UCSC genome browser

UNIVERSITY OF CALIFORNIA SANTA CRUZ Genomics Institute | UCSC **Genome Browser Gateway**

Genomes | Genome Browser | Tools | Mirrors | Downloads | My Data | Projects | Help | About Us

Browse/Select Species

POPULAR SPECIES

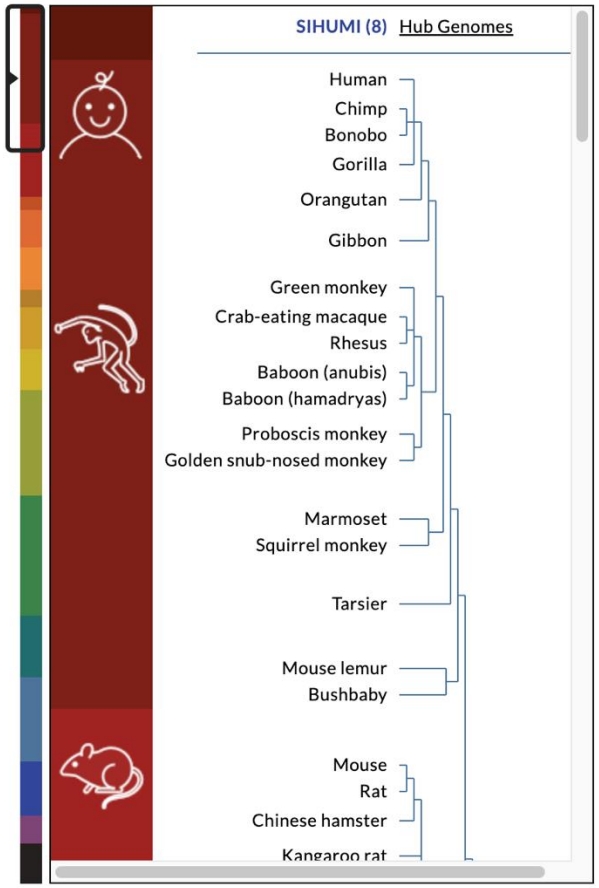
Human | Mouse | Rat | Zebrafish | Fruitfly | Worm | Yeast

Search through thousands of genome browsers

Enter species, common name or assembly ID

Unable to find a genome? Send us a request.

UCSC SPECIES TREE AND CONNECTED ASSEMBLY HUBS



Find Position

SIHUMI Hub Assembly

Escherichia coli

GO

Position/Search Term

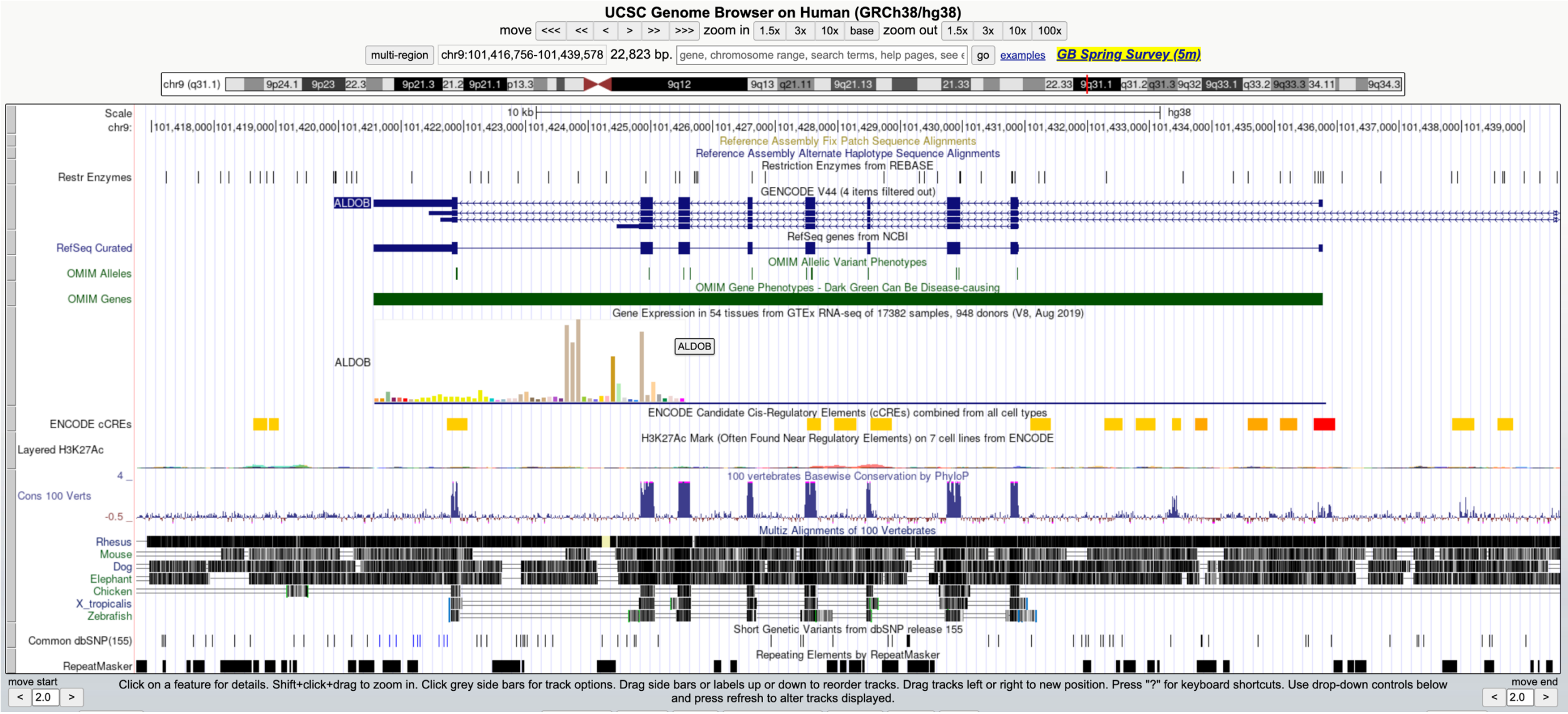
Enter position, gene symbol or search terms

Current position: U00096.3:90,001-110,000

Escherichia coli Genome Browser - ecoli assembly

Organism name: Escherichia coli str. K-12 substr. MG1655 (E. coli)
Infraspecific name: Strain: K-12 substr. MG1655
BioSample: SAMN02604091
BioProject: PRJNA225
Submitter: Univ. Wisconsin
Date: 2013/09/26
Assembly type: na
Assembly level: Complete Genome
Genome representation: full
RefSeq category: reference genome
GenBank assembly accession: GCA_000005845.2 (latest)
RefSeq assembly accession: GCF_000005845.2 (latest)
RefSeq assembly and GenBank assembly identical: yes

https://genome-euro.ucsc.edu/


UCSC Genome Browser on Human (GRCh38/hg38)
move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x
multi-region chr9:101,416,756-101,439,578 22,823 bp. gene, chromosome range, search terms, help pages, see e go examples GB Spring Survey (5m)
chr9 (q31.1) 9p24.1 9p23 22.3 9p21.3 21.2 9p21.1 p13.3 9q12 9q13 q21.11 9q21.13 21.33 22.33 9q31.1 q31.2 q31.3 9q32 9q33.1 q33.2 9q33.3 34.11 9q34.3
Scale
chr9:
10 kb
hg38
101,418,000 101,419,000 101,420,000 101,421,000 101,422,000 101,423,000 101,424,000 101,425,000 101,426,000 101,427,000 101,428,000 101,429,000 101,430,000 101,431,000 101,432,000 101,433,000 101,434,000 101,435,000 101,436,000 101,437,000 101,438,000 101,439,000
Reference Assembly Fix Patch Sequence Alignments
Reference Assembly Alternate Haplotype Sequence Alignments
Restriction Enzymes from REBASE
Restr Enzymes
GENCODE V44 (4 items filtered out)
ALDOB
RefSeq genes from NCBI
RefSeq Curated
OMIM Allelic Variant Phenotypes
OMIM Alleles
OMIM Gene Phenotypes - Dark Green Can Be Disease-causing
OMIM Genes
Gene Expression in 54 tissues from GTEx RNA-seq of 17382 samples, 948 donors (V8, Aug 2019)
ALDOB
ALDOB
ENCODE Candidate Cis-Regulatory Elements (cCREs) combined from all cell types
ENCODE cCREs
H3K27Ac Mark (Often Found Near Regulatory Elements) on 7 cell lines from ENCODE
Layered H3K27Ac
4
100 vertebrates Basewise Conservation by PhyloP
Cons 100 Verts
-0.5
Multiz Alignments of 100 Vertebrates
Rhesus
Mouse
Dog
Elephant
Chicken
X_tropicalis
Zebrafish
Short Genetic Variants from dbSNP release 155
Common dbSNP(155)
Repeating Elements by RepeatMasker
RepeatMasker
move start
< 2.0 >
Click on a feature for details. Shift+click+drag to zoom in. Click grey side bars for track options. Drag side bars or labels up or down to reorder tracks. Drag tracks left or right to new position. Press "?" for keyboard shortcuts. Use drop-down controls below and press refresh to alter tracks displayed.
move end
< 2.0 >

collapse all | track search | highlight | hide all | add custom tracks | configure | reverse | resize | expand all

Mapping and Sequencing

refresh

Base Position: dense	P14 Fix Patches: pack	P14 Alt Haplotypes: pack	Assembly: hide	Centromeres: hide	Chromosome Band: hide	Clone Ends: hide	Exome Probesets: hide
FISH Clones: hide	Gap: hide	GC Percent: hide	GRC Contigs: hide	GRC Incident: hide	Hg19 Diff: hide	INSDC: hide	LiftOver & ReMap: hide
LRG Regions: hide	Mappability: hide	Problematic Regions: hide	Recomb Rate: hide	RefSeq Acc: hide	Restr Enzymes: dense	Scaffolds: hide	Short Match: hide
STS Markers: hide							

Genes and Gene Predictions

refresh

GENCODE V44: pack	NCBI RefSeq: dense	CCDS: hide	CRISPR Targets: hide	Updated GENCODE Versions: hide	HGNC: hide	IKMC Genes Mapped: hide	LRG Transcripts: hide
MANE: hide	MGC Genes: hide	Non-coding RNA: hide	Old UCSC Genes: hide	ORFeome Clones: hide	Other RefSeq: hide	Pfam in GENCODE: hide	Prediction Archive: hide
RetroGenes V9: hide	TransMap V5: hide	UCSC Alt Events: hide	UniProt: hide				

Phenotype and Literature

refresh

OMIM Alleles: dense	COVID Rare Harmful Var: hide	New AbSplice Scores: hide	CADD: hide	Cancer Gene Expr: hide	ClinGen: hide	ClinGen CNVs: hide	ClinVar Variants: hide
Constraint scores: hide	Coriell CNVs: hide	COSMIC: hide	COSMIC Regions: hide	DECIPHER CNVs: hide	DECIPHER SNVs: hide	Development Delay: hide	New Dosage Sensitivity: hide
GenCC: hide	Gene Interactions: hide	GeneReviews: hide	GWAS Catalog: hide	HGMD public: hide	LOVD Variants: hide	OMIM Cyto Loci: hide	OMIM Genes: dense
Orphanet: hide	PanelApp: hide	REVEL Scores: hide	SNPedia: hide	TCGA Pan-Cancer: hide	UniProt Variants: hide	Updated Variants in Papers: hide	

Human Pangenome - HPRC

refresh

New Multiple Alignment: hide	New Pairwise Alignments: hide	New Rearrangements: hide	New Short Variants: hide

Single Cell RNA-seq

refresh

Blood (PBMC) Hao: hide	Colon Wang: hide	Cortex Velmeshev: hide	Cross Tissue Nuclei: hide	Fetal Gene Atlas: hide	Heart Cell Atlas: hide	Ileum Wang: hide	Kidney Stewart: hide
Liver MacParland: hide	Lung Travaglini: hide	Merged Cells: hide	Muscle De Micheli: hide	Pancreas Baron: hide	Placenta Vento-Tormo: hide	Rectum Wang: hide	Skin Sole-Boldo: hide
Tabula Sapiens: hide							

mRNA and EST

refresh

Human ESTs: hide	Human mRNAs: hide	Other ESTs: hide	Other mRNAs: hide	SIB Alt-Splicing: hide	Spliced ESTs: hide

Expression

refresh

GTEx Gene V8: pack	GTEx RNA-Seq Coverage: hide	Affy Archive: hide	EPDnew Promoters: hide	GNF Atlas 2: hide	GTEx Gene: hide	GTEx Transcript: hide	GWIPS-viz Riboseq: hide
miRNA Tissue Atlas: hide							

Regulation

refresh

ENCODE cCREs: dense	ENCODE Regulation: show	CpG Islands: hide	New FANTOM5: hide	GeneHancer: hide	GTEx cis-eQTLs: hide	Hi-C and Micro-C: hide	Updated JASPAR Transcription Factors: hide
ORegAnno: hide	RefSeq Func Elems: hide	ReMap ChIP-seq: hide	VISTA Enhancers: hide				

Comparative Genomics

refresh

Conservation: full	Cactus 241-way: hide	Cons 30 Primates: hide	Primate Chain/Net: hide	Placental Chain/Net: hide	Vertebrate Chain/Net: hide	Cactus 447-way: hide	CHM13 alignments: hide
Multiz 470-way: hide							

Variation

refresh

dbSNP 155: pack	COVID GWAS v4: hide	COVID GWAS v3: hide	1000G Archive: hide	Updated Array Probesets: hide	dbSNP Archive: hide	dbVar Common Struct Var: hide	DGV Struct Var: hide
Genome In a Bottle: hide	Updated gnomAD Variants: hide	Platinum Genomes: hide					

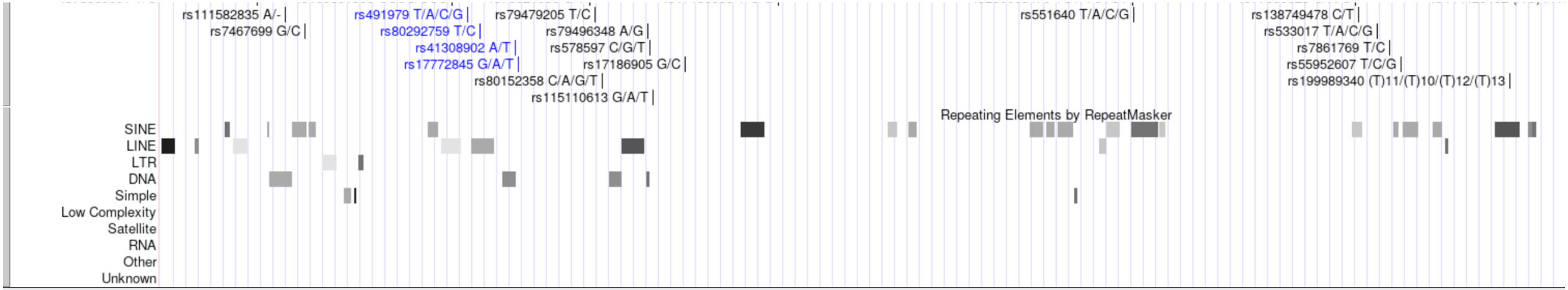
Repeats

refresh

RepeatMasker: dense	Interrupted Rpts: hide	Microsatellite: hide	RepeatMasker Viz.: hide	Segmental Dups: hide	Self Chain: hide	Simple Repeats: hide	WM + SDust: hide

Tons of pre-loaded annotations!

- Genes annotations
- Conservation scores
- Alignments with other species
- SNPs
- Expression profile across tissues for genes
- And many more



nove start
< 2.0 >

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collapse all track groups

collapse all | track search | highlight | hide all | add custom tracks | configure | reverse | resize | expand all

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Add Custom Tracks

clade Mammal genome Human assembly Dec. 2013 (GRCh38/hg38)

Display your own data as custom annotation tracks in the browser. Data must be formatted in bigBed, bigBarChart, bigChain, bigGenePred, bigInteract, bigLolly, bigMaf, bigPsl, bigWig, BAM, barChart, VCF, BED, BED detail, bedGraph, broadPeak, CRAM, GFF, GTF, hic, interact, MAF, narrowPeak, Personal Genome SNP, PSL, or WIG formats.

- You can paste just the URL to the file, without a "track" line, for bigBed, bigWig, bigGenePred, CRAM, BAM and VCF.
- To configure the display, set track and browser line attributes as described in the User's Guide.
  Examples are here. If you do not have web-accessible data storage available, please see the Hosting section of the Track Hub Help documentation.

Please note a much more efficient way to load data is to use Track Hubs, which are loaded from the Track Hubs Portal found in the menu under My Data.

Paste URLs or data: Or upload: Choose file No file chosen Submit

Clear

Optional track documentation: Or upload: Choose file No file chosen

Clear

Click here for an HTML document template that may be used for Genome Browser track descriptions.

Add the HCC1143 bam file

- Just paste the amazon link in the input field (it also needs a bai index file, in this case it will find it as it exists in the same online repository)
- Then go to chr21:19,000,000-20,000,000
- Explore the reads alignment
- A cleaner way to do it is to add metadata, such as

track type=bam name="HCC1143 normal" bigDataUrl=https://ngs-introduction-training.s3.eu-central-1.amazonaws.com/HCC1143.normal.21.19M-20M.bam

Add the HCC1143 bam file (2)

- Check if dbSNP is displayed, then find rs3827160
- It’s also possible to visualize the LTR and the deletion region as in the GenomeBrowser exercice (chr21:19,800,320-19,818,162)

Bed files are a simple way to specify coordinates

- A basic bed file contains chromosome, start, end
- They are often used as output of an analysis, eg methylation regions
- As a test, try manual input of the deletion: chr21:19,326,851-19,329,106

The syntax for a bed file in the UCSC genome browser is

track name=Deletion description="Deletion, manual input" useScore=1

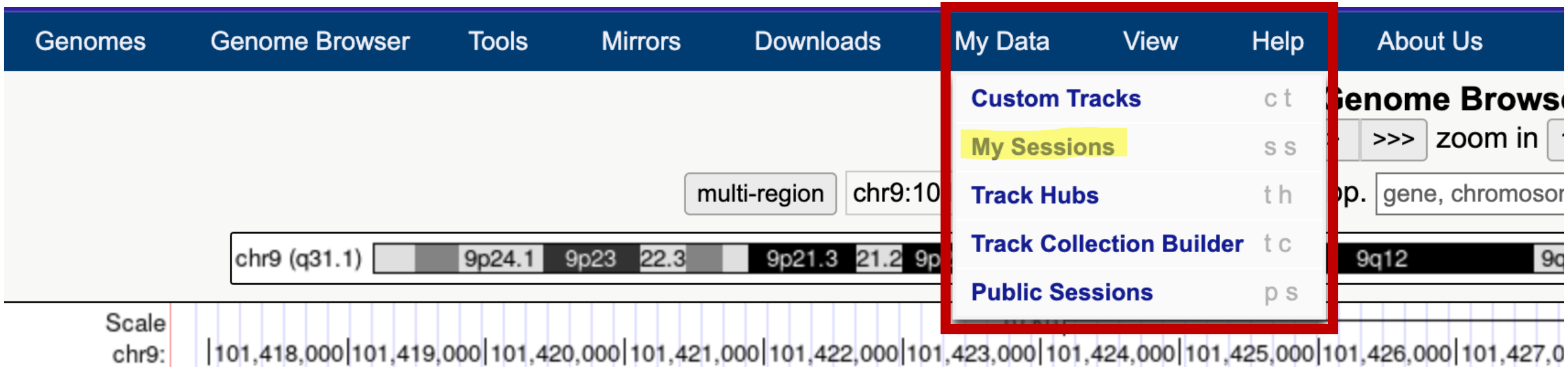
chr21 19326851 19329106

- Reference a bed file
  - https://github.com/fburdet/UCSC/raw/refs/heads/main/test.bed

Other formats commonly used

- bigBed: compressed bed files
- bigWig: coordinates with specific intensities, indexed
- vcf: used for variants data

Save and share session



Welcome fburdet

Your Account Information

Username: fburdet

Change password

Sign out

Session Management

See the Sessions User's Guide for more information about this tool. See the Session Gallery for example sessions.

Click here to reset the browser user interface settings to their defaults.

My Sessions

Show 10 entries Search:

session name (click to load)	created on	assembly	view/edit details	delete this session	share with others?	post in public listing?	send to mail
mm10_Miki_OCT2015_edited	2015-10-12	mm10	view/edit	delete	☑	☐	Email
mm10_Miki_OCT2015	2015-10-12	mm10	view/edit	delete	☑	☐	Email
mm10_3_datasets_merged_candidates	2015-09-24	mm10	view/edit	delete	☑	☐	Email
mm10_3_datasets_merged	2015-09-17	mm10	view/edit	delete	☑	☐	Email
mm10_Miki_ROSE_2rep	2015-09-08	mm10	view/edit	delete	☑	☐	Email
mm10_Miki_ROSE	2015-08-27	mm10	view/edit	delete	☑	☐	Email
mm10_Miki_TE_SE_normalized_size	2015-08-10	mm10	view/edit	delete	☑	☐	Email
mm10_Miki_TE_SE	2015-08-07	mm10	view/edit	delete	☑	☐	Email
mm10_merge_SE	2015-08-03	mm10	view/edit	delete	☑	☐	Email
mm10_miki_chippart_clean_3TP	2015-07-21	mm10	view/edit	delete	☑	☐	Email

Showing 1 to 10 of 33 entries Previous 1 2 3 4 Next

Save Settings

Save current settings as named session:

name: hg38 ☑ allow this session to be loaded by others submit

Save current settings to a local file:

file: file type returned: ◉ plain text ○ gzip compressed (ignored if output file is blank) submit

(leave file blank to get output in browser window)

Next step: hubs!

IGV vs UCSC genome browser

IGV

- Suitable for any genome
- Need to install it on each computer
- Files on local computer can be very big (mammal bam files)
- Not easy to share sessions
- No need for a file server
- Less available annotations

UCSC

- Genome must exist
- No local install or space needed
- Easy to share sesions with link and sessions
- Easier to manage if you have several custom annotations
- Need a file server for own tracks
- Tons of pre-loaded annotations

Bonus slides

Example: get bed & bigBed for 1 gene

```
wget https://ftp.ebi.ac.uk/pub/databases/gencode/Gencode_human/release_45/gencode.v45.annotation.gff3.gz

gzip -d gencode.v45.annotation.gff3.gz

grep ENST00000647789 gencode.v45.annotation.gff3 | grep exon | cut -f1,4,5 > ALDOB.bed

./fetchChromSizes hg38 > hg38.chromSize

sort -k1,1 -k2,2n ALDOB.bed > ALDOB.sorted.bed

./bedToBigBed ALDOB.sorted.bed hg38.chromSize ALDOB.bb
```

Example: bam to bigWig

```
samtools view -H DP003.merged.bam > DP003.T2D.ALDOB.sam
samtools view DP003.merged.bam "chr9:101420000-101437000" >> DP003.T2D.ALDOB.sam
samtools view -bS DP003.T2D.ALDOB.sam > DP003.T2D.ALDOB.bam
samtools index DP003.T2D.ALDOB.bam
bamCoverage -b DP003.T2D.ALDOB.bam -o DP003.T2D.ALDOB.bw
```