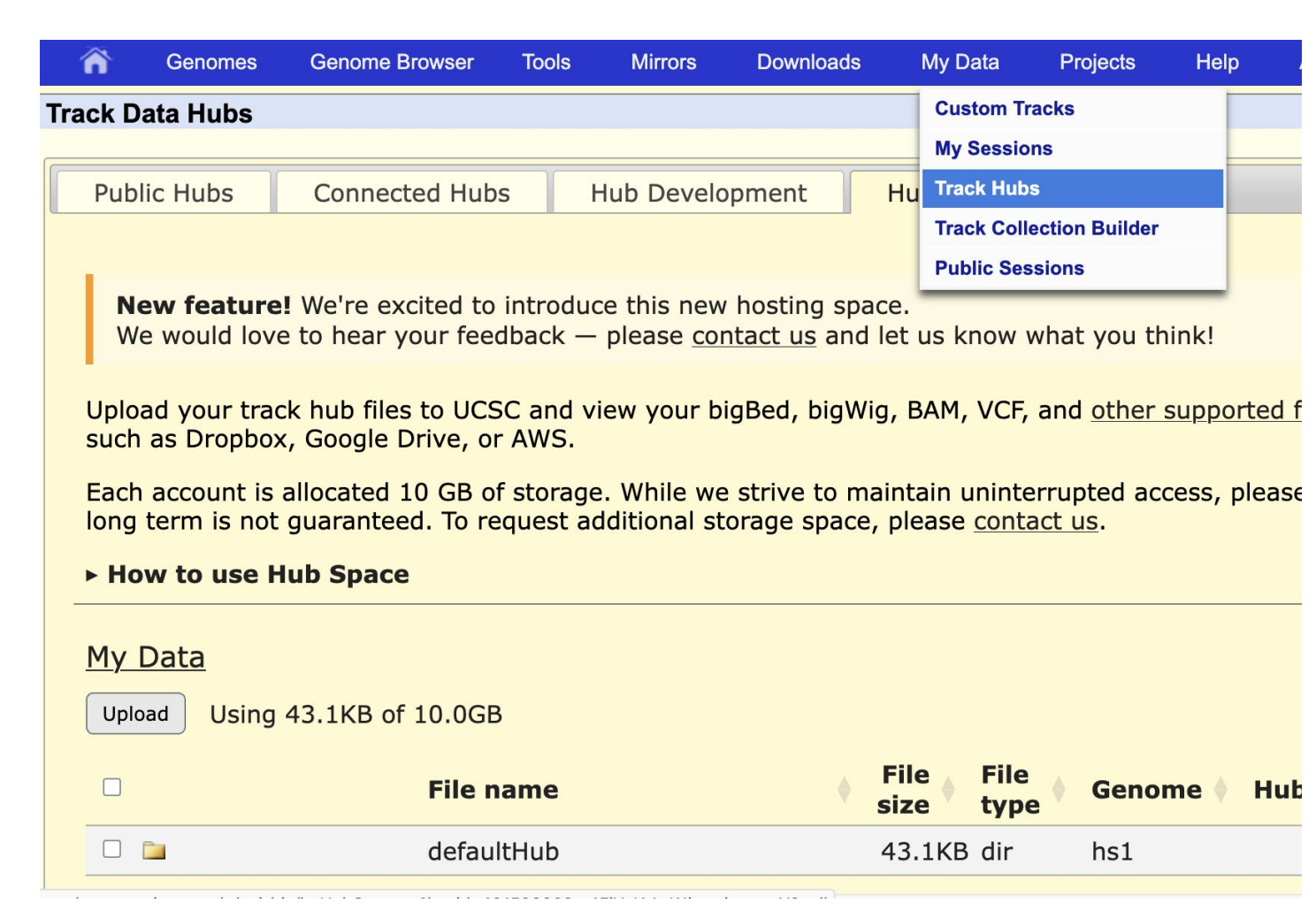


UCSC Genome Browser 2026: Storage for your track hubs, lift any tracks, edit annotations & new tracks: long-read SVs, short-read SNVs, tandem repeats and NMD escape

Maximilian Haeussler, Christopher Lee, Brian Raney, Galt Barber, Hiram Clawson, Jairo Navarro Gonzalez, Luis Nassar, Jonathan Casper, Anton Nekrutenko

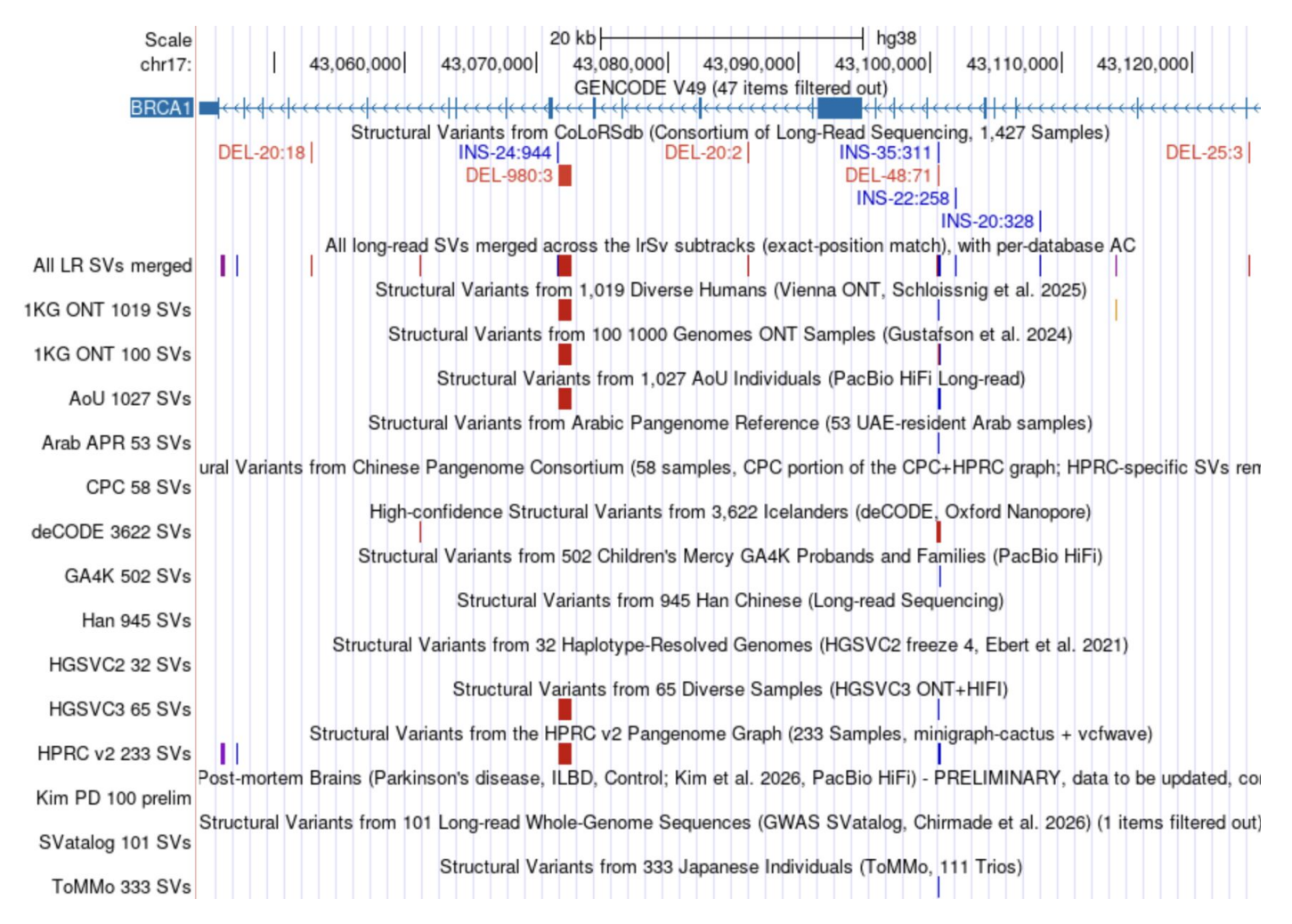
Need storage for your BAM/VCF/bigBed/Bigwig files and a track hub for a paper? Click **My Data > Track Hubs > Hub Upload**

- Upload files to UCSC, no need for DropBox, Github, etc accounts
- 10GB by default, much more upon request
- Files are stored on UCSC servers: fast and reliable
- Track hub config auto-generated: define track names and labels, mouse overs, colors, fields on click, etc
- Hubs can be loaded into IGV, Jbrowse2, IGB, Ensembl.
- Annotations can be on > 30k Genbank assemblies
- New assembly? Request via our form or upload your own sequence file (scheduled for June 2026)
- Share via a short link: **My Data > My Sessions**



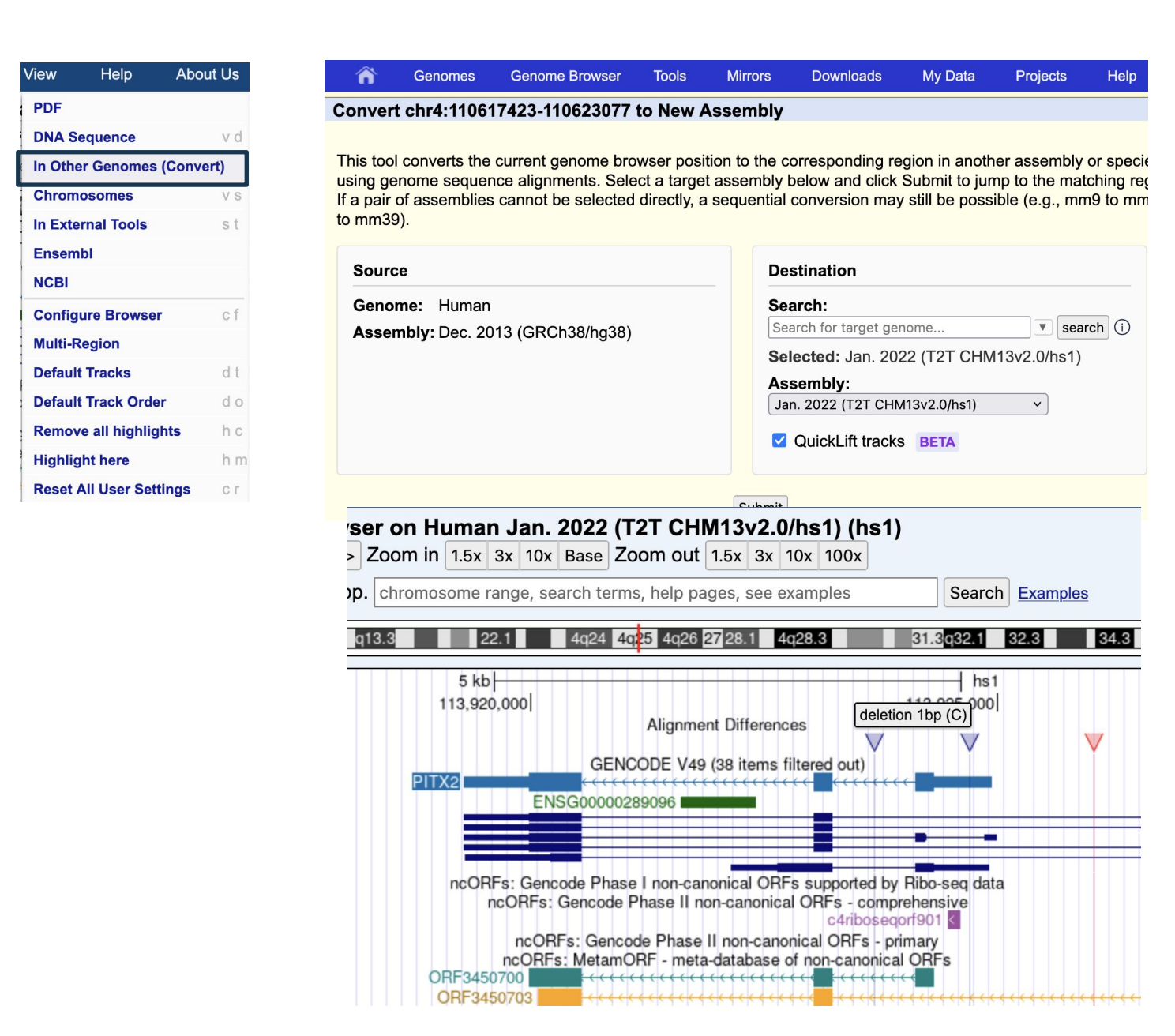
New Track: Structural long-read variants from more than 8000 genomes

- A collection of structural variants from CoLoRS DB, Japan TOMMO Biobank, 1000 Genomes (Vienna and ONT), Arabic Pangenome, deCODE, Children's Mercy GA4K, HGSVC, HPRC, Svatalog and a Parkinson's cohort from Kim et al. 2026
- Integrated into a single VCF or bigBed file, freely downloadable
- Release June 2026
- Suggestions for more datasets welcome!



Looking at annotations but need them to another genome? Click **View > In Other Genomes > Quick Lift**

- UCSC has thousands of whole-genome alignments in liftOver format, e.g. hg19 to hg38, hg38 to CHM13, etc
- QuickLift allows you to take the currently shown annotation tracks and lift them on-the-fly to another genome in real time.
- All currently displayed annotation tracks are lifted
- We add alignments on request by email. A request form for liftOver alignments is in development (release late 2026)
- Alignments will be computed on Galaxy servers and made available in the Genome Browser and QuickLift.
- They can be merged into multiple alignments (multiz)



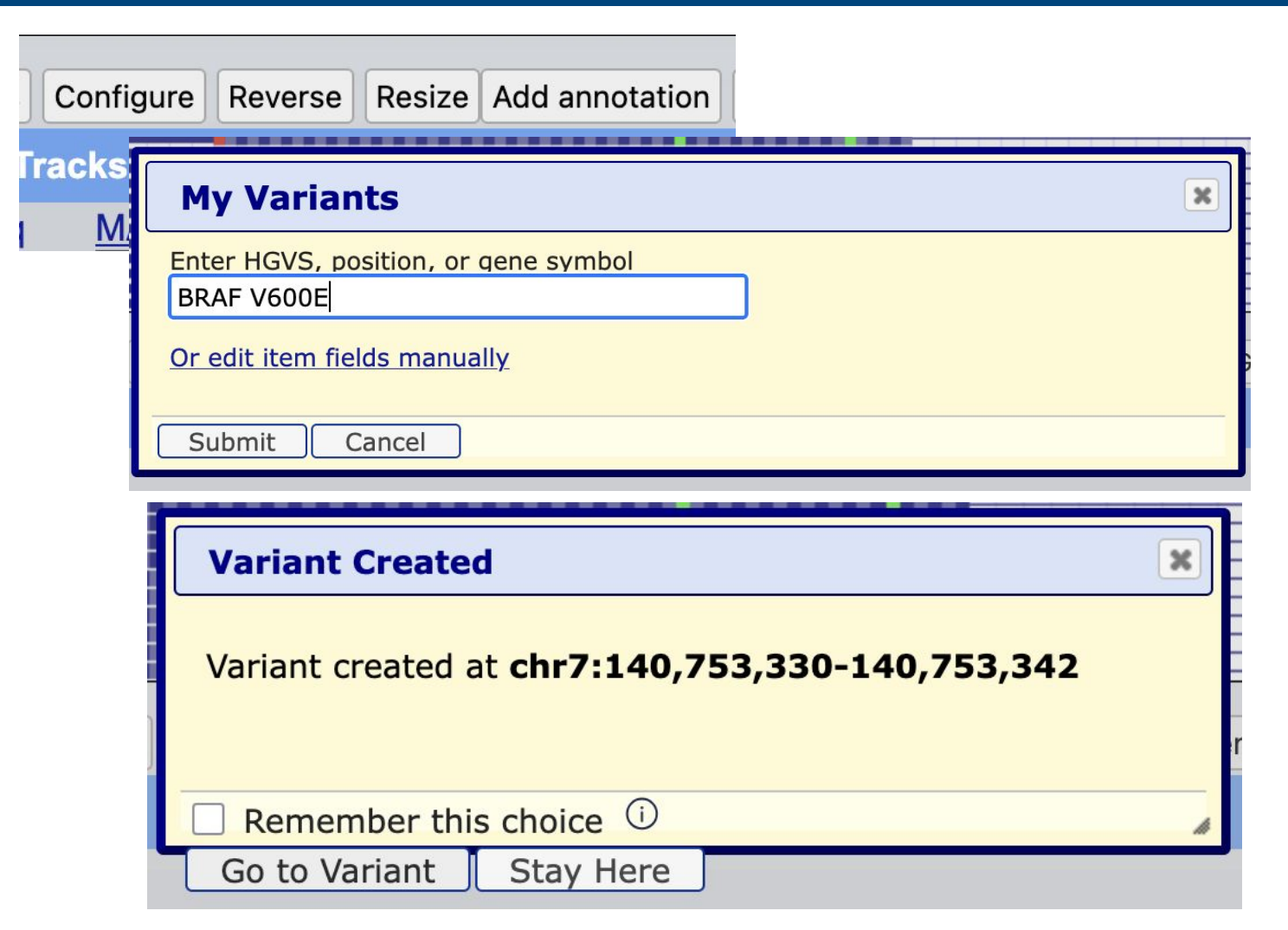
New Track: Short-read SNVs from 1.6 million genomes

- A collection of short-read variant frequencies, from: All of Us 245k, TOPMED 151k, SFARI Spark 152k, NCBI ALFA 409k, FinnGen 500k, SweGen 1k, SCHEMA 121k, Japan TOMMO Biobank 61k, Mexico Biobank 6k, SGDP 279, Indigenous Africans 180, HGDP and 1000 Genomes 4k, GREGoR rare diseases 3.5k, Australia MRGB 4k, Brazil AbraOM 1k, GenomeAsia 1.7k, HRC 30k, IndiGenomes 1k, Korea 1.9k, Saudi Genome 302, Singapore NPM 9.7k
- Release May/June 2026
- Suggestions on other projects welcome!
- **Seeking contacts at UK Biobank & Regeneron.**



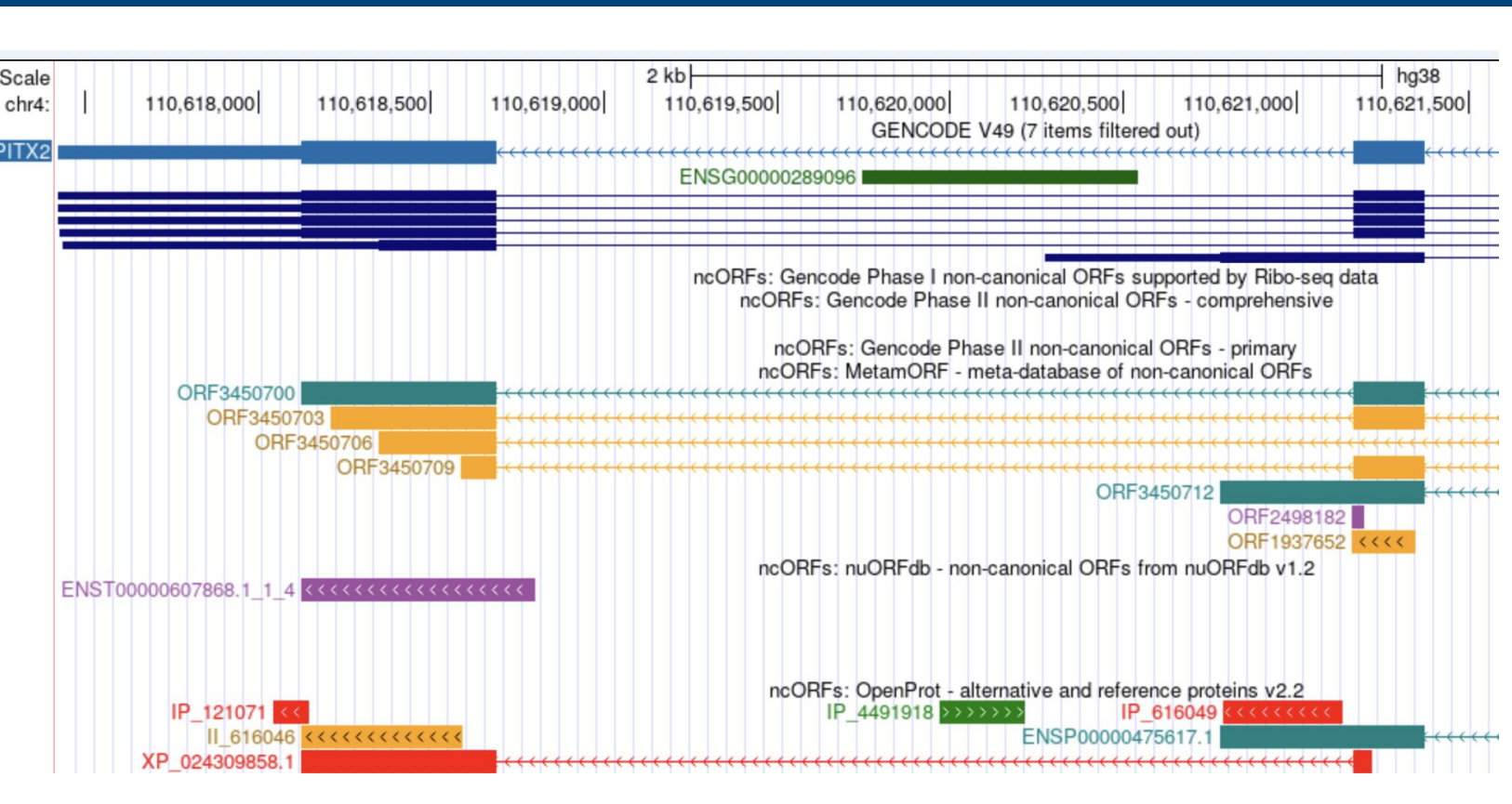
Need to edit annotations manually and collaborate on them? Click "Add annotation" (not released yet)

- We already have custom tracks, where you paste text files in special formats, but no interactive way to change a single annotation
- "Add annotation" creates special custom tracks with user-defined fields, e.g. variant, comments, publications
- Use cases: manual gene annotation, primer design, CRISPR target locus annotation, etc.
- Tracks can be shared with "editors" who can make changes
- Overlapping annotations can be pulled in from certain tracks, e.g. CADD or REVEL scores for variants, or from external APIs (e.g. SpliceAI Indels from the Broad Lookup Server)
- We appreciate suggestions on APIs to add



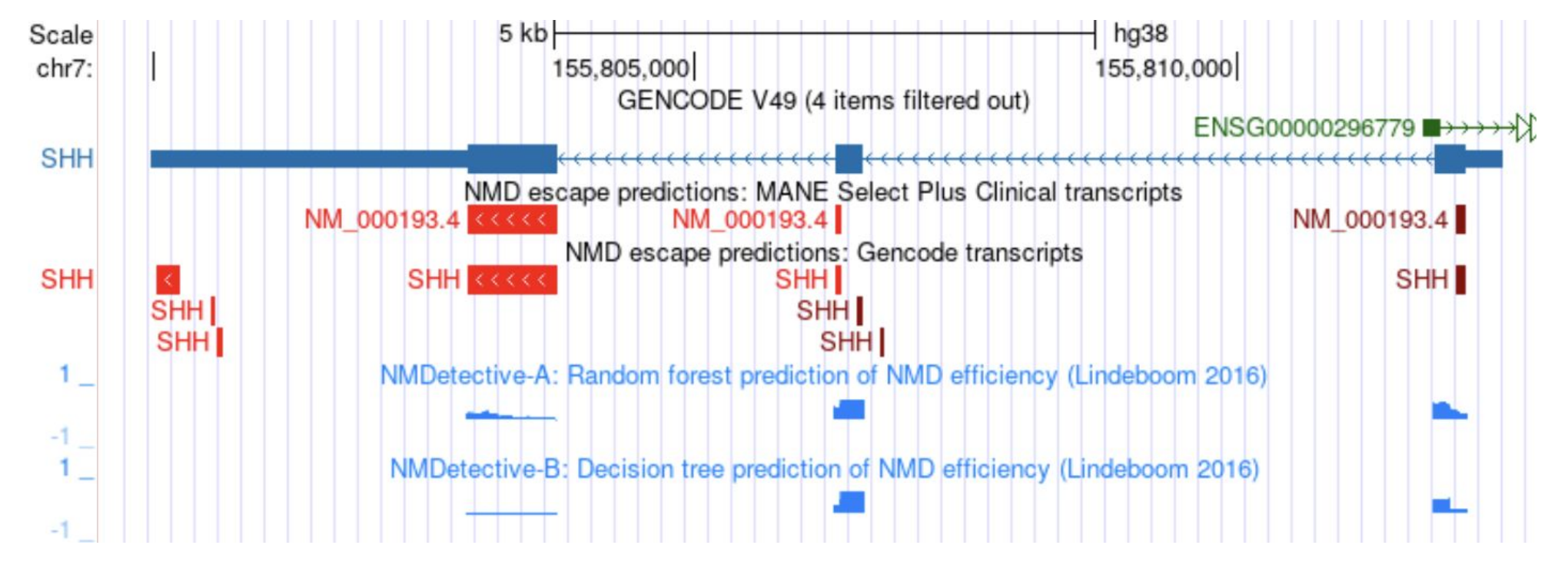
New Track: Non-canonical, short ORFs with RiboSeq and/or Mass-spec evidence

- Non-canonical ORFs from Gencode Phase I and II, MetaMorf/Sorfs.org, nuORFdb, OpenProt and UTRAnnotator

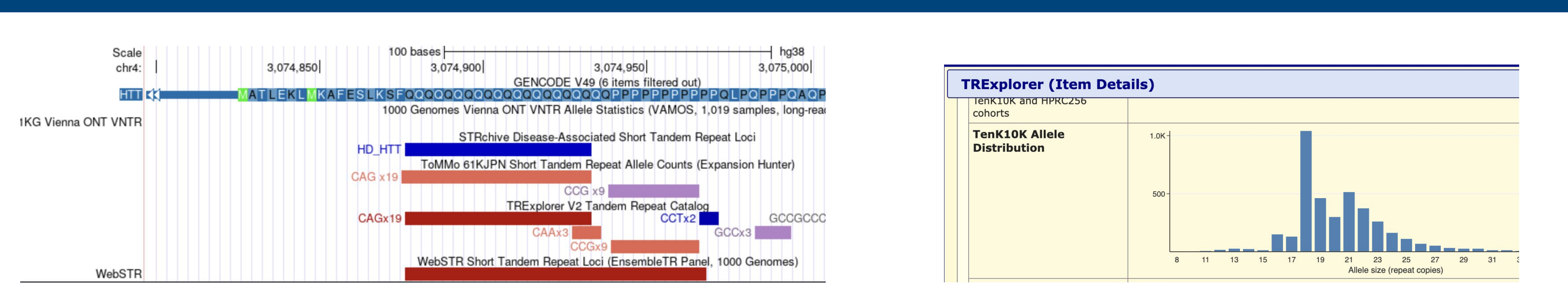


New Track: NMD Escape regions of Gencode or RefSeq Transcripts

- Nonsense-mediated decay destroys transcripts containing premature stop codons or frameshifts, except when these occur in certain regions of the gene (the 50/100/400 bp rules). Tracks show these regions for Gencode and RefSeq. The track also shows NMDetective, a prediction model for these regions.



New Track: Tandem repeat variation - WebSTR, TRExplorer, STRchive, TOMMO



Other tracks:

- PromoterAI, PrimateAI variant impact predictions
- Recount3: All Introns in human SRA RNA-seq datasets, Langmead Group
- DNA Methylation Atlas, Kaplan Group
- MethBase2 with 5600 Methylation Samples in the SRA, A. Smith USC
- ENCODE4 CCREs and also ENCODE4 TF/Chromatin data (coming)

Ideas for new tracks? E.g. long-read transcripts, non-coding, RNA modifications?

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Genome Browser tutorials and videos: <https://genome.ucsc.edu/training/index.html>