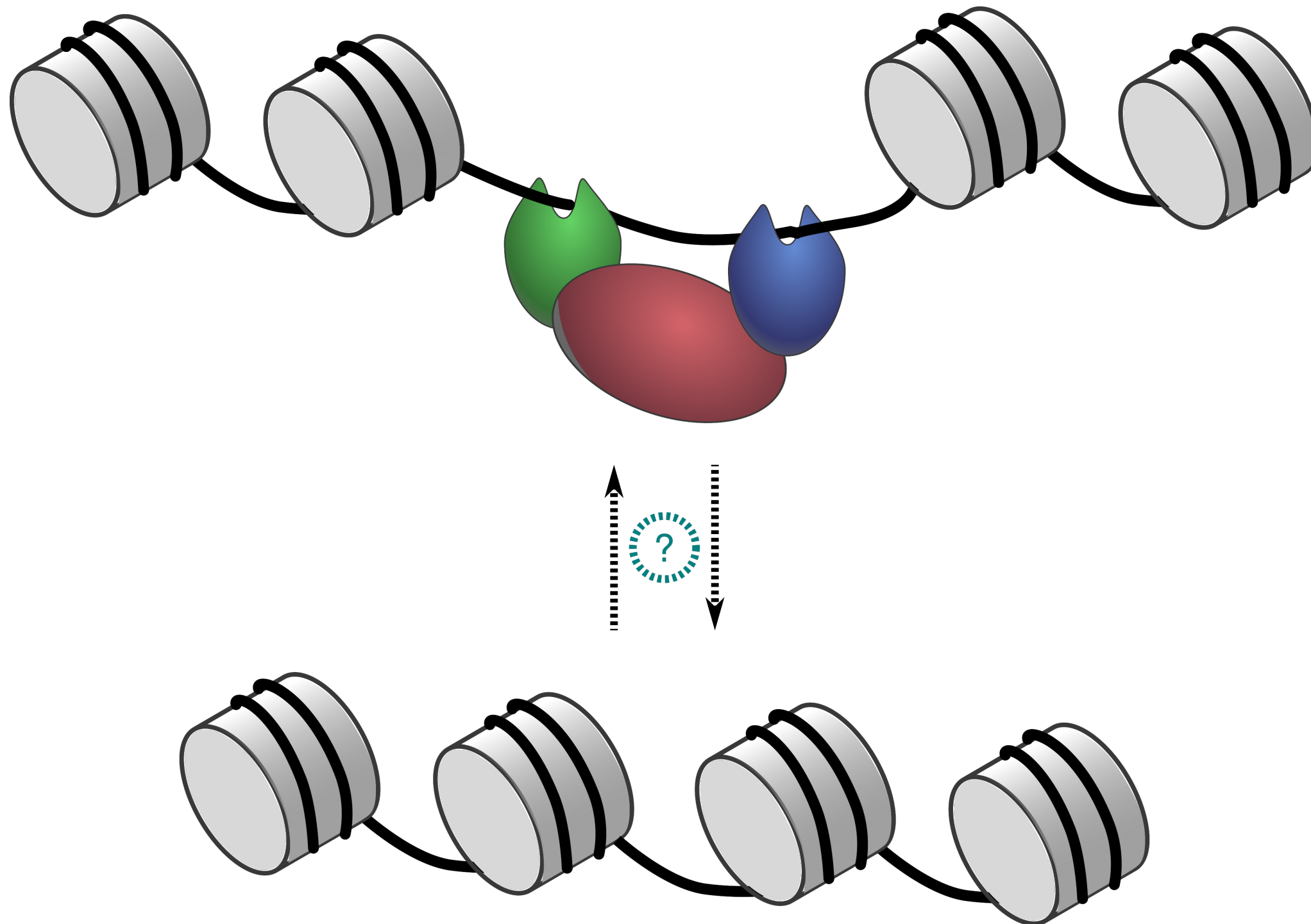


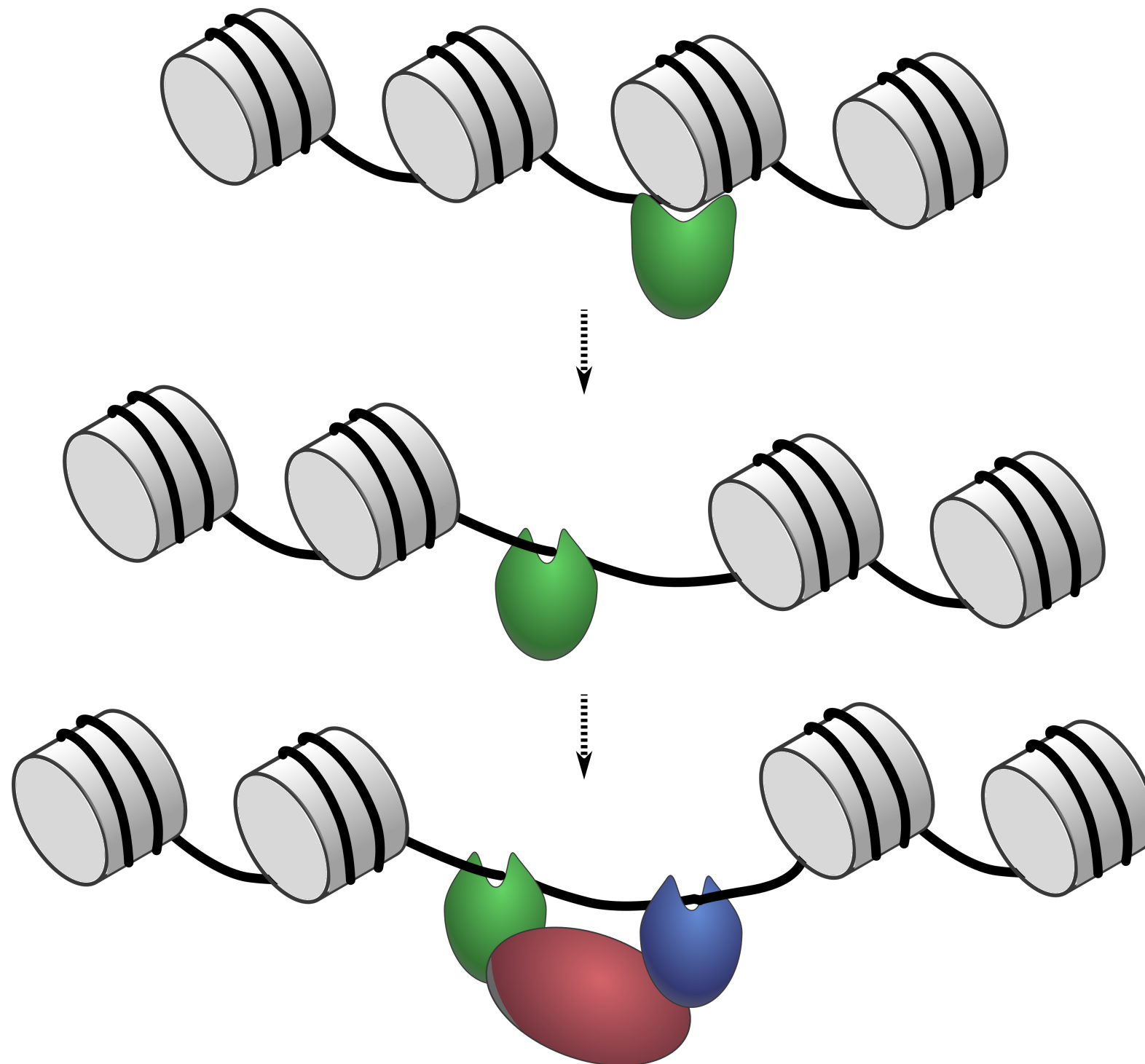
# Genome-wide association between transcription factor expression and chromatin accessibility reveals chromatin state regulators

David Lamparter

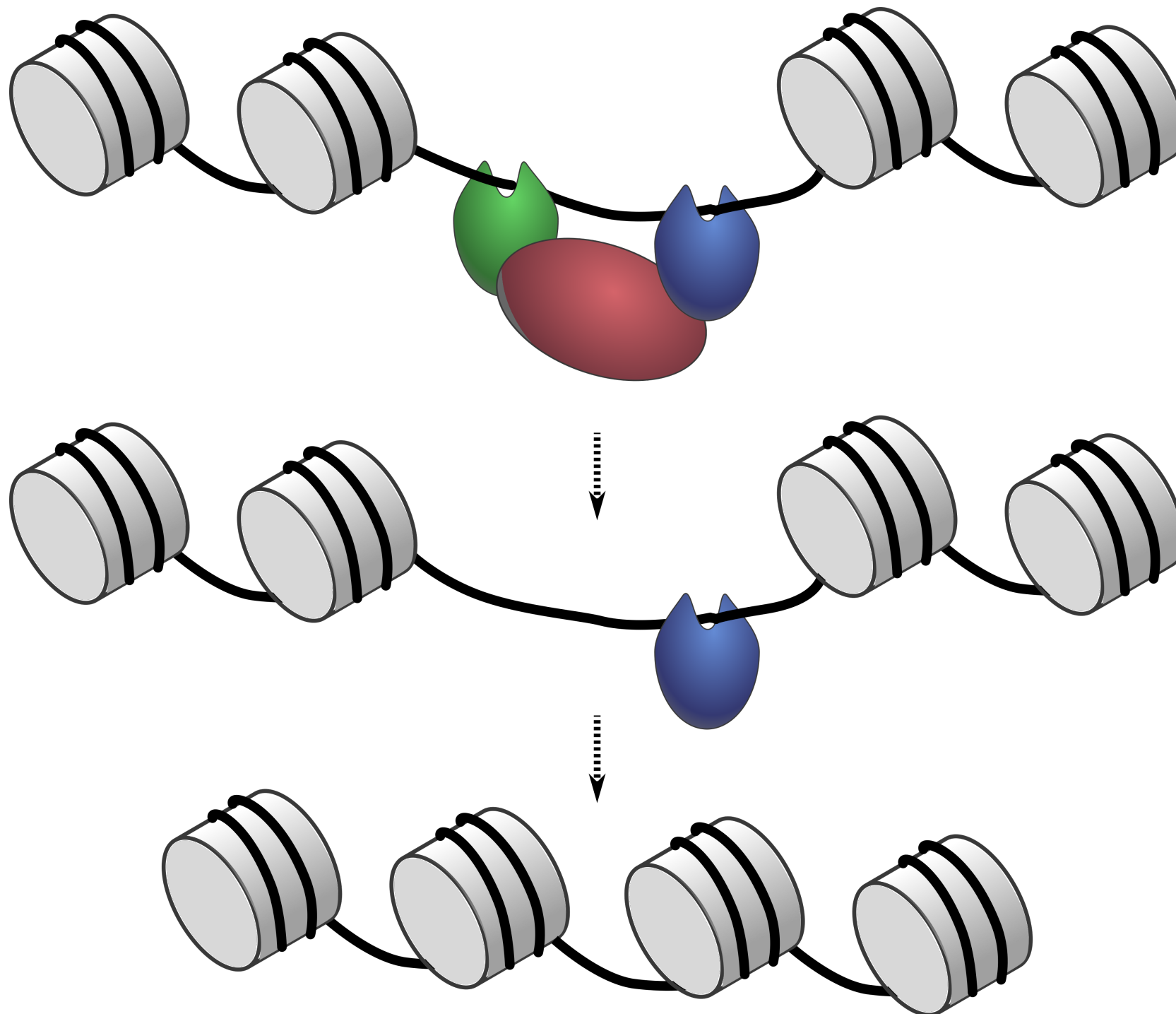
# Chromatin opening/closing: Which TFs relevant (CSRs)?



# Pioneer Factors

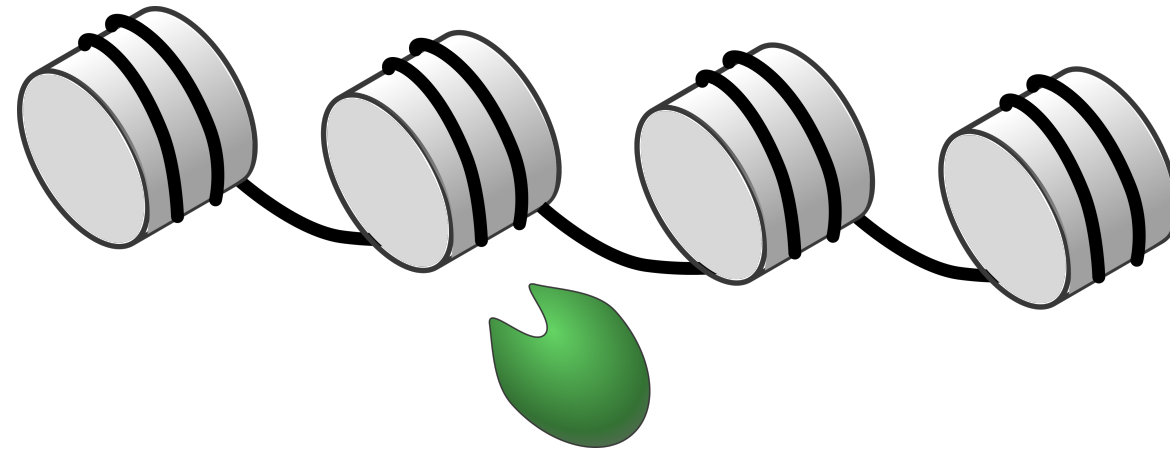


# Stability of TF Complex

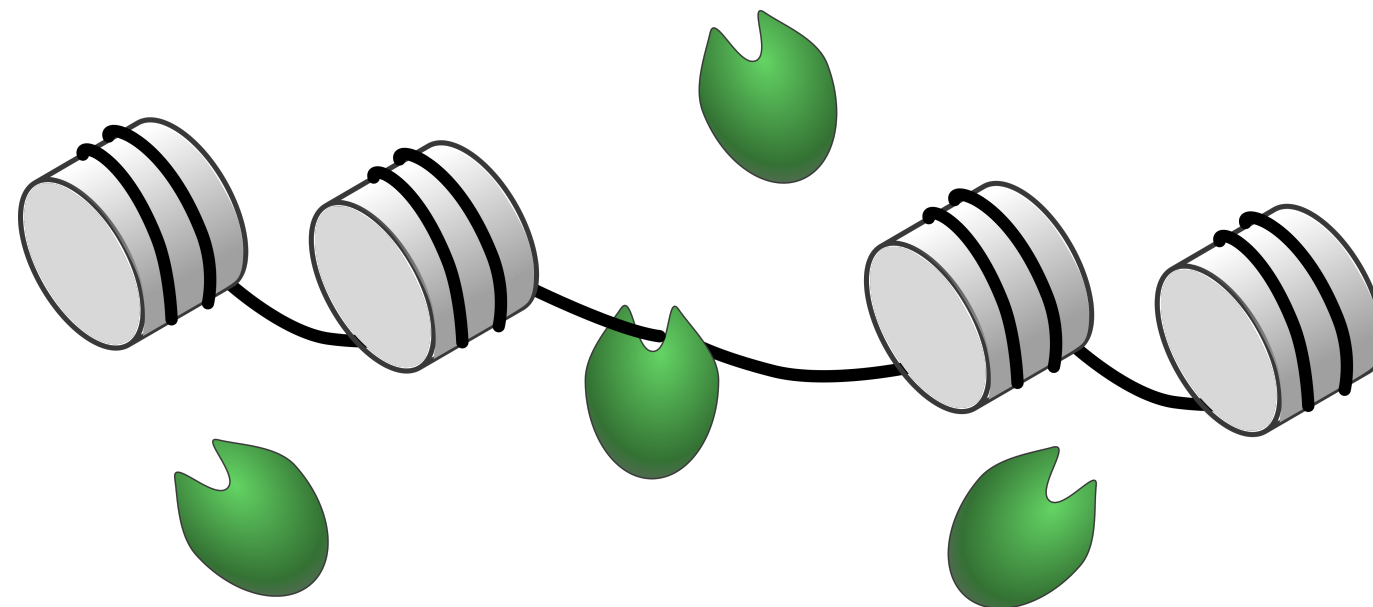




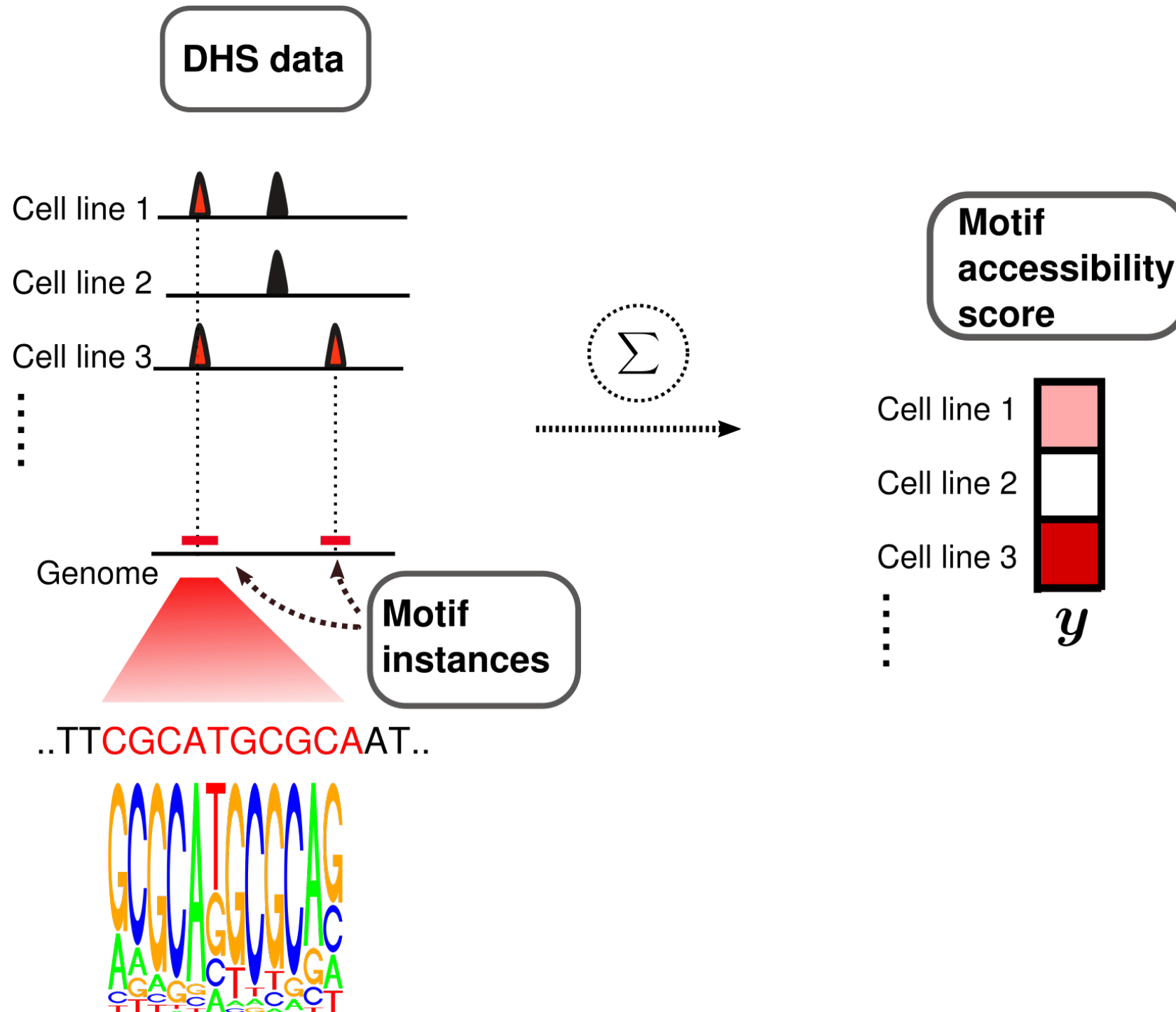
# The Basic Idea



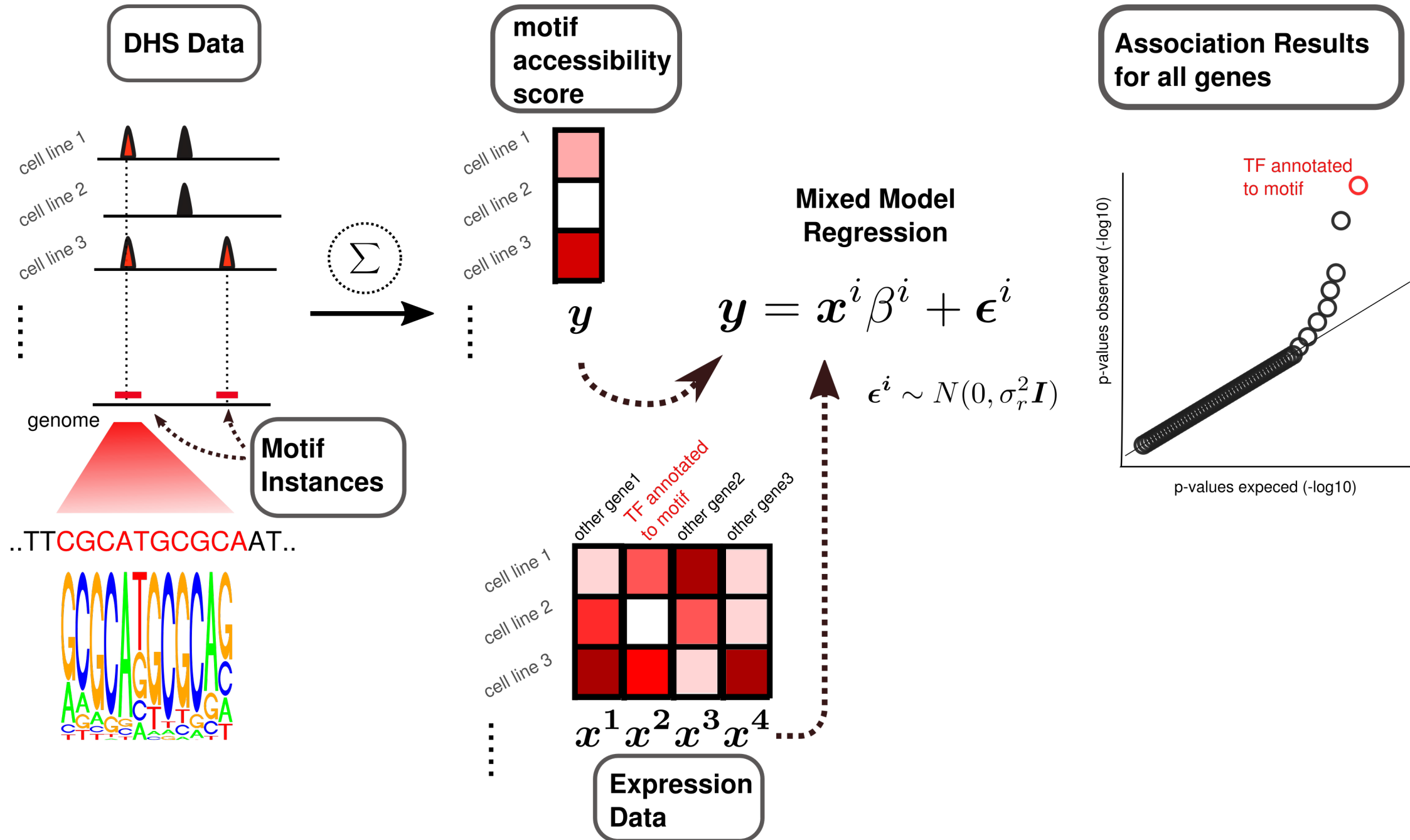
VS



# Accessibility Score of TF Motif



# Association Test across Genes

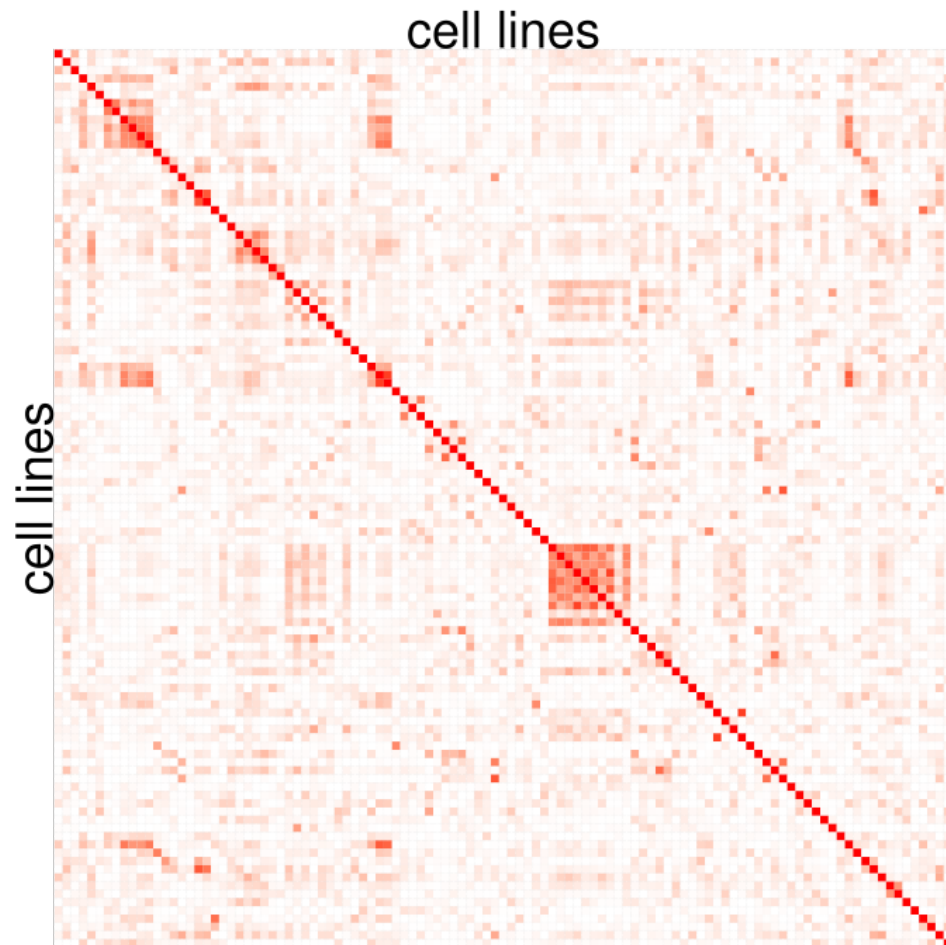


# Data Used

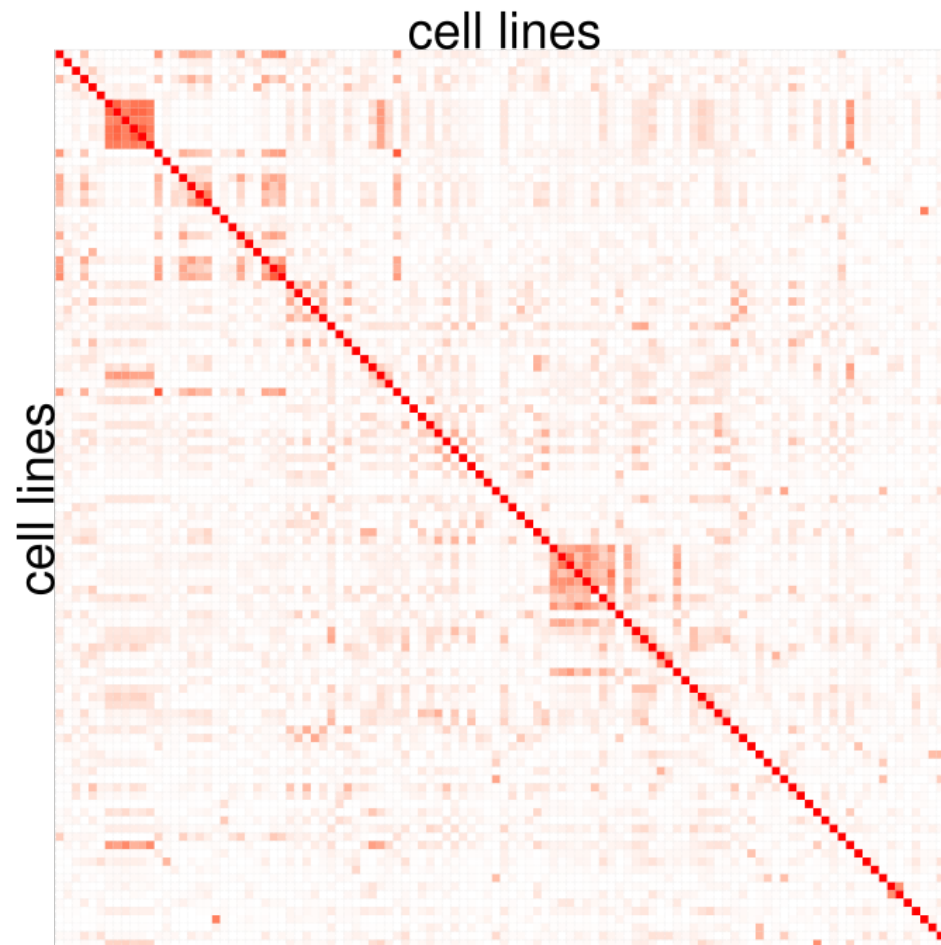
- Encode expression data (109 varied cell lines).
- Encode DHS data (109 varied cell lines).
- 344 TF motifs.

# Correlation<sup>2</sup> matrices

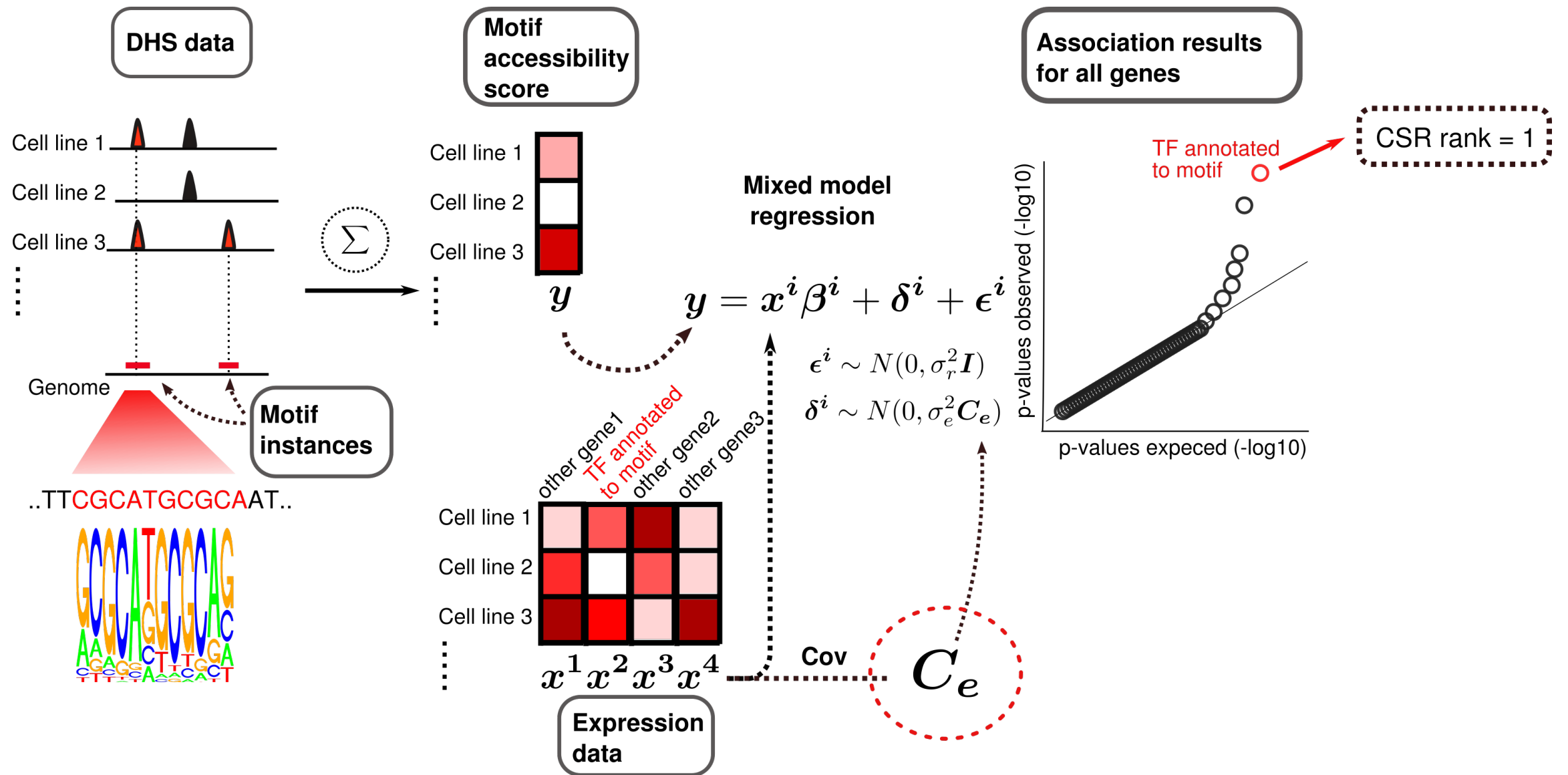
**Motif**



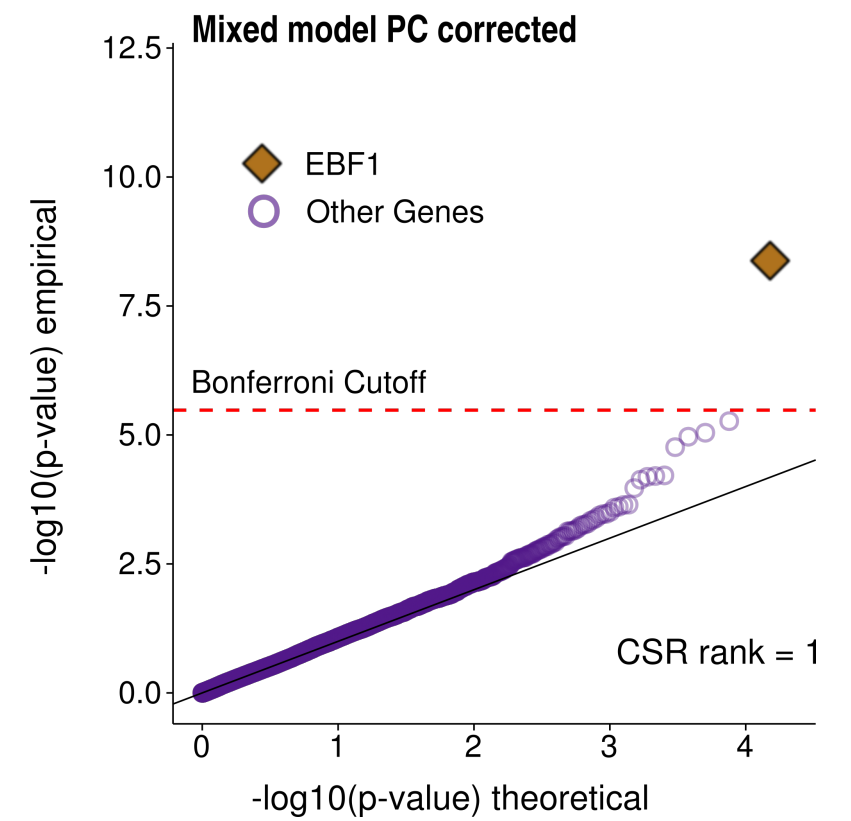
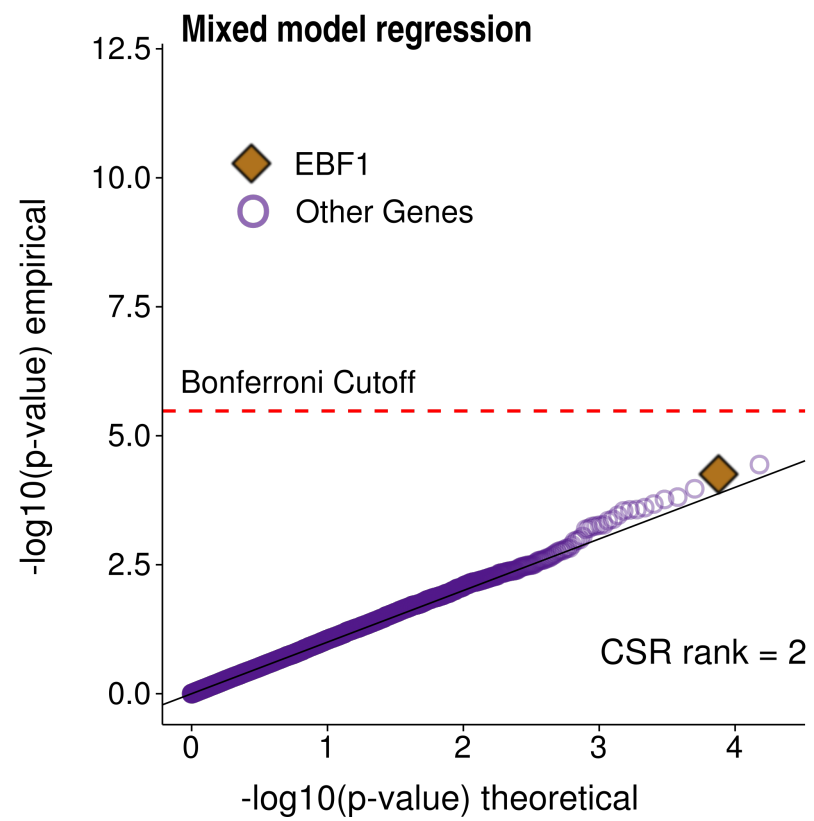
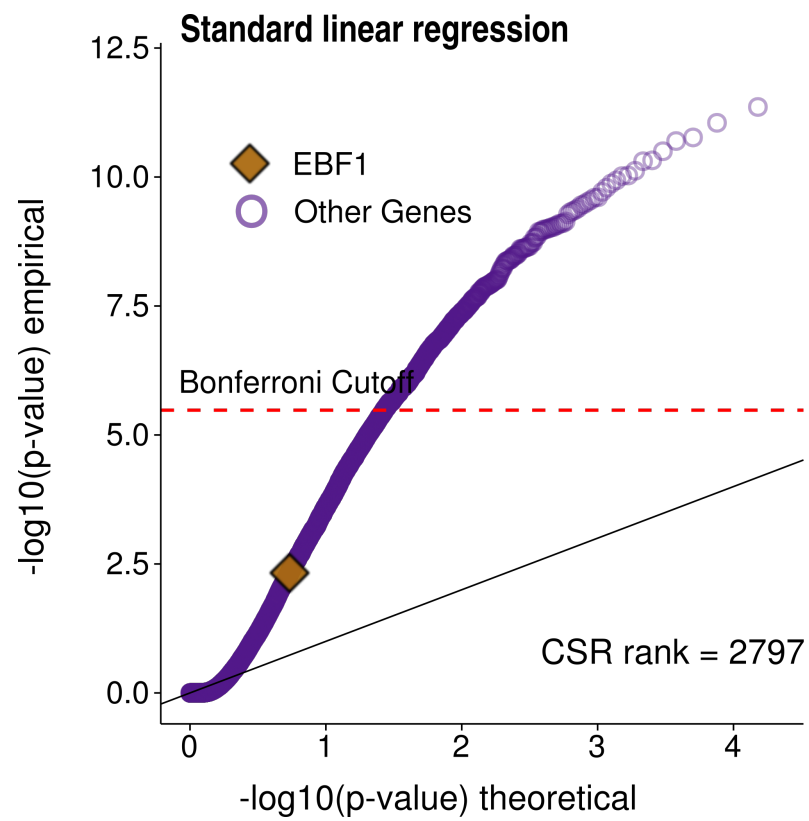
**Expression**



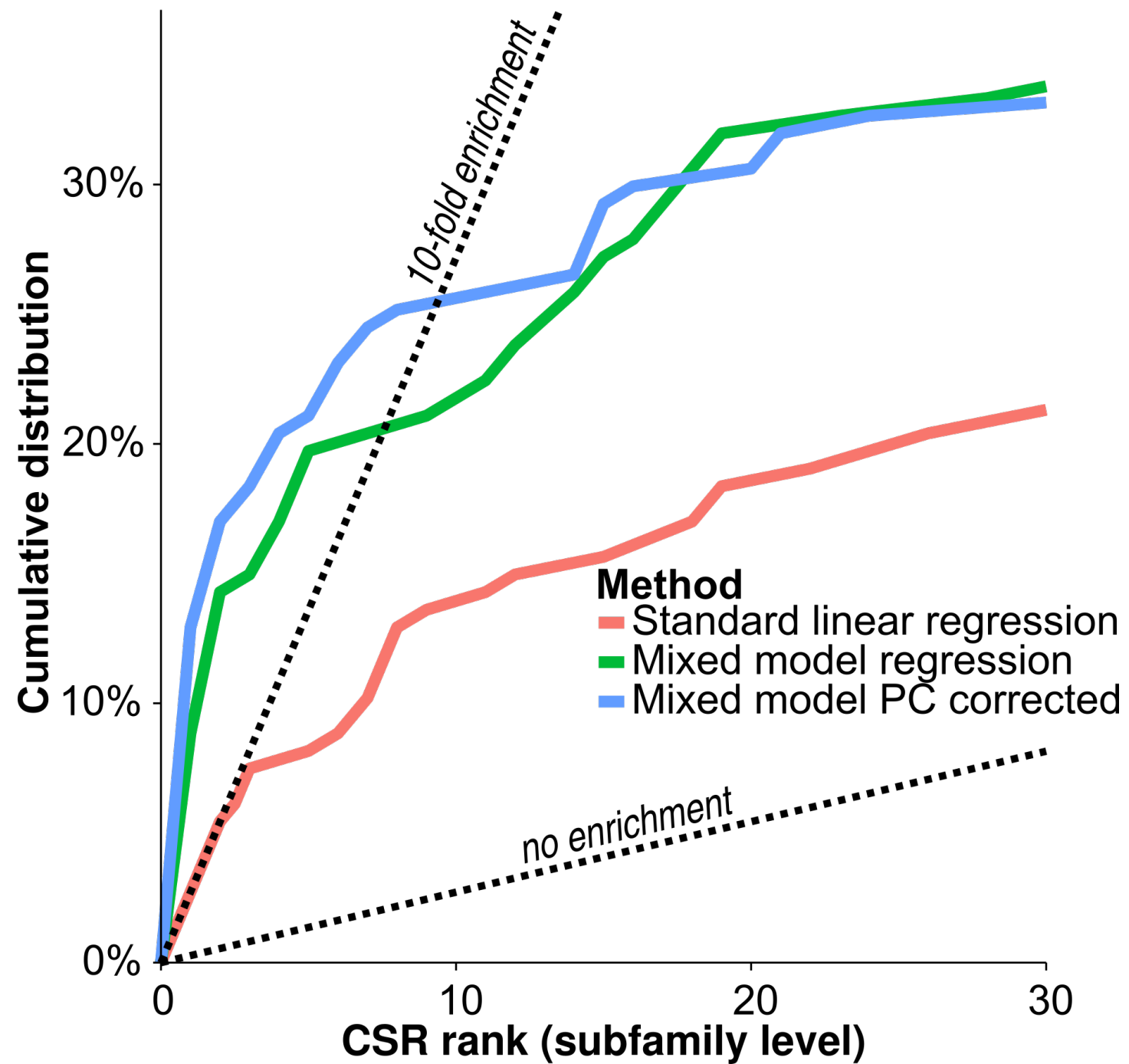
# Control population structure



# Example TF EBF1



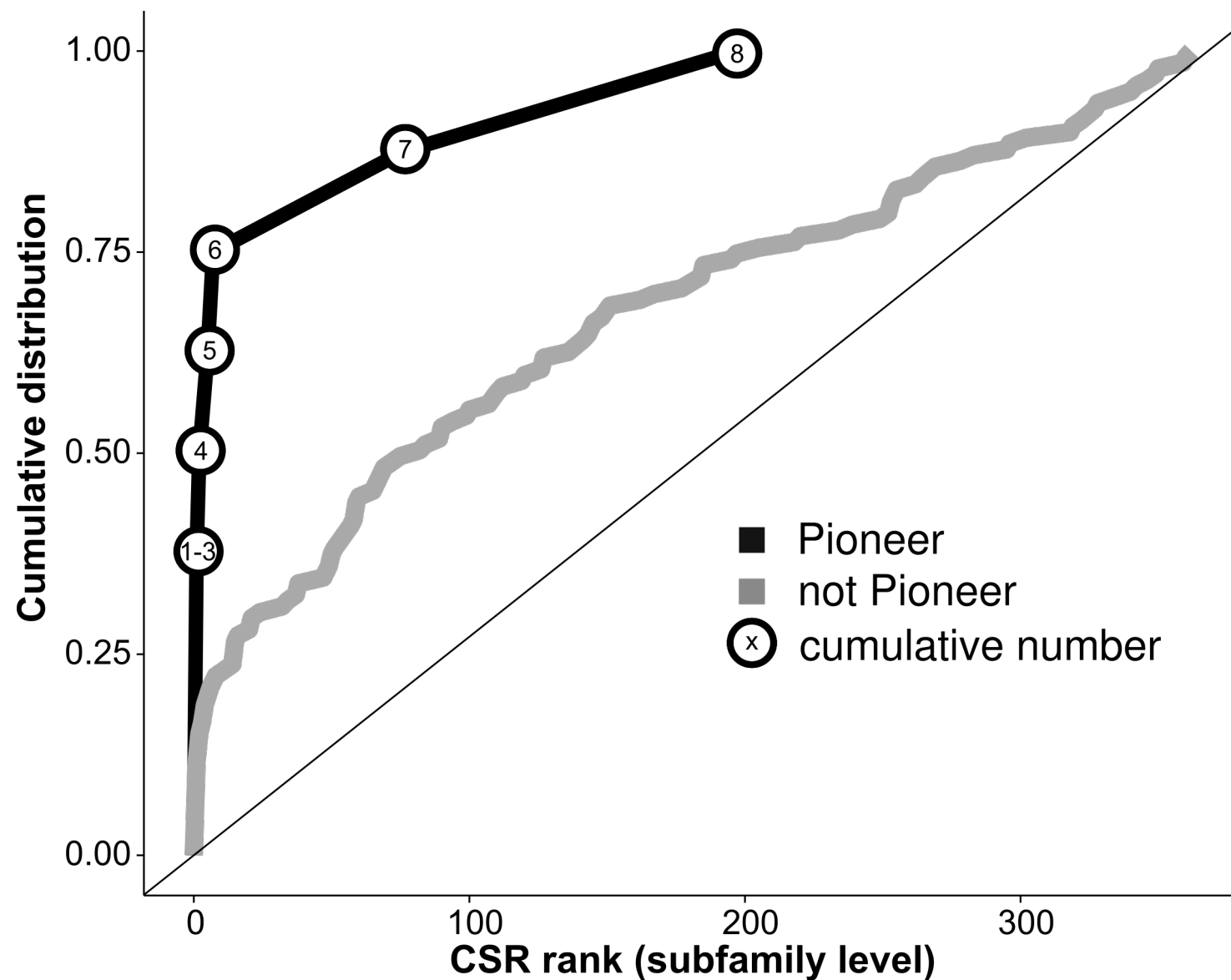
# Comprehensive CSR prediction





# Pioneers: most have low CSR ranks.

High confidence set. (Zaret et al. 2014)



Additionally mentioned in literature (evidence varies)

*TFAP2C,*  
*EBF1,*  
*CEBPD/B,*  
*OTX2,*  
*NFKB,*  
*STAT5,*  
*MYOG/D1*  
*RUNX1/2*

**>1/3 of predicted CSR.**

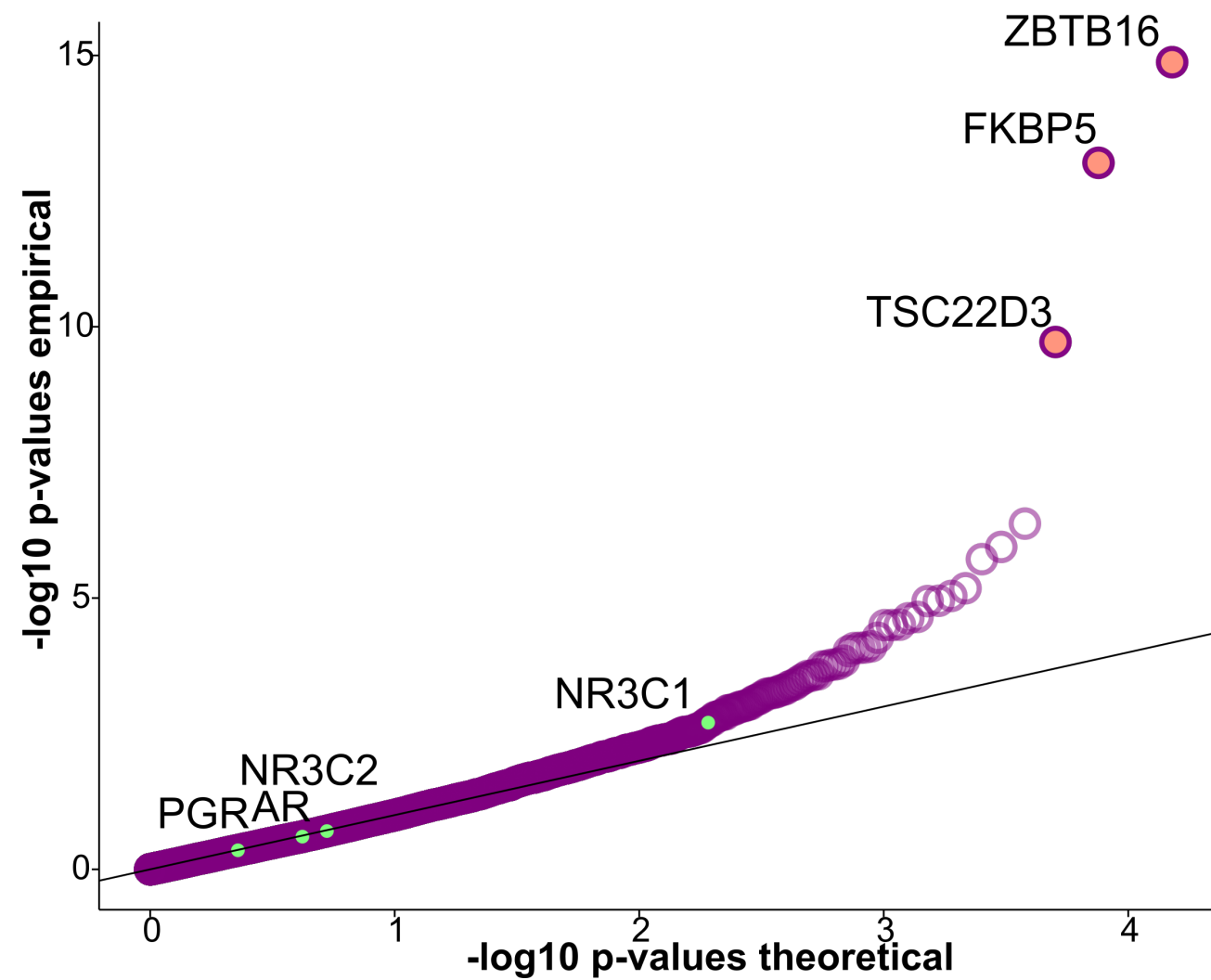
# Thanks



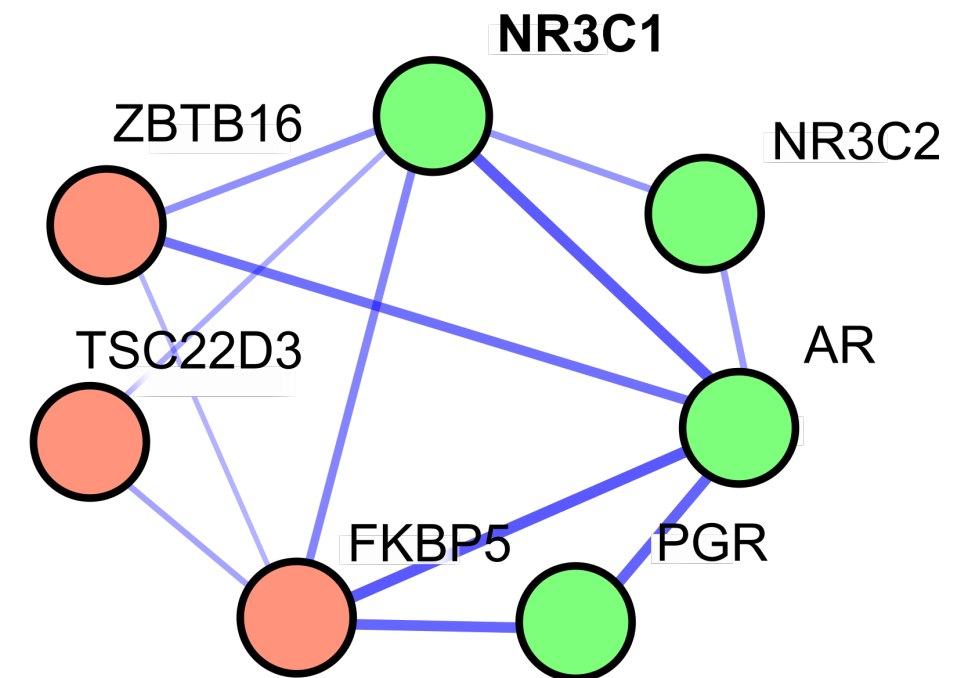
- Sven Bergmann
- Zoltan Kutalik
- Rico Rueedi
- Daniel Marbach

# Additional slides: NR3C1

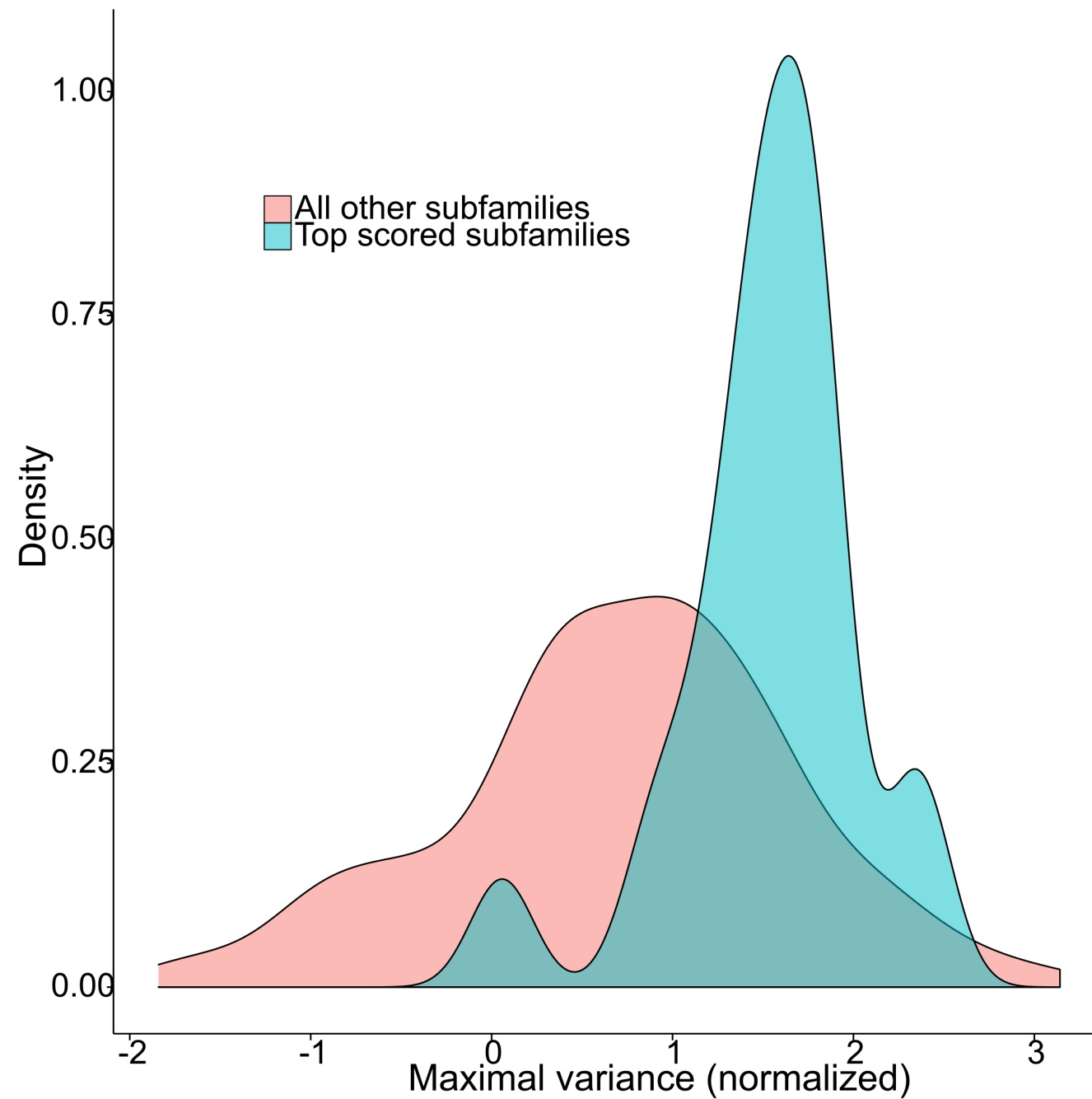
*NR3C1* motif vs all Genes



*STRINGdb* network



# Expression variance effect.



# POU5F1: SOX2 is guiding TF.

