

The manual for

# **ChIP-Atlas: Target Genes**

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The ChIP-Atlas Target Genes tool is useful for identifying the target genes of given transcription factors (TFs) based on binding data from ChIP-seq experiments.



## ChIP-Atlas: Target Genes

[Tutorial movie](#)

hg38

Search for genes bound by given transcription factors

[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. Choose Antigen

MYH11  
MYNN  
MYOCD  
**MYOD1**  
MYOG  
MYRF  
MZF1  
N6AMT1

MYOD1

### 2. Choose Distance from TSS

- ☐  $\pm 1k$   
☒  $\pm 5k$   
☐  $\pm 10k$

$\pm 5 kb$

View

View Potential Target Genes

Download (TSV)



This is an example to search for the target genes of MYOD1. The  $\pm 5 kb$  regions from the transcription start sites (TSS) of these genes are bound by MYOD1.

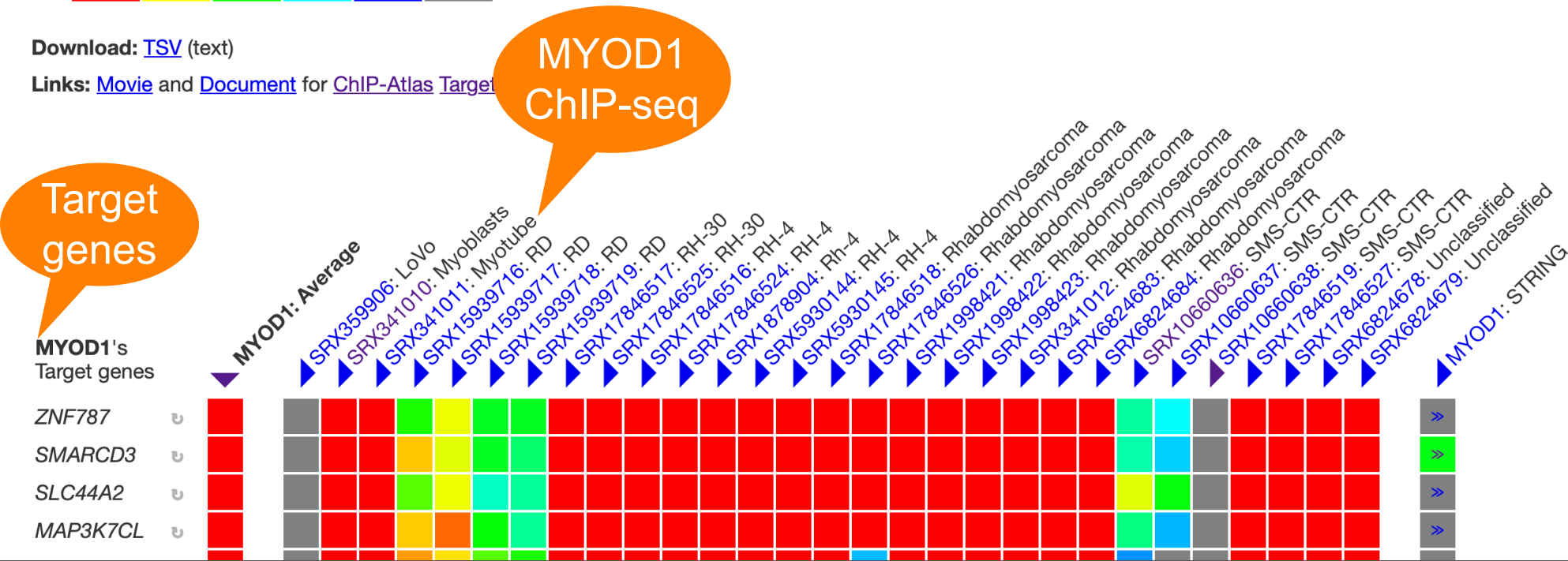
## ChIP-Atlas: Target genes

### Potential target genes for MYOD1

Query protein: MYOD1  
Distance from TSS:  $\pm 1$  kb  $\pm 5$  kb  $\pm 10$  kb  
Sort key: MYOD1 | Average

Color legends  
1000 750 500 250 1 0 (Values = Binding scores of MACS2 and STRING)

Download: [TSV](#) (text)  
Links: [Movie](#) and [Document](#) for [ChIP-Atlas Target](#)



The result matrix shows MYOD1 ChIP-seq experiments (columns) and potential target genes of MYOD1 (rows).

# Result

## ChIP-Atlas: Target genes

### Potential target genes for MYOD1

Que

Dist

Sort key

Color legends

MACS2 score

$\text{MACS2 score} = -10 \times \text{Log}_{10}[\text{Q value}]$

1000

750

500

250

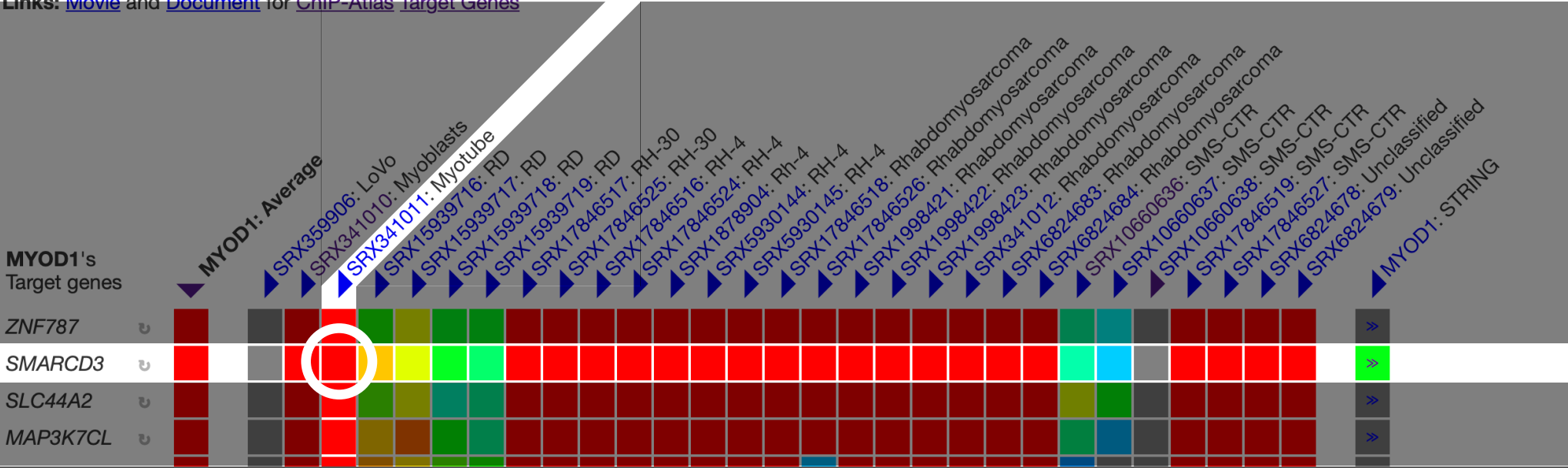
1

0

(Values = Binding scores of MACS2 and STRING)

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For example, this circled cell indicates that MYOD1 in the myotube binds to the TSS ± 5 kb region of the *SMARCD3* gene, with a MACS2 score of the ChIP-seq peak greater than 1,000.

# Result

## ChIP-Atlas: Target genes

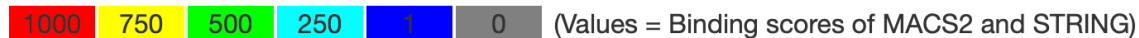
## Potential target genes for MYOD1

**Query protein: MYOD1**

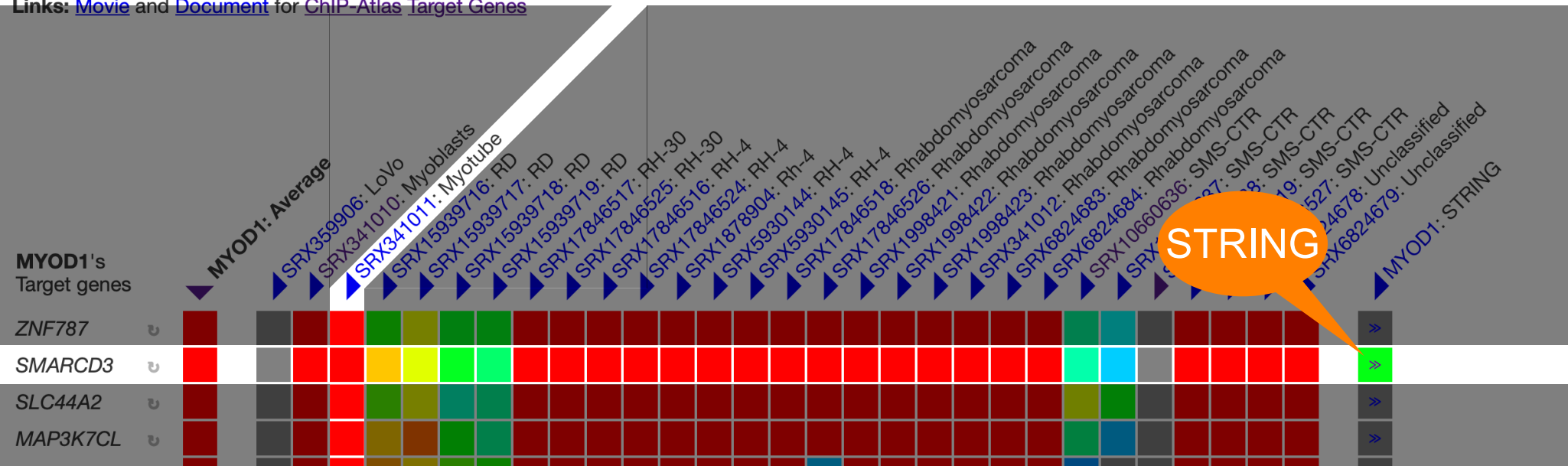
**Distance from TSS:** ± 1 kb ± 5 kb ± 10 kb

**Sort key:** MYOD1 | Average

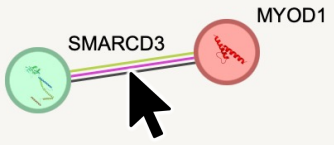
### Color legends

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



Click on the colored box to learn more about the MYOD1–SMARCD3 interaction in the STRING database.



Viewers >

Legend ▾

Settings >

Analysis >

Exports >

Clusters >

+ More

- Less

**Nodes:**

Network

splice is  
collapse  
produce

**Edges:**

Edges r

associa  
meanin  
shared  
they are

**Your Input**

MYOD1

SMARCD3

● MYOD1 [ENSP00000250003]

Myoblast determination protein 1; Acts as a transcriptional activator that promotes transcription of muscle-specific target genes and plays a role in muscle differentiation. Together with MYF5 and MYOG, co-occupies muscle-specific gene promoter core region during myogenesis. Induces fibroblasts to differentiate into myoblasts. Interacts with and is inhibited by the twist protein. This interaction probably involves the basic domains of both proteins (By similarity).



● SMARCD3 [ENSP00000262188]

SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 3; Involved in transcriptional activation and repression of select genes by chromatin remodeling (alteration of DNA-nucleosome topology). Component of SWI/SNF chromatin remodeling complexes that carry out key enzymatic activities, changing chromatin structure by altering DNA-histone contacts within a nucleosome in an ATP-dependent manner. Stimulates nuclear receptor mediated transcription. Belongs to the neural progenitors-specific chromatin remodeling complex (npBAF complex) and the neuron-spec [...]

**Evidence suggesting a functional link:**

|                                   |  |      |
|-----------------------------------|--|------|
| Neighborhood in the Genome:       | none / insignificant.  |      |
| Gene Fusions:                     | none / insignificant   |      |
| Cooccurrence Across Genomes:      | none / insignificant   |      |
| Co-Expression:                    | none, but putative homologs are coexpressed in other organisms (score 0.055).                              | show |
| Experimental/Biochemical Data:    | yes (score 0.316). In addition, putative homologs were found interacting in other organisms (score 0.054). | show |
| Association in Curated Databases: | none / insignificant   |      |
| Co-Mentioned in Pubmed Abstracts: | yes (score 0.986). In addition, putative homologs are mentioned together in other organisms (score 0.042). | show |

# Browsing ChIP-seq data

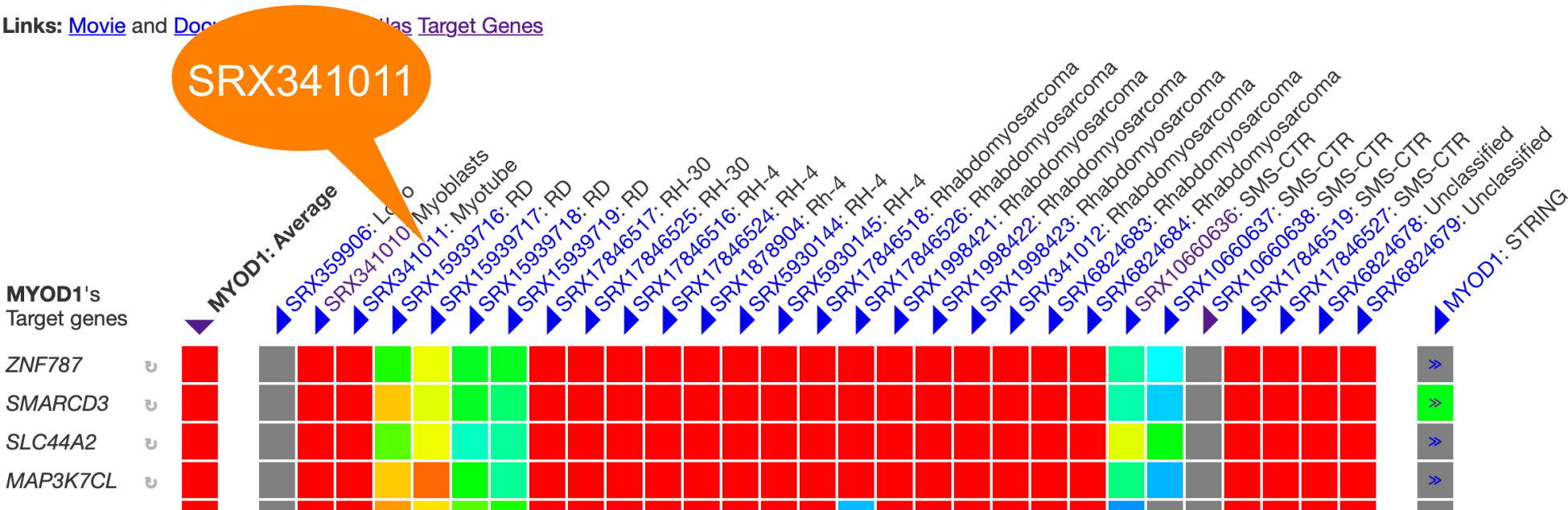
## ChIP-Atlas: Target genes

### Potential target genes for MYOD1

Query protein: MYOD1  
Distance from TSS:  $\pm 1$  kb  $\pm 5$  kb  $\pm 10$  kb  
Sort key: MYOD1 | Average

Color legends  
1000 750 500 250 1 0 (Values = Binding scores of MACS2 and STRING)

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Links: [Movie](#) and [Download ChIP-Atlas Target Genes](#)



Click on an experiment ID to browse the ChIP-seq data (e.g., SRX341011).

# Browsing ChIP-seq data

Peak Browser

Enrichment Analysis

Diff Analysis

Target

Publications

Docs

Find By ID

SRX018625

Go

Search

Visualize

Analyze

Download

Link Out

hg38

BigWig

Install and launch IGV before clicking data to visualize

For hg38

BigWig

Peak-call (q < 1E-05)

Peak-call (q < 1E-10)

Peak-call (q < 1E-20)

For hg19

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

MYOD1

Cell type

Cell type Class

Muscle

Cell type

Myotube

NA

NA

Attributes by original data submitter

Sample

source\_name

human m

tissue

myotube

chip antibody

MyoD

Sequenced DNA Library

library\_strategy

ChIP-Seq

library\_source

GENOMI

library\_selection

ChIP

IGV

Human (GRCh38/hg38)

All

Go

1

2

3

4

5

6

7

8

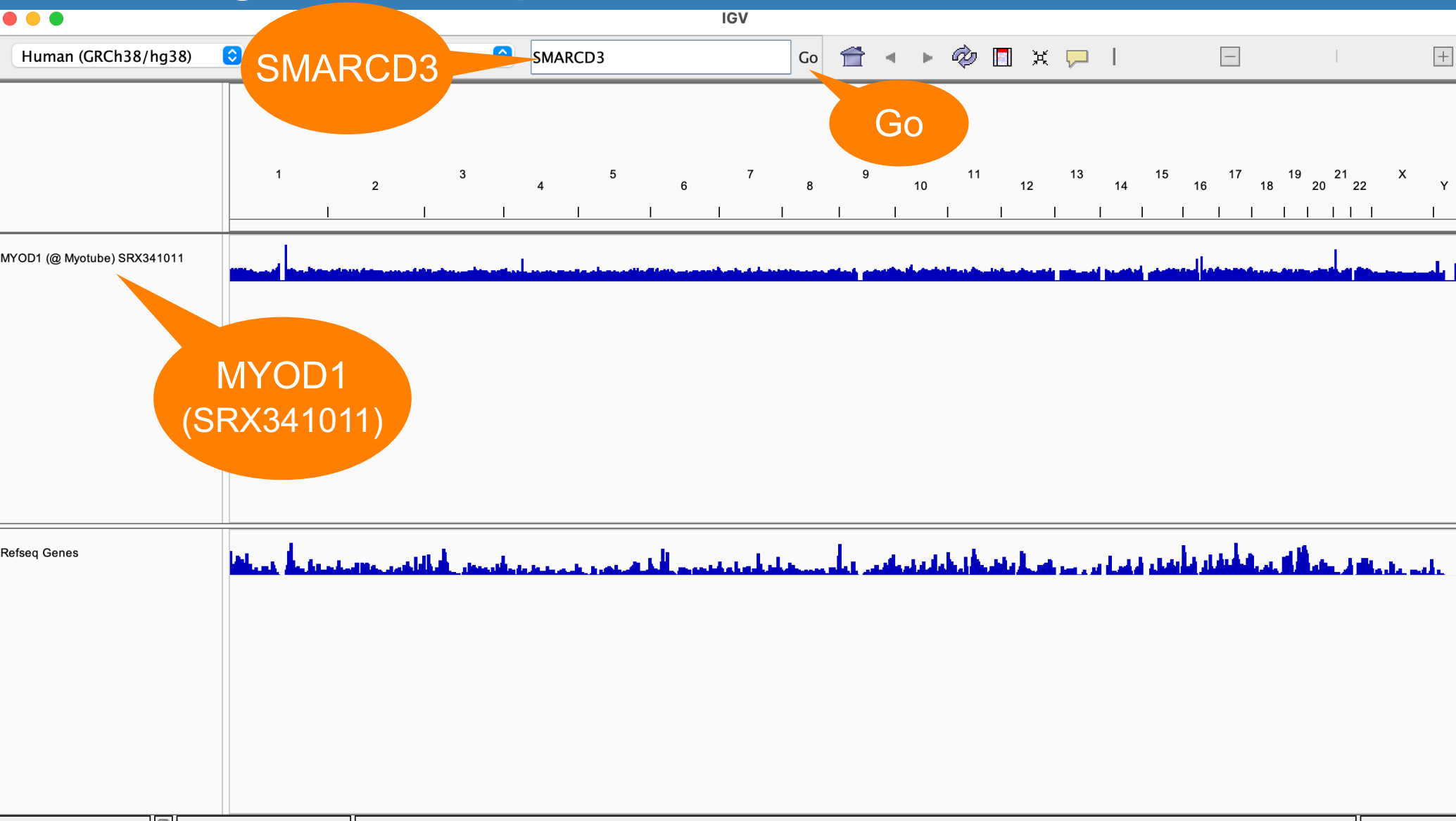
9

10

The detailed information of SRX341011 is displayed. Make sure that IGV has been launched before clicking on “Visualize” and “BigWig”.

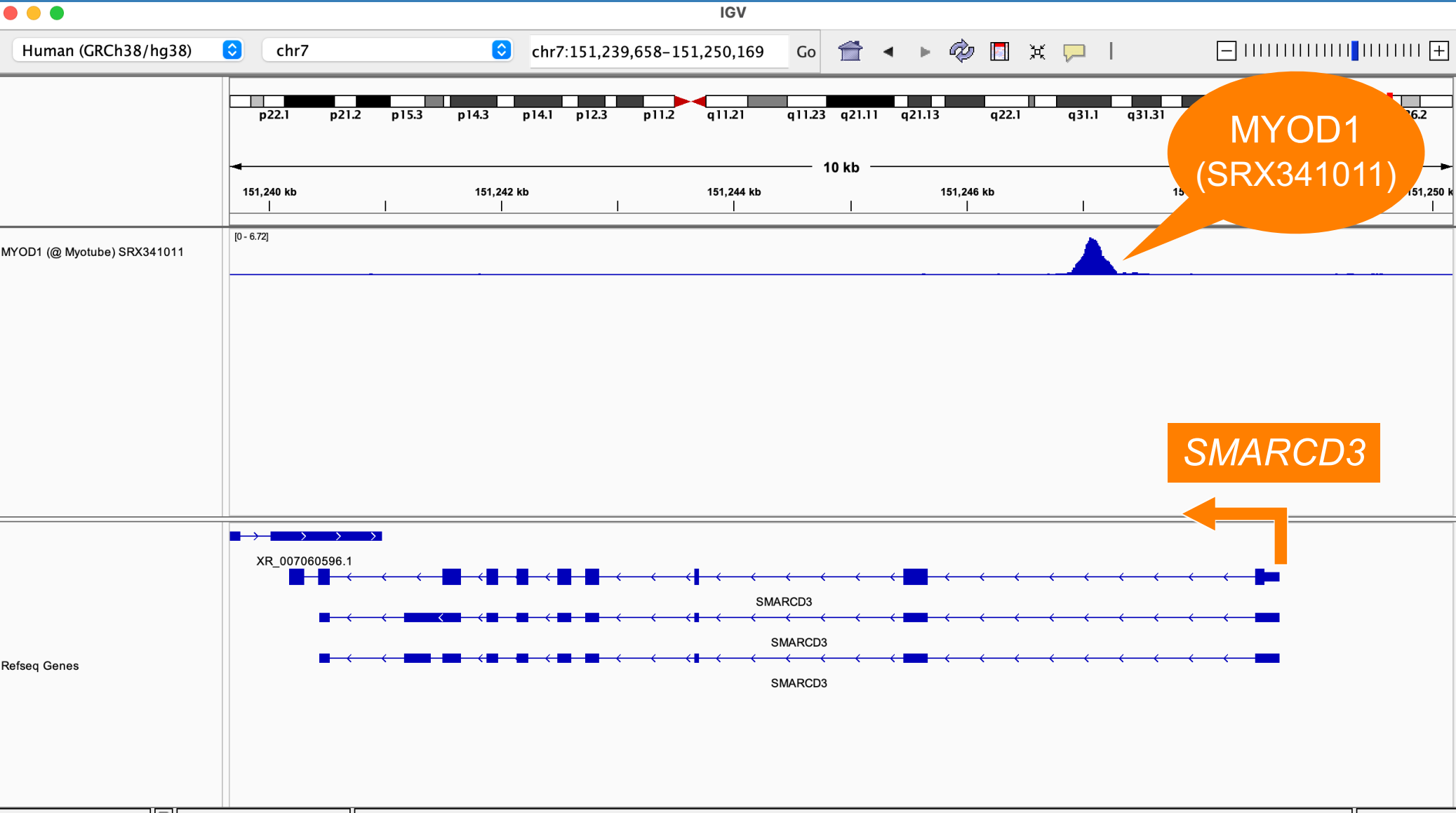


# Browsing ChIP-seq data



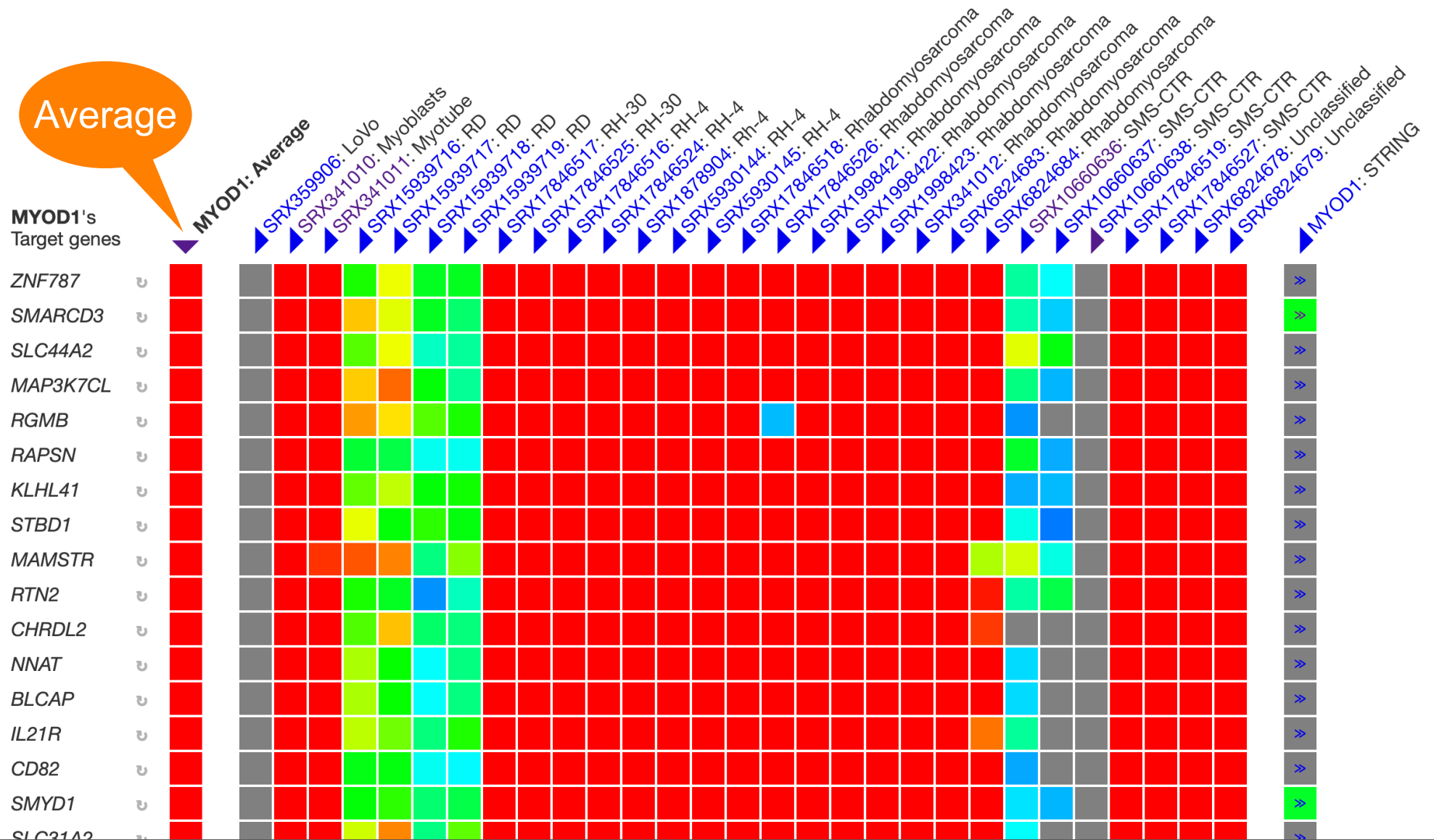
The ChIP-seq data of MYOD1 in the myotube (SRX341011) is loaded into the IGV. Enter the name of a potential target gene of MYOD1 (e.g., *SMARCD3*).

# Browsing ChIP-seq data



MYOD1 binding is evident around the *SMARCD3* gene locus.

# Sorting the result



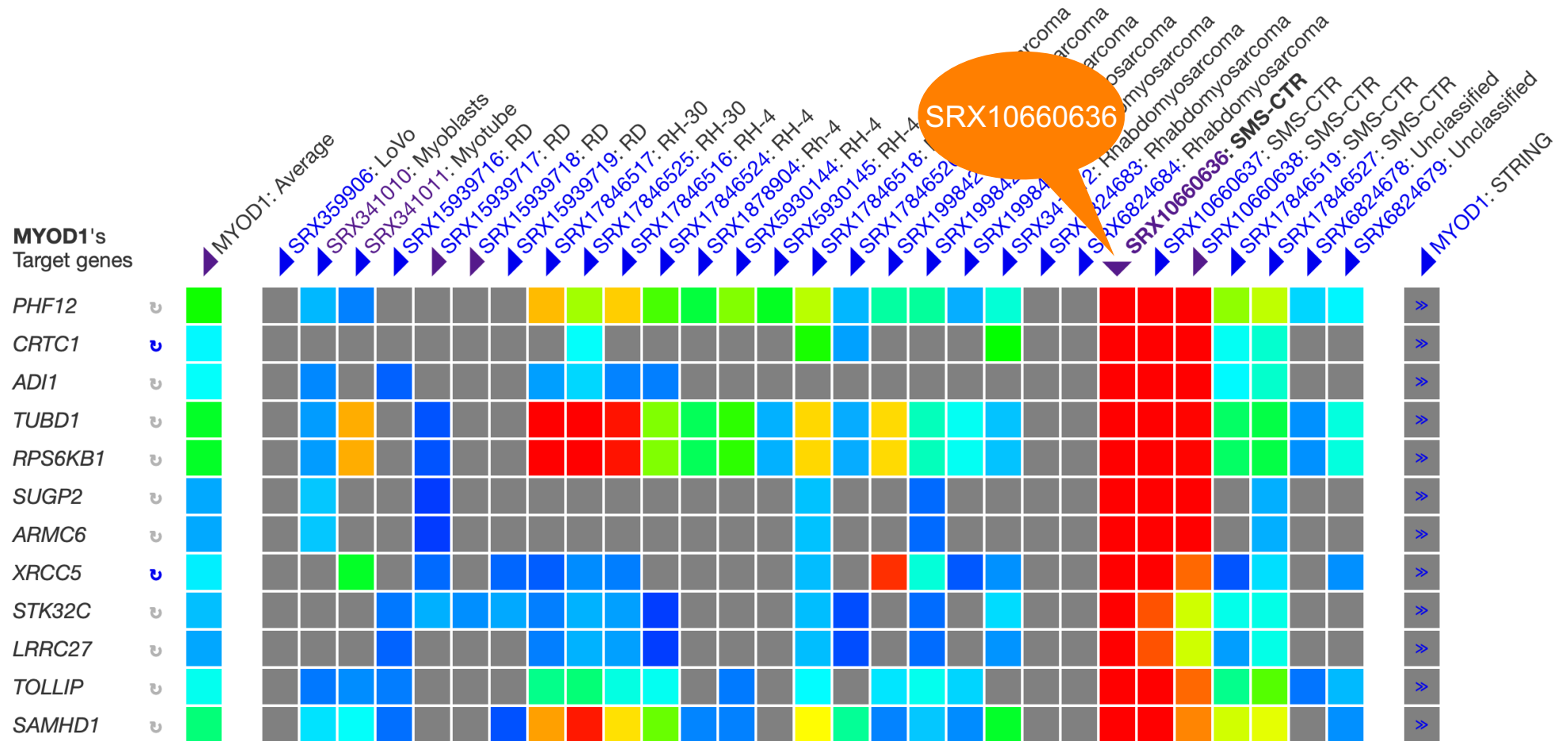
By default, the results matrix is sorted by the average of the MACS2 scores for each row.

## Sorting the result

### Color legends

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

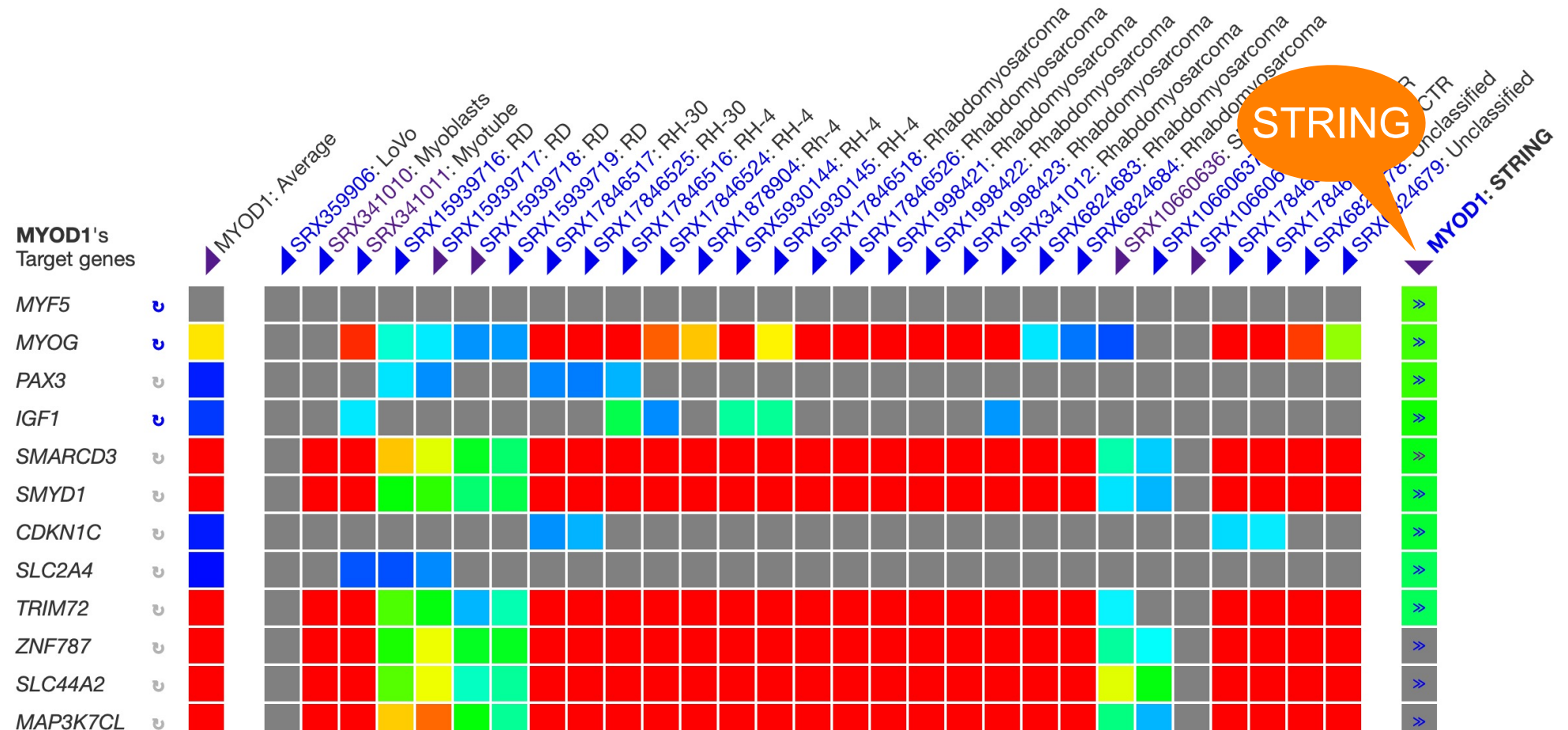
# Sorting the result

## Color legends

1000 750 500 250 1 0 (Values = Binding scores of MACS2 and STRING)

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