

UCSC Genome/Table Browser

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<http://sschmeier.github.io/bioinf-workshop/>

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UCSC Genome/Table browser

- Look at genes of interest and their genomic context
- Put your data into context of other publicly available data
- Easy download of public available data

UCSC Genome Bioinformatics

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About the UCSC Genome Bioinformatics Site

Welcome to the UCSC Genome Browser website. This site contains the reference sequence and working draft assemblies for a large collection of genomes. It also provides portals to [ENCODE](#) data at UCSC (2003 to 2012) and to the [Neandertal](#) project. Download or purchase the Genome Browser source code, or the Genome Browser in a Box ([GBiB](#)) at our [online store](#).

We encourage you to explore these sequences with our tools. The [Genome Browser](#) zooms and scrolls over chromosomes, showing the work of annotators worldwide. The [Gene Sorter](#) shows expression, homology and other information on groups of genes that can be related in many ways. [Blat](#) quickly maps your sequence to the genome. The [Table Browser](#) provides convenient access to the underlying database. [VisiGene](#) lets you browse through a large collection of *in situ* mouse and frog images to examine expression patterns. [Genome Graphs](#) allows you to upload and display genome-wide data sets.

The UCSC Genome Browser is developed and maintained by the Genome Bioinformatics Group, a cross-departmental team within the [UC Santa Cruz Genomics Institute](#) at the University of California Santa Cruz ([UCSC](#)). If you have feedback or questions concerning the tools or data on this website, feel free to contact us on our [public mailing list](#).

The Genome Browser project team relies on public funding to support our work. Donations are welcome -- we have many more ideas than our funding supports! If you have ideas, drop a comment in our [suggestion box](#).

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Mouse (*Mus musculus*) Genome Browser Gateway

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group	genome	assembly	position	search term
Mammal	Mouse	July 2007 (NCBI37/mm9)	chr12:57,795,963-57,815,592	enter position, gene symbol or search terms

[Click here to reset](#) the browser user interface settings to their defaults.

[track search](#) [add custom tracks](#) [track hubs](#) [configure tracks and display](#)

Mouse Genome Browser – mm9 assembly ([sequences](#))

The July 2007 mouse (*Mus musculus*) genome data were obtained from the Build 37 assembly by [NCBI](#) and the [Mouse Genome Sequencing Consortium](#). For more information about this assembly, see [MGSCv37](#) in the NCBI Assembly database.

Sample position queries

A genome position can be specified by the accession number of a sequenced genomic region, an mRNA or EST, a chromosomal coordinate range, or keywords from the GenBank description of an mRNA. The following list shows examples of valid position queries for the Mouse genome. See the [User's Guide](#) for more information.



Mus musculus
(Photo courtesy of [The Jackson Laboratory](#))



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group	genome	assembly	position	search term
Mammal	Mouse	July 2007 (NCBI37/mm9)	chr12:57,795,963-57,815,592	enter position, gene symbol or search terms

Choose species and genome built
[Click here to reset the browser user interface settings to their defaults.](#)

[track search](#) [add custom tracks](#) [track hubs](#) [configure tracks and display](#)

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Mus musculus
(Photo courtesy of [The Jackson Laboratory](#))

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group	genome	assembly	position	search term
Mammal	Mouse	July 2007 (NCBI37/mm9)	chr12:57,795,963-57,815,592	enter position, gene symbol or search terms

[Click here to reset](#) the browser user interface settings to their defaults.

[track search](#) [add custom tracks](#) [track hubs](#) [configure tracks and display](#)

Choose the genome location you want to visualise

Mouse Genome Browser – mm9 assembly ([sequences](#))

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Mus musculus
(Photo courtesy of [The Jackson Laboratory](#))

UCSC Genome Browser on Mouse July 2007 (NCBI37/mm9) Assembly

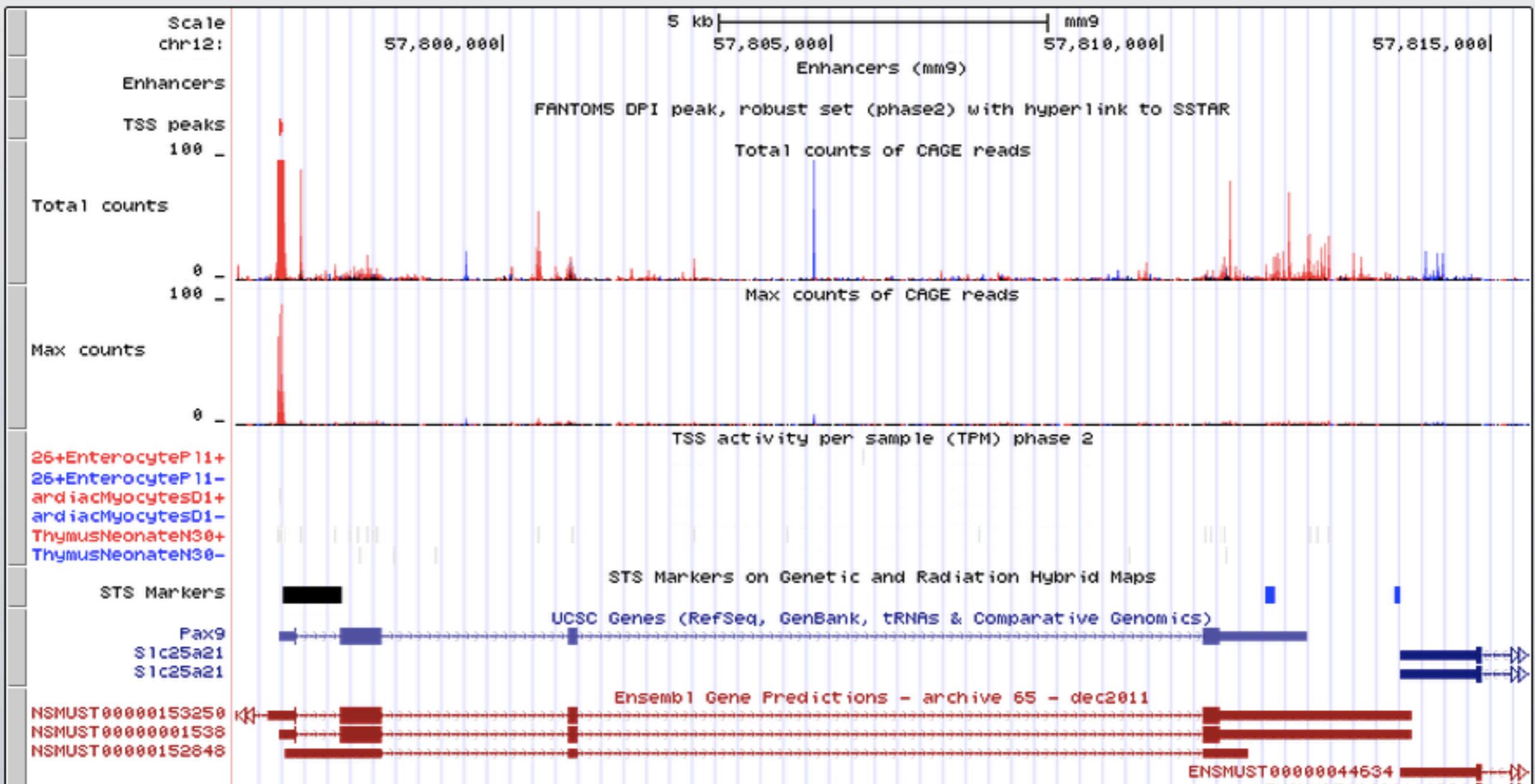
move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr12:57,795,963-57,815,592 19,630 bp.

enter position, gene symbol or search terms

go

chr12 (qC1) 12qA1.1 qA2 12qA3 qB1 12qB3 12qC1 qC2 12qC3 qD1 D2 12qD3 12qE 12qF1 qF2



UCSC Genome Browser on Mouse July 2007 (NCBI37/mm9) Assembly

move <<< << < > >> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

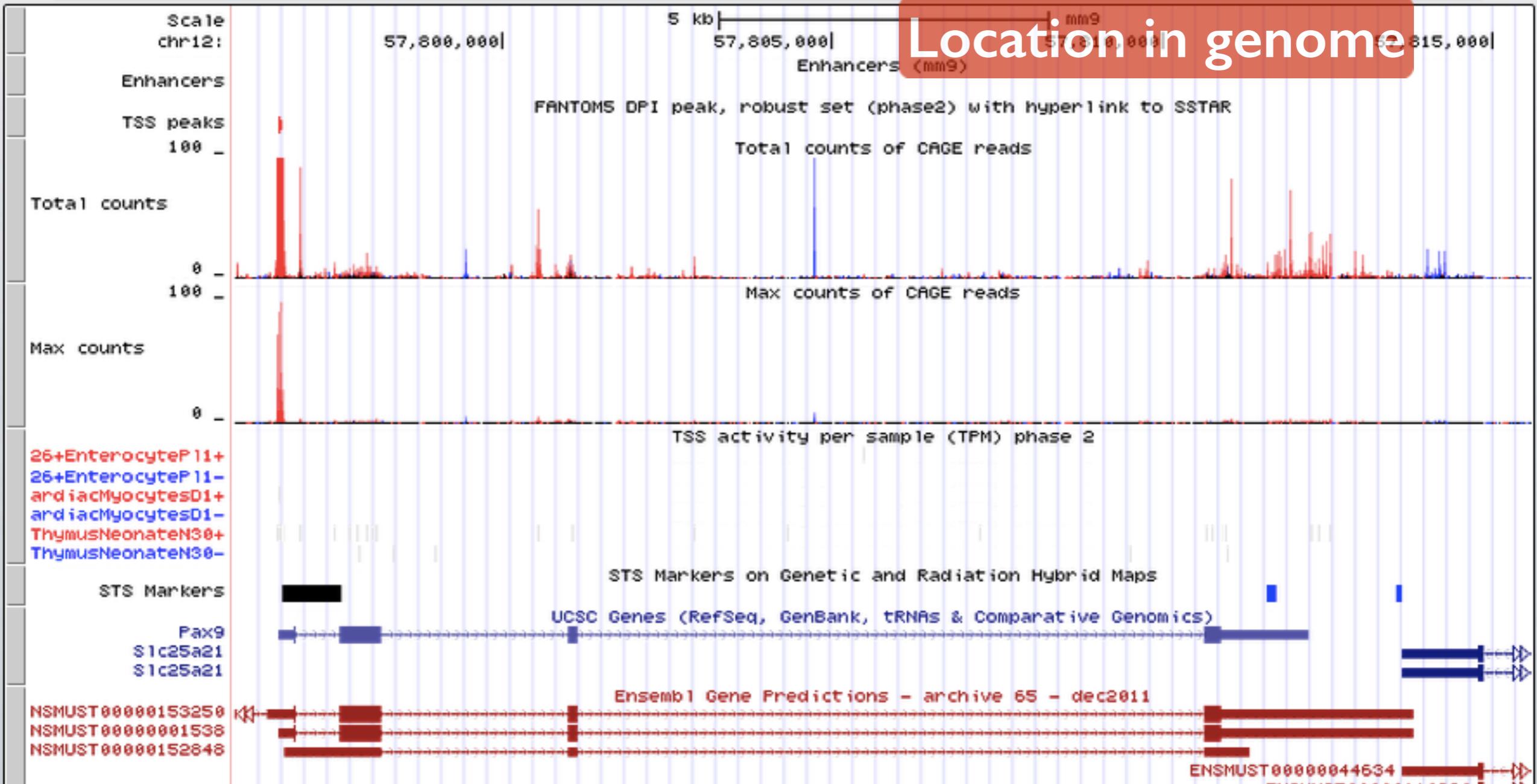
chr12:57,795,963-57,815,592 19,630 bp.

enter position, gene symbol or search terms

go

chr12 (qC1) 12qA1.1 qA2 12qA3 qB1 12qB3 12qC1 qC2 12qC3 qD1 D2 12qD3 12qE 12qF1 qF2

Location in genome



UCSC Genome Browser on Mouse July 2007 (NCBI37/mm9) Assembly



UCSC Genome Browser on Mouse July 2007 (NCBI37/mm9) Assembly

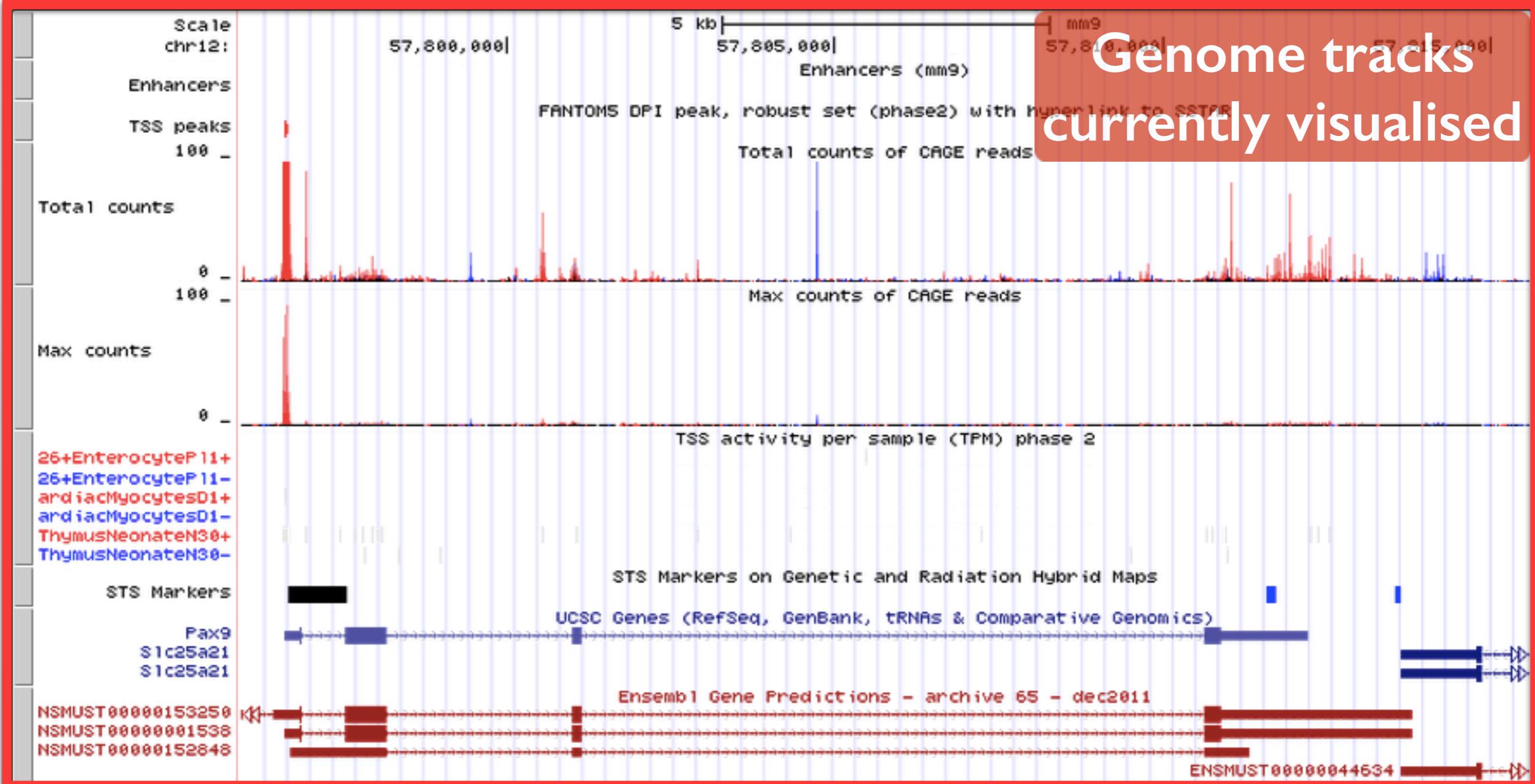
move <<< << < > >> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

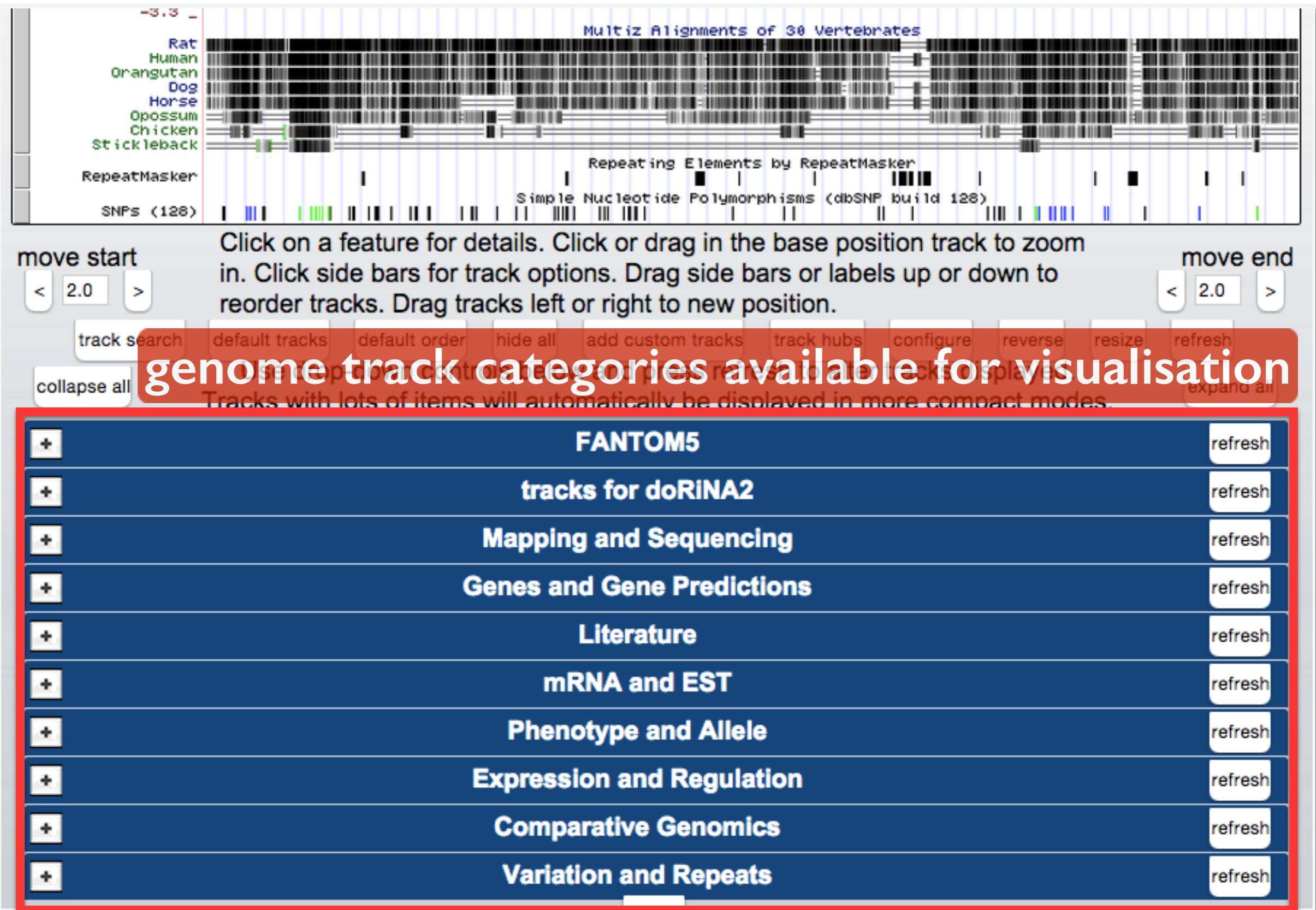
chr12:57,795,963-57,815,592 19,630 bp.

enter position, gene symbol or search terms

go

chr12 (qC1) 12qA1.1 qA2 12qA3 qB1 12qB3 12qC1 qC2 12qC3 qD1 D2 12qD3 12qE 12qF1 qF2





tracks for doRNA2

[refresh](#)

Mapping and Sequencing

[refresh](#)

Genes and Gene Predictions

[refresh](#)

Literature

[refresh](#)

mRNA and EST

[refresh](#)

Phenotype and Allele

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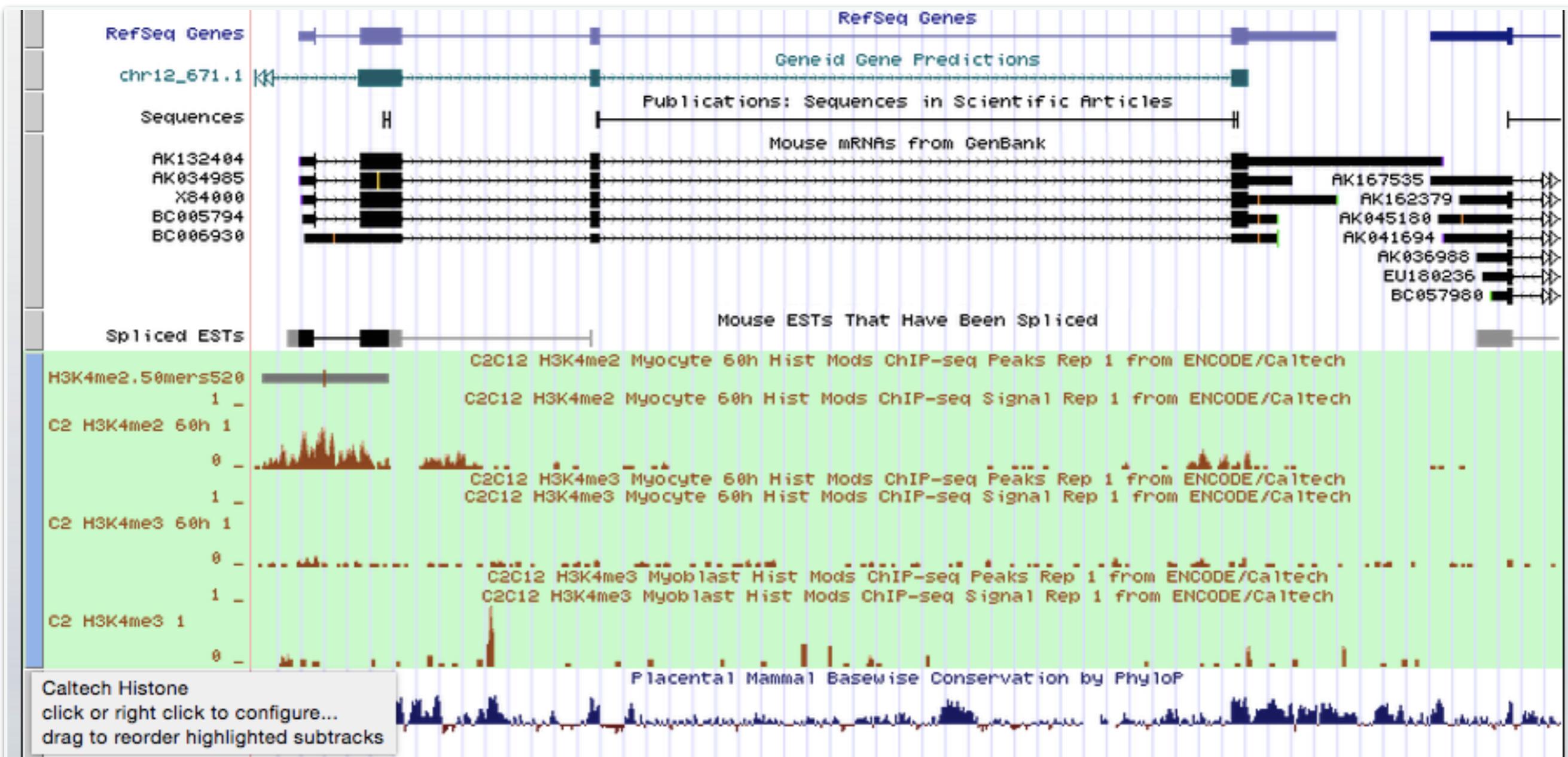
Expression and Regulation

[refresh](#)

Affy Exon...	Affy GNF1M	Affy MOE430	Affy U74	Allen Brain	Caltech Histone
hide	hide	hide	hide	hide	hide
<input checked="" type="checkbox"/> Caltech RNA-seq	<input checked="" type="checkbox"/> Caltech TFBS	CpG Islands...	<input checked="" type="checkbox"/> CSHL Long RNA-seq	FaceBase 24STypes	Repli-
hide	hide	hide	hide	hide	LICR RNA-
GNF Atlas 2	GNF U74A	GNF U74B	GNF U74C	<input checked="" type="checkbox"/> LICR Histone	<input checked="" type="checkbox"/> PSU Histone
hide	hide	hide	hide	hide	hide
<input checked="" type="checkbox"/> LICR TFBS	<input checked="" type="checkbox"/> NHGRI BiP	NKI Nuc Lamina...	ORegAnno	<input checked="" type="checkbox"/> PSU DNasel HS	<input checked="" type="checkbox"/> Stan/Yale RNA-seq
hide	hide	hide	hide	hide	hide
<input checked="" type="checkbox"/> PSU RNA-seq	<input checked="" type="checkbox"/> PSU TFBS	REST	<input checked="" type="checkbox"/> Stan/Yale Histone	<input checked="" type="checkbox"/> Stan/Yale TFBS	<input checked="" type="checkbox"/> TS miRNA sites
hide	hide	hide	hide	hide	hide
TS miRNA sites	UW DNasel DGF	UW DNasel HS	UW RNA-seq		
hide	hide	hide	hide		

Choose how to visualise

dense
squish
pack
full



Load your own data into the browser

UCSC Genome Browser (NCBI37/mm9) Assembly

chr12:57,795,963-57,815,592 19,630

Custom Tracks

chr12 (qC1) 12qA1.1 qA2 12qB3 qB1 12qB3 12qC1 qC2 12qC3 qD1 qD2 12qD3 12qE 12qF1 qF2

The screenshot shows a genomic track for chromosome 12 (chr12) from position 57,795,963 to 57,815,592. The track includes several types of data:

- ENCODE ChIP-seq tracks:** ENCCFF292UDW, ENCCFF364LWZ, ENCCFF931NAC, ENCCFF447VDV, ENCCFF448YKU.
- RefSeq genes:** Pax9, SLC25A21.
- Ensembl Gene Predictions:** NSMUST00000153250, NSMUST0000001538, NSMUST00000152648, ENSMUST00000044634, ENSMUST00000110688.
- Human Proteins Mapped by Chained tBLASTn:** PAX9, SLC25A21.
- Non-Mouse RefSeq Genes:** Other RefSeq.
- RefSeq Genes:** RefSeq Genes.
- MicroRNAs from miRBase:** Publications: Sequences in Scientific Articles.
- Mouse mRNAs from GenBank:** AK132404, AK034985, X84000, BC005794, BC006938, AK167535, AK162379, AK045180, AK041494.

The top navigation bar includes links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, View, Help, and About Us. The 'Custom Tracks' link in the 'My Data' menu is highlighted with a red box.



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clade

Mammal

genome

Human

assembly

Feb. 2009 (GRCh37/hg19)

Display your own data as custom annotation tracks in the browser. Data must be formatted in [bigBed](#), [bigGenePred](#), [bigWig](#), [BAM](#), [VCF](#), [BED](#), [BED detail](#), [bedGraph](#), [broadPeak](#), [GFF](#), [GTF](#), [MAF](#), [narrowPeak](#), [Personal Genome SNP](#), [PSL](#), or [WIG](#) formats. To configure the display, set [track](#) and [browser](#) line attributes as described in the [User's Guide](#). Data in the bigBed, bigWig, bigGenePred, BAM and VCF formats can be provided via only a URL or embedded in a track line in the box below. Examples are [here](#).

Paste URLs or data:

Or upload:

 No file chosen

https://genome.ucsc.edu/goldenPath/help/examples/ct_example1.txt

Optional track documentation: Or upload:

 No file chosen

Click [here](#) for an HTML document template that may be used for Genome Browser track descriptions.



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genome Human

assembly Feb. 2009 (GRCh37/hg19)

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Paste URLs or data:

Or upload: No file chosen

Submit

https://genome.ucsc.edu/goldenPath/help/examples/ct_example1.txt

chr19	6159262	6159269	ESR2_si	6.47	-
chr19	6159262	6159272	THA_f1	6.53	-
chr19	6159262	6159275	RORG_f1	8.4	-
chr19	6159262	6159279	THA_f2	9.66	-

Optional track documentation: Or upload: No file choseClick [here](#) for an HTML document template that may be used fo

I. Chromosome

2. Start

3. Stop

4. Name

5. Score

6. Strand

Mandatory



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clade genome assembly

Display your own data as custom annotation tracks in the browser. Data must be formatted in [bigBed](#), [bigGenePred](#), [bigWig](#), [BAM](#), [VCF](#), [BED](#), [BED detail](#), [bedGraph](#), [broadPeak](#), [GFF](#), [GTF](#), [MAF](#), [narrowPeak](#), [Personal Genome SNP](#), [PSL](#), or [WIG](#) formats. To configure the display, set [track](#) and [browser](#) line attributes as described in the [User's Guide](#). Data in the bigBed, bigWig, bigGenePred, BAM and VCF formats can be provided via only a URL or embedded in a track line in the box below. Examples are [here](#).

Paste URLs or data:

Or upload: No file chosen

```
##Example 1 from Custom Annotation Tracks User's Guide
browser position chr22:20100000-20100900
track name=coords description="Chromosome coordinates list" visibility=2
chr22 20100000 20100100
chr22 20100011 20100200
chr22 20100215 20100400
chr22 20100350 20100500
chr22 20100700 20100800
chr22 20100700 20100900
```

Optional track document

Click [here](#) for an HTML document template that may be used for Genome Browser track descriptions.

Manage Custom Tracks

genome: Human assembly: Feb. 2009 (GRCh37/hg19) [hg19]

Name	Description	Type	Doc	Items	Pos	delete	update	view in	Genome Browser	go
coords	Chromosome coordinates list	bed		6	chr22:					

Managing Custom Tracks

This section provides a brief description of the columns in custom track management table. For more details about managing custom tracks, see the Genome Browser [User's Guide](#).

- **Name** - a hyperlink to the update page where you can edit your track data.
- **Description** - the value of the "description" attribute from the track line, if present. If no description is included in the input file, this field contains the track name.
- **Type** - the track type, determined by the Browser based on the format of the data.
- **Doc** - displays "Y" (Yes) if a description page has been uploaded for the track; otherwise the field is blank.
- **Items** - the number of data items in the custom track file. An item count is not displayed for tracks lacking individual items (e.g. wiggle format data).
- **Pos** - the default chromosomal position defined by the track file in either the browser line "position" attribute or the first data line. Clicking this link opens the Genome Browser or Table Browser at the specified position (note: only the chromosome name is shown in this column). The Pos column remains blank if the track lacks individual items (e.g. wiggle format data) and the browser line "position" attribute hasn't been set.



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UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

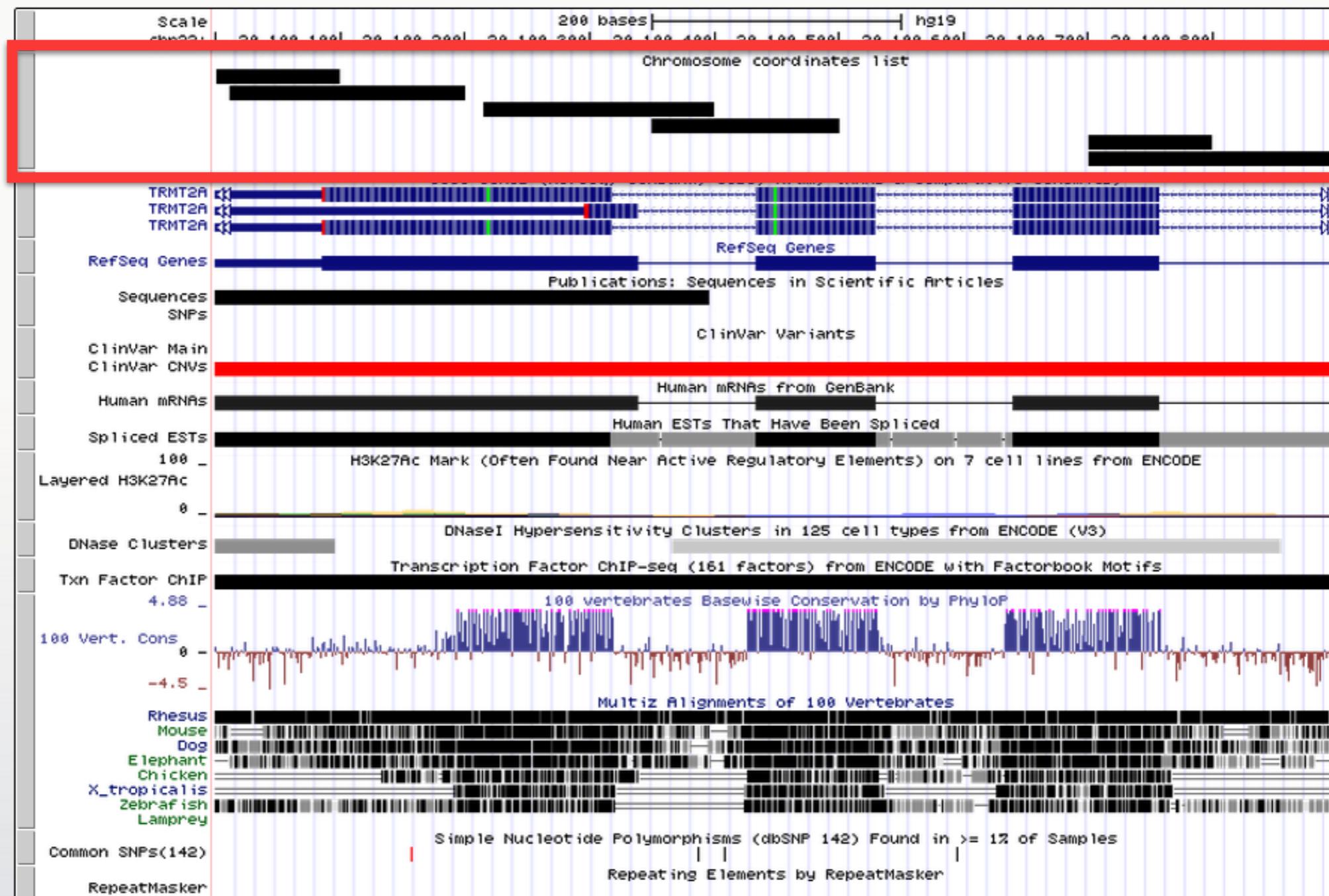
move <<< << < > >> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr22:20,100,000-20,100,900 901 bp. enter position, gene symbol or search terms



go

chr22 (q11.21) 22p13 22p12 p11.2 q11.21 q12.1 12.2 22q12.3 q13.1 q13.2 q13.31



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The Genome Browser project team relies on public funding to support our work. Donations are welcome -- we have many more ideas than our funding supports! If you have ideas, drop a comment in our [suggestion box](#).

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Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. For help in using this application see [Using the Table Browser](#) for a description of the controls in this form, the [User's Guide](#) for general information and sample queries, and the OpenHelix Table Browser [tutorial](#) for a narrated presentation of the software features and usage. For more complex queries, you may want to use [Galaxy](#) or our [public MySQL server](#). To examine the biological function of your set through annotation enrichments, send the data to [GREAT](#). Send data to [GenomeSpace](#) for use with diverse computational tools. Refer to the [Credits](#) page for the list of contributors and usage restrictions associated with these data. All tables can be downloaded in their entirety from the [Sequence and Annotation Downloads](#) page.

clade: Mammal **genome:** Mouse **assembly:** July 2007 (NCBI37/mm9)

group: Genes and Gene Predictions **track:** UCSC Genes [add custom tracks](#) [track hubs](#)

table: knownGene [describe table schema](#)

region: genome position chr12:57805505-57825134 [*](#) [lookup](#) [define regions](#)

identifiers (names/acccessions): [paste list](#) [upload list](#)

filter: [create](#)

intersection: [create](#)

correlation: [create](#)

output format: BED - browser extensible data [Send output to](#) [Galaxy](#) [GREAT](#) [GenomeSpace](#)

output file: [*](#) (leave blank to keep output in browser)

file type returned: plain text gzip compressed

[get output](#) [summary/statistics](#)

To reset **all** user cart settings (including custom tracks), [click here](#).



Table Browser

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clade: Mammal genome: Mouse assembly: July 2007 (NCBI37/mm9)

group: Genes and Gene Predictions track: UCSC Genes
Ensembl Genes
Human Proteins
Other RefSeq
RefSeq Genes
TransMap UCSC
TransMap RefGene
TransMap mRNA
TransMap ESTs
AceView Genes
Augustus
CCDS
Exoniphy
Gene Trap
Geneid Genes
Genscan Genes
IKMC Genes
MGC Genes
miRNA
N-SCAN
NIA Gene Index

table: knownGene description:
region: genome position chr12:57805

identifiers (names/acccessions): paste list

filter: [create](#)

intersection: [create](#)

correlation: [create](#)

output format: BED - browser extensible data

output file: *

file type returned: plain text gzip

[get output](#) [summary/statistics](#)

To reset all user cart settings (including current filters)

track hubs: [add custom tracks](#) [track hubs](#)

output to: Galaxy GREAT GenomeSpace

(or output in browser)

The UCSC Table browser allows you to download all data stored in the genome browser



Table Browser

Use this program to retrieve tracks, and to retrieve DNA Browser for a description of queries, and the OpenHelix usage. For more complex biological function of your GenomeSpace for use with usage restrictions associated and Annotation Downloads

clade: Mammal
group: Genes and Gene Predictions
table: knownGene
region: genome
identifiers (names/accession numbers)

filter:

intersection:

correlation:

output format: all fields from selected table

GenomeSpace

output file: * (leave blank to keep output in browser)

file type returned: plain text gzip compressed

Filter on Fields from mm9.knownGene

name	does <input type="button" value="↑"/> match *	<input type="text"/>	<input type="button" value="≡"/>	
chrom	does <input type="button" value="↑"/> match *	<input type="text"/>		AND
strand	does <input type="button" value="↑"/> match *	<input type="text"/>		AND
txStart	is <input style="background-color: #e0e0e0; color: black; border: 1px solid #ccc; width: 100px; height: 20px; vertical-align: middle;" type="button" value="ignored"/> <input type="button" value="↑"/>	0	<input type="text"/>	AND
txEnd	is <input style="background-color: #e0e0e0; color: black; border: 1px solid #ccc; width: 100px; height: 20px; vertical-align: middle;" type="button" value="ignored"/> <input type="button" value="↑"/>	0	<input type="text"/>	AND
cdsStart	is <input style="background-color: #e0e0e0; color: black; border: 1px solid #ccc; width: 100px; height: 20px; vertical-align: middle;" type="button" value="ignored"/> <input type="button" value="↑"/>	0	<input type="text"/>	AND
cdsEnd	is <input style="background-color: #e0e0e0; color: black; border: 1px solid #ccc; width: 100px; height: 20px; vertical-align: middle;" type="button" value="ignored"/> <input type="button" value="↑"/>	0	<input type="text"/>	AND
exonCount	is <input style="background-color: #e0e0e0; color: black; border: 1px solid #ccc; width: 100px; height: 20px; vertical-align: middle;" type="button" value="ignored"/> <input type="button" value="↑"/>	0	<input type="text"/>	AND
exonStarts	does <input type="button" value="↑"/> match *	<input type="text"/>		
exonEnds	does <input type="button" value="↑"/> match *	<input type="text"/>		
proteinID	does <input type="button" value="↑"/> match *	<input type="text"/>		AND
alignID	does <input type="button" value="↑"/> match *	<input type="text"/>		AND

AND Free-form query:

Filter for specific elements



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clade: Mammal genome: Mouse assembly: July 2007 (NCBI37/mm9)

group: Genes and Gene Predictions track: UCSC Genes add custom tracks track hubs

table: knownGene describe table schema

region: genome position chr12:57805505-57825134 * lookup define regions

identifiers (names/accessions): [paste list](#) [upload list](#)

filter: [create](#) all fields from selected table
selected fields from primary and related tables

intersection: [sequence](#)
[GTF - gene transfer format](#)
[CDS FASTA alignment from multiple alignment](#)

correlation: [c](#)

output format: BED - browser extensible data Send output to [Galaxy](#) [GREAT](#) [GenomeSpace](#)
 custom track
 hyperlinks to Genome Browser

output file: (to keep output in browser)

file type returned: plain text gzip compressed

[get output](#) [summary/statistics](#)

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clade: Mammal genome: Mouse a
group: Genes and Gene Predictions track: UCSC Genes

table: knownGene describe table schema
region: genome position chr12:57805505-57825134
identifiers (names/accessions): paste list upload list
filter: create all fields from selected table
selected fields from primary and related tables
intersection: sequence
correlation: GTF - gene transfer format
CDS FASTA alignment from multiple alignment
output format: ✓ BED - browser extensible data
output file: custom track hyperlinks to Genome Browser
file type returned: plain text gzip compressed

chr19	6159262	6159269	ESR2_si	6.47	-	ciated
chr19	6159262	6159272	THA_f1	6.53	-	s page.
chr19	6159262	6159275	RORG_f1	8.4	-	
chr19	6159262	6159279	THA_f2	9.66	-	

1. Chromosome
2. Start
3. Stop
4. Name
5. Score
6. Strand

Space

To reset **all** user cart settings (including custom tracks), [click here](#).



Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. For help in using this application see [Using the Table Browser](#) for a description of the controls in this form, the [User's Guide](#) for general information and sample queries, and the OpenHelix Table Browser [tutorial](#) for a narrated presentation of the software features and usage. For more complex queries, you may want to use [Galaxy](#) or our [public MySQL server](#). To examine the biological function of your set through annotation enrichments, send the data to [GREAT](#). Send data to [GenomeSpace](#) for use with diverse computational tools. Refer to the [Credits](#) page for the list of contributors and usage restrictions associated with these data. All tables can be downloaded in their entirety from the [Sequence and Annotation Downloads](#) page.

clade: Mammal **genome:** Mouse **assembly:** July 2007 (NCBI37/mm9)

group: Genes and Gene Predictions **track:** UCSC Genes **add custom tracks** **track hubs**

table: knownGene **describe table schema**

region: genome position chr12:57805505-57825134 ***** **lookup** **define regions**

identifiers (names/accessions): **paste list** **upload list**

filter: **create**

intersection: **create**

correlation: **create**

output format: BED - browser extensible data **Send output to** [Galaxy](#) [GREAT](#) [GenomeSpace](#)

output file: ***** (leave blank to keep output in browser)

file type returned: plain text gzip compressed

get output **summary/statistics**

To reset **all** user cart settings (including custom tracks), [click here](#).

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Output knownGene as BED

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to analyze DNA sequence covered by a track. For help in using this application see [Using the Table Browser](#) and the [General Table Browser tutorial](#) for a narrated presentation of the software features and sample queries, and usage. For more complex queries, you may want to use [Galaxy](#) or our [public MySQL server](#). To examine the biological function of your set through annotation enrichments, send the data to [GREAT](#). Send data to [GenomeSpace](#) for use with Create one BED record per:

Whole Gene All tables can be downloaded in their entirety from the [Sequence and Annotation Downloads](#) page.

Upstream by 200 bases genome: Mouse assembly: July 2007 (NCBI37/mm9)

Exons plus 0 bases at each end

Introns plus 0 bases at each end

5' UTR Exons

Coding Exons

3' UTR Exons

Downstream by 200 bases

Note: if a feature is close to the end of a chromosome they may be truncated in the output.

get BED cancel create

output format: BED

output file:

file type returned:

get output summary/stats

To reset all user cart settings (including custom tracks), [click here](#).

chr	start	end	name	score	strand	thickStart	thickEnd	color
chr1	3195984	3205713	uc007aet.1	0	-	3195984	3195984	0
chr1	3204562	3661579	uc007aeu.1	0	-	3206102	3661429	0
chr1	3638391	3648985	uc007aev.1	0	-	3638391	3638391	0
chr1	4280926	4399322	uc007aew.1	0	-	4283061	4399268	0
chr1	4333587	4350395	uc007aex.2	0	-	4334680	4342906	0
chr1	4481008	4483816	uc007aey.1	0	-	4481796	4483487	0
chr1	4481008	4486494	uc007aez.1	0	-	4481796	4483487	0
chr1	4481008	4486494	uc007afa.1	0	-	4481796	4485236	0
chr1	4481008	4486494	uc007afb.1	0	-	4481796	4482672	0
chr1	4481008	4486494	uc007afc.1	0	-	4481796	4483487	0
chr1	4763278	4775807	uc007aff.2	0	-	4766544	4775758	0
chr1	4763278	4775807	uc007afd.2	0	-	4764532	4775758	0
chr1	4763278	4775807	uc007afe.2	0	-	4763278	4763278	0
chr1	4797973	4832908	uc007afg.1	0	+	4798009	4831240	0

References

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Mangan MEI et al.. The UCSC Genome Browser: What Every Molecular Biologist Should Know. *Curr Protoc Mol Biol.* 2014 Jul 1;107:19.9.1-19.9.36.

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