

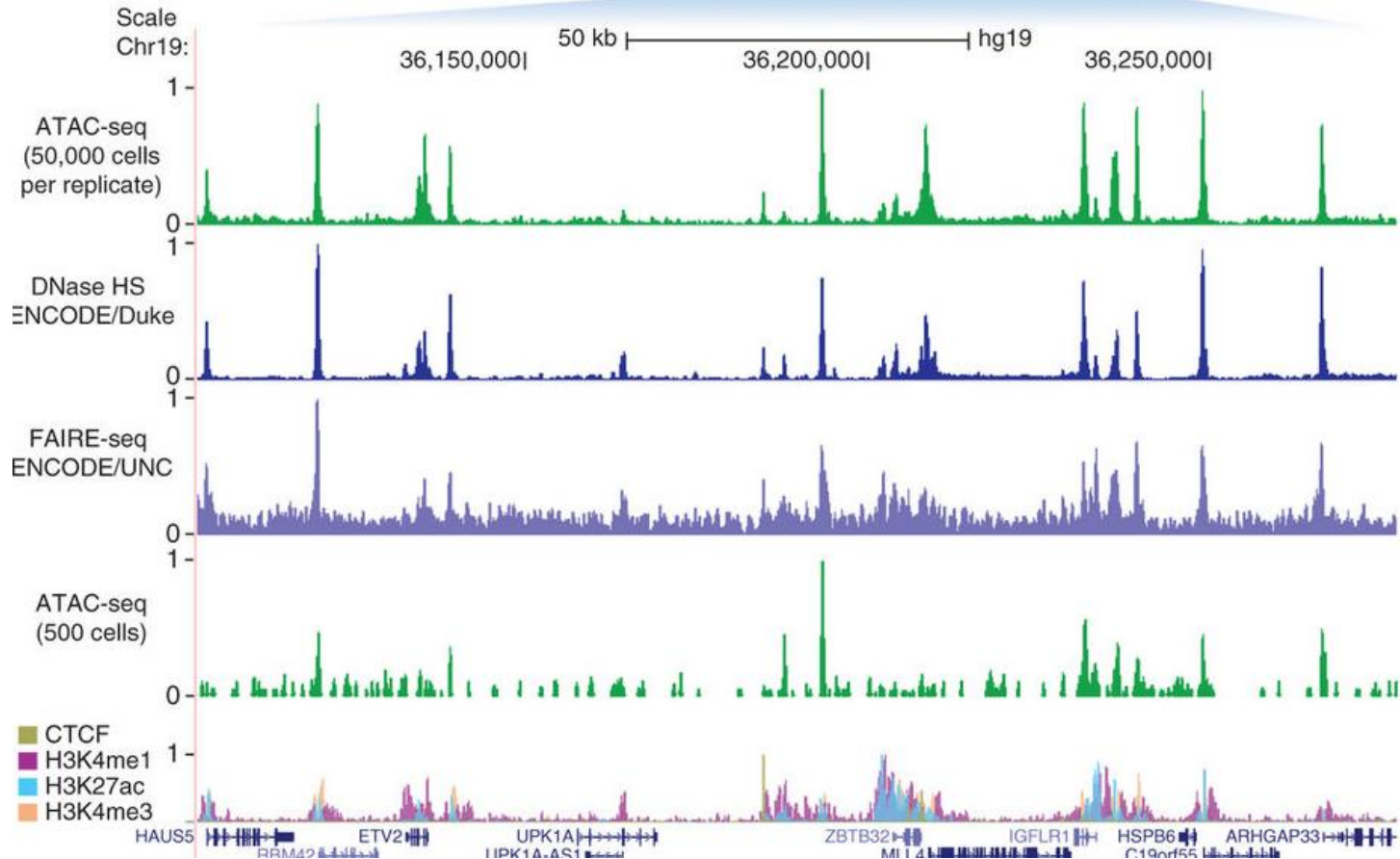
# LONG-RANGE SINGLE MOLECULE MAPPING OF ACCESSIBLE CHROMATIN IN EUKARYOTES

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**GREENLEAF & KUNDAJE LABS**

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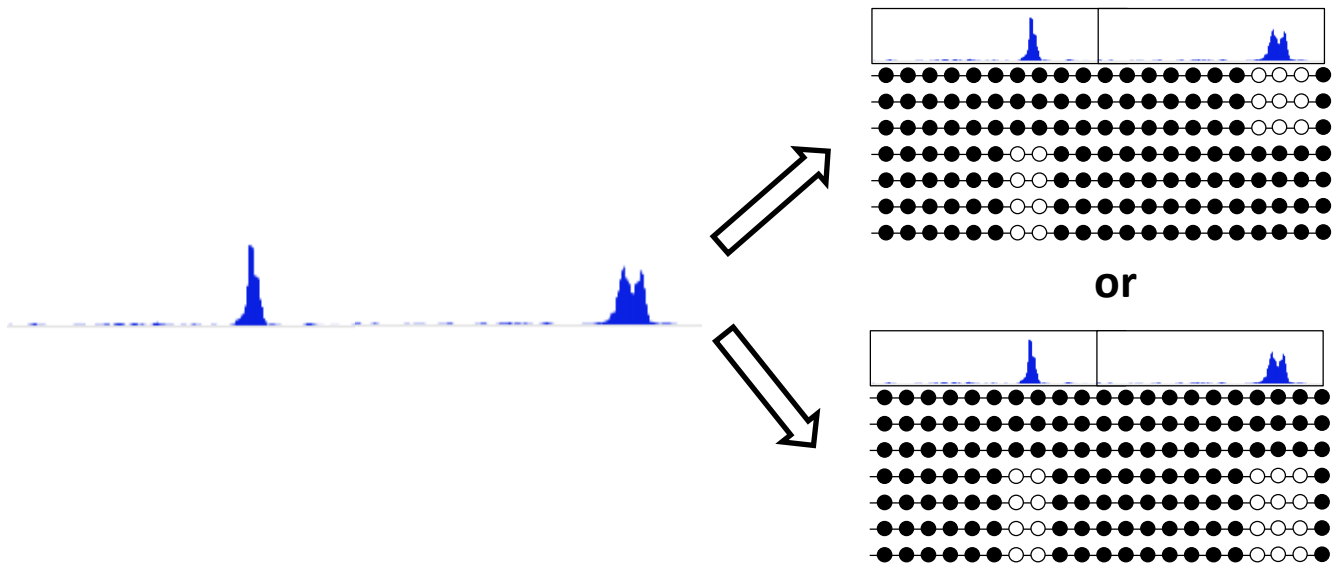


# ACCESSIBLE CHROMATIN LANDSCAPE IN MAMMALS



## QUESTIONS:

- Is the accessibility of distant open chromatin regions independently regulated or are they correlated?
- What is the distribution of open chromatin states within the population?
- Note: scATAC does not answer these questions because of sparseness, noise and diploidy



# SINGLE-MOLECLE LONG READ ACCESSIBLE CHROMATIN MAPPING

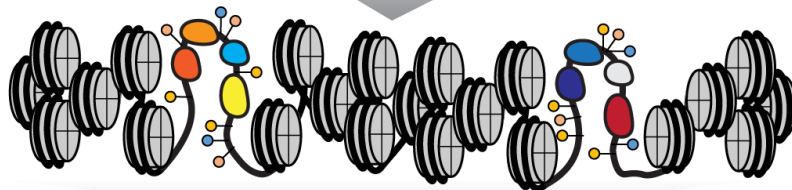
## SMAC-SEQ



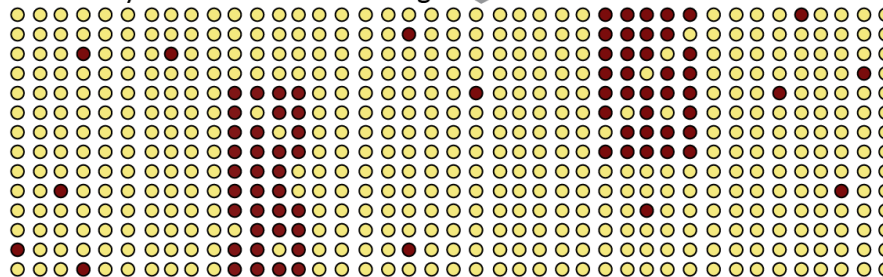
M.CviPI (GpC 5mC)

EcoGII (m<sup>6</sup>A)

M.SssI (CpG 5mC)



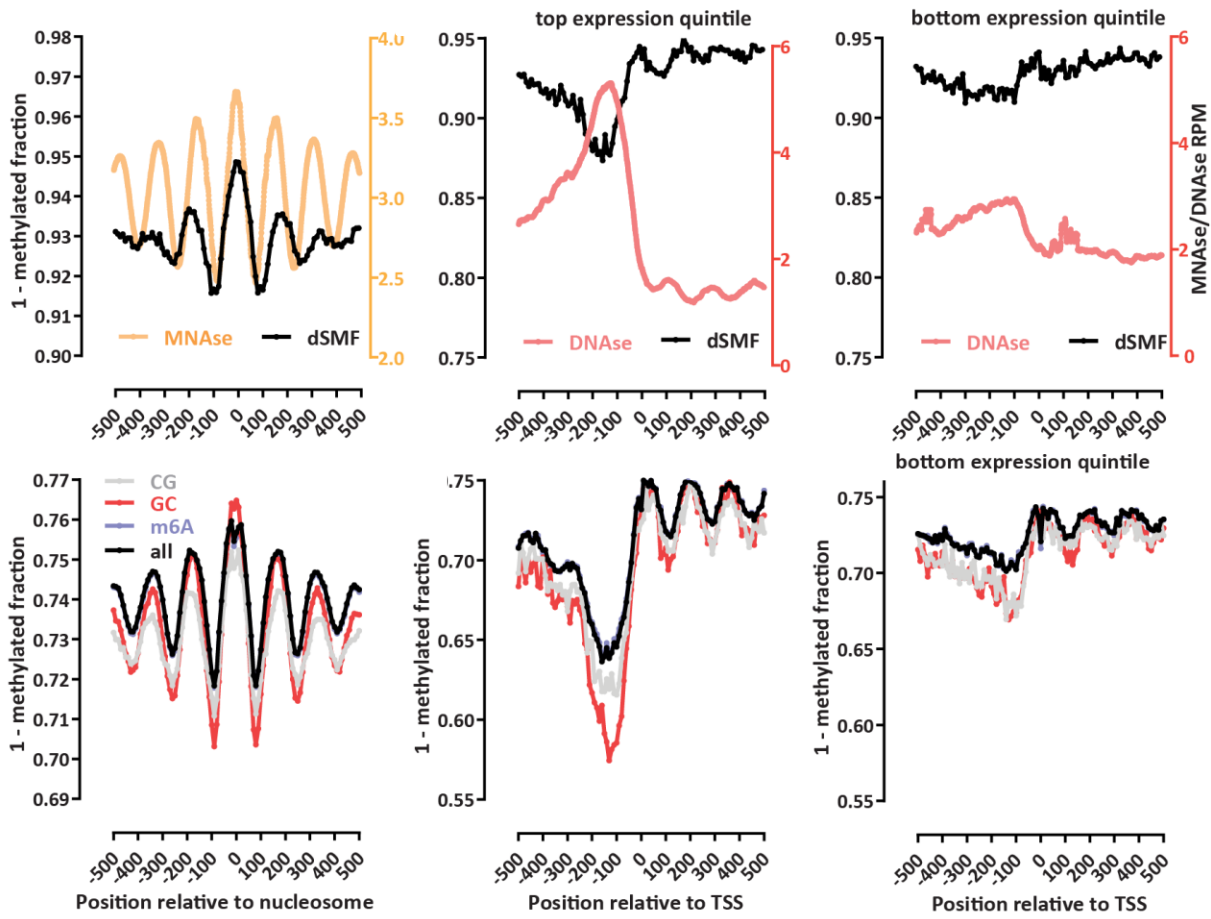
- HMW DNA extraction
- nanopore sequencing
- methylation-aware base calling



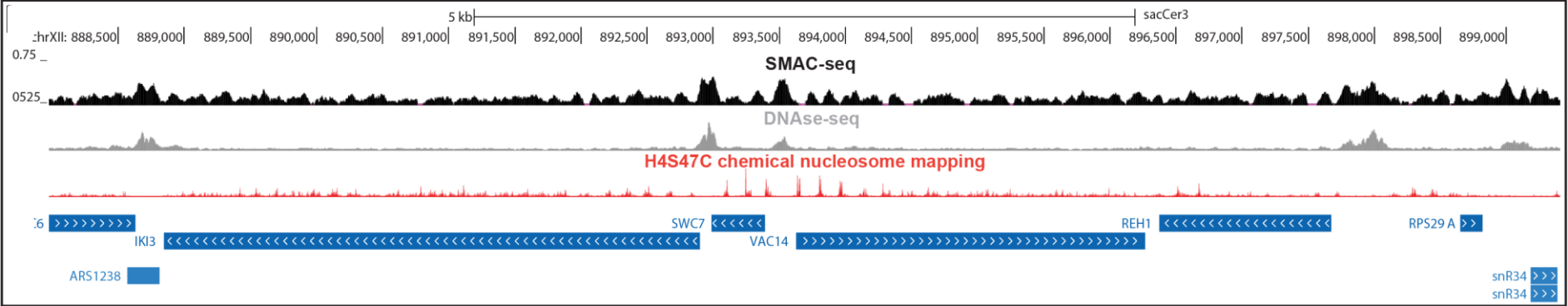
Single-Molecule long-range Accessibility of Chromatin footprints  
●●●● closed/protected ●●●● open/accessible

# **PILOT STUDY IN YEAST**

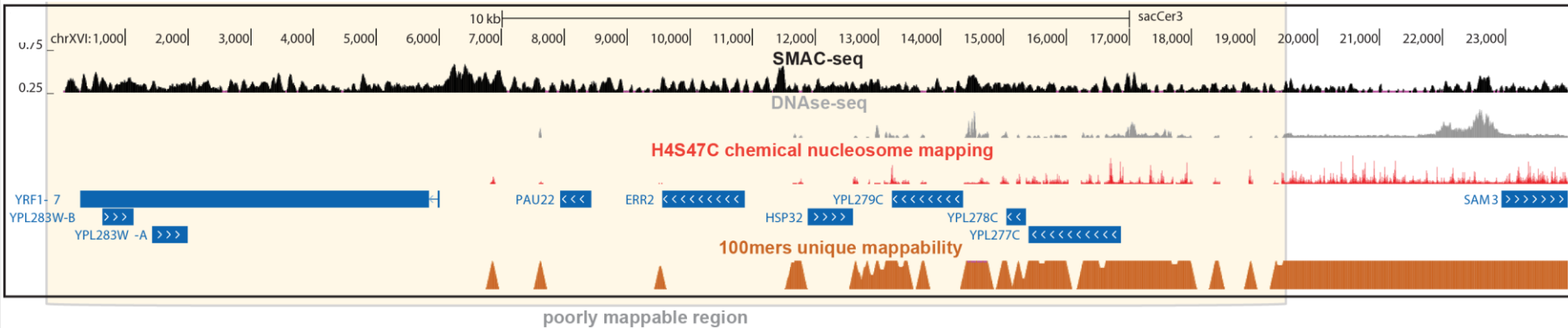
# KNOWN FEATURES OF ACCESSIBLE CHROMATIN ARE REPRODUCED



# SIMULTANEOUS MAPPING OF OPEN CHROMATIN AND NUCLEOSOMES

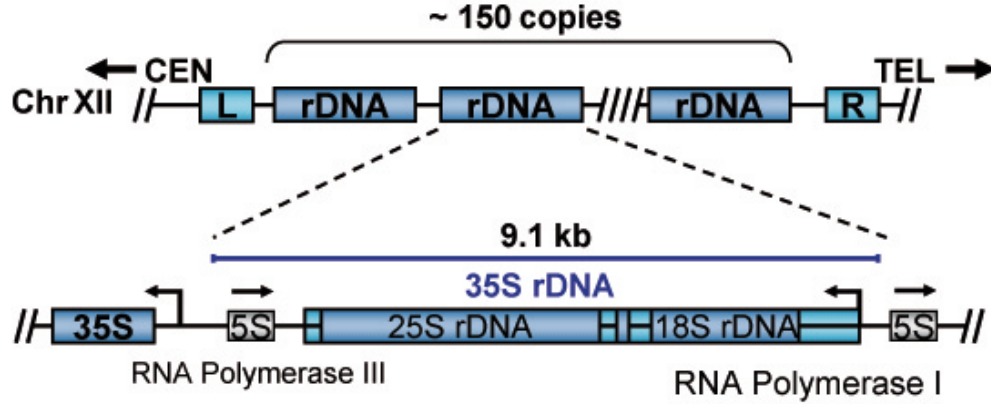


# MAPPING OF OPEN CHROMATIN AND NUCLEOSOMES IN REPEATS

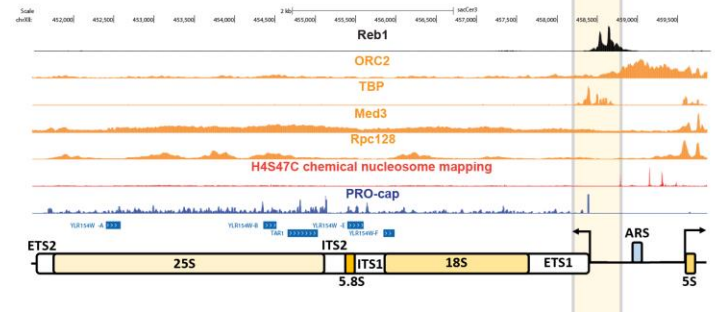
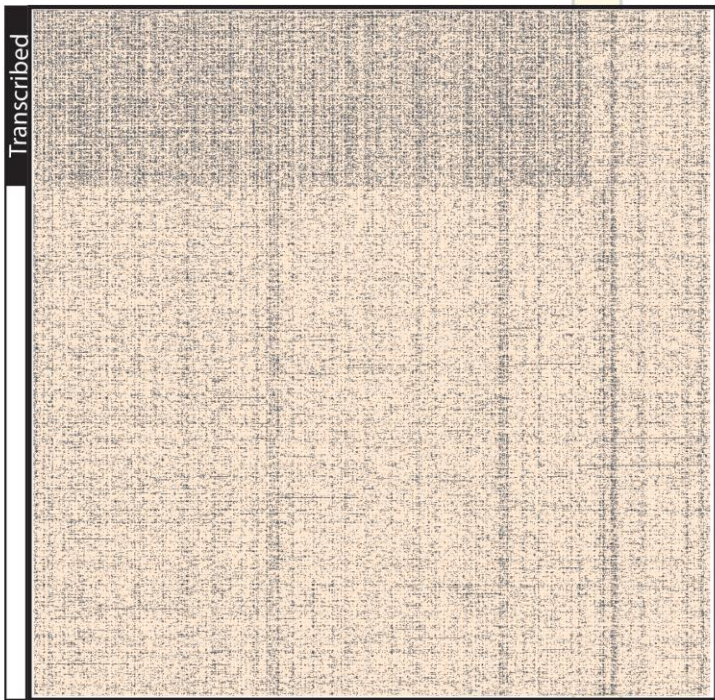




# RIBOSOMAL DNA CASE STUDY

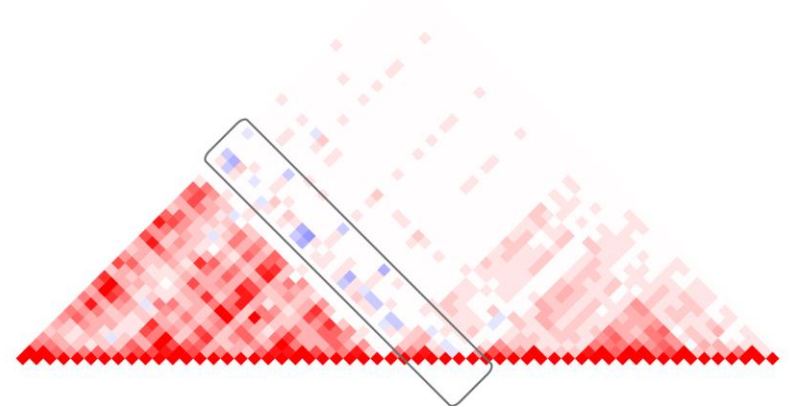
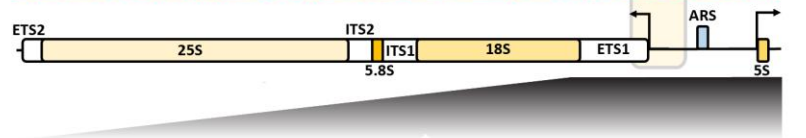
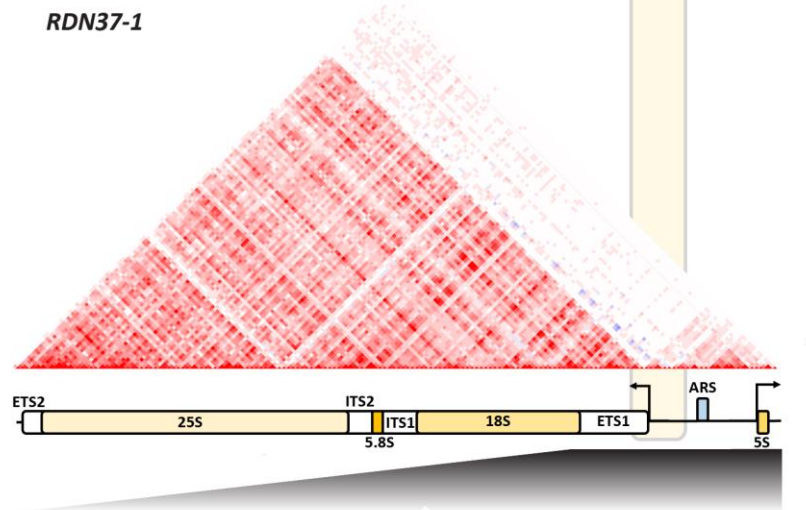


- Not uniquely mappable
- Present in arrays of 150-200 copies in the genome (but the whole arrays are not included in the genome assembly)
- Extremely highly transcribed and thought to be almost devoid of chromatin when active

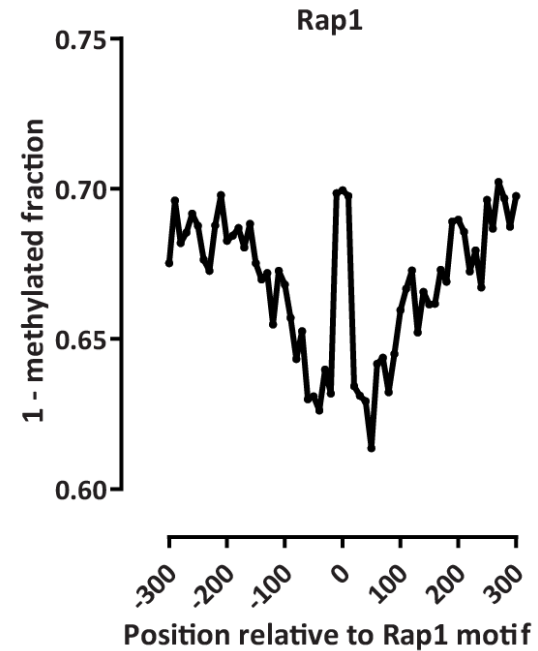
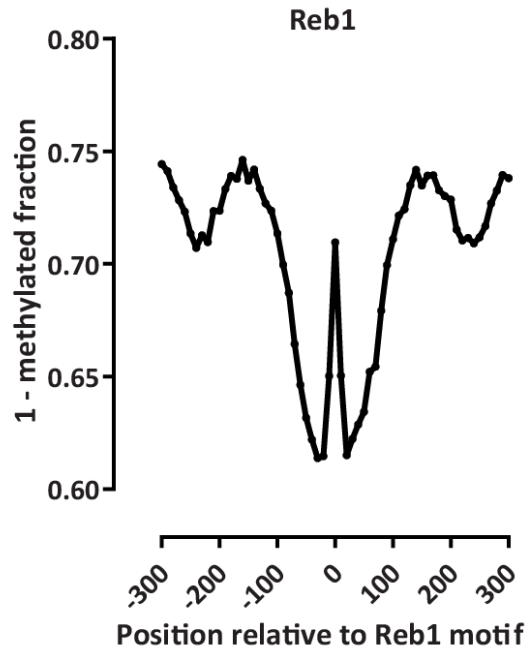
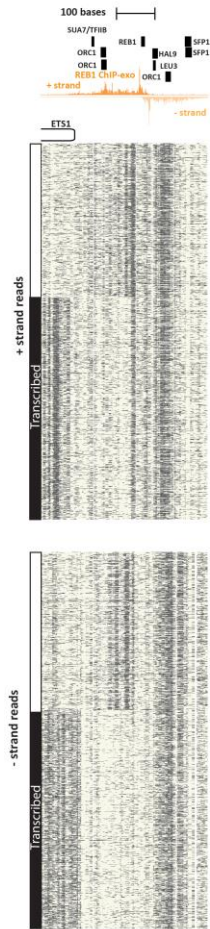


NMI: -0.10 0 0.10

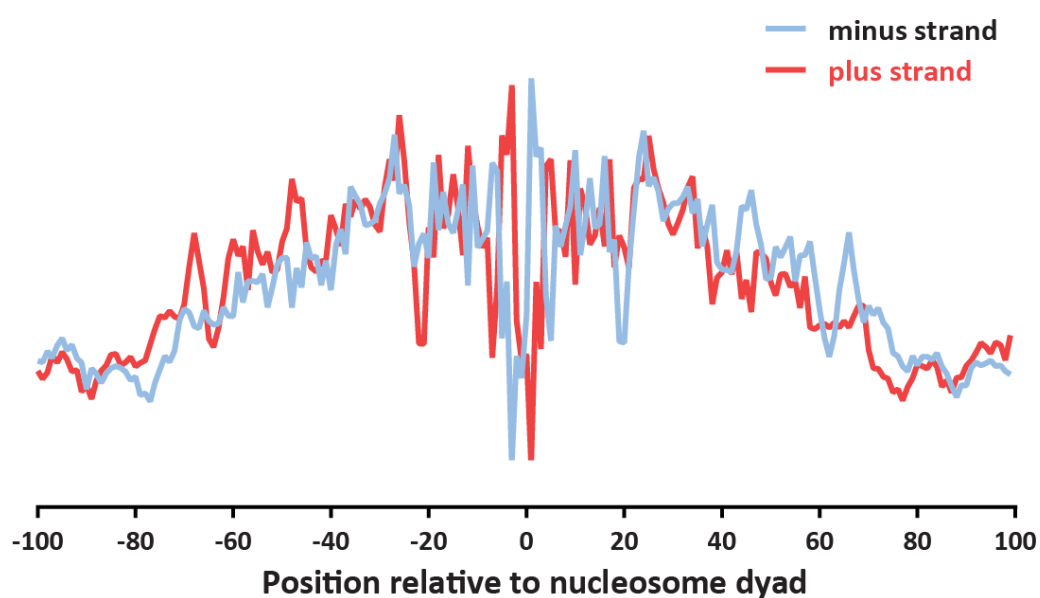
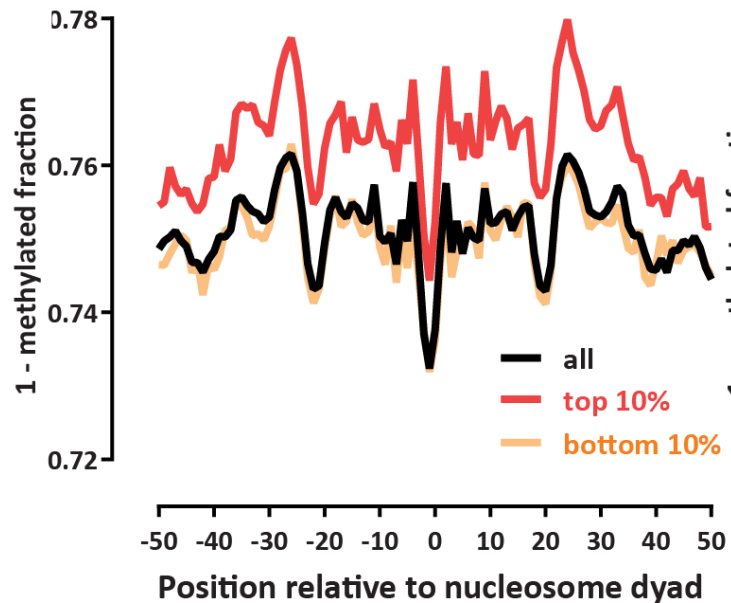
*RDN37-1*



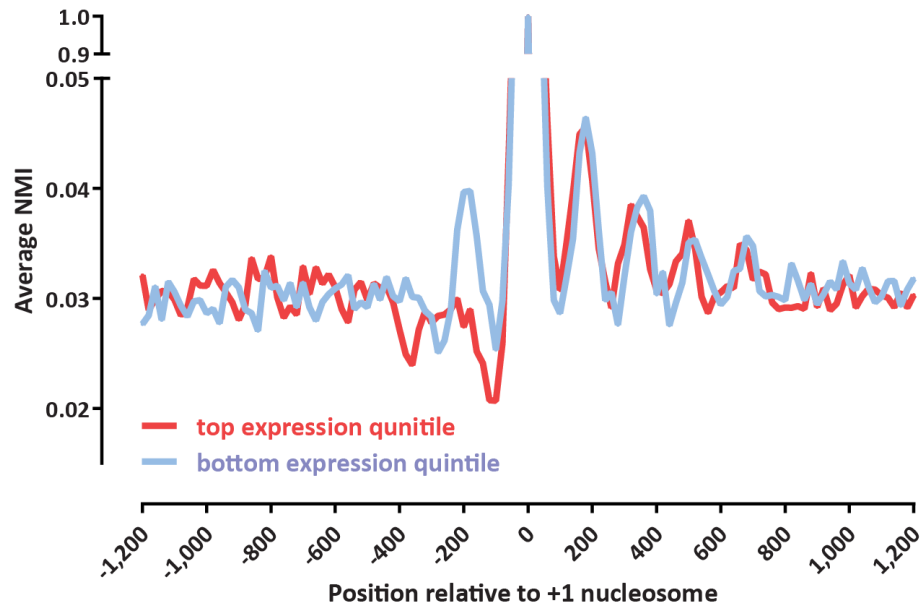
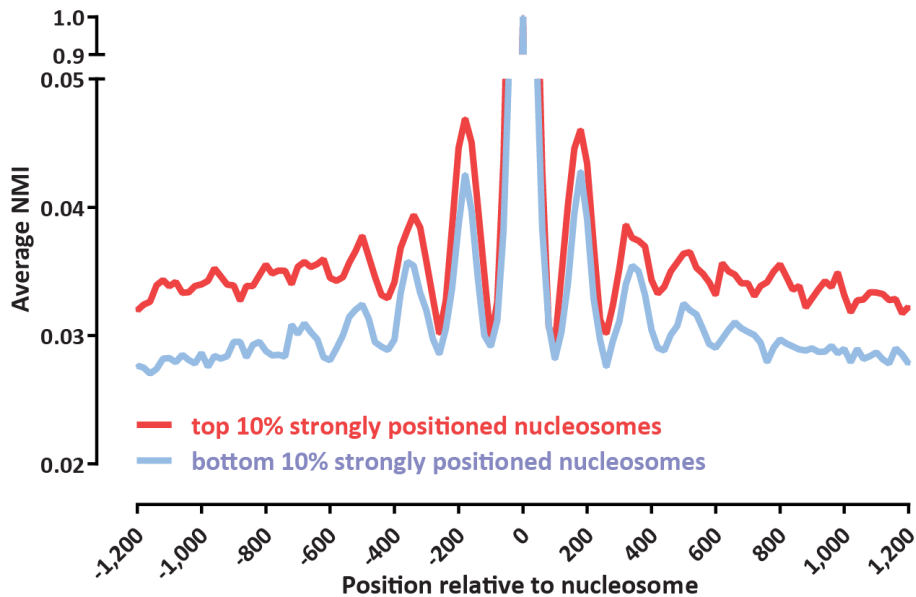
# TRANSCRIPTION FACTOR FOOTPRINTING



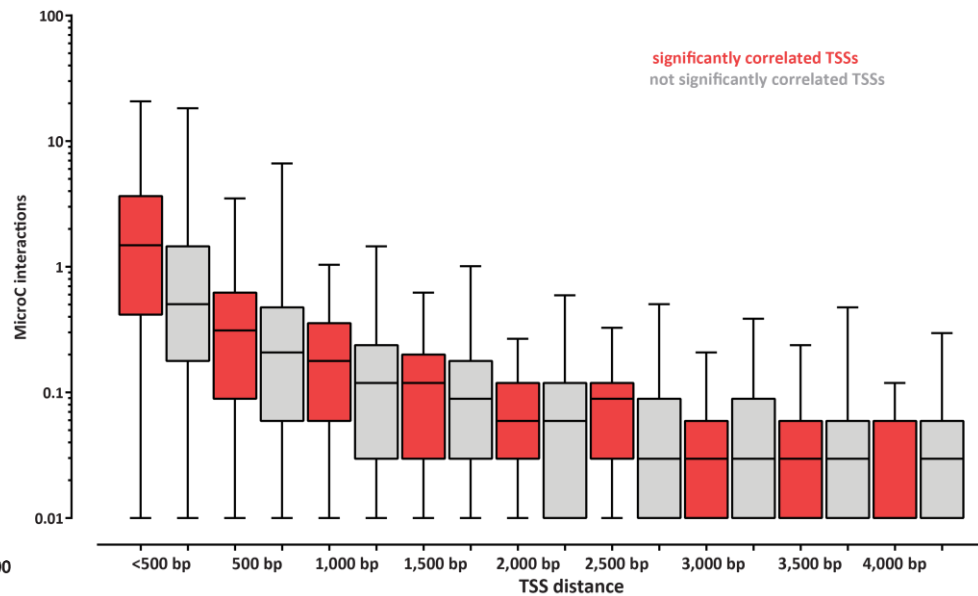
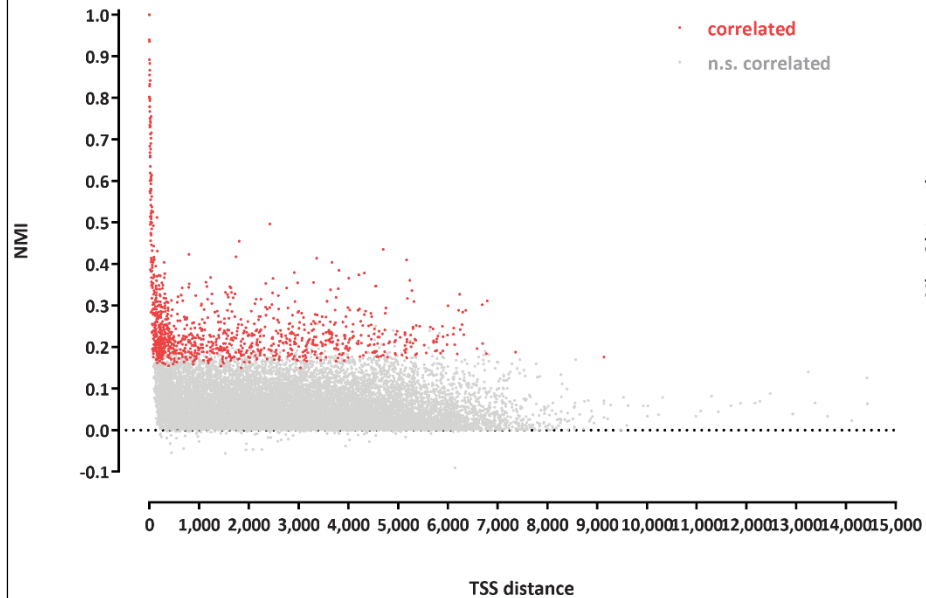
# FINE-SCALE NUCLEOSOME OCCUPANCY FEATURES



# LOCAL ACCESSIBILITY/PROTECTION CORRELATIONS



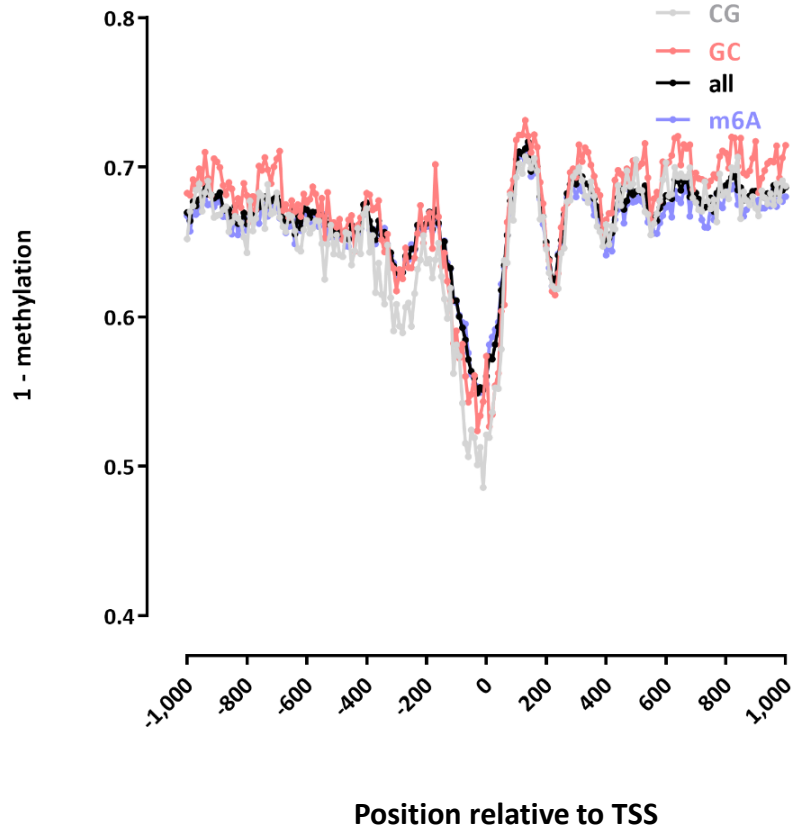
# GLOBAL ACCESSIBILITY/PROTECTION CORRELATIONS



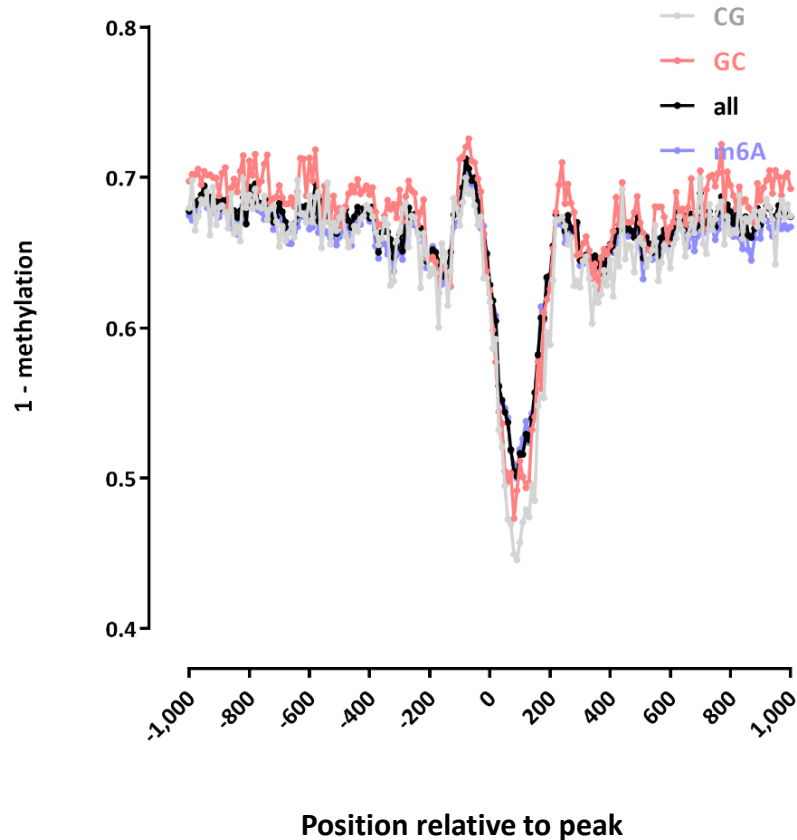


# SMAC-SEQ IN *DROSOPHILA*

## Top 20% expressed genes in S2 cells



## BEAF32 peaks



# ACKNOWLEDGEMENTS

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