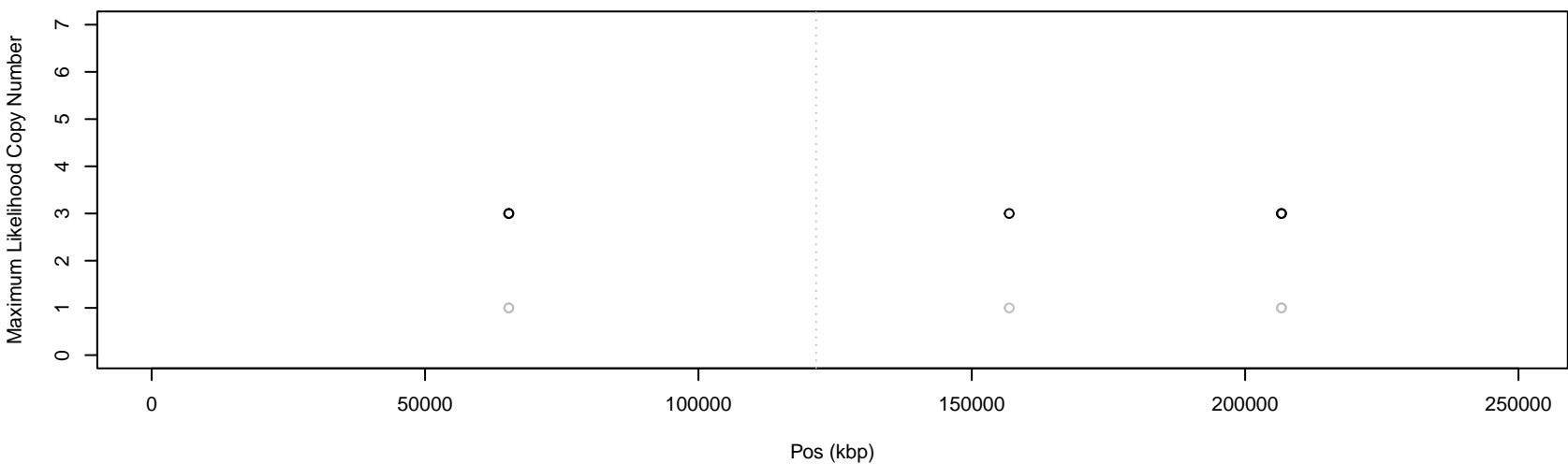
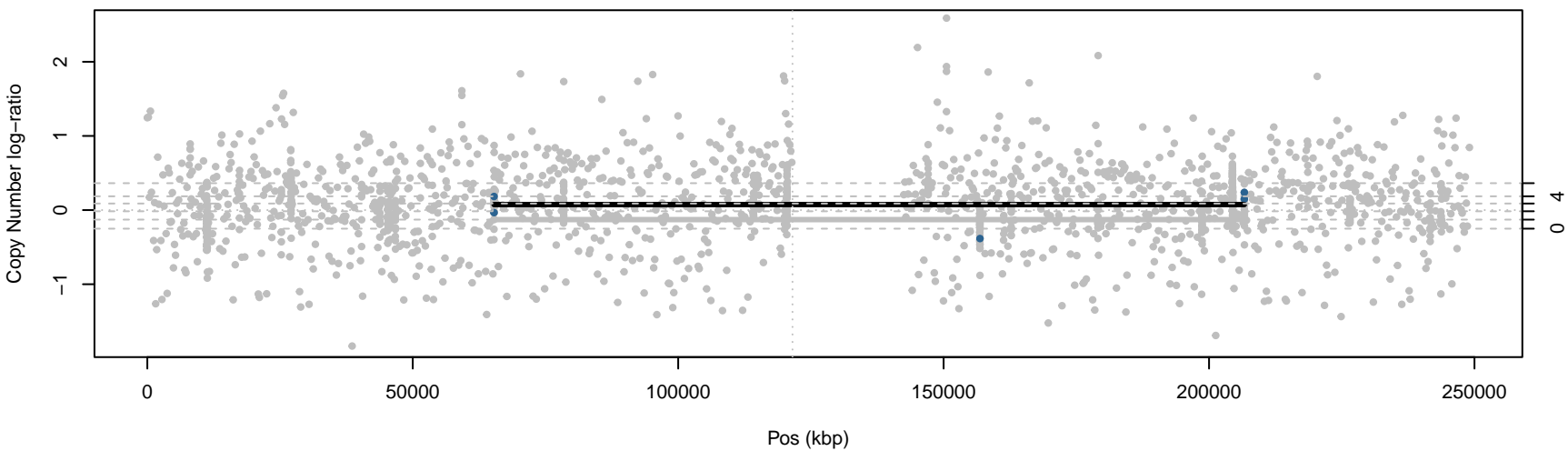
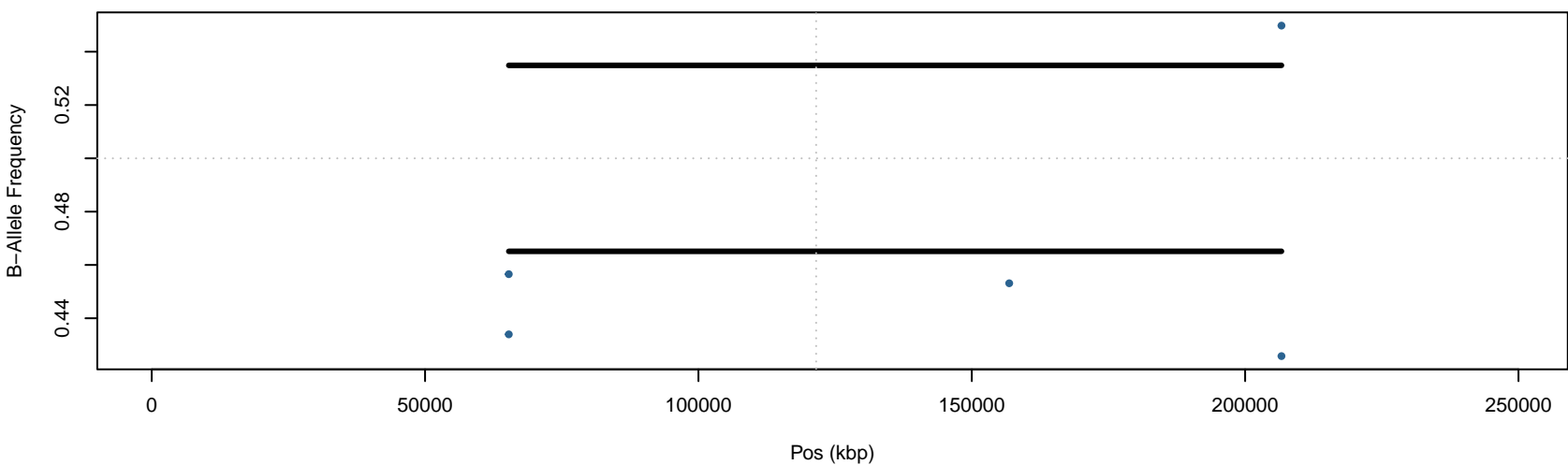
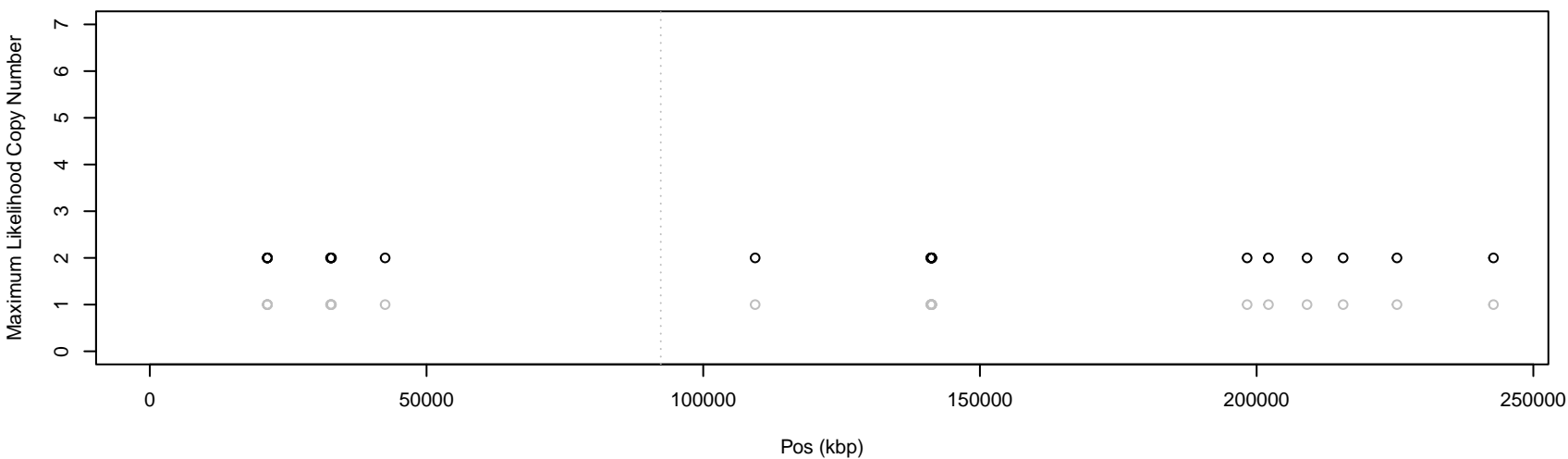
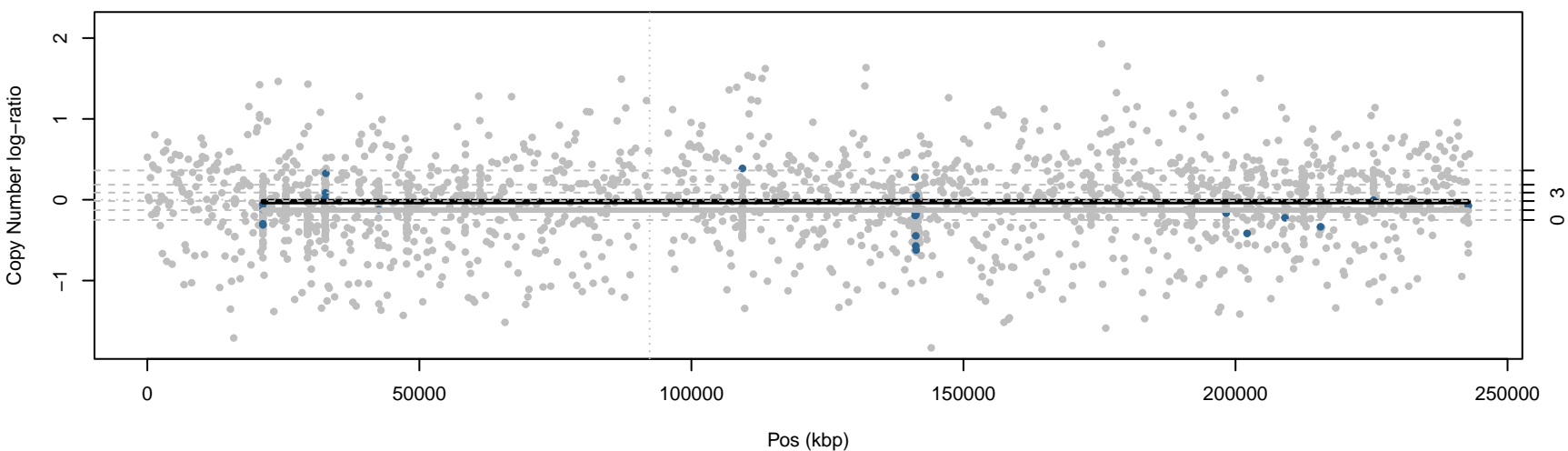
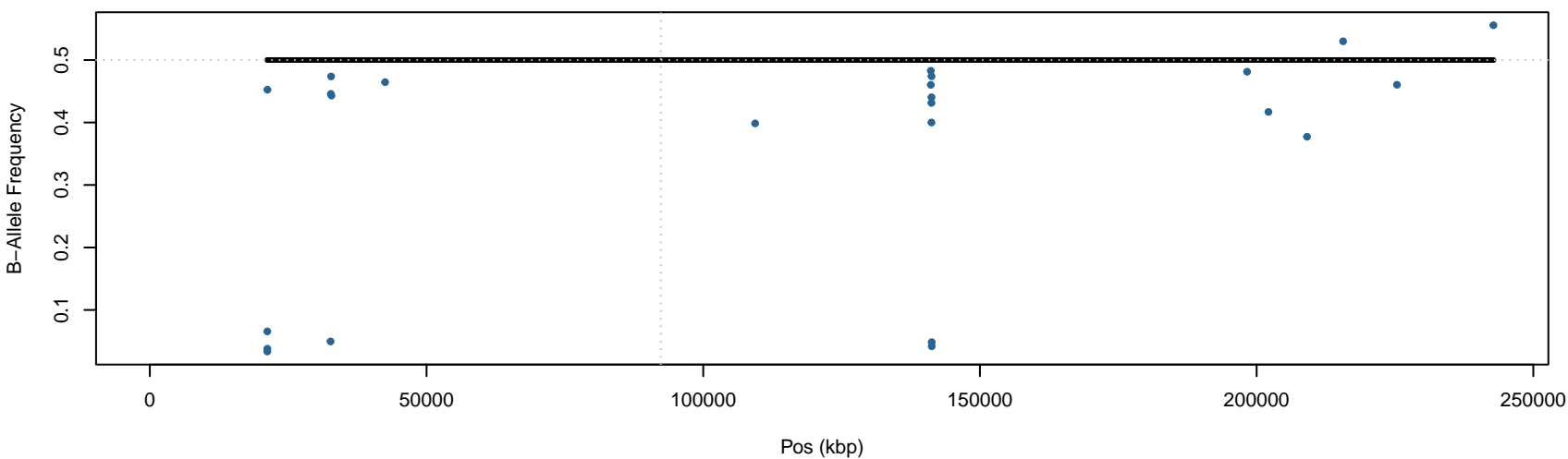


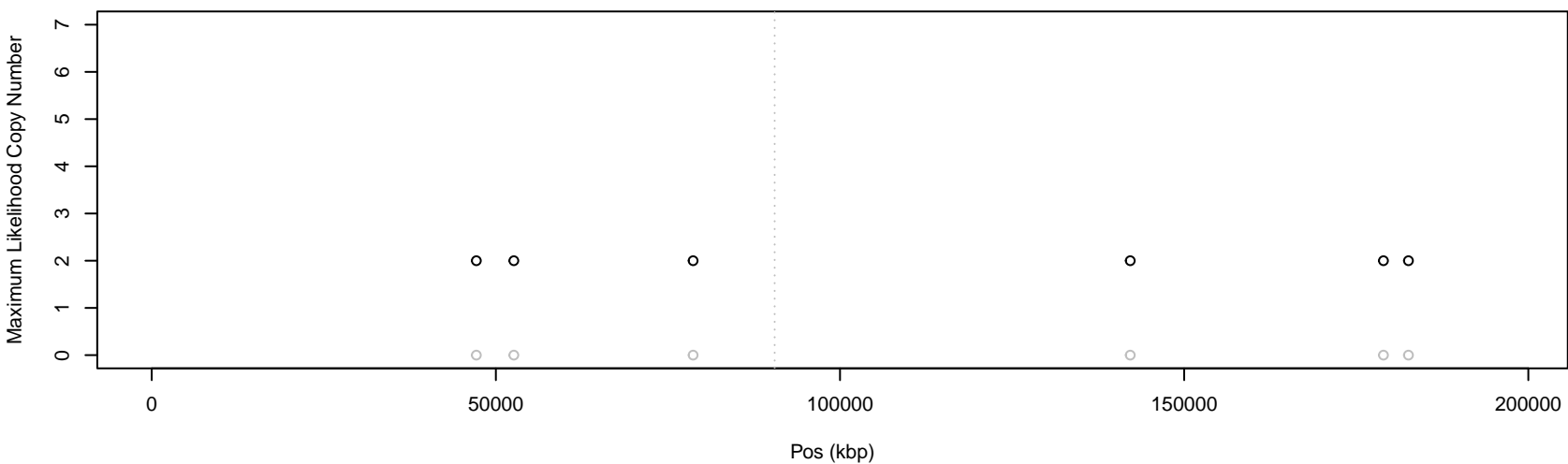
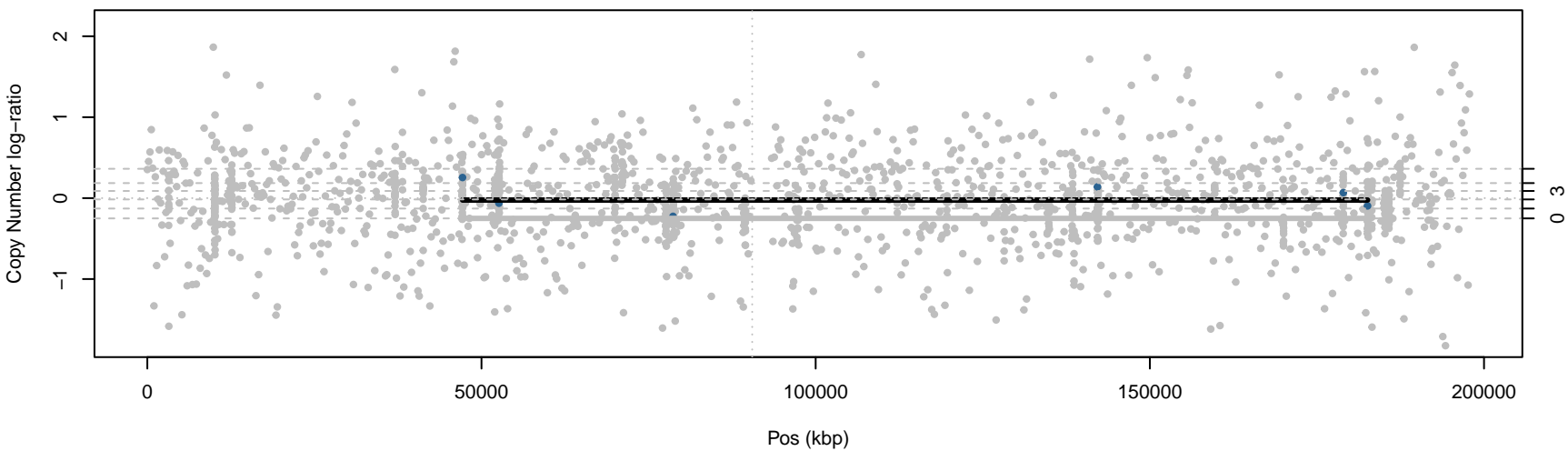
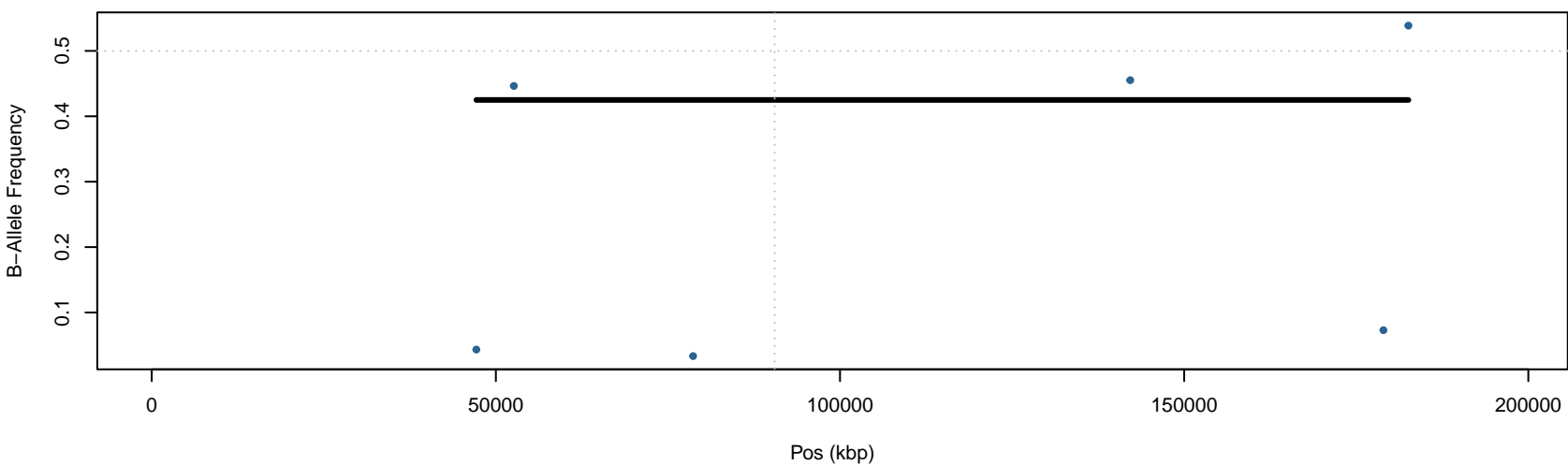
Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108,387 Chromosome: 1



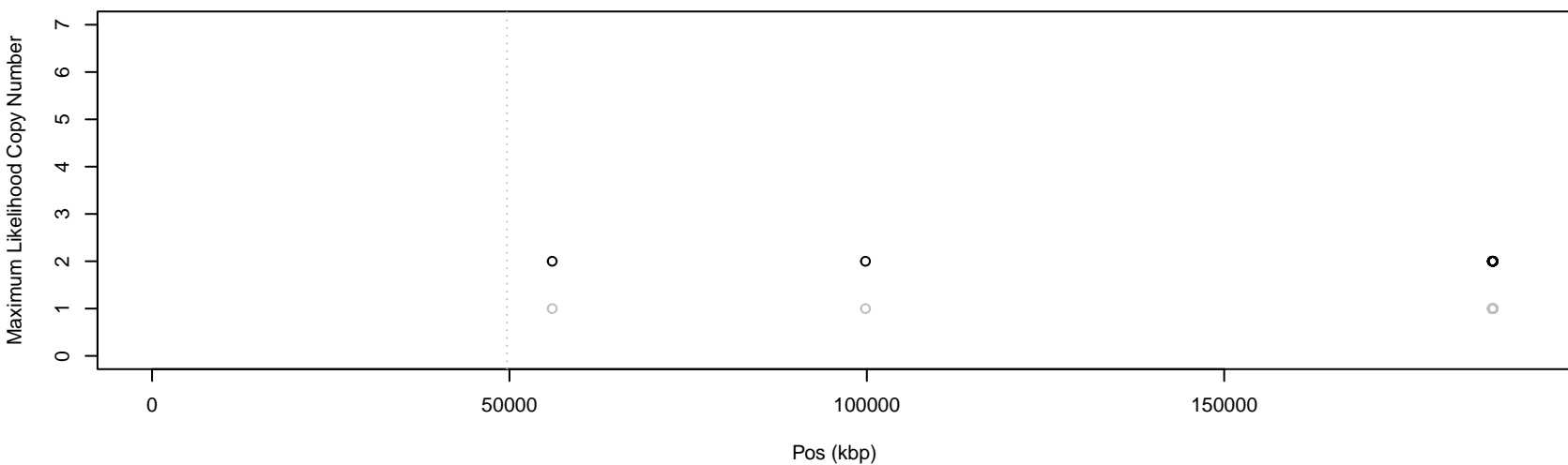
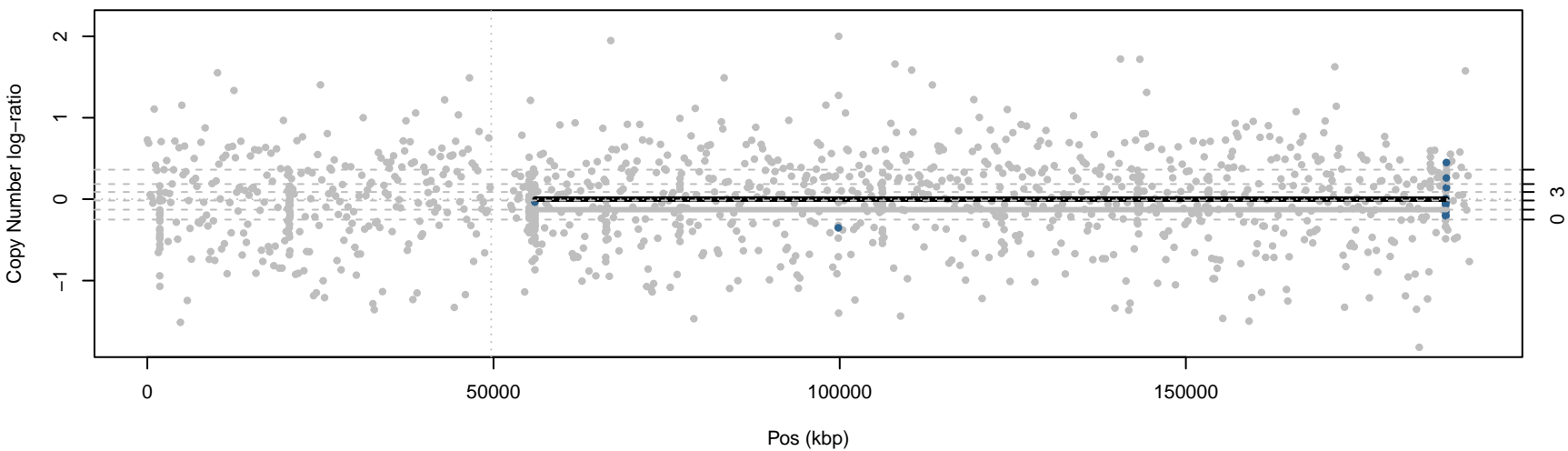
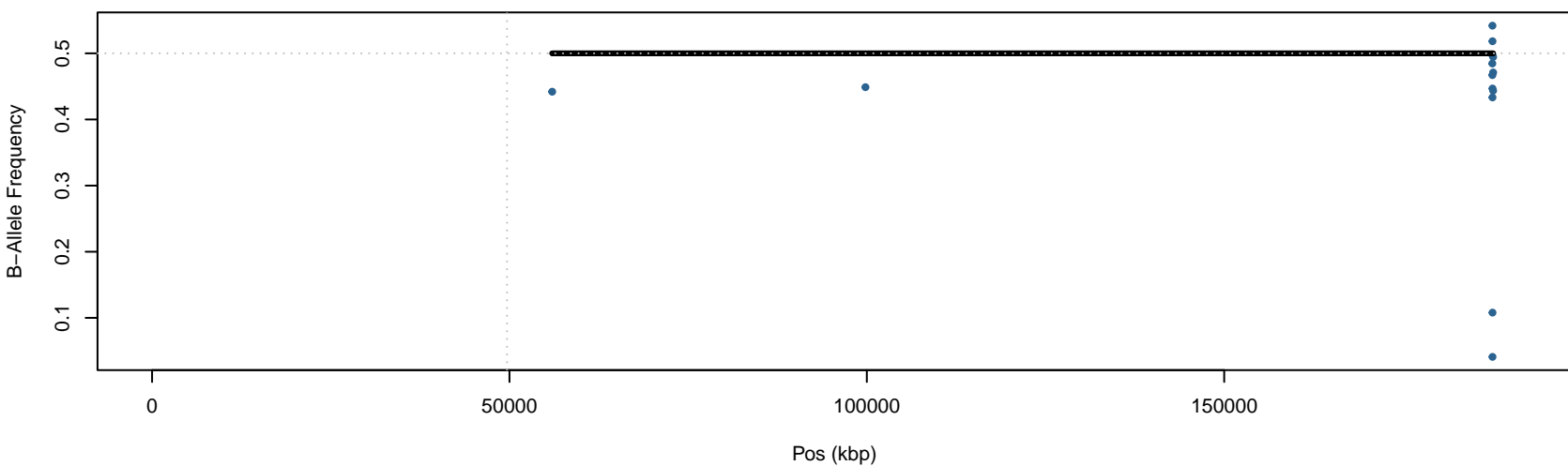
Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108,387 Chromosome: 2



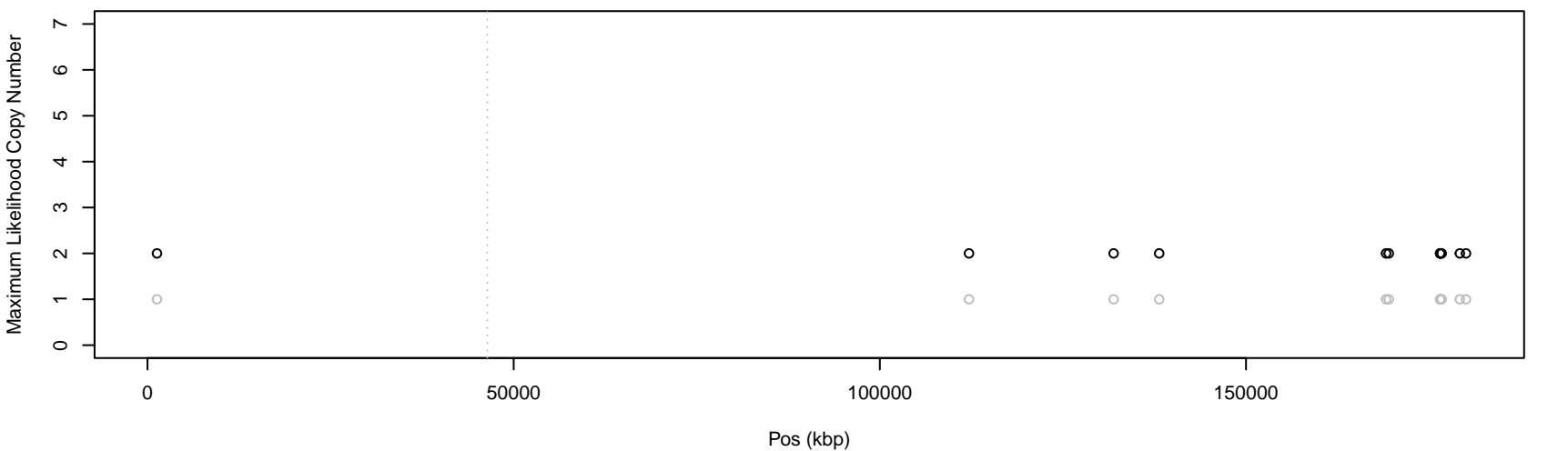
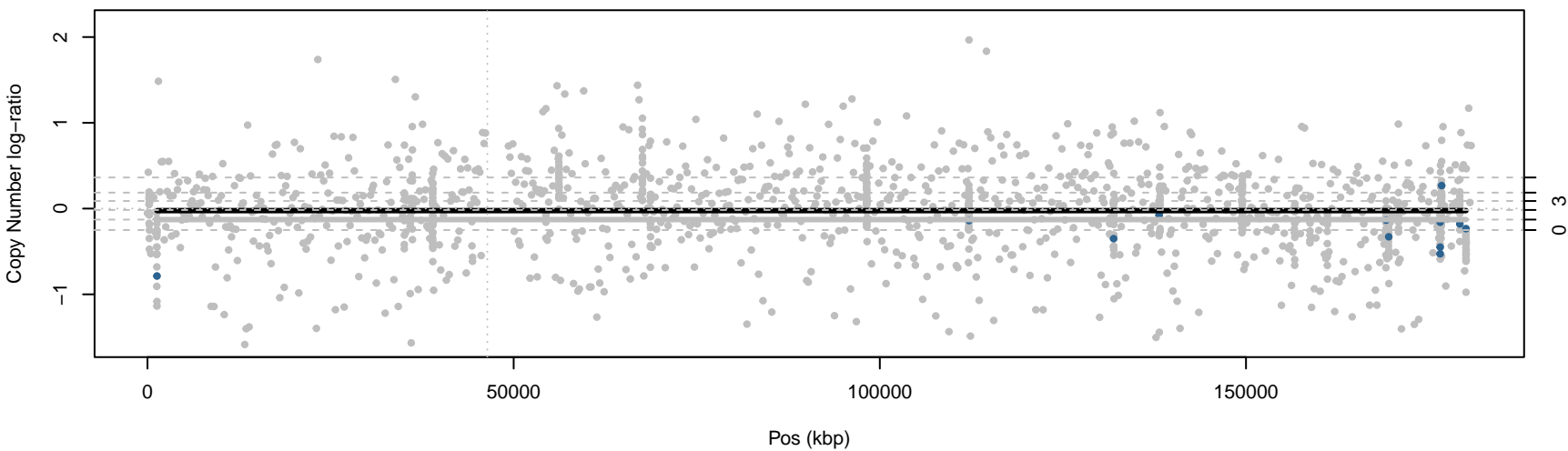
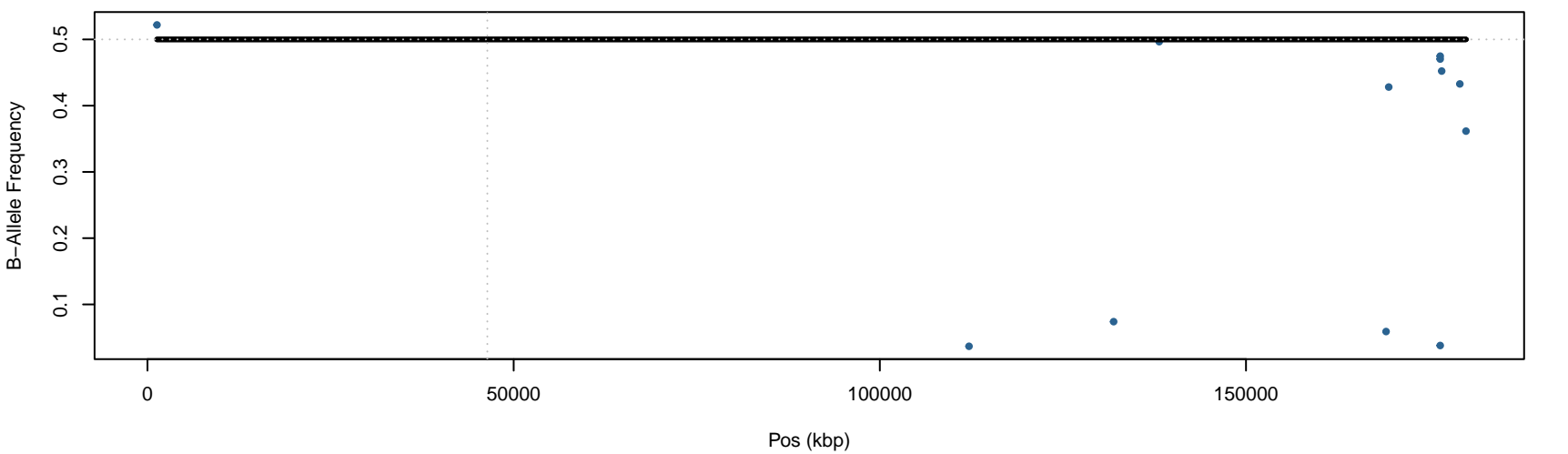
Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108;387 Chromosome: 3



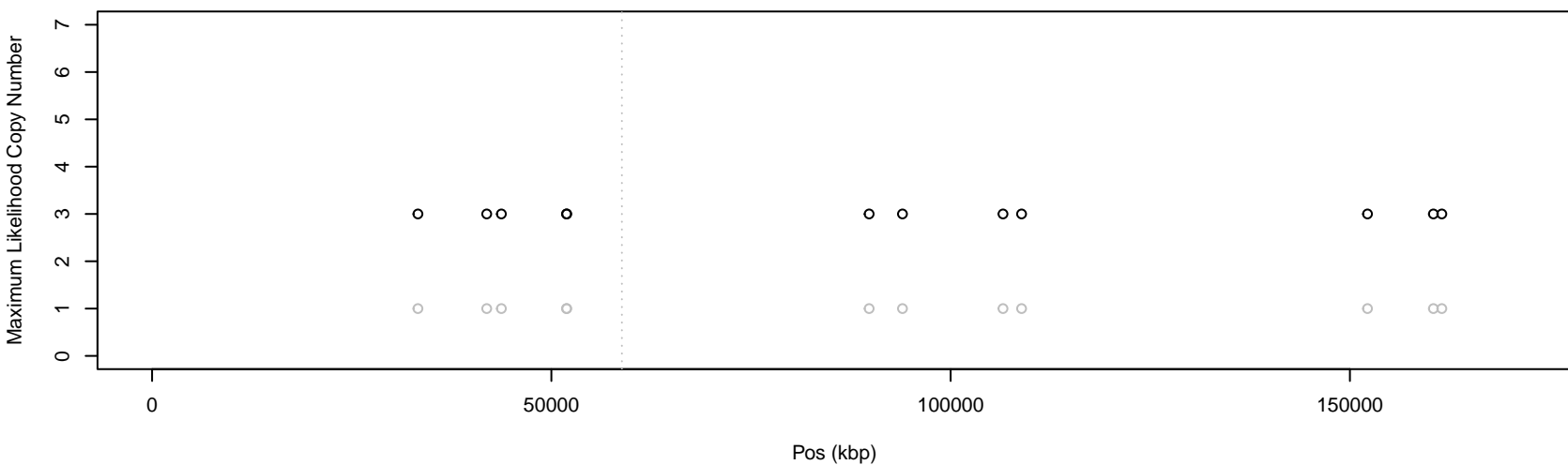
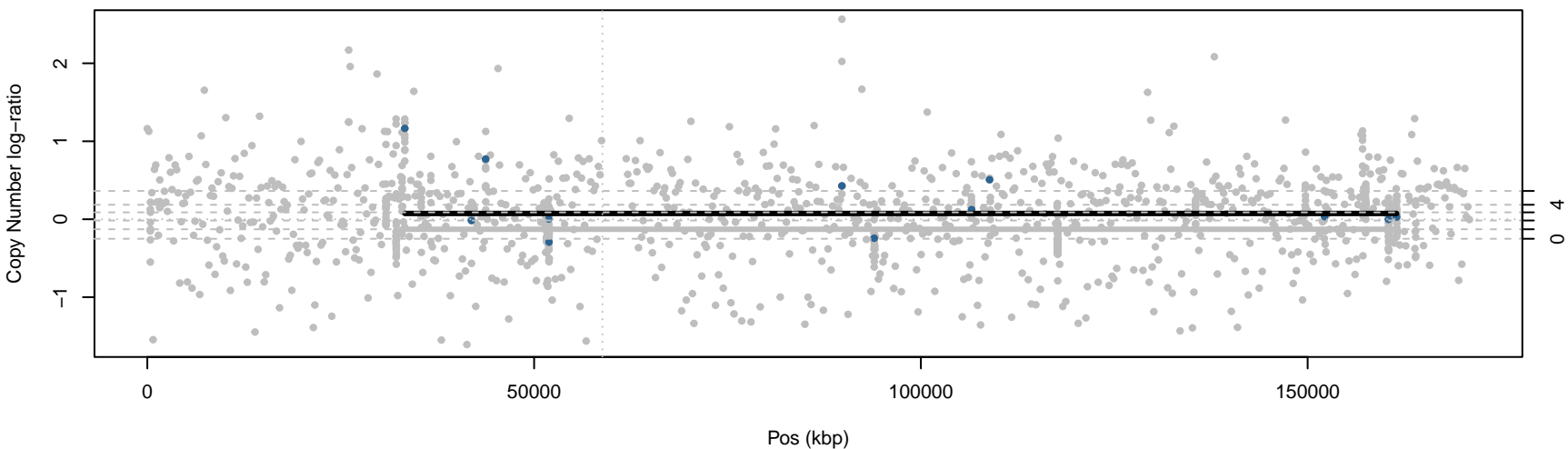
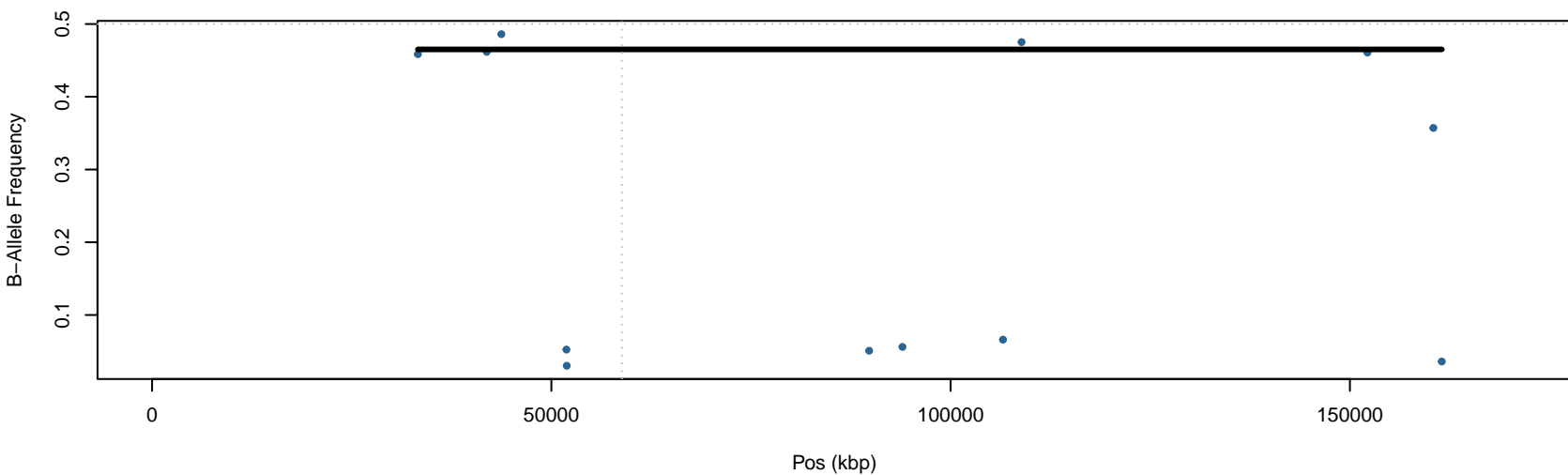
Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108;387 Chromosome: 4



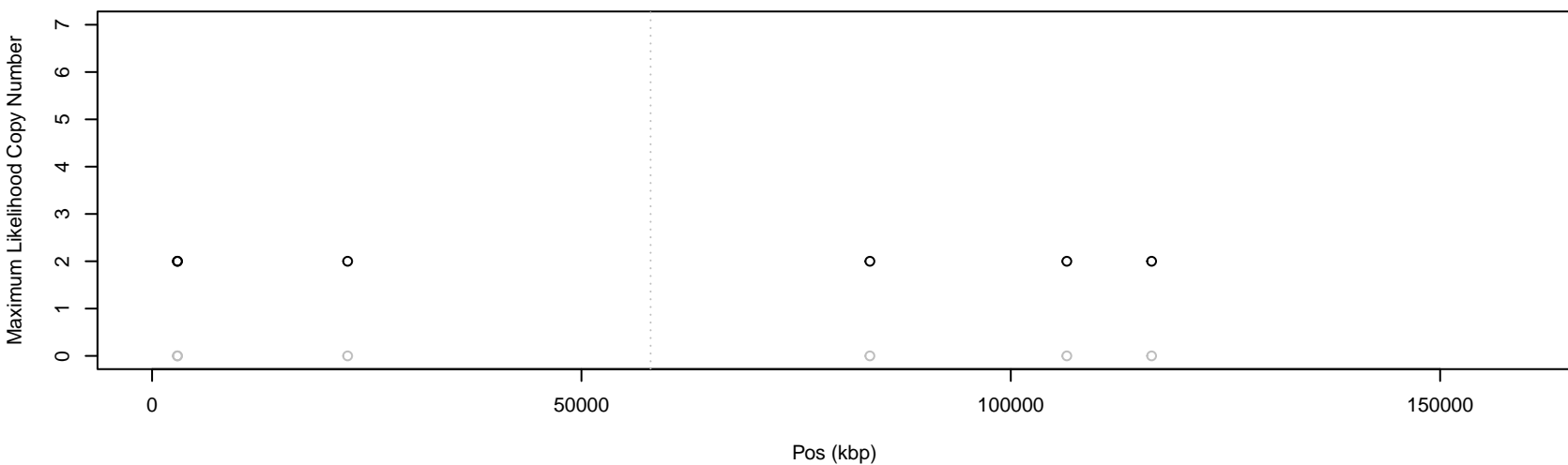
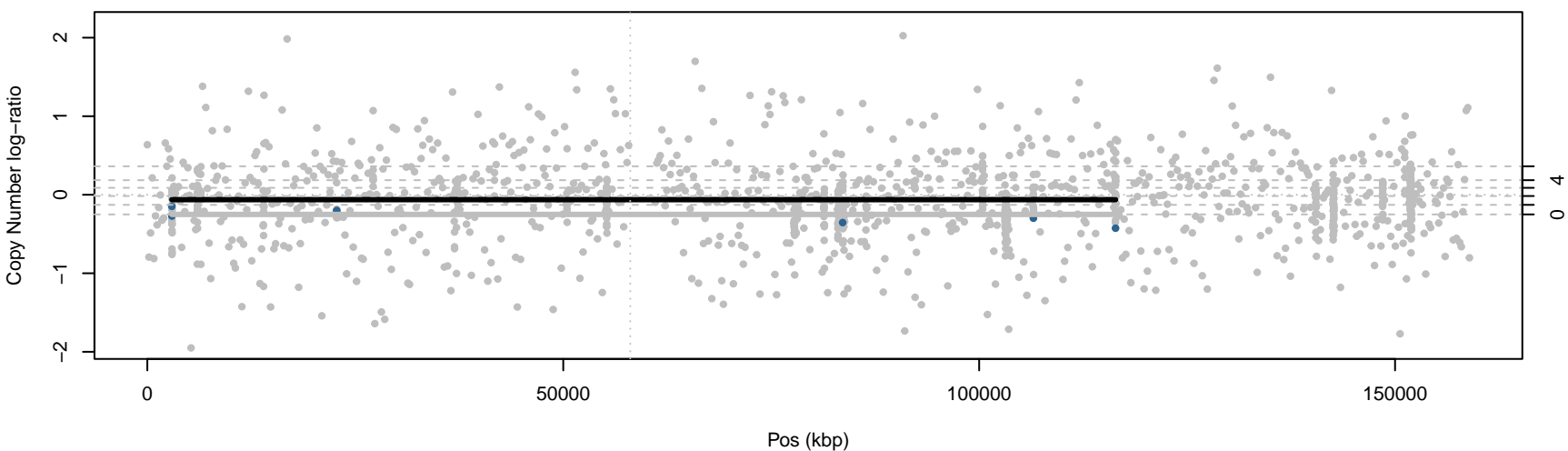
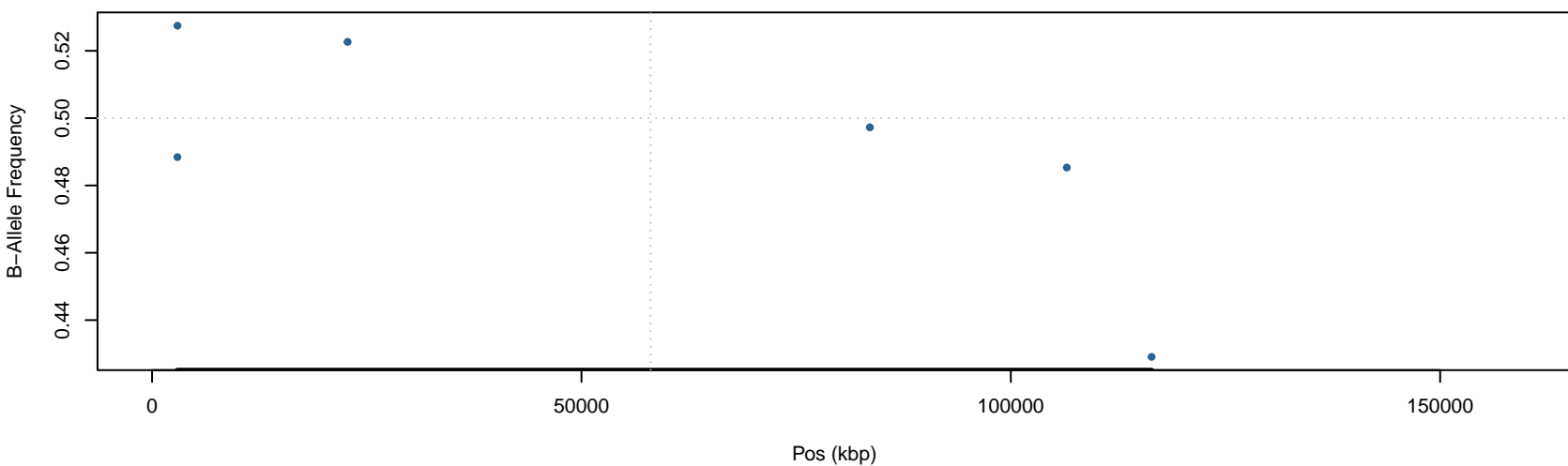
Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108;387 Chromosome: 5



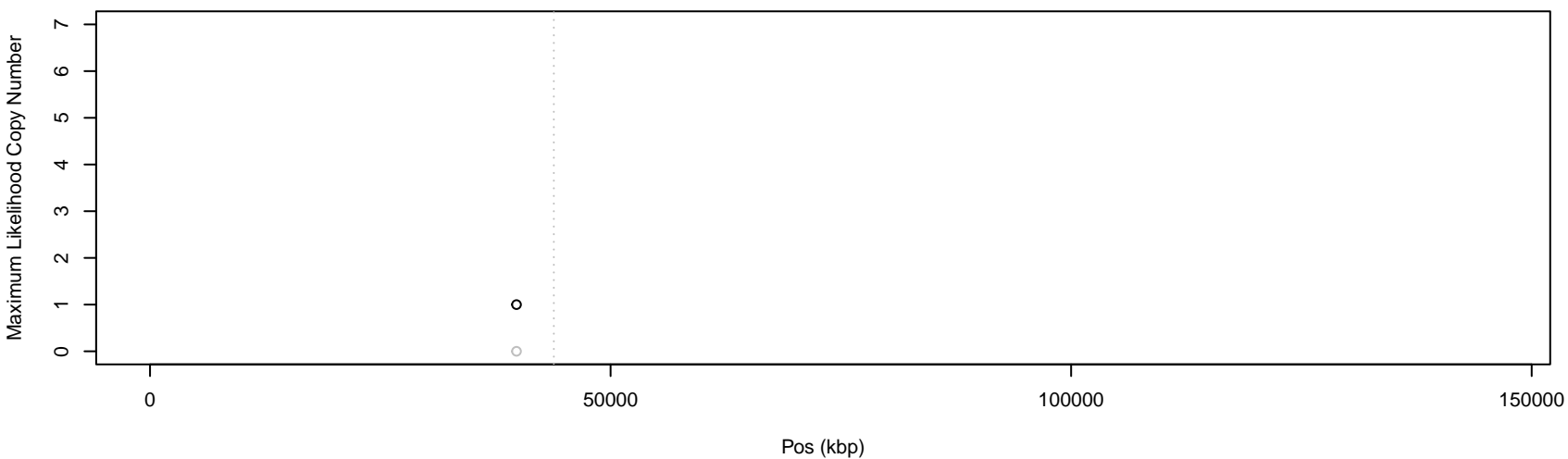
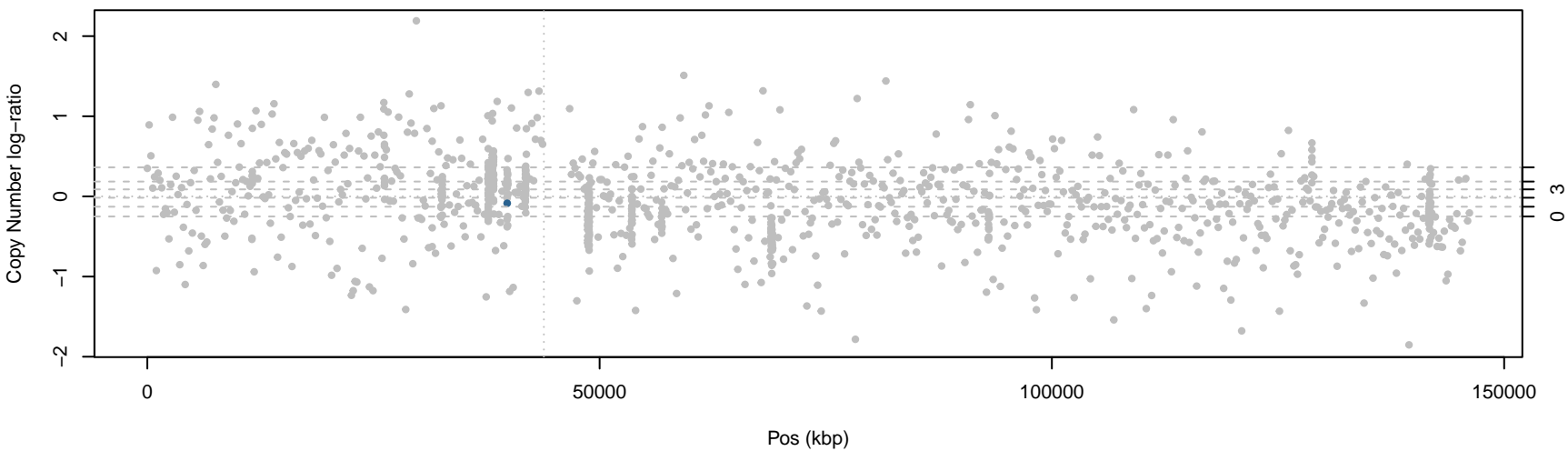
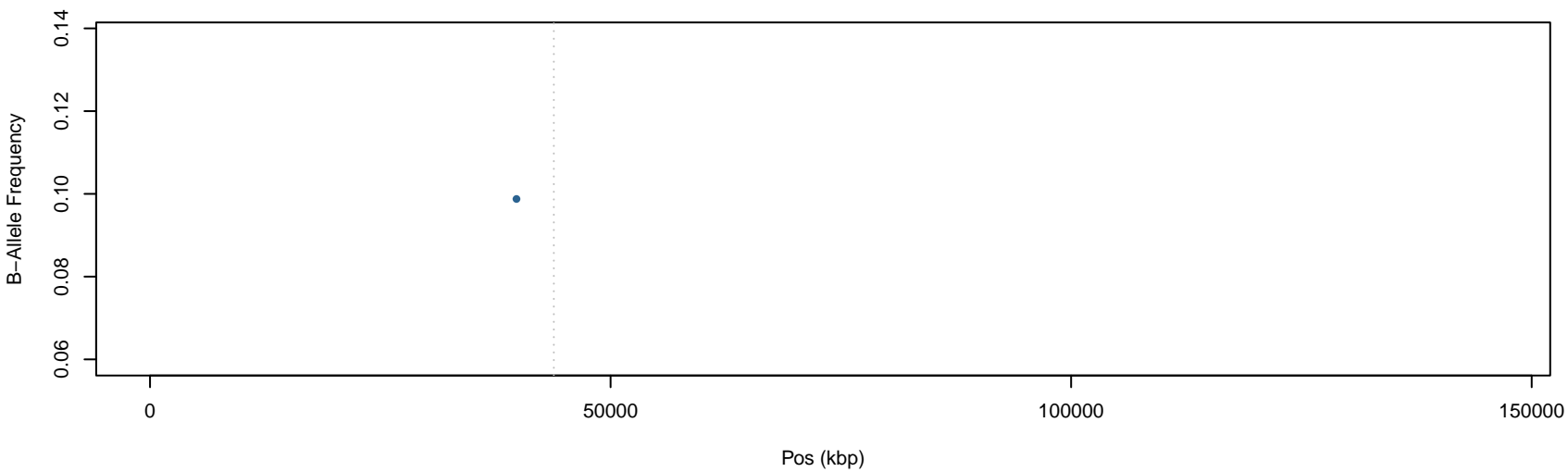
Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108;387 Chromosome: 6



Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108,387 Chromosome: 7

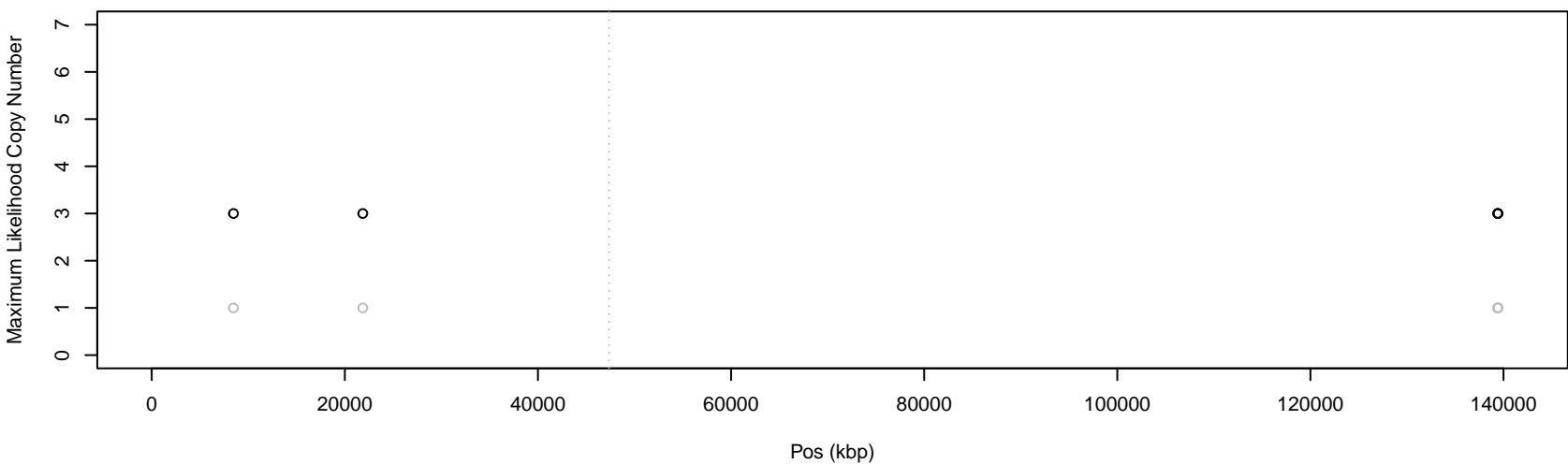
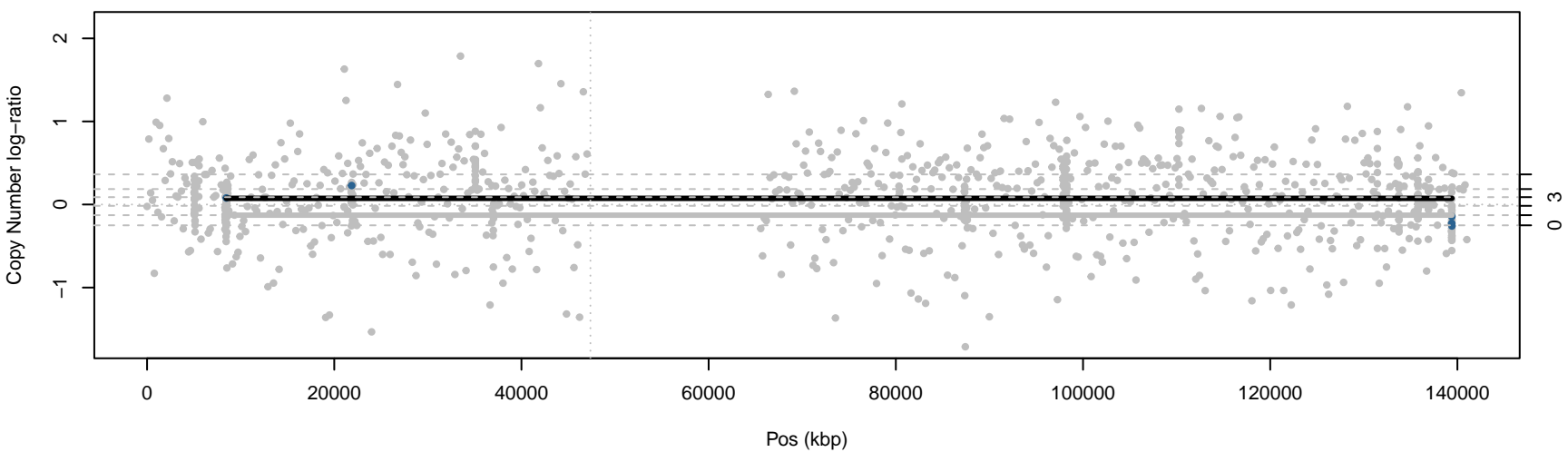
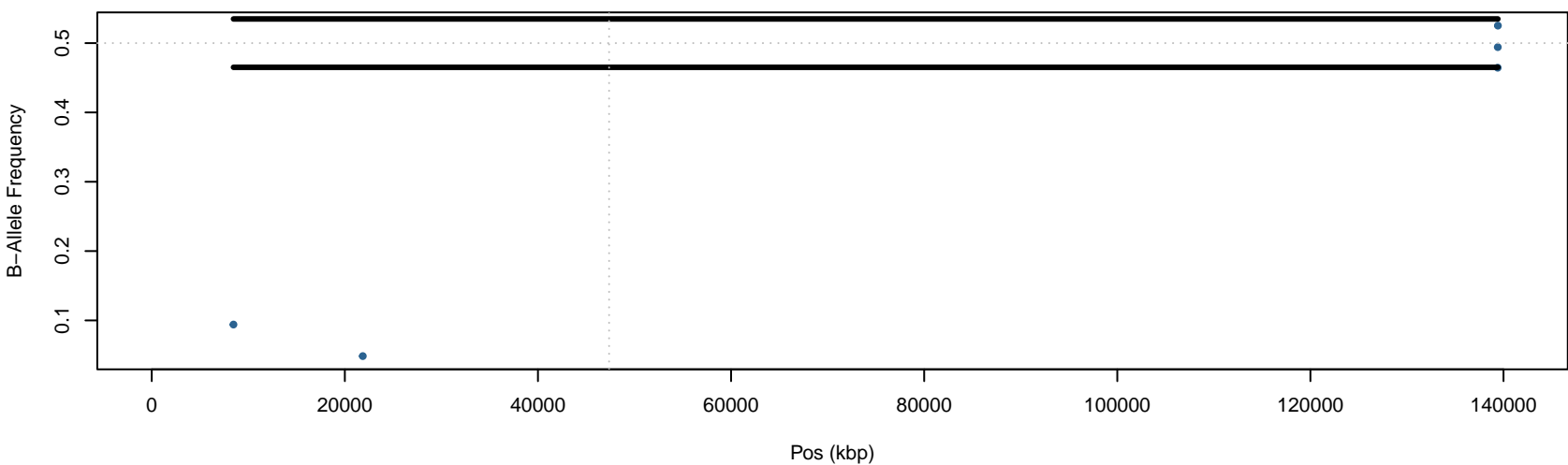


Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108,387 Chromosome: 8

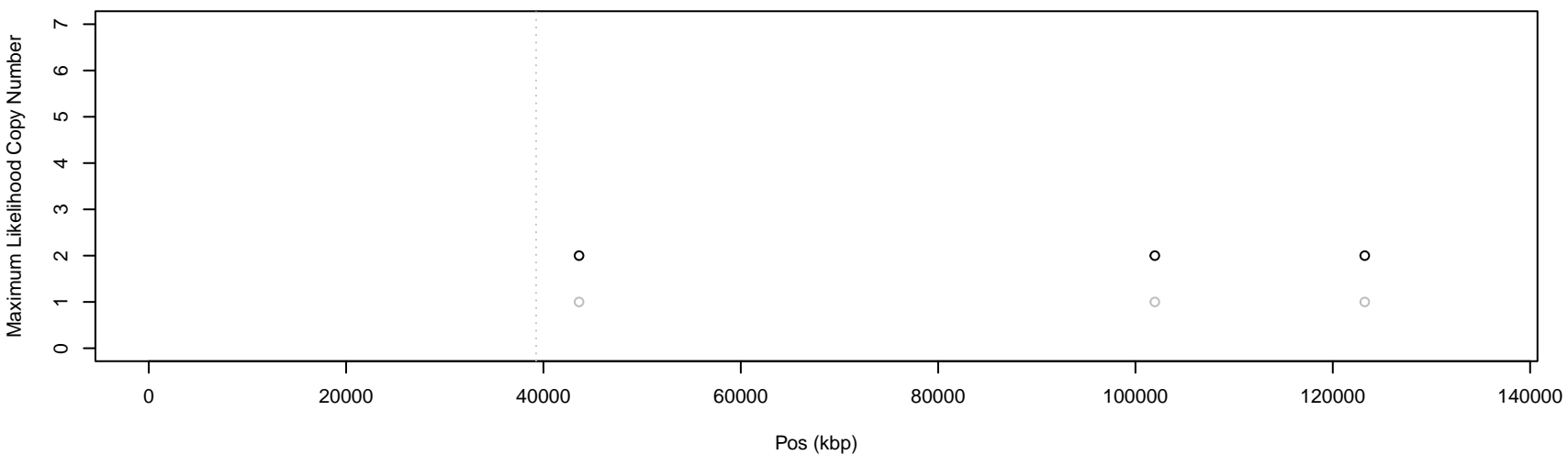
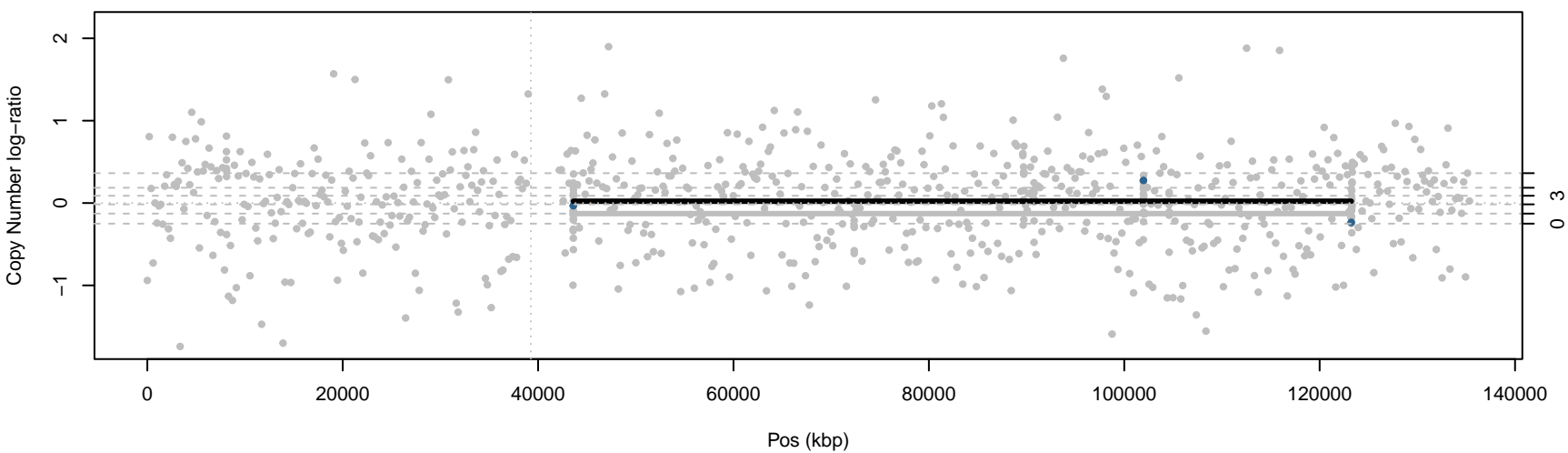
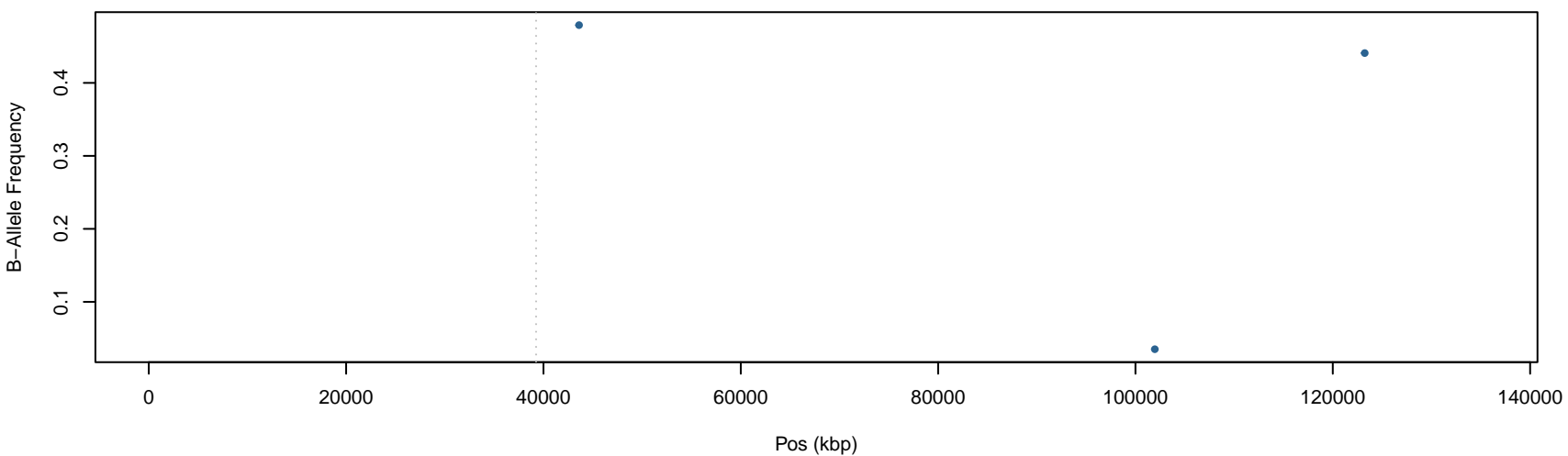




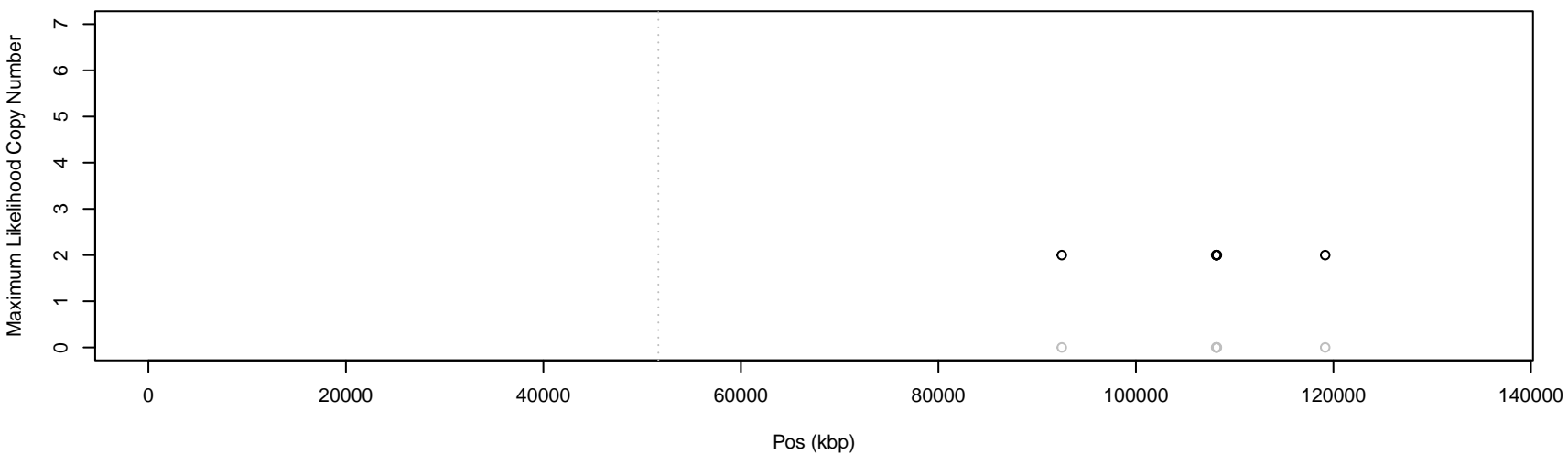
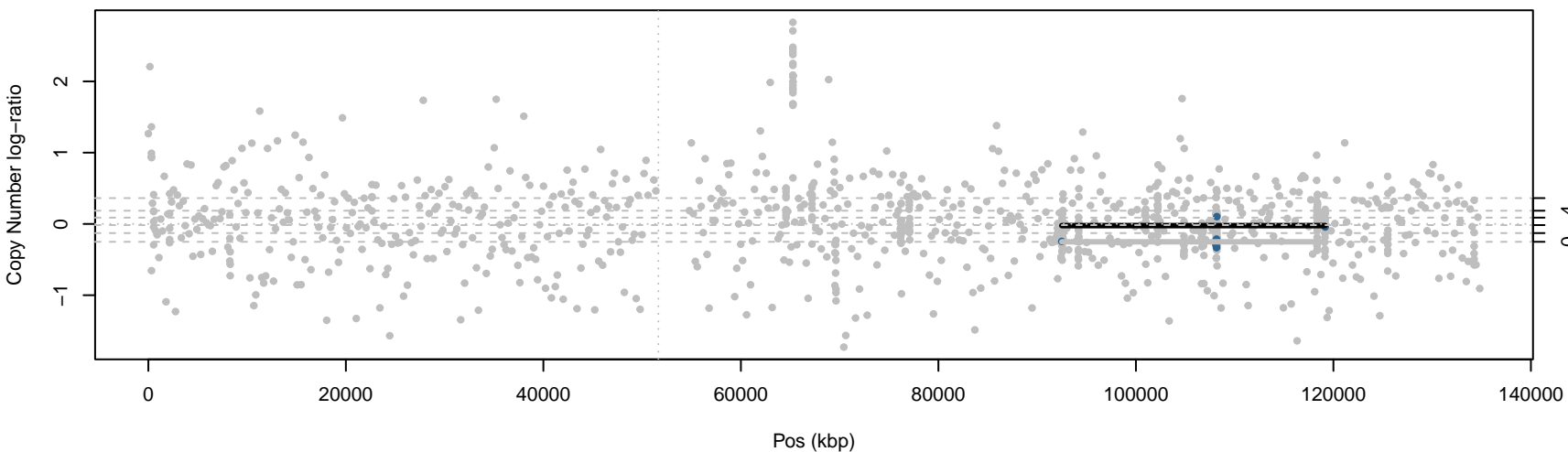
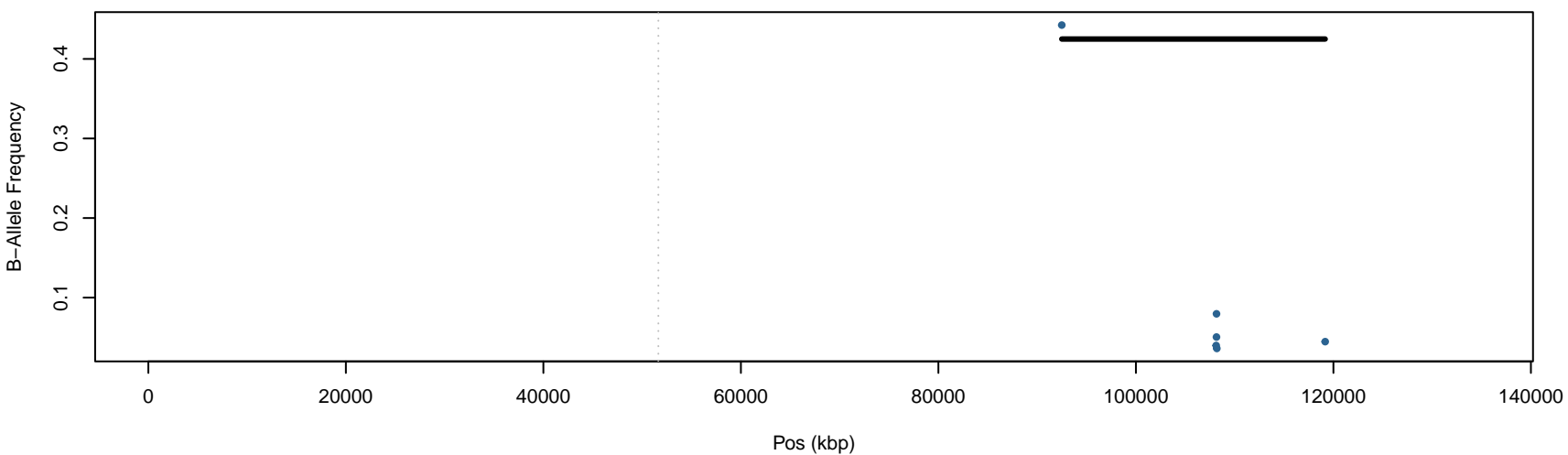
Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108;387 Chromosome: 9



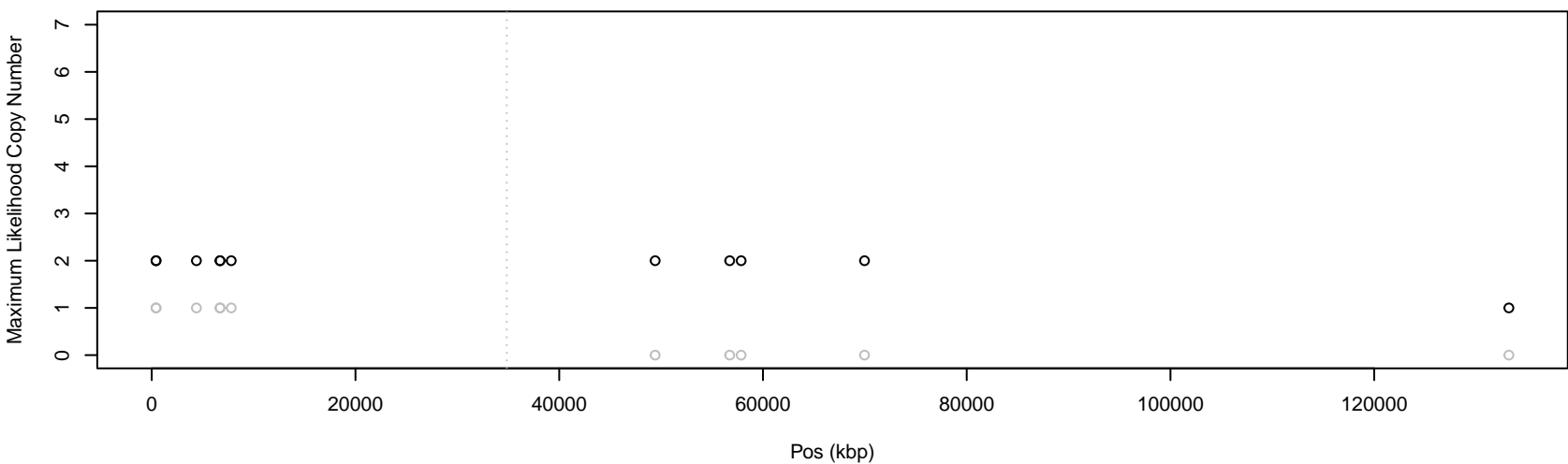
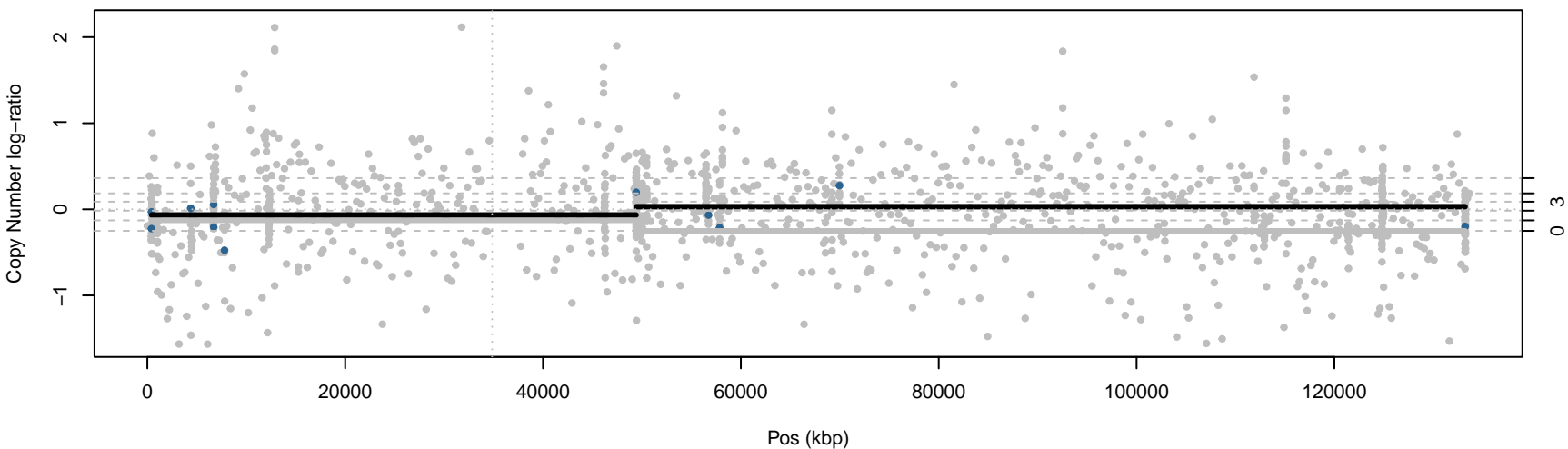
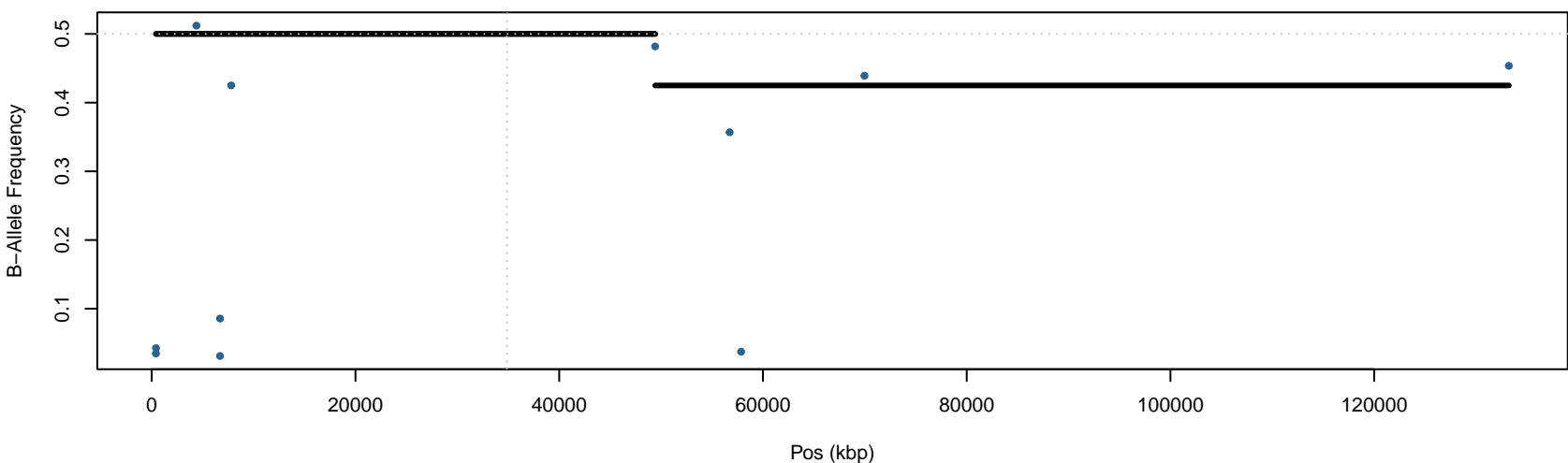
Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108;387 Chromosome: 10



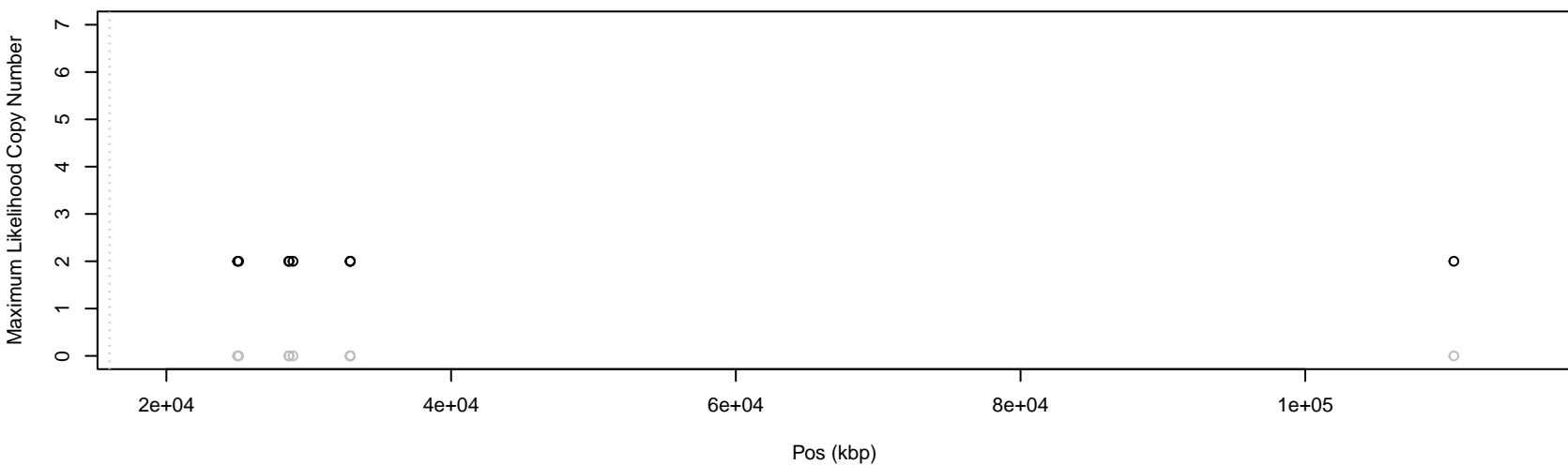
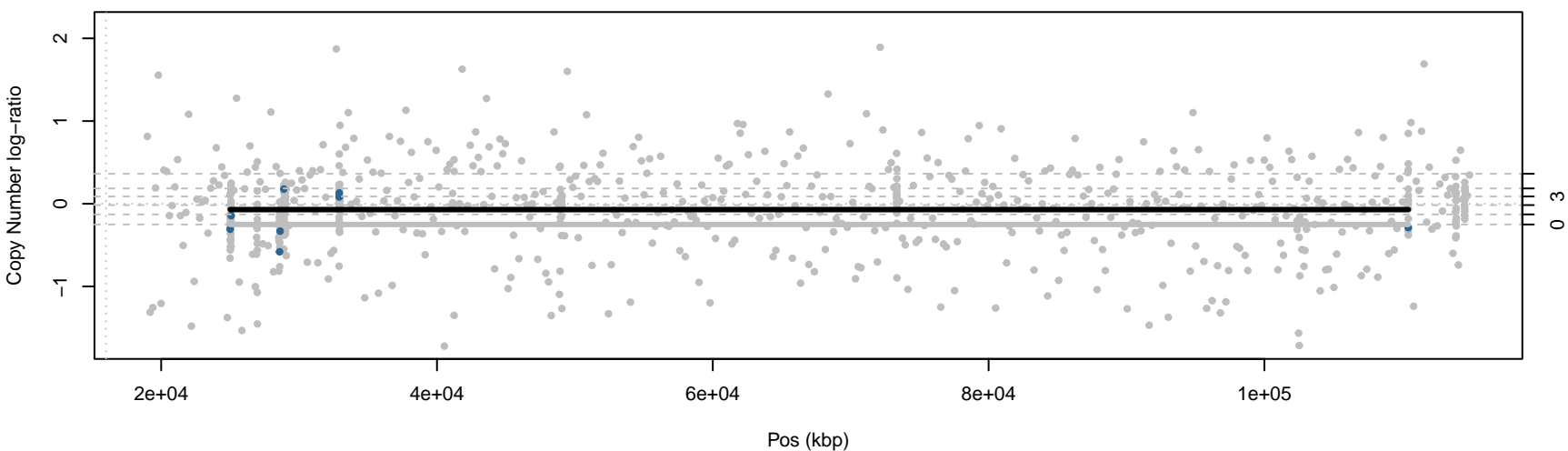
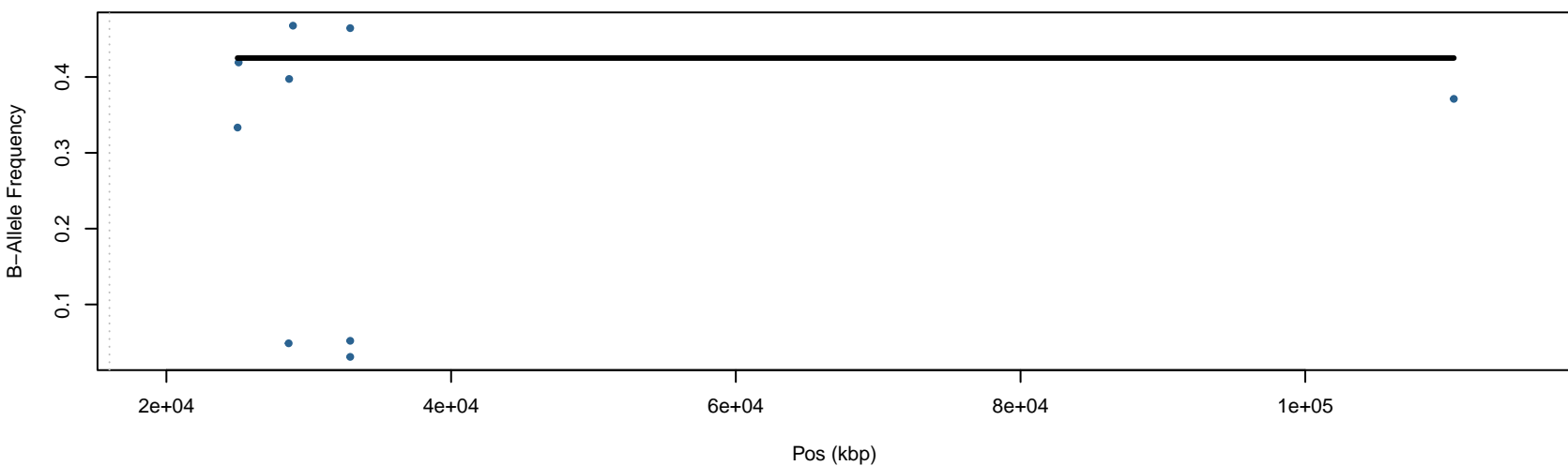
Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108;387 Chromosome: 11



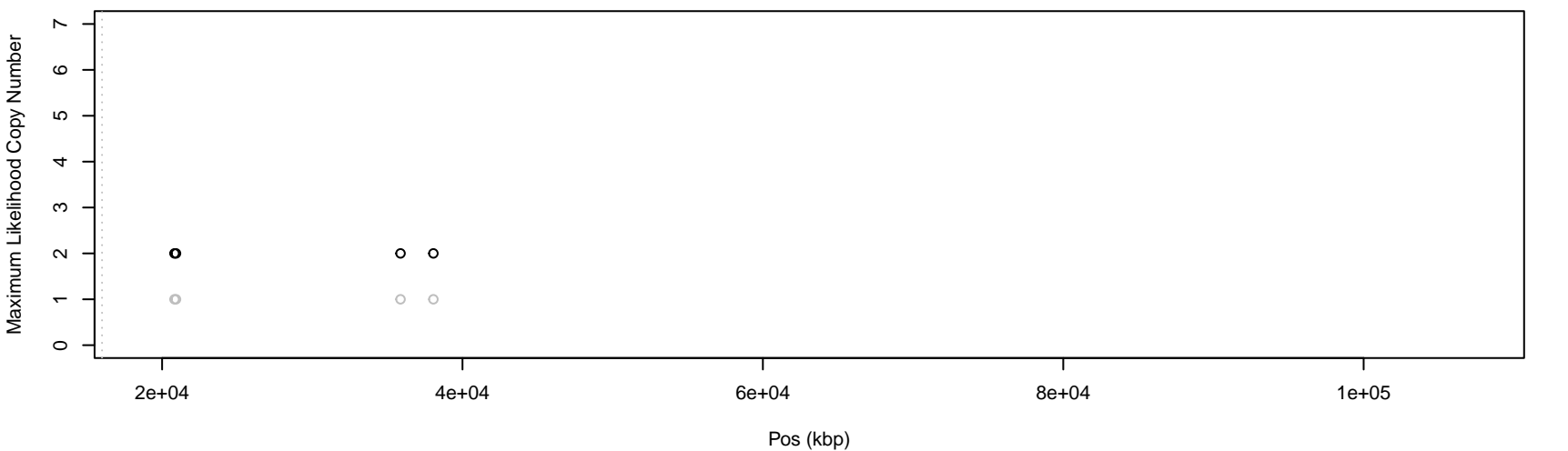
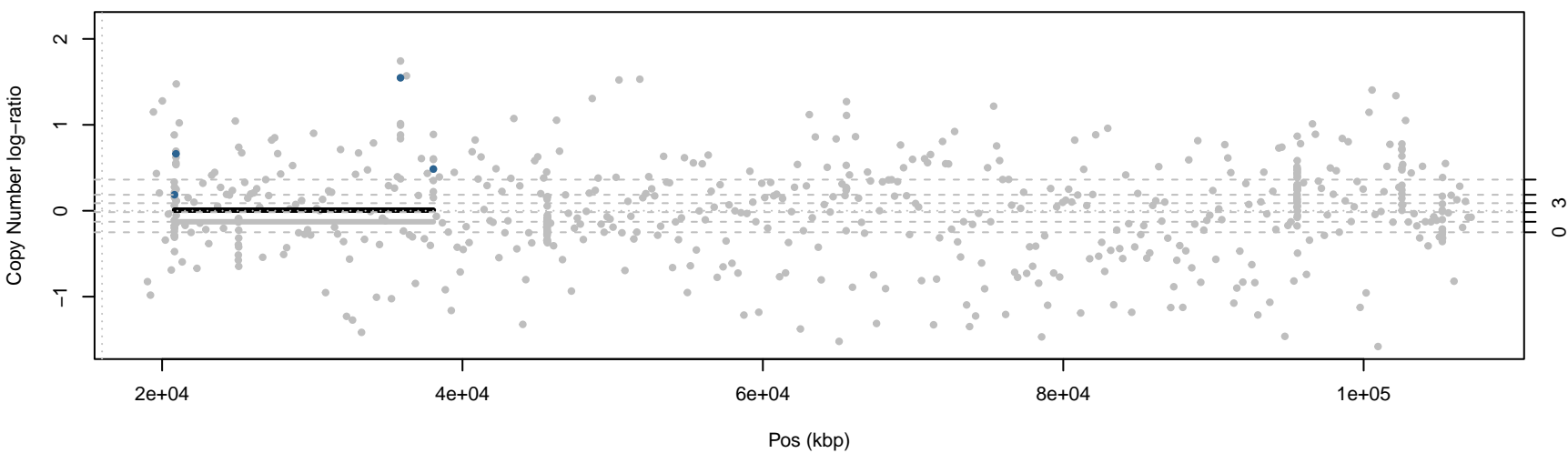
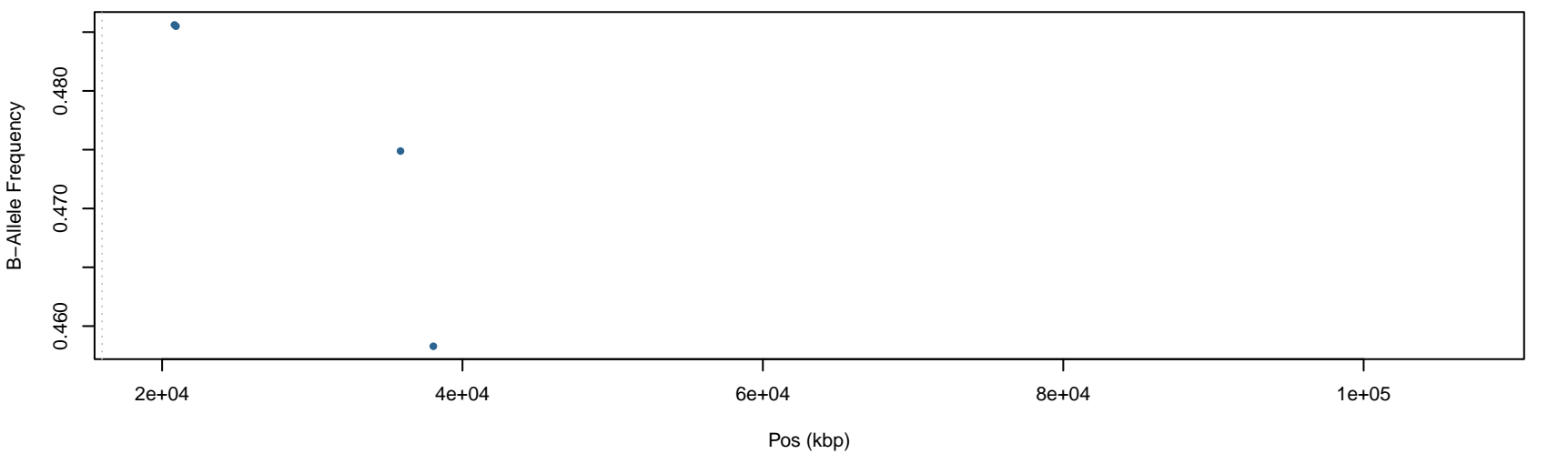
Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108;387 Chromosome: 12



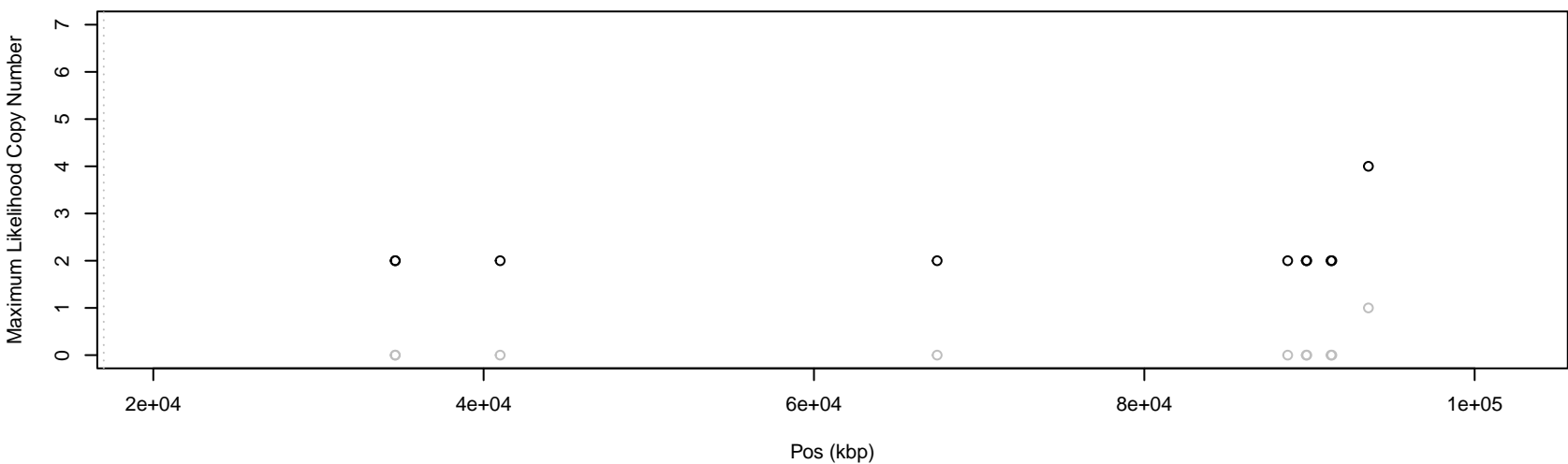
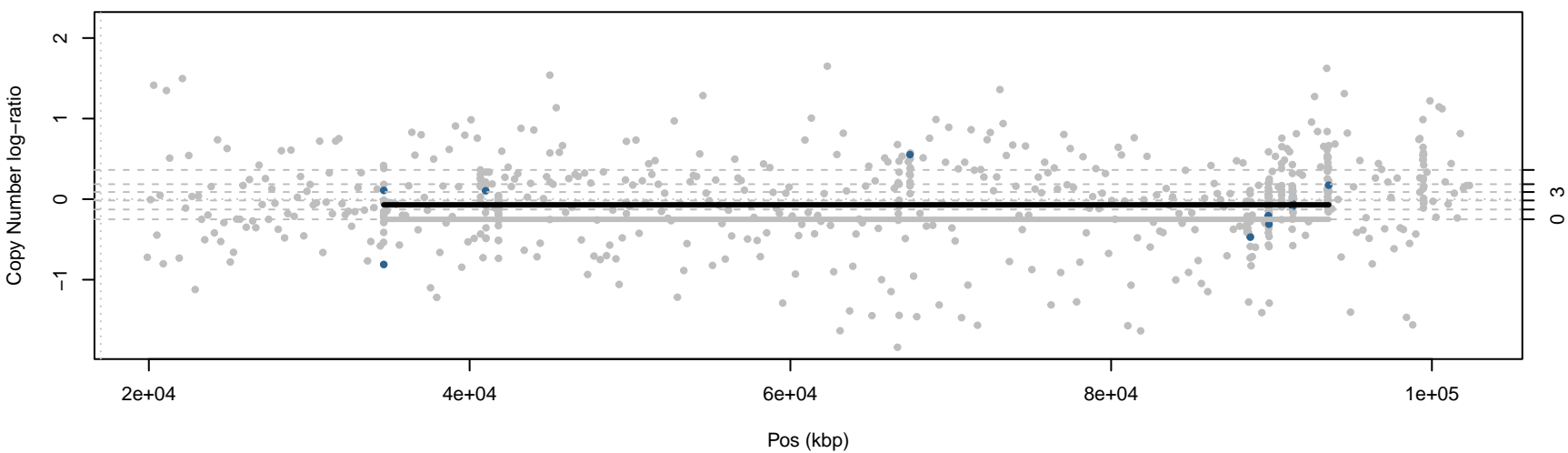
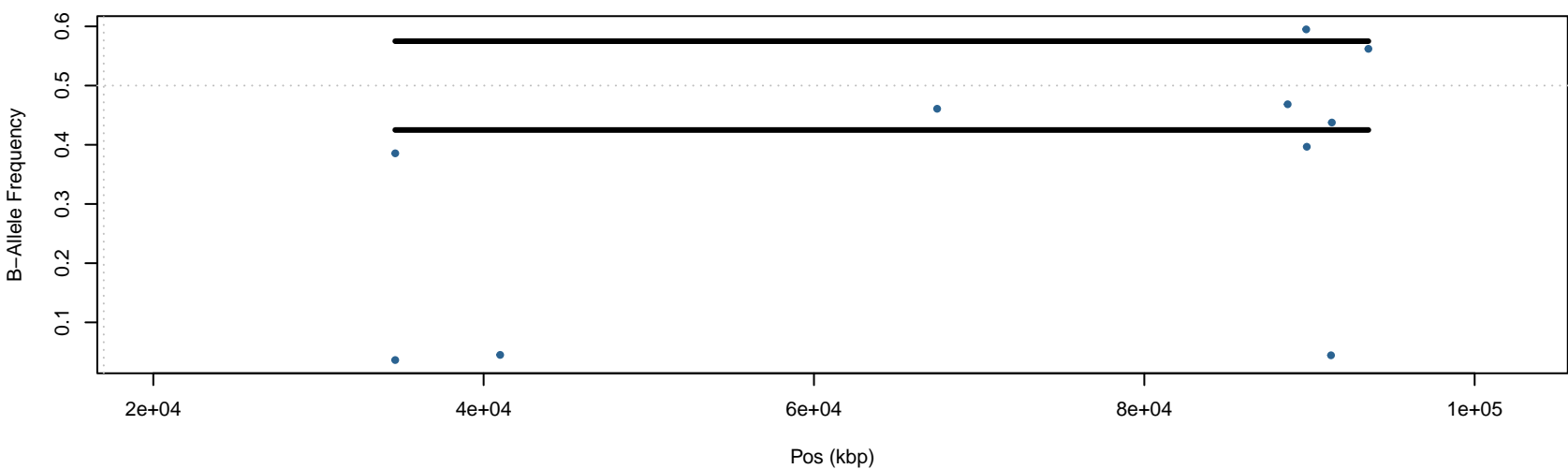
Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108;387 Chromosome: 13



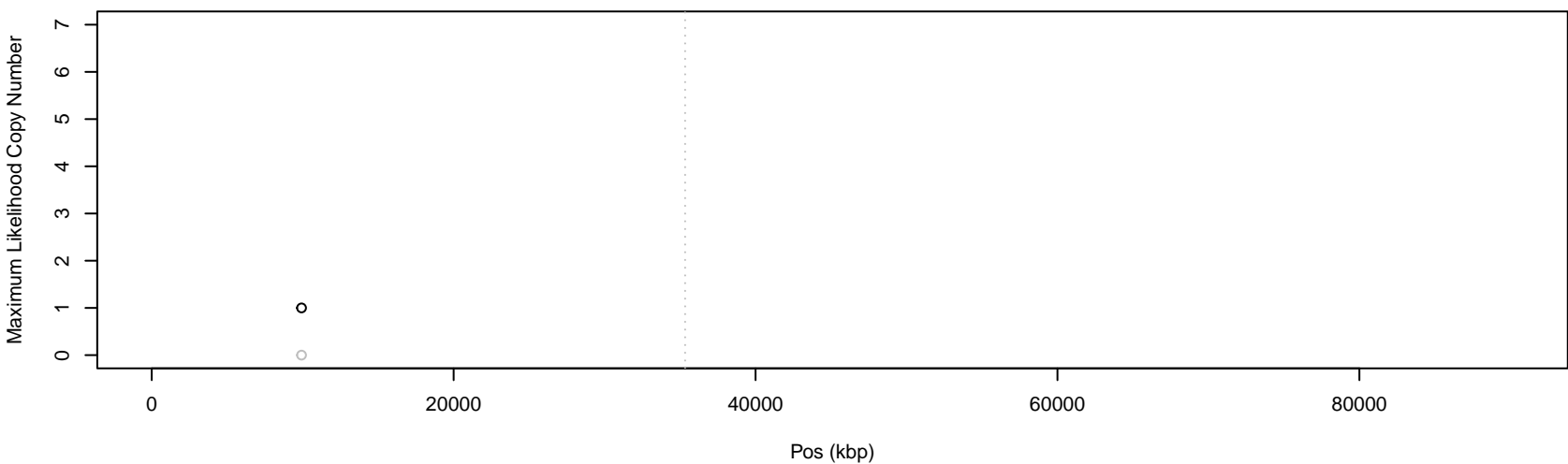
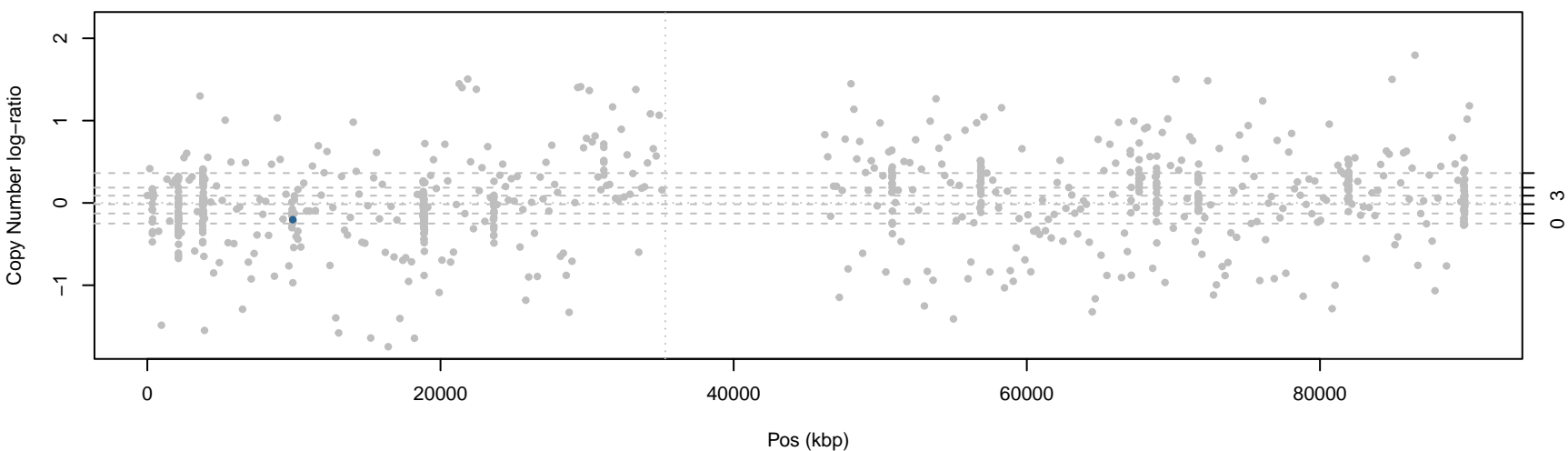
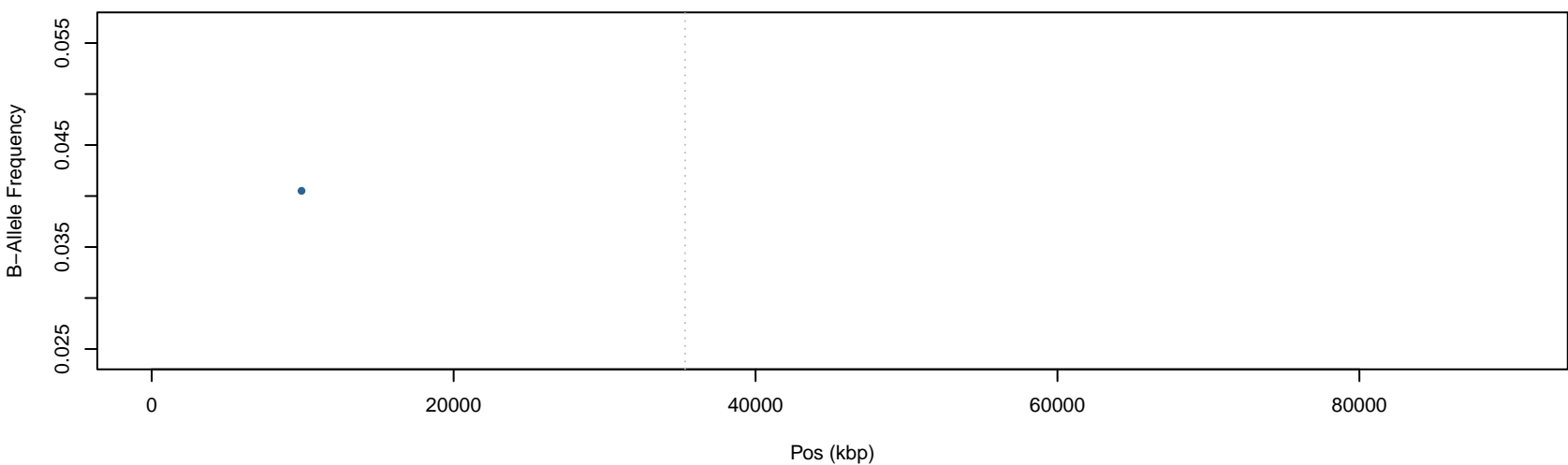
Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108;387 Chromosome: 14



Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108;387 Chromosome: 15

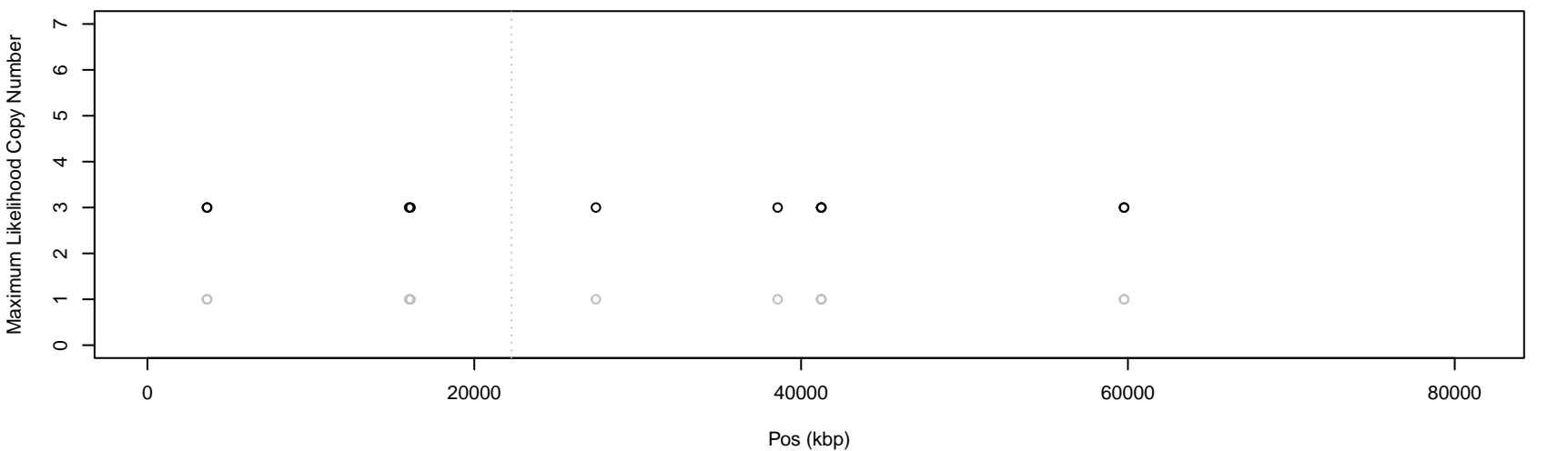
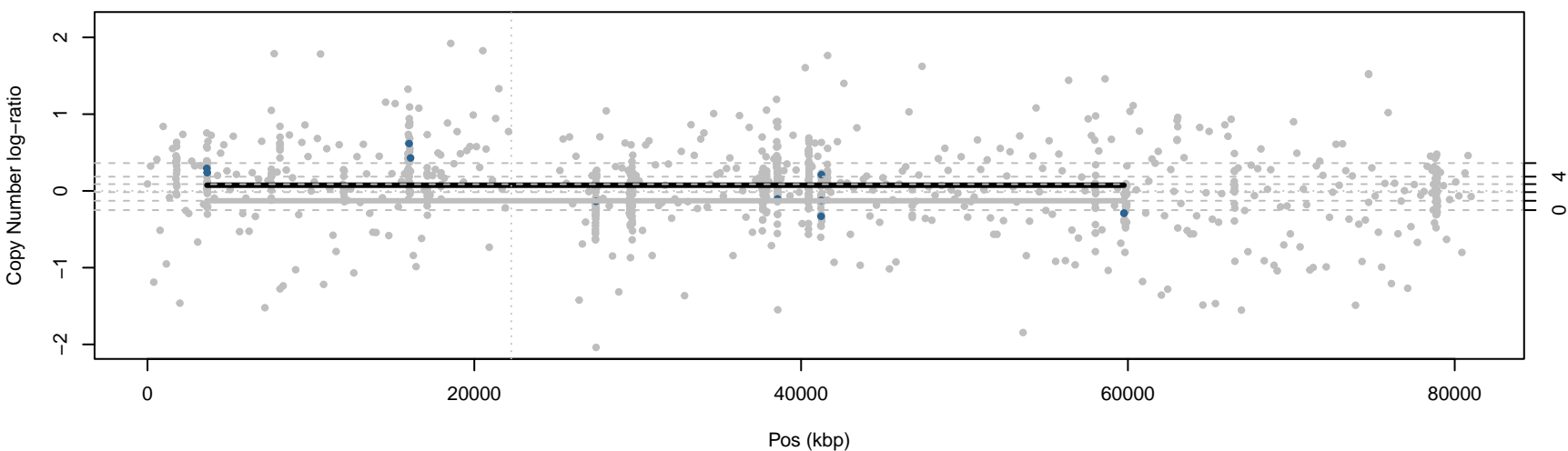
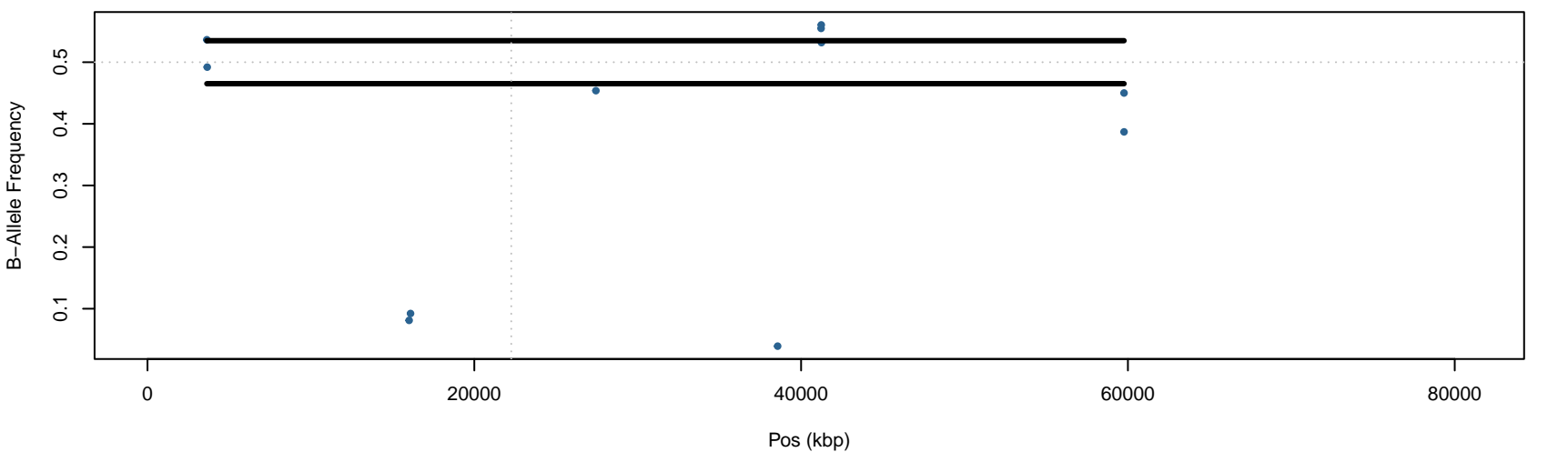


Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108;387 Chromosome: 16

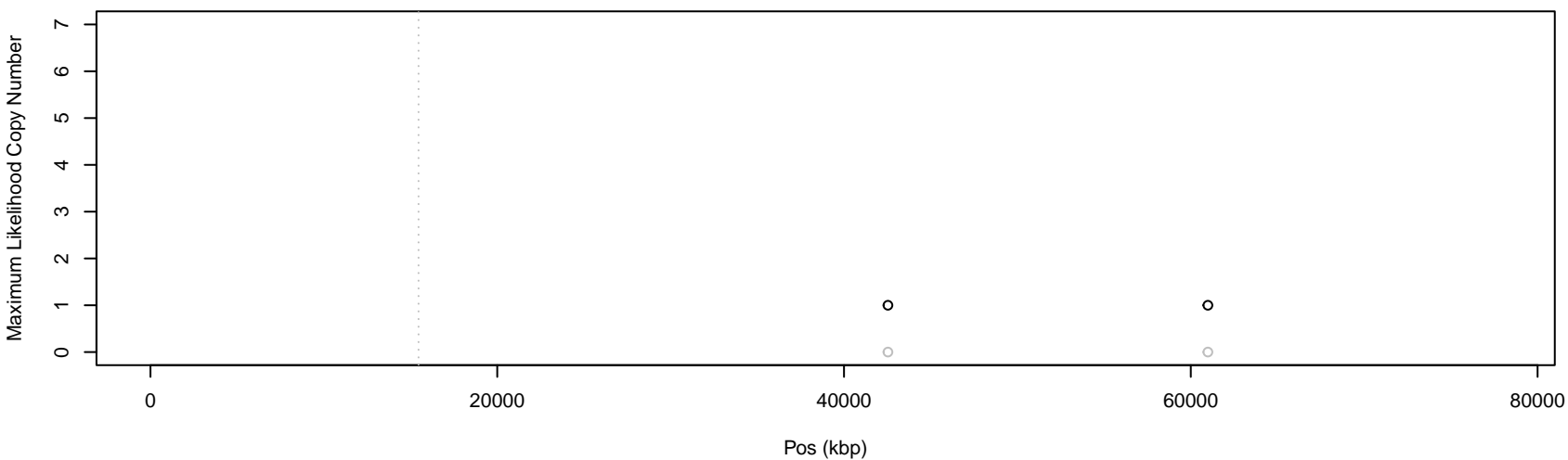
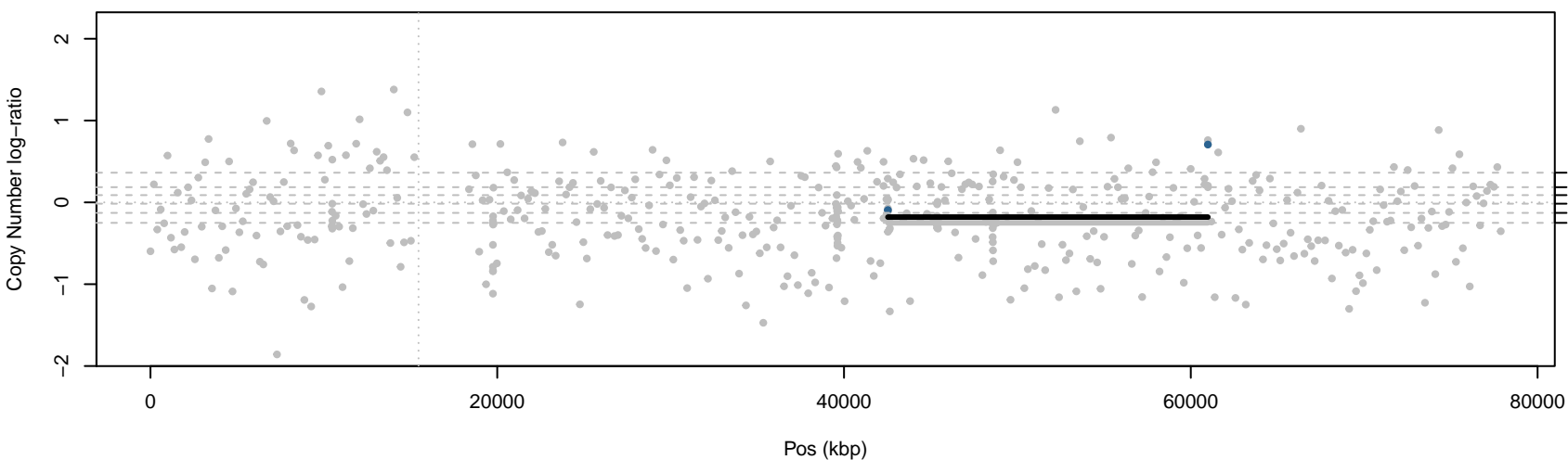
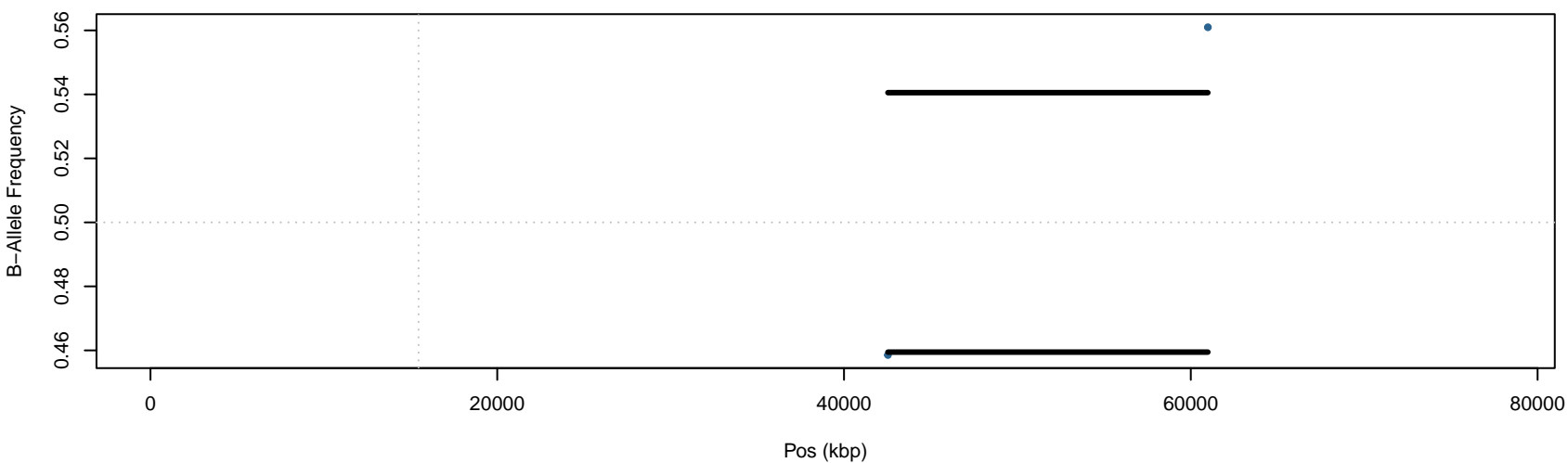




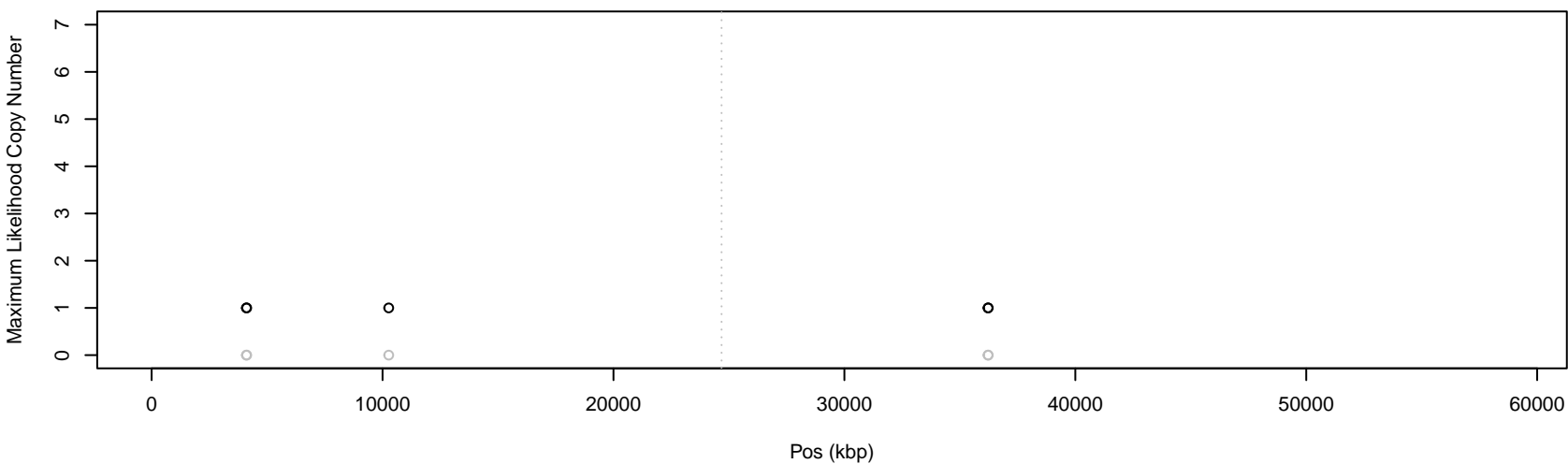
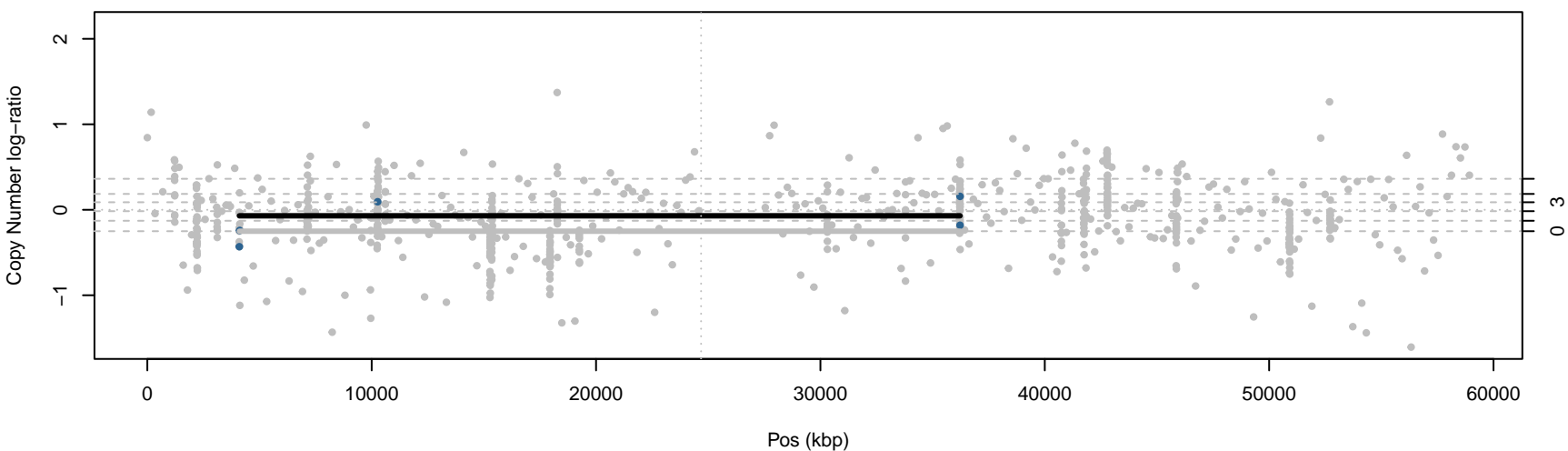
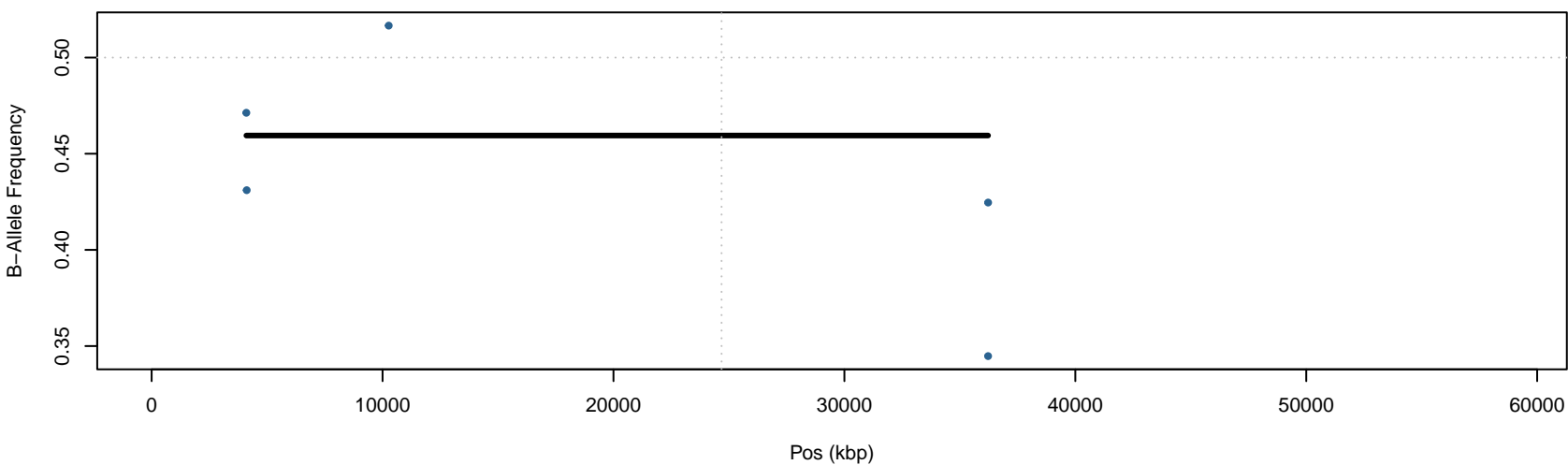
Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108;387 Chromosome: 17



Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108;387 Chromosome: 18



Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108;387 Chromosome: 19



Purity: 0.15 Tumor ploidy: 2.149 SNV log-likelihood: -16.21 GoF: 95.1% Mean coverage: 108;387 Chromosome: 22

