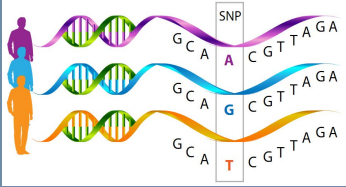
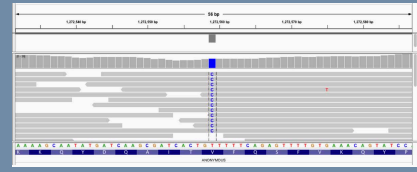


Harvard Chan Bioinformatics Core

presents:



Introduction to Variant Calling



This **in-person** workshop will introduce participants to best practices for **calling variants in paired tumor/normal datasets**. We will walk through the workflow beginning from raw sequence reads through to visualization and use of the cBioPortal platform.

During this hands-on workshop participants will learn how to:

- Evaluate **QC metrics** for the variant calling workflow
- **Call variants** and filter them to retain high quality calls
- Annotate and prioritize variants
- **Visualize variants** and compare against large-scale cancer datasets

***Introduction to the command-line interface and HPC is a prerequisite for this **advanced** workshop.*

Please check link below for eligibility requirements.

May 28th, 31st, June 4th and 7th 2024
(9:30am - 12pm each day)

More information & registration link at <https://tinyurl.com/HBC-VariantCalling>

Registration fee: \$65

Workshop Location: **In-person (Longwood Medical Area)**