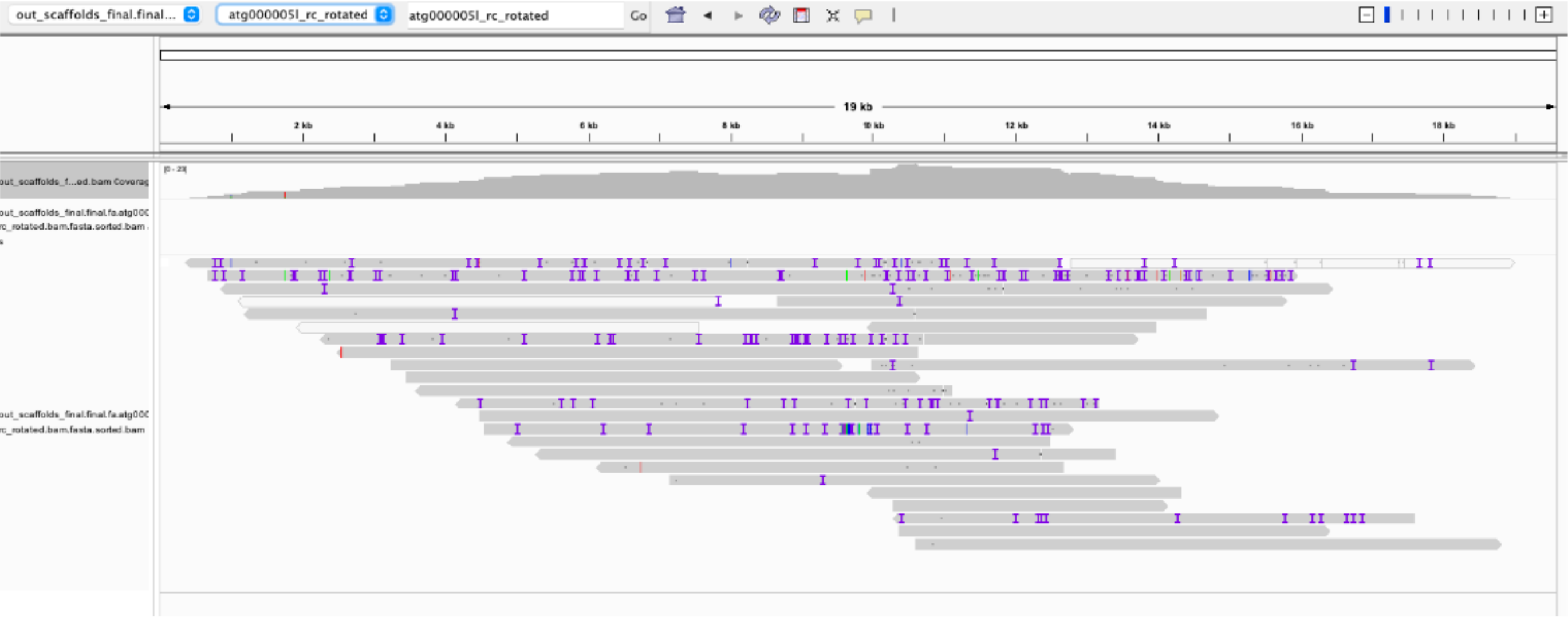


Additional Figure 2: Screenshots of IGV plots of reads mapped back to Andrea bucephala mitogenome before and after NUMTs reads were removed.

A



B



Supplementary Figure 2: Panel **A** shows an IGV plot of all MitoHiFi filtered reads mapped back to the final_mitogenome.fasta of *Andrena bucephala*. In Panel **B**, when reads are mapped to the final_mitogenome.fasta together with the nuclear genome, NUMTs reads are attracted to map at their nuclear locations and the variation track is gone.