

Viewing Human ENCODE RNA-seq Data

(Updated October 2013)

ENCODE has a wide variety of RNA-seq data available for a wide assortment of cell types. The Experiment Matrix provides access to, and a quick visual summary of, what is available.

1) Navigate to the Human Experiment Matrix from the ENCODE portal:

Go to <http://encodeproject.org/> or the UCSC browser. Directly select the Human Experiment Matrix link (bottom arrow).

Alternatively visit the Resources & FAQ page link (top arrow) first. Notice other useful links (such as to Tutorials, Cell Types, Antibodies, Publications, and Track and File Search). Click the link to the Human Experiment Matrix.

Assays	DNA Methylation	Methyl Array	Methyl RRBS	Open Chromatin	DNase-seq	FAIRE-seq	RNA Binding Proteins	RIP Gene ST	RIP Tiling Array	RIP Validation	RIP-seq	RNA Profiling	CAGE	Exon Array	RNA-chip	RNA-PET	RNA-seq	Small RNA-seq	TFBS & Histones	ChIP-seq	Other	5C	Hi-C
Tier 1																							
GM12878	1	1		2	1		7	4		4		6	2	6	2	12	5		133			2	
H1-hESC	1	1		2	1		3					4	1		1	10			91			1	
K562	1	1		3	16	3		6	4		4	9	7	9	6	17			224			2	
Tier 2																							
A549	1	1		1	2	1						3	2		3	10	9		87				
CD20+												1			2	1			4				

2) From the Experiment Matrix, ensure tracks selected, and click link to the RNA-seq experiments in the Cell Type of interest, such as GM12878:

3) From the resulting Track Search page, change the visibility of the desired tracks from hide to pack (left arrow).

Search for Tracks in the Human Feb. 2009 (GRCh37/hg19) Assembly

Search Advanced

Track Name: contains

and Description: contains

and Group: is Any

and Data Format: is Any

and Experiment (Assay) type: is among RNA-seq

and Cell, tissue or DNA sample: is among GM12878

and RNA Extract: is among Long PolyA+ RNA, Long PolyA- RNA, PolyA+ RNA, Total RNA

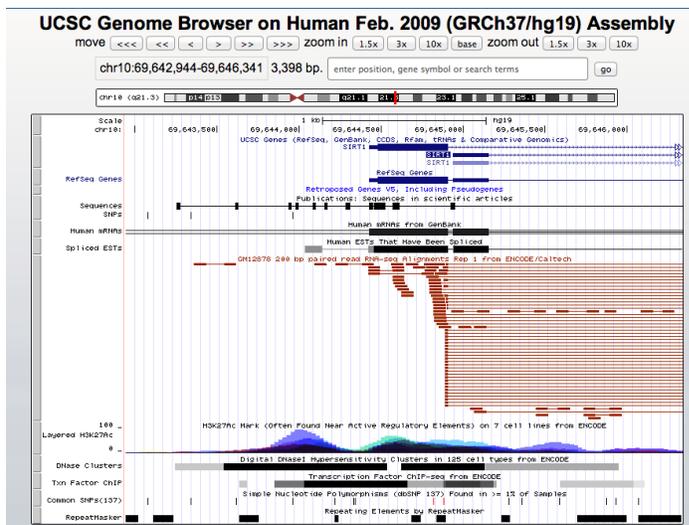
and View - Peaks or Signals: is among Any

View in Browser (1 of 77 selected)

Visibility	Track Name	Sort: by Relevance Alphabetical
<input checked="" type="checkbox"/> pack	GM12878 2x75 A 1	GM12878 200 bp paired read RNA-seq Alignments Rep 1 from EN
<input type="checkbox"/> hide	GM12878 2x75 A 2	GM12878 200 bp paired read RNA-seq Alignments Rep 2 from EN

Alternatively, modify or add new Track Search parameters (right arrow).

4) Click the “View in Browser” button to see track displayed. Then click the left bar to click through to the related RNA-seq Track Setting page.



5) From the Track Setting page, you can see other related subtracks (such as Raw Signal) as well as read the Track Description at the bottom of the page:

Caltech RNA-seq Track Settings ENCODE Downloads Subtracks Description Contact

RNA-seq from ENCODE/Caltech (ENC RNA-seq)

Maximum display mode: full Submit Cancel Reset to defaults

Select views (help): Raw Signal hide Plus Raw Signal hide Minus Raw Signal hide Splice Sites hide Alignments squish

Select subtracks by read type and cell line:

Replicate: 1 2 3 4

Cell Line	Paired 75 nt (200 bp)	Paired 75 nt (400 bp)	Single Strand-Specific 75 nt
GM12878 (Tier 1)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
H1-hESC (Tier 1)	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>