



## Agenda for Three-Day Genome Browser Virtual Workshop

### DAY 1

#### Intro to the UCSC Genome Browser – features and navigation.

A tour of the basic parts of the UCSC Genome Browser:

- General overview of the Browser, what it is, history
- Display configuration
- Track settings
- Exporting Browser .pdf images for publication
- Searches: for regions/positions, gene names, motifs, other keywords
- Searches: BLAT, short match track for sequences
- Searches: PCR for primers
- Demo of example searches: Gene of interest, regions of interest, dataset/publication of interest
- Navigation: drag-and-zoom, drag-reorder tracks, switching genome assemblies and organisms via homology
- Keeping track of your thinking by saving and sharing sessions

#### Genome Browser data

- Starting points for browsing our data:
  - genomic position, sequence, gene, HGVS nomenclature
- Data types – BED files, wiggle, BAM, VCF, dbSNP
- New Data types – barChart, interact, Hi-C, , lollipop
- Variants – CNVs and SNPs, benign and pathogenic
- Data – genesets, annotation, 1000 Genomes, GnomAD, OMIM, GTEx expression data, CRISPR guides, pathways, Epigenomics ...

- Publications / gene interactions
- Proteomics
- How to find more info about a track or track item
- Variants – Understanding various SNP tracks

## DAY 2

### More features

- Table Browser and extracting data
- Custom tracks - uploading and displaying your own data in the Browser
- Custom track examples – BED files. Sequences data: coverage (BAM files), variant calls (VCF), RNA-seq (wiggle)
- The Variant Annotation Integrator – predicting biochemical consequences of short variants
- Public Assembly Hubs
- How to download our data
- How to get DNA for the region you are viewing
- Short Match, BLAT and isPCR
- Getting gene sequences using the Table Browser

## DAY 3

### Getting more out of the Browser

- Multi-Region mode
  - Exon-only display
  - Viewing discontinuous regions of your choice (e.g., pathways)
  - Alternate haplotypes in human genome assemblies
- Table Browser advanced examples – Intersection, Filtering
  - Finding the table that goes with your track
- Data Integrator – combining data from multiple tables
- New feature: Track collections – co-configure multiple wiggle tracks

### Large and remote datasets and sensitive data

- Track Hubs, including making your own
- Assembly Hubs – A Browser for your genome of interest
- Genome Browser in a Box: Hosting a local copy of the Genome Browser on your laptop – solution for sensitive data inside your firewall

**Cementing your knowledge: Problem session to work on example problems**

- Use the Browser to investigate a biological problem.