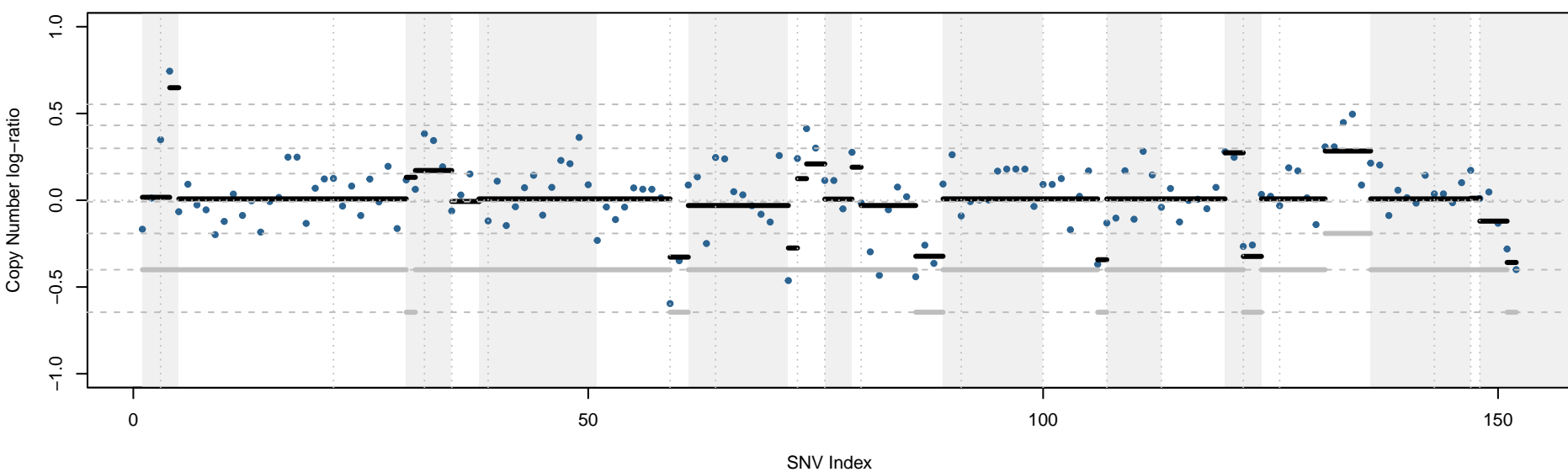
Purity: 0.27 Tumor ploidy: 3.05

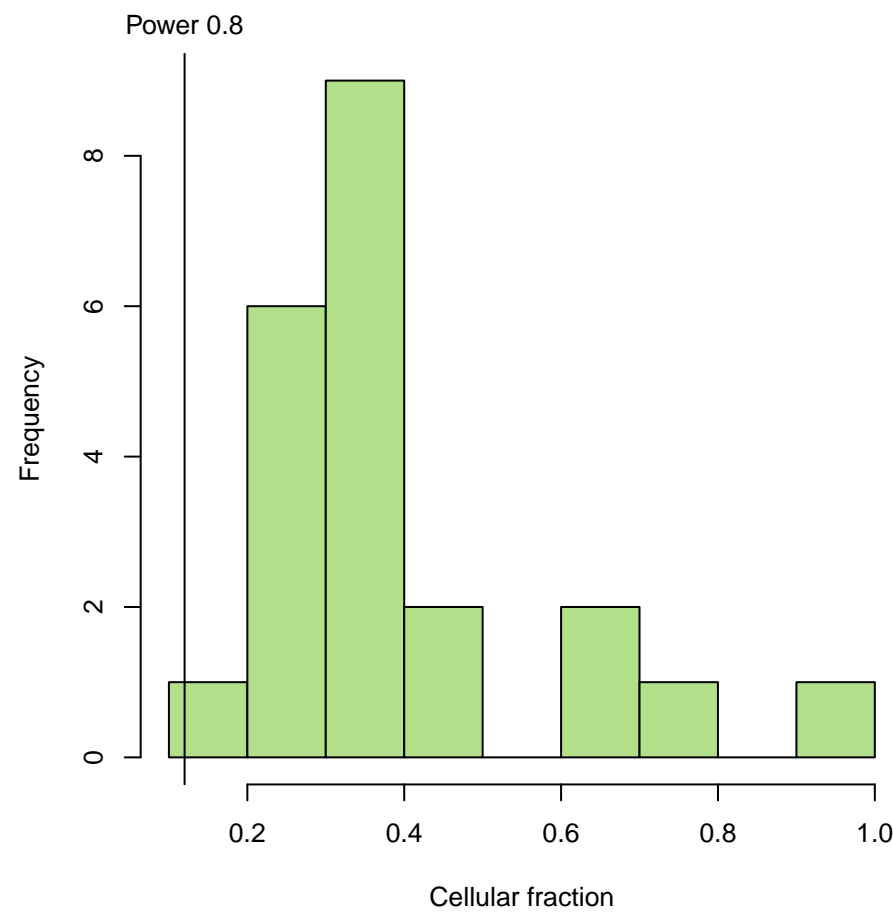
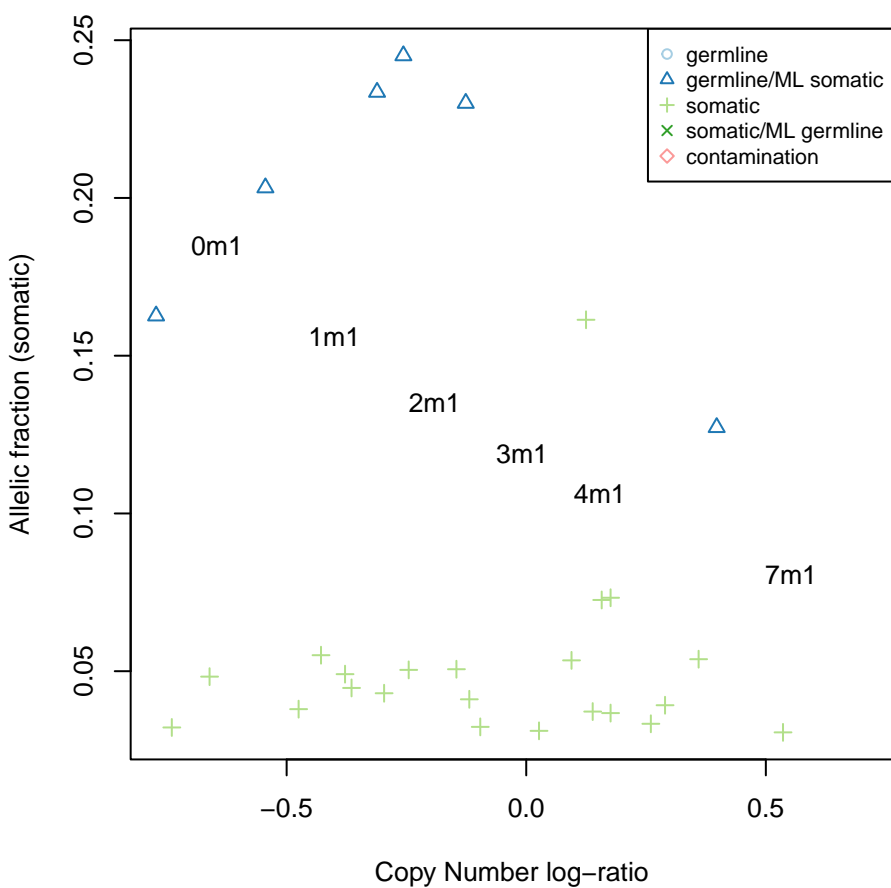
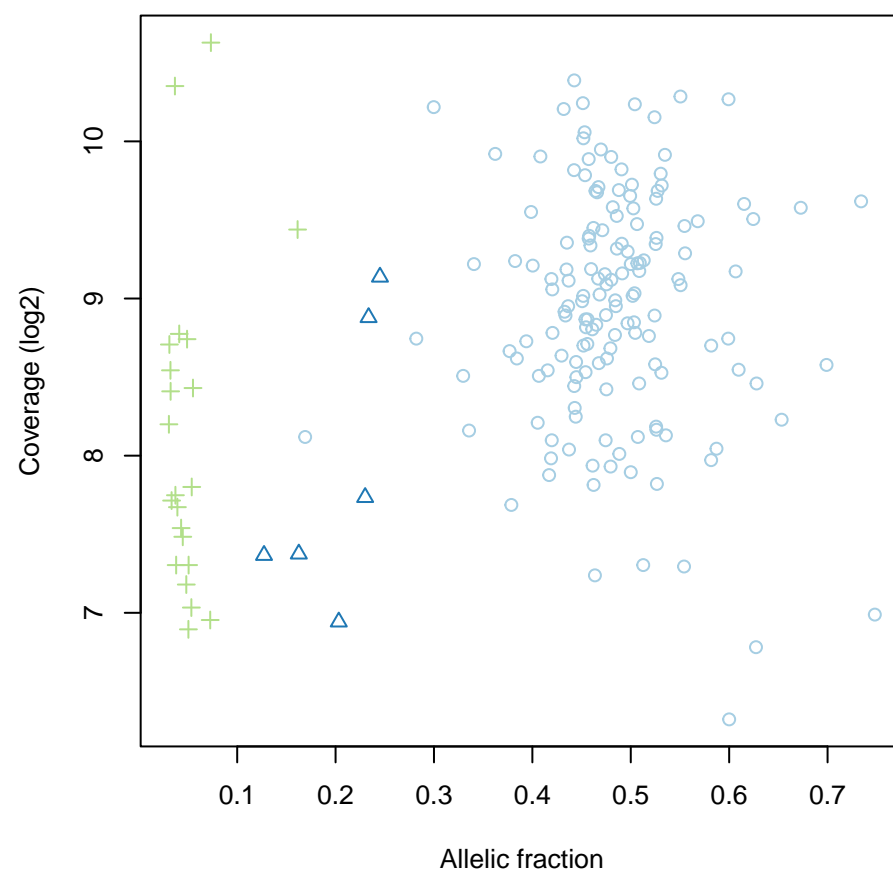
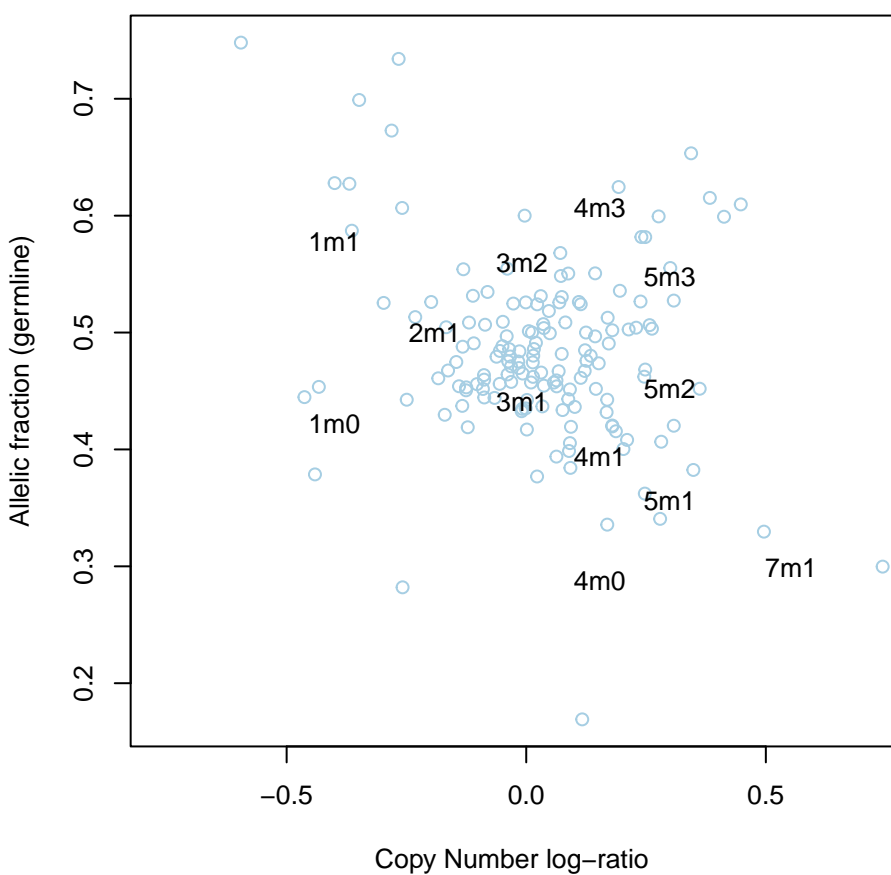


Purity: 0.27 Tumor ploidy: 3.05 SNV log-likelihood: -172.33 GoF: 93.1% Mean coverage: 527;500

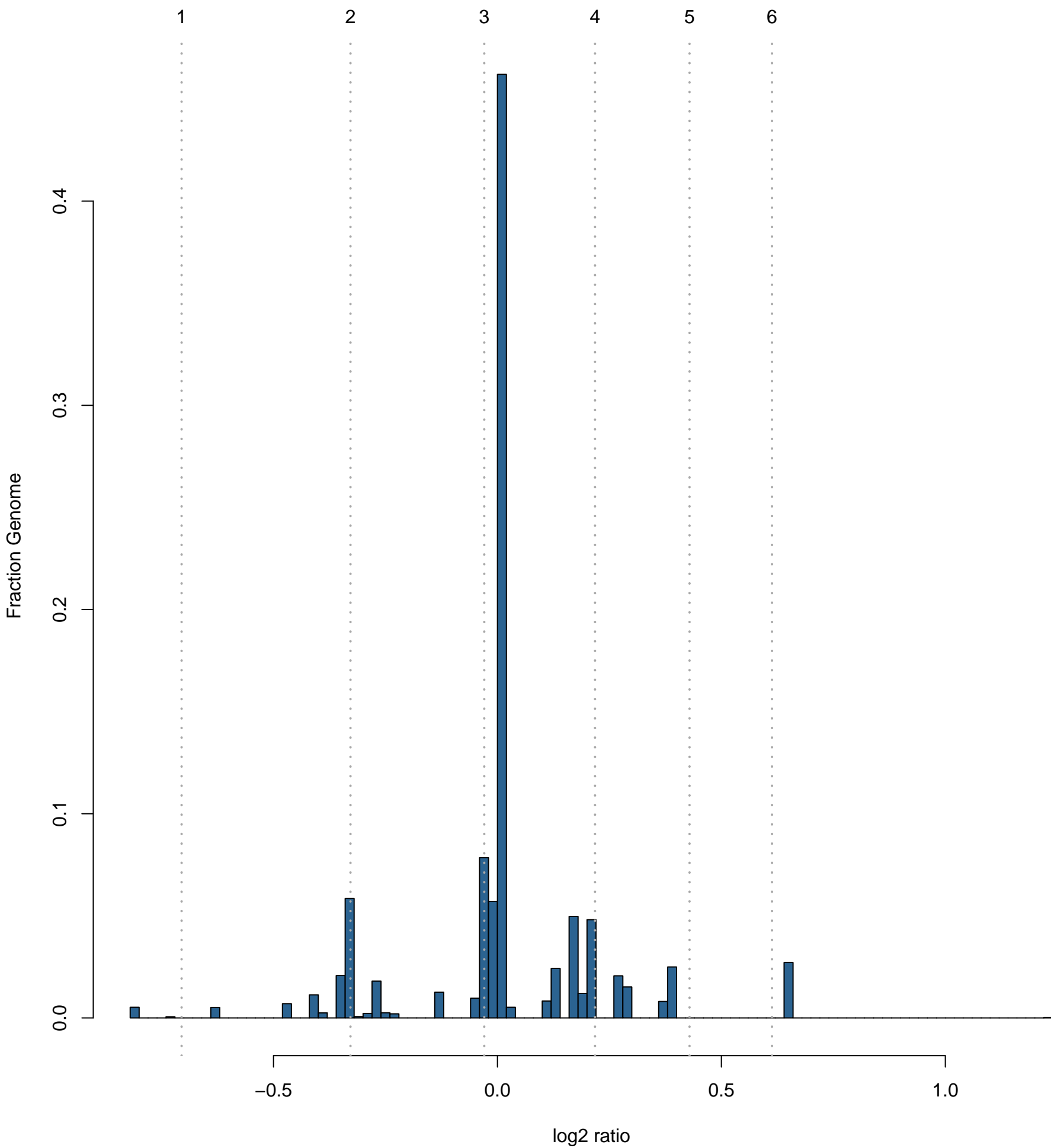


SCNA-fit log-likelihood: -4543.15

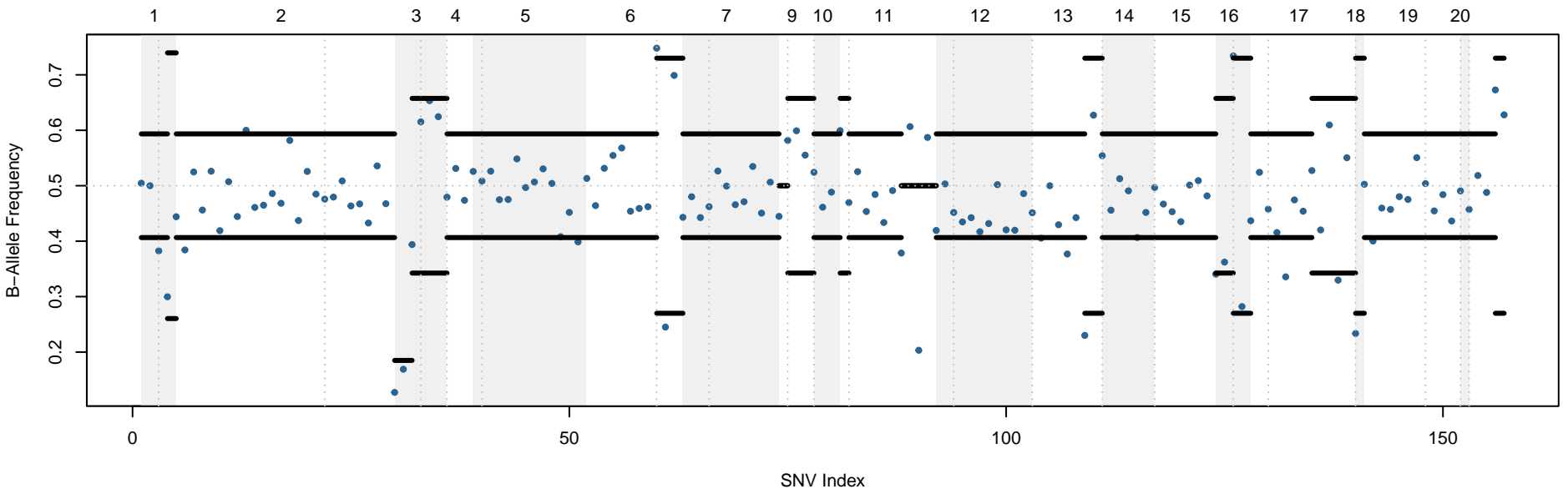




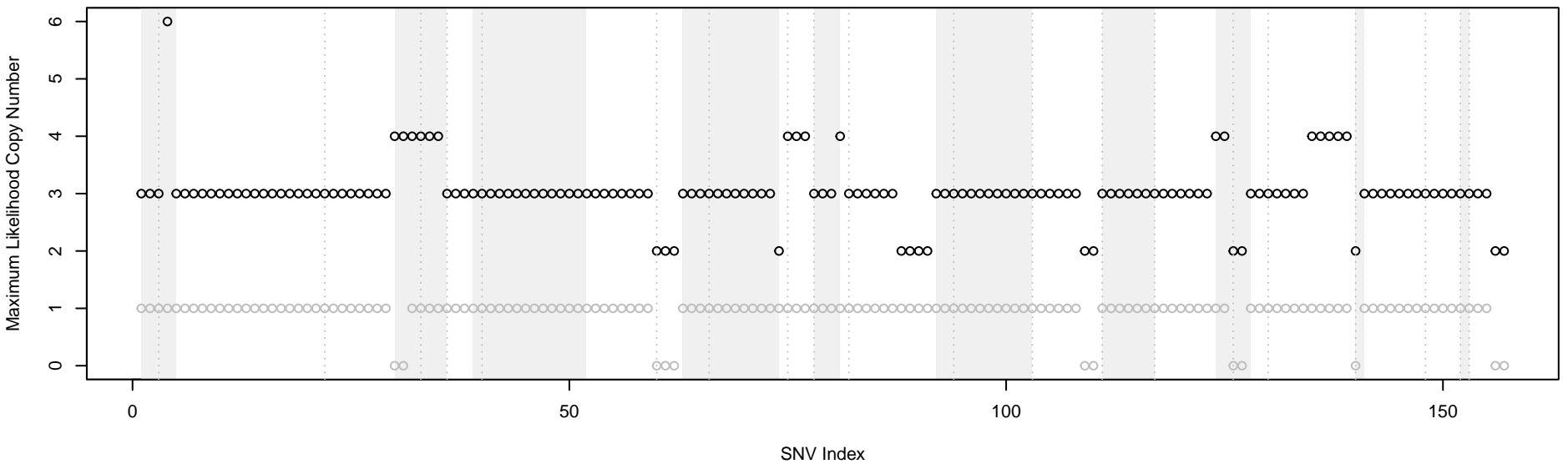
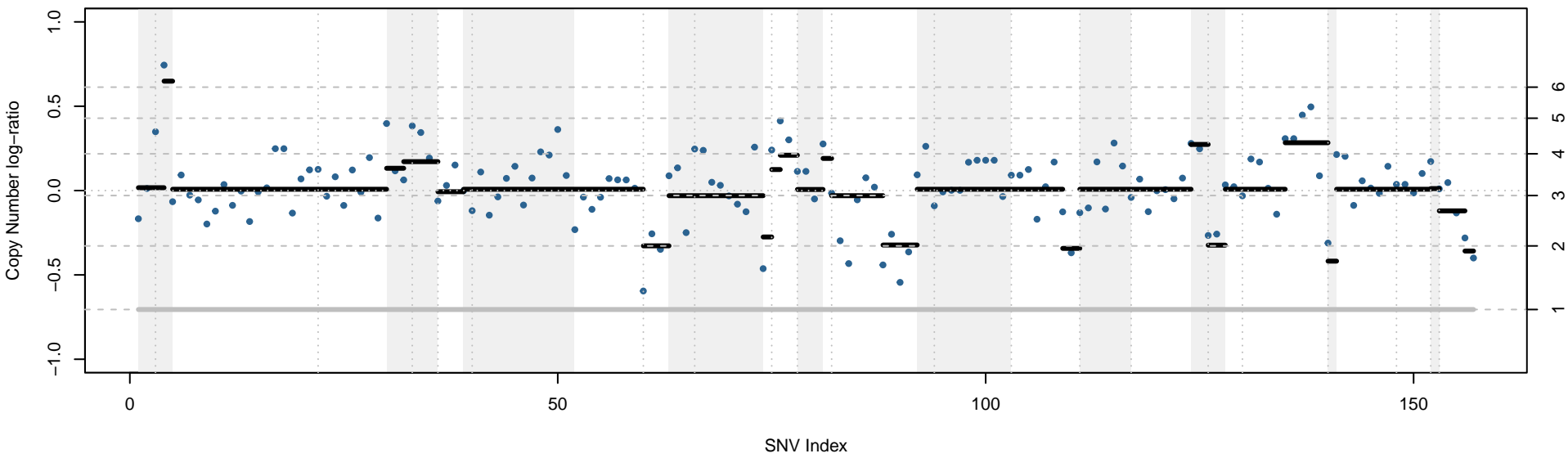
Purity: 0.46 Tumor ploidy: 3.11

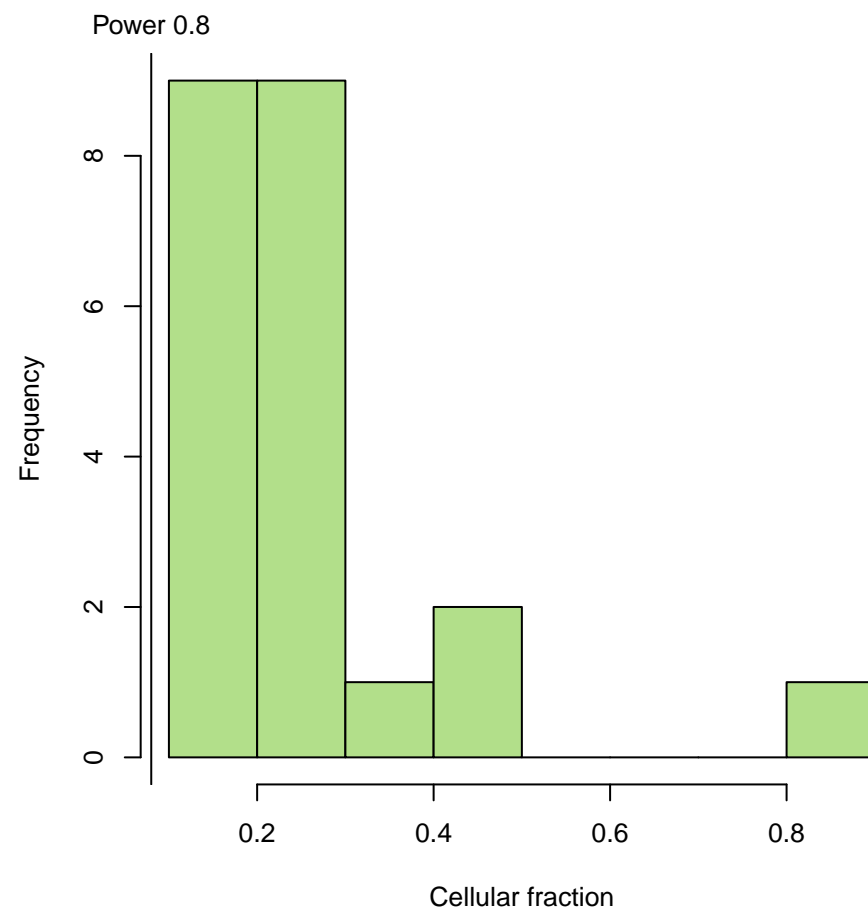
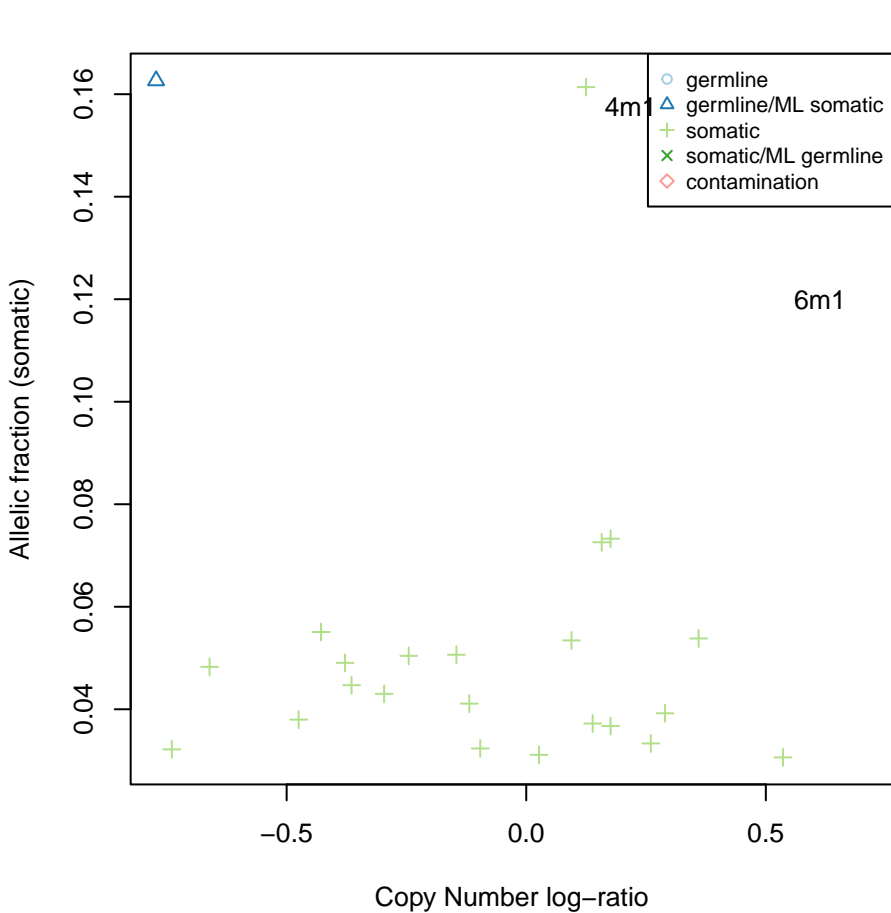
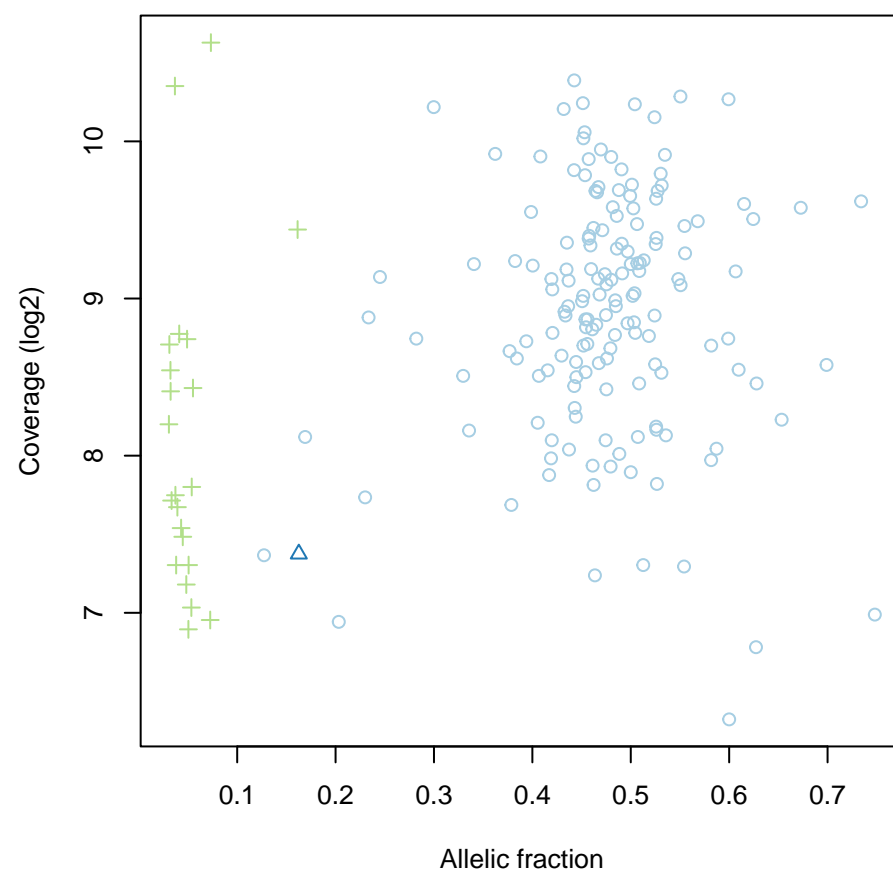
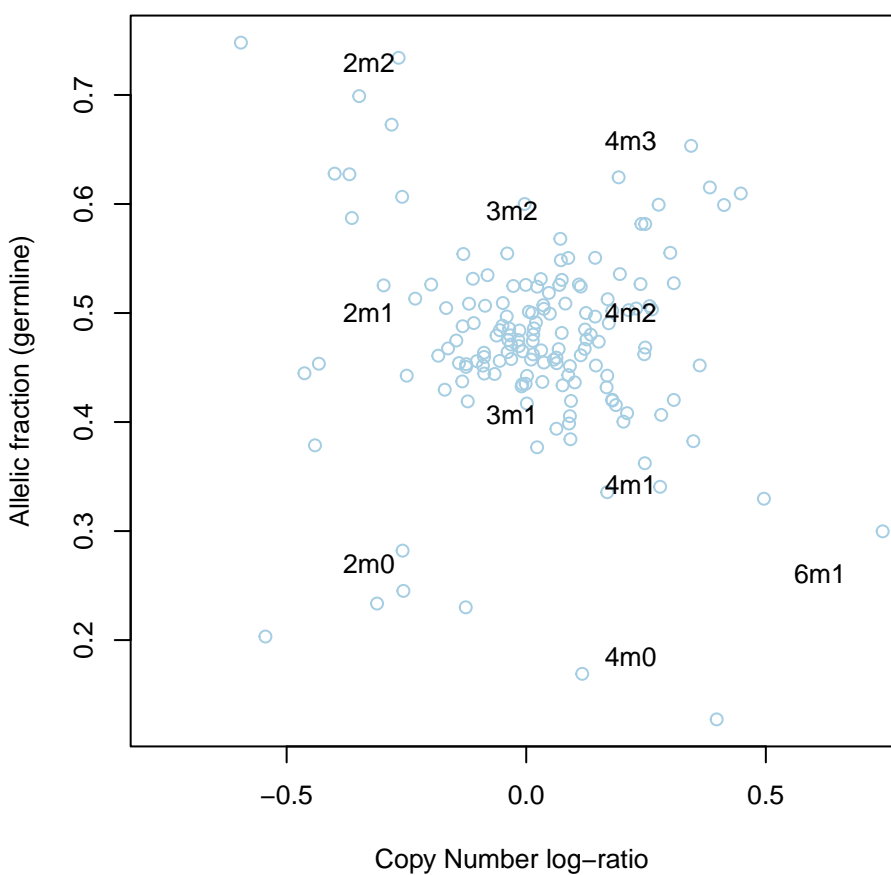


Purity: 0.46 Tumor ploidy: 3.11 SNV log-likelihood: -306.25 GoF: 84.3% Mean coverage: 527;500

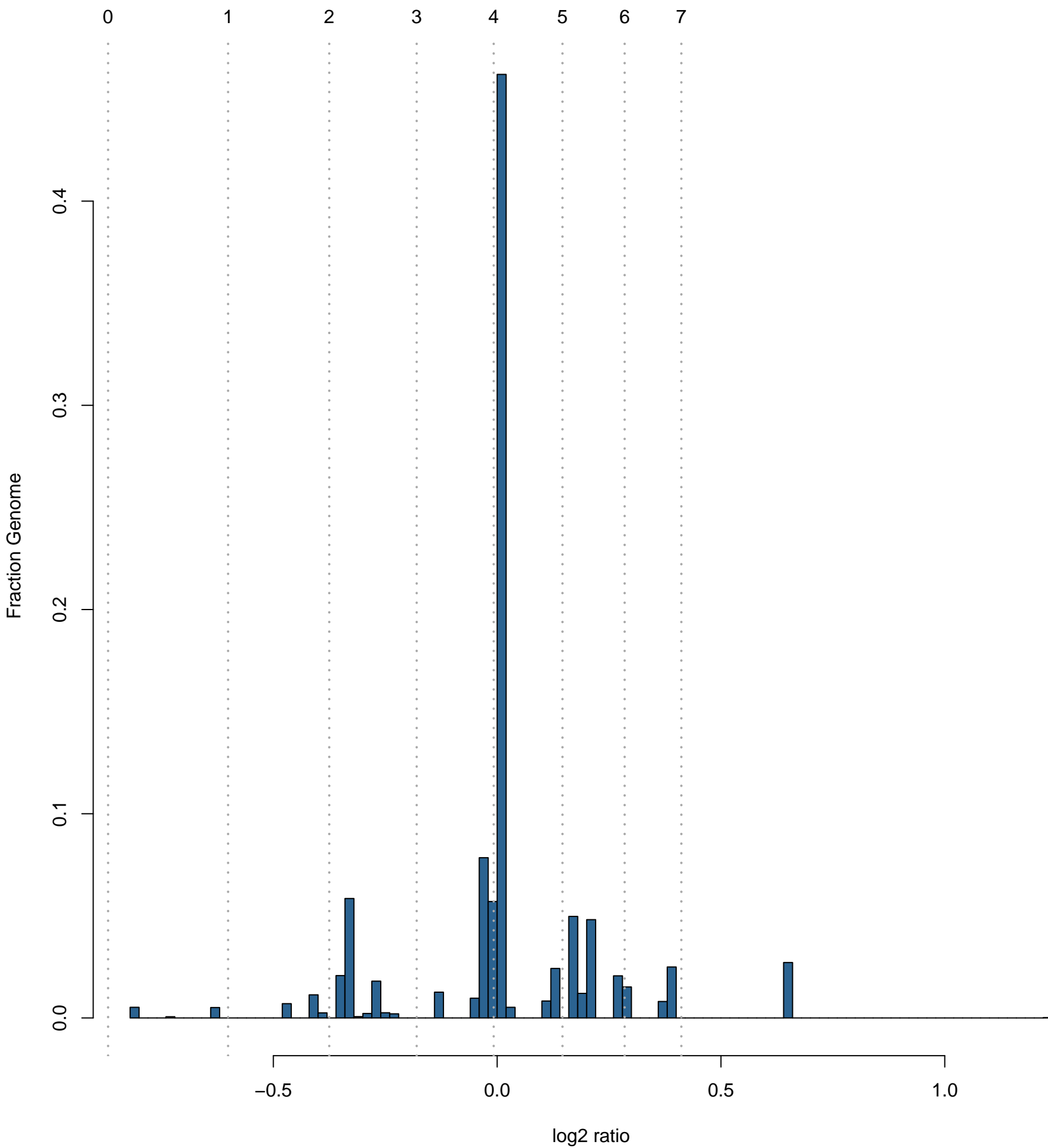


SCNA-fit log-likelihood: -4572.11



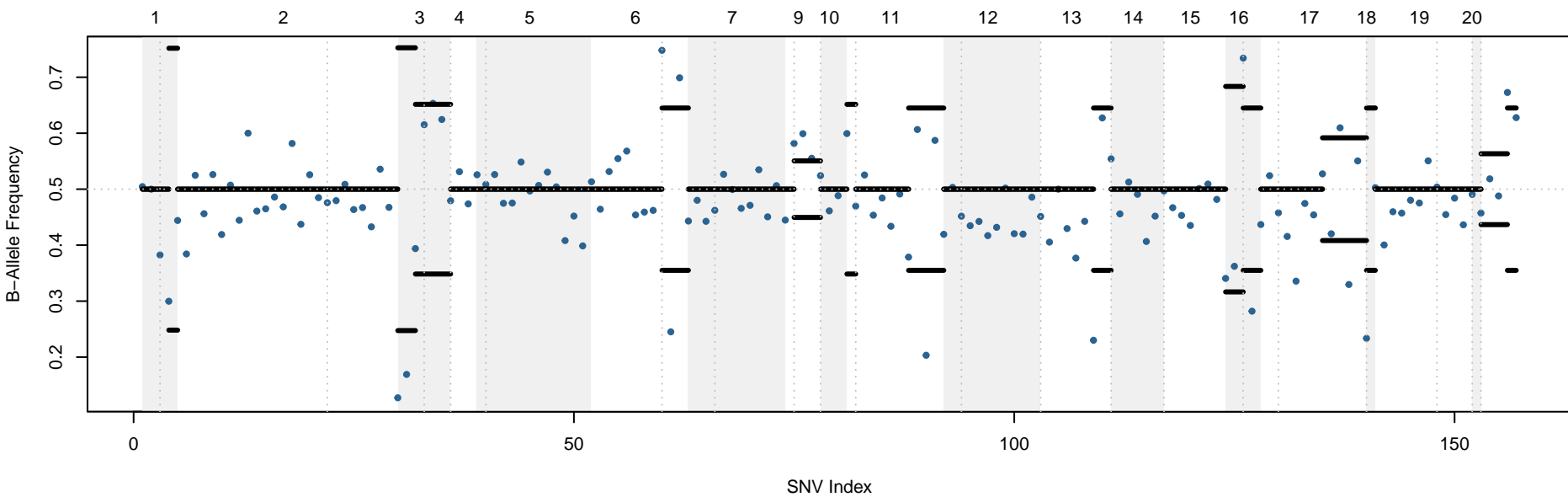


Purity: 0.29 Tumor ploidy: 4.048

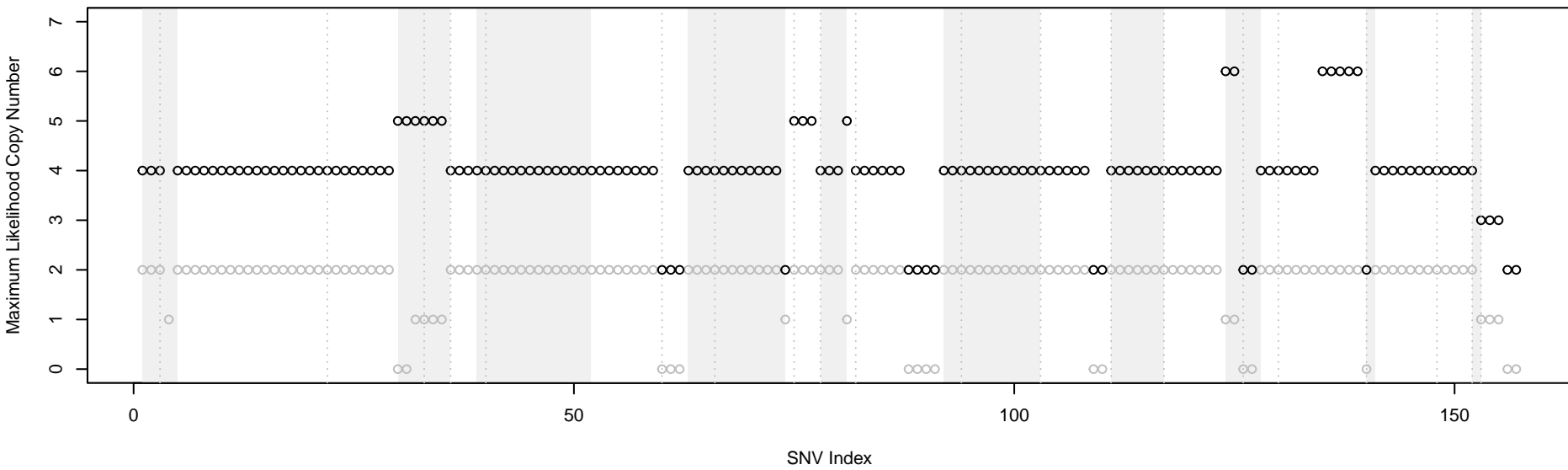
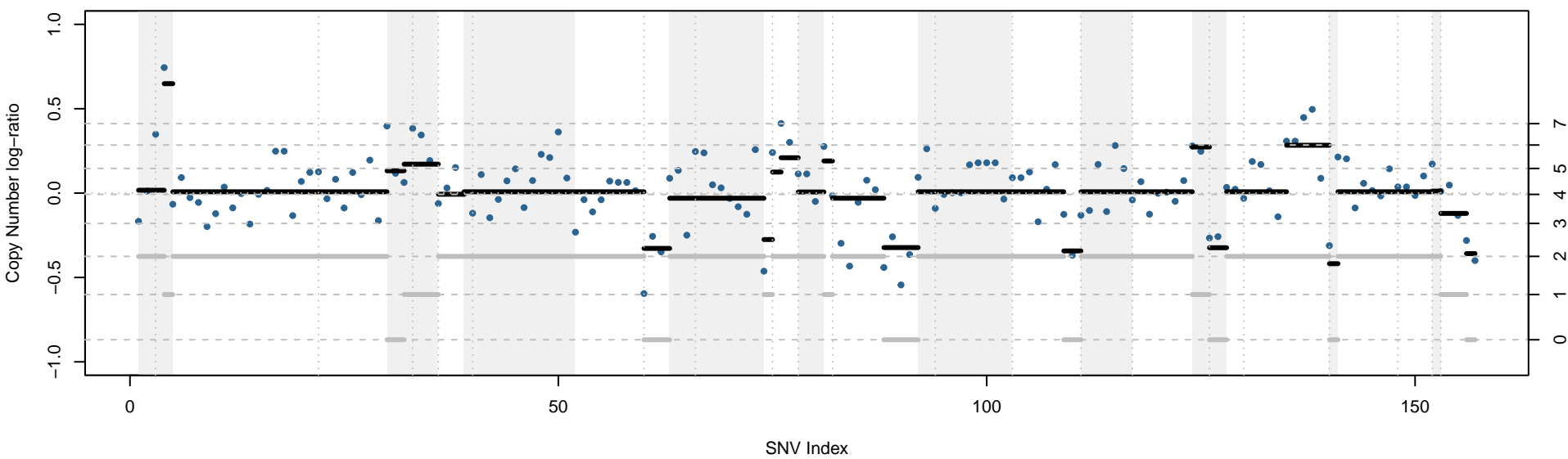


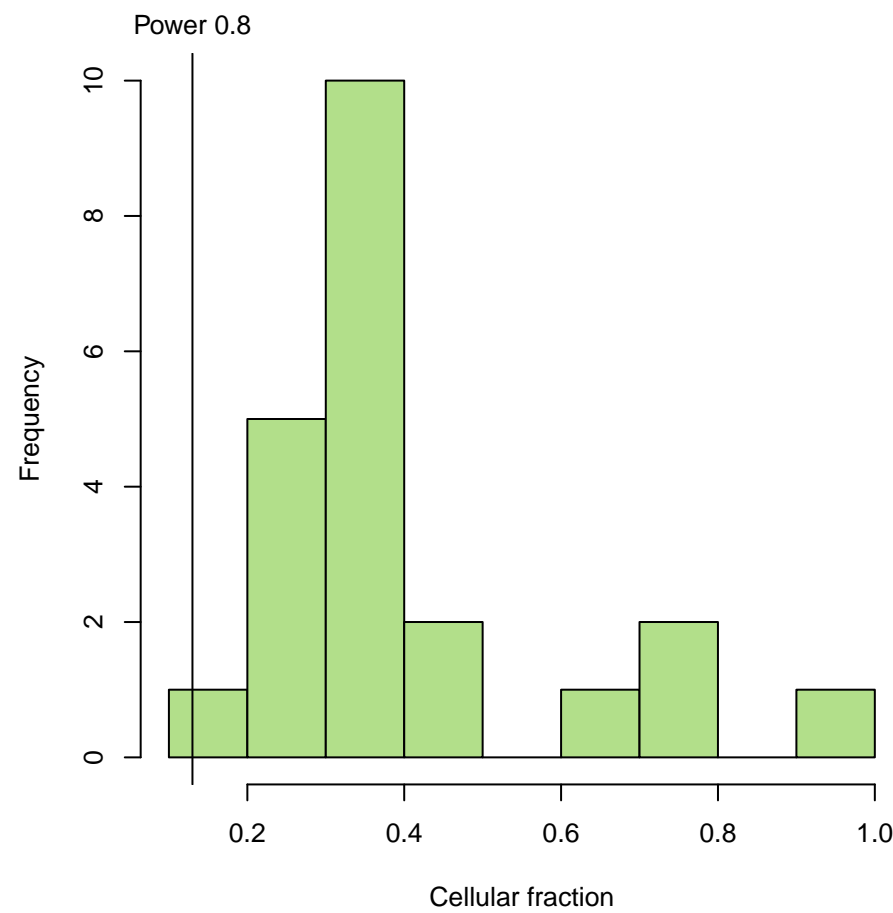
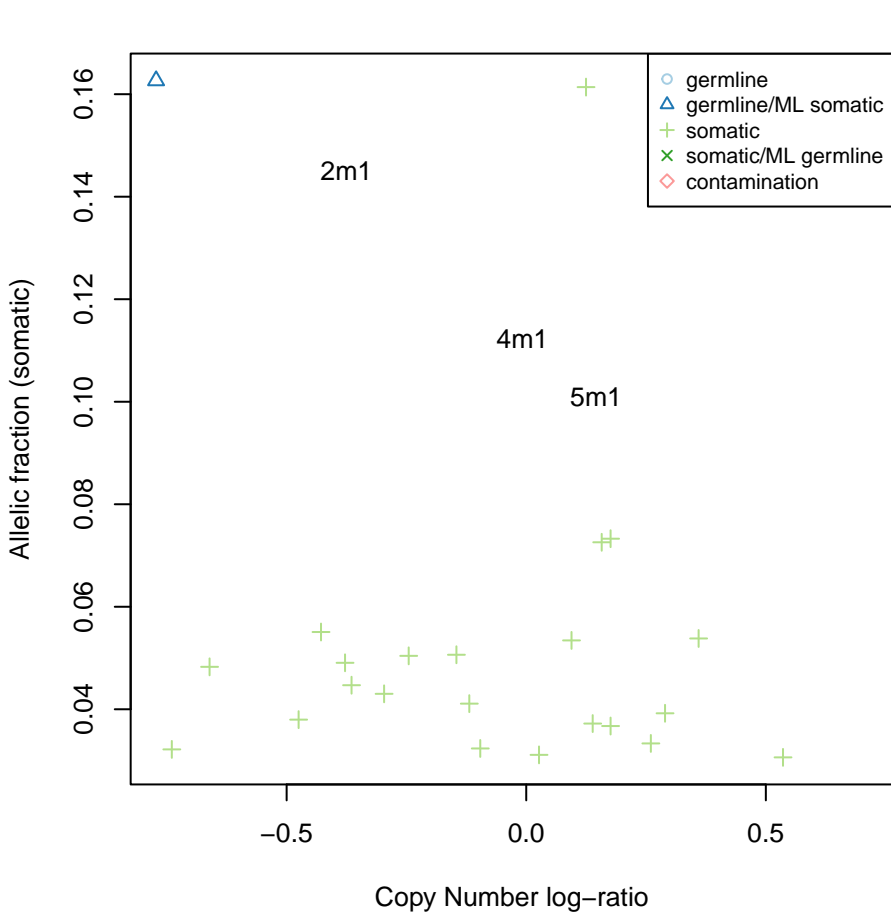
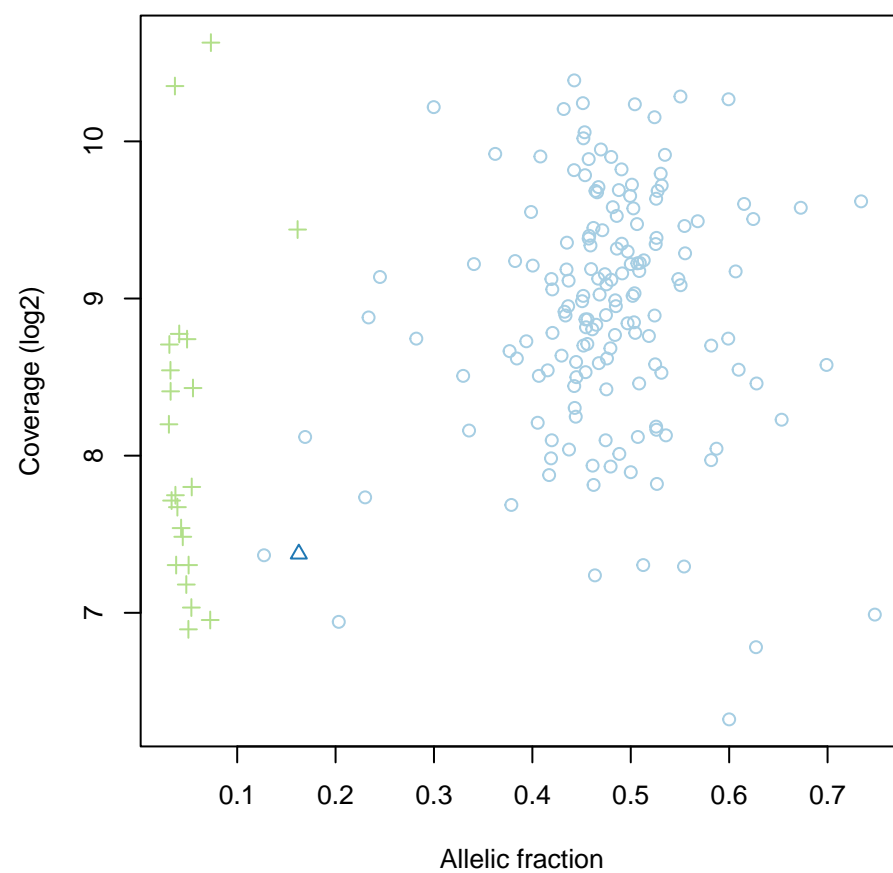
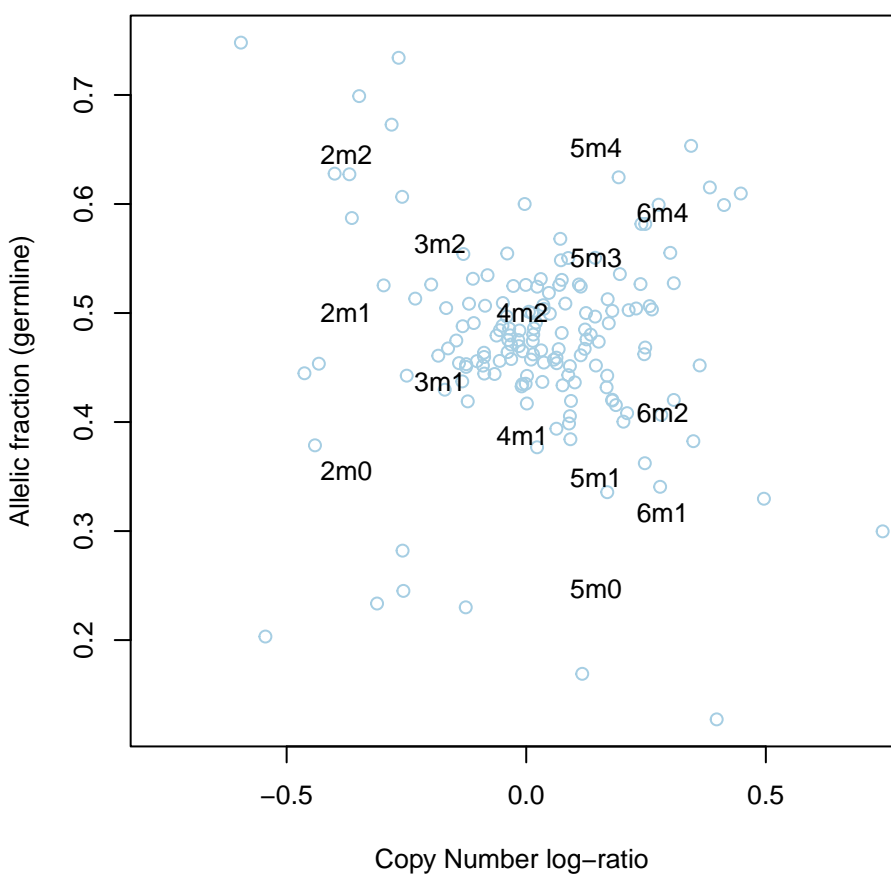


Purity: 0.29 Tumor ploidy: 4.048 SNV log-likelihood: -113.58 GoF: 92.3% Mean coverage: 527,500

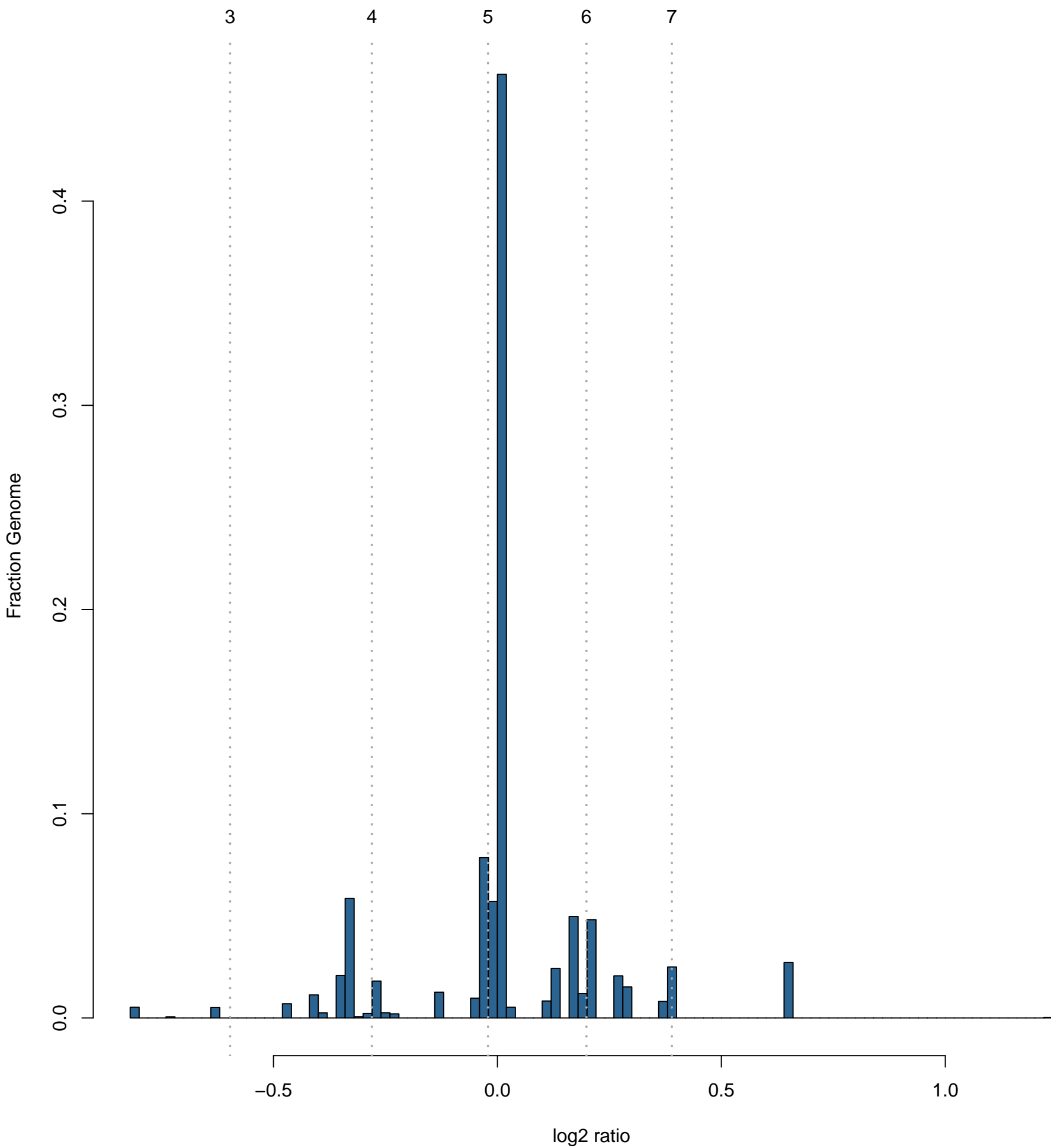


SCNA-fit log-likelihood: -4941.63

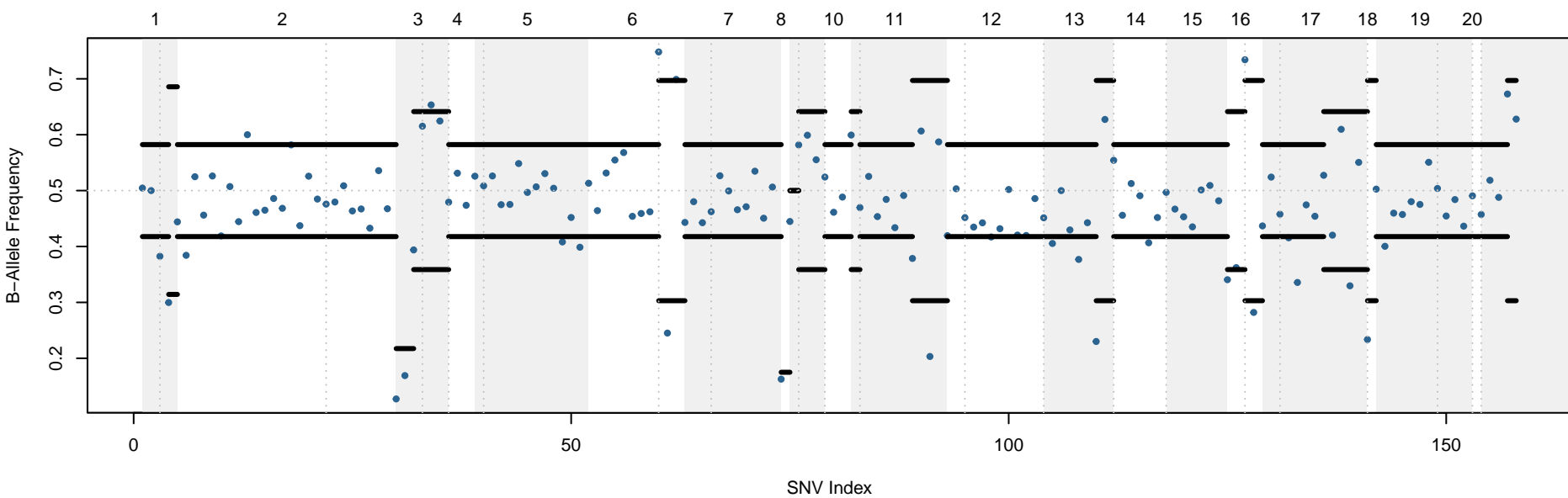




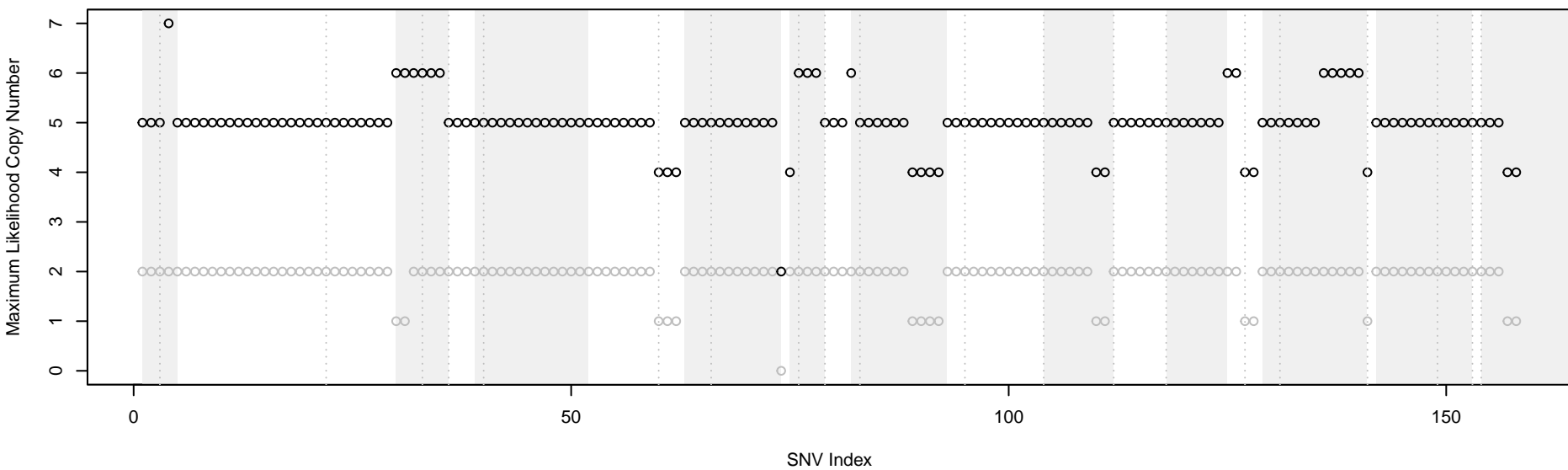
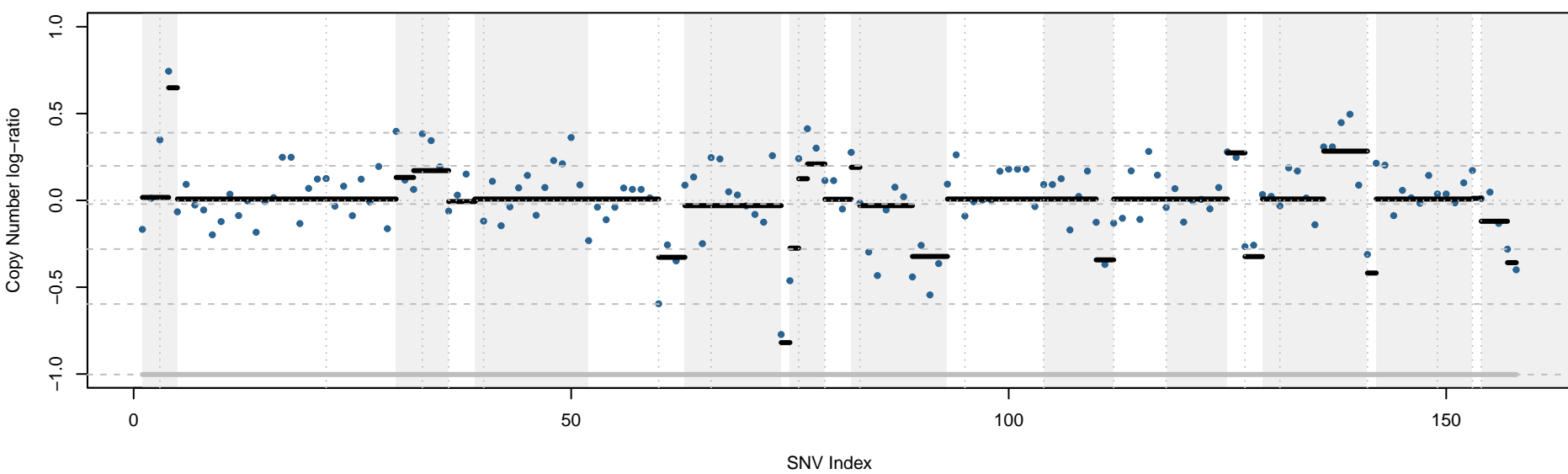
Purity: 0.65 Tumor ploidy: 5.089

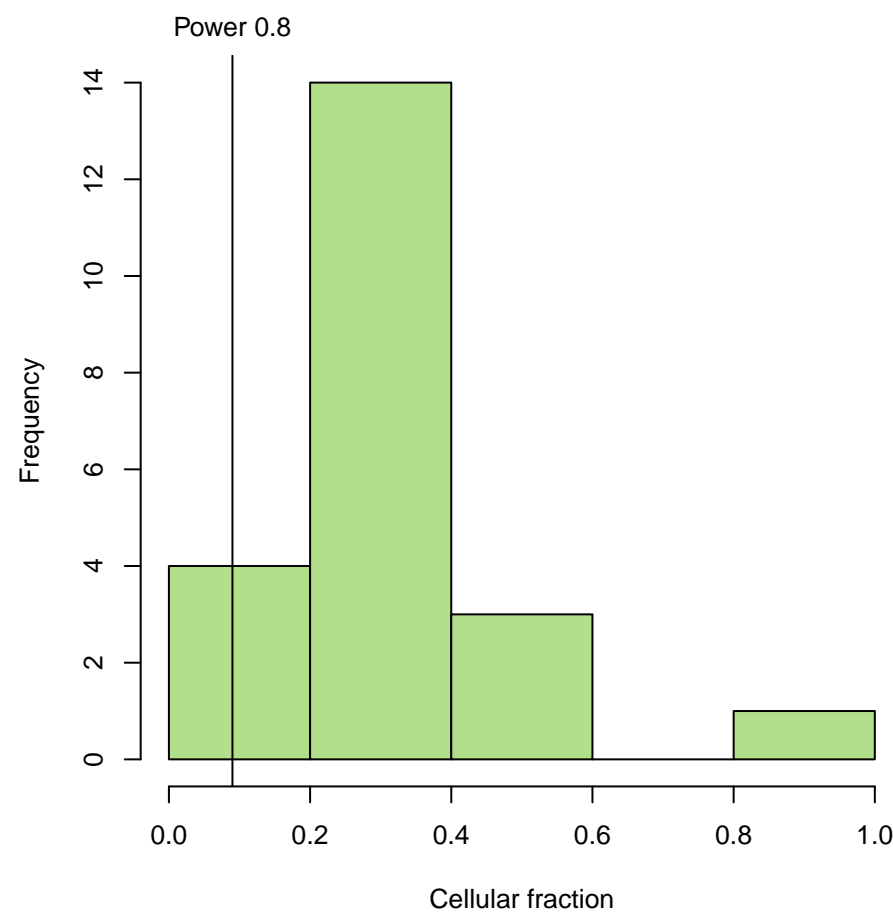
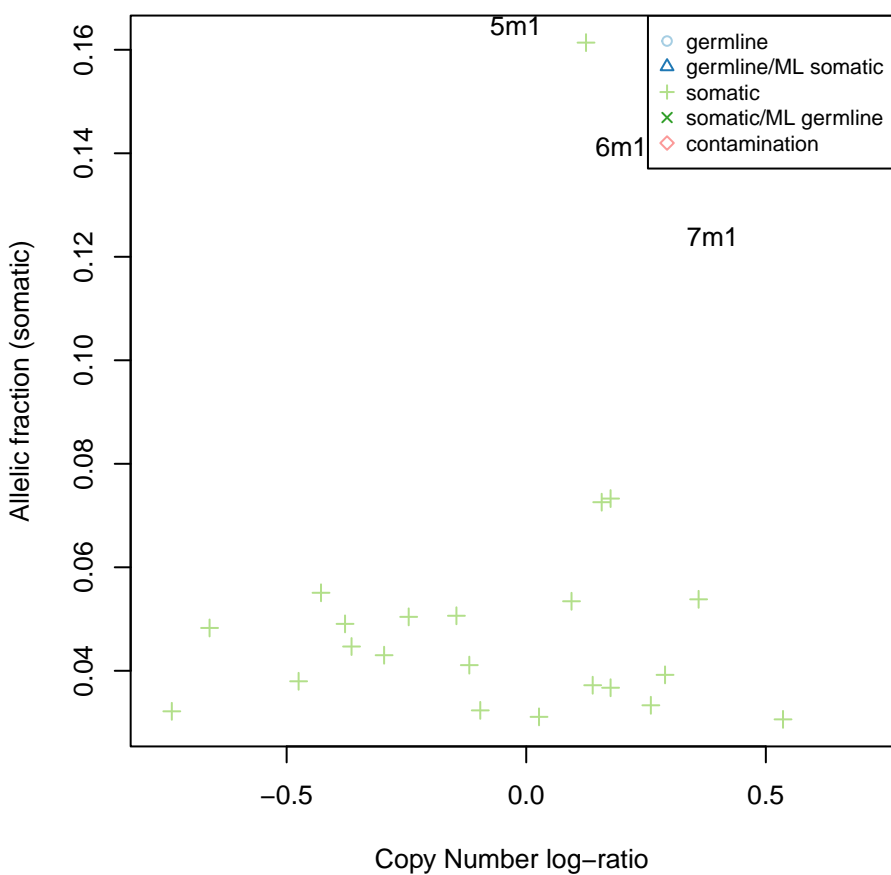
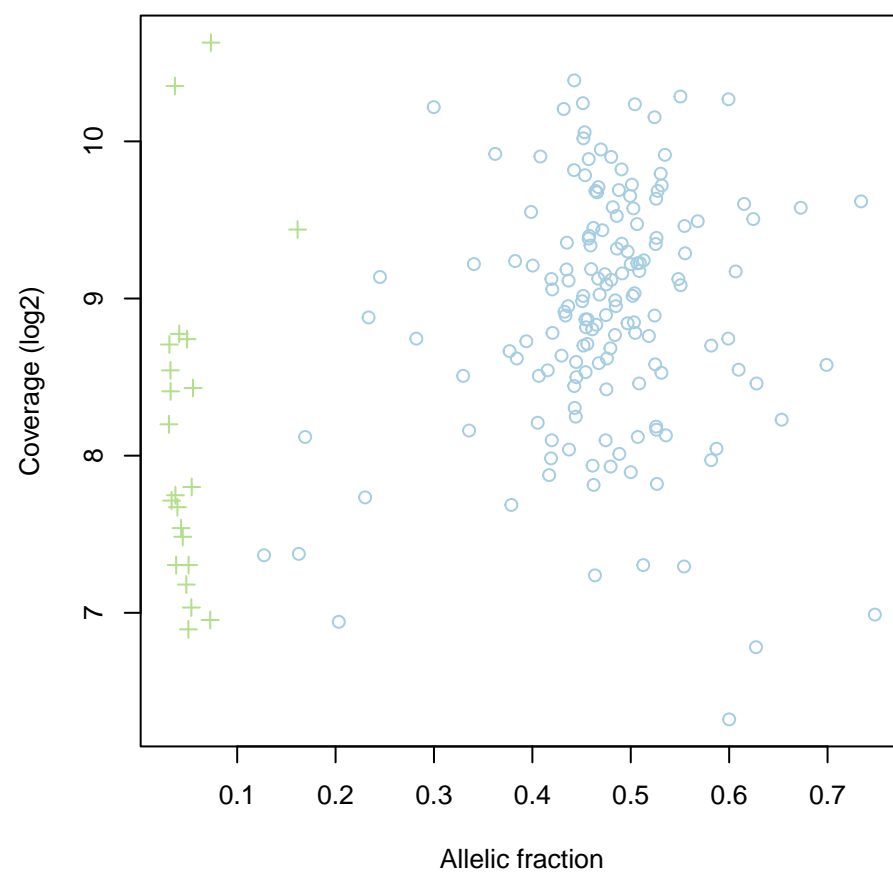
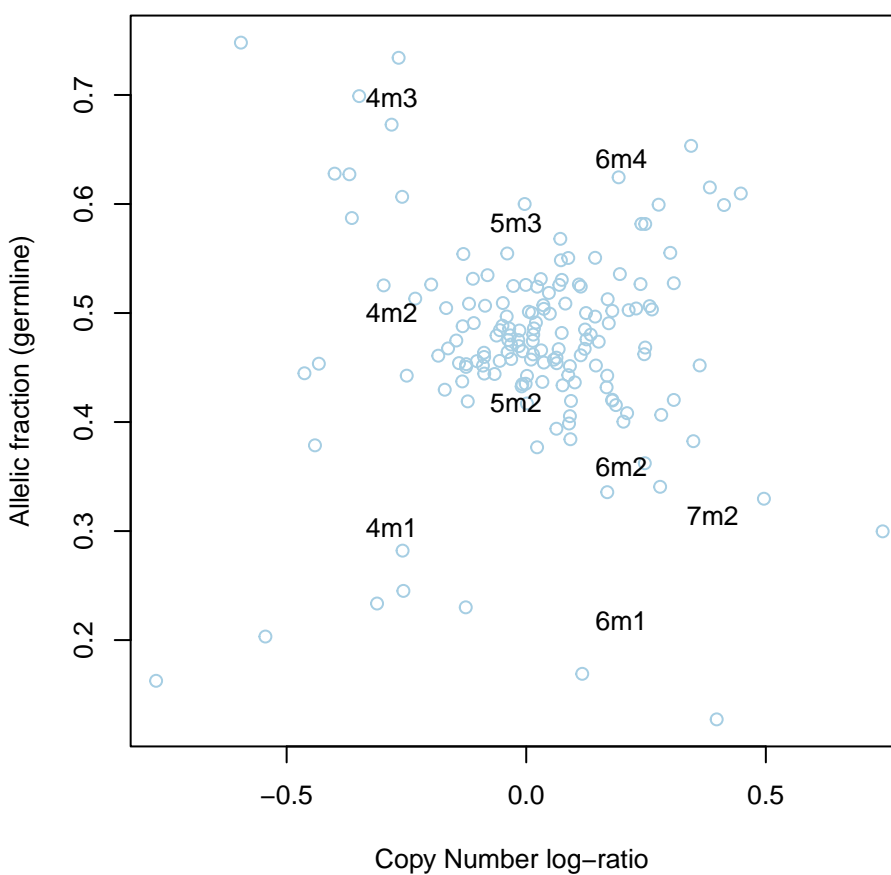


Purity: 0.65 Tumor ploidy: 5.089 SNV log-likelihood: -263.02 GoF: 88.3% Mean coverage: 527,500

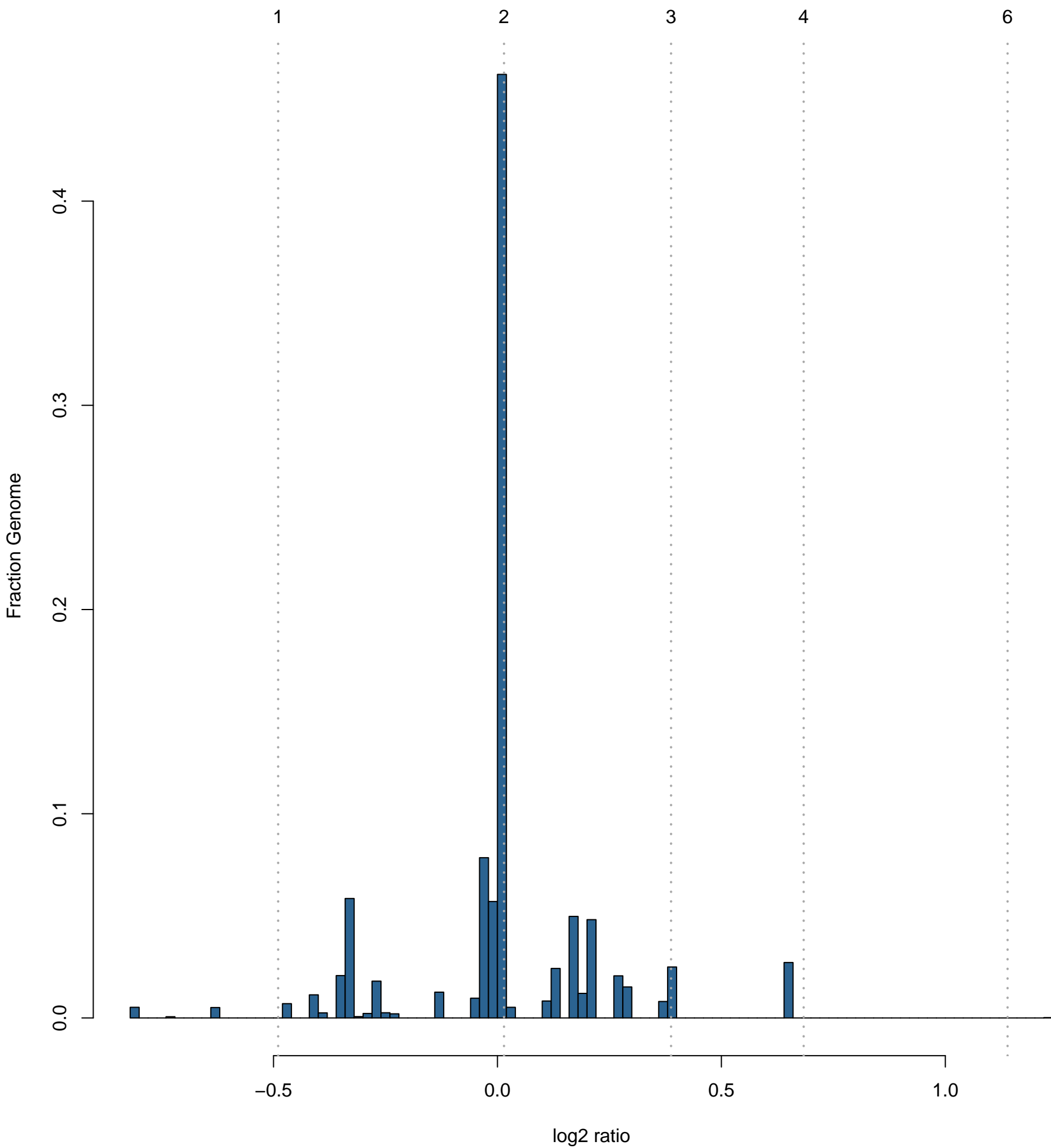


SCNA-fit log-likelihood: -4712.23

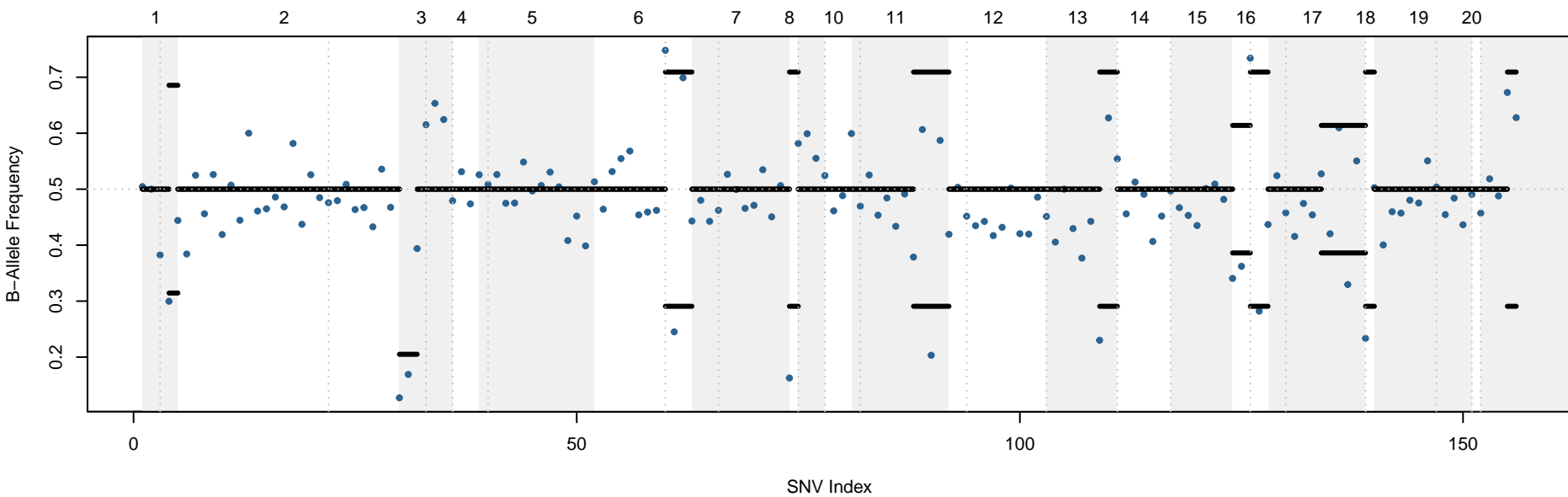




Purity: 0.59 Tumor ploidy: 1.966



Purity: 0.59 Tumor ploidy: 1.966 SNV log-likelihood: -153.57 GoF: 68.4% Mean coverage: 527,500



SCNA-fit log-likelihood: -5084.65

