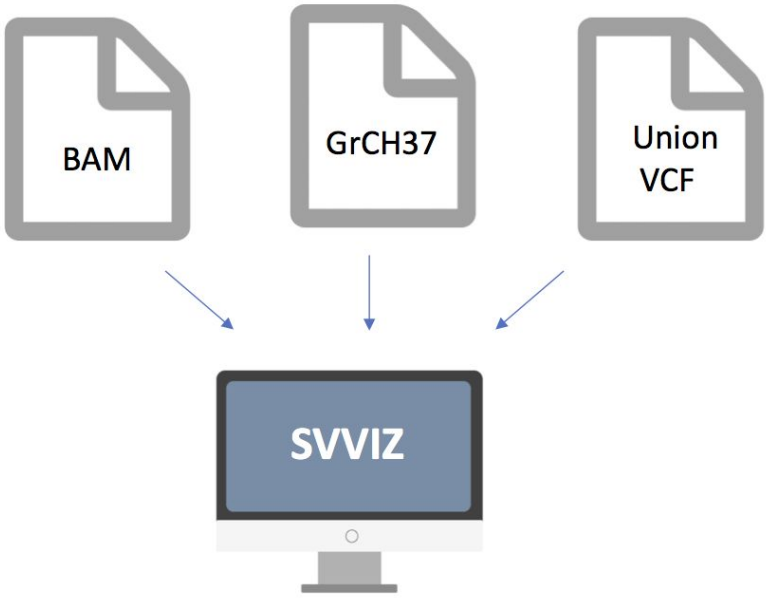
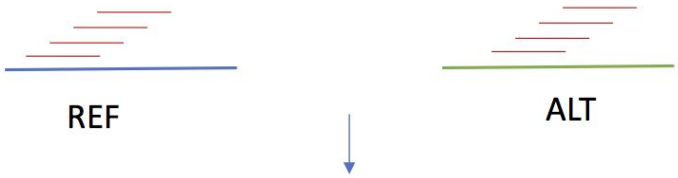
1

SVVIZ takes in:
-<u>read data</u> in BAM format from short read and long read sequencing technologies
- <u>reference genome</u>
- <u>putative SVs</u> listed in a VCF



2

Reads from the BAM file are mapped to **reference allele** (from GrCH37)



Reads from the BAM file are mapped to **alternate allele** (from union VCF). Reads that do not map better to the ref or alt allele are placed in an **ambiguous** bin

3

SVVIZ generates read aligned images (right), dotplots, and summary statistics.