

Genome 540 Discussion

Feb. 26th 2026



HW7 Questions?

HW7 Overview

- Take the D-segments identified from HW6
 - a) Generate a new scoring scheme based on log-likelihood ratios
 - b) Generate a simulated read count file
- Run D-segments again, using updated scoring scheme and $S = -D = 5$
- Answer some questions about the comparison of simulated and real data

HW7 Running D-Segments:

New Scheme:

0 = ?

1 = ?

2 = ?

>3 = ?

S = -D = 5

real sequence:

5 {# of segments with score ≥ 5 }

6 {# of segments with score ≥ 6 }

7 {# of segments with score ≥ 7 }

.

.

.

list all the segment score counts for scores
between 5 and 30

(only first/last 3 shown here)

.

.

.

28 {# of segments with score ≥ 28 }

29 {# of segments with score ≥ 29 }

30 {# of segments with score ≥ 30 }

simulated sequence:

5 {# of segments with score ≥ 5 }

6 {# of segments with score ≥ 6 }

7 {# of segments with score ≥ 7 }

.

.

.

list all the segment score counts for scores
between 5 and 30

(only first/last 3 shown here)

.

.

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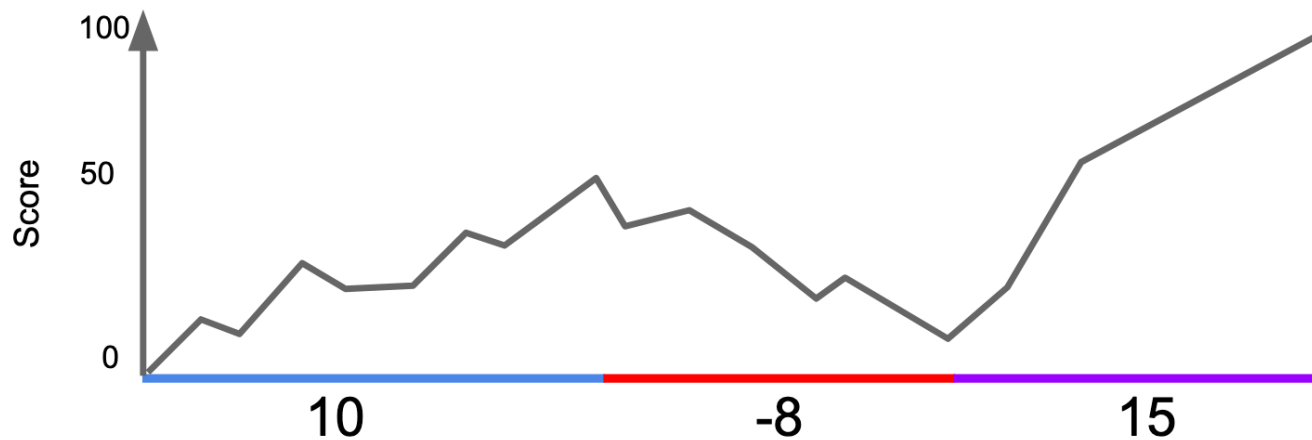
28 {# of segments with score ≥ 28 }

29 {# of segments with score ≥ 29 }

30 {# of segments with score ≥ 30 }

HW7 Running D-Segments:

As you find D-segments, you can add to the histogram:



5: 2
6: 2
7: 2
8: 2
9: 2
10: 2
11: 1
12: 1
13: 1
14: 1
15: 1
16: 0
17: 0
...
30: 0

HW7: BG Distribution

Finally, we want to understand the shape of the BG distribution:

Ratios of simulated data:

$N_seg(5)/N_seg(6)$ {# of segments with score ≥ 5 / # of segments with score ≥ 6 }

$N_seg(6)/N_seg(7)$ {# of segments with score ≥ 6 / # of segments with score ≥ 7 }

$N_seg(7)/N_seg(8)$ {# of segments with score ≥ 7 / # of segments with score ≥ 8 }

.

.

.

list all ratios

(only first/last 3 shown here)

.

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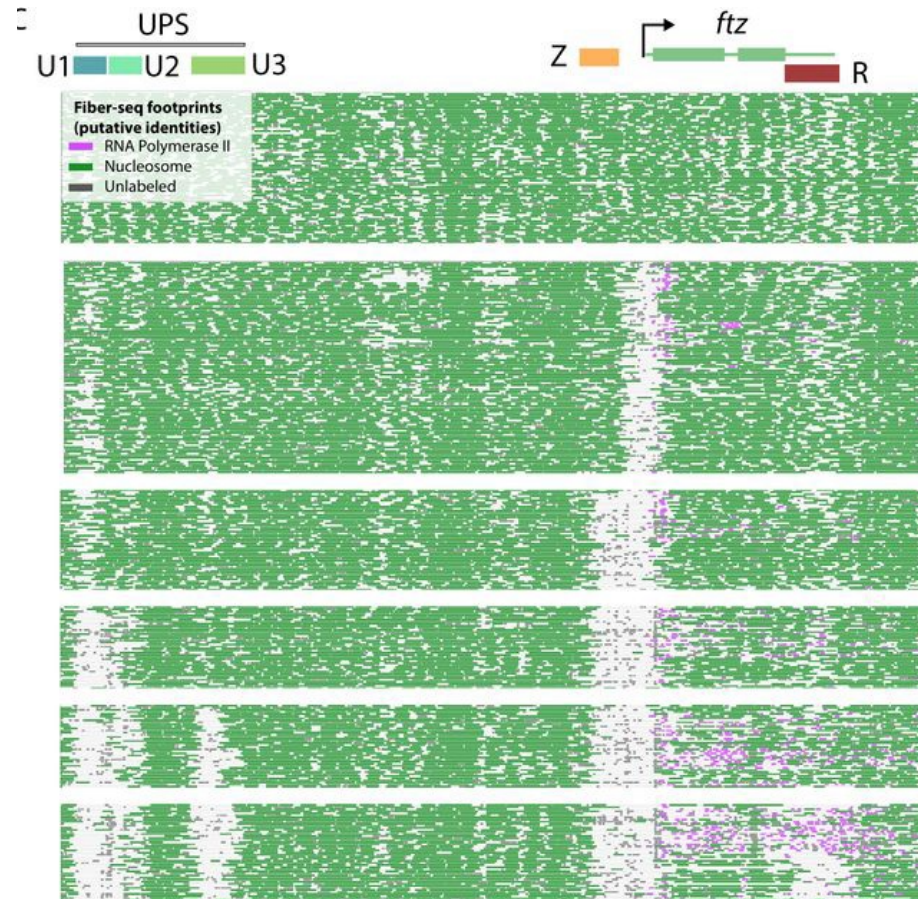
.

$N_seg(27)/N_seg(28)$ {# of segments with score ≥ 27 / # of segments with score ≥ 28 }

$N_seg(28)/N_seg(29)$ {# of segments with score ≥ 28 / # of segments with score ≥ 29 }

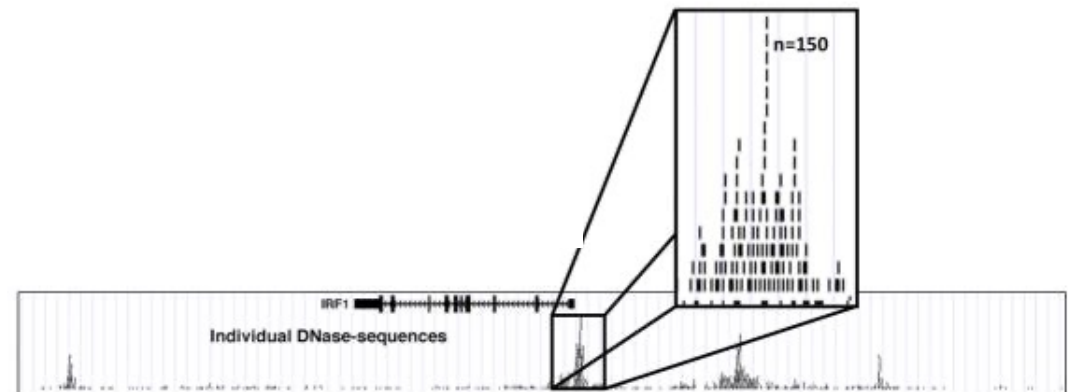
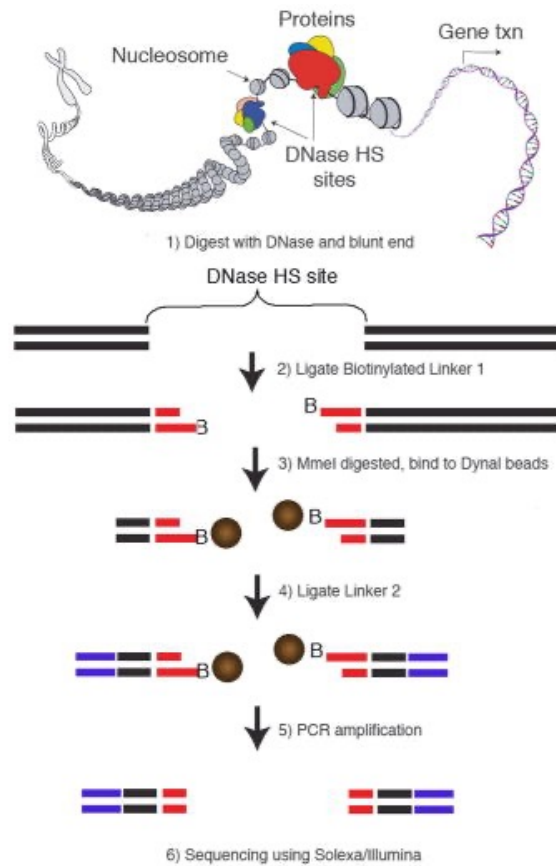
$N_seg(29)/N_seg(30)$ {# of segments with score ≥ 29 / # of segments with score ≥ 30 }

FIBER-HMM



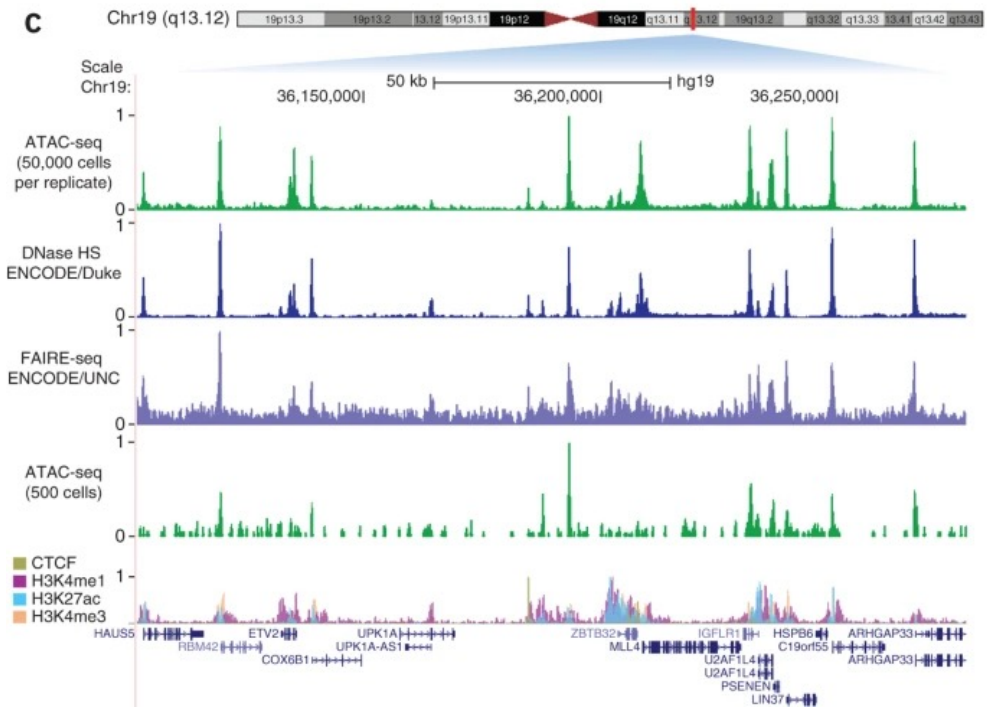
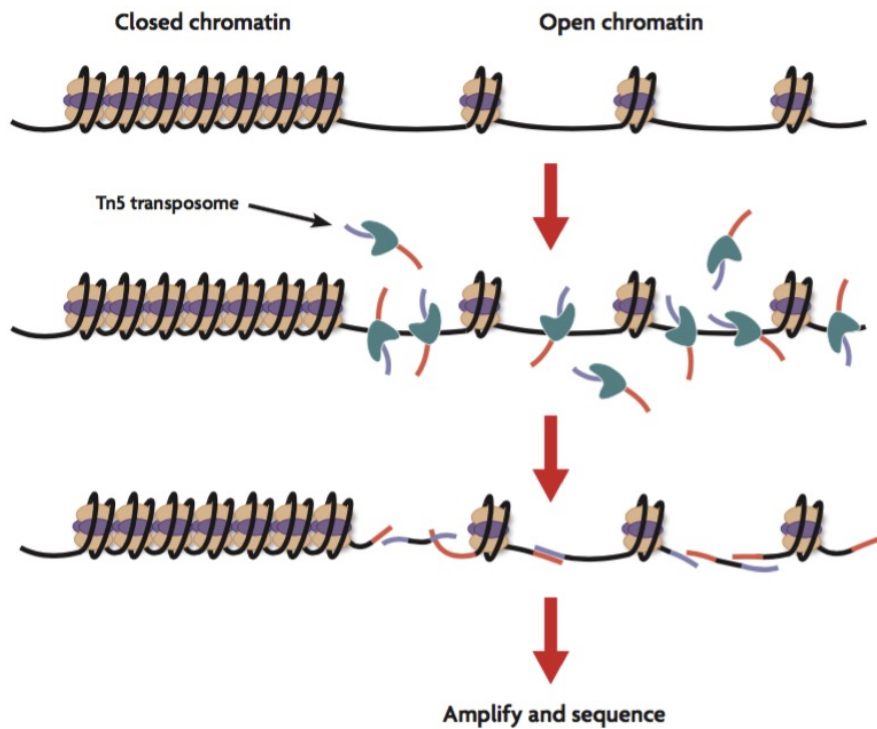
<https://doi.org/10.1101/2025.10.28.685222>

DNase-seq



doi: [10.1101/pdb.prot5384](https://doi.org/10.1101/pdb.prot5384)

ATAC-seq

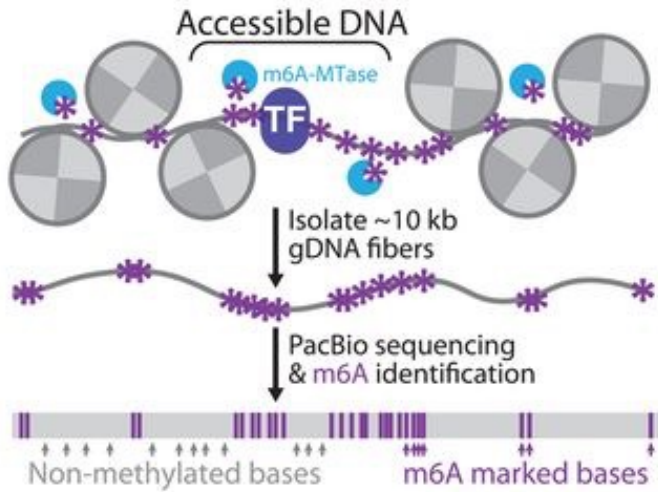


<https://www.activemotif.com/blog-atac-seq>

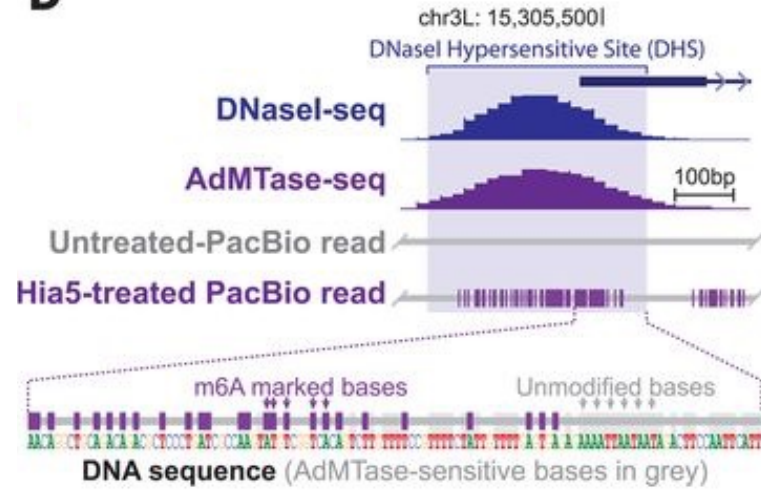
<https://doi.org/10.1038/nmeth.2688>

FIBER-seq

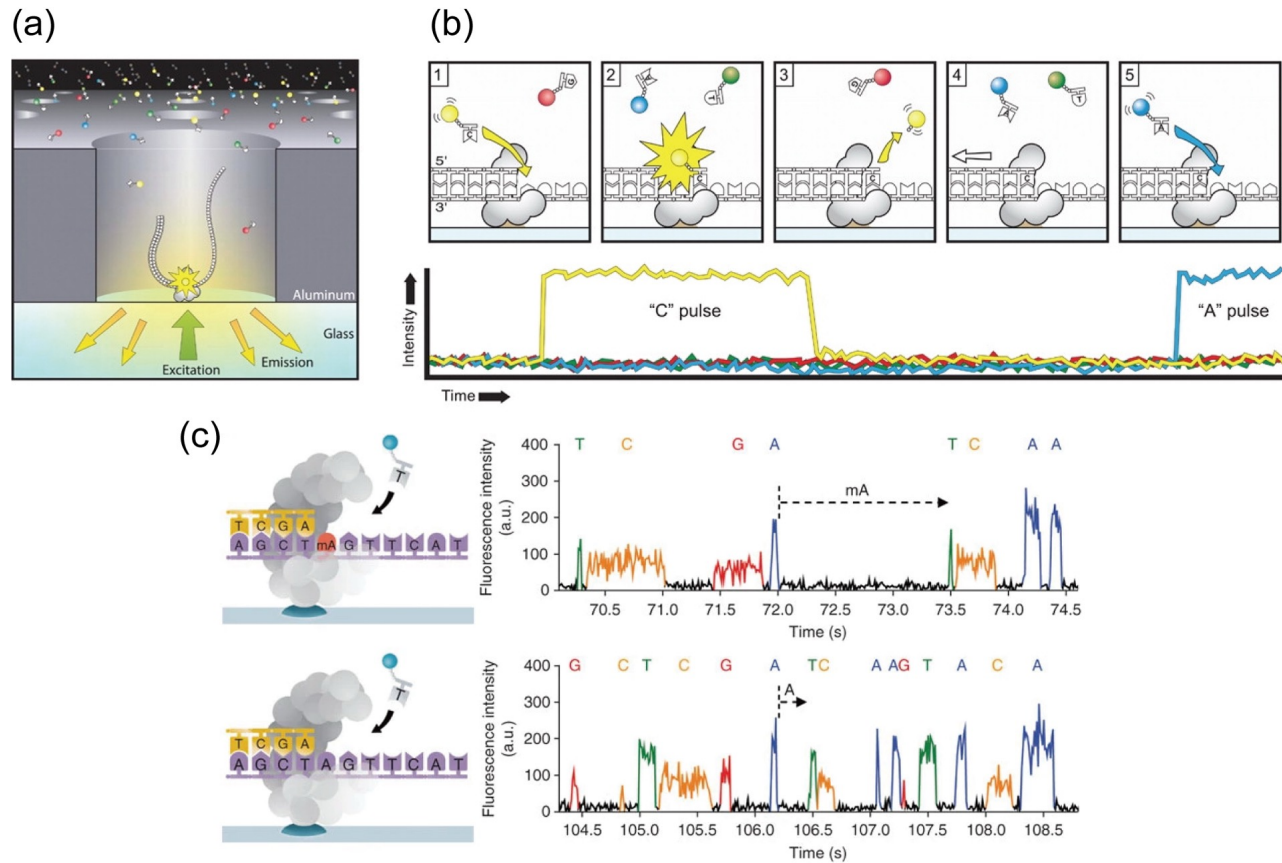
A



D

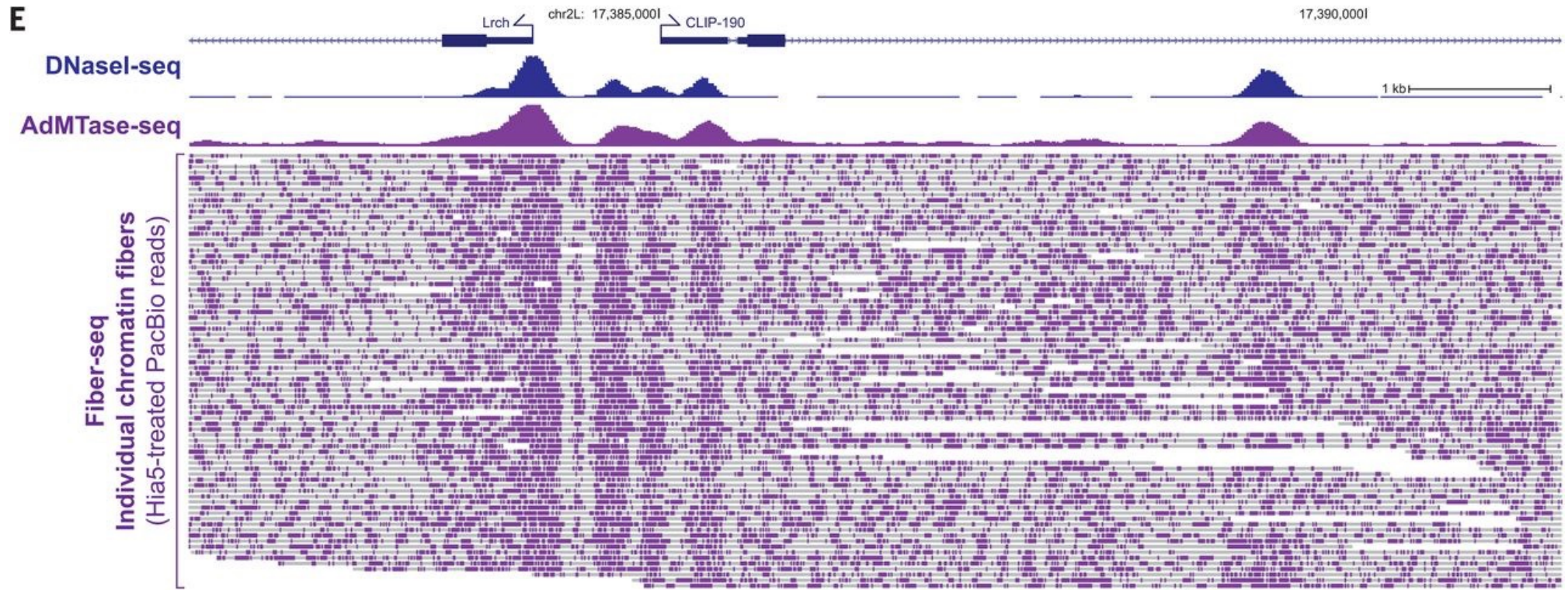


Quick PacBio Aside:



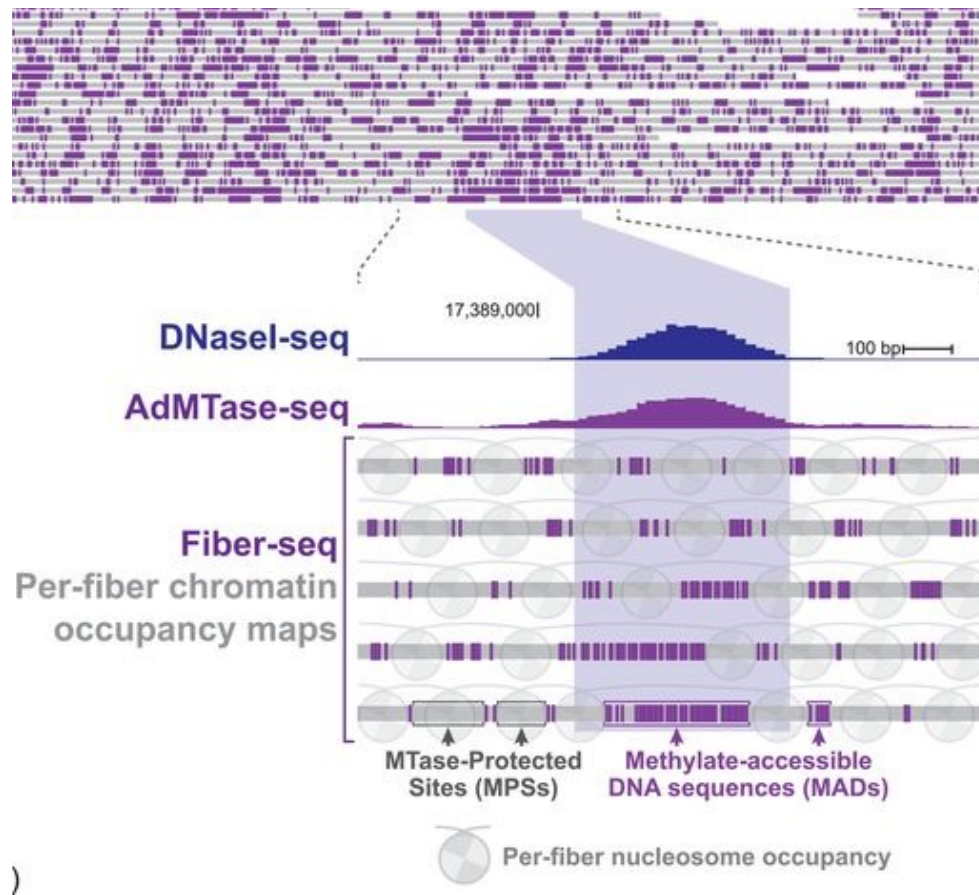
<https://doi.org/10.2142/biophysico.bppb-v19.0032>

Back to FIBER-seq



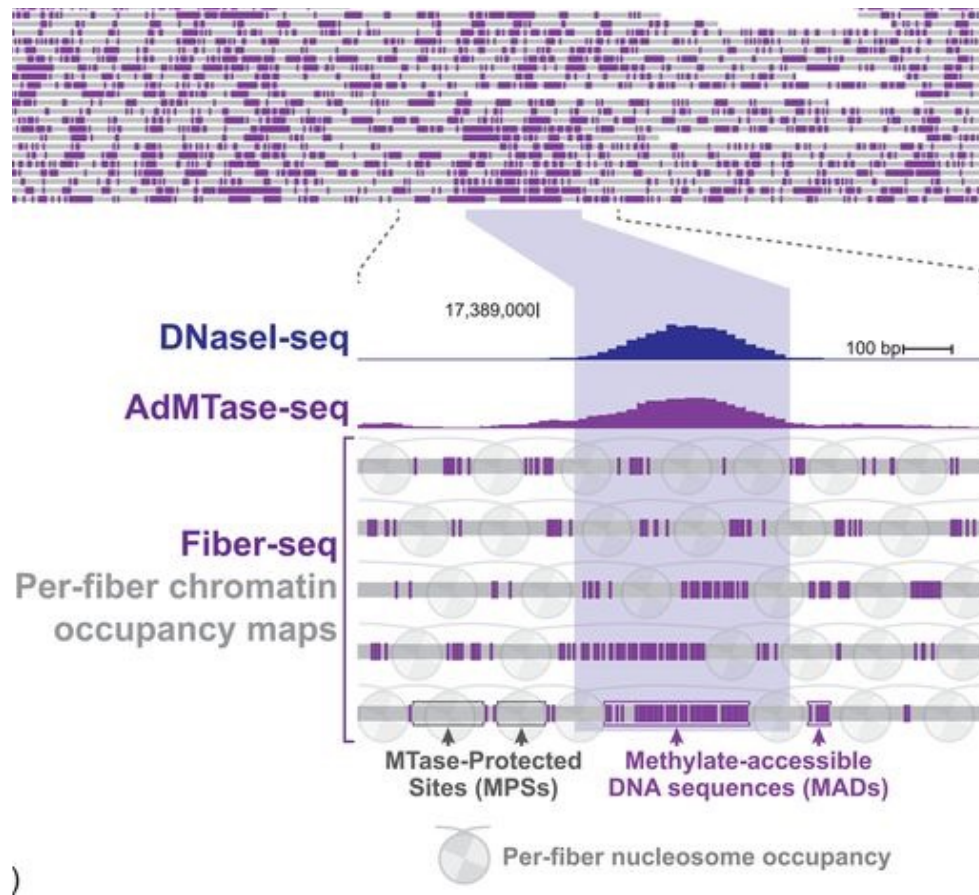
[DOI: 10.1126/science.aaz1646](https://doi.org/10.1126/science.aaz1646)

Back to FIBER-seq



DOI: [10.1126/science.aaz1646](https://doi.org/10.1126/science.aaz1646)

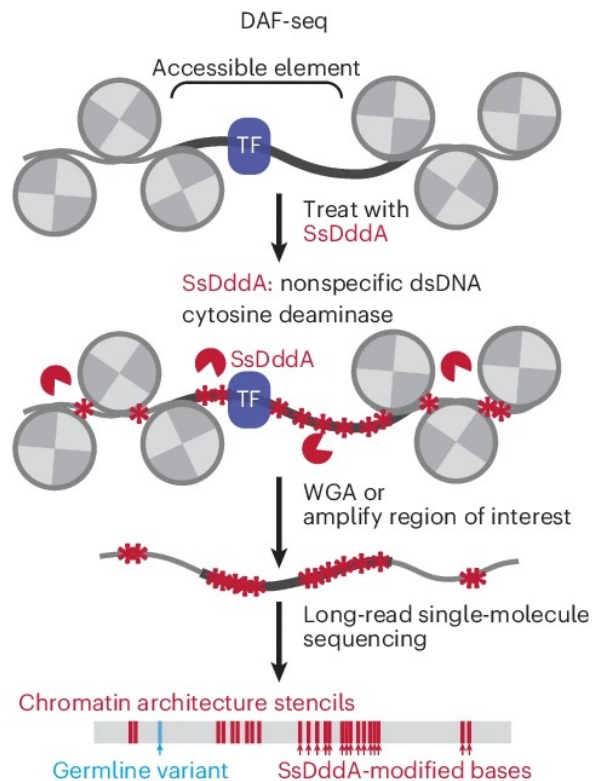
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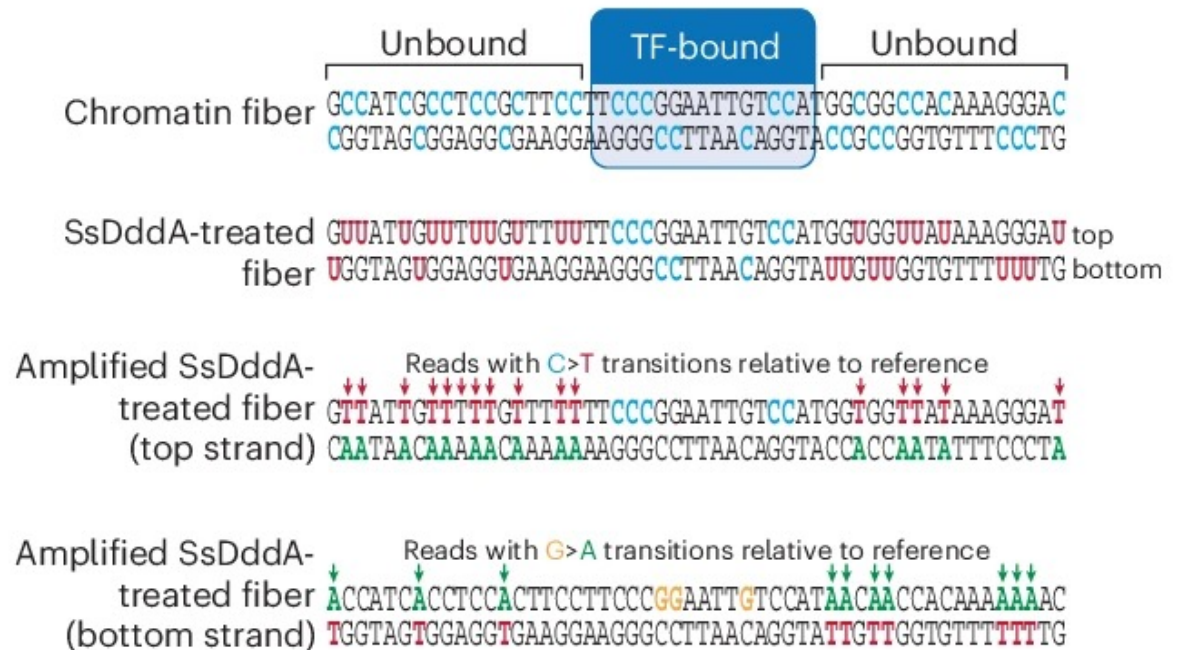
DOI: [10.1126/science.aaz1646](https://doi.org/10.1126/science.aaz1646)

DAF-seq

a

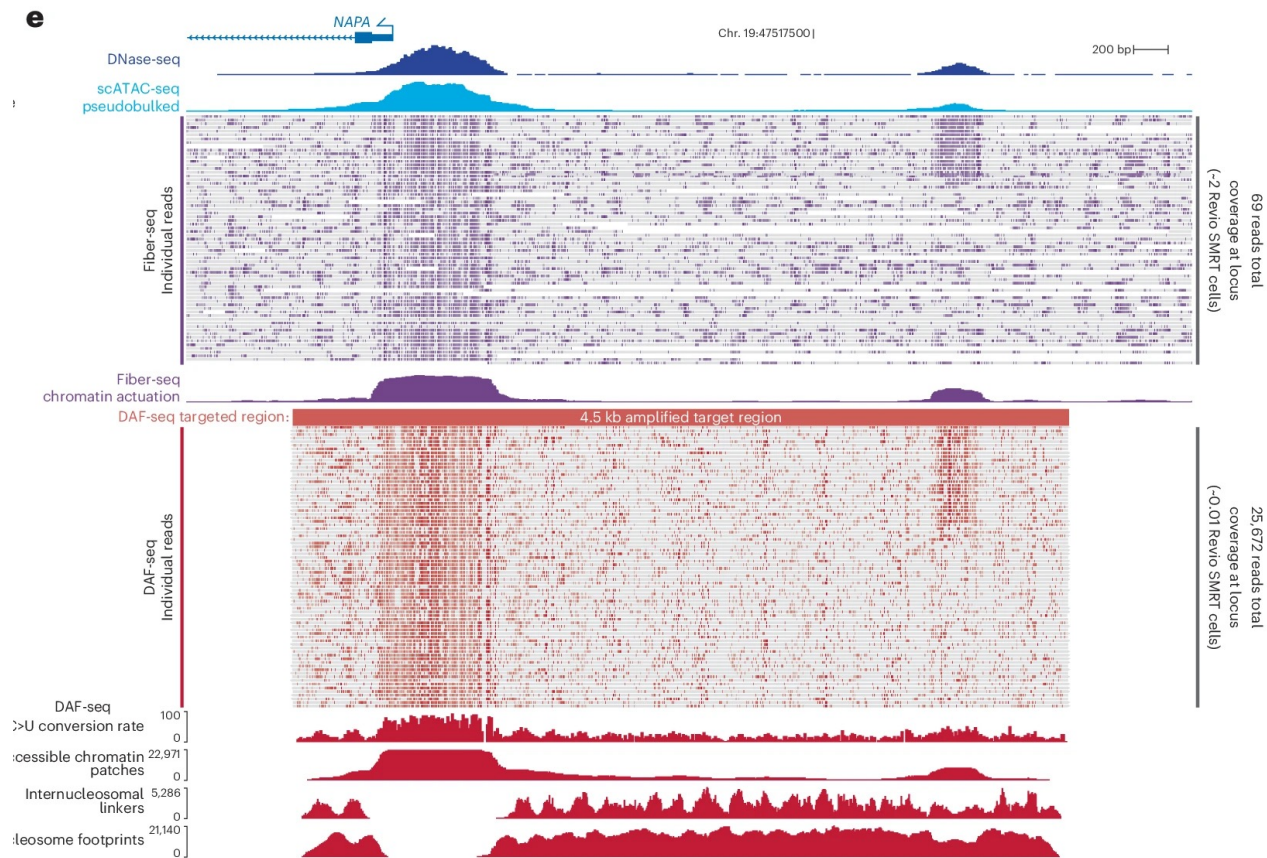


b



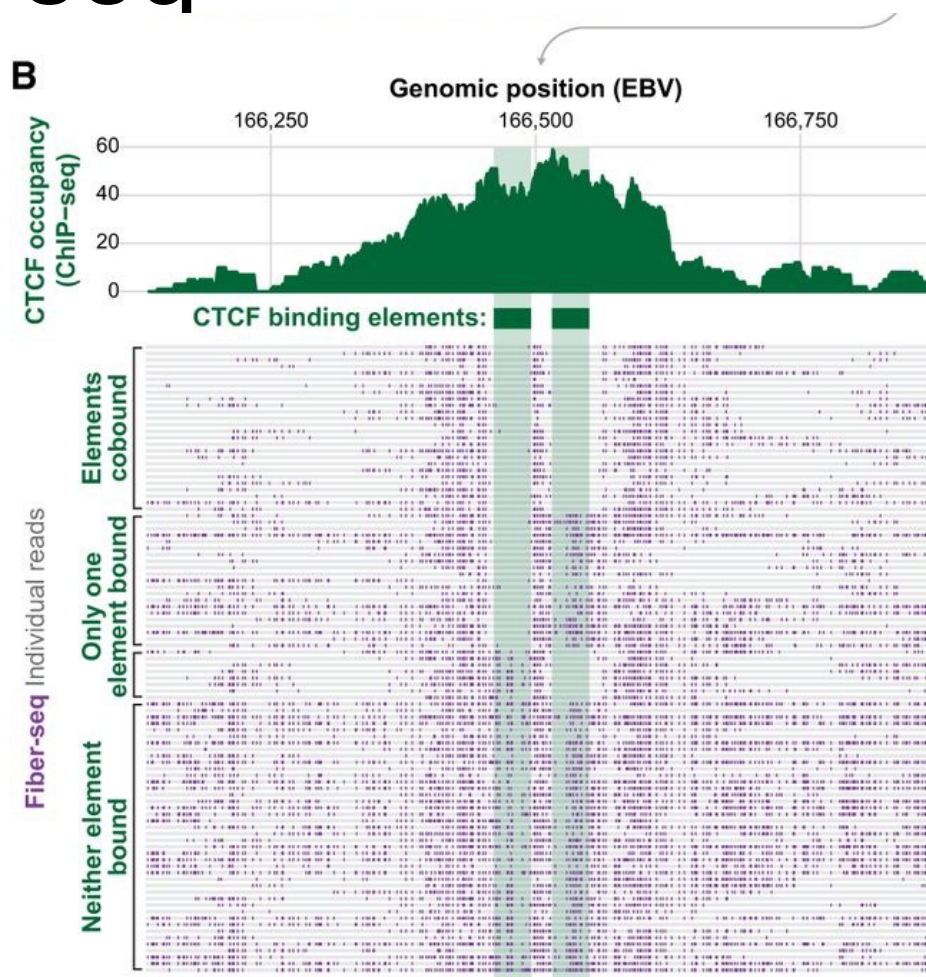
<https://doi.org/10.1038/s41587-025-02914-3>

DAF-seq



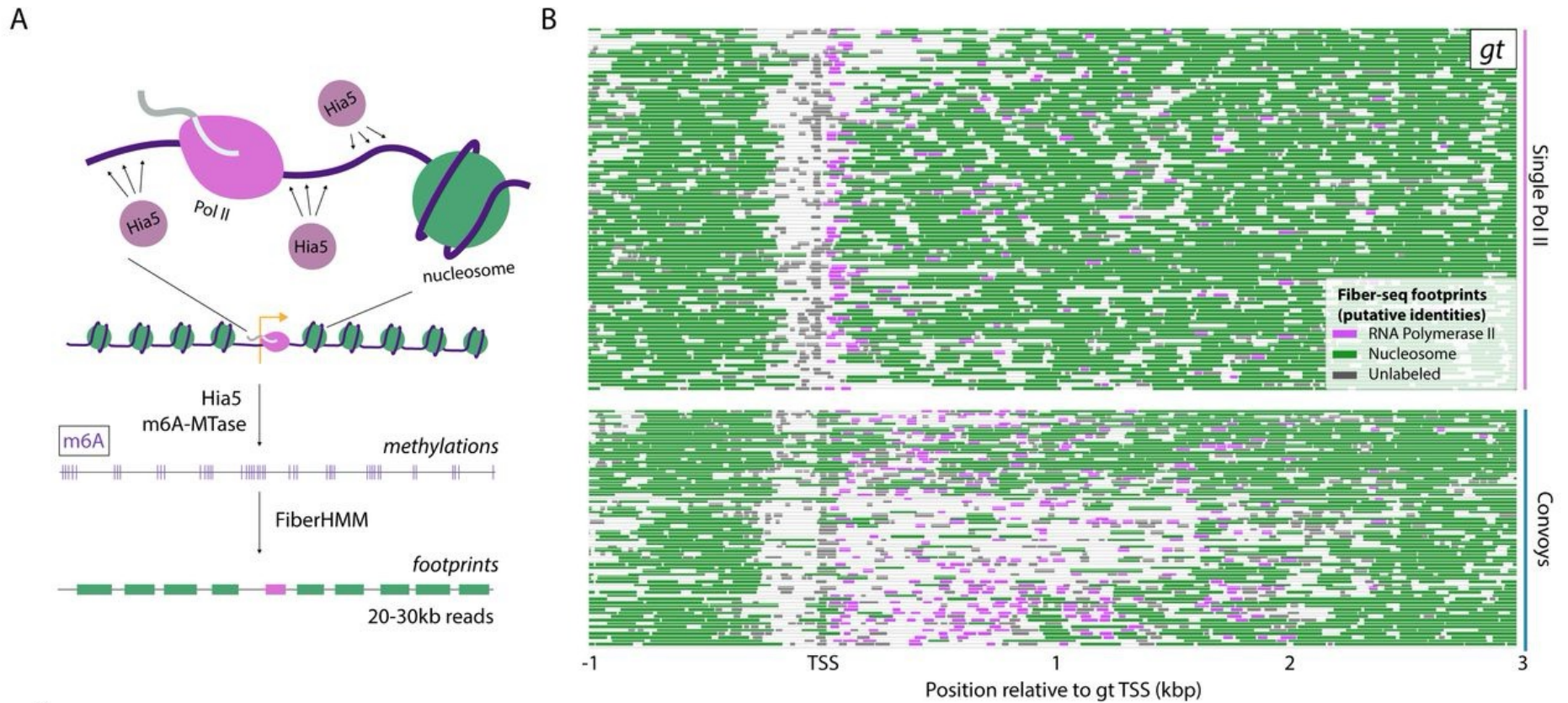
<https://doi.org/10.1038/s41587-025-02914-3>

FIBER-seq



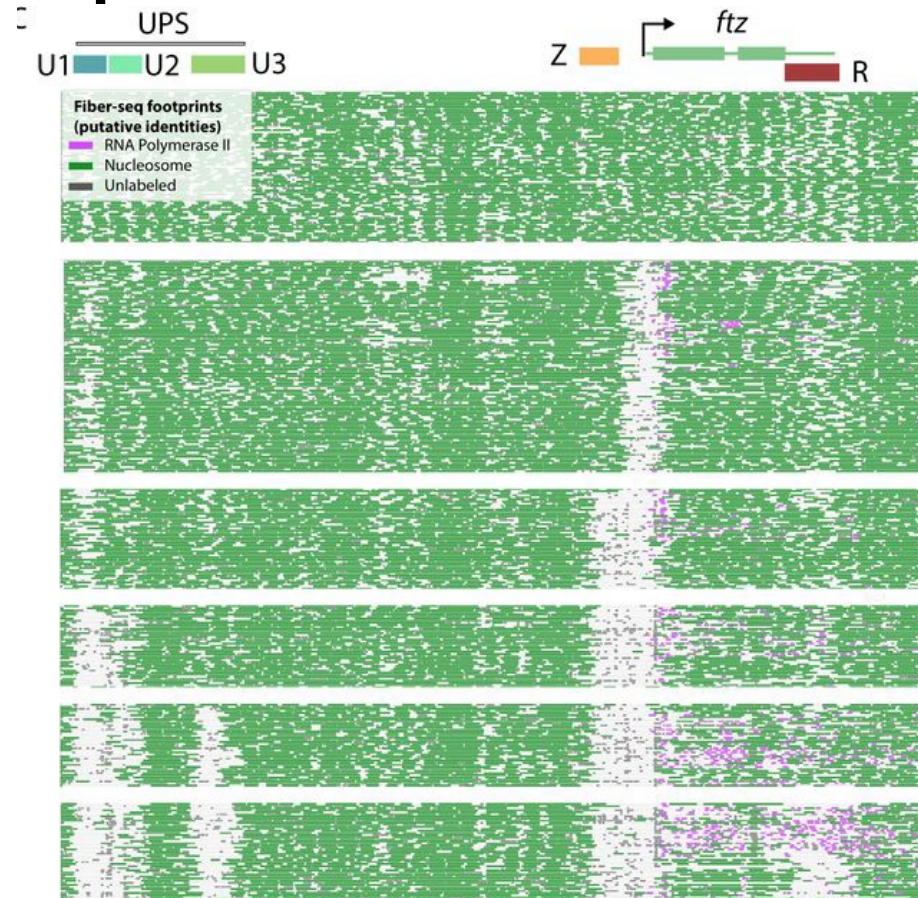
doi: 10.1101/gr.279095.124

FIBER-seq



<https://doi.org/10.1101/2025.10.28.685222>

FIBER-seq



<https://doi.org/10.1101/2025.10.28.685222>