

Varant: An Open Source Variant Annotation Tool

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Why we developed this tool ?

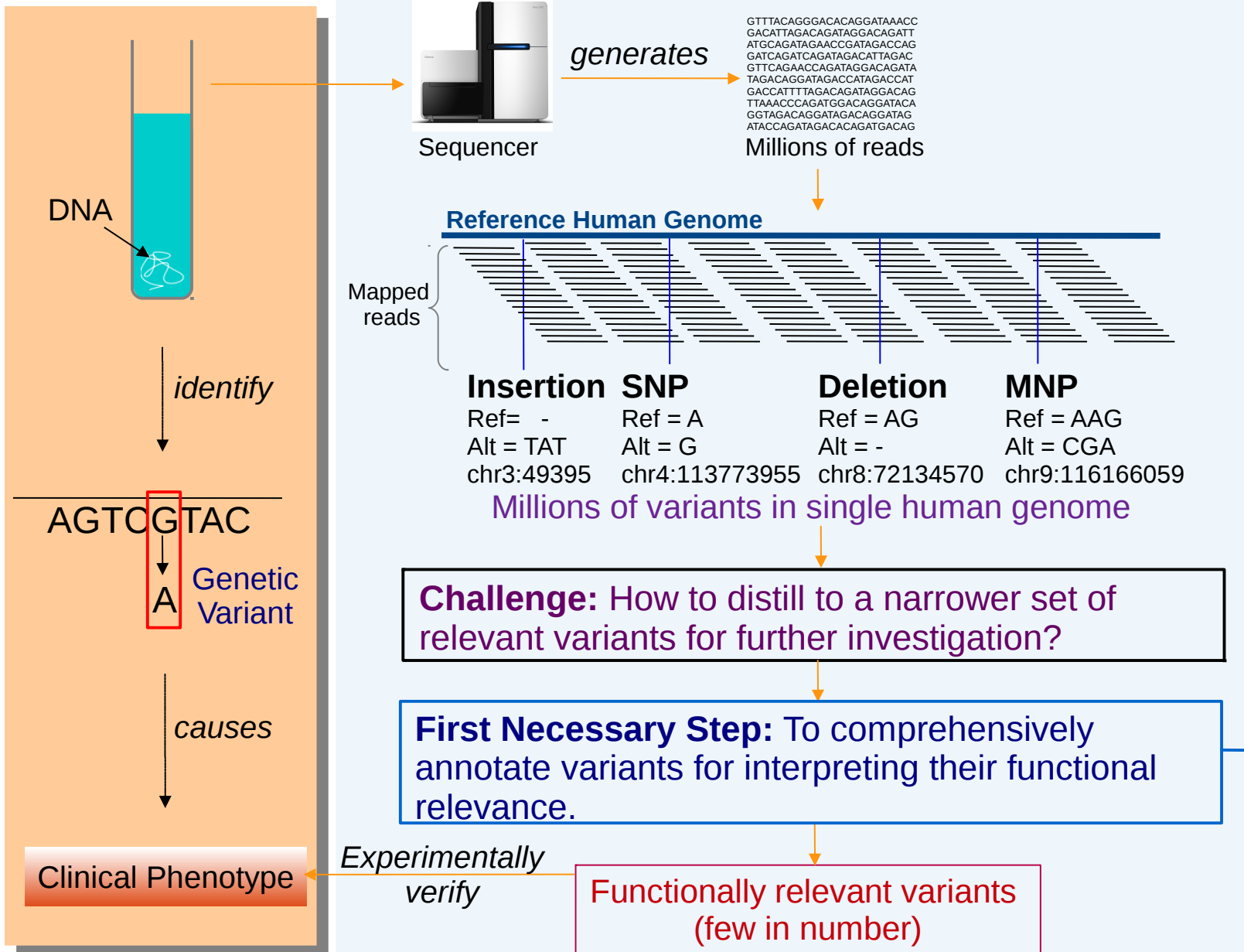
How does this tool work ?

What is the accuracy of this tool ?

Motivation

Why we developed this tool ?

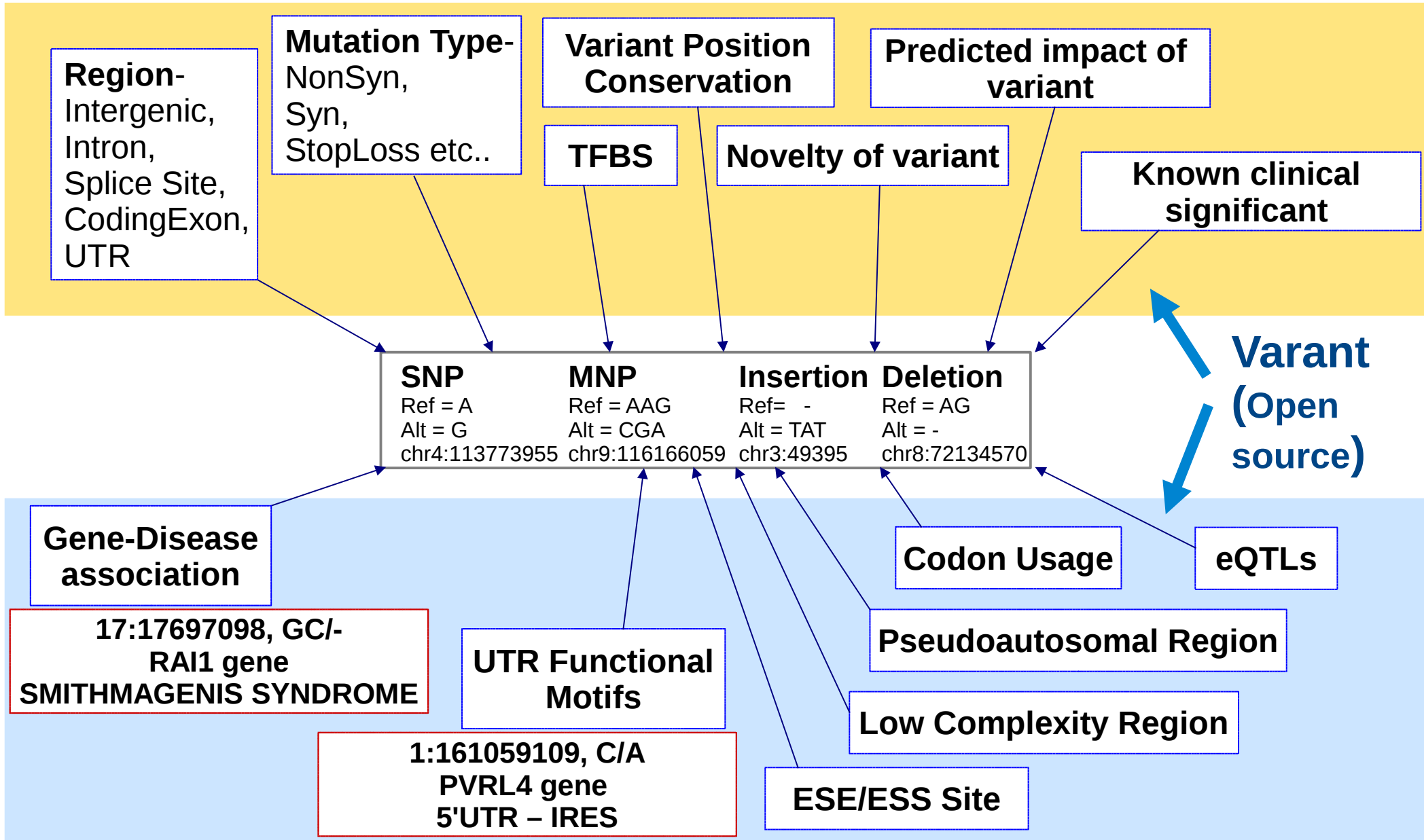
AIM in clinical study



With this outlook we have developed a **comprehensive** and **extensible** **open source** tool for human genome variation annotation called **Varant**.

Annotation Types

Annovar (Commercial), SnpEff (Open source)



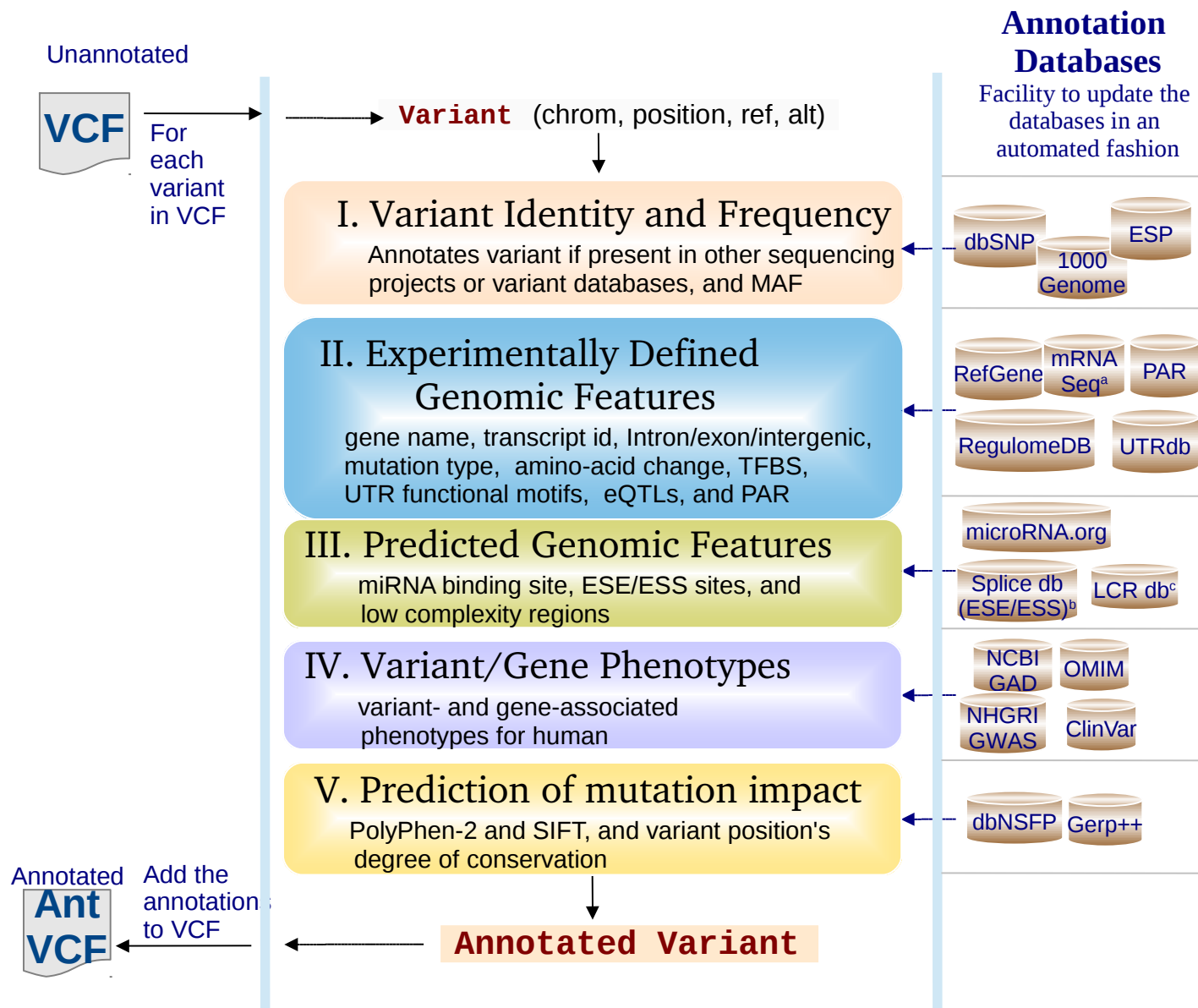
Installation and Working

How does this tool work ?

1. Download data sources
(Variant depends upon 17 data sources)

2. Create SQLite databases

3. Set path to locations of data sources and their SQLite databases



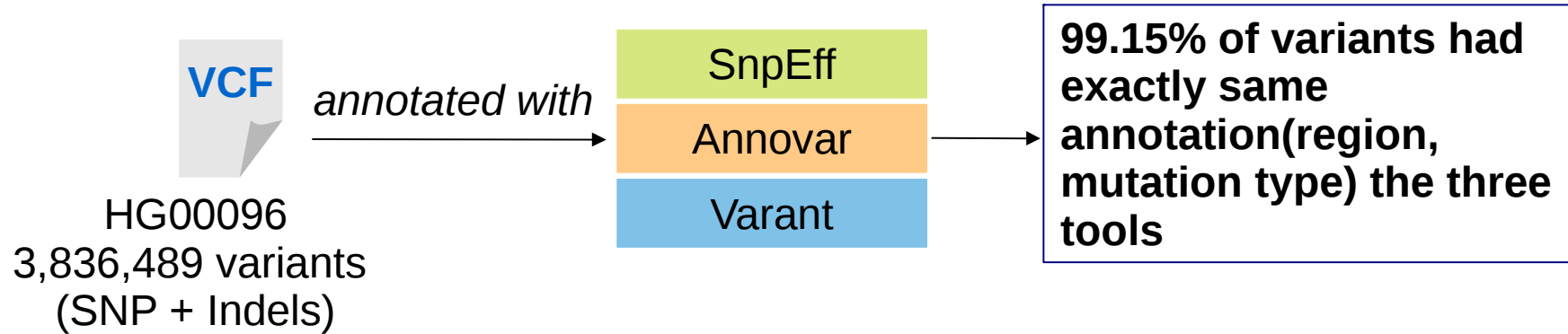
^aComputed from reffgene definition and using reference genome.

^bComputed using Burge et al. hexamer data on ESS/ESE.

^cComputed using the mdust Program (<http://bit.ly/mdust-LC>)

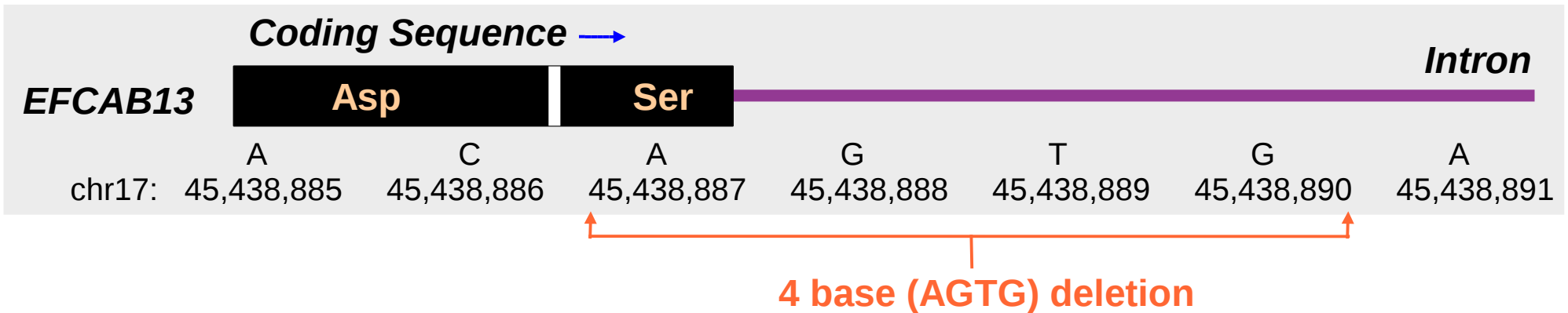
Annotation Accuracy

What is the accuracy of this tool ?



When Varant disagrees with other methods, its predictions are superior

Annotation of a deletion variant that spans intron exon boundary



SnEff – splicing

Annovar – exonic;frameshift

Varant – intron-exon boundary;splicing (*better precision*)

Annotation Accuracy

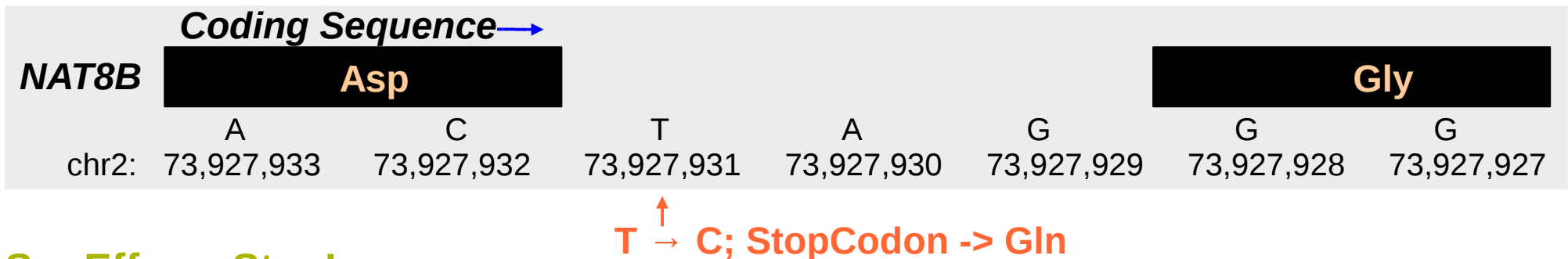
What is the accuracy of this tool ?

Annotation of Indels that do not alter coding sequence



- SnEff** – frameshift (incorrect)
- AnnoVar** – frameshift (incorrect)
- Variant** – NoCDSChange (correct)

Annotation of variants that alters stop codon in CDS



- SnEff** – StopLoss
- AnnoVar** – exonic (mutation type not computed)
- Variant** – Ambiguous_StopLoss (better precision)

Summary

- Varant provides a broad range of annotations for interpreting the relevance of genetic variants.
- Varant is easily deployed.
- Varant is accurate: annotations are equal or better than other commonly used tools.
- Varant is open source.

Acknowledge



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Thank You...