Tutorial

for

RiceENCODE: a comprehensive epigenomic database

as rice Encyclopedia of DNA Elements

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\texttt{http://glab.hzau.edu.cn/RiceENCODE}

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In RiceENCODE (http://glab.hzau.edu.cn/RiceENCODE), we have integrated a large number of epigenetic data (ChIP-Seq, Hi-C, ChIA-PET, ATAC-Seq, MNase-Seq, FAIRE-Seq, BS-Seq) and transcriptome data (RNA-Seq) from different species and tissues of plants from GEO, which provides an important browsing and searching module for the study in plant epigenomics. We hope that such a comprehensive rice epigenome database could serve as an important platform for studying molecular breeding, subgroup comparison, and differences of epigenetic regulation in rice.

1. Home page

Part 1:

The top navigation menu gathers general functions of the database, including links to different search modules.
Part 2:

Schematic diagram of the introduction to the RiceENCODE search module. Each orange part can jump to the page respectively.

1.1 Quick search.

Quick search engine to help users query the histone modification, DNA interaction information, and tissue expression flexibly. This kind of global search can help users quickly locate the marker histone modification or DNA interaction, especially when users have no clear target histone modifications to search. Select target genome and tissues then submit the gene ID and click on the search button.

For example (OsPsbS) the genome browser in results like this:
2. Genome Browser.

In Genome Browser module, RiceENCODE provides a WashU Epigenome Browser instance to better visualize large number of epigenetic datasets.
2.1 Select the assembly and genome region you interested

2.2 Select the annotated track and public hub

2.3 Choose the data hub
2.4 Select the data type from tissues and species

2.5 Add the data track you chose
2.6 Genome browser for your track

3. Browse and search Histone modification in different samples.

In histone modification module, users can easily search for histone modification signals in different tissues.

3.1 Select genomes tissues and histone modifications.

To get the histone modification signals information, you can either select a query genome region or a target gene after you selected target genome, histone mark and tissues. Click on the Search button to get the results.

3.2 Histone modification overview

The histone modification viewer provides and tabular layouts for the resulted blocks.
Corresponding to peak regions in different tissues

4. Browse and search chromatin accessibility.

In chromatin accessibility module, users can easily search for chromatin accessibility signals (ATAC-Seq, MNase-Seq, FAIRE-Seq) in different tissues.
5. Browse and search interaction from gene to gene and gene to regions.

In 3D interaction search module, users can easily search for gene-gene interactions, gene-region interactions and region-region interactions in different genome, tissues and sequencing.

The meanings of part are listed below:

Part 1:

Shows the selector for genome and sequencing.

Part 2:

In the loop ID search module, fill in the blanks with a loop ID (MH63_H3K4me3_Loop1) then click the search button and resulted tabular layout looks like this:
Part 3:

In the gene-region search module, users may have some interesting gene and want to know the interactive regions. Filling the gene ID (Ghd7.1) and the resulted tabular layout looks like this:

Click orange part the result look like this:
Part 4:

In the region-region search module, users may have some interesting region and want to know the interactive regions. Filling the chr:start-end and the resulted tabular layout looks like this:

For example click the loop ID (MH63_H3K4me3_Loop1) the result look like this:
Part 5 and 6:

In the gene-gene search module, users may have some interesting genes and want to know the interactive gene. Filling the gene ID or gene name in part 5 and choose the extend degree in part 6 (extend degree means the network connectivity). The resulted (Ghd7.1) tabular and network layout looks like this:
6. Browse and search gene expression.

In gene expression search module, users can easily search for FPKM from different tissues transcriptome data (RNA-Seq) we collected.

6.1 Select genomes and submit the gene ID or gene name.

To get the gene expression level information, you can either select a query genome and a target gene. Click on the Search button to get the results.
6.2 Gene expression overview

The gene (OsPsbS/MH01g0710600) expression viewer provides and bar plot for the resulted blocks.

7. Browse and search DNA methylation level.

In DNA methylation search module, users can easily search DNA methylation level for genes, regions and DMR between different tissues.

The meanings of part are listed below:

Part 1:

Choose species.

Part 2:

In the gene ID search module, fill in the blanks with a gene ID or gene name then click the search button and resulted layout looks like this:
Part 3:

In the DNA methylation region search module, fill in the blanks with the chr:start-end then click the search button and resulted layout looks like this:

Part 4 and 5:

In the DMR search module, fill in the blanks with the chr:start-end then click the DMR search button and resulted layout looks like this:
For example click the DMR number (CHG-DMR_32210) the result look like this:

8. Browse and search Chromatin state in different tissues and species

RiceENCODE provides chromatin states search module. Users are only allowed to search limited tissues. The easily online search module can help user better understand the epigenetic regulation of interested regions or genes.

The resulted tabular layout looks like this:
9. Download all the bigwig and peaks file for different datasets.

Rice ENCODE provides bigwig and peak file for users downloading.
Contact:

If you have any problem, comments or suggestions about our database, please contact us. All comments and suggestions on this database will be highly appreciated.

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