

Aim 2

- Develop and integrate novel computational tools into the **Functional annotation pipeline (SVIM)** pipeline to evaluate the impact of SVs by
 - identifying genomic elements affected by a variant and the type of impact
 - assessing the impact based on the types of SV and disruption mechanism
 - up-weighting SVs associated with certain functional features
- Using the new pipeline, prioritize SVs from the **reference set** to identify **high-impact variants**

