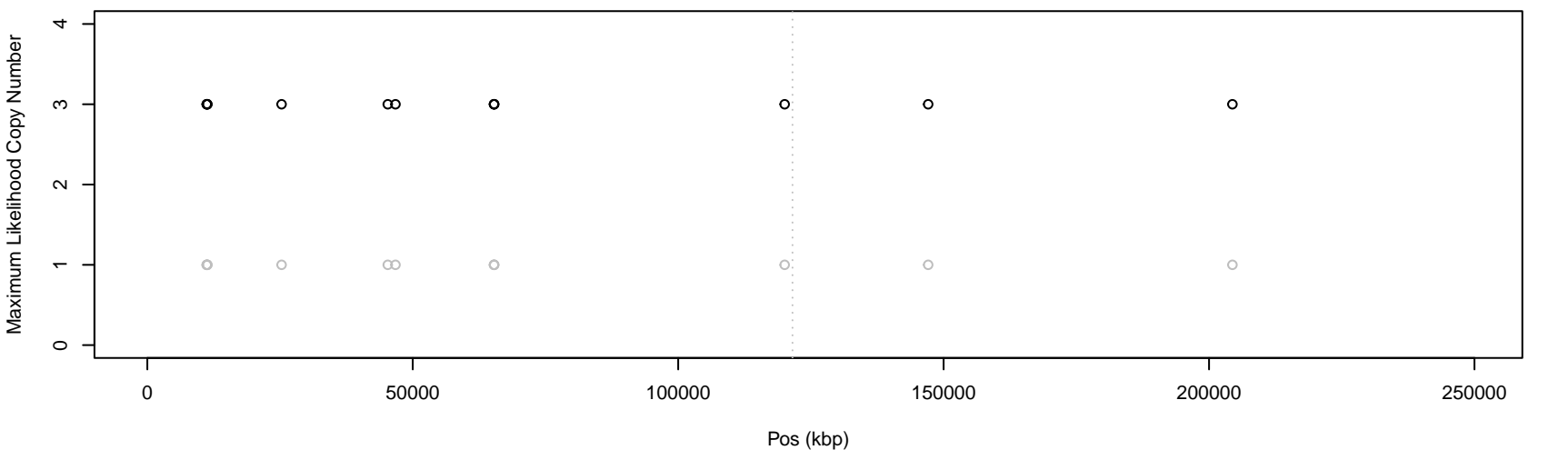
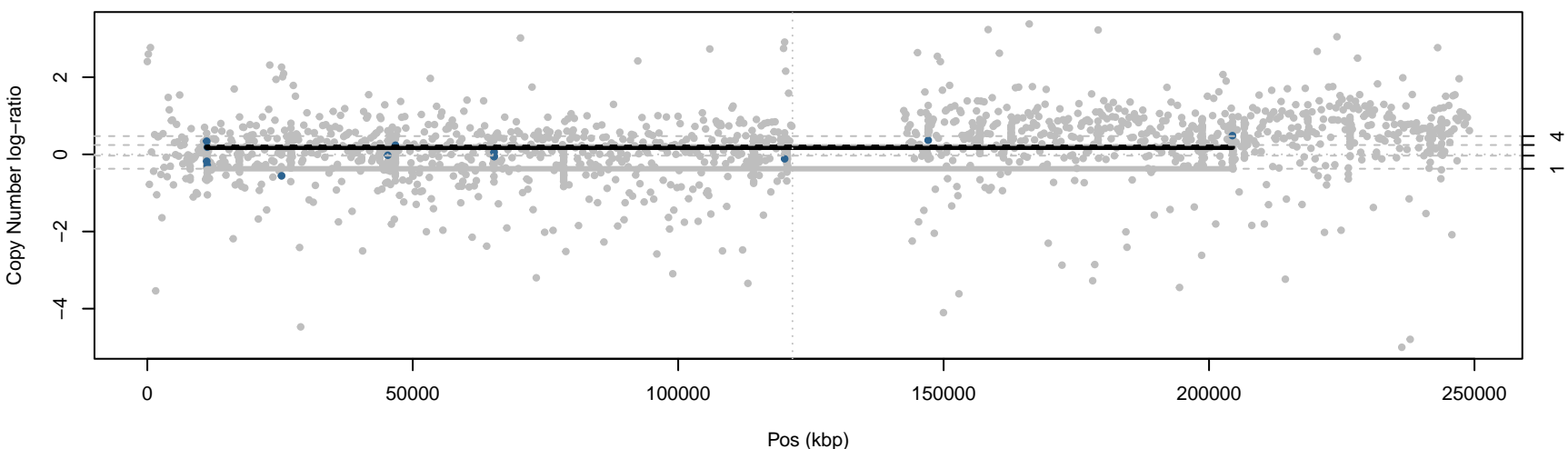
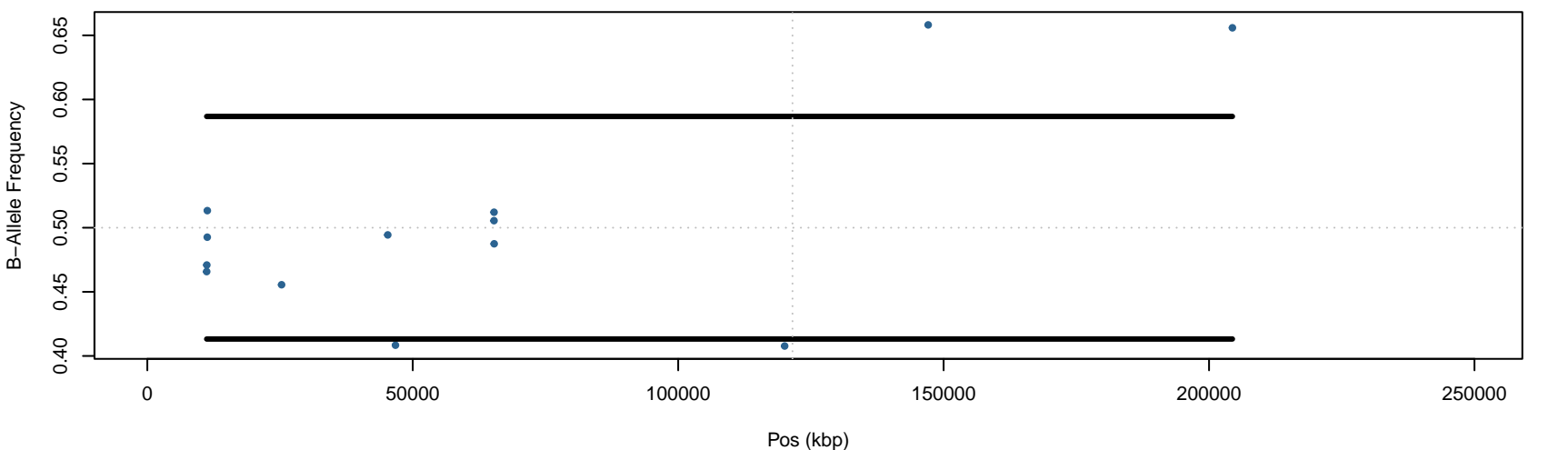
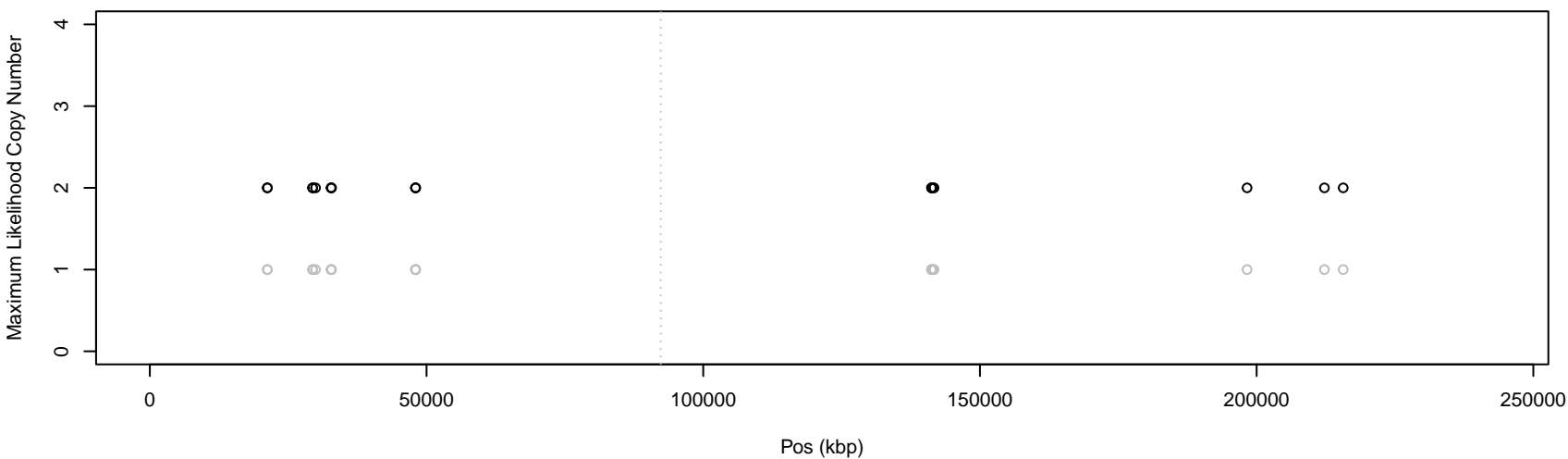
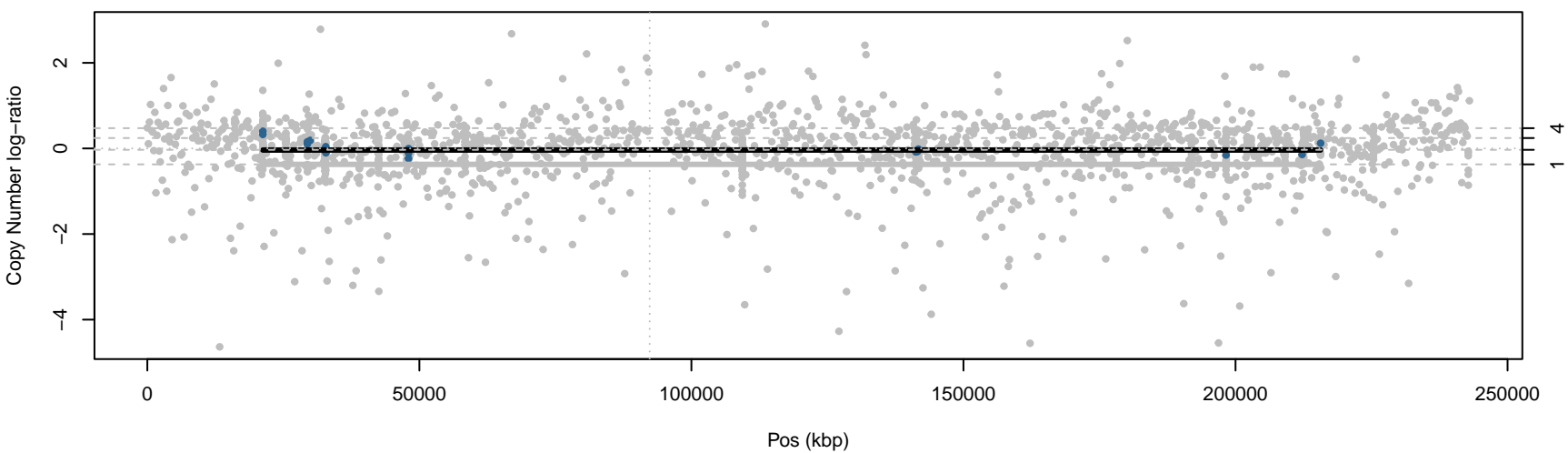
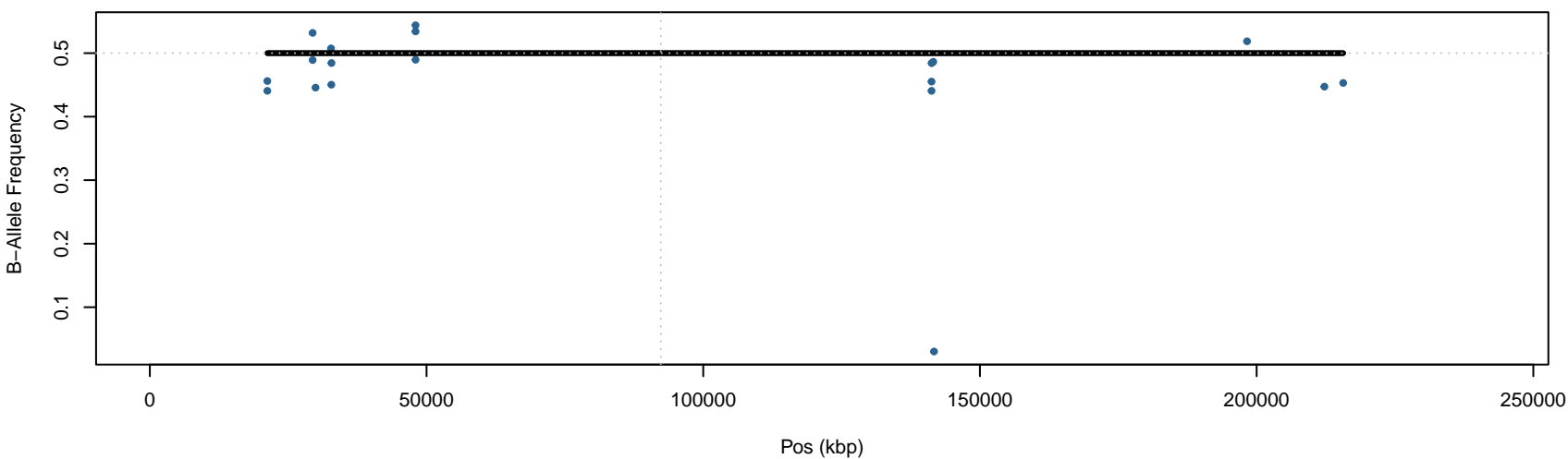


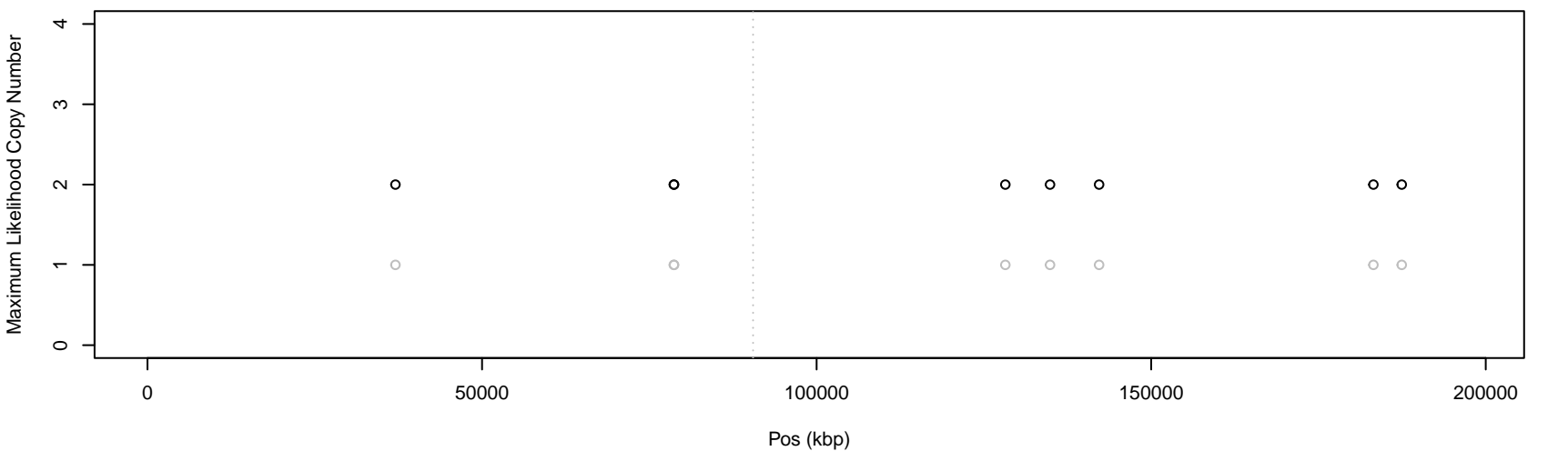
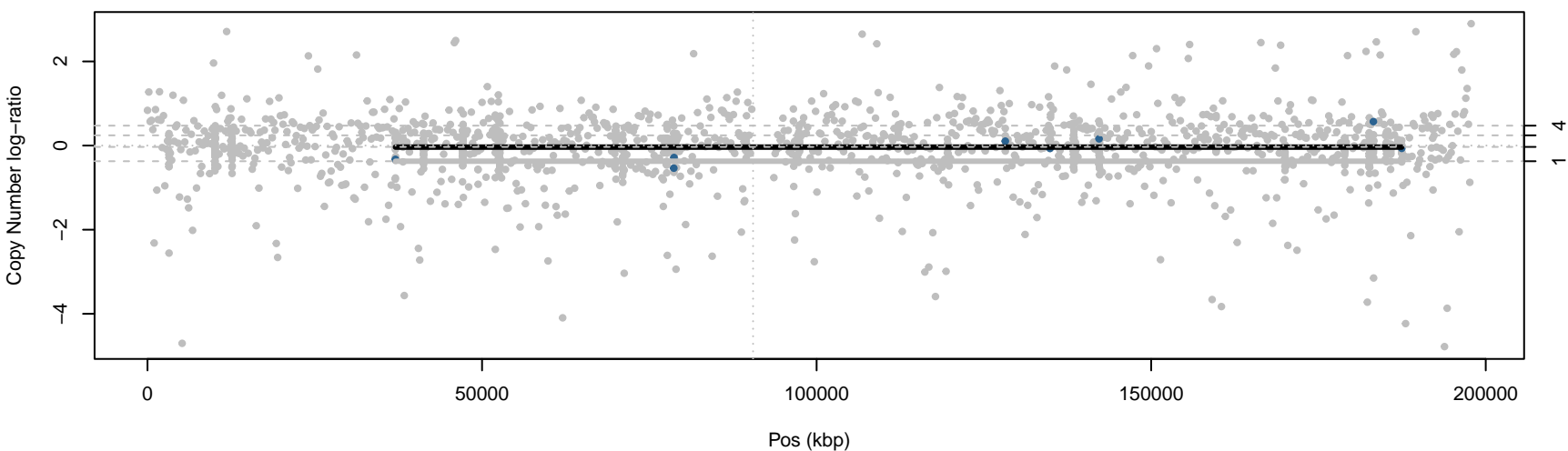
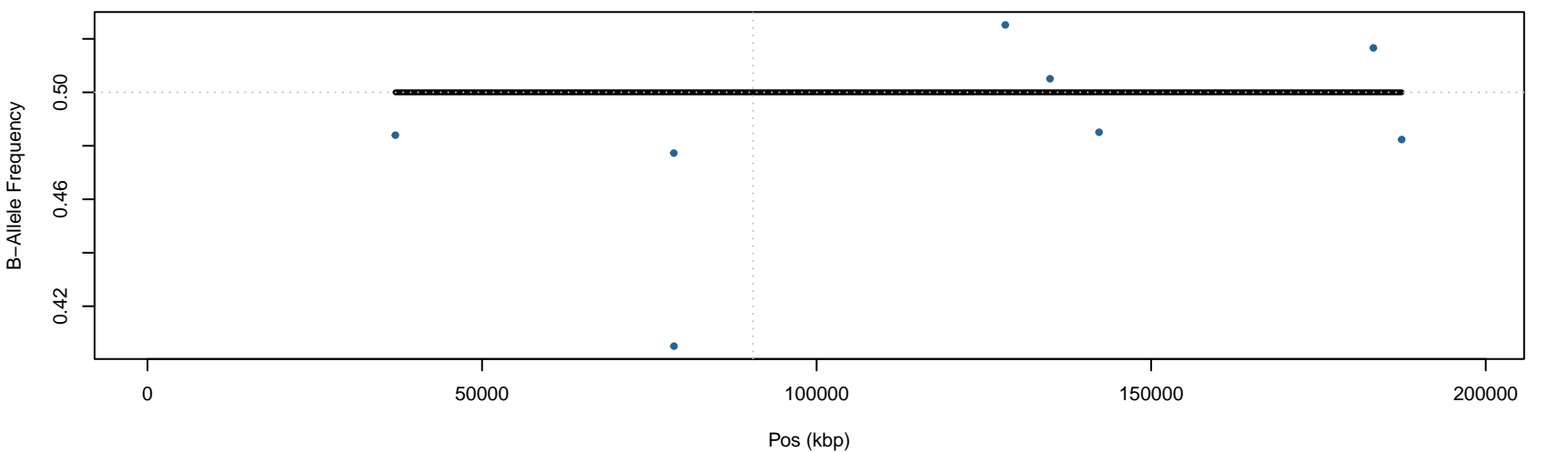
Purity: 0.42 Tumor ploidy: 2.108 SNV log-likelihood: -30.49 GoF: 86% Mean coverage: 774;145 Chromosome: 1



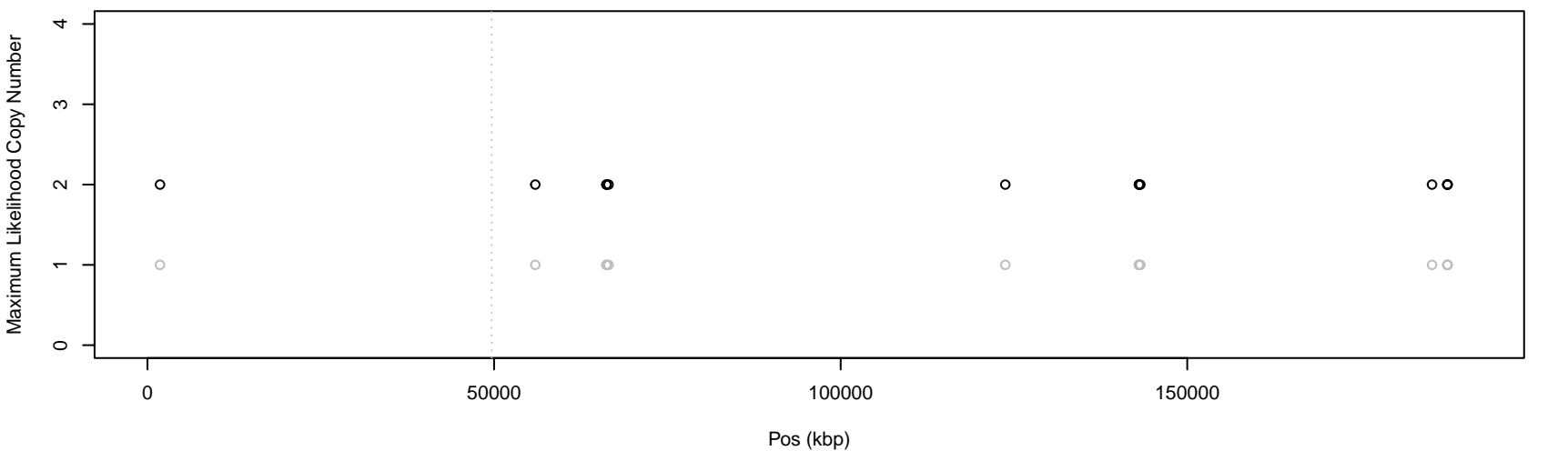
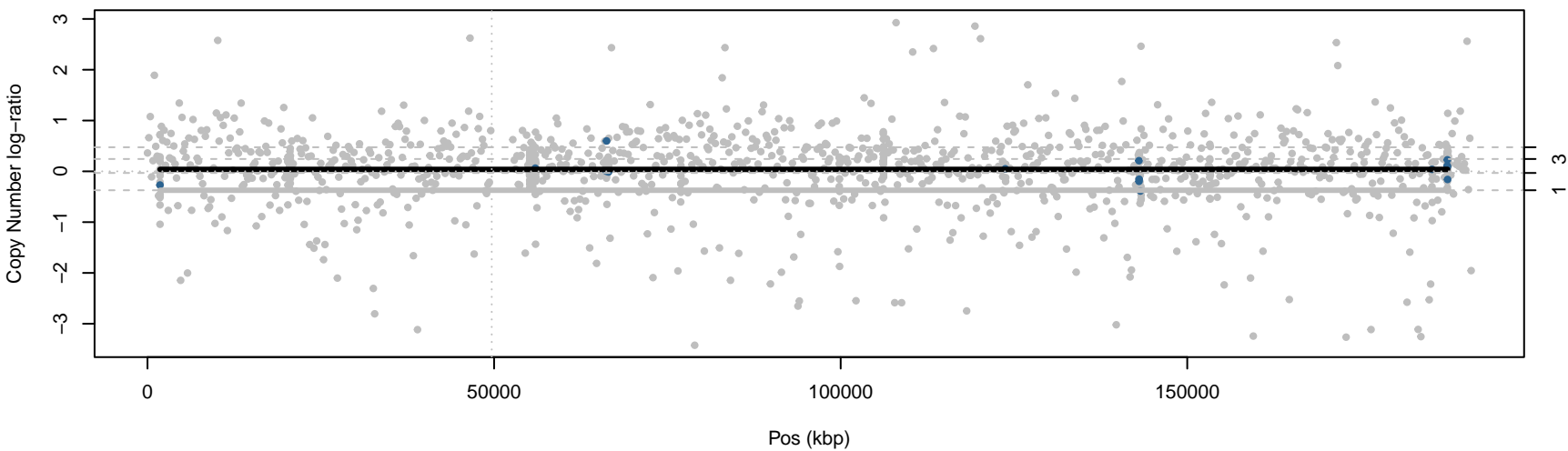
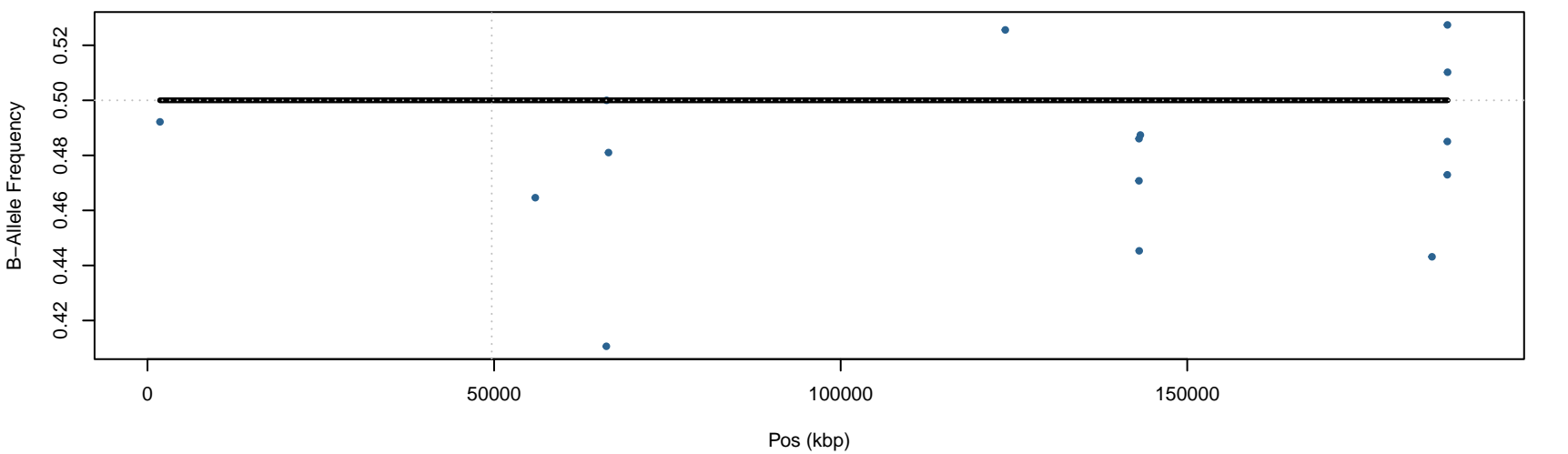
Purity: 0.42 Tumor ploidy: 2.108 SNV log-likelihood: -30.49 GoF: 86% Mean coverage: 774;145 Chromosome: 2



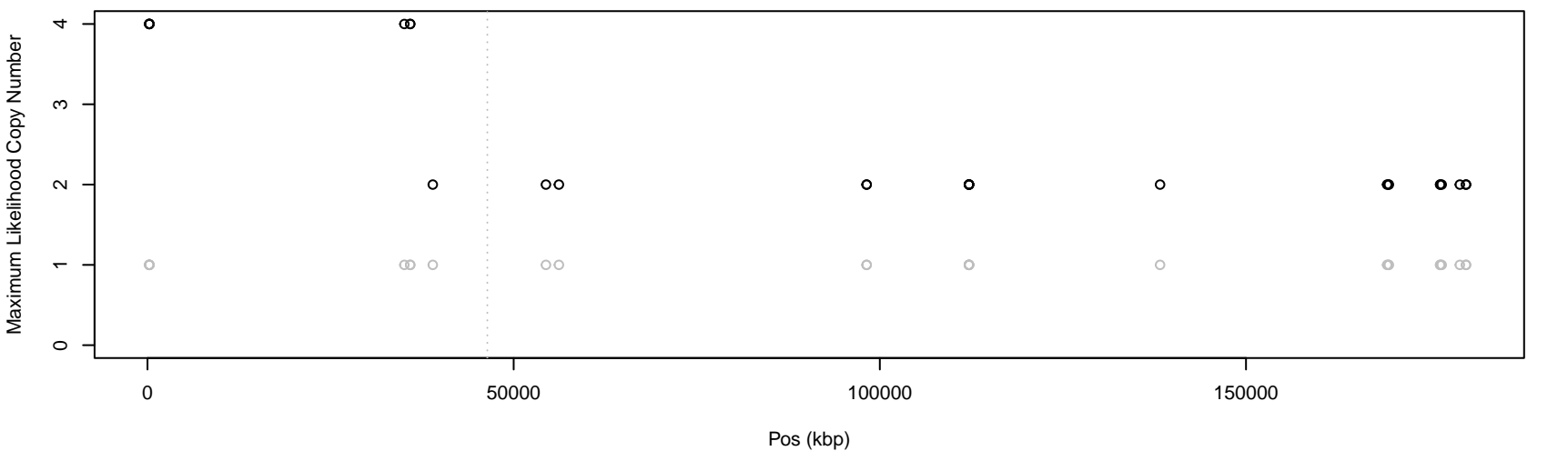
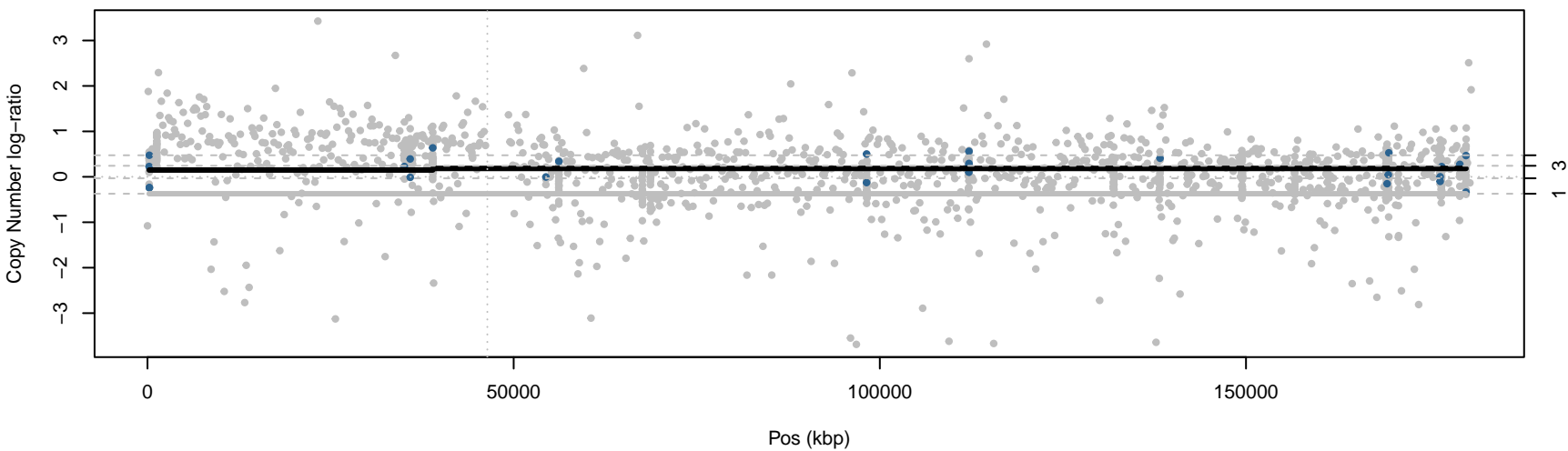
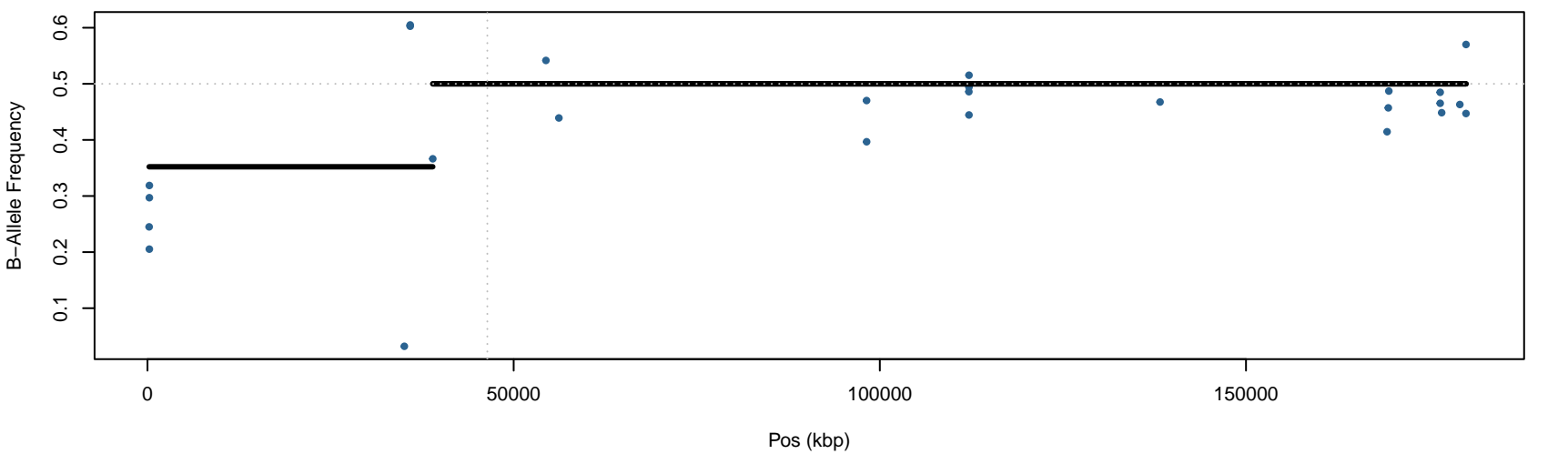
Purity: 0.42 Tumor ploidy: 2.108 SNV log-likelihood: -30.49 GoF: 86% Mean coverage: 774;145 Chromosome: 3



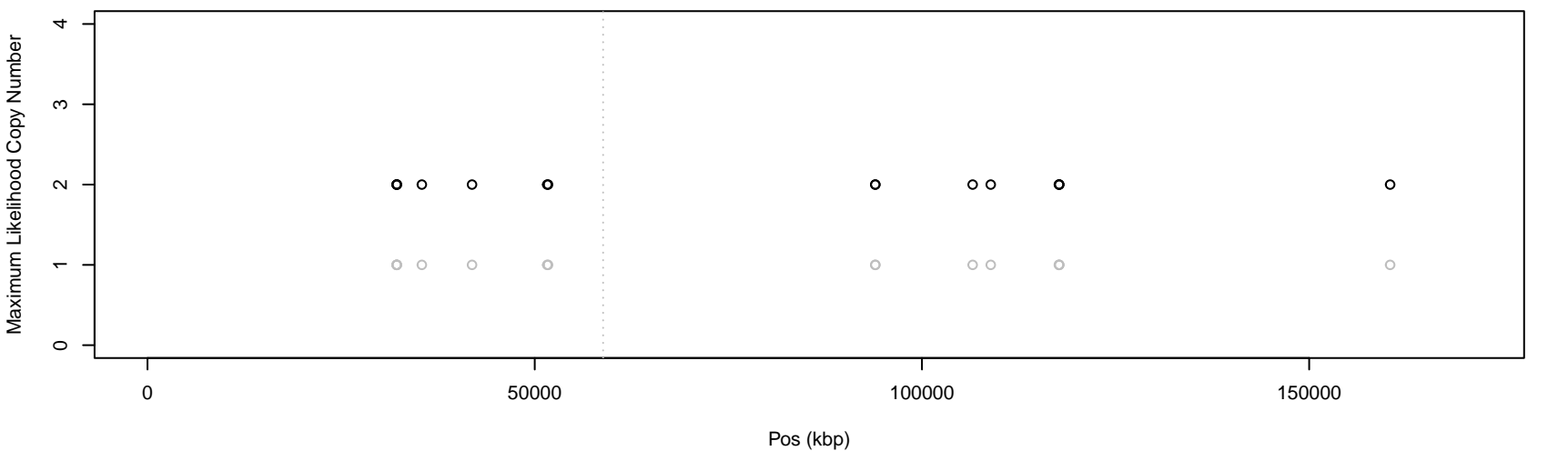
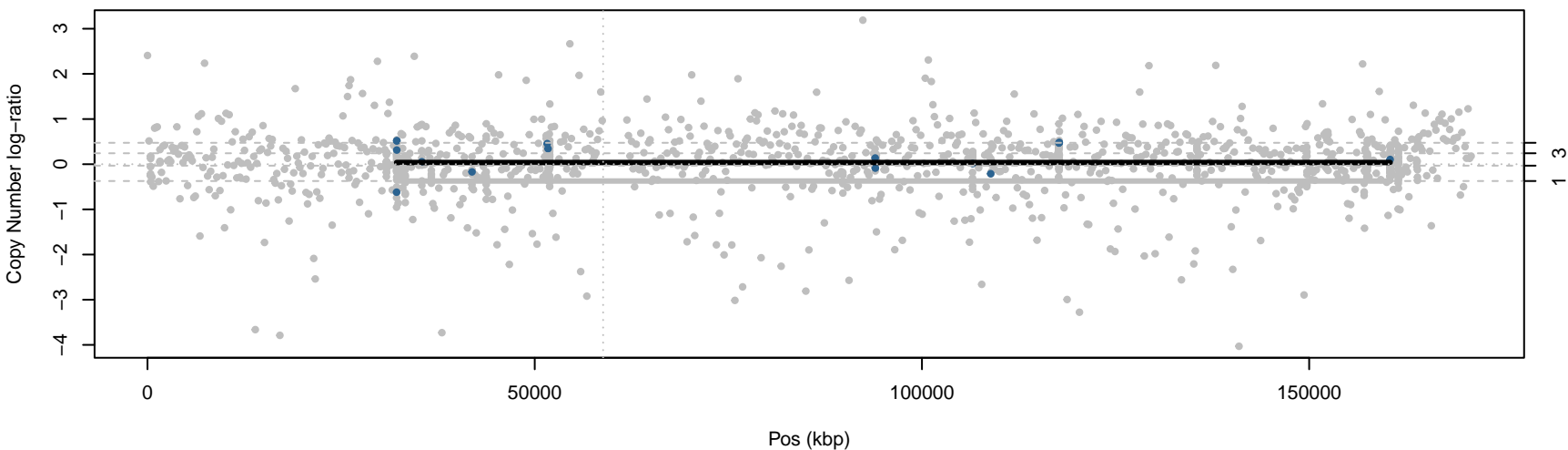
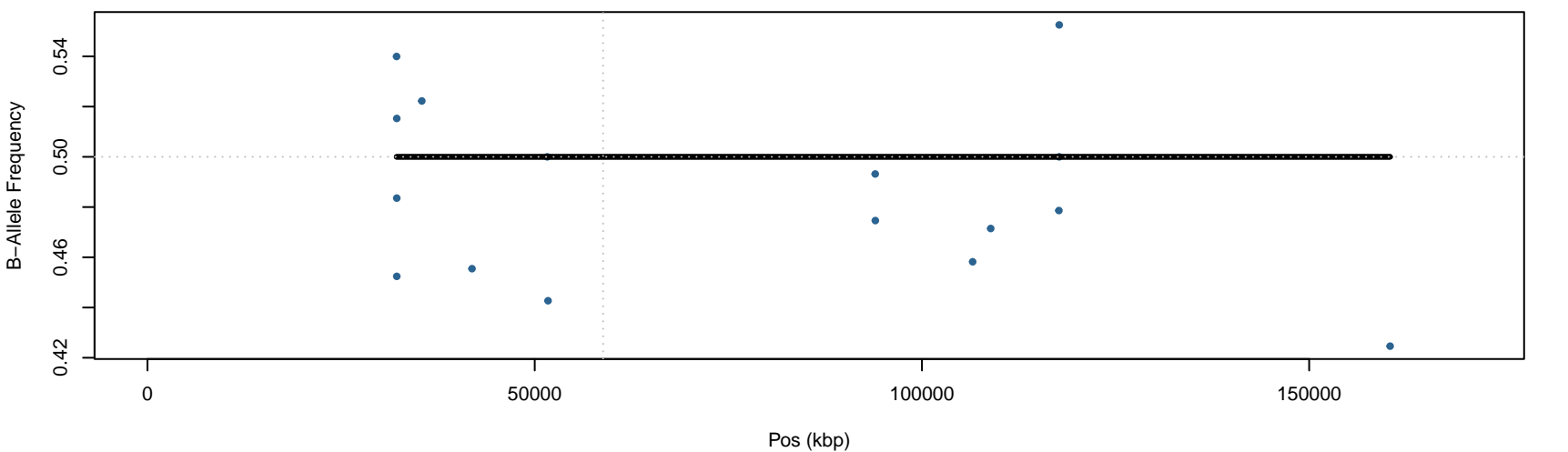
Purity: 0.42 Tumor ploidy: 2.108 SNV log-likelihood: -30.49 GoF: 86% Mean coverage: 774;145 Chromosome: 4



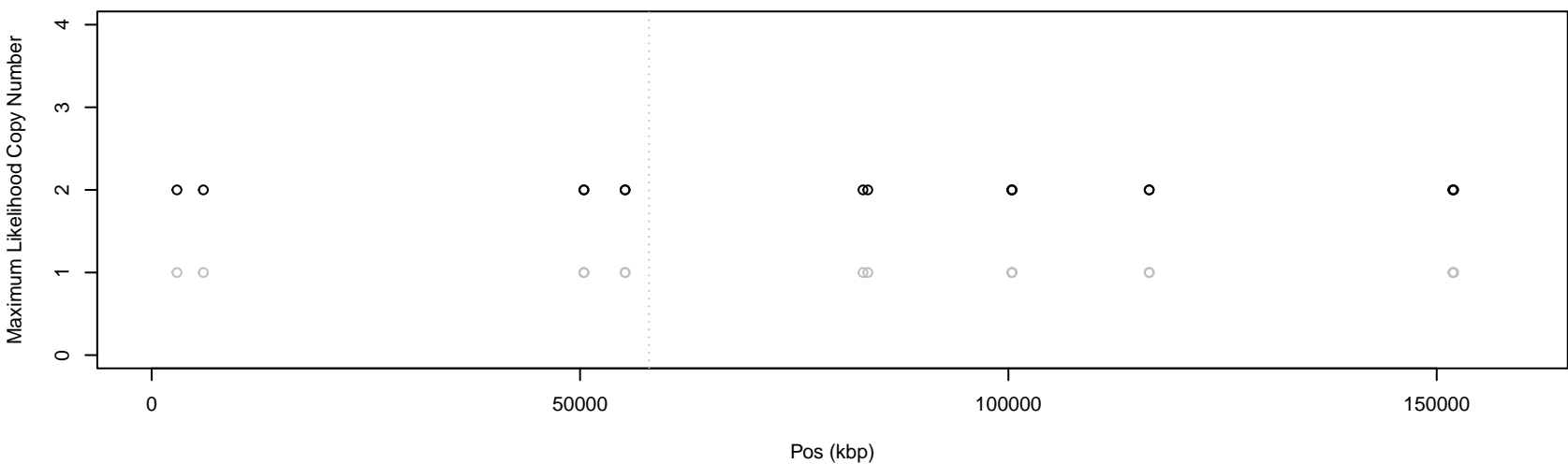
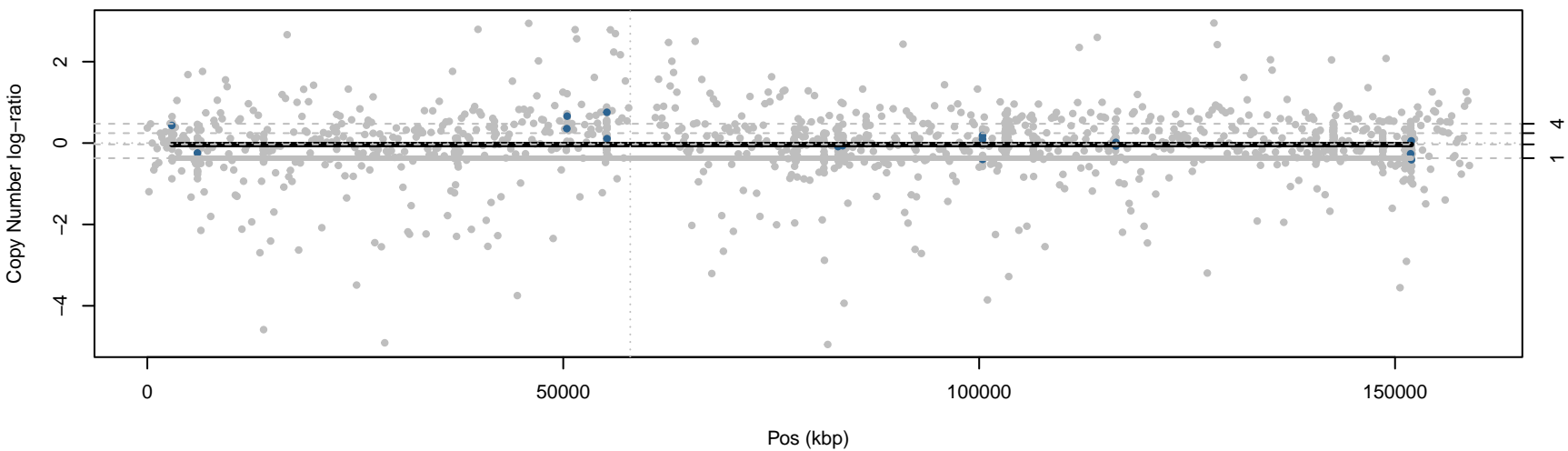
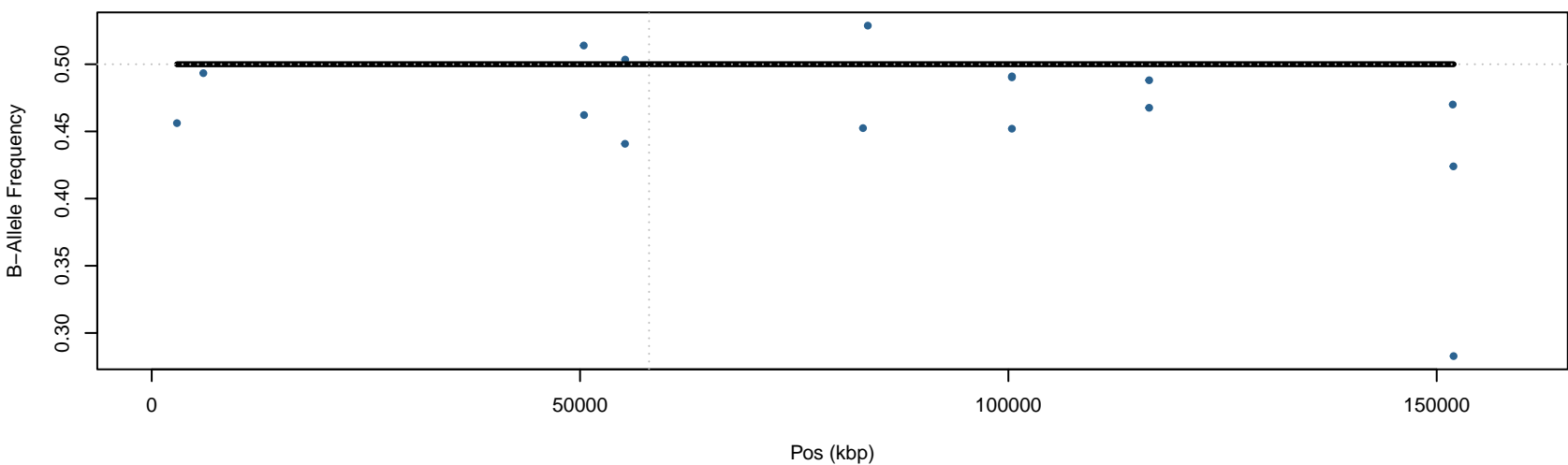
Purity: 0.42 Tumor ploidy: 2.108 SNV log-likelihood: -30.49 GoF: 86% Mean coverage: 774;145 Chromosome: 5



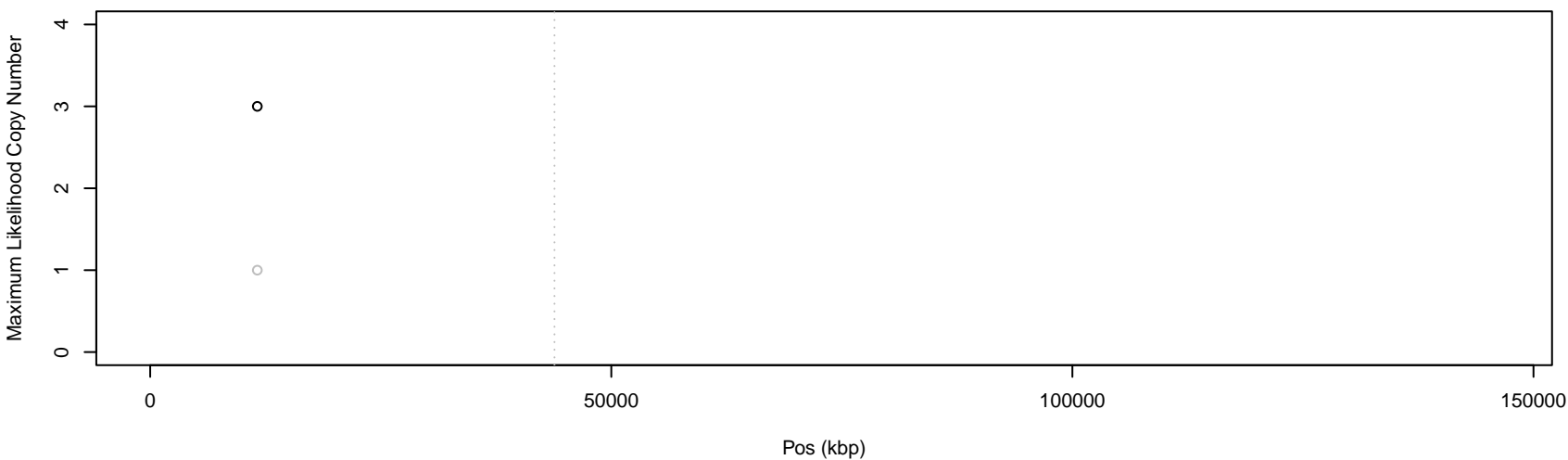
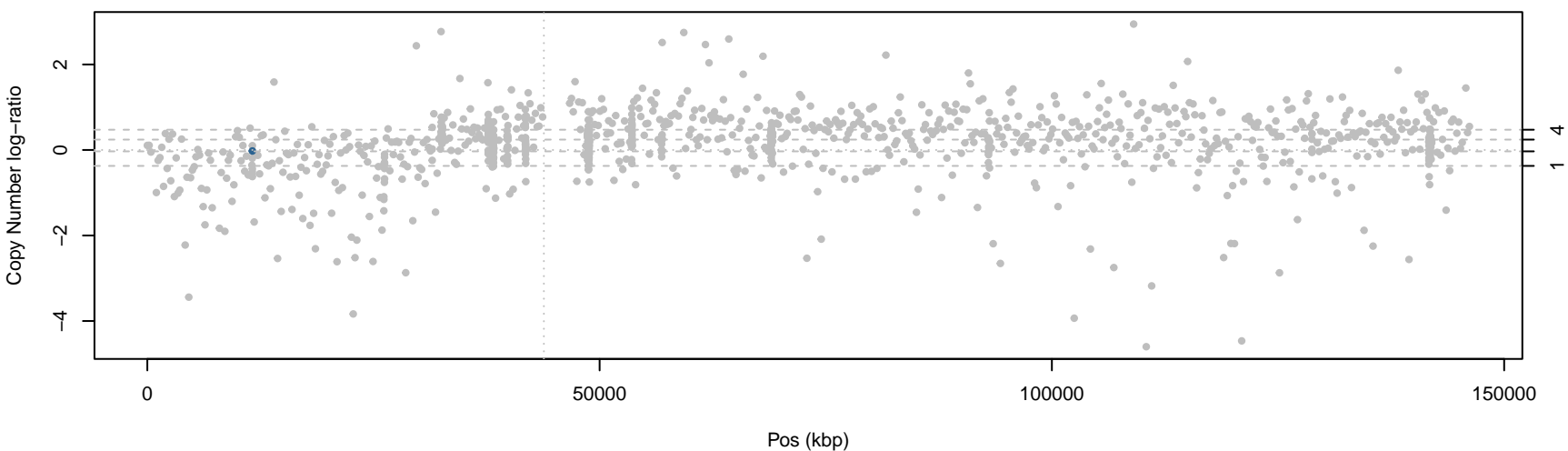
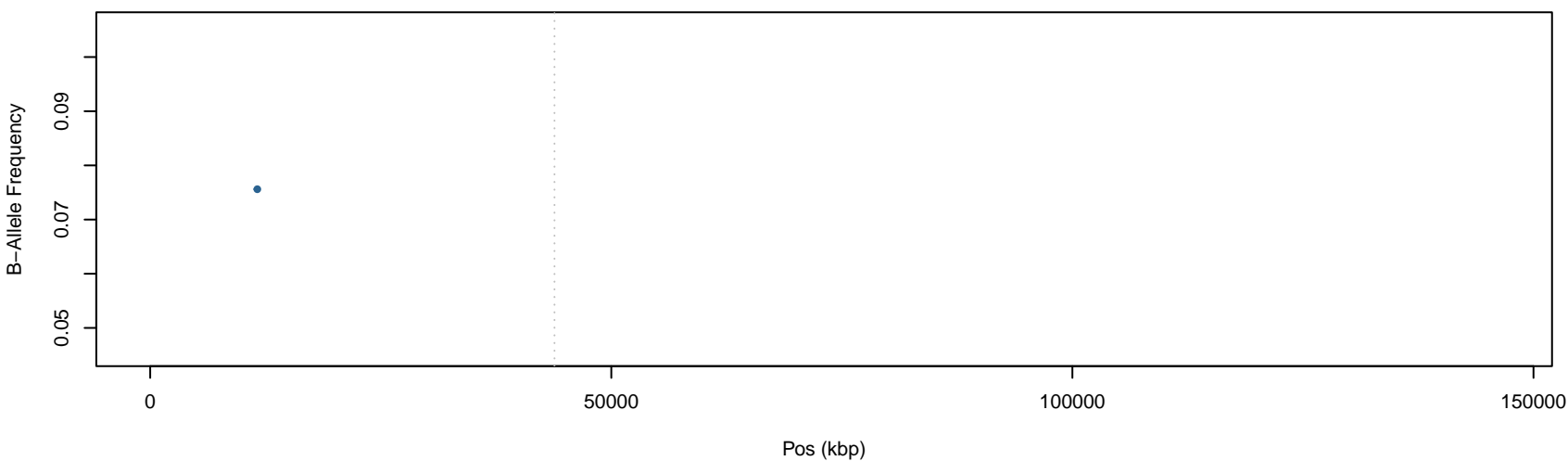
Purity: 0.42 Tumor ploidy: 2.108 SNV log-likelihood: -30.49 GoF: 86% Mean coverage: 774;145 Chromosome: 6



Purity: 0.42 Tumor ploidy: 2.108 SNV log-likelihood: -30.49 GoF: 86% Mean coverage: 774;145 Chromosome: 7

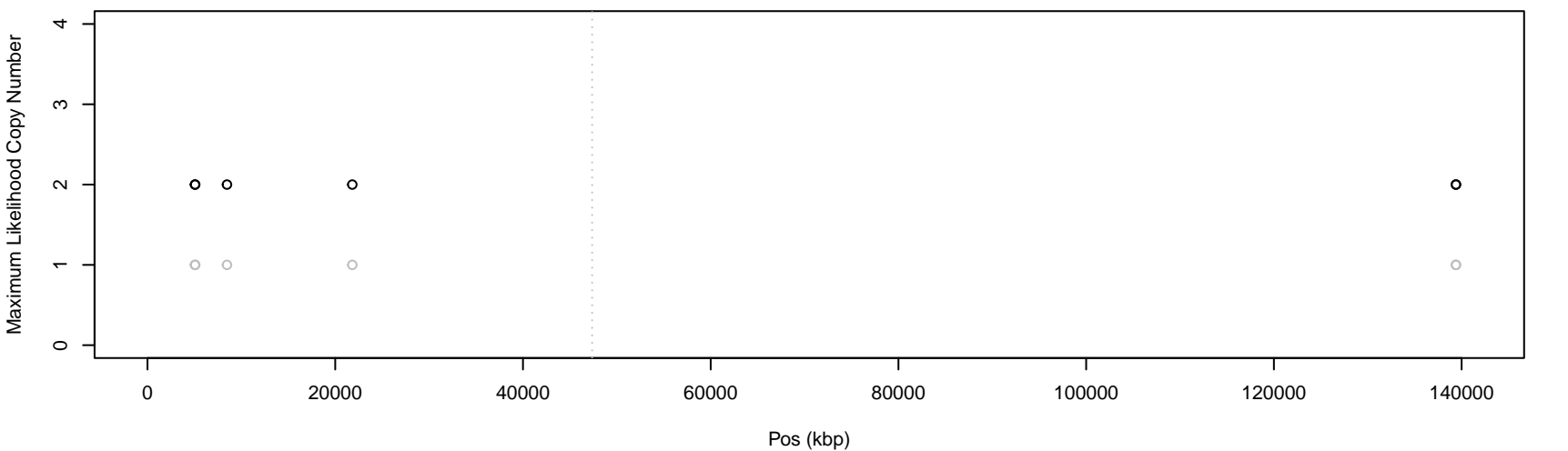
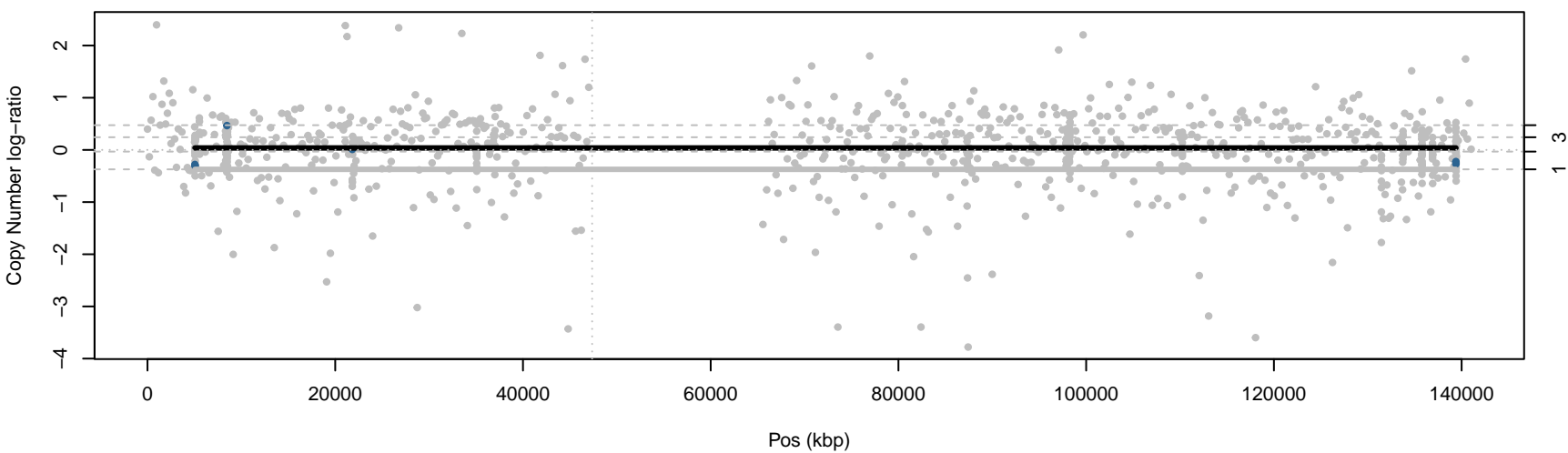
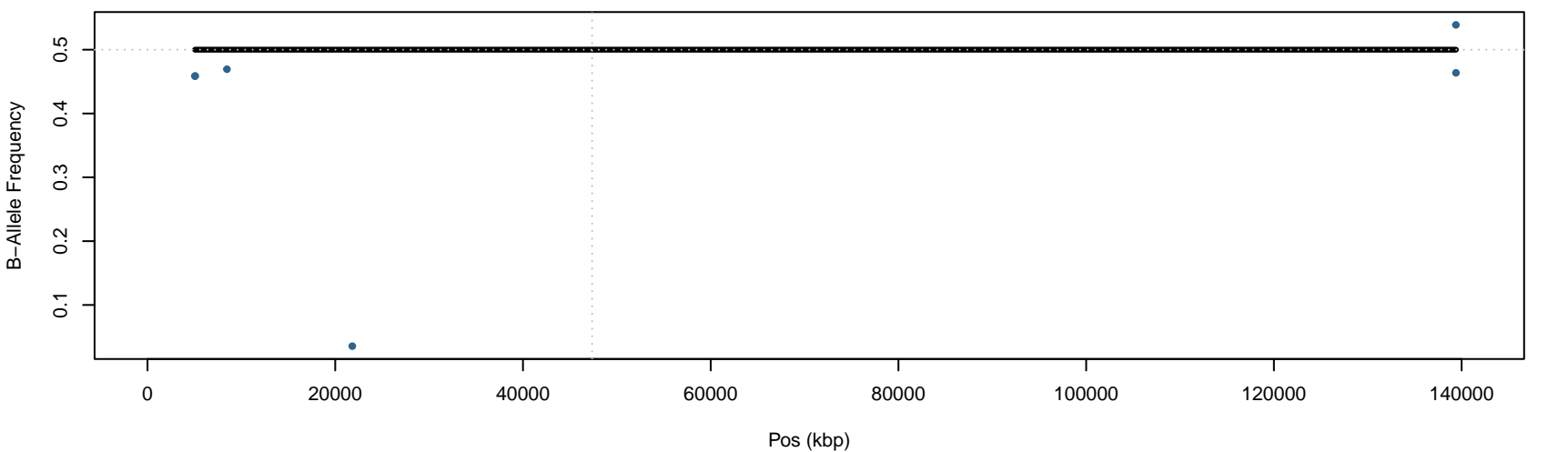


Purity: 0.42 Tumor ploidy: 2.108 SNV log-likelihood: -30.49 GoF: 86% Mean coverage: 774;145 Chromosome: 8

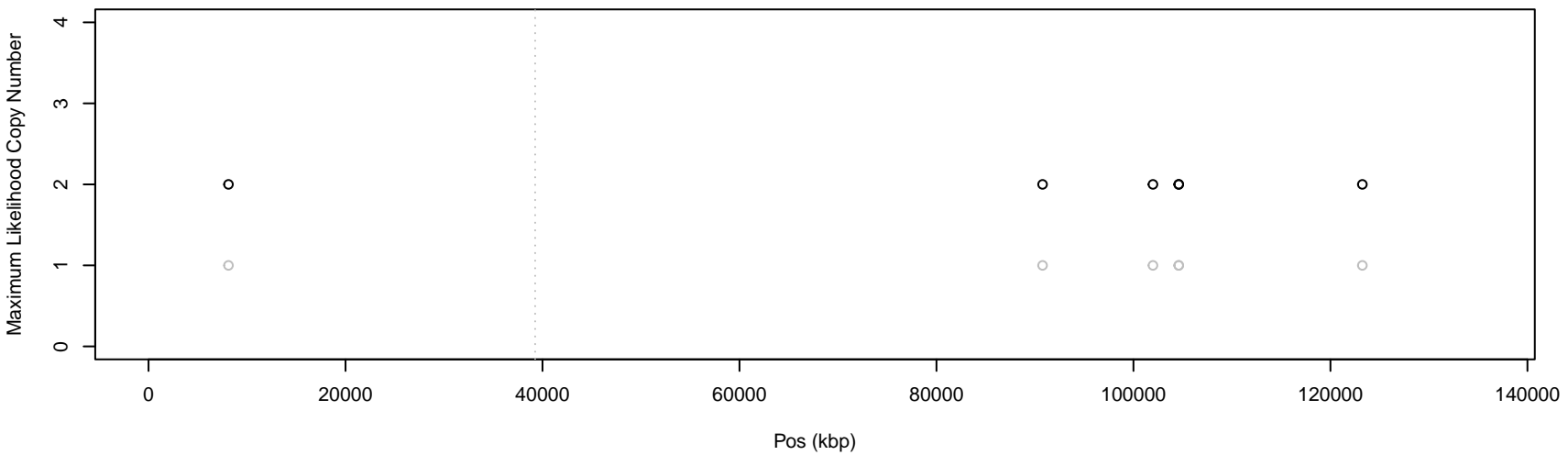
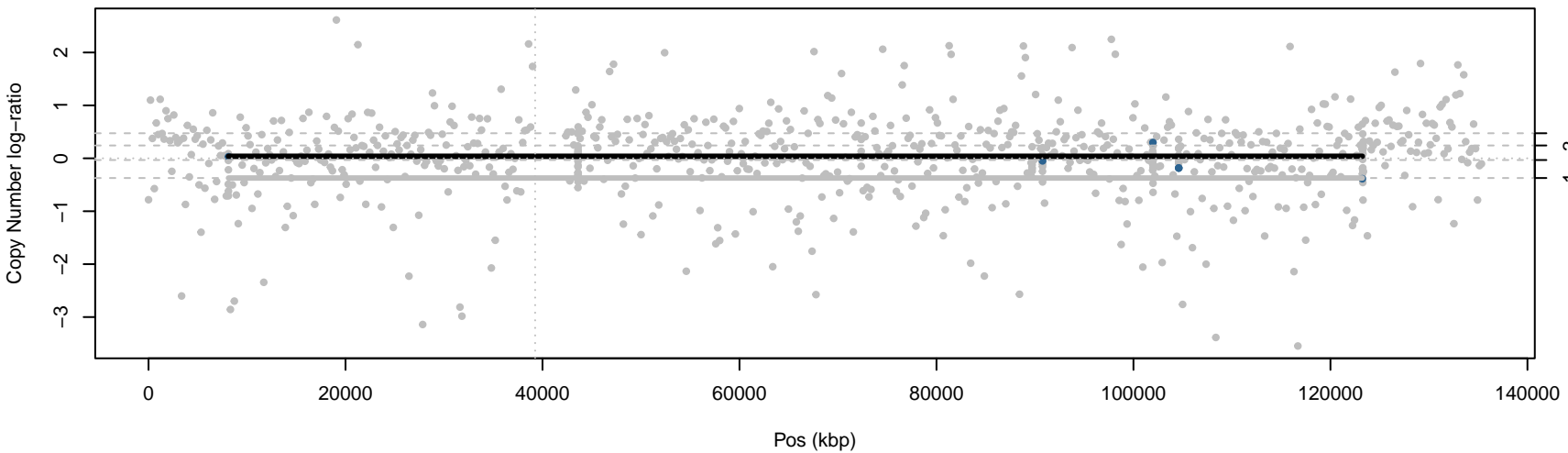
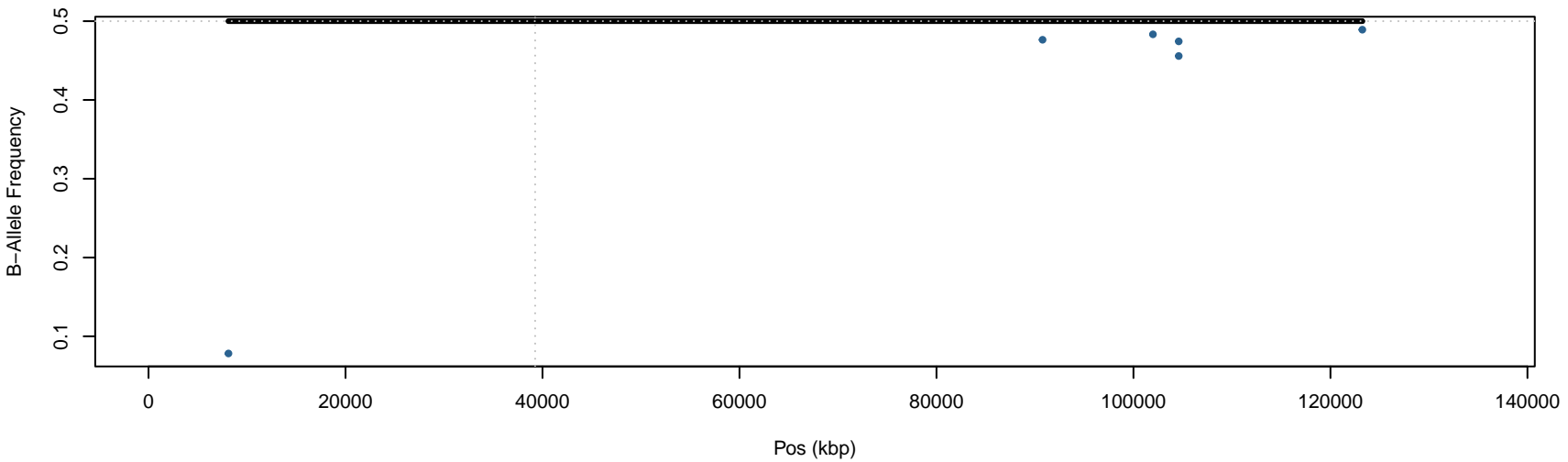




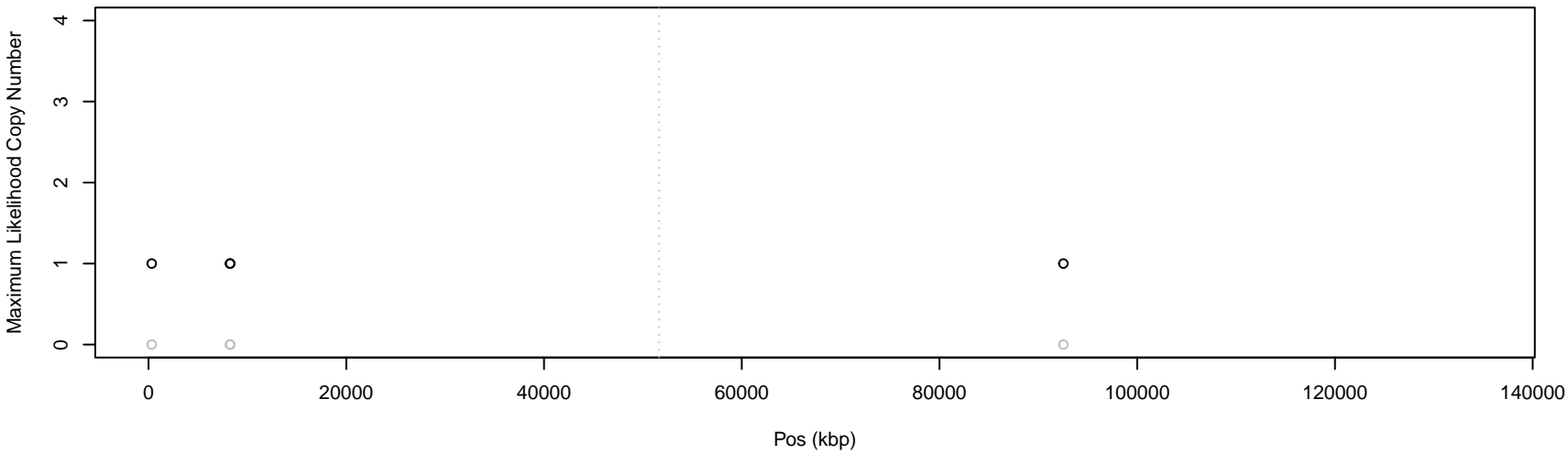
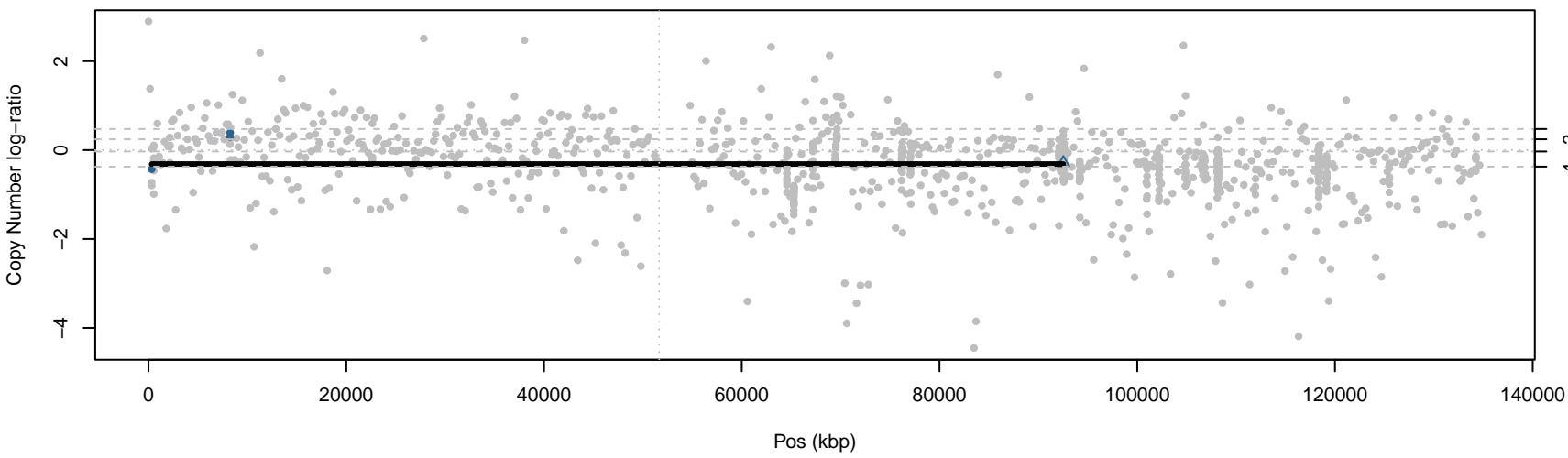
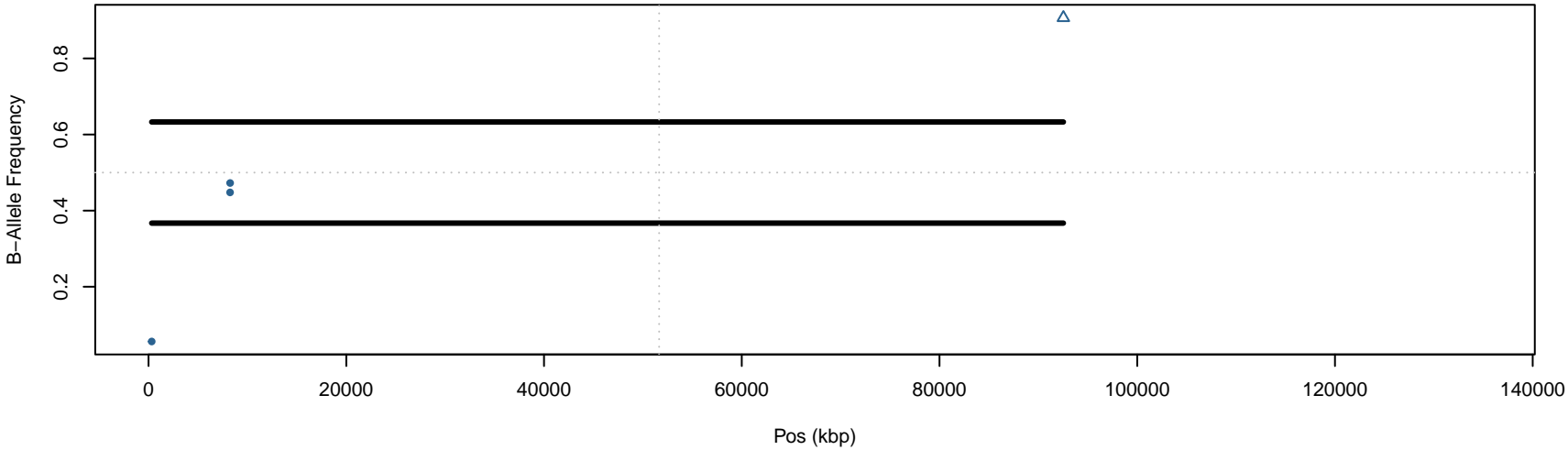
Purity: 0.42 Tumor ploidy: 2.108 SNV log-likelihood: -30.49 GoF: 86% Mean coverage: 774;145 Chromosome: 9



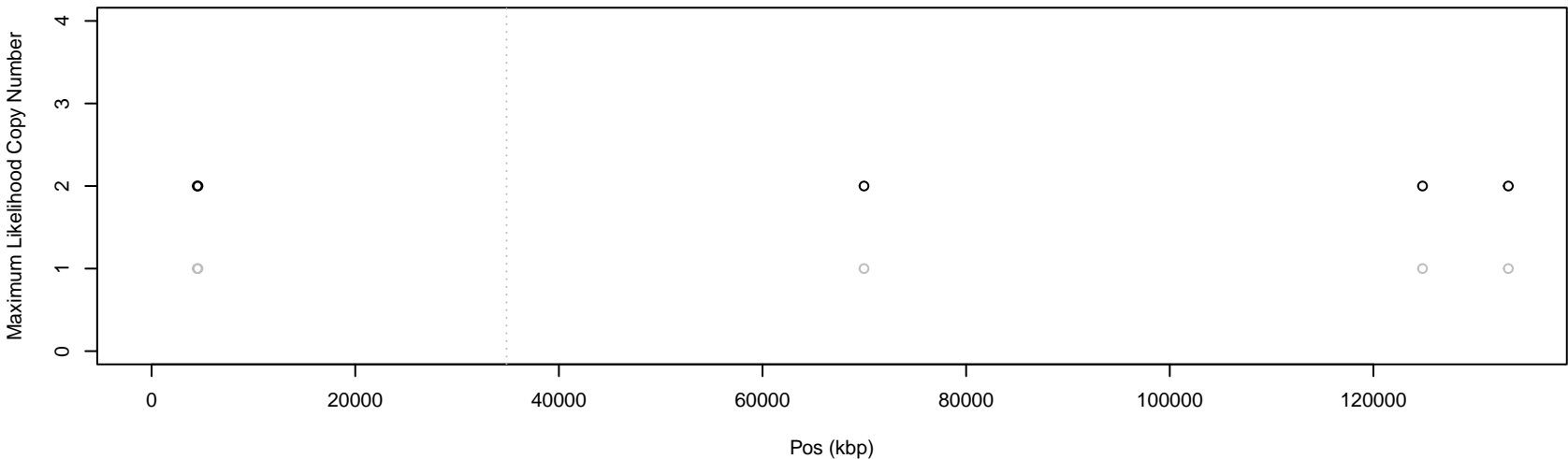
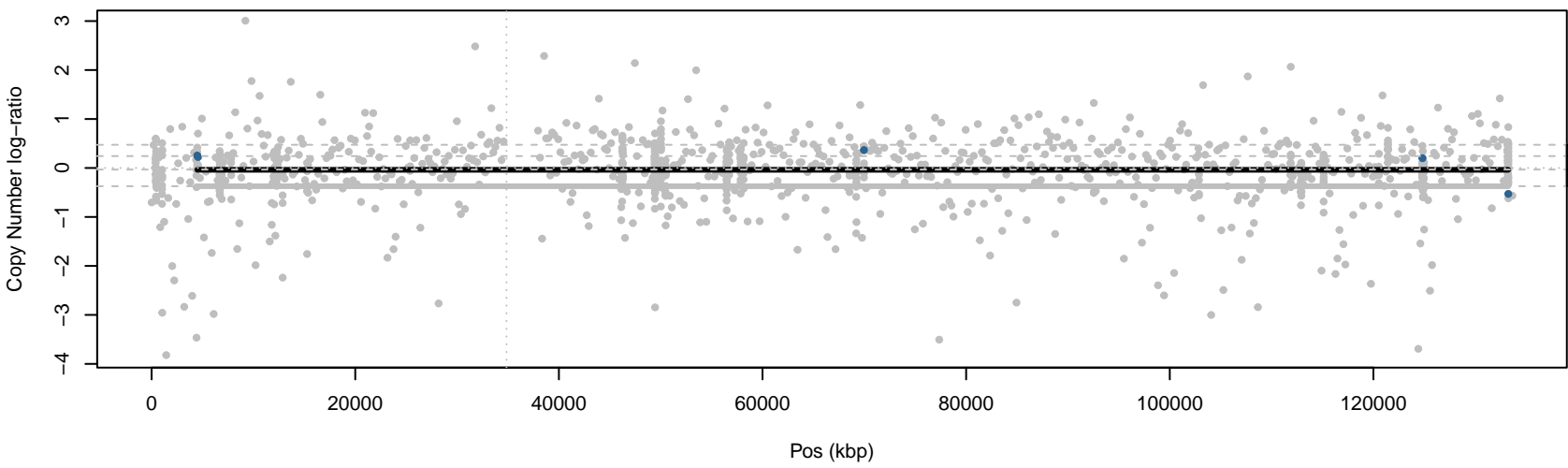
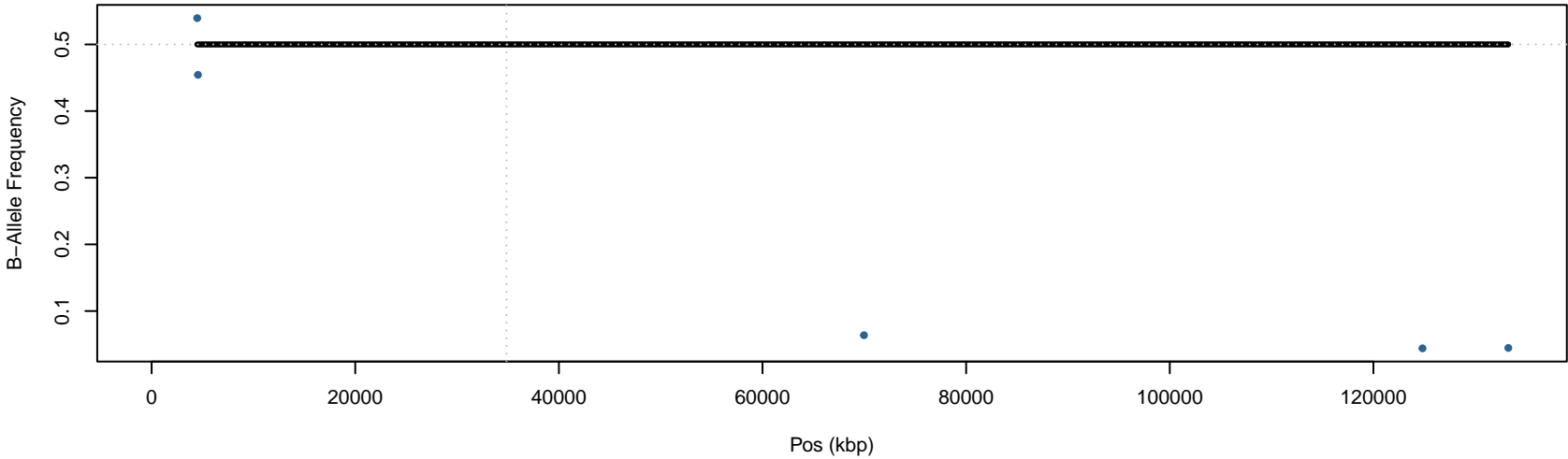
Purity: 0.42 Tumor ploidy: 2.108 SNV log-likelihood: -30.49 GoF: 86% Mean coverage: 774;145 Chromosome: 10



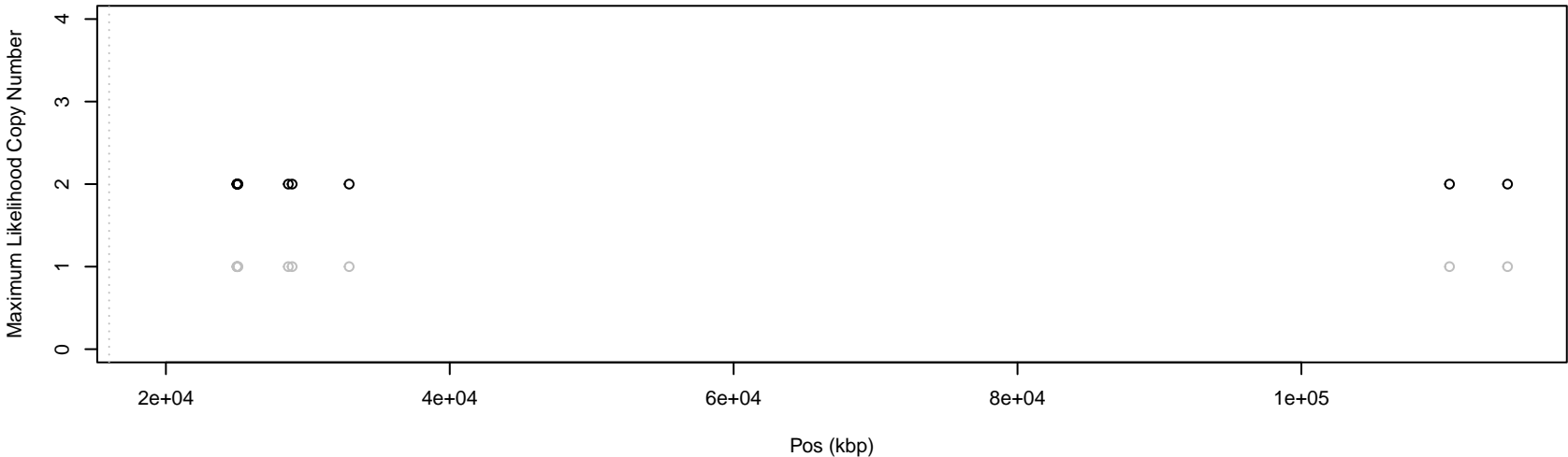
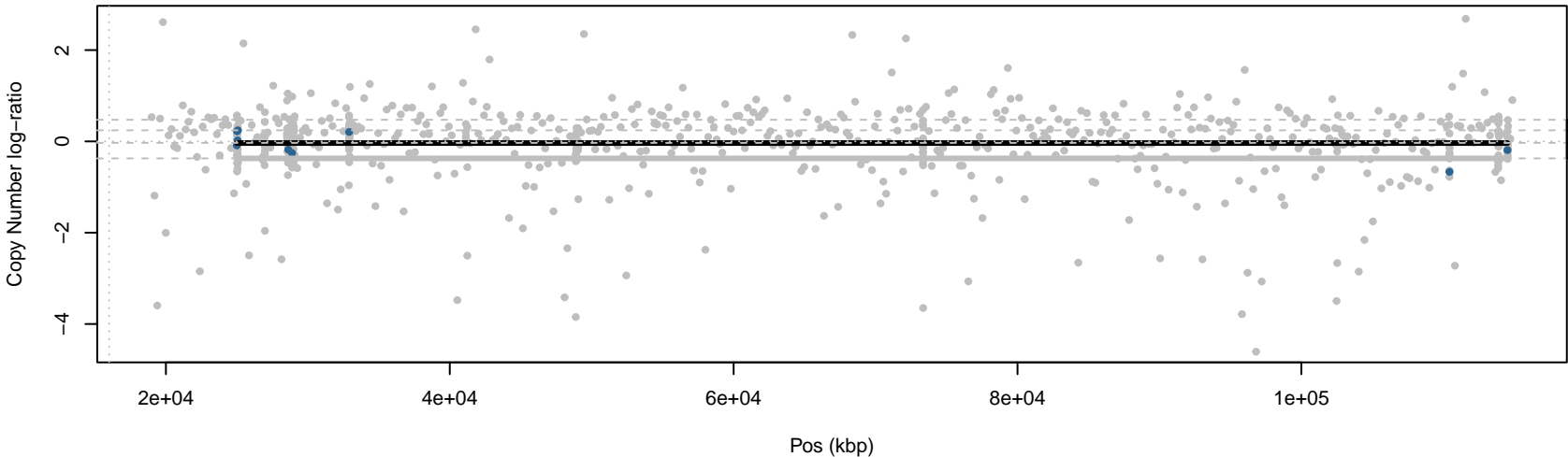
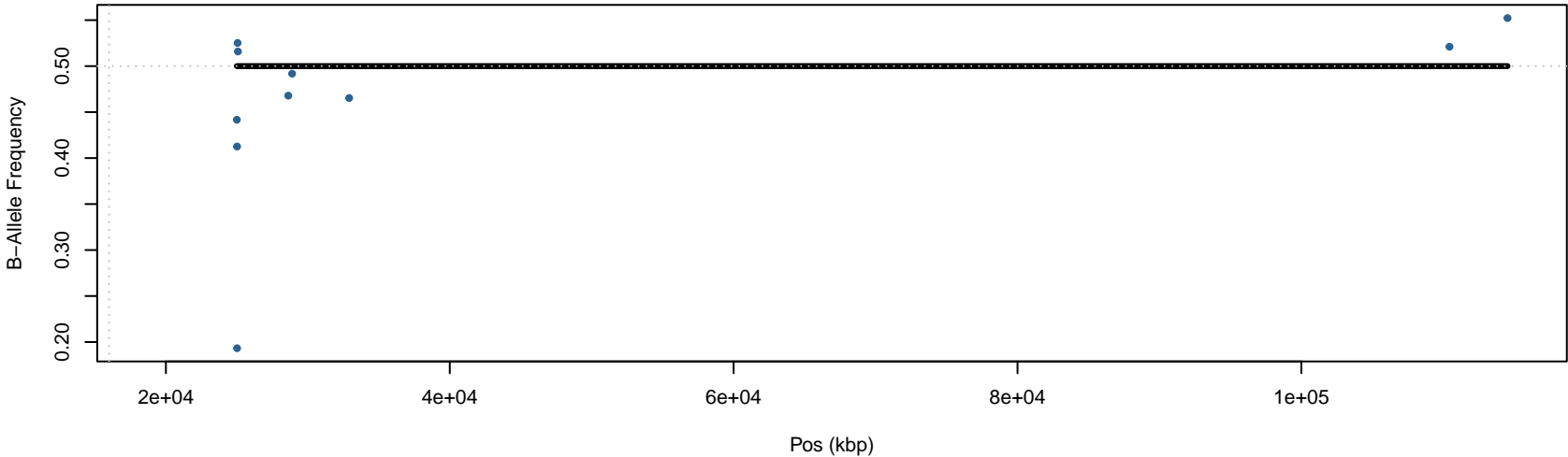
Purity: 0.42 Tumor ploidy: 2.108 SNV log-likelihood: -30.49 GoF: 86% Mean coverage: 774;145 Chromosome: 11



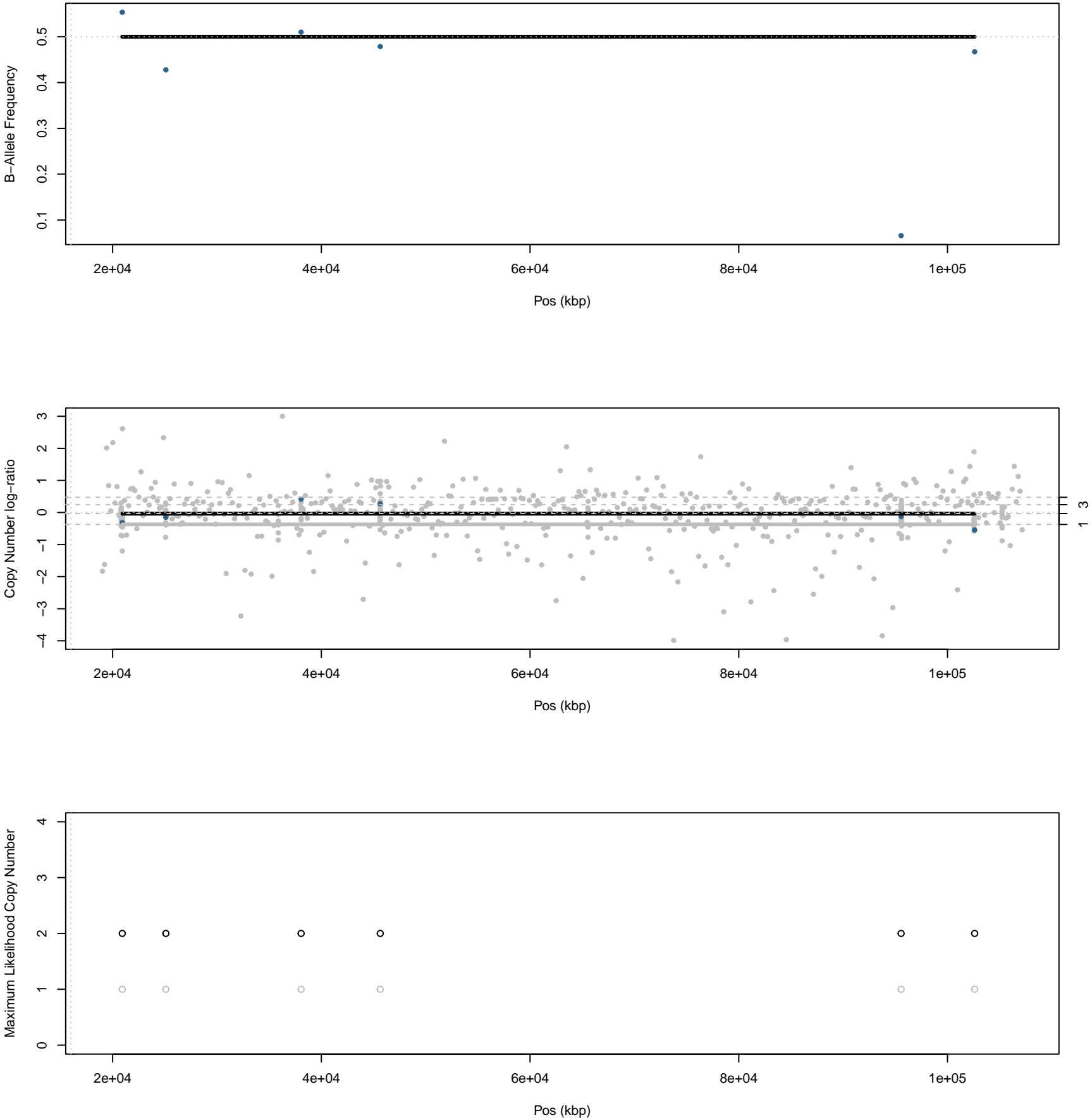
Purity: 0.42 Tumor ploidy: 2.108 SNV log-likelihood: -30.49 GoF: 86% Mean coverage: 774;145 Chromosome: 12



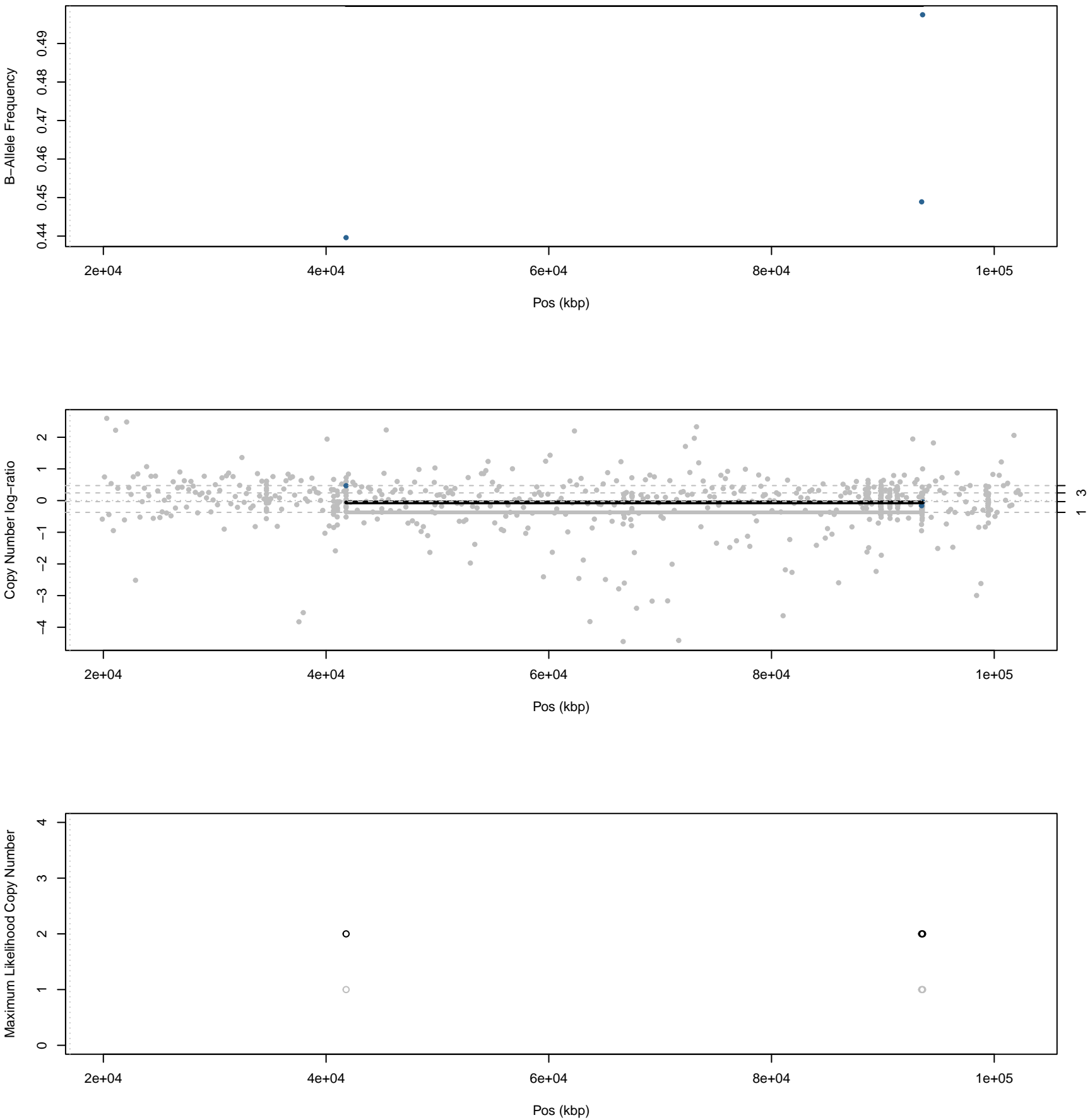
Purity: 0.42 Tumor ploidy: 2.108 SNV log-likelihood: -30.49 GoF: 86% Mean coverage: 774;145 Chromosome: 13



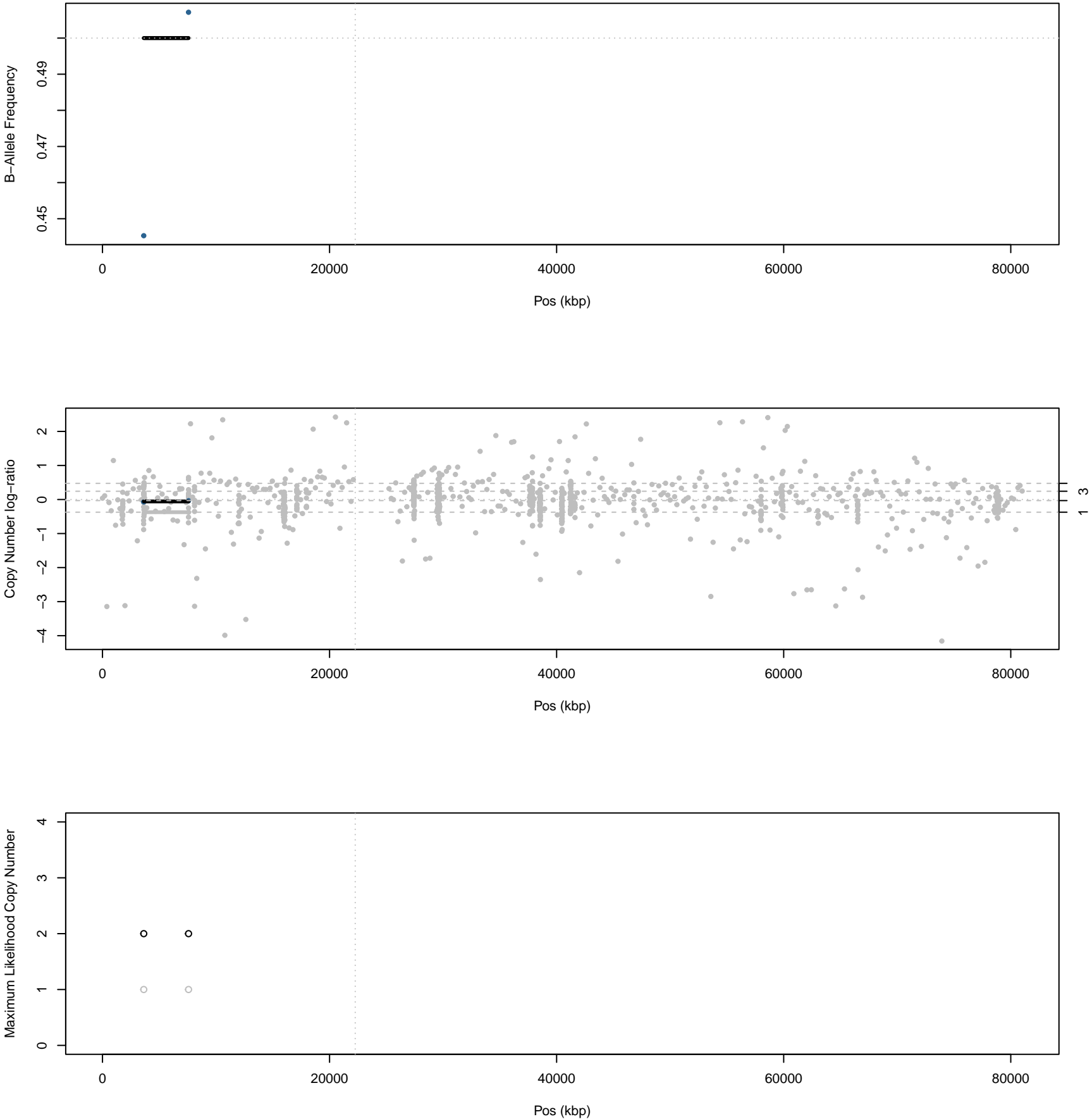
Purity: 0.42 Tumor ploidy: 2.108 SNV log-likelihood: -30.49 GoF: 86% Mean coverage: 774;145 Chromosome: 14



Purity: 0.42 Tumor ploidy: 2.108 SNV log-likelihood: -30.49 GoF: 86% Mean coverage: 774;145 Chromosome: 15

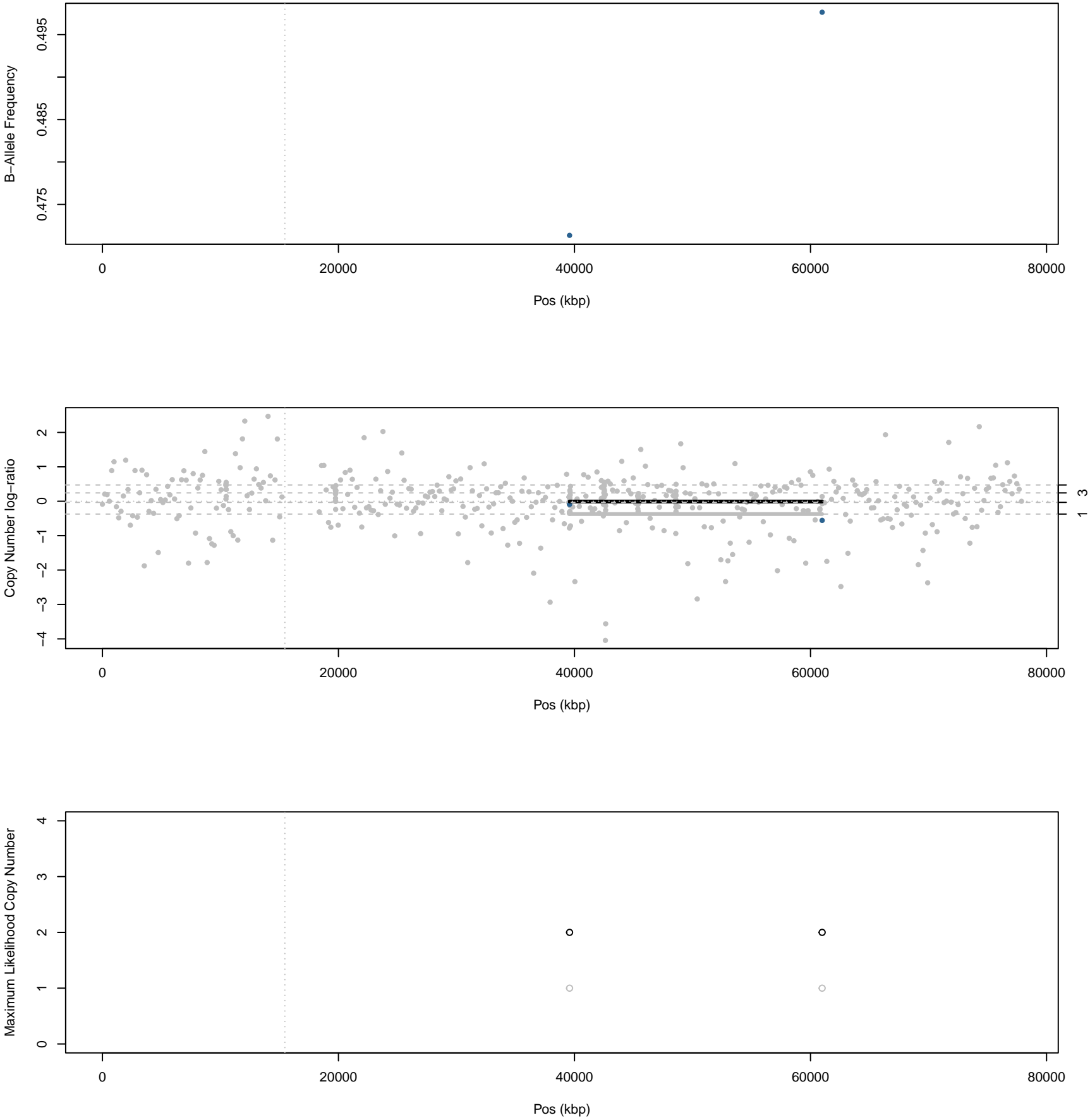


Purity: 0.42 Tumor ploidy: 2.108 SNV log-likelihood: -30.49 GoF: 86% Mean coverage: 774;145 Chromosome: 17

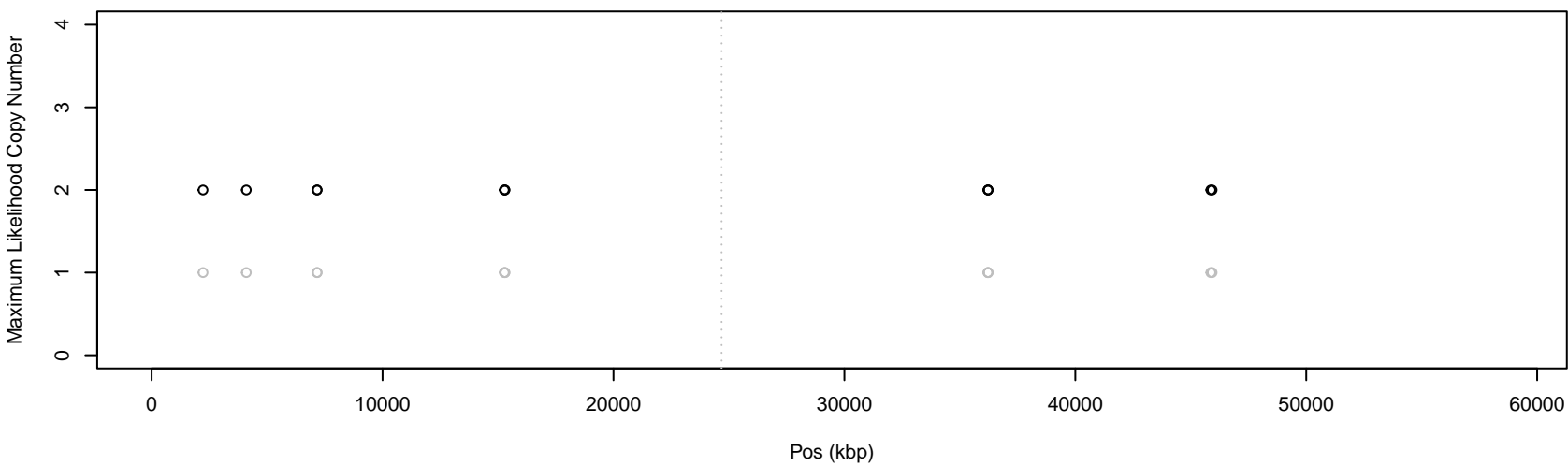
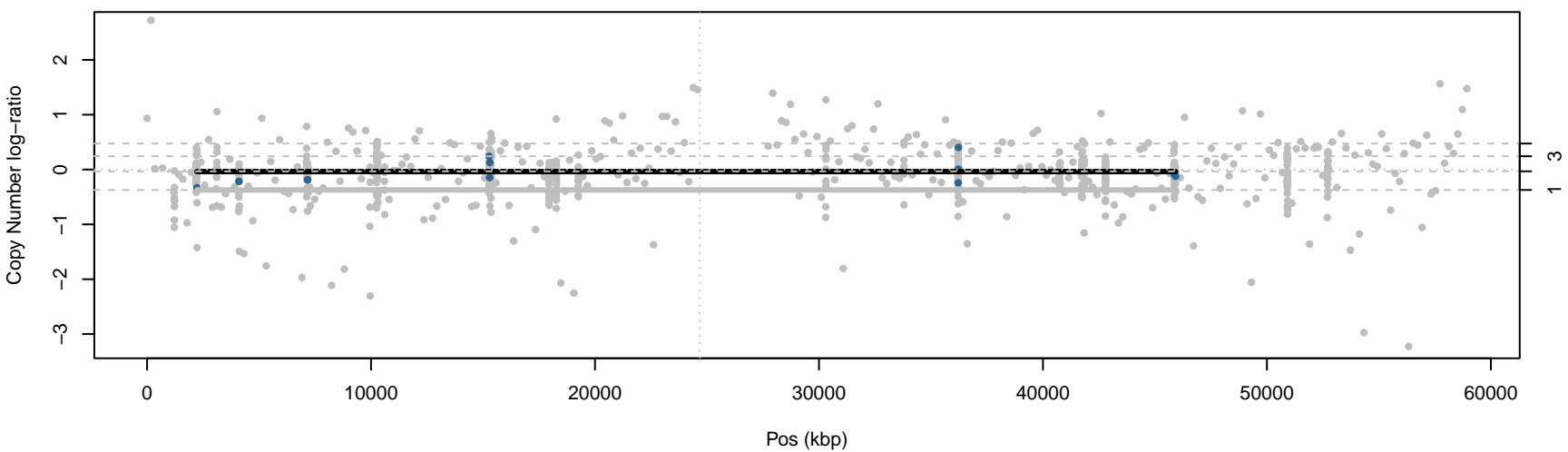
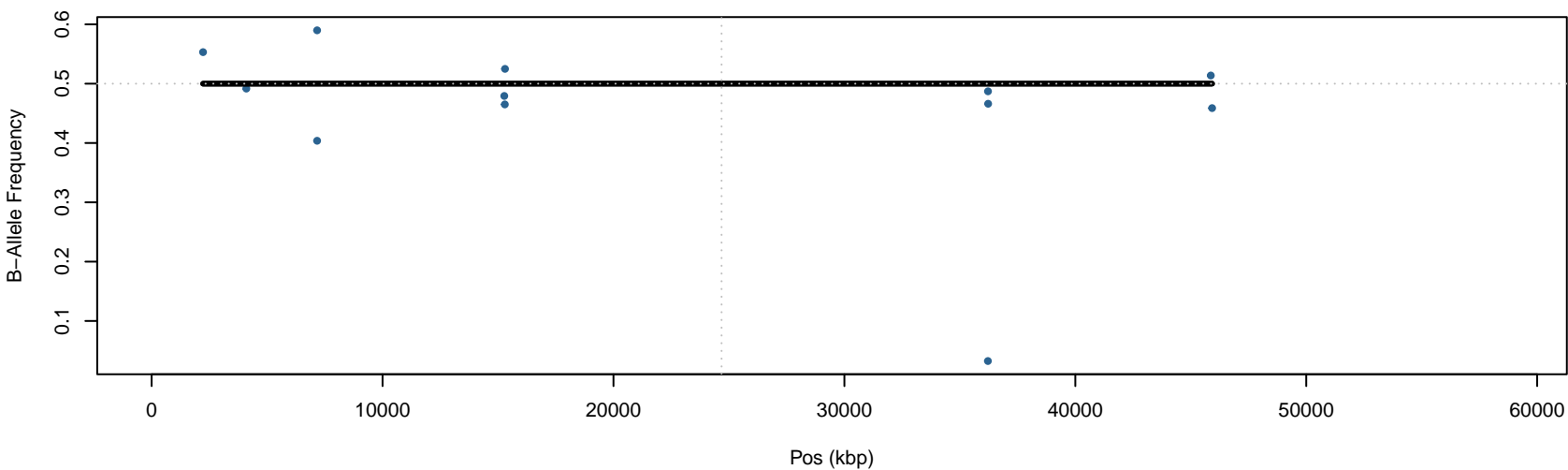




Purity: 0.42 Tumor ploidy: 2.108 SNV log-likelihood: -30.49 GoF: 86% Mean coverage: 774;145 Chromosome: 18



Purity: 0.42 Tumor ploidy: 2.108 SNV log-likelihood: -30.49 GoF: 86% Mean coverage: 774;145 Chromosome: 19



Purity: 0.42 Tumor ploidy: 2.108 SNV log-likelihood: -30.49 GoF: 86% Mean coverage: 774;145 Chromosome: 22

