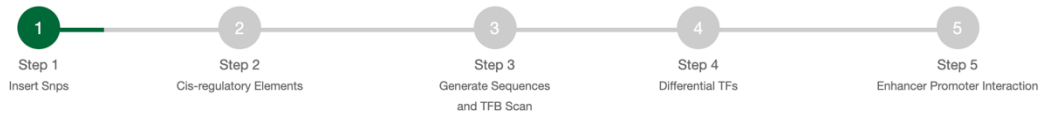
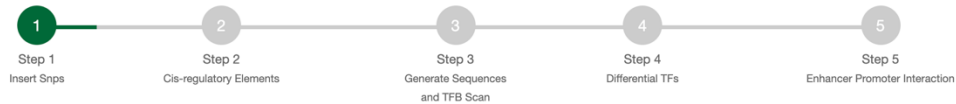


REGULOMIX TUTORIAL

After you've logged in, you will see steps that were designed to ease the process of using REGULOMIX. To use REGULOMIX, you'll have to follow each step below.



Step 1 – Insert SNPs:



Step 1 Insert Snps

First step is to insert snps id into its respective field. Click run to get snp information by its id. Or you can insert an .xlsx file with your SNPs, create one column named SNPS, and write down all SNPs IDs

 or

Nenhum arquivo selecionado

Search:

| Snp Name | Location | Chromossome | Allele Wild Type | Allele Variation | Row Actions |
|----------------------------|----------|-------------|------------------|------------------|-------------|
| No data available in table | | | | | |

Showing 0 to 0 of 0 entries

Insert your SNPs manually at the blank text field inside the red box. After that, press the green “Run” button.



Step 1 Insert Snps

First step is to insert snps id into its respective field. Click run to get snp information by its id. Or you can insert an .xlsx file with your SNPs, create one column named SNPS, and write down all SNPs IDs

 or

Nenhum arquivo selecionado

Search:

| Snp Name | Location | Chromossome | Allele Wild Type | Allele Variation | Row Actions |
|----------------------------|----------|-------------|------------------|------------------|-------------|
| No data available in table | | | | | |

Showing 0 to 0 of 0 entries

OR

You can create a table in .xlsx to use you list of SNPs faster. To do that, you'll have to follow the example below.

| | A | B | C | D | E | F |
|----|----------|---|---|---|---|---|
| 1 | SNPS | | | | | |
| 2 | rs3333 | | | | | |
| 3 | rs356168 | | | | | |
| 4 | | | | | | |
| 5 | | | | | | |
| 6 | | | | | | |
| 7 | | | | | | |
| 8 | | | | | | |
| 9 | | | | | | |
| 10 | | | | | | |

Example of an excel sheet containing SNP IDs. For the algorithm to work, create a file in .xlsx with only one column with header named SNPS and write in each row one SNP ID.

1

Step 1

Insert Snps

2

Step 2

Cis-regulatory Elements

3

Step 3

Generate Sequences and TFB Scan

4

Step 4

Differential TFs

5

Step 5

Enhancer Promoter Interaction

Step 1 Insert Snps

First step is to insert snps id into its respective field. Click run to get snp information by its id. Or you can insert an .xlsx file with your SNPs, create one column named SNPS, and write down all SNPs IDs

or

Nenhum arquivo selecionado

Search:

| Snp Name | Location | Chromossome | Allele Wild Type | Allele Variation | Row Actions |
|----------------------------|----------|-------------|------------------|------------------|-------------|
| No data available in table | | | | | |

Showing 0 to 0 of 0 entries

Choose your SNP chart file to be uploaded by clicking the "Choose File" button and select you own .xlsx file. After that, press the green "Run" button.

1

Step 1

Insert Snps

2

Step 2

Cis-regulatory Elements

3

Step 3

Generate Sequences and TFB Scan

4

Step 4

Differential TFs

5

Step 5

Enhancer Promoter Interaction

Step 1 Insert Snps

First step is to insert snps id into its respective field. Click run to get snp information by its id. Or you can insert an .xlsx file with your SNPs, create one column named SNPS, and write down all SNPs IDs

or

testedb.xlsx

Search:

| Snp Name | Location | Chromossome | Allele Wild Type | Allele Variation | Row Actions |
|----------------------------|----------|-------------|------------------|------------------|-------------|
| No data available in table | | | | | |

Showing 0 to 0 of 0 entries

25%

SNP 1:3333 is done being processed from a total of 4

A progress bar will appear showing the percentage of SNPs that already had been processed, the SNP id of the SNP that had just been processed and its index. The progress bar will not be shown if the user close the browser tab, but the progress will continue and the user will be notified by email when it's done.

REGULOMIX

This step-by-step guide will give you instructions on how to put snps and analyze it. Steps 2 and 5 are bound only by step1, step 4 is bound to steps 1 and 3, and step 3 is bound to step 1 and optionally by step 2.

Step 1: Insert Snps

Step 2: Cis-regulatory Elements

Step 3: Generate Sequences Upload TF Matrix

Step 4: Differential TFs

Step 5: Enhancer Promoter Interaction

| Snp Name | Location | Chromosome | Allele Wild Type | Allele Variation | Row Actions |
|----------|----------|------------|------------------|------------------|---------------------------------------------|
| rs3333 | 96115111 | 5 | G | A | Edit Delete |

Showing 1 to 1 of 1 entries

Previous 1 Next

Use the Scroll Down Bar (red arrow) to see the information about the SNP inserted at the chart below.

Step 2 – Cis-regulatory Elements:

REGULOMIX uses, in STEP 2, ROADMAP Epigenomics Project data and servers. To verify Cis-regulatory elements, you'll have to enter the ID of the tissue from ROADMAP Epigenomics Project, present in the ID Catalogue.

Welcome, admin

GENERAL

- Home
- Regulomix
- ID Catalogue
- About

ID Catalogue

Search for... Go!

ENCODE+Roadmap Tissues

Use in step 2 and 5

| ID | Tissue |
|------|-----------------------------------------------|
| E001 | ES-i3 Cells |
| E002 | ES-WA7 Cells |
| E003 | H1 Cells |
| E004 | H1 BMP4 Derived Mesendoderm Cultured Cells |
| E005 | H1 BMP4 Derived Trophoblast Cultured Cells |
| E006 | H1 Derived Mesenchymal Stem Cells |
| E007 | H1 Derived Neuronal Progenitor Cultured Cells |
| E008 | H9 Cells |
| E009 | H9 Derived Neuronal Progenitor Cultured Cells |
| E010 | H9 Derived Neuron Cultured Cells |
| E011 | hESC Derived CD184+ Endoderm Cultured Cells |
| E012 | hESC Derived CD56+ Ectoderm Cultured Cells |
| E013 | hESC Derived CD56+ Mesoderm Cultured Cells |
| E014 | HUES48 Cells |

Tissues ID are in the ID Catalogue (1). To access the ID Catalogue (1), click on "ID Catalogue" at the left green panel. The tissues ID (2) will be at the first column.

Step 2 Verify Cis-Regulatory Elements

Second step verify if the snps are in a cis-regulatory element. See ID Catalogue to insert in field. To enter more than one tissue, write | between them.

Copy CSV Print

| Snp Name | State Model | Tissue | Regulatory Element |
|----------------------------|-------------|--------|--------------------|
| No data available in table | | | |

Showing 0 to 0 of 0 entries

At Step 2, the first thing you'll need to do is enter the tissue ID at the textbox. You can enter multiple tissues by using the symbol “|” between them!

Step 2 Verify Cis-Regulatory Elements

Second step verify if the snps are in a cis-regulatory element. See ID Catalogue to insert in field. To enter more than one tissue, write | between them.


Copy CSV Print

| Snp Name | State Model | Tissue | Regulatory Element |
|----------|--------------|--------|----------------------------------------------------------------|
| rs3333 | 25 18 15 | E074 | Transcription 3' Strong transcription Strong transcription |
| rs3333 | 25 18 15 | E071 | Transcription 3' Weak transcription Weak transcription |
| rs356168 | 25 18 15 | E074 | Active Enhancer 2 Active Enhancer 1 Enhancers |
| rs356168 | 25 18 15 | E071 | Active Enhancer 1 Active Enhancer 1 Enhancers |

After entering the tissue ID, press the green “Run” button to the right of the tissue ID textbox. It will appear that it is processing your request with the same progress bar as the step 1. It is going to show the tissue ID, the SNP that just finished being processed and its index.

Step 2 Verify Cis-Regulatory Elements

Second step verify if the snps are in a cis-regulatory element. See ID Catalogue to insert in field. To enter more than one tissue, write | between them.

25%

TISSUE E071: rs12694823, id: 1, is done being processed from a total of 4

Copy CSV Print

Search:

| Snp Name | State Model | Tissue | Regulatory Element |
|----------------------------|-------------|--------|--------------------|
| No data available in table | | | |

Showing 0 to 0 of 0 entries

Previous Next

After REGULOMIX process your SNPs inside tissue data from ROADMAP Epigenomics, the information will be displayed at the table below.

Step 2 Verify Cis-Regulatory Elements

Second step verify if the snps are in a cis-regulatory element. See ID Catalogue to insert in field. To enter more than one tissue, write | between them.

E074 ▶ Run

Copy CSV Print Search:

| Snp Name | State Model | Tissue | Regulatory Element |
|----------|--------------|--------|----------------------------------------------------------------|
| rs3333 | 25 18 15 | E074 | Transcription 3' Strong transcription Strong transcription |
| rs356168 | 25 18 15 | E074 | Active Enhancer 2 Active Enhancer 1 Enhancers |

Showing 1 to 2 of 2 entries

Previous 1 Next

You can use the “Search” textbox to look for any value in the table such as: SNPs, Tissues and Regulatory Elements.

Step 2 Verify Cis-Regulatory Elements

Second step verify if the snps are in a cis-regulatory element. See ID Catalogue to insert in field. To enter more than one tissue, write | between them.

E074|E071 ▶ Run

Copy CSV Print Search:

| Snp Name | State Model | Tissue | Regulatory Element |
|----------|--------------|--------|----------------------------------------------------------------|
| rs3333 | 25 18 15 | E074 | Transcription 3' Strong transcription Strong transcription |
| rs3333 | 25 18 15 | E071 | Transcription 3' Weak transcription Weak transcription |
| rs356168 | 25 18 15 | E074 | Active Enhancer 2 Active Enhancer 1 Enhancers |
| rs356168 | 25 18 15 | E071 | Active Enhancer 1 Active Enhancer 1 Enhancers |

Showing 1 to 4 of 4 entries

Previous 1 Next

Step 2 Verify Cis-Regulatory Elements

Second step verify if the snps are in a cis-regulatory element. See ID Catalogue to insert in field. To enter more than one tissue, write | between them.

E074|E071 ▶ Run

Copy CSV Print Search: rs3333

| Snp Name | State Model | Tissue | Regulatory Element |
|----------|--------------|--------|----------------------------------------------------------------|
| rs3333 | 25 18 15 | E074 | Transcription 3' Strong transcription Strong transcription |
| rs3333 | 25 18 15 | E071 | Transcription 3' Weak transcription Weak transcription |

Showing 1 to 2 of 2 entries (filtered from 4 total entries)

Previous 1 Next

Step 2 Verify Cis-Regulatory Elements

Second step verify if the snps are in a cis-regulatory element. See ID Catalogue to insert in field. To enter more than one tissue, write | between them.

E074|E071 ▶ Run

Copy CSV Print Search: E074

| Snp Name | State Model | Tissue | Regulatory Element |
|----------|--------------|--------|----------------------------------------------------------------|
| rs3333 | 25 18 15 | E074 | Transcription 3' Strong transcription Strong transcription |
| rs356168 | 25 18 15 | E074 | Active Enhancer 2 Active Enhancer 1 Enhancers |

Showing 1 to 2 of 2 entries (filtered from 4 total entries)

Previous 1 Next

Step 2 Verify Cis-Regulatory Elements

Second step verify if the snps are in a cis-regulatory element. See ID Catalogue to insert in field. To enter more than one tissue, write | between them.

E074|E071 ▶ Run

Copy CSV Print Search: Enhancer

| Snp Name | State Model | Tissue | Regulatory Element |
|----------|--------------|--------|---------------------------------------------------|
| rs356168 | 25 18 15 | E074 | Active Enhancer 2 Active Enhancer 1 Enhancers |
| rs356168 | 25 18 15 | E071 | Active Enhancer 1 Active Enhancer 1 Enhancers |

Showing 1 to 2 of 2 entries (filtered from 4 total entries)

Previous 1 Next

It is possible to “Copy”, “Print” or download a “.csv” file of your data from STEP 2 using the buttons below “Tissue” text field.</p>

Step 2 Verify Cis-Regulatory Elements

Second step verify if the snps are in a cis-regulatory element. See ID Catalogue to insert in field. To enter more than one tissue, write | between them.

Copy CSV Print

Search:

| Snp Name | State Model | Tissue | Regulatory Element |
|----------|--------------|--------|----------------------------------------------------------------|
| rs3333 | 25 18 15 | E074 | Transcription 3' Strong transcription Strong transcription |
| rs356168 | 25 18 15 | E074 | Active Enhancer 2 Active Enhancer 1 Enhancers |

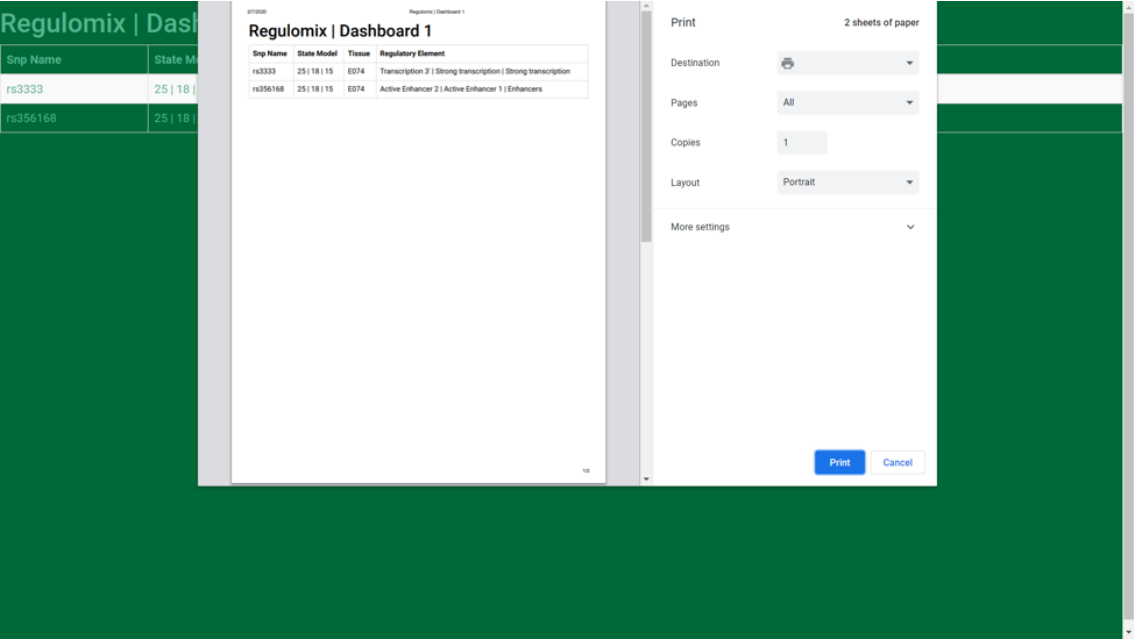
Showing 1 to 2 of 2 entries

Previous

1

Next

Pressing “Copy” will copy the Cis-regulatory Elements analysis data to your Clipboard. You can paste it in whatever program you want to save the information. Pressing “CSV” will download a .csv file with the information of the Cis-regulatory Elements analysis. Pressing “Print” will open a new tab with only the Cis-regulatory Elements analysis table information and it will open a printer information window.



If you want to exclude SNPs from next steps, you can write the name of that SNP inside the Delete SNPs textbox and press “Delete”.

Step 2 Verify Cis-Regulatory Elements

Second step verify if the snps are in a cis-regulatory element. See ID Catalogue to insert in field. To enter more than one tissue, write | between them.

| Snp Name | State Model | Tissue | Regulatory Element |
|----------|--------------|--------|----------------------------------------------------------------|
| rs3333 | 25 18 15 | E074 | Transcription 3' Strong transcription Strong transcription |
| rs3333 | 25 18 15 | E071 | Transcription 3' Weak transcription Weak transcription |
| rs356168 | 25 18 15 | E074 | Active Enhancer 2 Active Enhancer 1 Enhancers |
| rs356168 | 25 18 15 | E071 | Active Enhancer 1 Active Enhancer 1 Enhancers |

Showing 1 to 4 of 4 entries

Step 2.1 Delete SNPs from Tables

Delete SNPs if you dont want to analyze them for third and fourth steps

Choose regulatory element you want to keep snps from. The rest is going to be deleted.

After pressing delete, you'll notice that the SNP will be deleted from the table above.

Step 2 Verify Cis-Regulatory Elements

Second step verify if the snps are in a cis-regulatory element. See ID Catalogue to insert in field. To enter more than one tissue, write | between them.

| Snp Name | State Model | Tissue | Regulatory Element |
|----------|--------------|--------|---------------------------------------------------|
| rs356168 | 25 18 15 | E074 | Active Enhancer 2 Active Enhancer 1 Enhancers |
| rs356168 | 25 18 15 | E071 | Active Enhancer 1 Active Enhancer 1 Enhancers |

Showing 1 to 2 of 2 entries

Step 2.1 Delete SNPs from Tables

Delete SNPs if you dont want to analyze them for third and fourth steps

Choose regulatory element you want to keep snps from. The rest is going to be deleted.

If you want to continue to STEP 3, you should select one of the tissues analyzed and any of the respectively regulatory element you want, then press "Submit".

Second step verify if the snps are in a cis-regulatory element. See ID Catalogue to insert in field. To enter more than one tissue, write | between them.

| E074 E071 | |  | |
|-----------|--------------|-----------------------------------------------------------------------------------|----------------------------------------------------------------|
| Copy | CSV | Print | |
| Snp Name | State Model | Tissue | Regulatory Element |
| rs3333 | 25 18 15 | E074 | Transcription 3' Strong transcription Strong transcription |
| rs3333 | 25 18 15 | E071 | Transcription 3' Weak transcription Weak transcription |
| rs356168 | 25 18 15 | E074 | Active Enhancer 2 Active Enhancer 1 Enhancers |
| rs356168 | 25 18 15 | E071 | Active Enhancer 1 Active Enhancer 1 Enhancers |

Showing 1 to 4 of 4 entries

Step 2.1 Delete SNPs from Tables

Delete SNPs if you dont want to analyze them for third and fourth steps

Choose regulatory element you want to keep snps from. The rest is going to be deleted.

Select Tissue
E074

☐ Active TSS
☐ Promoter Downstream TSS
☐ Transcription
☐ Weak transcription
☒ Transcription 5' Enhancer
☒ Transcription Weak Enhancer
☒ Active Enhancer 2
☒ Weak Enhancer 1
☒ Enhancer Acetylation Only
☐ ZNF genes & repeats
☒ Poised Promoter
☐ Repressed PolyComb
☐ Flanking TSS
☐ Flanking TSS Downstream
☒ Genic Enhancer 1
☒ Weak Enhancer
☒ Bivalent Enhancer
☐ Flanking Active TSS
☒ Genic enhancers
☐ Flanking Bivalent TSS/Enh

☒ Promoter Upstream TSS
☐ Promoter Downstream TSS with DNase
☐ Transcription 5'
☐ Transcription 3'
☐ Transcription regulatory
☐ Transcription 3' Enhancer
☒ Active Enhancer 1
☒ Active Enhancer Flank
☒ Weak Enhancer 2
☐ DNase only
☐ Heterochromatin
☒ Bivalent Promoter
☐ Quiescent/Low
☐ Flanking TSS Upstream
☐ Strong Transcription
☒ Genic Enhancer 2
☐ Bivalent/Poised TSS
☐ Weak Repressed PolyComb
☐ Transcr. at gene 5' and 3'
☒ Enhancers



Step 3 – Generate Sequences and TFB Scan:

In Step 3, REGULOMIX is going to create sequences of 63 nucleotides long with each SNP filtered from Step 2 in different positions within the sequence. These sequences will be used with JASPAR matrixes to identify which Transcription Factors to bind in each SNP filtered.

To select one of the matrixes from JASPAR already in our server, click on the drop-down list box to choose. Matrix information can be found at Jaspar website, inside “About” section: <http://jaspar.genereg.net/about/>

You can also upload matrixes in meme format to be used in REGULOMIX, that uses FIMO in the background, by clicking “Choose File”. After you choose your file, you should click “Upload”.

You can select a different value for p-value parameter in FIMO or you can select q-value to use "q-value" as FIMO threshold parameter

Click “Generate and Scan” to request to Generate Sequences and process sequences in FIMO.

REGULOMIX

This step-by-step guide will give you instructions on how to put snps and analyze it. Steps 2 and 5 are bound only by step1, step 4 is bound to steps 1 and 3, and step 3 is bound to step 1 and optionally by step 2.

Step 1 Insert Snps Step 2 Cis-regulatory Elements **Step 3 Generate Sequences and TFB Scan** Step 4 Differential TFs Step 5 Enhancer Promoter Interaction

Step 3 Generate Sequences and TFB Scan

Your generated sequences will show up here. click on the generate button

Select Matrix: **JASPAR_CNE_2008** or Escolher arquivo Nenhum arquivo selecionado Upload

P-value: 1E-4

Generate Sequences and Scan

Previous Next

SIMPLTON - Based on Template by Colorlib

When the generation of sequences is over, it will appear a popup message saying it's done.

regulomix.unifor.br diz
DONE

REGULOMIX

This step-by-step guide will give you instructions on how to put snps and analyze it. Steps 2 and 5 are bound only by step1, step 4 is bound to steps 1 and 3, and step 3 is bound to step 1 and optionally by step 2.

Step 1 Insert Snps Step 2 Cis-regulatory Elements **Step 3 Generate Sequences and TFB Scan** Step 4 Differential TFs Step 5 Enhancer Promoter Interaction

Step 3 Generate Sequences and TFB Scan

Your generated sequences will show up here. click on the generate button

Select Matrix: JASPAR2018_CORE_vertbrates_non-redundant or Escolher arquivo Nenhum arquivo selecionado Upload

P-value: 1E-4 Use q-value

Generate Sequences and Scan

```
>sequence_wild_type|rs12694823|2|G|32
ACCAAAACTTAGCAGCTTAAATAACCATTTGATTTGGGCAATCCCGTGGCTCATGCCTGT
>sequence_variation|rs12694823|2|A|32
ACCAAAACTTAGCAGCTTAAATAACCATTTAATTTGGGCAATCCCGTGGCTCATGCCTGT
>sequence_variation|rs12694823|2|C|32
ACCAAAACTTAGCAGCTTAAATAACCATTTGATTTGGGCAATCCCGTGGCTCATGCCTGT
>sequence_wild_type|rs356168|4|G|32
TGCAAAACGCTTCTGTTTGGATTGGTAAATTGGAACAATCAGGGCACAACCTGCAAGGTCAC
>sequence_variation|rs356168|4|A|32
TGCAAAACGCTTCTGTTTGGATTGGTAAATTAGAACAATCAGGGCACAACCTGCAAGGTCAC
>sequence_wild_type|rs3333|5|G|32
CATCAGACAGAGTATCTCTGCTCTAGACCTCGCTGGAGTTCAAGCTTGAATTATTATATGCAA
>sequence_variation|rs3333|5|A|32
CATCAGACAGAGTATCTCTGCTCTAGACCTCGCTGGAGTTCAAGCTTGAATTATTATATGCAA
>sequence_wild_type|rs1560747|13|A|32
```

You will be able to see the sequences generated below the “Generate and Scan” Button.

Step 3 Generate Sequences and TFB Scan

Your generated sequences will show up here, click on the generate button

Select Matrix JASPAR2018_CORE vertebrates non-redundant or Escolher arquivo Nenhum arquivo selecionado Upload

P-value 1E-4

Use q-value ☐

▶ Generate Sequences and Scan

```
>sequence_wild_type|rs12694823|2|G|32
ACCAAACTTAGCAGCTTAAATAACCAATTTGATTTTGGGCAATCCCGTGGCTCATGCCTG
>sequence_variation|rs12694823|2|A|32
ACCAAACTTAGCAGCTTAAATAACCAATTTAATTTTGGGCAATCCCGTGGCTCATGCCTG
>sequence_variation|rs12694823|2|C|32
ACCAAACTTAGCAGCTTAAATAACCAATTTTATTTTGGGCAATCCCGTGGCTCATGCCTG
>sequence_wild_type|rs356168|4|G|32
TGCAAAACGCTTCTGTTTGTGTTGTTGTAATTGGAACAATCAGGGCACAACGCAAGGTGCA
>sequence_variation|rs356168|4|A|32
TGCAAAACGCTTCTGTTTGTGTTGTTGTAATTAGAACAATCAGGGCACAACGCAAGGTGCA
>sequence_wild_type|rs3333|5|G|32
CATCAGACAGAGTATCTCTGCTCTAGACCTCGCTGGAGTTCAAGCTTGAATTATTATATGCA
>sequence_variation|rs3333|5|A|32
CATCAGACAGAGTATCTCTGCTCTAGACCTCACTGGAGTTCAAGCTTGAATTATTATATGCA
>sequence_wild_type|rs1560747|13|A|32
TAAAAACAACCAAGAAACACCTTCCCCCACTAGAGTAGATTGTAATCTCTGTGTGGATG
>sequence_variation|rs1560747|13|C|32
TAAAAACAACCAAGAAACACCTTCCCCCACTAGAGTAGATTGTAATCTCTGTGTGGATG
>sequence_variation|rs1560747|13|G|32
```

You can press “Next” to continue to Step 4.

Step 4 – Differential Transcription Factors:

In Step 4, you’ll be able to request analyses of which Transcription Factors bind to each sequence generated in Step 3. Therefore, it’s possible to manually search for Differential Transcription Factors.

To request the Differential Transcription Factors analyses, press the green “Run” button.

REGULOMIX

This step-by-step guide will give you instructions on how to put snps and analyze it. Steps 2 and 5 are bound only by step1, step 4 is bound to steps 1 and 3, and step 3 is bound to step 1 and optionally by step 2.



Step 4 Differential Transcription Factors

Here is showing up all the differential transcription factors

▶ Run

Copy CSV Print

Search:

| Motif ID | Motif Alt ID | Sequence Name | Strand | Start | End | p-value | q-value | Matched Sequence |
|----------------------------|--------------|---------------|--------|-------|-----|---------|---------|------------------|
| No data available in table | | | | | | | | |

Showing 0 to 0 of 0 entries

Previous Next

When the Differential Transcription Factor Analyses is over, it will appear a popup message saying it’s done. After the analysis is over, it will appear a table below the “Run” button to visualize each TF binding for each sequence.

Step 4 Differential Transcription Factors

Here is showing up all the differential transcription factors

Run

CopyCSVPrint

Search

| Motif ID | Motif Alt ID | Sequence Name | Strand | Start | End | p-value | q-value | Matched Sequence |
|----------|--------------|------------------------------------|--------|-------|-----|-------------------------|---------|------------------|
| MA0075.2 | Prrx2 | sequence_wild_type rs356168 4 G 32 | - | 26 | 33 | 0.000057499999999999995 | 0.0235 | CCAATTAC |
| MA0132.2 | PDX1 | sequence_variation rs356168 4 A 32 | + | 26 | 33 | 0.0000218 | 0.00898 | GTAATTAG |
| MA0612.1 | EMX1 | sequence_variation rs356168 4 A 32 | - | 25 | 34 | 0.0000483 | 0.0191 | TCTAATTACC |
| MA0618.1 | LBX1 | sequence_variation rs356168 4 A 32 | + | 26 | 33 | 0.0000966 | 0.0425 | GTAATTAG |
| MA0642.1 | EN2 | sequence_wild_type rs356168 4 G 32 | - | 25 | 34 | 0.000048100000000000004 | 0.0204 | TCCAATTACC |
| MA0661.1 | MEOX1 | sequence_variation rs356168 4 A 32 | - | 25 | 34 | 0.000039 | 0.0166 | TCTAATTACC |
| MA0666.1 | MSX1 | sequence_wild_type rs356168 4 G 32 | - | 26 | 33 | 0.000035799999999999996 | 0.0157 | CCAATTAC |
| MA0705.1 | Lhx8 | sequence_variation rs356168 4 A 32 | - | 26 | 33 | 0.0000435 | 0.0191 | CTAATTAC |
| MA0706.1 | MEOX2 | sequence_variation rs356168 4 A 32 | + | 25 | 34 | 0.0000706 | 0.0282 | GGTAATTAGA |
| MA0707.1 | MNX1 | sequence_variation rs356168 4 A 32 | + | 25 | 34 | 0.000036099999999999997 | 0.0151 | GGTAATTAGA |

Showing 1 to 10 of 31 entries

Showing 1 to 10 of 31 entries

Previous 1 2 3 4 Next

Previous Next

It is possible to “Copy”, “Print” or download a “.csv” file of your data from STEP 4 using the buttons below “Run” button.

Step 4 Differential Transcription Factors

Here is showing up all the differential transcription factors

Copy

CSV

Print

Search:

| Motif ID | Motif Alt ID | Sequence Name | Strand | Start | End | p-value | q-value | Matched Sequence |
|----------|--------------|------------------------------------|--------|-------|-----|-------------------------|---------|------------------|
| MA0075.2 | Prrx2 | sequence_wild_type rs356168 4 G 32 | - | 26 | 33 | 0.000057499999999999995 | 0.0235 | CCAATTAC |
| MA0132.2 | PDX1 | sequence_variation rs356168 4 A 32 | + | 26 | 33 | 0.0000218 | 0.00898 | GTAATTAG |
| MA0612.1 | EMX1 | sequence_variation rs356168 4 A 32 | - | 25 | 34 | 0.0000483 | 0.0191 | TCTAATTACC |
| MA0618.1 | LBX1 | sequence_variation rs356168 4 A 32 | + | 26 | 33 | 0.0000966 | 0.0425 | GTAATTAG |
| MA0642.1 | EN2 | sequence_wild_type rs356168 4 G 32 | - | 25 | 34 | 0.000048100000000000004 | 0.0204 | TCCAATTACC |
| MA0661.1 | MEOX1 | sequence_variation rs356168 4 A 32 | - | 25 | 34 | 0.000039 | 0.0166 | TCTAATTACC |
| MA0666.1 | MSX1 | sequence_wild_type rs356168 4 G 32 | - | 26 | 33 | 0.000035799999999999996 | 0.0157 | CCAATTAC |
| MA0705.1 | Lhx8 | sequence_variation rs356168 4 A 32 | - | 26 | 33 | 0.0000435 | 0.0191 | CTAATTAC |
| MA0706.1 | MEOX2 | sequence_variation rs356168 4 A 32 | + | 25 | 34 | 0.0000706 | 0.0282 | GGTAATTAGA |
| MA0707.1 | MNX1 | sequence_variation rs356168 4 A 32 | + | 25 | 34 | 0.000036099999999999997 | 0.0151 | GGTAATTAGA |

Showing 1 to 10 of 31 entries

Previous

1

2

3

4

Next

Showing 1 to 10 of 31 entries

Previous 1 2 3 4 Next

Pressing “Copy” will copy the Step 4 analysis data to your Clipboard. You can paste it in whatever program you want to save the information.

Pressing “CSV” will download a .csv file with the information of the Step 4 analysis.

Pressing “Print” will open a new tab with only the Step 4 analysis table information and it will open a printer information window.

Regulomix | Dash

| Motif ID | Motif Alt ID | Seq |
|----------|--------------|-----|
| MA0075.2 | Prrx2 | seq |
| MA0132.2 | PDX1 | seq |
| MA0612.1 | EMX1 | seq |
| MA0618.1 | LBX1 | seq |
| MA0642.1 | EN2 | seq |
| MA0661.1 | MEOX1 | seq |
| MA0666.1 | MSX1 | seq |
| MA0705.1 | Lhx8 | seq |
| MA0706.1 | MEOX2 | seq |
| MA0707.1 | MNX1 | seq |
| MA0708.1 | MSX2 | seq |
| MA0709.1 | Msx3 | seq |
| MA0710.1 | NOTO | seq |
| MA0722.1 | VAX1 | seq |

Regulomix | Dashboard 1

| Motif ID | Sequence Name | Strand | Start | End | p-value | q-value | Matched Se |
|----------|------------------------------------|--------|-------|-----|-------------------------|---------|------------|
| MA0075.2 | sequence_wild_type rs356168 4 G 32 | - | 26 | 33 | 0.000057499999999999995 | 0.0235 | CCAATTAC |
| MA0132.2 | sequence_variation rs356168 4 A 32 | + | 26 | 33 | 0.0000218 | 0.00898 | GTAATTAG |
| MA0612.1 | sequence_variation rs356168 4 A 32 | - | 25 | 34 | 0.0000483 | 0.0191 | TCTAATTACC |
| MA0618.1 | sequence_variation rs356168 4 A 32 | + | 26 | 33 | 0.0000966 | 0.0425 | GTAATTAG |
| MA0642.1 | sequence_wild_type rs356168 4 G 32 | - | 25 | 34 | 0.000048100000000000004 | 0.0204 | TCCAATTACC |
| MA0661.1 | sequence_variation rs356168 4 A 32 | - | 25 | 34 | 0.000039 | 0.0166 | TCTAATTACC |
| MA0666.1 | sequence_wild_type rs356168 4 G 32 | - | 26 | 33 | 0.000035799999999999996 | 0.0157 | CCAATTAC |
| MA0705.1 | sequence_variation rs356168 4 A 32 | - | 26 | 33 | 0.0000435 | 0.0191 | CTAATTAC |
| MA0706.1 | sequence_variation rs356168 4 A 32 | + | 25 | 34 | 0.0000706 | 0.0282 | GGTAATTAGA |
| MA0707.1 | sequence_variation rs356168 4 A 32 | + | 25 | 34 | 0.000036099999999999997 | 0.0151 | GGTAATTAGA |

Print

2 sheets of paper

Destination

Pages

Copies

Layout

More settings

Print

Cancel

| | | | | | | | | |
|----------|--------|------------------------------------|---|----|----|-------------------------|----------------------|----------------|
| MA0723.1 | VAX2 | sequence_variation rs356168 4 A 32 | - | 26 | 33 | 0.0000218 | 0.00897 | CTAATTAC |
| MA0725.1 | VX1 | sequence_variation rs356168 4 A 32 | - | 26 | 33 | 0.0000435 | 0.0166 | CTAATTAC |
| MA0726.1 | VX2 | sequence_variation rs356168 4 A 32 | - | 26 | 33 | 0.0000435 | 0.0163 | CTAATTAC |
| MA0784.1 | POU1F1 | sequence_variation rs356168 4 A 32 | + | 20 | 33 | 0.0000656 | 0.022000000000000002 | ATTGGTGTAATTAG |
| MA0876.1 | BSX | sequence_wild_type rs356168 4 G 32 | - | 26 | 33 | 0.000035799999999999996 | 0.0159 | CCAATTAC |

Step 5 – Enhancer Promoter Interaction:

In Step 5, you'll be able to request enhancer-promoter interaction (EPI). REGULOMIX uses JEME, joint effect of multiple enhancers (Cao, Qin et al., 2016), in Step 5 to identify EPI. The prediction uses a learned random forest model with cross-validation for predicting enhancer targets. For more information about how JEME works, go to doi:10.1038/ng.3950.

Use the "ROADMAP Epigenomics tissue ID" of the tissue you want to use for the analysis in the textbox. You can enter multiple tissues by using the symbol "|" between them.

REGULOMIX

This step-by-step guide will give you instructions on how to put snps and analyze it. Steps 2 and 5 are bound only by step1, step 4 is bound to steps 1 and 3, and step 3 is bound to step 1 and optionally by step 2.



Step 5 Enhancer Promoter Interaction

This part shows enhancer and promoter interaction pairs of snps inside enhancer region. See ID Catalogue to insert in field. To enter more than one tissue, write | between them.

Copy CSV Print

| SNP | Location | Gene ID | Gene | Gene Location | Score | Tissue | File Type |
|----------------------------|----------|---------|------|---------------|-------|--------|-----------|
| No data available in table | | | | | | | |

Showing 0 to 0 of 0 entries

Previous Next

After the REGULOMIX is done, a table will appear below the tissue textbox.

REGULOMIX

This step-by-step guide will give you instructions on how to put snps and analyze it. Steps 2 and 5 are bound only by step1, step 4 is bound to steps 1 and 3, and step 3 is bound to step 1 and optionally by step 2.



Step 5 Enhancer Promoter Interaction

This part shows enhancer and promoter interaction pairs of snps inside enhancer region. See ID Catalogue to insert in field. To enter more than one tissue, write | between them.

Copy CSV Print

| SNP | Location | Gene ID | Gene | Gene Location | Score | Tissue | File Type |
|-------------|-------------------------|--------------------|--------|-----------------|-------|--------------------------|-----------|
| rs117310449 | chr19:45392200-45393600 | ENSG00000104853.11 | CLPTM1 | chr19:45457842+ | 0.39 | Brain Hippocampus Middle | Lasso |
| rs117310449 | chr19:45392200-45393600 | ENSG00000130202.5 | PVR12 | chr19:45349432+ | 0.37 | Brain Hippocampus Middle | Lasso |
| rs117310449 | chr19:45392200-45393600 | ENSG00000130203.5 | APOE | chr19:45409011+ | 0.72 | Brain Hippocampus Middle | Lasso |
| rs117310449 | chr19:45392200-45393600 | ENSG00000130204.8 | TOMM40 | chr19:45393826+ | 0.43 | Brain Hippocampus Middle | Lasso |

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The meaning of each column in step 5:

SNP: SNP ID/RefSNP number of the SNP contained in the sequence being analyzed.

Location: Location of the SNP contained in the sequence being analyzed.

Gene ID: Ensembl Gene ID of the Gene predicted to interact with the sequence being analyzed.

Gene: The gene that potentially interacts with the sequence being analyzed.

Gene Location: Localization of the Gene predicted to interact with the sequence being analyzed.

File Type: Statistic regression method used in the prediction of EPI.

For more information about how JEME works, go to [doi:10.1038/ng.3950](https://doi.org/10.1038/ng.3950).

This step-by-step guide will give you instructions on how to put snps and analyze it. Steps 2 and 5 are bound only by step 1, step 4 is bound to steps 1 and 3, and step 3 is bound to step 1 and 3, and step 3 is bound to step 1 and 3, and step 3 is bound to step 1 and 3, and step 3 is bound to step 1 and 3.

```

graph LR
    S1((Step 1  
Insert Snps)) --- S2((Step 2  
Cis-regulatory Elements))
    S2 --- S3((Step 3  
Generate Sequences  
Upload TF Matrix))
    S3 --- S4((Step 4  
Differential TFs))
    S4 --- S5((Step 5  
Enhancer Promoter Interaction))

```

Step 5 Enhancer Promoter Interaction

This part shows enhancer and promoter interaction pairs of snps inside enhancer region. See ID Catalogue to insert in field. To enter more than one tissue, write | between them.

E071 Run

Copy | CSV | Print

| SNP | Location | Gene ID | Gene | Gene Location | Score | Tissue | File Type |
|-------------|-------------------------|---------------------|--------|-----------------|-------|--------------------------|-----------|
| rs117310449 | chr19:45392200-45393600 | ENS0000000104853.11 | CLPTM1 | chr19-45457842+ | 0.39 | Brain Hippocampus Middle | Lasso |
| rs117310449 | chr19:45392200-45393600 | ENS0000000130202.5 | PVRL2 | chr19-45349432+ | 0.37 | Brain Hippocampus Middle | Lasso |
| rs117310449 | chr19:45392200-45393600 | ENS0000000130203.5 | APOE | chr19-45409011+ | 0.72 | Brain Hippocampus Middle | Lasso |
| rs117310449 | chr19:45392200-45393600 | ENS0000000130204.8 | TOMM40 | chr19-45393826+ | 0.43 | Brain Hippocampus Middle | Lasso |

Search:

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[illegible]

Pressing “CSV” will download a .csv file with the information of the Step 5 analysis.

Pressing “Print” will open a new tab with only the Step 5 analysis table information and it will open a printer information window.