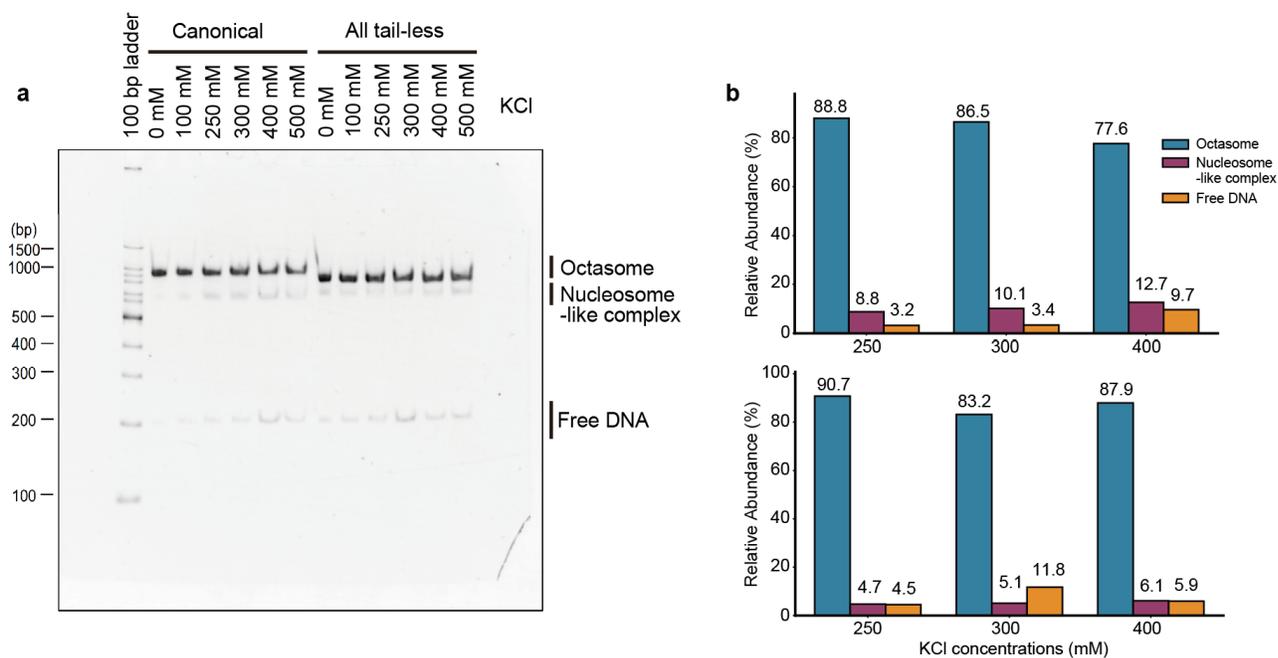
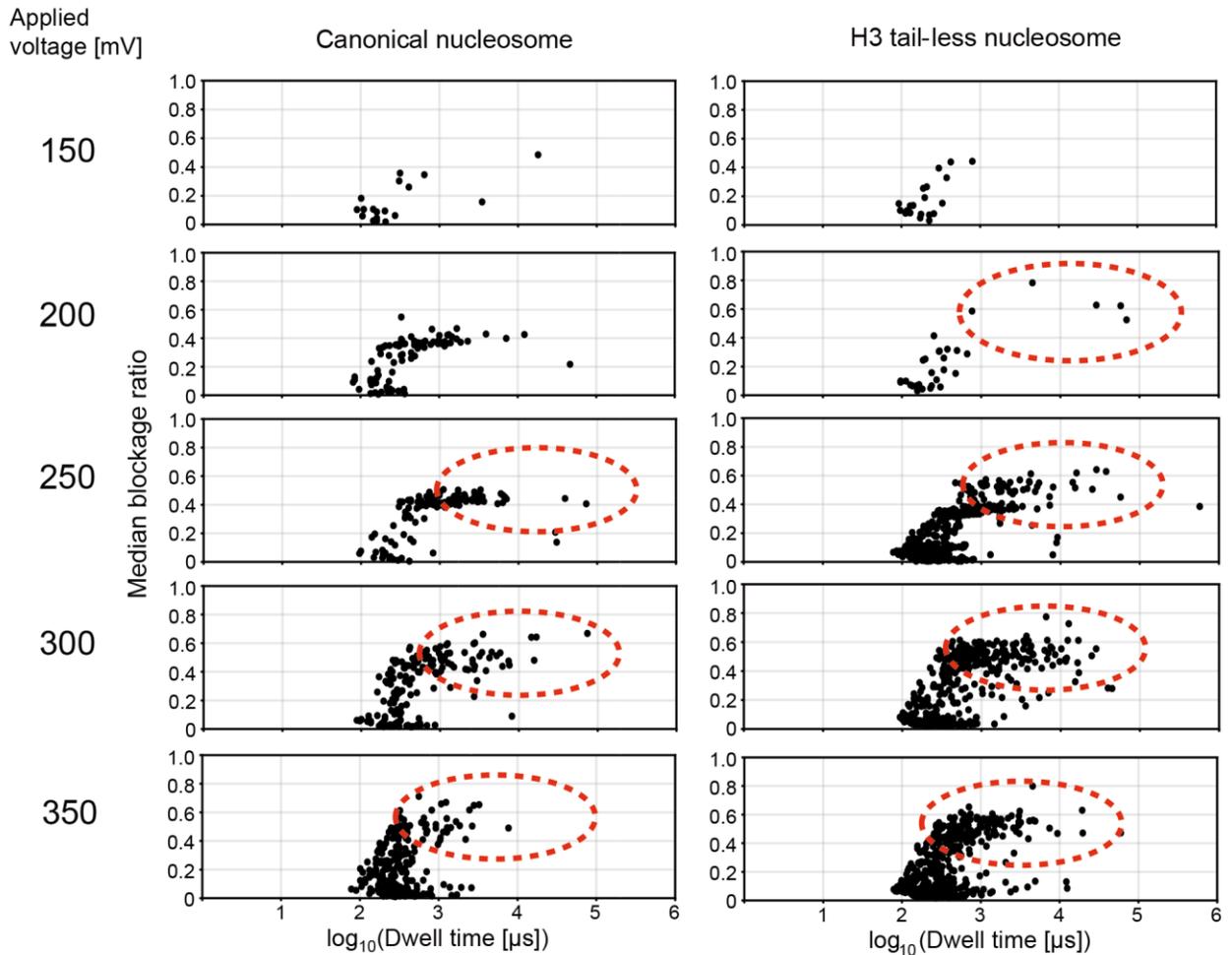


Supplementary Information



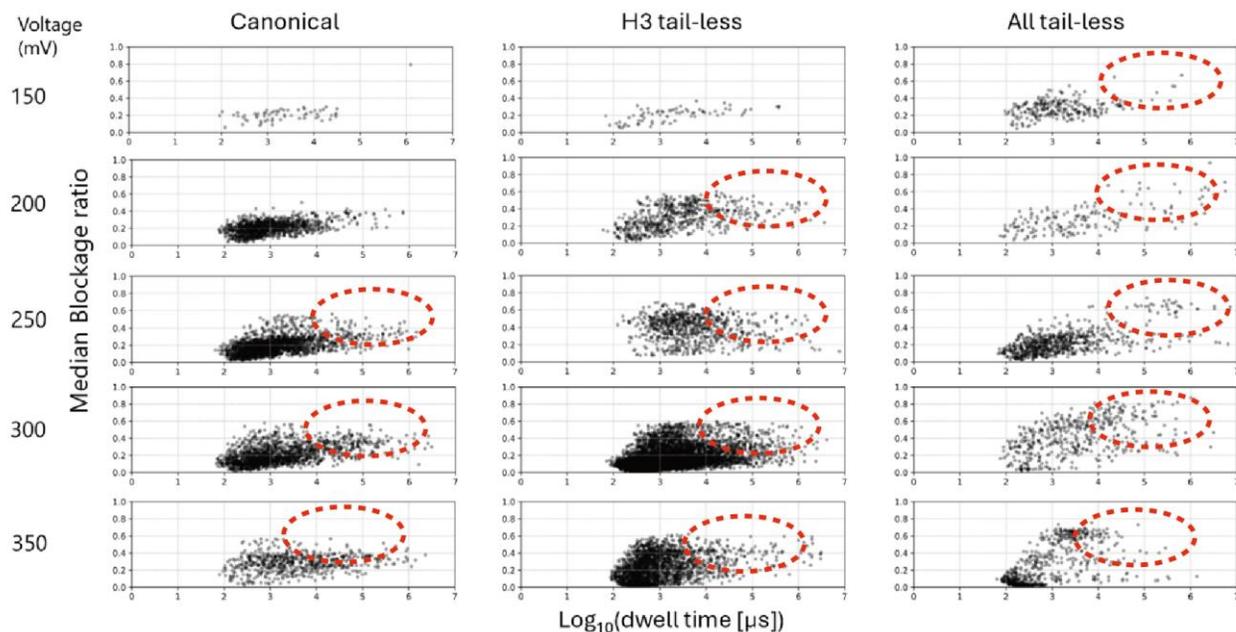
Supplementary Fig. S1: Non-denaturing polyacrylamide gel electrophoresis for nucleosome samples at various KCl concentrations

a. Canonical nucleosomes and all tail-less nucleosomes incubated under each KCl concentration condition were analyzed by non-denaturing 6% polyacrylamide gel electrophoresis with ethidium bromide staining. **b.** Quantification of the relative abundance (%) of octasome, nucleosome-like complex, and free DNA species for canonical nucleosomes (upper) and all tail-less nucleosomes (lower) at 250, 300, and 400 mM KCl, as determined by densitometric analysis of the gel shown in **a**.



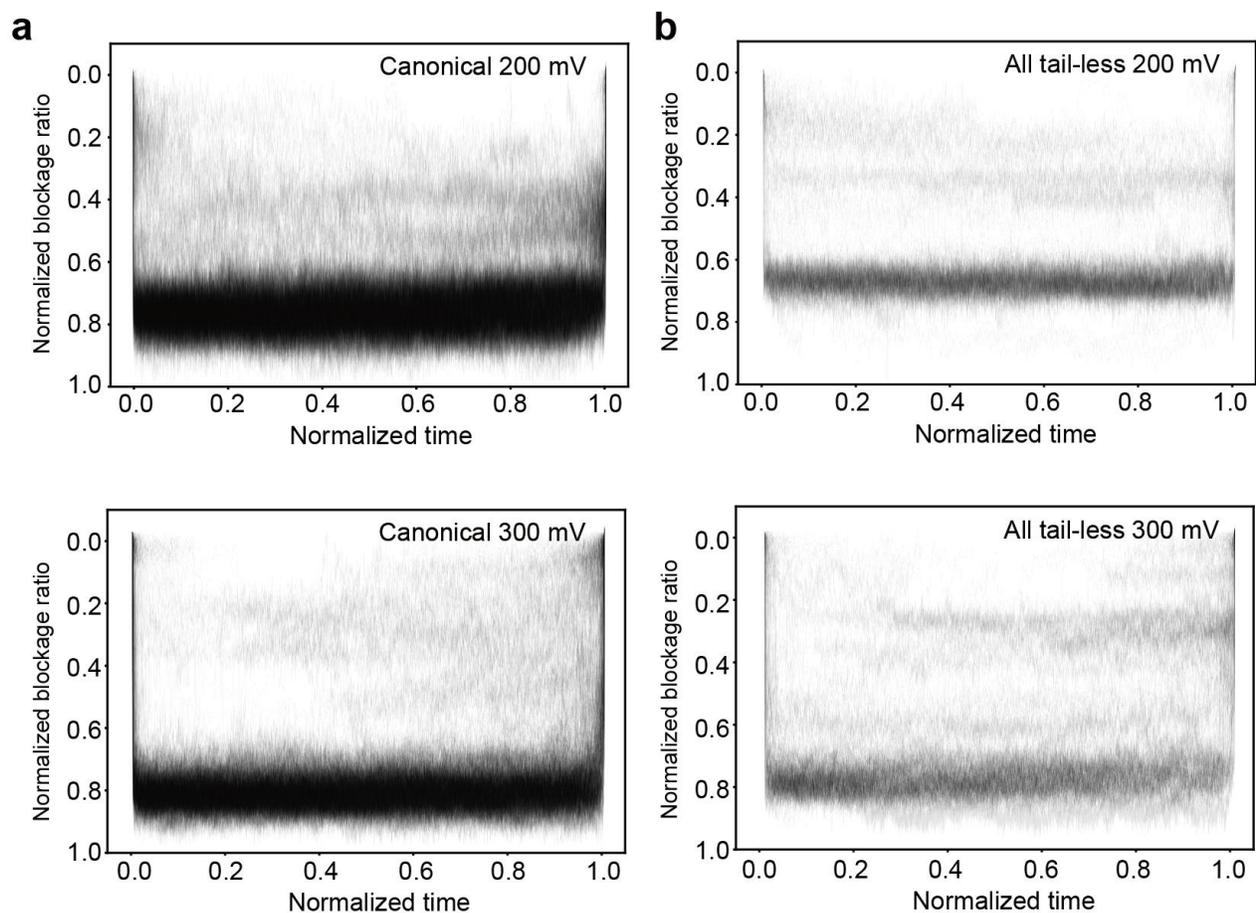
Supplementary Fig. S2: Scatter plots of nanopore signals from canonical and H3 tail-less nucleosomes.

Scatter plots of median blockage ratio ($\Delta I/I_0$) versus dwell time for canonical nucleosomes (left) and H3 tail-less nucleosomes (right) under different applied voltages (150, 200, 250, 300, and 350 mV). Red dot circles indicate the emergence of event populations with high blockage ratios and long dwell times, corresponding to complete DNA unwinding. The final number of analyzed events for canonical nucleosomes was 18 at 150 mV, 86 at 200 mV, 118 at 250 mV, 166 at 300 mV, and 277 at 350 mV. For H3 tail-less nucleosomes, the number of events was 21 at 150 mV, 33 at 200 mV, 389 at 250 mV, 395 at 300 mV, and 527 at 350 mV. Data were acquired at a nucleosome concentration of 5 nM.



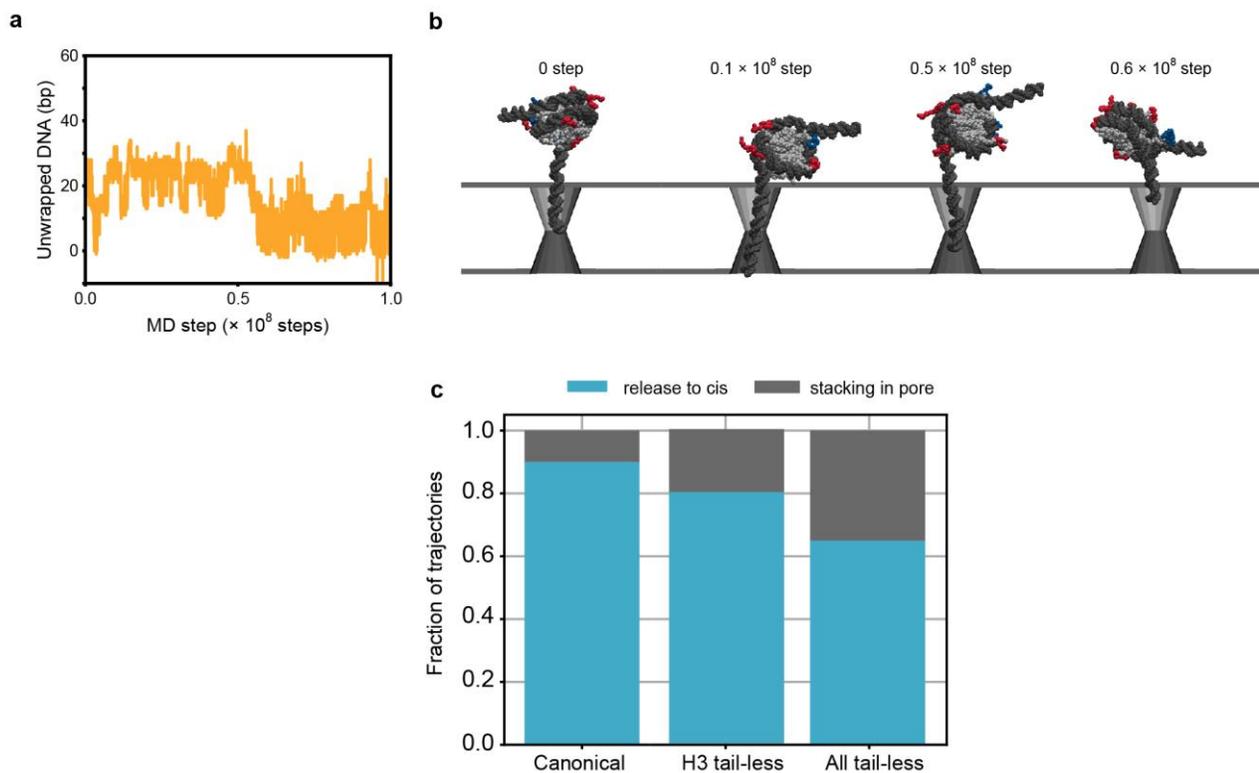
Supplementary Fig. S3: Scatter plots of nanopore signals obtained under reversed electric field polarity (*trans-to-cis* direction).

Scatter plots of median blockage ratio ($\Delta I/I_0$) versus dwell time for canonical nucleosomes (left), H3 tail-less nucleosomes (middle), and all tail-less nucleosomes (right) under *trans-to-cis* voltage application. In the standard measurement configuration used in the main text (Figs. 1 and 2), DNA translocation was driven in the *cis-to-trans* direction. Here, the electric field polarity was reversed to drive DNA translocation in the *trans-to-cis* direction. The overall trends—specifically, the shift of the complete DNA unwinding population to lower voltages upon histone tail removal—were reproduced under reversed polarity conditions. The final number of analyzed events for canonical nucleosomes was 63 at 150 mV, 1119 at 200 mV, 1859 at 250 mV, 1604 at 300 mV, and 639 at 350 mV. For H3 tail-less nucleosomes, the number of events was 73 at 150 mV, 627 at 200 mV, 740 at 250 mV, 6089 at 300 mV, and 2132 at 350 mV. For all tail-less nucleosomes, the number of events was 252 at 150 mV, 170 at 200 mV, 712 at 250 mV, 462 at 300 mV, and 621 at 350 mV. Data were acquired at a nucleosome concentration of 20 nM.



Supplementary Fig. S4: Post-synchronization analysis of nanopore current traces from canonical and all tail-less nucleosomes.

Post-synchronization analysis of canonical nucleosomes (left, **a**) and all tail-less nucleosomes (right, **b**). The raw current traces of individual DNA unwinding events were temporally normalized and overlaid to examine intermediate states during the unwinding process. Upper panels show the results at 200 mV, and lower panels at 300 mV. The final number of analyzed events for canonical nucleosomes was 239 at 200 mV and 533 at 300 mV. For all tail-less nucleosomes, the number of events was 91 at 200 mV and 188 at 300 mV.



Supplementary Fig. S5: Coarse-grained MD simulation trajectories at 50 mV.

a. Representative time course of nucleosomal DNA unwrapping for a canonical nucleosome at 50 mV, showing a failed unwinding attempt in which DNA partially entered the nanopore but rewrapped and returned to the *cis* side. **b.** Snapshots from the trajectory shown in **a** at the indicated time points. **c.** Fraction of trajectories classified as "release to *cis*" or "stacking in pore" for each nucleosome construct at 50 mV ($n = 20$ per condition). No complete translocation was observed under this sub-threshold voltage.