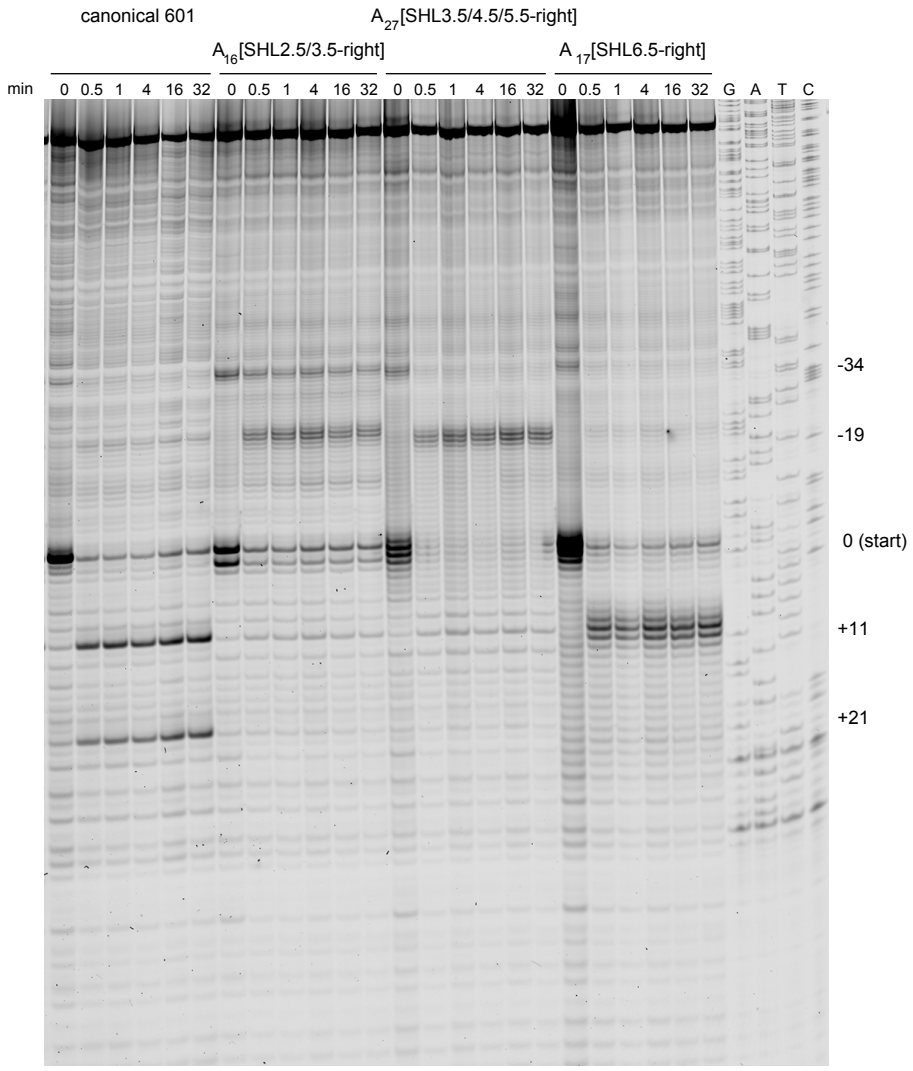
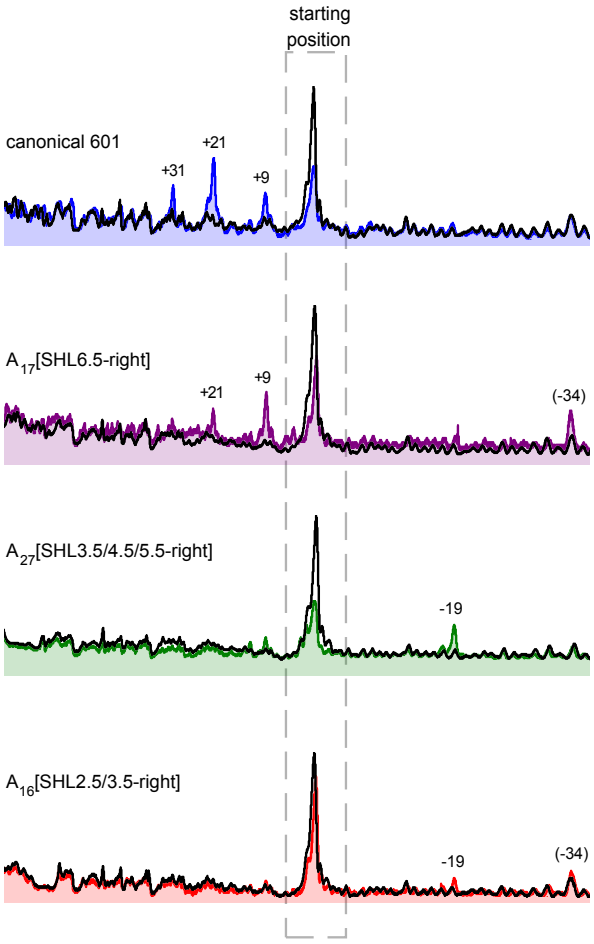
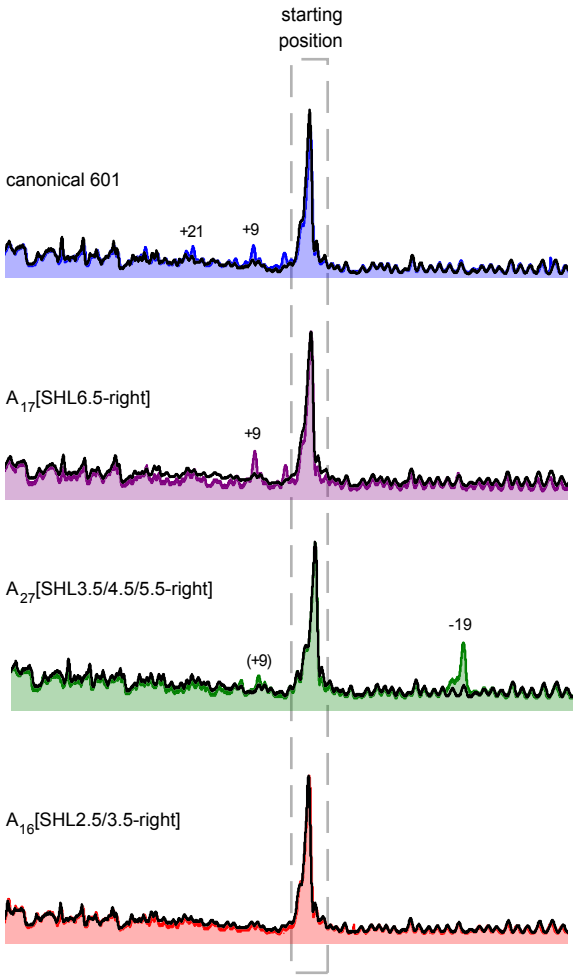


FAM scan (bottom strand)

Supplementary Figure S1. Chd1 remodeling reactions rapidly reach equilibrium.
Remodeling reactions were carried out with 150 nM 40-N-40 nucleosomes and 300 nM Chd1, and the nucleosome positions were detected by histone mapping with H2B(S53C). These reactions were resolved on a urea denaturing gel, visualized with the FAM label, and are representative of similar experiments carried out more than five times.

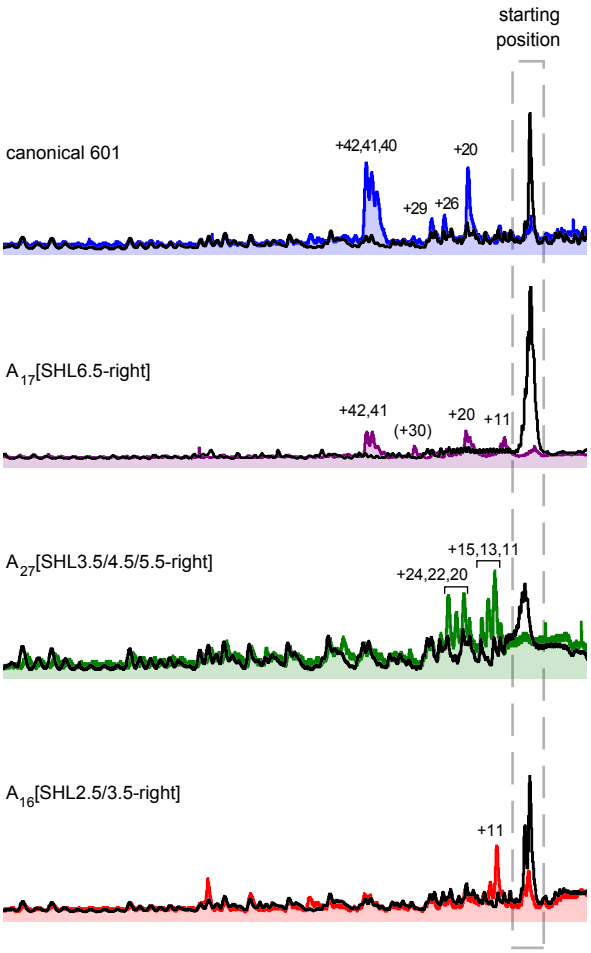


Supplementary Figure S2. The presence of internal poly(dA:dT) tracts bias nucleosome sliding in the opposite direction.
Cross-linking distributions of 40-N-40 nucleosomes before and after sliding by Chd1, monitored with Cy5 (top strand) scans. Black traces show starting nucleosome positions prior to remodeling, and colored traces show distributions 32 min after addition of 2 mM ATP and 300 nM Chd1. The positions of peaks that are weak but reproducibly show up in different experiments are given in parentheses. Scans are oriented with the bottom of the gel on the right. These scans are representative of three or more experiments.

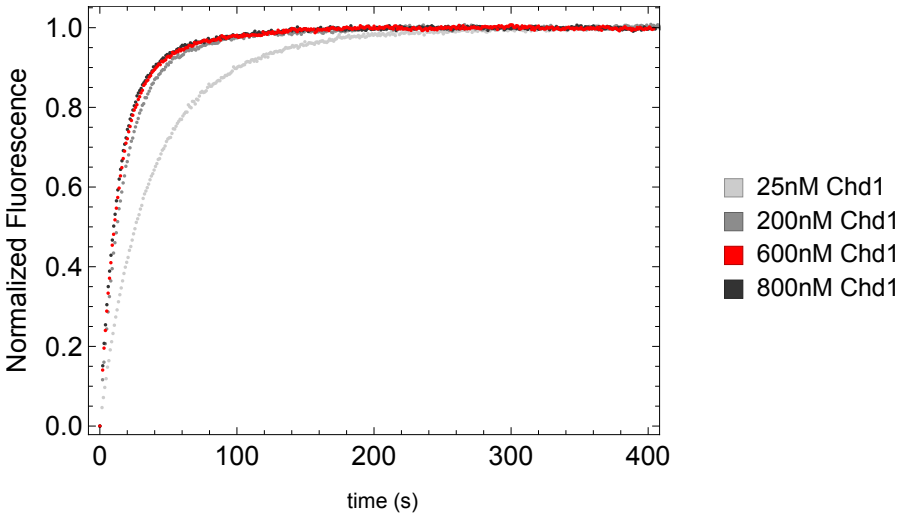


Supplementary Figure S3. Internal poly(dA:dT) tracts influence nucleosome sliding by Chd1 independently of the DNA-binding domain

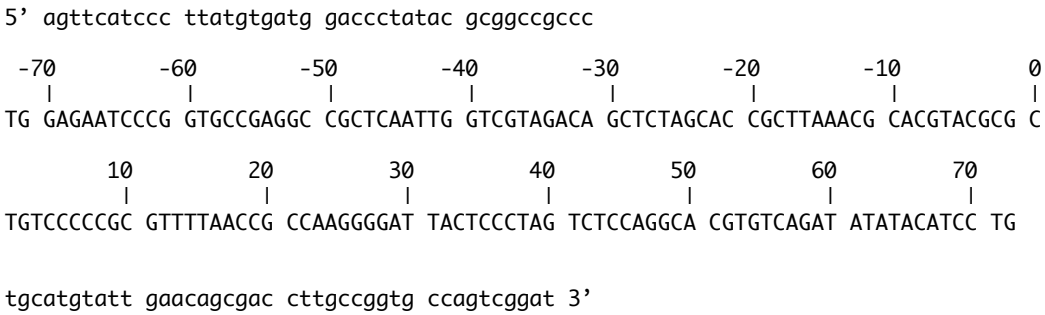
Cross-linking distributions of 40-N-40 nucleosomes before and after addition of Chd1[ΔDBD], monitored with Cy5 (top strand) scans. Black traces show starting nucleosome positions prior to remodeling, and colored traces show distributions 32 min after addition of 2 mM ATP and 300 nM Chd1[ΔDBD]. The positions of peaks that are weak but reproducibly show up in different experiments are given in parentheses. Scans are oriented with the bottom of the gel on the right. These scans are representative of three or more experiments.



Supplementary Figure S4. Chd1 can pull internal poly(dA:dT) tracts further onto the nucleosome
Histone mapping reactions of 0-N-80 nucleosomes before and after sliding by Chd1, followed with the FAM (bottom strand) label. Black traces show starting nucleosome positions prior to remodeling, and colored traces show distributions 16 min (for A_{17}[SHL6.5-right]) or 64 min (all others) after addition of 2 mM ATP and 50 nM Chd1 to 150 nM nucleosomes. These data are representative of three or more experiments.



Supplementary Figure S5. Rate of remodeling saturates at 600 nM Chd1
Shown are progress curves of remodeling reactions followed using Cy3B-Dabcyl SQOF, with increasing fluorescence correlated to movement of the histone octamer away from the short DNA end of 0-N-80 nucleosomes. Reactions contained 10 nM nucleosome, 25 μM ATP, and the indicated concentrations of Chd1. These results are representative of three similar titrations.



Supplementary Figure S6. Sequence of the Widom 601 positioning sequence with flanking DNA. The core 145 bp, which directly contact the histone core, are capitalized, whereas the flanking DNA outside the nucleosome core is lowercase. Numbering is relative to the dyad, given as zero.