

The manual for

# **ChIP-Atlas: Colocalization**

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The ChIP-Atlas Colocalization tool is useful for identifying the transcription factors (TFs) whose bindings are colocalized with a given TF in a genome-wide manner.



## ChIP-Atlas: Colocalization

[Tutorial](#)

Predict potential protein complexes with given TFs

[H. sapiens \(hg38\)](#)[H. sapiens \(hg19\)](#)[M. musculus \(mm10\)](#)[M. musculus \(mm9\)](#)[R. norvegicus \(rn6\)](#)[D. melanogaster \(dm6\)](#)[D. melanogaster \(dm3\)](#)[C. elegans \(ce11\)](#)[C. elegans \(ce10\)](#)[S. cerevisiae \(sacCer3\)](#)

### 1. Search mode

☒ Antigens → Cell Type☐ Cell Type → Antigen

### 2. Choose Antigen

Tbx3  
Tbx4  
Tbx5  
Tcf12  
**Tcf3**  
Tcf4  
Tcf7  
Tcf7l1

### 3. Choose Cell Type Class

Blood  
Embryo  
Epidermis  
Liver  
Muscle  
Neural  
**Pluripotent stem cell**

[View Colocalization Data](#)[Download \(TSV\)](#)[Download \(GML\)](#)

mm10

Tcf3

PSC

View

This is an example of searching for TFs that may colocalize with Tcf3 in pluripotent stem cells (PSCs).

# Result

## Color legends

ChIP-seq data: H-H H-M M-M H-L M-L L-L N.D. Same (Peak intensities are **H**igh, **M**iddle or **L**ow)

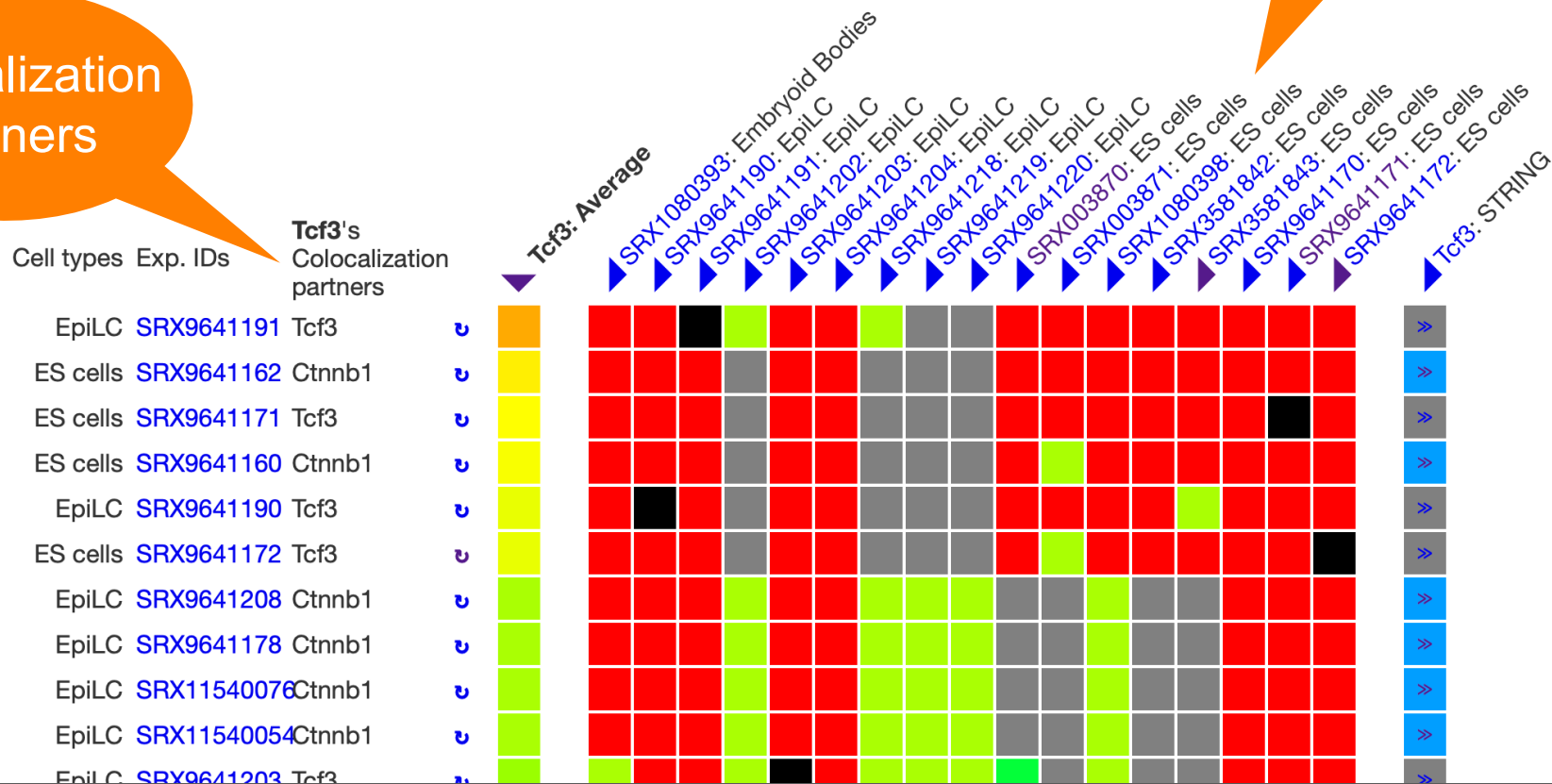
STRING data: 1000 750 500 250 0 N.D. (Values = STRING's binding scores)

Downloads: [TSV](#) (text), [GML](#) (Cytoscape)

Links: [Movie](#) and [Document](#) for [ChIP-Atlas](#) [Colocalization](#)

Colocalization partners

Tcf3 ChIP-seq



The result matrix shows ChIP-seq experiments of Tcf3 (columns) and TFs showing similar binding patterns to Tcf3 (rows).

# Result

## Color legends

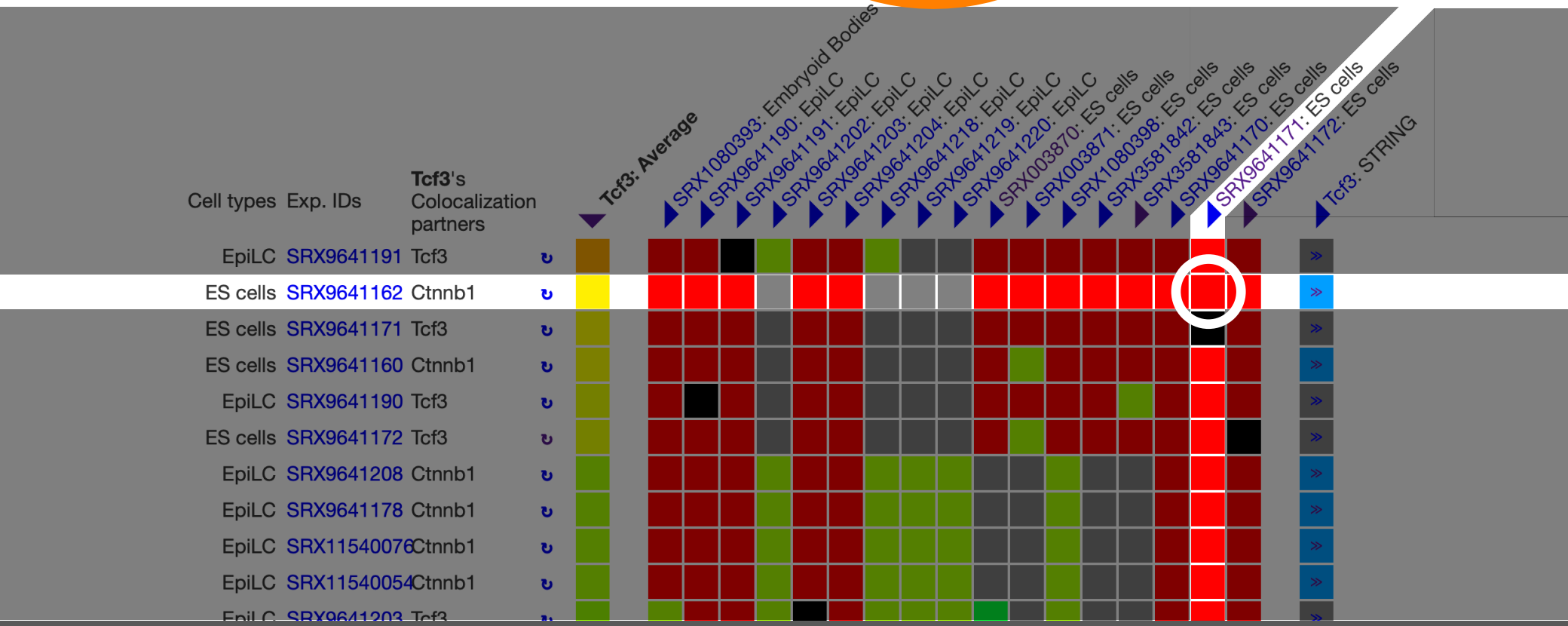
ChIP-seq data: H-H H-M M-M H-L M-L L-L N.D. Same (Peak intensities are High, Middle or Low)

STRING data: 1000 750 500 250 0 N.D. (Values = STRING binding score)

Downloads: [TSV](#) (text), [GML](#) (Cytoscape)

Links: [Movie](#) and [Document](#) for [ChIP-Atlas Colocalization](#)

Colocalization score



This is an example showing that the binding patterns of SRX9641171 (Tcf3) and SRX9641162 (Ctnnb1) are very similar, suggesting the possibility of Tcf3–Ctnnb1 colocalization in ES cells.

# Result

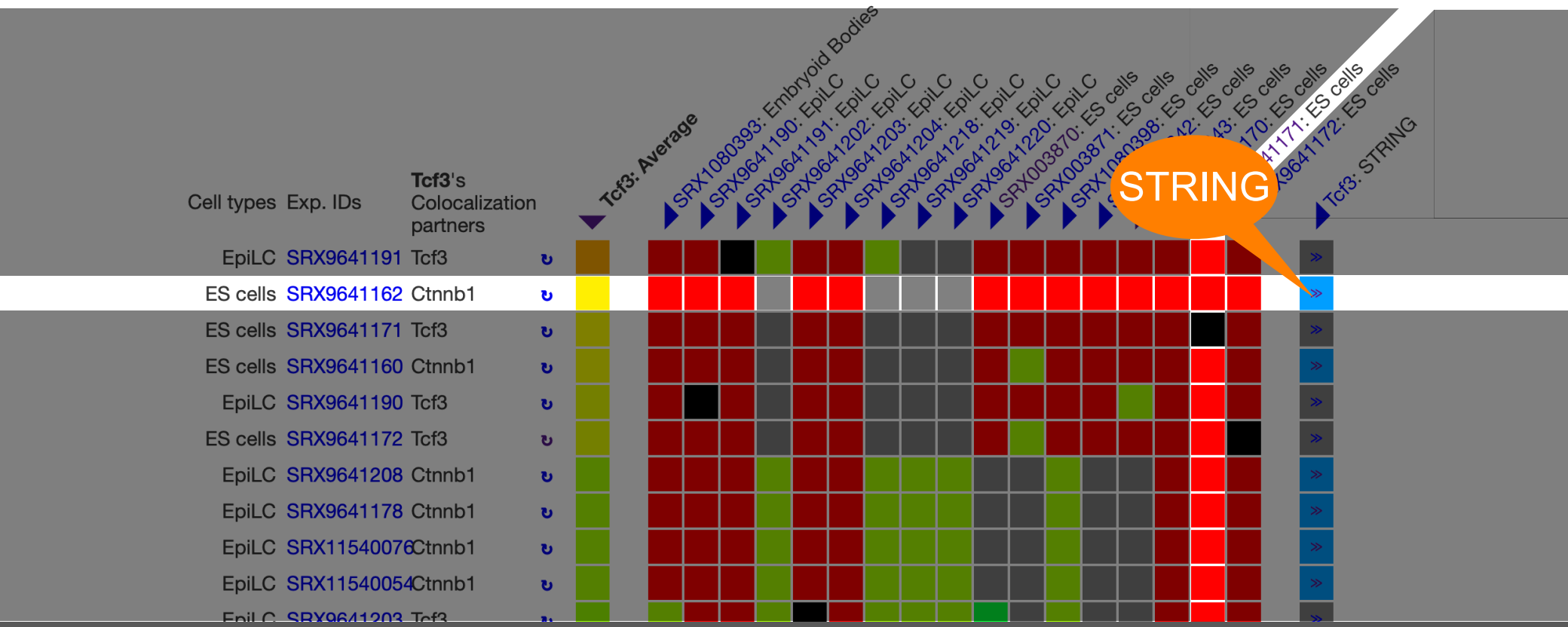
## Color legends

ChIP-seq data: H-H H-M M-M H-L M-L L-L N.D. Same (Peak intensities are **H**igh, **M**iddle or **L**ow)

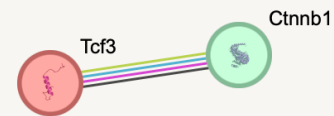
STRING data: 1000 750 500 250 0 N.D. (Values = STRING's binding scores)

Downloads: [TSV](#) (text), [GML](#) (Cytoscape)

Links: [Movie](#) and [Document](#) for [ChIP-Atlas](#) [Colocalization](#)



Click on the colored box to learn more about the Tcf3–Ctnnb1 interaction in the STRING database.



Viewers >

Legend ▾

Settings >

Analysis >

Exports >

Clusters >

+ More

- Less

**Nodes:**

Network no

splice isofo  
collapsed, i  
produced by

**Edges:**

Edges repre

association  
meaningful  
shared func  
they are phy

**Your Input:**

- Tcf3
- h
- bl
- se
- C

Interaction

Ctnnb1 [ENSMUSP00000007130]

Catenin beta-1; Key downstream component of the canonical Wnt signaling pathway. In the absence of Wnt, forms a complex with AXIN1, AXIN2, APC, CSNK1A1 and GSK3B that promotes phosphorylation on N-terminal Ser and Thr residues and ubiquitination of CTNNB1 via BTRC and its subsequent degradation by the proteasome. In the presence of Wnt ligand, CTNNB1 is not ubiquitinated and accumulates in the nucleus, where it acts as a coactivator for transcription factors of the TCF/LEF family, leading to activate Wnt responsive genes. Involved in the regulation of cell adhesion, as component of an [...]

Tcf3 [ENSMUSP00000100979]

Transcription factor E2-alpha; Transcriptional regulator. Involved in the initiation of neuronal differentiation. Heterodimers between TCF3 and tissue-specific basic helix-loop-helix (bHLH) proteins play major roles in determining tissue-specific cell fate during embryogenesis, like muscle or early B- cell differentiation. Dimers bind DNA on E-box motifs: 5'-CANNTG-3'. Binds to the kappa-E2 site in the kappa immunoglobulin gene enhancer. Binds to IEB1 and IEB2, which are short DNA sequences in the insulin gene transcription control region.

↔

Evidence suggesting a functional link:

Neighborhood in the Genome:	none / insignificant.	
Gene Fusions:	none / insignificant	
Cooccurrence Across Genomes:	none / insignificant	
Co-Expression:	yes (score 0.061). In addition, putative homologs are coexpressed in other organisms (score 0.049).	show
Experimental/Biochemical Data:	none, but putative homologs were found interacting in other organisms (score 0.265).	show
Association in Curated Databases:	yes (score 0.900).	show
Co-Mentioned in PubMed Abstracts:	yes (score 0.687)	show

The details of Tcf3–Ctnnb1 interaction is shown in the STRING website, which is an interaction database of proteins and genes based on the information from many research papers.

# Browsing the colocalization

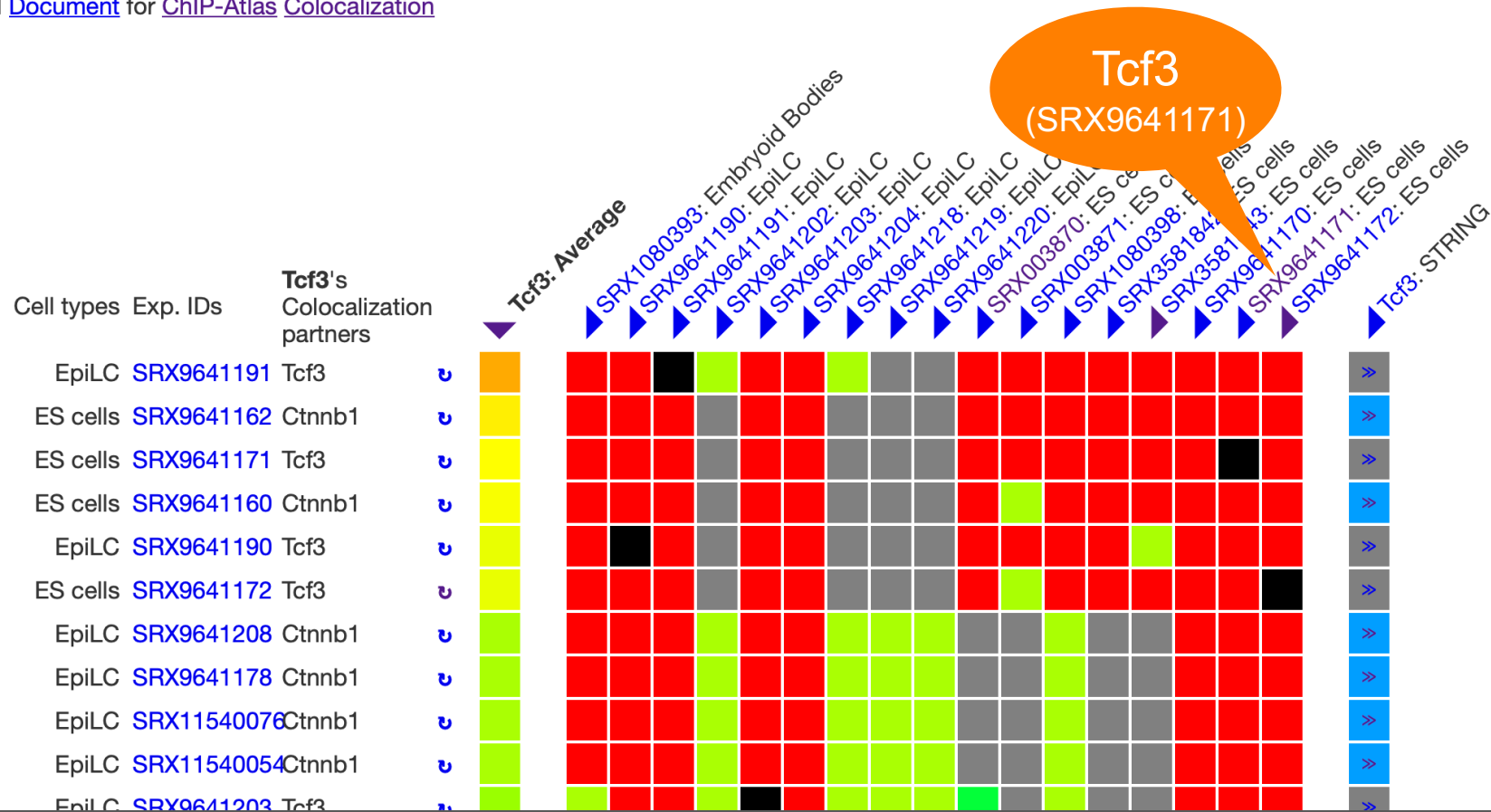
## Color legends

ChIP-seq data: H-H H-M M-M H-L M-L L-L N.D. Same (Peak intensities are **H**igh, **M**iddle or **L**ow)

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**Links:** [Movie](#) and [Document](#) for [ChIP-Atlas Colocalization](#)



Click on an experiment ID to browse the ChIP-seq data (e.g., SRX9641171).

# Browsing ChIP-seq data

SRX9641171

GSM4959636: WT NAIVE TCF3 IP ChIP-seq bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted March 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

## Sample information curated by ChIP-Atlas

### Antigen

**Antigen Class** TFs and others  
**Antigen** Tcf3

### Cell type

**Cell type Class** Pluripotent stem cell  
**Cell type** ES cells  
**NA** NA

## Attributes by original data submitter

### Sample

**source\_name** Undifferentiated r  
**chip antibody** TCF3 (Santa Cruz)  
**strain** HM1 (129)  
**genotype** wild-type  
**time point** 72h  
**treatment** none

### Sequenced DNA Library

Visualize

mm10

BigWig

IGV

Visualize ▾

Analyze ▾

Download ▾

Link Out ▾

Install and launch IGV before selecting data to visualize

For mm10

BigWig

Peak-call (q < 1E-05)

Peak-call (q < 1E-10)

Peak-call (q < 1E-20)

For mm9

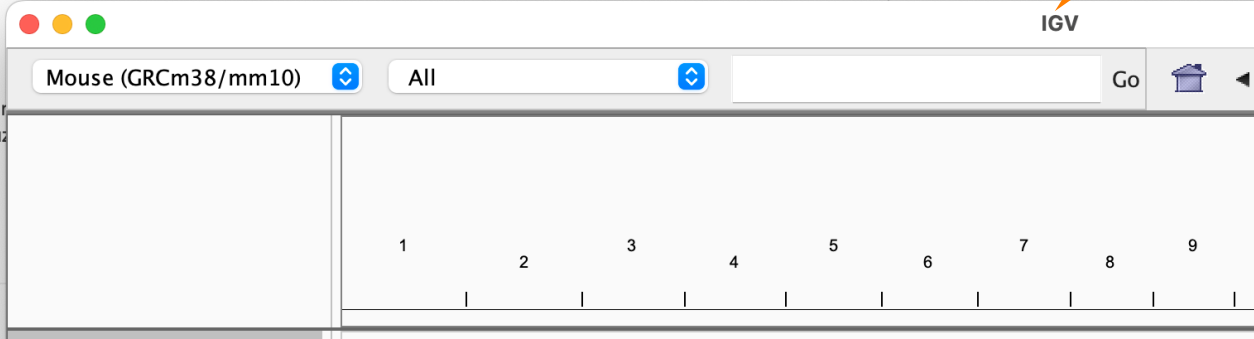
BigWig

Peak-call (q < 1E-05)

Peak-call (q < 1E-10)

Peak-call (q < 1E-20)

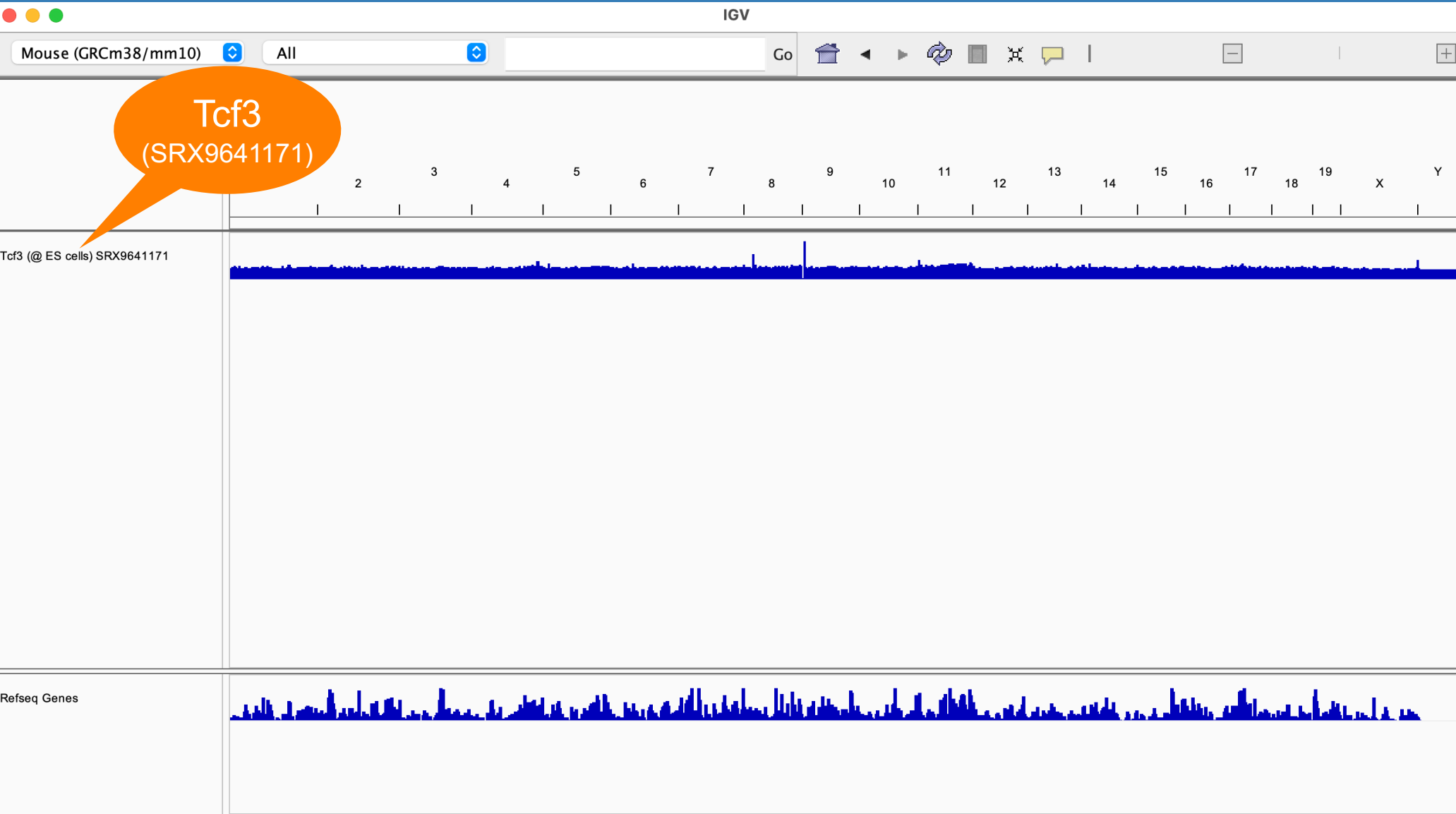
Error connecting to IGV?



The detailed information of SRX9641171 is displayed. Make sure that IGV has been launched before clicking on “Visualize” and “BigWig”.



# Browsing ChIP-seq data



The ChIP-seq data of Tcf3 (SRX9641171) is loaded into the IGV.

# Browsing the colocalization

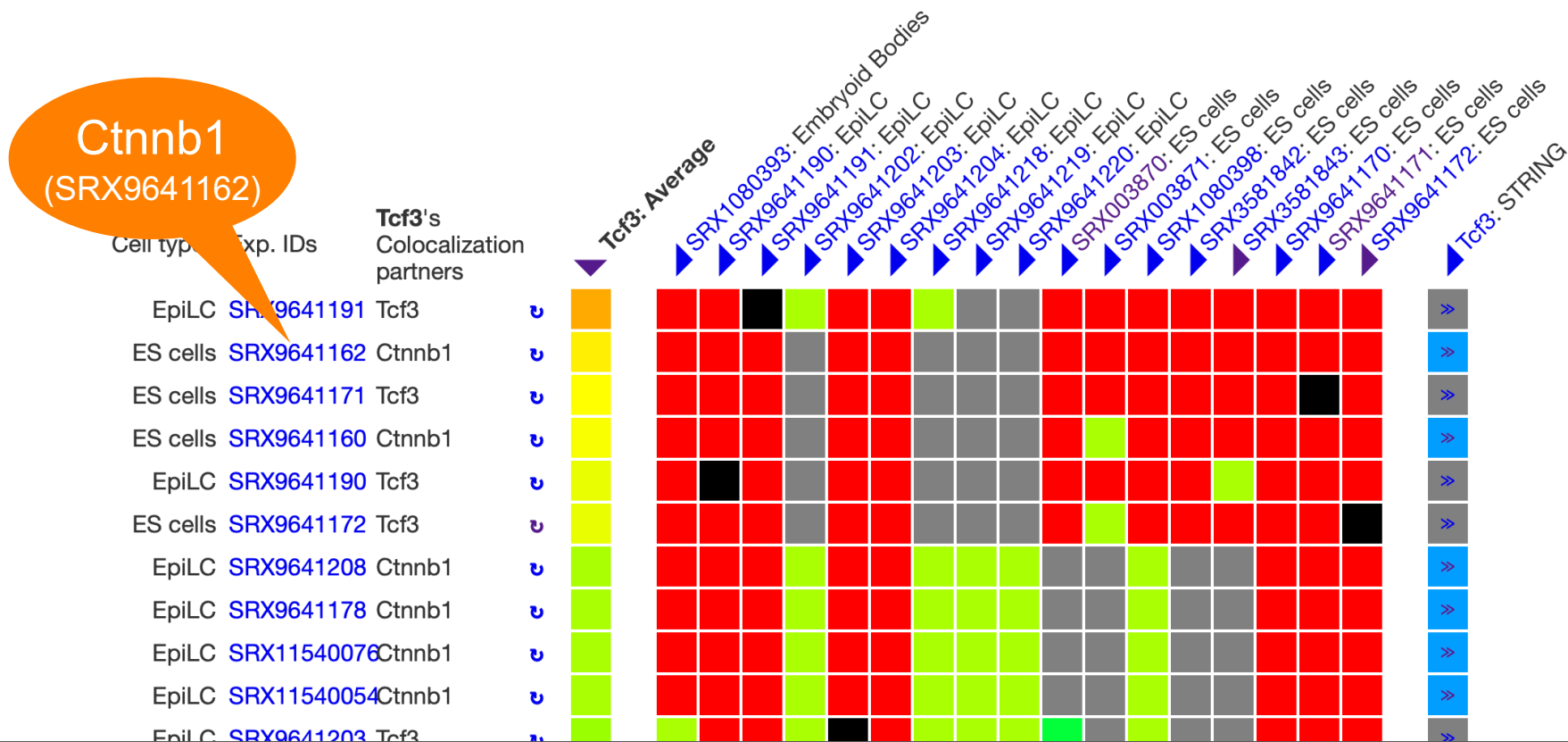
## Color legends

ChIP-seq data: H-H H-M M-M H-L M-L L-L N.D. Same (Peak intensities are **H**igh, **M**iddle or **L**ow)

STRING data: 1000 750 500 250 0 N.D. (Values = STRING's binding scores)

**Downloads:** [TSV](#) (text), [GML](#) (Cytoscape)

**Links:** [Movie](#) and [Document](#) for [ChIP-Atlas Colocalization](#)



Next, click another experiment ID to browse the ChIP-seq data (e.g., SRX9641162).

# Browsing ChIP-seq data

Peak Browser

Enrichment Analysis

Diff Analysis

Target

Visualization

Publications

Docs

Find By ID

SRX018625

Go

Search

Visualize

mm10

BigWig

SRX9641162

GSM4959627: WT NAIVE BCATENIN IP ChIP-seq replicate 3;

Visualize

Analyze

Download

Link Out

Install and launch IGV before selecting data to visualize

For mm10

BigWig

Peak-call (q < 1E-05)

Peak-call (q < 1E-10)

Peak-call (q < 1E-20)

For mm9

BigWig

Peak-call (q < 1E-05)

Peak-call (q < 1E-10)

Peak-call (q < 1E-20)

Error connecting to IGV?

Sample information curated by ChIP-Atlas

Antigen

Antigen Class

TFs and others

Antigen

Ctnnb1

Cell type

Cell type Class

Pluripotent stem cell

Cell type

ES cells

NA

NA

Attributes by original data submitter

Sample

source\_name

Undifferentiated naïve pluripotent embryonic stem cells

chip antibody

Bcatenin (Invitrogen 71-2700 rabbit)

strain

HM1 (129)

genotype

wild-type

time point

72h

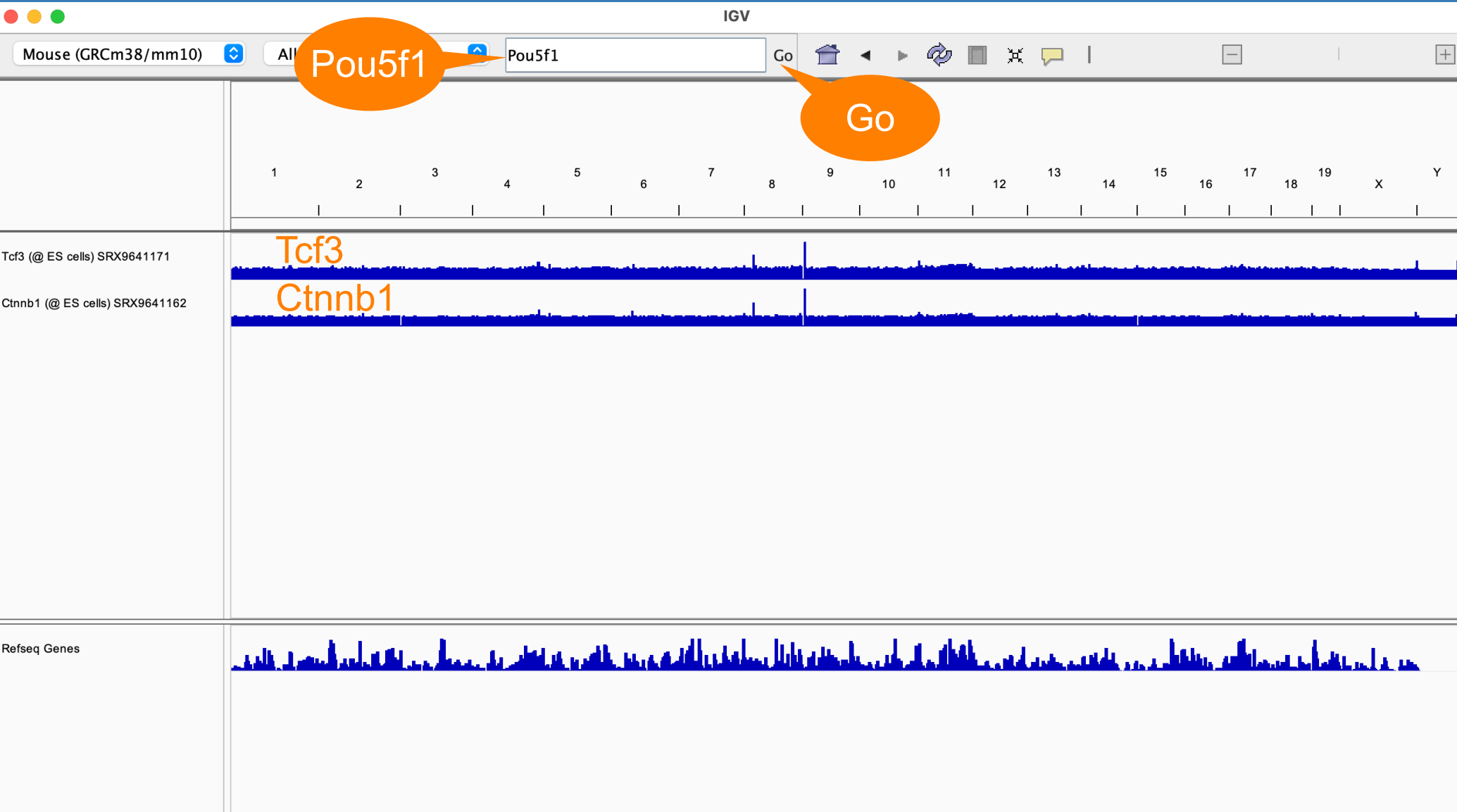
treatment

none

Sequenced DNA Library

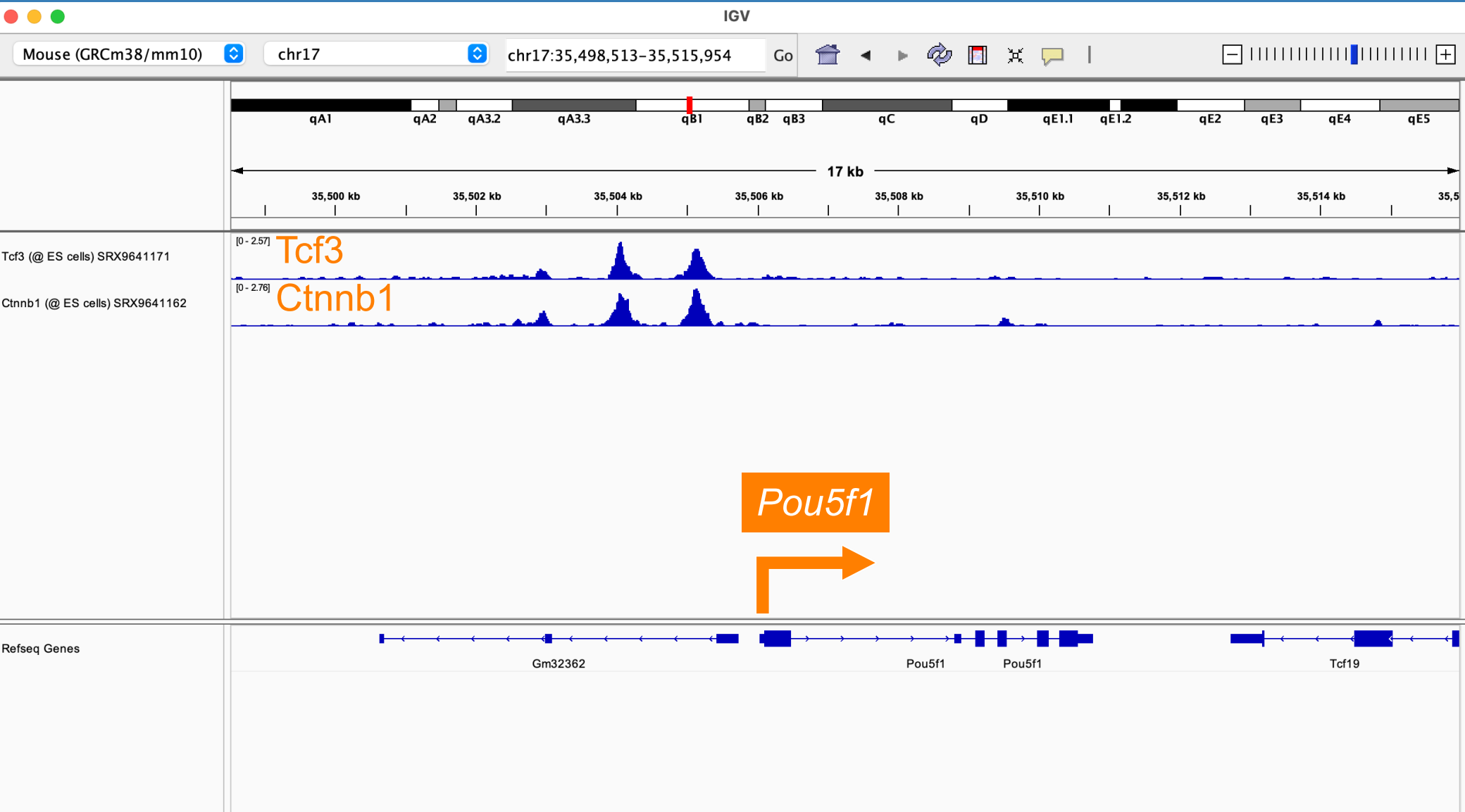
The detailed information of SRX9641162 is displayed. Click on “Visualize” and “BigWig”.

# Browsing ChIP-seq data



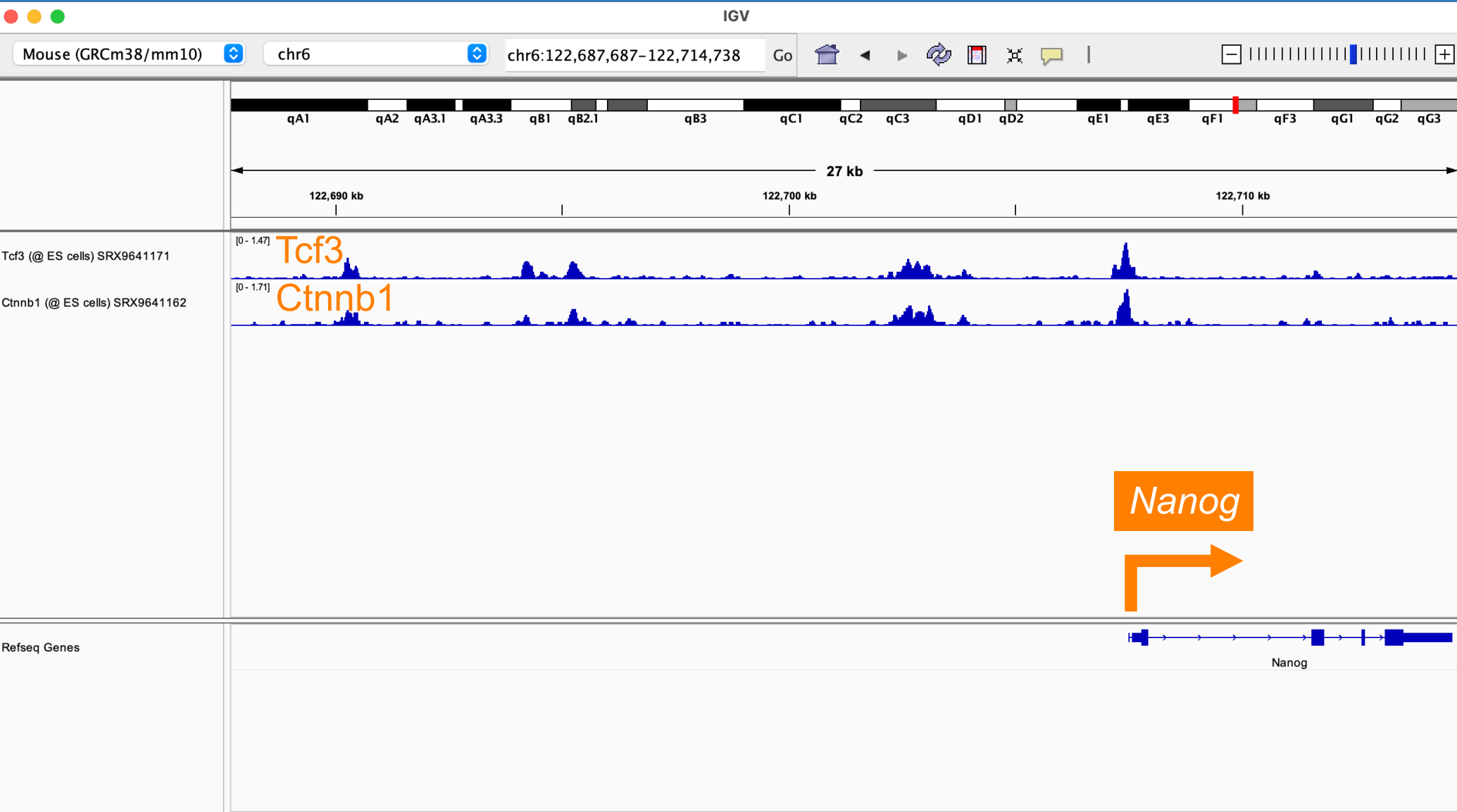
The ChIP-seq data of Tcf3 (SRX9641171) and Ctnnb1 (SRX9641162) are loaded into the IGV. Enter a gene name of your interest (e.g., *Pou5f1*).

# Browsing ChIP-seq data



Tcf3 and Ctnnb1 show a similar binding pattern around the *Pou5f1* gene locus.

# Browsing ChIP-seq data



Tcf3 and Ctnnb1 show a similar binding pattern around the *Nanog* gene locus.

# Sorting the result

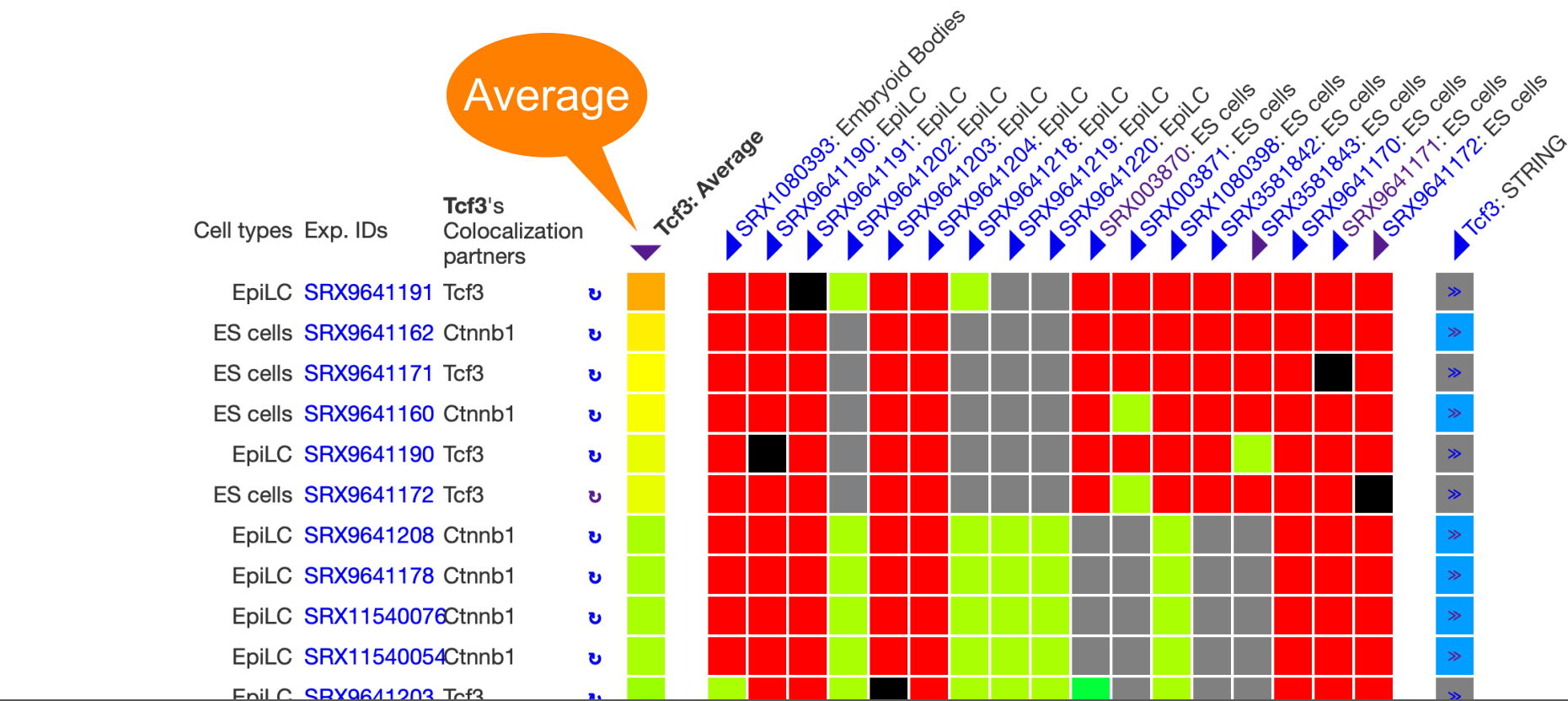
## Color legends

ChIP-seq data: H-H H-M M-M H-L M-L L-L N.D. Same (Peak intensities are **H**igh, **M**iddle or **L**ow)

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By default, the results matrix is sorted by the average of the colocalization scores for each row.

# Sorting the result

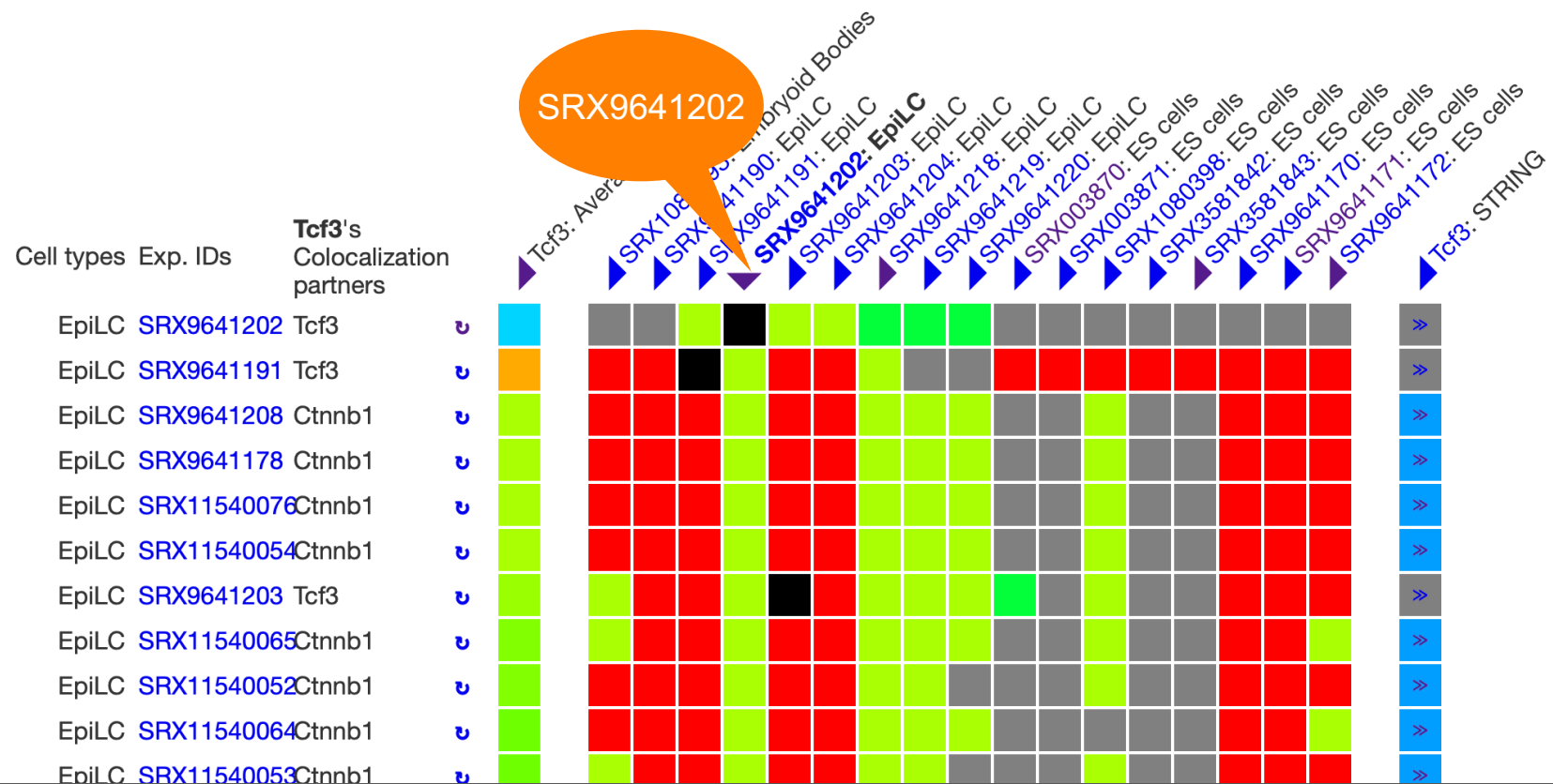
## Color legends

ChIP-seq data: H-H H-M M-M H-L M-L L-L N.D. **Same** (Peak intensities are **H**igh, **M**iddle or **L**ow)

STRING data: 1000 750 500 250 0 N.D. (Values = STRING's binding scores)

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You can sort the result matrix by the data of your interest by clicking on the ► symbol.



## Sorting the result

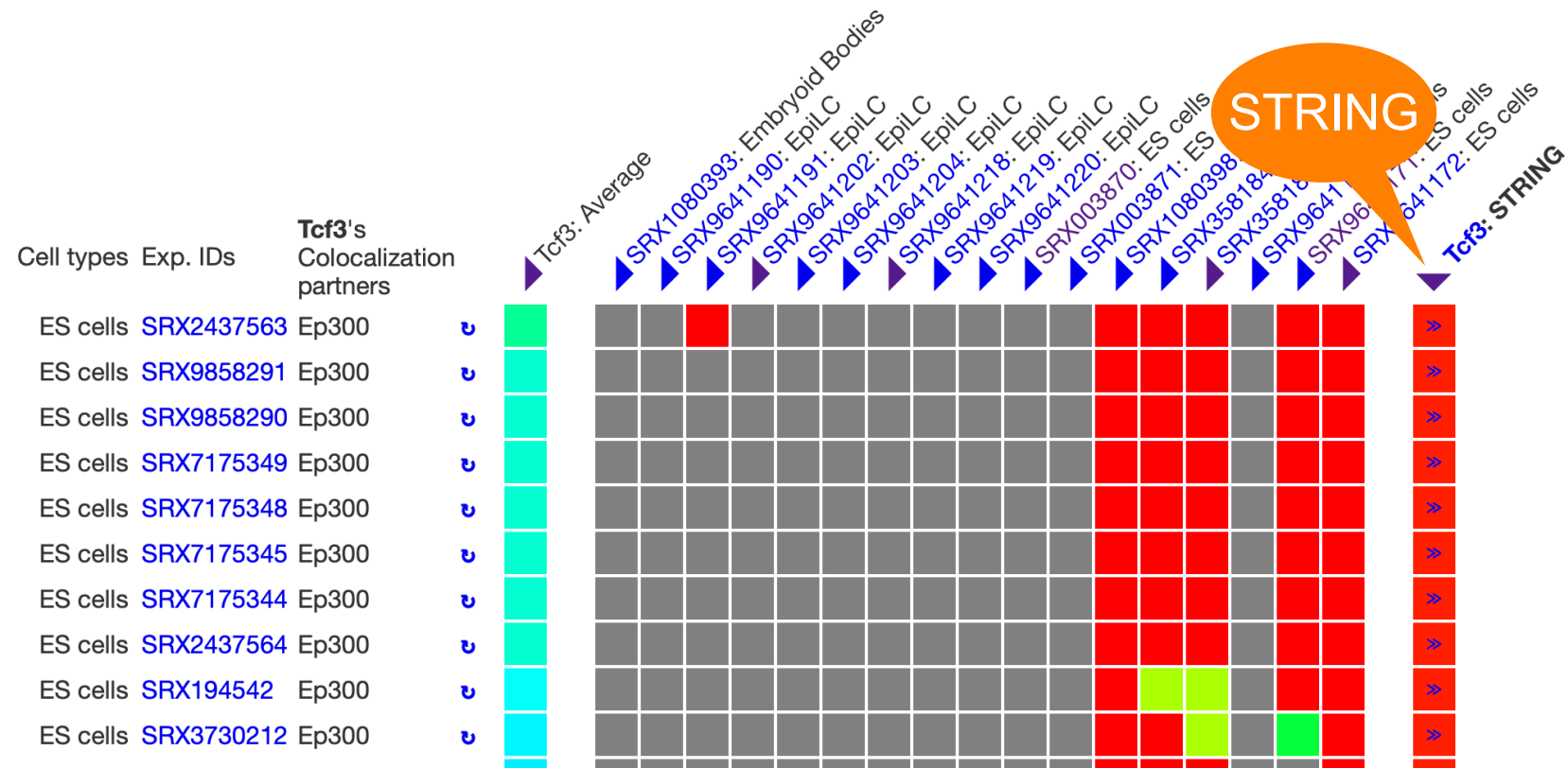
### Color legends

ChIP-seq data: **H-H** **H-M** **M-M** **H-L** **M-L** **L-L** **N.D.** **Same** (Peak intensities are **H**igh, **M**iddle or **L**ow)

STRING data: 1000 750 500 250 0 N.D. (Values = STRING's binding scores)

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