

Input DRS data

Control condition

(low or no modifications)

- ↳ Replicate 1
- ↳ Replicate 2
- ↳ Replicate

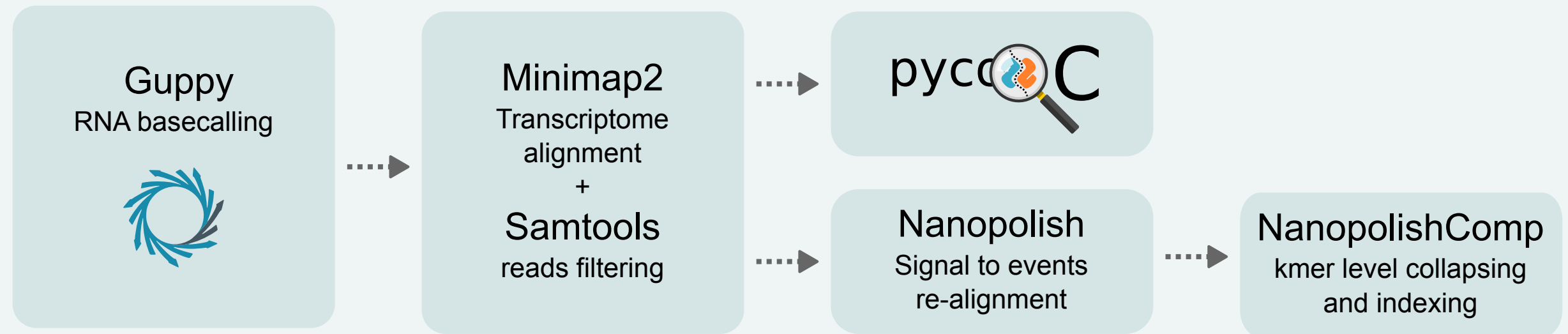
Test condition

(wild type)

- ↳ Replicate 1
- ↳ Replicate 2
- ↳ Replicate ...

A

nextflow Preprocessing pipeline



B

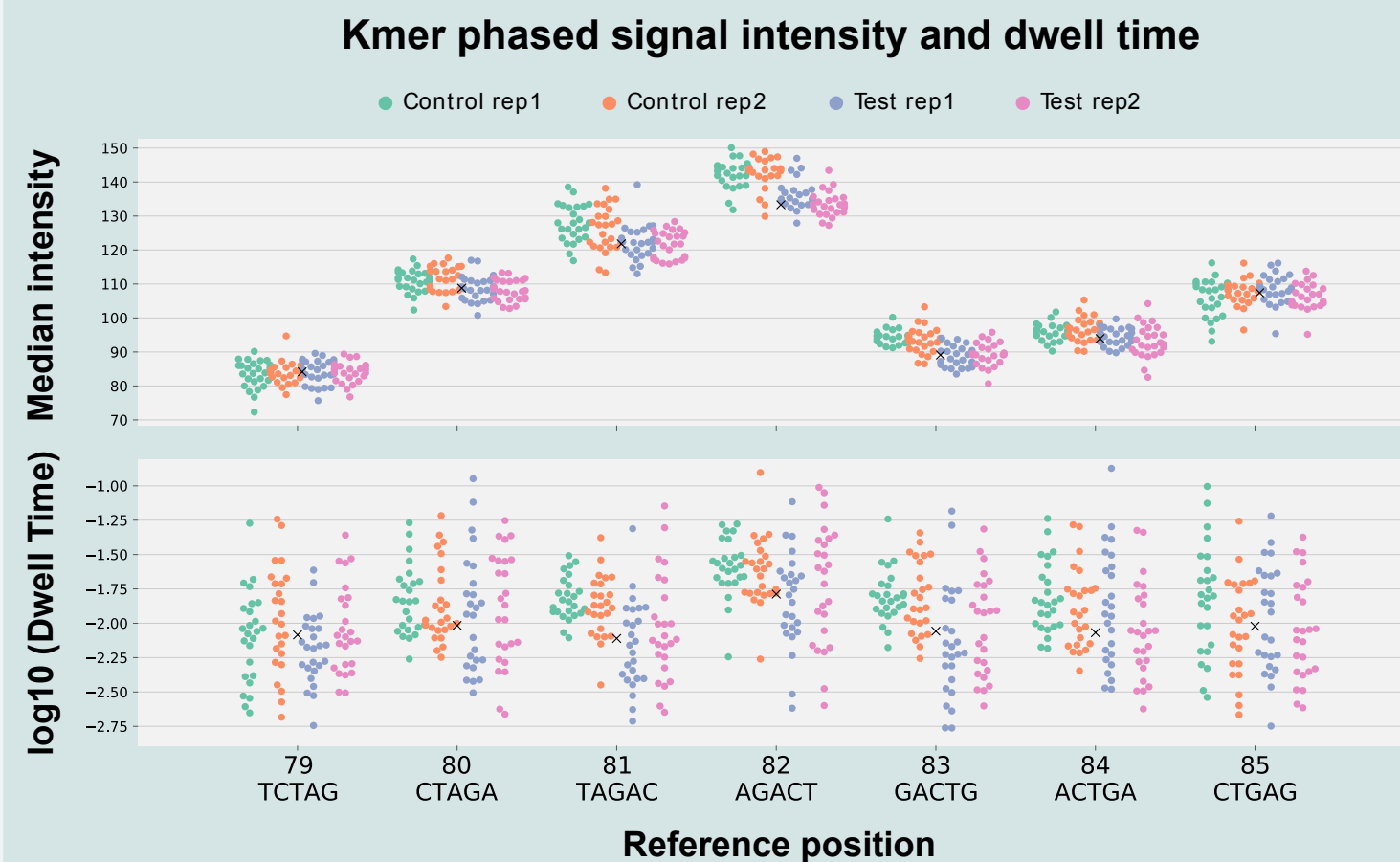
Whitelist

Select reads mapped on transcripts with sufficient coverage



Position-wise data aggregation

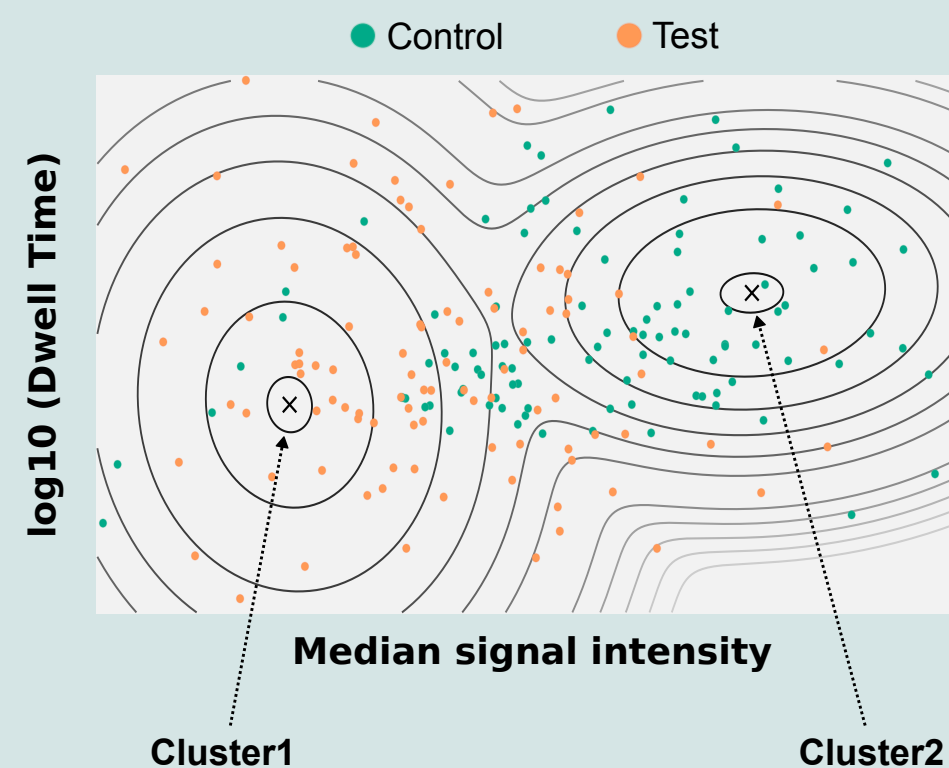
Intensity and dwell time values are collected at transcript position level. The replicate structure is conserved



Statistical pairwise comparison

- Mann-Whitney, Kolmogorov-Smirnov or T test
- Gaussian mixture model clustering + ANOVA or logit regression
- Complex statistical design (multi-factor, batch effects ...)

1 2D GMM clustering



2 Compare GMM clusters against condition labels

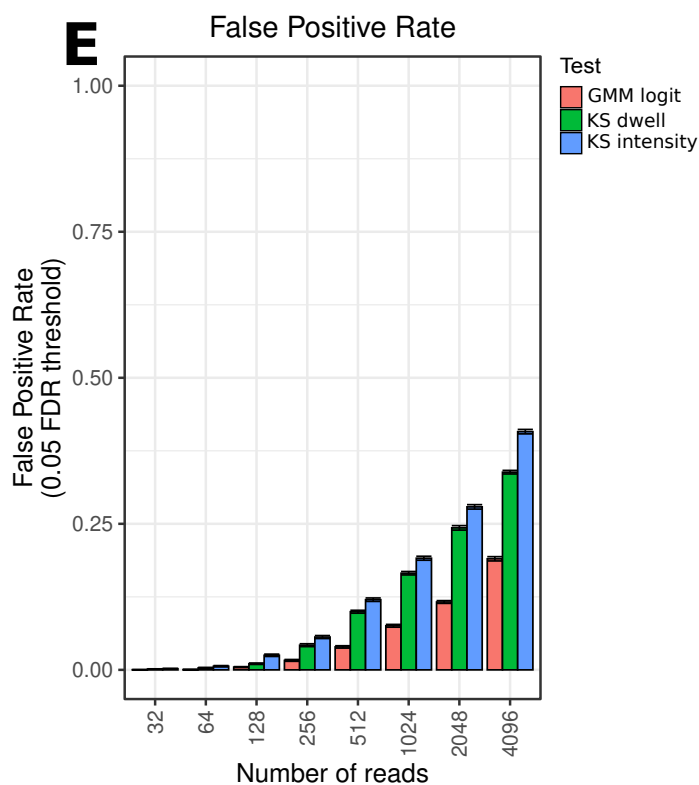
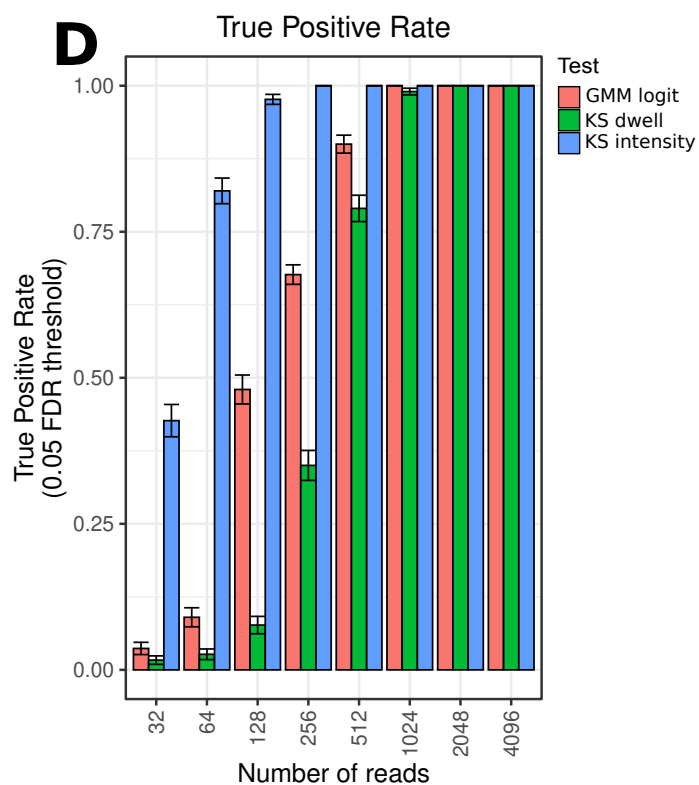
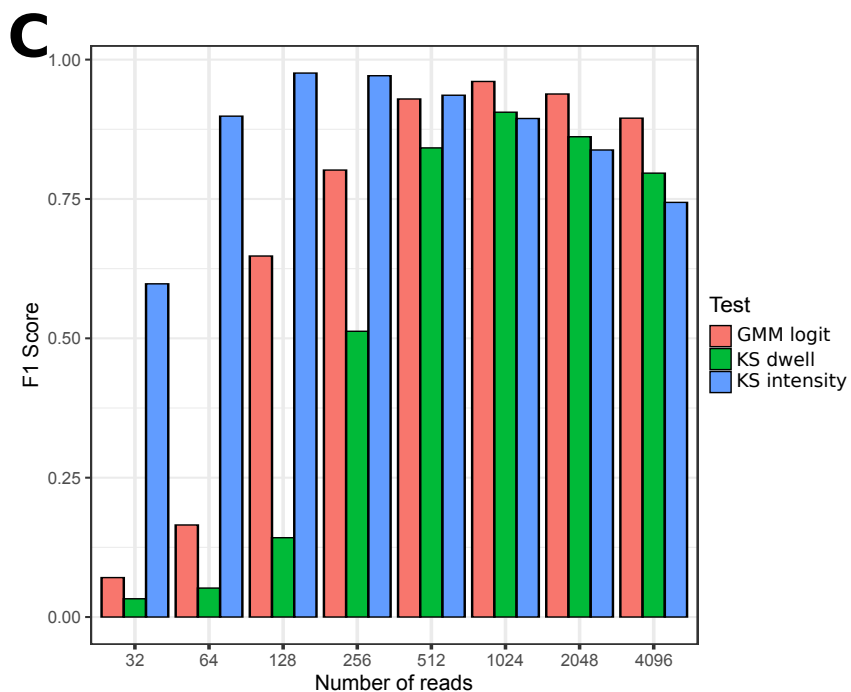
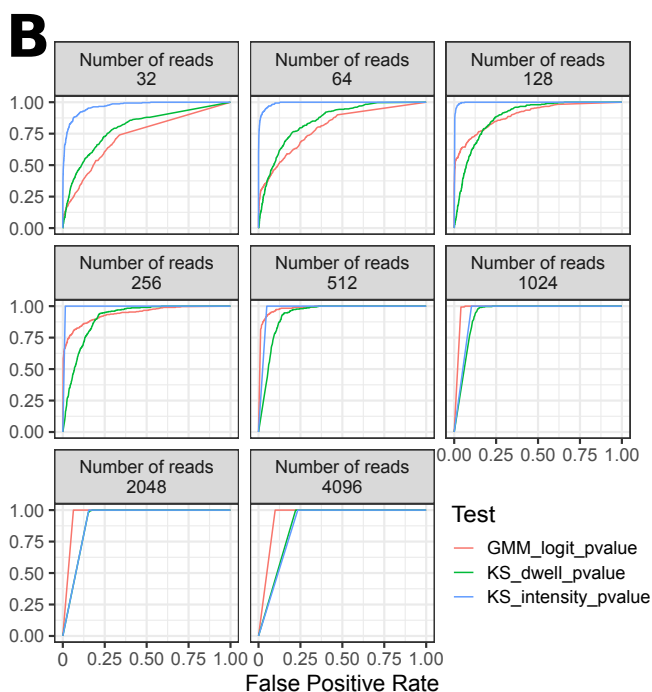
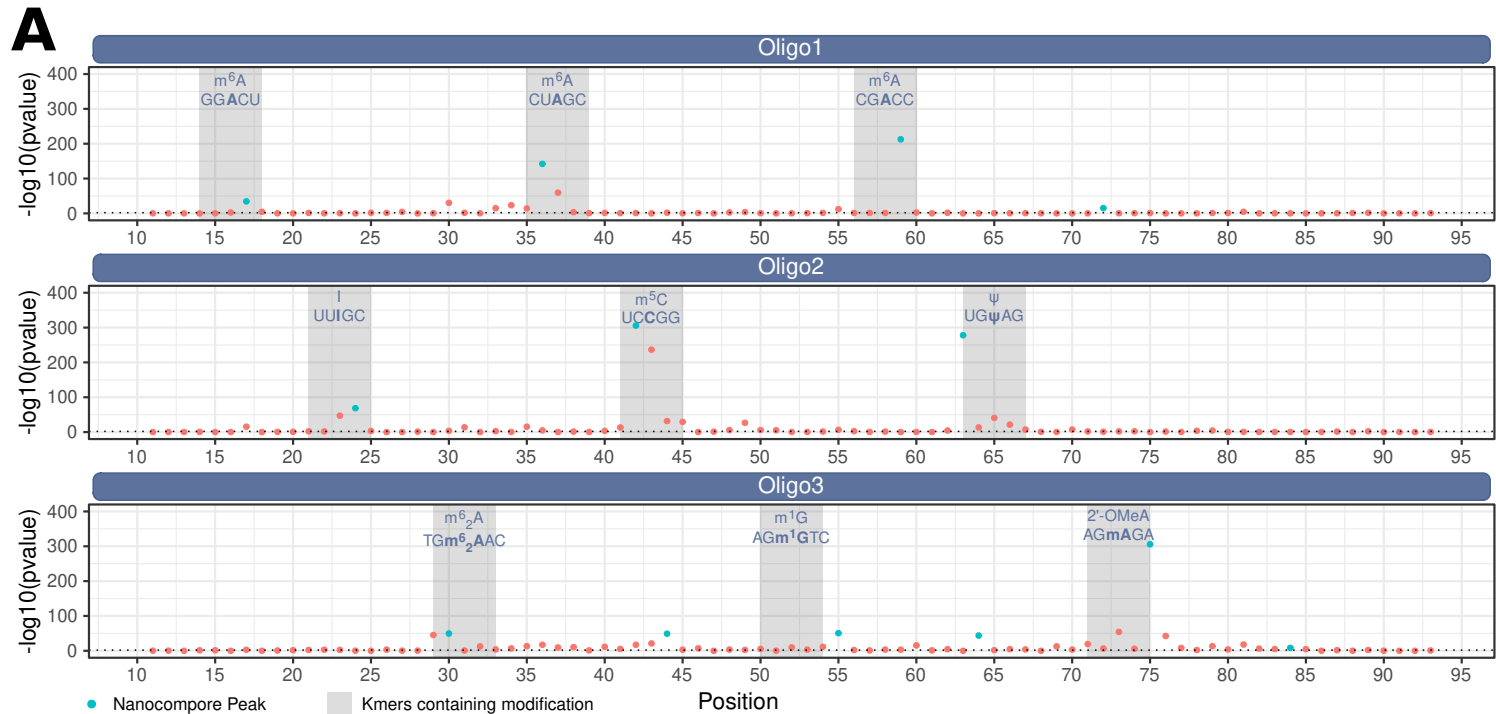
- ANOVA if replicates OR
- Logistic regression

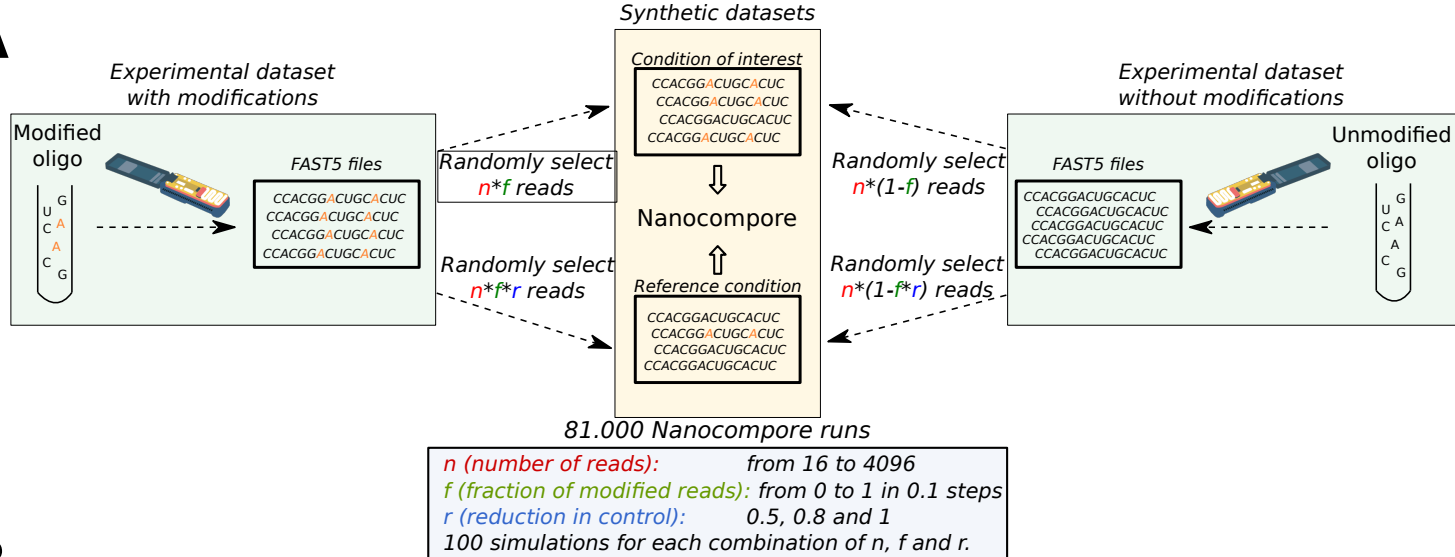
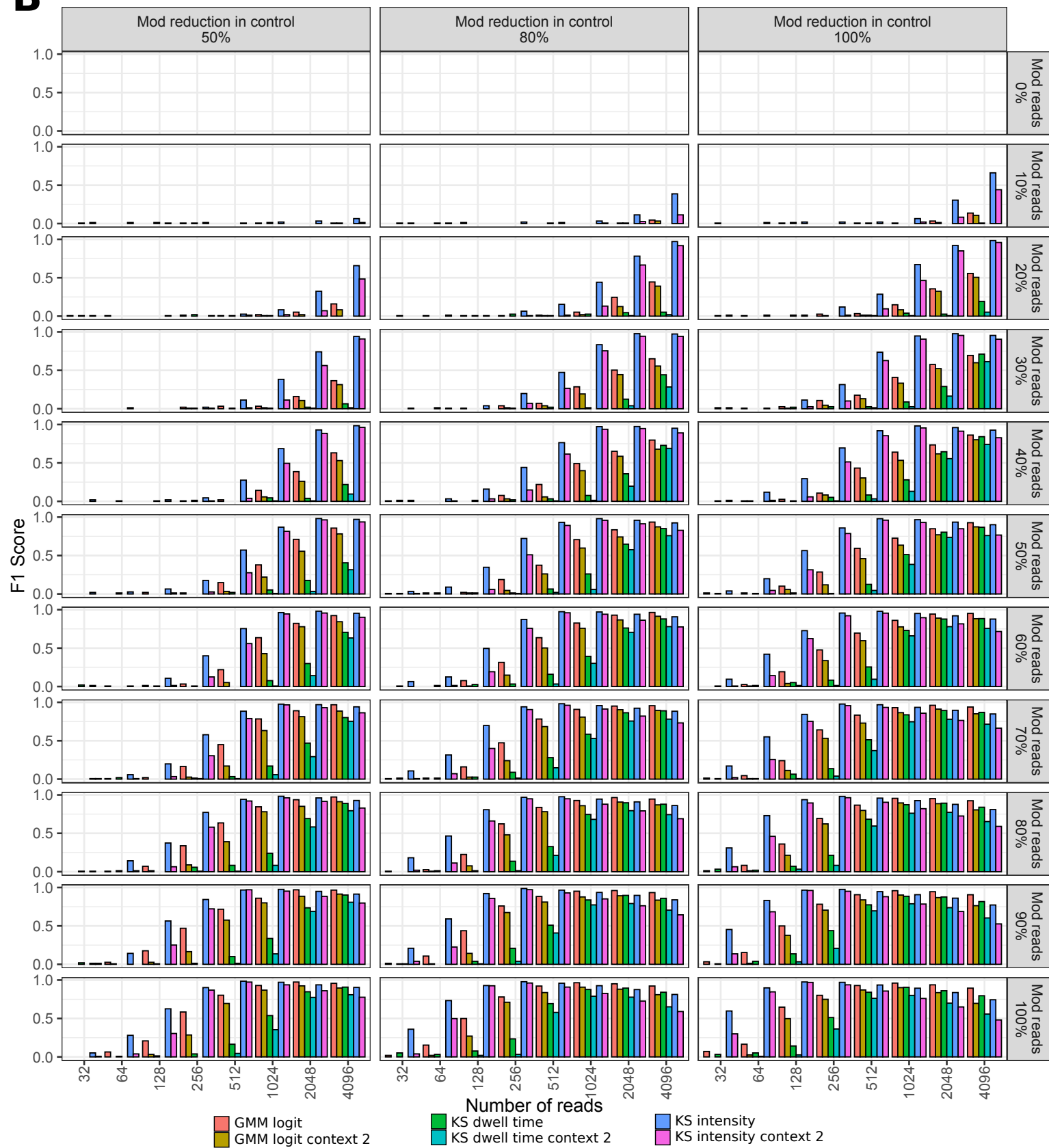
3 Multiple tests correction

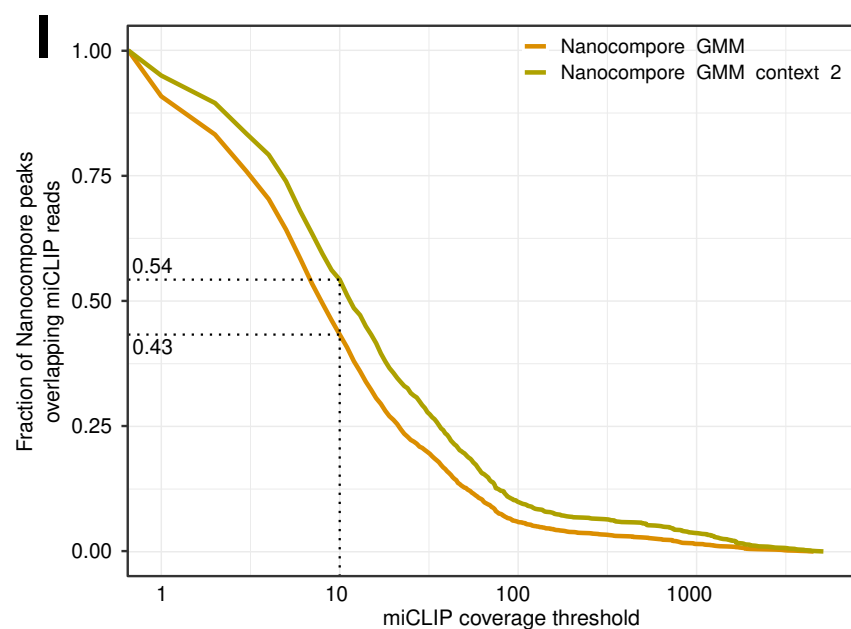
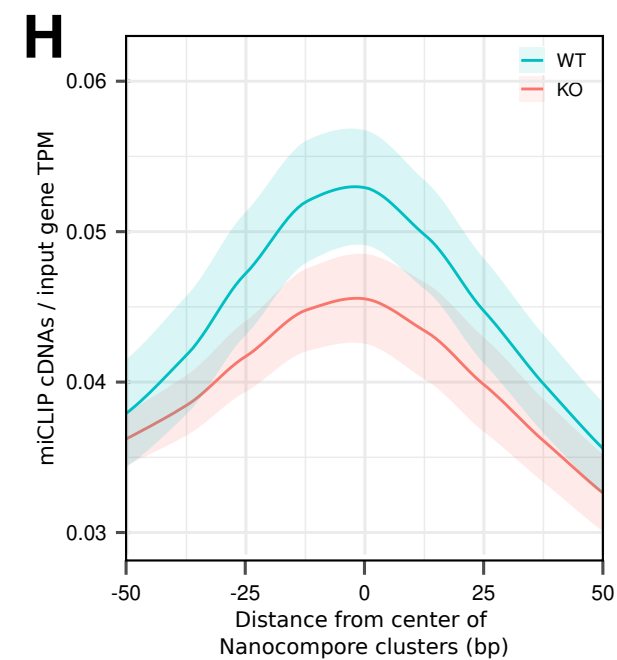
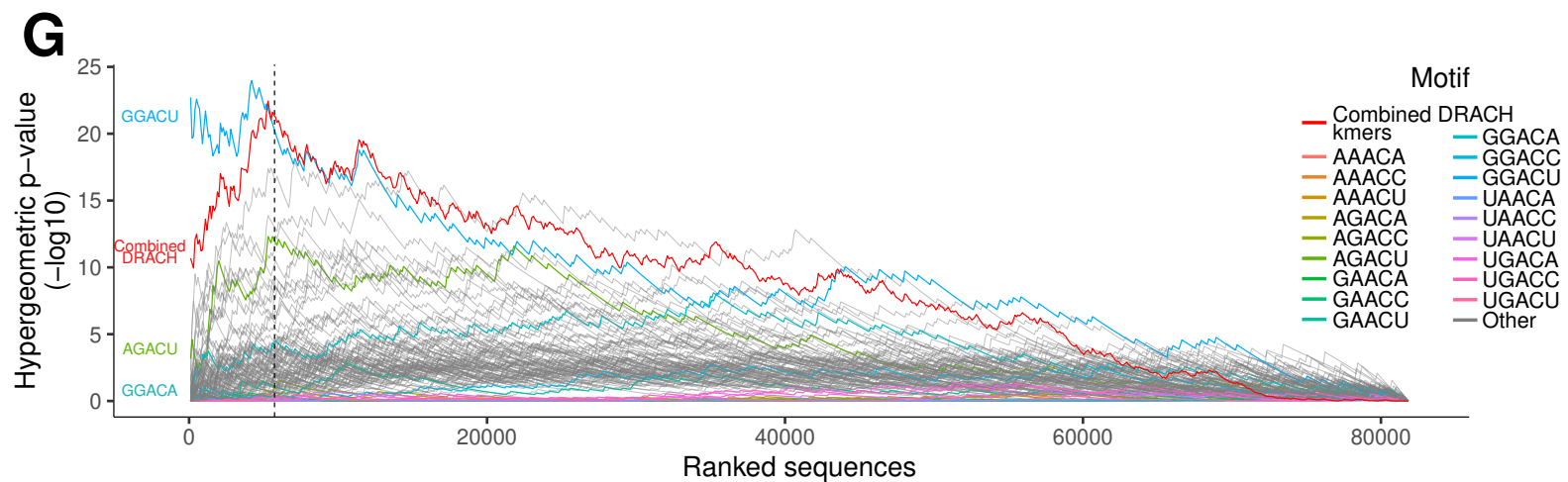
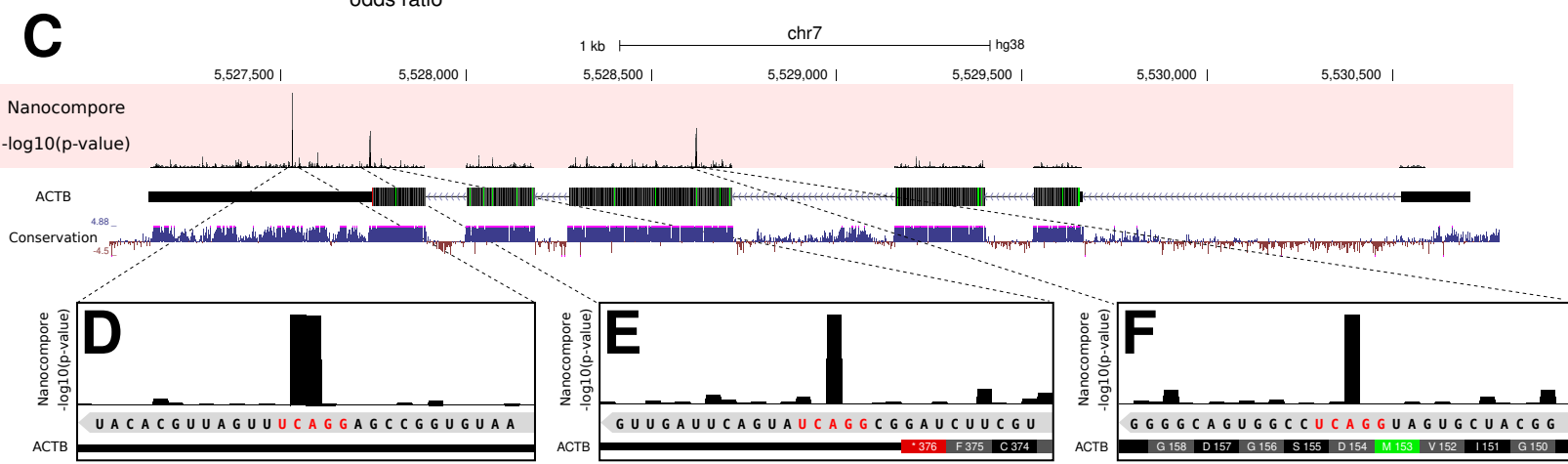
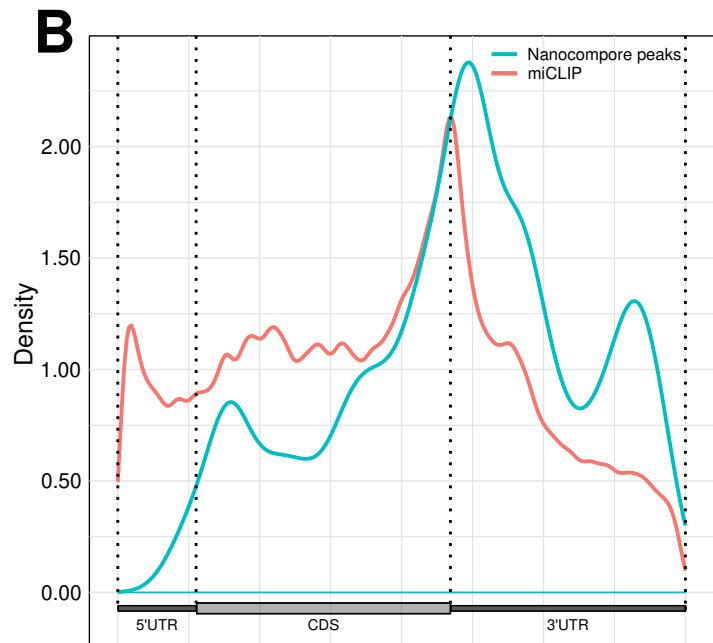
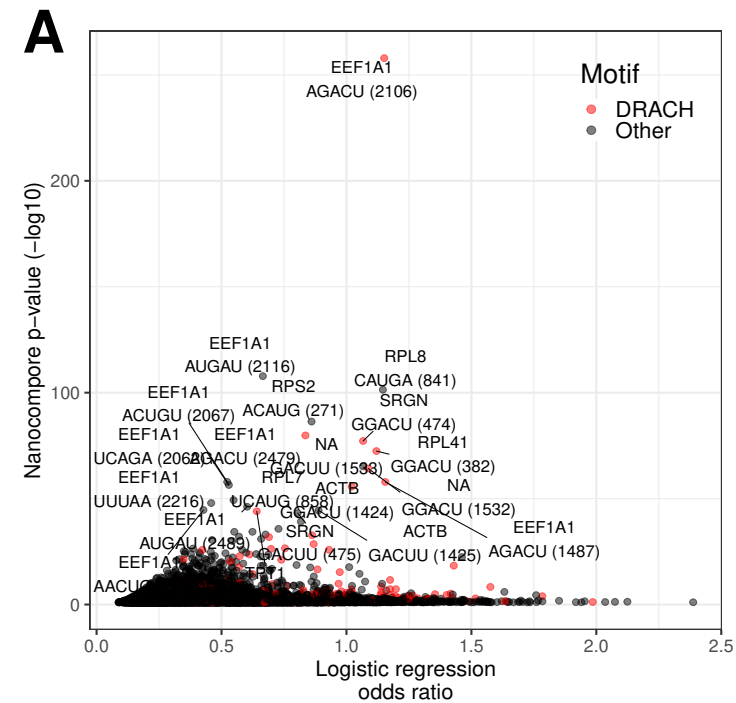
- Benjamini/Hochberg

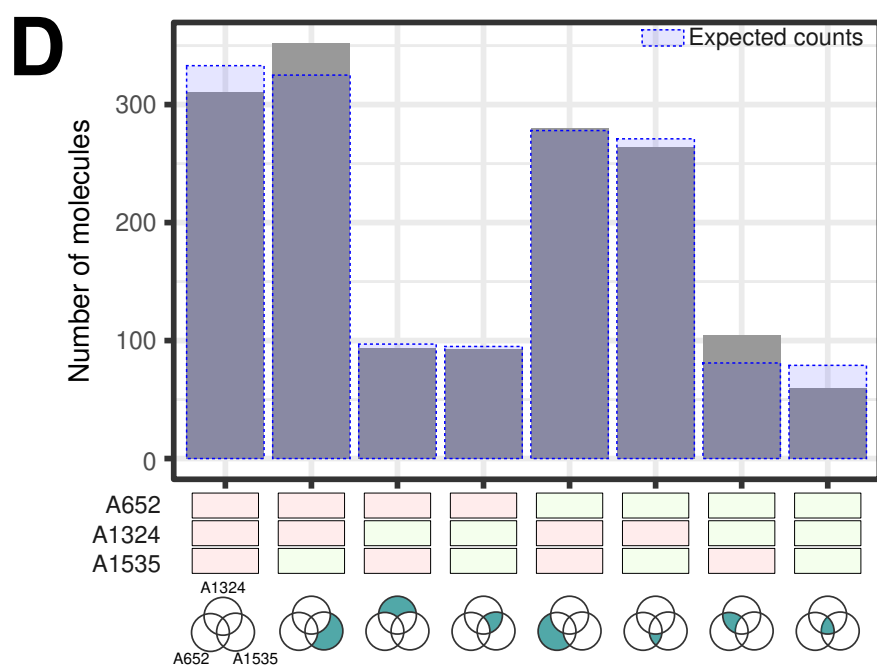
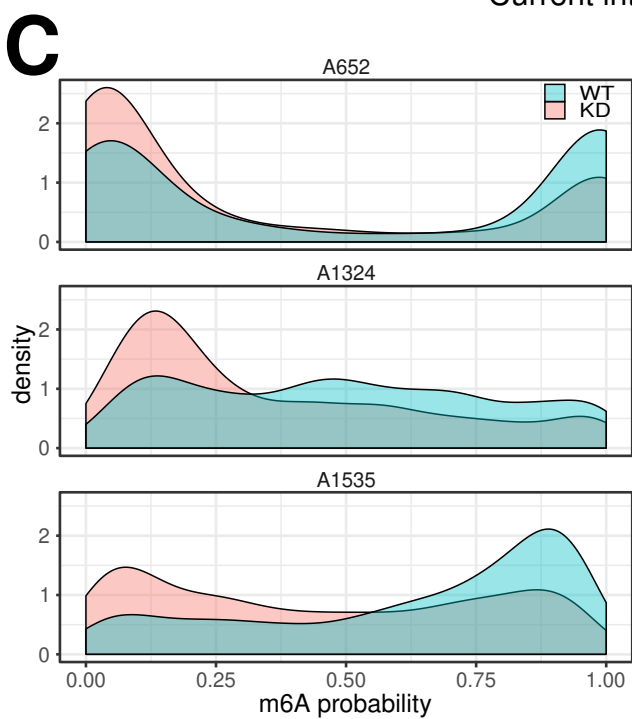
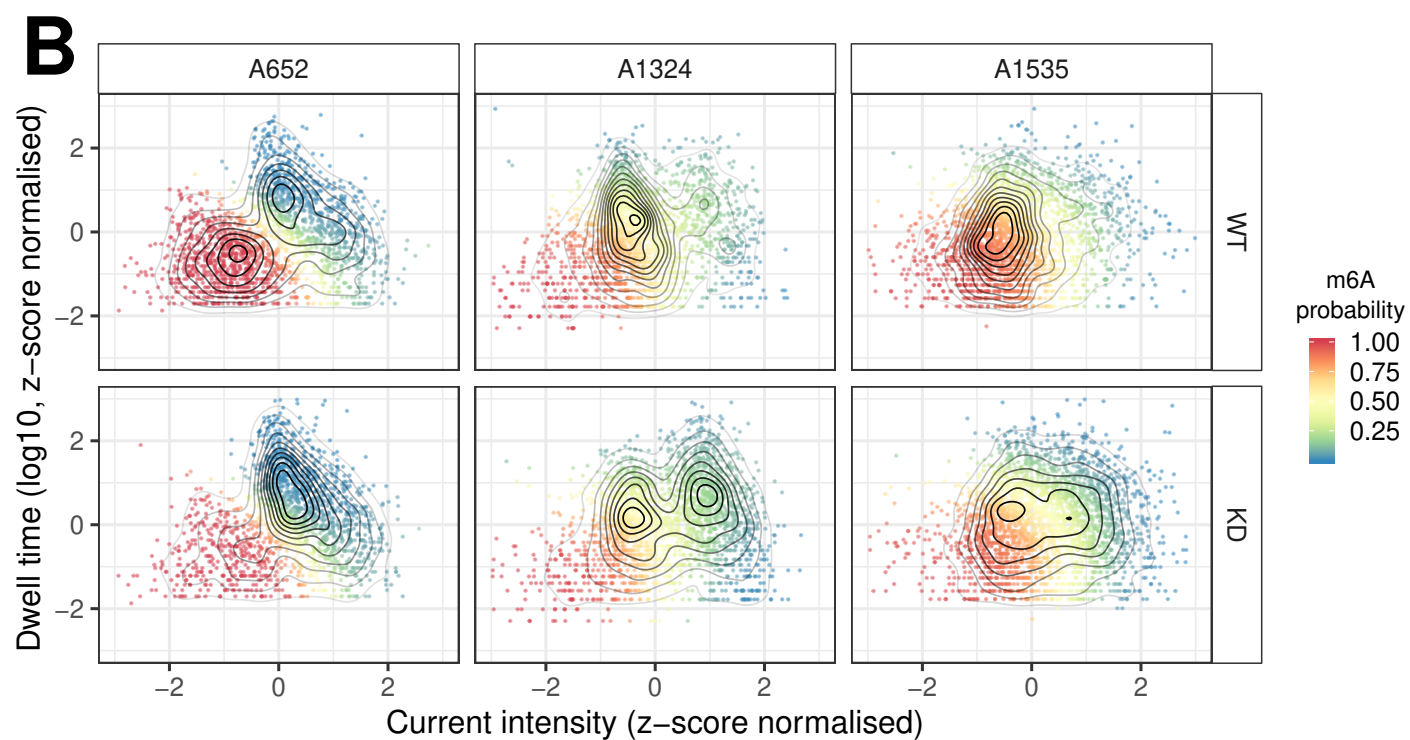
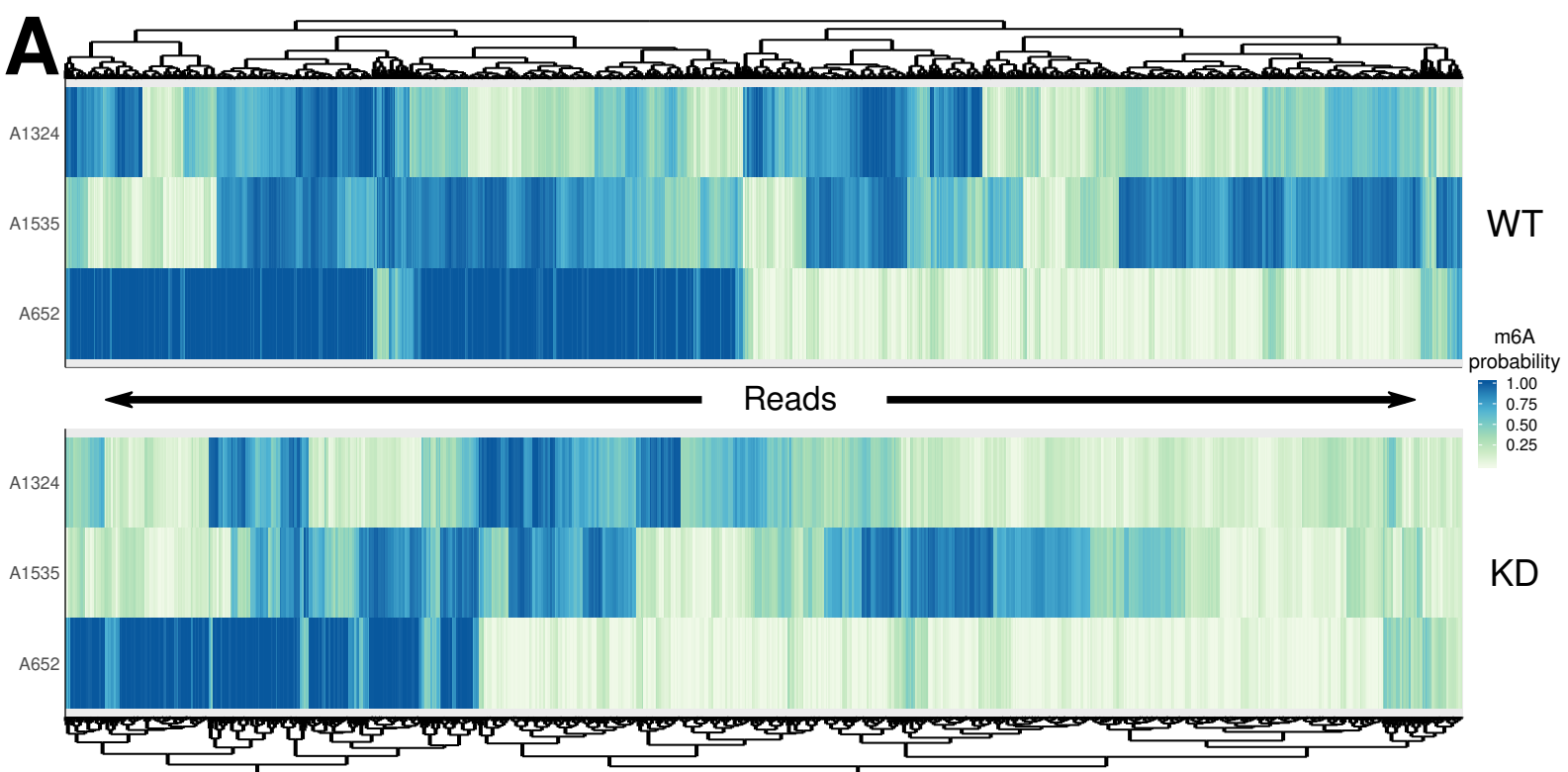
4 Results saving and analysis

- Save data in GDBM database
- Plot data with plotting API
- Export data



A**B**

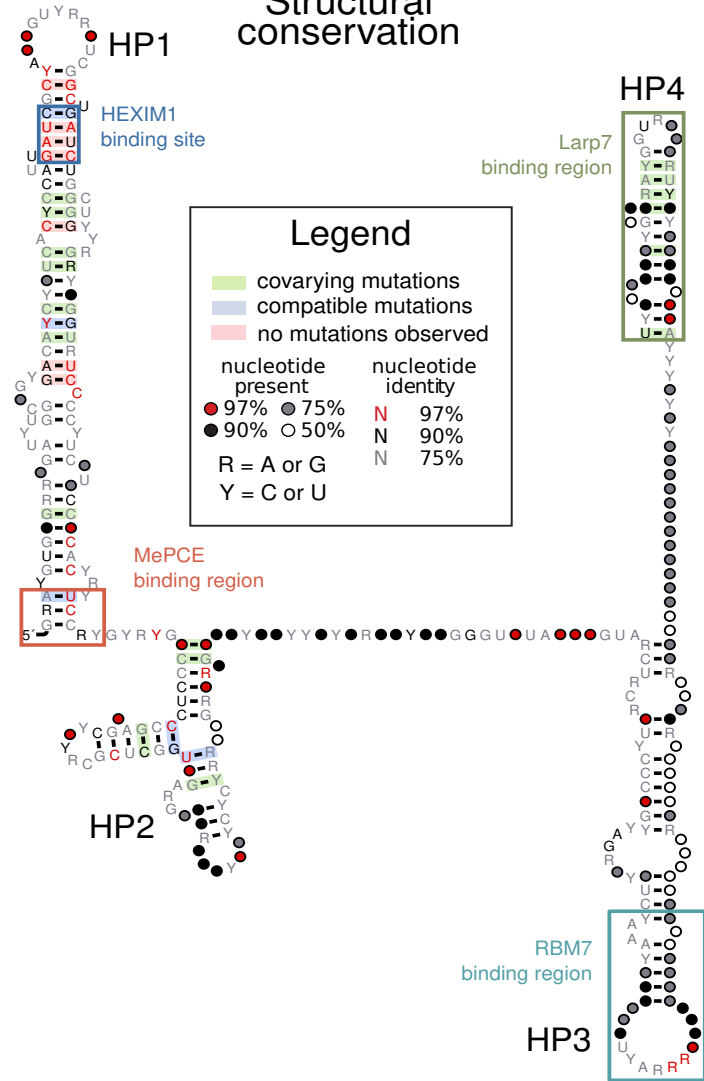




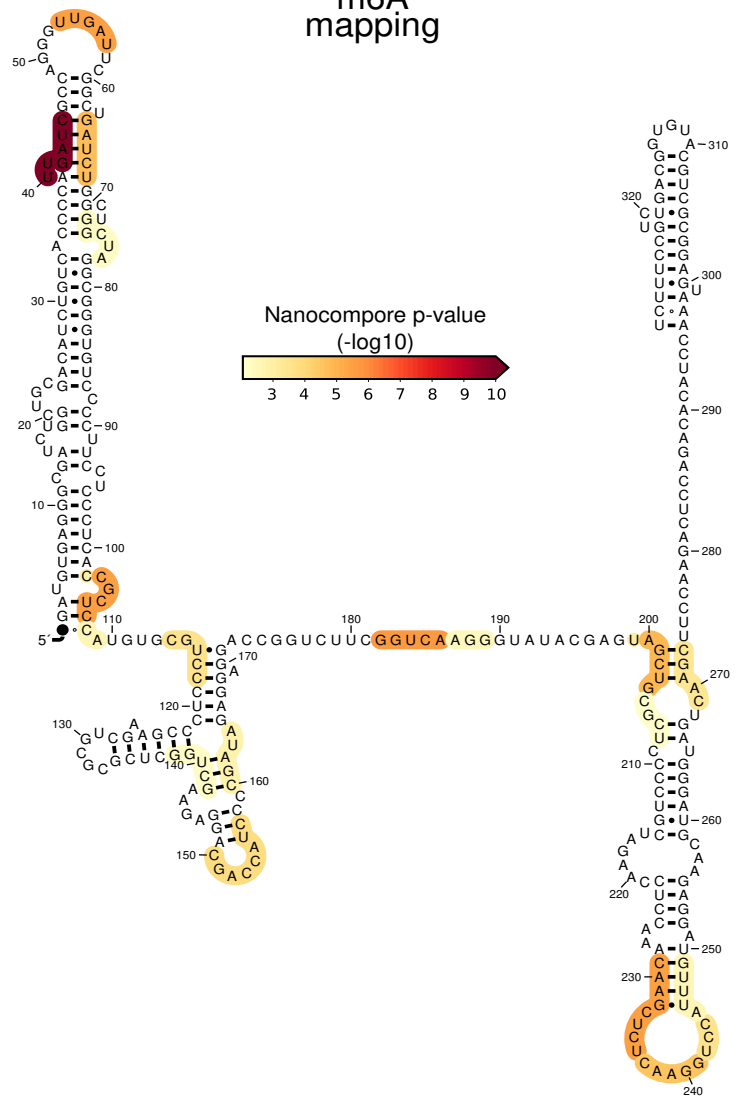
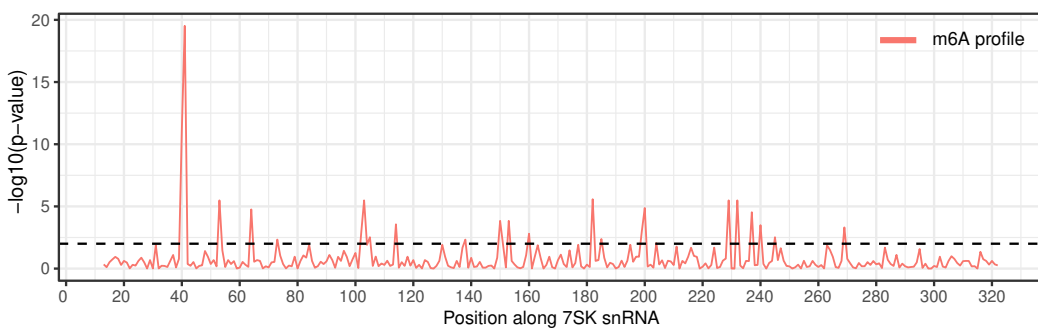
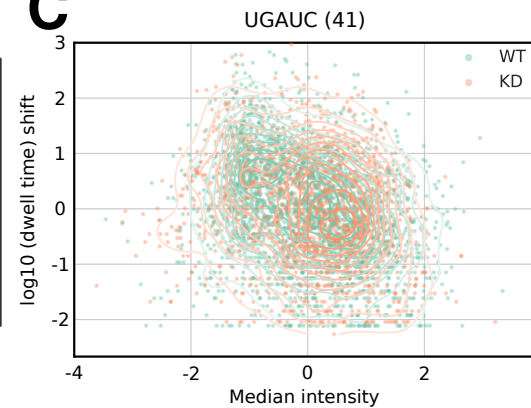
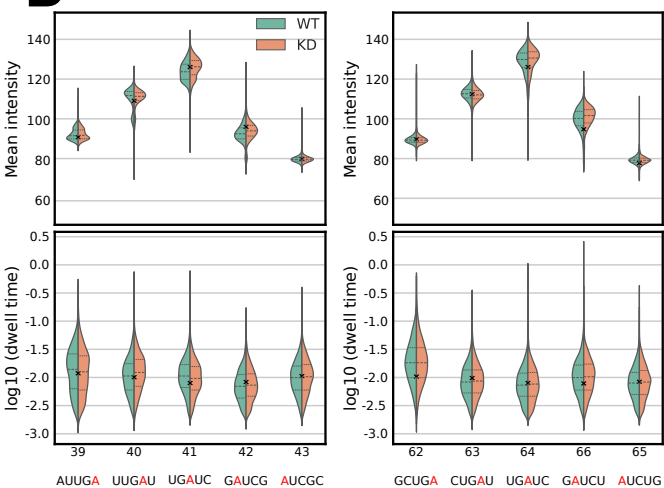
A

snRNA 7SK

Structural conservation



m6A mapping

**B****C****D****E**