Supporting materials

Nucleosome Array Compaction and Aggregation Modulated by CpG Location and Methylation Status

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1. **Supporting tables**
2. **Supporting figures**

1. Supporting tables

Table S1. DNA sequences of all four constructs used in this study. Linker DNA sequence is in italics and highlighted. CpG sites are in bold and underlined.

Construct	DNA sequence	Number of CpG sites
Widom-601 (4x177)	*ATCAGTACT*C TGGAGAATCC **CG**GTGC**CG**AG GC**CG**CTCAAT TGGT**CG**TAGA CAGCTCTAGC AC**CG**CTTAAA **CG**CA**CG**TA**CG** **CG**CTGTCCCC **CGCG**TTTTAA C**CG**CCAAGGG GATTACTCCC TAGTCTCCAG GCA**CG**TGTCA GATATATACA TCCTGT*ACTT* *A**CGCG**GC**CG**C ACAGTACTAC TTA**CG**C*CTGG AGAATCC**CG**G TGC**CG**AGGC**C G**CTCAATTGG T**CG**TAGACAG CTCTAGCAC**C** **G**CTTAAA**CG**C A**CG**TA**CGCG**C TGTCCCC**CGC G**TTTTAAC**CG** CCAAGGGGAT TACTCCCTAG TCTCCAGGCA **CG**TGTCAGAT ATATACATCC TGT*TCTAGAC TTA**CGCG**AGT ACTACTTA**CG*** ***CG***G*CTGGAGA ATCC**CG**GTGC **CG**AGGC**CG**CT CAATTGGT**CG** TAGACAGCTC TAGCAC**CG**CT TAAA**CG**CA**CG** TA**CGCG**CTGT CCCC**CGCG**TT TTAAC**CG**CCA AGGGGATTAC TCCCTAGTCT CCAGGCA**CG**T GTCAGATATA TACATCCTGT *ACTTA**CGCG**G* *CCAGTACTAC TTA**CGCG**GGC* CTGGAGAATC C**CG**GTGC**CG**A GGC**CG**CTCAA TTGGT**CG**TAG ACAGCTCTAG CAC**CG**CTTAA A**CG**CA**CG**TA**C GCG**CTGTCCC C**CGCG**TTTTA AC**CG**CCAAGG GGATTACTCC CTAGTCTCCA GGCA**CG**TGTC AGATATATAC ATCCTGT*GCT AGCAGTACTA C**CG**GTGAT*	65
Central dyad (4x177)	*GATCTTCATG GATATCCC*CT GGAGAATCC**C G**GTGC**CG**AGG C**CG**CTCAATT GGT**CG**TAGAC AGCTCTAGCA C**CG**CTTAAA**C** **G**CA**CG**TA**CGC GCGCGCG**CC**C GCG**TTTTAAC **CG**CCAAGGGG ATTACTCCCT AGTCTCCAGG CA**CG**TGTCAG ATATATACAT CCTGT*G**CG**AT AT**CG**ATGGAT CTTCATGGAT ATCCC*CTGGA GAATCC**CG**GT GC**CG**AGGC**CG** CTCAATTGGT **CG**TAGACAGC TCTAGCAC**CG** CTTAAA**CG**CA **CG**TA**CGCGCG CGCG**CC**CGCG** TTTTAAC**CG**C CAAGGGGATT ACTCCCTAGT CTCCAGGCA**C** **G**TGTCAGATA TATACATCCT GT*G**CG**ATAT**C G**ATGGATCTT* *CATGGATATC CC*CTGGAGAA TCC**CG**GTGC**C G**AGGC**CG**CTC AATTGGT**CG**T AGACAGCTCT AGCAC**CG**CTT AAA**CG**CA**CG**T A**CGCGCGCGC G**CC**CGCG**TTT TAAC**CG**CCAA GGGGATTACT CCCTAGTCTC CAGGCA**CG**TG TCAGATATAT ACATCCTGT*G* ***CG**ATAT**CG**AT GGATCTTCAT GGATATCCC*C TGGAGAATCC **CG**GTGC**CG**AG GC**CG**CTCAAT TGGT**CG**TAGA CAGCTCTAGC AC**CG**CTTAAA **CG**CA**CG**TA**CG CGCGCGCG**CC **CGCG**TTTTAA C**CG**CCAAGGG GATTACTCCC TAGTCTCCAG GCA**CG**TGTCA GATATATACA TCCTGT*G**CG**A TAT**CG**ATG*	72
Major groove (4x177)	*GATCTTCATG GATATCCC*CT GGAGAATCC**C G**GTGC**CG**AGG C**CG**CTCAATT GGT**CG**TAGAC AGCTCTAGCA C**CG**CTTAAA**C** **G**CA**CG**TA**CGC G**CTGTCCCC**C GCG**TTTTAAC **CGCG**AAGGGG	76

	AT**CG**CTCCCT AG**CG**TCCAGG CA**CG**TGTCAG AT**CG**ATACAT CCTGT*G**CG**AT AT**CG**ATGGAT CTTCATGGAT ATCCC*CTGGA GAATCC**CG**GT GC**CG**AGGC**CG** CTCAATTGGT **CG**TAGACAGC TCTAGCAC**CG** CTTAAA**CG**CA **CG**TA**CGCG**CT GTCCCC**CGCG** TTTTAAC**CGC G**AAGGGGAT**C G**CTCCCTAG**C G**TCCAGGCA**C** **G**TGTCAGAT**C G**ATACATCCT GT*G**CG**ATAT**C G**ATGGATCTT* *CATGGATATC CC*CTGGAGAA TCC**CG**GTGC**C G**AGGC**CG**CTC AATTGGT**CG**T AGACAGCTCT AGCAC**CG**CTT AAA**CG**CA**CG**T A**CGCG**CTGTC CCC**CGCG**TTT TAAC**CGCG**AA GGGGAT**CG**CT CCCTAG**CG**TC CAGGCA**CG**TG TCAGAT**CG**AT ACATCCTGT*G* ***CG**ATAT**CG**AT GGATCTTCAT GGATATCCC*C TGGAGAATCC **CG**GTGC**CG**AG GC**CG**CTCAAT TGGT**CG**TAGA CAGCTCTAGC AC**CG**CTTAAA **CG**CA**CG**TA**CG** **CG**CTGTCCCC **CGCG**TTTTAA C**CGCG**AAGGG GAT**CG**CTCCC TAG**CG**TCCAG GCA**CG**TGTCA GAT**CG**ATACA TCCTGT*G**CG**A TAT**CG**ATG*	
Minor groove (4x177)	*GATCTTCATG GATATCCC*CT GGAGAATCC**C G**GTGC**CG**AGG C**CG**CTCAATT GGT**CG**TAGAC AGCTCTAGCA C**CG**CTTAAA**C** **G**CA**CG**TA**CGC G**CTGTCCCC**C GCG**TTTT**CG**C **CG**CCAAG**CG**G ATTACTC**CG**T AGTCTCC**CG**G CA**CG**TGT**CG**G ATATATACAT CCTGT*G**CG**AT AT**CG**ATGGAT CTTCATGGAT ATCCC*CTGGA GAATCC**CG**GT GC**CG**AGGC**CG** CTCAATTGGT **CG**TAGACAGC TCTAGCAC**CG** CTTAAA**CG**CA **CG**TA**CGCG**CT GTCCCC**CGCG** TTTT**CG**C**CG**C CAAG**CG**GATT ACTC**CG**TAGT CTCC**CG**GCA**C** **G**TGT**CG**GATA TATACATCCT GT*G**CG**ATAT**C G**ATGGATCTT* *CATGGATATC CC*CTGGAGAA TCC**CG**GTGC**C G**AGGC**CG**CTC AATTGGT**CG**T AGACAGCTCT AGCAC**CG**CTT AAA**CG**CA**CG**T A**CGCG**CTGTC CCC**CGCG**TTT T**CG**C**CG**CCAA G**CG**GATTACT C**CG**TAGTCTC C**CG**GCA**CG**TG T**CG**GATATAT ACATCCTGT*G* ***CG**ATAT**CG**AT GGATCTTCAT GGATATCCC*C TGGAGAATCC **CG**GTGC**CG**AG GC**CG**CTCAAT TGGT**CG**TAGA CAGCTCTAGC AC**CG**CTTAAA **CG**CA**CG**TA**CG** **CG**CTGTCCCC **CGCG**TTTT**CG** C**CG**CCAAG**CG** GATTACTC**CG** TAGTCTCC**CG** GCA**CG**TGT**CG** GATATATACA TCCTGT*G**CG**A TAT**CG**ATG*	80

2. Supporting figures

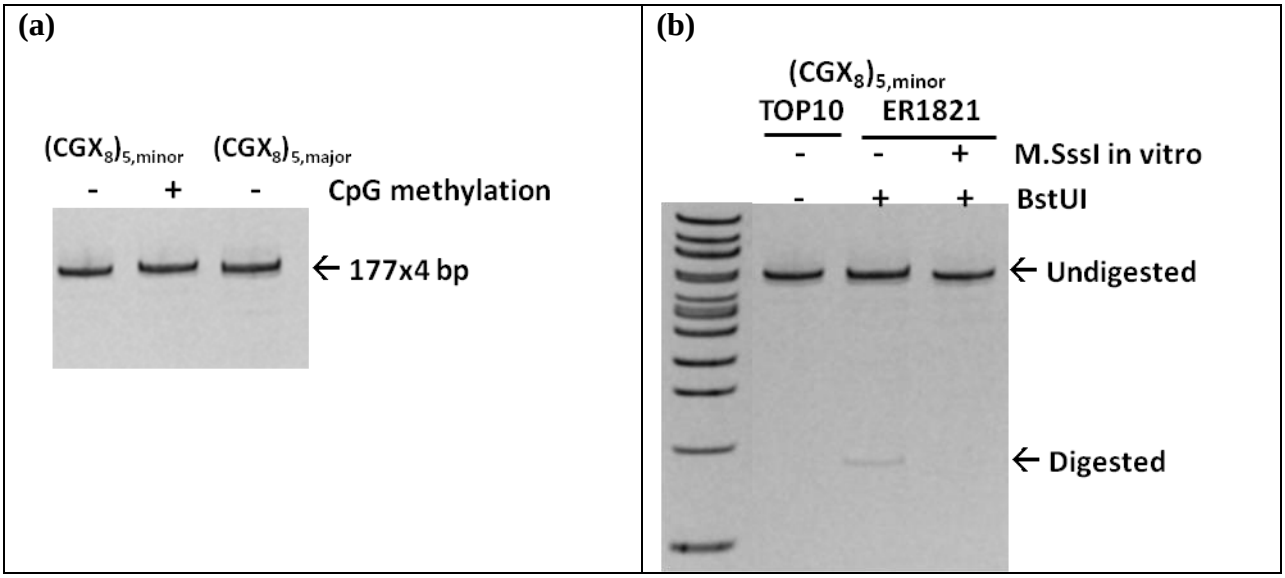

Figure S1. (a) Typical 5% PAGE gel of DNA repeats for preparation of tetra-nucleosomes. **(b)** Typical digestion pattern of DNA fragments with BstUI restriction enzyme examined using a 5% PAGE gel.

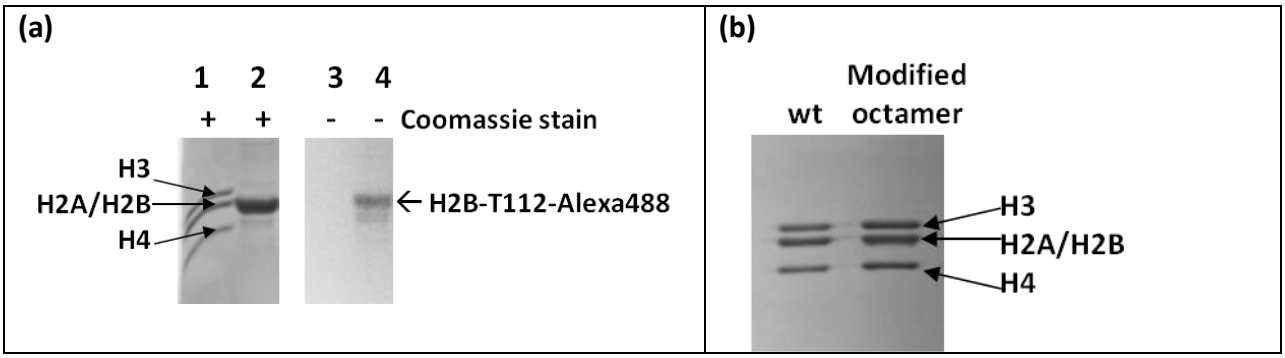

Figure S2. (a) Histone H2B proteins labeled with Alexa488 at the T112C position. Lane 1 and 3: wild-type core histone proteins with and without coomassie blue staining. Lane 2 and 4: H2B-T112-Alexa488 with and without coomassie blue staining. It is possible to observe the H2B band without staining due to the presence of Alexa488. (b) 18% SDS-PAGE of the refolded wild-type (wt) and modified histone octamers labeled with Alexa488 at position H2BT112C.

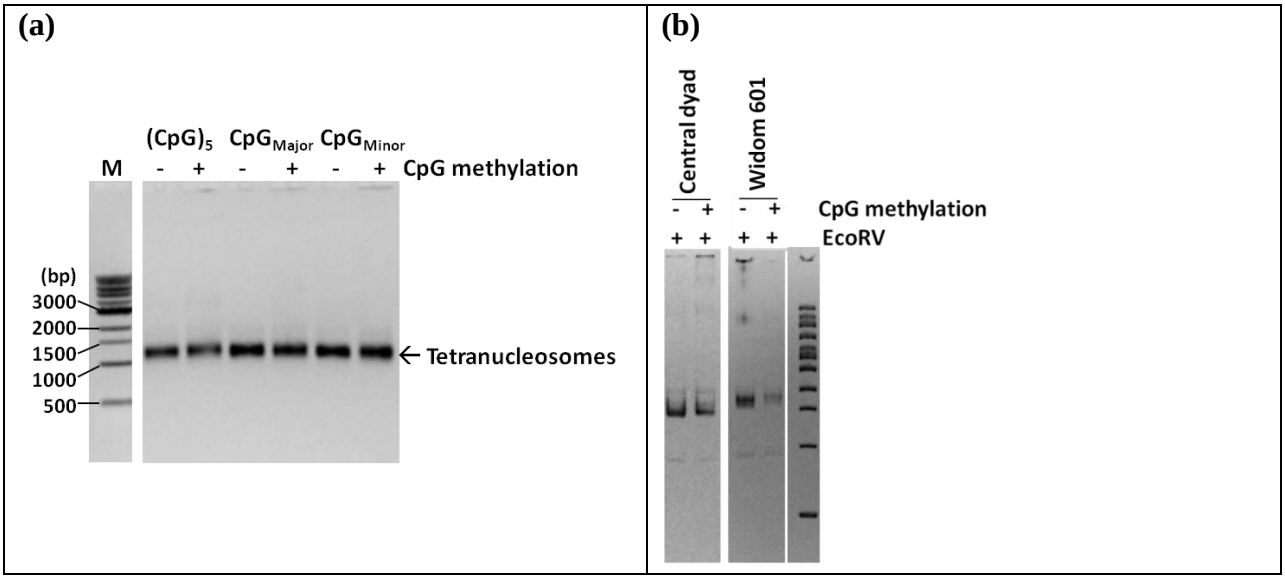

Figure S3. (a) Tetra-nucleosome arrays in a 0.8% agarose gel. **(b)** Digestion pattern of the tetra-nucleosome arrays with EcoRV.

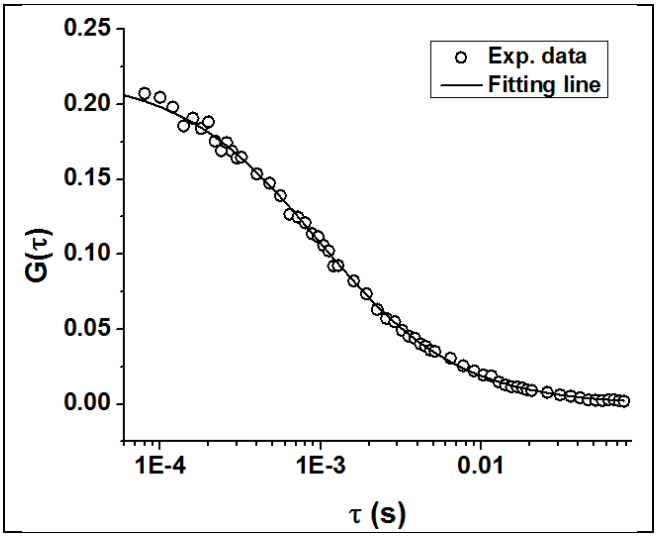

Figure S4. Typical autocorrelation curve obtained from FCS experiments. D = 13.9μm^2/s, χ^2 = 0.60. Tetra-nucleosome with CpG_{Major} pattern at 100mM KCl.

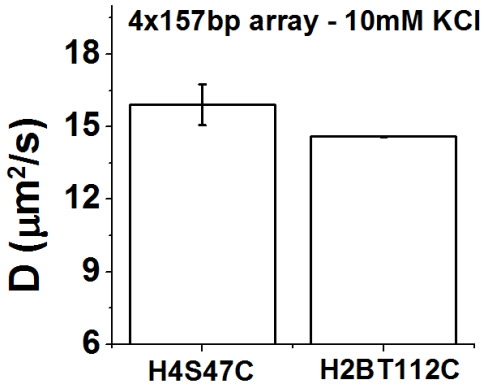

Figure S5. Comparison of the diffusivity of Widom-601 tetranucleosome arrays with fluorescent labels at position H4S47C and H2BT112C. The calculated diffusivity is 15.91 ± 0.85 and 14.59 ± 0.02 for the arrays labeled at histone H4 and H2B respectively.

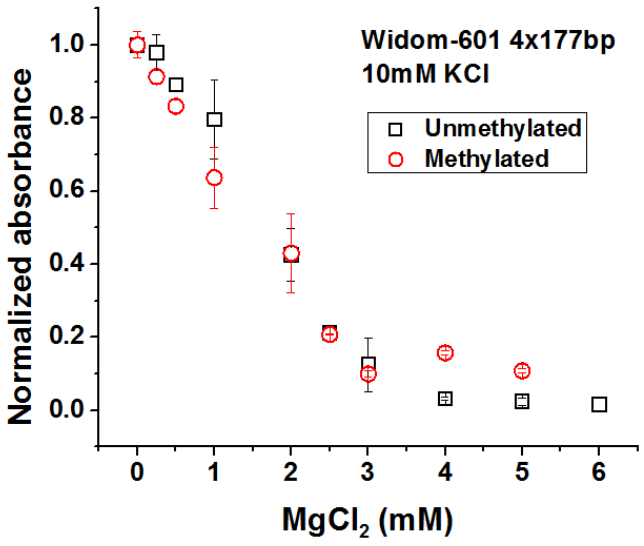

Figure S6. Sedimentation assay of Widom-601 tetranucleosome arrays. In this assay, tetra-nucleosome samples with different $MgCl_2$ concentrations (0-6mM) were incubated at room temperature for 15 min. The samples were then spun at 15000rpm for 15 min at room temperature. The absorbance of the soluble fraction at 256nm was recorded using a spectropohotometer (Cary 100 Bio, Cary Varian). The normalized absorbance was calculated as the absorbance at different $MgCl_2$ concentrations divided by that of tetra-nucleosomes without $MgCl_2$.