

Tutorial

for

RiceENCODE: a comprehensive epigenomic database

as rice Encyclopedia of DNA Elements

Liang Xie^{1,2}, Minghao Liu^{1,2}, Kai Cao^{1,2}, Peng Wang^{1,2}, Wenhao Xu^{1,2}, Lun Zhao¹,
Xingwang Li^{1*} & Guoliang Li^{1,2*}

<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

The screenshot shows the RiceENCODE database home page. At the top, there is a navigation menu with the following links: Home, Browser, Search, Data, Download, and Help. Below the menu, the page welcomes users to the RiceENCODE database Vo.1. The main content area contains a detailed description of the database, highlighting its comprehensive nature and the types of data it includes. A diagram at the bottom of the page illustrates various genomic and epigenetic features, including 3D Genome, histone modification, chromatin accessibility, chromatin state, DNA methylation, and transcriptome. Red arrows and circles highlight the navigation menu and the diagram.

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

Choose species and Tissues: MH63 Young leaves

Gene ID Search: SearchGene Example: MH01g0710600; Ghd7;

Comments or Questions

For any questions please [Contact us](#)

Recommended browsers

The recommended browsers are Chrome, Firefox, Safari, and Edge.

Citations

Researchers who wish to use RiceENCODE are encouraged to refer to our publication or more: [RiceENCODE](#).

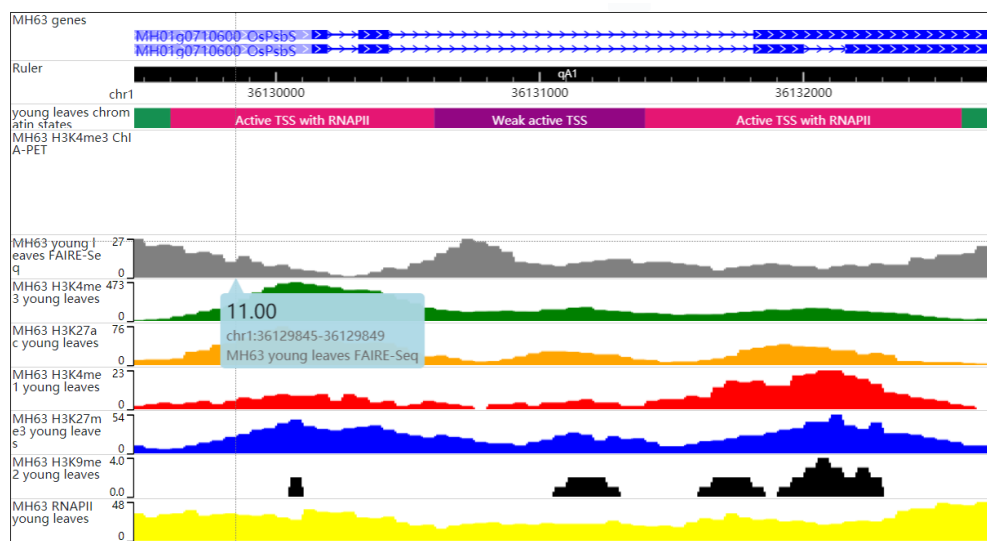
Guoliang's Bioinformatics Lab

Welcome to Guoliang's Lab Website of Bioinformatics at College of Informatics, Huazhong Agricultural University (HZAU). Our main research interests are in the field of three-dimensional (3D) Genomics.

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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:



The resulted tabular layout looks 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

The screenshot shows the WASHU EPIGENOME BROWSER interface. A search box labeled "Gene search" contains the text "LOC_Os01g01010". Below the search box, two gene entries are listed: "gene chr1:2983-10562" and "gene chr1:2902-10817", both described as "TBC domain containing protein, expressed". A "Coordinate" input field is visible below the search results, with a "Go" button next to it. Red arrows point to the search box and the coordinate field.

2.2 Select the annotated track and public hub

The screenshot shows the WASHU EPIGENOME BROWSER interface with the "Tracks" menu open. The menu options include "Annotations Tracks", "Public Data Hubs", "Track Facet Table", "Remote Tracks", "Local Tracks", "Local Text Tracks", and "Track List". A red arrow points to the "Public Data Hubs" option. Below the menu, a track labeled "Public data hub" is visible. The main browser area shows a genomic track with annotations for "LOC_Os01g01010" and "LOC_Os01g01030".

2.3 Choose the data hub

Public data hubs

Collection	Hub name	Tracks	Add
Rice CHIP-Seq datasets	Rice CHIP-Seq datasets	358	+
Rice Open Chromatin datasets	Rice open chromatin datasets	70	+
Rice RNA-Seq datasets	Rice RNA-Seq datasets	43	+
Rice DNA methylation datasets	Rice DNA methylation datasets	23	+
Rice Chromatin states	Rice Chromatin states	4	+
Rice Hi-C datasets	Rice Hi-C datasets	13	+
SNP/INDEL	19 varieties SNPs and INDELS	38	+

Page 1 of 1 | 10 rows

No tracks from data hubs yet. Load a hub first.

2.4 Select the data type from tissues and species

Species and Tissues	Assay	Epigenetic Mark	Histone Mark	Data type						
				RNAPII	H3K9me2	H3K27me3	H3K4me1	H3K27ac	H3K4me3	
<i>EjSample</i>										
<i>EjZS97</i>		0/36	0/36	0/30	0/36	0/36	0/36	0/30	0/30	0/36
mature leaves			0/36		0/36		0/30			0/36
panicles		0/36		0/36		0/30		0/36		
roots			0/36			0/36				0/30
young leaves			0/36			0/36				0/36
<i>EjNipponare</i>			0/30			0/36				
mature leaves							0/6	0/6		0/6
panicles	0/6	0/6	0/6				0/6	0/6	0/6	0/6
roots	0/6	0/6	0/6					0/6	0/6	0/6
young leaves	0/6	0/6	0/6				0/6	0/6	0/6	0/6
<i>EjMH63</i>	0/6	0/6	0/6							
mature leaves							0/6	0/6		0/6
panicles	0/6	0/6	0/6				0/6	0/6	0/6	0/6
roots	0/6	0/6	0/6					0/6	0/6	0/6
young leaves	0/6	0/6	0/6				0/6	0/6	0/6	0/6

2.5 Add the data track you chose

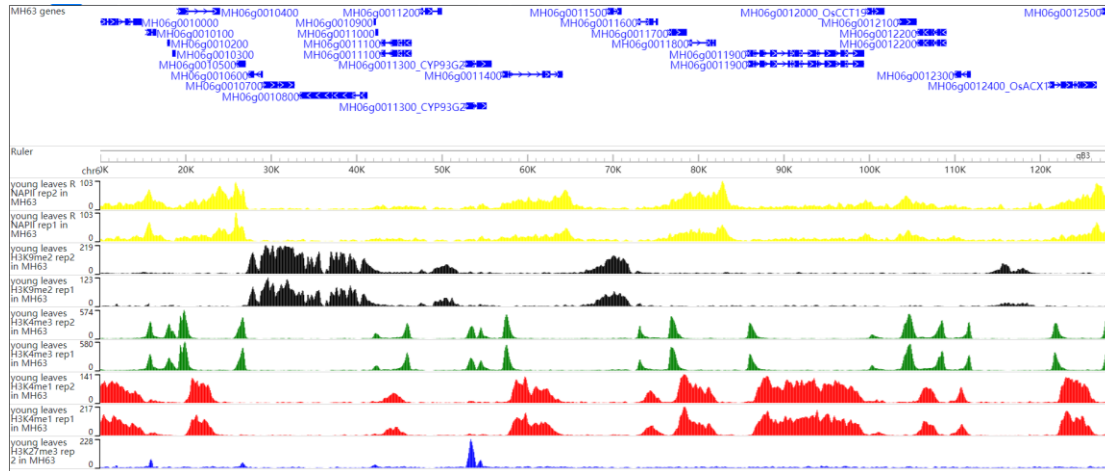
Track table

Search tracks Search track type

Free text search over track labels and metadata.

Name	Data hub	Sample	Assay	Format	Add
		Filter...	Filter...		
young leaves H3K4me3 rep1 in MH63	Rice ChIP-Seq datasets	MH63 > young leaves	Epigenetic Mark > Histone Mark > H...	bigwig	<input type="button" value="+"/>
young leaves H3K4me3 rep2 in MH63	Rice ChIP-Seq datasets	MH63 > young leaves	Epigenetic Mark > Histone Mark > H...	bigwig	<input type="button" value="+"/>
roots H3K4me3 rep1 in MH63	Rice ChIP-Seq datasets	MH63 > roots	Epigenetic Mark > Histone Mark > H...	bigwig	<input type="button" value="+"/>
roots H3K4me3 rep2 in MH63	Rice ChIP-Seq datasets	MH63 > roots	Epigenetic Mark > Histone Mark > H...	bigwig	<input type="button" value="+"/>
panicles H3K4me3 rep1 in MH63	Rice ChIP-Seq datasets	MH63 > panicles	Epigenetic Mark > Histone Mark > H...	bigwig	<input type="button" value="+"/>
panicles H3K4me3 rep2 in MH63	Rice ChIP-Seq datasets	MH63 > panicles	Epigenetic Mark > Histone Mark > H...	bigwig	<input type="button" value="+"/>
mature leaves H3K4me3 rep1 in MH63	Rice ChIP-Seq datasets	MH63 > mature leaves	Epigenetic Mark > Histone Mark > H...	bigwig	<input type="button" value="+"/>
mature leaves H3K4me3 rep2 in MH63	Rice ChIP-Seq datasets	MH63 > mature leaves	Epigenetic Mark > Histone Mark > H...	bigwig	<input type="button" value="+"/>
young leaves H3K27ac rep1 in MH63	Rice ChIP-Seq datasets	MH63 > young leaves	Epigenetic Mark > Histone Mark > H...	bigwig	<input type="button" value="+"/>

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.

Histone Modification Search

Gene ID/ Gene name

Choose species and histone modification:

Gene ID Search: Example: MH01g0710600; Ghd7;

Chr Start: End:

Annotations: Red arrows point to 'Select genome,tissues and histone modification' (pointing to the dropdowns), 'Genome region' (pointing to the Gene ID Search input), and 'Search' (pointing to the Search button).

3.2 Histone modification overview

The histone modification viewer provides and tabular layouts for the resulted blocks.

Histone Modification Search

Choose species and histone modification: MH63 Young leaves H3K4me3

Gene ID Search: SearchGene Example: MH01g0710600; Ghd7; Click histone button shows the screenshots for this peak

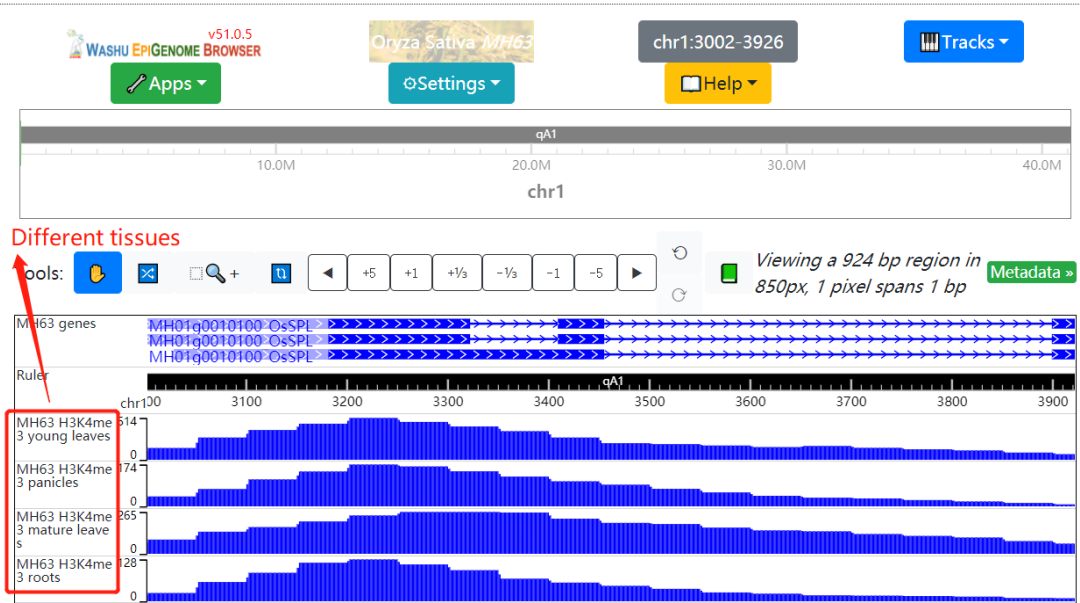
Chr: Start: End: Search download table

chr	start	end	pileup	-log10pvalue	fold enrichment	-log10qvalue	Histone
chr1	3002	3926	57.63	42.6963	10.769	40.2016	H3K4me3
chr1	24209	25394	47.82	33.8953	9.76441	31.8469	H3K4me3
chr1	25810	27164	39.42	26.1717	8.35432	24.3822	H3K4me3
chr1	28925	30607	41.02	29.2353	9.10328	27.3545	H3K4me3
chr1	32500	33725	59.43	46.0769	11.5275	43.3464	H3K4me3
chr1	40130	41703	67.23	58.3173	14.1032	53.8959	H3K4me3
chr1	49746	51054	57.63	41.6627	10.3837	39.2357	H3K4me3
chr1	57273	58817	35.22	21.4453	7.18576	19.781	H3K4me3
chr1	86572	87616	34.02	17.6571	5.83595	16.083	H3K4me3
chr1	94165	95437	67.23	48.833	10.6385	45.8286	H3K4me3

Total number: 13 Page: 1-10 <<First PRE 1 2 NEXT LastPage>>

Corresponding to peak regions in different tissues

Browser screen



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.

Open Chromation Region Search → Select genome tissues and sequencing

Choose species and Sequence: MH63 Young leaves FAIRE-Seq

Gene ID Search: MH01g0710600 Example: MH01g0710600; Ghd7;

Overlap Region: Gene Body TSS500 TSS1000 TSS1500 SearchGene → Gene region select

Chr: Start: End: Search download table → Genome region select button

Chr	start	end	pileup	-log10pvalue	fold enrichment	-log10qvalue	Sequencing
chr1	36129324	36129652	34	6.34684	2.46827	4.27201	FAIRE-Seq

Total number: 1 Page: 1-1 → Peak button for browser screen <<First PRE 1 NEXT LAST>>

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.

Chromatin interaction Search

Choose species and histone modification: Oryza Sativa MH63RS1 H3K4me3 ChIA-PET ①

Loop ID Search: SearchLoop ② Gene ID Search: MH01g0710600 SearchGenetoRegion ③

Chr: Start: End: Search ④

Gene to Gene loop Search: MH01g0710600 SearchGeneToGene download table Example: MH01g0710600; Ghd7.1; ⑤

Extend 3 ⑥
 Extend 2
 Extend 1

Extend number means connection layers to search gene in the network. We limit the searching number of extend number here.

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 then click the search button and resulted tabular layout looks like this:

Chr	Start	End	Chr	Start	End	PETcount	LoopID
chr1	100139	101453	chr1	120643	122793	5	MH63_H3K4me3_Loop19

Total number:1 Page:1-1

Shows the loop region in browser

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 and the resulted tabular layout looks like this:

Gene	Chr	Start	End	PETCount	LoopID
MH01g0710600	chr1	36142775	36145109	18	MH63_H3K4me3_Loop1165
MH01g0710600	chr1	36152816	36154193	8	MH63_H3K4me3_Loop1166

Total number:2 Page:1-2

Shows the loop in browser

<<First PRE 1 NEXT LAST>>

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:

Chr	Start	End	Chr	Start	End	PETcount	LoopID
chr1	2908	4018	chr1	32376	33847	4	MH63_H3K4me3_Loop1
chr1	25673	27299	chr1	39971	41860	6	MH63_H3K4me3_Loop2
chr1	28755	30775	chr1	39971	41860	6	MH63_H3K4me3_Loop3
chr1	28755	30775	chr1	49614	51184	6	MH63_H3K4me3_Loop4
chr1	32376	33847	chr1	39971	41860	8	MH63_H3K4me3_Loop5
chr1	32376	33847	chr1	49614	51184	4	MH63_H3K4me3_Loop6
chr1	39971	41860	chr1	49614	51184	15	MH63_H3K4me3_Loop7
chr1	39971	41860	chr1	97678	99044	4	MH63_H3K4me3_Loop8
chr1	39971	41860	chr1	100139	101453	6	MH63_H3K4me3_Loop9
chr1	49614	51184	chr1	97678	99044	7	MH63_H3K4me3_Loop10

Total number:86 Page:1-10

Shows the loop region in browser

<<First PRE 1 2 3 4 5 6 7 .. NEXT LastPage>>

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

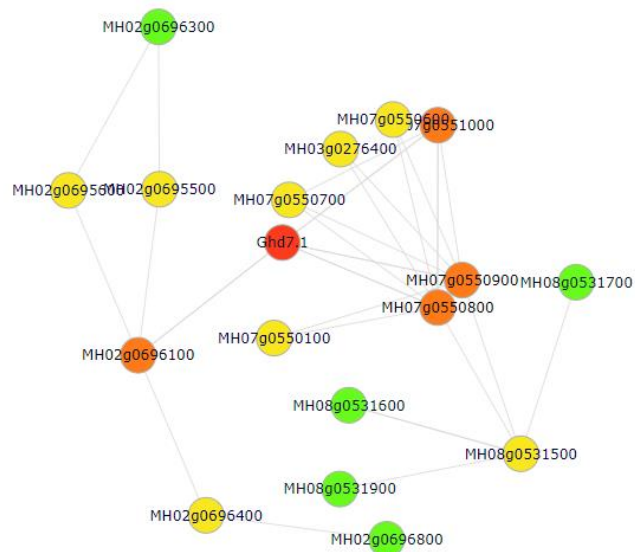
extend degree in part 6(extend degree means the network connectivity). The resulted(Ghd7.1) tabular and network layout looks like this:

Gene	FPKM	Gene	FPKM	Pvalue
MH02g0696100	49	Ghd7.1	73.21	1.76e-06
MH07g0550800	18	Ghd7.1	73.21	2.18e-06
MH07g0550900	842	Ghd7.1	73.21	2.18e-06
MH07g0551000	45	Ghd7.1	73.21	1.01e-08
MH02g0695500	1	MH02g0696100	48.99	1.18e-16
MH02g0695600	210	MH02g0696100	48.99	1.18e-16
MH02g0696100	49	MH02g0696400	131.37	5.73e-06
MH03g0276400	6	MH07g0550800	17.88	1.07e-05
MH07g0550100	50	MH07g0550800	17.88	4.73e-10
MH07g0550600	6	MH07g0550800	17.88	7.83e-12

Total number:44 Page:1-10

<<First PRE 1 2 3 4 5 NEXT LastPage>>

- Search gene
- Extend 1 hoop
- Extend 2 hoop
- Extend 3 hoop



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.

Gene Expression Search

Choose species : Choose genome

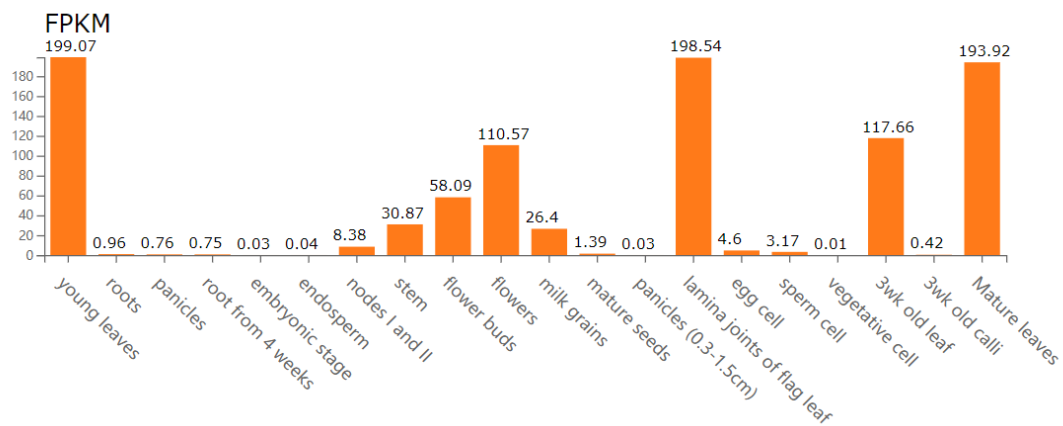
MH63 ZS97 Nipponbare

Gene ID Search: Gene ID/Gene name

Example: MH01g0710600; Ghd7;

6.2 Gene expression overview

The gene 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.

DNA methylation Search

Choose species and histone modification: 1

Gene ID Search: 2 Example: MH01g0710600; Ghd7;

Chr: Start: End: 3

Compare Tissues: VS DNAmethylation type: 4

5

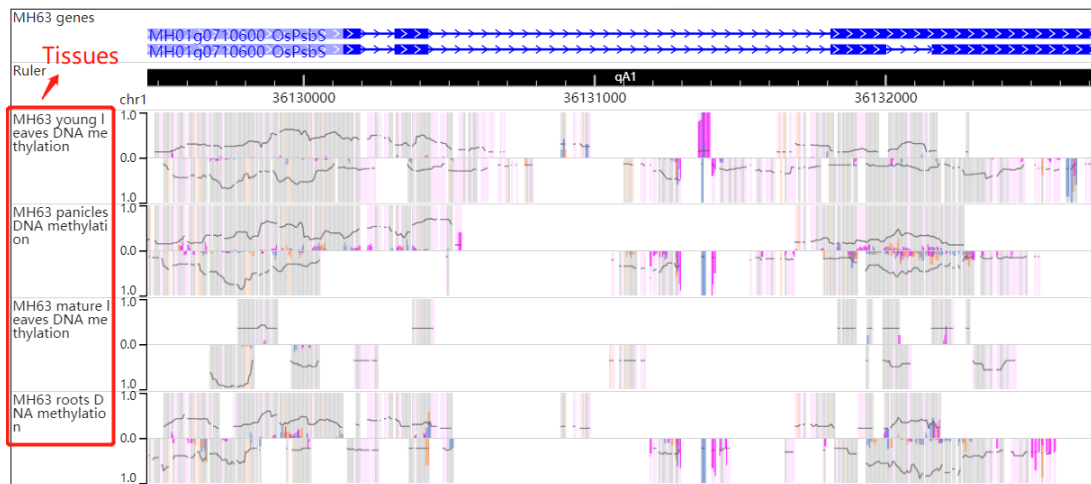
The meanings of part are listed below:

Part 1:

Choose species.

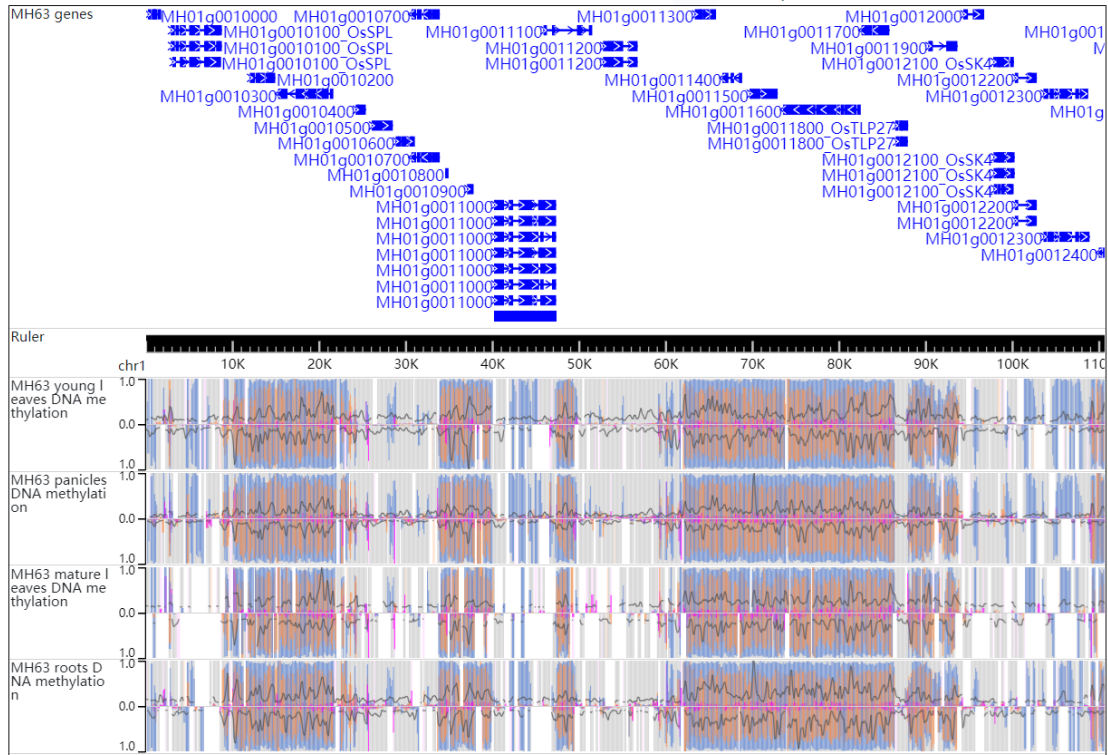
Part 2:

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:

Chr: Start: End:

Compare Tissues: VS DNAmethylation type:

Chr	start	end	Pvalue	foldchange	Compare	DMR_ID
chr1	33001	34000	3.01e-02	-0.18	Panicles VS Young leaves	CG-DMR_30610
chr1	102001	103000	4.87e-02	-0.16	Panicles VS Young leaves	CG-DMR_30611

Total number: 2 Page: 1-2 [Show DMR region in browser](#) <<First PRE 1 NEXT LAST>>

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.

Chromatin State Search

Choose species and histone modification: **Oryza Sativa MH63** **Mature leaves**

Gene ID Search: **MH01g0710600** **SearchGene** Example: MH01g0710600; Ghd7;

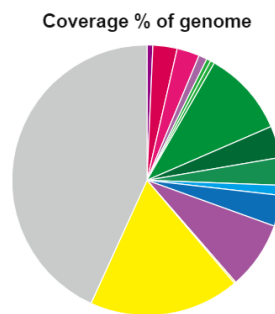
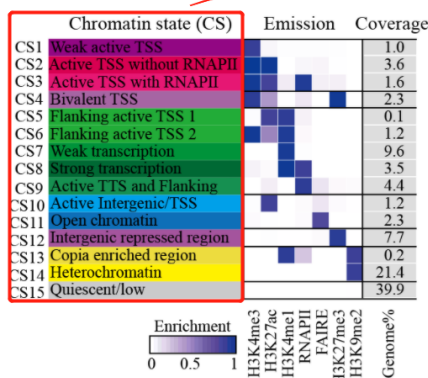
Chr: Start: End: **Search** **download table**

The resulted tabular layout looks like this:

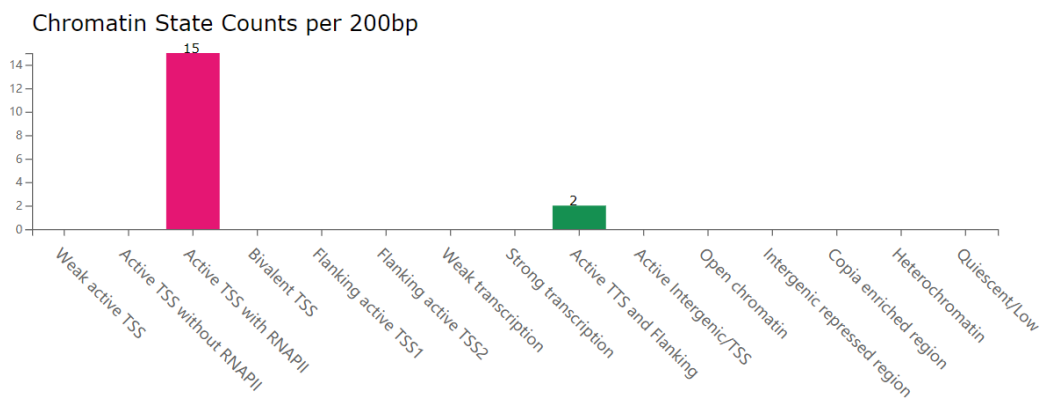
Chr	start	end	Chromatin State
chr1	36129400	36129600	Active TTS and Flanking
chr1	36129600	36132600	Active TSS with RNAPII
chr1	36132600	36132800	Active TTS and Flanking

Total number: 3 Page: 1-3 <<First PRE 1 NEXT LAST>>

MH63 Mature leaves ChromHMM chromatin states



Bar plot for chromatin state counts:



9. Download all the bigwig and peaks file for different datasets.

RiceENCODE provides bigwig and peak file for users downloading.

Dataset Download Treetable

You can download bigwig and bed files here.

[Expand all](#) [Collapse all](#)

Files	Tissues	Type	SRA
▼ Oryza Sativa	--	Folder	--
▼ Peaks	--	Folder	--
▼ MH63	--	Folder	--
▶ histone modification	--	Folder	--
▶ chromatin accessibility	--	Folder	--
▼ ZS97	--	Folder	--
▶ histone modification	--	Folder	--
▶ chromatin accessibility	--	Folder	--
▼ Nipponbare	--	Folder	--
▶ histone modification	--	Folder	--
▶ chromatin accessibility	--	Folder	--
▼ BigWig	--	Folder	--
▼ MH63	--	Folder	--
▶ histone modification	--	Folder	--
▶ chromatin accessibility	--	Folder	--
▼ ZS97	--	Folder	--
▶ histone modification	--	Folder	--
▶ chromatin accessibility	--	Folder	--
▼ Nipponbare	--	Folder	--
▶ histone modification	--	Folder	--
▶ chromatin accessibility	--	Folder	--

FTP download sites

[Peaks sites](#) Peaks or interaction loop files for search module in RiceENCODE

[BigWig sites](#) BigWig files for browser module in RiceENCODE

Welcome to visit RiceENCODE!

<http://glab.hzau.edu.cn/RiceENCODE>