

Esercitazione UCSC – Table Browser.

Obiettivi dell'esercitazione:

- i. caricare nel Genome Browser una lista di identificativi di geni umani di interesse
- ii. estrarre un file in formato BED (Browser Extensible Data) con le loro coordinate genomiche, relative alla versione del genoma umano del febbraio 2009 (GRCh37/hg19)
- iii. importare e visualizzare la traccia BED appena creata nel Genome Browser, come traccia di colore verde

parte I:

caricare nel Genome Browser una lista di identificativi di geni di interesse

1. apri una pagina del UCSC genome browser <http://genome.ucsc.edu>
2. dal menù principale --> Tools --> Table Browser

The screenshot shows the UCSC Genome Browser homepage. The browser's address bar displays <https://genome.ucsc.edu>. The main navigation bar includes links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, Help, and About Us. A left-hand sidebar lists various tools: Genome Browser, Blat, Table Browser, Gene Sorter, In Silico PCR, Genome Graphs, Galaxy, VisiGene, Utilities, Downloads, Release Log, Custom Tracks, and Cancer Browser. The 'Tools' menu is currently open, showing a list of options: Blat, Table Browser (highlighted), Variant Annotation Integrator, Data Integrator, Gene Sorter, Genome Graphs, In-Silico PCR, LiftOver, VisiGene, and Other Utilities. The main content area features the heading 'About the UCSC Genome Browser' and a welcome message. It describes the browser's purpose and provides links to the 'Genome Browser in a Box' and 'Genome Browser source code'. A paragraph encourages exploration of the browser's features, mentioning the 'Gene Sorter', 'Blat', 'VisiGene', and 'Genome Graphs'. A 'DONATE NOW' button is visible. Below this, a 'News' section with social media icons (Twitter and Facebook) and a 'News Archives' link is shown. The latest news item is dated '23 September 2015' and titled 'New keyboard shortcuts on the Genome Browser!'. The text of the news item states: 'We are excited to announce the addition of keyboard shortcuts to navigate the Genome Browser display! It's now possible to zoom in and out, navigate left and right, hide all tracks, configure the browser display and much more using only your keyboard. Use the "?" key to view the entire list of shortcuts. Happy browsing!'. The URL <https://genome.ucsc.edu/cgi-bin/hgTables> is visible at the bottom of the page.

UCSC Genome Browser

Genomes Genome Browser Tools Mirrors Downloads My Data Help About Us

Genome Browser
Blat
Table Browser
Gene Sorter
In Silico PCR
Genome Graphs
Galaxy
VisiGene
Utilities
Downloads
Release Log
Custom Tracks
Cancer Browser

About the UCSC Genome Browser

Welcome to the UCSC Genome Browser. The browser also provides portals to [ENCODE](#) and the [Genome Browser in a Box](#) (Genome Browser in a Box).

We encourage you to explore the browser's features worldwide. The [Gene Sorter](#) allows you to sort a sequence to the genome. The [Blat](#) tool allows you to map *situ* mouse and frog images to the genome.

The UCSC Genome Browser is 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](#).

News [News Archives](#)

To receive announcements of new genome assembly releases, new software features, updates and training seminars by email, subscribe to the [genome-announce](#) mailing list. Please see our [blog](#) for posts about Genome Browser tools, features, projects and more.

23 September 2015 — New keyboard shortcuts on the Genome Browser!

We are excited to announce the addition of keyboard shortcuts to navigate the Genome Browser display! It's now possible to zoom in and out, navigate left and right, hide all tracks, configure the browser display and much more using only your keyboard. Use the "?" key to view the entire list of shortcuts. Happy browsing!

<https://genome.ucsc.edu/cgi-bin/hgTables> aeussler for implementing this new feature.

3. definisci i criteri di ricerca come segue:

clade:Mammal genome:Human assembly: Feb.2009(GRCh37/hg19)
group:Genes and Gene Predictions track: UCSC Genes
table:knownGene
region:genome

The screenshot shows the UCSC Table Browser web application. The browser's address bar displays the URL `https://genome.ucsc.edu/cgi-bin/hgTables`. The navigation bar includes links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, Help, and About Us. The main content area, titled "Table Browser", contains a detailed instruction paragraph and a form for specifying search criteria. A red rectangular box highlights the form fields for clade, genome, assembly, group, track, table, and region. Below this box, additional options for identifiers, filters, intersections, correlations, output format, output file, and file type are visible.

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:** Human **assembly:** Feb. 2009 (GRCh37/hg19)

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

table: knownGene describe table schema

region: ☒ genome ☐ ENCODE Pilot regions ☐ position chr21:33031597-33041570 lookup define regions

identifiers (names/accessions): paste list upload list

filter: create

intersection: create

correlation: create

output format: all fields from selected table 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

4. carica la lista dei geni interesse (file “Lista_geni_di_interesse.txt” che accompagna il tutorial) per caricare il file:
--> “upload list” --> “browse” (naviga fino al file da caricare) --> “submit”

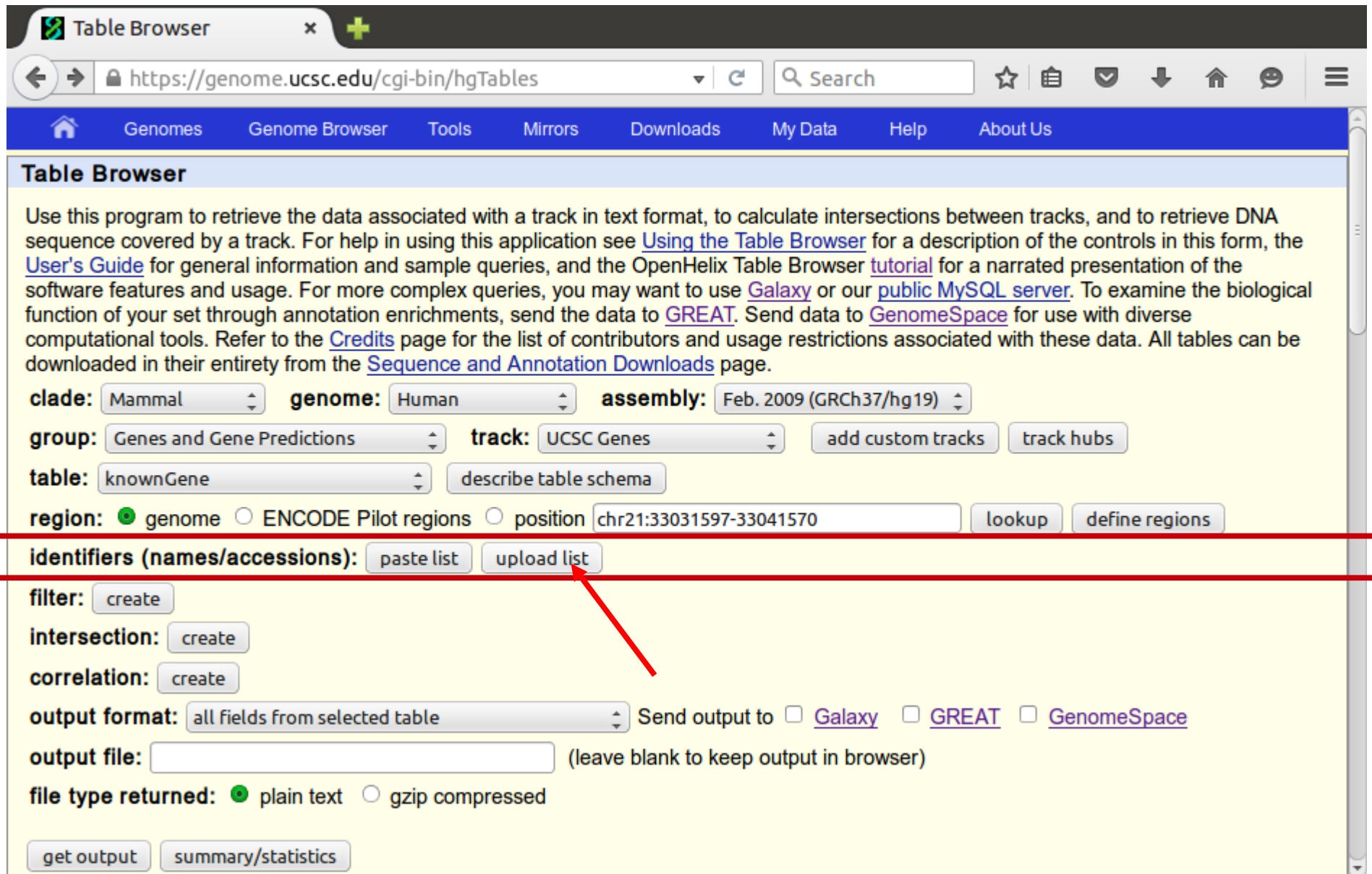


Table Browser

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clade: Mammal **genome:** Human **assembly:** Feb. 2009 (GRCh37/hg19)

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

table: knownGene [describe table schema](#)

region: ☒ genome ☐ ENCODE Pilot regions ☐ position chr21:33031597-33041570 [lookup](#) [define regions](#)

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

filter: [create](#)

intersection: [create](#)

correlation: [create](#)

output format: all fields from selected table ☐ 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](#)

4. carica la lista dei geni interesse (file “Lista_geni_di_interesse.txt” che accompagna il tutorial) per caricare il file:
--> “upload list” --> “browse” (naviga fino al file da caricare) --> “submit”

Firefox Web Browser

↑↓ It (79%) 15:50

Upload Identifiers for UCSC Genes - Mozilla Firefox

Upload Identifiers f... x +

https://genome.ucsc.edu/cgi-bin/hgTables

Genomes Genome Browser Tools Mirrors Downloads My Data Help About Us

Upload Identifiers for UCSC Genes

Please enter the name of a file from your computer that contains a space, tab, or line separated list of the items you want to include. The items must be values of the **name** field of the currently selected table, **knownGene**, or the **alias** field of the alias table **kgAlias**. (The "describe table schema" button shows more information about the table fields.) Some example values:

uc004dxd.4
uc003fon.3
uc011efo.2
Q86US5
AF394064
PDZK8

Browse... No file selected.

submit cancel

File Upload

mie_slides UCSC - tutorial ed esercizi tutorial #2

Location: Lista_geni_di_interesse.txt

Places	Name	Size	Modified
Search	Figures		15:49
Recently Used	Lista_geni_di_interesse.txt	604 bytes	15:46
teresa	presentazione_esercitazione_U...	859,6 kB	15:22
Desktop	presentazione_esercitazione_U...	704,8 kB	15:19
File System	esercitazione_UCSC_estrai_ma...	28,2 kB	05/12/2014
Documents	esercitazione_UCSC_estrai_ma...	6,0 kB	05/12/2014
Music			
Pictures			
Videos			

All Files

Cancel Open

parte II:

estrarre un file in formato BED (Browser Extensible Data) con le loro coordinate genomiche, relative alla versione del genoma umano del febbraio 2009 (GRCh37/hg19)

1. definisci il formato di output desiderato e indica un nome per il file di output.
2. premi il pulsante “get output” per scaricare il risultato.

Table Browser (Input Identifiers)

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: Human assembly: Feb. 2009 (GRCh37/hg19)

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

table: knownGene describe table schema

region: ☒ genome ☐ ENCODE Pilot regions ☐ position chr21:33031597-33041570 lookup

define regions

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

filter: create

intersection: create

correlation: create

output format: all fields from selected table Send output to

output file: all fields from selected table blank to keep o

file type return: sequence

GTF - gene transfer format

CDS FASTA alignment from multiple alignment

BED - browser extensible data

custom track

hyperlinks to Genome Browser

get output

To reset all user

Firefox Web Browser

Table Browser (Input Identifiers) - Mozilla Firefox

https://genome.ucsc.edu/cgi-bin/hgTables

Table Browser (Input Identifiers)

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: Human assembly: Feb. 2009 (GRCh37/hg19)

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

table: knownGene describe table schema

region: ☒ genome ☐ ENCODE Pilot regions ☐ position chr21:33031597-33041570 lookup

define regions

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

filter: create

intersection: create

correlation: create

output format: BED - browser extensible data Send output to ☐ Galaxy ☐ GREAT ☐ GenomeSpace

output file: geni_di_interesse.bed (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](#).

Nota: l'output verrà scaricato in un file con il nome specificato al punto 5. Qualora lo spazio del nome venga lasciato in bianco, l'output verrebbe visualizzato a schermo.

3. spuntare l'opzione "Include custom track header" e scegliere un nome e una descrizione per la nostra traccia. Queste informazioni verranno mostrate nel Genome Browser.

Output knownGene as BED

☐ Include custom track header:

name=

description=

visibility=

url=

Create one BED record per:

☒ Whole Gene

☐ Upstream by bases

☐ Exons plus bases at each end

☐ Introns plus bases at each end

☐ 5' UTR Exons

☐ Coding Exons

☐ 3' UTR Exons

☐ Downstream by bases

Note: if a feature is close to the beginning or end of a chromosome and upstream/downstream bases are added, they may be truncated in order to avoid extending past the edge of the chromosome.

4. scegliere l'intervallo genomico di interesse nella sezione “Create one BED record per”

Output knownGene ...

https://genome.ucsc.edu/cgi-bin/hgTables

Search

Genomes

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Tools

Mirrors

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Output knownGene as BED

☐ Include custom track header:

name= selected genes

description= table browser query on knownGene for some gene of interest

visibility= pack

url=

Create one BED record per:

☒ Whole Gene

☐ Upstream by 200 bases

☐ 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 beginning or end of a chromosome and upstream/downstream bases are added, they may be truncated in order to avoid extending past the edge of the chromosome.

get BED

cancel

Opening geni_di_interesse.bed

You have chosen to open:

geni_di_interesse.bed

which is: BIN file

from: https://genome.ucsc.edu

Would you like to save this file?

Cancel

Save File

5. premere il pulsante “get BED” -->
scegliere di salvare il file dal pop-up che comparirà.

parte III:

importare e visualizzare la traccia BED appena creata nel Genome Browser, come
traccia di colore verde

Per visualizzare la nostra traccia di geni di interesse (file BED) nel browser genomico UCSC:

1. Aprire il browser web su <http://genome.ucsc.edu/>
2. Selezionare "Genome Browser" dal menu a sinistra della home page.
3. Dal menù della finestra selezionare i valori appropriati per genoma e versione del genoma. Nel nostro caso:
 - group: "Mammal"
 - genome: "Human"
 - assembly: "Feb.2009 (GRCh37 / hg19)"
4. Premere il pulsante "add custom tracks"

Human (Homo sapie... x

https://genome-euro.ucsc.edu/cgi-bin/hgGateway?hgsid=209854105_JRIWxGqvAyFZWf8cganOW3osOiAR Search

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Human (*Homo sapiens*) Genome Browser Gateway

The UCSC Genome Browser was created by the [Genome Bioinformatics Group of UC Santa Cruz](#).
Software Copyright (c) The Regents of the University of California. All rights reserved.

group genome assembly position search term

Mammal Human Feb. 2009 (GRCh37/hg19) chr21:33,031,597-33,041,570 enter position, gene symbol or search terms submit

[Click here to reset](#) the browser user interface settings to their defaults. **hg38 replaces hg19 as default human assembly**

track search **add custom tracks** track hubs configure tracks and display

Add your own custom tracks

Human Genome Browser – hg19 assembly (sequences)

The February 2009 human reference sequence (GRCh37) was produced by the [Genome Reference Consortium](#). For more information about this assembly, see [GRCh37](#) in the NCBI Assembly database.

Sample position queries

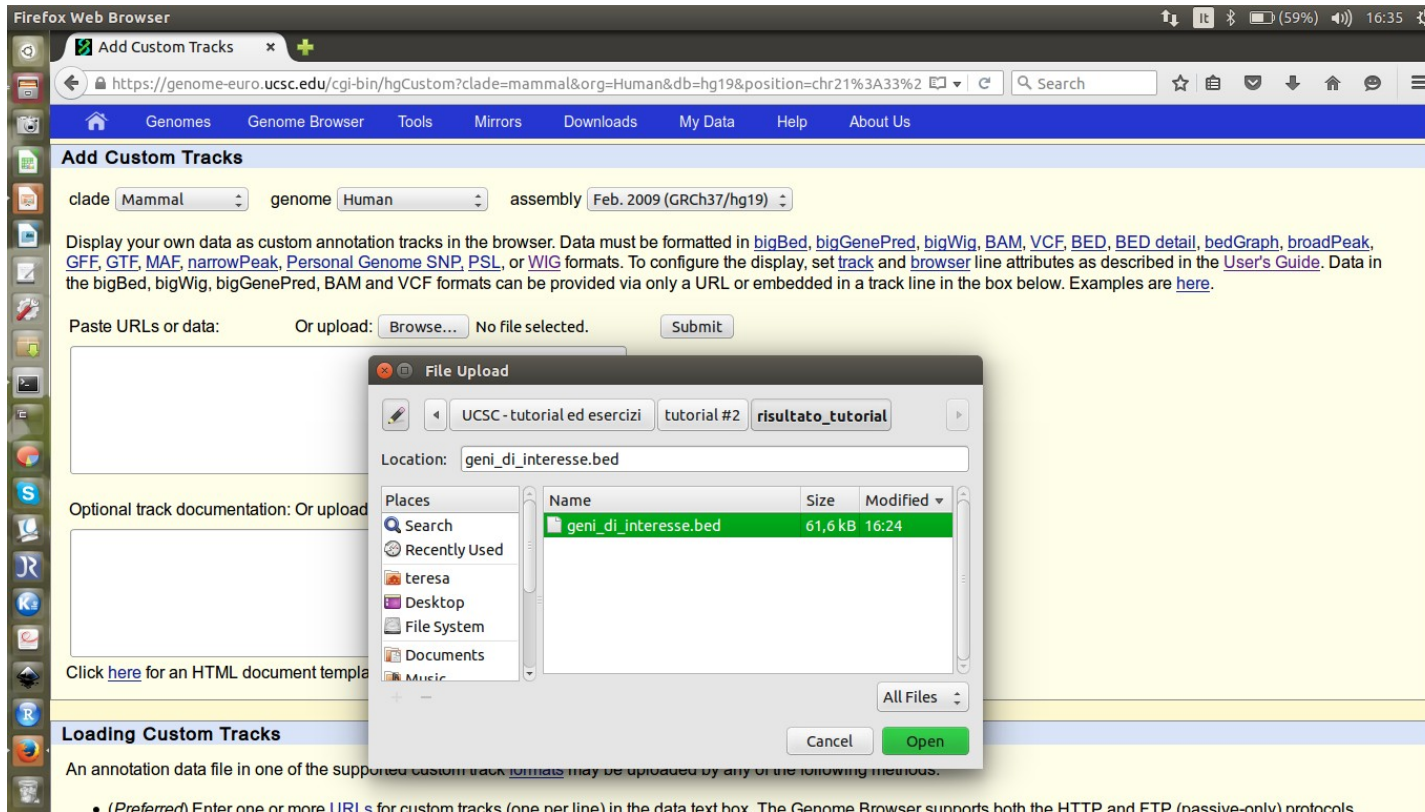
A genome position can be specified by the accession number of a sequenced genomic clone, an mRNA or EST or STS marker, a chromosomal coordinate range, or keywords from the GenBank description of an mRNA. The following list shows examples of valid position queries for the human genome. See the [User's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

Request:	Genome Browser Response:
chr7	Displays all of chromosome 7
chrUn_gl000212	Displays all of the unplaced contig gl000212
20p13	Displays region for band p13 on chr 20
chr3:1-1000000	Displays first million bases of chr 3, counting from p-arm telomere
chr3:1000000+2000	Displays a region of chr3 that spans 2000 bases, starting with position 1000000
BU18064:BU180475	Displays region between genome landmarks such as the STS markers BU18064 and BU180475 on chromosome

U C S C

Homo sapiens
(Graphic courtesy of [CBSE](#))

5. Dalla schermata che ora permette l'upload di file, premere "Browse" e caricare il file di interesse i (nel nostro caso, il file "geni_di_interesse.bed" che avrete salvato sul vostro pc).
6. Premere il pulsante "scegli file" e caricare il file, quindi premere il pulsante "submit".



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Manage Custom Tracks

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

Name	Description	Type	Doc	Items	Pos	delete
selected_genes	table browser query on knownGene for some gene of interest	bed		341	chr1:	<input type="checkbox"/>

view in Genome Browser go

[add custom tracks](#)

Nota: a questo punto, la traccia BED relativa ai nostri geni di interesse è già visualizzabile nel Genome Browser, lo potete verificare premendo il tasto “GO”.

Questo vi porterà a visualizzare il primo elemento presente nel file BED appena caricato (nel nostro caso: il gene “AUNIP”, o “uc001bkw.1”, che si trova sul cromosoma 1 alle coordinate: 26,160,496-26,185,848).

Ma per completare il nostro tutorial, cioè per far sì che la nostra traccia BED sia visualizzata in verde nel genome browser dobbiamo tornare al menù delle “custom tracks” e specificare il colore della traccia nel suo header. Così:

1. premi il pulsante “Manage custom tracks” dalla finestra del genome browser (per tornare al menù delle nostre tracce)

The screenshot displays the UCSC Genome Browser interface for Human chromosome 1 (chr1:26,160,496-26,185,848). The main header shows the assembly version (GRCh37/hg19) and navigation controls. Below the main track, a search bar contains the coordinates and a 'go' button. A yellow highlight is placed over the 'go' button with the text 'replaces hg19 as default human assembly'. The main track area shows the gene uc001bkw.1 (AUNIP) and its coordinates. Below the main track, a 'Custom Tracks' panel is visible, containing a search bar, a 'Manage your custom tracks' button, and a list of tracks including 'Roadmap Epigenomics Data Complete Collection at Wash U VizHub'. The 'Custom Tracks' panel also includes a 'refresh' button and a 'pack' dropdown menu.

2. premi il pulsante “Manage custom tracks” dalla finestra del genome browser (per tornare al menù delle nostre tracce)

The screenshot displays the UCSC Genome Browser interface for Human chr1:261604... The browser window shows the URL <https://genome-euro.ucsc.edu/cgi-bin/hgTracks?db=hg19&position=chr1%3A261>. The main heading is "UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly". Below the heading, there are navigation controls including "move" buttons (left, right, zoom in, zoom out) and a search bar. The search bar contains the text "chr1:26,160,496-26,185,848 25,353 bp." and a "go" button. A yellow highlight is placed over the text "replaces hg19 as default human assembly" below the search bar. The main track display shows a genomic region with various tracks, including "chr1 (p36.11)", "uc001bkw.1", and "RUNIP". A red arrow points to the "manage custom tracks" button in the "Custom Tracks" section. The "Custom Tracks" section also includes a "refresh" button and a "collapse all" button. The "Roadmap Epigenomics Data Complete Collection at Wash U VizHub" track is also visible.

Human chr1:261604... x

https://genome-euro.ucsc.edu/cgi-bin/hgTracks?db=hg19&position=chr1%3A261

Search

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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

chr1:26,160,496-26,185,848 25,353 bp. enter position, gene symbol or search terms go **hg38**

replaces hg19 as default human assembly

chr1 (p36.11) 33 31.3 1p31.1 1q12 q32.1 1q41 1q43 q44

Scale chr1: 26,165,000 10 kb 26,170,000 26,175,000 hg19 26,180,000

uc001bkw.1

RUNIP

table browser query on knownGene for some gene of interest

UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics)

move start < 2.0 >

Click on a feature for details. Click or drag in the base position track to zoom in. Click side bars for track options. Drag side bars labels up or down to reorder tracks. Drag tracks left or right to new position.

track search default tracks default order hide all **manage custom tracks** track hubs configure reverse resize refresh

collapse all Use drop-down controls below and press refresh to alter tracks displayed. Tracks with lots of items will automatically be displayed in more compact modes. expand all

Custom Tracks refresh

selected genes pack

Roadmap Epigenomics Data Complete Collection at Wash U VizHub refresh

UCSC-JRC-JSC

3. premi sul nome della traccia (per noi “selected genes”) per poter editare l'header della traccia

Manage Custom Tracks - Mozilla Firefox

Manage Custom Tra... x +

https://genome-euro.ucsc.edu/cgi-bin/hgCustom?hgsid=209854105_JRiWxGqvAj Search

Genomes Genome Browser Tools Mirrors Downloads My Data Help About Us

Manage Custom Tracks

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

Name	Description	Type	Doc	Items	Pos	delete
selected genes	table browser query on knownGene for some gene of interest	bed		341	chr1:	<input type="checkbox"/>

view in Genome Browser go

add custom tracks

4. nella sezione “Edit configuration” (dove compare la riga di header) aggiungi la scritta “color=0,255,0”, che corrisponde al colore verde nel sistema RGB (una guida ai colori qui: http://www.rapidtables.com/web/color/RGB_Color.htm) (Approfittiamo anche per cancellare “url=”, visto che non abbiamo usato questa opzione). Premi “submit”.

Update Custom Tra... x +

https://genome-euro.ucsc.edu/cgi-bin/hgCustom?hgsid=209854105_JRiWxGq Search

Genomes Genome Browser Tools Mirrors Downloads My Data Help About Us

Update Custom Track: table browser query on knownGene for some gene of interest [hg19]

Update your custom track configuration, data, and/or documentation. 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](#).

Edit configuration: Submit

```
track name="selected genes" description="table browser query on knownGene for some gene of interest" visibility=3 color=0,255,0
```


Ora premendo di nuovo il tasto "GO" siamo pronti a visualizzare la nostra traccia di geni di interesse in verde.

Manage Custom Tracks - Mozilla Firefox

https://genome-euro.ucsc.edu/cgi-bin/hgCustom?hgsid=209854105_JRIWxGqvA...

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Manage Custom Tracks

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

Name	Description	Type	Doc	Items	Pos	delete
selected genes	table browser query on knownGene for some gene of interest	bed		341	chr1:	<input type="checkbox"/>

view in



Human chr1:261604... x

https://genome-euro.ucsc.edu/cgi-bin/hgTracks?db=hg19&position=chr1%3A261

Genomes Genome Browser Tools Mirrors Downloads My Data View Help About Us

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

chr1:26,160,496-26,185,848 25,353 bp. enter position, gene symbol or search terms **hg38**

replaces hg19 as default human assembly

chr1 (p36.11) 33 31.3 1p31.1 1q12 q32.1 1q41 1q43 q44

Scale chr1: 26,165,000 | 10 kb | 26,170,000 | 26,175,000 | hg19 26,180,000 |

uc001bkw.1 table browser query on knownGene for some gene of interest

RUNIP UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics)

move start < 20 >

Click on a feature for details. Click or drag in the base position track to zoom in. Click side bars for track options. Drag side b labels up or down to reorder tracks. Drag tracks left or right to new position.

track search default tracks default order hide all manage custom tracks track hubs configure reverse resize refresh

collapse all Use drop-down controls below and press refresh to alter tracks displayed. Tracks with lots of items will automatically be displayed in more compact modes. expand all

Custom Tracks refresh