Appendix A: Supplementary Data

Human OGG1 activity in nucleosomes is facilitated by transient unwrapping of DNA and is influenced by the local histone environment

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Scheme S1. Oligonucleotide sequences used in this work

The 145mer oligomers were synthesized as three component oligomers. Each strand was divided into a 45mer, a 40mer, and a 60mer, as indicated by the vertical lines. The component oligomers were assembled for ligation using the scaffolds listed. The table below details the base identity at locations X (lesion strand) or Y (complement strand) explored in this study.

145mer lesion strand (numbering based on "I strand" of Vasudevan *et. al.*) [36]

5′- ATC AGA ATC CCG GTG CCG X^{-54}GX^{-52} CCX^{-49} CTC AAT TGG TCG TAG ACA GCT|CTA GCA CCG CTT AAA CGC ACG TAC GCG CTG TCC CCC GCG T|TT TAA CCG CCA AGG GGA TTA CTC CCT AGT CTC CAG GCA CGT GTC AGA TAT ATA CAT CGA T -3′

Scaffold 1:

5′- TTT AAG CGG TGC TAG AGC TGT CTA CGA CCA -3′

Scaffold 2:

5′- CCC TTG GCG GTT AAA ACG CGG GGG ACA GCG -3′

145mer complement strand (numbering based on "J strand" of Vasudevan *et. al.*) [36]

5′- ATC GAT GTA TAT ATC TGA CAC GTG CCT GGA GAC TAG GGA GTA ATC|CCC TTG GCG GTT AAA ACG CGG GGG ACA GCG CGT ACG TGC G|TT TAA GCG GTG CTA GAG CTG TCT ACG ACC AAT TGA GY^{+49}G GY^{+52}C Y^{+54}CG GCA CCG GGA TTC TGA T -3′

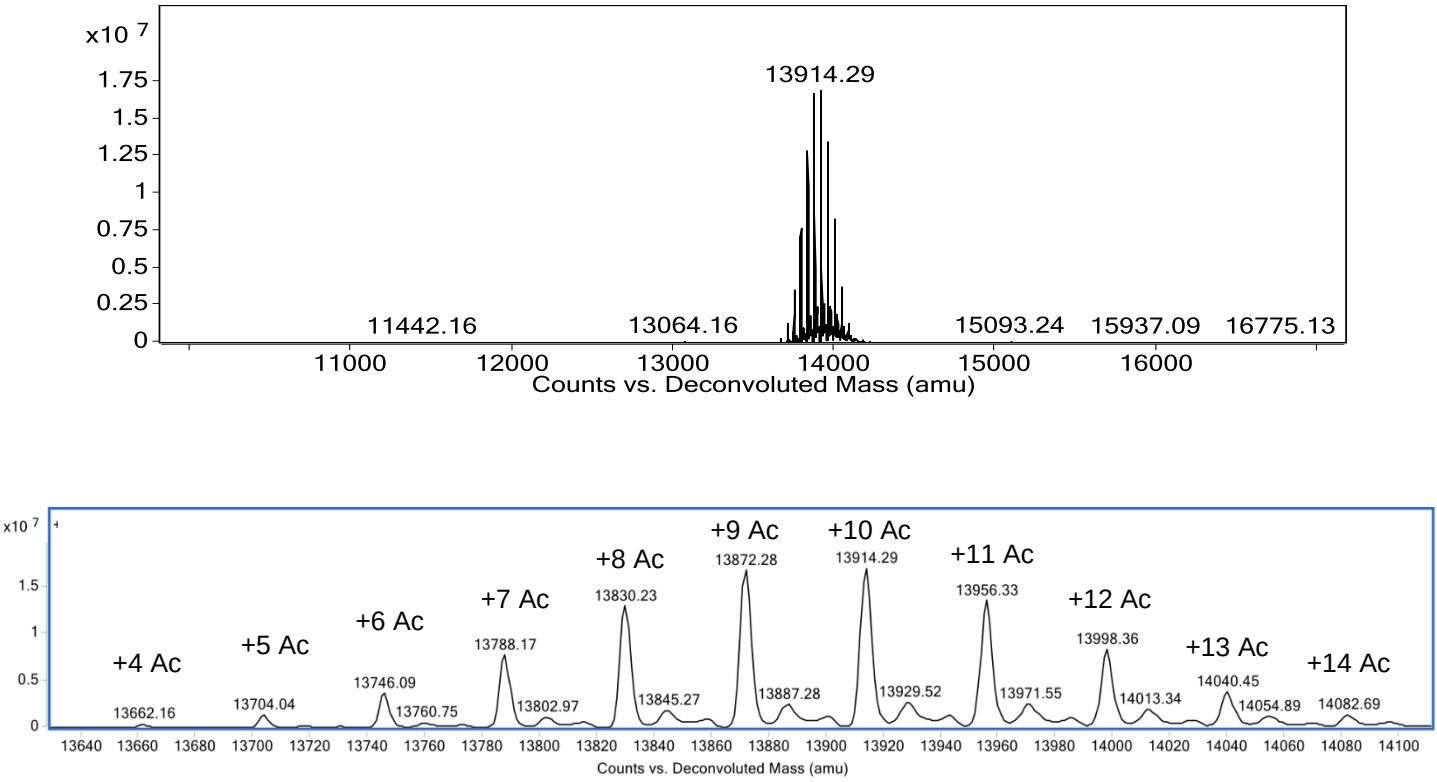
Scaffold 3:

5′- TTT AAC CGC CAA GGG GAT TAC TCC CTA GTC -3′

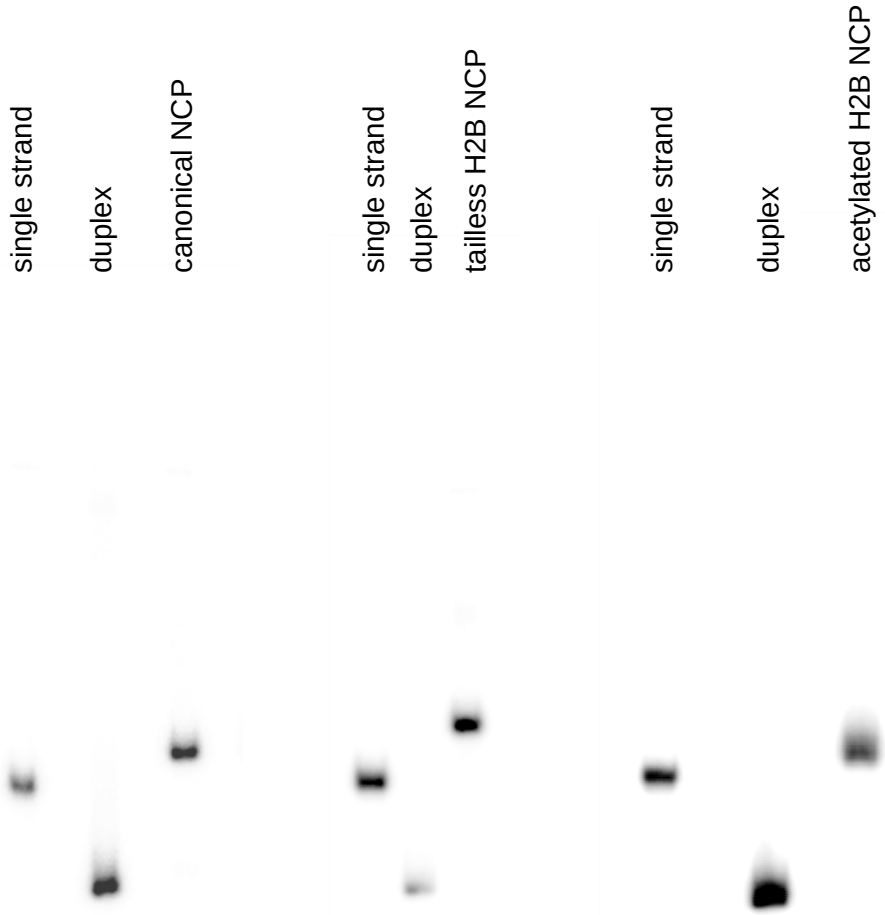
Scaffold 4:

5′- CTA GCA CCG CTT AAA CGC ACG TAC GCG CTG -3′

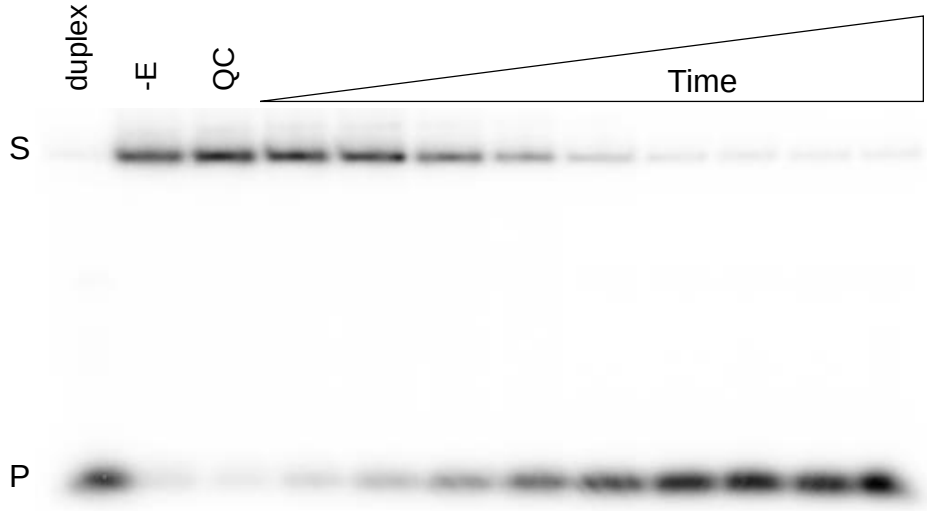
Substrate	**X^{-49}**	**Y^{+49}**	**X^{-52}**	**Y^{+52}**	**X^{-54}**	**Y^{+54}**
8-oxoG^{OUT}	8-oxoG	C	G	C	G	C
8-oxoG^{MID}	G	C	8-oxoG	C	G	C
8-oxoG^{IN}	G	C	G	C	8-oxoG	C
U^{OUT}	U	G	C	G	C	G
U^{MID}	C	G	U	G	C	G
U^{IN}	C	G	C	G	U	G



Supplementary Data Fig. 1. Electrospray ionization mass spectrometry was used to evaluate the acetylation of H2B. **(A)** Mass spectrometry reveals H2B acetylation. The peak at 13914.29 amu corresponds to the addition of 10 acetyl groups. **(B)** A zoomed in view of the mass spectra reveals a distribution in the number of acetyl group added. Peaks corresponding to the addition of 4-14 acetyl groups were observed.



Supplementary Data Fig. 2. Representative native PAGE for evaluating the reconstitution of canonical, tailless H2B, and acetylated H2B NCPs. Radiolabeled samples were loaded on a 1 mm thick 7% native gel (60:1 acrylamide:bisacrylamide, 0.25X TBE). The gel was run at 4°C for 3 hours at 150 V. Variable migration distances are observed for single strand, duplex, and NCP-incorporated DNA samples.



Supplementary Data Fig. 3. A representative denaturing PAGE showing the formation of product by UDG in a single turnover experiment. The reaction buffer used in all glycosylase kinetics experiments was 20 mM Tris-HCl (pH 7.6), 25 mM NaCl, 75 mM KCl, 1 mM EDTA, 1 mM DTT, 200 μg/ml BSA. The conversion of the lesion containing NCP substrates (S) to nicked product (P) is observed with increasing time. A positive control of UDG acting on free duplex ("duplex" lane) is included to verify the activity of UDG. The "–E" lane is a negative control prepared by incubating the NCP substrate in the absence of UDG at 37 °C for the duration of the longest time point. The "QC" lane is a second negative control that was prepared by adding 1 M NaOH quench (16 μL) to substrate (8 μL) followed by addition of UDG (8 μL) before incubation at 37 °C for the duration of the longest time point. As NaOH prevents glycosylase activity, this control serves to reveal any pre-existing damage or incidental damage. Radiolabeled samples were loaded on a 0.4 mm thick 8% denaturing sequencing gel. The gel was run for 45 min at 80 W to achieve adequate separation of substrate and product. The bands corresponding to substrate and product were quantified using densitometry.