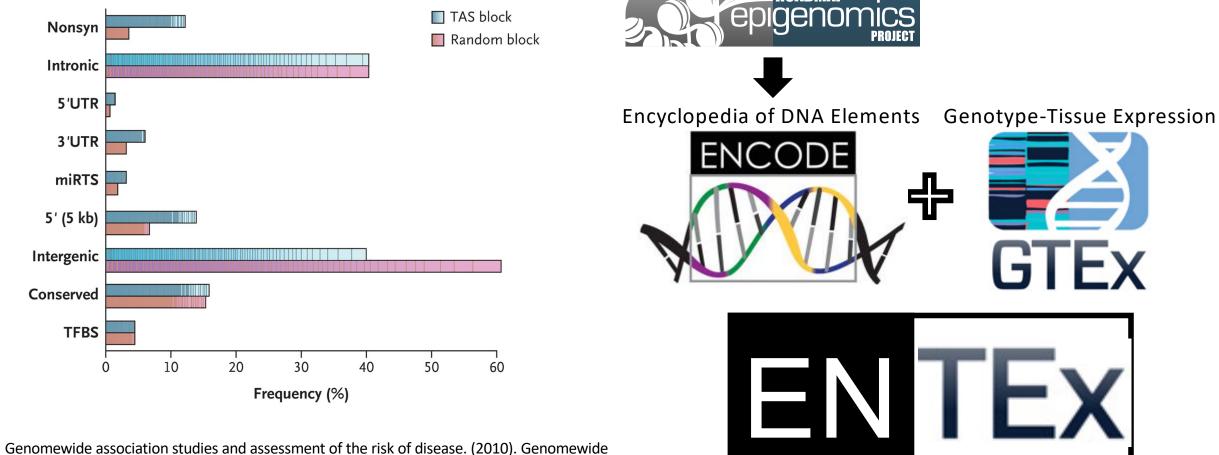
Uniformly collected and processed functional genomics assays provide a way to interpret non-coding variants in terms of tissue of action

Fabio Navarro – Yale University ASHG 2018

# Agenda

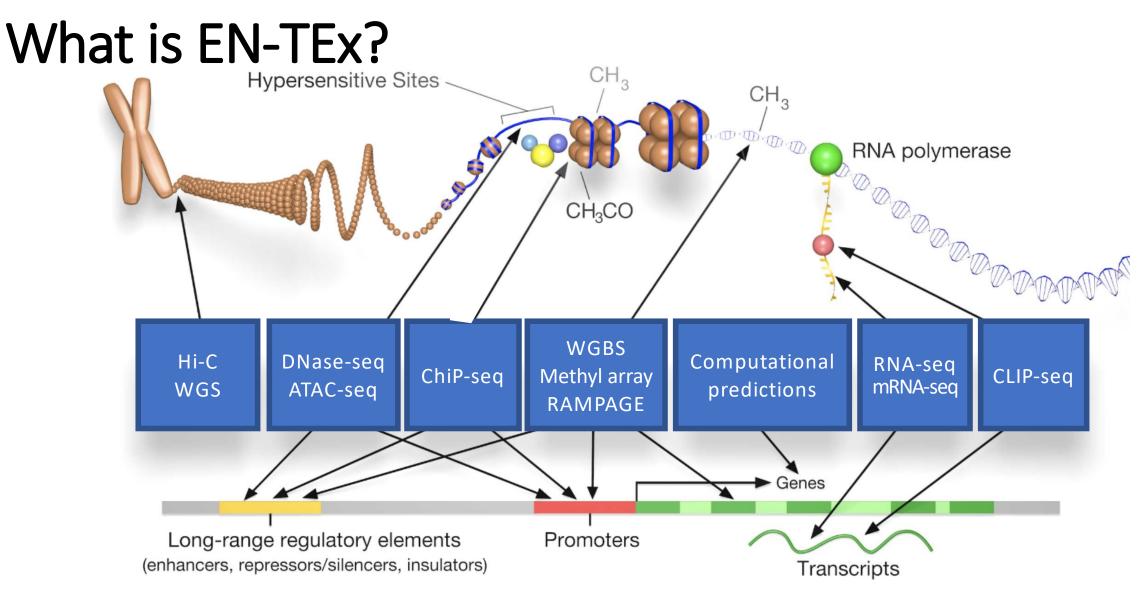
- What is EN-TEx?
- The EN-TEx resource
- Our first findings

## EN-TEx is the follow up of GTEx and ENCODE

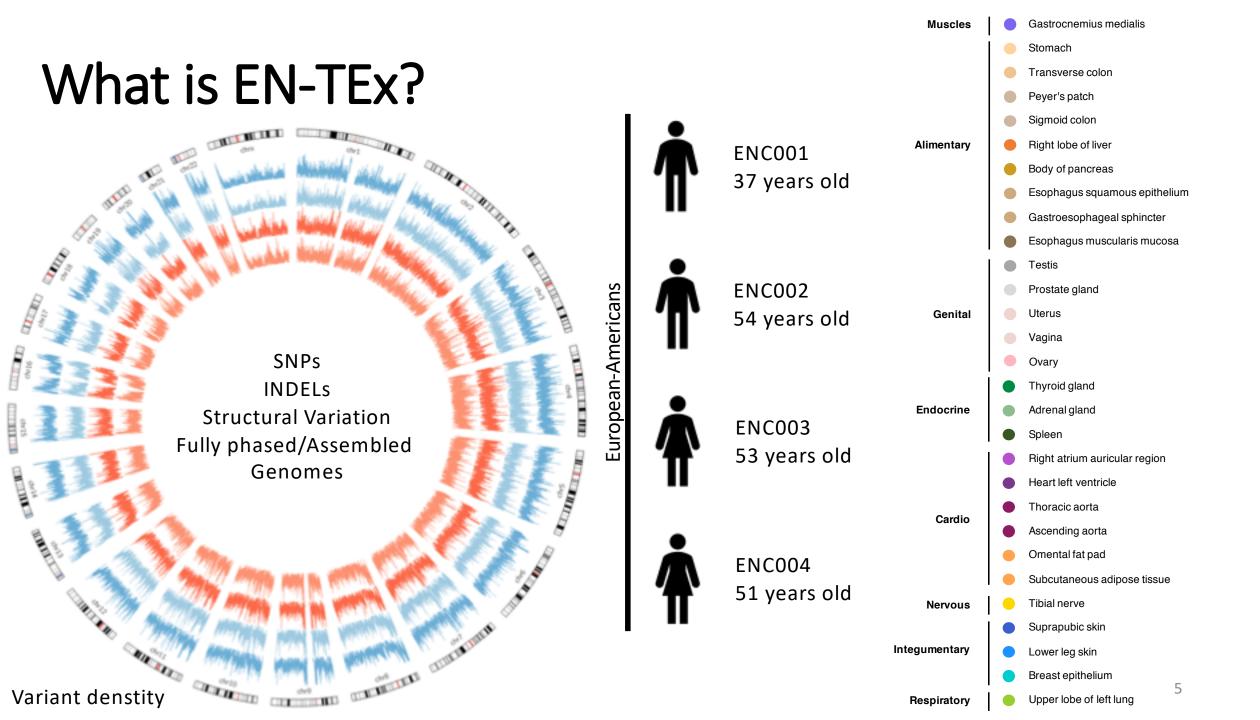


ROADMAP

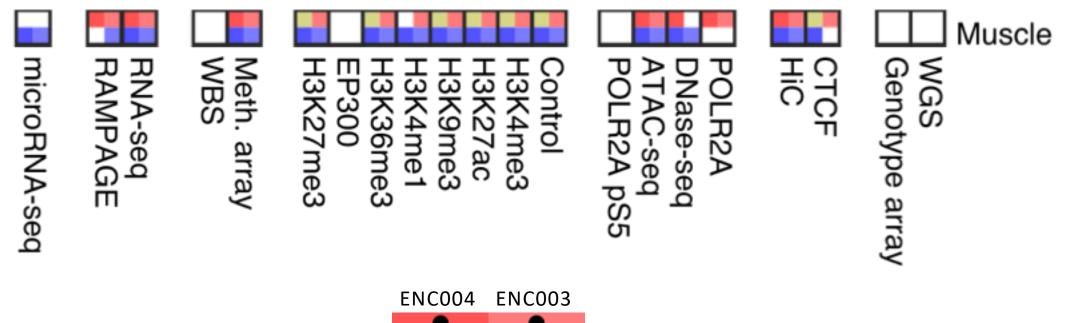
Genomewide association studies and assessment of the risk of disease. (2010). Genomewide association studies and assessment of the risk of disease., *363*(2), 166–176. http://doi.org/10.1056/NEJMra0905980

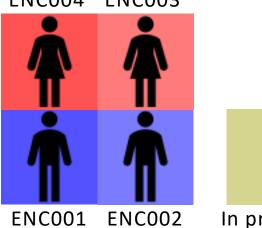






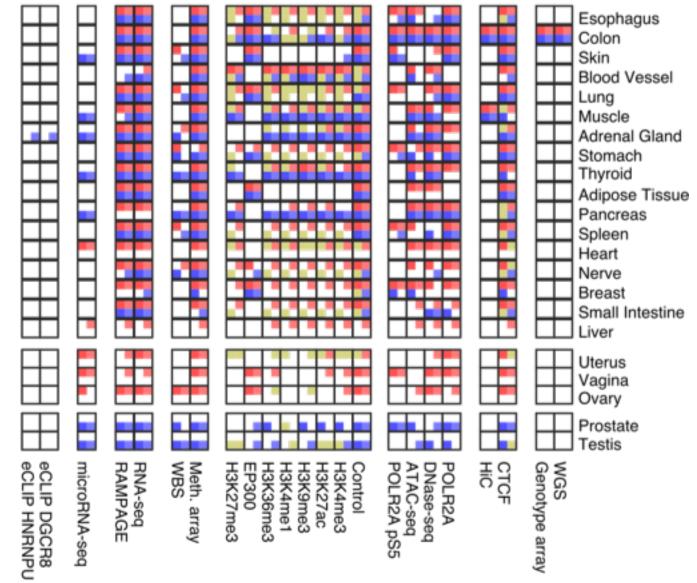
## The EN-TEx dataset



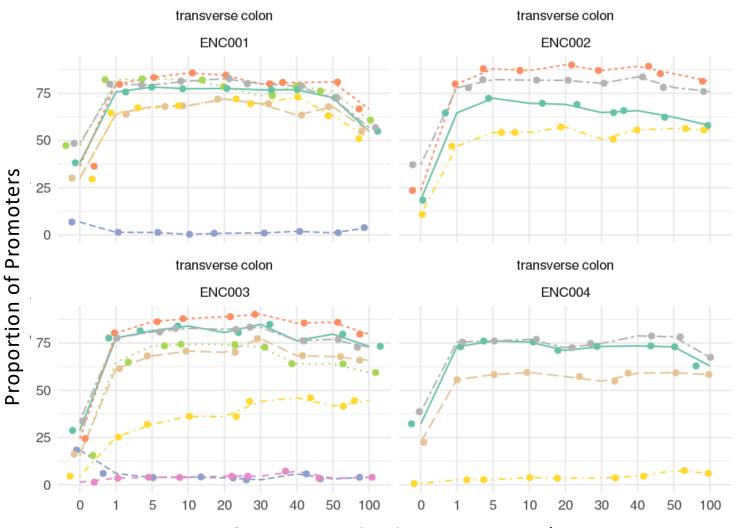


In progress

## The EN-TEx dataset

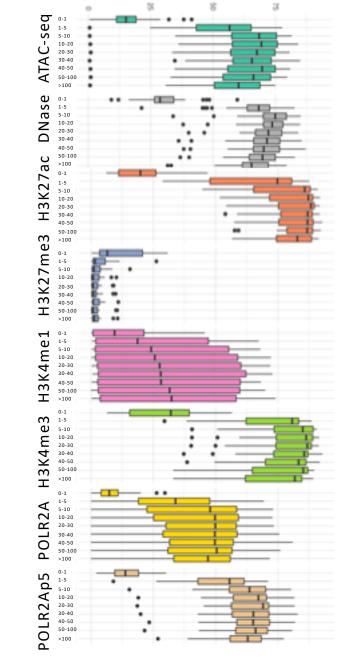


#### Variation across tissues

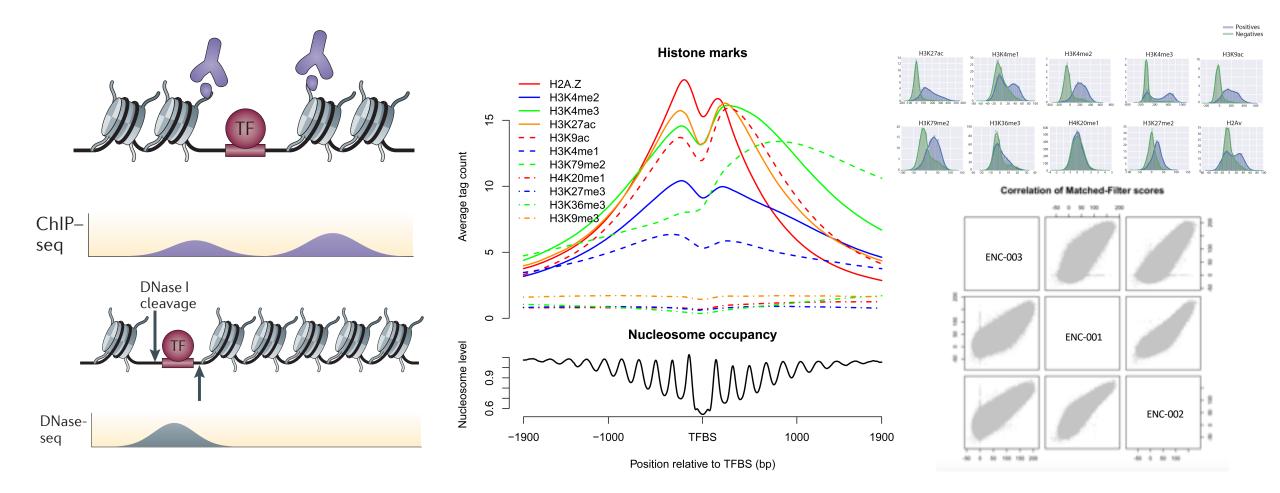


Gene expression in transverse colon

#### Proportion of Promoters Across all EN-TEx samples



## Integrative methods for calling regulatory regions

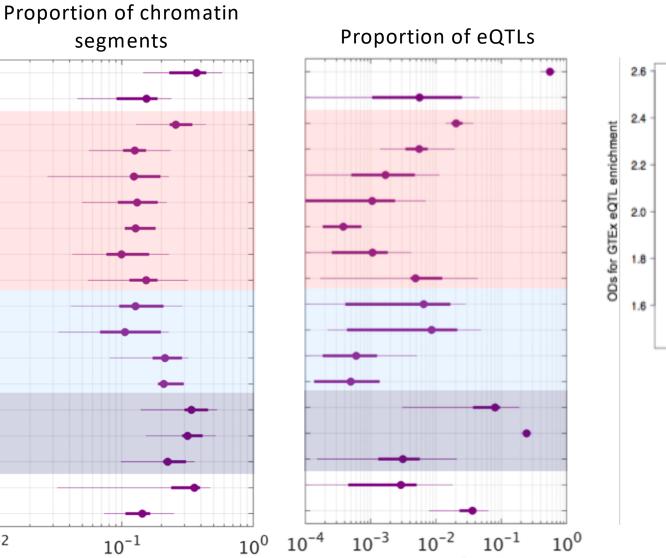


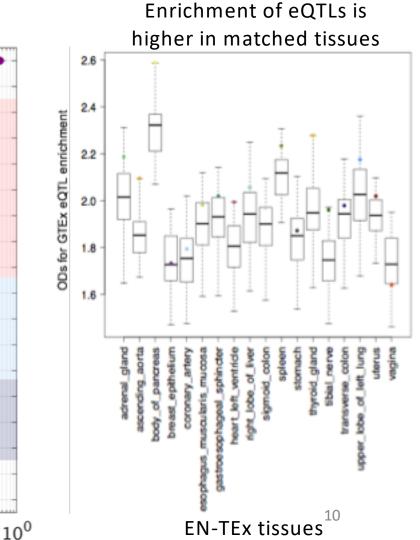
## eQTLs are enriched in tissue regulatory regions

Quiescent Heterochromatin **Active Promoter Inactive Promoter Active Flanking Promoter Inactive Flanking Promoter Active Bivalent Promoter** Inactive Bivalent Promoter **Polycomb Silenced Promoter Active Enhancer Inactive Enhancer Active Exonic Enhancer Inactive Exonic Enhancer Strong Transcription** Weak Transcription H3K27ac + H3K36me3 H3K9me3 + H3K36me3 H3K27ac

10<sup>-2</sup>

**Chromatin State** 





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GENCODE GTEx consortium Roadmap Epigenomics project