* Specificity vs sensitivity (if in exonic DNA and not in RNA then the sensitivity is bad, and the kind of variation should be matching between the DNA and RNA \_sensitivity)
* Correct position variant and genotype (related the sensitivity and specificity)
* Filter the variation that occurred in exonic regions.
* are all the variations that happened in the RNAseq already exist in the DNAseq?
* Re calibration and realignment
* One round vs two round
* Generate bam file from variant calling output
* Explanation for vsf compare
* match and mismatch (is it based on the DNA vs RNA?)
* RNA editing positions (look for software).
* Convert the vsf to exonic and non-exonic (what is the criteria of spilitting?).
* Bam to bid graph bed tool (bam to bid)
* Every place covered be RNAseq is covered

1. Generate bam file from the variant calling
2. Bit graph
3. RNA editing software.
4. Vsf file interpreting

Converting the BAM-out file to BED-graph (make sure to include the whole RNA data) then convert it to BED file and then use it to split the VCF file to exonic (select and non-select)