

The “Neopolitan Ice Cream” World of Genome Browsing:

- UCSC Genome Browser
 - <http://genome.cse.ucsc.edu/>
- Ensembl
 - <http://www.ensembl.org/>
- NCBI Map Viewer
 - <http://www.ncbi.nlm.nih.gov/mapview/>

The underlying data is common for all three “flavors” of Genome Browsers.

- NCBI, UCSC and Ensembl use the same human genome assembly that is generated by NCBI but release timing is different between sites.
- Note version of assembly to which you are referring, since available precomputed info and locations of features will be different between assemblies.
- On March 14, 2005 they were using build 35.

Let's compare the view of the NRG1 gene in all three genome browsers..

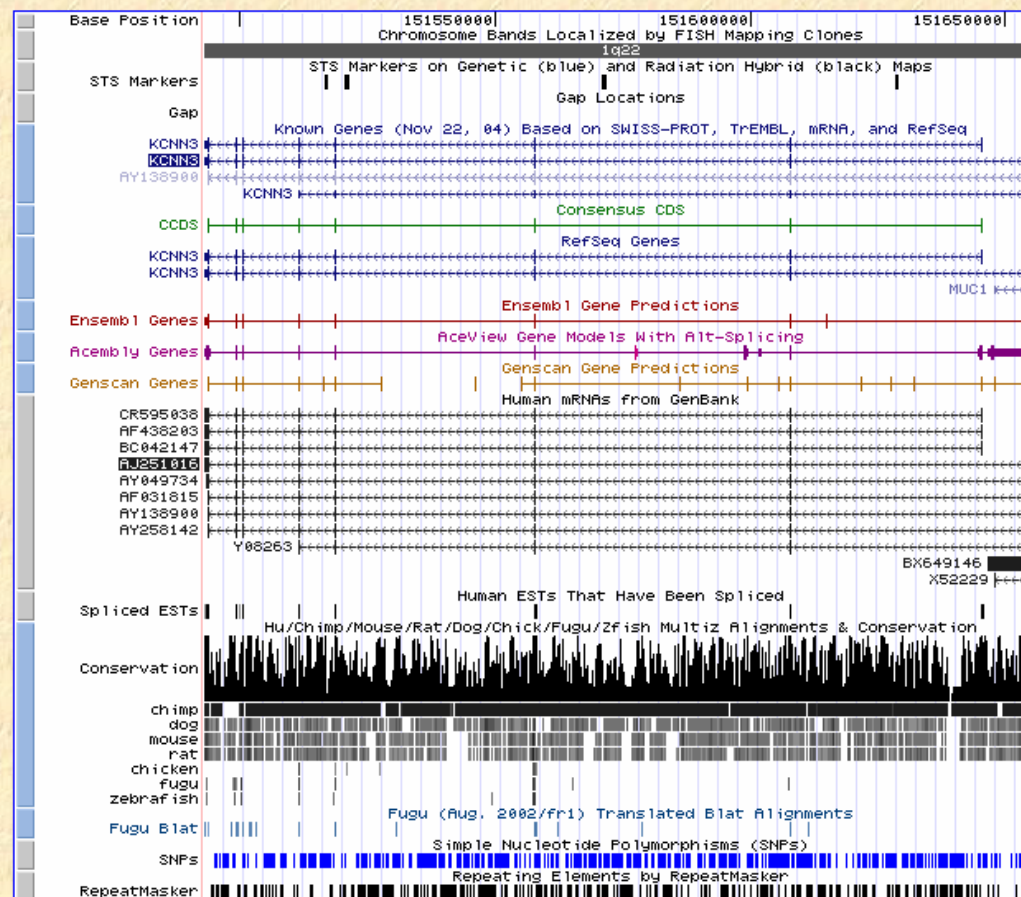
- Compare the view of the genomic region on chr 1 that contains the human KCNN3 gene
 - Common features:
 - Coordinate system is based on the build
 - Zoom in and out
 - Annotations displayed – ie. Gene features
 - Major Differences:
 - Each Browser has a very different look and feel
 - Annotation information displayed
 - Navigating through the information

UCSC Genome Browser on Human May 2004 Assembly

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

position chr1:151,492,989-151,655,827 jump clear size 162,839 bp. configure

chr1 (q22) 

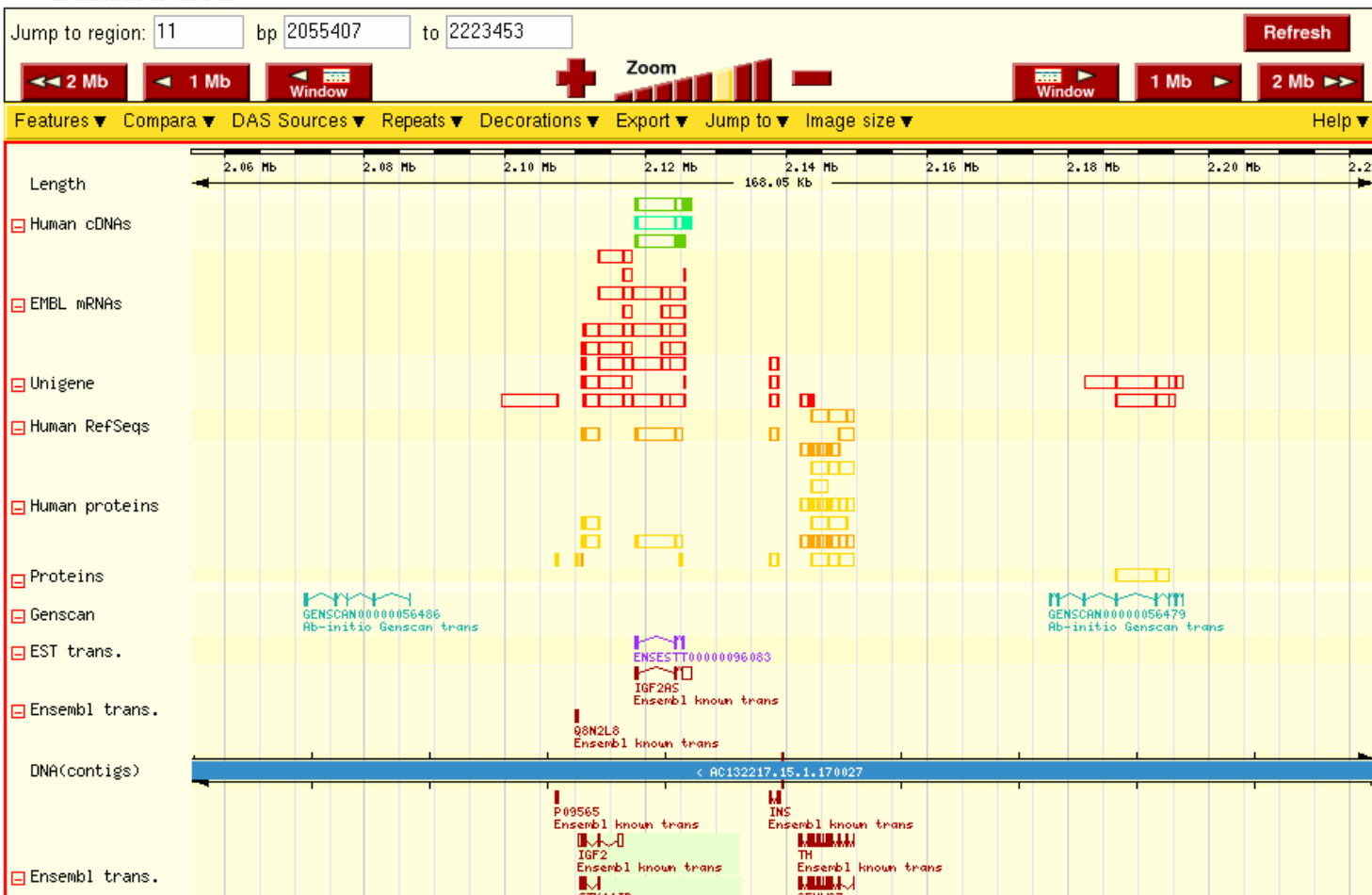


Chromosome 11



Overview

Detailed view





[PubMed](#)
[Entrez](#)
[BLAST](#)
[OMIM](#)
[Taxonomy](#)
[Structure](#)

[Map Viewer Home](#)

[Map Viewer Help](#)
[Human Maps Help](#)
[FTP](#)
[Data As Table View](#)

[Maps & Options](#)

Compress Map ☒

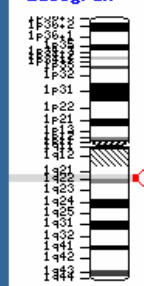
Region Shown:

149M

152M

You are here:

[Ideogram](#)



☒ default
☐ master

[Homo sapiens build 35.1](#)

Chromosome: [[1](#)] [2](#) [3](#) [4](#) [5](#) [6](#) [7](#) [8](#) [9](#) [10](#) [11](#) [12](#) [13](#) [14](#) [15](#) [16](#) [17](#) [18](#) [19](#) [20](#) [21](#) [22](#) [X](#) [Y](#) [MT](#)

Query: KCNN3

Master Map: Genes On Sequence

[Summary of Maps](#)

[Maps & Options](#)

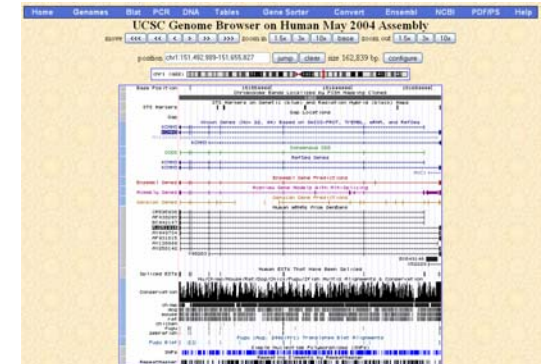
Region Displayed: 149M-152M bp

[Download/View Sequence/Evidence](#)

Gen...	HsUniG	Genes_seq	Symbol	O	LinkOut	E	Cyto	Description
		149.5M	PGLYRP3	↑	OMIM sv pr dl ev mm hm ccds	C	1q21	peptidoglycan recognit
		149.6M	PGLYRP4	↑	OMIM sv pr dl ev mm hm	C	1q21	peptidoglycan recognit
		149.7M	NPR1	↓	OMIM sv pr dl ev mm hm ccds	C	1q21-q22	natriuretic peptide recep
		149.8M	FLJ21919	↓	sv pr dl ev mm hm ccds	C	1q21.3	hypothetical protein FL
		149.9M	P66beta	↑	sv pr dl ev mm hm ccds	C	1q21.3	transcription repressor j
		150M	KIAA0476	↑	sv pr dl ev mm hm	C	1p36.13-q31.3	KIAA0476
		150.1M	LOC91181	↑	sv pr dl ev mm hm	C	1q21.3	nuclear pore membrane
		150.2M	TPM3	↑	OMIM sv pr dl ev mm hm ccds	C	1q21.2	tropomyosin 3
		150.3M	NICE-3	↑	sv pr dl ev mm hm ccds	C	1q21.2	NICE-3 protein
		150.4M	NICE-4	↓	sv pr dl ev mm hm ccds	C	1q21.3	NICE-4 protein
		150.5M	ATP8B2	↓	OMIM sv pr dl ev mm hm ccds	C	1q21.3	ATPase, Class I, type 8
		150.6M	IL6R	↓	OMIM sv pr dl ev mm hm ccds	C	1q21	interleukin 6 receptor
		150.7M	LOC126669	↑	sv pr dl ev mm hm	C	1q21.3	hypothetical protein LO
		150.8M	DKFZp434M202	↓	sv pr dl ev mm	C	1q21.3	hypothetical protein DK
		150.9M	ADAR	↑	OMIM sv pr dl ev mm hm ccds	C	1q21.1-q21.2	adenosine deaminase, R
		151M	KCNN3	↑	OMIM sv pr dl ev mm hm ccds	C	1q21.3	potassium intermediate/
		151.1M	PMVK	↑	OMIM sv pr dl ev mm hm ccds	C	1p13-q23	phosphomevalonate kin
		151.2M	PBXIP1	↑	sv pr dl ev mm hm ccds	C	1q22	pre-B-cell leukemia tran
		151.3M						

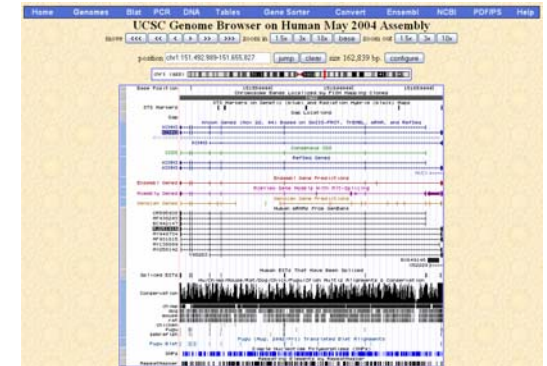
UCSC Genome Browser: Overview

- Site contains working drafts for:
 - human, chimp, dog, cow, mouse, rat, opossum, chicken, *X. tropicalis*, zebrafish, tetraodon, fugu, *C. intestinalis*, fly, honey bee, mosquito, *C. elegans*, *C. briggsae*, yeast, SARS, and target 1 of NISC comparative genomics sequencing project with tracks of sequence annotations.
- The Genome Browser and the data it displays are freely available for academic, nonprofit, and personal use with a few exceptions



UCSC Genome Browser: Useful Features & Highlights

- Useful Features
 - User Guide
 - News Archives esp. Dec 23 on genome status - Seven chromosomes are considered to be in a finished state: 6, 7, 13, 20, 21, 22, and Y.
 - Mailing List subscription and archive, via Contact page
- Highlights to Explore:
 - Genome Browser
 - Entry into genome sequence via BLAT
 - Table Browser
 - Create pdf



Ensembl: Overview



- Site produces and maintains automatic annotations on eukaryote genomes.
 - Human, mouse, zebrafish, rat (pre), chicken, mosquito, fugu, fruitfly, chimp, honeybee, tetraodon, dog, C. elegans, X. tropicalis, S. cerevisiae, cow (pre), opossum (pre)
- Access to all the data produced by the project, and to the software used to analyse and present it, is provided free and without constraints.

Ensembl: Useful Features & Highlights

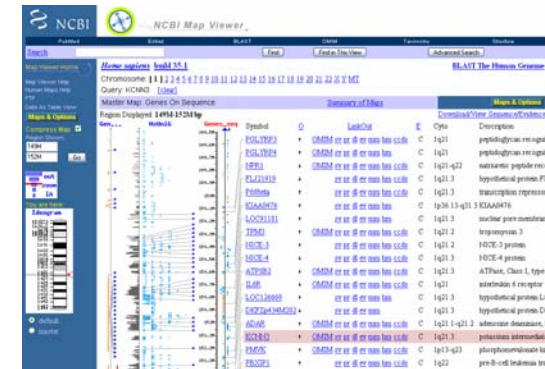
- Useful Info:
 - Help and Documentation
 - News
 - Announcements Mailing List

- Highlights to Explore:
 - Ensembl Mart
 - Entry into genome sequence via SSAHA

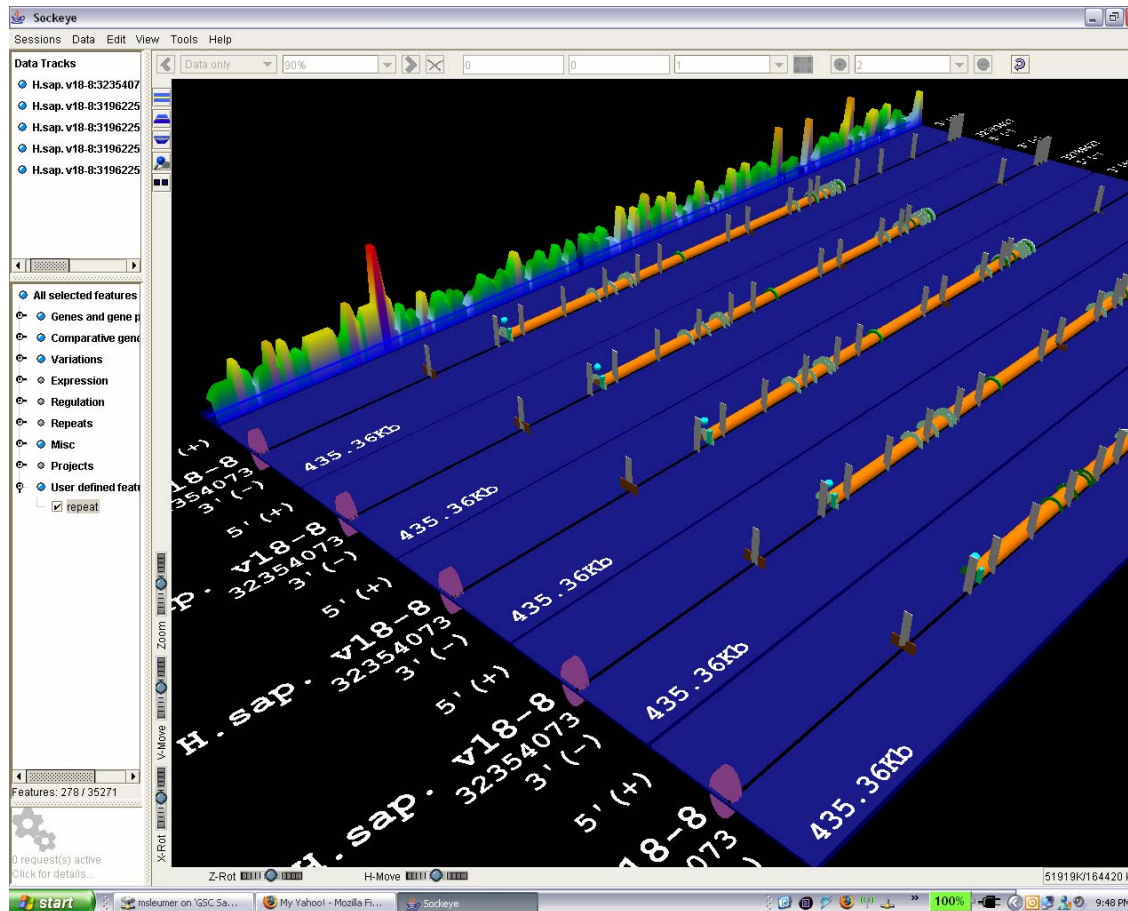


Entrez Map Viewer: Overview

- Contains genome information for:
 - Vertebrates (human, mouse, cow, dog, cat, sheep, chimp, rat, pig, zebrafish, chicken), Invertebrates (mosquito, honeybee, fruitfly, nematode), Protozoa (1 genome), Fungi (11), Plants (thale cress, oat, barley, rice, wheat, corn, tomato, soybean), Bacteria (+++), Organelles (+++), Viruses (++++)
- NCBI is the source of the assembly data (or builds) that other genome browsers use. Data is freely available for download



There are other flavors!



<http://www.bcgsc.ca/gc/bomge/sockeye/>

Applied Workshops in Bioinformatics: Mining the Genome: Using Genome Browsers to their Full Potential

Workshop Website:

http://bioinformatics.ubc.ca/applied_workshops/genome

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