Human Epigenome Browser

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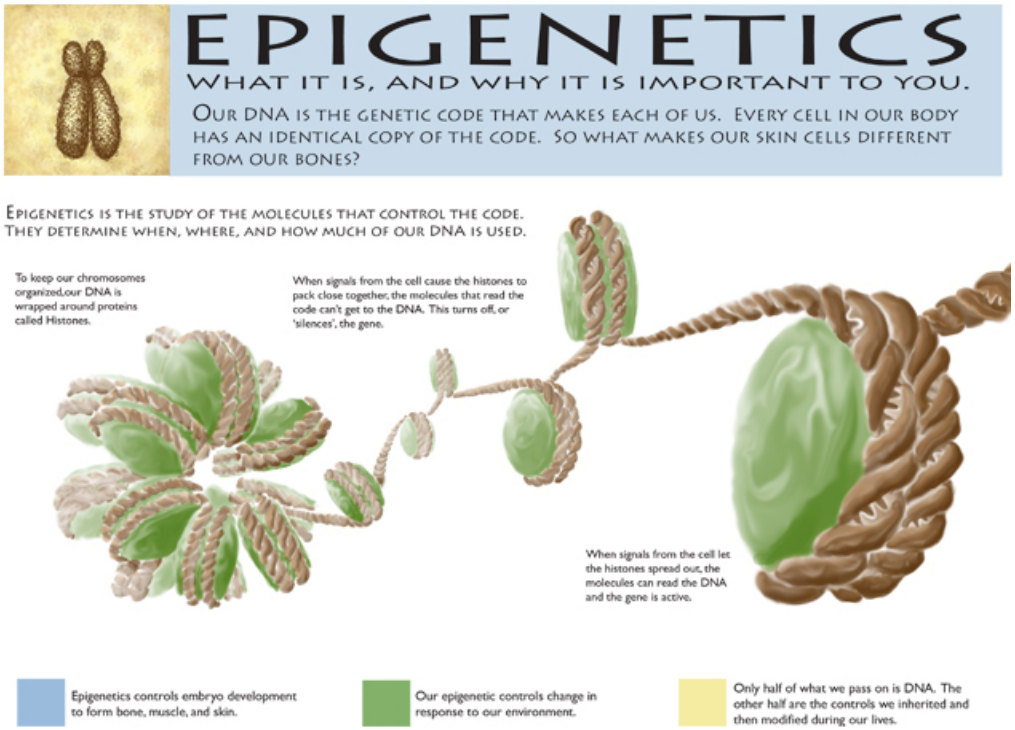
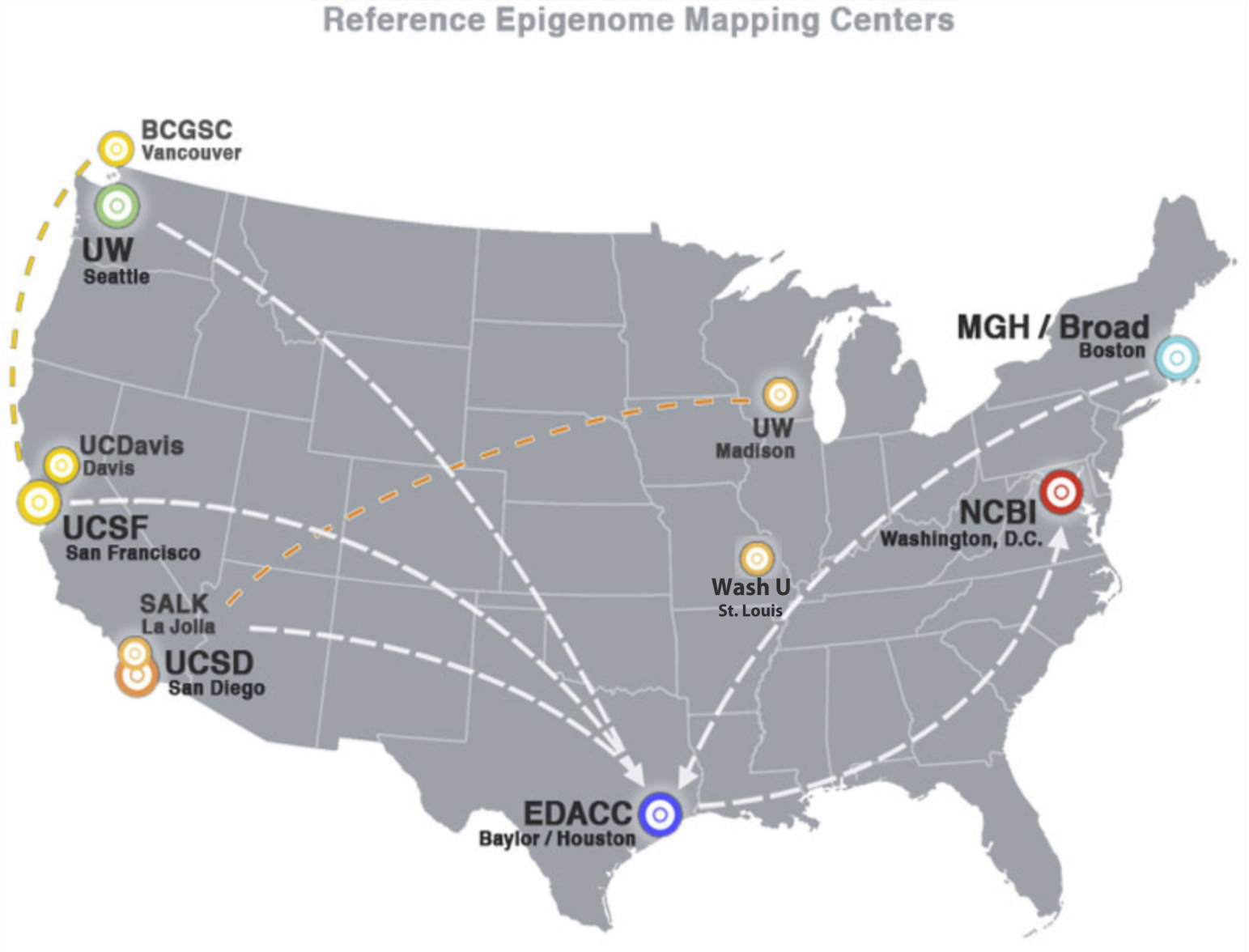
Background



Agouti mice

ROADMAP epigenomics PROJECT

http://www.roadmapepigenomics.org/



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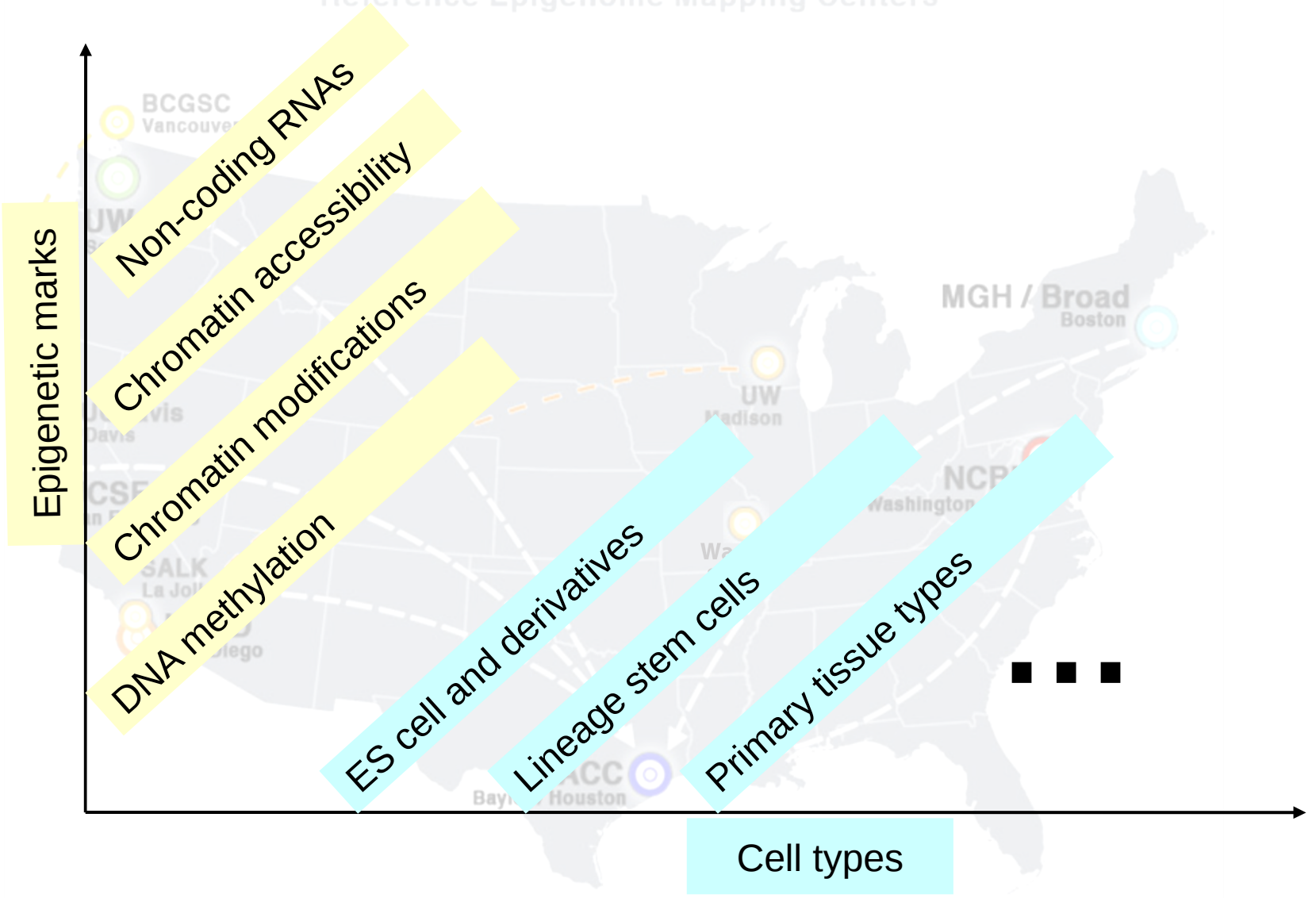


ROADMAP epigenomics PROJECT

http://www.roadmapepigenomics.org/

Reference Epigenome Mapping Centers

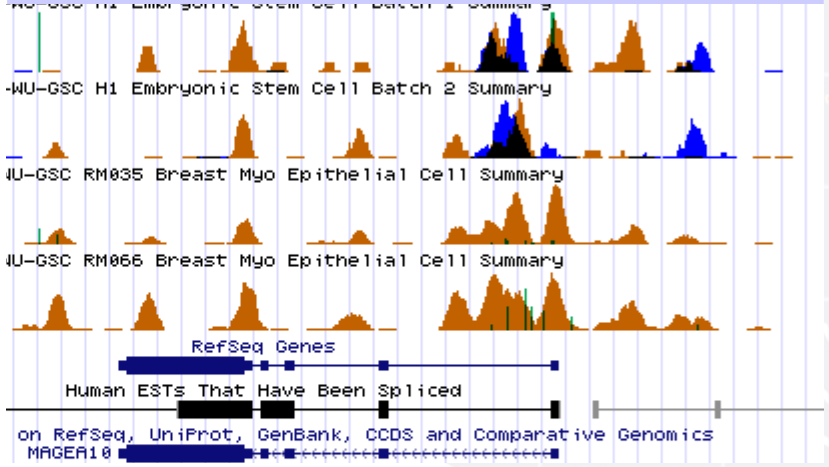
BCGSC Vancouver

UW

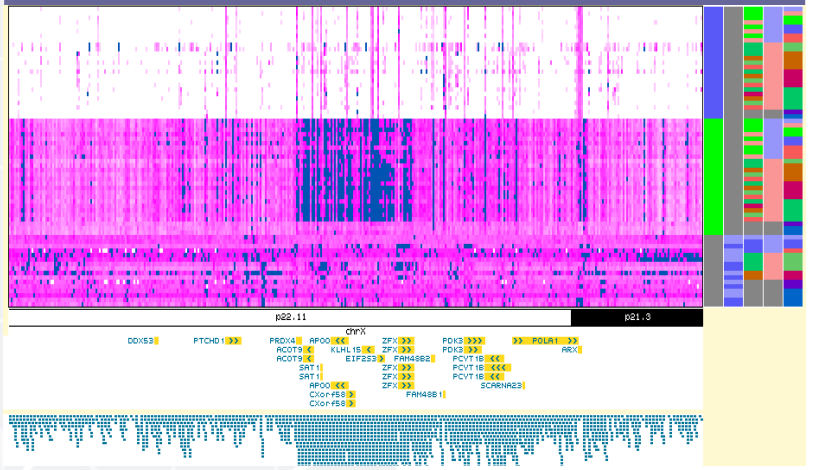
EDACC Baylor / Houston

VizHub @ WashU (Ting's lab)

UCSC Genome browser mirror site

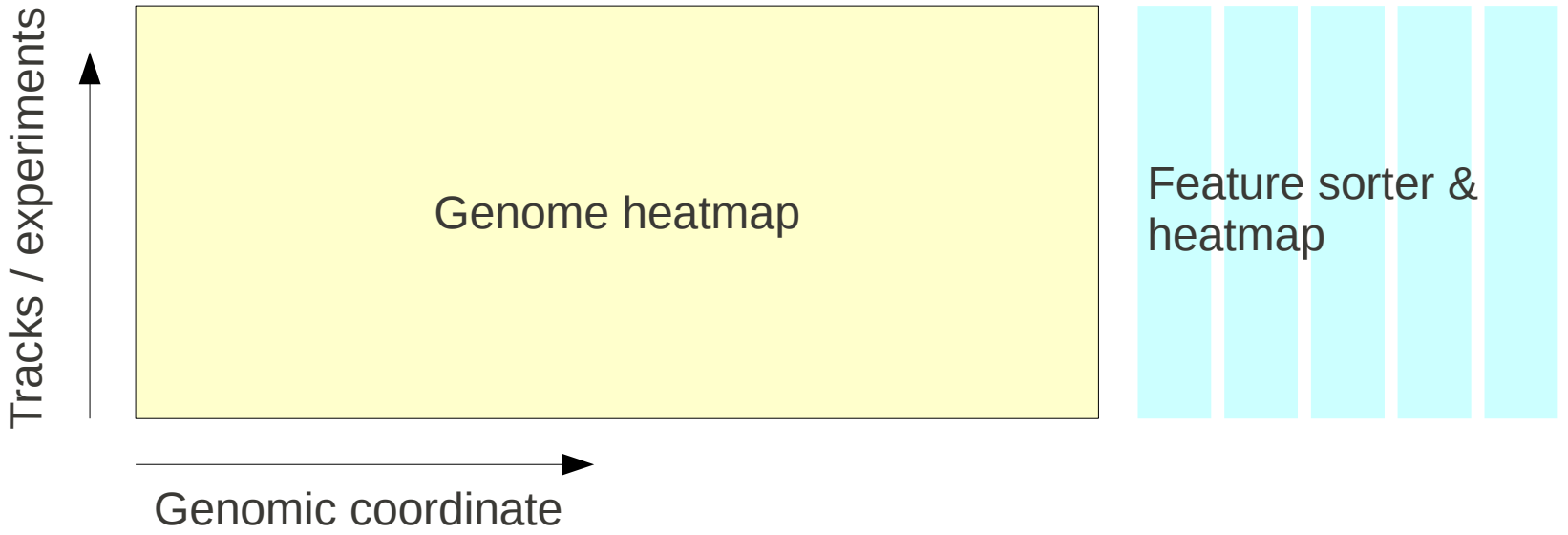


Human Epigenome Browser



Human epingenome browser

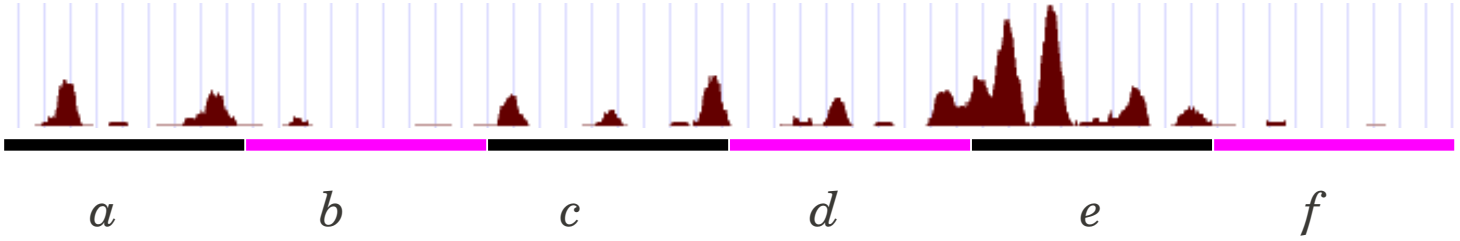
- Adopt the UCSC Cancer Browser display style



Data transformation

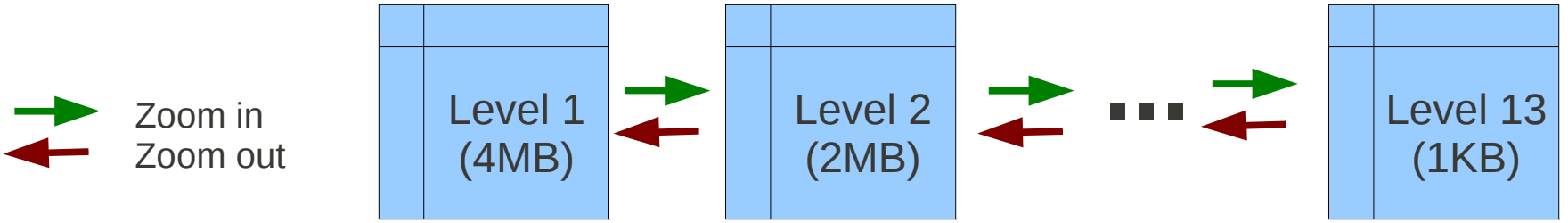
Step 1: divide genome into bins

Step 2: compute score for each bin using sequencing data



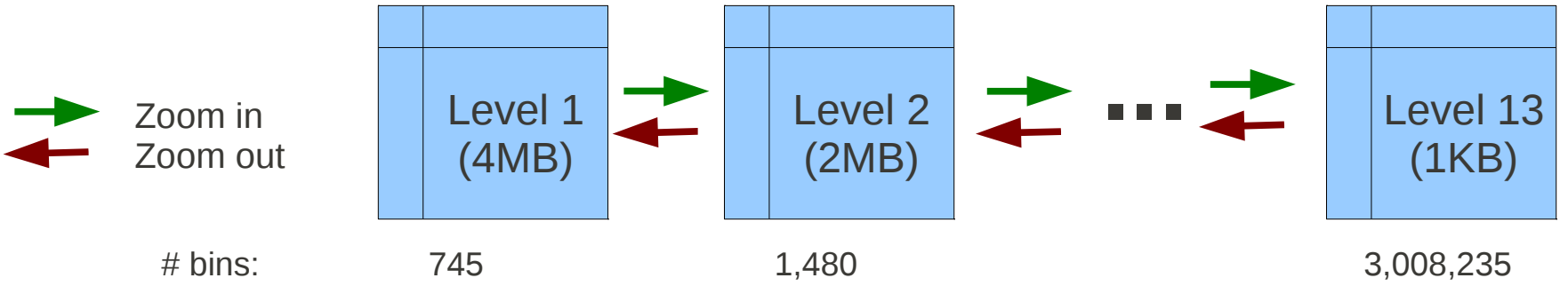
Step 3: apply steps 1-2 to multiple level of bins

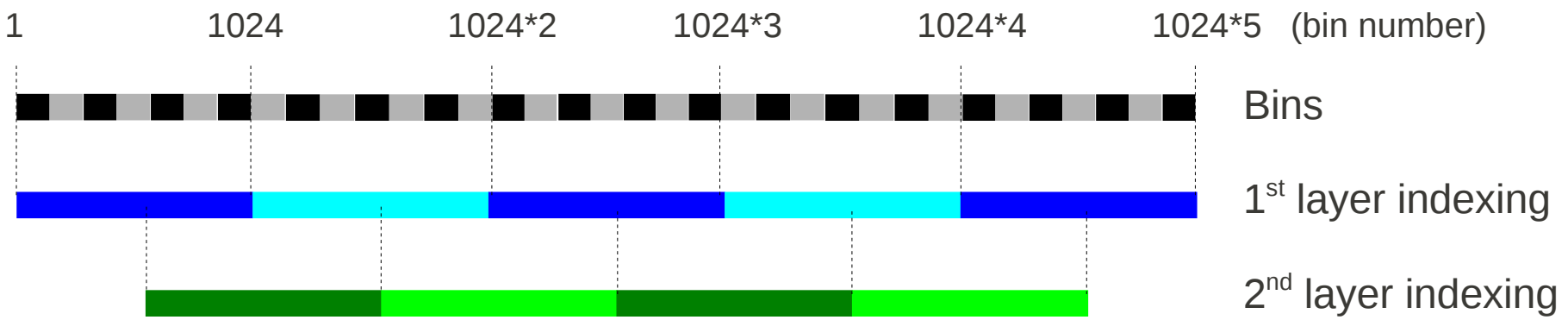
Database design



# bins:	745	1,480	3,008,235

Database design





(number of displayed bins is always 400)

Software implementation

- Server-side
  - MySQL
  - C, Kent source tree
    - CGI, MySQL communication, image rendering
  - R
- Front-end
  - JavaScript, Ajax

Human Epigenome Browser

*** Displaying genome ***

- start: chr1 1398784
- stop: chr1 1809408
- spanning 401 kb

Normalize data by 95 percentile of track

View current region
in UCSC genome browser

Zoom in | Zoom out | <<< | << | < | > | >> | >>>

Track height: 4 pixels

Position [ ] gene [CDK11B] Jump Clear

e.g. chr1:1397760-1808384
separator could be space, tab, dash, colon or single chromosome name

e.g. CDK11B, IL1RAPL1
case insensititve

- Choose genomic features (horizontal axis)
- Draw decorative tracks
- Select data tracks (vertical axis)
- Track score & genomic feature density correlation analysis
- Hypothesis test
- Get data in tabular format

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*** Displaying genome ***

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View current region
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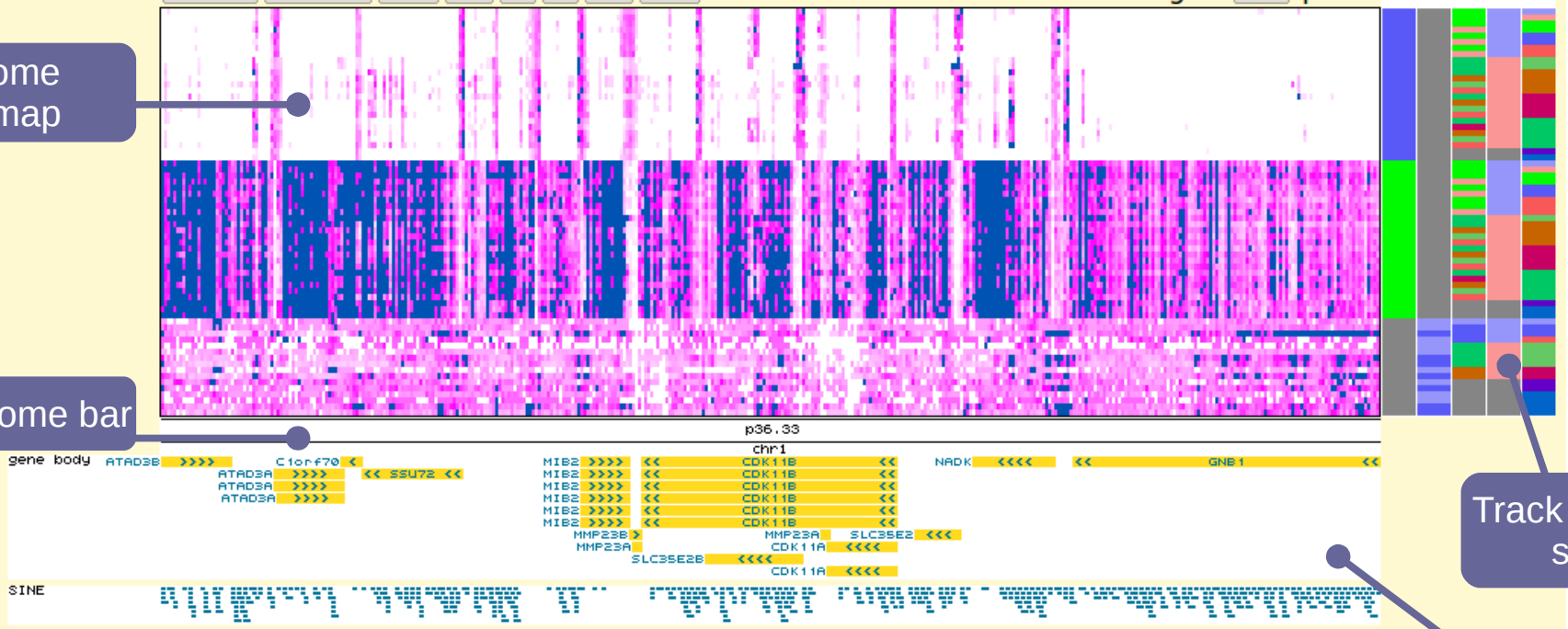
Zoom in | Zoom out | <<< | << | < | > | >> | >>>

Track height: 4 pixels

DNA methylation
Histone modification
Individual
Tissue / organ
Cell type



Genome heatmap

Chromosome bar

Track attribute & sorting

"Decorative" track

Jump to region

Position [ ] gene [CDK11B] Jump Clear

e.g. chr1:1397760-1808384
separator could be space, tab, dash, colon or single chromosome name

e.g. CDK11B, IL1RAPL1
case insensititve

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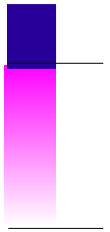
Control panel

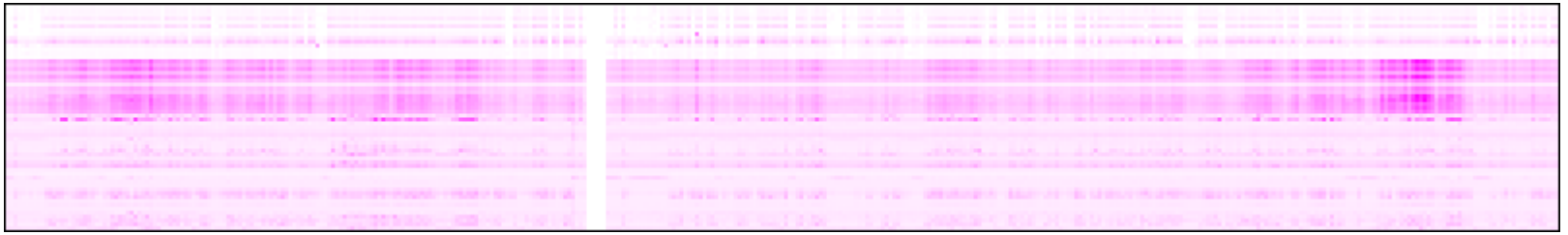
Heatmap coloring



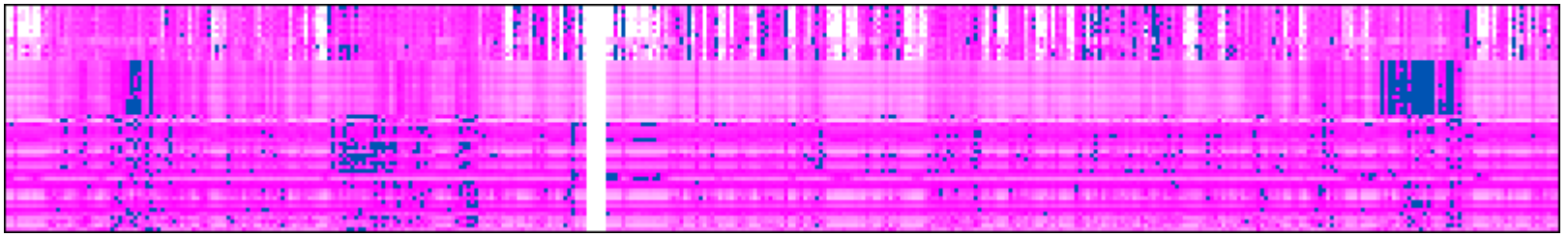
threshold

min

Different thresholds

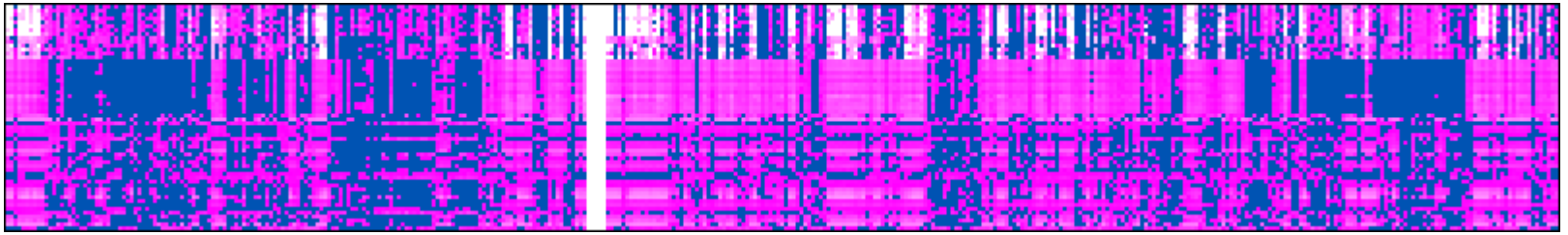


Track max



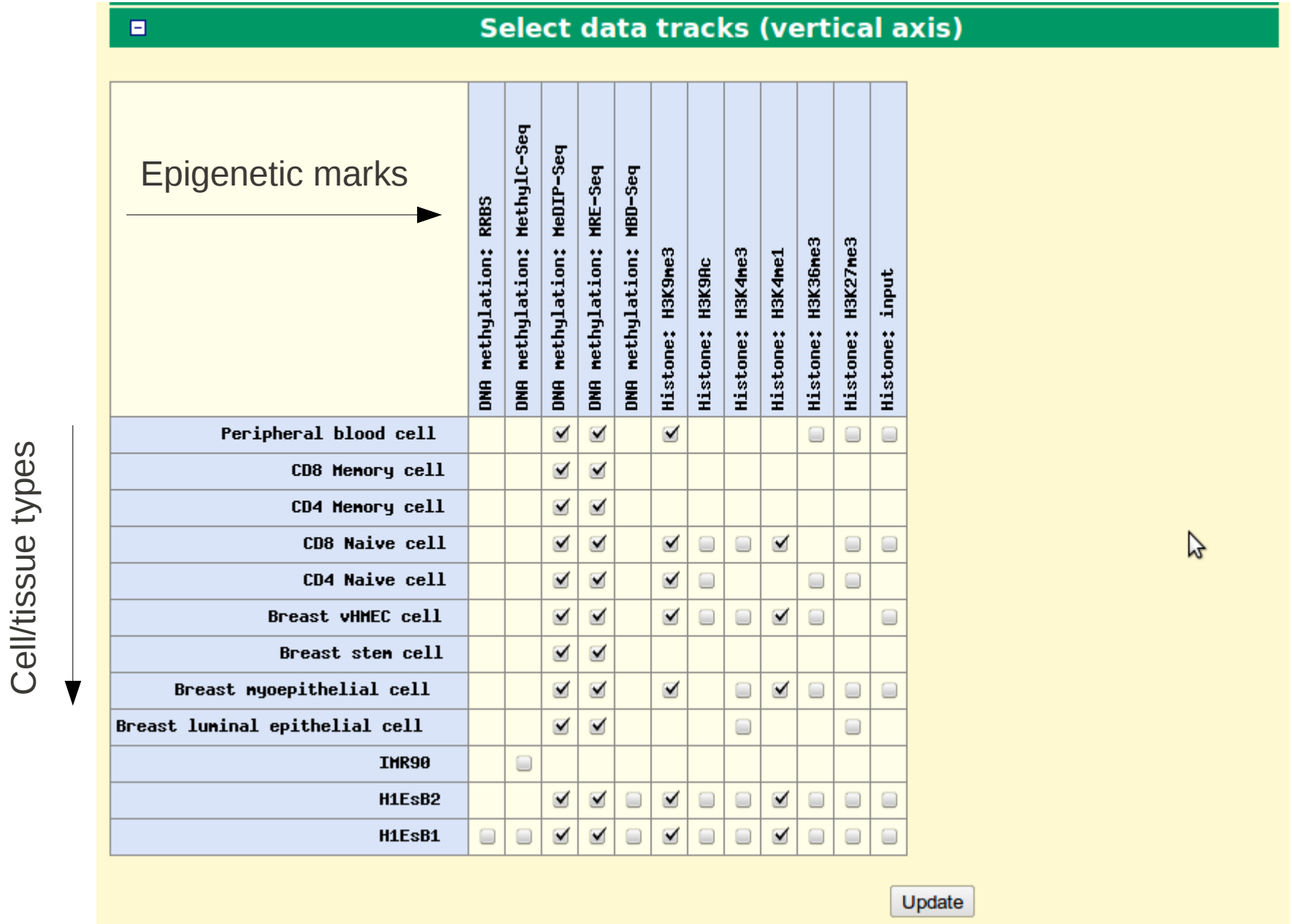
95 percentile of track

(90, 80, 70 percentiles)



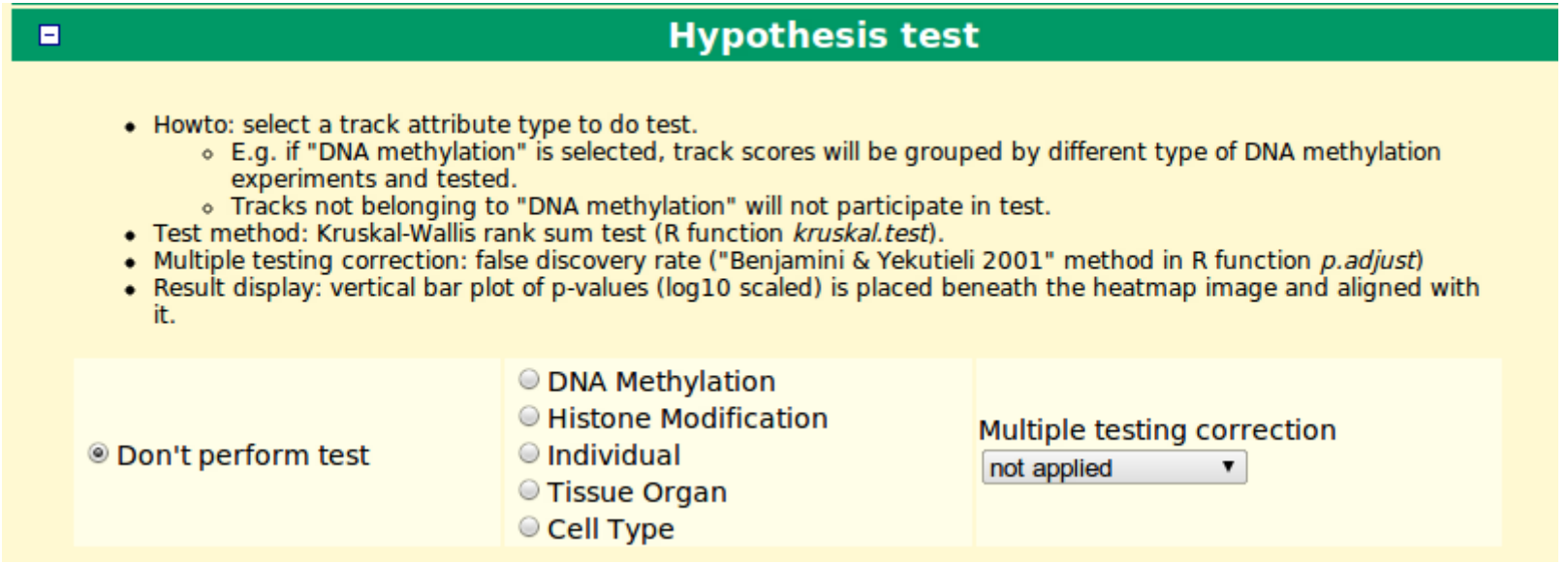
60 percentile of track

Track selection



Hypothesis test

on bin scores across groups of tracks



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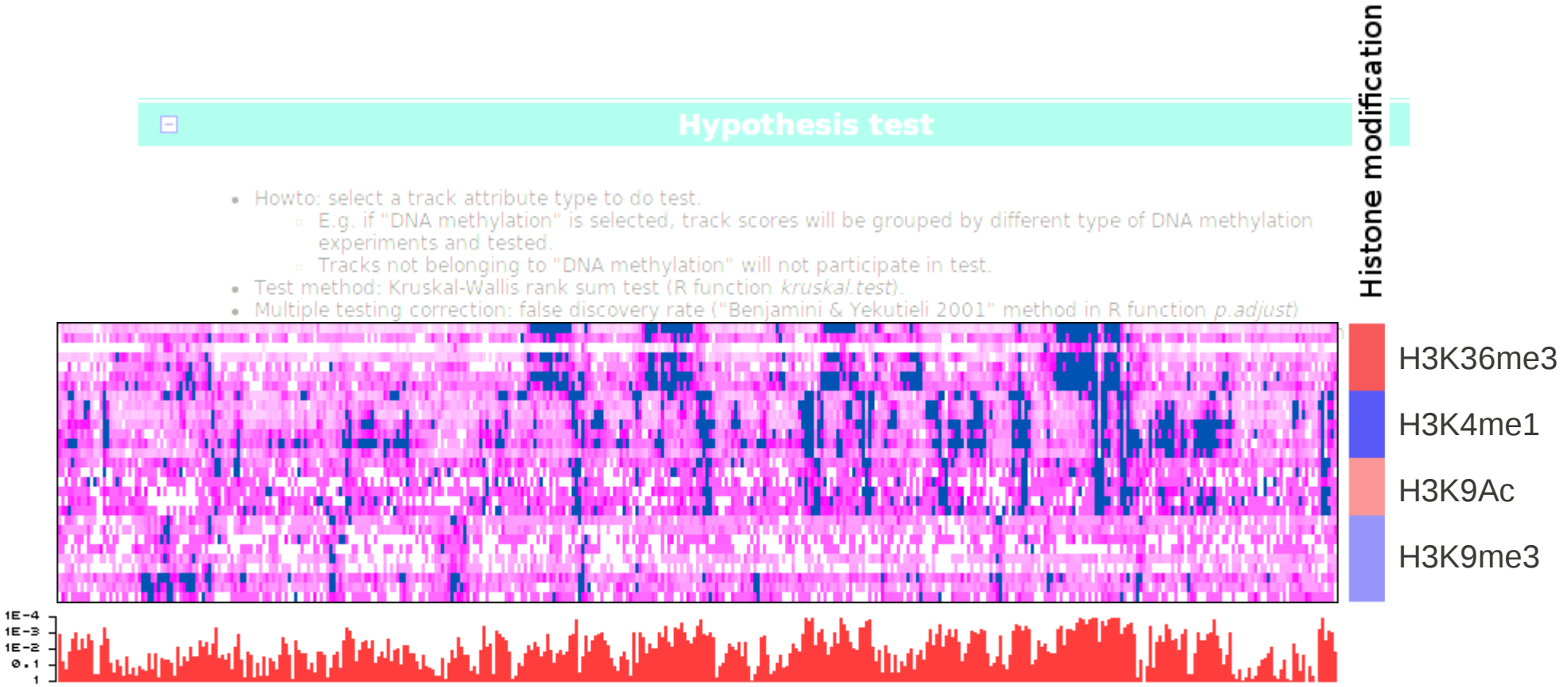
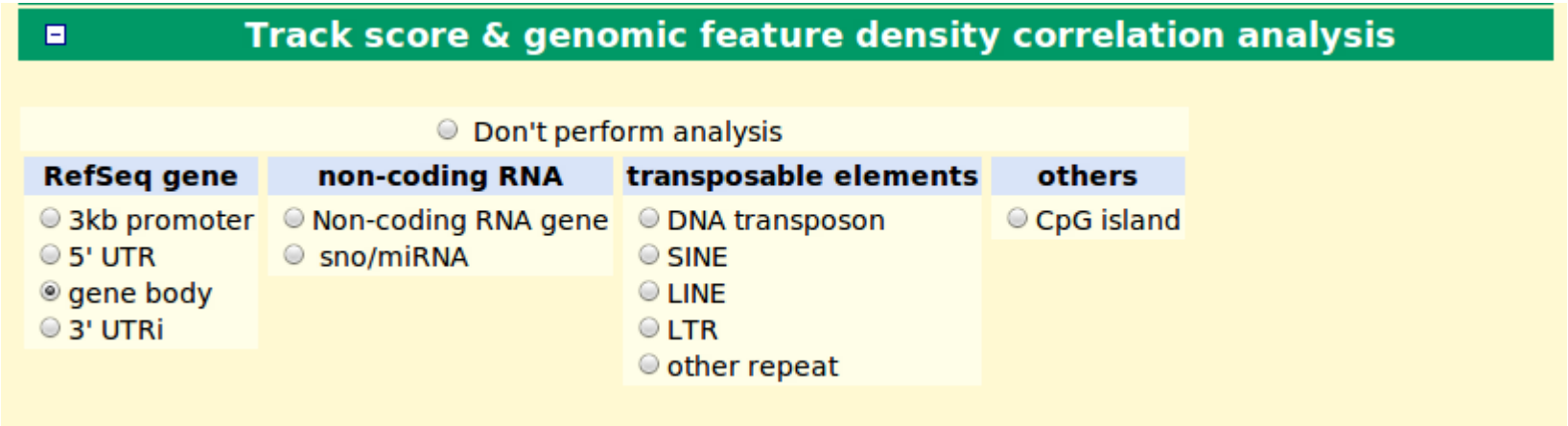


Correlation analysis

Track scores & genomic feature density



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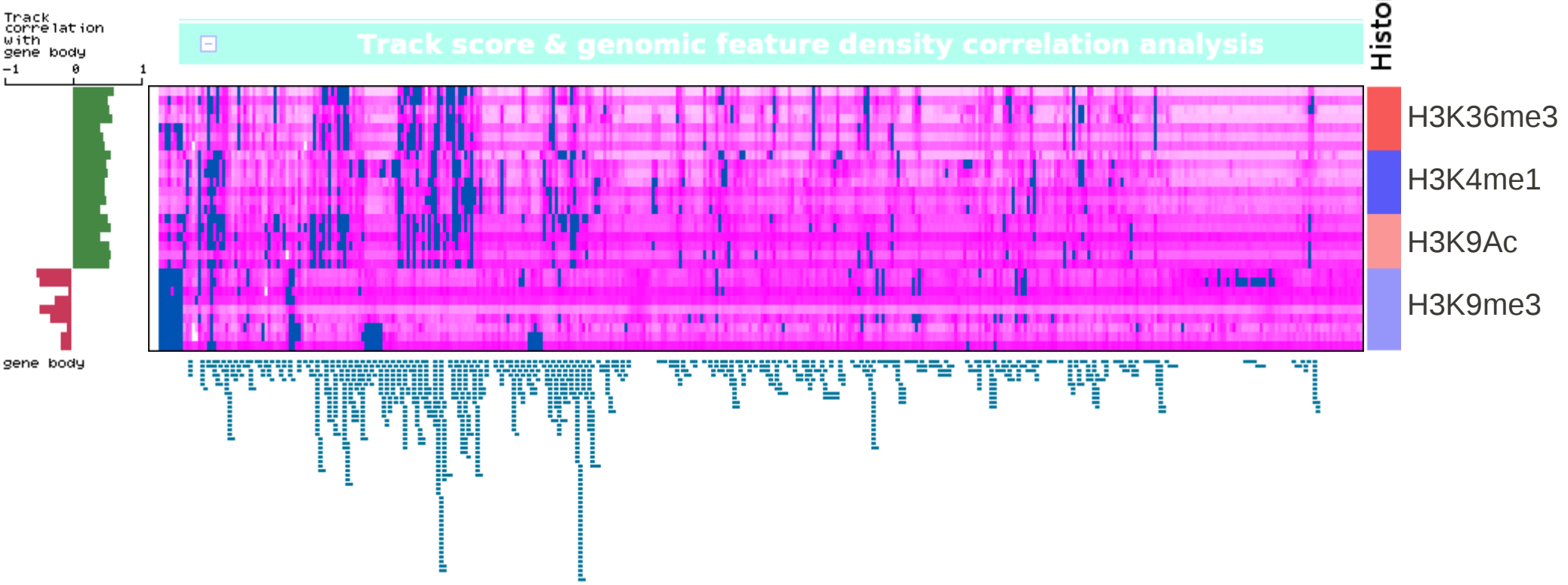
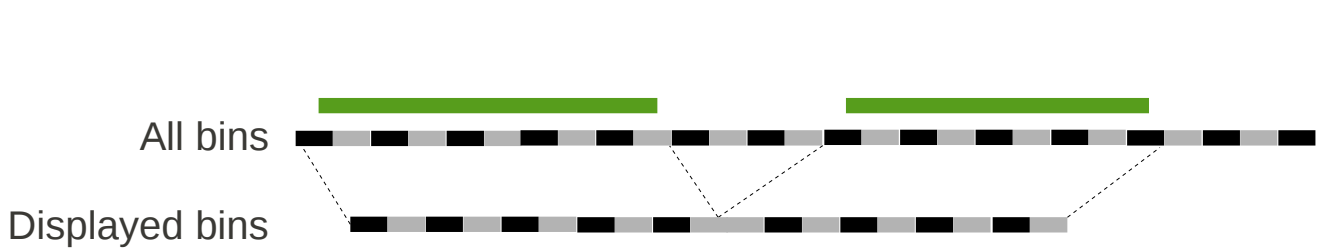
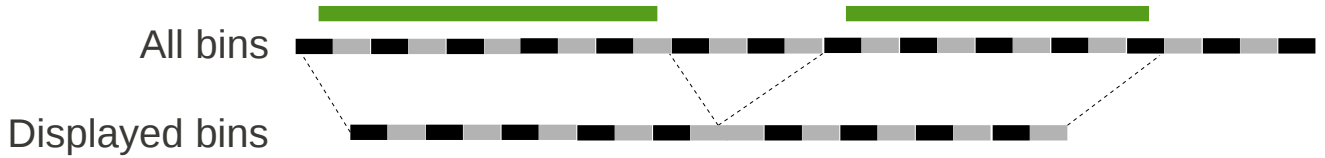


Focusing on genomic features



Focusing on genomic features



Choose genomic features (horizontal axis)

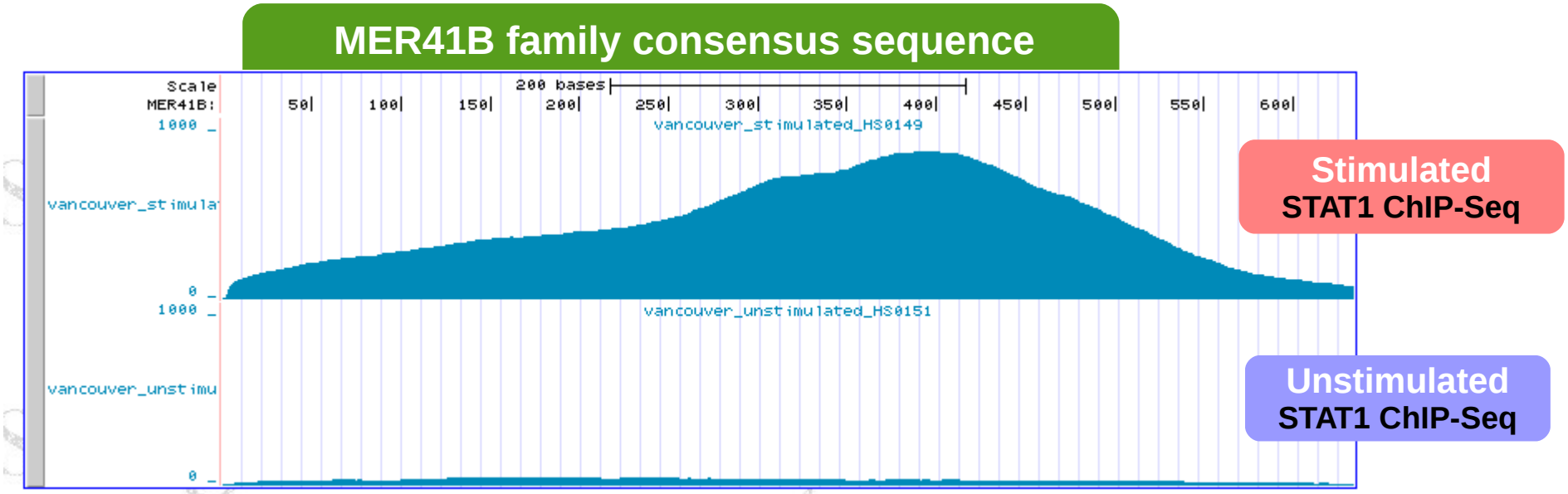
genome	RefSeq gene	non-coding RNA	transposable elements	others
○ genome	◉ 3kb promoter	○ non-coding RNA gene	○ DNA transposon	○ CpG island
	○ 5' UTR	○ sno/miRNA	○ SINE	
	○ gene body		○ LINE	
	○ exon		○ LTR	
	○ intron		○ other repeat	
	○ 3' UTR			

Problem to solve

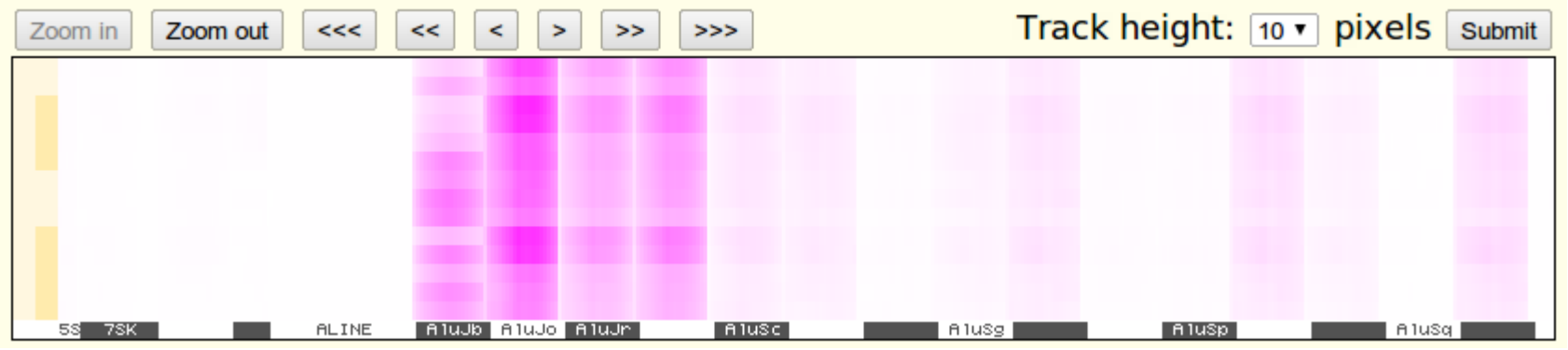
- Data transformation
- Database design
- Comments and suggestions are appreciated

Future work

- A focus on transposable elements
  - Carry TF binding sites around
  - Shape the landscape of mammalian regulatory network



Future work: a browser for transposable elements



- Adapt the code of epigenome browser
- Family centric view
- Reprocess REMC epigenome dataset, display on this browser

Acknowledgement

- Ting Wang's lab

- Brett Maricque
-
- Vasavi Sundaram

-
- Mingchao Xie

-
- Xiaoyun Xing