Supplementary Data for
Cisplatin fastens chromatin irreversibly even at a high chloride concentration.

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SUPPLEMENTARY MATERIALS AND METHODS

Gel electrophoresis analysis of DNA plasmids treated with cisplatin in various ionic conditions.

Buffers for cisplatin binding reactions: Numerous ion species besides Cl\(^-\) exist inside a live cell. Cytosol is rich in K\(^+\) and PO\(_4\)\(^3-\) (~140 mM and 80 mM, respectively) and much less so in Na\(^+\) and Cl\(^-\) (~10 mM). As cisplatin functions in the presence of various ions, we tested cisplatin binding to DNA in different buffers with various ionic conditions. Three buffers (namely, NaCl, NaNO\(_3\), and KNO\(_3\) buffers) were basically 1.6 mM Na-HEPES buffer (pH = 7.4) with the indicated salt concentrations. The pH of these buffers was adjusted to be 7.4. Sodium phosphate buffer was prepared by mixing Na\(_2\)HPO\(_4\) and NaH\(_2\)PO\(_4\), with [Na\(^+\)]/[PO\(_4\)\(^3-\)] ~ 1.77 for pH = 7.4. Sodium carbonate buffer was prepared by adjusting its pH to 7.4 by adding HNO\(_3\). These two buffers were prepared at various concentrations as indicated in Figure S4. The “cytosol-mimicking” buffer is composed of [Na\(^+\)] = 10 mM, [K\(^+\)] = 140 mM, [Cl\(^-\)] = 4 mM, [Mg\(^2+\)] = 2 mM, [CO\(_3\)\(^2-\)] = 10 mM, and [PO\(_4\)\(^3-\)] = 75 mM.

Gel electrophoresis analysis: Although the effect of Cl\(^-\) on cisplatin activity has been closely examined (1), little attention has been paid to the effect of Na\(^+\) on the binding affinity of cisplatin (2,3). To investigate the effect of Na\(^+\) on DNA platination, we substituted Cl\(^-\) by another anion, NO\(_3\). NO\(_3\) is known to have little effect on hydrolysis of cisplatin (4). As shown in Figure S4A (lanes 13-17), the mobility of the bands depends on the concentration of NaNO\(_3\). As the concentration of NaNO\(_3\) decreased from 180 to 10 mM (lanes 13-17), the SC DNA bands were gradually retarded towards the NC DNA band, but were more retarded than the SC DNA bands at the same concentrations of [NaCl] (lanes 3-7). K\(^+\), major cation in cytosol, also appeared to suppress cisplatin binding to DNA (lanes 8-12) similarly to Na\(^+\) (lanes 13-17). Considering that the effect of NO\(_3\) is known to promote cisplatin binding to DNA (4,5), which is opposite to other anions, weak inhibition of cisplatin binding by NaNO\(_3\) and KNO\(_3\) would be attributed to the effect of cations. To compare the effects of phosphate and carbonate with that of Cl\(^-\), sodium carbonate buffers (lanes 8-12 in Figure S4B) and sodium phosphate buffers (lanes 13-17 in Figure S4B) with the indicated concentrations of CO\(_3\)\(^2-\) and PO\(_4\)\(^3-\), respectively, were used. Interestingly, carbonate and phosphate ions suppressed cisplatin binding to DNA more effectively than Cl\(^-\). Overall, carbonates turned out to be the most effective ion species for suppression of cisplatin binding. This experimental result is in good agreement with our previous study that verifies the effect of carbonates on cisplatin binding to DNA, that is, the formation of mono-functional adducts (6). Such kink-free cisplatin-DNA adducts, presumably clinically inactive form, does not affect gel mobility because the superhelical state of DNA remains unchanged. Our results ascertain the importance of other ions in the activity of cisplatin (4,7,8).

We also tested cisplatin binding to DNA in the “cytosol-mimicking” buffer (the right of Figure S4C), whose ionic composition is similar to that of cytosol (see Supplementary materials and methods). Again, binding
of cisplatin (lanes 3-8 in the right of Figure S4C) was effectively suppressed for all tested concentrations of cisplatin, similarly to the case of [NaCl] = 180 mM (lanes 3-8 in the left of Figure S4C).

**ICP-MS measurement.**

2 µg of pUC19 plasmid in 100 µl of reaction solution containing 1.6 mM HEPES (pH 7.4) and various concentrations of NaCl (0, 20, 60, 90, and 180 mM) was incubated with cisplatin (final [cisplatin] = 0.1 mM and 3.3 mM). After incubation at 24 °C for 1 hour, the cisplatin-treated pUC19 was purified using Qiagen PCR Purification kit (cat. No. 28104, Germany) and suspended in 600 µl of TE buffer. Next, we added 3 M sodium-acetate solution (60 µl, pH 5.2), 528 µl of isopropanol, and 5 µl of glycerol to the purified DNA sample. This mixture was incubated in -80 °C for overnight. The mixture was centrifuged at 20,000 g for 1 hour and was subsequently rid of supernatant. It was then provided with 70 % ethanol (1 ml), centrifuged at 20,000 g for 1 hour and rid of supernatant. Finally, the DNA pellet was air-dried for ICP-MS measurements. Then, the air-dried DNA pellets were wet-digested for ICP-MS measurements as follows: (i) each DNA pellet was heated at 70 °C for 1 hour after suspended in 75 µl of 70% HNO₃, and (ii) 75 µl of H₂O₂ was added into each suspended DNA sample and then heated again at 70 °C for 3 hours. These suspended DNA samples were finally diluted by HPLC-grade water containing 10 nM thallium (Tl) to final concentration of 3.5% HNO₃.

In all ICP-MS experiments, the Agilent 7700 instrument (Agilent Technologies, USA) was used with a micromist nebulizer and quartz double-pass Scott-type spray chamber at 2°C. The wet digested DNA samples were analysed with ICP-MS under helium gas mode. For external calibration, ^{195}\text{Pt} (0 – 100 ppb) and ^{31}\text{P} (0 – 100 ppb) standard solutions were prepared. The amount of DNA-bound platinum and DNA in the prepared DNA samples was quantified by analysis of ^{195}\text{Pt} and ^{31}\text{P}, respectively. When DNA was treated in 3.3 mM cisplatin solution, the purification of DNA sample failed likely because DNA molecules were heavily cross-linked by cisplatin, exceeding the size limit of our purification column.
Figure S1. MNase digestion patterns for NAP1-assisted nucleosome array. After treated with 1 mU MNase for 10 min at 24 °C, it was analysed by 1.2 % agarose gel electrophoresis with ethidium bromide staining to measure nucleosome repeat lengths in three different lanes (–: nucleosomal DNA, +: 0.05 mM cisplatin-treated N-DNA, and ++: 0.1 mM cisplatin-treated N-DNA). The bands of mono-N-DNA are clearly visible with three higher bands of multiple-N-DNA in both cases of cisplatin-free (–) and cisplatin-treated lines at two different concentrations (+: 0.05 and ++: 0.1 mM). The length of DNA used for MNase digestion assay was 5.4 kb.
Figure S2. MT measurement of the elastic property for a bare DNA molecule at [NaCl] = 180 mM. The force-extension curve was fitted by the WLC model with $\phi_0 = 50$ nm. Inset: schematic configuration of the DNA molecule and MT system used in our experiments.
Table S1. Modified persistence length ($\xi_p$) of DNA molecules measured at three different concentrations of [NaCl] (20, 60, and 90 mM)

| NaCl (mM) | $\xi$ of DNA by the WLC model | $\xi$ at high-tension regime | $\xi$ at low-tension regime |
|-----------|-------------------------------|-----------------------------|----------------------------|
| 20$^\circ$ | 9.5 nm                        | 14 nm                       |
| 20$^\circ$ | 9 nm                          | 12.5 nm                     |
| 60$^\circ$ | 21.5 nm                       | 26 nm                       |
| 60$^\diamond$ | 26 nm                       | 32 nm                       |
| 60$^\diamond$ | 29 nm                       | 34 nm                       |
| 90$^\circ$ | 41 nm                        | 41 nm                       |
| 90$^\diamond$ | 38 nm                       | 42 nm                       |
| 90$^\diamond$ | 35.5 nm                      | 38 nm                       |

Here, the data of $\xi_p$ with hat, asterisk, and dagger were taken from Figure 1 of this work, ref (6), and ref (9), respectively. For all experimental measurements, the concentration of cisplatin used was 3.3 mM and free cisplatin was washed out after 30-minute incubation.
Table S2. Quantification of the degree of cisplatin binding to DNA under various [NaCl] by ICP-MS

| NaCl (mM) | 0.1 mM cisplatin | 3.3 mM cisplatin |
|-----------|-------------------|-----------------|
| 0         | 0.0591 ± 0.0260   | –               |
| 20        | 0.0256 ± 0.0096   | –               |
| 60        | 0.0088 ± 0.0038   | –               |
| 90        | 0.0056 ± 0.0024   | 0.1238 ± 0.0160 |
| 180       | 0.0028 ± 0.0010   | 0.0661 ± 0.0145 |

For ICP-MS measurements, the pUC19 DNA plasmid (closed circular, 2686 bp) was used and incubated with cisplatin for 1 hour. Here, the p value is defined and calculated by $2 \times \left( \frac{^{195}\text{Pt} (\mu\text{M})}{^{31}\text{P} (\mu\text{M})} \right)$, fraction of platinum-bound DNA base pairs. Below a low salt concentration ([NaCl] ≤ 90 mM), DNA molecules treated by 3.3 mM cisplatin solution seem to form aggregates by crosslinking, which are too large to enter the purification column, making it difficult to purify cisplatin-DNA adducts for ICP-MS measurements. Thus, (–) symbols indicate lack of reliable data points in ICP-MS measurements. In ICP-MS data, the errors represent the standard deviation of 4- and 3-independent measurements for 0.1- and 3.3-mM cisplatin treatments, respectively.
Figure S3. Drastic condensation of DNA observed in the presence of free cisplatin. (A) Time course measurement of DNA extension in the presence of free cisplatin. At tension below 0.4 pN (yellow-boxed area), a DNA molecule is rapidly condensed in discrete steps. The raw DNA extension data (black) were averaged with the time window of 1 s (red). The magnetic force measured at each time point was also shown (blue line). For comparison, the extension of bare DNA (raw: green; time-average (1 s): violet) measured for the same range of applied forces was also drawn. (B) Blown-up of the boxed part in (A). The trace (orange line) generated by the same step-detection algorithm (Figures S5 and S6) (10) reveals transition steps shown in (C). (C) Histogram of the step size during cisplatin-induced DNA condensation obtained from two independent measurements. The descending events (blue and right-hatched) were only observed to occur below ~ 0.4 pN. During cisplatin-induced condensation, ascending events (yellow and left-hatched) were also observed but rarely and with small steps, indicating that they resulted from usual random fluctuations. The concentration of cisplatin was 3.3 mM.
Figure S4. Gel assay displaying the binding efficiency of cisplatin to DNA under various ionic conditions. (A) Electrophoretic mobility of the 15-kb DNA incubated with cisplatin in buffers with different concentrations of NaCl (lanes 3-7), KNO₃ (lanes 8-12), and NaNO₃ (lanes 13-17). (B) Electrophoretic mobility of the 15-kb DNA incubated with cisplatin in buffers with different anionic species (NaCl: lanes 3-7, NaHCO₃: lanes 8-12, and sodium phosphate buffer: lanes 13-17). In sodium phosphate buffer, the molar ratio of [PO₄³⁻] and [Na⁺] was 1:1.77 after the pH of the solution was adjusted to be 7.4. Thus, x is 1.23. (C) Electrophoretic mobility of the 15-kb DNA incubated with different concentrations of cisplatin in either salt solution ([NaCl] = 180 mM; lanes 3-8 in the left gel) or cytosol-mimicking buffer (lanes 3-8 in the right gel). For the composition of the cytosol-mimicking buffer, see Supplementary material and methods. For all the gel assays, 125 ng of DNA in 50 µl of buffer solution was incubated with cisplatin for 1 hour at 24 °C. Cisplatin solutions were prepared to desired salt concentrations by mixing pre-hydrolysed cisplatin with buffer mixtures. SC and NC stand for supercoiled and nicked circular DNA, respectively. Cisplatin is in 1 mM unless noted otherwise.
Figure S5. Stepwise decrease of DNA extension due to NAP1-assisted formation of individual nucleosomes in the presence of $F \sim 0.95$ pN for the same DNA molecule shown in Figure 2B. (A) After incubating a single DNA tether with a mixture of NAP1 proteins and core histones in the reaction buffer for nucleosome assembly under $F \sim 10$ pN for 30 minutes, the tension was lowered below 1 pN to observe individual steps due to formation of individual NCPs. Here, raw data for z-position of a 2.8 µm magnetic bead and the step trace found by the step detection algorithm are in grey and red, respectively. (B) Blow-up of the green boxed area in (A). Raw data were moving-averaged with a 1-s window (blue line). (C) Size distribution of individual steps found by the step detection algorithm. The distribution has a main peak at $-25 \pm 0.9$ nm which corresponds to wrapping of one turn of DNA around a histone octamer. At the same time, unwrapping events were also observed, but with much less frequency (see the peak at 25 nm in the histogram).
Figure S6. Mechanically-induced rupturing of a N-DNA (See Figure 2B). (A) After forming a N-DNA, $F$ was elevated from 1 to 40 pN (blue line). The first unwinding step in the N-DNA was observed from $F \sim 3$ pN. At $F \sim 40$ pN, its extension was restored to 95% of the original DNA length. (B) Blow-up of the green-boxed area in (A), which shows stepwise increase in DNA extension at a low force regime ($3.3 \sim 4.2$ pN). In (A) and (B), raw extension data and the step trace are drawn in grey and red lines, respectively. (C) Size distribution of individual steps (black) found in the rupturing process of N-DNA in (A) (bin size: 5 nm) and its Gaussian fit (red) showing the location of a main peak at $27.2 \pm 0.4$ nm.
Figure S7

Figure S7. Evidence of residual histones associated with once-overstretched N-DNA and origin of the hysteresis in the intermediate regime of tension. Force-extension behaviors of bare DNA (black) and a N-DNA (red) in a S-R cycle. (See Figure 2F). Even after a N-DNA is overstretched, it exhibits a sudden collapse below 1 pN in a relaxation run because residual histones trigger N-DNA formation.
Figure S8. Two independent data sets (A-F and G-L) illustrating the structural fixation of a single N-DNA molecule induced by cisplatin crosslinking at two different cisplatin concentrations, 3.3 and 0.1 mM. (A-F) Samples #2 in Table S3. (A) Stretching and relaxation of a bare DNA molecule used in (B, C) by changing applied $F$. Because a nicked DNA molecule was used, it exhibited the OST around $F \sim 65$ pN. (B) Structural fixation of a N-DNA molecule crosslinked by cisplatin at a high concentration of 3.3 mM in PBS solution. At $F \sim 20$ pN, its length ($l \sim 2.8 \mu m$; point “a” in (B)) remains collapsed to 70% of the length of the same DNA molecule ($l \sim 3.9 \mu m$; point “a” in (A)). This collapsed structure was stably maintained in the high force regime below 65 pN, much larger than a rupturing force ($F \sim 15$ pN) for a N-DNA molecule previously reported. The OST occurred at the higher onset force, $F \sim 70$ pN, but the overstretched extension of the CBN-DNA under the maximum force applicable ($F \sim 75$ pN) (point “b” in (B)) was still shorter than that of the same DNA molecule under the same tension (point “b” in (A)). (C) Imperfect relaxation of a CBN-DNA
molecule after changing buffer to 3 M NaCl solution from (B). At $F \sim 20$ pN, a length of the collapsed CBN-DNA molecule increased gradually to 85% of bare DNA extension in (A) and its OST was observed at $F \sim 65$ pN. (D) Stretching and relaxation of another bare DNA molecule used in (E, F). (E) Structural modification of a N-DNA molecule crosslinked by cisplatin at a low concentration of 0.1 mM in PBS solution. It behaved like a typical N-DNA molecule without treatment of cisplatin under $F \sim 40$ pN (Figure 2B), but the OST was not observed (below $F \sim 75$ pN), indicating that this CBN-DNA would be torsionally-constrained by wrapping DNA nick sites around histones. (F) Full relaxation of a CBN-DNA molecule after changing buffer to 3 M NaCl solution from (E). At $F \sim 60$ pN, its length was restored to the full extension of the same DNA in (D) ($\sim 4.0 \mu m$). The OST happened beyond $F \sim 60$ pN and the overstretched extension of the CBN-DNA was the same as the extension observed in its bare form in (D). Insets in (A-F) show the regime of OST highlighted by green boxed areas in (A-F), and the vertical dotted lines drawn in insets indicate the onset of OST. (G-L) Samples #3 in Table S3. The two sets (A-F, G-L) of samples were acquired in a similar manner and also yielded similar results in general. Panels (G) and (J) show the stretching and relaxation of bare DNA molecules used in (H,I) and (K,L), respectively. (H,I) Structural fixation of N-DNA by 3.3 mM cisplatin in 1× PBS (H) and the same CBN-DNA in 3 M NaCl (I). (K,L) Structural fixation of N-DNA by 0.1 mM cisplatin in 1× PBS (K) and the same CBN-DNA in 3 M NaCl (L). In (G-I), we were able to apply the exceptionally high force ($> 100$ pN) to the DNA molecule likely because the bead attached to it contained an unusually high magnet content. The heterogeneity between the two independent measurements conducted under the same experimental conditions likely arose from a different number and distribution of nucleosomes assembled on a long DNA tether. For the actual extension of molecules measured from (A-F) and (G-L), see #2’s and #3’s in Table S3, respectively.
Figure S9. Mechanically-induced rupturing of the CBN-DNA prepared with 0.1 mM cisplatin (Figure 3E). (A) After treating a N-DNA with 0.1 mM cisplatin, $F$ was increased from 0.3 to 60 pN (blue line). Stepwise N-DNA rupturing events were continually observed in a high force regime, and its extension reached to 2.5 µm at $F \sim 60$ pN (raw extension trace, black; step trace, red). (B) Size distribution of individual steps found by the step detection algorithm from raw data in (A). The distribution has a main peak at $20 \pm 0.3$ nm, which is slightly shorter than one turn of DNA around a histone octamer, $\sim 25$ nm. The bin size is 5 nm.
### Table S3. Full extension of DNA samples in different states measured by single-molecule MT assay.

| # of tested DNA samples | Bare DNA | N-DNA | CBN-DNA | CBN-DNA at high F in 180 mM NaCl | CBN-DNA at high F in 3M mM NaCl |
|-------------------------|----------|-------|---------|---------------------------------|---------------------------------|
|                         | $L_{DNA}$ | $L_{N-DNA}$ | $\Delta L$ | $\#$ of nucleosome s |                                  |                                  |
| 1                       | 4.39     | 2.10  | 2.28    | 46                             | 1.94                            | 1.95                            |
| 2                       | 4.04     | 2.78  | 1.26    | 25                             | 4.91                            | 6.21                            |
| 3                       | 4.68     | 1.88  | 2.80    | 56                             | 4.94                            | 6.56                            |
| 4                       | 3.86     | 2.17  | 1.69    | 34                             | 3.00                            | 3.54                            |
| 5                       | 4.32     | 1.77  | 2.55    | 51                             | Not measured                    | 1.41                            |
| 6                       | 4.35     | 1.64  | 2.71    | 54                             | Not measured                    | 2.51                            |
| 7                       | 4.20     | 1.24  | 2.96    | 59                             | Not measured                    | 1.68                            |
| 1                       | 4.21     | 2.43  | 1.78    | 35                             | 4.25                            | 5.97                            |
| 2                       | 4.07     | 2.41  | 1.65    | 33                             | 4.41                            | 7.11                            |
| 3                       | 3.96     | 1.34  | 2.62    | 52                             | 3.48                            | 7.02                            |
| 4                       | 4.09     | 2.19  | 1.90    | 38                             | 2.29                            | 3.93                            |
| 5                       | 3.69     | 1.23  | 2.46    | 49                             | 2.70                            | Not measured                    |

The complete set of the data includes all the measurements from three different states, bare DNA, N-DNA, and CBN-DNA. There are seven and five independent data sets from DNA molecules treated with 3.3 mM and 0.1 mM cisplatin, respectively. Some data sets are incomplete, missing some experimental conditions. Data sets, #1’s, #2’s, and #3’s, are presented in Figure 3, Figures S8A-F, and Figures S8G-L, respectively. Here, $\Delta L = L_{DNA} - L_{N-DNA}$. 
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