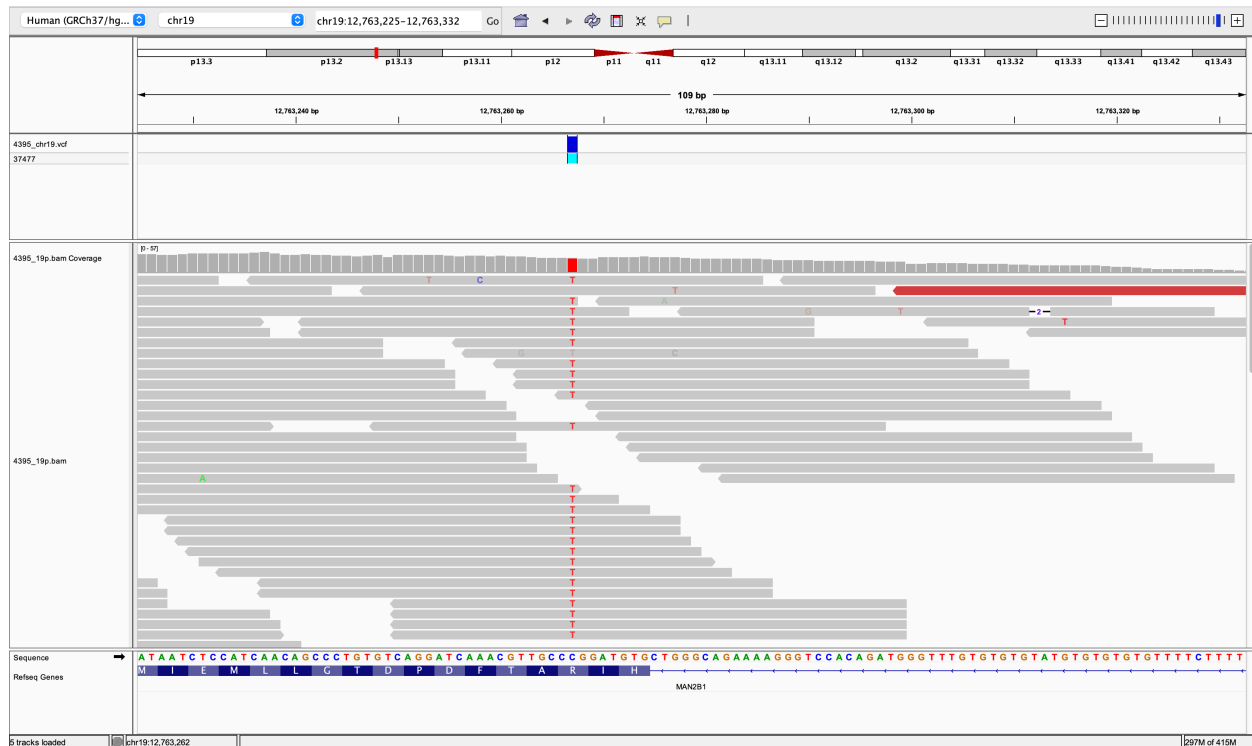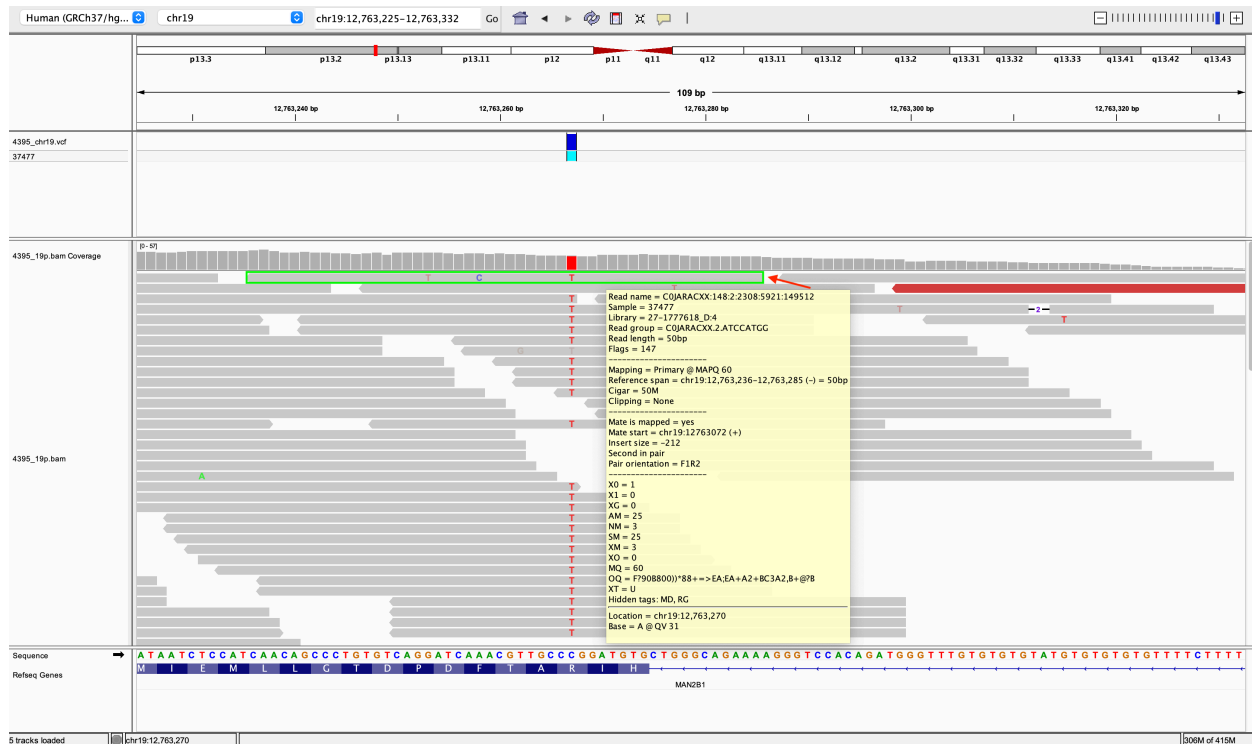## 5. **Load 4395_19p.bam and go to location chr19:12,763,225-12,763,332.**

Identify read name: C0JARACXX:148:2:2308:5921:149512 from center of the top row.

Report MAPQ score and insert size for this read.

MAPQ score: 60
Insert Size: -212

Is it color coded?

No.
The read is neither red or blue.

What is the range of depth for this Read?

26-39
We can look at all of the depths for the read that span between the start of the read and the end. The max depth was 39 and the min depth was 26.

**Is there any base calling different from reference on this read?**

Yes.
We can see that three of the base callings are different from the reference sequence (letters) which are listed across the bottom of the screen. These are the reference sequence genes, and we can see that there are two "T"s and one "C" in the read that are difference than the reference sequence genes.

If so, how many?

3
There are three base callings in the read that are difference than the reference sequence genes, two "T"s and one "C".

Is there any variant called by the VCF file?
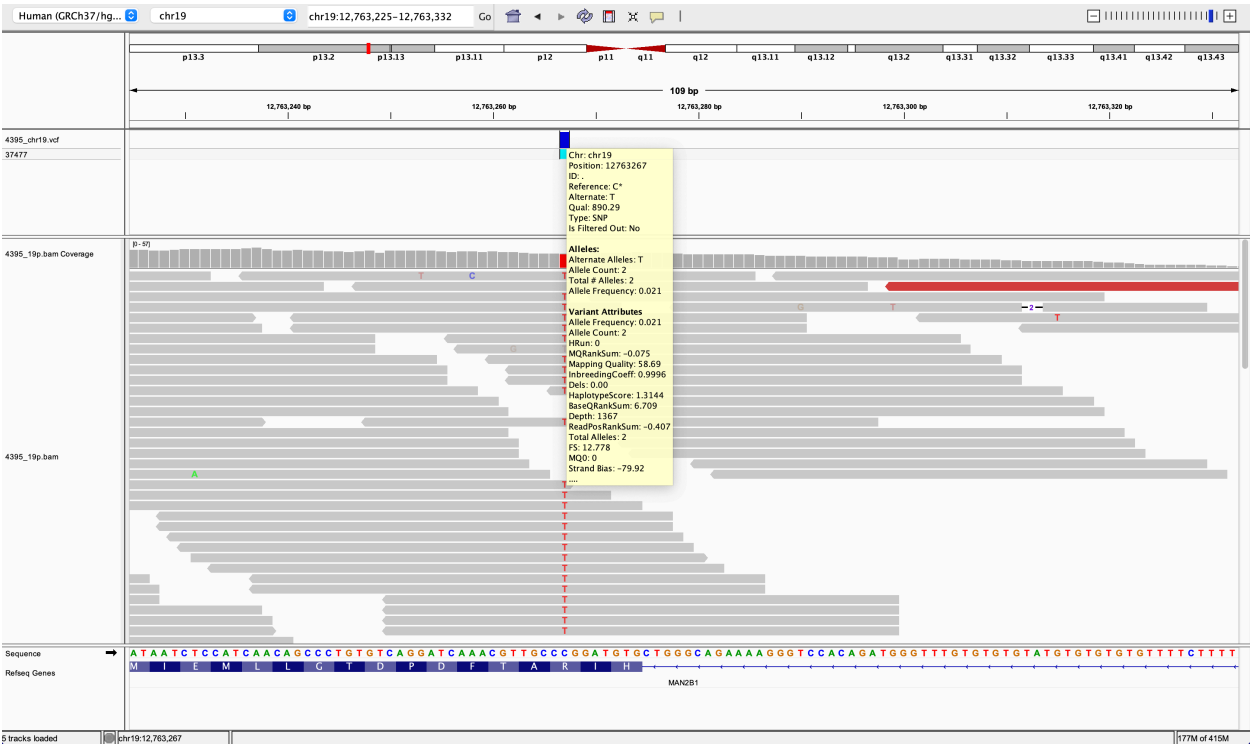
Yes. See variant information below: