Puzzles in massively parallel genome biology

await GPU solutions

Oleksiy Karpenko
Bioinformatics Program
University of Illinois at Chicago

Super Computing 2011
Seattle, WA

SC11 Seattle, WA | Connecting communities through HPC

NSF

UIC UNIVERSITY OF ILLINOIS AT CHICAGO COLLEGE OF ENGINEERING

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Human genome for computer scientists

…ACGTTGGATCGAGACATGACGATG…

- 4 letter alphabet of DNA: {**A**, **C**, **G**, **T**}
- ~3 GB letters long

Human genome for computer scientists

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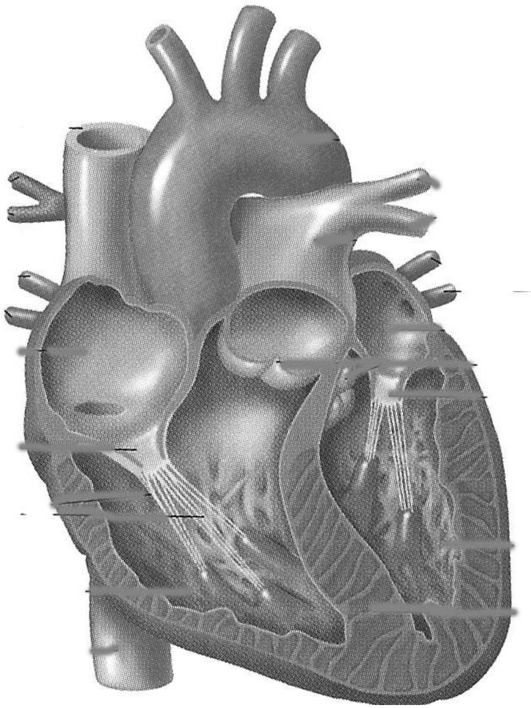
- ~3 GB letters long
- 2% are genes coding for proteins
- 98% formerly known as “junk DNA”

DNA is the same
but active genes are different



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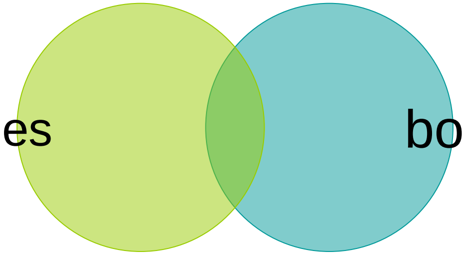

heart genes

bone genes

http://www.bio.aps.anl.gov/scihi/img/heart.jpg, http://www.sciencephoto.com/image/190555/large/F0014577-The_femur-SPL.jpg

Human genome for computer scientists

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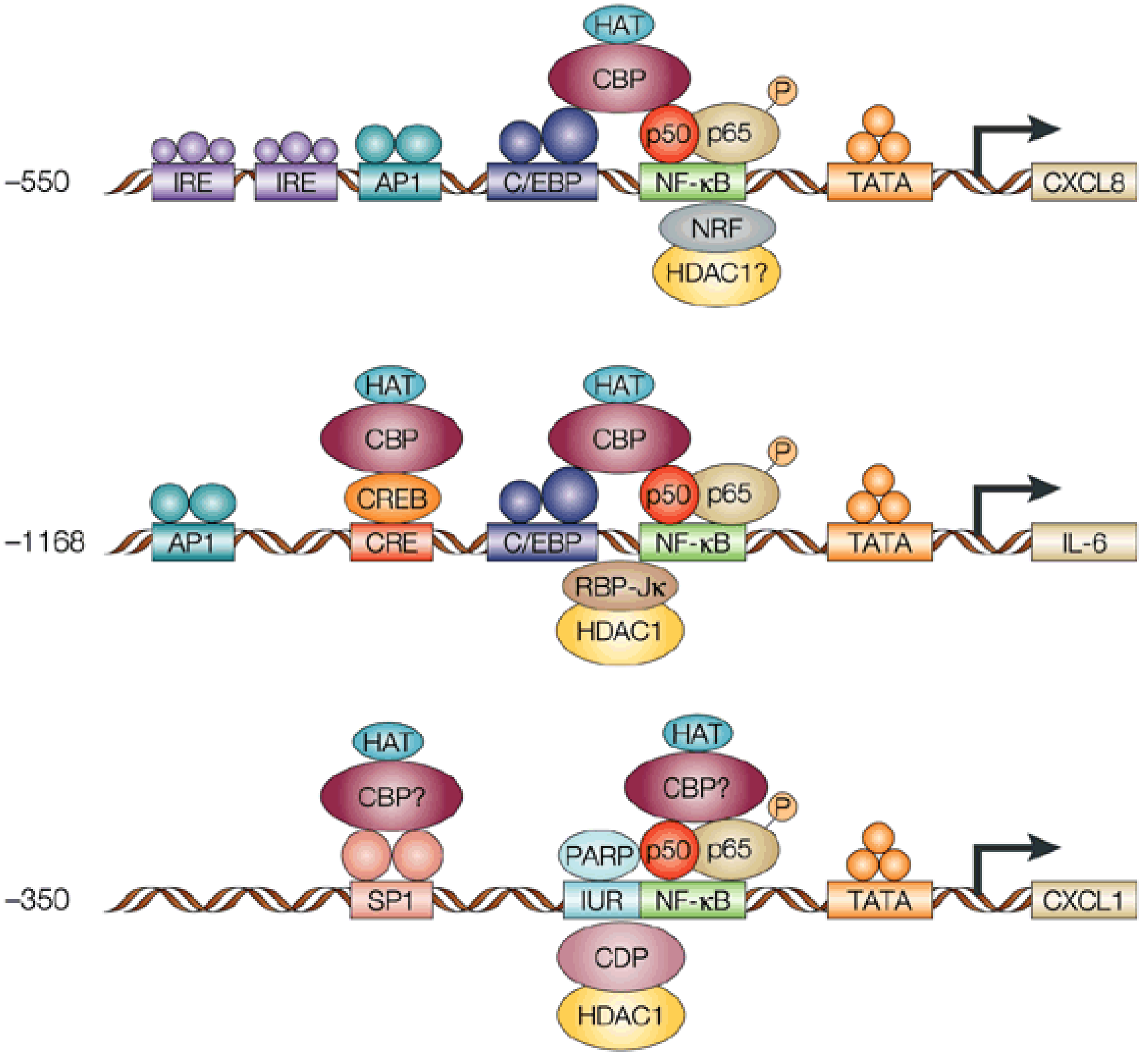
- 4 letter alphabet of DNA: {**A, C, G, T**}
- ~3 GB letters long
- 2% are genes coding for proteins
- 98% formerly known as “junk DNA”
- the non-coding regions host important regulatory sites

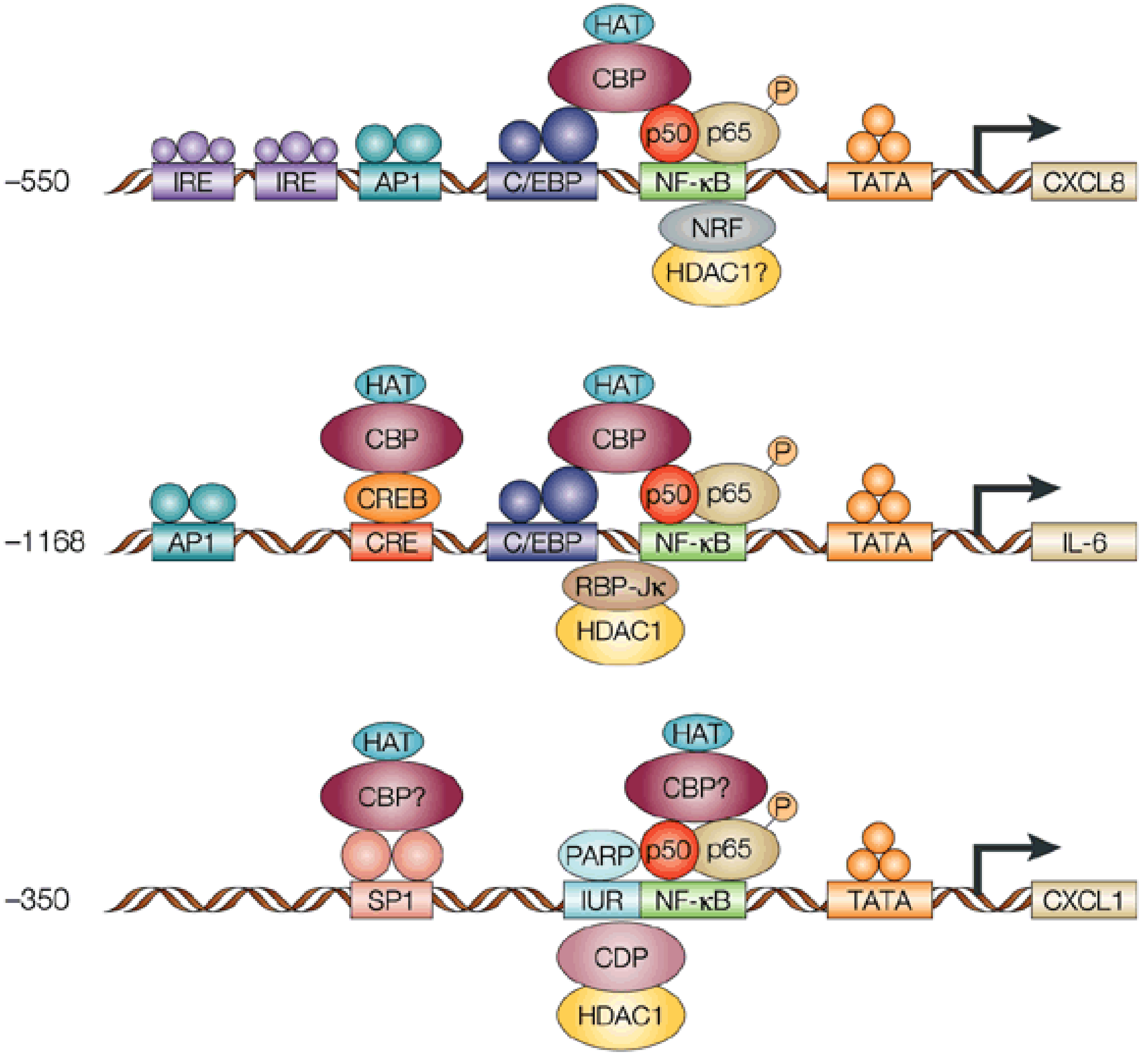
1) Transcription factors



Nature Reviews | Immunology

http://www.nature.com/nri/journal/v2/n9/images/nri887-f2.gif

1) Transcription factors



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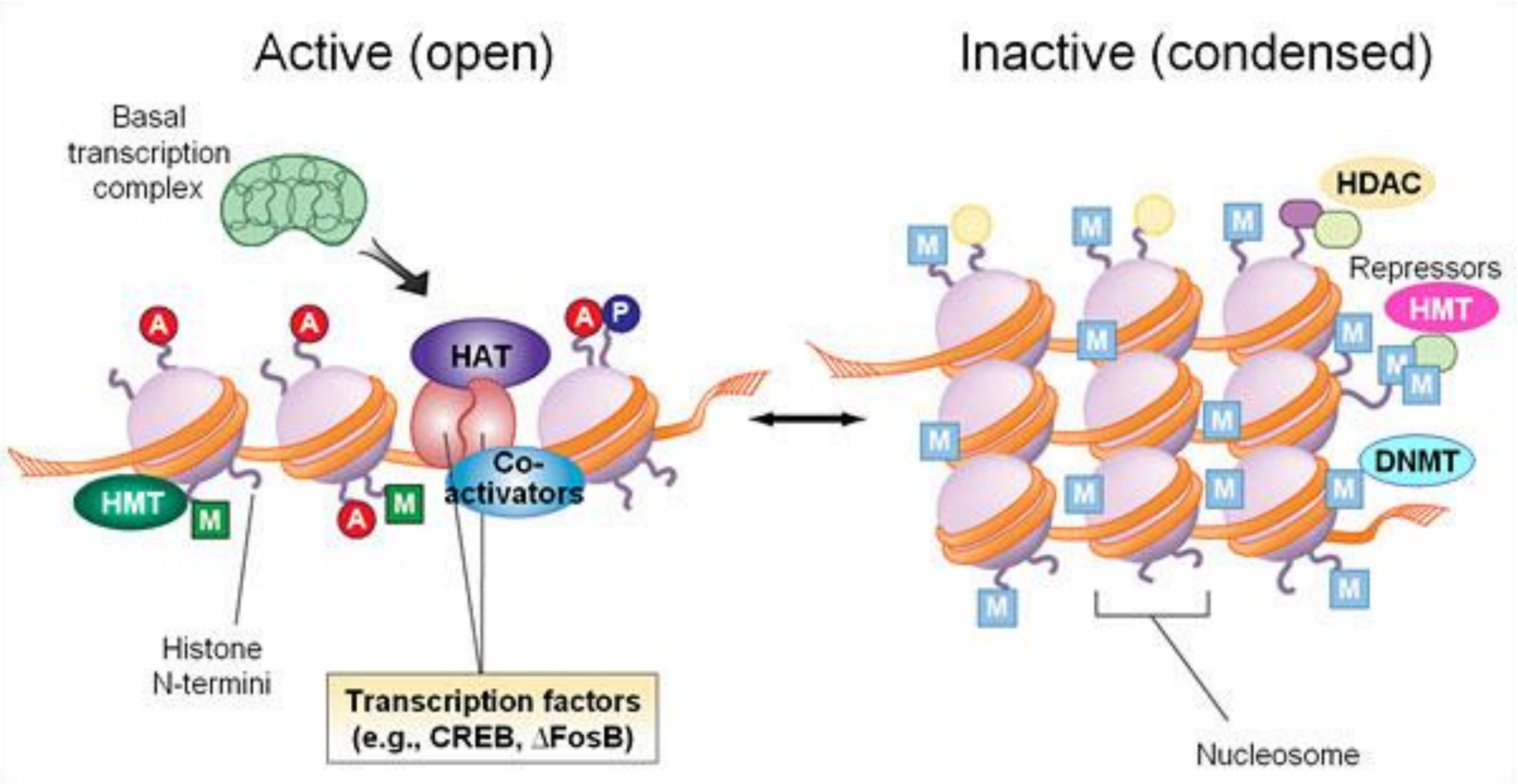
http://www.nature.com/nri/journal/v2/n9/images/nri887-f2.gif

2) Histone modifications



http://www.nyas.org/image.axd?id=a261ff6e-1e42-442c-8dc6-428a60574df4&t=634329511969400000

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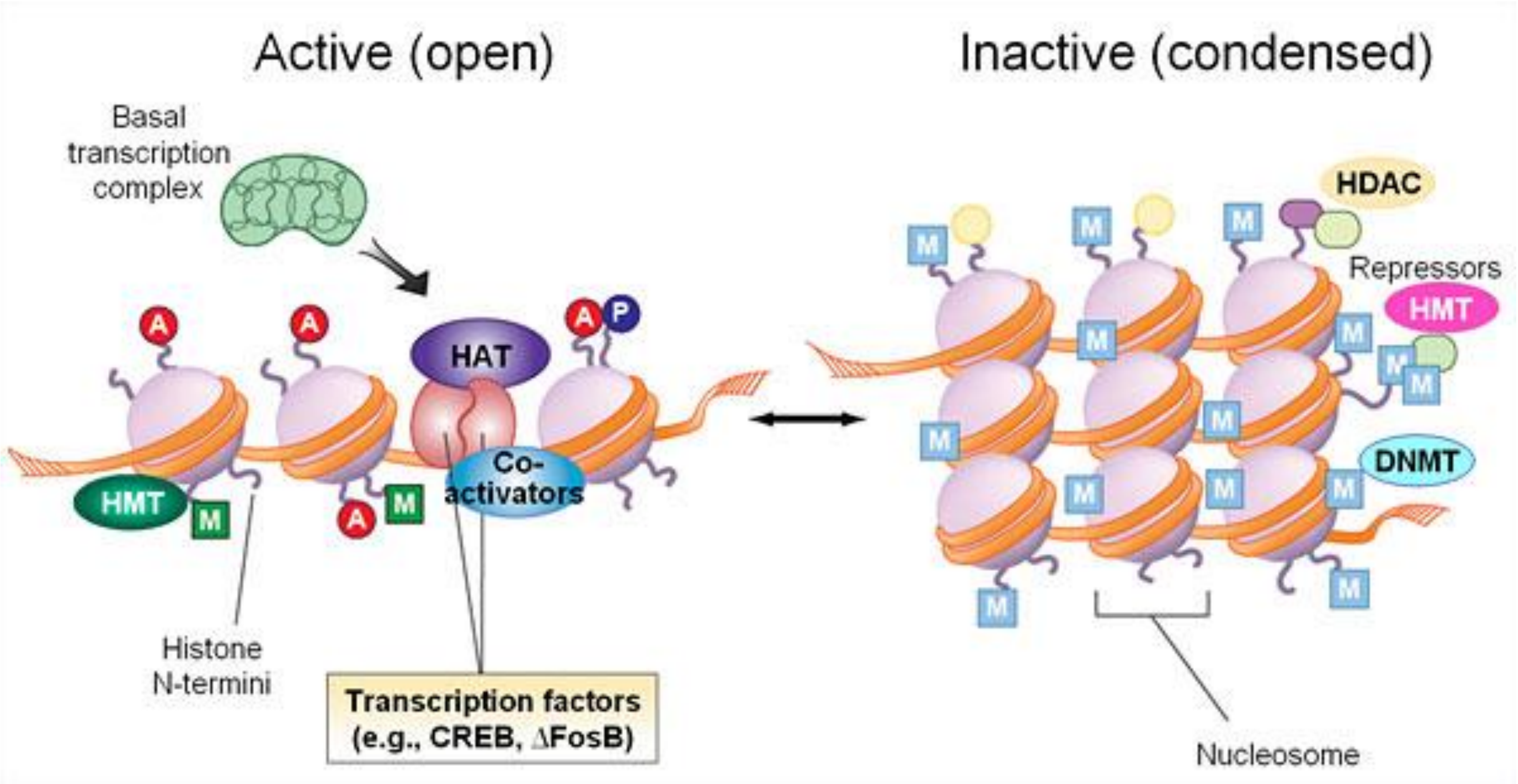

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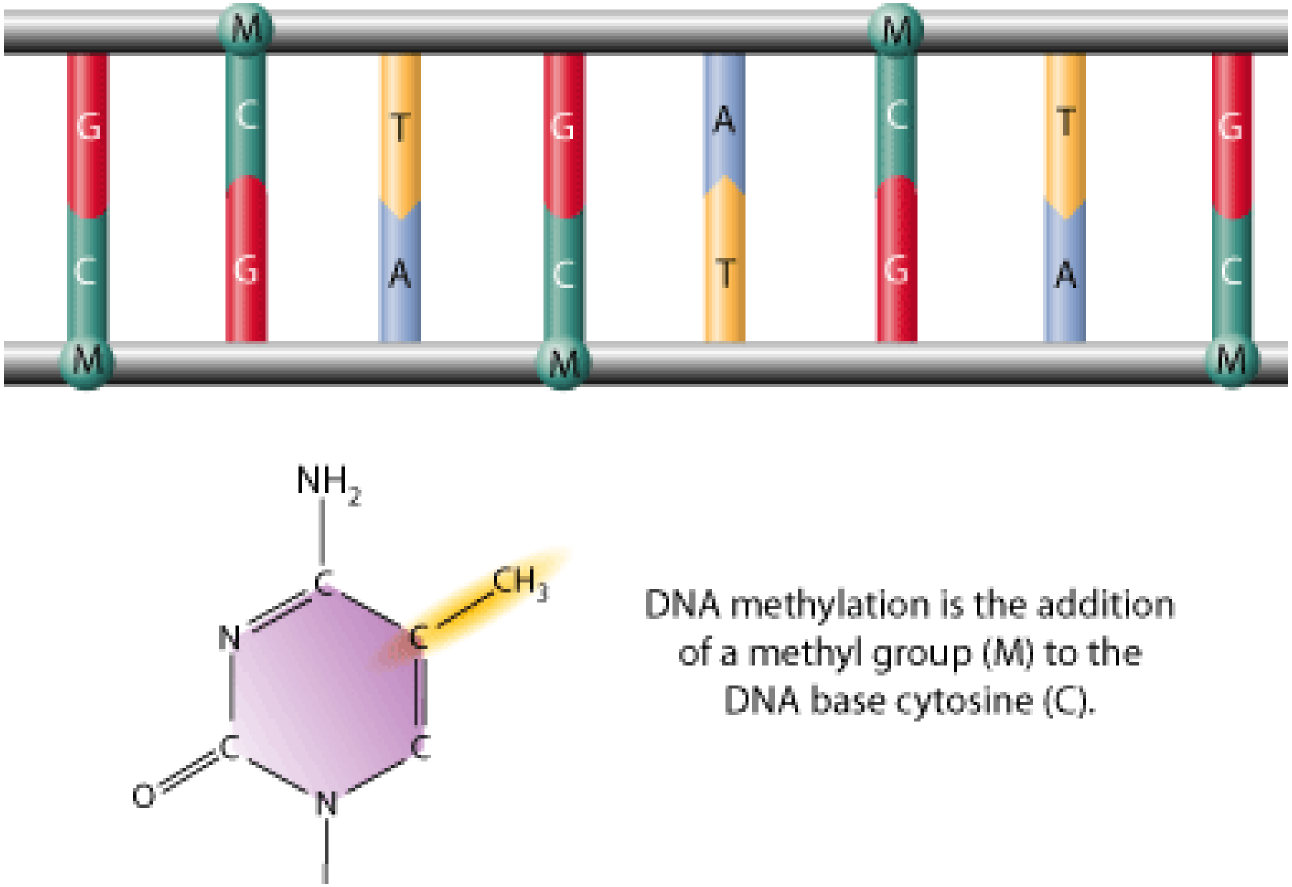
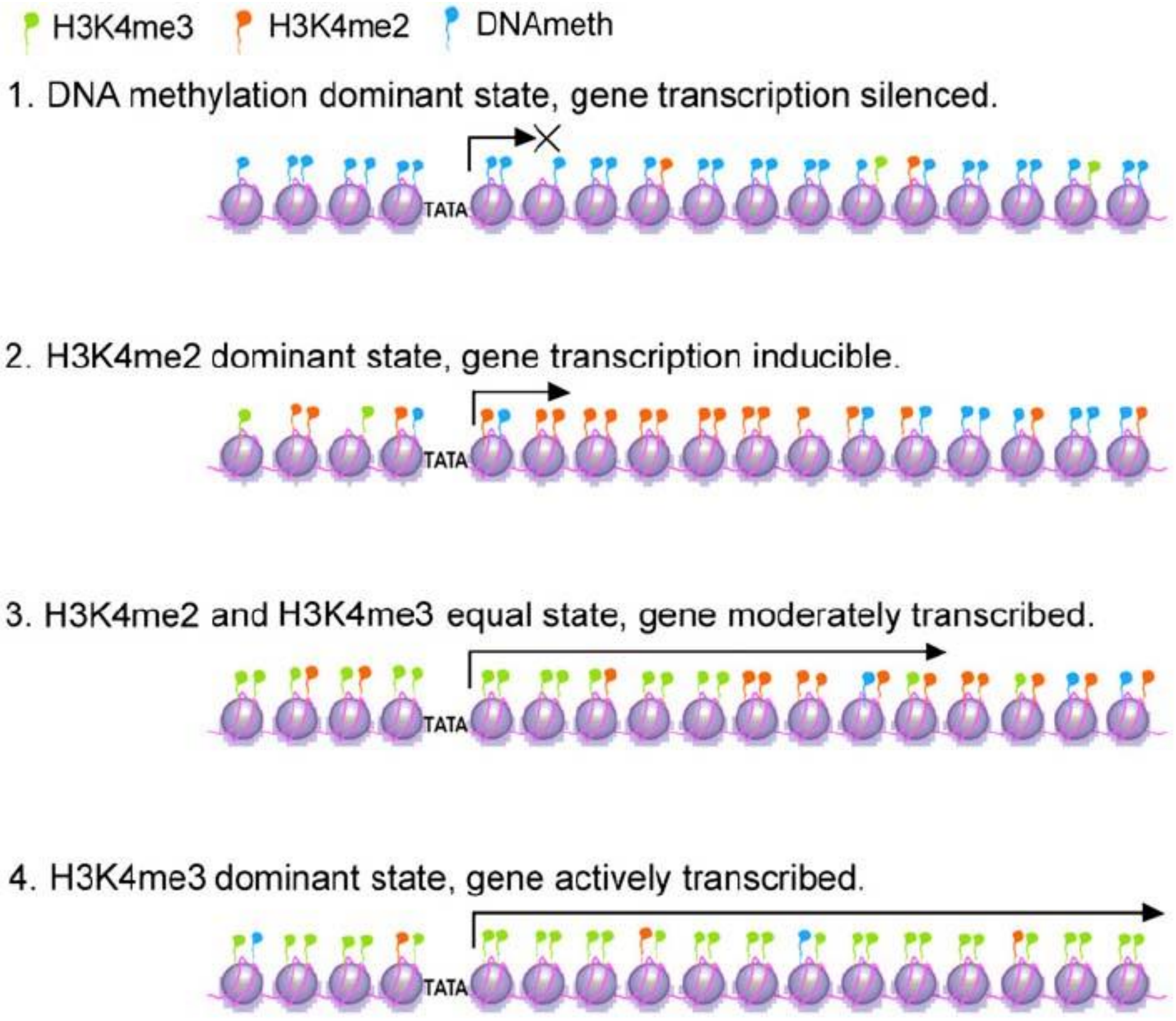
3) DNA methylation



DNA methylation is the addition of a methyl group (M) to the DNA base cytosine (C).

http://www.scq.ubc.ca/wp-content/uploads/2006/08/methylation[1]-GIF.gif

Some known regulatory rules



1. DNA methylation dominant state, gene transcription silenced.

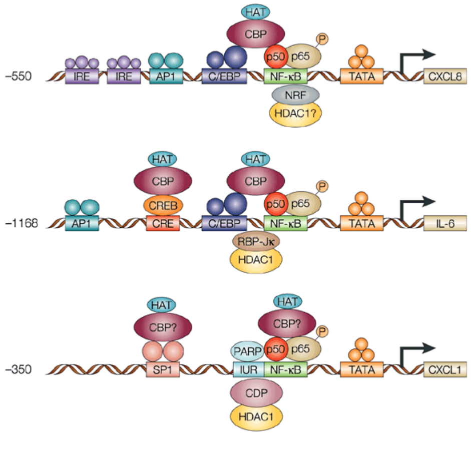
2. H3K4me2 dominant state, gene transcription inducible.

3. H3K4me2 and H3K4me3 equal state, gene moderately transcribed.

4. H3K4me3 dominant state, gene actively transcribed.

http://ag.arizona.edu/research/xwang/milestones/Rice_Chipchip.jpg

Genome site signals detected individually



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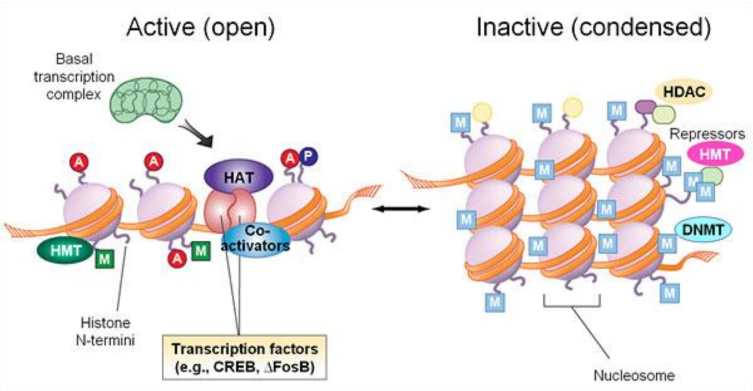

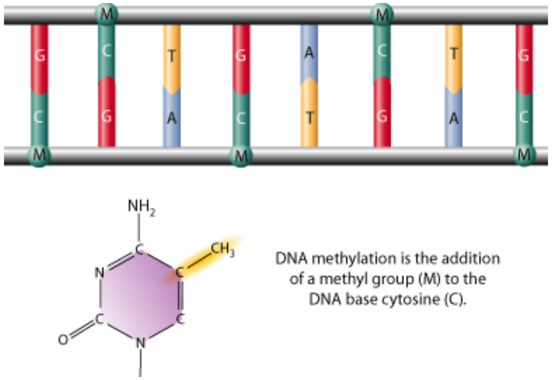

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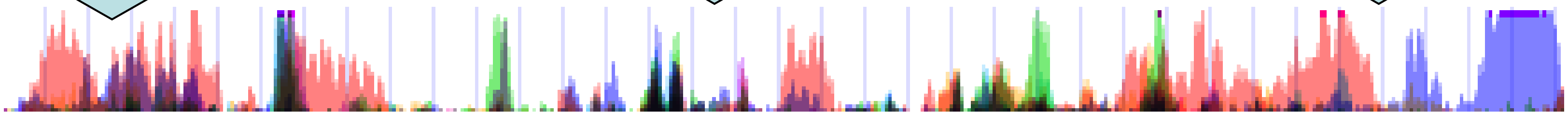
Single transcription factor binding sites

Single histone modifcation sites

DNA methylation sites



...ACGTTGGATCGAGACATGACGATG...

Different signals for different tissues

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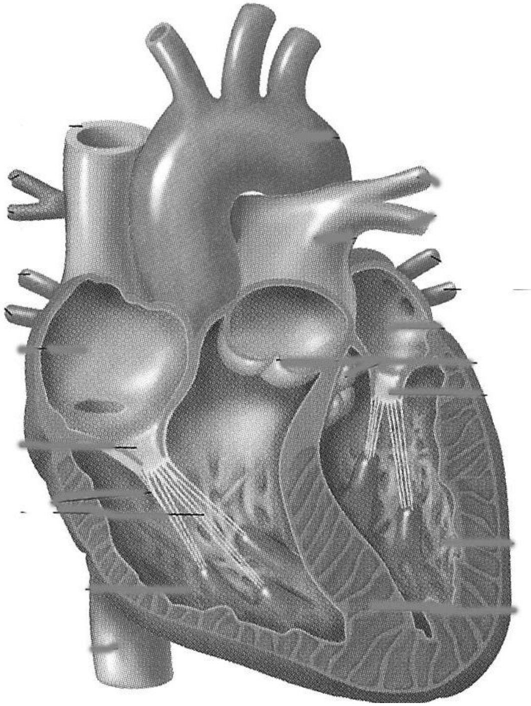

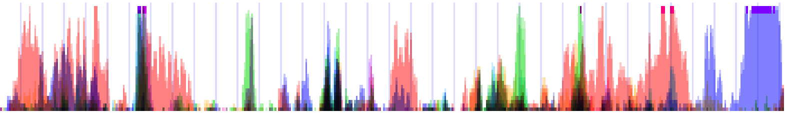

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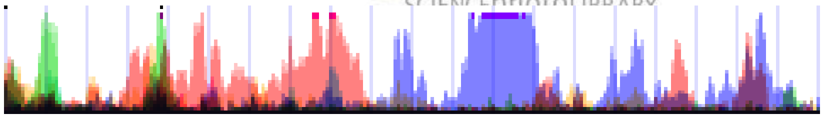
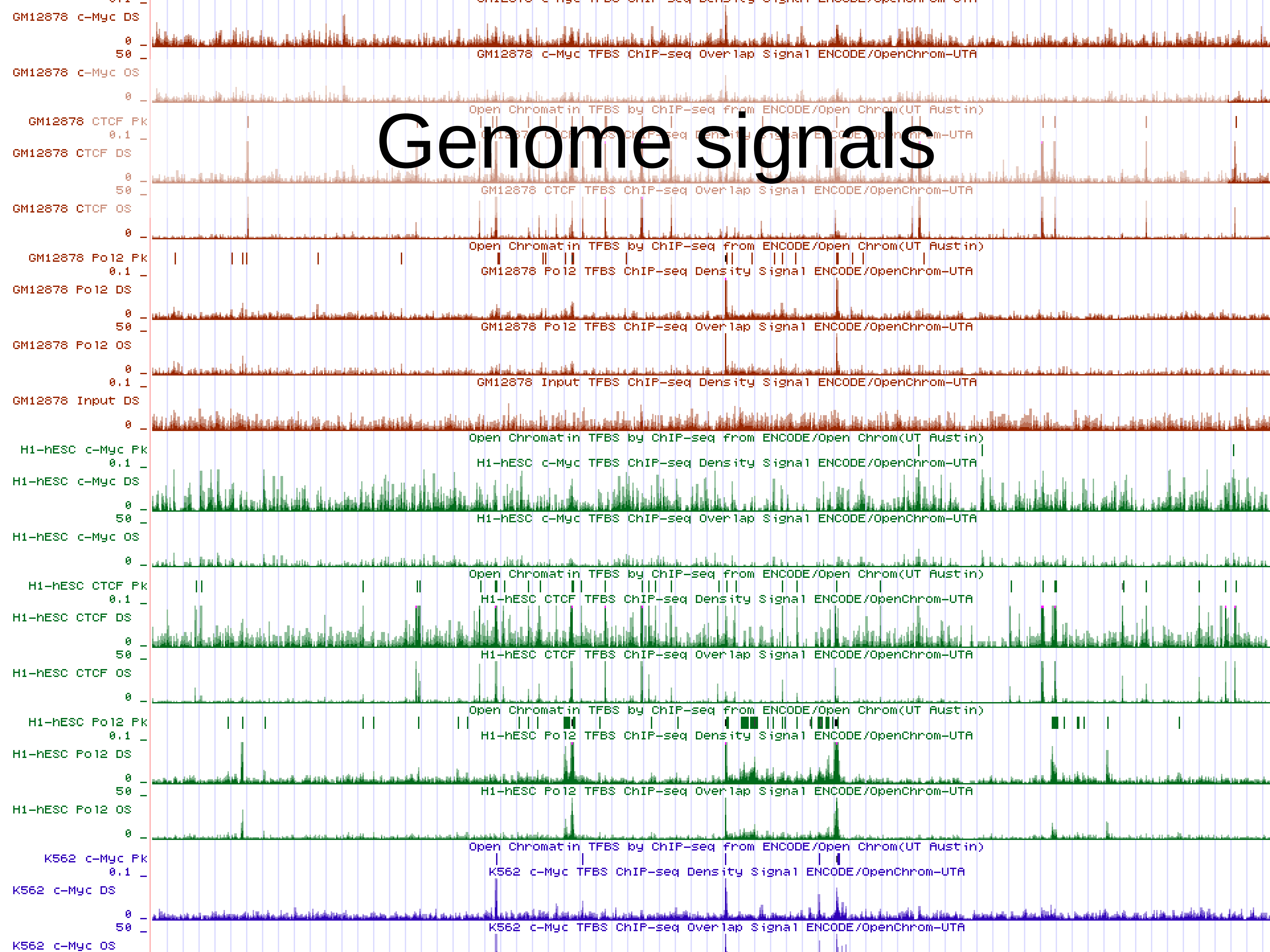


Complexity?

Consider a combination of

- ~2600 transcription factors
- ~210 unique cell types
- dozens of histone modifications

Genome signals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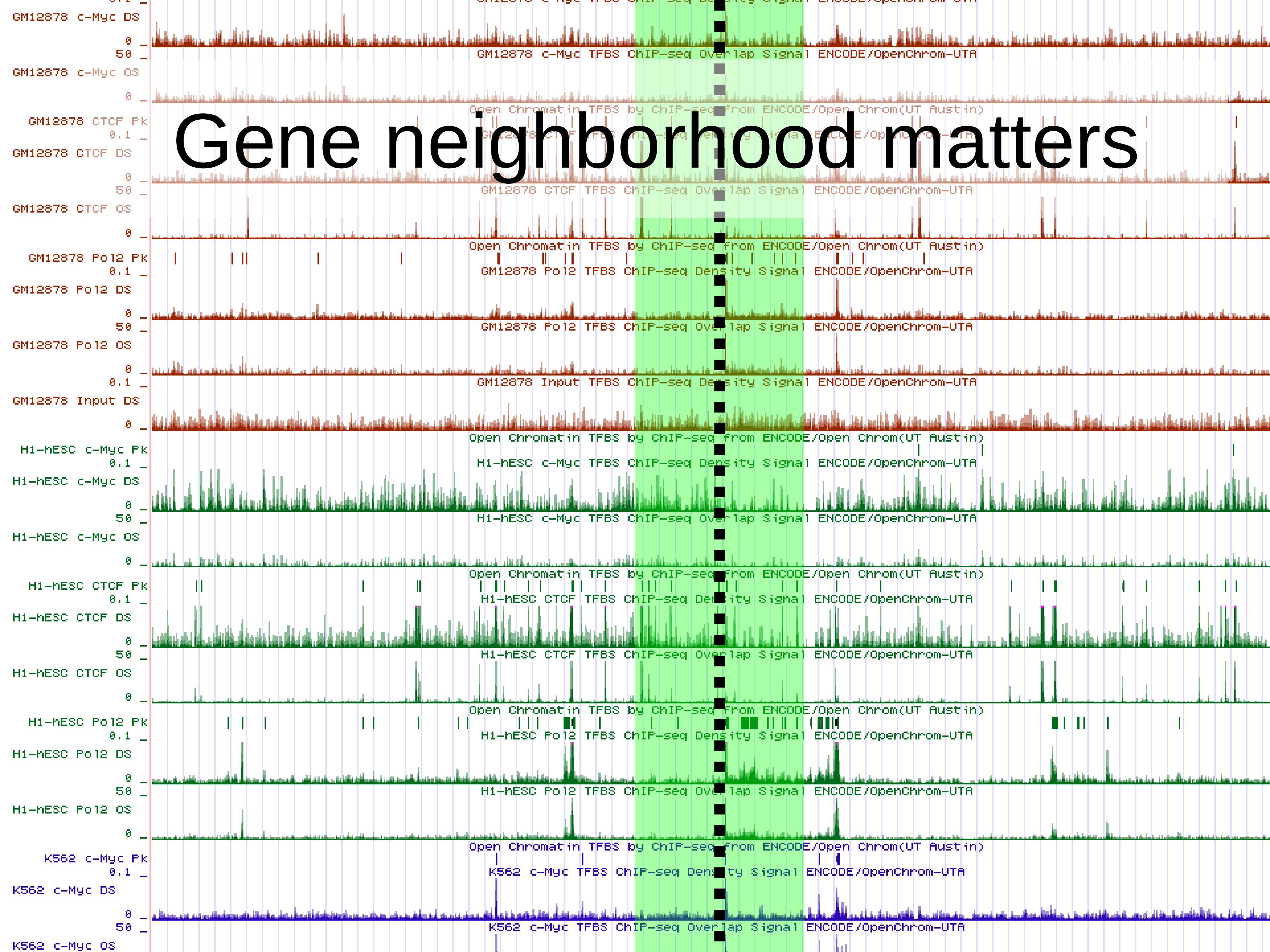
Gene neighborhood matters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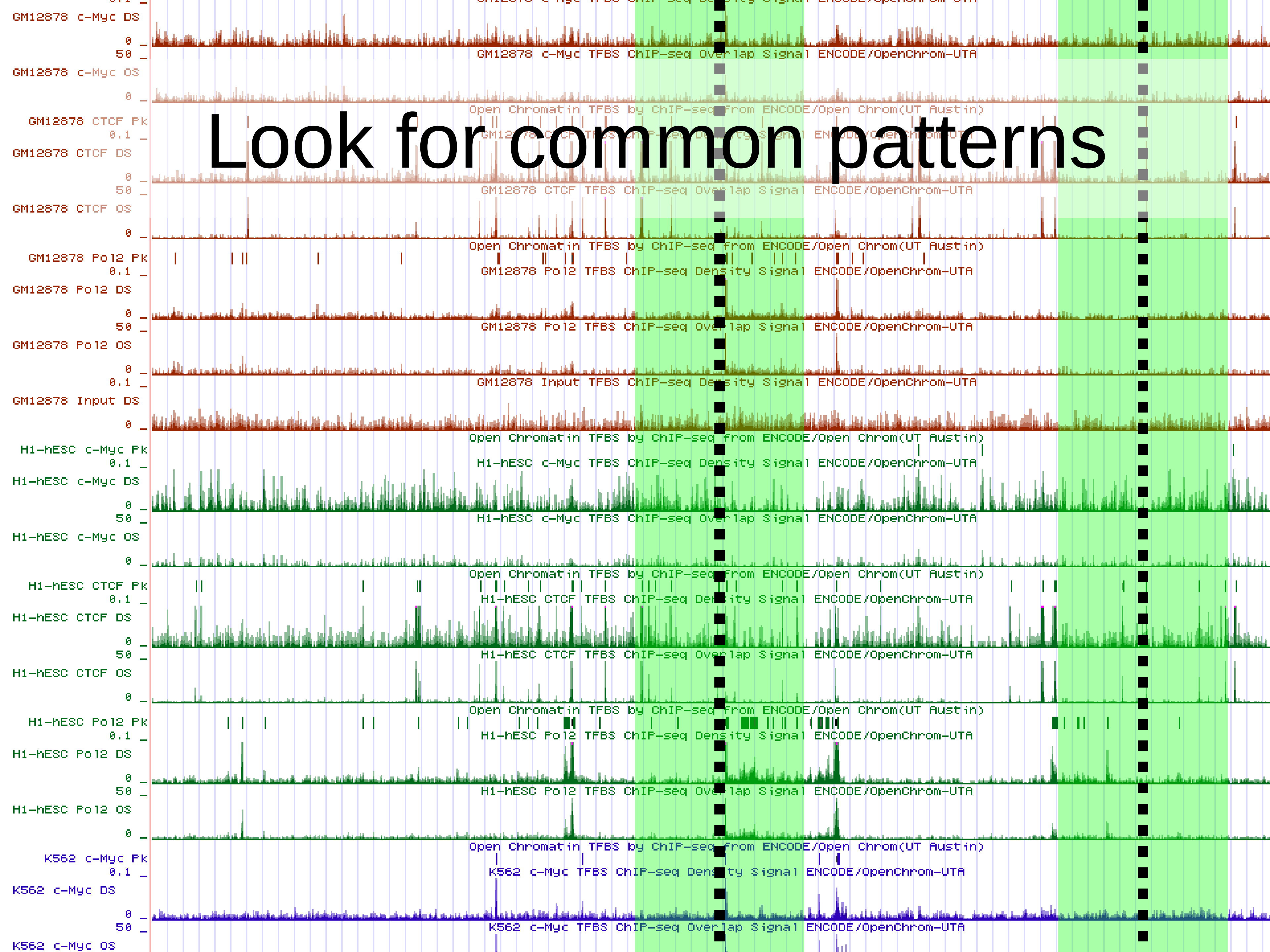
Look for common patterns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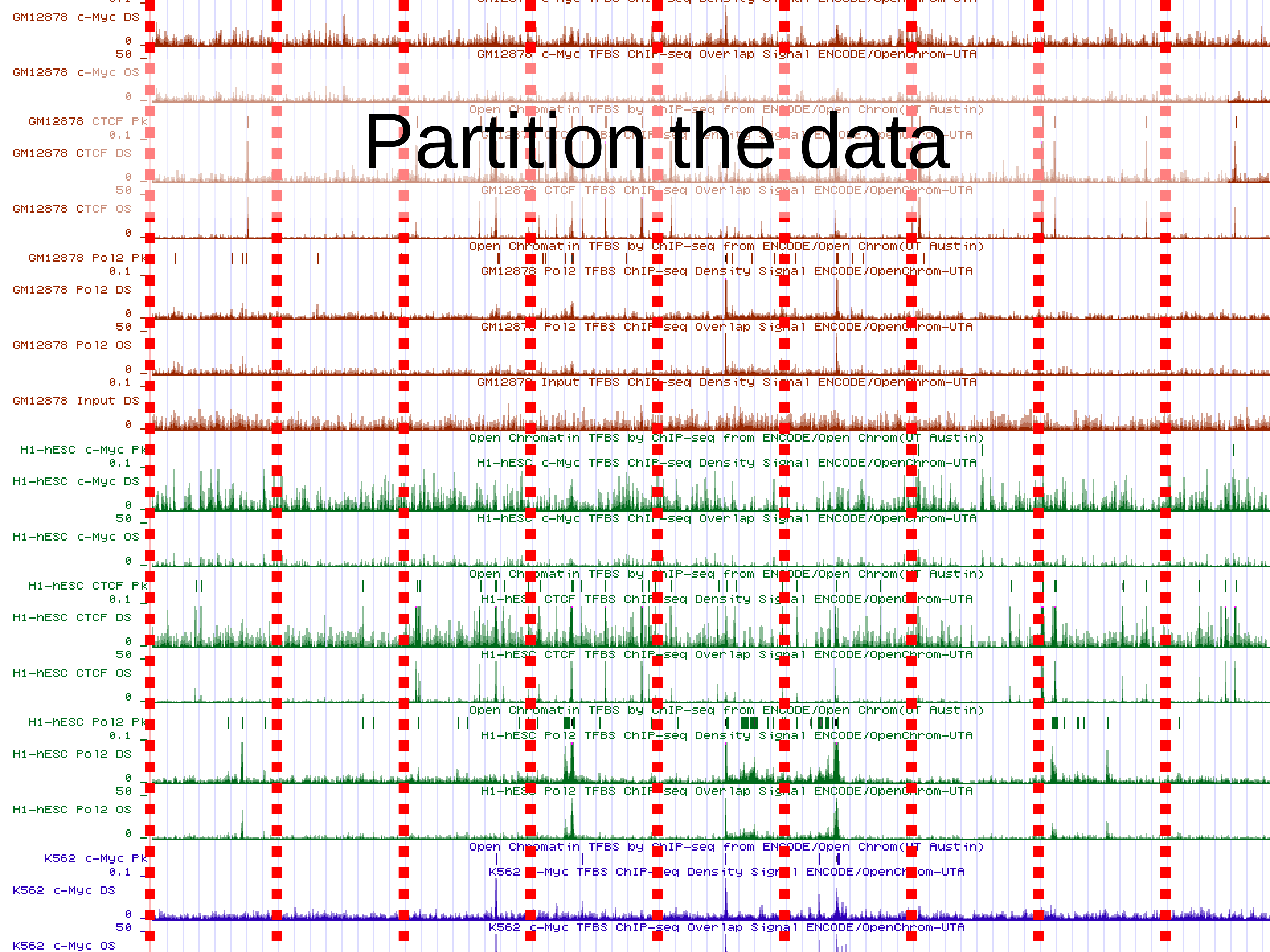
Partition the data



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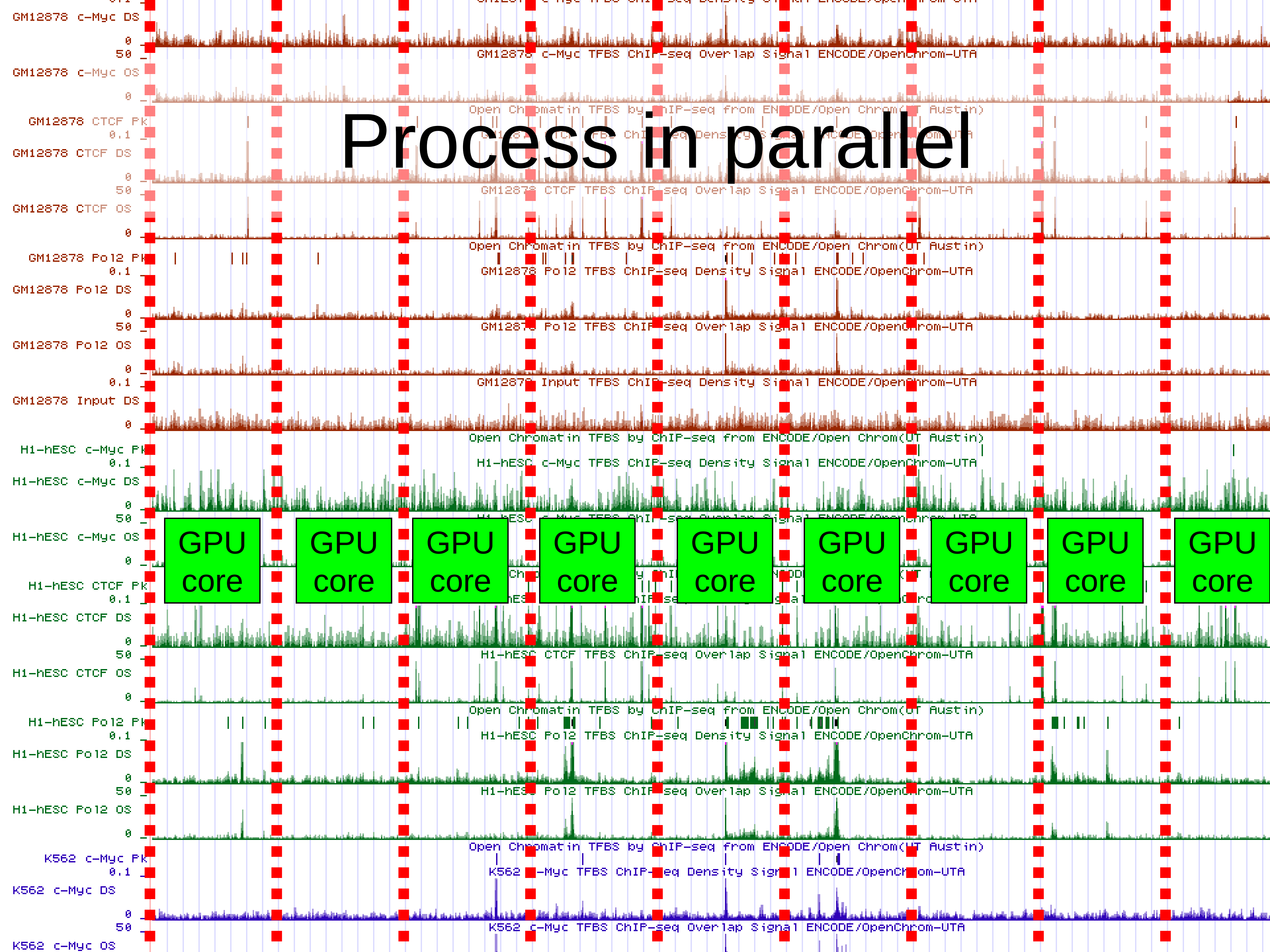
Process in parallel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GPU core
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Take home message

- Biology as a science is becoming more computationally oriented
- Genome biology is massively parallel by its nature
- GPUs fit perfectly for solving problems in genome biology