* Specificity vs sensitivity
* Correct position variant and genotype
* 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
* RNA editing positions (look for software).
* Convert the vsf to exonic and non-exonic.
* 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