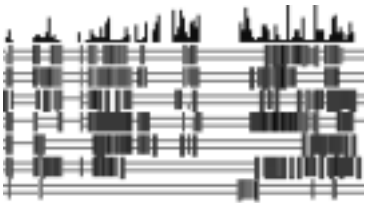
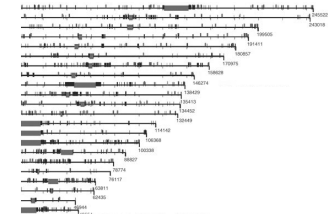


GersteinLab.org Overview

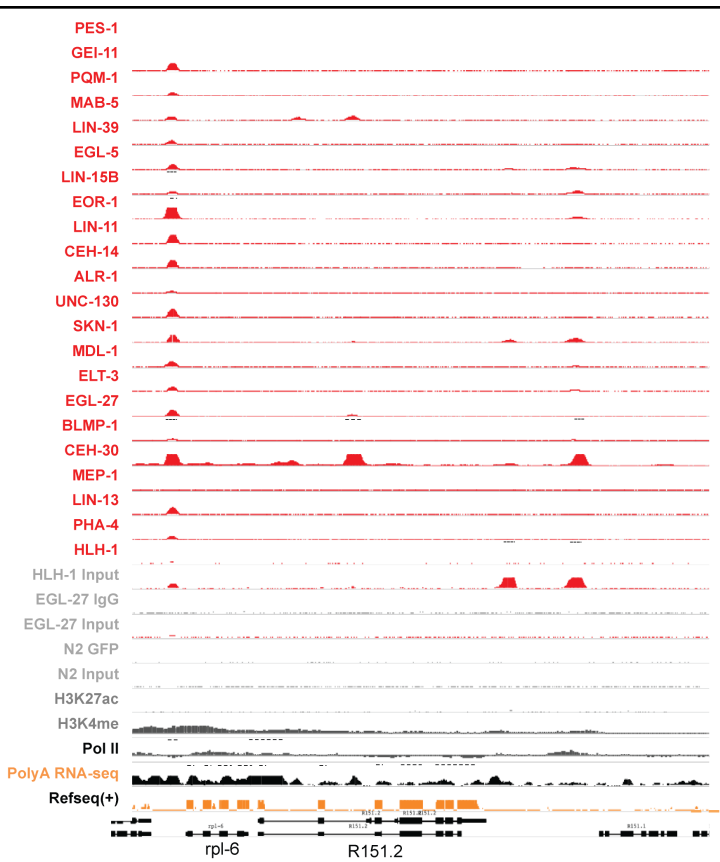
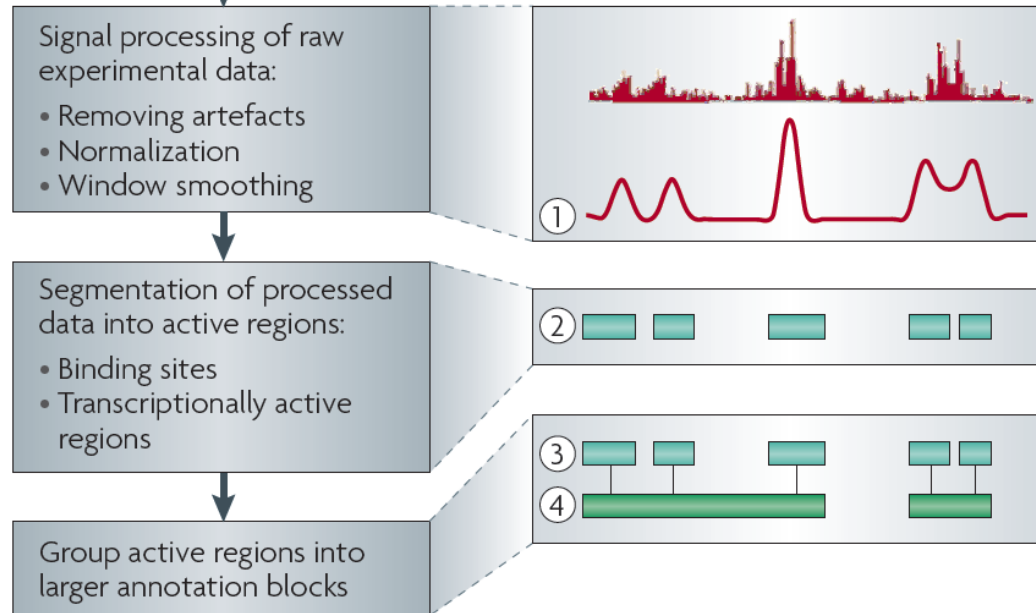
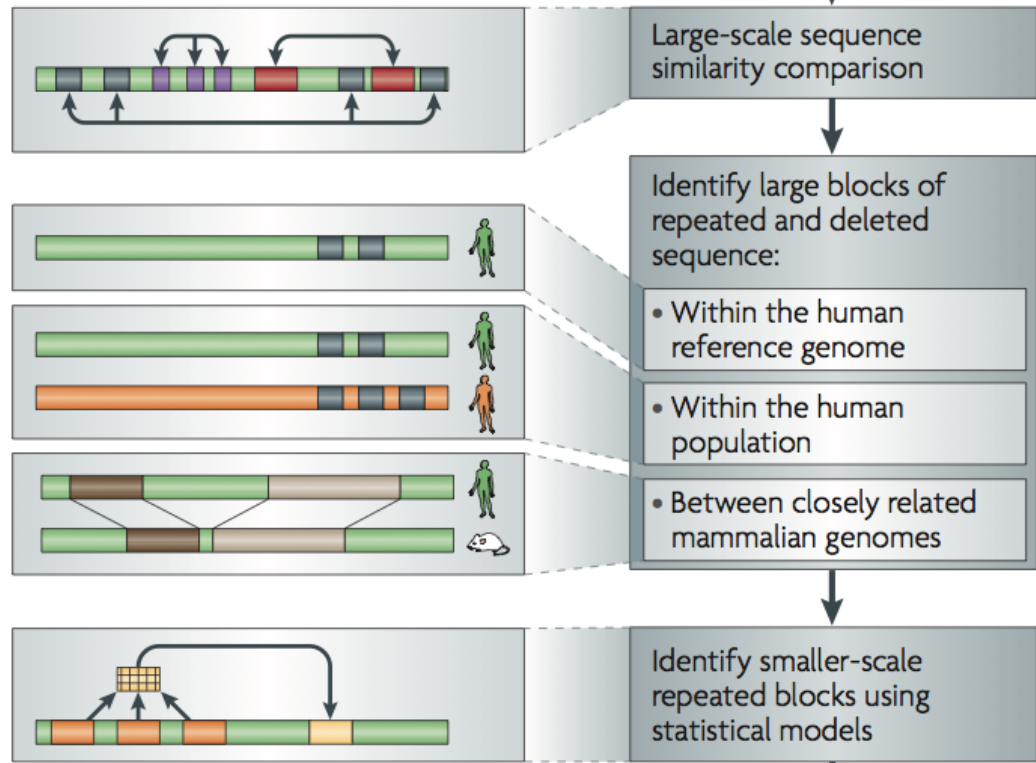


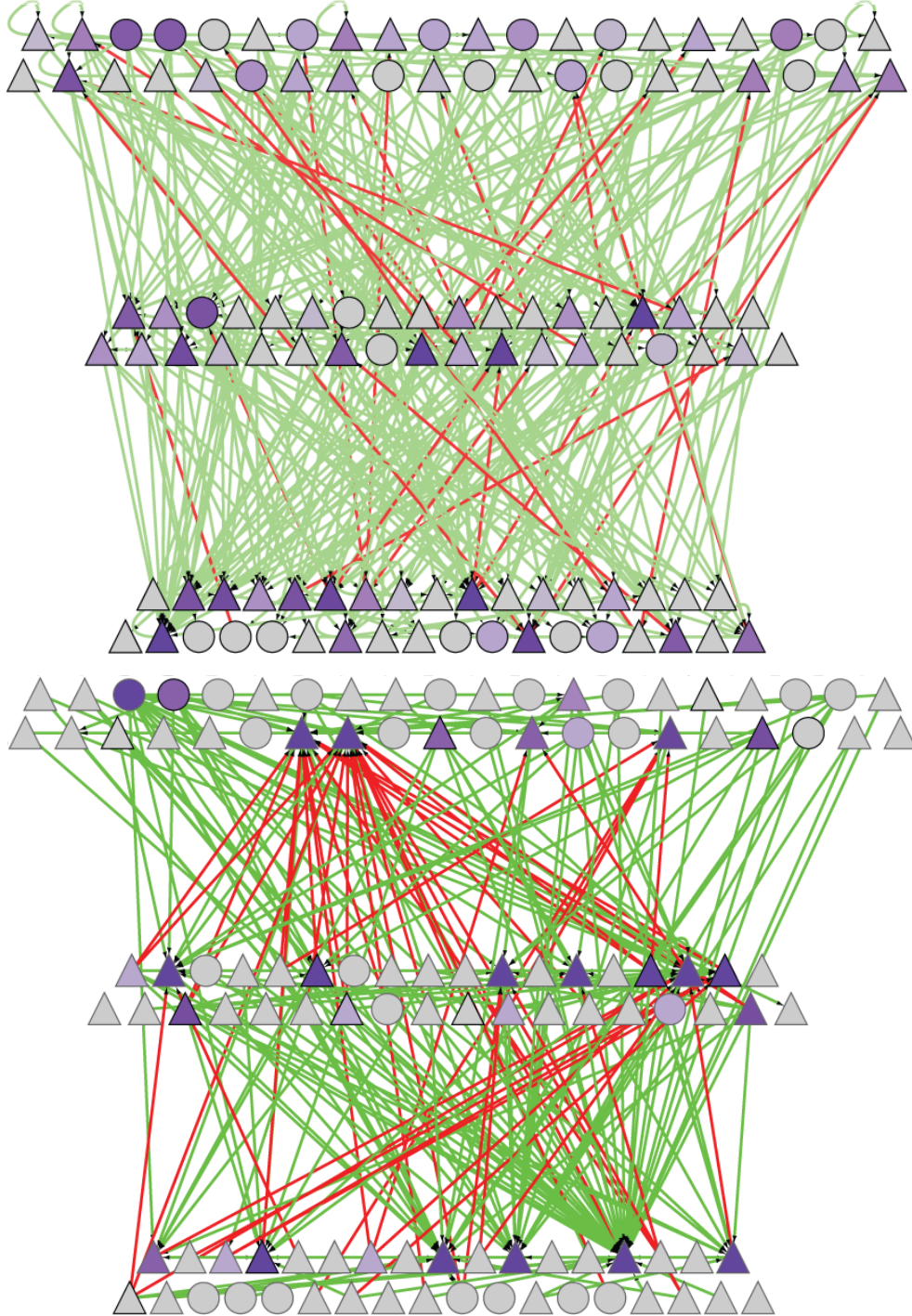
- Biological Knowledge Representation, Literature Mining, **Genomic Privacy**
- Genome Structural Variation & **Personal Genomics**
- **Human Genome Annotation & Disease Genomics**
- **Networks of Genes** & Protein Pathways
- Macromolecular Structures & Motions

Big Data Analysis & Mining

Simulation & Modeling

Annotating the Human Genome: Comparative & Functional



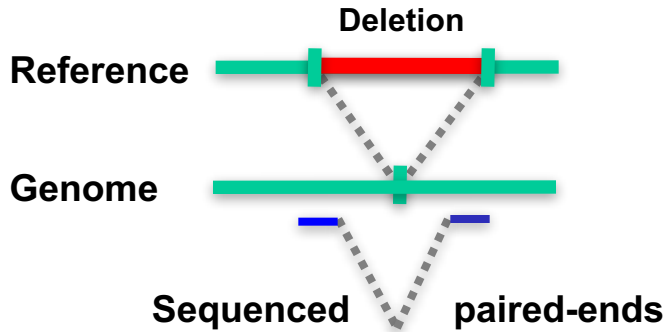


**Recasting
Genome
Annotation as
Networks:**

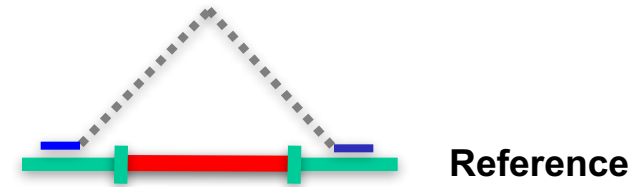
**Comparing
Proximal
&
Distal
Networks**

Methods to Find Variants (SVs) in Personal Genomes

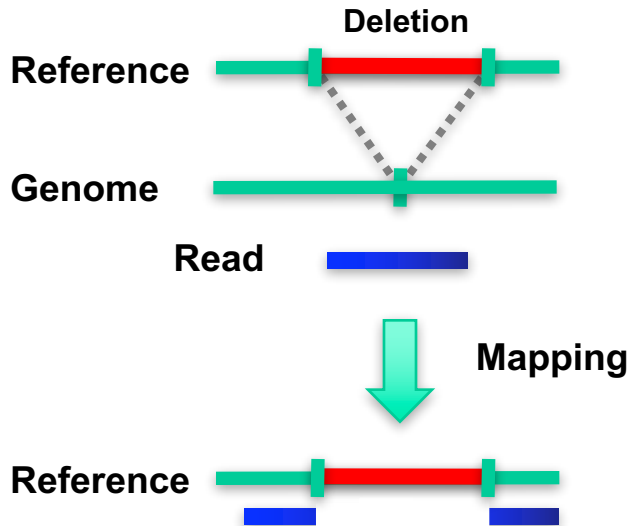
1. Paired ends



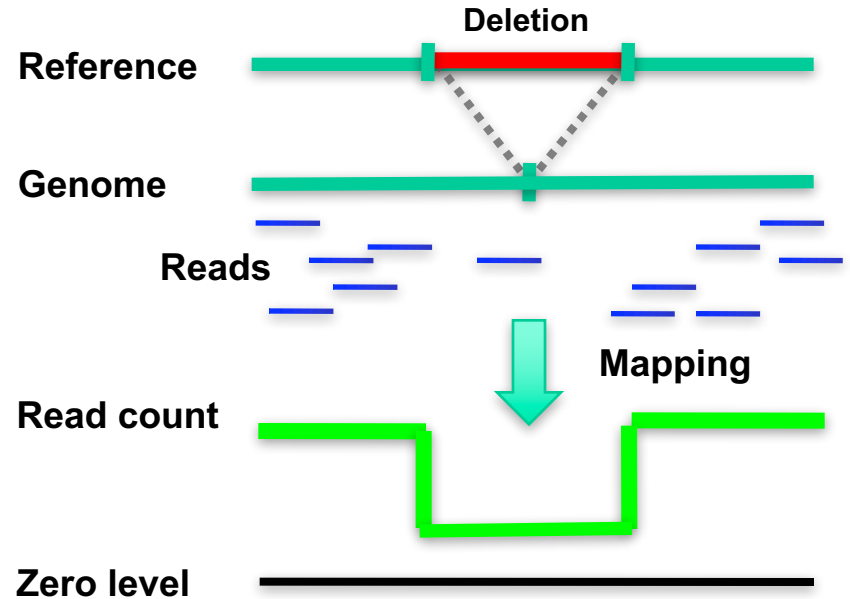
Mapping



2. Split read

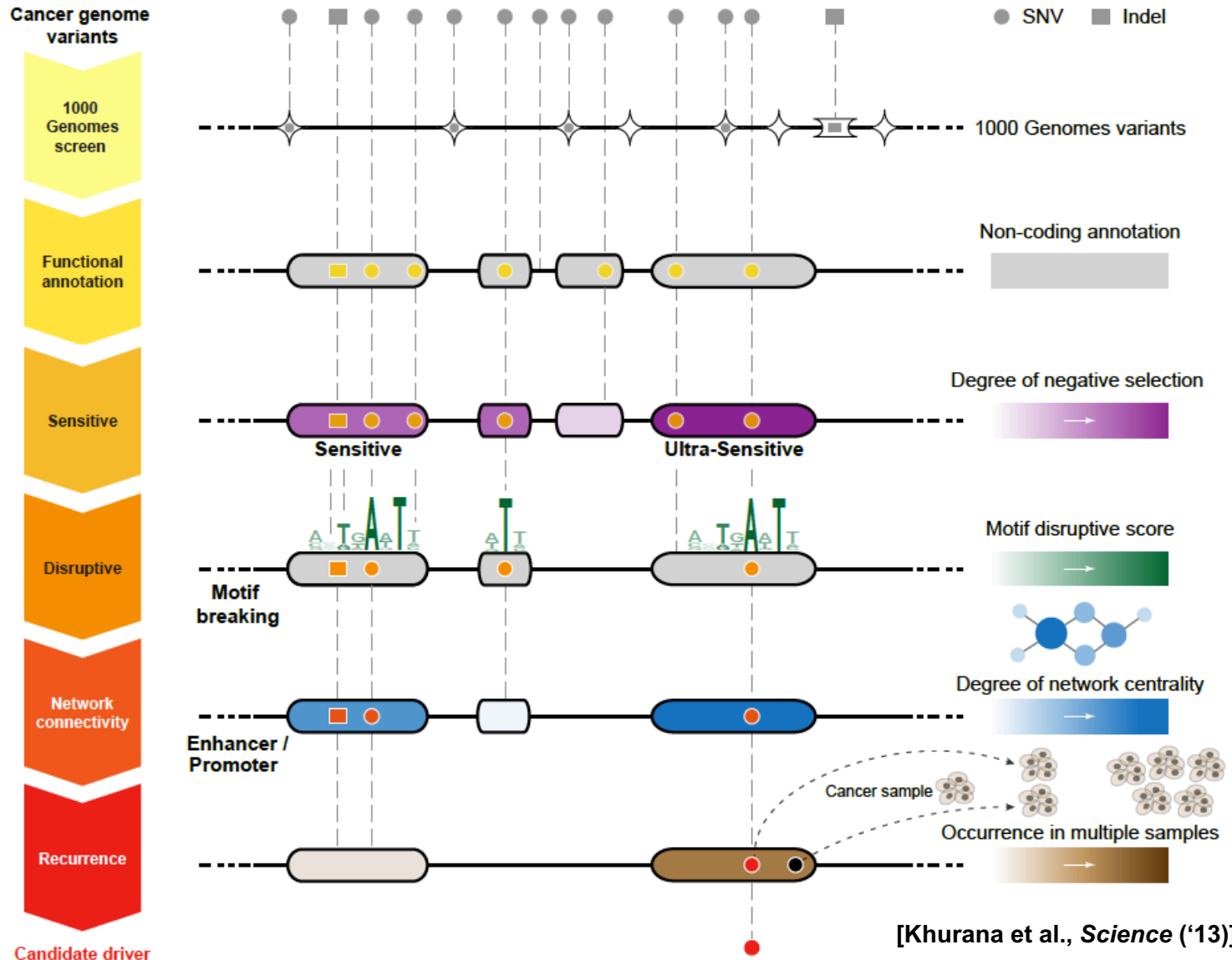


3. Read depth

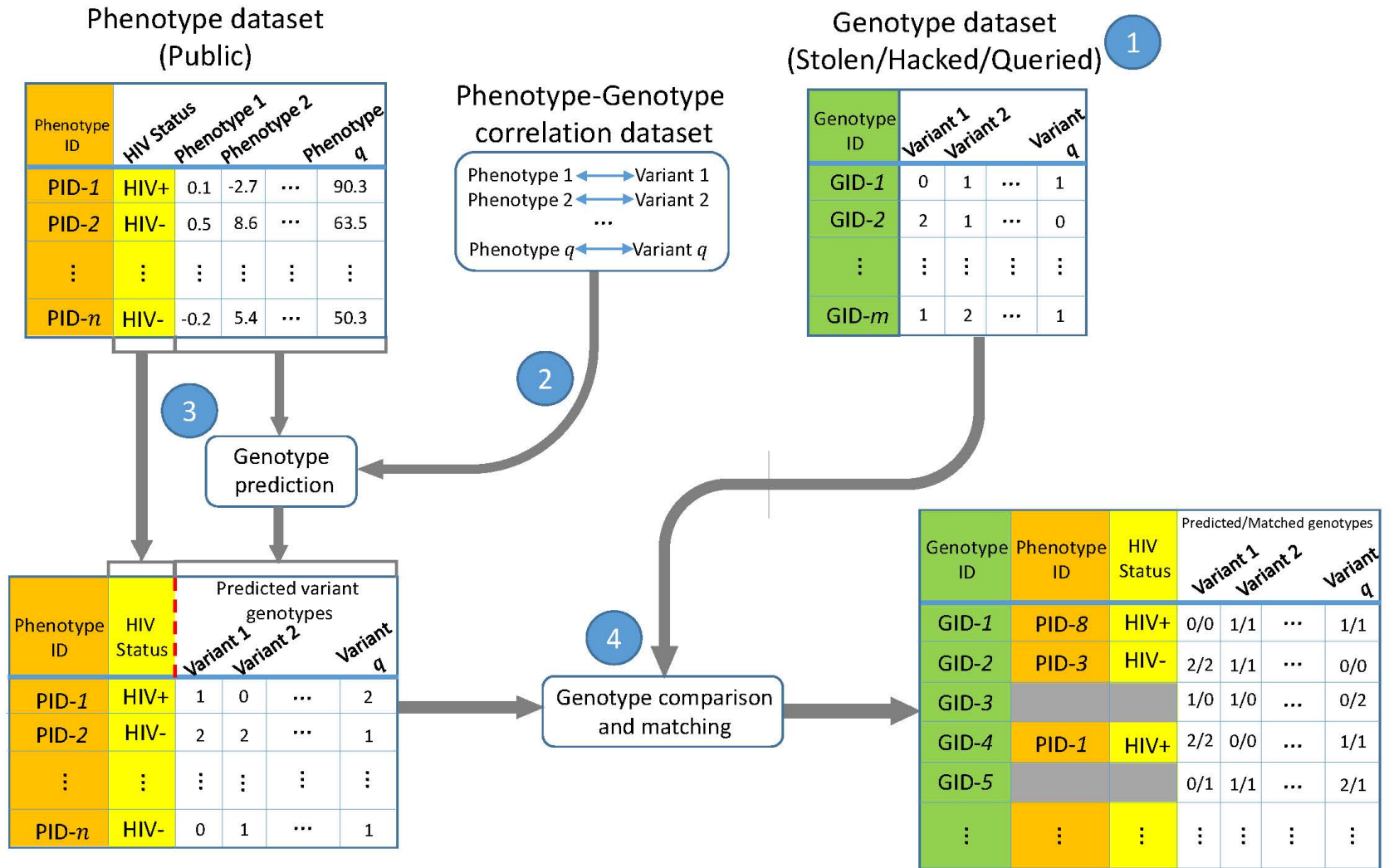


[Snyder et al. Genes & Dev. ('10)]

Identification of non-coding candidate drivers amongst somatic variants, using genome annotation & patterns of natural variation



Biological Data Science: Protecting Genomic Privacy from linking attacks



Predicting Allosterically-Important Residues at the Surface via **simulation**, to characterize deleterious variants

PDB: 3PFK

