# quickLift: Lifting UCSC Genome Browser annotations on demand

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## Problem

With the rapid increase in high-quality genomes, in particular human genomes (such as HPRC genomes), research is becoming more broad and less centralized on a single reference assembly such as GRCh38/hg38. One problem with this is that annotations are typically mapped to a reference. So while new genomes may be attractive for various reasons, their research value is often limited by the available annotations.

## Solution

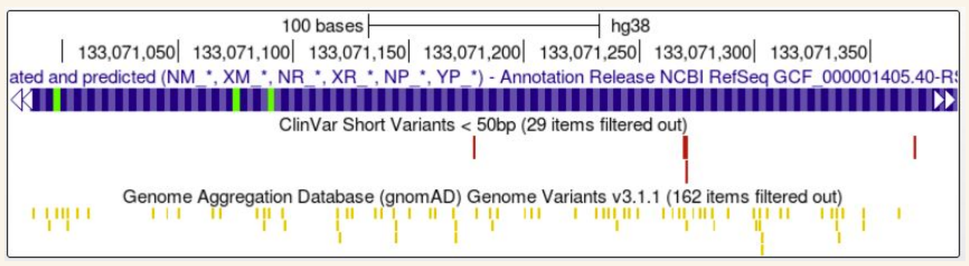
We introduce **quickLift**: A feature that allows you to convert (lift) annotations between assemblies on demand. This includes annotations from GRCh38/hg38 to new assemblies such as T2T CHM13v2.0/hs1. You can also lift custom data (hubs and custom tracks) from your own genome of interest to a reference and vice versa. This empowers users with interests in non-reference genomes without requiring difficult and timely data conversions.

## Design details

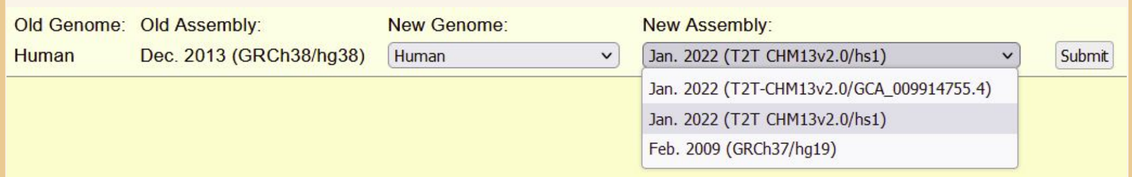
- **Chain files** between the assemblies can be UCSC generated or user-created and web-accessible
- First implementation will support **bigBed** format, both UCSC-hosted and custom data
- **Regional conversions** lead to quick results
- Results may be **downloaded** or **saved** freely

## How it works

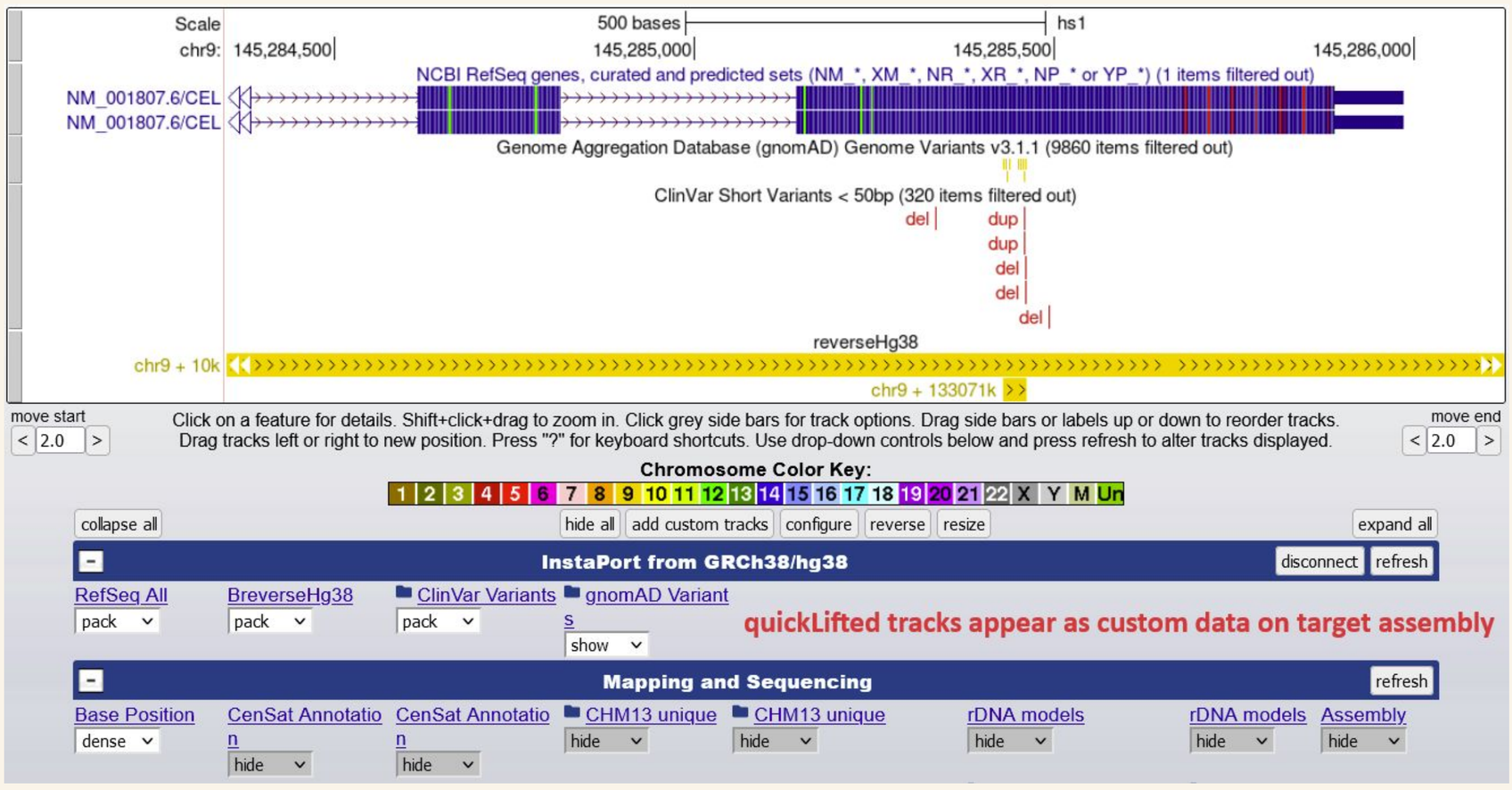
**1.** Select region and annotations from original assembly




**2.** Select target assembly




**3.** See resulting region on target with chosen annotations




Example above shows a **quickLift** of two exons of the CEL gene on hs1 with the following data from hg38:

**1.** RefSeq models
**2.** GnomAD v3.1.1 track showing only missense variants
**3.** ClinVar variants track showing only pathogenic variants
**4.** A chain track, which shows the alignment between the two assemblies. This is particularly important to see where there may be gaps in the target (in this case hs1) assembly

## Get involved!

This feature is still in the **testing phase** of development. If you are interested in testing the feature, providing any feedback, or have suggestions please get in touch with us at genome-www@soe.ucsc.edu.

We also encourage anyone to share how they would specifically use this feature so that it may be taken into consideration.

## More information

View this poster:

For any questions or comments, email us at genome@soe.ucsc.edu or scan the QR code.

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Make a suggestion: