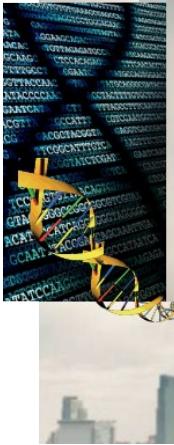


PART OF



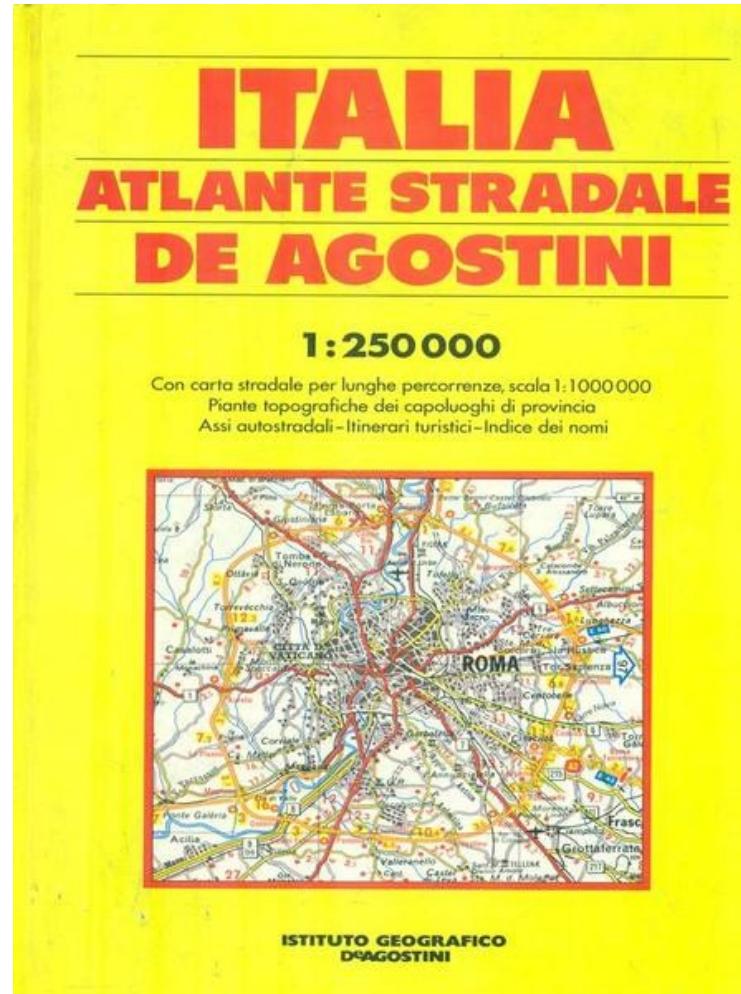
Consiglio Nazionale
delle Ricerche

30/09/2020
Teresa Colombo, IBPM-CNR



A spasso nel tuo genoma: un tour virtuale tra geni apparsi sui titoli dei giornali

Chi se lo ricorda?





- ✓ Qualunque posto noto alla portata di tutti
- ✓ Mappe arricchite di informazioni utili
- ✓ Possibilità di zoom dinamico



sapienza university of rome

Sapienza University of Rome

4.1 ★★★★★ (458)
Public university

Directions Save Nearby Send to your phone Share

Educational institution, founded in 1303, with 11 faculties, 120,000 students & research centers.

Piazzale Aldo Moro, 5, 00185 Roma RM
WG37+GQ Rome, Metropolitan City of Rome
uniroma1.it
06 49911
Add a label

Suggest an edit



Search Google Maps

See travel times, traffic and nearby places

Piazzale Aldo Moro
Rome, Lazio

Street View - Apr 2019

Map data ©2019 Google Italy Terms

Images Street View Photo Sphere Click highlighted areas to see images

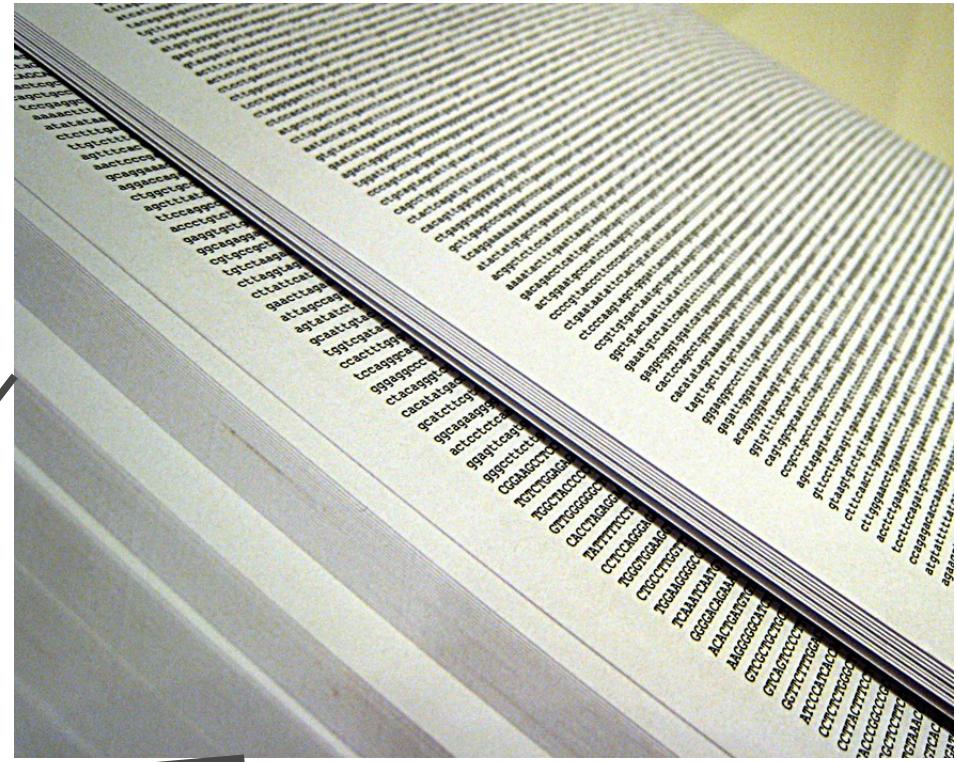
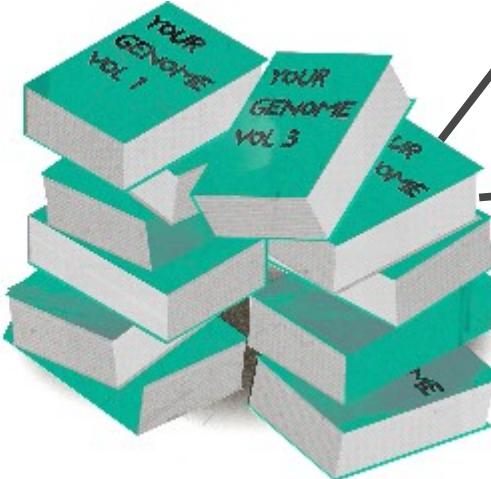
Map data ©2019 Italy Terms Send feedback 10 km

della Matematica

di Roma

Google

La visualizzazione dei dati
facilita la capacità degli esseri umani
di
assorbire e comprendere le
informazioni



Se iniziassi adesso a leggere tutti e 23 i volumi che conservano l'intera sequenza del genoma umano (3 Miliardi di lettere) e leggessi ad una velocità di 1 lettera al secondo 24h su 24, finiresti tra 9 anni?

Browser genomici



The UCSC Genome Browser homepage features a large blue DNA double helix graphic on the left. The main navigation bar includes links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, Projects, Help, and About Us. A sidebar titled "Our tools" lists various analytical tools: Genome Browser, BLAT, Table Browser, Variant Annotation Integrator, Data Integrator, Gene Sorter, Genome Browser in a Box (GBIB), In-Silico PCR, and LiftOver. The background has a yellow border.

UCSC Genome Browser

University of California Santa Cruz (UCSC)



The Ensembl homepage shows a search interface for "All species" with a placeholder "e.g. BRCA2 or rat". It includes sections for "Tools", "BioMart", "BLAST/BLAT", and "Variant Effect Predictor". Below these are "All genomes" and "Favourite genomes" lists, which include Human (GRCm38.p12), Mouse (GRCm38.p6), and Zebrafish (GRCz11). A sidebar highlights "Ensembl Release 97 (July 2019)" with news items about new GENCODE gene sets, changes to InPFA, and a new Regulatory Build.

Ensembl

Wellcome Trust Sanger Institute – EBI



The Genome Data Viewer homepage for Homo sapiens (human) shows a phylogenetic tree of eukaryotic genomes. The tree branches from a root node through various species including fruit fly, mouse, and dog. On the right, a sidebar provides details about the assembly (GRCh38.p13), including RefSeq accession GCF_000001005.39, GCA_000001005.38, and submission information. It also lists annotation details: Annotation Release 109, Release date 2019-06-14, and a Feedback link.

Genome Data Viewer

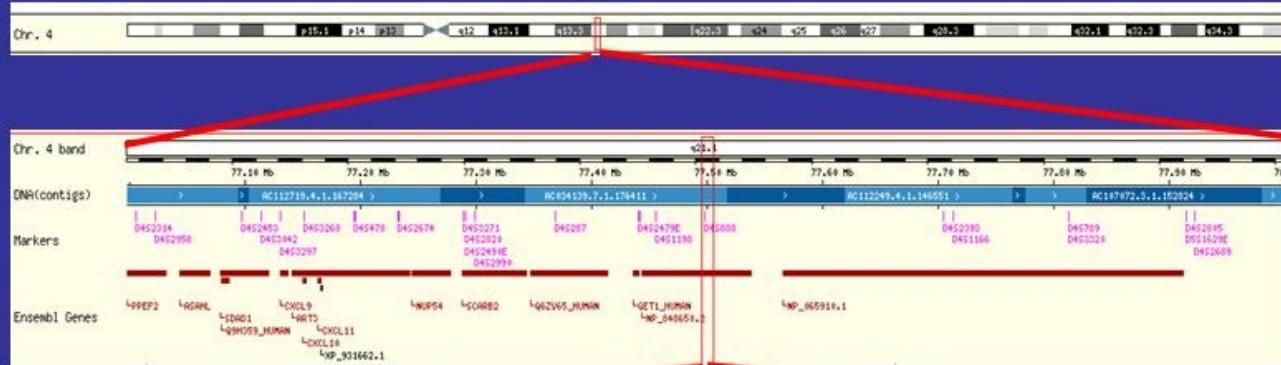
National Center for Biotechnology Information (NCBI)

Che cosa è un browser genomico:

un programma accessibile via WWW (→ A TUTTI ←) che consente all'utente di interrogare e visualizzare graficamente i dati genomici

Browser genomici

200 Mb



1 Mb



10 Kb



200 bp





Genomes

Genome Browser

Tools

Mirrors

Downloads

My Data

Projects

Help

About Us

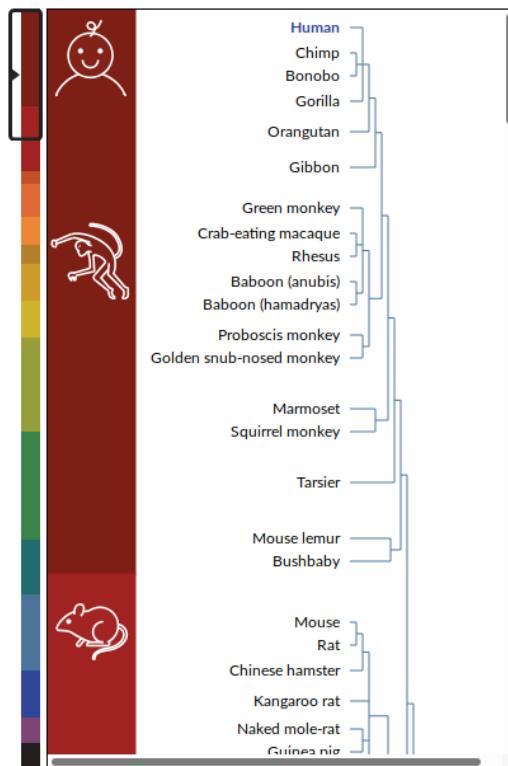
Browse>Select Species

POPULAR SPECIES



Enter species or common name

REPRESENTED SPECIES



Find Position

Human Assembly

Dec. 2013 (GRCh38/hg38)

<https://genome-euro.ucsc.edu/cgi-bin/hgGateway>

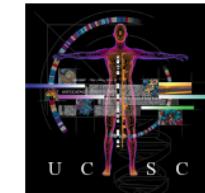
GO

Position/Search Term

Enter position, gene symbol or search terms

Current position: chr17:43,044,295-43,125,483

Human Genome Browser - hg38 assembly

[view sequences](#)**UCSC Genome Browser assembly ID: hg38****Sequencing/Assembly provider ID:** Genome Reference Consortium Human GRCh38.p12 (GCA_000001405.27)**Assembly date:** Dec. 2013 initial release; Dec. 2017 patch release 12**Assembly accession:** GCA_000001405.27**NCBI Genome ID:** 51 (Homo sapiens (human))**NCBI Assembly ID:** 5800238 (GRCh38.p12, GCA_000001405.27)**BioProject ID:** PRJNA31257

Homo sapiens

(Graphic courtesy of CBSE)

Search the assembly:

- **By position or search term:** Use the "position or search term" box to find areas of the genome associated with many different attributes, such as a specific chromosomal coordinate range; mRNA, EST, or STS marker names; or keywords from the GenBank description of an mRNA. [More information](#), including sample queries.
- **By gene name:** Type a gene name into the "search term" box, choose your gene from the drop-down list, then press "submit" to go directly to the assembly location associated with that gene. [More information](#).
- **By track type:** Click the "track search" button to find Genome Browser tracks that match specific selection criteria. [More information](#).

Download sequence and annotation data:

- [Using rsync](#) (recommended)
- [Using FTP](#)
- [Using HTTP](#)
- [Data use conditions and restrictions](#)
- [Acknowledgments](#)

Assembly Details

The GRCh38 assembly is the first major revision of the human genome released in more than four years. As with the previous GRCh37 assembly, the [Genome Reference Consortium](#) (GRC) is now the primary source for human genome assembly data submitted to GenBank. Beginning with this release, the UCSC Genome Browser version numbers for the human assemblies now match those of the GRC to minimize version confusion. Hence, the GRCh38 assembly is referred to as "hg38" in the Genome Browser datasets and documentation. For a glossary of assembly-related terms, see the [GRC Assembly Terminology](#) page.



Genomes

Genome Browser

Tools

Mirrors

Downloads

My Data

Projects

Help

About Us

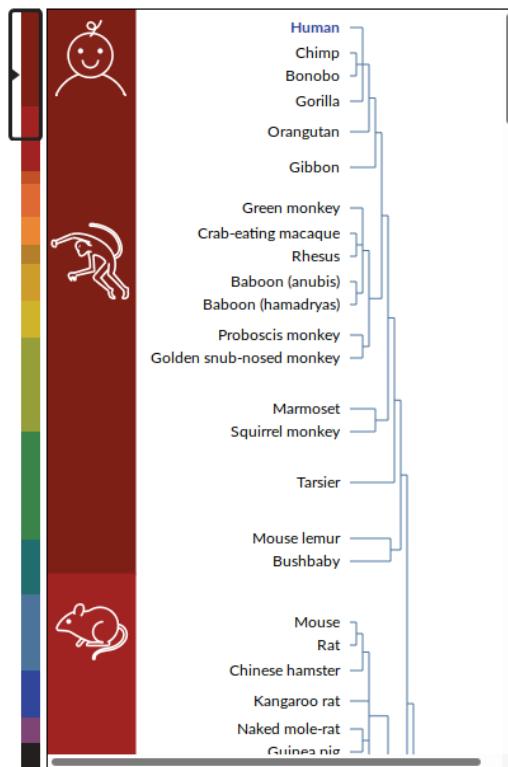
Browse>Select Species

POPULAR SPECIES



Enter species or common name

REPRESENTED SPECIES



Find Position

Human Assembly

Dec. 2013 (GRCh38/hg38)

GO

Position/Search Term

Enter position, gene symbol or search terms

Current position: chr17:43,044,295-43,125,483

Human Genome Browser - hg38 assembly

view sequences

UCSC Genome Browser assembly ID: hg38

Sequencing/Assembly provider ID: Genome Reference Consortium Human GRCh38.p12 (GCA_000001405.27)

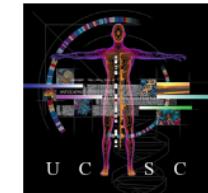
Assembly date: Dec. 2013 initial release; Dec. 2017 patch release 12

Assembly accession: GCA_000001405.27

NCBI Genome ID: 51 (Homo sapiens (human))

NCBI Assembly ID: 5800238 (GRCh38.p12, GCA_000001405.27)

BioProject ID: PRJNA31257



Homo sapiens

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- [Using FTP](#)
- [Using HTTP](#)
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<https://genome-euro.ucsc.edu/cgi-bin/hgGateway>



Genomes

Genome Browser

Tools

Mirrors

Downloads

My Data

Projects

Help

About Us

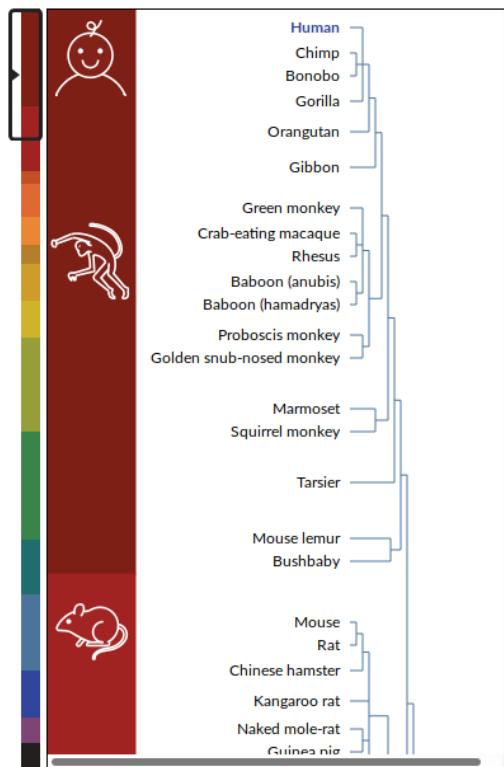
Browse>Select Species

POPULAR SPECIES



Enter species or common name

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Human Assembly

Dec. 2013 (GRCh38/hg38)

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Enter position, gene symbol or search terms

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Human Genome Browser - hg38 assembly

[view sequences](#)

UCSC Genome Browser assembly ID: hg38

Sequencing/Assembly provider ID: Genome Reference Consortium Human GRCh38.p12 (GCA_000001405.27)

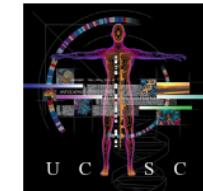
Assembly date: Dec. 2013 initial release; Dec. 2017 patch release 12

Assembly accession: GCA_000001405.27

NCBI Genome ID: 51 (Homo sapiens (human))

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BioProject ID: PRJNA31257



Homo sapiens

(Graphic courtesy of CBSE)

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- [Acknowledgments](#)

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Suggerimenti per la ricerca

Di seguito sono riportati alcuni esempi di ricerche su Google Maps:

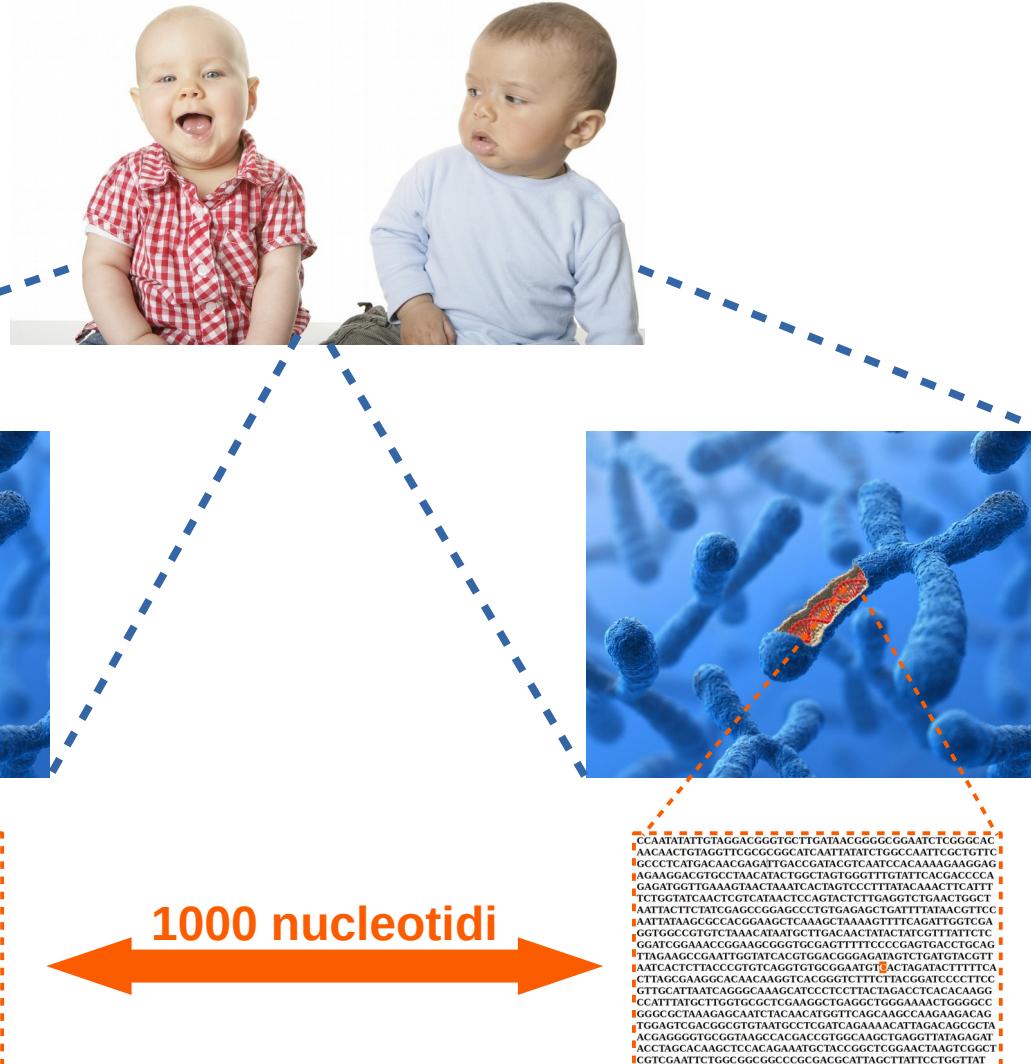
- Attività specifiche: [Starbucks](#).
- Tipi di luoghi: [bar vicino al Colosseo](#).
- Circoscrivi i risultati indicando la città e la provincia: [negozi di alimentari a Empoli, FI](#).
- Circoscrivi i risultati indicando il codice postale: [benzinai in 80127](#).
- Cerca un incrocio: [via Roma e via Dalmazia](#).
- Indirizzo, città, provincia, nazione o aeroporto: [1600 Amphitheater Parkway Mountain View, California, LAX, aeroporto di Los Angeles o Everest, Nepal](#).
- Coordinate di latitudine e longitudine: [41.40338, 2.17403](#).
- Amici e altri contatti (devi avere effettuato l'accesso): [Paolo Rossi](#).
- Altri nomi di utenti nei tuoi [Contatti di G Suite](#).



Suggerimenti per la ricerca

- Un cromosoma intero: [chr22](#)
- Un intervallo genomico (crom.:da-a): [chr4:3,074,681-3,243,960](#)
- Il nome di un gene: [BRCA1](#)
- Una regione cromosomica (banda): [20p13](#)
- Un termine (per cercare geni/regioni associati/e): [Huntington](#)
- Una coordinata genomica: [chr13:20189547-20189547](#)
- Una variante allelica (SNP): [rs80338939](#)

Uguali al 99.9% con ogni altro essere umano

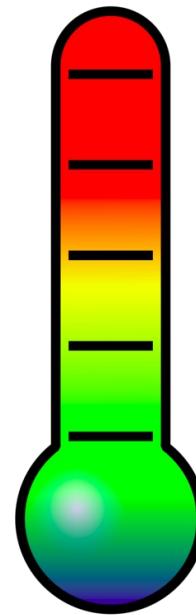
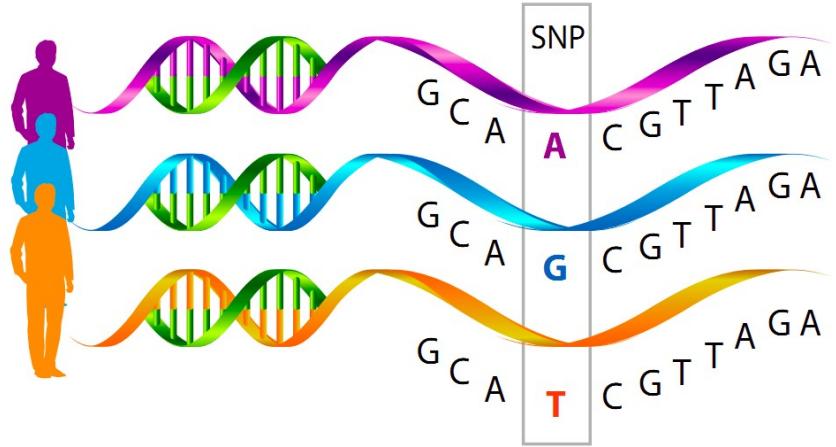


1 nucleotide ogni 1000 diverso (0.1% di variazione)

CCAATATATTGTAGGACGGGTGCTTGATAACGGGGCGGAATCTCGGGCAC
AACAACTGTAGGTTCGCGCGGCATCAATTATATCTGGCCAATTGCGCTGTTG
GCCCTCATGACAACGAGATTGACCGATACTCAATCCACAAAAGAAGGAG
AGAAGGACGTGCCTAACATACTGGCTAGTGGTTGTATTGACGACCCCCA
GAGATGGTTGAAAGT
TCTGGTATCAAACTCGTT
AATTACTTCTATCGAG
AATTATAAGCGCCACGGAAAGT
GGTGGCCGTGTCTAACACATAATGCTT
GGATCGGAAACCGGAAGCGGGTGCAGT
TTAGAAGCCGAATTGGTATCACGTGGACGGGAGATAGTCTGATGTACGTT
AATCACTCTTACCCGTGTCAGGTGTGCGGAATGTC
CTTAGCGAAGGCACAACAAGGTACCGGTCTTACGGATCCCTTCC
GTTGCATTAATCAGGGCAAAGCATCCCTCCTTACTAGACCTCACACAAGG
CCATTATGCTTGGTGCCTCGAAGGCTGAGGCTGGAAAAGTGGGCC
GGGCCTAAAGAGCAATCTACAACATGGTTCAGCAAGCCAAGAAGACAG
TGGAGTCGACGGCGTGTAAATGCCTCGATCAGAAAACATTAGACAGCGCTA
ACGAGGGGTGCGGTAAGCCACGACCGTGGCAAGCTGAGGTTATAGAGAT
ACCTAGCACAAGCTCCACAGAAATGCTACCGGCTCGGAACTAAGTCGGCT
CGTCGAATTCTGGCGGCGGGCGACGCATTAGCTTATTCCCTGGTTAT

Polimorfismo a Singolo Nucleotide (SNP)

Conseguenze associate a variazioni di singolo nucleotide



VERY
HOT

Variante responsabile di malattia monogenica di tipo dominante

HOT

Variante responsabile di malattia monogenica di tipo recessivo (in eterozigosi)

WARM

Variante associata a predisposizione genetica a determinate patologie multifattoriali

COOL

Variante non associata a fenotipo oppure associata a variabilità fisiologica (colore degli occhi, altezza, colore della pelle, propensione al canto, ...)

La gravità o meno dipenderà dalla funzione (più o meno fondamentale) del nucleotide coinvolto



Genomes

Genome Browser

Tools

Mirrors

Downloads

My Data

Projects

Help

About Us

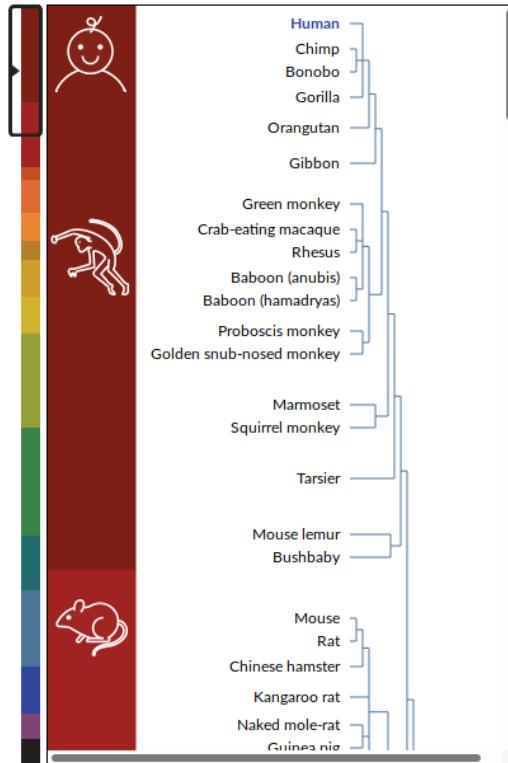
Browse>Select Species

POPULAR SPECIES



Enter species or common name

REPRESENTED SPECIES



Find Position

Human Assembly

Dec. 2013 (GRCh38/hg38)

GO

Position/Search Term

ADRB1 Gene symbol or search terms
chr17:43,044,295-43,125,483

At Salute&Benessere

ANSA.it > Salute&Benessere > Stili di Vita > Scoperto il gene che fa dormire di meno

Scoperto il gene che fa dormire di meno

Studio individua una sua mutazione che porta a svegliarsi 2 ore prima



Redazione ANSA ROMA 29 agosto 2019 14:37

Download sequence and annotation data:

- Using rsync (recommended)
- Using FTP
- Using HTTP
- Data use conditions and restrictions
- Acknowledgments

Assembly Details

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Genomes

Genome Browser

Tools

Mirrors

Downloads

My Data

View

Help

About Us

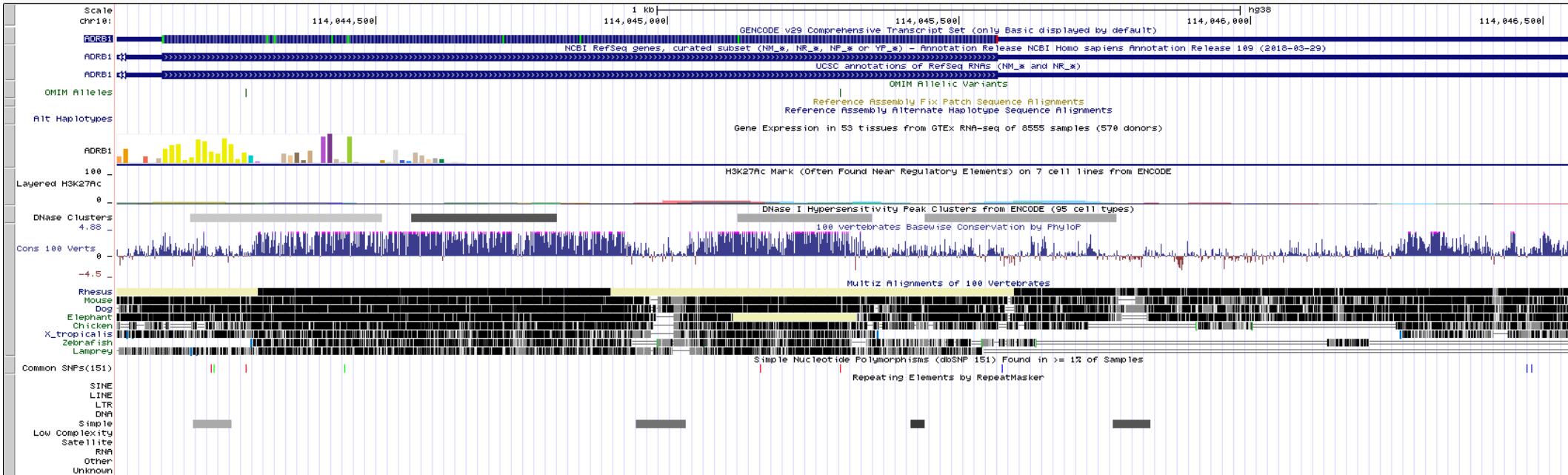
UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

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

chr10:114,044,056-114,046,908 2,853 bp enter position, gene symbol, HGVS or search terms

go

chr10 (q25.3) p15.3 p15.1 10p14 10p13 p12.31 10p12.1 11.22 p11.21 q11.21 q11.22 10q21.1 q21.2 10q21.3 10q22.1 q22.2 10q22.3 10q23.1 q23.31 23.q24.1 q24.2 10q25.1 q25.2 q25.3 q26.13 q26.2 10q26.3



move start

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 or labels up or down to reorder tracks. Drag tracks left or right to new position. Press "?" for keyboard shortcuts.

< 2.0 >

track search default tracks default order hide all add custom tracks track hubs configure multi-region 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



Mapping and Sequencing

refresh



Genes and Gene Predictions

refresh

P12 GENCODE v29

pack

NCBI RefSeq

pack

P12 Other RefSeq

hide

P12 Updated All
GENCODE...

hide

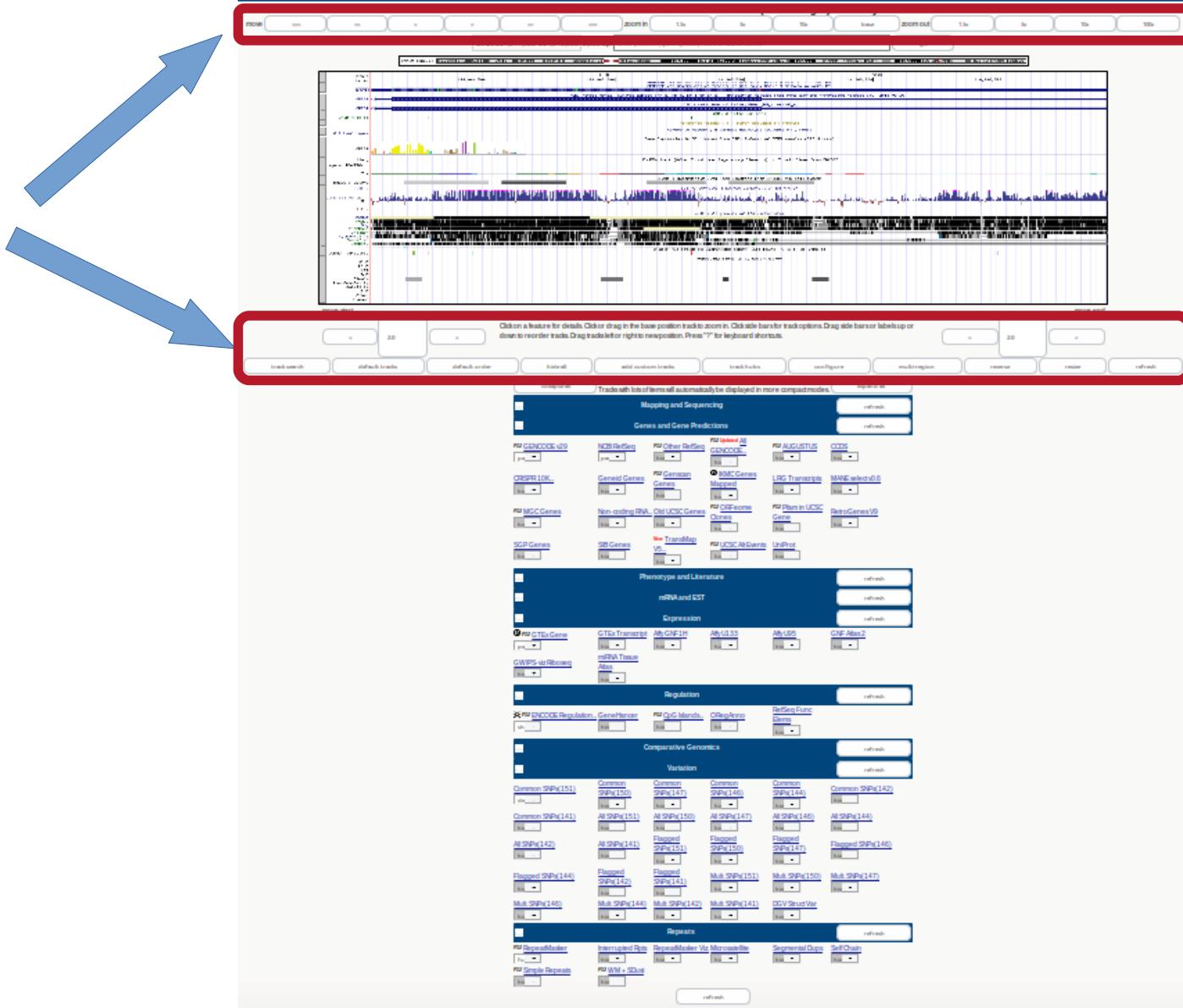
P12 AUGUSTUS

hide

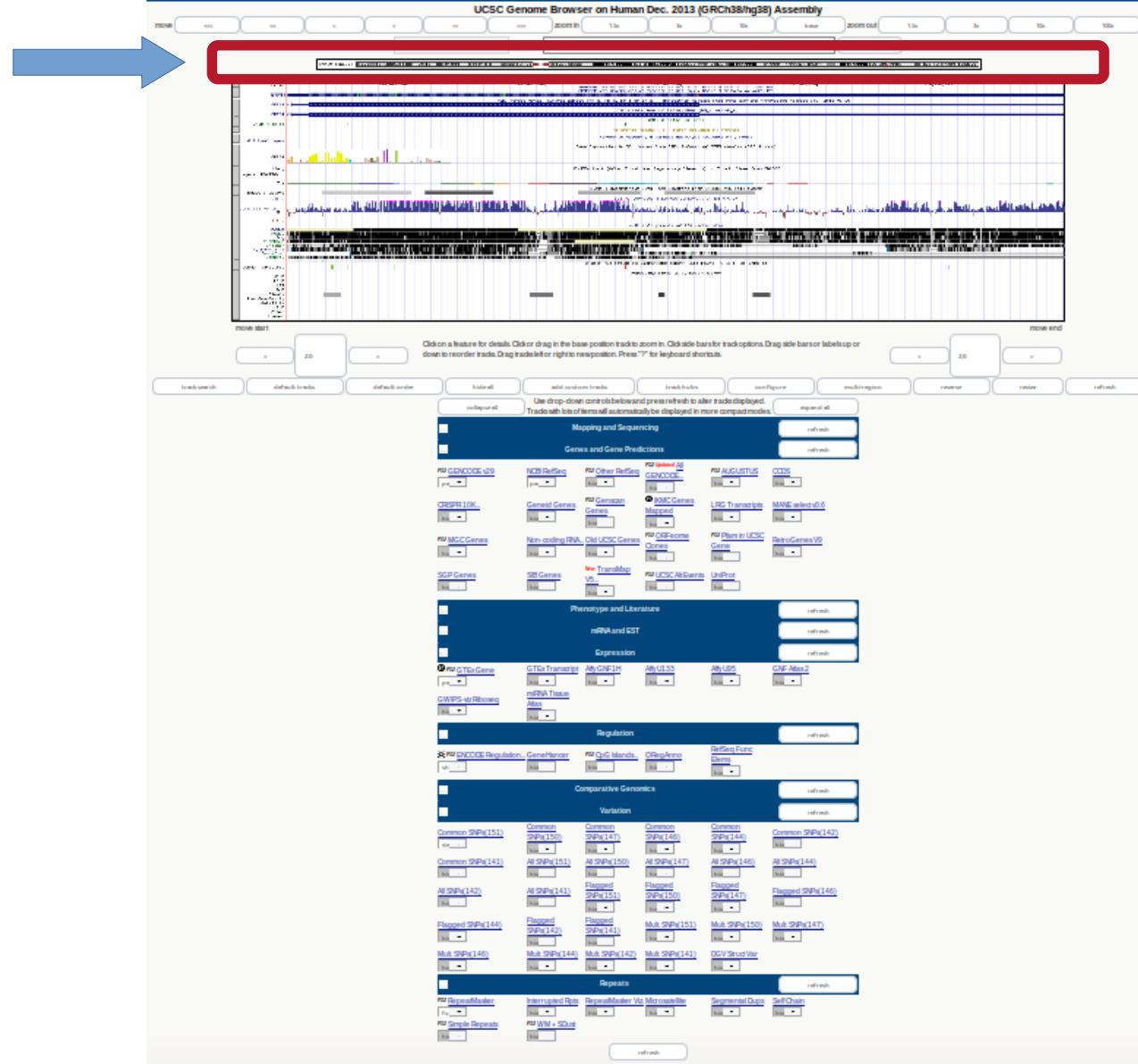
CCDS

hide

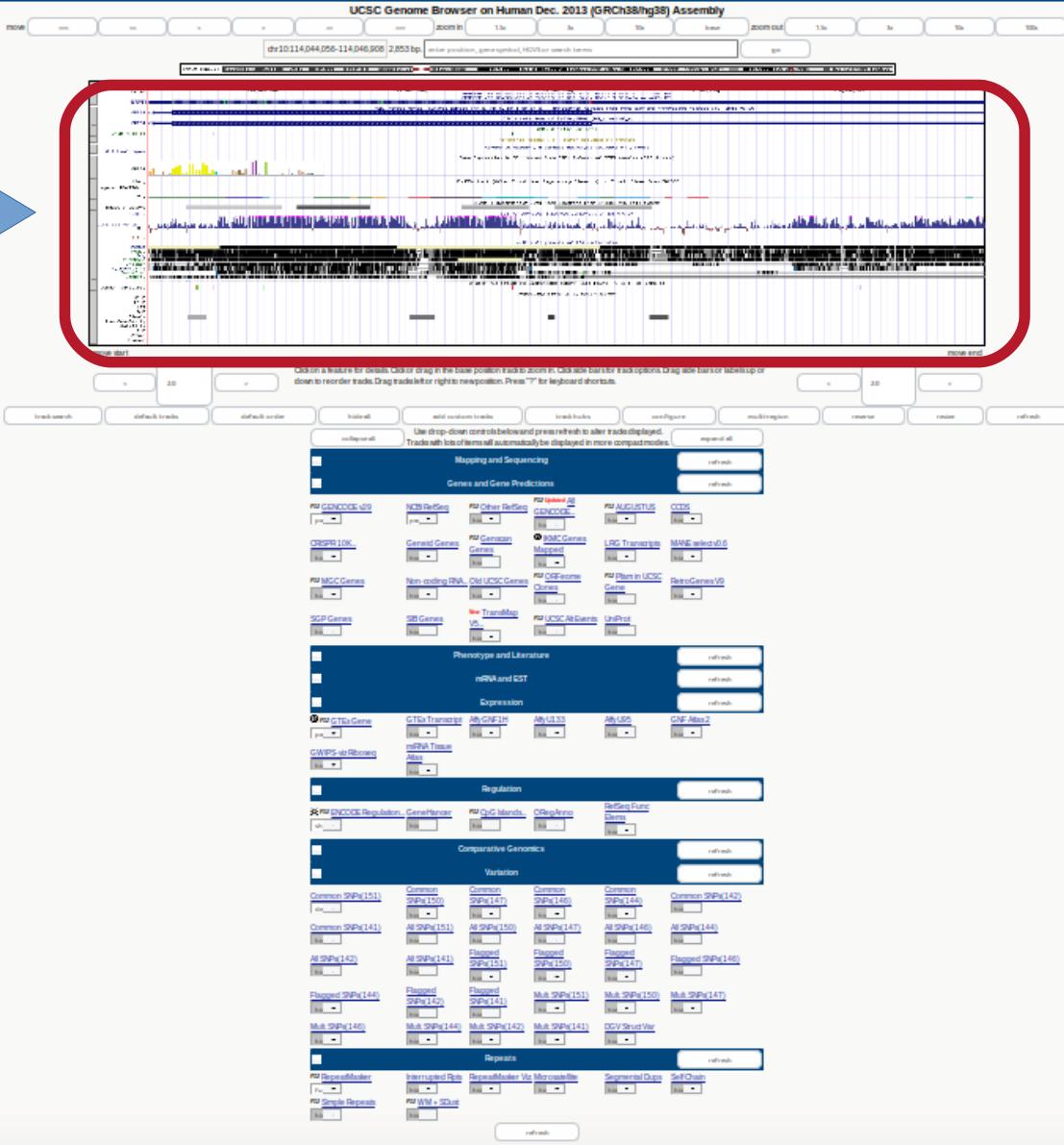
Bottoni di controllo e modifica
(es. Zoom IN/OUT, Spostamento laterale)



Rappresentazione grafica del cromosoma
che stiamo navigando



Finestra di visualizzazione delle annotazioni
(es. Geni, conservazione, presenza di
varianti nucleotidiche tra la popolazione)



Blocchi di annotazioni disponibili,
divise per categorie (es. Geni, espressione,
conservazione, variazione, etc).
Da qui si possono aggiungere o togliere
tracce di annotazione dalla finestra di
visualizzazione

The image shows a screenshot of the UCSC Genome Browser interface. At the top, a header reads "UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly". Below the header is a search bar with the query "chr10:114,044,056-114,046,908 2,853 bp". The main area displays a genomic track with various data layers. At the bottom of the browser window, there is a large red rounded rectangle highlighting the "track controls" section. This section contains a grid of checkboxes for selecting different types of annotations. The categories visible include:

- Mapping and Sequencing: GENECODE v20, NCBI RefSeq, Other RefSeqs, GENCODE, AUGUSTUS, CODE.
- Genes and Gene Predictions: CDS v10K, GenBank Genes, Ensembl Genes, Mapped, LRG Transcripts, MANE select v0.5.
- Non-coding RNA: ncRNA, Old UCSC Genes, Old UCSC Genes, Rfam in UCSC, RetroElements v8.
- Protein Domains: SWISSPROT, TrEMBL vs., UniProt.
- Phenotype and Literature: mRNA and EST, Expression.
- Expression: GTEx Transcriptome, Affy GNF1k, Affy U133, Affy U150, GNF Allx2.
- Regulation: ENCODE Regulation, ChIP-seq, CTC Islands, ChIP-seq.
- Comparative Genomics: RefSeq Fasta, UCSC Genome Browser.
- Variation: Common SNPs (151), Common SNPs (150), Common SNPs (147), Common SNPs (146), Common SNPs (144), Common SNPs (142).
- Repeats: Repetitive Elements, Insertion Bias, RepeatMasker Up, Microsatellites, Segmented Dups, SelfCheck.

Below the track controls, there are buttons for "refresh" and "track start/end" with a zoom level of 2.0.

VOI SIETE QUI



Traccia: GENCODE

- bright green codons/lines: methionine, including start codons
- cyan text: partial codon, either spliced or truncated
- red "*": stop codons
- black "X": error (e.g. truncated last codon)

Traccia: OMIM

- **Locus:** downstream_gene_variant, upstream_gene_variant
- **Coding - Synonymous:** synonymous_variant
- **Coding - Non-Synonymous:** stop_gained, missense_variant, stop_lost, frameshift_variant, inframe_indel
- **Untranslated:** 5_prime_UTR_variant, 3_prime_UTR_variant
- **Intron:** intron_variant
- **Splice Site:** splice_acceptor_variant, splice_donor_variant

Traccia: dbSNP

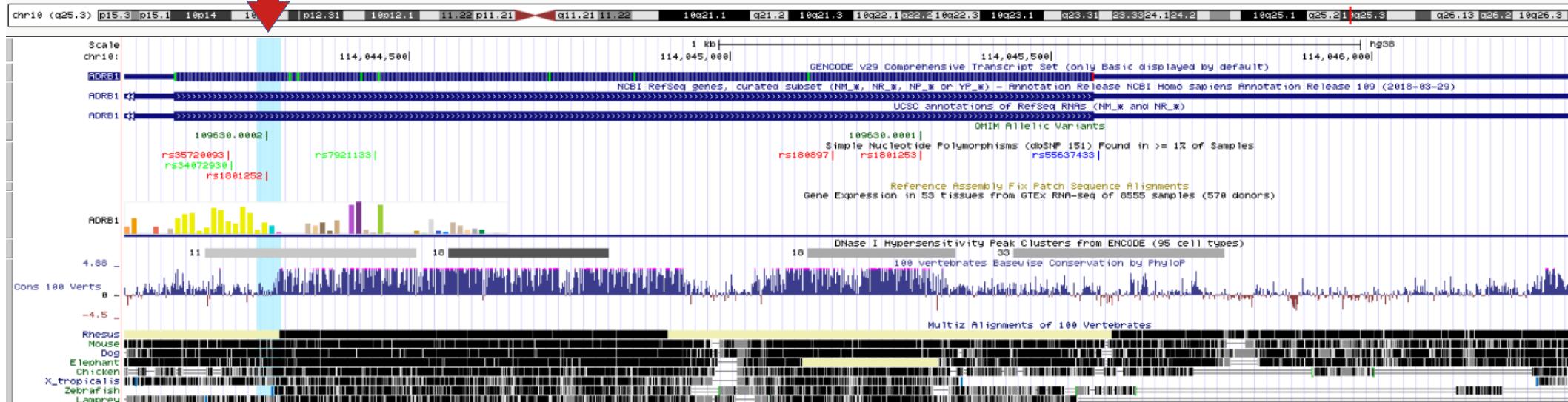
| | | | | | | | |
|--------------|-------|--------|-------|---------------------|-------|-------------------------|-----|
| Unknown | black | Locus | black | Coding - Synonymous | green | Coding - Non-Synonymous | red |
| Untranslated | blue | Intron | black | Splice Site | red | | |

rs1801252

Gene: [ADRB1](#), adrenoceptor beta 1 (plus strand)

| Molecule type | Change | Amino acid[Codon] | SO Term |
|----------------------------|------------------------|-------------------|-------------------------|
| ADRB1 transcript | NM_000684.3:c.145A>G | S [AGC] > G [GGC] | Coding Sequence Variant |
| beta-1 adrenergic receptor | NP_000675.1:p.Ser49Gly | S (Ser) > G (Gly) | Missense Variant |

La variante allelica (A/G)
che incide sulla nostra
frequenza cardiaca a riposo



Traccia: GENCODE

- bright green codons/lines: methionine, including start codons
- cyan text: partial codon, either spliced or truncated
- red "*": stop codons
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Traccia: OMIM

- Locus: downstream_gene_variant, upstream_gene_variant
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- Coding - Non-Synonymous: stop_gained, missense_variant, stop_lost, frameshift_variant, inframe_indel
- Untranslated: 5_prime_UTR_variant, 3_prime_UTR_variant
- Intron: intron_variant
- Splice Site: splice_acceptor_variant, splice_donor_variant

Traccia: dbSNP

| | | | | | | | |
|--------------|-------|--------|-------|---------------------|-------|-------------------------|-----|
| Unknown | black | Locus | black | Coding - Synonymous | green | Coding - Non-Synonymous | red |
| Untranslated | blue | Intron | black | Splice Site | red | | |



Genomes

Genome Browser

Tools

Mirrors

Downloads

My Data

View

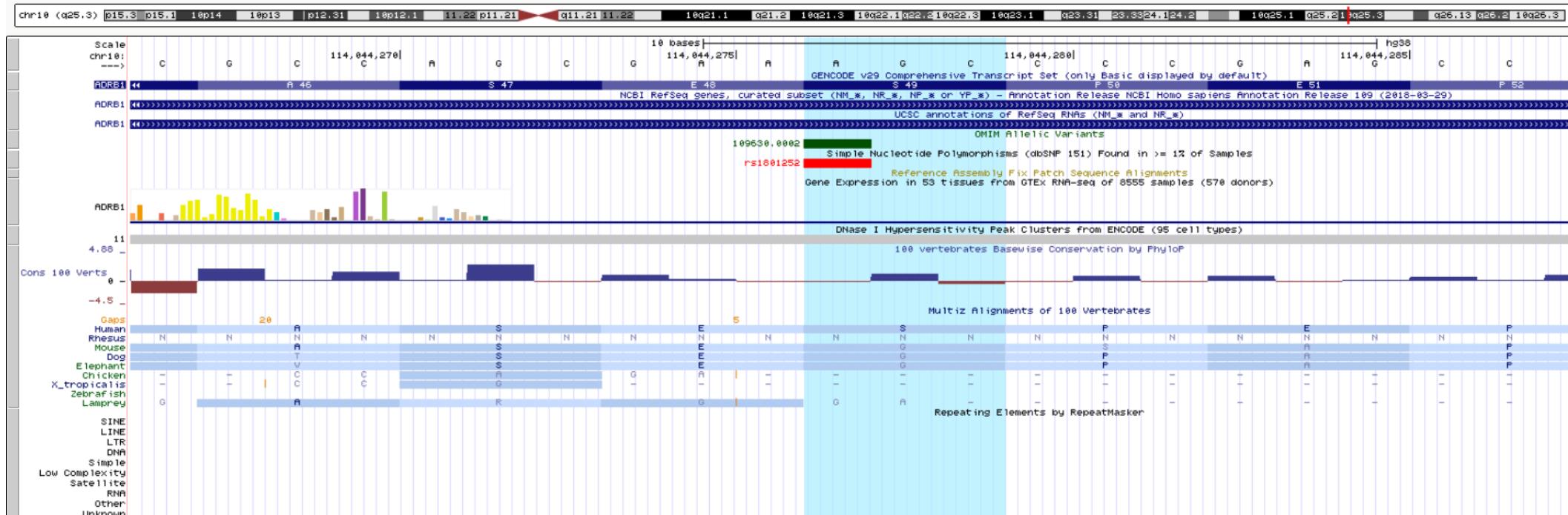
Help

About Us

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

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

chr10:114,044,267-114,044,293 27 bp. enter position, gene symbol, HGVS or search terms go



move start

< 2.0 >

track search

default tracks

default order

hide all

add custom tracks

track hubs

configure

multi-region

reverse

resize

refresh

collapse all

expand 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.



Mapping and Sequencing

refresh



Genes and Gene Predictions

refresh



Phenotype and Literature

refresh

DIAMO UNO SGUARDO AL CONTESTO → ZOOM OUT 10 X



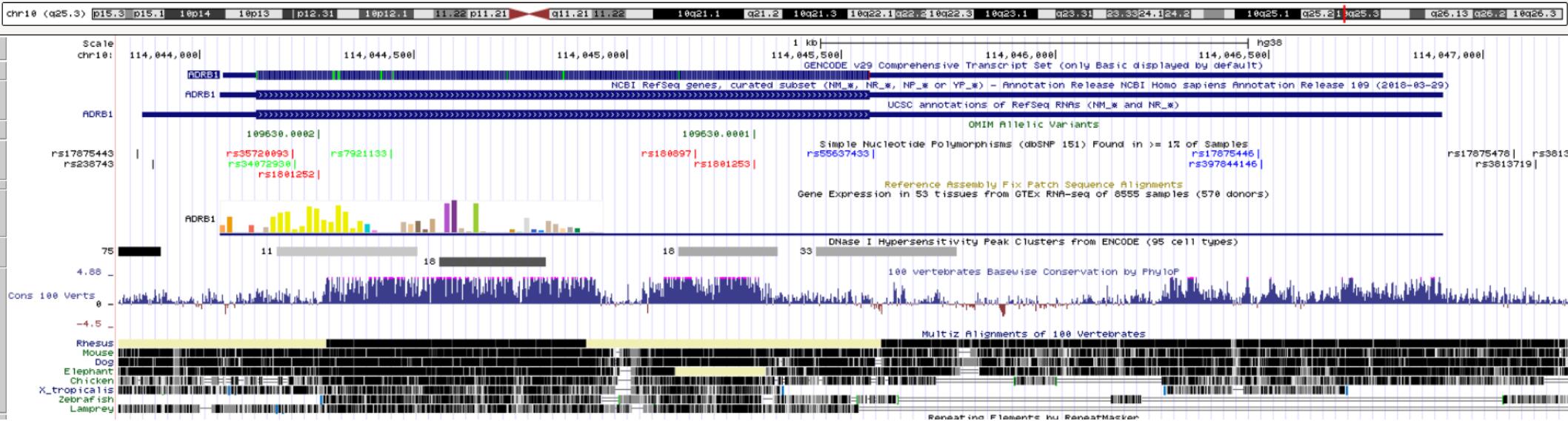
zoom out

1.5x

3x

10x

100x



Traccia: dbSNP

| | | | | | | | | | | | |
|--------------|-------|---|--------|-------|---|---------------------|-------|---|-------------------------|-----|---|
| Unknown | black | ▼ | Locus | black | ▼ | Coding - Synonymous | green | ▼ | Coding - Non-Synonymous | red | ▼ |
| Untranslated | blue | ▼ | Intron | black | ▼ | Splice Site | red | ▼ | | | |

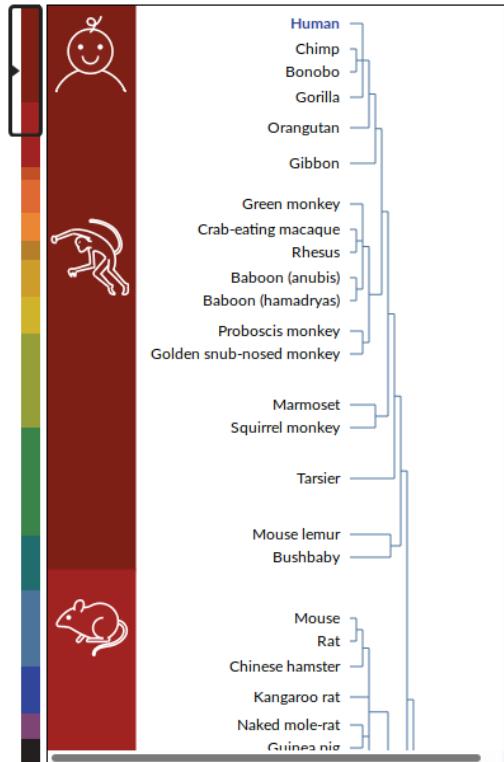
Browse>Select Species

POPULAR SPECIES



Enter species or common name

REPRESENTED SPECIES



Find Position

Human Assembly

Dec. 2013 (GRCh38/hg38)

GO

Position/Search Term

CMAHP

Gene symbol or search terms

743,044,295-43,125,483

Human Genome Browser - hg38 assembly

[view sequences](#)

il Giornale.it cronache 8 Gennaio 2019

Scoperto il "gene del maratoneta"

Si chiama Cmah, durante l'evoluzione si è «spento». Aiuta la resistenza nella corsa



Assembly Details

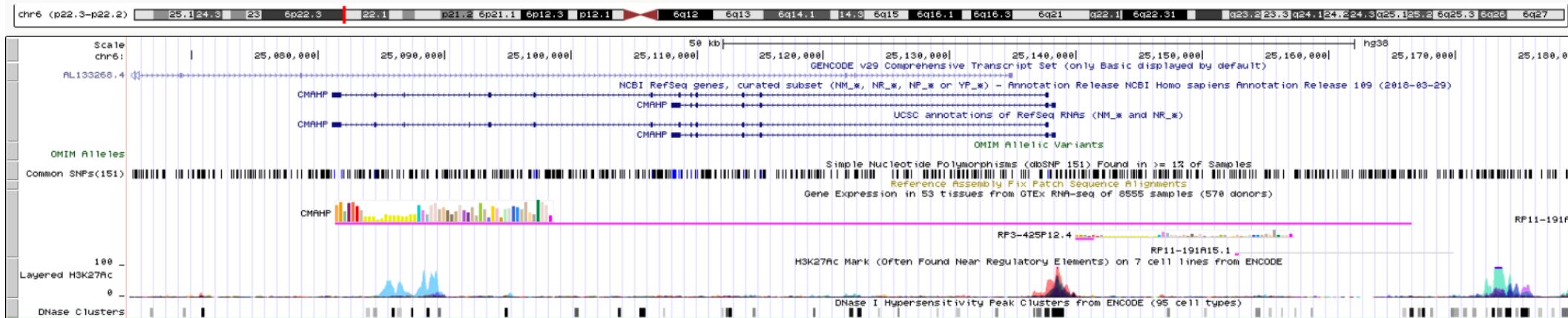
The GRCh38 assembly is the first major revision of the human genome released in more than four years. As with the previous GRCh37 assembly, the [Genome Reference Consortium](#) (GRC) is now the primary source for human genome assembly data submitted to GenBank. Beginning with this release, the UCSC Genome Browser version numbers for the human assemblies now match those of the GRC to minimize version confusion. Hence, the GRCh38 assembly is referred to as "hg38" in the Genome Browser datasets and documentation. For a glossary of assembly-related terms, see the [GRC Assembly Terminology](#) page.

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

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

chr6:25,065,073-25,209,052 143,980 bp. enter position, gene symbol, HGVS or search terms

go



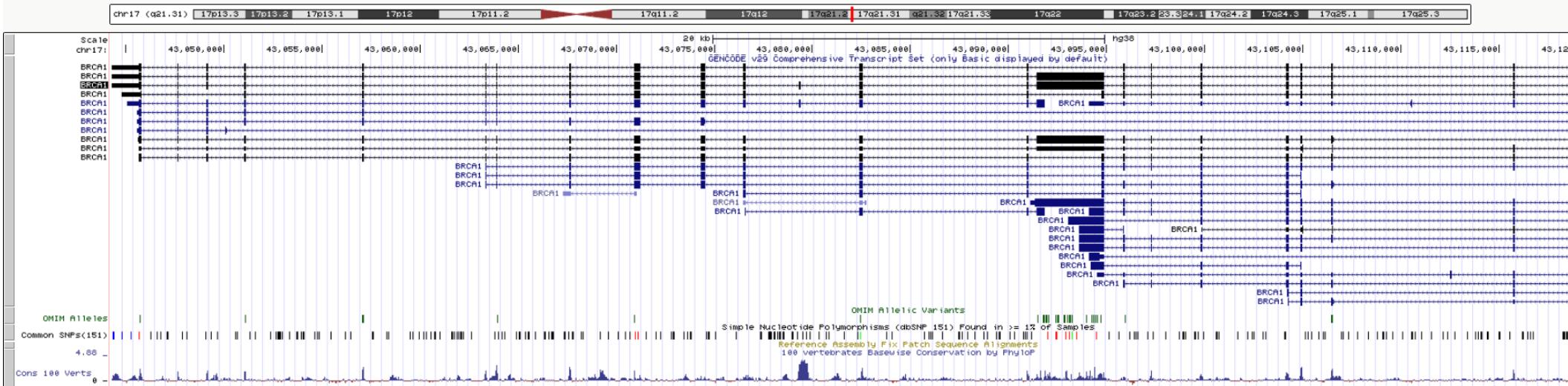
tra parentesi... che cos'è un gene?

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

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

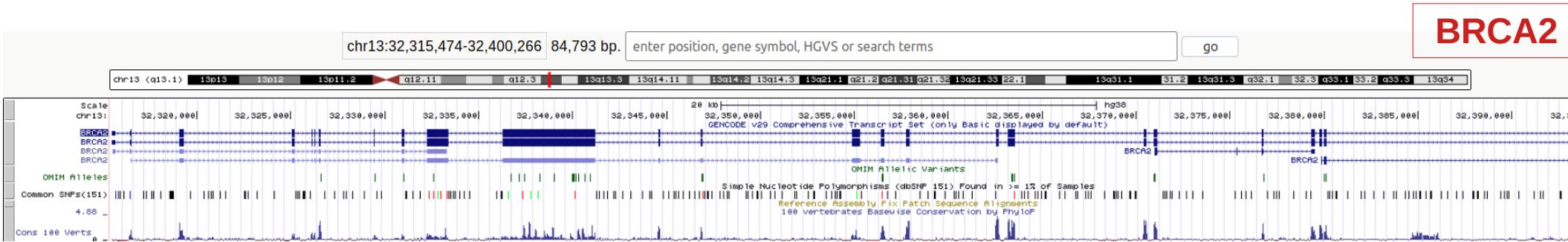
chr17:43,044,295-43,125,483 81,189 bp. enter position, gene symbol, HGVS or search terms

BRCA1



chr13:32,315,474-32,400,266 84,793 bp. enter position, gene symbol, HGVS or search terms

BRCA2





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Help

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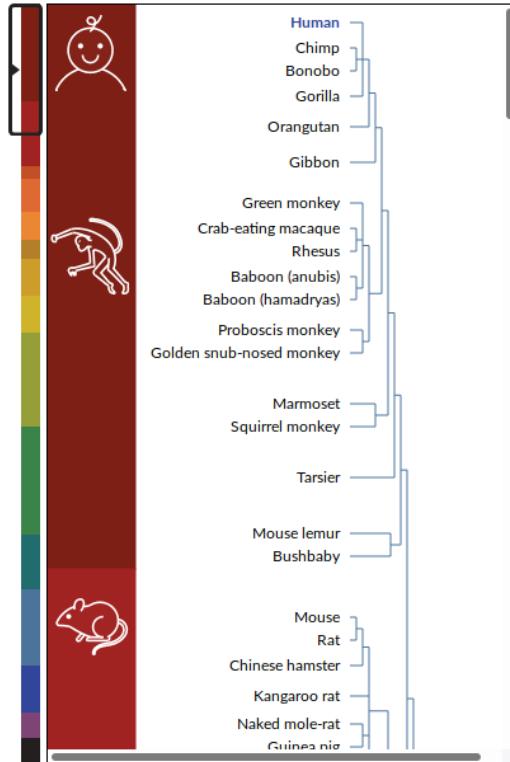
Browse>Select Species

POPULAR SPECIES



Enter species or common name

REPRESENTED SPECIES



Find Position

Human Assembly

Dec. 2013 (GRCh38/hg38)

GO

Position/Search Term

LIMS1

Type symbol or search terms

743,044,295-43,125,483

Human Genome Browser - hg38 assembly

UCSC Genome Browser assembly ID: hg38
Sequencing/Assembly provider ID: GenBank
Assembly date: Dec. 2013 initial release
Assembly accession: GCA_000001405
NCBI Genome ID: 51 (Homo sapiens (human))
NCBI Assembly ID: 5800238 (GRCh38)
BioProject ID: PRJNA31257

Search the assembly:

- **By position or search term:** Use the coordinate range; mRNA, EST, or Search term.
- **By gene name:** Type a gene name associated with that gene. [More information](#)
- **By track type:** Click the "track search" link.

Download sequence and annotation data

- [Using rsync \(recommended\)](#)
- [Using FTP](#)
- [Using HTTP](#)
- [Data use conditions and restrictions](#)
- [Acknowledgments](#)

Assembly Details

The GRCh38 assembly is the first major genome assembly released by the International Human Genome Sequencing Consortium (GRC). It is now the primary source for human genome assembly data submitted to GenBank. Beginning with this release, the UCSC Genome Browser version numbers for the human assemblies now match those of the GRC to minimize version confusion. Hence, the GRCh38 assembly is referred to as "hg38" in the Genome Browser datasets and documentation. For a glossary of assembly-related terms, see the GRC [Assembly Terminology](#) page.

17 Maggio 2019**Il Messaggero.it**

Trapianti, scoperto il gene che provoca il rigetto: si potranno ridurre i casi di incompatibilità

SALUTE > RICERCA

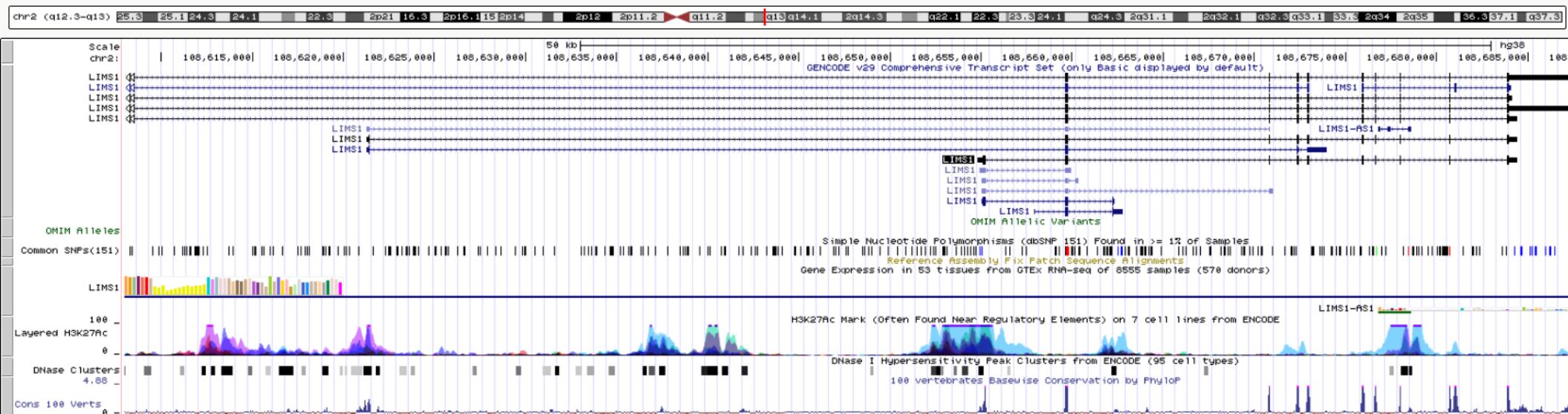


UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

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

chr2:108,607,982-108,708,007 100,026 bp. enter position, gene symbol, HGVS or search terms

go



La nostra idea di *locus genico*
PRIMA e DOPO
Il Progetto Genoma Umano



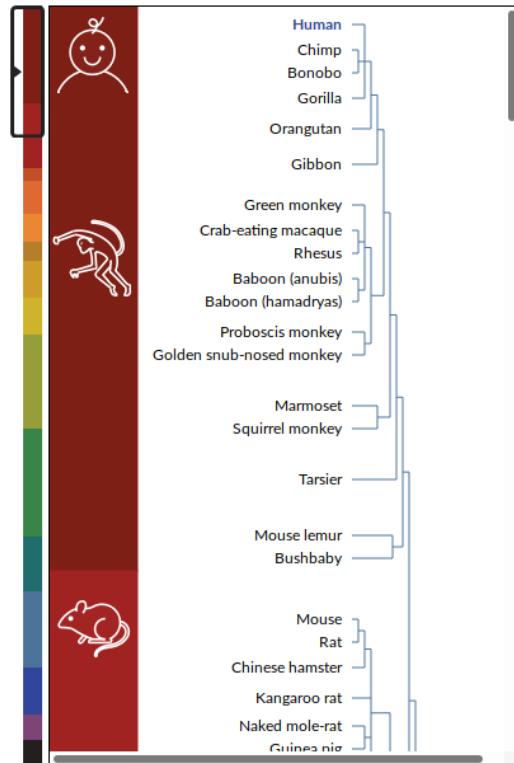
Browse>Select Species

POPULAR SPECIES



Enter species or common name

REPRESENTED SPECIES



Find Position

Human Assembly

Dec. 2013 (GRCh38/hg38)

GO

Position/Search Term

ACE2

Gene symbol or search terms

743,044,295-43,125,483

CARDIOLOGIA

Fabio Di Todaro

PUBBLICATO IL 29-04-2020



TAG:

[IPERTENSIONE](#) [ACE-INIBITORI](#)
[ANTICORPI](#) [POLMONITE](#)
[RICERCA CORONAVIRUS](#)
[BAMBINI CORONAVIRUS](#)

Coronavirus, ACE2 a due facce: e se proteggesse donne e bambini?

ACE2 è la «porta» d'accesso per il virus, ma anche un possibile «alleato» nella forma solubile. L'ipotesi di Elena Ciaglia, sostenuta da Fondazione Veronesi

IP
P

I TOOL DE

I CONTROL
FARE

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

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

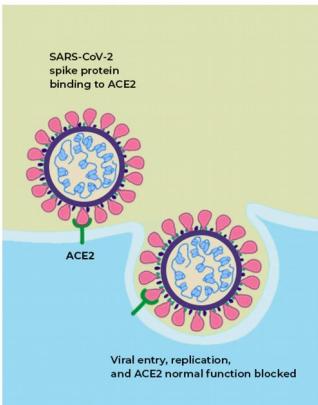
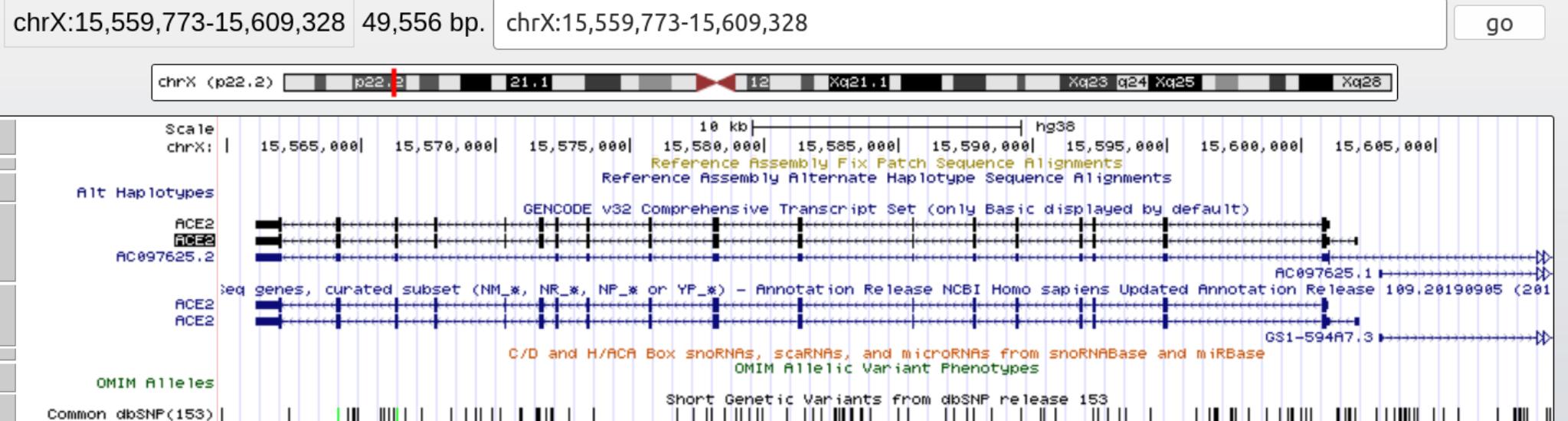


Figura tratta da:

The Conversation, What is the ACE2 receptor, how is it connected to coronavirus and why might it be key to treating COVID-19? May 14, 2020



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Tools

Mirrors

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Projects

Help

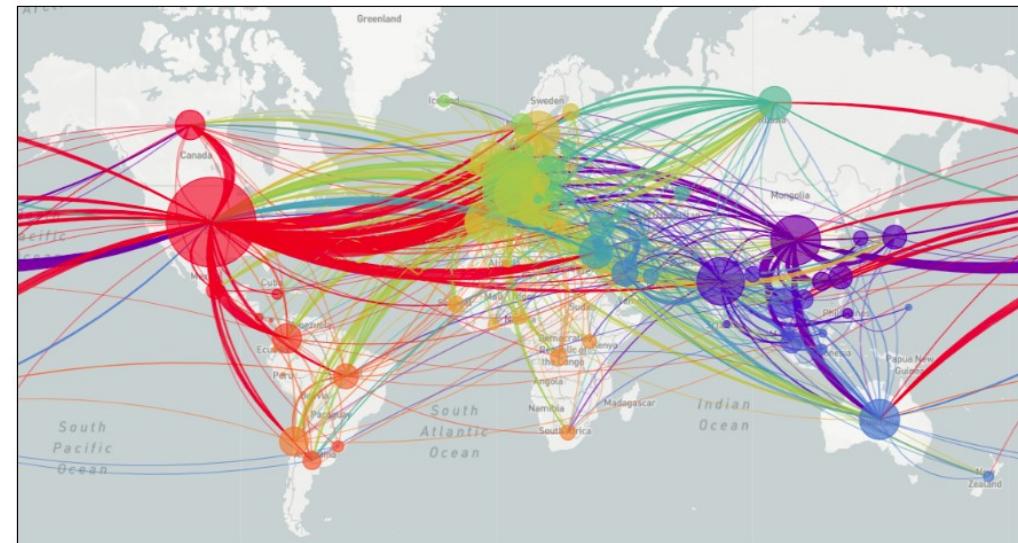
About Us

COVID-19 Pandemic Resources at UCSC

Updated: September 8, 2020

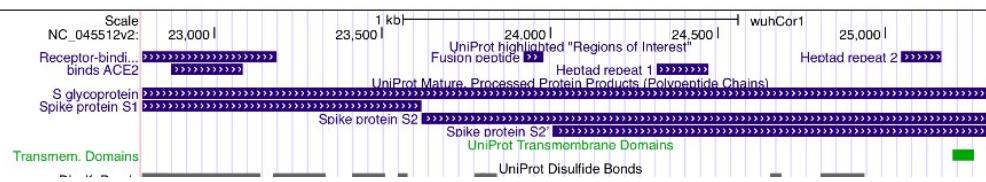
The SARS-CoV-2 coronavirus emerged in December 2019 as a novel human pathogen causing a severe acute respiratory syndrome (COVID-19). In the following months, the disease spread internationally and was **declared a pandemic by the World Health Organization** on March 11, 2020.

We at the **UC Santa Cruz Genomics Institute** are responding to the urgency of supporting biomedical research aimed at developing therapeutics and a vaccine for this devastating illness by fast-tracking the **UCSC Genome Browser for SARS-CoV-2** and incorporating relevant biomedical datasets such as single-cell lung gene expression into the **UCSC Cell Browser**. A manuscript describing this work, **The UCSC SARS-CoV-2 Genome Browser**, is *in press* and currently available from the **bioRxiv** preprint server.



COVID-19 transmission as of May 30, 2020
Latest situation report from Nextstrain.org

UCSC Genome Browser view of SARS-CoV-2 genomic datasets



COVID-19 and Lung gene expression data in the UCSC Cell Browser:

COVID-19 Datasets:

- **Bronchoalveolar Immune Cells in COVID-19**
- **COVID-19 Airways**

Grazie per l'attenzione!



Domande?

teresa.colombo@cnr.it

