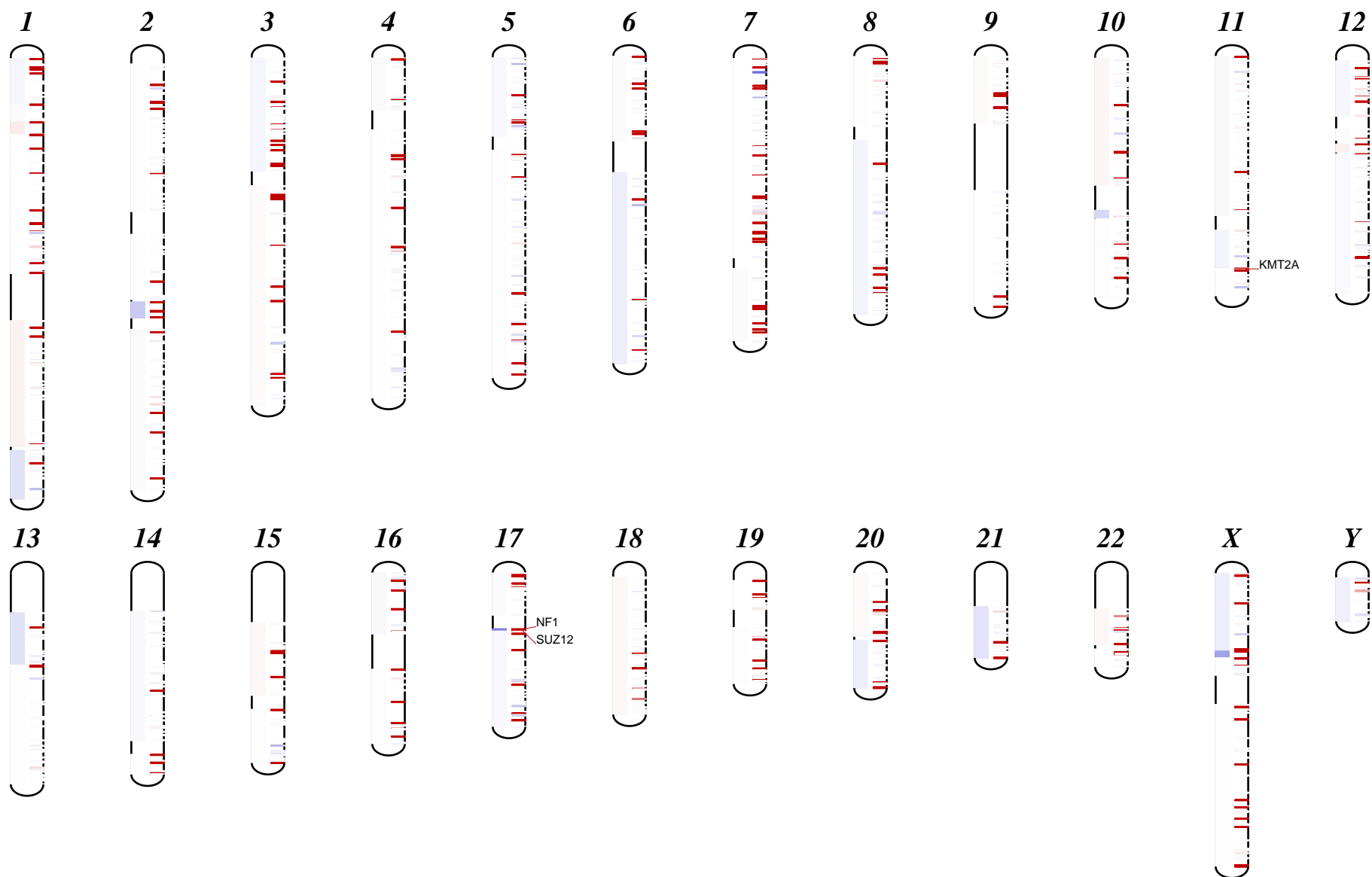
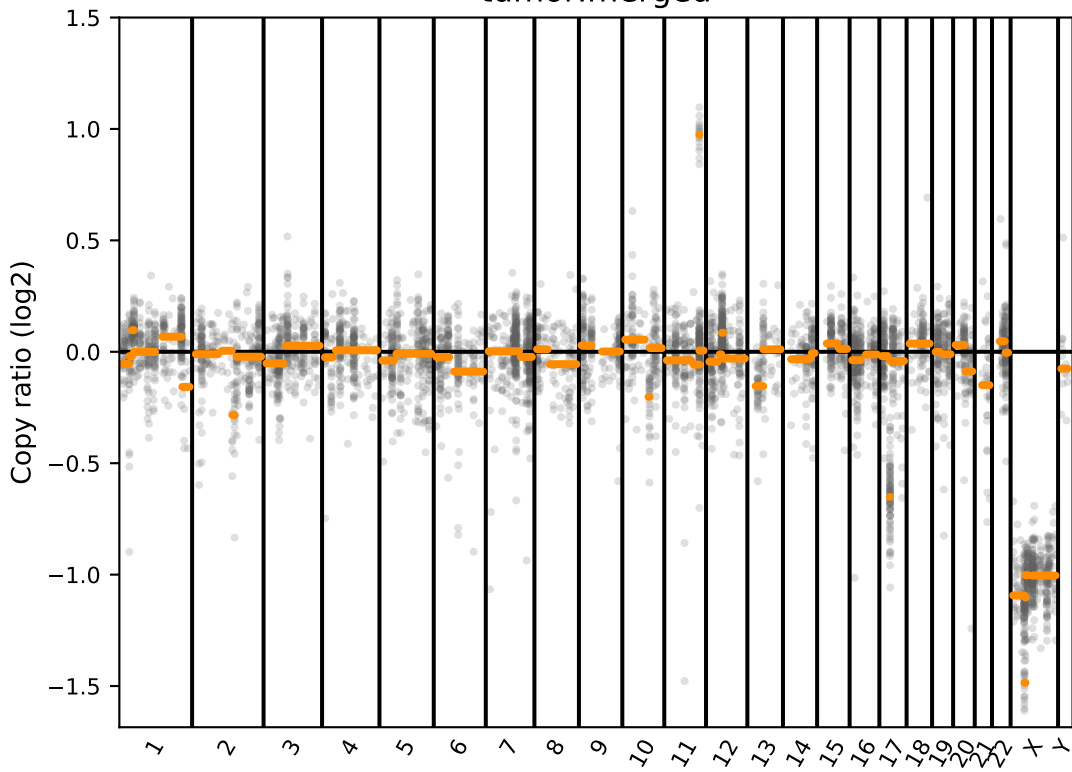


## Sample tumor.merged

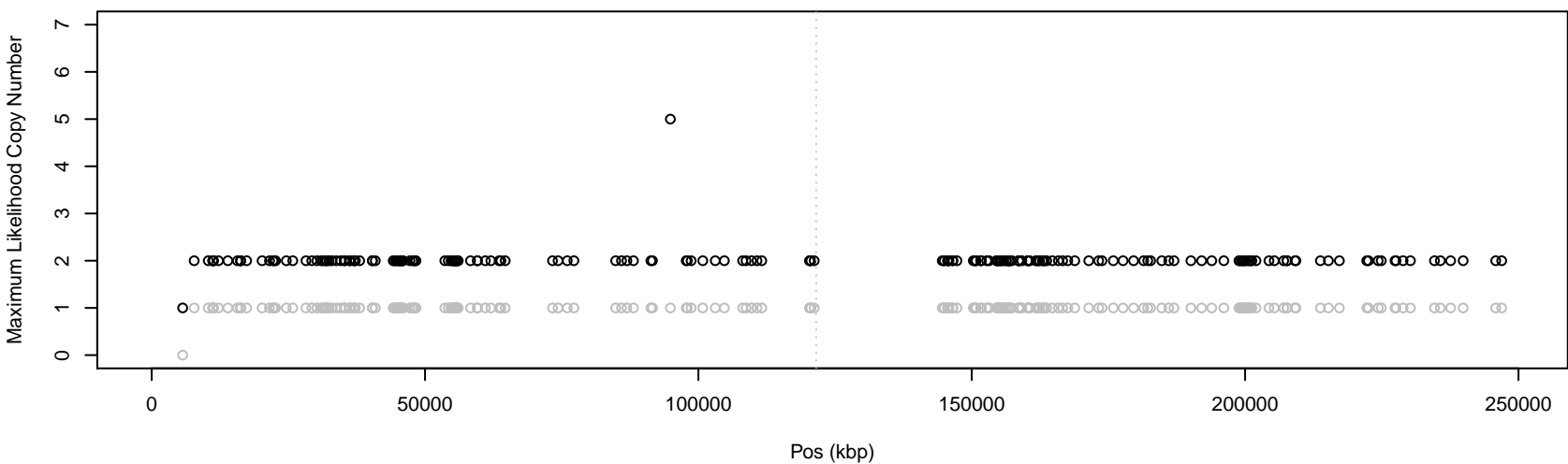
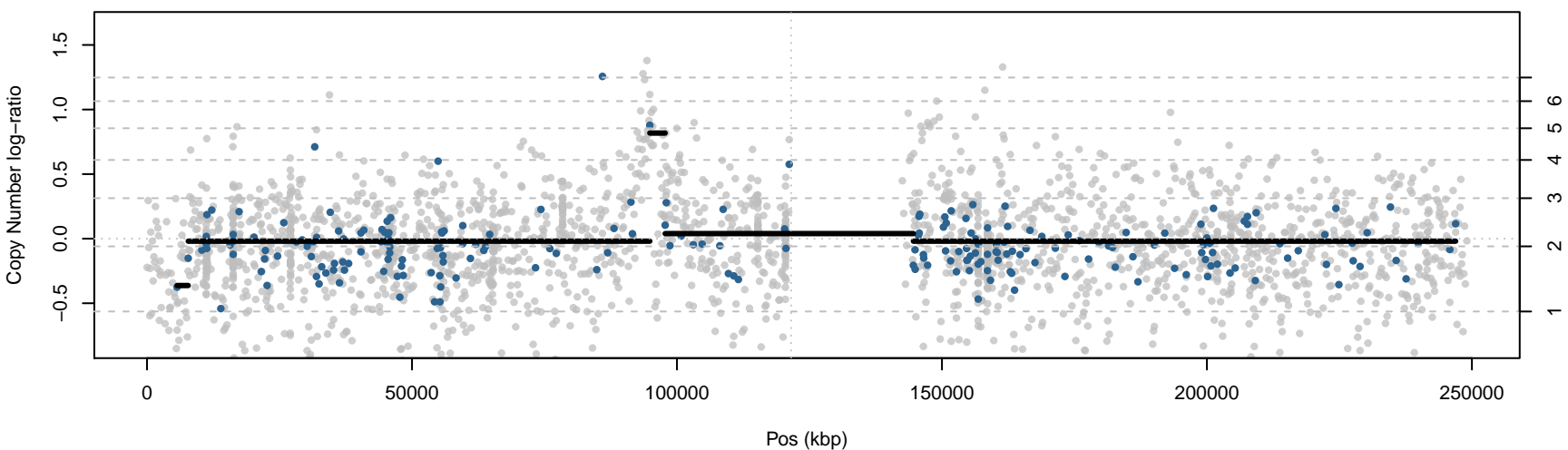
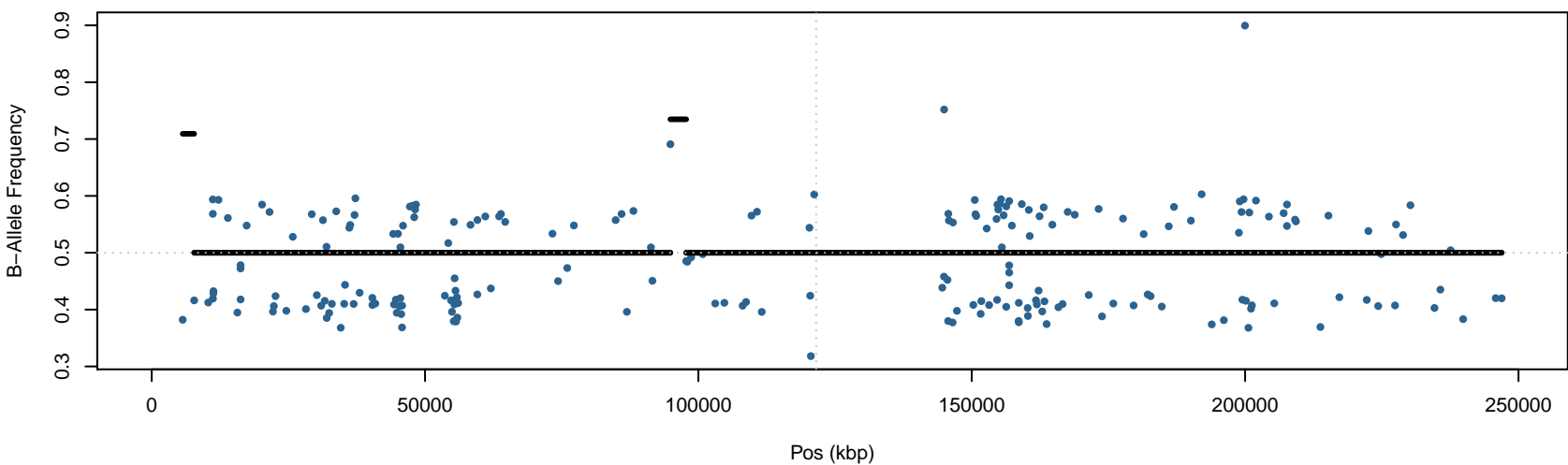


 Gain  Loss

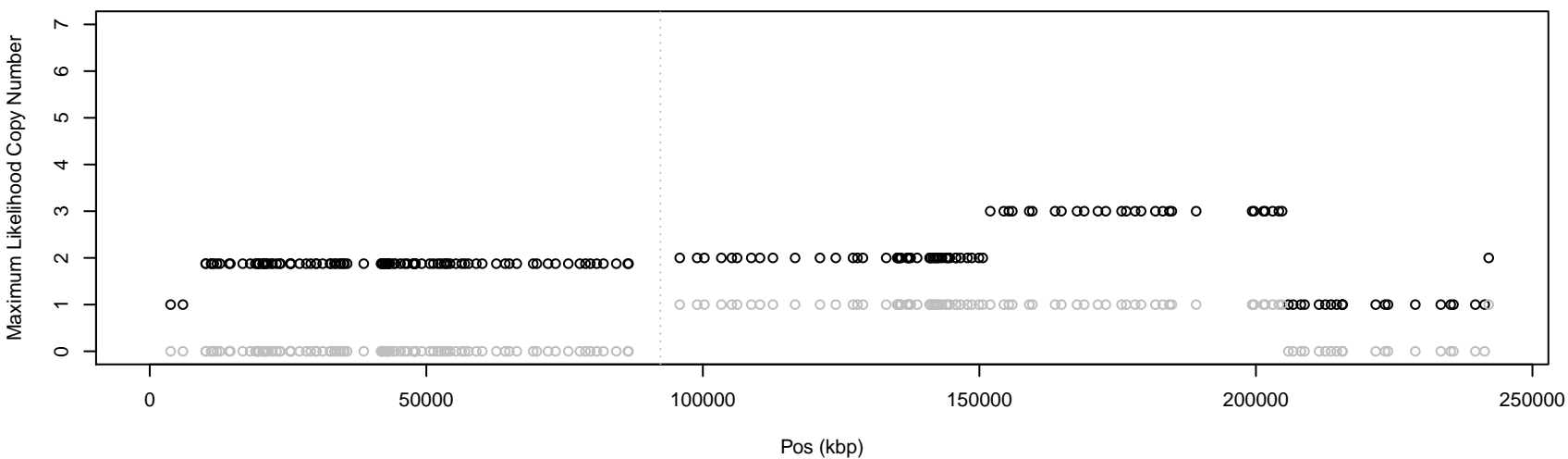
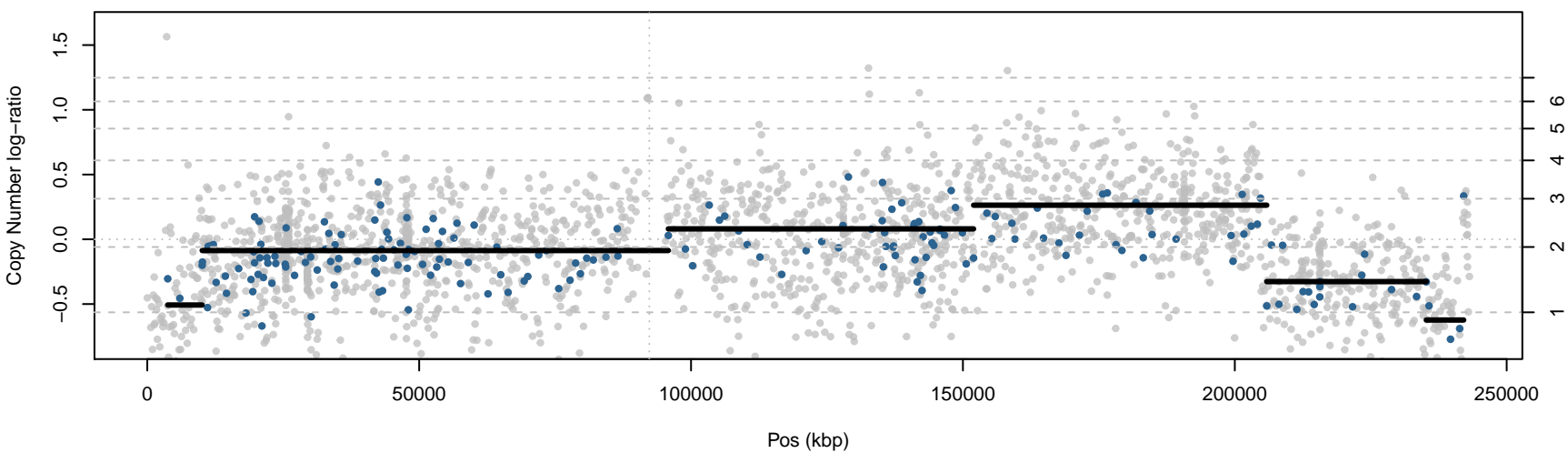
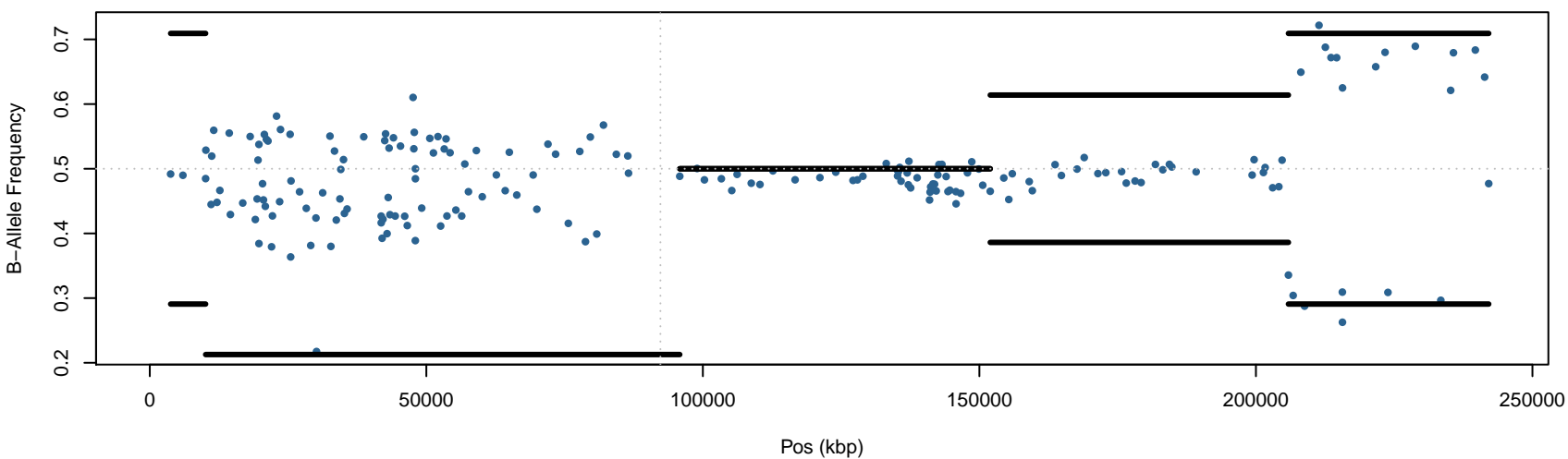
tumor.merged



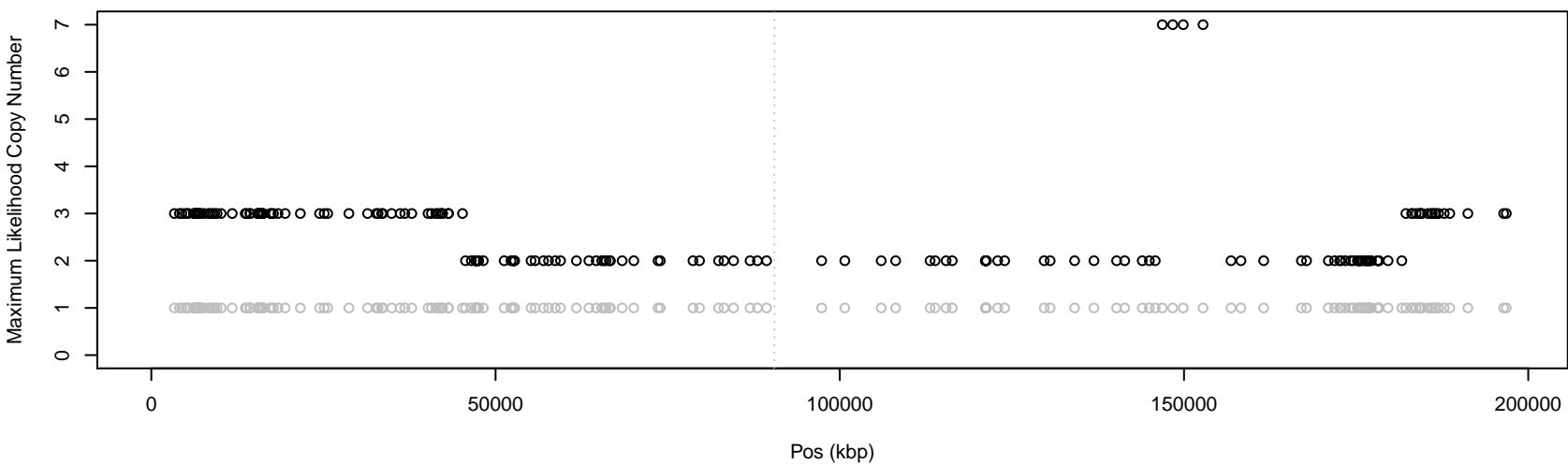
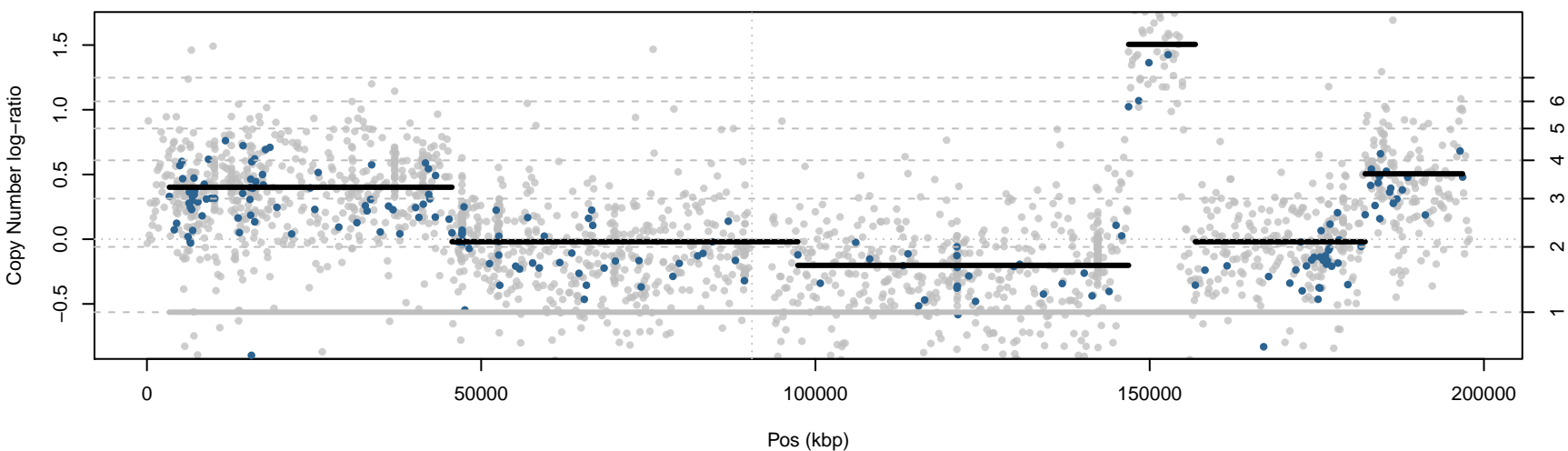
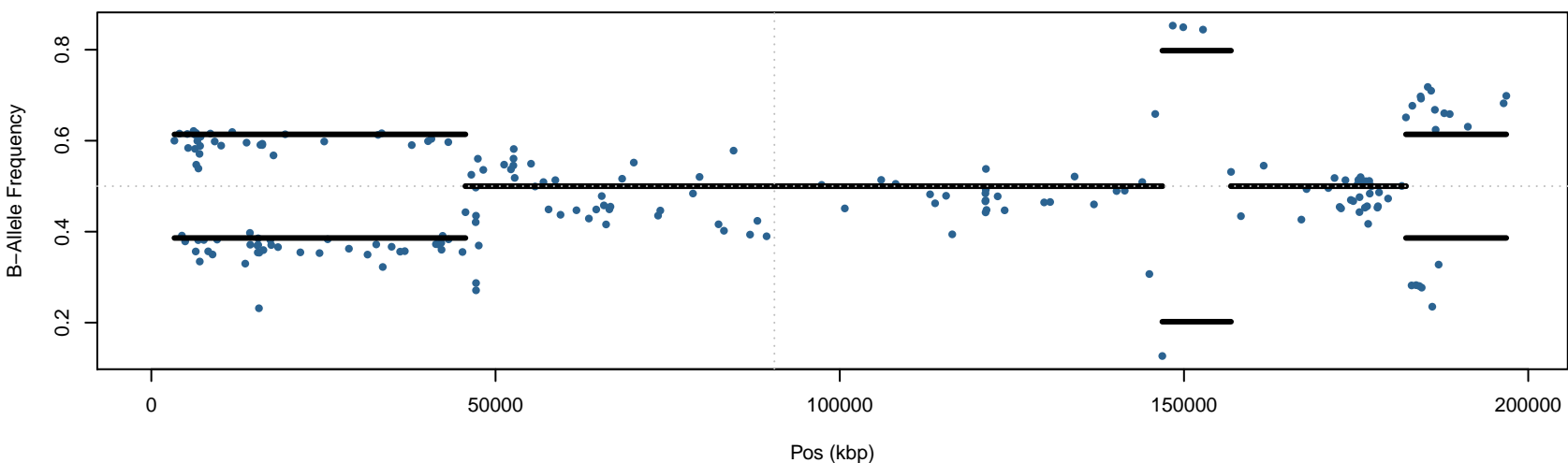
Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 1



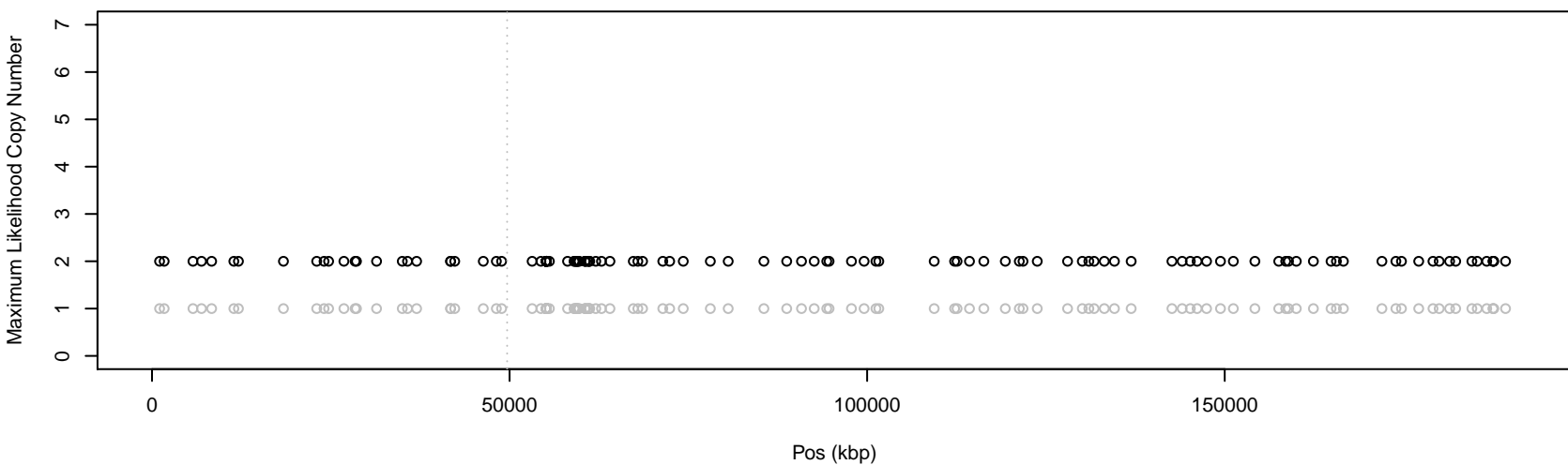
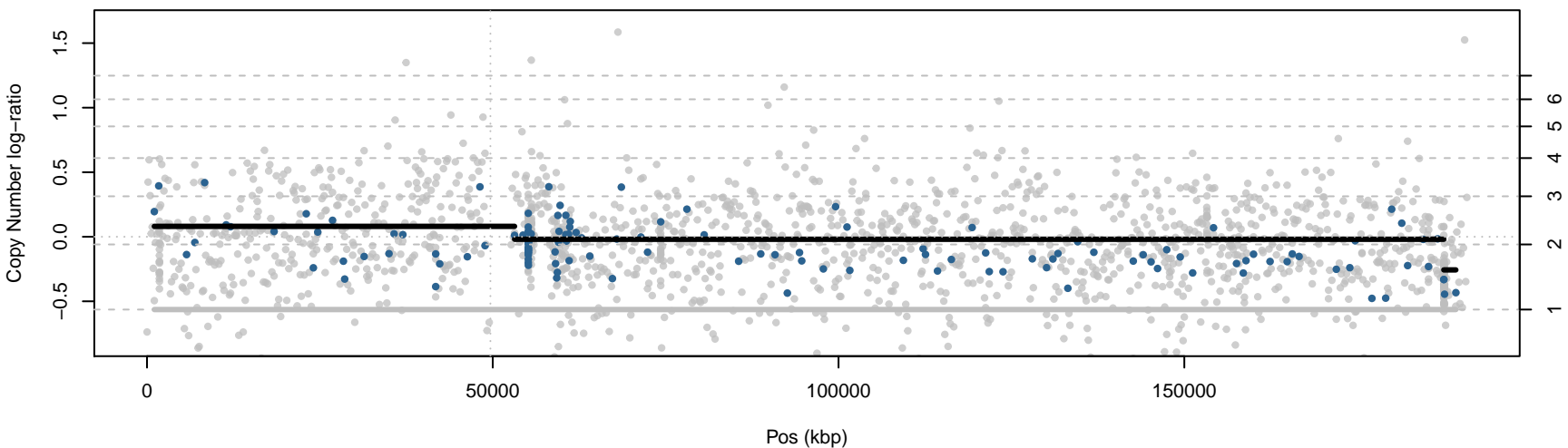
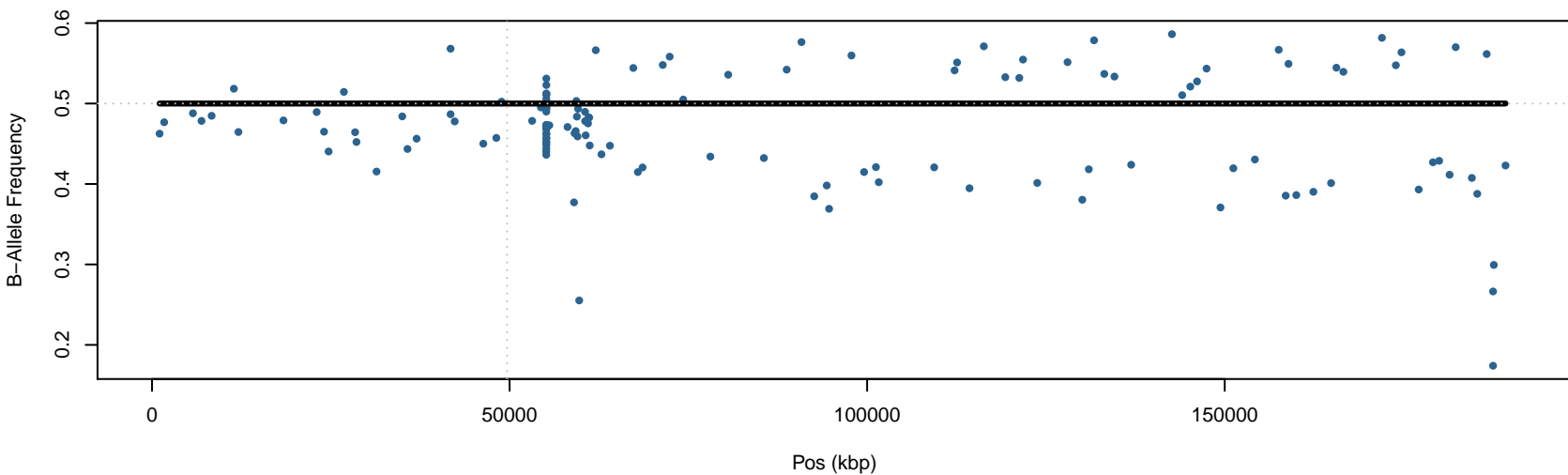
Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 2



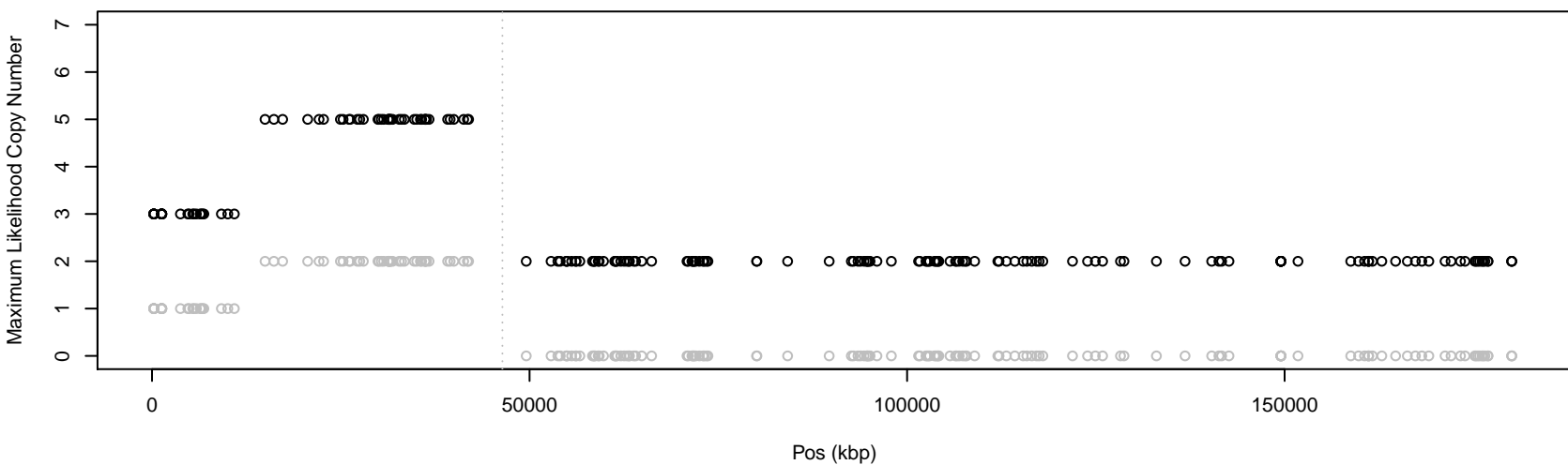
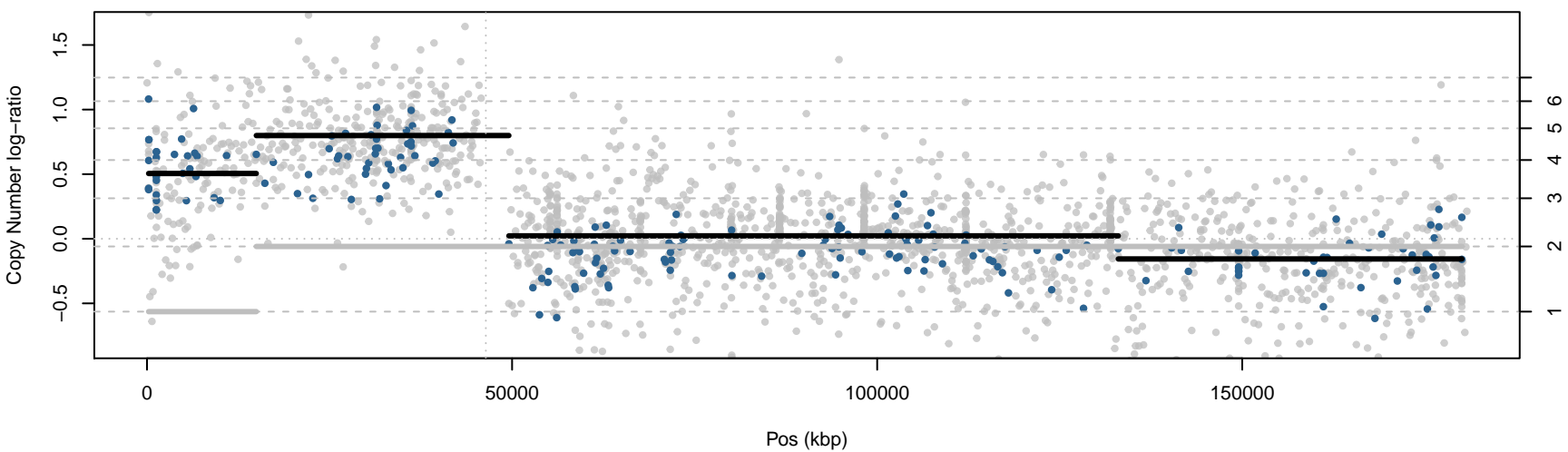
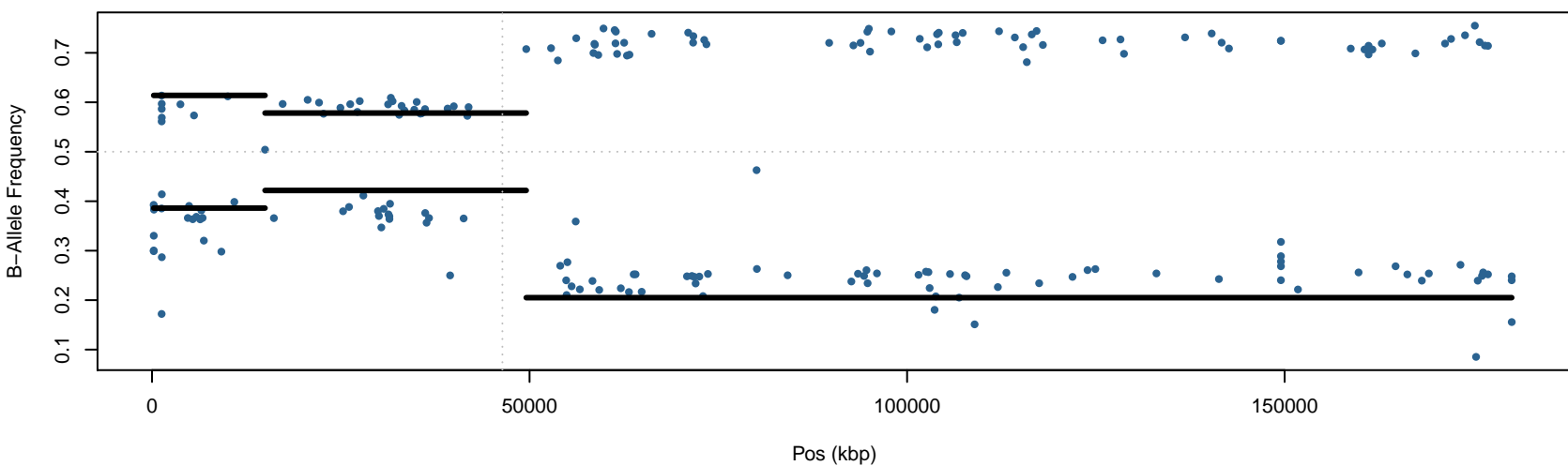
Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 3



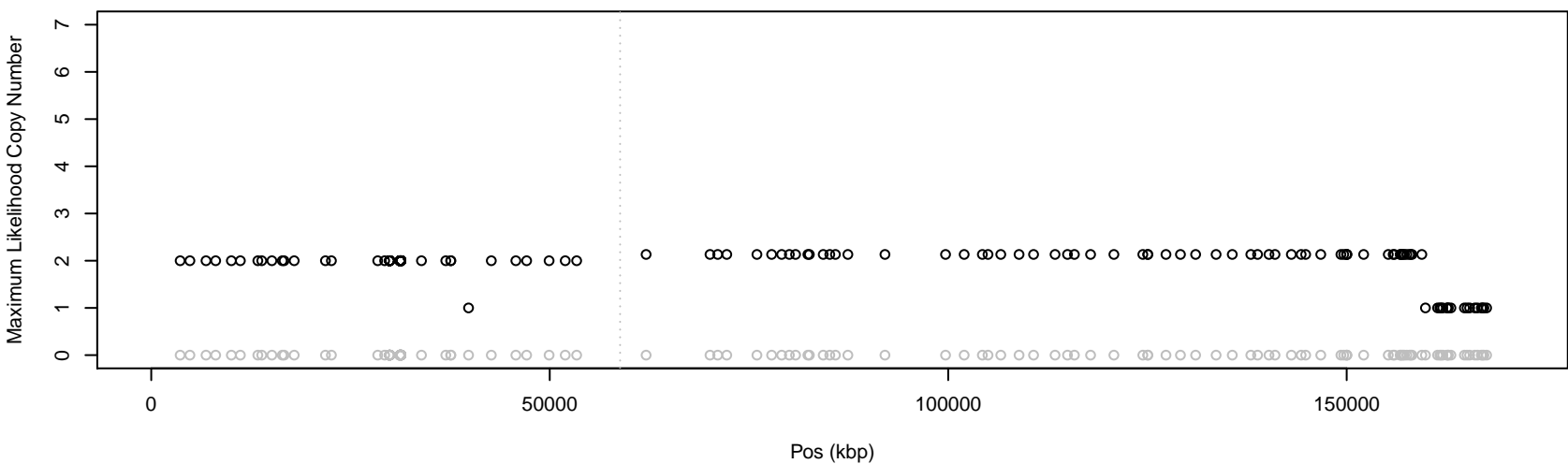
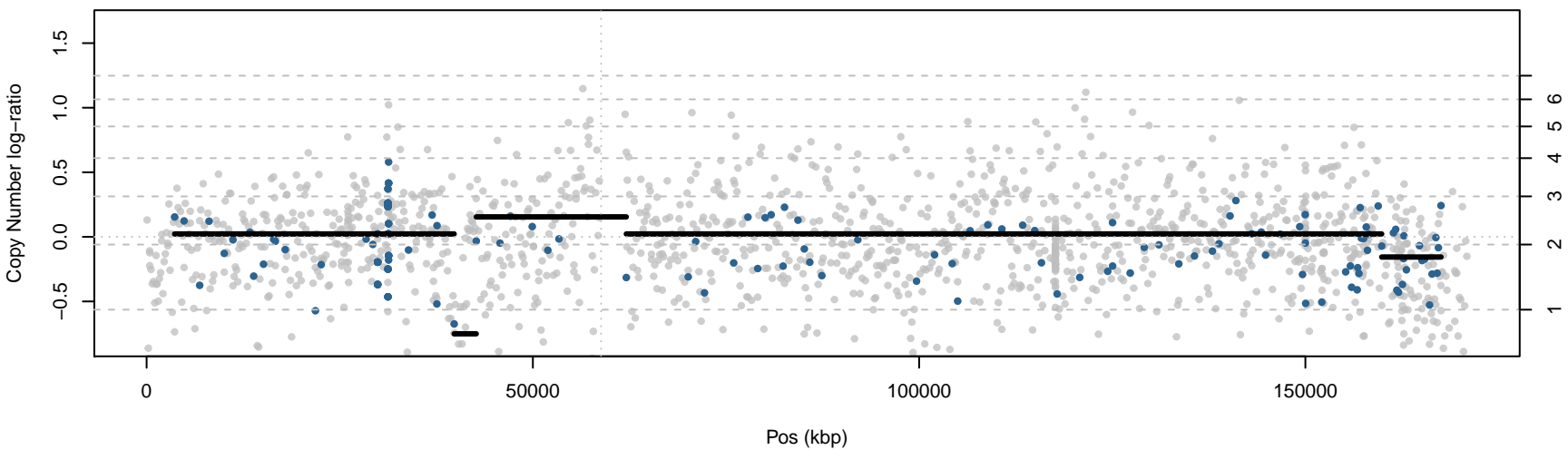
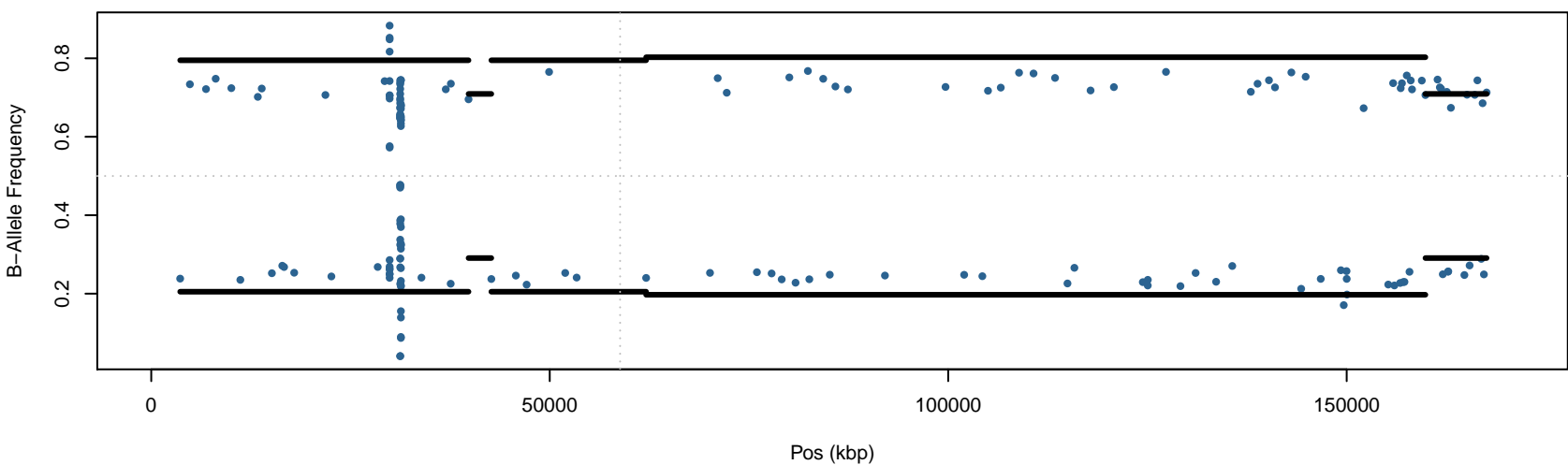
Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 4



Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 5

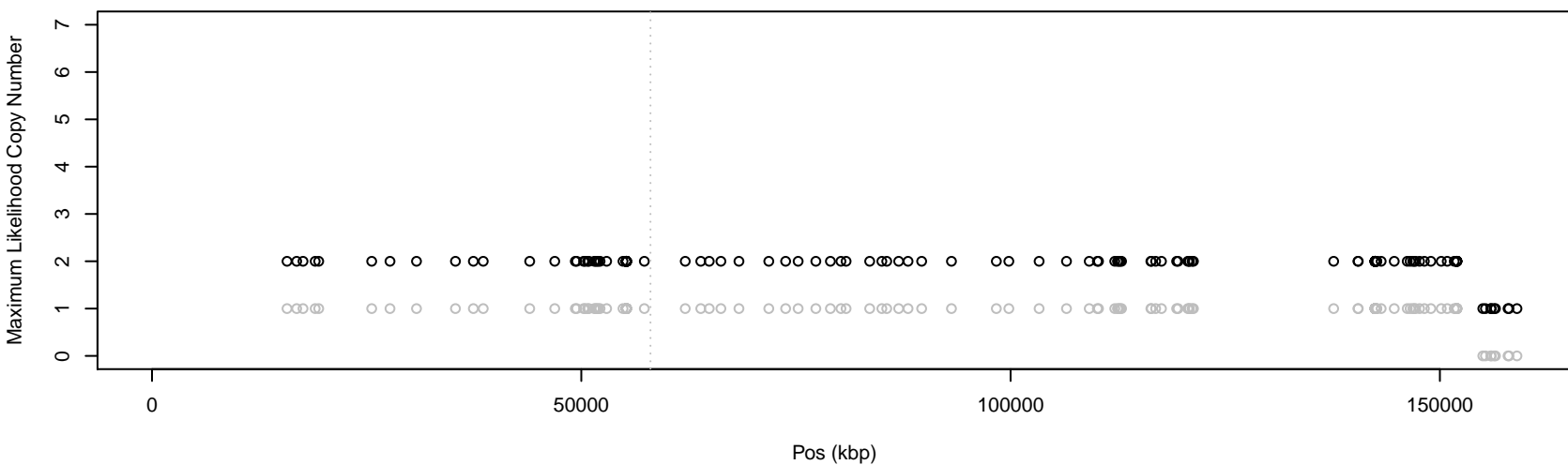
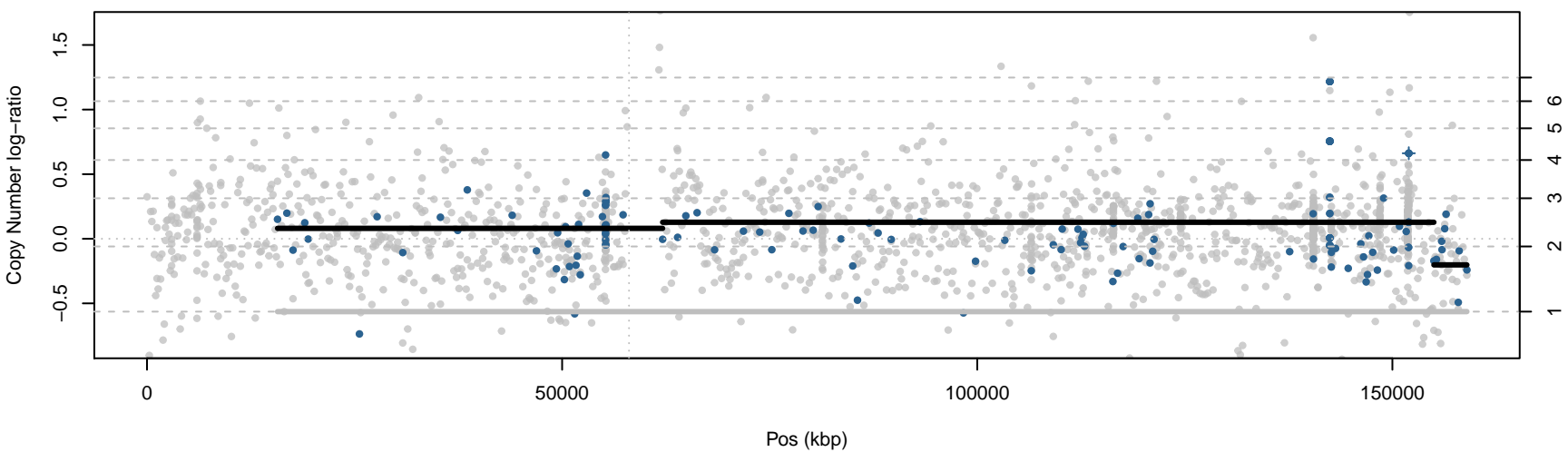
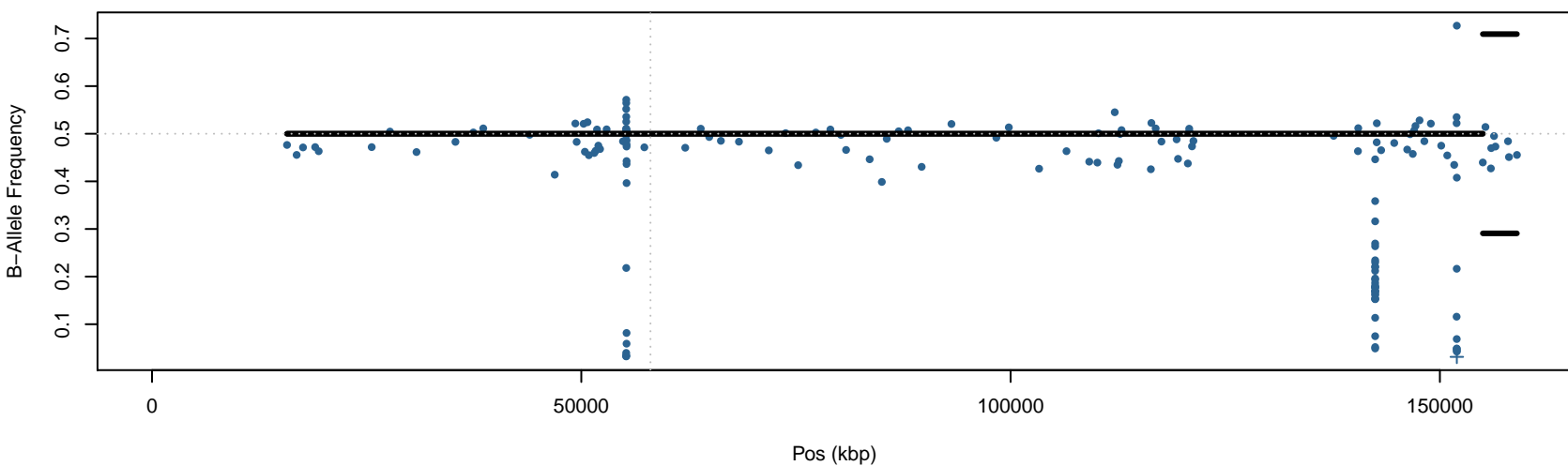


Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 6

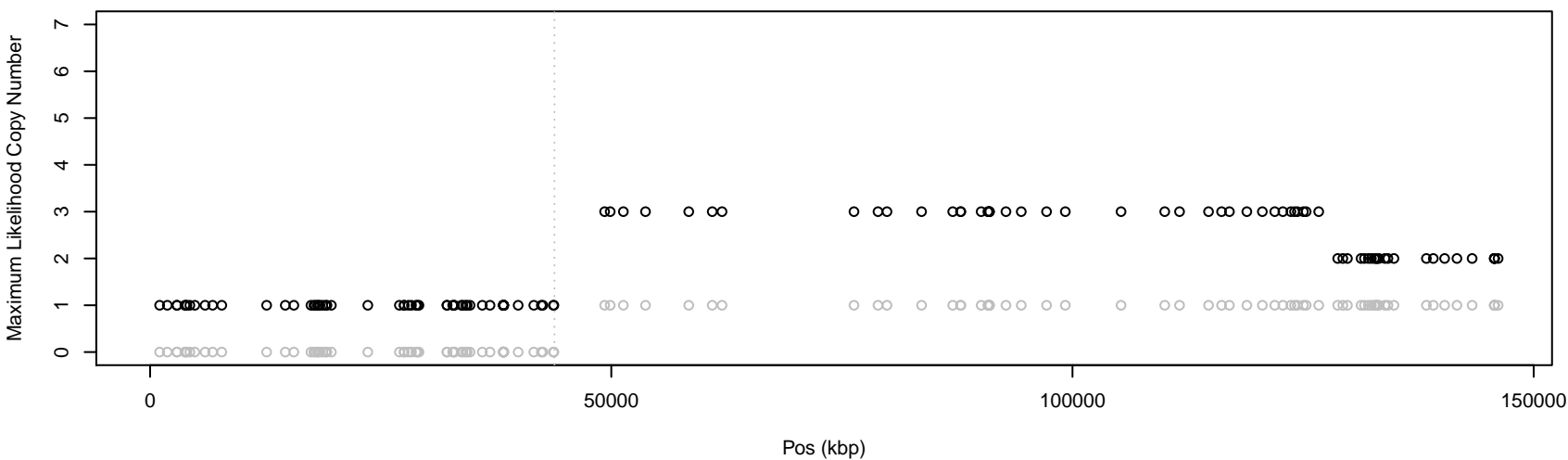
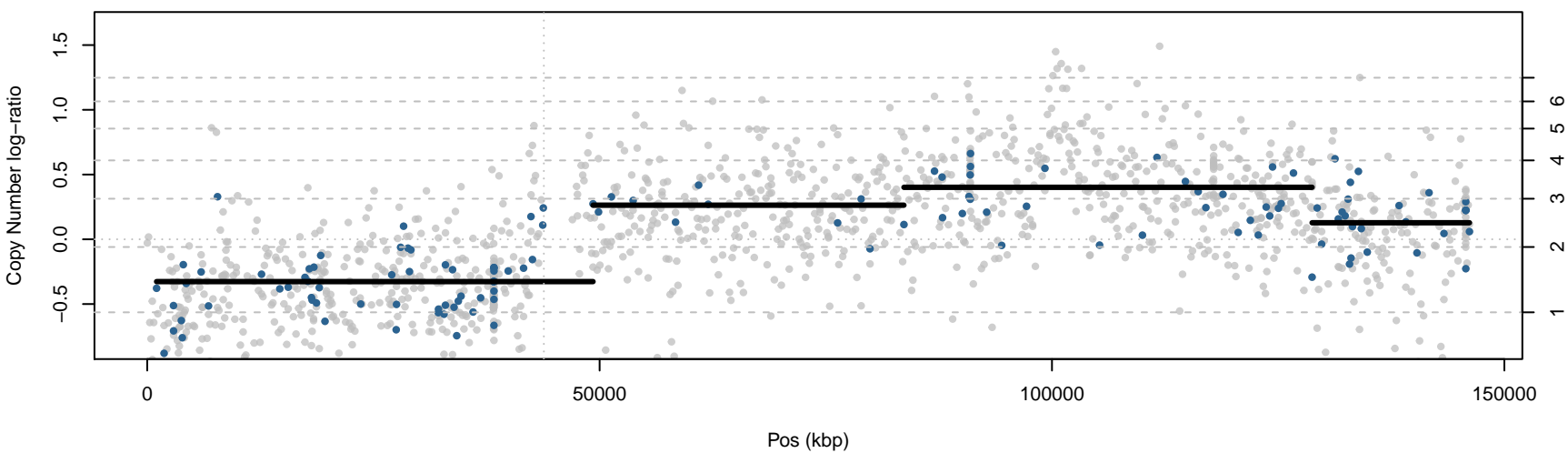
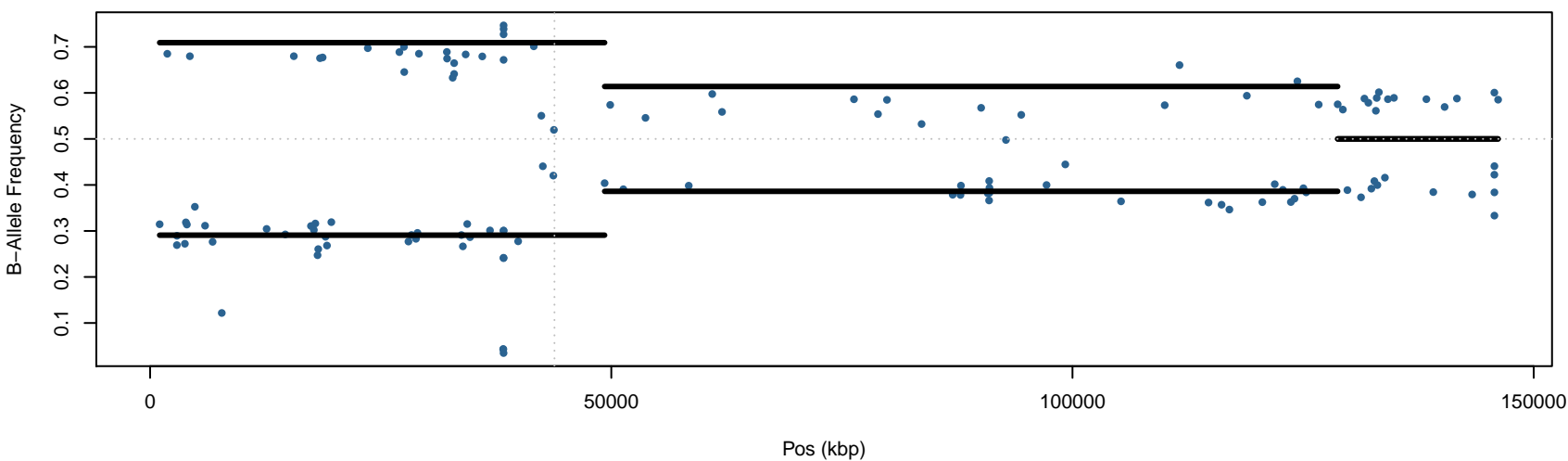




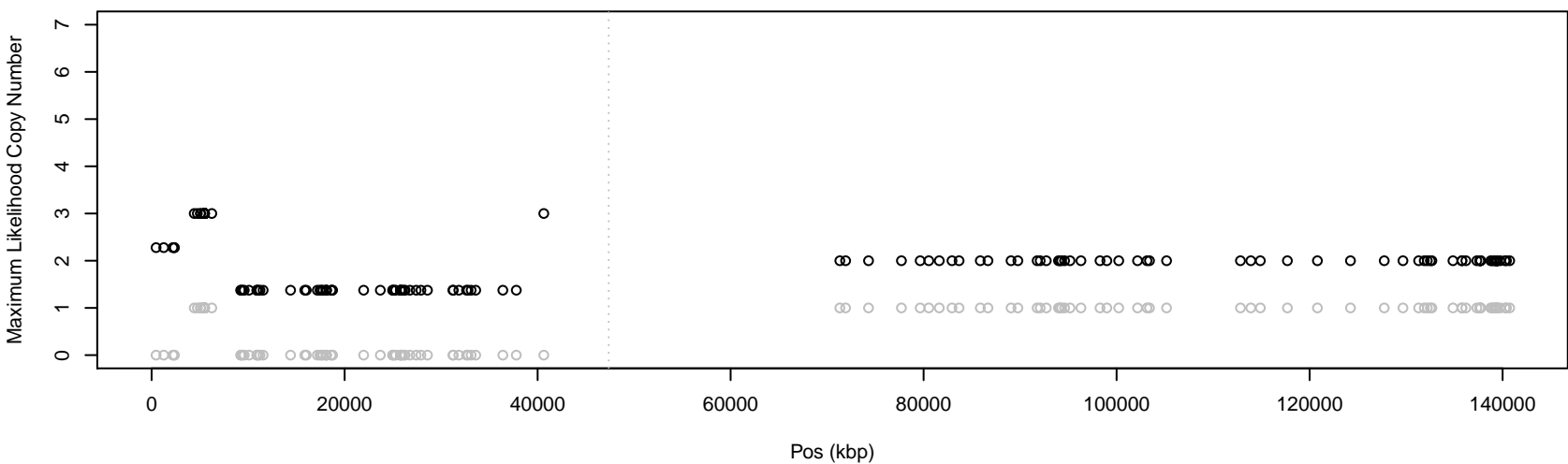
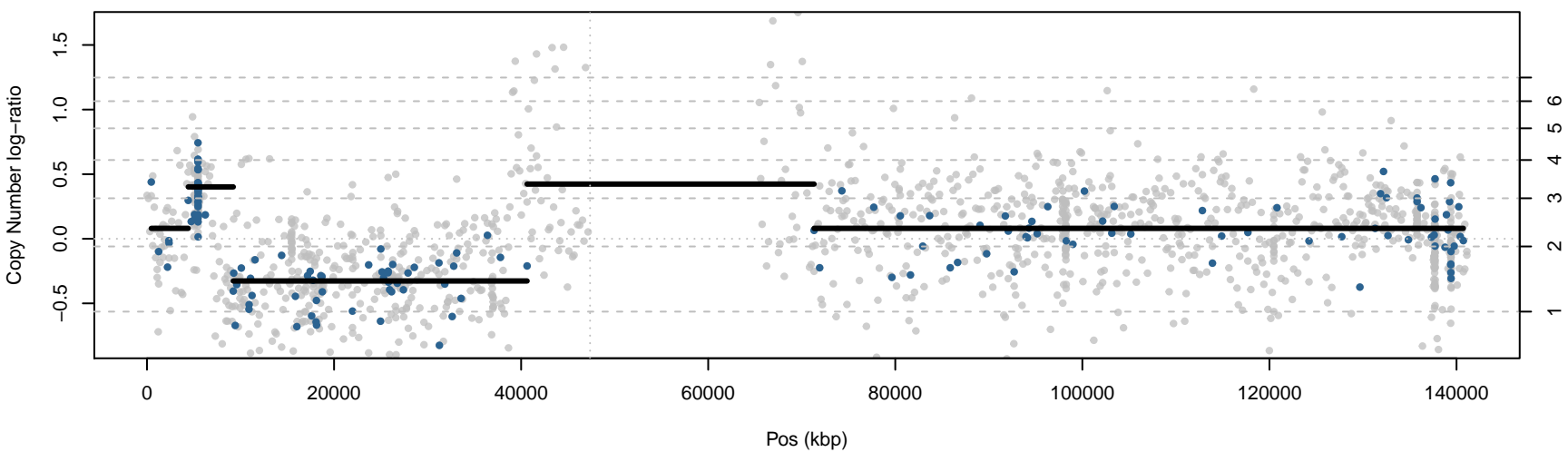
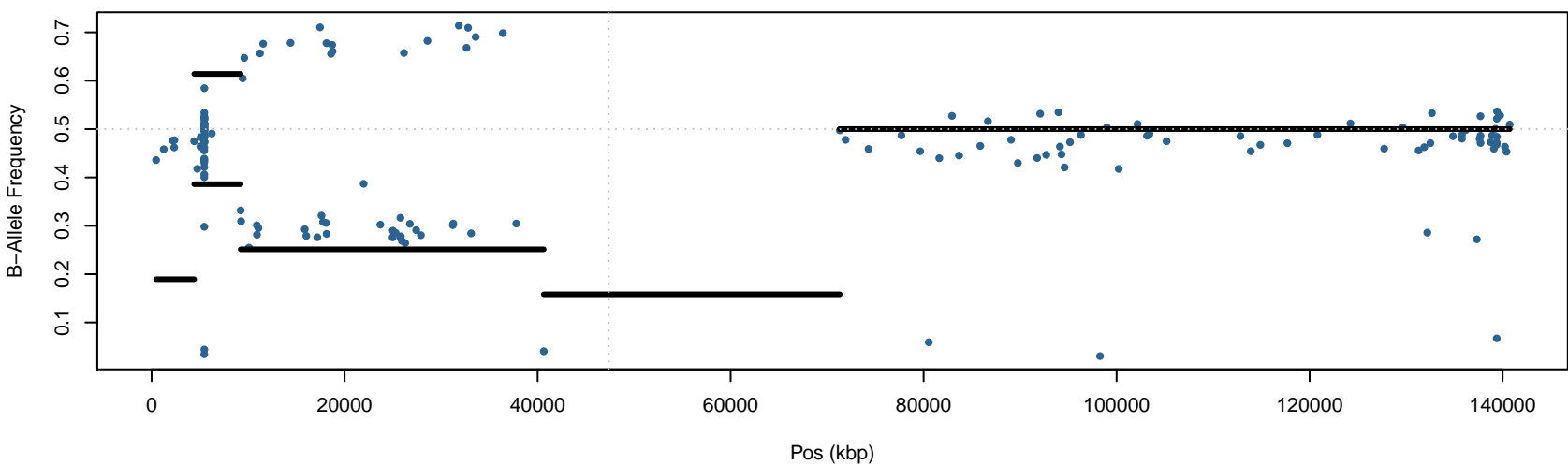
Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 7



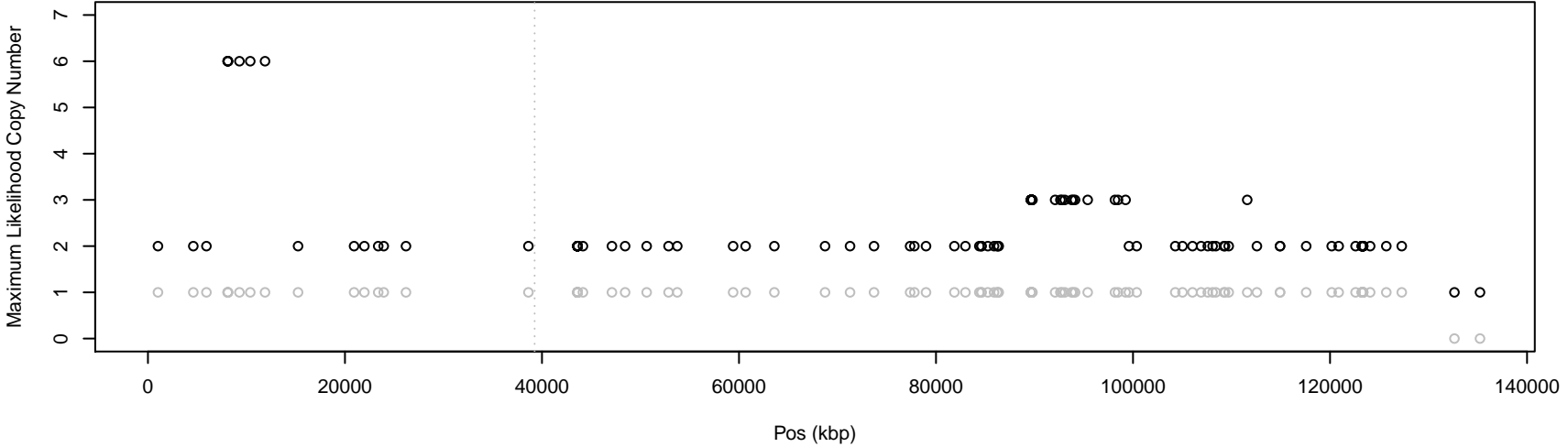
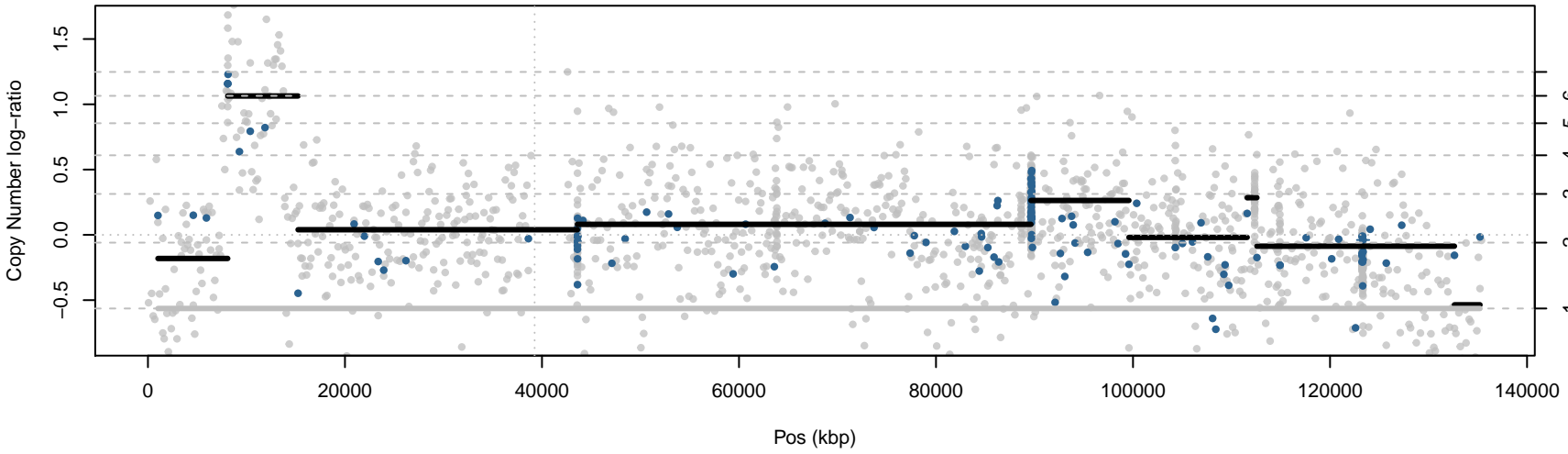
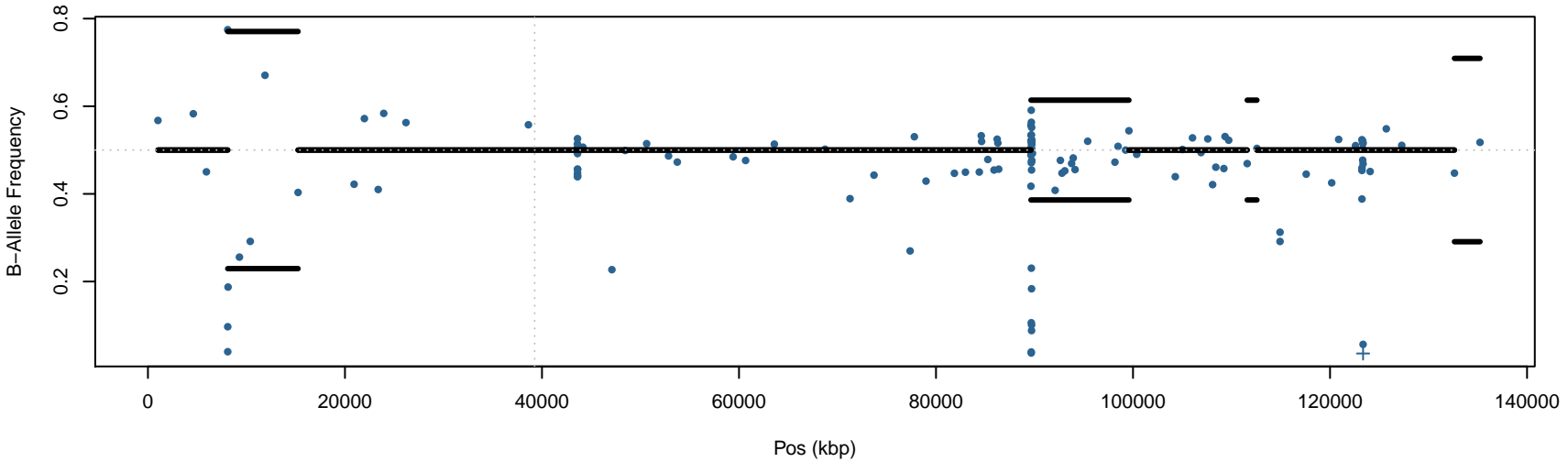
Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 8



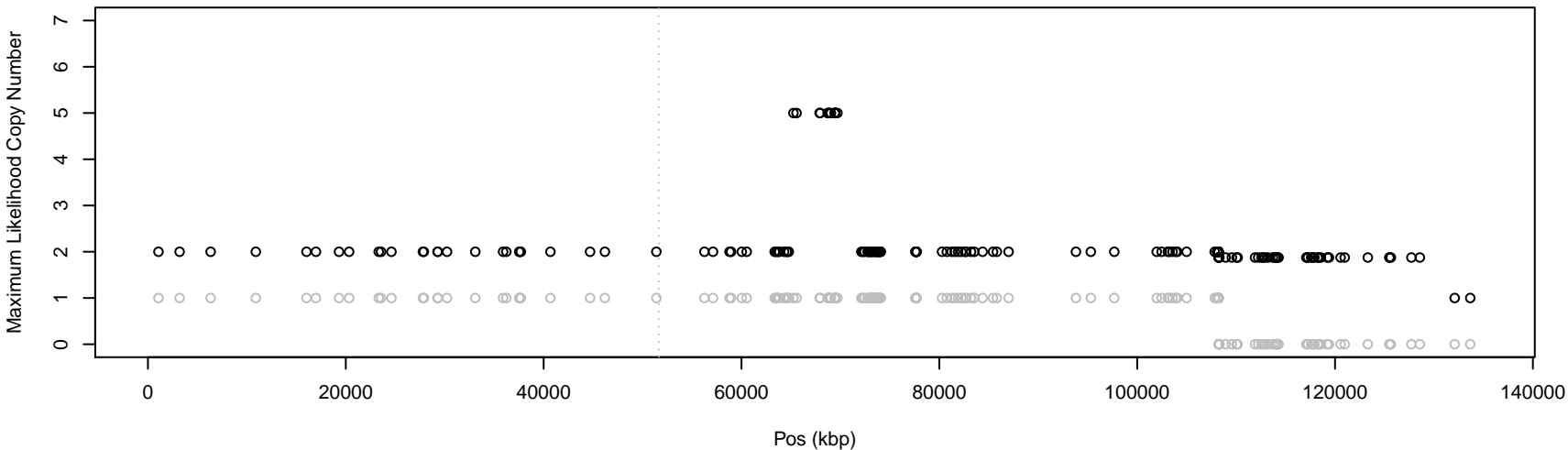
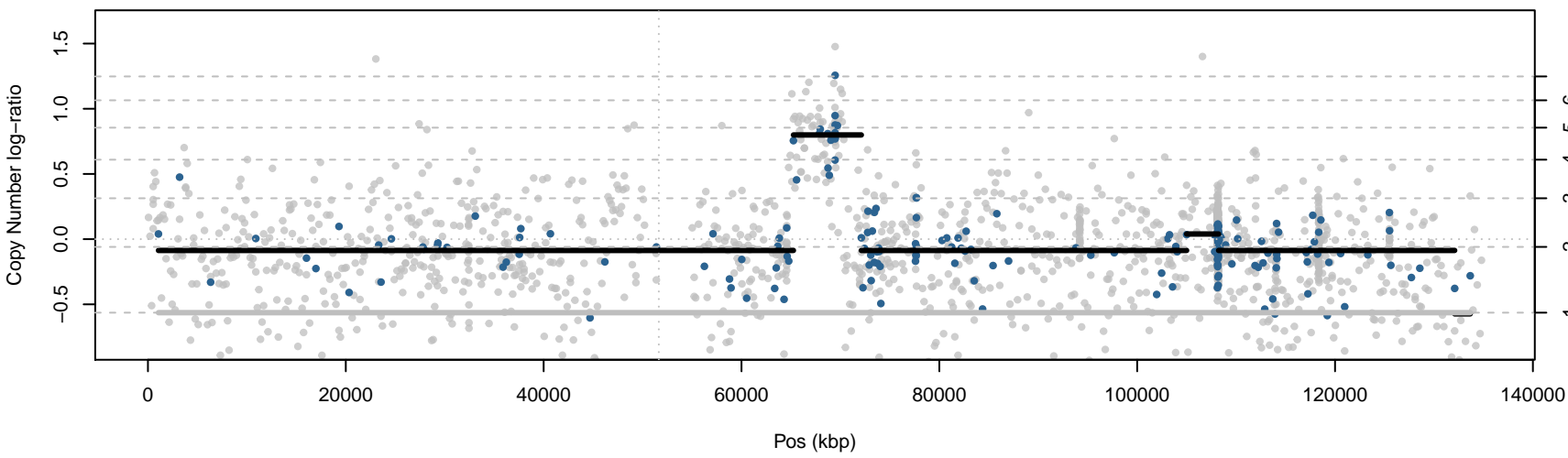
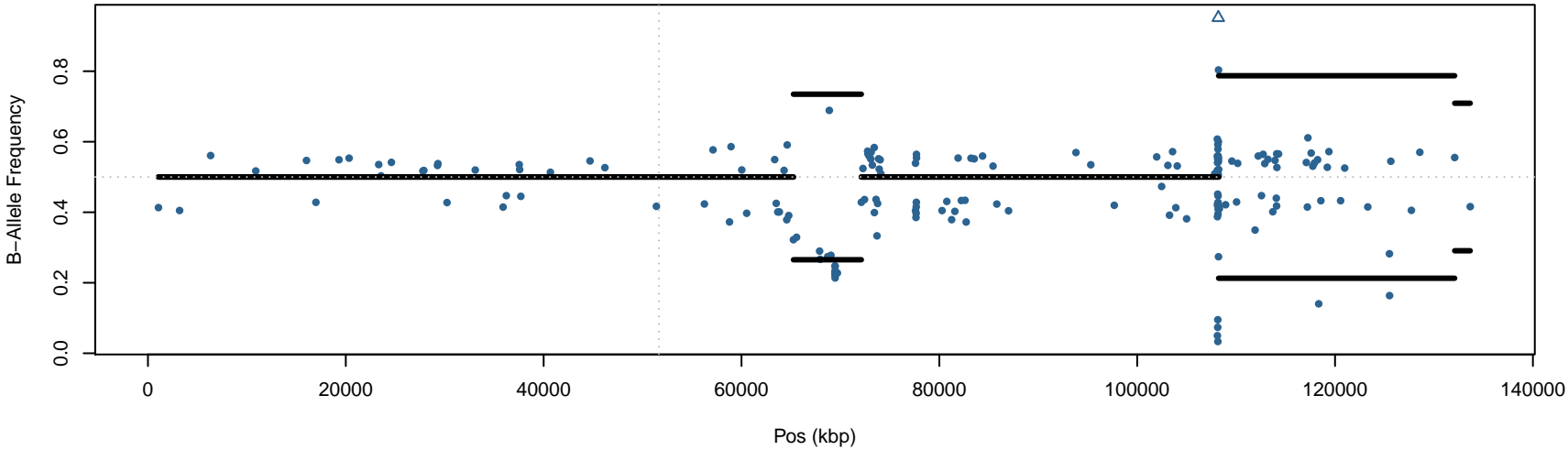
Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 9



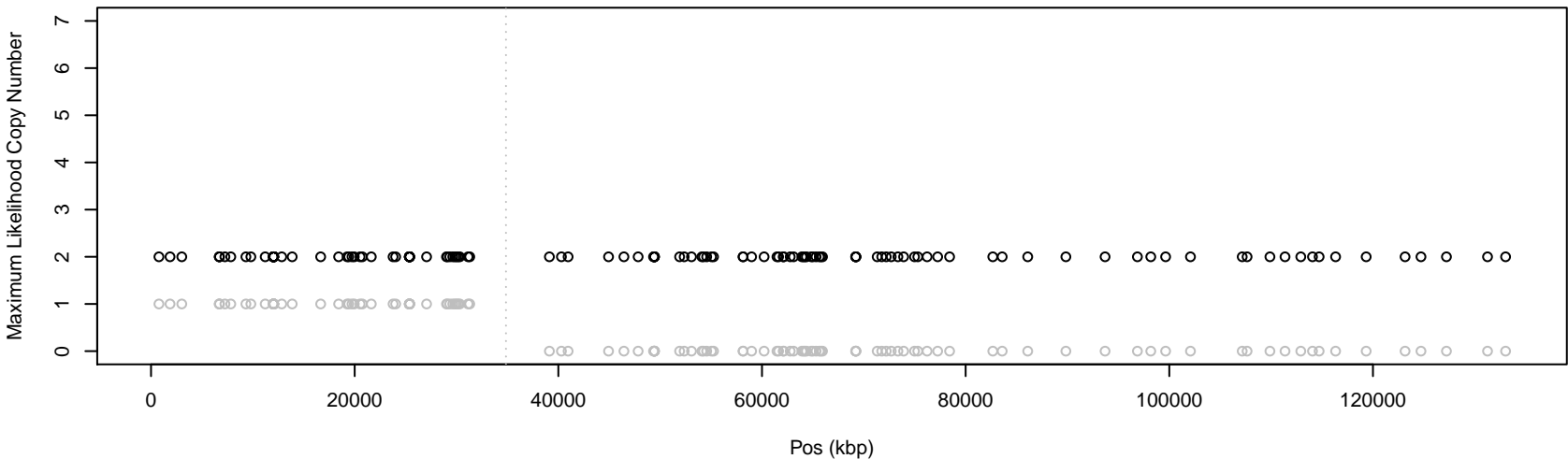
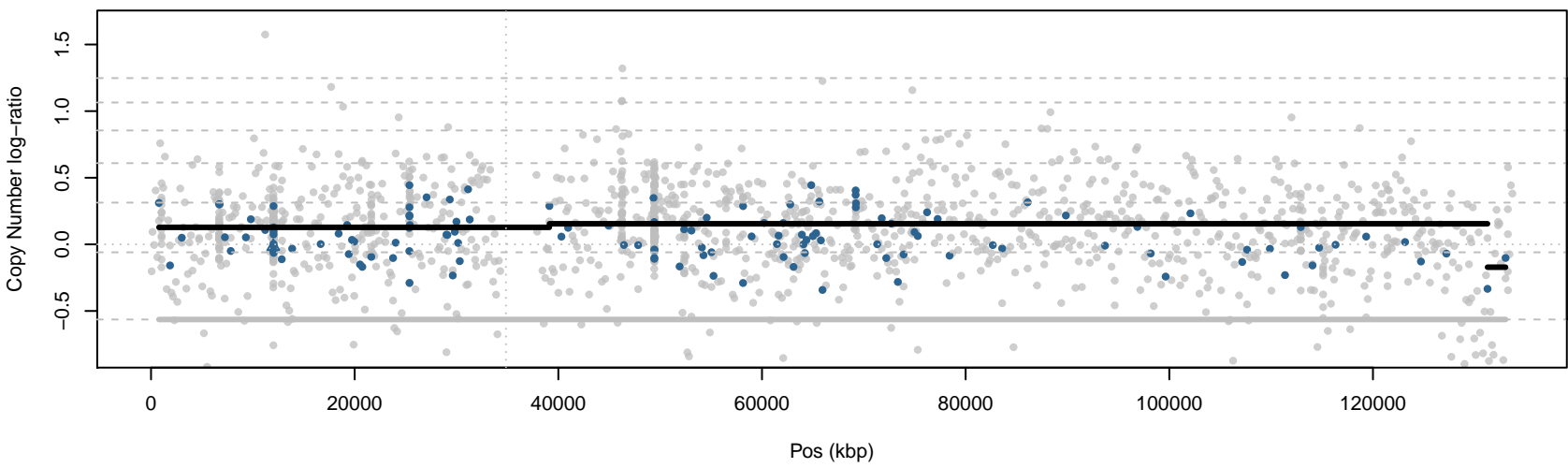
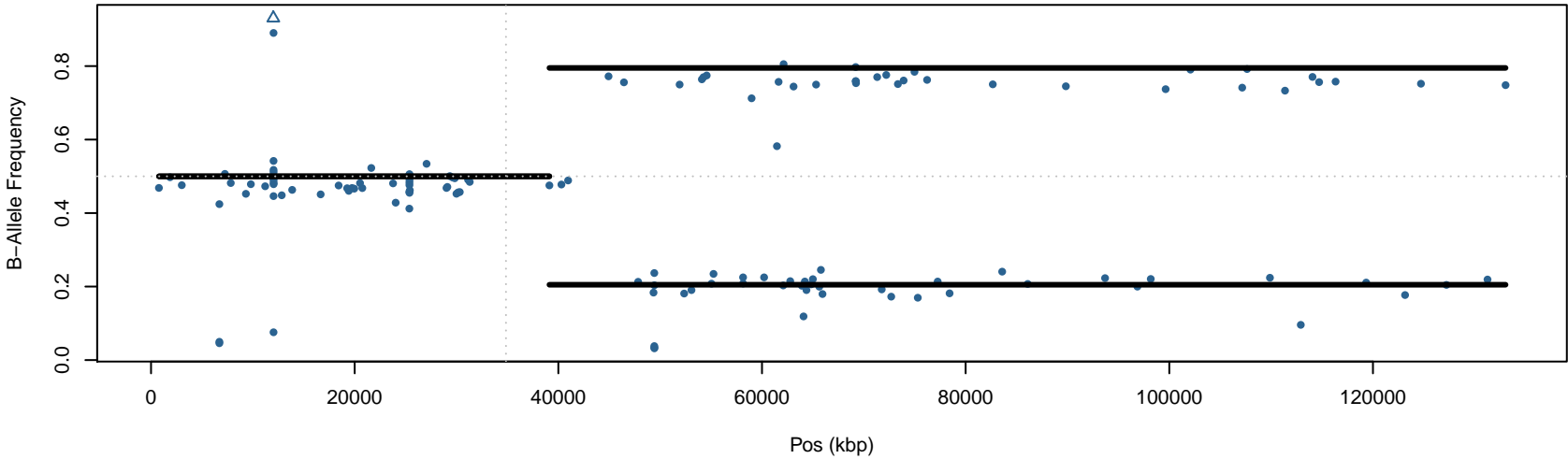
Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 10



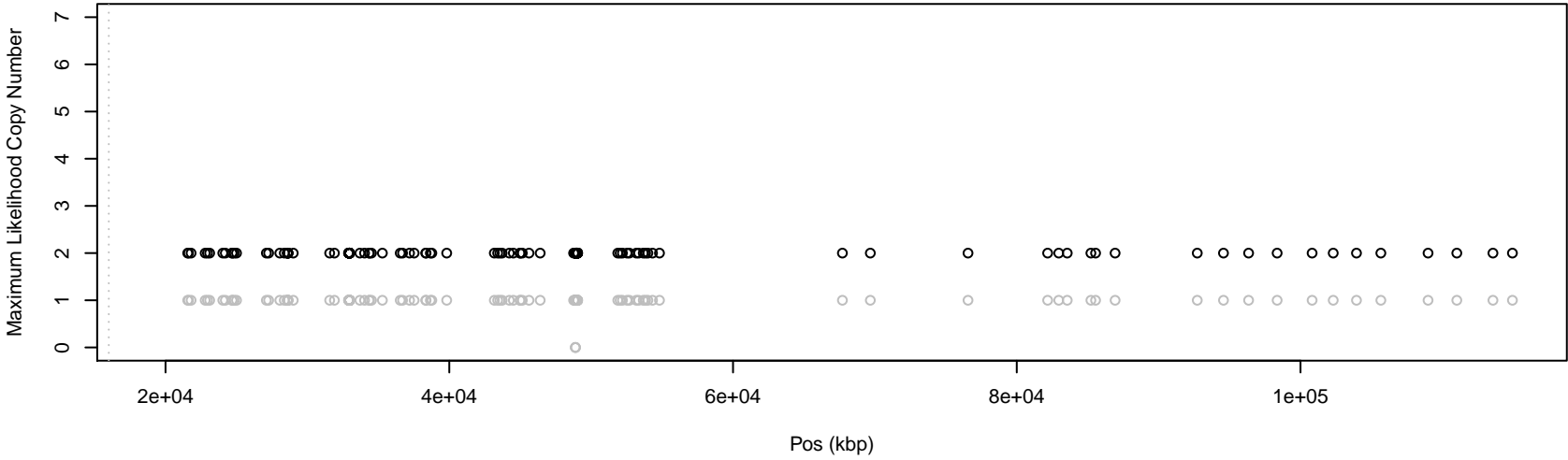
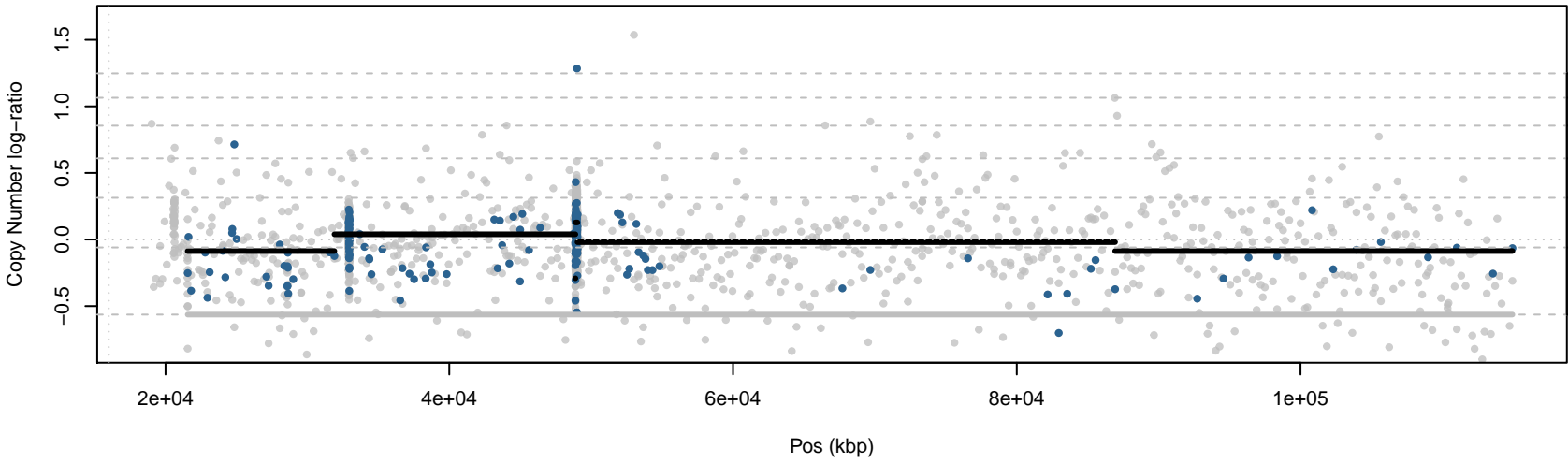
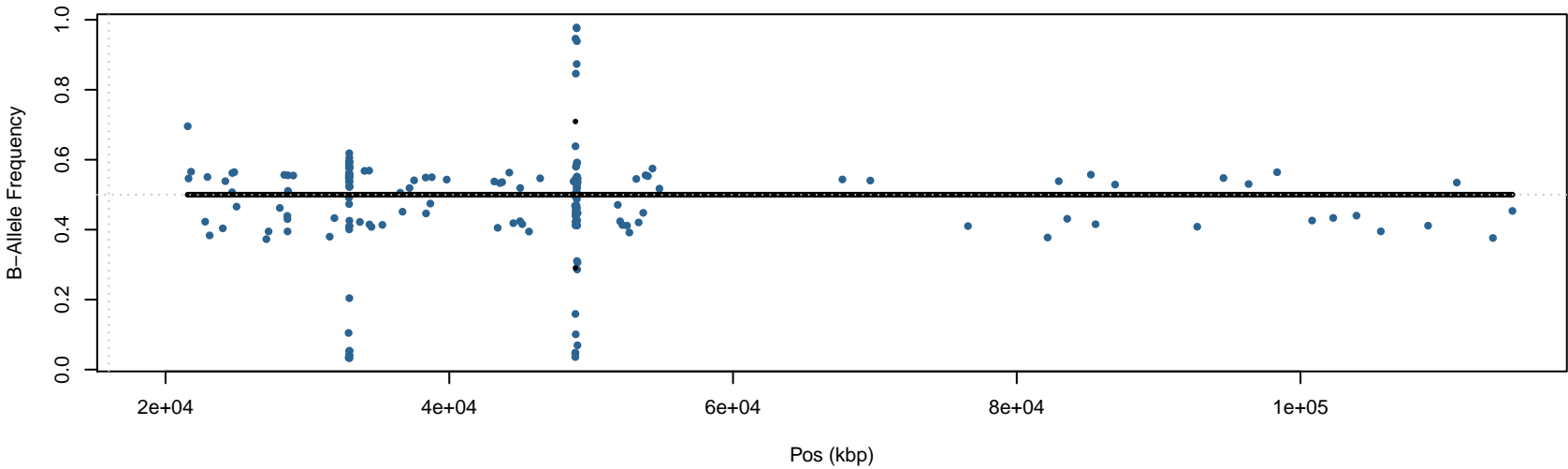
Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 11



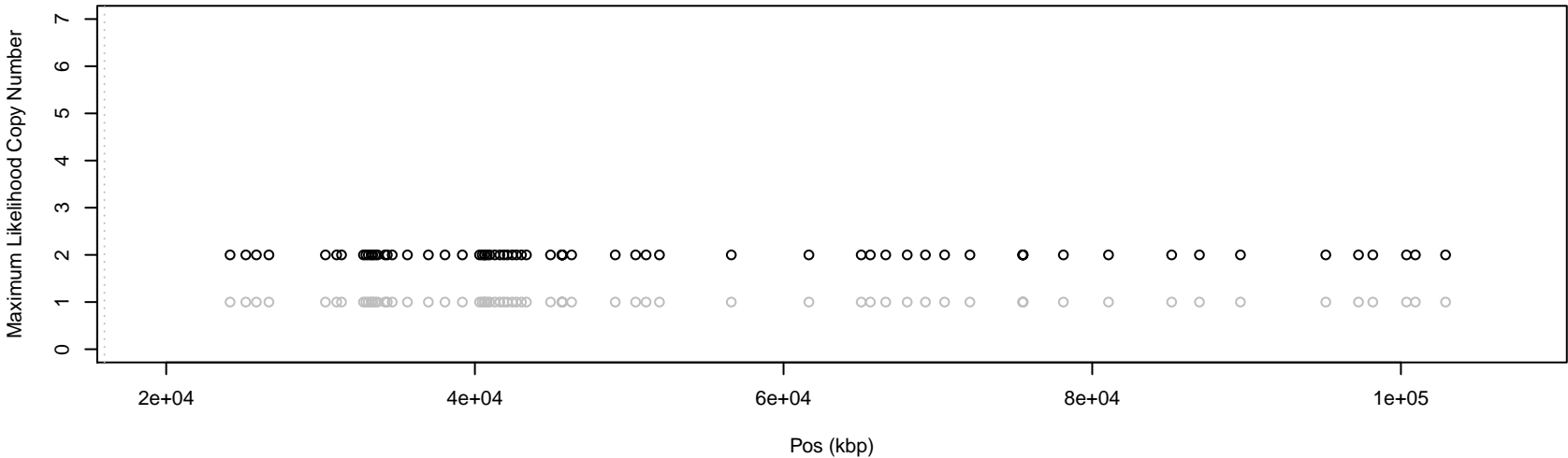
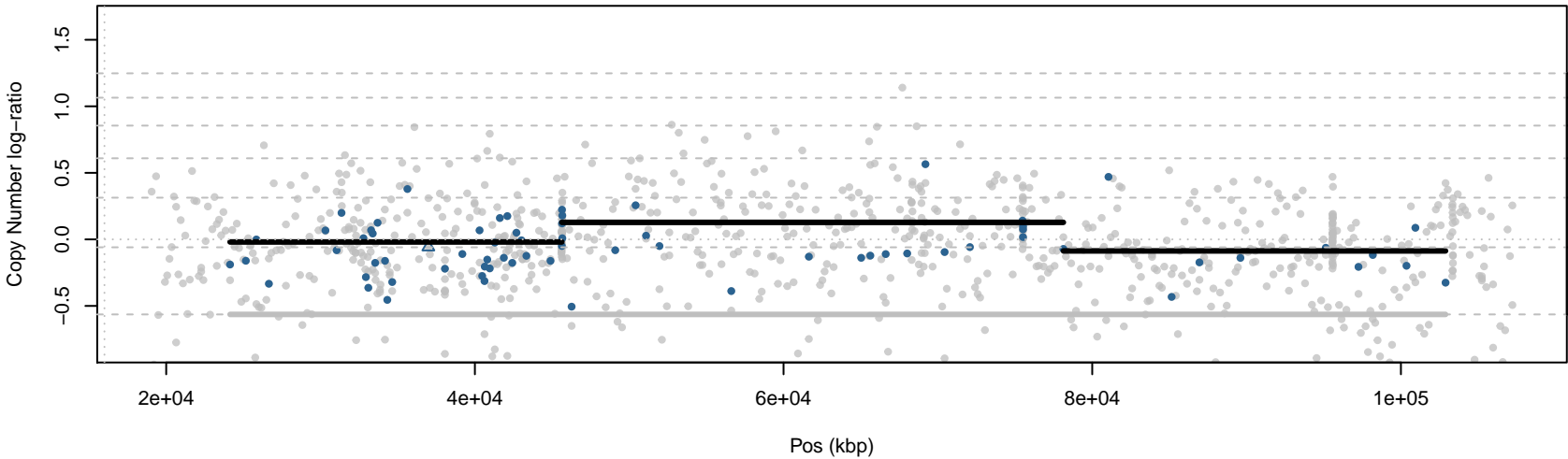
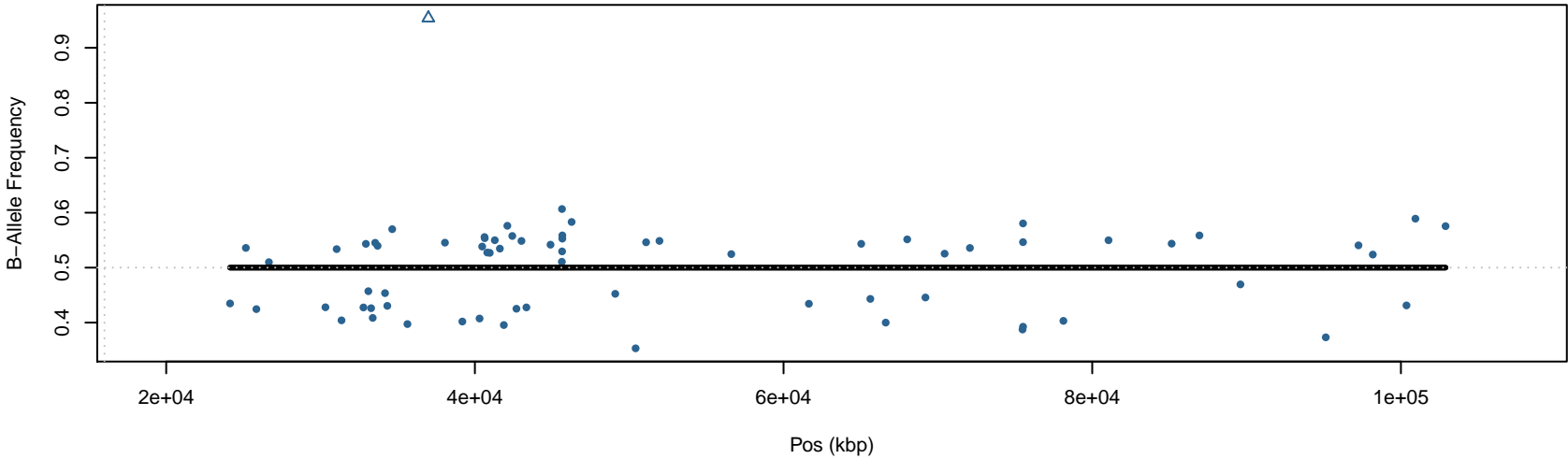
Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 12



Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 13

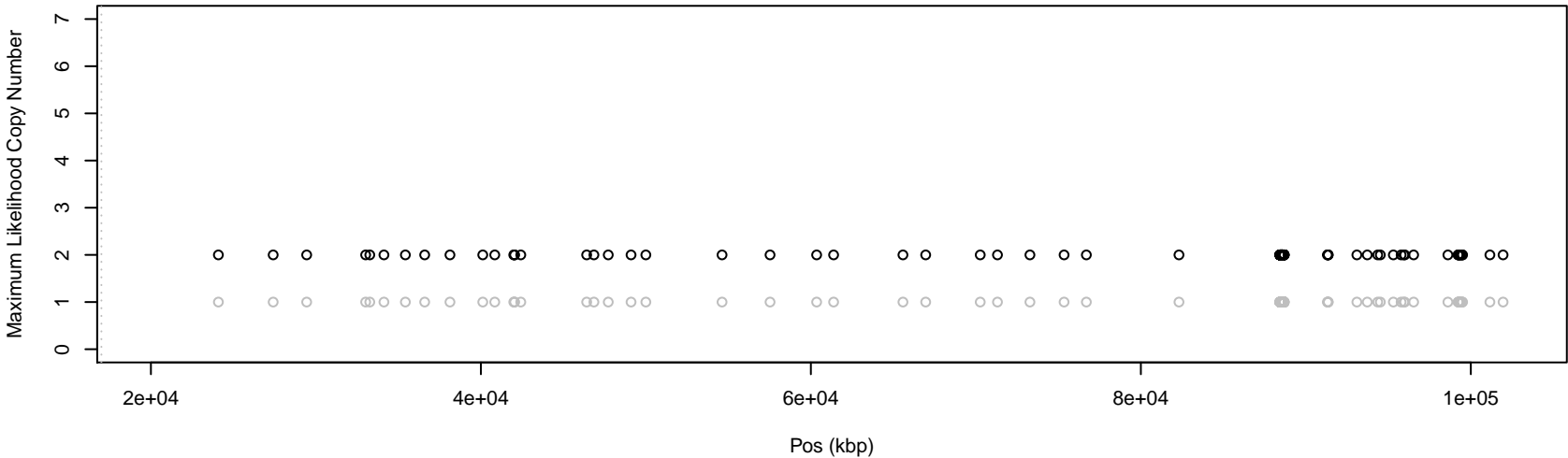
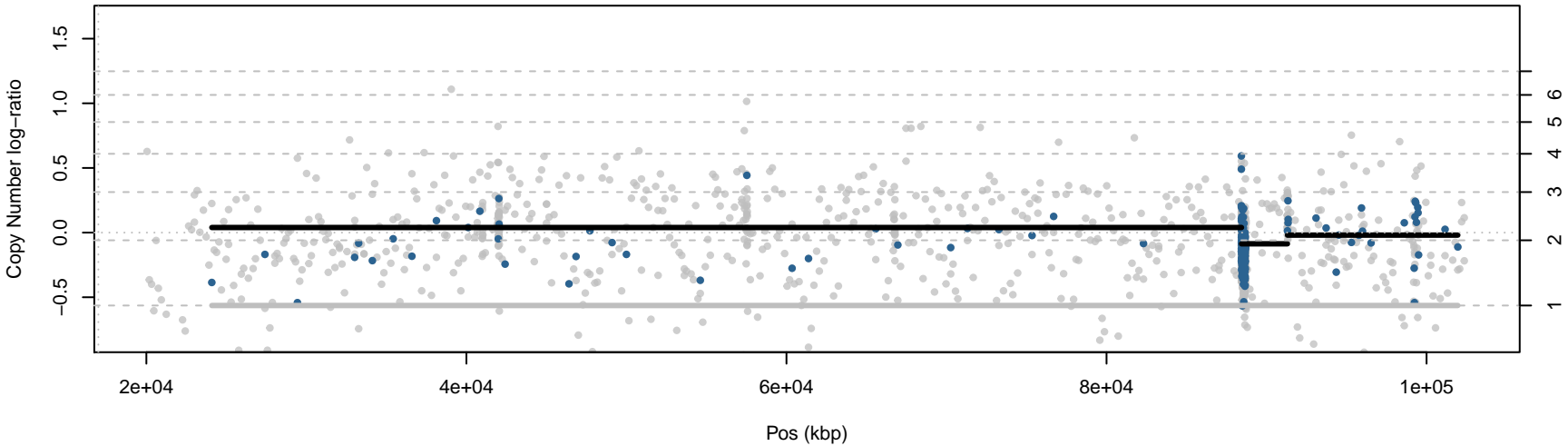
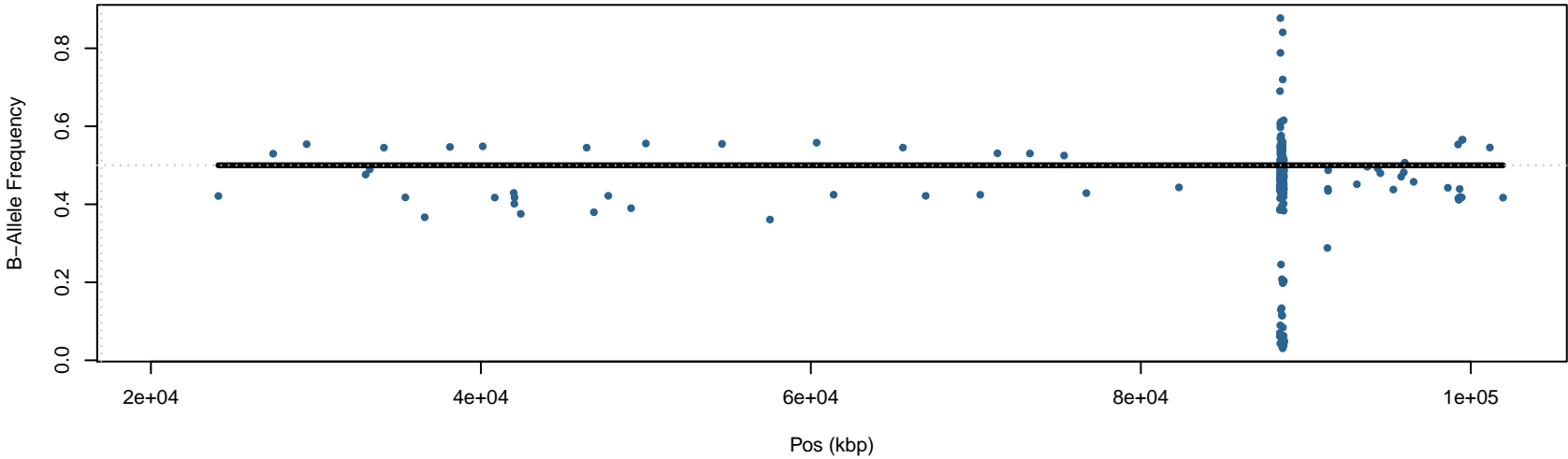


Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 14

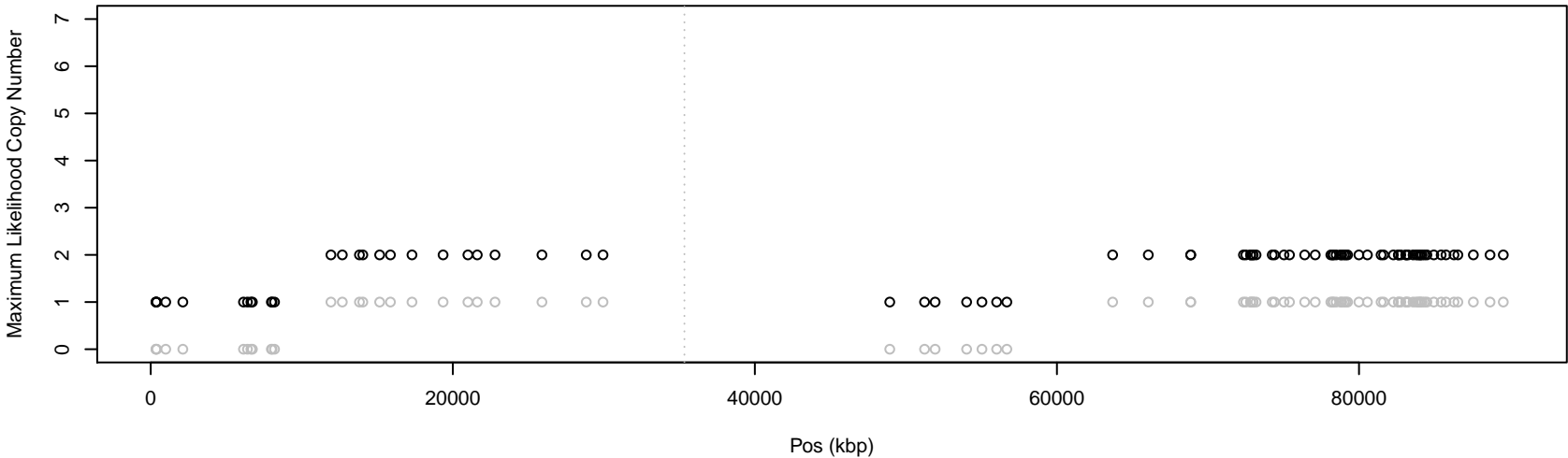
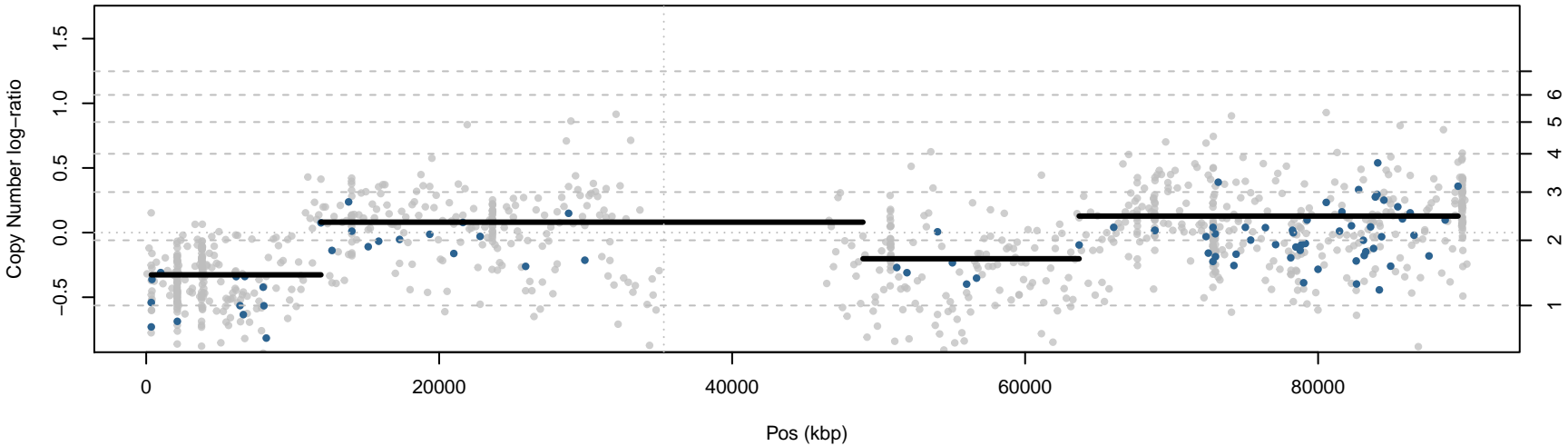
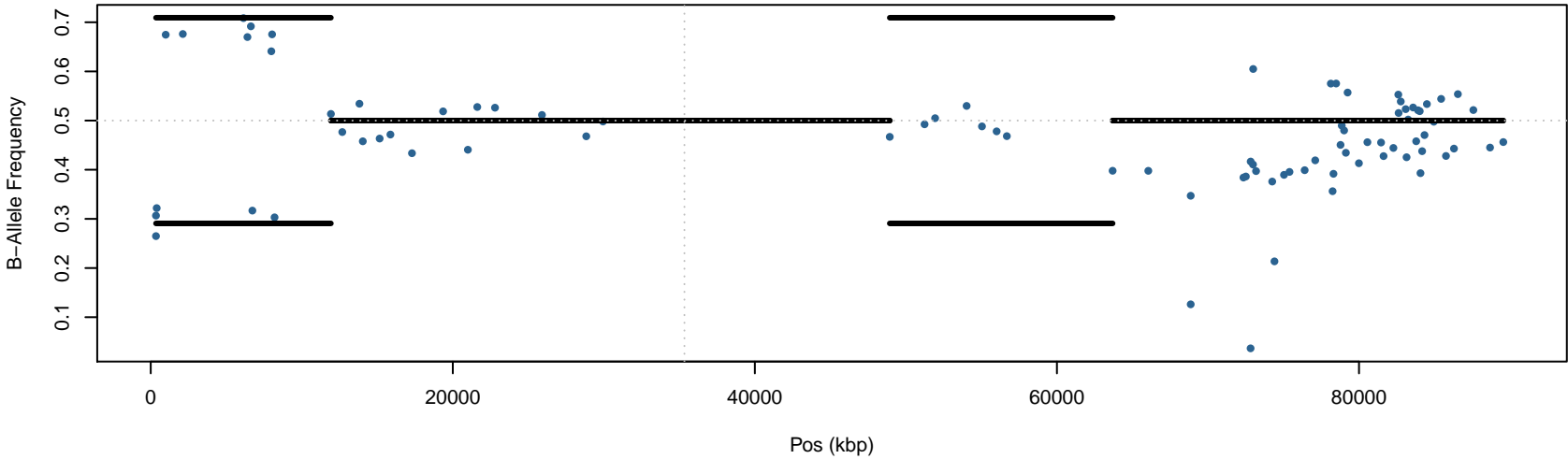




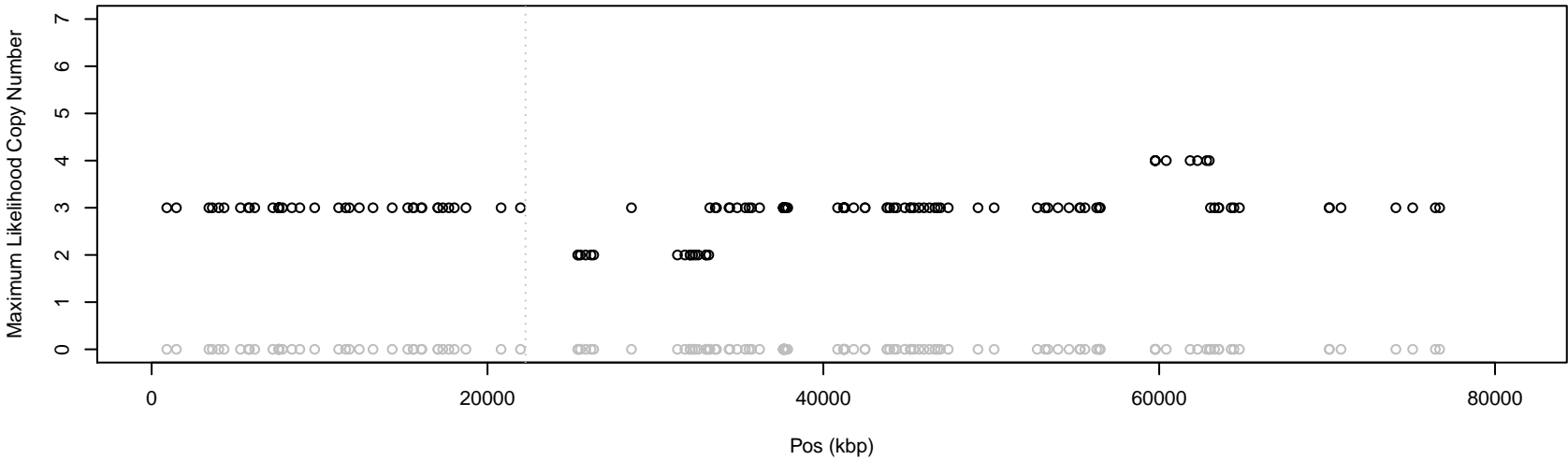
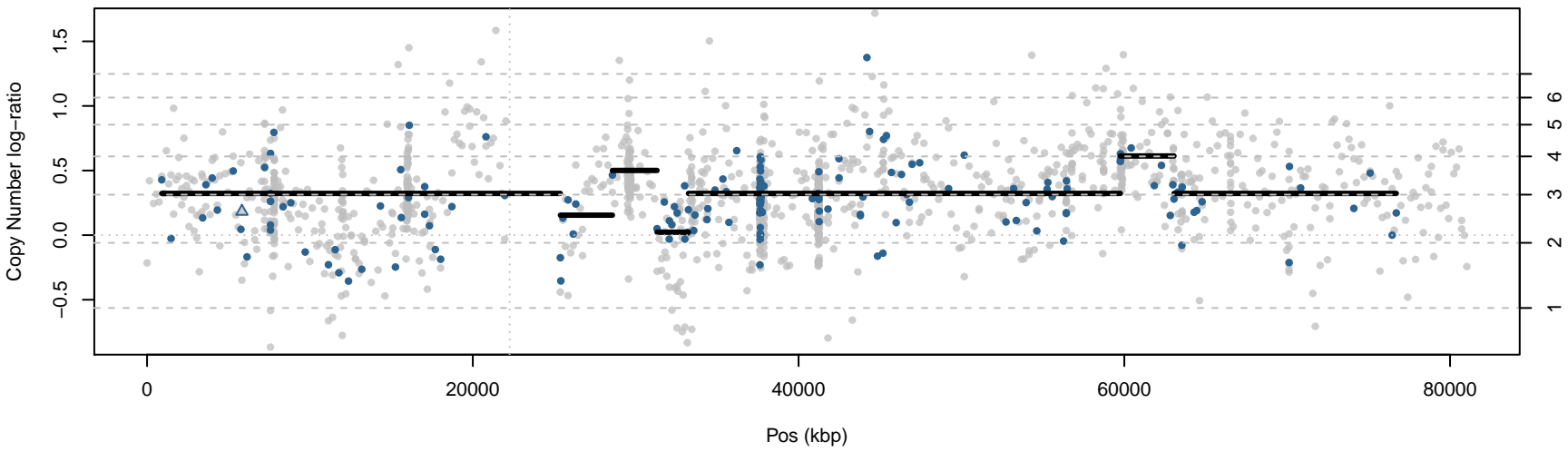
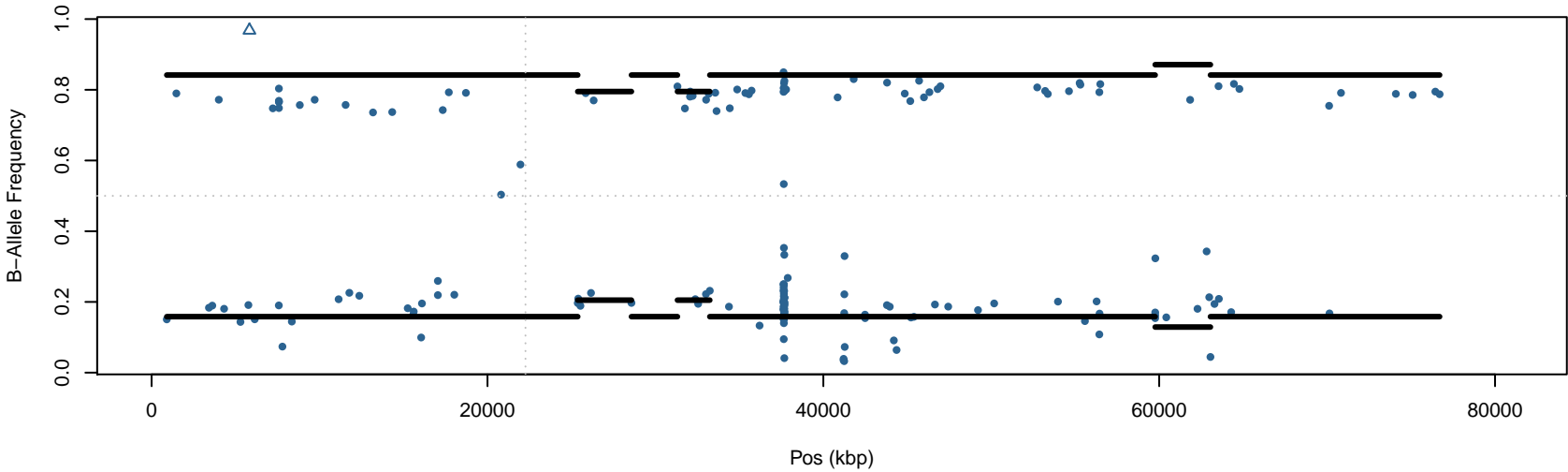
Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 15



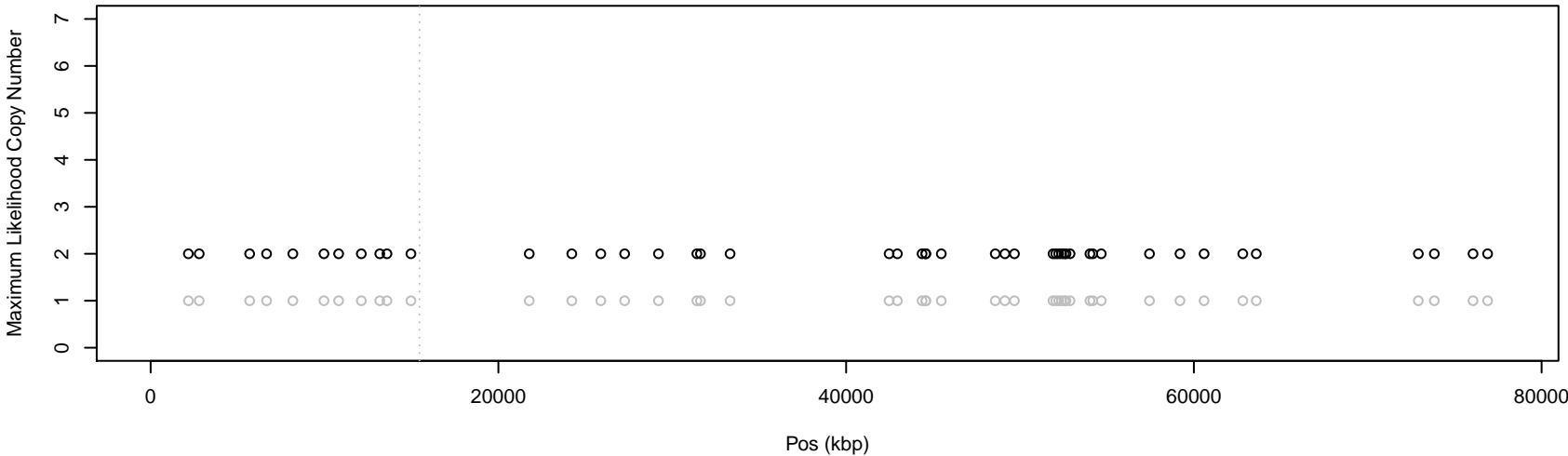
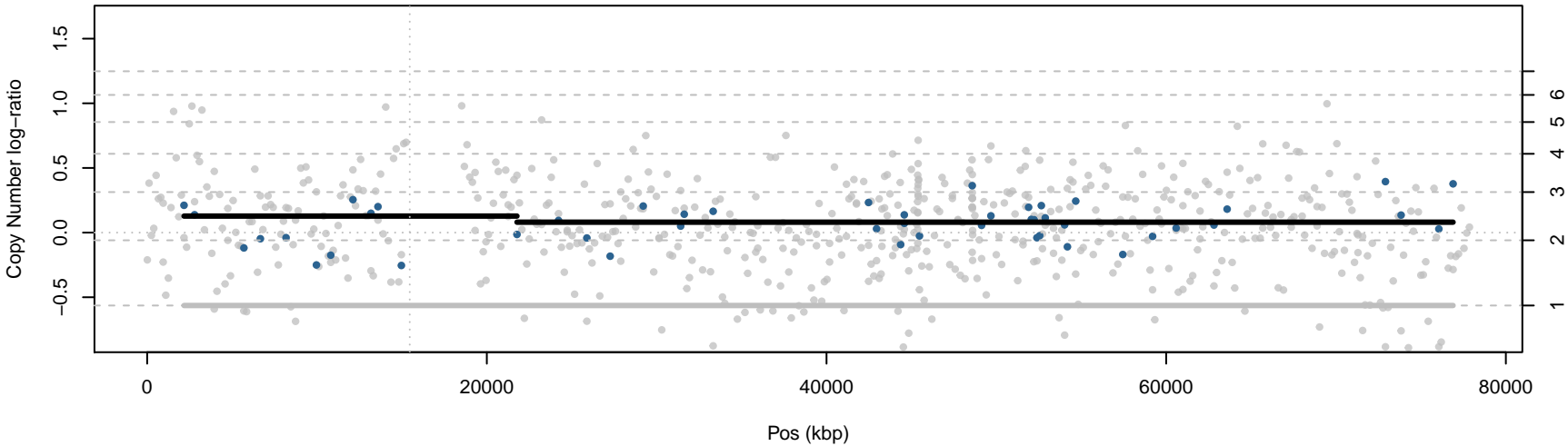
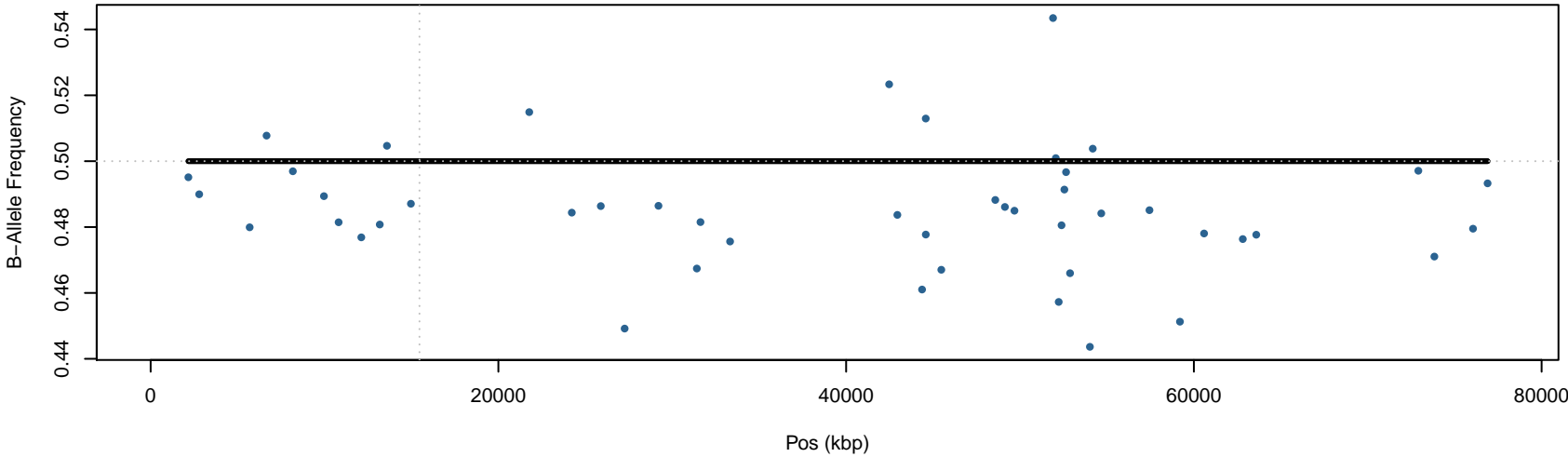
Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 16



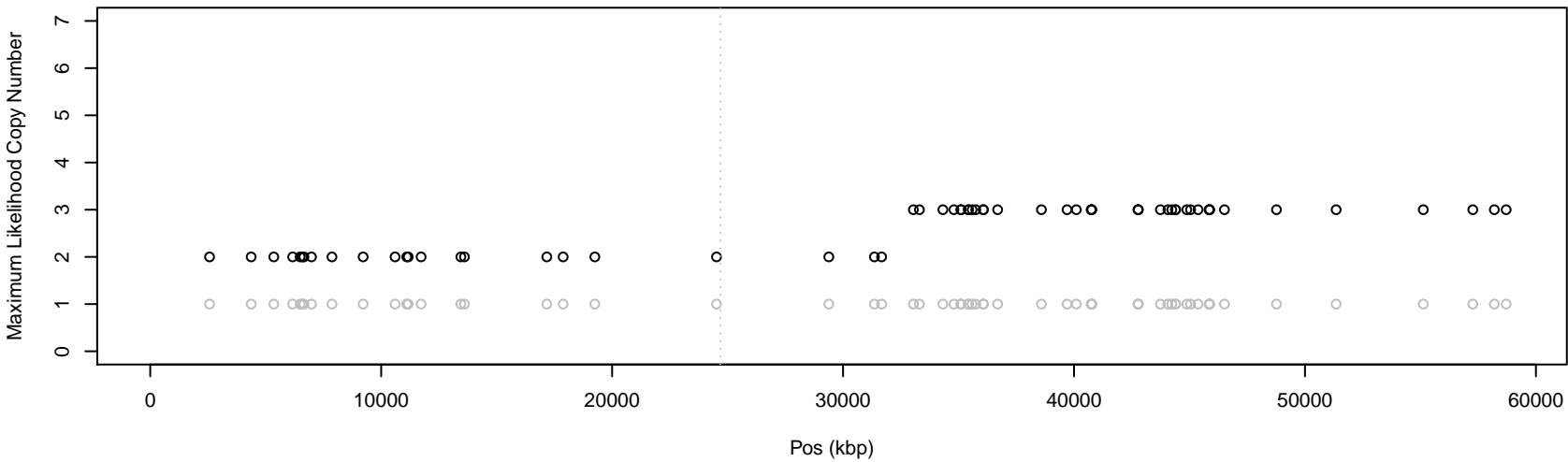
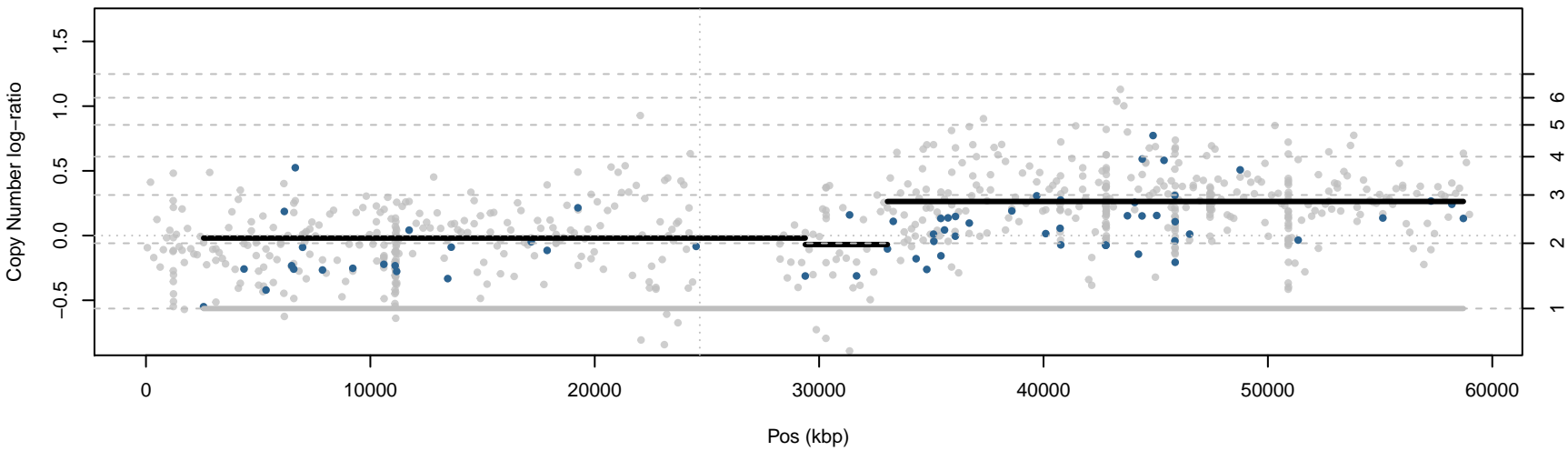
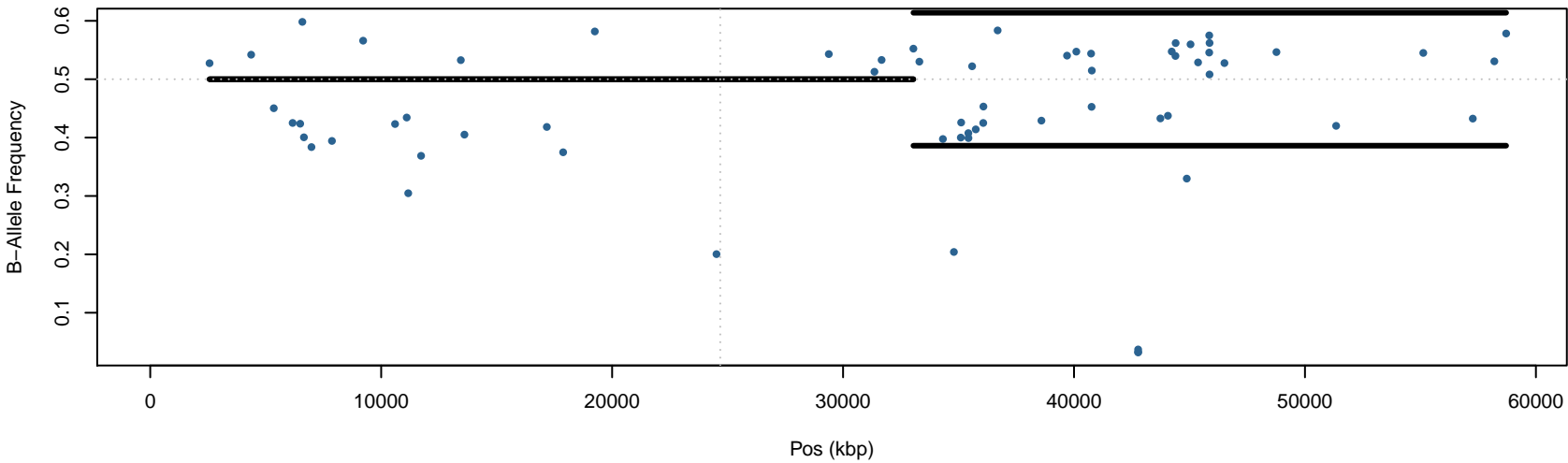
Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 17



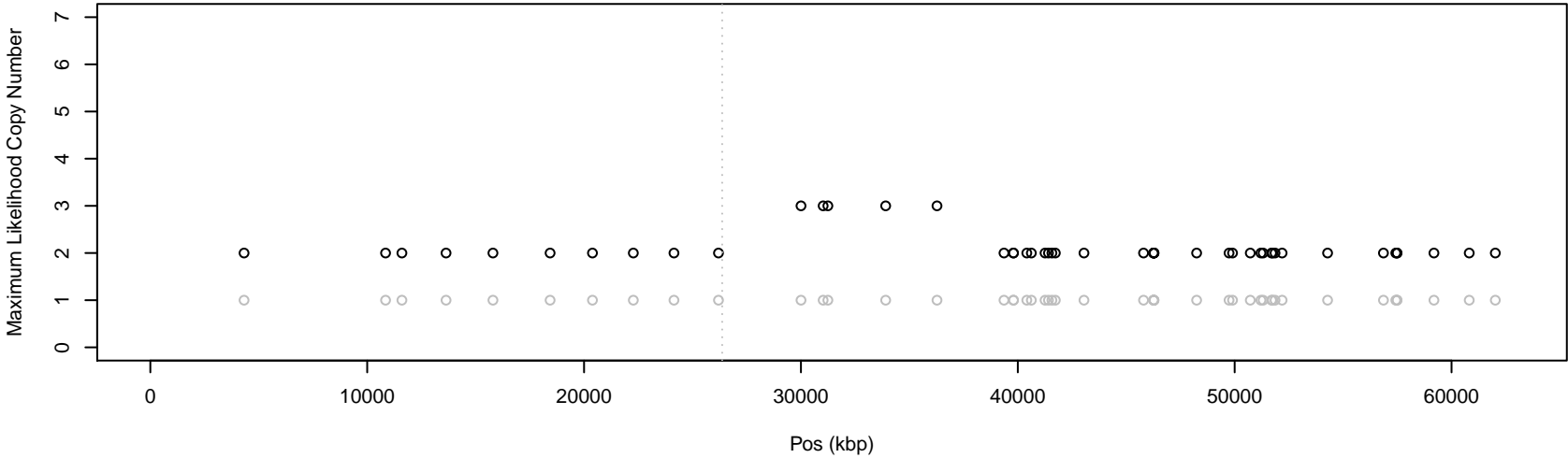
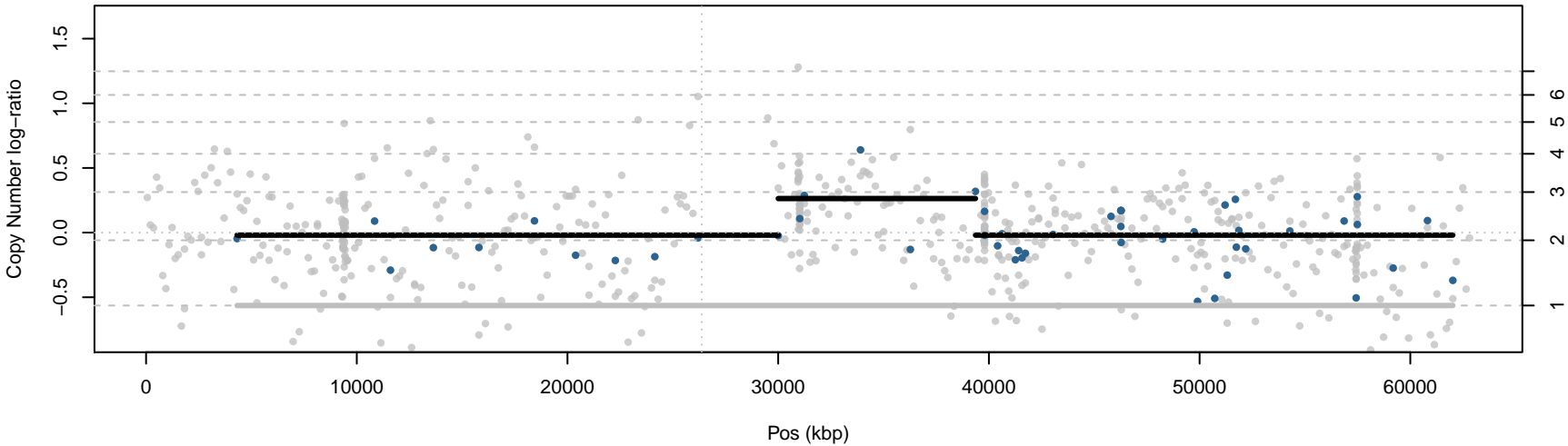
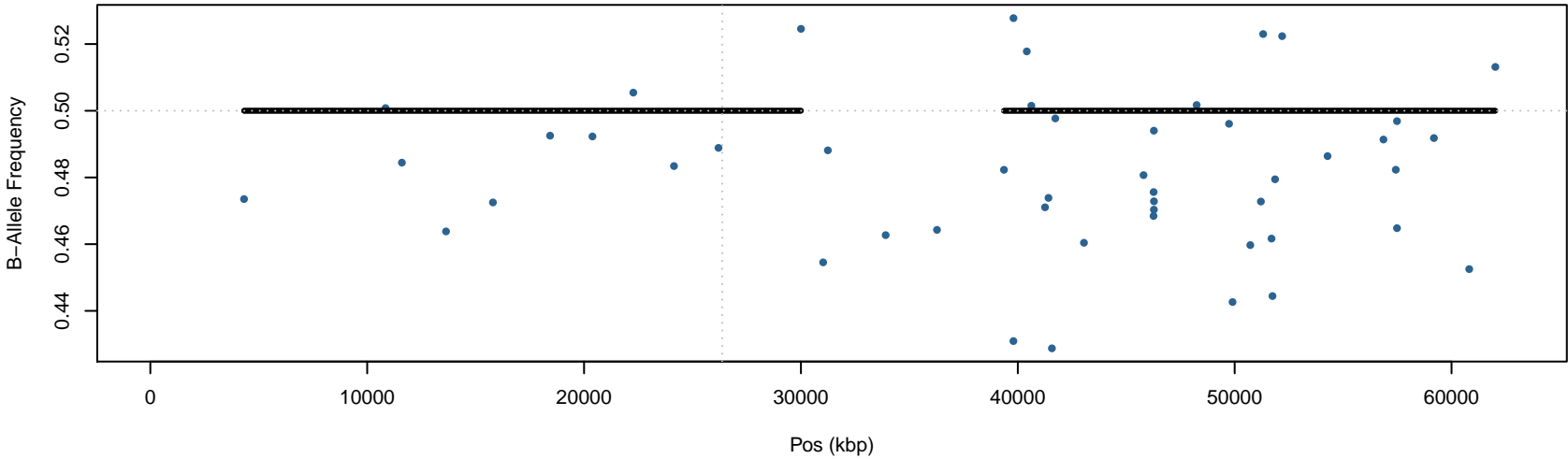
Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 18



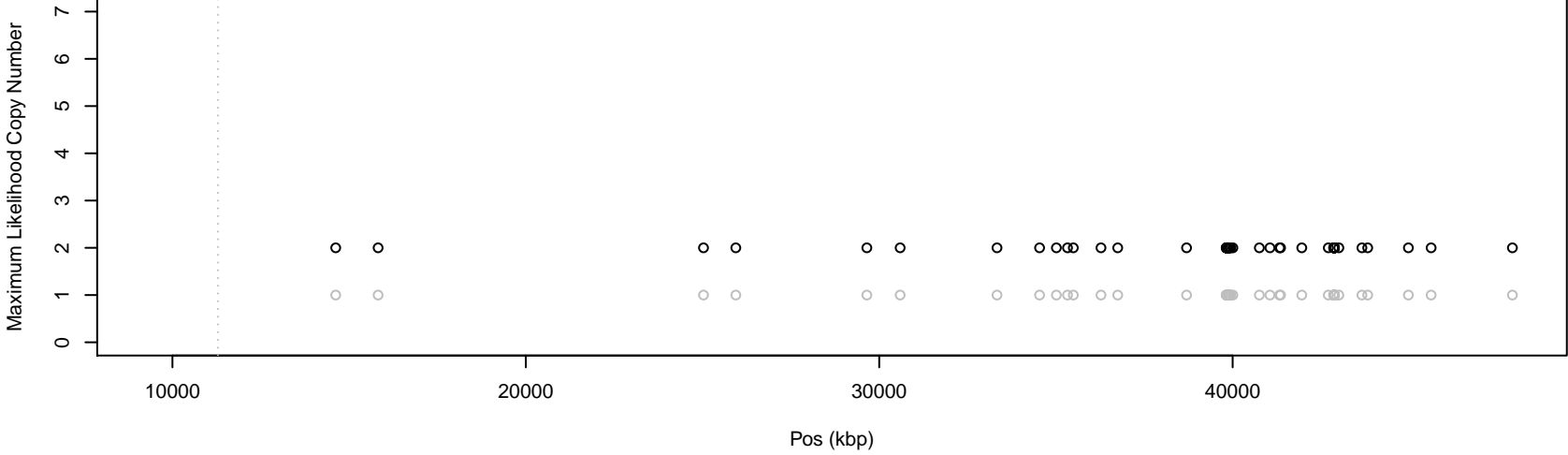
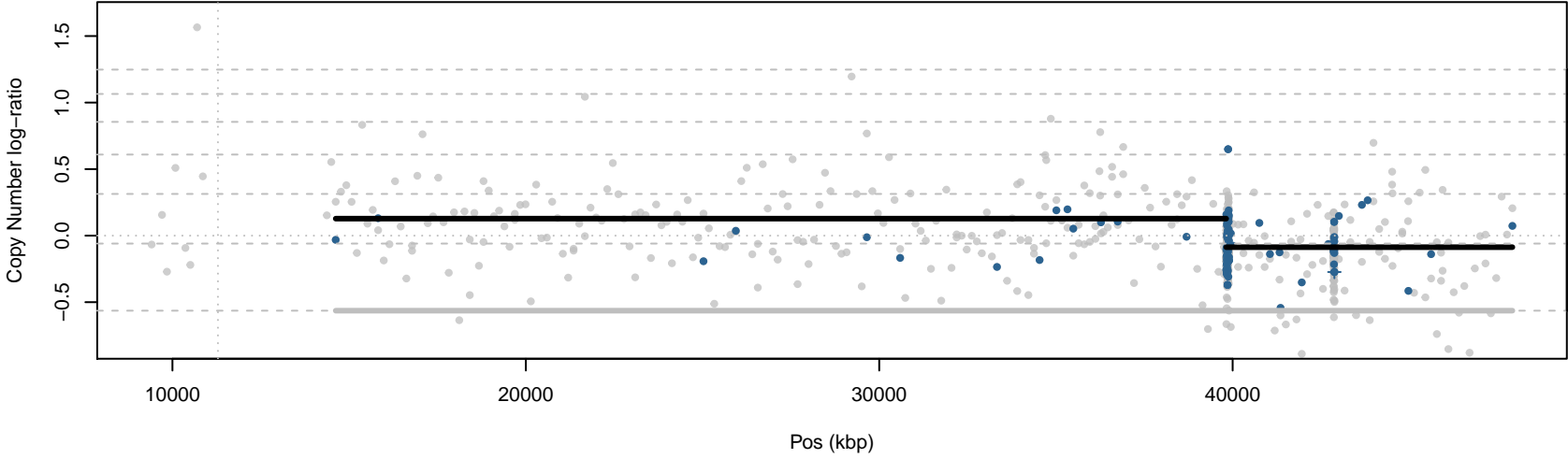
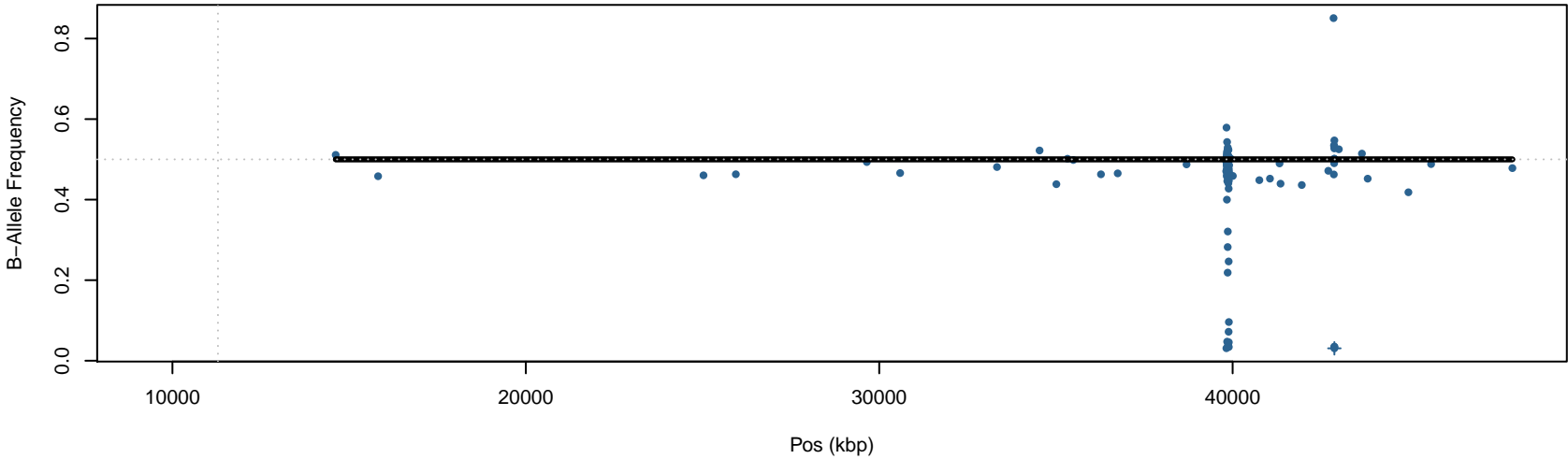
Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 19



Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 20



Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 21



Purity: 0.59 Tumor ploidy: 2.143 SNV log-likelihood: -4250.77 GoF: 86.2% Mean coverage: 868 Chromosome: 22

