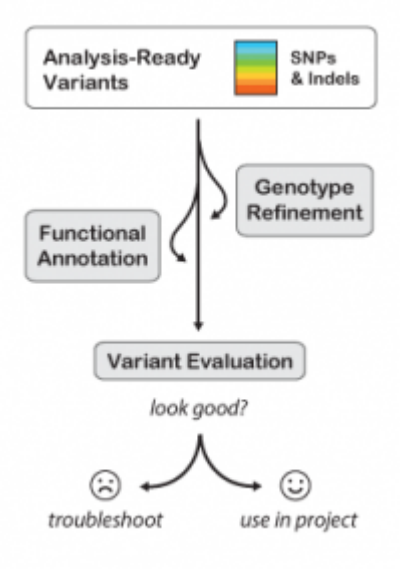
the thir dpahse of GATK's bioinforamtic process consist on running some prelimianry analysis that willinfomr us on the quality of our data and that will leave it ready for cosnequent statistical anlaysis.

It consists on “three” steps, as suggested by GATK's Best Practices for Varaint Discovery workflow section BP3.0.



Once you have generated and filtered your callset according to our recommendations, you have several options for evaluating and refining the variant and genotype calls further, before moving on with your study. We do not provide comprehensive guidelines for this step because different studies will have different requirements, but we do provide tools and general advice.

The main options available through GATK are:

- Genotype Refinement
- Functional Annotation
- Variant Evaluation

Some of the tools involved in those processes (such as SnpEff and BEAGLE) are third-party tools that are not part of GATK. We recommend those specific tools because we are most familiar with them, but there may be alternative software that would work just as well or even better with your particular data. Also, please understand that we cannot provide support for those tools; if you have any problems with them we suggest you seek out the corresponding documentation form the tool project websites, and contact their developers with any questions you may have.