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# PEREpigenomics Profile Explorer of Roadmap Epigenomics data

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# PEREpigenomics

## Profile Explorer of Roadmap Epigenomics data

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 @G\_Devailly

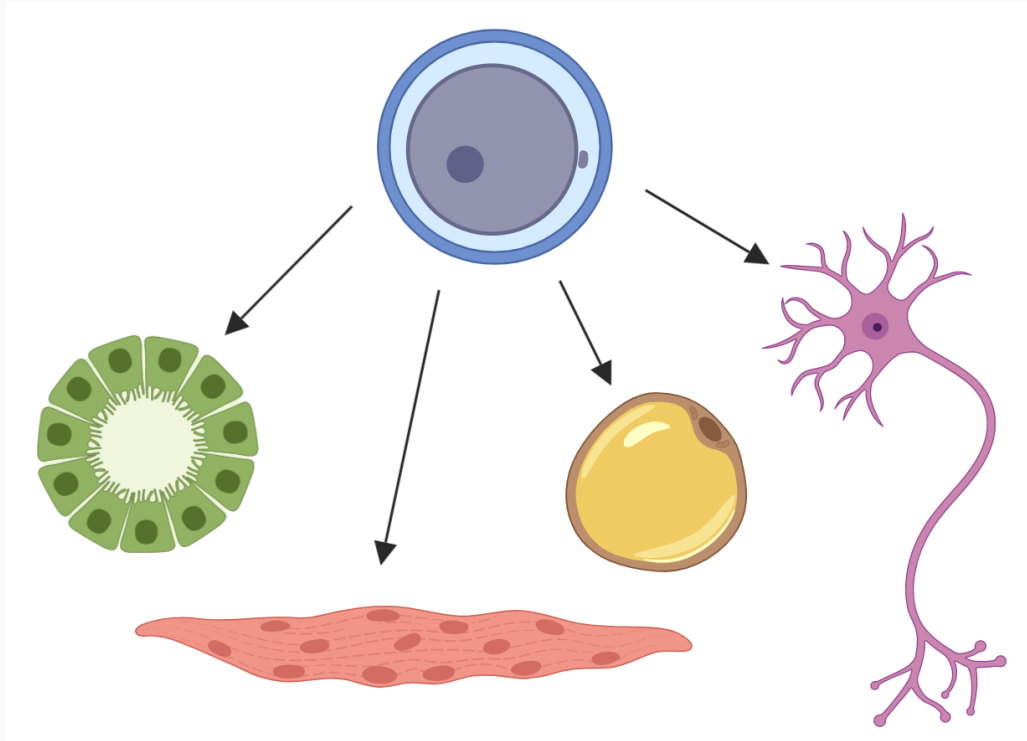
Guillaume Devailly

useR!2019

2019/07/09



# One genome, many cell types



Differential gene expression =  
cellular environment + epigenetics

# Epigenetics data

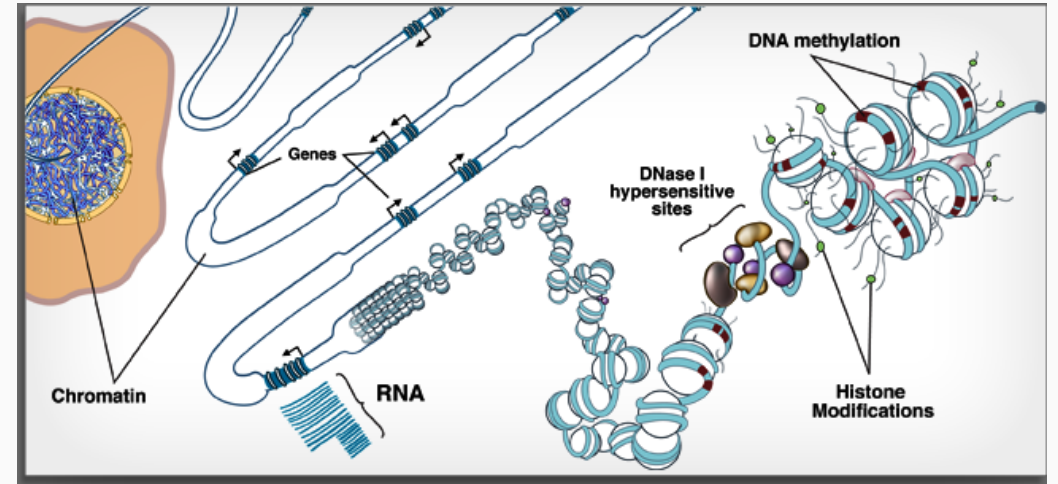
Many existing datasets and databases.

## Dataset:



- RNA-seq
- DNase1
- WGBS,
- 10 different histone methylations
- 17 different histone acetylations

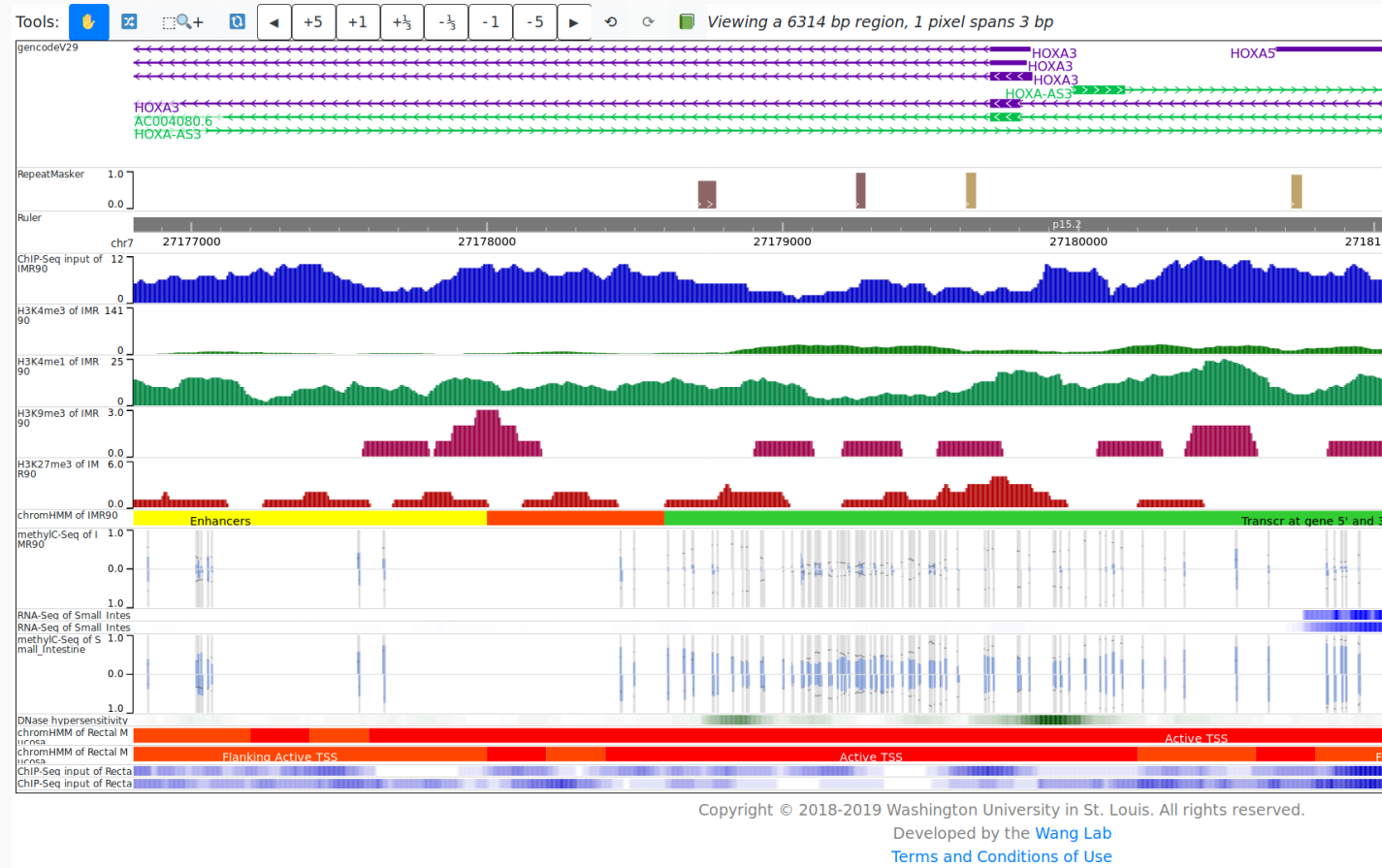
in 33 human cell lines & tissues,  
uniformly processed.





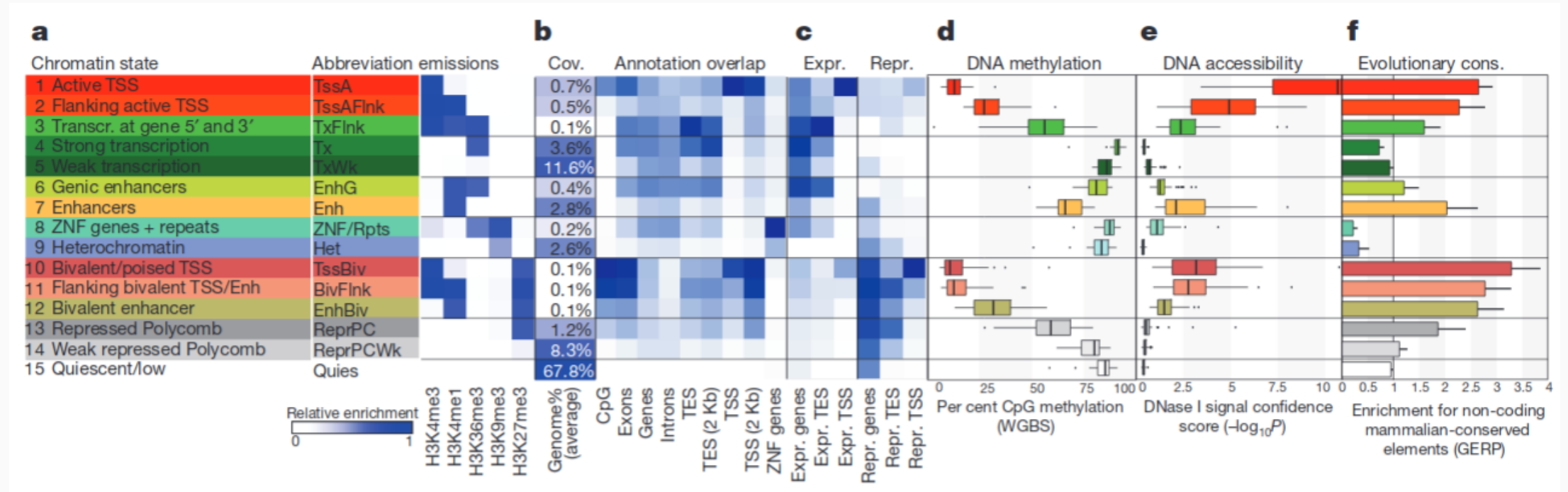
# What to do with big dataset?

Link data to genome browser:



# What to do with big dataset?

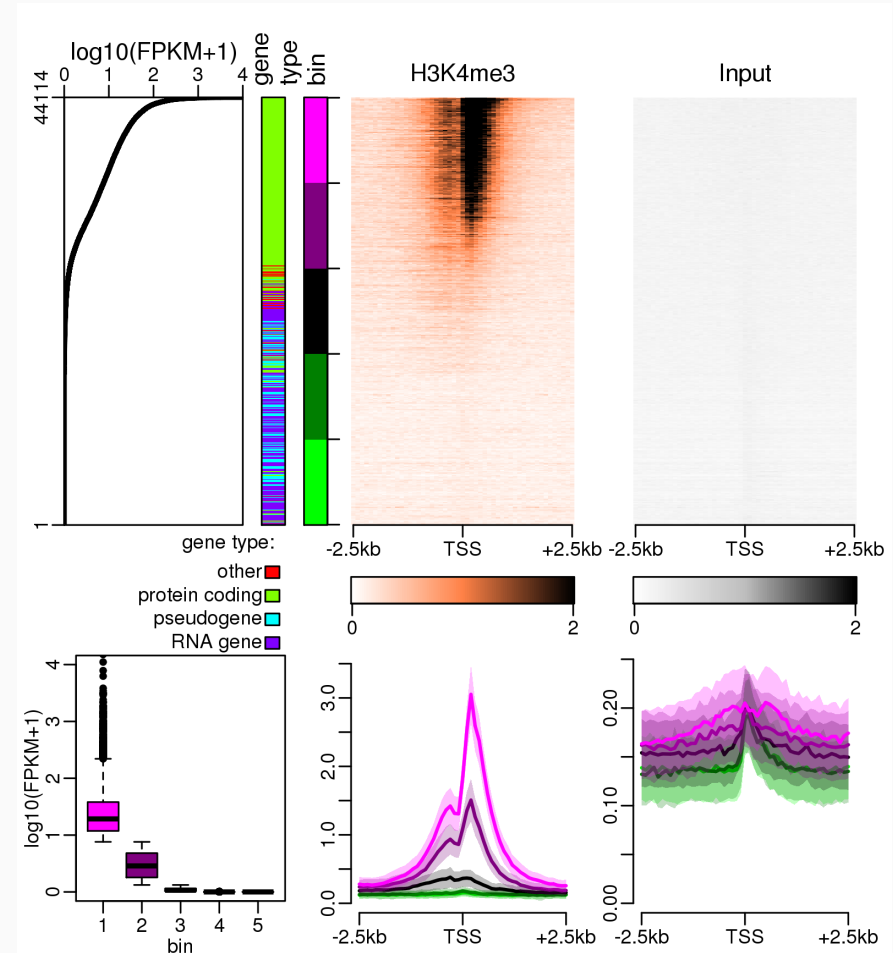
Machine learning:



Kundaje, Meuleman, Ernst, Bilenky et al., 2015, [10.1038/nature14248](https://doi.org/10.1038/nature14248)

# Objectives

- Visualisation of marks, sorted by **gene** transcription level:
  - at TSS (gene start)
  - at TTS (gene end)
- Visualisation of marks at **middle exons** starts, sorted by:
  - transcription level
  - inclusion ratio
- For **all** genes/exons in **each** cell type.
- For **each** gene/exon in **all** cell types.

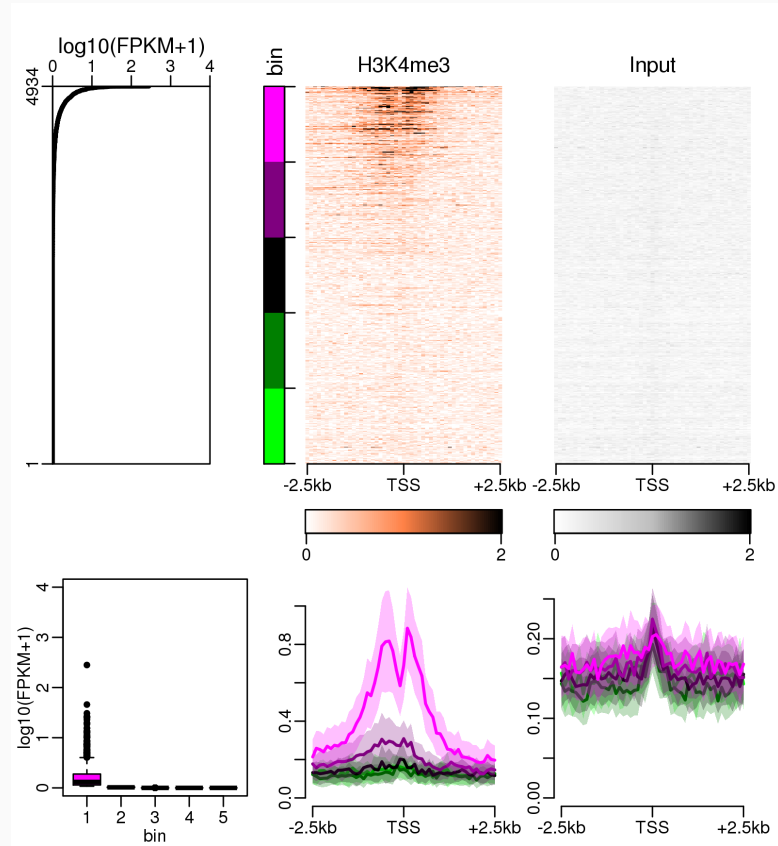




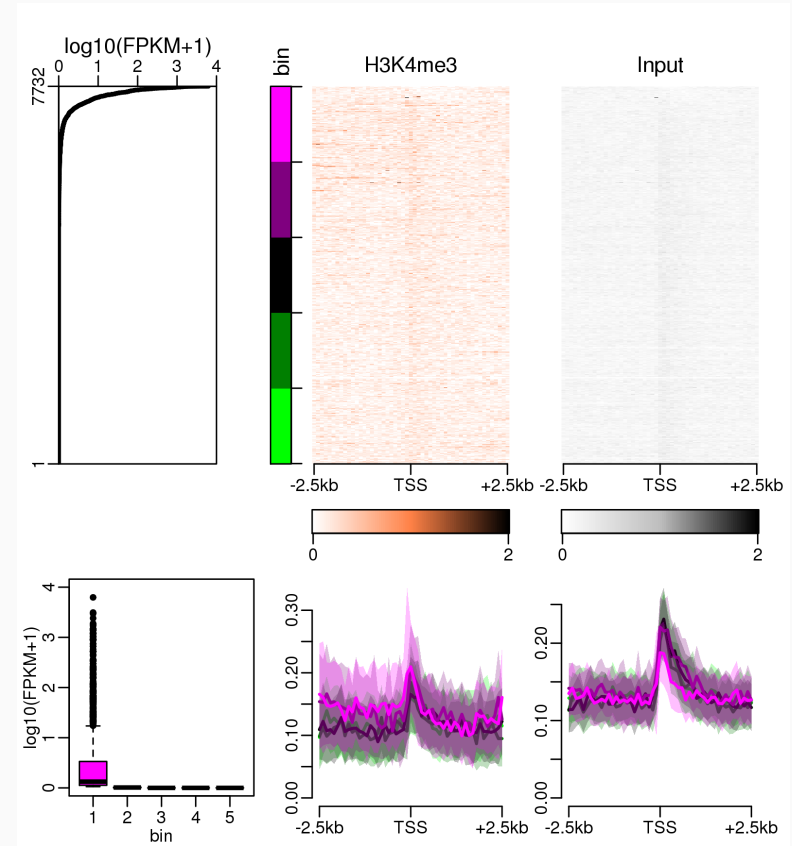
# H3K4me3, TSS, small intestine

# Different gene types, different associations

## lincRNA

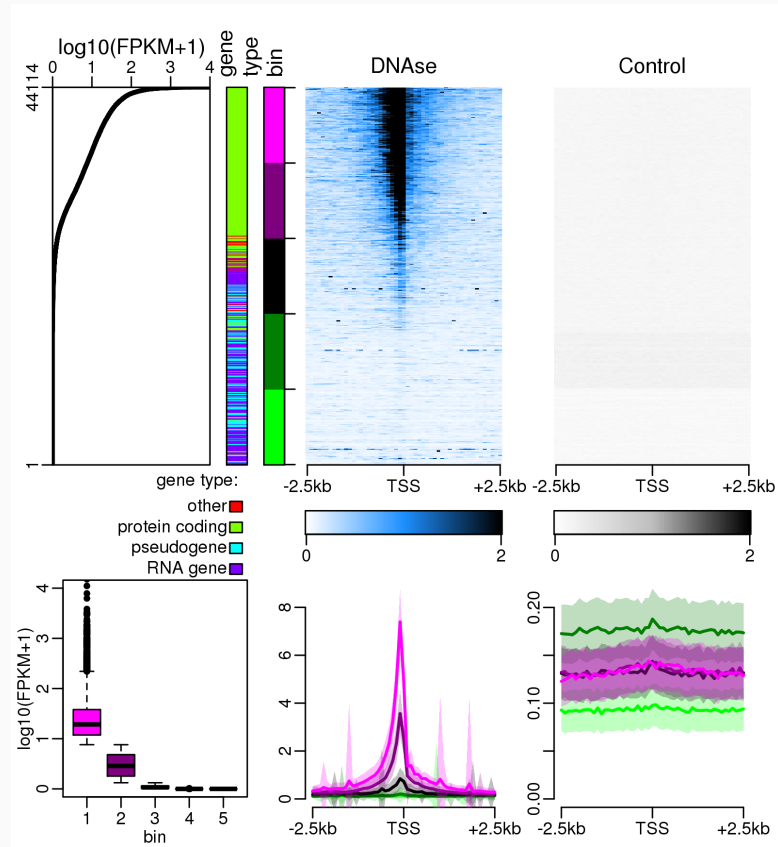


## processed pseudogenes

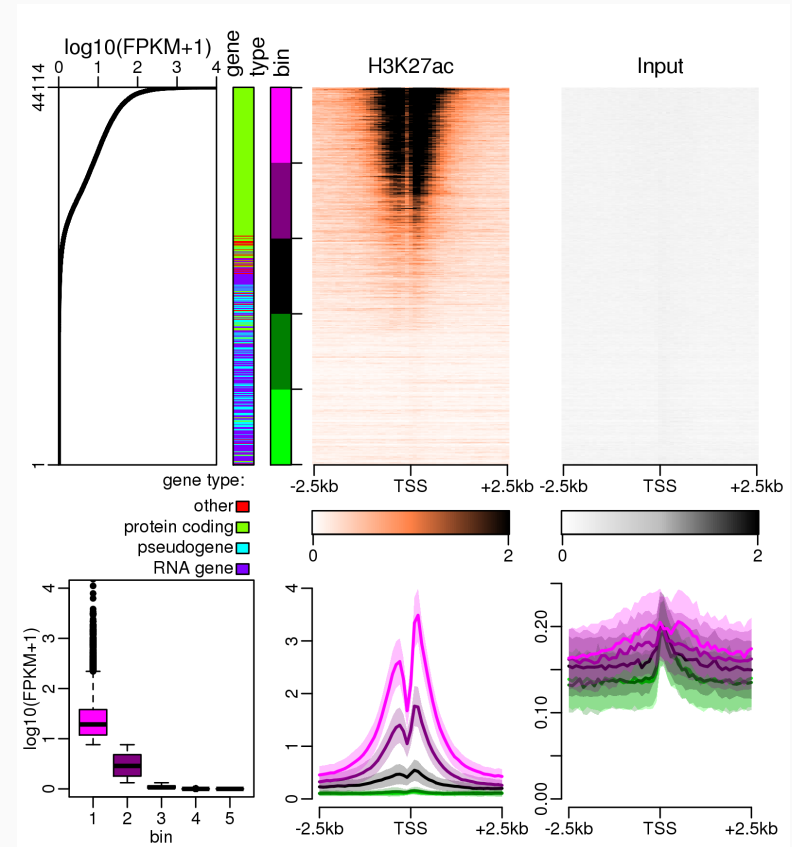


# Position of signal matters

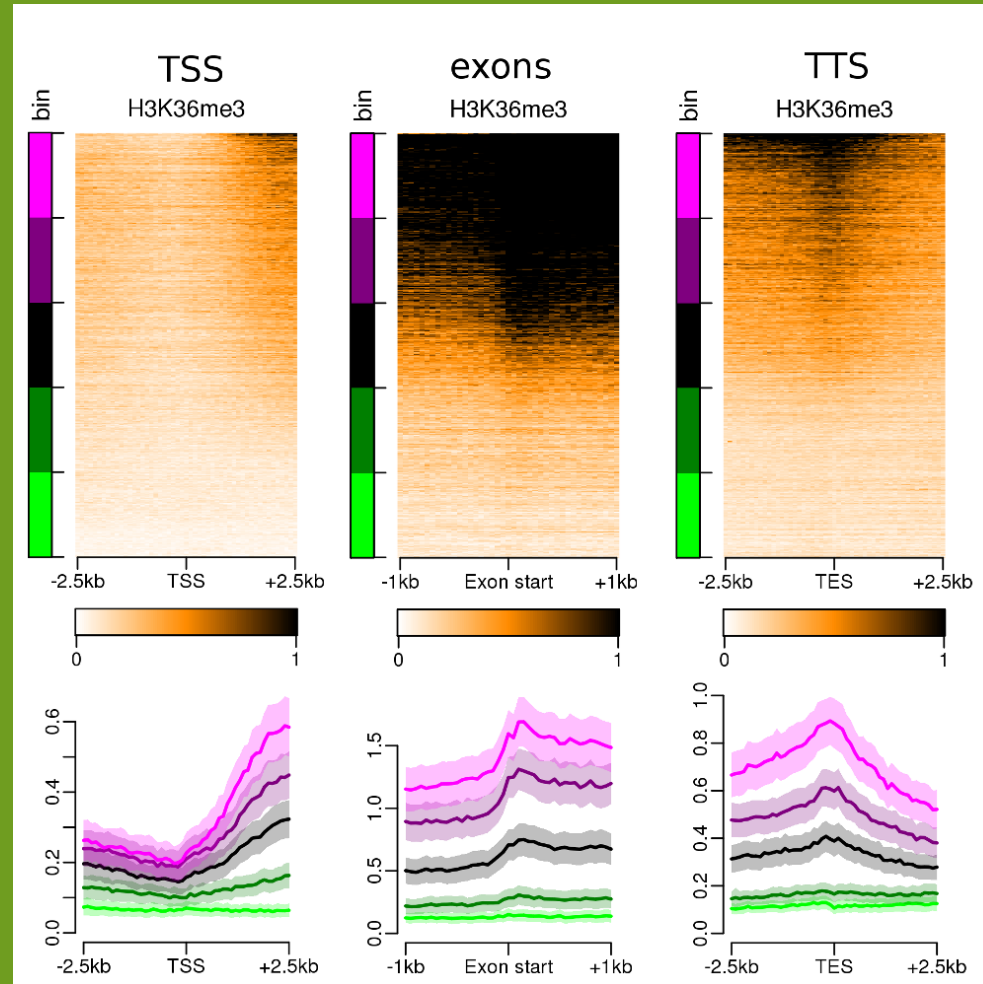
## DNase 1 (accessible chromatin)



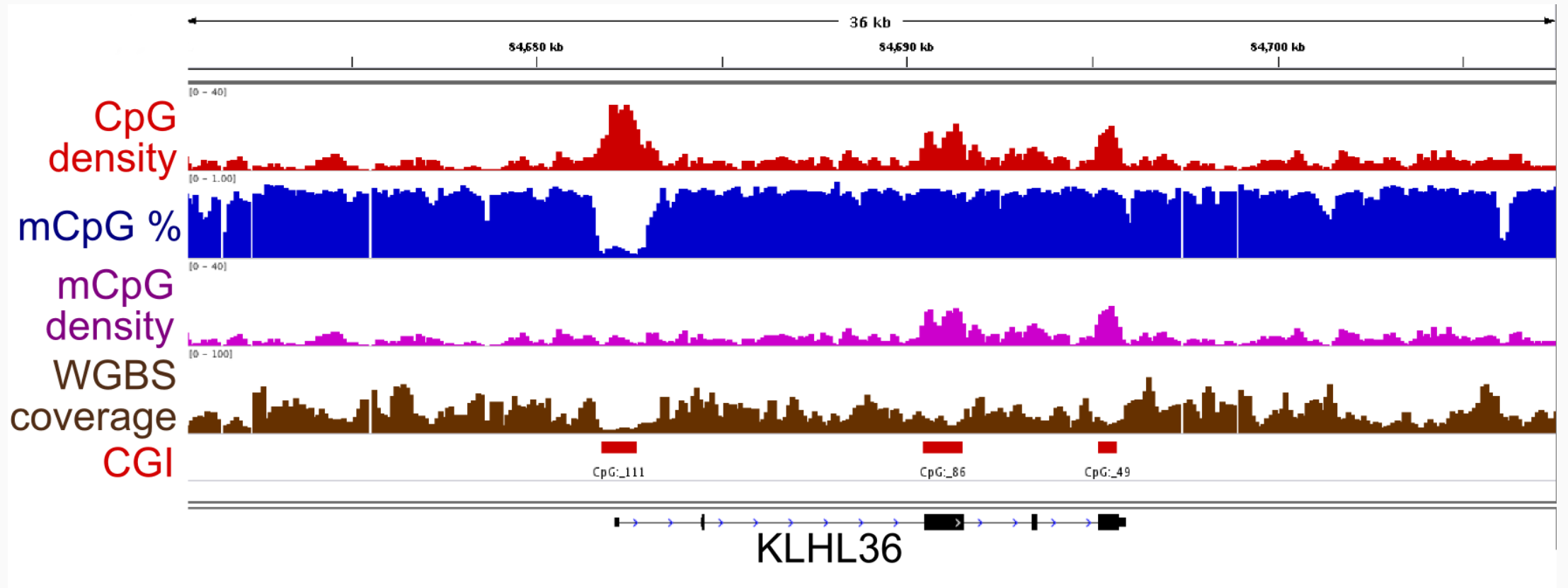
## H3K27ac



# Exonic mark: H3K36me3, fetal large intestine

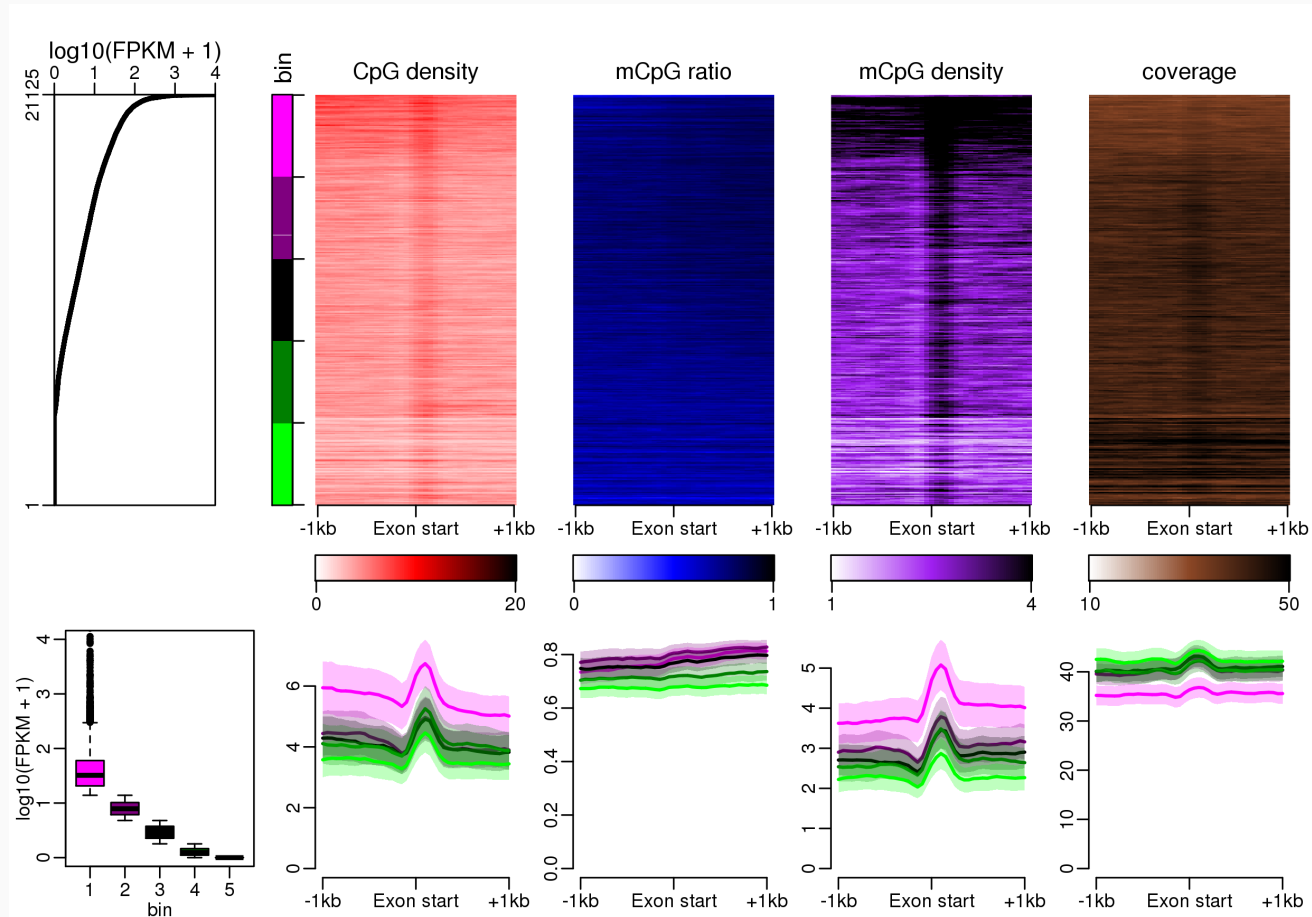


# DNA methylation: ratio *and* density



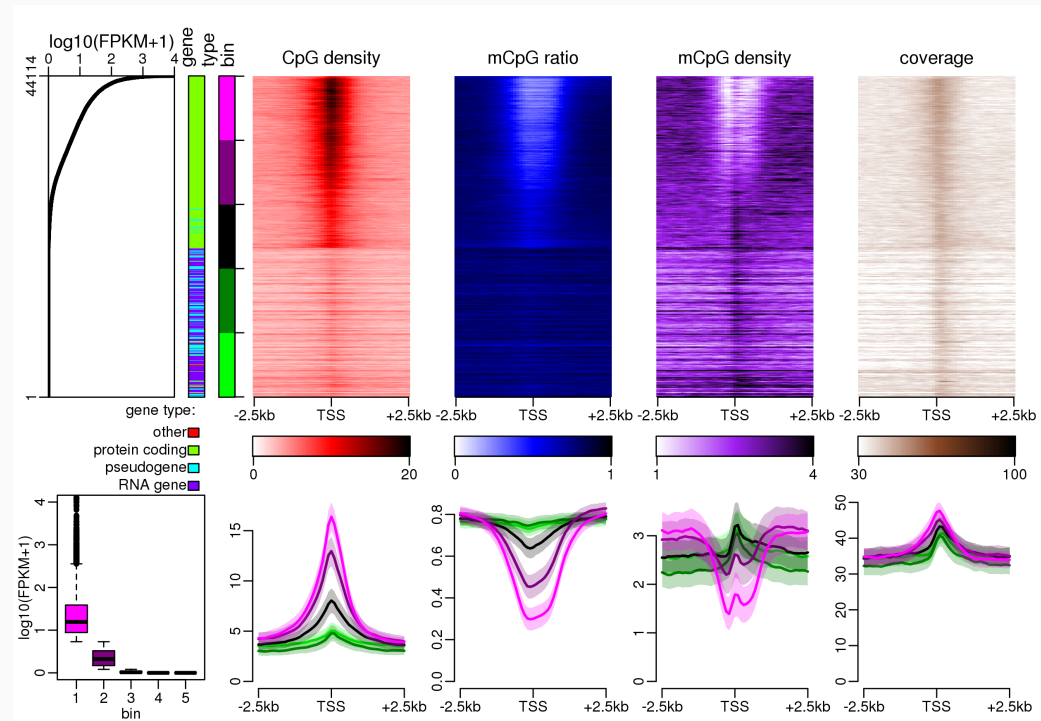
# Exonic DNA methylation

WGBS, pancreas

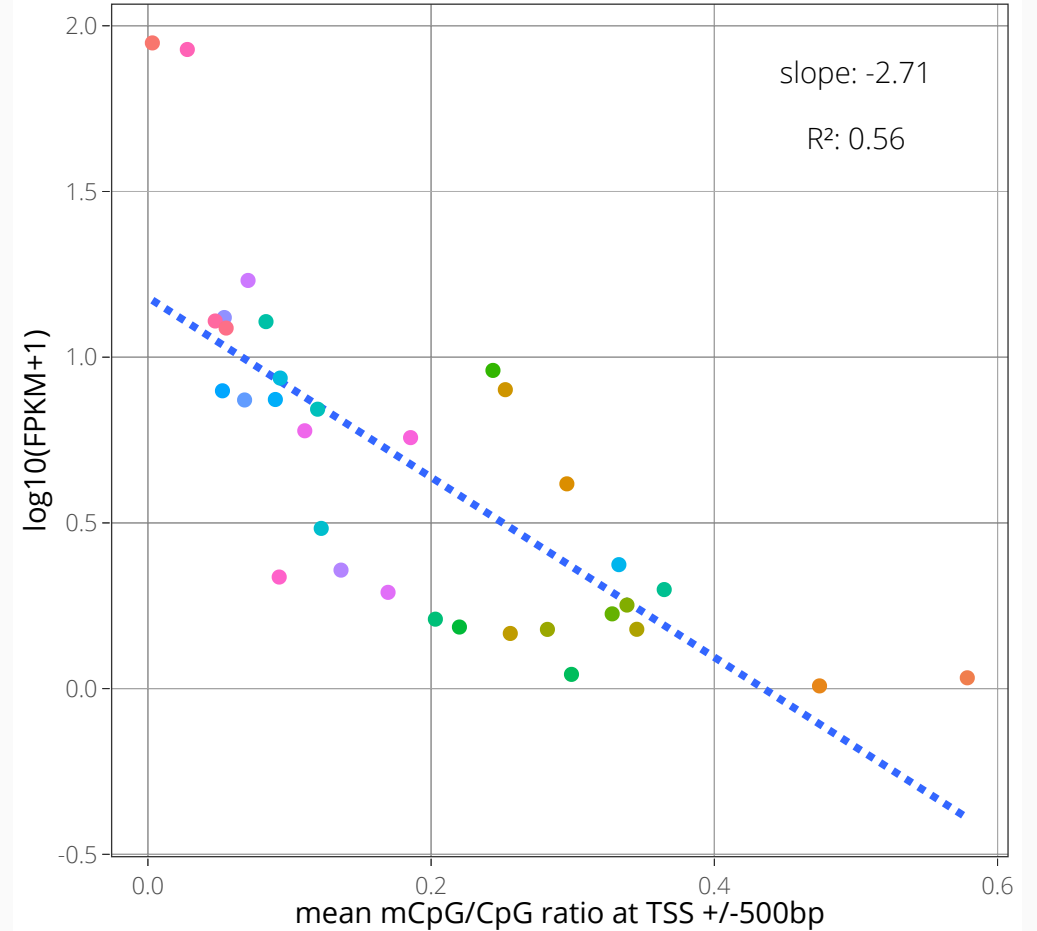


# Cell by cell vs gene by gene

## WGBS, adult liver

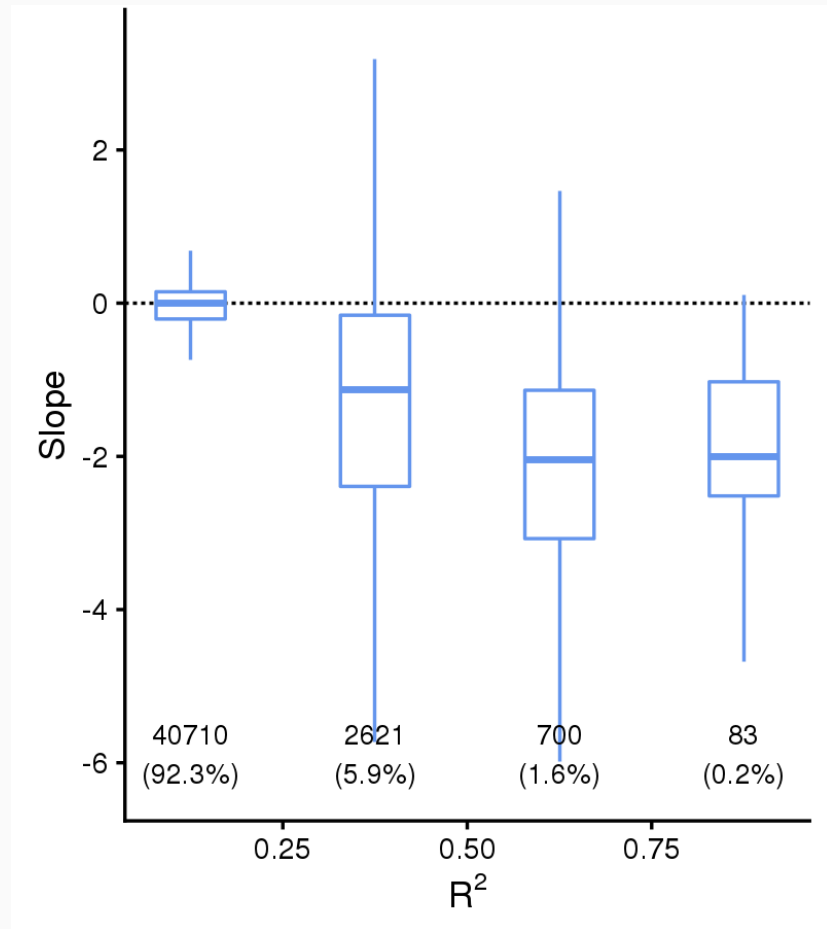


## LYL1 (ENSG00000104903)

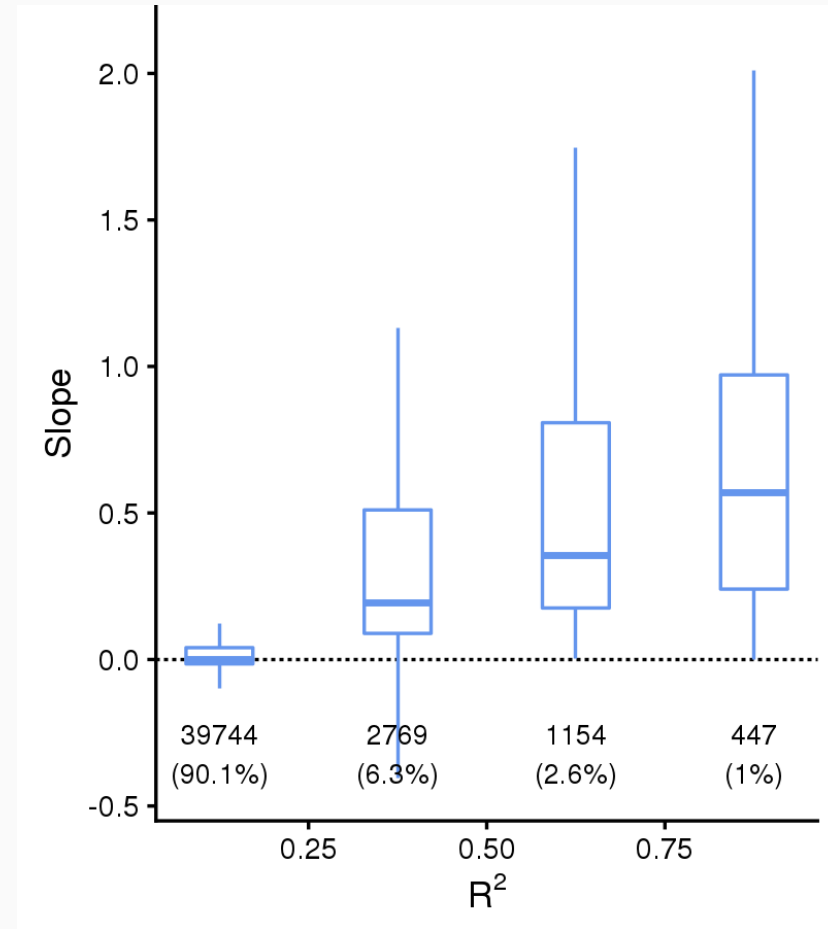


# Repressing and activating marks

## mCpG ratio

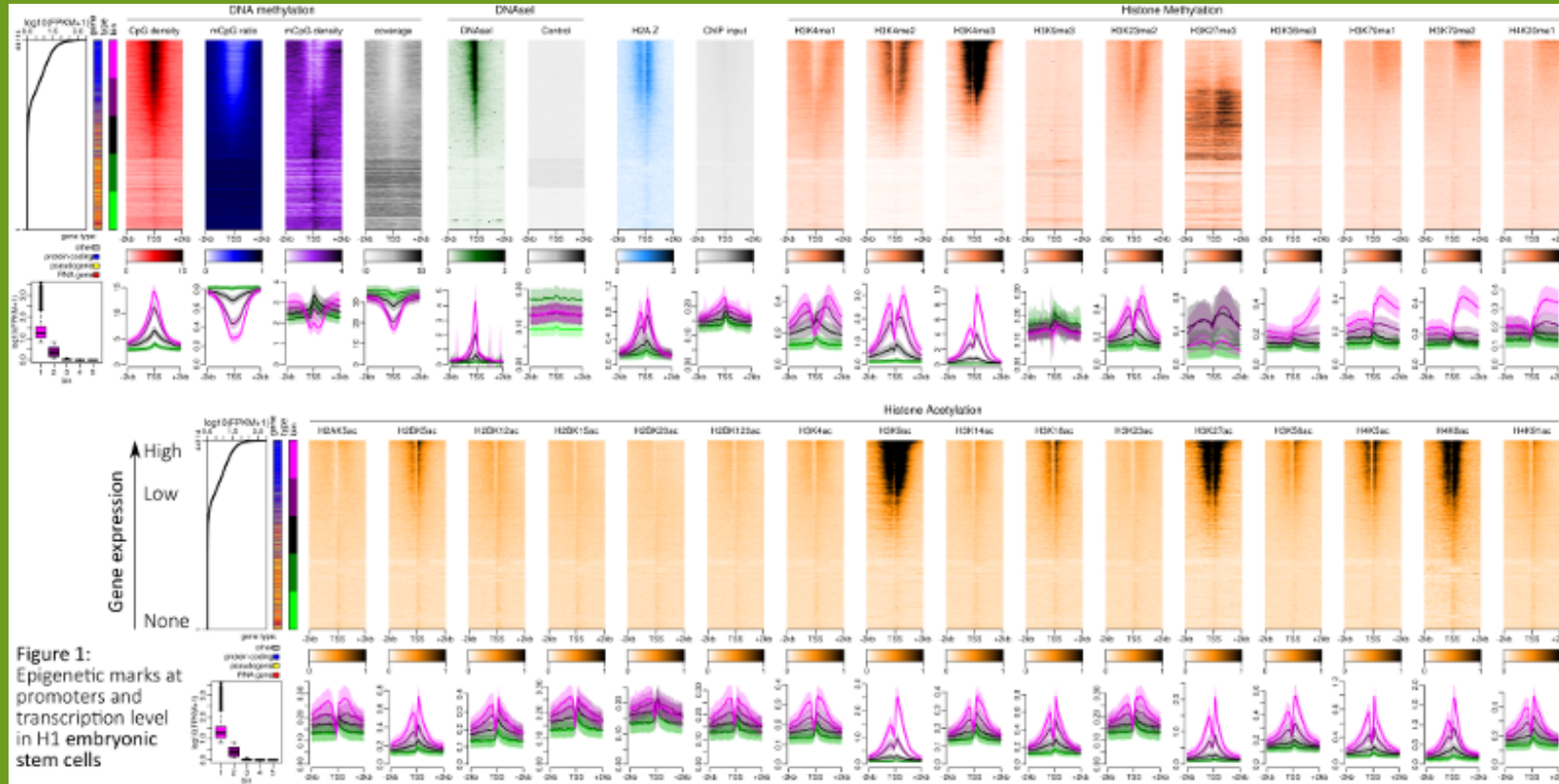


## H3K4me3





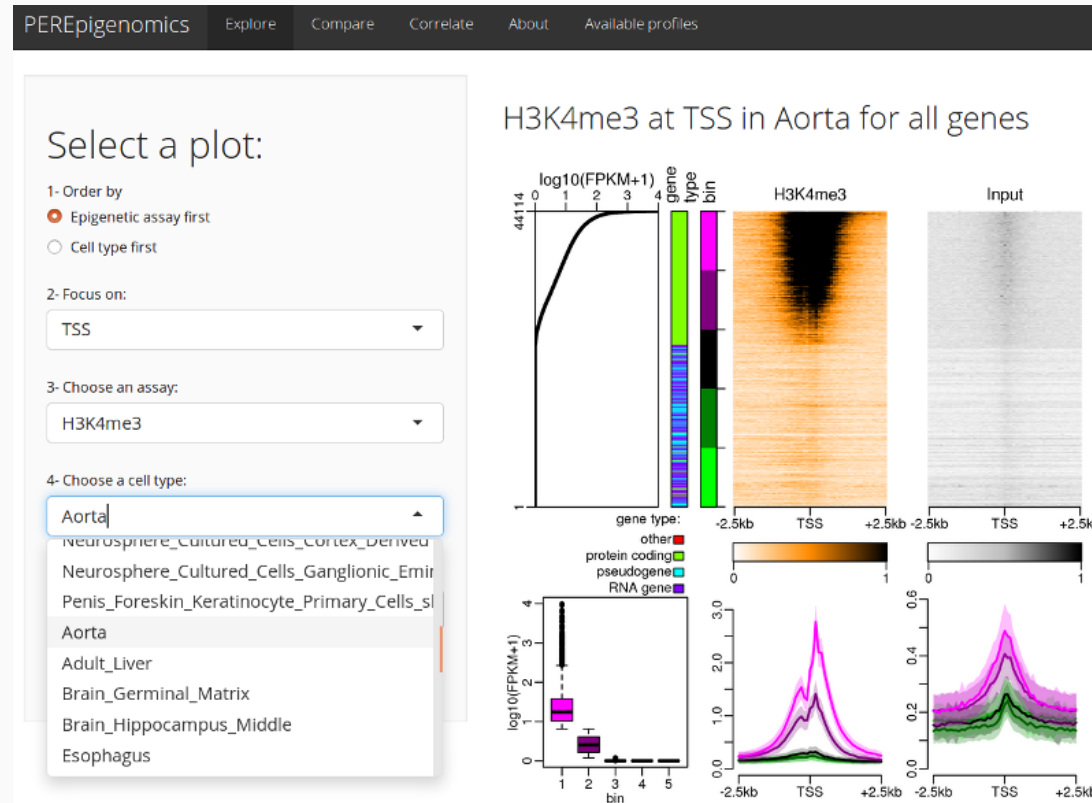
# Too many plots?



# PEREpigenomics

Profile Explorer of Roadmap *Epigenomic* data

[www.perepigenomics.roslin.ed.ac.uk](http://www.perepigenomics.roslin.ed.ac.uk)



# Summary of results

mark	cell type by cell type	gene by gene	center on TSS
WGBS	negative	negative	
DNase	positive	positive	
H2A.Z	positive	balanced	
H3K4me1	positive	positive	
H3K4me2	positive	positive	
H3K4me3	positive	positive	
H3K9me3	unclear	unclear	no
H3K23me2	positive	NA	
H3K27me3	negative – variable	negative	
H3K36me3	positive	positive	no
H3K79me1	positive	positive	no
H3K79me2	positive	balanced	no

mark	cell type by cell type	gene by gene	center on TSS
H2AK5ac	positive	positive	
H2BK120ac	positive	positive	
H2BK12ac	positive	positive	
H2BK15ac	positive	balanced	
H2BK20ac	neutral	NA	
H2BK5ac	positive	positive	
H3K4ac	positive	positive	
H3K9ac	positive	positive	
H3K14ac	positive	positive	
H3K18ac	positive	positive	
H3K23ac	positive	positive	
H3K27ac	positive	positive	
H3K56ac	positive	NA	
H4K8ac	positive	positive	
H4K12ac	positive	NA	
H4K91ac	positive	positive	

## Conclusions

PEREpigenomics offers interesting visualisations of epigenetic data gathered by Roadmap Epigenomics.

## Perspectives

- update with new annotation data (ongoing)
- preprint & source code available soon
- develop similar approach for **FAANG** (Functional Annotation of the Animal Genomes) data

# Thanks

Anagha Joshi

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Deepti Vipin



THE UNIVERSITY  
of EDINBURGH

