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Database issue

The UCSC Genome Browser database: 2027 update

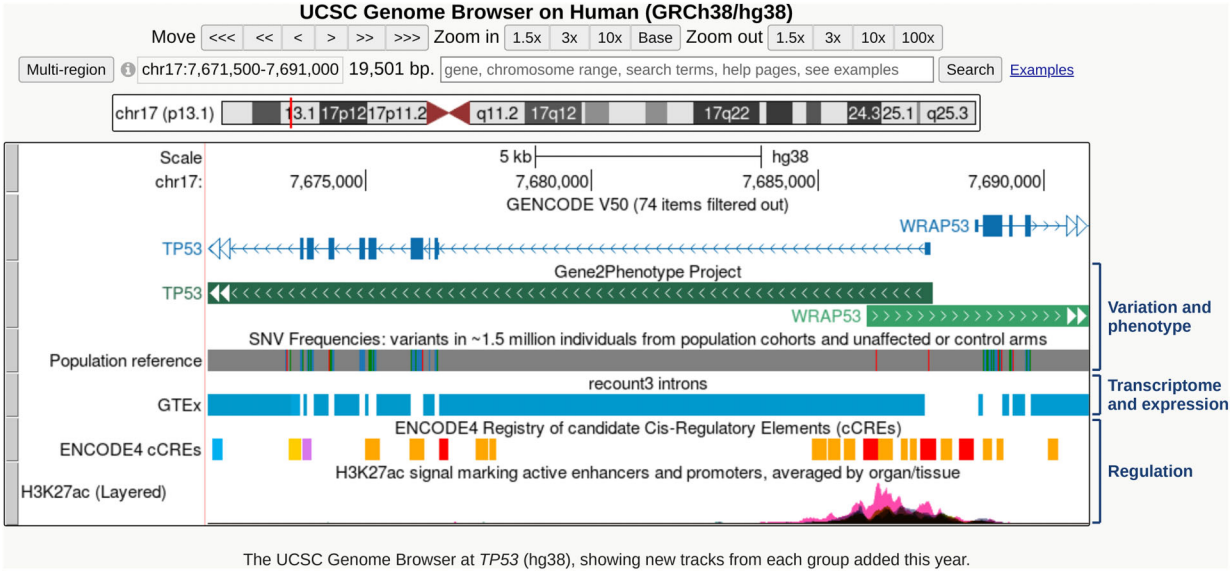
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Abstract

Since 2000, the UCSC Genome Browser (https://genome.ucsc.edu) has served as a standard tool for visualizing and comparing annotations across thousands of genome assemblies. Users can browse and visualize a wide range of data types from gene annotations to regulatory regions and comparative genome alignments. Once the data view is configured, the Genome Browser image can be exported for use in publications. Beyond visualization, users can use our tools to compare and export the annotations for further analysis. This year's feature updates include the full release of a tool to copy annotations between related assemblies, QuickLift; feature additions to our data-hosting service HubSpace to enable live editing of configuration files; two new display configurability options: "My Annotations" and custom item coloring; and several improvements to genome assembly discovery and track management. Beyond these new features, 28 new annotation tracks have been added across three broad categories: variant databases and interpretation, gene regulation, and transcriptome and gene expression. These include ENCODE4 cCREs and other ENCODE4 regulatory annotations, variant frequencies and phased variants from national sequencing projects, and two massively parallel reporter assay tracks.

Graphical abstract



The UCSC Genome Browser at *TP53* (hg38), showing new tracks from each group added this year.

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Introduction

The UCSC Genome Browser ("the Browser") serves as one of the primary visualization tools for genomic data, collecting and displaying data from both public and proprietary genomic databases [1, 2]. The Browser now covers over 50 000 genome assemblies, with new ones added through an assembly request system. Each assembly includes several basic sets of features mapped to assembly regions, such as GC Percentage, repeat elements from RepeatMasker (http://www.repeatmasker.org), and RefSeq gene annotations when available. More popular assemblies, such as hg38/GRCh38 and mm39/GRCm39, often receive numerous additional data tracks—>6000 tracks are available for the two most recent human genome reference assemblies. These tracks provide annotations on topics as diverse as splicing, pseudogenes, genome uniqueness, array probes, segmental duplications, and microsatellites. Many tracks are updated automatically, including ClinVar [3], RefSeq [4], and OMIM [5], rather than being snapshots of a database or publication. Users can also load their own data into the Browser and visualize it alongside these public data tracks through custom tracks or hubs. Users who believe their data would be of value to the wider genomics community can submit their hub to our public hub list. For assemblies with limited annotations, groups can submit tracks to be added. Beyond visualization, the Browser provides access to the underlying data through interactive web-based tools (the Table Browser), a REST API that can be programmed against, and a static downloads server.

Data track updates

Over the last year, the UCSC Genome Browser has continued to steadily expand its catalog of available data tracks. Data tracks are either continuous data, such as RNA-seq expression, or discrete annotations, such as variants or genes. Users can hover their cursor over an annotation in the visualization or click that item to see more details or links to the original database. The new data track additions primarily fit into three groups: (i) variant databases and interpretation, (ii) gene regulation, and (iii) transcriptome and gene expression. Here, we highlight a small selection of newly added tracks in each of these groups for the GRCh38/hg38 human genome assembly. A full list of new data tracks, alongside a brief description and available assemblies, can be found in Table 1.

Variation and phenotype tracks

Variation and phenotype tracks display simple and structural variants that appear in the genome. While variation tracks focus on enumerating observed variants (e.g. large public databases like dbSNP and [6] gnomAD [7]), phenotype tracks, in contrast, attempt to link variants to disease phenotypes or predict the deleteriousness of mutations (e.g. OMIM, G2P [8, 9], and CADD [10]). For example, Fig. 1 shows a collection of new variant and phenotype tracks a user might combine to annotate a new variant [10]. The Browser added four notable tracks under this group this year.

SNV Frequencies

This track collection presents 34 variant tracks from various research cohorts, such as All of Us or TOPMed, and national sequencing projects, including those from Australia, Finland, China, India, and more. The tracks cover nearly 1.7 million genomes, exomes, and genotyping arrays across these global populations. In addition to the individual data tracks for each of these projects, we created three tracks that aggregate variants across these projects along different axes. The "population reference" track is the default view and pools 1.24 billion variants from across the general population and biobank cohorts, as well as the control arms of disease databases. The disease cohorts track collects 133 million variants from the affected arms of five disease cohorts. Finally, the genotyping array databases track pools together 14.7 million variants from three array cohorts. These aggregate tracks alongside each of the cohort tracks provide an easy way to compare a variant's frequency across populations, ancestries, and disease cohorts [11–39].

Phased variants

This collection brings together phased variant databases from several sources, including Mexico Biobank, the Human Genome Diversity Project (HGDP), gnomAD, the Simons Genome Diversity Project, and several others. While similar to the SNV Frequencies data, the phased variants have the advantage of allowing users to determine similarity between samples and understand how different loci are inherited [11, 28, 32, 40–42].

Gene2Phenotype

This track displays data from the Gene2Phenotype (G2P) project at EBI, which provides expert-curated gene–disease models that link gene loci to specific disease phenotypes. Alongside our OMIM and GenCC [43] data tracks, the G2P data track can provide genetic counselors and clinical geneticists with a high-level starting point for exploring curated gene–disease associations [8, 9].

Ancient hominids

This collection of two tracks from the Archaic Sequence Hub (ArcSeqHub) group remaps high-quality Altai Neanderthal and Denisovan sequencing data to the hg38/GRCh38 genome assembly. From the remapped data, ArcSeqHub has identified sequence variants, highlighting those different from the human reference genome, and, as such, users can check if a newly identified variant derives from one of these ancient genomes [44].

Regulation tracks

The Genome Browser also provides access to many regulation tracks. These tracks cover a wide range of data, from ATAC-seq to DNase and histone marks to summary tracks that merge these different modalities. These tracks can assist users with identifying regulatory regions in the genome, such as promoters or enhancers. A clinical geneticist could use such regulatory elements to determine how a new variant might affect the expression of a downstream or distal gene. Different data tracks in this group can be combined to understand the potential regulatory role of a region and what gene it may regulate. For example, Fig. 2 shows a selection of these new tracks a user might combine to understand the effect of mutations on the TERT promoter. Here, we highlight five new tracks of regulatory data.

ENCODE cCREs

These tracks annotate candidate cCREs generated by the ENCODE Project Phase 4. Data from across all four ENCODE phases was integrated to annotate regions of the genome as

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Table 1. New Tracks in 2026

Data track title	Category	Short description	Assemblies
SNV Frequencies*		Collection of 34 variant tracks from national projects and other sequencing projects and three aggregate tracks	hg38
Phased variants*	Variation	Phased variants from HGDP, gnomAD, and more	hg38, hg19
Ancient hominids*	Variation	Altai Neanderthal and Denisova variants	hg38
gnomAD MPC	Variation	Identifies missense-depleted regions that are enriched for ClinVar pathogenic variants	hg19
gnomAD coverage	Variation	Shows how many times genomic and exomic regions were sequenced	hg38, hg19
Tandem repeat variation	Variation	Collection of tracks displaying population-level variation at tandem repeat loci	hg38
CoLoRSdb variants	Variation	Single nucleotide and structural variants derived from PacBio long-reads from CoLoRSdb	hg38, T2T-CHM13v2 (hs1)
EVA SNP release 8	Variation	SNP database covering non-human organisms	Over 40 assemblies
Varaico variants and varaico variants (suppl)	Variation	Variants mined from full-text publications and, now, from publication supplemental files	hg38, hg19
Gene2Phenotype*	Phenotype	Displays expert-curated gene–disease models, linking genes to specific disease phenotypes	hg38, hg19
Pubtator	Phenotype	Variants from PubMed abstracts, PMC Open Access publications, and other full-text articles	hg38, hg19
PrimateAI-3D	Phenotype	Predicts the pathogenicity of all possible missense variants in the human genome	hg38, hg19
PromoterAI	Phenotype	Predicts expression impact of SNVs in gene promoter regions	hg38
SpliceAI wildtype	Phenotype	Shows splice prediction scores for the genome itself without variants	hg38
popEVE	Phenotype	A proteome-wide missense deleteriousness model built on EVE and calibrated with human population data	hg38
EVE scores	Phenotype	Applies an evolutionary model to predicting the effect of missense variants	hg38
ClinPred	Phenotype	Machine-learning prediction of missense variant effects combining existing pathogenicity scores with gnomAD frequencies	hg38, hg19
MPRAs*	Regulation	Results of MPRAs to measure the regulatory activity of genomic regions	hg38
MethBase2*	Regulation	Methylation profiles from uniformly processed SRA data	hg38
Human methylation atlas	Regulation	Genome-wide methylation profiles across 39 human cell types	hg38, hg19
JASPAR 2026 update	Regulation	Genome-wide transcription binding site predictions based on curated binding profiles	hg38, mm39, and more
ENCODE cCREs*	Regulation	Cis-regulatory elements identified using data from all ENCODE phases	hg38
ENCODE4 regulation*	Regulation	Summary and individual tracks of DNase-seq, ChIP-seq, and ATAC-seq data	hg38
EpigenCentral	Regulation	Collection of CpG probes from published DNA methylation signatures associated with genetic disorders	hg38
NMD escape*	Regulation/genes	Regions containing premature termination codons predicted to escape NMD and be translated	hg38
Non-canonical ORFs	Genes	Collects databases of ORFs that fall outside annotated protein−coding genes	hg38
recount3*	RNA	Uniformly reprocessed RNA-seq data and metadata from SRA, GTEx, and more	hg38, mm10
ENCODE expression*	RNA/expression	Mouse ENCODE developmental time course RNA-seq expression	mm39, mm10

A full list of the data tracks released on the UCSC Genome Browser in 2026. Tracks are labeled with their broad category, e.g. "Variation," a short description, and what assemblies the track is available for. Tracks marked with a * are discussed in the body of the paper.

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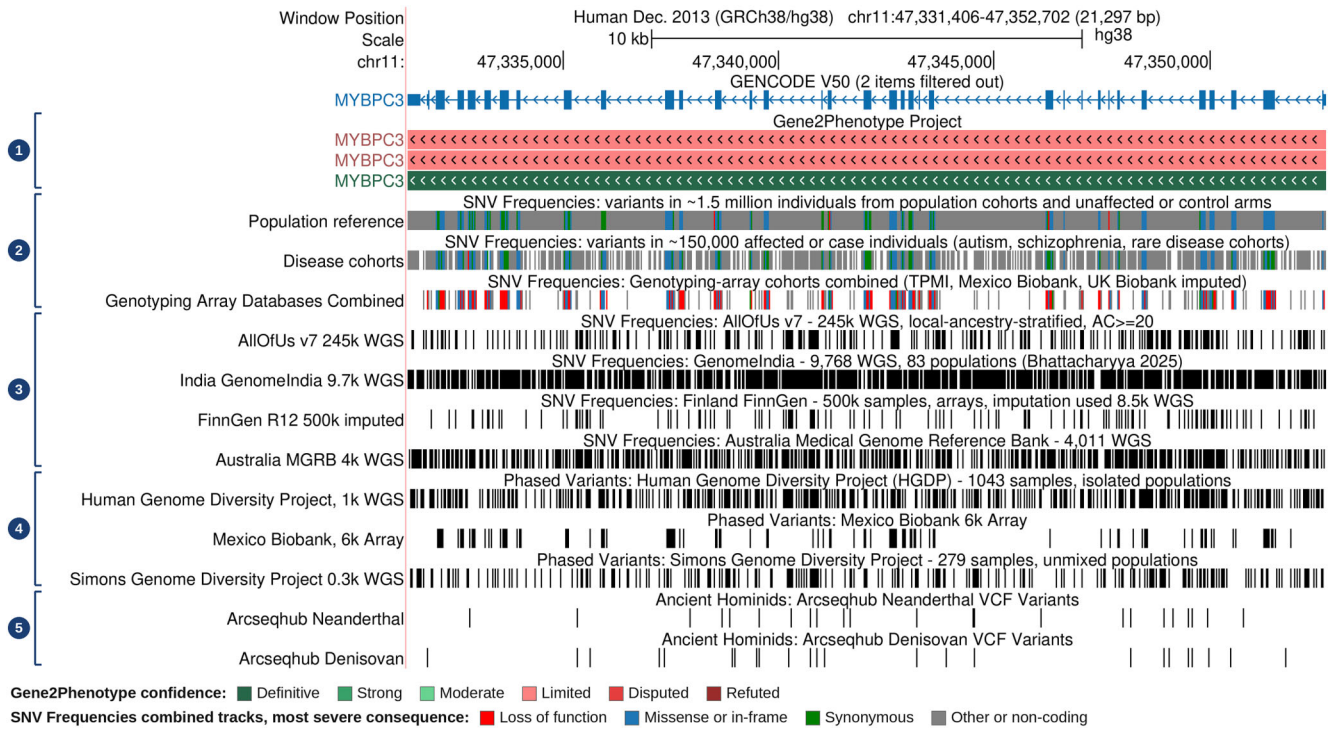


Figure 1. New variation and phenotype tracks on hg38. The "MYBPC3" gene (chr11:47 331 406–47 352 702) with the GENCODE V50 gene model at the top. Numbered brackets correspond to the items below, and the color key is given beneath the image. (1) Gene2Phenotype (G2P) gene–disease records for "MYBPC3," one item per record, colored by the curators' confidence in the association: hypertrophic cardiomyopathy (definitive), and dilated cardiomyopathy and arrhythmogenic right ventricular cardiomyopathy (both limited). The disease name, allelic requirement, variant consequence, molecular mechanism, and supporting publications are shown on mouseover and on the details page opened by clicking an item. (2) The three combined SNV Frequencies tracks, which pool variants from population cohorts and the unaffected arms of disease studies (population reference), from affected individuals in disease cohorts, and from genotyping-array cohorts. In this display mode each vertical line is one variant, colored by its most severe predicted consequence. (3) Four of the individual cohort tracks in the SNV Frequencies collection (All of Us, GenomeIndia, FinnGen, and the Australian Medical Genome Reference Bank), in which each line marks a variant reported by that cohort. For the tracks in (2) and (3), allele counts and frequencies are shown on mouseover or on the details page of a variant, and at base-level zoom the alleles are drawn directly. (4) Three Phased Variants collections (HGDP, Mexico Biobank, and the Simons Genome Diversity Project), which can also display the phased haplotypes of individual samples. (5) The Ancient Hominids tracks, marking positions at which the Altai Neanderthal and Denisovan sequences, remapped to hg38 by ArcSeqHub, differ from the reference genome. The view can be reproduced from the session https://genome.ucsc.edu/s/mspeir/GBUpdate2026_Fig1.

promoter-like, proximal or distal enhancer-like, and more. The ENCODE4 cCREs subtrack combines chromatin accessibility and ChIP-seq across thousands of biosamples, while the ENCODE4 cCREs Core Collection provides the biosample-specific signals and annotations. Since these cCREs tracks integrate several different assays, they can provide users with a high-level understanding of the regulatory potential of a given region [45, 46].

ENCODE4 Regulation

This collection of 10 tracks contains DNase, ATAC, H3K4me3, H3K27ac, CTCF, and Transcription data for numerous organs. For example, the layered DNase track averages this data across 41 organs, while the layered H3K27ac track averages across 38 organs. Beyond this, container tracks allow users to visualize the thousands of underlying DNase, ATAC, Histone, CTCF, RNA-seq, and ChIP-seq tracks used to create the layered visualizations. Alongside the cCREs, these provide a comprehensive view of the biochemical activity of the human genome [45, 46].

MPRAs

This collection of two MPRA tracks hosts data from two databases: MPRAbase and MPRAVarDB. MPRAs measure the activity of thousands of candidate regulatory elements using high-throughput methods. The MPRAbase track collects tested enhancer elements from ten reporter assays across six cell lines (HepG2, HUES64, mESC, NPC, HEK293FT, and UACC903). Alongside this, the MPRAVarDB track shows the impact of a single-nucleotide variant in a regulatory element relative to its wild-type sequence for nearly 240 000 curated variants across >30 cell lines and several different diseases or traits [47, 48].

MethBase2

This collection displays DNA methylation profiles for thousands of public data sets from the NCBI Sequence Read Archive (SRA) database, all analyzed uniformly by the Smith Lab at the University of Southern California (USC), Los Angeles, and verified to meet data quality criteria. Each entry in the collection includes a "levels" track with single-CpG methylation levels and a "reads" track to indicate the amount of data informing each genomic locus. The MethBase2 interface includes controls to search methylomes according to their accompanying metadata in SRA. This means a user could filter down these thousands of tracks to those for their specific set of tissues or conditions and understand genomic methylation states across these [49].

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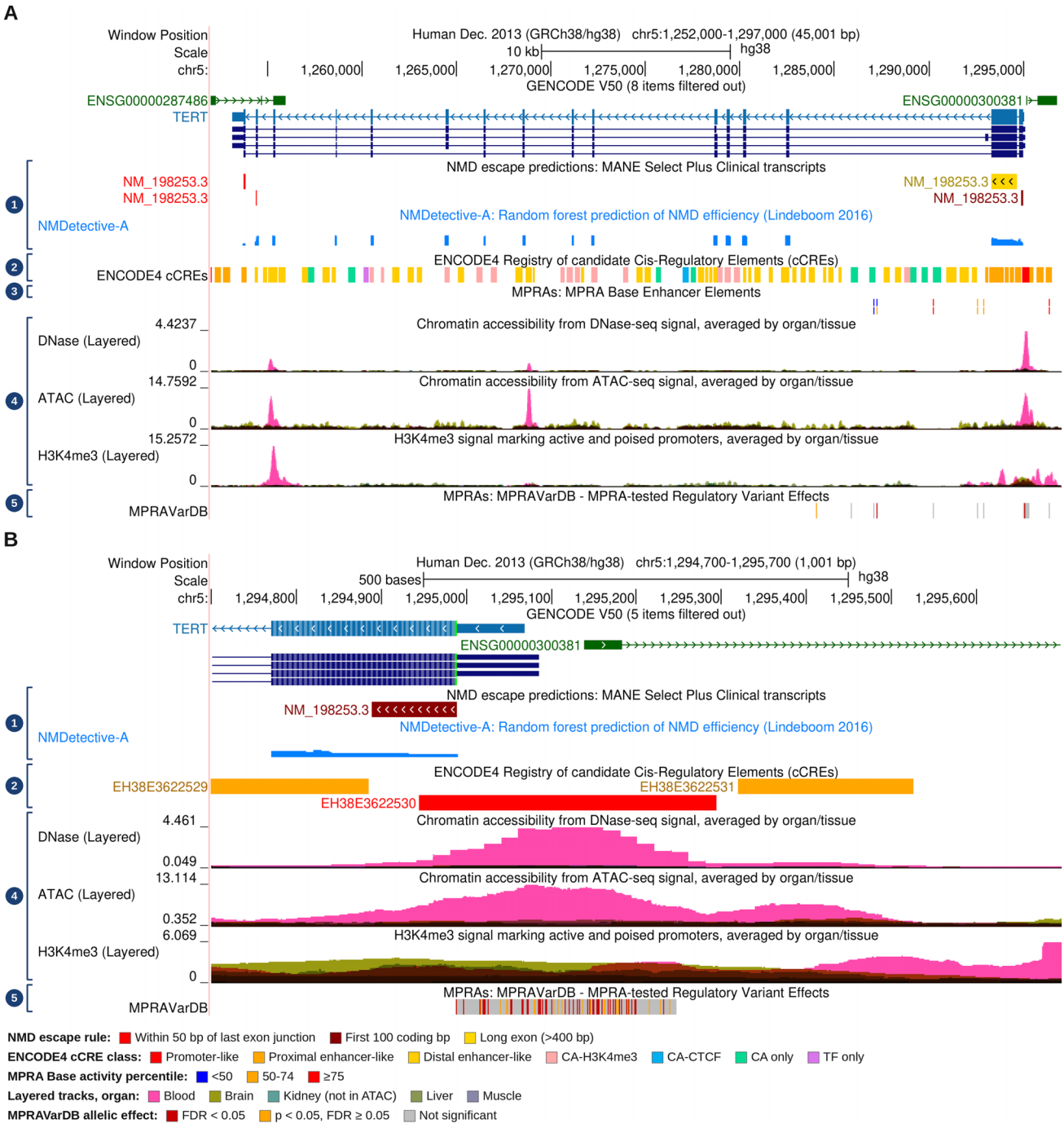


Figure 2. New regulation tracks on hg38. Numbered brackets correspond to the items below, and the color key is given beneath panel (B). (**A**) The "TERT" gene (chr5:1 252 000–1 297 000) with GENCODE V50 gene models. (1) Nonsense-mediated decay (NMD) Escape predictions for the MANE Select transcript NM_198253.3, marking the coding regions in which a premature termination codon is predicted to escape NMD, colored by the rule that applies; below it, the NMDetective-A score gives the predicted NMD efficiency for a premature stop codon at each coding position. (2) ENCODE4 candidate *cis*-regulatory elements (cCREs), colored by element class. (3) Massively Parallel Reporter Assay (MPRA) Base enhancer elements tested by lentiviral MPRA in HEK293FT and UACC903 cells, colored by activity percentile within each experiment. (4) Three of the 10 ENCODE4 Regulation layered tracks (DNase, ATAC, and H3K4me3). Each track overlays the mean signal for each organ in its own semi-transparent color; the five organs shown by default are blood, brain, kidney, liver, and muscle (no kidney ATAC data are available), and other organs can be selected on the track settings page. (5) MPRAVarDB variants with regulatory effects measured by MPRA, colored by statistical significance. Item details are shown on mouseover and on the details page opened by clicking an item: for MPRA Base, the cell line, assay, activity score, and citation; for MPRAVarDB, the alleles, cell line, $\log_2$ fold change, *P*-value, and false discovery rate (FDR). (**B**) The "TERT" promoter (chr5:1 294 700–1 295 700). The promoter-like cCRE EH38E3622530 (red) coincides with the DNase and ATAC peaks, which are highest in blood (pink); H3K4me3 signal in blood is highest immediately upstream of it. MPRAVarDB contains 3896 entries across 259 consecutive positions in this window (chr5:1 294 989–1 295 246); 1464 of them have an FDR below 0.05. The views can be reproduced from the sessions https://genome.ucsc.edu/s/mspeir/GBUpdate2026_Fig2A and https://genome.ucsc.edu/s/mspeir/GBUpdate2026_Fig2B.

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NMD escape

These two groups of tracks display regions where premature termination codons are expected to escape nonsense-mediated mRNA decay (NMD), a cellular mechanism that normally degrades transcripts with such premature stop codons. The NMD Escape tracks contain predictions of such premature stop codons in transcripts from MANE Select Plus Clinical [50], GENCODE v49 [51], and NCBI RefSeq [4] based on several published rules. NMDetective is a set of machine-learning tracks providing an NMD score for every possible premature termination codon. These tracks can help clinical geneticists interpret the clinical significance of truncating variants, which is important under the ACMG/AMP PVS1 criterion [52–55].

Transcriptome and expression

Finally, we added two new tracks displaying tissue-specific gene expression and RNA-seq-driven transcript structure.

ENCODE expression for mouse

This set of tracks from the Wold lab at Caltech displays RNA-seq expression for 17 tissues across eight time points in mouse embryos. Expression signal tracks are provided alongside the primary visualization of expression bar charts. Together, these tracks can aid users in identifying how a specific gene might be differentially expressed in a specific tissue across different time points. These tracks are available for the GRCm39/mm39 and GRCm38/mm10 assemblies [56].

recount3

The recount3 project has uniformly reprocessed and reanalyzed the RNA-seq data from several sources, including the NCBI SRA database and NIH's Genotype-Tissue Expression (GTEx) project. The recount3 track focuses on identifying introns in the RNA-seq data from these sources. Thus, a user could combine them with the ENCODE Regulation tracks above to understand how splicing might reflect regulatory differences in different biosamples. On the GRCh38/hg38 human assembly, there are intron tracks for GTEx, TCGA, SRA, and CCLE, while on the GRCm38/mm10 mouse assembly, only SRA introns are available [57, 58].

Feature updates

The Browser provides several features that allow users to manipulate, intersect, and export data from our databases as well as visualize their own data alongside what we host. The first two subsections describe two new, individual features: first the new QuickLift feature for transferring annotations between assemblies, and then additions to our free data-hosting service HubSpace. The next two subsections describe new improvements to existing features, specifically adjustments to assembly search, data track discovery and management, and greater customization of the primary visualization.

QuickLift

Genomic annotations are mapped to specific assemblies (e.g. GRCh38 or GRCm39), and some databases may never reannotate their data on a new assembly, meaning useful data can be stuck on older assembly releases. The QuickLift feature, released in full this year, addresses this by allowing users to remap genomic features between genome assemblies during a browsing session. Users can now move to a newer assembly and lift over preferred annotation tracks, whether personal data or publicly available tracks only mapped to an older assembly. This new feature can be found under "View" > "In Other Genomes (Convert)." Once there, users can select which of the currently visible tracks they would like to lift to the new assembly.

Alongside this, we added a request form for creating LiftOver files (https://genome.ucsc.edu/liftRequest.html). First, a user must log into their Genome Browser account, then enter the two assemblies for which they want a LiftOver file. If the alignment already exists, it provides links to the existing files. Otherwise, the system will then generate the LiftOver file and notify the requester at the email associated with the account that the new files are available both on our download servers and in the web-based LiftOver tool.

HubSpace

UCSC Track Hubs allow any user to create Genome Browser tracks, using all the options available for our "native" tracks, but track hubs require a web server to store the data. Certain custom track types, bigBed, bigWig, and other "big" types, also require the data to be hosted on a web server. Our HubSpace service provides users with 10 GB of free storage for genomic data. We made several notable improvements to the HubSpace service over the last year. First, we added support for assembly hubs, allowing users to upload their custom assemblies to HubSpace. Second, we added the ability for users to edit their files in place on HubSpace, rather than having to edit these files locally and re-upload them. Alongside this new editing ability, we added an interface to recommend features a user might wish to enable for their track. Users can contact us at genome-www@soe.ucsc.edu to increase their storage limit.

Improved genome assembly and track management

The number of genome assemblies in the UCSC Genome Browser has expanded over the last few years, particularly with the introduction of our GenArk Repository, to cover over 50 000 genomes from mammals to bacteria and plants. Our GenArk Repository uses our track hub infrastructure to provide access to genome assemblies from GenBank and RefSeq alongside a limited set of annotations [59]. Since 2016, we have provided a tree view of the available assemblies, but as the number of genome assemblies has expanded, it has been unable to capture the diversity of genomes we host. We replaced this with an improved assembly search box and a list of recently viewed genomes. We also added this new assembly search interface to other tools on our site that require a user to search and select assemblies, including BLAT, isPCR, LiftOver, and our Table Browser.

Beyond assembly discovery, we improved the track management experience through several new features. First, we added a "Visible Tracks" group that collects all the tracks in the current display, allowing users to find and manage those in the display. Second, we added a new "gear" and "x" icon along the left-hand side of the display to allow users to configure the track display settings or quickly hide a specific track. Third, we improved the configuration page for supertracks, which are collections of individual tracks or track containers, making it easier to turn tracks on and off and control the current display settings for subtracks. Fourth, and finally, with the help of the Smith Lab at USC, we created a new faceted track settings page aimed at improving the discovery, selection, and management of tracks within a track collection of hundreds

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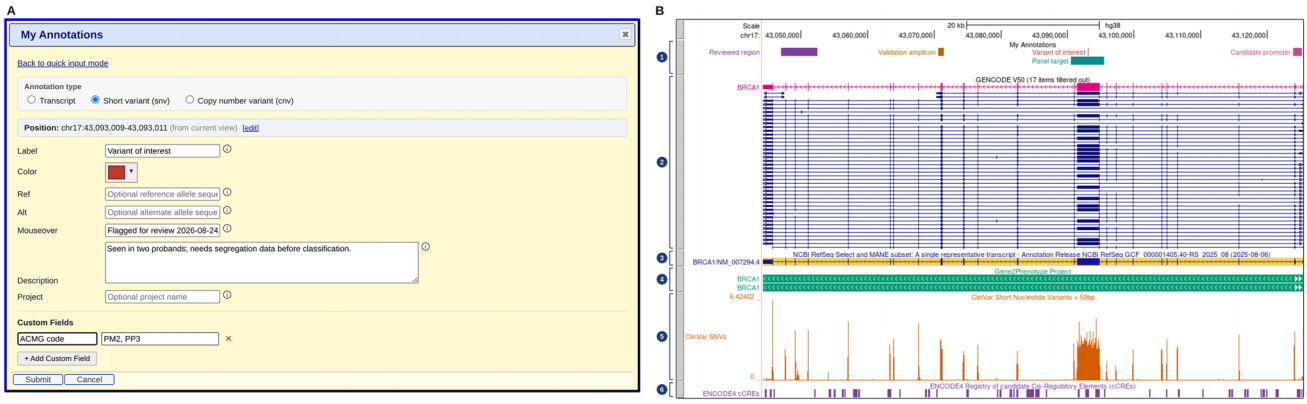


Figure 3. Custom annotations and colors. (**A**) The My Annotations dialog in manual mode, available to users logged in to a Genome Browser account. The annotation type (transcript, short variant, or copy-number variant) determines which fields are offered, and the position is taken from the current view and can be edited. For a short variant, as here, the fields are the item label, color, optional reference and alternate alleles, mouseover text, description, project name, and any number of user-named custom fields. (**B**) The "BRCA1" locus (hg38 chr17:43 044 295–43 125 364) after annotation and recoloring. (1) The My Annotations track, holding five user-created items drawn in the colors assigned to them. (2) GENCODE V50, in which the MANE Select transcript ENST00000357654.9 has been recolored (magenta) with the "Color [item name]" option in the right-click menu. (3) The RefSeq Select and MANE track, in which NM_007294.4 has been given a yellow background highlight in the same way. (4) Gene2Phenotype, (5) ClinVar short variants, and (6) ENCODE4 cCREs, each recolored as a whole with "Change Track Color." At this scale ClinVar contains more variants than can be drawn individually, so the Browser displays it as a density graph in which the *y*-axis gives the mean number of ClinVar variants overlapping each base; the highest density is over exon 10 of "BRCA1," its largest exon. These changes affect only the display, not the underlying data, and are saved with the session.

or thousands of tracks (e.g. the "TF ChIP-seq" track under ENCODE4 Regulation).

Display configurability

While the Genome Browser provides several options for configuring the display, such as selectable fonts or the ability to hide track labels, we added two new features to help users create publication-ready figures: "My Annotations" and custom item coloring.

First, users can create new annotations directly in the Browser using the "My Annotations" feature (Fig. 3). To add a new annotation, users can click the "Add Annotation" below the main visualization or select the "My Annotations" option from the "My Data" menu. This will open a dialog allowing the entry of annotation details like position (which will be pre-filled based on their current location or via item search), label, mouseover, item color, and custom fields. Users can also share their annotations with other Genome Browser users, either by entering specific account names or by leaving this blank to allow anyone with the link to view them. With this feature, users can improve their Genome Browser publication figures by creating custom items as needed, highlighting specific variants, or collaboratively building a custom view.

Second, users can set a custom color for specific items in the display or whole tracks, overriding the default color for that track or track items. To change the color of a track, right-click it and select "Change Track Color" from the menu, then choose the desired color. Users can also change the color of or add a background highlight to a single annotation by instead selecting "Color [annotation name]" from the right-click menu. Together, these features allow users to highlight specific transcripts, variants, tracks, or other items in the Genome Browser display when making a publication figure.

Future updates

Upcoming feature additions aim to make it simpler to find data tracks in the UCSC Genome Browser as well as add the ability to visualize local files. As noted above, there are thousands of tracks on the latest human genome assemblies, with an increasing number added each year. To address data discoverability, we plan to overhaul the data track selection interface. This selection interface would allow users to use keyword searches and an array of tags to filter the increasingly long list of data tracks. Next, we are working closely with the IGV team on integrating the IGV viewer as a parallel display alongside the primary display in the UCSC Genome Browser. This would allow the visualization of local BAM files without needing to upload them to Genome Browser servers or place them in a publicly accessible web location, as is required with data visualized in the Browser via standard methods.

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Conflict of interest

J.C., M.L.S., B.J.R., G.P., L.R.N., C.M.L., A.S.H., J.N.G., C.F., M.D., H.C., G.P.B., D.H., W.J.K., and M.H. receive royalties from the sale of UCSC Genome Browser source code, LiftOver, GBiB, and GBiC licenses to commercial entities. W.J.K. owns Kent Informatics.

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Data availability

The UCSC Genome Browser website and APIs are freely available for all users. Most data files provided by UCSC are also freely available, and much of the Genome Browser source code is provided under the MIT license. See our License page (https://genome.ucsc.edu/license/) for full details. Files can be found on our download server at https://hgdownload.soe.ucsc.edu.

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